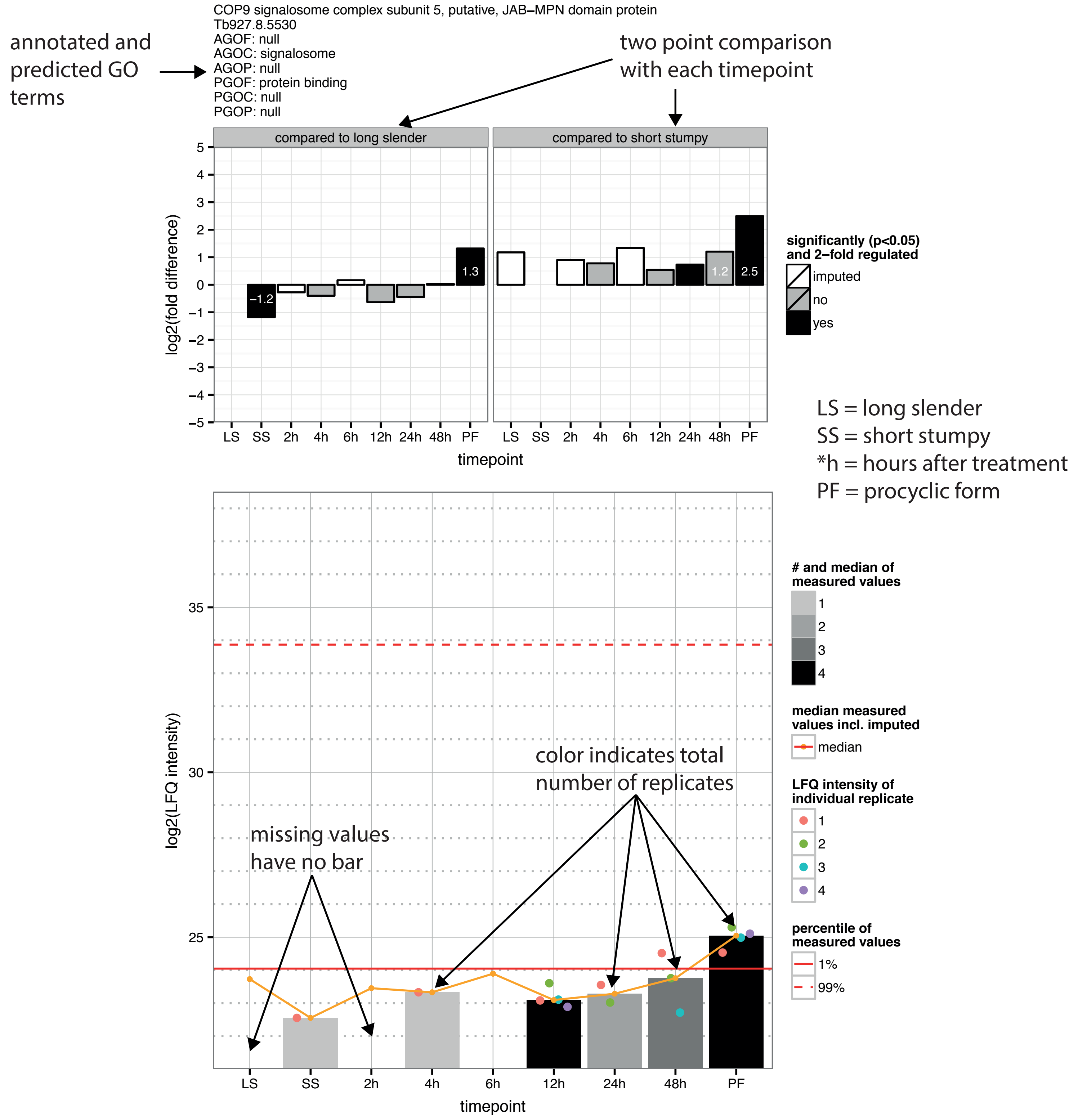
Supplemental figure 1

Quantitative proteomics uncovers novel factors for developmental differentiation of *Trypanosoma brucei*

Mario Dejung, Ines Subota, Ferdinand Brucerius, Gülcin Dindar, Anja Freiwald,
Markus Engstler, Michael Boshart, Falk Butter, Christian Janzen

Note: Please switch on table of contents.

Example page:



COP9 signalosome complex subunit 5, putative, JAB–MPN domain protein
Tb927.8.5530
AGOF: null
AGOC: signalosome
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

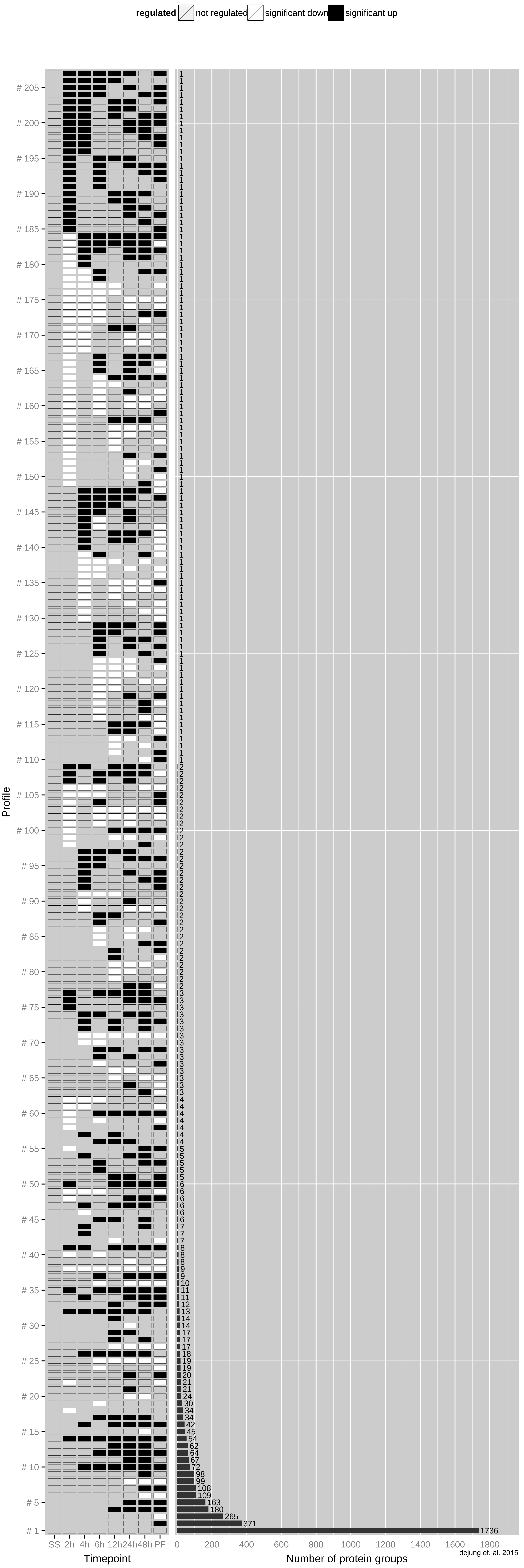
annotated and predicted GO terms

two point comparison with each timepoint

missing values have no bar

color indicates total number of replicates

LS = long slender
SS = short stumpy
*h = hours after treatment
PF = procyclic form


regulated
not regulated
significant down
significant up
Profile
205
200
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190
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180
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130
125
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115
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70
65
60
55
50
45
40
35
30
25
20
15
10
5
1
SS
2h
4h
6h
12h
24h
48h
PF
Timepoint
0
200
400
600
800
1000
1200
1400
1600
1800
Number of protein groups
1736
371
265
180
163
109
108
99
98
72
67
64
62
54
45
42
34
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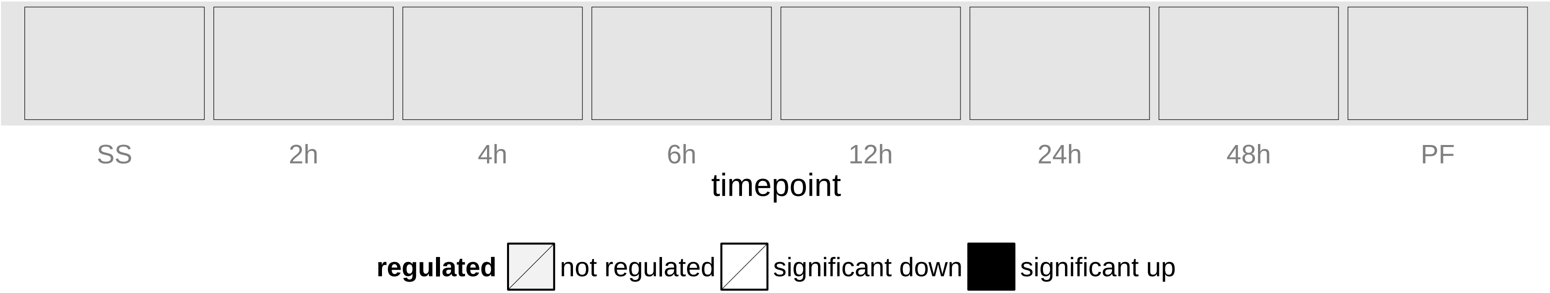

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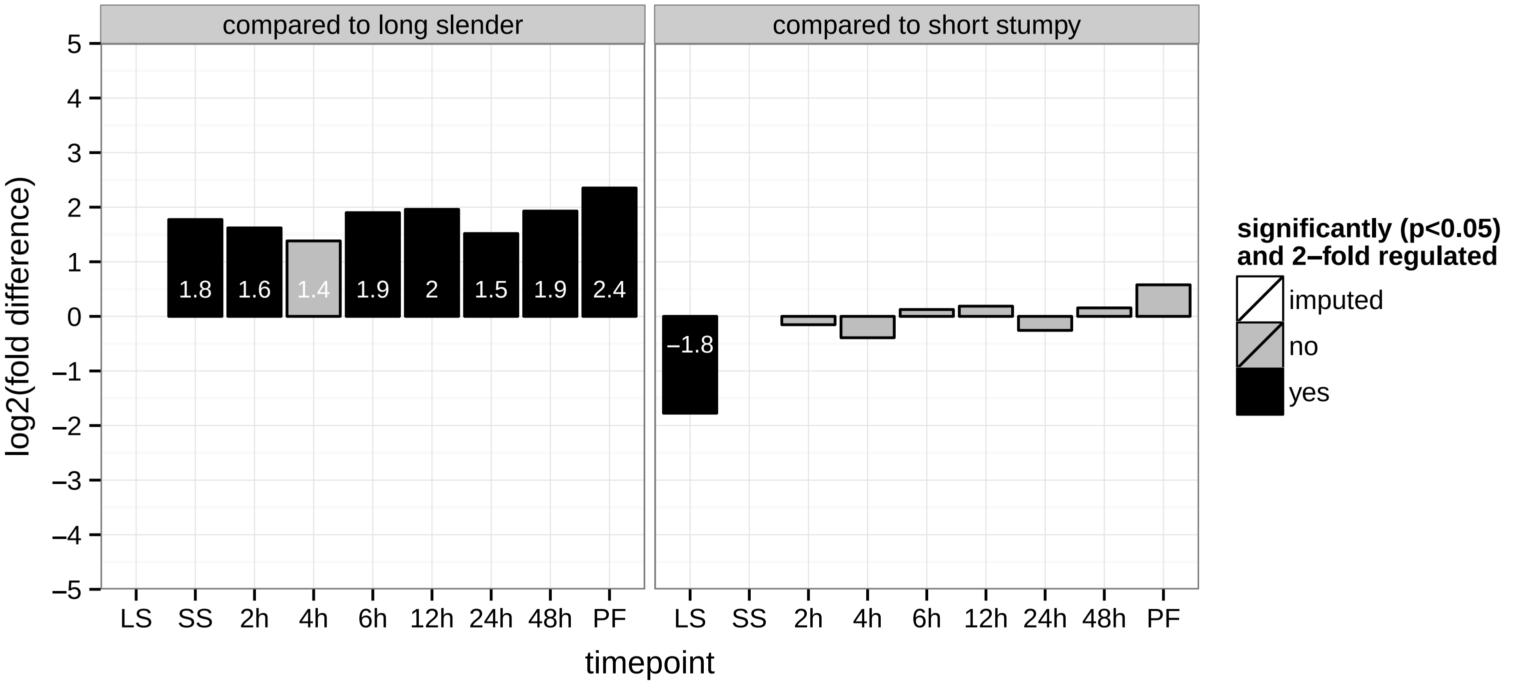
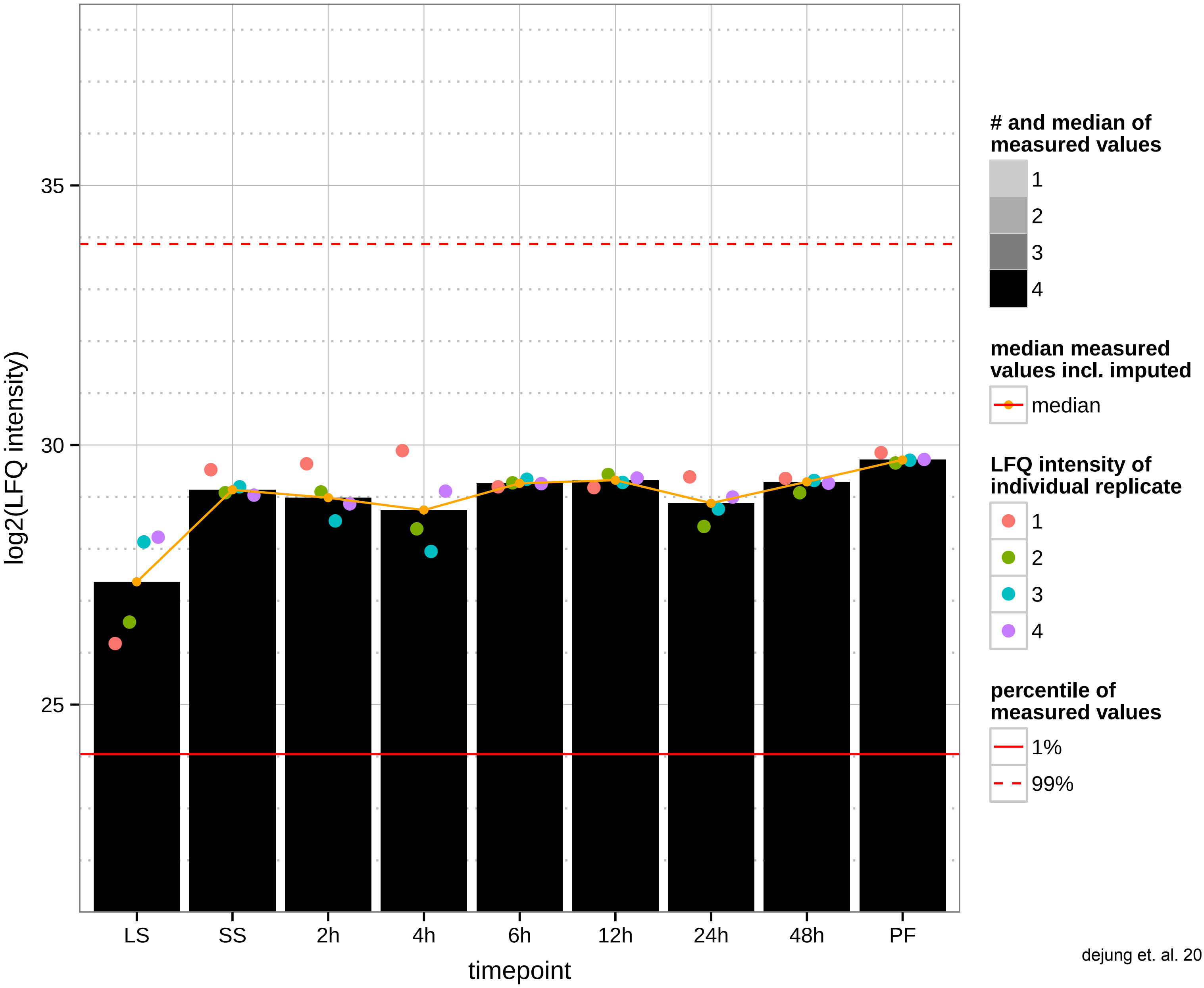
major vault protein, putative, BAC from homologous region on chr5, putative (MVP)
Tb927.5.4460;Tb05.5K5.110;Tb11.v5.0866
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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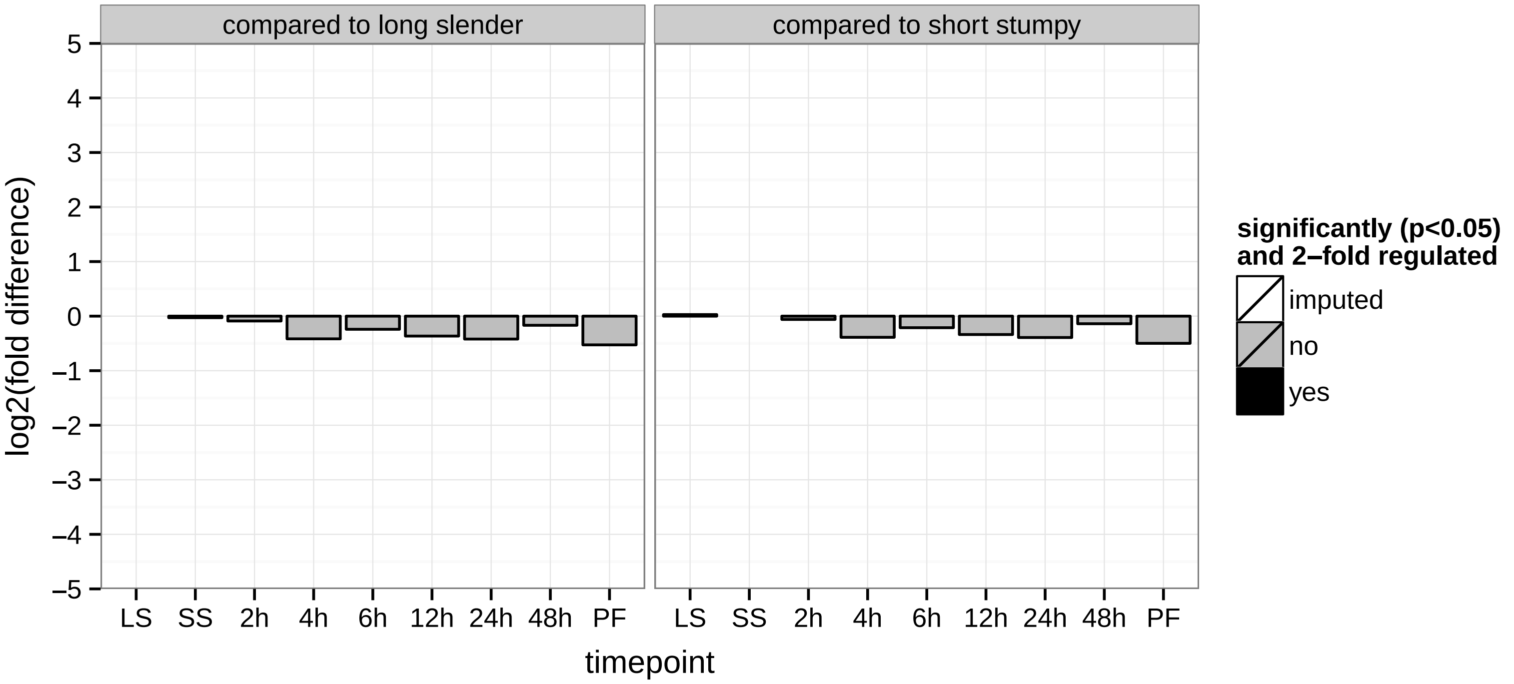
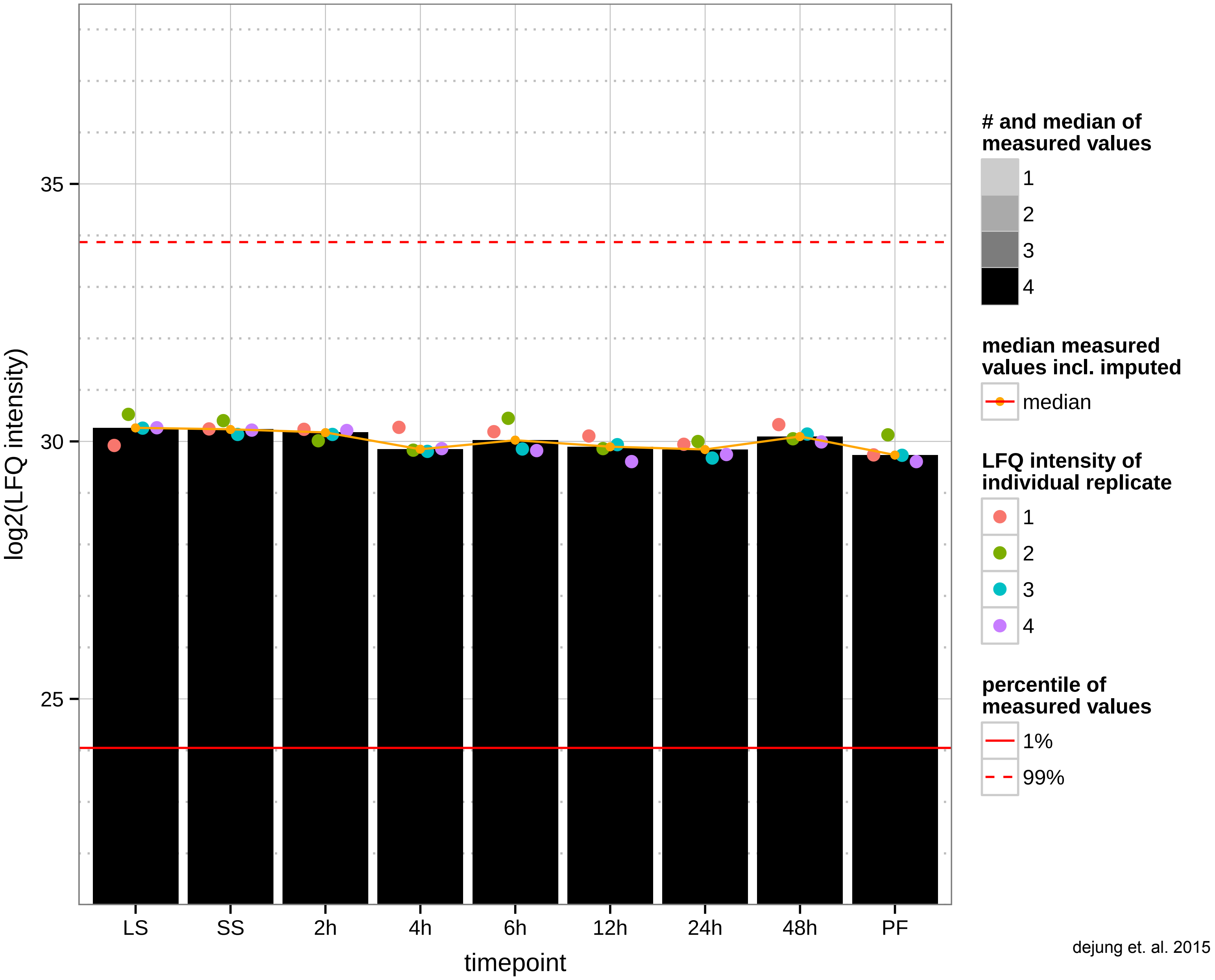
paraflagellar rod component par4, putative, BAC from homologous region on chr5
Tb927.5.4480;Tb05.5K5.130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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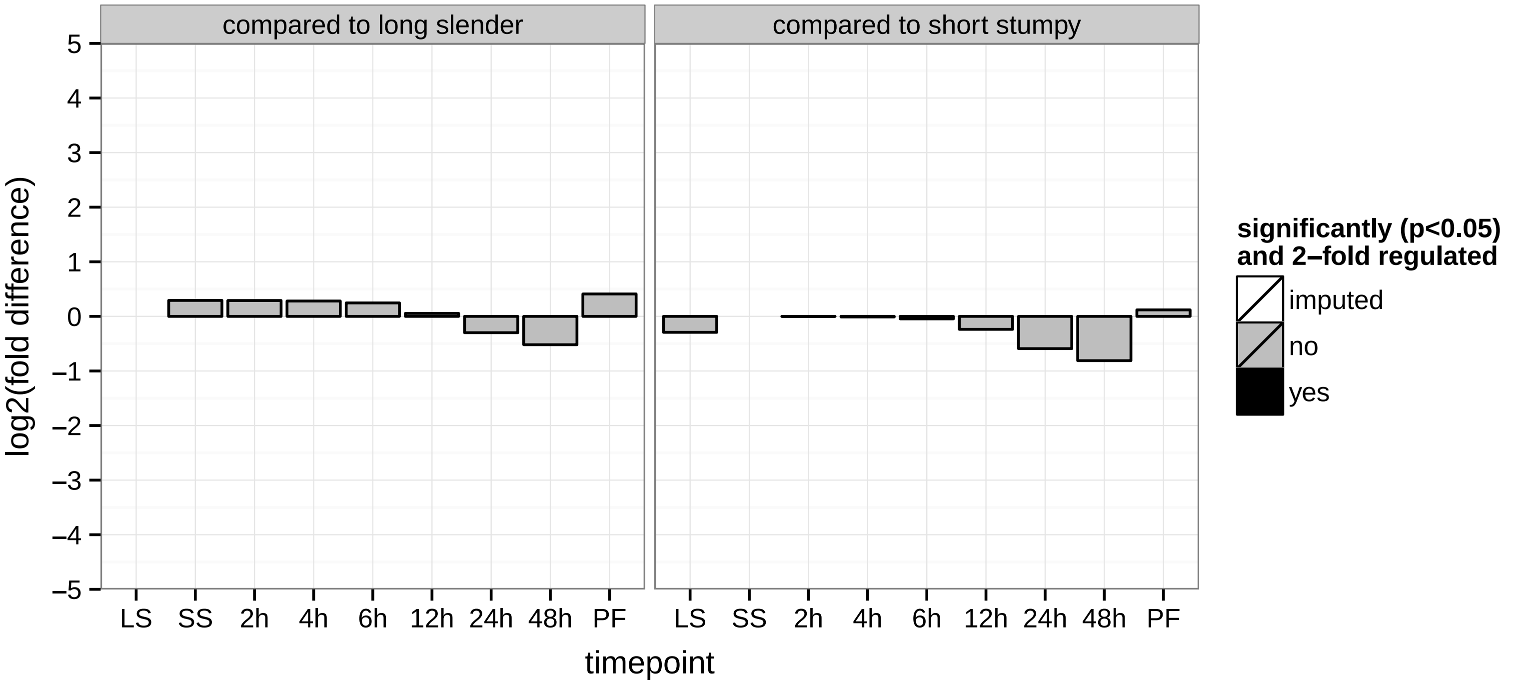
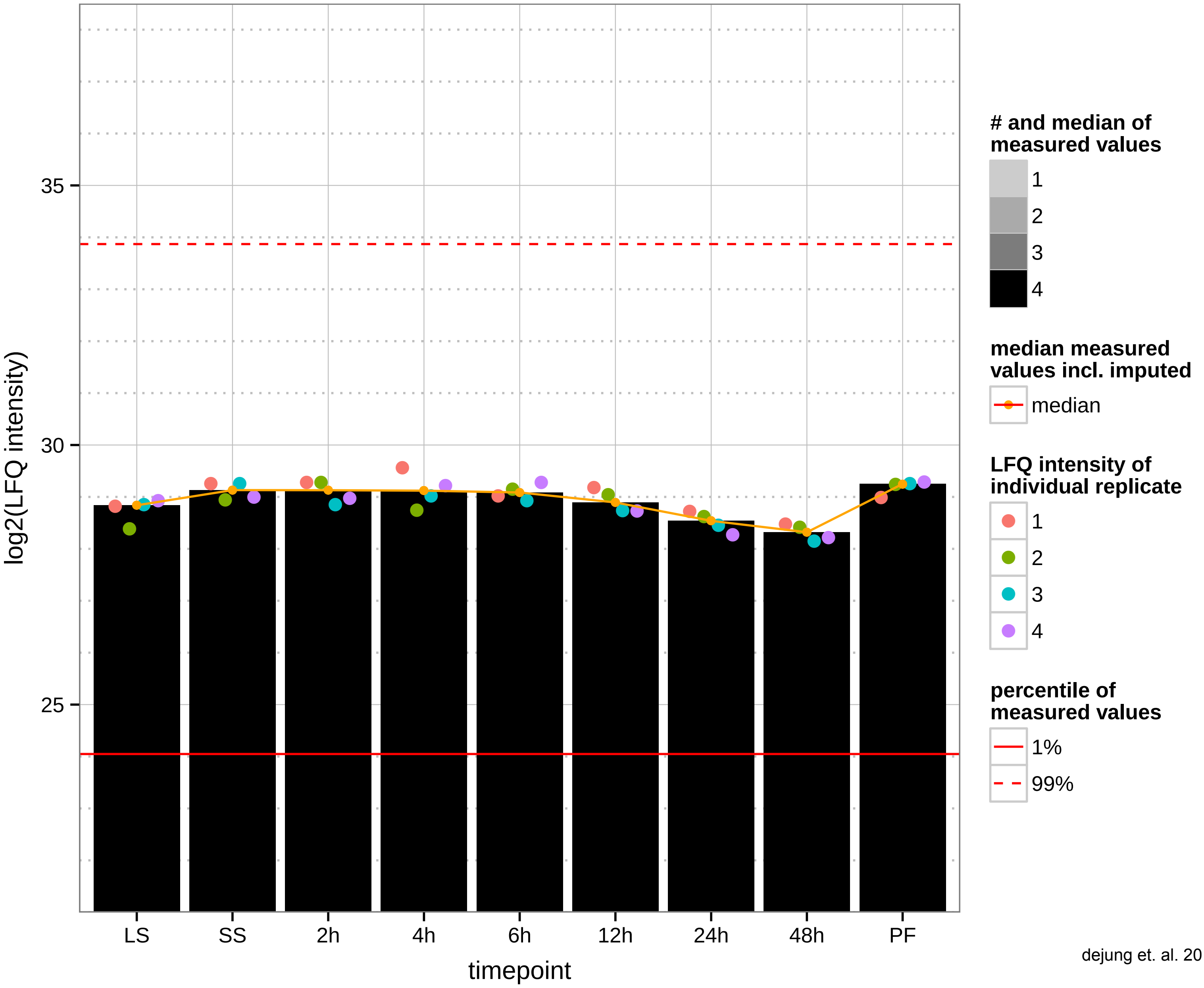
guanine deaminase, putative, guanase, guanine aminase, guanine aminohydrolase, BAC from homologous region on chr5
Tb927.5.4560;Tb11.v5.0409;Tb05.5K5.200
AGOF: guanine deaminase activity, zinc ion binding, null
AGOC: null
AGOP: null
PGOF: guanine deaminase activity, hydrolase activity, acting on carbon–nitrogen (but not peptide) bonds, zinc ion binding
PGOC: null
PGOP: null





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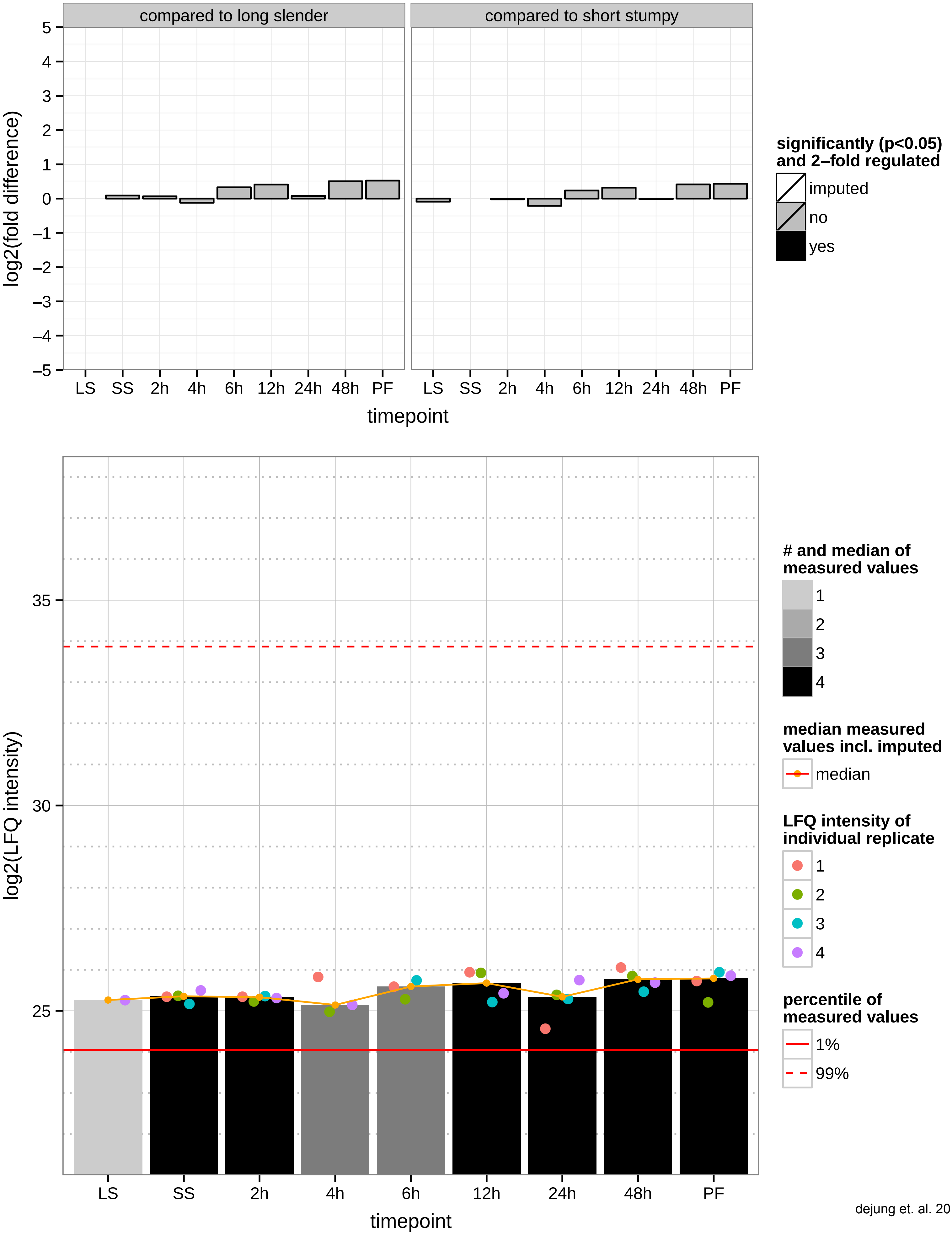
hypothetical protein, conserved, BAC from homologous region on chr5
Tb927.5.4400;Tb05.5K5.50
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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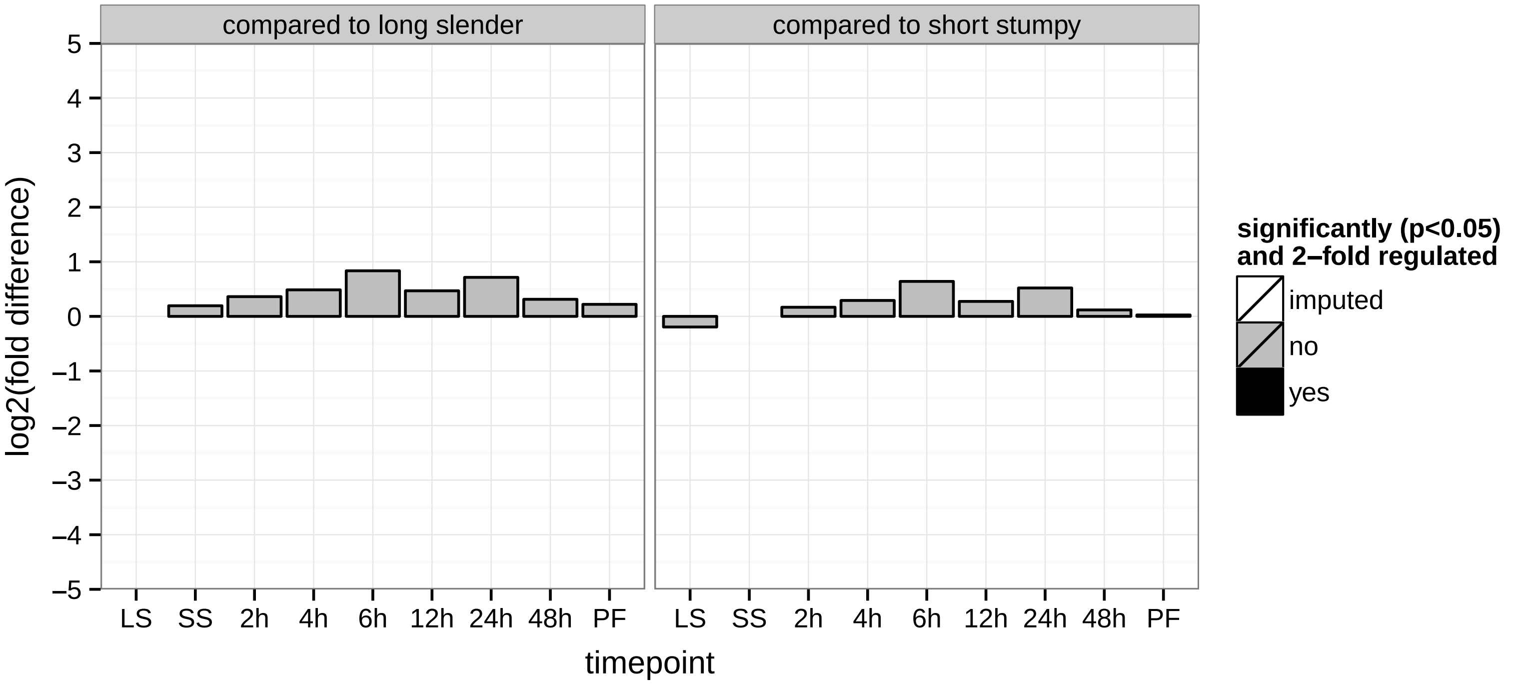
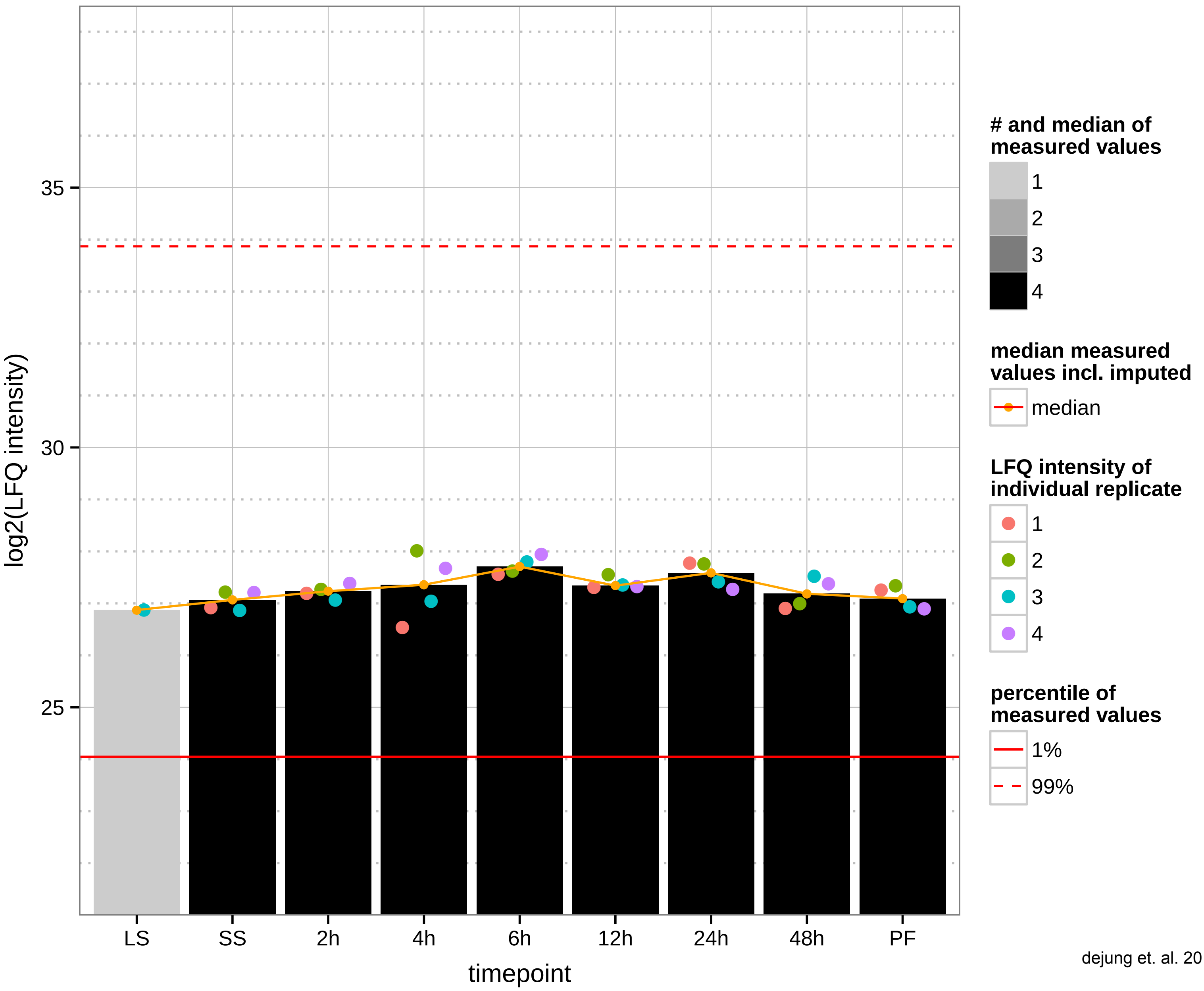
hypothetical protein, conserved, BAC from homologous region on chr5
Tb927.5.4410;Tb05.5K5.60
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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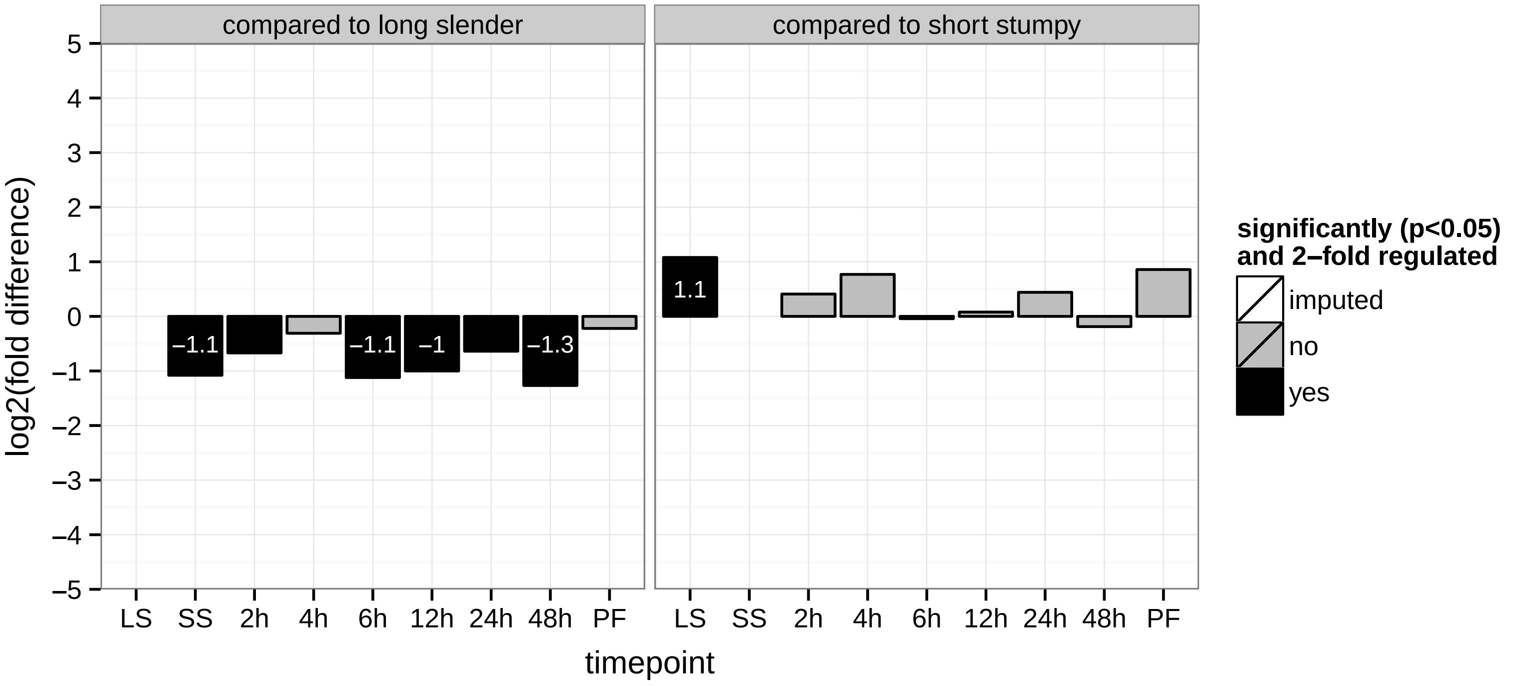
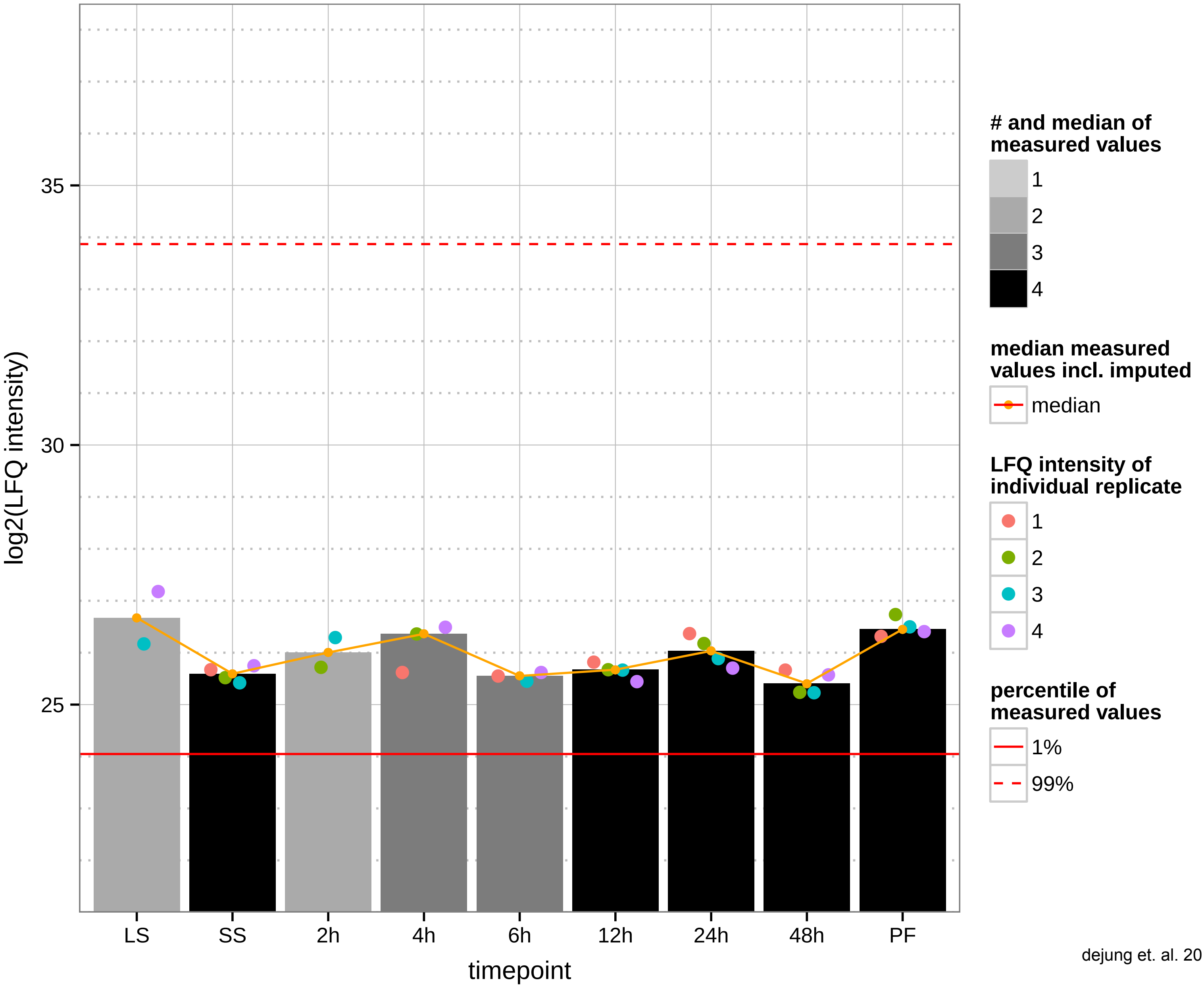
dynein light chain, putative, BAC from homologous region on chr5
Tb927.5.4440;Tb05.5K5.90
AGOF: microtubule motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based process
PGOF: null
PGOC: microtubule associated complex
PGOP: microtubule–based process





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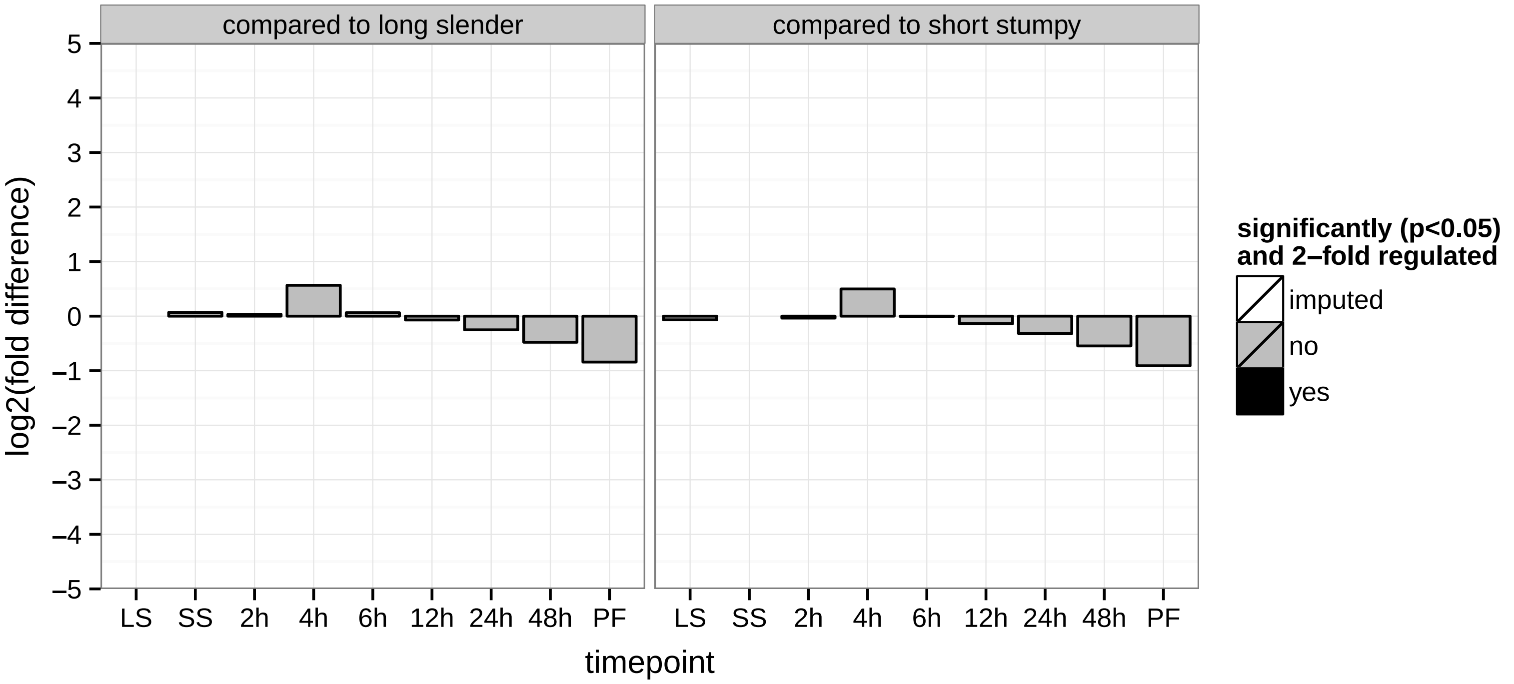
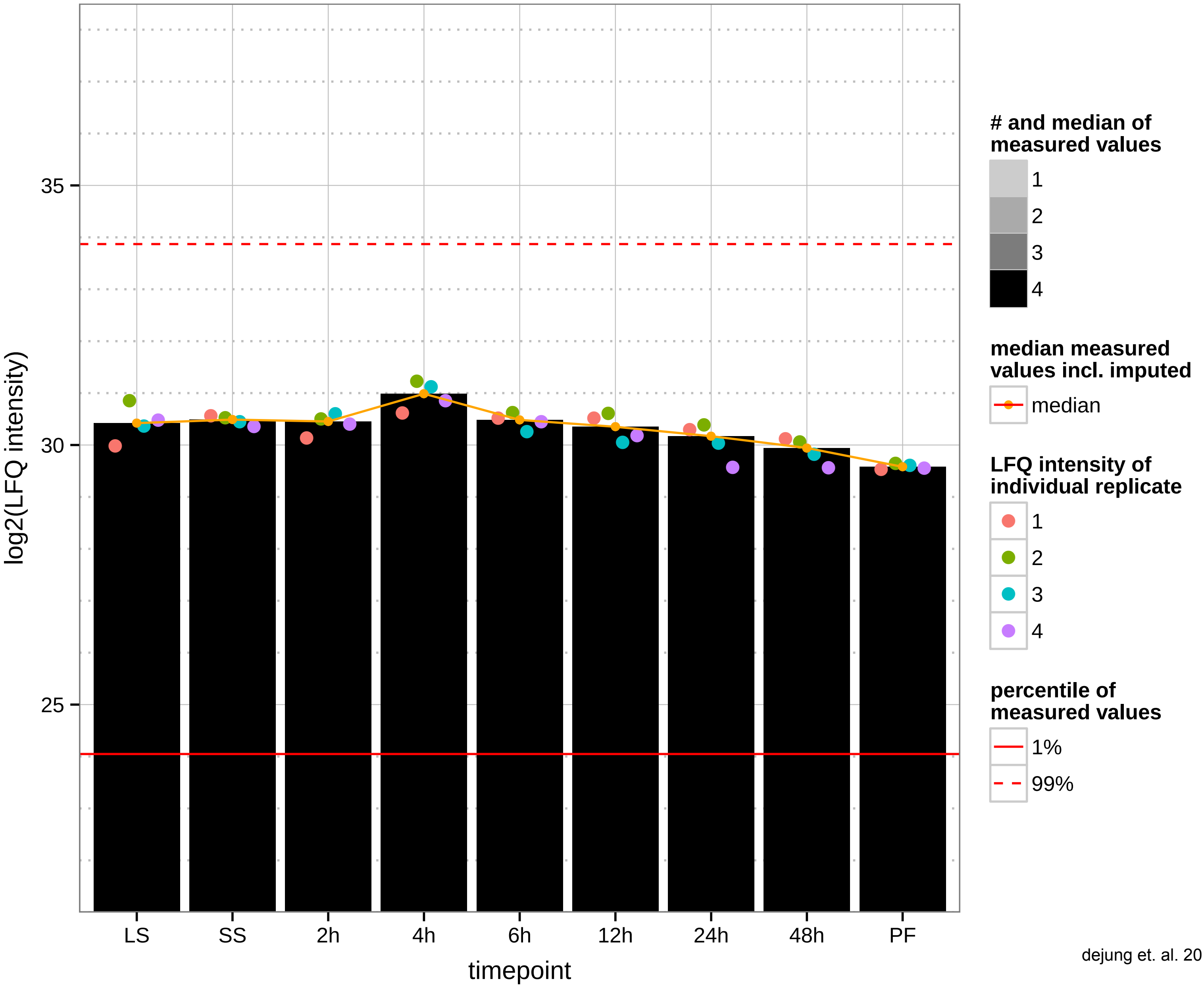
stress–inducible protein STI1–like, putative, chrX additional, unordered contigs, variant surface glycoprotein, fragment
Tb927.10.4450;Tb10.v4.0035;Tb11.v5.0757
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding, null
PGOC: null
PGOP: null





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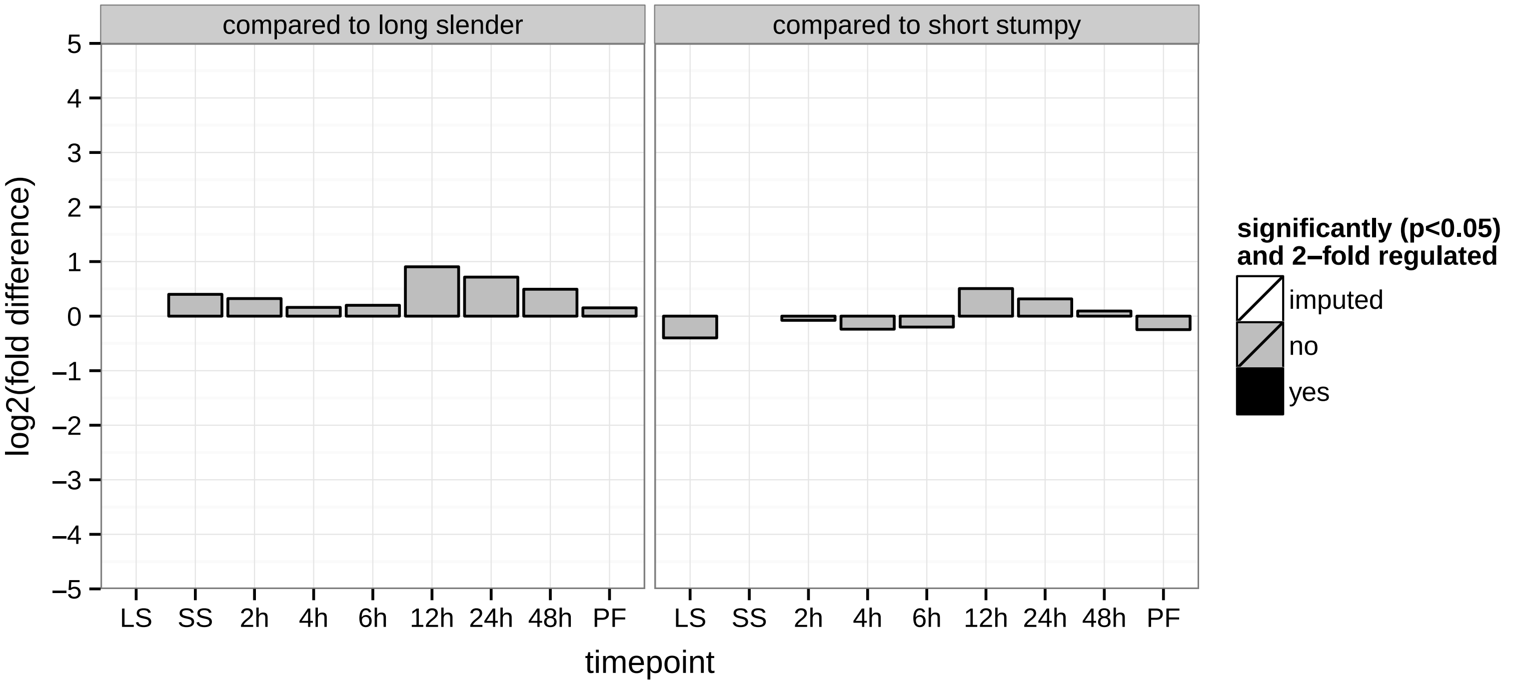
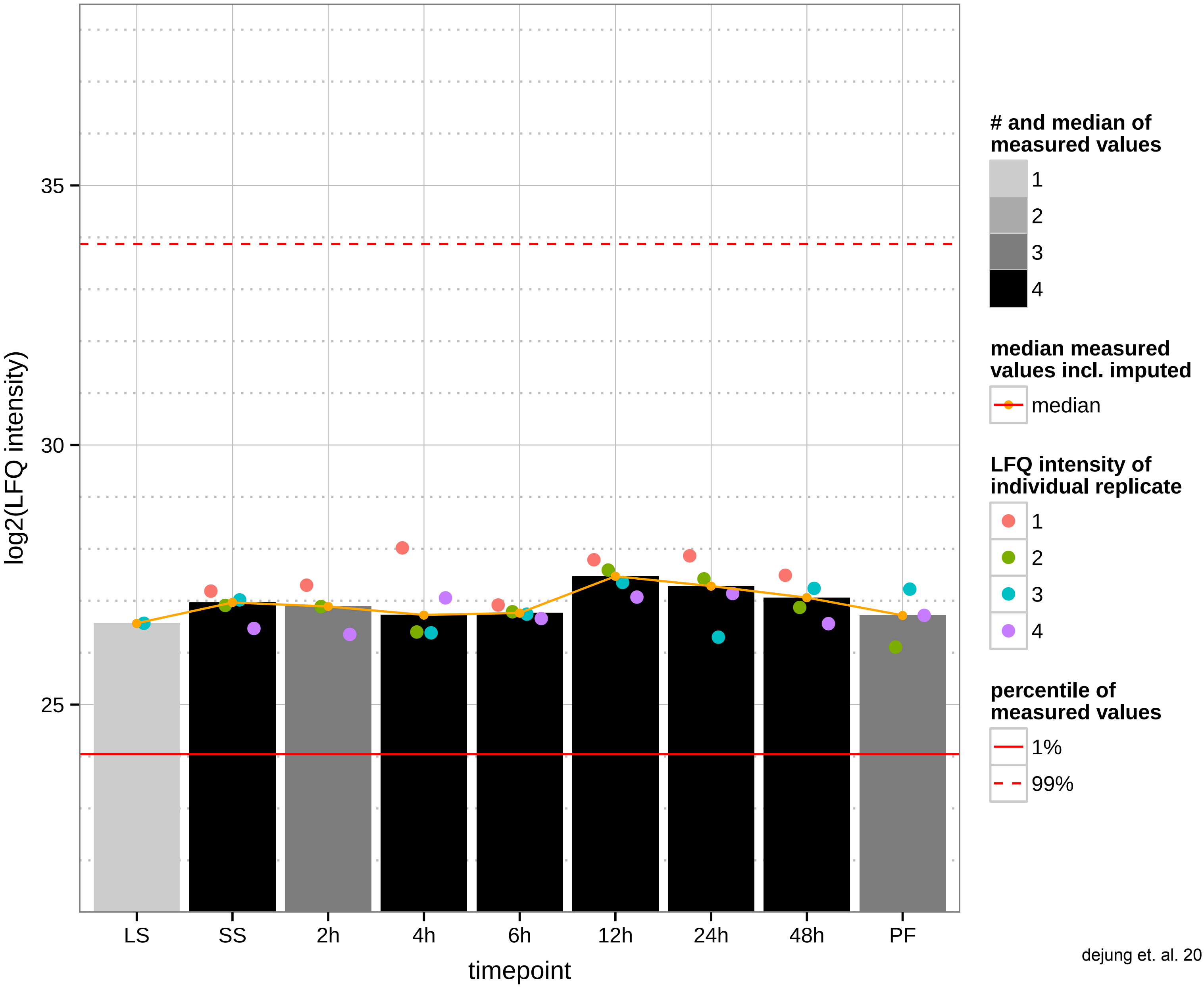
leucine carboxyl methyltransferase, putative, chrX additional, unordered contigs
Tb927.10.4460;Tb10.v4.0036
AGOF: methyltransferase activity, protein C−terminal carboxyl O−methyltransferase activity
AGOC: null
AGOP: null, cellular protein modification process
PGOF: methyltransferase activity
PGOC: null
PGOP: null





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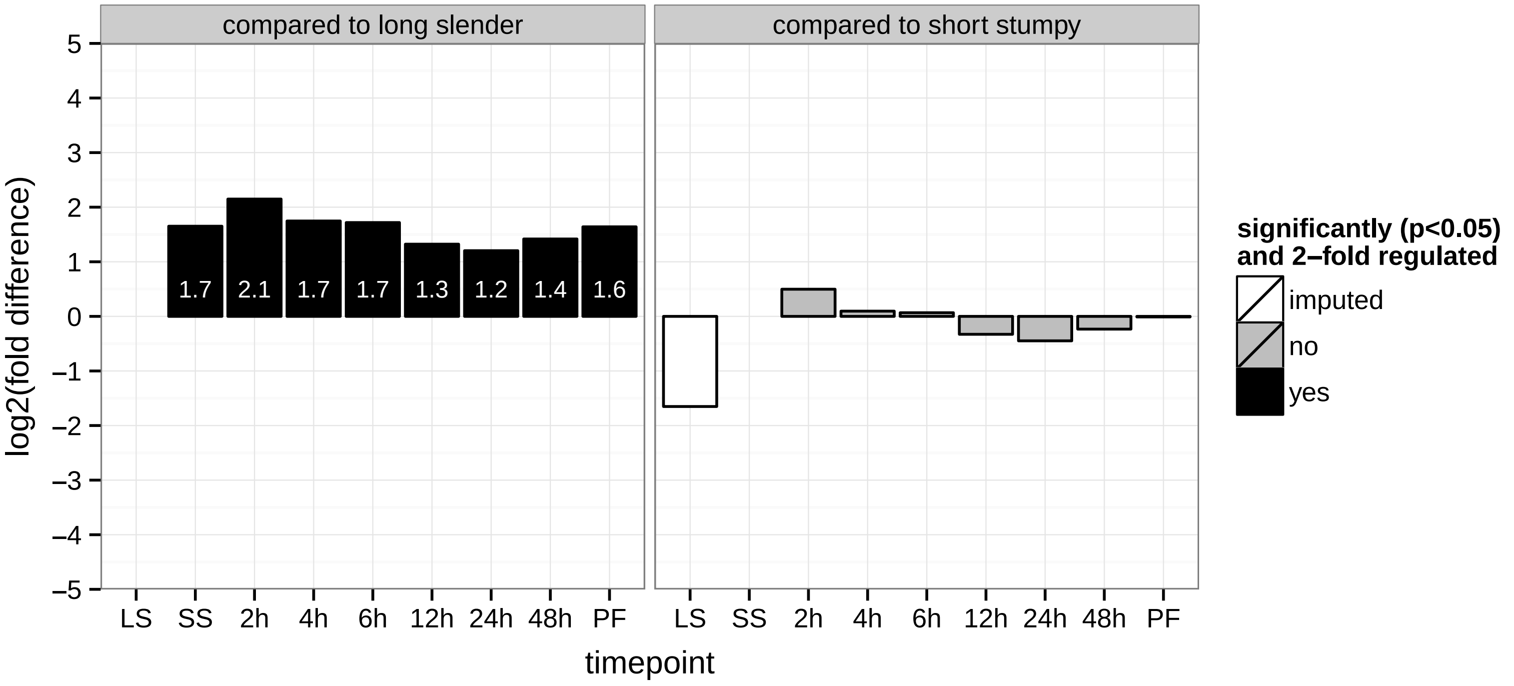
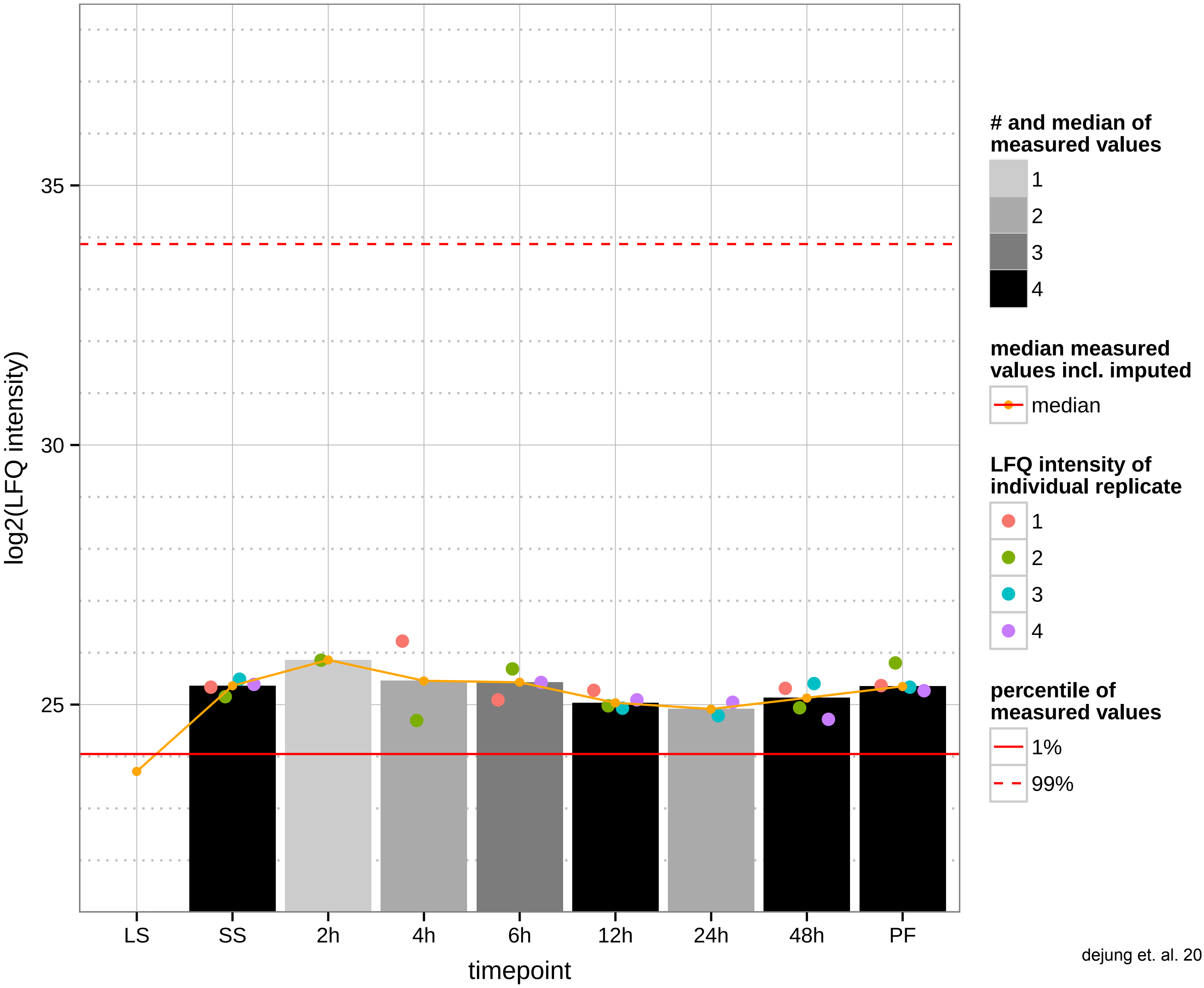
mRNA capping methyltransferase, putative, chrX additional, unordered contigs
Tb927.10.4500;Tb10.v4.0040
AGOF: null, methyltransferase activity
AGOC: null
AGOP: 7−methylguanosine mRNA capping
PGOF: null
PGOC: null
PGOP: 7−methylguanosine mRNA capping





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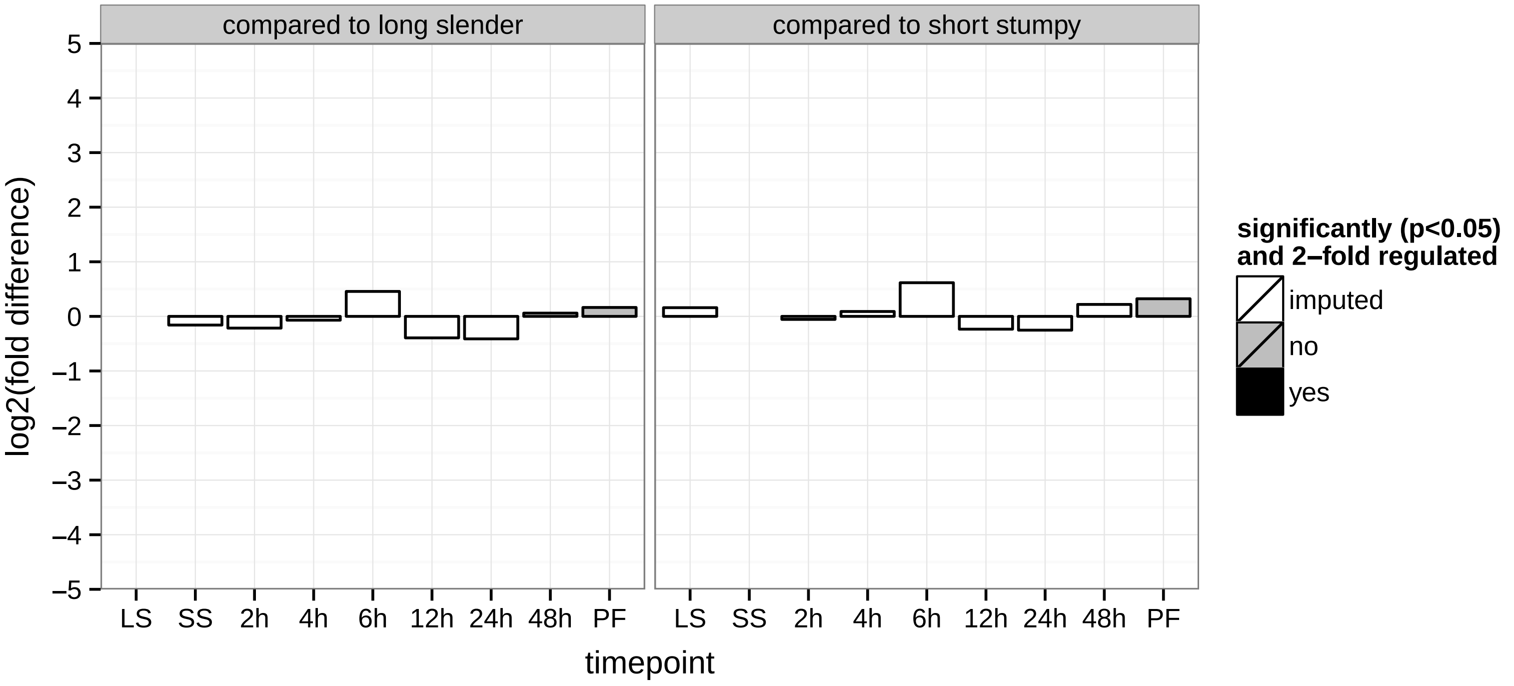
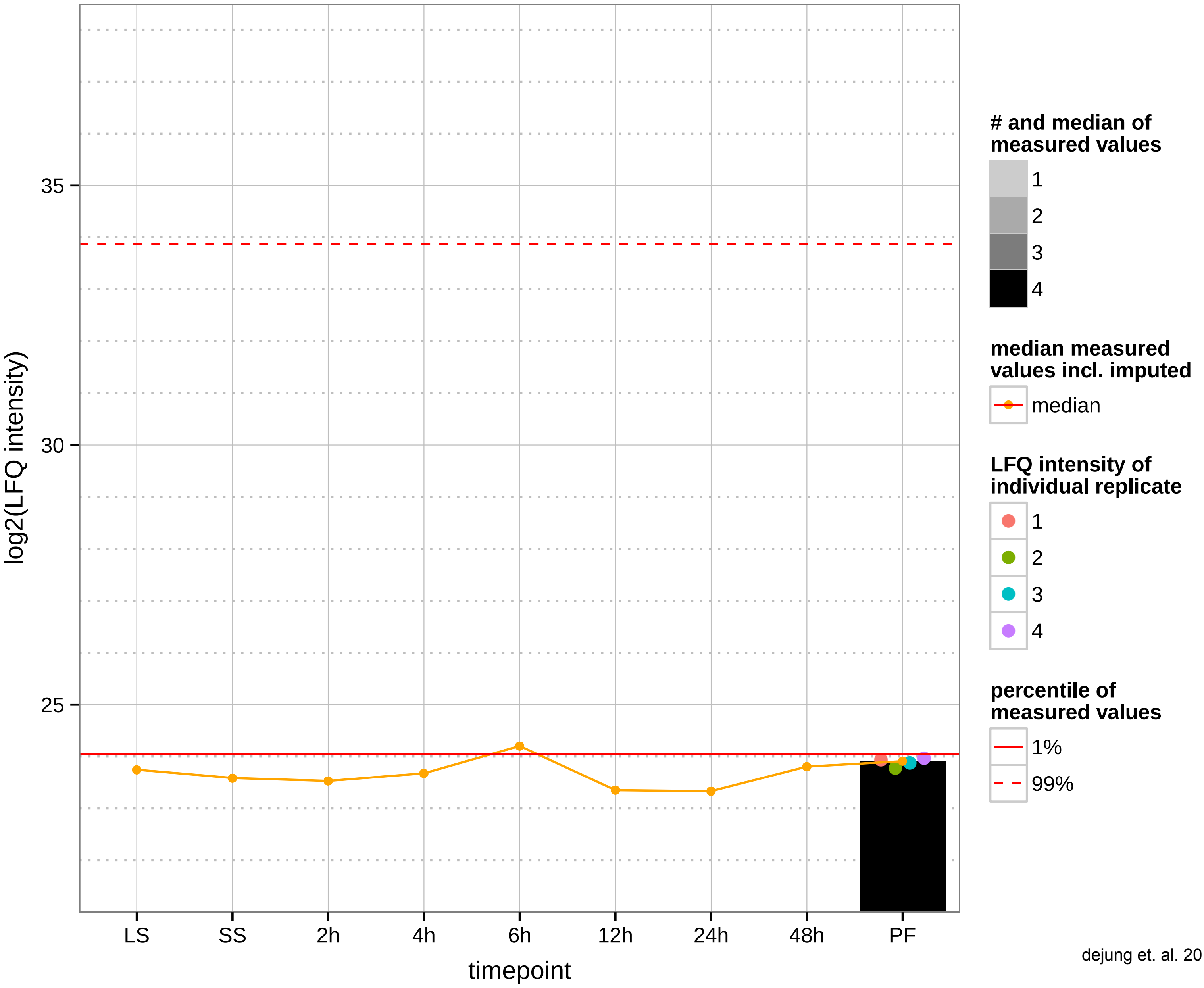
mitochondrial edited mRNA stability factor 1 subunit, putative
Tb927.11.7218;Tb11.02.5120b
AGOF: RNA binding
AGOC: null
AGOP: RNA polyadenylation, mRNA stabilization
PGOF: null
PGOC: null
PGOP: null





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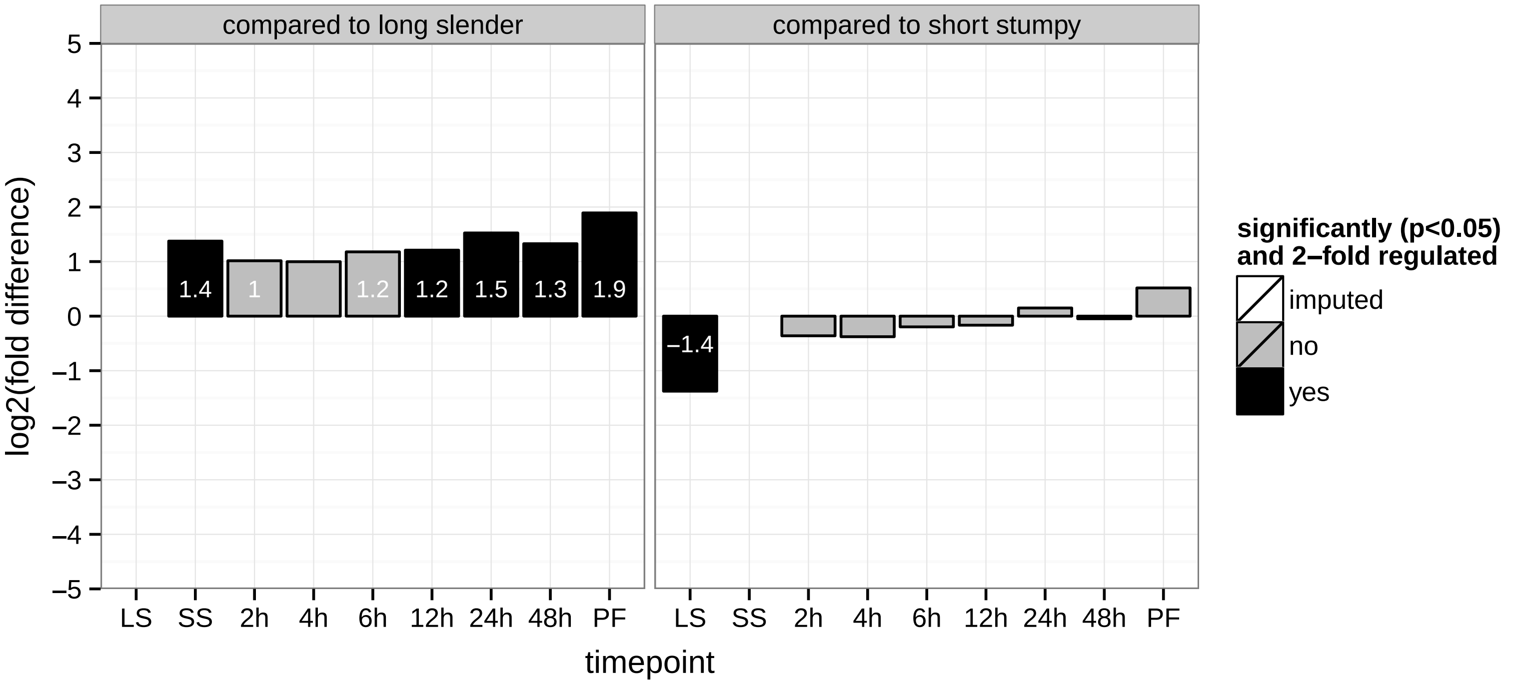
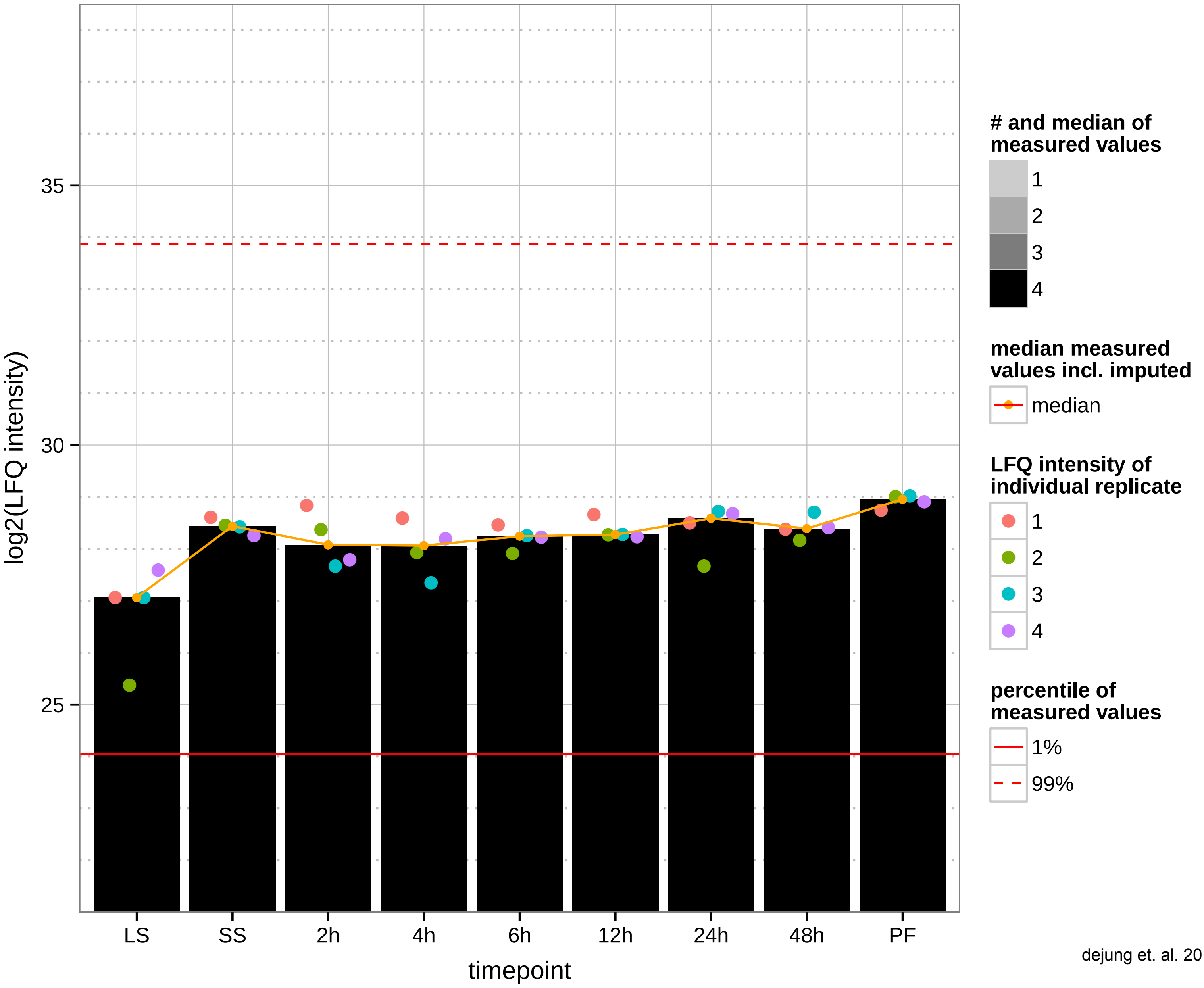
NADPH–cytochrome p450 reductase, putative (CPR), putative
Tb11.02.5420b;Tb11.02.5420
AGOF: FMN binding, electron carrier activity, iron ion binding, oxidoreductase activity
AGOC: integral to membrane
AGOP: oxidation–reduction process
PGOF: FMN binding, oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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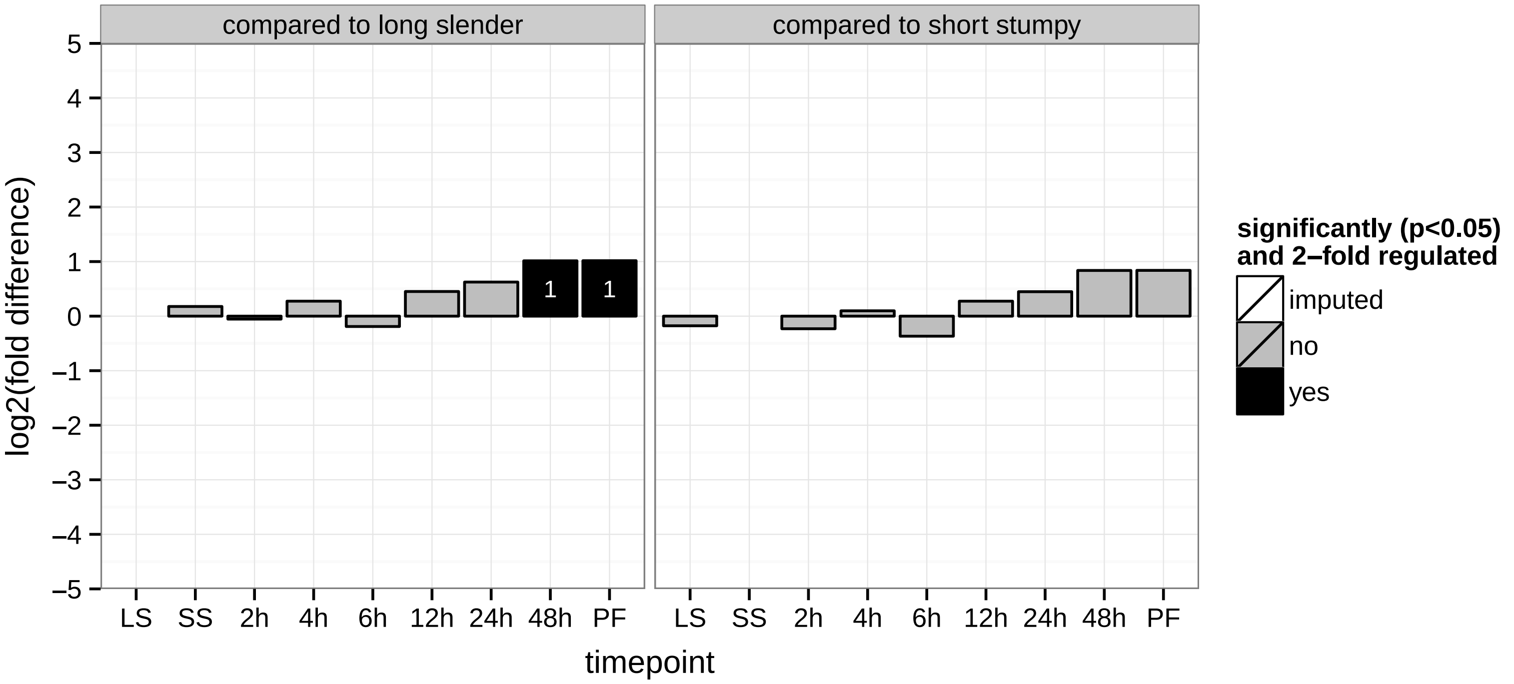
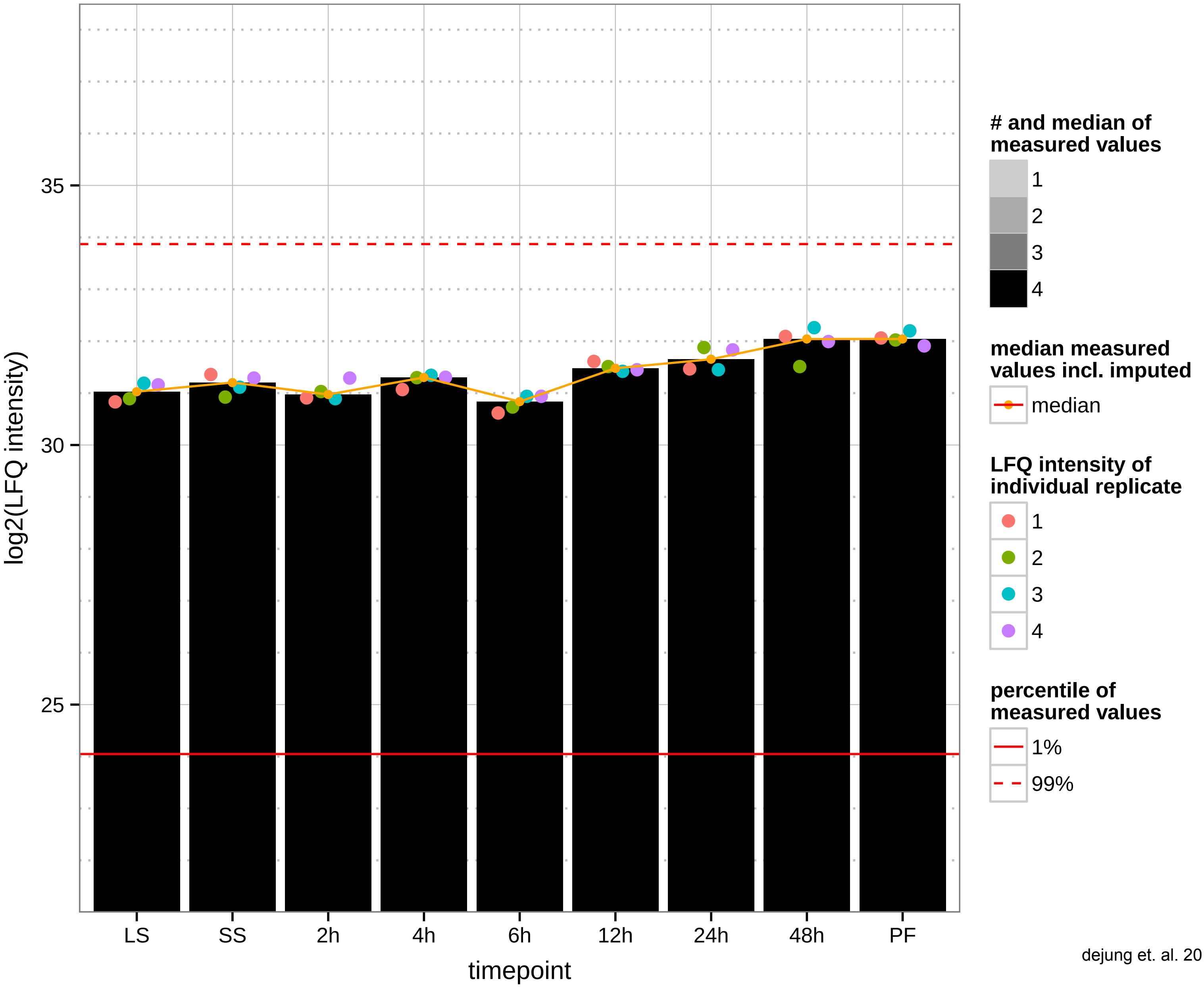
40S ribosomal protein S14, putative, chrXI additional, unordered contigs (RPS14), 40S ribosomal protein S14 (RPS14)
Tb927.6.4980;Tb11.0390;Tb11.0290
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome, small ribosomal subunit
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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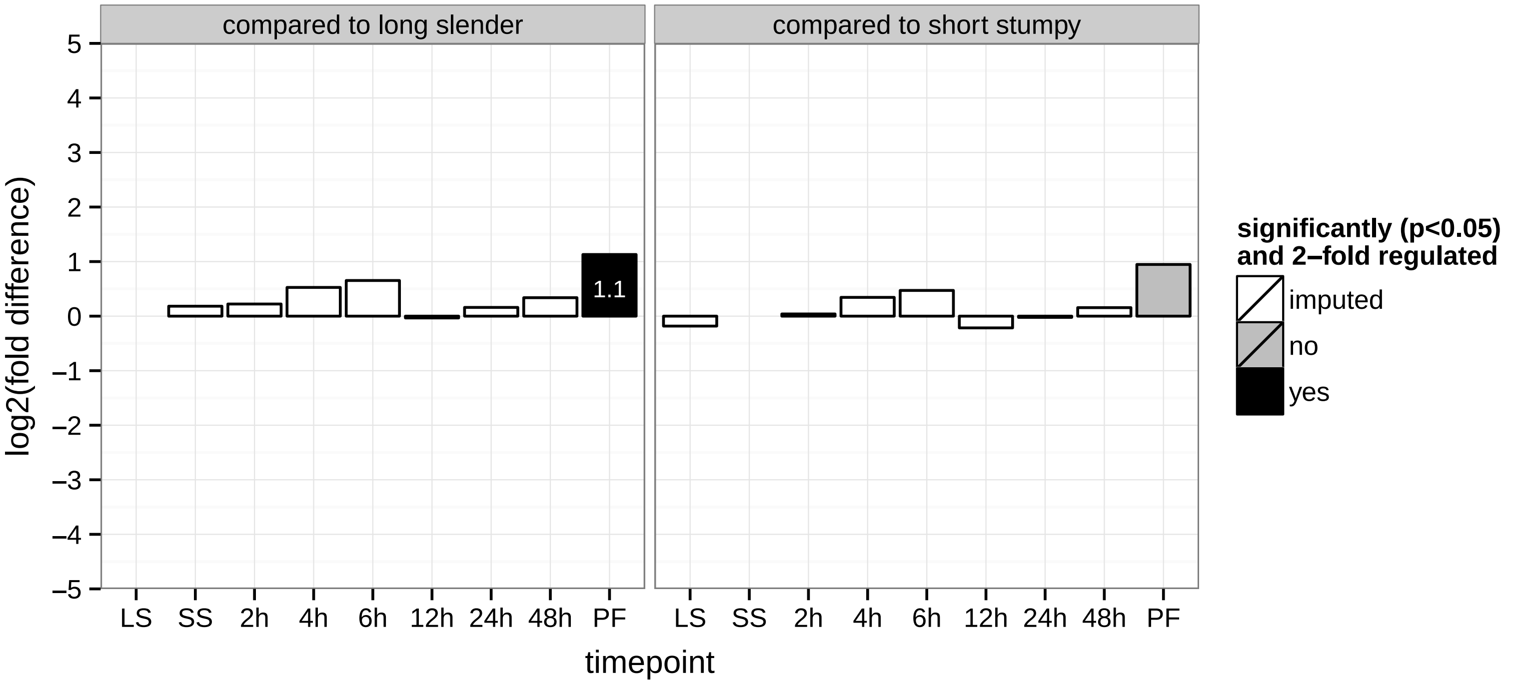
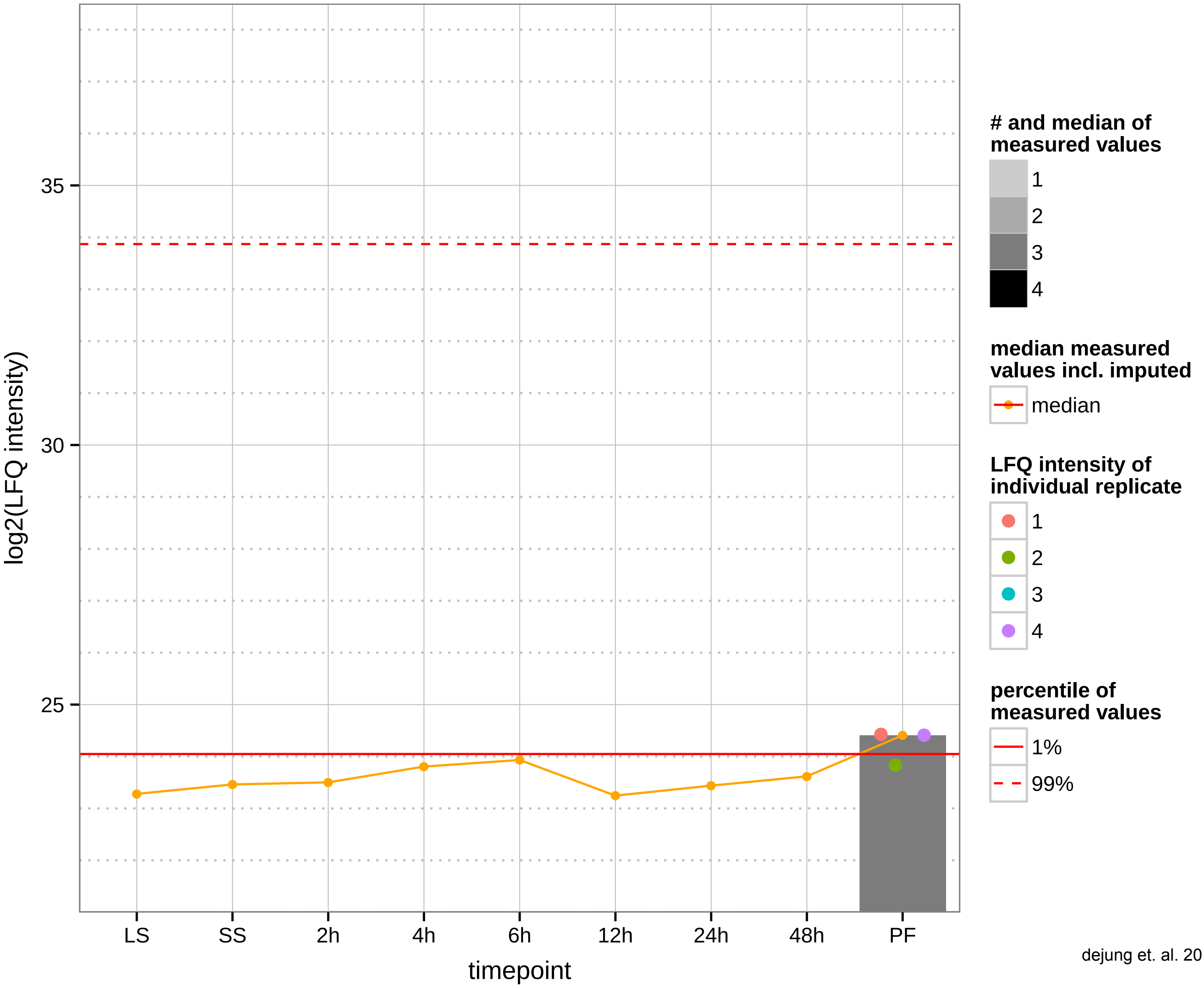
hypothetical protein, chrXI additional, unordered contigs
Tb927.11.7670;Tb11.0330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: cytoplasm
PGOP: peptide cross–linking





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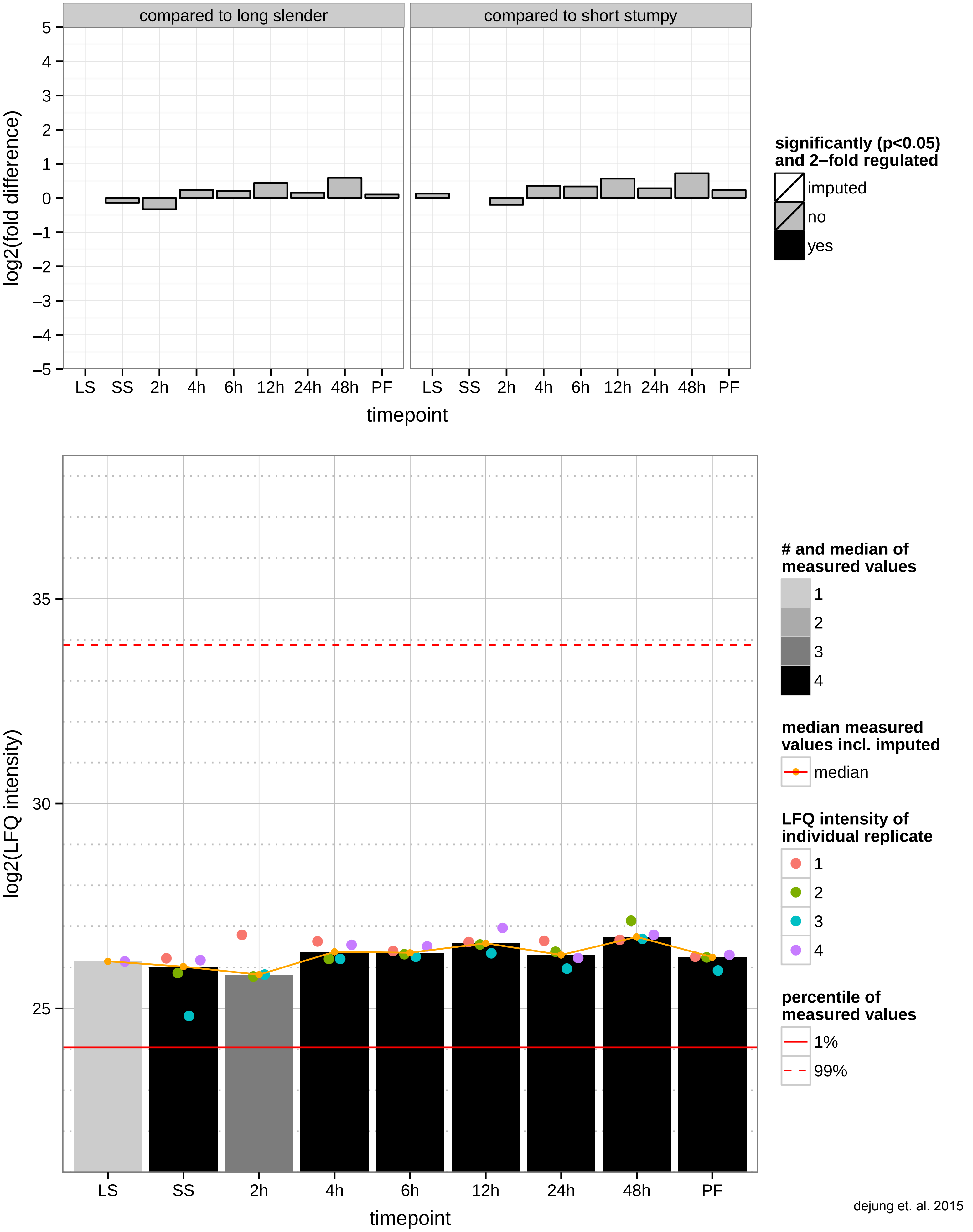
hypothetical protein, chrXI additional, unordered contigs
Tb927.11.7650;Tb11.0350
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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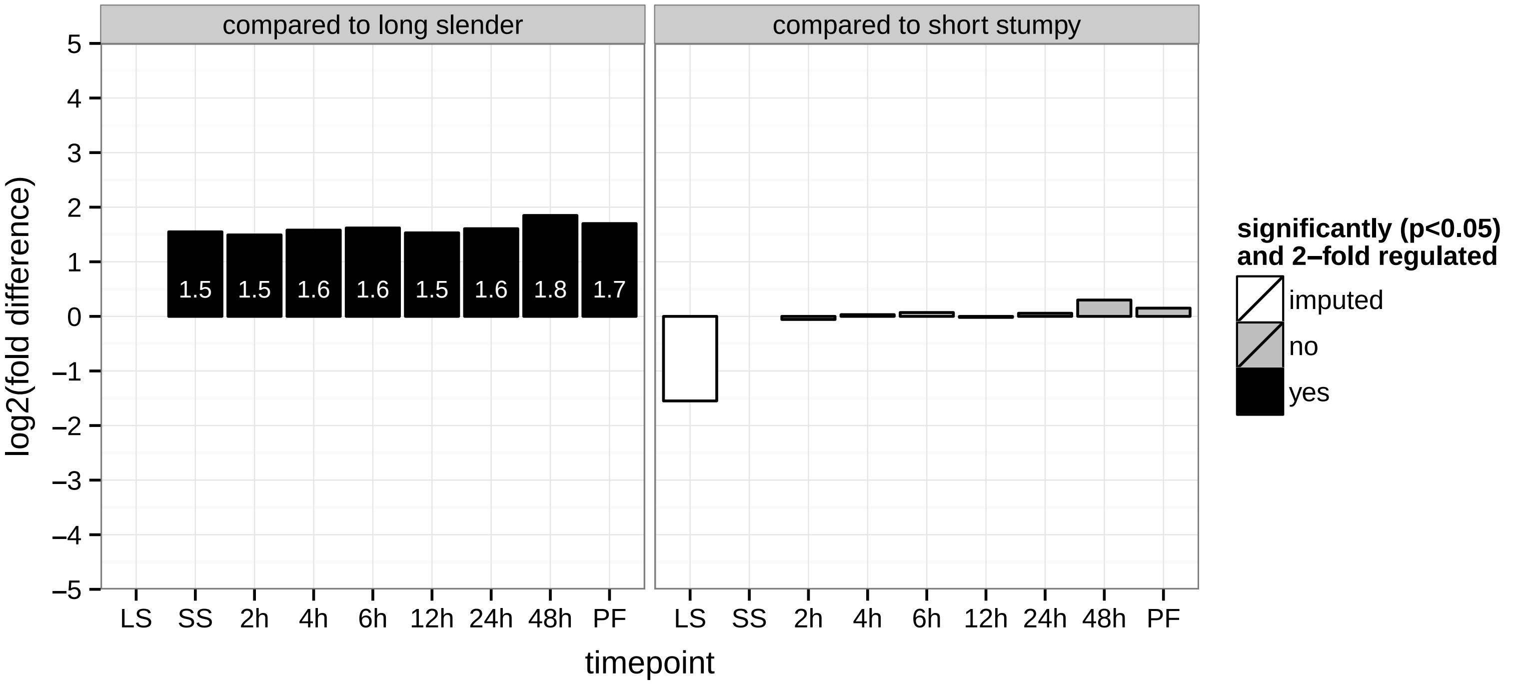
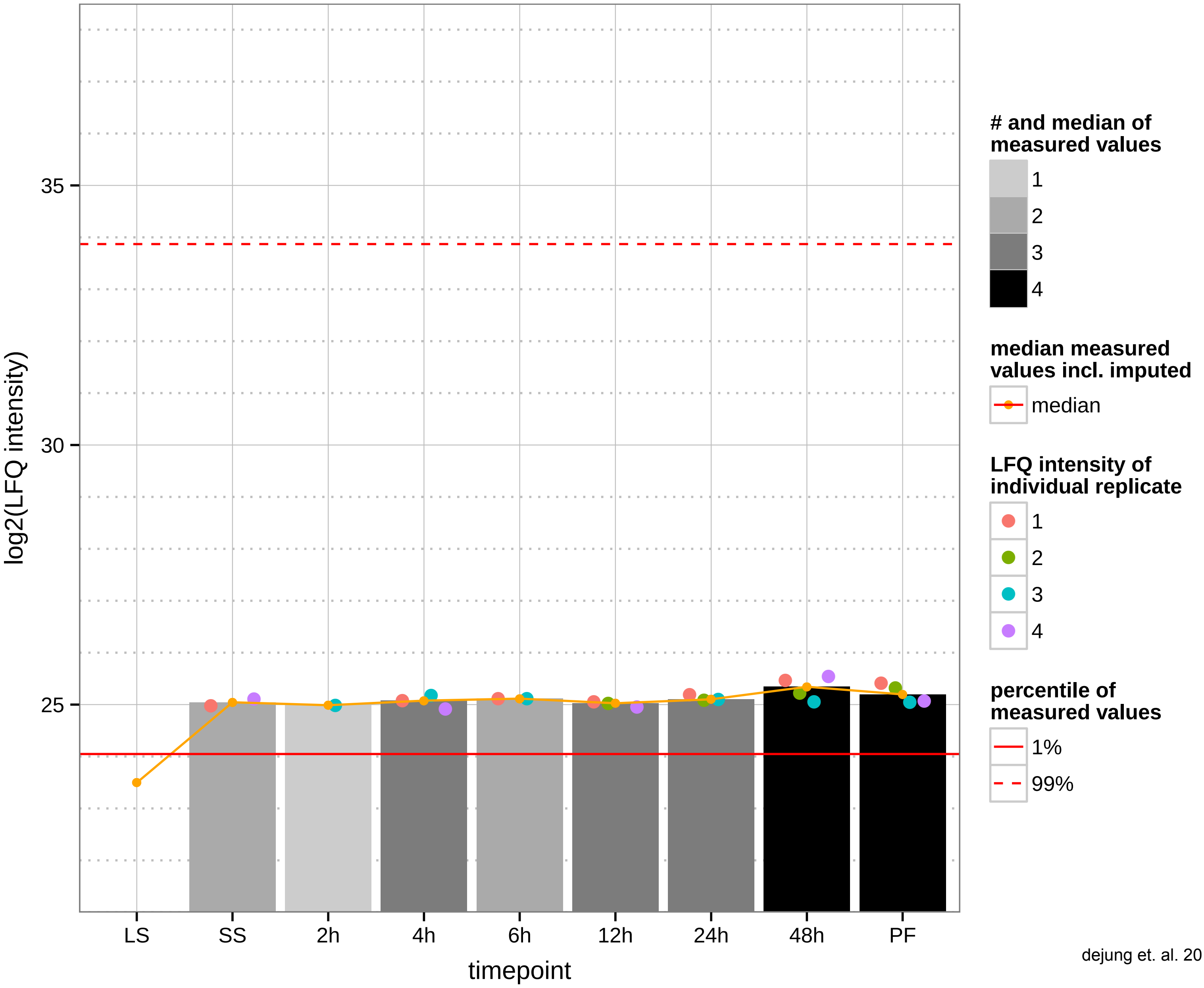
chrX additional, unordered contigs, dynein light chain, putative, dynein arm light chain, axonemal
Tb927.10.1130;Tb11.0520
AGOF: null, microtubule motor activity
AGOC: null, axonemal dynein complex
AGOP: null, cellular component movement
PGOF: null
PGOC: null
PGOP: null





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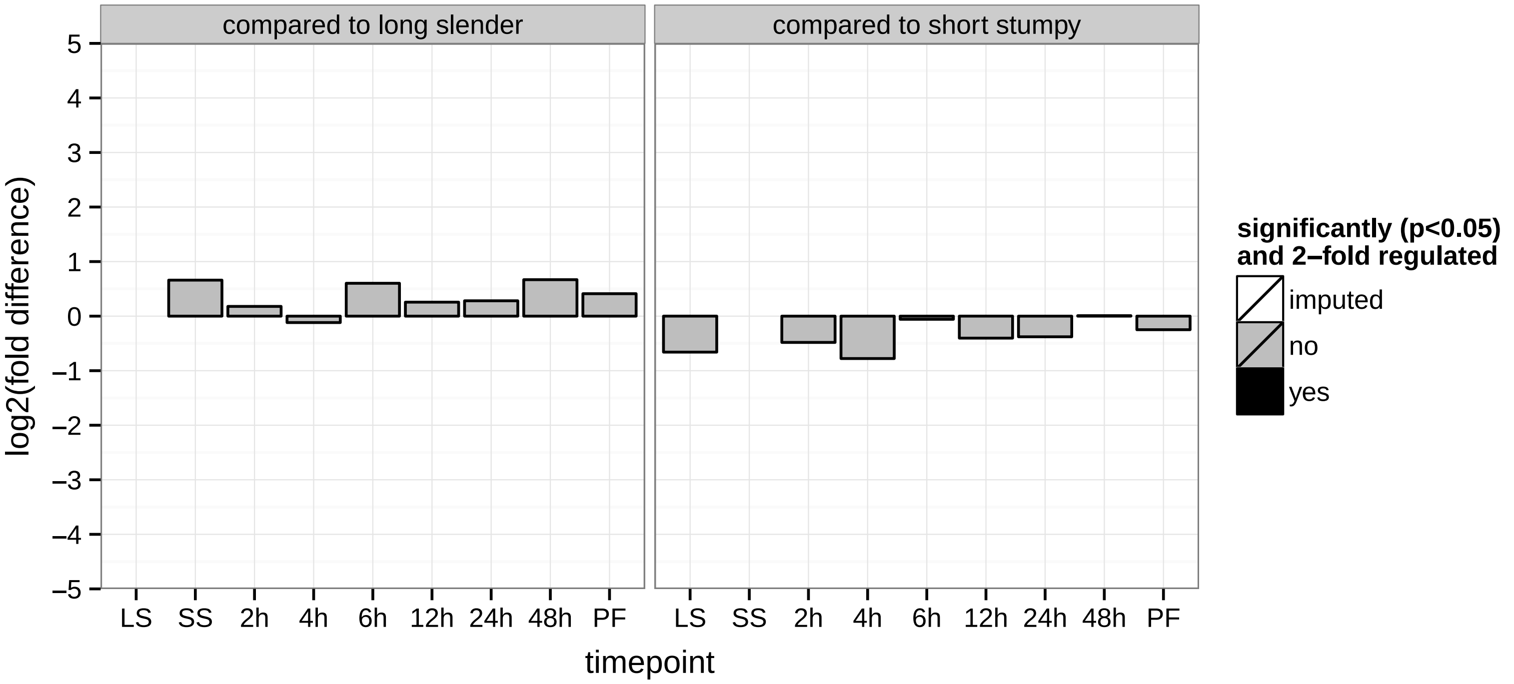
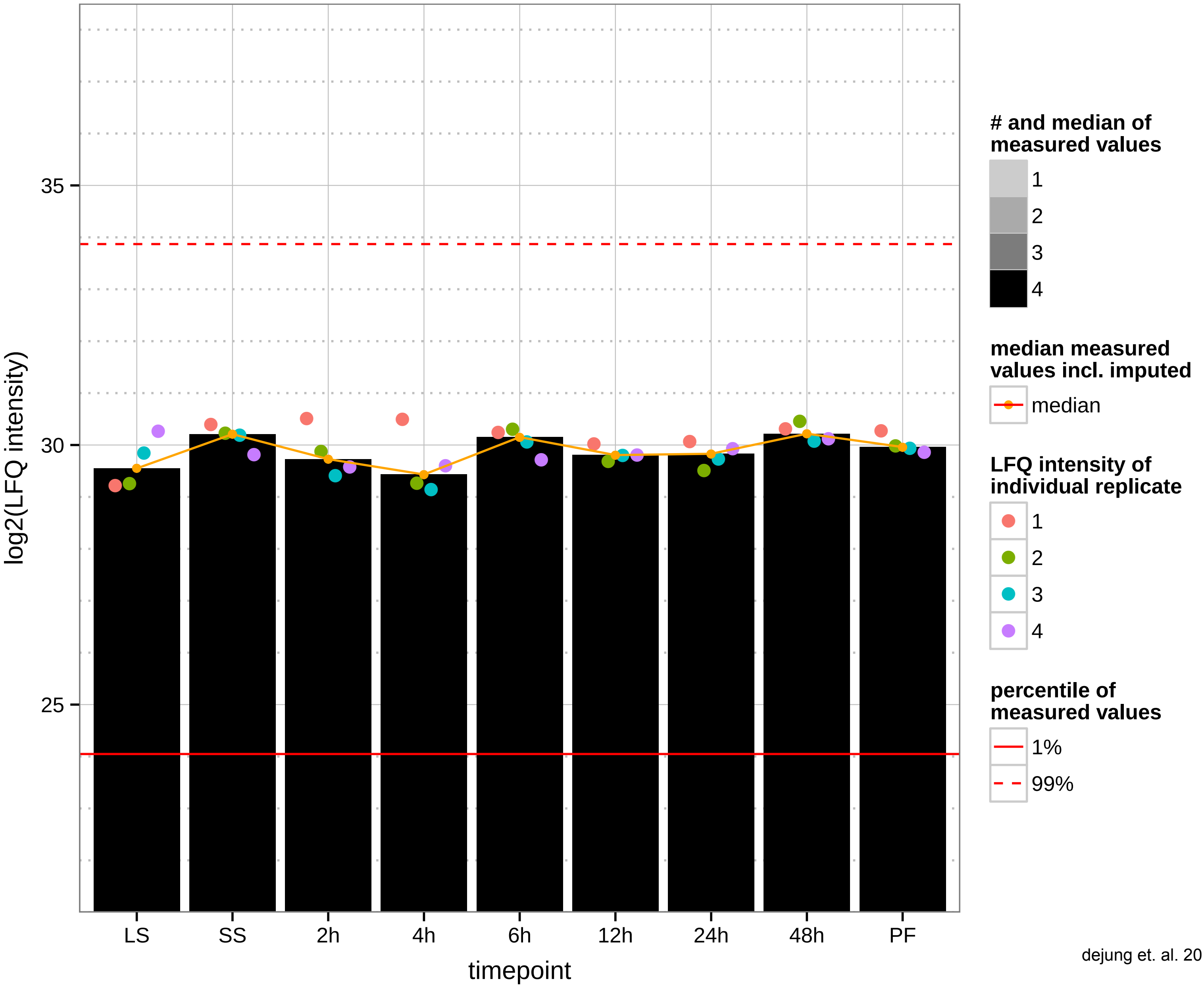
hypothetical protein, chrXI additional, unordered contigs, conserved, paraflagellar rod component, putative (PFC15)
Tb11.v5.0996;Tb11.1220;Tb927.10.15250
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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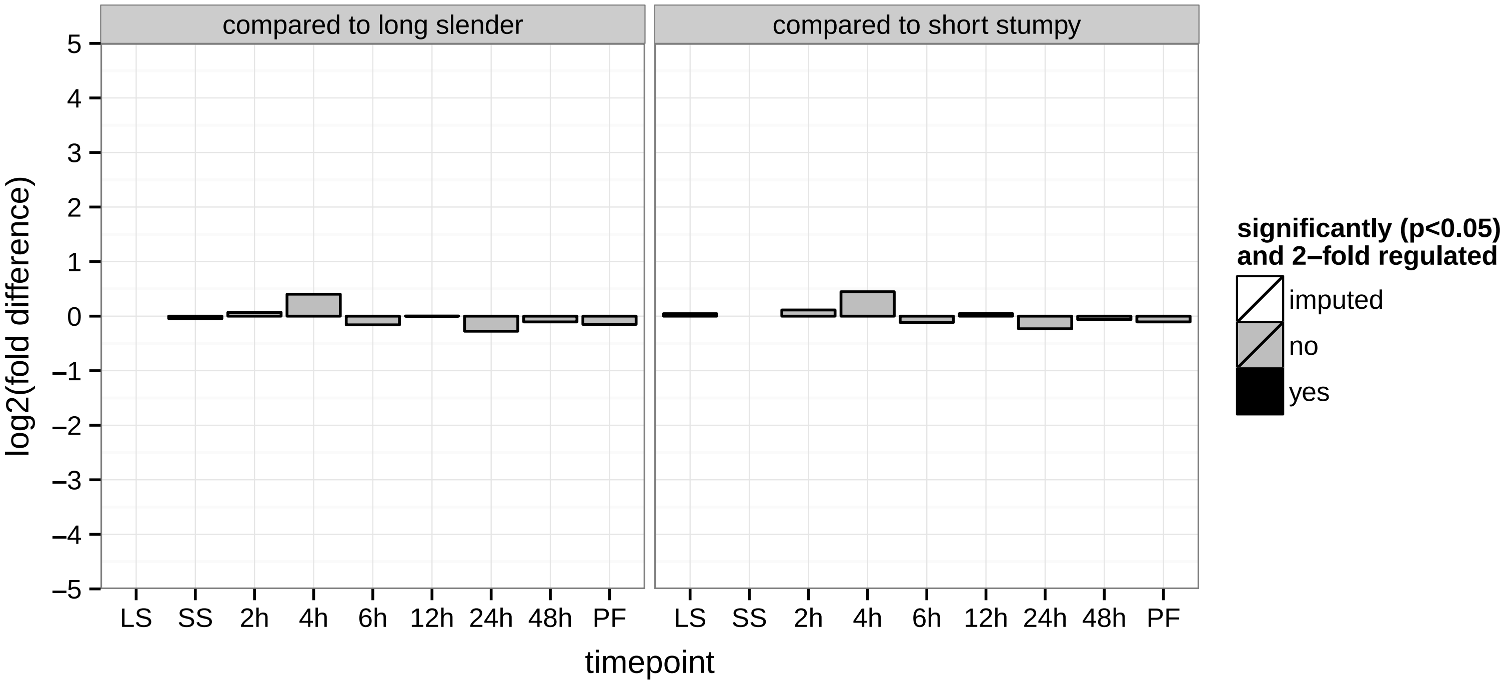
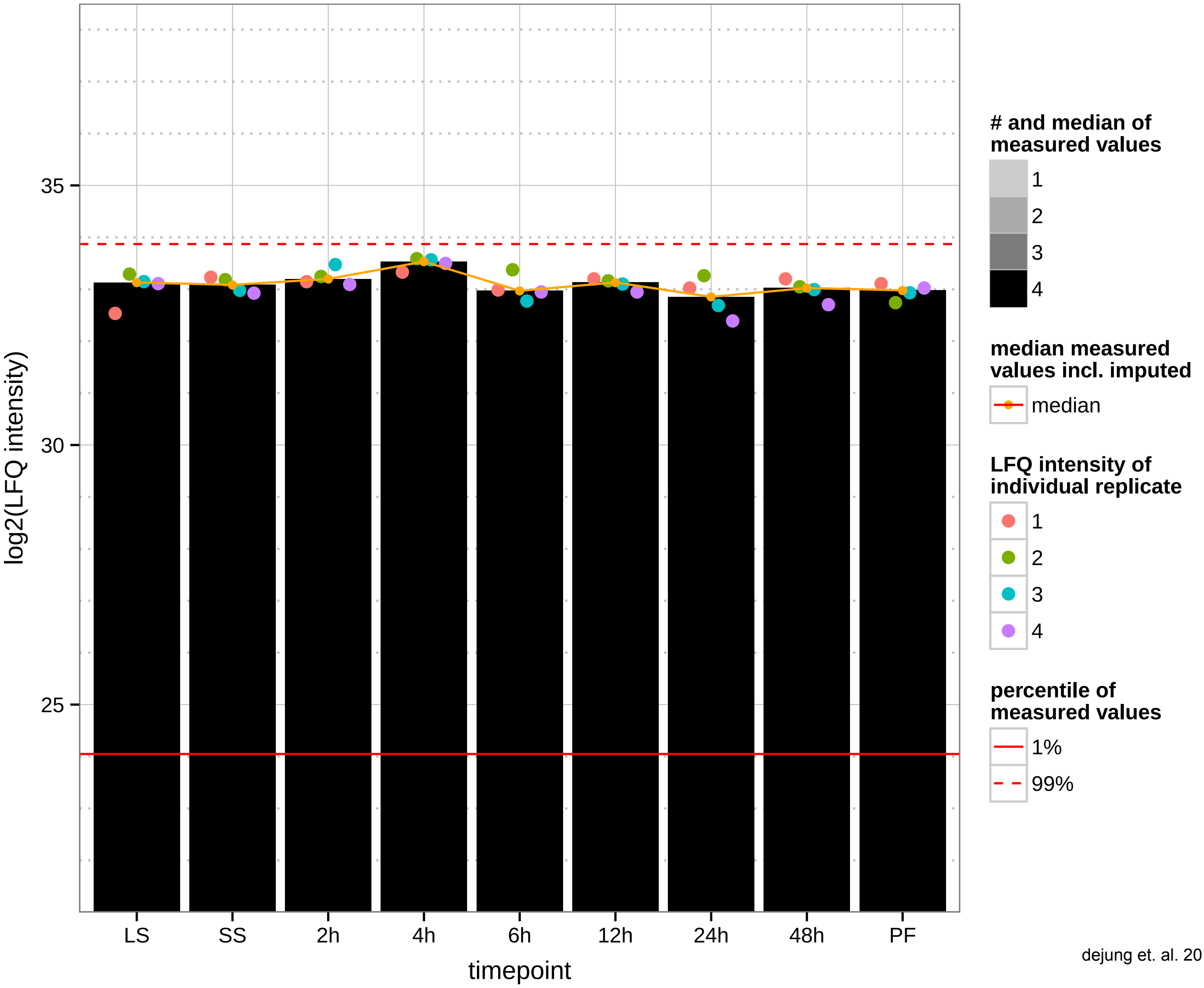
hypothetical protein, conserved
Tb927.11.1840;Tb11.1380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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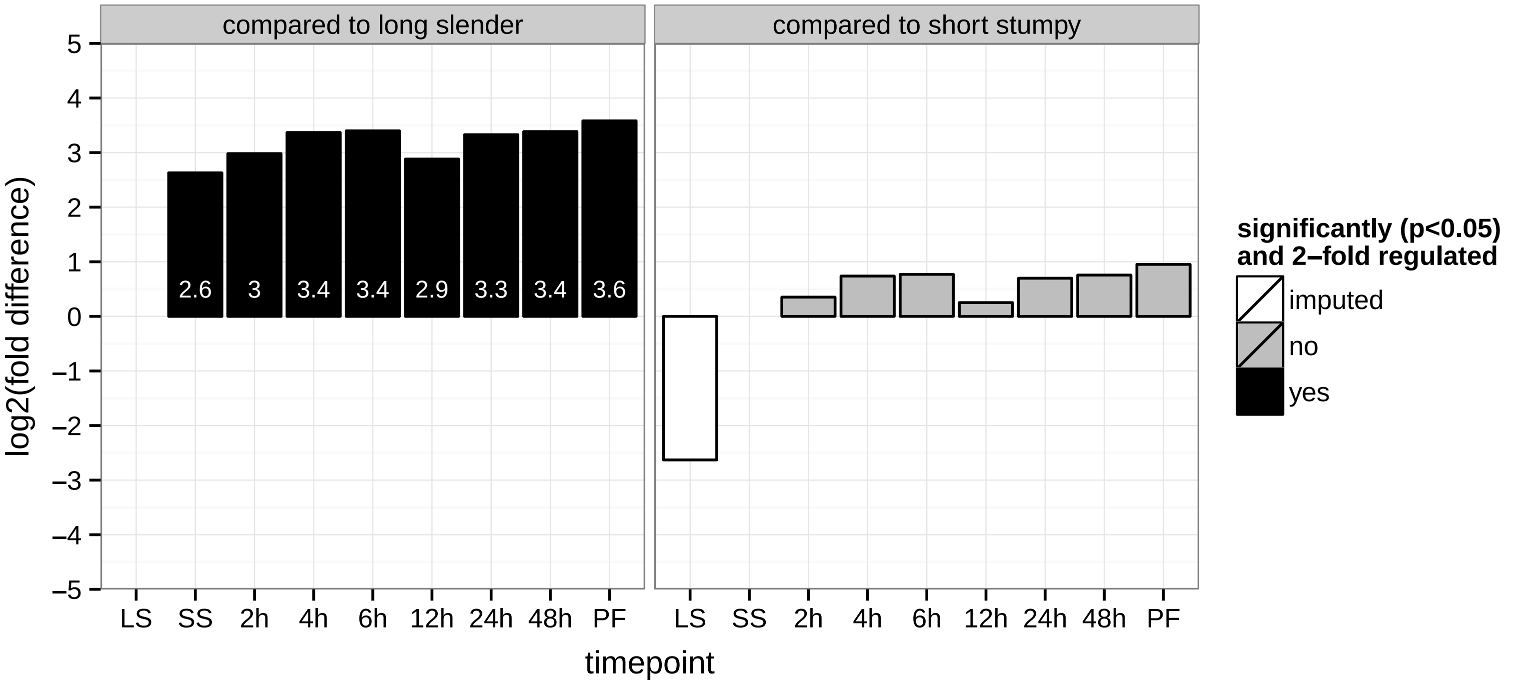
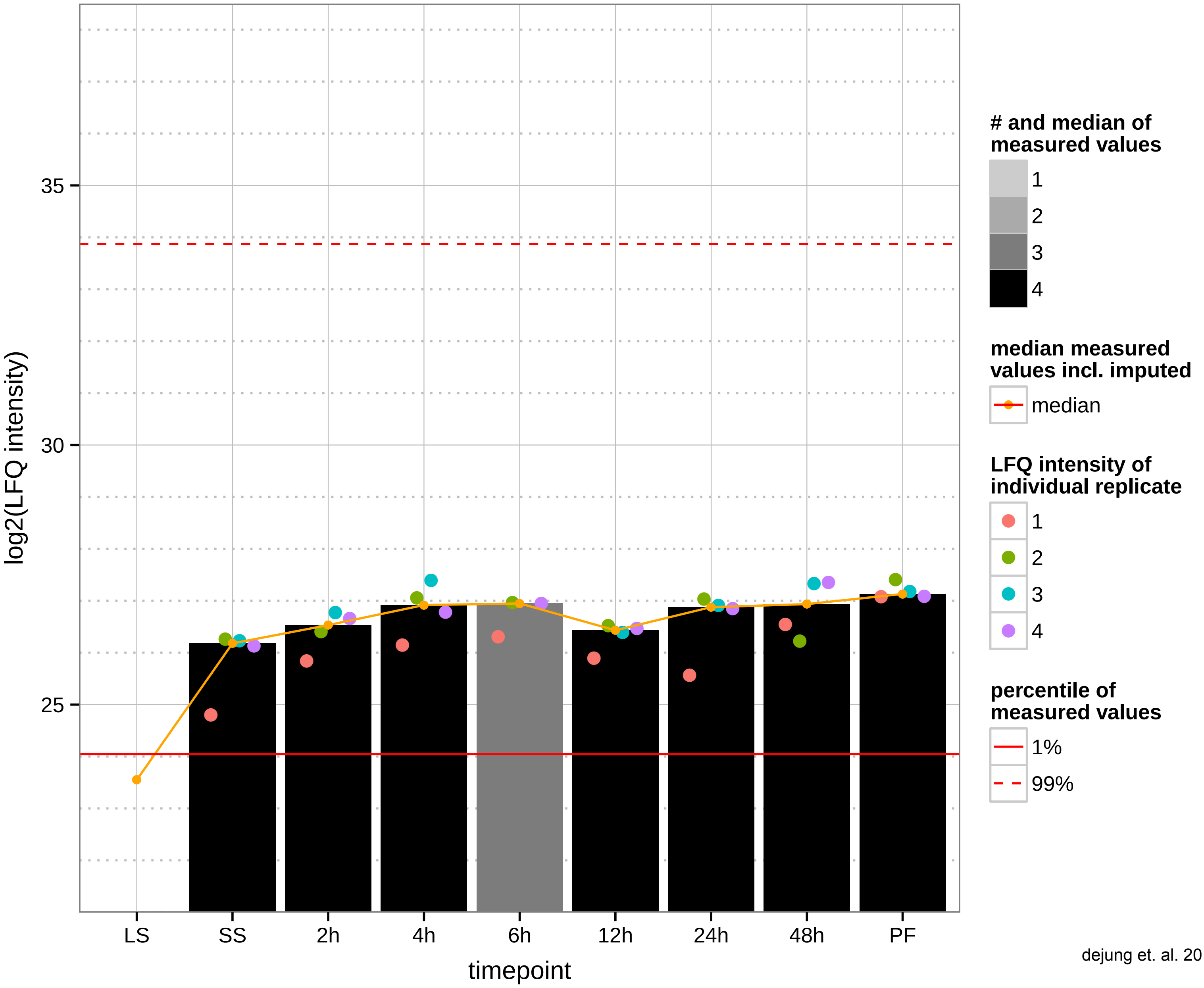
hypothetical protein, conserved
Tb927.11.1830;Tb11.1390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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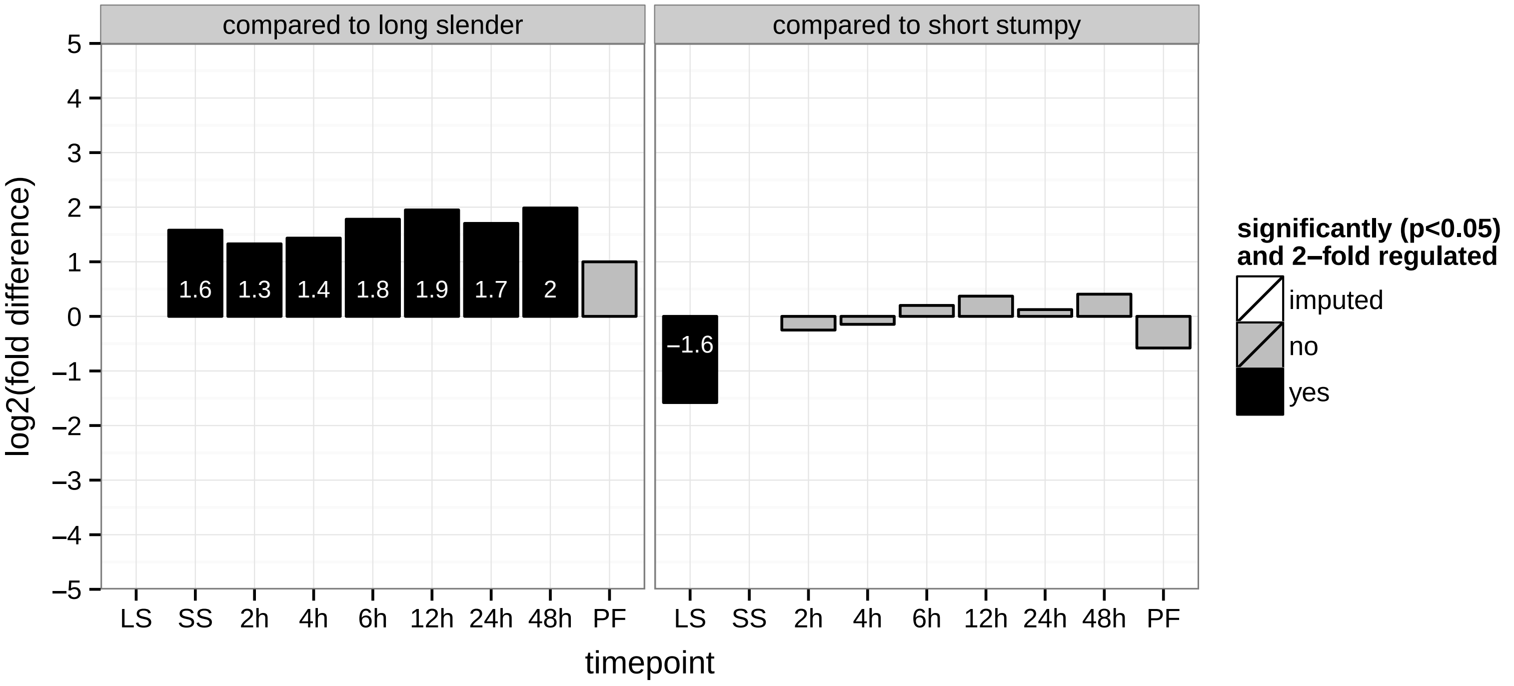
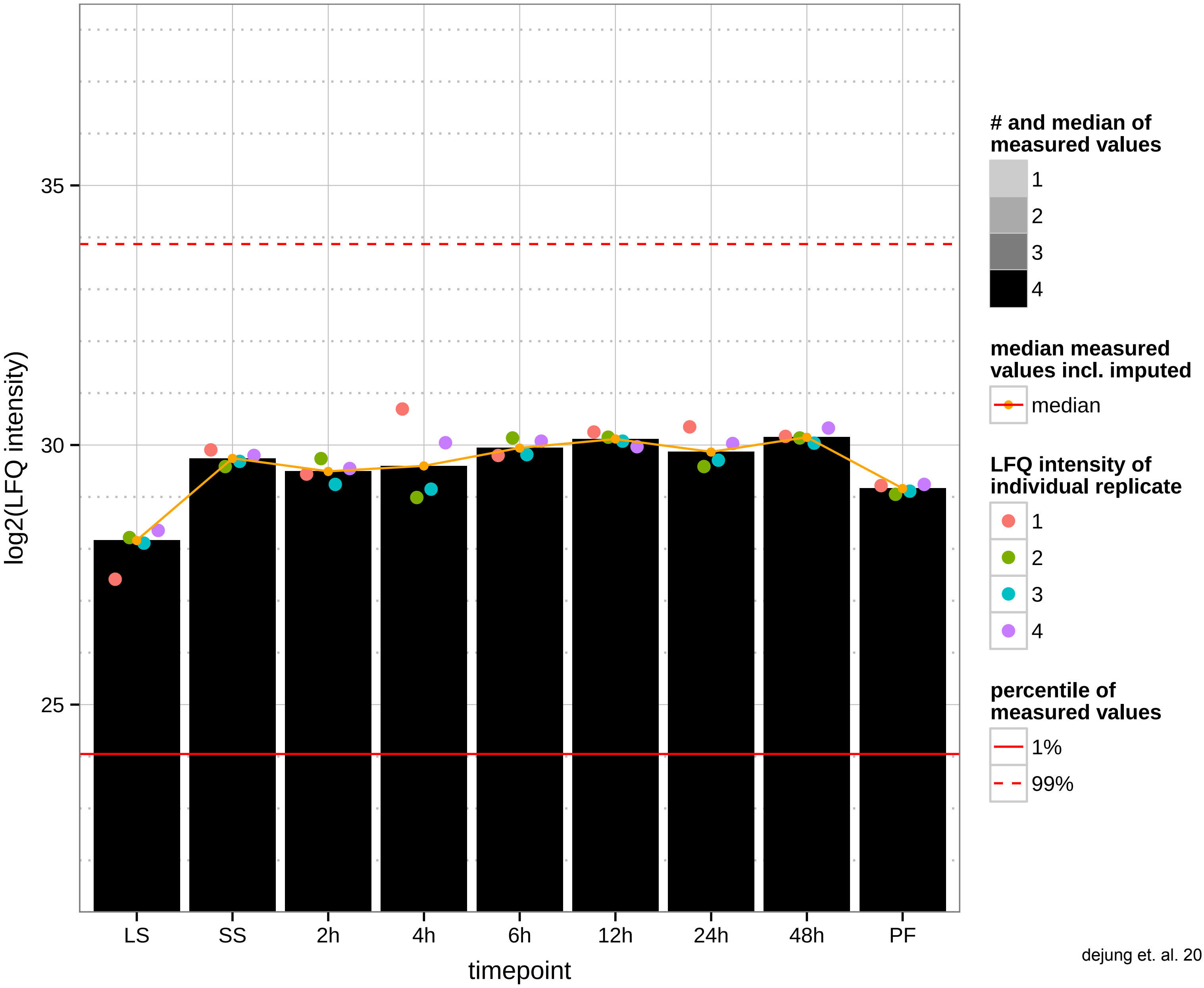
retrotransposon hot spot protein 1 (RHS1, pseudogene), putative
Tb11.1780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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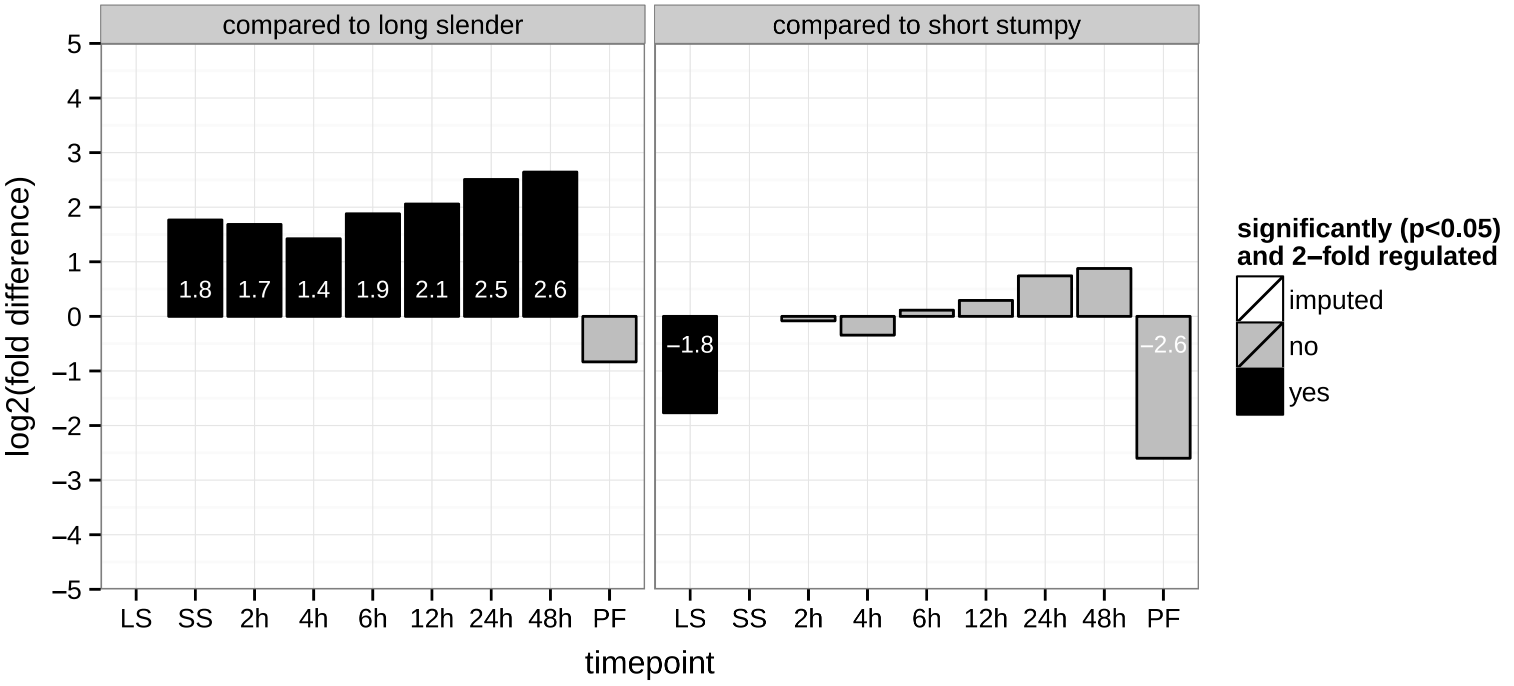
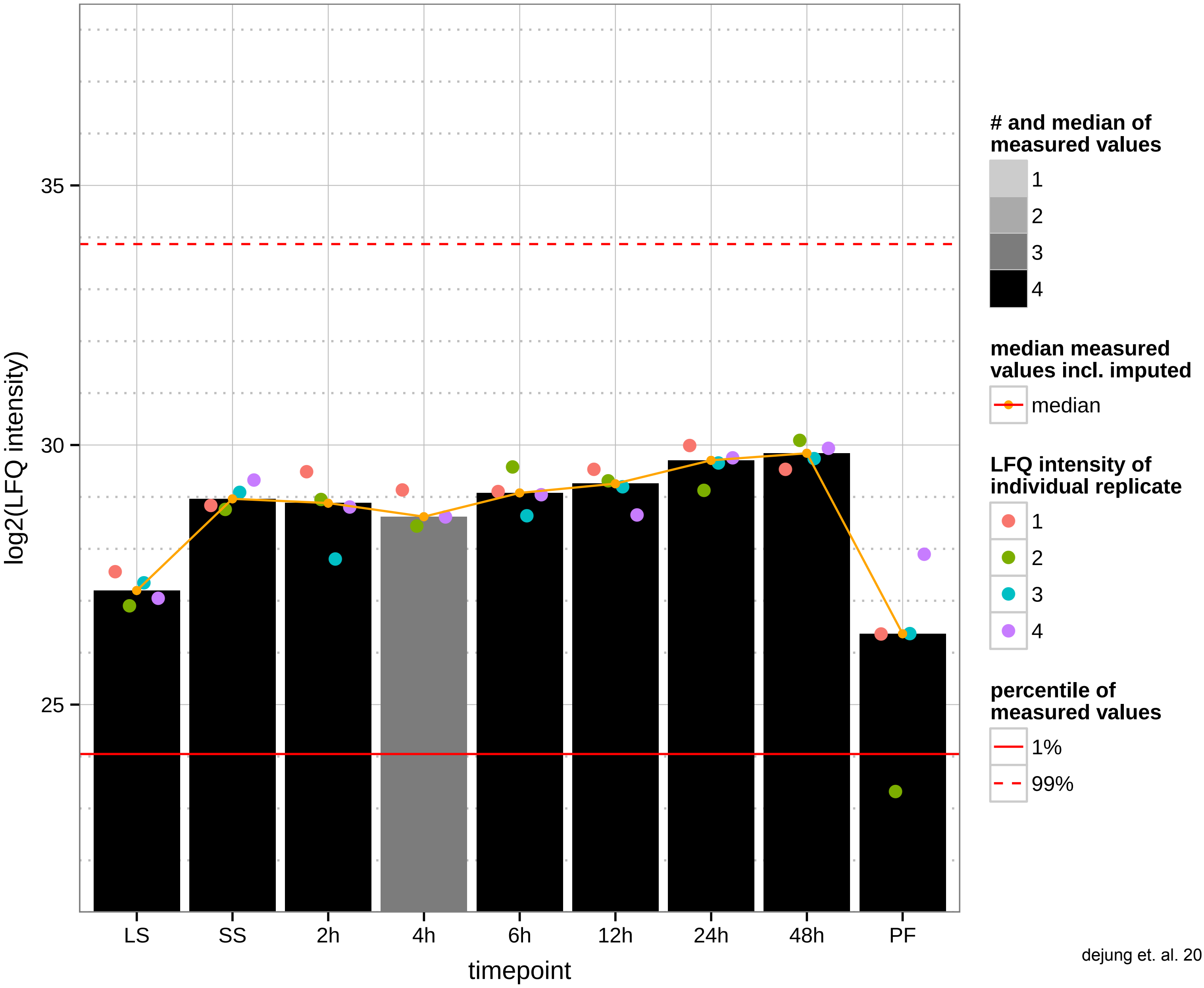
retrotransposon hot spot protein (RHS, pseudogene), putative
Tb11.1790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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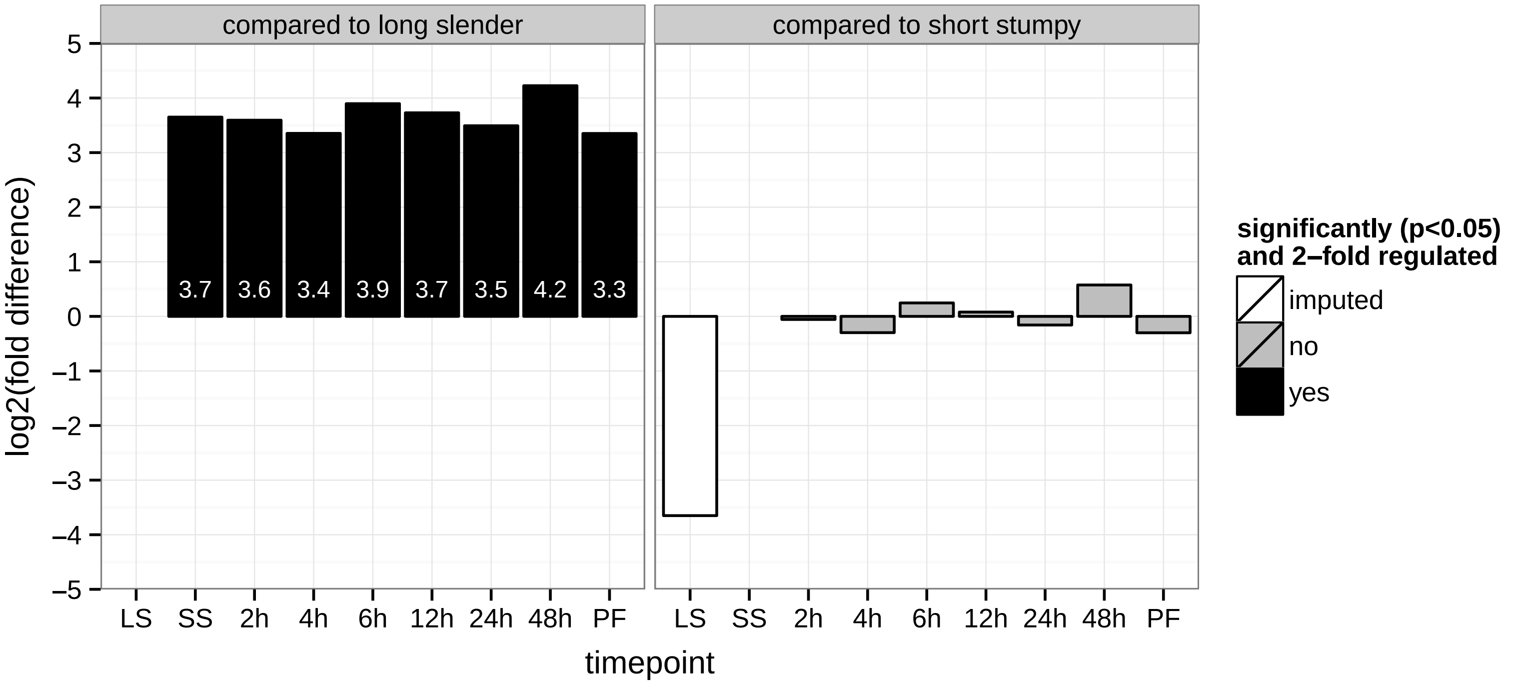
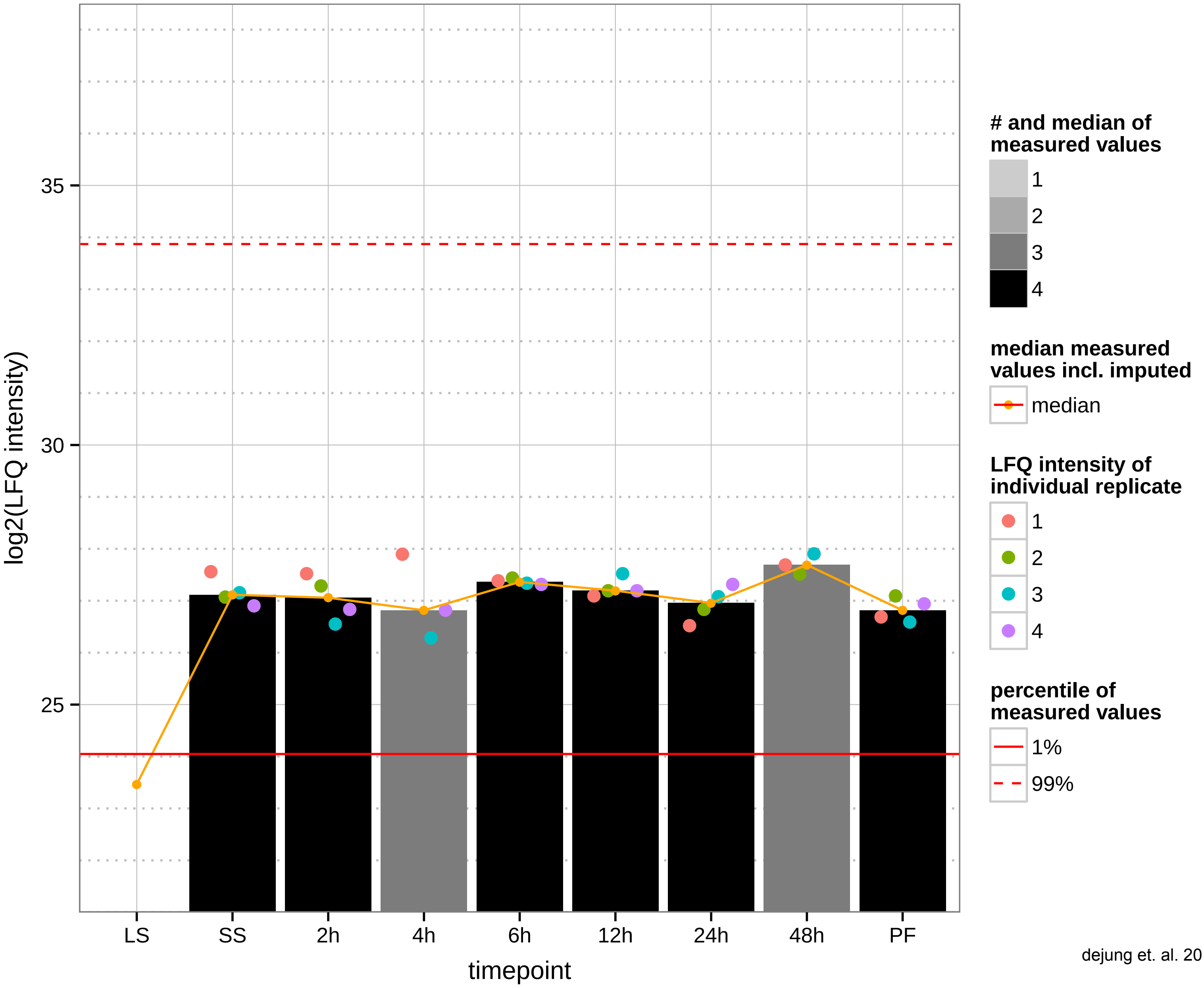
retrotransposon hot spot (RHS) protein, (pseudogene), putative, retrotransposon hot spot protein (RHS, pseudogene)
Tb11.1810b;Tb11.1810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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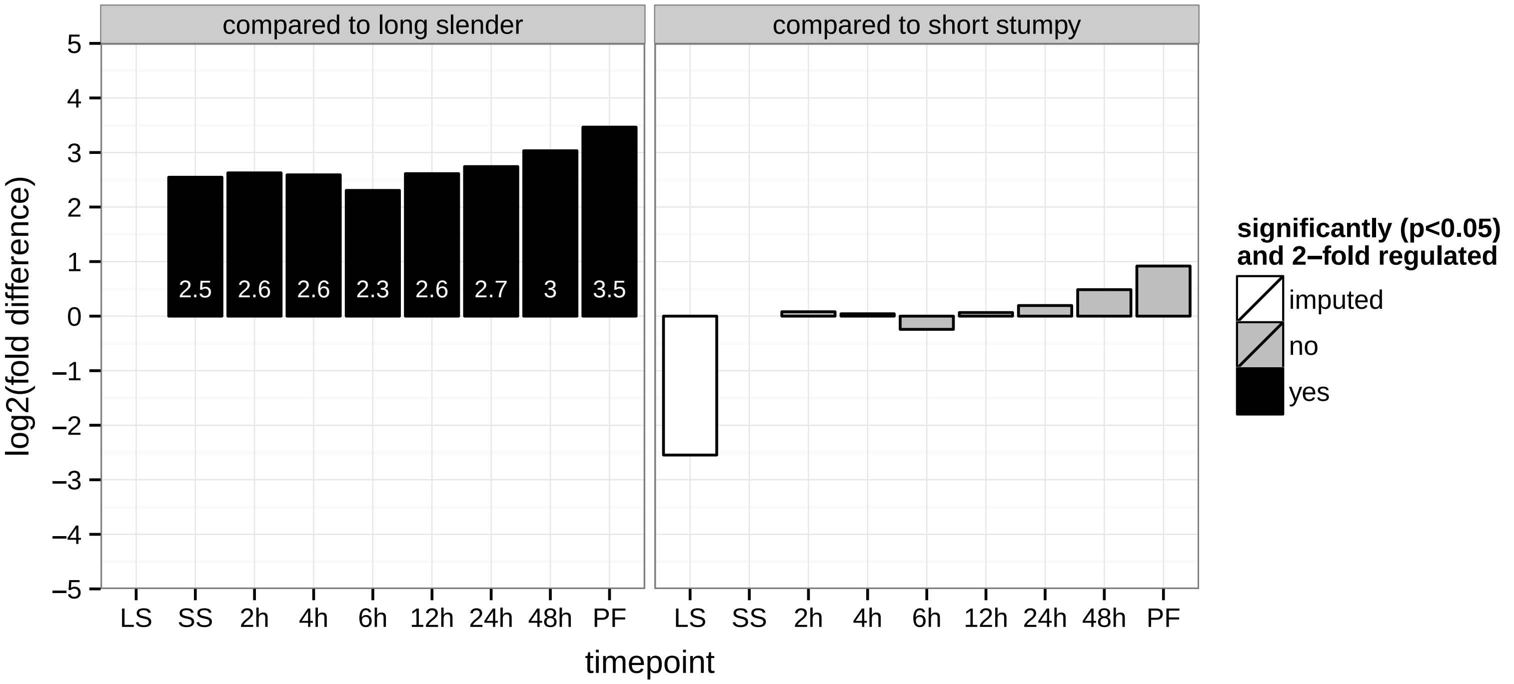
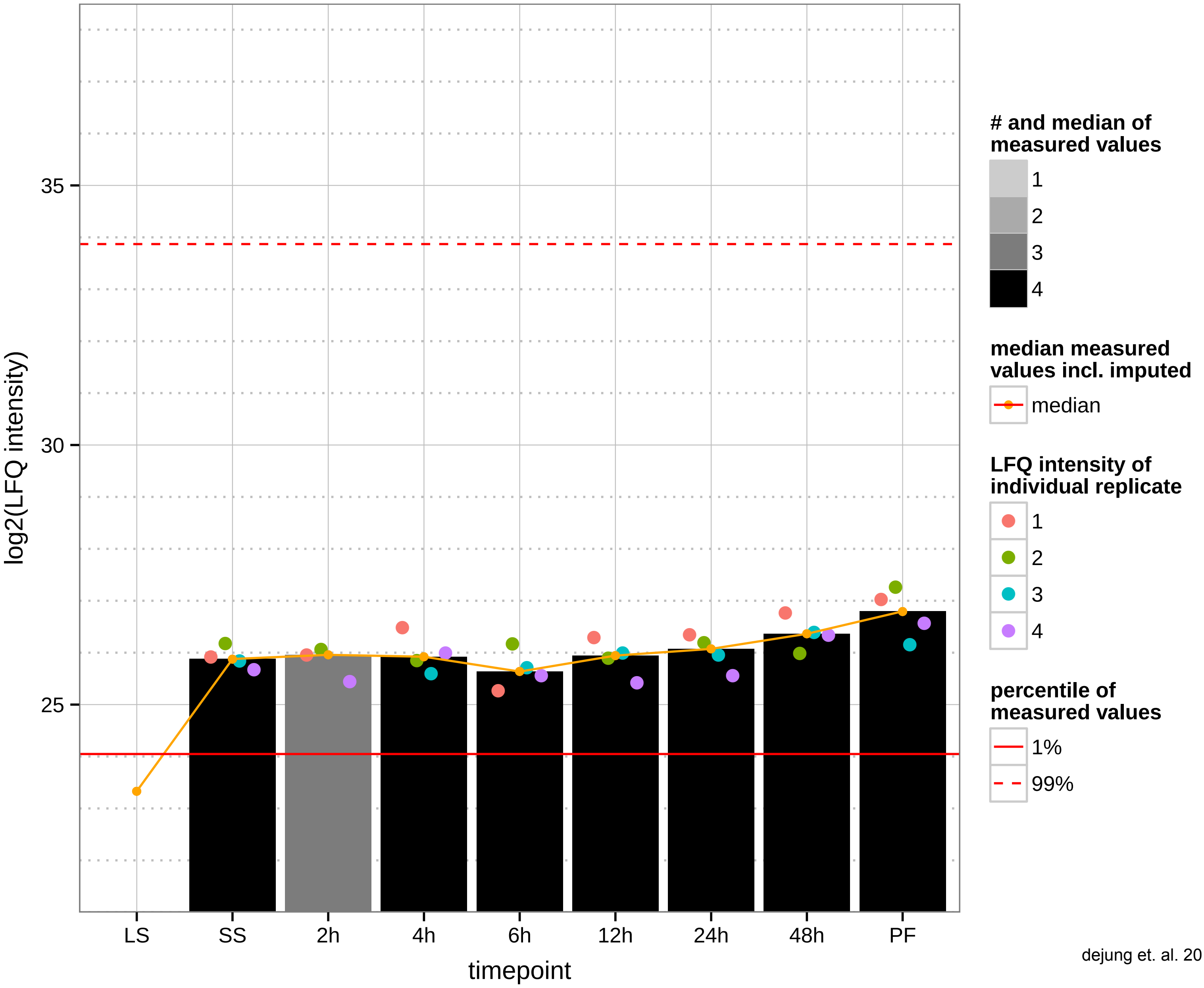
ribosomal RNA processing protein 4, putative, exosome complex exonuclease (RRP4)
Tb927.7.4670;Tb11.v5.0152
AGOF: null, 3'−5'−exoribonuclease activity, RNA binding
AGOC: null, cytoplasmic exosome (RNase complex), exosome (RNase complex), nuclear exosome (RNase complex)
AGOP: null, cell growth, rRNA processing
PGOF: RNA binding
PGOC: null
PGOP: null





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hypothetical protein, conserved
Tb11.v5.0154
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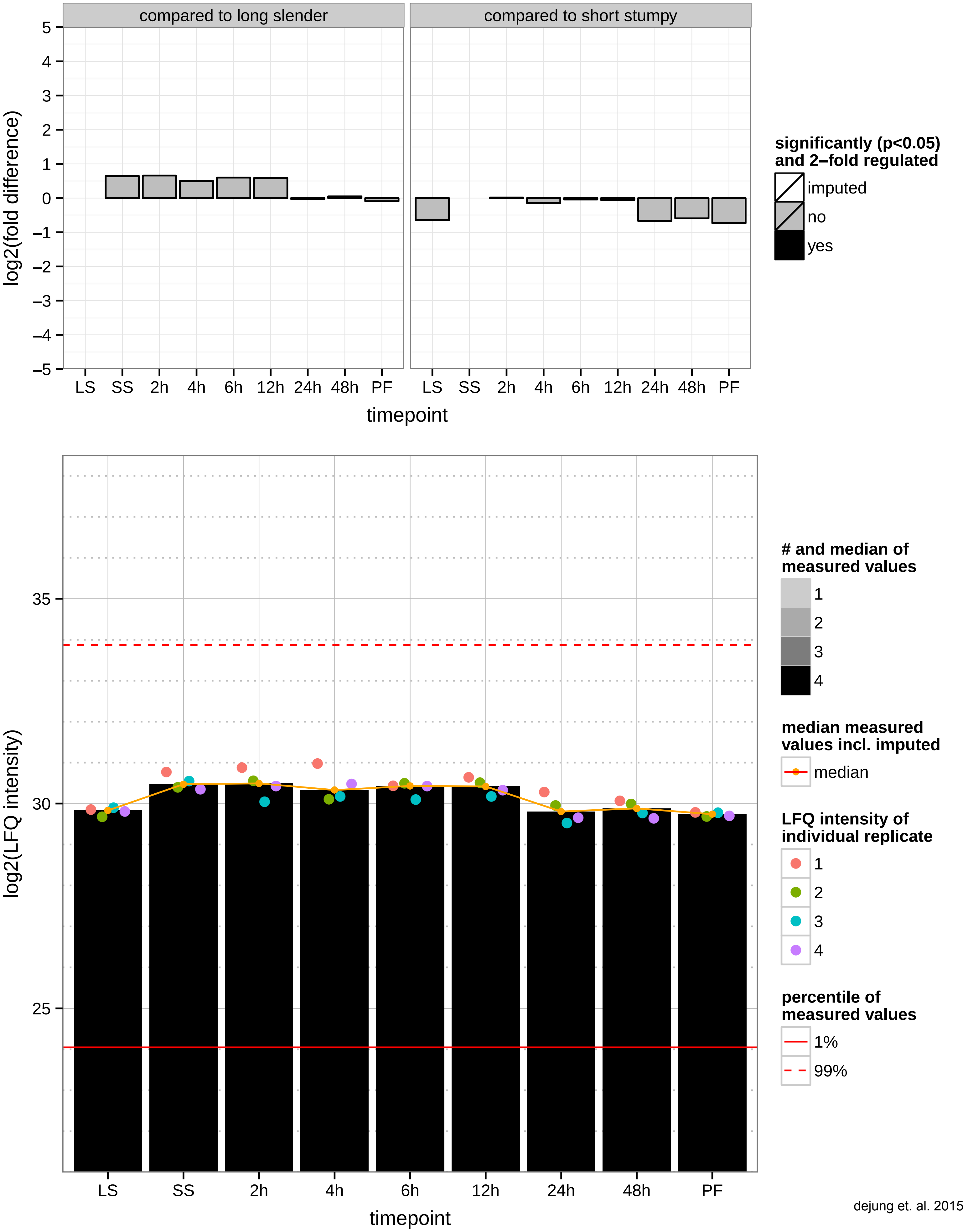
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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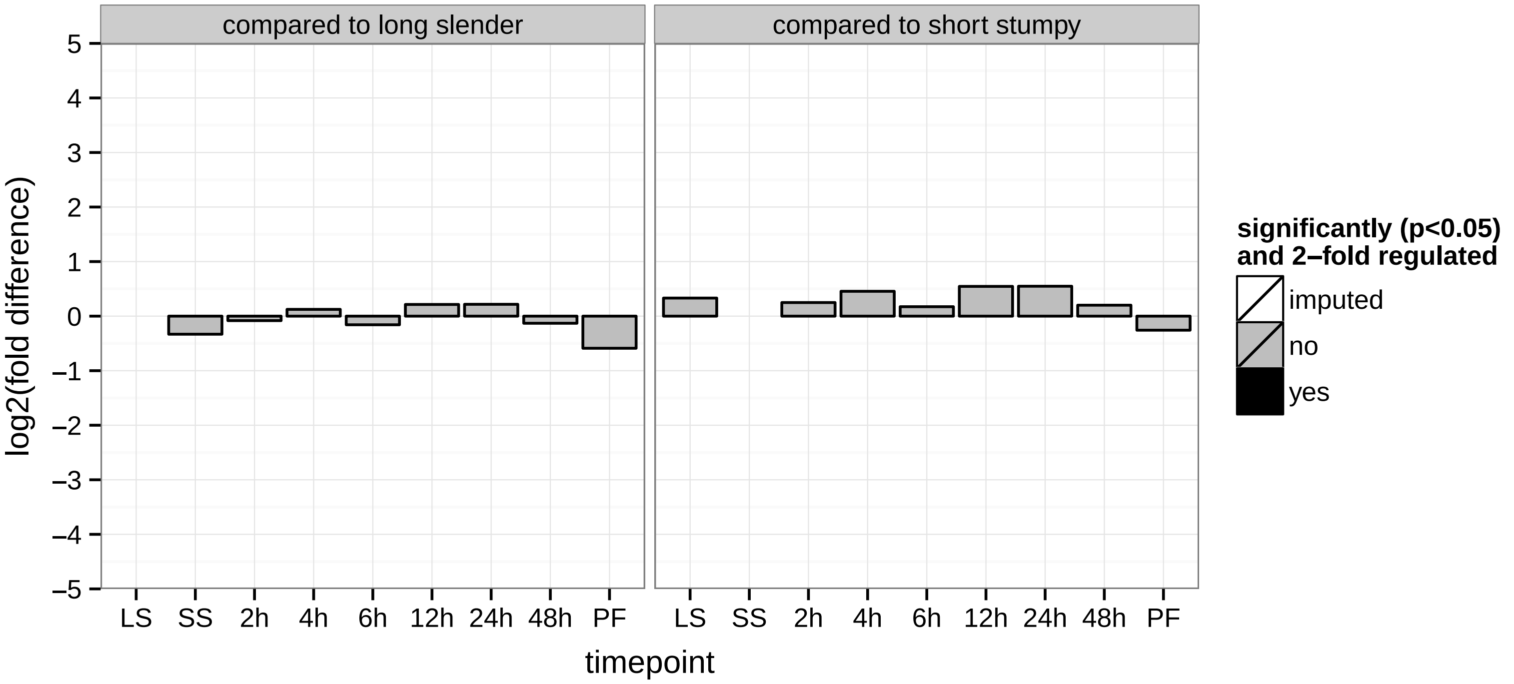
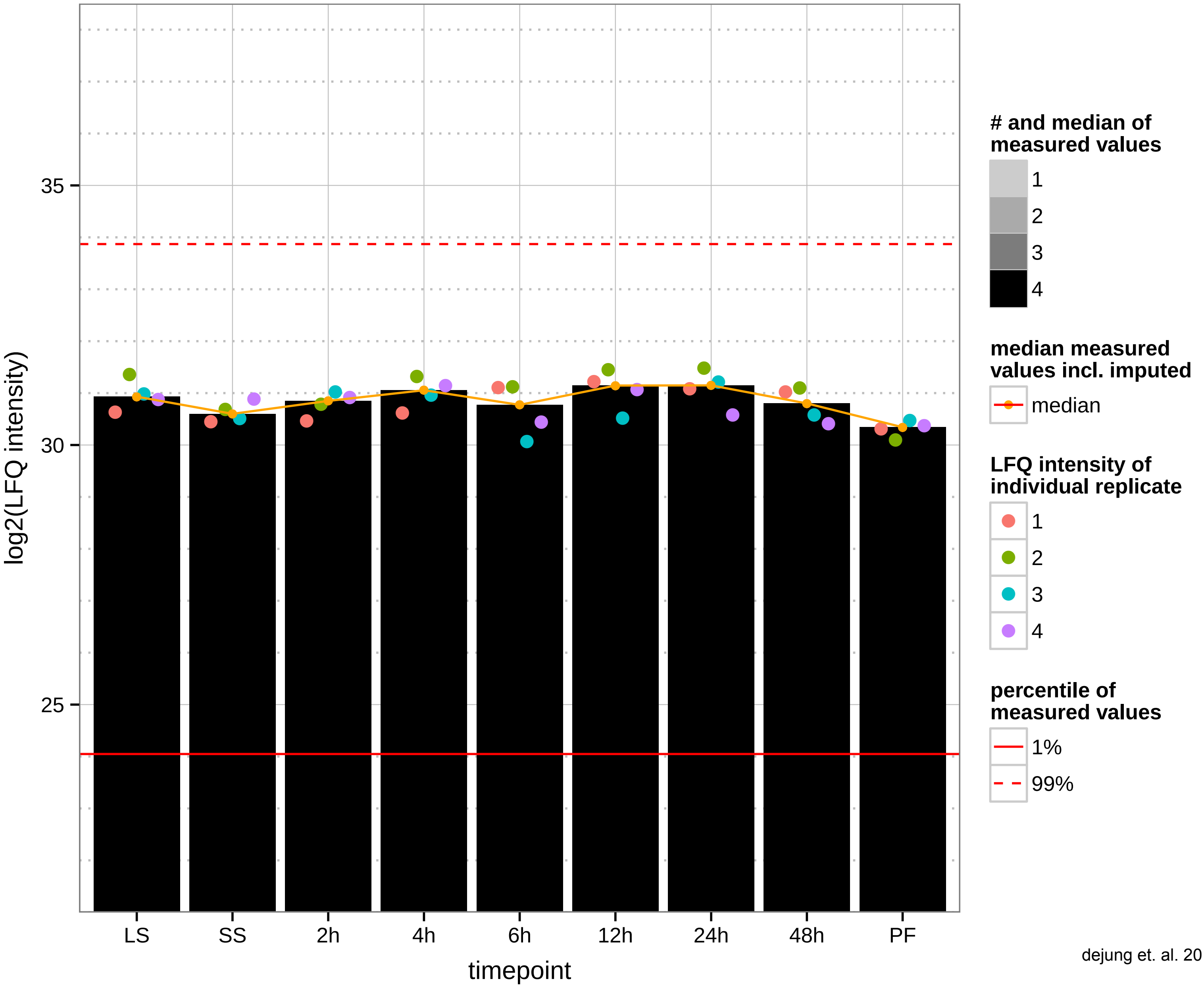
cyclophilin–type peptidyl–prolyl cis–trans isomerase, putative, putative (PPIase)
Tb11.v5.0160;Tb927.7.4770
AGOF: null, peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: null, protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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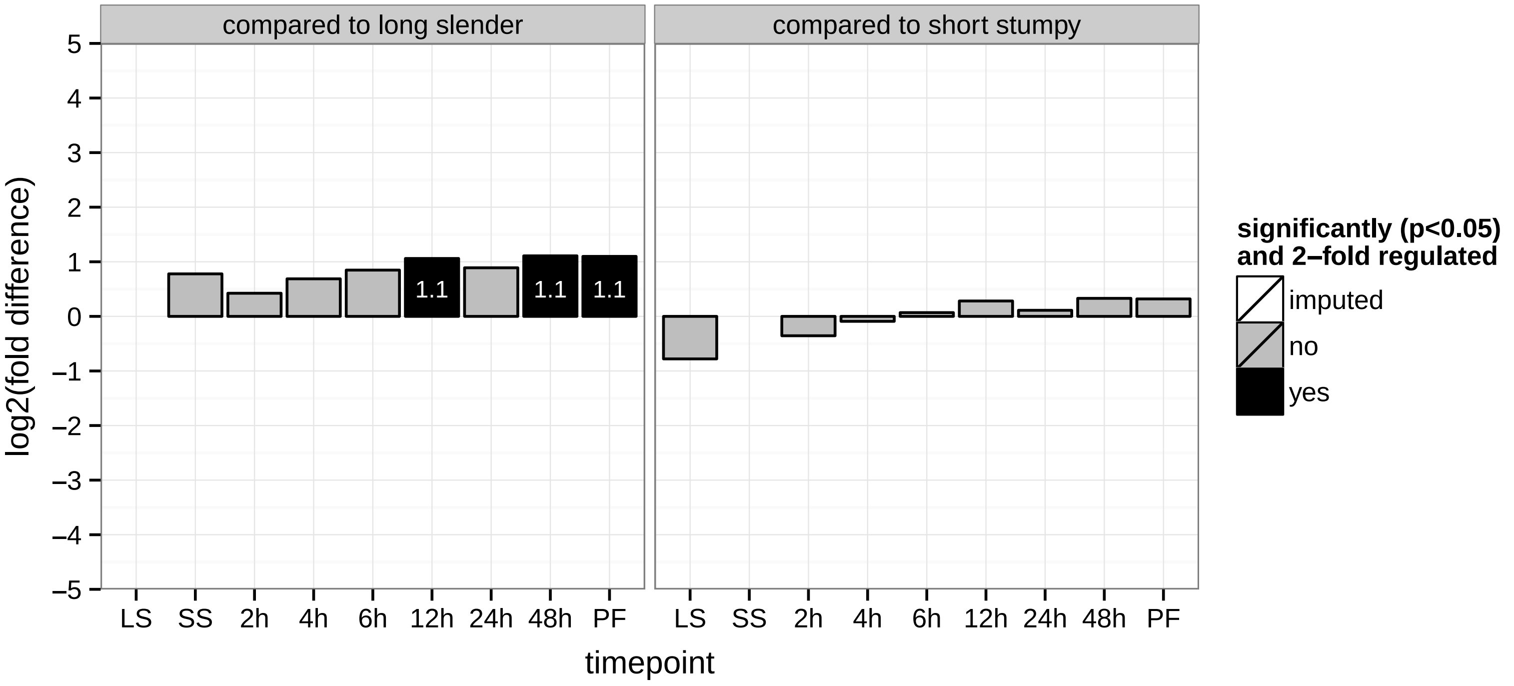
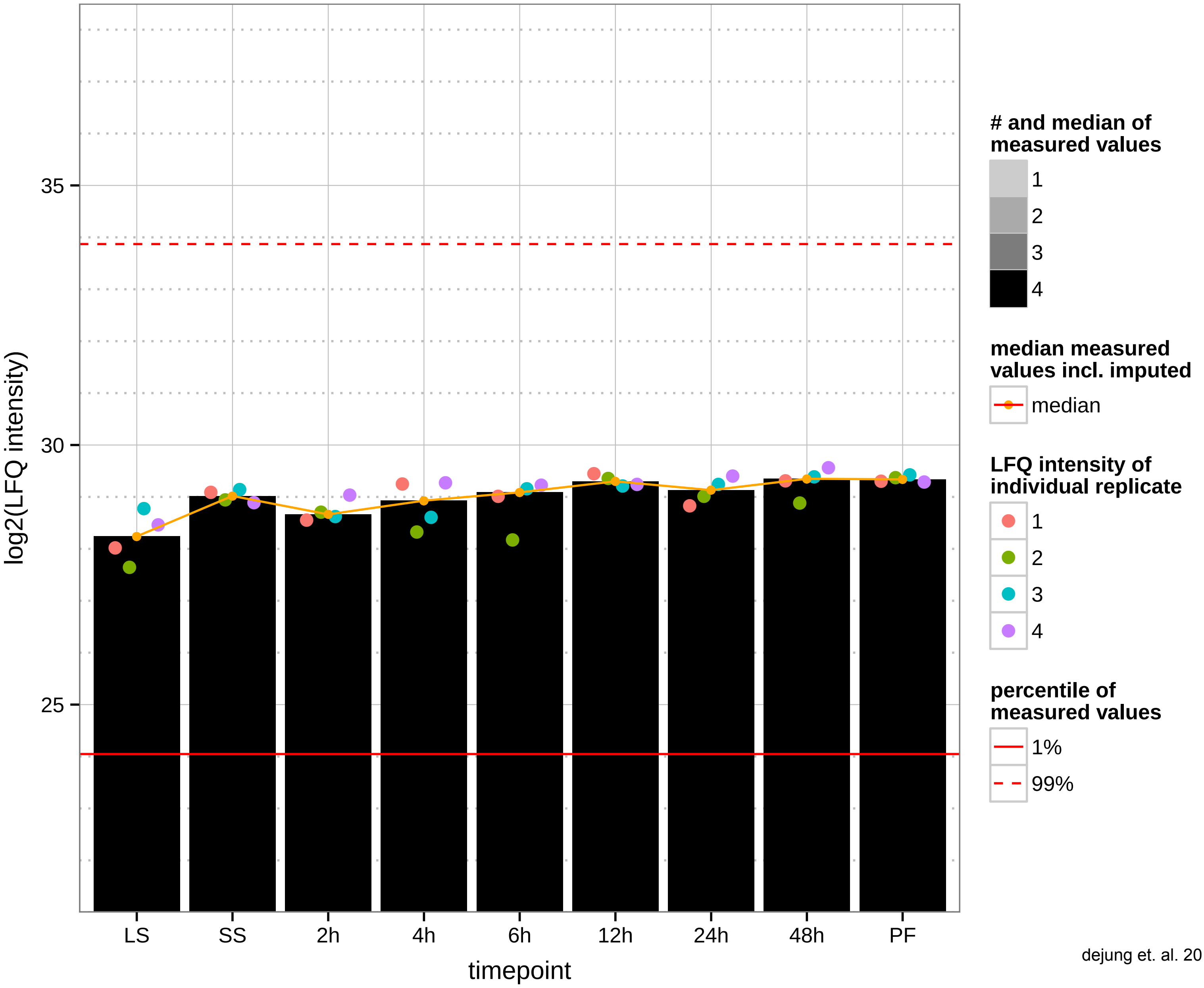
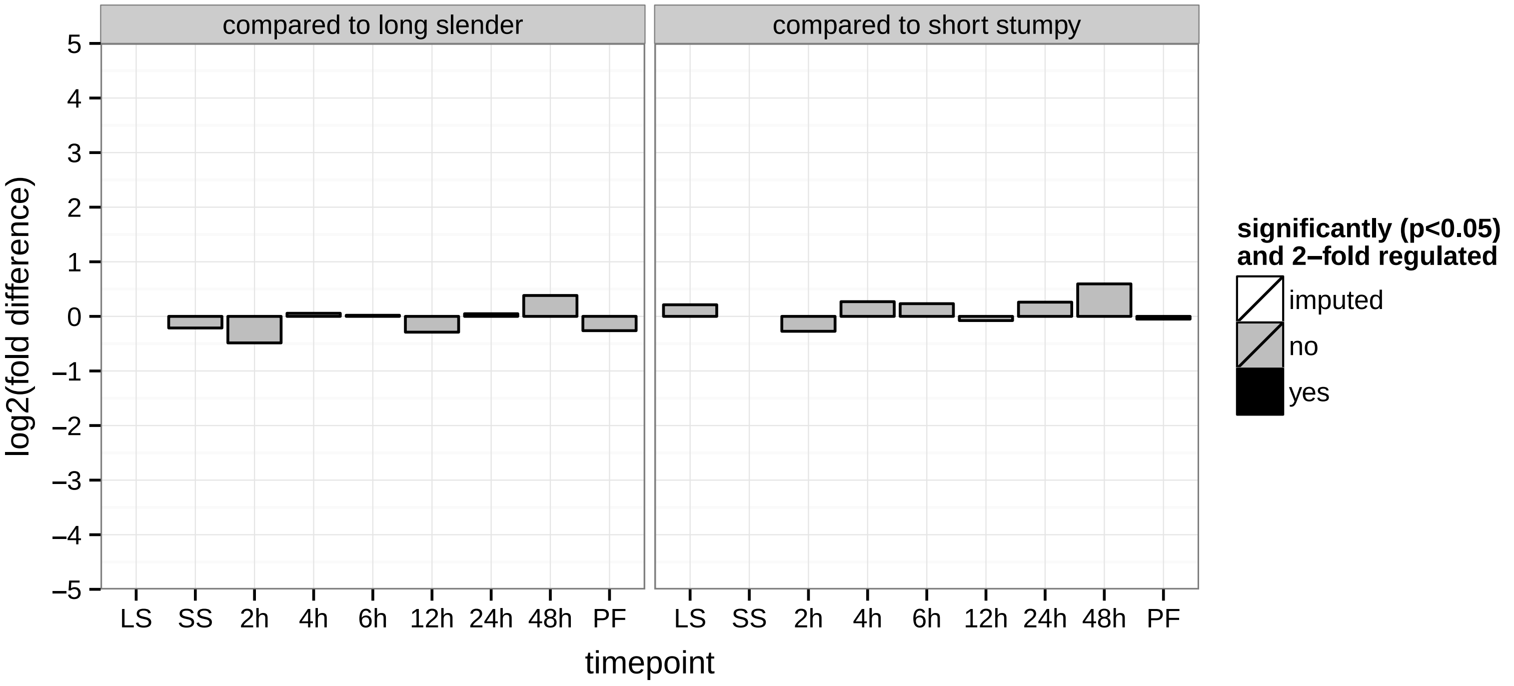
proteasome beta 6 subunit, 20S proteasome beta 6 subunit, putative (BETA6)
Tb927.7.4790;Tb11.v5.0162
AGOF: null, endopeptidase activity, threonine–type endopeptidase activity
AGOC: null, proteasome core complex, proteasome core complex, beta–subunit complex
AGOP: null, ubiquitin–dependent protein catabolic process
PGOF: threonine–type endopeptidase activity
PGOC: proteasome core complex
PGOP: proteolysis involved in cellular protein catabolic process

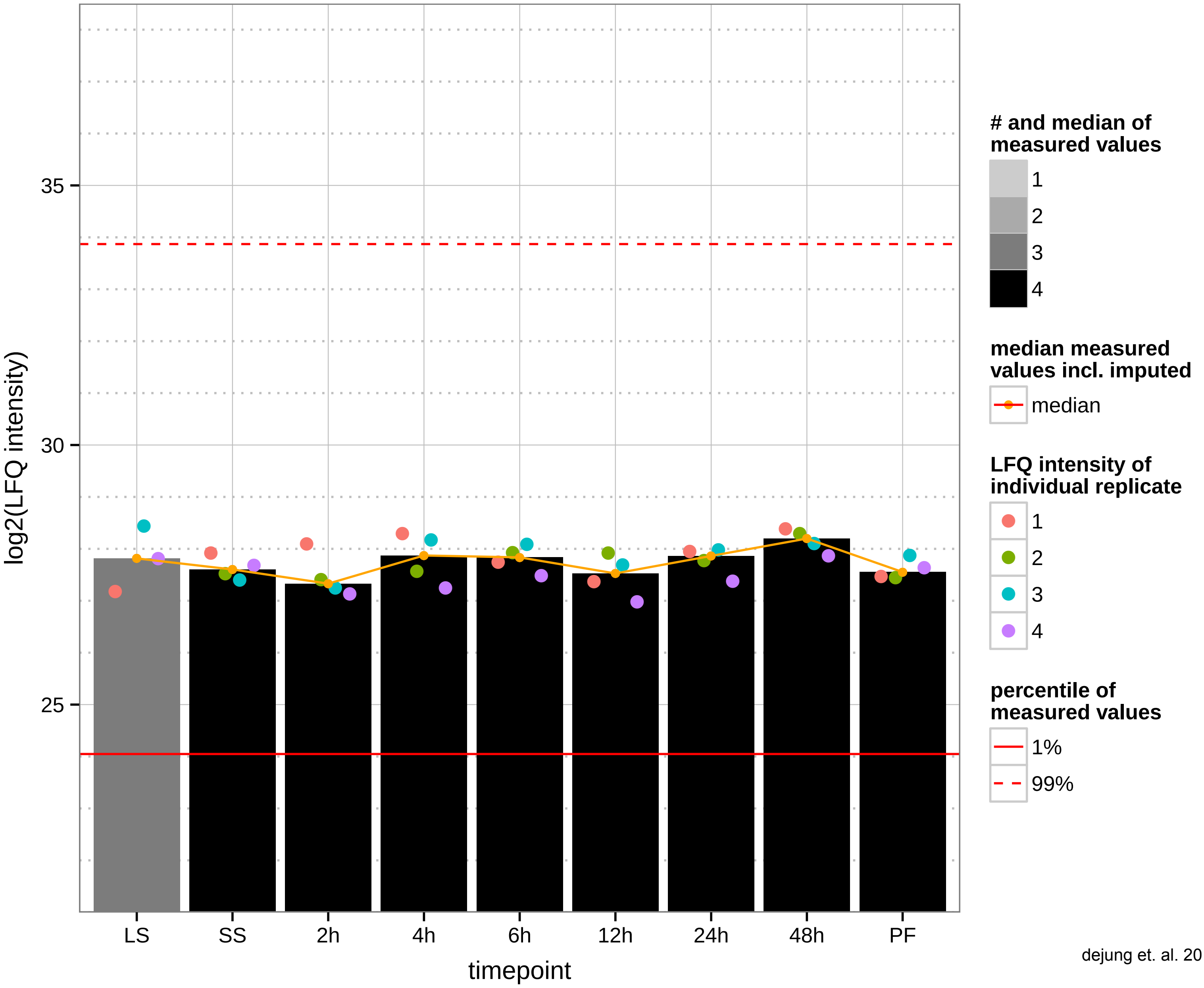




dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.4870;Tb11.v5.0169
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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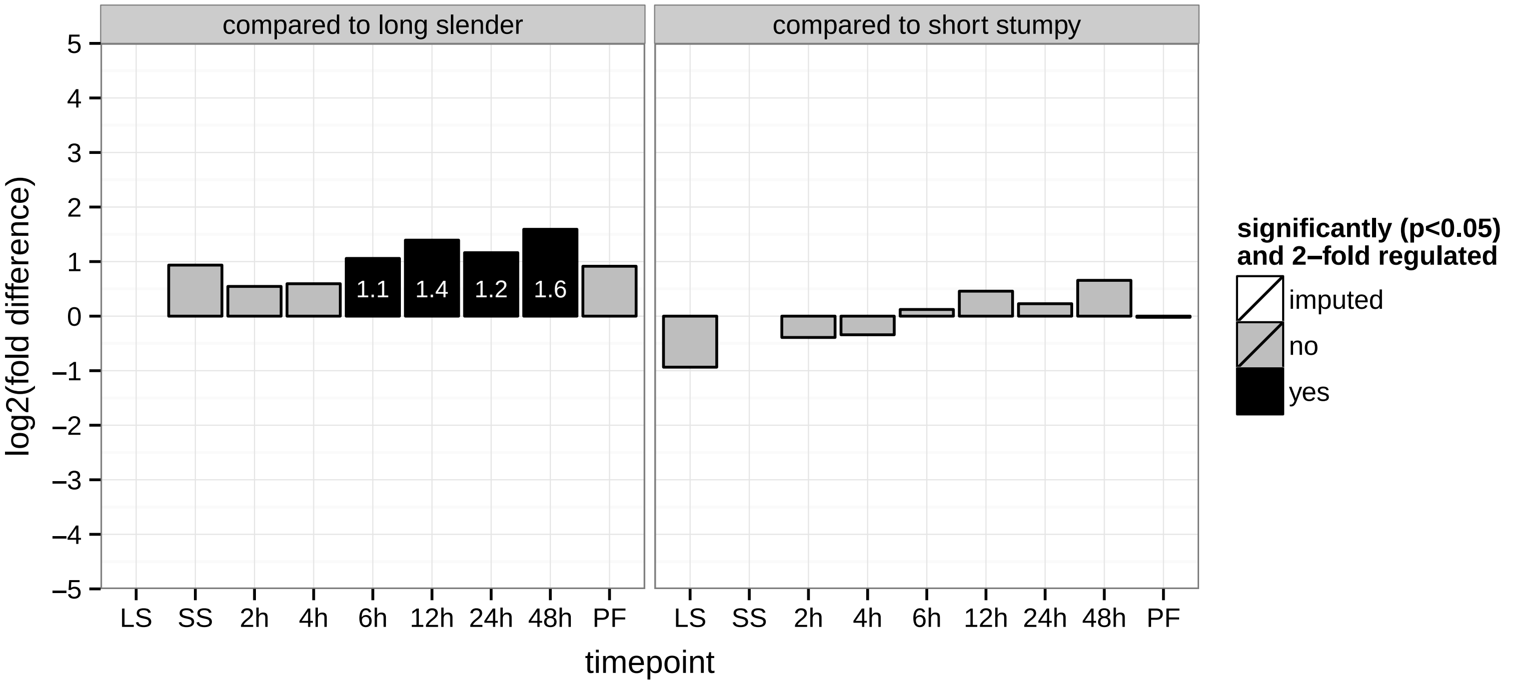
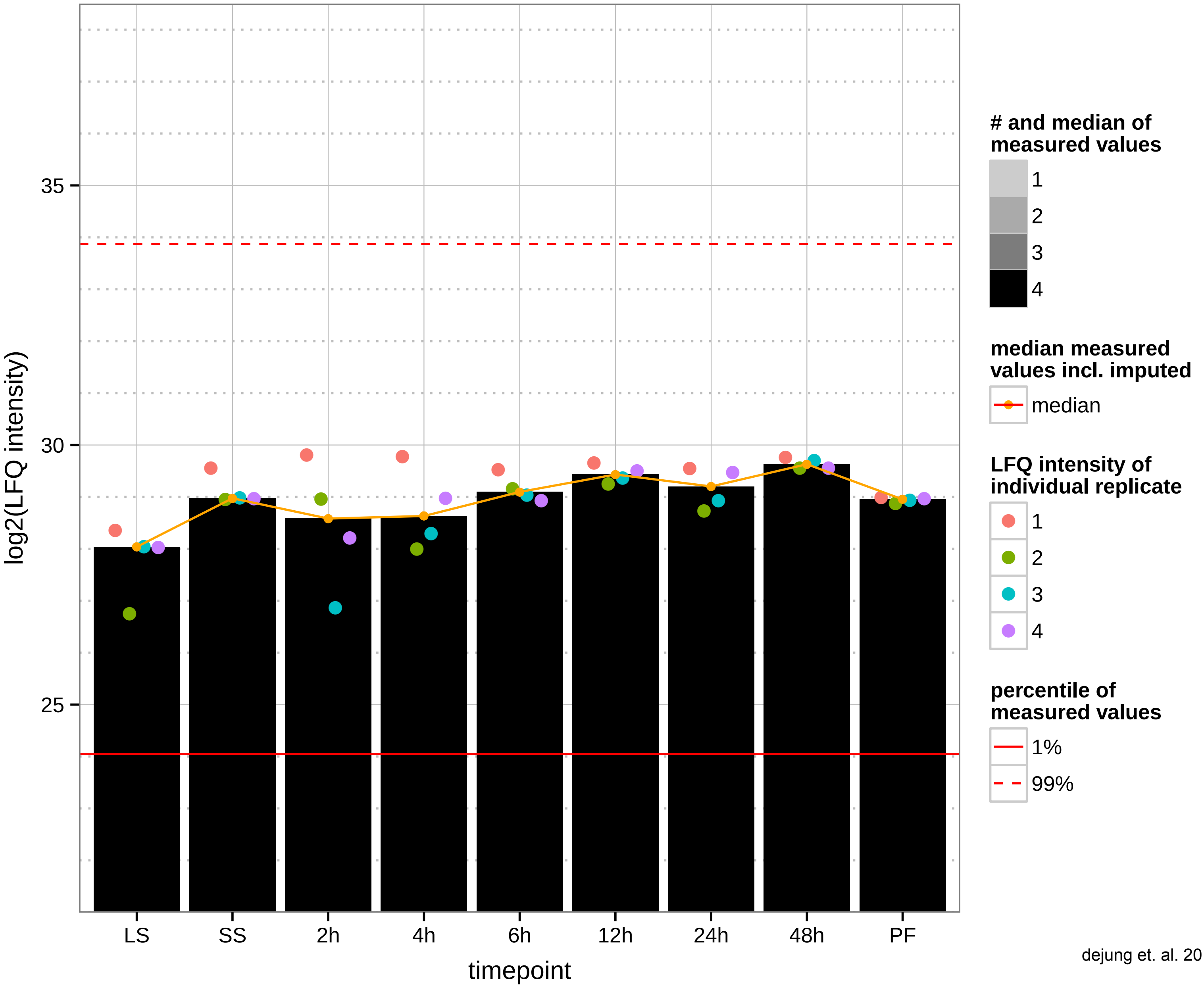
5'–3' exonuclease XRNA, putative, exoribonuclease 1, putative (XRNA)
Tb927.7.4900;Tb11.v5.0171
AGOF: null, exonuclease activity, nucleic acid binding
AGOC: null, intracellular
AGOP: null
PGOF: exonuclease activity, nucleic acid binding
PGOC: intracellular
PGOP: null





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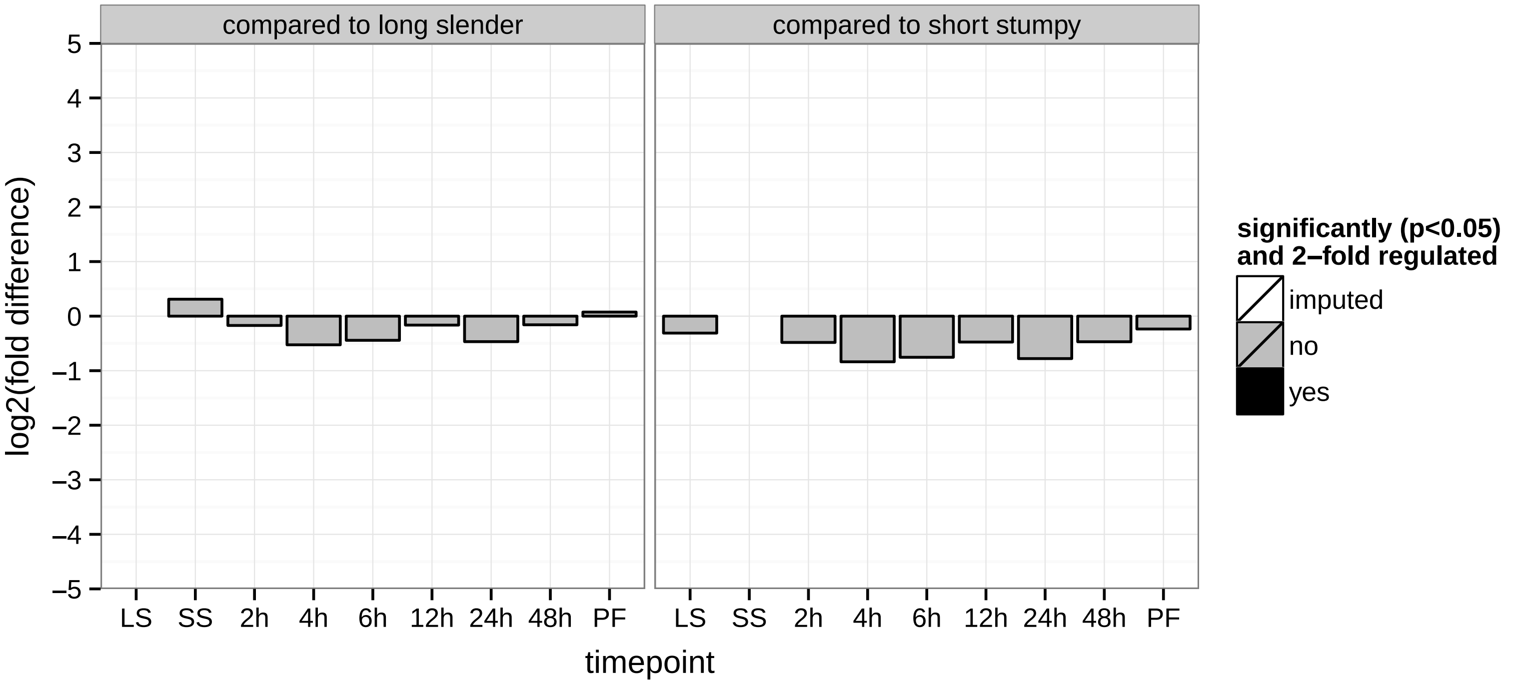
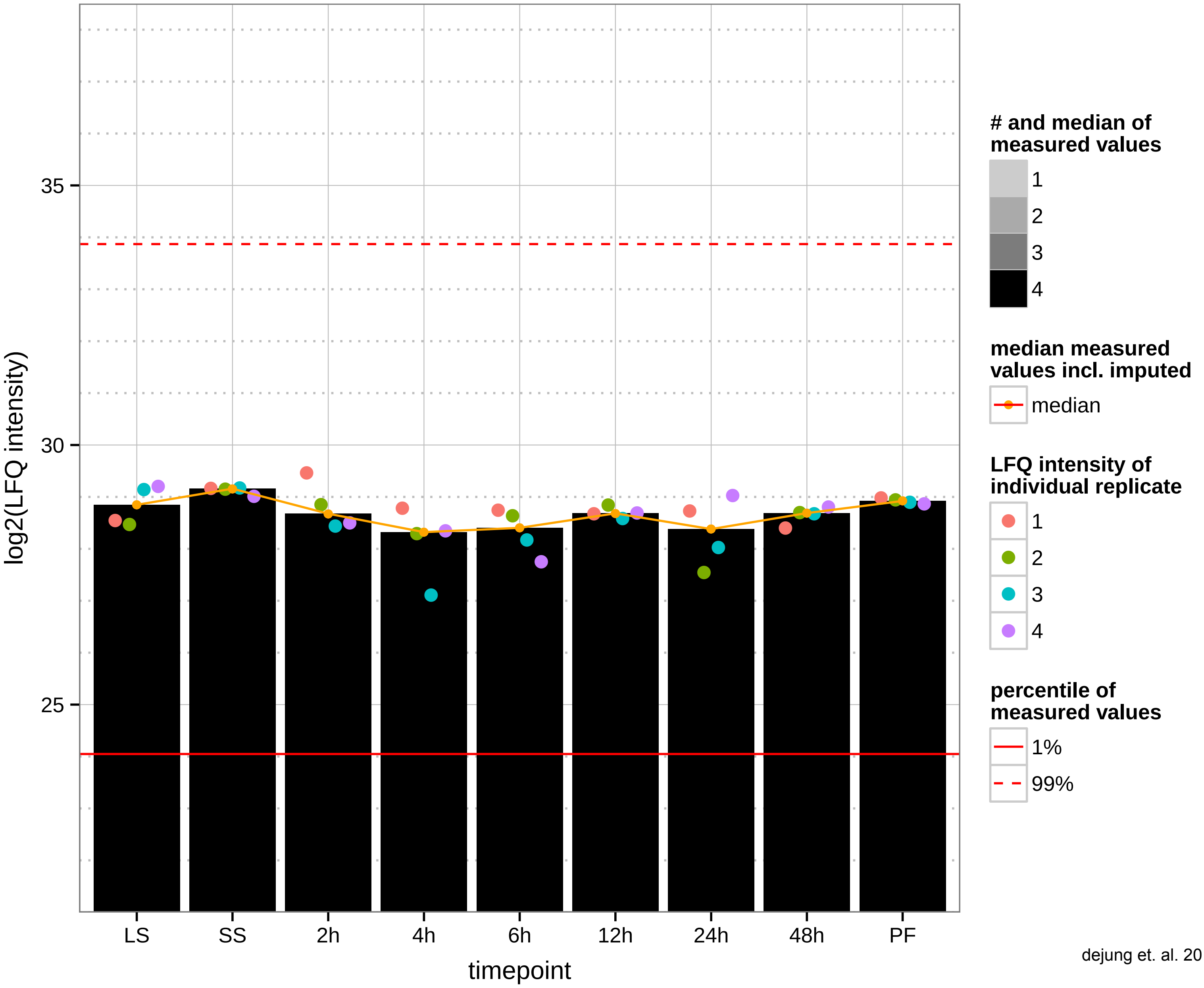
hypothetical protein, conserved
Tb927.7.4910;Tb11.v5.0172
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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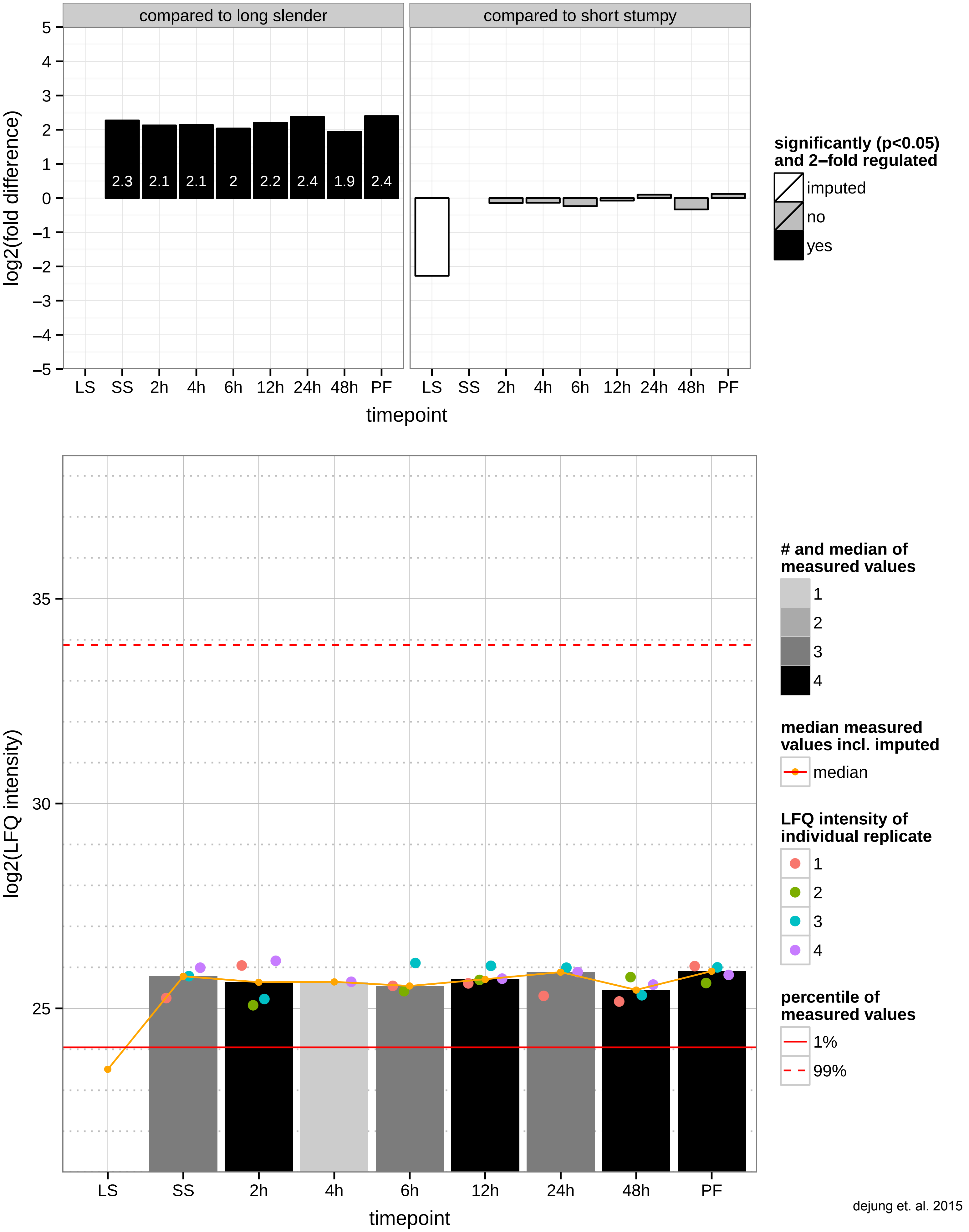
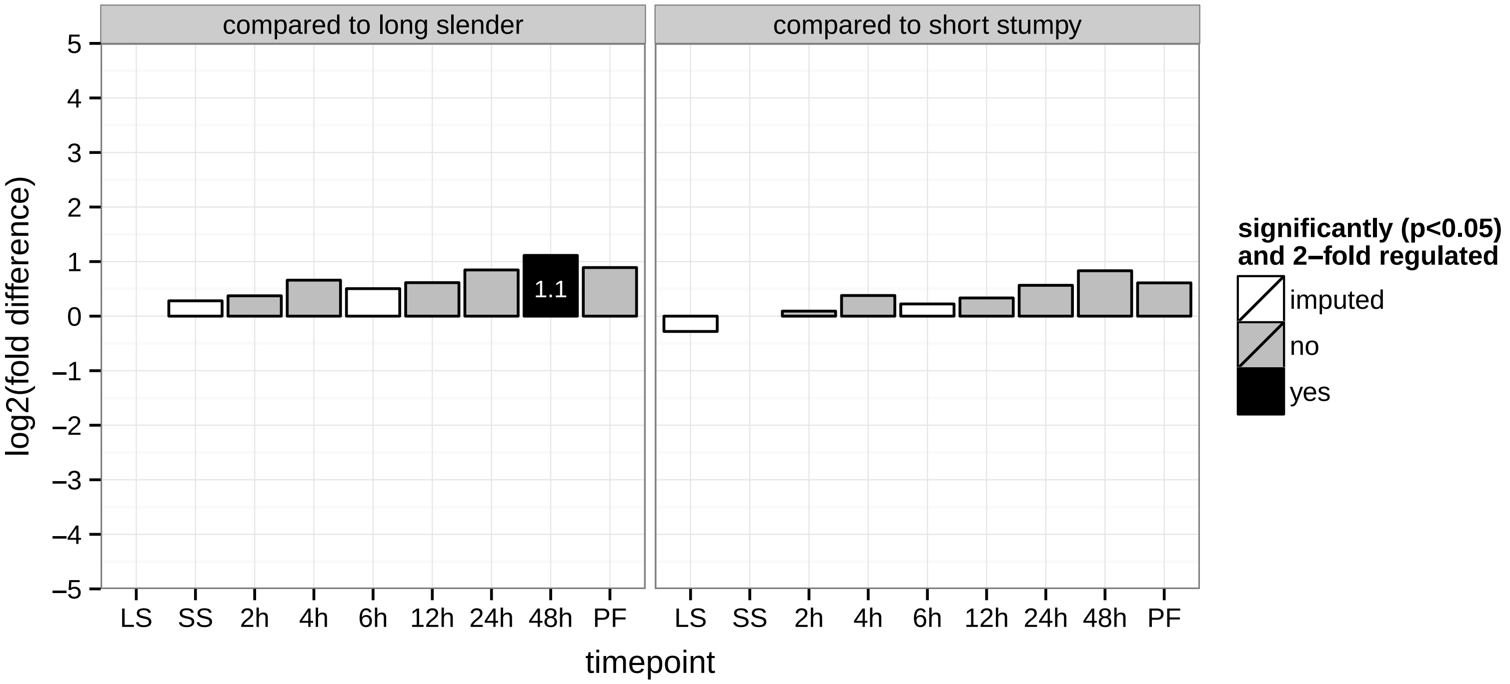
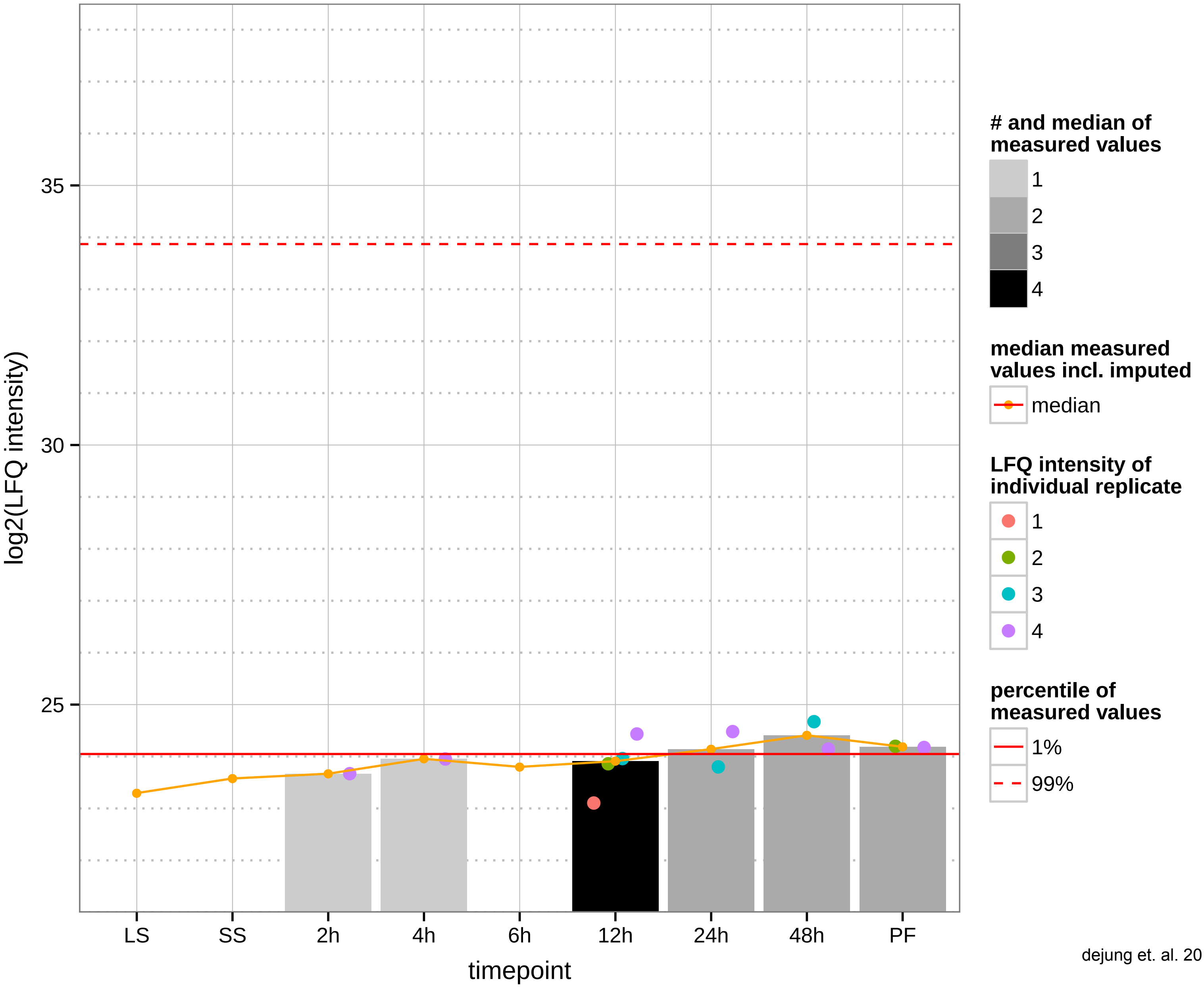
hypothetical protein, conserved
Tb927.7.4960;Tb11.v5.0177
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



hypothetical protein, conserved, zinc finger protein family member, putative (ZC3H23)
Tb927.7.4980;Tb11.v5.0179
AGOF: null, RNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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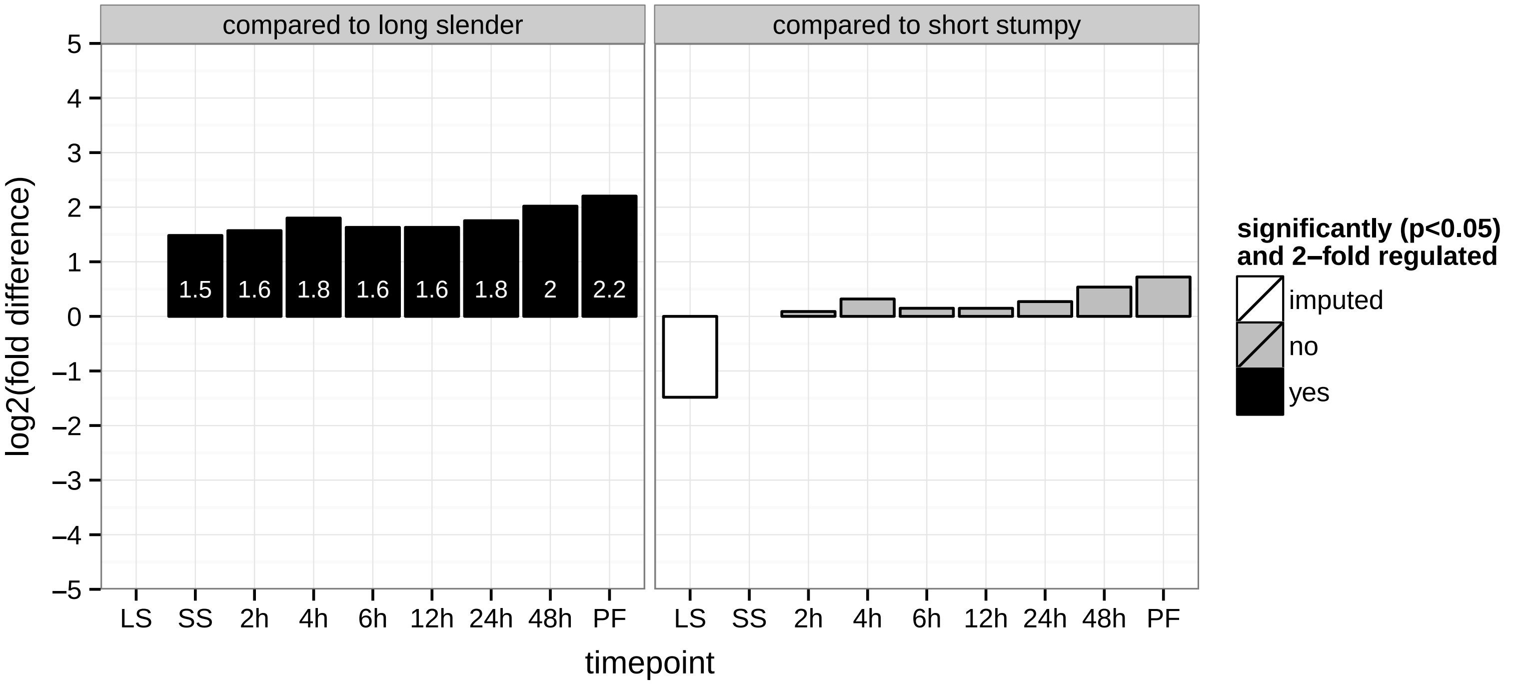
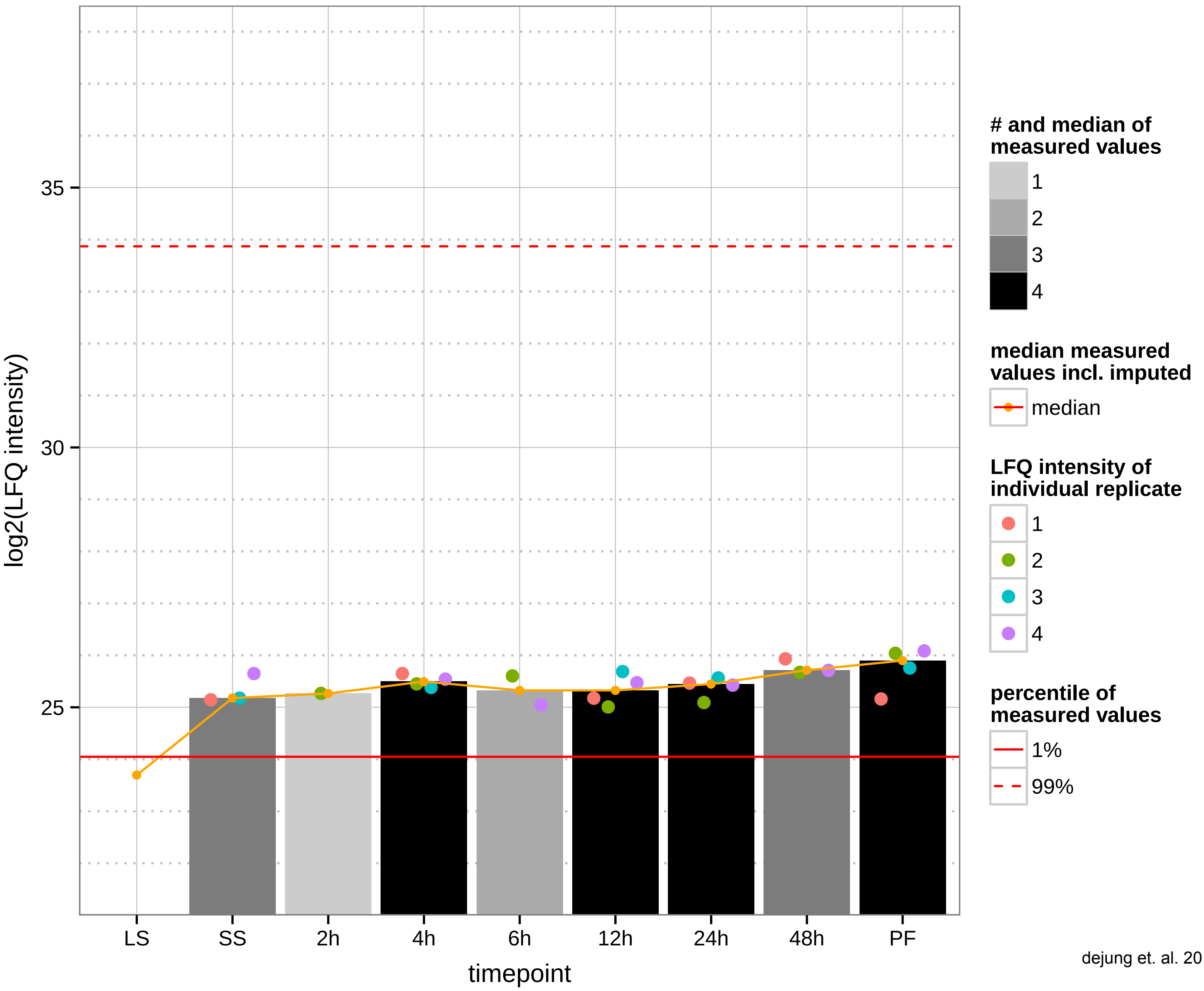
hypothetical protein, conserved
Tb927.7.4990;Tb11.v5.0180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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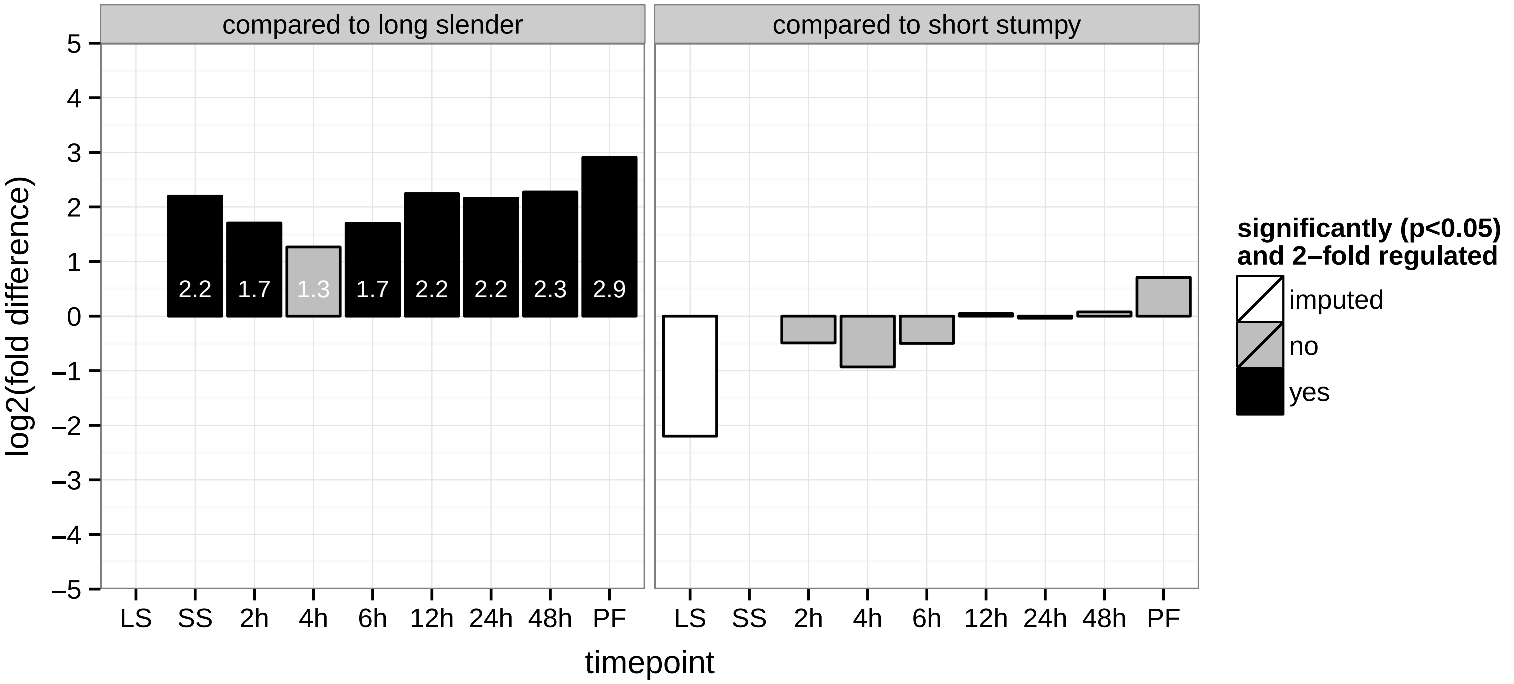
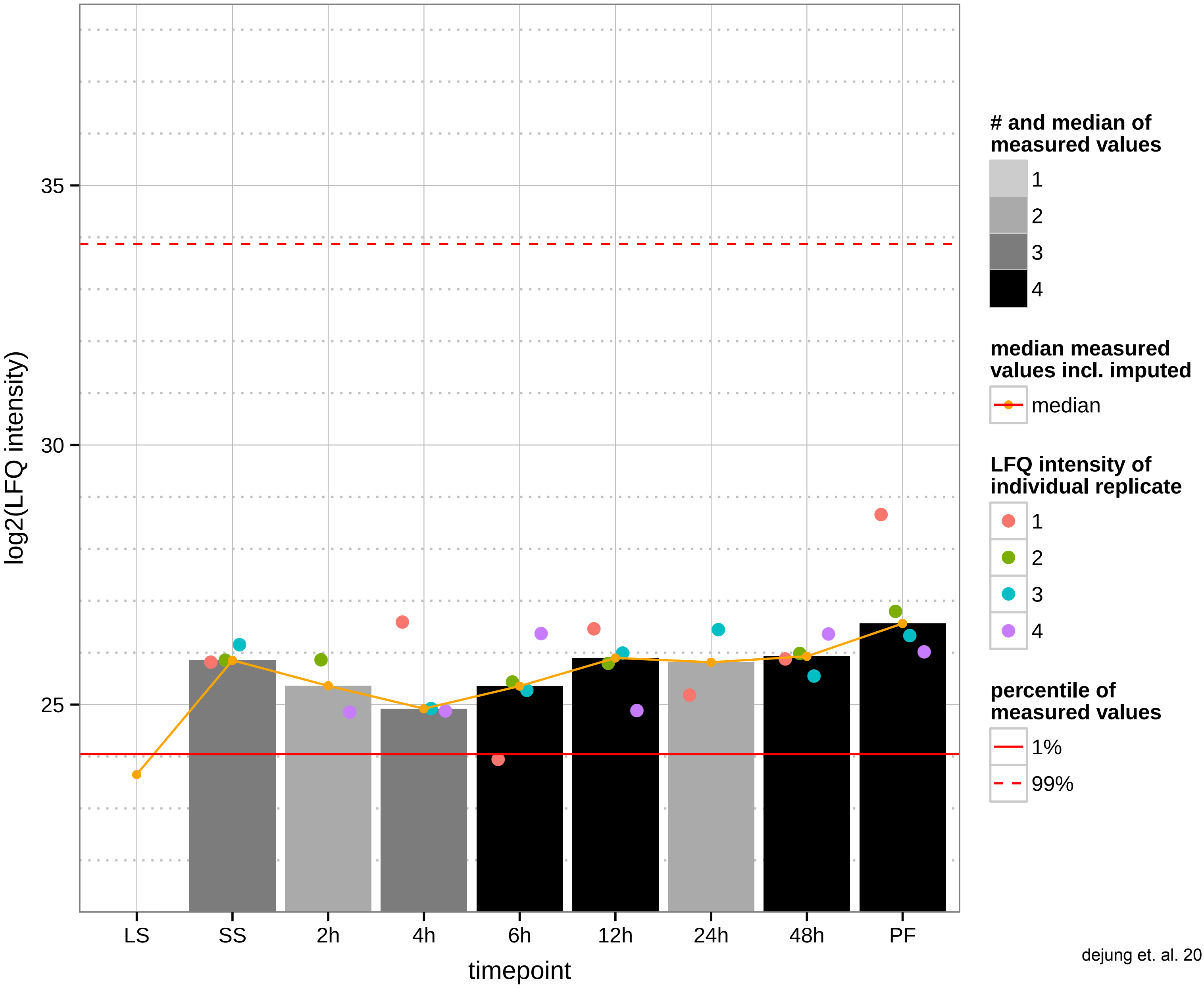
hypothetical protein, conserved
Tb927.7.5030;Tb11.v5.0183
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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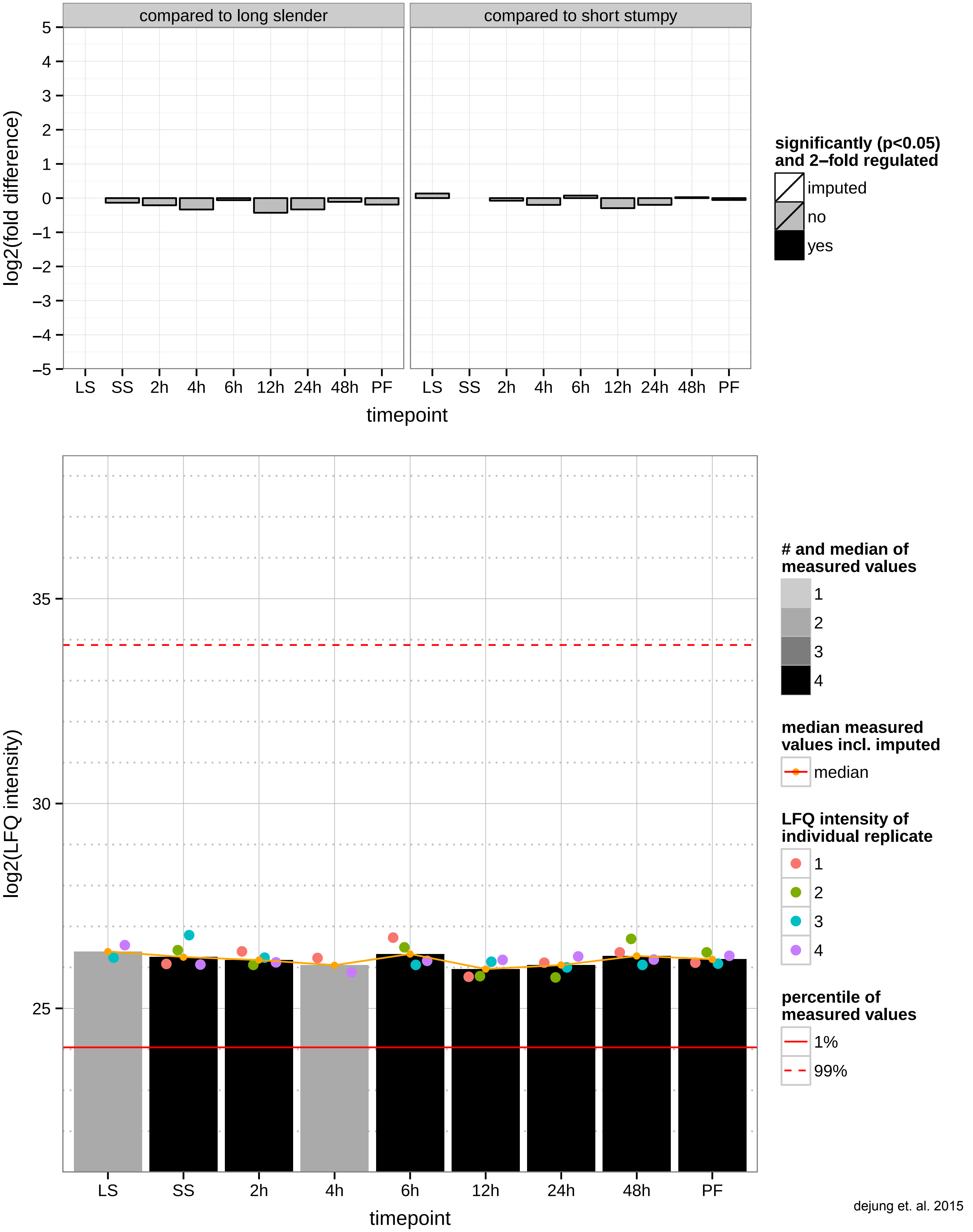
hypothetical protein, conserved
Tb927.7.5050;Tb11.v5.0185
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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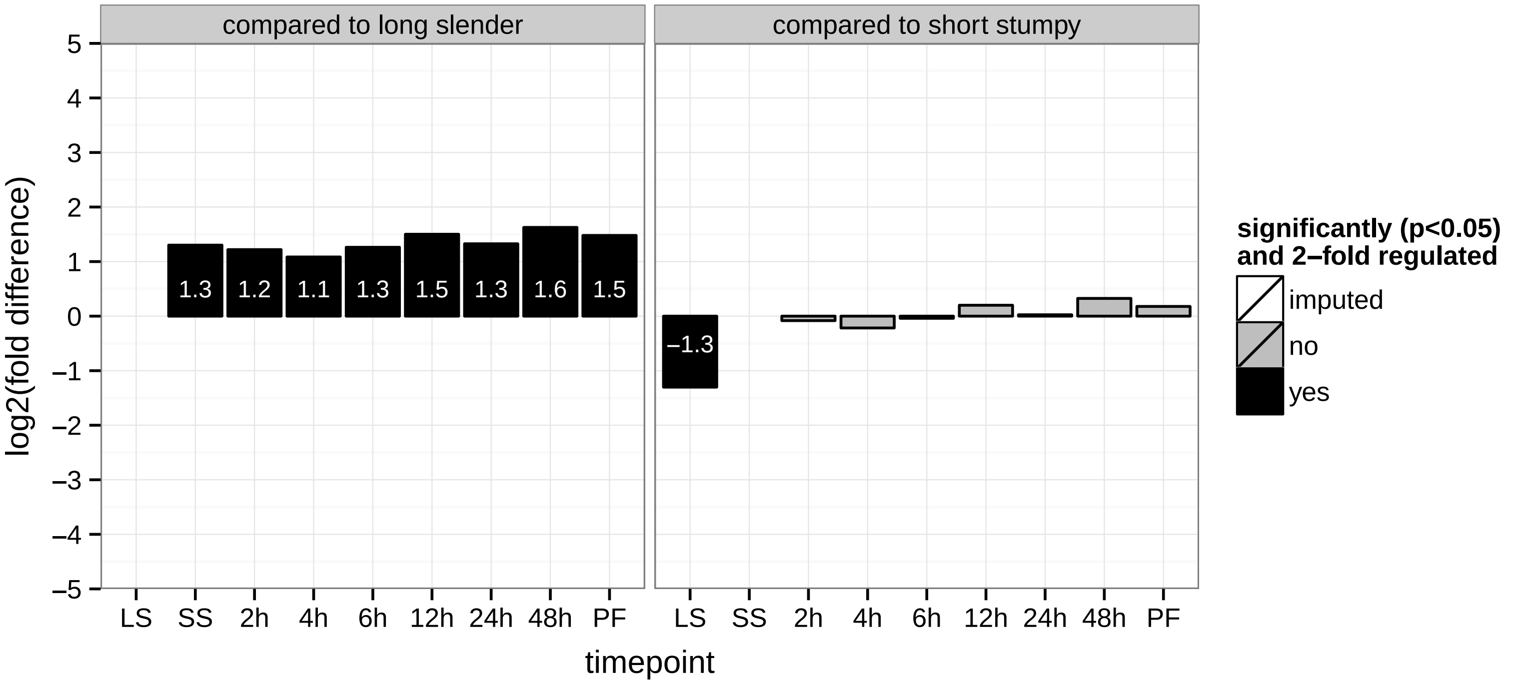
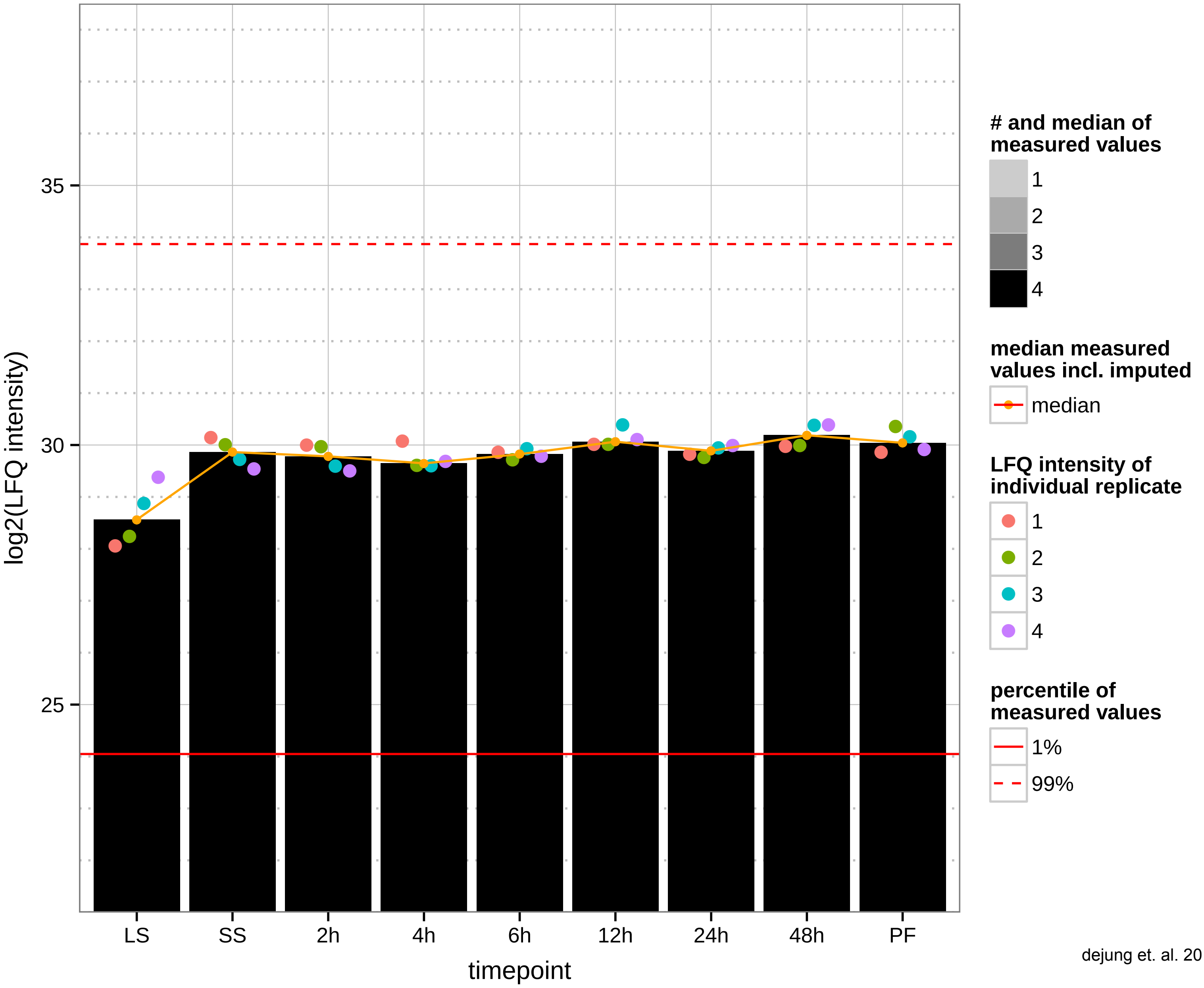
protein kinase, putative, (OTHER) NEK family, HsNEK1–like
Tb927.10.5950;Tb11.v5.0190
AGOF: null, ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null, modulation of development of symbiont involved in interaction with host, protein phosphorylation, quorum sensing
PGOF: ATP binding, phospholipid binding, protein binding, protein kinase activity, transferase activity, transferring phosphorus
PGOC: null
PGOP: protein phosphorylation





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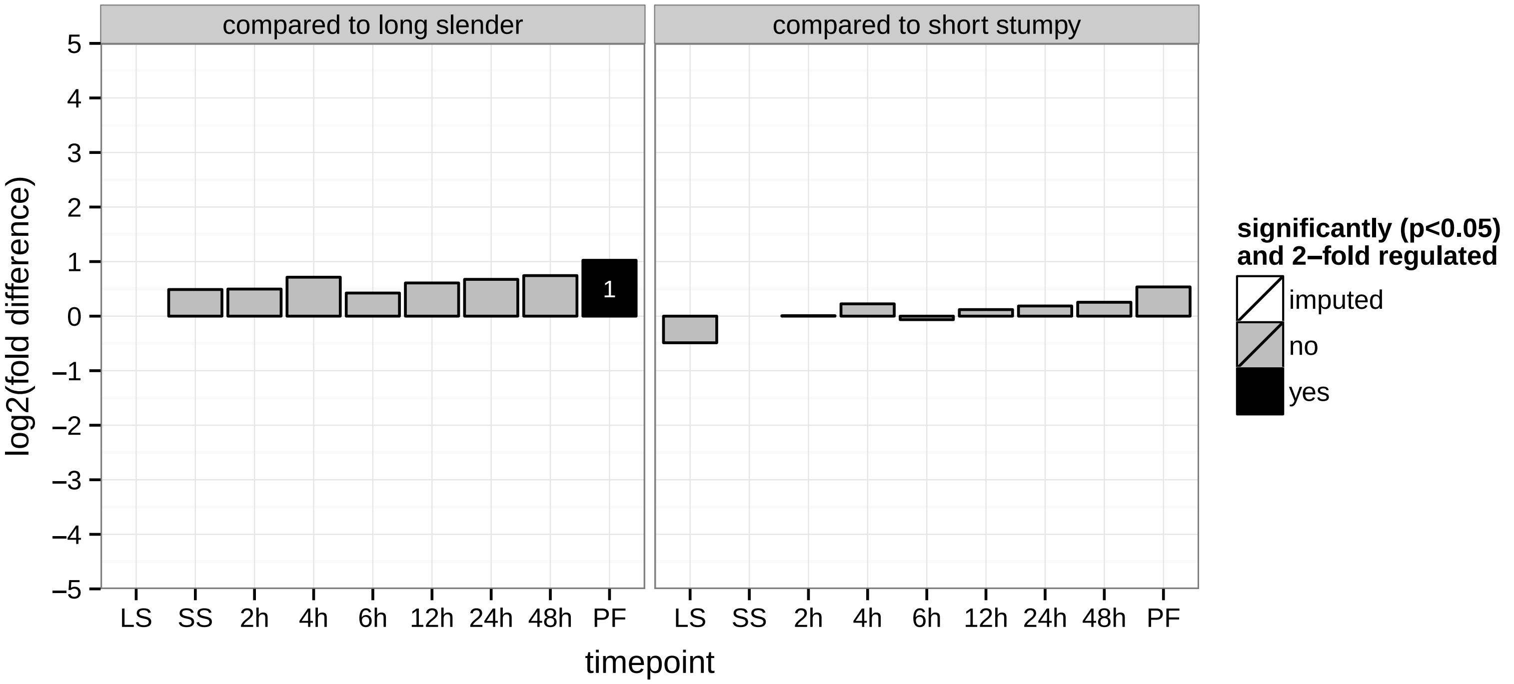
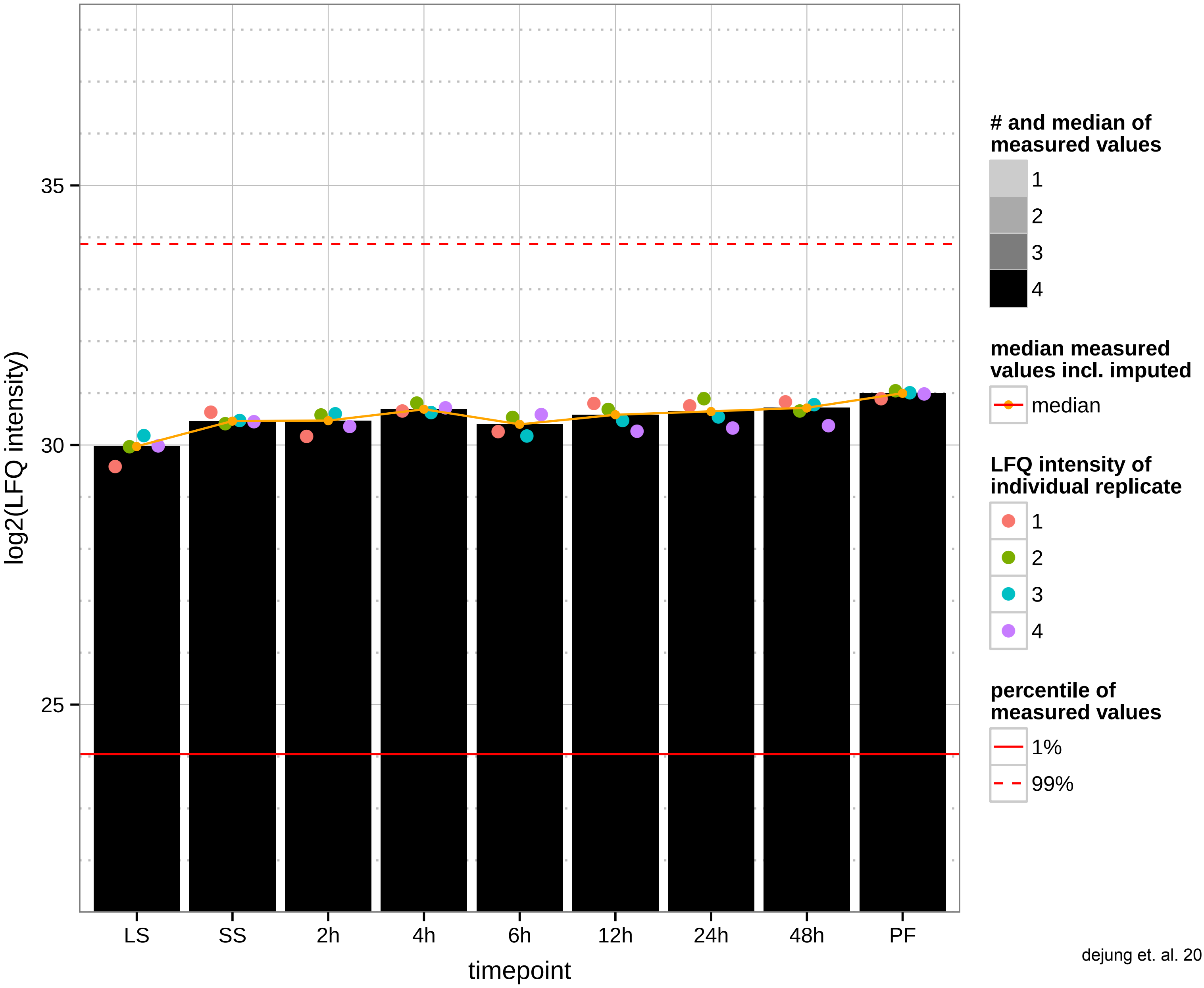
hypothetical protein, conserved, proteasome alpha 1 subunit, putative, 20S proteasome subunit alpha–6, (putative) (TbPSA6)
Tb11.v5.0196;Tb927.10.6030
AGOF: null, endopeptidase activity, threonine–type endopeptidase activity
AGOC: null, mitochondrion, proteasome core complex
AGOP: null, ubiquitin–dependent protein catabolic process
PGOF: endopeptidase activity, threonine–type endopeptidase activity
PGOC: proteasome core complex, proteasome core complex, alpha–subunit complex
PGOP: proteolysis involved in cellular protein catabolic process, ubiquitin–dependent protein catabolic process





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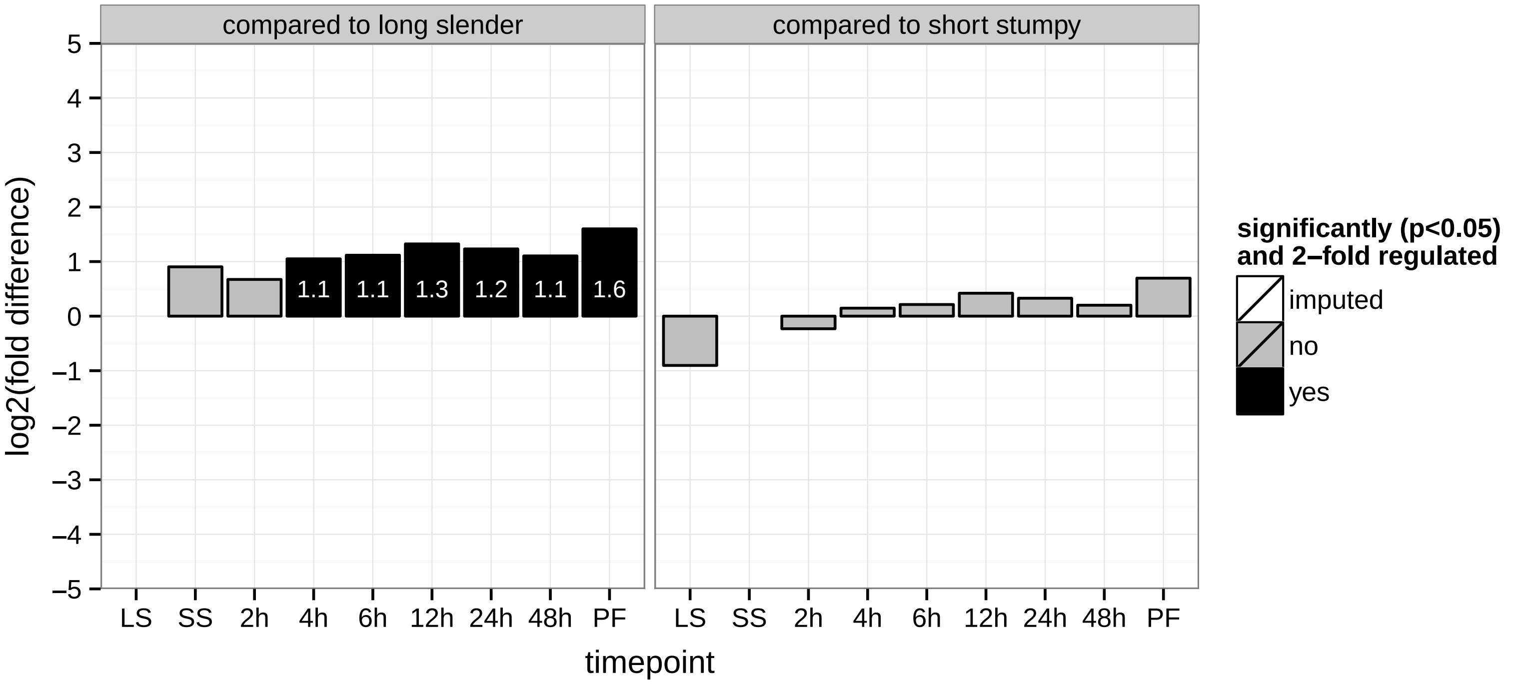
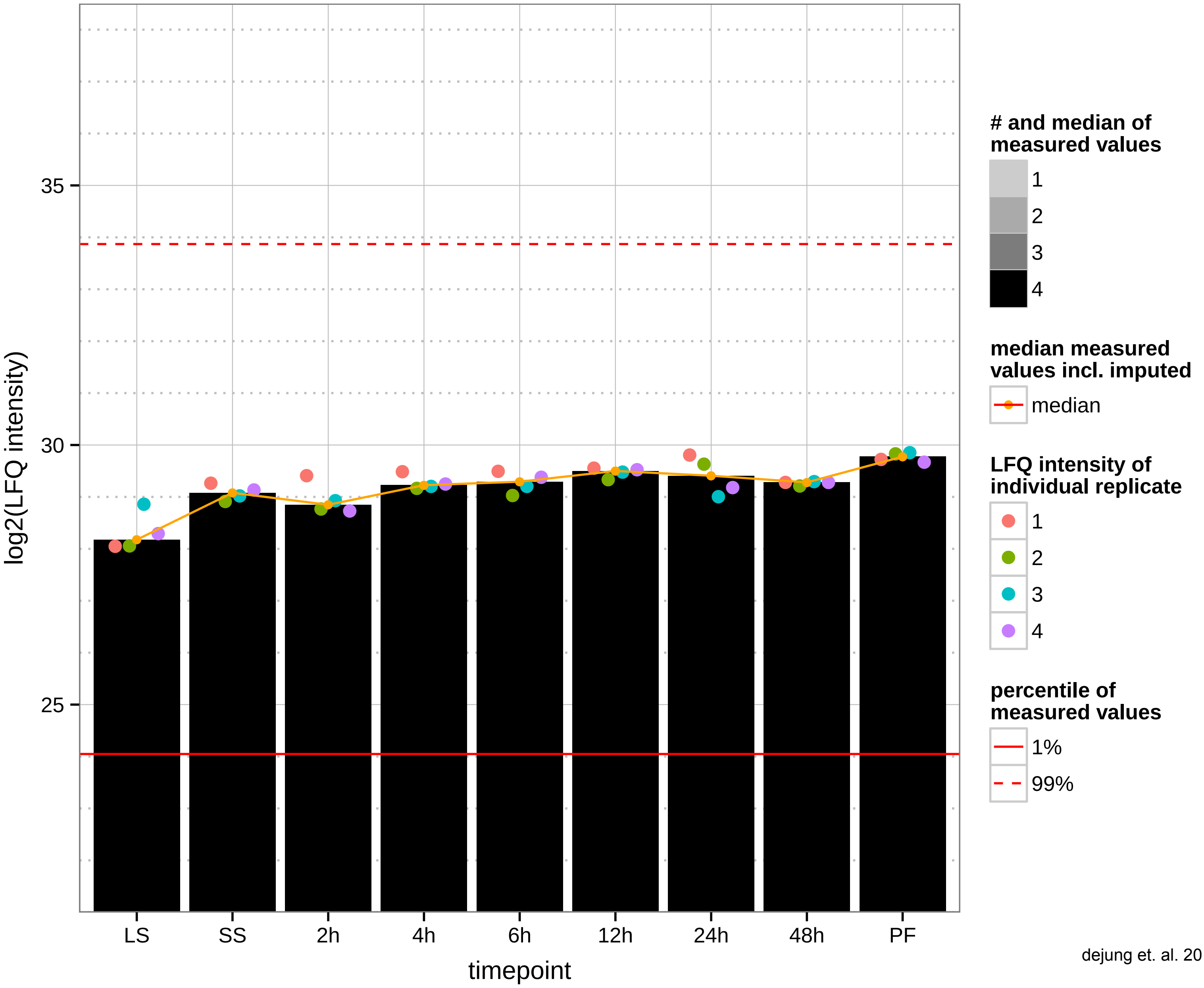
proteasome beta 5 subunit, putative, proteasome beta 5 subunit (PRCE)
Tb927.10.6080;Tb11.v5.0200
AGOF: null, endopeptidase activity, threonine–type endopeptidase activity
AGOC: null, proteasome core complex, proteasome core complex, beta–subunit complex
AGOP: null, ubiquitin–dependent protein catabolic process
PGOF: threonine–type endopeptidase activity
PGOC: proteasome core complex
PGOP: proteolysis involved in cellular protein catabolic process





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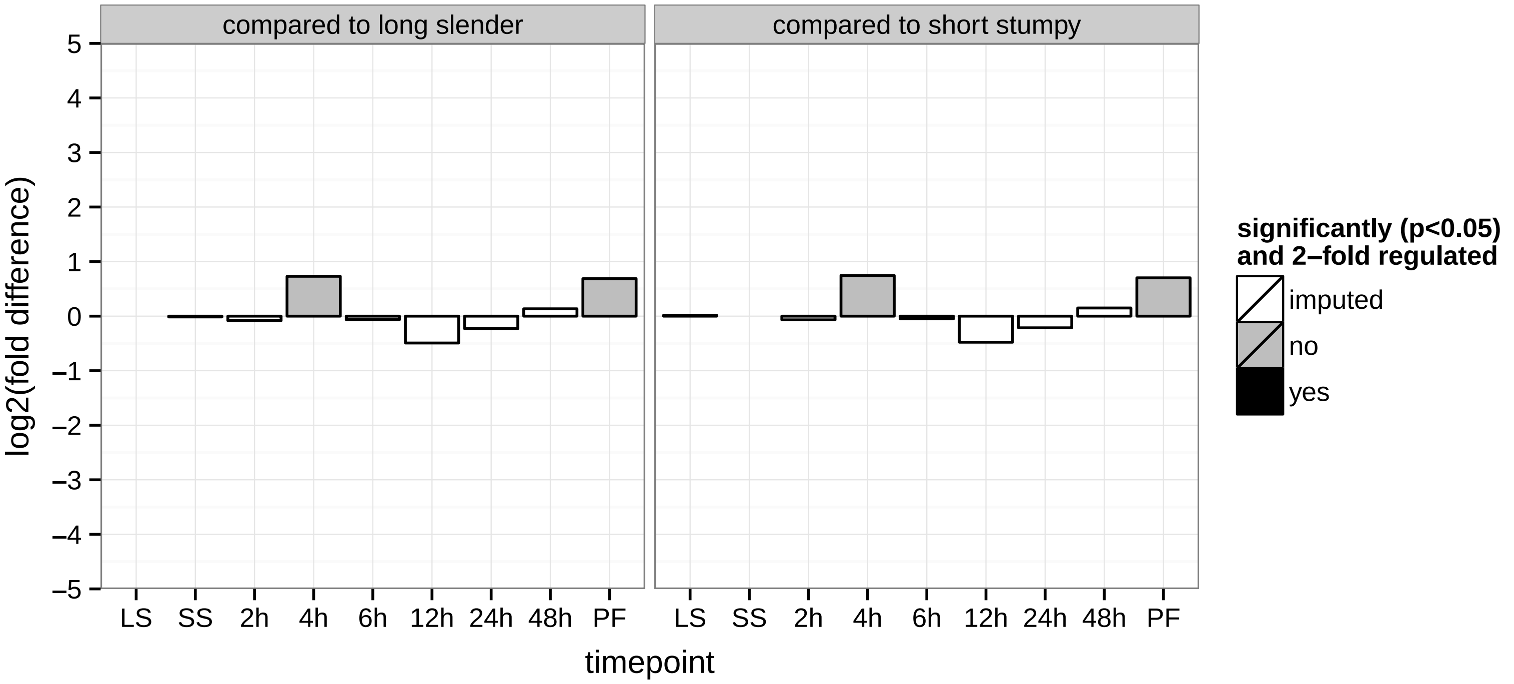
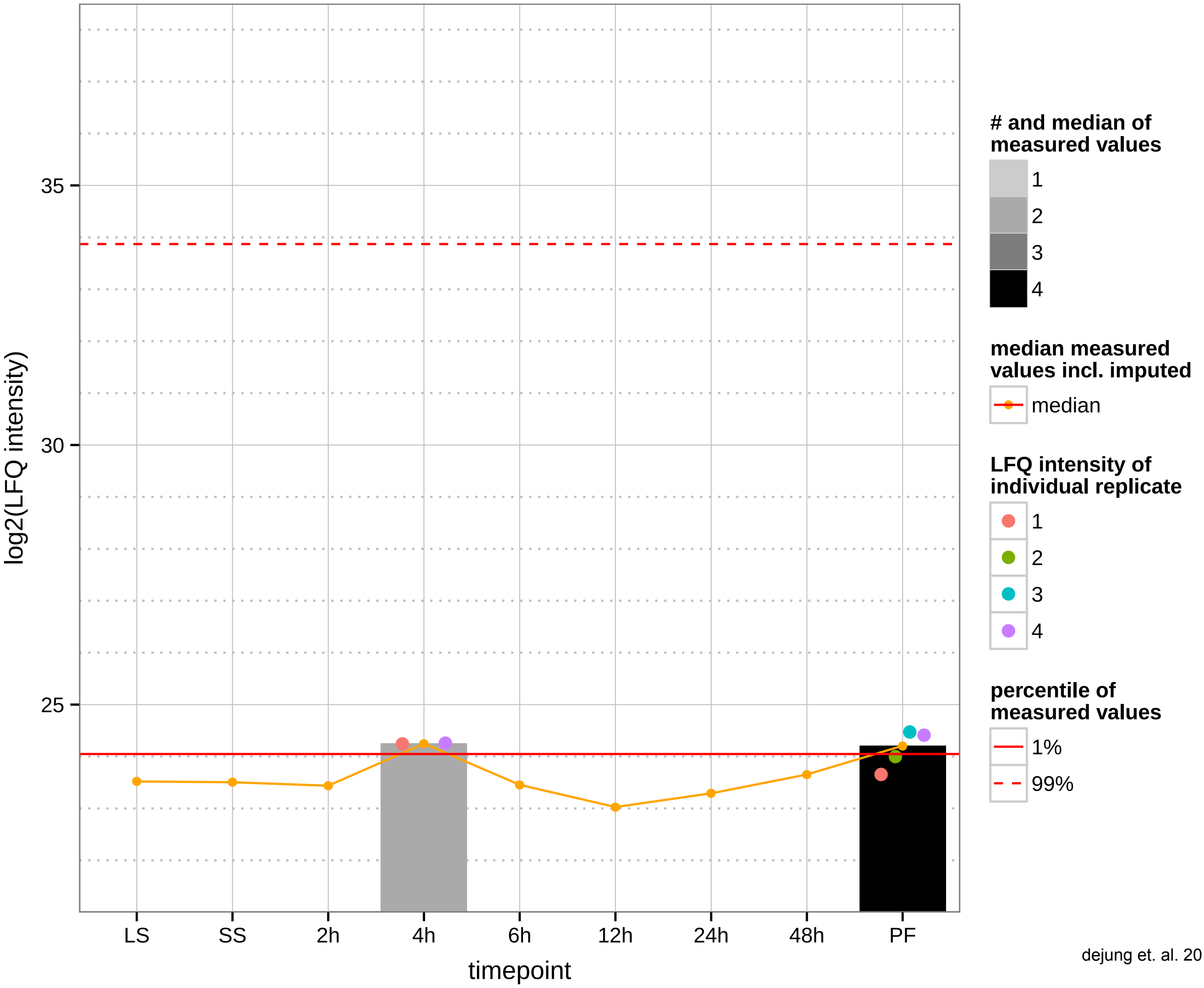
tRNA pseudouridine synthase A, putative
Tb11.v5.0201;Tb927.10.6090
AGOF: null, RNA binding, pseudouridine synthase activity
AGOC: null
AGOP: null, pseudouridine synthesis
PGOF: RNA binding, pseudouridine synthase activity
PGOC: null
PGOP: RNA modification, pseudouridine synthesis





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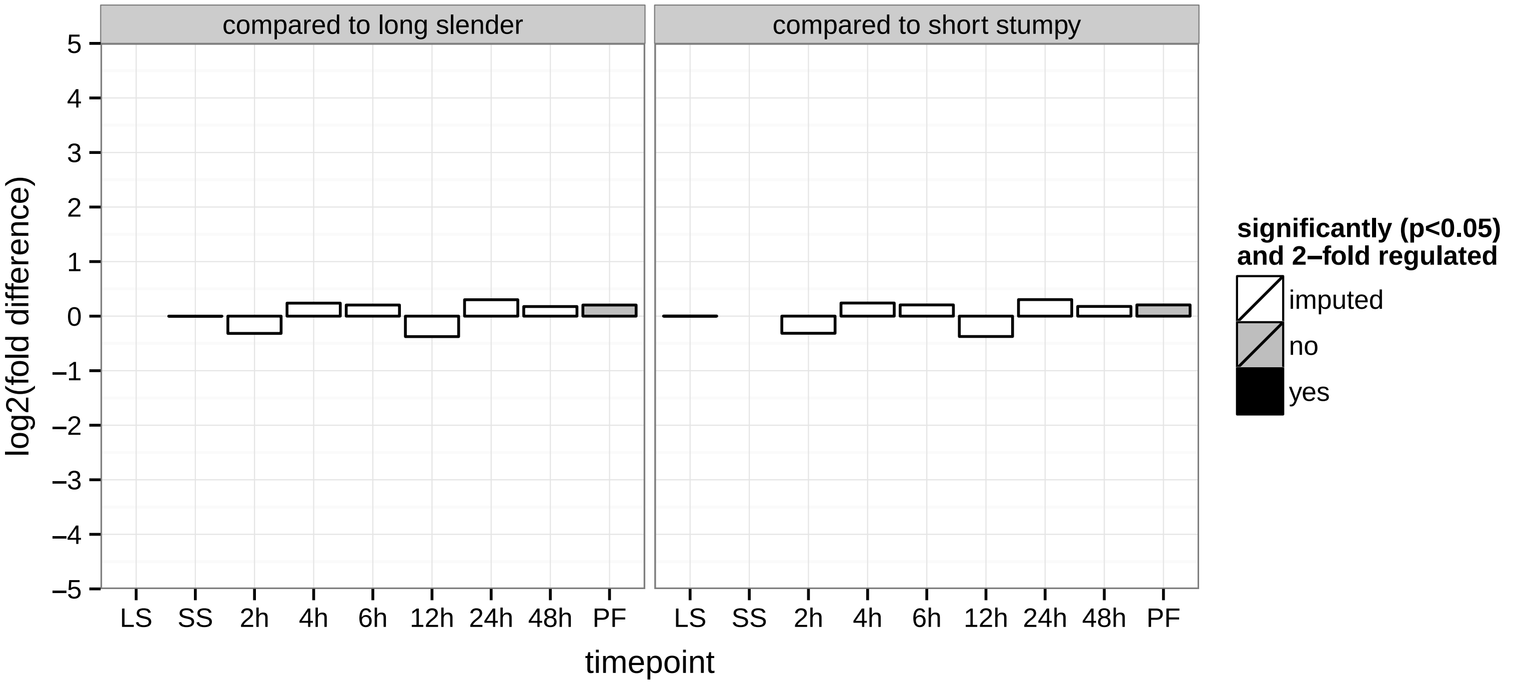
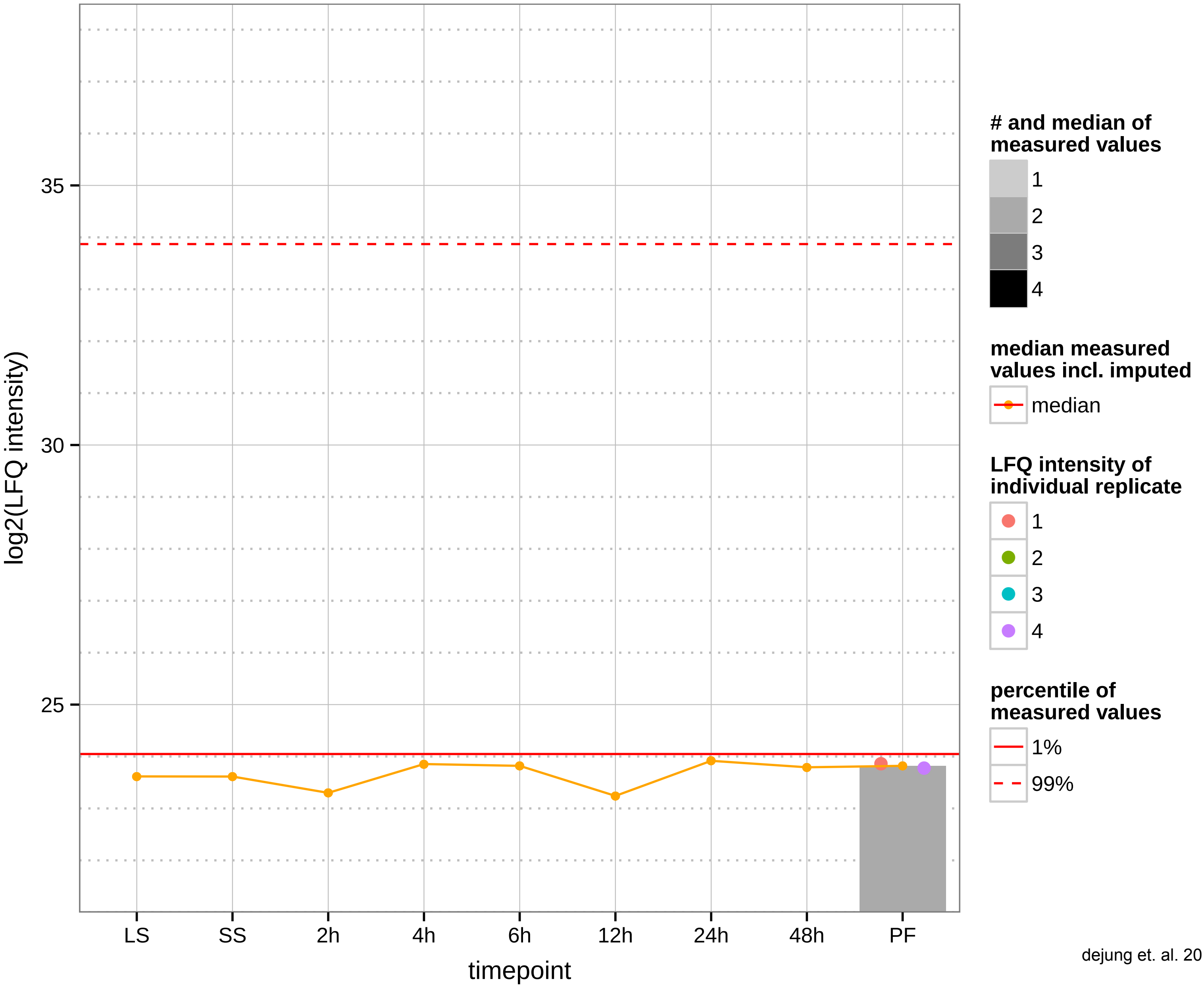
iron/ascorbate oxidoreductase family protein, putative, thymine−7−hydroxylase, putative (TLP5), 2−oxoglutarate (2OG) and Fe
Tb927.5.300b;Tb927.5.300;Tb11.v5.0215
AGOF: null, ferrous iron binding, oxidoreductase activity, iron ion binding
AGOC: null
AGOP: null, metabolic process
PGOF: oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular o
PGOC: null
PGOP: oxidation−reduction process





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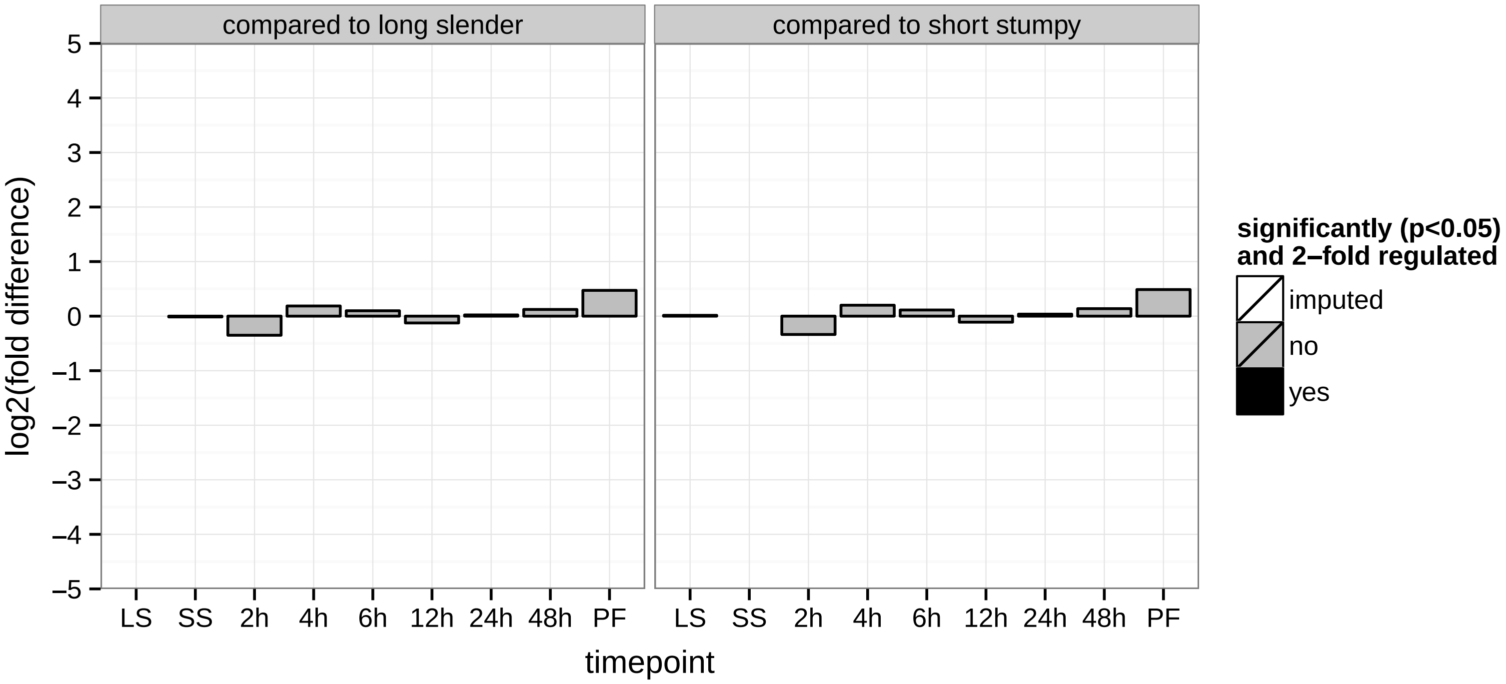
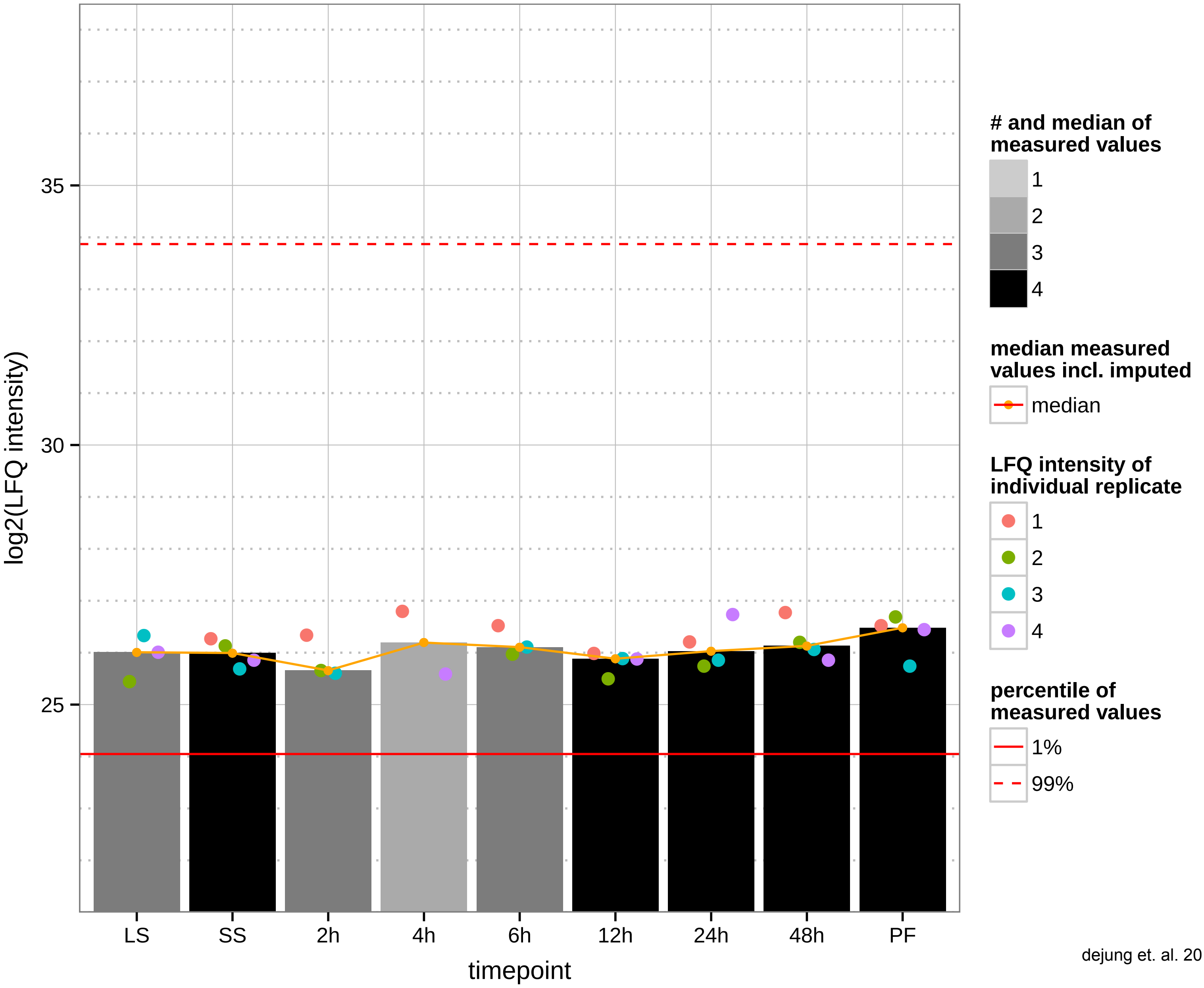
hypothetical protein, conserved
Tb927.5.500;Tb11.v5.0218
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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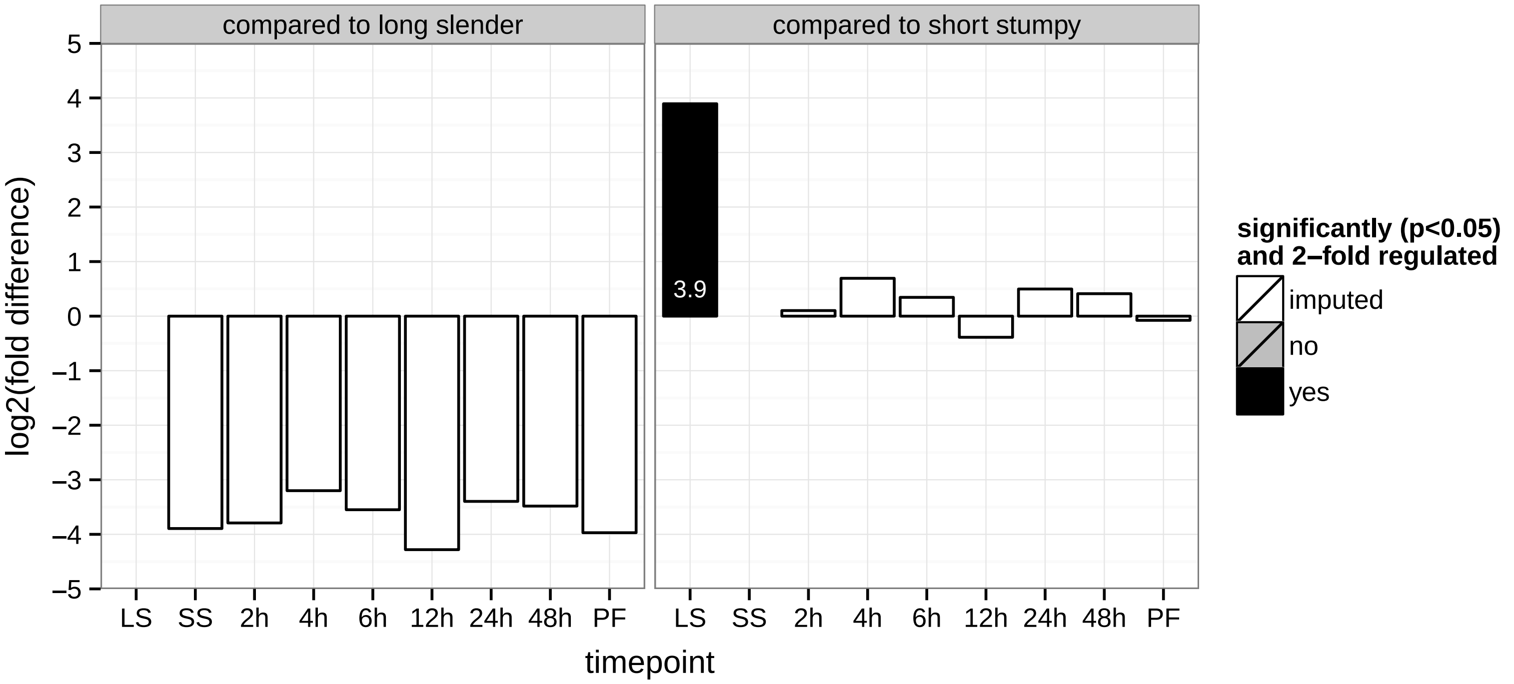
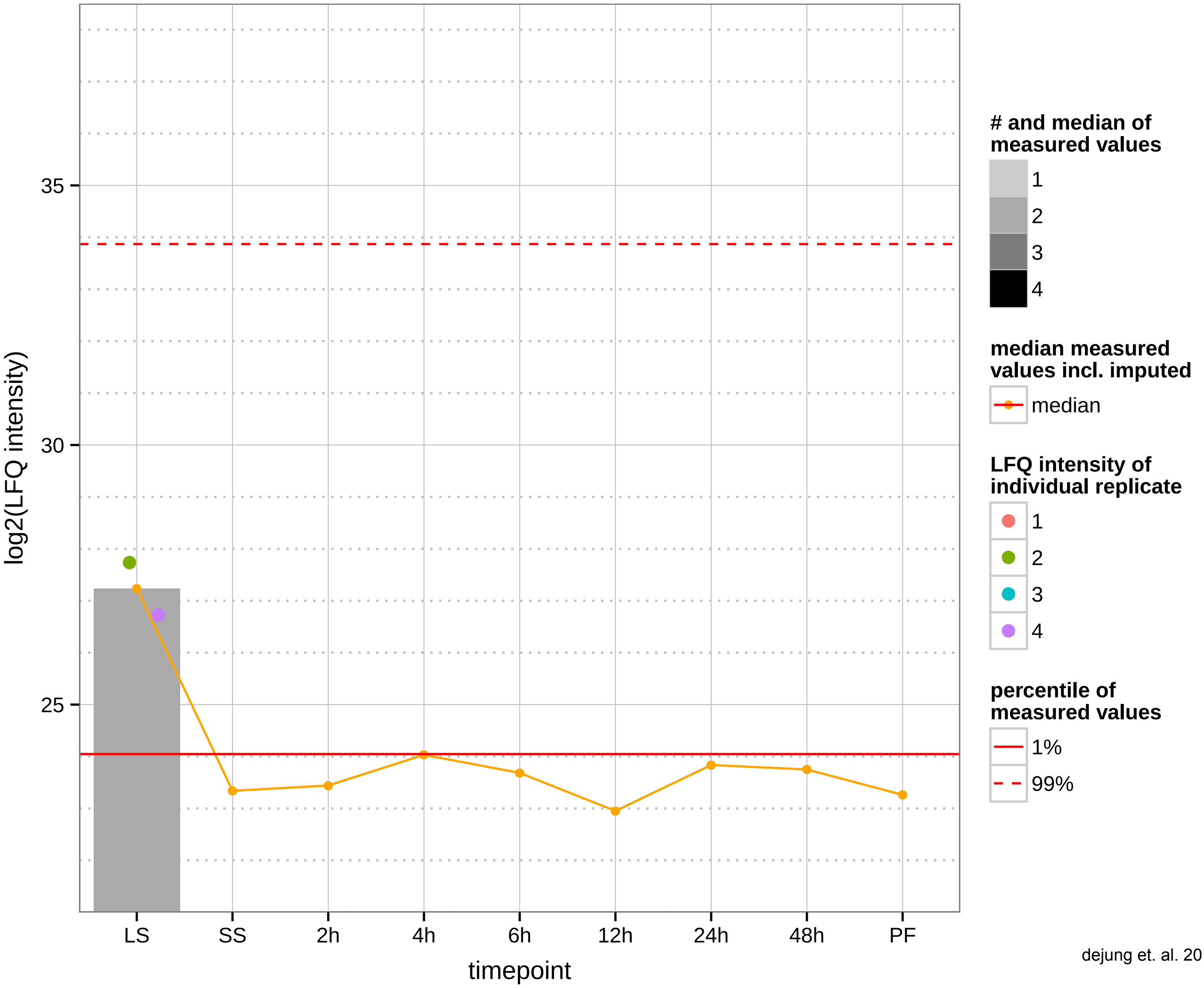
75 kDa invariant surface glycoprotein, putative, putative (ISG75)
Tb927.5.400;Tb11.v5.0227;Tb927.5.350;Tb11.v5.0421
AGOF: null
AGOC: null, plasma membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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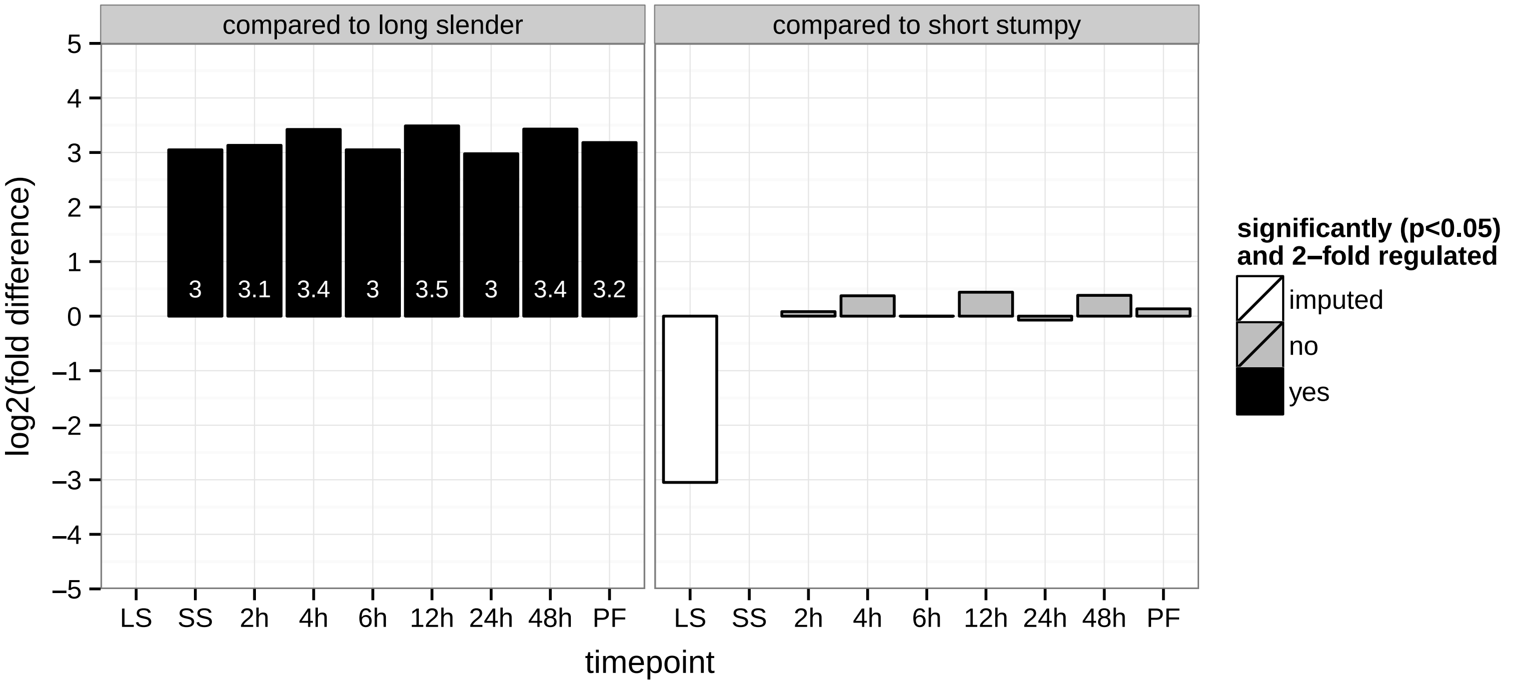
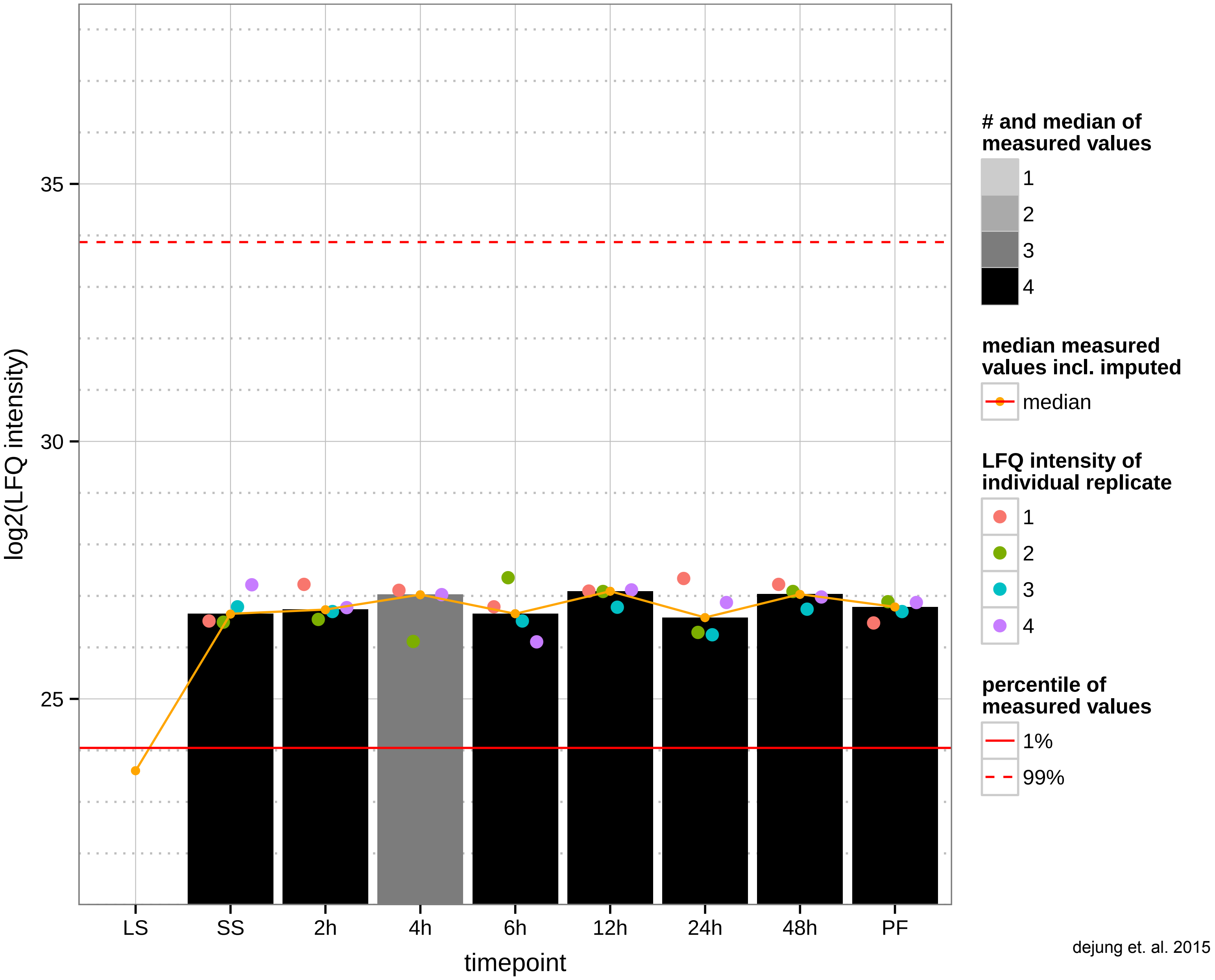
protein kinase, putative, SNF1–related protein kinases
Tb927.10.5310;Tb11.v5.0245
AGOF: null, ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null, protein phosphorylation
PGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity, transferring phosphoru
PGOC: null
PGOP: protein phosphorylation





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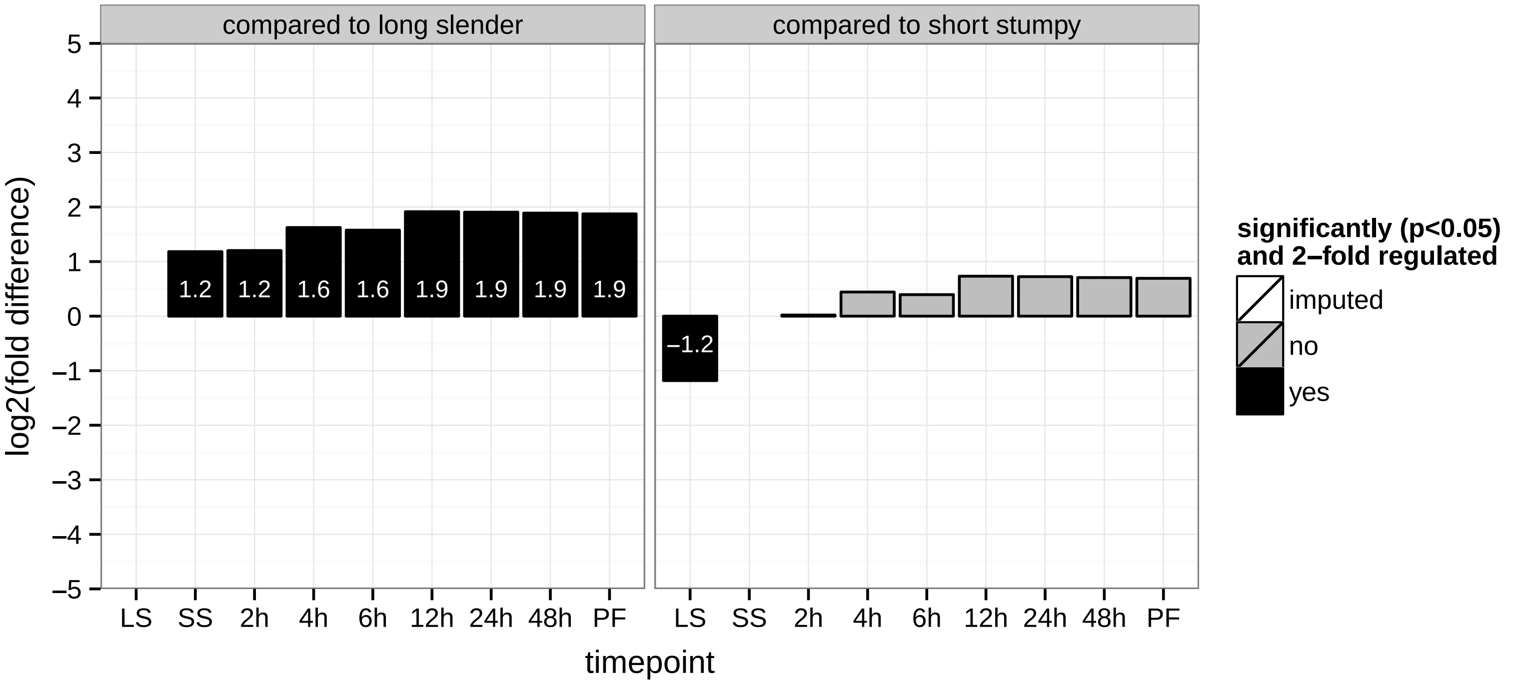
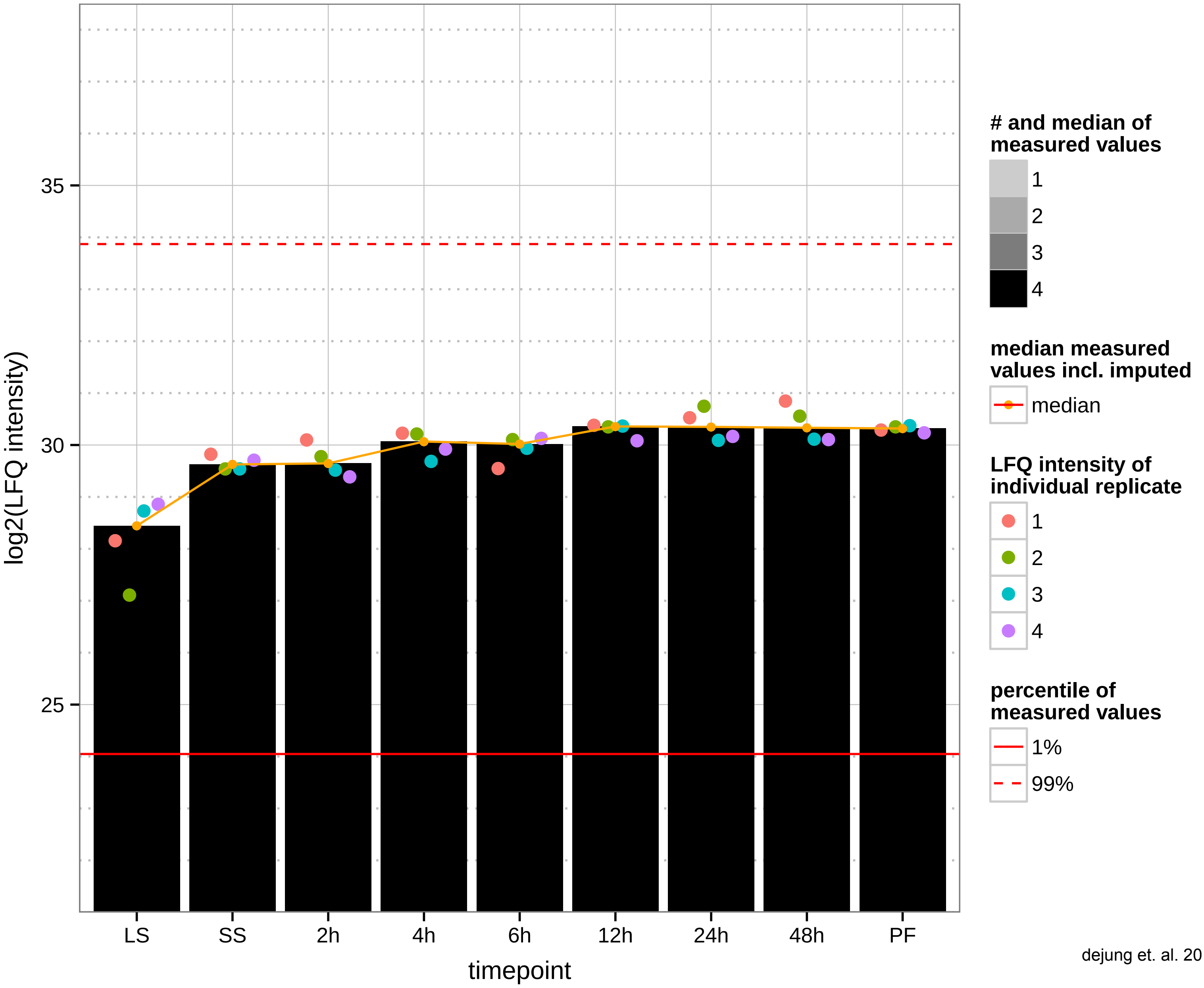
eukaryotic translation initiation factor 6, putative, eukaryotic translation initiation factor 6 (eIF−6)
Tb927.10.5300;Tb11.v5.0246
AGOF: null, ribosome binding
AGOC: null
AGOP: null, mature ribosome assembly
PGOF: ribosome binding
PGOC: null
PGOP: mature ribosome assembly





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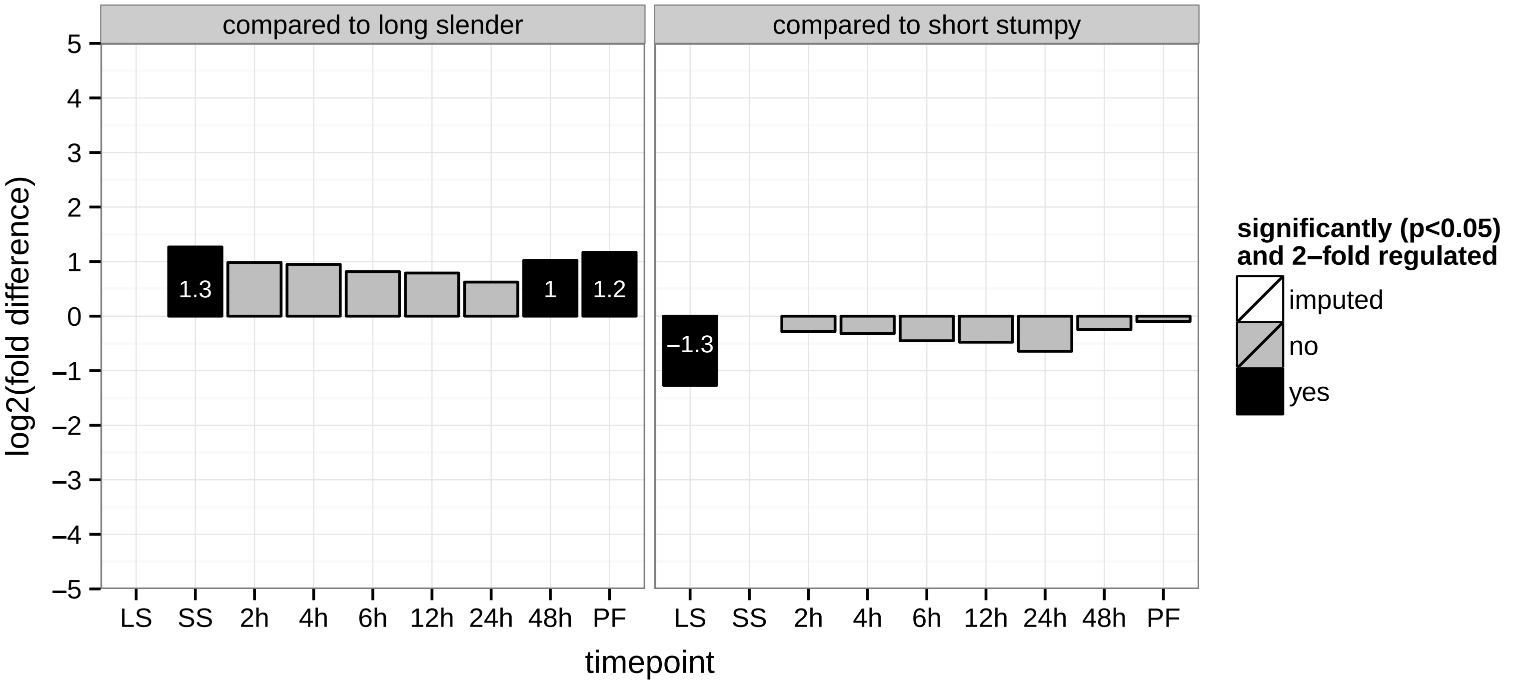
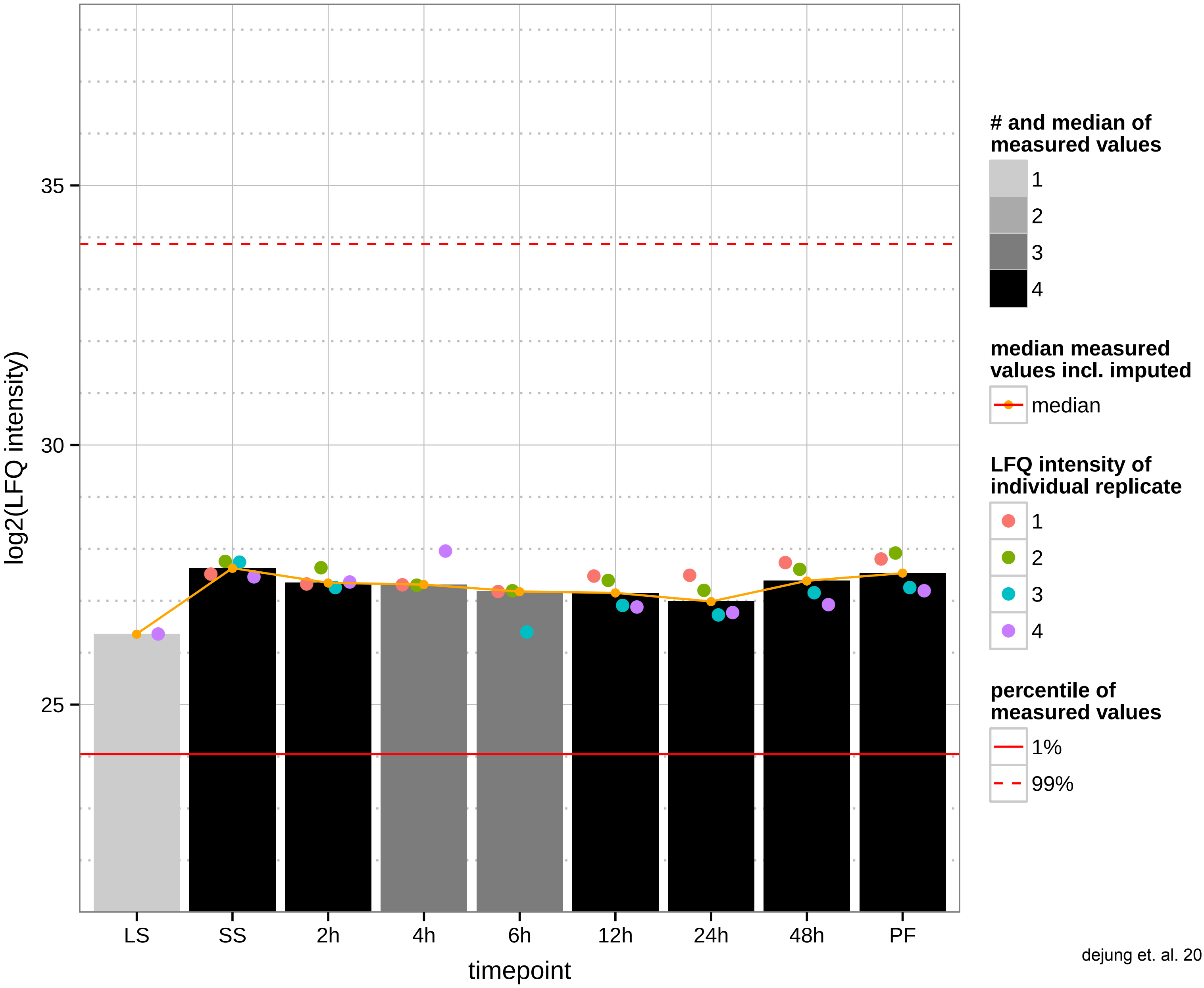
RNA binding protein, putative
Tb927.11.7310;Tb11.v5.0252
AGOF: null, RNA binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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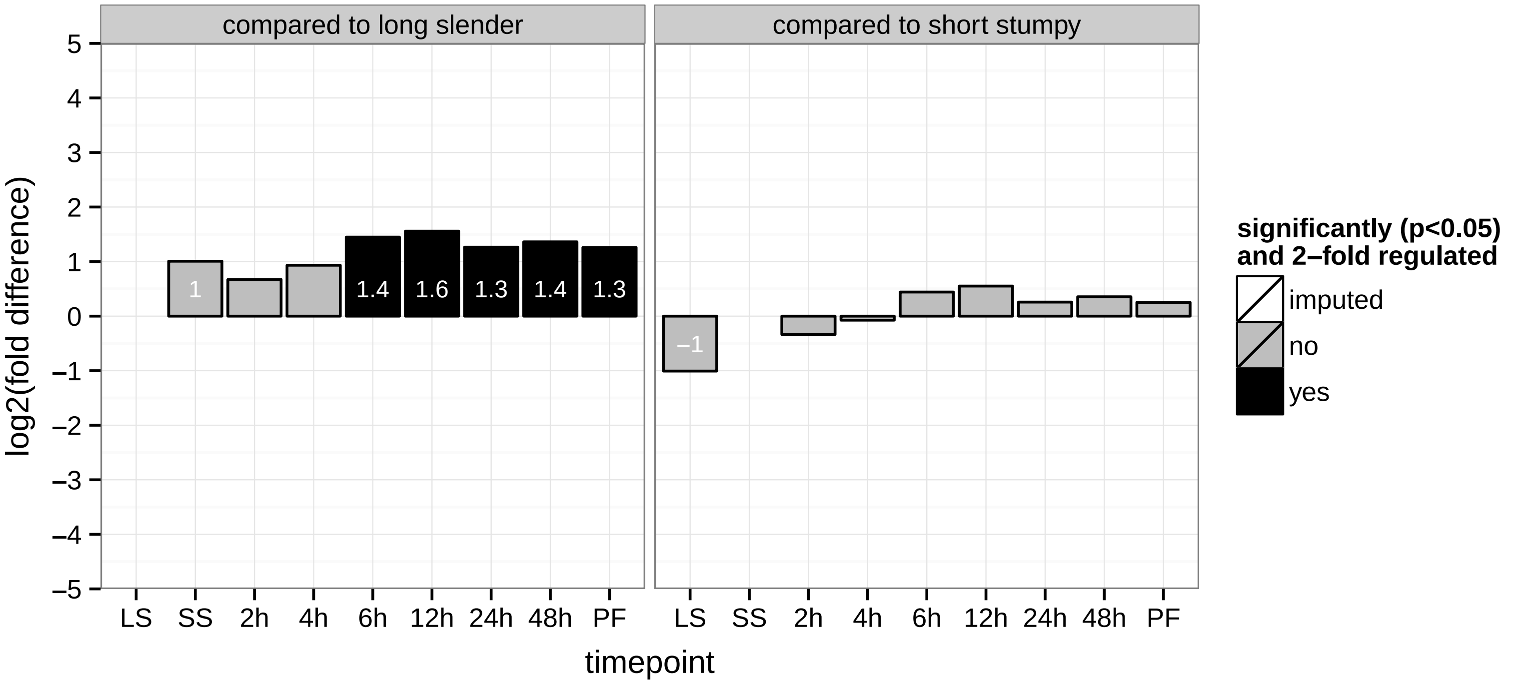
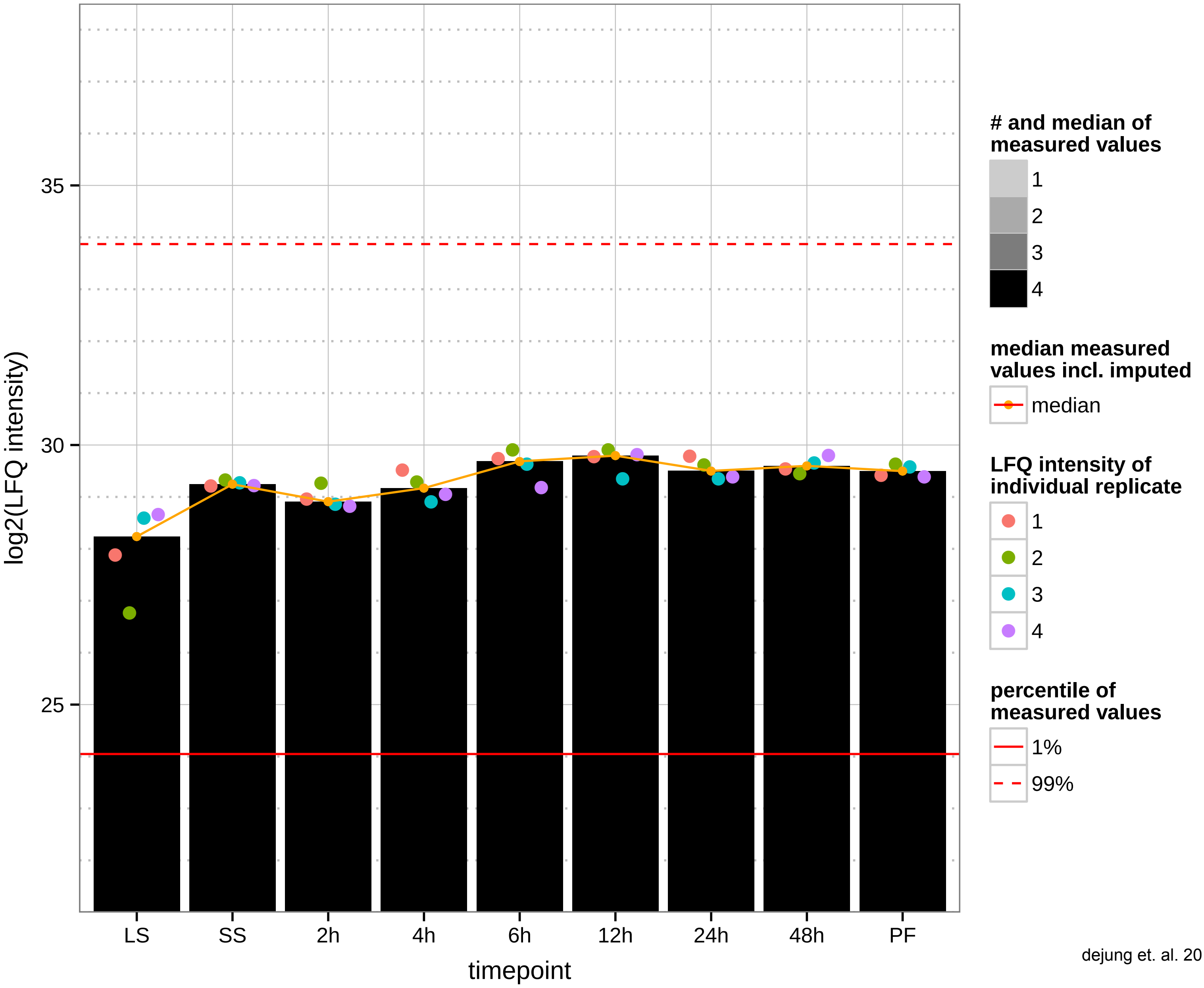
proteasome beta 3 subunit, putative, putative (PSB3)
Tb927.11.7270;Tb11.v5.0256
AGOF: null, endopeptidase activity, threonine−type endopeptidase activity
AGOC: null, proteasome core complex, proteasome core complex, beta−subunit complex
AGOP: null, ubiquitin−dependent protein catabolic process
PGOF: threonine−type endopeptidase activity
PGOC: proteasome core complex
PGOP: proteolysis involved in cellular protein catabolic process





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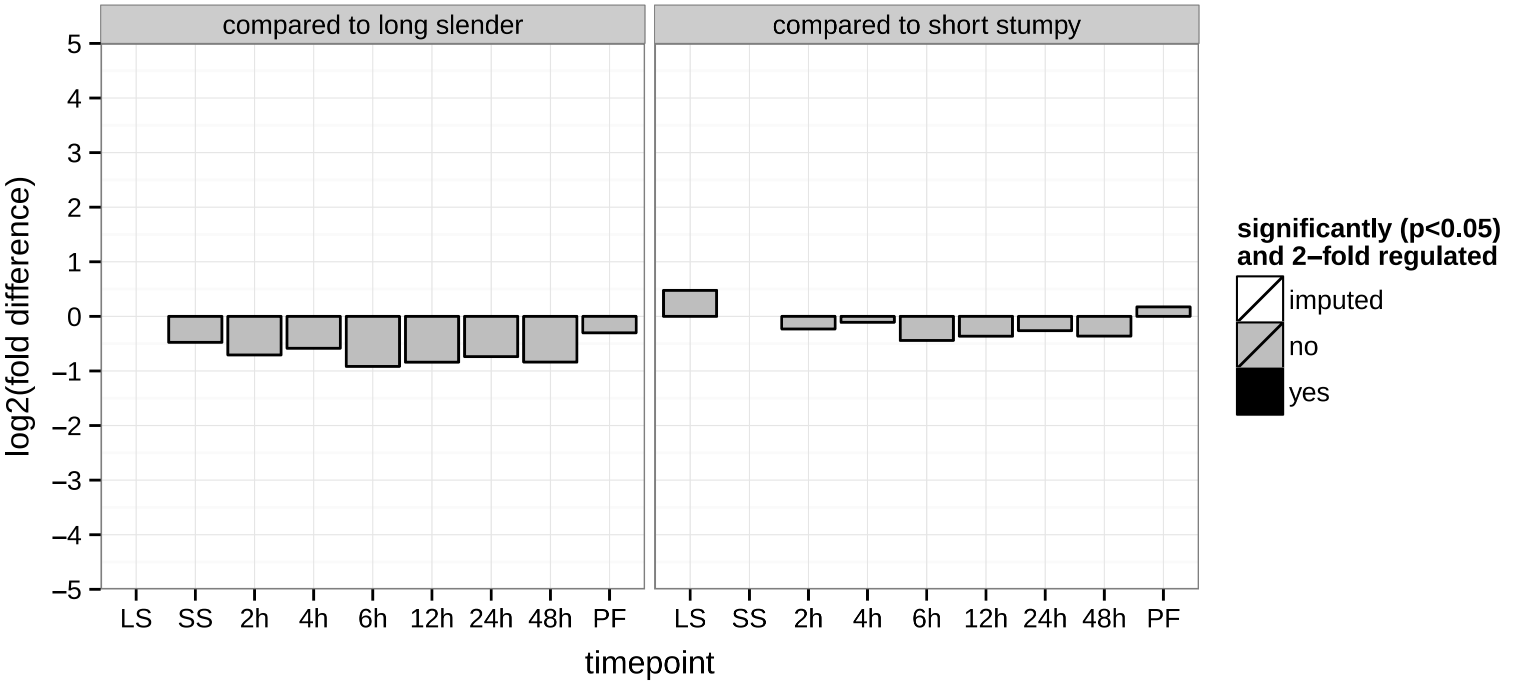
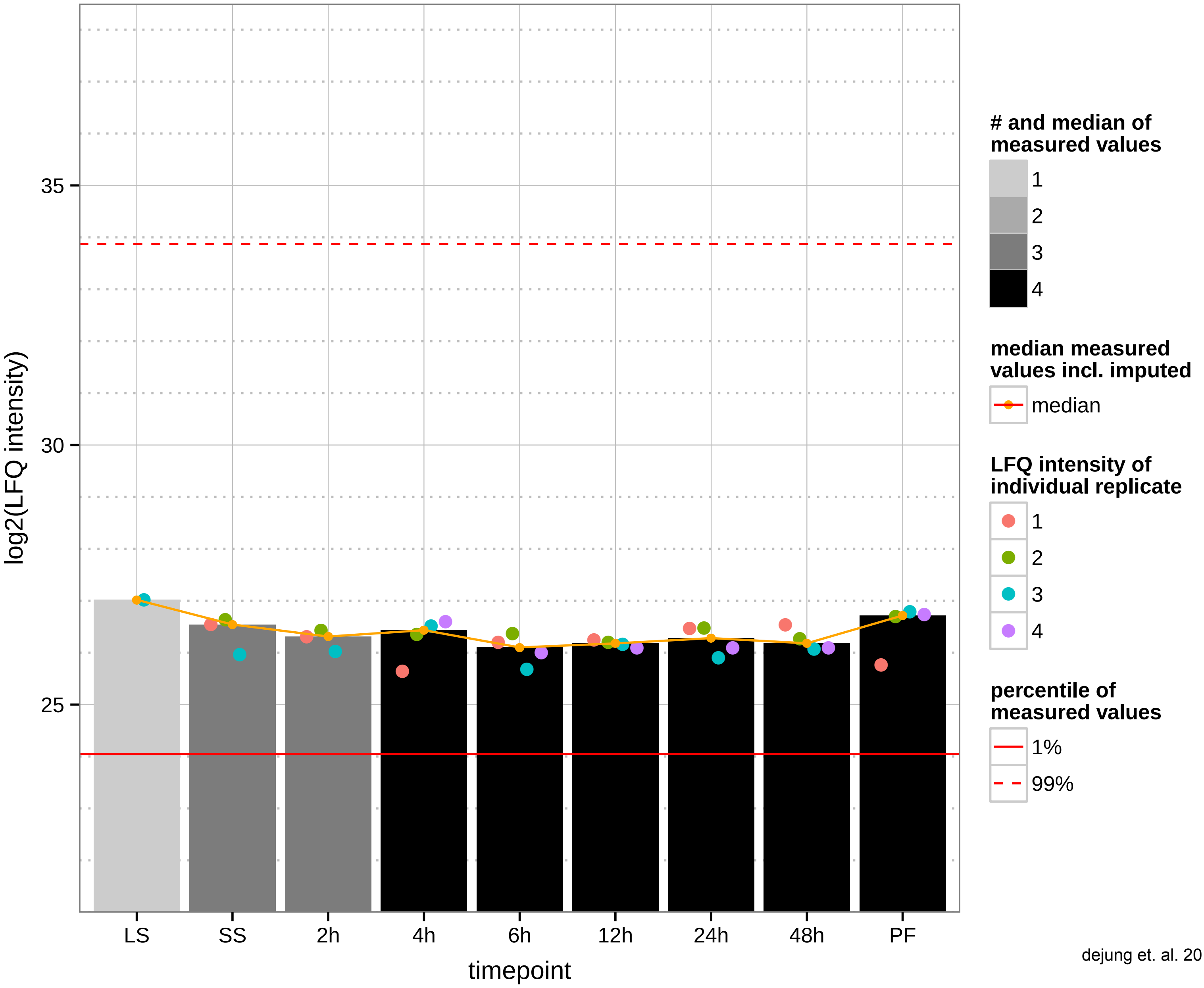
hypothetical protein, conserved, dynein regulatory complex subunit (CMF70)
Tb927.11.7240;Tb11.v5.0258
AGOF: null
AGOC: null, axonemal dynein complex, cilium
AGOP: null, ciliary cell motility, ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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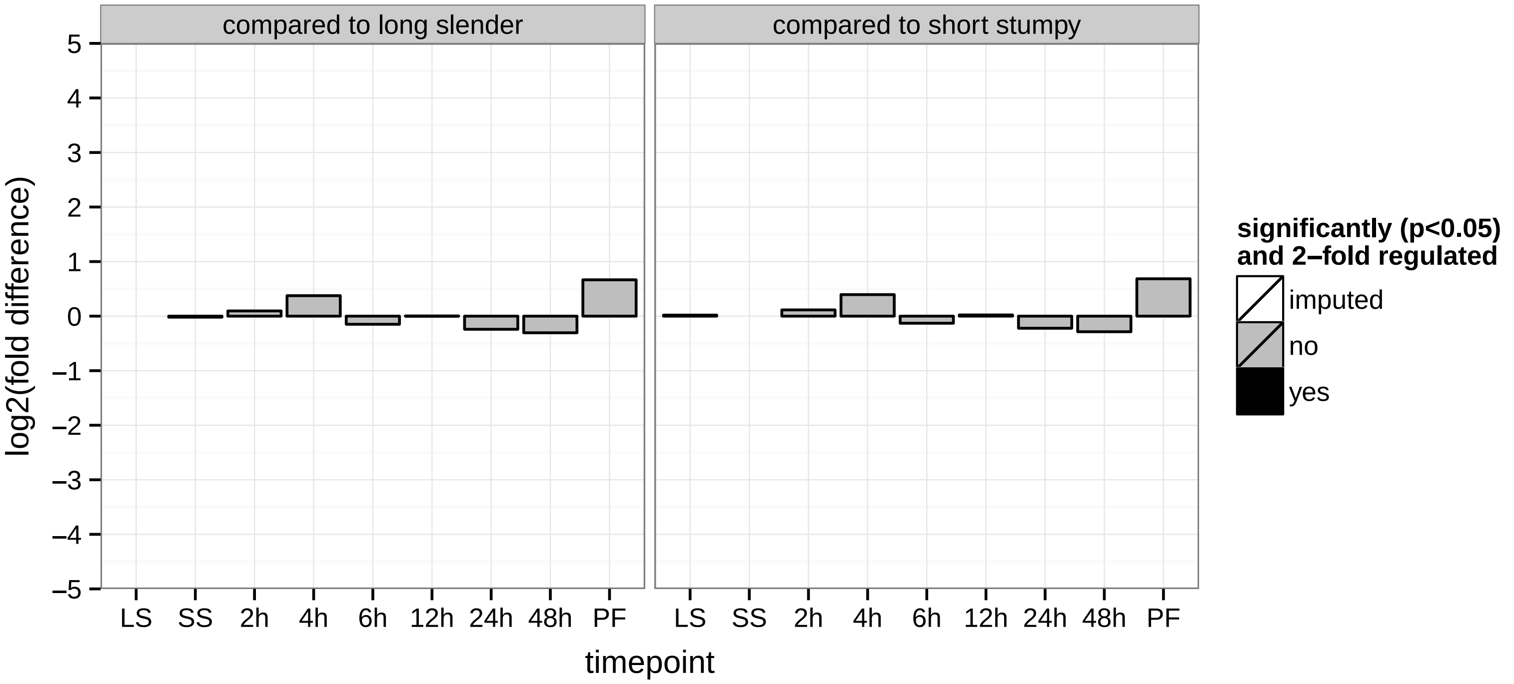
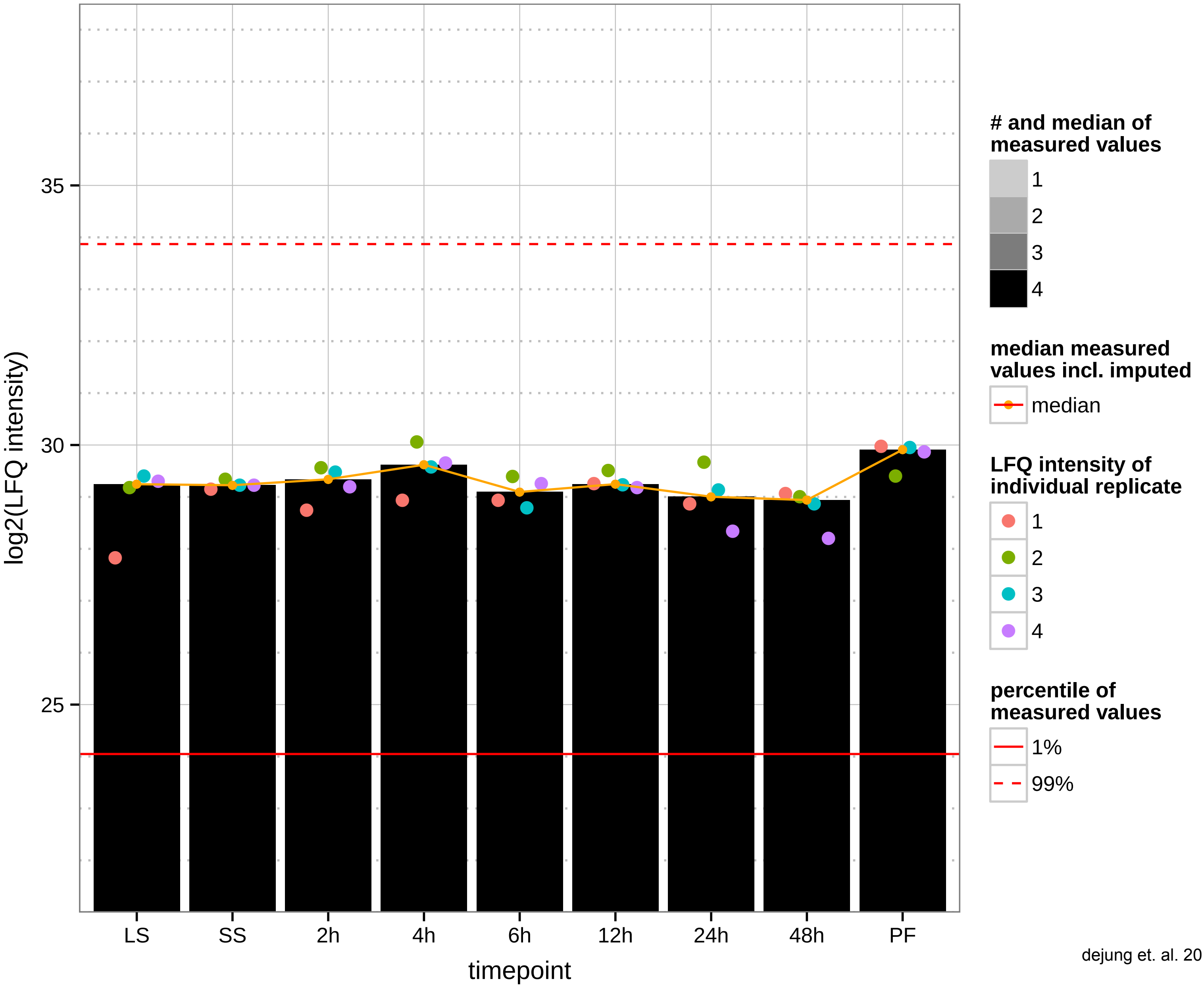
adenosine 5'–monophosphoramidase, putative
Tb927.7.4480;Tb11.v5.0261
AGOF: null, catalytic activity
AGOC: null
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null





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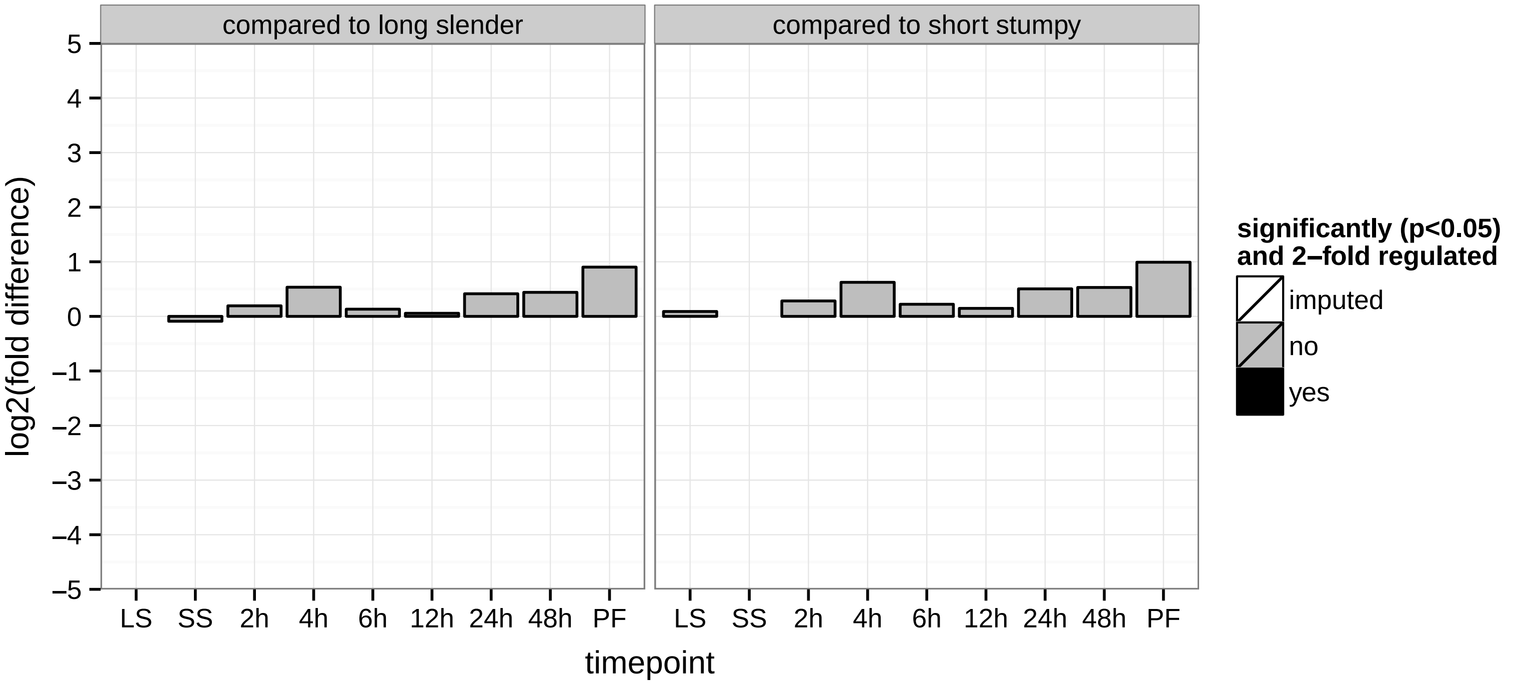
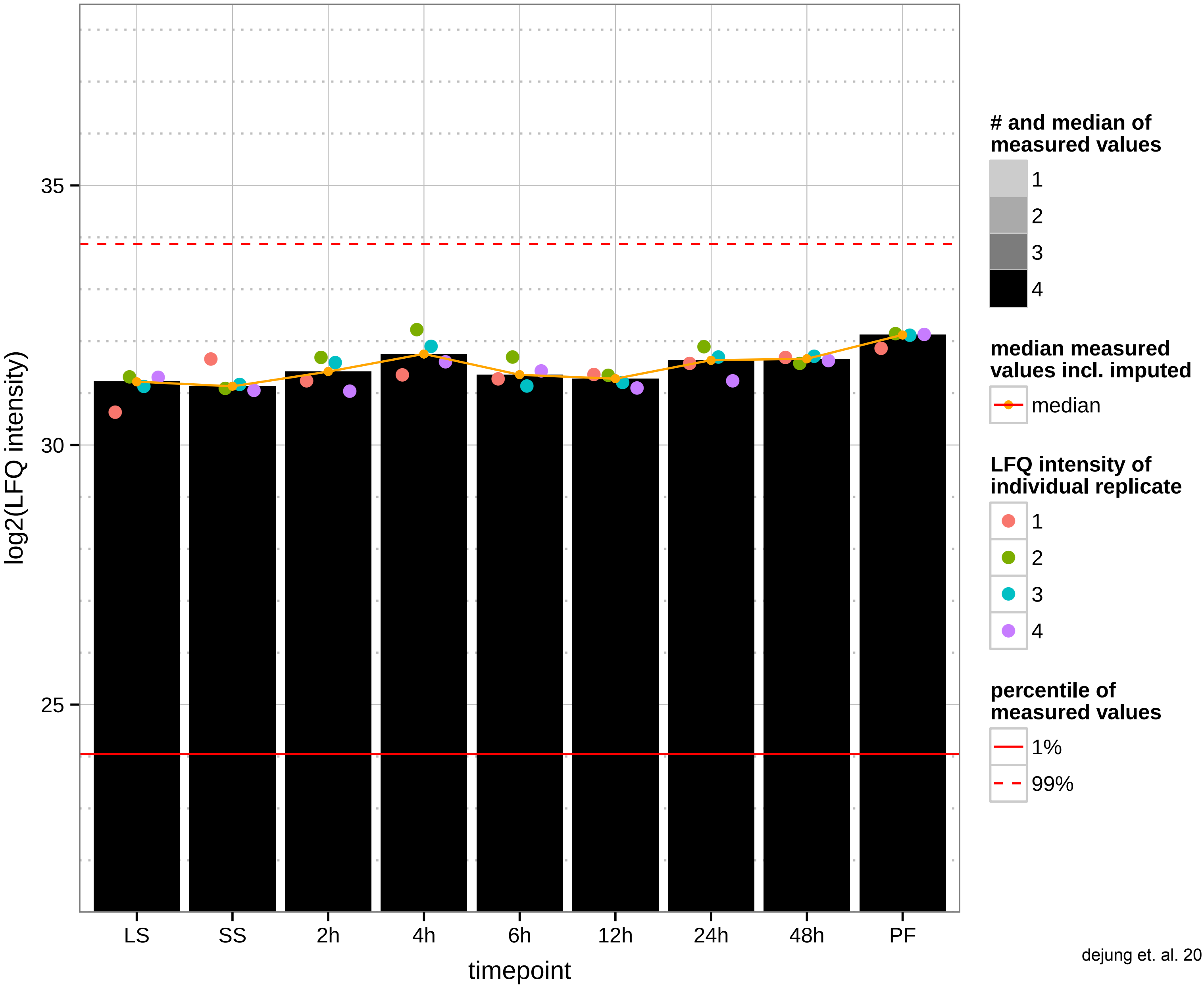
hypothetical protein, conserved
Tb927.7.4520;Tb11.v5.0265
AGOF: null
AGOC: null
AGOP: null, cell redox homeostasis
PGOF: null
PGOC: null
PGOP: null





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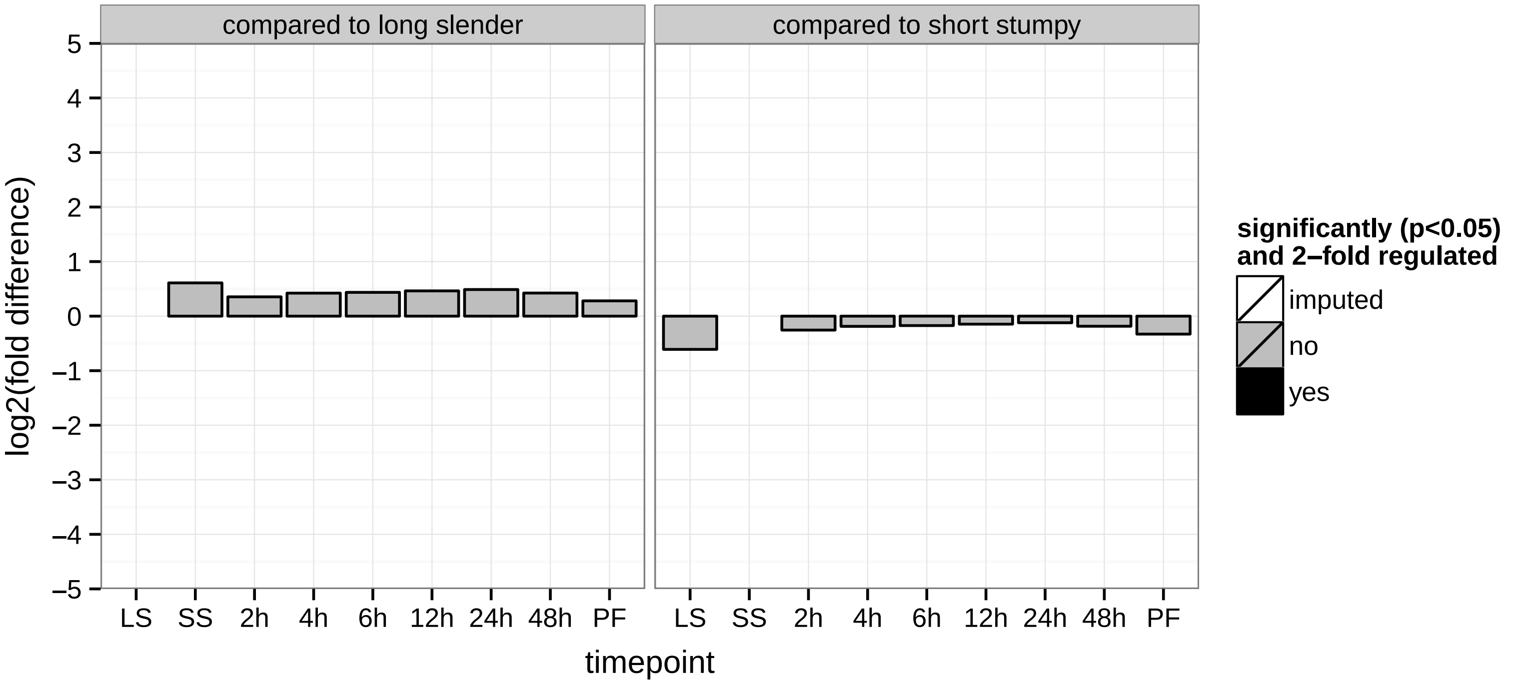
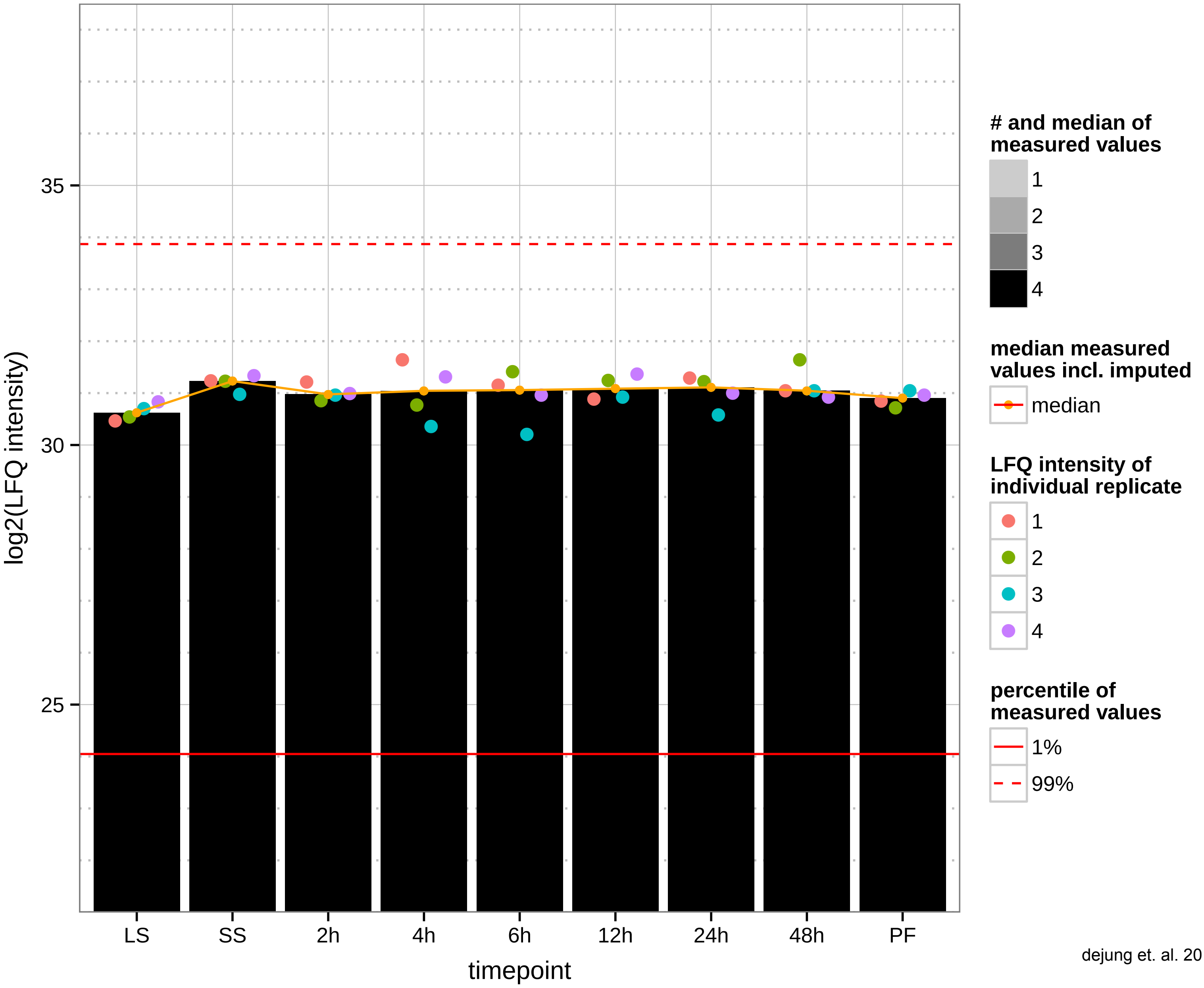
nucleoside hydrolase, putative, inosine–guanine nucleoside hydrolase (IG–NH)
Tb927.7.4570;Tb11.v5.0270
AGOF: null, inosine nucleosidase activity
AGOC: null
AGOP: null, guanosine salvage, inosine salvage
PGOF: null
PGOC: null
PGOP: null





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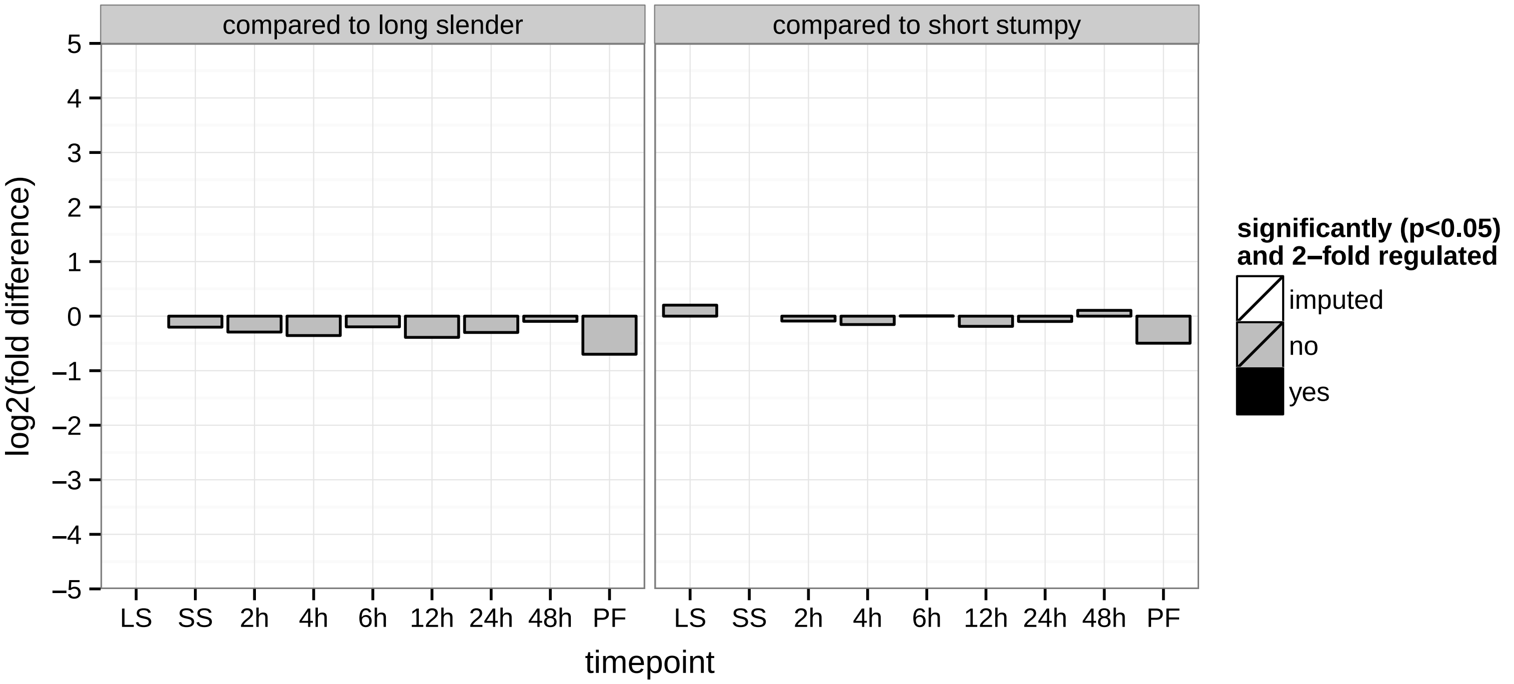
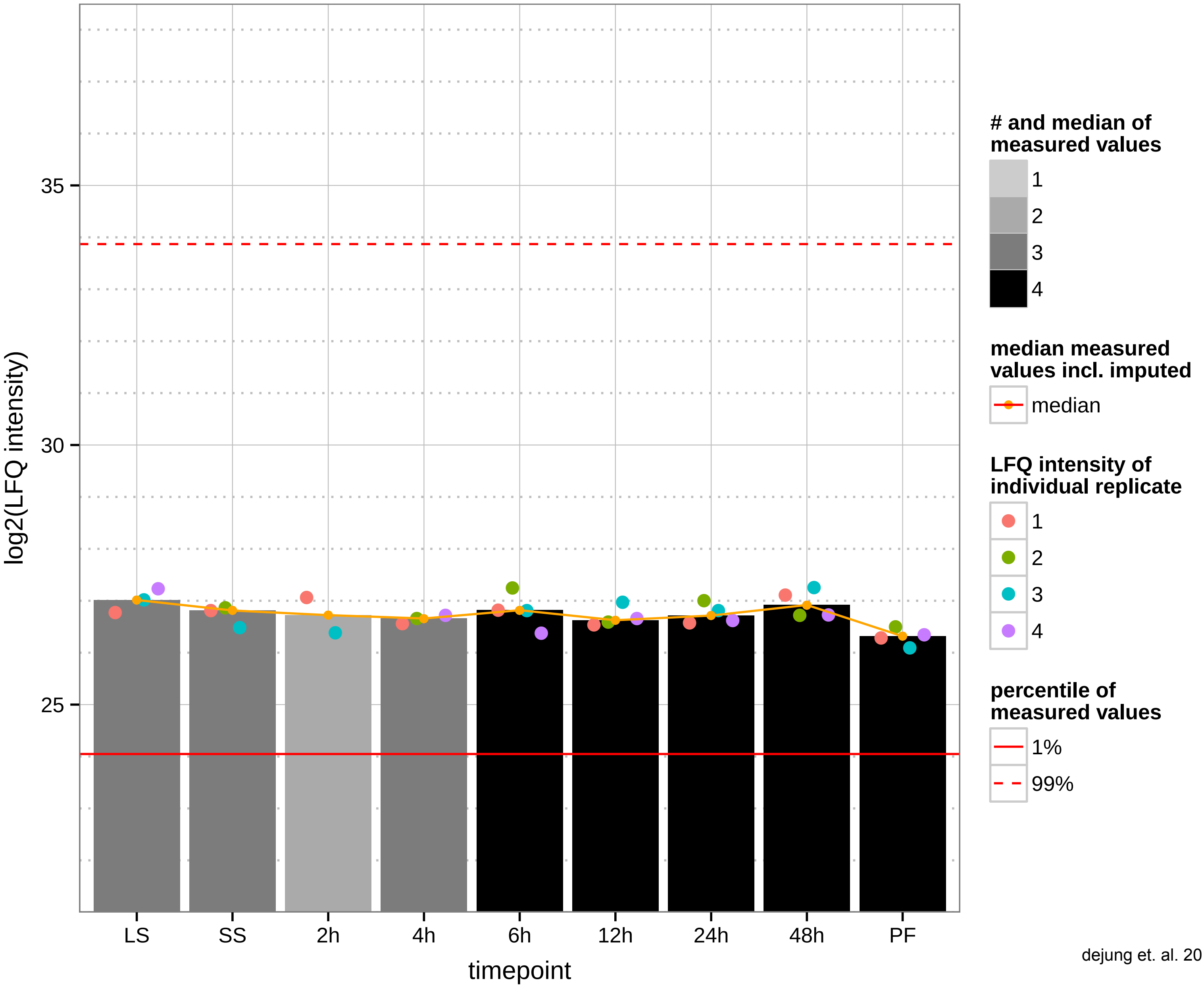
trypanin, putative, trypanin (trypanin)
Tb927.10.6350;Tb11.v5.0271
AGOF: null
AGOC: null, cilium
AGOP: null, cellular component movement
PGOF: null
PGOC: microtubule–based flagellum
PGOP: cell motility





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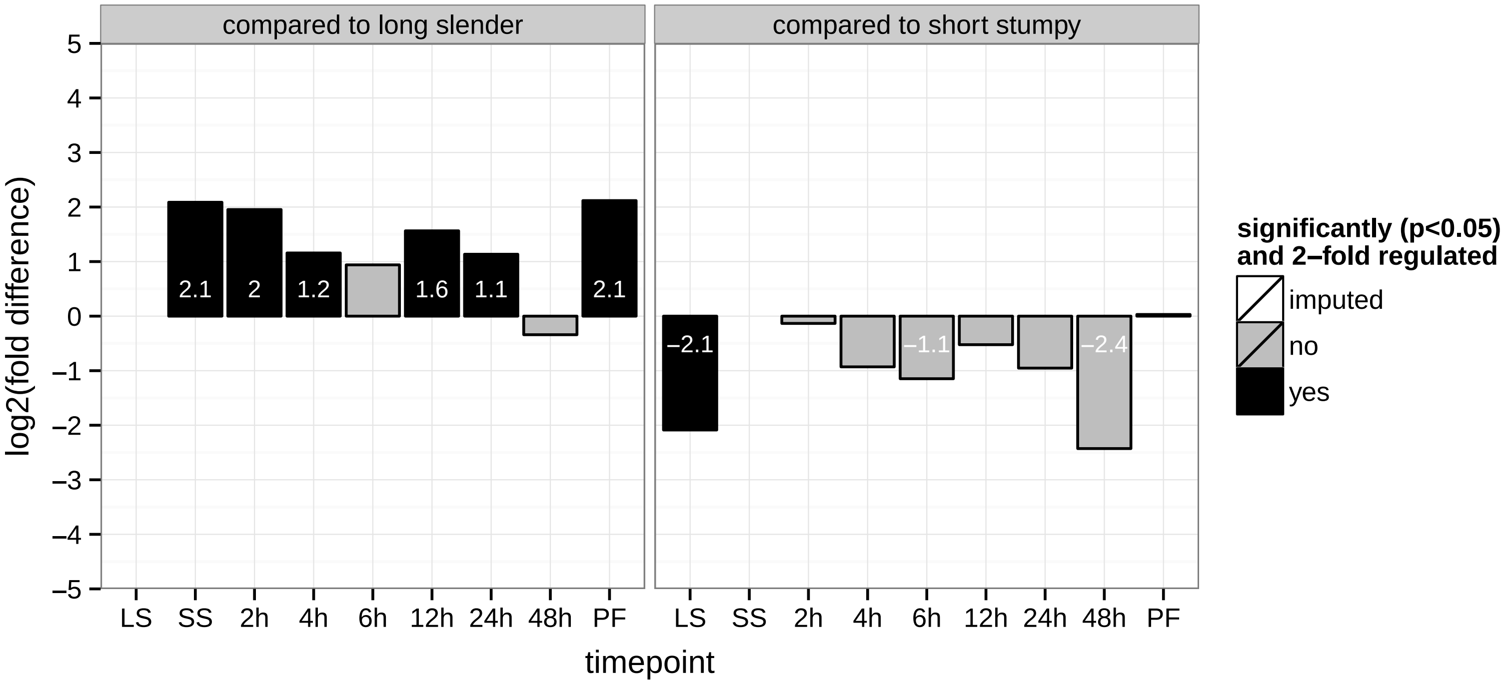
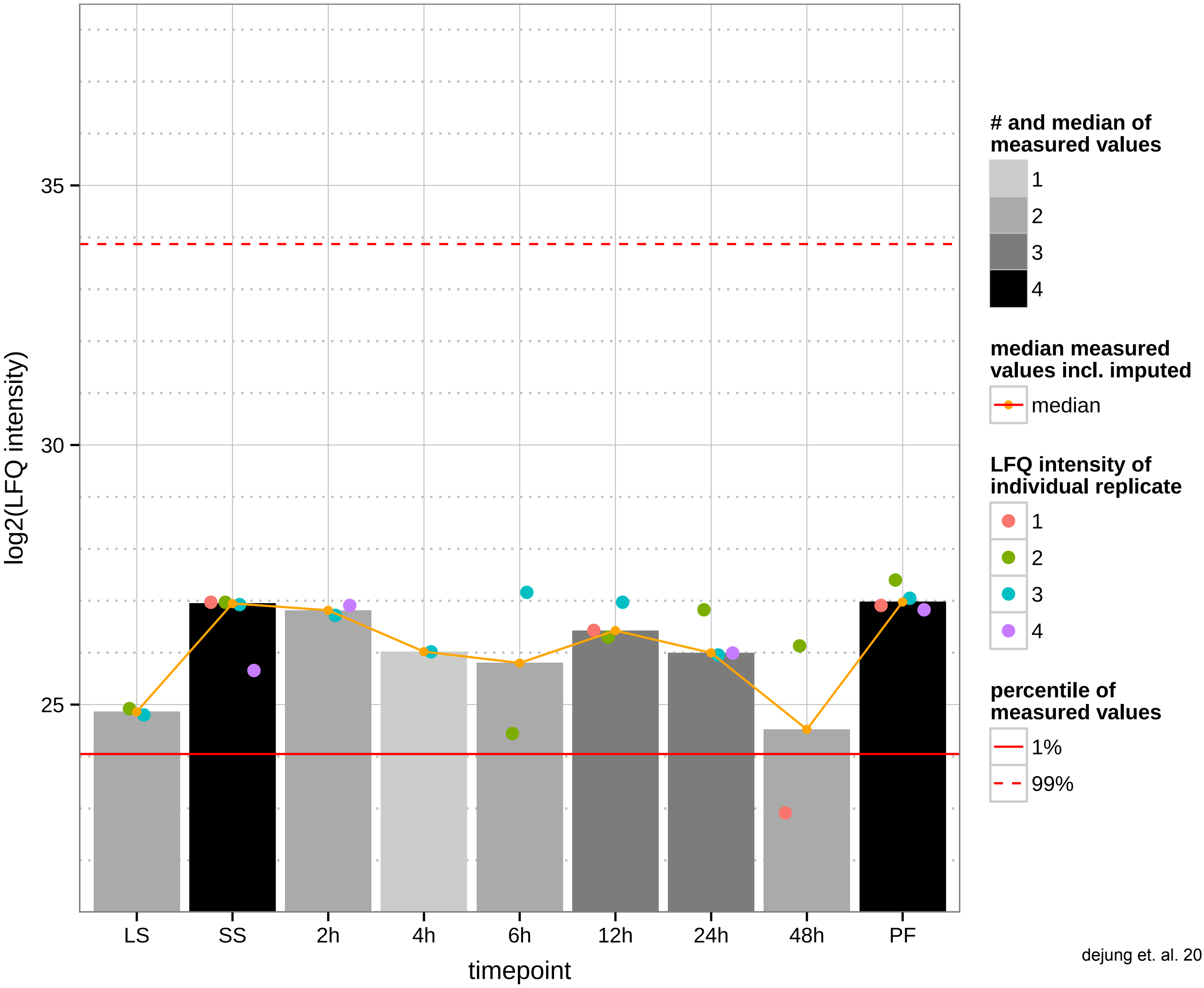
hypothetical protein, conserved, kinetoplastid kinetochore protein 1 (kkt1)
Tb927.10.6330;Tb11.v5.0273
AGOF: null
AGOC: null, kinetochore
AGOP: null, chromosome segregation
PGOF: null
PGOC: null
PGOP: null





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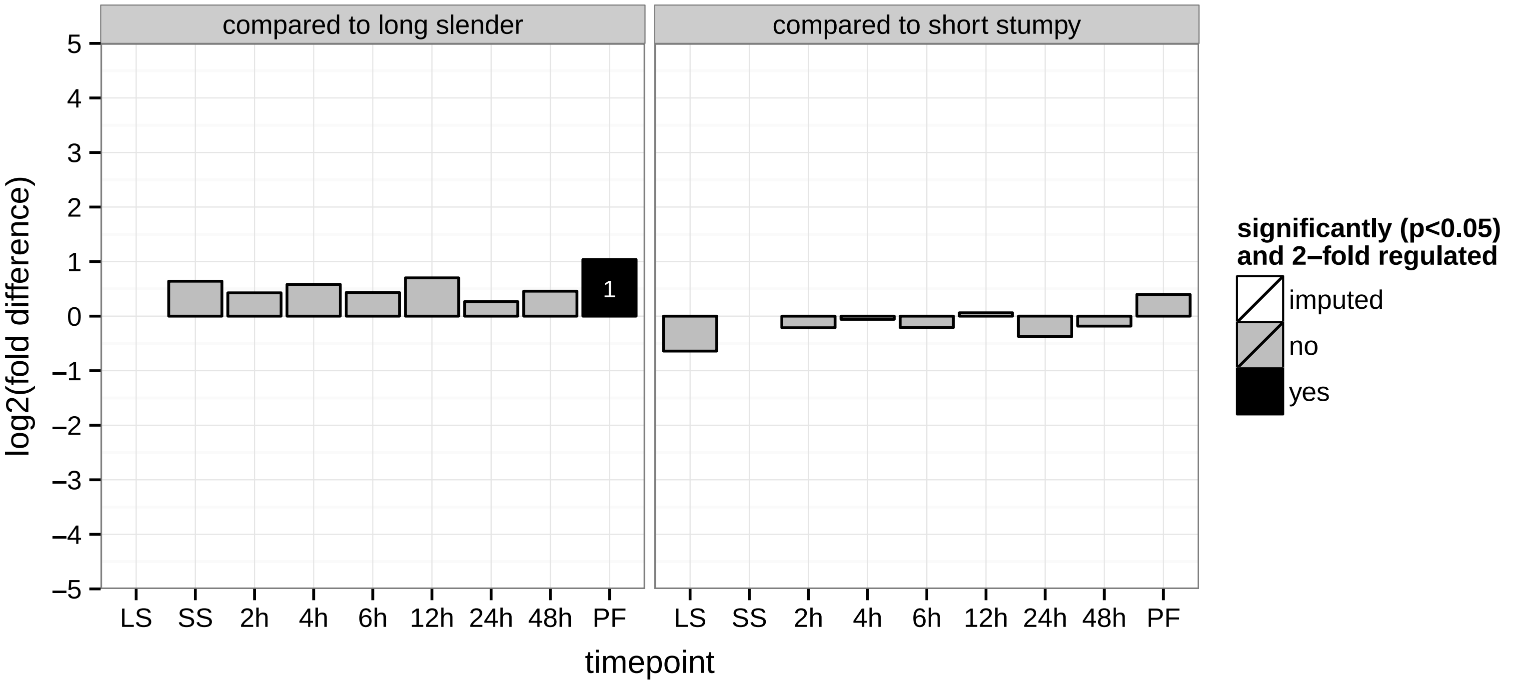
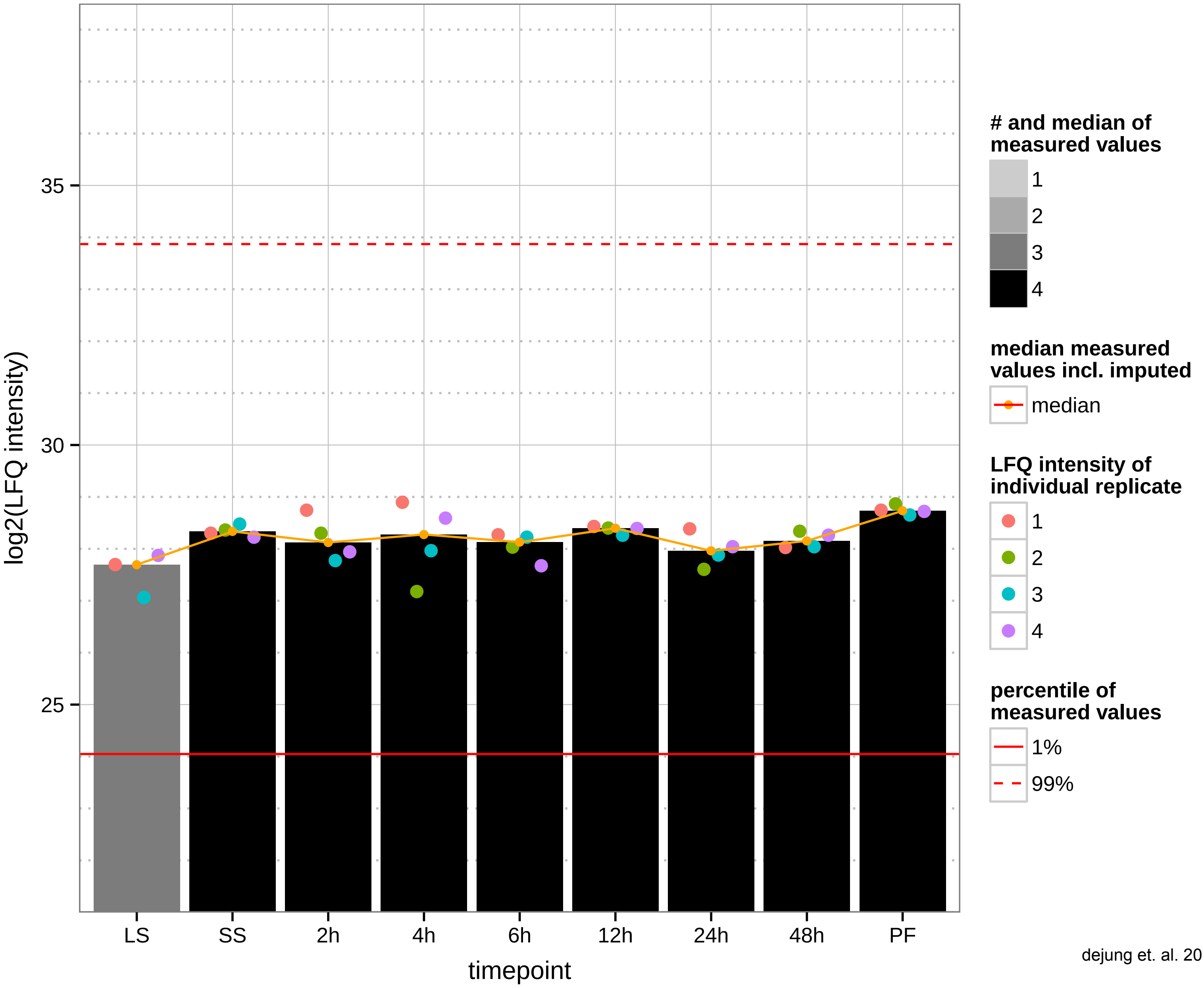
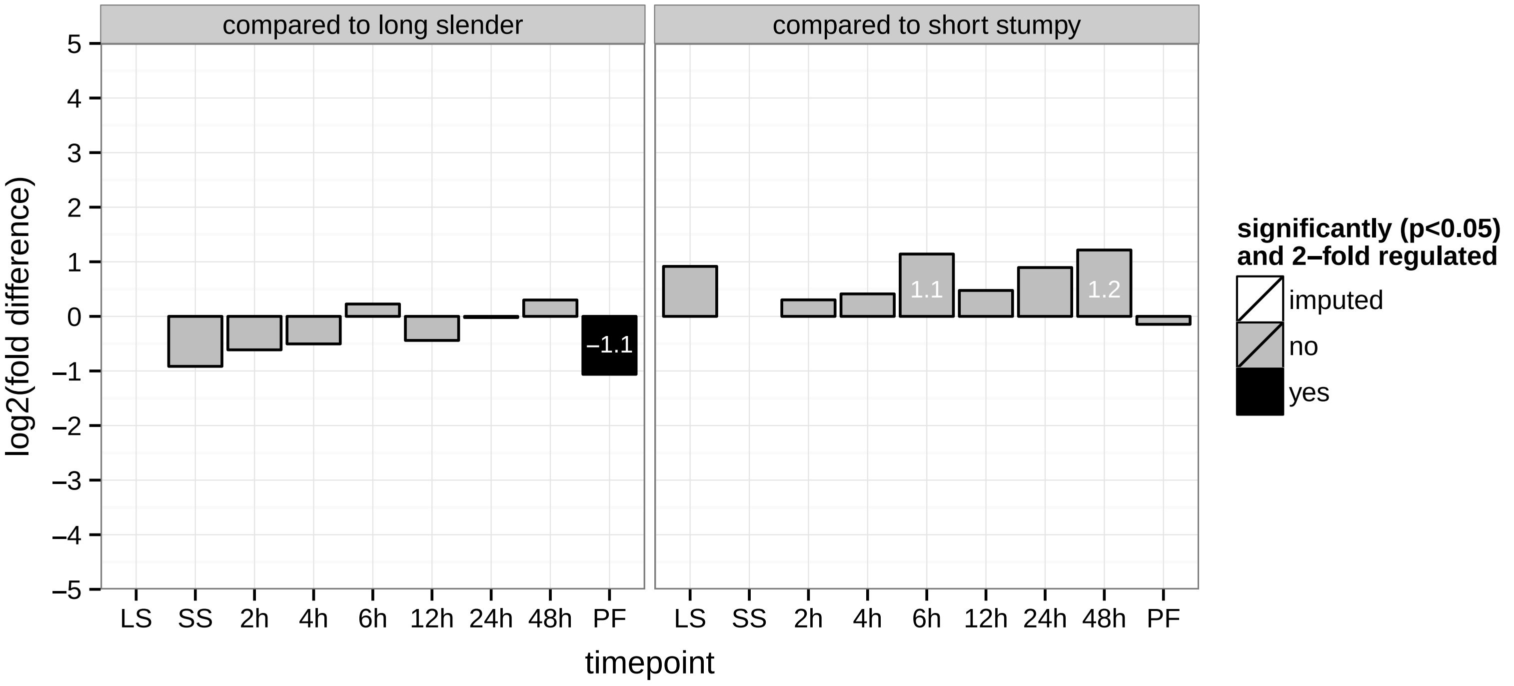
major vault protein, putative, putative (MVP)
Tb927.10.6310;Tb11.v5.0275
AGOF: null
AGOC: null
AGOP: null, negative regulation of signaling
PGOF: null
PGOC: null
PGOP: null

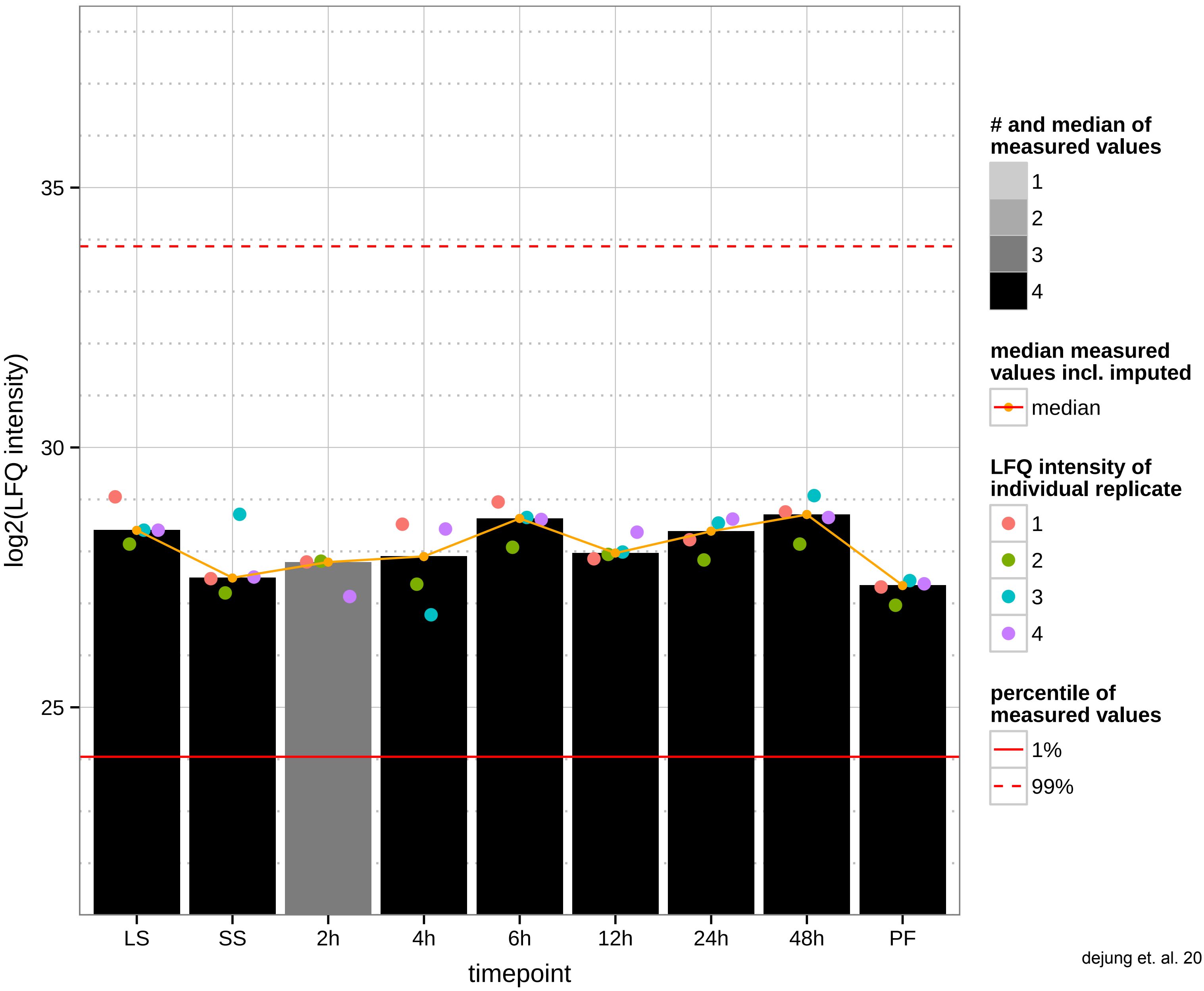




dejung et. al. 2015

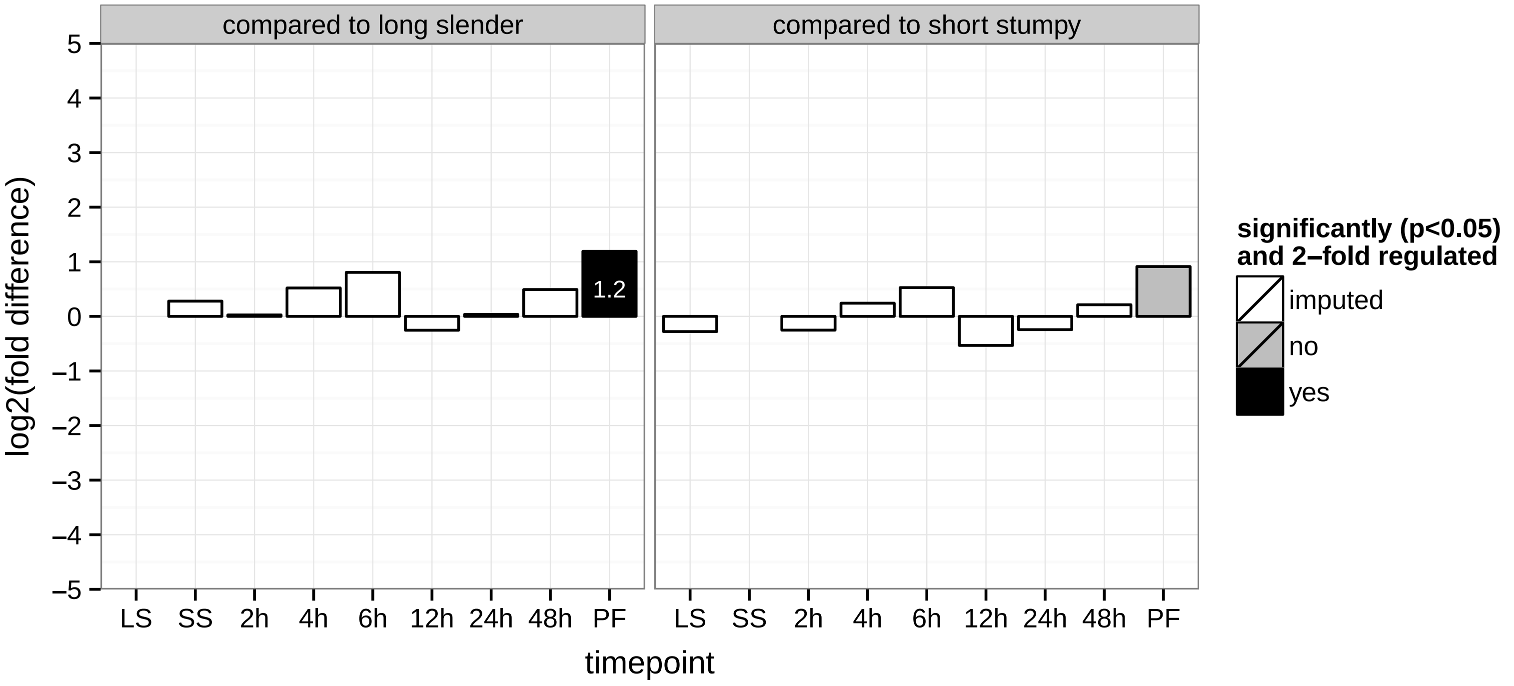
ATP−dependent DEAD/H RNA helicase, putative
Tb927.10.6290;Tb11.v5.0277
AGOF: null, ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: null, nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null

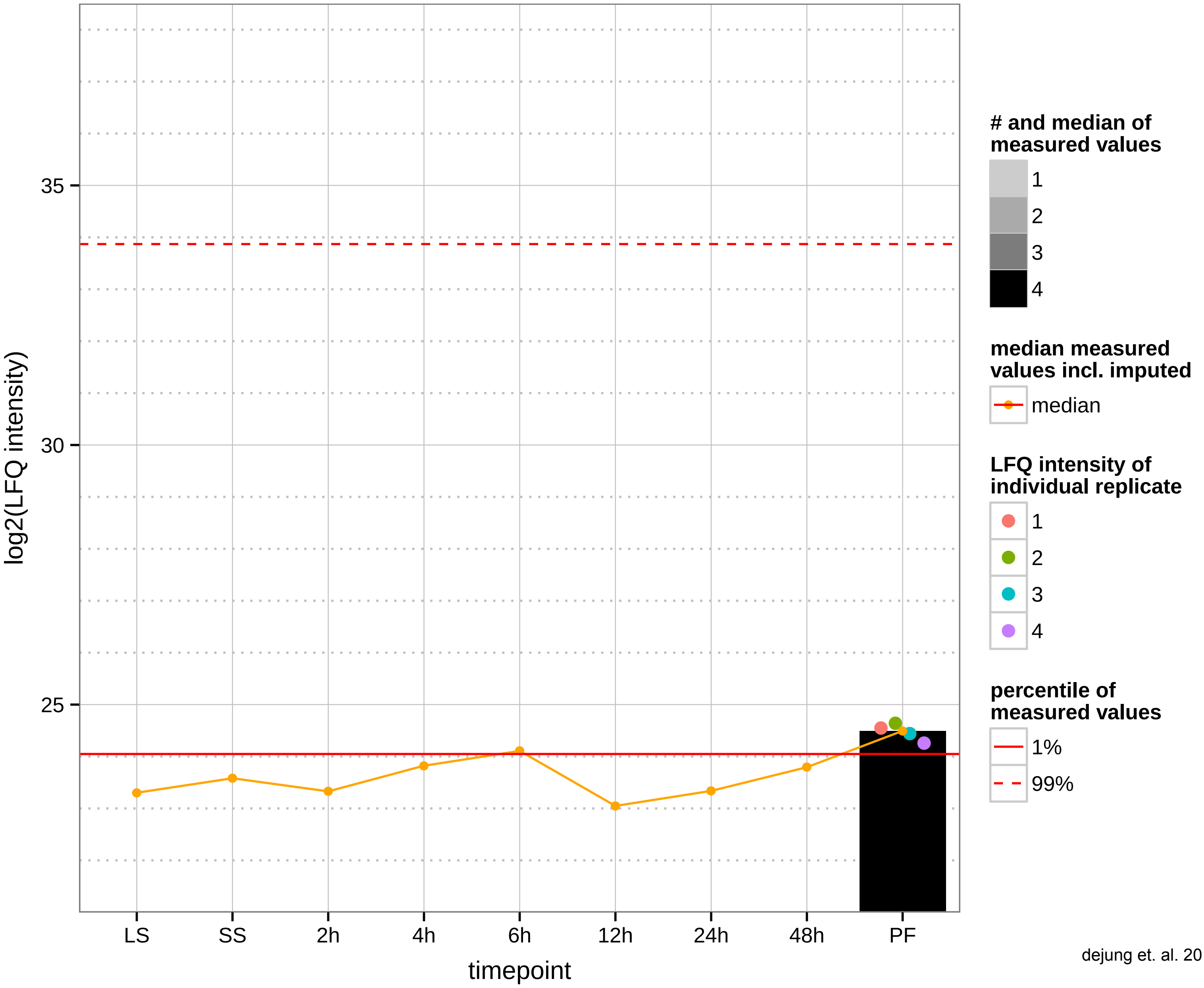




dejung et. al. 2015

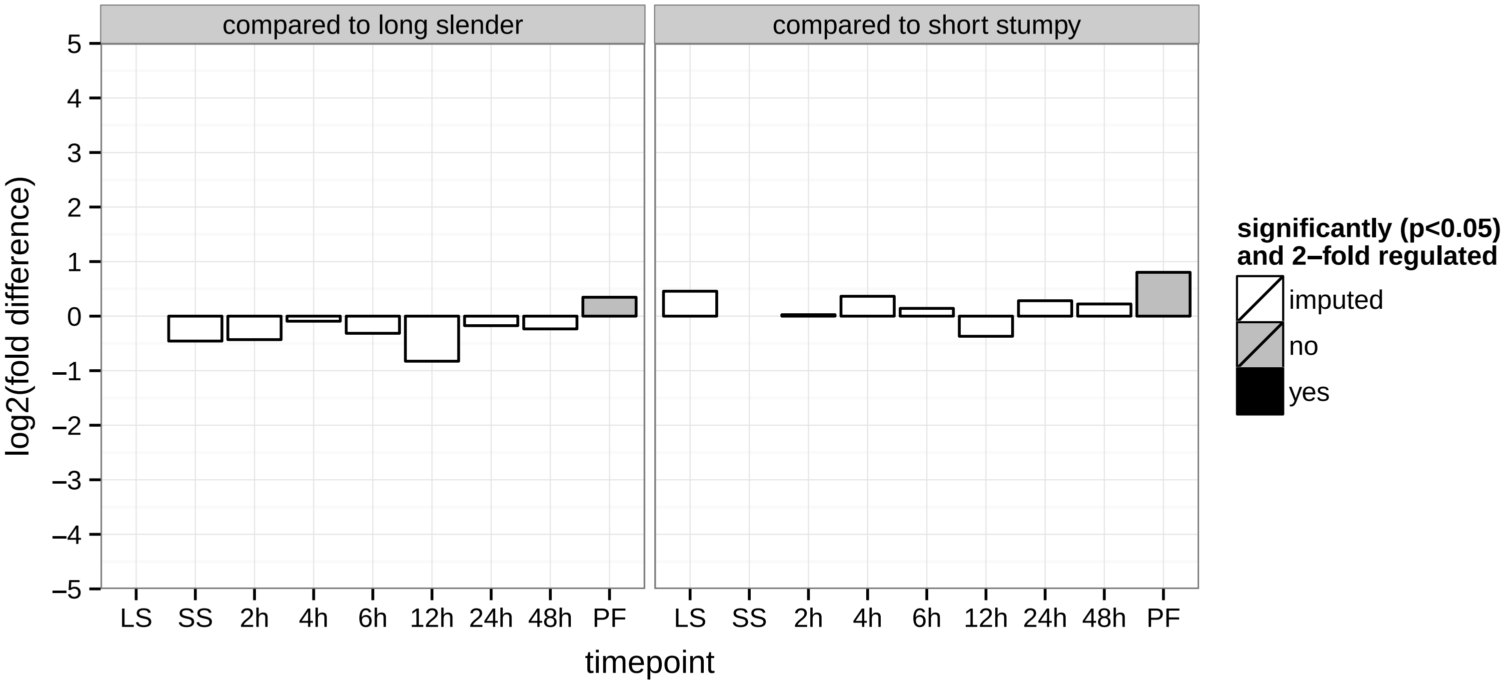
cleavage and polyadenylation specificity factor 30 kDa subunit, putative, CPSF 30 kDa subunit, NS1 effector domain– binding
Tb927.11.12750;Tb11.v5.0291
AGOF: null, RNA binding, nucleic acid binding, zinc ion binding
AGOC: null, mRNA cleavage and polyadenylation specificity factor complex
AGOP: null, RNA processing
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null

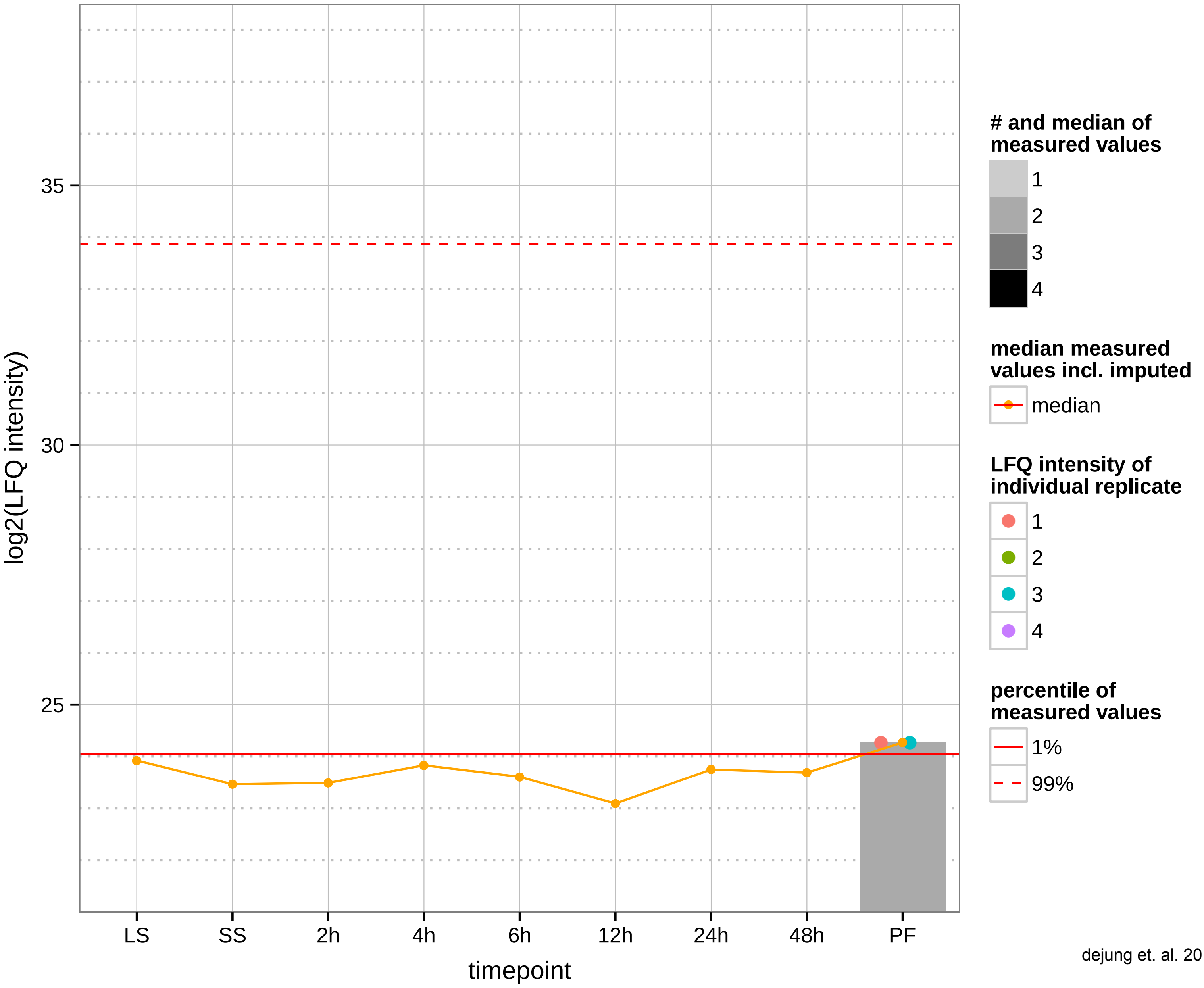




dejung et. al. 2015

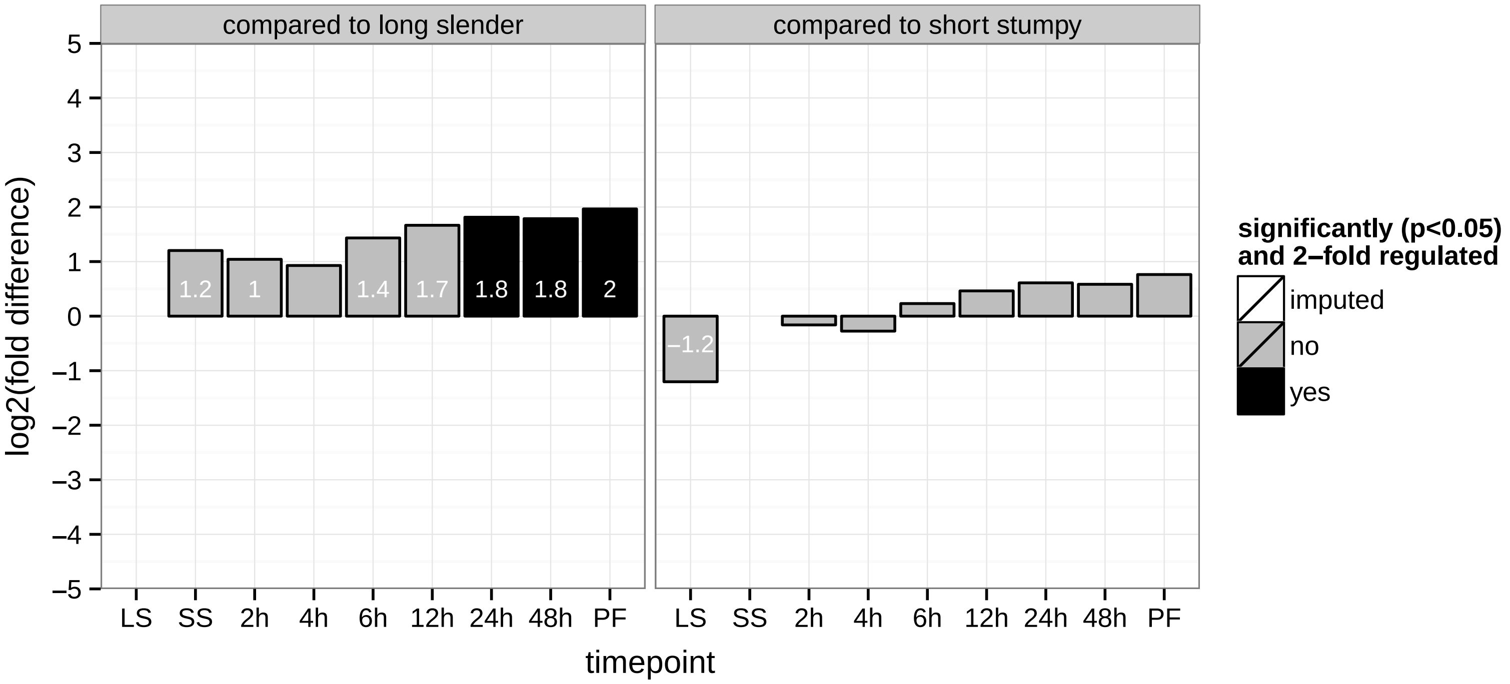
TFIID–like protein, putative, putative (TRF4)
Tb927.10.15950;Tb11.v5.0305
AGOF: null, DNA binding
AGOC: null, nucleus, transcription factor TFIID complex
AGOP: null, regulation of transcription, DNA–dependent, transcription initiation from RNA polymerase II promoter
PGOF: DNA binding
PGOC: null
PGOP: regulation of transcription, DNA–dependent, transcription initiation from RNA polymerase II promoter

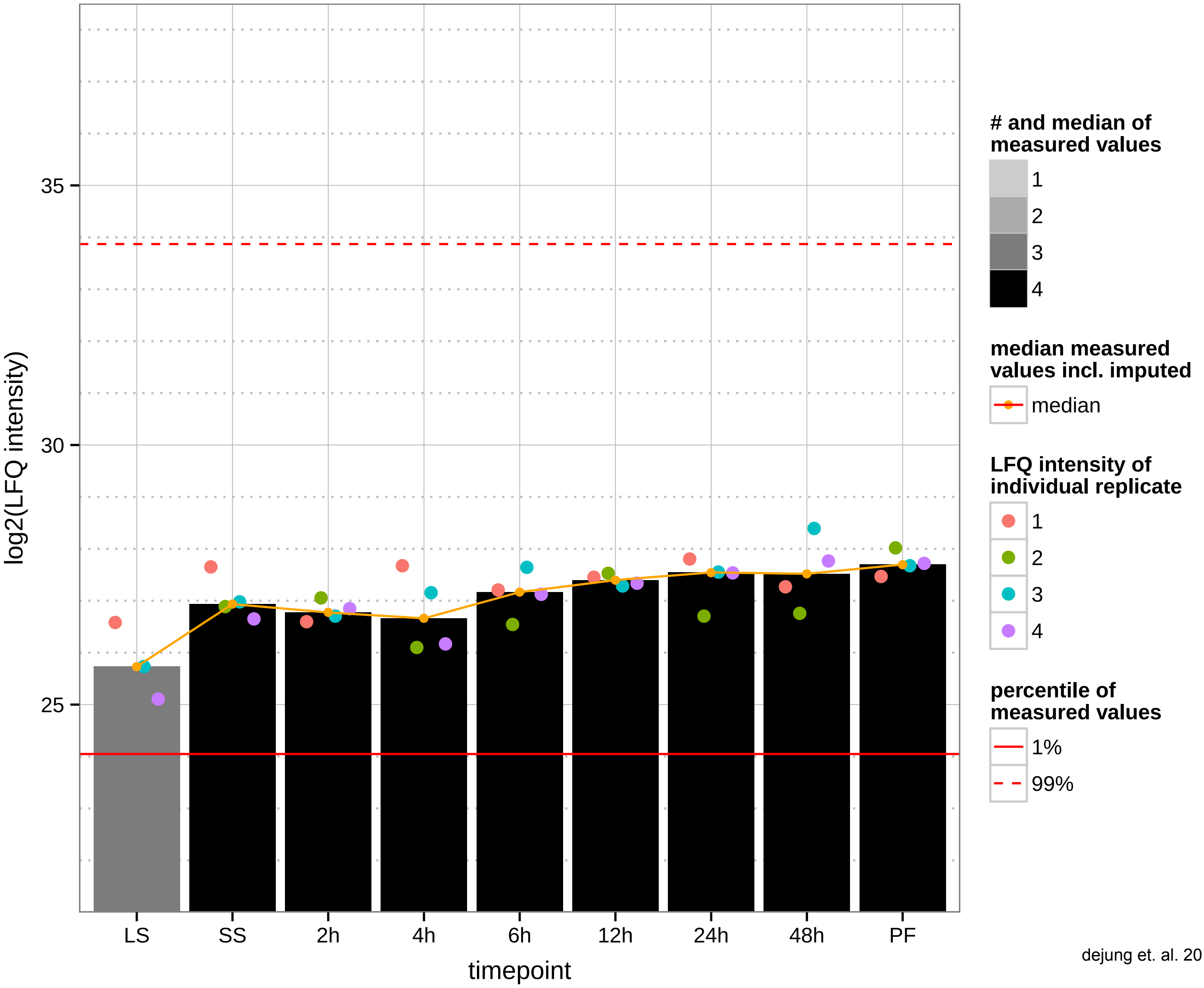




dejung et. al. 2015

retrotransposon hot spot (RHS) protein, putative
Tb11.v5.0325
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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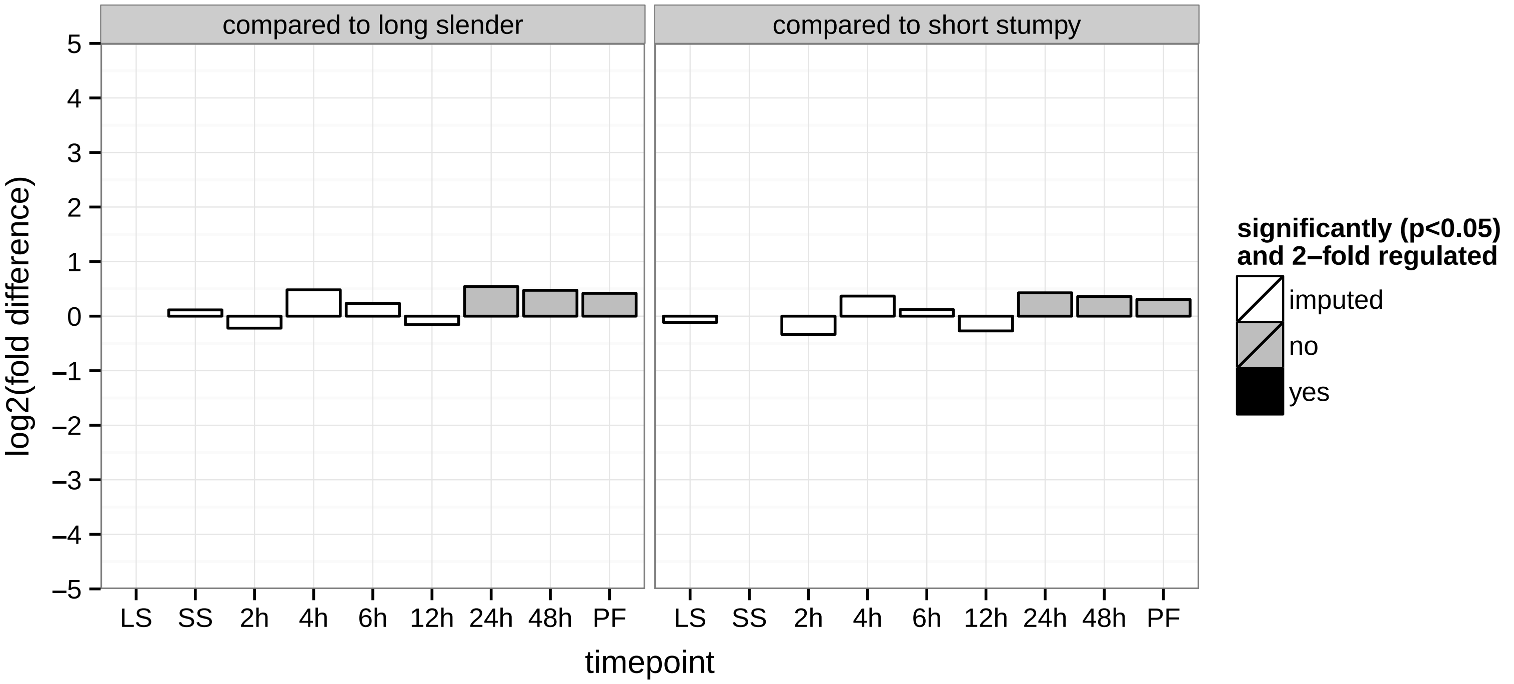
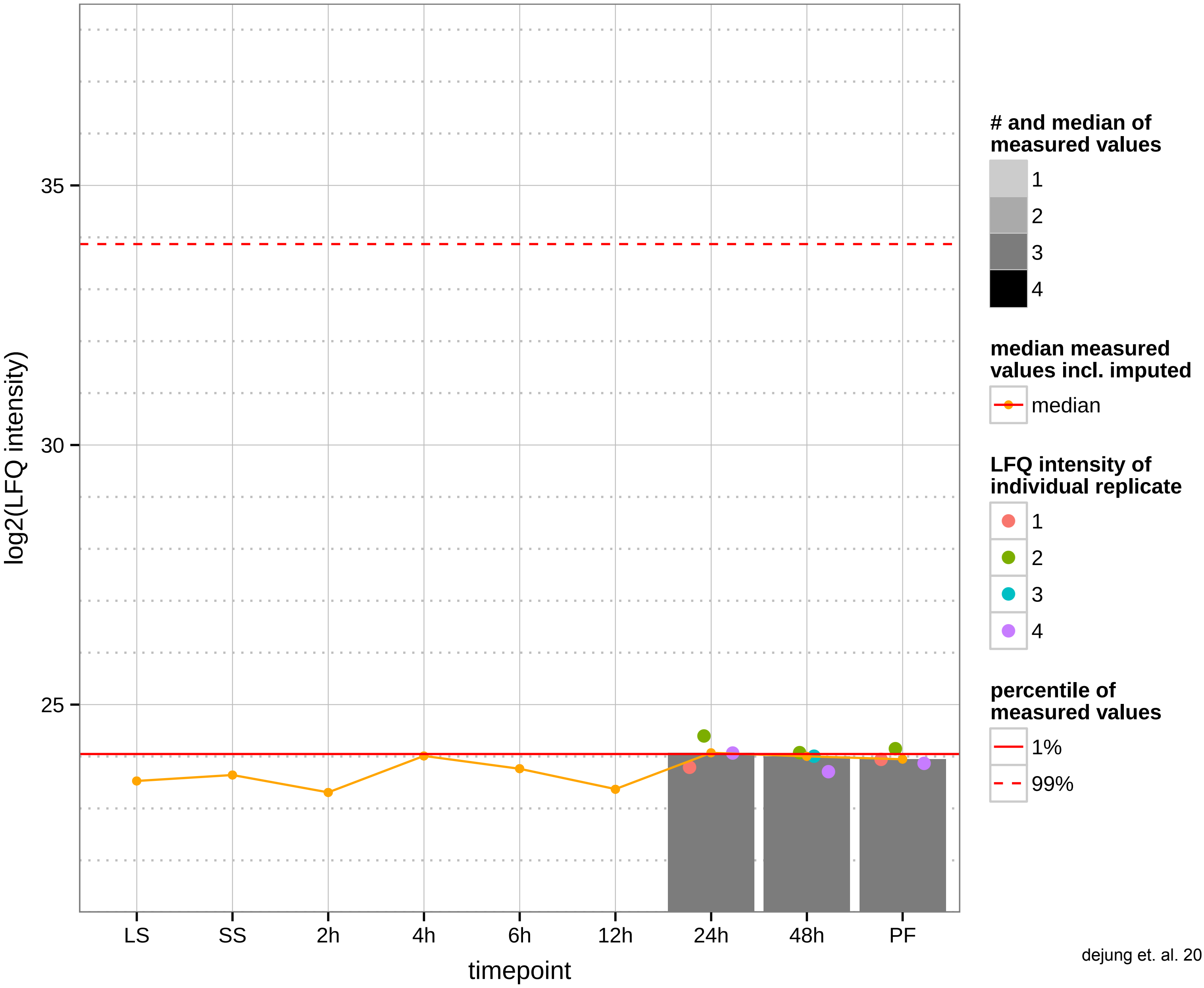
hypothetical protein, conserved, ribonuclease H, putative
Tb927.10.5070;Tb11.v5.0340
AGOF: null, RNA binding, ribonuclease H activity
AGOC: null, nucleus
AGOP: null, RNA catabolic process
PGOF: nucleic acid binding, ribonuclease H activity
PGOC: null
PGOP: RNA metabolic process





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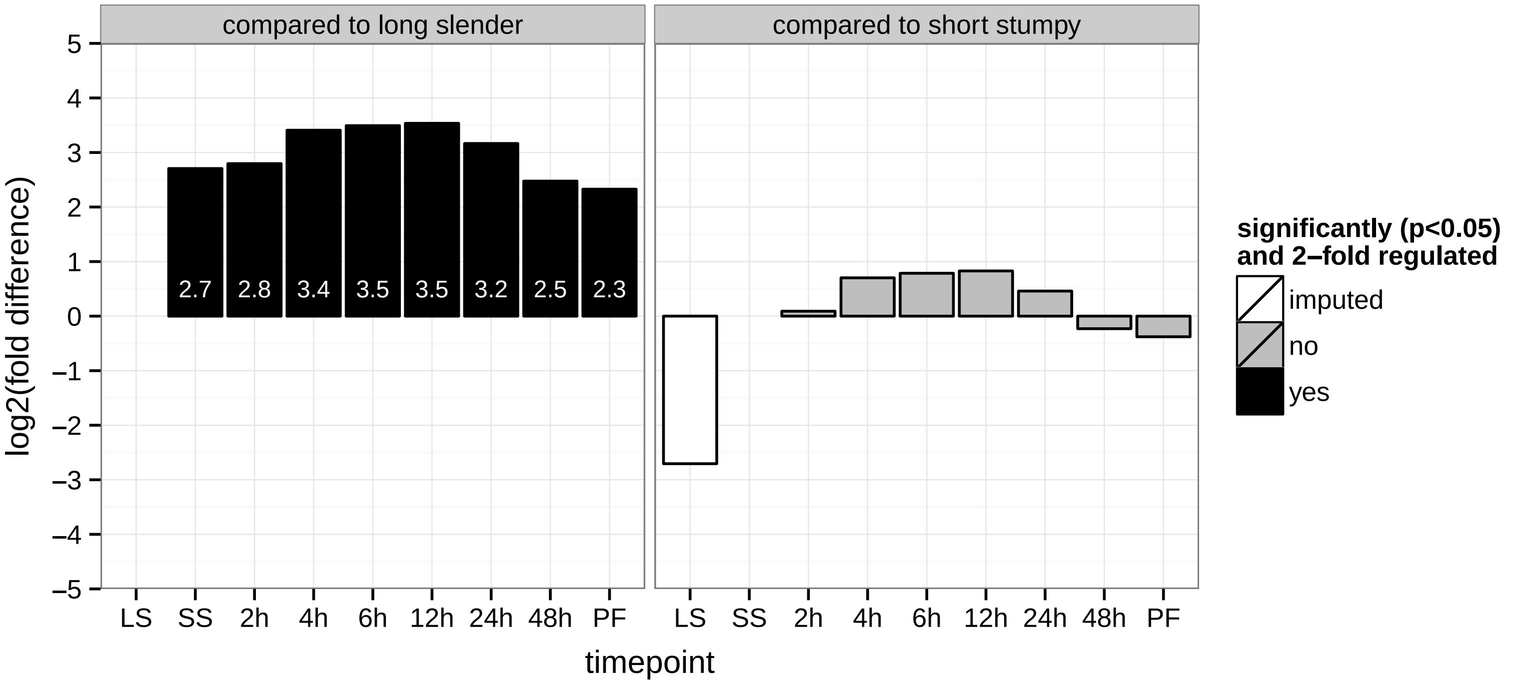
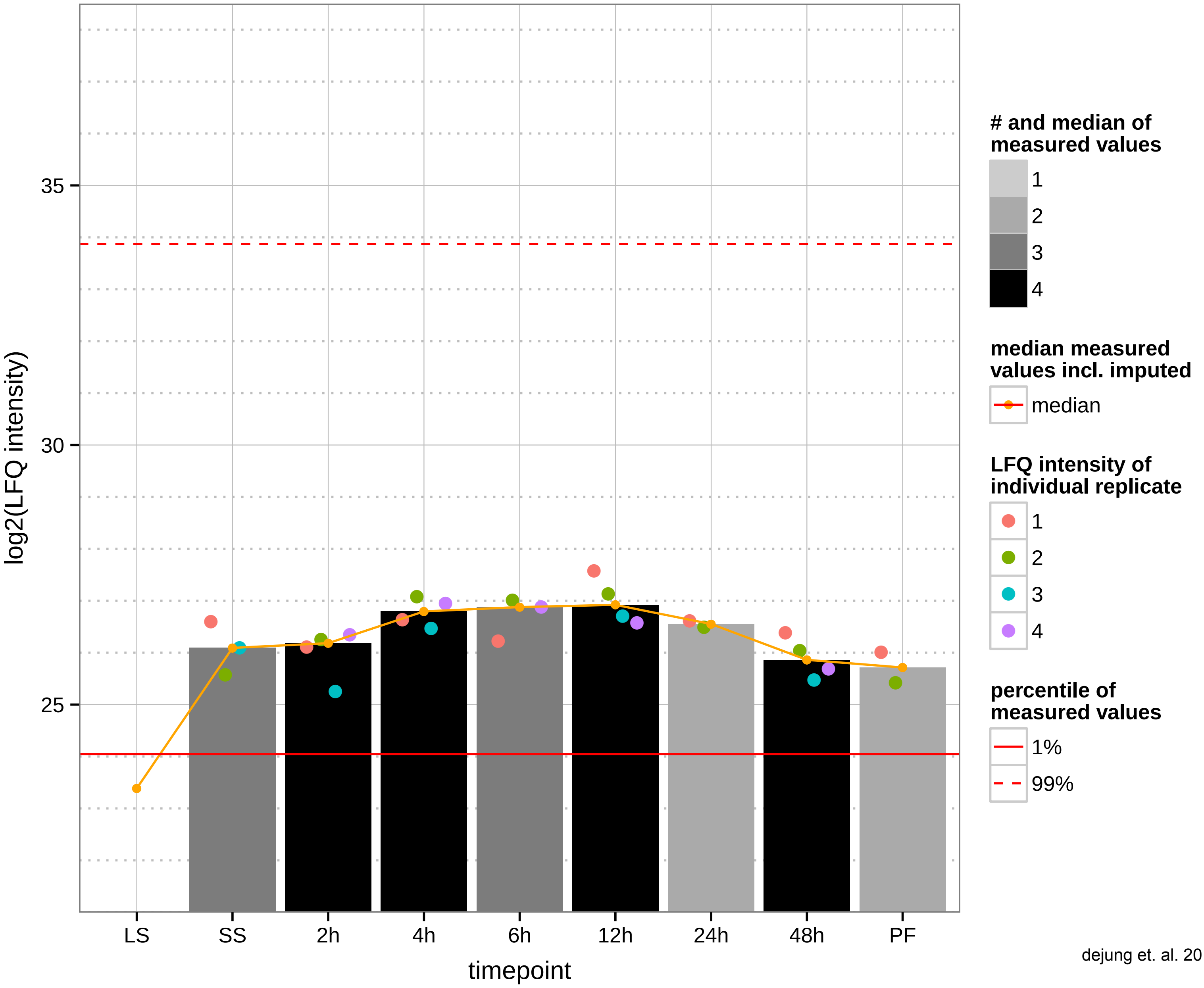
chaperone protein DNAj, putative
Tb927.10.5040;Tb11.v5.0342
AGOF: null, heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: null, protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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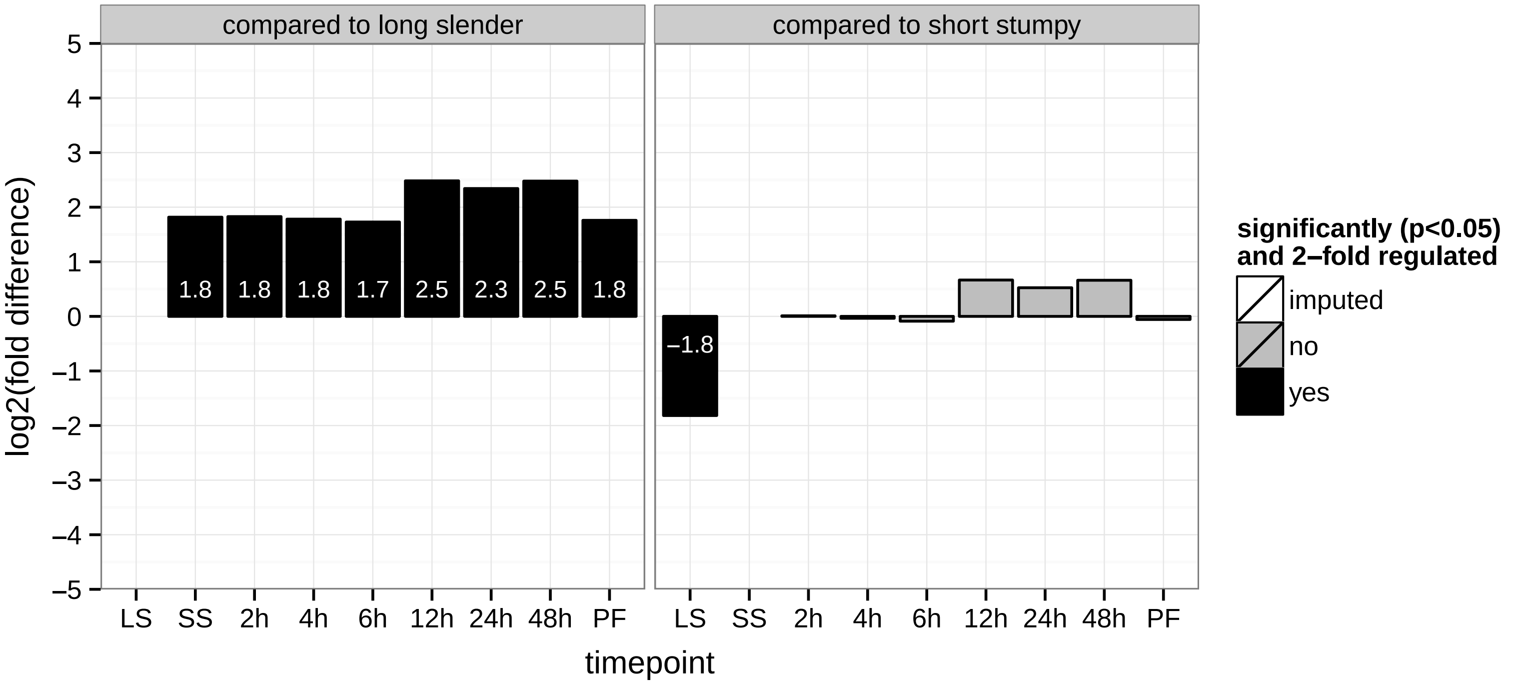
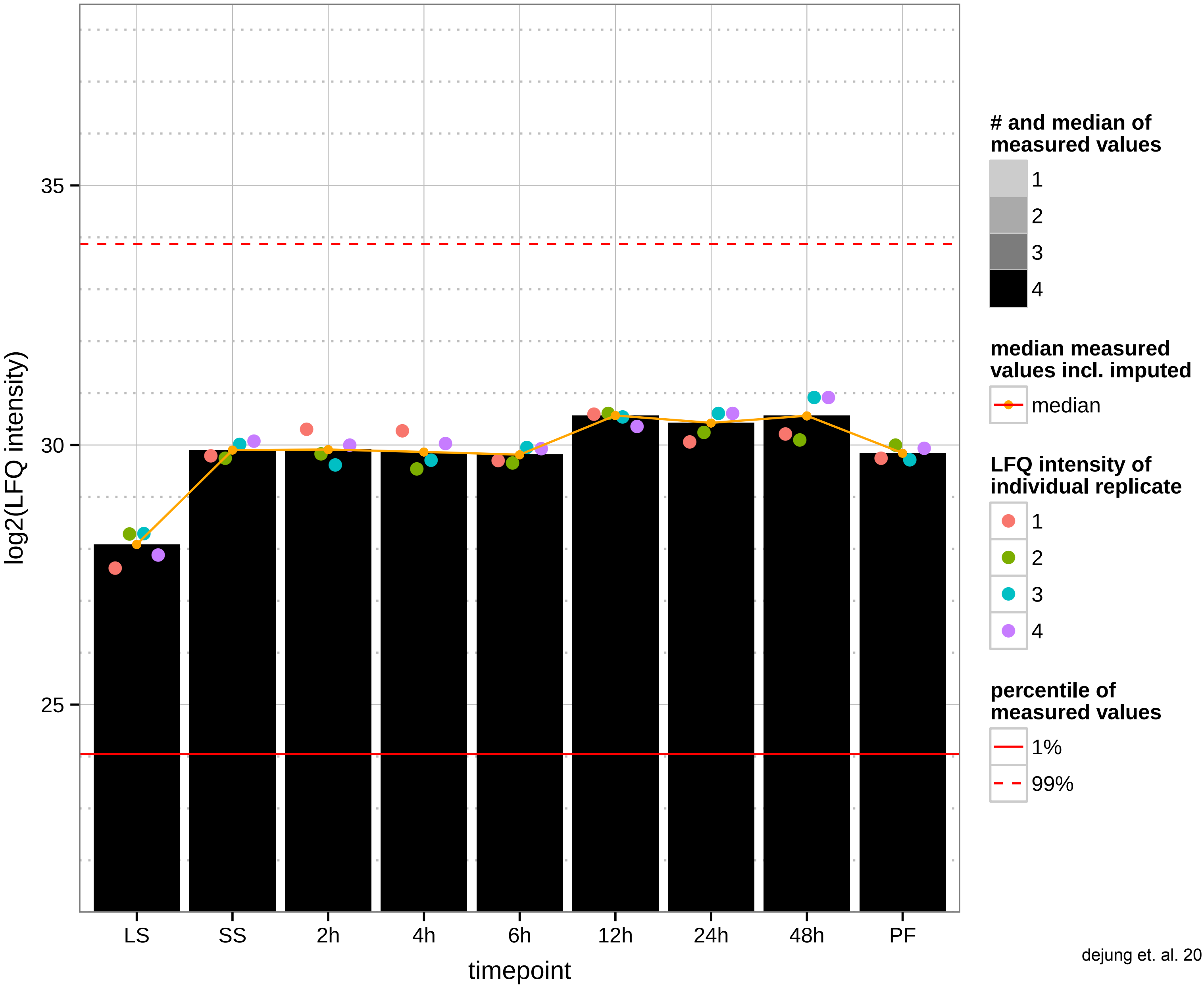
cytidine triphosphate synthase, putative
Tb927.1.1240;Tb11.v5.0356
AGOF: null, CTP synthase activity
AGOC: null, cytosol
AGOP: null, CTP biosynthetic process
PGOF: CTP synthase activity
PGOC: null
PGOP: pyrimidine nucleotide biosynthetic process





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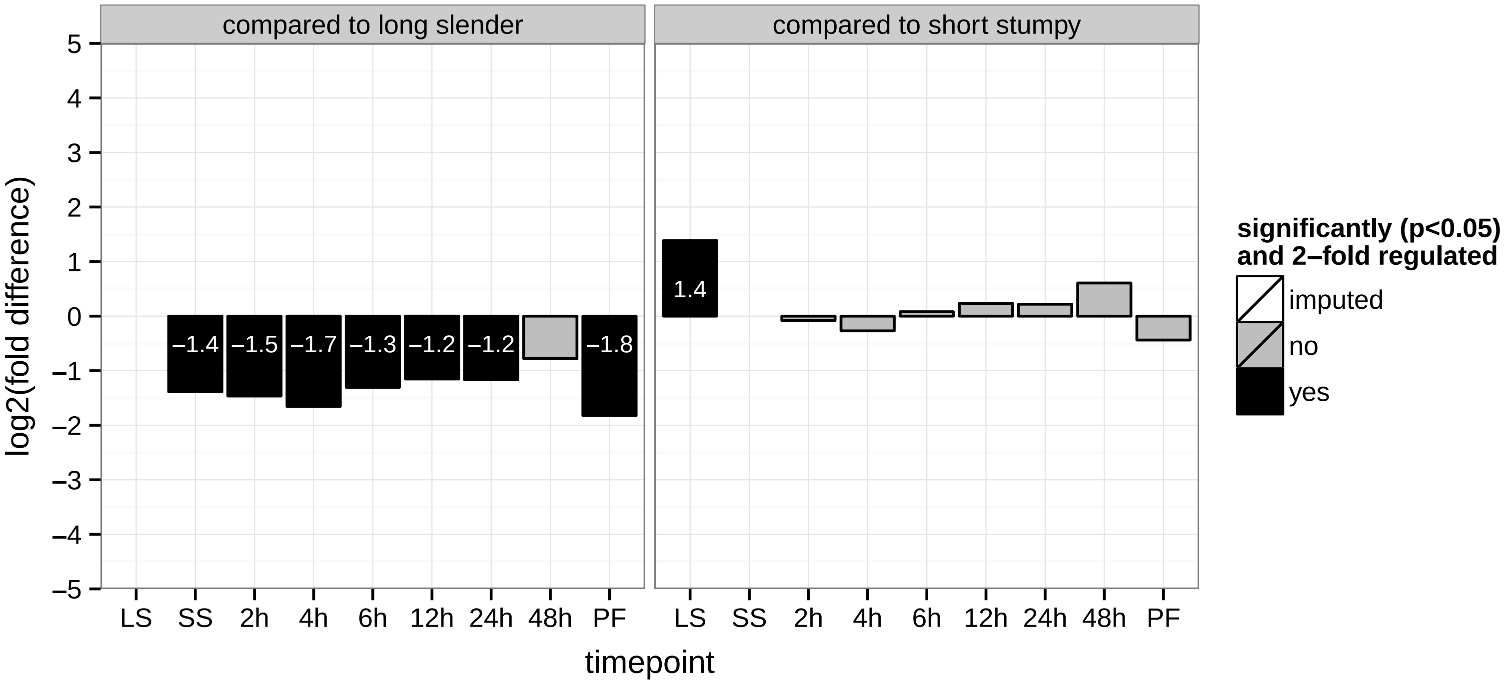
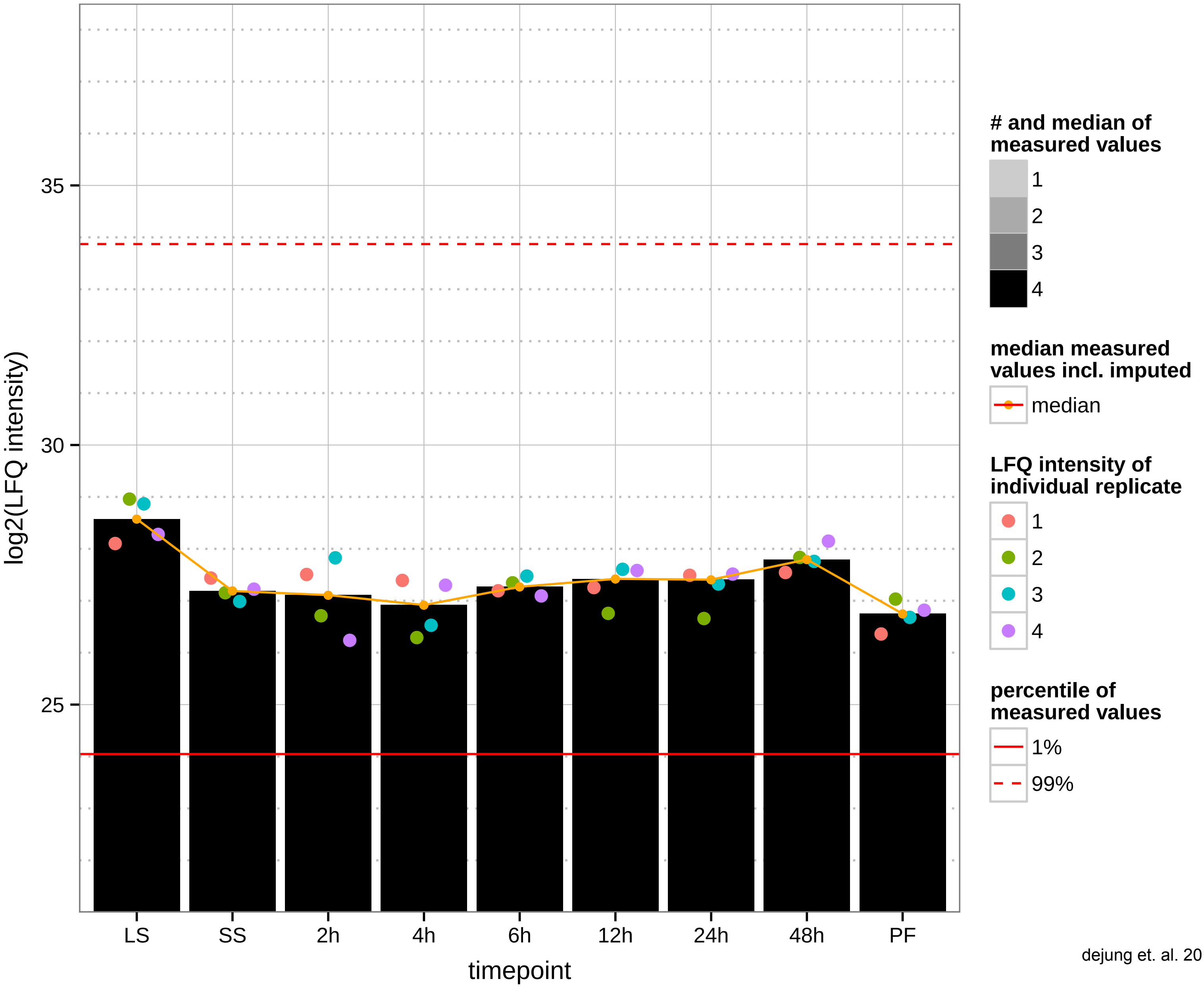
hypothetical protein, conserved, conserved protein
Tb11.v5.0366;Tb927.11.12880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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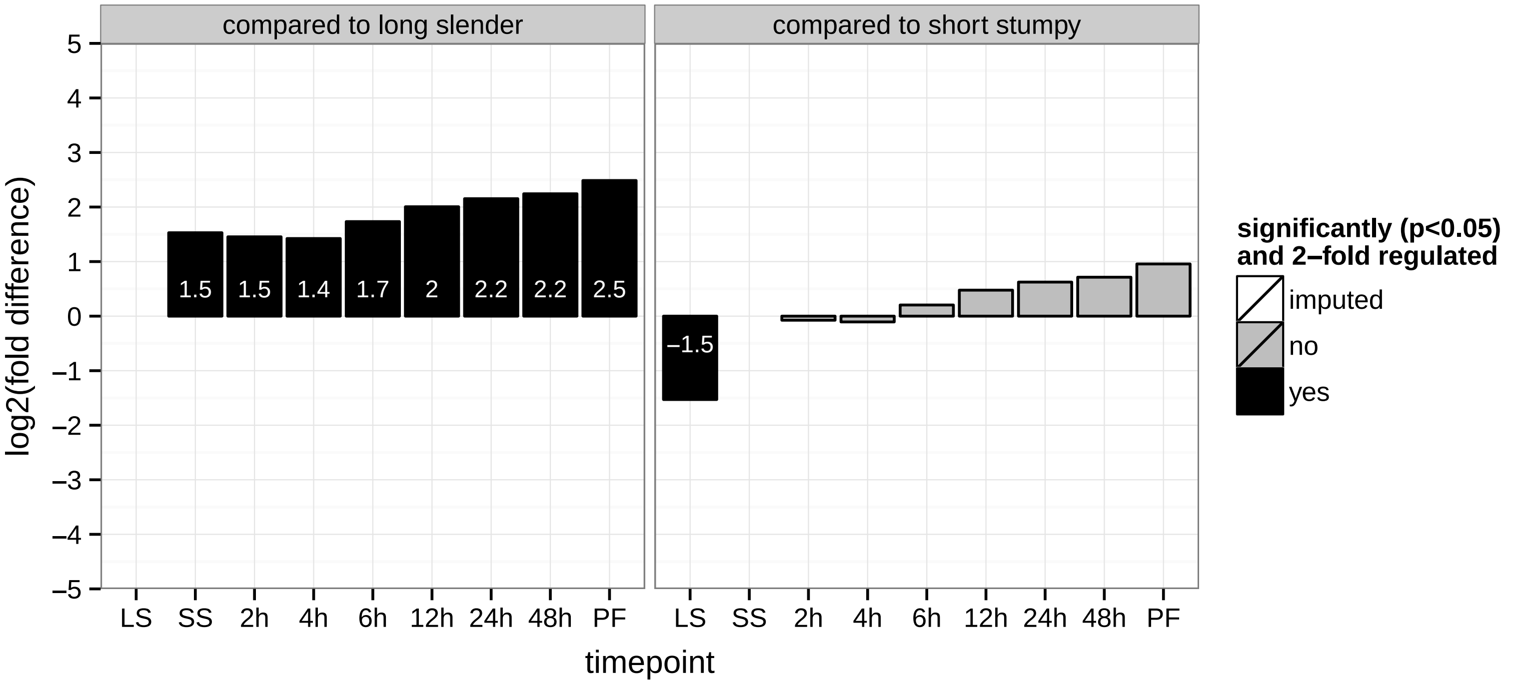
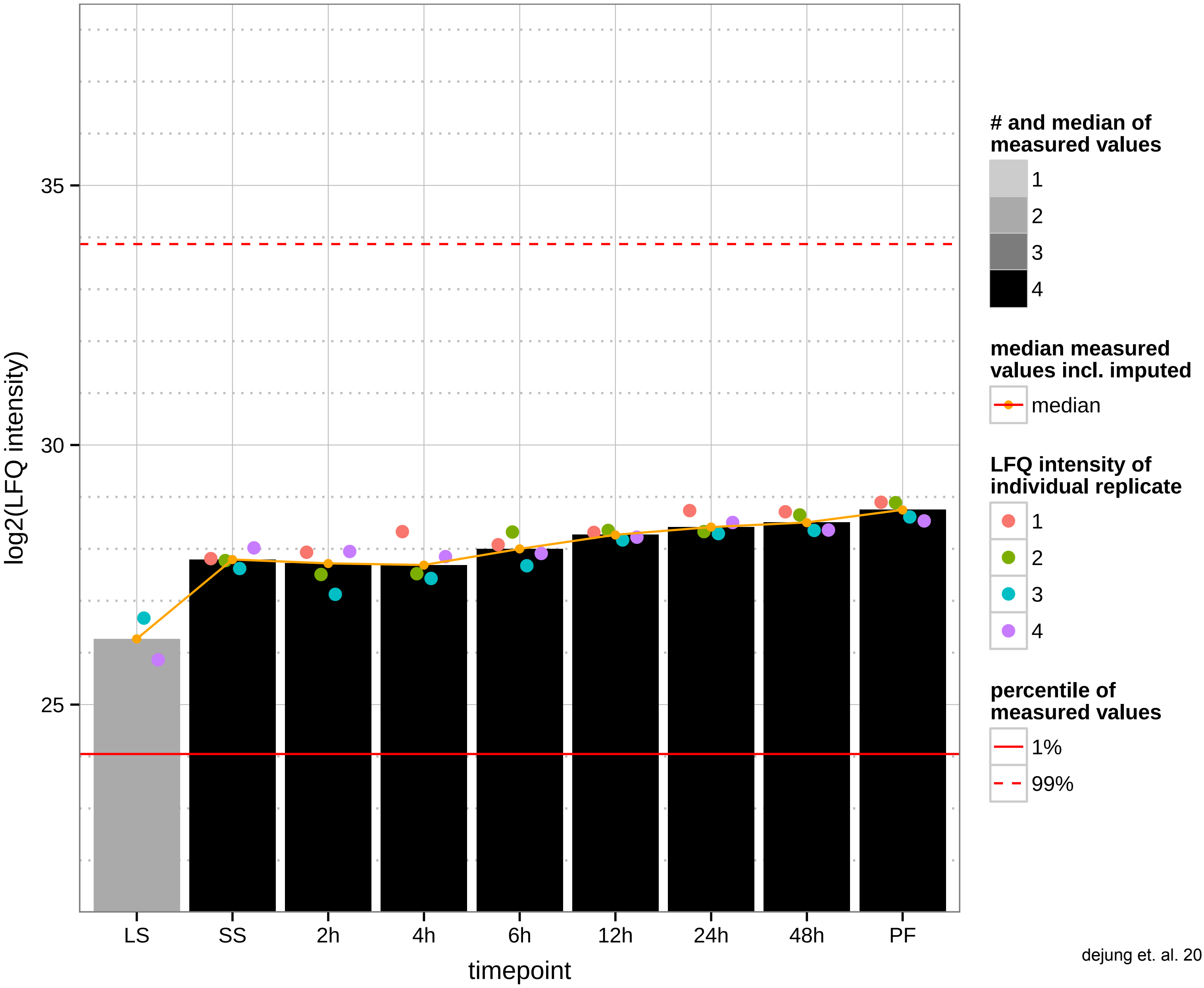
rRNA biogenesis protein, putative
Tb927.1.1370;Tb11.v5.0391
AGOF: null, RNA binding
AGOC: null
AGOP: null, rRNA processing
PGOF: null
PGOC: null
PGOP: null





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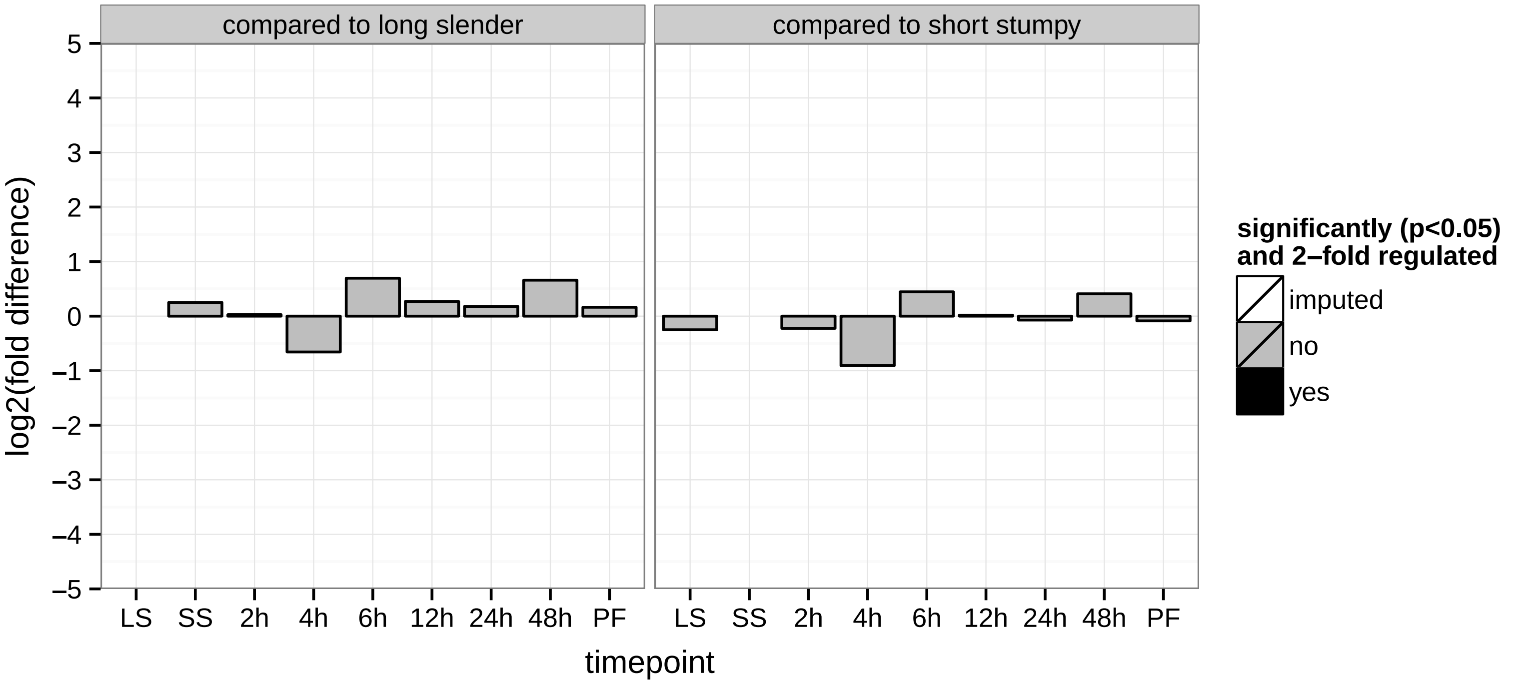
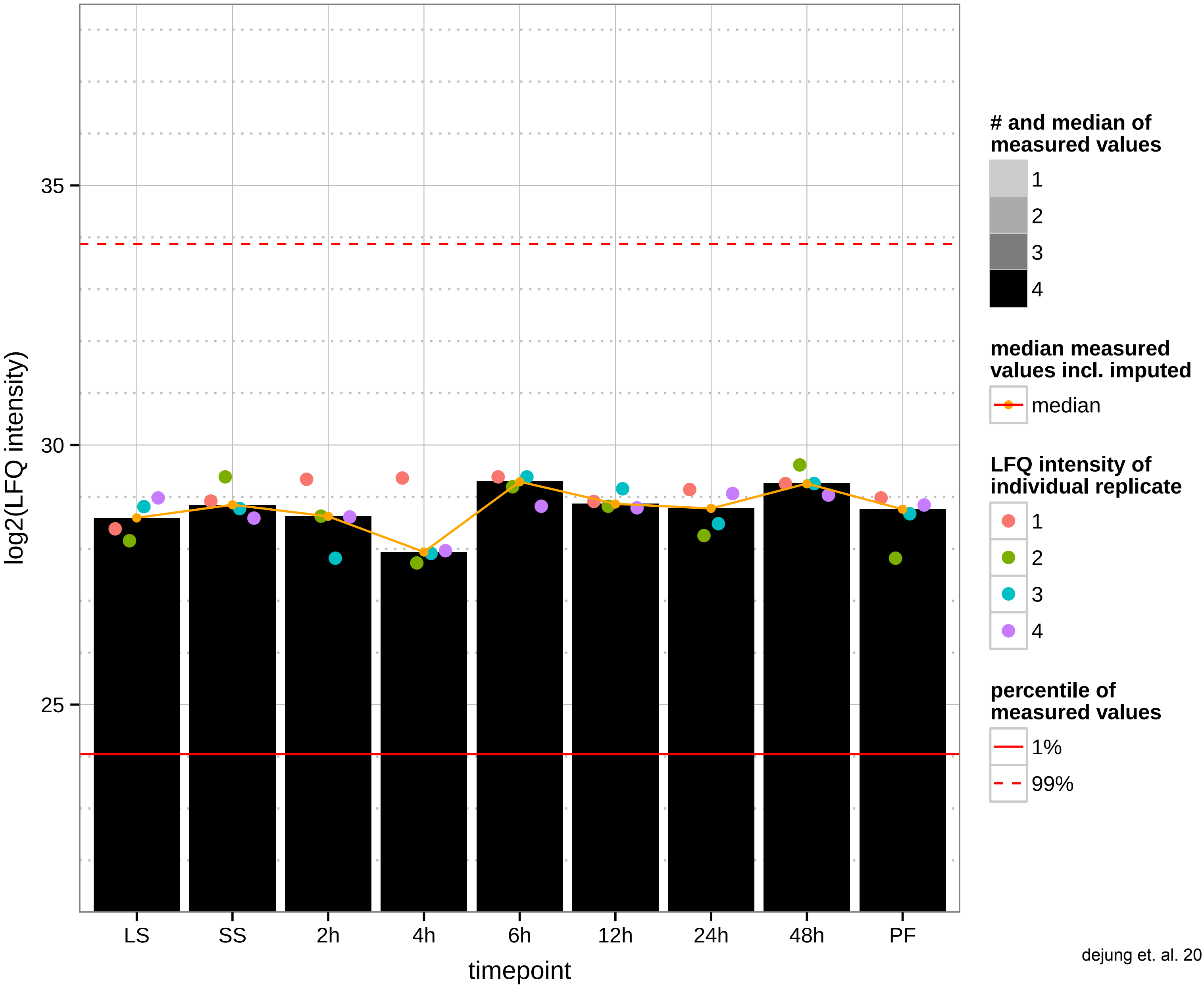
hypothetical protein, conserved
Tb11.v5.0394;Tb927.10.15750
AGOF: null, zinc ion binding
AGOC: null, bacterial–type flagellum basal body
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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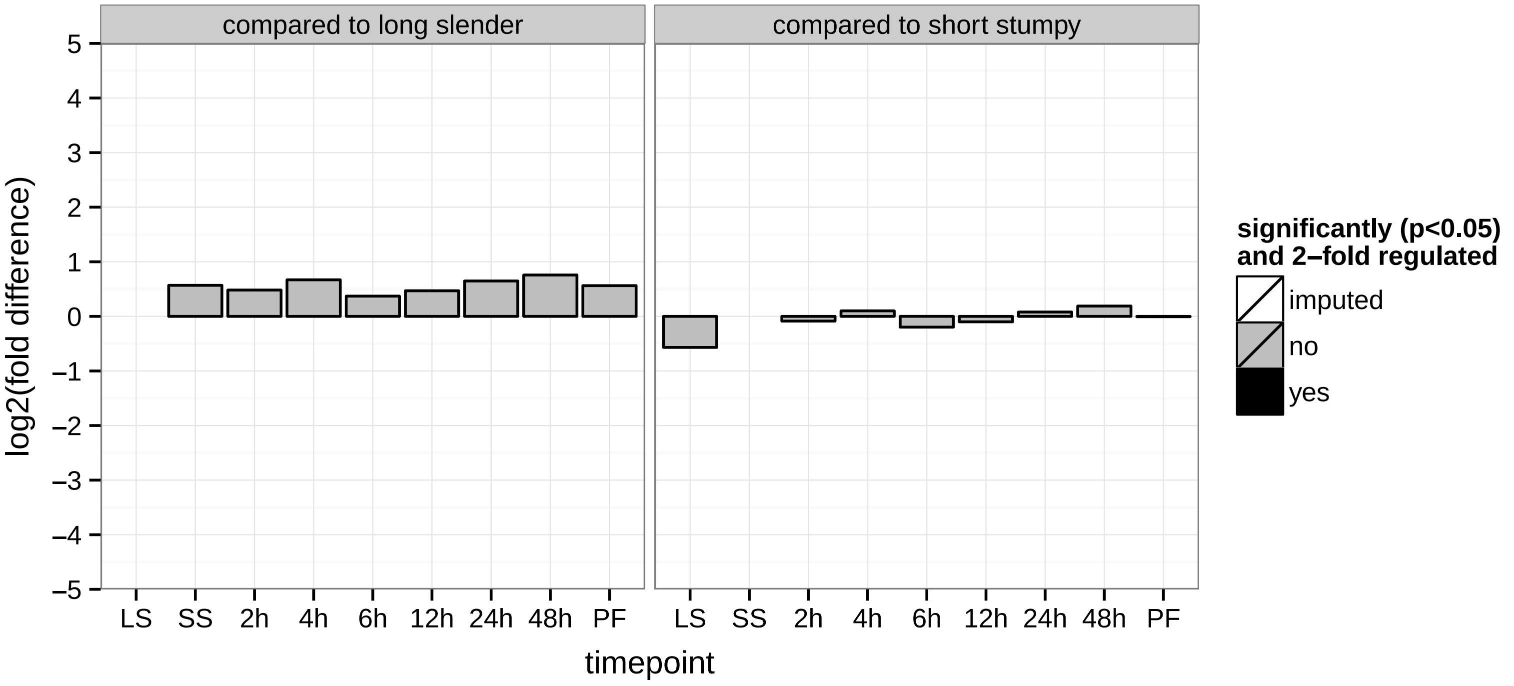
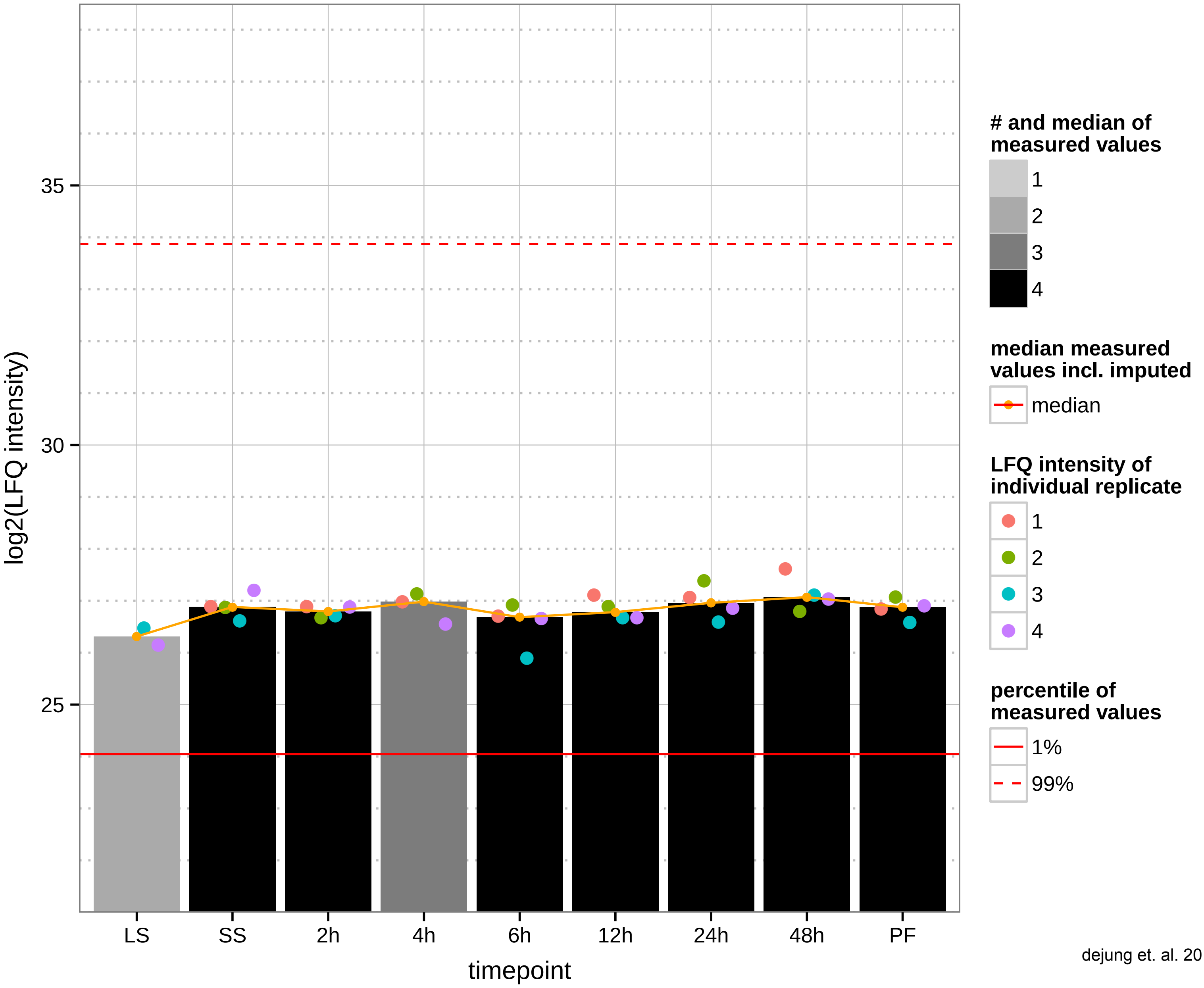
potassium voltage–gated channel, putative
Tb927.10.16170;Tb11.v5.0396
AGOF: null, ATP–activated inward rectifier potassium channel activity, voltage–gated potassium channel activity
AGOC: null, membrane, mitochondrion, voltage–gated potassium channel complex
AGOP: null, potassium ion transport
PGOF: null
PGOC: null
PGOP: protein homooligomerization





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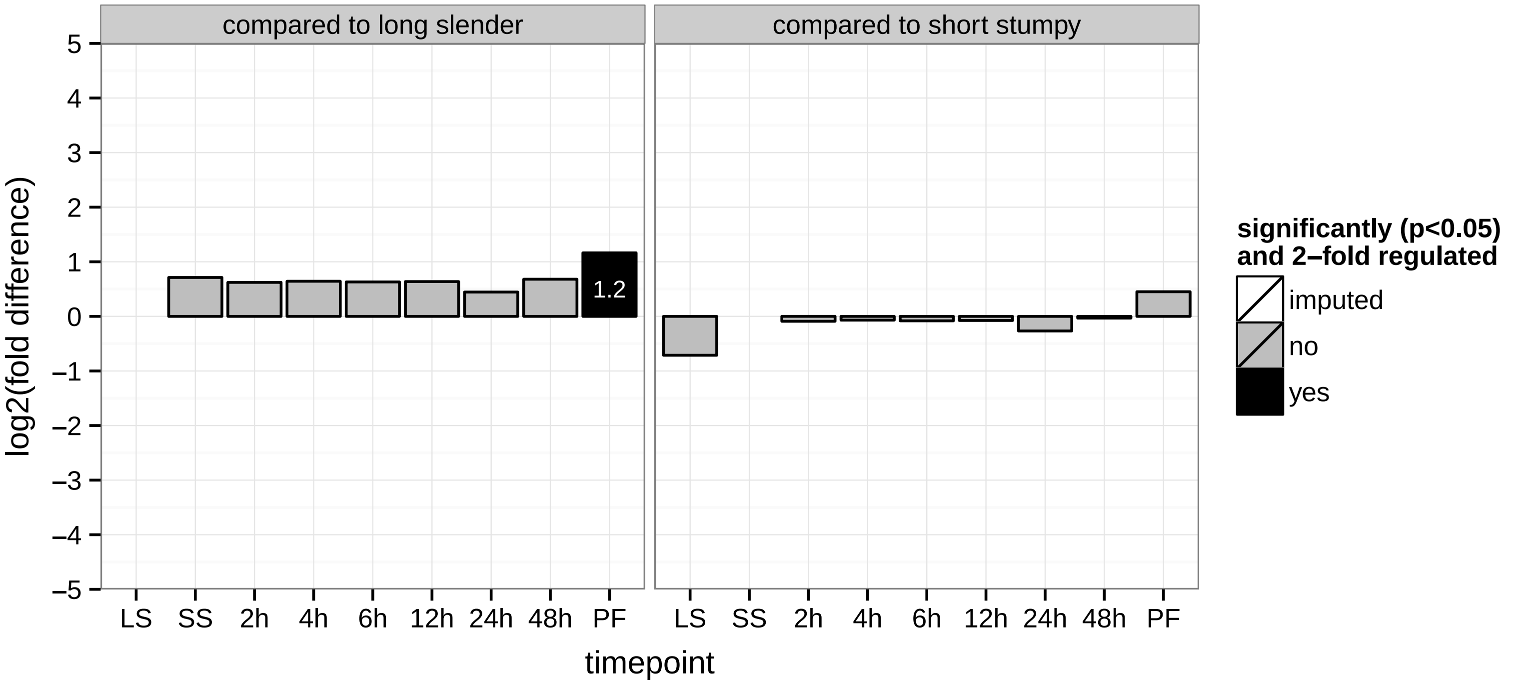
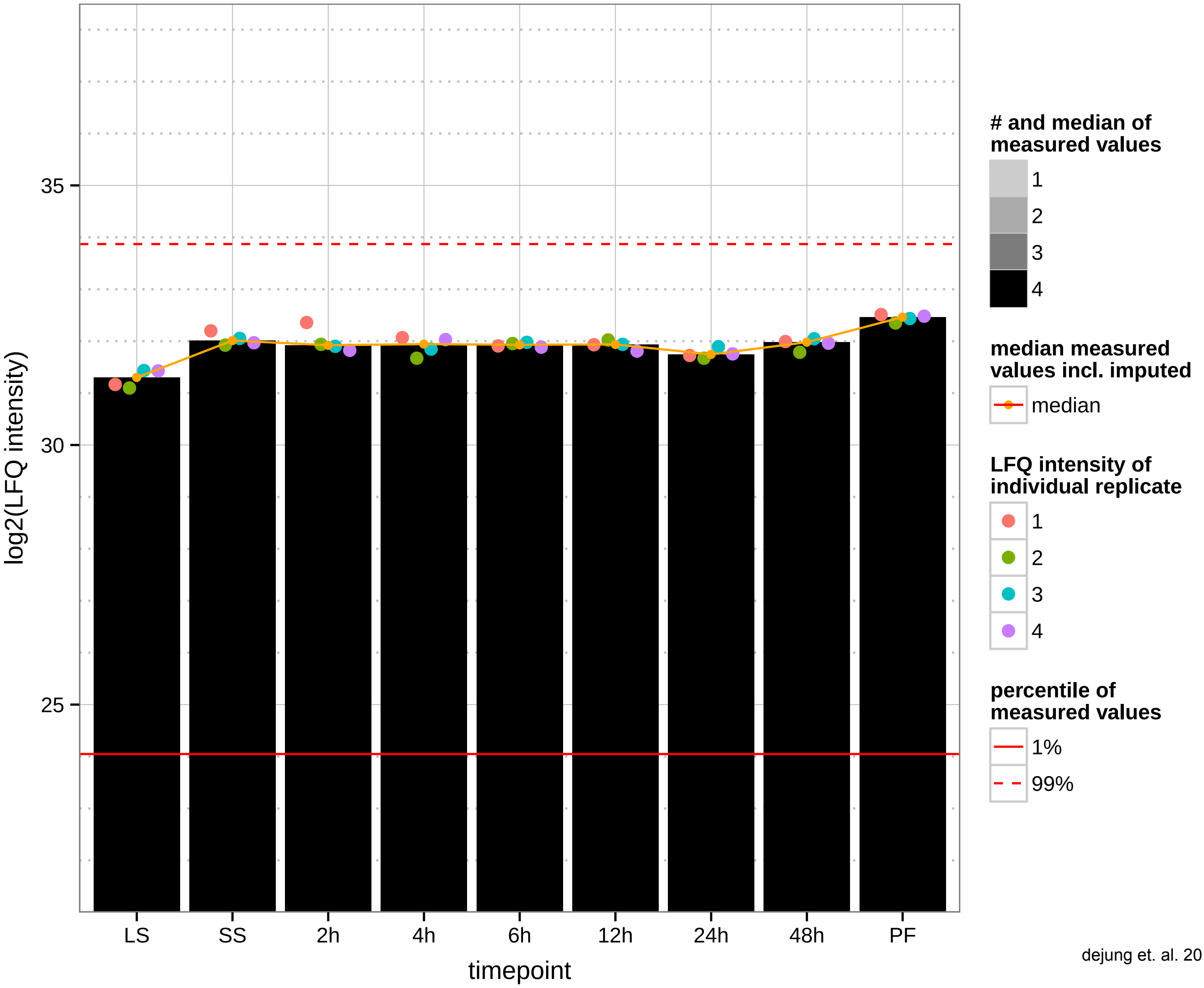
ATP–dependent DEAD/H RNA helicase, putative, DEAD box RNA helicase
Tb927.10.540;Tb11.v5.0414
AGOF: null, ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: null
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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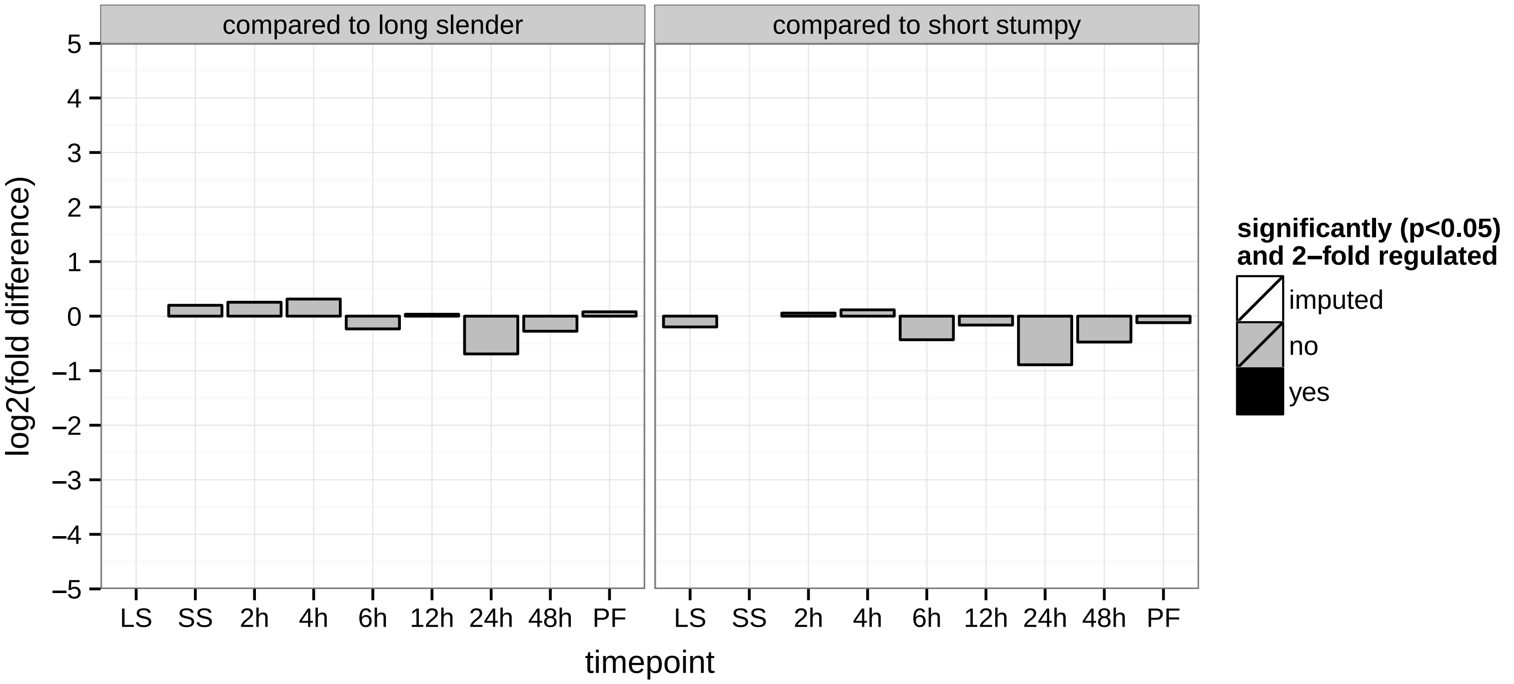
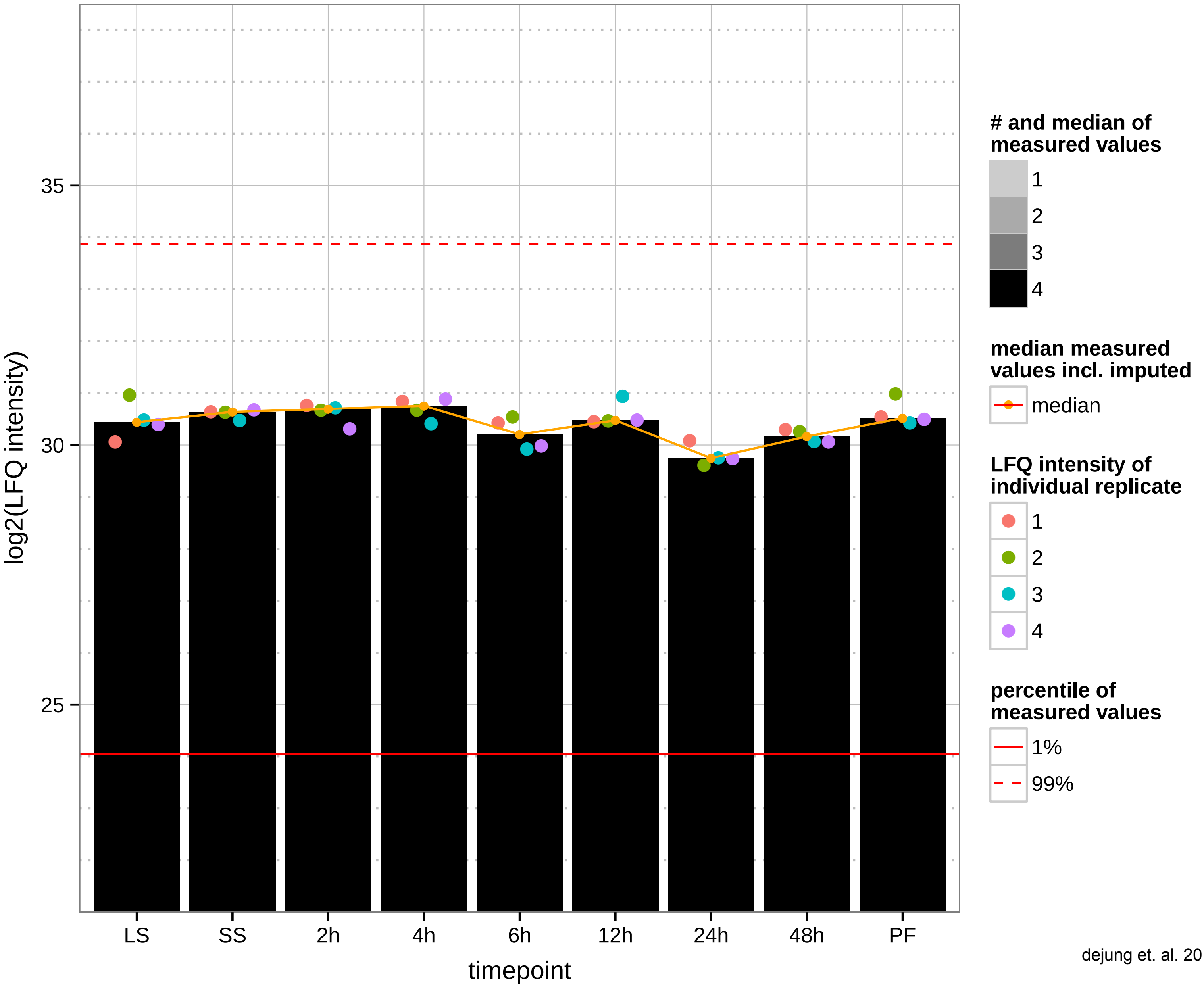
hypothetical protein, conserved
Tb927.10.14490;Tb11.v5.0420
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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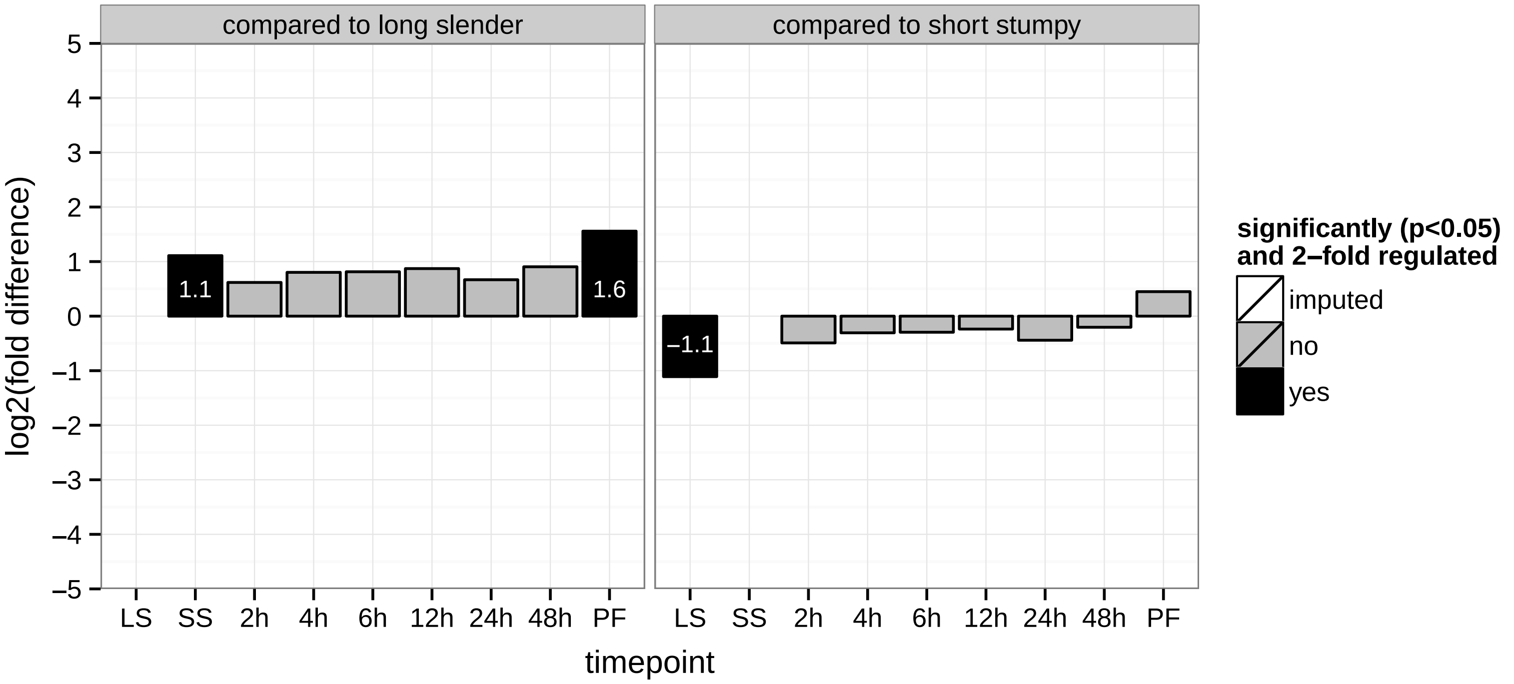
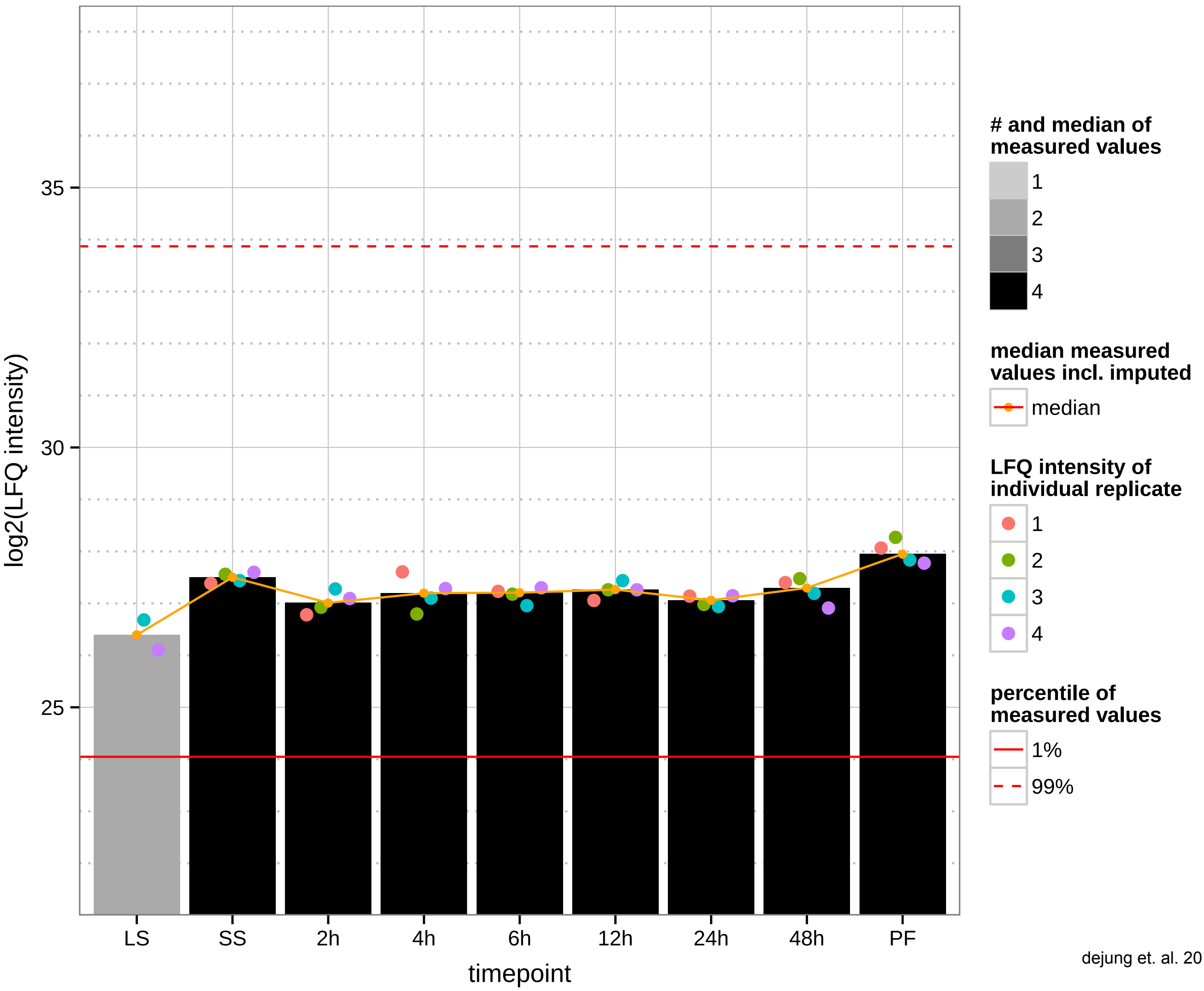
peroxisome assembly protein, putative, peroxin 12, putative (PEX12)
Tb927.10.15850;Tb11.v5.0427
AGOF: null
AGOC: null, glycosome, glycosome membrane, integral to membrane, peroxisomal membrane
AGOP: null, peroxisome organization
PGOF: null
PGOC: null
PGOP: null





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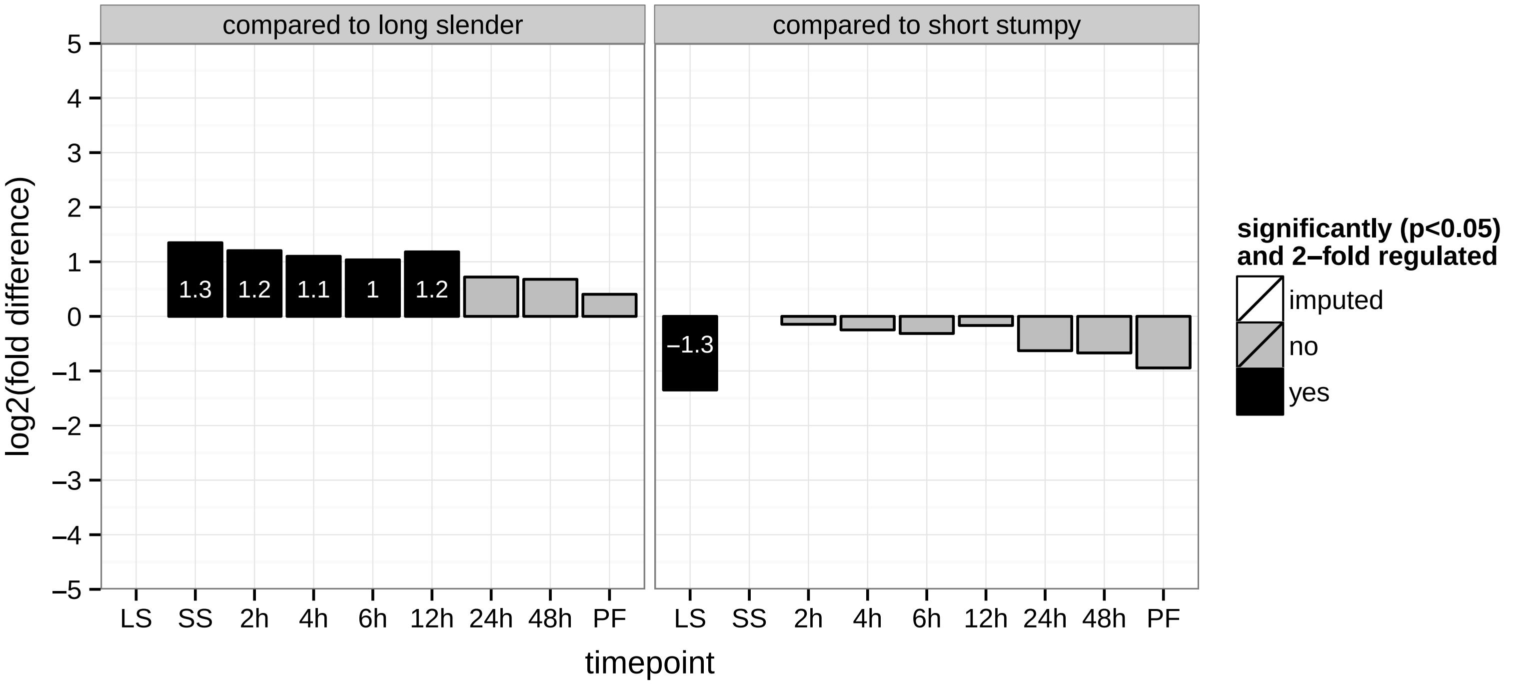
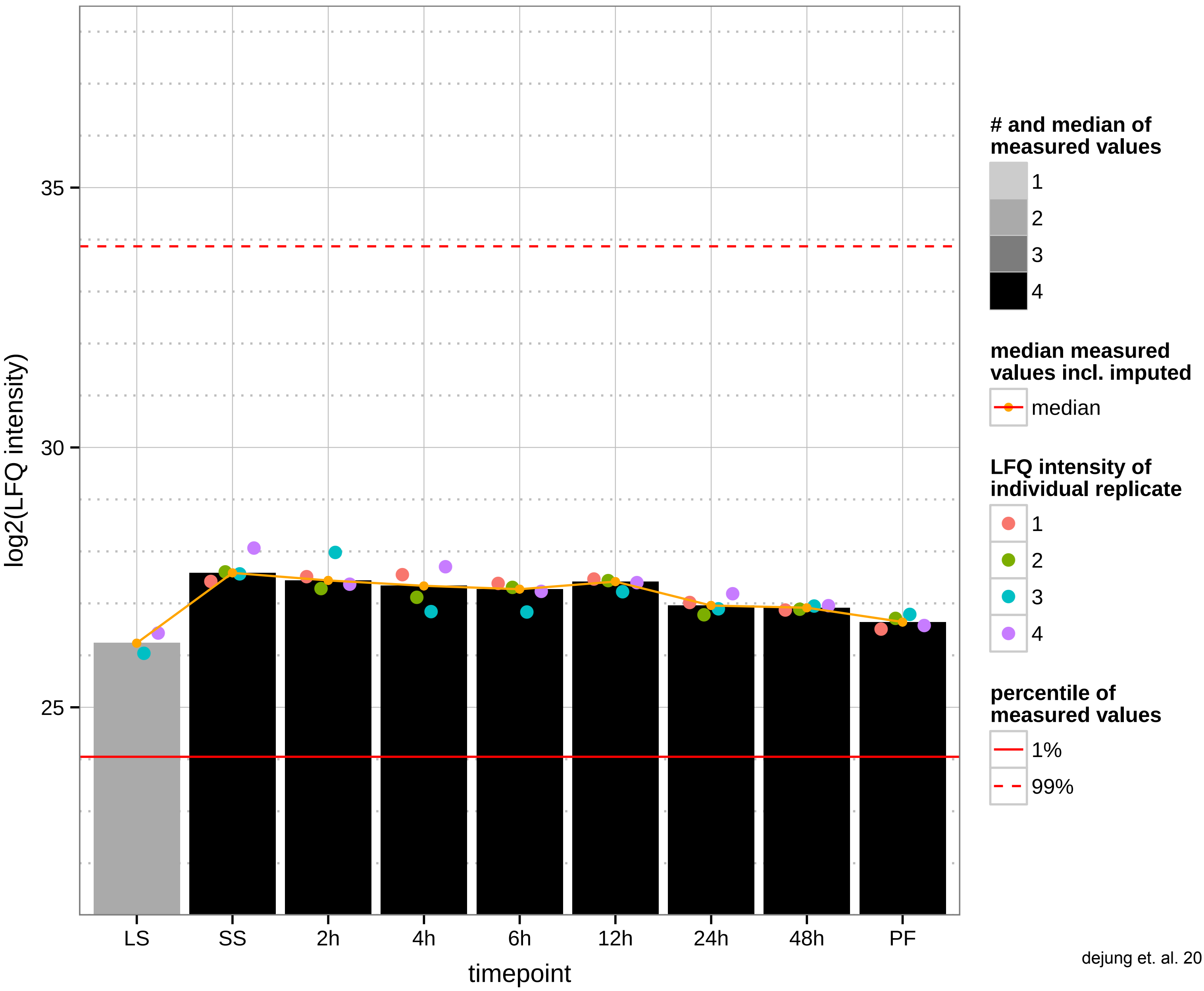
hypothetical protein, conserved, leucine−rich repeat protein (LRRP), putative
Tb927.1.1030;Tb11.v5.0436
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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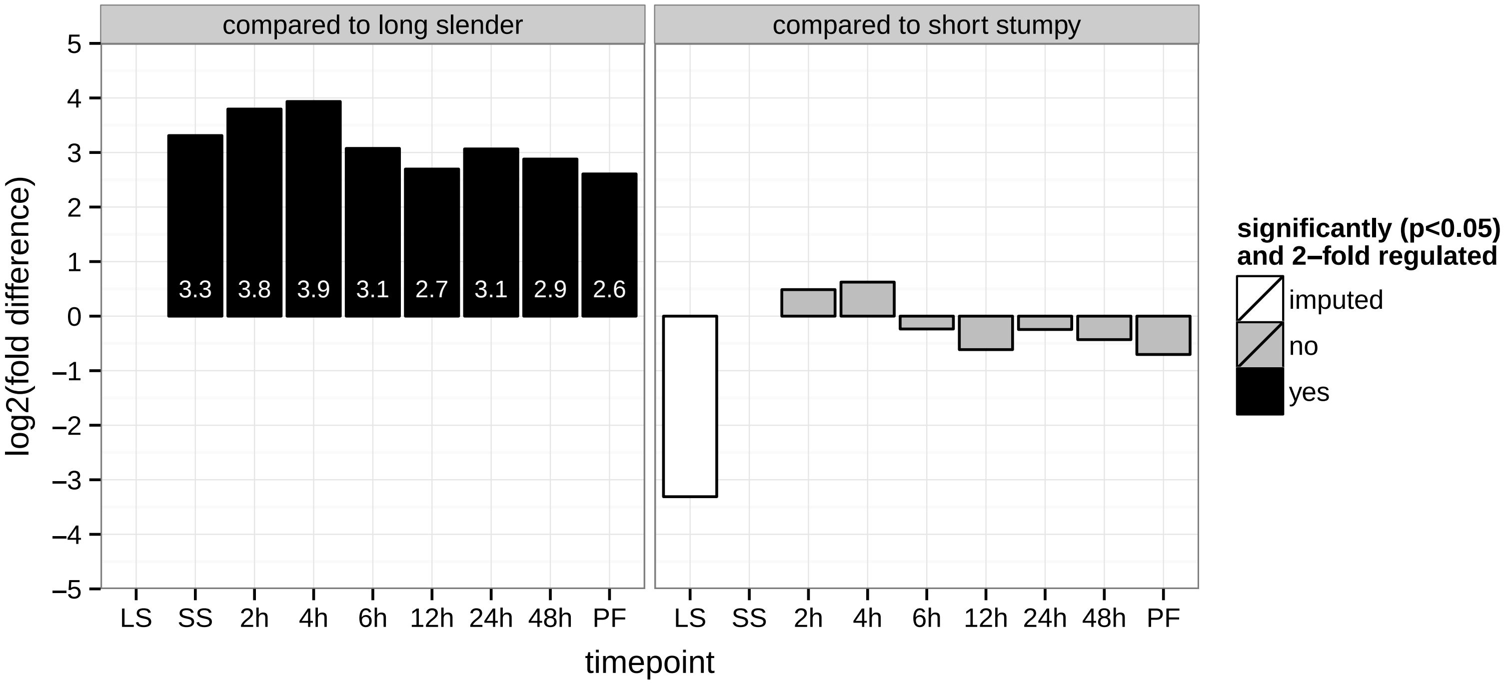
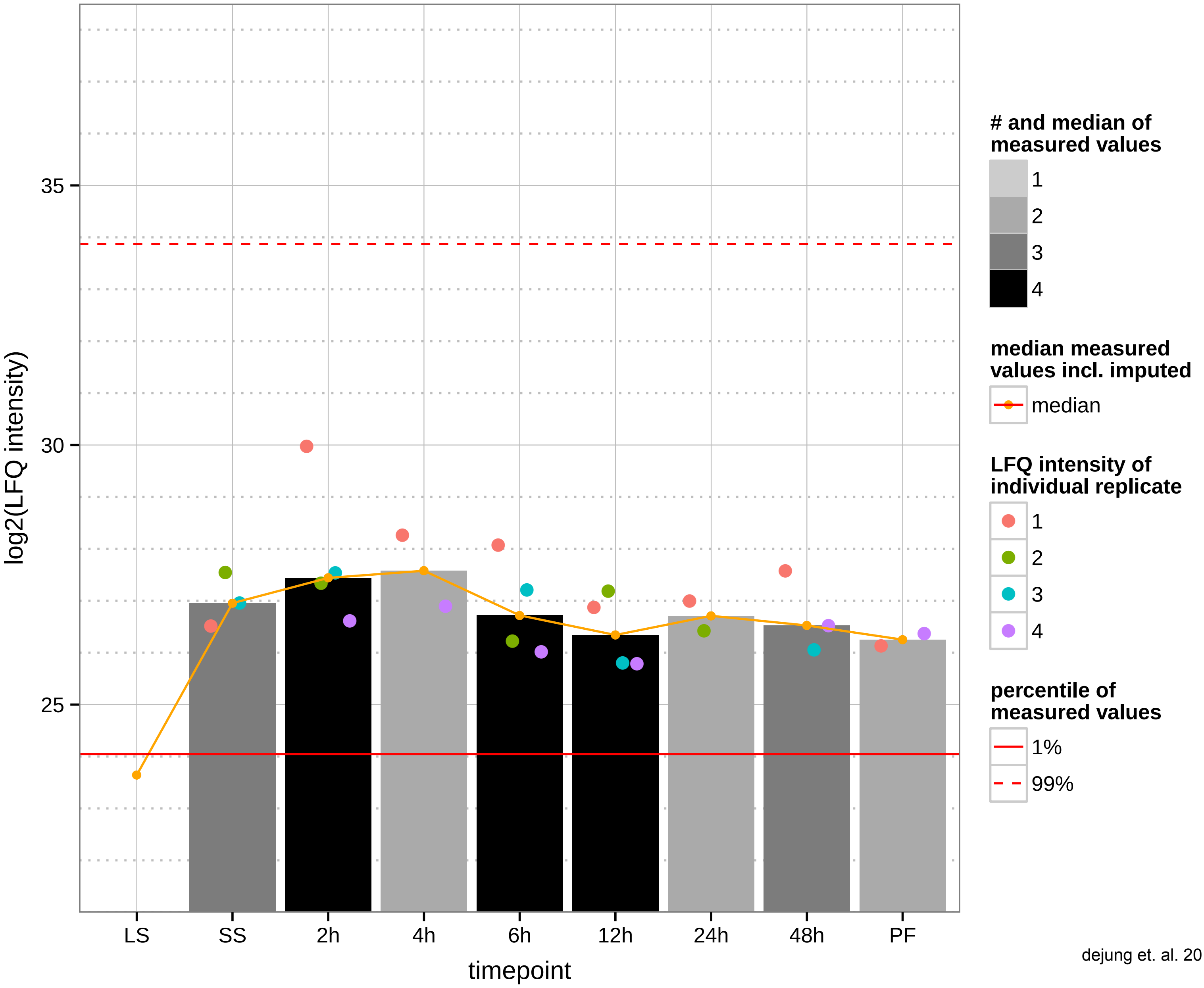
alpha tubulin, putative
Tb11.v5.0468
AGOF: null
AGOC: null
AGOP: null
PGOF: GTP binding, GTPase activity
PGOC: protein complex
PGOP: GTP catabolic process, protein polymerization





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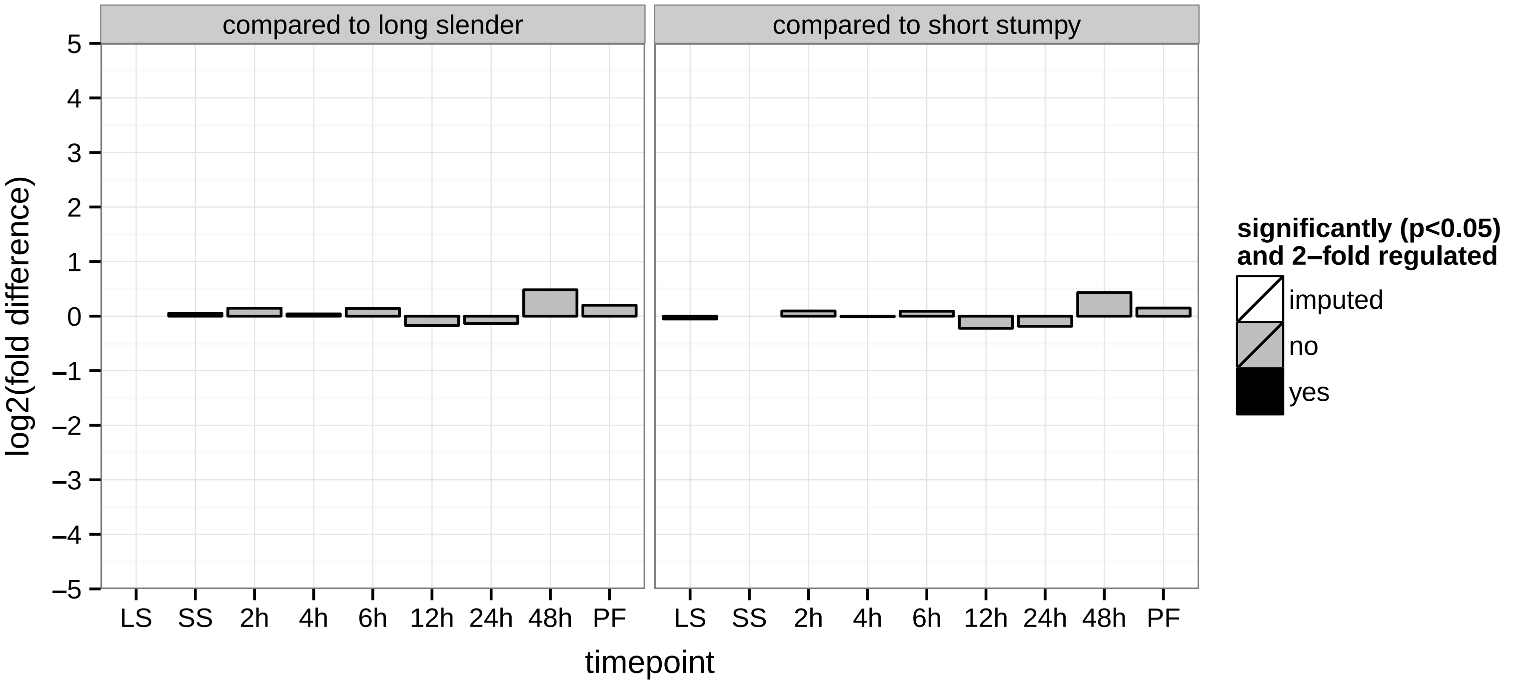
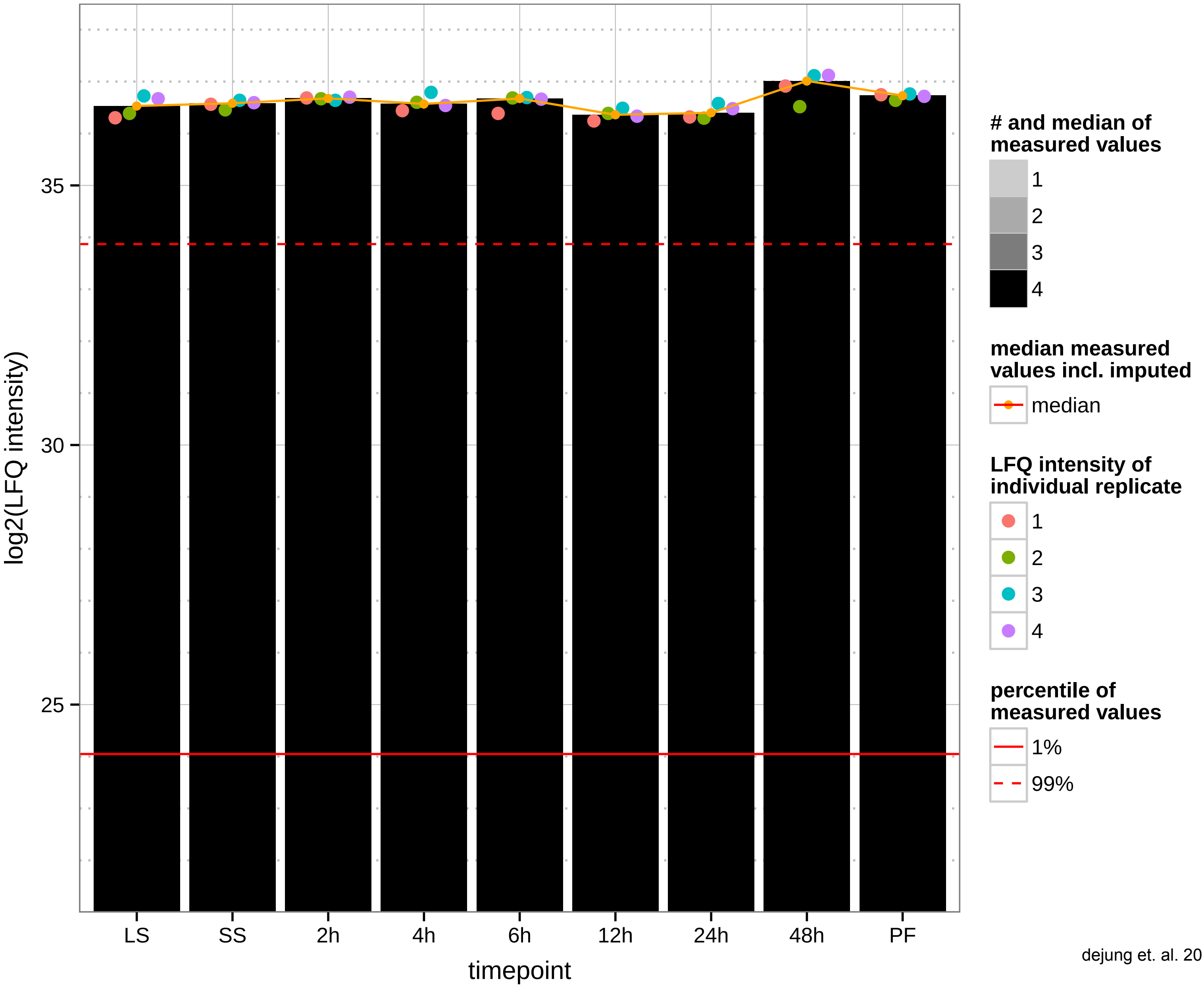
beta tubulin, putative, pseudogene
Tb927.1.2390;Tb927.1.2370;Tb927.1.2350;Tb927.1.2330;Tb11.v5.0469;Tb927.1.2410
AGOF: null, GTP binding, GTPase activity, structural constituent of cytoskeleton, structural molecule activity
AGOC: null, microtubule, protein complex
AGOP: null, cellular component movement, microtubule cytoskeleton organization, microtubule–based movement, protein poly
PGOF: GTP binding, GTPase activity, null
PGOC: protein complex, null
PGOP: GTP catabolic process, protein polymerization, null





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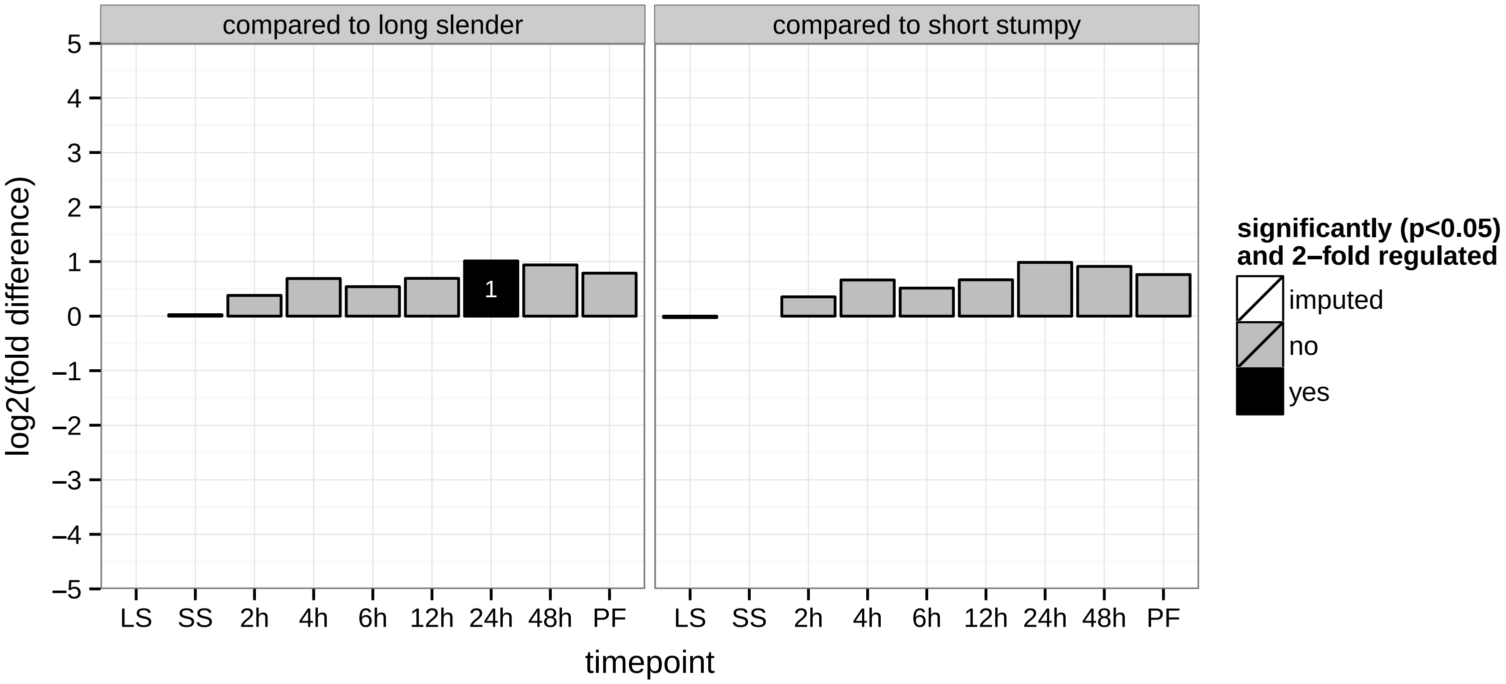
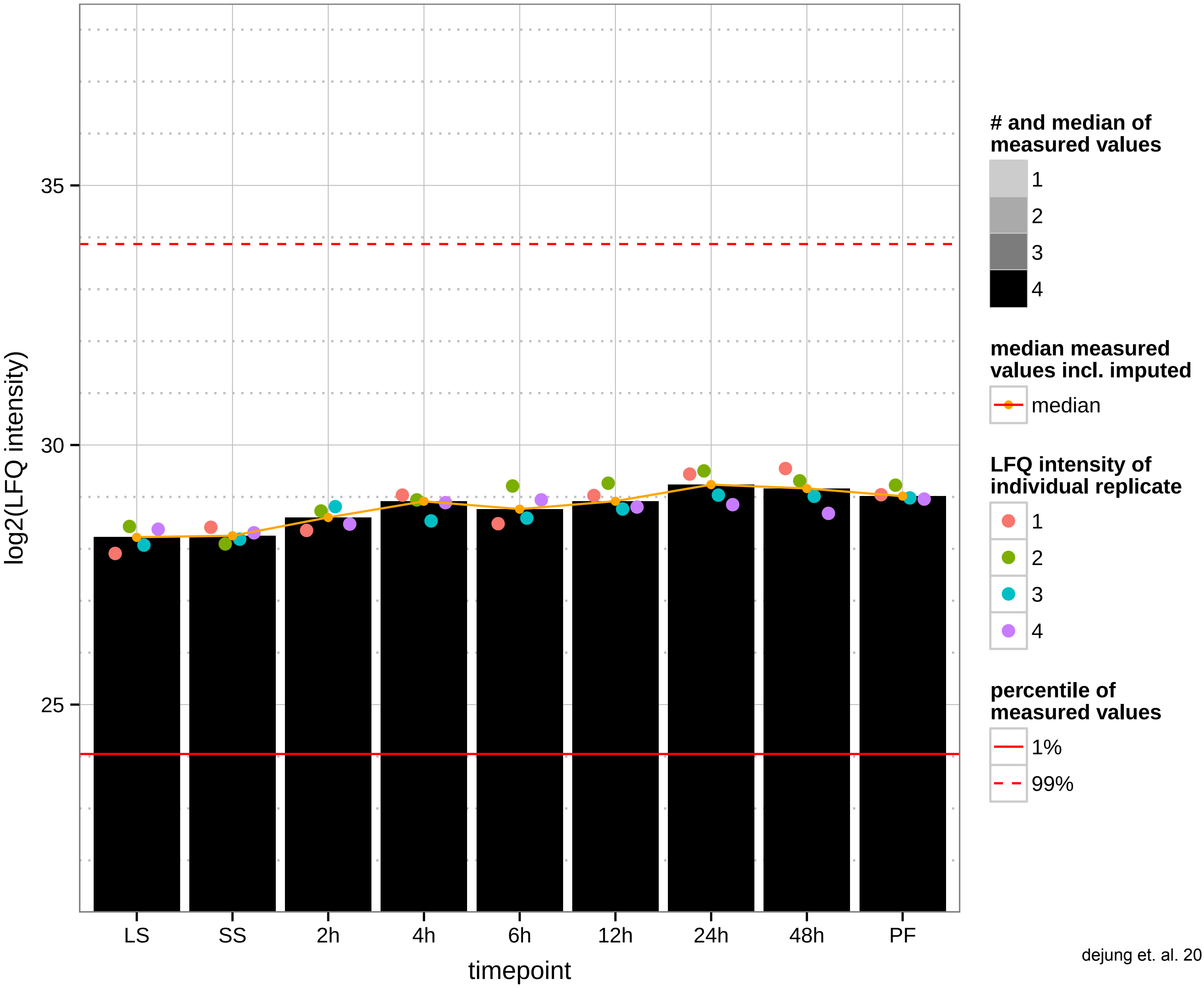
DNA–directed RNA polymerase, alpha subunit, putative, DNA–directed RNA polymerases I and III subunit RPAC1, putative (F
Tb11.v5.0480;Tb927.10.15370
AGOF: null, DNA binding, DNA–directed RNA polymerase activity, protein dimerization activity
AGOC: null
AGOP: null, transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity, protein dimerization activity
PGOC: null
PGOP: transcription, DNA–dependent





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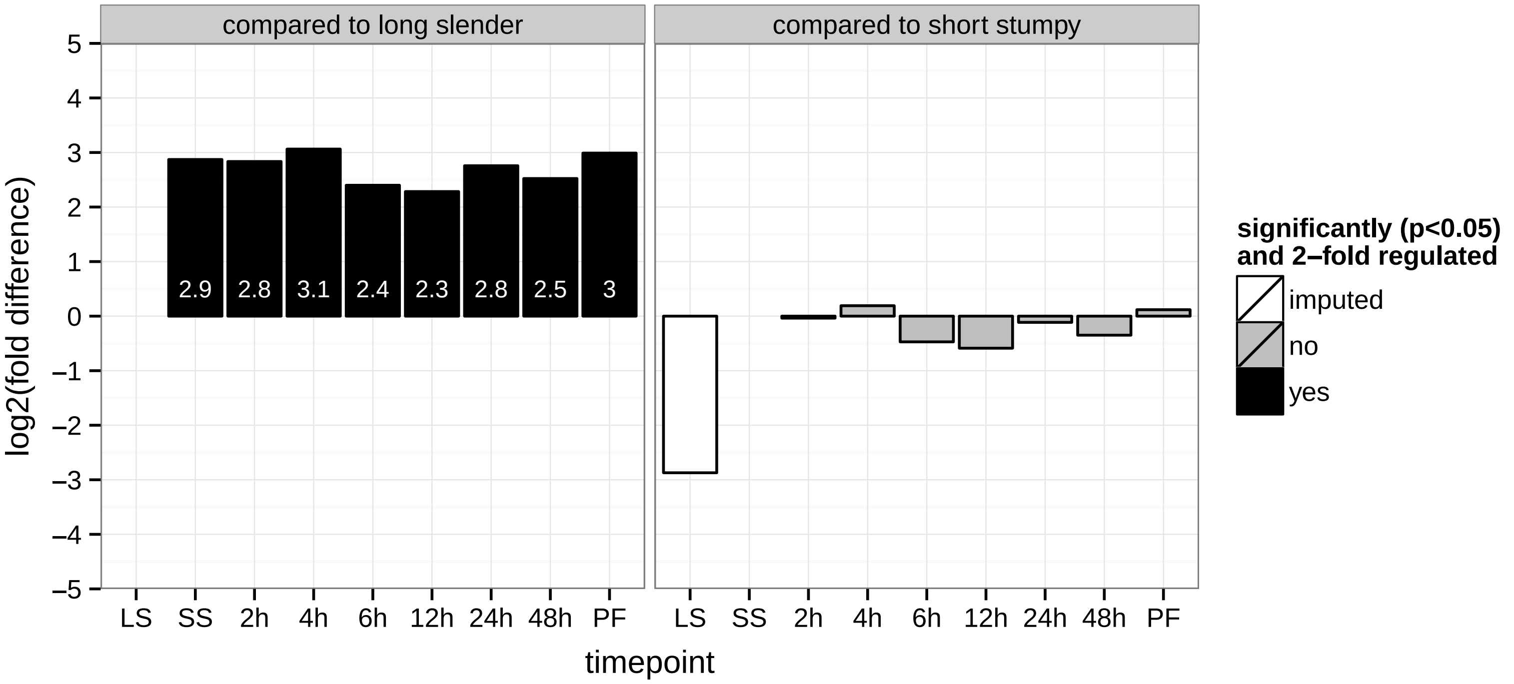
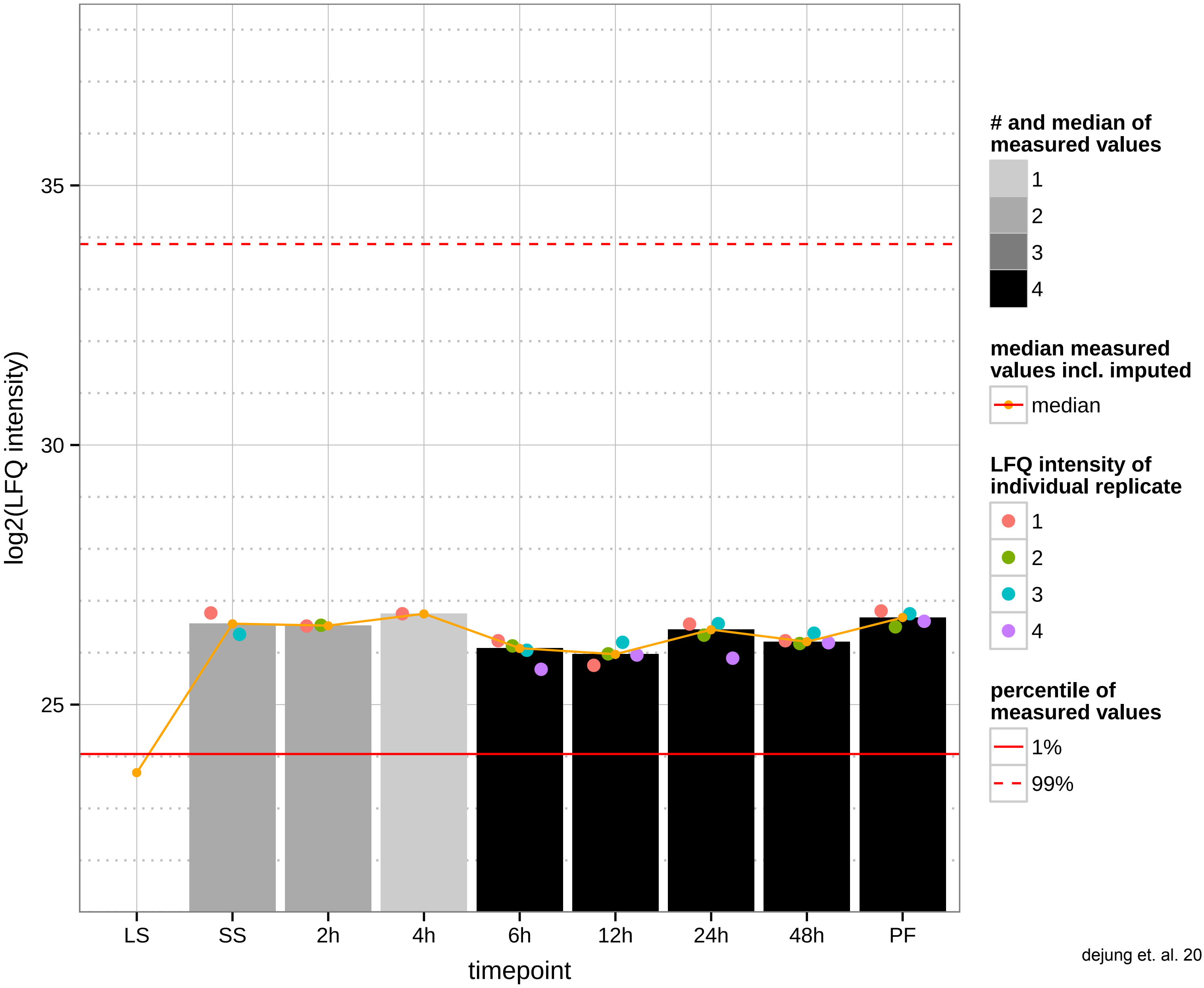
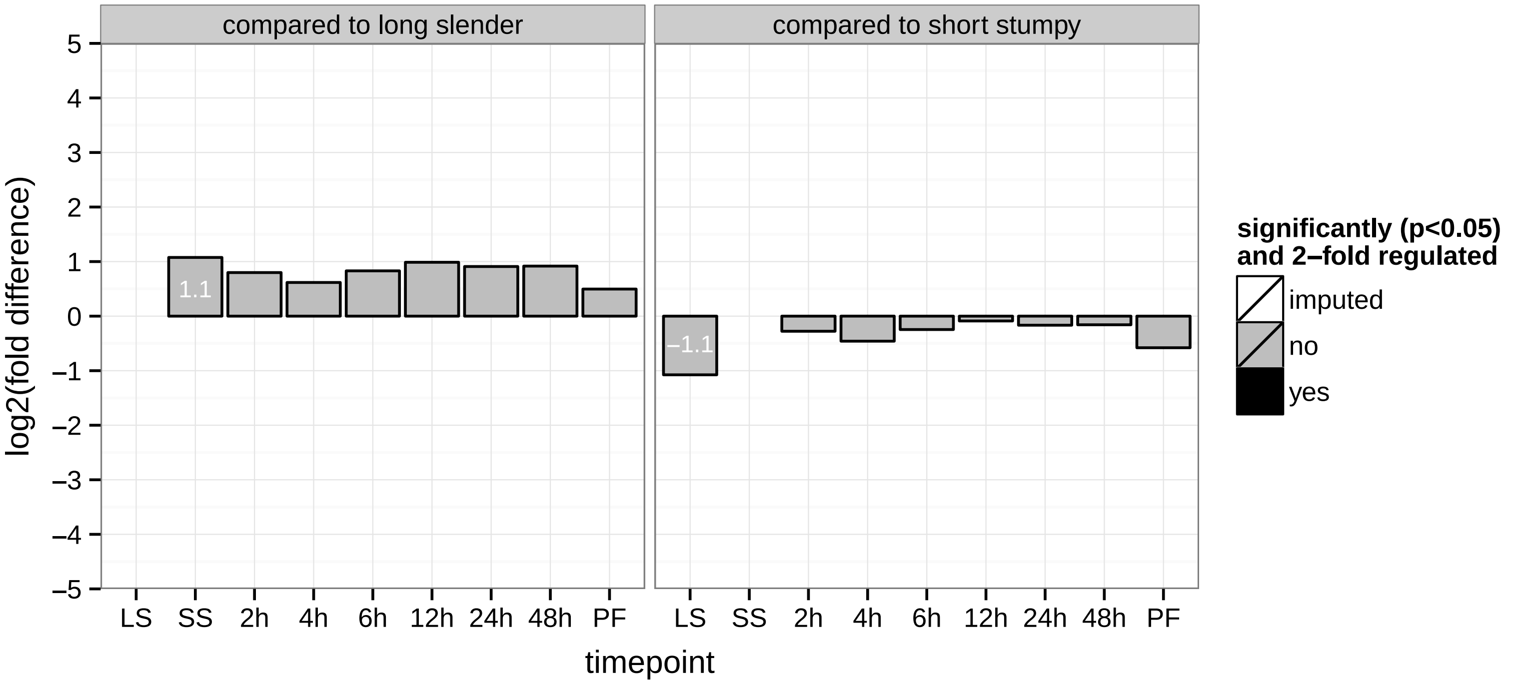
U3 snoRNA–associated protein UTP11, putative
Tb927.10.15380;Tb11.v5.0481
AGOF: null
AGOC: null, ribonucleoprotein complex, small–subunit processome
AGOP: null, rRNA processing
PGOF: null
PGOC: small–subunit processome
PGOP: rRNA processing

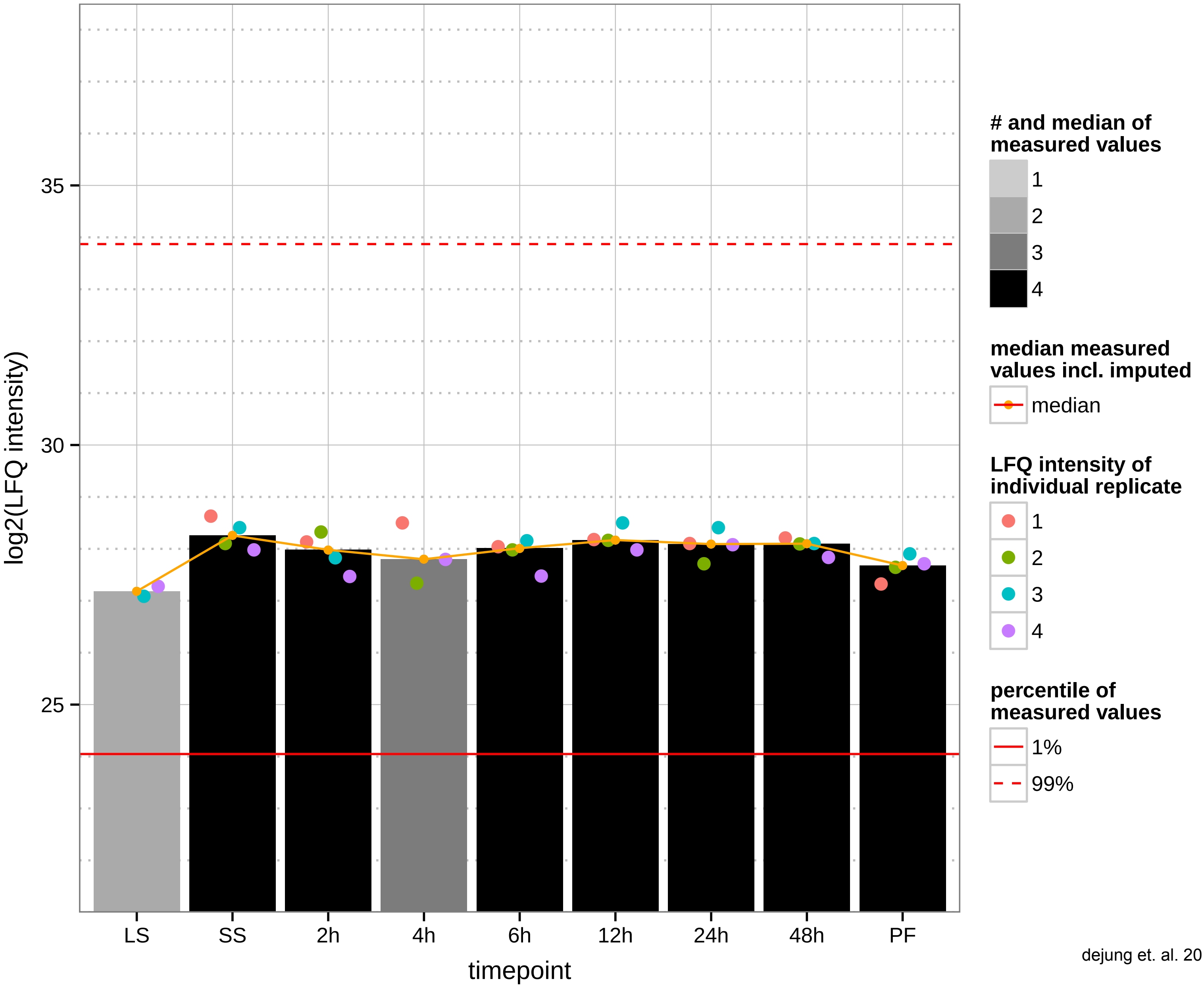




dejung et. al. 2015

retrotransposon hot spot (RHS) protein, putative
Tb11.v5.0489
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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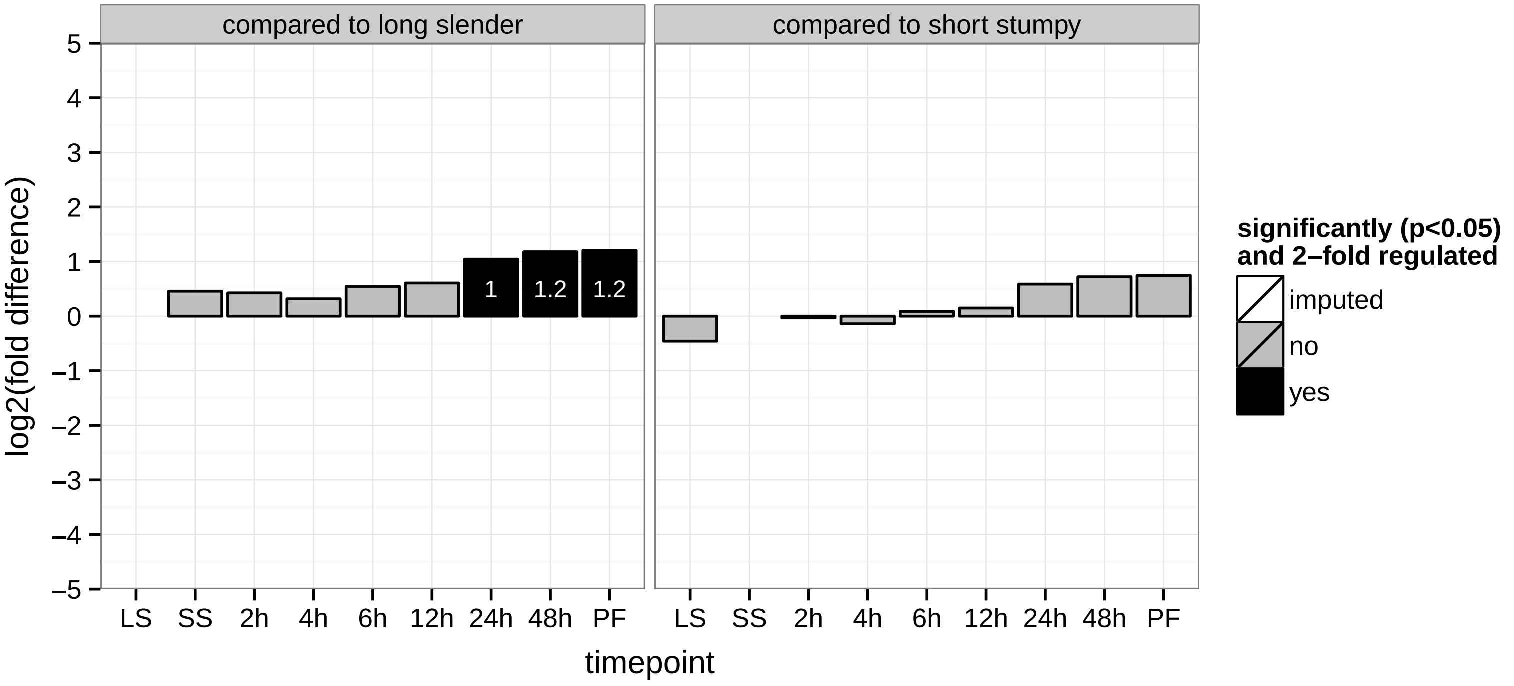
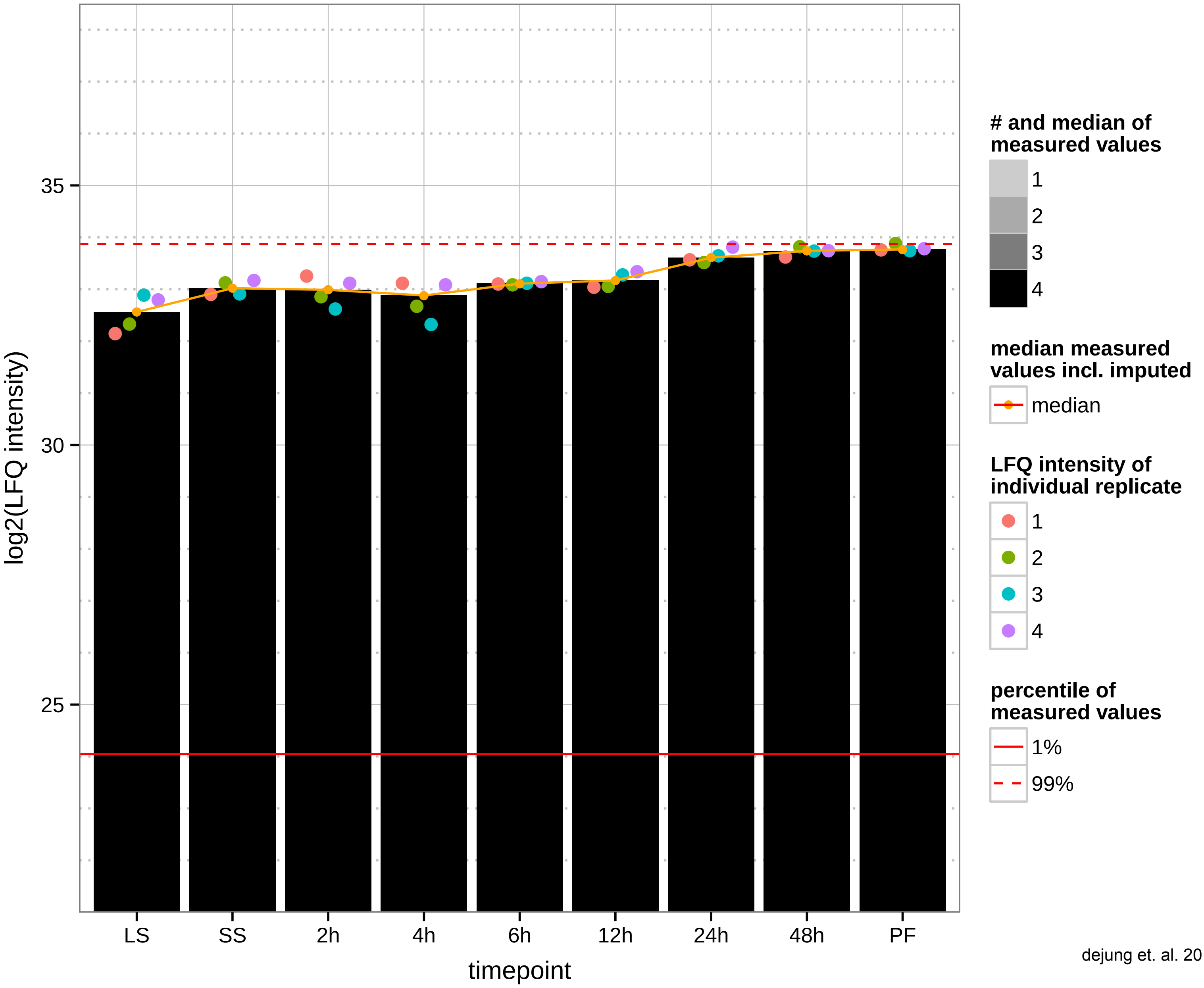
40S ribosomal protein S3A, putative
Tb927.10.3940;Tb11.v5.0501;Tb927.10.3930
AGOF: null, structural constituent of ribosome
AGOC: null, intracellular, ribosome
AGOP: null, translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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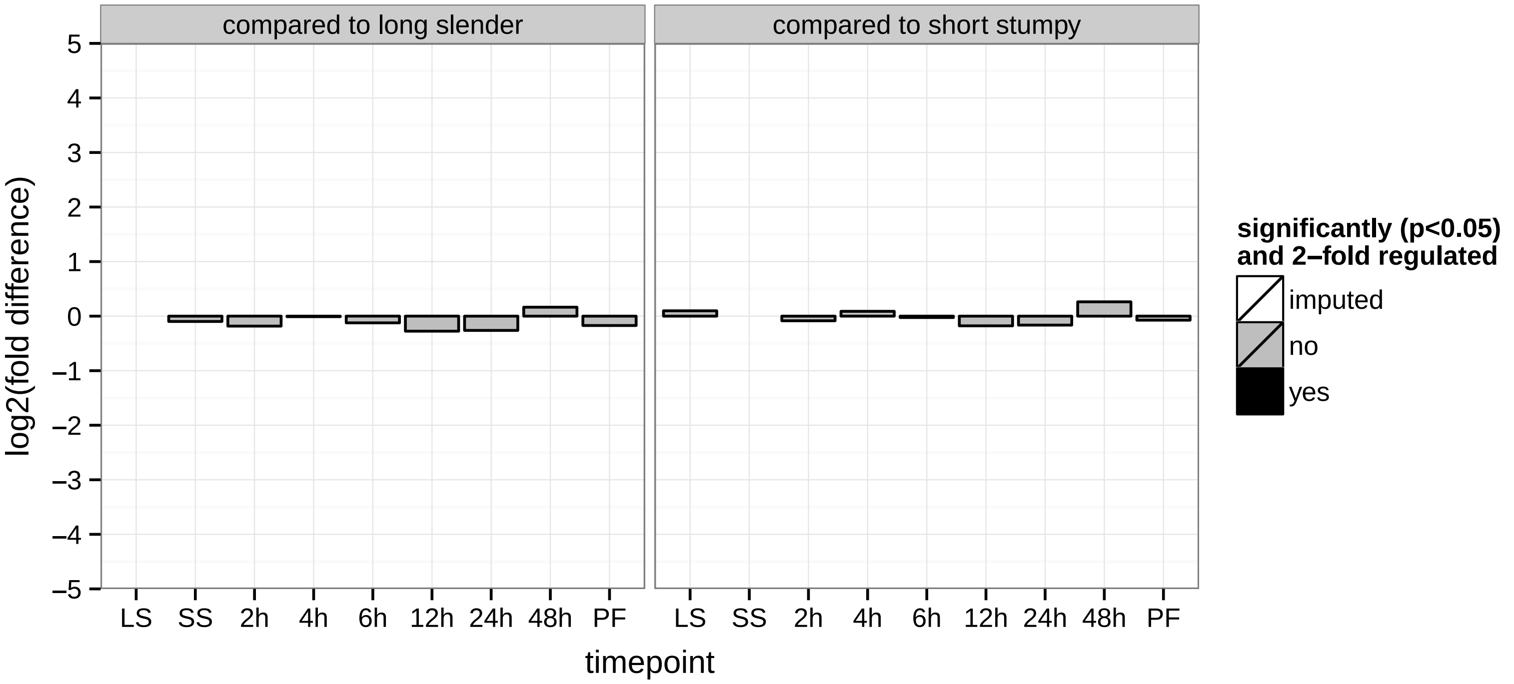
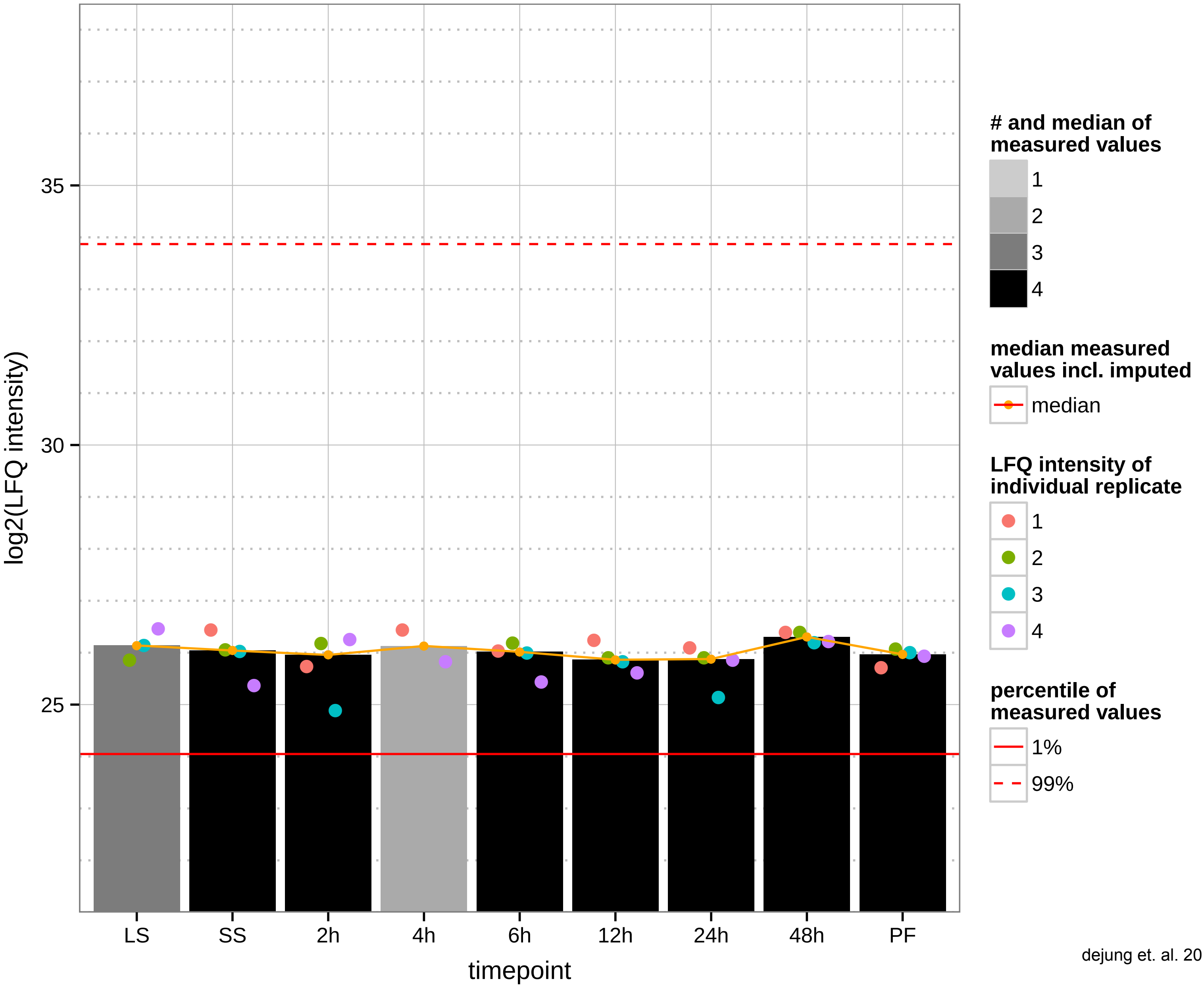
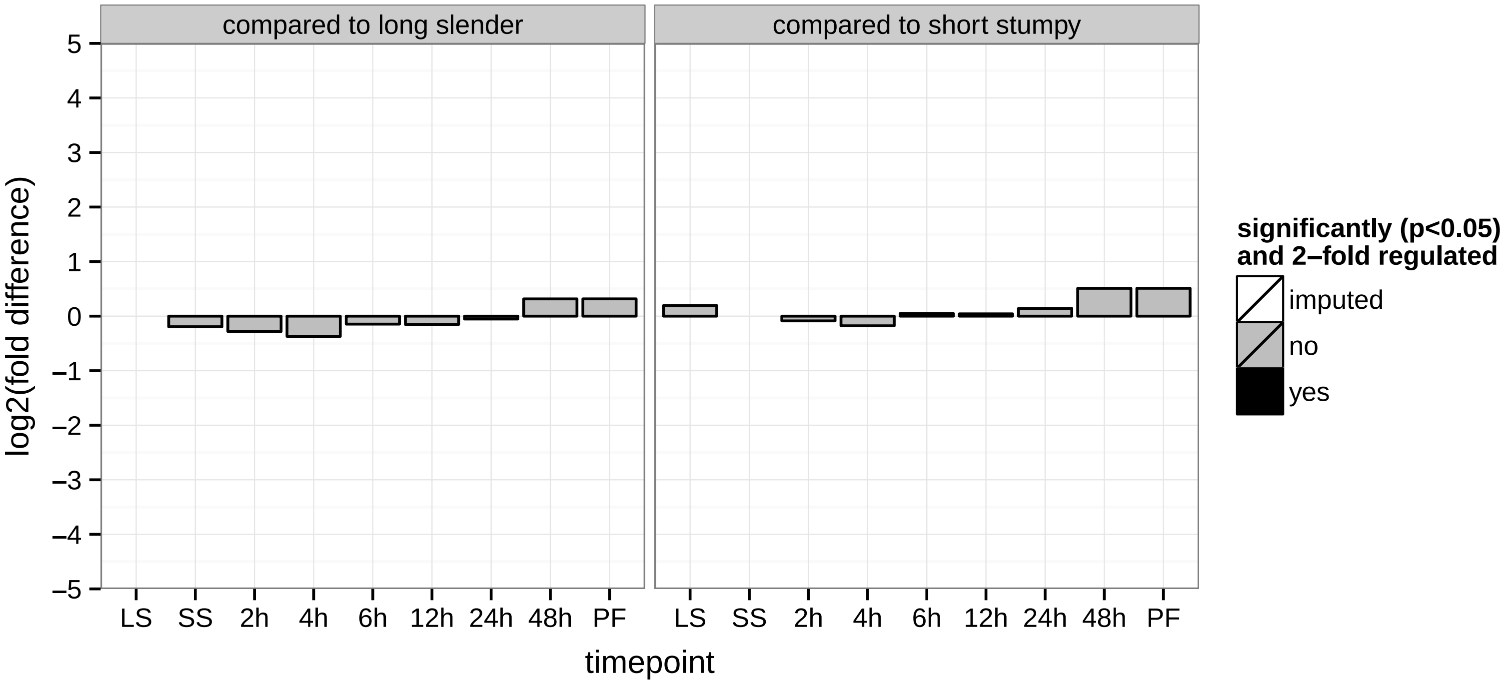
hypothetical protein, conserved
Tb927.10.3920;Tb11.v5.0502
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

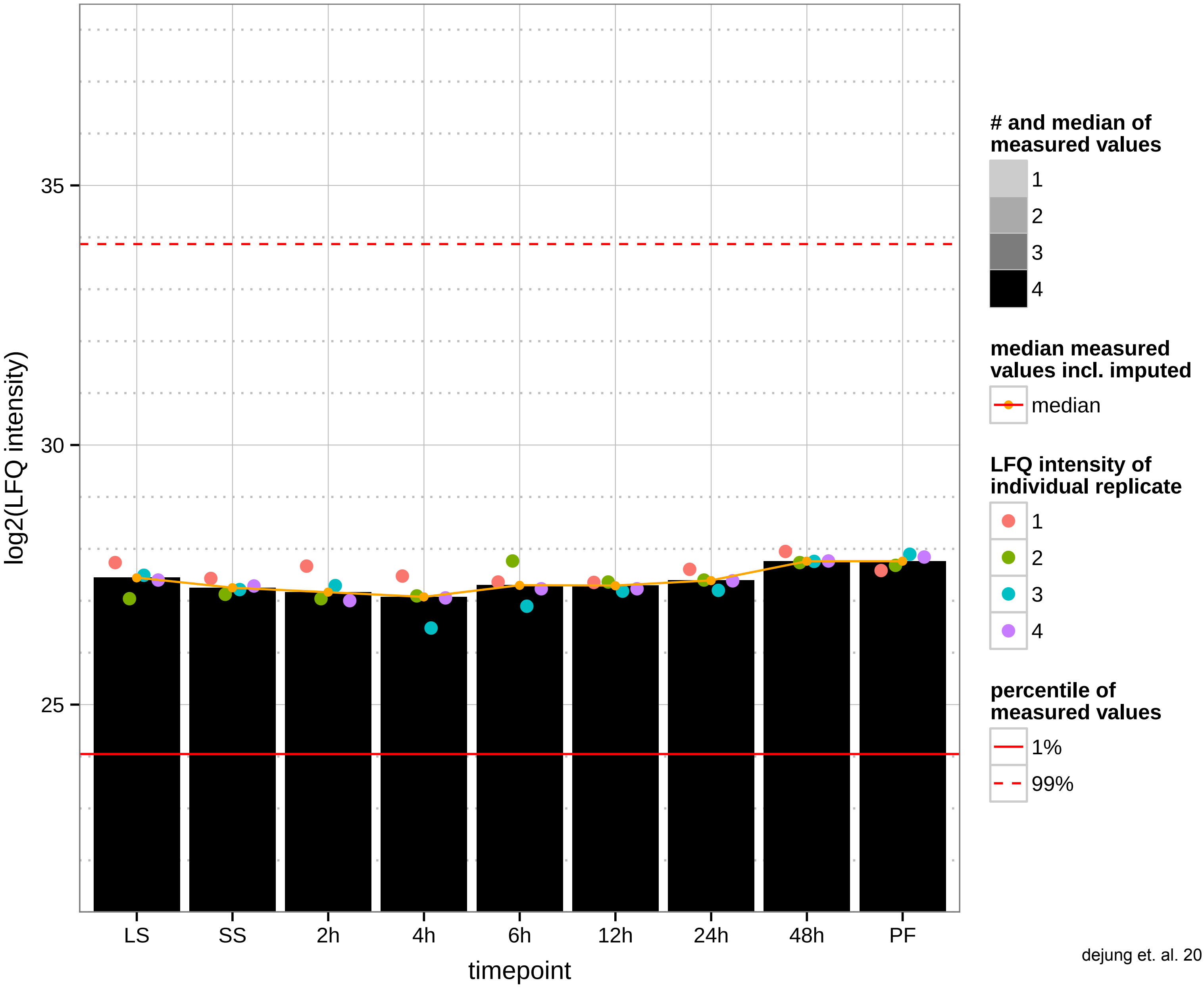




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.16110;Tb11.v5.0527
AGOF: null
AGOC: null
AGOP: null, ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null





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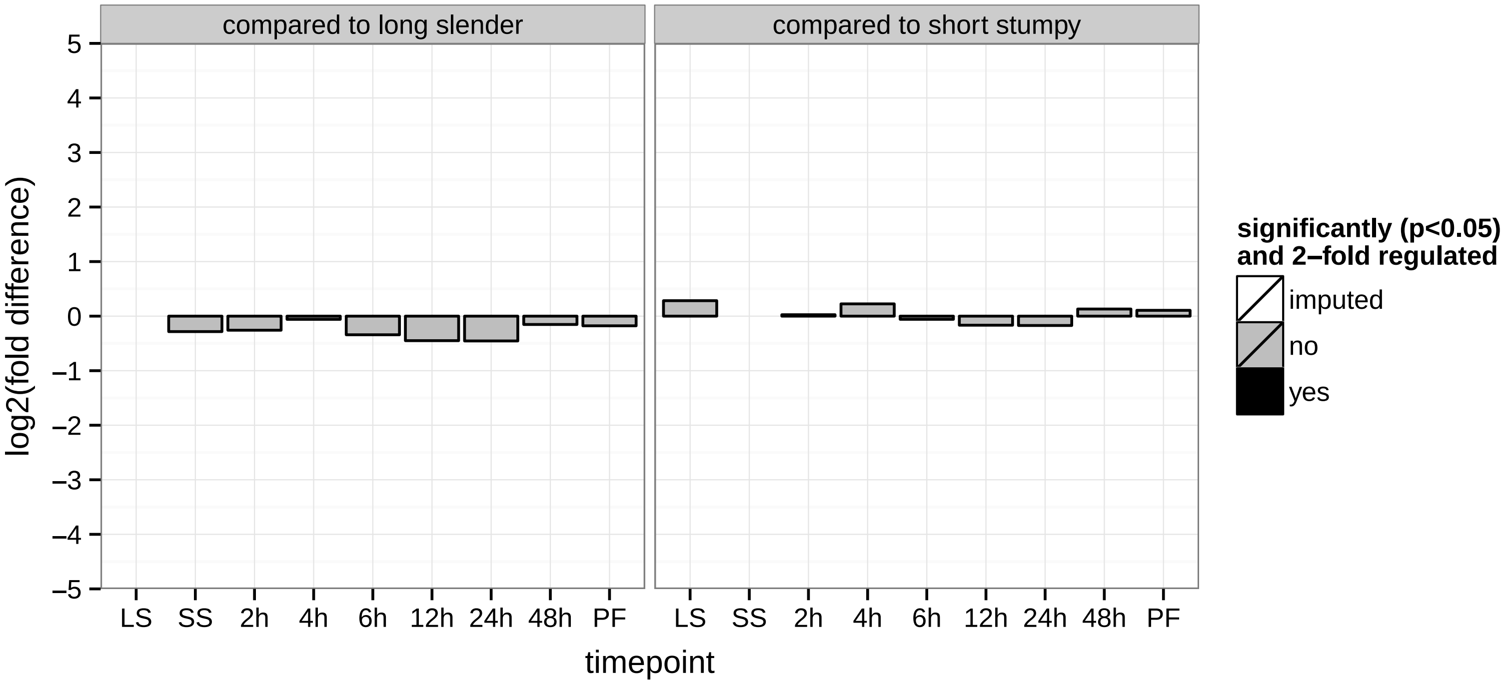
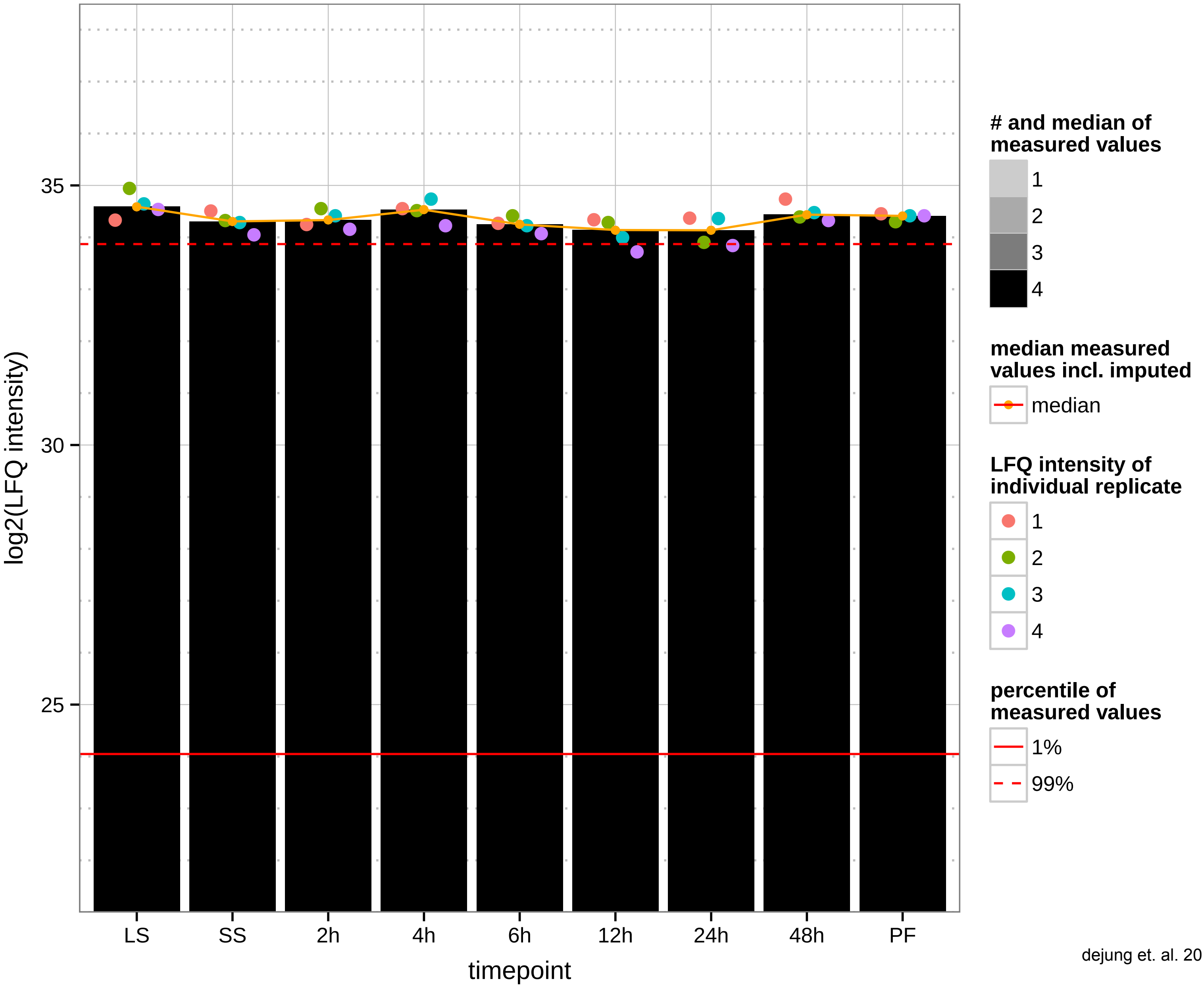
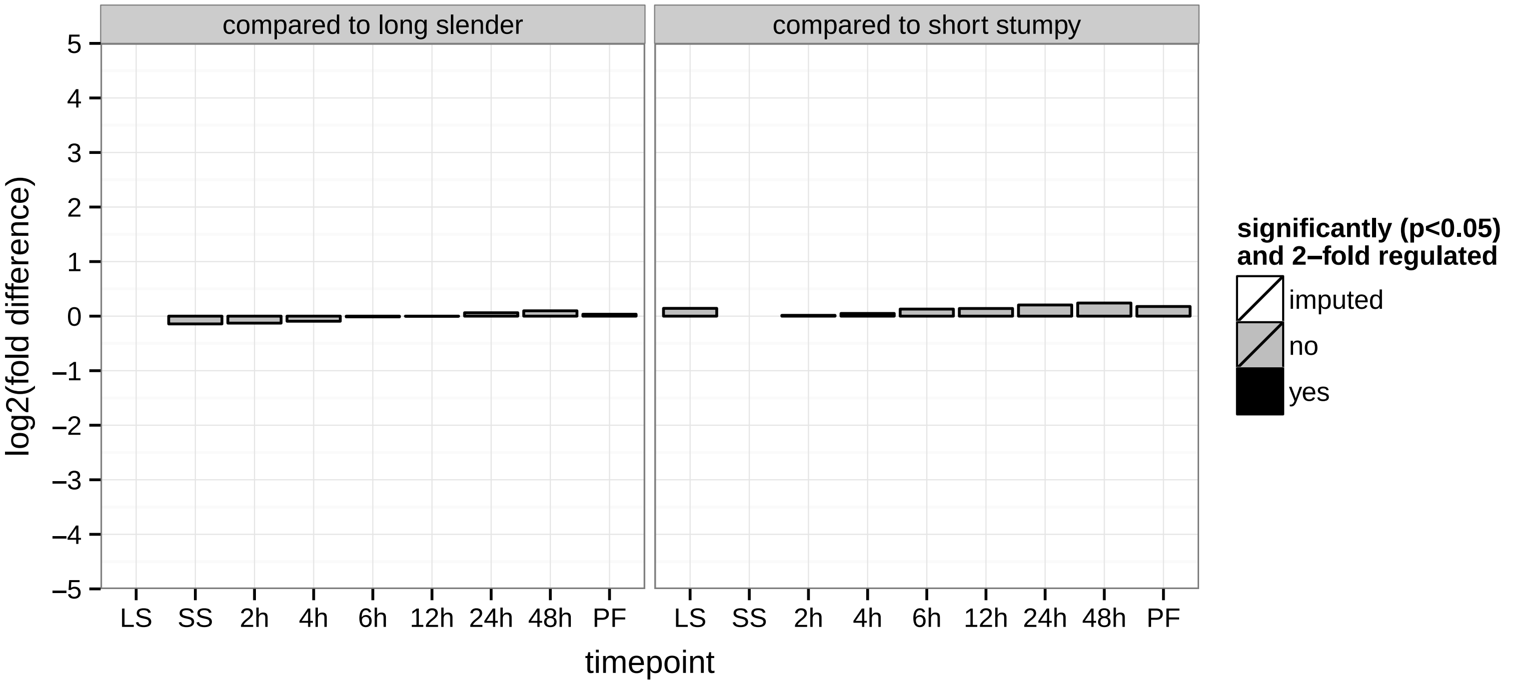
69 kDa paraflagellar rod protein, putative, Paraflagellar rod protein 2, Paraflagellar rod protein A (PFR2)
Tb927.8.5010;Tb927.8.5000;Tb927.8.4990;Tb927.8.4980;Tb927.8.4970;Tb11.v5.0538
AGOF: null, calmodulin binding
AGOC: null, cilium, microtubule–based flagellum
AGOP: null, cellular component movement, forward locomotion
PGOF: calmodulin binding, null
PGOC: microtubule–based flagellum, null
PGOP: null

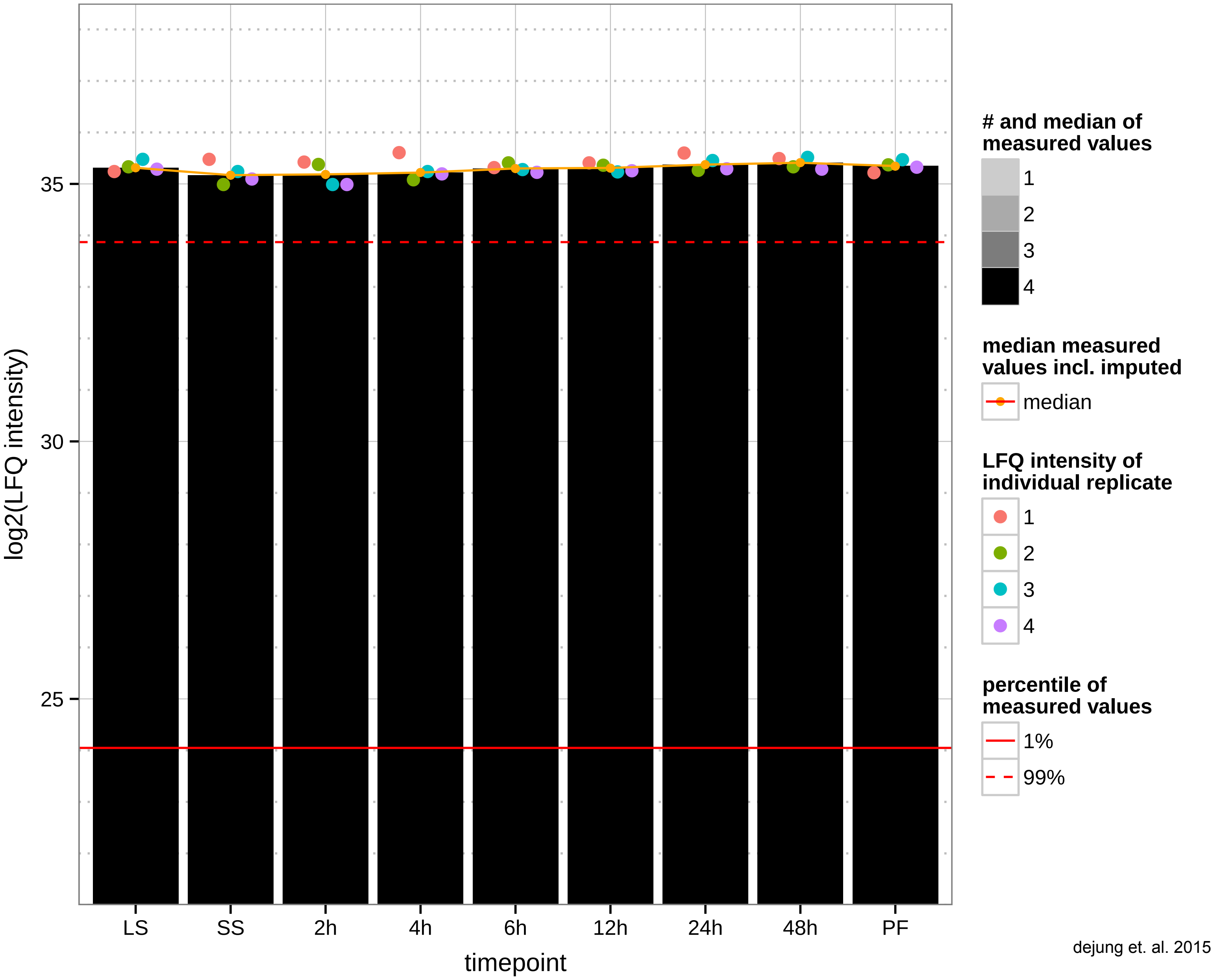




dejung et. al. 2015

Heat shock protein 83, putative, heat shock protein, heat shock protein 90
Tb927.10.10960;Tb927.10.10950;Tb927.10.10940;Tb927.10.10920;Tb927.10.10900;Tb927.10.10890;Tb11.v5.0543;Tb927.1
AGOF: null, ATP binding, unfolded protein binding, ATPase activity, coupled
AGOC: null, centrosome
AGOP: null, protein folding, response to stress, protein refolding, response to unfolded protein
PGOF: ATP binding, unfolded protein binding, null
PGOC: null
PGOP: protein folding, response to stress, null





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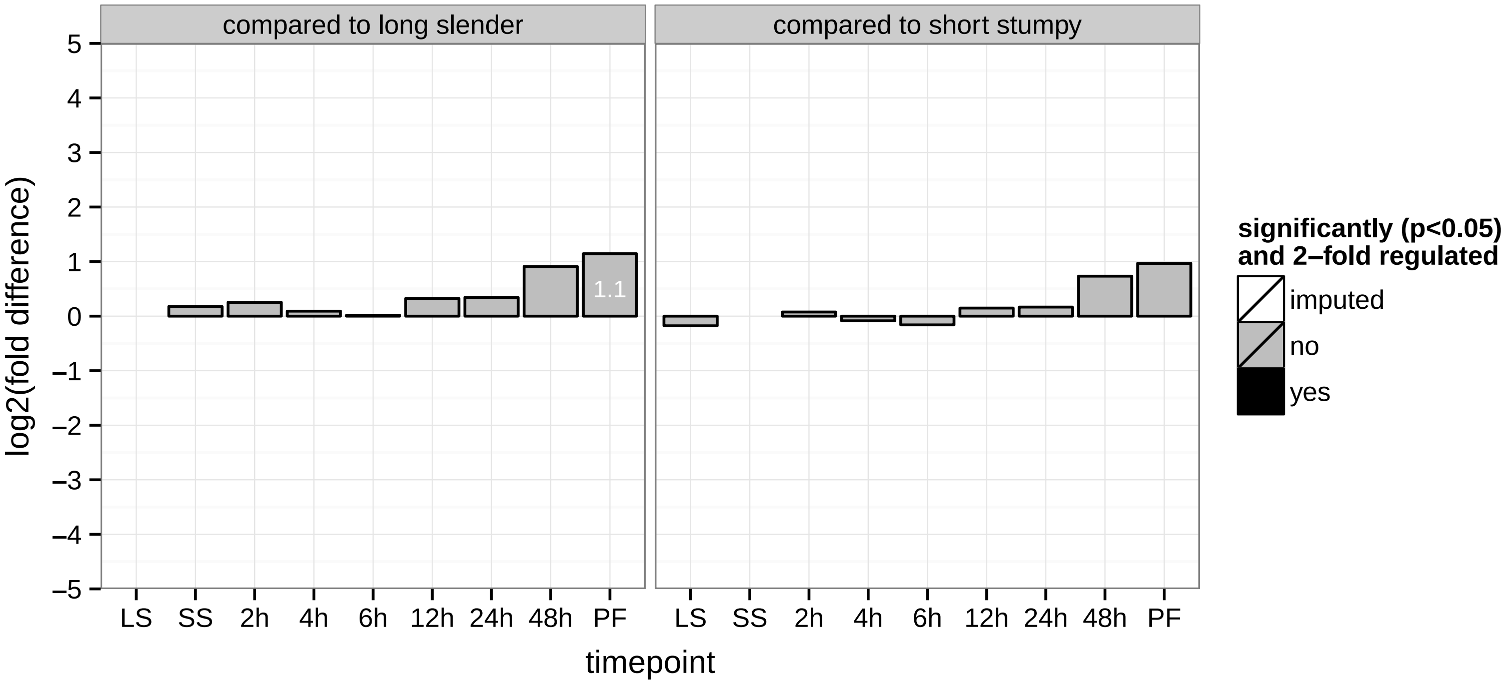
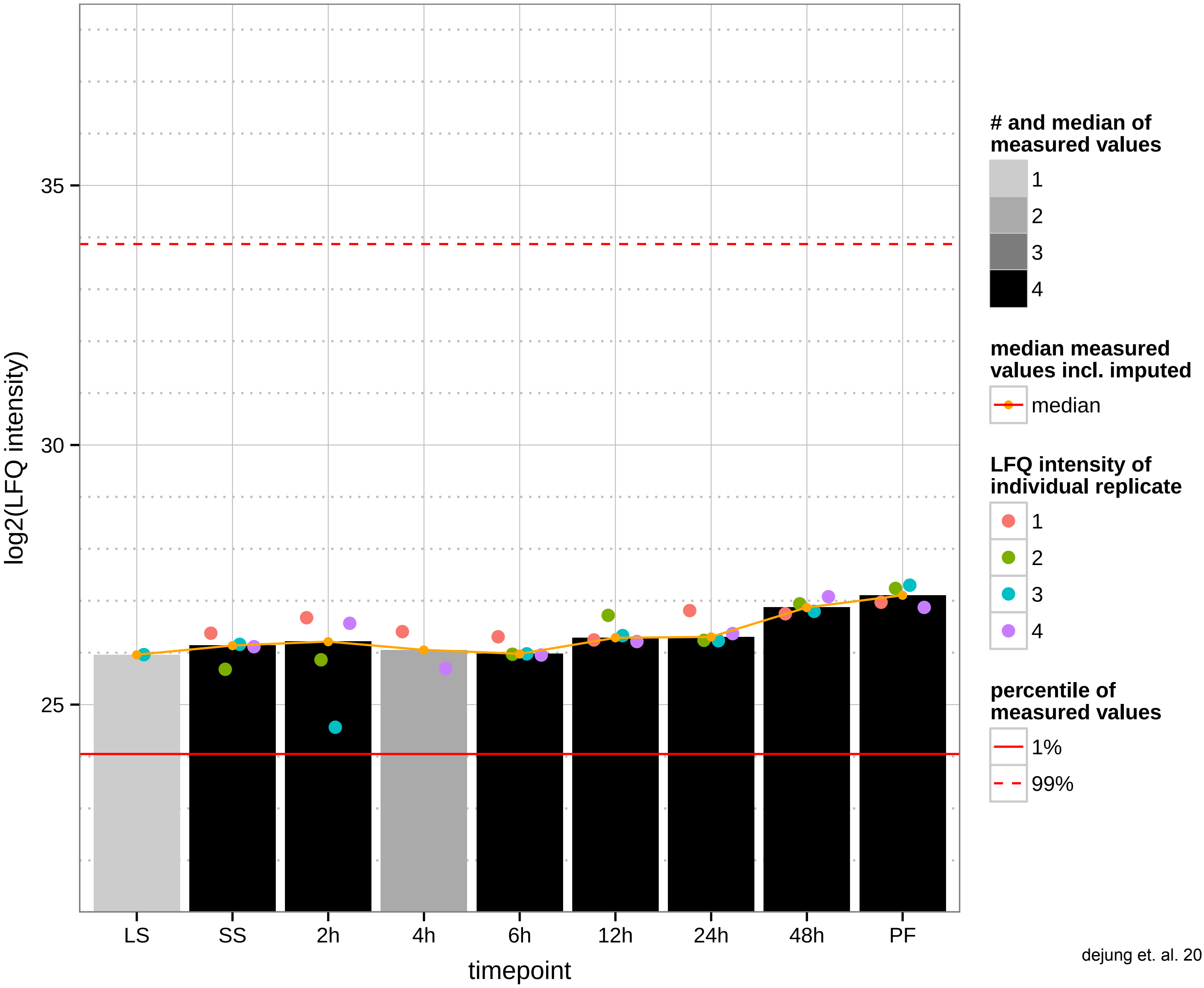
protein kinase, putative
Tb927.10.350;Tb11.v5.0564
AGOF: null, ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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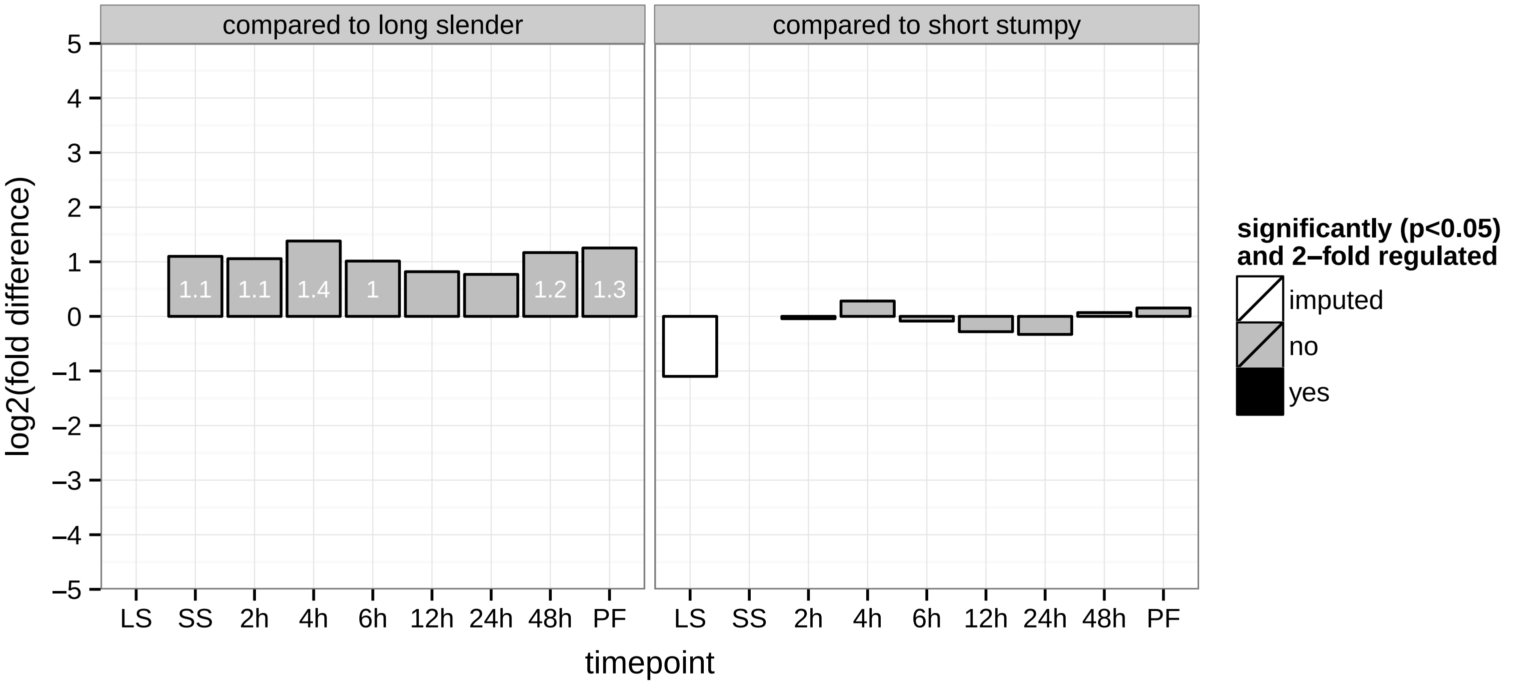
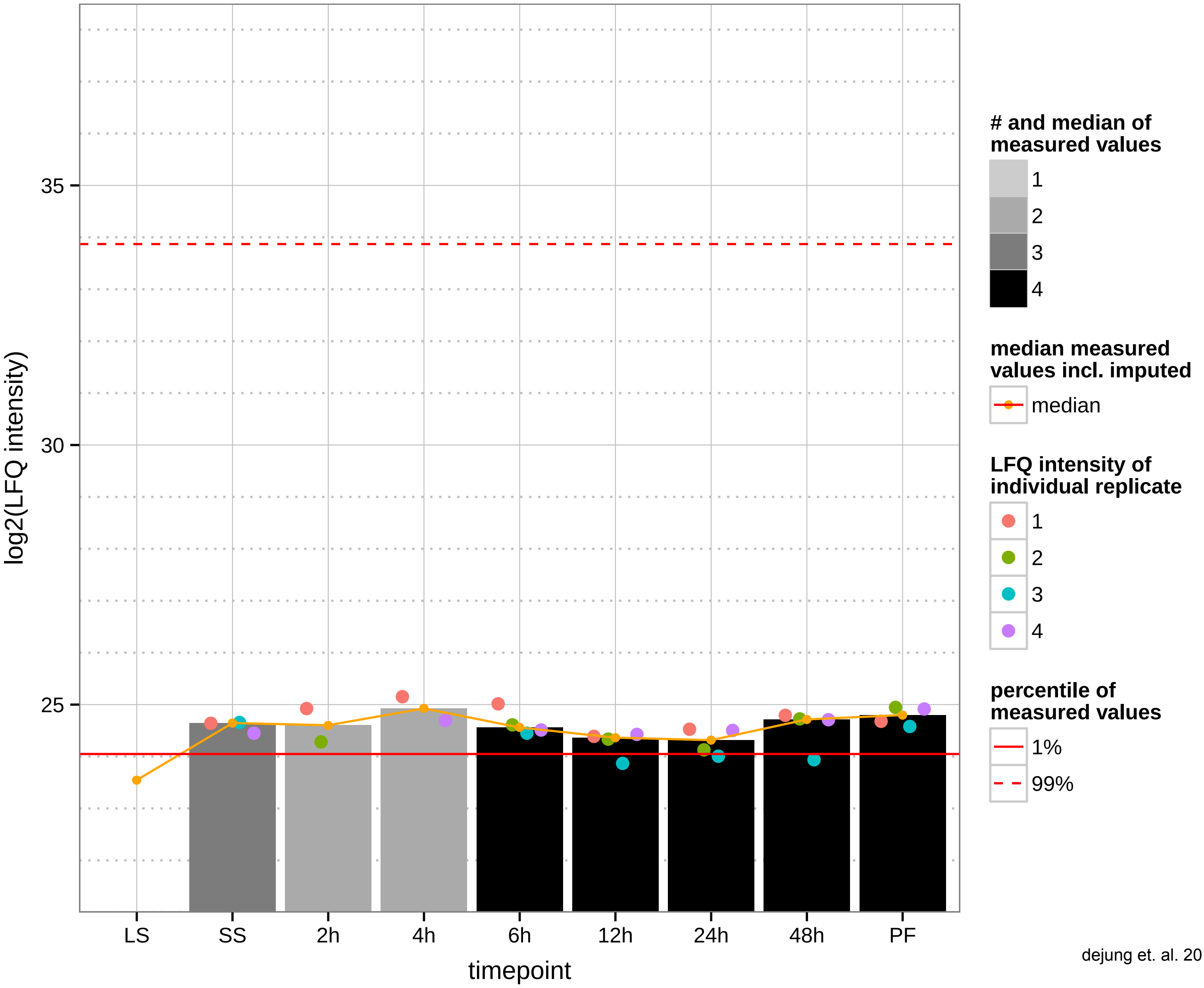
hypothetical protein, conserved
Tb927.7.5620;Tb11.v5.0590
AGOF: null, zinc ion binding
AGOC: null
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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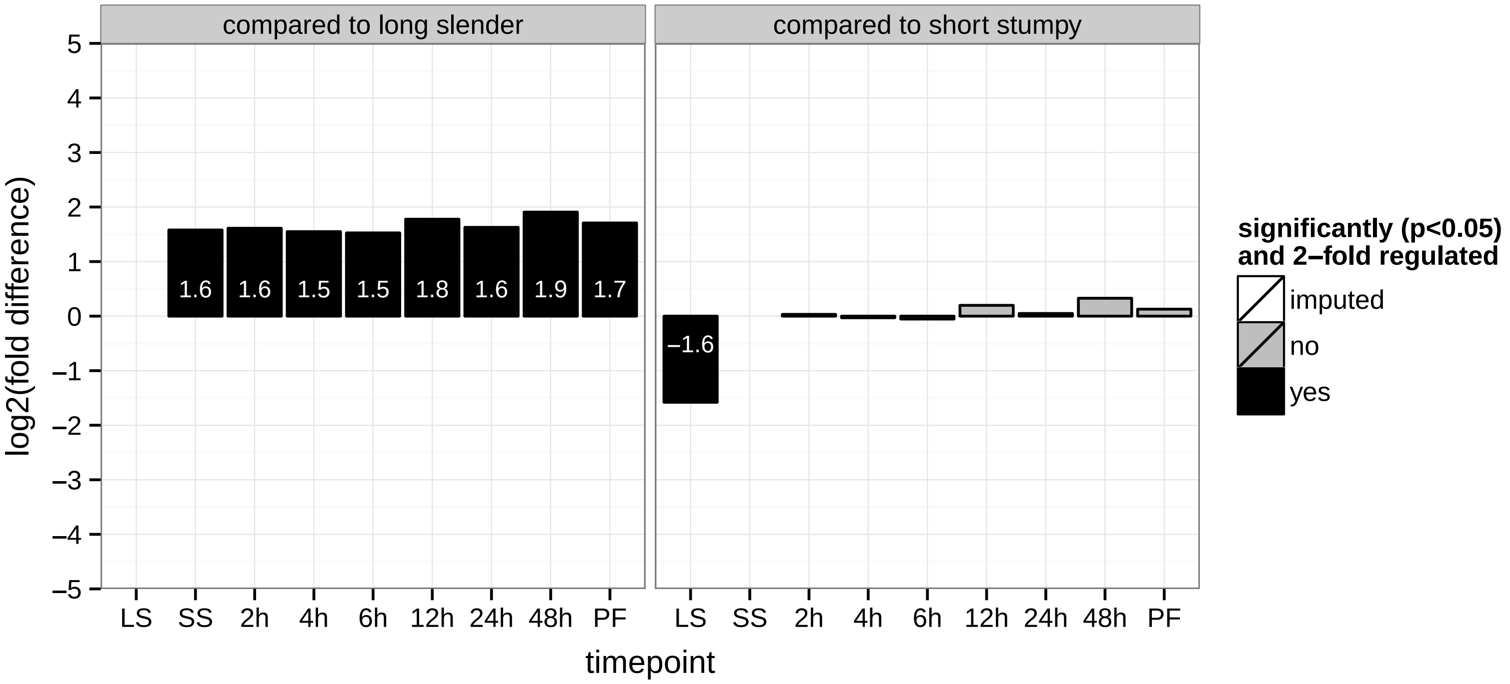
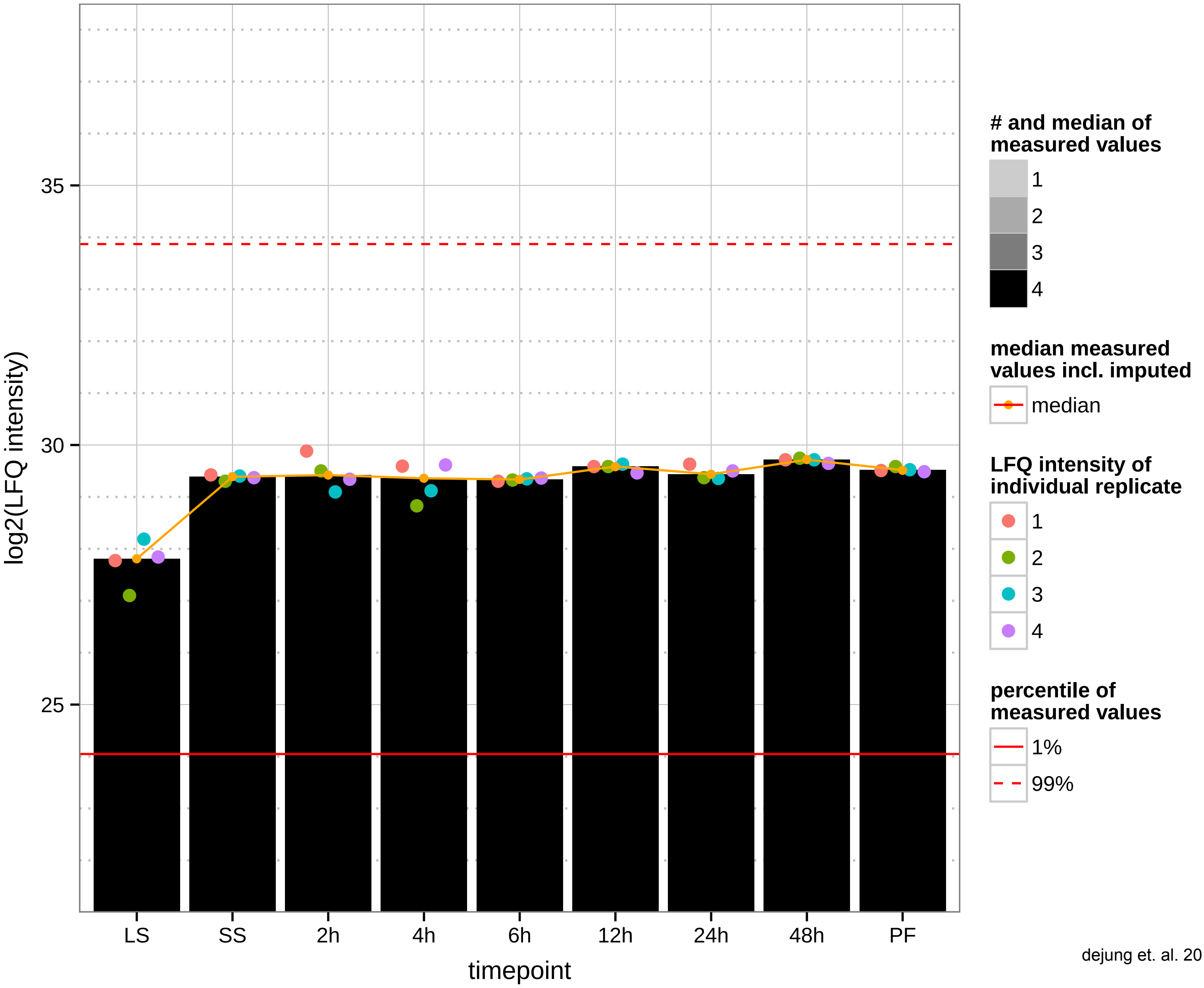
hypothetical protein, conserved, guide RNA associated protein, GAP2, mitochondrial RNA binding protein 1
Tb927.7.2570;Tb11.v5.0611
AGOF: null, mRNA binding
AGOC: null, mitochondrion
AGOP: null, mitochondrial RNA processing
PGOF: null
PGOC: null
PGOP: null





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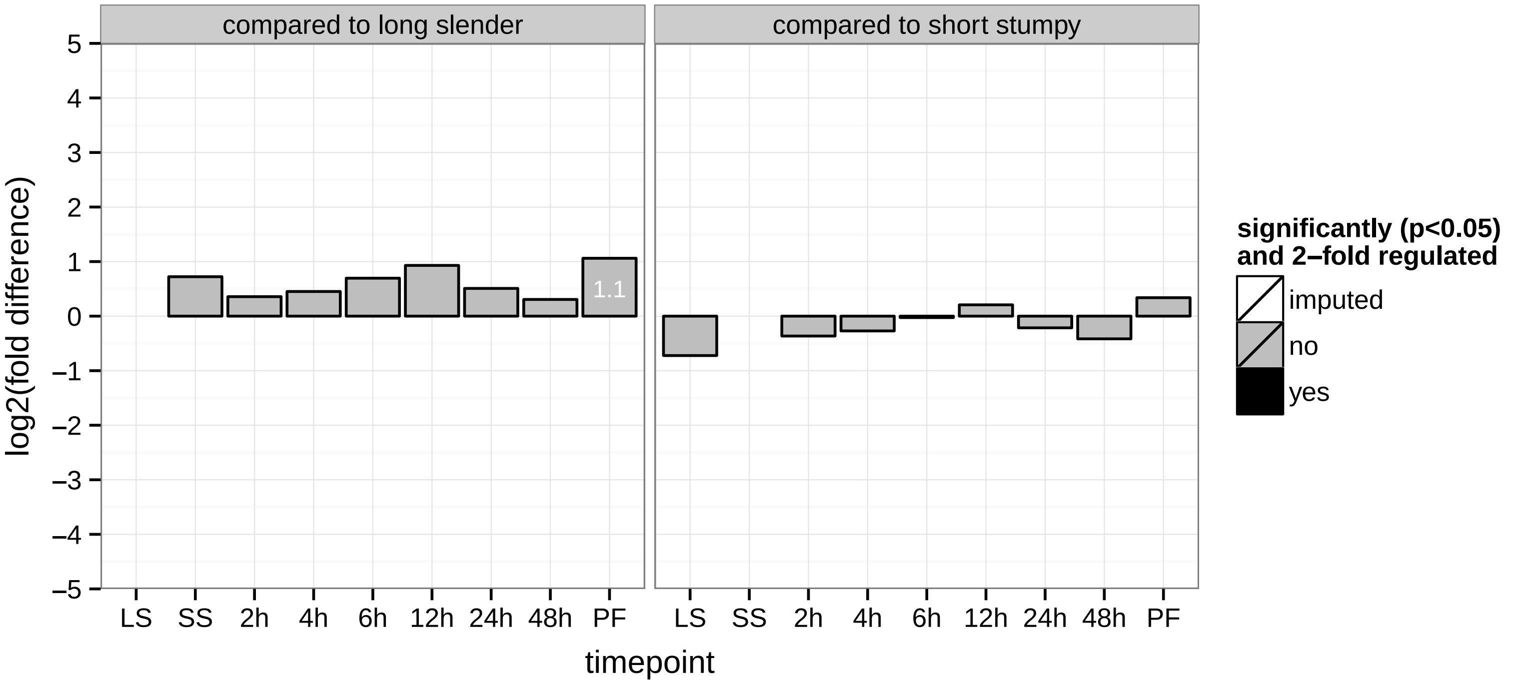
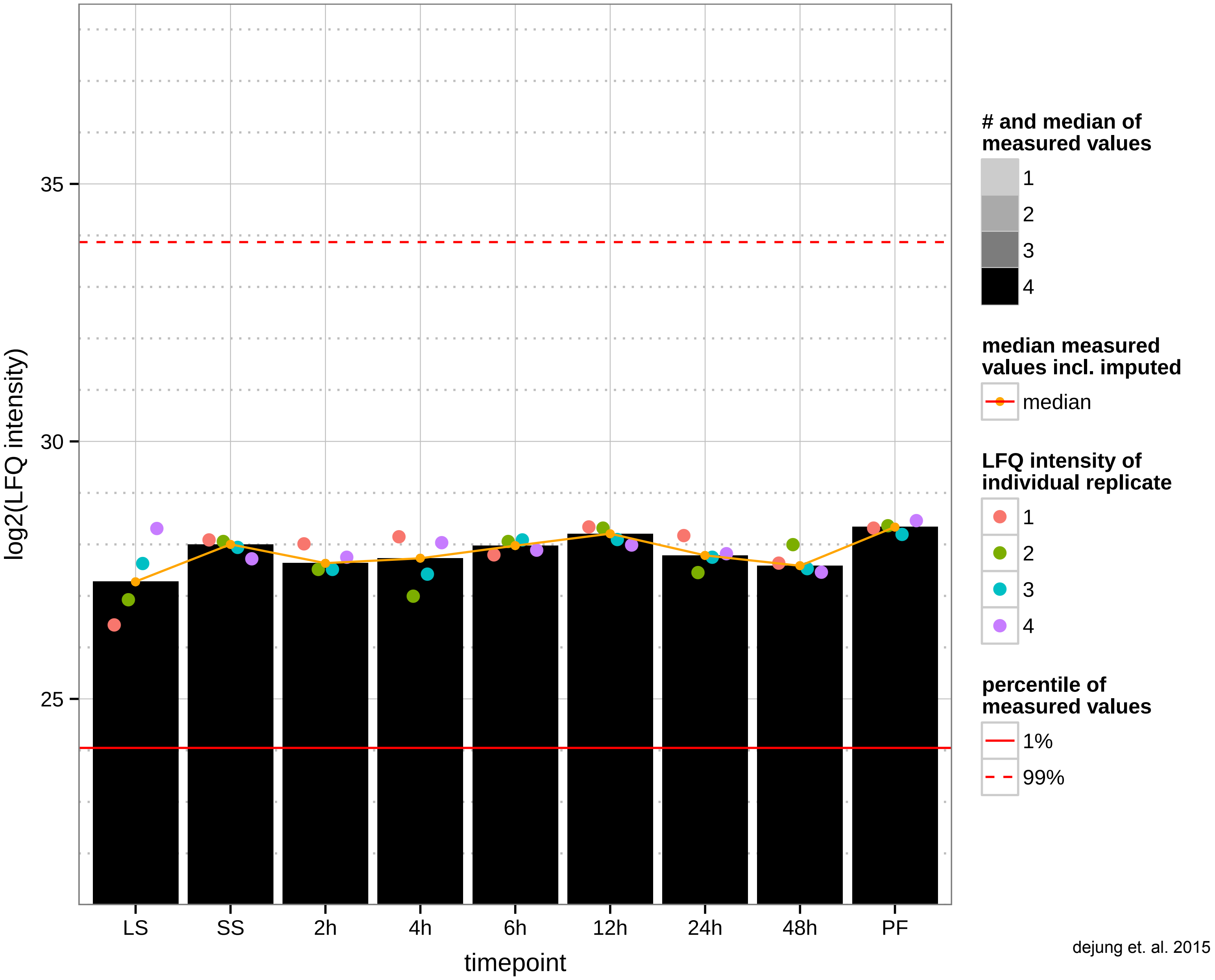
hypothetical protein, conserved
Tb927.7.7070;Tb11.v5.0612
AGOF: null, zinc ion binding
AGOC: null
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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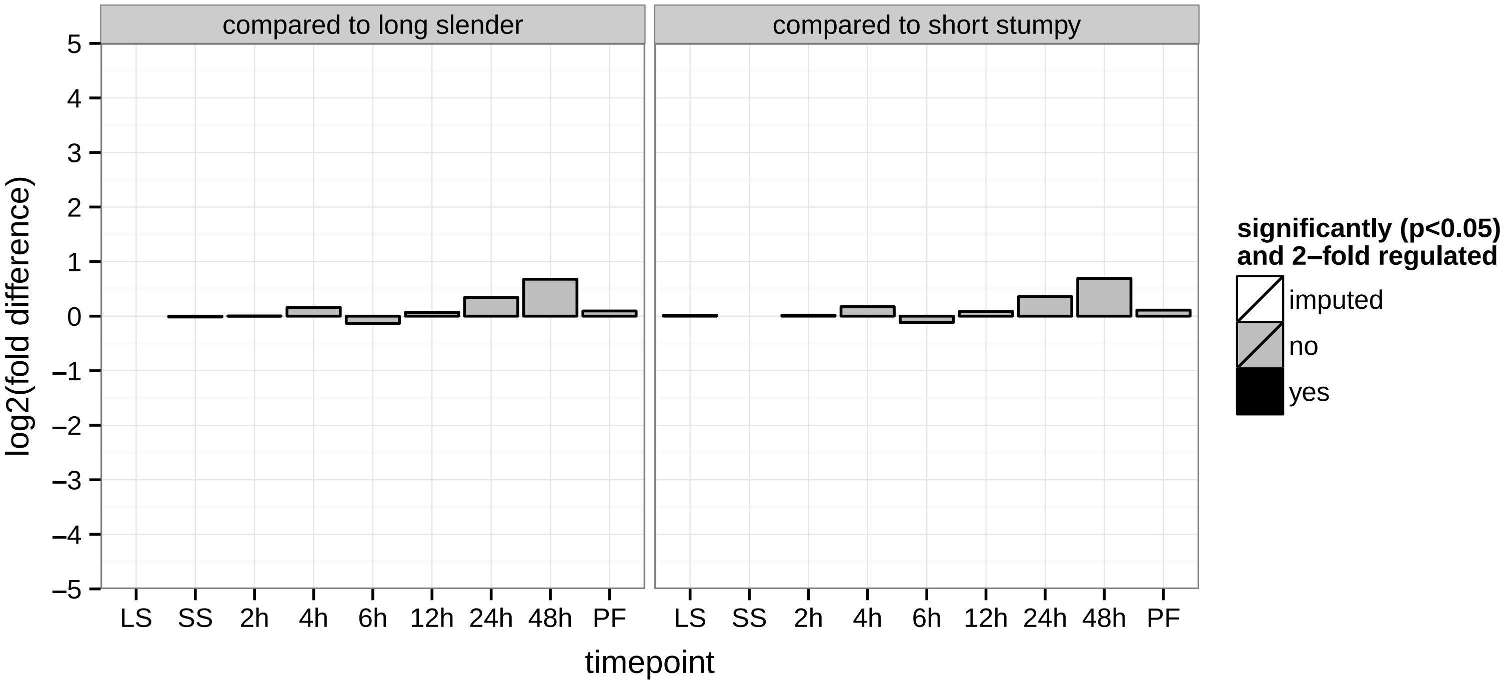
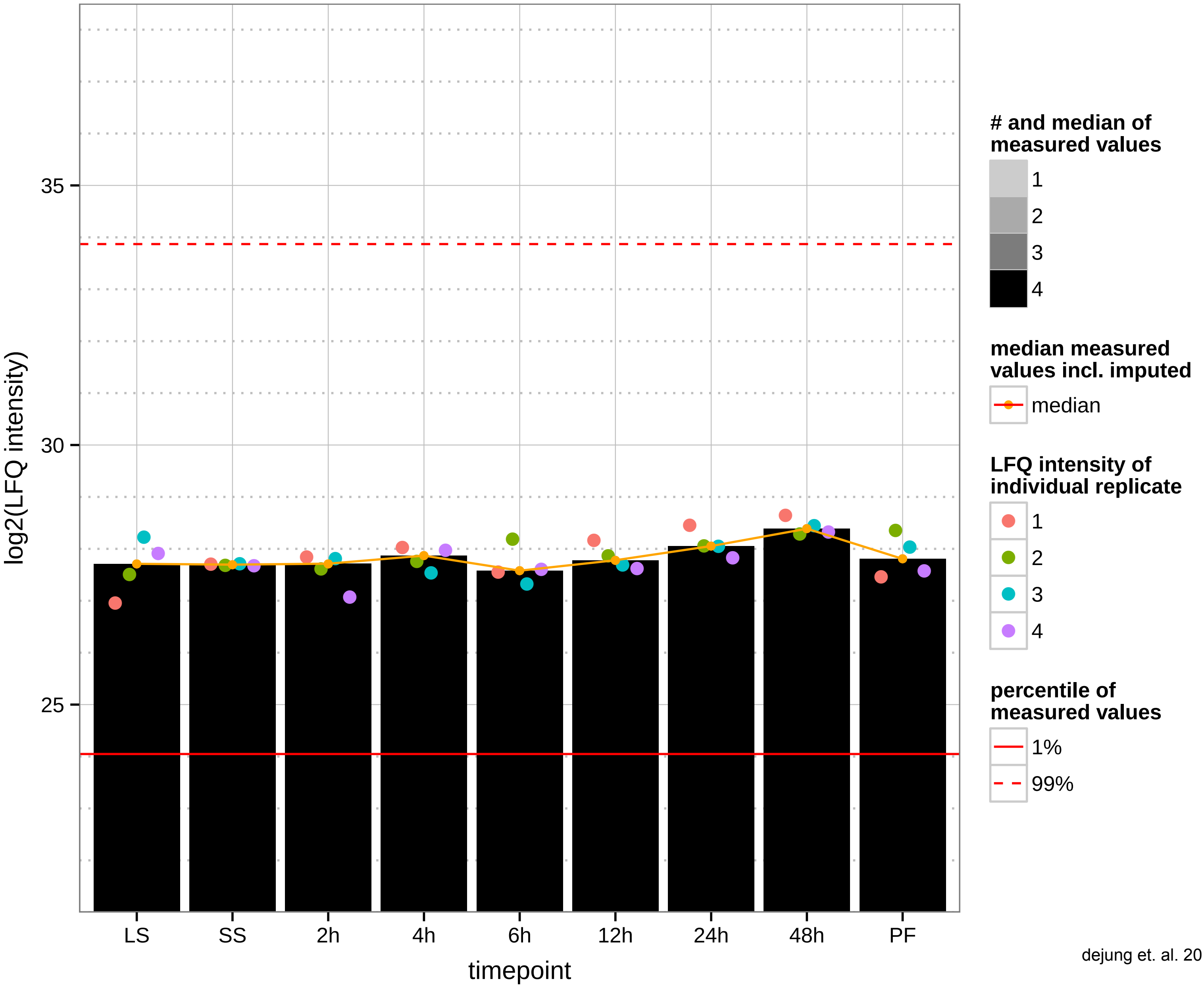
paraflagellar rod protein, putative
Tb11.v5.0616
AGOF: null
AGOC: null
AGOP: null
PGOF: calmodulin binding
PGOC: microtubule–based flagellum
PGOP: null





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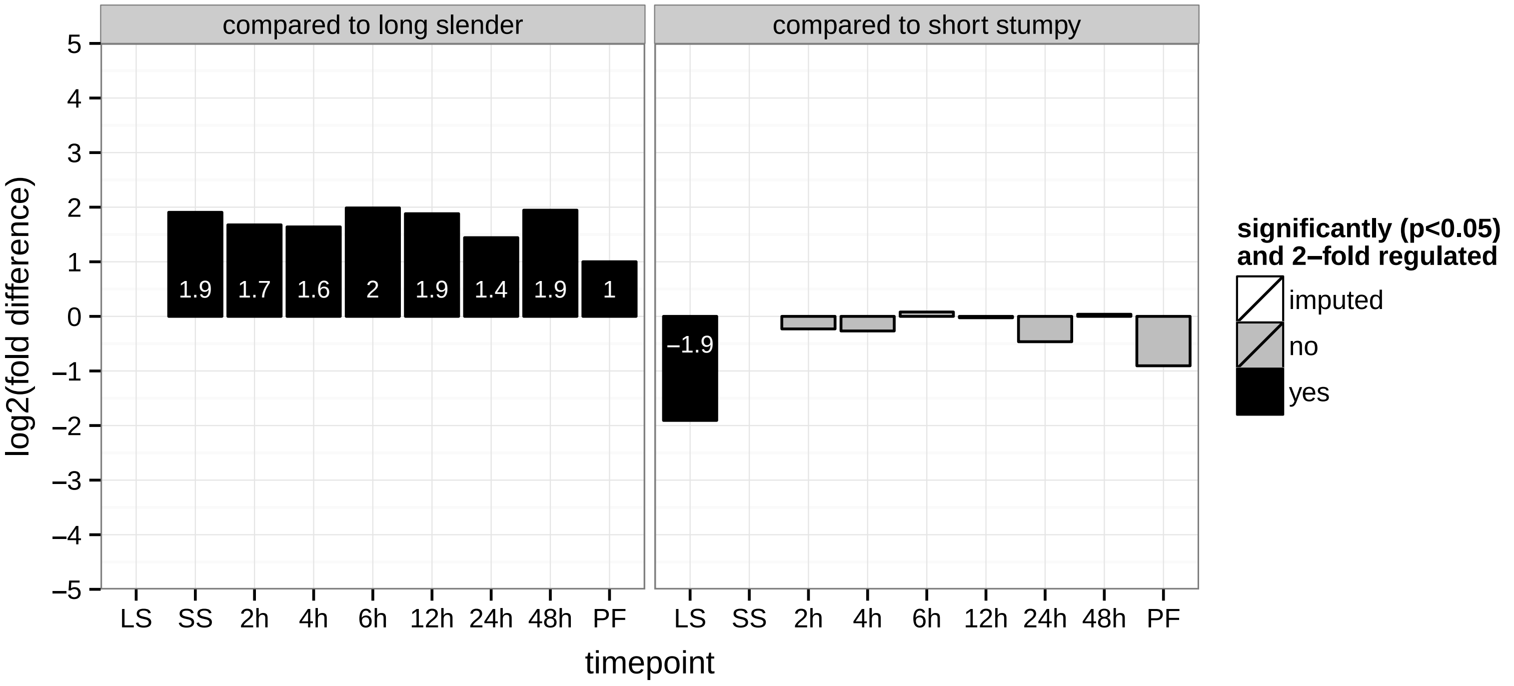
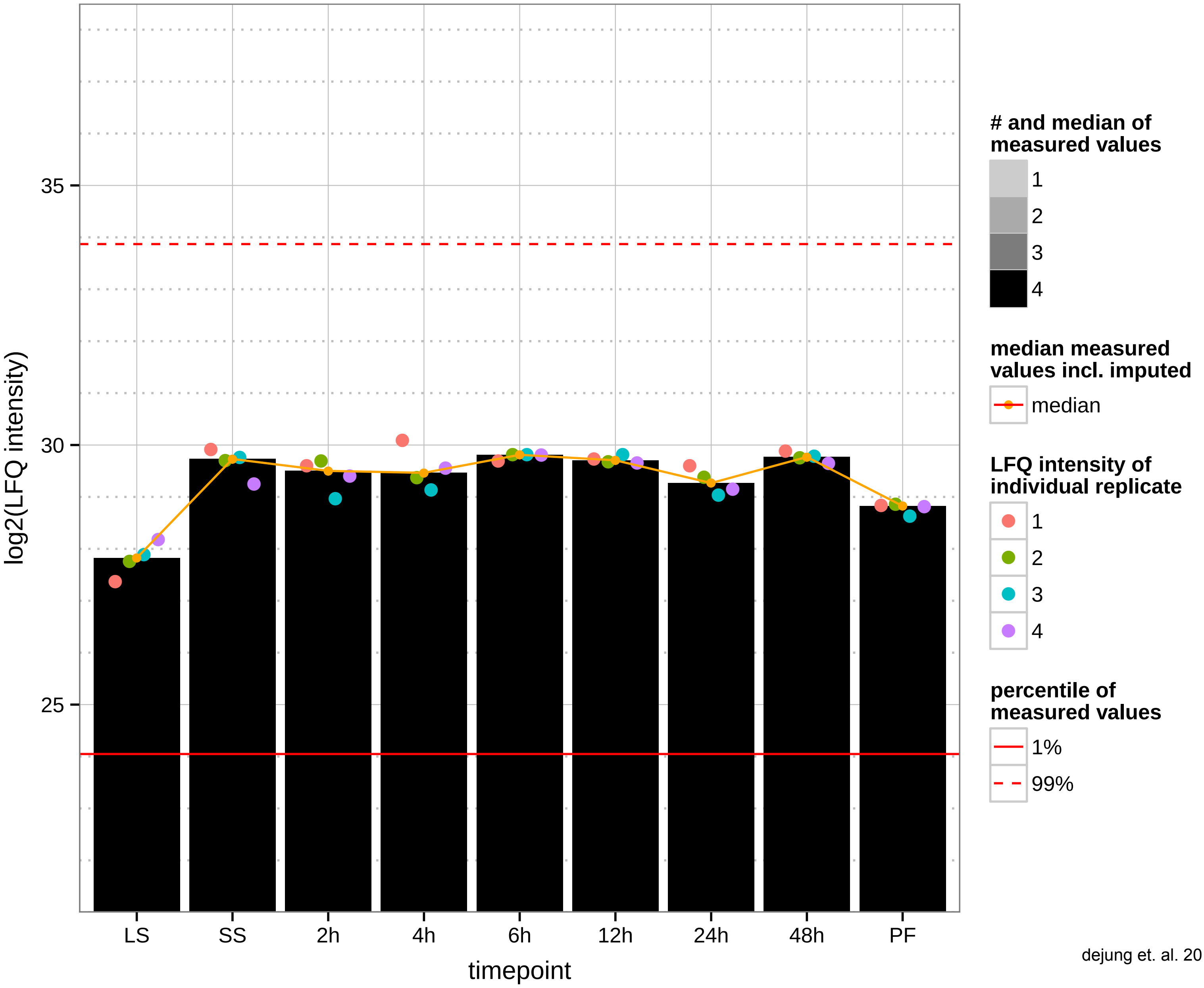
retrotransposon hot spot protein (PHS), putative
Tb11.v5.0624
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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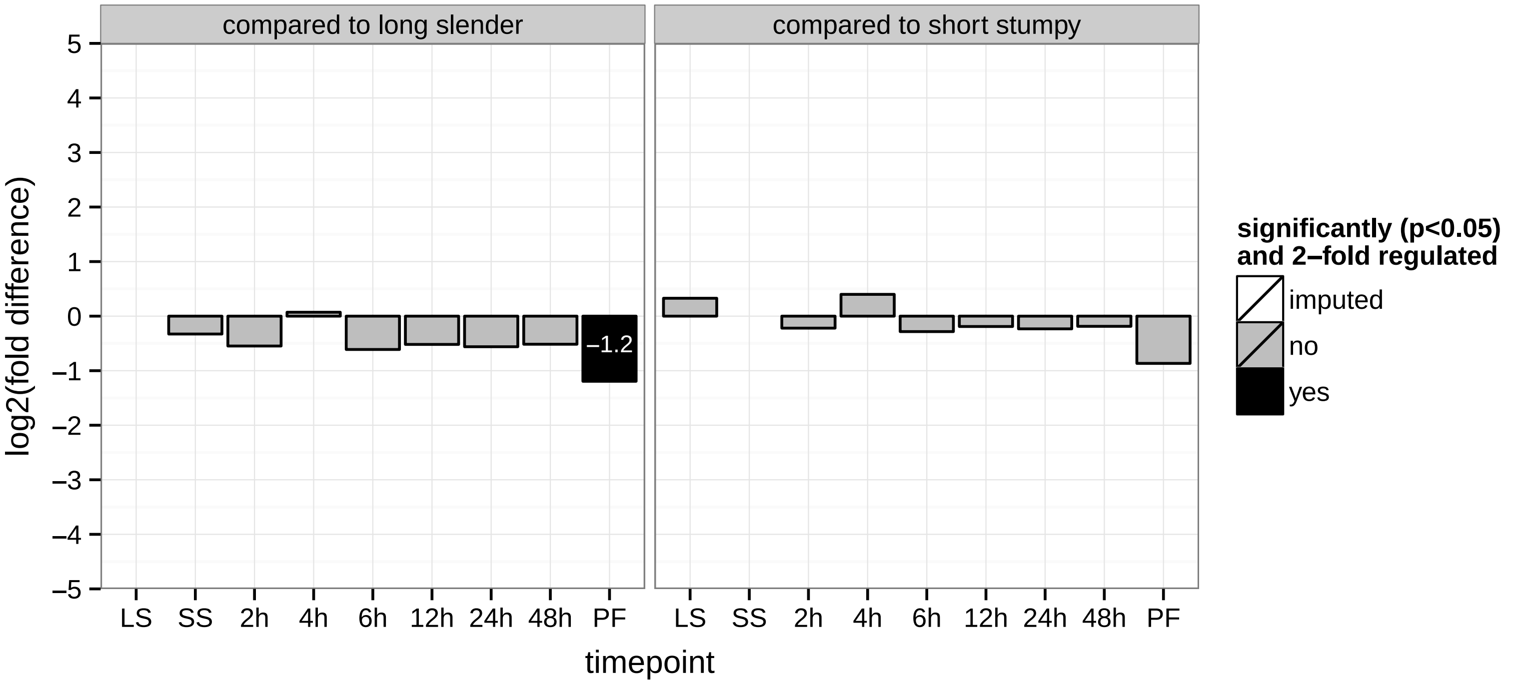
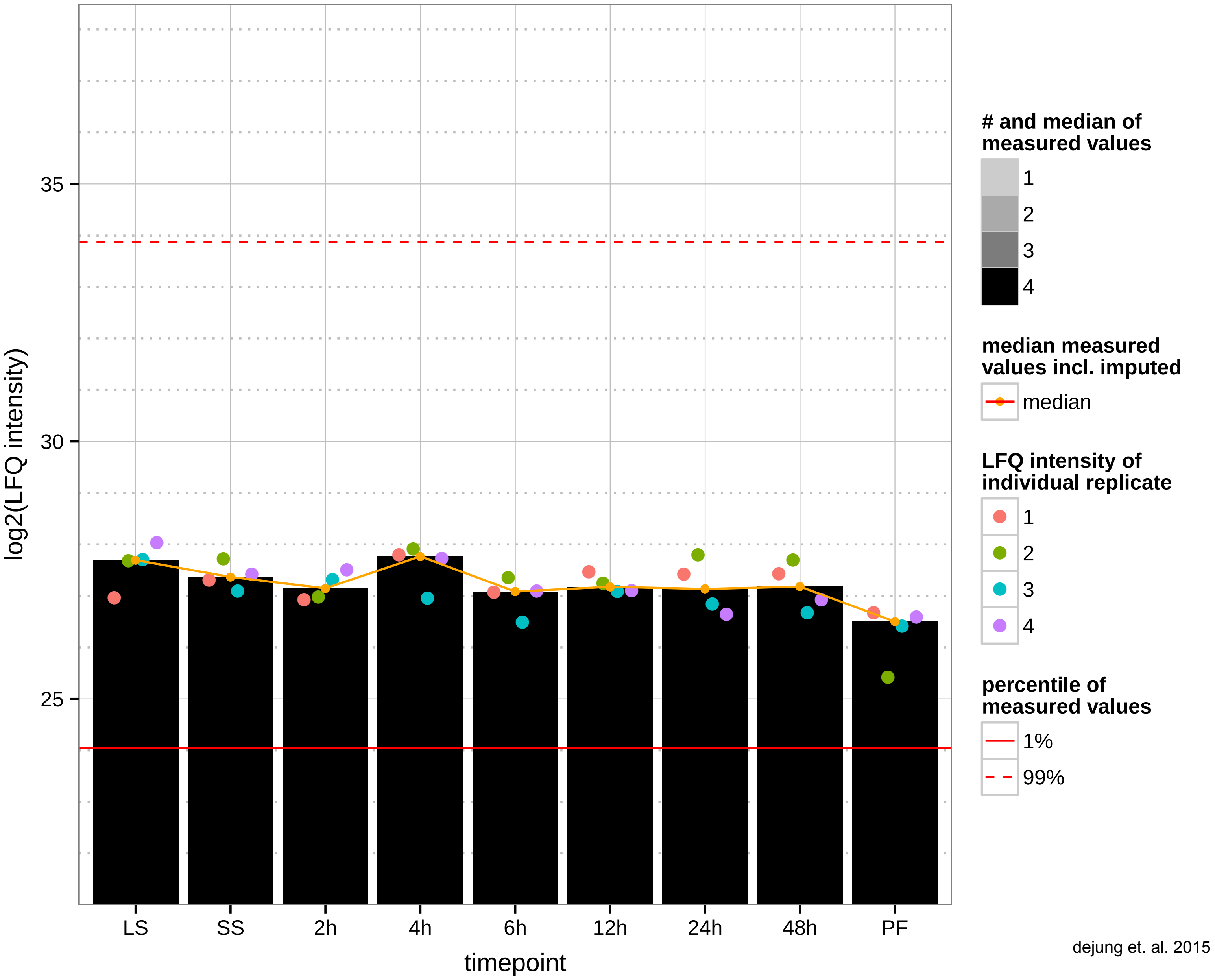
hypothetical protein, conserved
Tb927.5.1230;Tb11.v5.0639
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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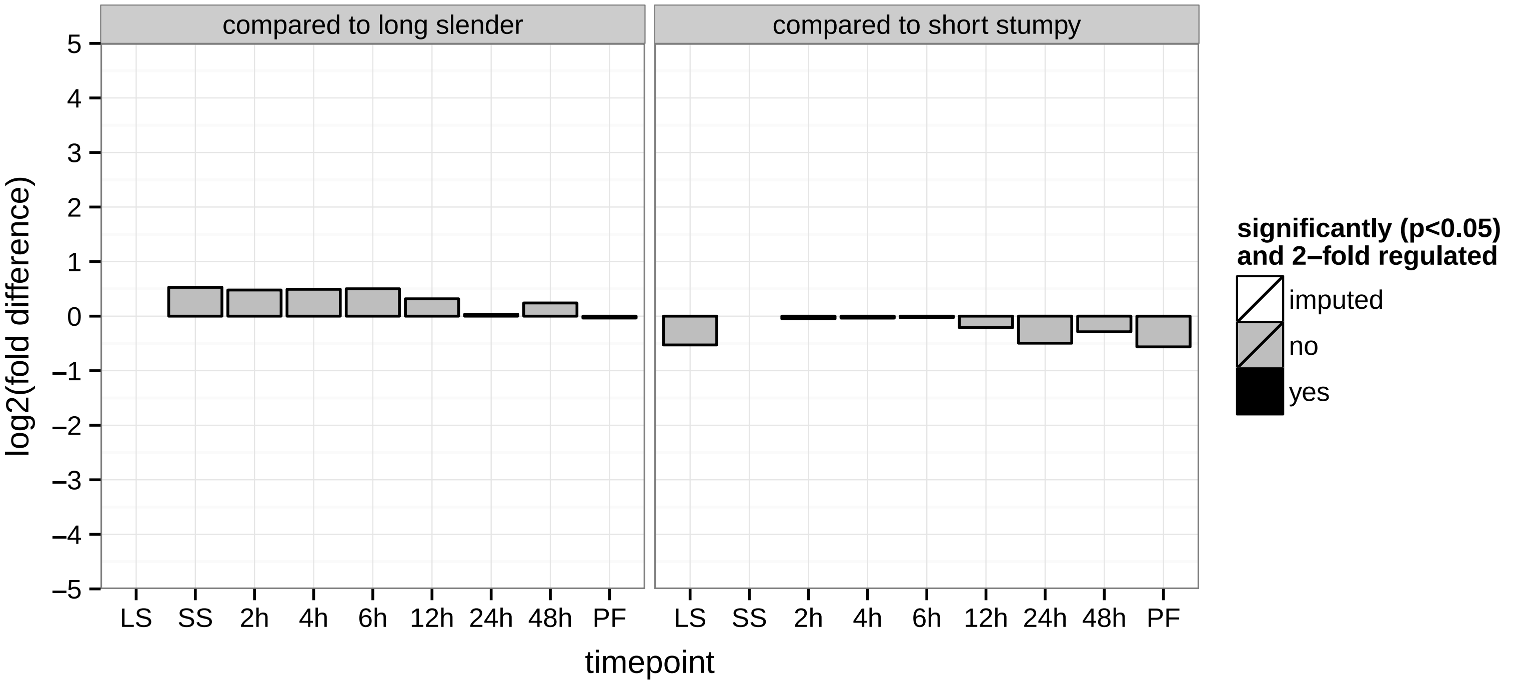
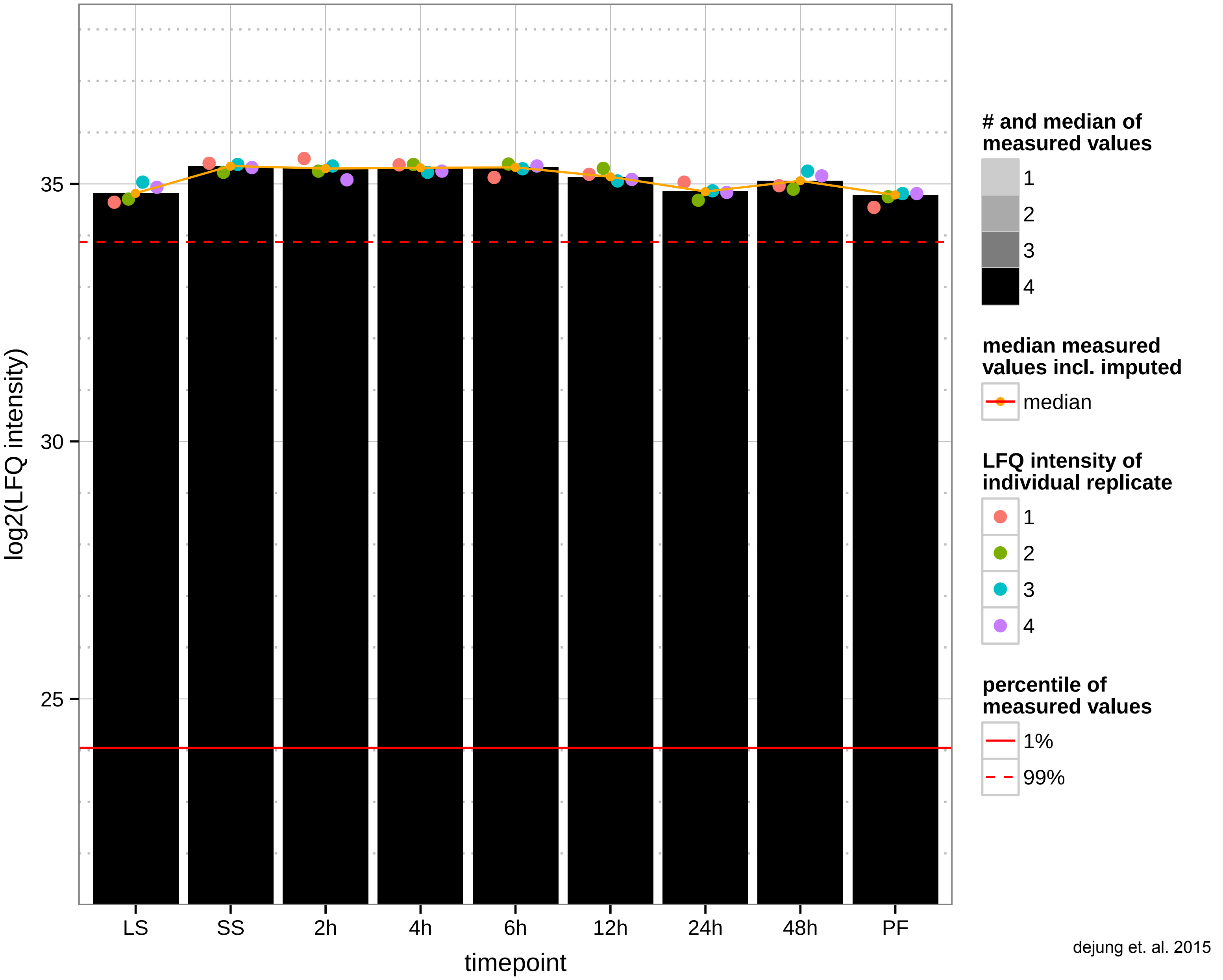
enolase, putative
Tb927.10.2890;Tb11.v5.0650
AGOF: null, magnesium ion binding, phosphopyruvate hydratase activity
AGOC: null, phosphopyruvate hydratase complex
AGOP: null
PGOF: magnesium ion binding, phosphopyruvate hydratase activity
PGOC: phosphopyruvate hydratase complex
PGOP: glycolysis





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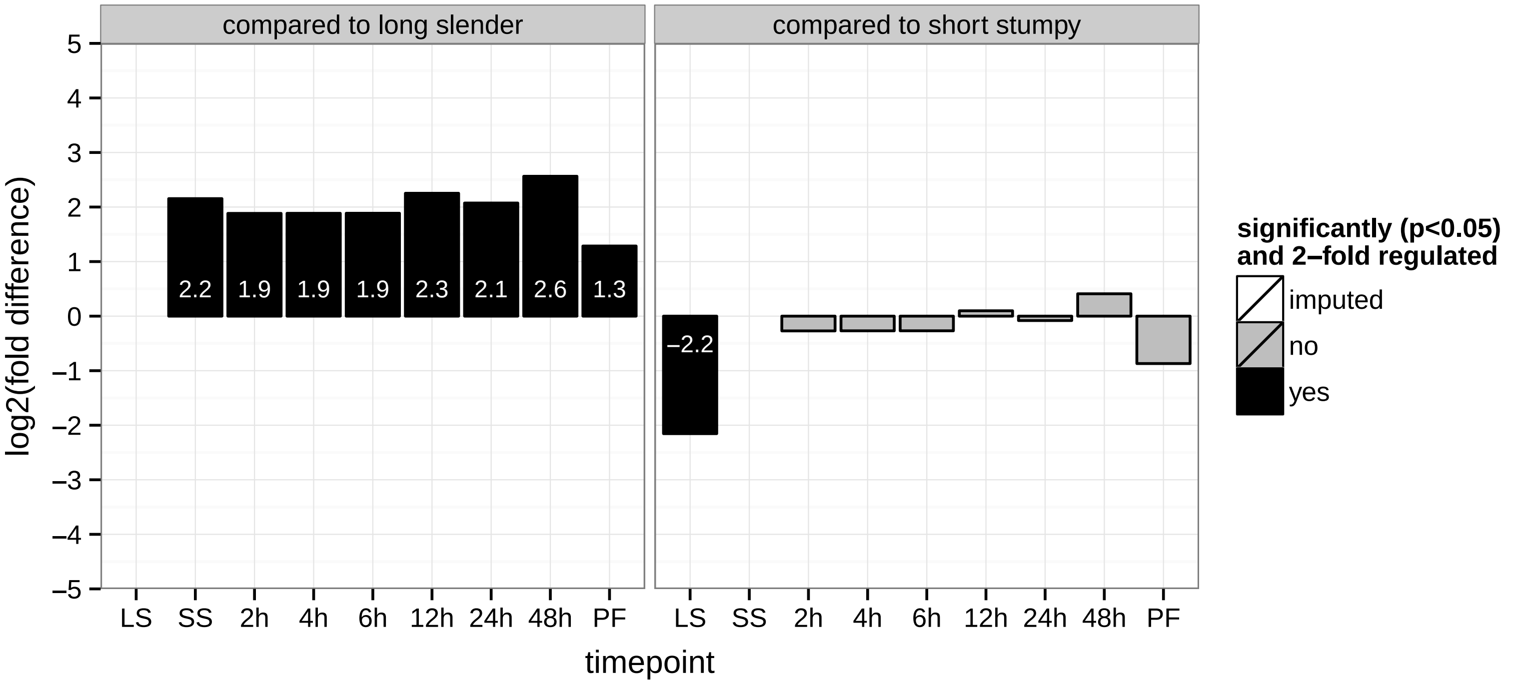
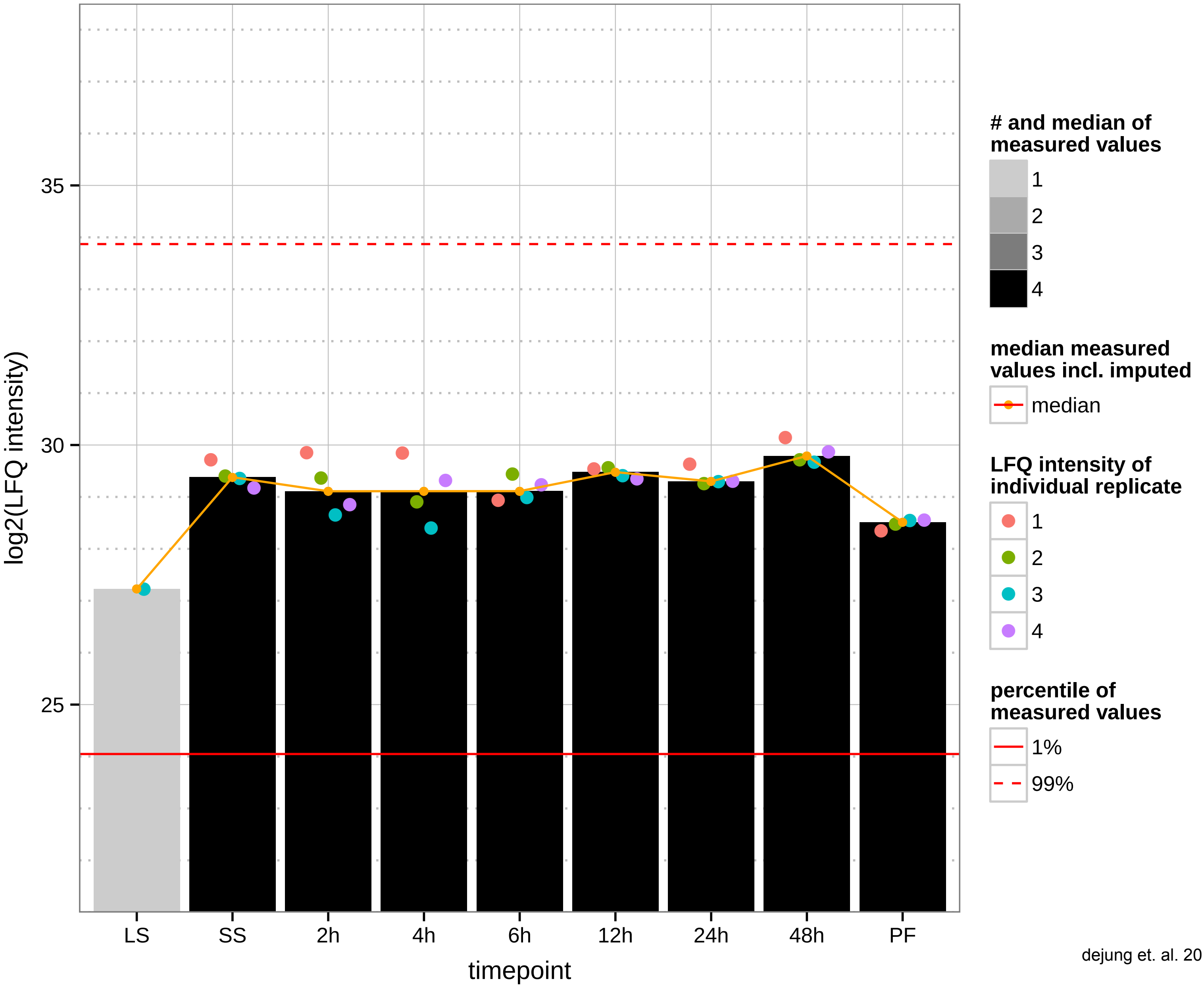
hypothetical protein, conserved, retrotransposon hot spot protein (RHS, pseudogene), putative, retrotransposon hot spot prote
Tb927.2.830;Tb11.v5.0655
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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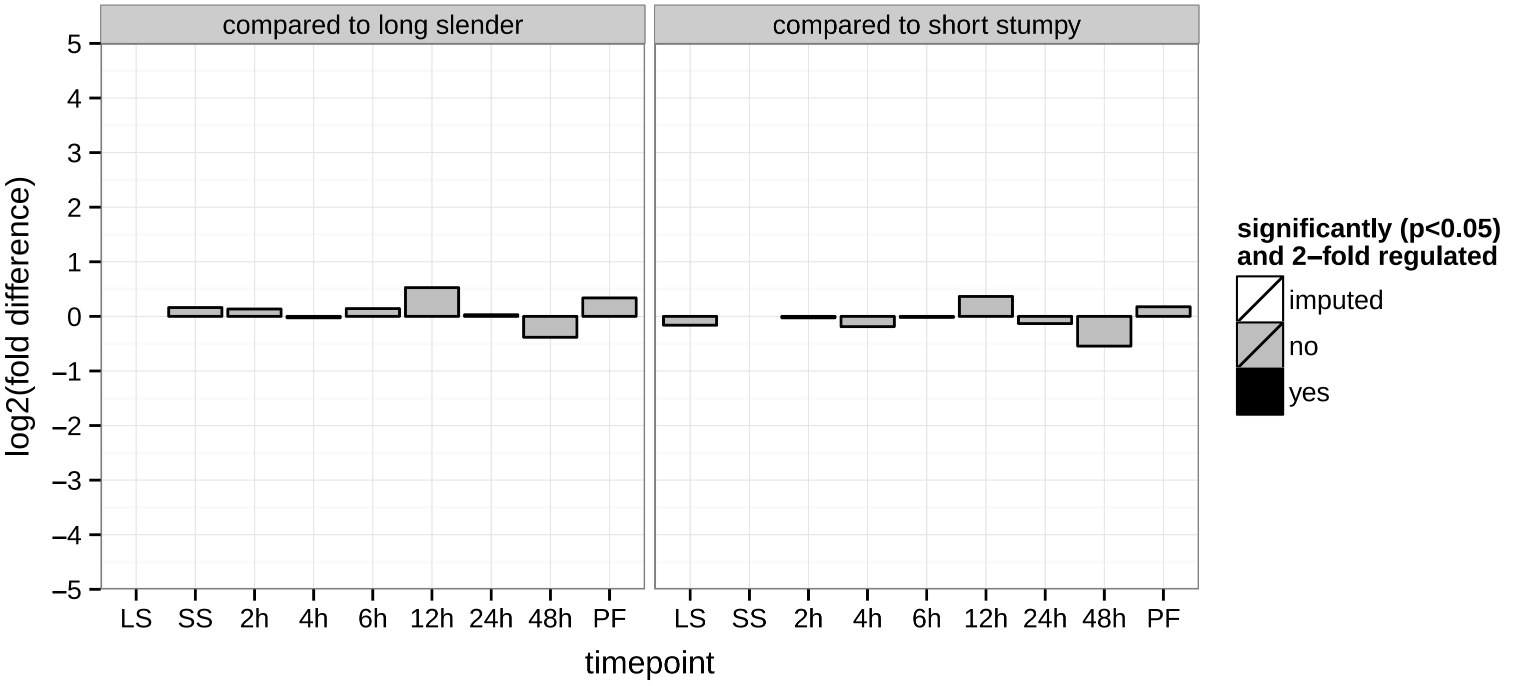
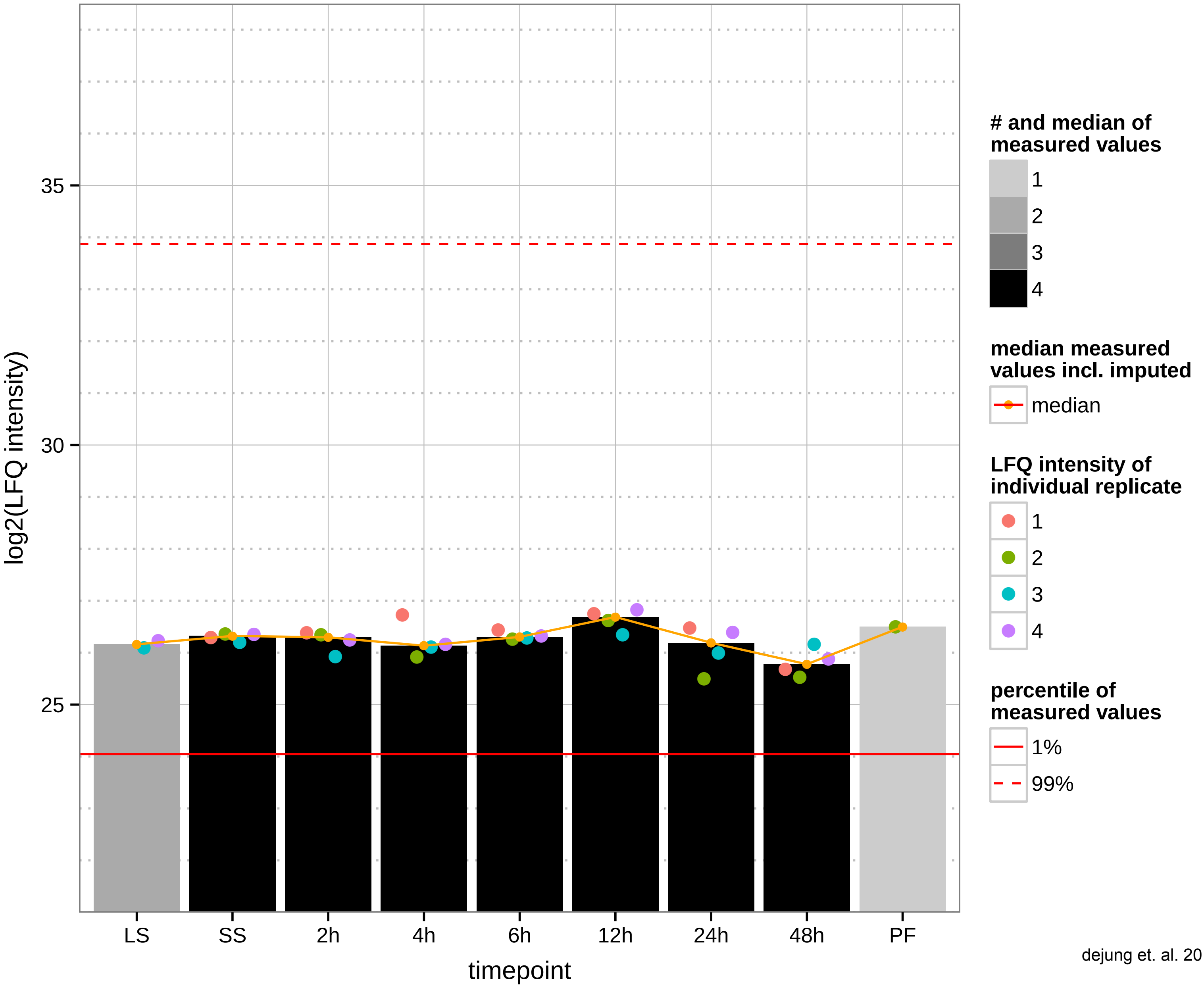
histone deacetylase, putative, histone deacetylase 3 (HDAC3)
Tb11.v5.0660;Tb927.2.2190
AGOF: null, histone deacetylase activity, zinc ion binding
AGOC: null, nucleus
AGOP: null, negative regulation of chromatin silencing, regulation of transcription, DNA−dependent
PGOF: null
PGOC: null
PGOP: null





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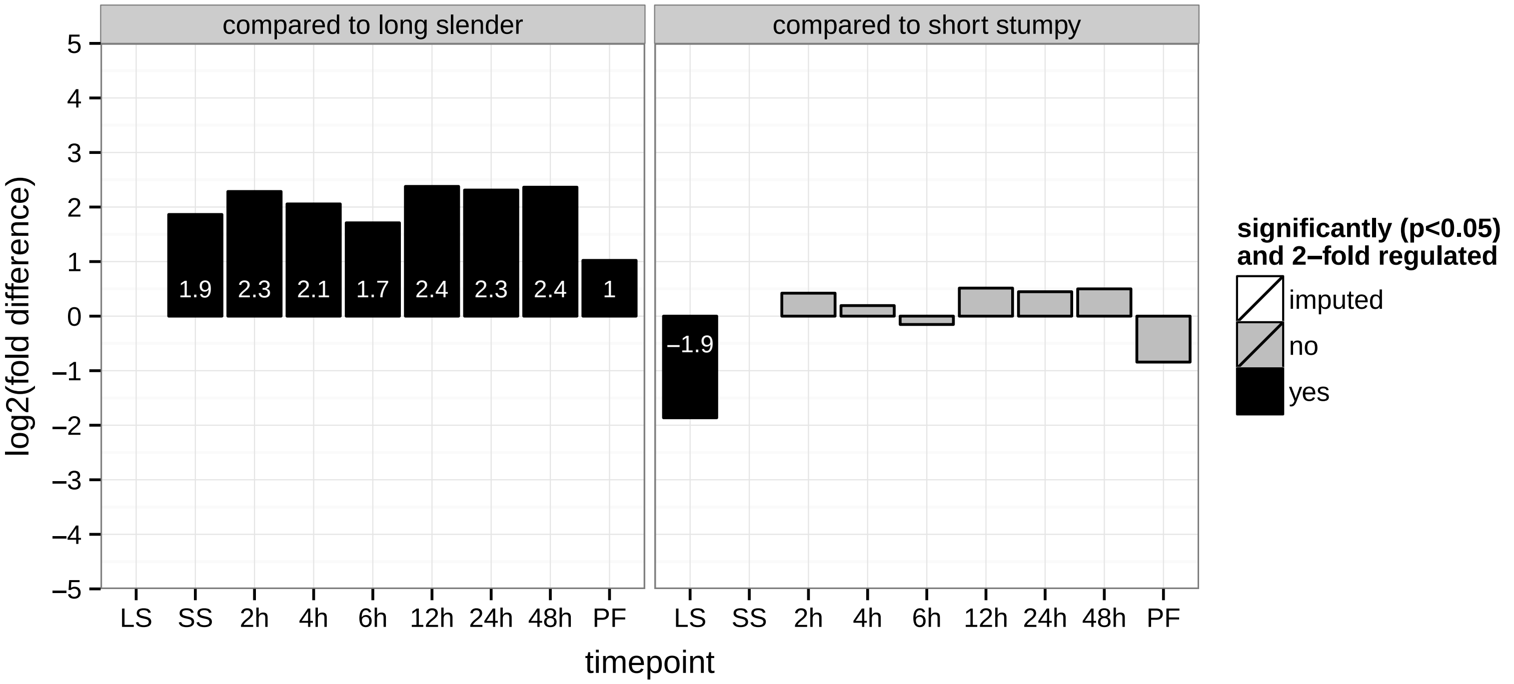
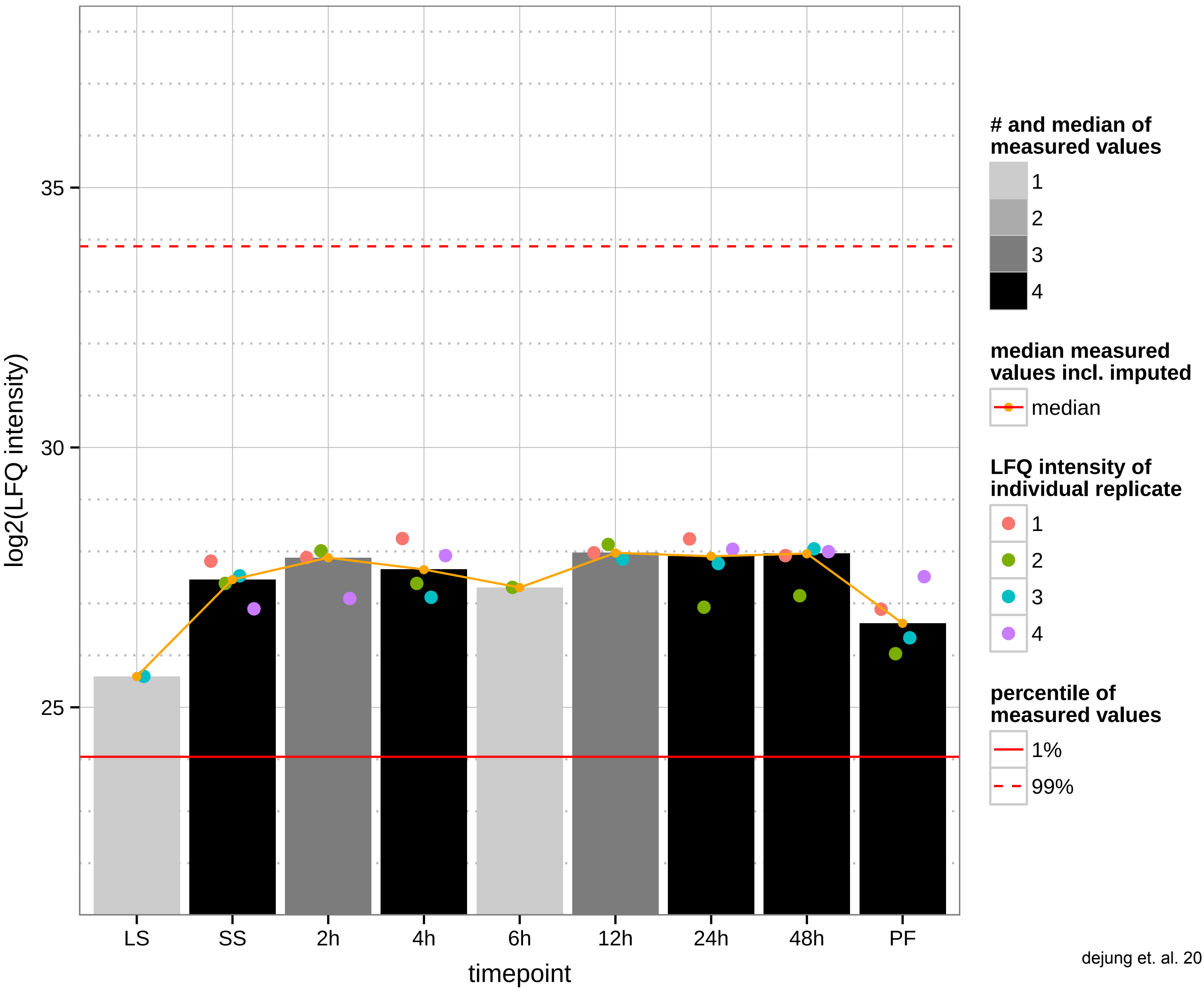
retrotransposon hot spot (RHS) protein, putative
Tb11.v5.0670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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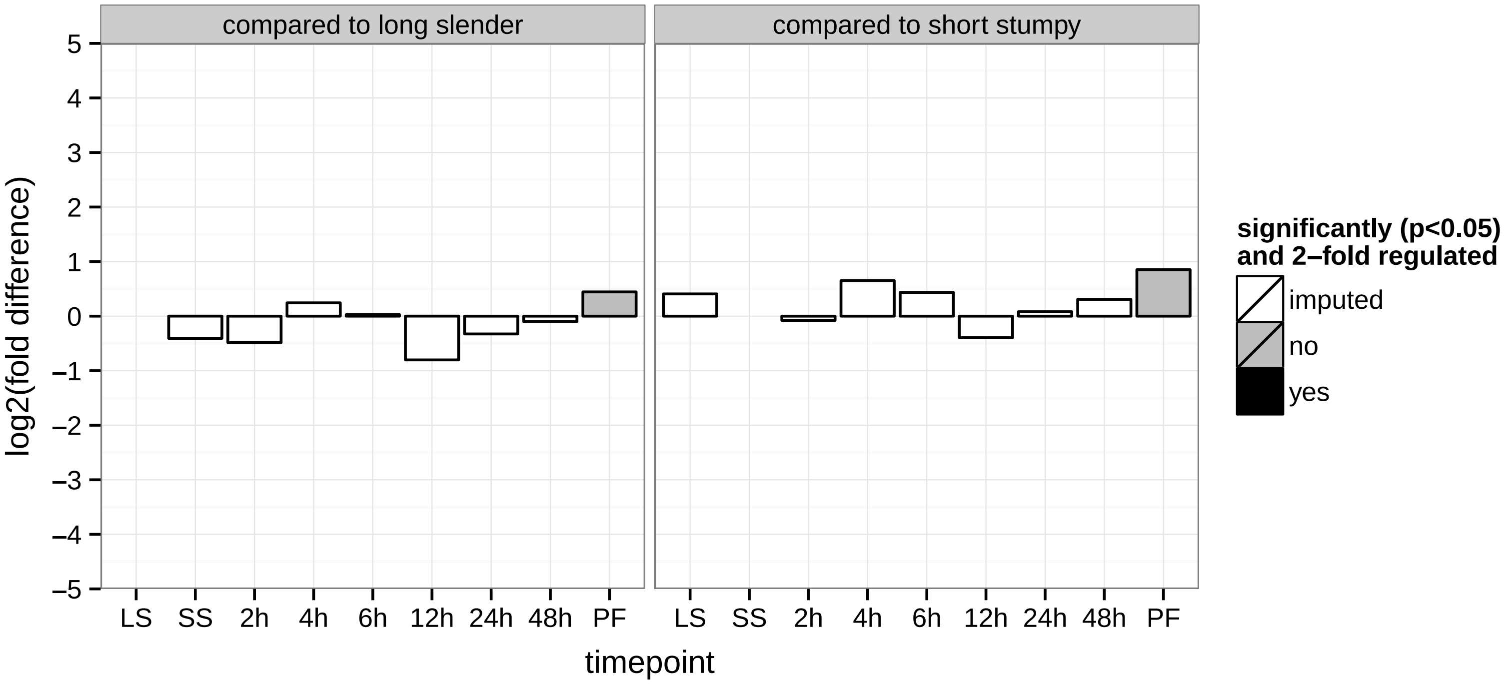
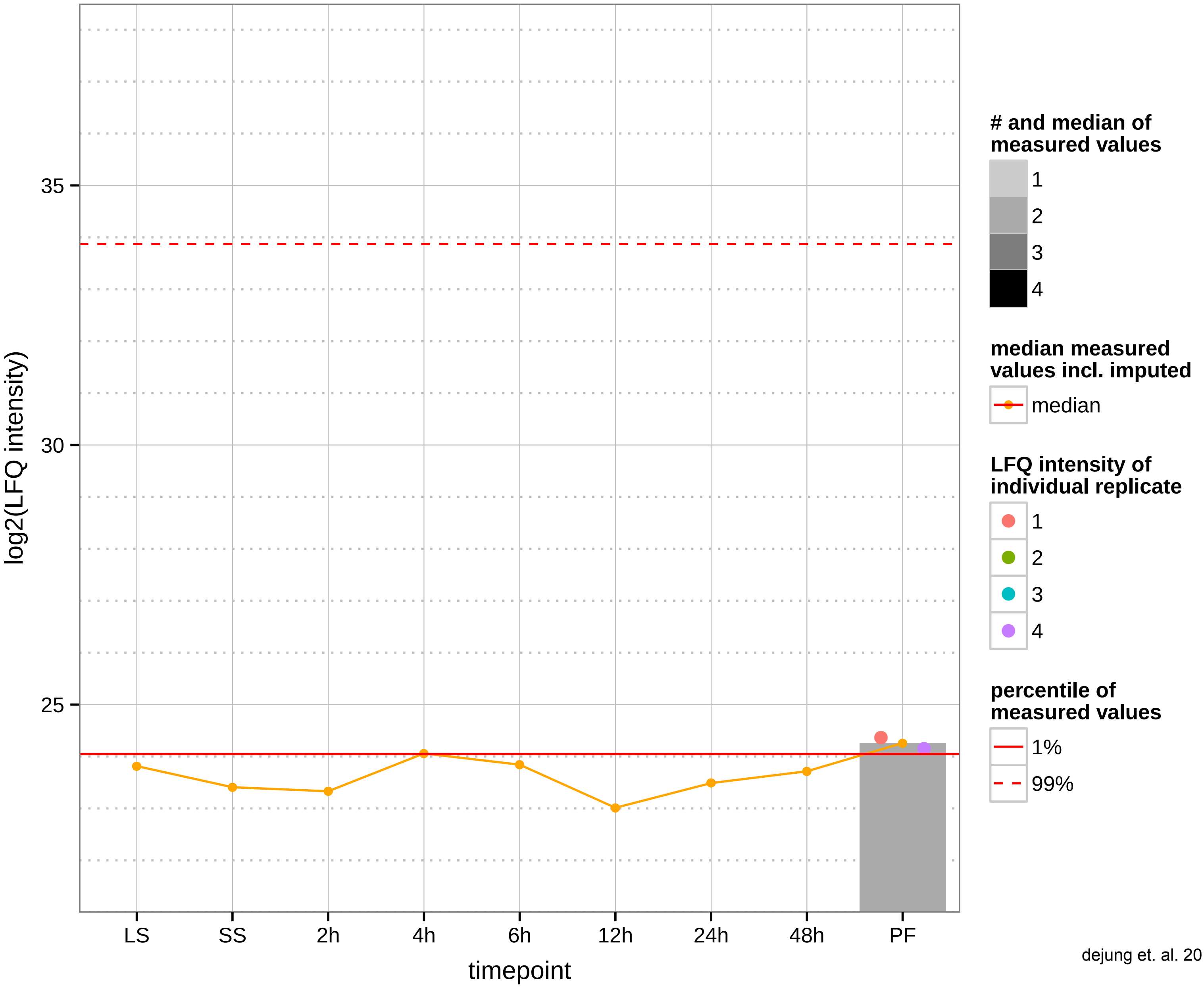
hypothetical protein, conserved
Tb11.v5.0692;Tb927.5.3000
AGOF: null, thiopurine S−methyltransferase activity
AGOC: null, cytoplasm, mitochondrion
AGOP: null, metabolic process
PGOF: S−adenosylmethionine−dependent methyltransferase activity
PGOC: null
PGOP: null





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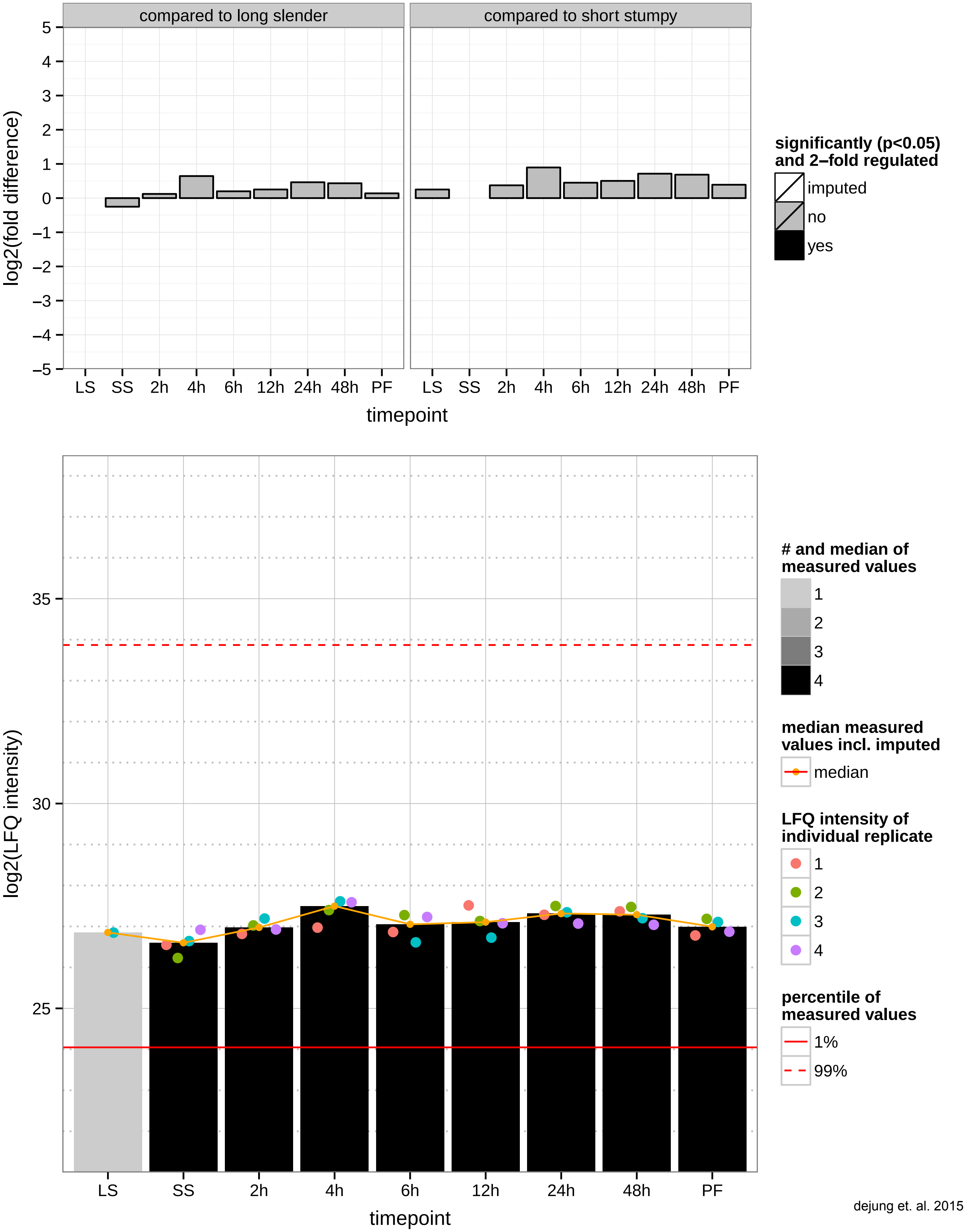
hypothetical protein, conserved
Tb927.10.8650;Tb11.v5.0707
AGOF: null
AGOC: null
AGOP: null, intracellular transport
PGOF: null
PGOC: null
PGOP: intracellular transport



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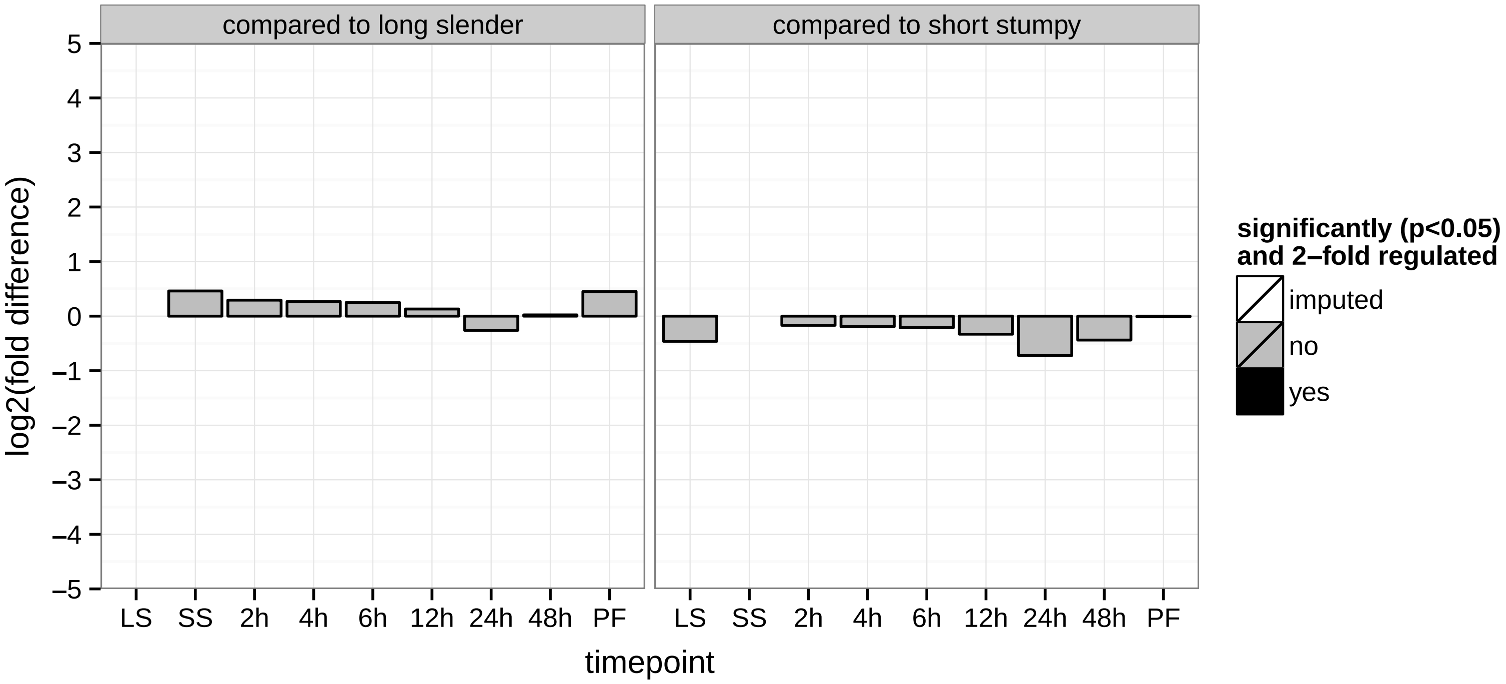
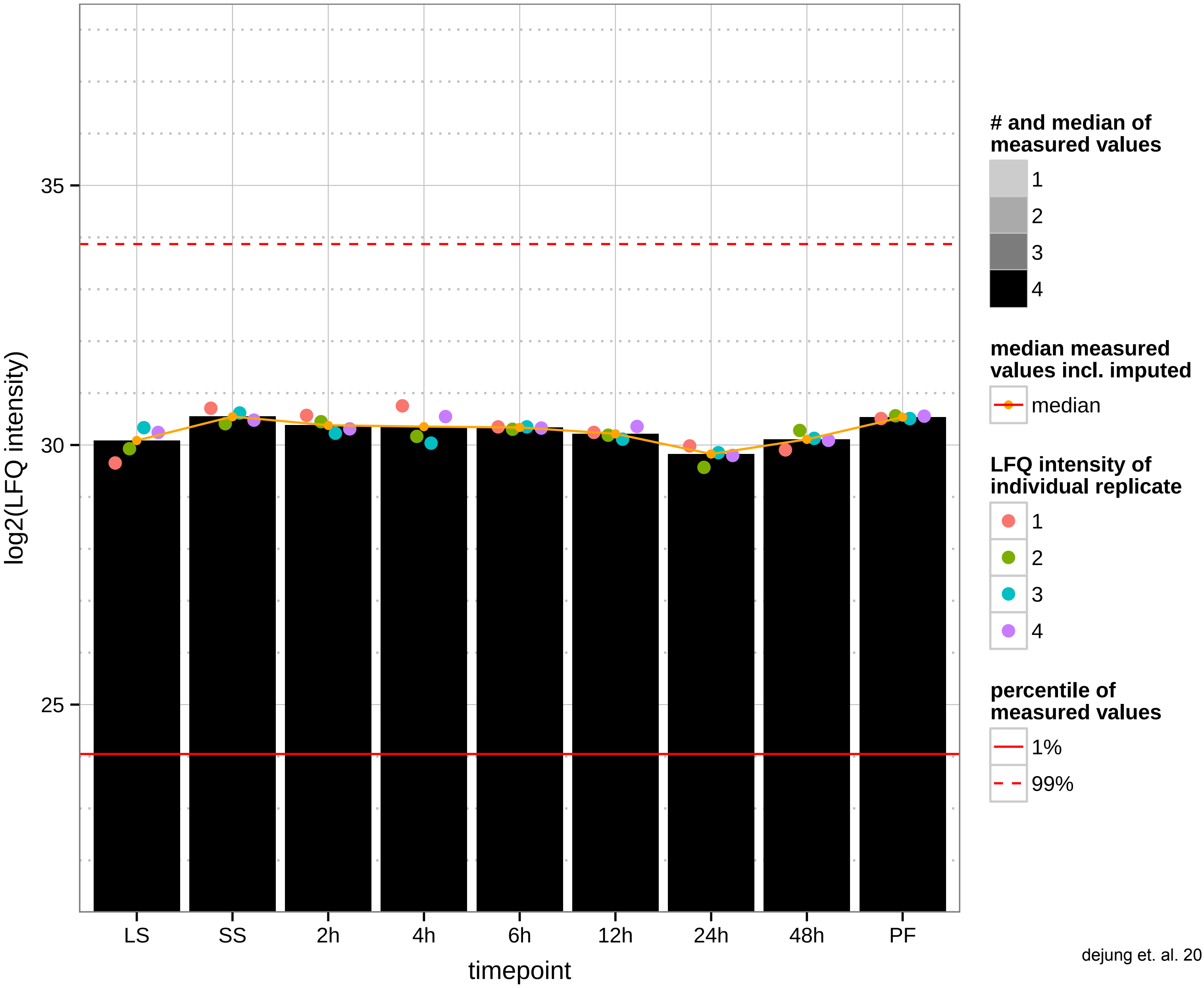
protein kinase, putative, glycogen synthase kinase 3 (GSK3), glycogen synthase kinase−3 alpha
Tb927.10.13780;Tb11.v5.0718
AGOF: null, ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity, protein kinase activity
AGOC: null
AGOP: null, growth, protein phosphorylation, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus−containing groups
PGOC: null
PGOP: protein phosphorylation





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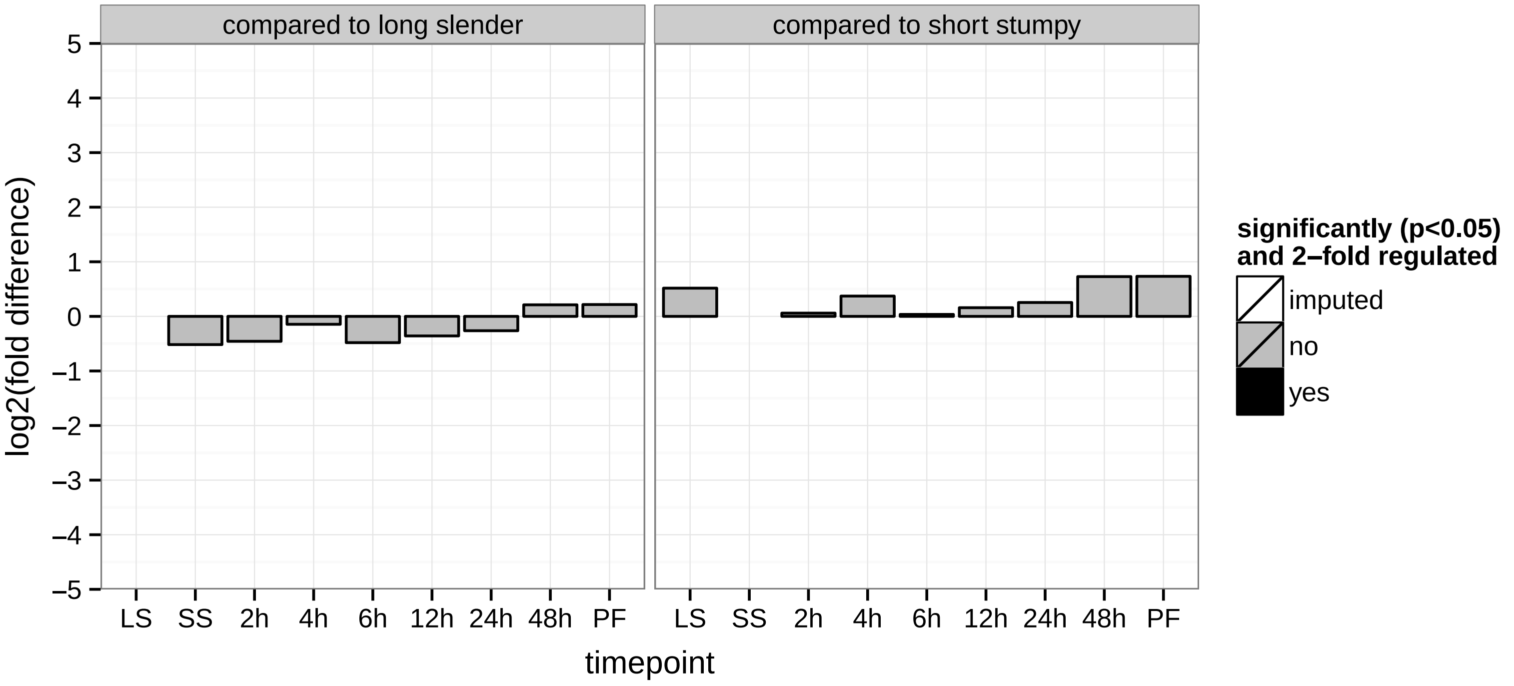
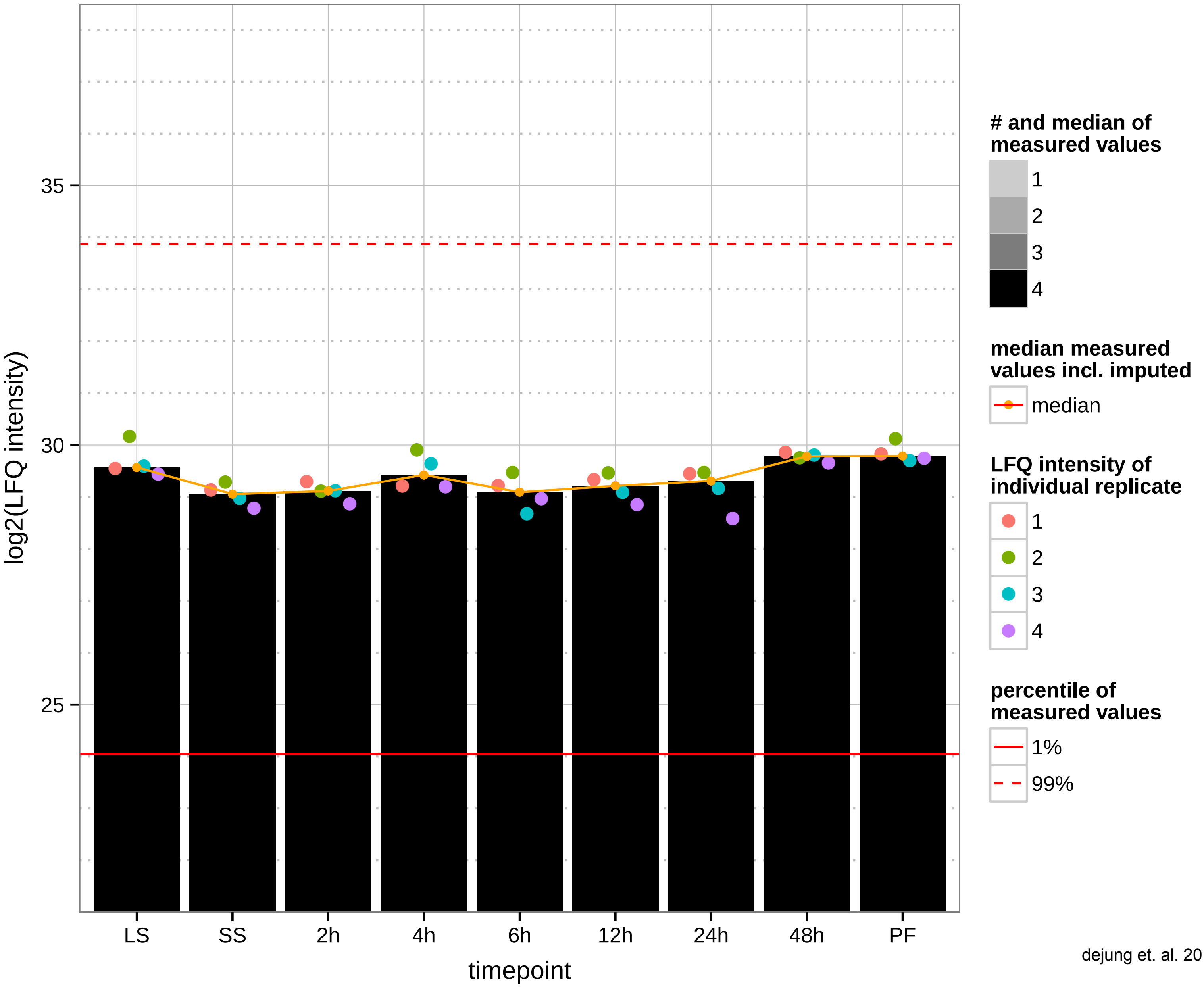
hypothetical protein, conserved, paraflagellar rod component, putative (PFC6)
Tb927.3.3790;Tb927.3.3770;Tb11.v5.0741
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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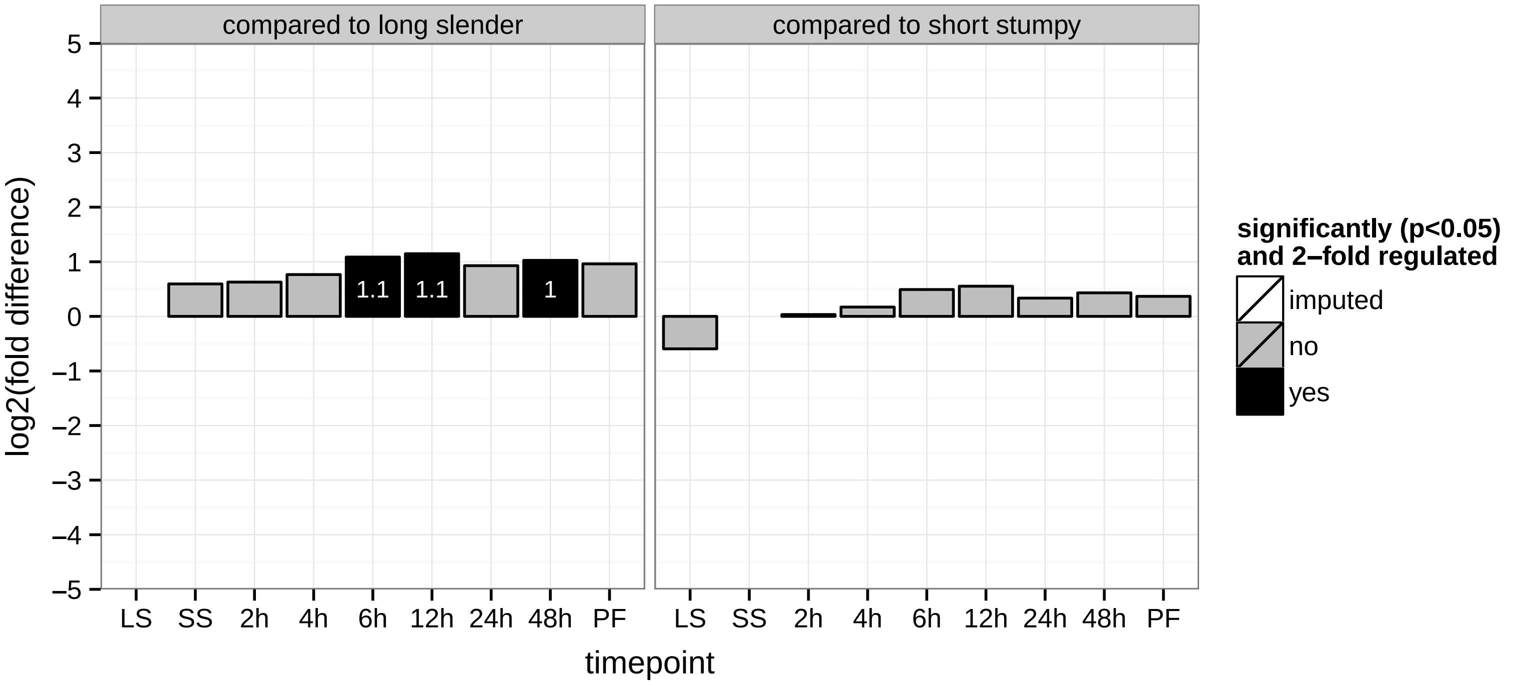
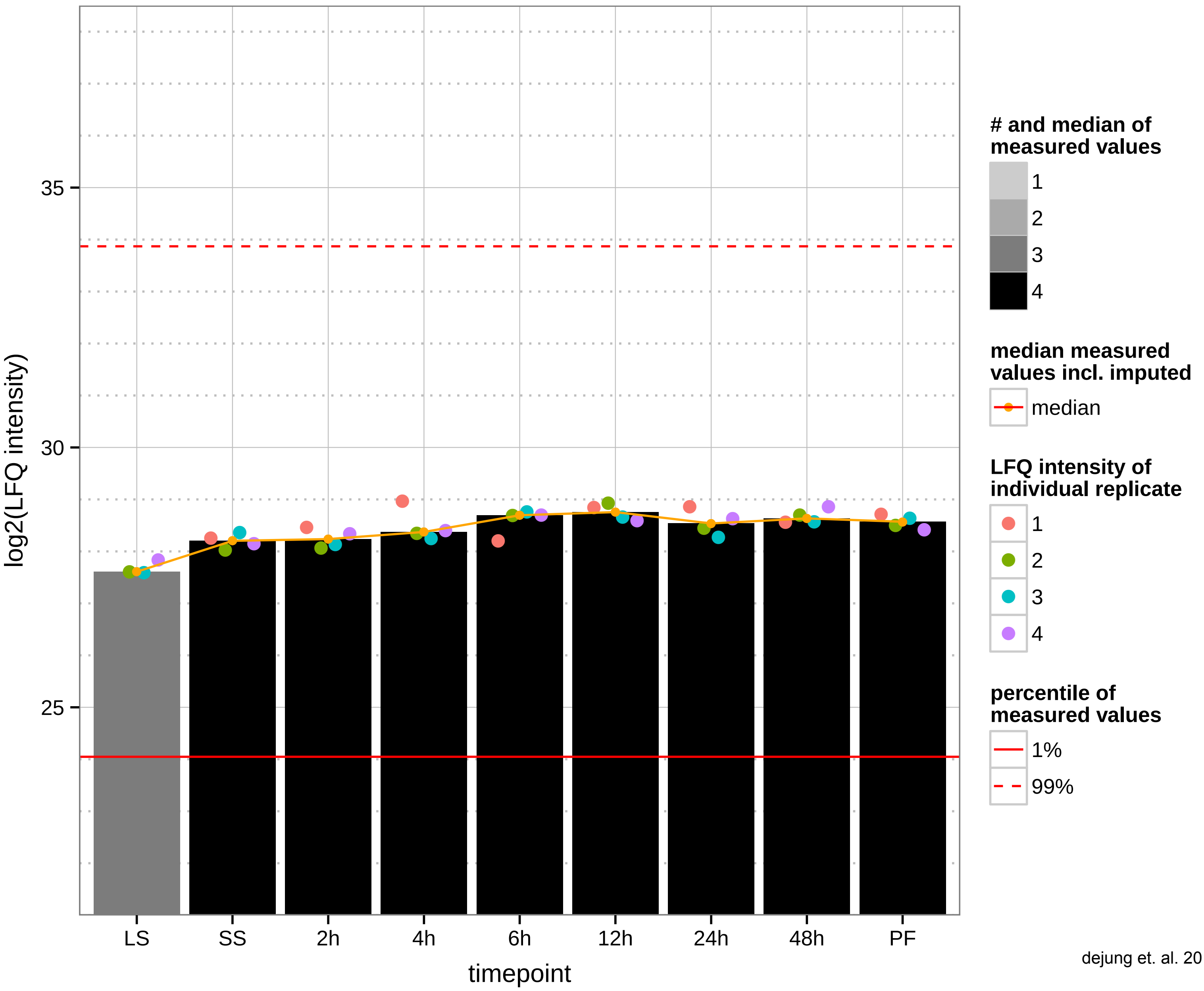
proteasome beta–1 subunit, putative, putative (TbPSB1)
Tb927.6.1260;Tb11.v5.0742
AGOF: null, peptidase activity, acting on L–amino acid peptides, threonine–type endopeptidase activity
AGOC: null, proteasome core complex, proteasome core complex, beta–subunit complex
AGOP: null, protein metabolic process, proteolysis involved in cellular protein catabolic process
PGOF: threonine–type endopeptidase activity
PGOC: proteasome core complex
PGOP: proteolysis involved in cellular protein catabolic process





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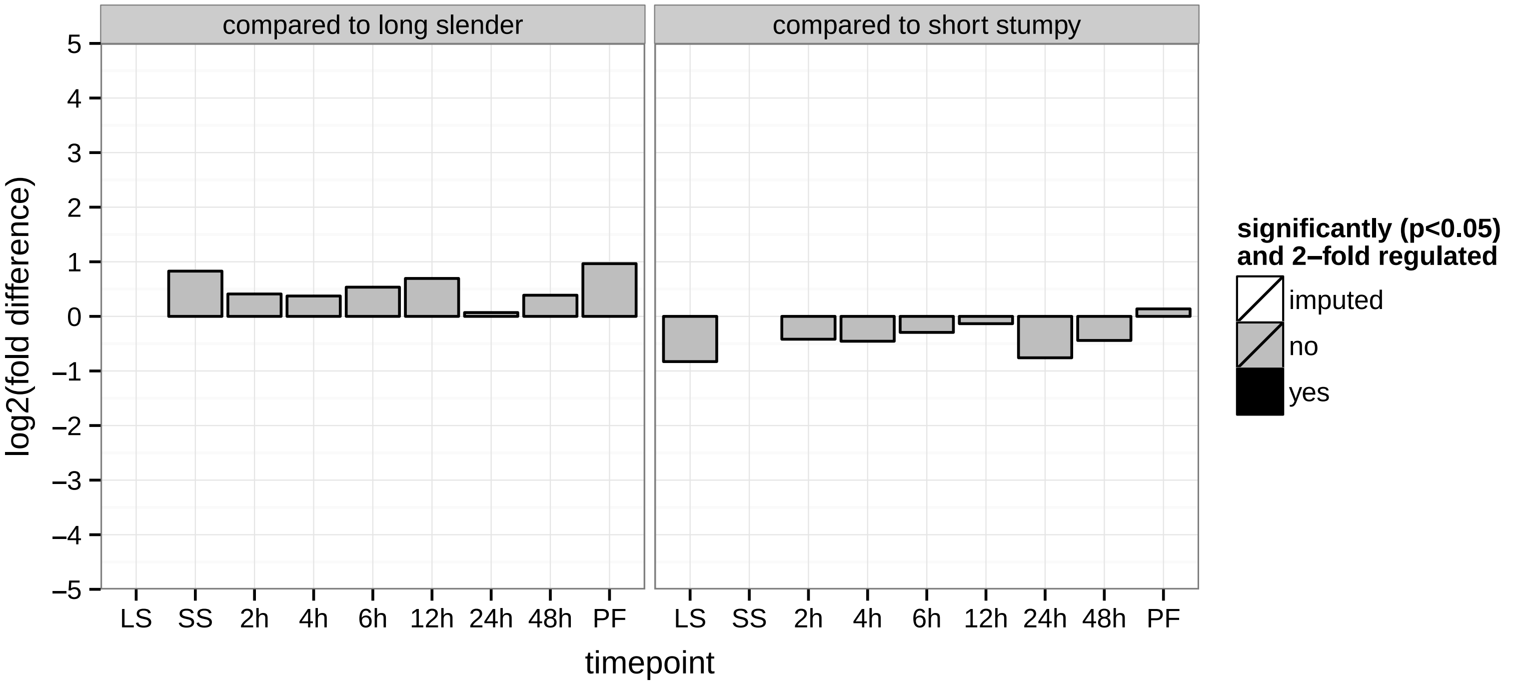
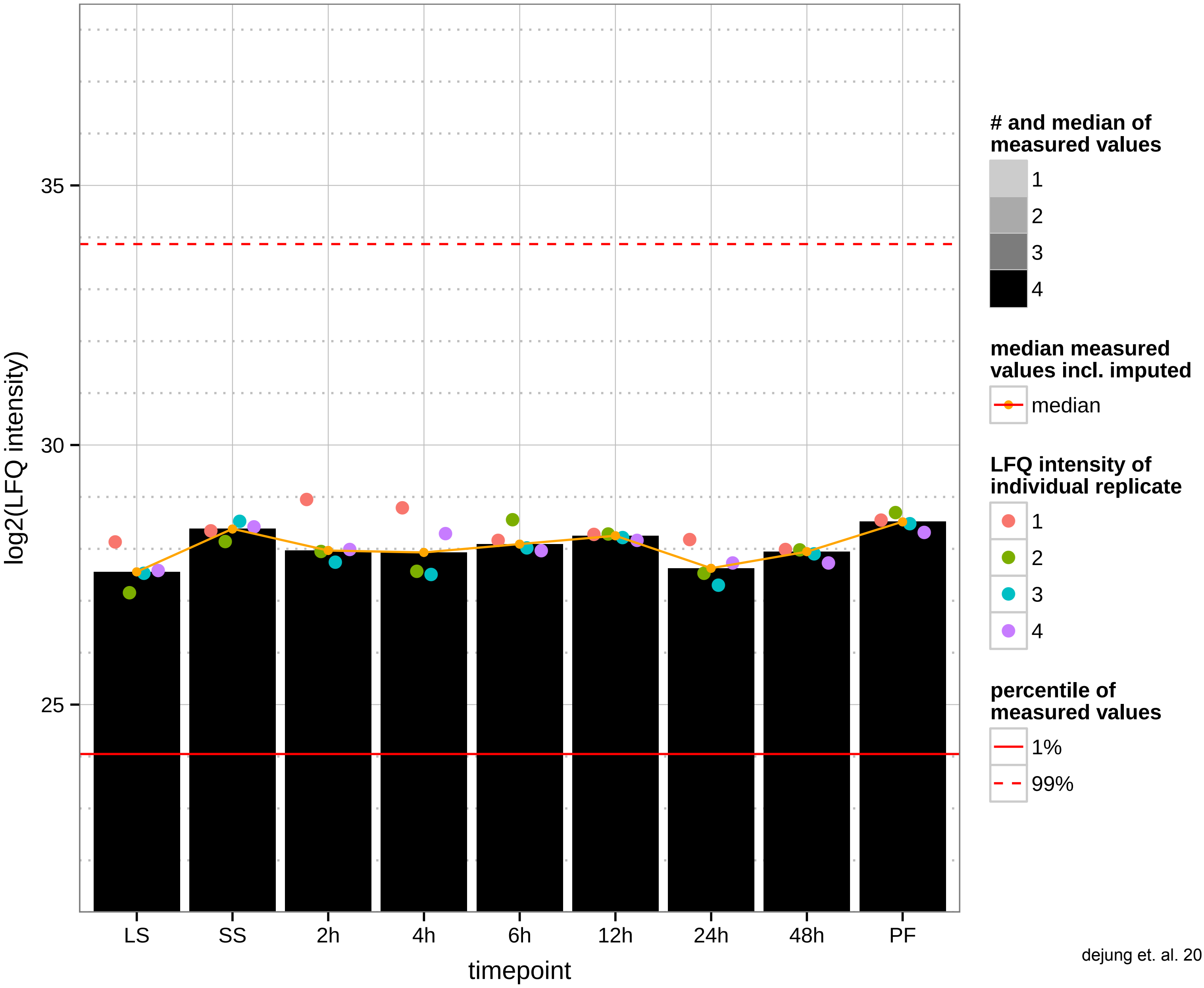
ribonuclease, putative, Poly(A)–specific ribonuclease PARN–3 (parn3)
Tb11.v5.0807;Tb927.9.13510
AGOF: null, nucleic acid binding
AGOC: null, nucleus
AGOP: null
PGOF: nucleic acid binding
PGOC: nucleus
PGOP: null





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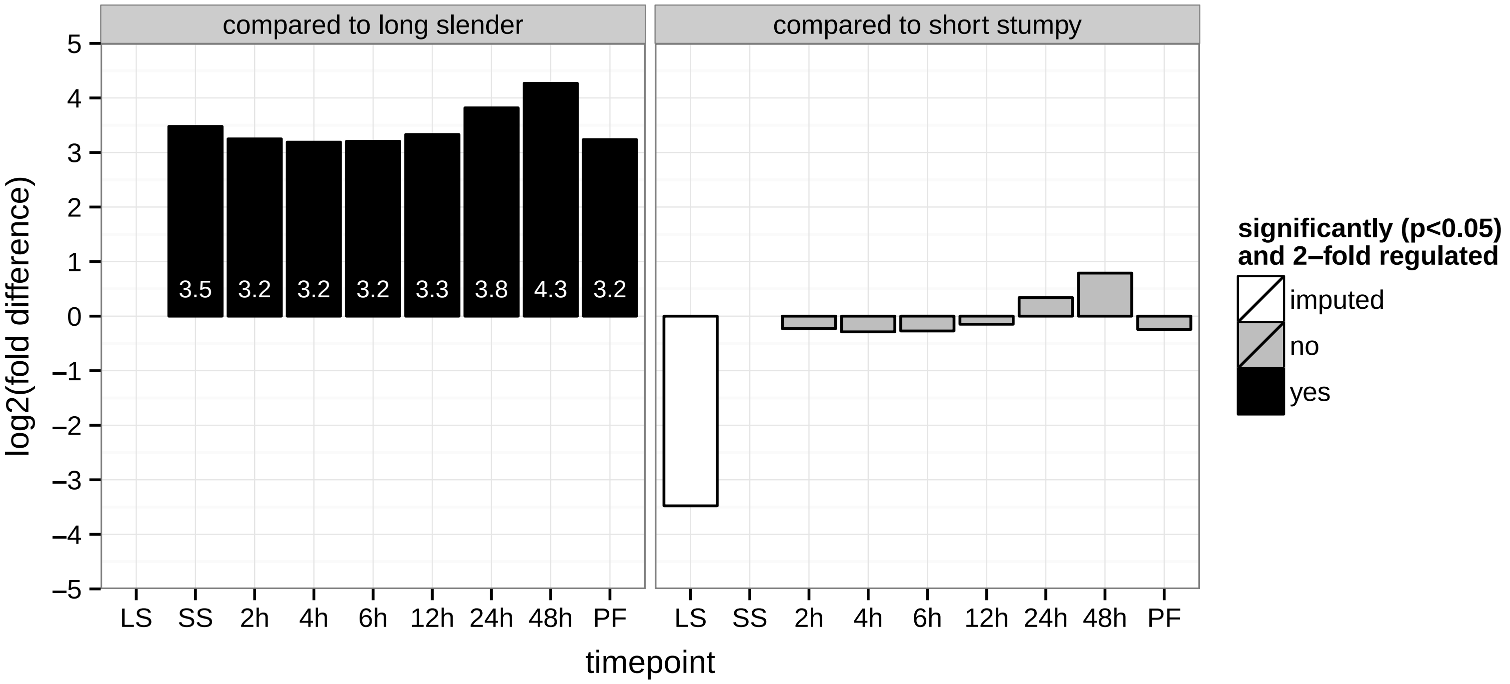
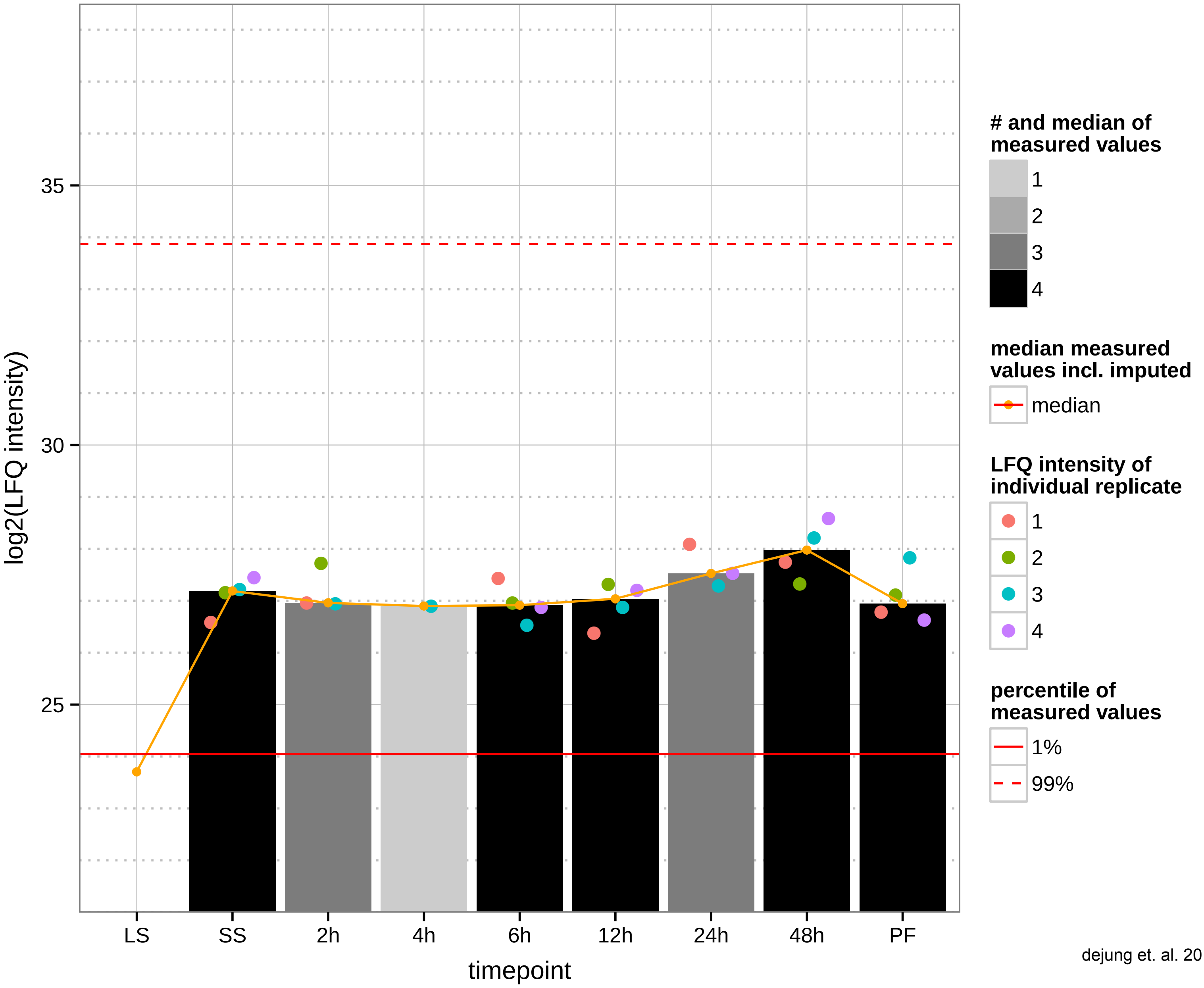
peroxin–2, putative, glycosome import protein (gim1) (PEX2)
Tb927.3.2340;Tb11.v5.0818
AGOF: null, zinc ion binding
AGOC: null, glycosome membrane, peroxisomal membrane
AGOP: null, glycolysis, peroxisome membrane biogenesis, peroxisome organization, protein import
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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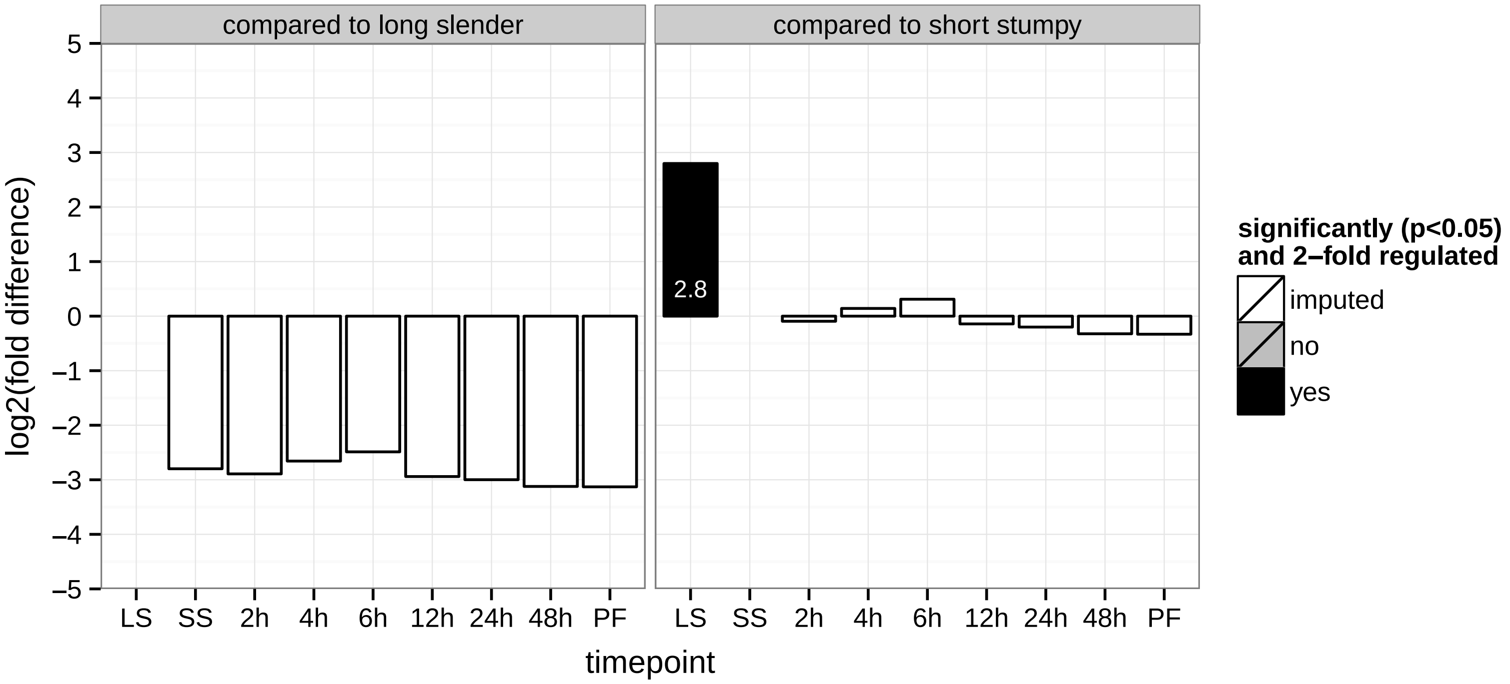
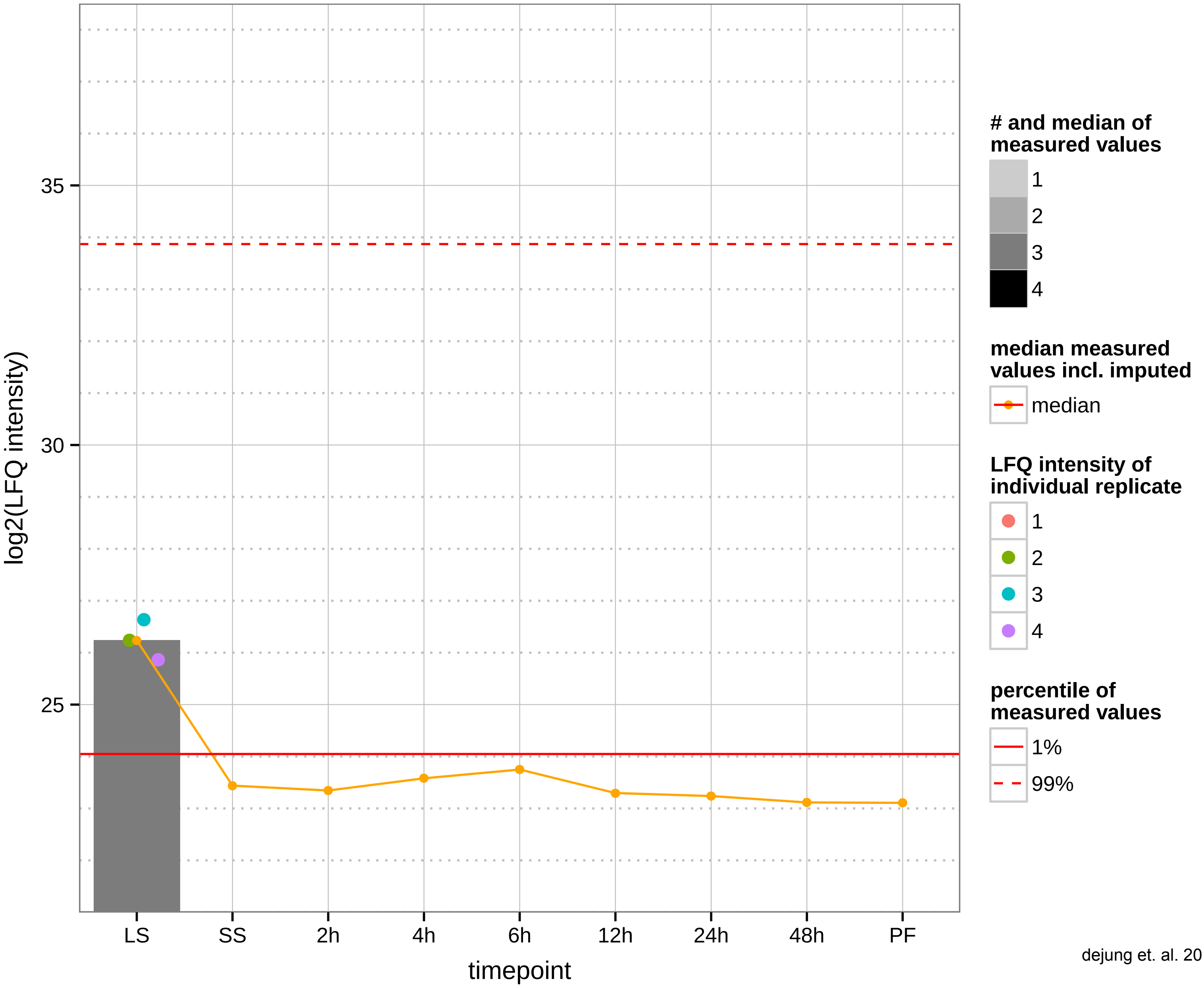
procyclin–associated gene 2–like protein, putative
Tb927.11.14600;Tb11.v5.1026
AGOF: null
AGOC: null
AGOP: null, evasion or tolerance of host immune response
PGOF: null
PGOC: null
PGOP: evasion or tolerance of host immune response





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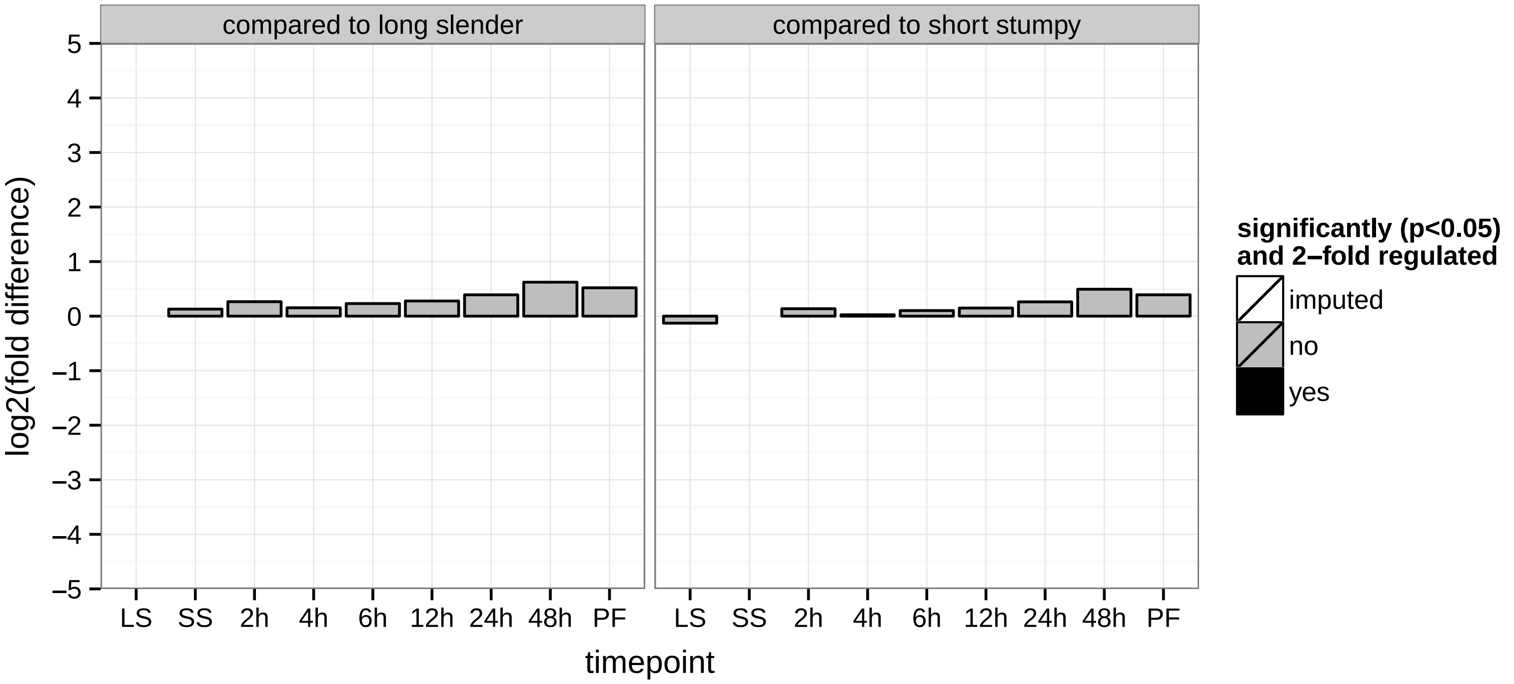
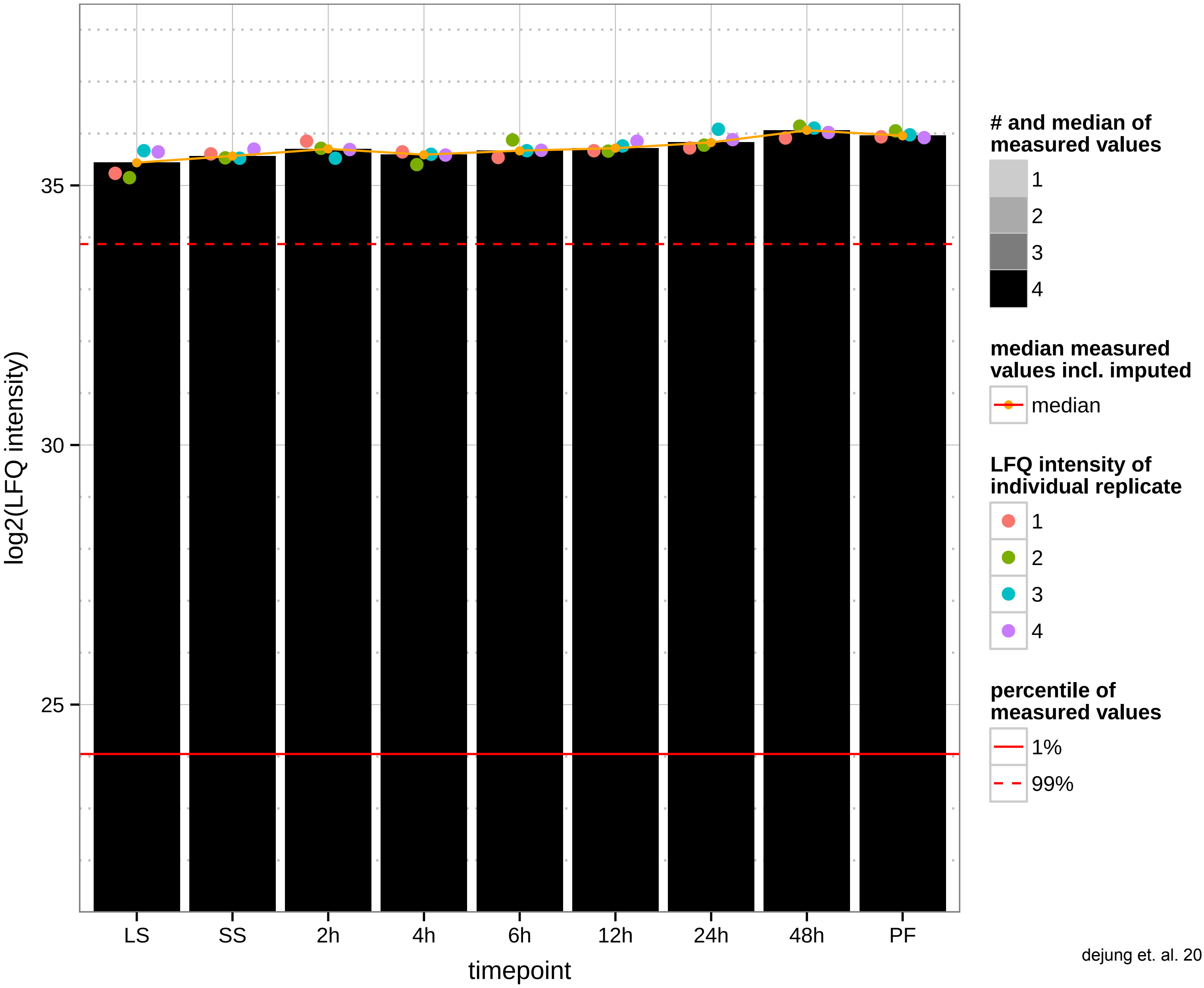
elongation factor 1–alpha, putative, EF–1–alpha (TEF1), elongation factor 1–alpha (TEF1)
Tb927.10.2110;Tb927.10.2100;Tb11.v5.1046;Tb927.10.2090
AGOF: null, GTP binding, GTPase activity, calmodulin binding, translation elongation factor activity
AGOC: null, cytoplasm
AGOP: null, calcium–mediated signaling, microtubule–based process, translational elongation
PGOF: GTP binding, GTPase activity, translation elongation factor activity
PGOC: cytoplasm
PGOP: translational elongation





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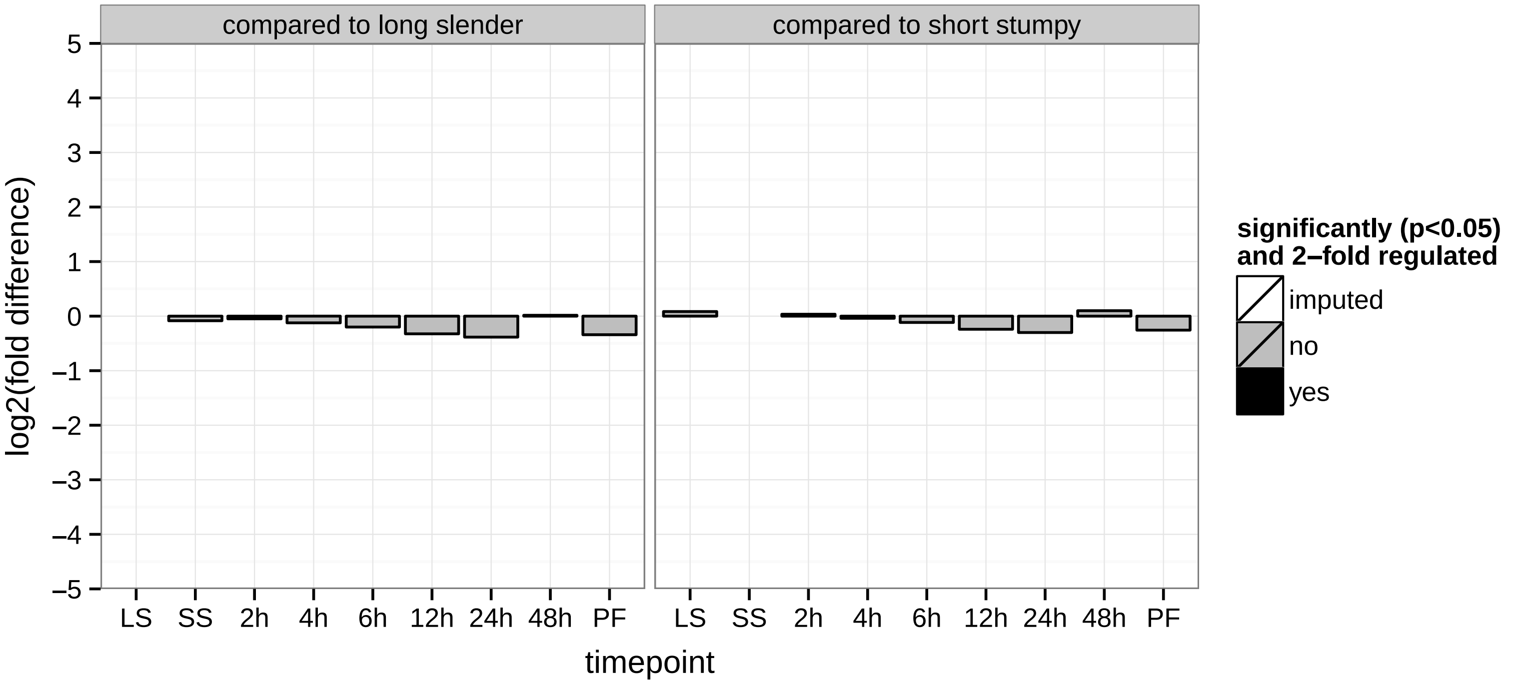
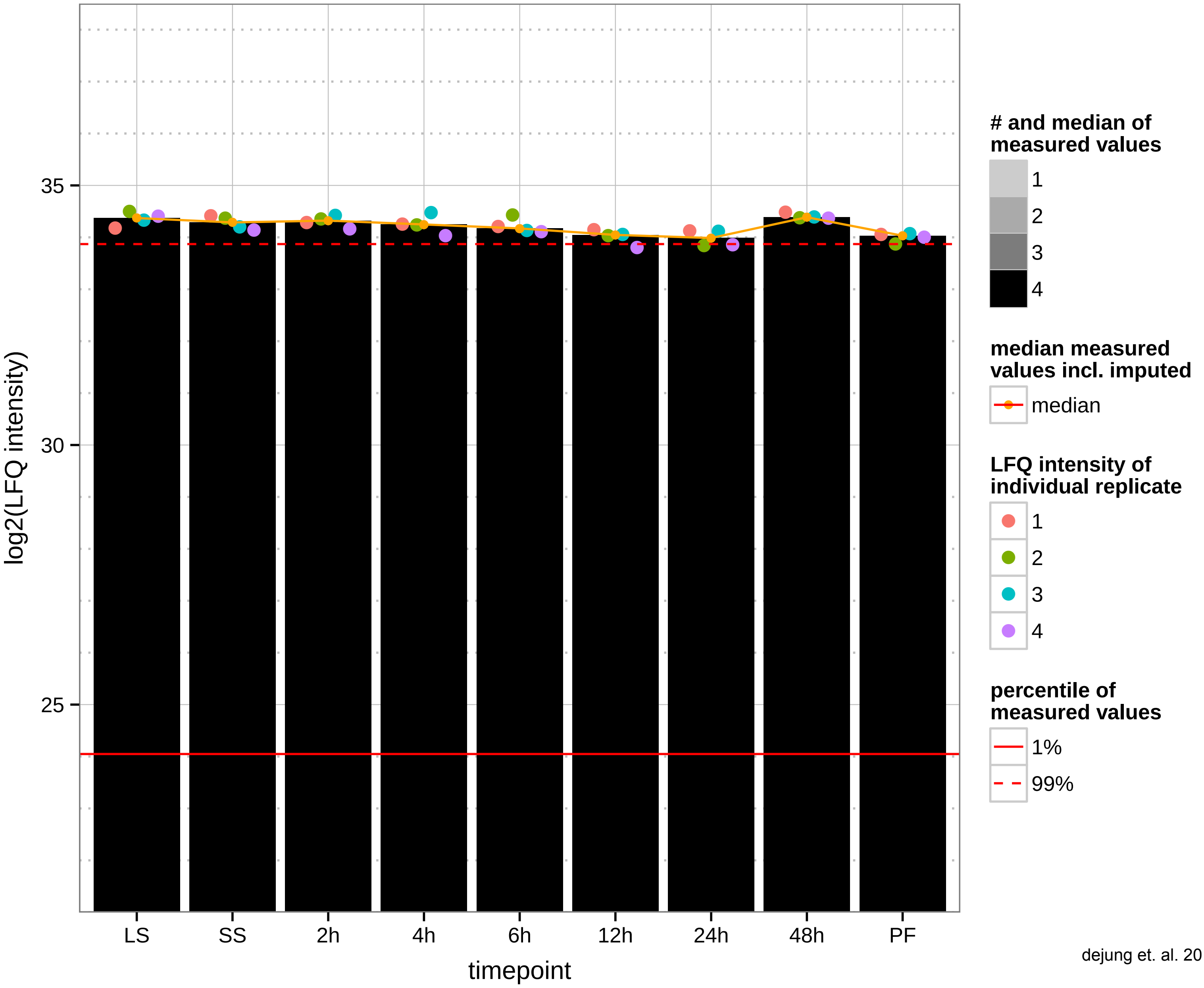
73 kDa paraflagellar rod protein, putative, PFR1 (PFR1)
Tb927.3.4330;Tb927.3.4320;Tb927.3.4310;Tb927.3.4300;Tb927.3.4290;Tb11.v5.1055
AGOF: null, calmodulin binding, molecular_function
AGOC: null, cilium, microtubule–based flagellum
AGOP: null, cellular component movement, forward locomotion
PGOF: calmodulin binding, null
PGOC: microtubule–based flagellum, null
PGOP: null





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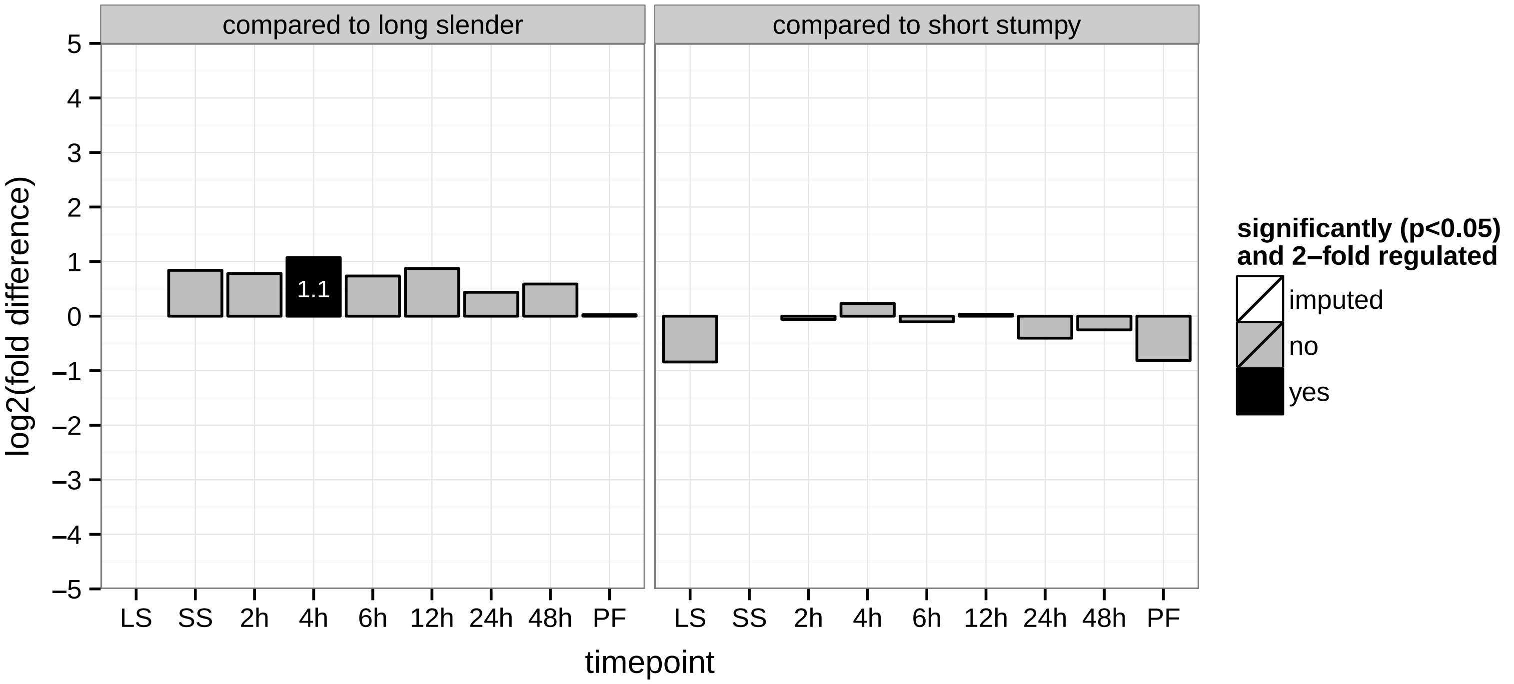
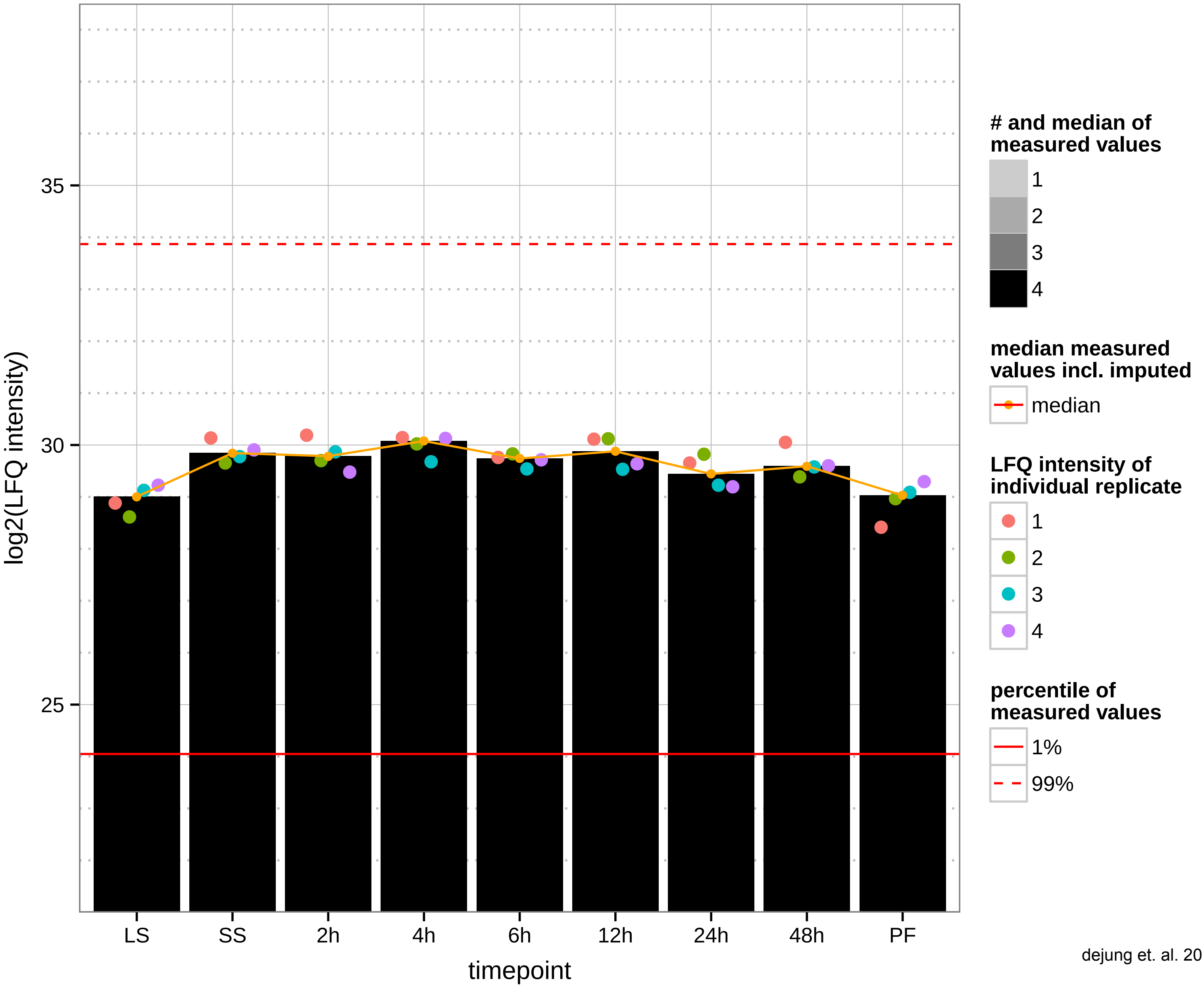
protein kinase, putative, mitogen–activated protein kinase 11
Tb927.10.12040;Tb11.v5.1057
AGOF: null, ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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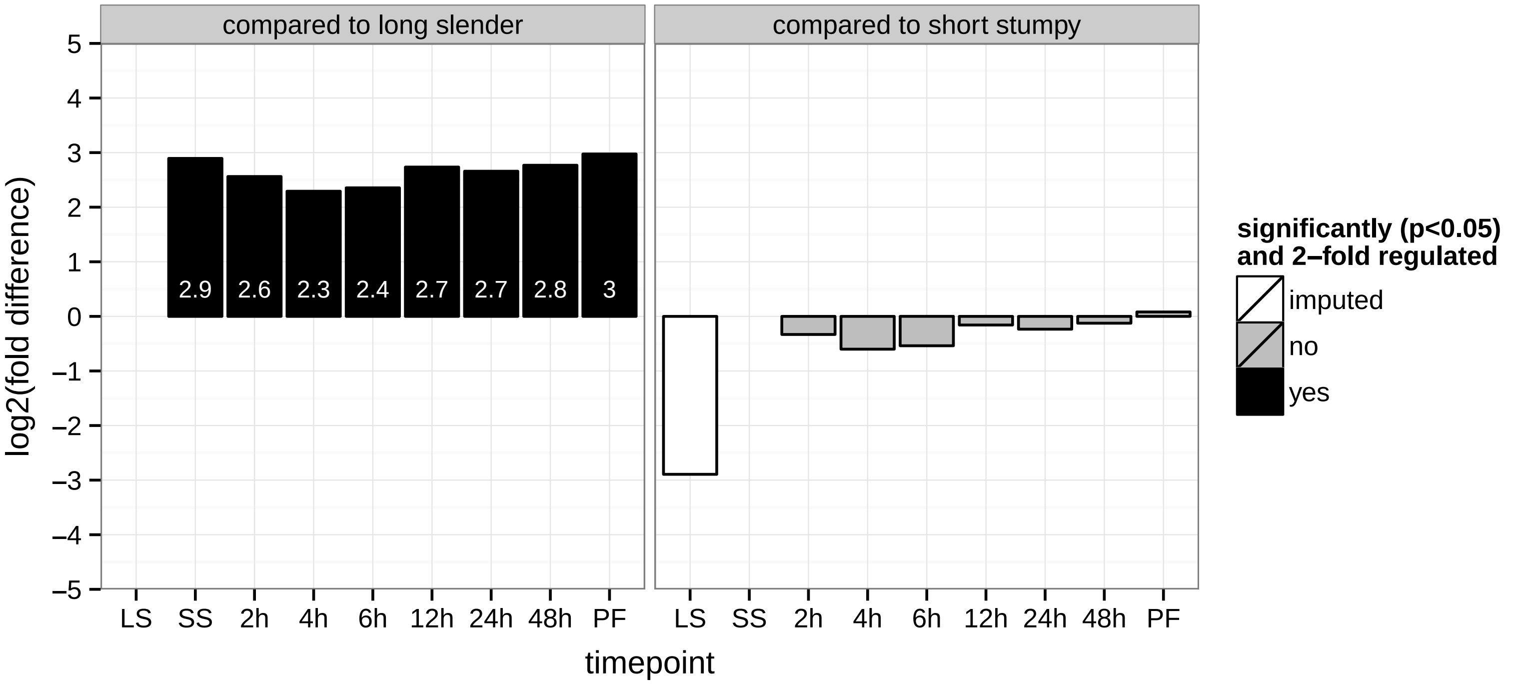
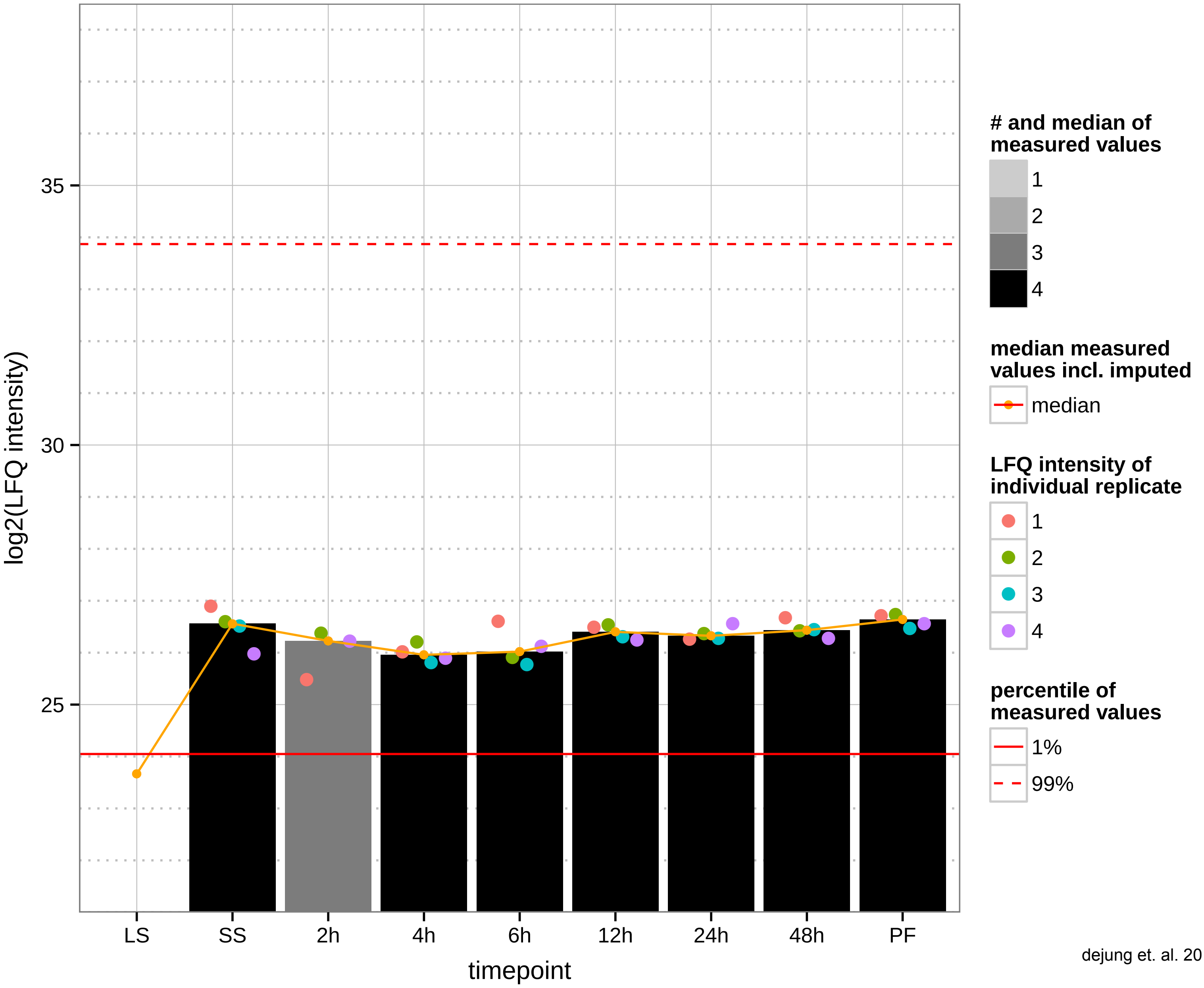
developmentally regulated phosphoprotein
Tb927.1.1000
AGOF: ATP binding
AGOC: mitochondrion
AGOP: null
PGOF: ATP binding
PGOC: null
PGOP: null





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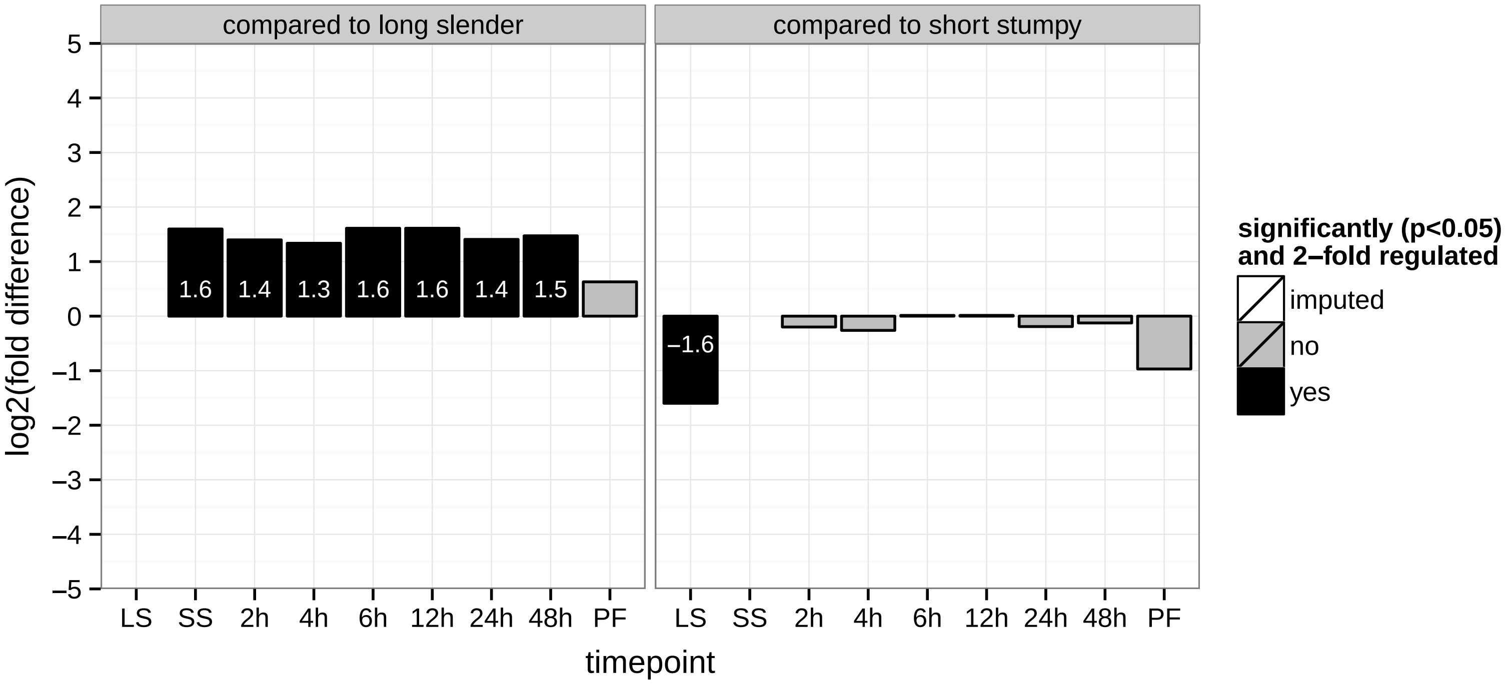
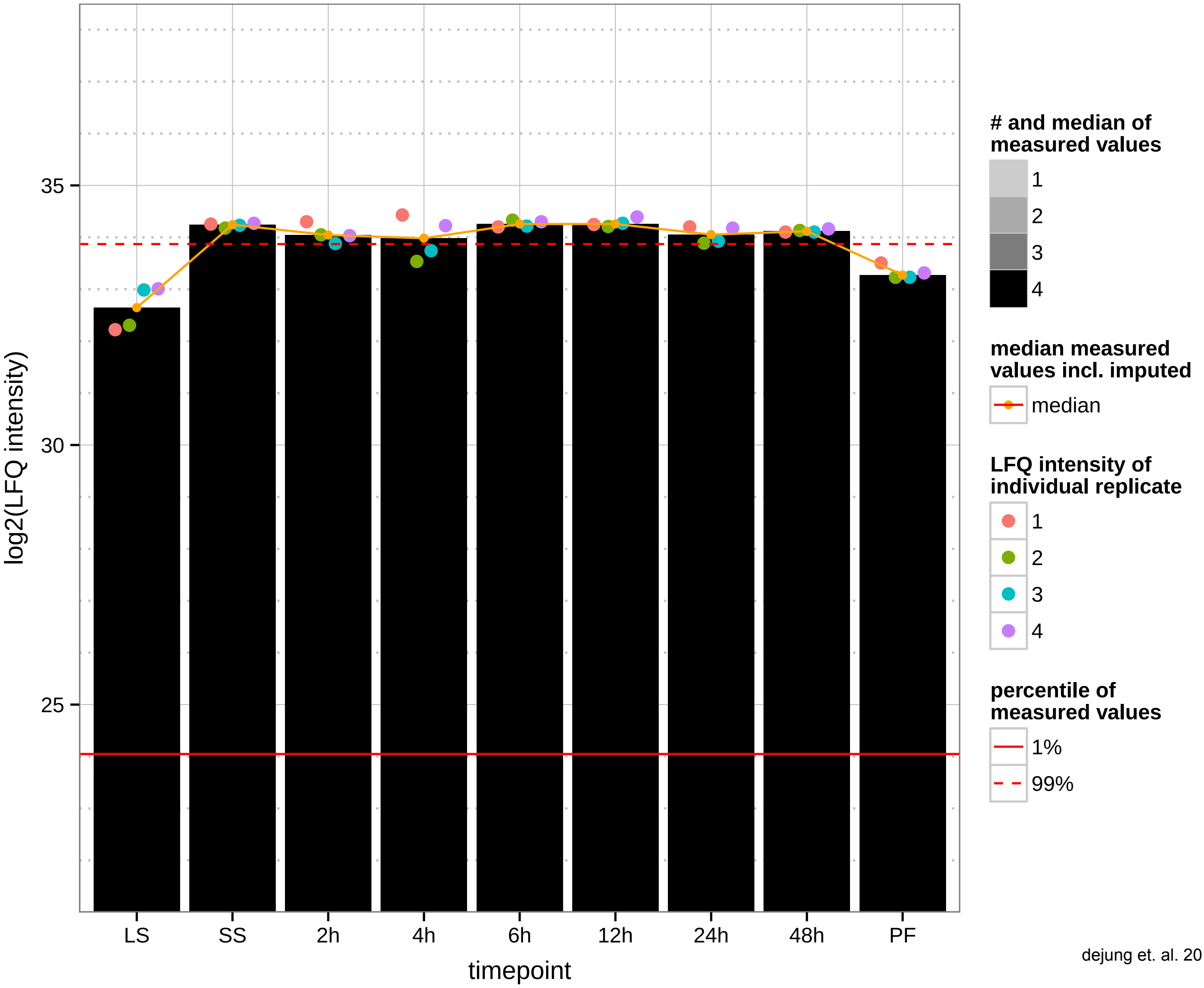
retrotransposon hot spot protein 4 (RHS4), putative
Tb927.1.120
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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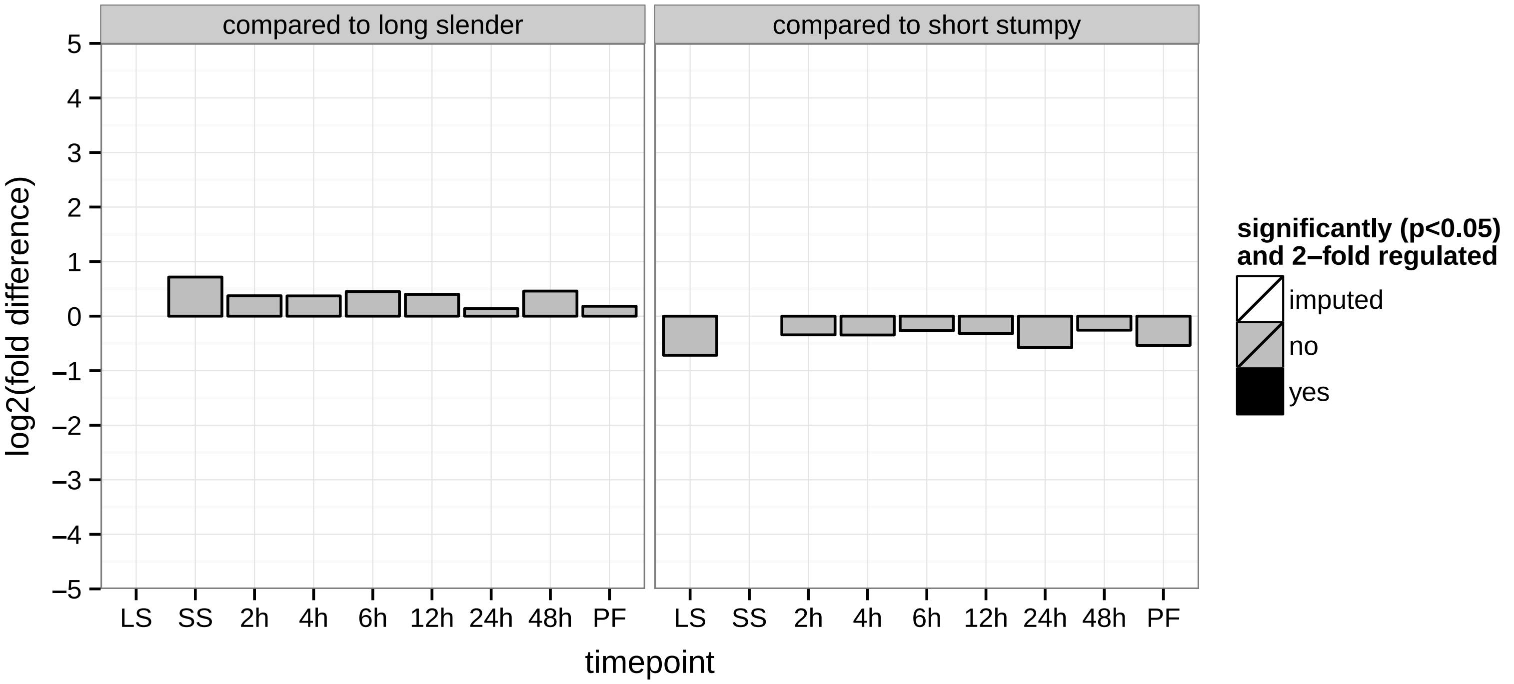
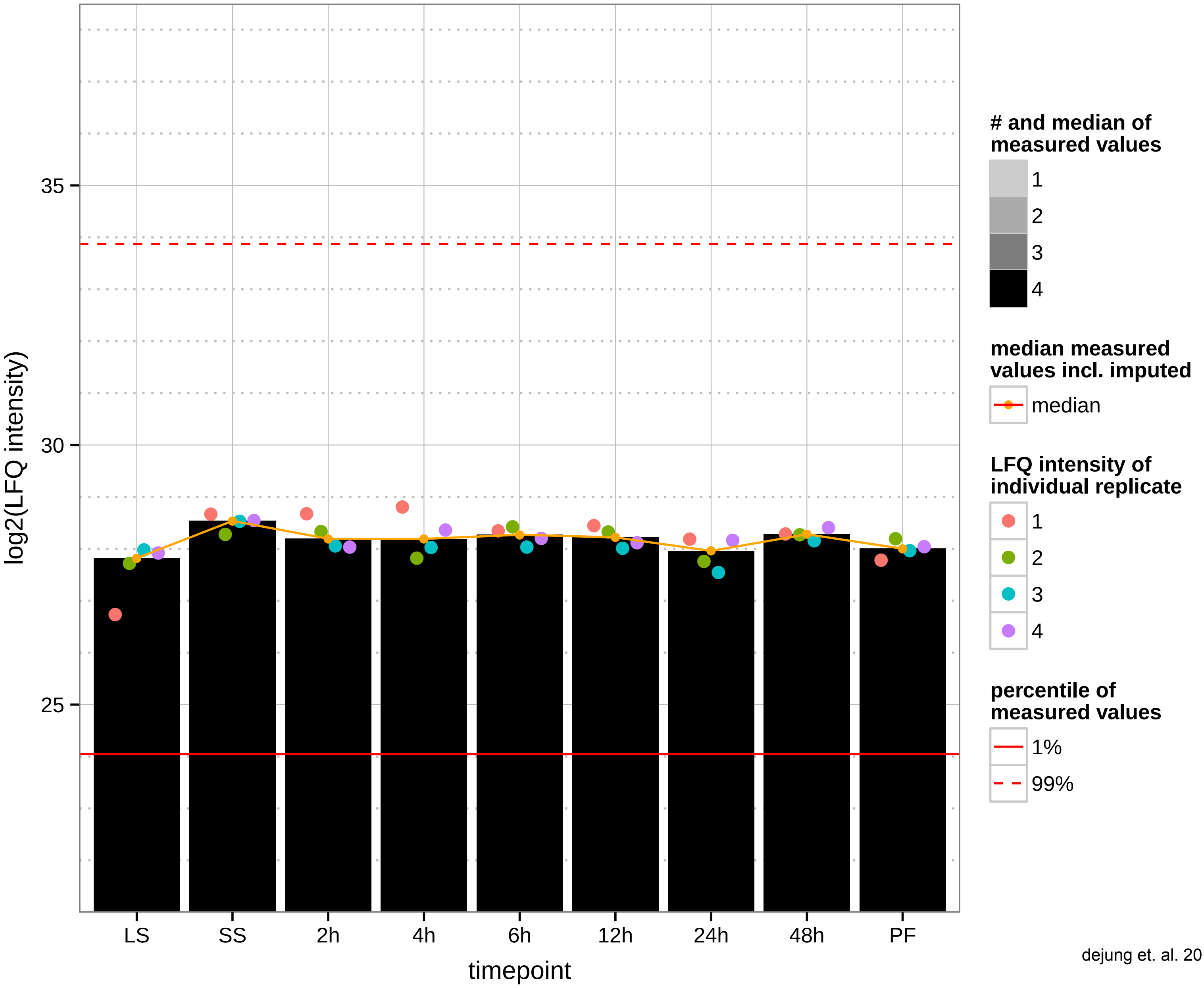
serine/threonine protein phosphatase 2A regulatory subunit, putative
Tb927.1.1380;Tb11.v5.0390
AGOF: null
AGOC: null, protein serine/threonine phosphatase complex
AGOP: null, protein dephosphorylation
PGOF: binding
PGOC: null
PGOP: null





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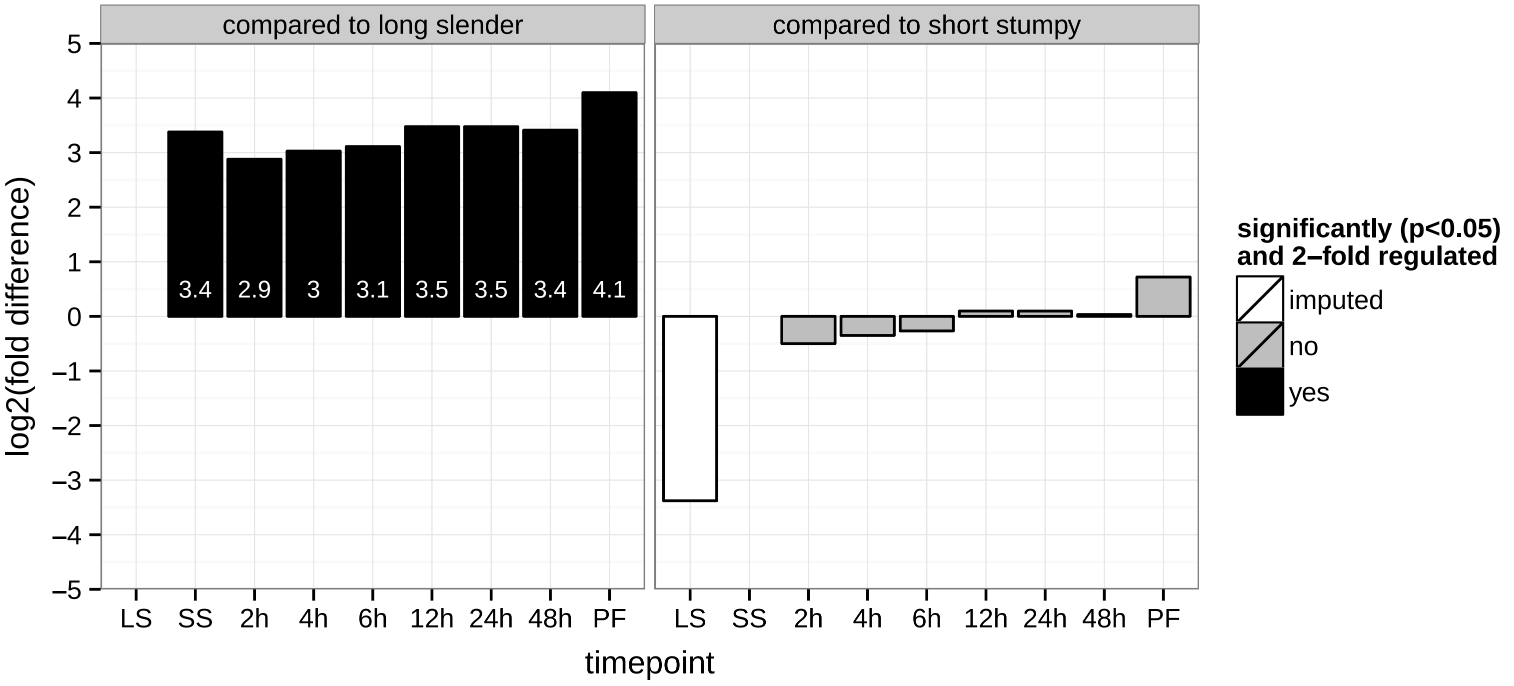
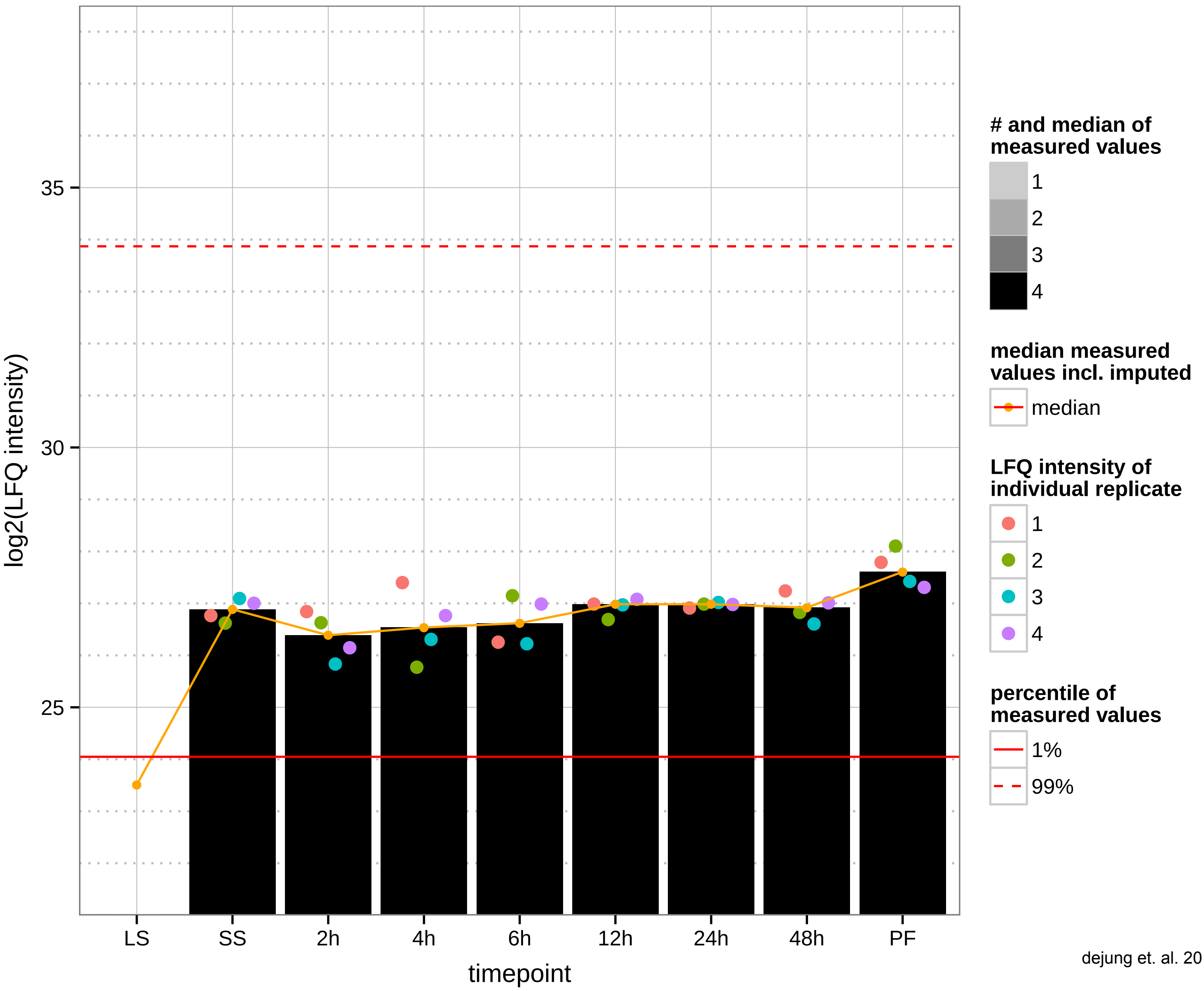
ATP−dependent DEAD/H RNA helicase, putative
Tb927.1.1620
AGOF: null, ATP binding, ATP−dependent RNA helicase activity, nucleic acid binding
AGOC: null
AGOP: null, RNA metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, nucleic acid binding, helicase activity
PGOC: null
PGOP: null





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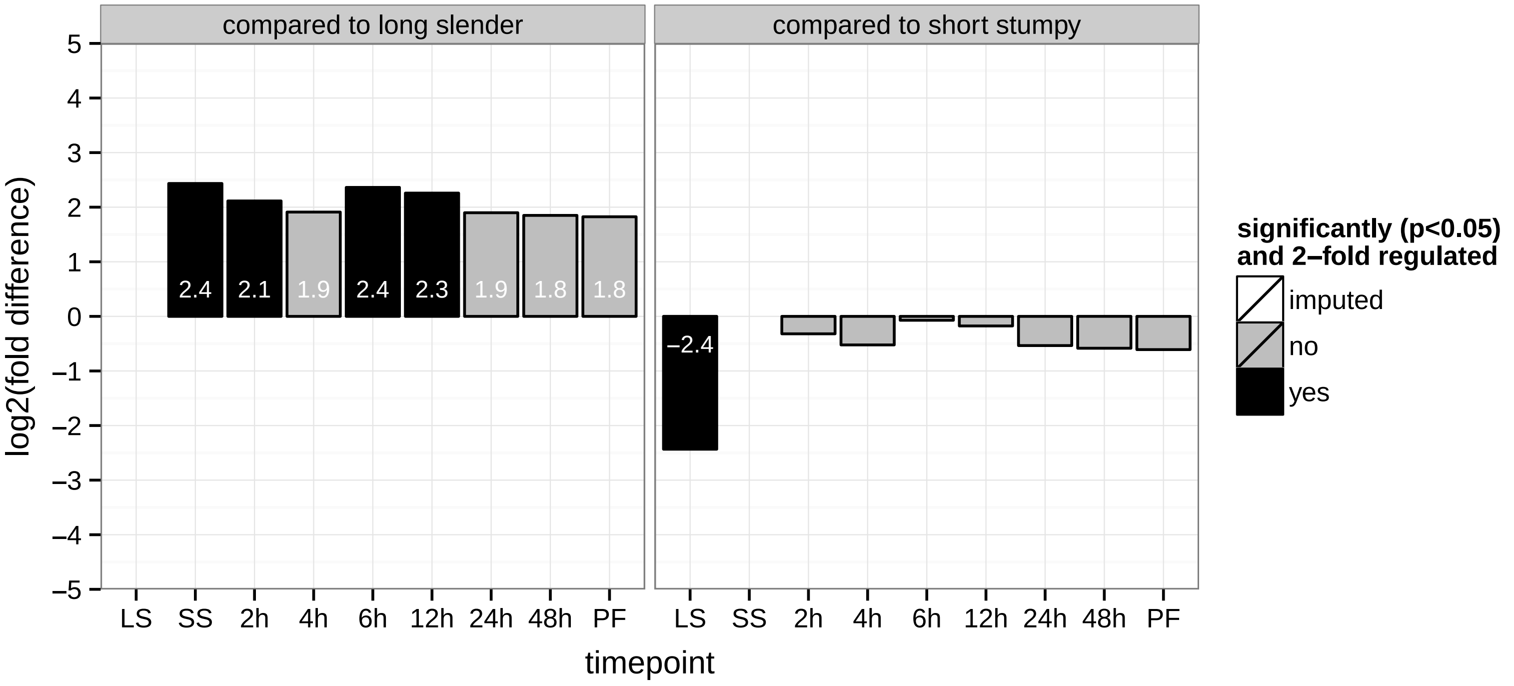
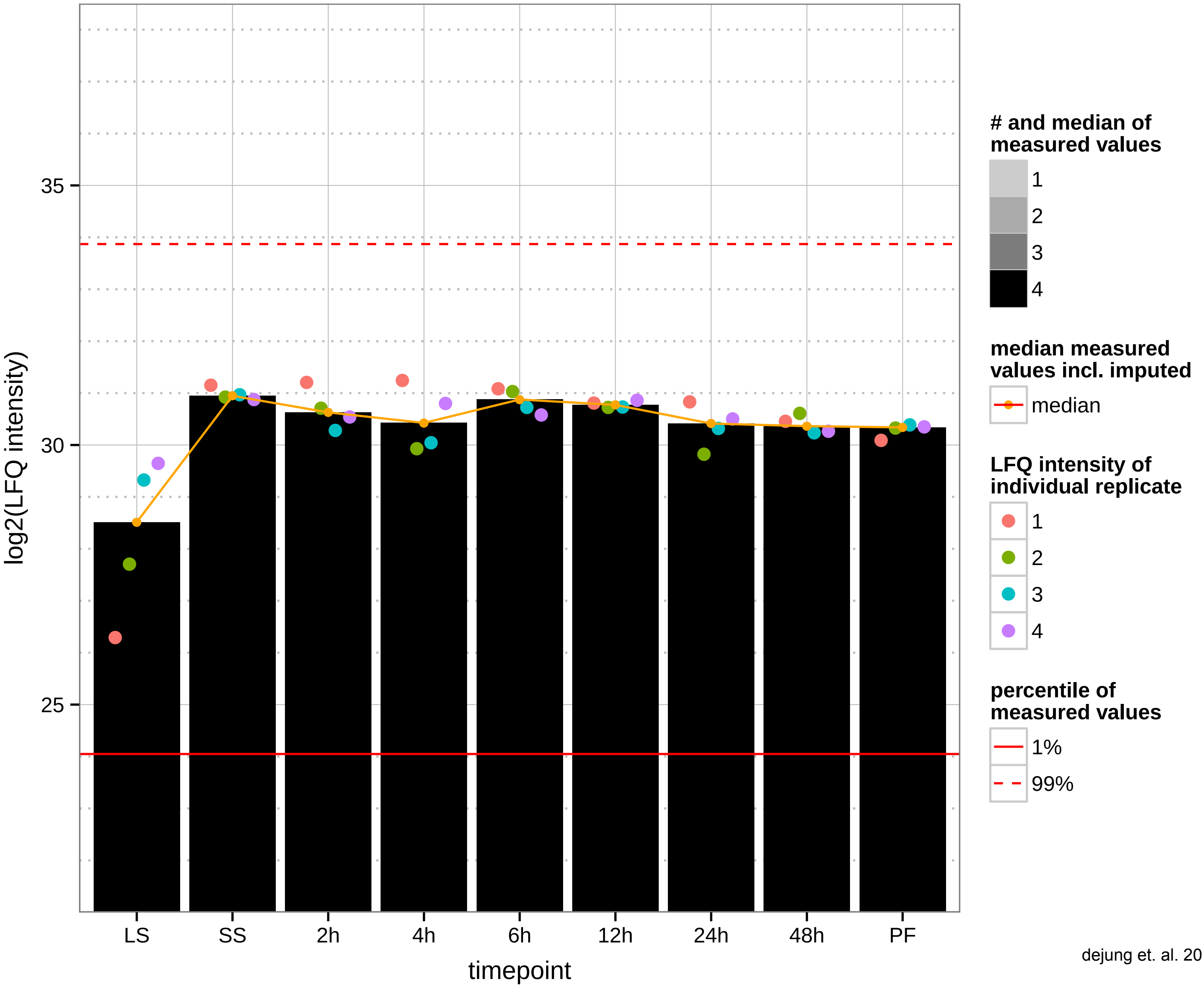
hypothetical protein, conserved, ARM–like helical domain–containing protein
Tb927.1.1670
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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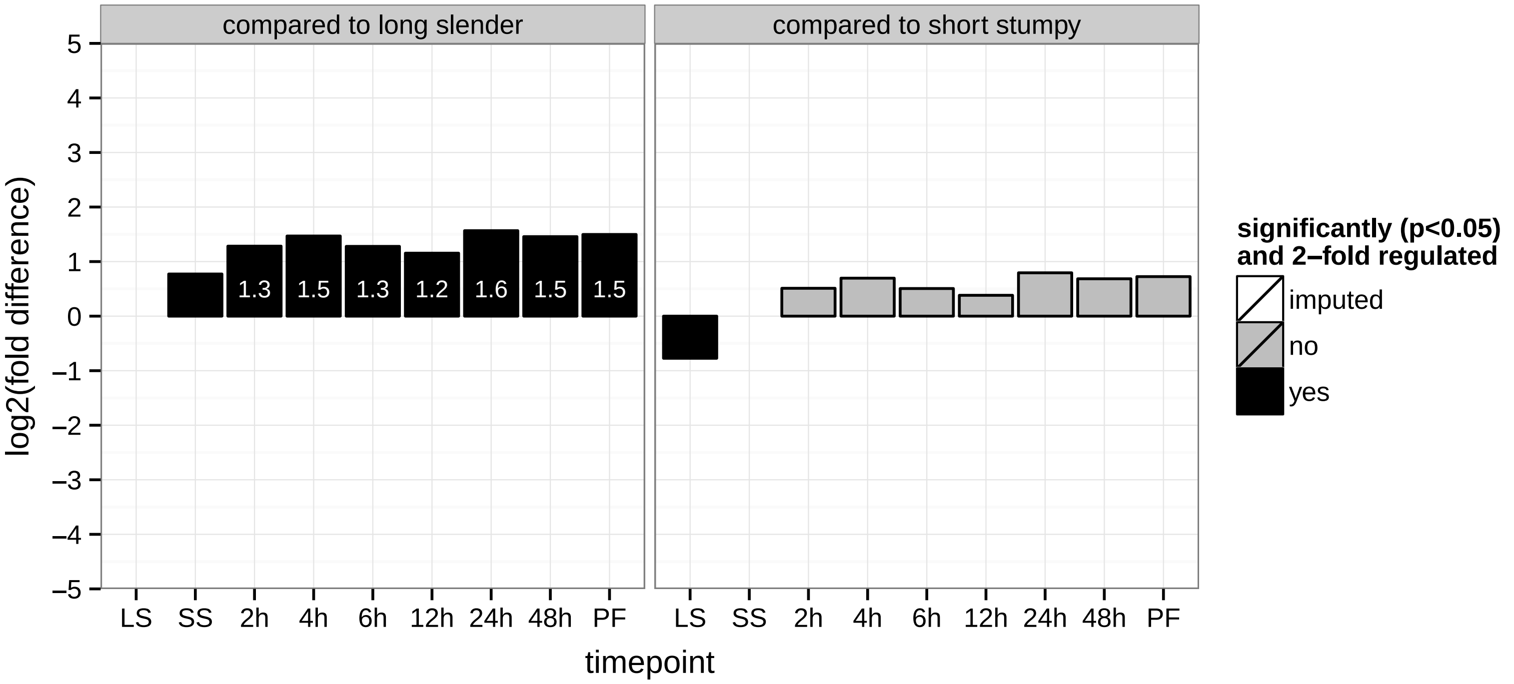
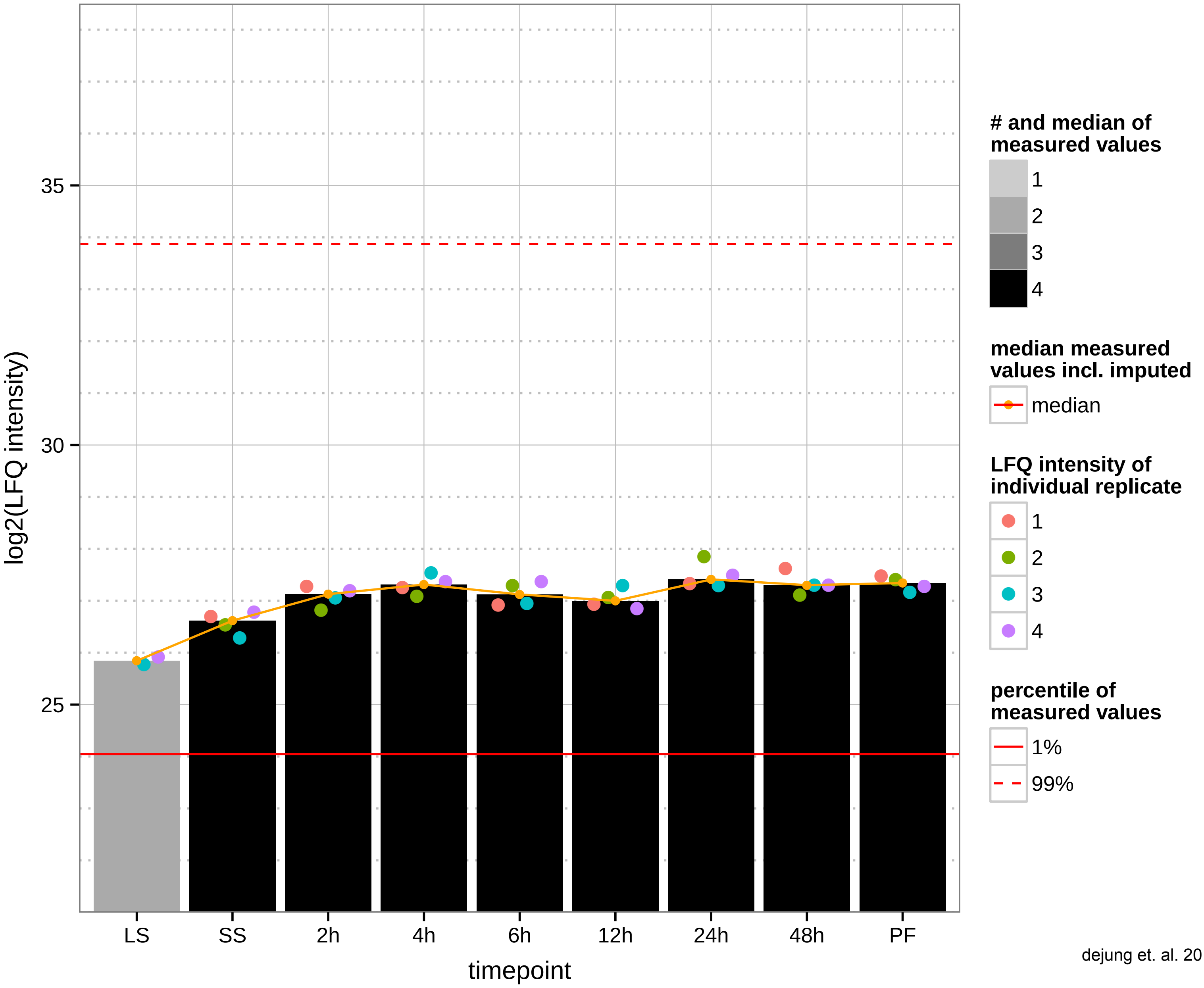
AATF protein, putative
Tb927.1.1700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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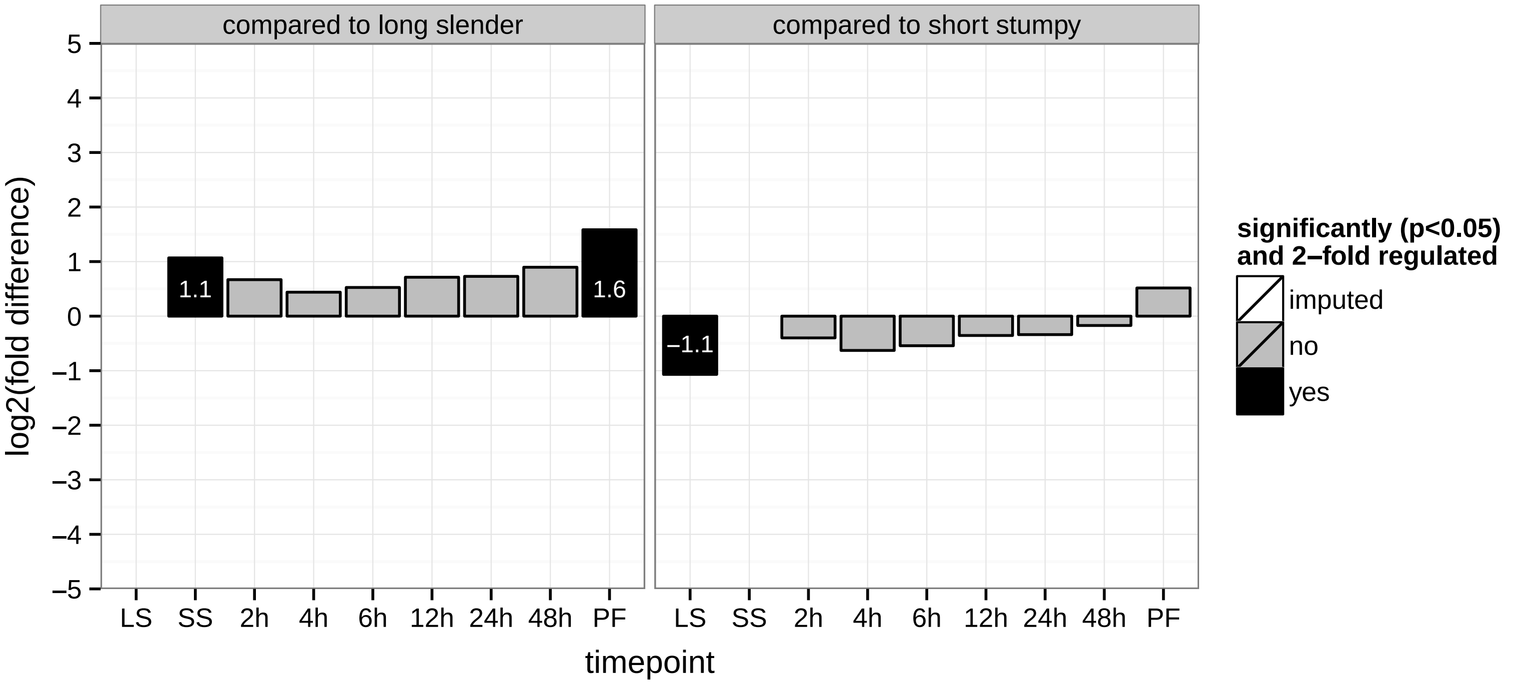
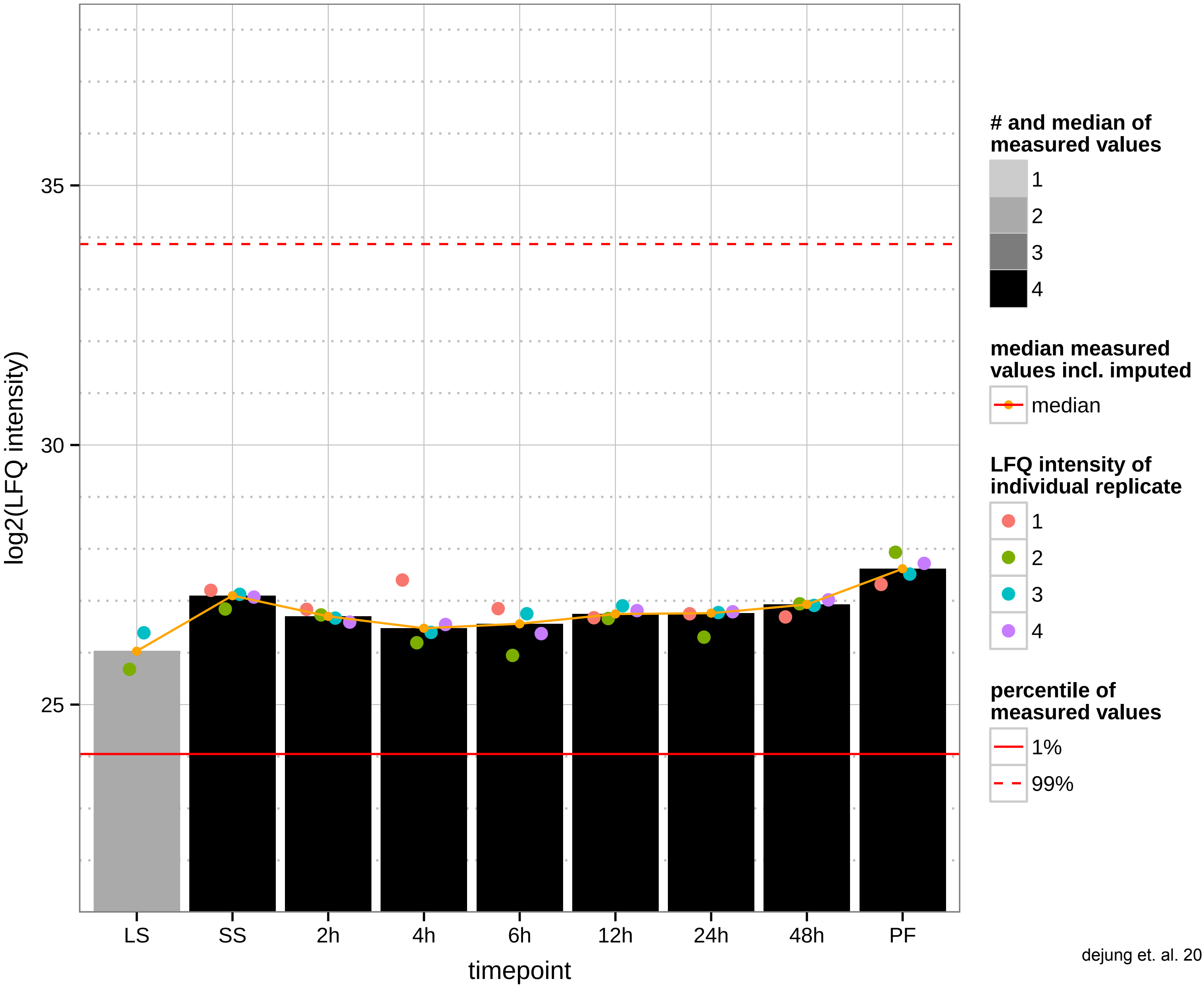
transmembrane protein, conserved
Tb927.1.1710
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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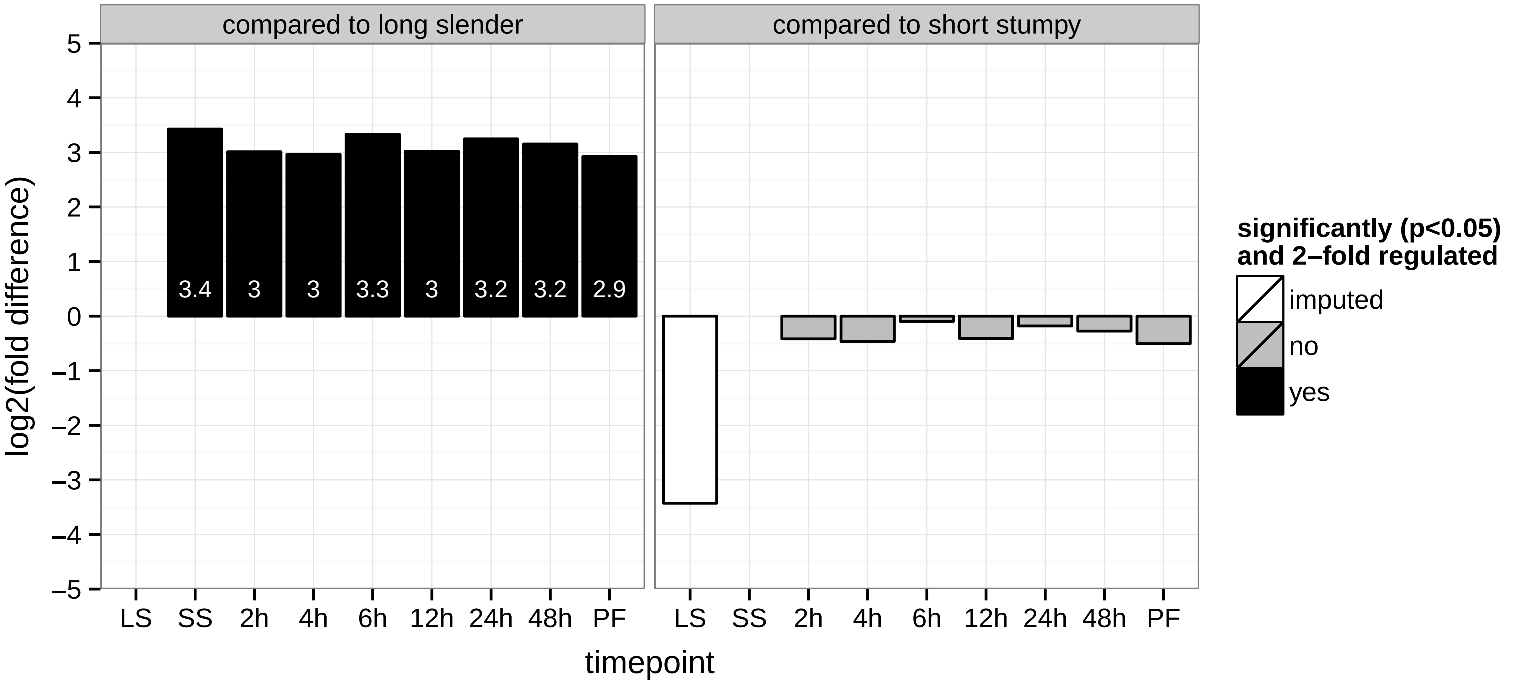
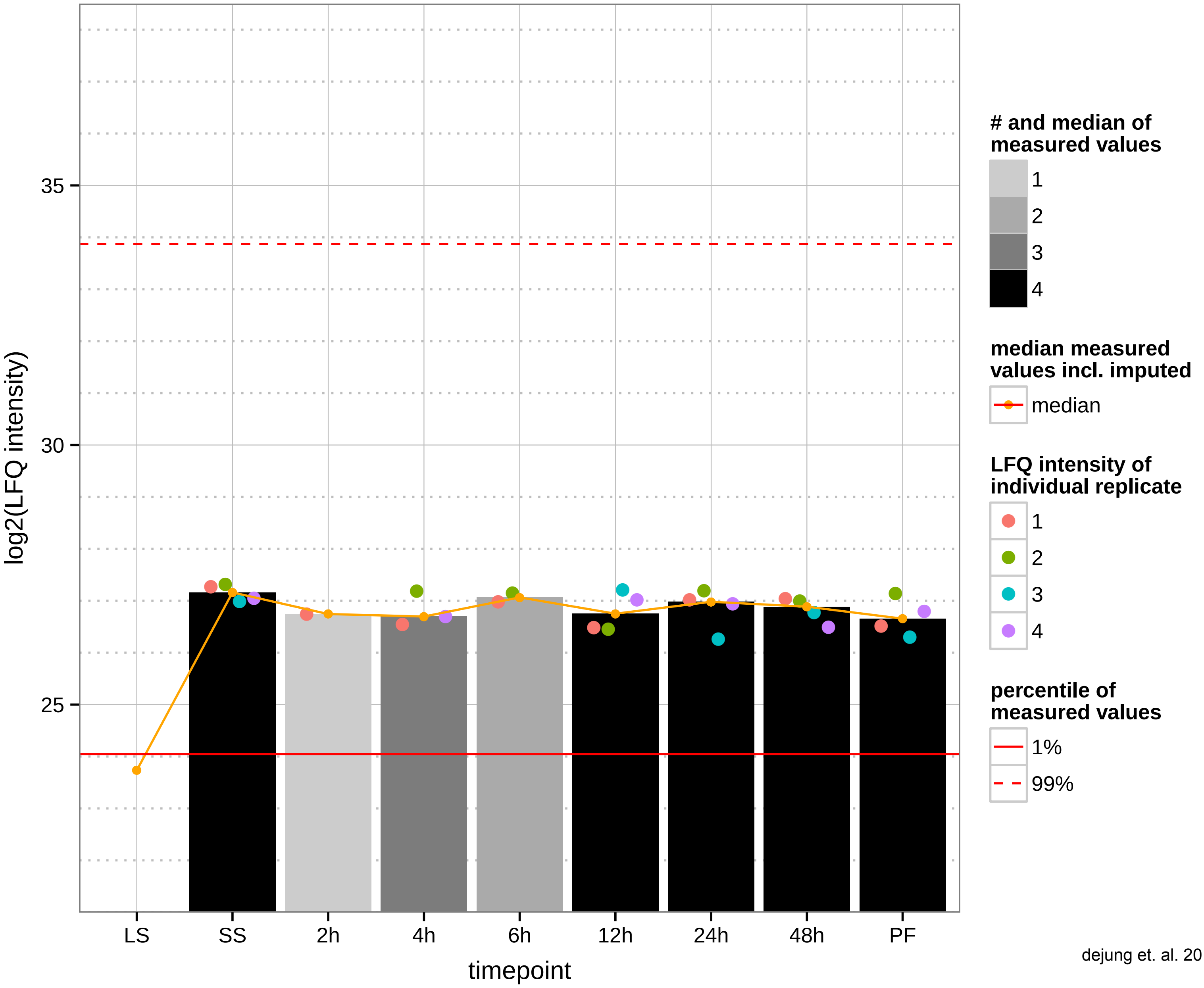
cyclophilin 15, putative
Tb927.1.1720
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: null
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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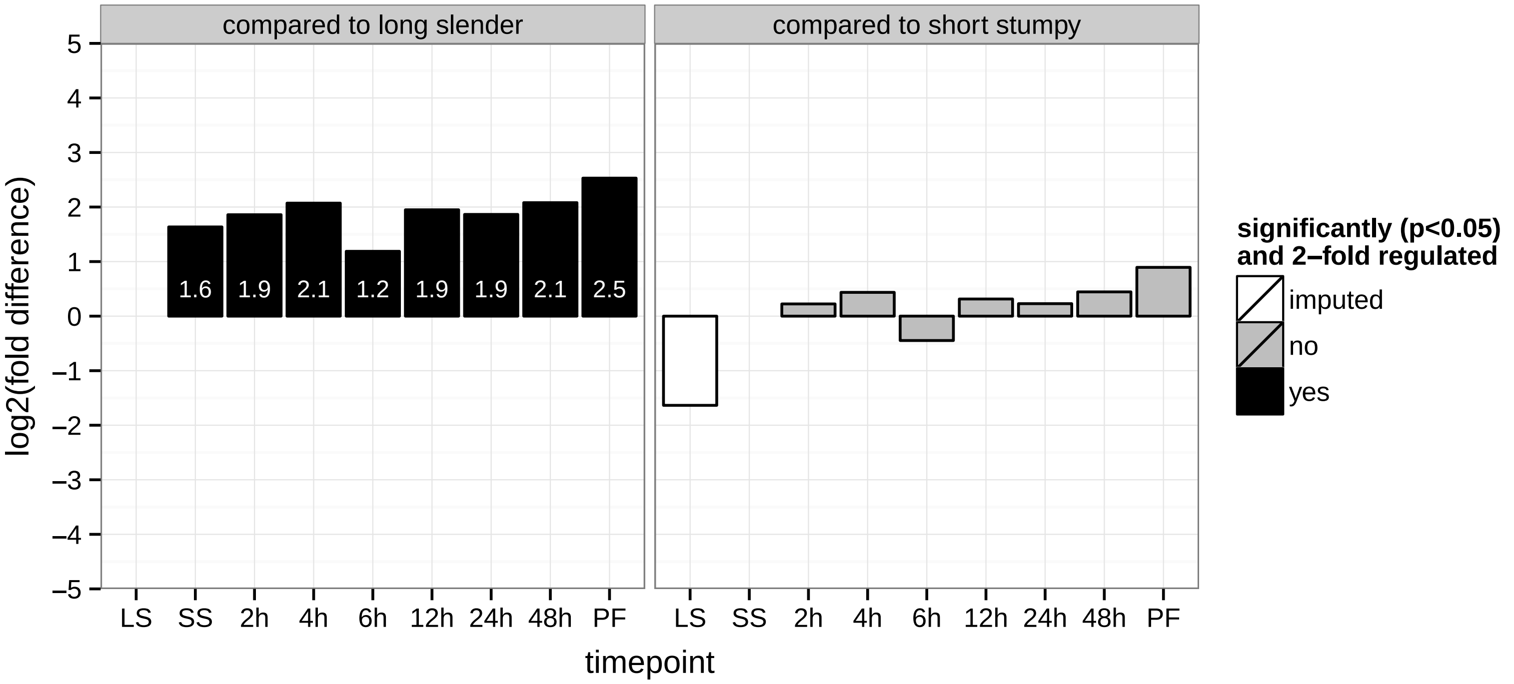
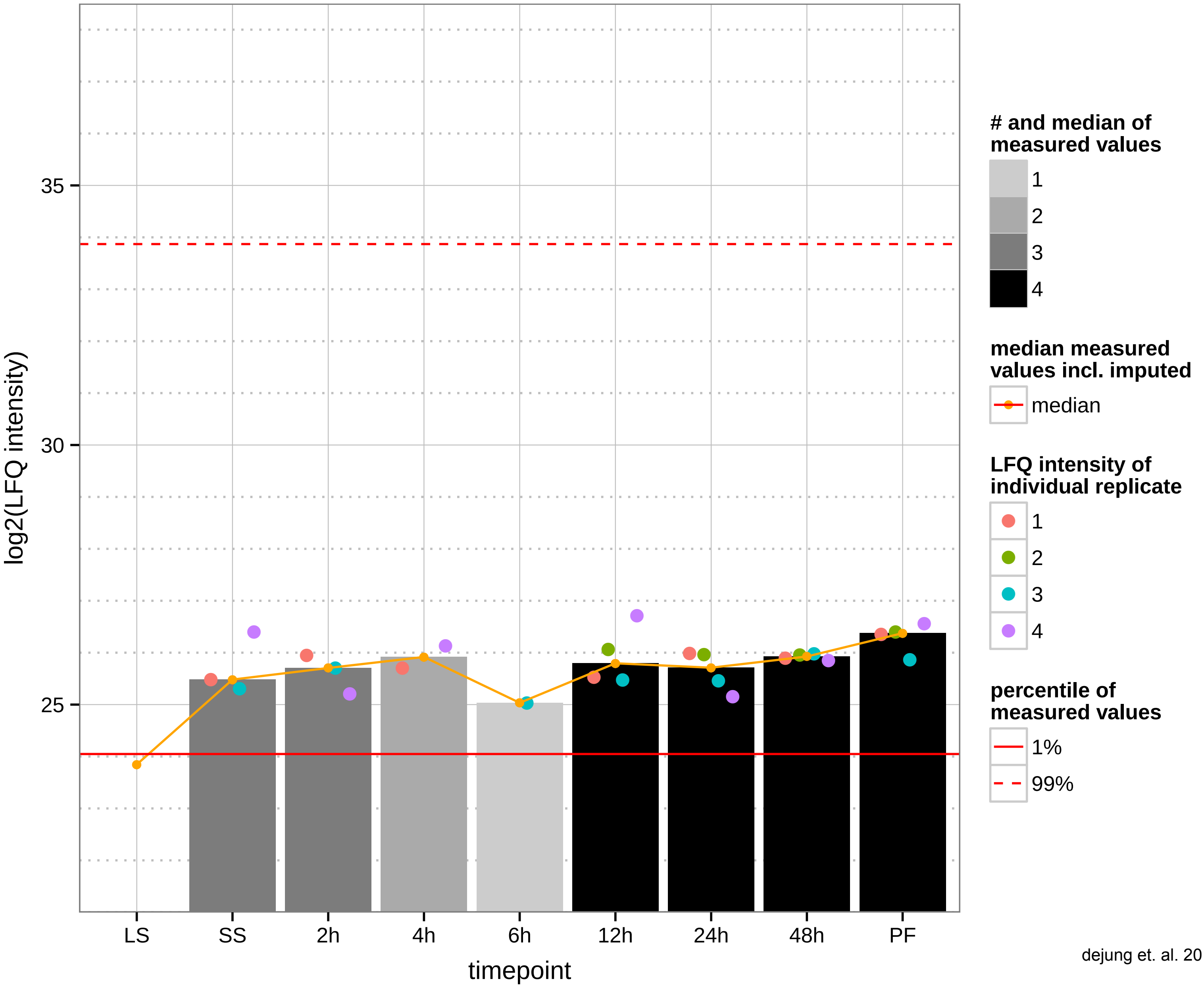
conserved protein, unknown function
Tb927.1.1730
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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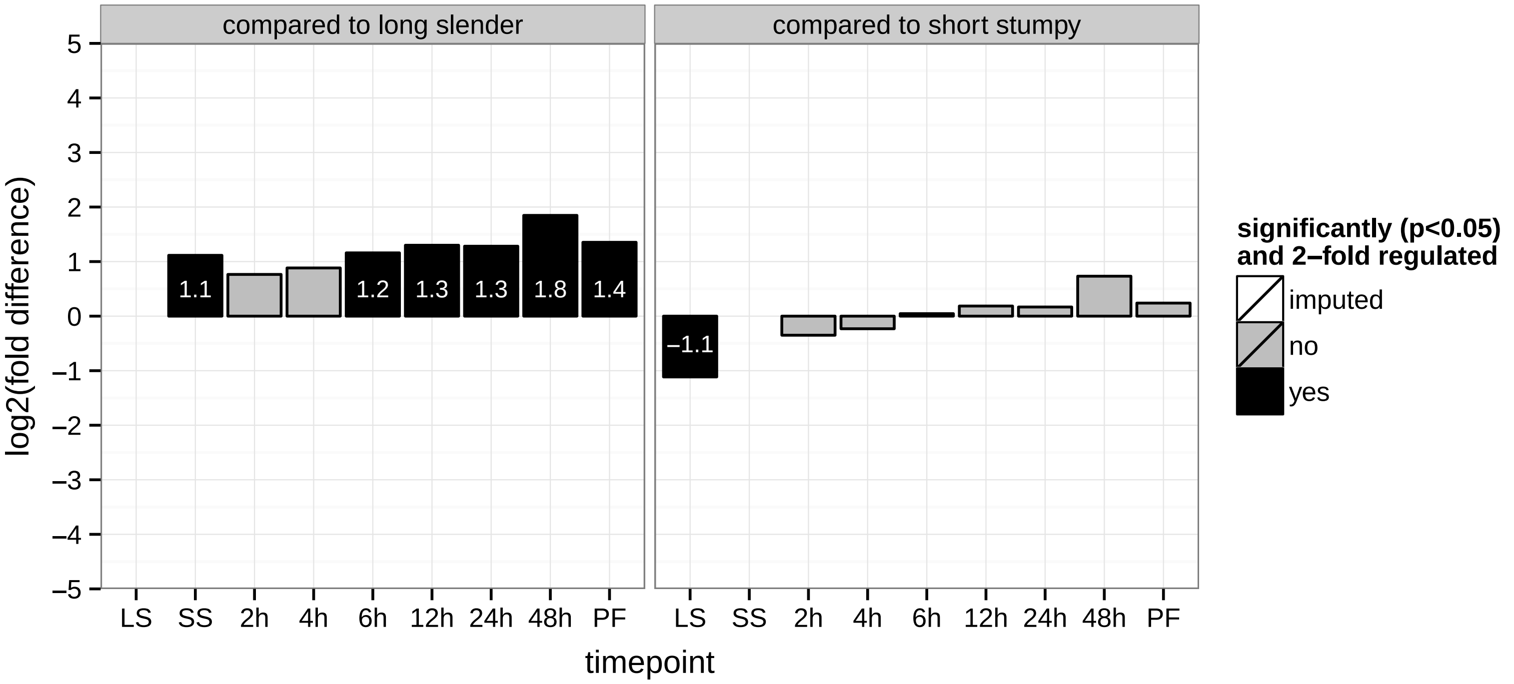
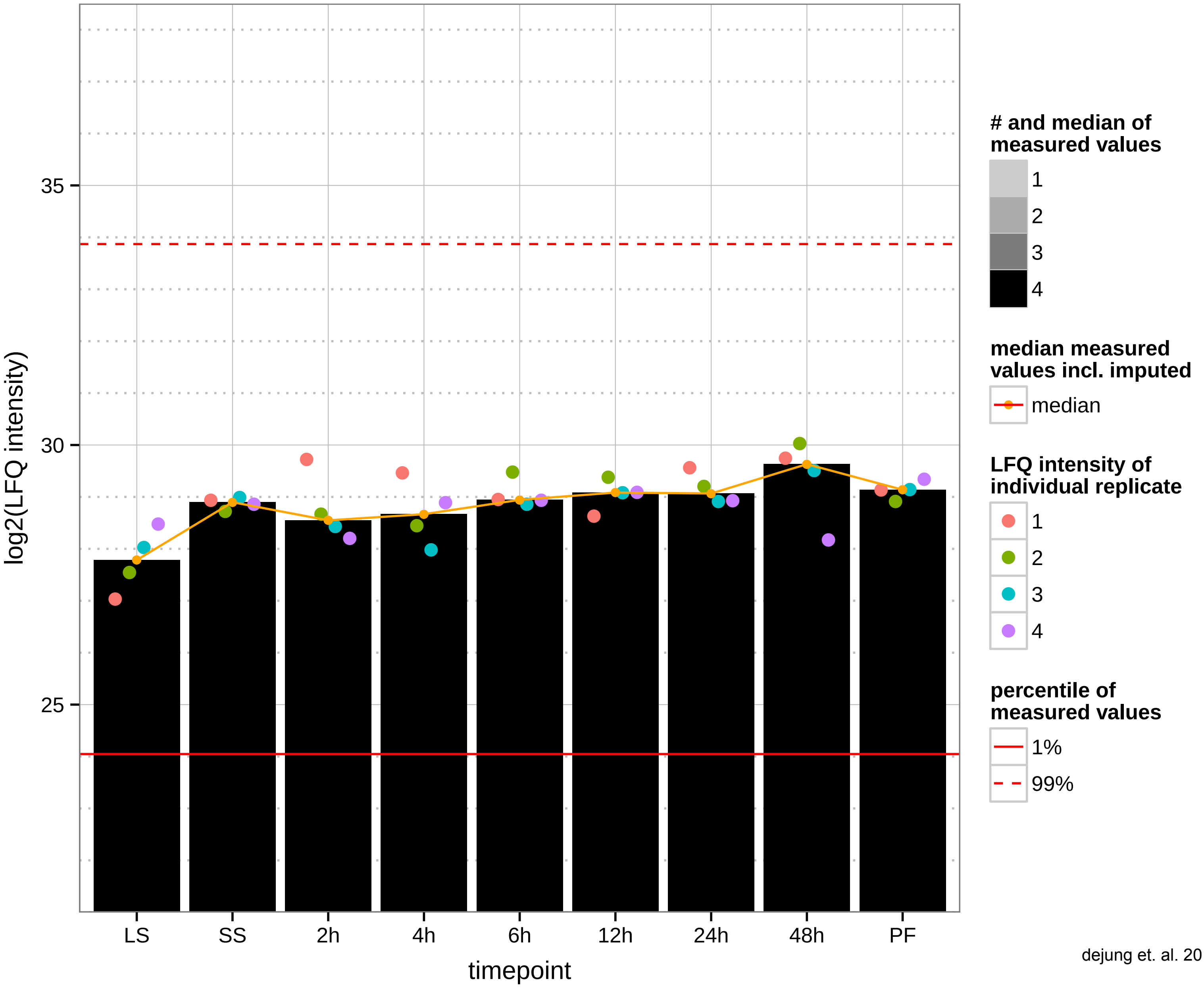
retrotransposon hot spot protein 1 (RHS1), putative
Tb927.1.180
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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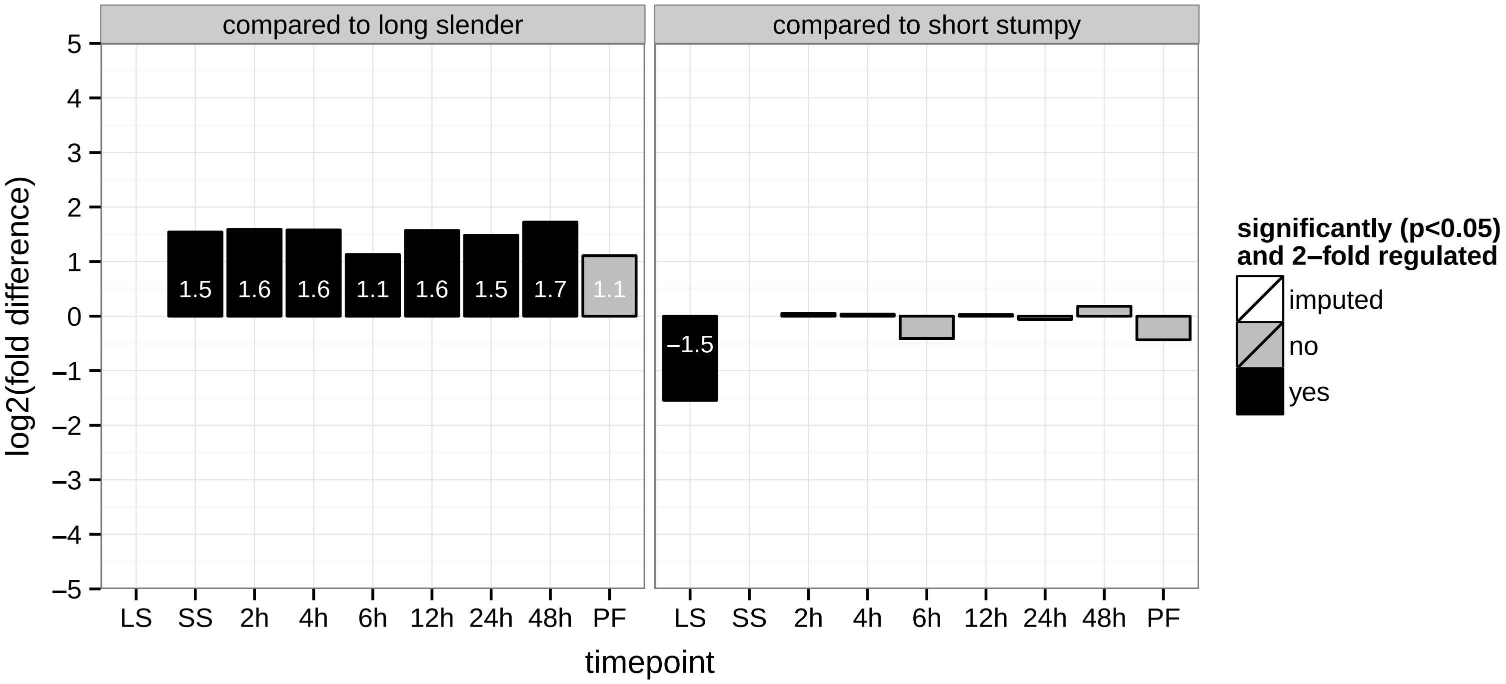
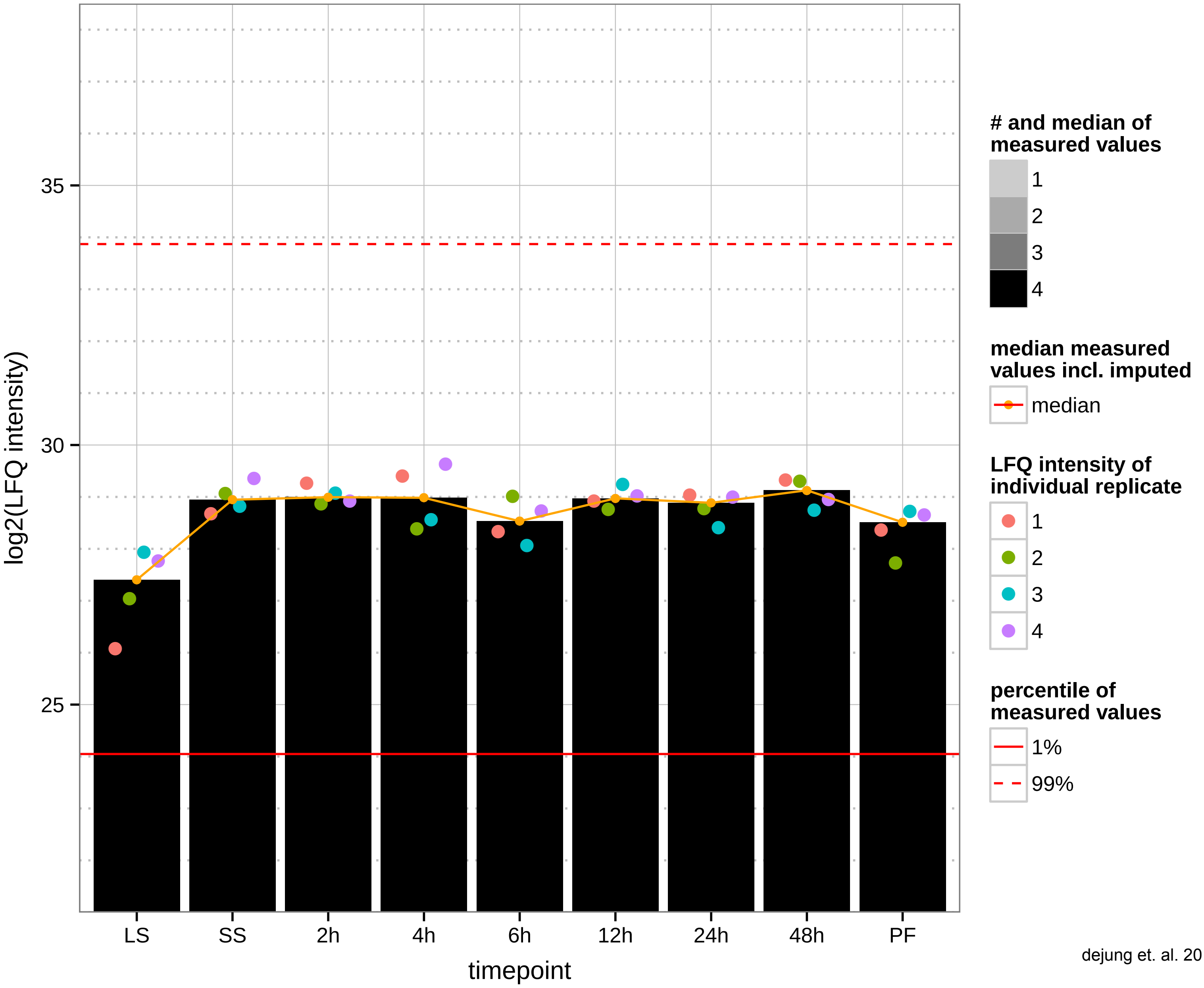
retrotransposon hot spot protein (RHS, pseudogene), putative
Tb927.1.190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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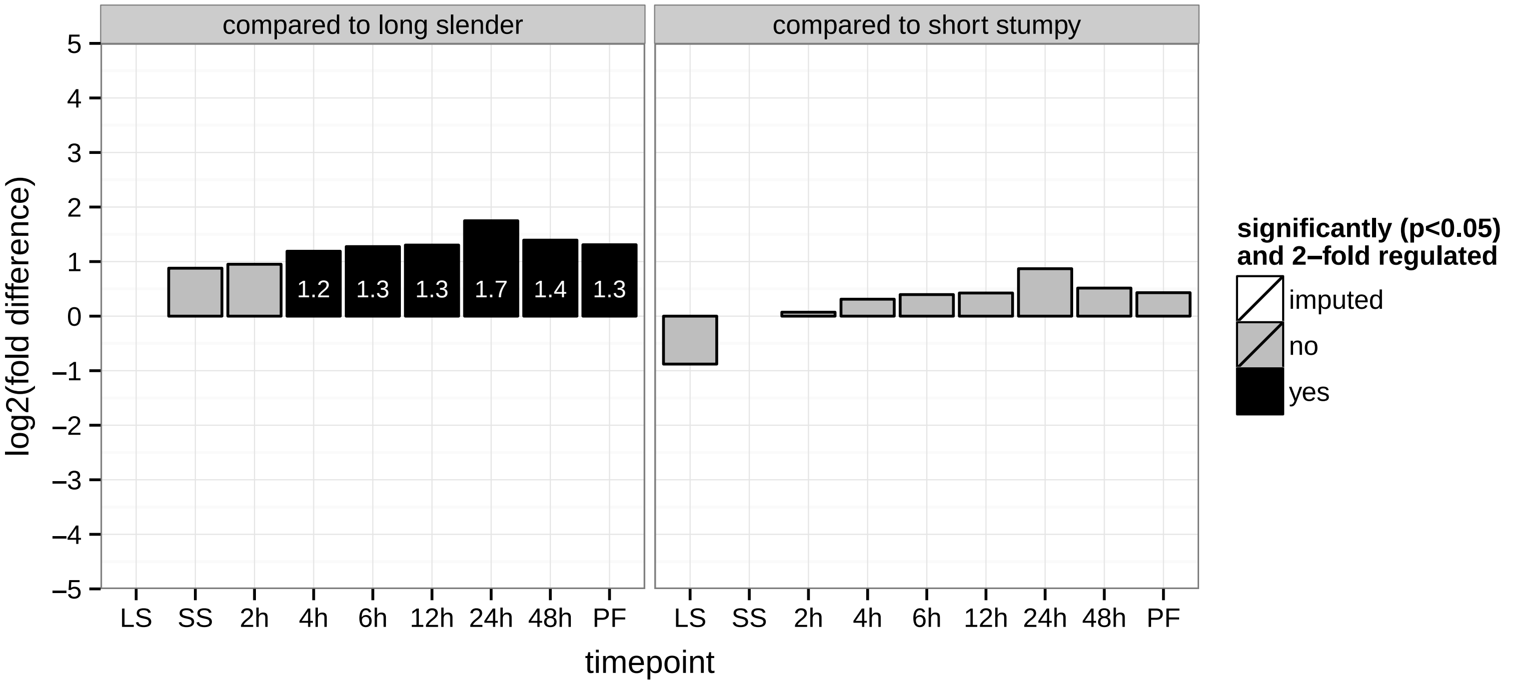
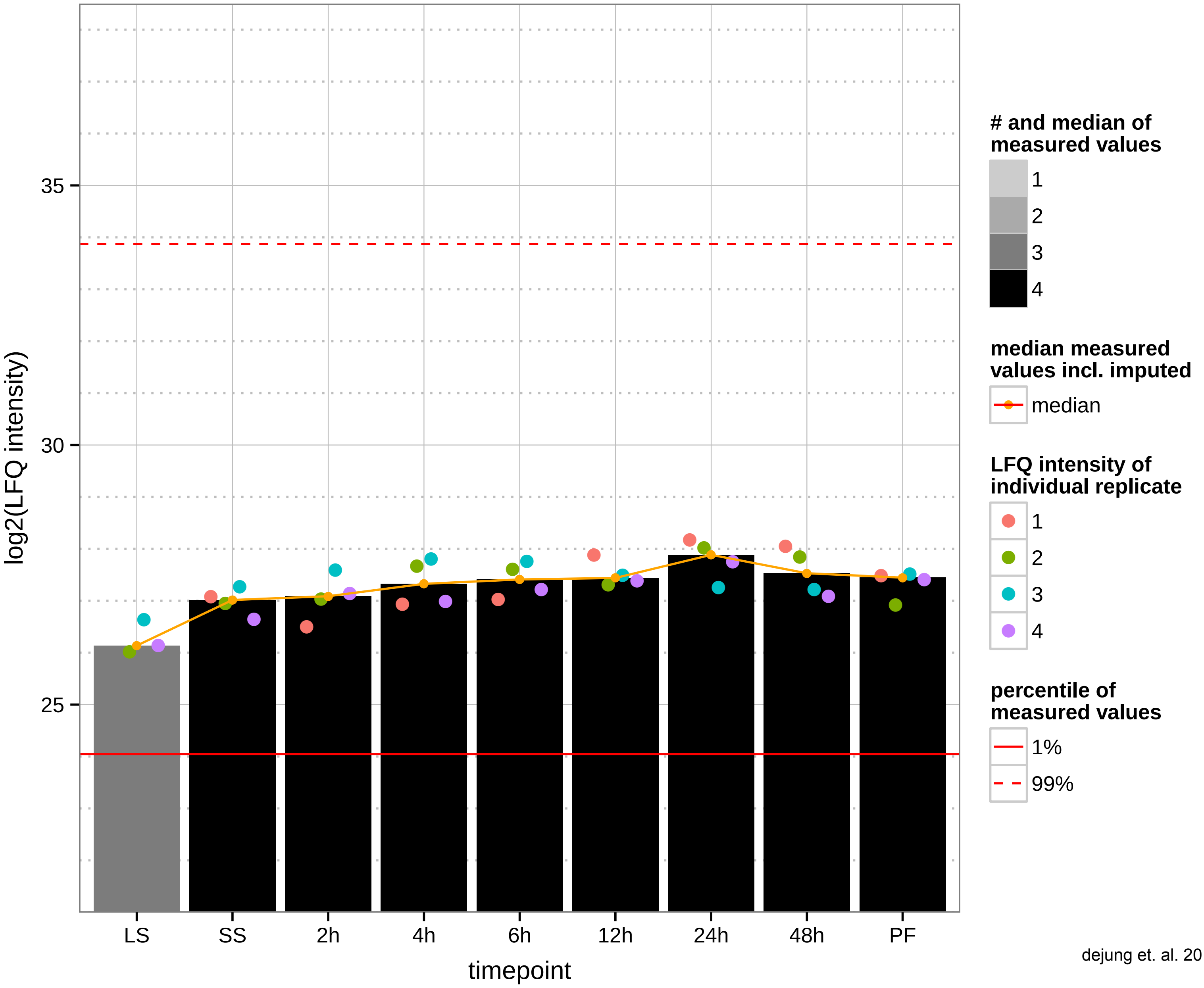
chaperone protein DNAj, putative
Tb927.1.1960
AGOF: DNA binding, heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: DNA binding, heat shock protein binding
PGOC: null
PGOP: null





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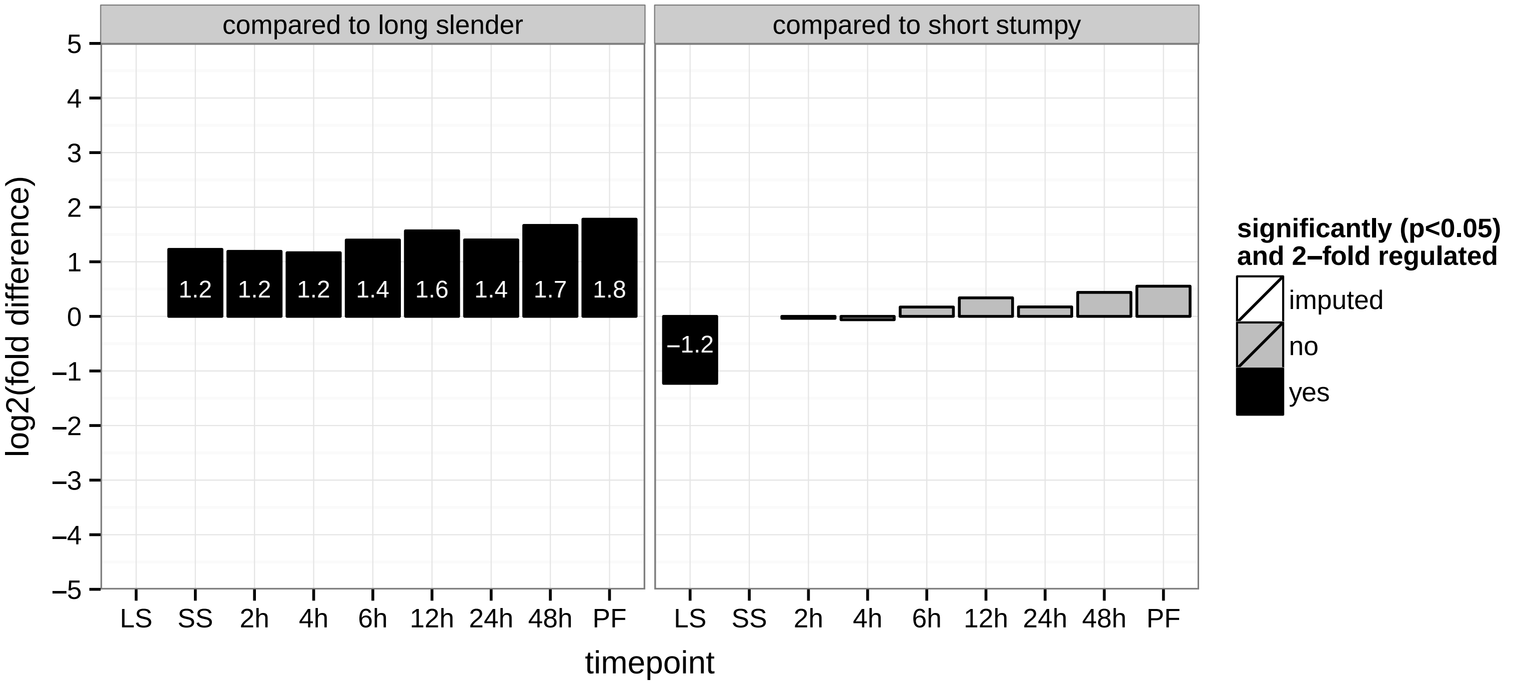
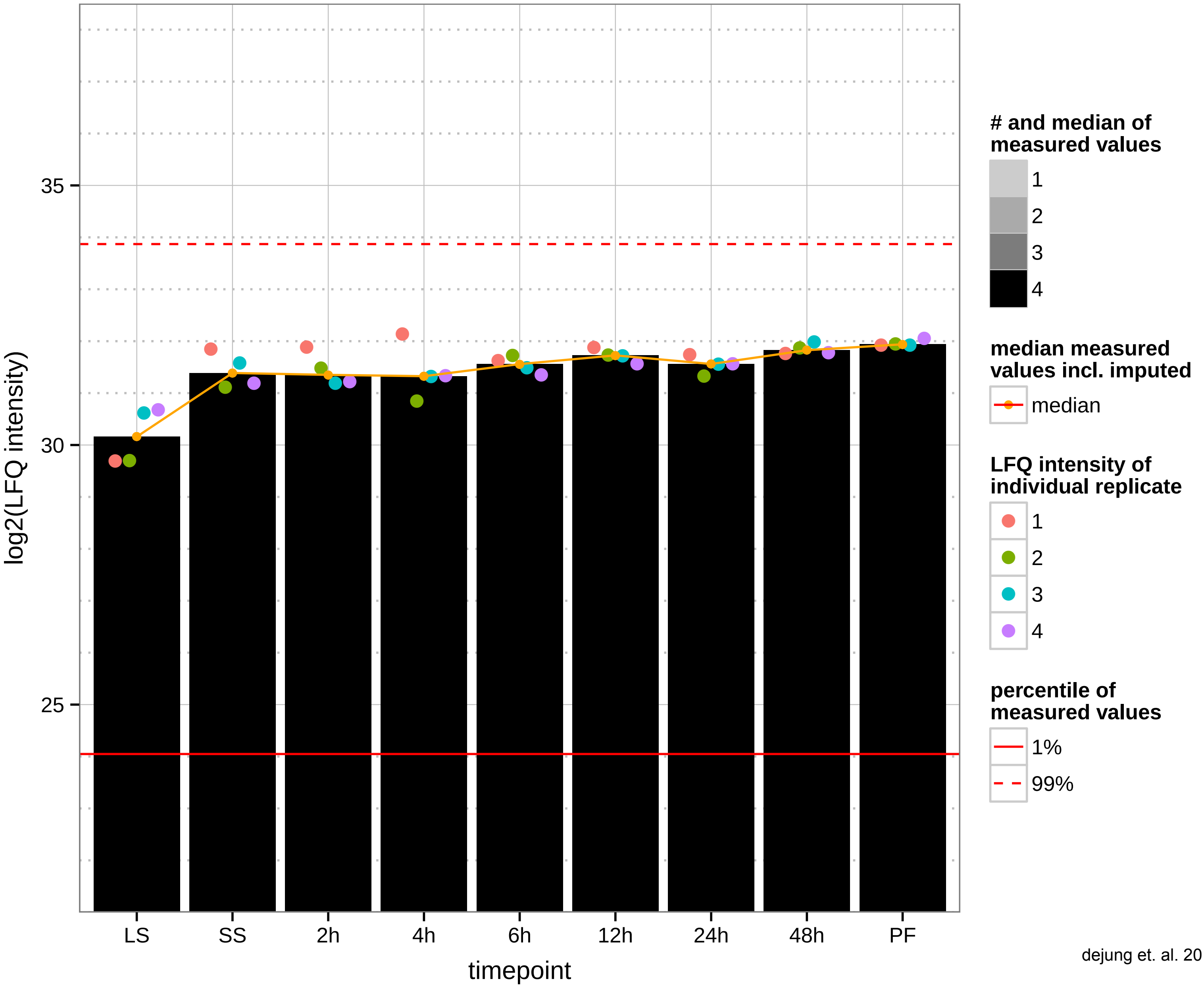
cysteine peptidase, Clan CA, family C2, putative, calpain–like cysteine peptidase
Tb927.1.2100
AGOF: calcium–dependent cysteine–type endopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: calcium–dependent cysteine–type endopeptidase activity
PGOC: intracellular
PGOP: proteolysis





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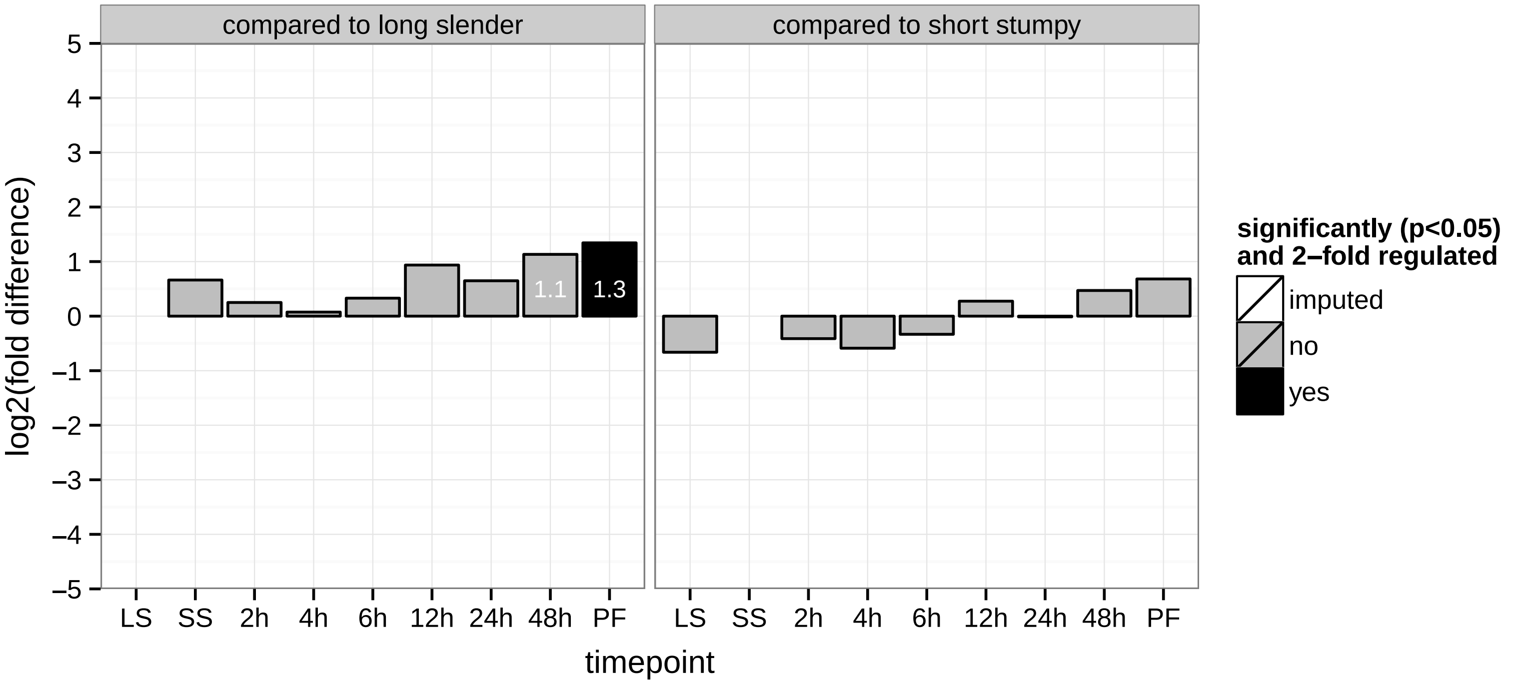
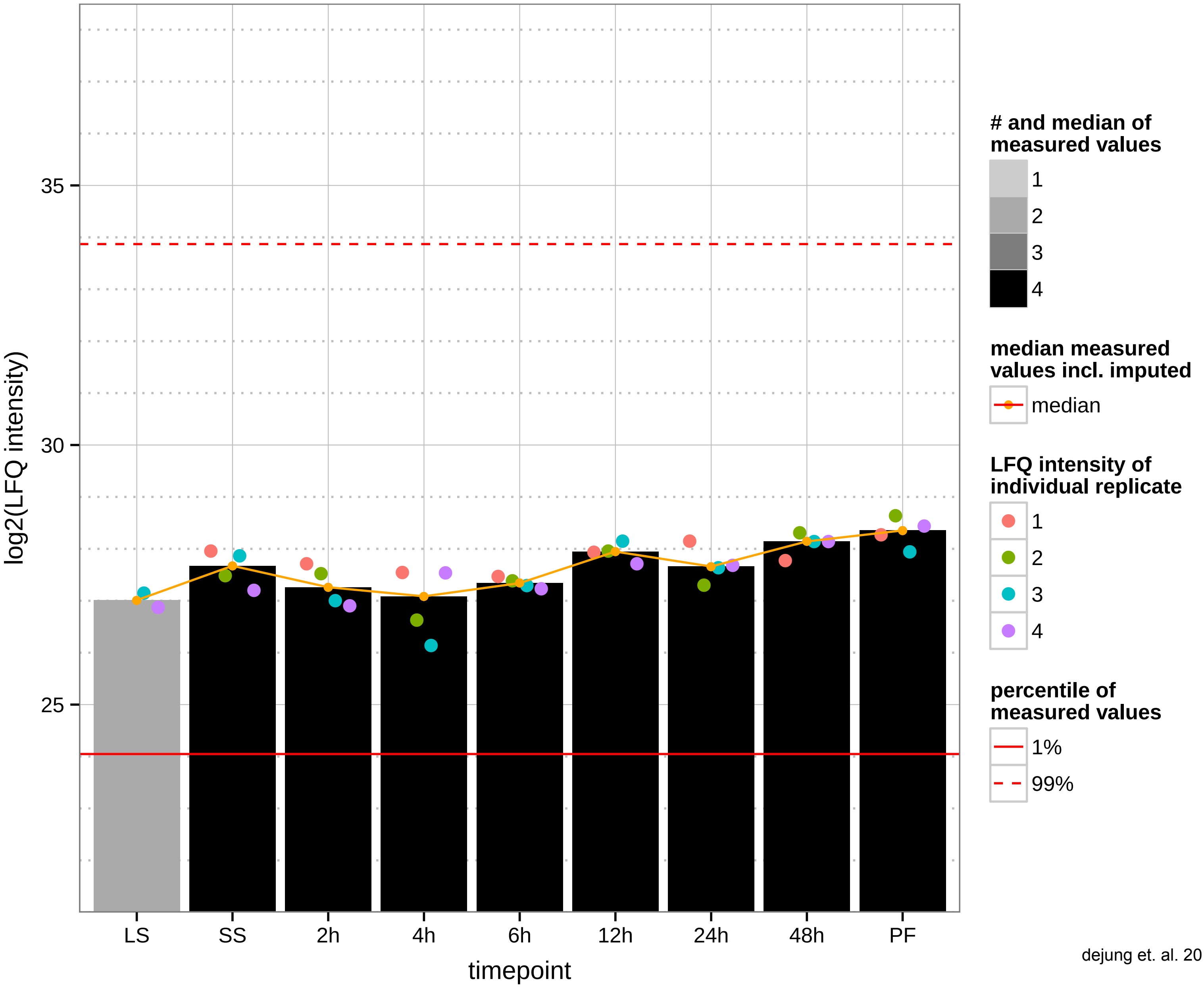
calpain, putative, cysteine peptidase, Clan CA, family C2
Tb927.1.2120
AGOF: calcium−dependent cysteine−type endopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: calcium−dependent cysteine−type endopeptidase activity
PGOC: intracellular
PGOP: proteolysis





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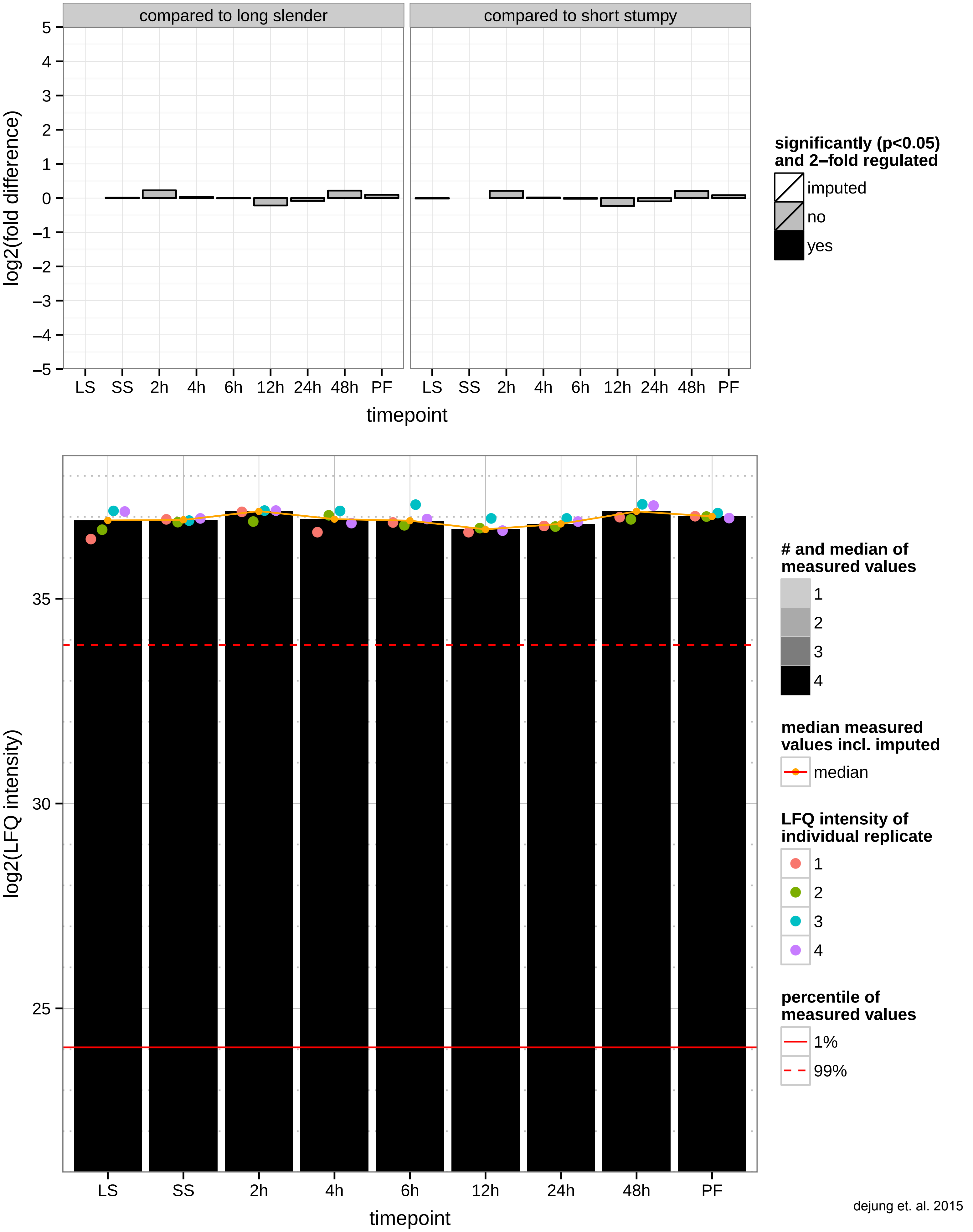
alpha tubulin
Tb927.1.2400;Tb927.1.2380;Tb927.1.2360;Tb927.1.2340
AGOF: GTP binding, GTPase activity, structural constituent of cytoskeleton
AGOC: microtubule, protein complex
AGOP: cellular component movement, microtubule cytoskeleton organization, microtubule–based movement, protein polymer
PGOF: GTP binding, GTPase activity, null
PGOC: protein complex, null
PGOP: GTP catabolic process, protein polymerization, null



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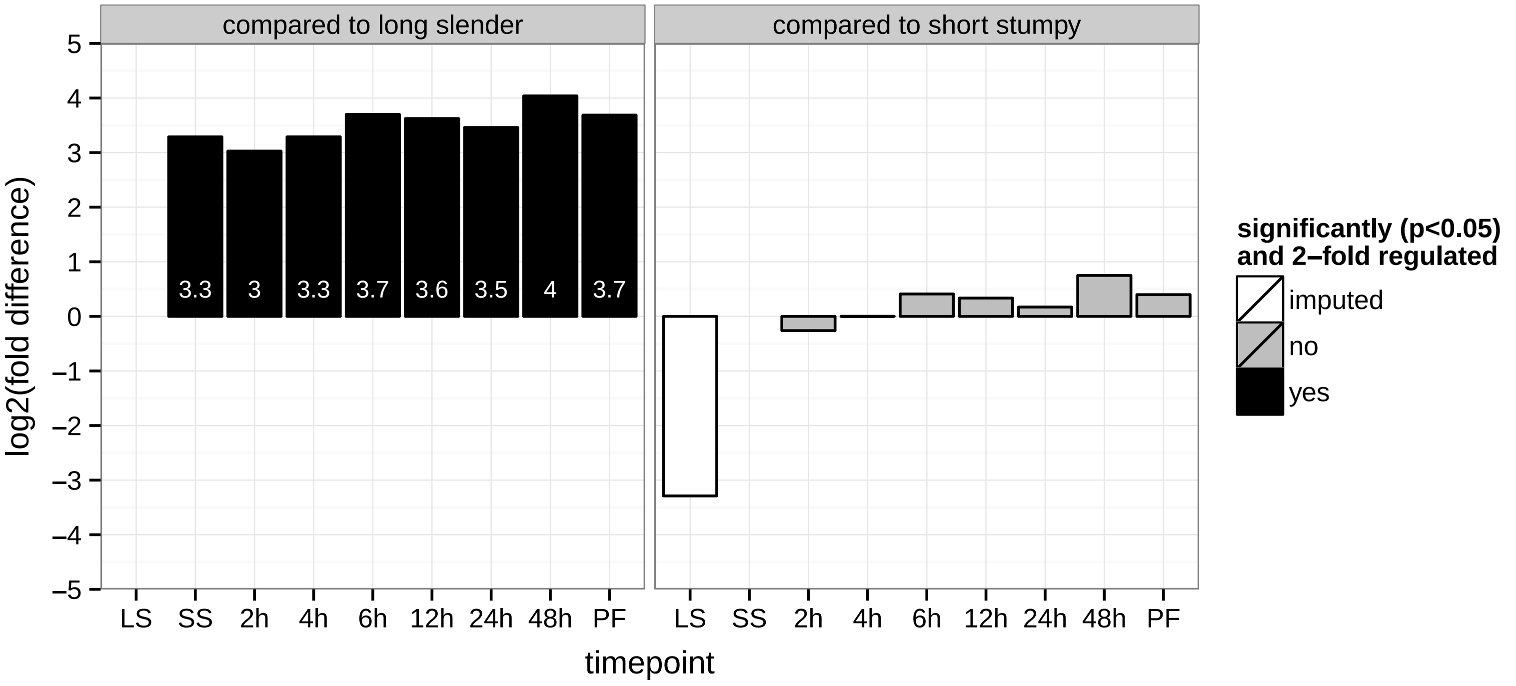
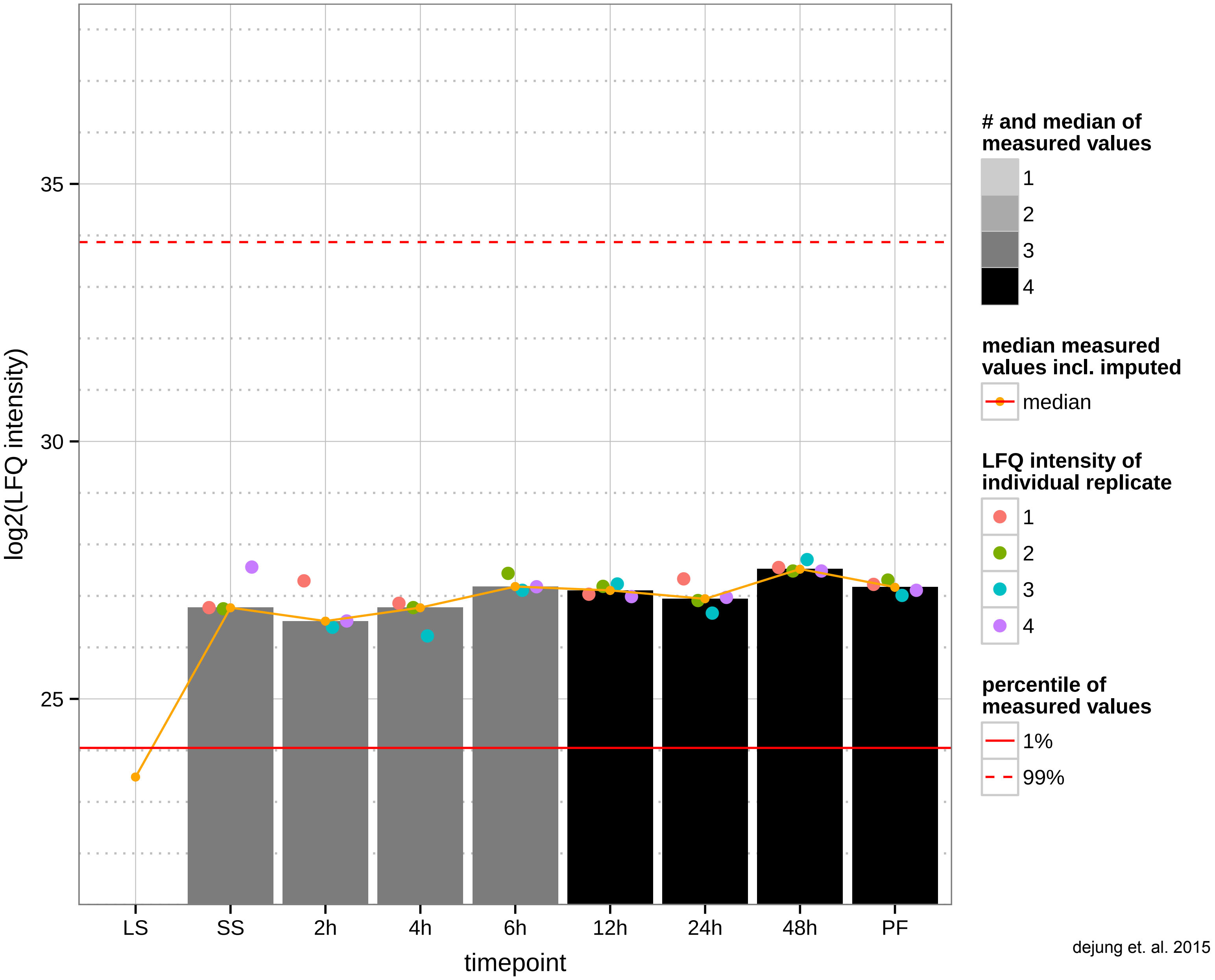
retrotransposon hot spot protein (RHS, pseudogene), putative
Tb927.1.240
AGOF: RNA binding, RNA–directed DNA polymerase activity, ribonuclease H activity, zinc ion binding
AGOC: intracellular
AGOP: RNA–dependent DNA replication
PGOF: RNA binding, RNA–directed DNA polymerase activity, nucleic acid binding, ribonuclease H activity, zinc ion binding
PGOC: intracellular
PGOP: RNA–dependent DNA replication





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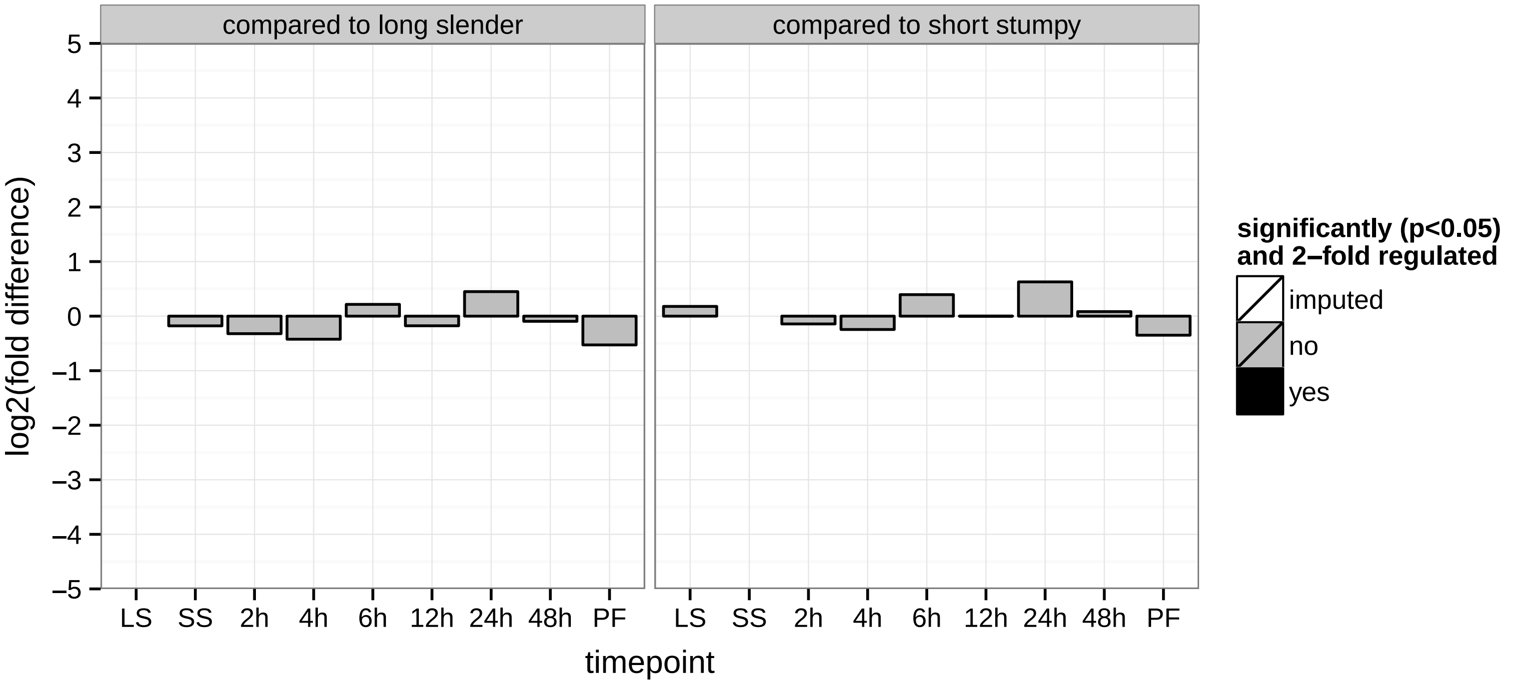
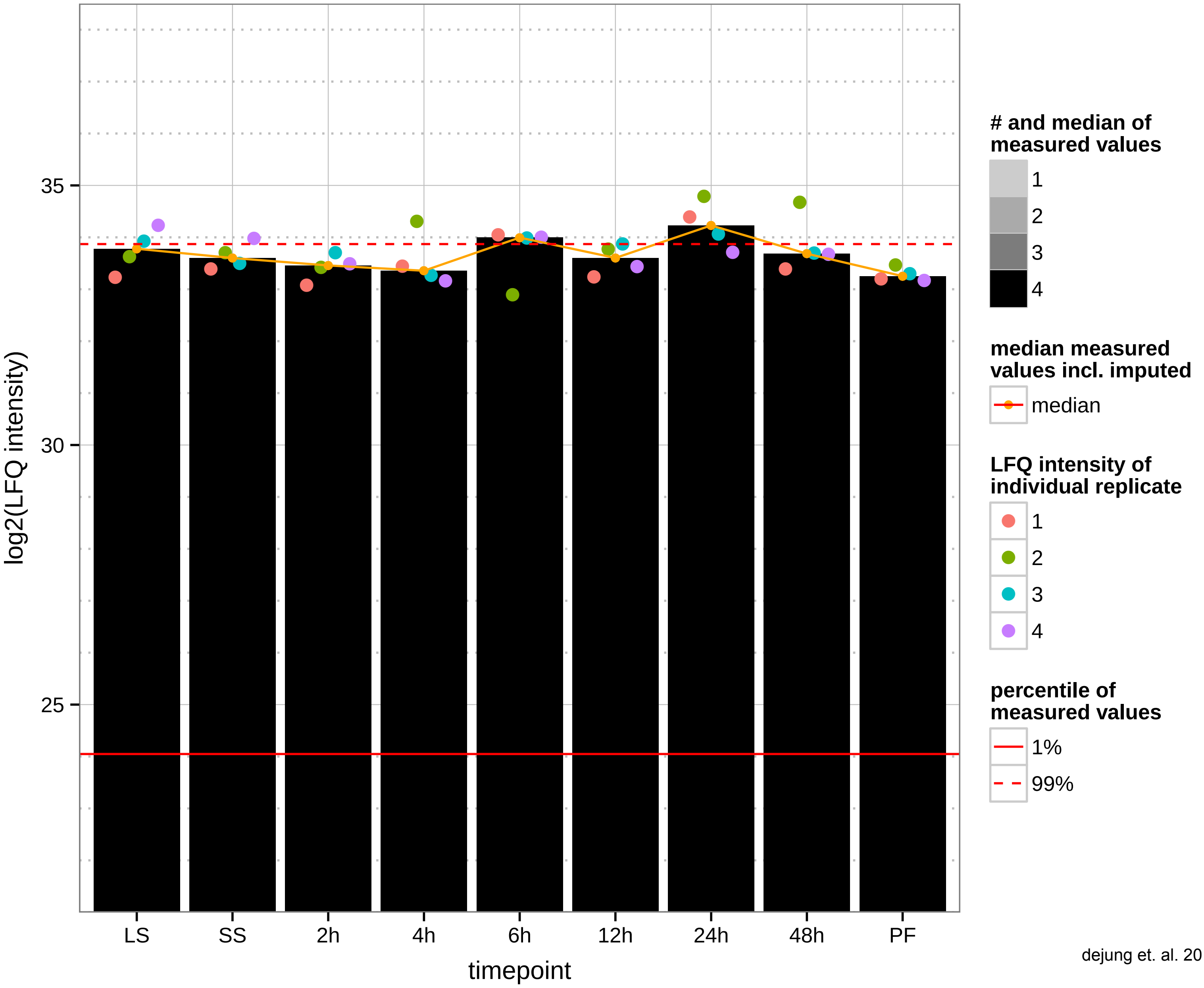
histone H3, putative
Tb927.1.2550;Tb927.1.2530;Tb927.1.2510;Tb927.1.2490;Tb927.1.2470;Tb927.1.2450;Tb927.1.2430
AGOF: DNA binding
AGOC: nucleosome, nucleus
AGOP: nucleosome assembly
PGOF: null, DNA binding
PGOC: null, nucleosome
PGOP: null, nucleosome assembly





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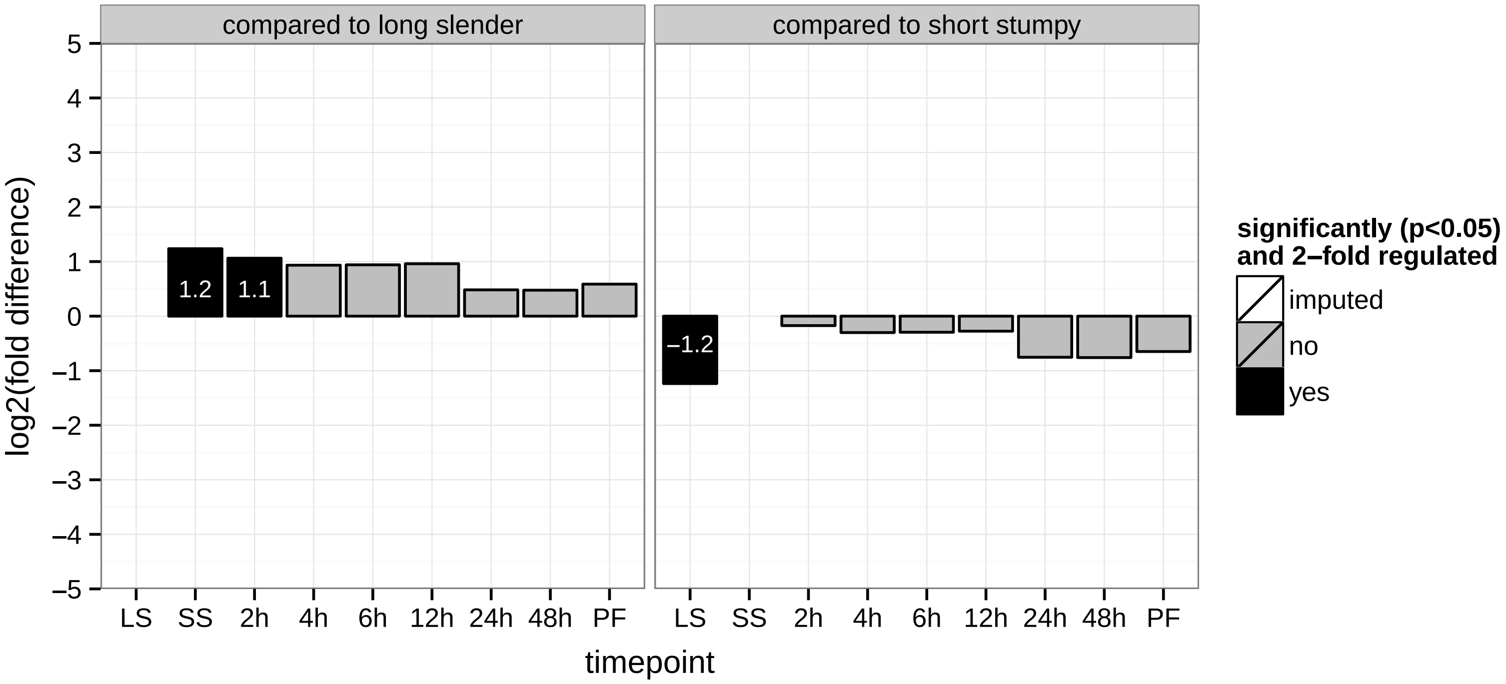
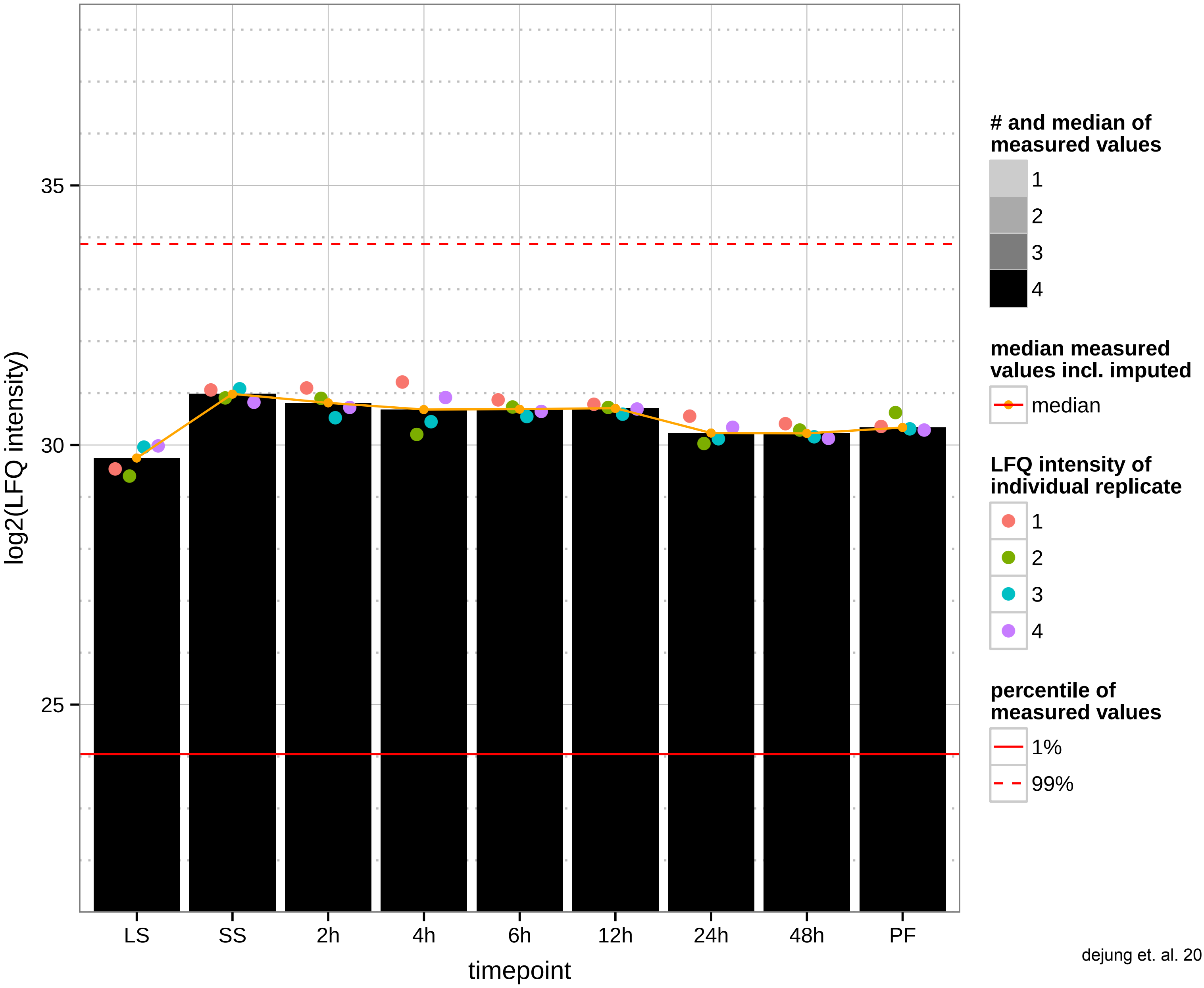
coatomer beta subunit (beta–coP)
Tb927.1.2570
AGOF: structural molecule activity
AGOC: membrane coat
AGOP: intracellular protein transport, vesicle–mediated transport
PGOF: binding, structural molecule activity
PGOC: COPI vesicle coat, cytoplasm, membrane coat
PGOP: intracellular protein transport, vesicle–mediated transport





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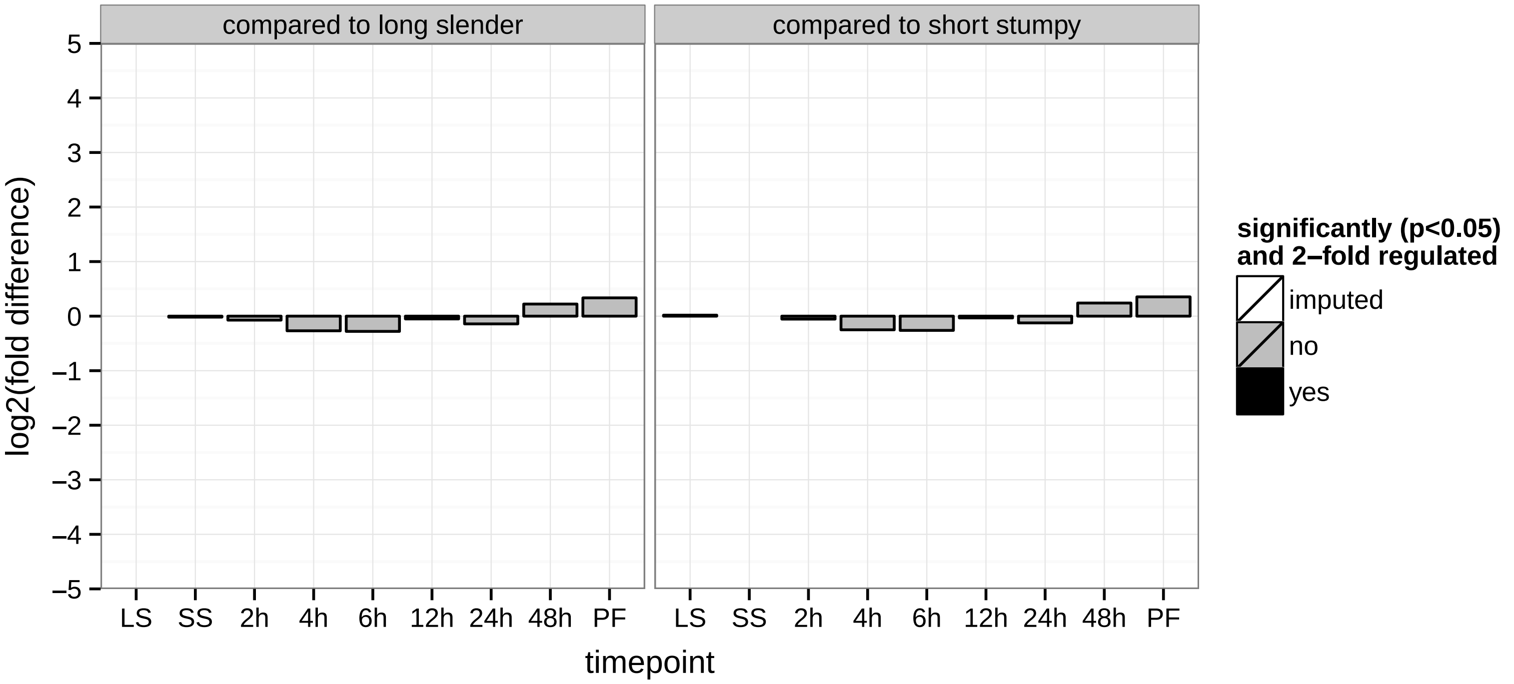
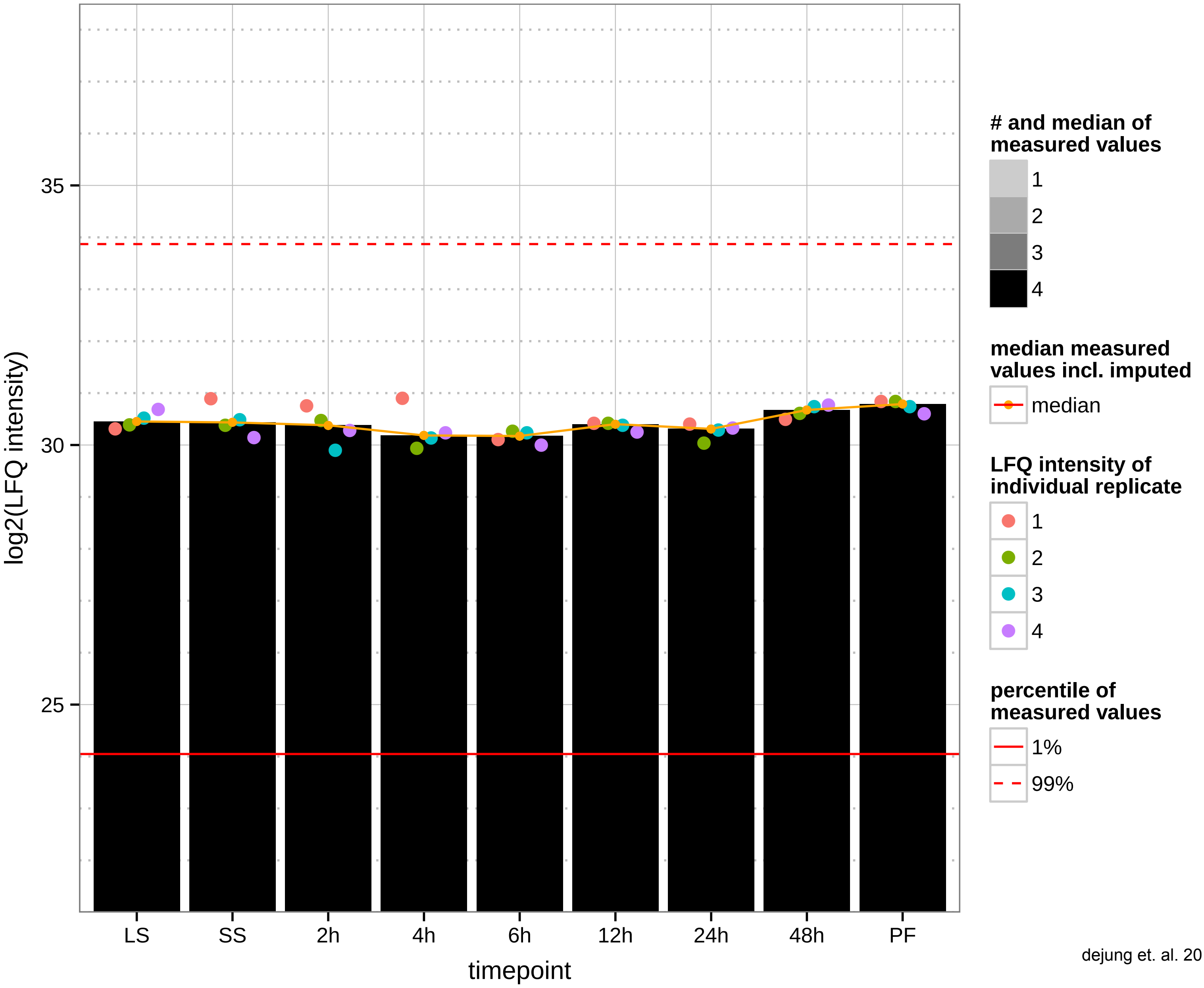
flagellar protein PF16, axoneme central apparatus protein
Tb927.1.2670
AGOF: null
AGOC: axoneme
AGOP: axoneme assembly, ciliary or flagellar motility
PGOF: binding, protein binding
PGOC: null
PGOP: null





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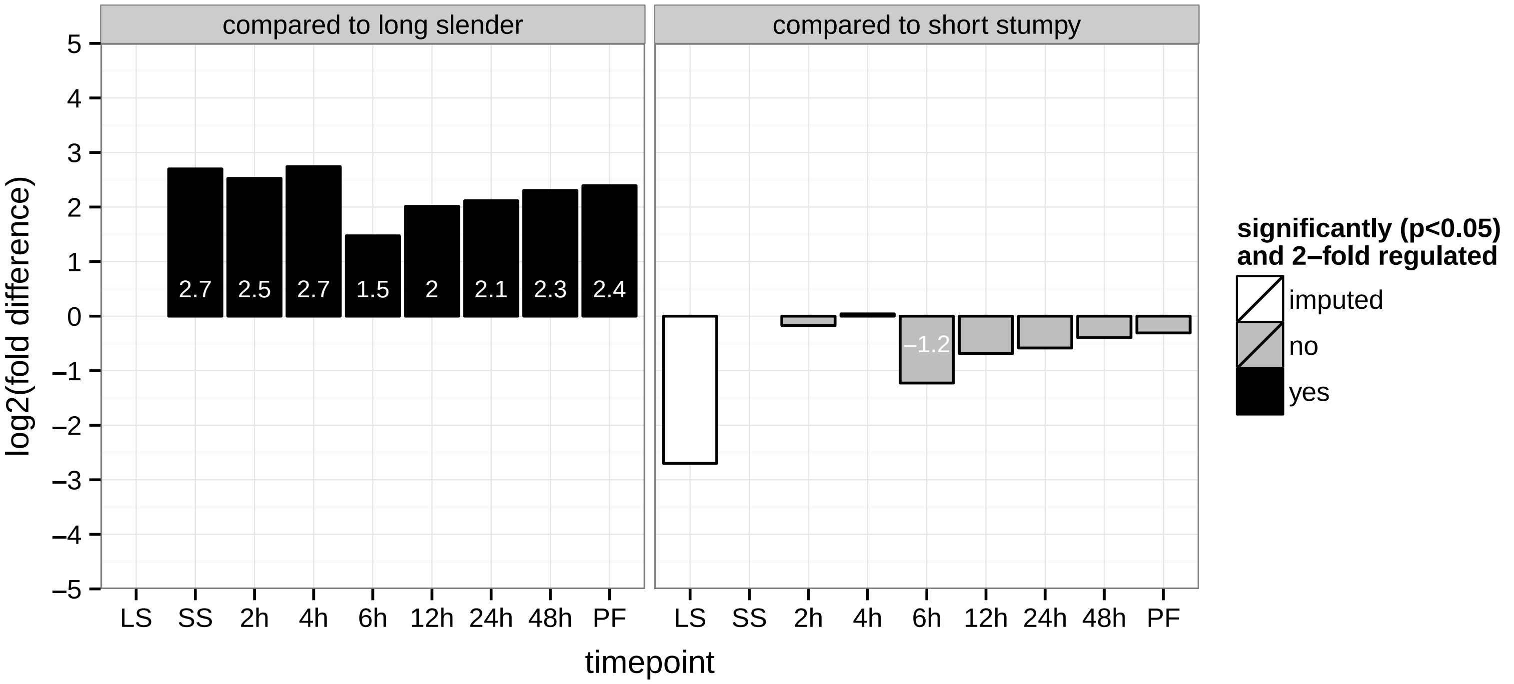
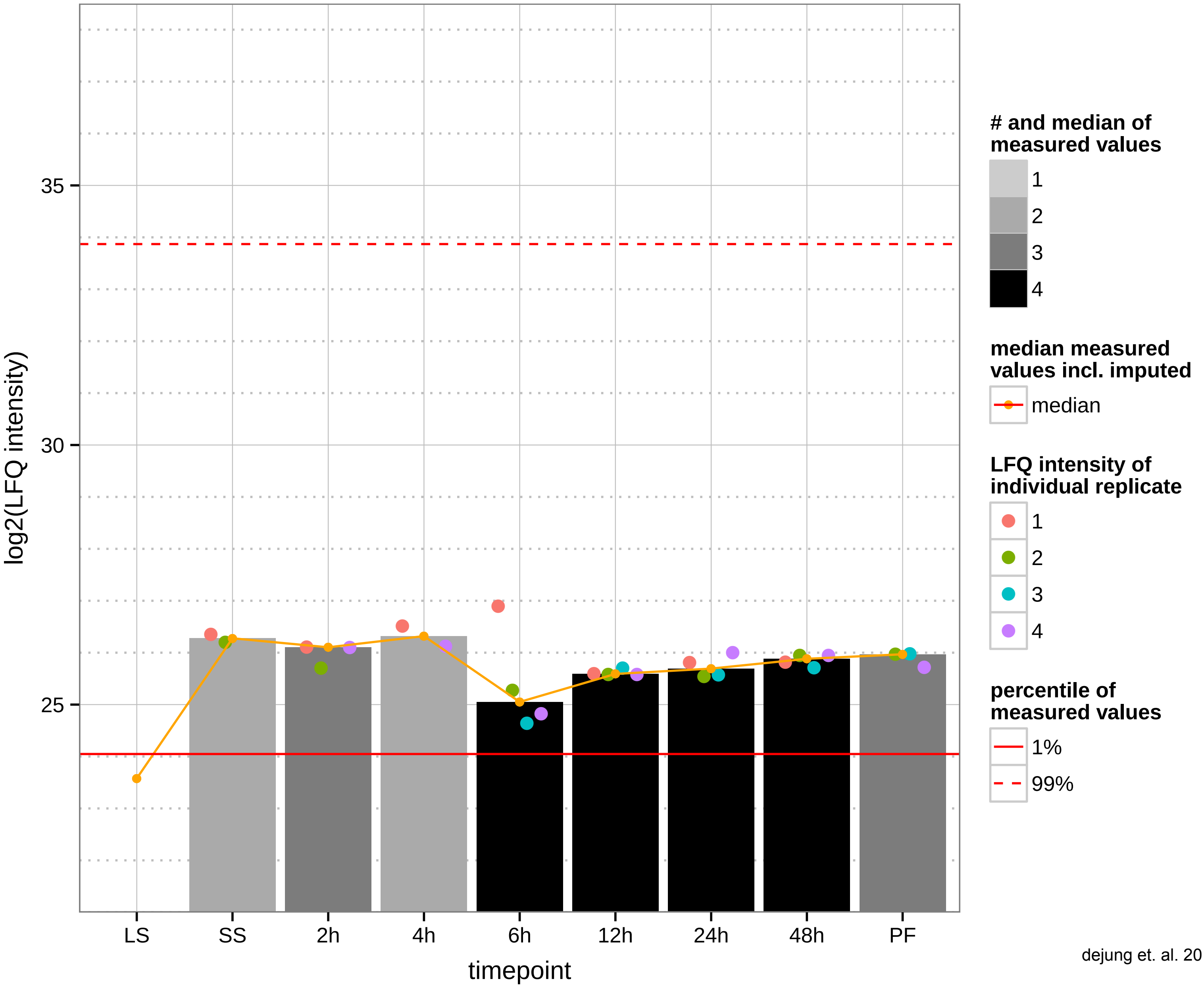
KREL2, RNA–editing complex protein, RNA editing ligase (KREL2)
Tb927.1.3030
AGOF: ATP binding, RNA ligase (ATP) activity
AGOC: mRNA editing complex, mitochondrial mRNA editing complex, mitochondrion
AGOP: mRNA modification
PGOF: ATP binding, RNA ligase (ATP) activity, ligase activity
PGOC: null
PGOP: null





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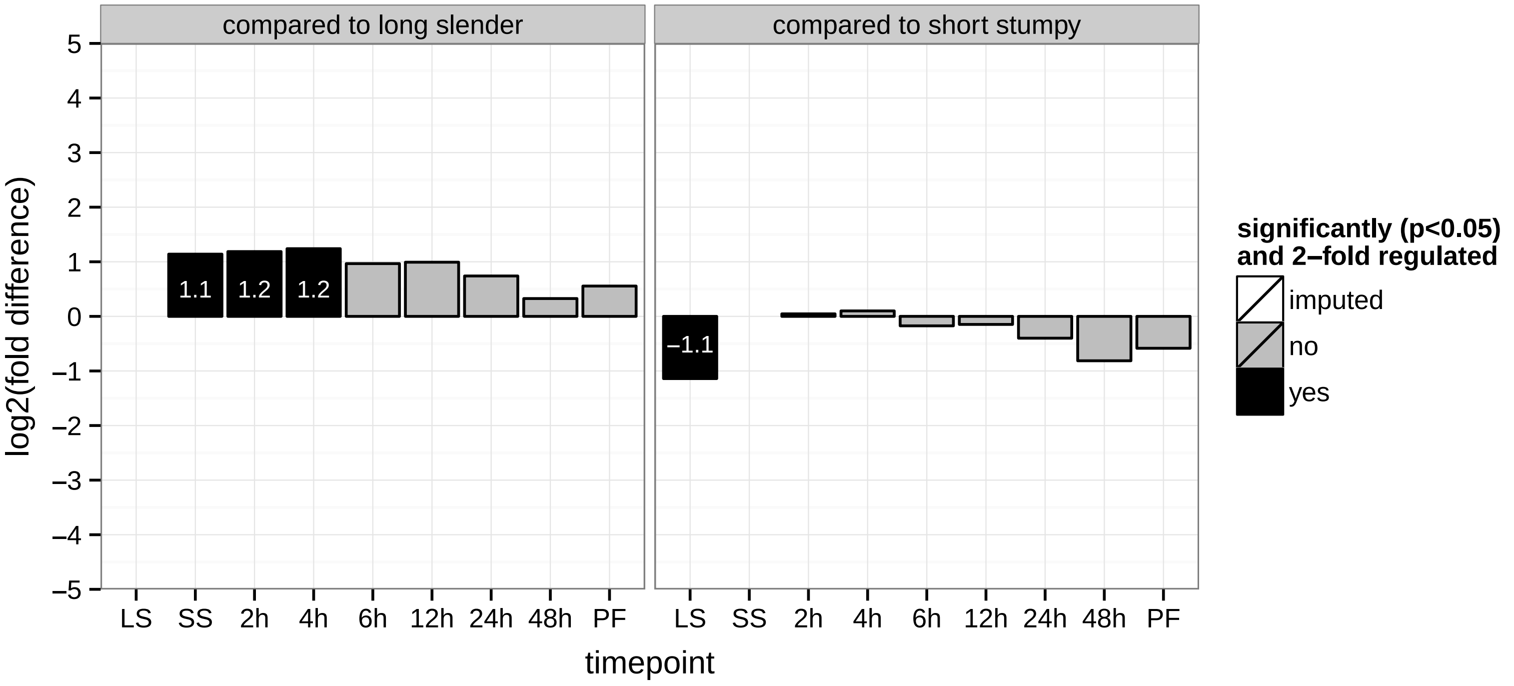
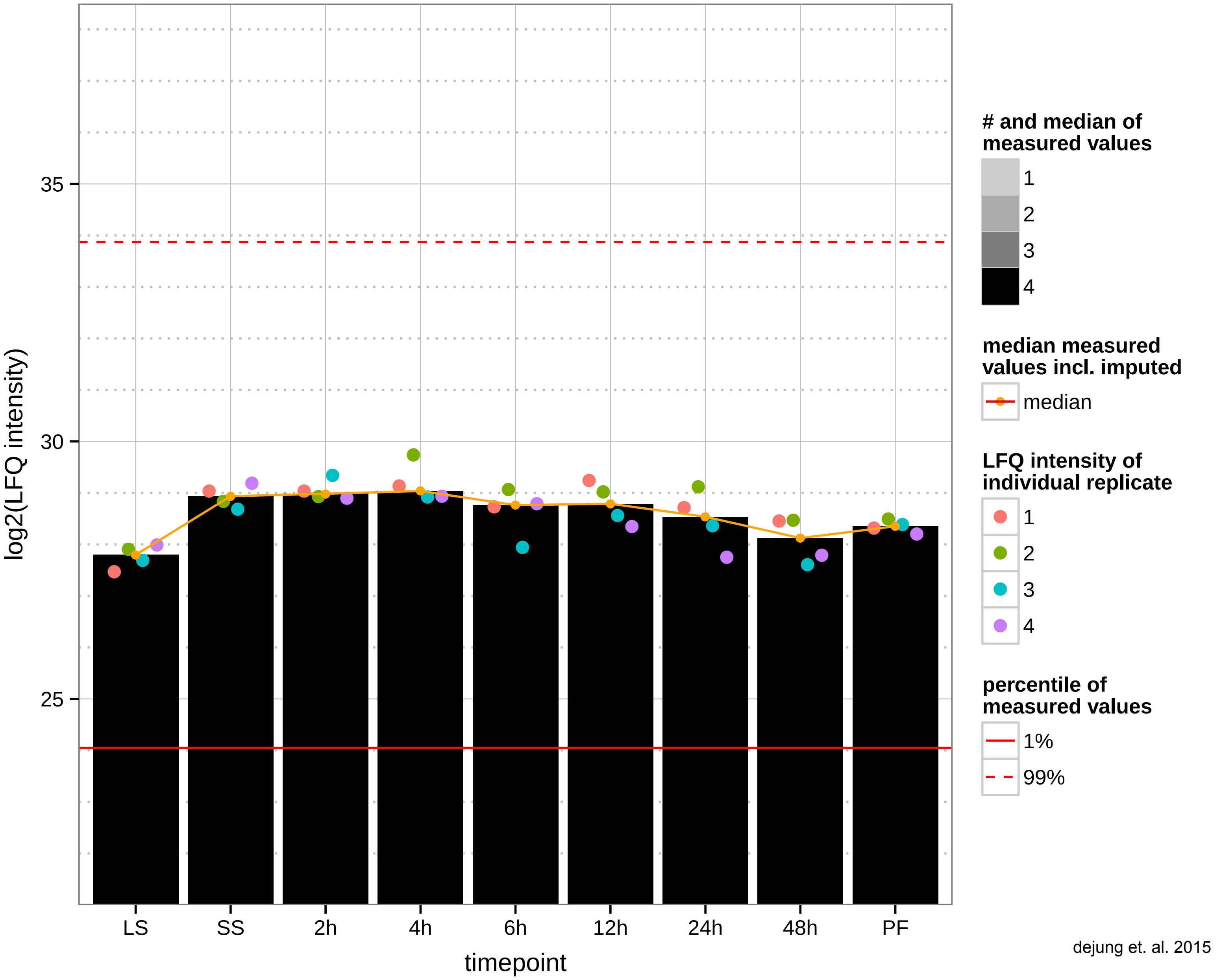
soluble N–ethylmaleimide sensitive factor (NSF) attachment protein, putative
Tb927.1.3110
AGOF: soluble NSF attachment protein activity
AGOC: Golgi apparatus, endoplasmic reticulum
AGOP: intracellular protein transport
PGOF: null
PGOC: null
PGOP: null





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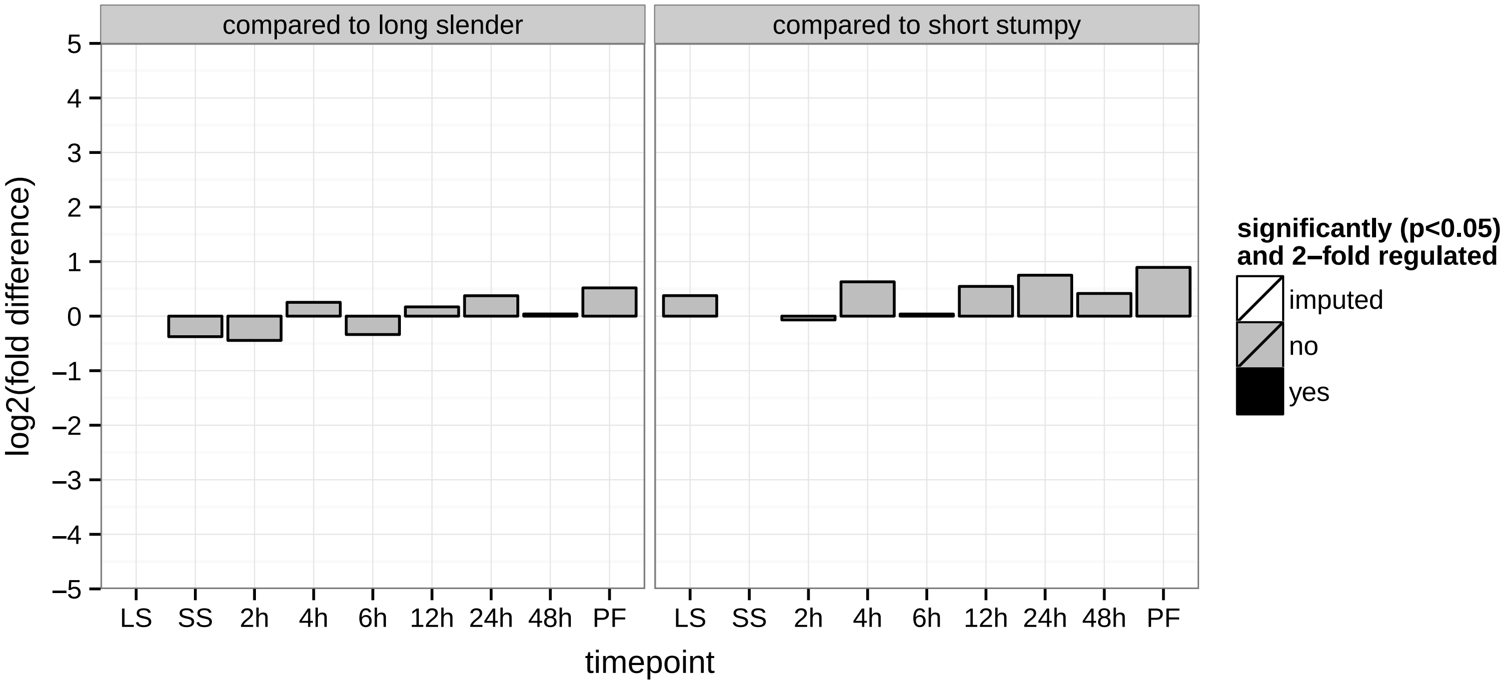
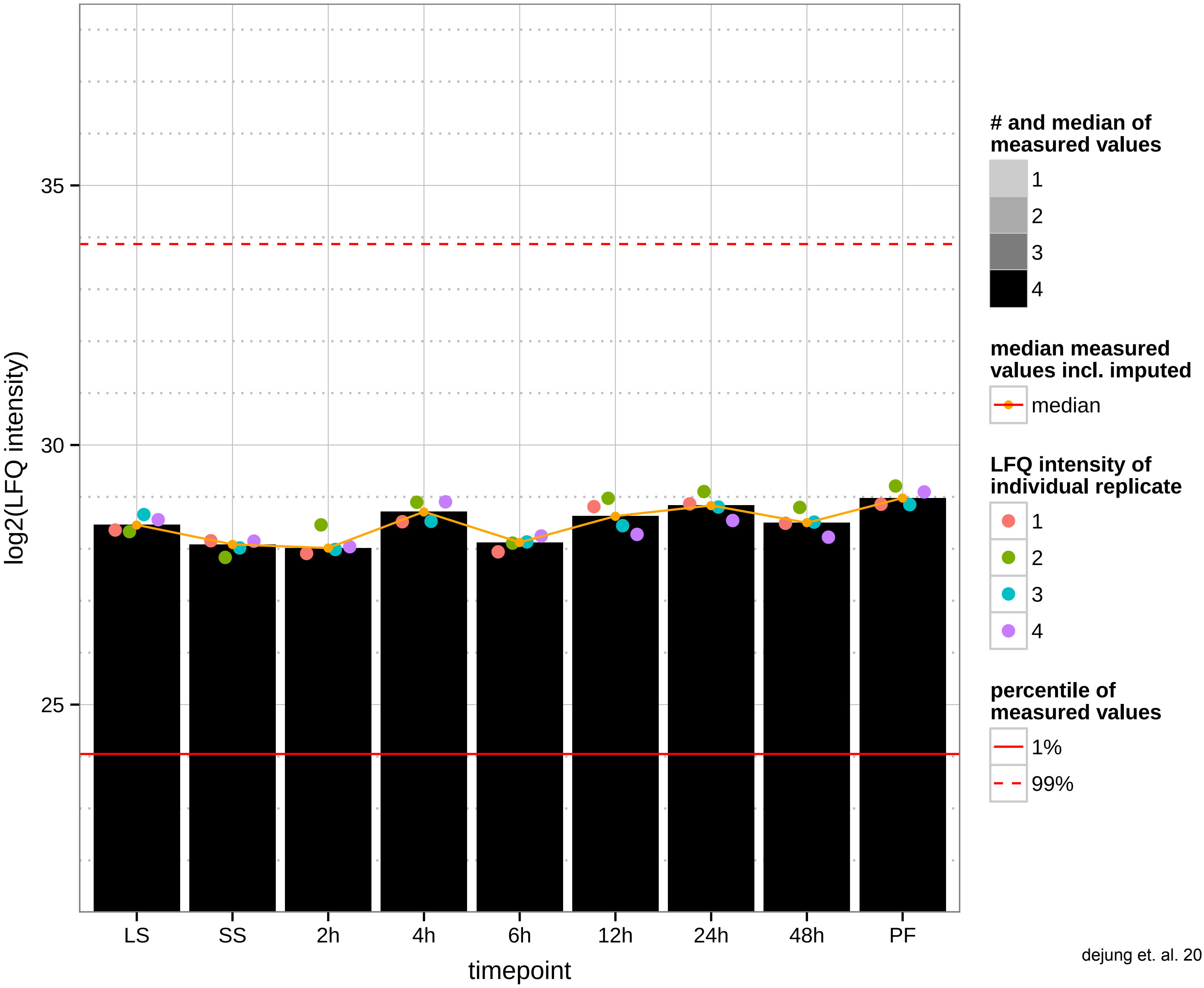
Suppressor of G2 allele of SKP1, putative
Tb927.1.3200
AGOF: null
AGOC: ubiquitin ligase complex
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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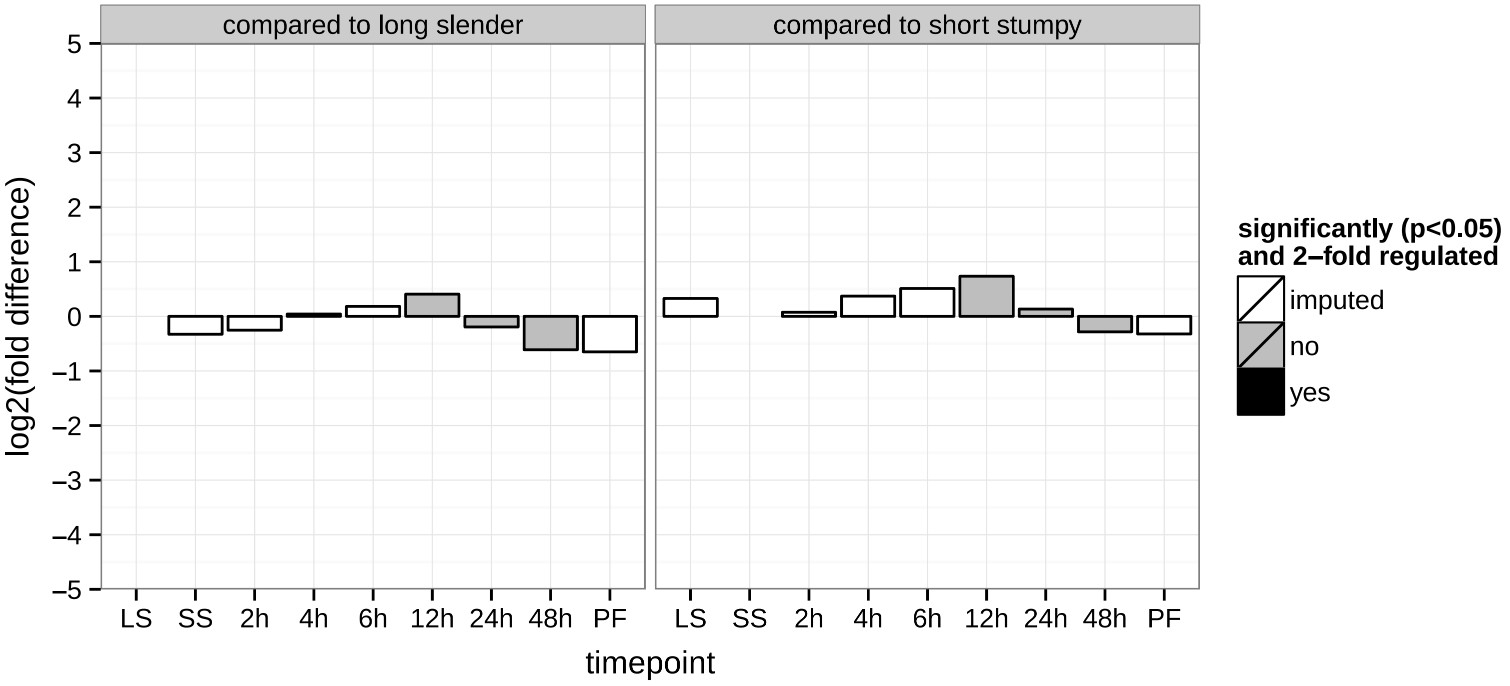
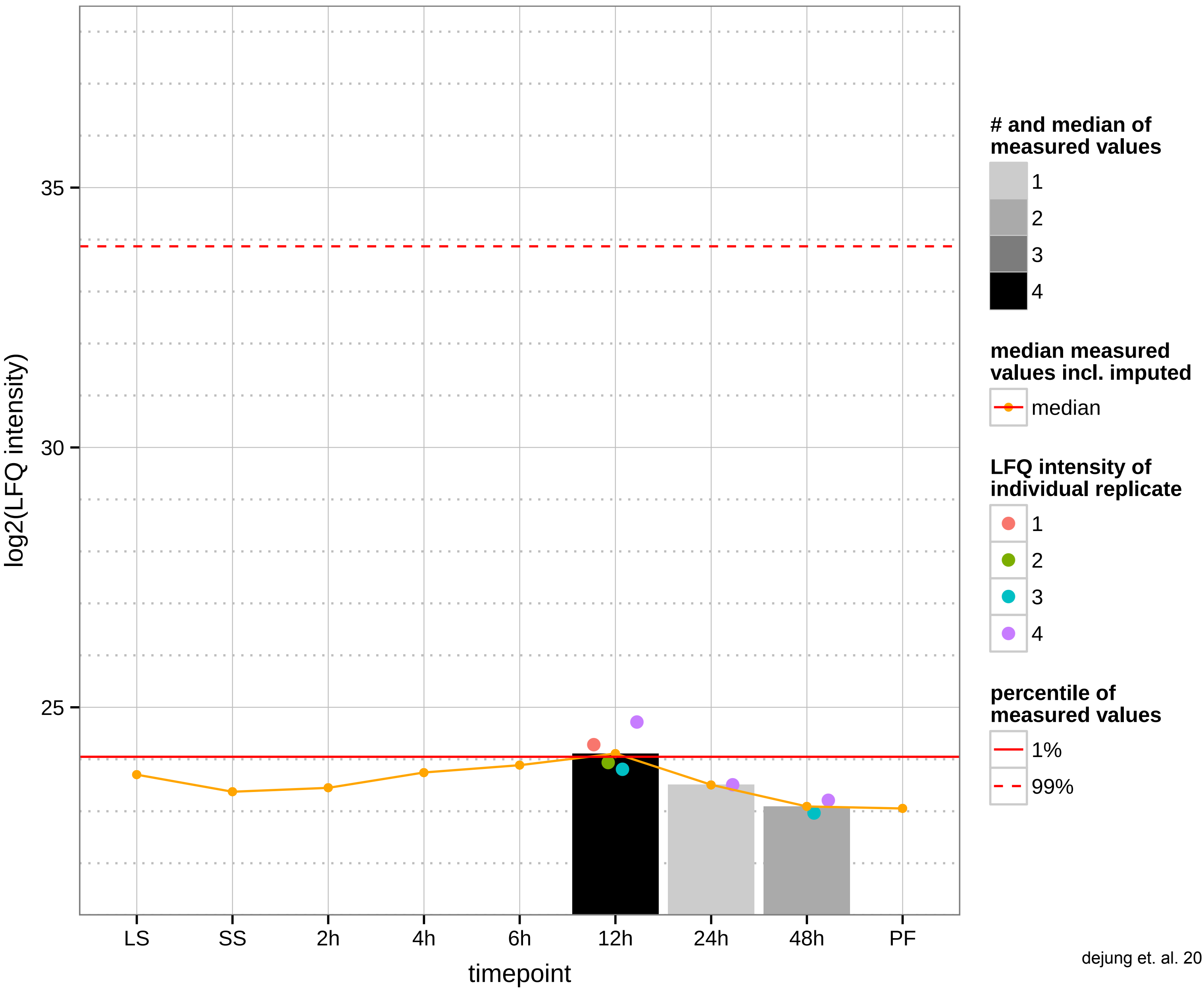
TBC1 domain family member 20/GTPase, putative
Tb927.1.3220
AGOF: Rab GTPase activator activity
AGOC: intracellular
AGOP: regulation of Rab GTPase activity
PGOF: Rab GTPase activator activity
PGOC: intracellular
PGOP: regulation of Rab GTPase activity





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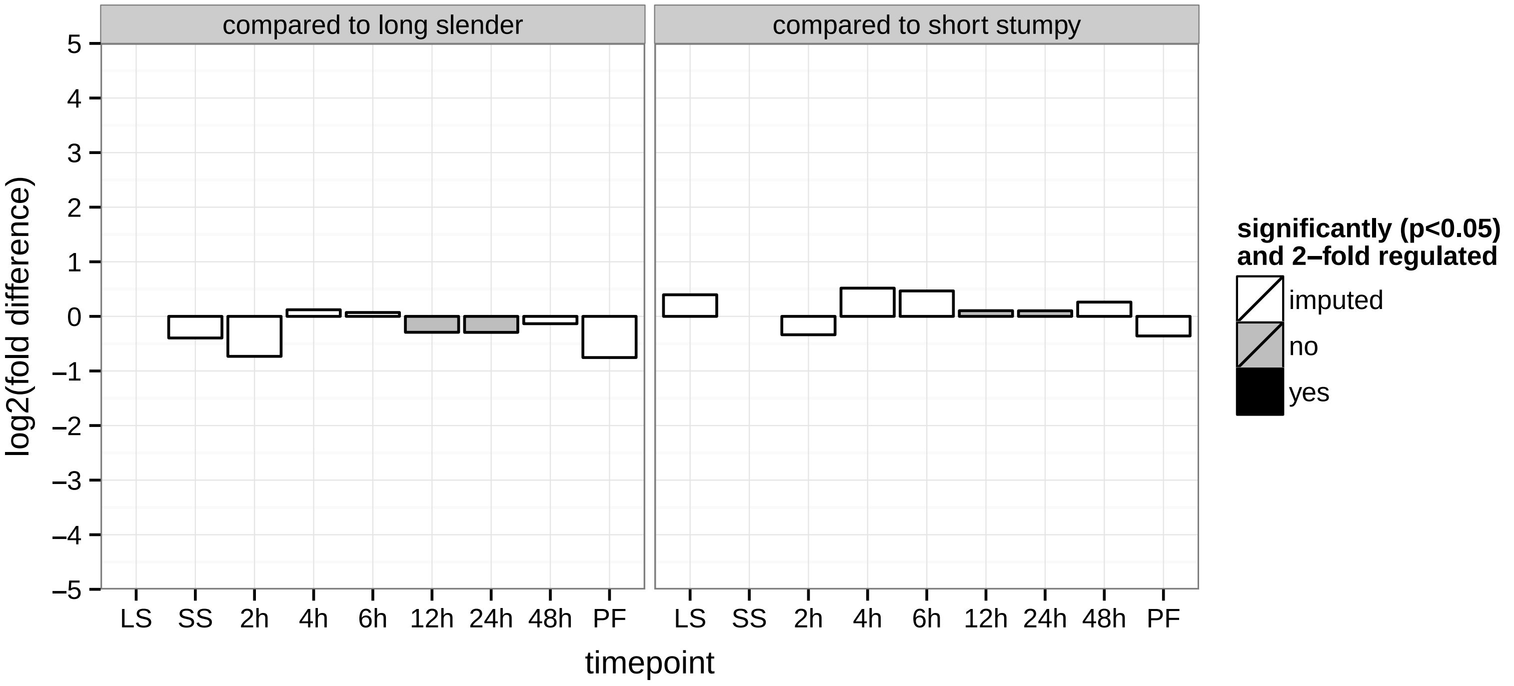
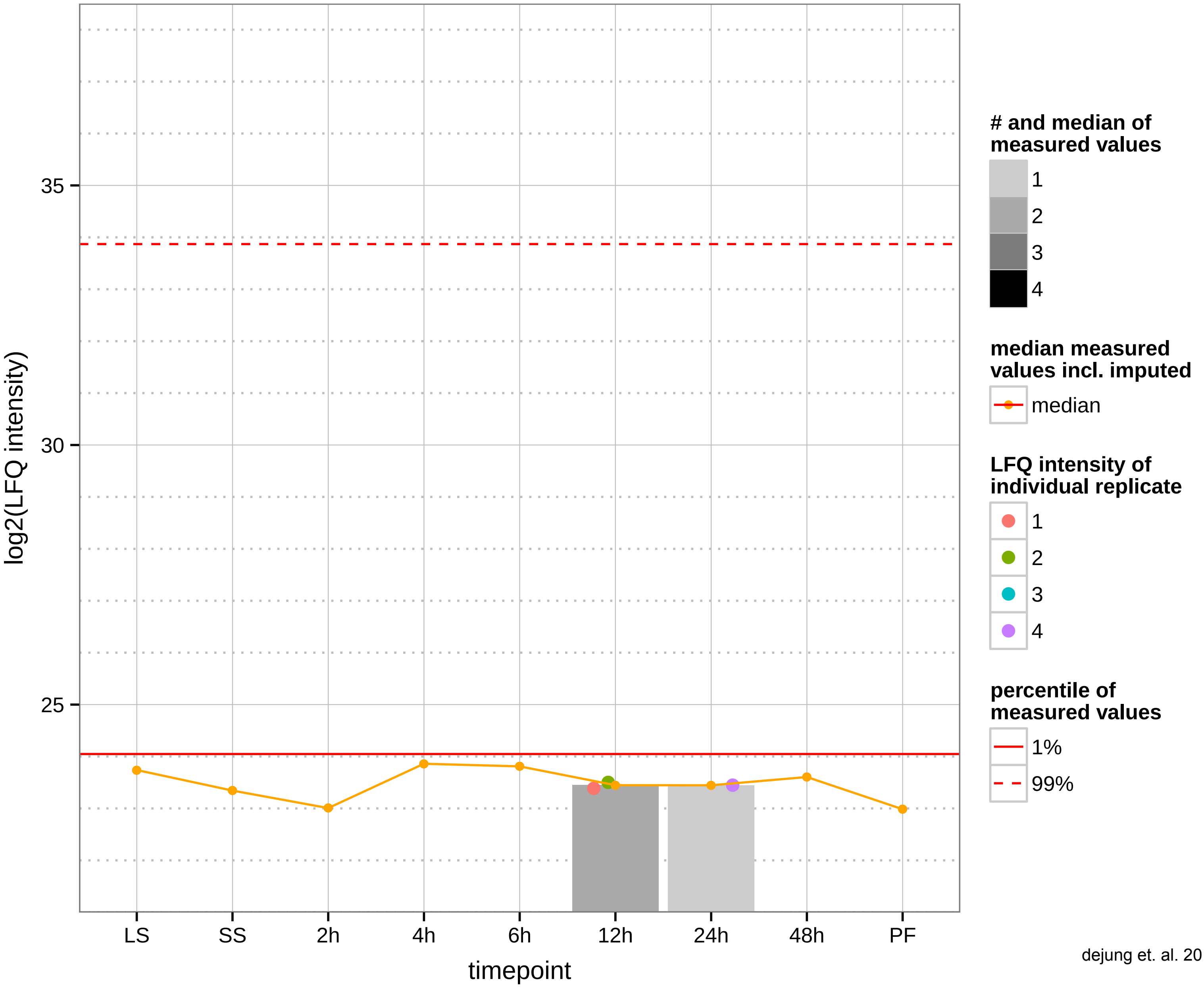
cell division cycle protein, putative
Tb927.1.3230
AGOF: ATP binding, nucleoside−triphosphatase activity
AGOC: null
AGOP: null
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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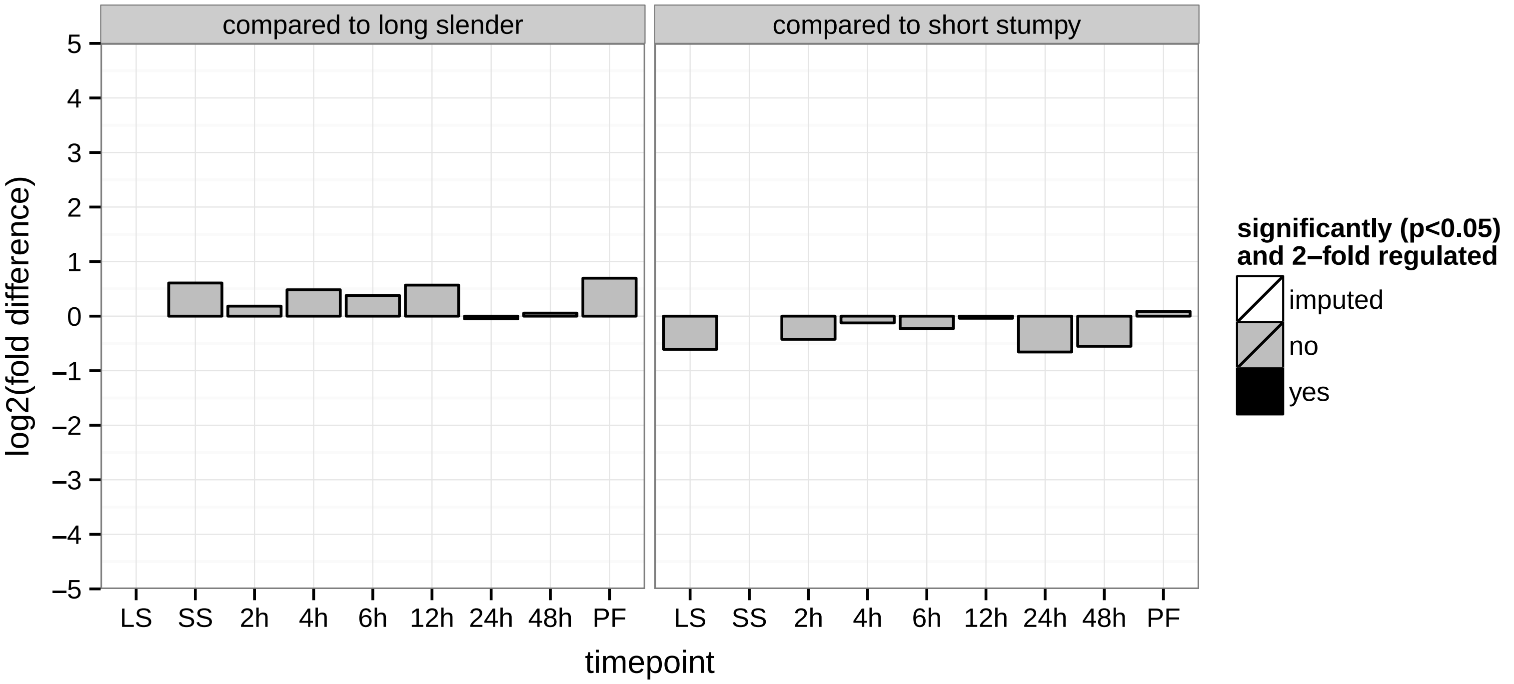
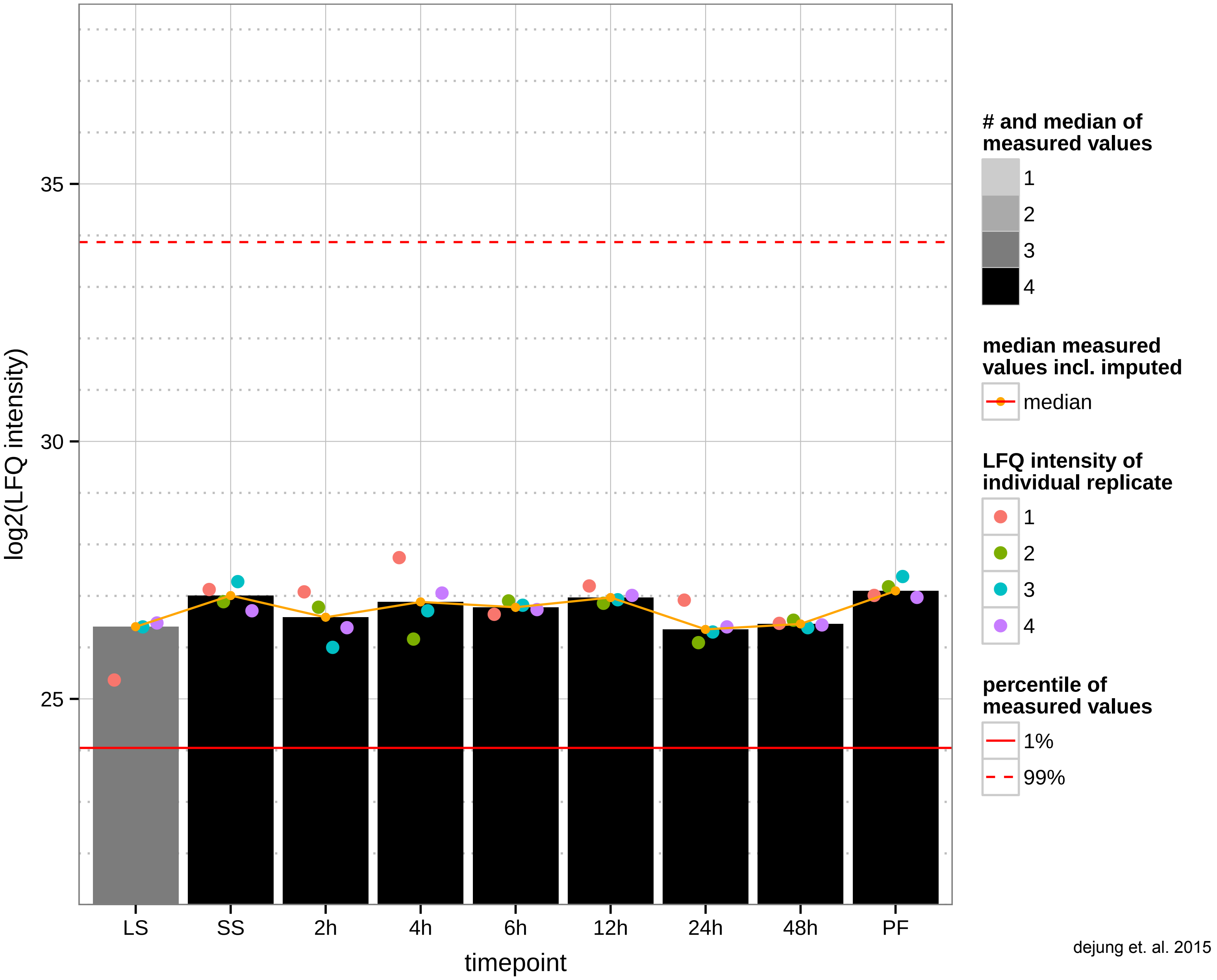
myotubularin, putative, zinc−binding phosphatase
Tb927.1.3300
AGOF: phosphatase activity
AGOC: null
AGOP: dephosphorylation
PGOF: metal ion binding, phosphatase activity
PGOC: null
PGOP: dephosphorylation





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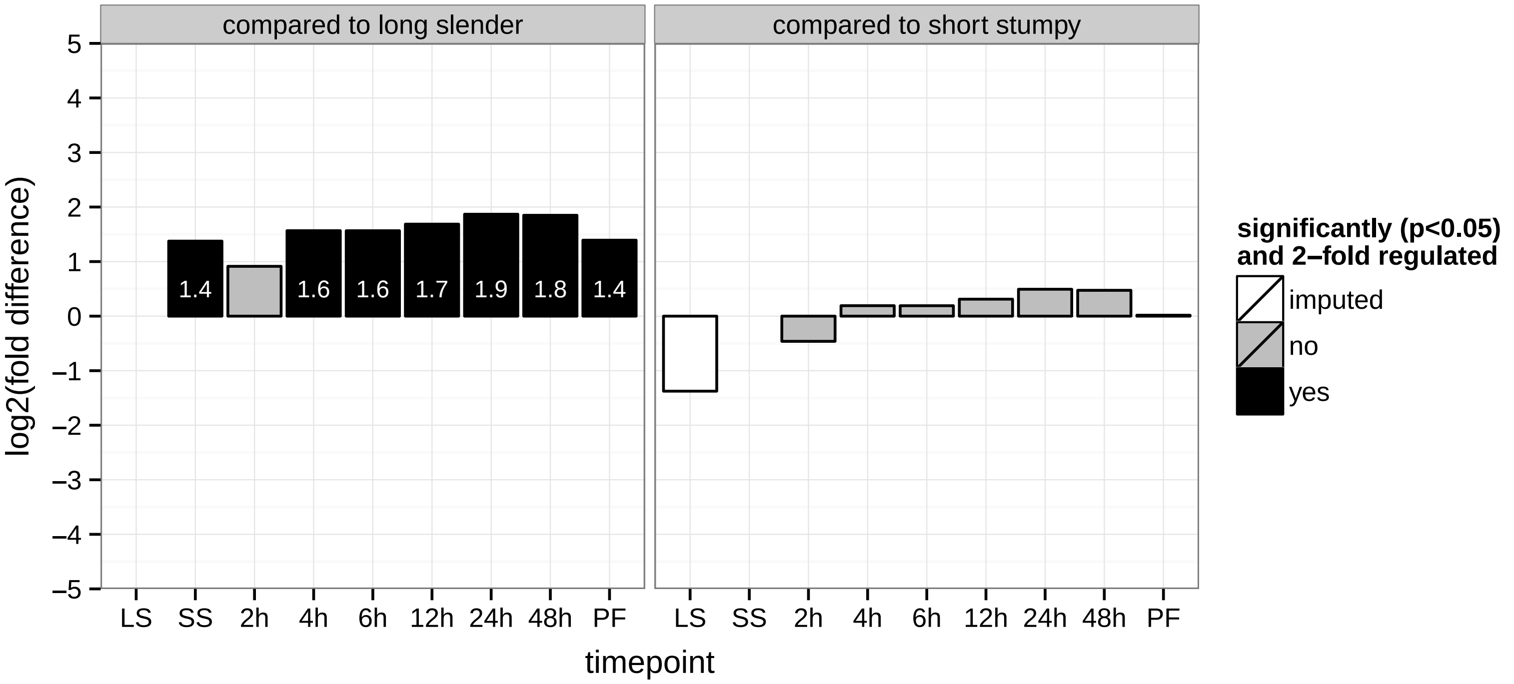
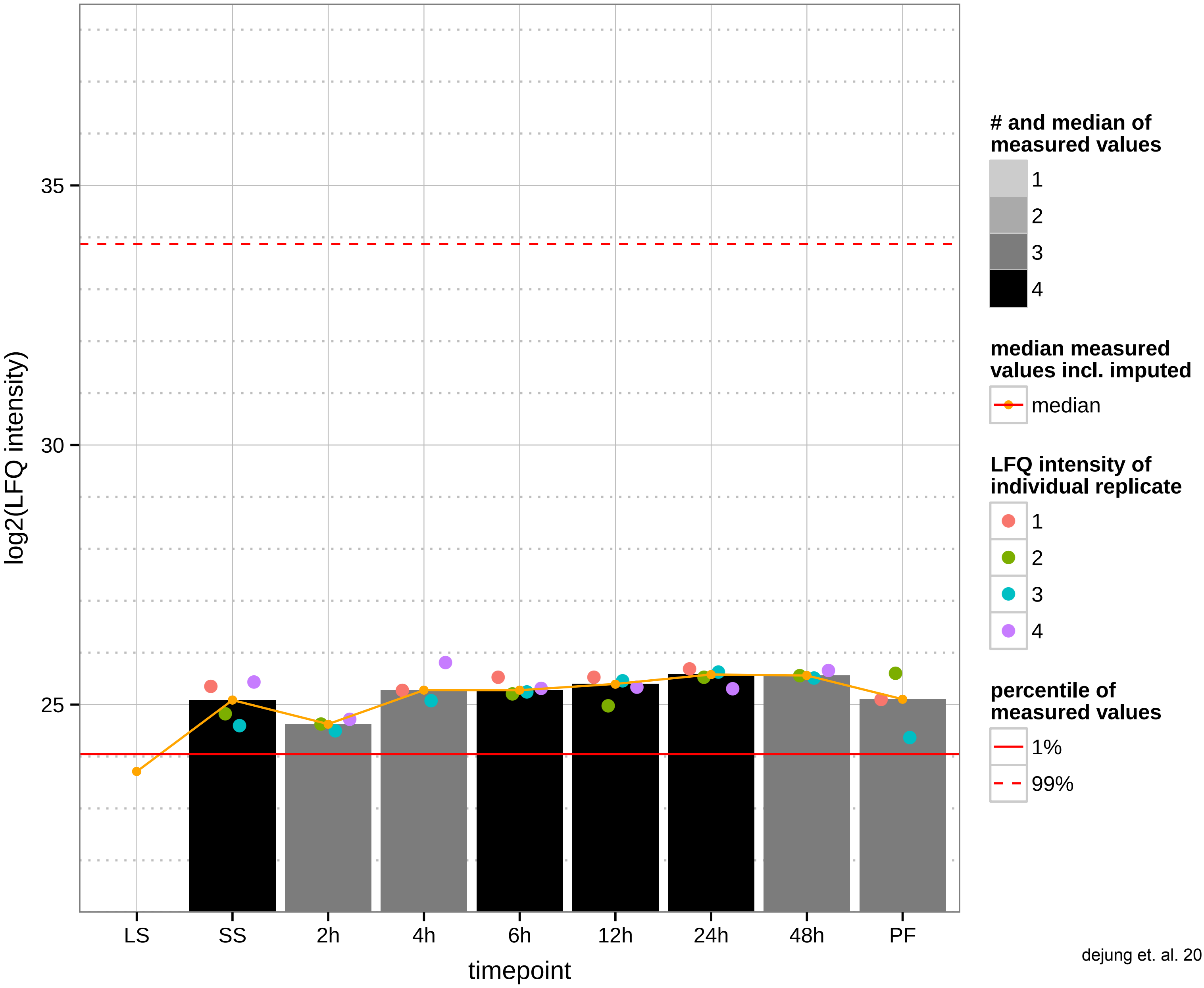
hypothetical protein, conserved
Tb927.1.3450;Tb11.v5.0619
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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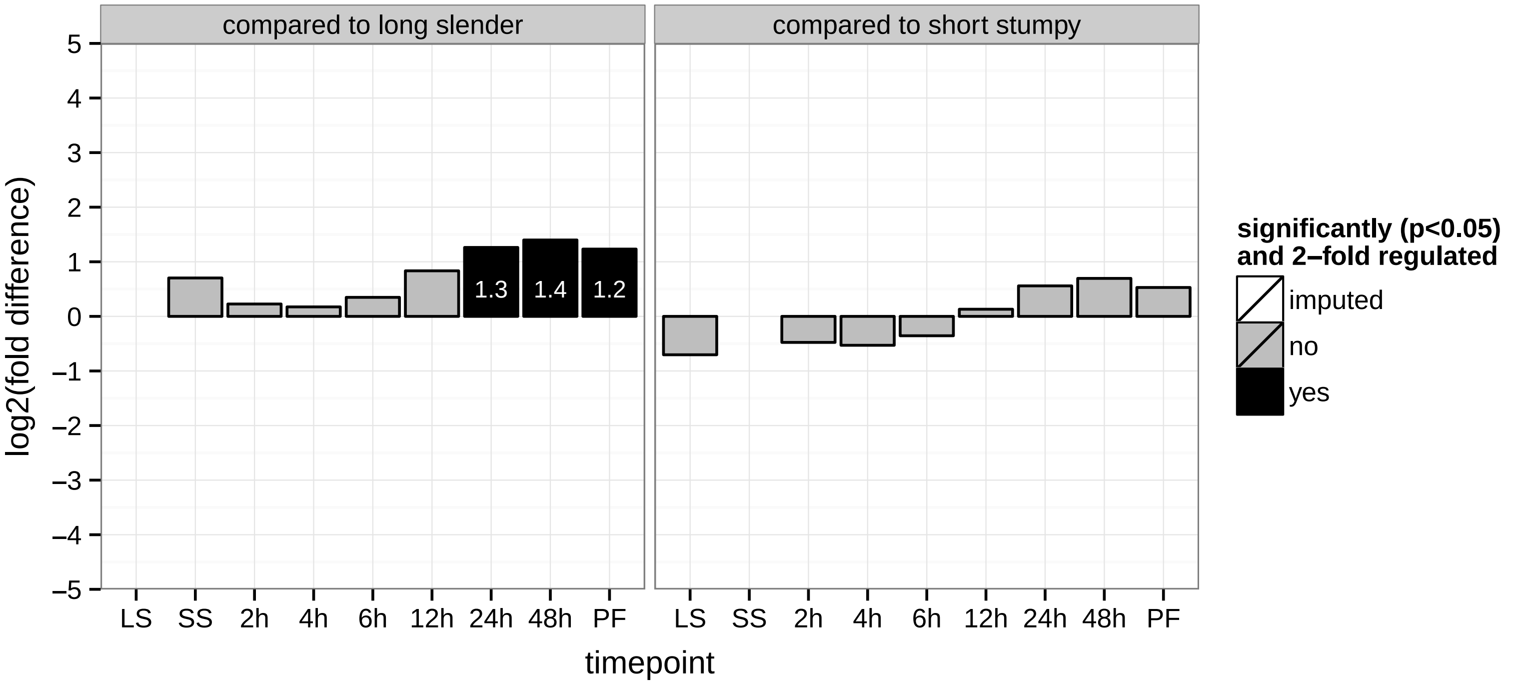
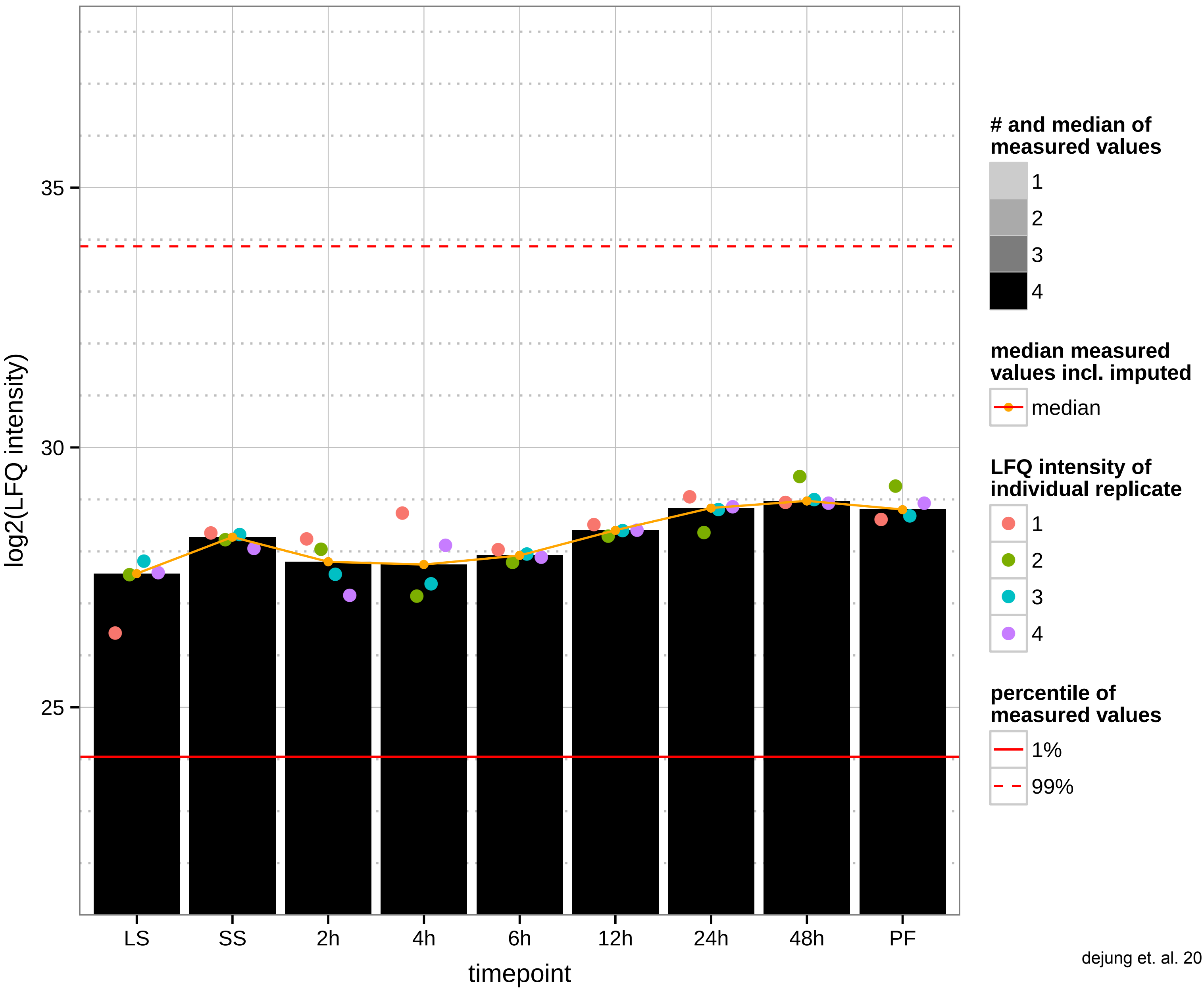
protein phosphatase with EF–Hand domains (PPEF), ser/thr protein phosphatase, putative
Tb927.1.4050
AGOF: protein serine/threonine phosphatase activity
AGOC: protein serine/threonine phosphatase complex
AGOP: protein dephosphorylation
PGOF: hydrolase activity
PGOC: null
PGOP: null





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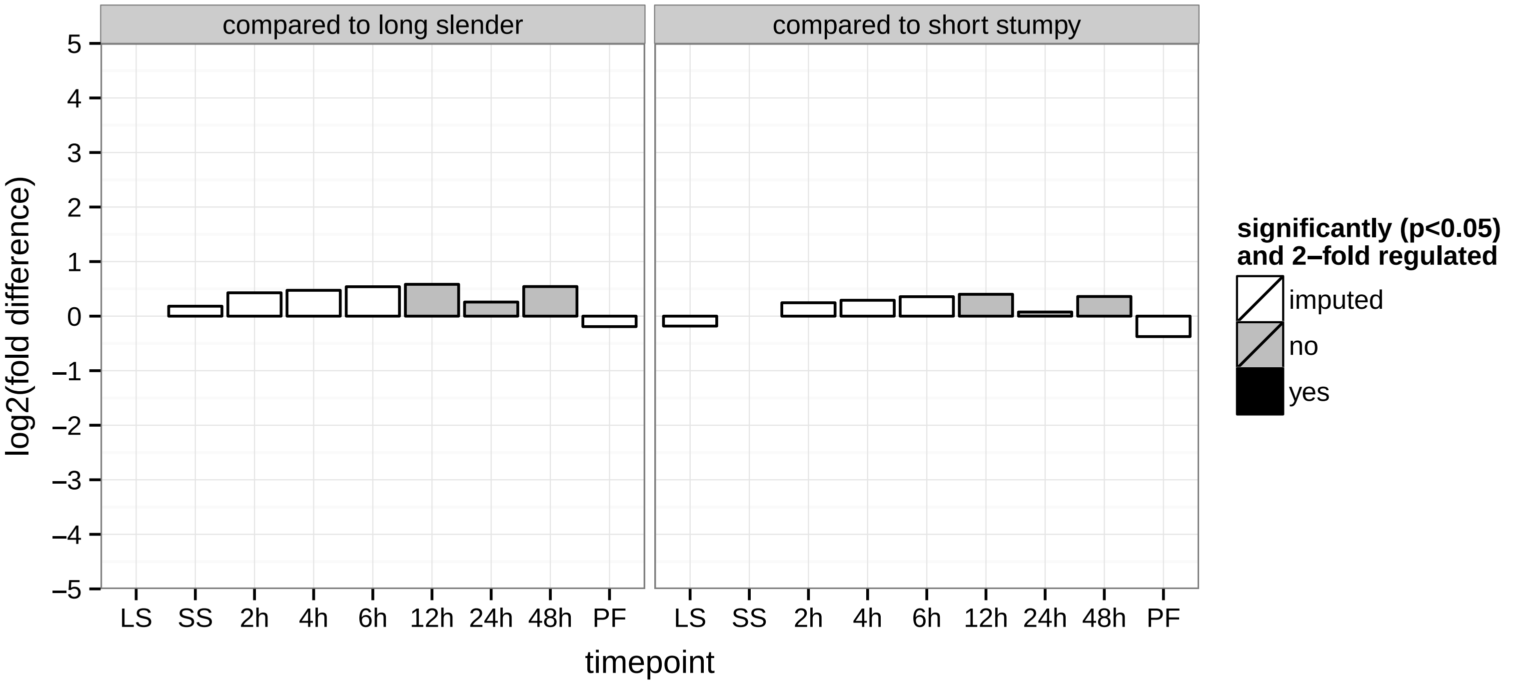
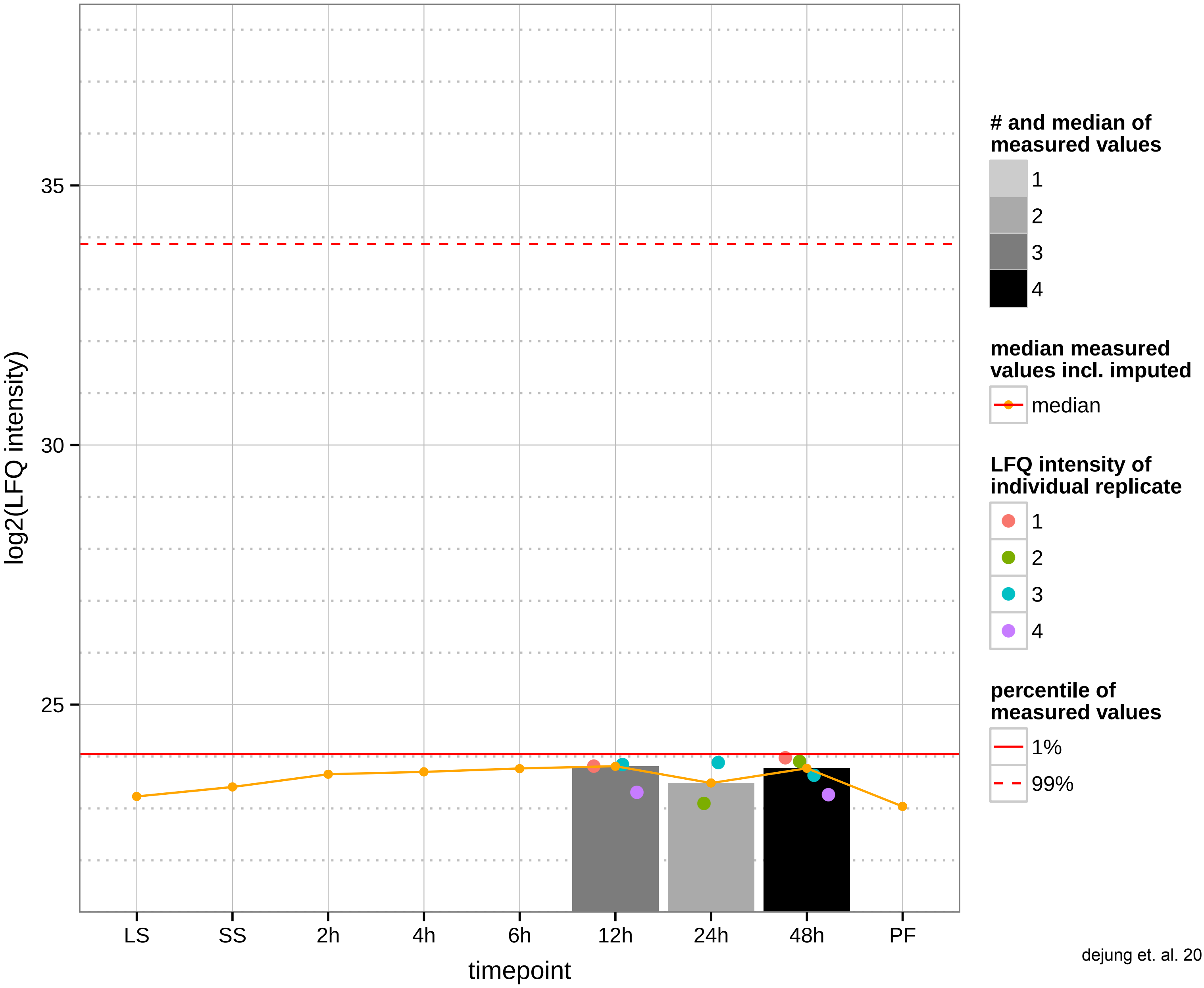
hypothetical protein, conserved
Tb927.1.4250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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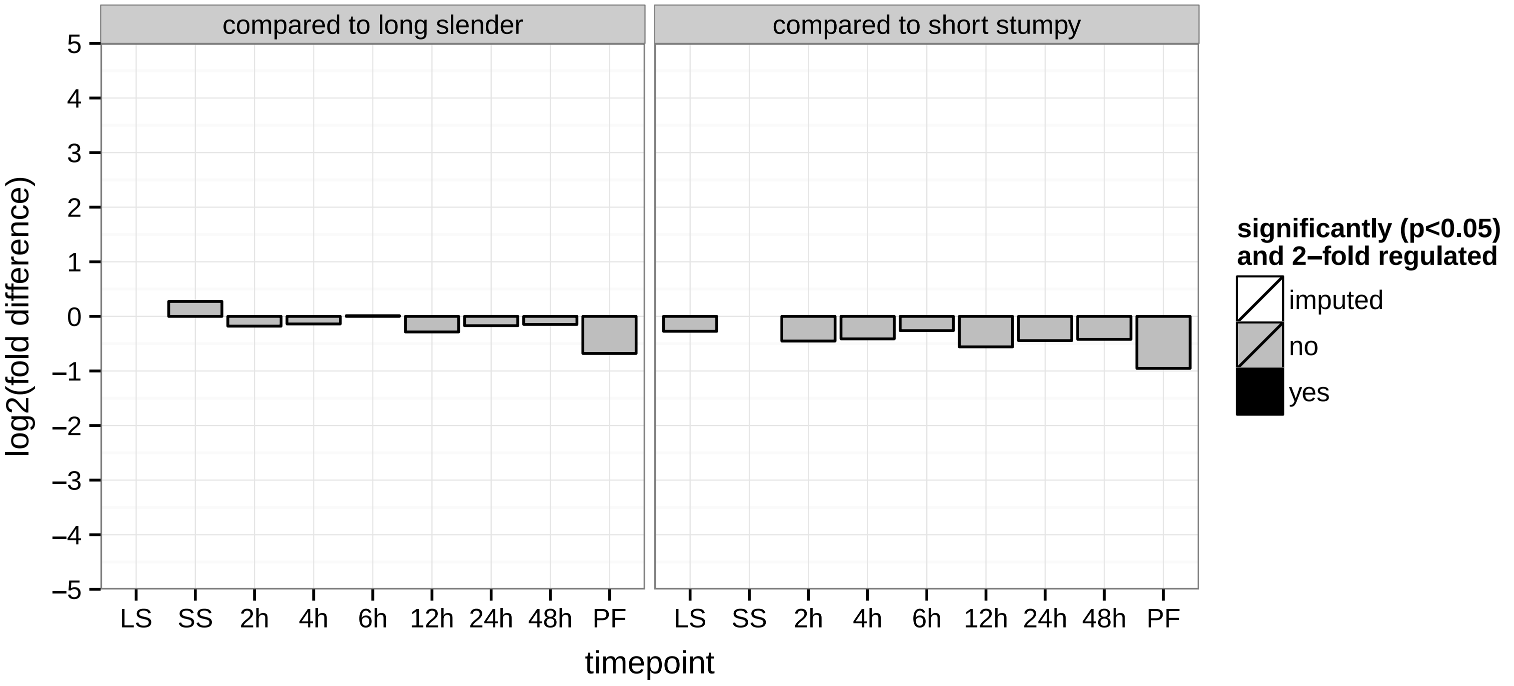
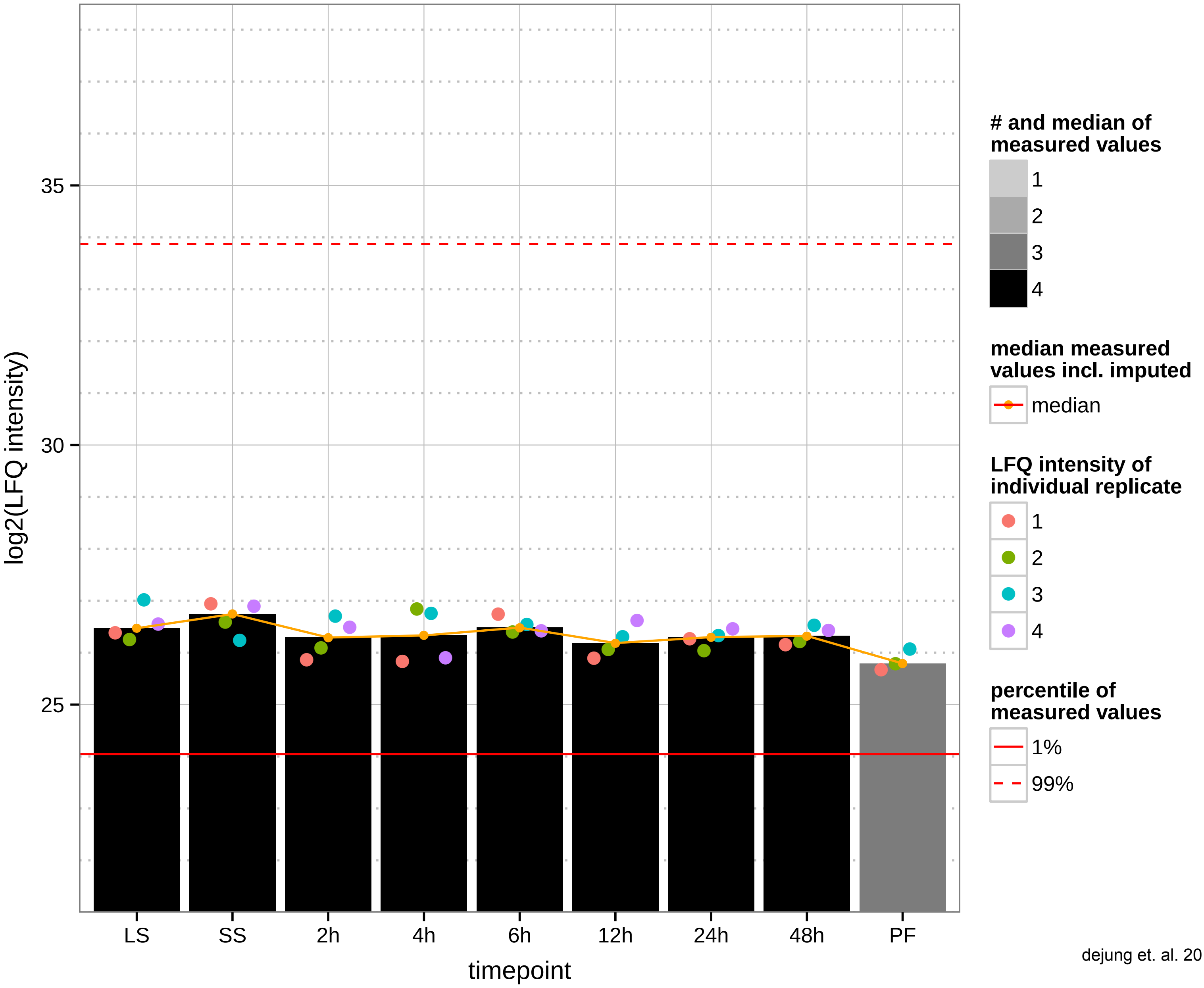
hypothetical protein, conserved
Tb927.1.4280
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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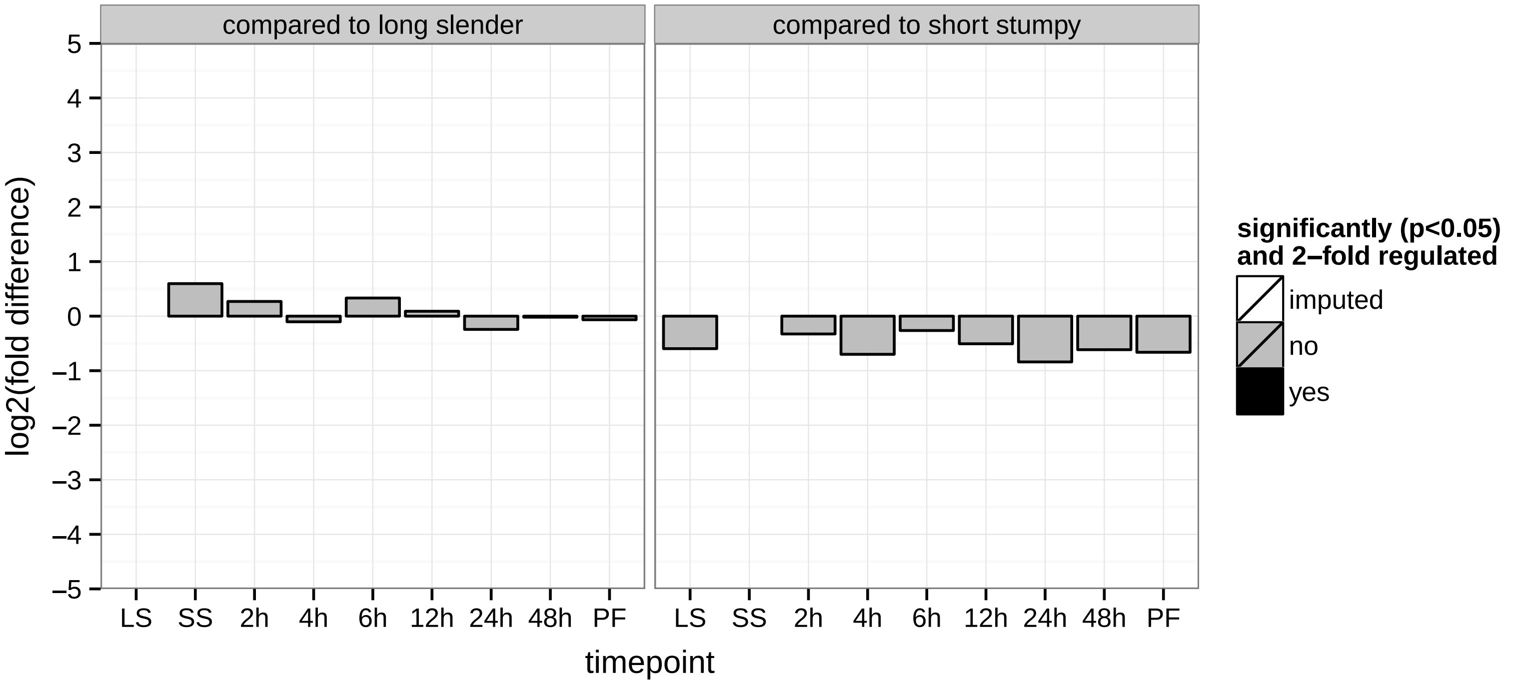
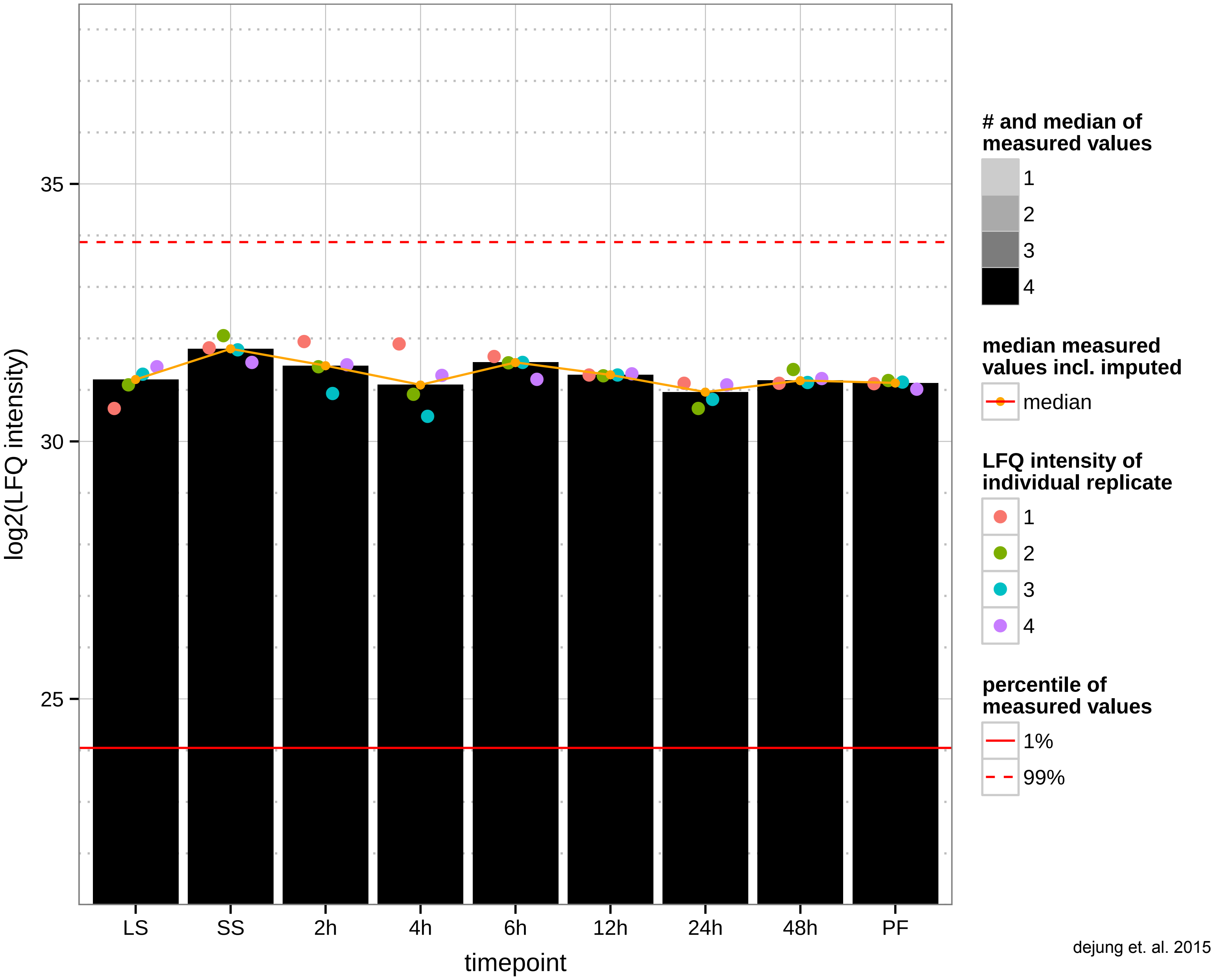
hypothetical protein, conserved
Tb927.1.4310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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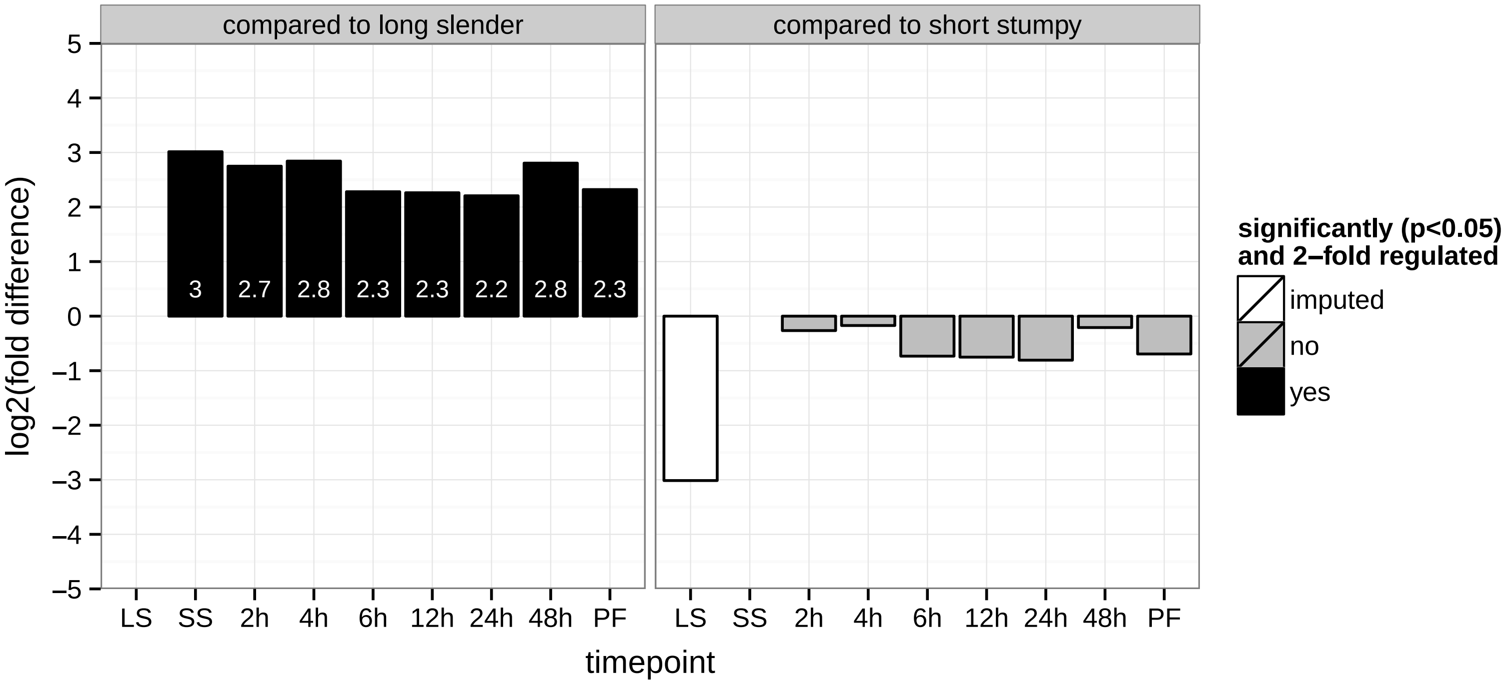
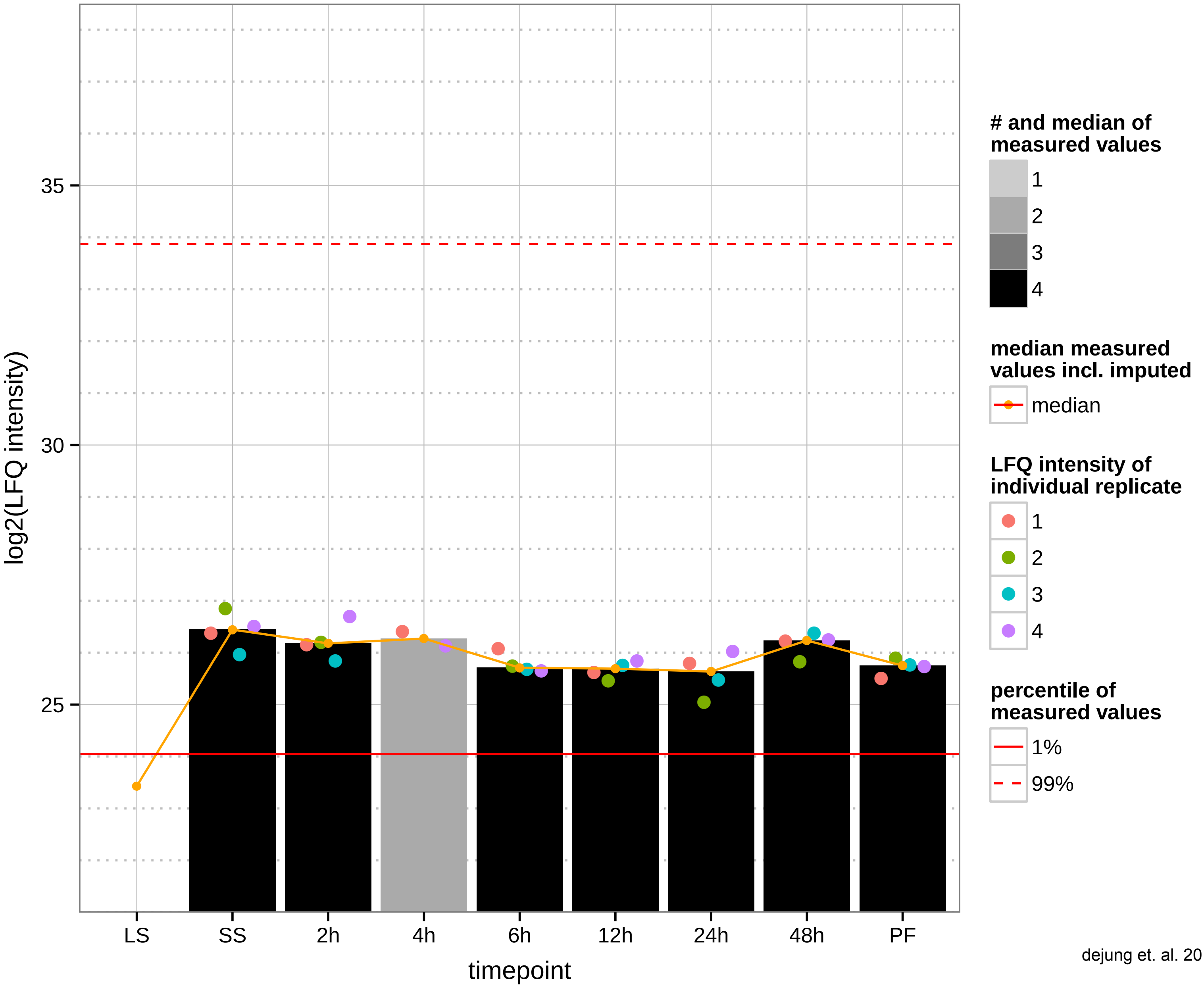
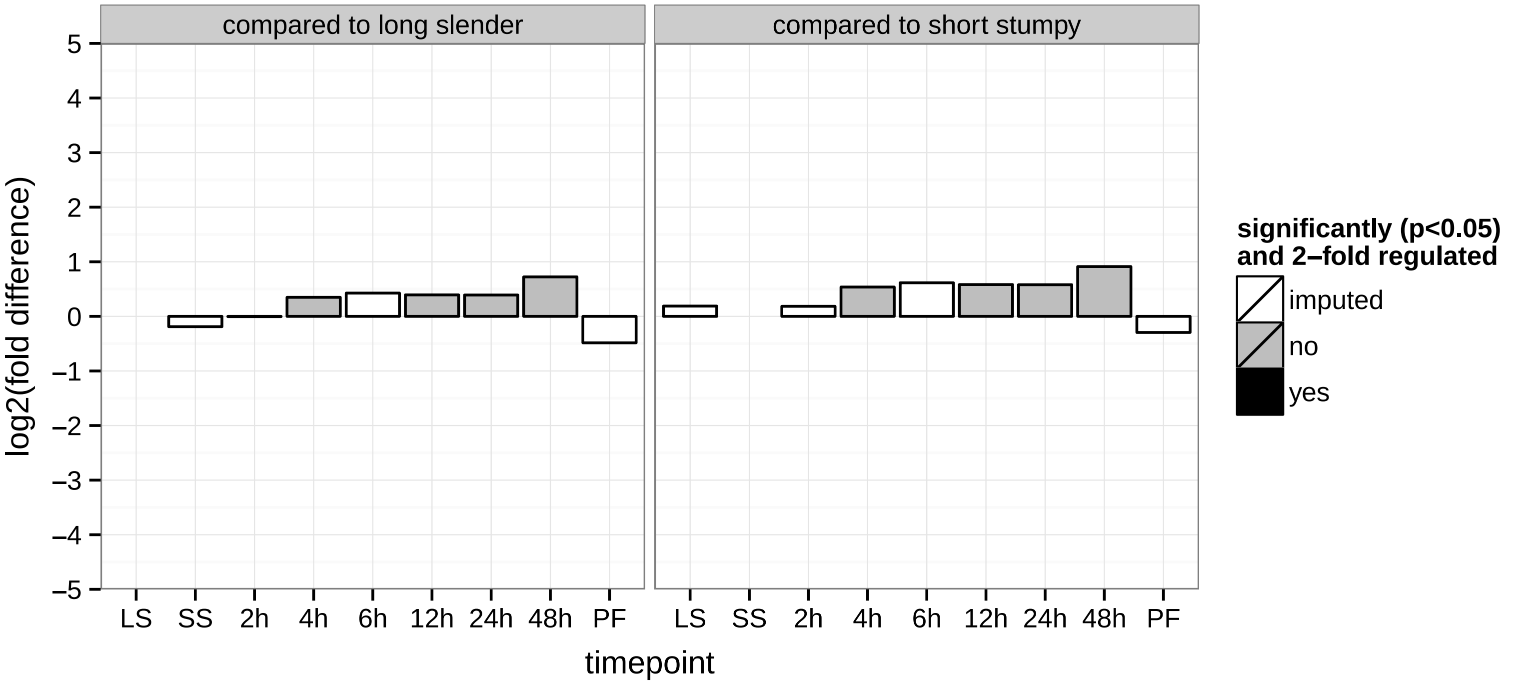
hypothetical protein, conserved
Tb927.1.4340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

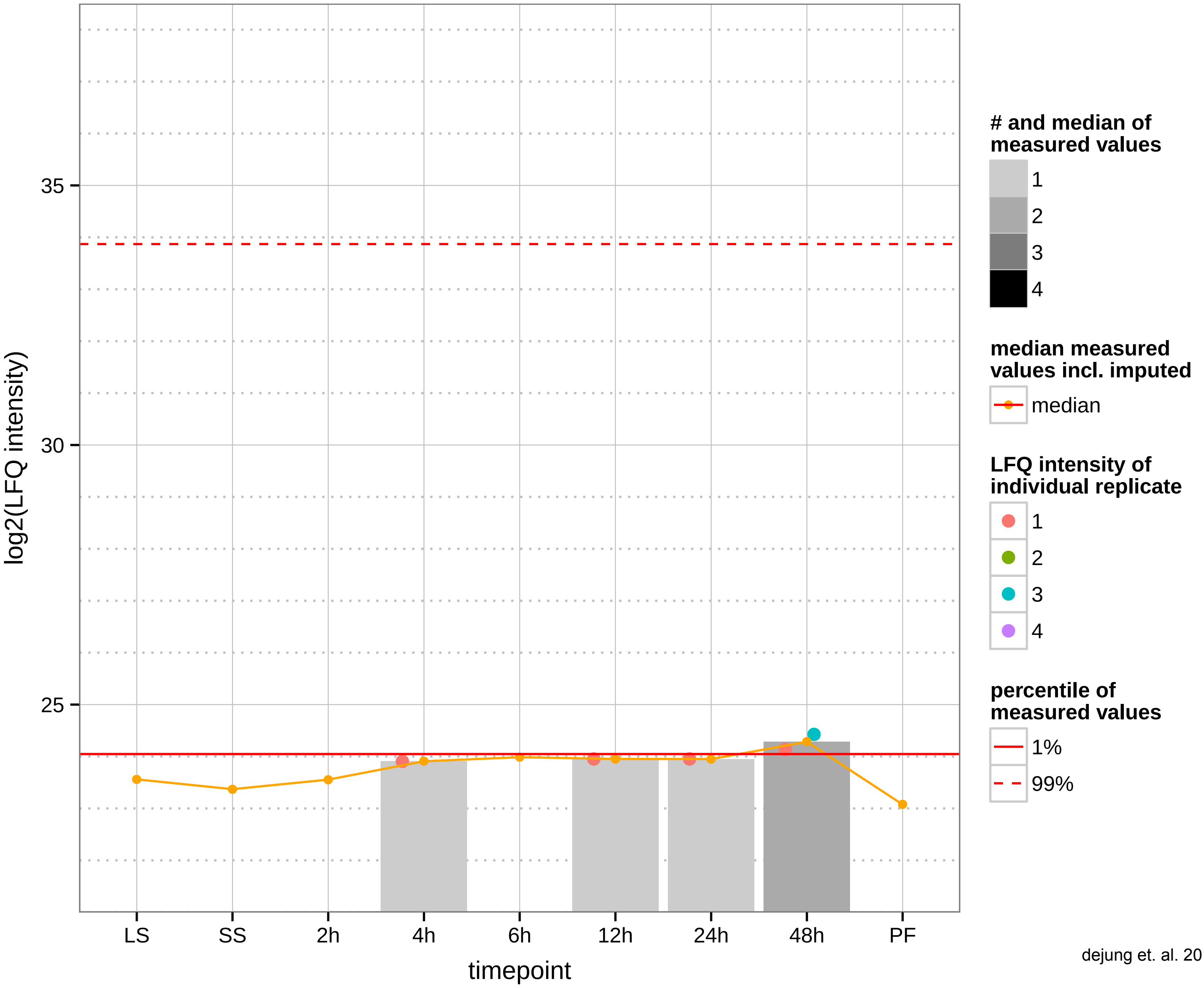




dejung et. al. 2015

hypothetical protein, conserved
Tb927.1.4410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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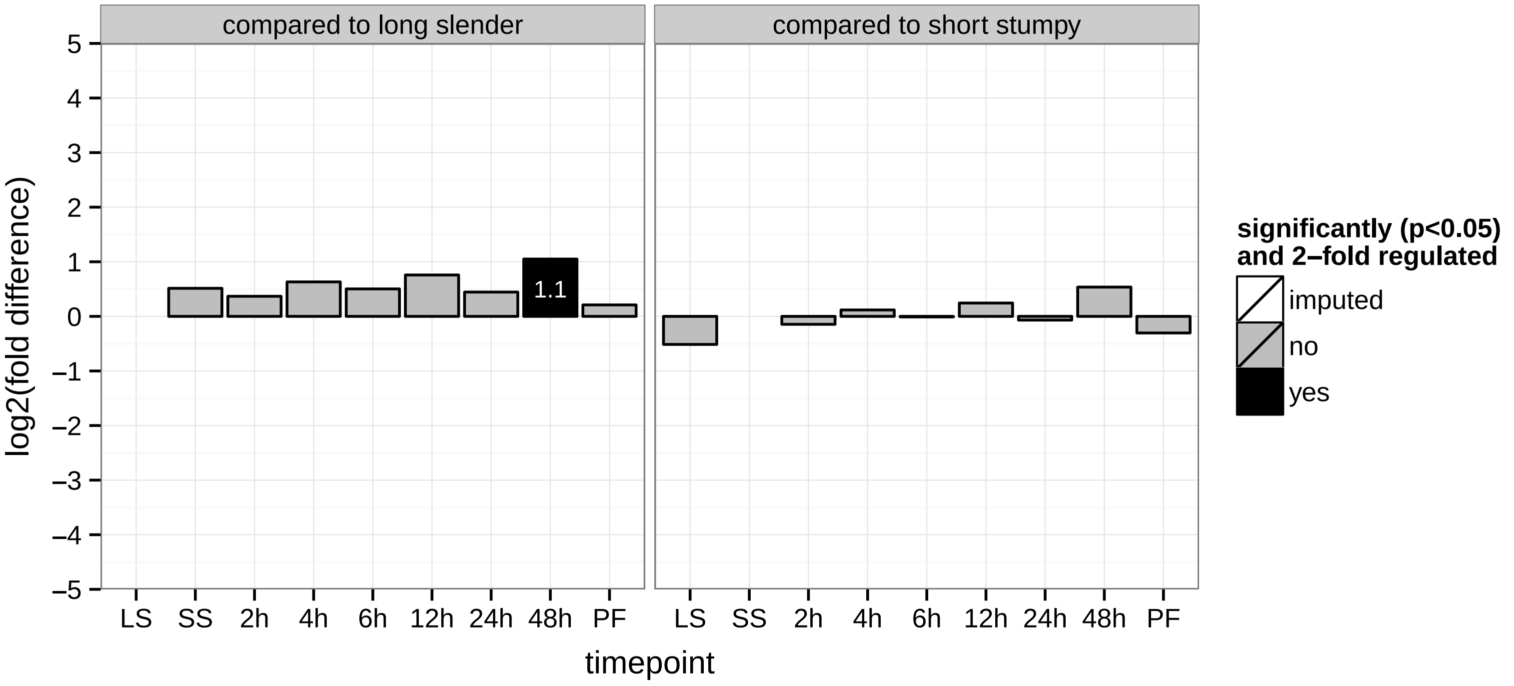
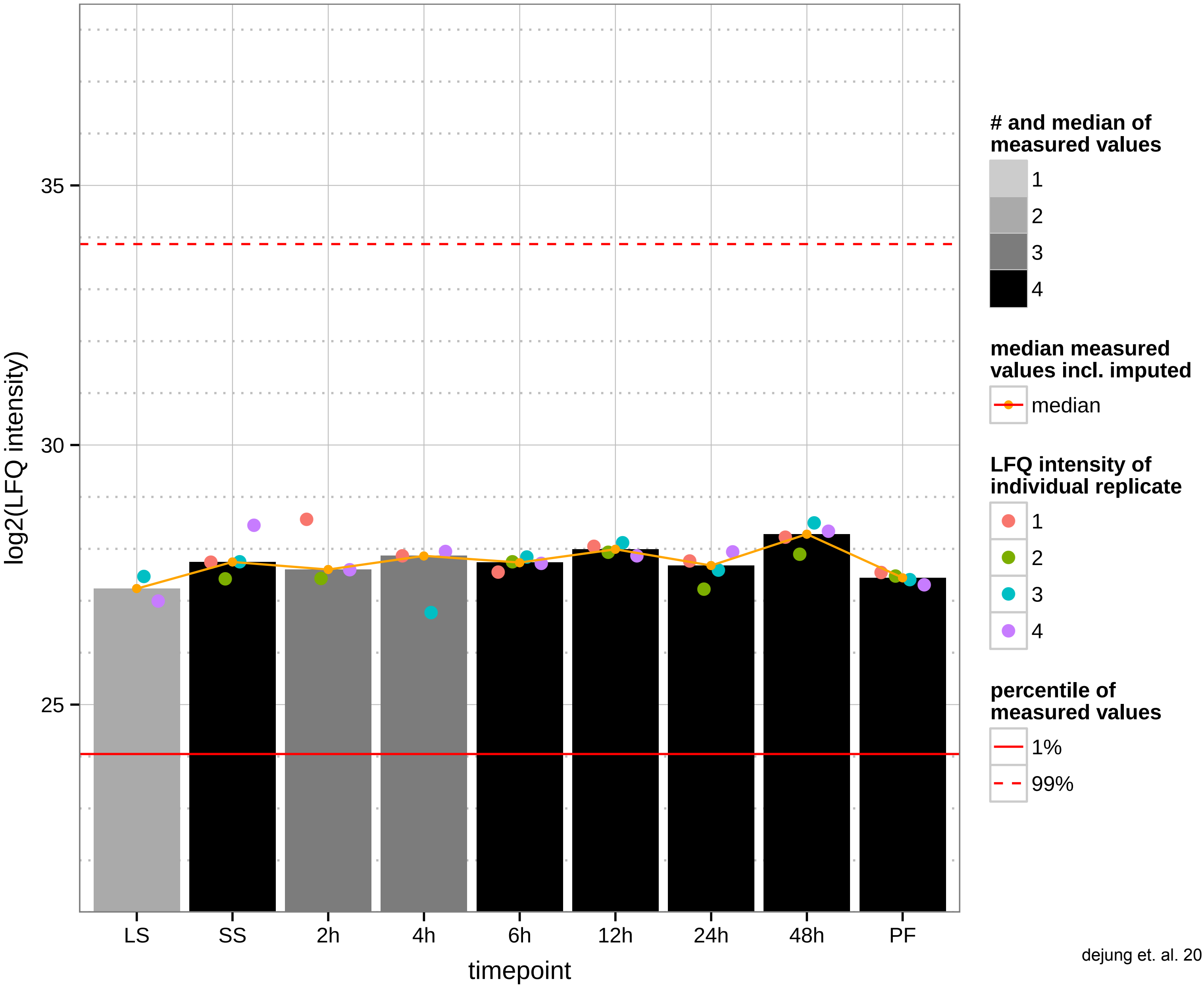
retrotransposon hot spot protein (RHS, pseudogene), putative
Tb927.1.450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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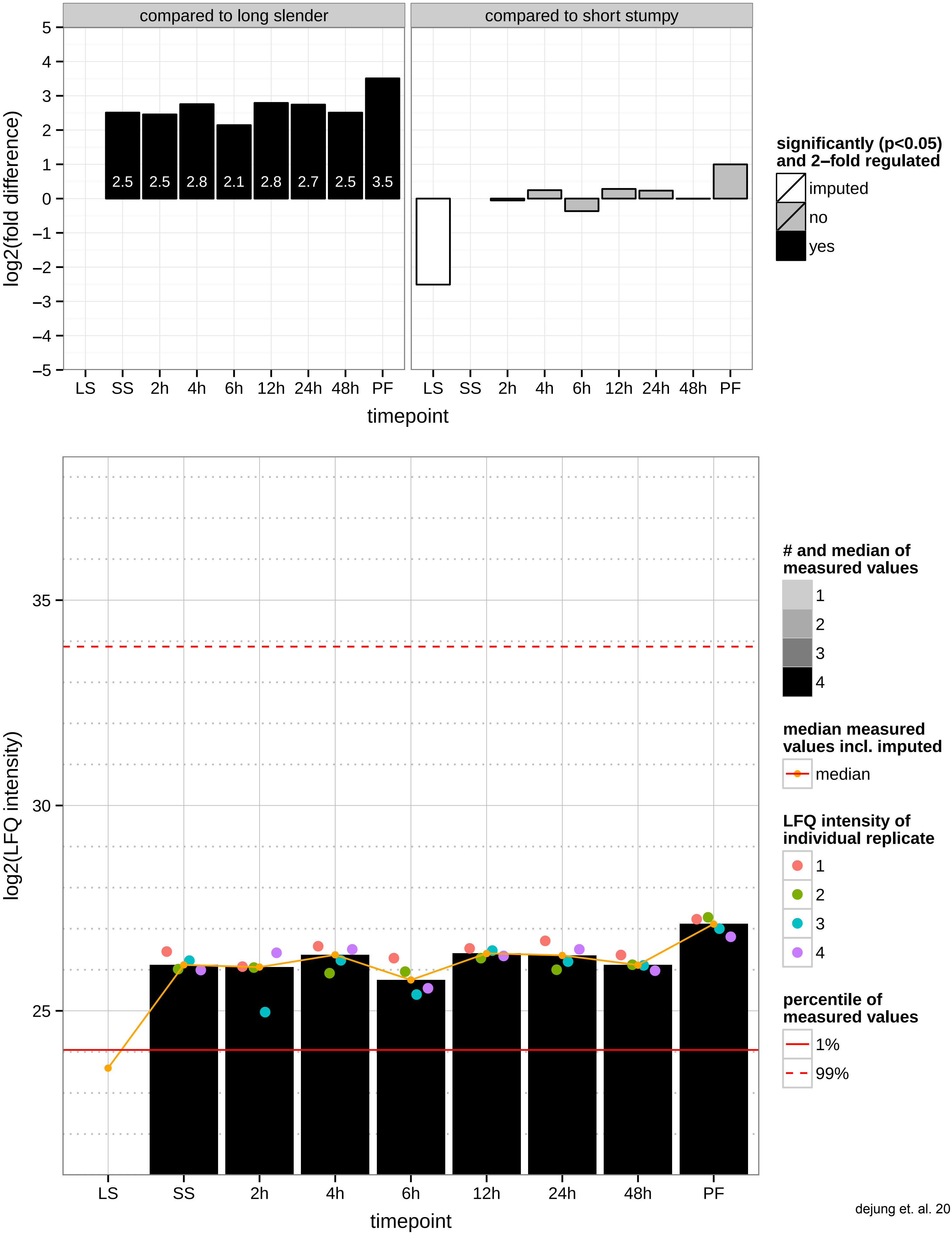
hypothetical protein, conserved
Tb927.1.4680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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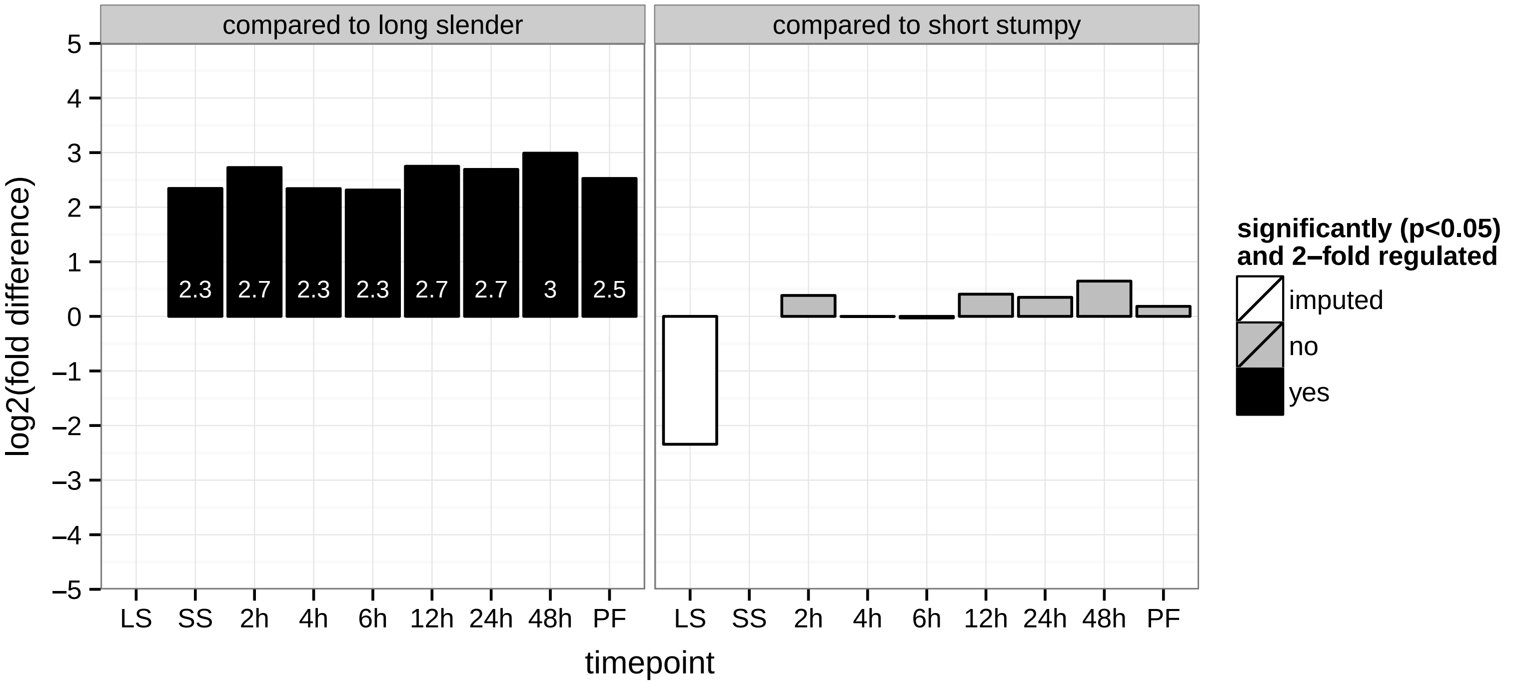
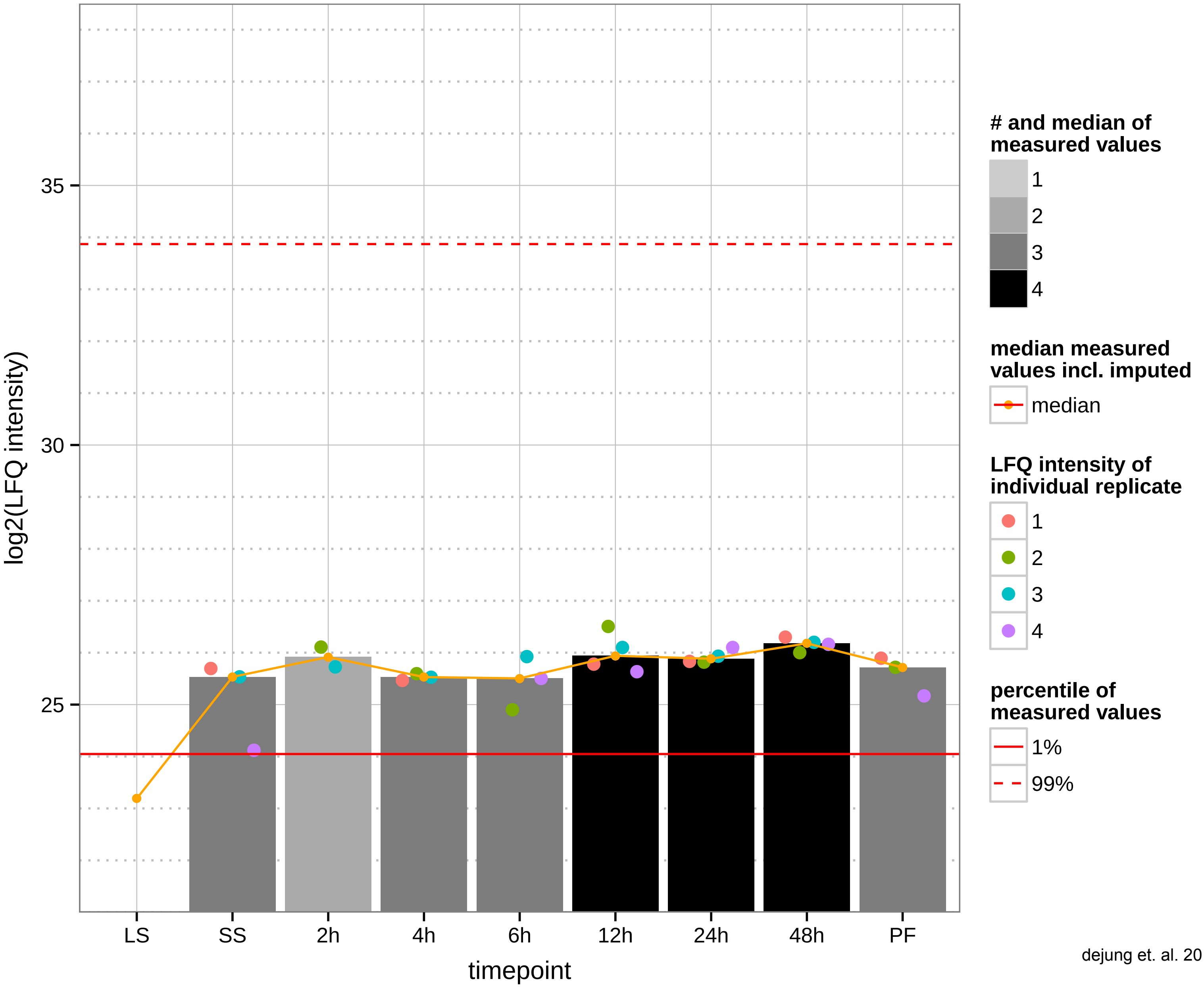
hypothetical protein, conserved
Tb927.1.4720
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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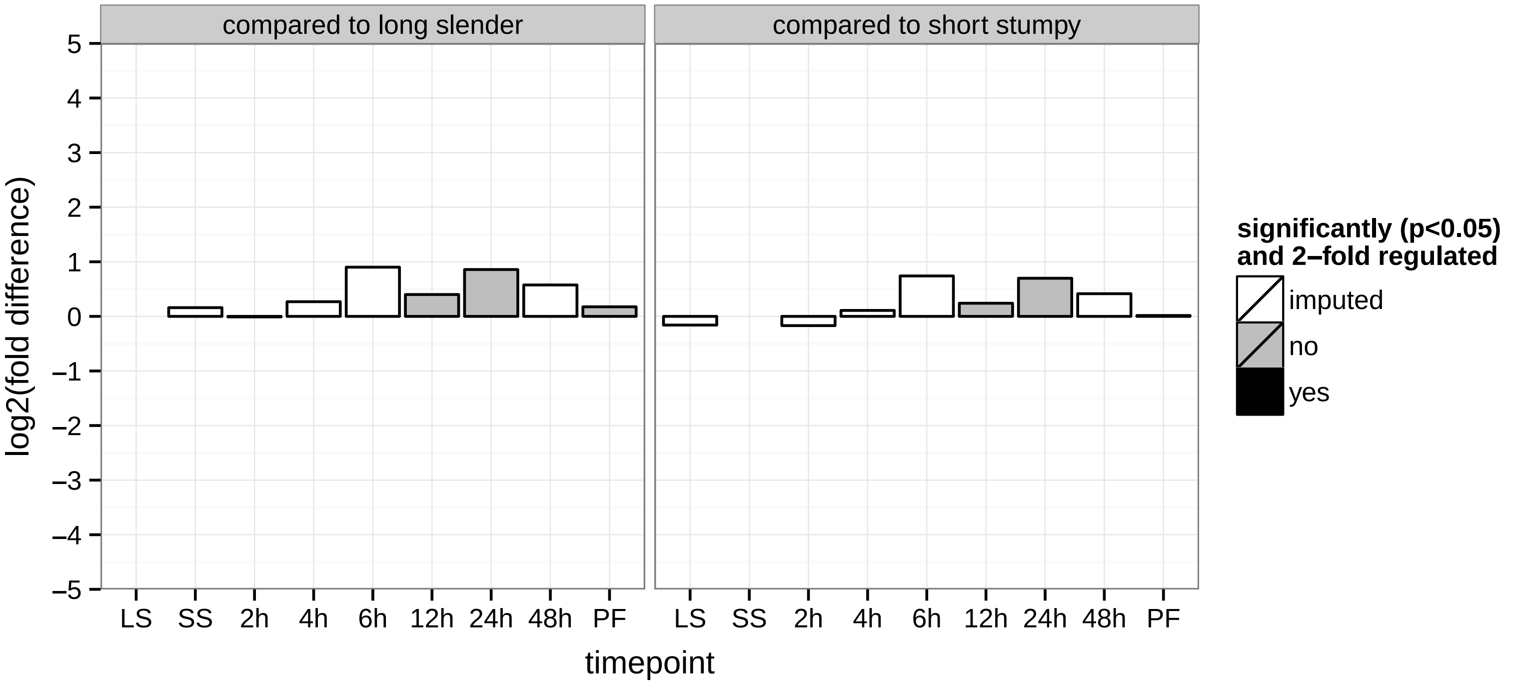
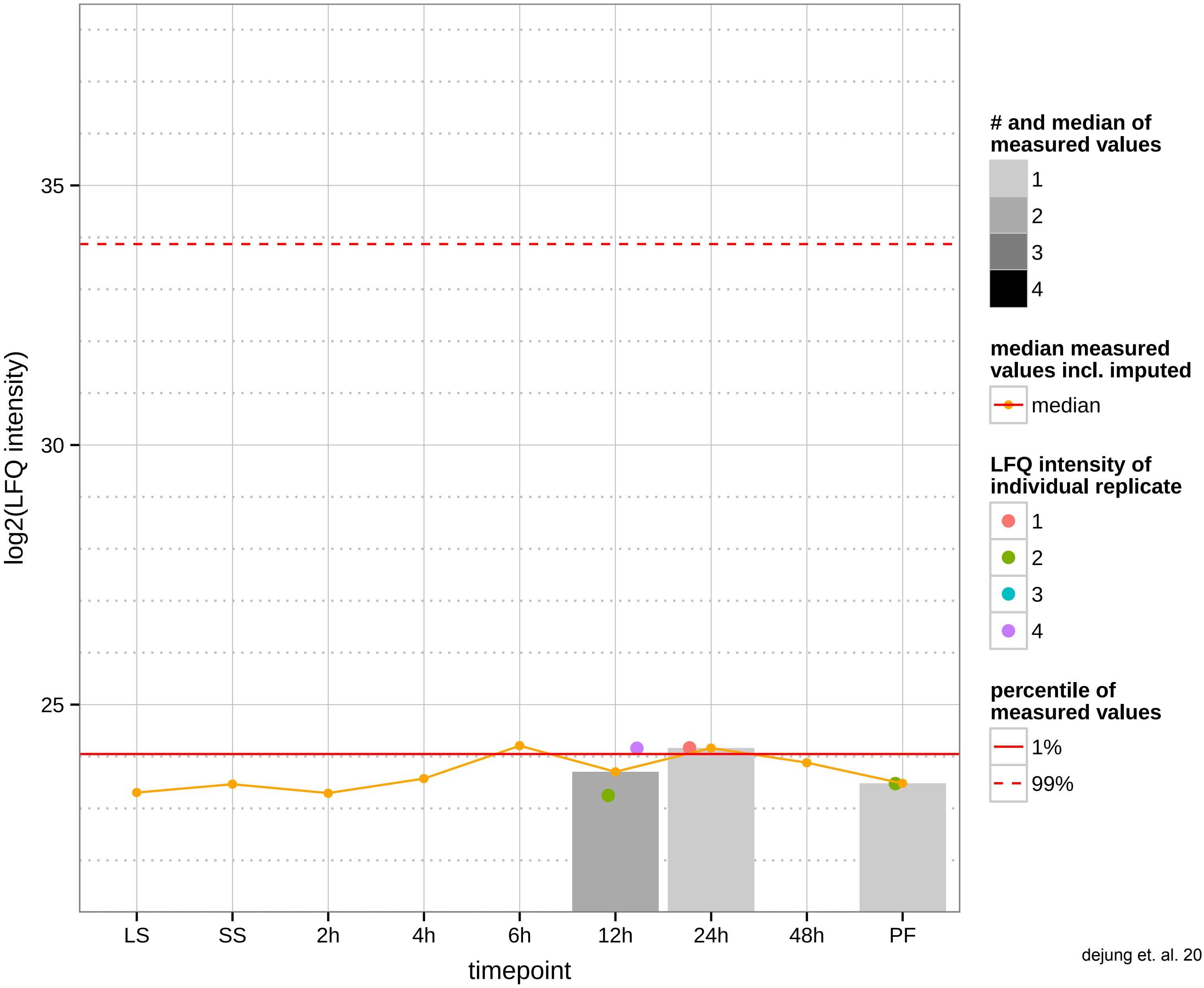
hypothetical protein, conserved
Tb927.1.4740
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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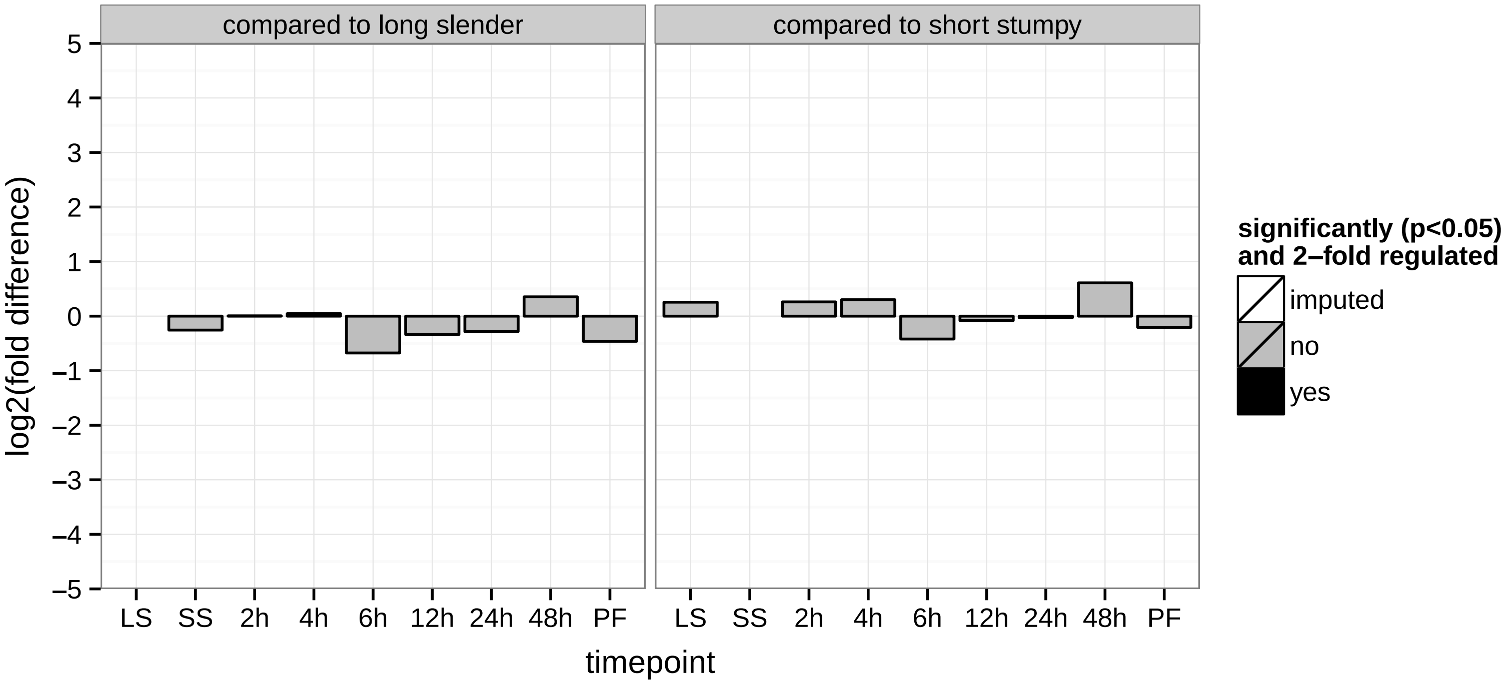
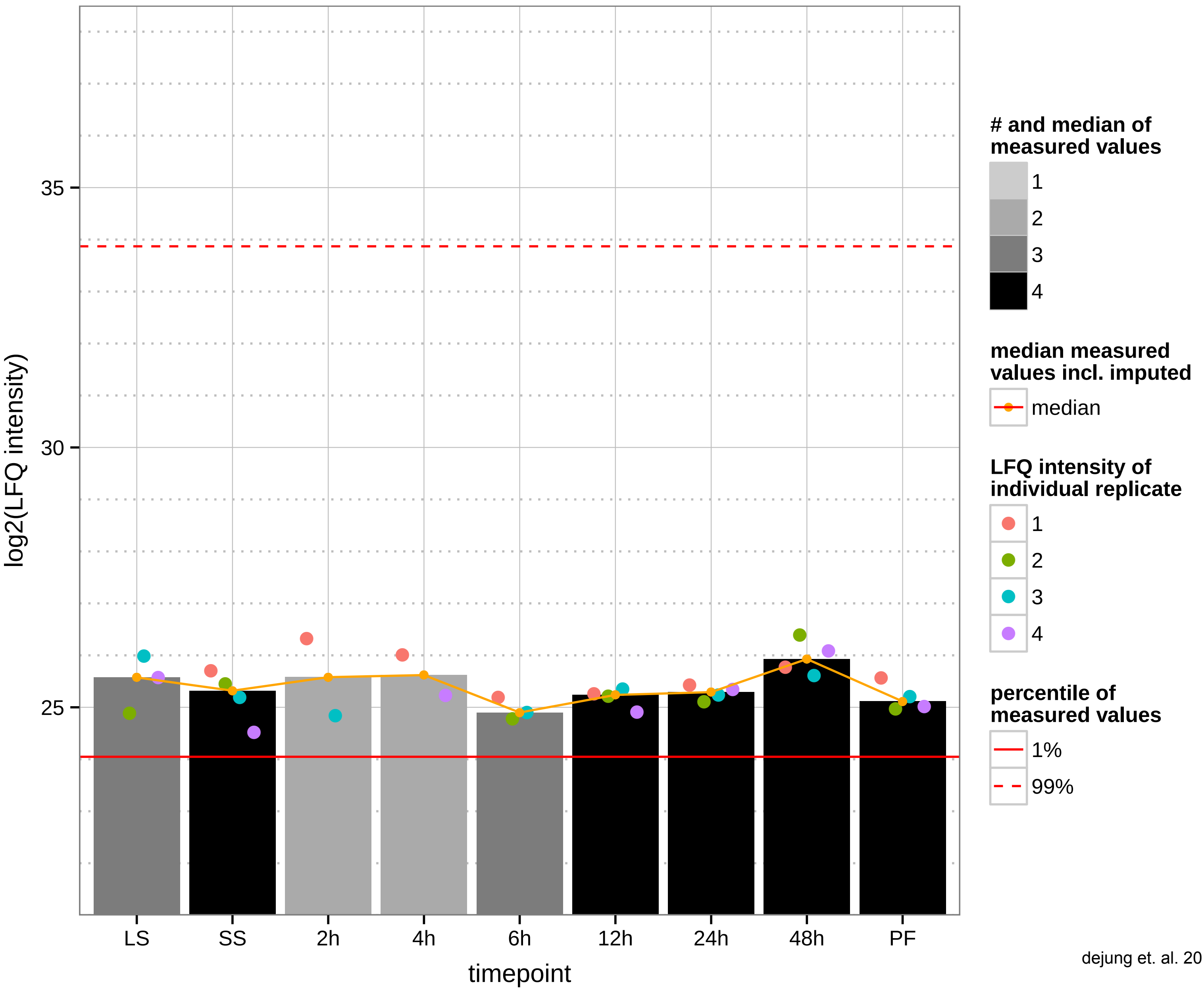
leucine–rich repeat protein (LRRP), putative
Tb927.1.5030
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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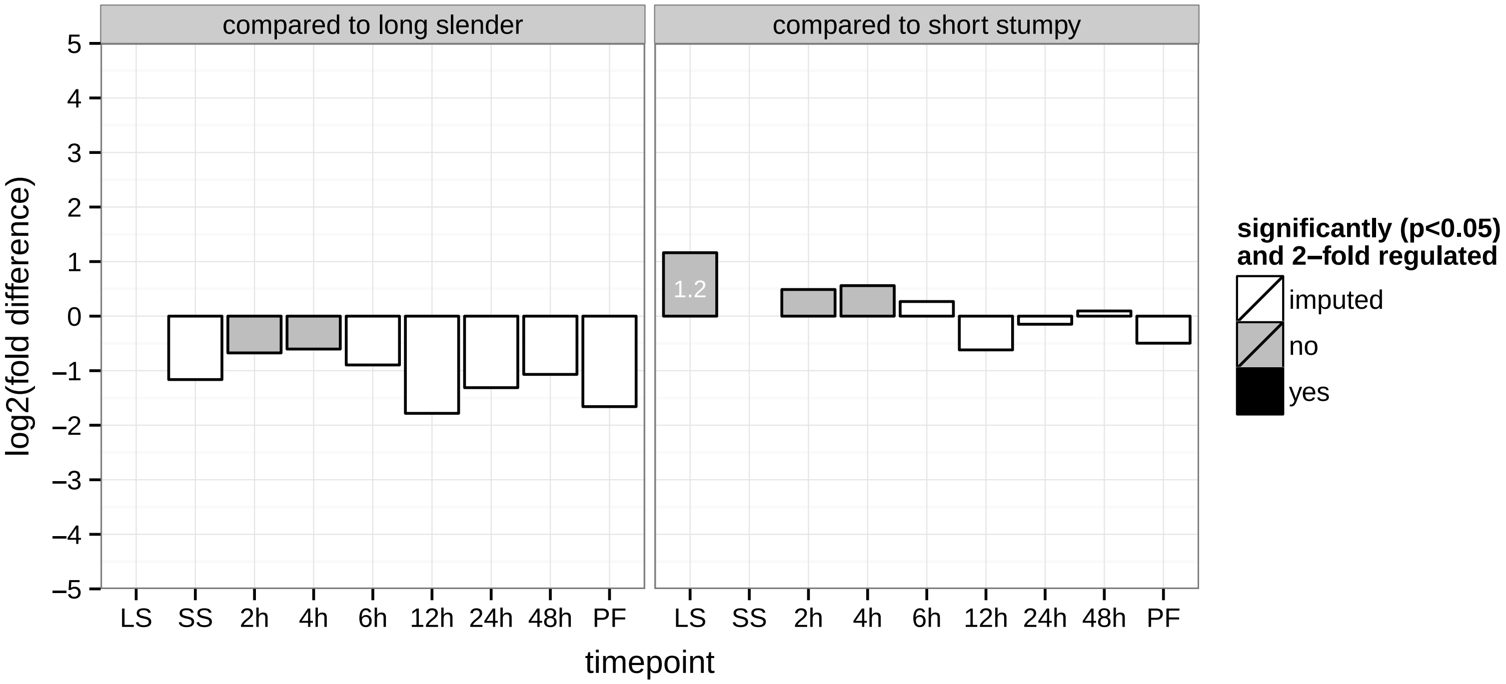
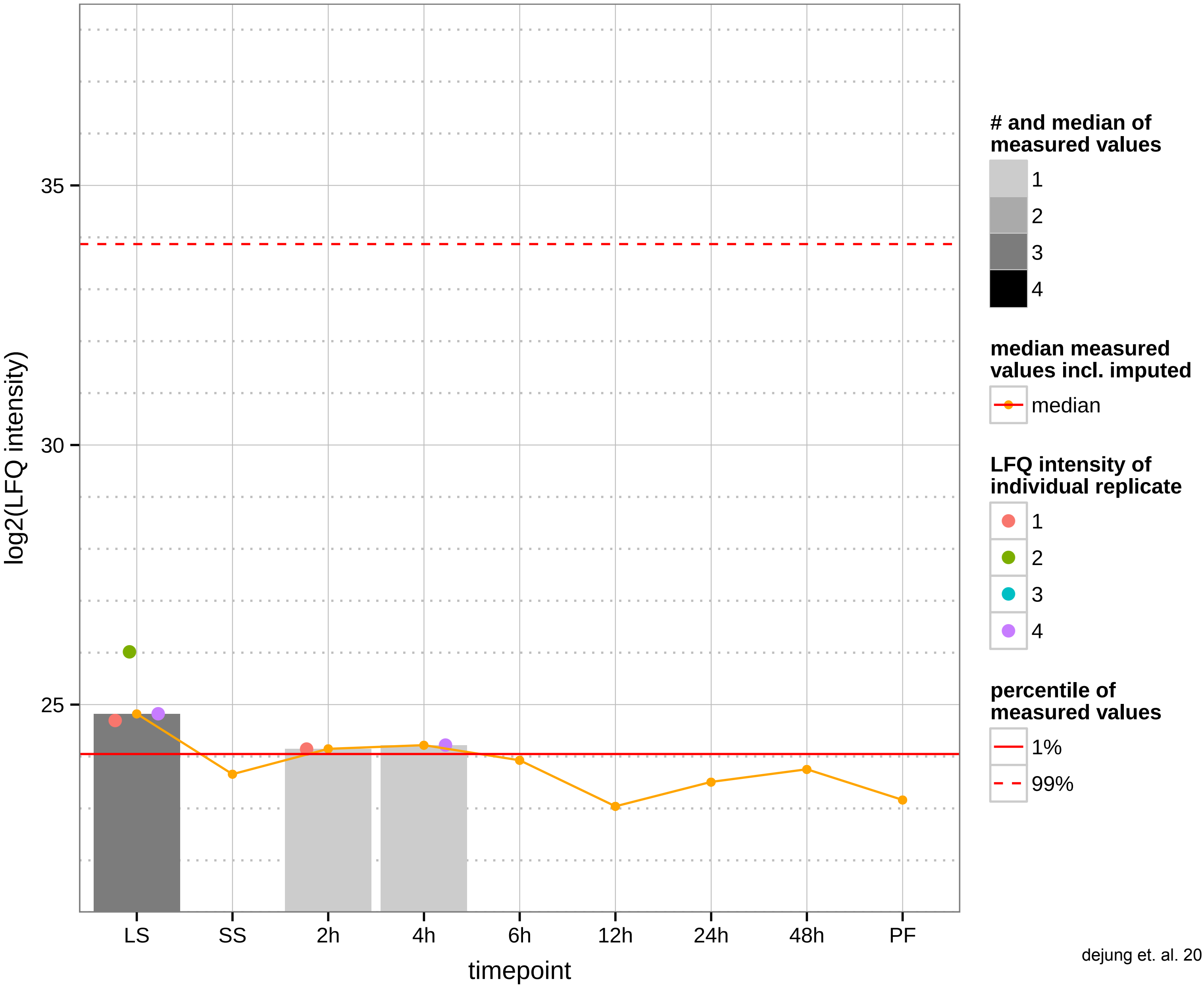
variant surface glycoprotein (VSG)–related, putative
Tb927.1.5170
AGOF: host cell surface receptor binding
AGOC: integral to membrane
AGOP: antigenic variation, symbiosis, encompassing mutualism through parasitism
PGOF: null
PGOC: null
PGOP: null





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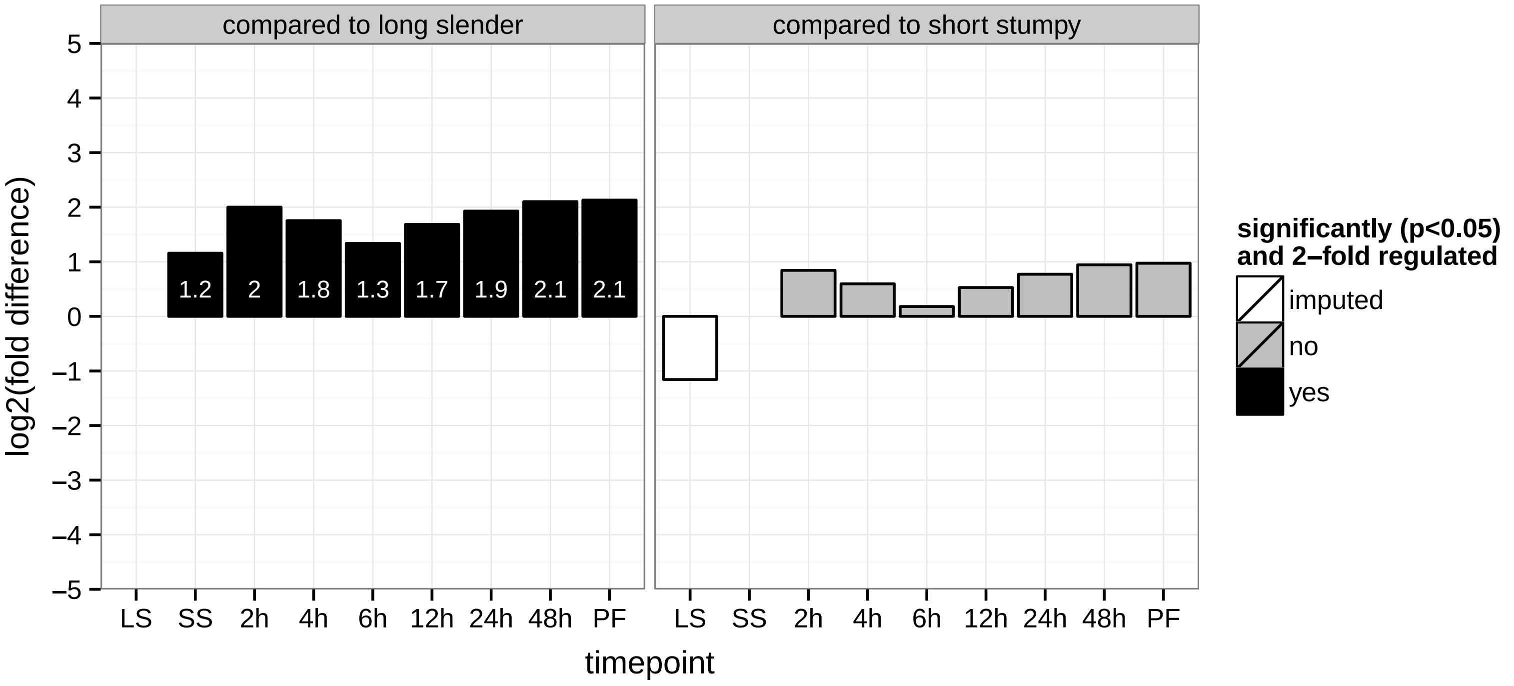
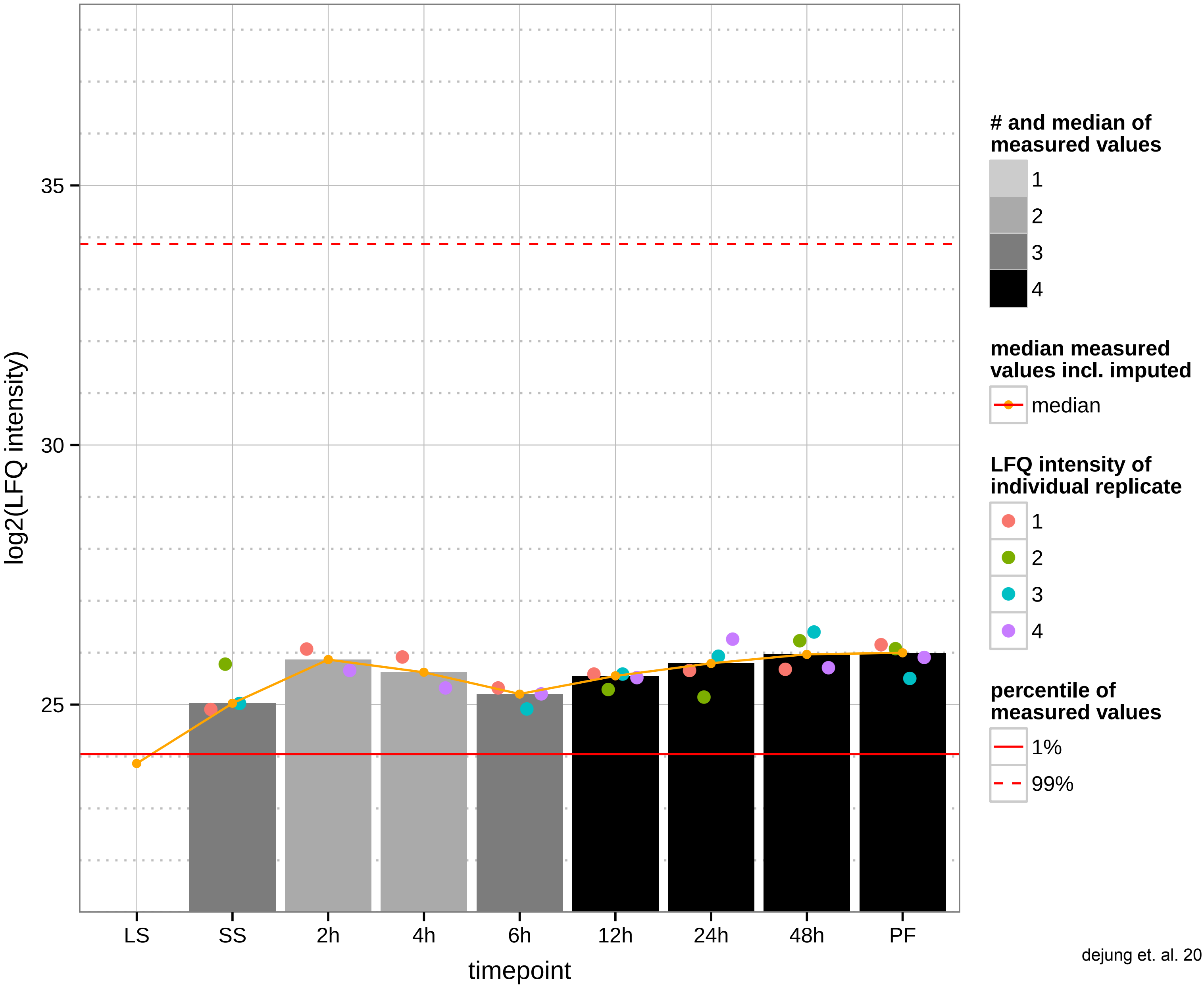
DNA–directed RNA polymerase III, putative, RNA polymerase subunit, putative (RPC128), RNA polymerase (pseudogene), D
Tb927.1.540
AGOF: DNA binding, DNA–directed RNA polymerase activity, ribonucleoside binding
AGOC: DNA–directed RNA polymerase III complex, null
AGOP: transcription from RNA polymerase III promoter, transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA–dependent





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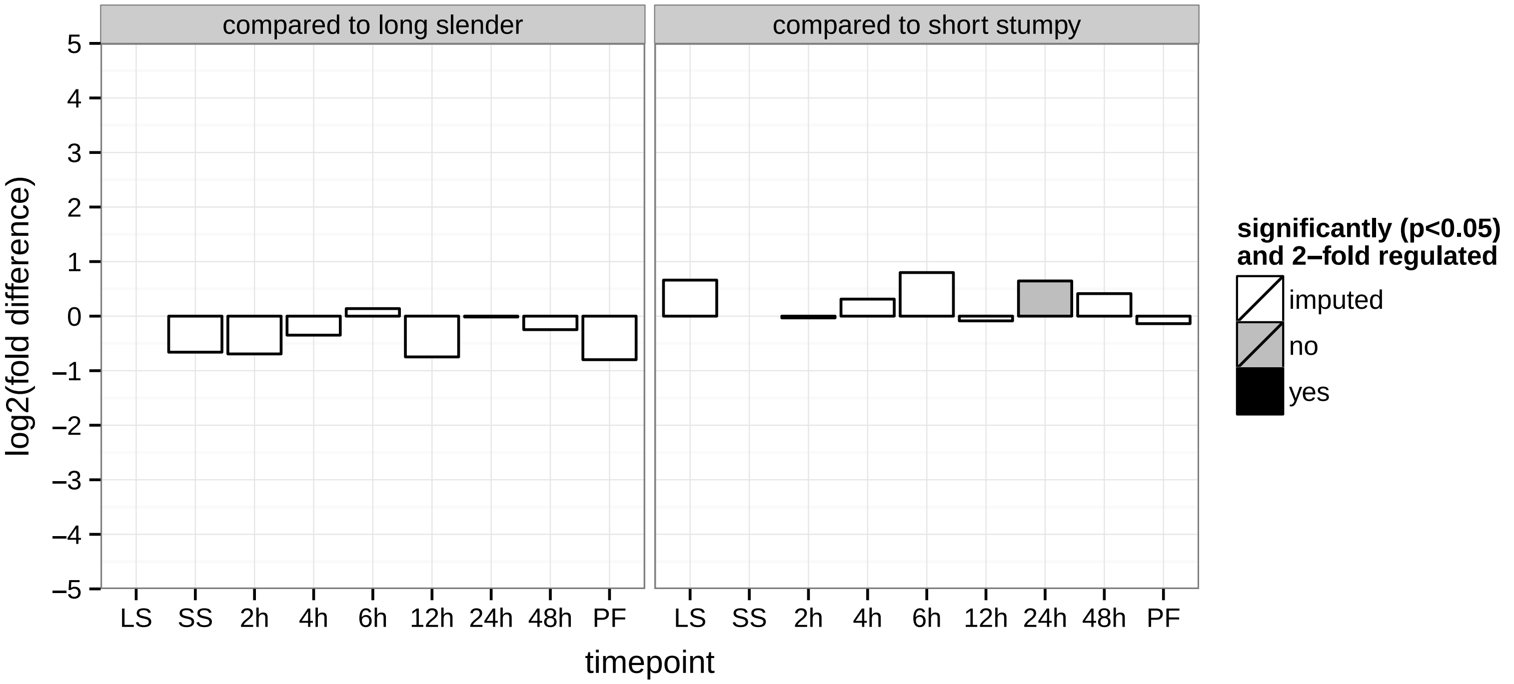
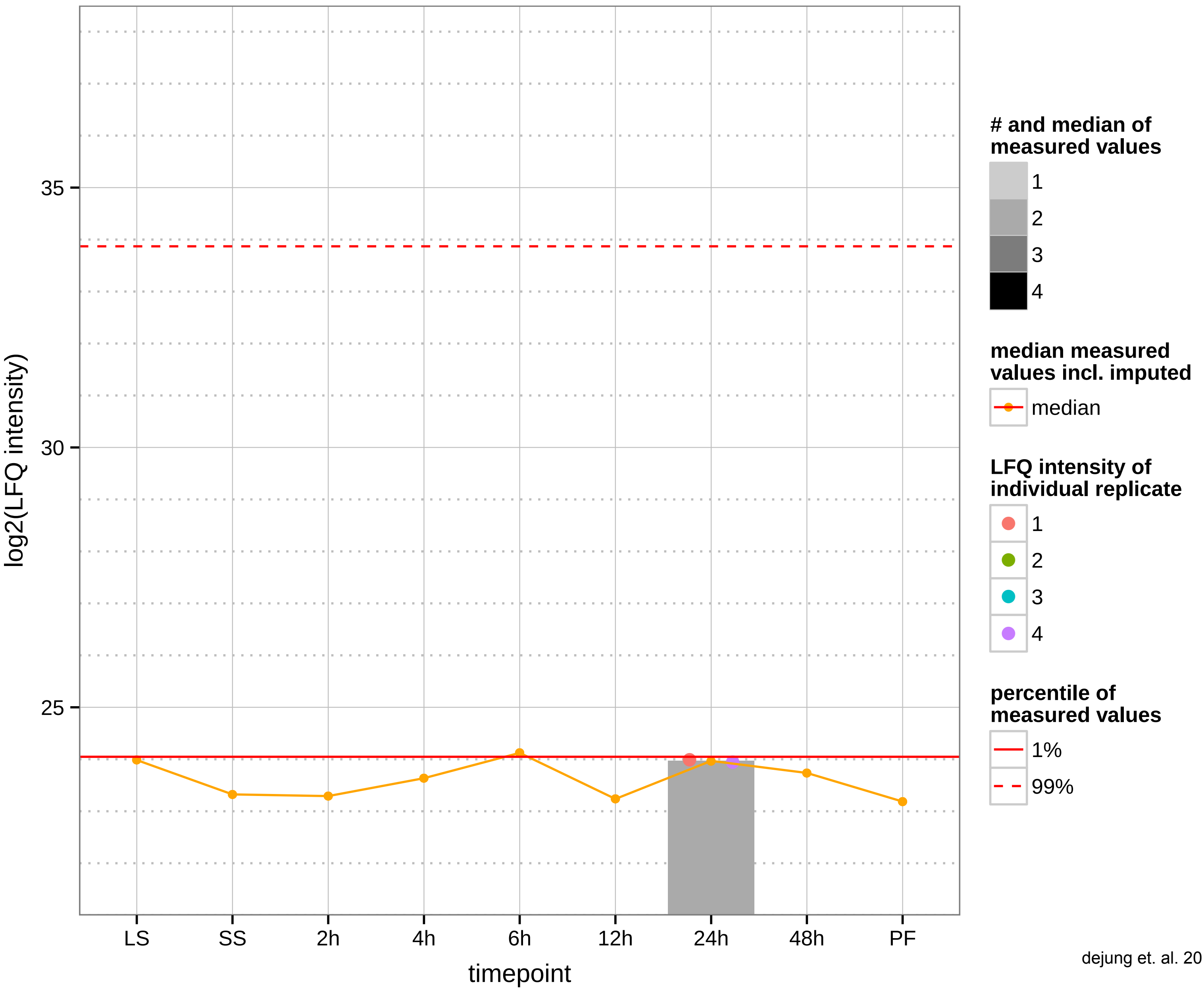
BRCA2
Tb927.1.640
AGOF: damaged DNA binding
AGOC: nucleus
AGOP: antigenic variation
PGOF: null
PGOC: null
PGOP: double–strand break repair via homologous recombination





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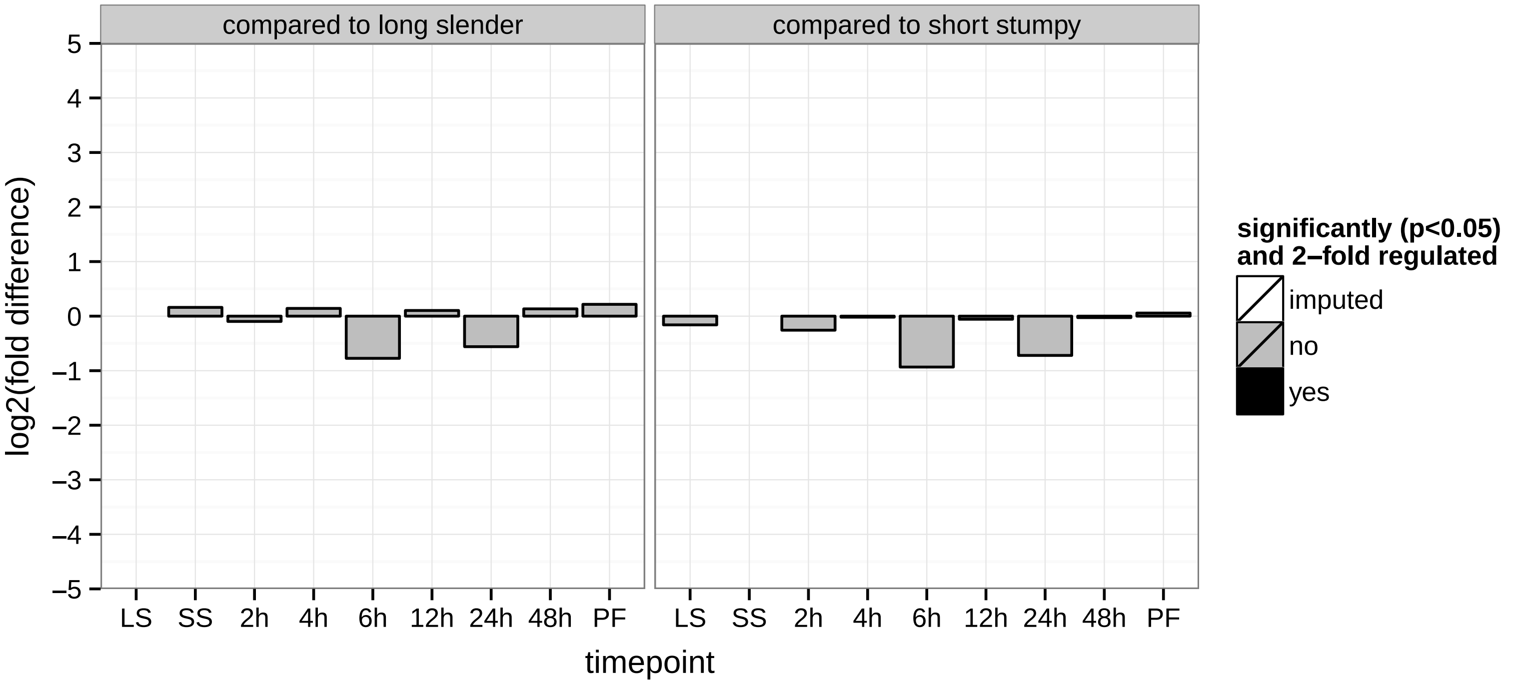
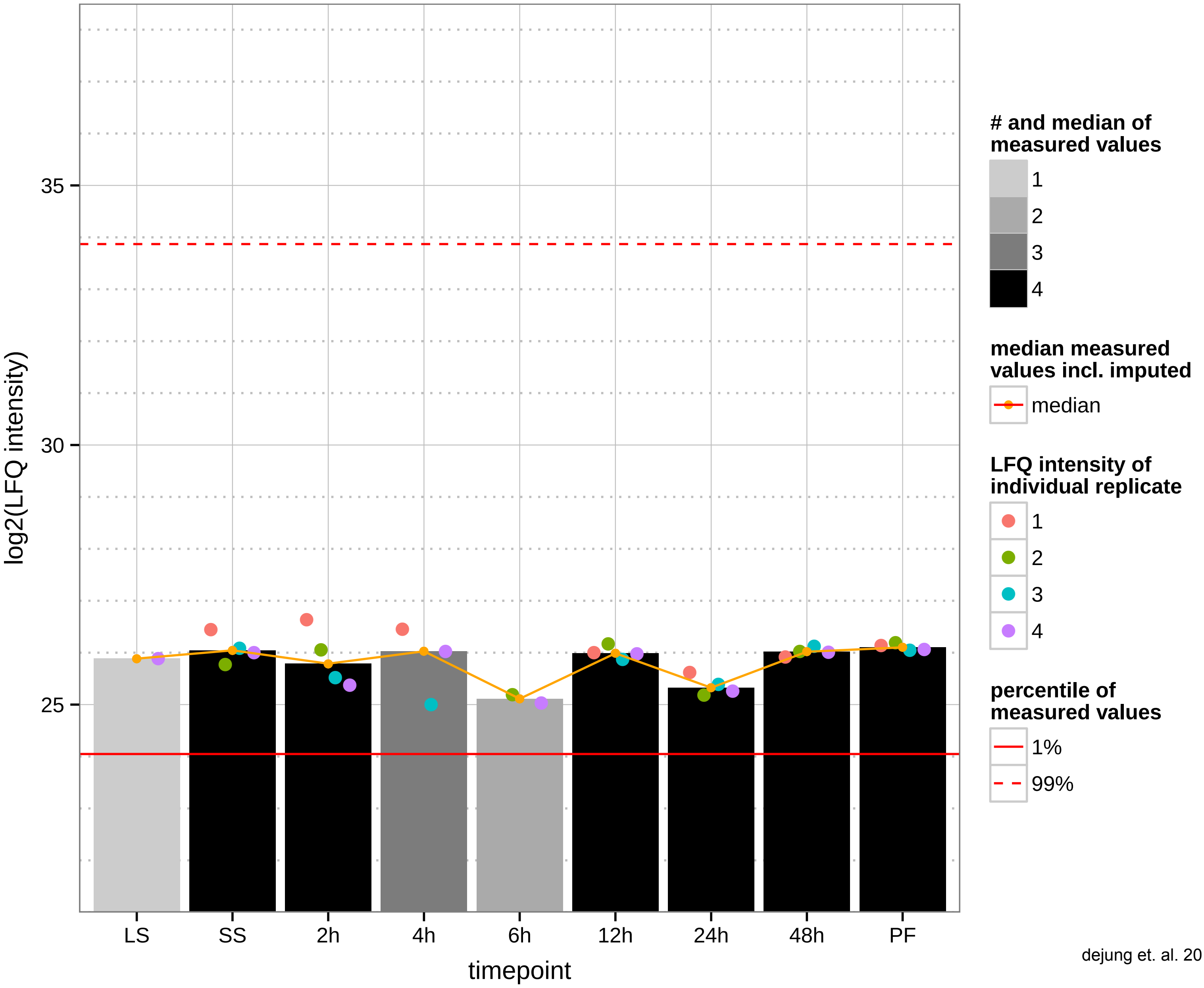
conserved protein, unknown function
Tb927.1.670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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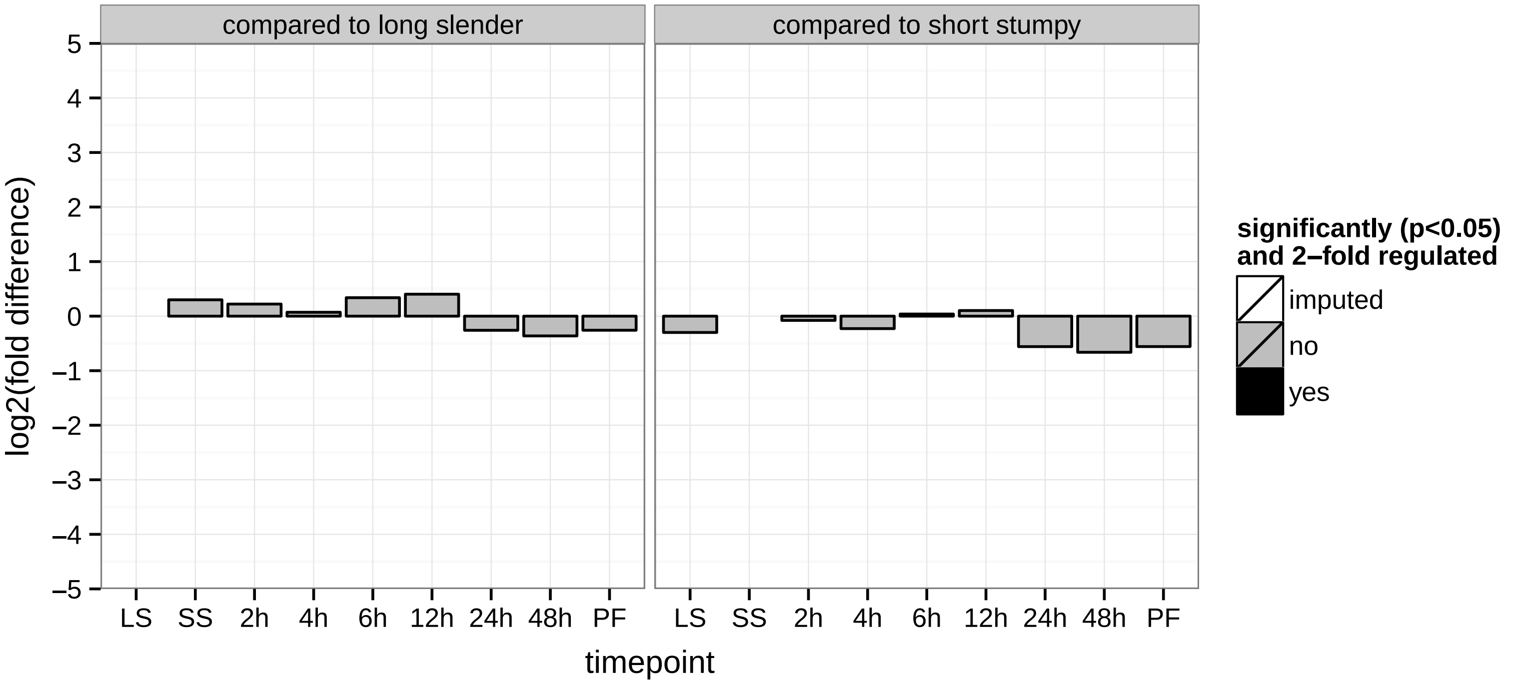
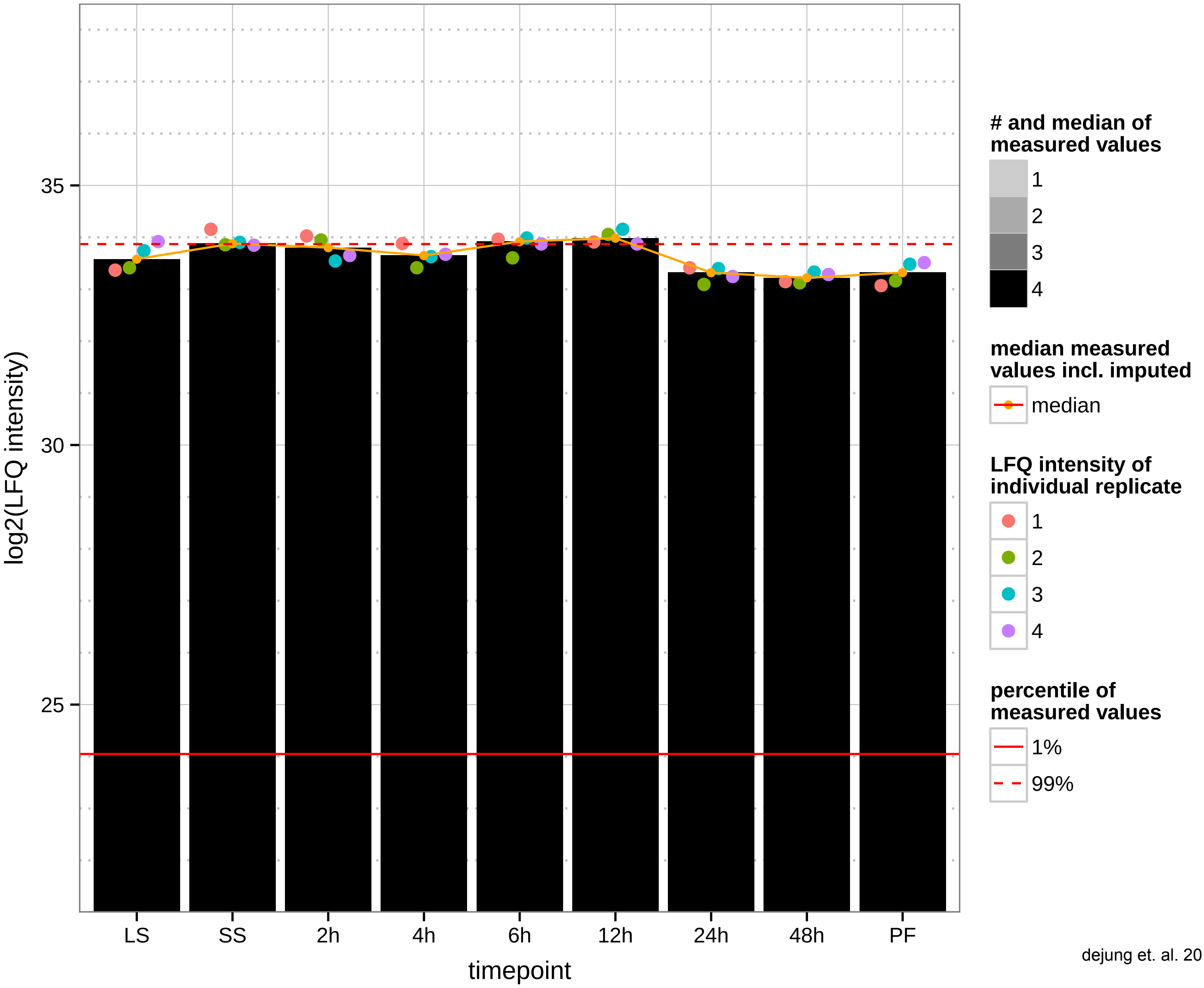
phosphoglycerate kinase (PGKC)
Tb927.1.700
AGOF: phosphoglycerate kinase activity
AGOC: glycosome
AGOP: glycolysis
PGOF: phosphoglycerate kinase activity
PGOC: null
PGOP: glycolysis





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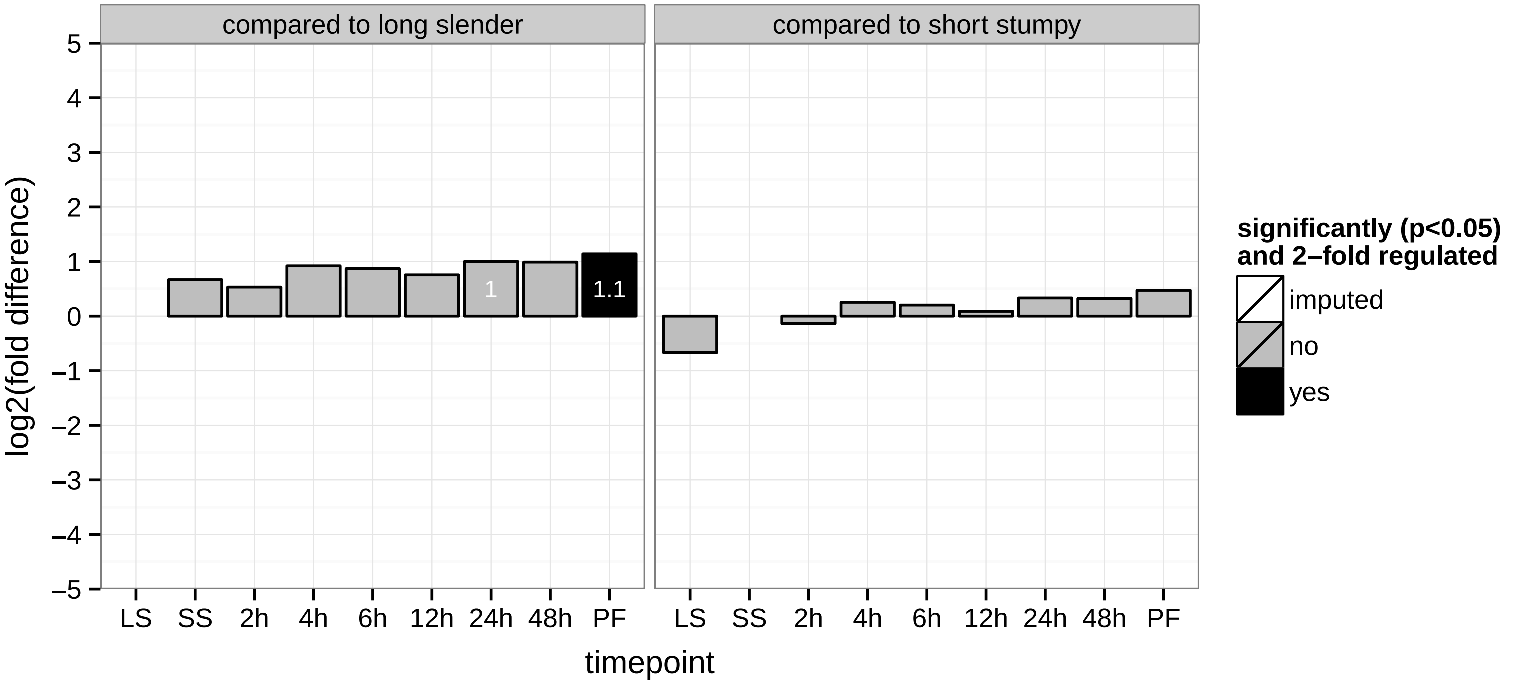
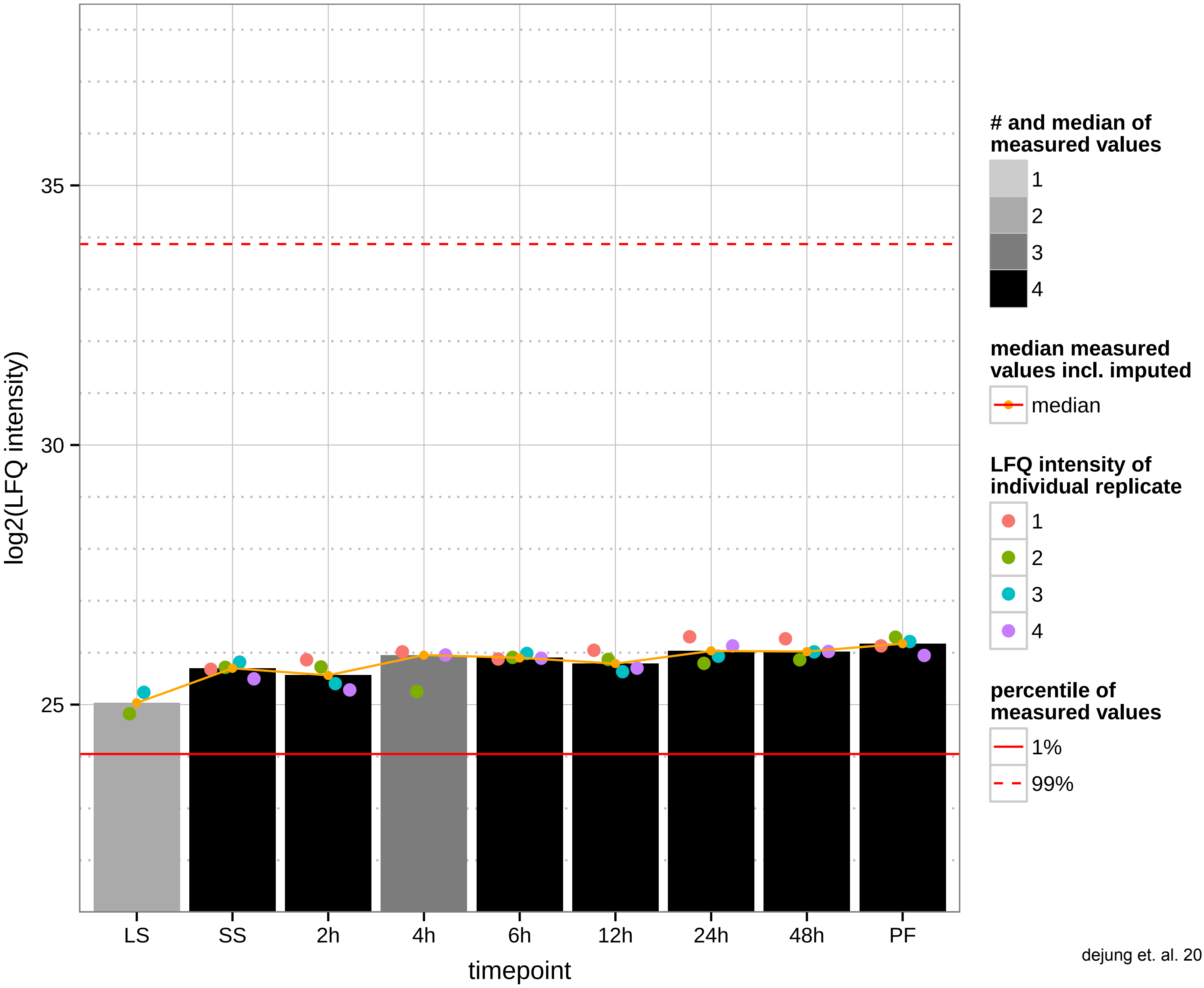
deoxyhypusine synthase, putative
Tb927.1.870
AGOF: null
AGOC: null
AGOP: deoxyhypusine biosynthetic process from spermidine, peptidyl–lysine modification to hypusine
PGOF: null
PGOC: null
PGOP: peptidyl–lysine modification to hypusine





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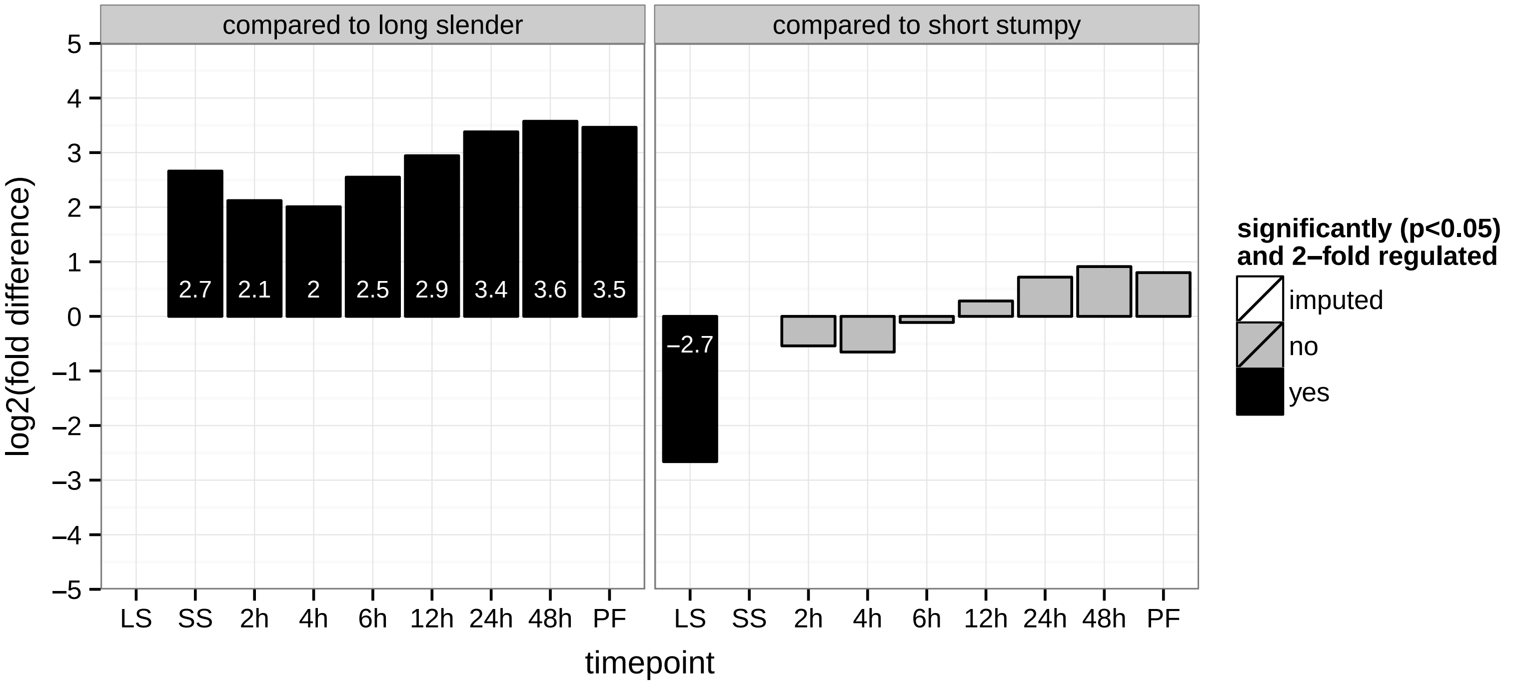
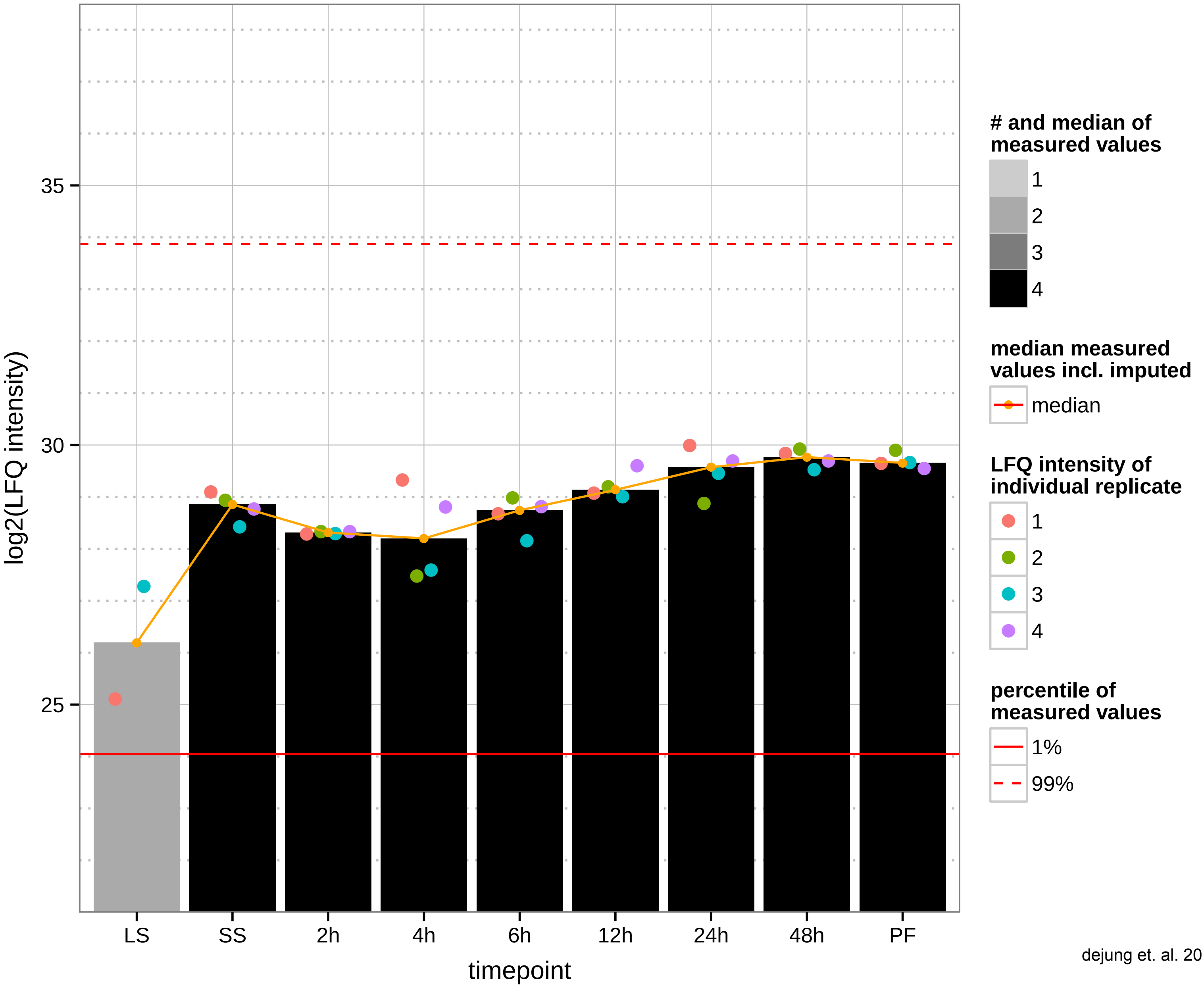
hypothetical protein, conserved, Midasin, putative (MDN1)
Tb927.1.880
AGOF: null, ATP binding, ATPase activity
AGOC: null, nucleus
AGOP: null, regulation of protein complex assembly
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding, protein binding
PGOC: null, nucleus
PGOP: null, protein complex assembly





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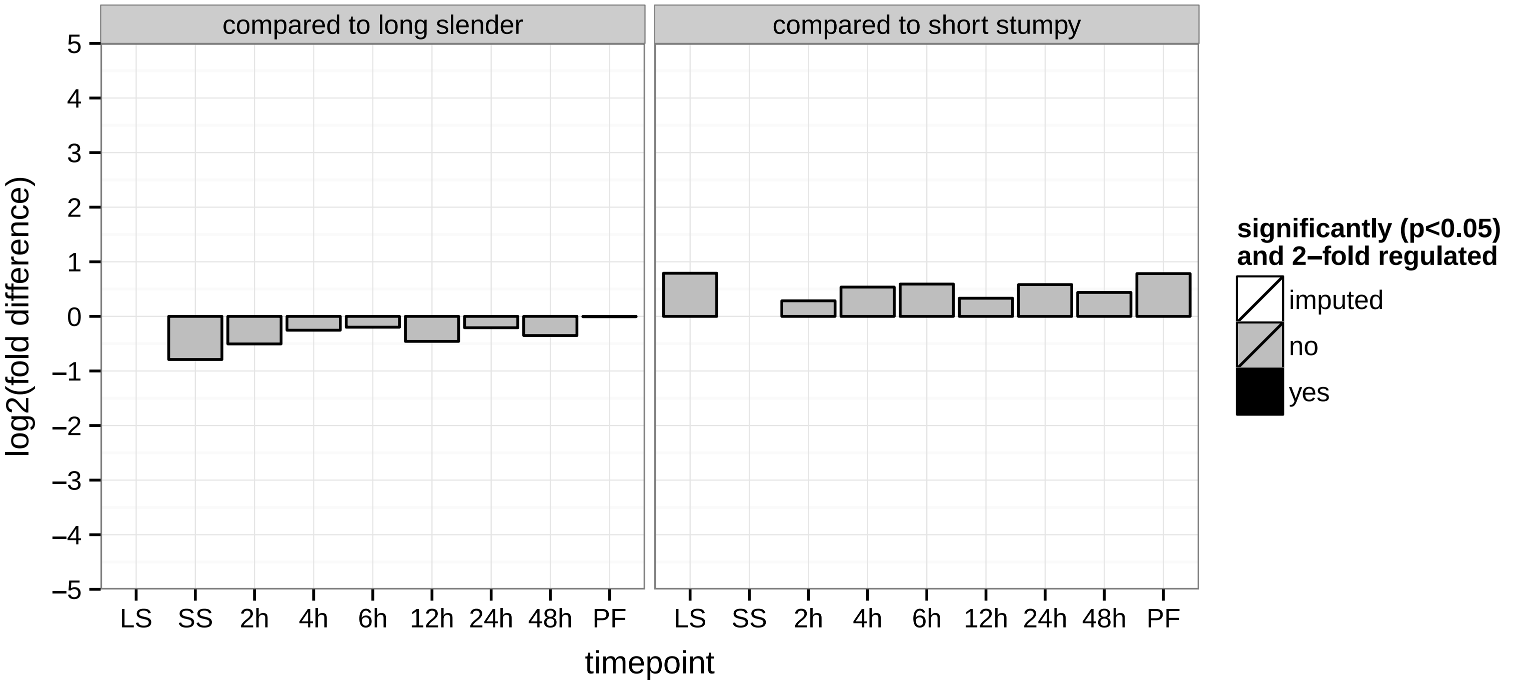
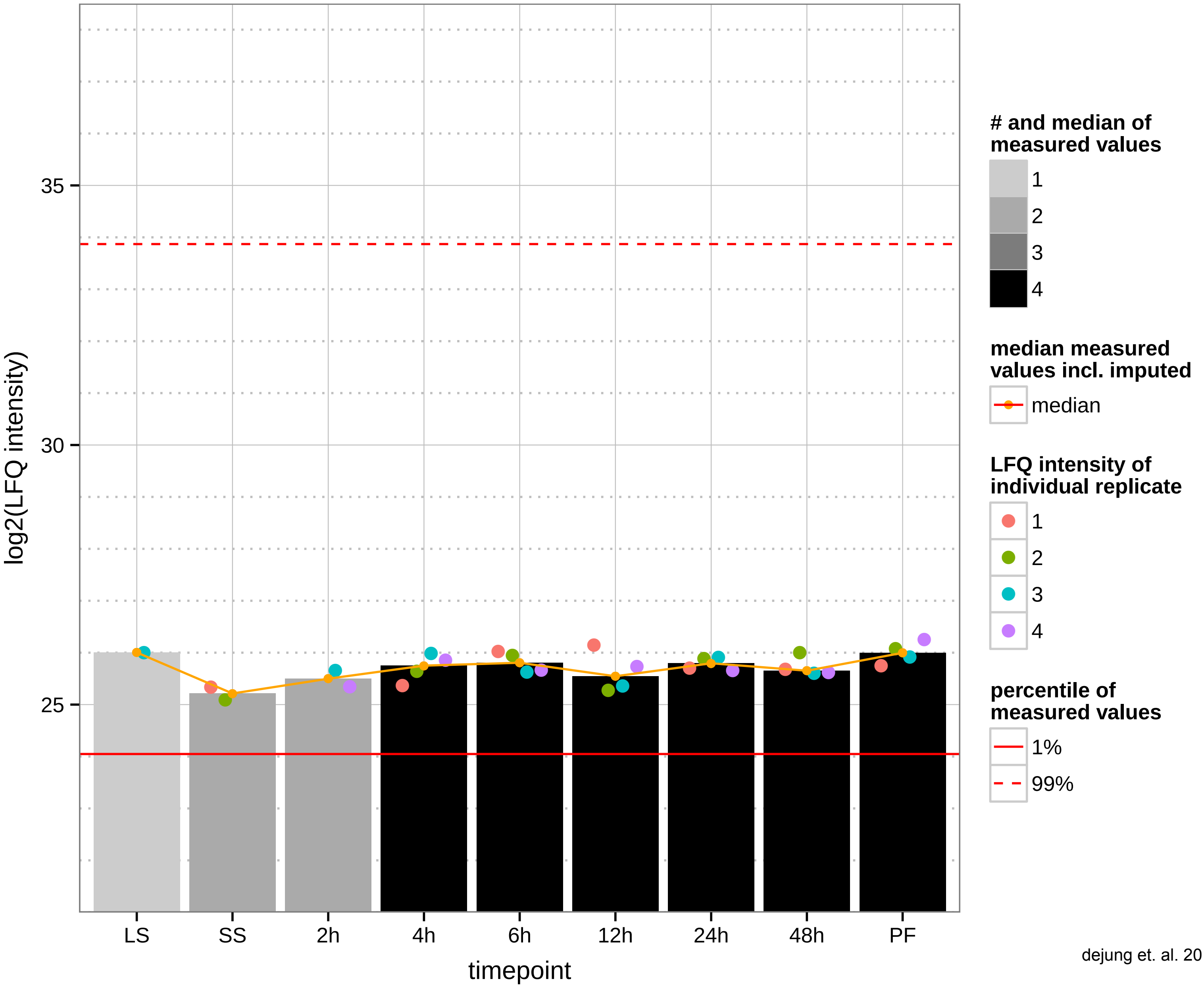
Enkuring domain–containig protein
Tb927.1.990
AGOF: calmodulin binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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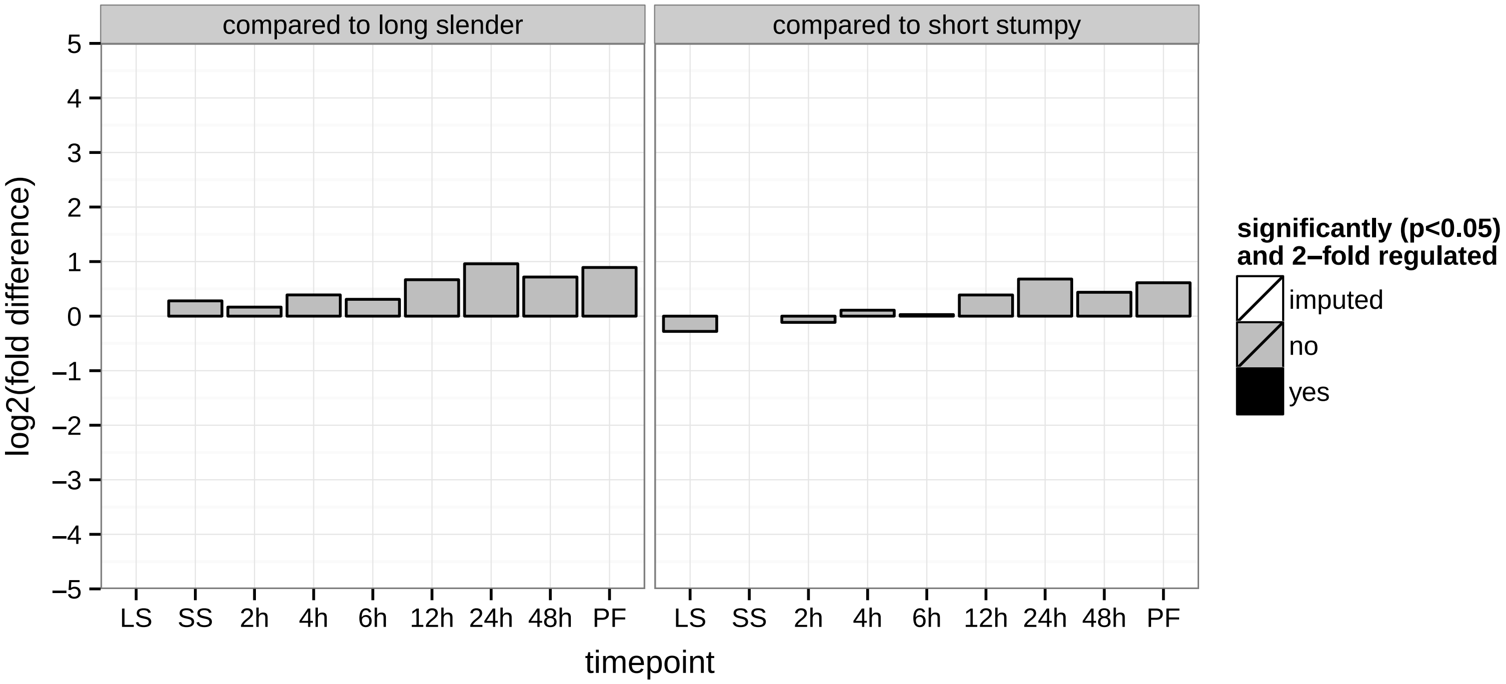
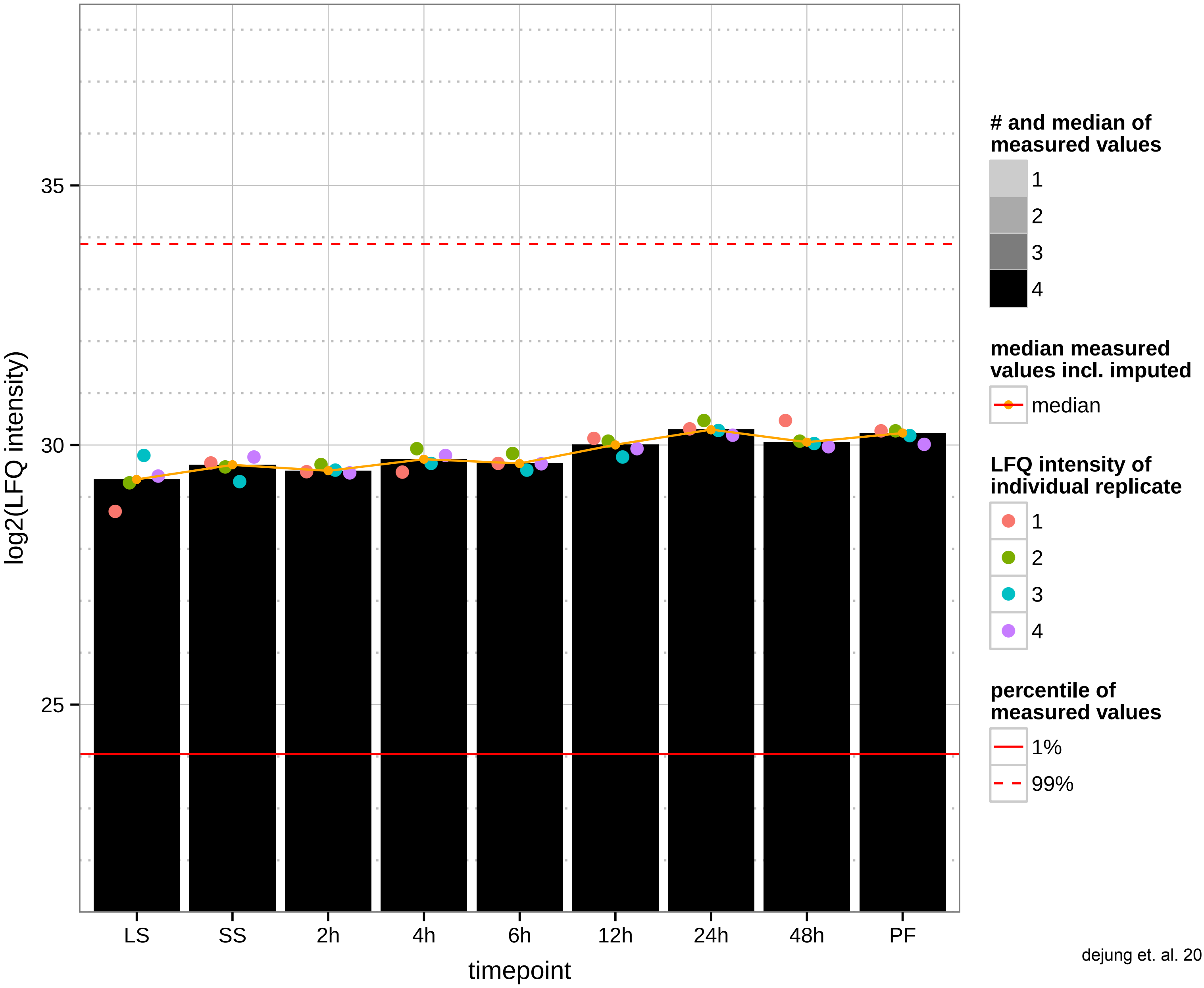
60S acidic ribosomal protein, putative
Tb927.10.10010
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null
PGOC: intracellular
PGOP: ribosome biogenesis





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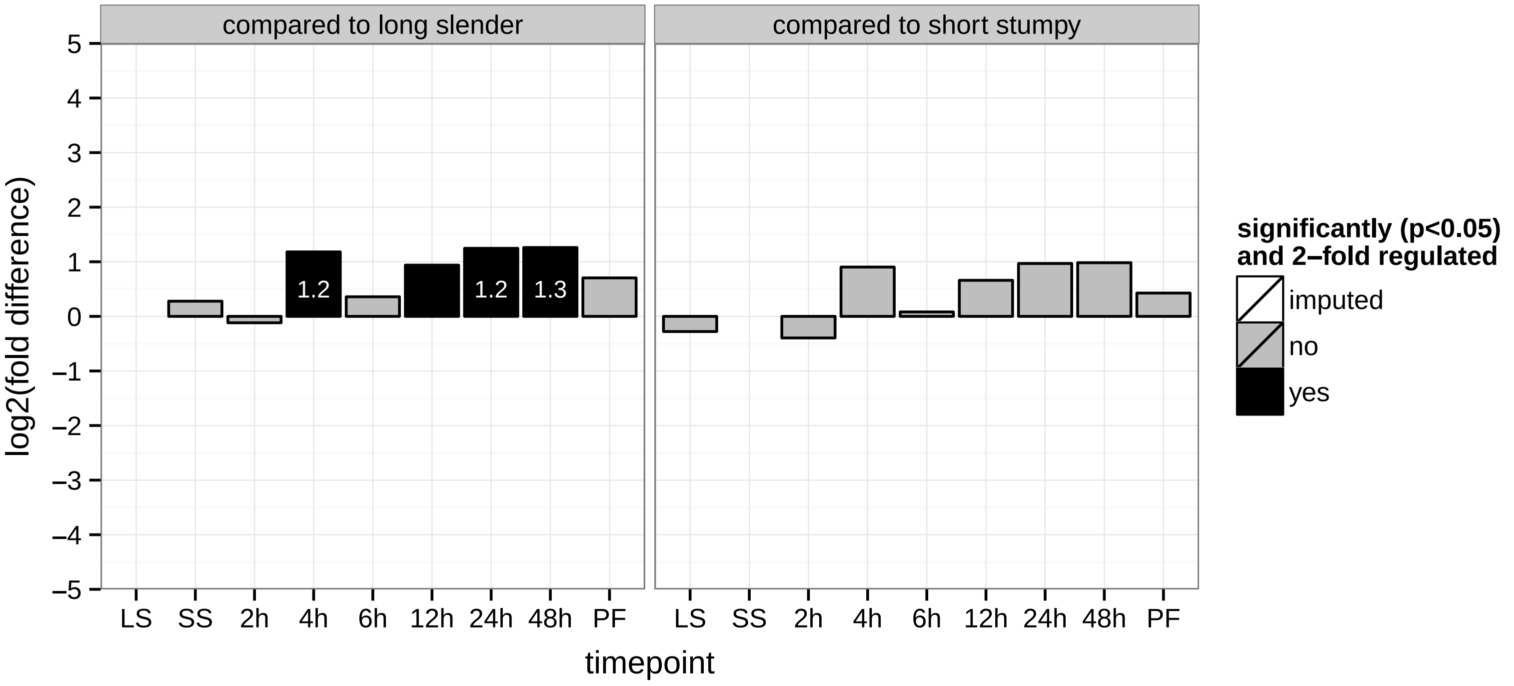
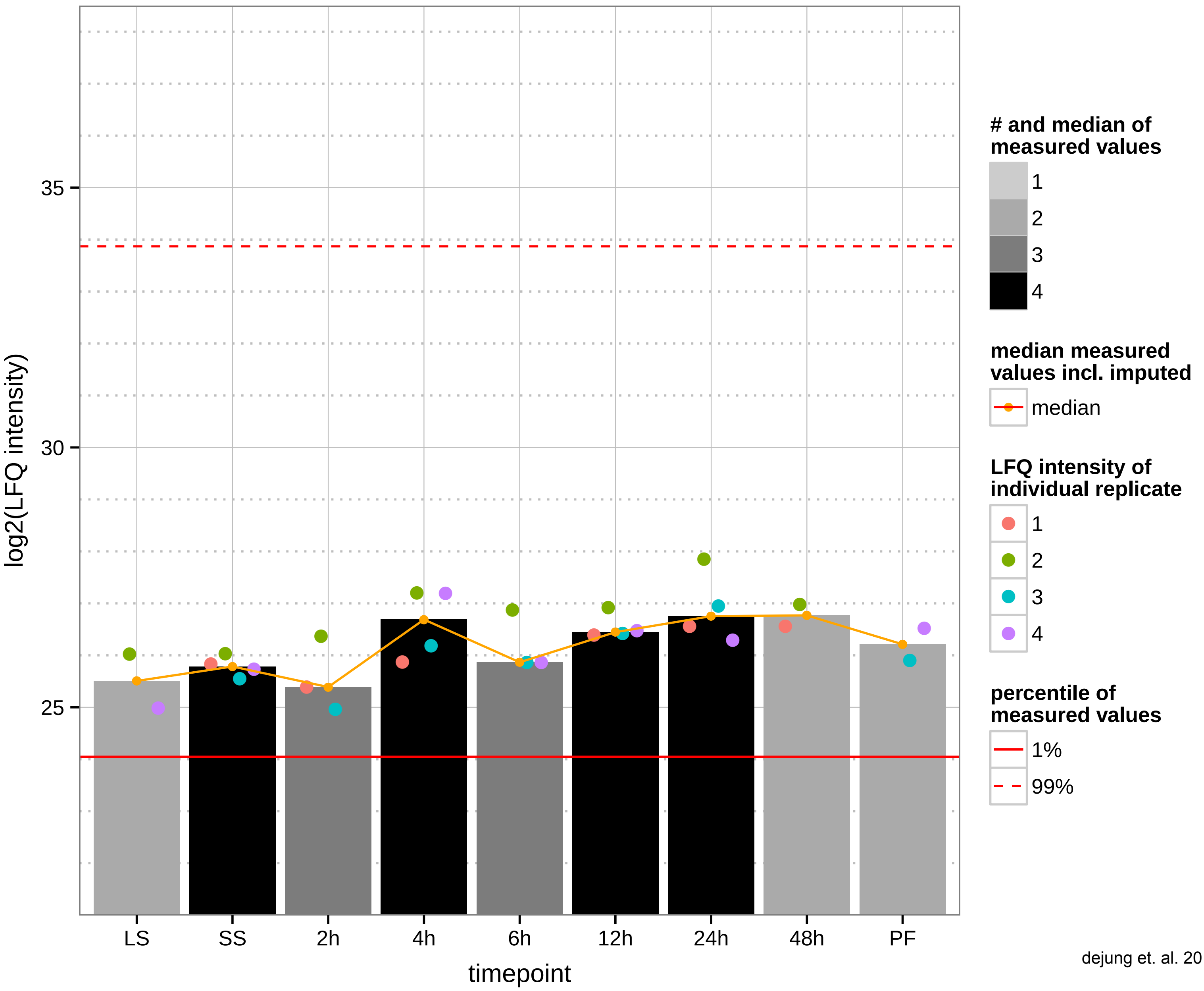
hypothetical protein, conserved
Tb927.10.10030
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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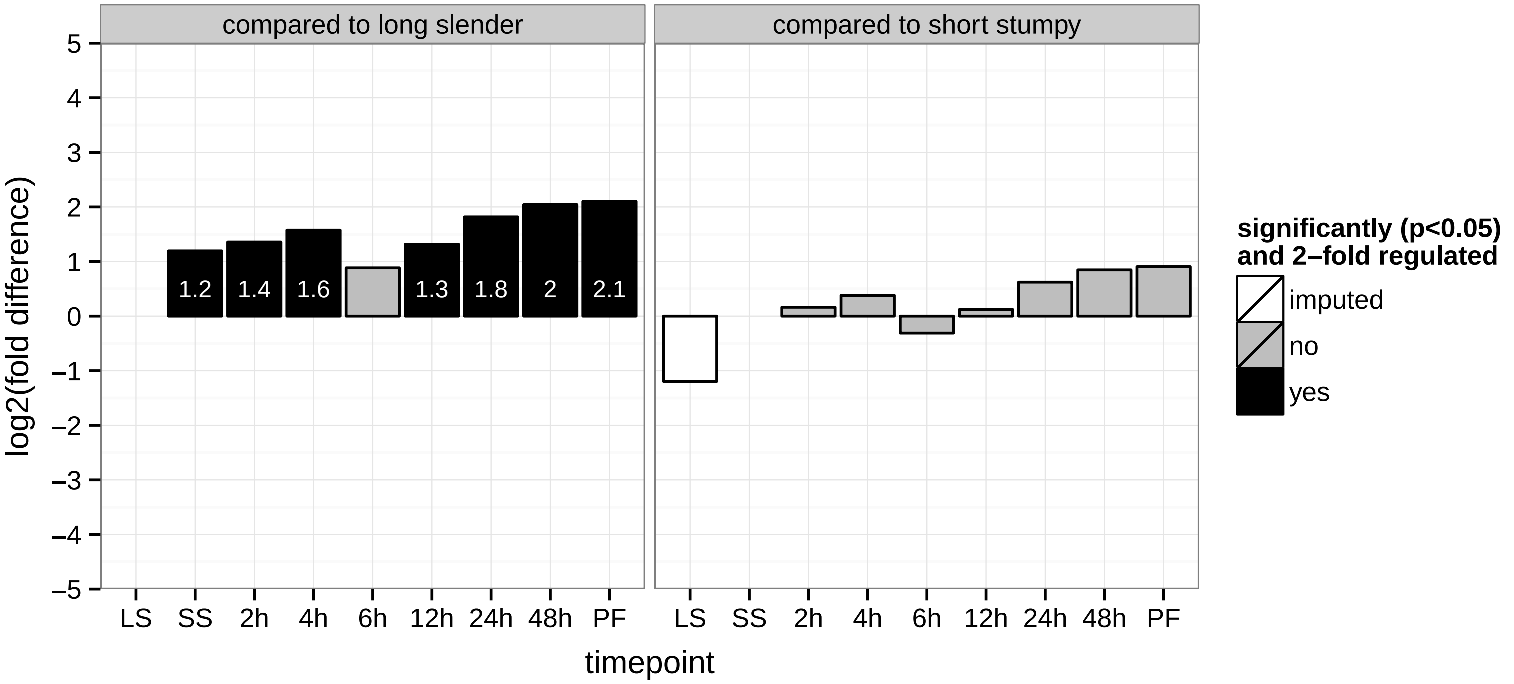
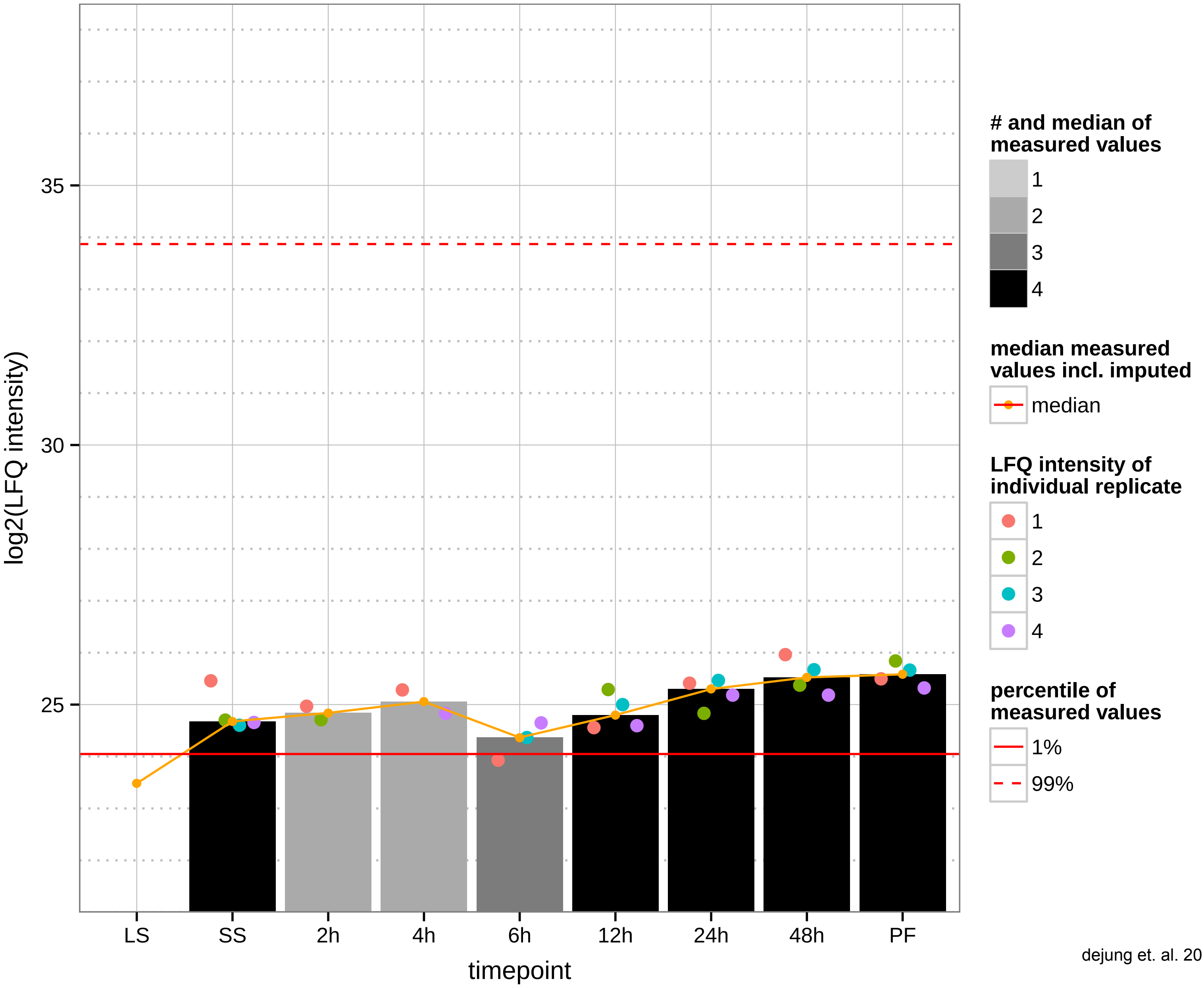
mitochondrial RNA binding complex 1 subunit (MRB10130)
Tb927.10.10130
AGOF: RNA binding
AGOC: mitochondrion
AGOP: cytidine to uridine editing, mRNA stabilization
PGOF: binding
PGOC: null
PGOP: null





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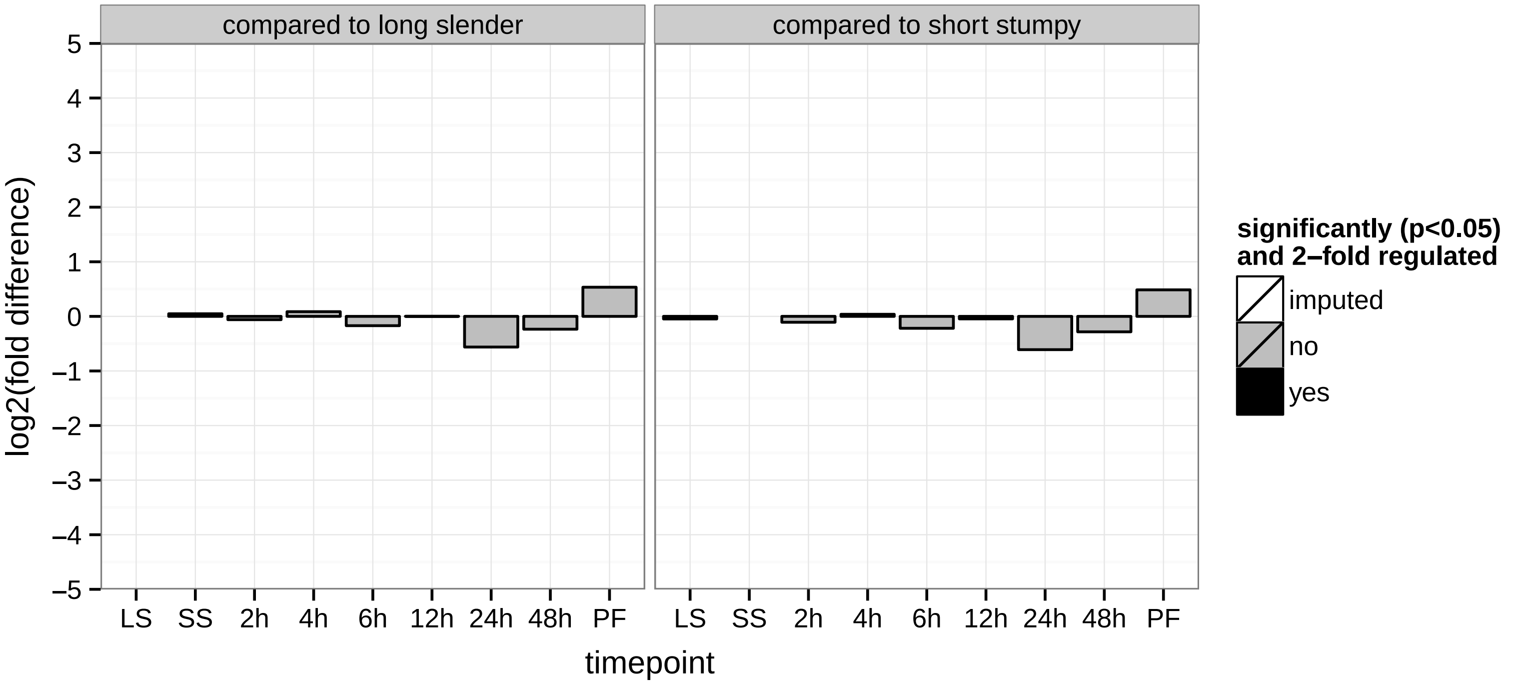
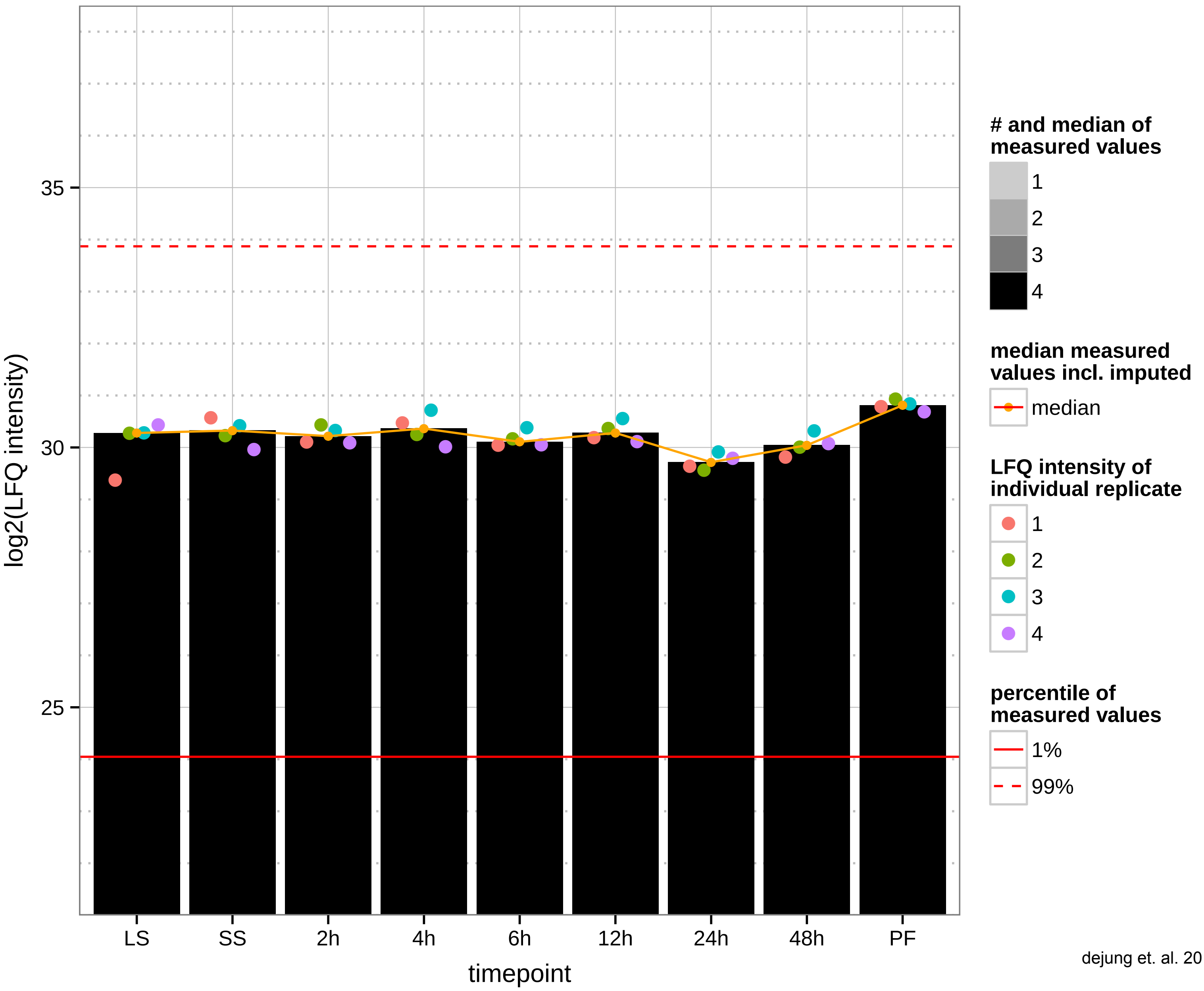
paraflagellar rod component, putative (PFC19)
Tb927.10.10140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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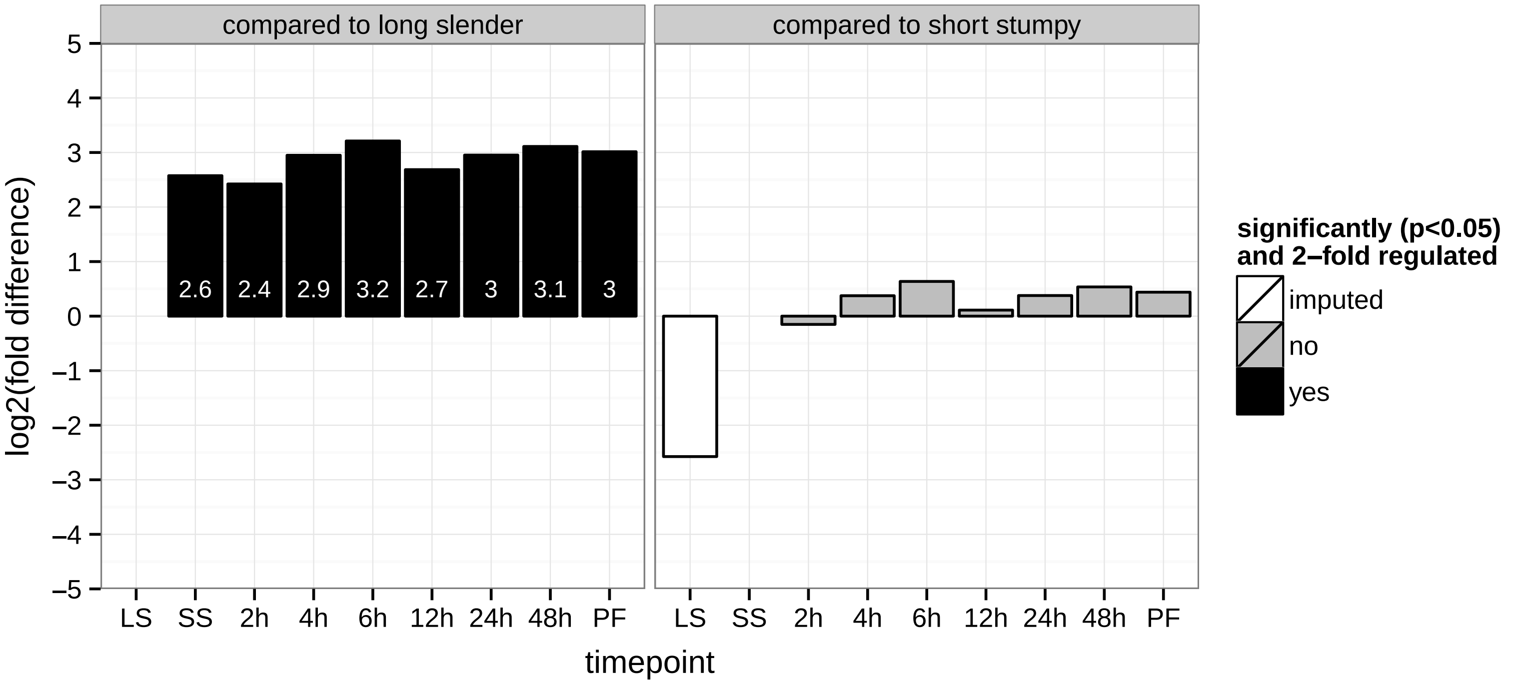
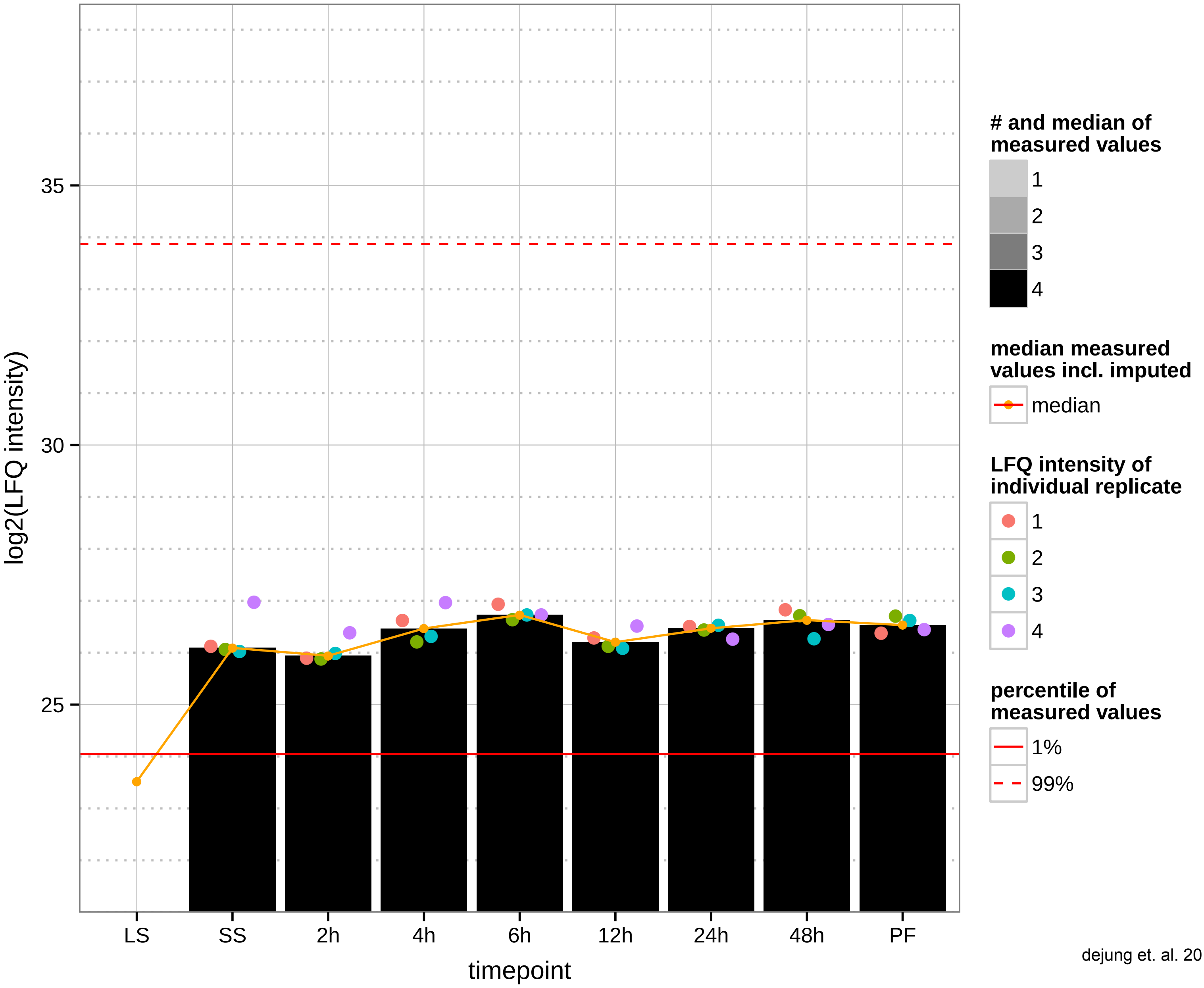
hypothetical protein, conserved
Tb927.10.10160
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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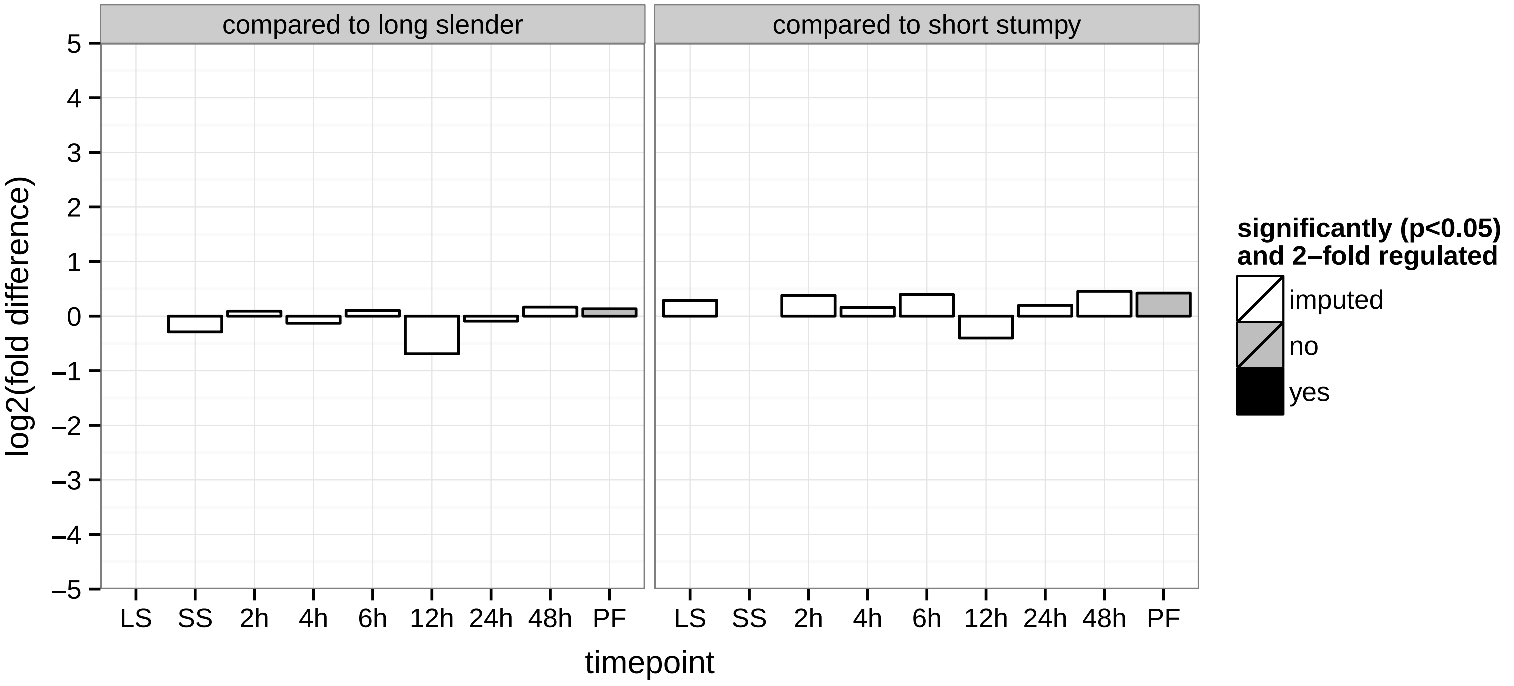
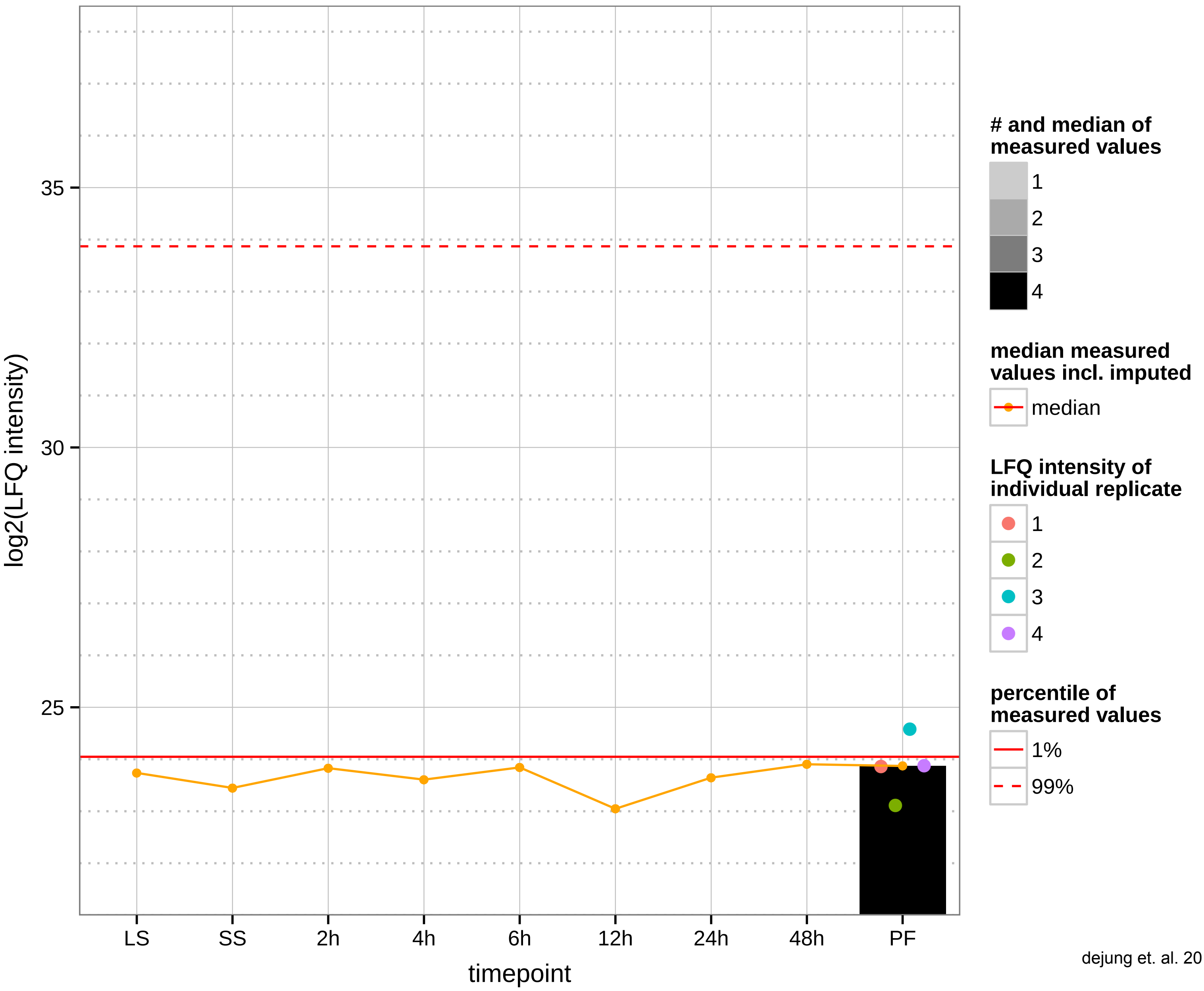
hypothetical protein, conserved
Tb927.10.10330
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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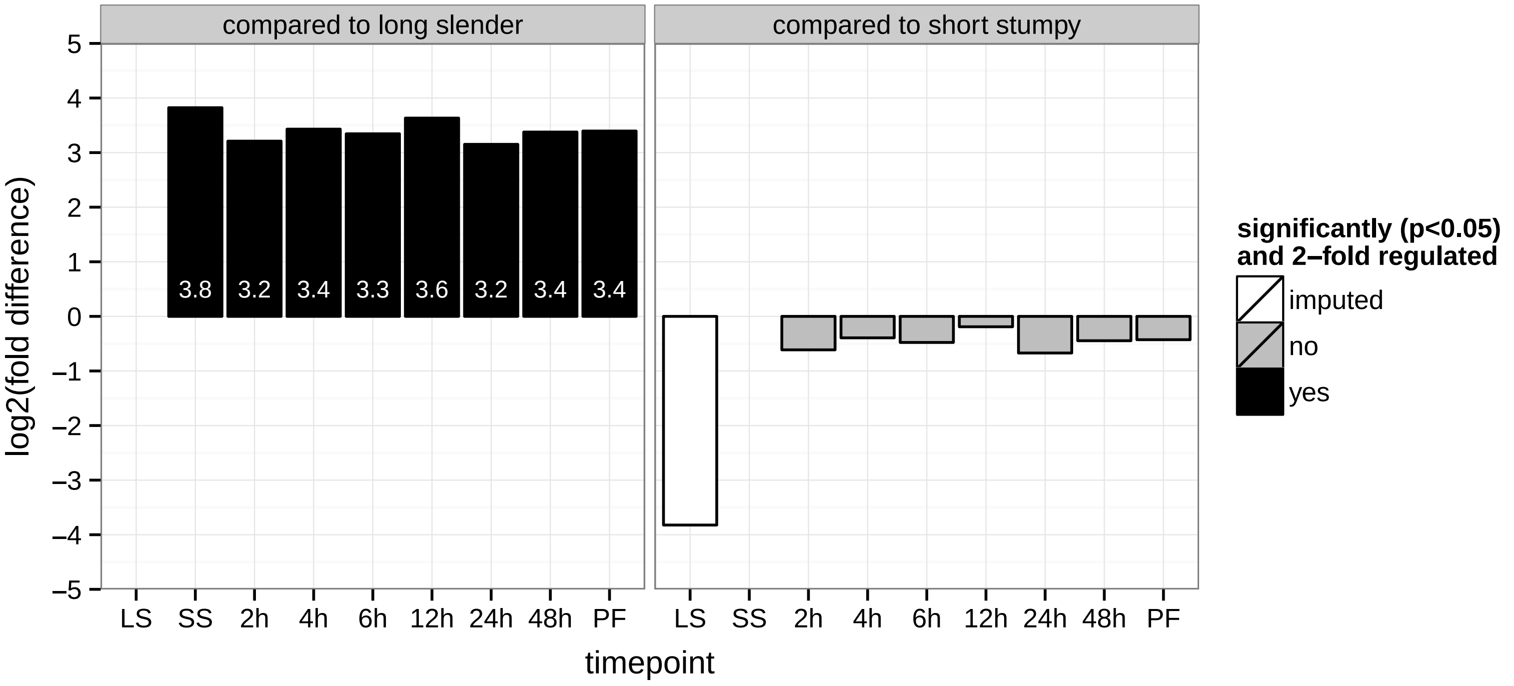
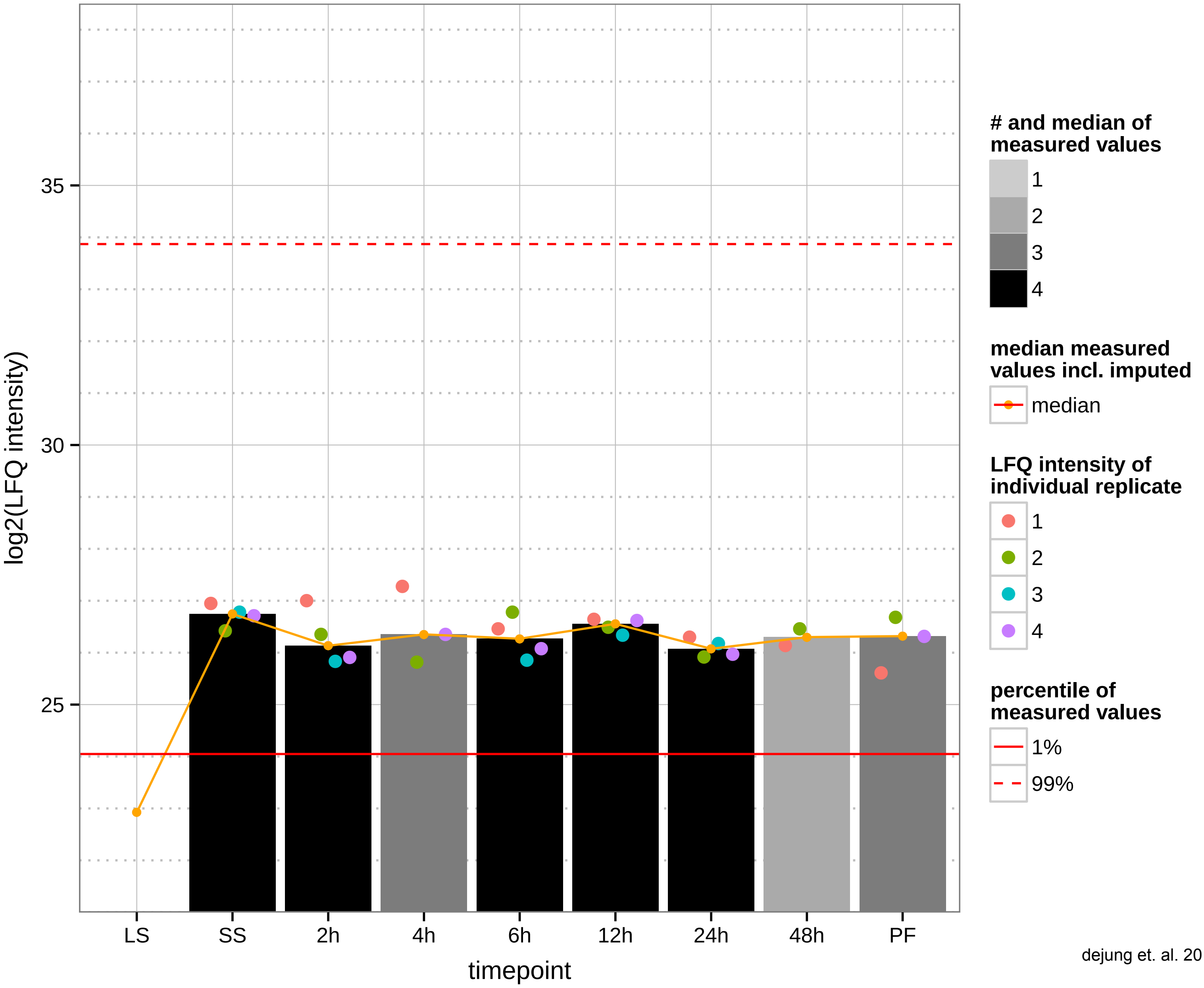
protein kinase, putative
Tb927.10.10350
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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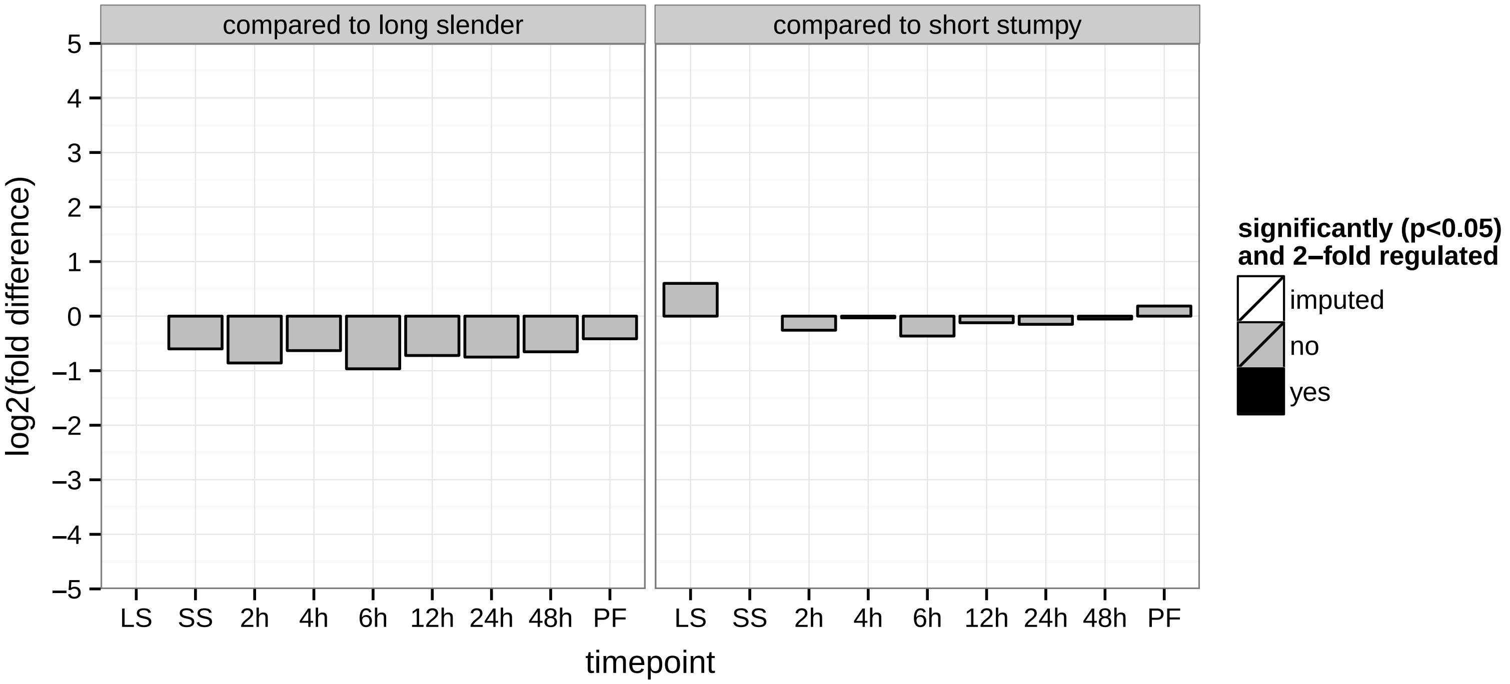
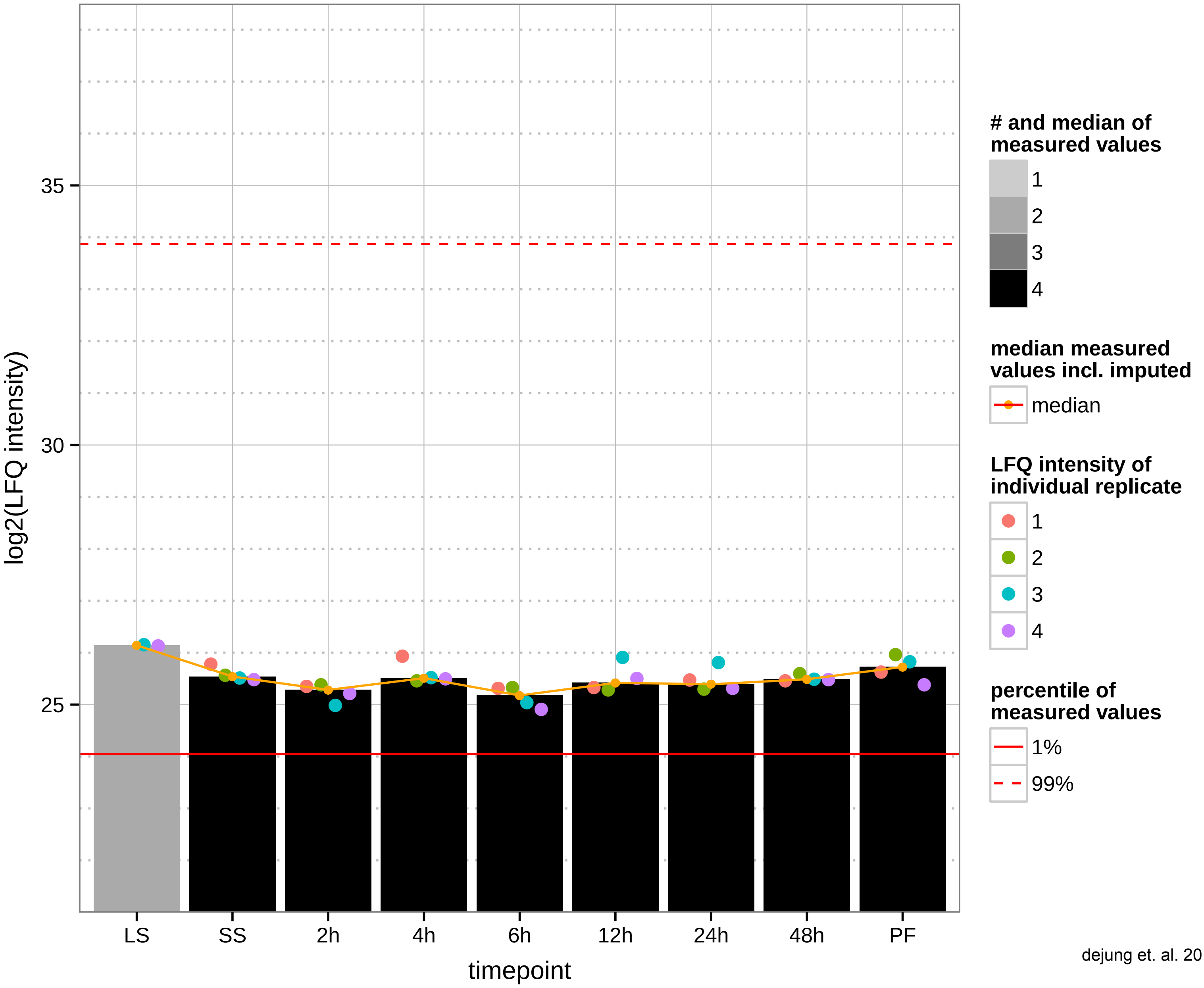
hypothetical protein, conserved
Tb927.10.10370;Tb927.10.10290
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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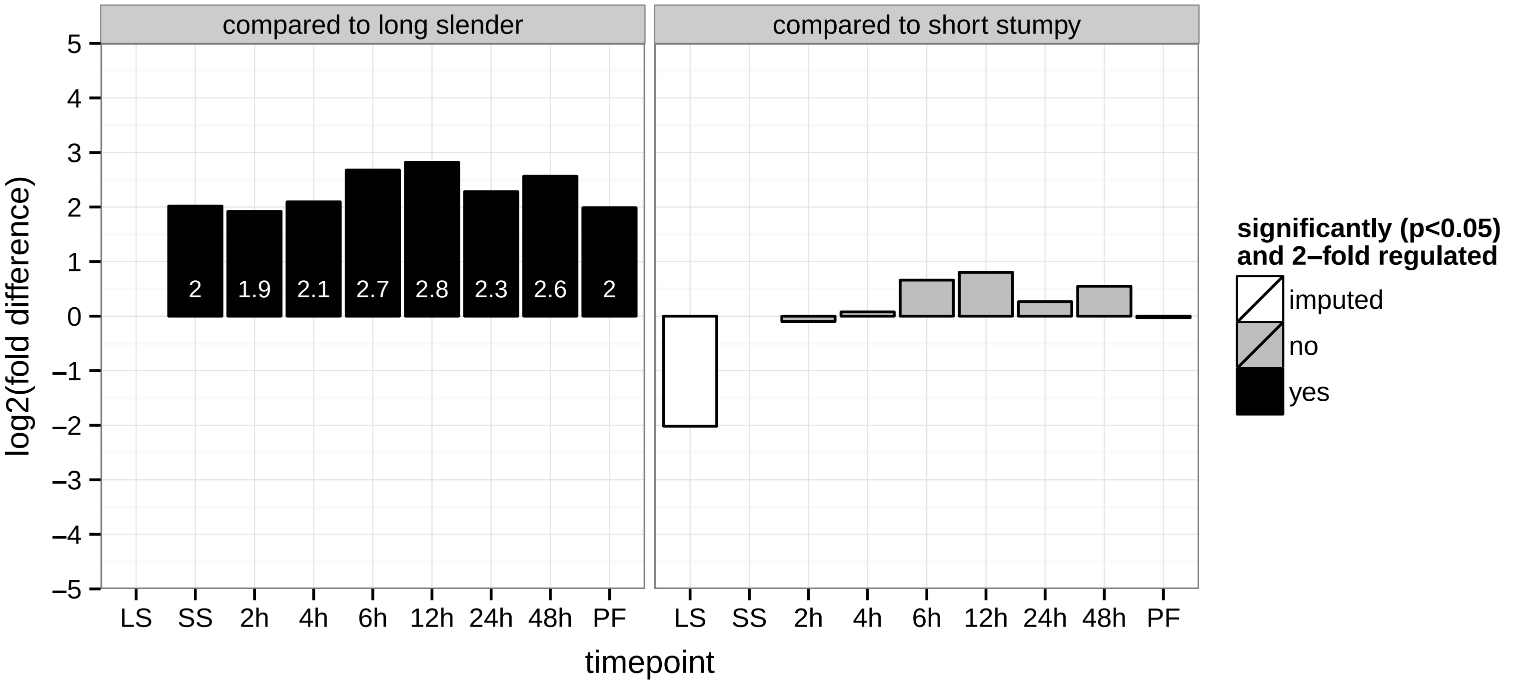
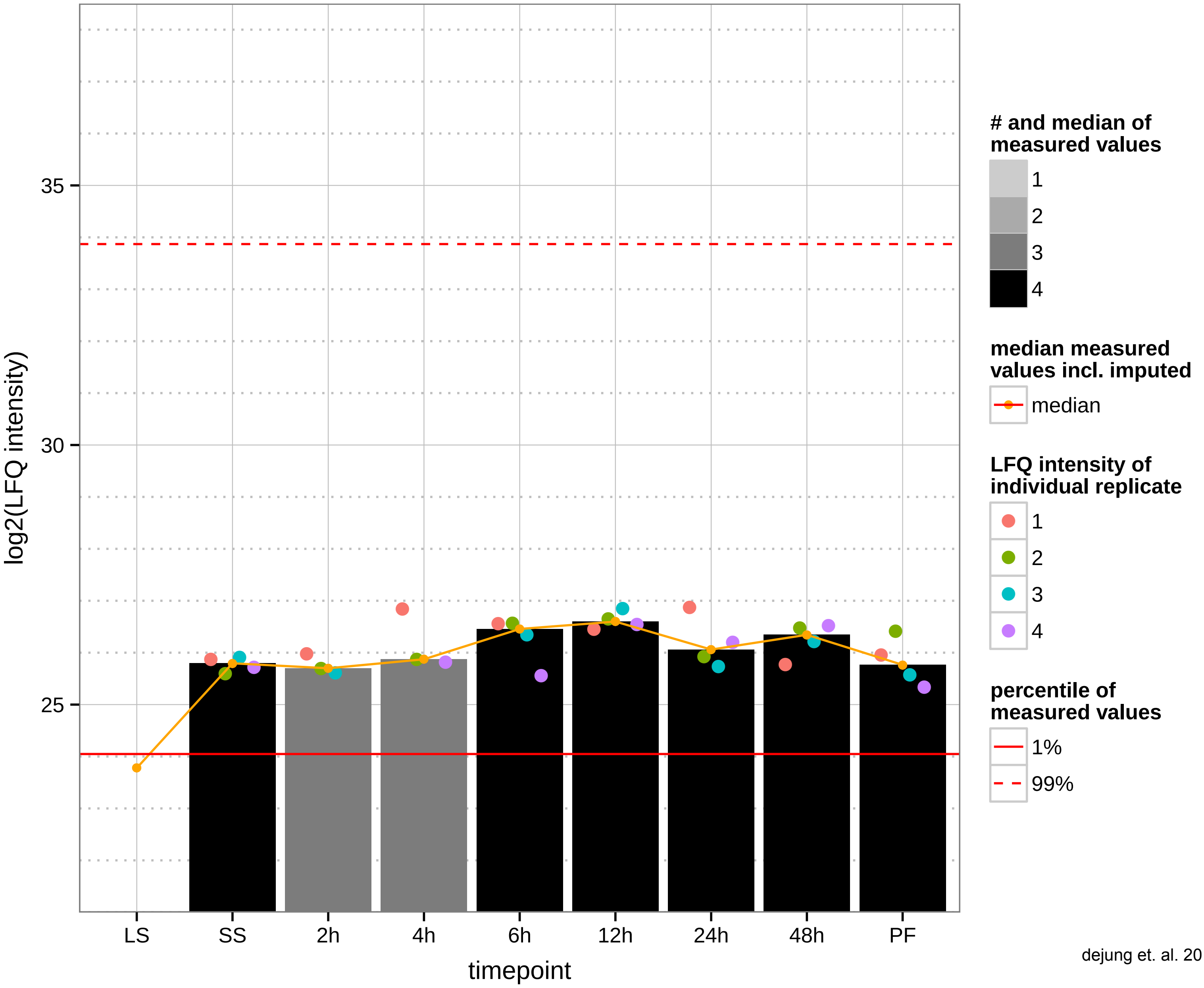
ATP−dependent DEAD/H RNA helicase, putative
Tb927.10.10380
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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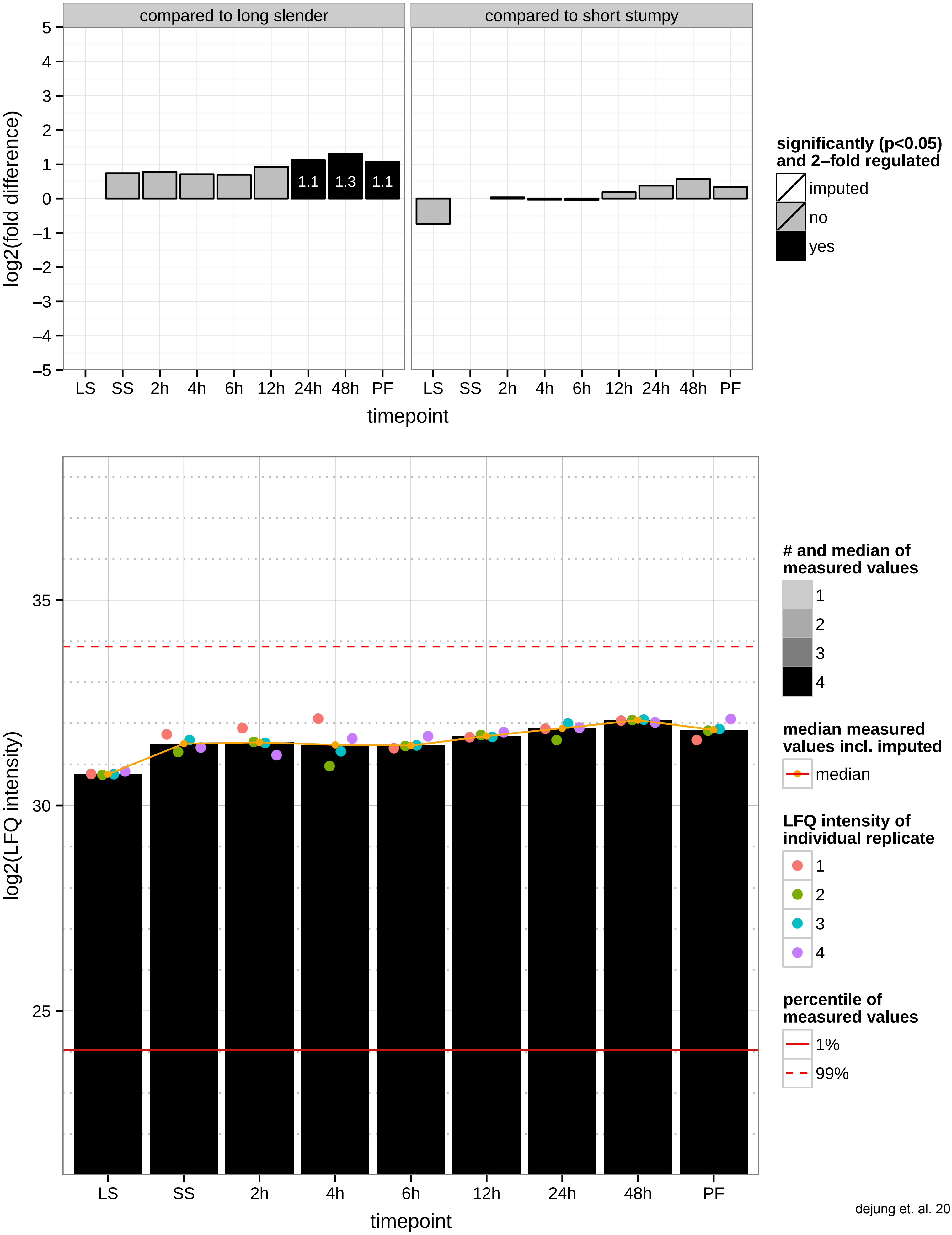
trypanothione reductase
Tb927.10.10390
AGOF: disulfide oxidoreductase activity, flavin adenine dinucleotide binding, trypanothione–disulfide reductase activity
AGOC: cytoplasm
AGOP: cell redox homeostasis, oxidation–reduction process
PGOF: disulfide oxidoreductase activity, flavin adenine dinucleotide binding, oxidoreductase activity
PGOC: cytoplasm
PGOP: cell redox homeostasis, oxidation–reduction process



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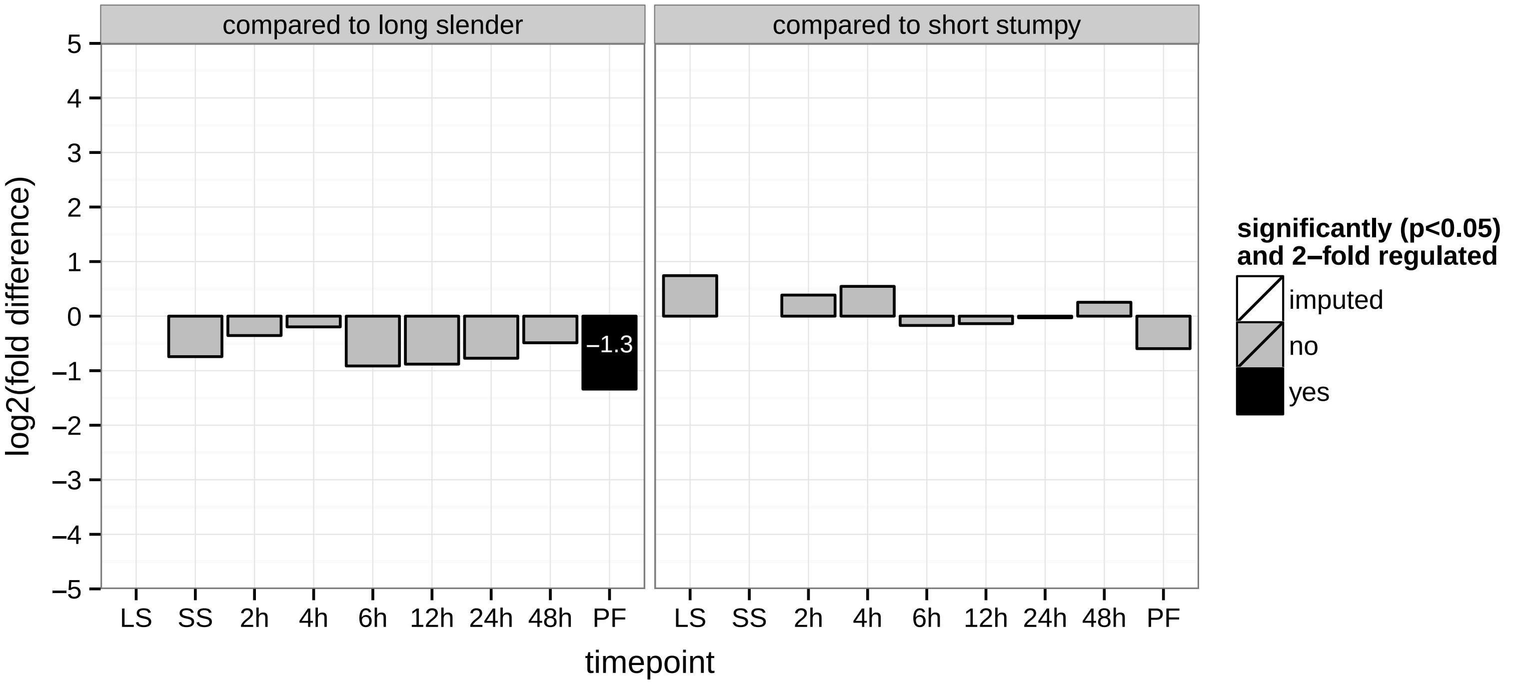
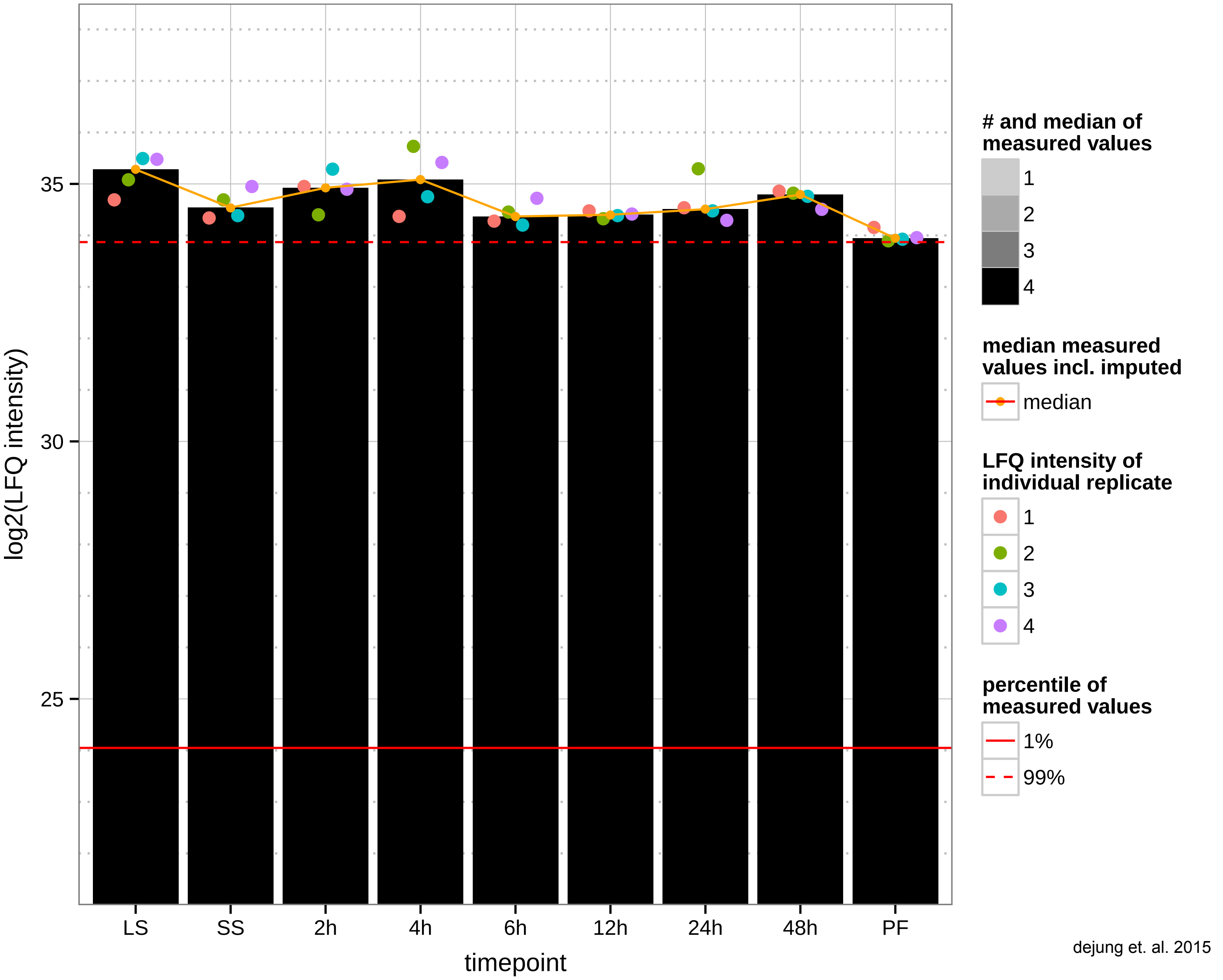
histone H2B, putative
Tb927.10.10590;Tb927.10.10580;Tb927.10.10570;Tb927.10.10560;Tb927.10.10550;Tb927.10.10540;Tb927.10.10530;Tb92
AGOF: DNA binding
AGOC: nucleosome, nucleus
AGOP: chromosome organization, nucleosome assembly
PGOF: null, DNA binding
PGOC: null, nucleosome, nucleus
PGOP: null, nucleosome assembly





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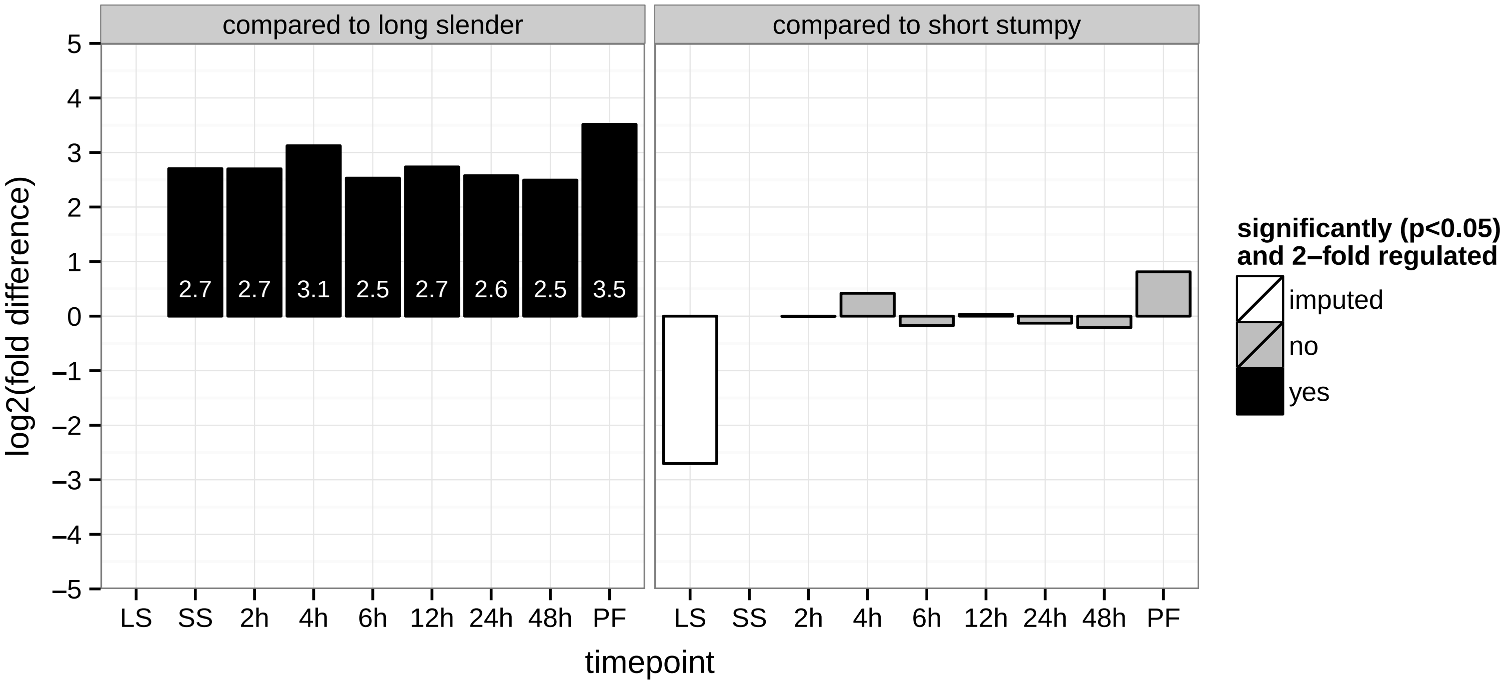
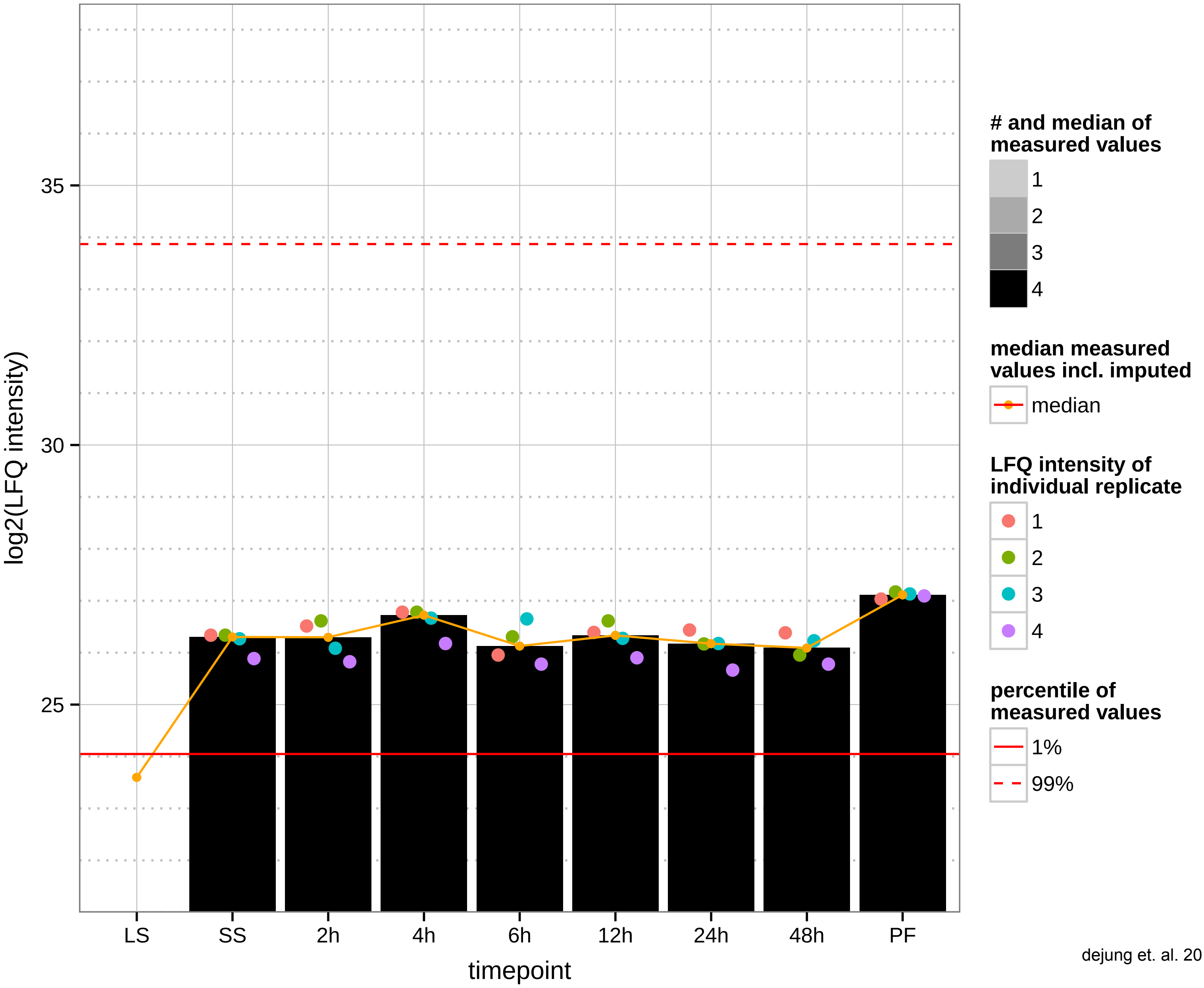
hypothetical protein, conserved
Tb927.10.10620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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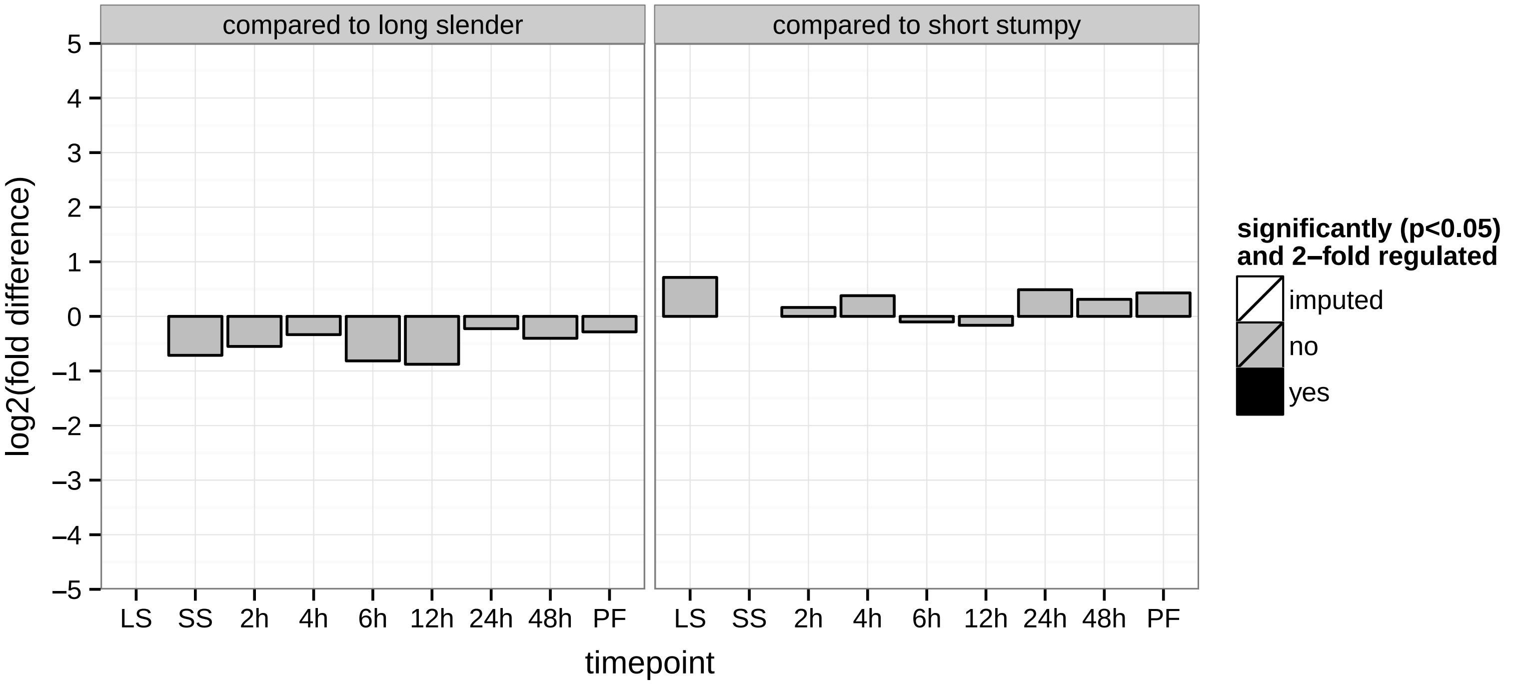
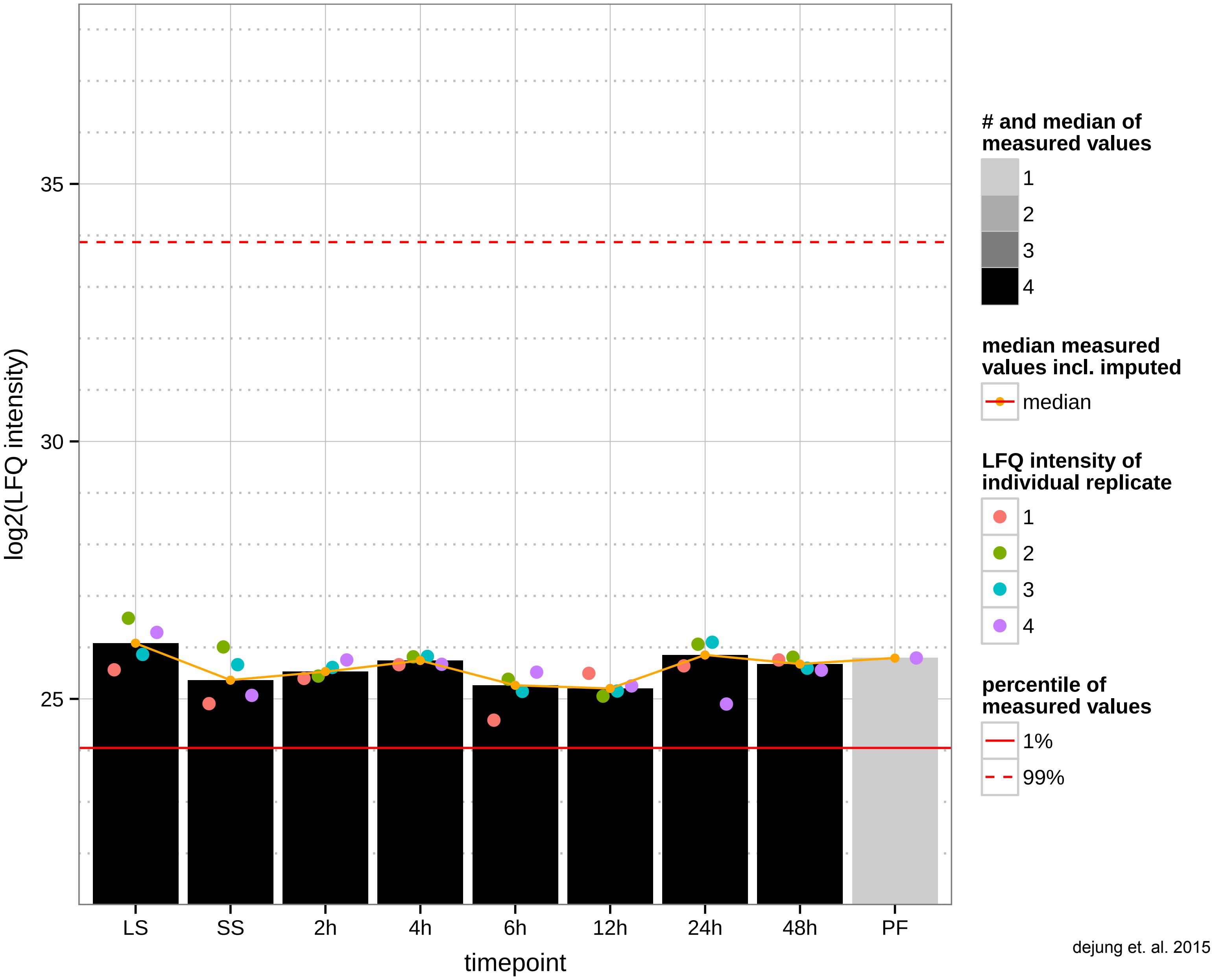
hypothetical protein, conserved
Tb927.10.10630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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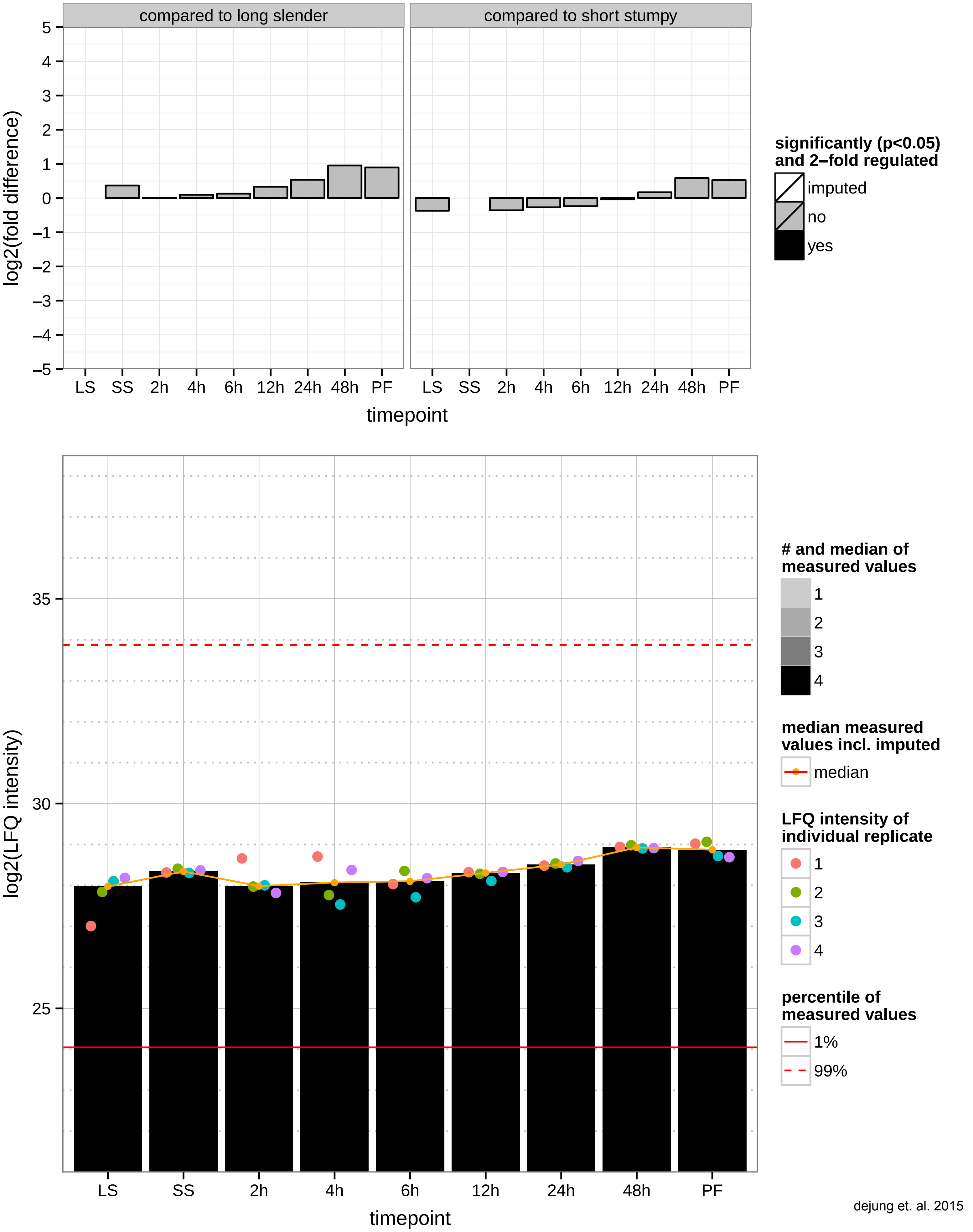
cdc2–related kinase 1, putative, cell division protein kinase 2 homolog 1 (CRK1)
Tb927.10.1070
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: cytosol
AGOP: cell cycle, growth, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation



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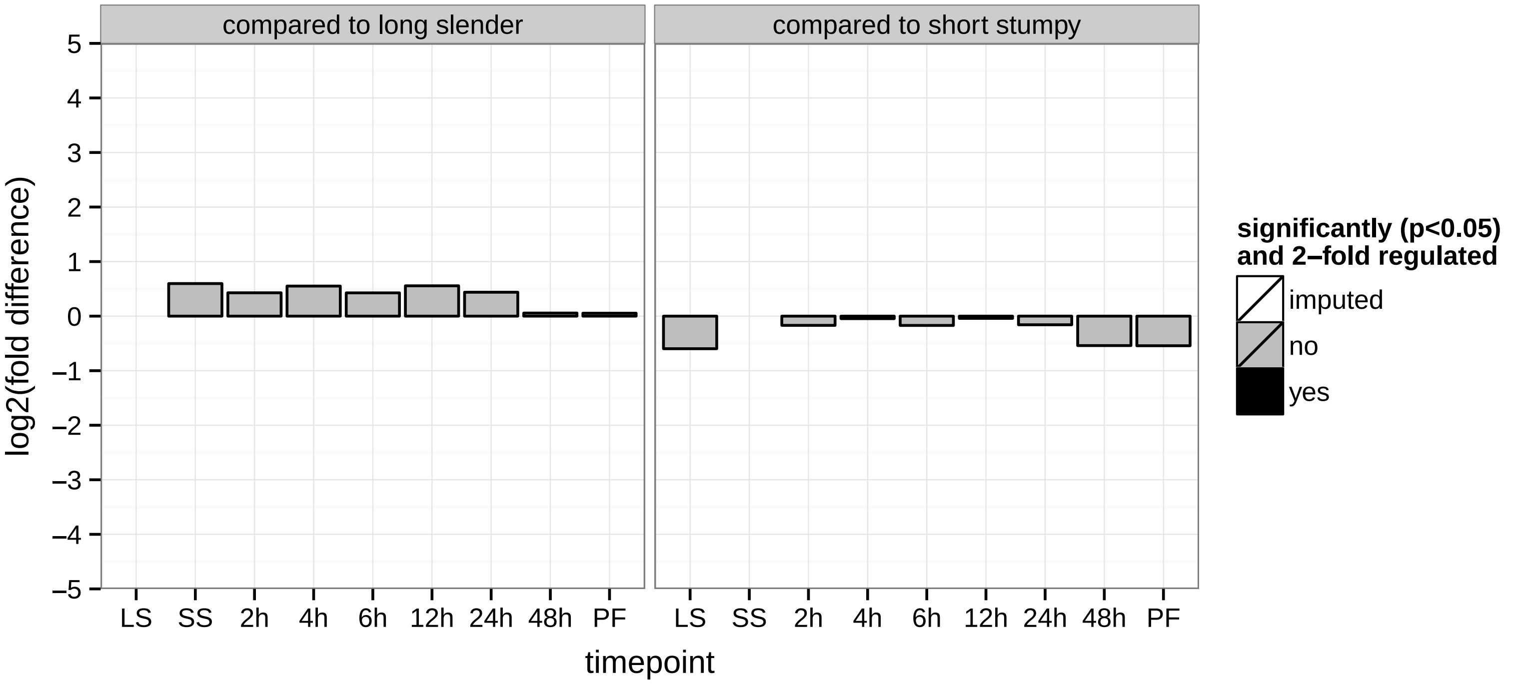
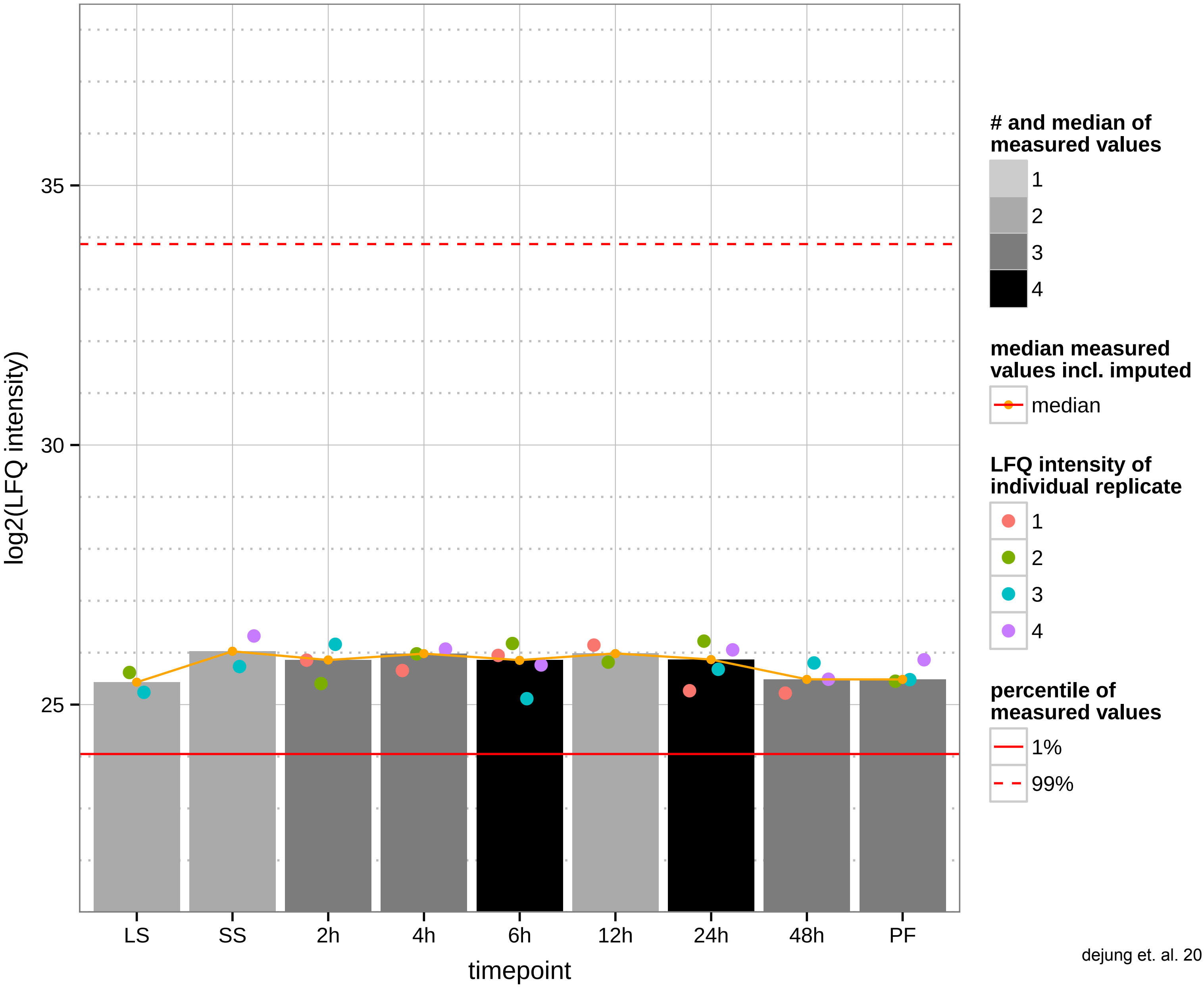
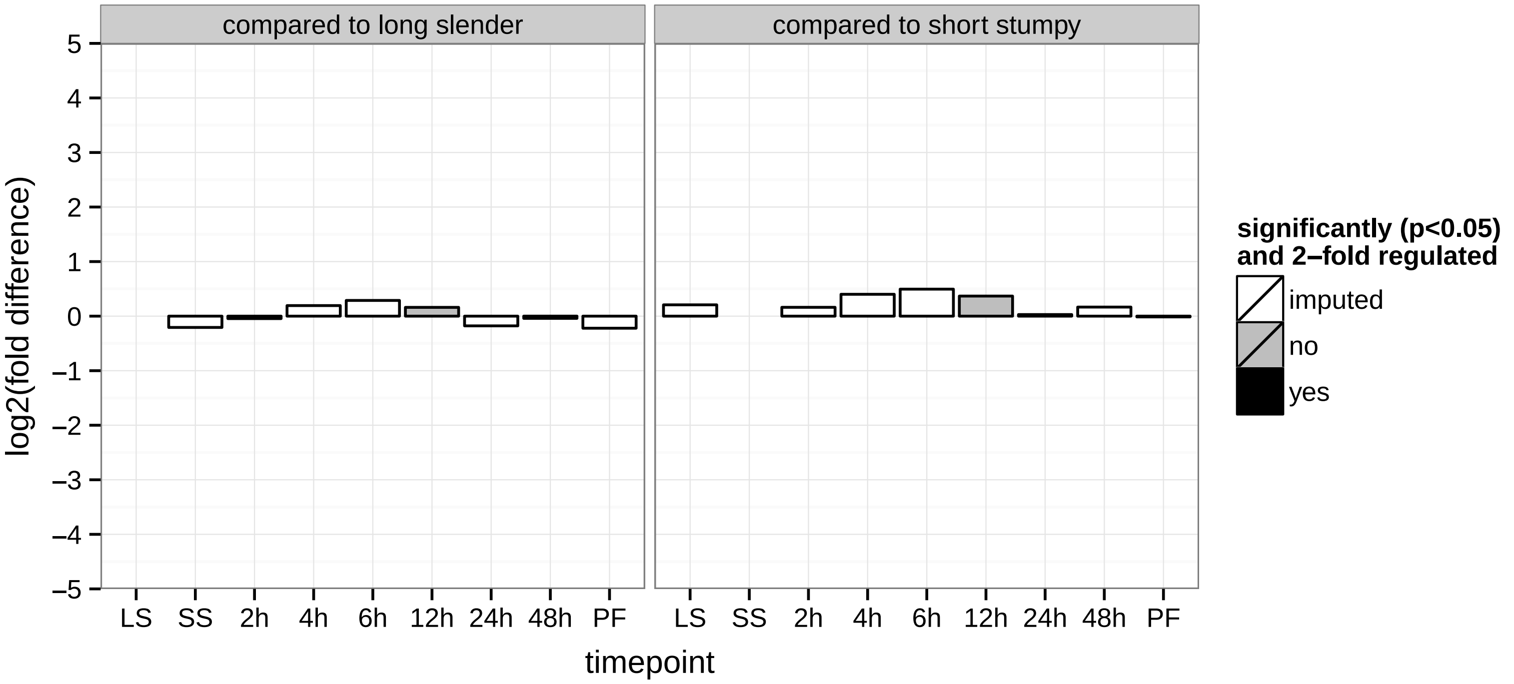
hypothetical protein, conserved
Tb927.10.10720
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: integral to membrane
PGOP: null

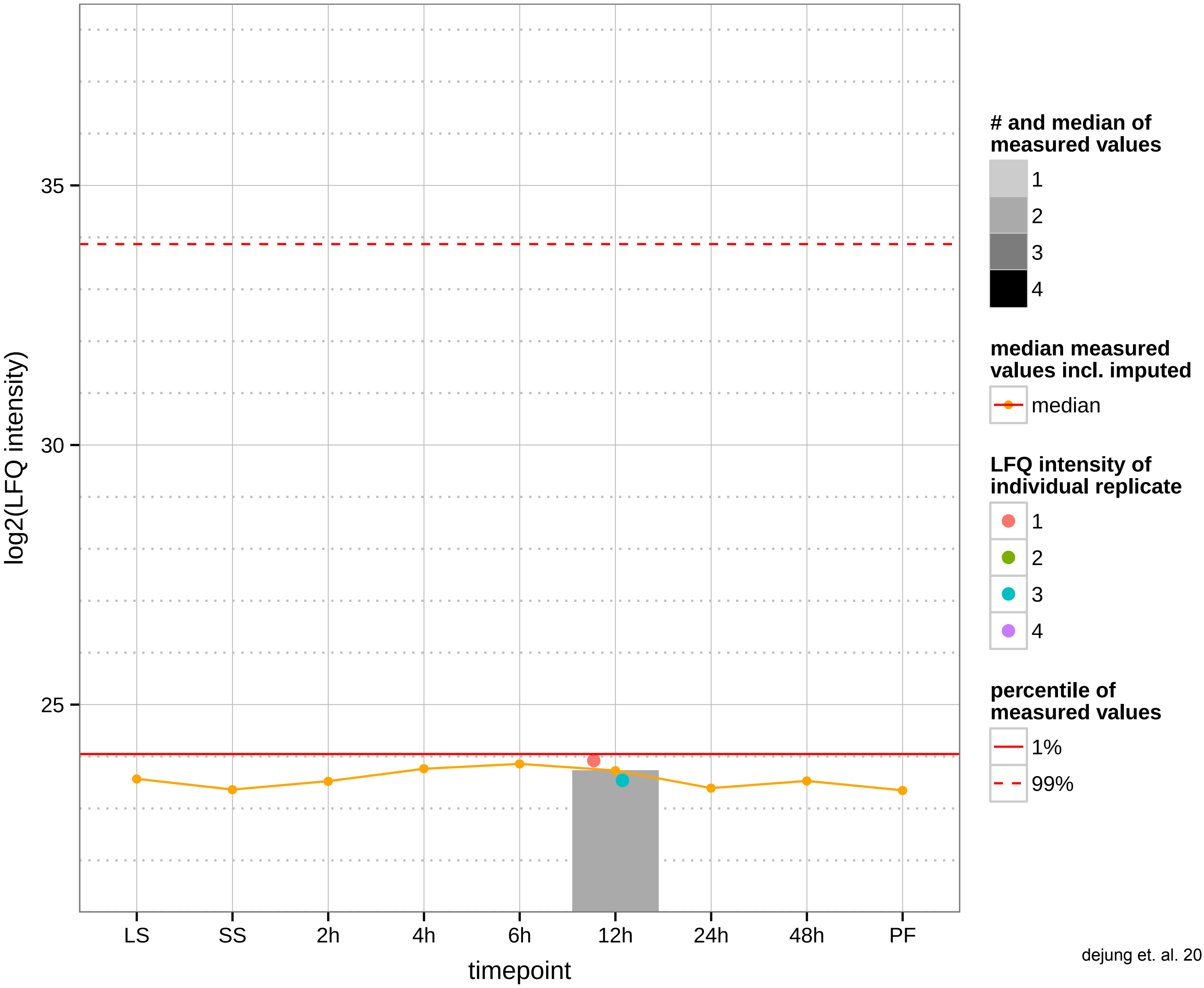




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.10740
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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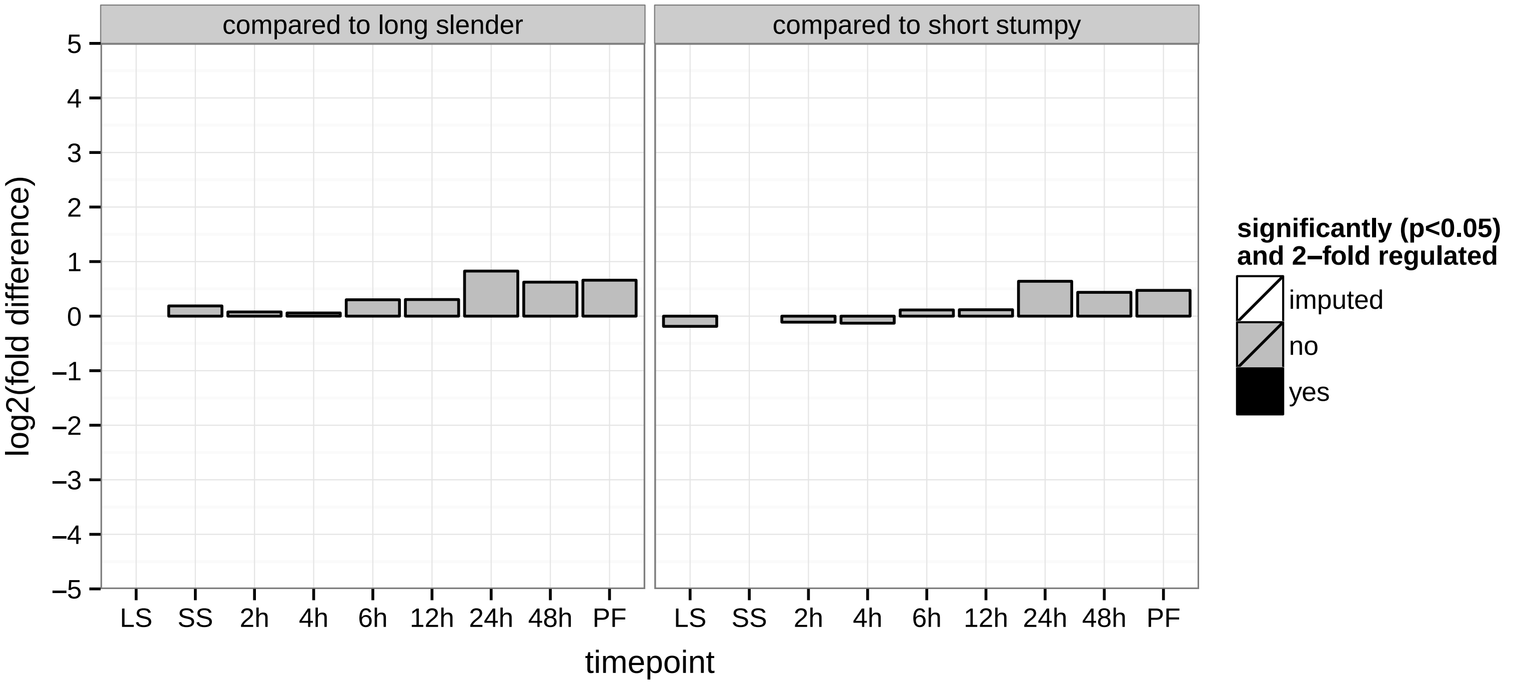
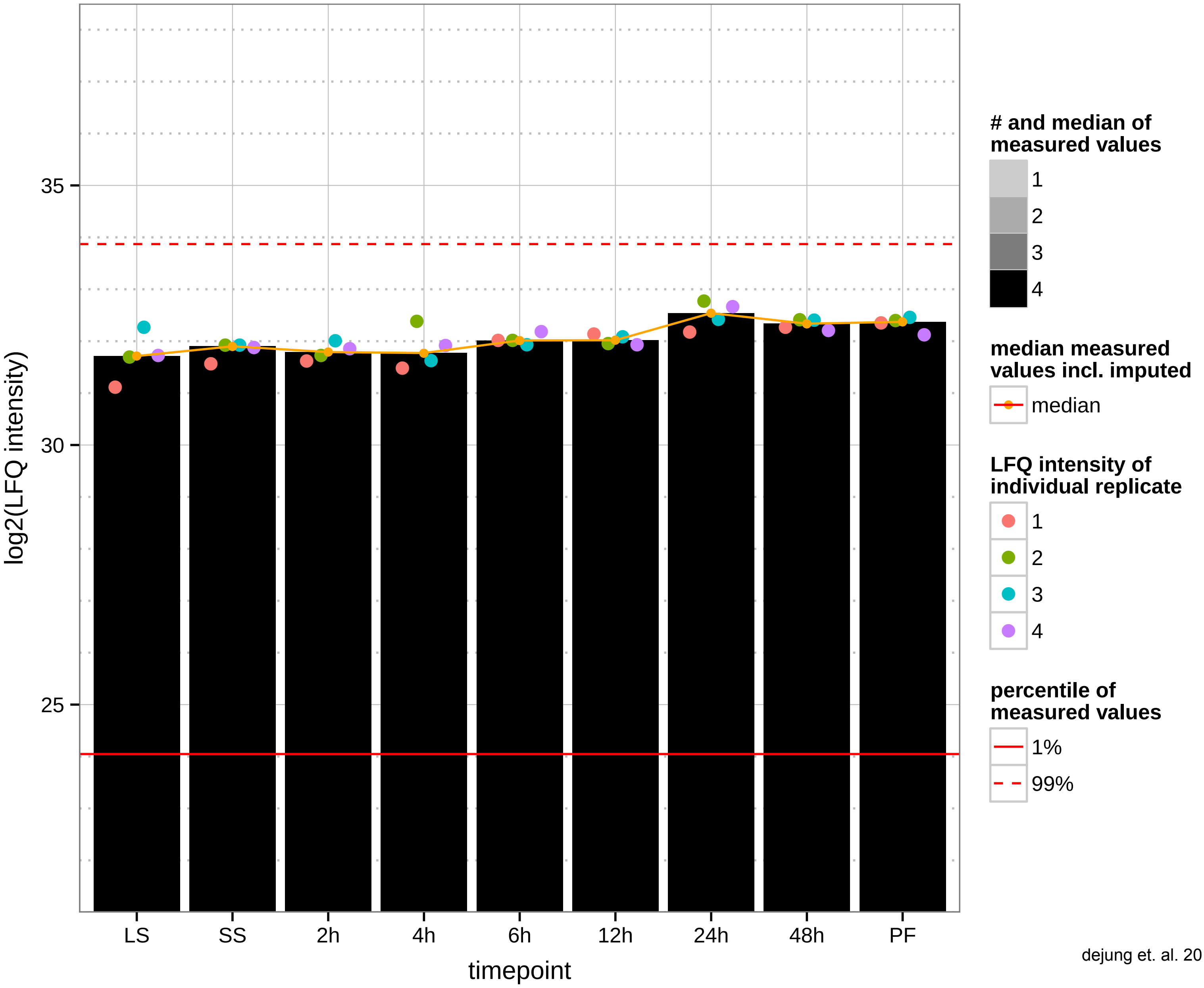
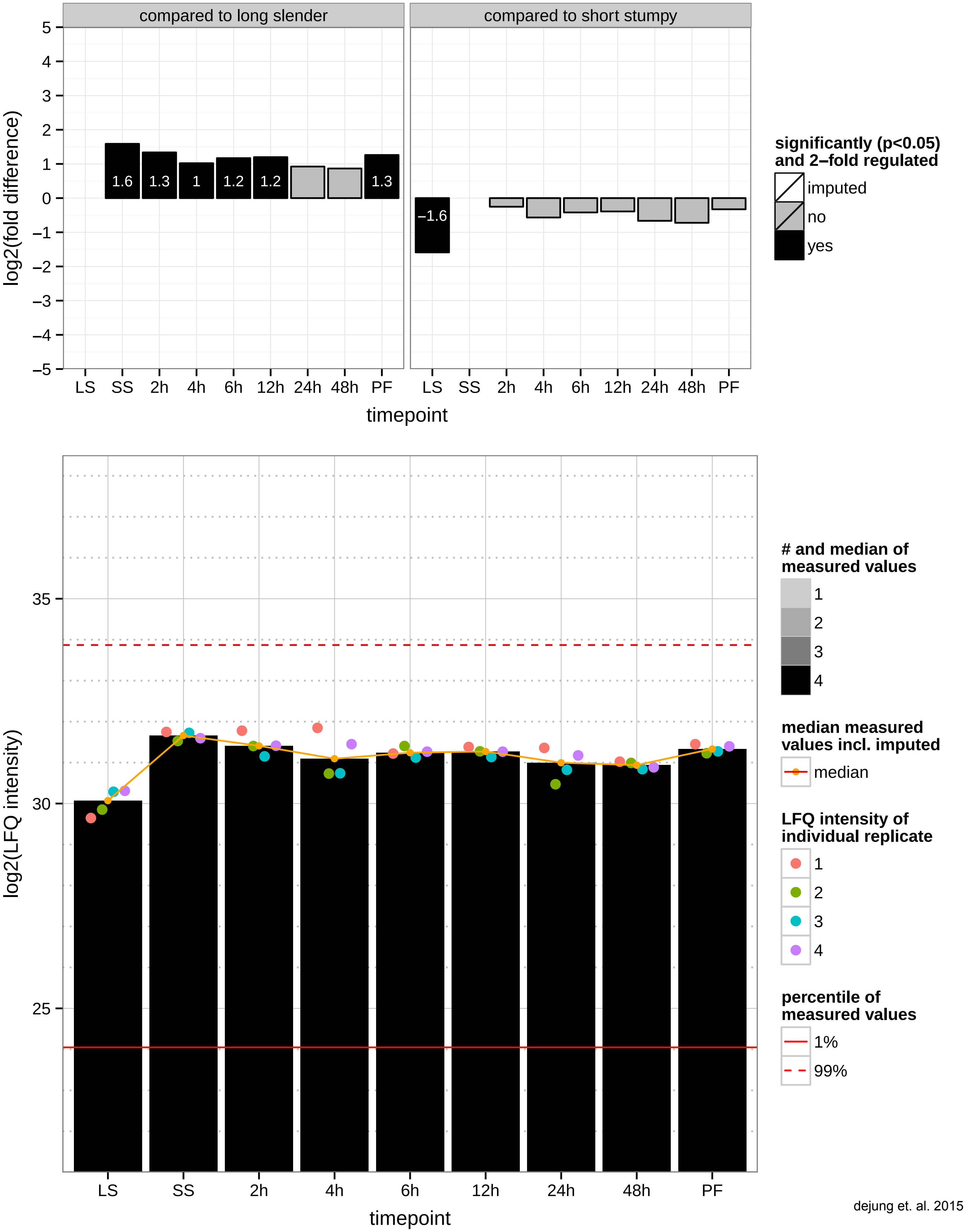
40S ribosomal protein S23, putative (RPS23)
Tb927.10.1090;Tb927.10.1080
AGOF: RNA binding, structural constituent of ribosome
AGOC: intracellular, ribosome, small ribosomal subunit
AGOP: translation
PGOF: structural constituent of ribosome, null
PGOC: intracellular, ribosome, small ribosomal subunit, null
PGOP: translation, null





dejung et. al. 2015

argonaute–like protein (AGO1)
Tb927.10.10850
AGOF: ribosome binding
AGOC: cytoplasm
AGOP: RNA interference, production of siRNA involved in RNA interference
PGOF: nucleic acid binding, protein binding
PGOC: null
PGOP: null



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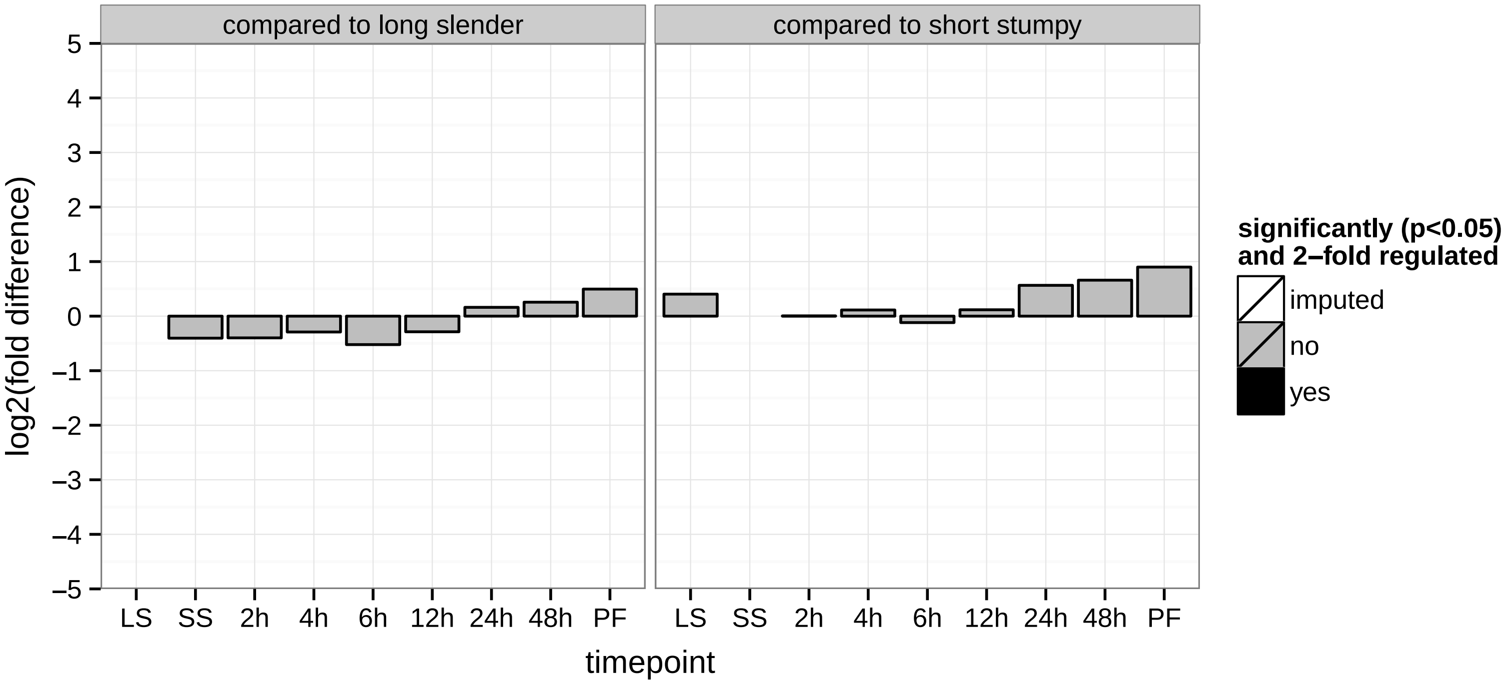
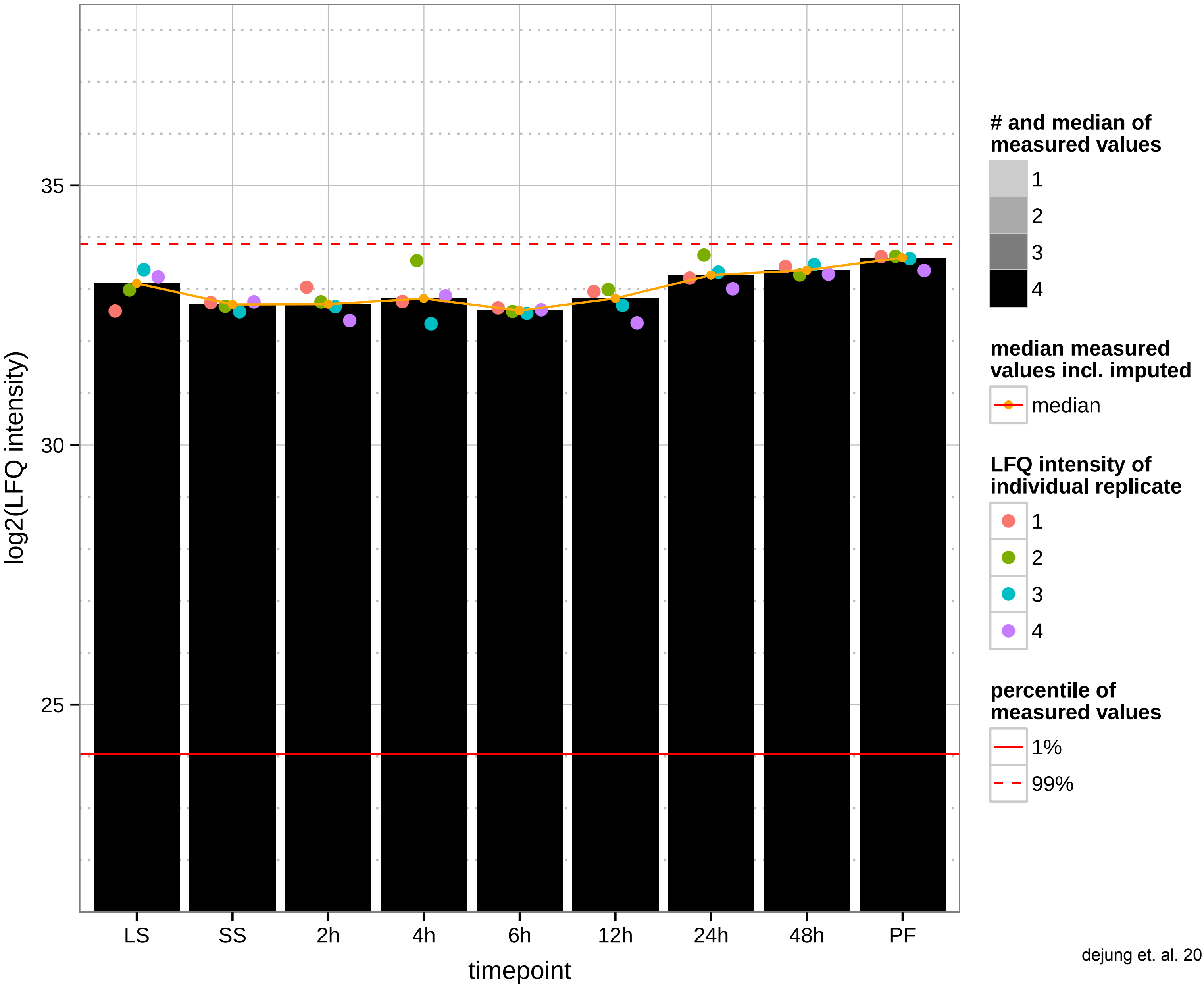
60S ribosomal protein L9, putative
Tb927.10.1100;Tb927.6.4690
AGOF: rRNA binding, structural constituent of ribosome
AGOC: ribosome
AGOP: ribosome biogenesis, translation
PGOF: rRNA binding, structural constituent of ribosome
PGOC: ribosome
PGOP: translation





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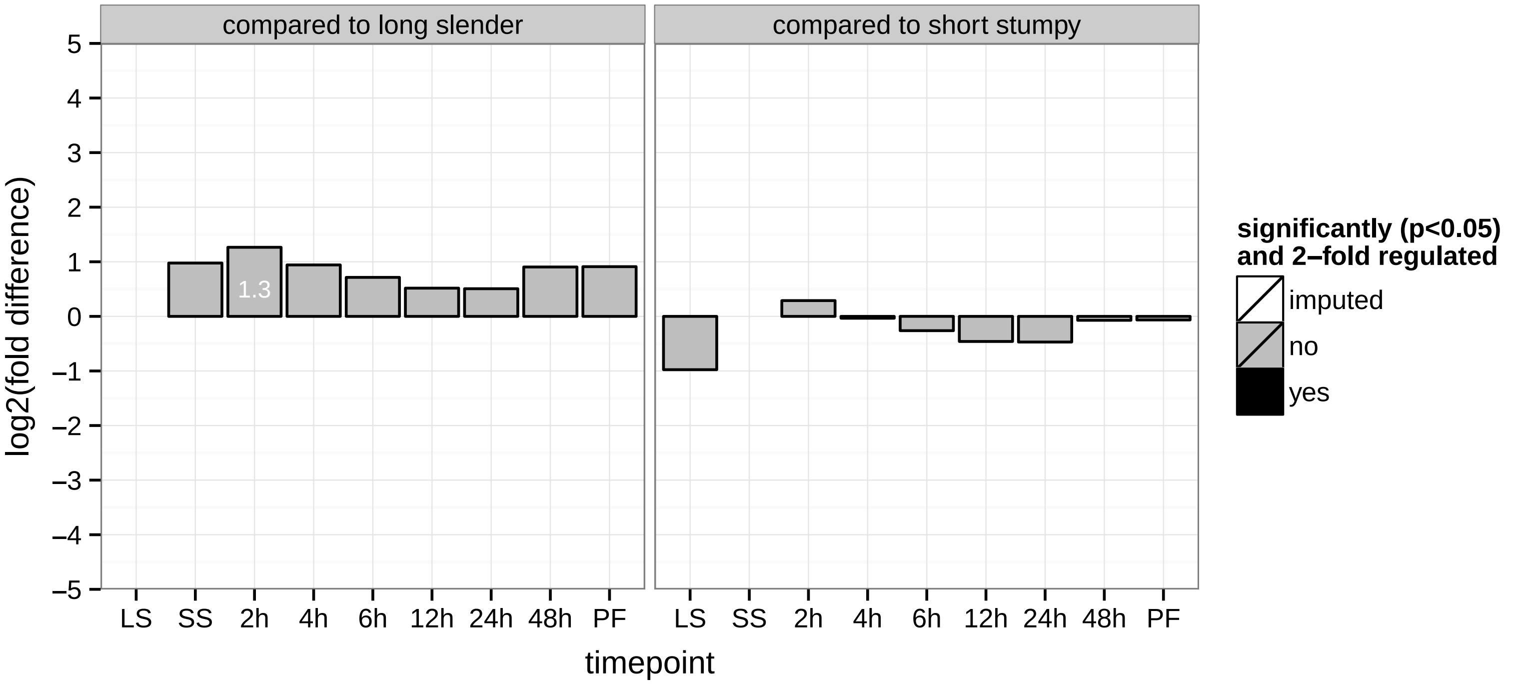
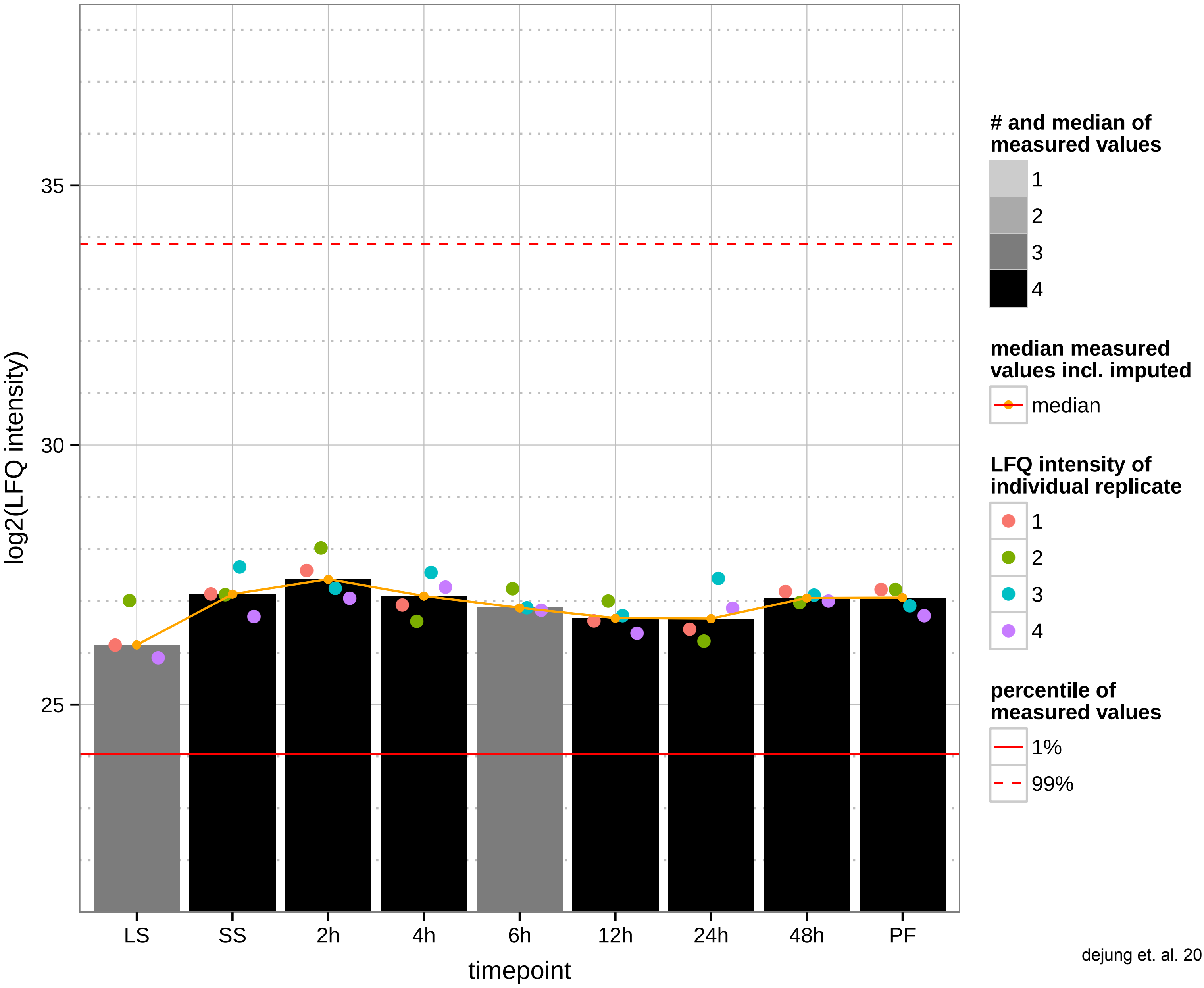
paraflagellar rod protein
Tb927.10.11080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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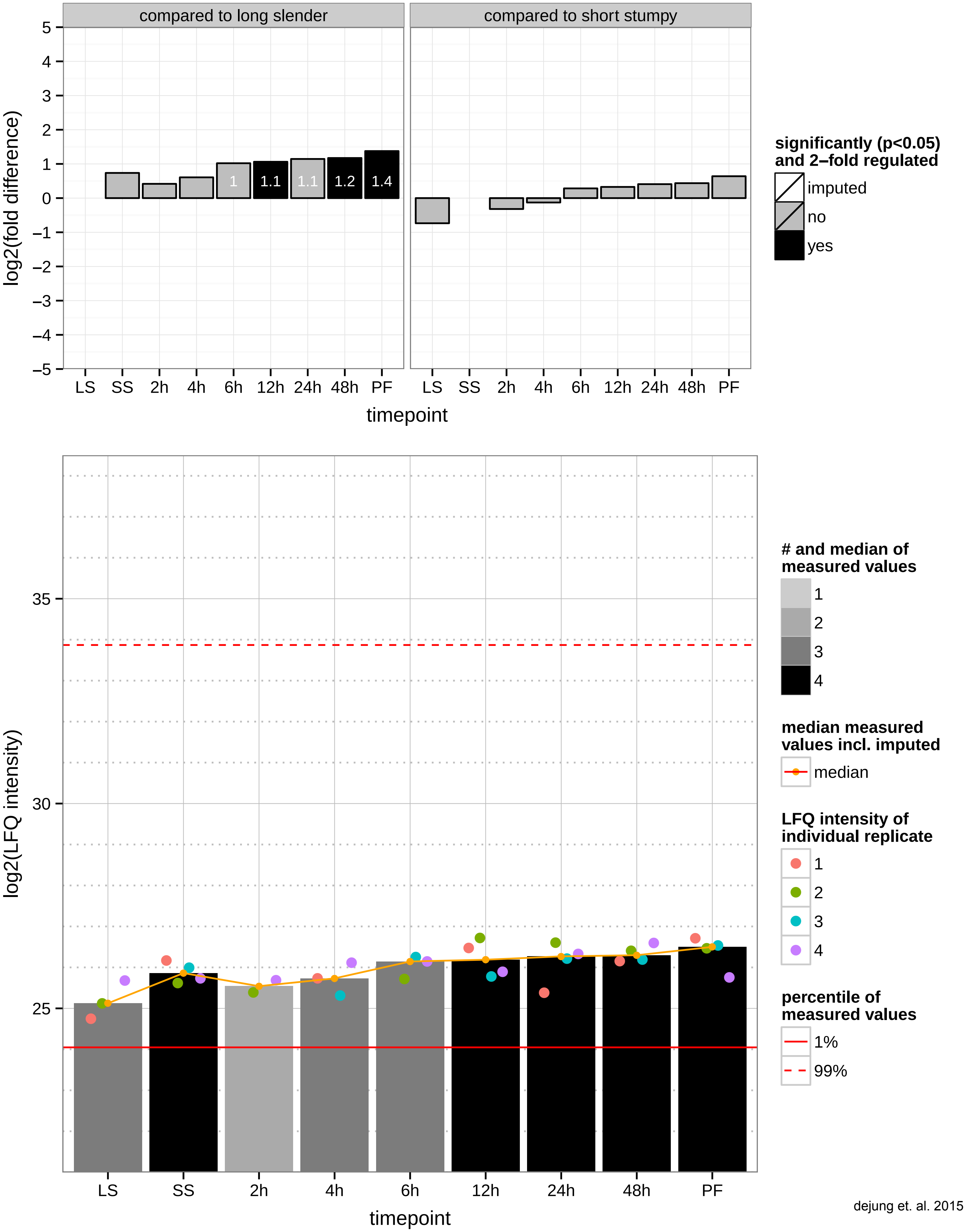
hypothetical protein, conserved
Tb927.10.11150
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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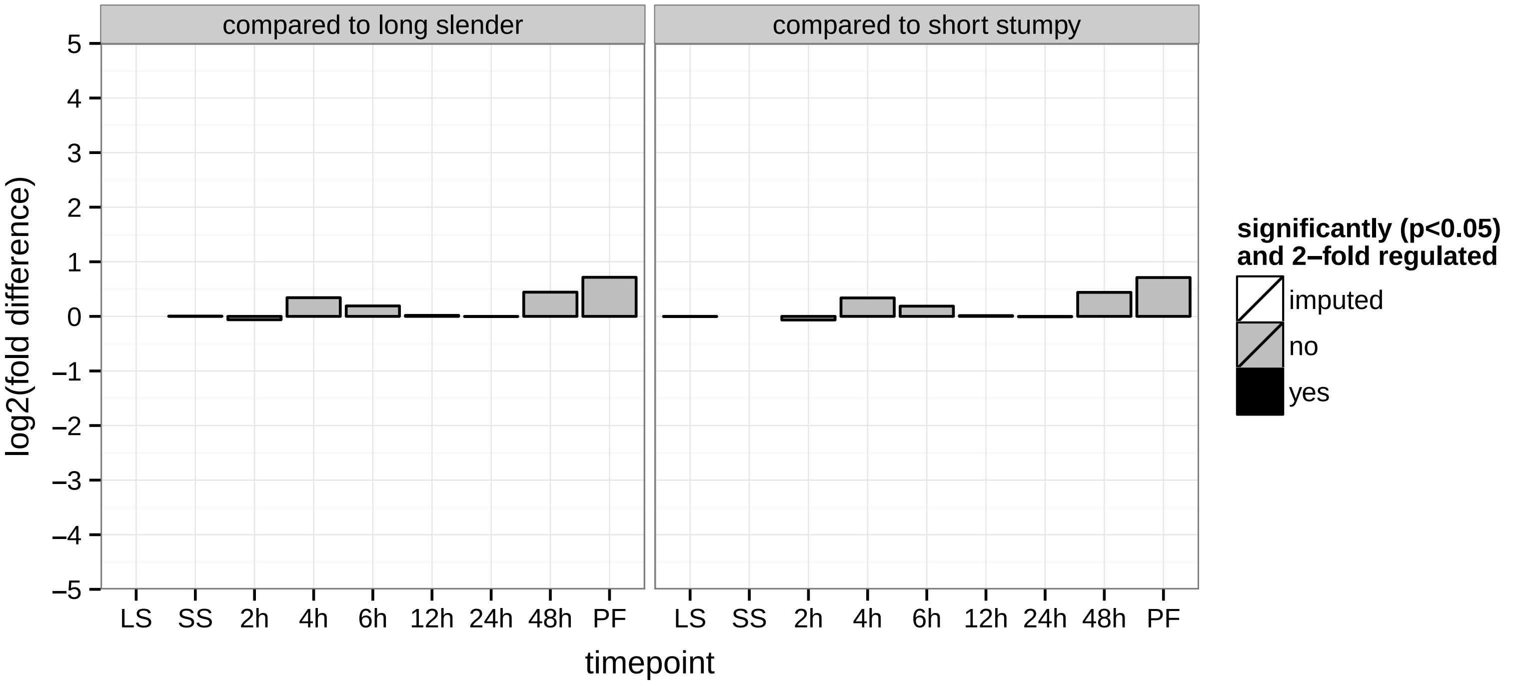
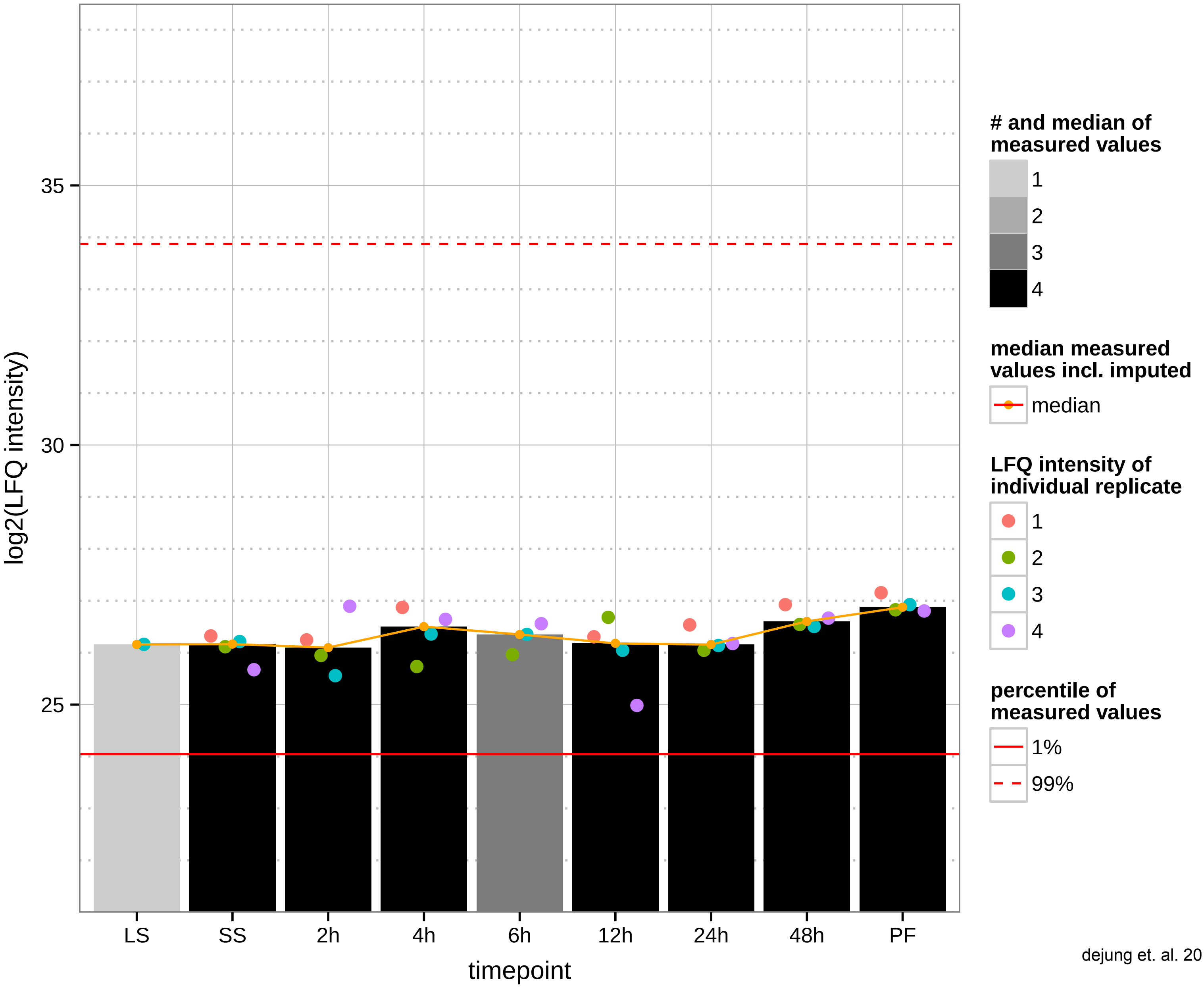
hypothetical protein, conserved
Tb927.10.11210
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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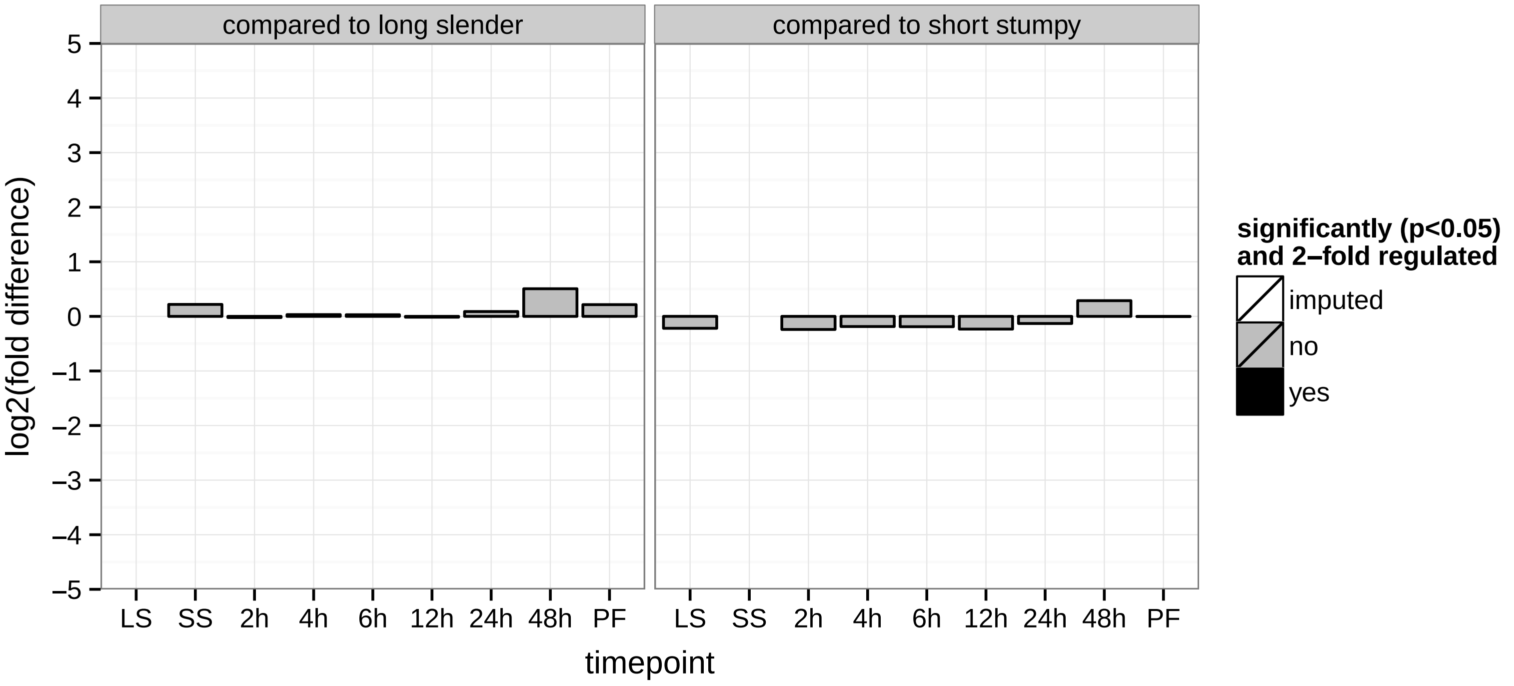
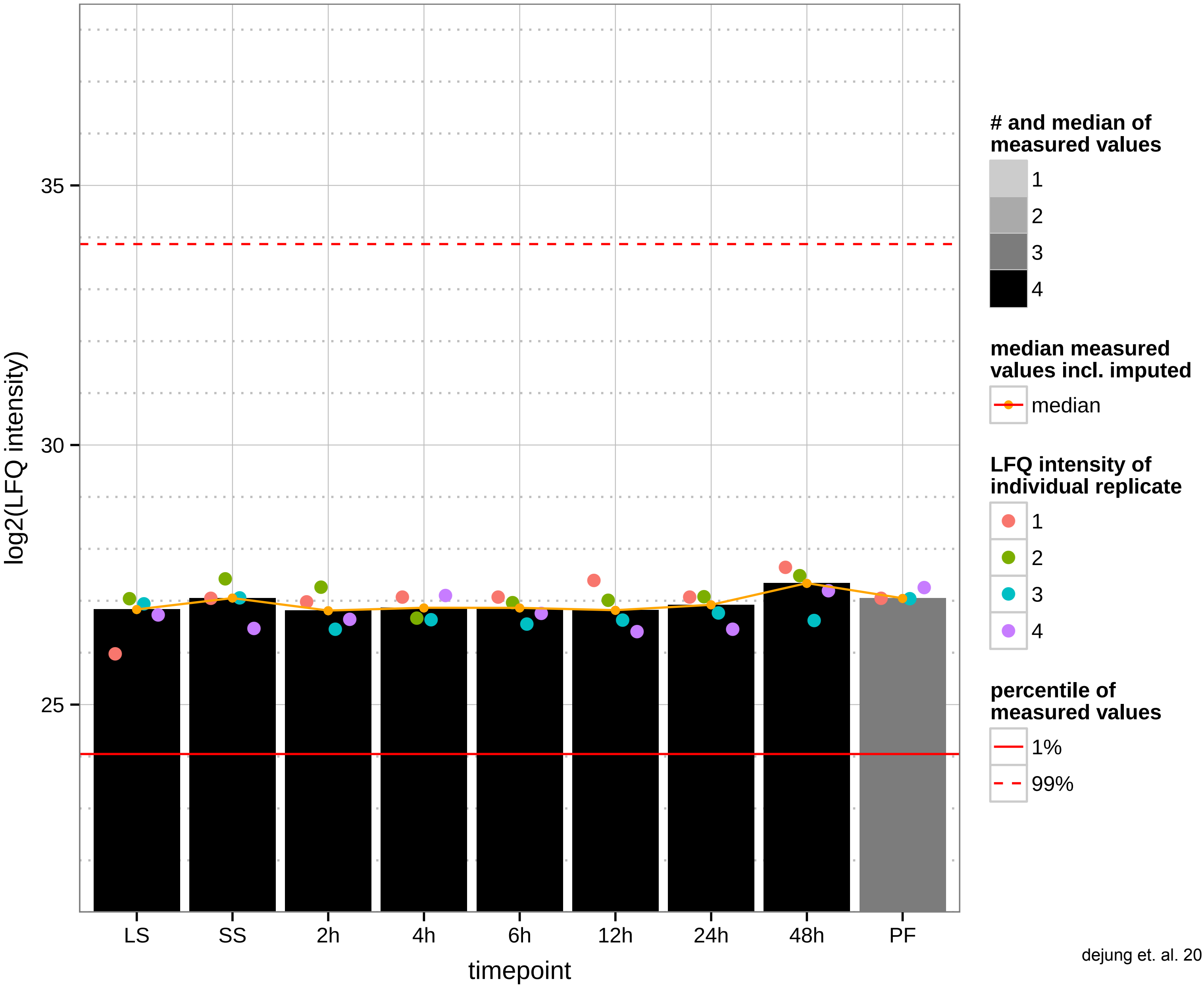
hypothetical protein, conserved
Tb927.10.11250;Tb11.v5.0575
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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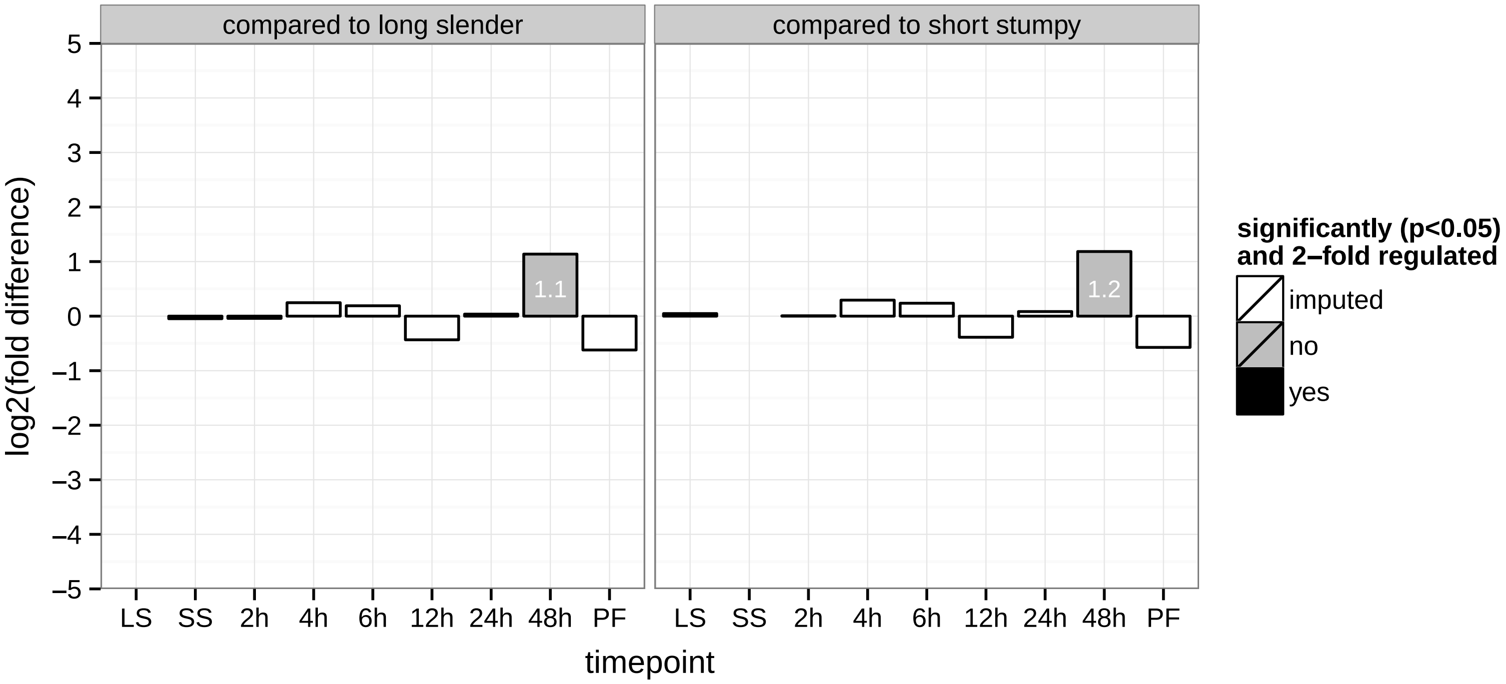
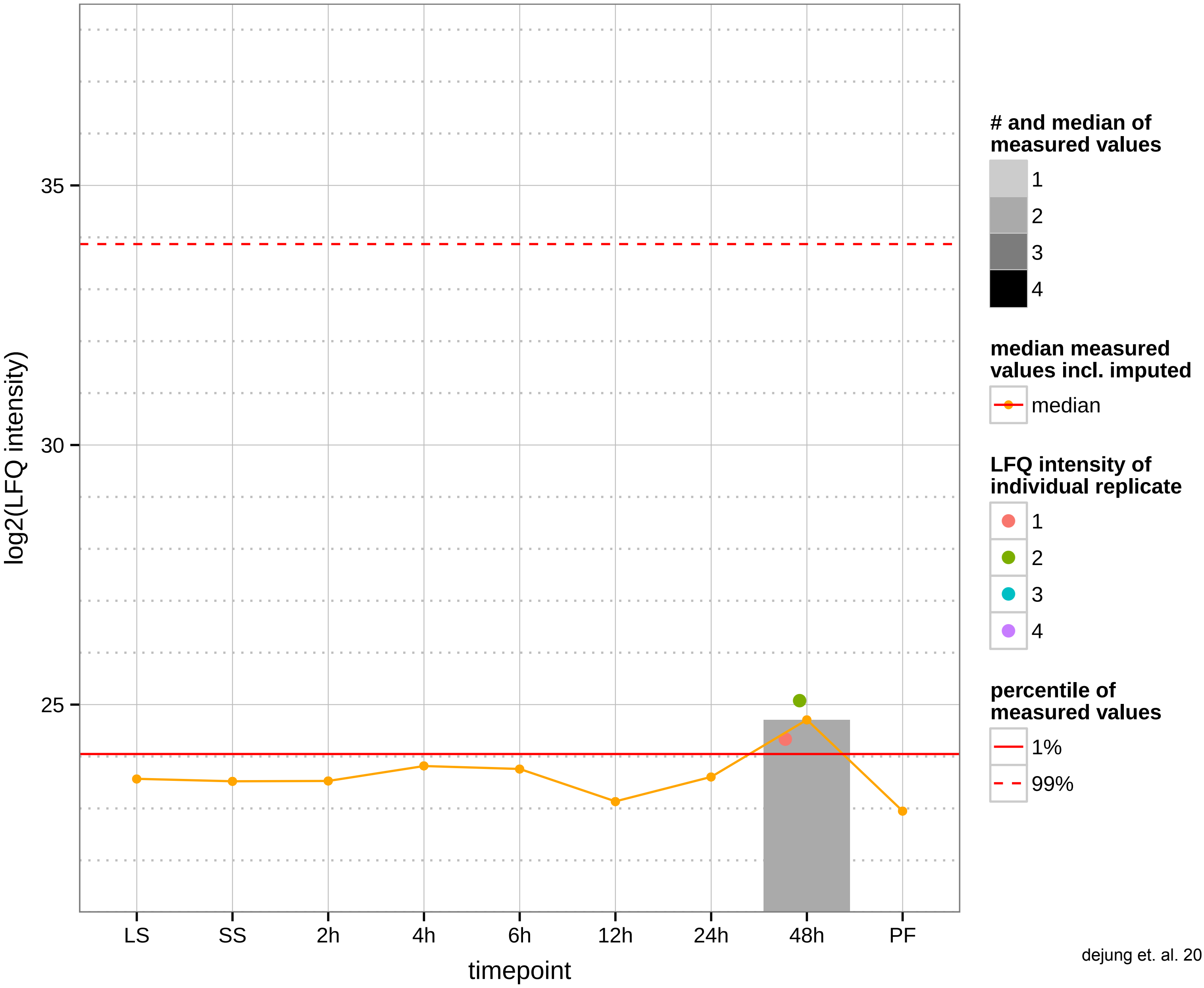
hypothetical protein, conserved
Tb927.10.11260
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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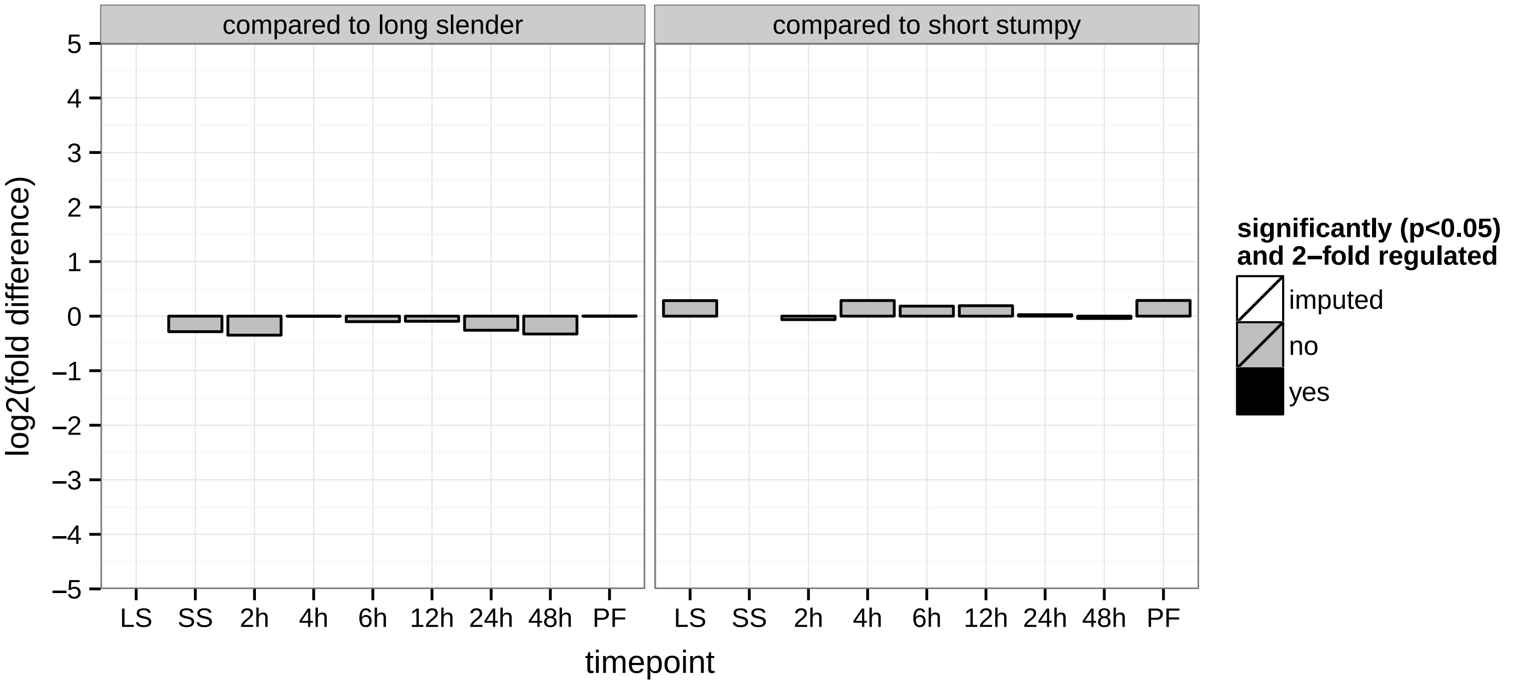
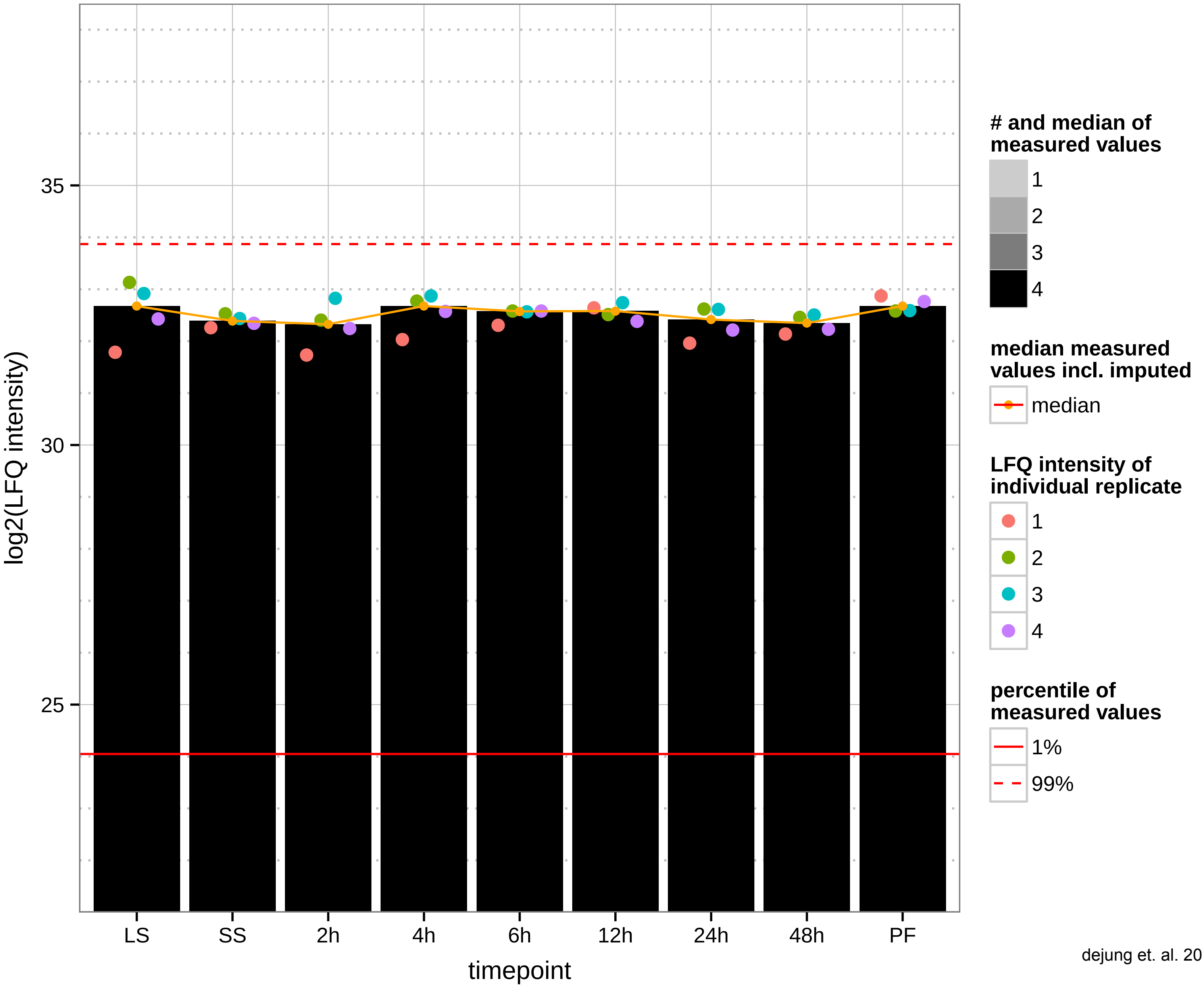
paraflagellar rod component, putative (PFC16)
Tb927.10.11300
AGOF: null
AGOC: eukaryotic translation initiation factor 4F complex
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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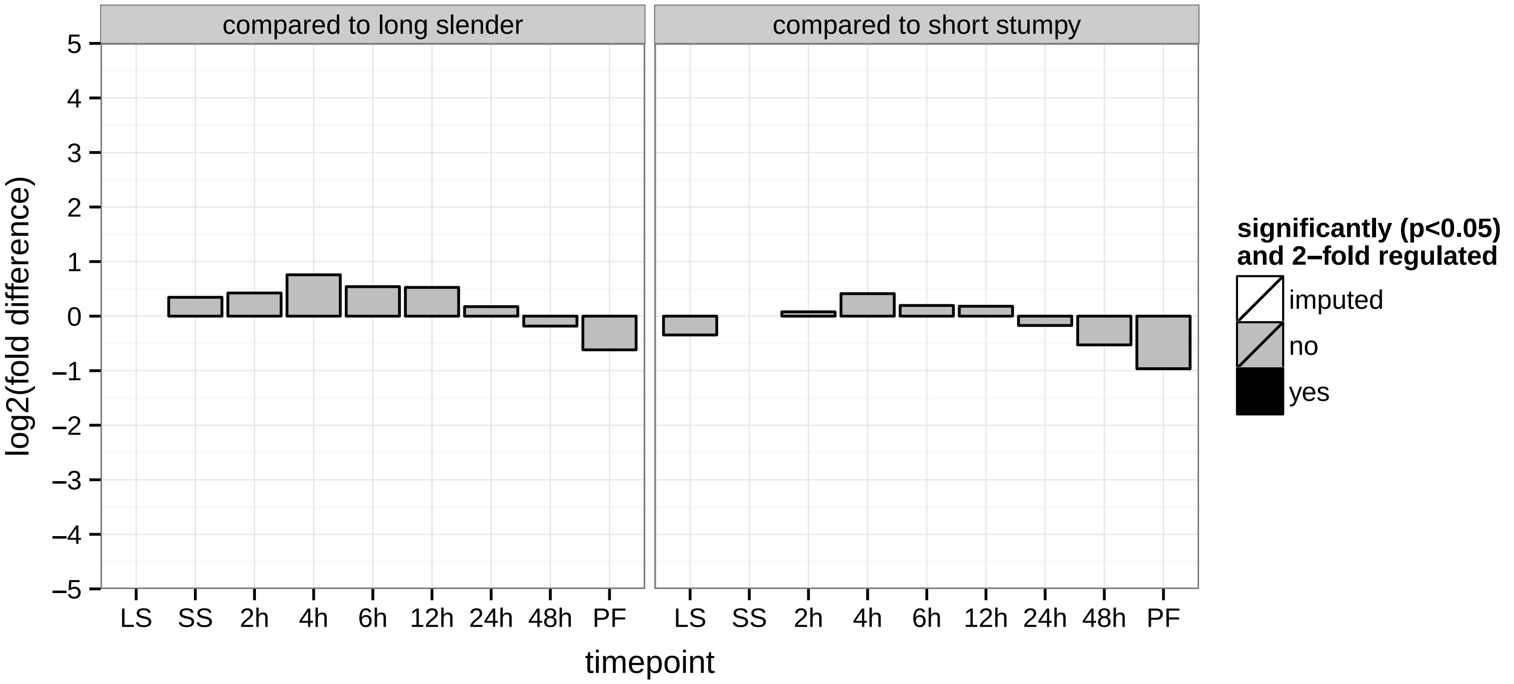
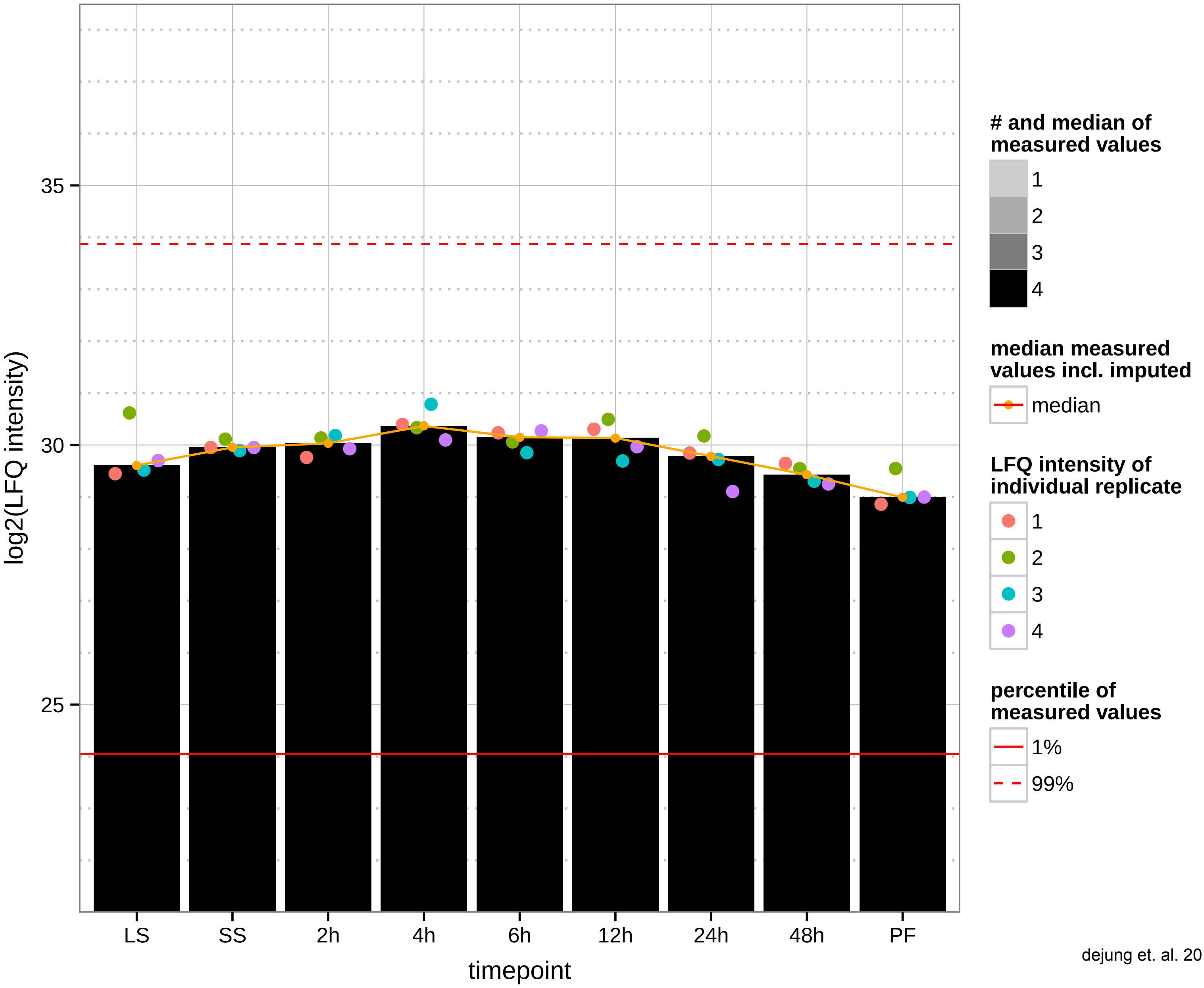
intraflagellar transport protein IFT55/IFT57, putative (IFT57/55)
Tb927.10.11310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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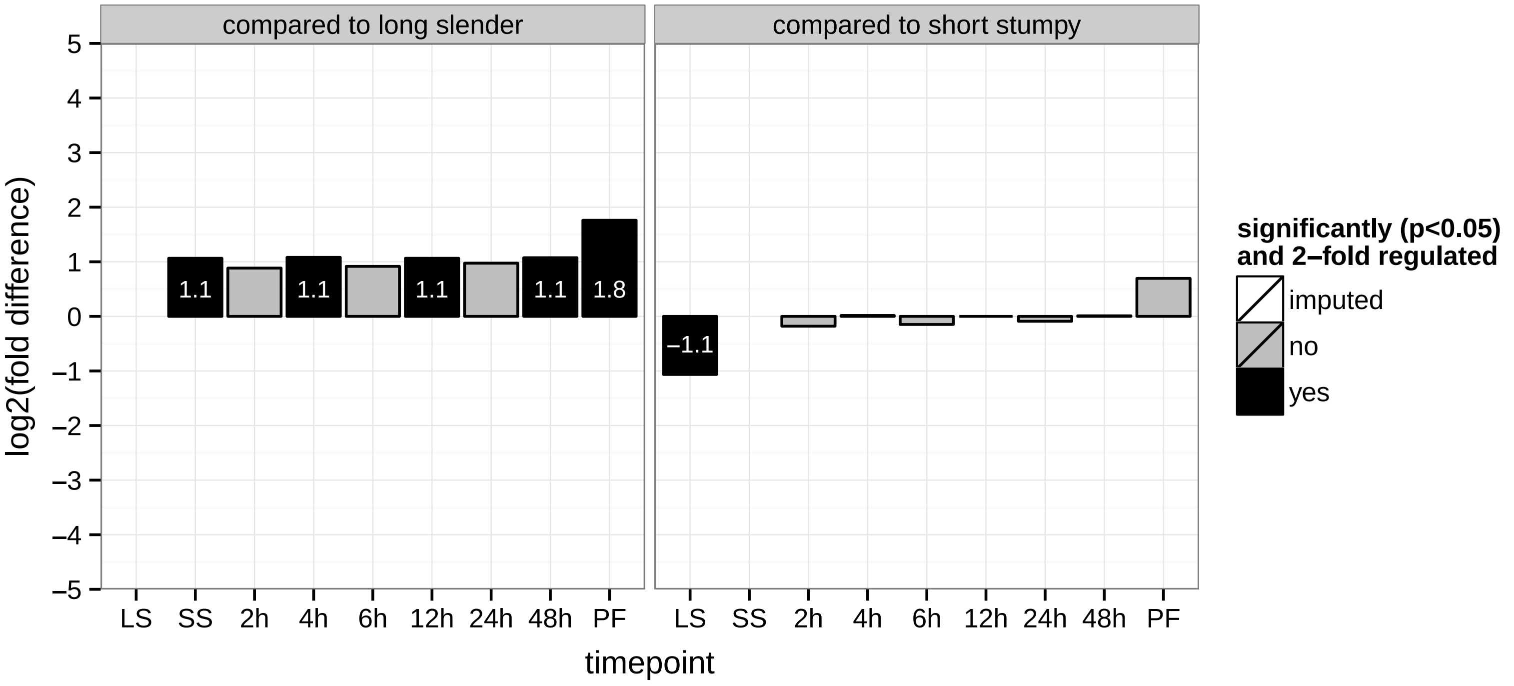
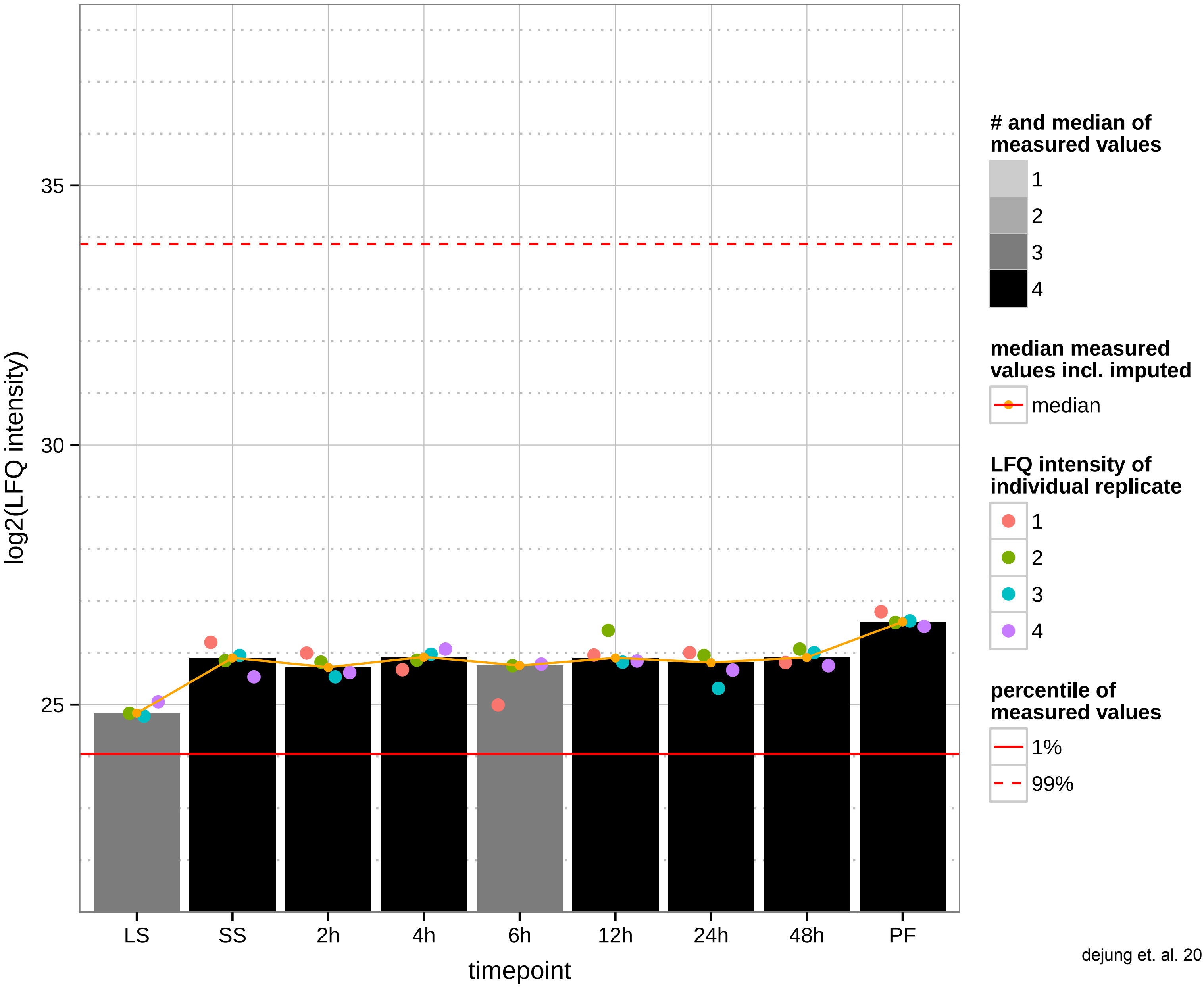
hypothetical protein, conserved
Tb927.10.11510
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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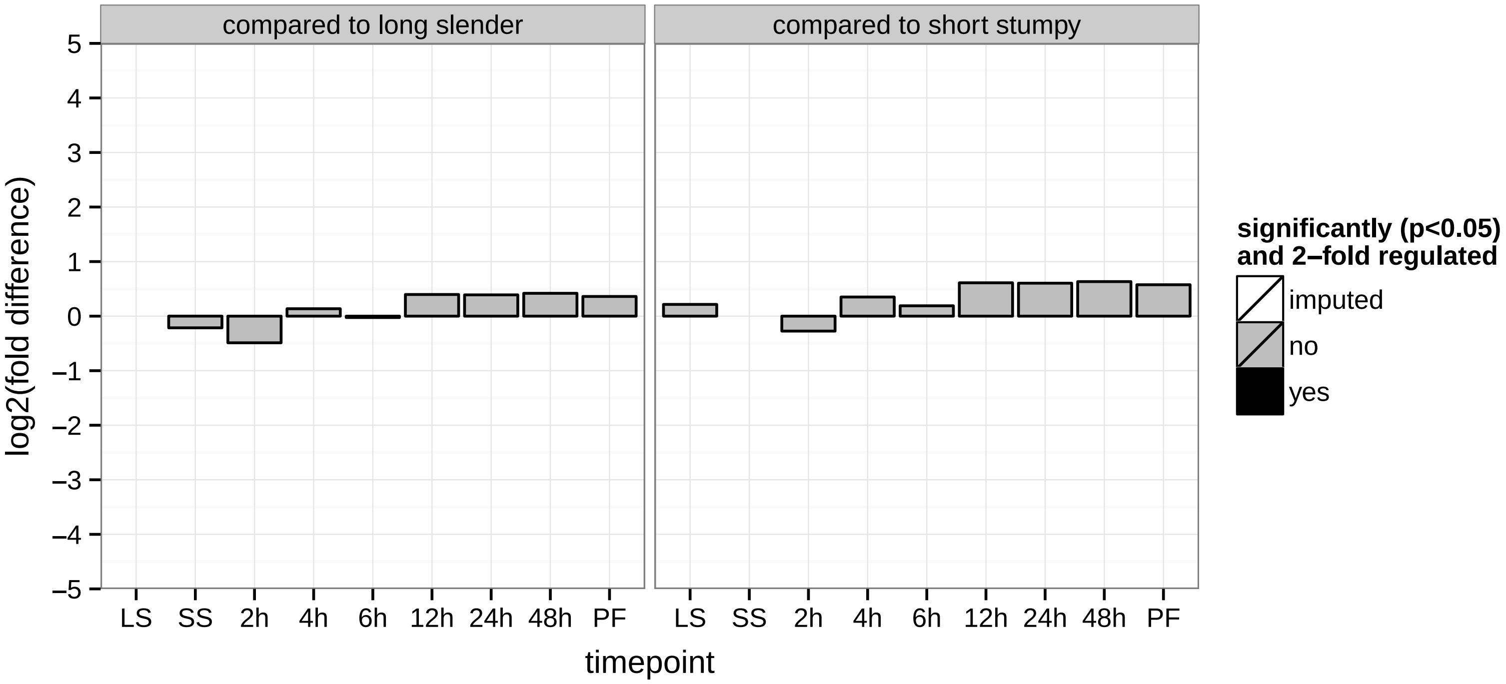
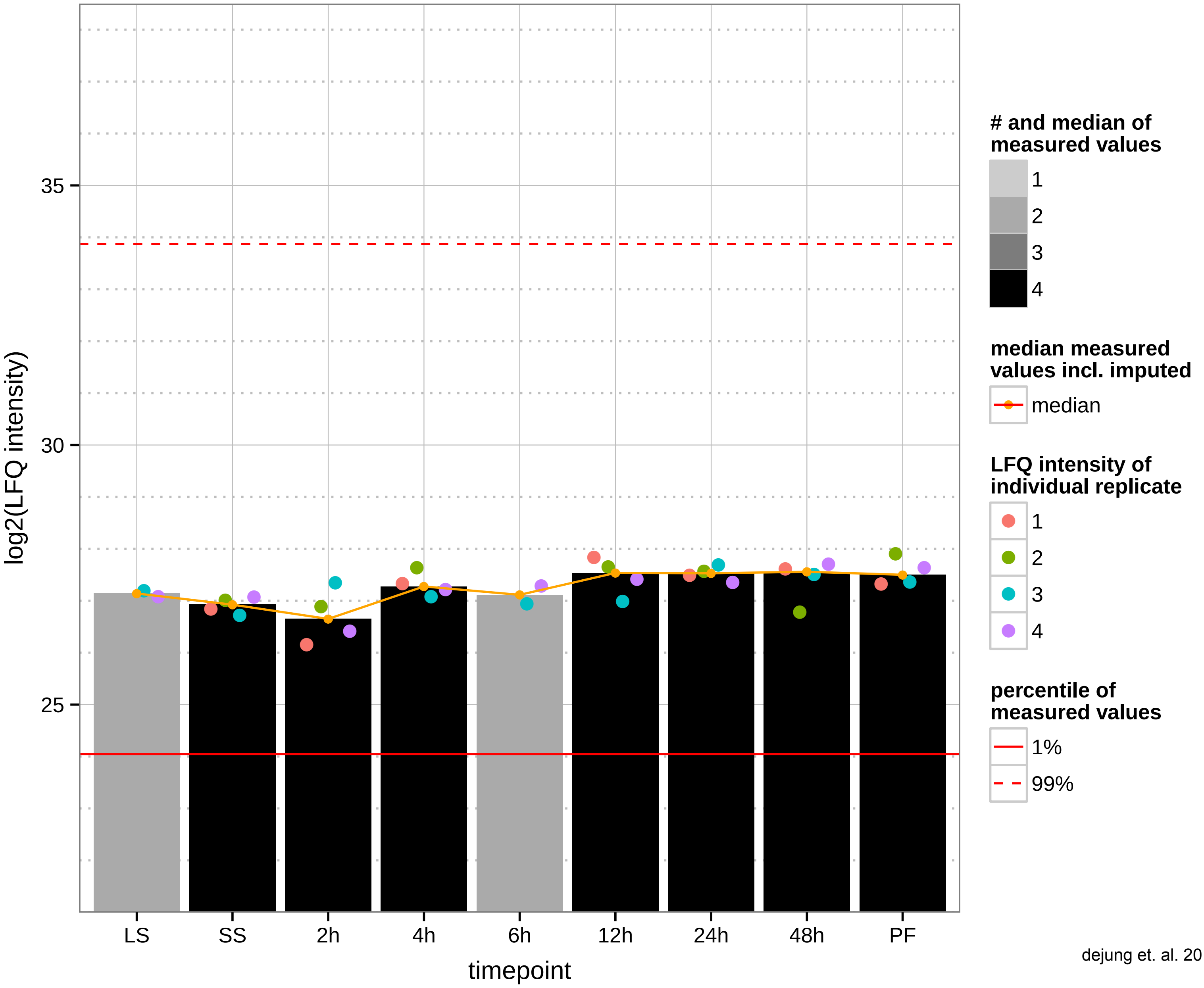
hypothetical protein, conserved
Tb927.10.11530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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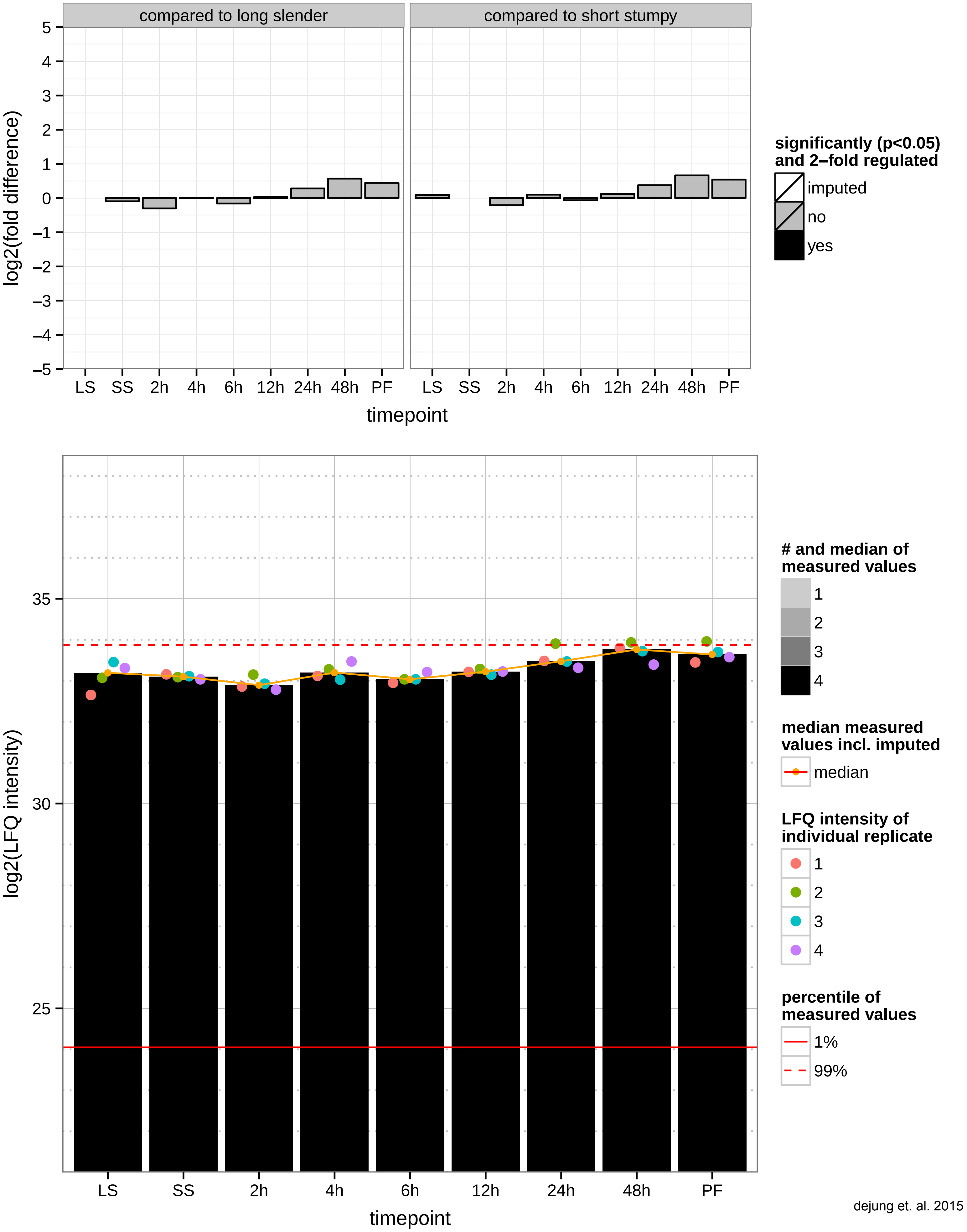
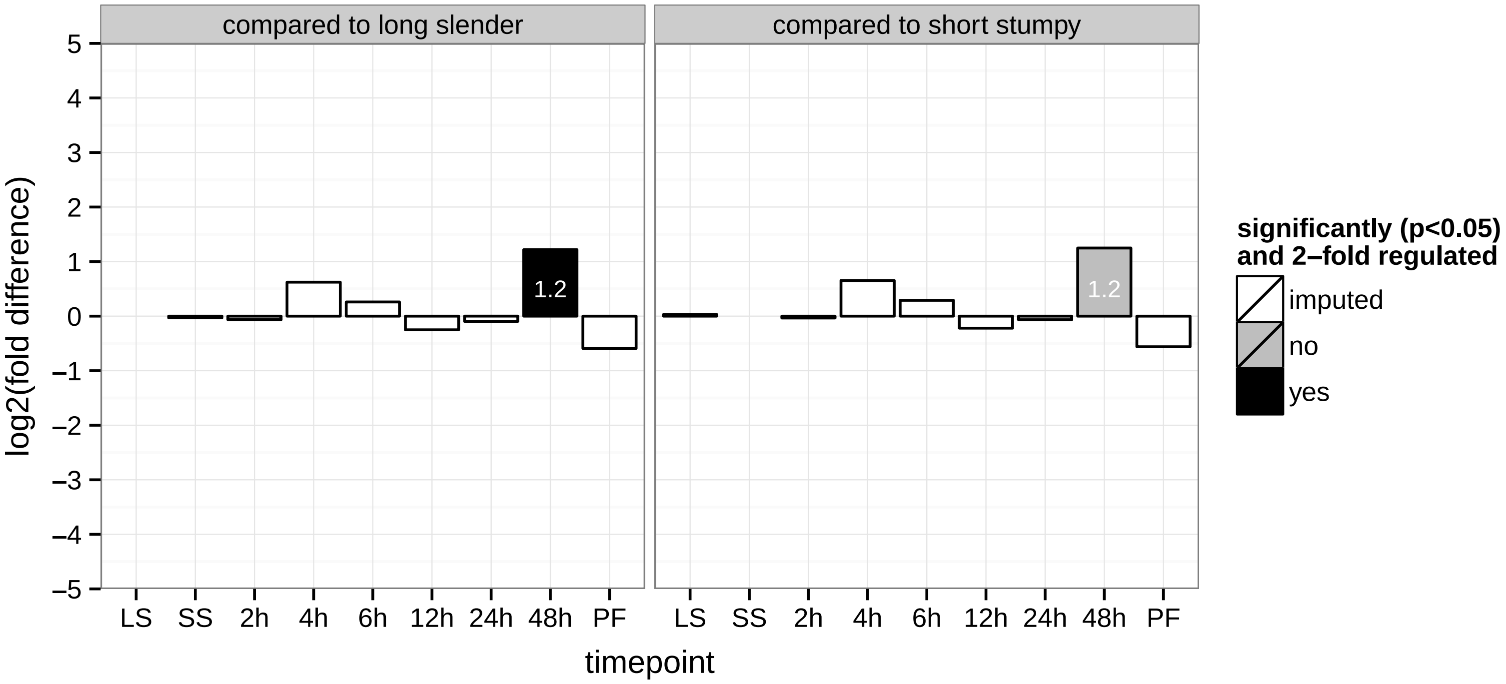
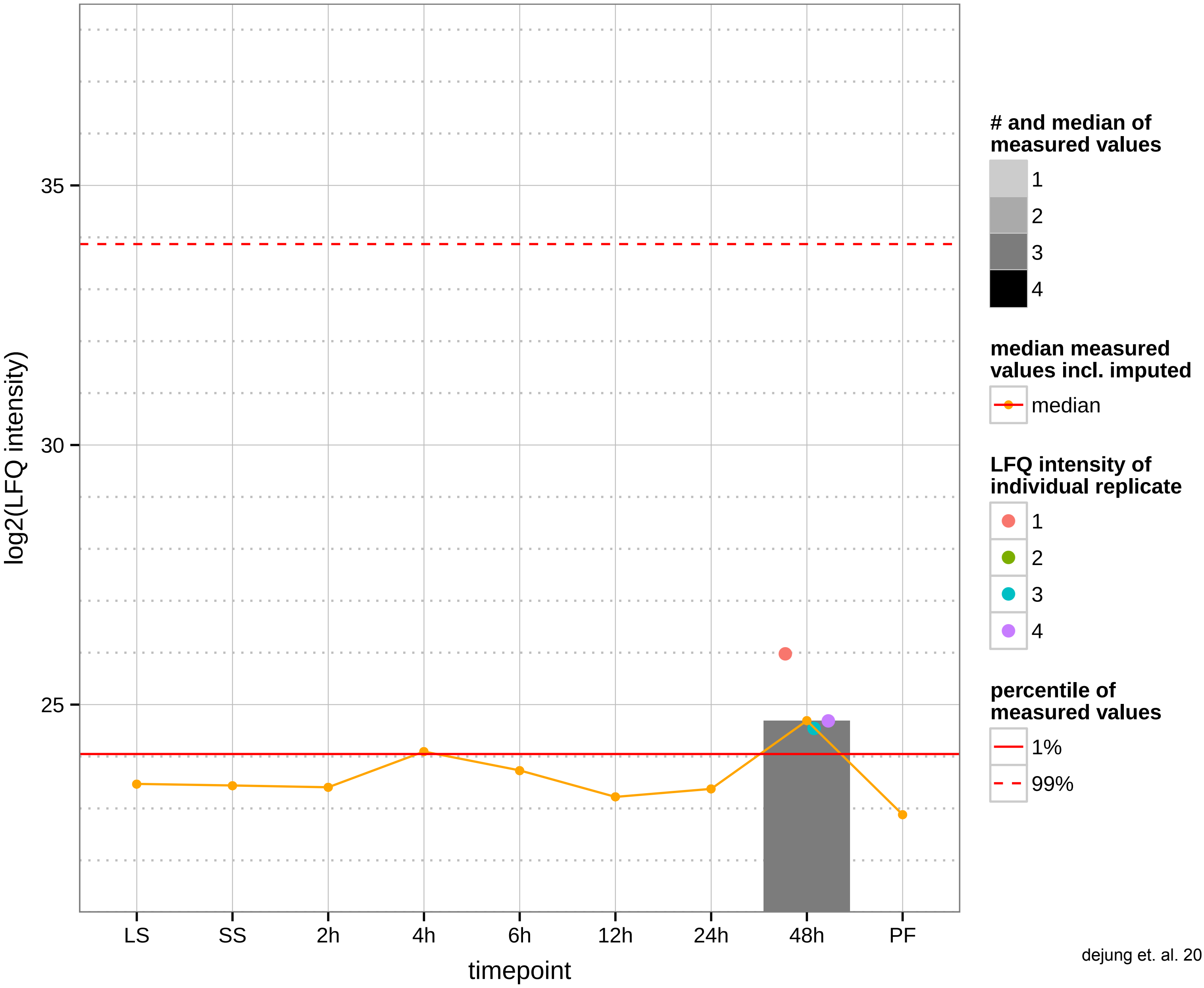
40S ribosomal protein S3, putative (RPS3)
Tb927.9.6070;Tb927.10.11540
AGOF: RNA binding, nucleic acid binding, structural constituent of ribosome
AGOC: intracellular, ribosome, small ribosomal subunit
AGOP: ribosome biogenesis, translation
PGOF: RNA binding, structural constituent of ribosome
PGOC: intracellular, ribosome, small ribosomal subunit
PGOP: translation



hypothetical protein, conserved
Tb927.10.11660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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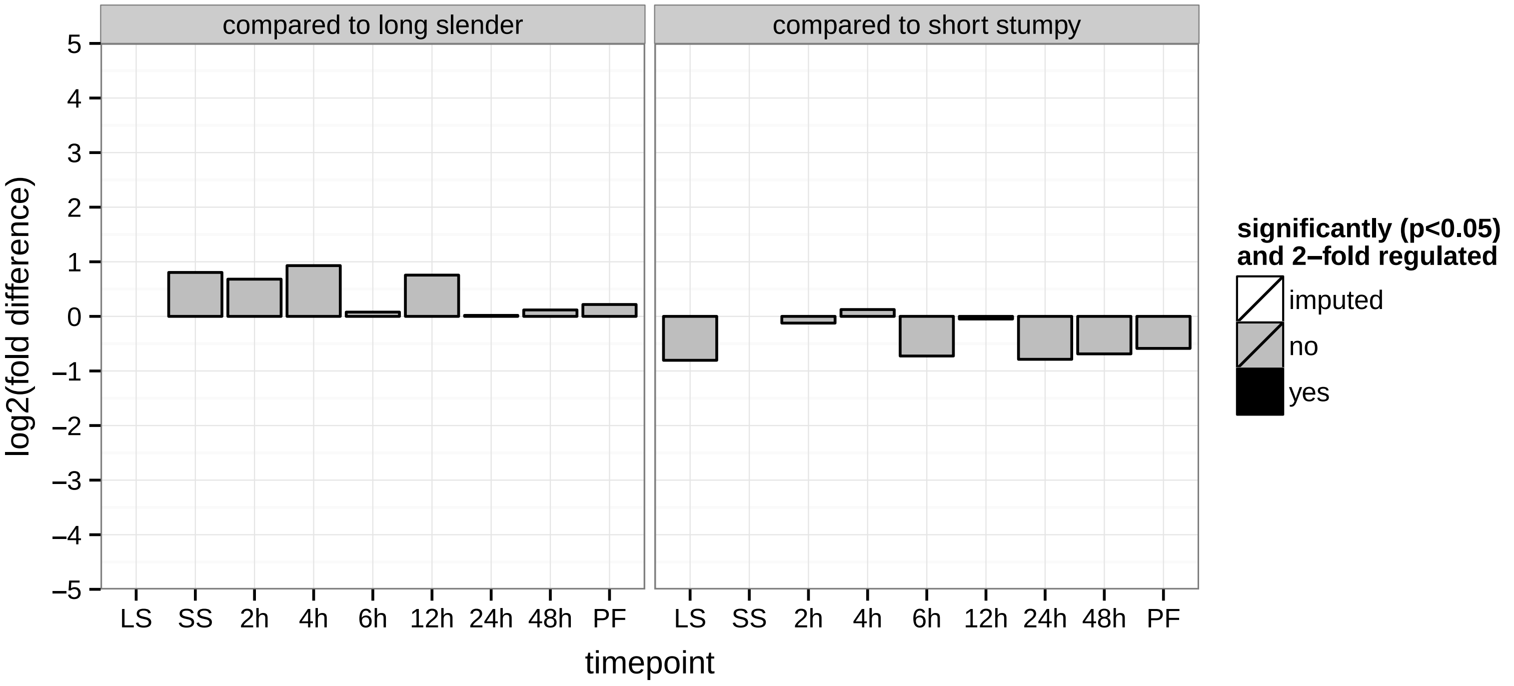
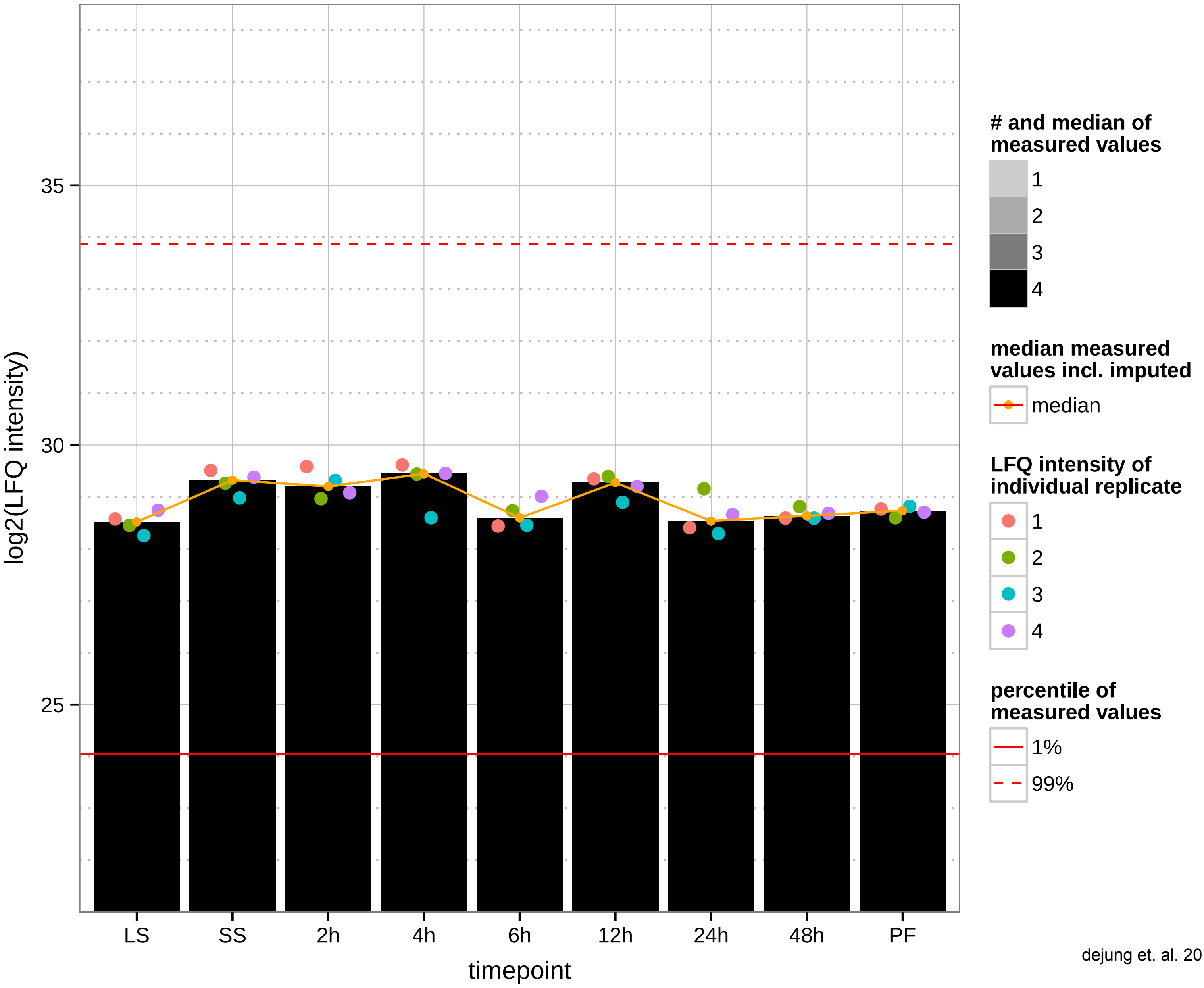
guanylate kinase, putative
Tb927.10.11700
AGOF: guanylate kinase activity
AGOC: null
AGOP: nucleobase−containing small molecule interconversion
PGOF: protein binding
PGOC: null
PGOP: null





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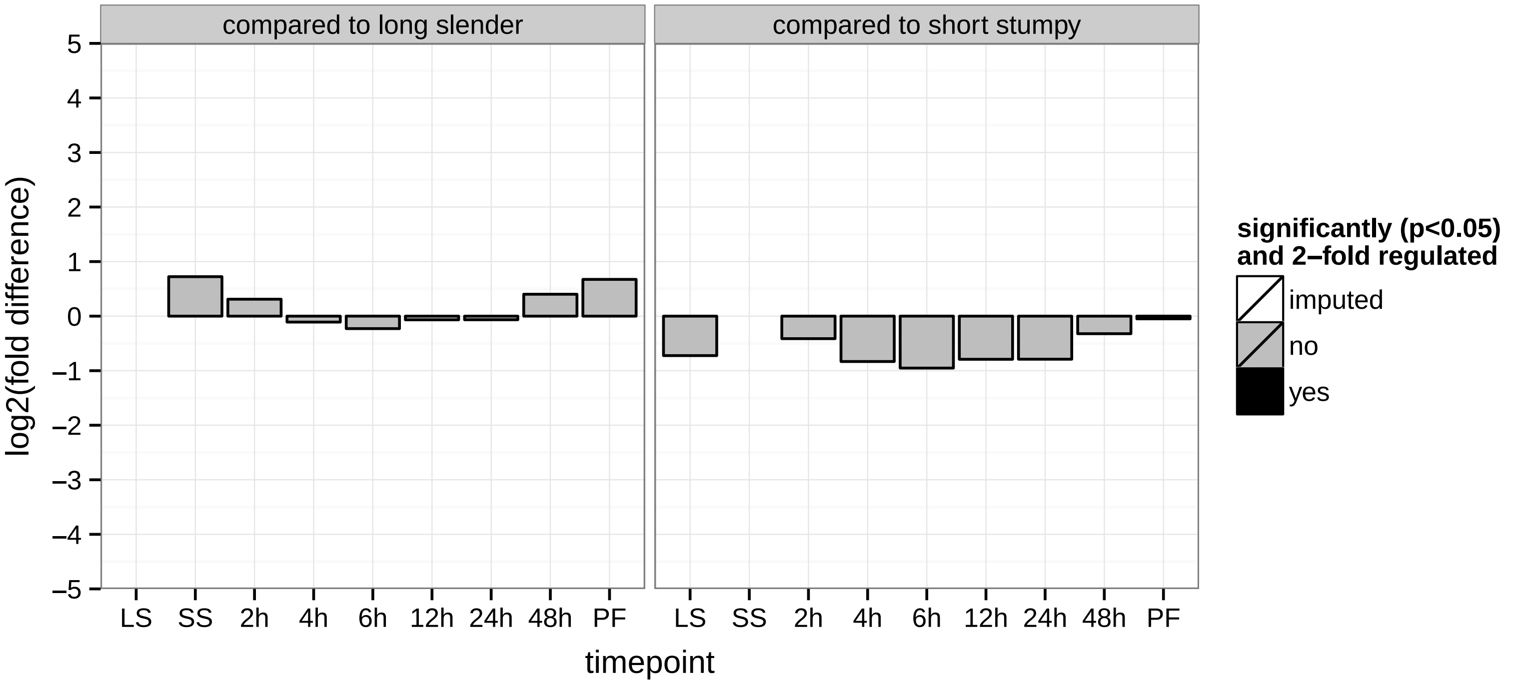
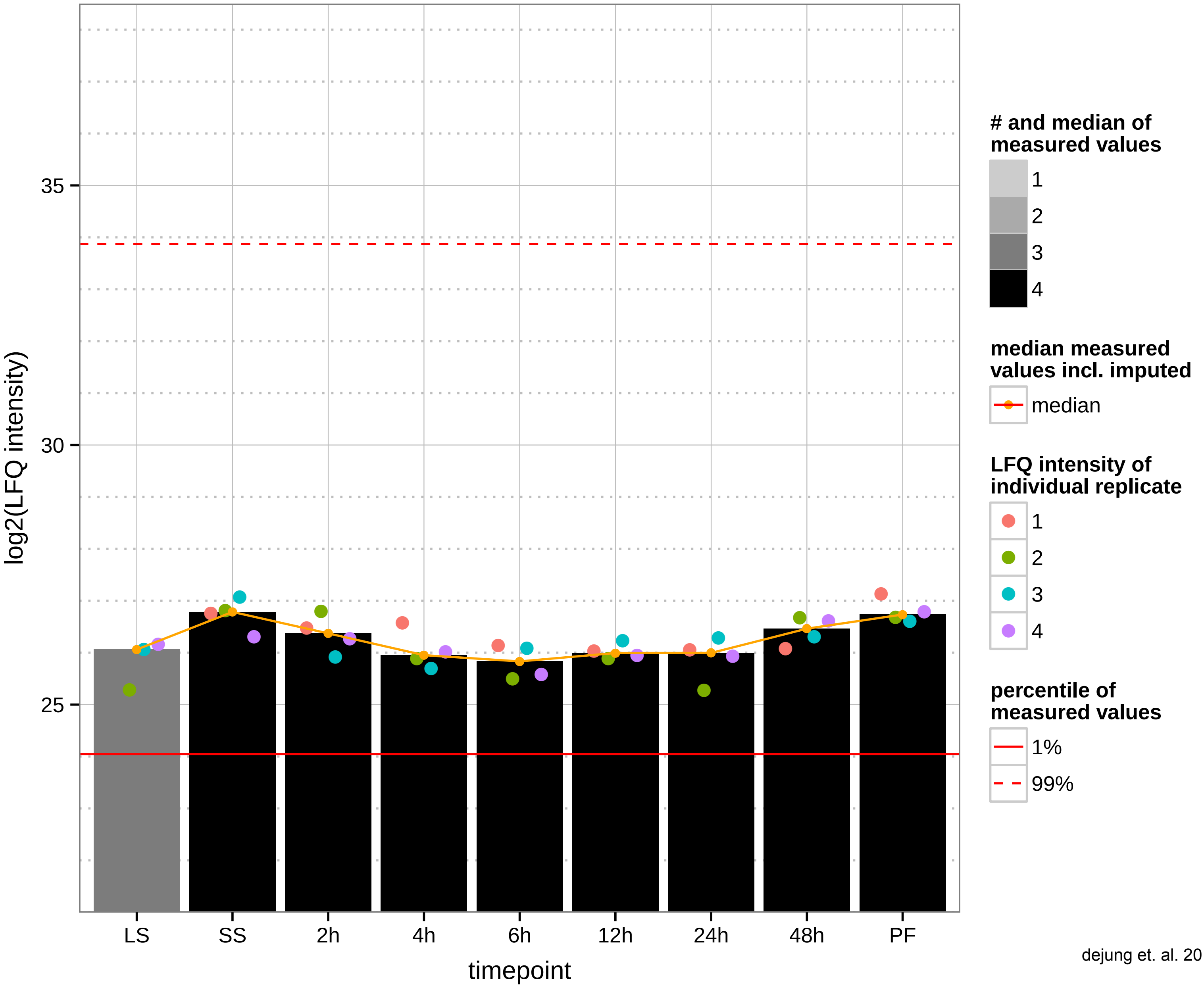
hypothetical protein, conserved
Tb927.10.11780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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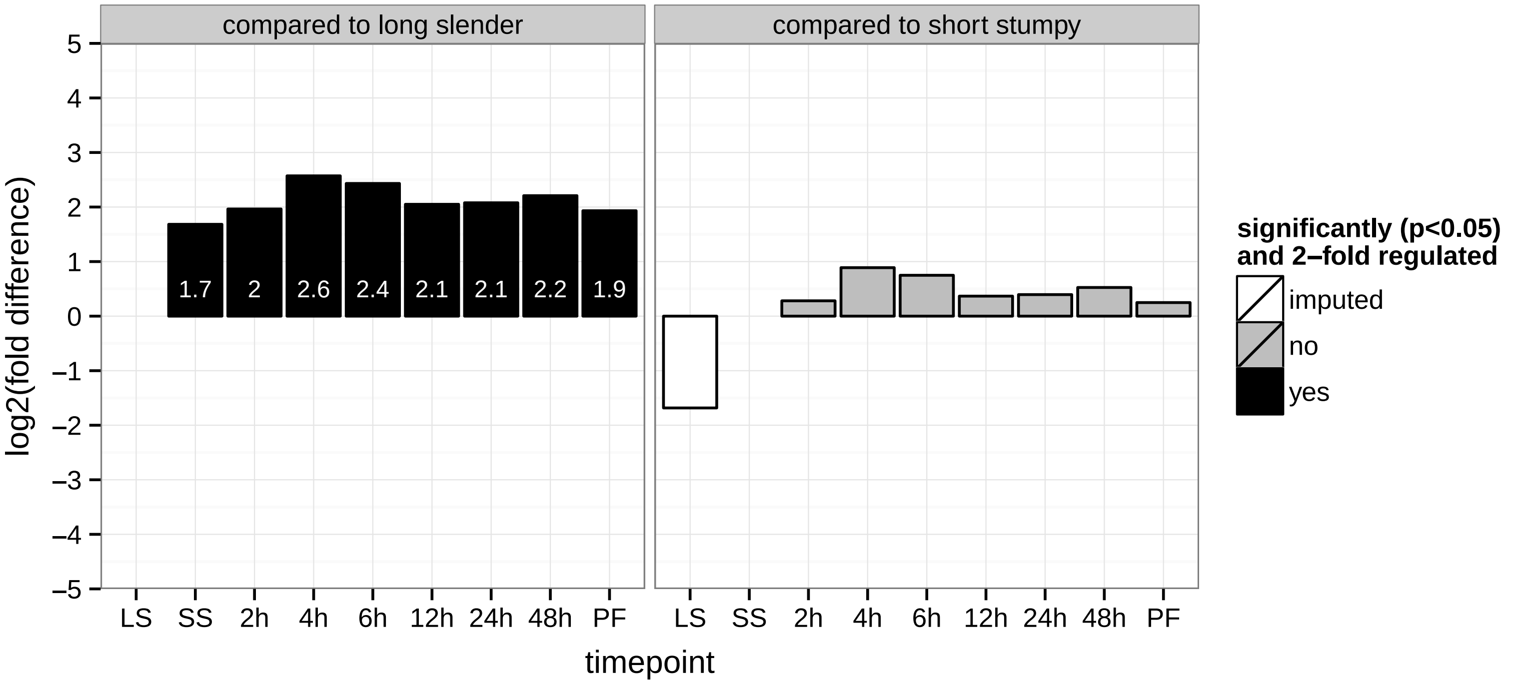
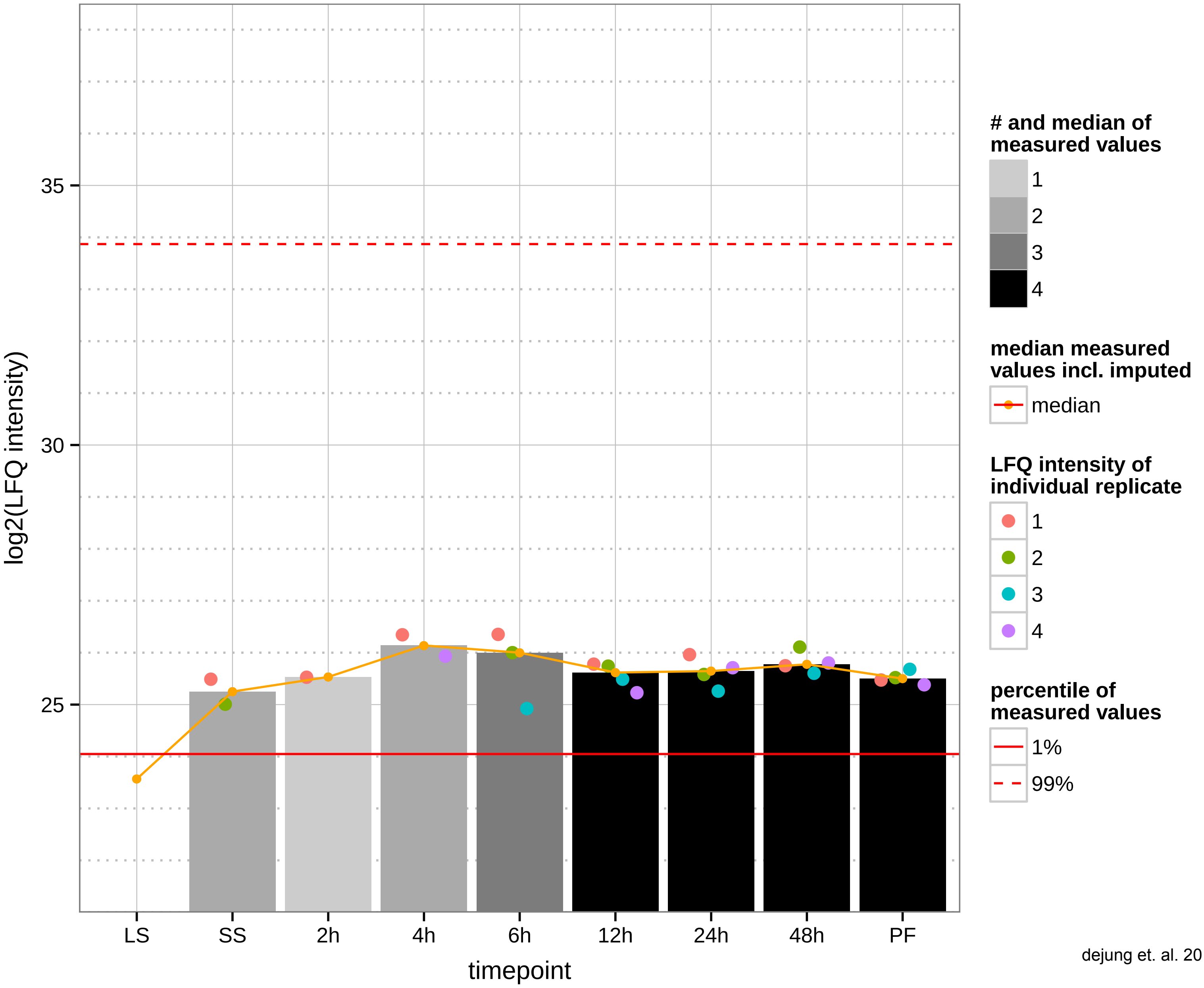
Axonemal inner arm dynein light chain, putative
Tb927.10.11800
AGOF: microtubule motor activity
AGOC: null
AGOP: microtubule−based movement
PGOF: null
PGOC: null
PGOP: null





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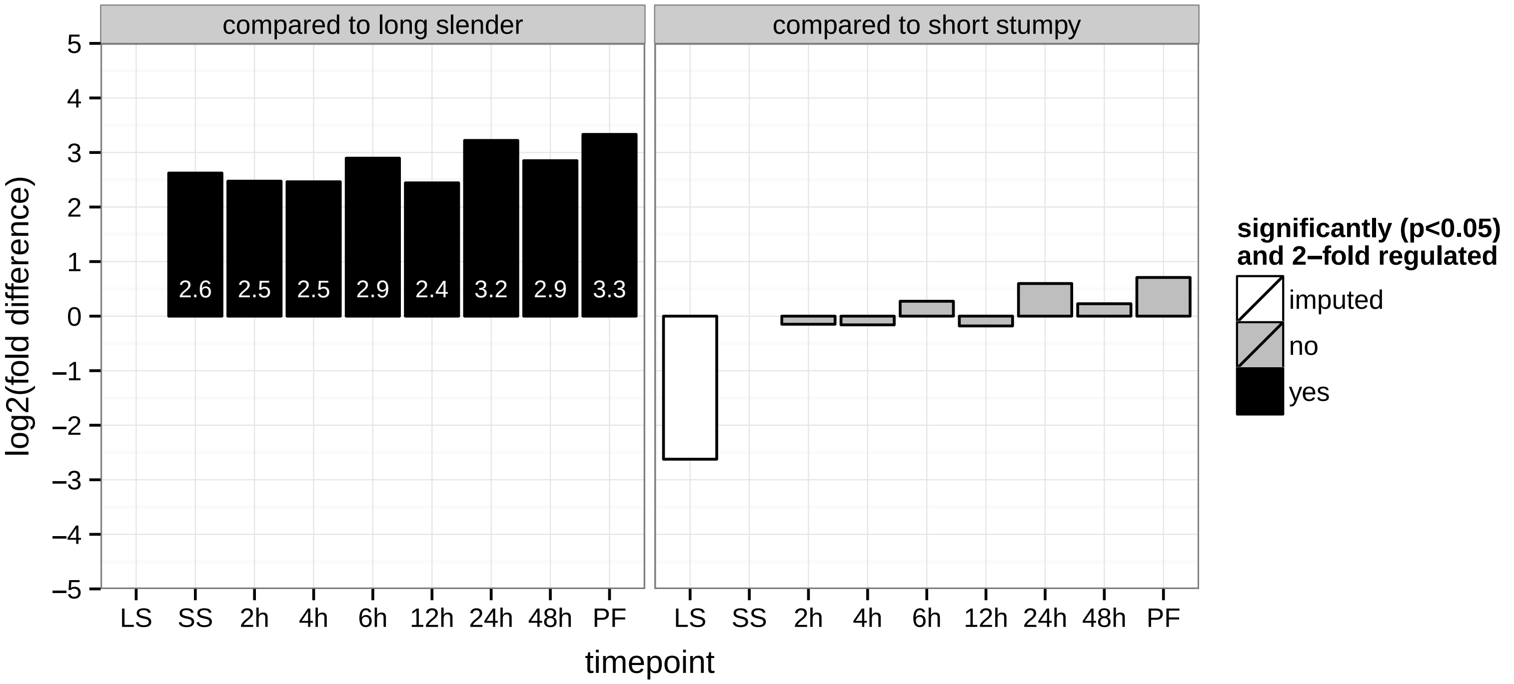
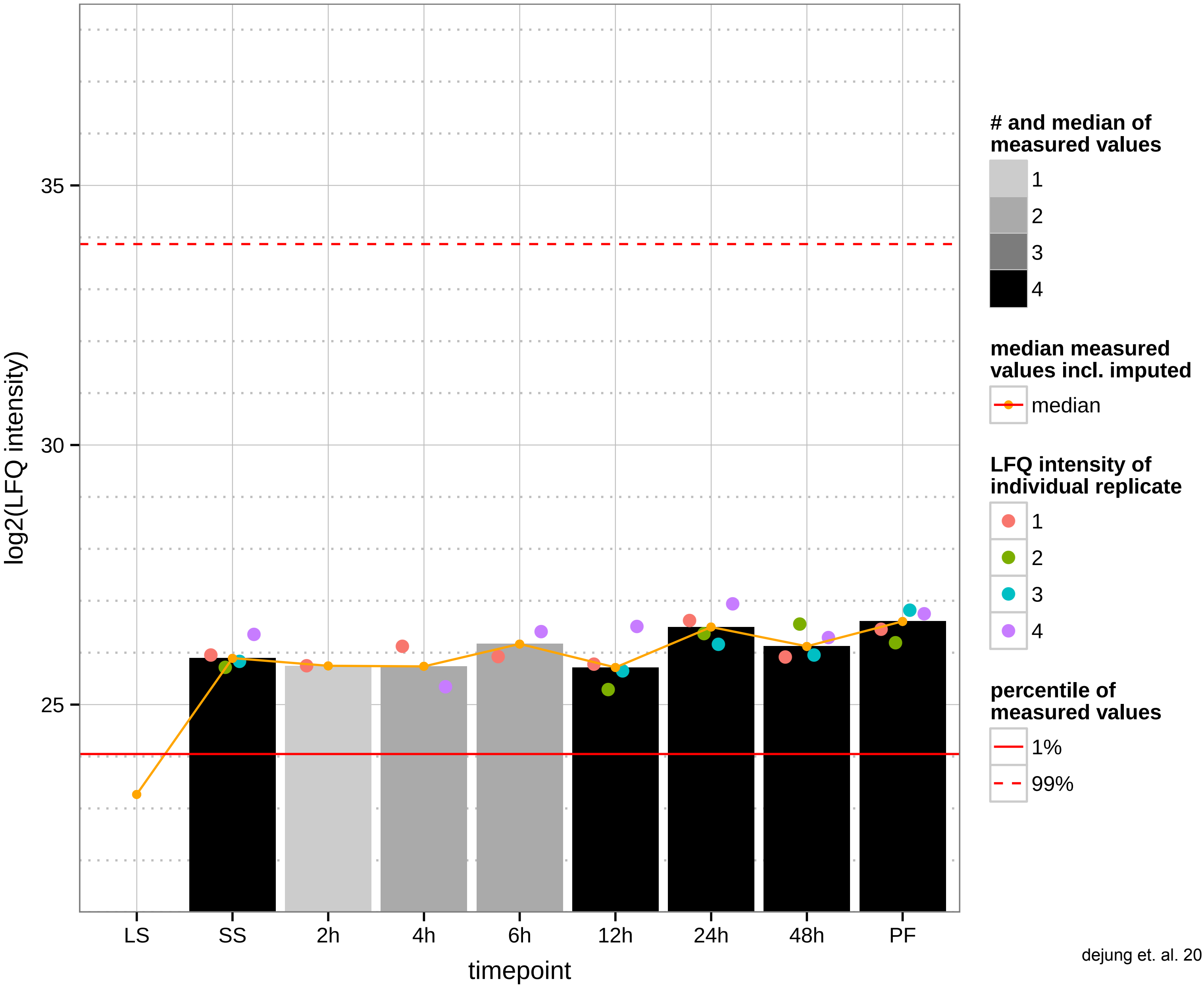
mitochondrial RNA binding protein (MRB11870)
Tb927.10.11870
AGOF: RNA binding
AGOC: mitochondrion
AGOP: RNA metabolic process
PGOF: null
PGOC: null
PGOP: null





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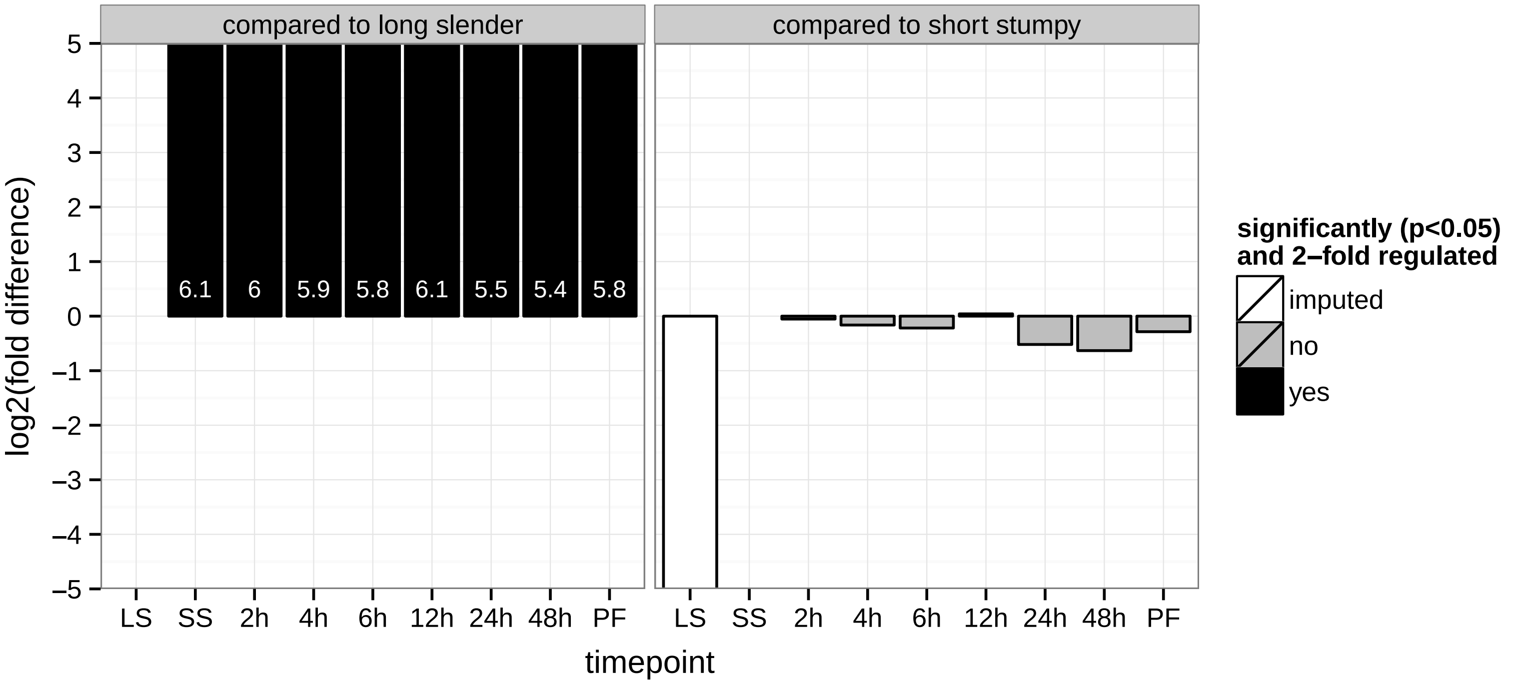
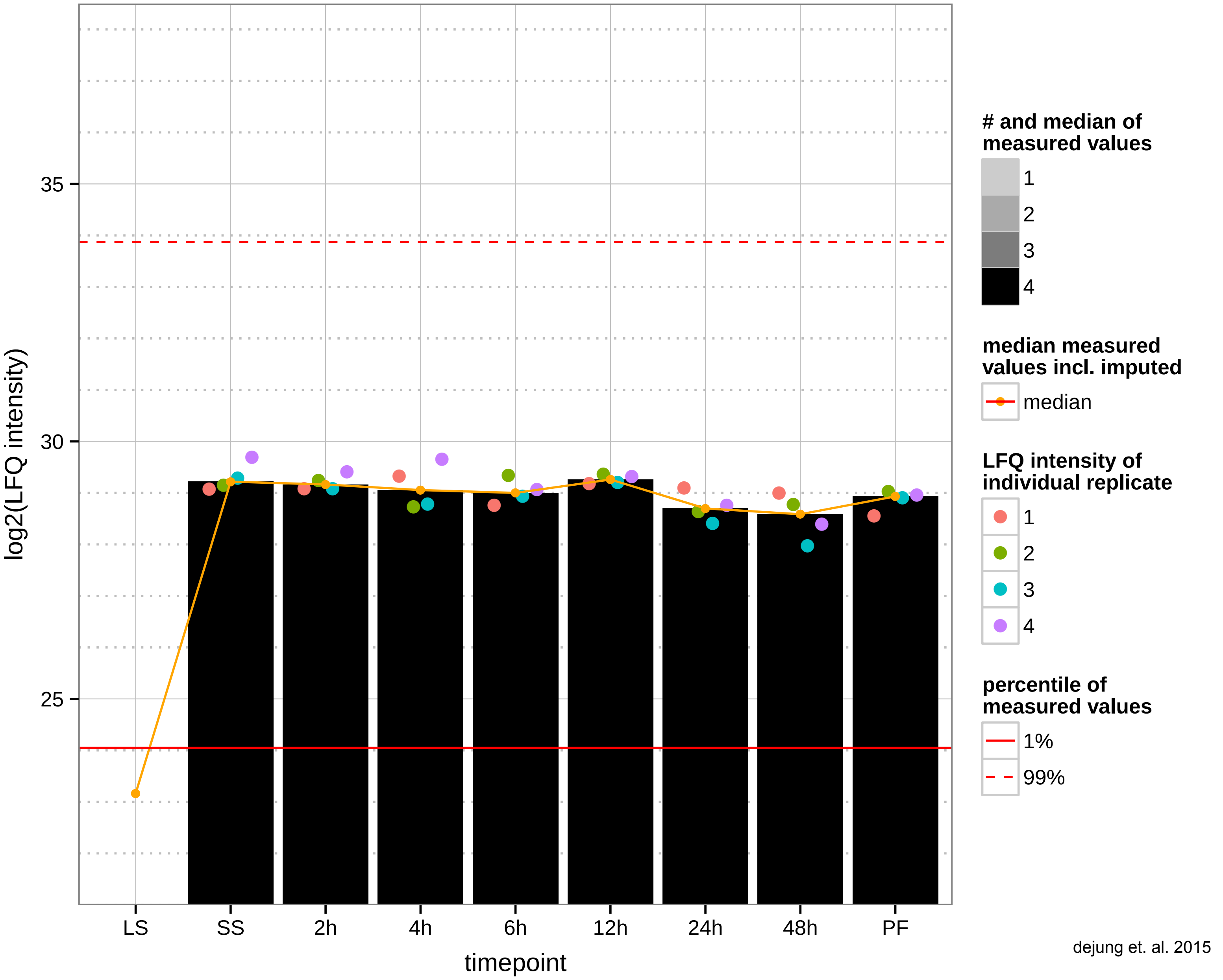
glutamine aminotransferase (GlnAT) (GlnAT)
Tb927.10.11970
AGOF: 1−aminocyclopropane−1−carboxylate synthase activity, L−cysteine:2−oxoglutarate aminotransferase activity, L−glutam
AGOC: cytosol
AGOP: biosynthetic process
PGOF: pyridoxal phosphate binding, transferase activity
PGOC: null
PGOP: biosynthetic process





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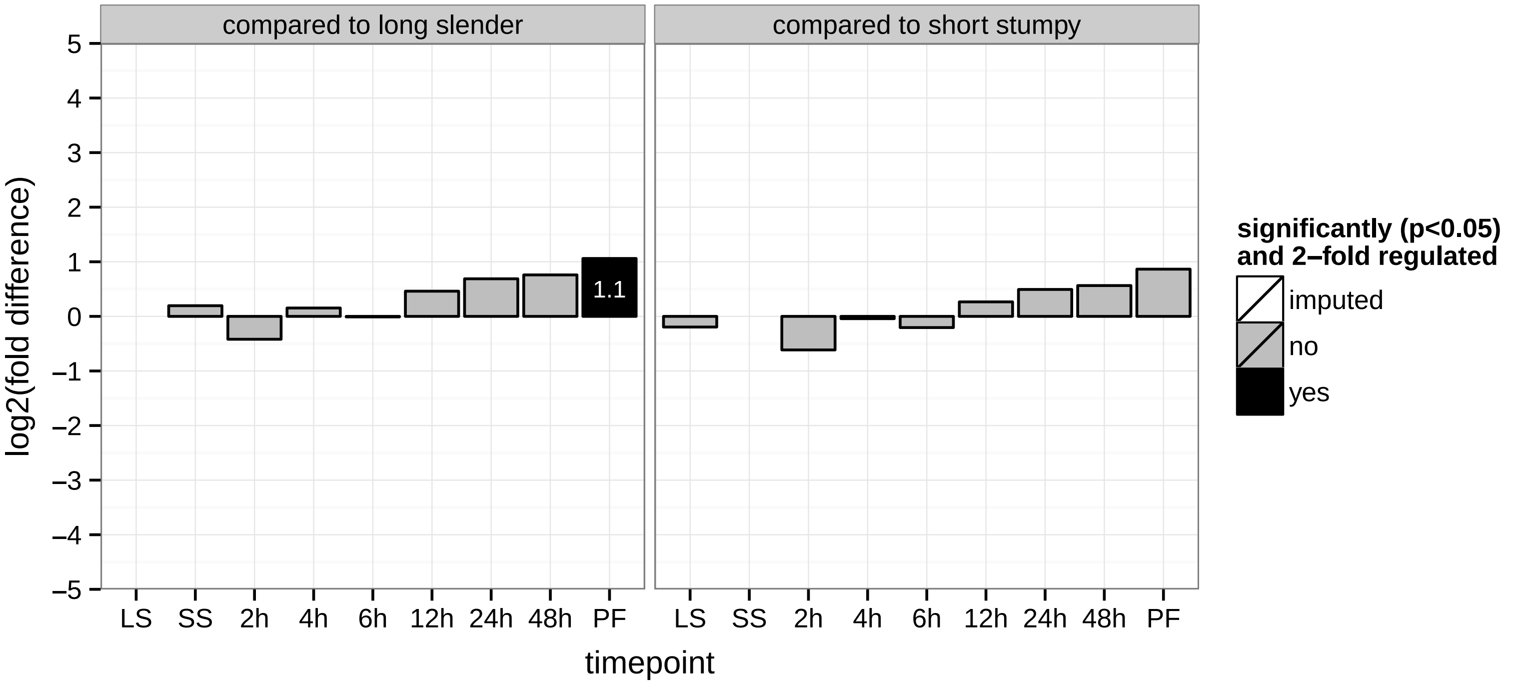
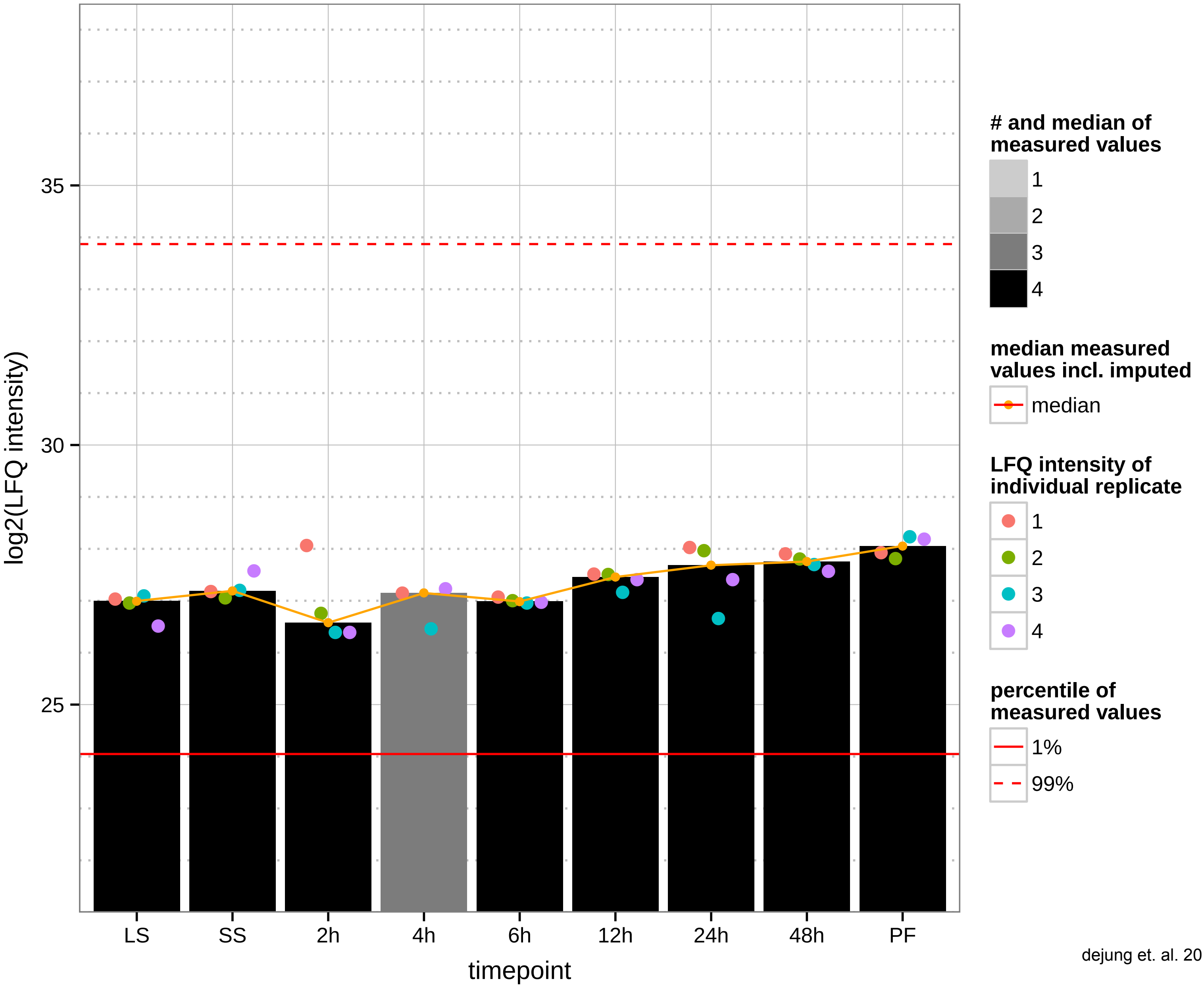
RNA–binding protein
Tb927.10.11990
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: RNA binding
PGOC: nucleus
PGOP: ribosome assembly





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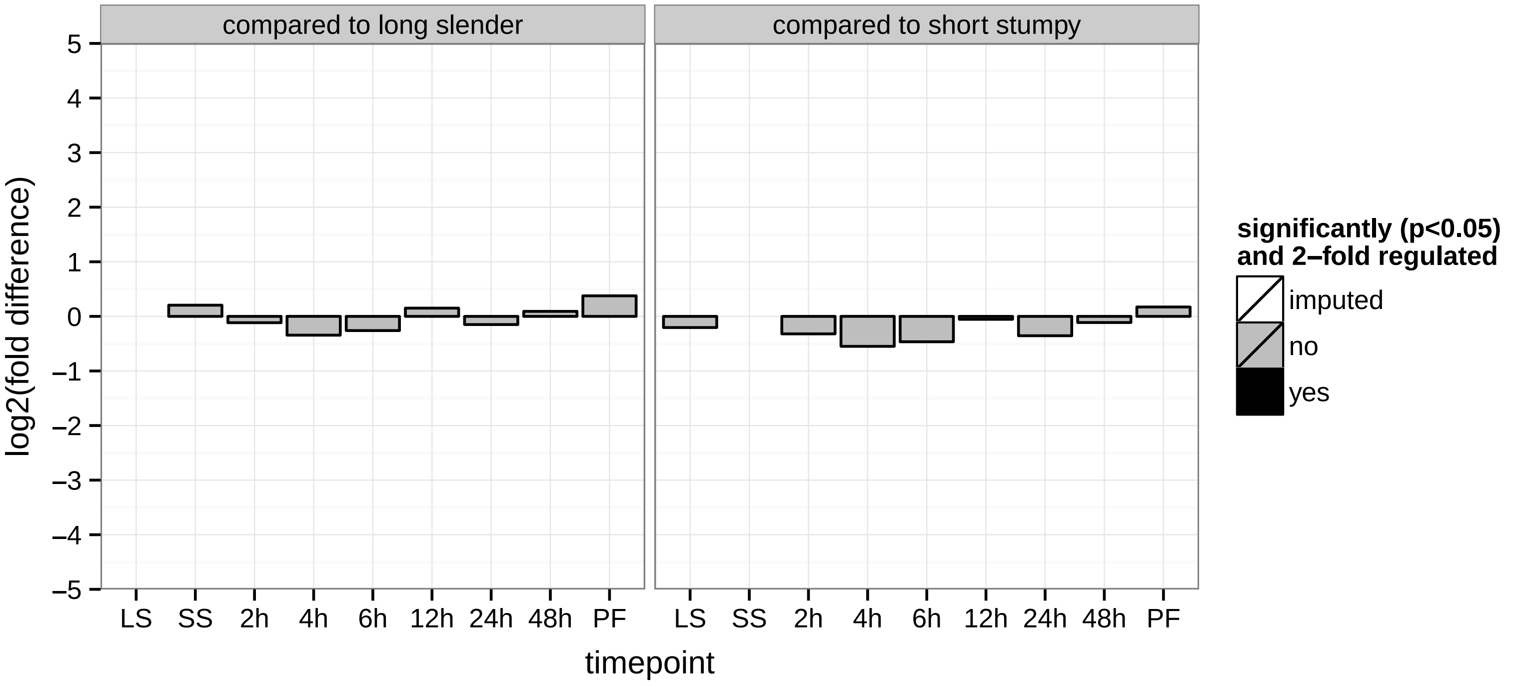
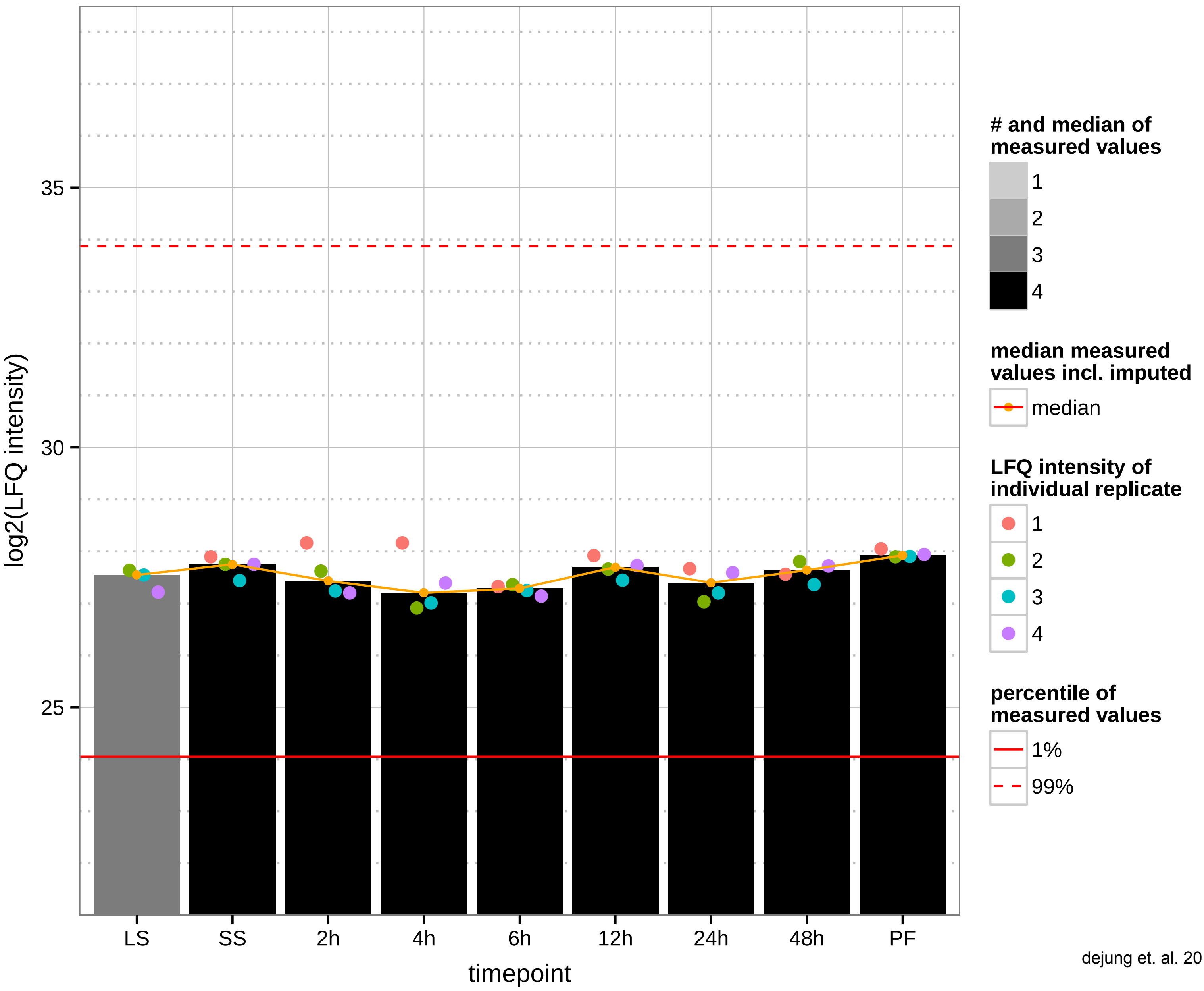
katanin, putative
Tb927.10.1210
AGOF: null, ATP binding, ATPase activity
AGOC: null, katanin complex
AGOP: null, endosomal transport
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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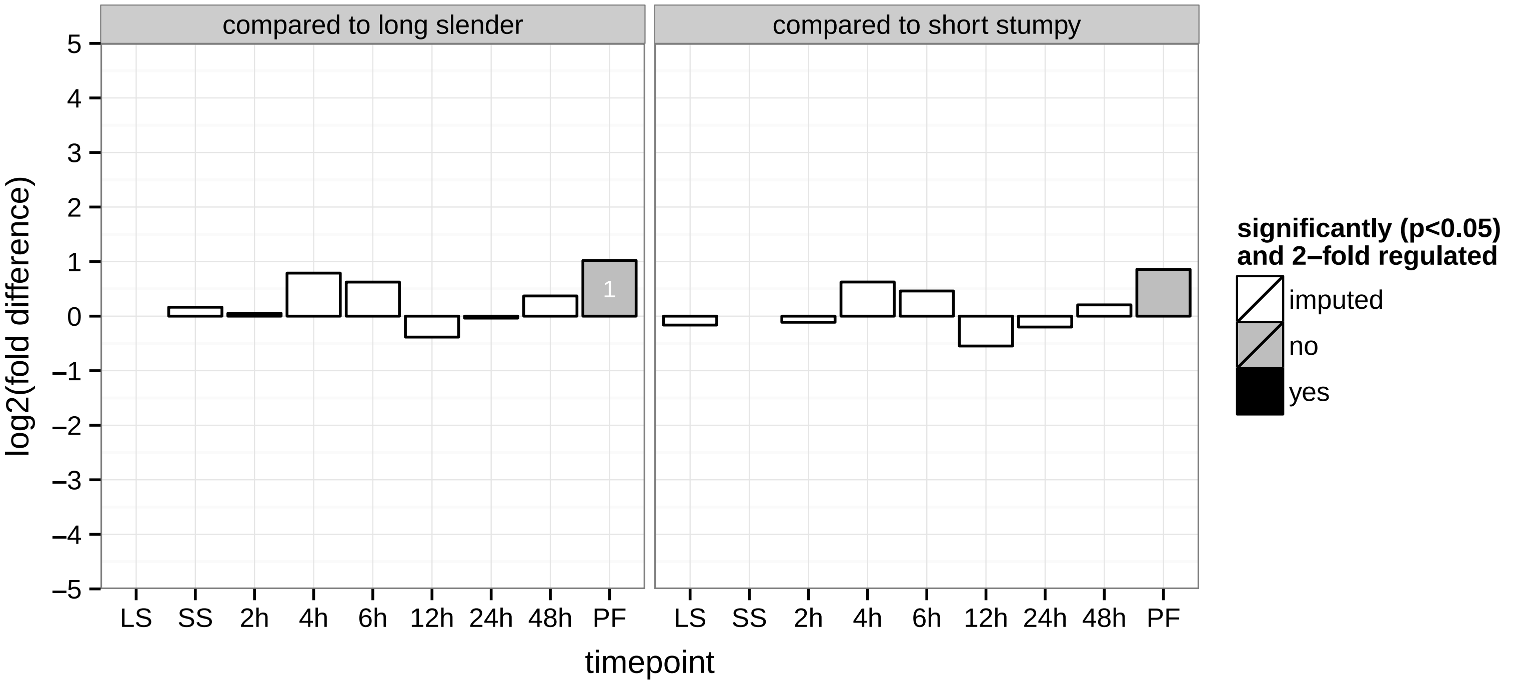
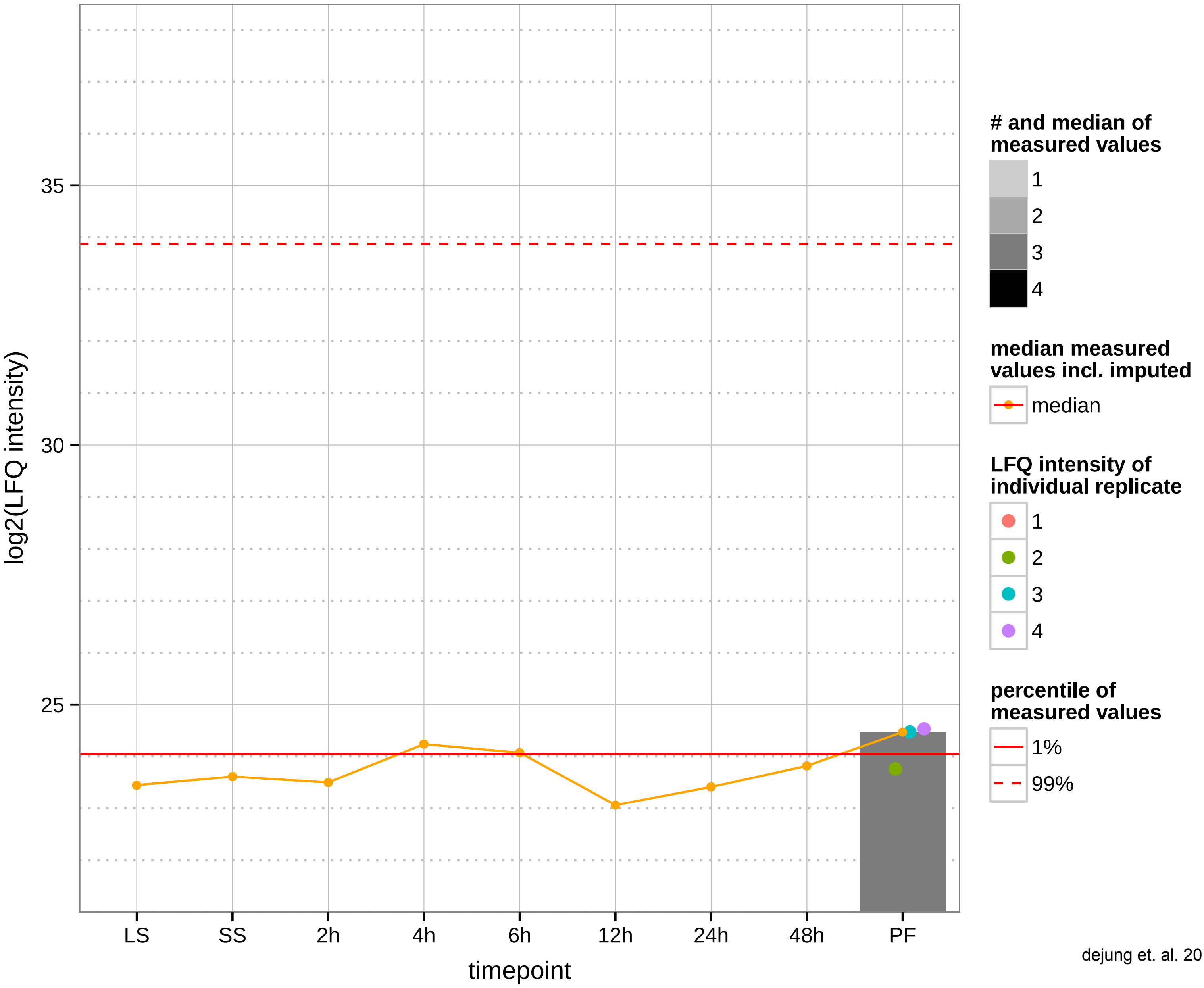
hypothetical protein, conserved
Tb927.10.12110
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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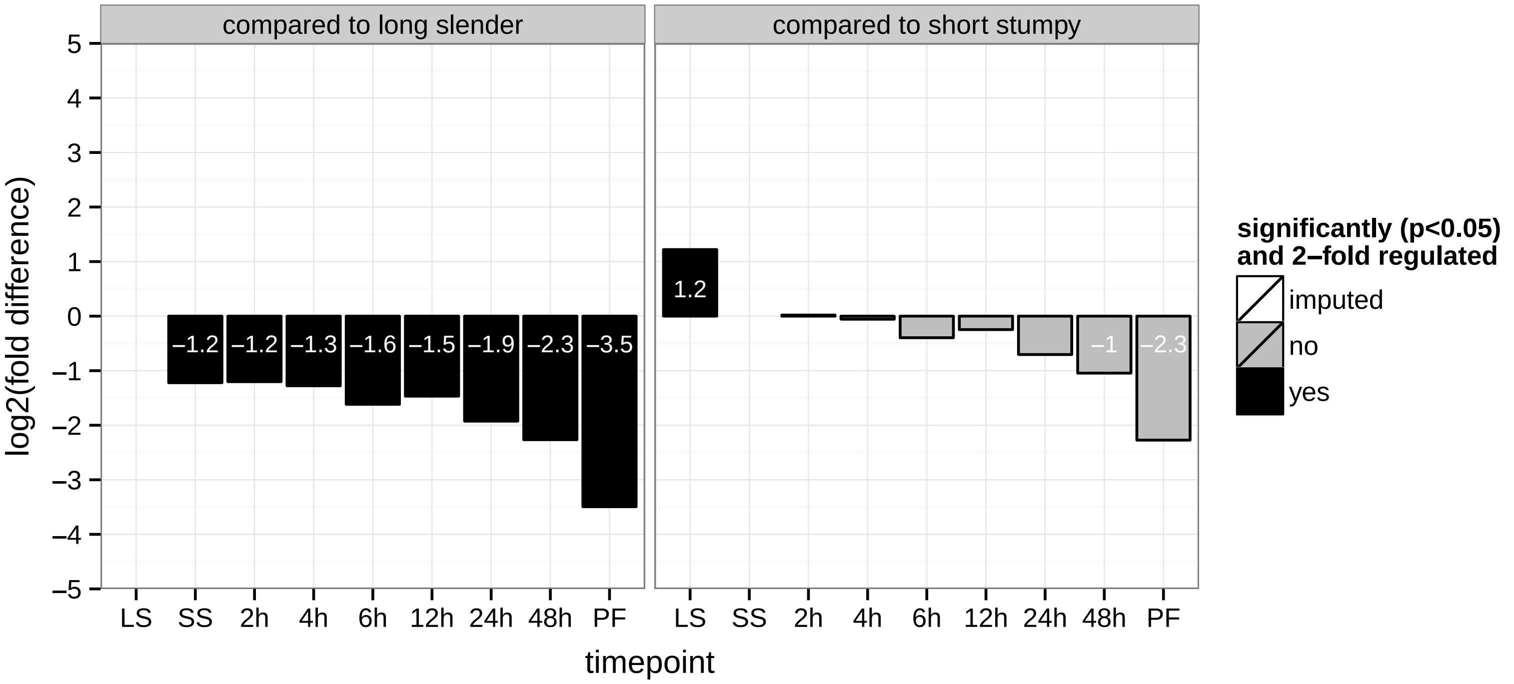
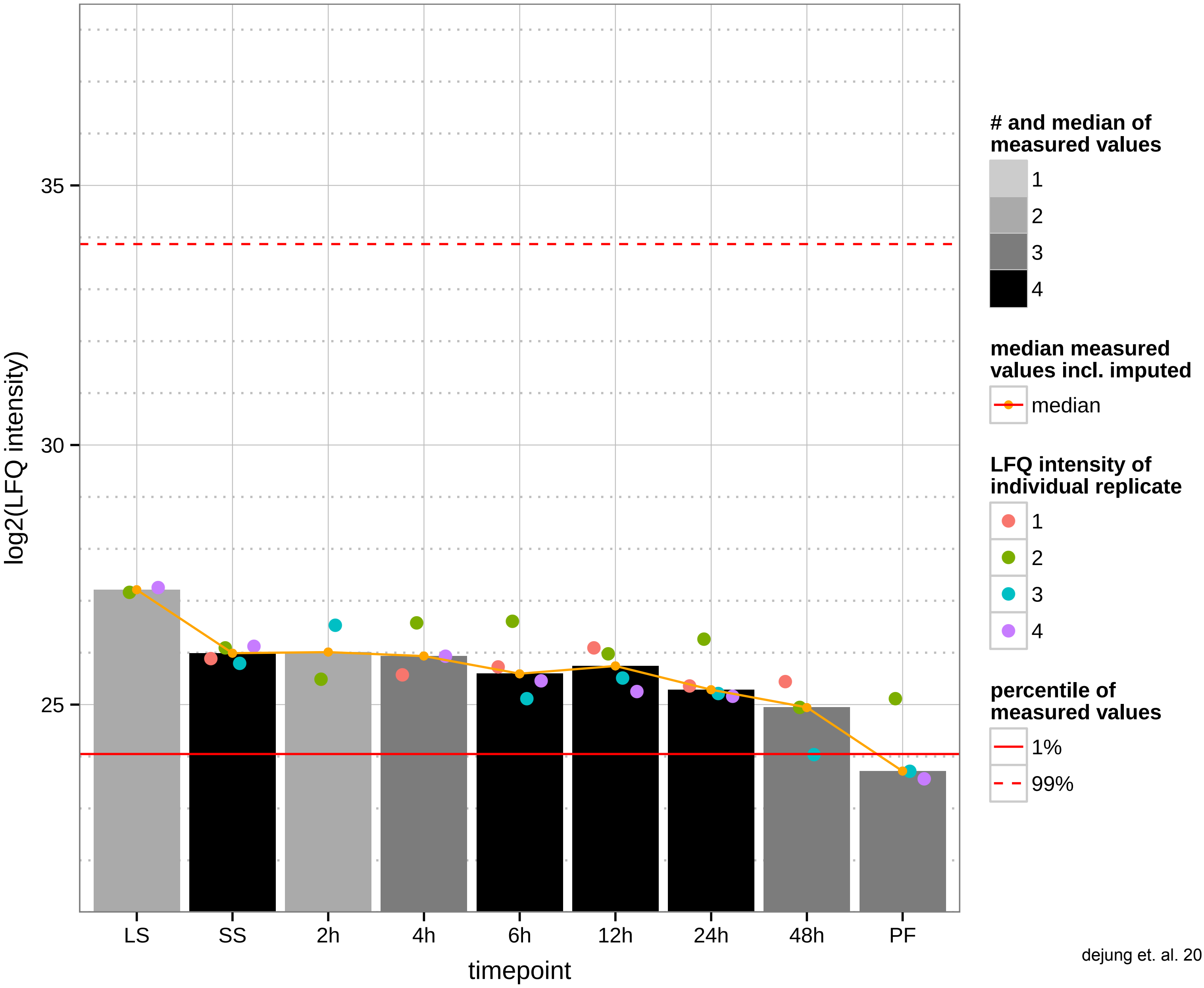
RAB–interacting protein, putative
Tb927.10.12190
AGOF: Rab GTPase binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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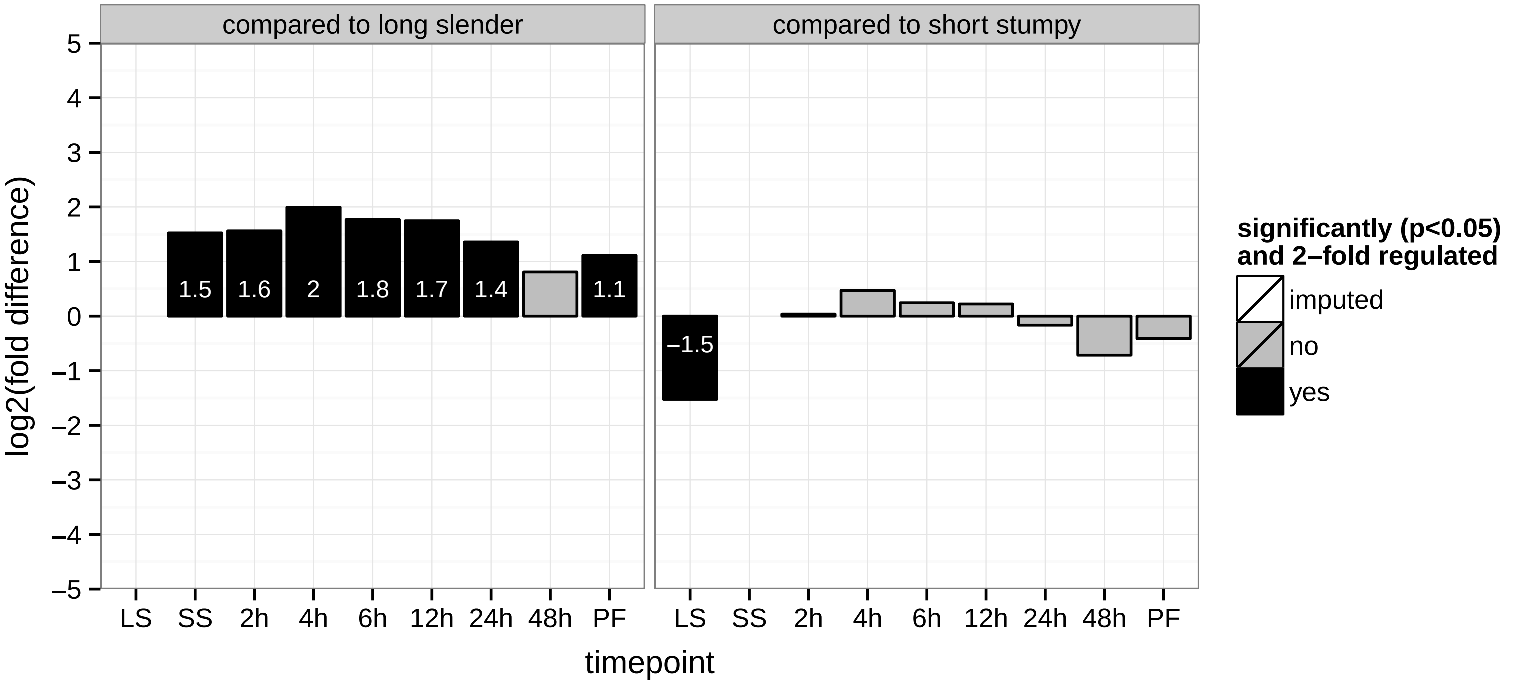
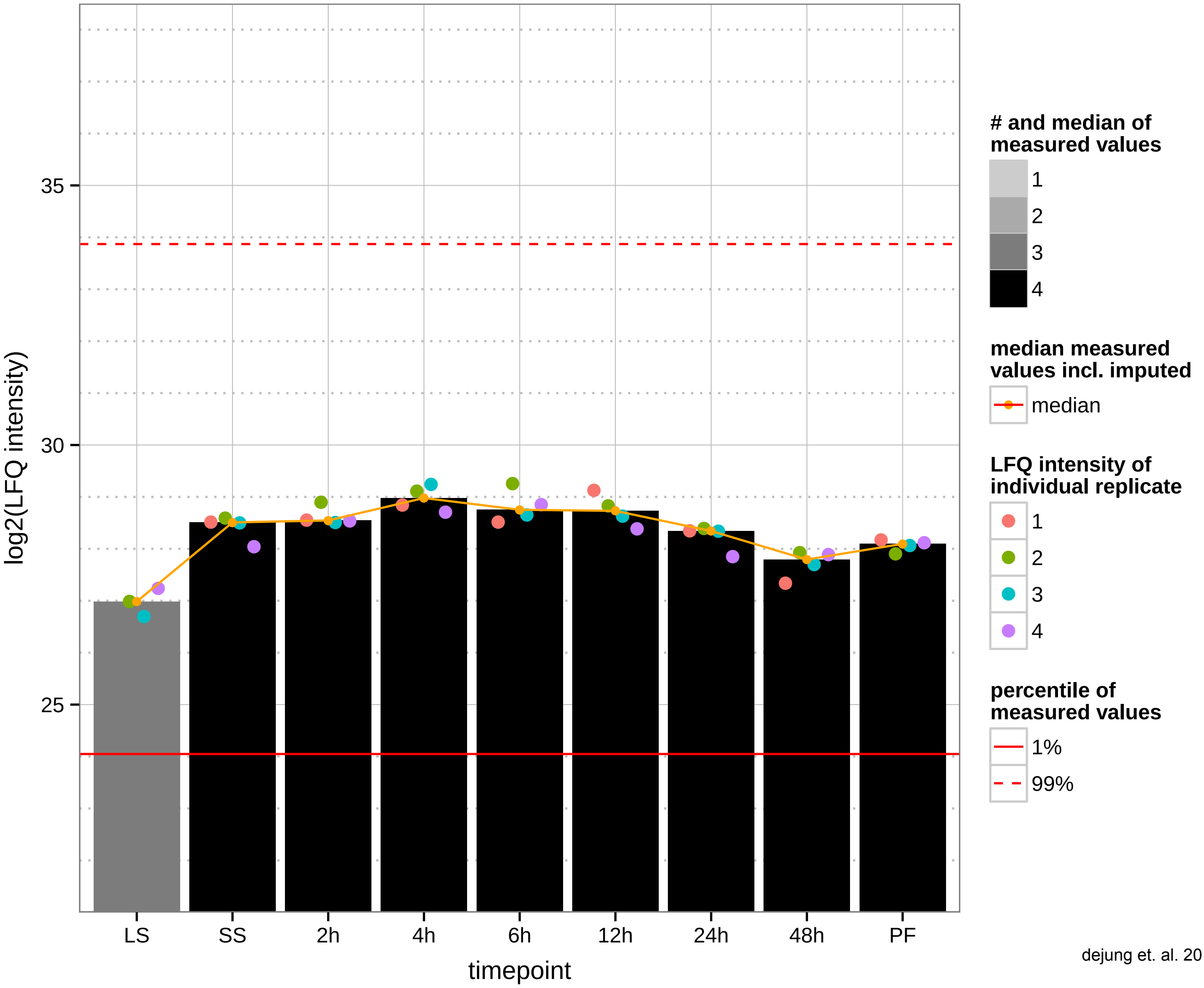
hypothetical protein, conserved
Tb927.10.12360
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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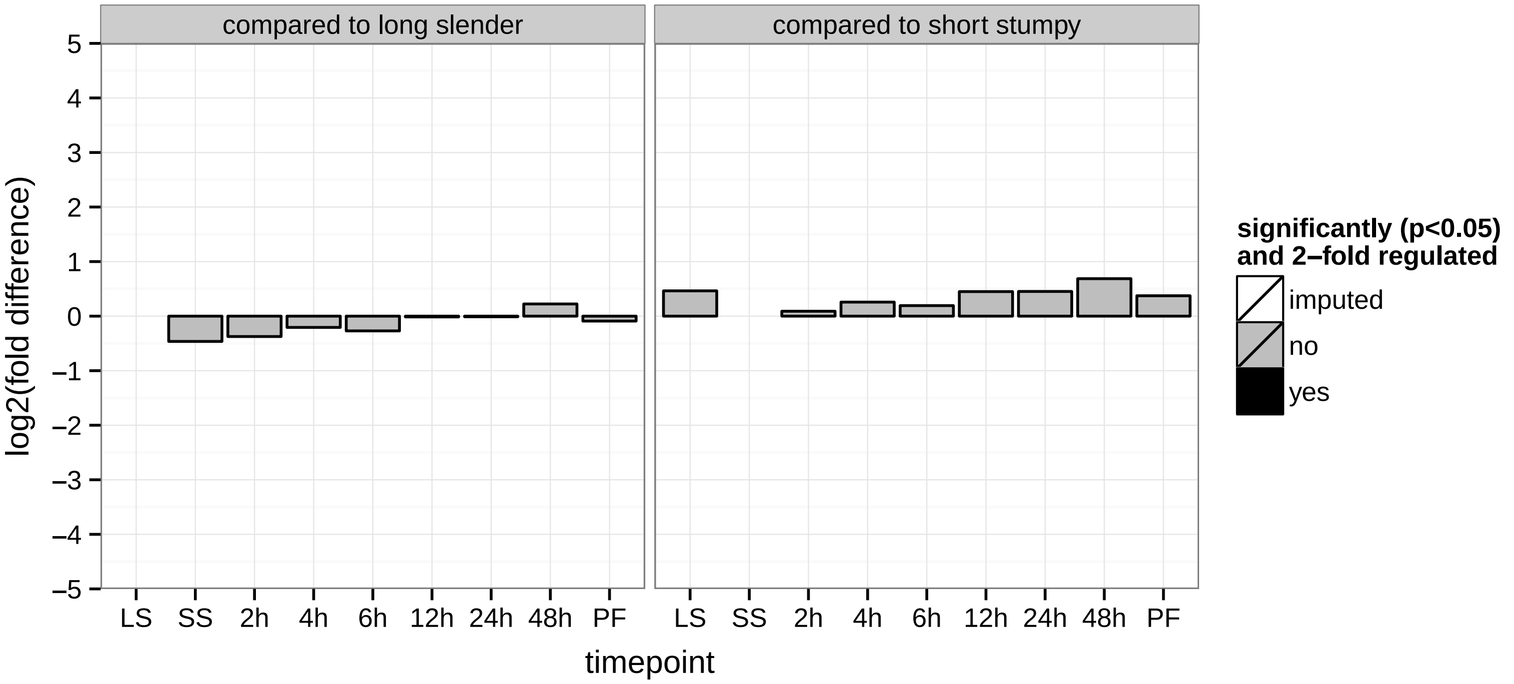
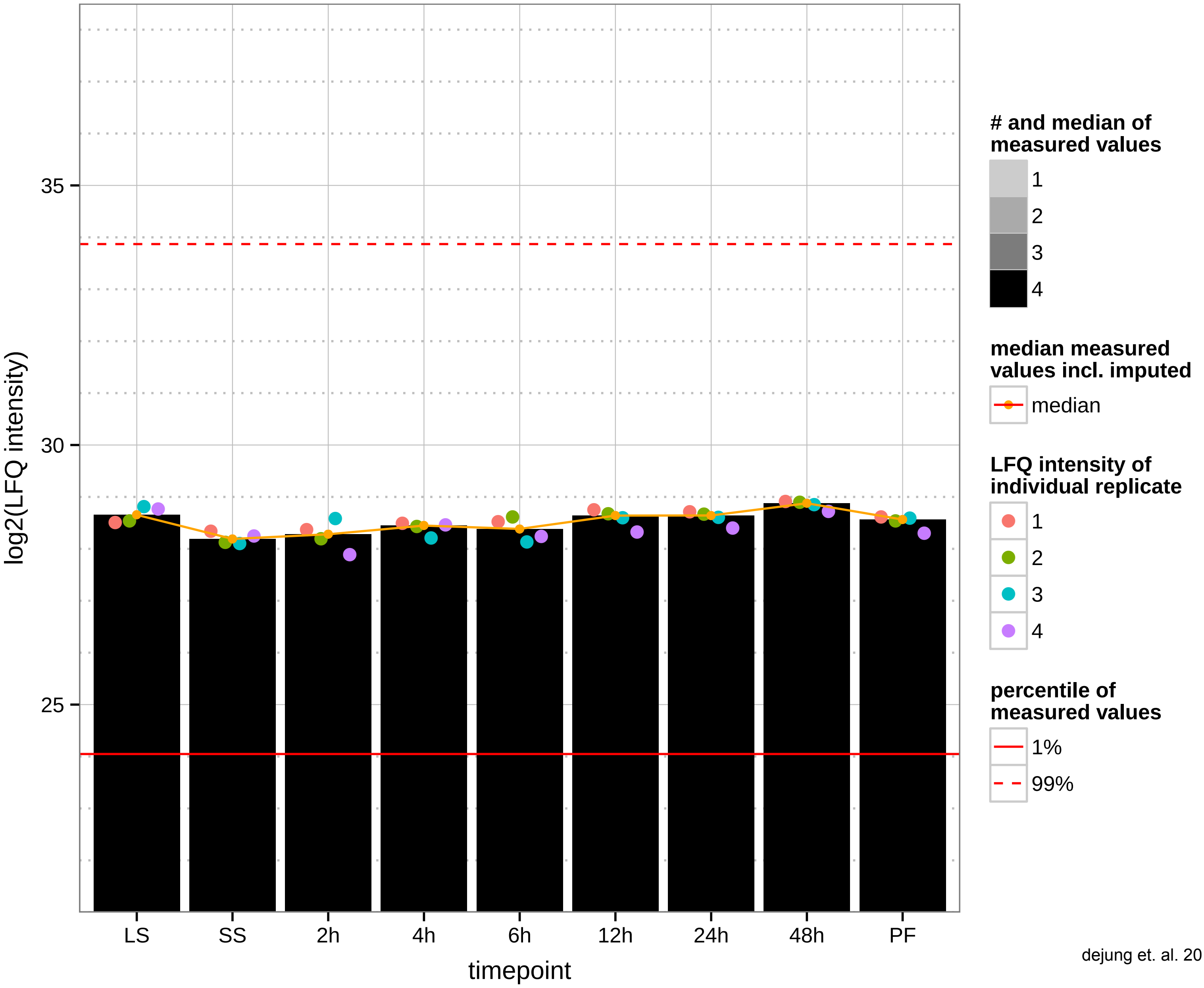
hypothetical protein, conserved
Tb927.10.12410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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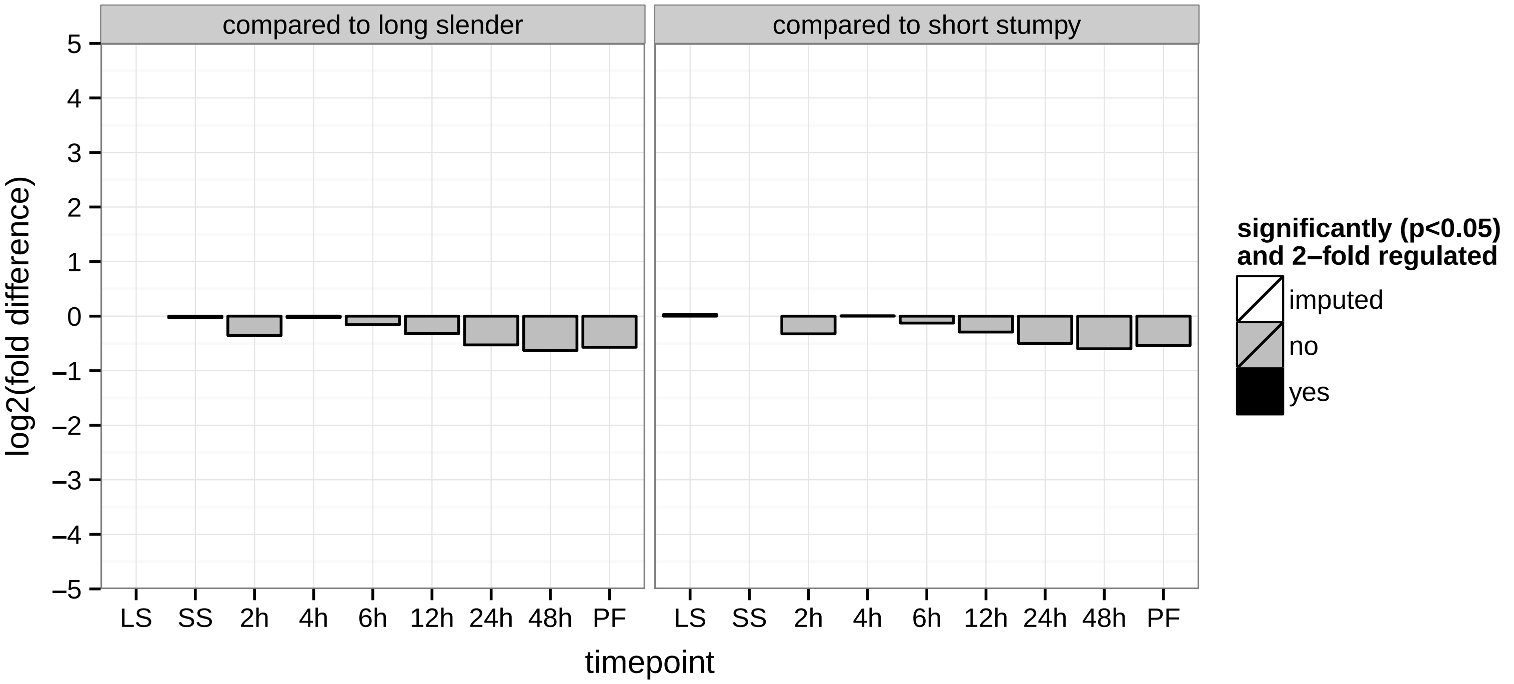
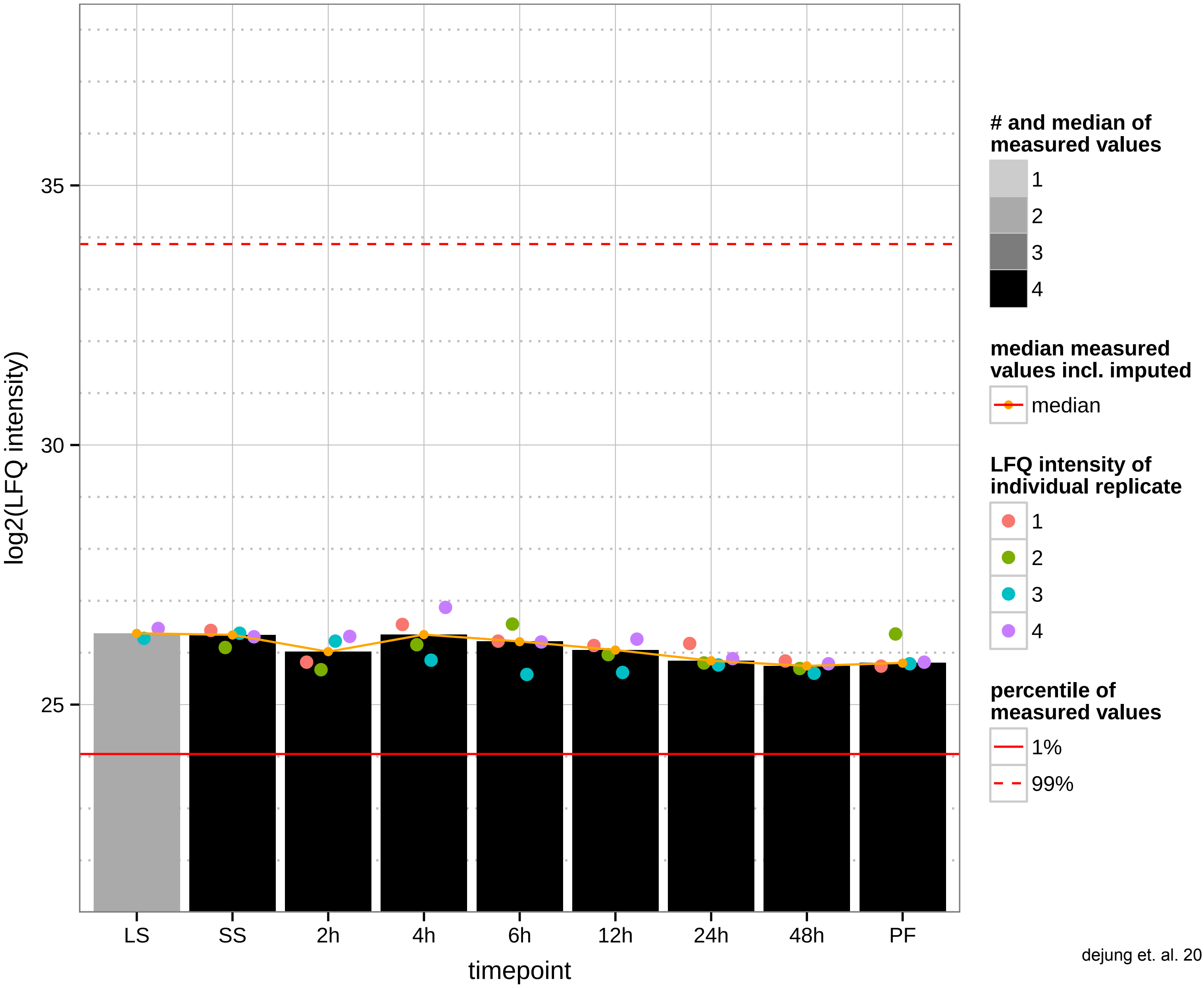
predicted S. cerevisiae Got1 homologue
Tb927.10.12420
AGOF: null
AGOC: null
AGOP: vesicle–mediated transport
PGOF: null
PGOC: null
PGOP: vesicle–mediated transport





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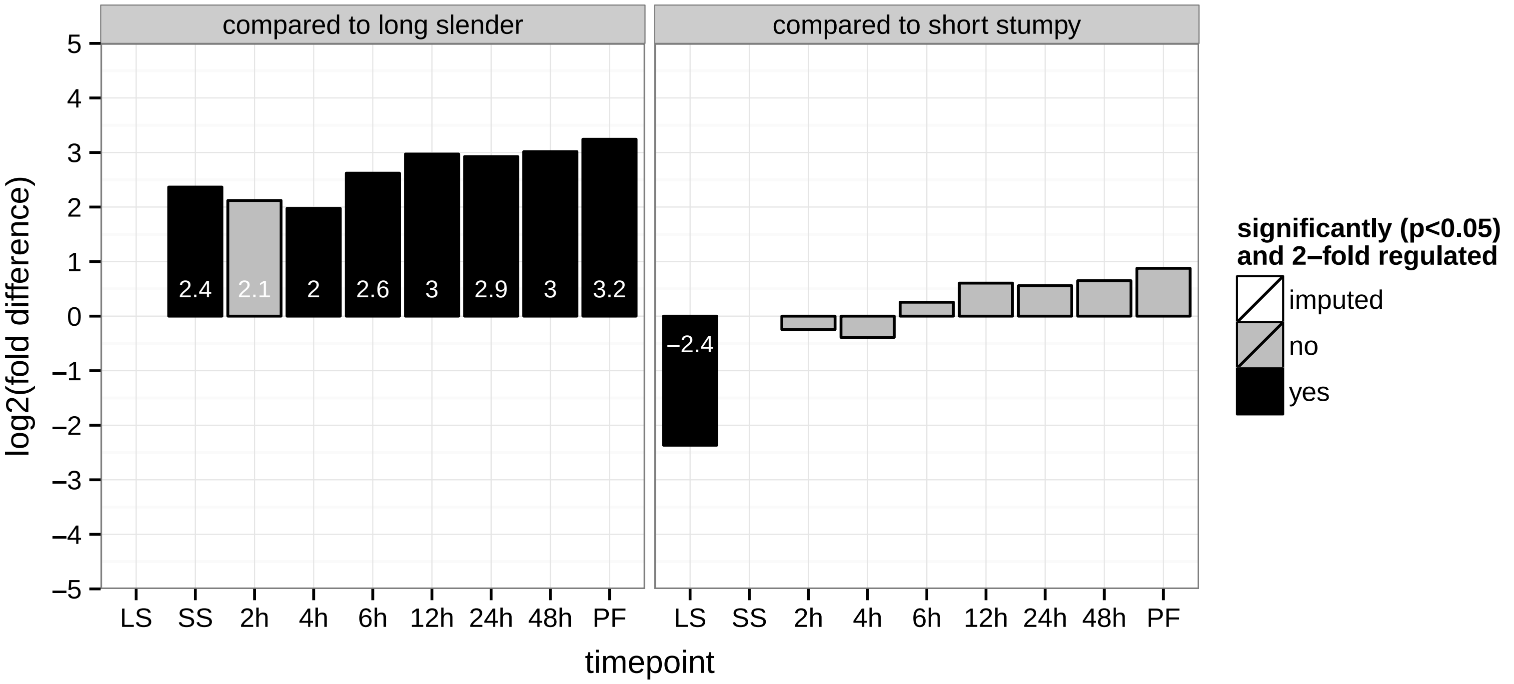
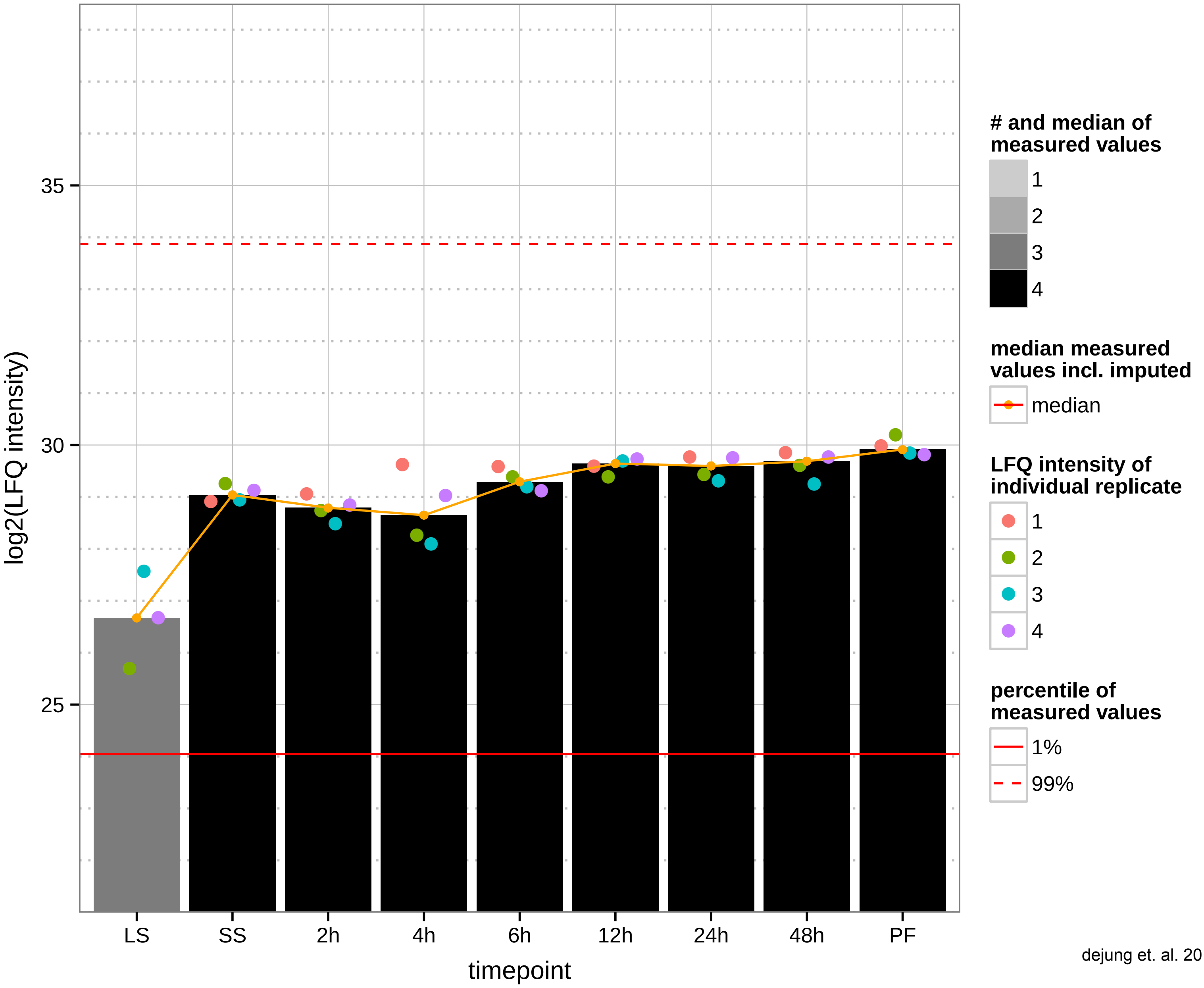
hypothetical protein, conserved
Tb927.10.12430
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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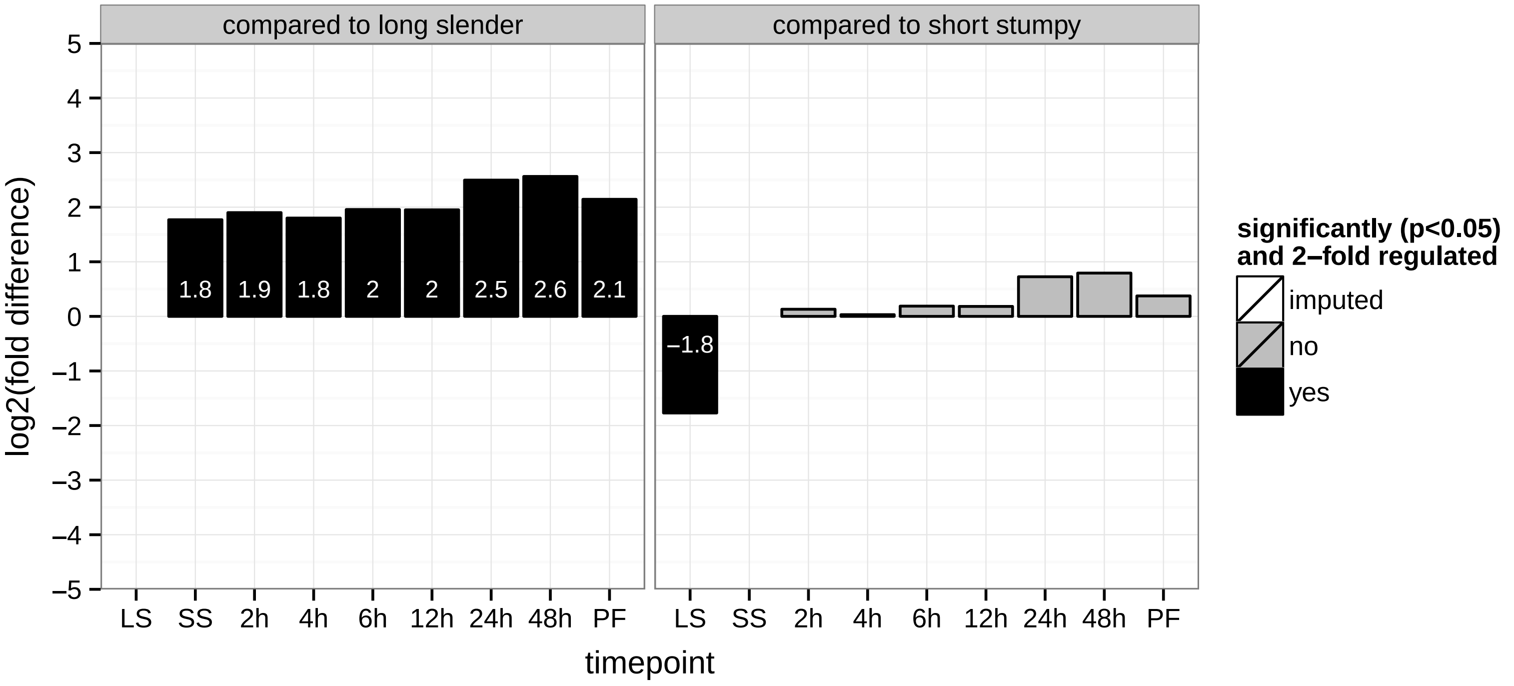
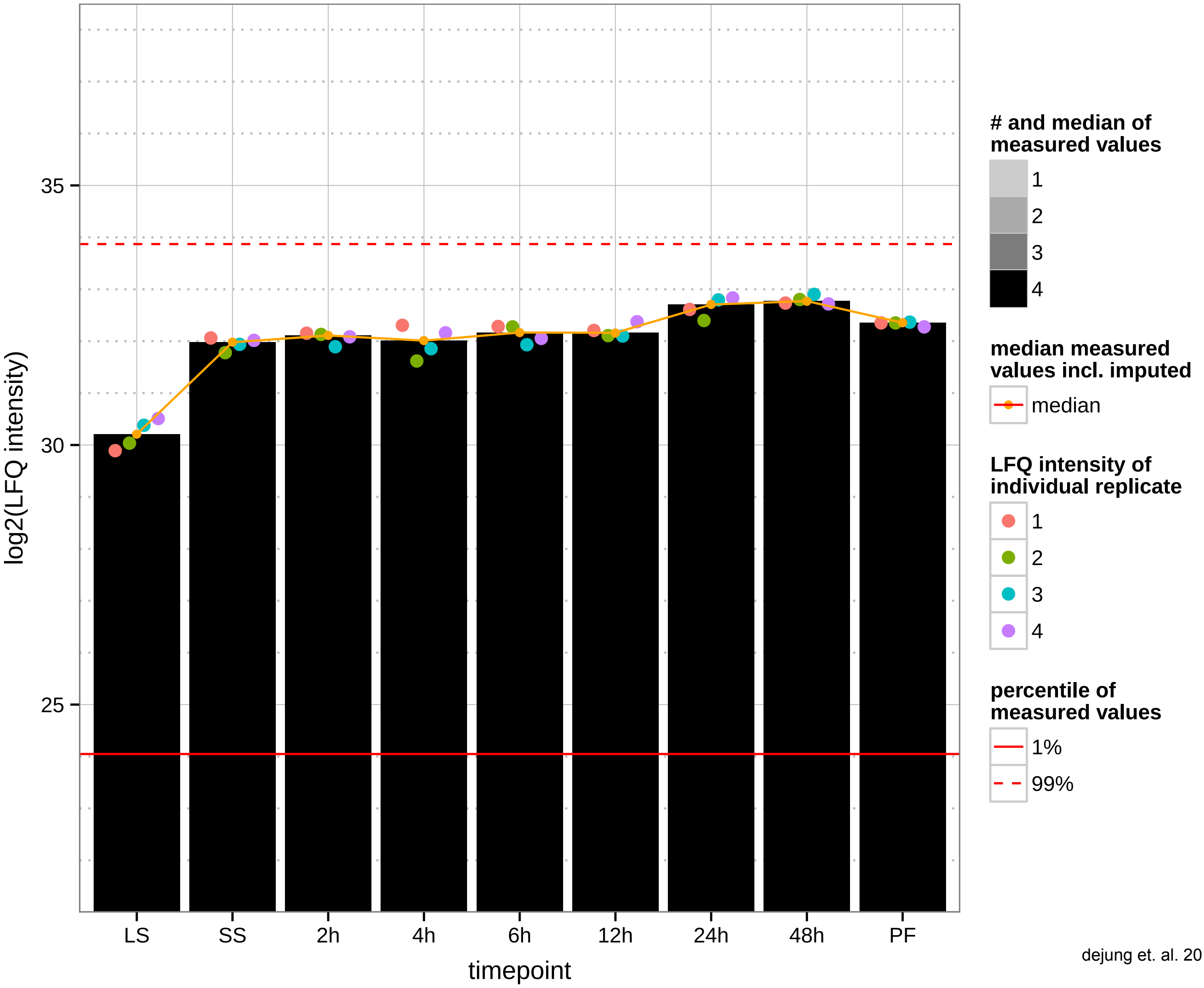
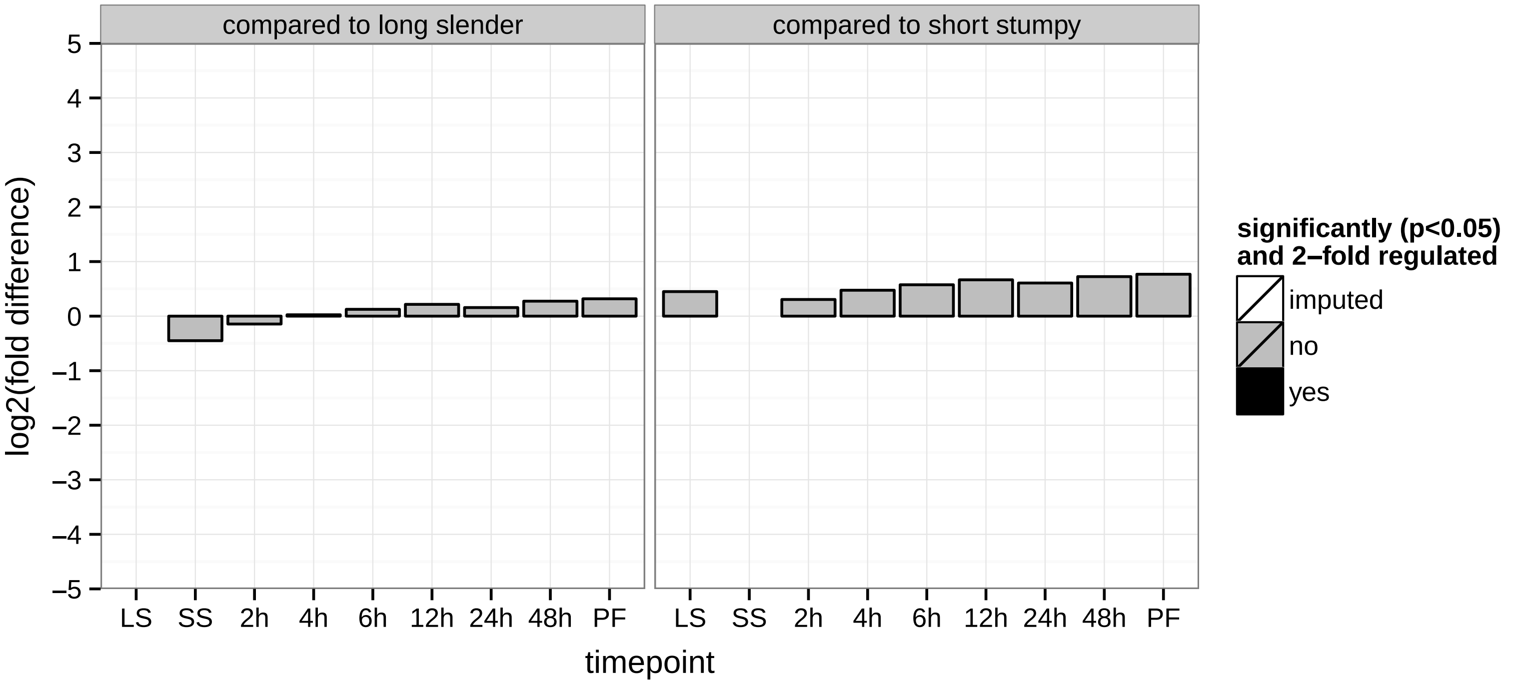
P–type H+–ATPase, putative
Tb927.10.12500
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism
AGOC: integral to membrane, plasma membrane
AGOP: ATP biosynthetic process, metabolic process, proton transport
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, catalytic acti
PGOC: integral to membrane, membrane
PGOP: ATP biosynthetic process, ATP catabolic process, cation transport, metabolic process

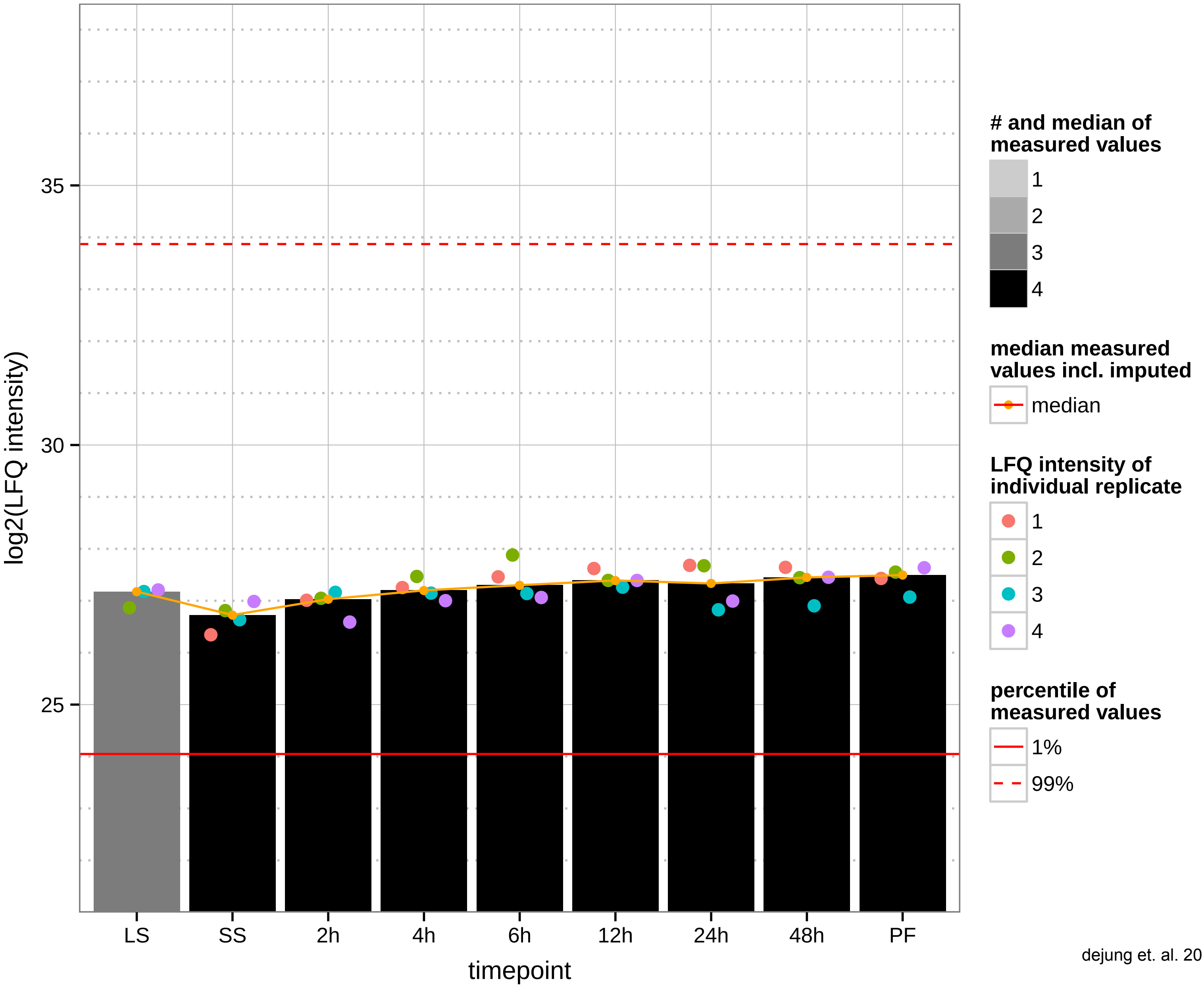




dejung et. al. 2015

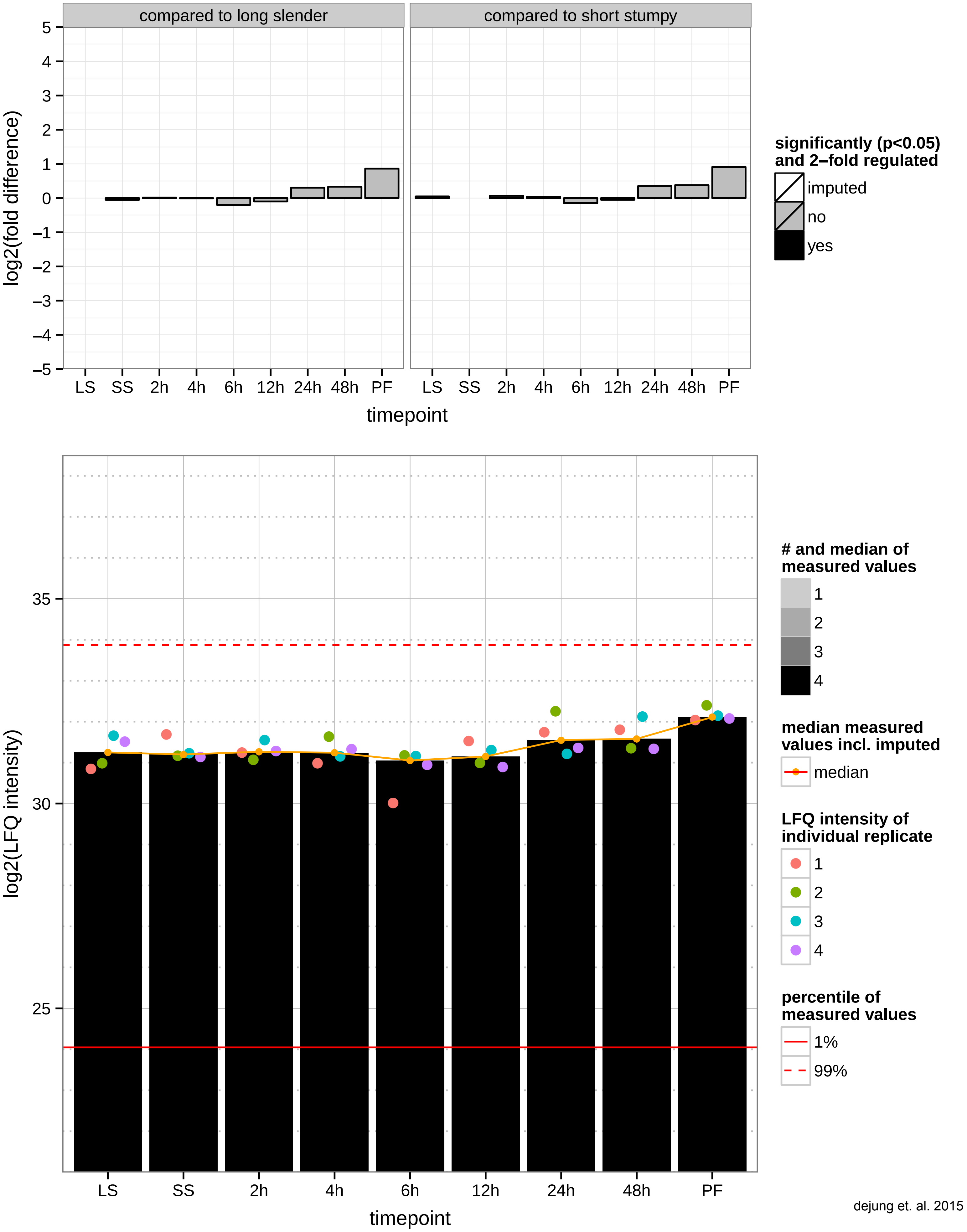
hypothetical protein, conserved
Tb927.10.12630
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





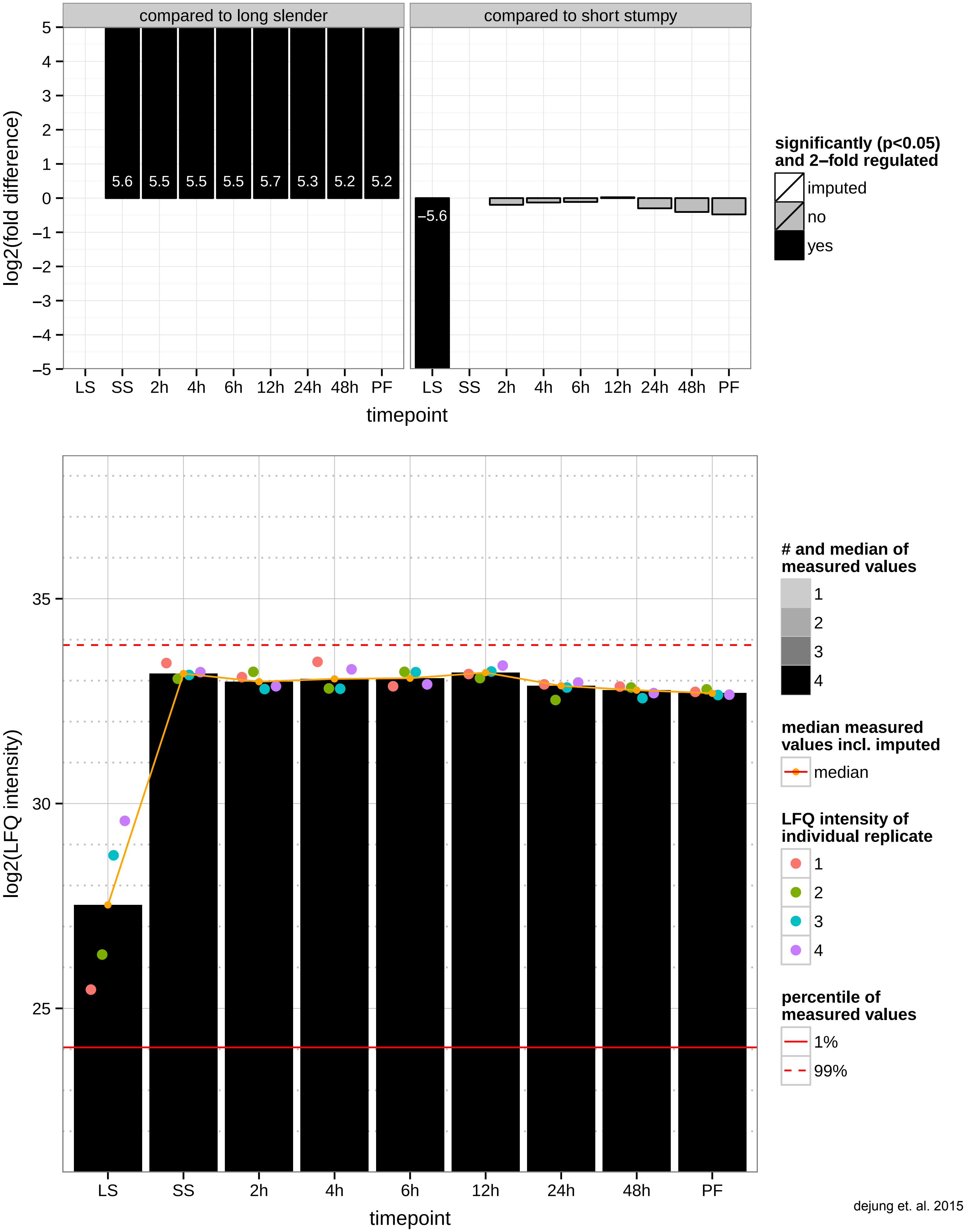
dejung et. al. 2015

60S ribosomal protein L34, putative
Tb927.11.9730;Tb927.10.12680
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation



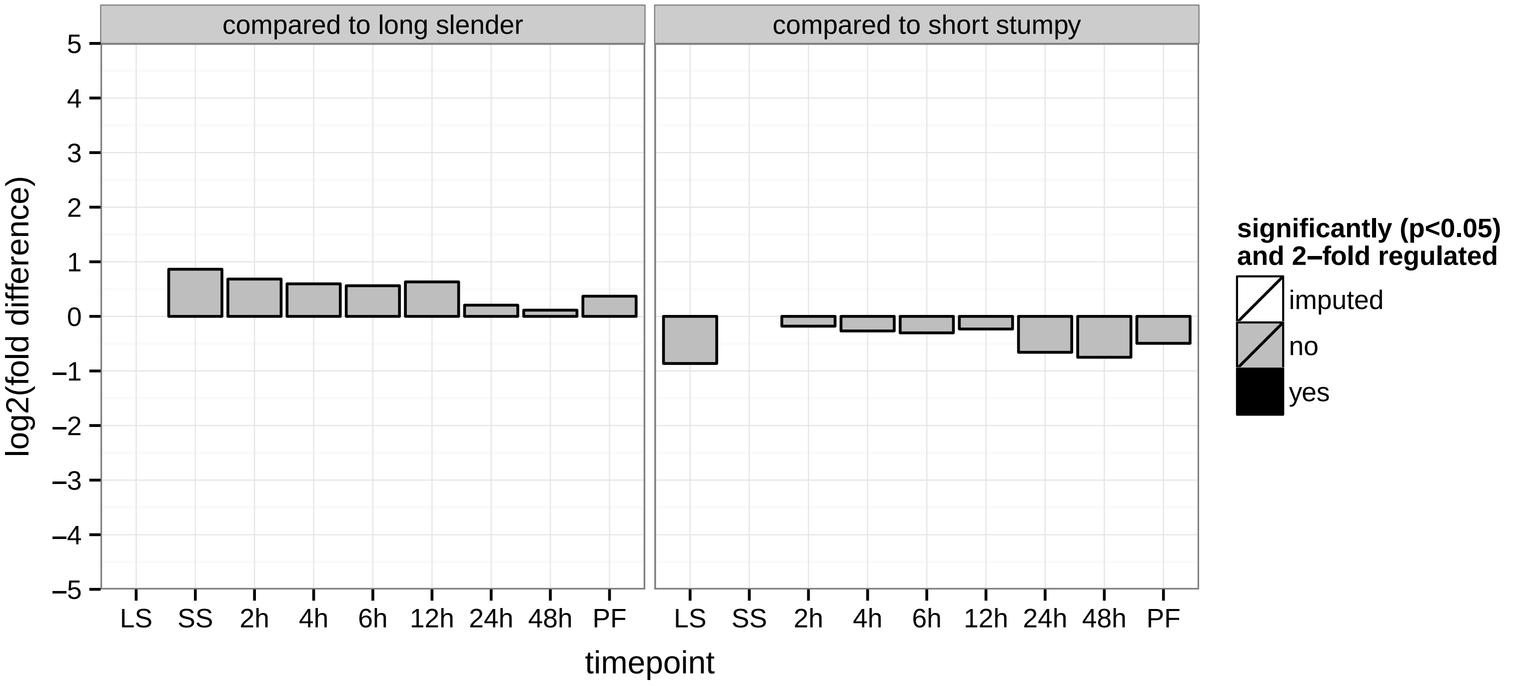
dejung et. al. 2015

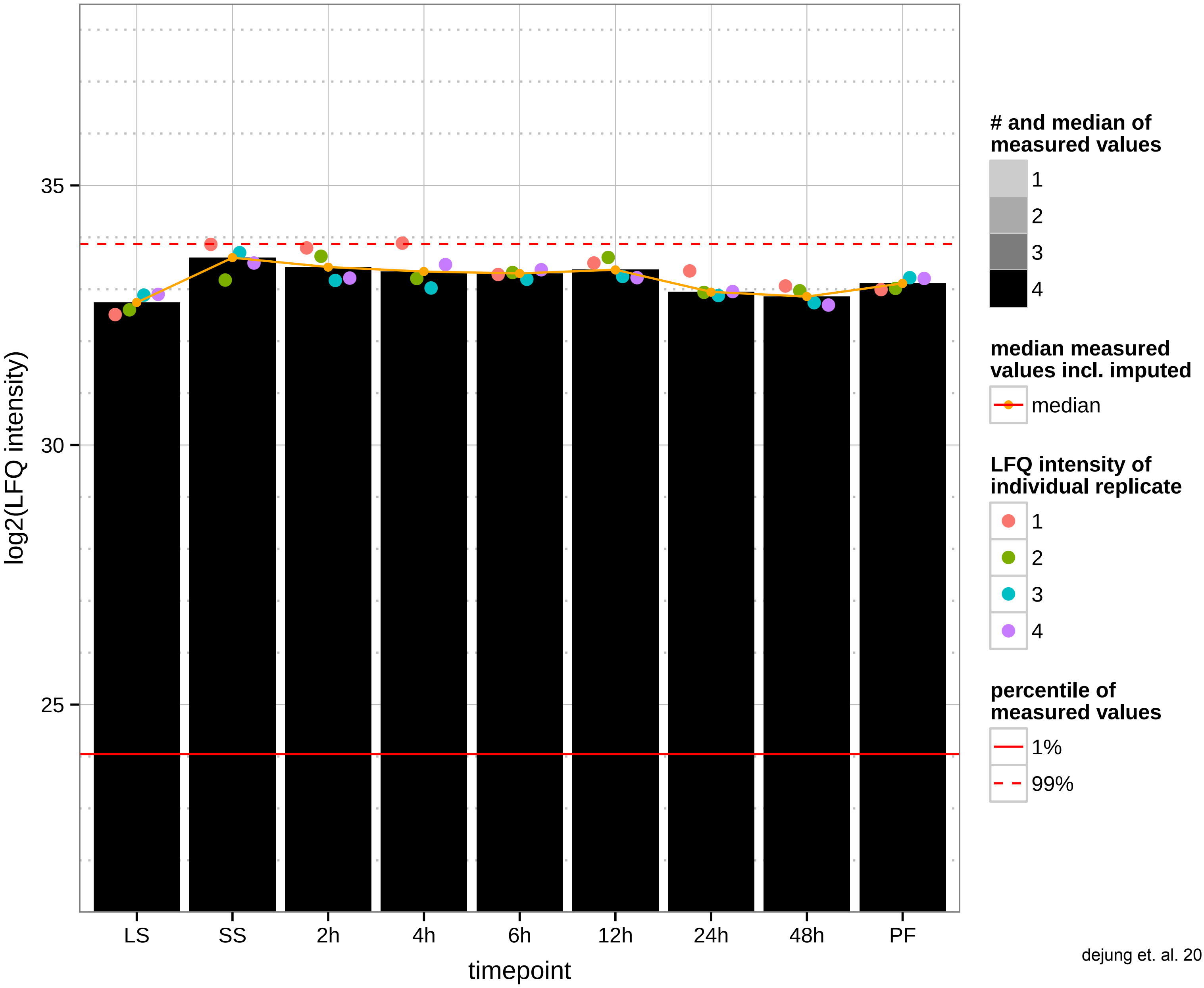
pyruvate dehydrogenase E1 alpha subunit, putative
Tb927.10.12700
AGOF: oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
AGOC: mitochondrion
AGOP: null
PGOF: oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
PGOC: null
PGOP: metabolic process



dejung et. al. 2015

heat shock protein 110, putative
Tb927.10.12710
AGOF: ATP binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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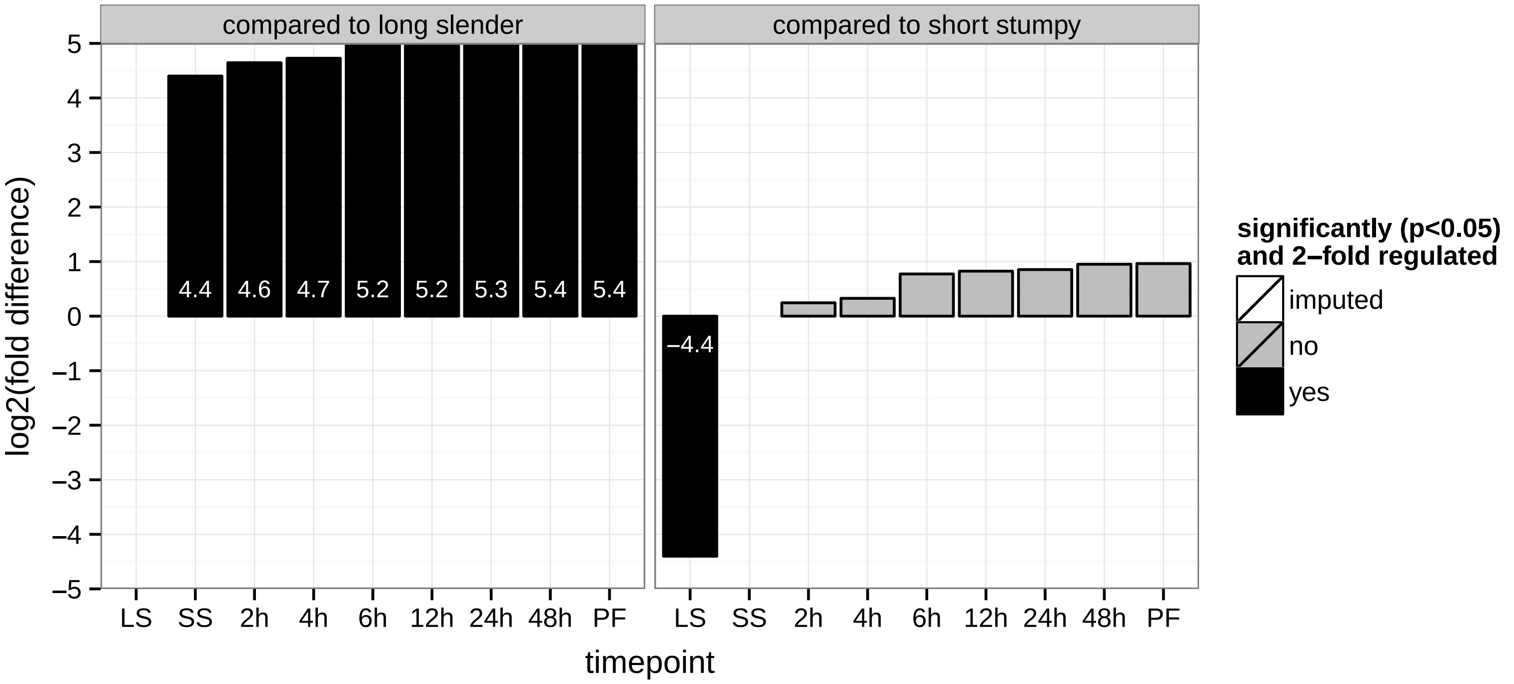
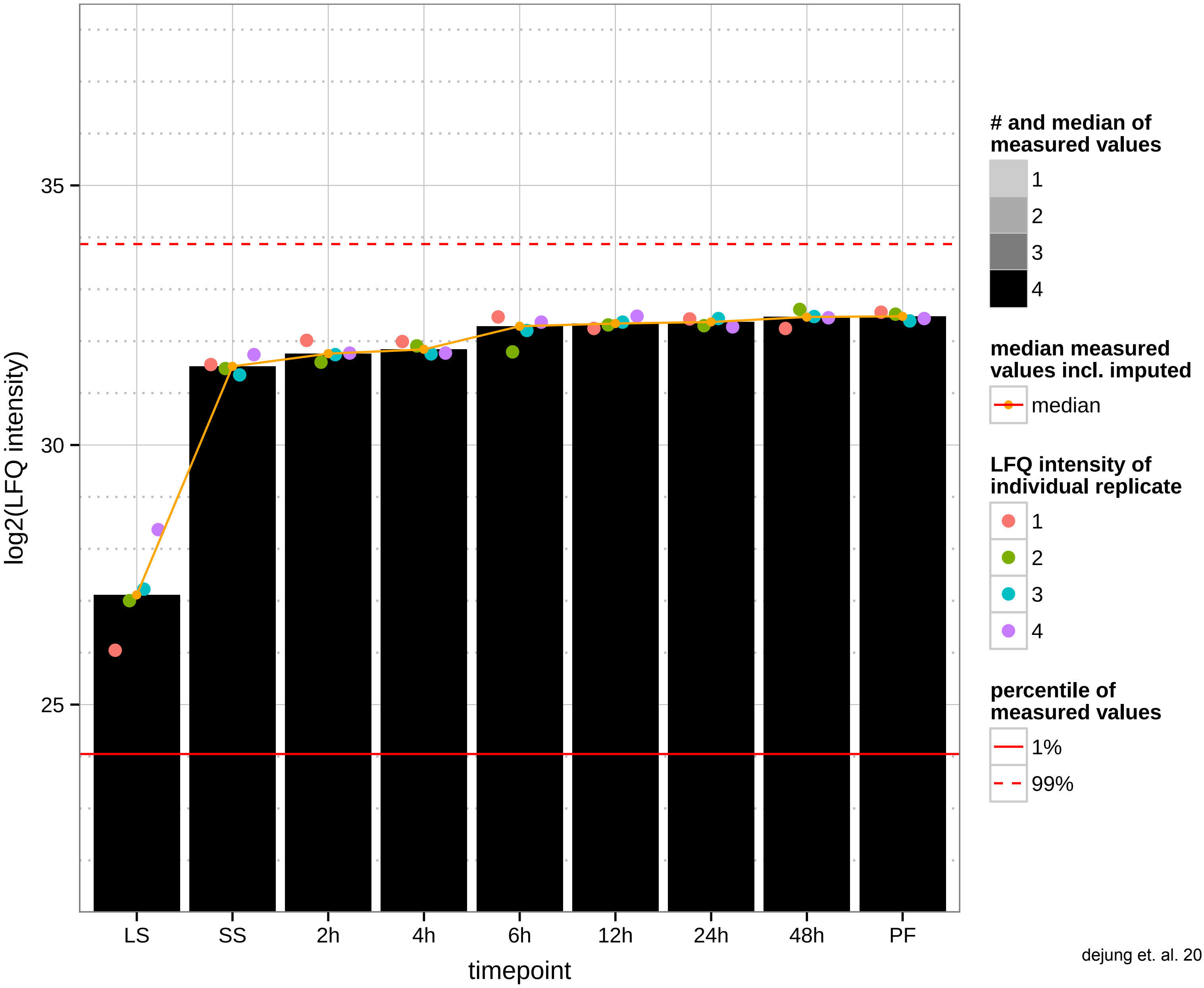
mitochondrial carrier protein (MCP12)
Tb927.10.12840
AGOF: null
AGOC: membrane, mitochondrial inner membrane, mitochondrial part
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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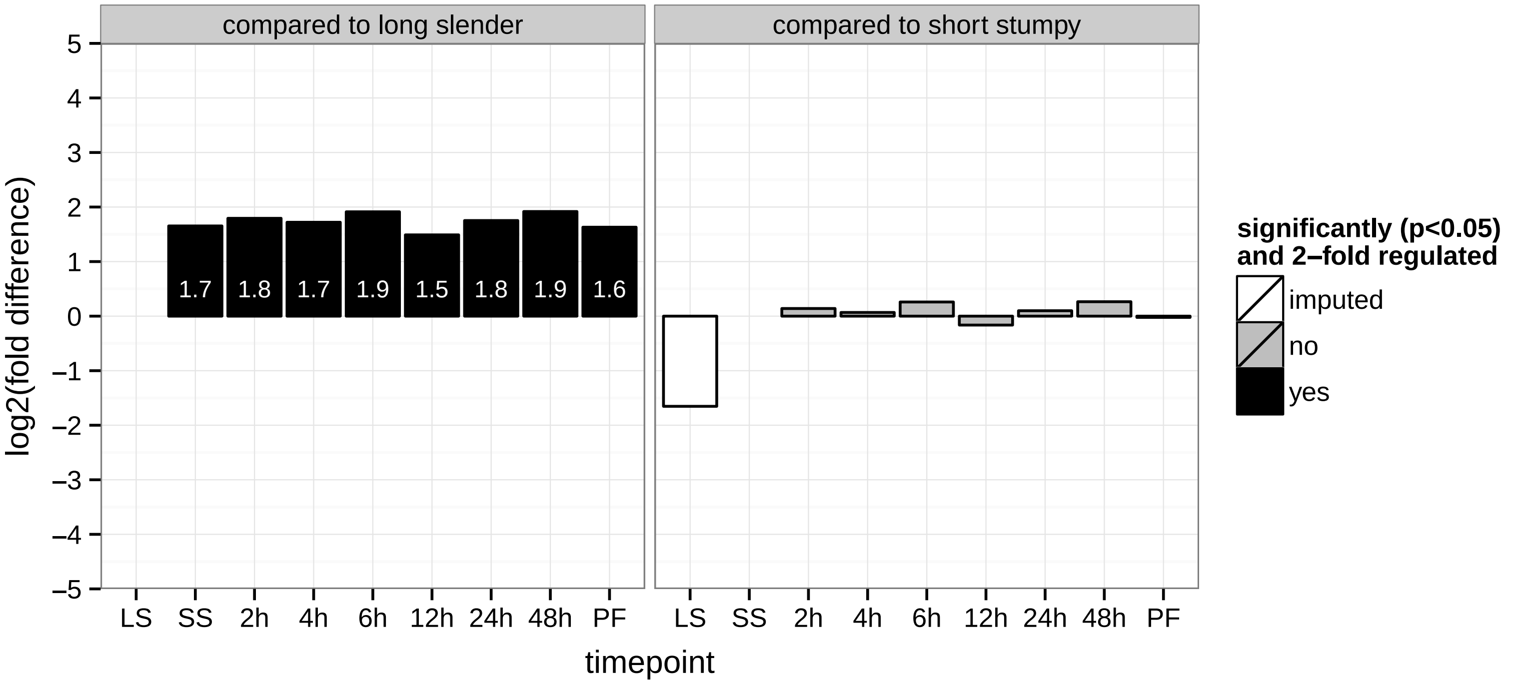
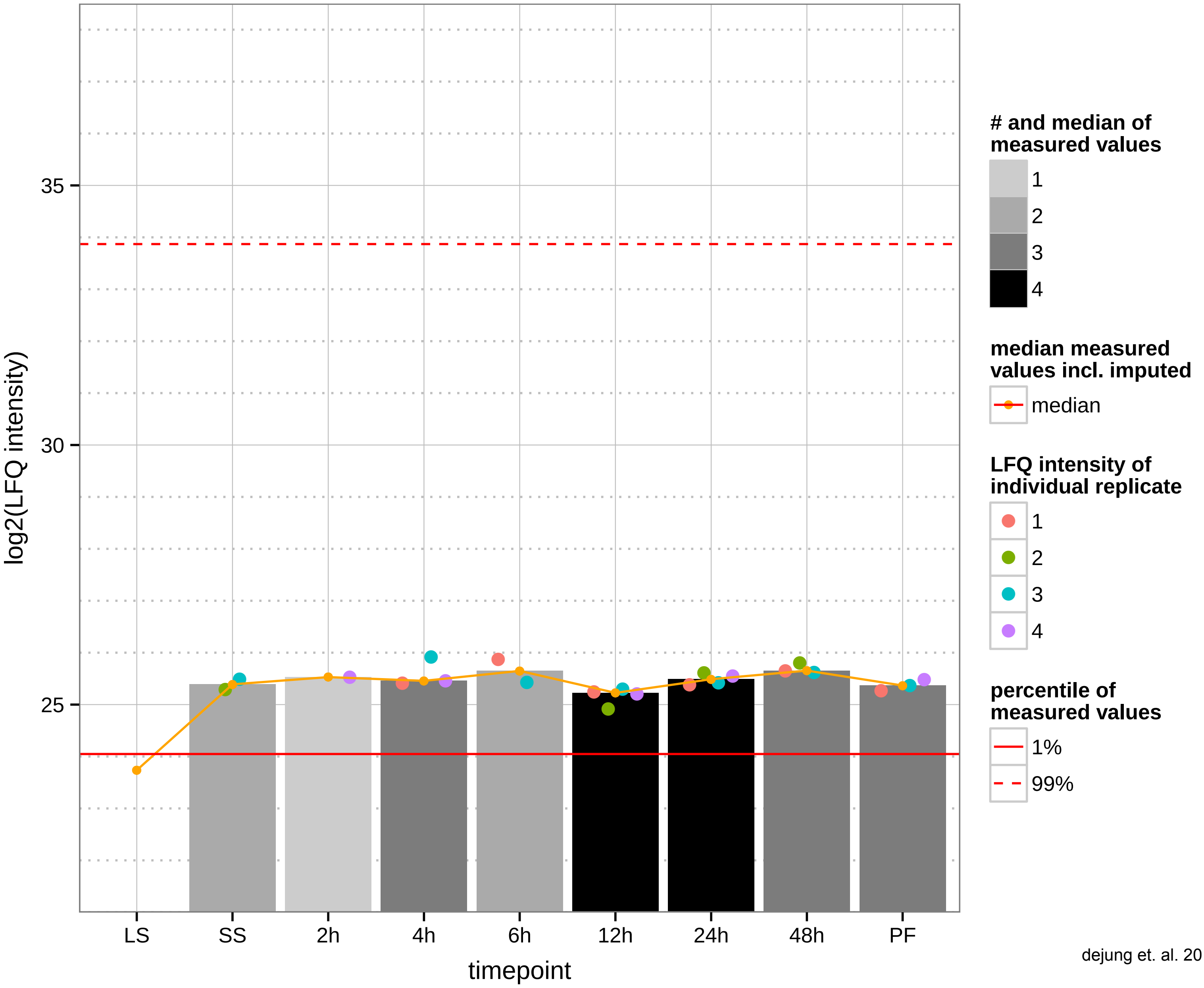
ttaggg binding factor
Tb927.10.12850
AGOF: null
AGOC: null
AGOP: null
PGOF: DNA binding
PGOC: null
PGOP: null





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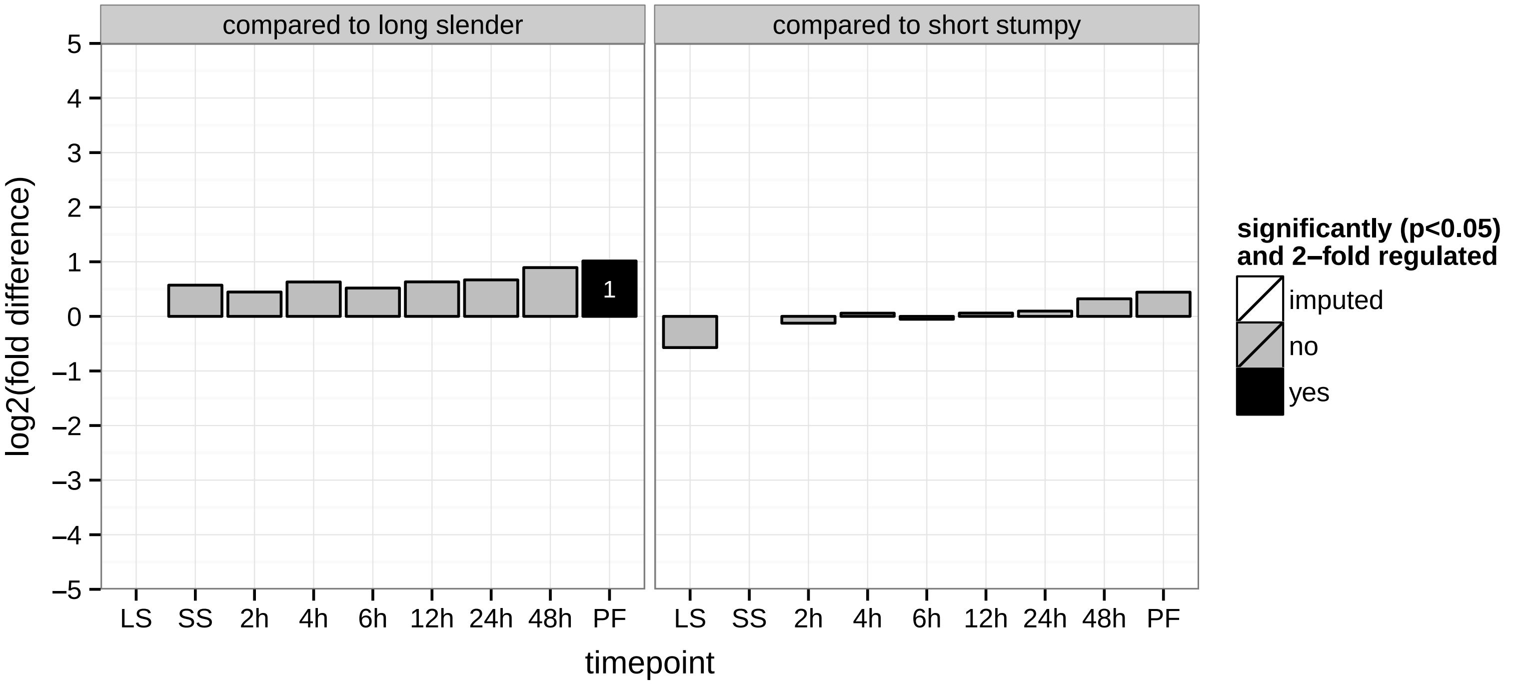
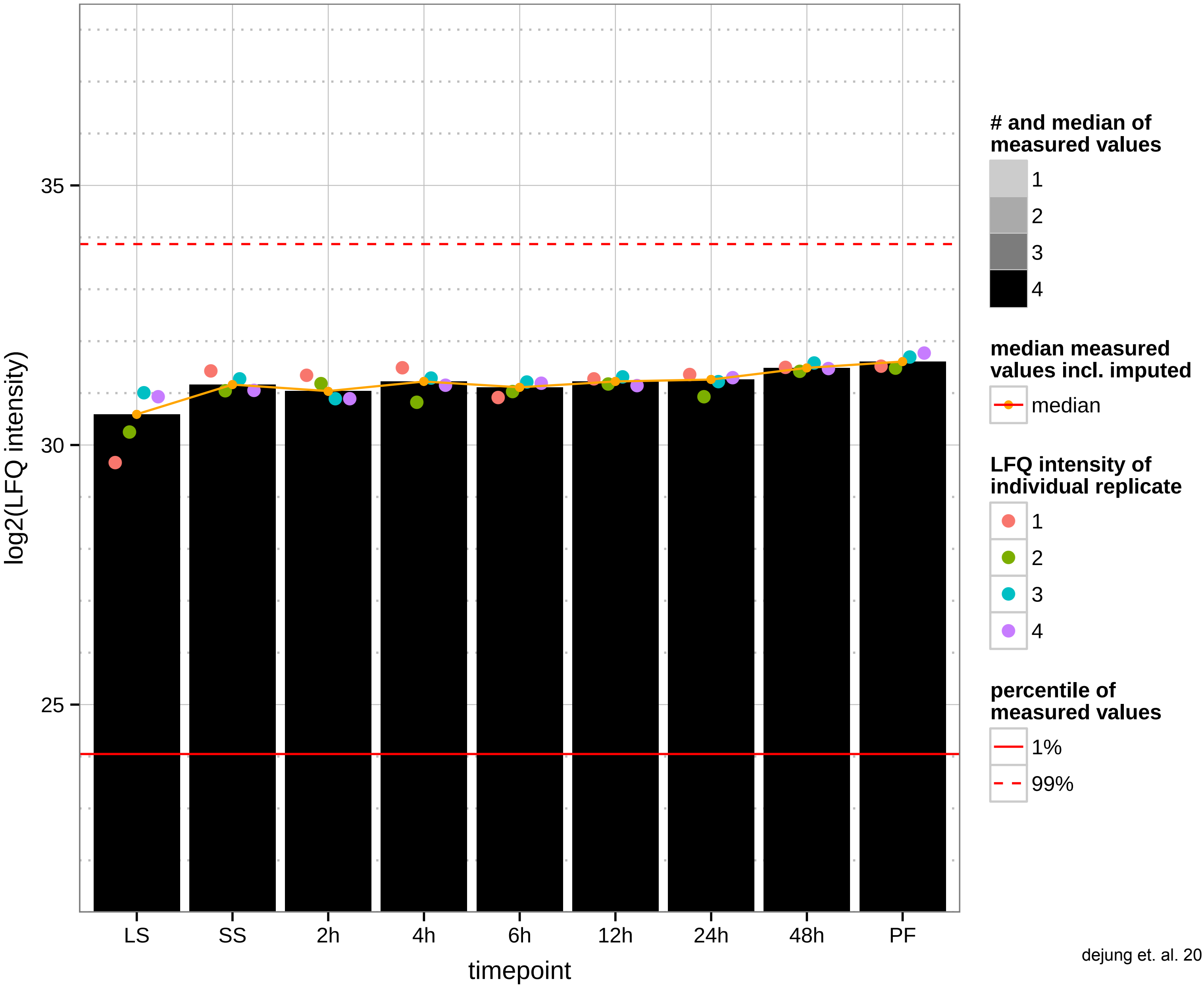
bifunctional aminoacyl–tRNA synthetase, putative
Tb927.10.12890
AGOF: ATP binding, proline–tRNA ligase activity
AGOC: cytoplasm, mitochondrion
AGOP: prolyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, nucleotide binding, proline–tRNA ligase activity
PGOC: cytoplasm
PGOP: prolyl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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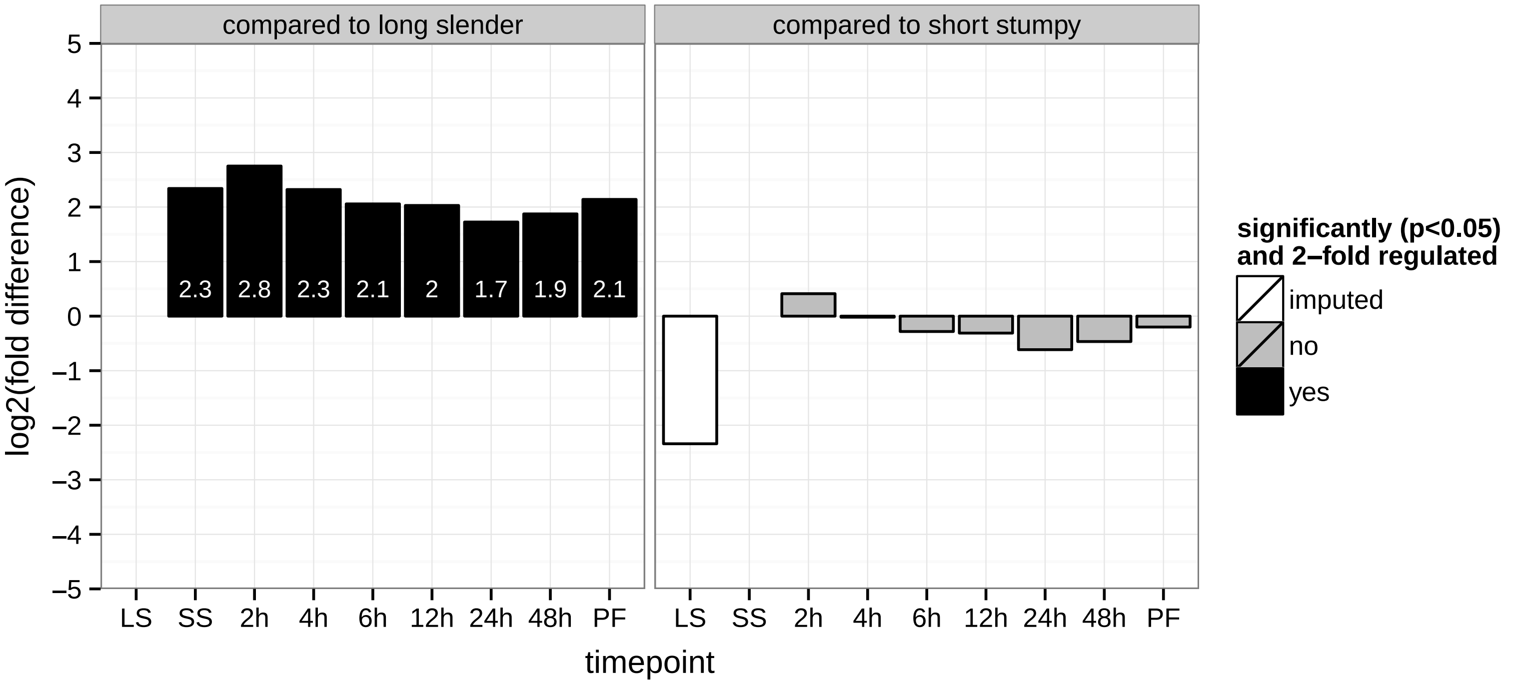
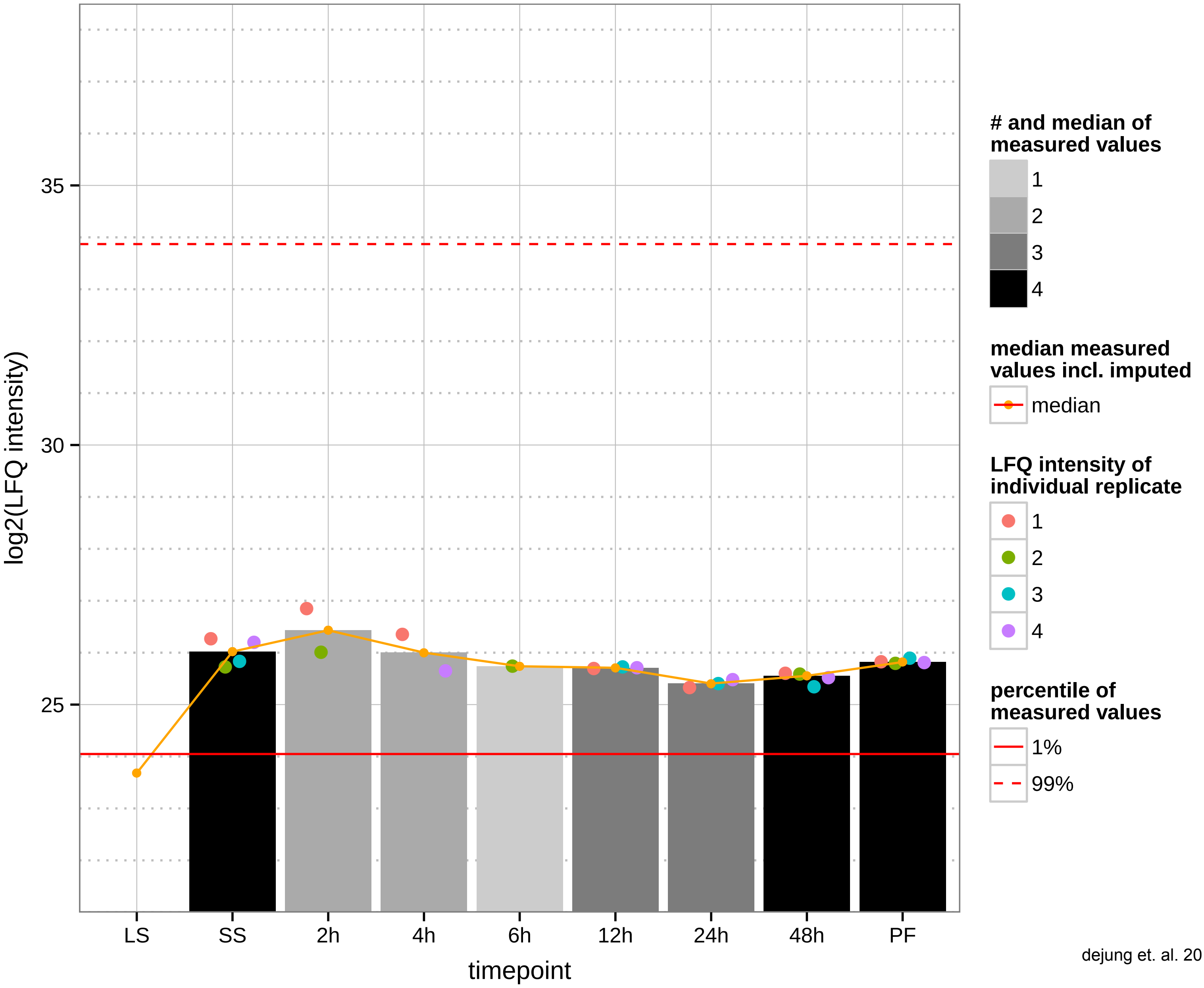
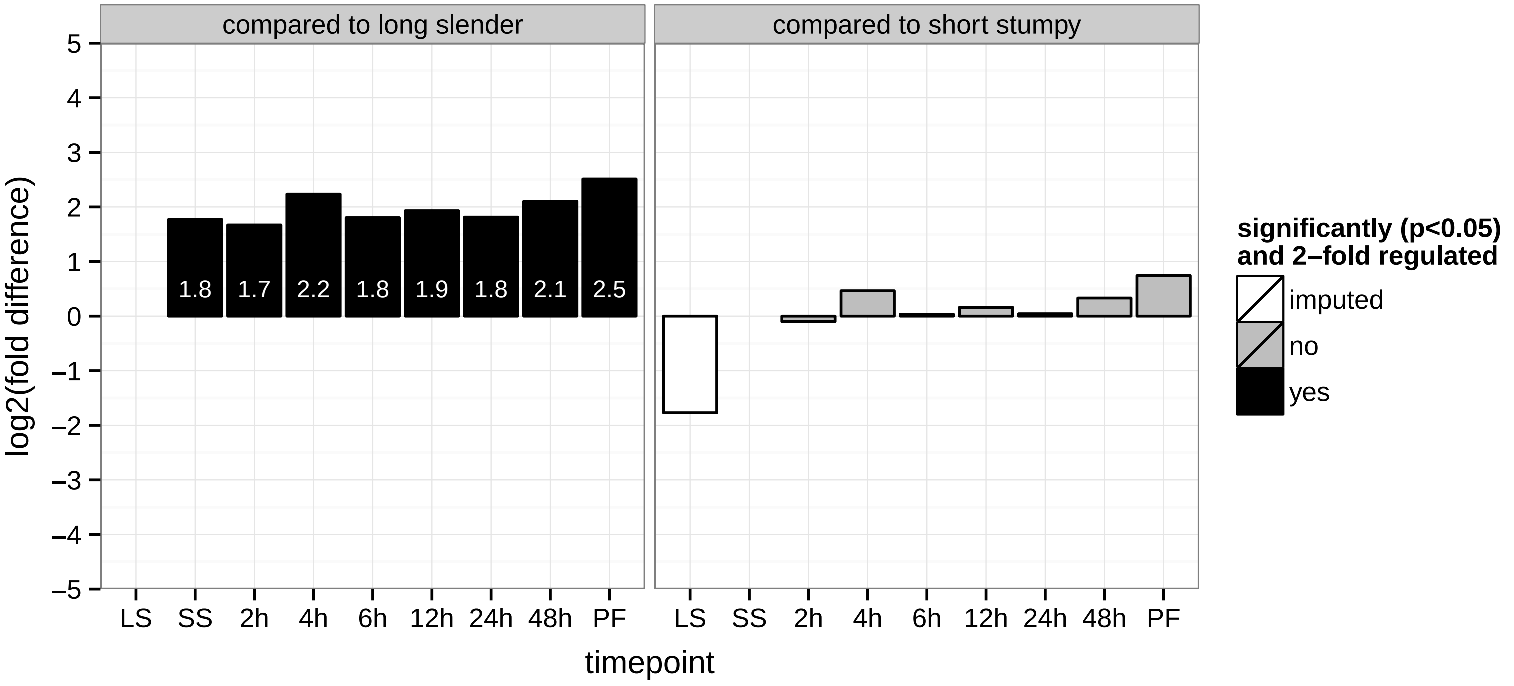
Multisite−specific tRNA:(cytosine−C(5))−methyltransferase, putative, NCL1(Yeast)−related NOL1/NOP2/FMU(SUN) domain−c
Tb927.10.12980
AGOF: null
AGOC: mitochondrion
AGOP: tRNA methylation
PGOF: null
PGOC: null
PGOP: null

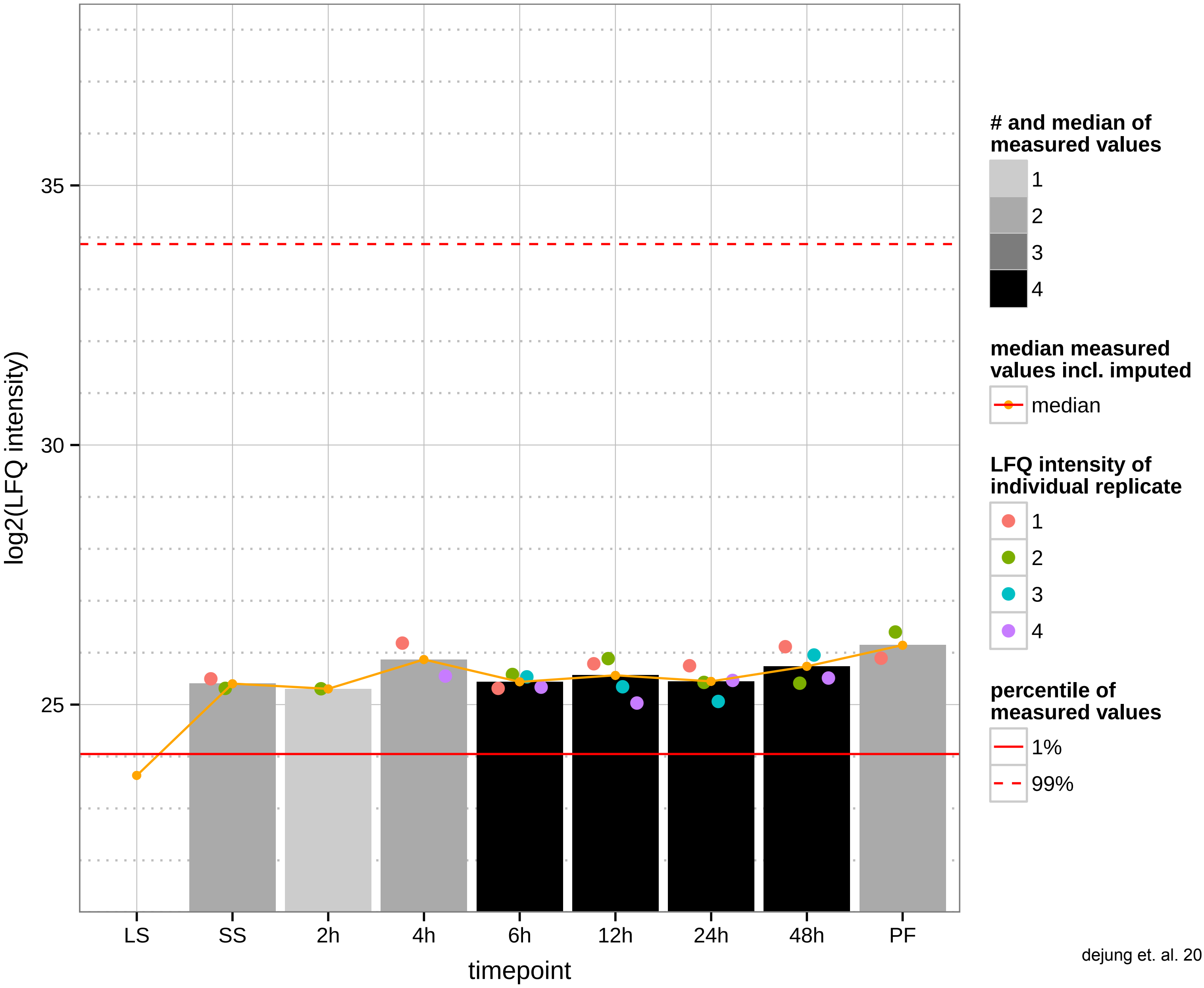




dejung et. al. 2015

predicted ankyrin repeat family protein
Tb927.10.12990
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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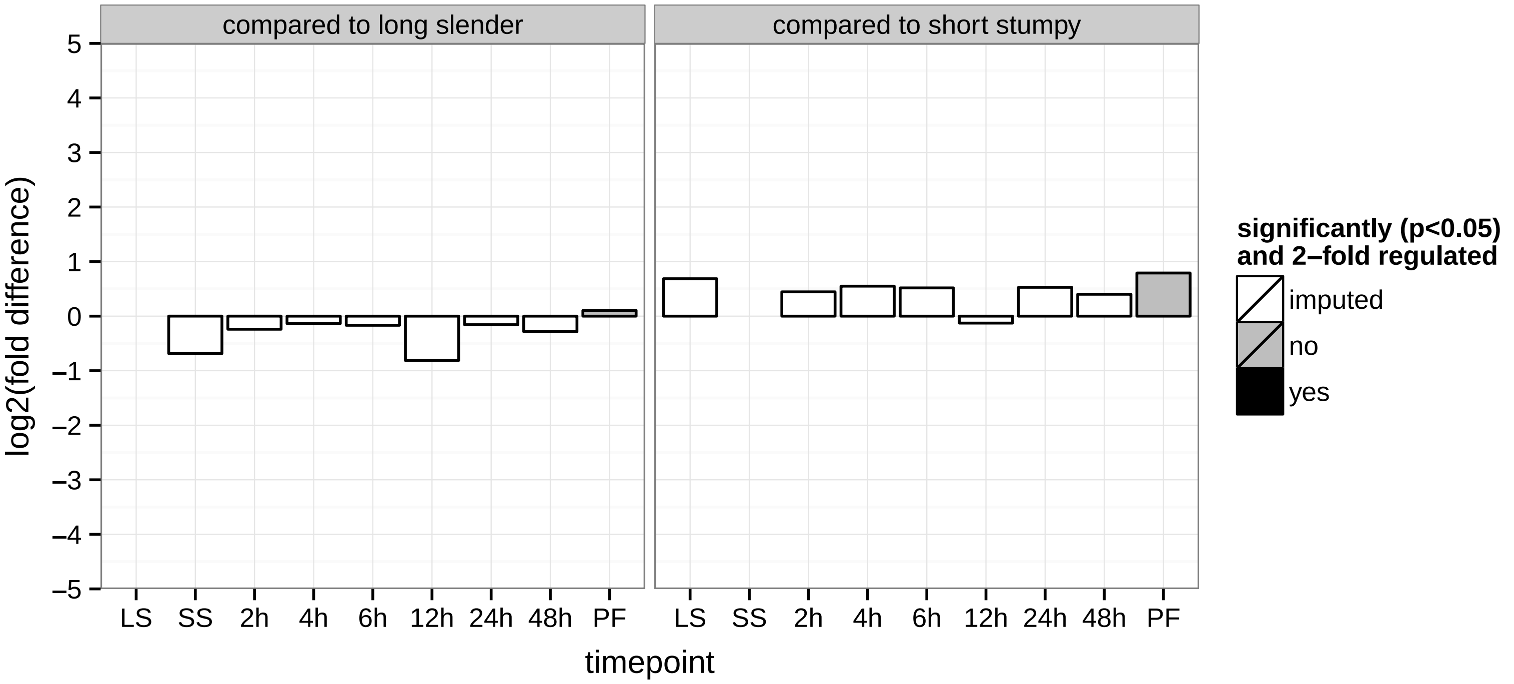
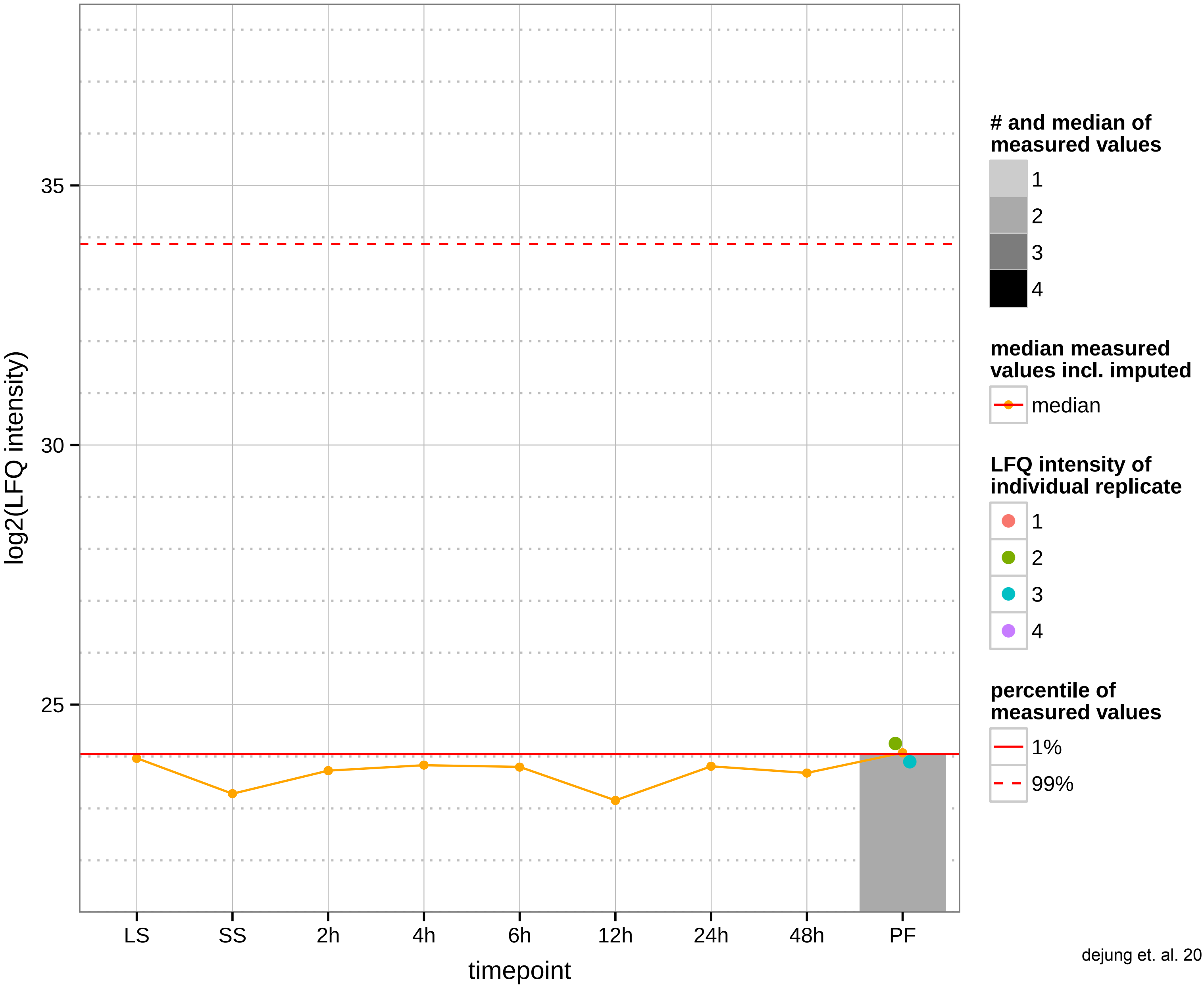
receptor–type adenylate cyclase GRESAG 4, putative, gene related to ESAG4, putative (GRESAG4)
Tb927.10.13040
AGOF: adenylate cyclase activity
AGOC: null
AGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction
PGOF: phosphorus–oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction





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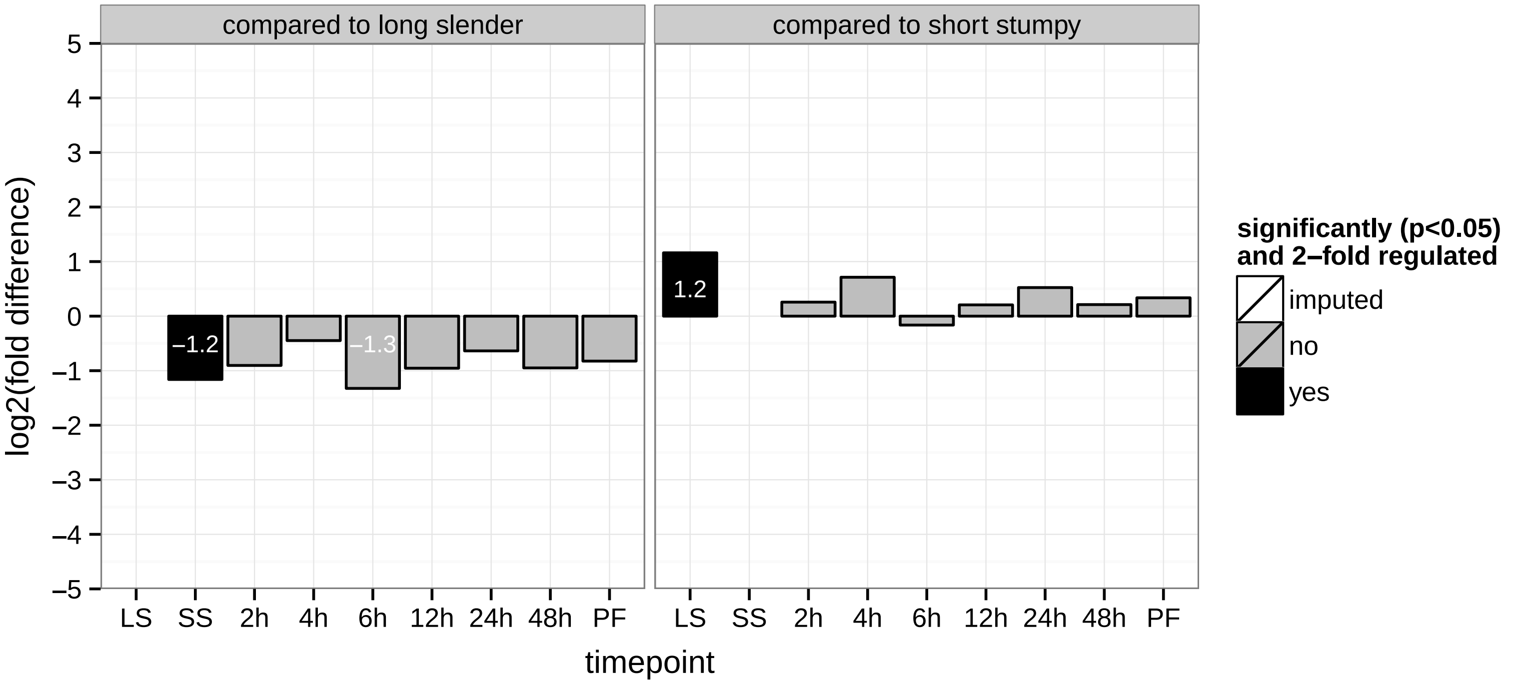
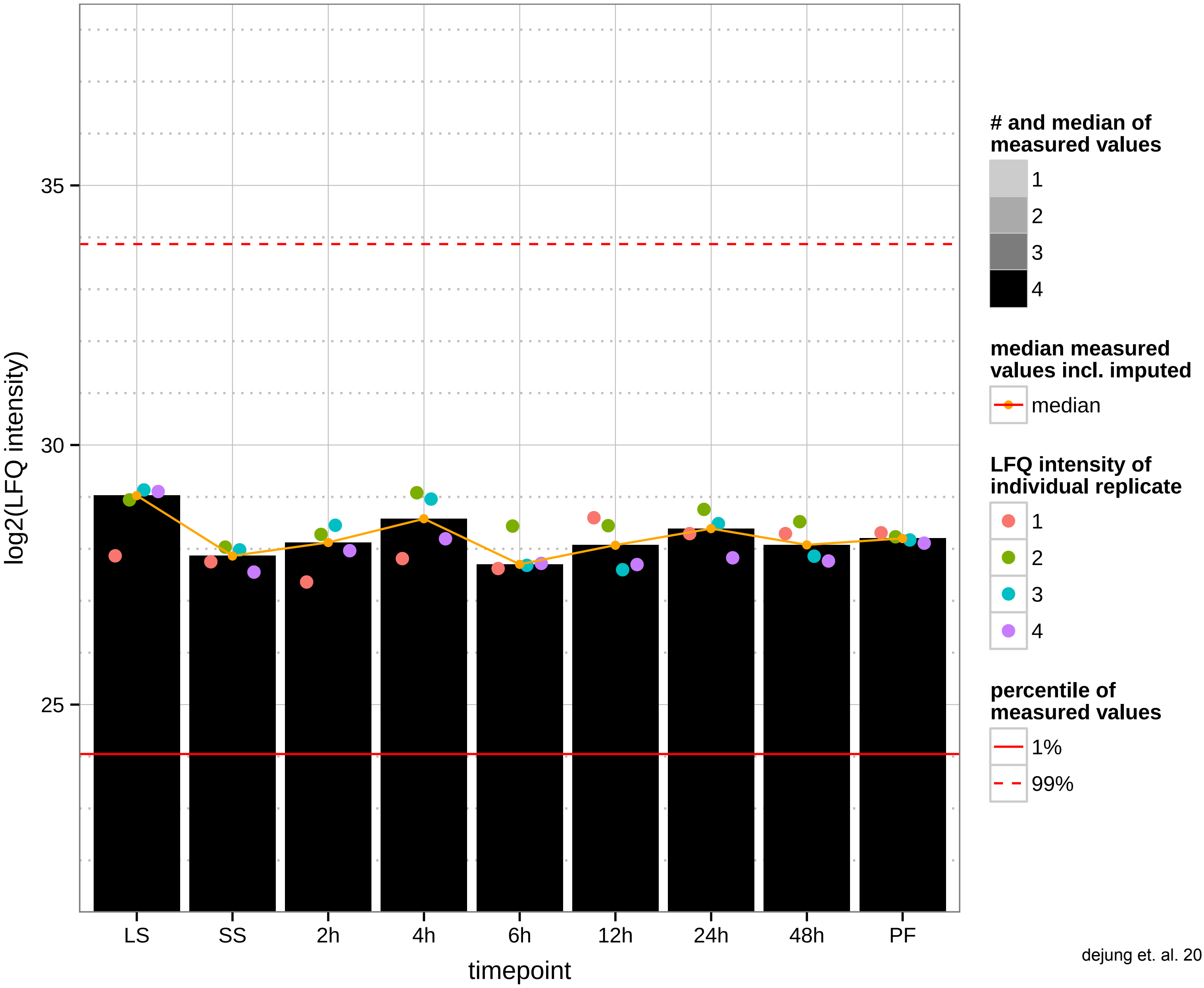
Dynein light chain roadblock–type protein, putative
Tb927.10.13110
AGOF: microtubule motor activity
AGOC: cytoplasmic dynein complex
AGOP: microtubule–based movement
PGOF: null
PGOC: null
PGOP: null





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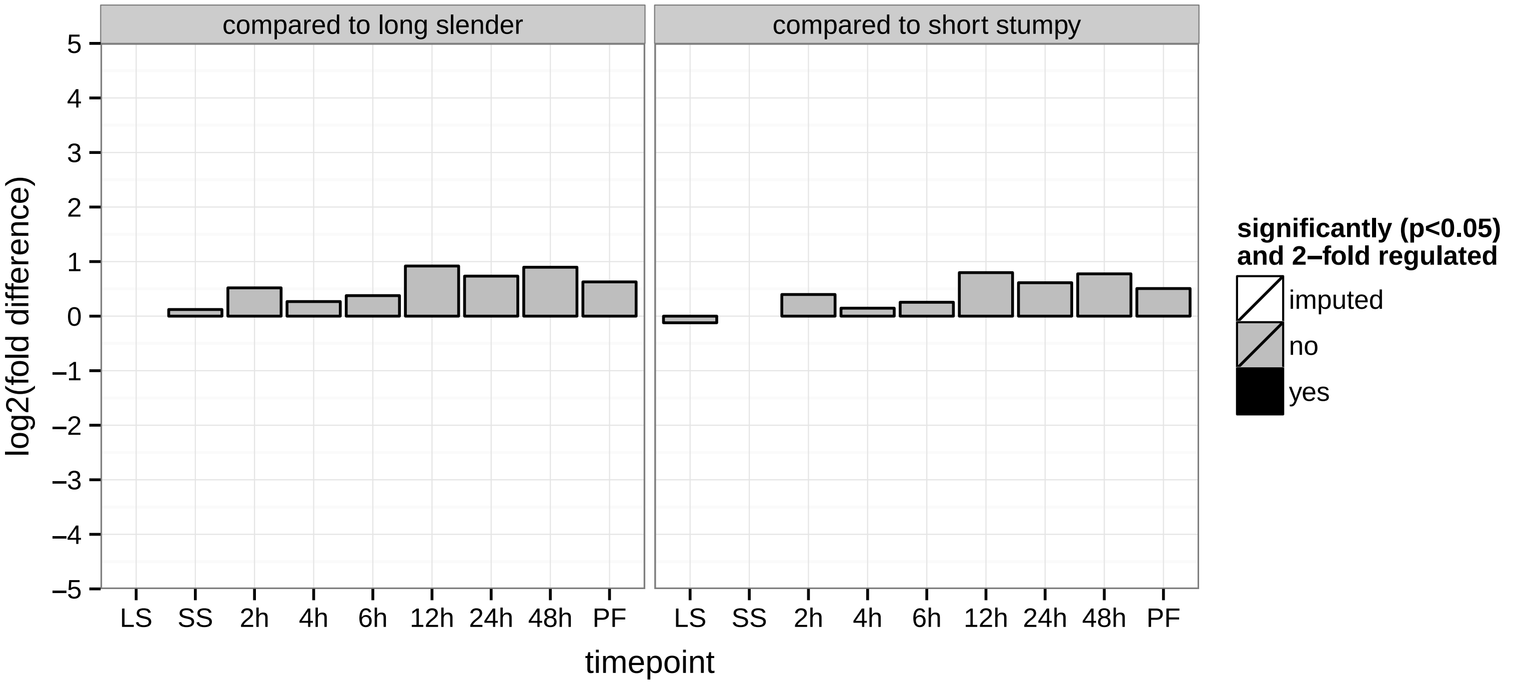
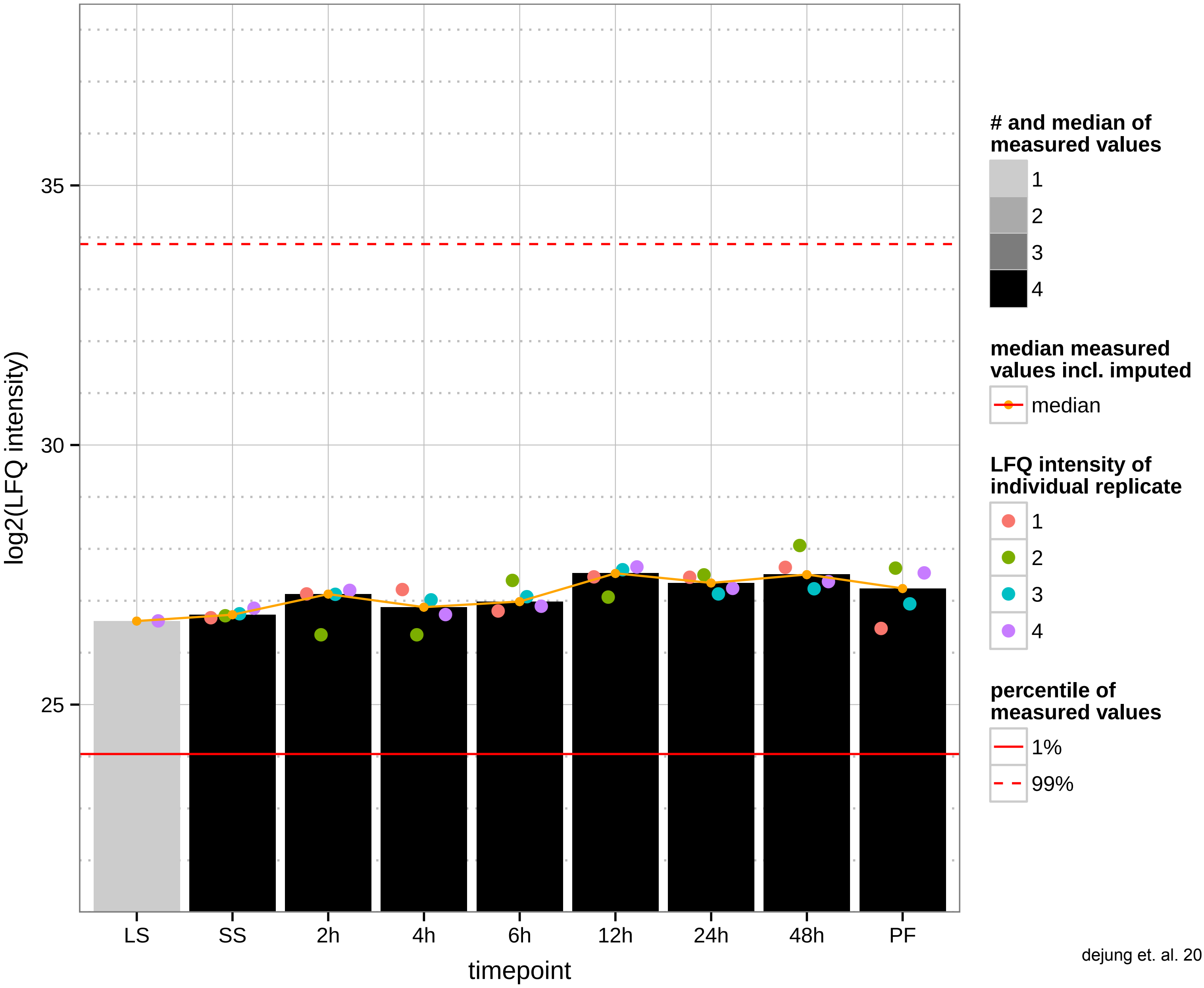
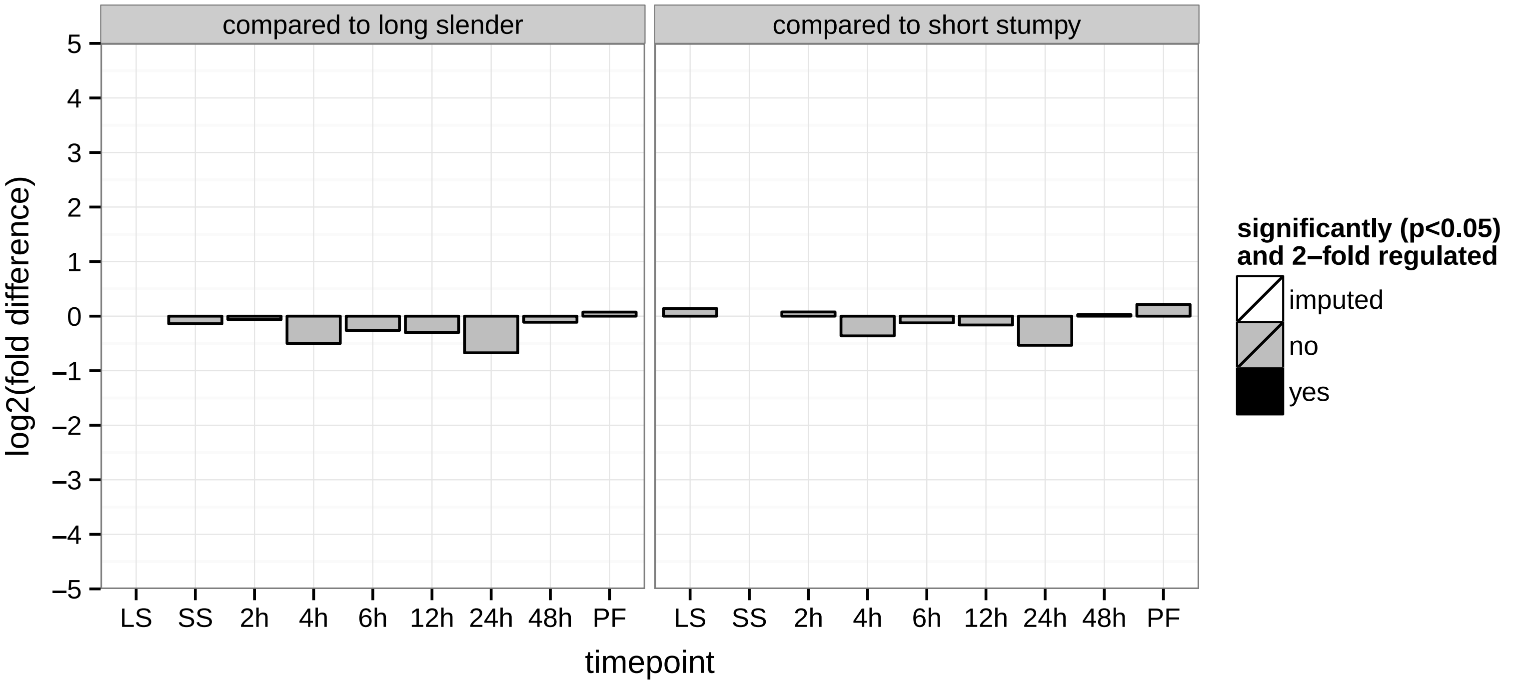
UTP−glucose−1−phosphate uridylyltransferase
Tb927.10.13130
AGOF: UTP:glucose−1−phosphate uridylyltransferase activity, metal ion binding, nucleotidyltransferase activity
AGOC: glycosome
AGOP: UDP−glucose metabolic process
PGOF: nucleotidyltransferase activity
PGOC: null
PGOP: metabolic process

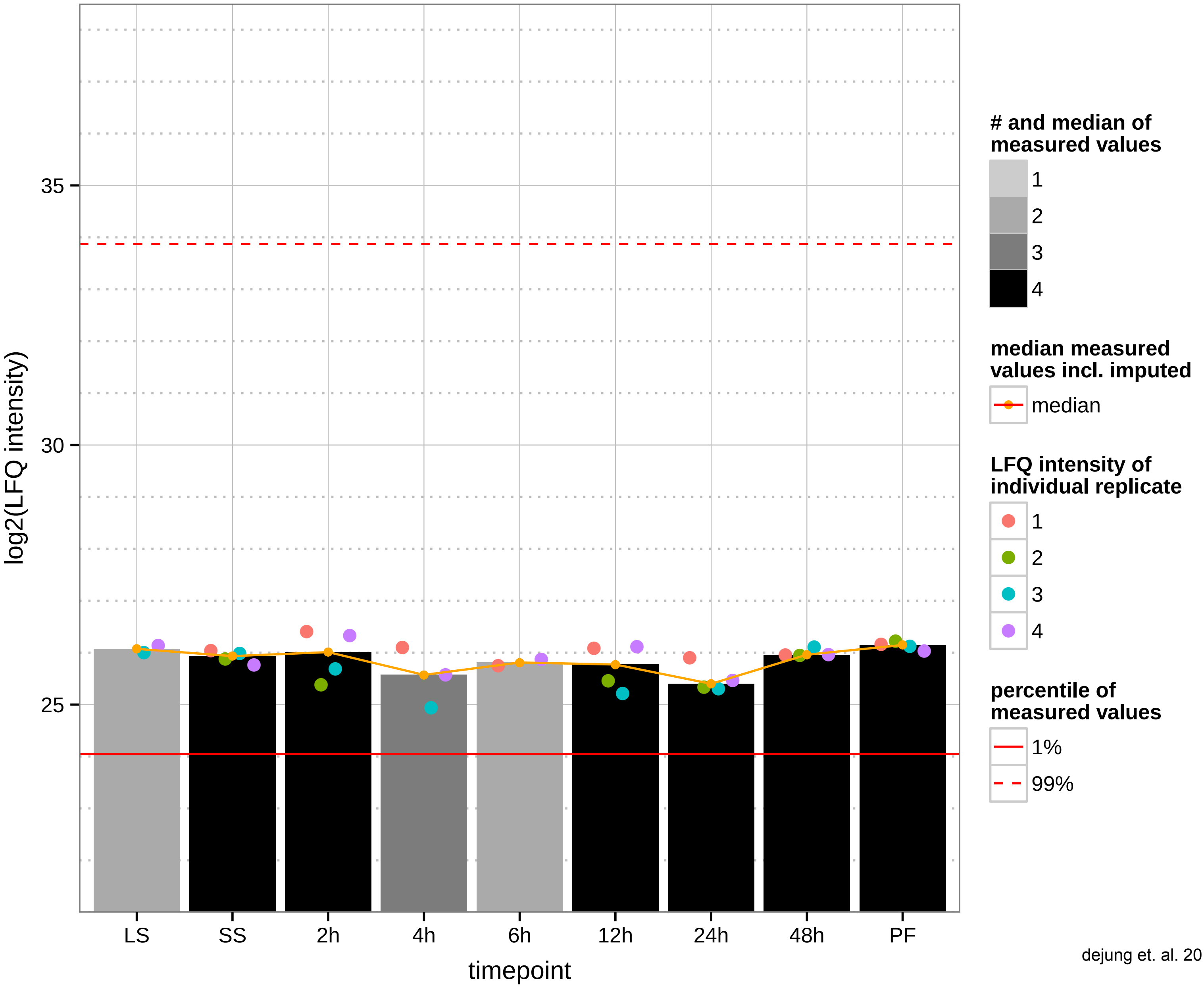




dejung et. al. 2015

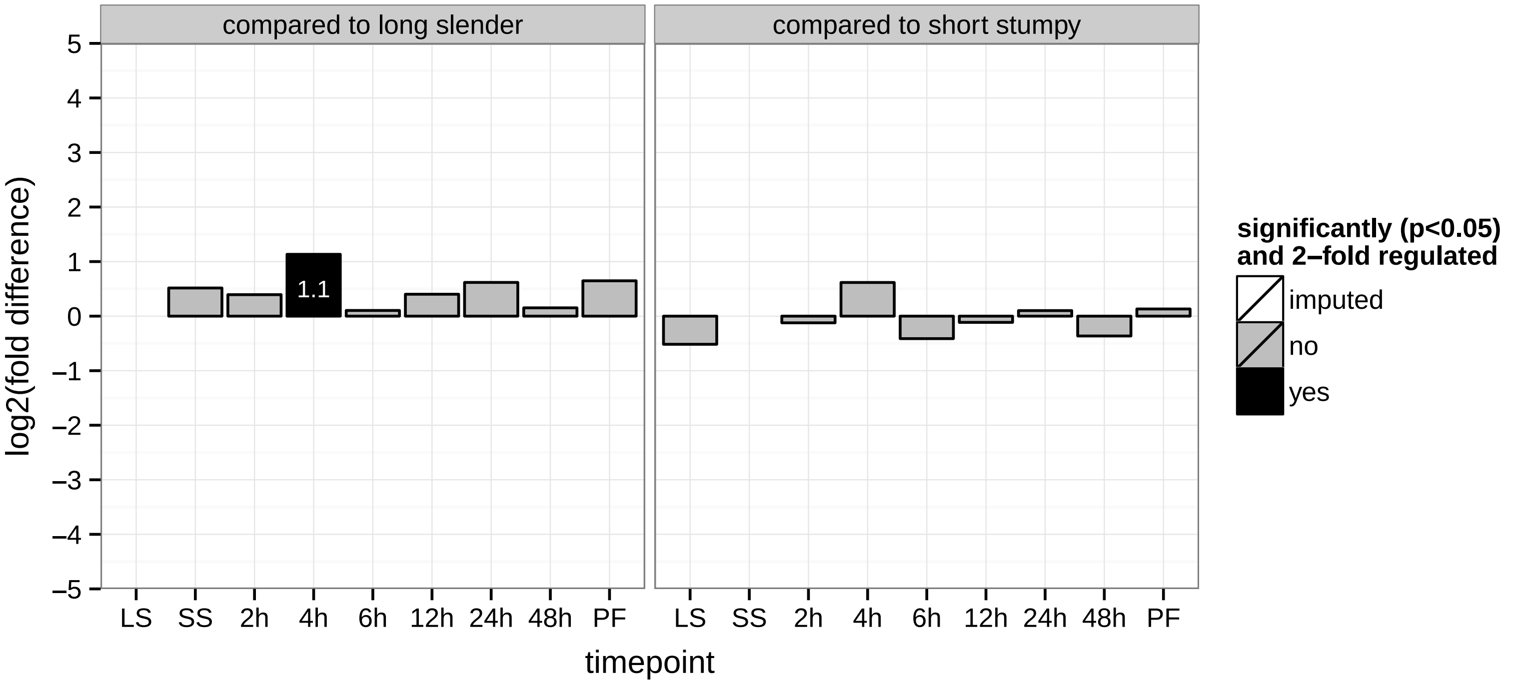
hypothetical protein, conserved
Tb927.10.1320
AGOF: ATP binding, protein kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

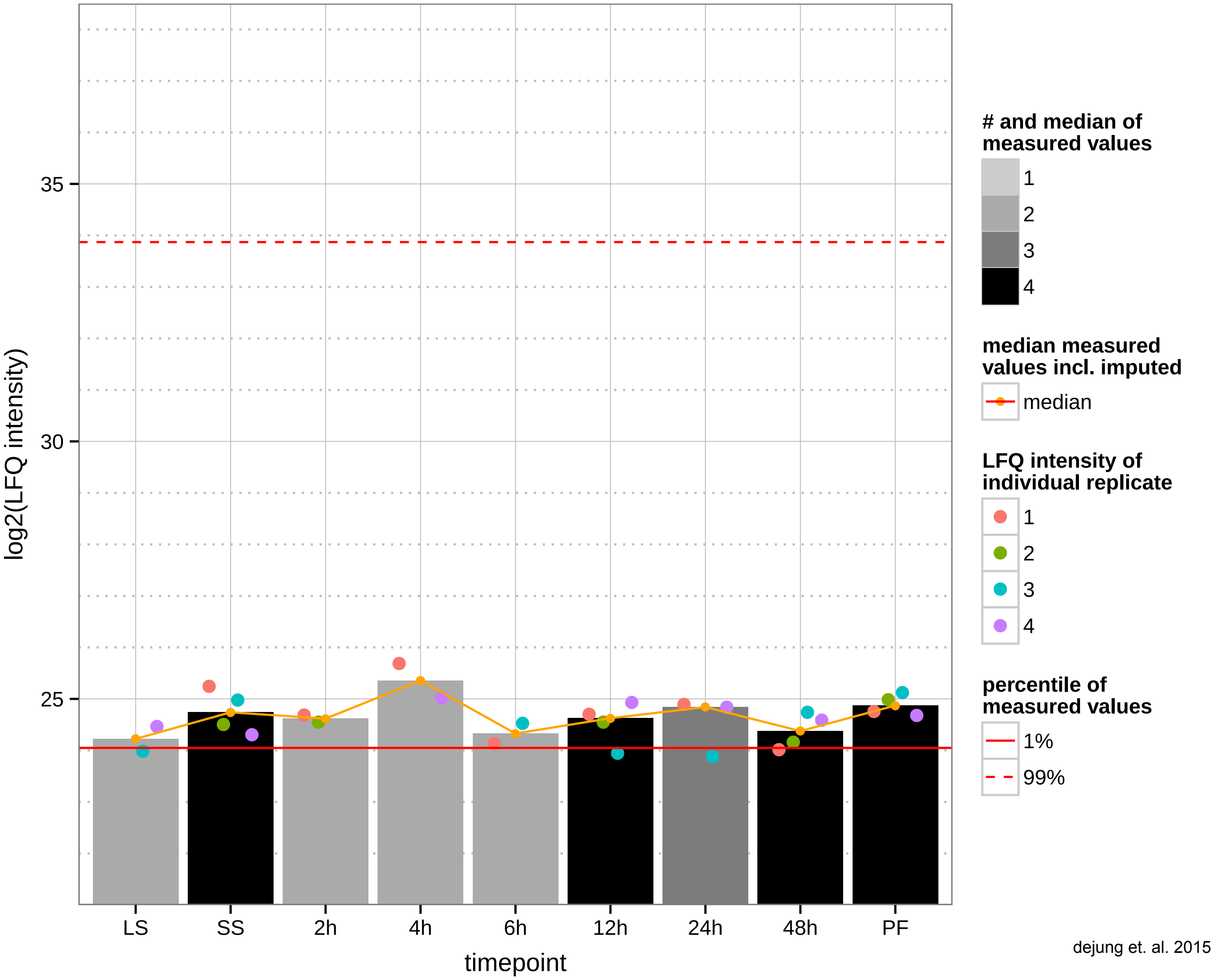




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.13250
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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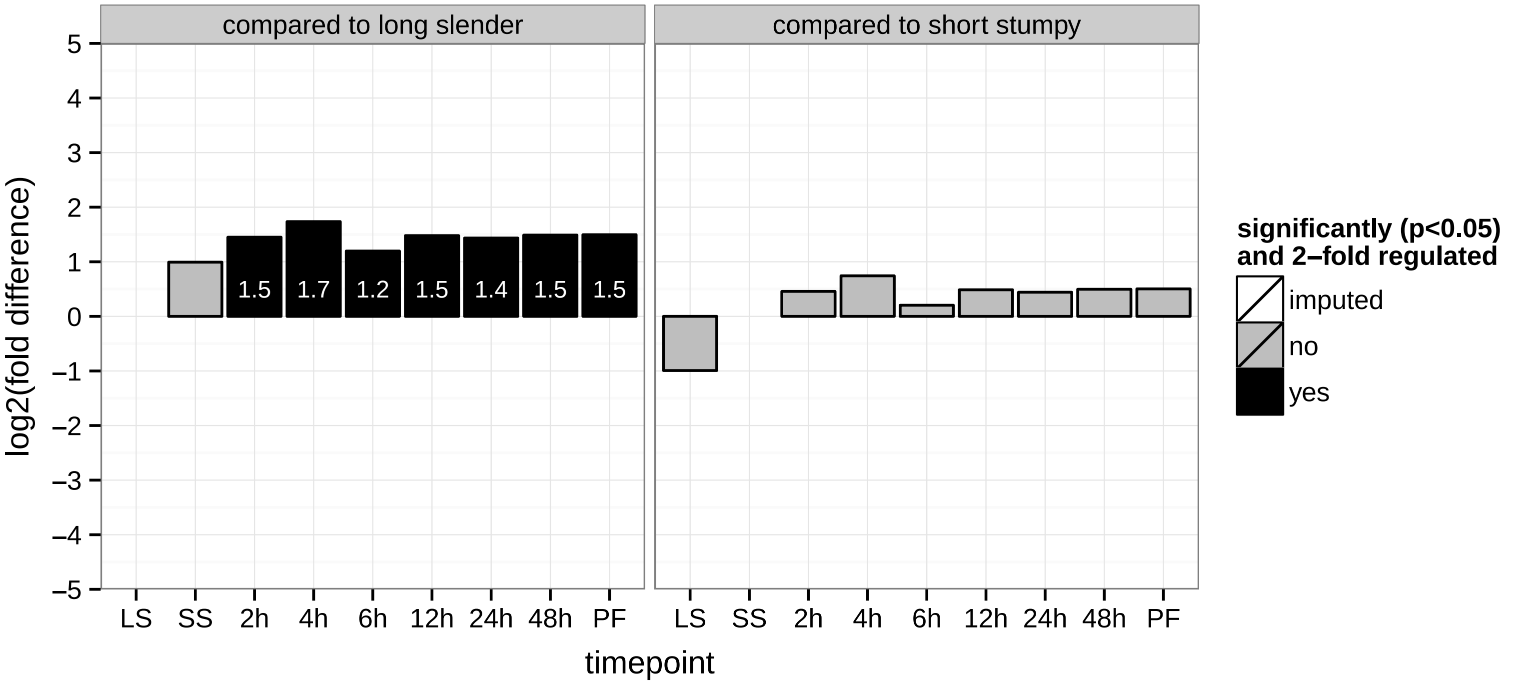
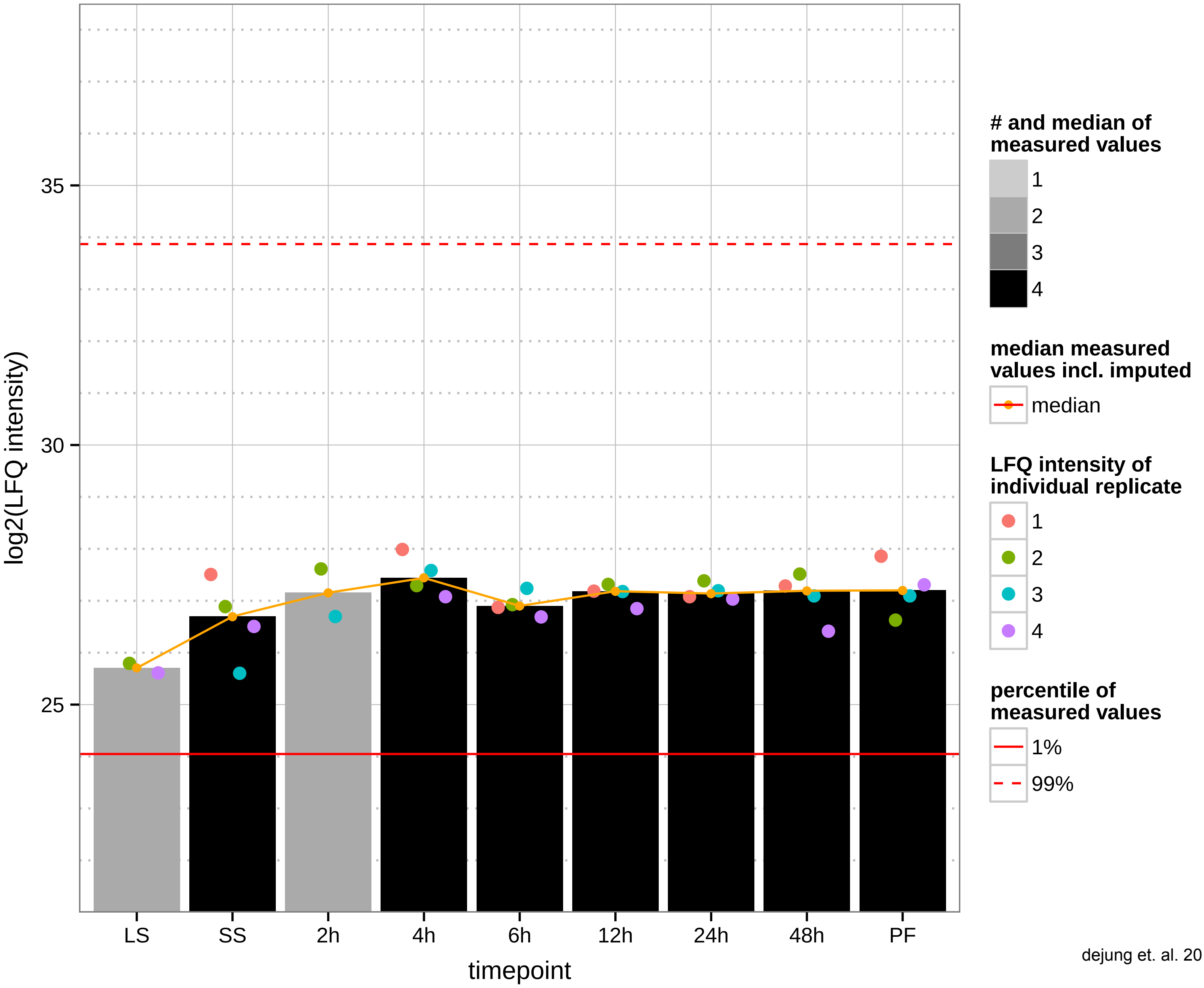
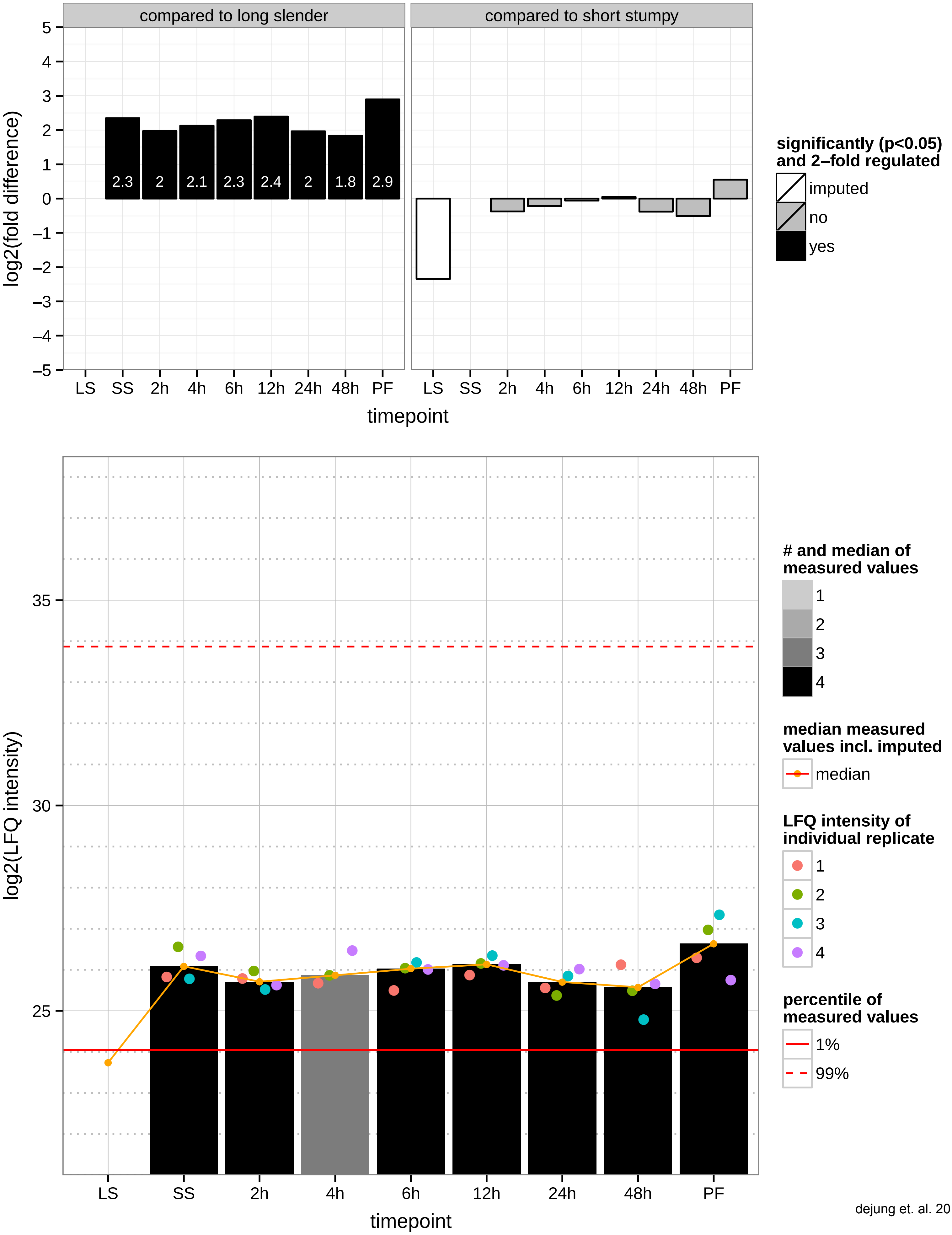
DNA–directed RNA polymerase II/III subunit, putative (RPB5)
Tb927.10.13320
AGOF: DNA binding, DNA–directed RNA polymerase activity
AGOC: nucleus
AGOP: transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: nucleus
PGOP: transcription, DNA–dependent





dejung et. al. 2015

citrate synthase, putative
Tb927.10.13430
AGOF: transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer
AGOC: mitochondrion
AGOP: cellular carbohydrate metabolic process
PGOF: transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer
PGOC: null
PGOP: cellular carbohydrate metabolic process



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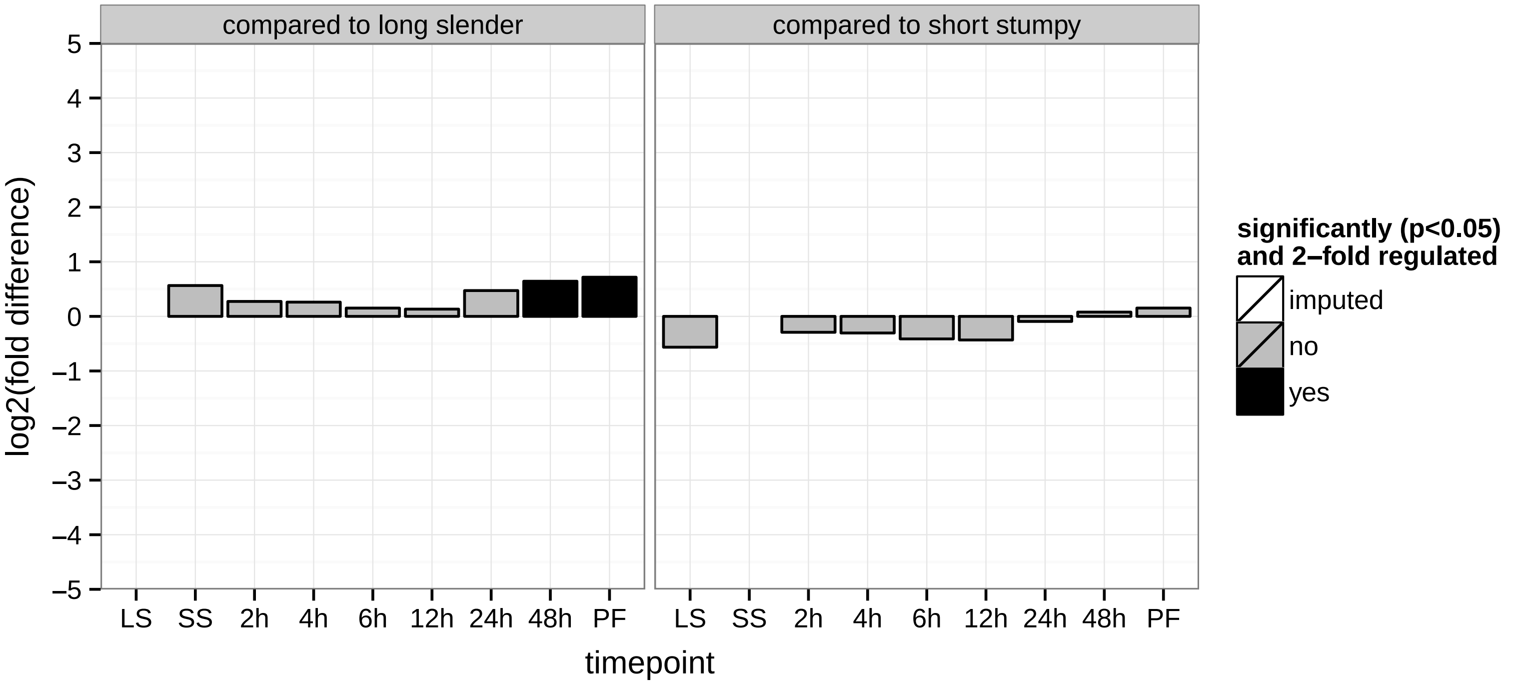
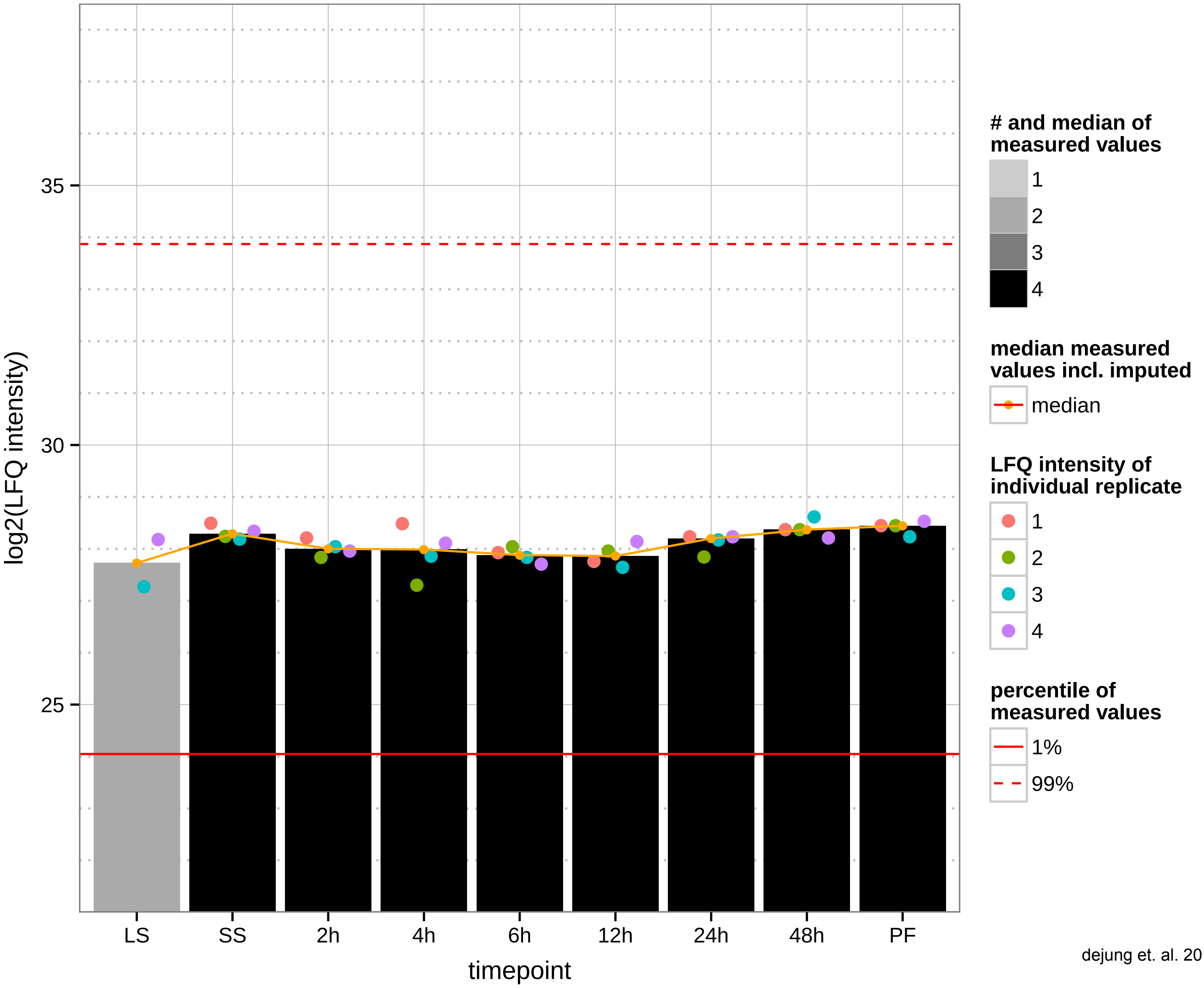
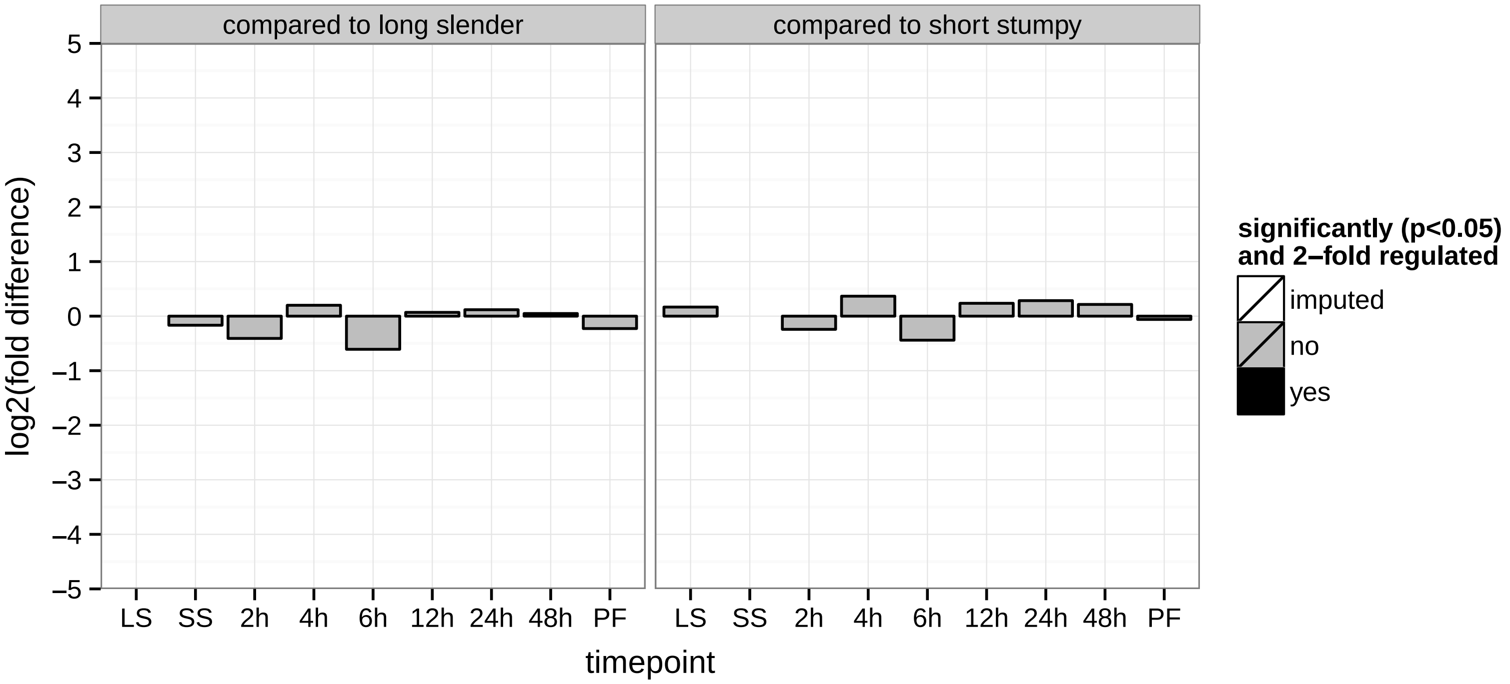
hypothetical protein, conserved
Tb927.10.13450
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

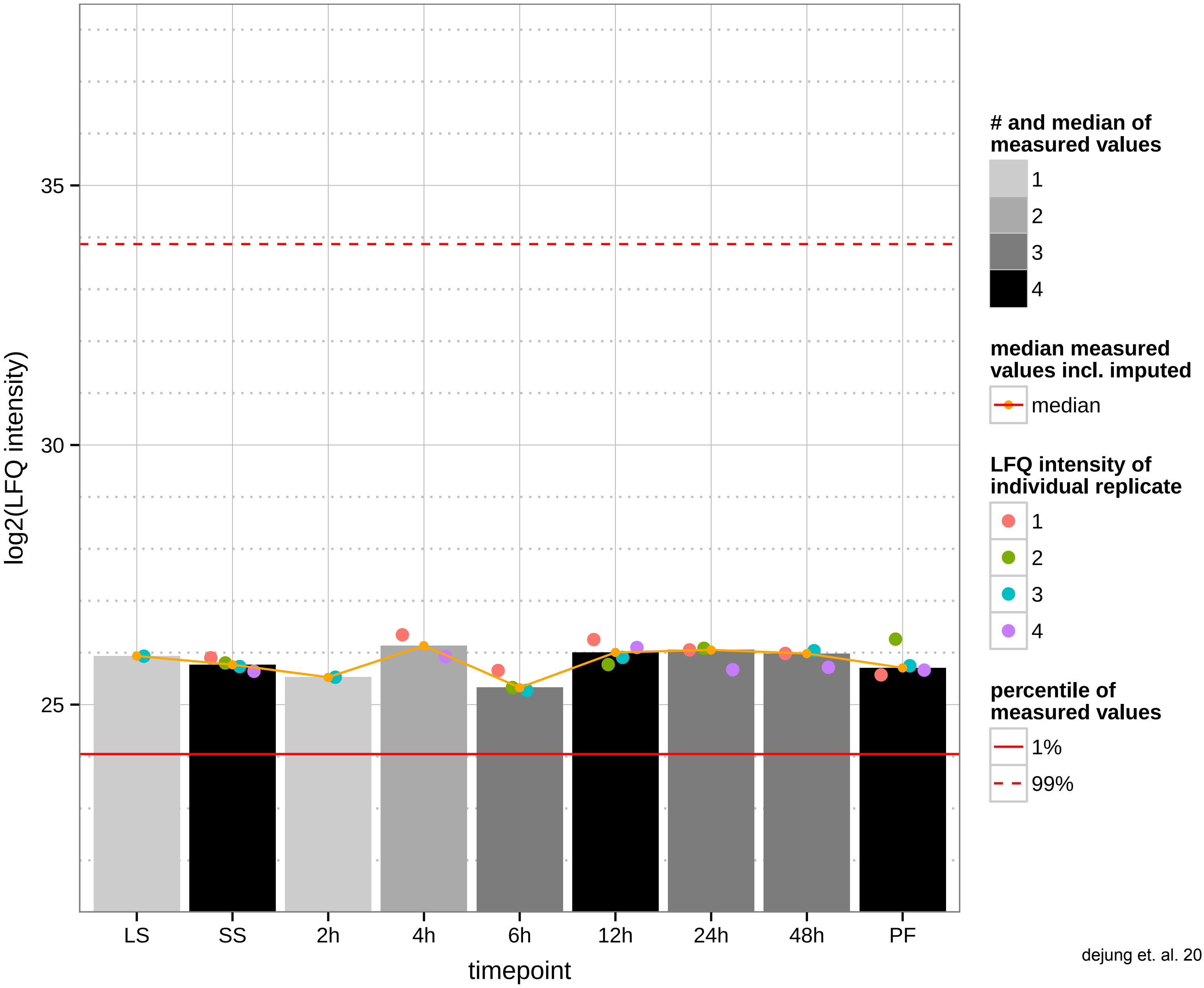




dejung et. al. 2015

protein kinase, putative
Tb927.10.13480
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: mitochondrion
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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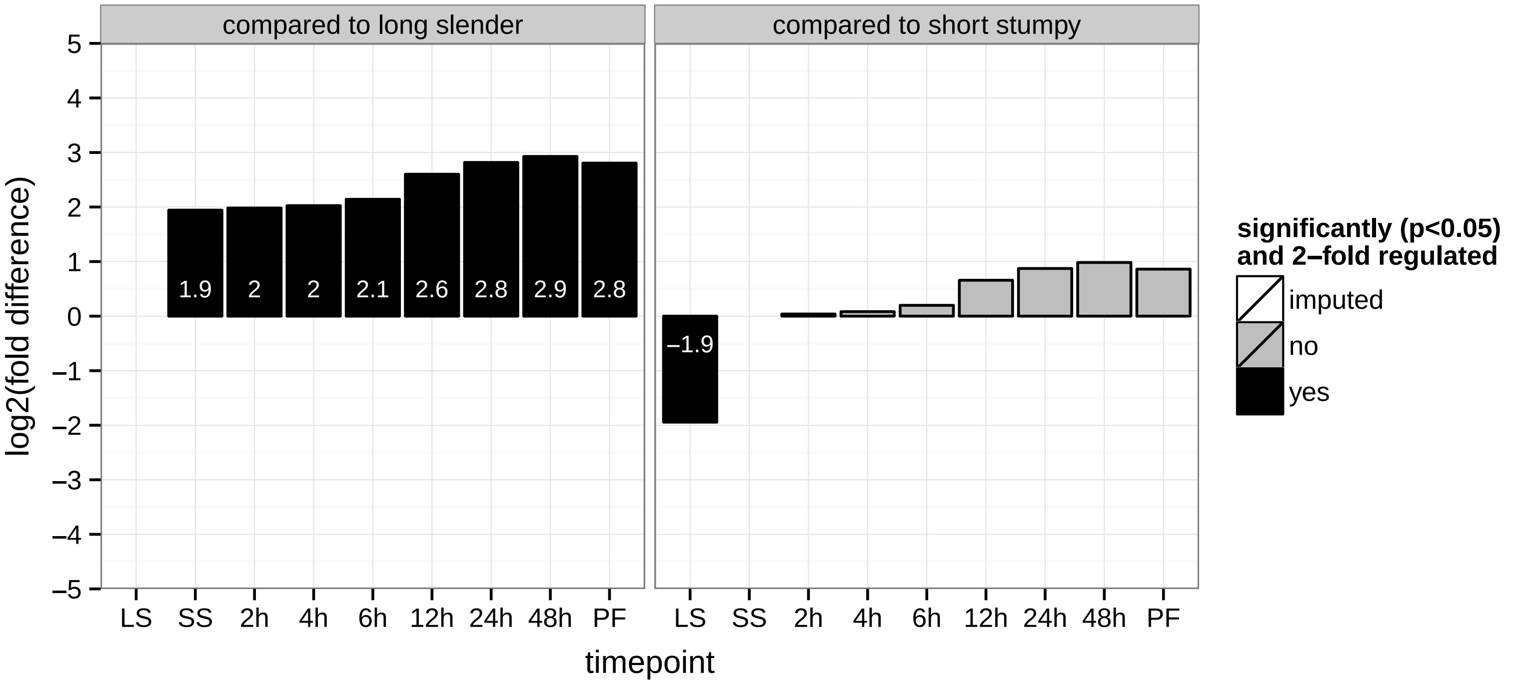
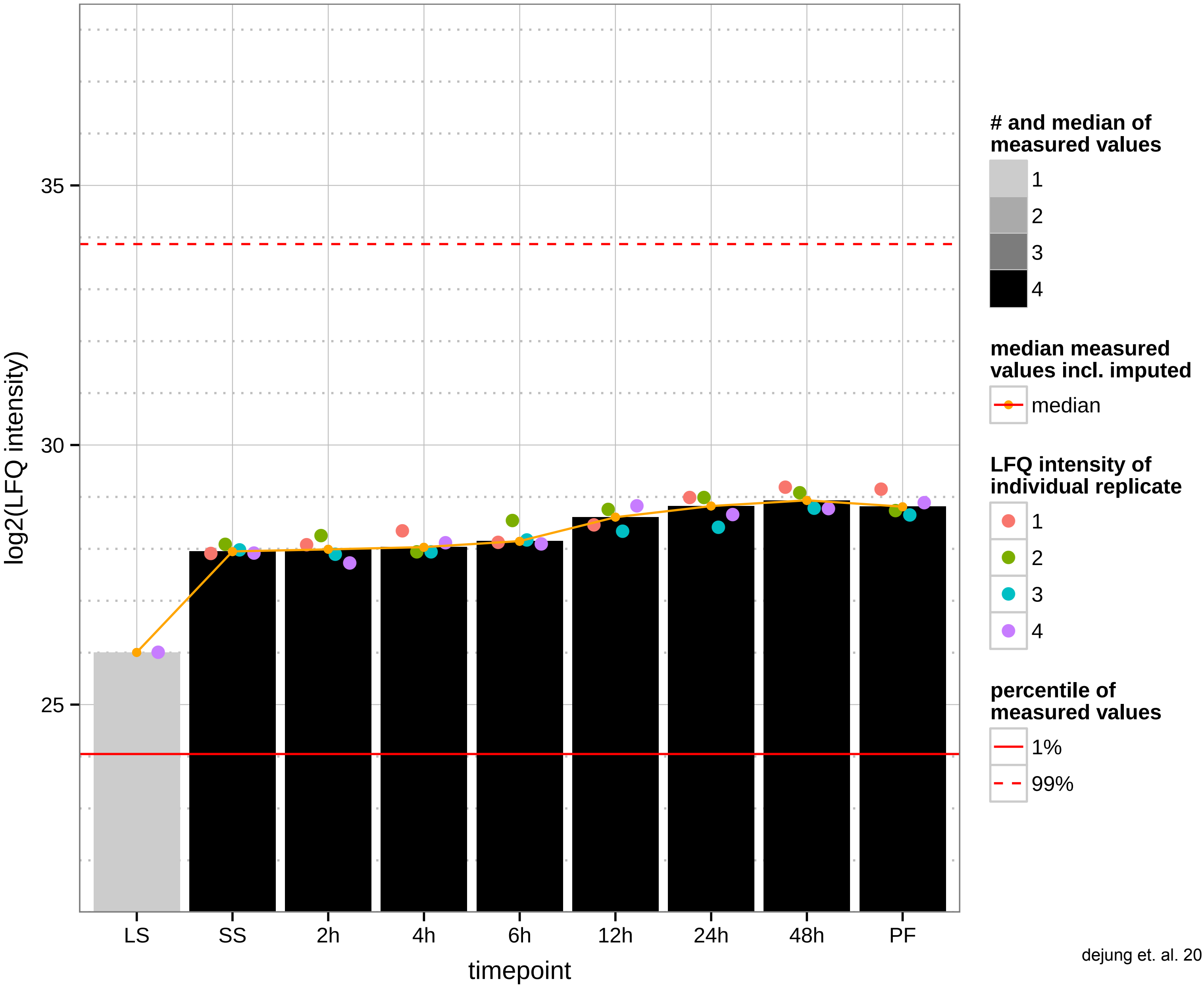
zinc metallopeptidase, putative
Tb927.10.13510
AGOF: ATP binding, metalloendopeptidase activity, nucleoside–triphosphatase activity
AGOC: null
AGOP: proteolysis
PGOF: ATP binding, metalloendopeptidase activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: proteolysis





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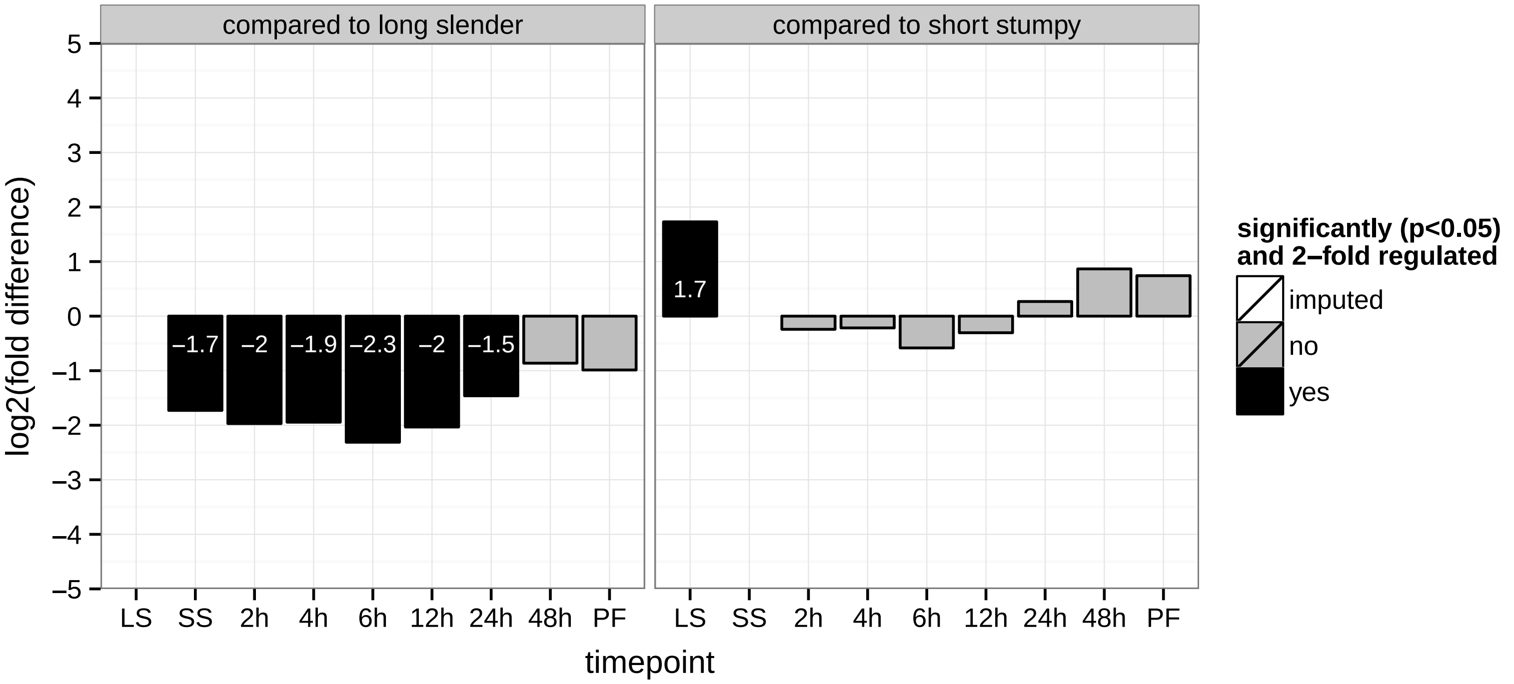
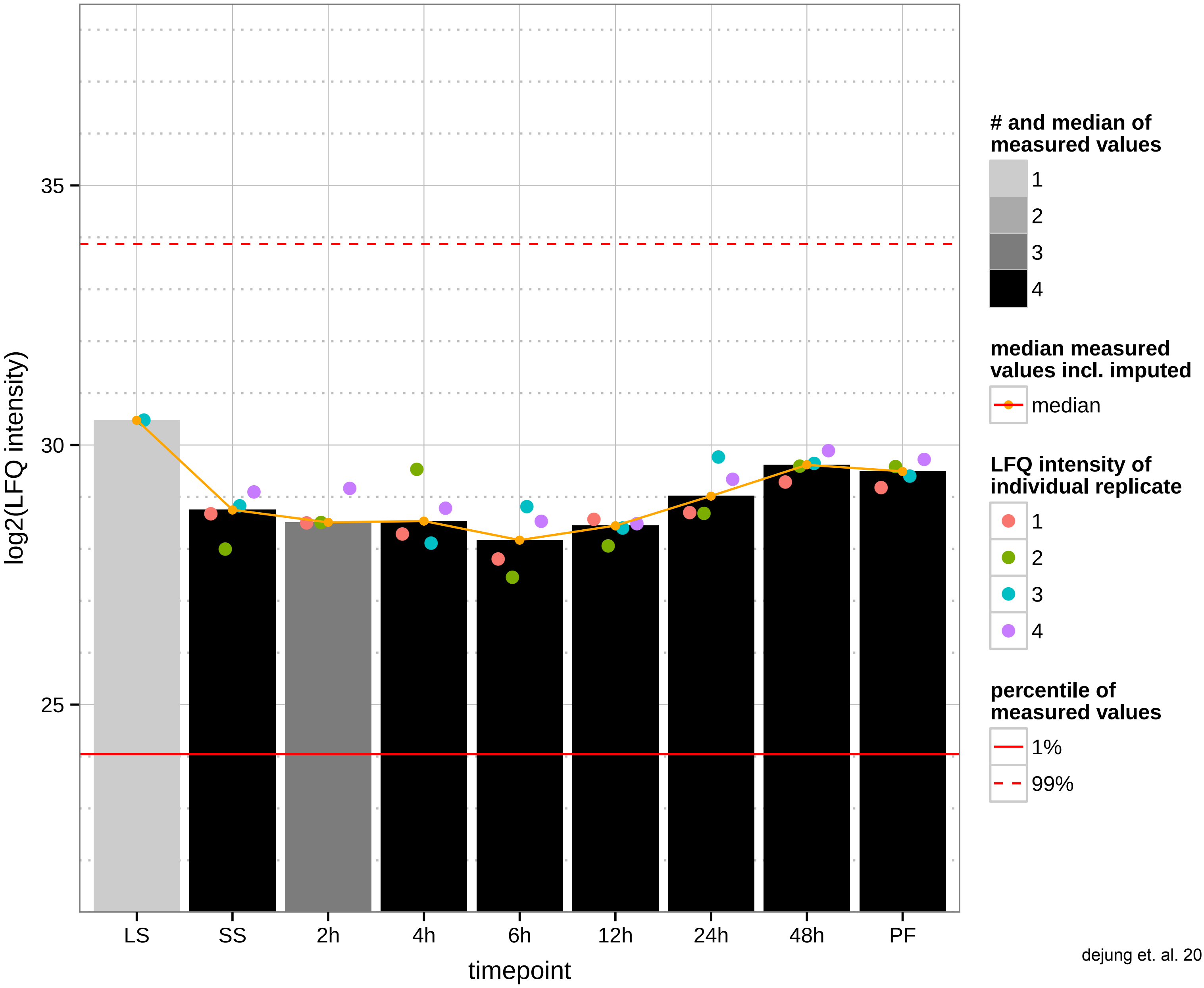
mevalonate–diphosphate decarboxylase, mevalonate diphosphate decarboxylase
Tb927.10.13560;Tb927.10.14070
AGOF: ATP binding, diphosphomevalonate decarboxylase activity, kinase activity
AGOC: null
AGOP: isoprenoid biosynthetic process, phosphorylation
PGOF: ATP binding, diphosphomevalonate decarboxylase activity
PGOC: null
PGOP: isoprenoid biosynthetic process





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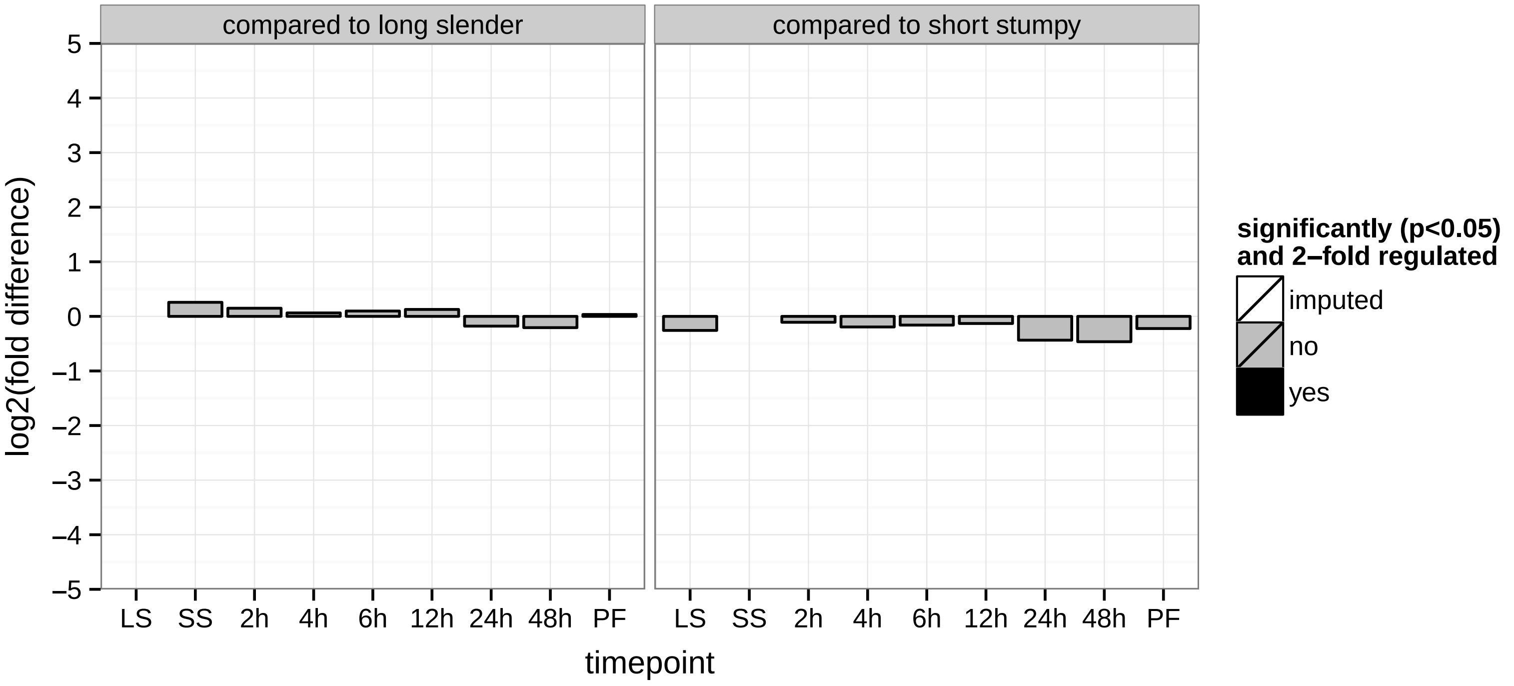
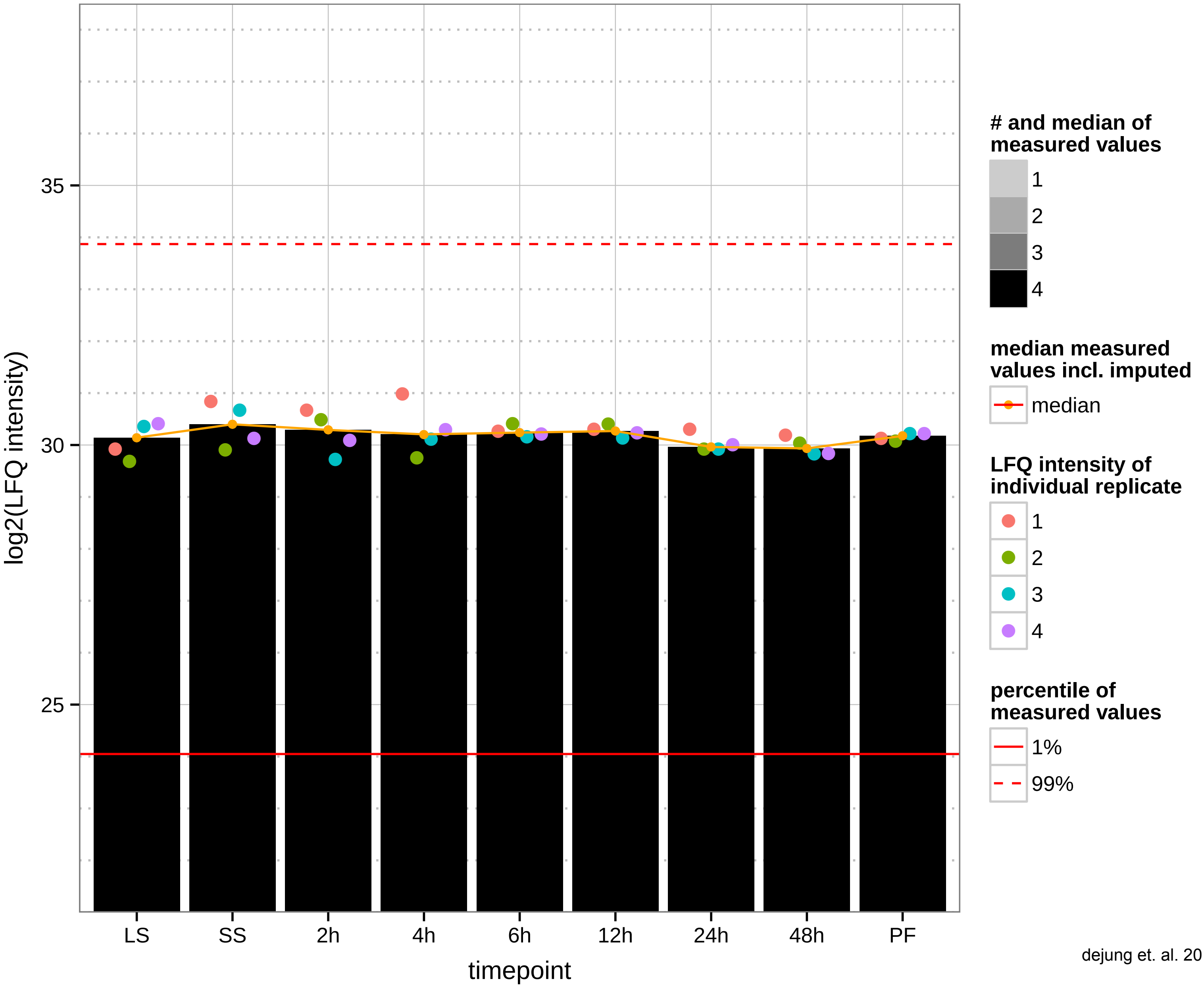
glucosidase, putative
Tb927.10.13630
AGOF: hydrolase activity, hydrolyzing O–glycosyl compounds
AGOC: null
AGOP: carbohydrate metabolic process
PGOF: carbohydrate binding, catalytic activity, hydrolase activity, hydrolyzing O–glycosyl compounds
PGOC: null
PGOP: carbohydrate metabolic process





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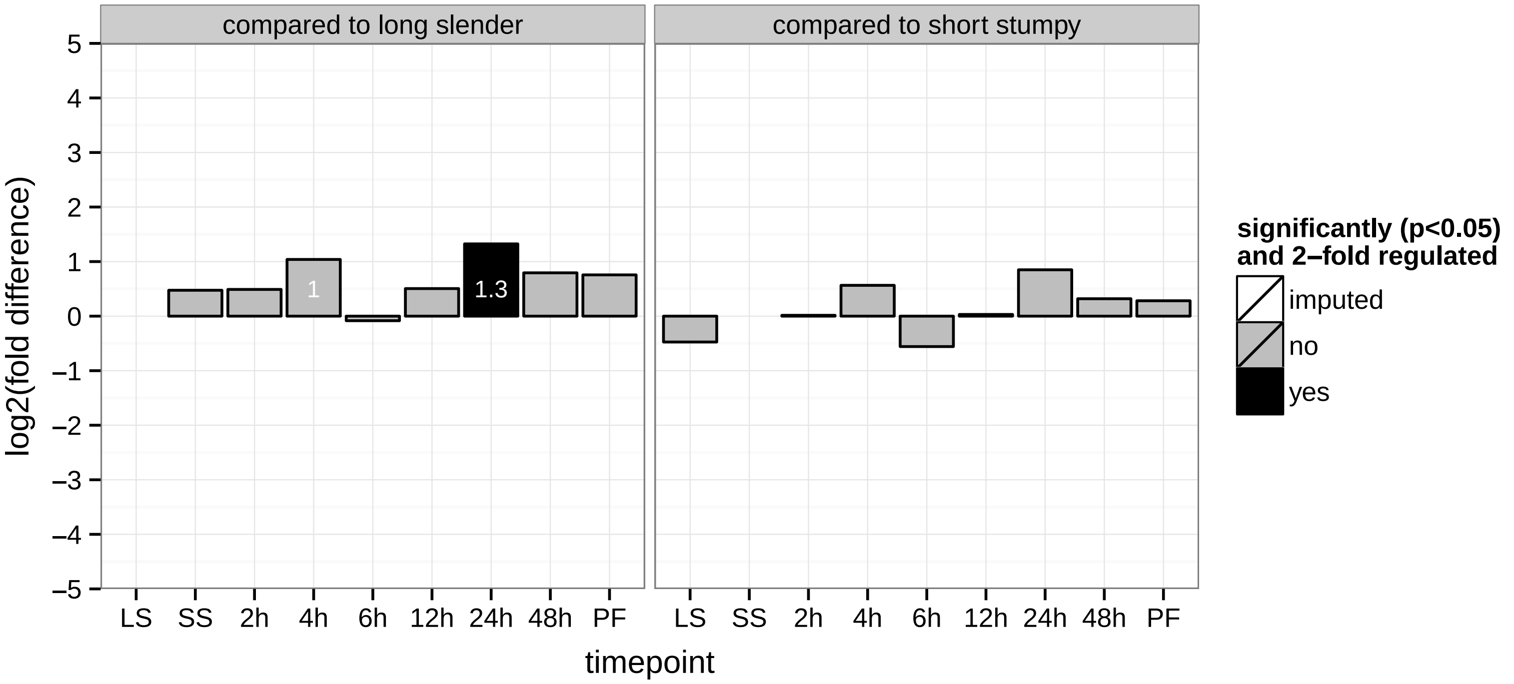
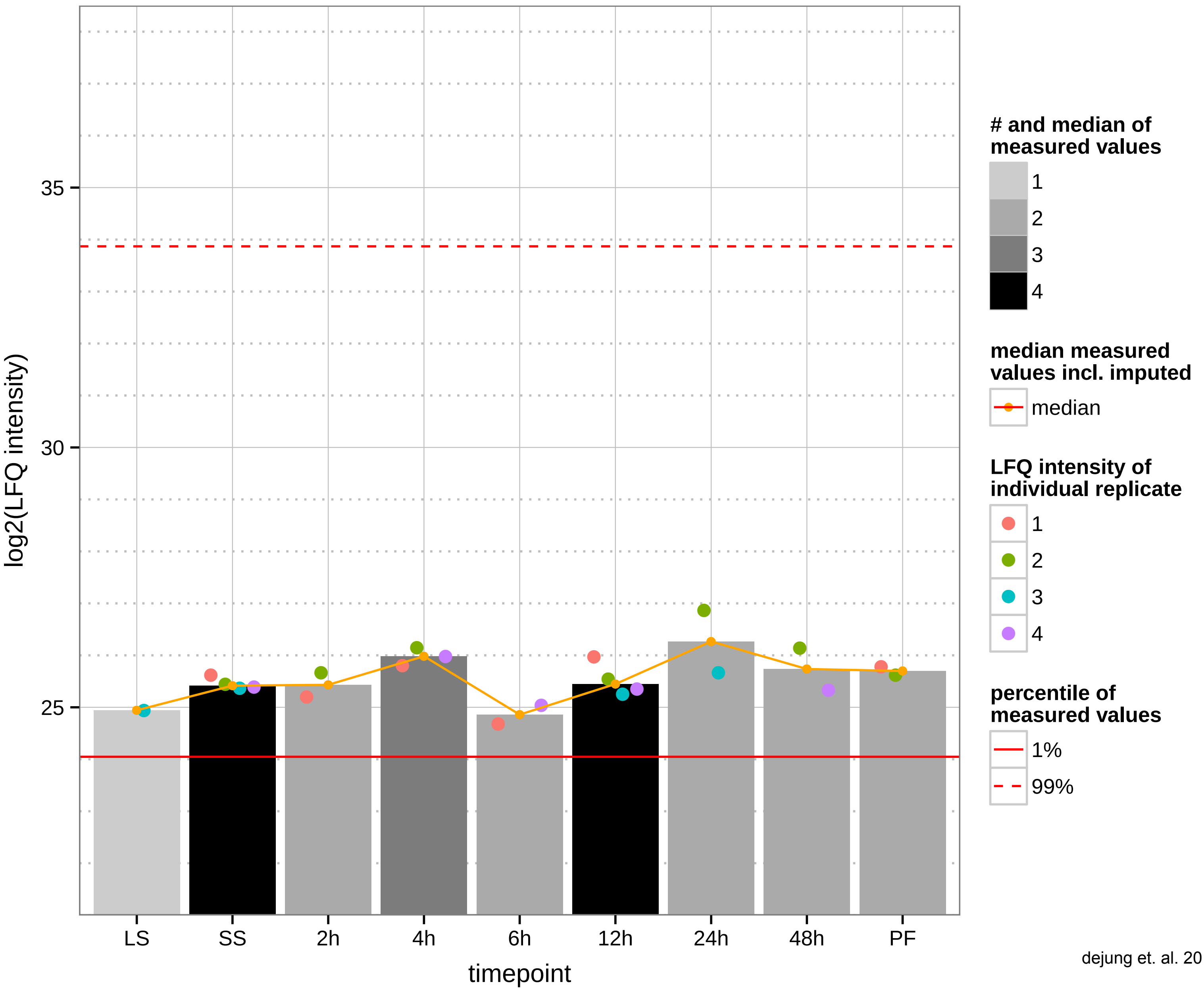
ARF–like 2–binding protein, putative, BART
Tb927.10.13650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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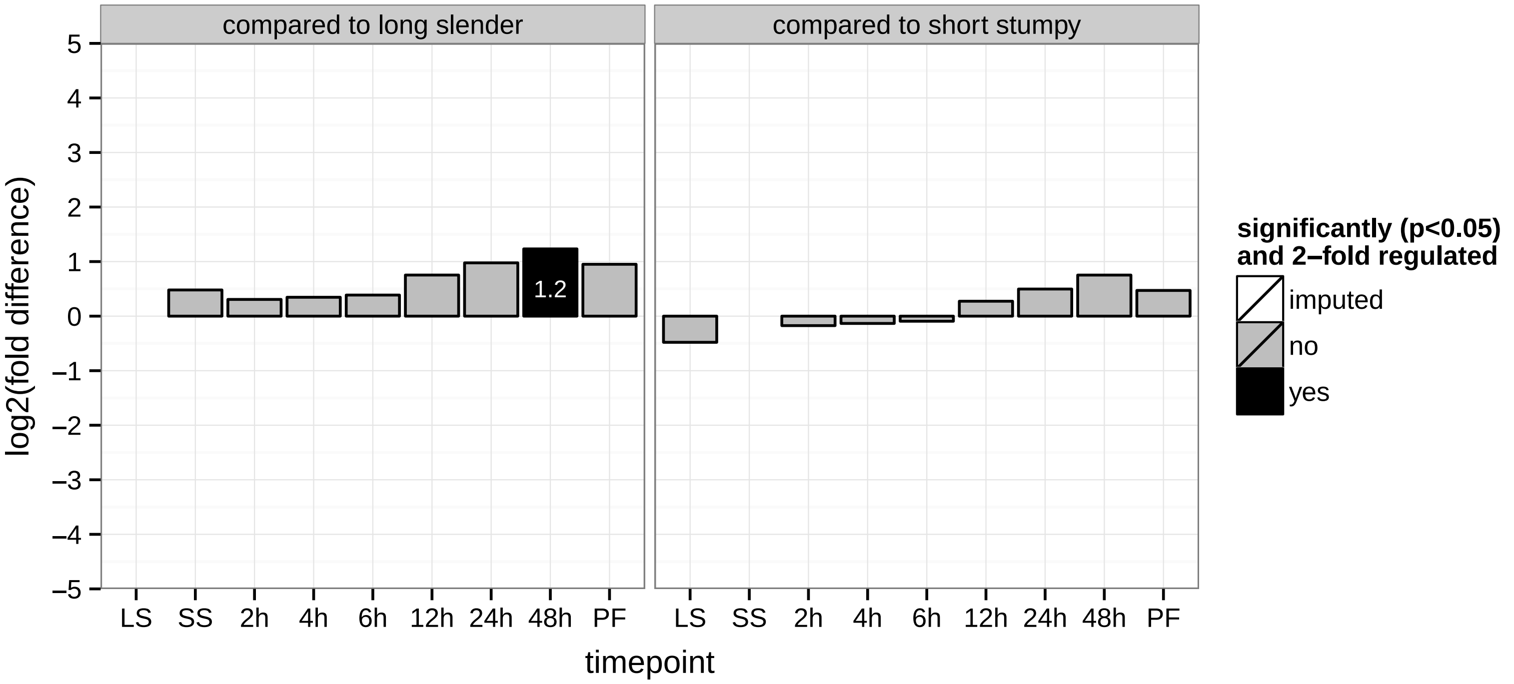
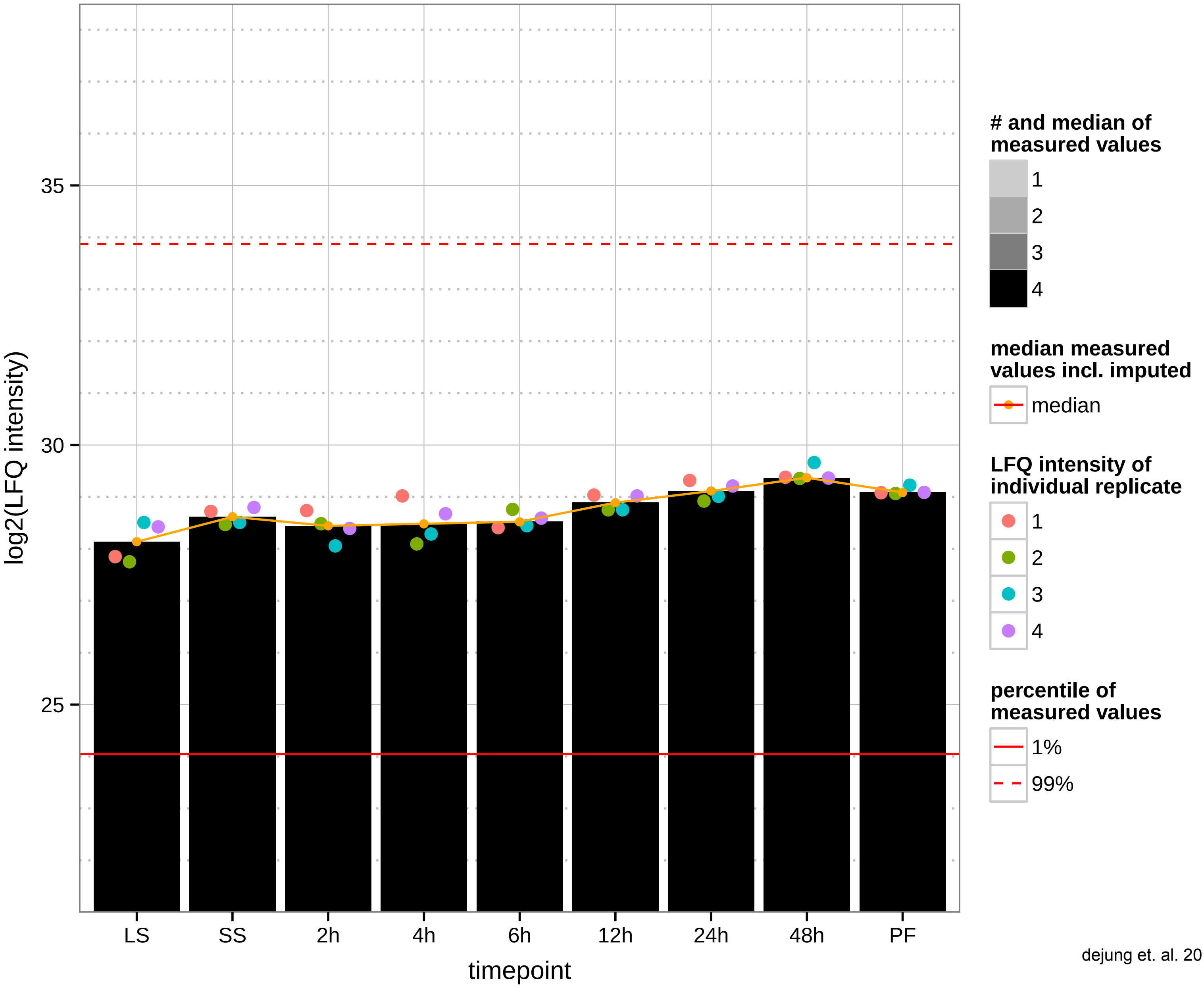
serine/threonine protein phosphatase 5
Tb927.10.13670
AGOF: metal ion binding, protein serine/threonine phosphatase activity
AGOC: cytoplasm, nucleus
AGOP: protein dephosphorylation
PGOF: hydrolase activity, phosphoprotein phosphatase activity, protein binding
PGOC: cytoplasm, nucleus
PGOP: protein dephosphorylation





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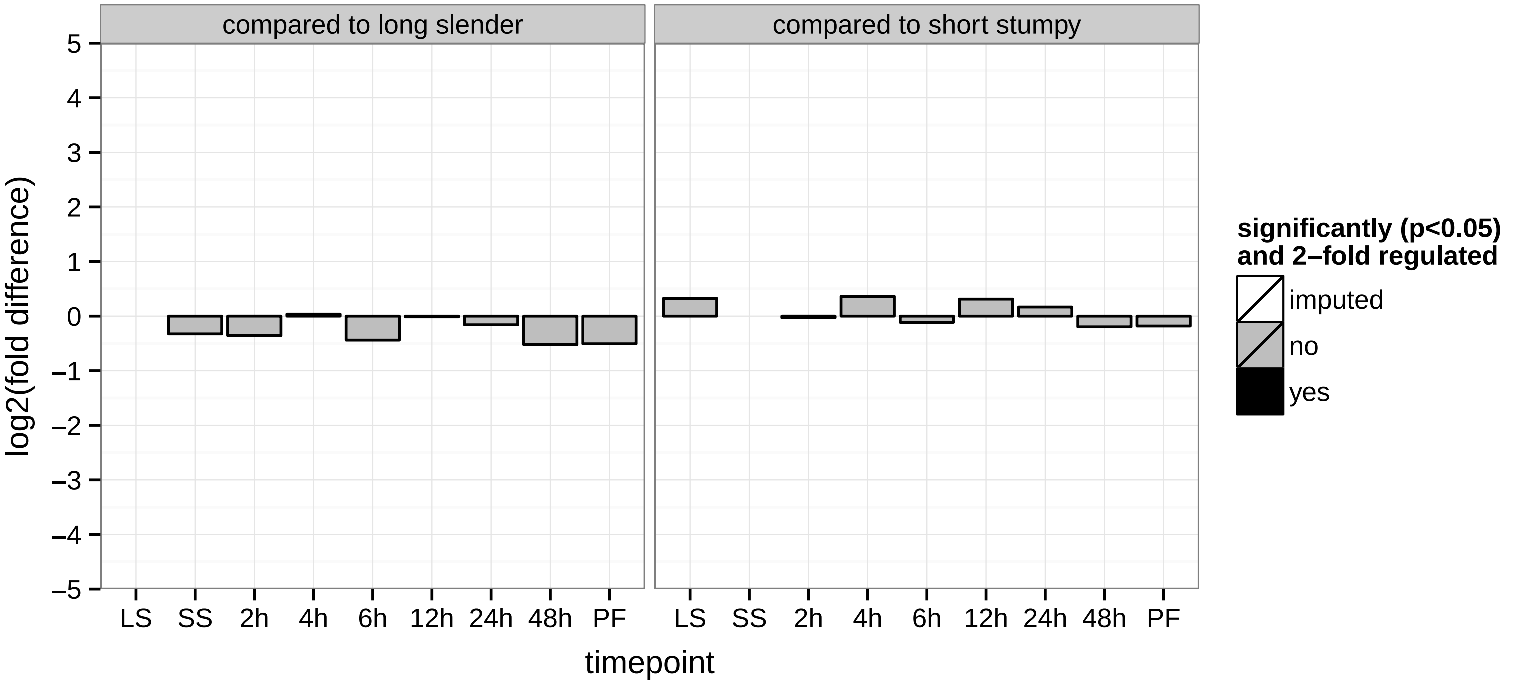
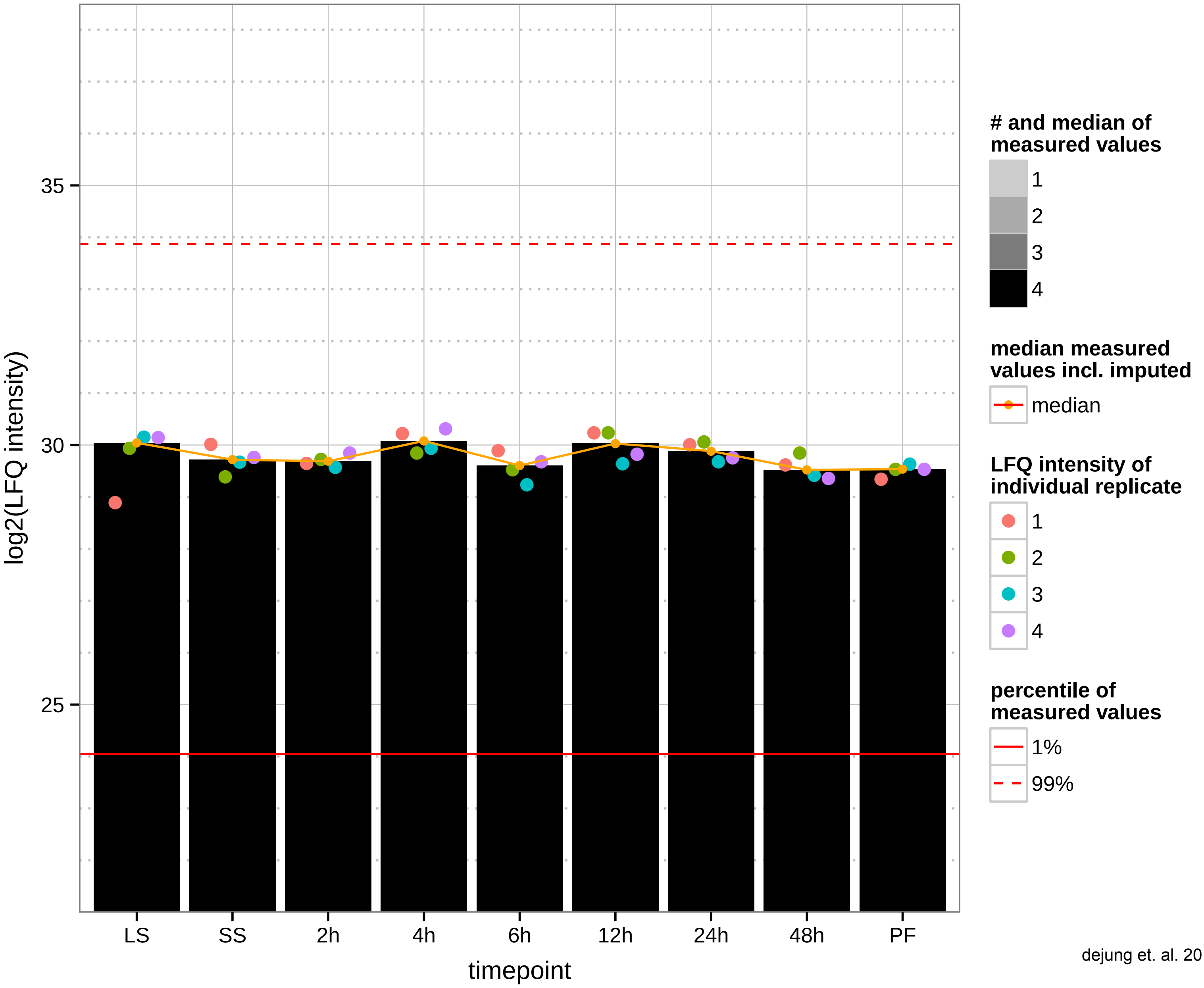
hypothetical protein, conserved
Tb927.10.13710
AGOF: ATPase activator activity, chaperone binding
AGOC: cytoplasm
AGOP: response to stress
PGOF: ATPase activator activity, chaperone binding
PGOC: null
PGOP: response to stress





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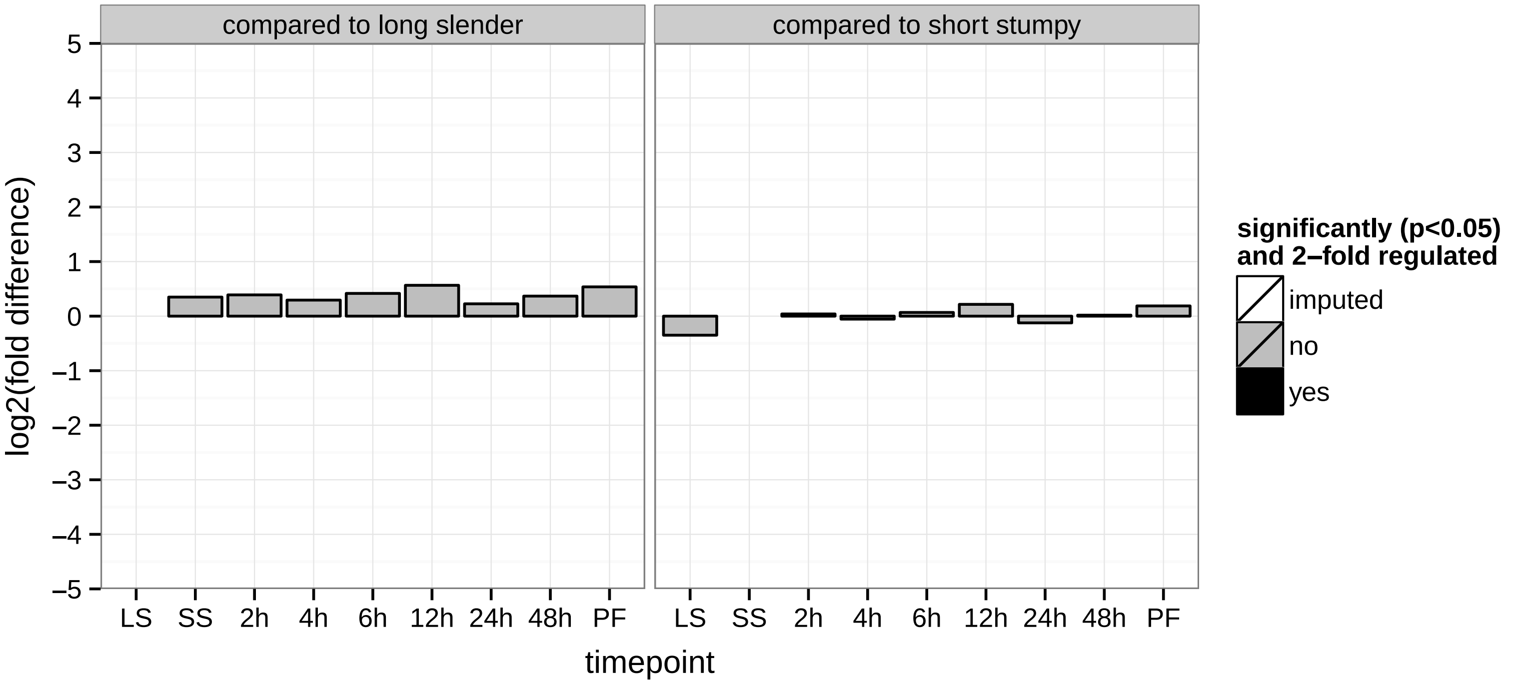
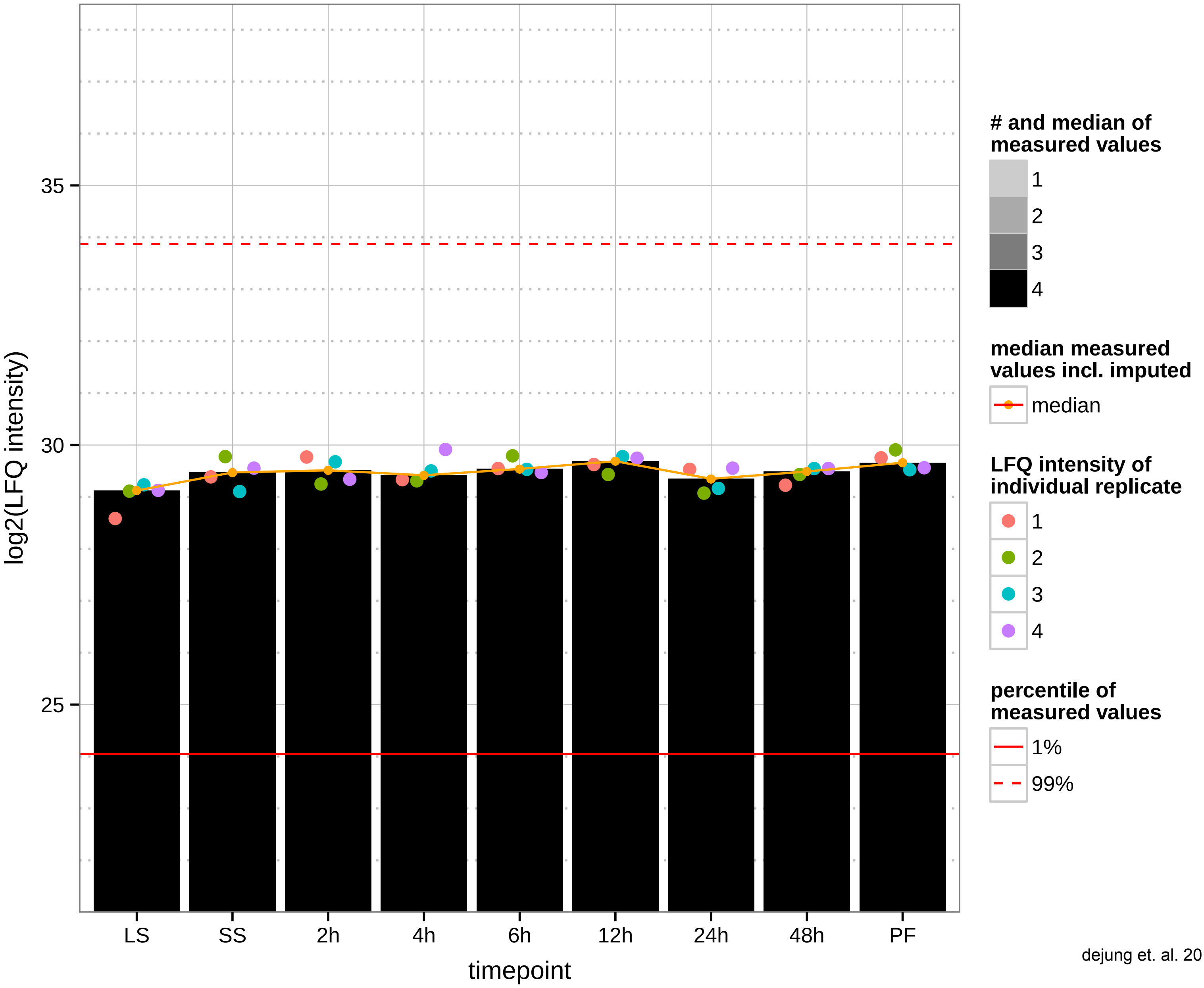
RNA–binding protein 29, putative (RBP29)
Tb927.10.13720
AGOF: RNA binding
AGOC: nucleus
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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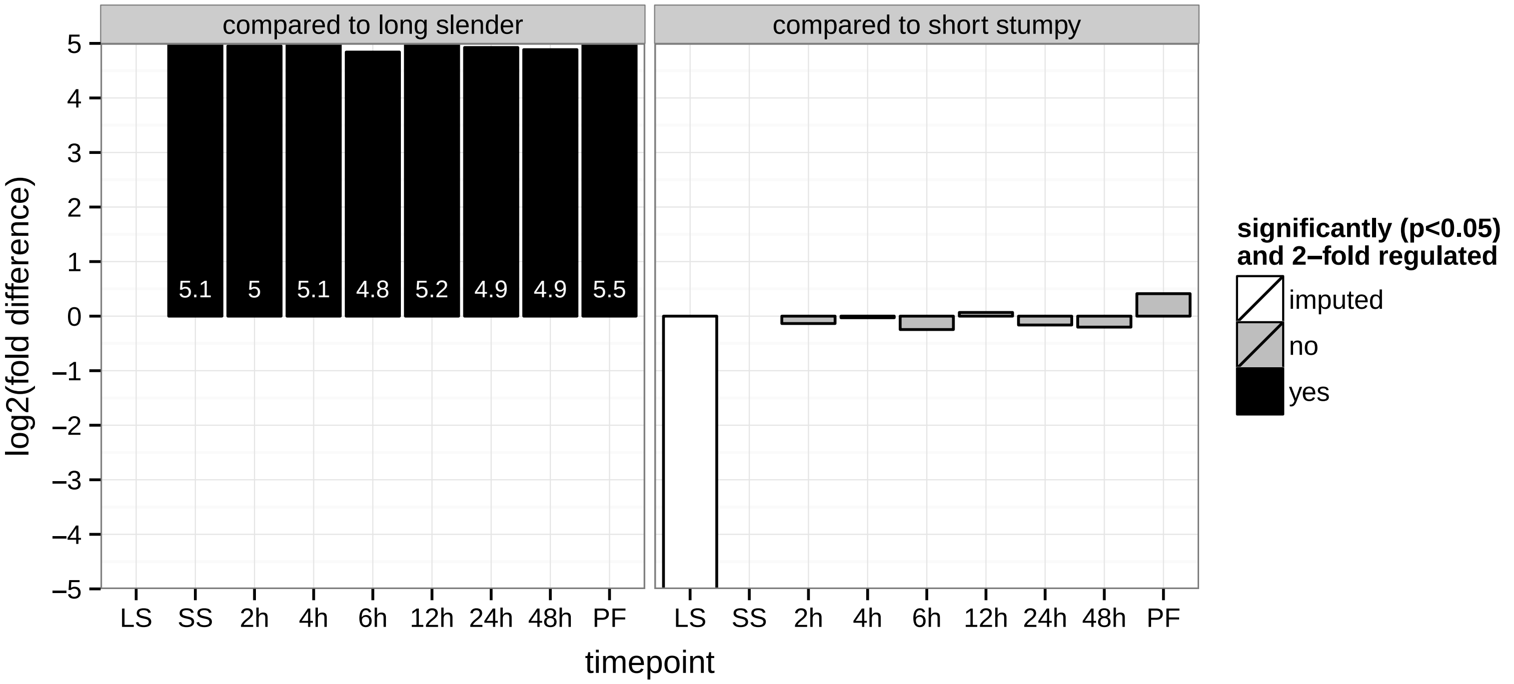
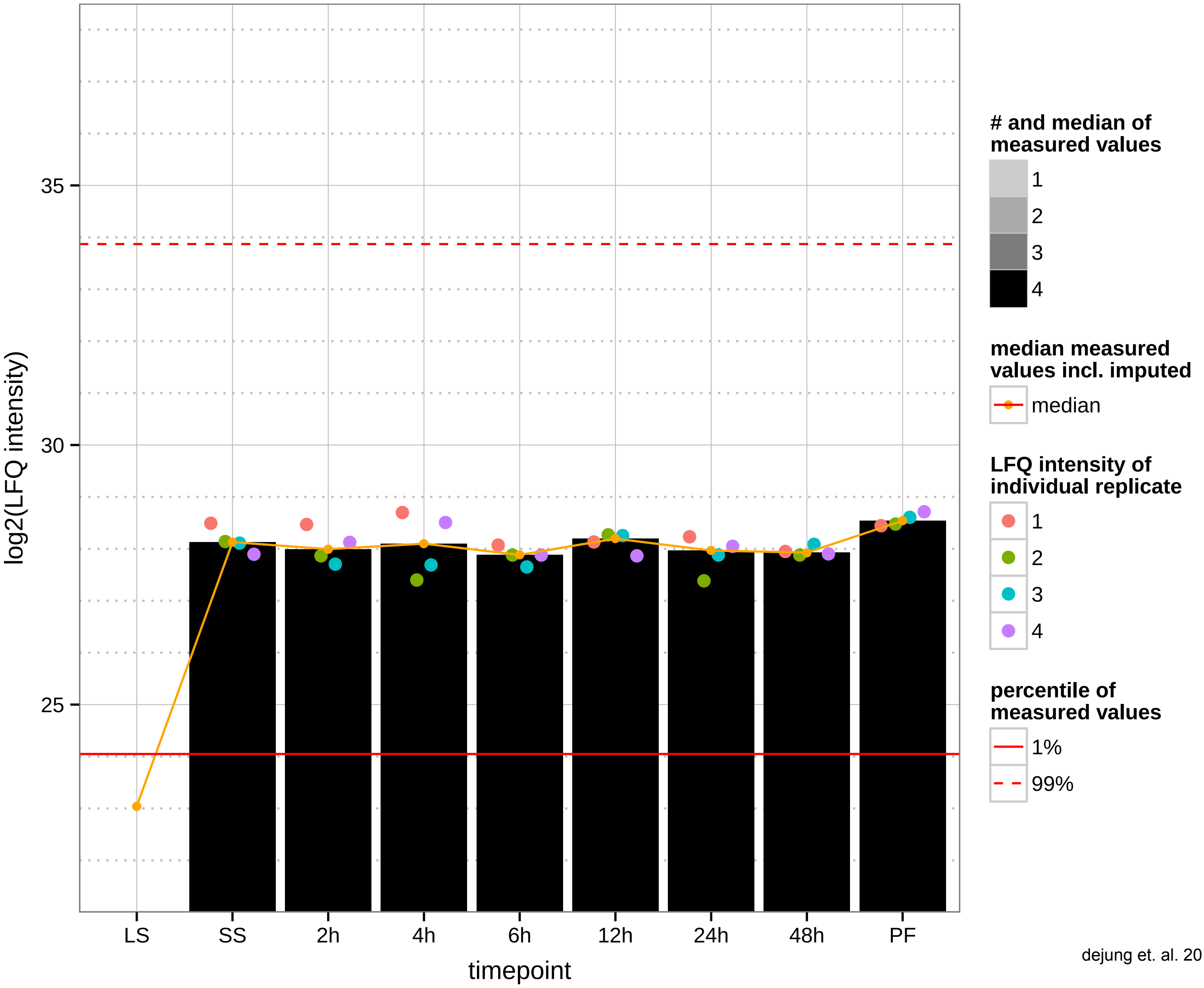
synaptotagmin, putative, calcium–dependent lipid binding protein
Tb927.10.13740
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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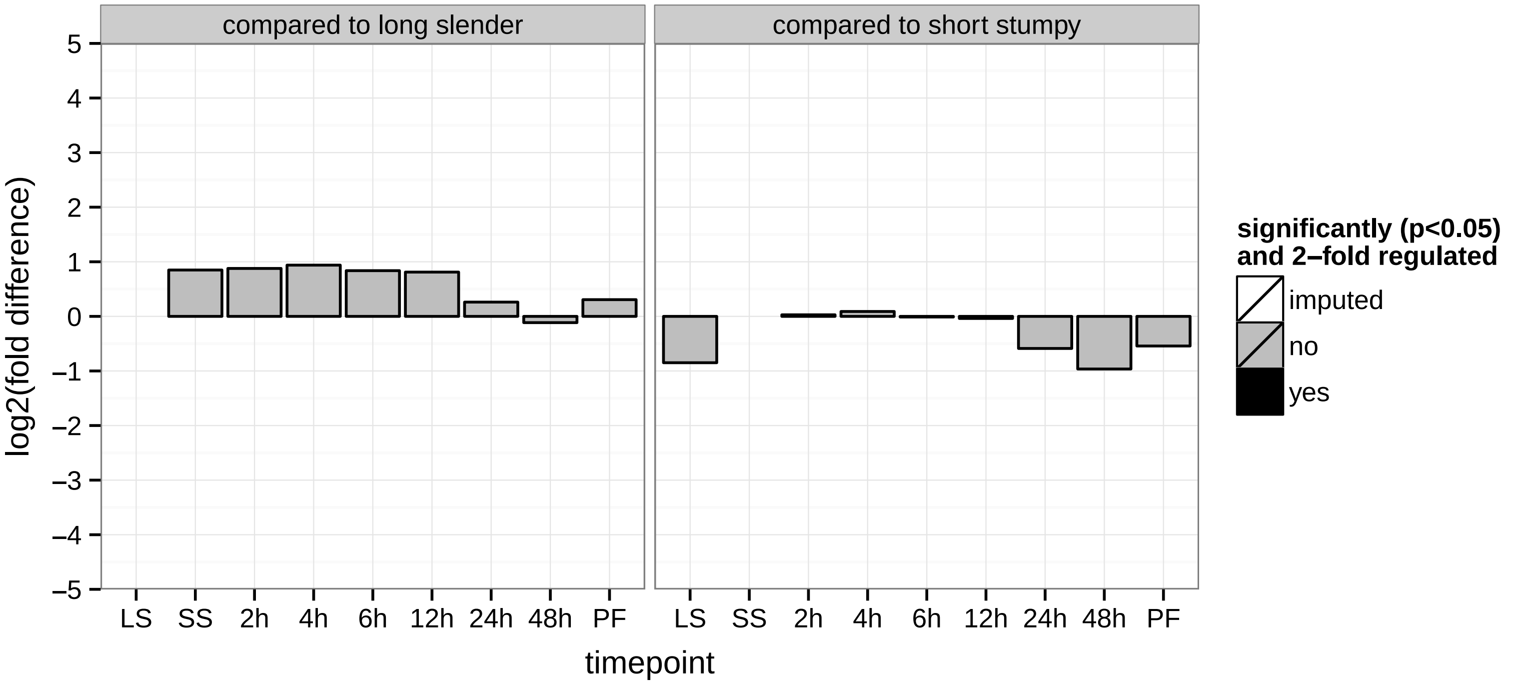
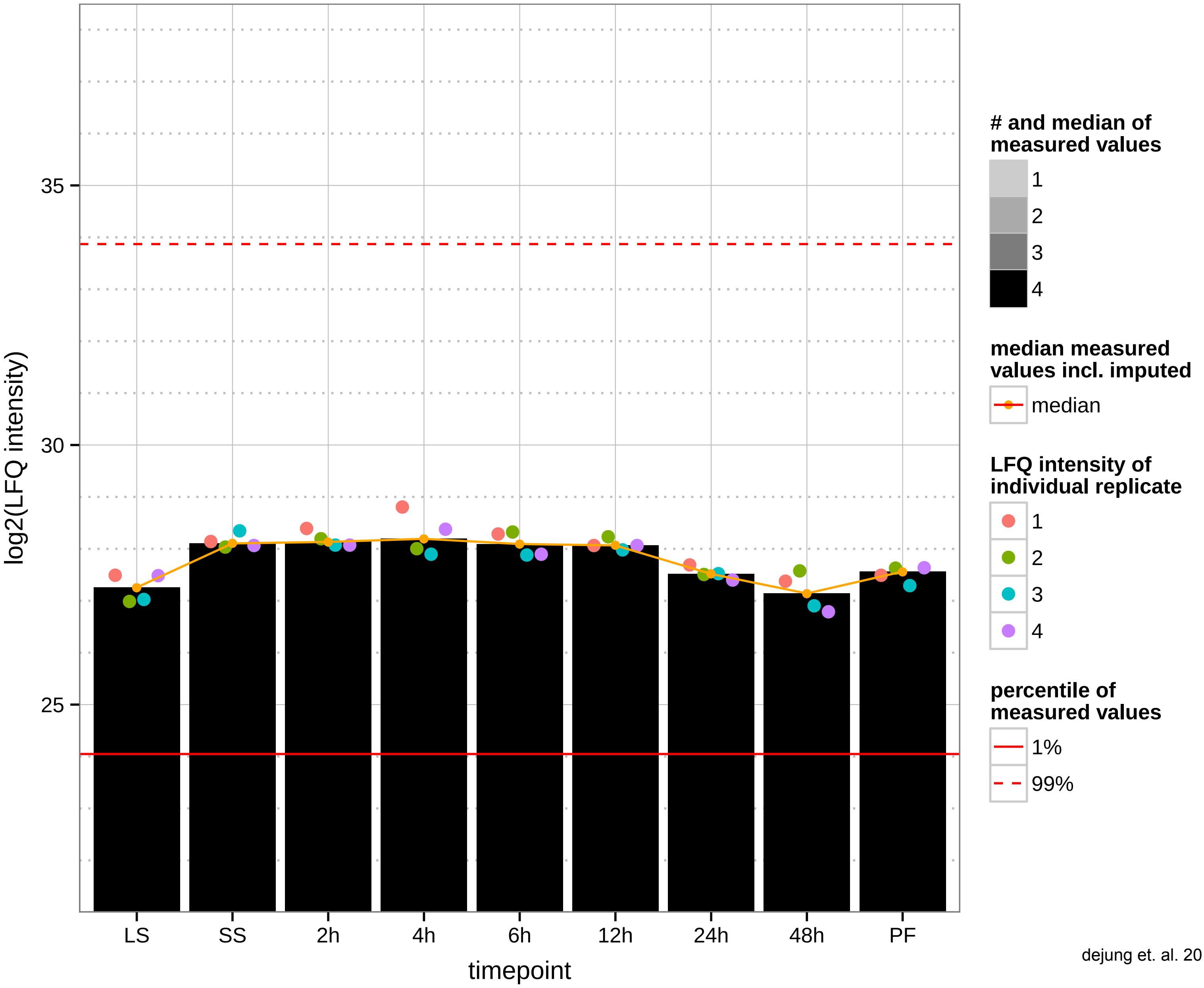
GPI−anchor transamidase subunit 8 (GPI8), cysteine peptidase, Clan CD, family C13
Tb927.10.13860
AGOF: cysteine−type endopeptidase activity
AGOC: null
AGOP: proteolysis
PGOF: cysteine−type endopeptidase activity
PGOC: null
PGOP: proteolysis





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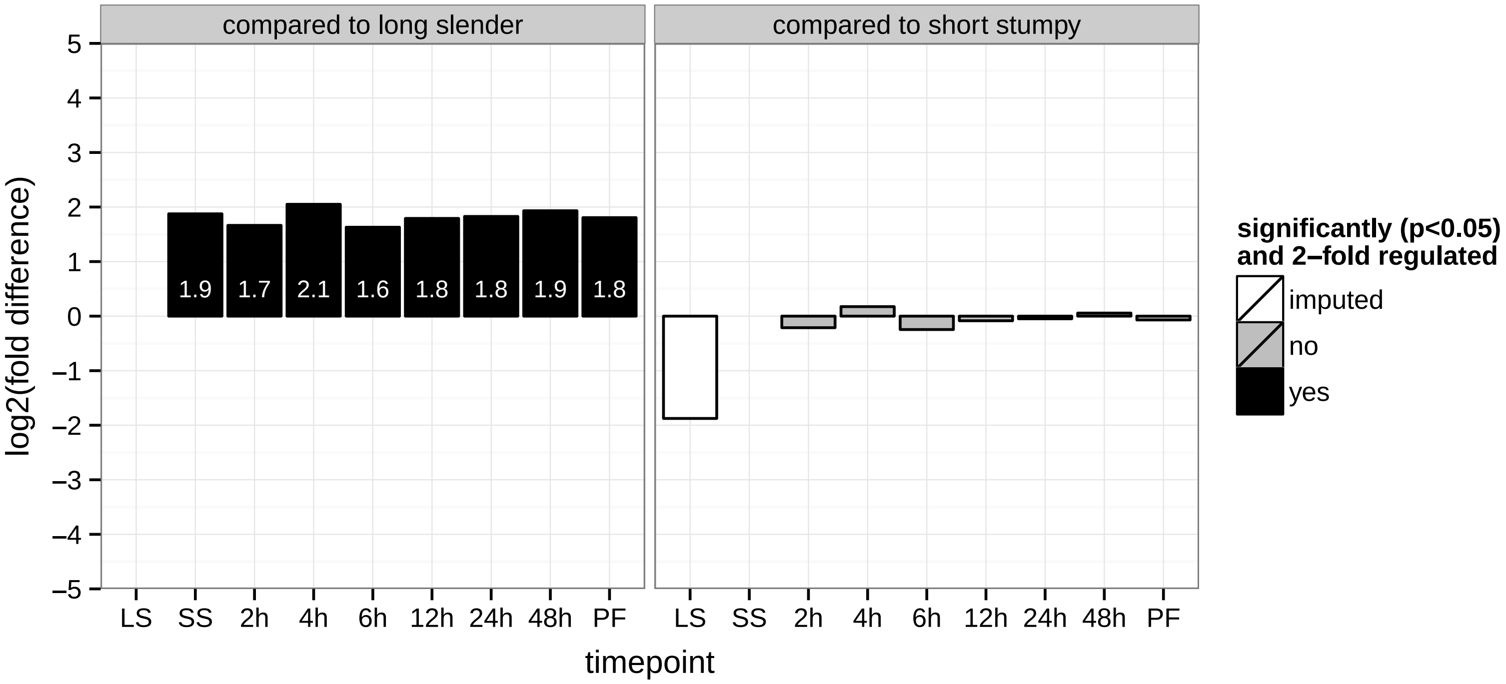
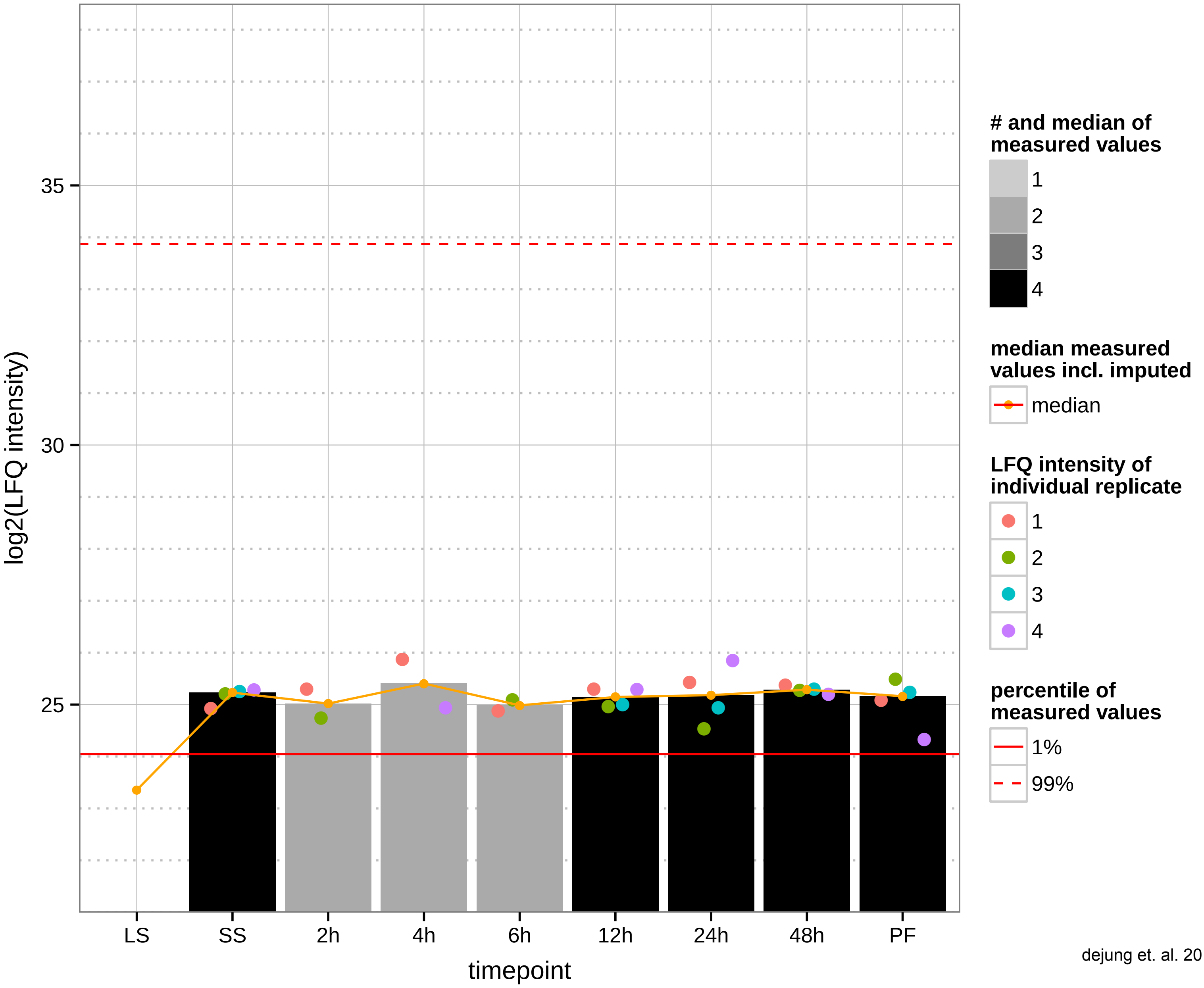
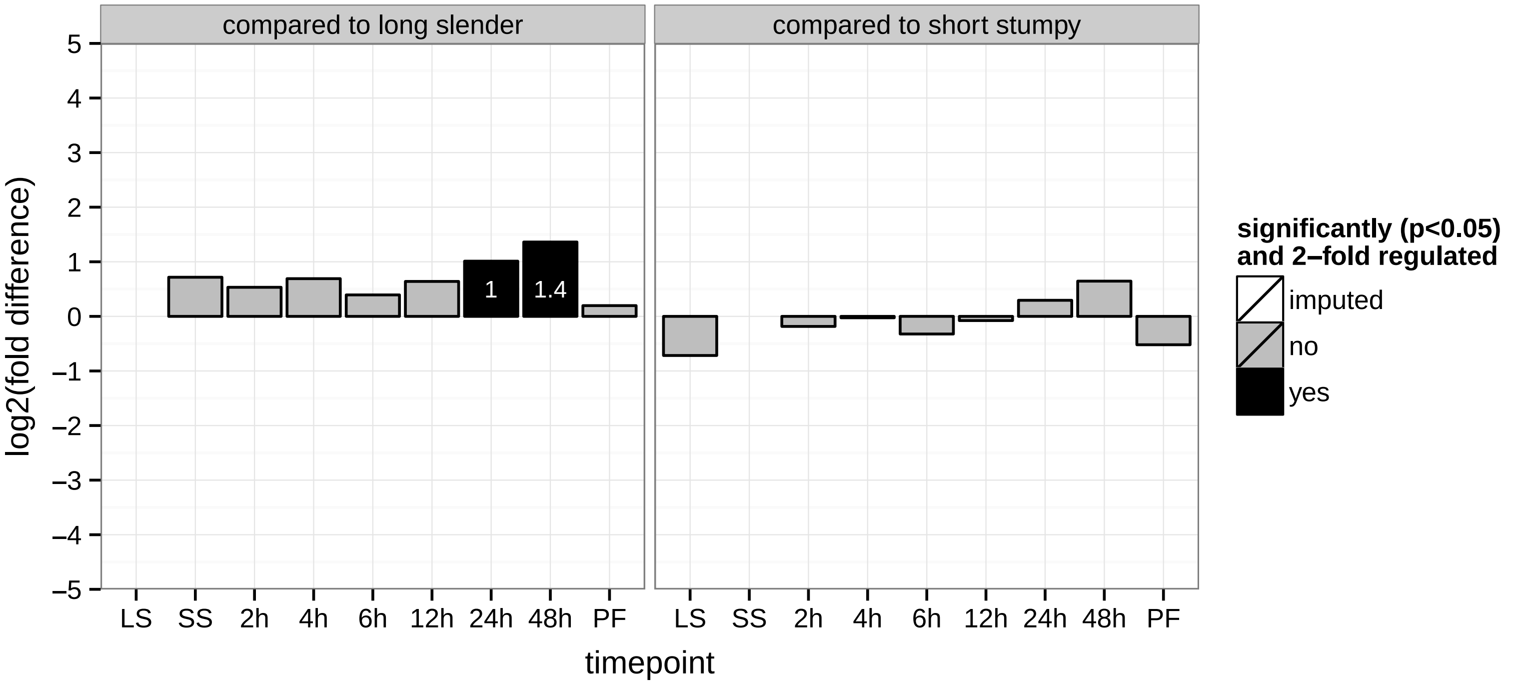
hypothetical protein, conserved
Tb927.10.13880
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

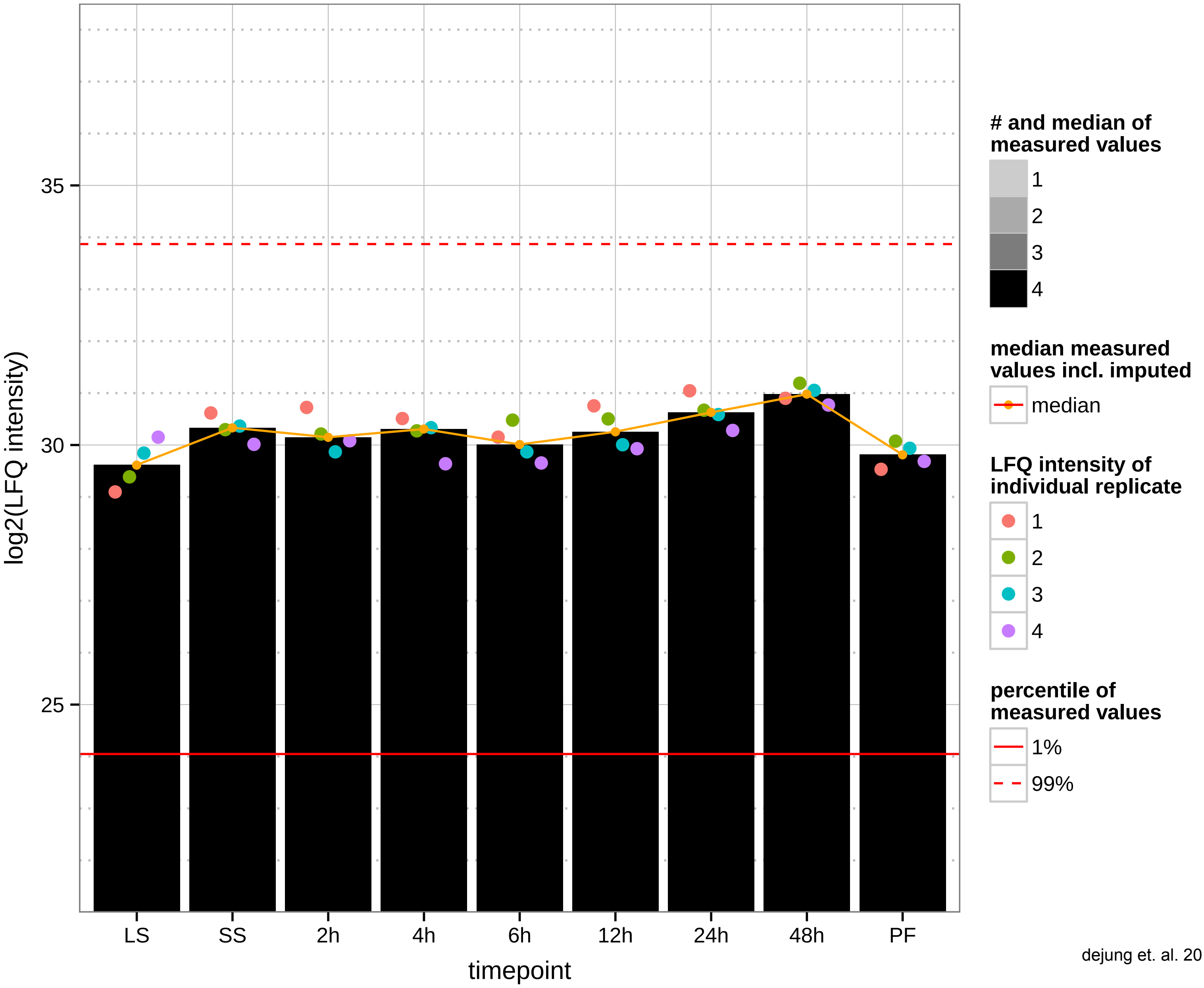




dejung et. al. 2015

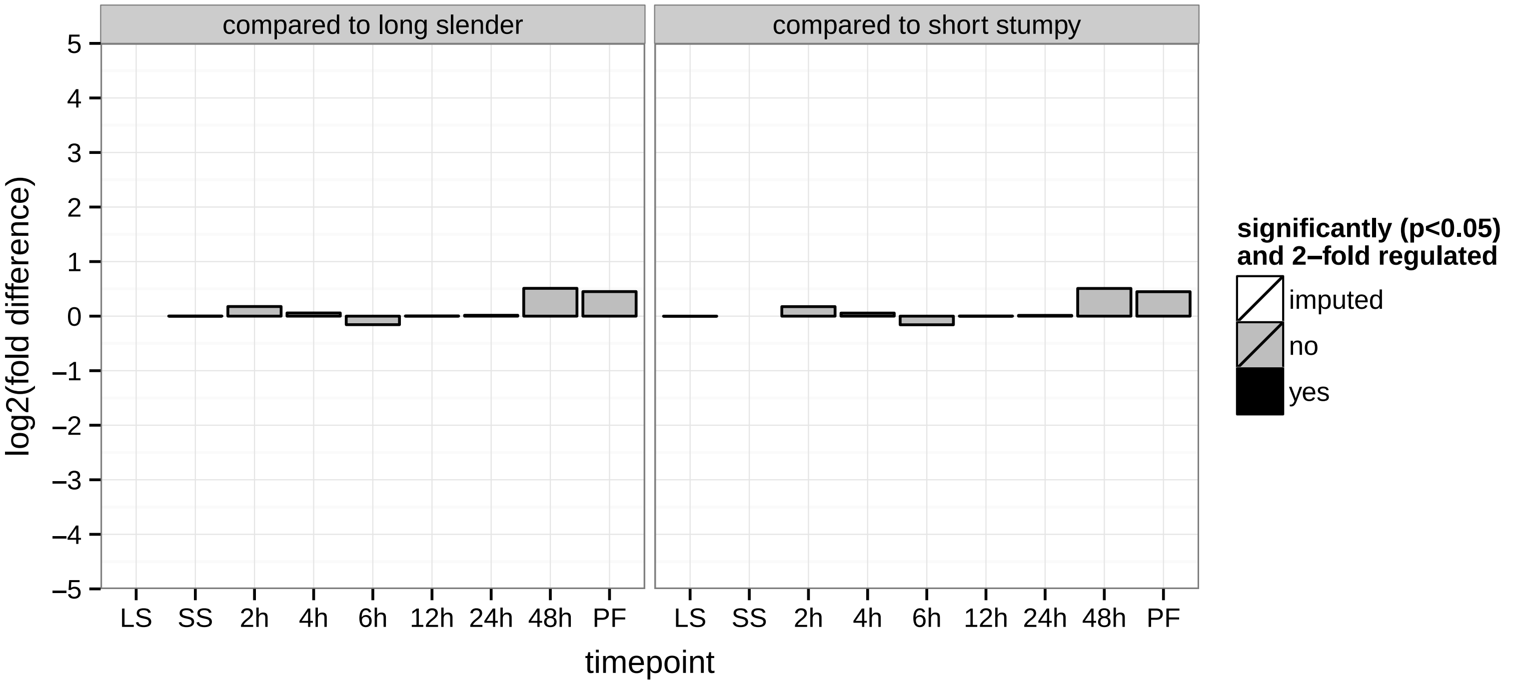
hypoxanthine–guanine phosphoribosyltransferase (HGPRT)
Tb927.10.1400;Tb927.10.1470
AGOF: hypoxanthine phosphoribosyltransferase activity
AGOC: cytoplasm
AGOP: purine ribonucleoside salvage
PGOF: hypoxanthine phosphoribosyltransferase activity
PGOC: cytoplasm
PGOP: nucleoside metabolic process, purine ribonucleoside salvage

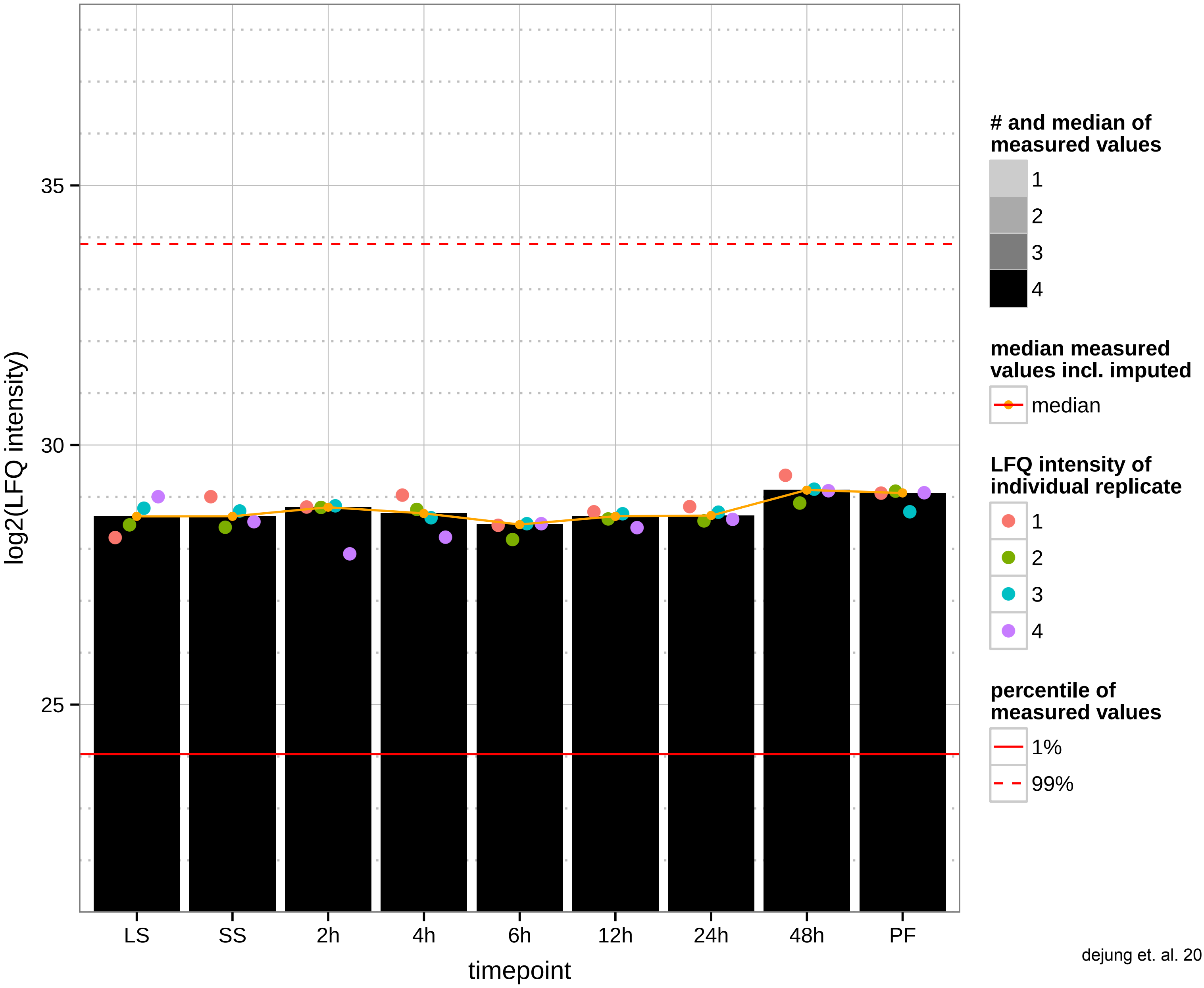




dejung et. al. 2015

tubulin cofactor C domain–containing protein RP2 (rp2)
Tb927.10.14010
AGOF: GTPase activator activity
AGOC: cilium basal body
AGOP: cell morphogenesis, motile cilium assembly, spindle assembly
PGOF: protein binding
PGOC: microtubule organizing center
PGOP: microtubule anchoring





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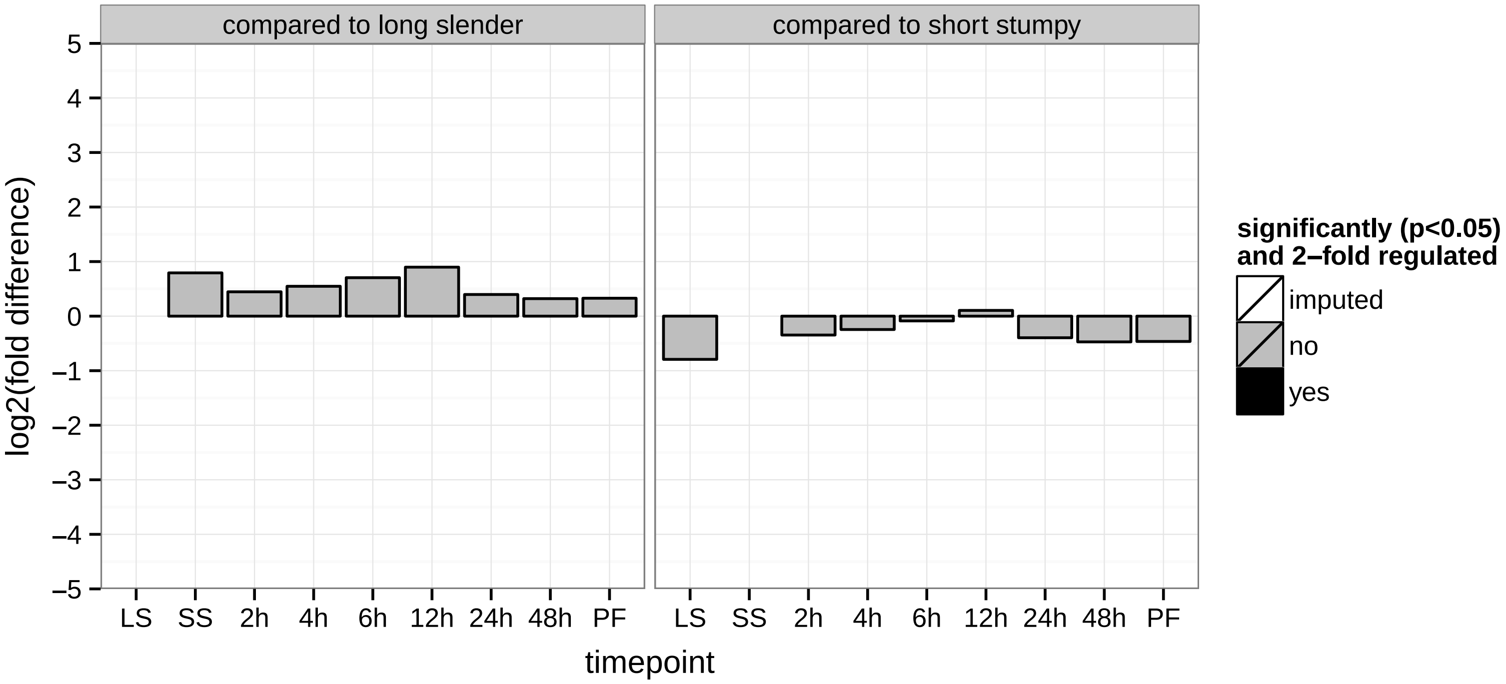
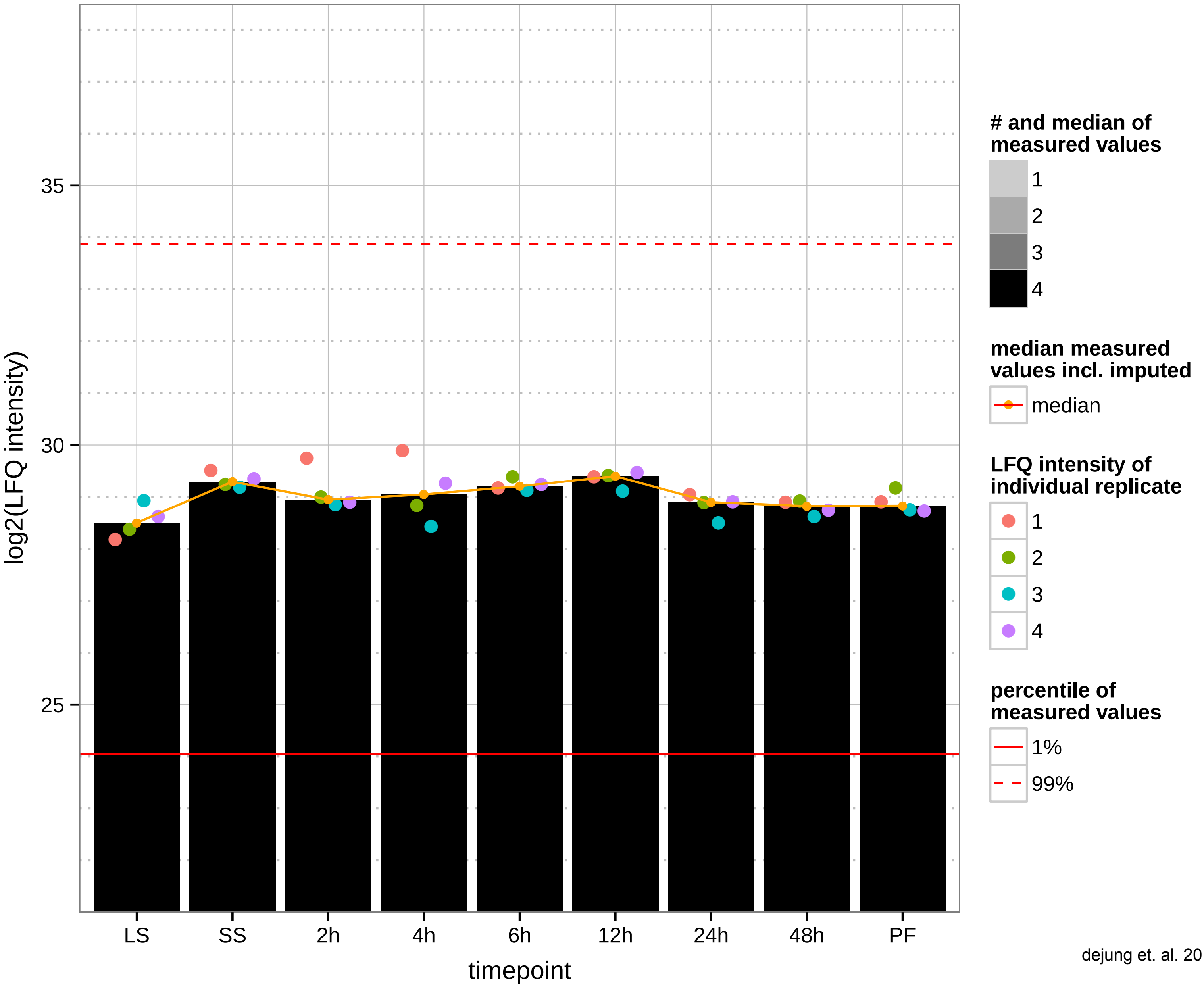
vacuolar ATP synthase subunit c, putative
Tb927.10.14040
AGOF: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances
AGOC: proton−transporting V−type ATPase, V1 domain, proton−transporting two−sector ATPase complex
AGOP: ATP synthesis coupled proton transport
PGOF: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances
PGOC: proton−transporting V−type ATPase, V1 domain
PGOP: ATP hydrolysis coupled proton transport





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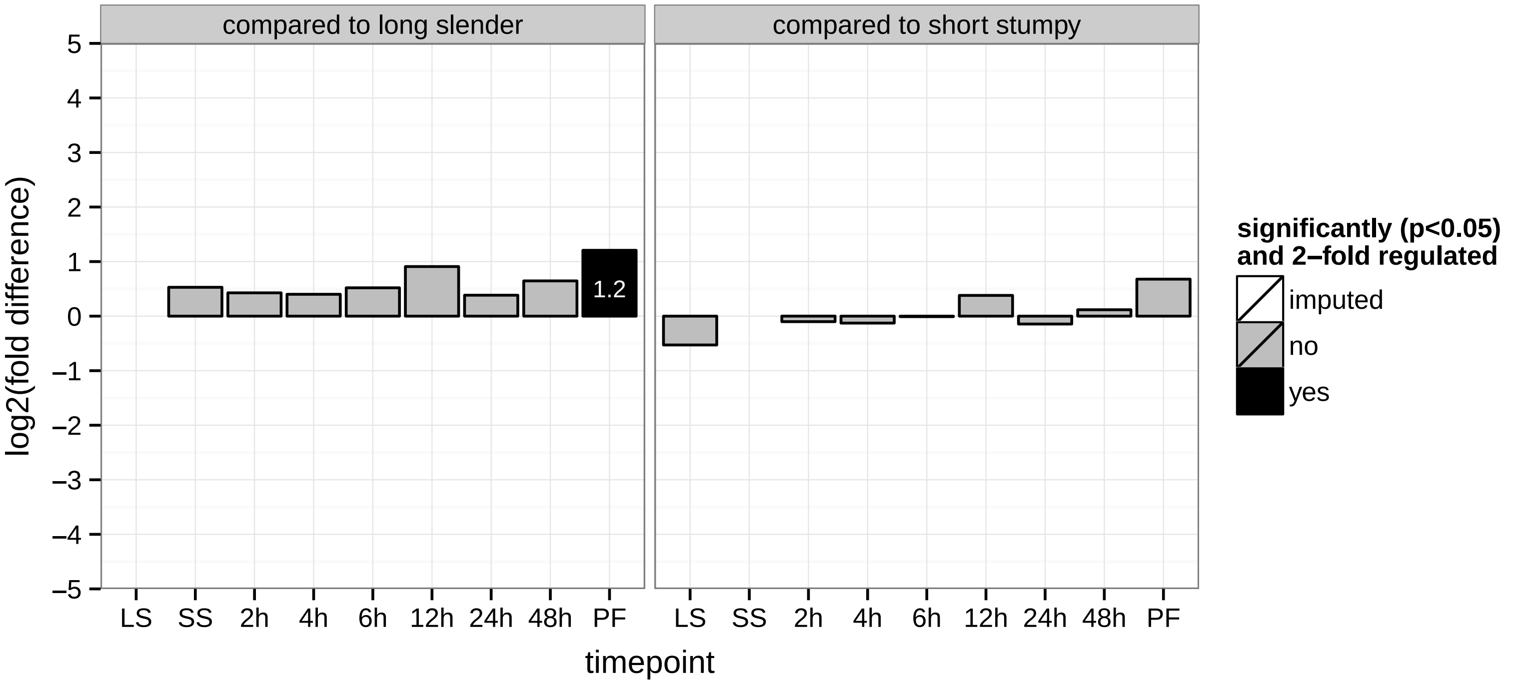
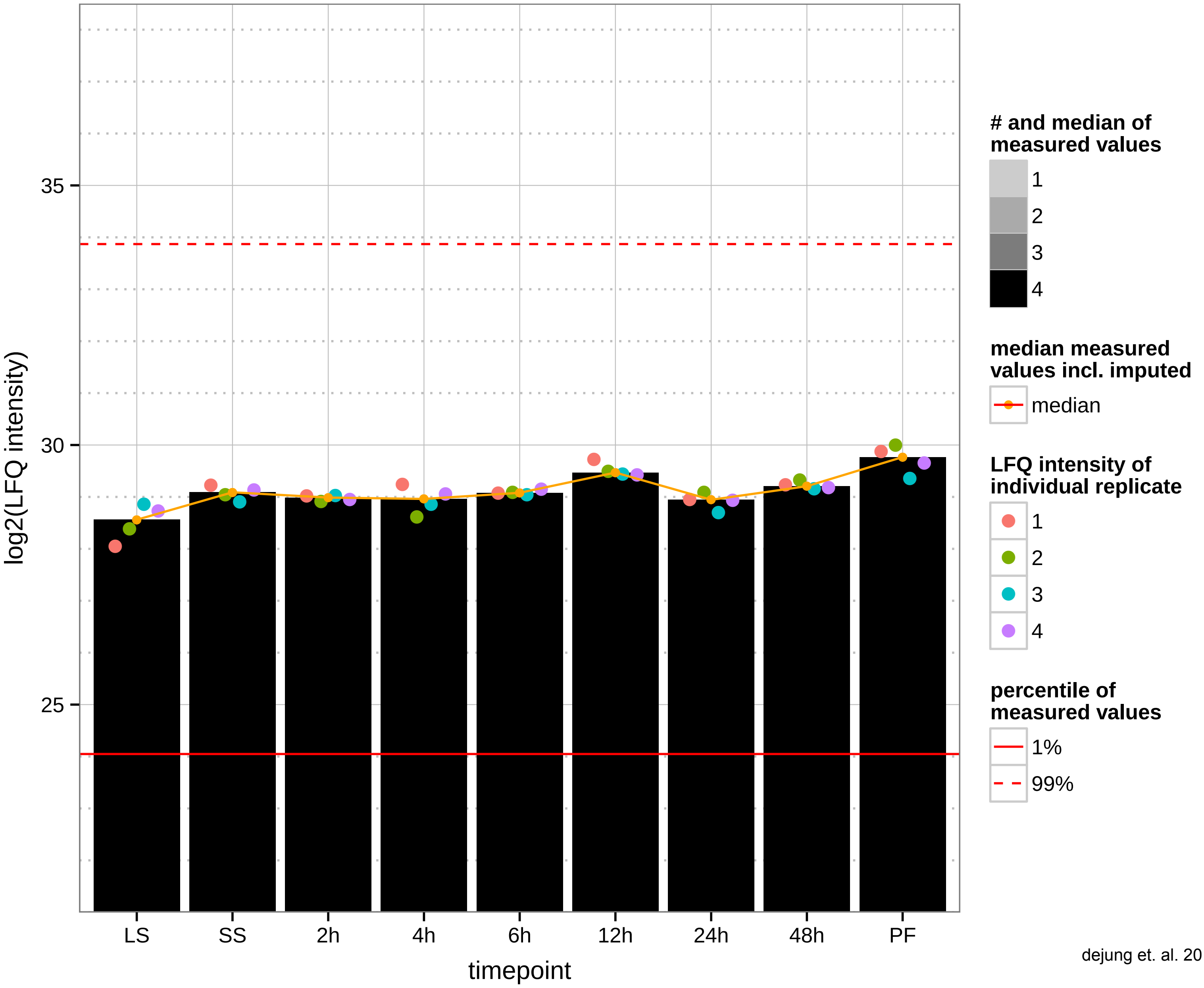
protein transport protein SEC13, putative
Tb927.10.14180
AGOF: null
AGOC: null
AGOP: intracellular protein transport, membrane budding
PGOF: protein binding
PGOC: null
PGOP: null





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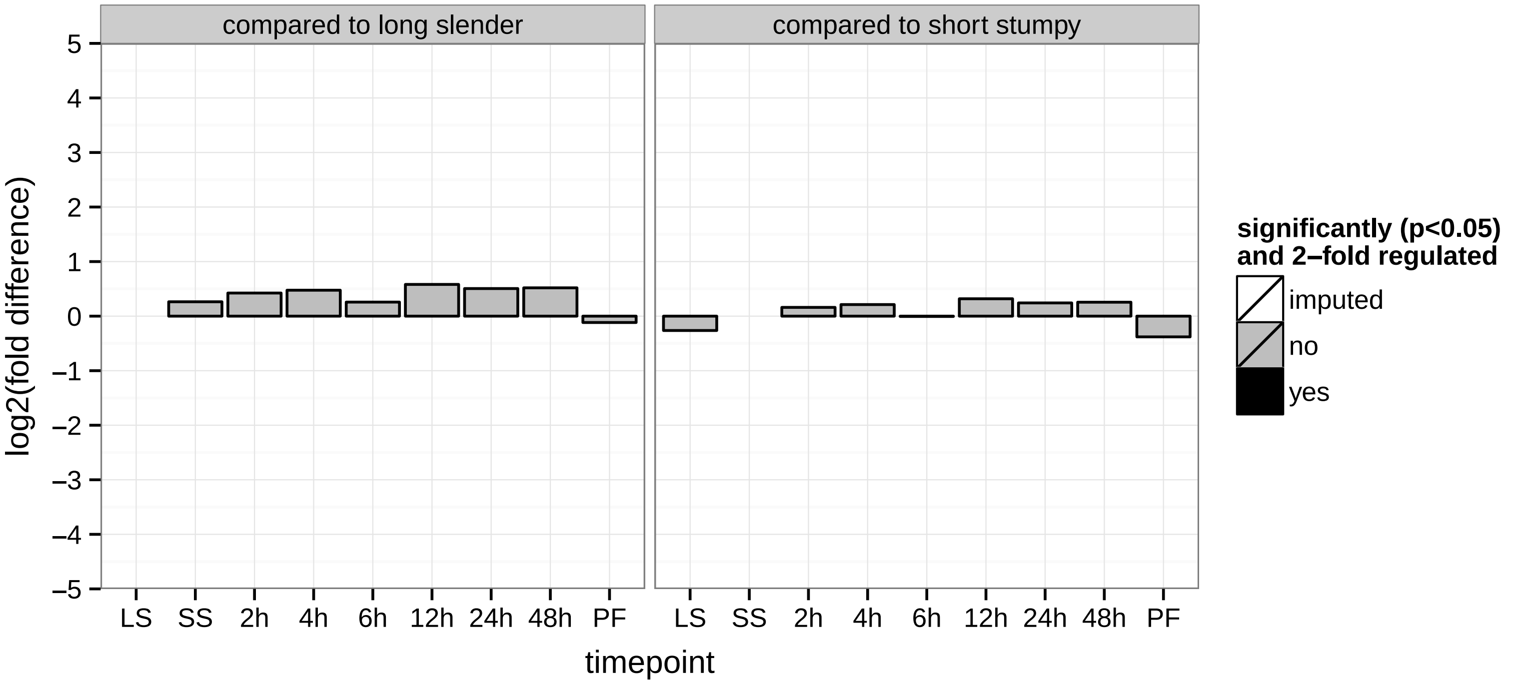
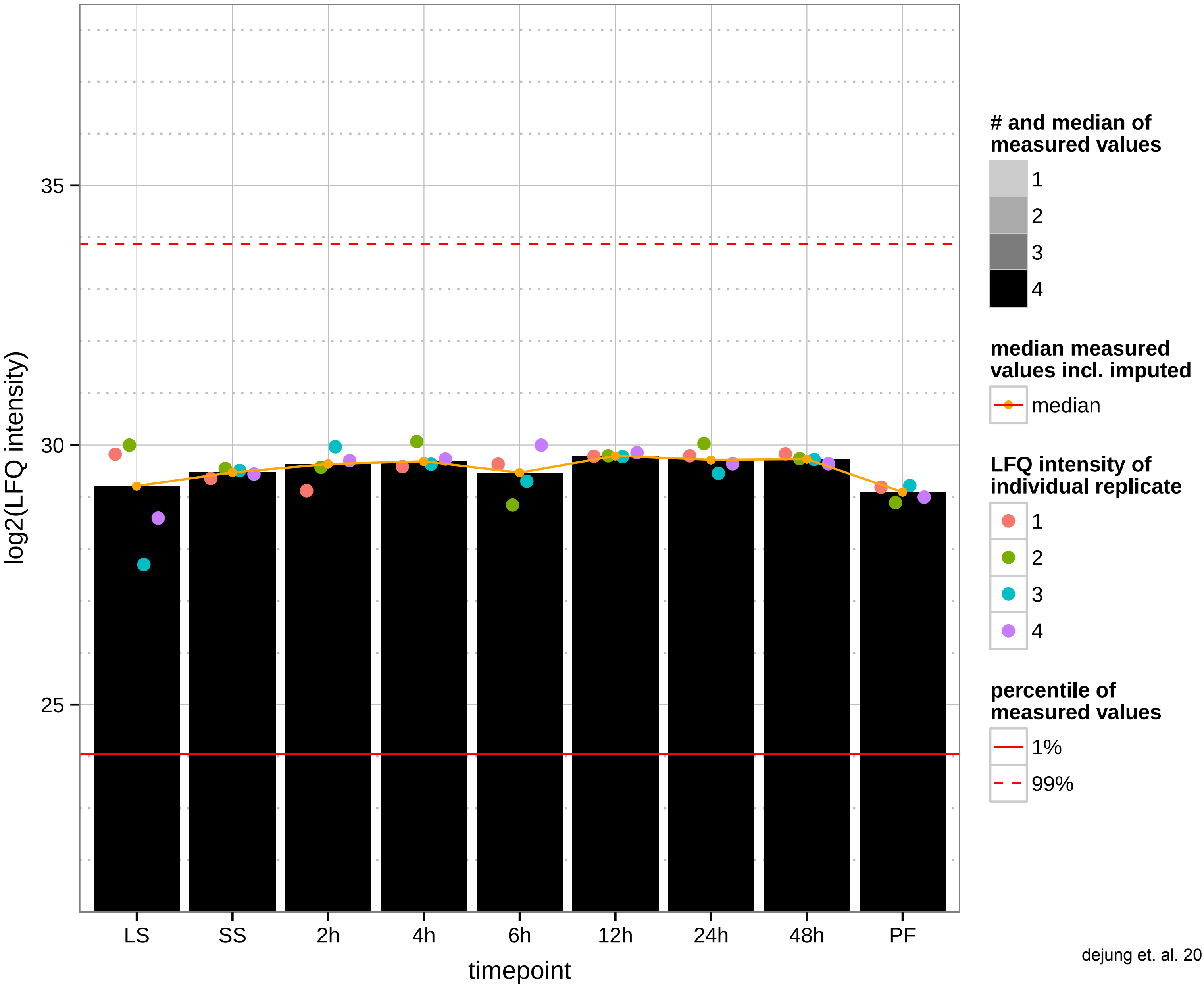
methionine aminopeptidase 2, putative, metallo–peptidase, Clan MG, Family M24, putative (MetAP2)
Tb927.10.1420
AGOF: null, aminopeptidase activity, metallopeptidase activity
AGOC: null
AGOP: null, cellular process, proteolysis
PGOF: null, aminopeptidase activity, metalloexopeptidase activity
PGOC: null
PGOP: cellular process, proteolysis





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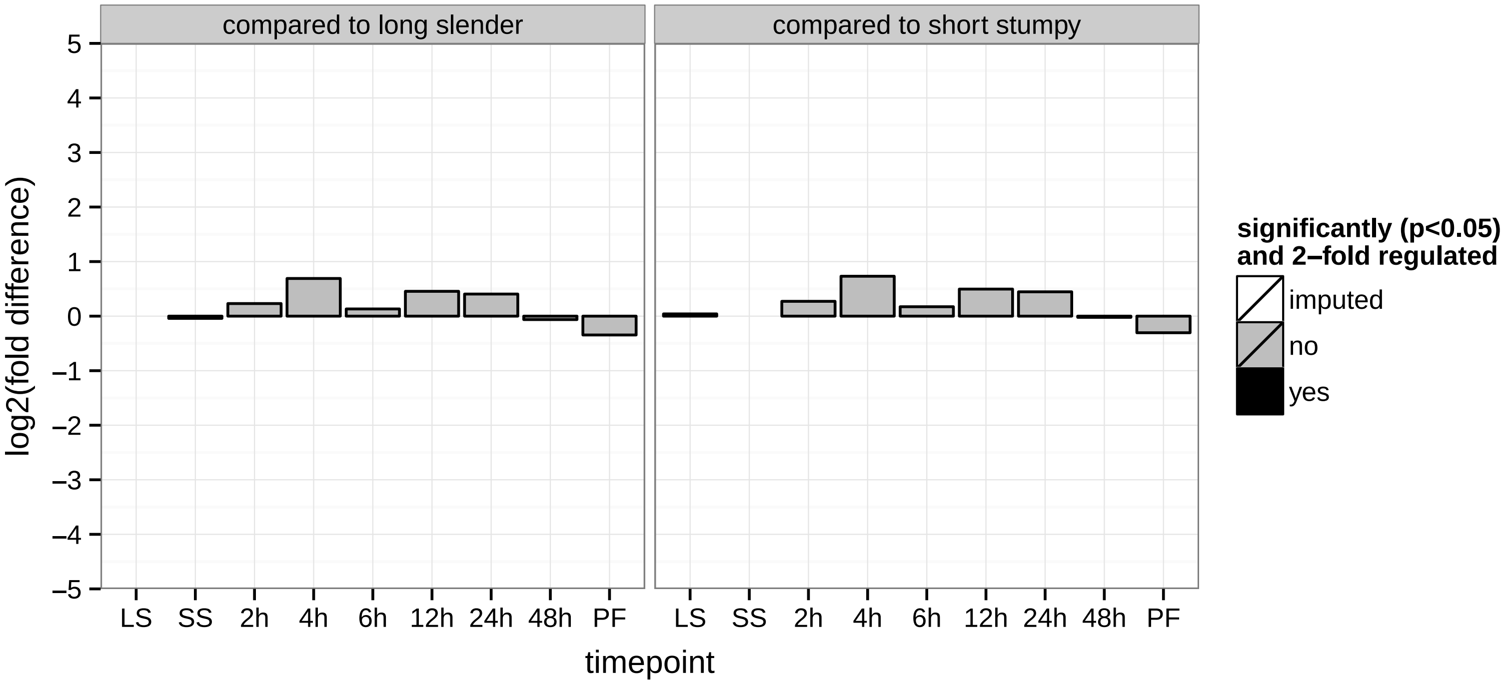
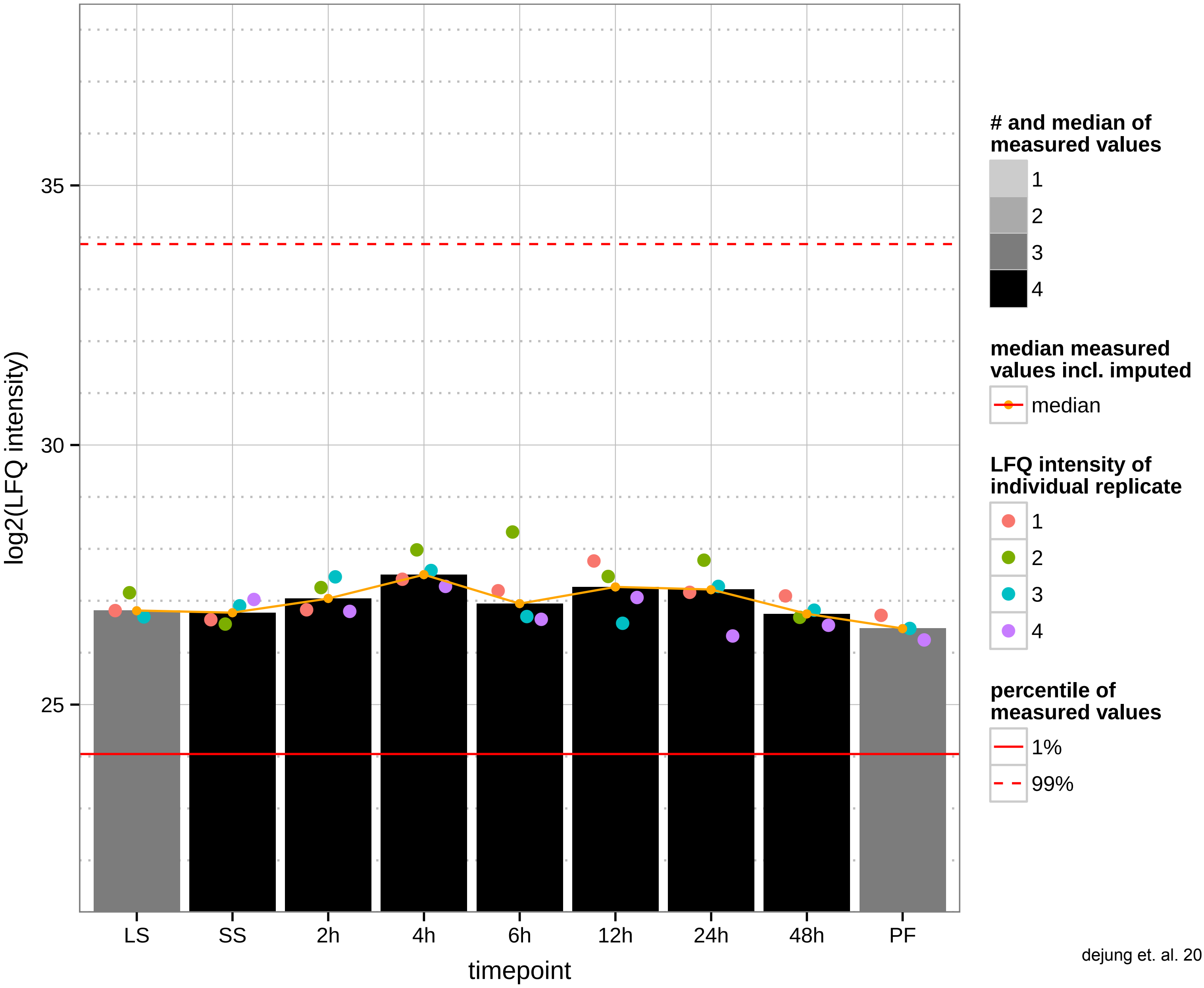
syntaxin 5
Tb927.10.14200
AGOF: SNAP receptor activity
AGOC: membrane
AGOP: membrane fusion, vesicle–mediated transport
PGOF: protein binding
PGOC: membrane
PGOP: vesicle–mediated transport





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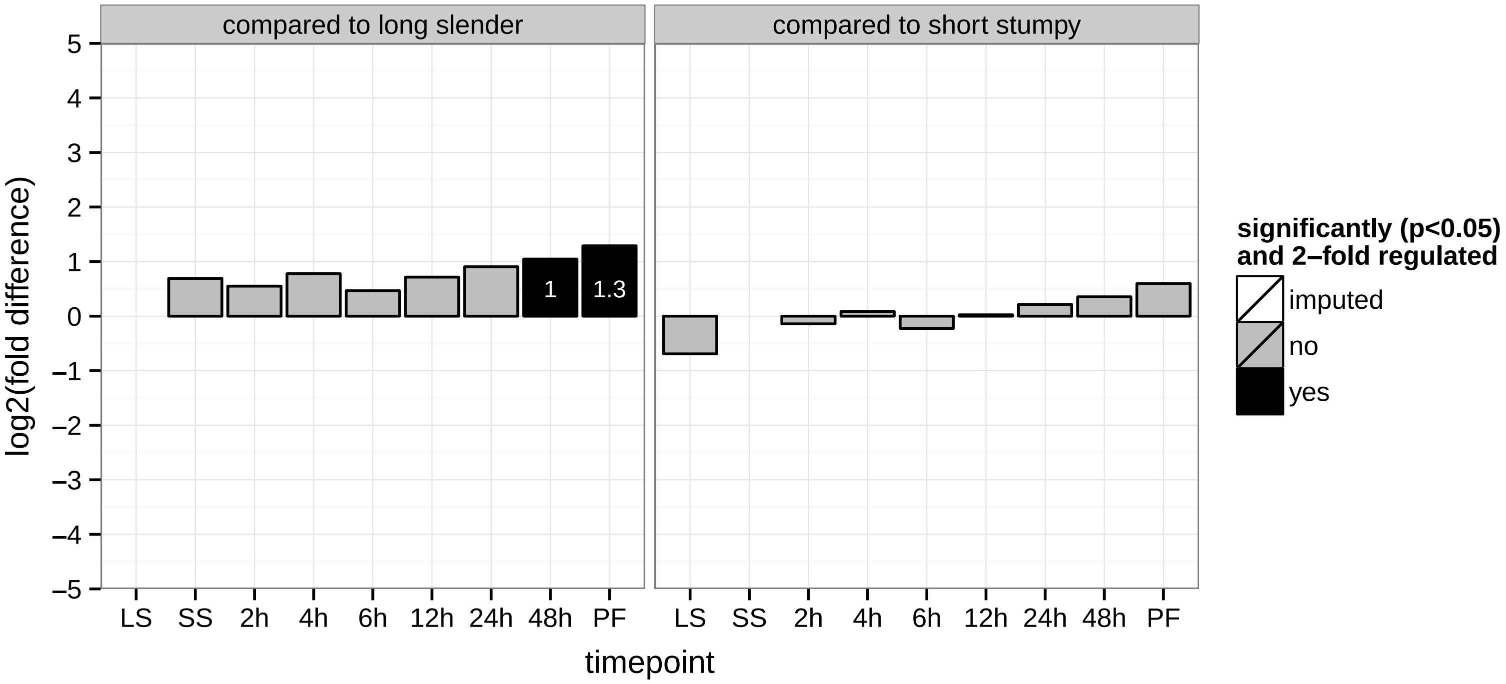
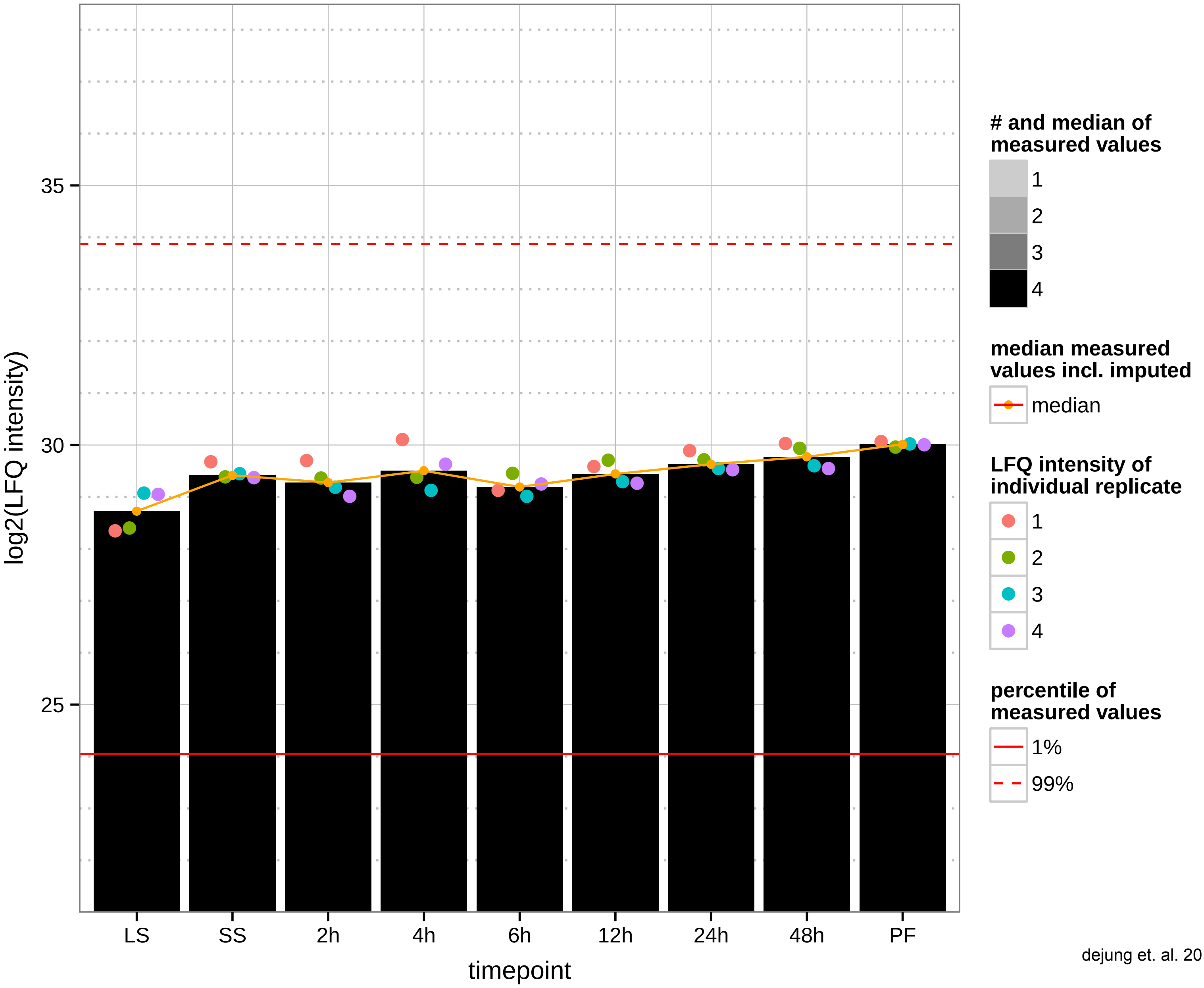
N–myristoyl transferase, putative, N–myristoyltransferase (NMT)
Tb927.10.14240;Tb11.v5.0859
AGOF: null, glycylpeptide N–tetradecanoyltransferase activity, myristoyltransferase activity
AGOC: null
AGOP: null, N–terminal protein myristoylation
PGOF: glycylpeptide N–tetradecanoyltransferase activity
PGOC: null
PGOP: N–terminal protein myristoylation





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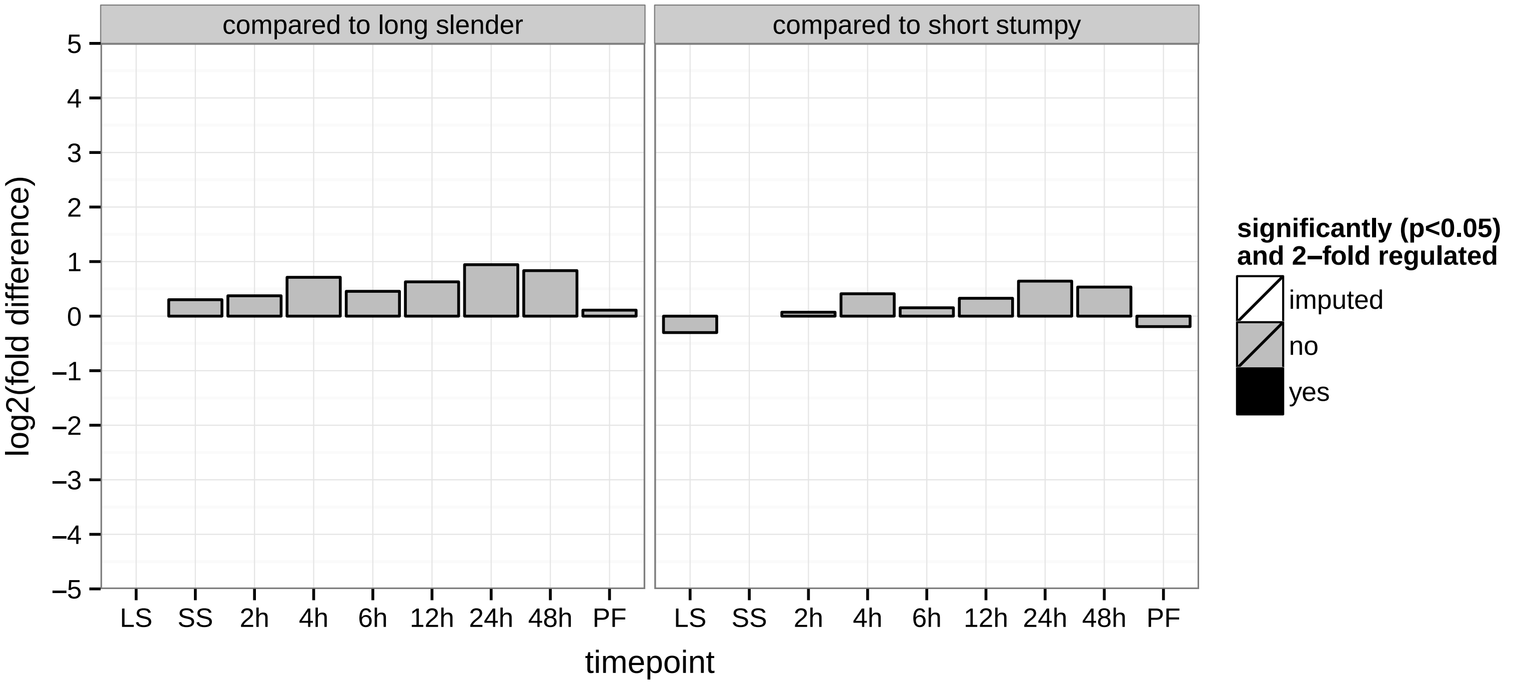
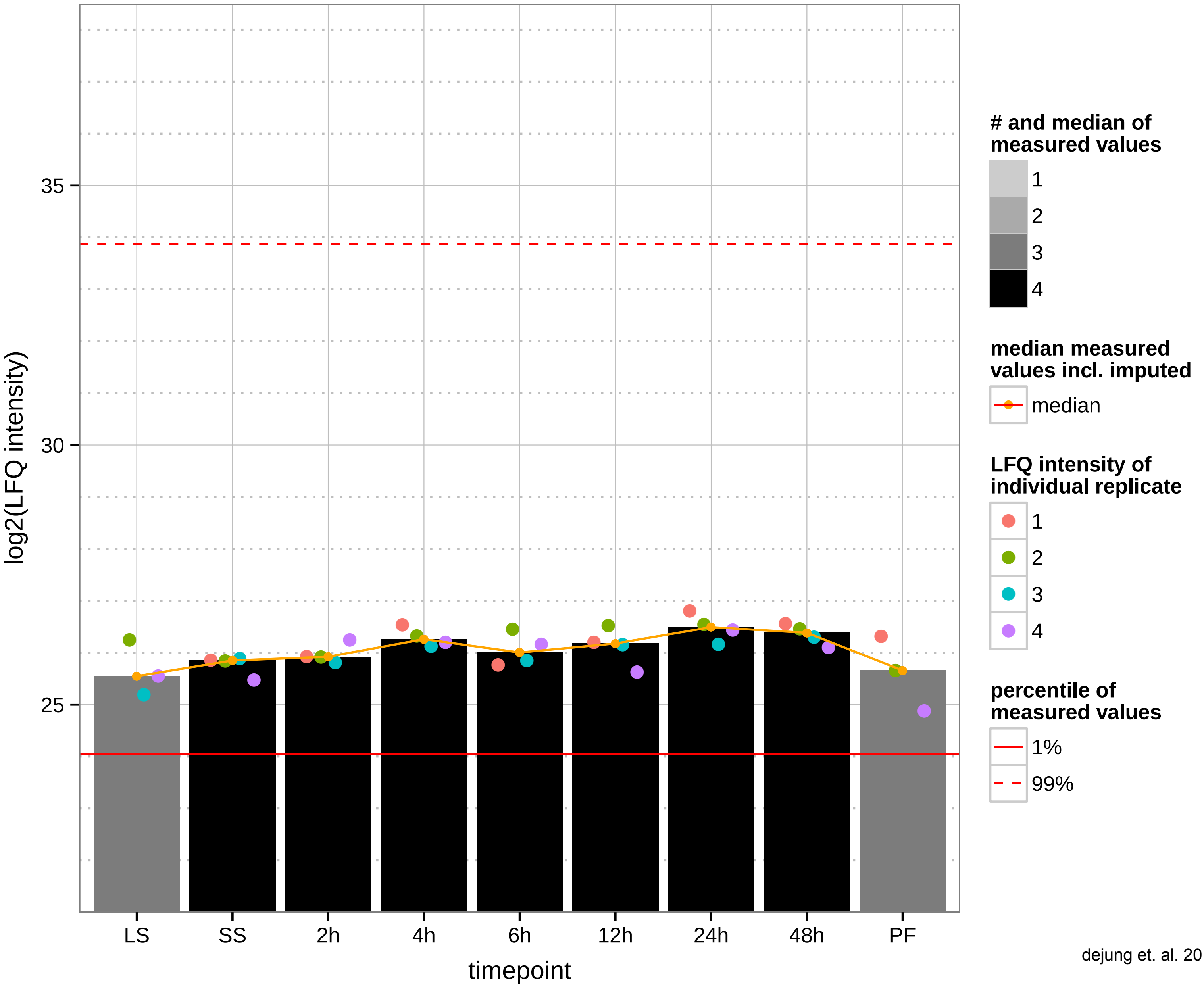
U2 small nuclear ribonucleoprotein 40K (U2_40K)
Tb927.10.14360
AGOF: mRNA binding
AGOC: U2 snRNP
AGOP: nuclear mRNA cis splicing, via spliceosome
PGOF: null
PGOC: null
PGOP: null





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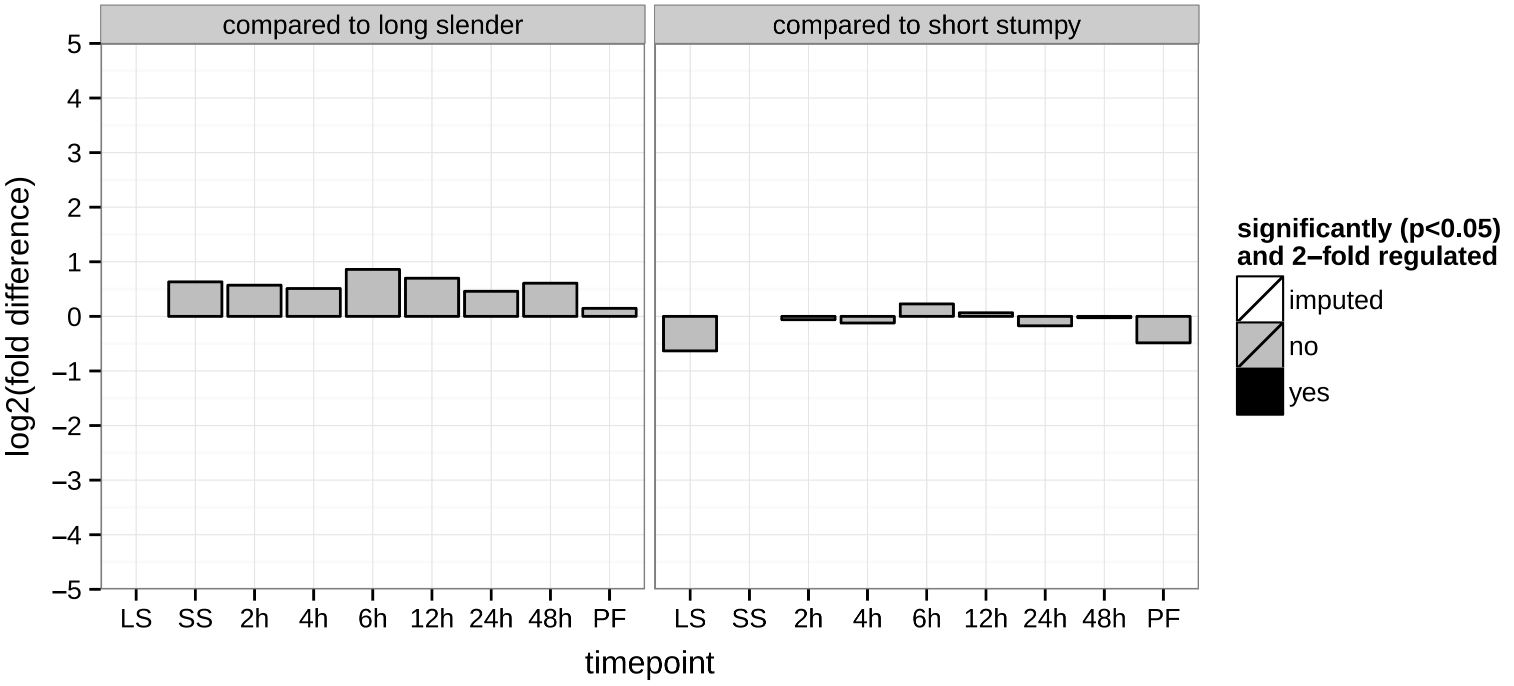
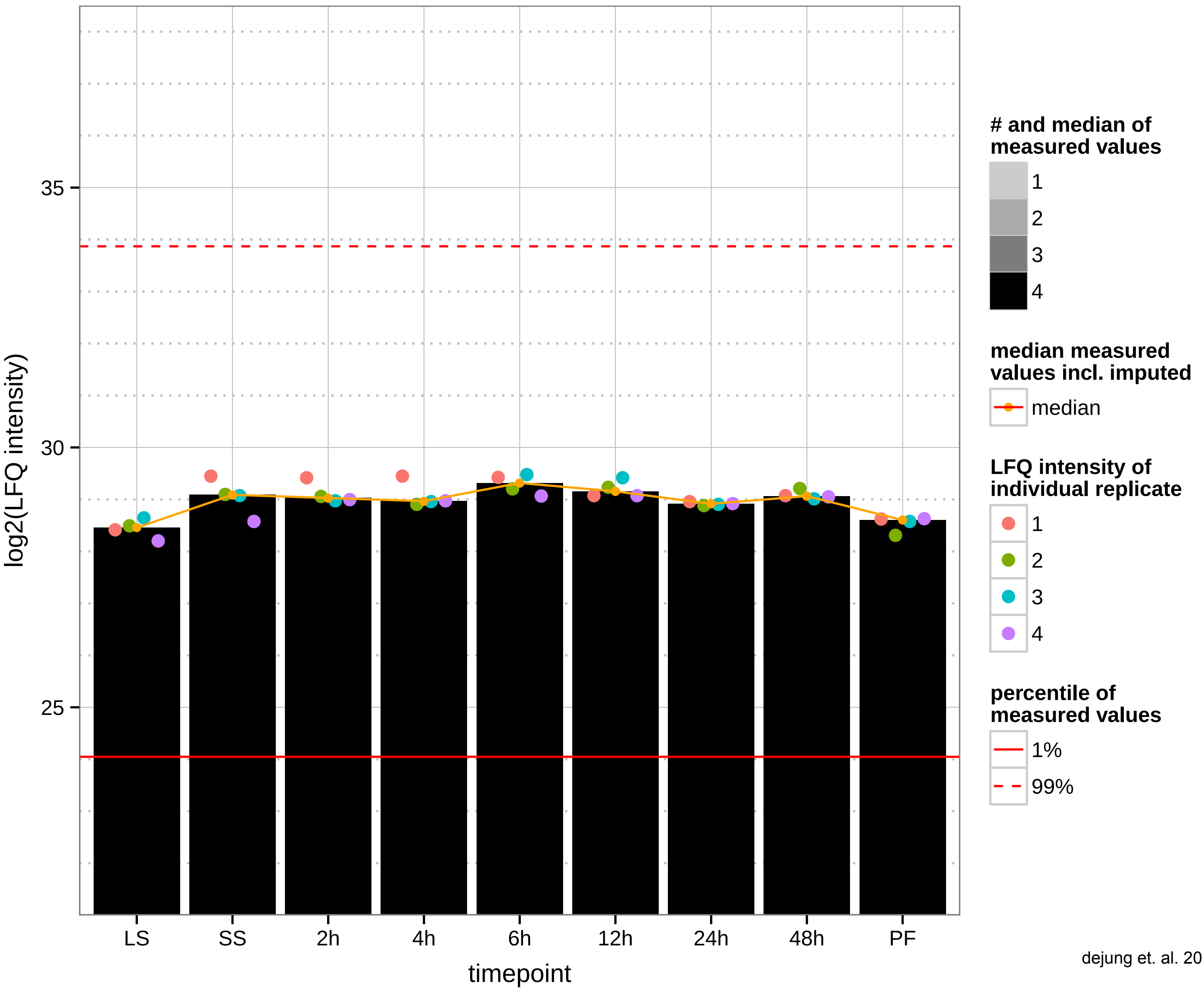
hypothetical protein, conserved
Tb927.10.14390
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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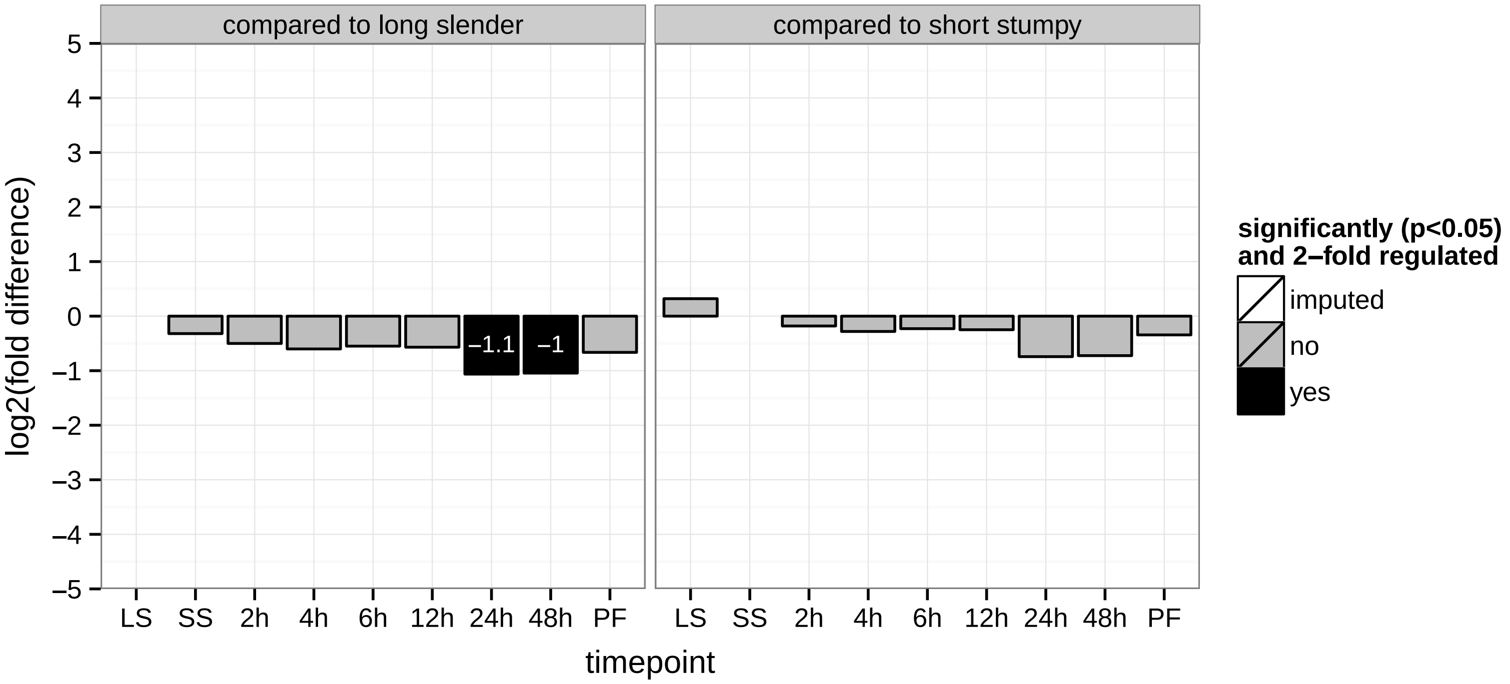
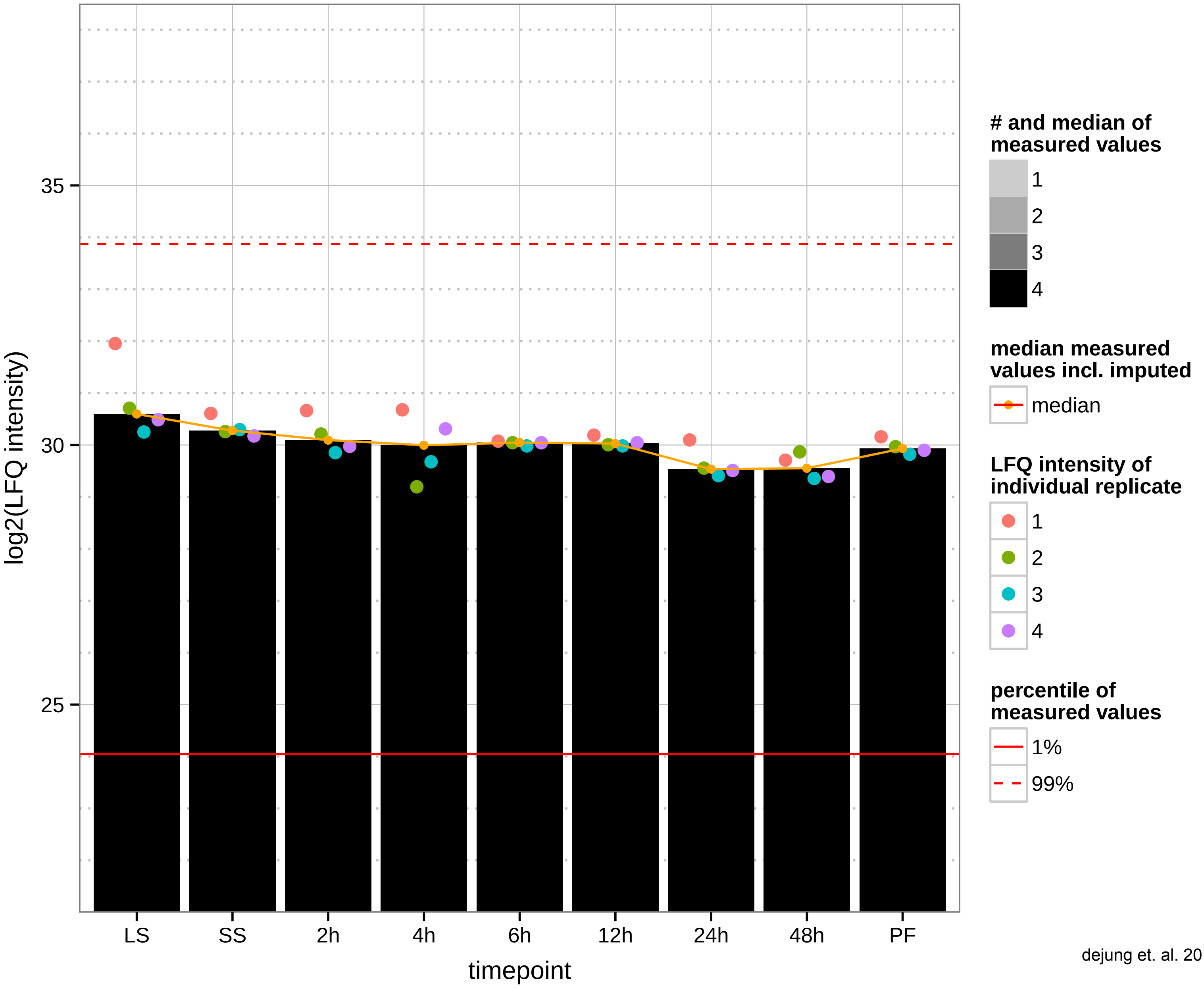
intraflagellar transport protein IFT140, putative (IFT140)
Tb927.10.14470
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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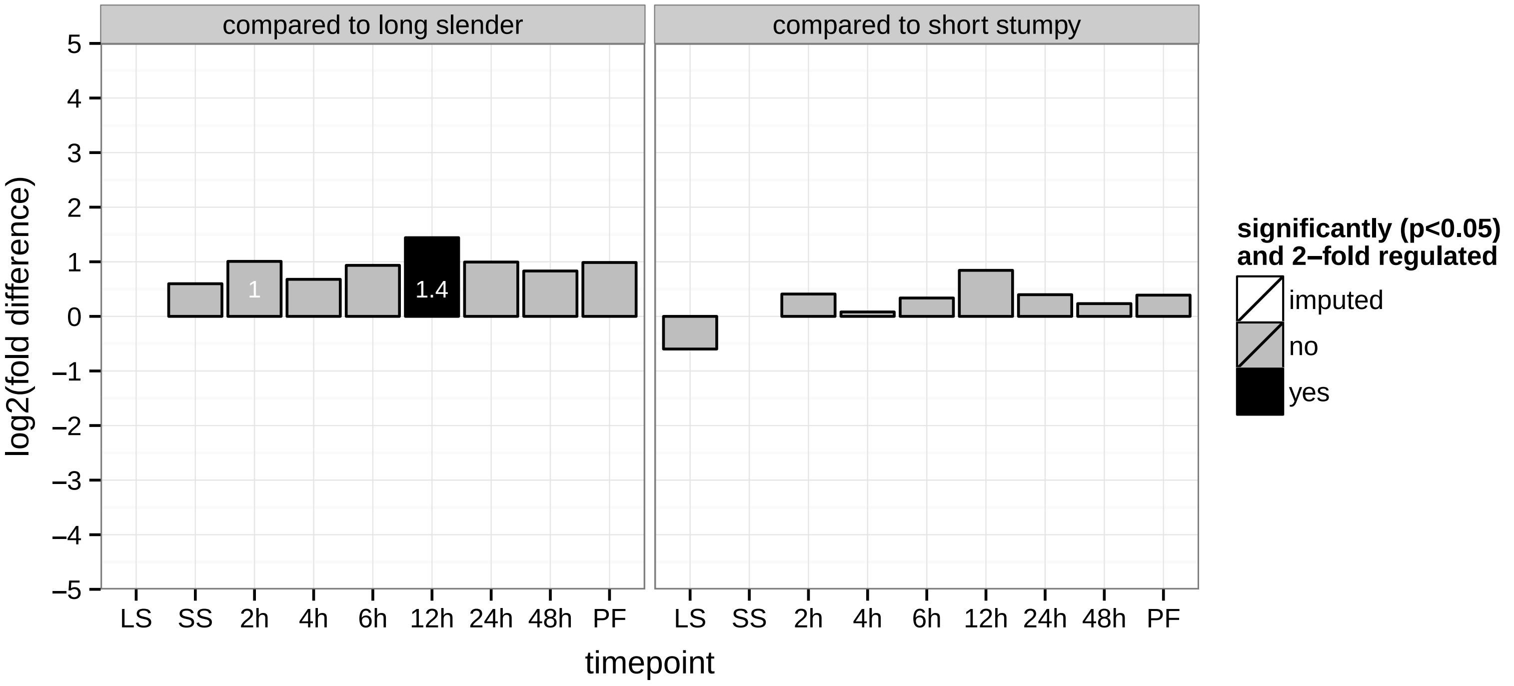
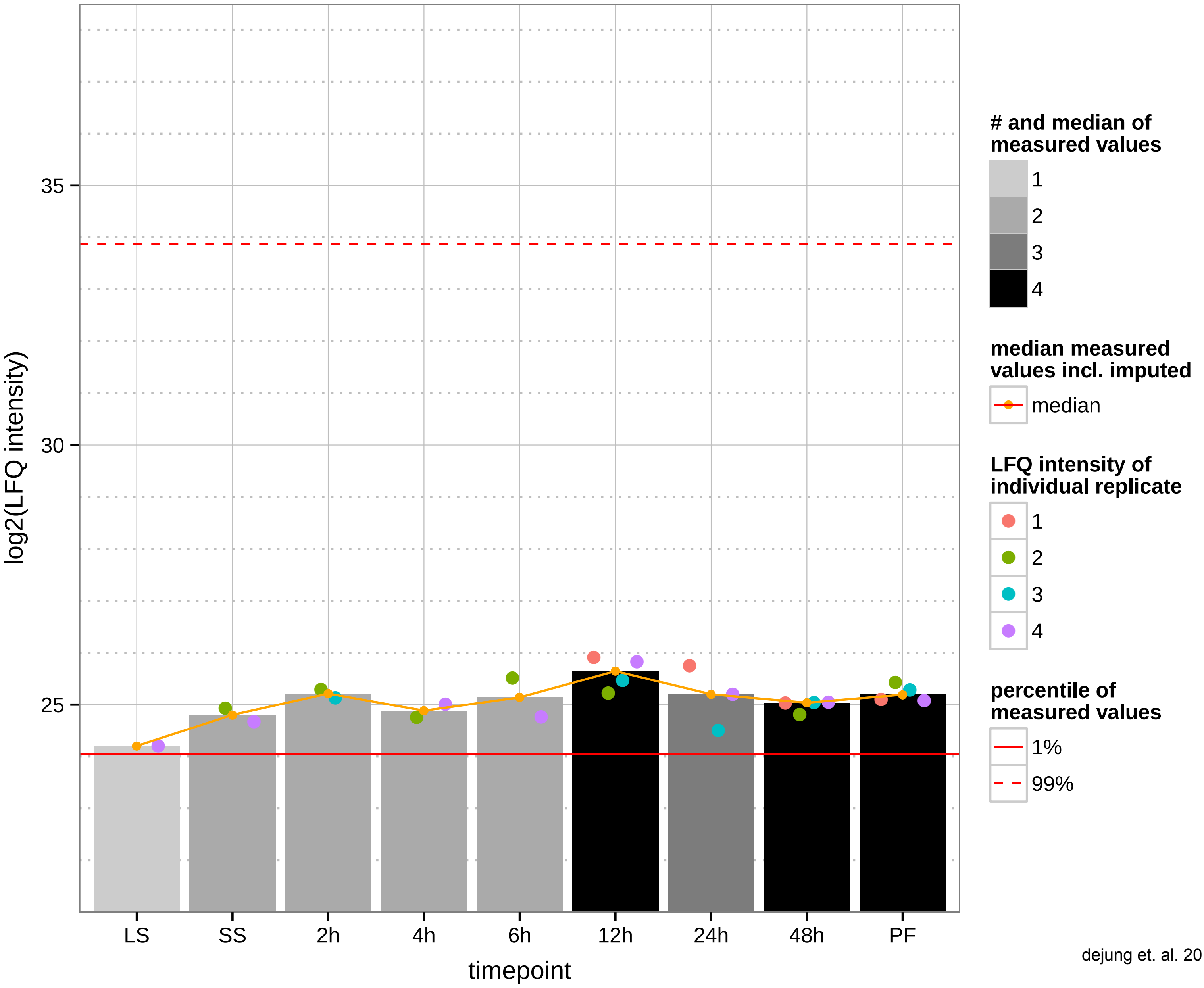
hypothetical protein, conserved
Tb927.10.14480
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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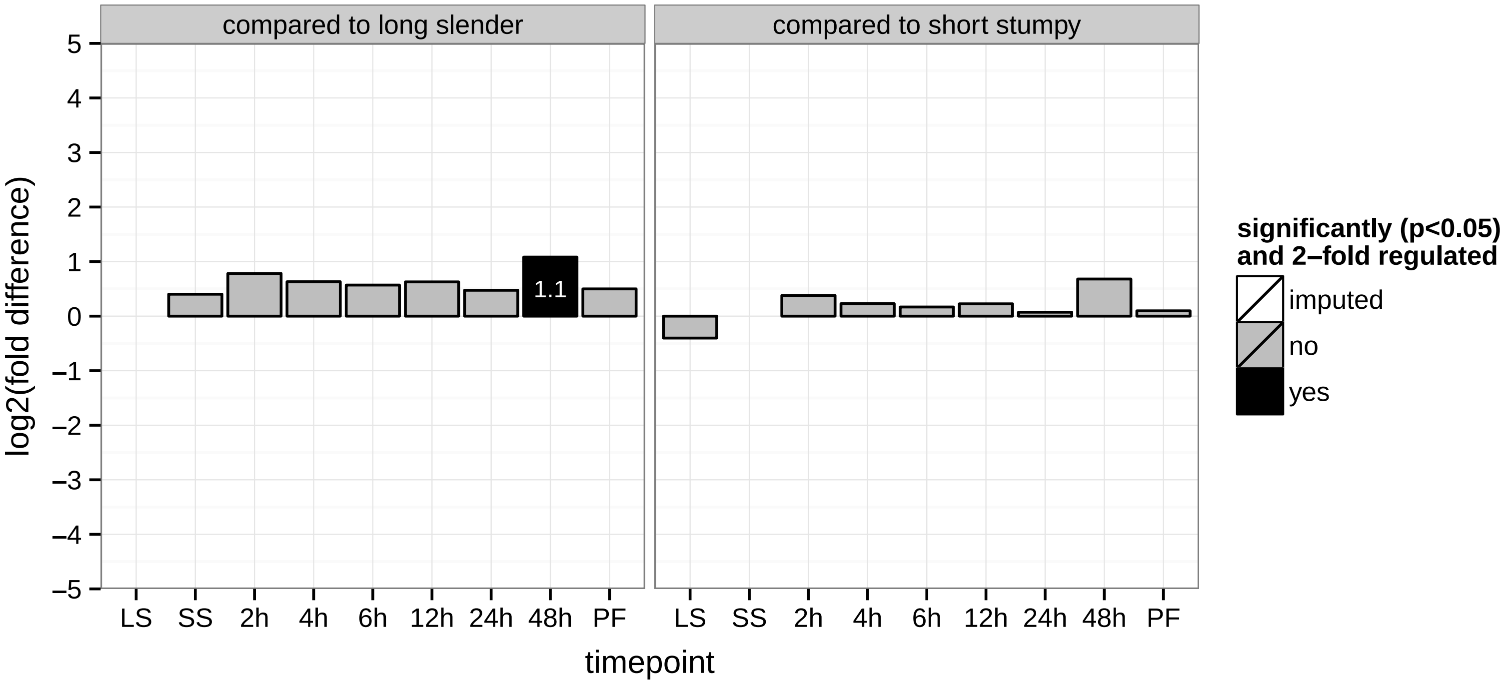
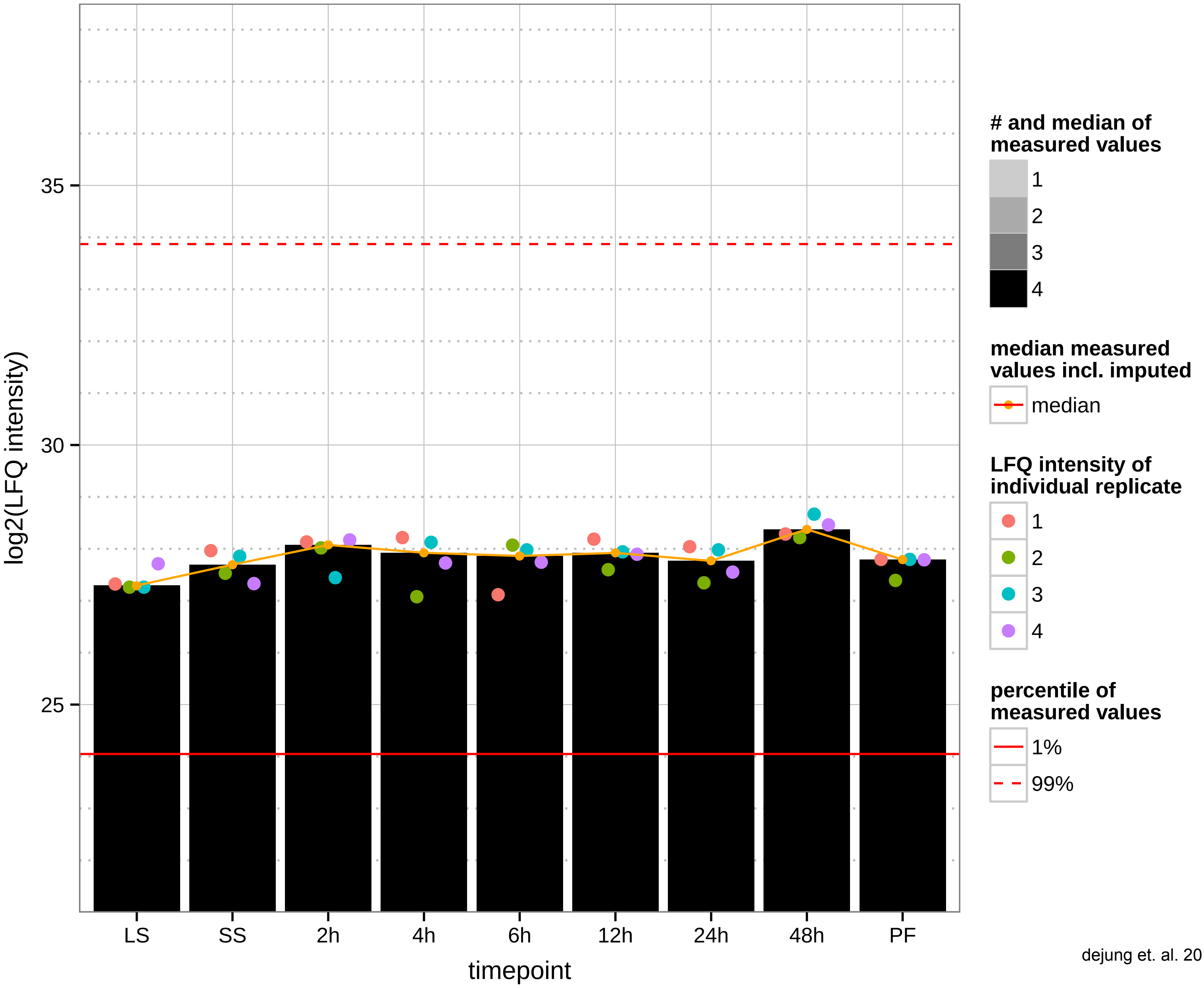
hypothetical protein, conserved
Tb927.10.1450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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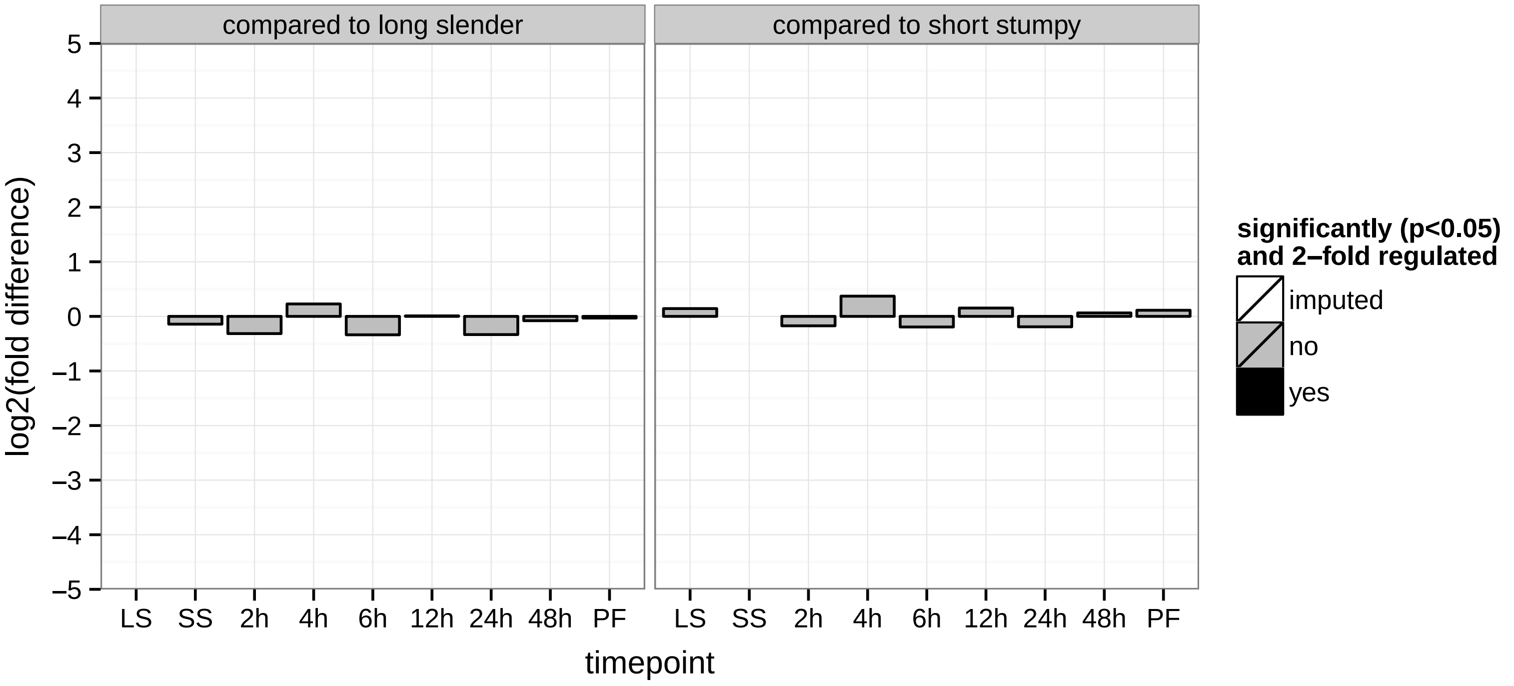
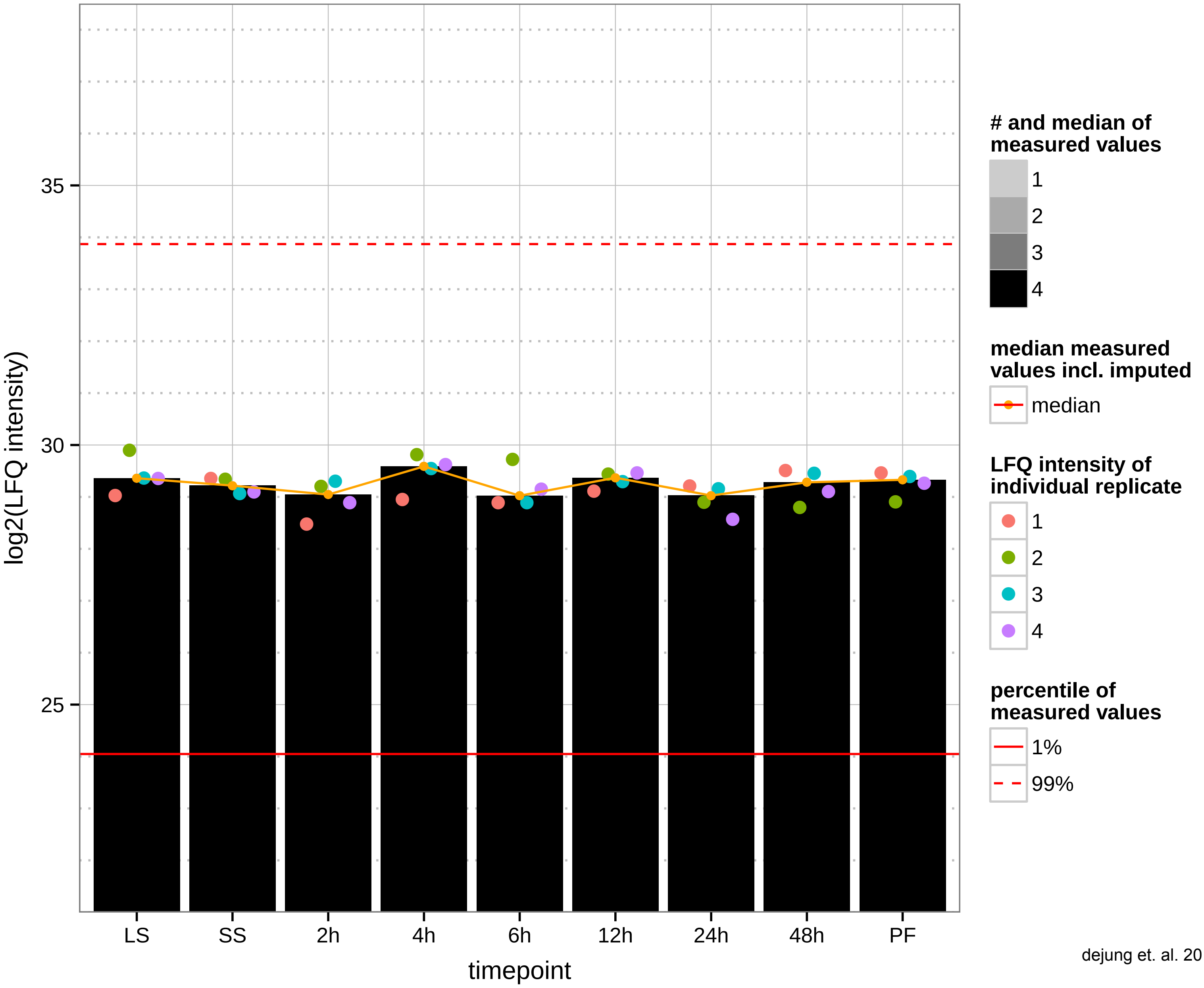
hypothetical protein, conserved
Tb927.10.14500
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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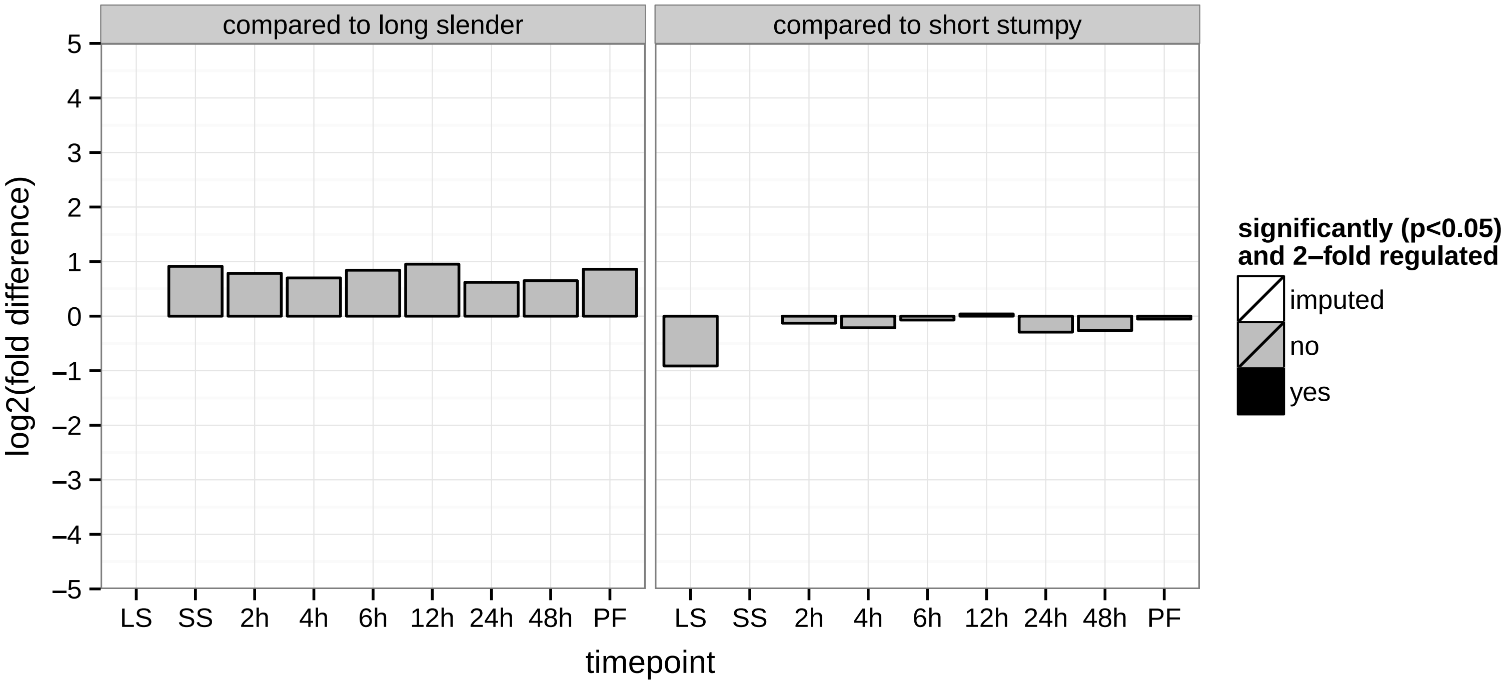
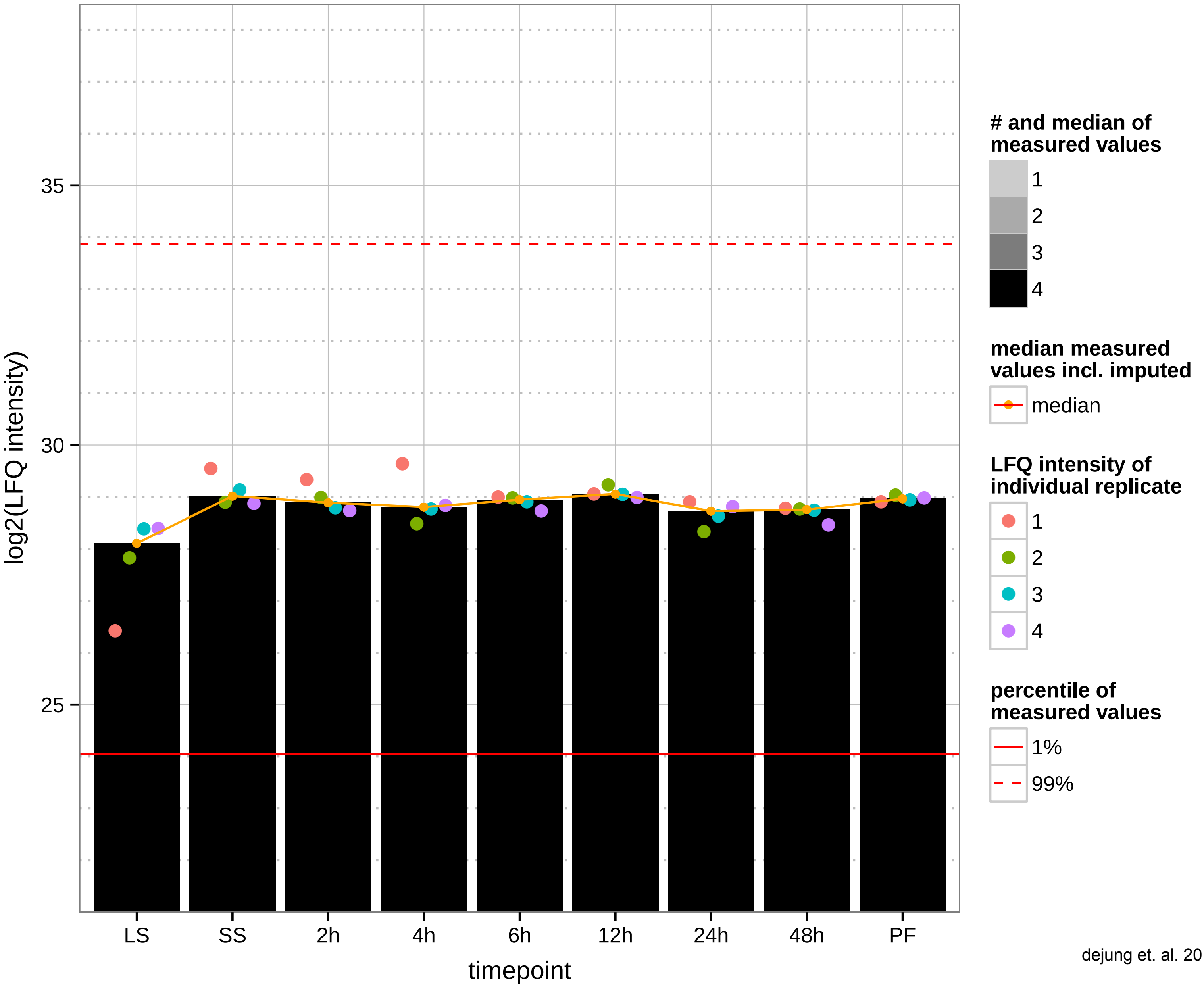
hypothetical protein, conserved
Tb927.10.14510
AGOF: null
AGOC: null
AGOP: null
PGOF: hydrolase activity, acting on acid anhydrides
PGOC: null
PGOP: null





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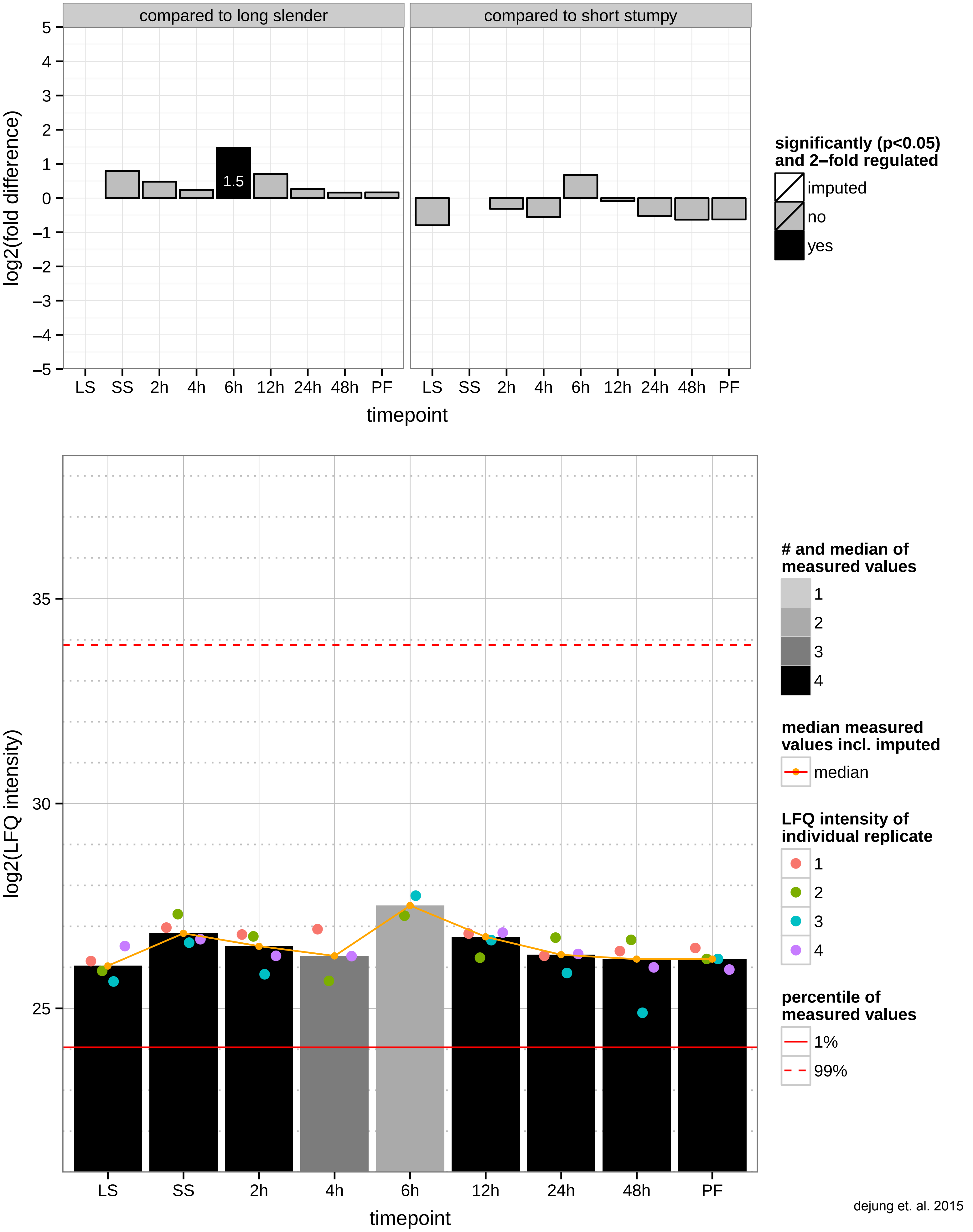
hypothetical protein, conserved
Tb927.10.14520
AGOF: null
AGOC: bacterial–type flagellum basal body
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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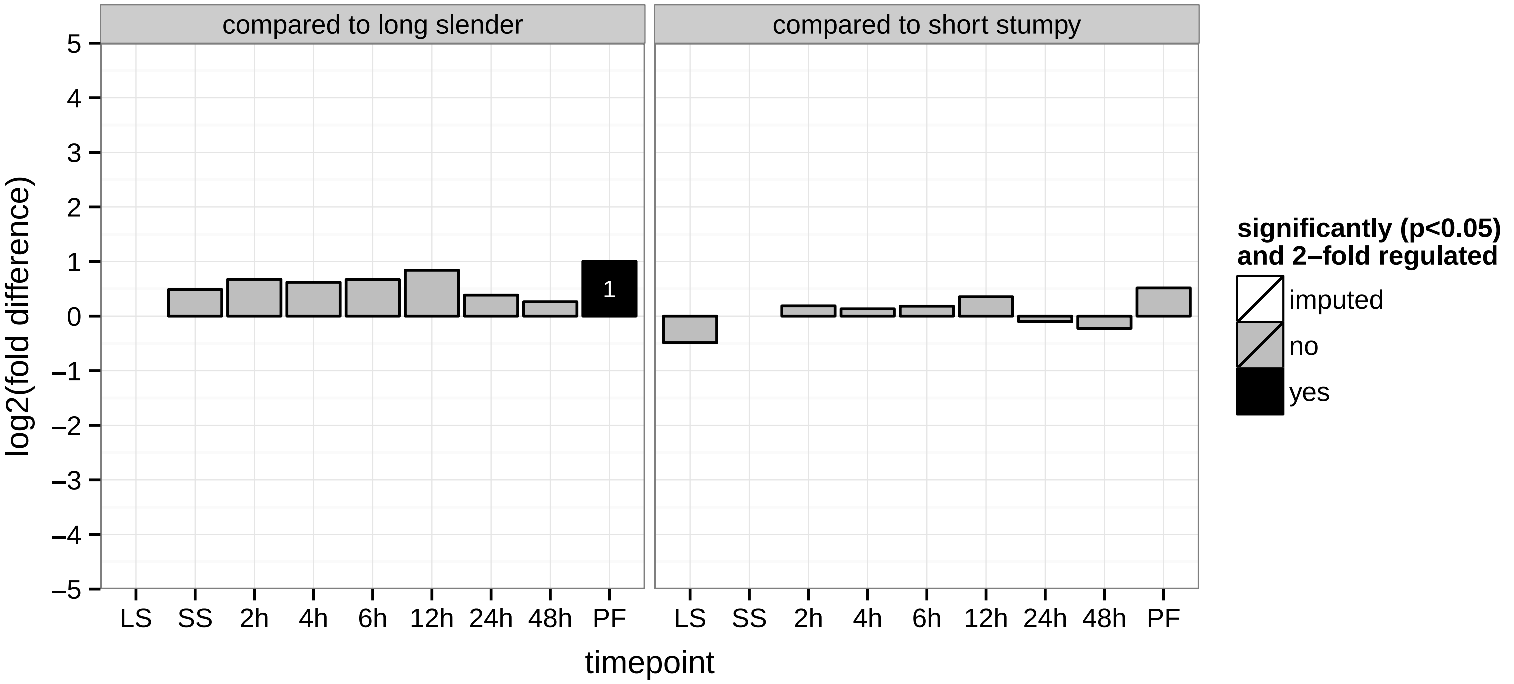
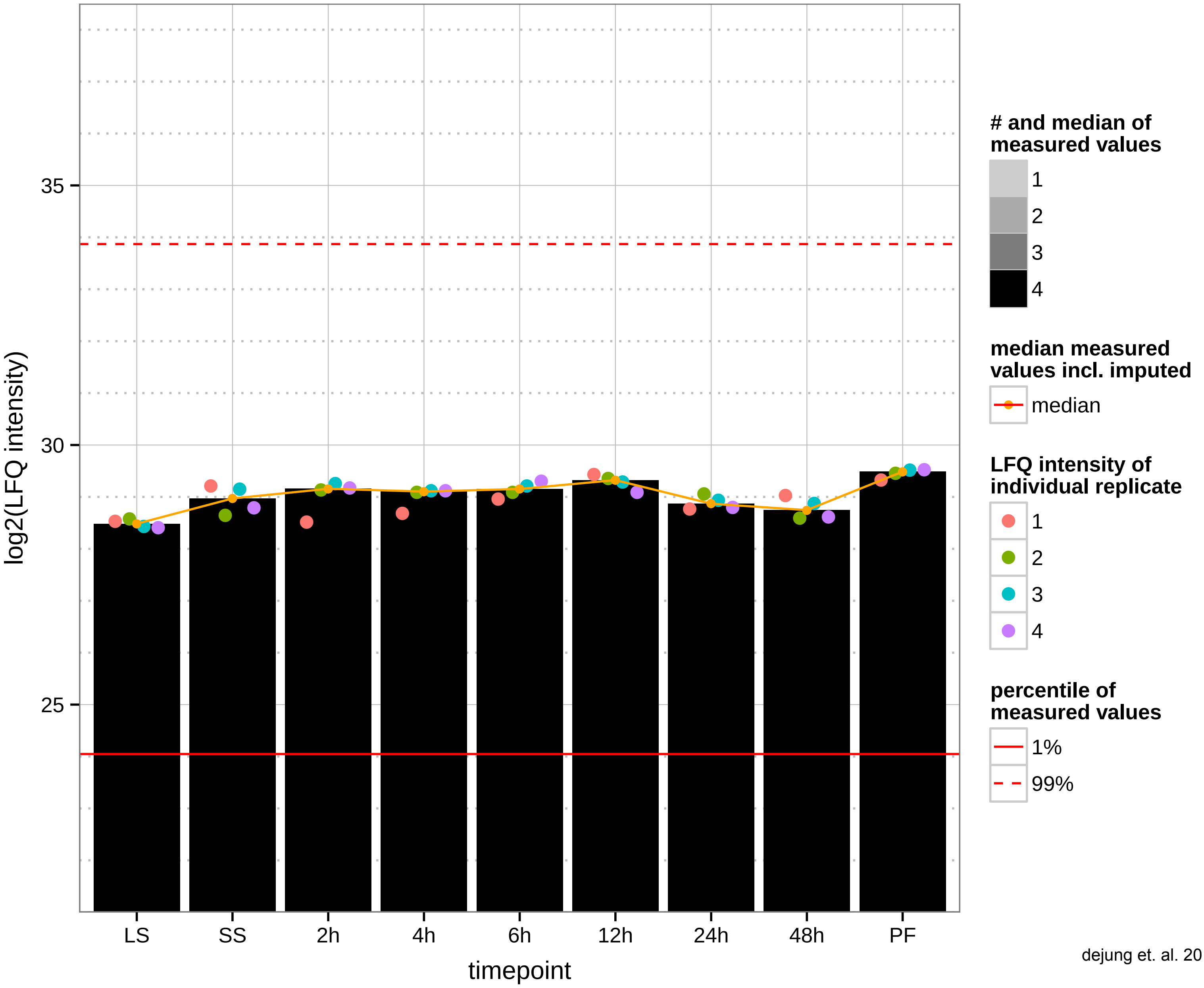
19S proteasome non–atpase subunit 8, 26s proteasome non–atpase regulatory subunit 8 (Rpn8)
Tb927.10.14530
AGOF: endopeptidase activity
AGOC: proteasome regulatory particle
AGOP: cell growth, ubiquitin–dependent protein catabolic process
PGOF: protein binding
PGOC: null
PGOP: null





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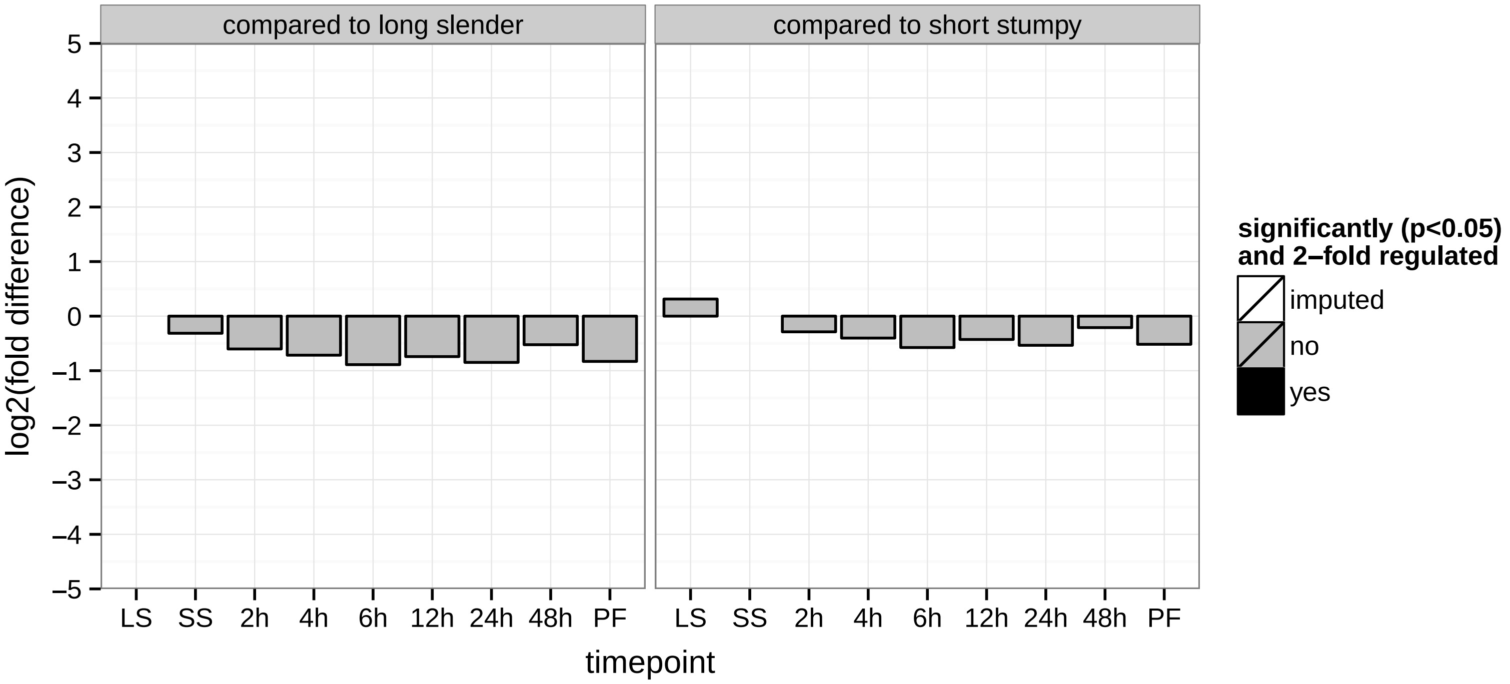
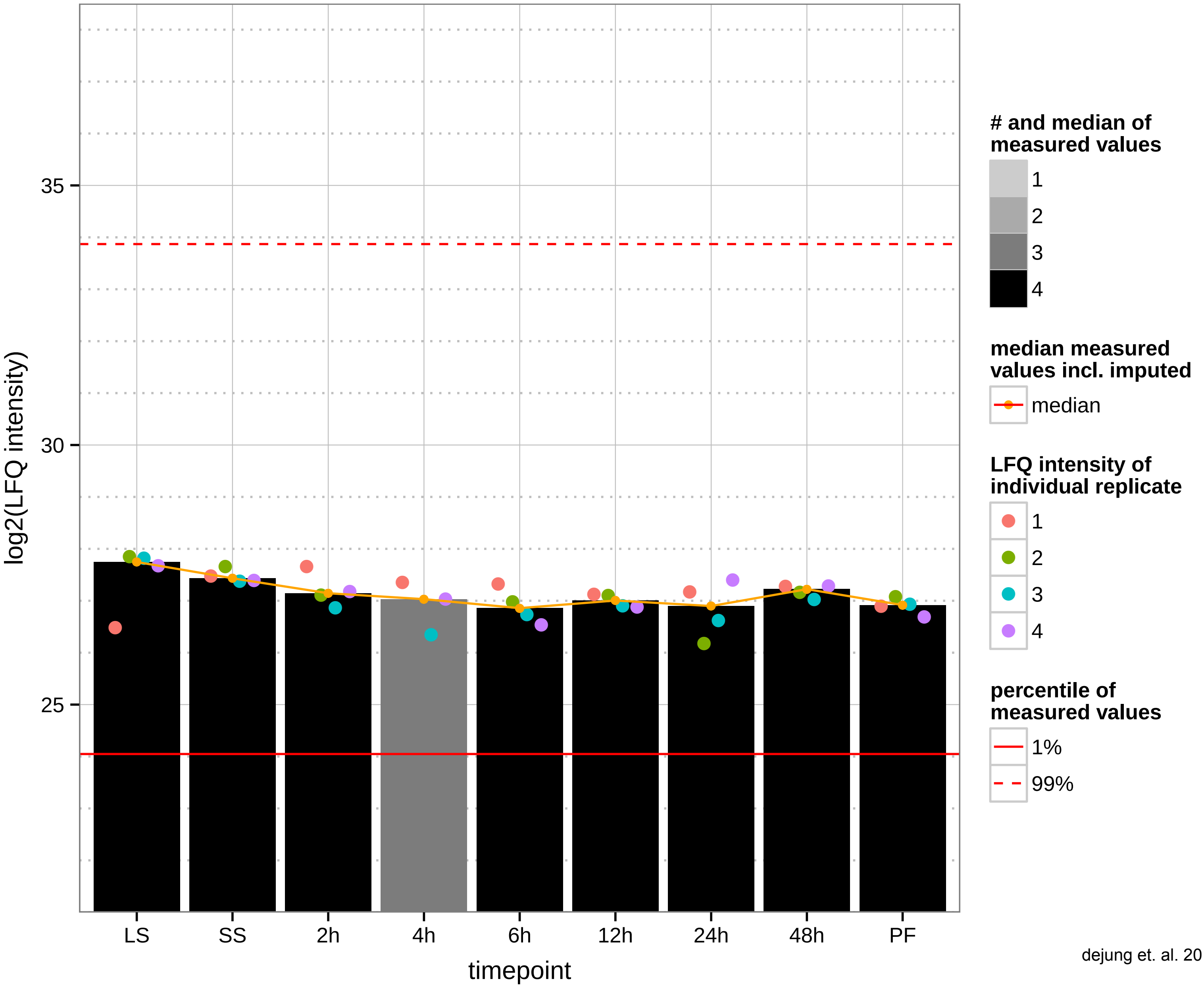
hypothetical protein, conserved
Tb927.10.14570
AGOF: ATP binding, microtubule motor activity
AGOC: null
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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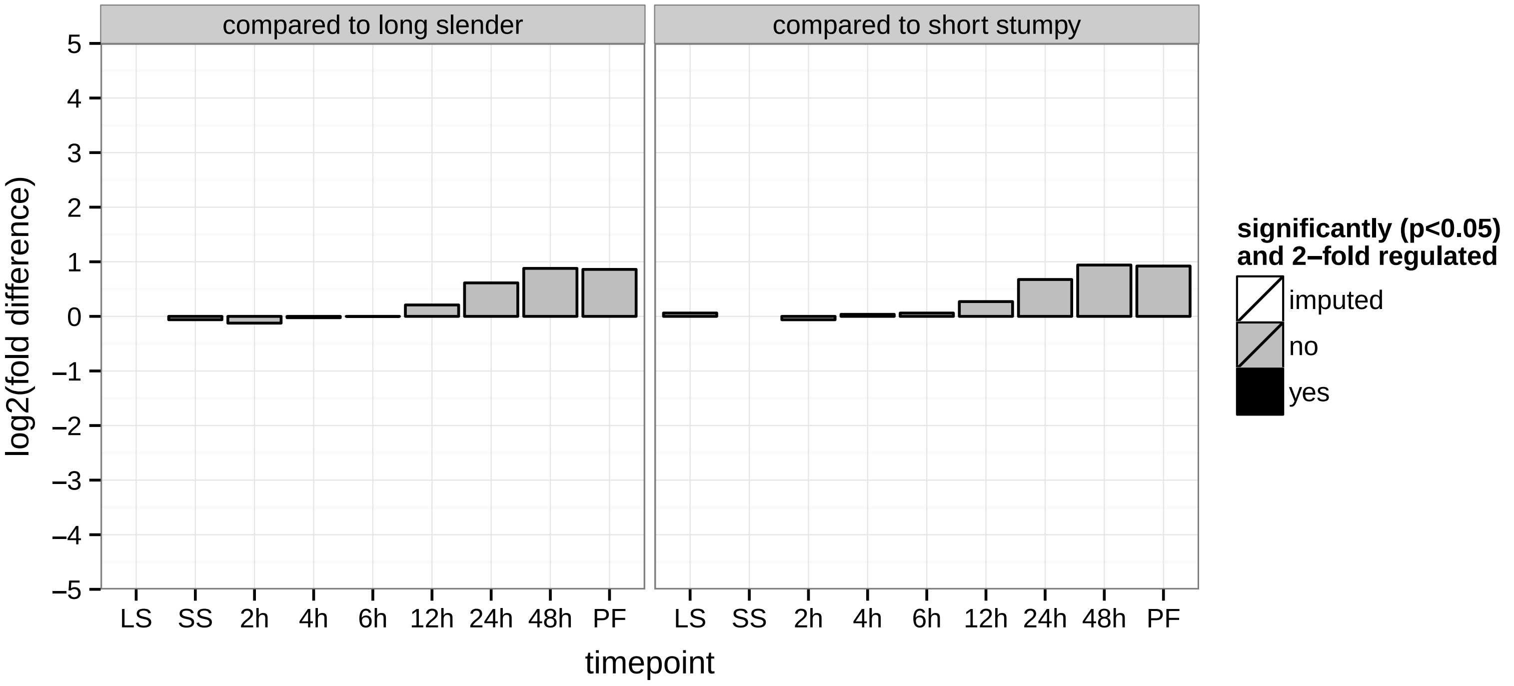
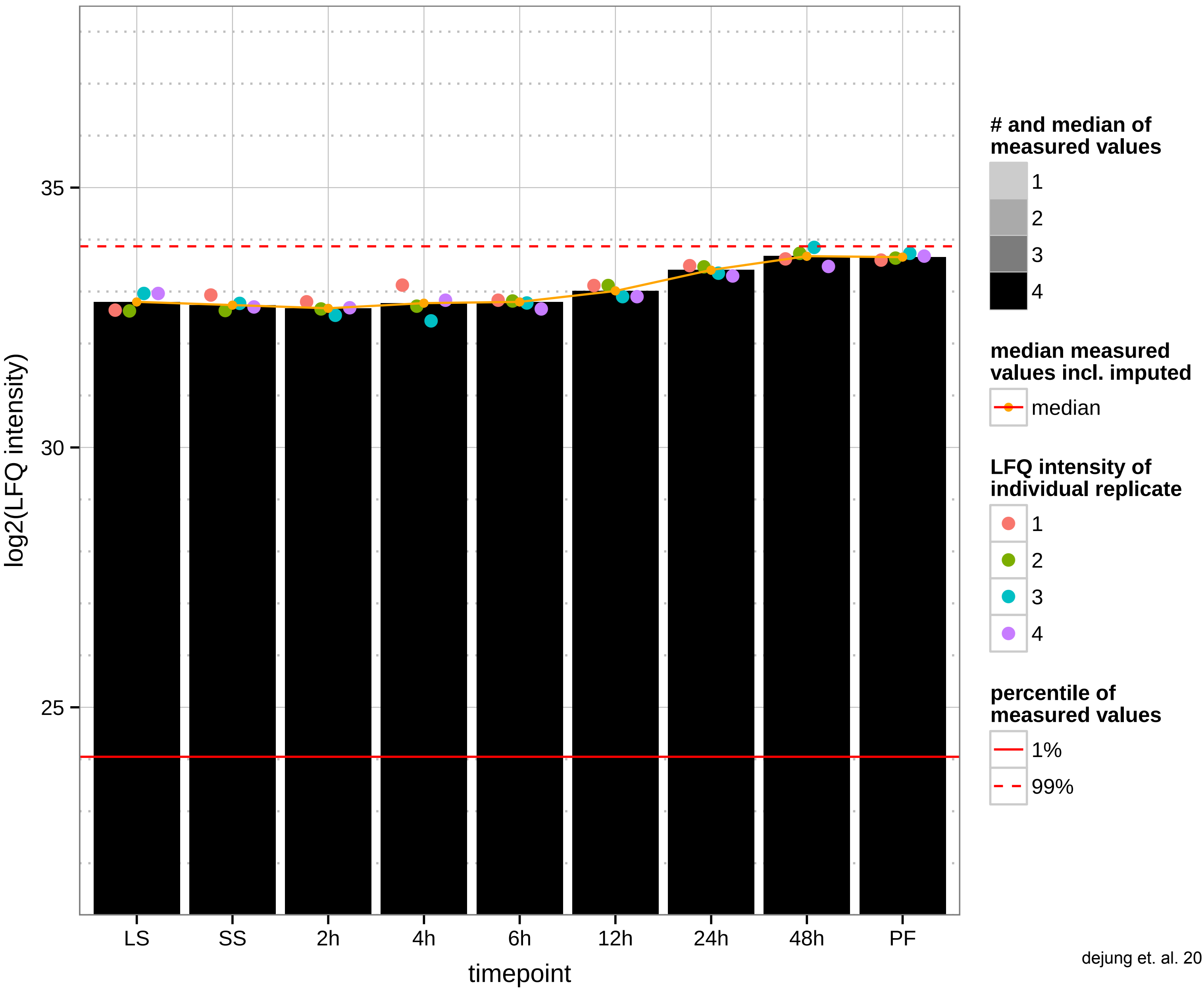
40S ribosomal protein S2, putative (RPS2)
Tb927.10.14710;Tb927.10.14600
AGOF: RNA binding, structural constituent of ribosome
AGOC: intracellular, ribosome, small ribosomal subunit
AGOP: translation
PGOF: RNA binding, structural constituent of ribosome
PGOC: intracellular, ribosome, small ribosomal subunit
PGOP: translation





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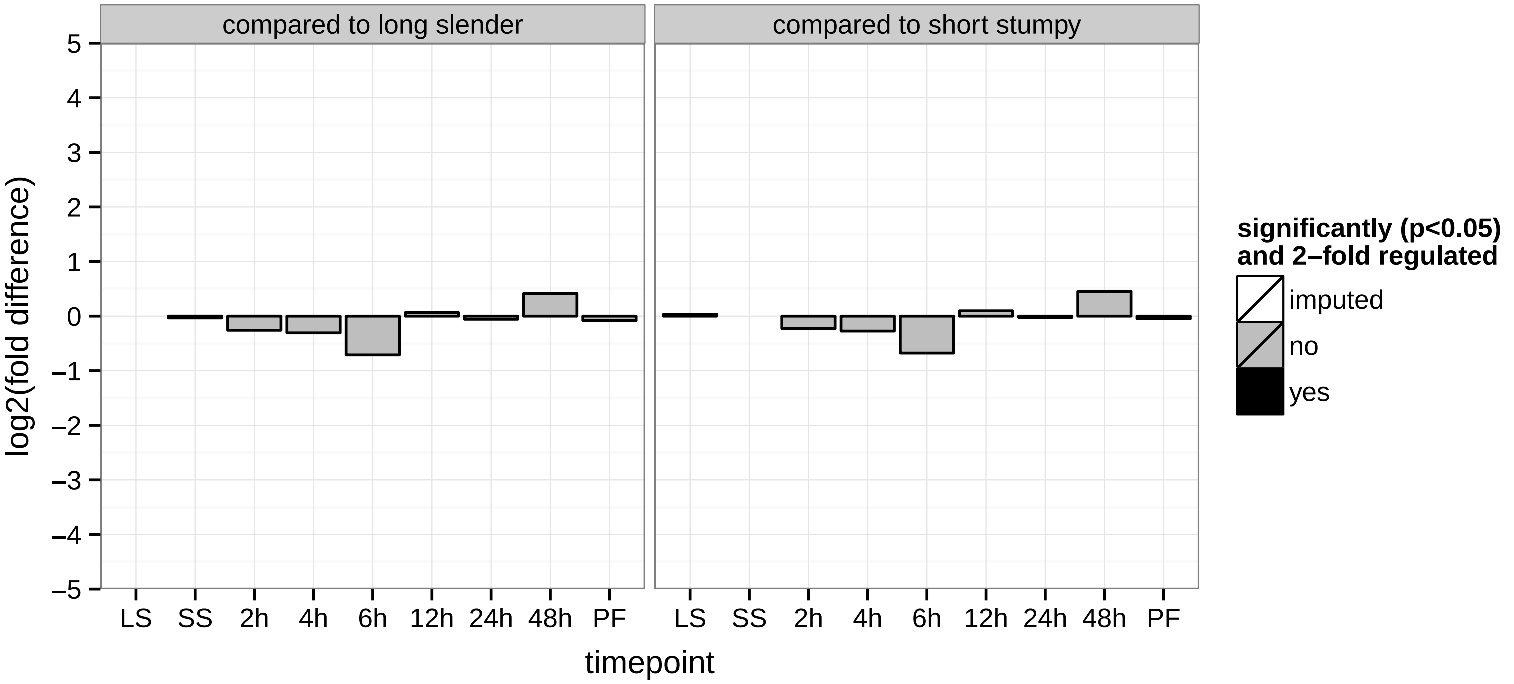
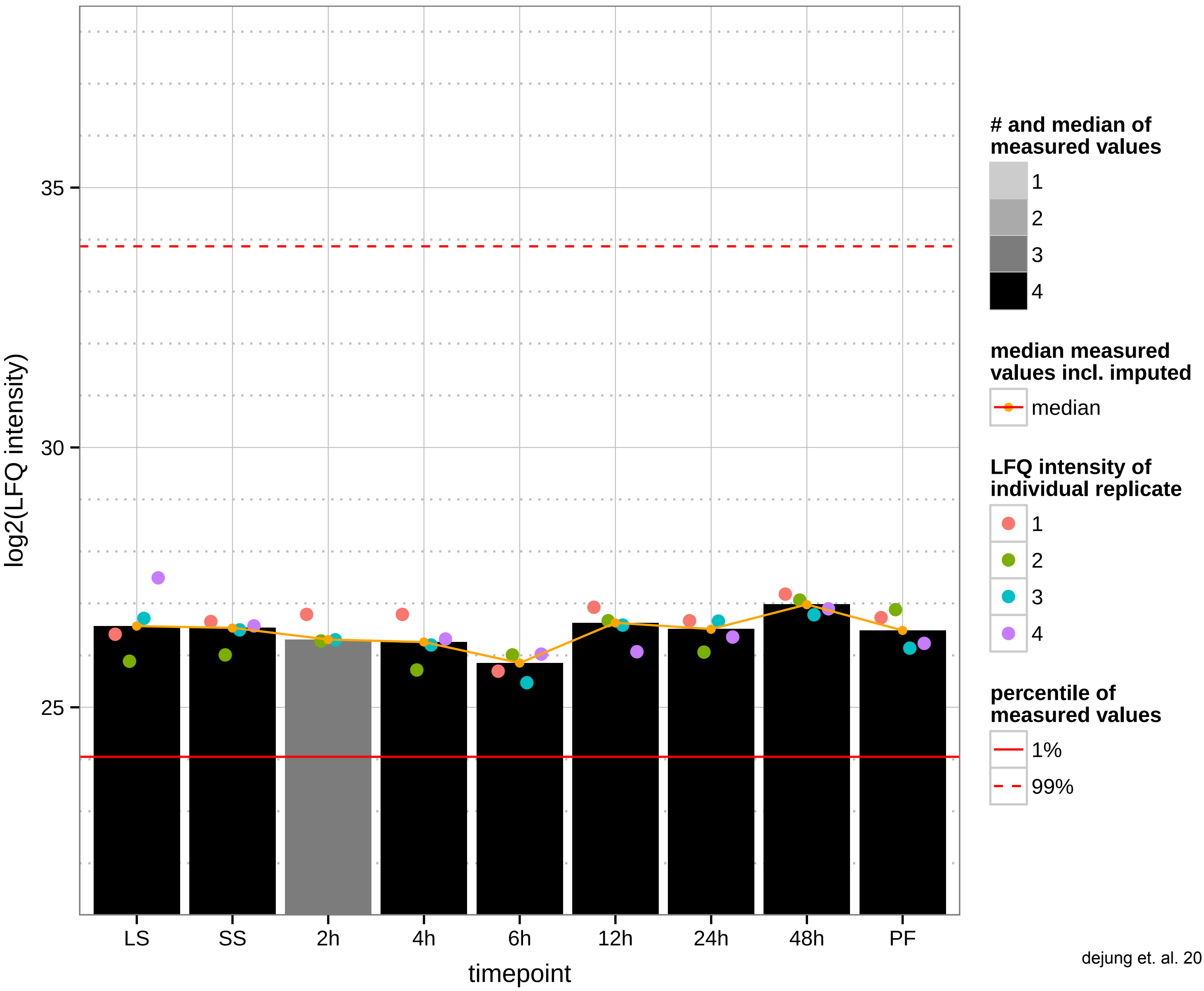
leucine–rich repeat protein (LRRP), putative
Tb927.10.14610
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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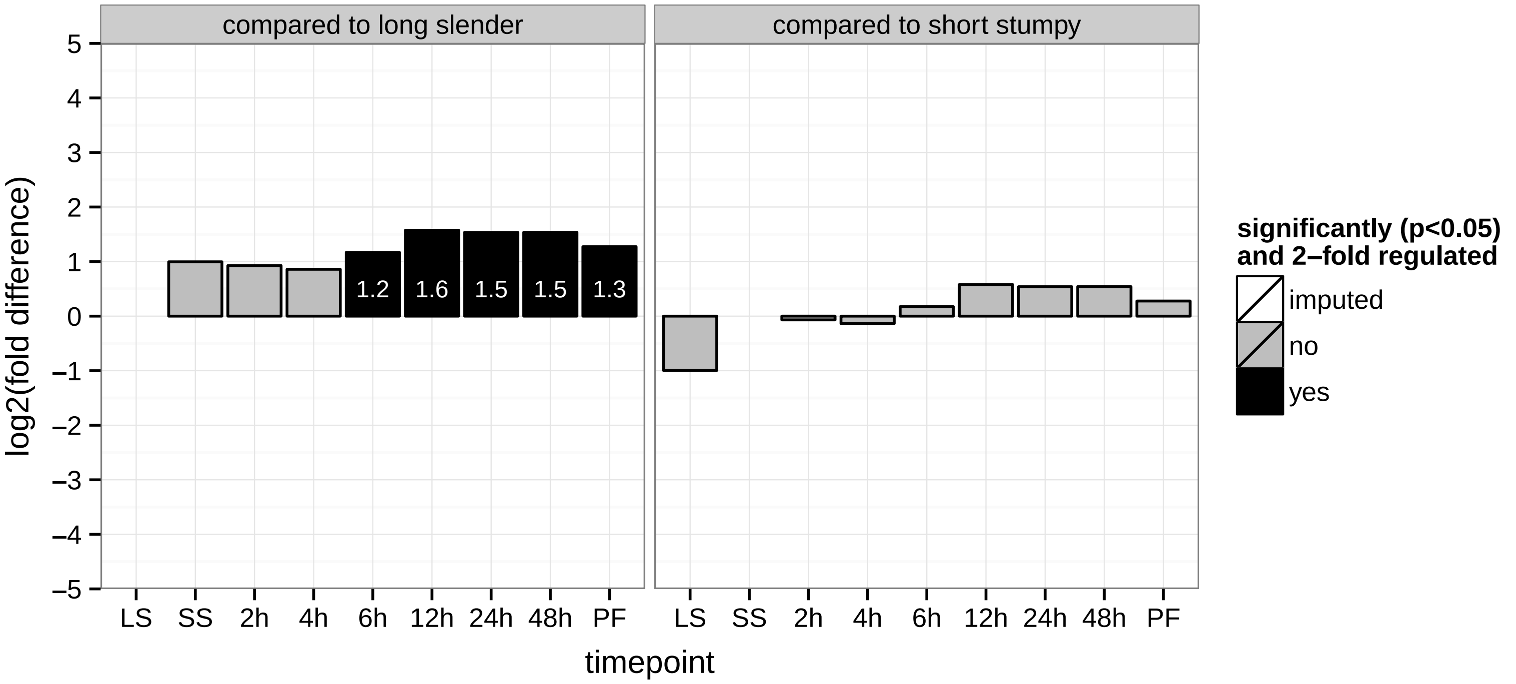
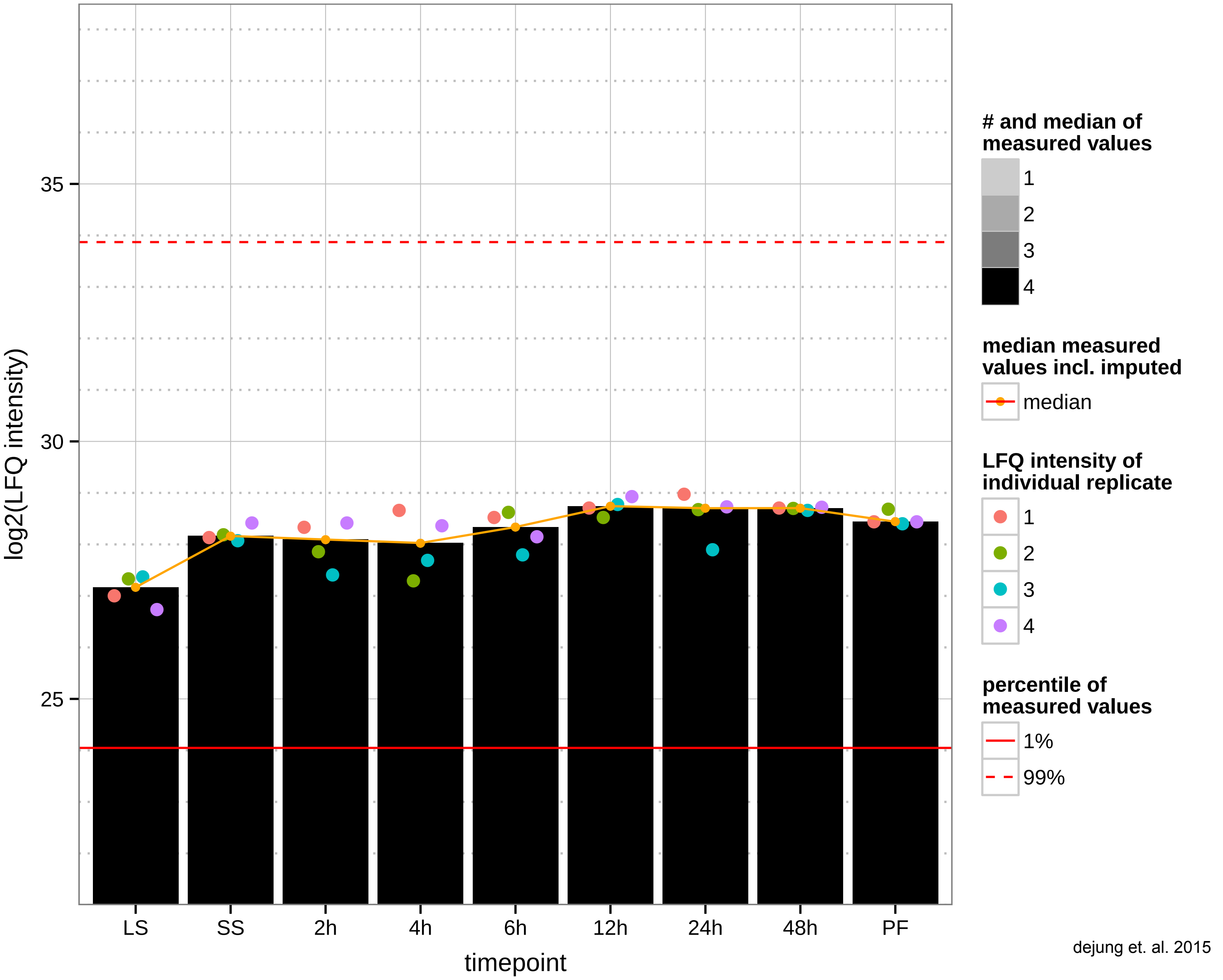
ribosome biogenesis protein, putative
Tb927.10.14680
AGOF: rRNA binding
AGOC: nucleolus
AGOP: ribosomal large subunit assembly
PGOF: null
PGOC: null
PGOP: null





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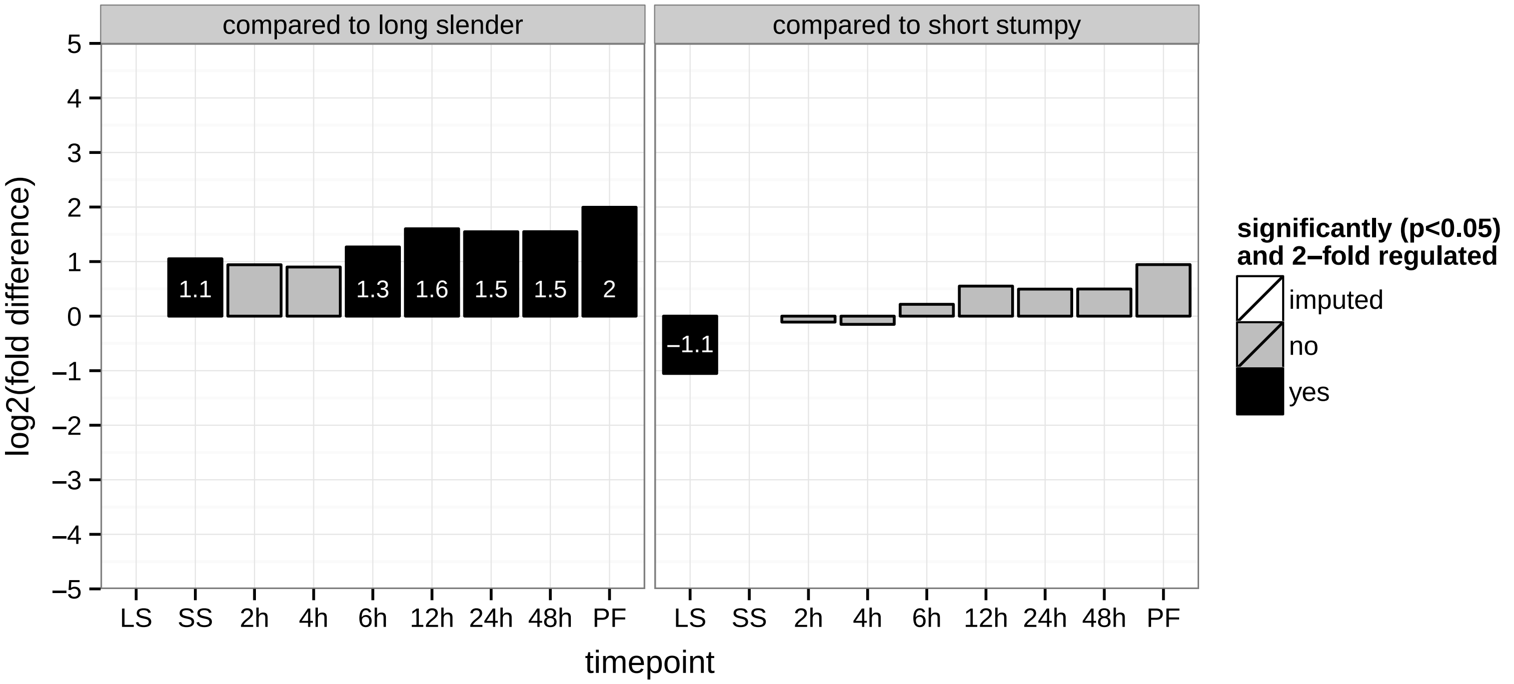
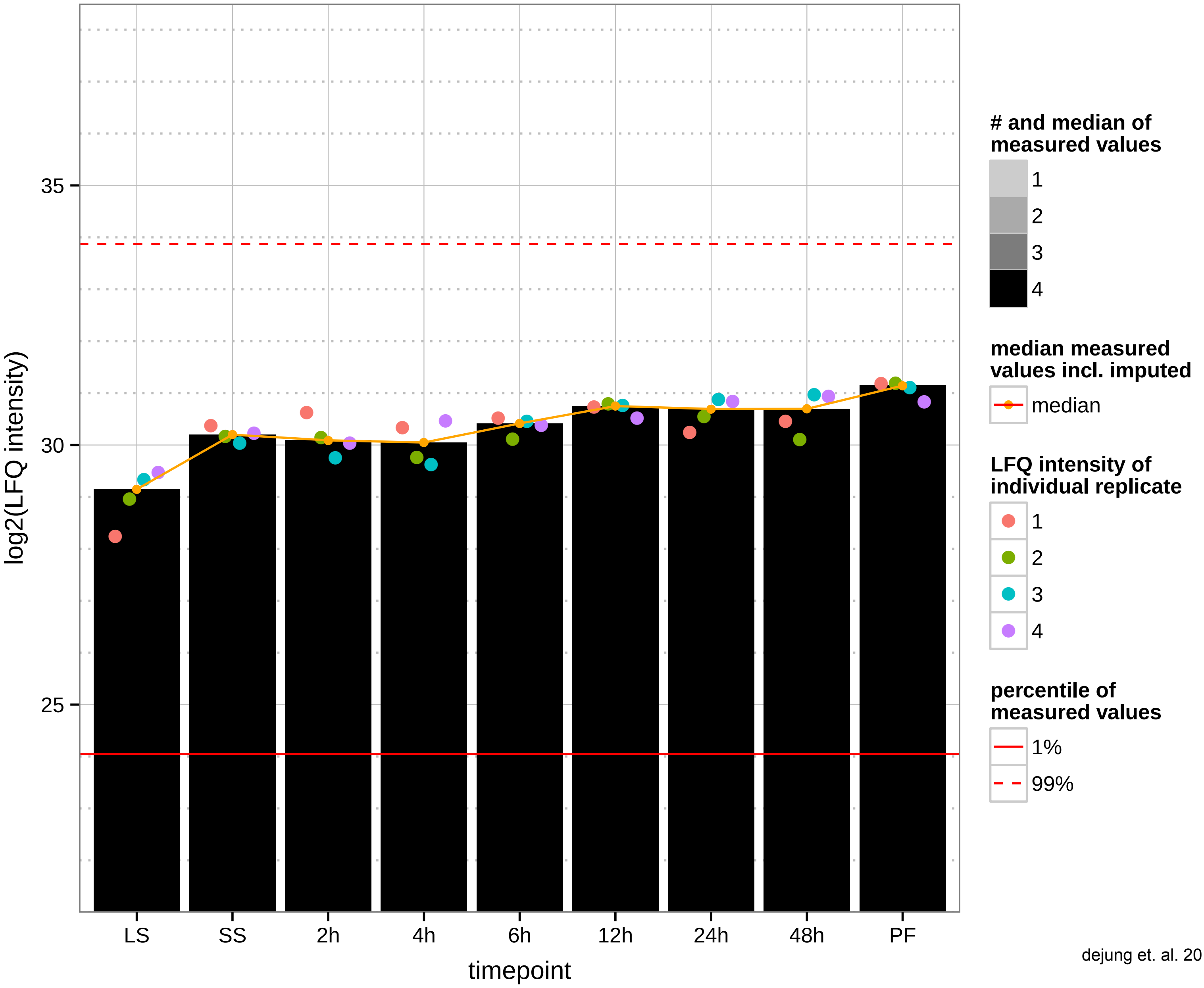
fibrillarin, putative
Tb927.10.14750;Tb927.10.14630
AGOF: RNA binding
AGOC: nucleus
AGOP: rRNA processing
PGOF: RNA binding, methyltransferase activity
PGOC: null
PGOP: rRNA processing, tRNA processing





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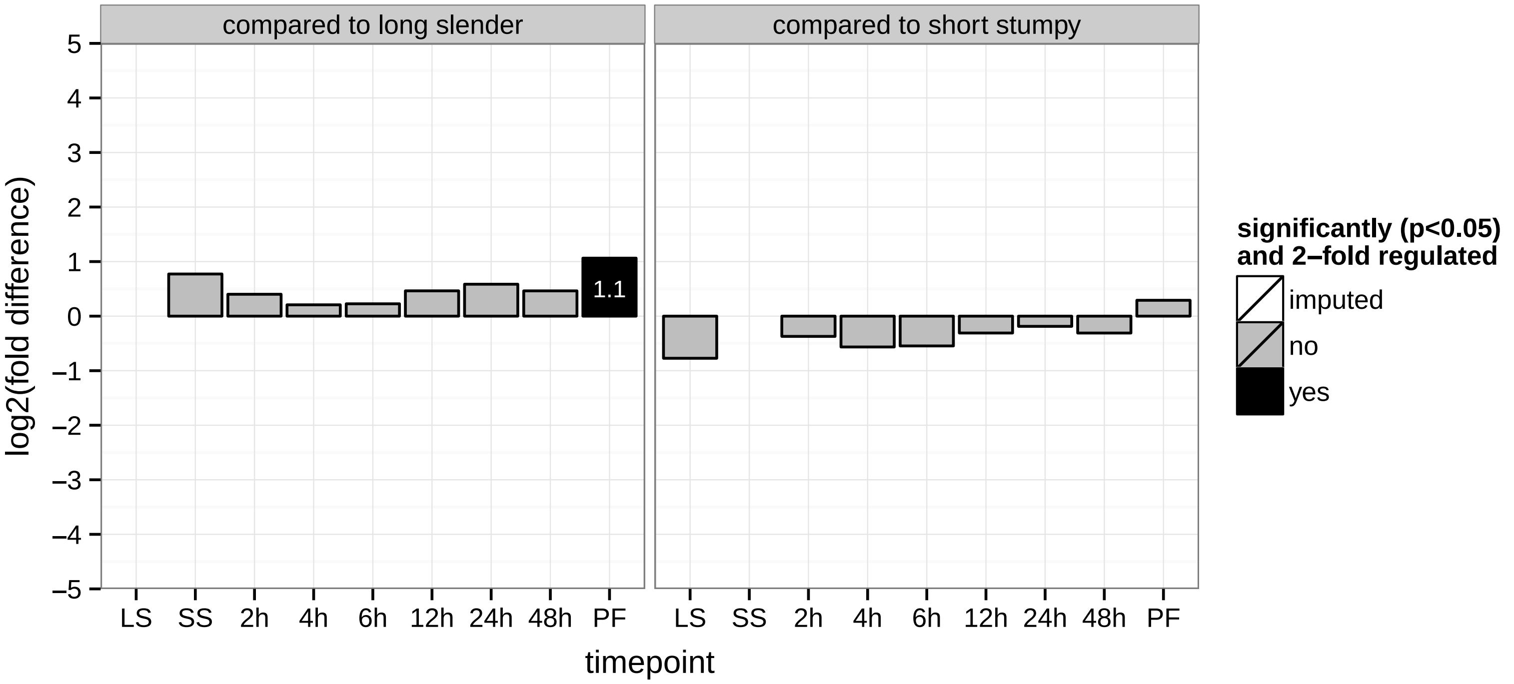
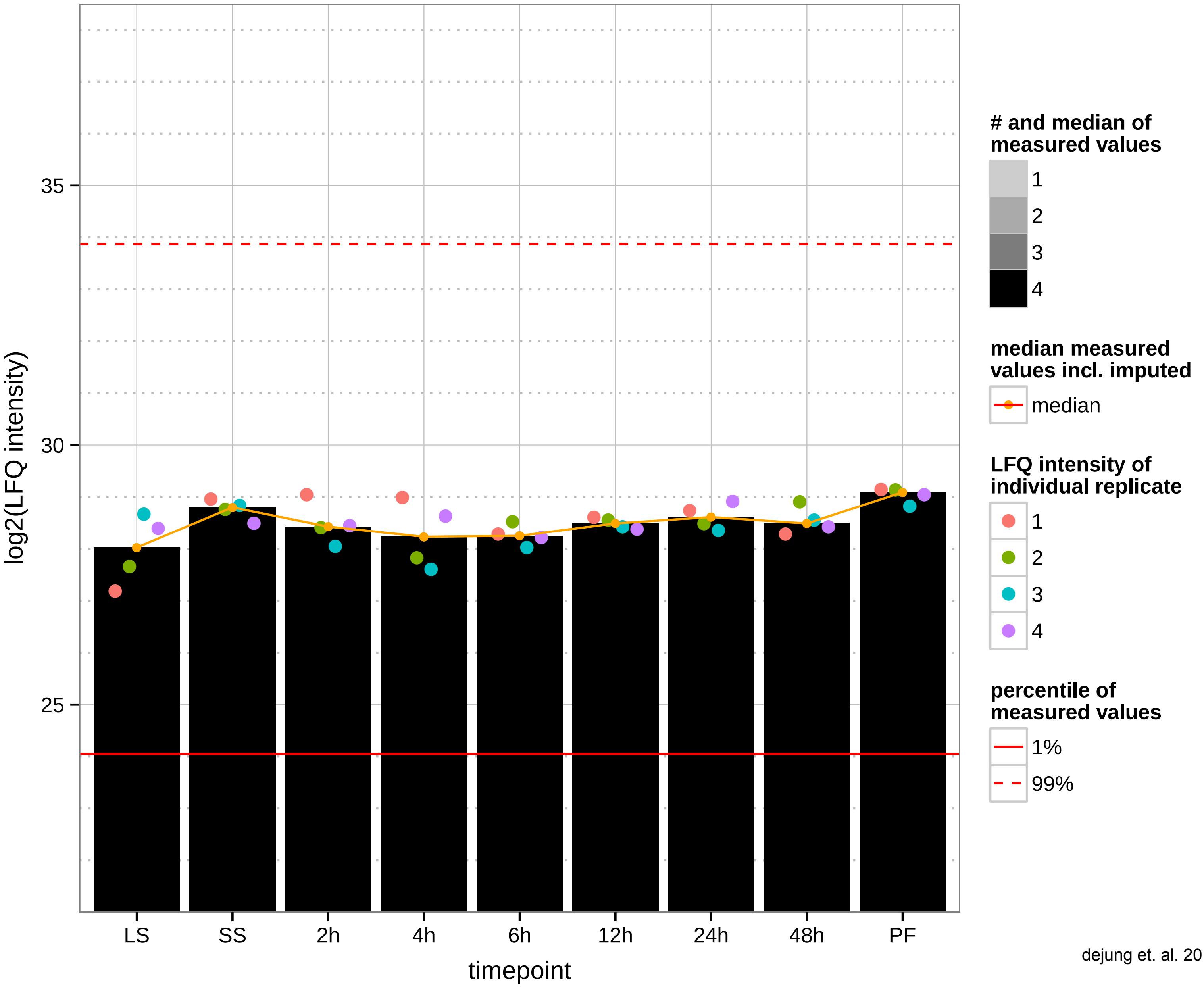
protein kinase, putative
Tb927.10.14770
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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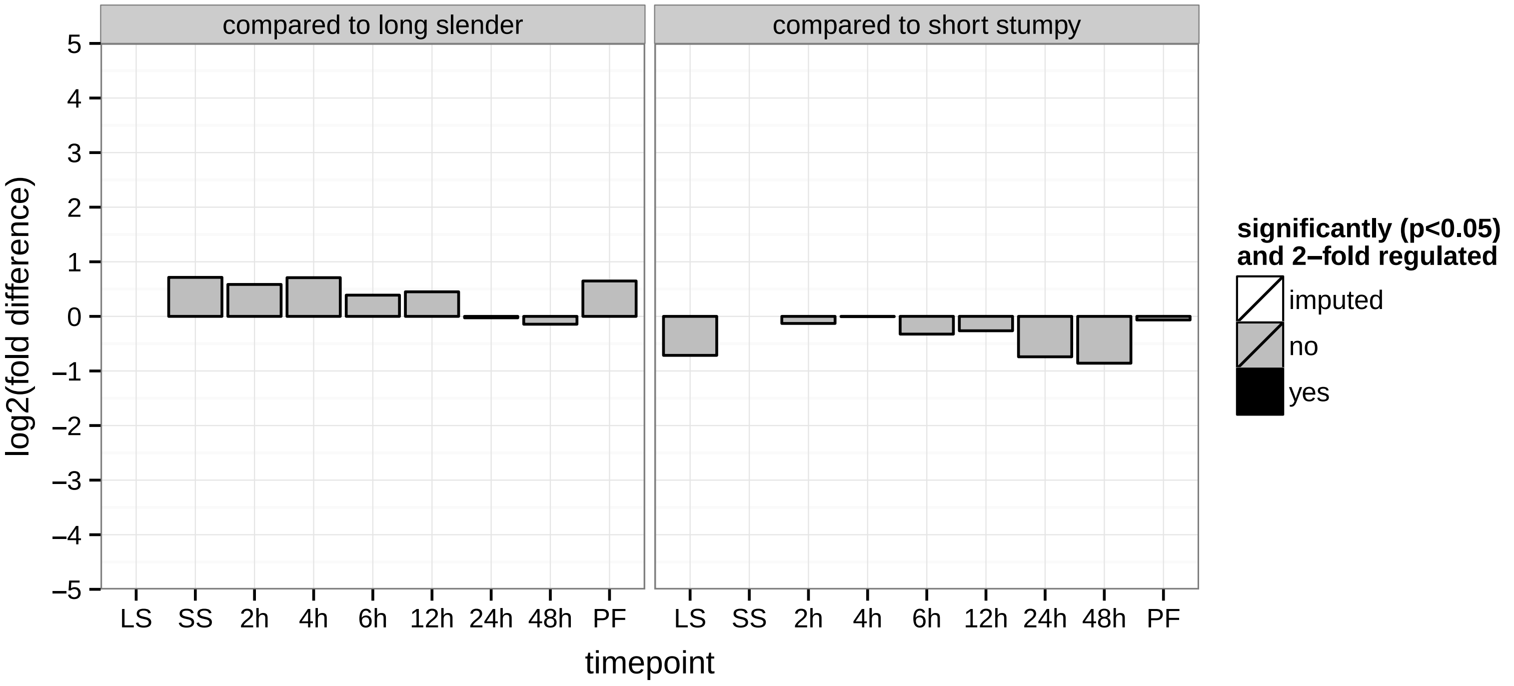
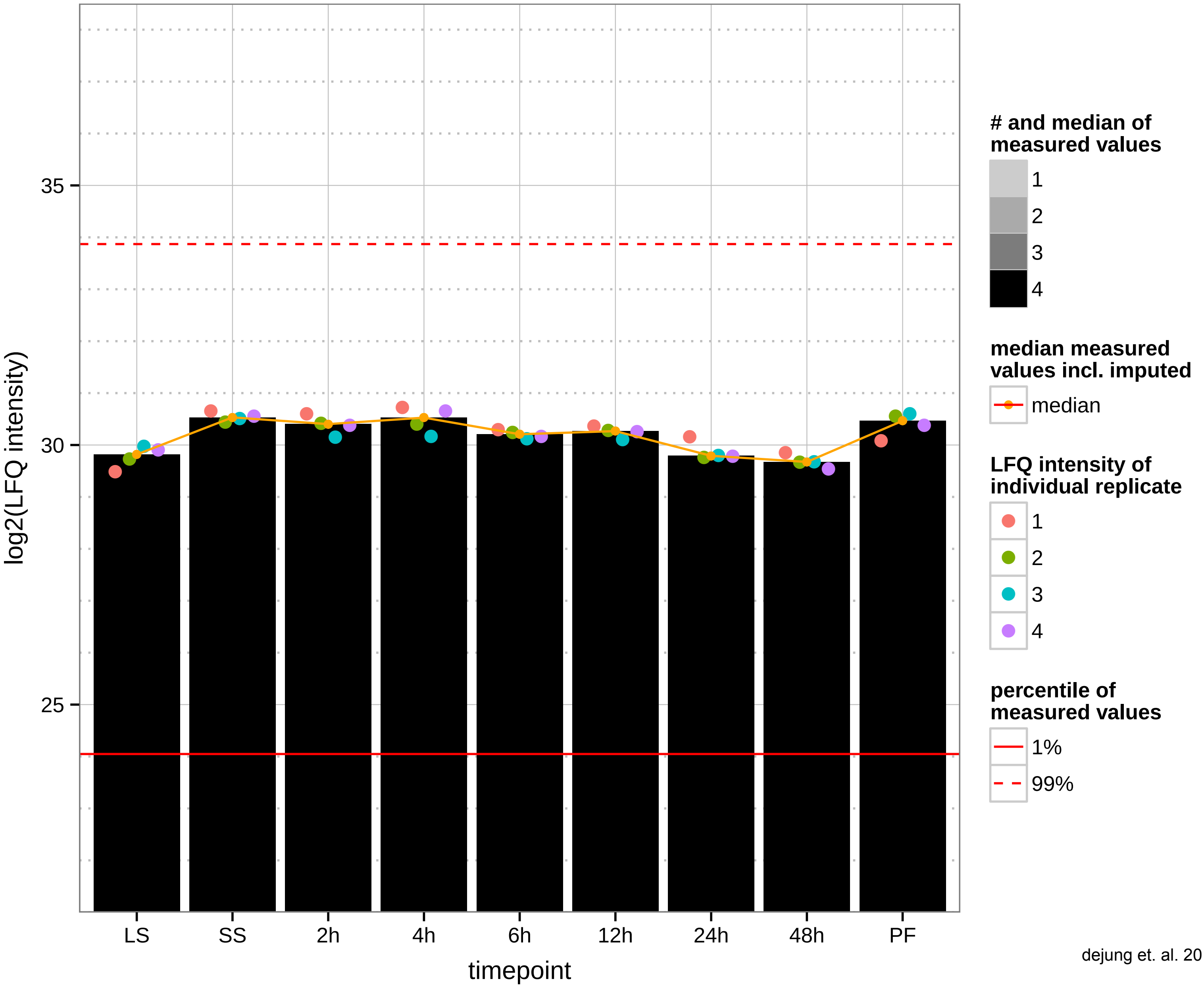
mitogen–activated protein kinase kinase kinase, putative, canertinib–binding protein kinase–1 (CBPK1)
Tb927.10.14780
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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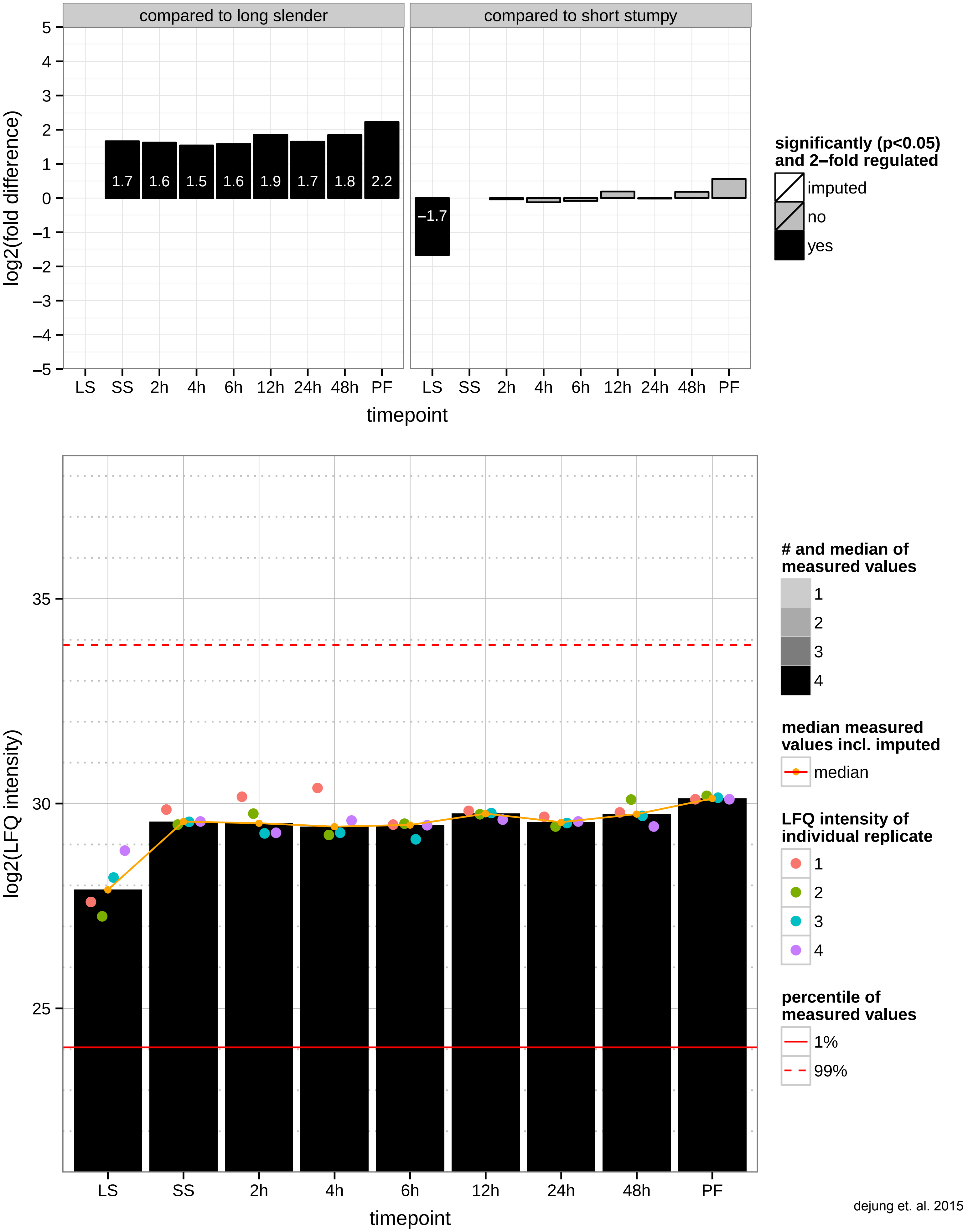
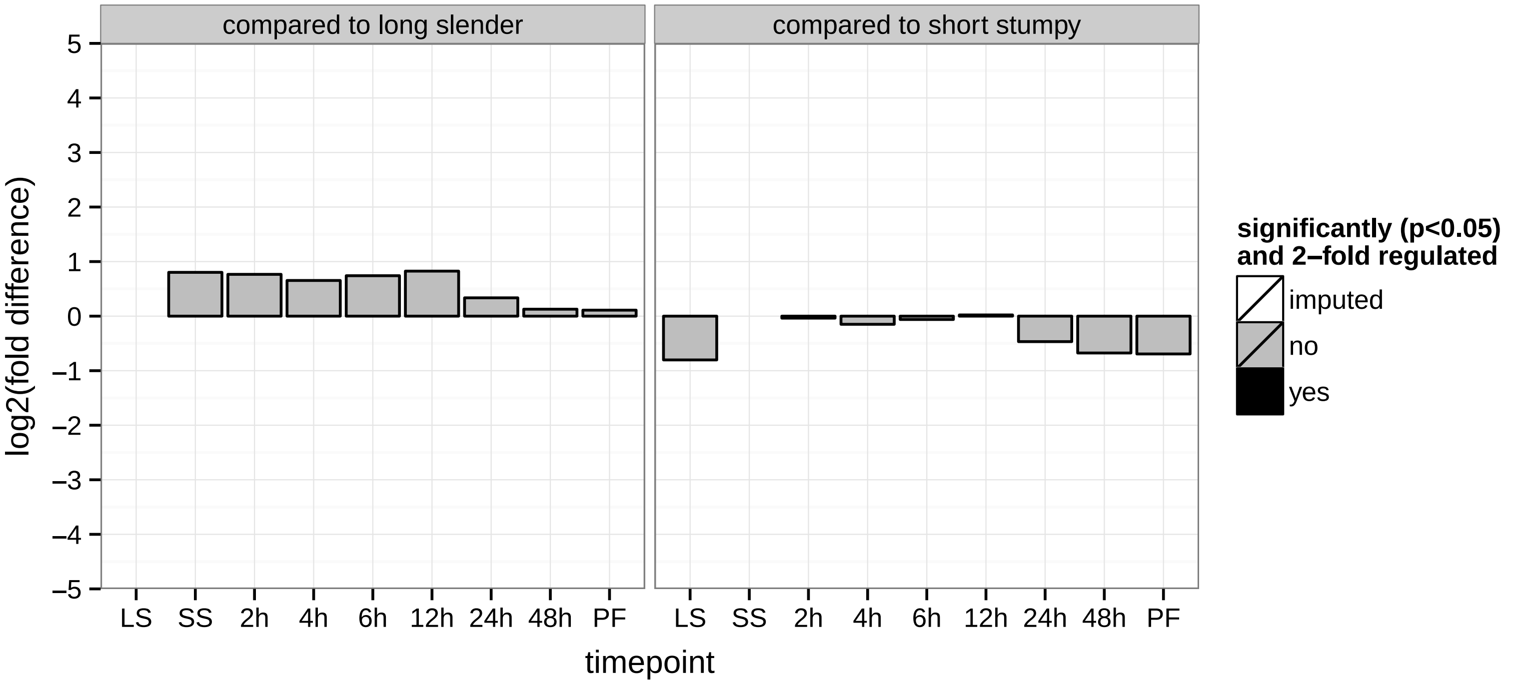
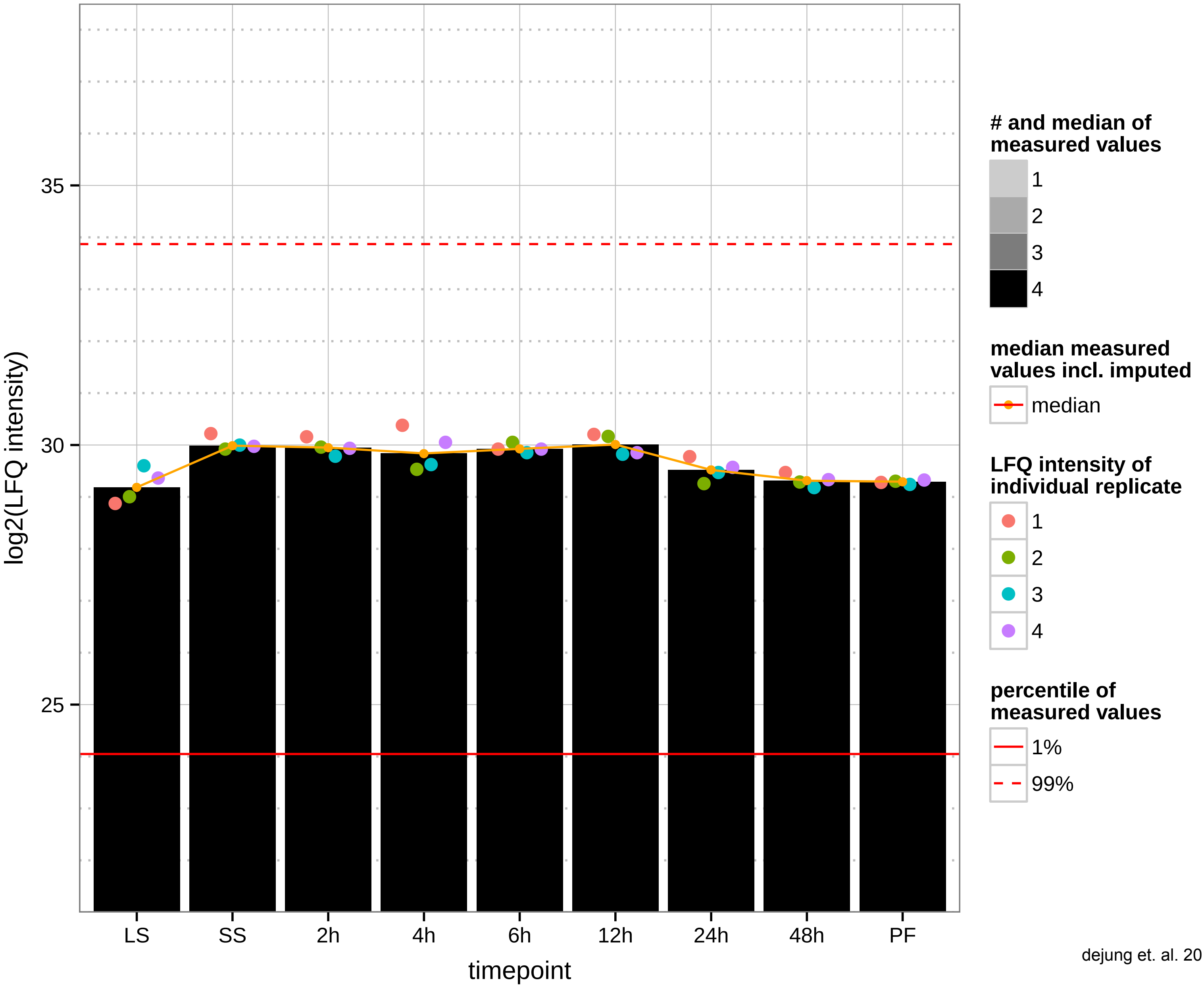
hypothetical protein, conserved
Tb927.10.1490
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



intraflagellar transport protein IFT52, putative (IFT52)
Tb927.10.14980
AGOF: null
AGOC: cilium
AGOP: intraflagellar transport
PGOF: null
PGOC: null
PGOP: null





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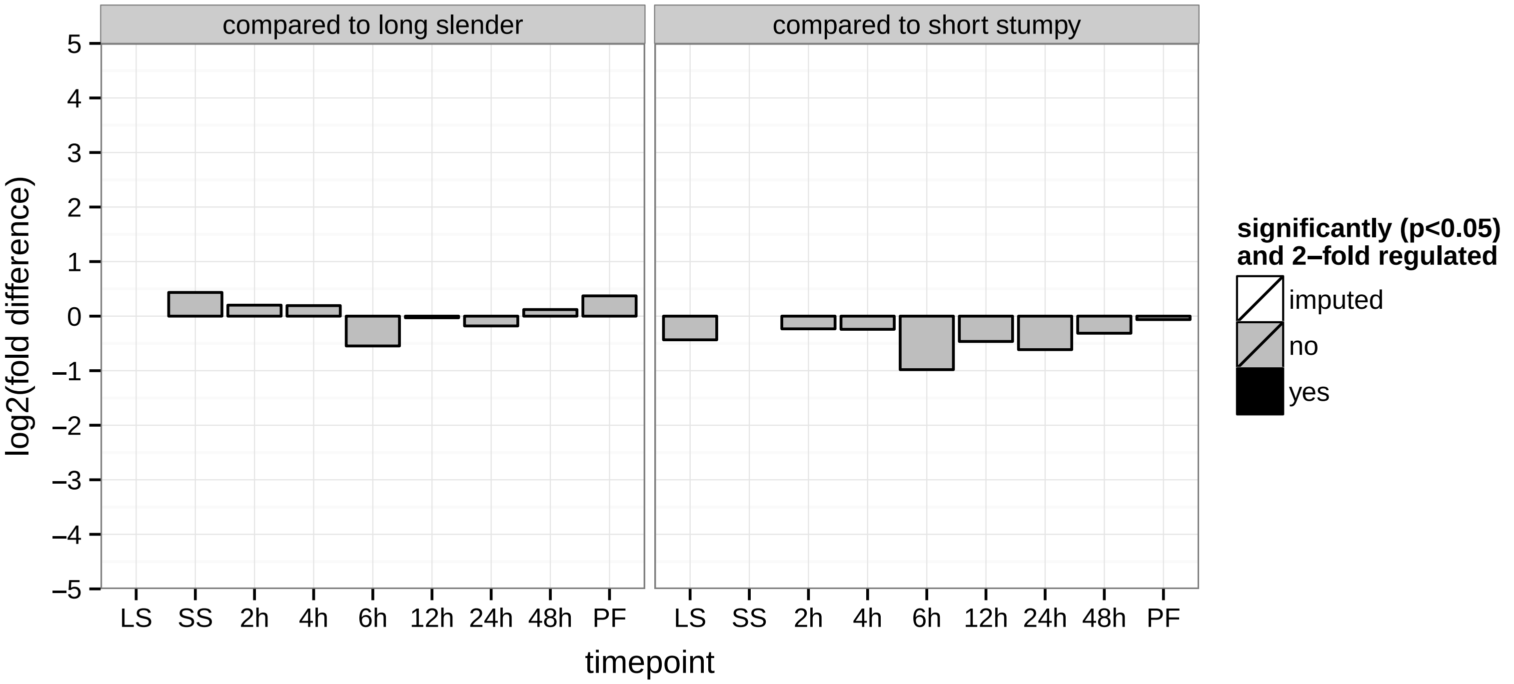
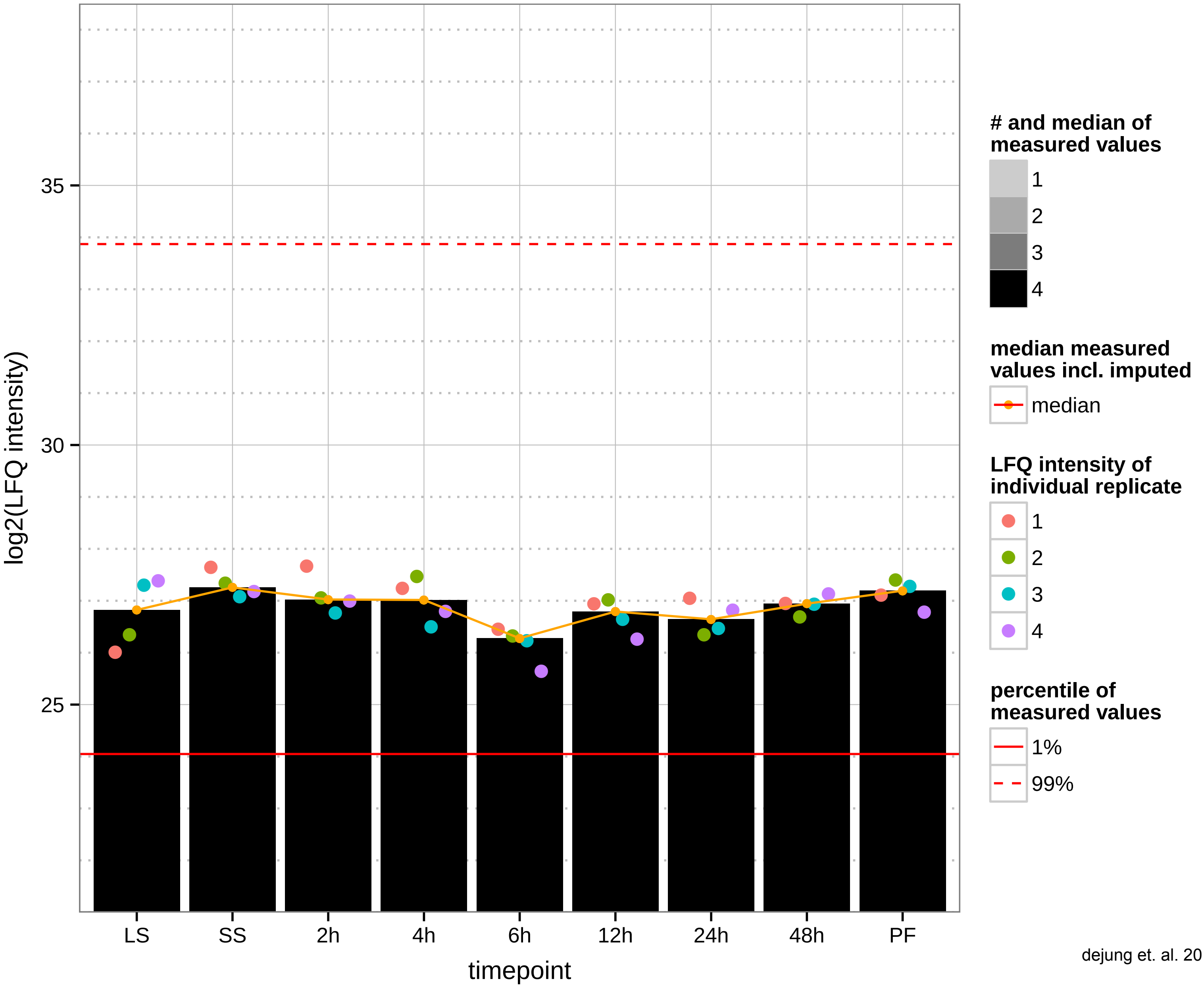
hypothetical protein, conserved
Tb927.10.15000
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: nucleus
PGOP: null





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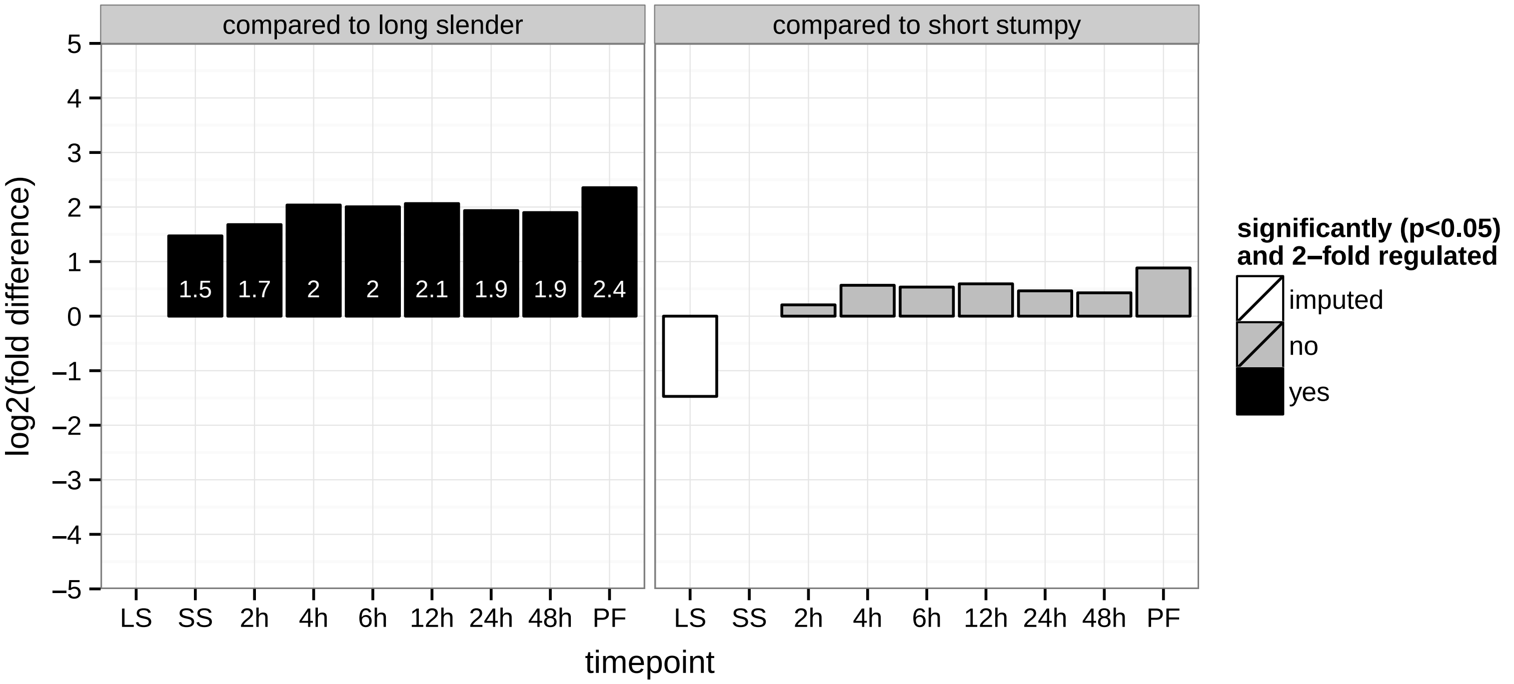
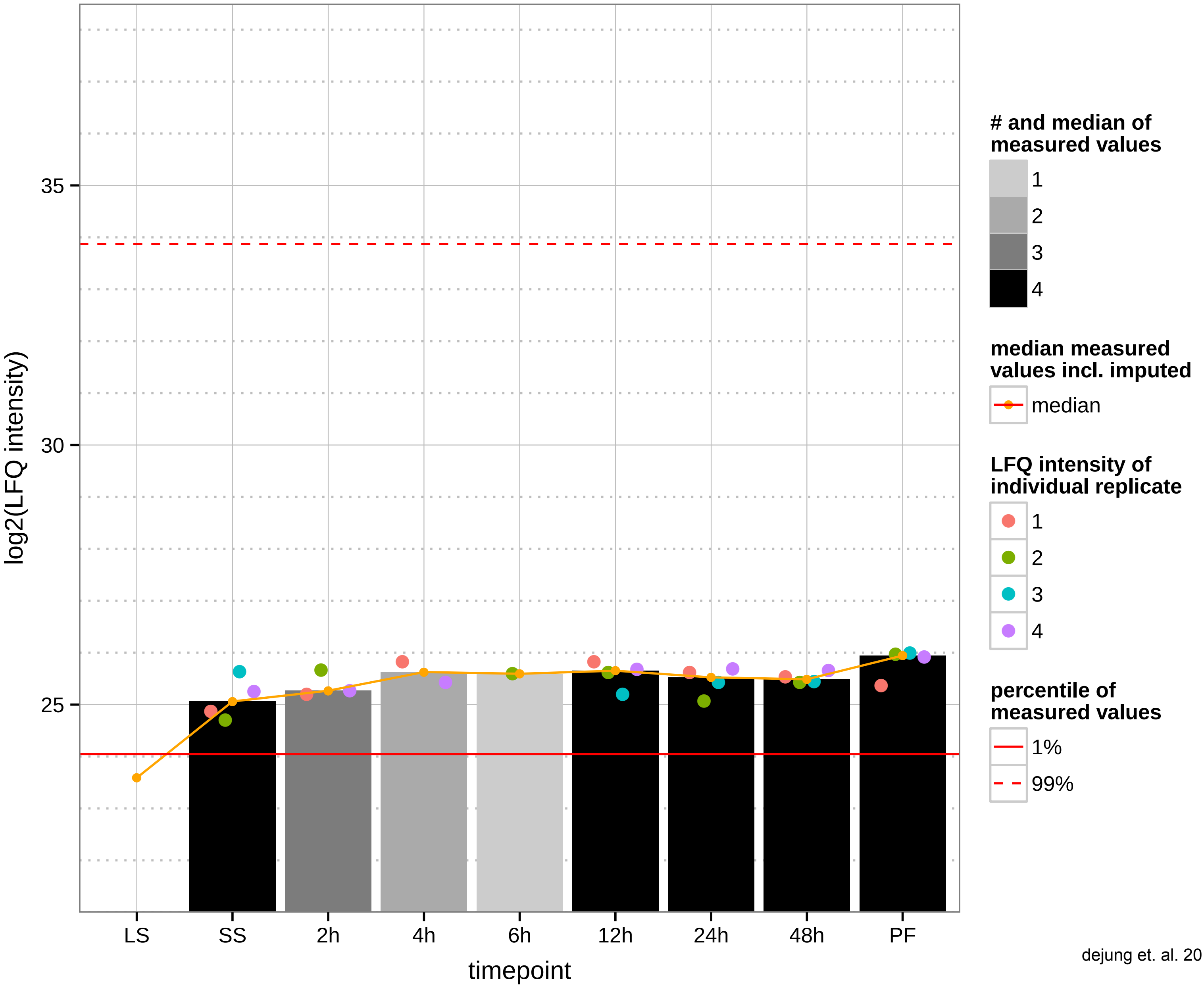
lipoic acid synthetase, mitochondrial precursor, putative
Tb927.10.15010
AGOF: 4 iron, 4 sulfur cluster binding, iron ion binding, lipoate synthase activity
AGOC: mitochondrion
AGOP: lipoate biosynthetic process
PGOF: 4 iron, 4 sulfur cluster binding, catalytic activity, iron–sulfur cluster binding, lipoate synthase activity
PGOC: null
PGOP: lipoate biosynthetic process





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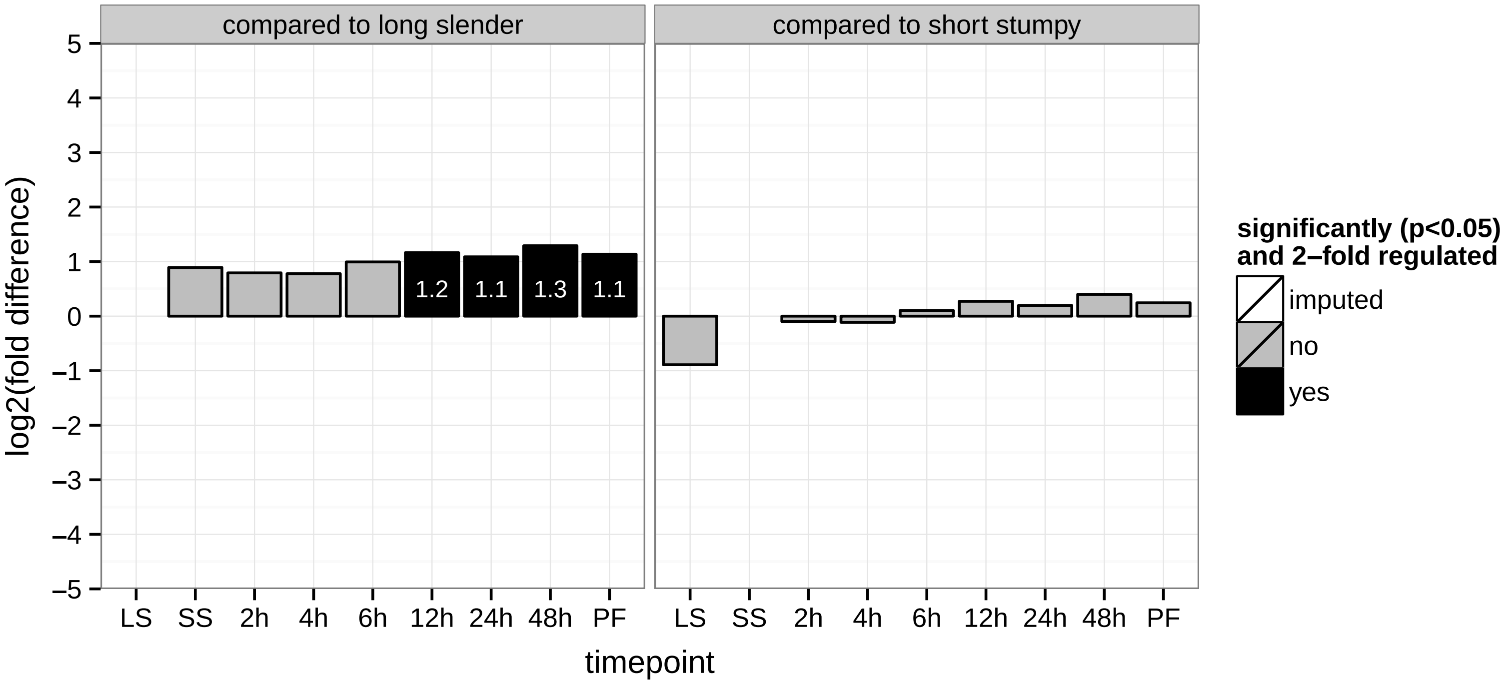
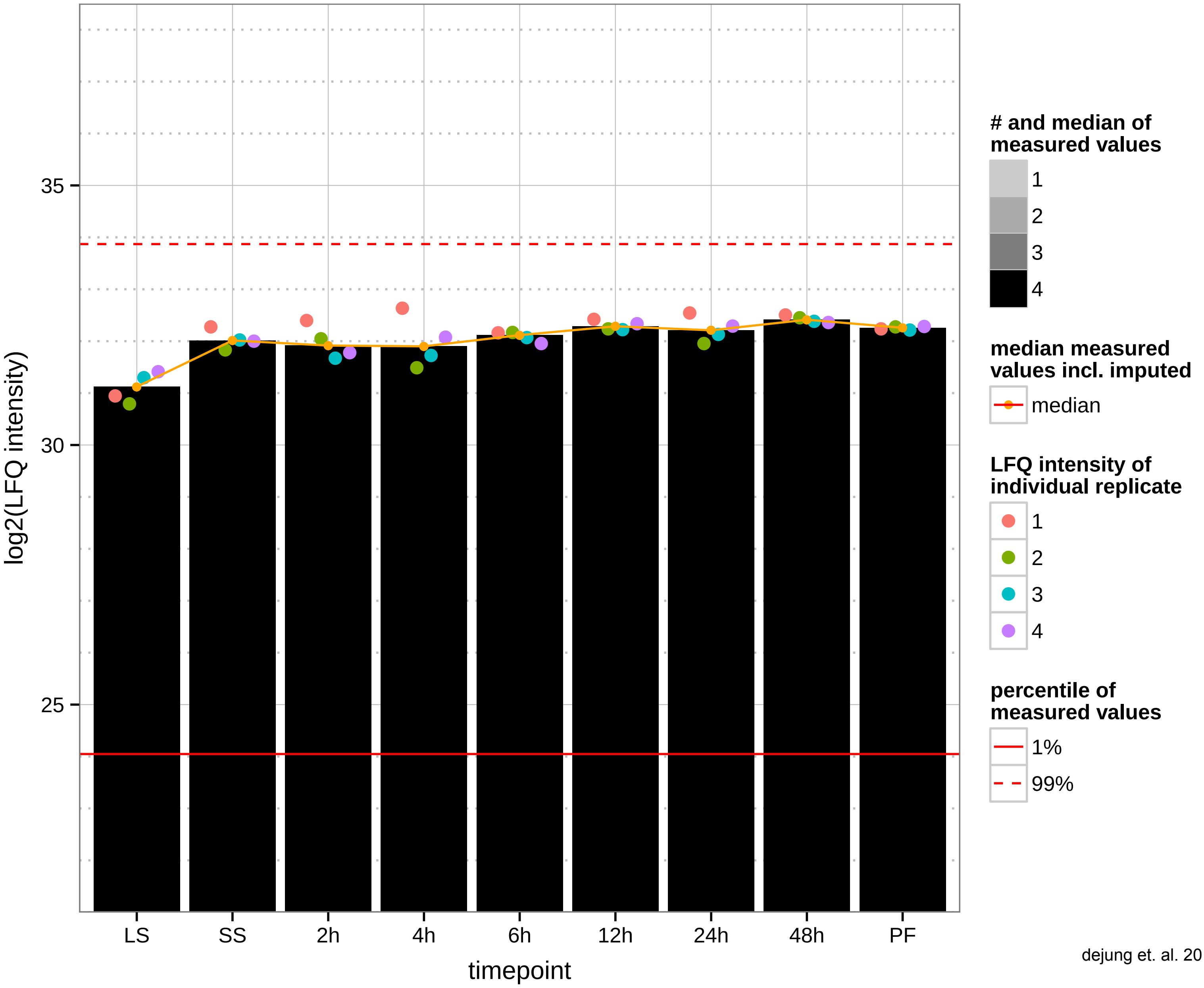
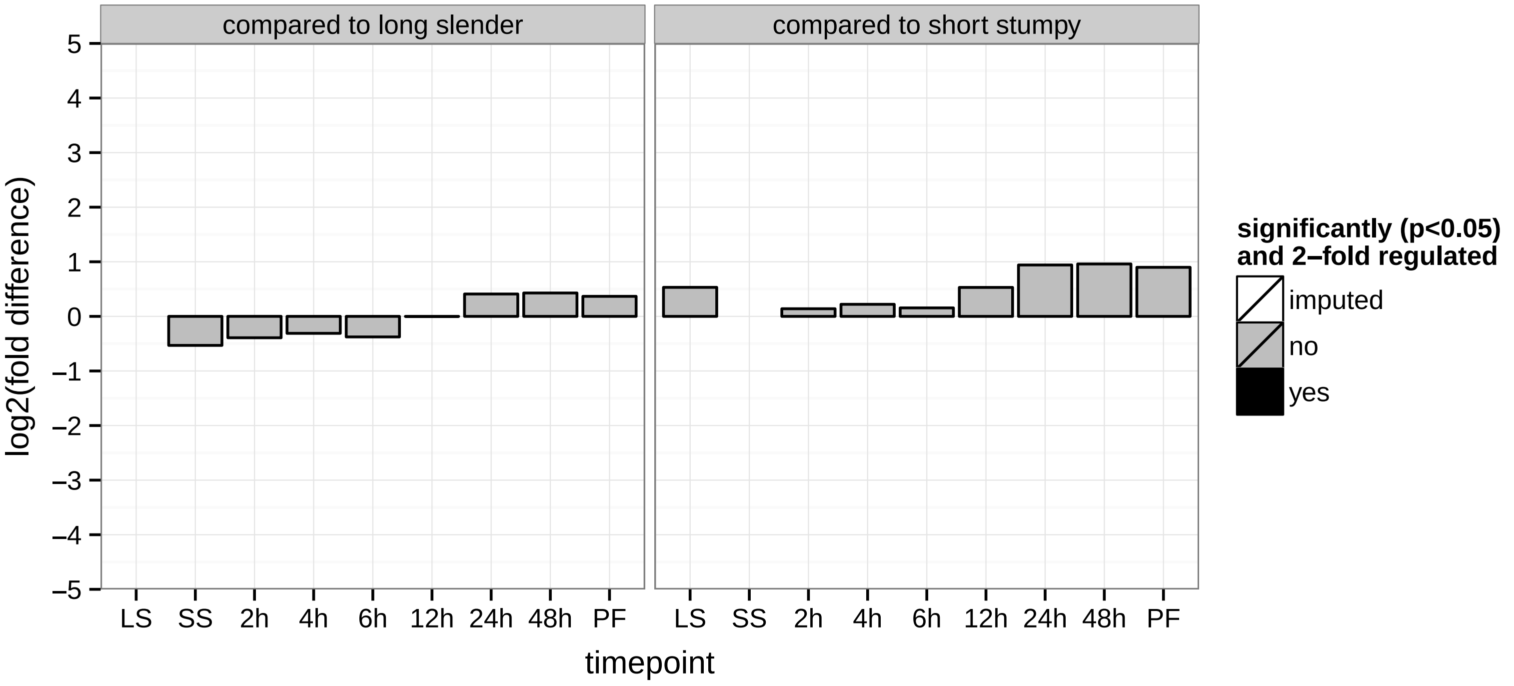
NOT1 (NOT1)
Tb927.10.1510
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

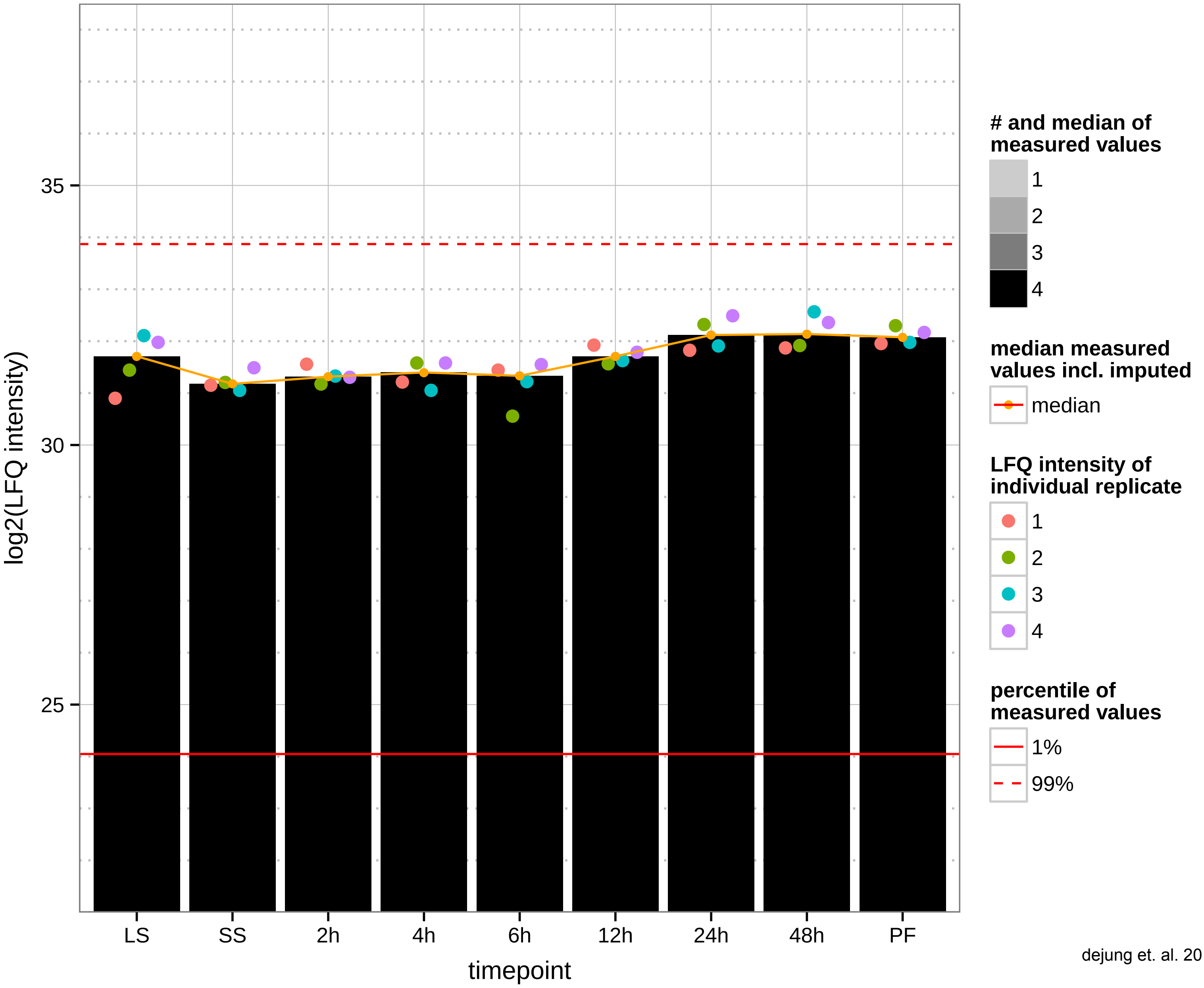




dejung et. al. 2015

40S ribosomal protein S13, putative
Tb927.2.5910;Tb927.10.15120
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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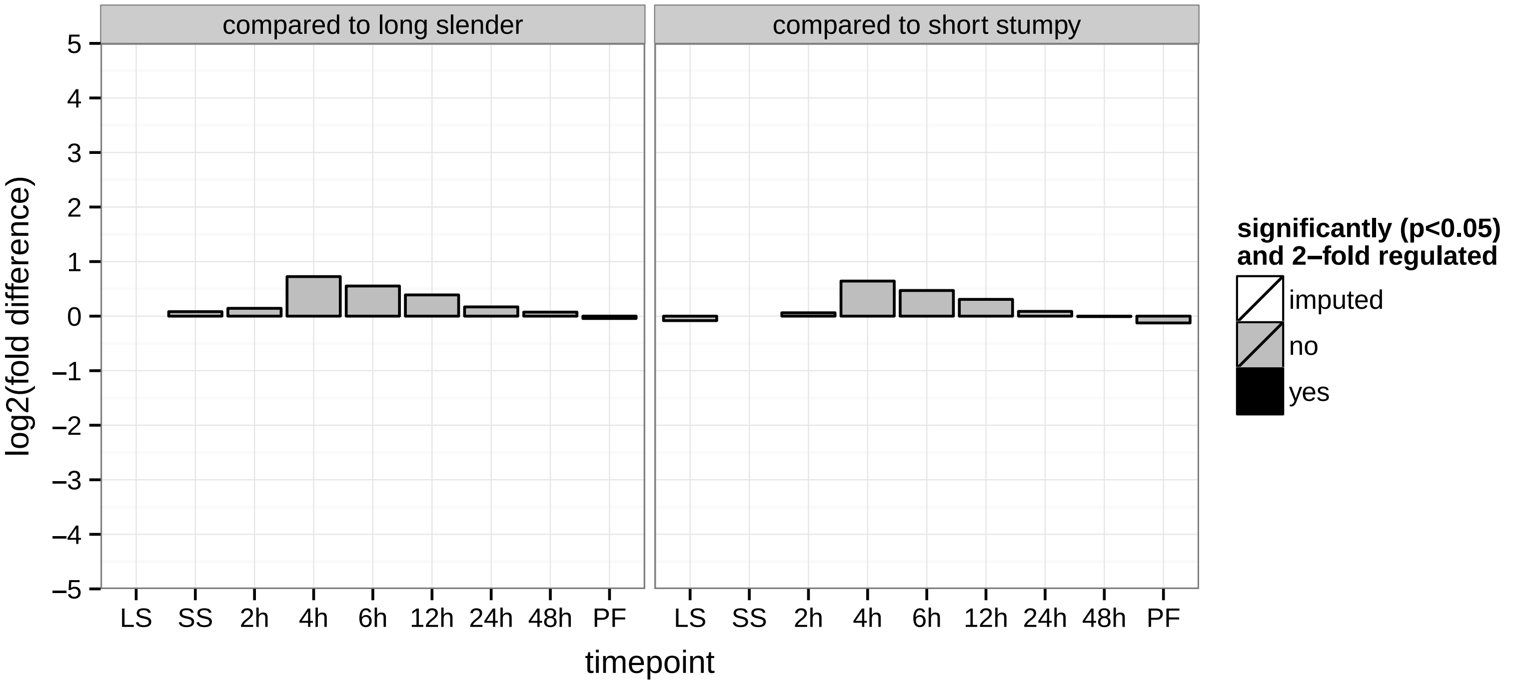
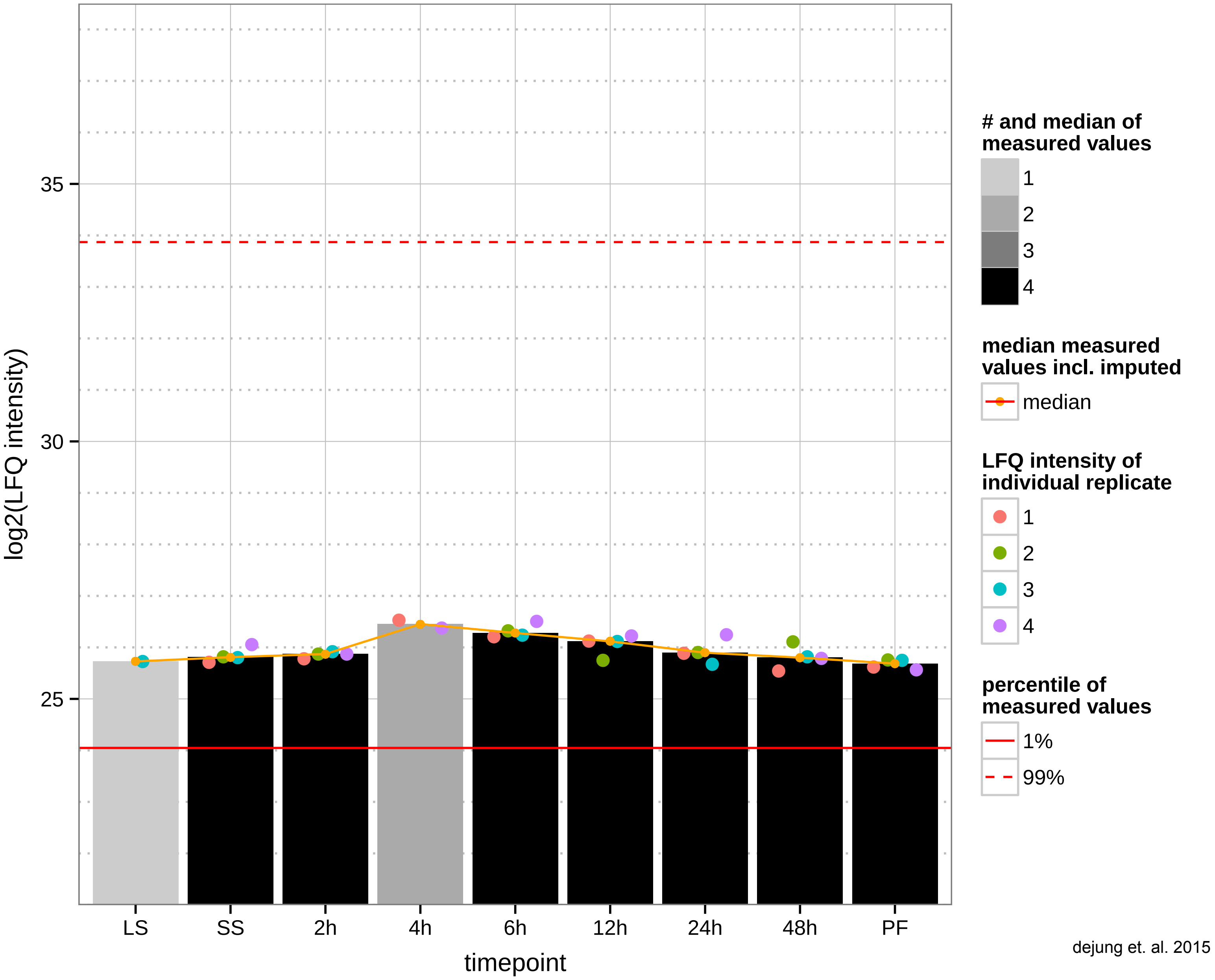
Vesicle–trafficking protein SEC22, putative, putative (SEC22)
Tb927.10.15130
AGOF: SNAP receptor activity
AGOC: integral to membrane
AGOP: vesicle targeting, vesicle–mediated transport
PGOF: null
PGOC: integral to membrane
PGOP: transport, vesicle–mediated transport





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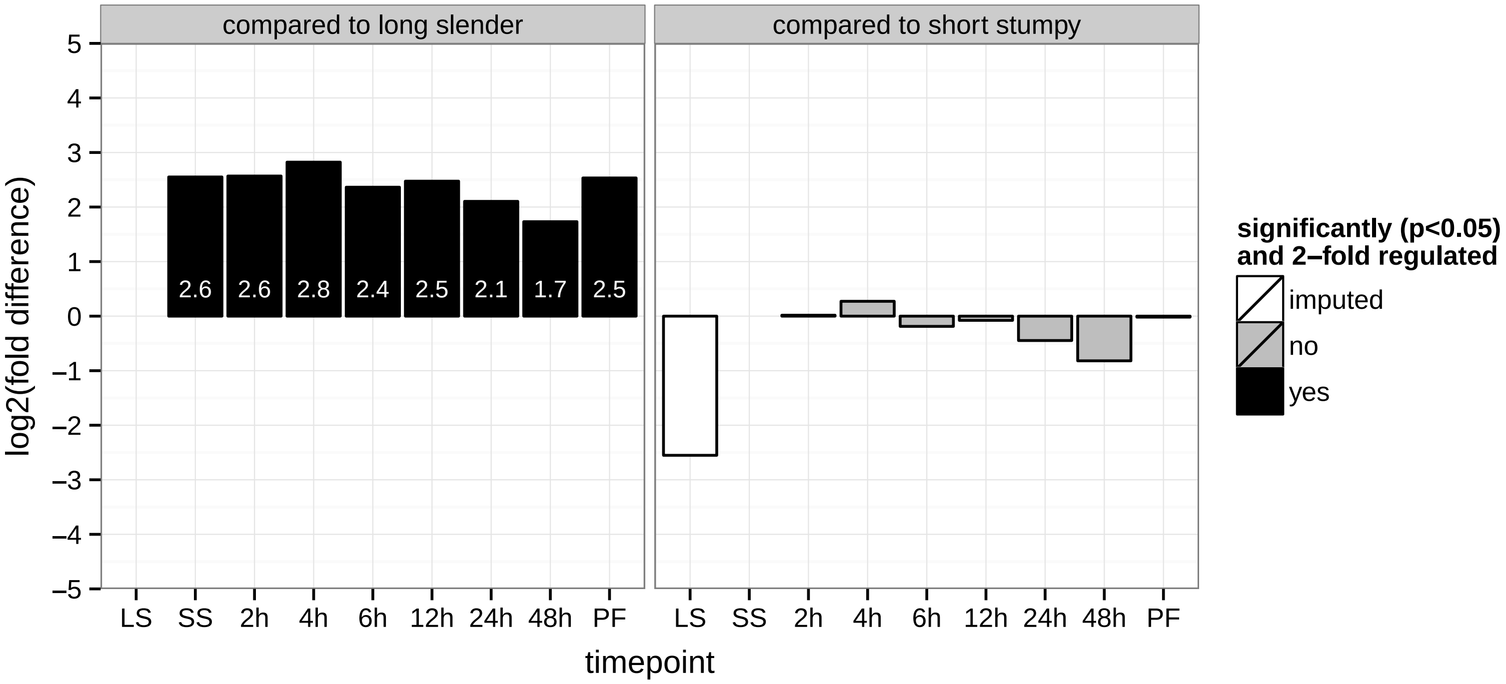
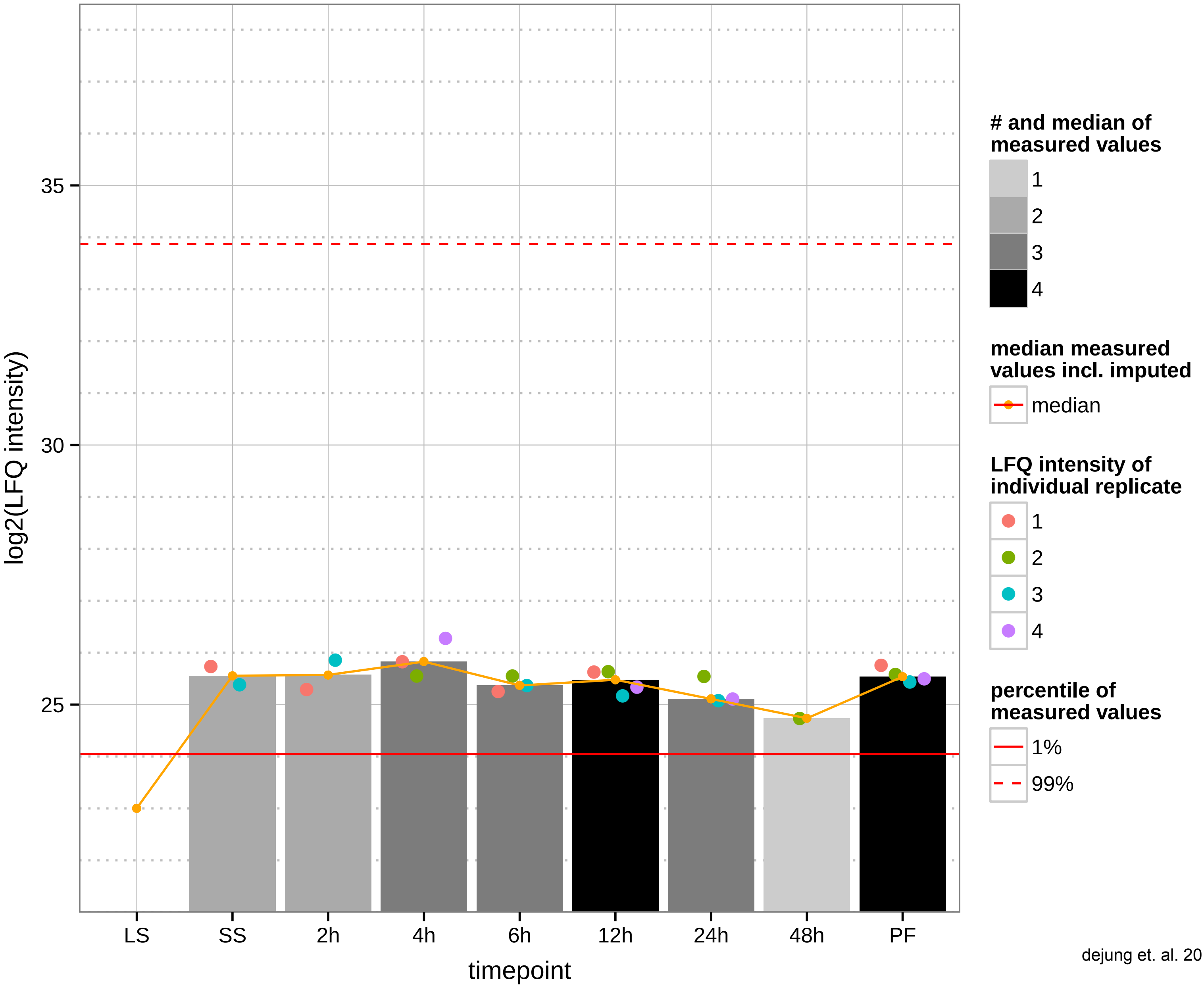
nuclear cap binding complex subunit CBP30 (CBP30)
Tb927.10.15210
AGOF: null
AGOC: mitochondrion, nuclear cap binding complex, nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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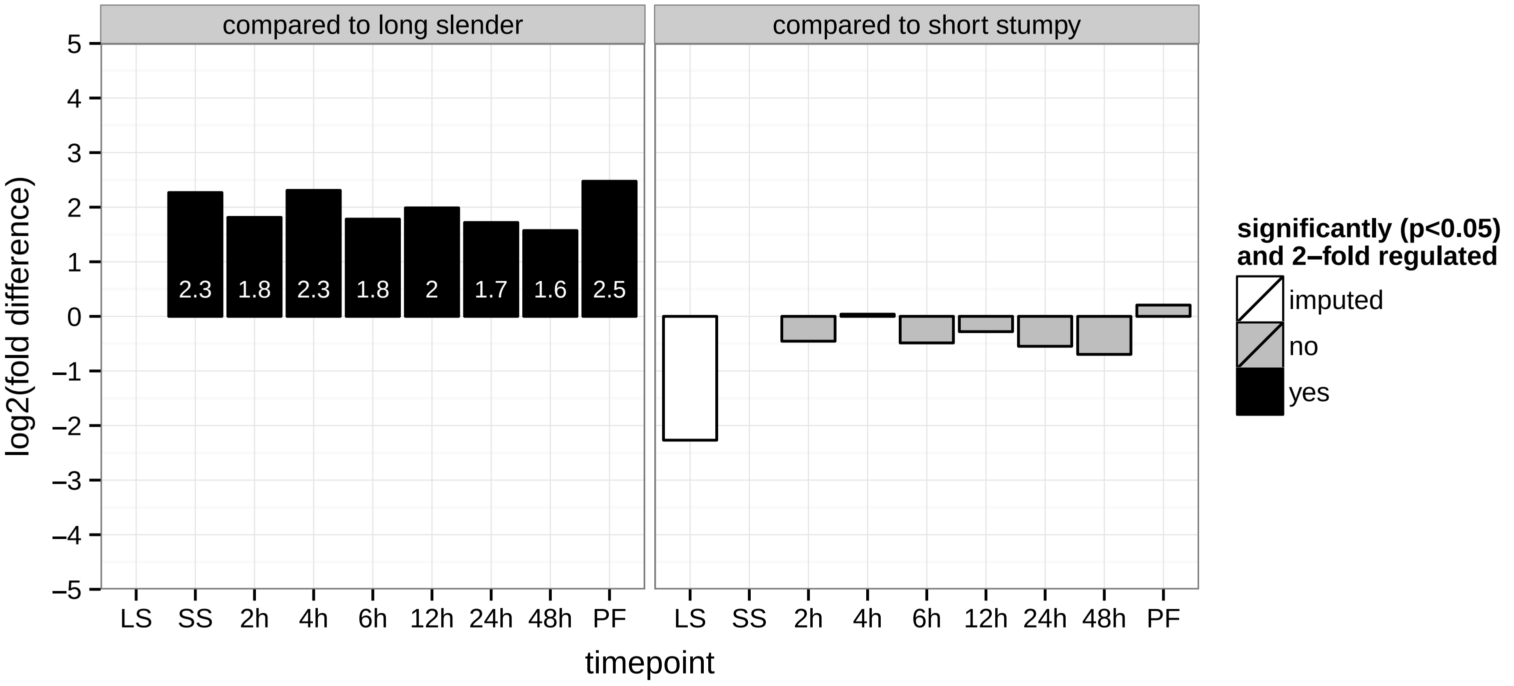
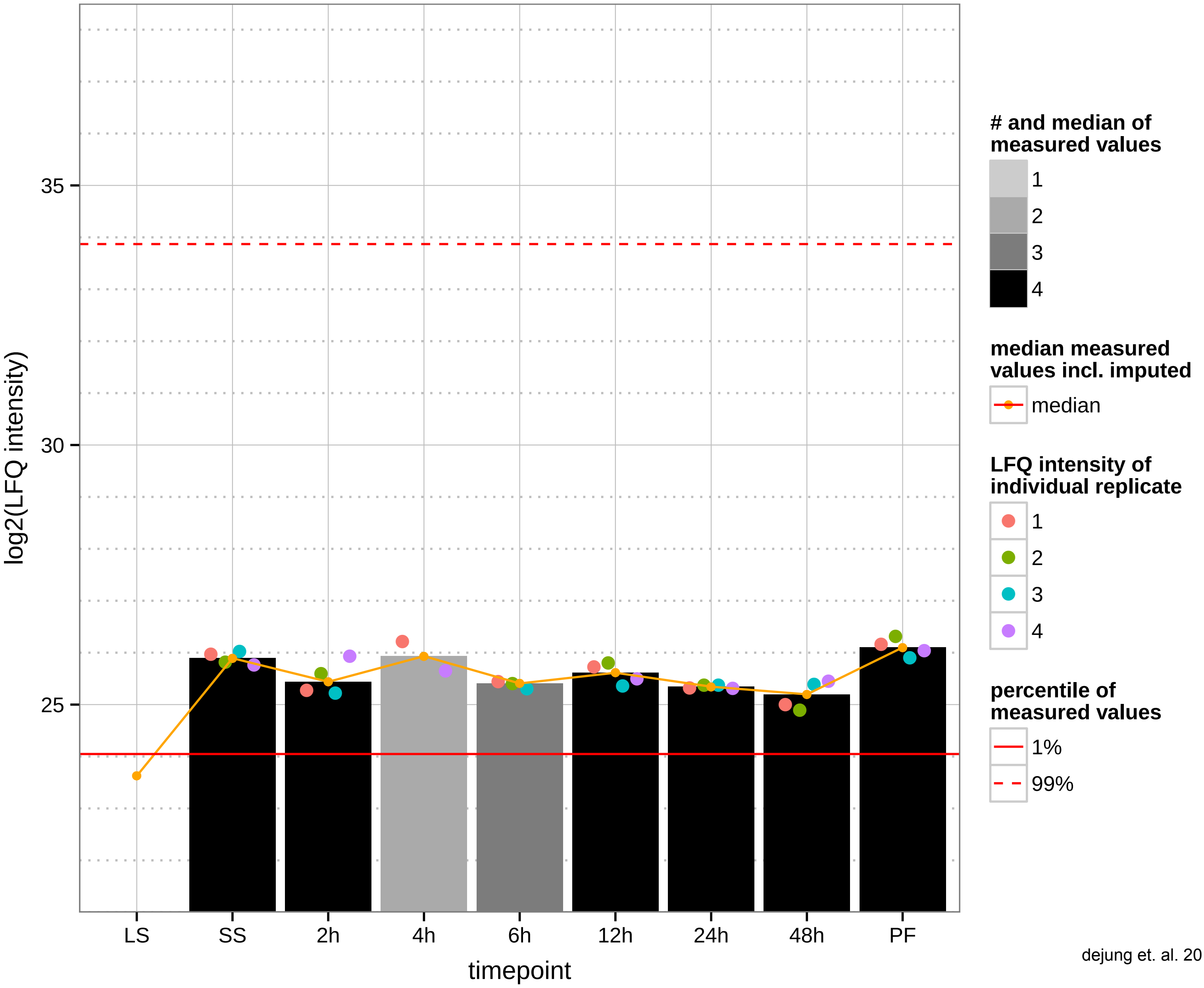
hypothetical protein, conserved
Tb927.10.15290
AGOF: null, ATP binding, protein kinase activity
AGOC: null
AGOP: null, protein phosphorylation
PGOF: null, ATP binding, protein kinase activity, transferase activity, transferring phosphorus−containing groups
PGOC: null
PGOP: null, protein phosphorylation





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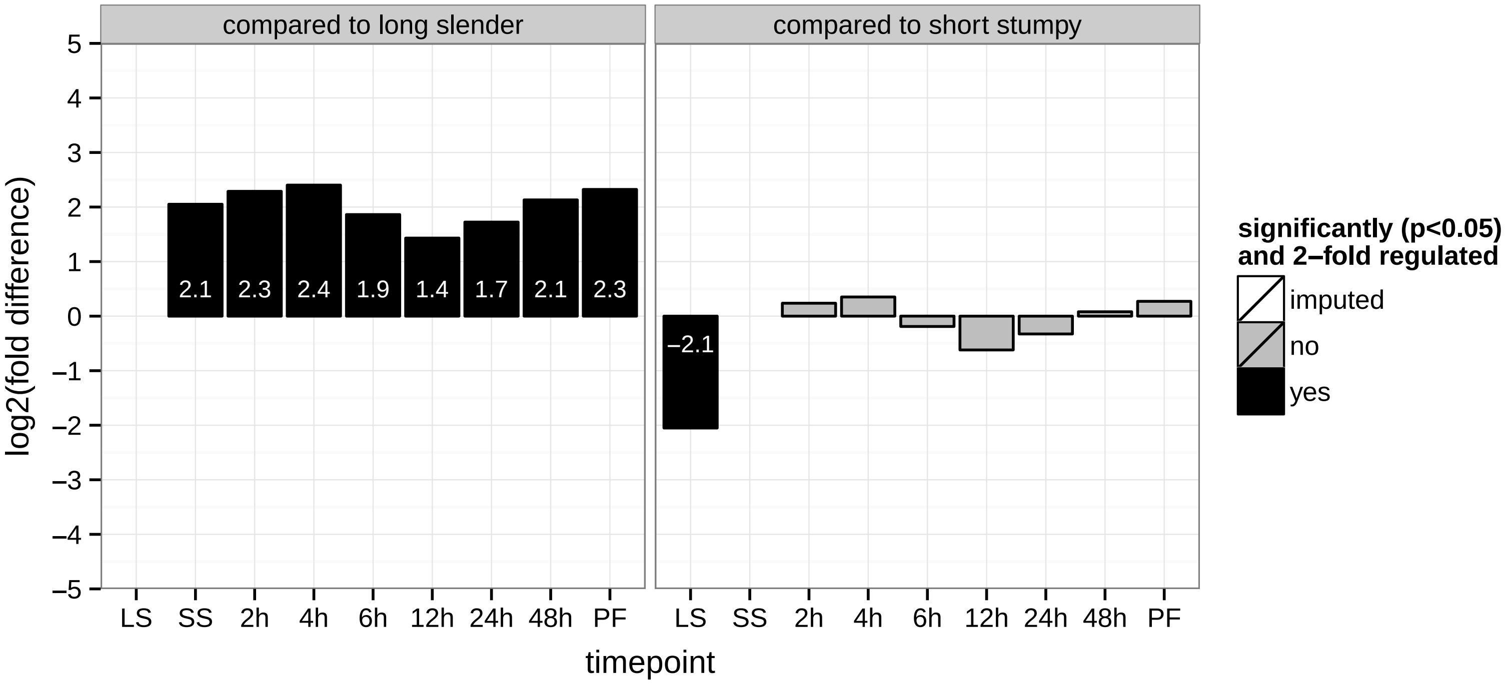
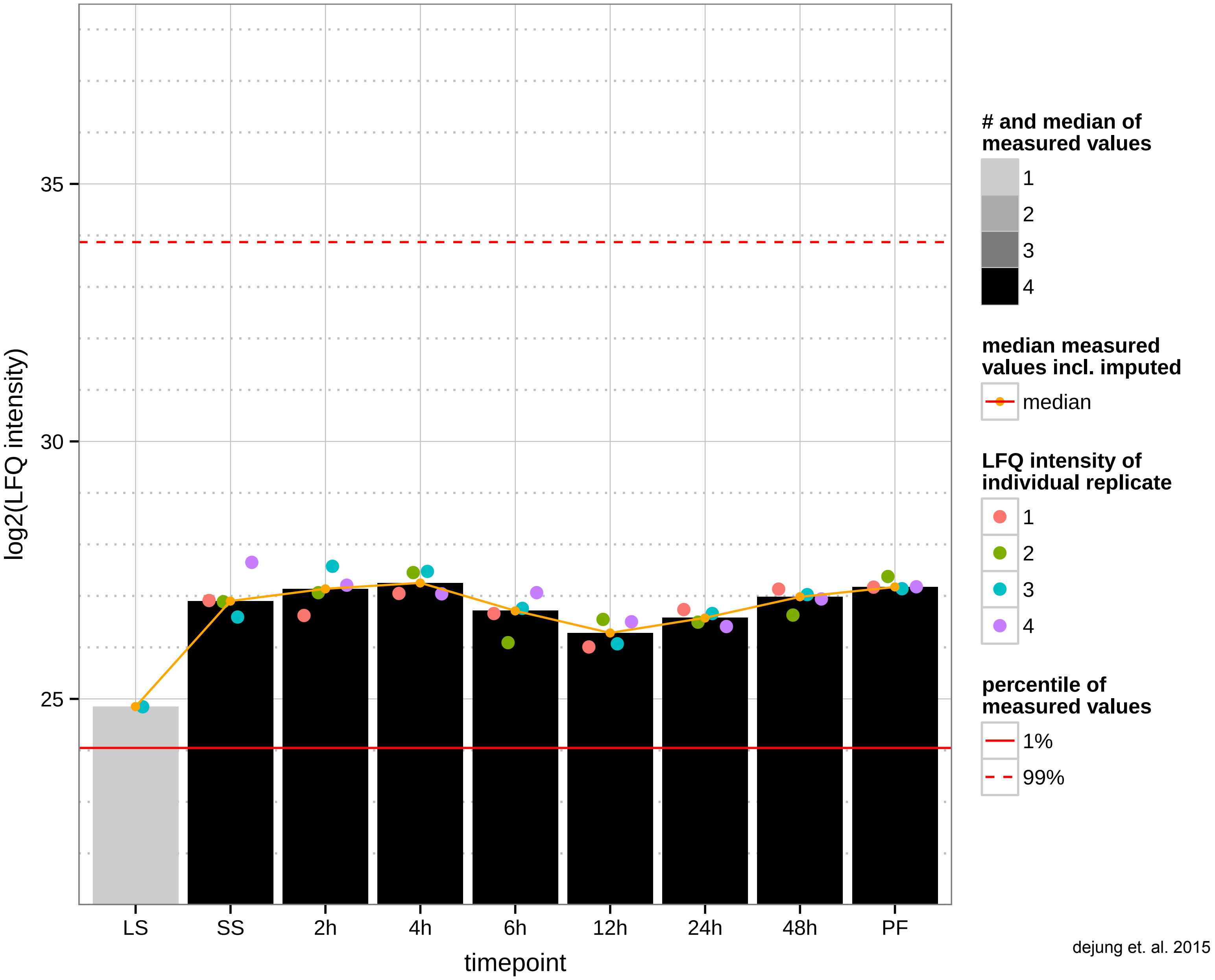
hypothetical protein, conserved
Tb927.10.15310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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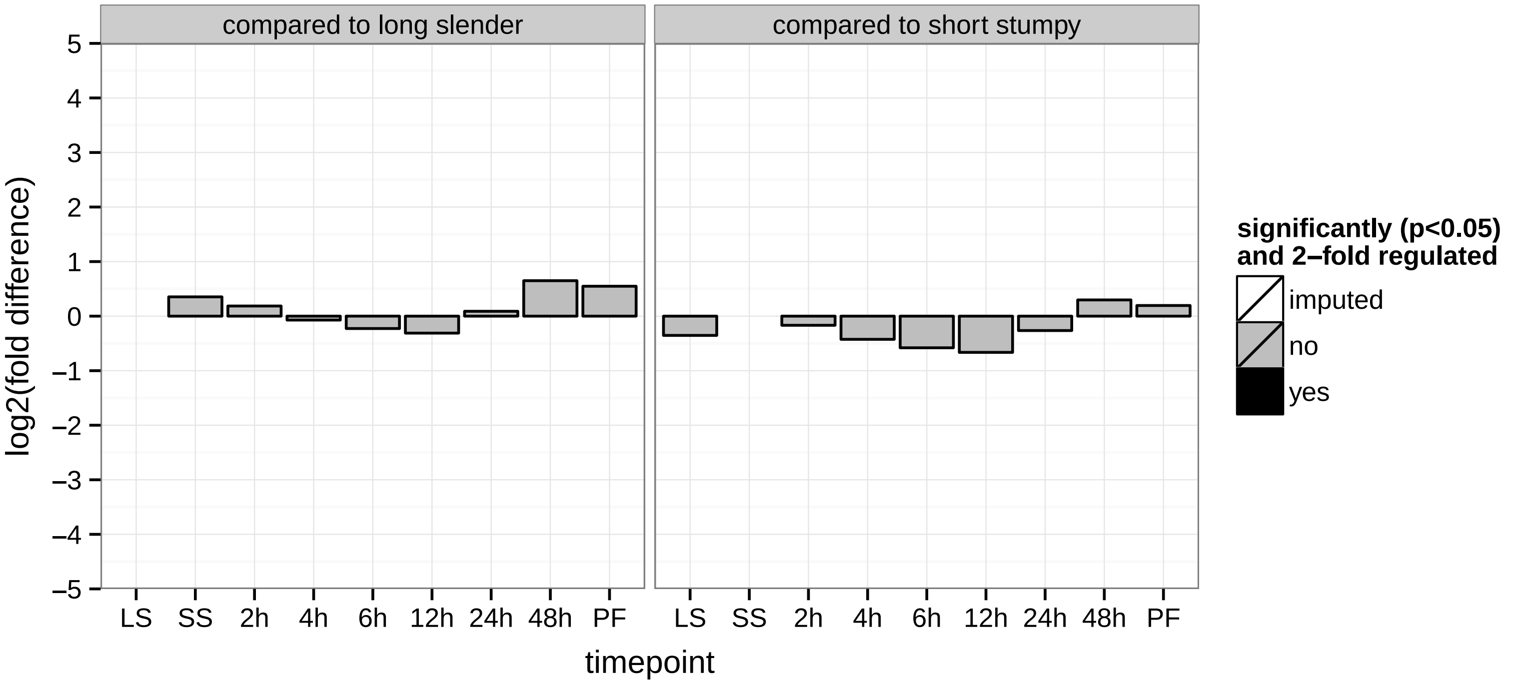
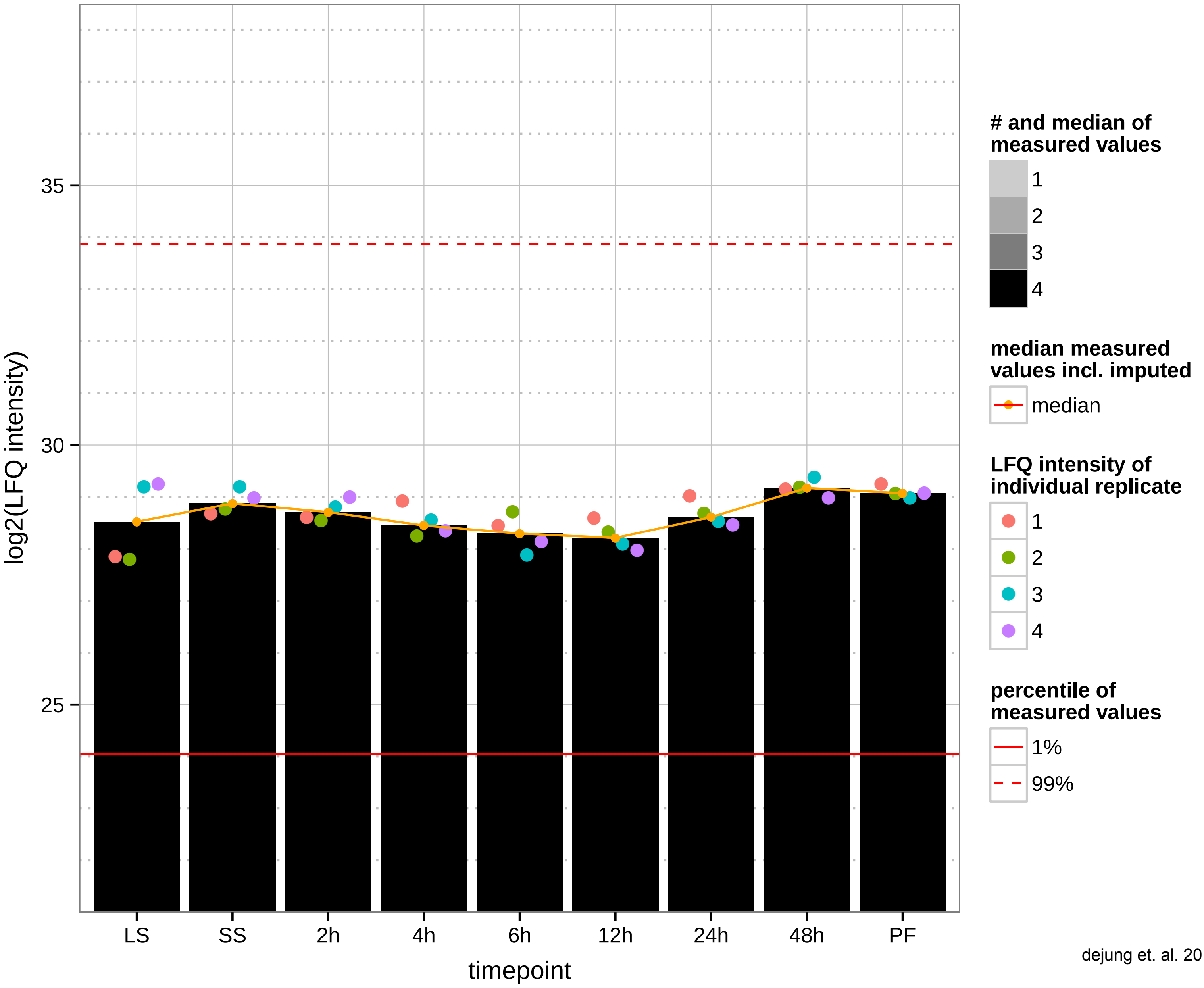
hypothetical protein, conserved
Tb927.10.15330;Tb11.v5.0348
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null, phosphate–containing compound metabolic process





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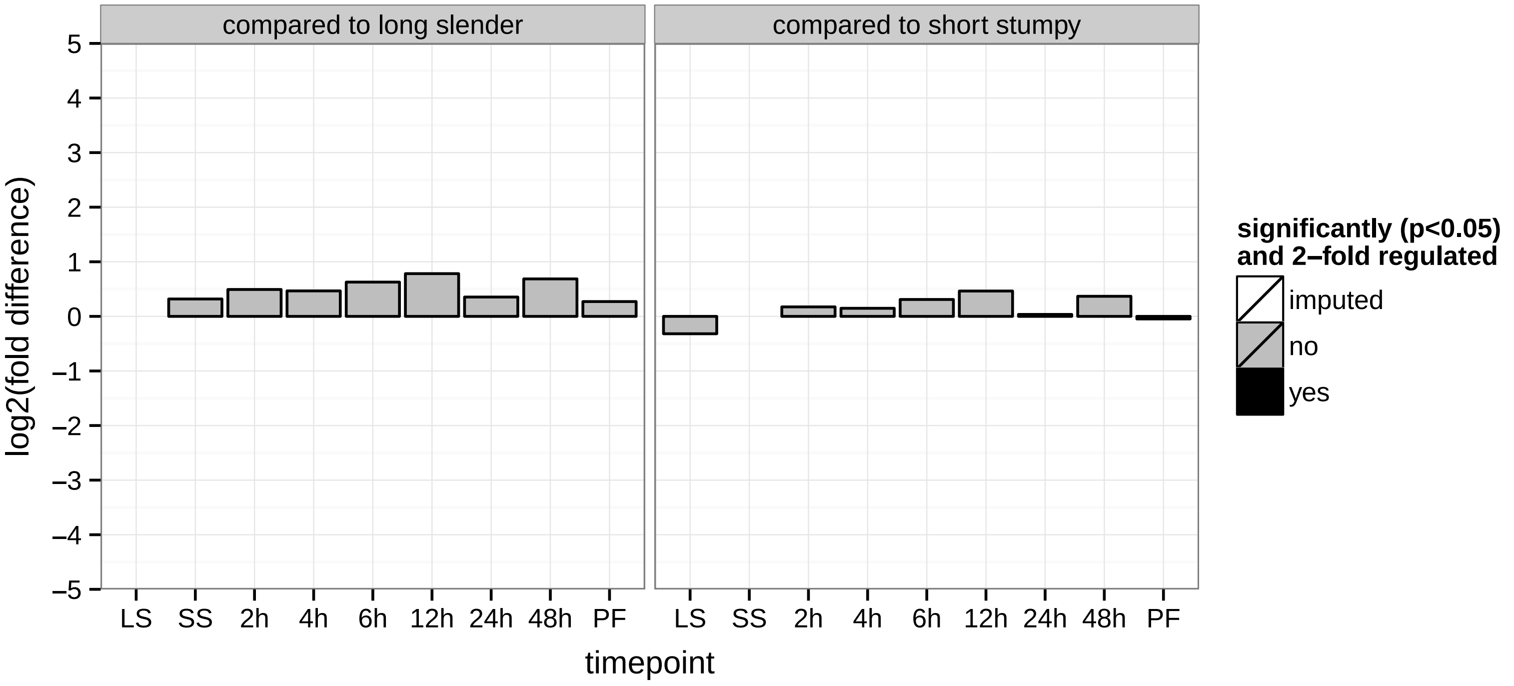
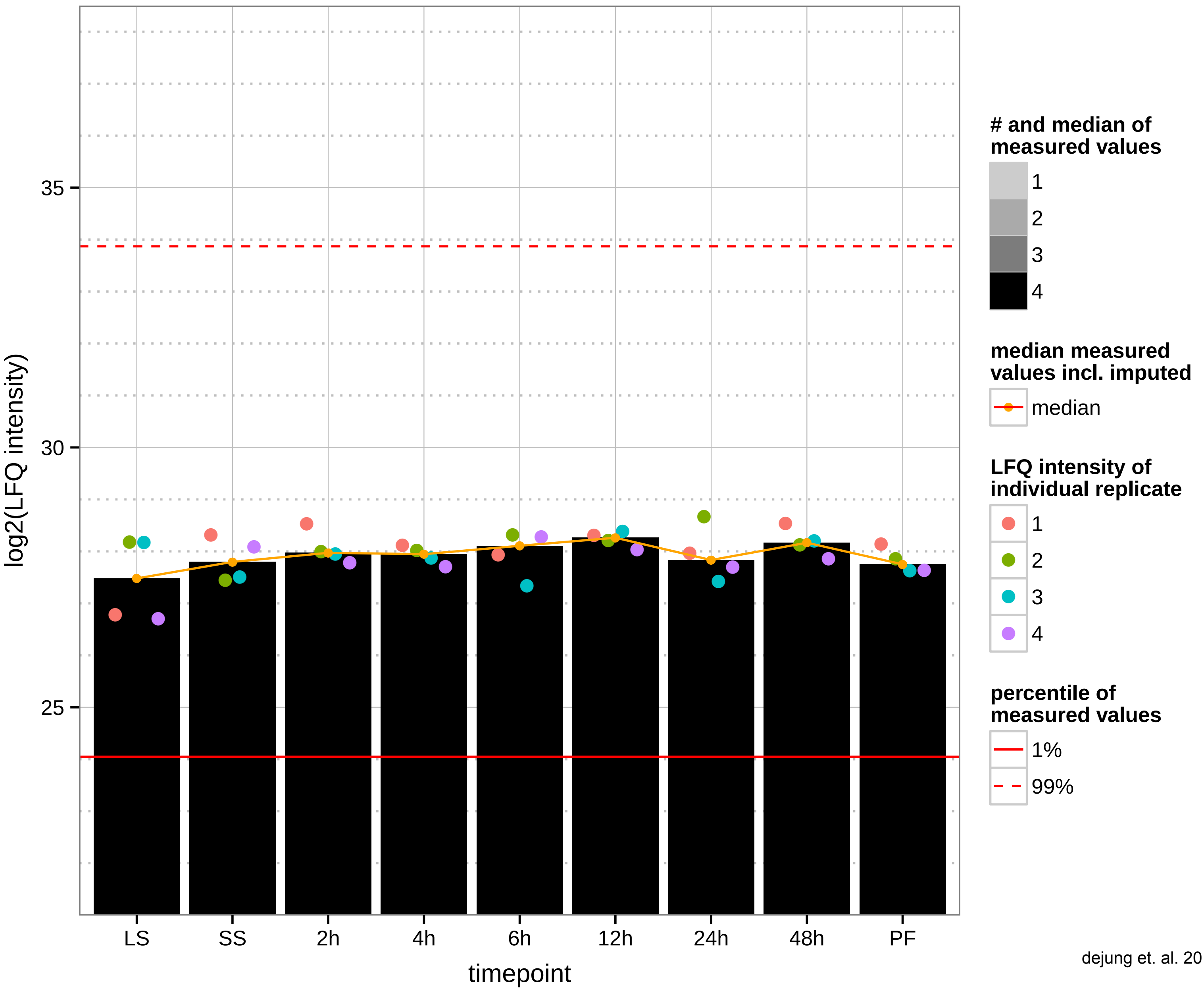
histone H3 variant, H3V (h3vaR)
Tb927.10.15350
AGOF: DNA binding
AGOC: chromosome, telomeric region, nucleosome, nucleus
AGOP: chromosome organization, nucleosome assembly, termination of RNA polymerase II transcription
PGOF: DNA binding
PGOC: nucleosome
PGOP: nucleosome assembly





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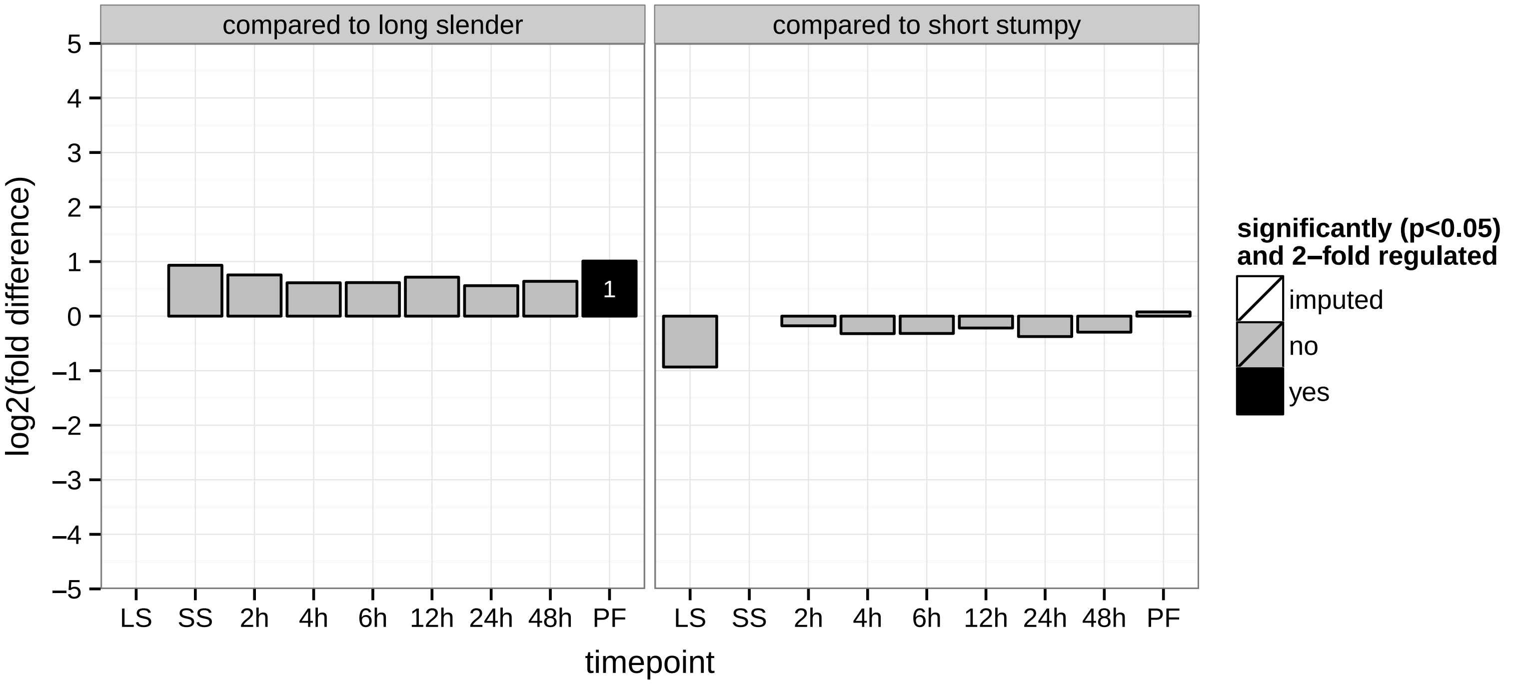
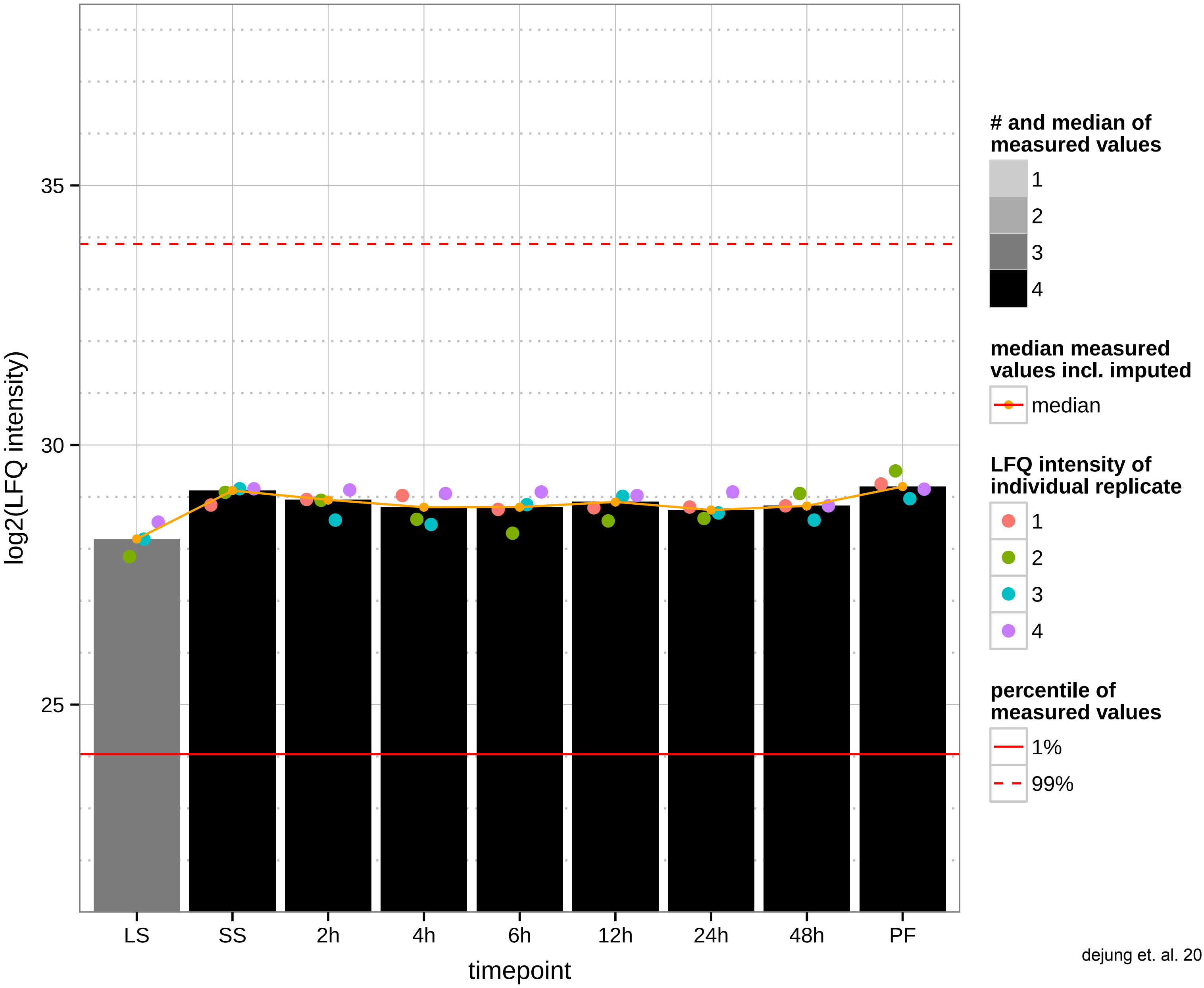
hypothetical protein, conserved
Tb927.10.15360
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: ATP binding, ATP−dependent helicase activity, RNA binding, nucleic acid binding
PGOC: null
PGOP: RNA processing





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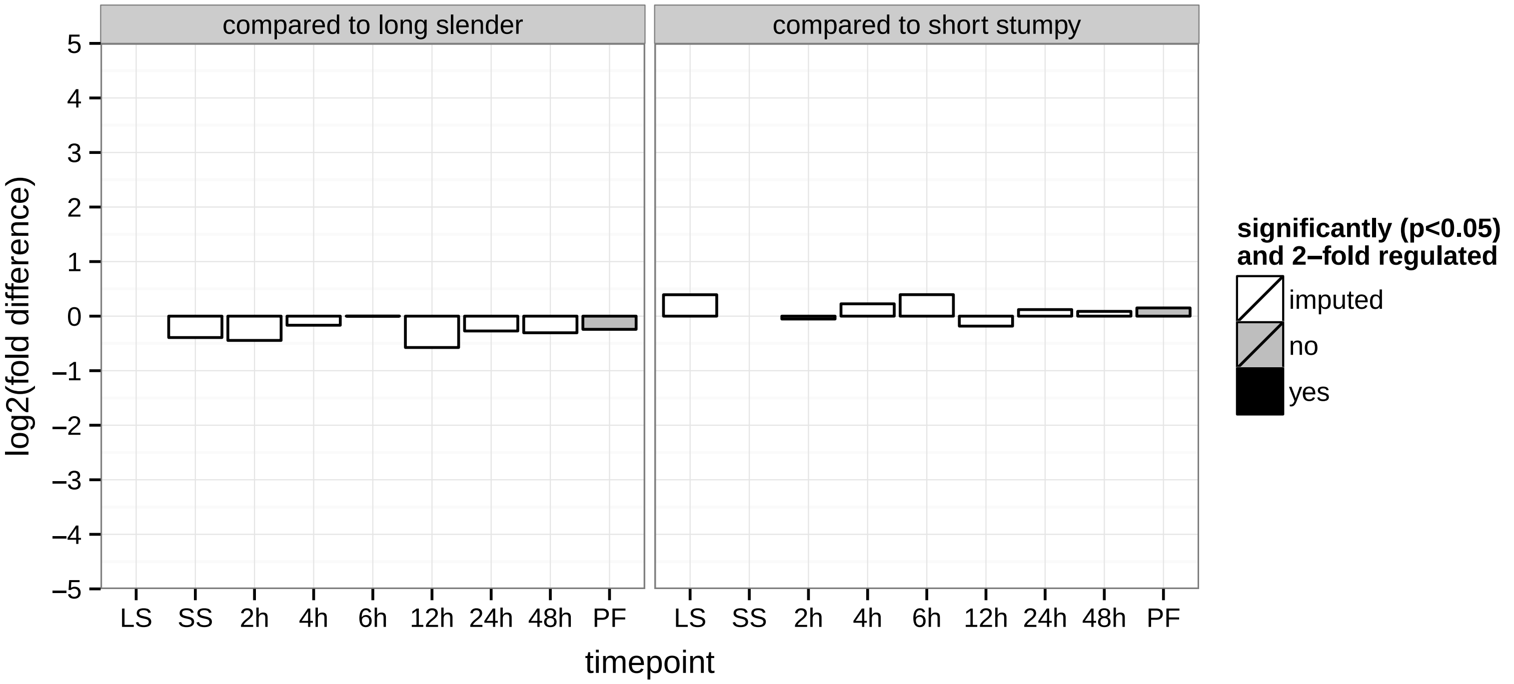
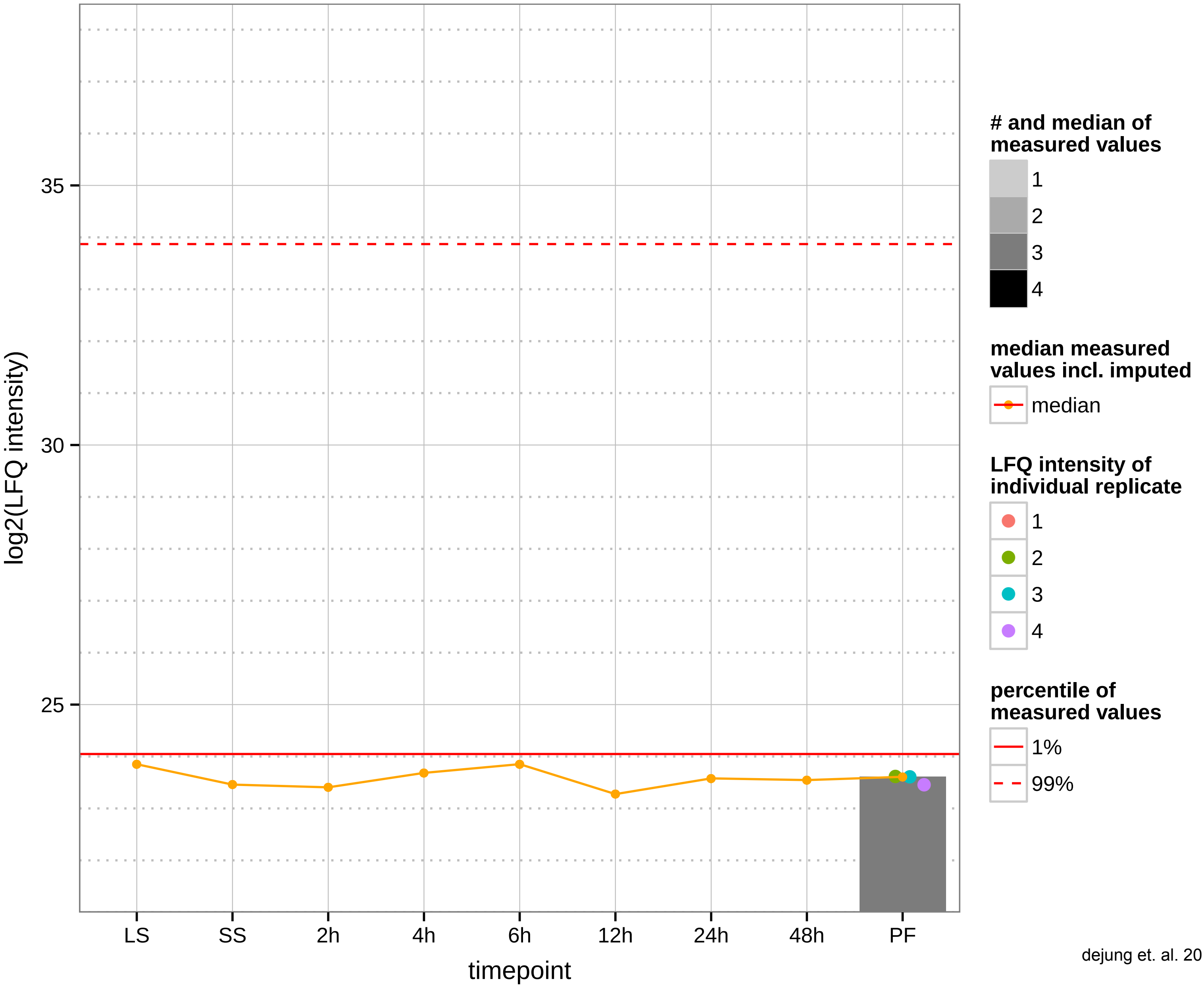
kinesin, putative, hypothetical protein, conserved
Tb927.10.15400;Tb11.v5.0849
AGOF: null, ATP binding, microtubule motor activity, motor activity
AGOC: null, kinesin complex, microtubule associated complex
AGOP: null, microtubule–based movement
PGOF: null, ATP binding, microtubule motor activity
PGOC: null
PGOP: null, microtubule–based movement





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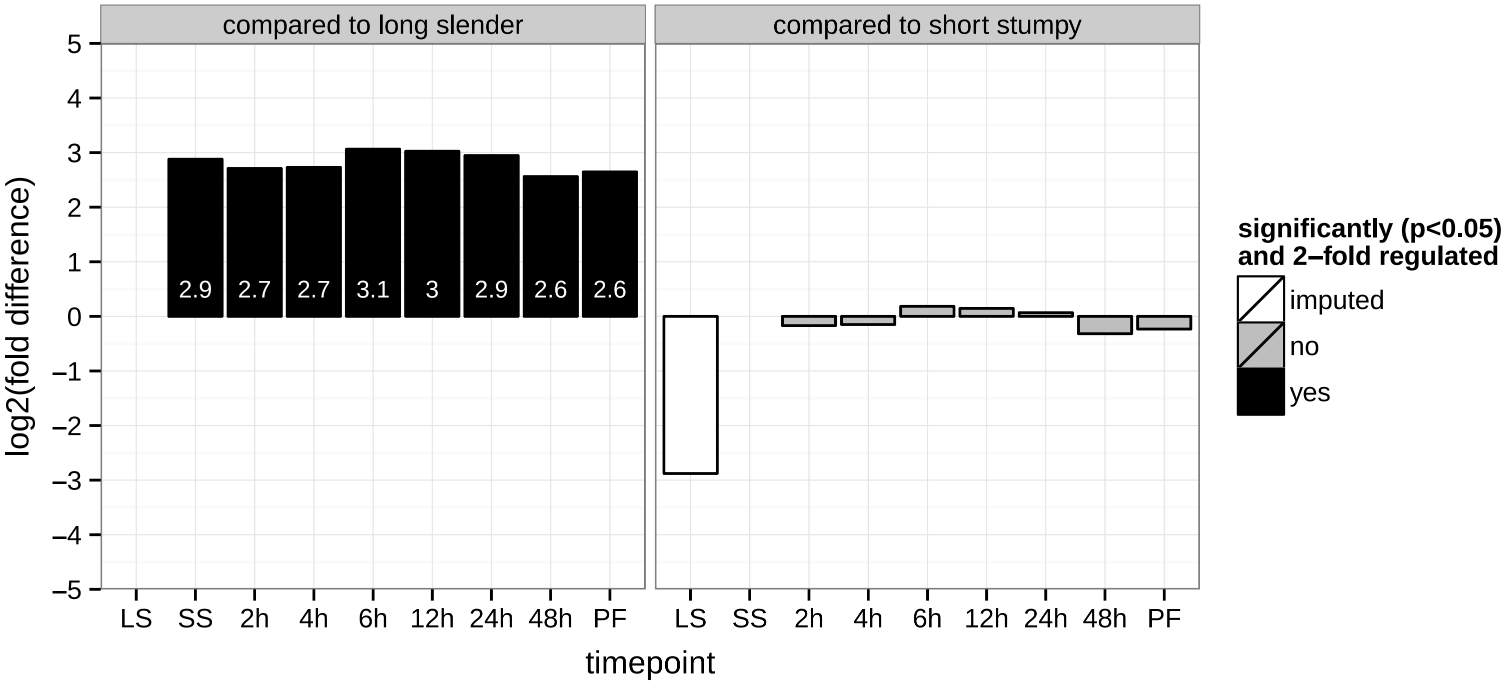
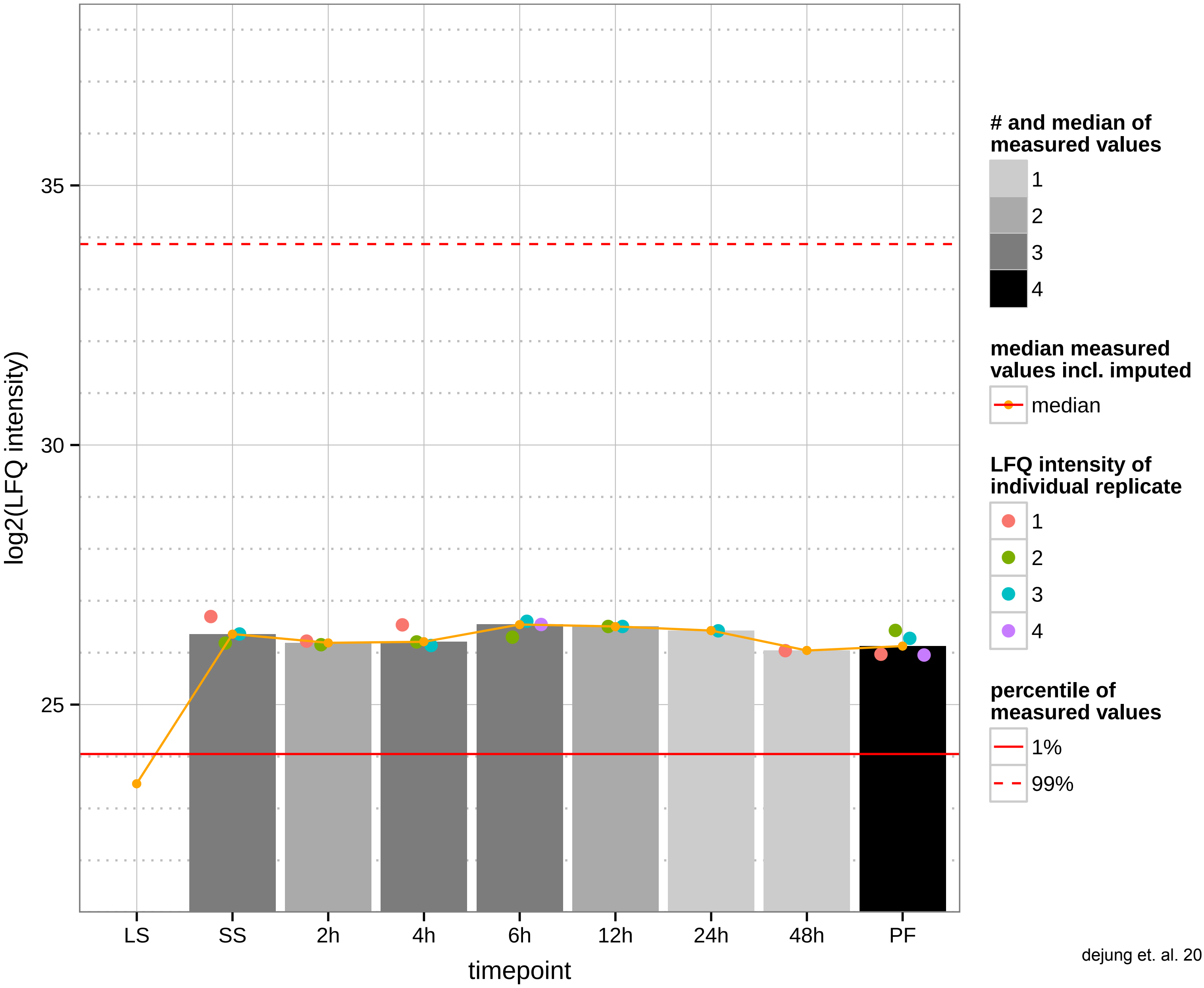
hypothetical protein, conserved
Tb927.10.15470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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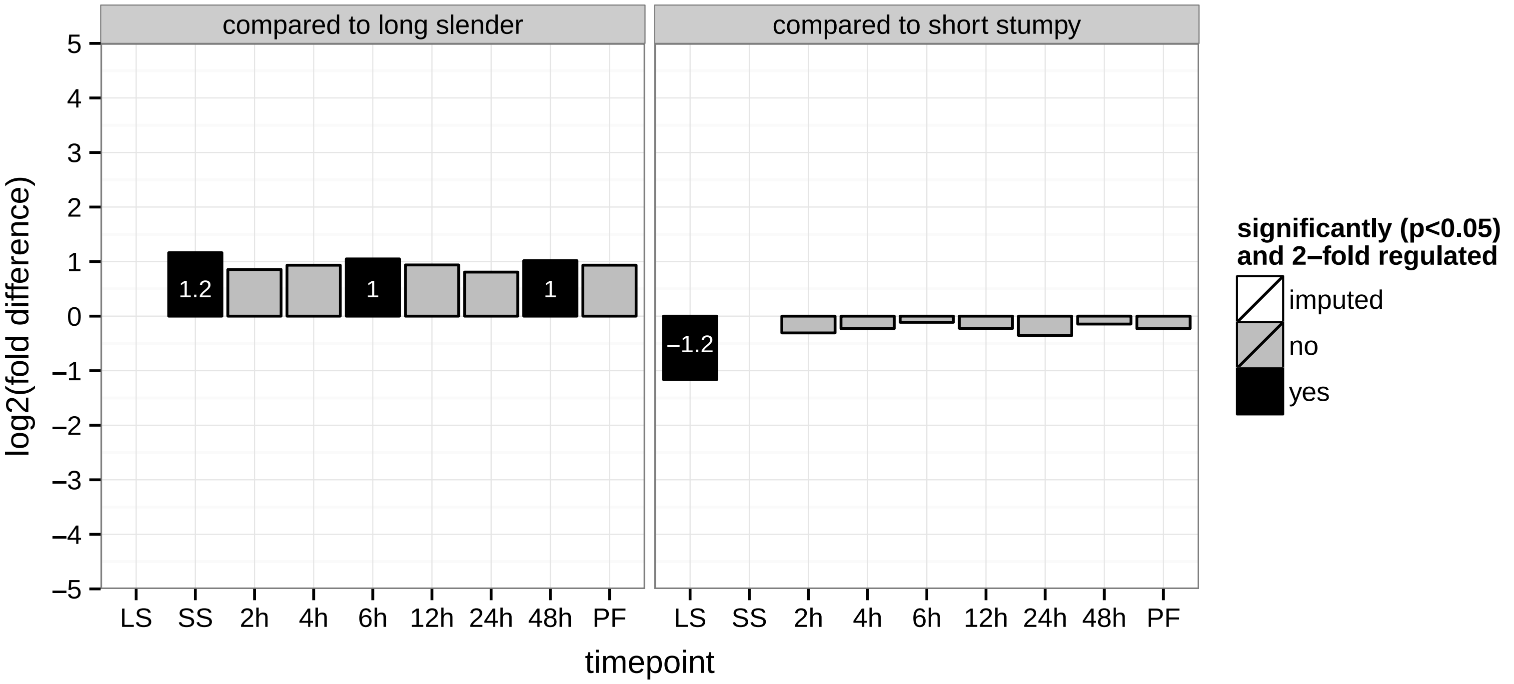
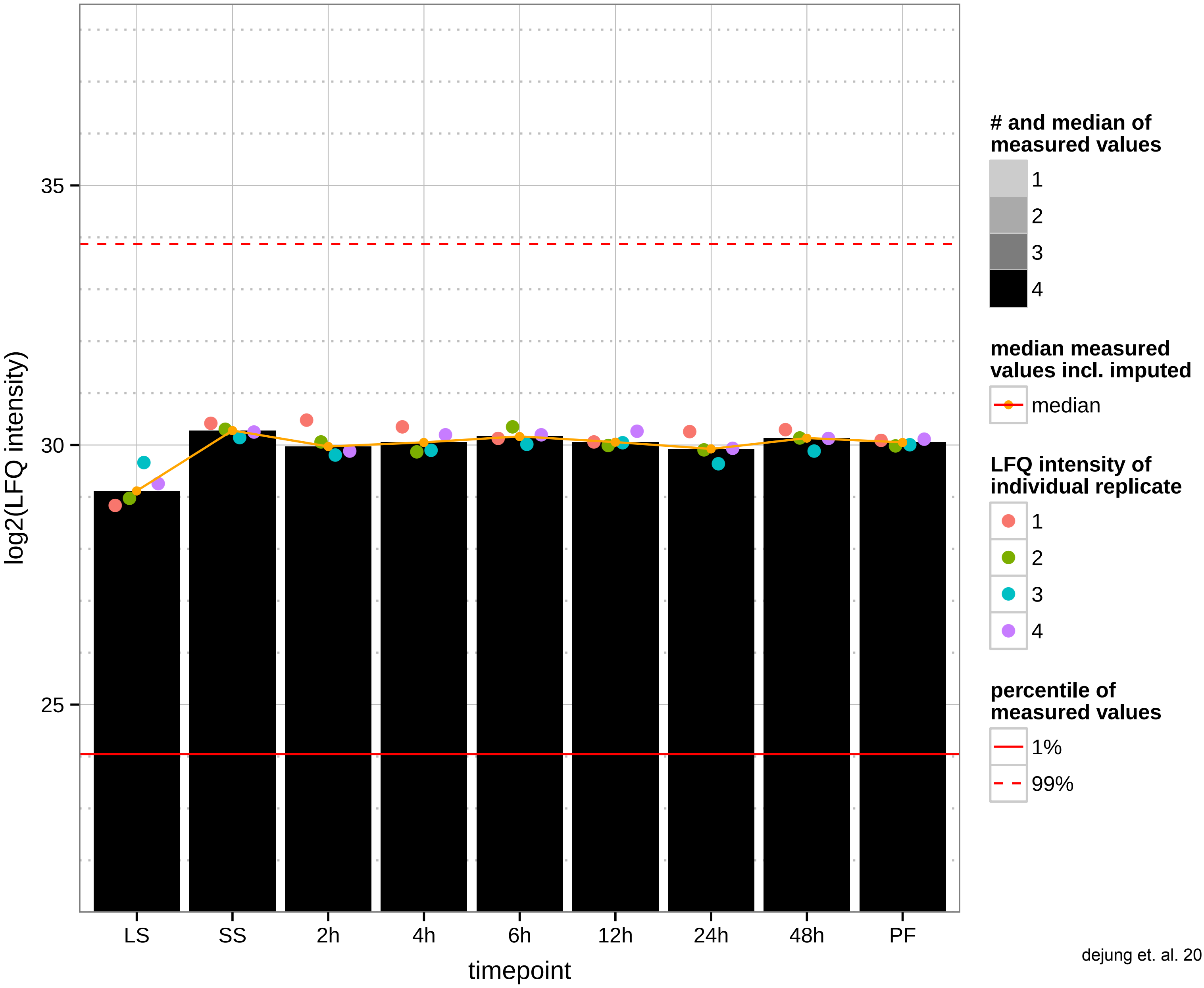
proteasome regulatory non–ATP–ase subunit 5, 19S proteasome regulatory subunit 5 (RPN5)
Tb927.10.1550
AGOF: endopeptidase activity
AGOC: proteasome regulatory particle
AGOP: ubiquitin–dependent protein catabolic process
PGOF: protein binding
PGOC: null
PGOP: null





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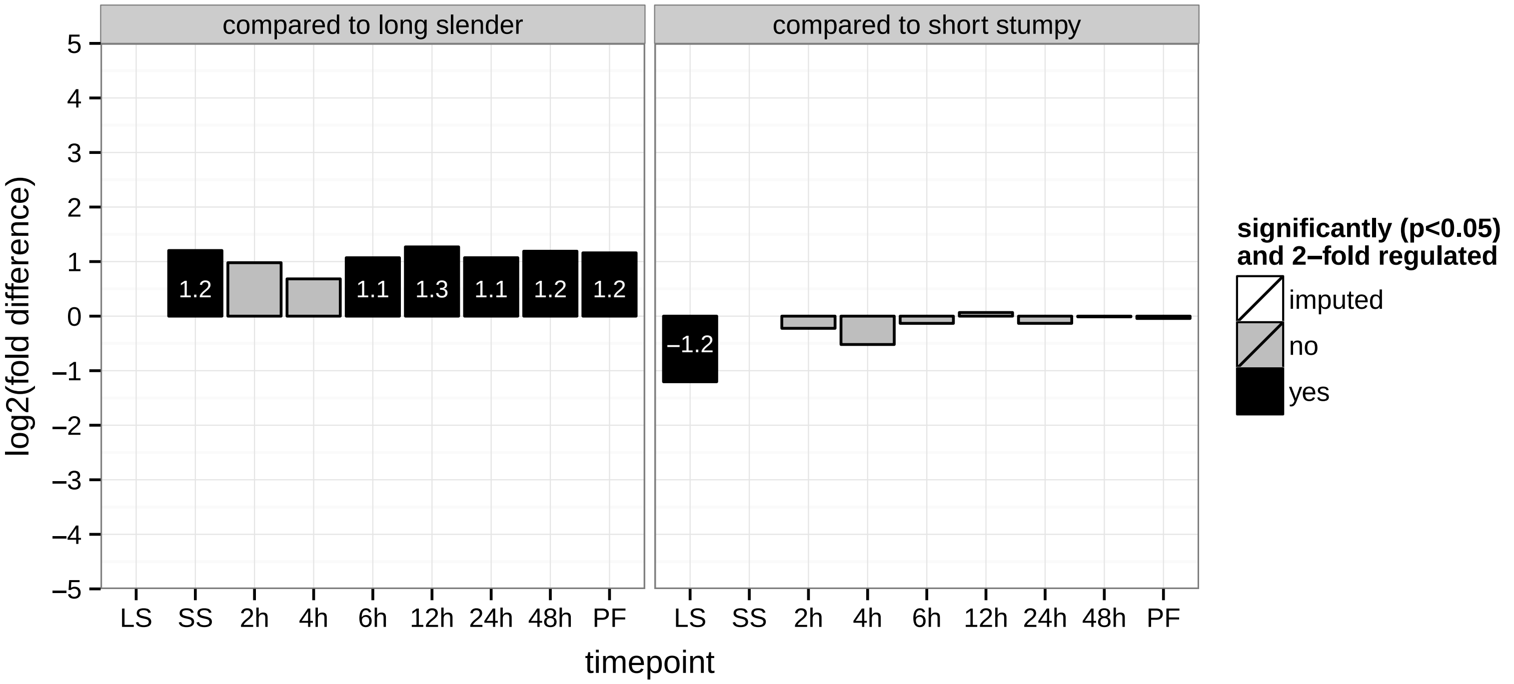
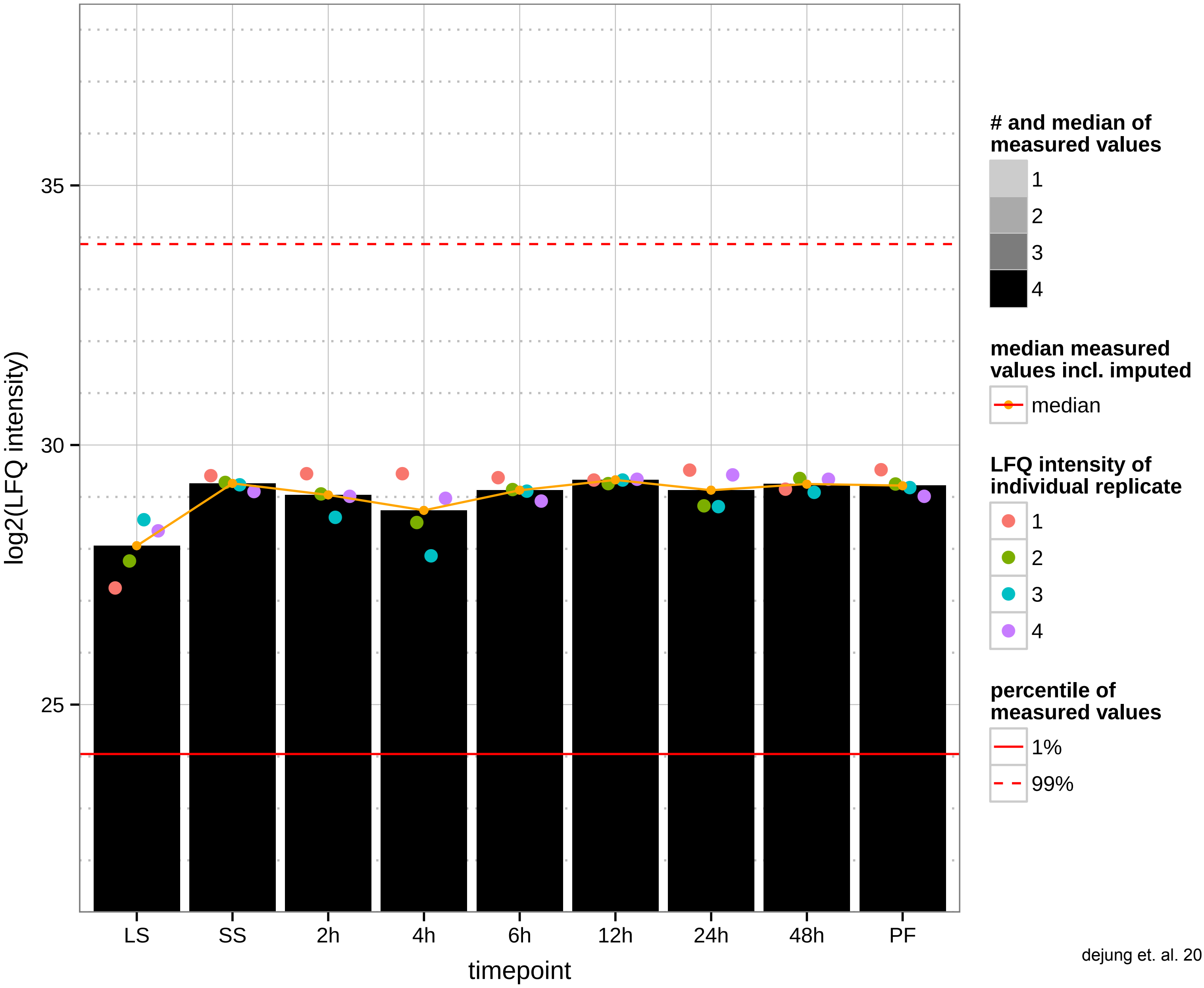
signal recognition particle protein, putative
Tb927.10.15520
AGOF: 7S RNA binding
AGOC: signal recognition particle
AGOP: SRP−dependent cotranslational protein targeting to membrane
PGOF: 7S RNA binding
PGOC: signal recognition particle
PGOP: SRP−dependent cotranslational protein targeting to membrane





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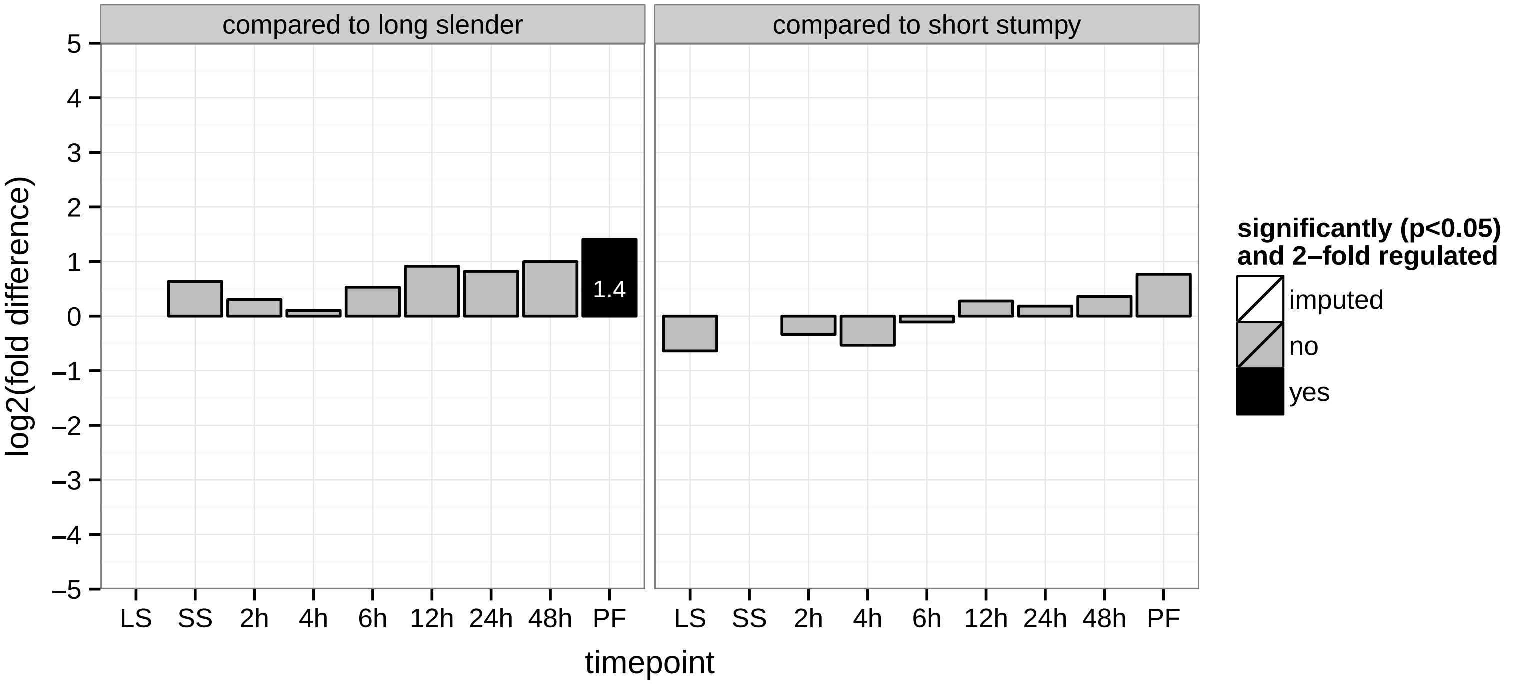
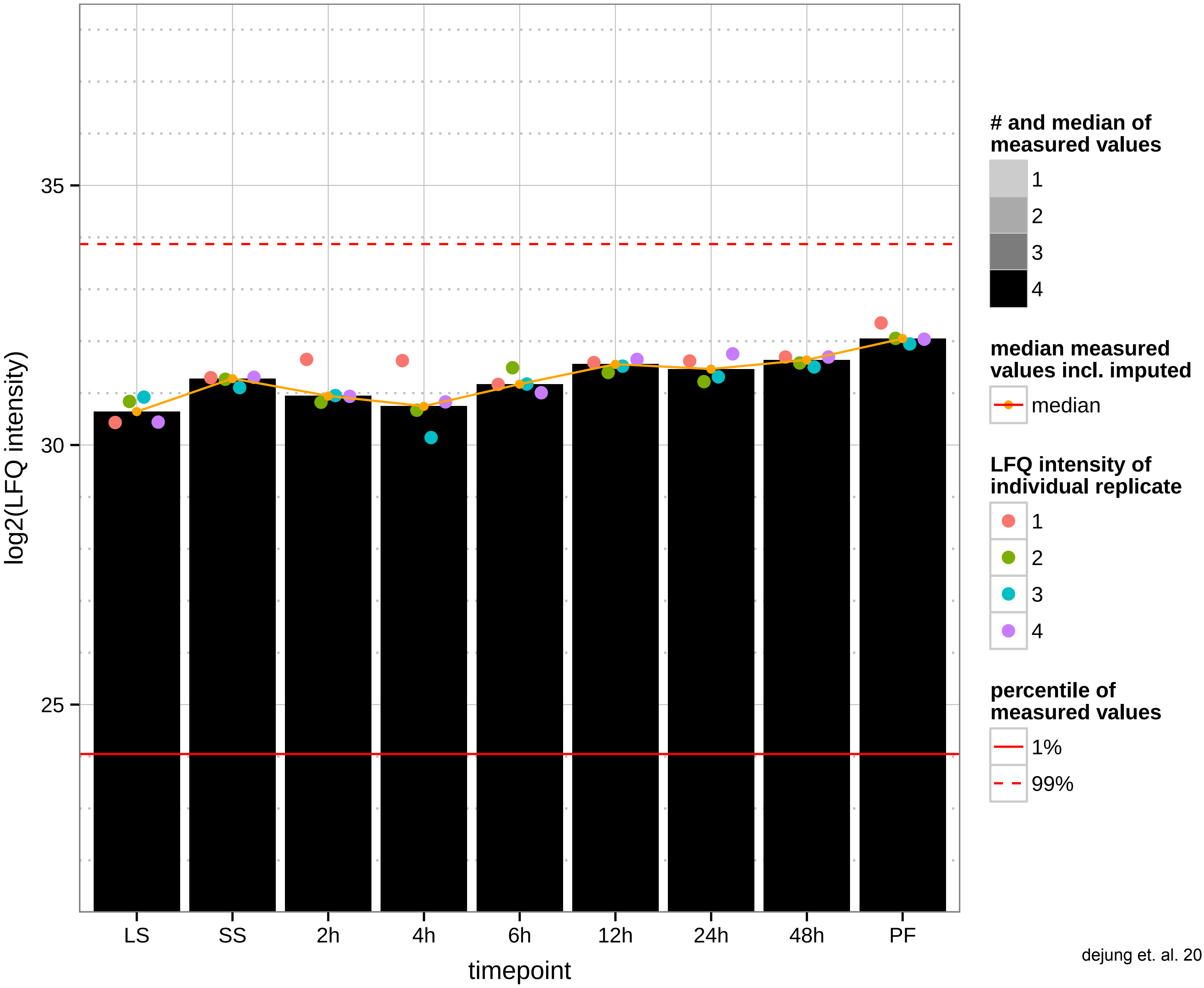
hypothetical protein, conserved
Tb927.10.1560
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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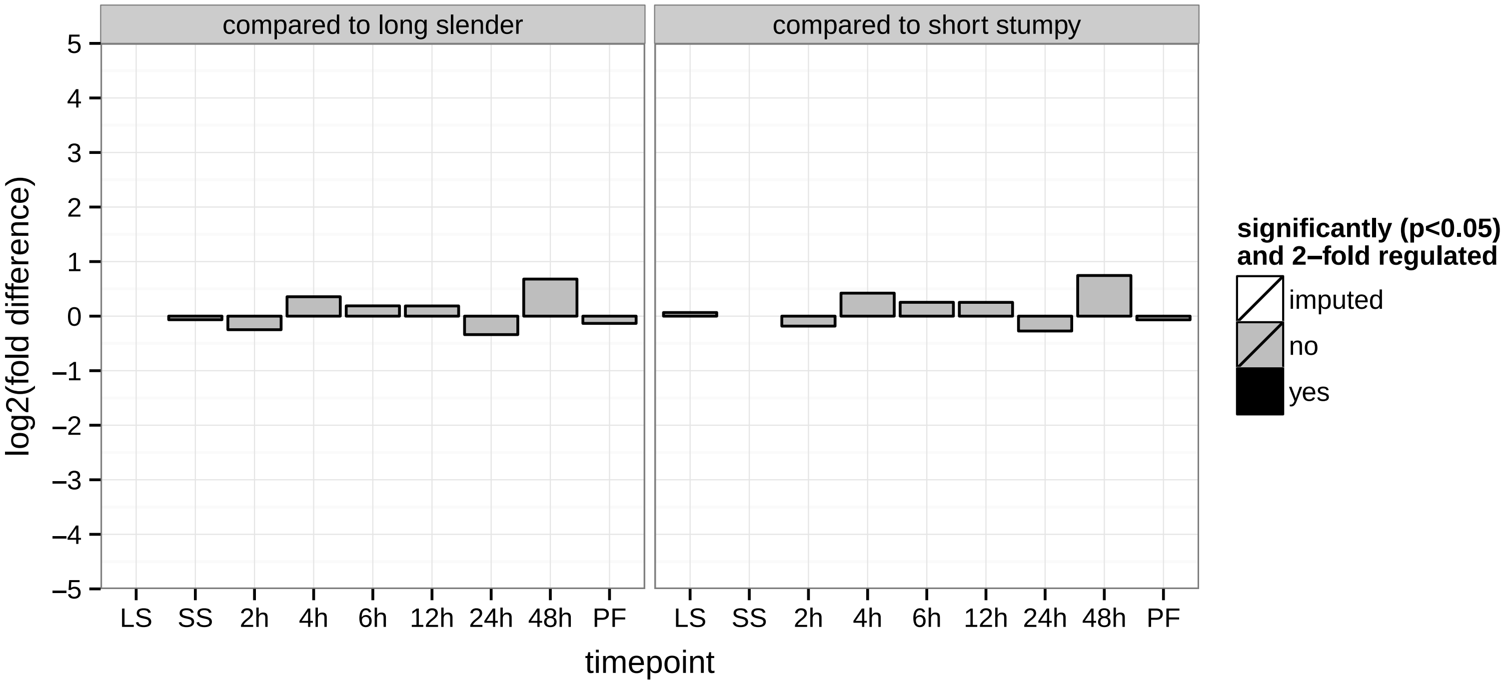
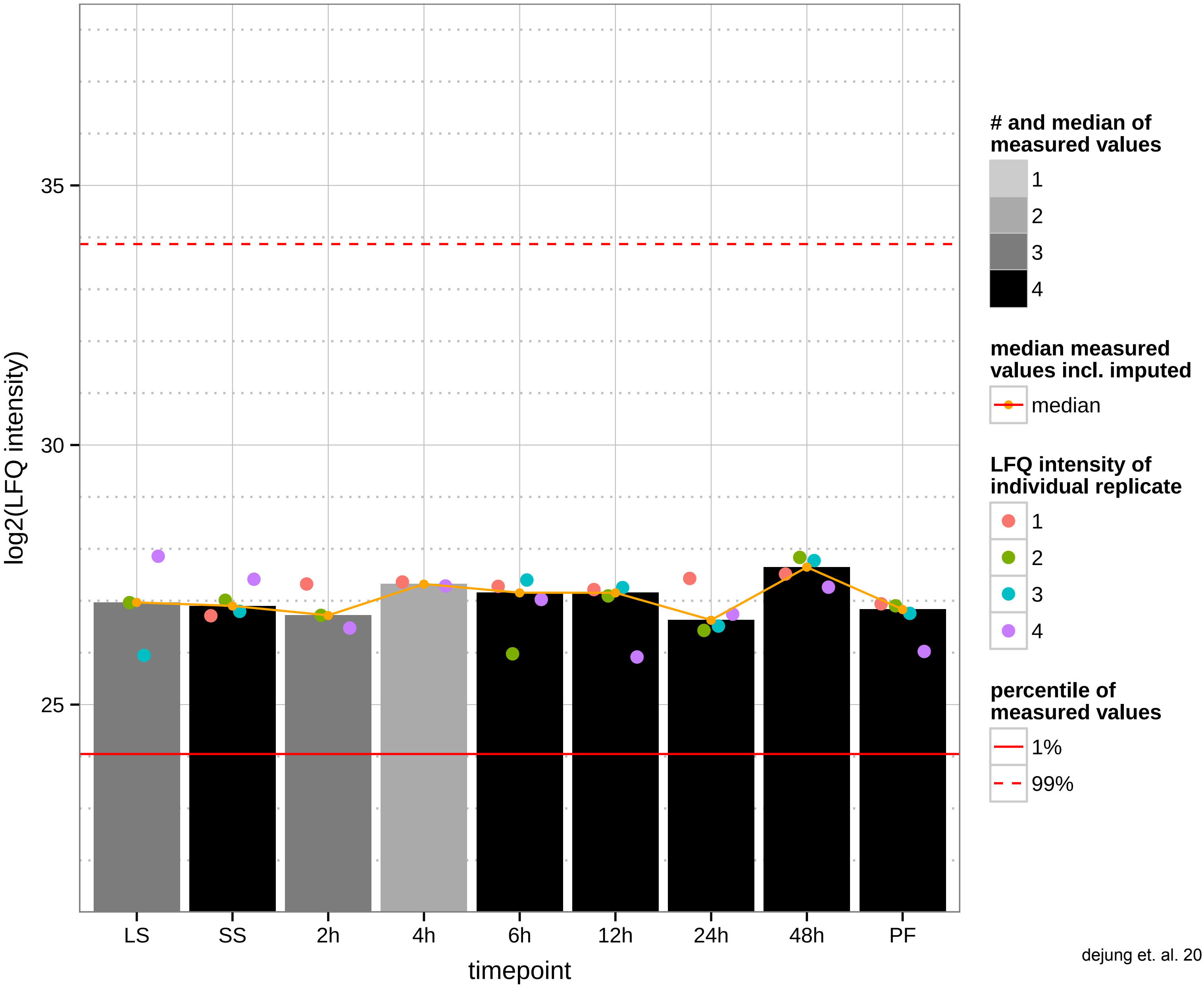
hypothetical protein, conserved
Tb927.10.15660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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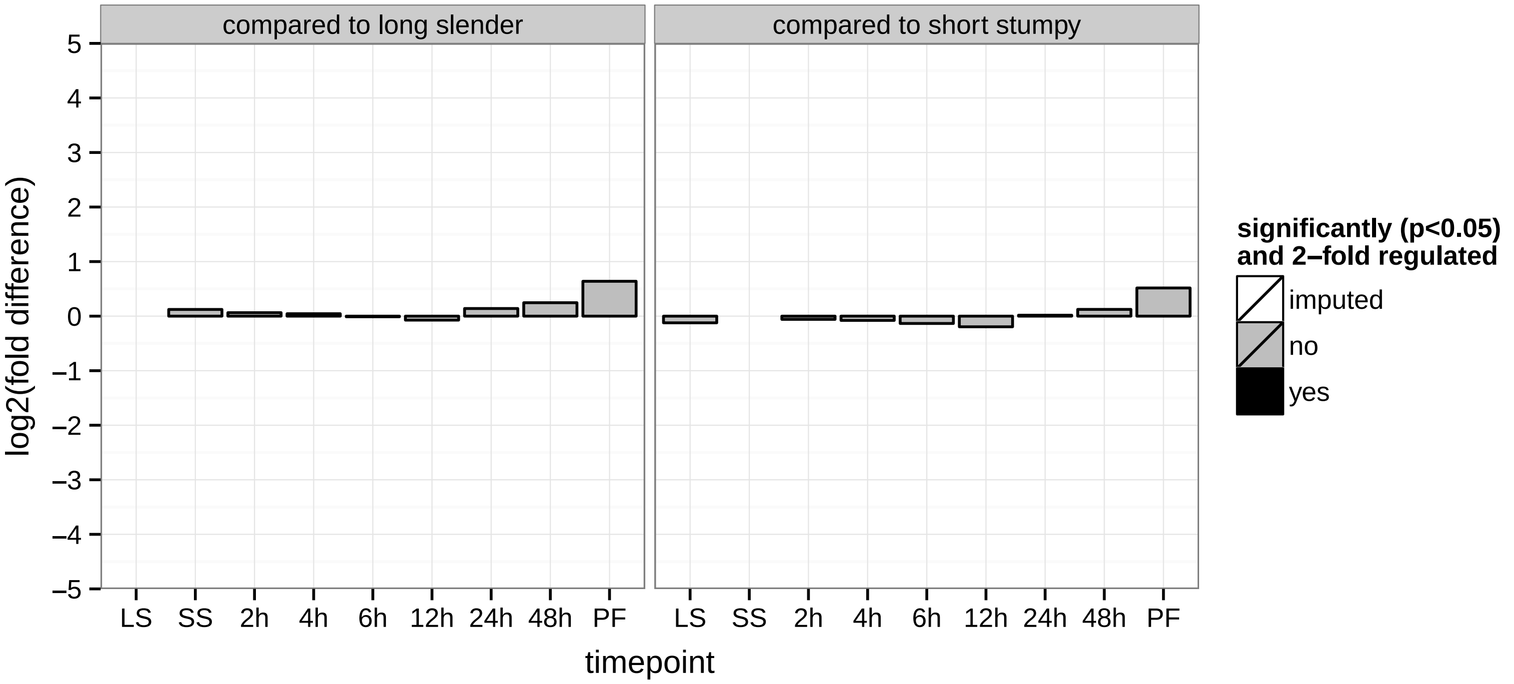
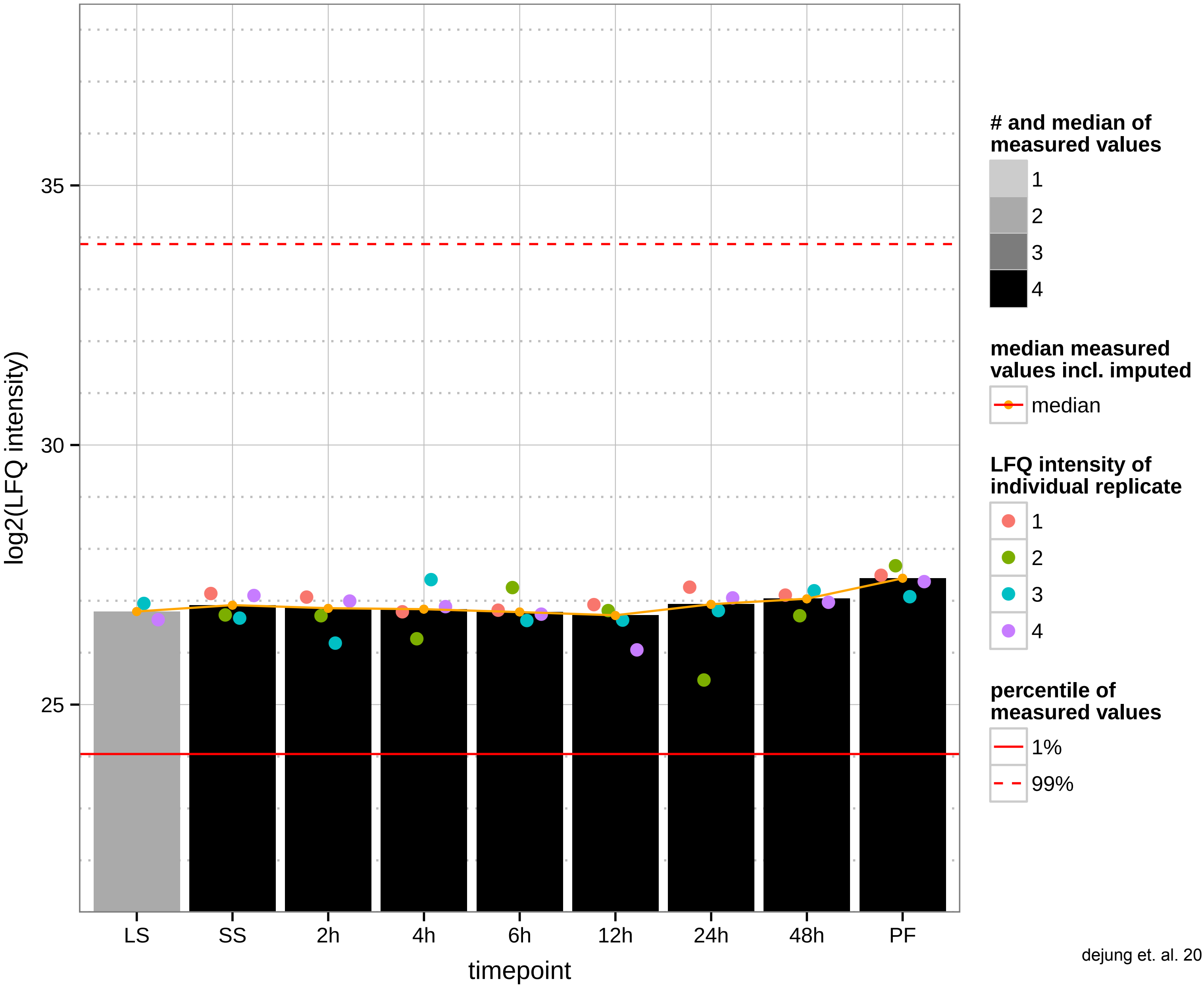
mitochondrial carrier protein (MCP7)
Tb927.10.15710
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrial part
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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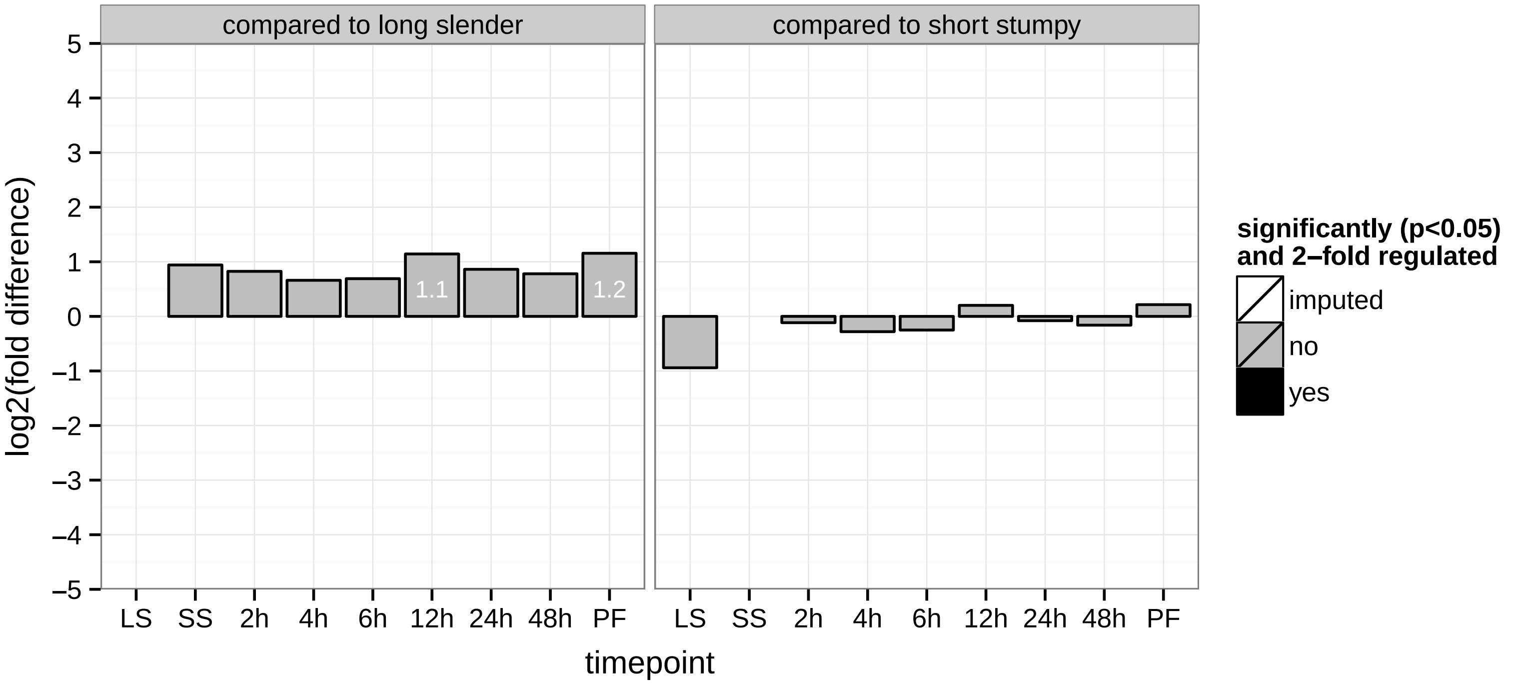
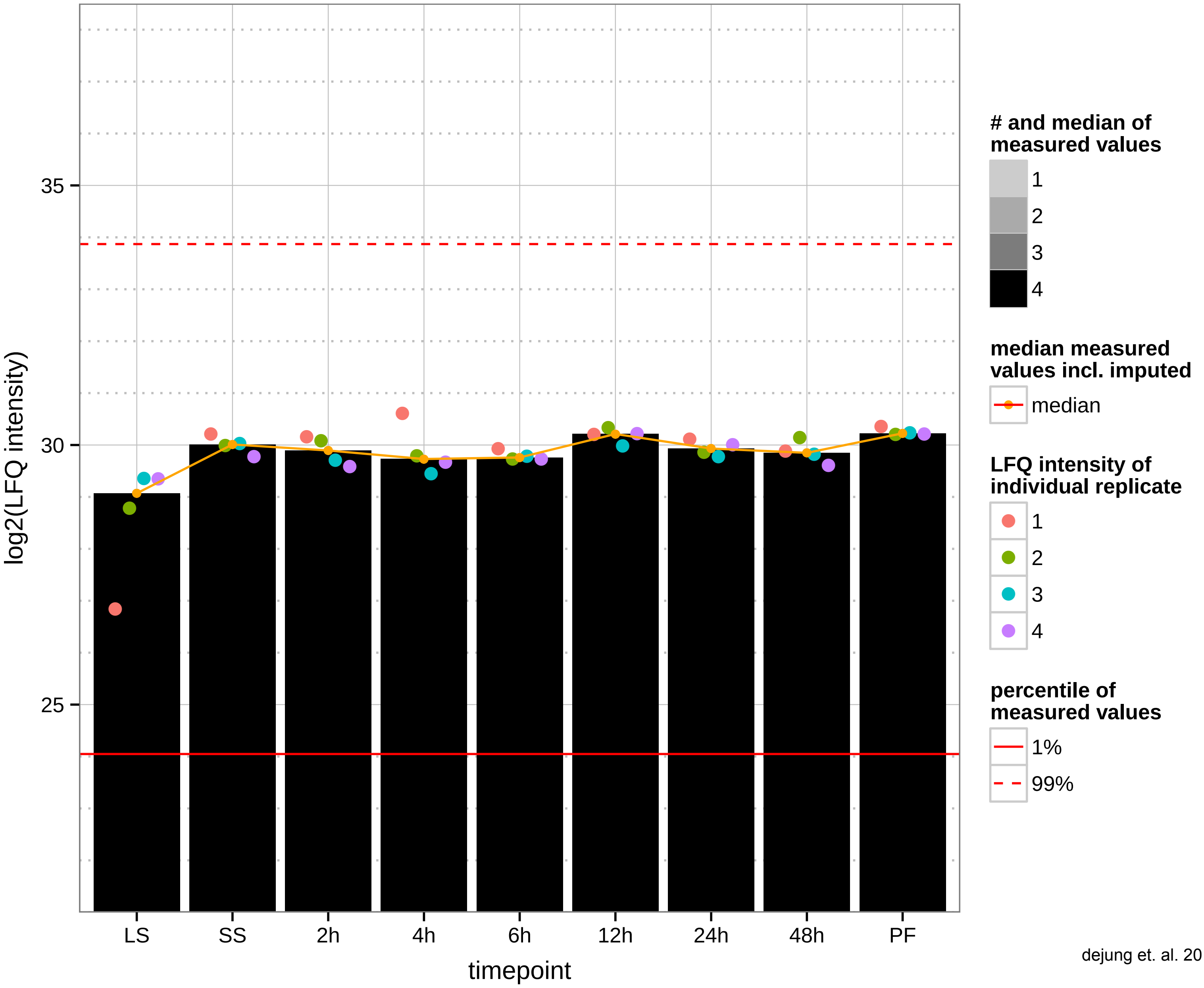
proteasome regulatory non–ATP–ase subunit 9, 19S proteasome regulatory subunit 9 (RPN9)
Tb927.10.15720
AGOF: endopeptidase activity
AGOC: proteasome regulatory particle
AGOP: ubiquitin–dependent protein catabolic process
PGOF: protein binding
PGOC: null
PGOP: null





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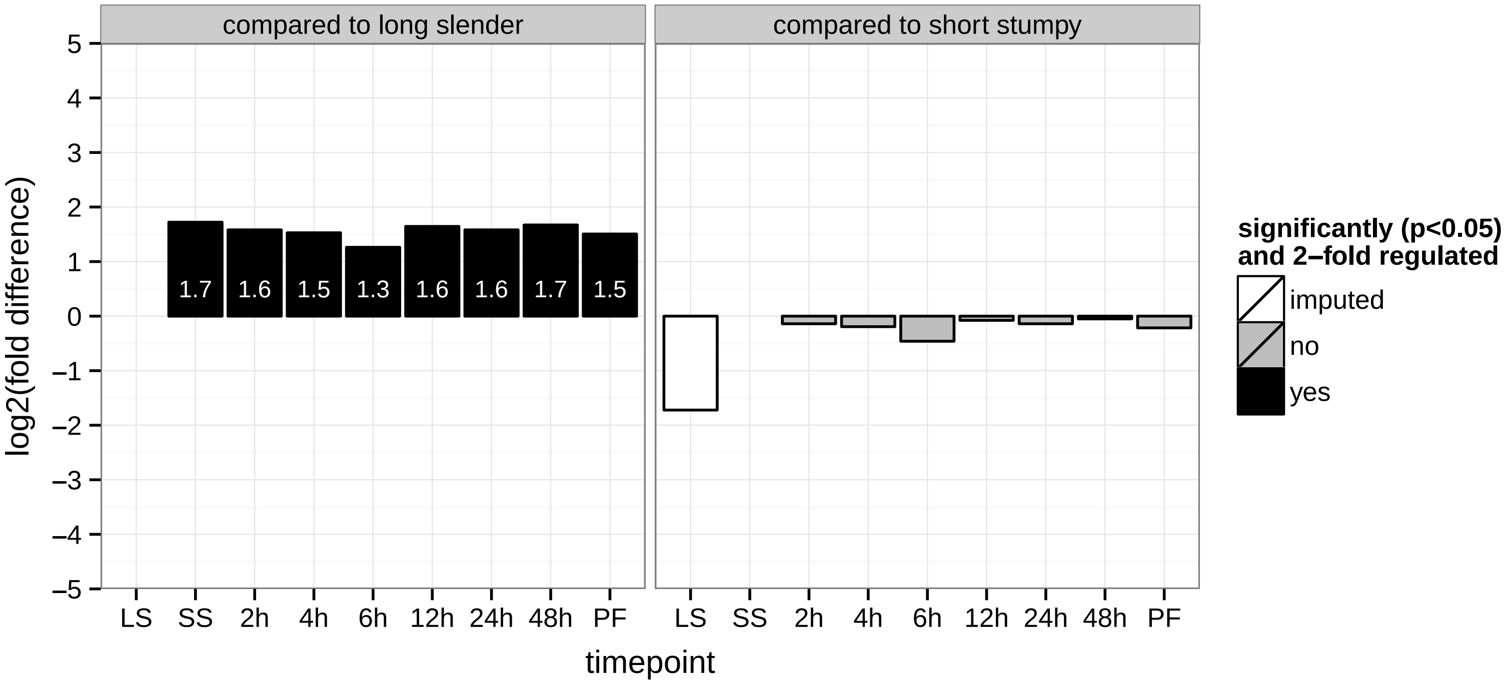
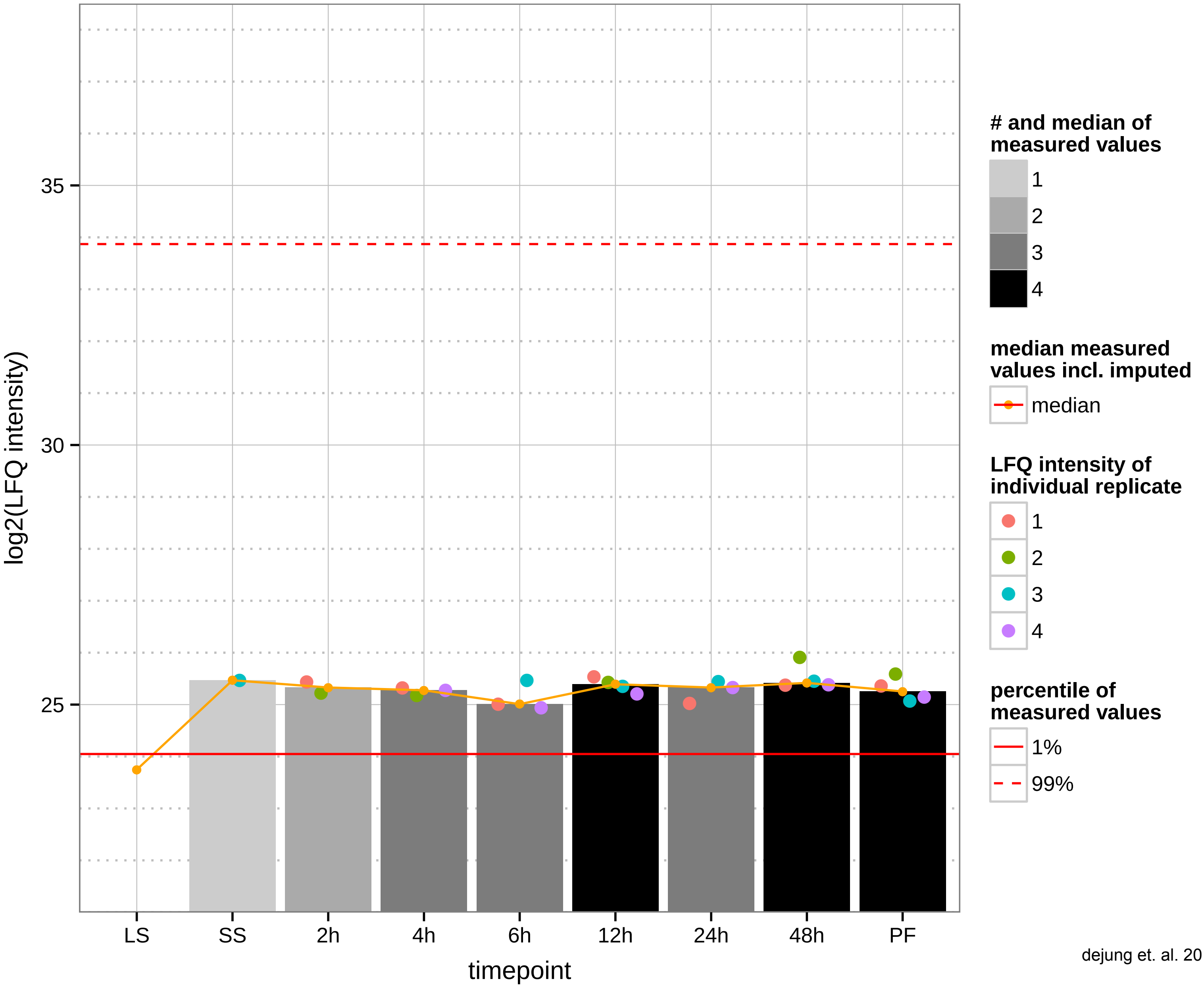
hypothetical protein, conserved
Tb927.10.15740
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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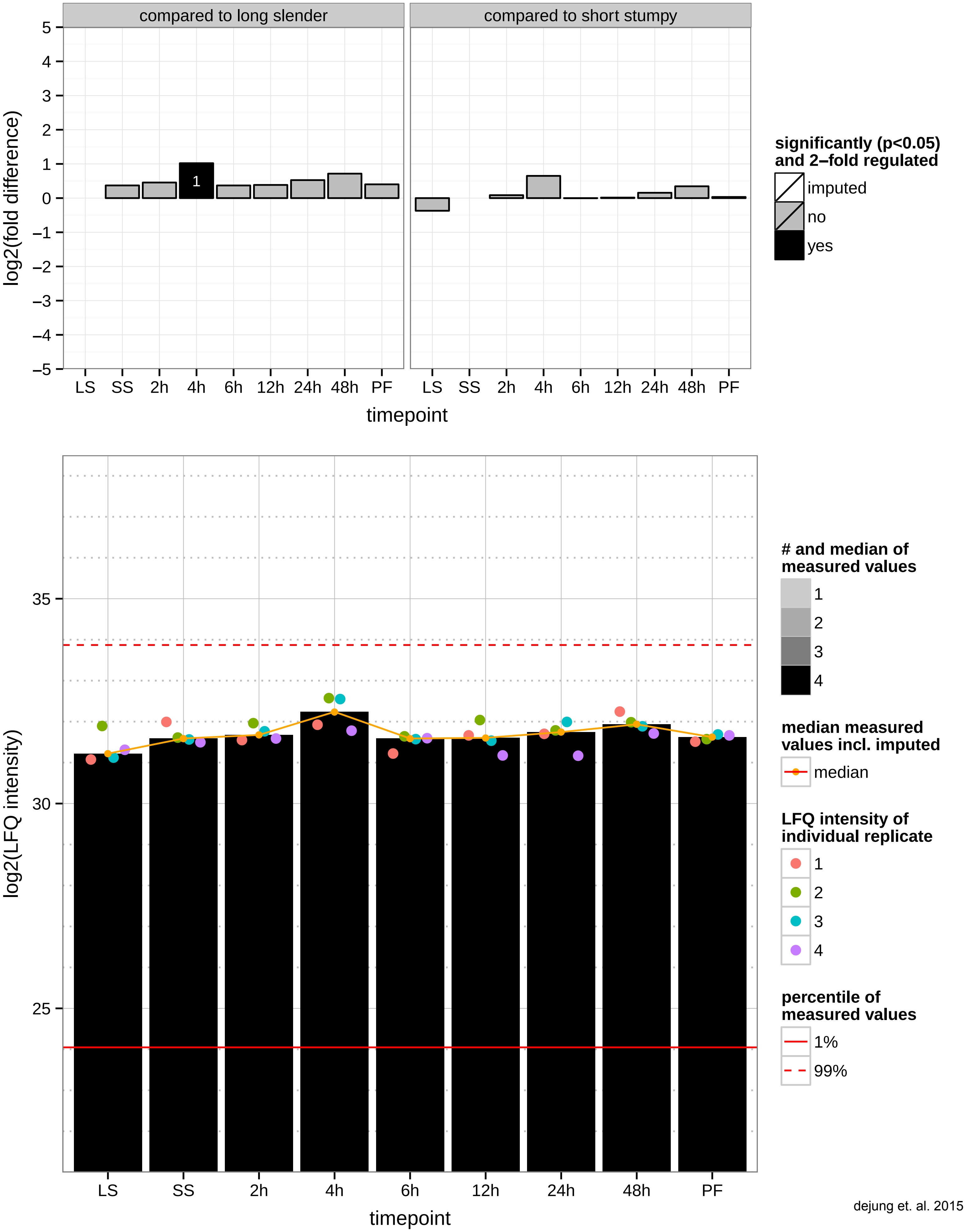
hypothetical protein, conserved
Tb927.10.15760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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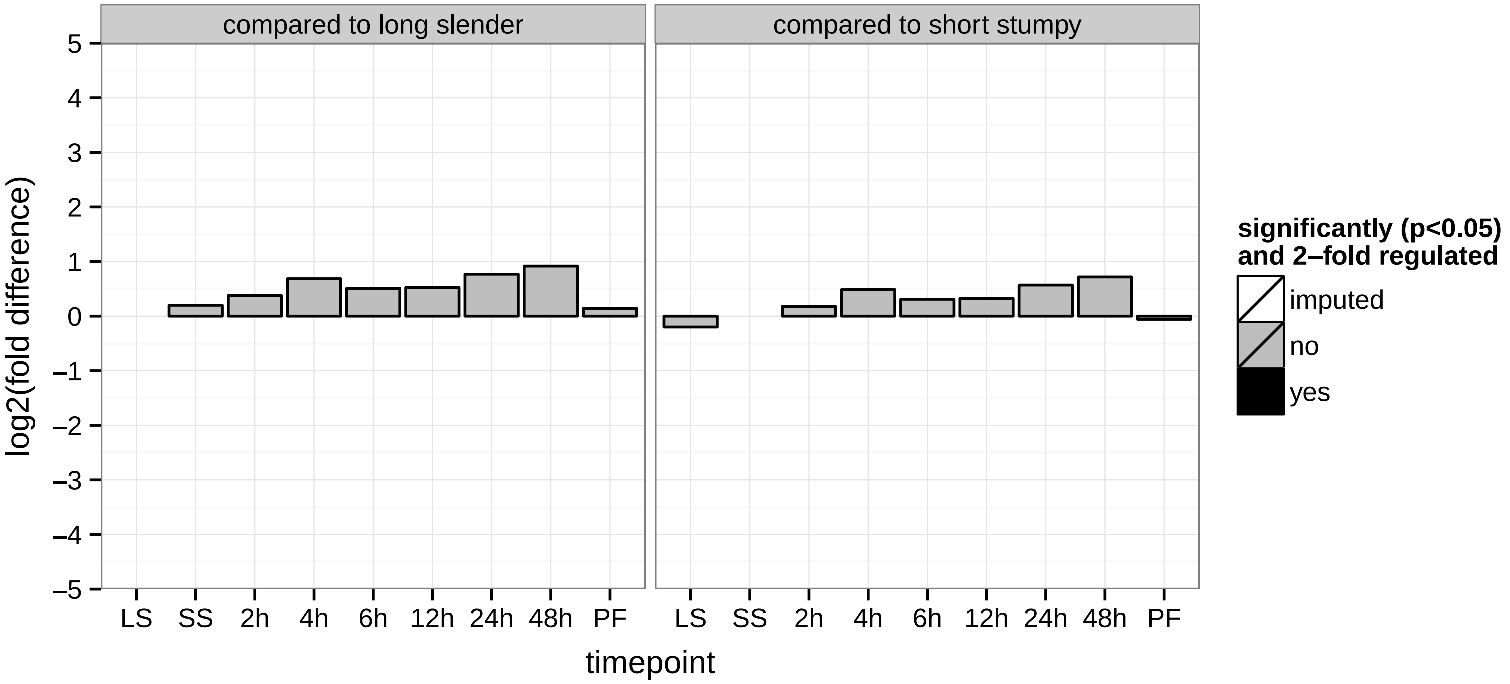
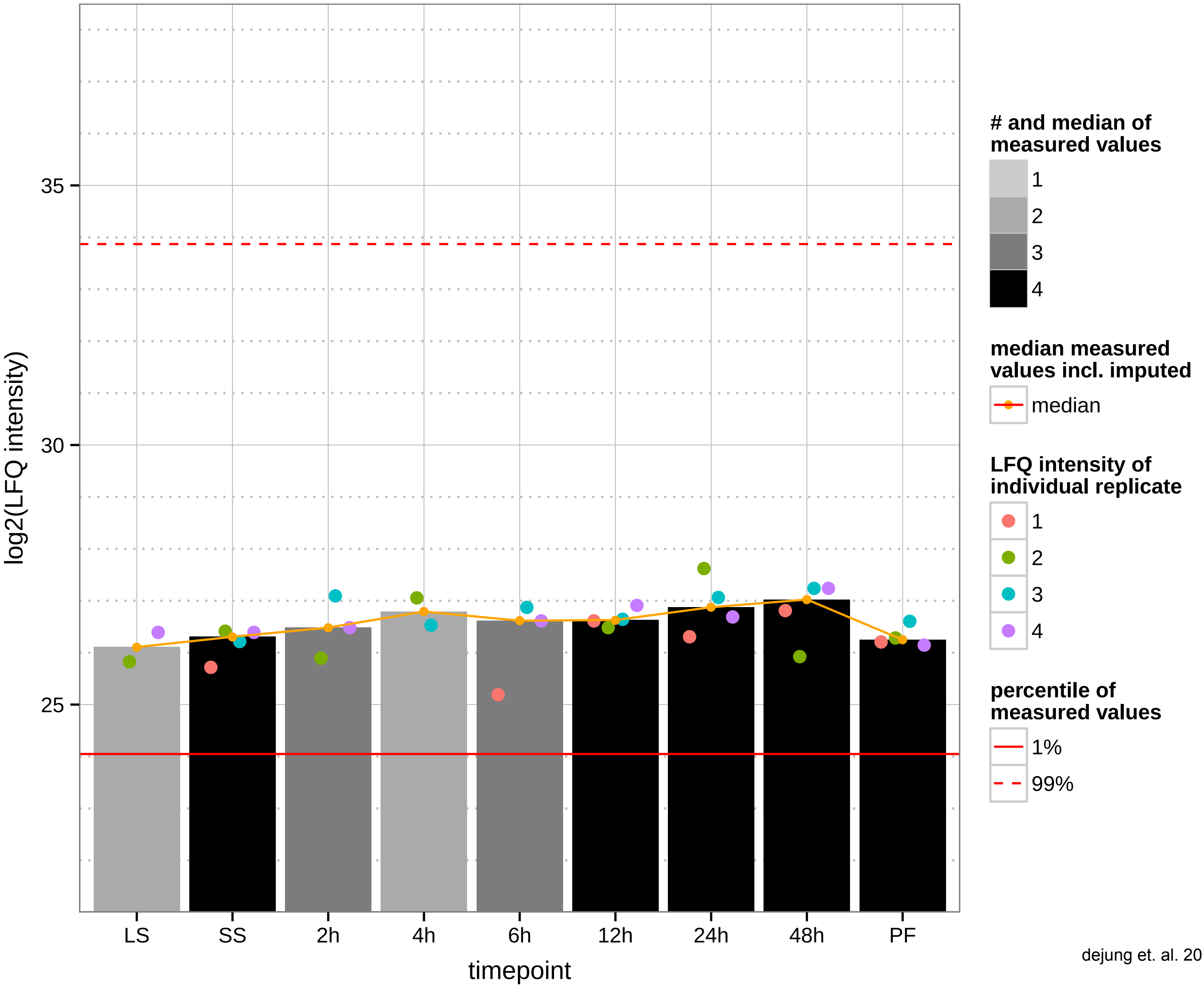
hypothetical protein, conserved
Tb927.10.1580
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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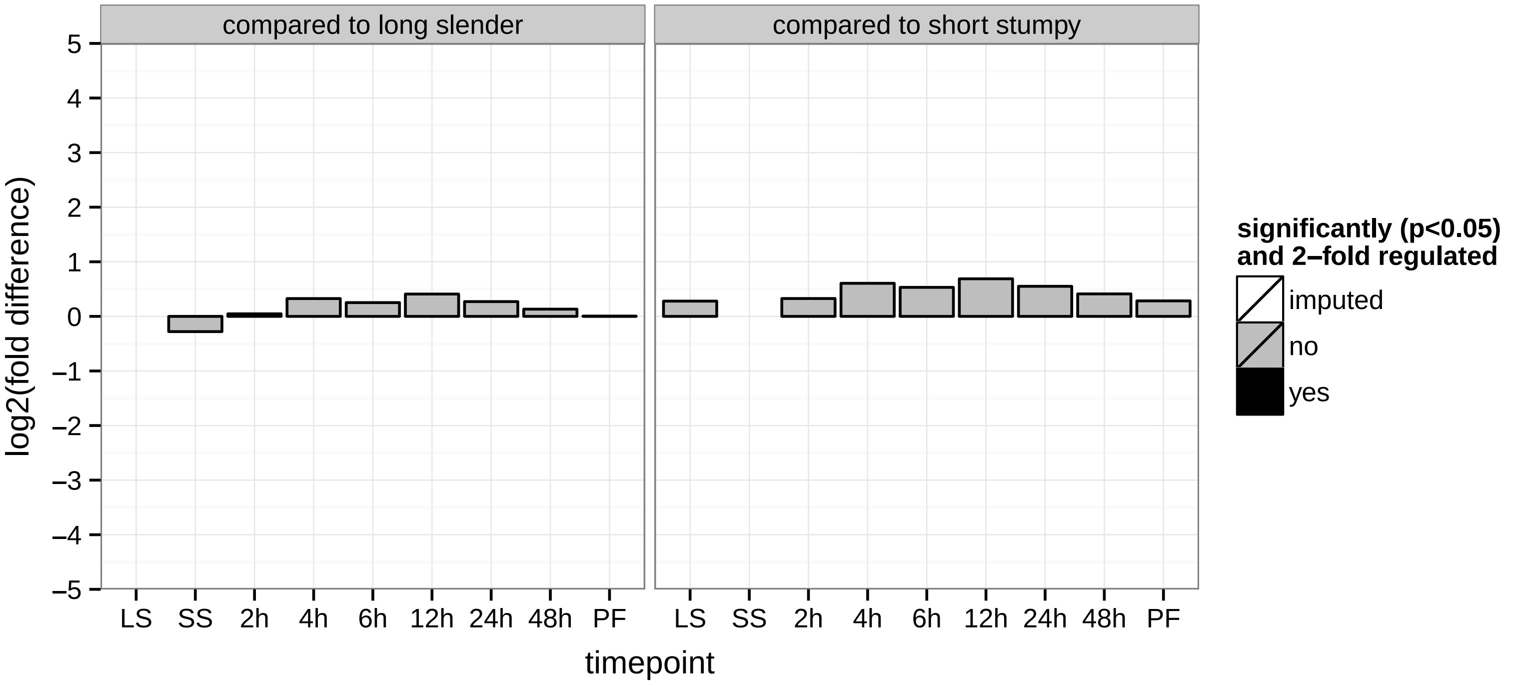
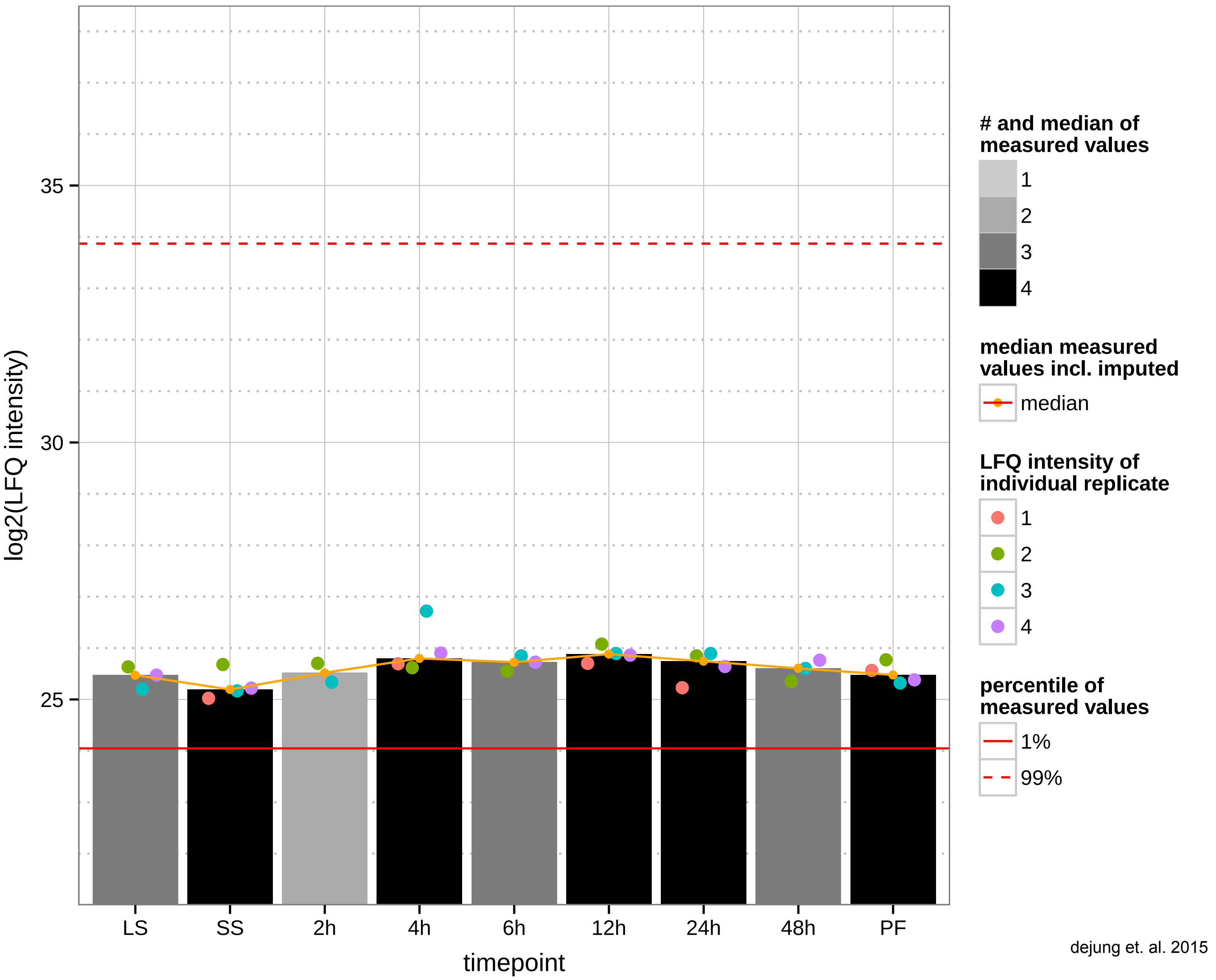
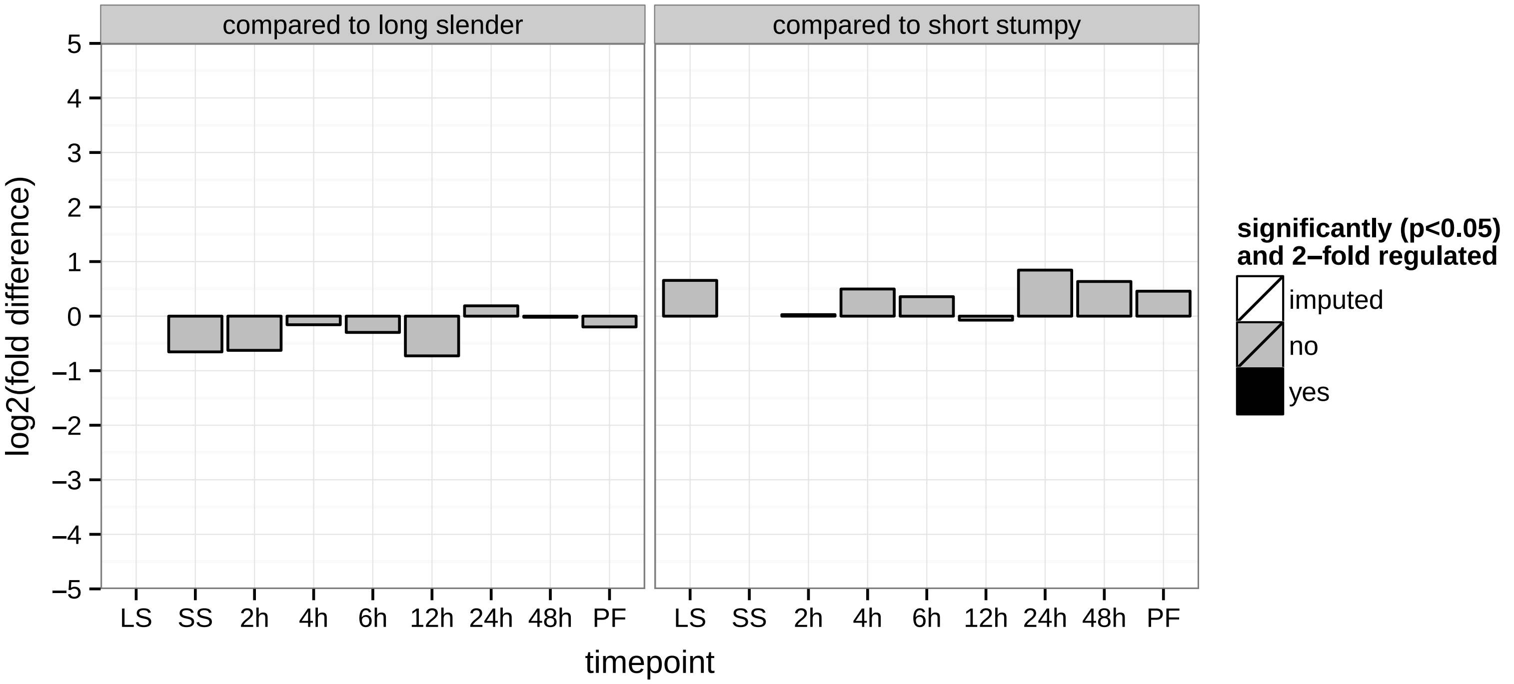
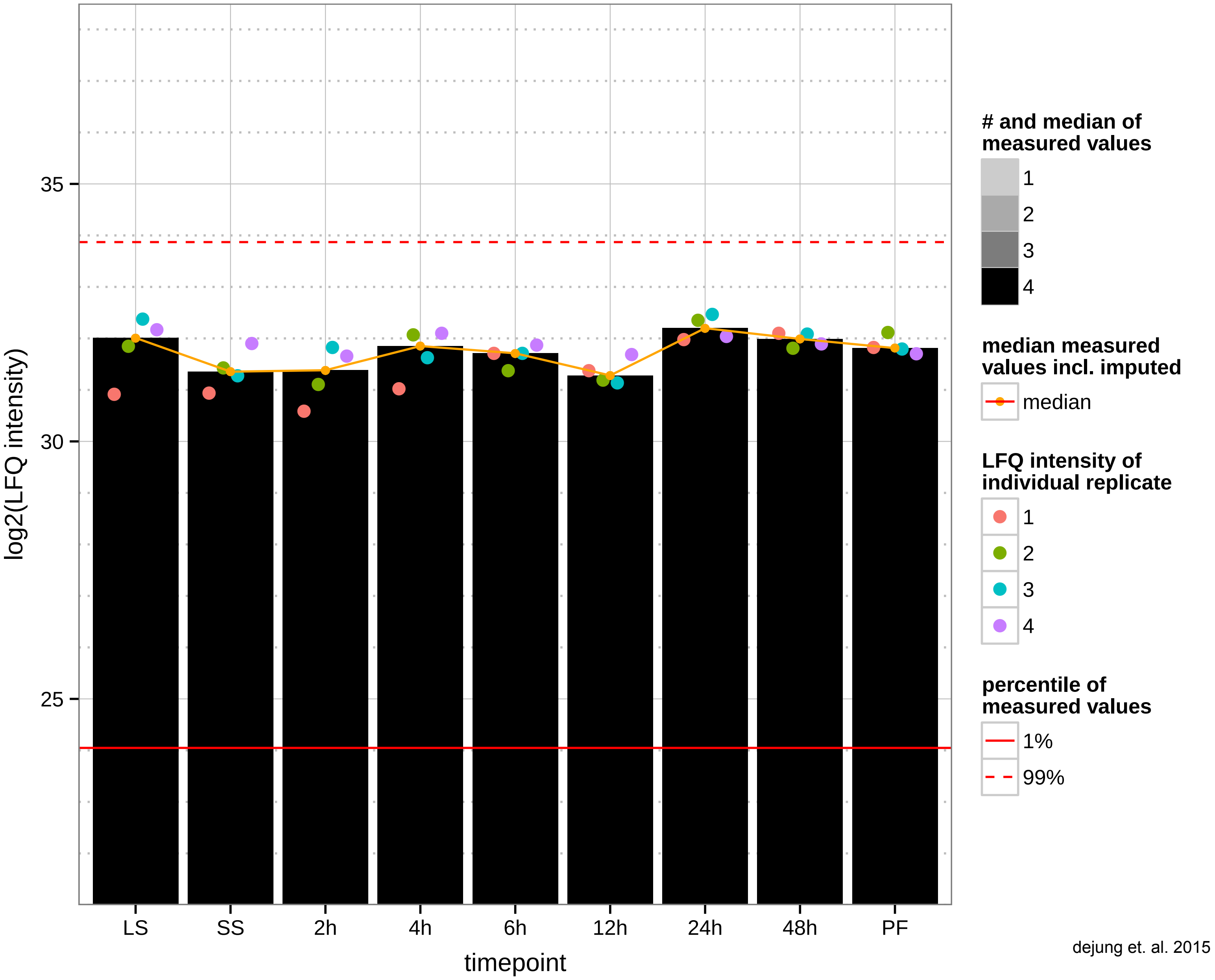
RNA binding protein, putative
Tb927.10.15870
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: RNA binding
PGOC: null
PGOP: RNA processing





ribosomal protein L36, putative
Tb927.9.15210;Tb927.10.1590
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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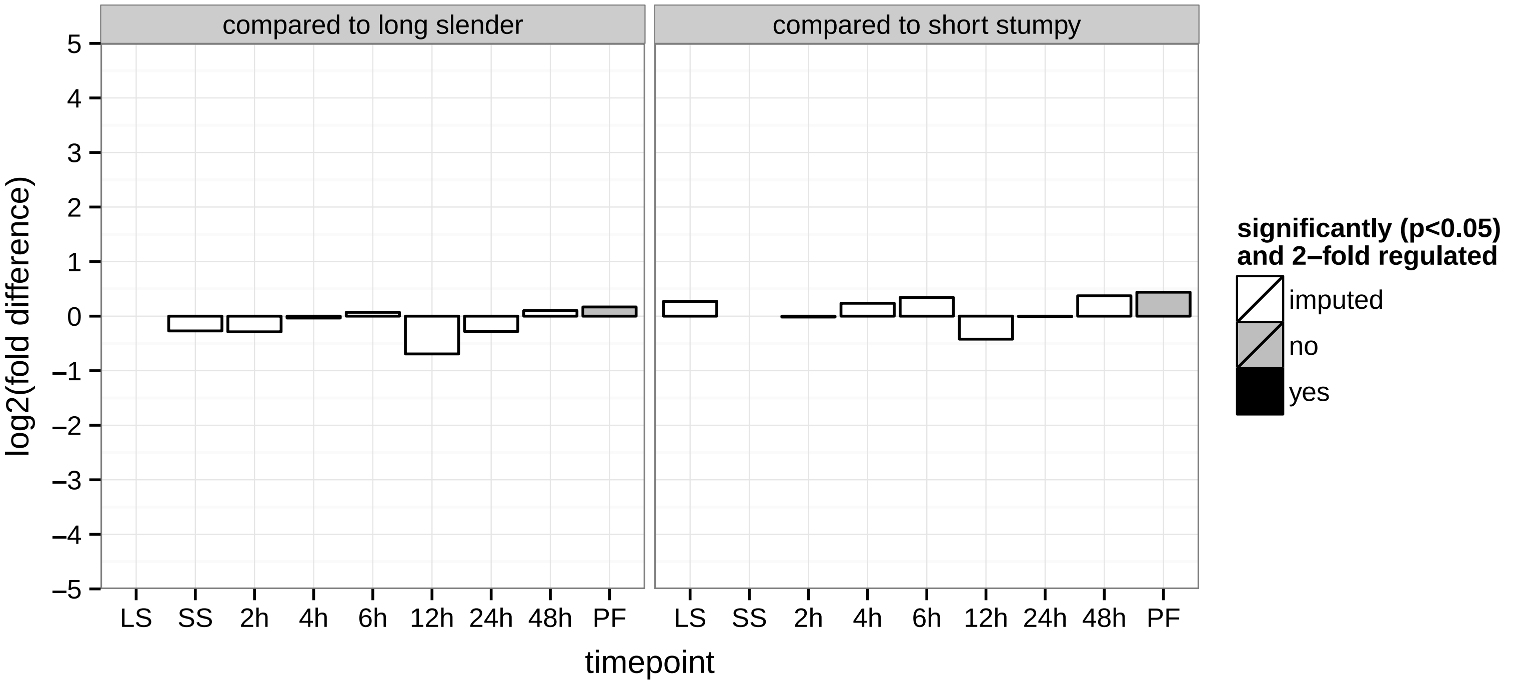
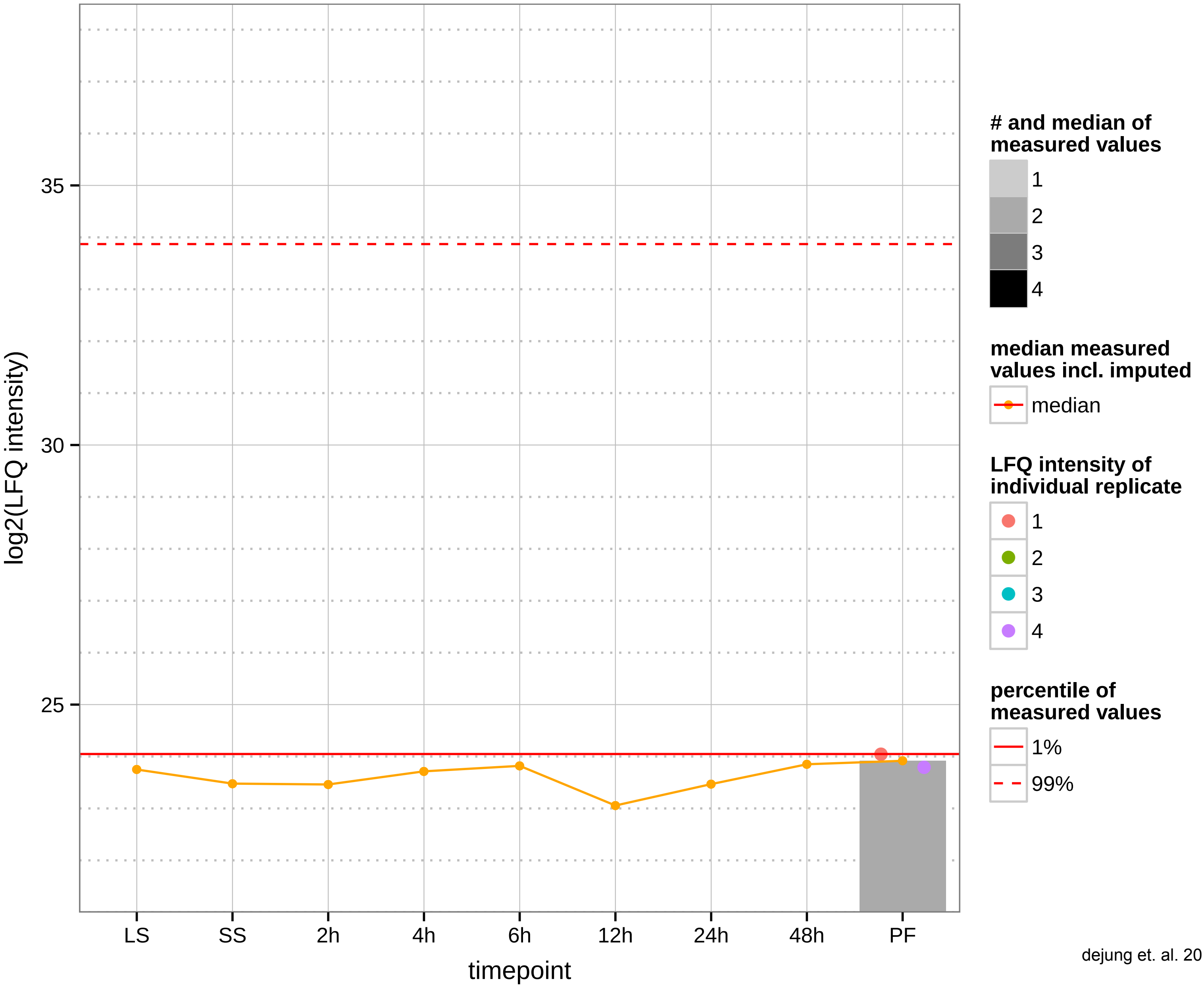
Triglyceride lipase, putative, class 3 lipase
Tb927.10.15970;Tb11.v5.0306
AGOF: triglyceride lipase activity, zinc ion binding
AGOC: null
AGOP: lipid metabolic process
PGOF: triglyceride lipase activity
PGOC: null
PGOP: lipid metabolic process





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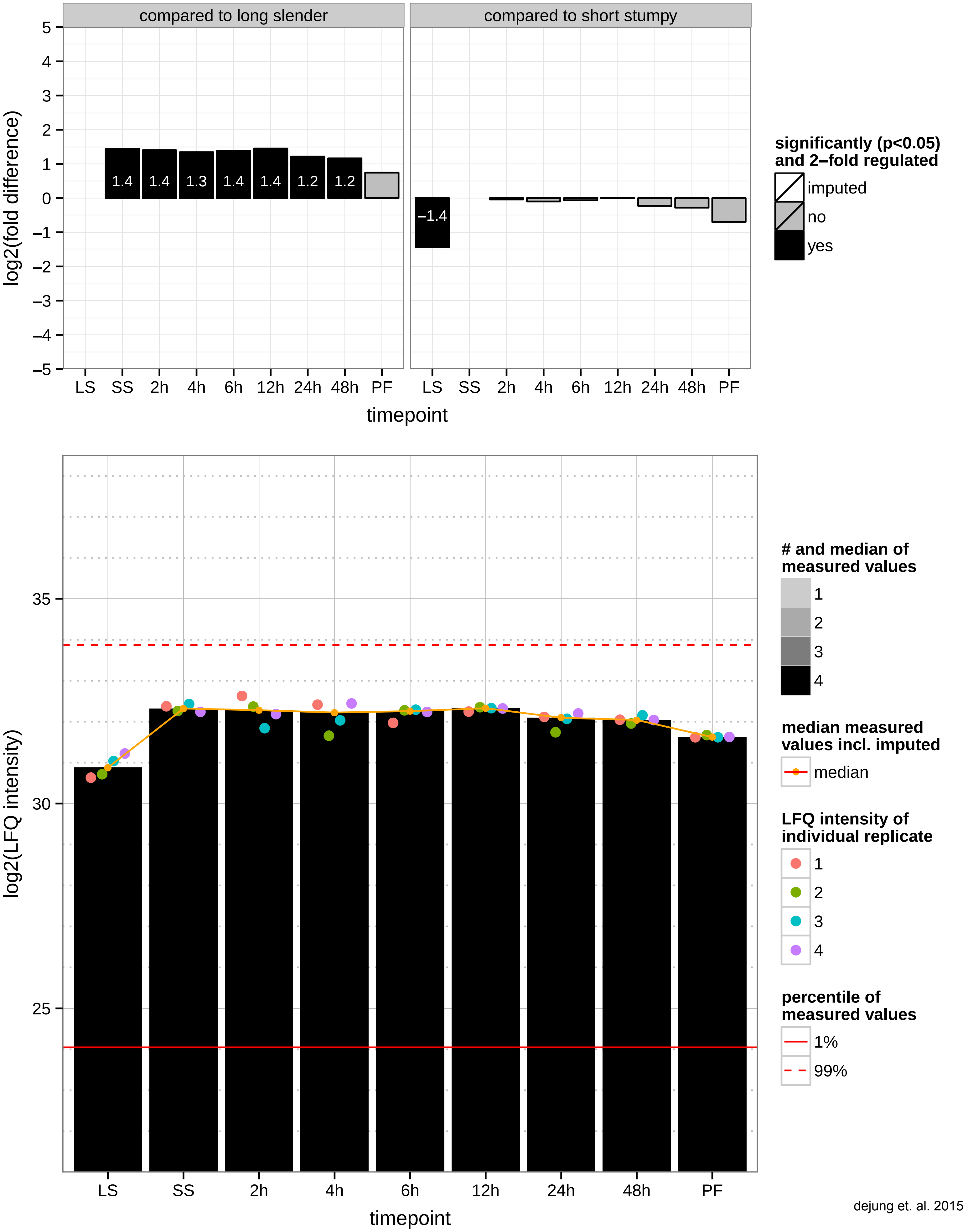
inosine–5'–monophosphate dehydrogenase, IMP dehydrogenase
Tb927.10.16120
AGOF: IMP dehydrogenase activity
AGOC: null
AGOP: oxidation–reduction process, purine ribonucleotide biosynthetic process
PGOF: IMP dehydrogenase activity, catalytic activity, protein binding
PGOC: null
PGOP: oxidation–reduction process



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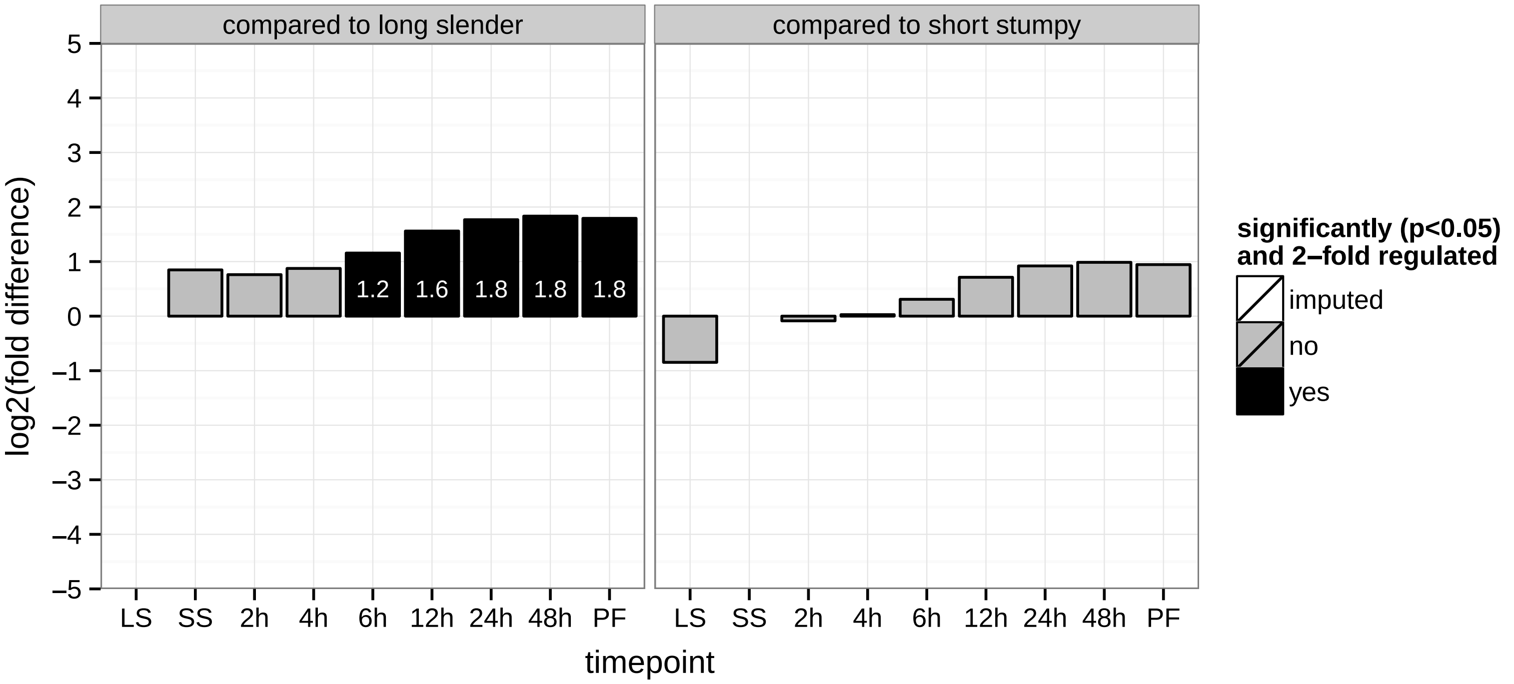
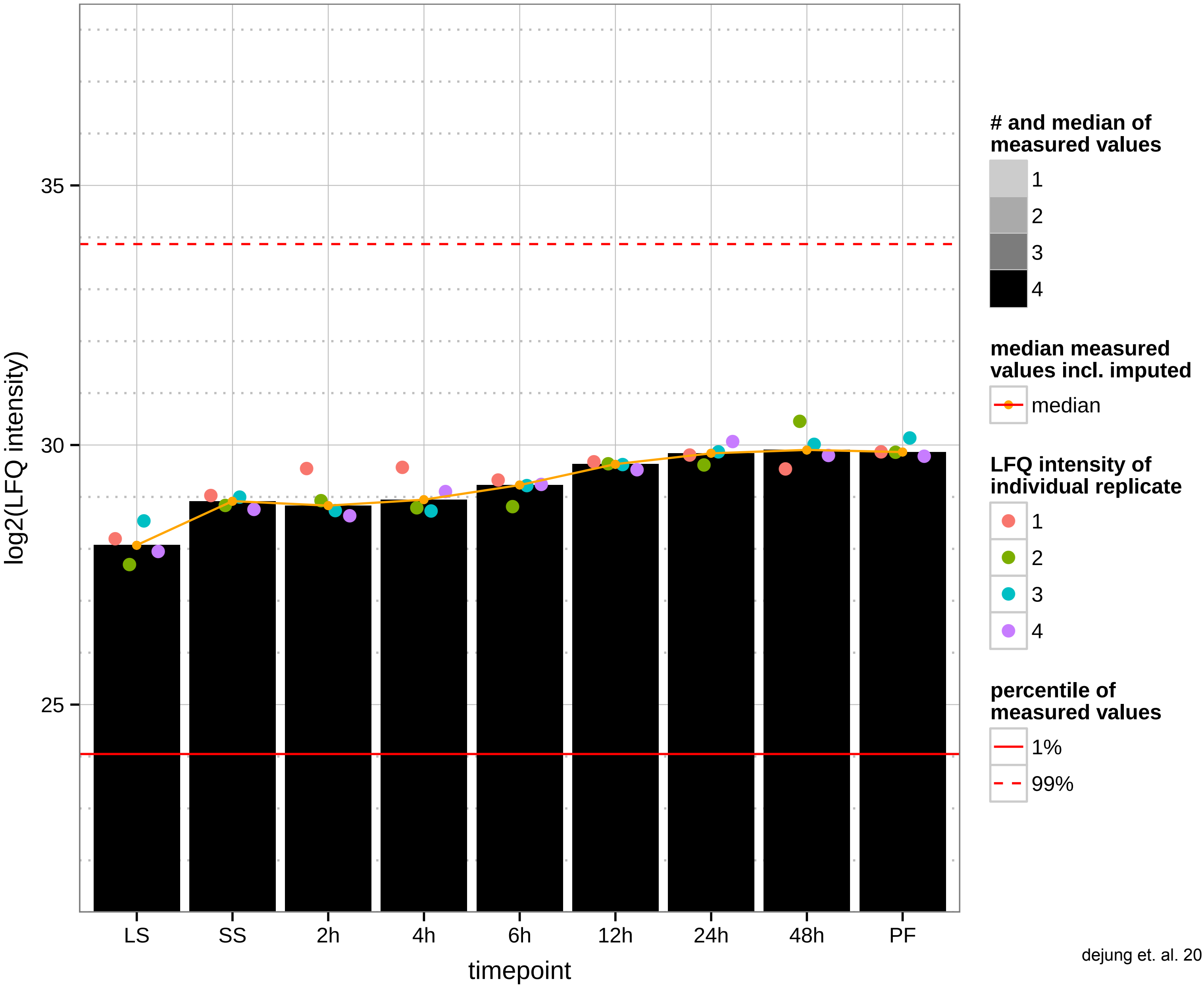
atp–binding cassette sub–family e member 1 (ABCE1)
Tb927.10.1630
AGOF: ATP binding, ATPase activity, electron carrier activity, iron–sulfur cluster binding, ribonuclease activity
AGOC: cytoplasm
AGOP: nuclear–transcribed mRNA catabolic process, exonucleolytic
PGOF: ATP binding, ATPase activity, electron carrier activity, iron–sulfur cluster binding, nucleoside–triphosphatase activity, nu
PGOC: null
PGOP: null





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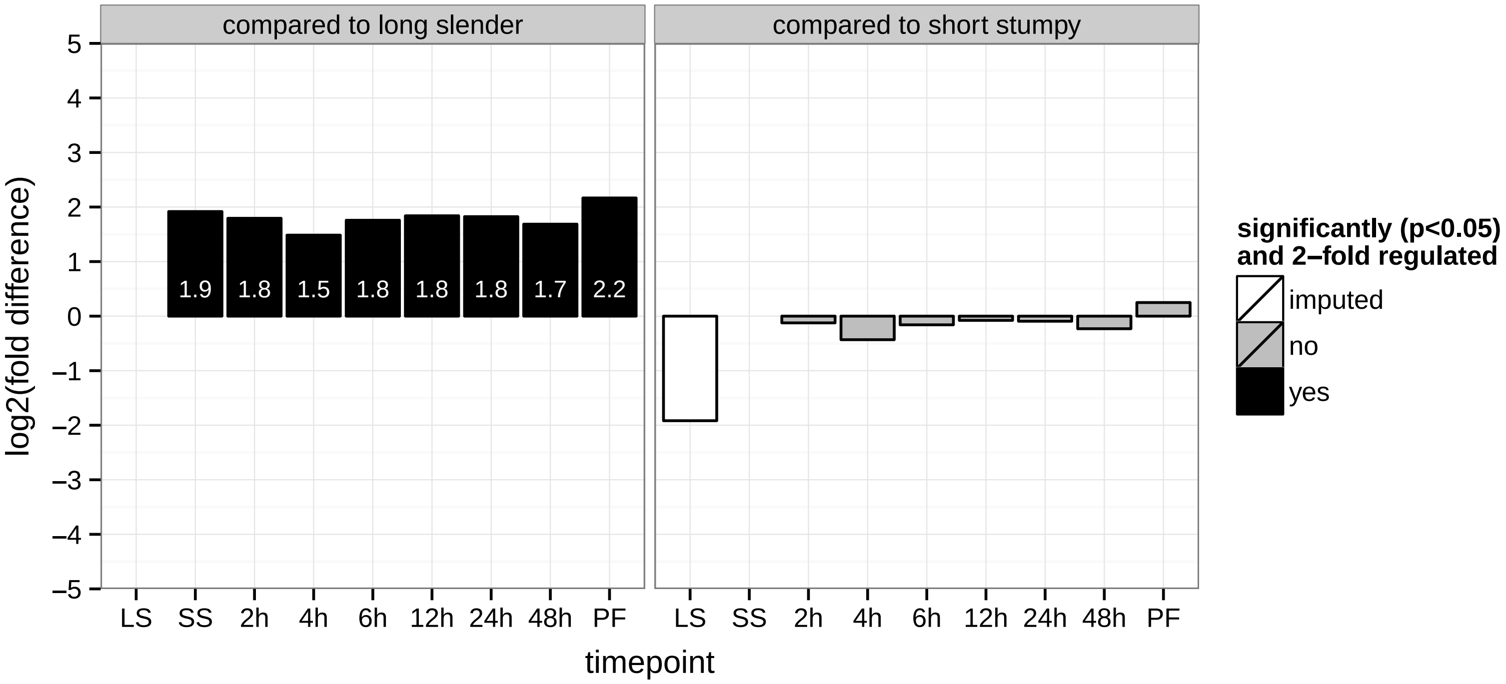
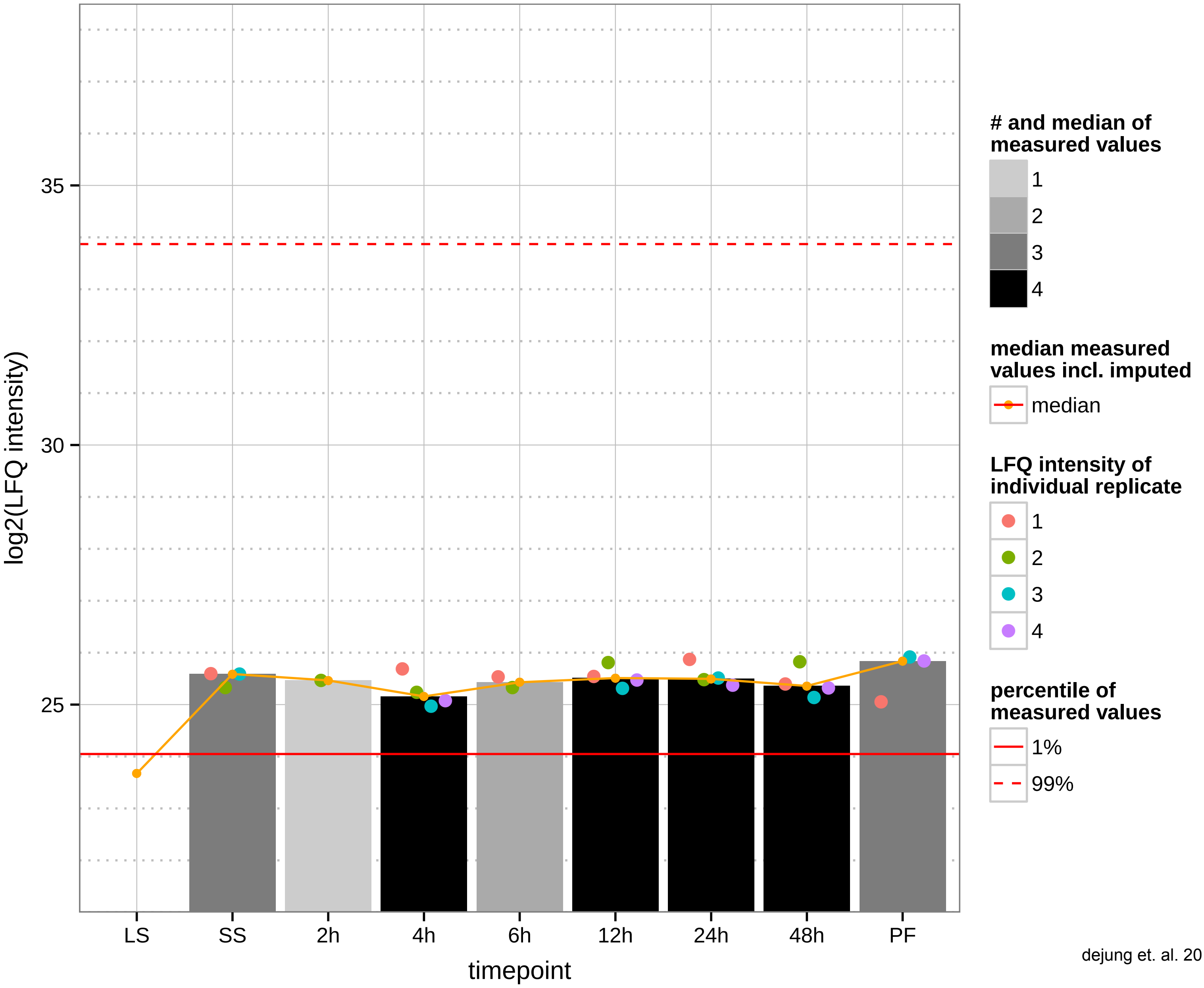
nucleotide binding protein, putative (NBP 1)
Tb927.10.1690
AGOF: nucleotide binding
AGOC: cytosol
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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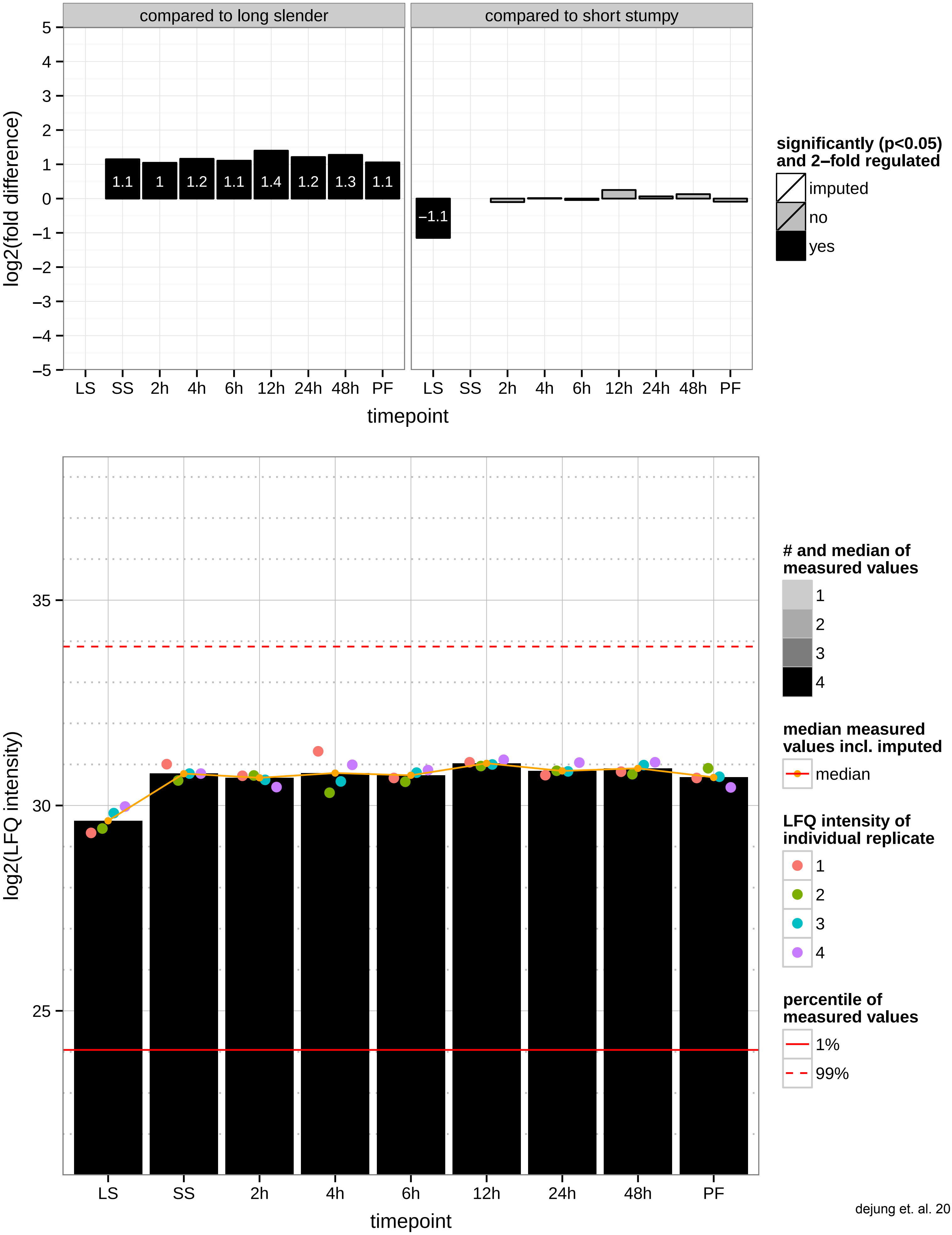
pseudouridine synthase, Cbf5p
Tb927.10.170
AGOF: RNA binding, pseudouridine synthase activity, pseudouridylate synthase activity
AGOC: nucleus
AGOP: RNA processing, pseudouridine synthesis, rRNA modification, tRNA modification
PGOF: RNA binding, pseudouridine synthase activity
PGOC: null
PGOP: RNA modification, RNA processing, pseudouridine synthesis



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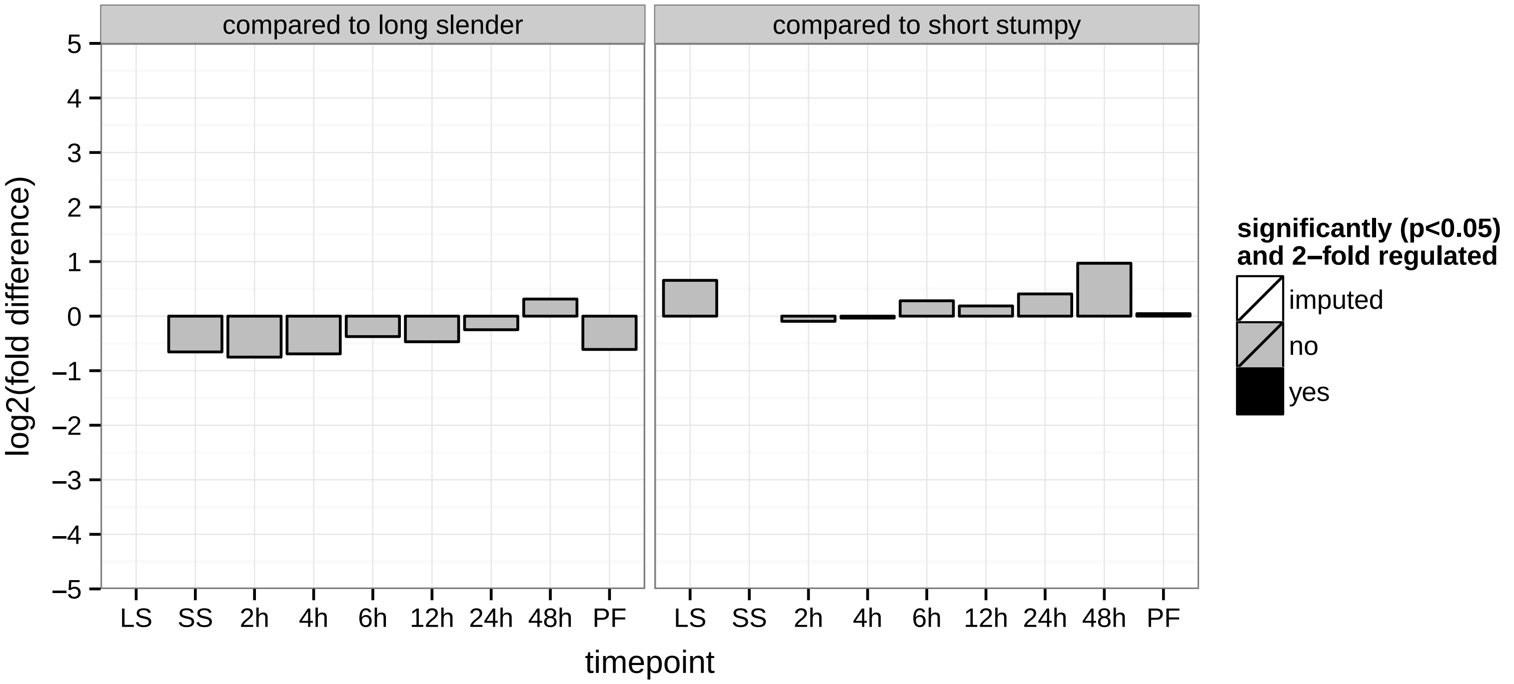
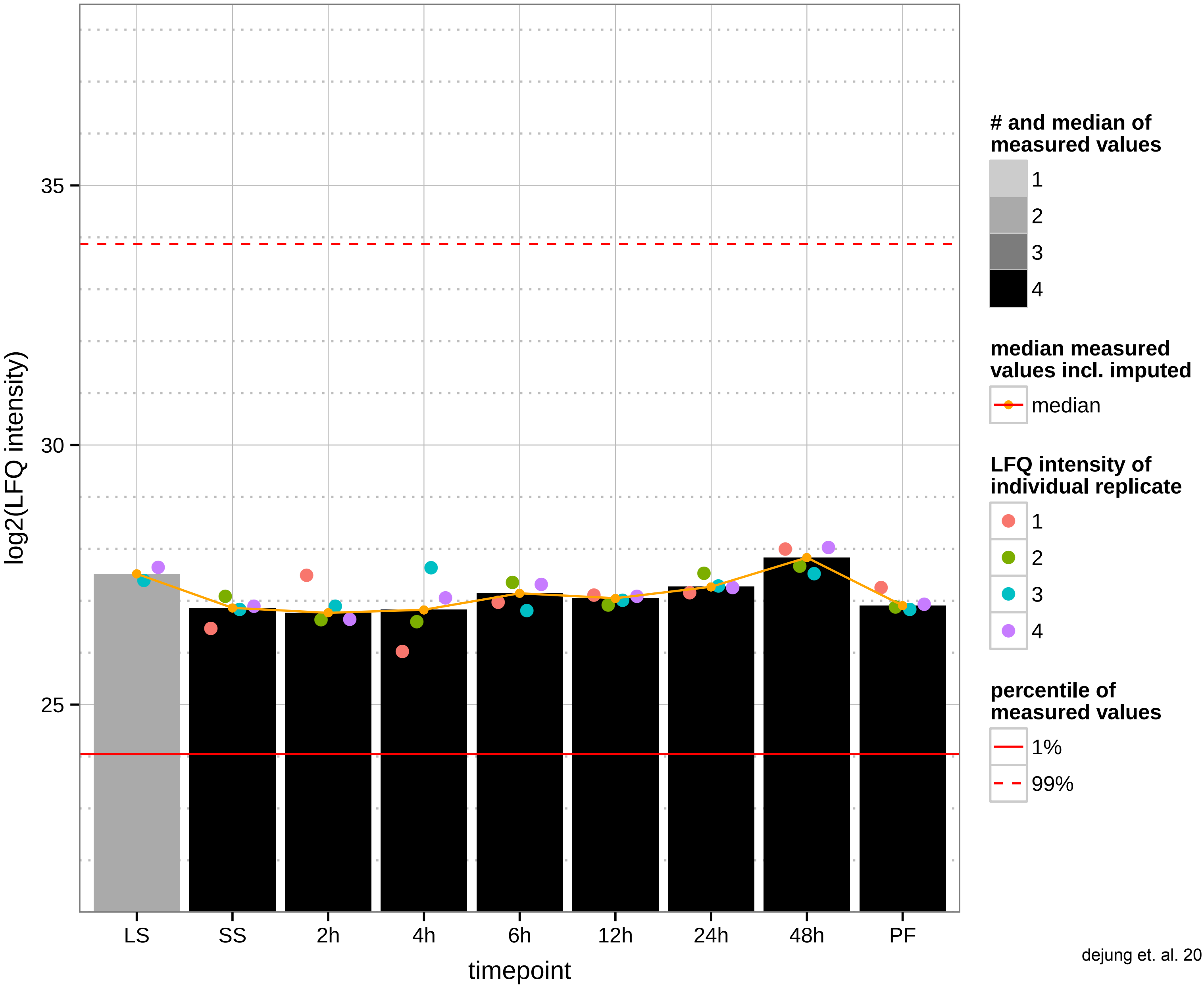
hypothetical protein, conserved
Tb927.10.1860
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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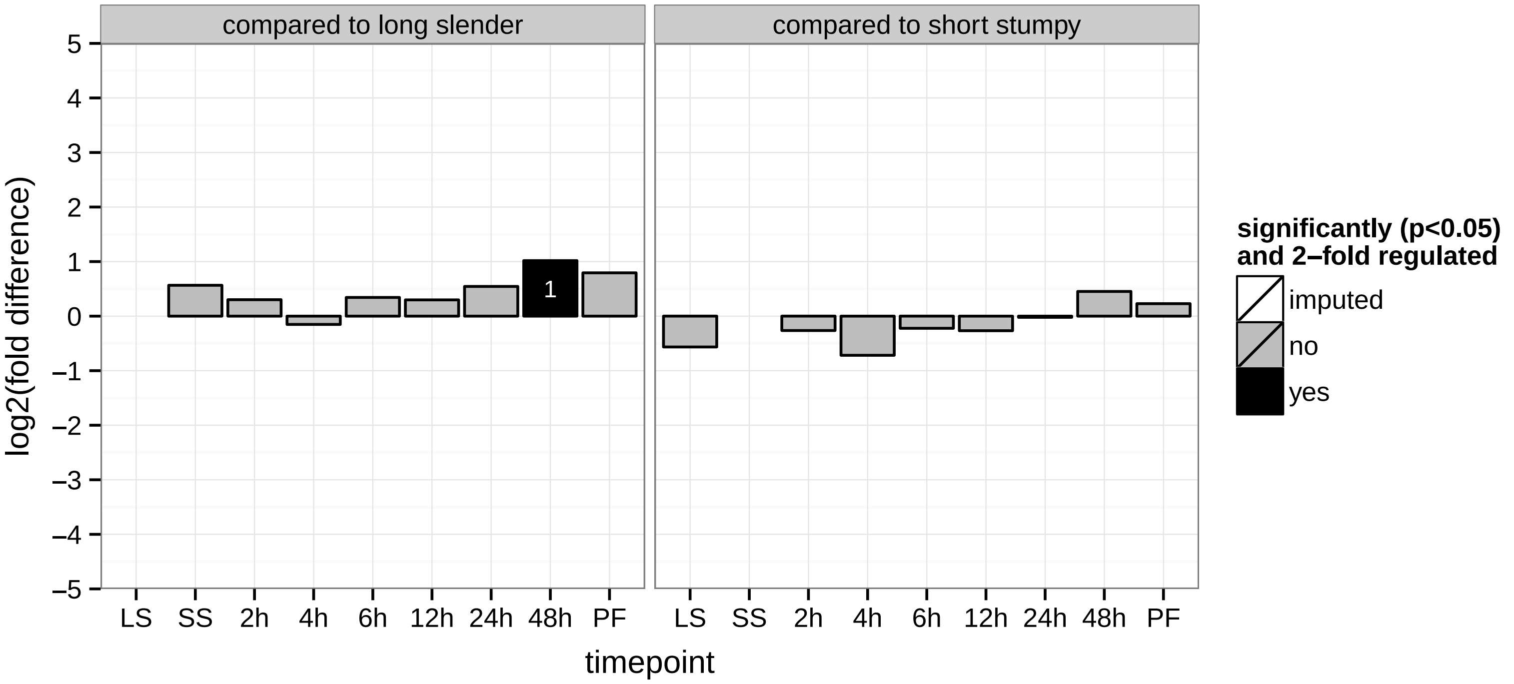
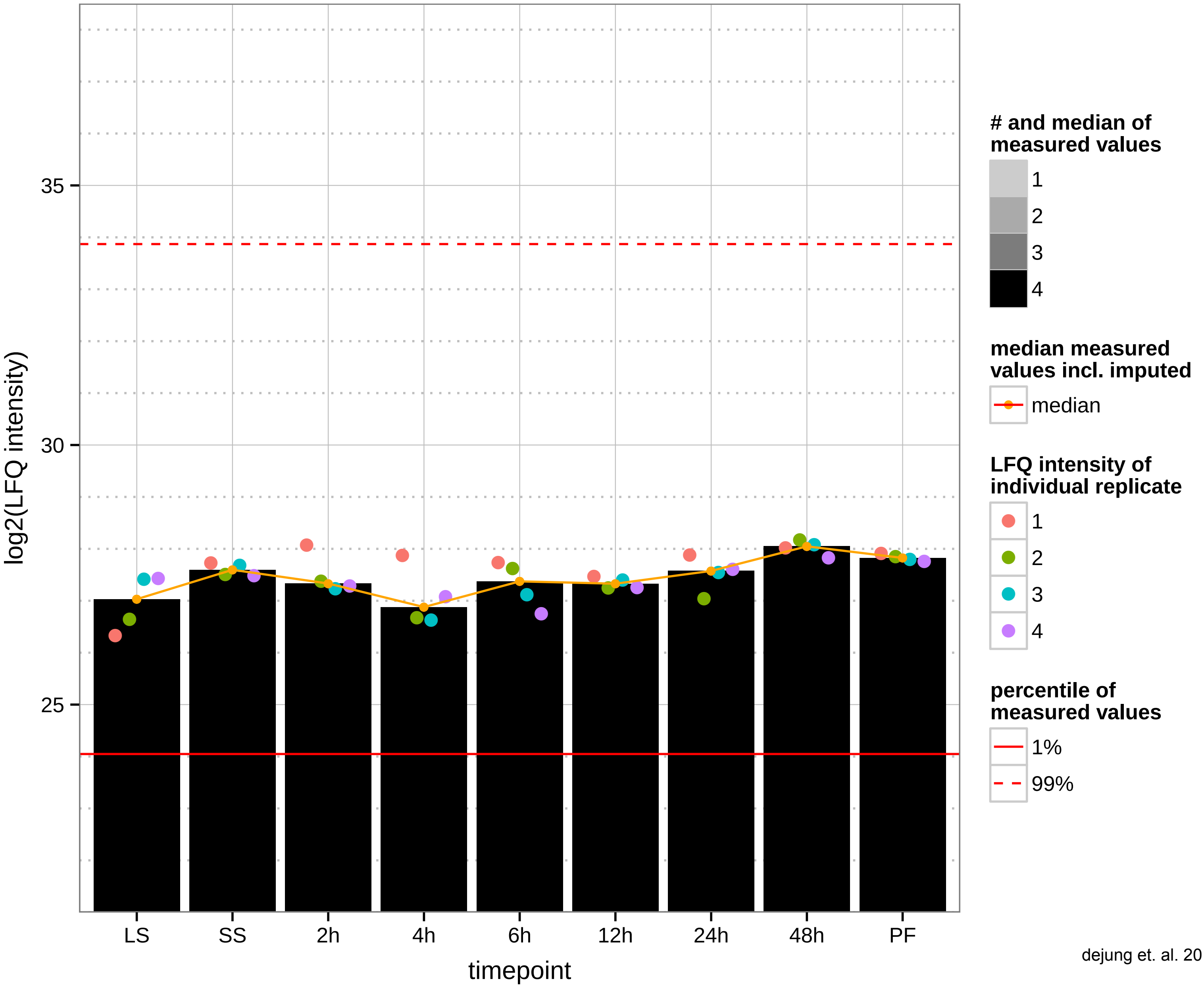
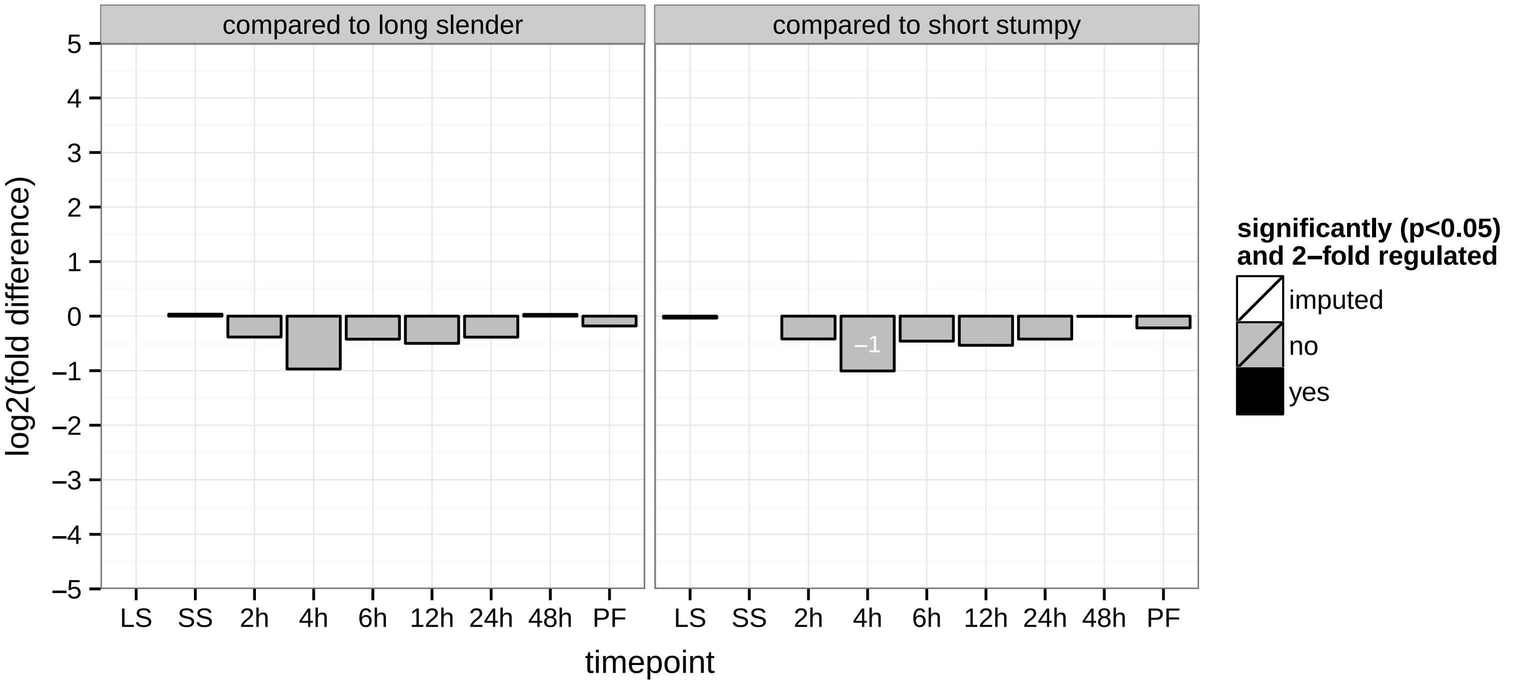
cysteine peptidase, Clan CA, family C2, putative, calpain
Tb927.10.1890
AGOF: calcium–dependent cysteine–type endopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: calcium–dependent cysteine–type endopeptidase activity
PGOC: intracellular
PGOP: proteolysis

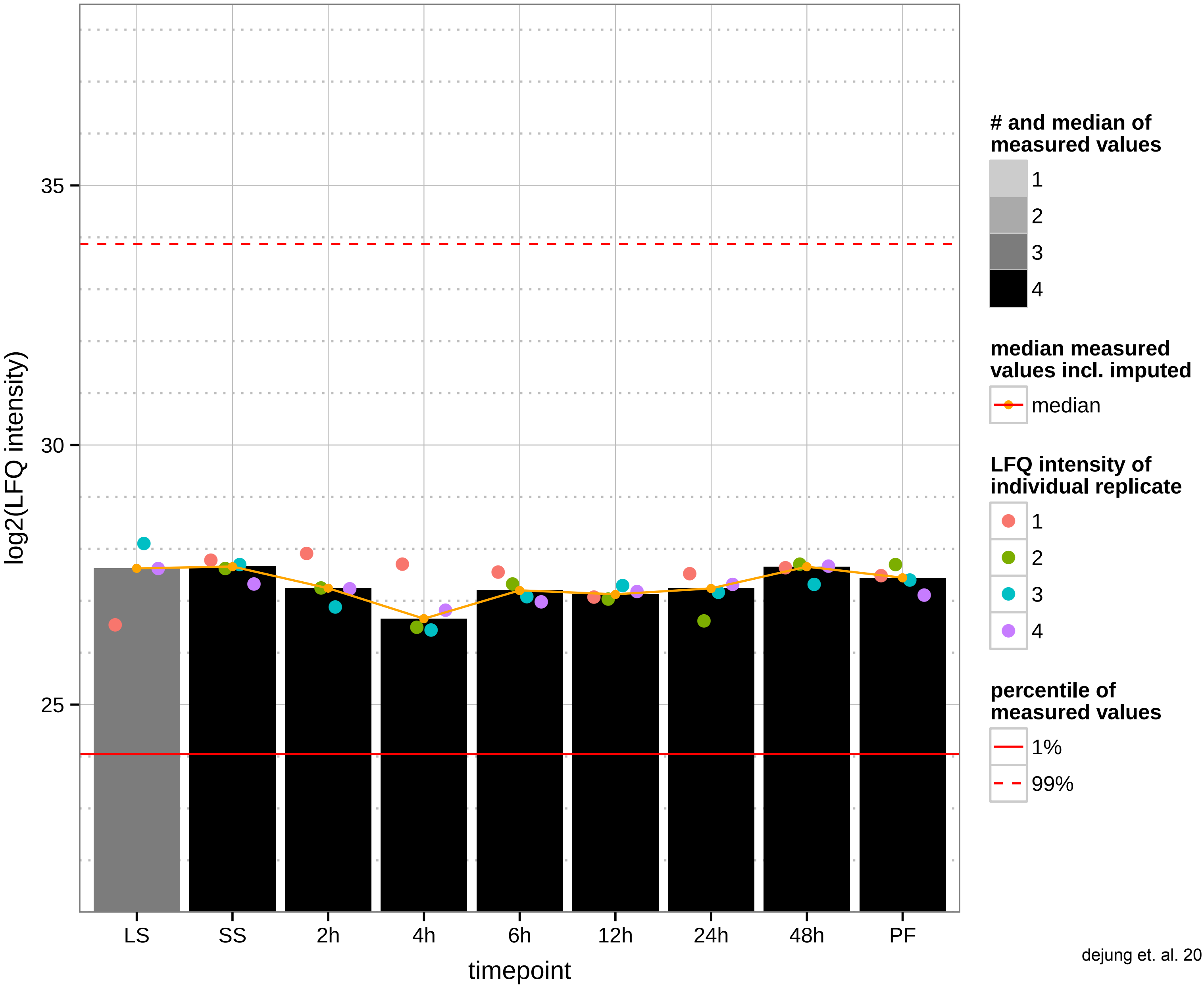




dejung et. al. 2015

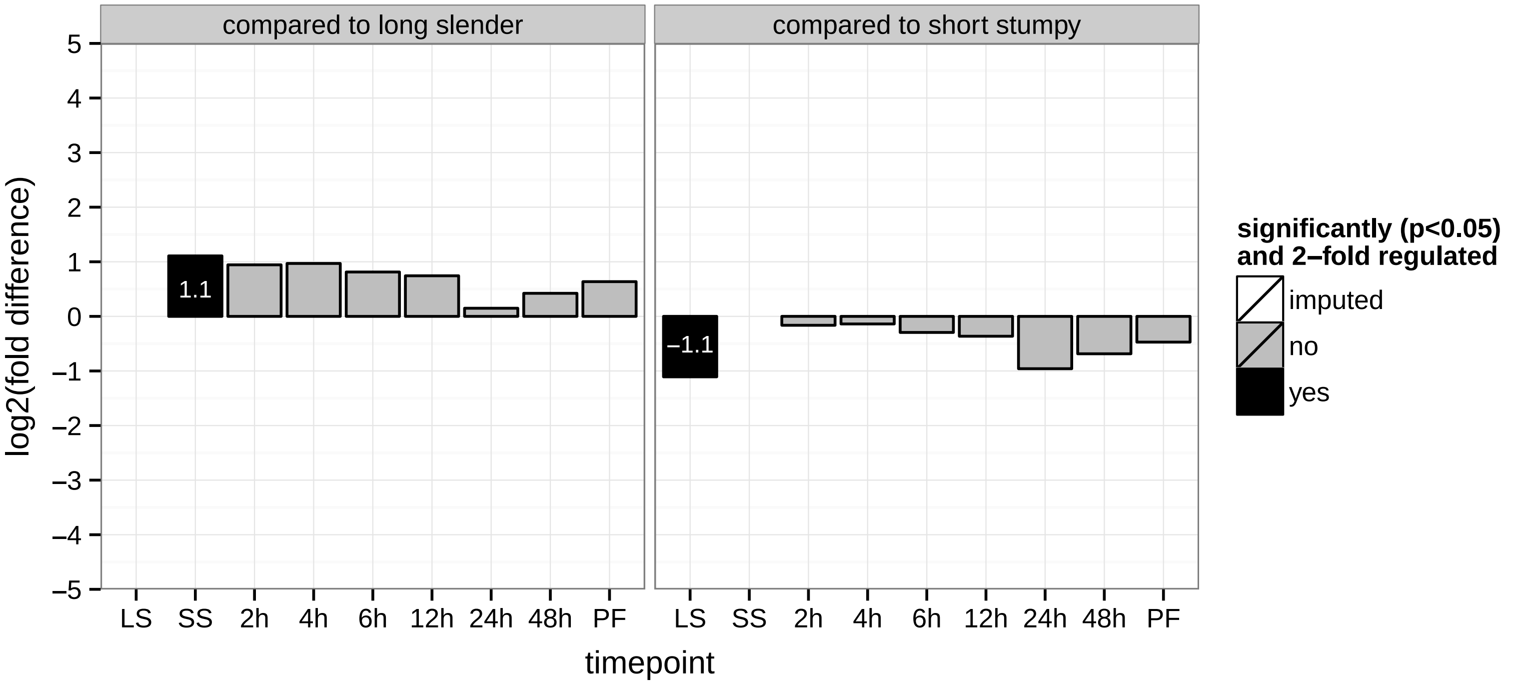
hypothetical protein, conserved
Tb927.10.1970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

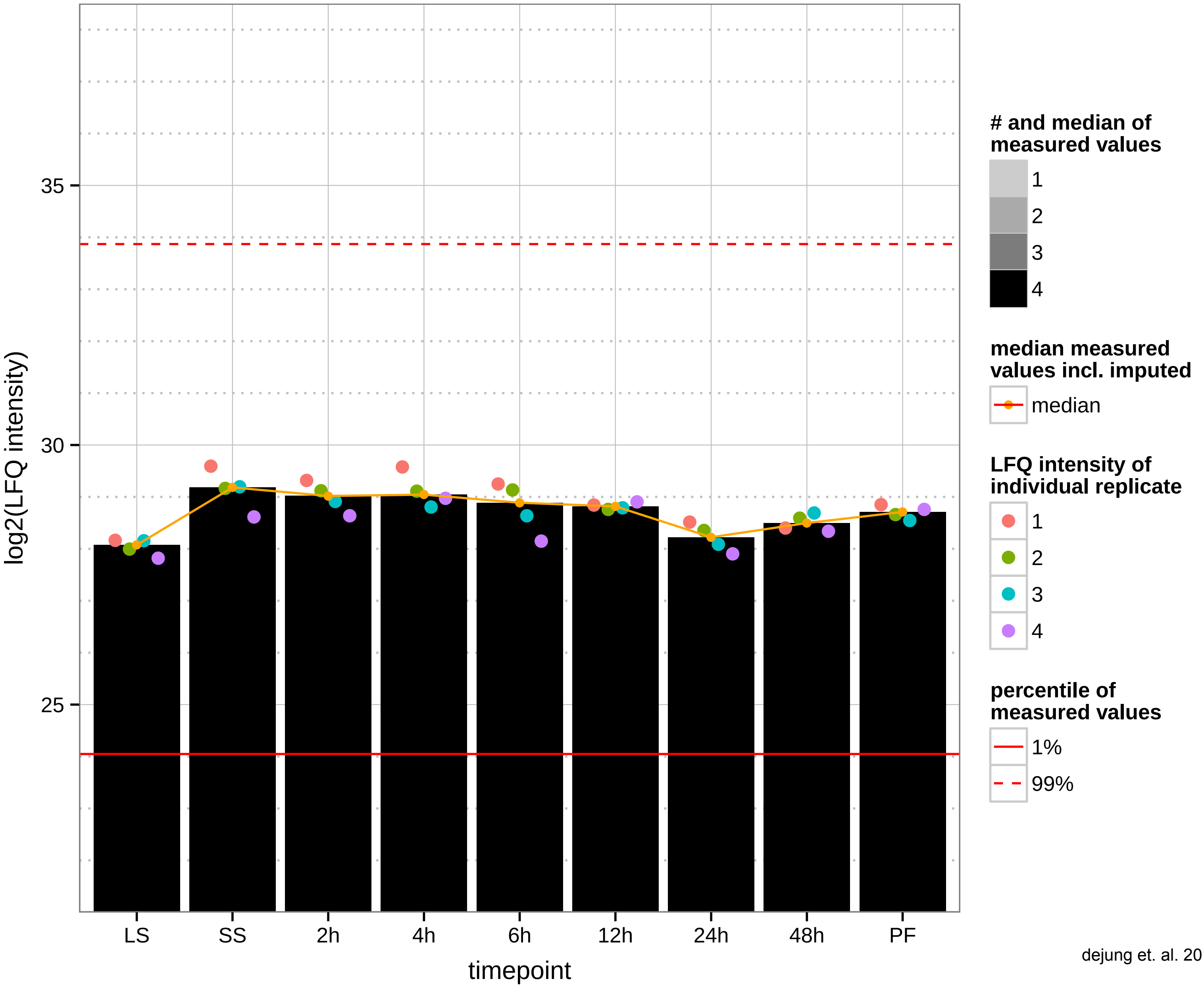




dejung et. al. 2015

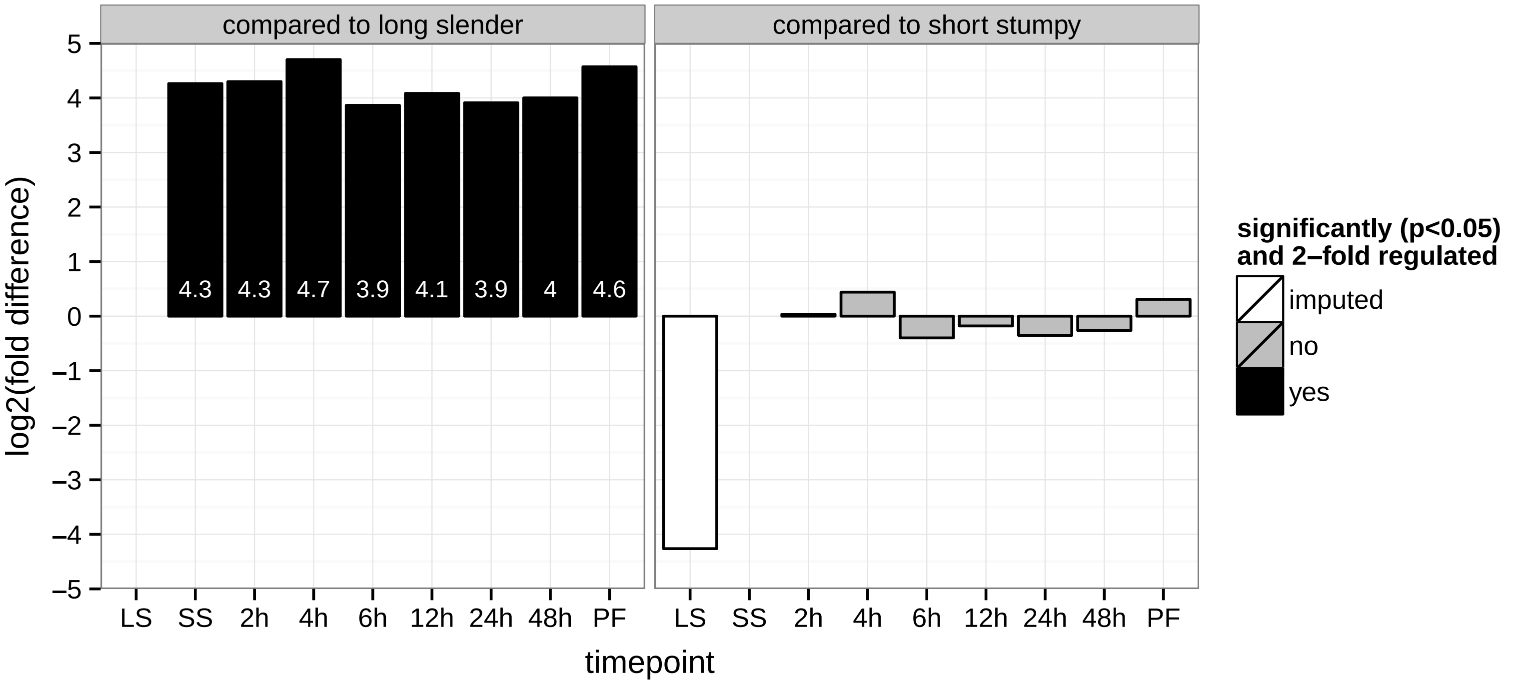
major vault protein, putative, putative (MVP)
Tb927.10.1990
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

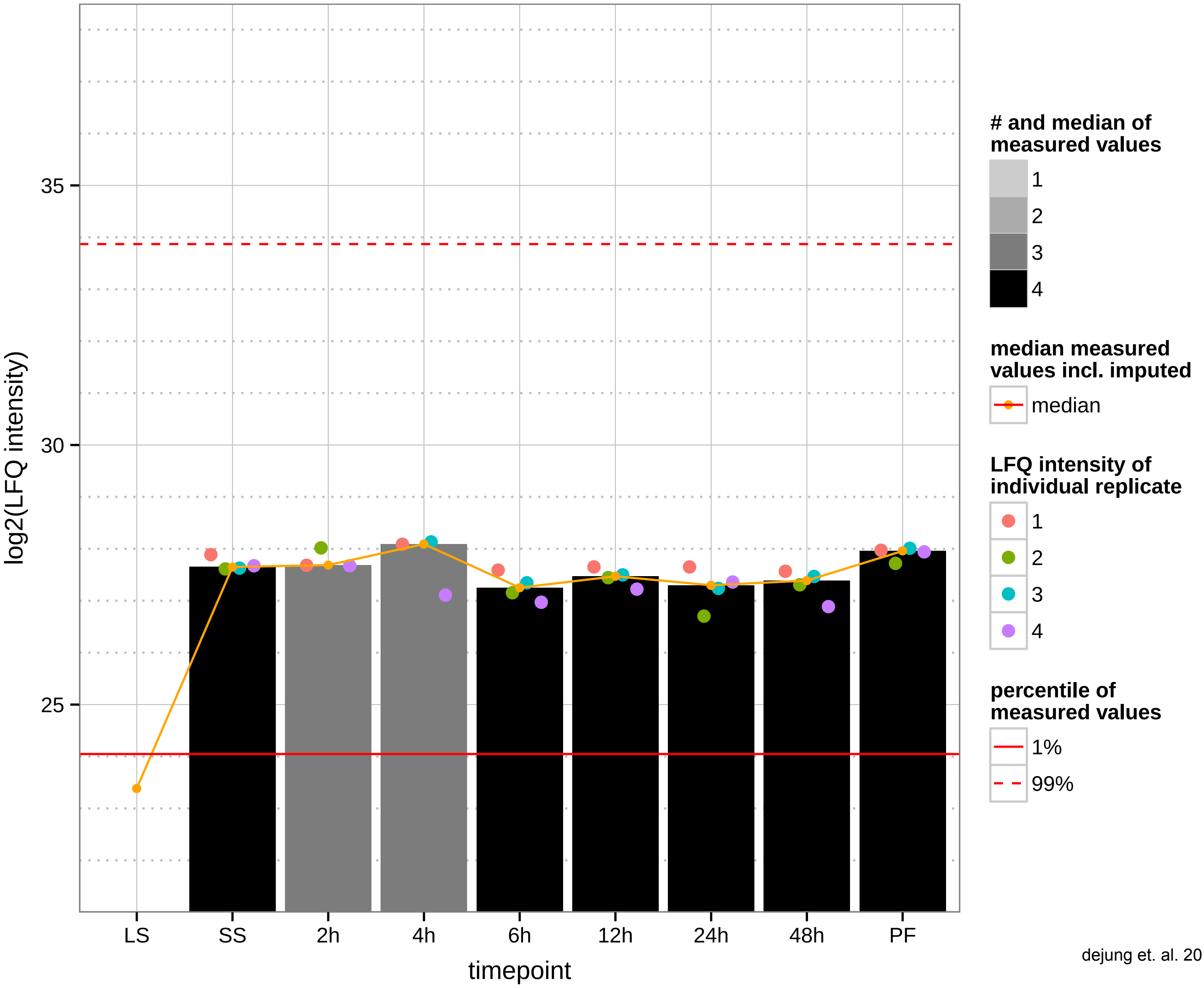




dejung et. al. 2015

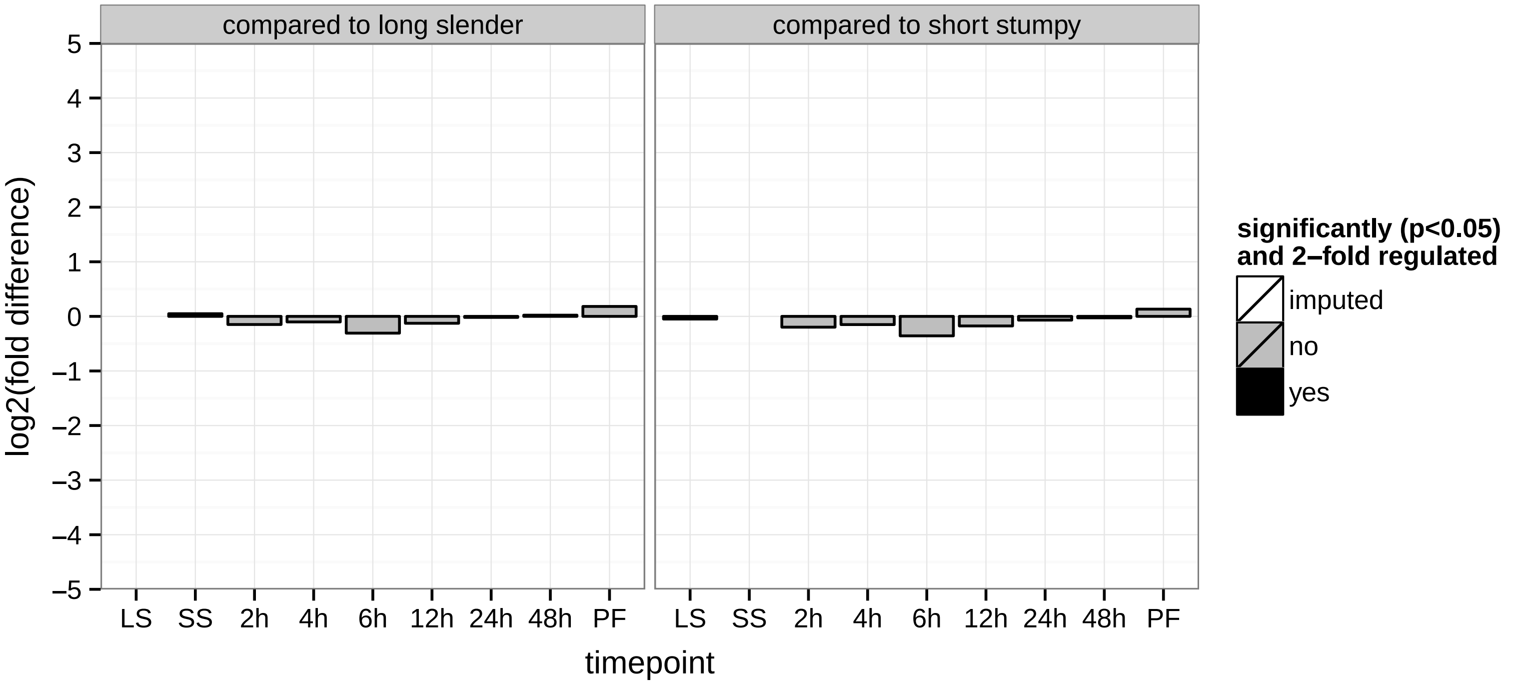
protein kinase, putative
Tb927.10.2040
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

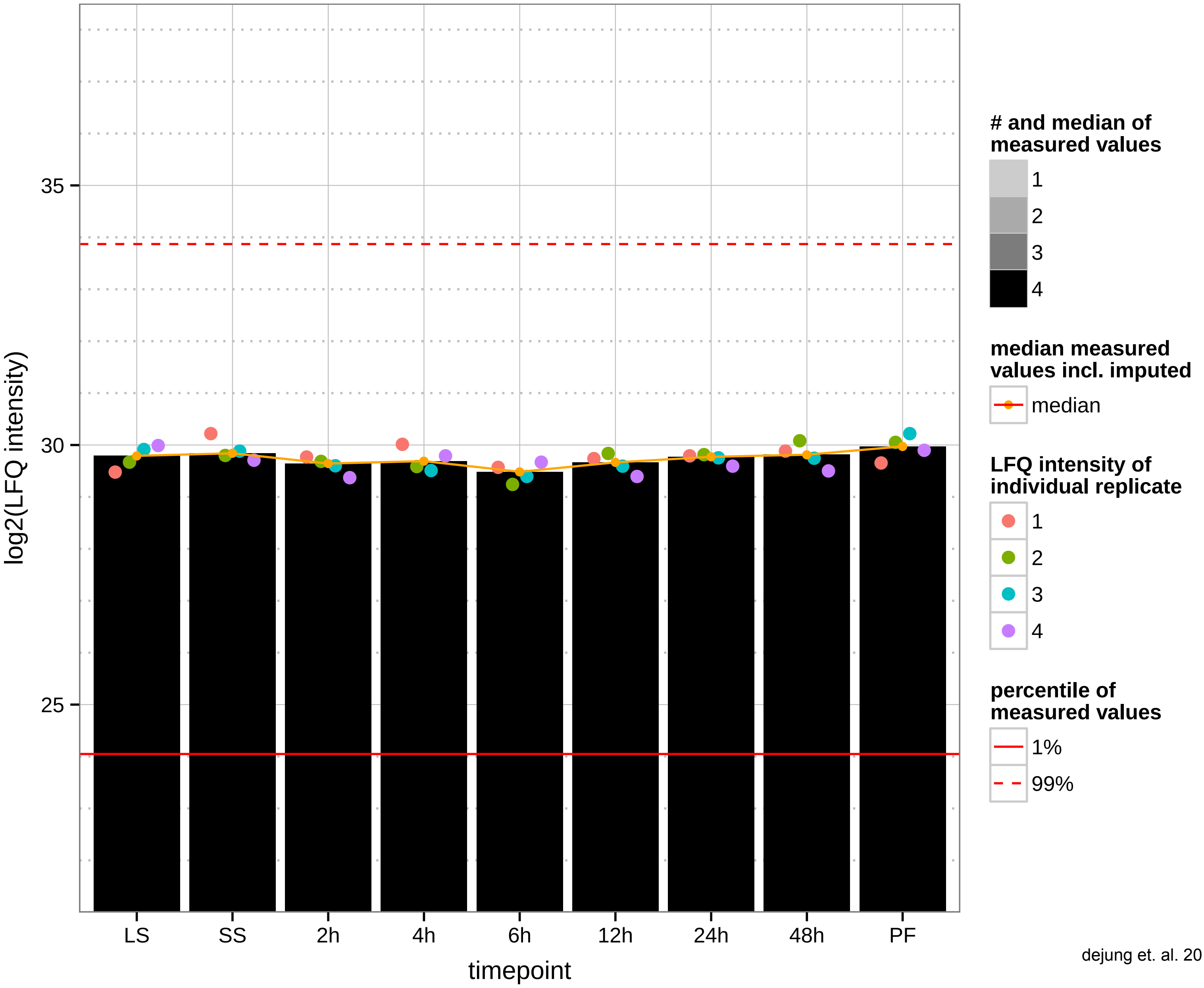




dejung et. al. 2015

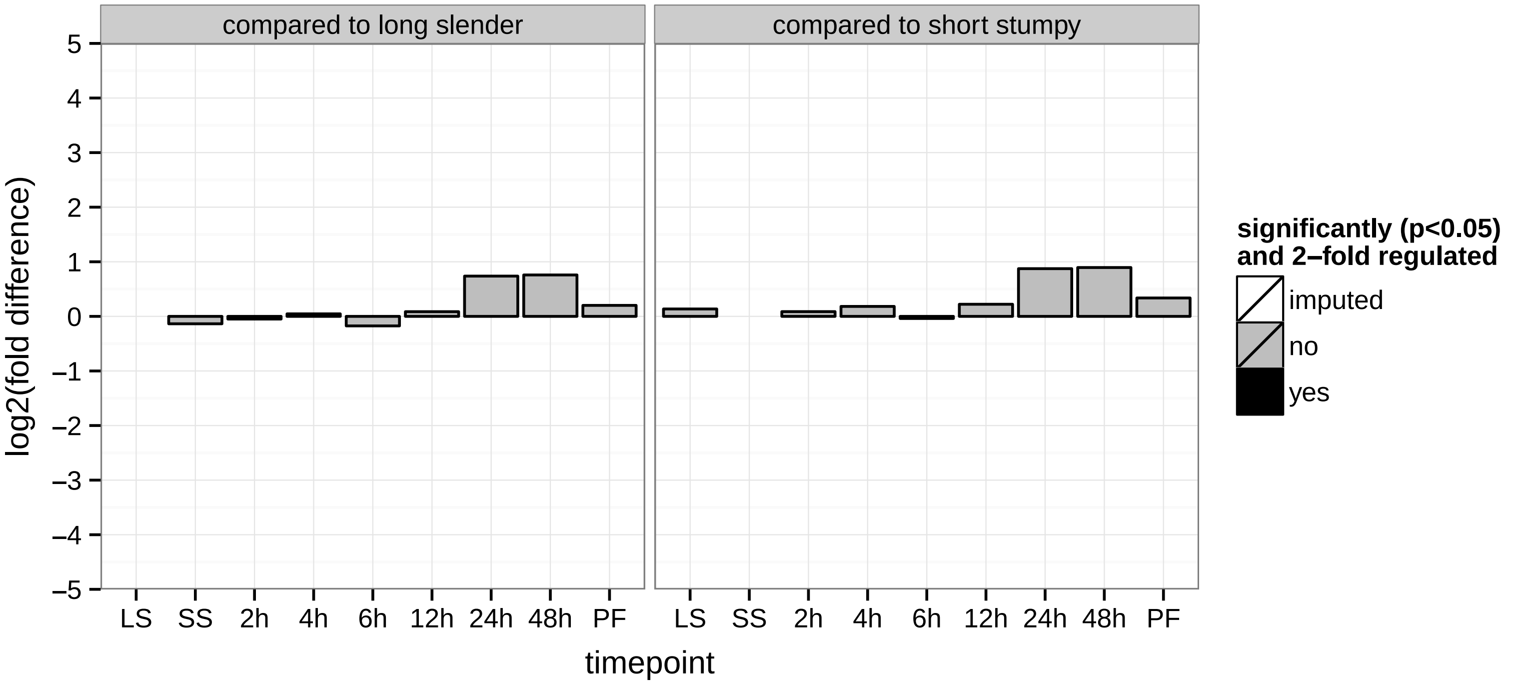
hypothetical protein, conserved
Tb927.10.2190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

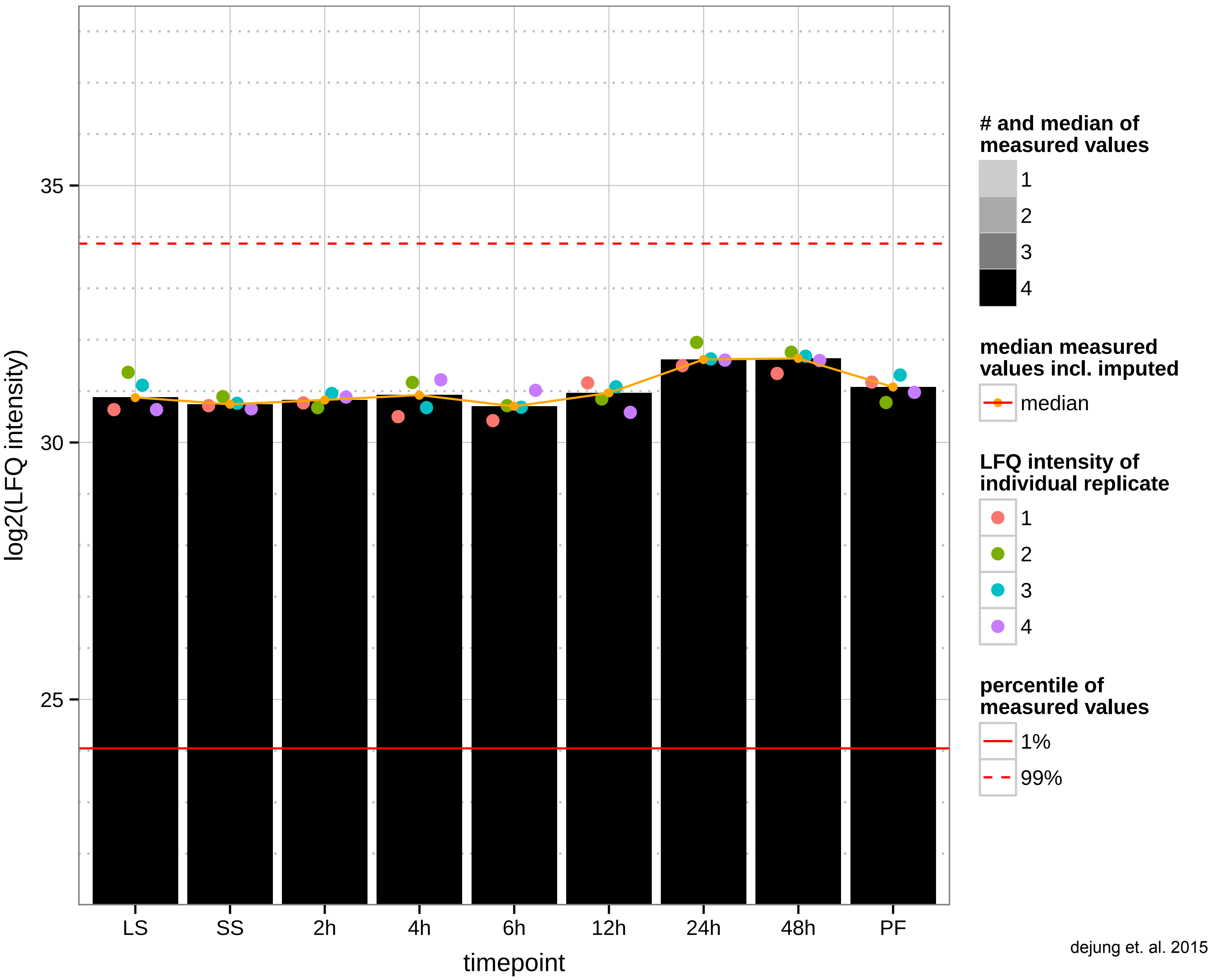




dejung et. al. 2015

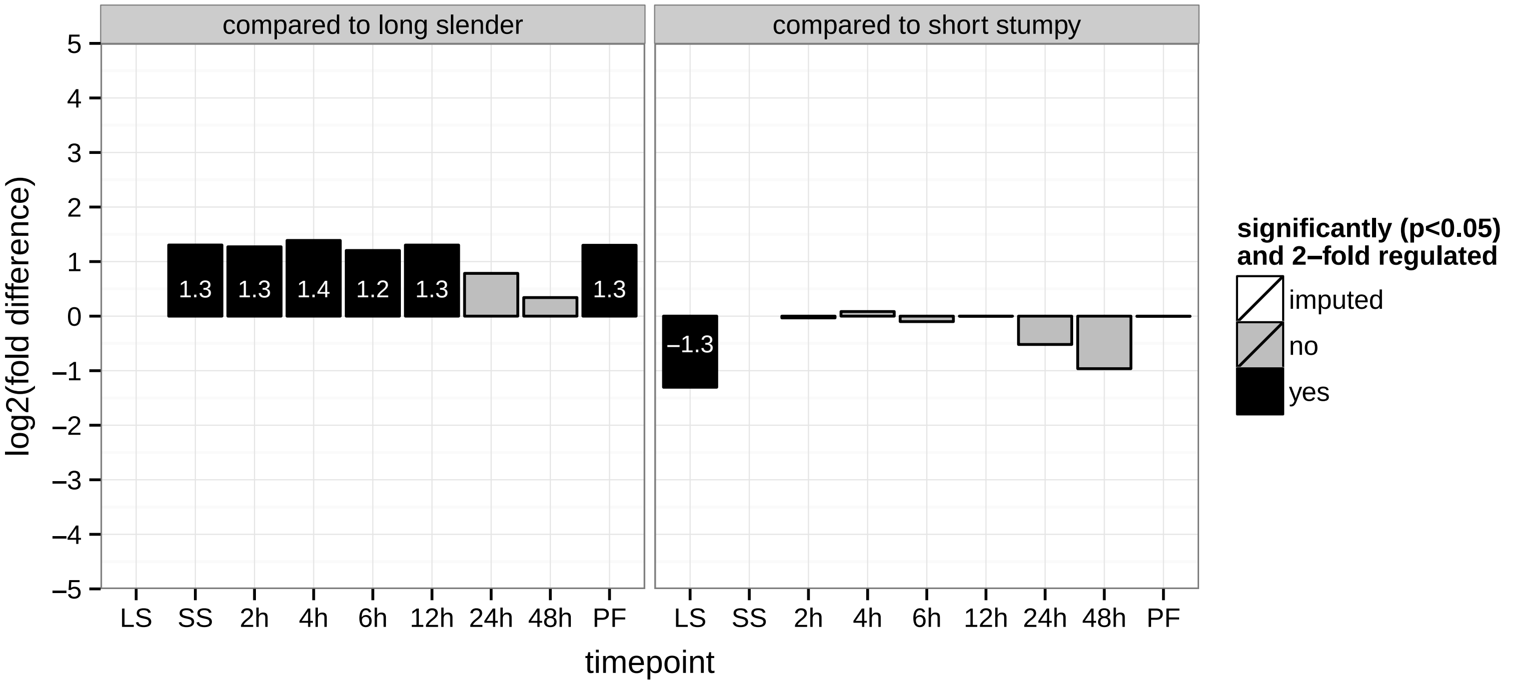
60S ribosomal protein L37a, putative, 60S ribosomal proteins L37
Tb927.10.6370;Tb927.10.220
AGOF: structural constituent of ribosome, zinc ion binding
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation

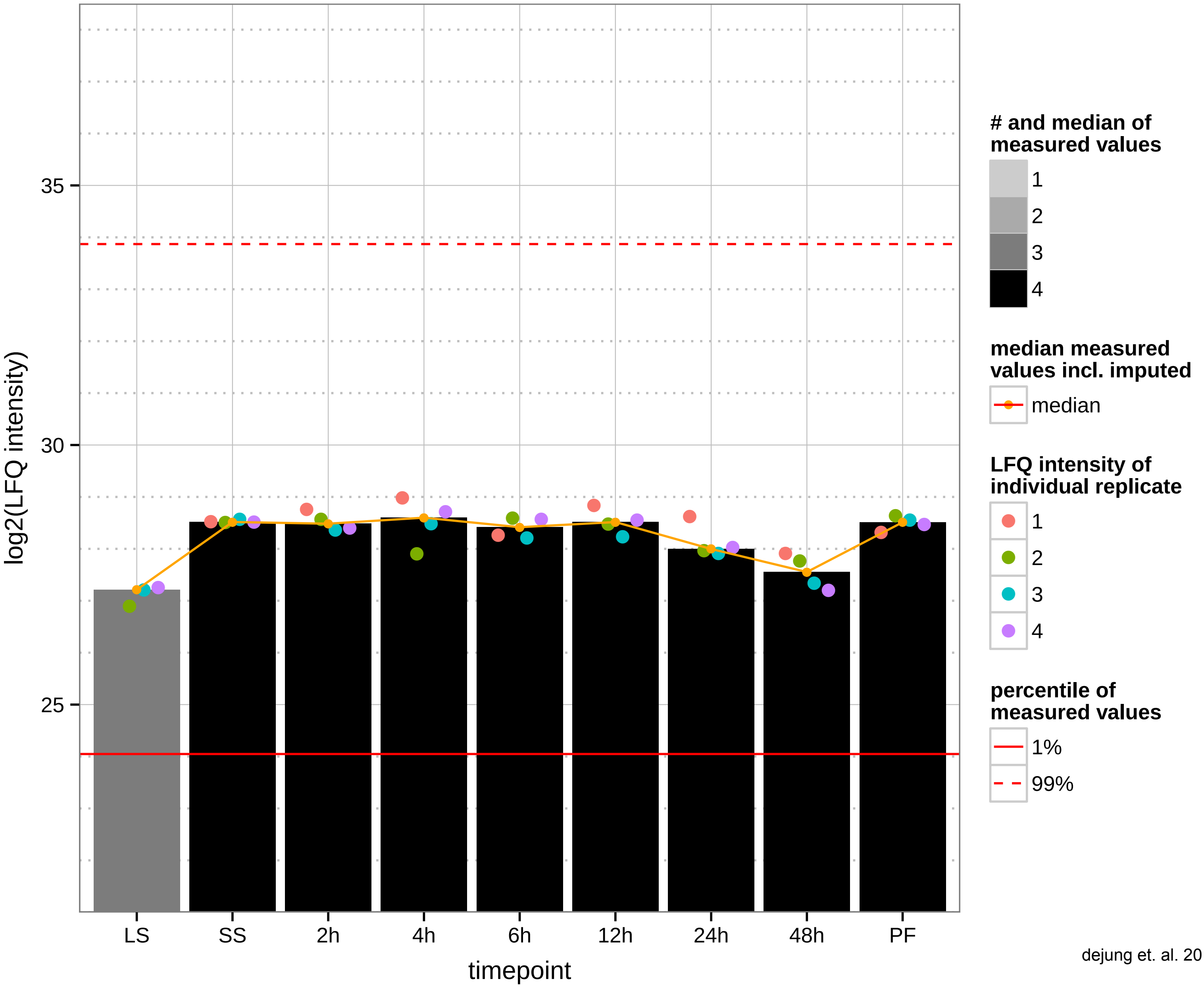




dejung et. al. 2015

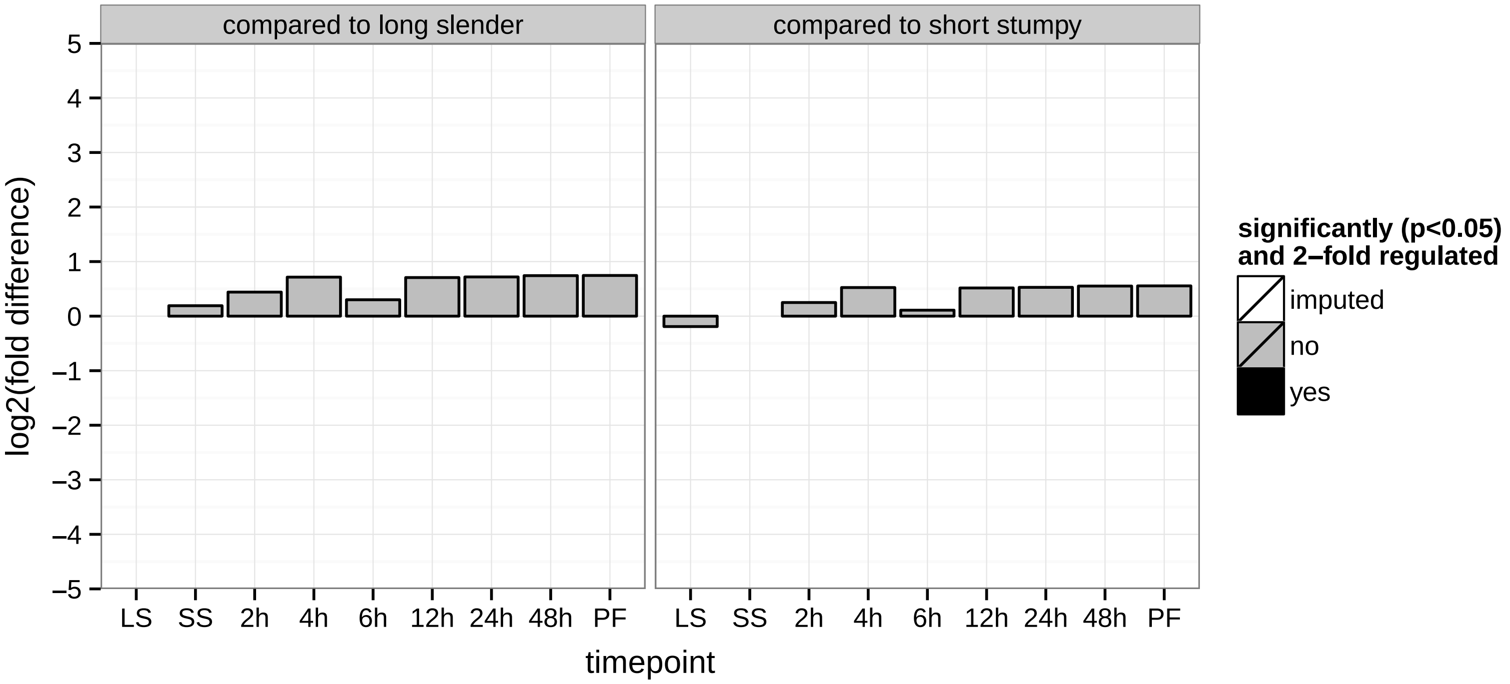
vacuolar protein sorting–associated protein 35, putative
Tb927.10.2270
AGOF: null
AGOC: cytoplasm, membrane
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

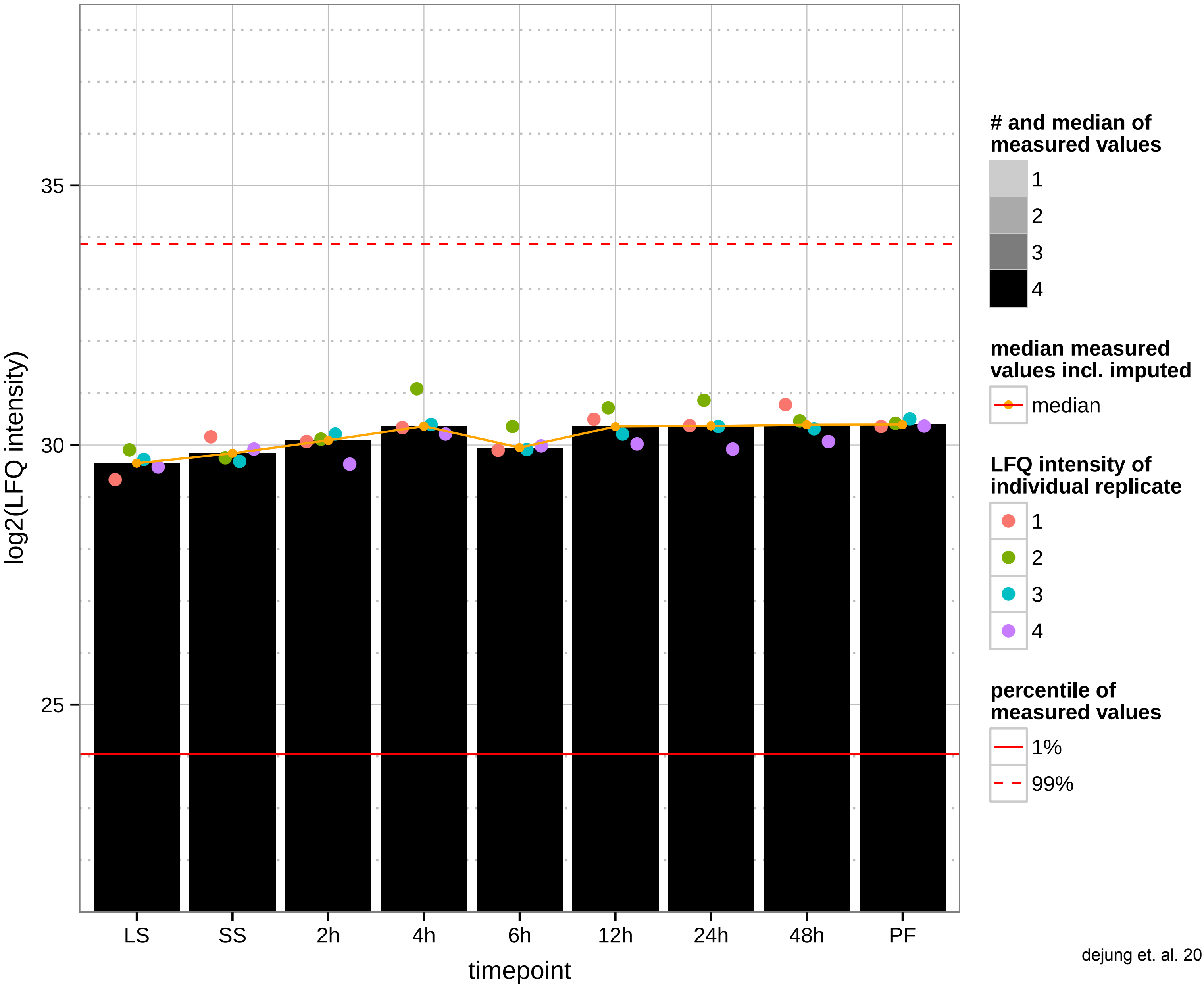




dejung et. al. 2015

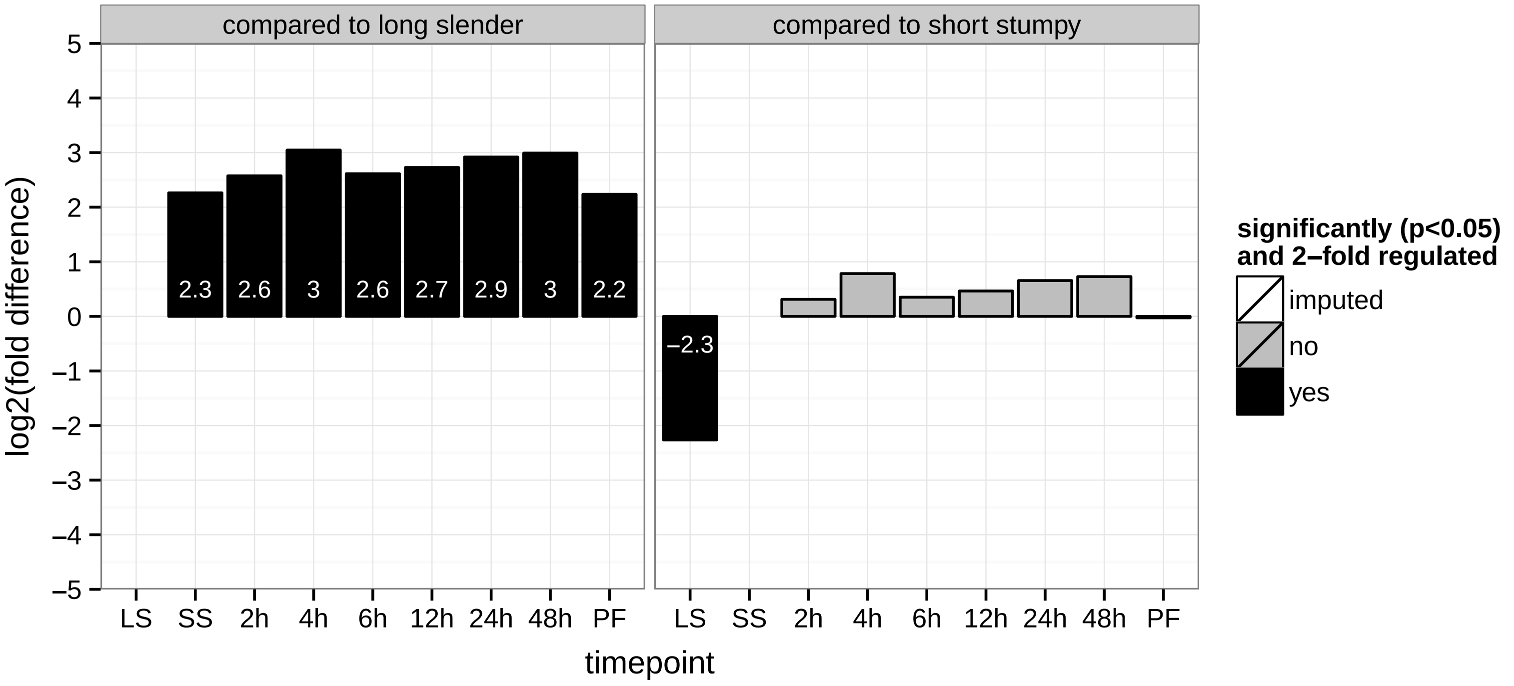
proteasome subunit alpha type–5, putative, 20S proteasome subunit alpha 5
Tb927.10.230
AGOF: threonine–type endopeptidase activity
AGOC: cytosol, nucleus, proteasome core complex
AGOP: ubiquitin–dependent protein catabolic process
PGOF: endopeptidase activity, threonine–type endopeptidase activity
PGOC: proteasome core complex, proteasome core complex, alpha–subunit complex
PGOP: proteolysis involved in cellular protein catabolic process, ubiquitin–dependent protein catabolic process

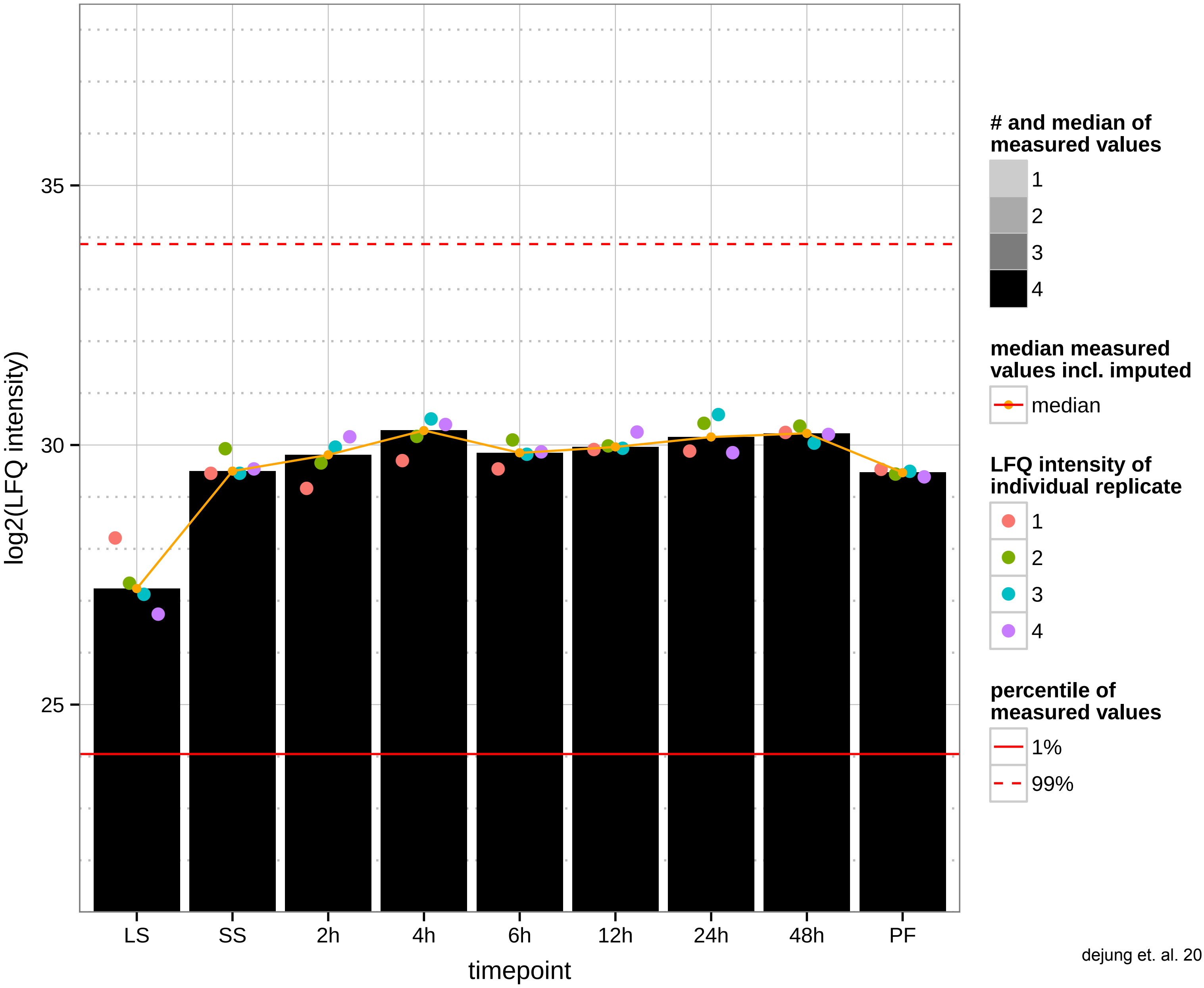




dejung et. al. 2015

pyruvate dehydrogenase complex E3 binding protein, putative
Tb927.10.2350
AGOF: biotin binding, dihydrolipoyllysine–residue acetyltransferase activity
AGOC: mitochondrion, pyruvate dehydrogenase complex
AGOP: generation of precursor metabolites and energy
PGOF: null
PGOC: null
PGOP: null





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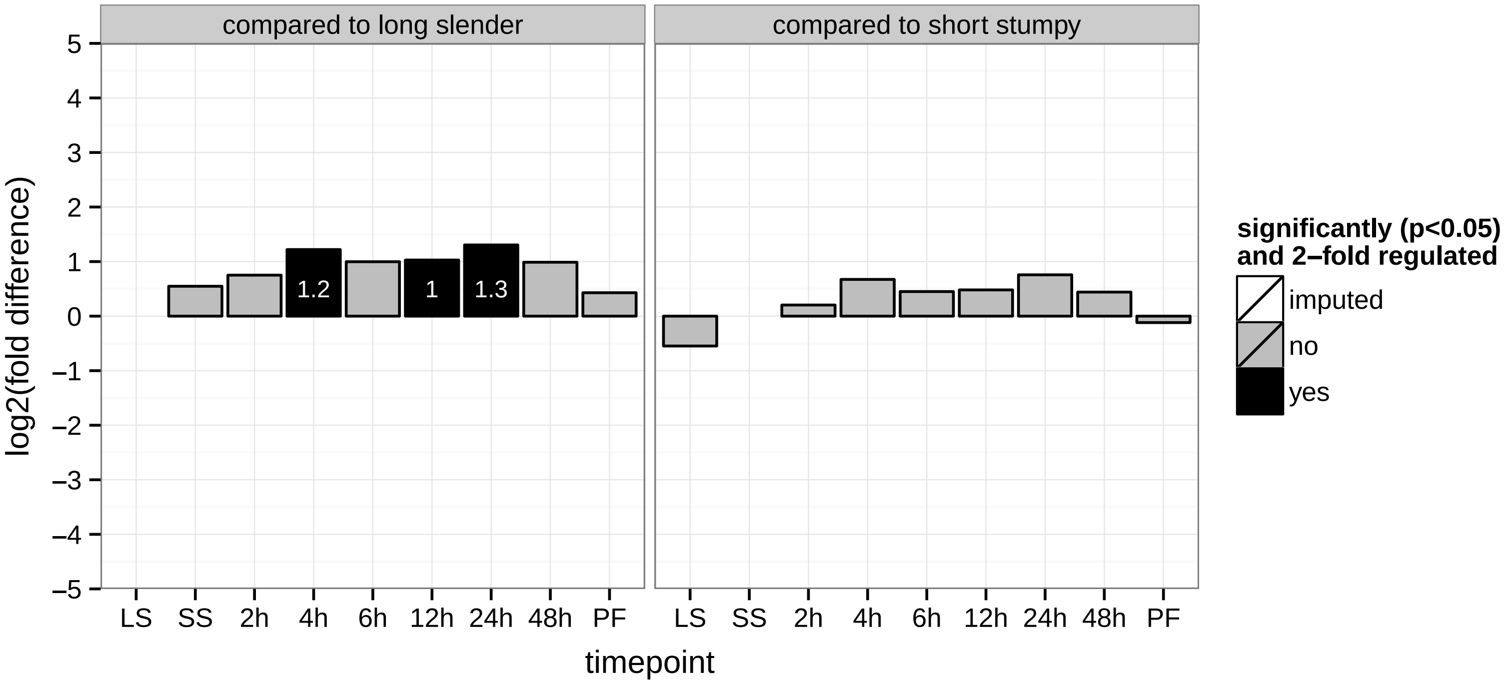
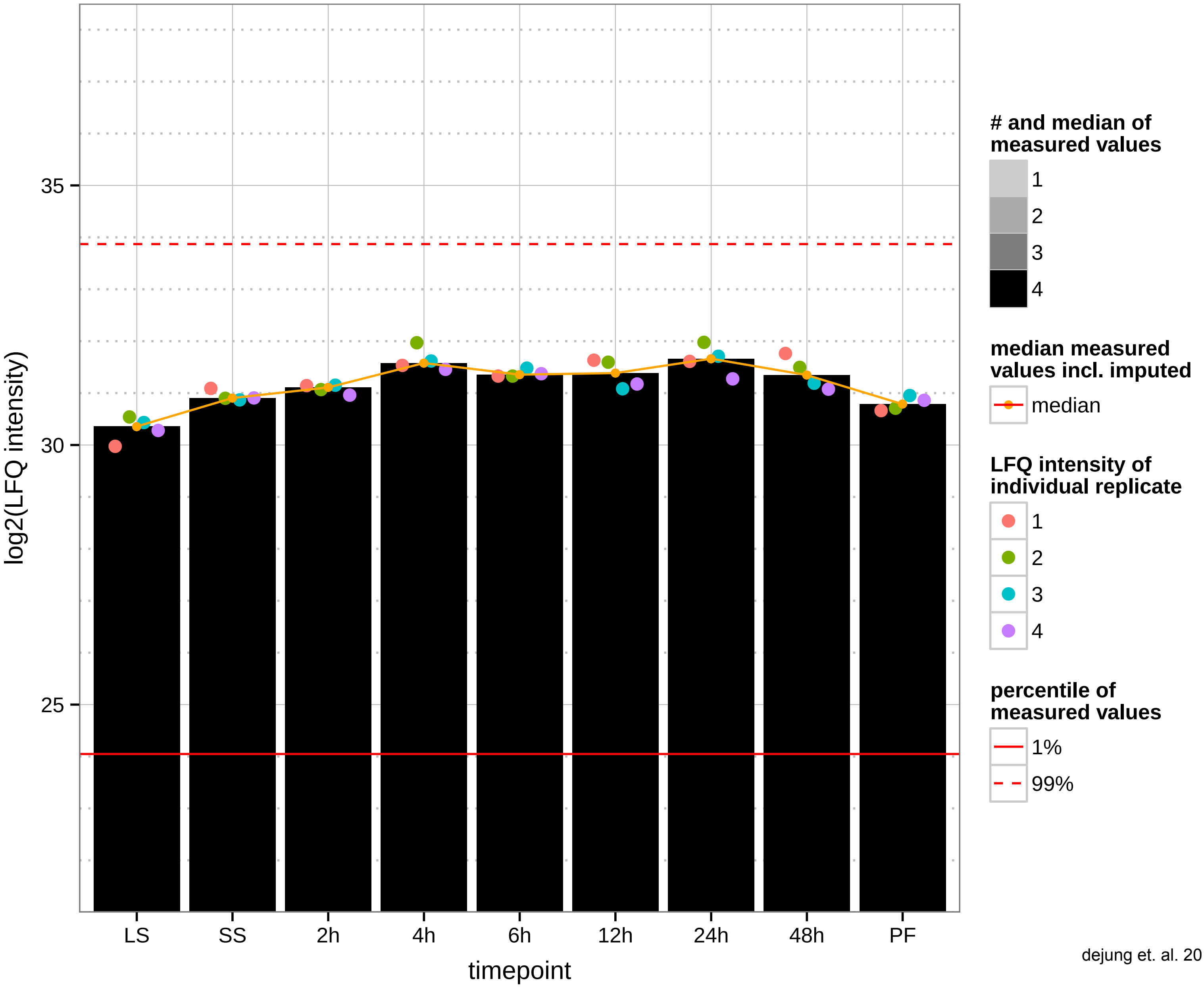
RNA–binding protein, putative (LA)
Tb927.10.2370
AGOF: RNA binding
AGOC: nucleus, ribonucleoprotein complex
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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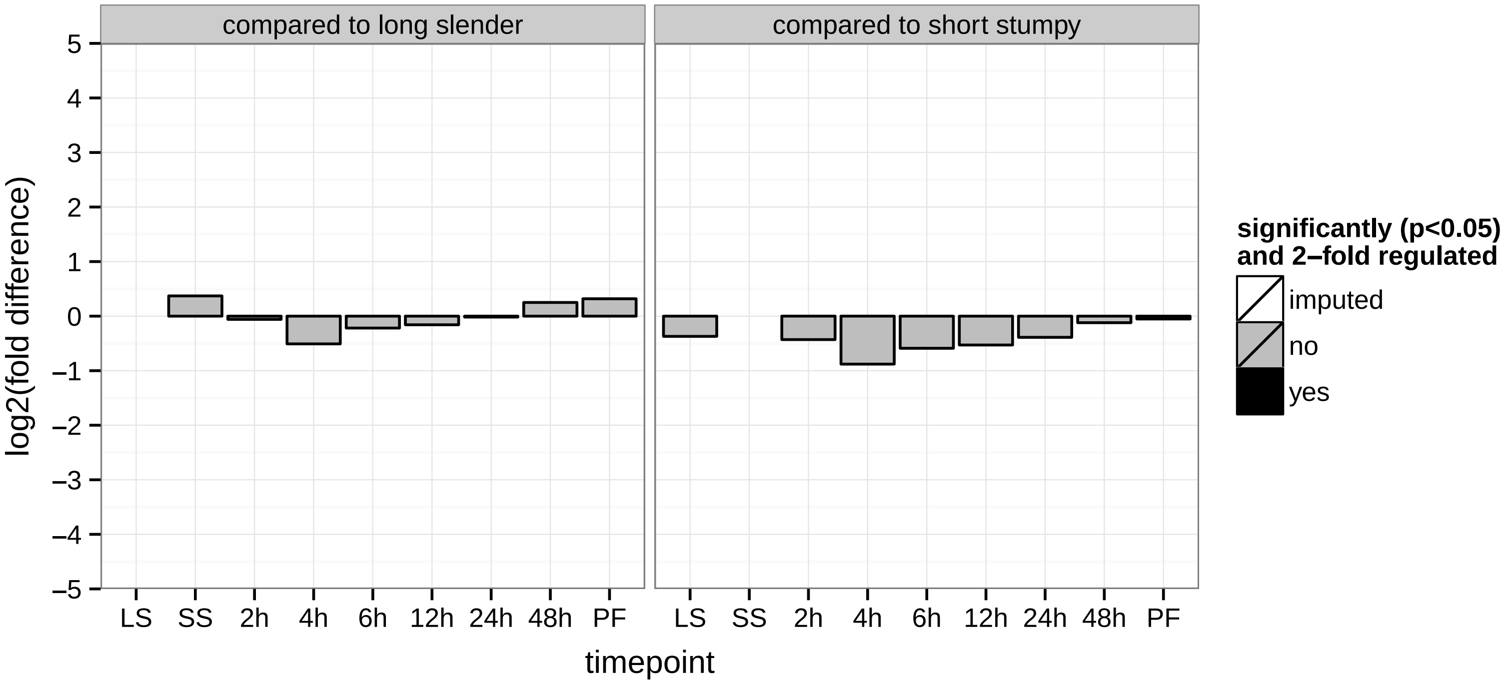
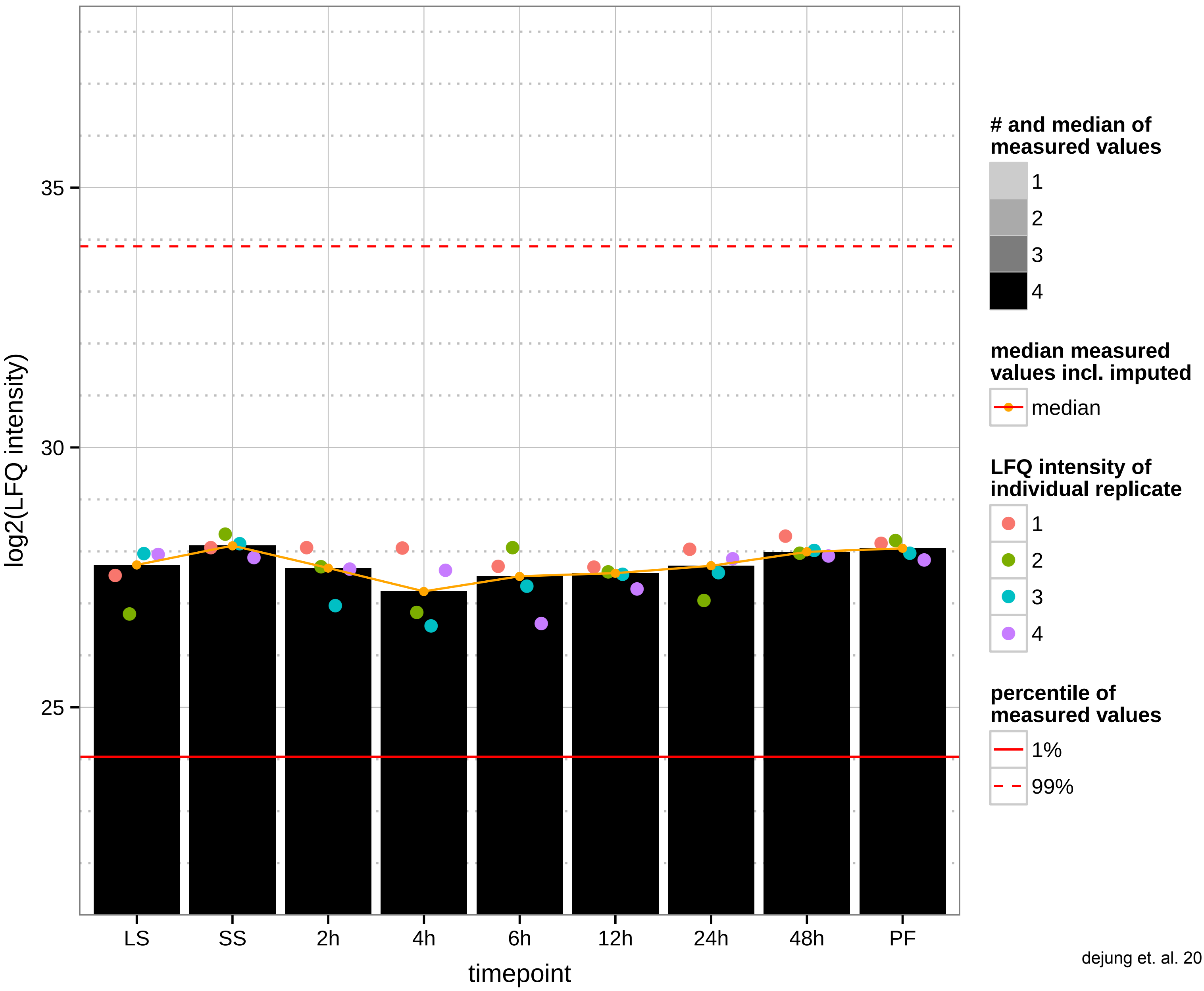
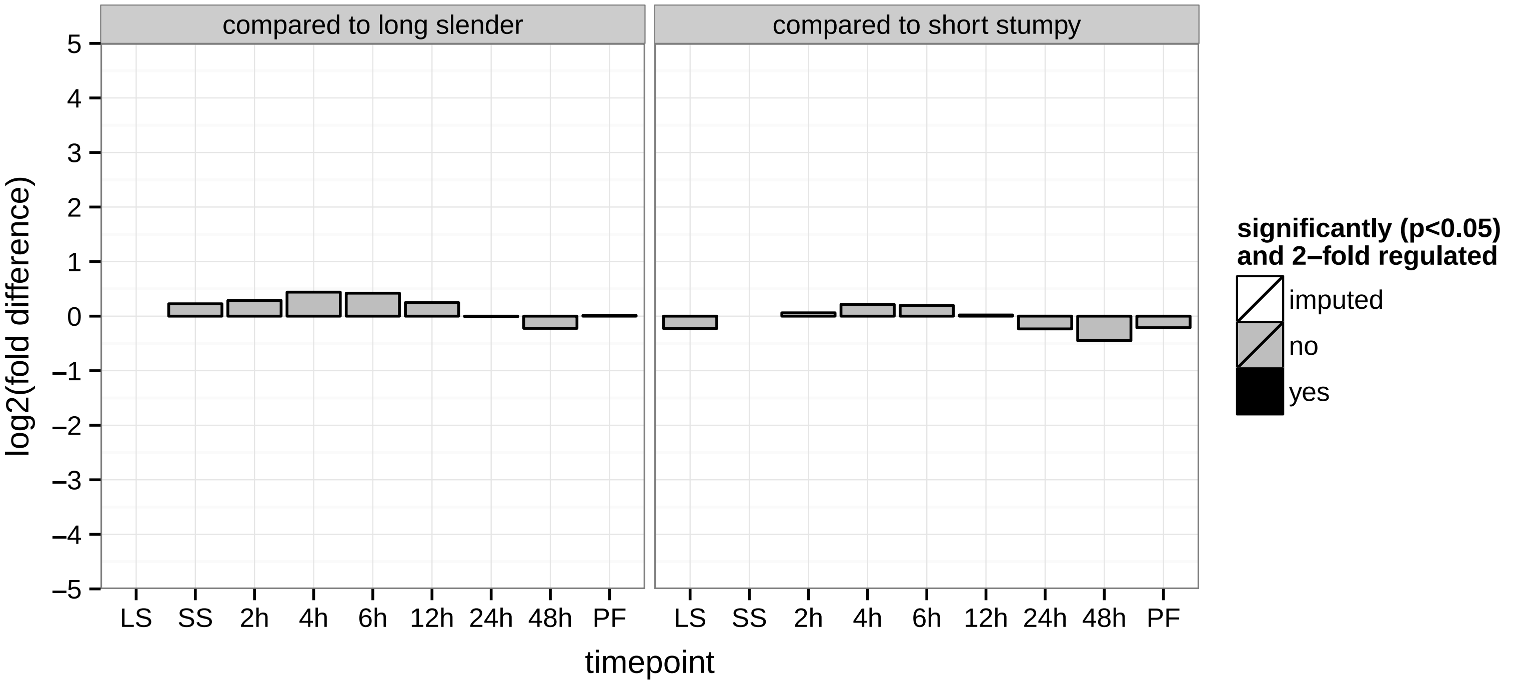
hypothetical protein, conserved
Tb927.10.2380
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

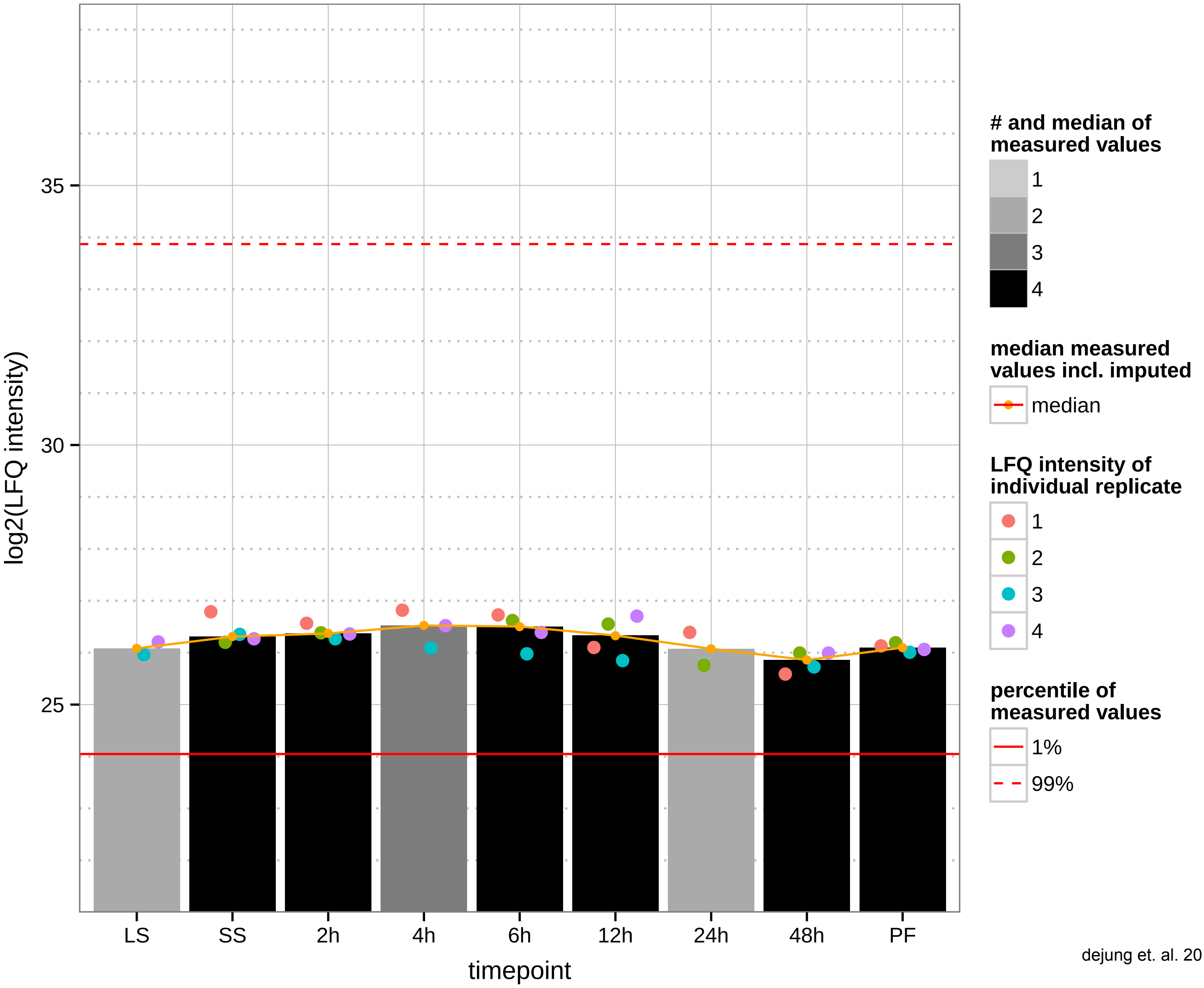




dejung et. al. 2015

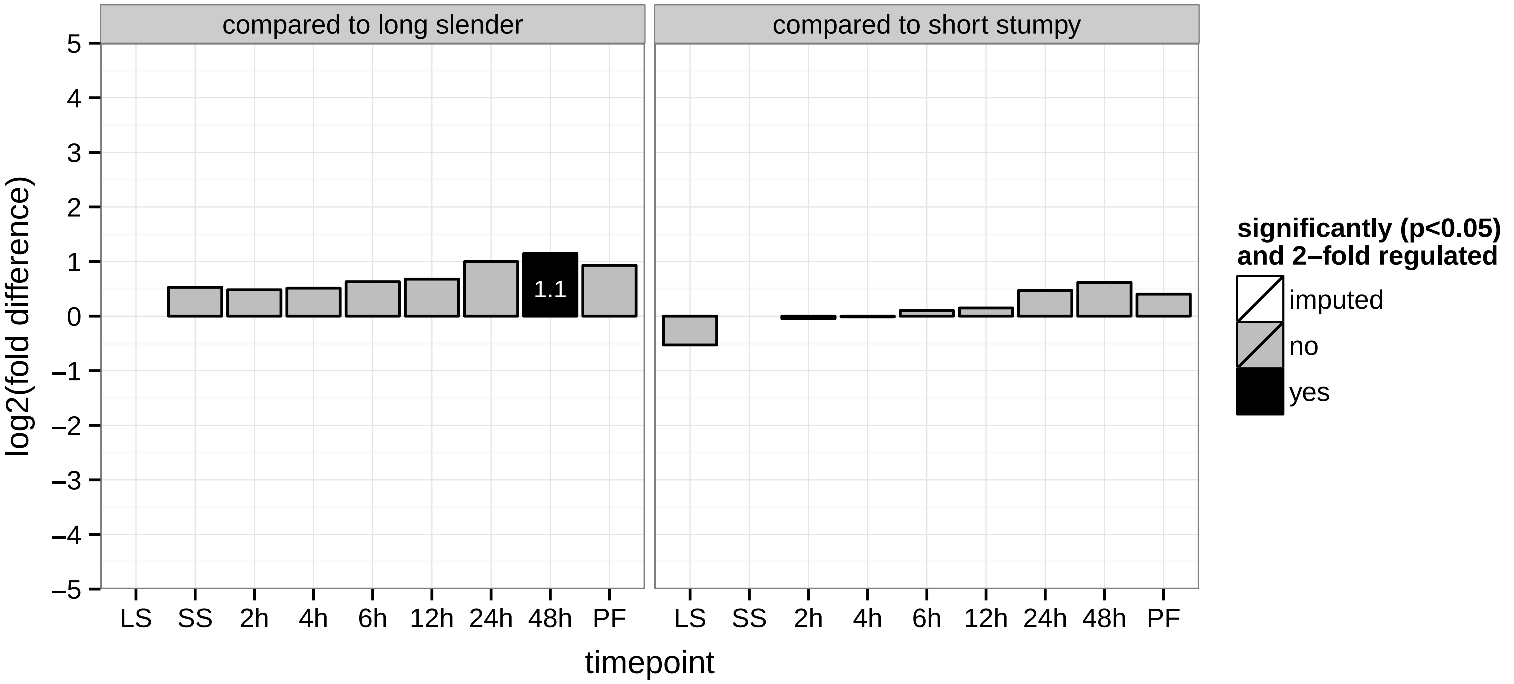
hypothetical protein, conserved
Tb927.10.2470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

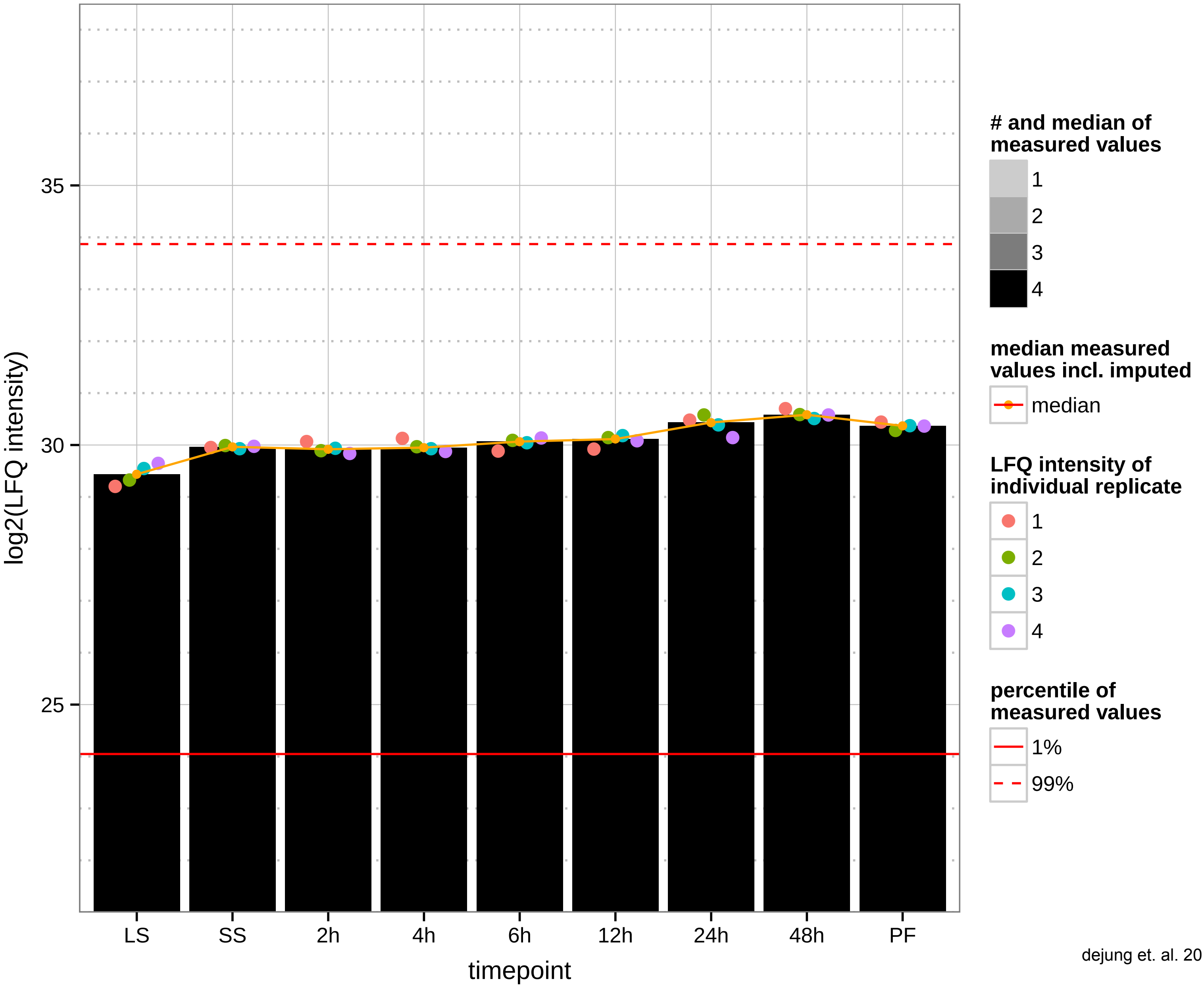




dejung et. al. 2015

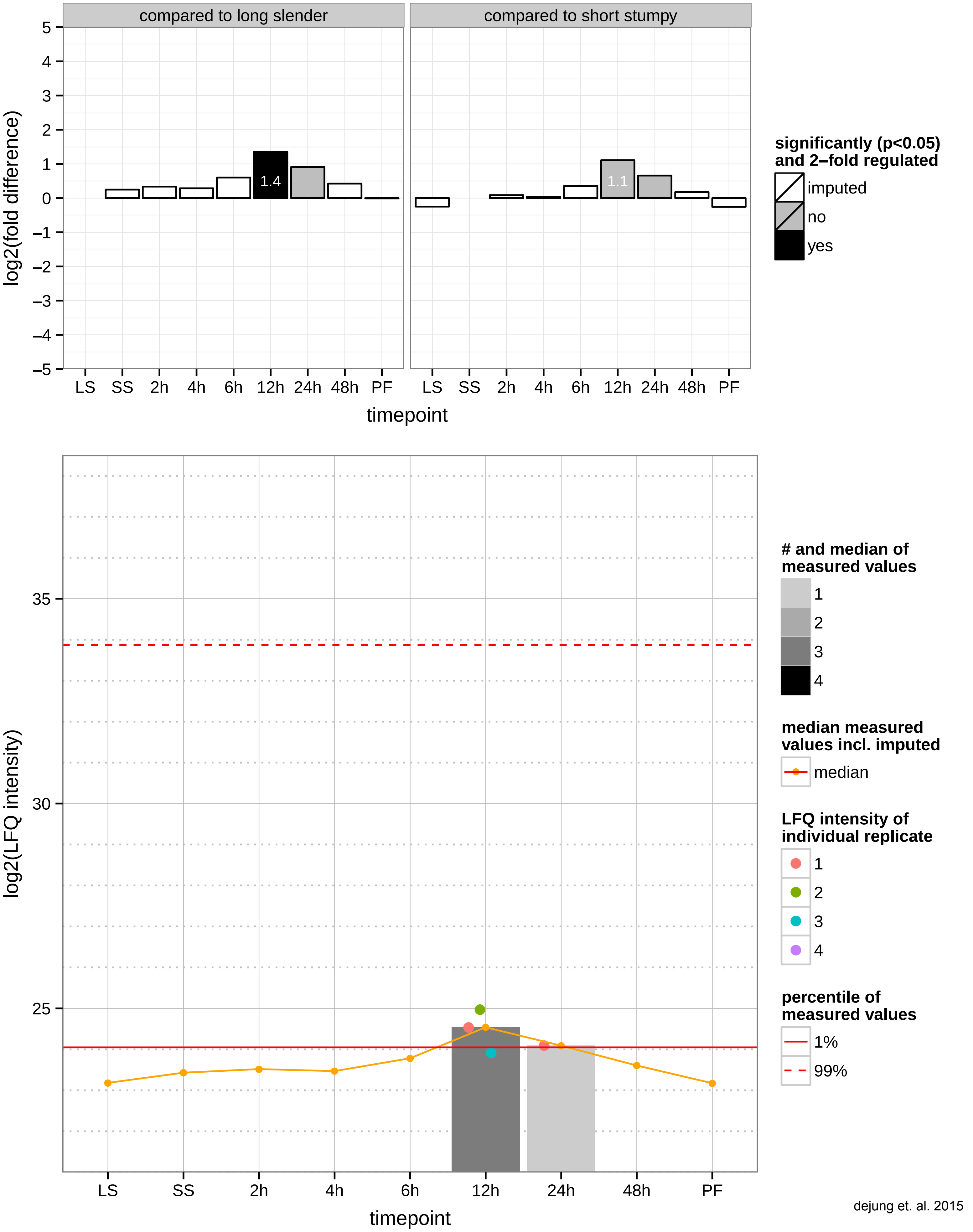
adenylate kinase, putative
Tb927.10.2530
AGOF: ATP binding, adenylate kinase activity
AGOC: null
AGOP: nucleobase–containing compound metabolic process, purine ribonucleotide biosynthetic process
PGOF: ATP binding, adenylate kinase activity, nucleobase–containing compound kinase activity, nucleotide kinase activity, ph
PGOC: null
PGOP: nucleobase–containing compound metabolic process, nucleotide phosphorylation



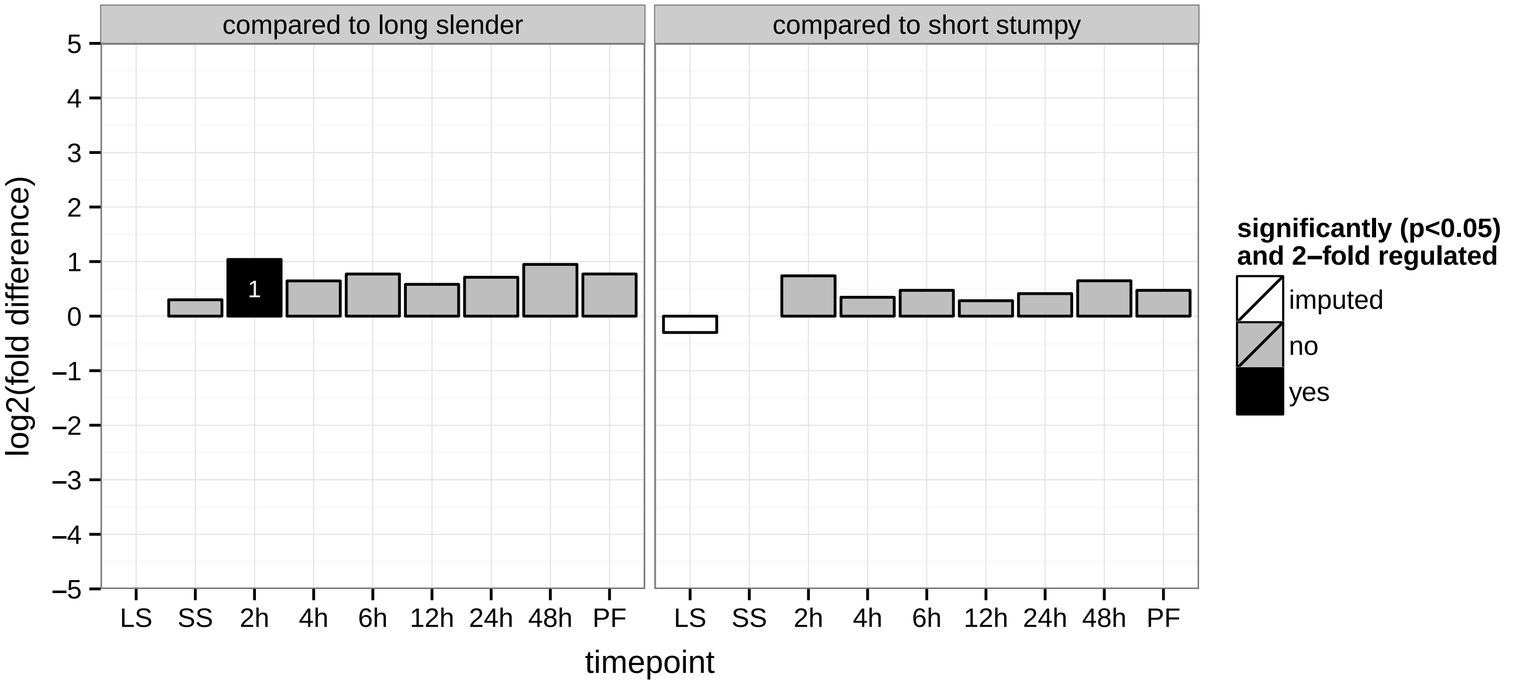


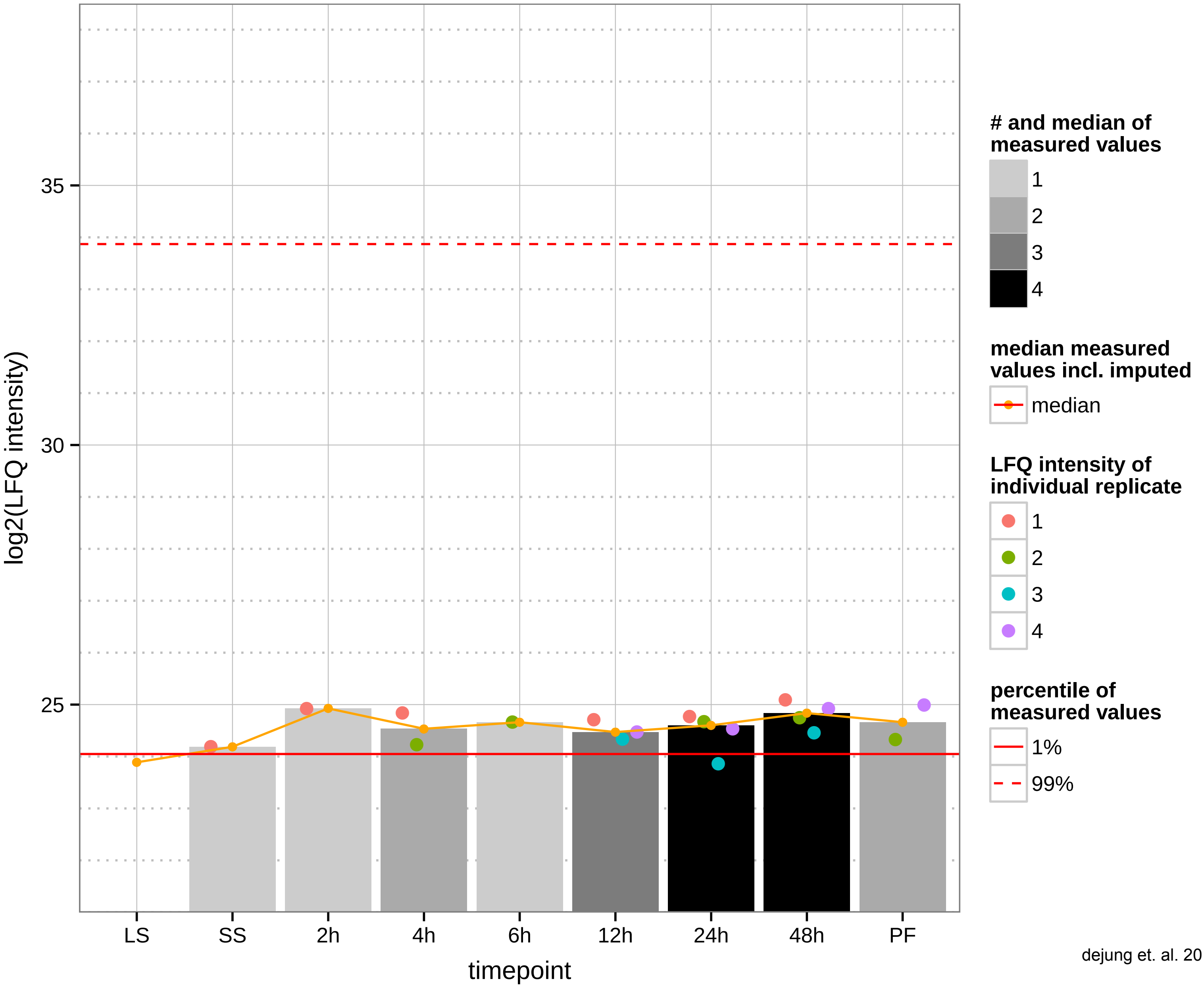
dejung et. al. 2015

adenylate kinase, putative
Tb927.10.2540
AGOF: ATP binding, adenylate kinase activity
AGOC: cytosol, glycosome, mitochondrion
AGOP: nucleobase–containing compound metabolic process
PGOF: ATP binding, adenylate kinase activity, nucleobase–containing compound kinase activity
PGOC: null
PGOP: nucleobase–containing compound metabolic process



hypothetical protein, conserved
Tb927.10.2630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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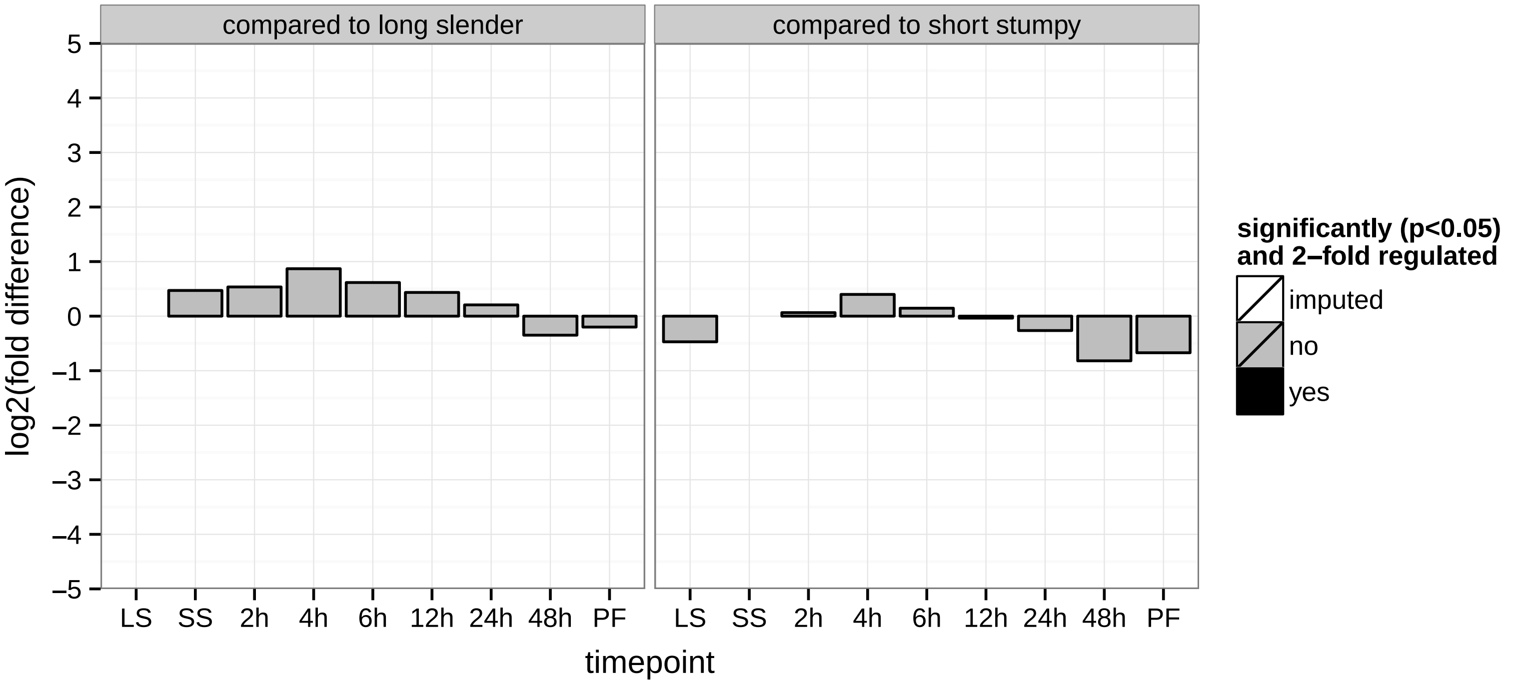
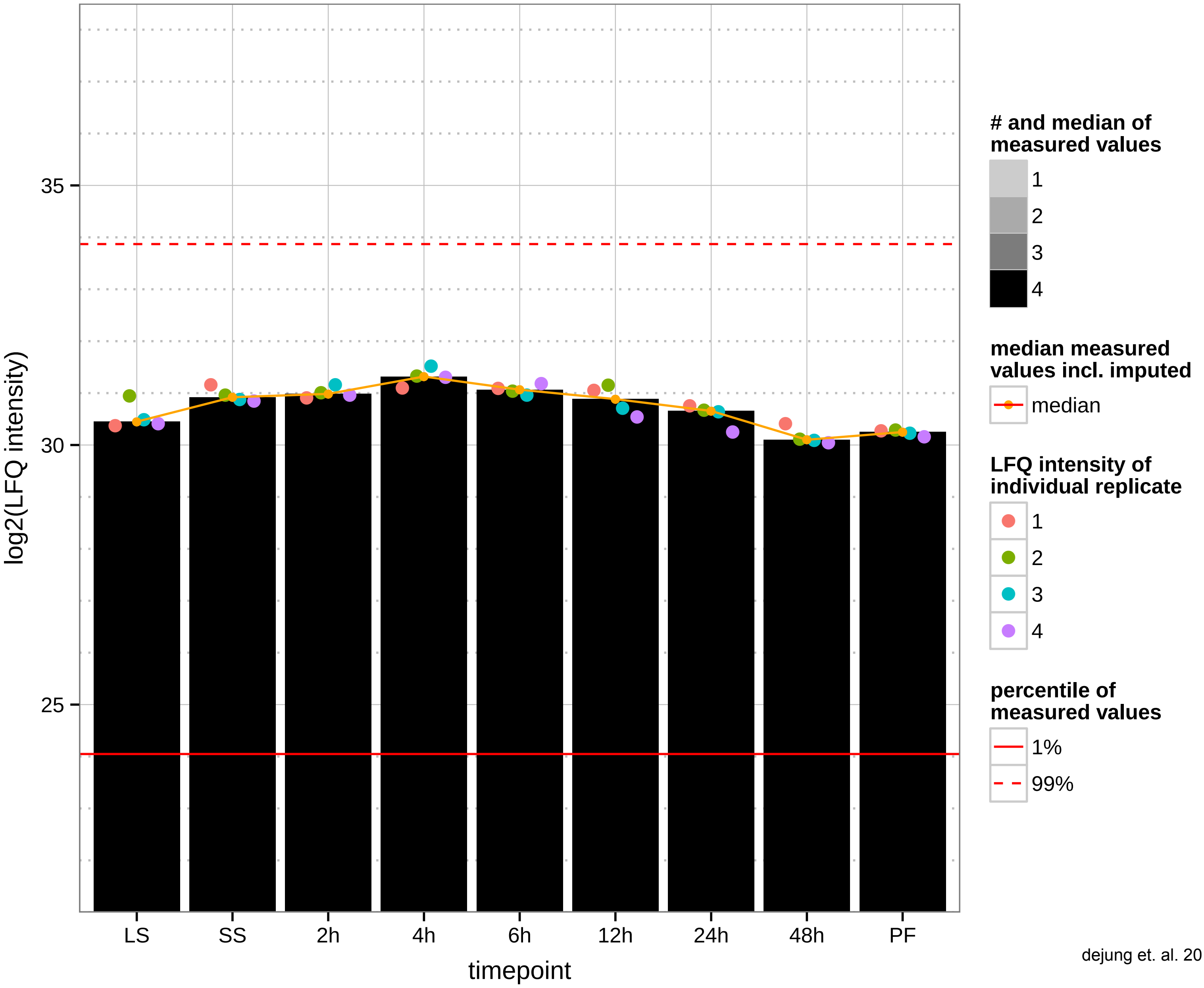
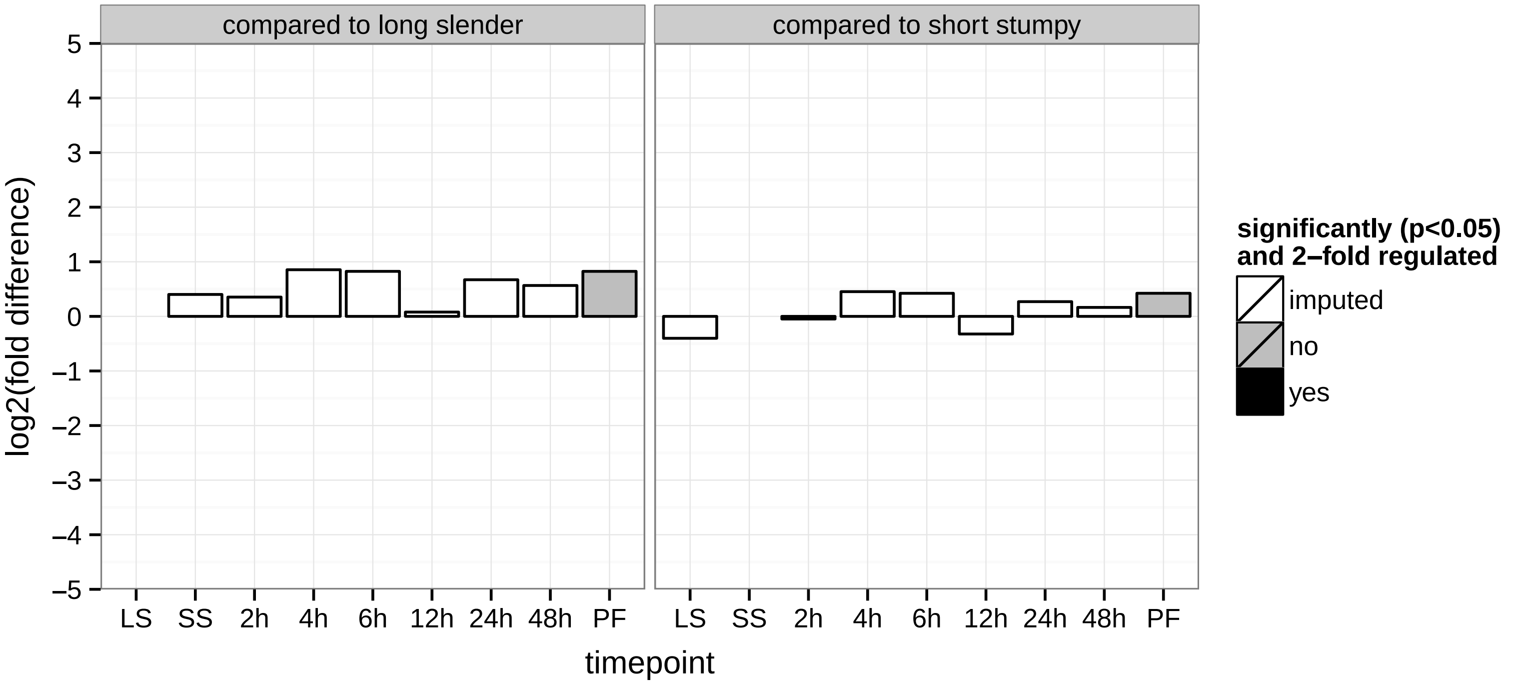
hypothetical protein, conserved, intraflagellar transport protein IFT81, putative
Tb927.10.2640;Tb11.v5.0525
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

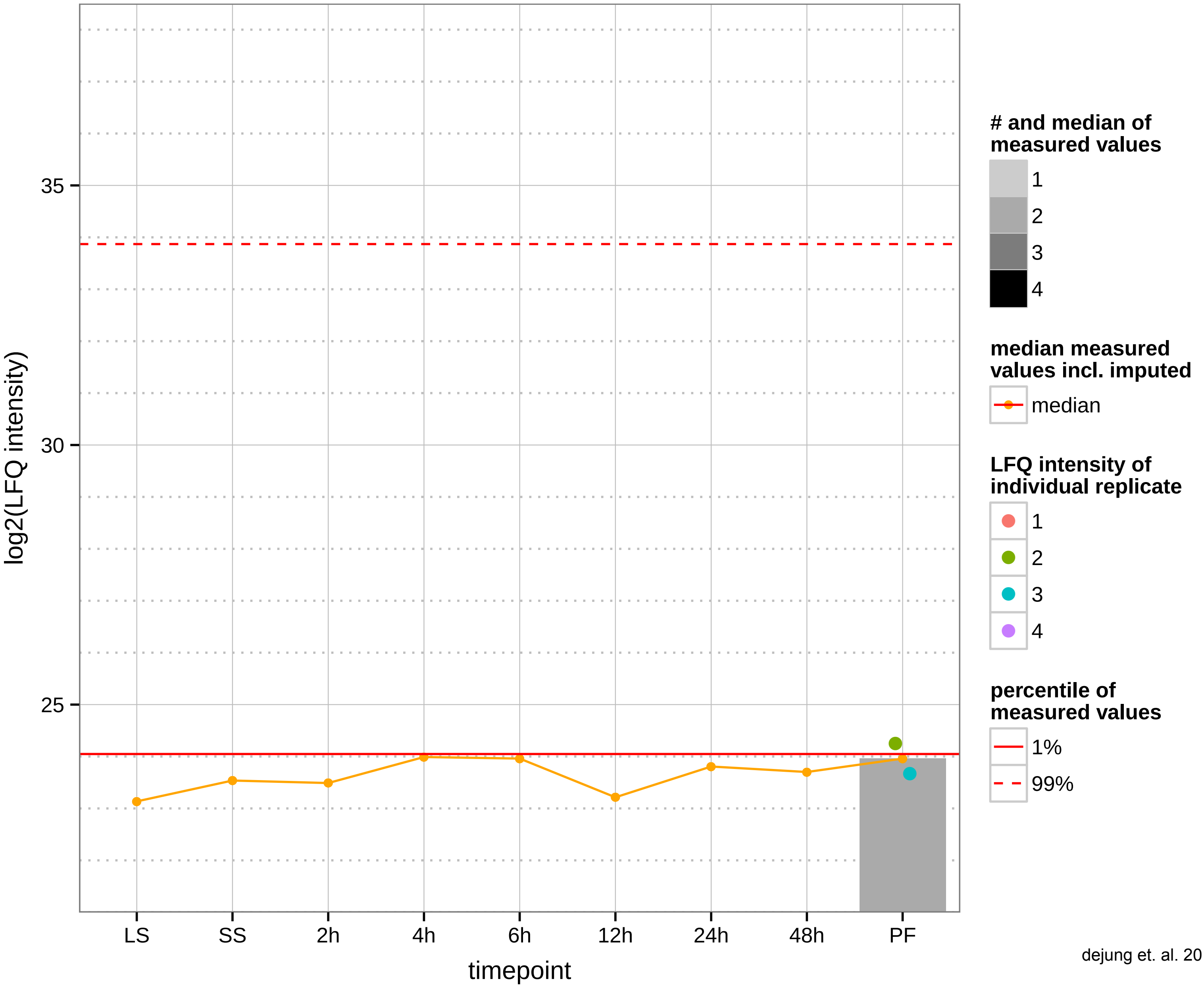




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.2650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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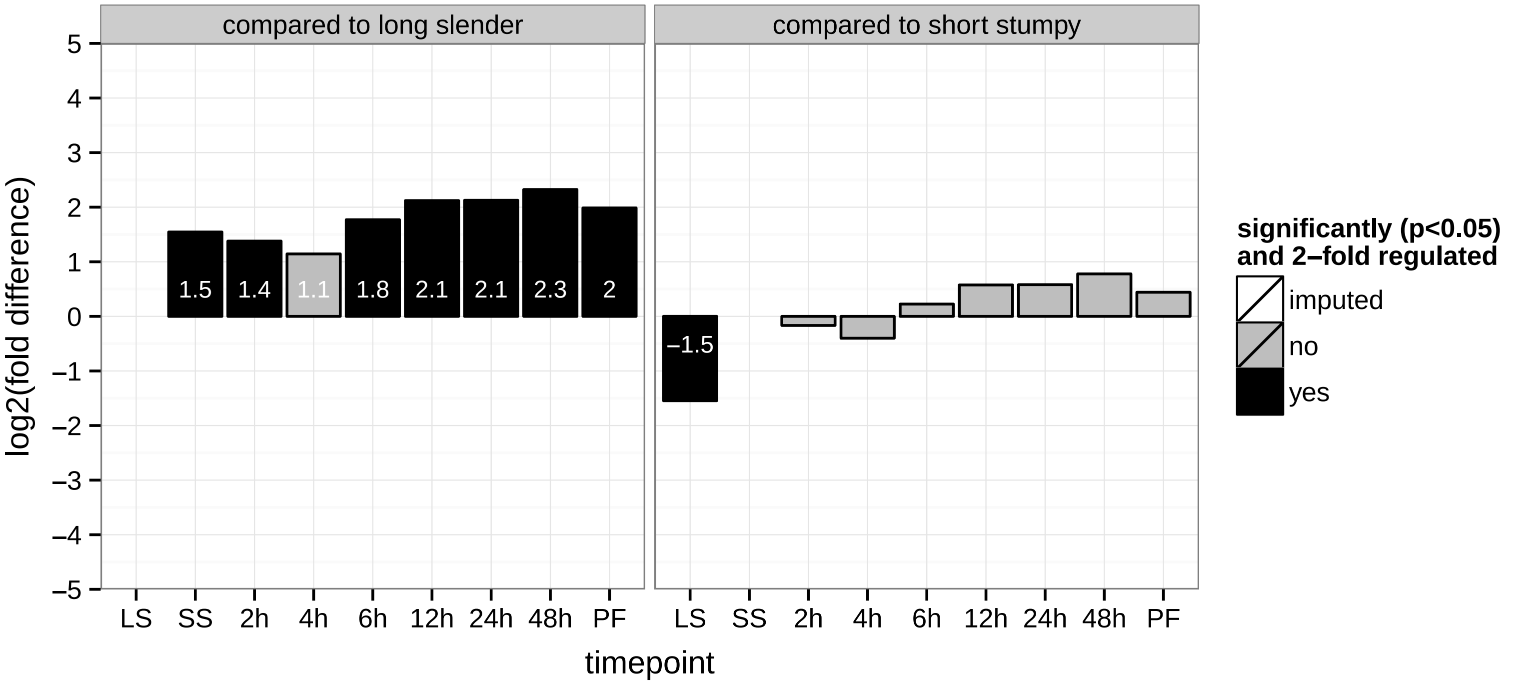
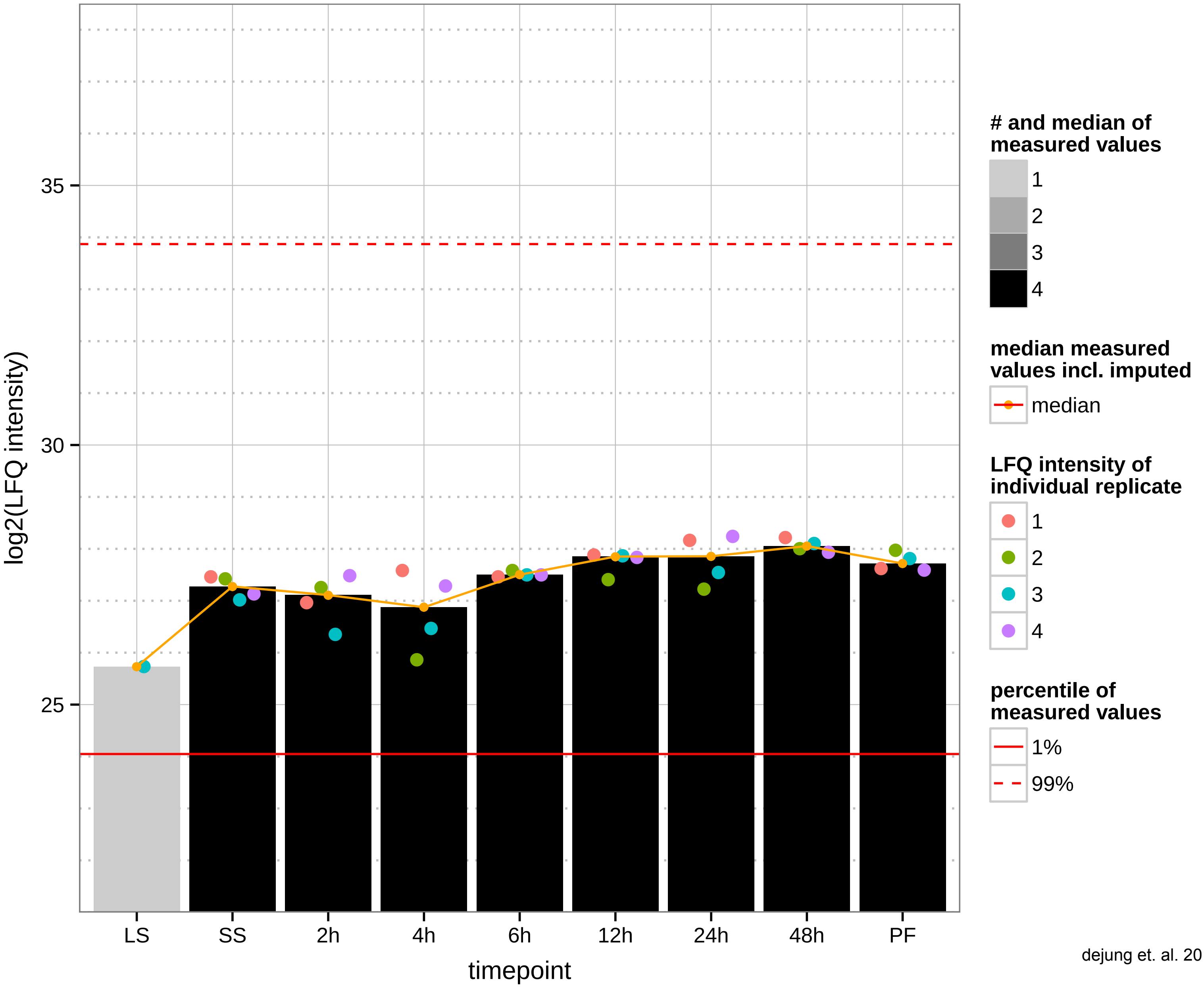
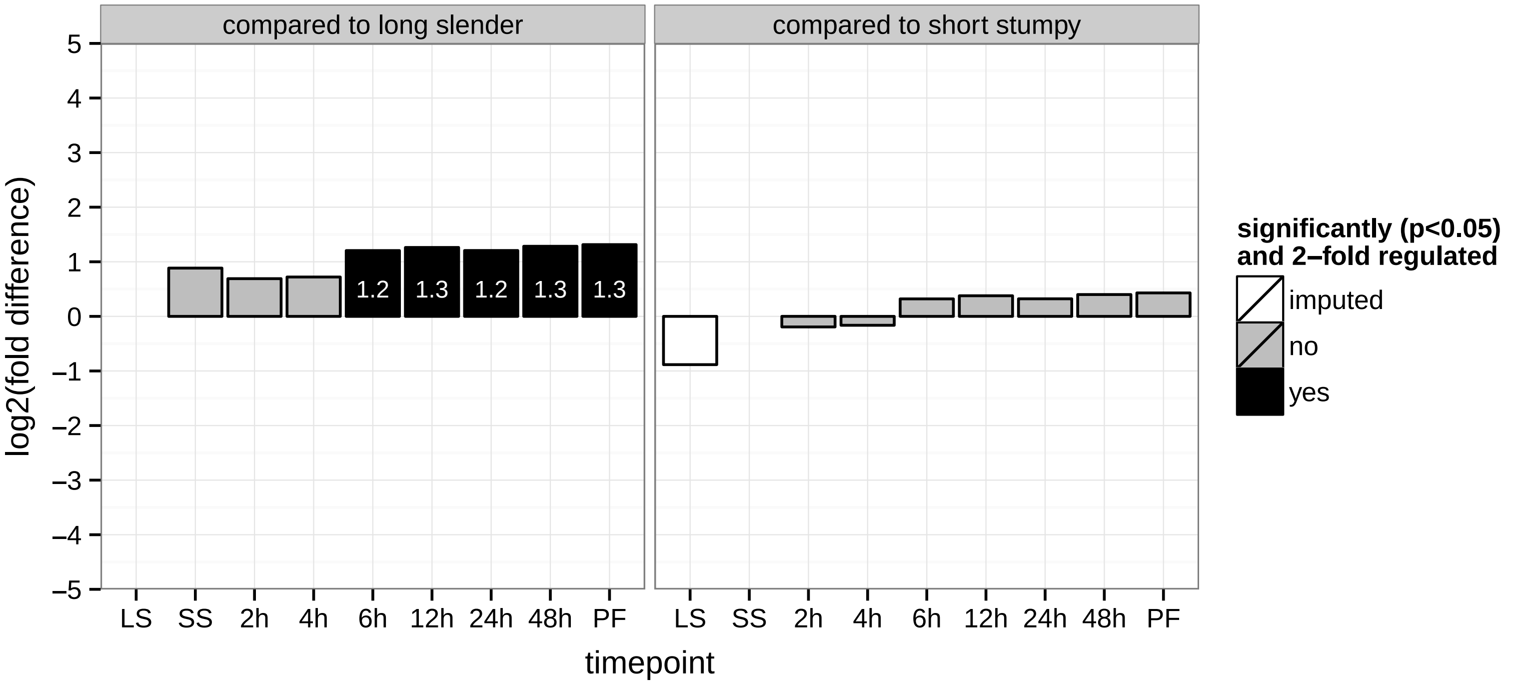
predicted WD40 repeat protein
Tb927.10.2700
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

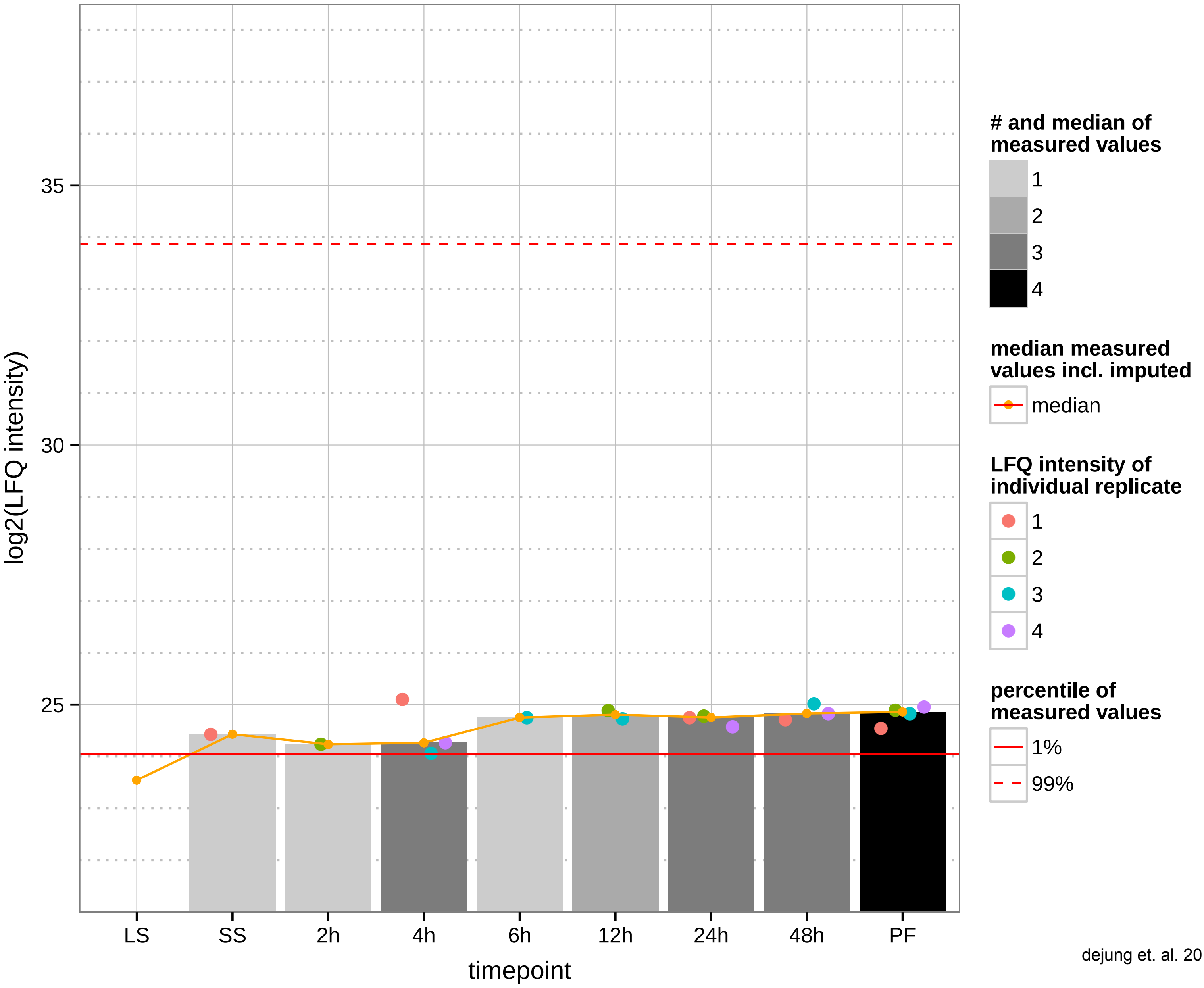




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.2720
AGOF: RNA binding, pseudouridine synthase activity
AGOC: null
AGOP: pseudouridine synthesis
PGOF: RNA binding, pseudouridine synthase activity
PGOC: null
PGOP: RNA modification, pseudouridine synthesis





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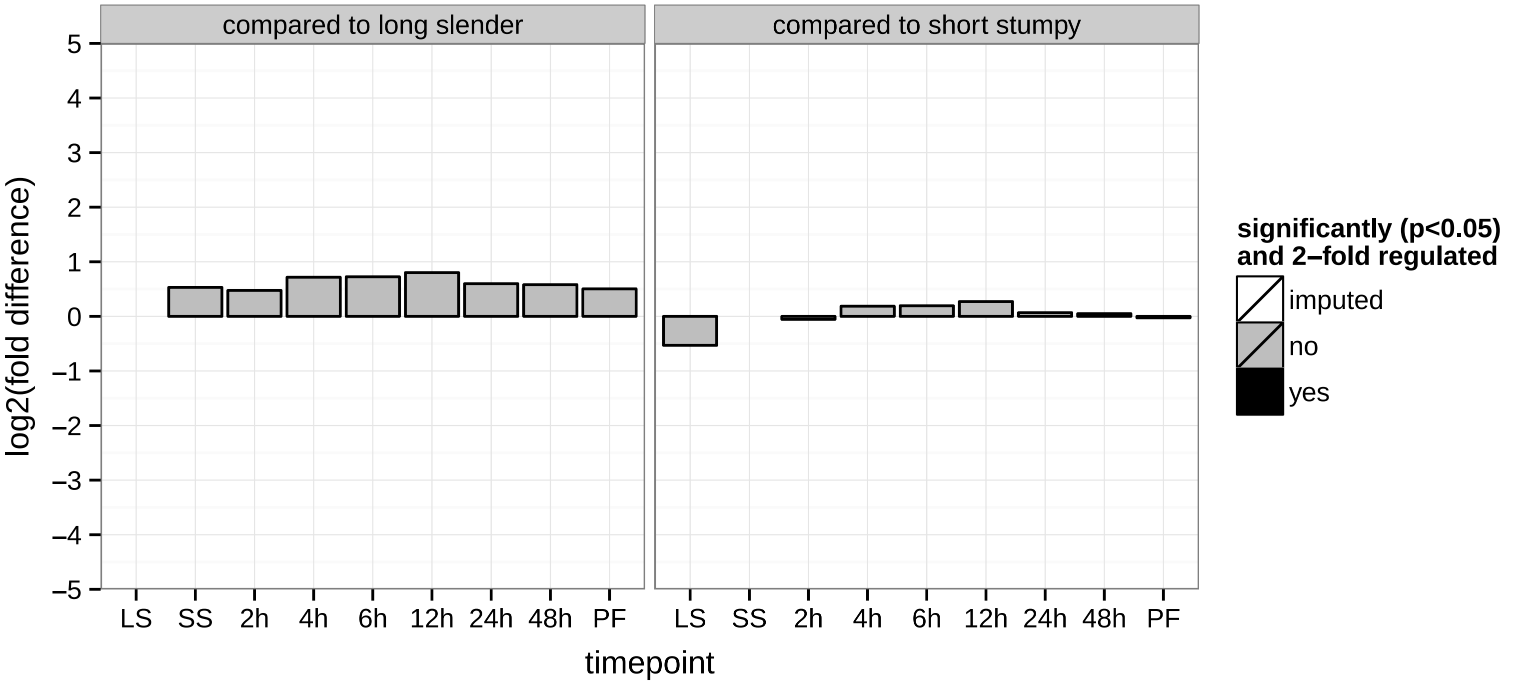
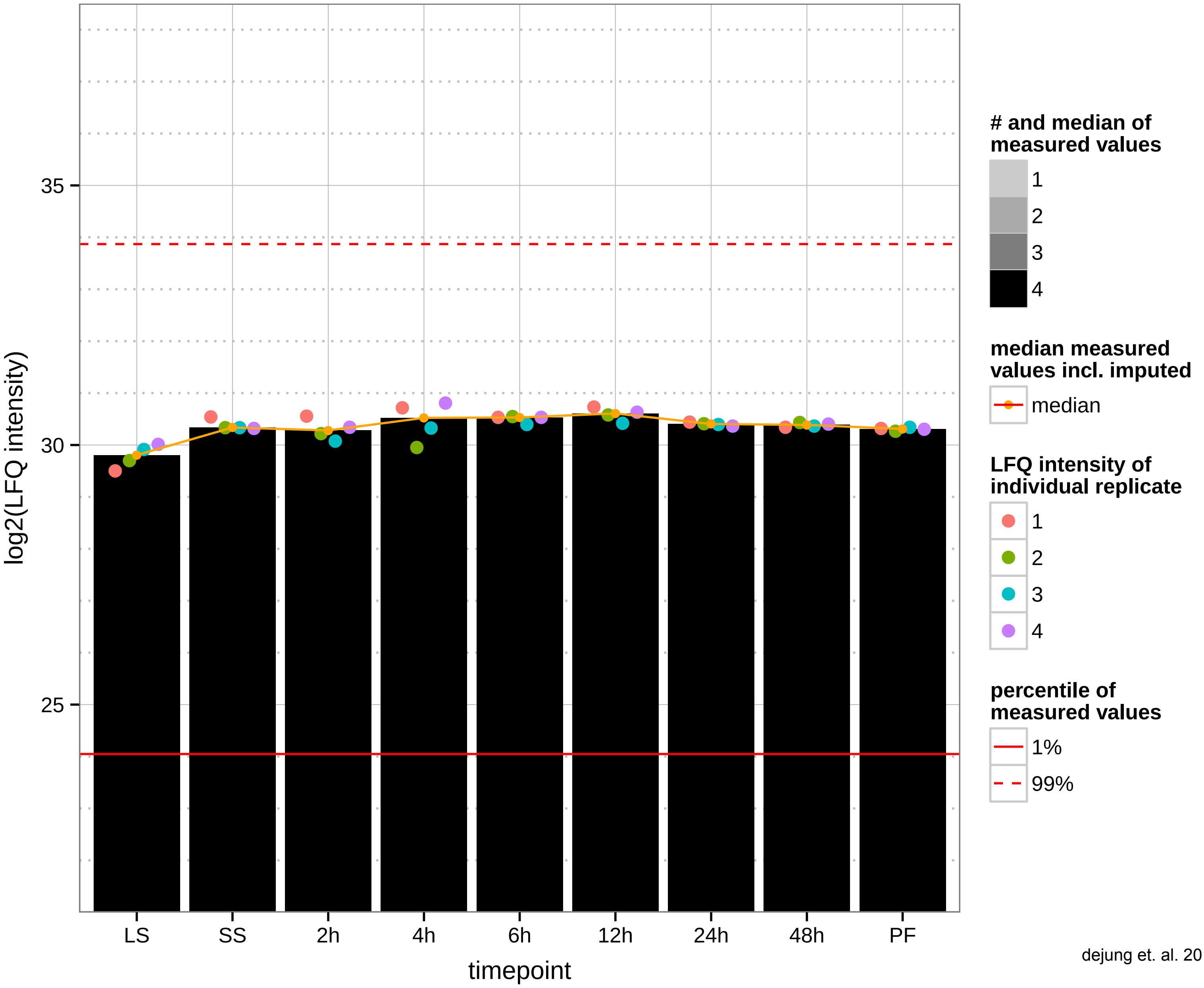
hypothetical protein, conserved
Tb927.10.2730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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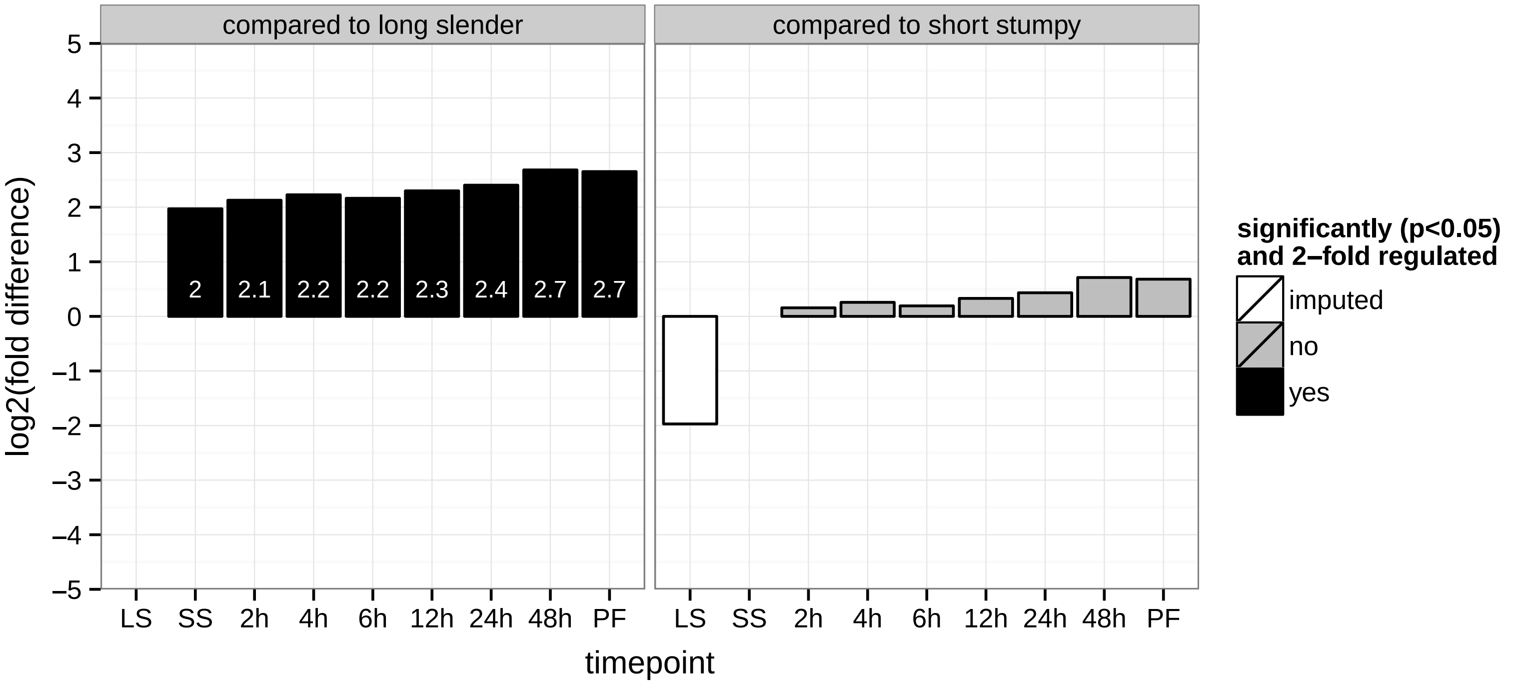
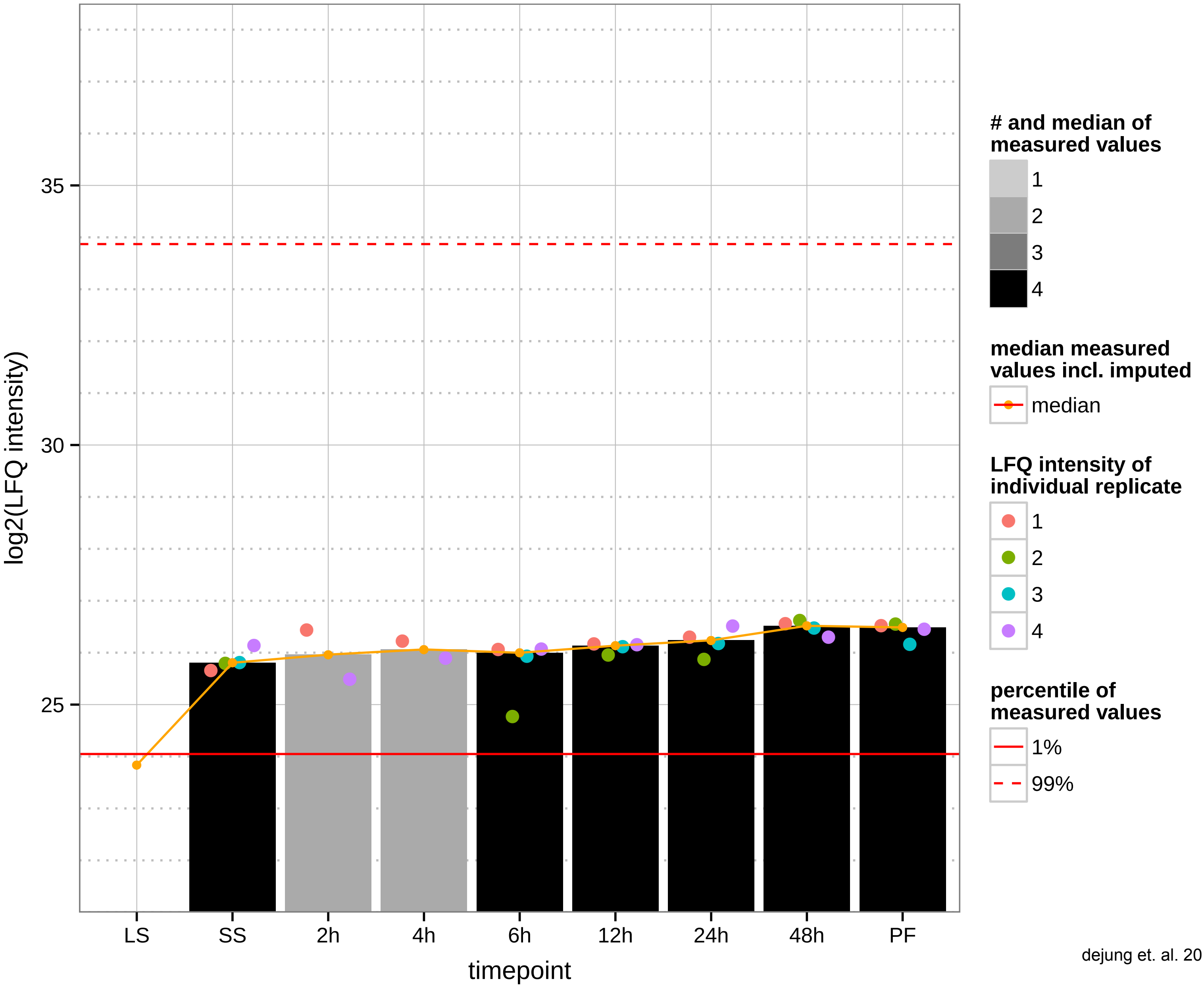
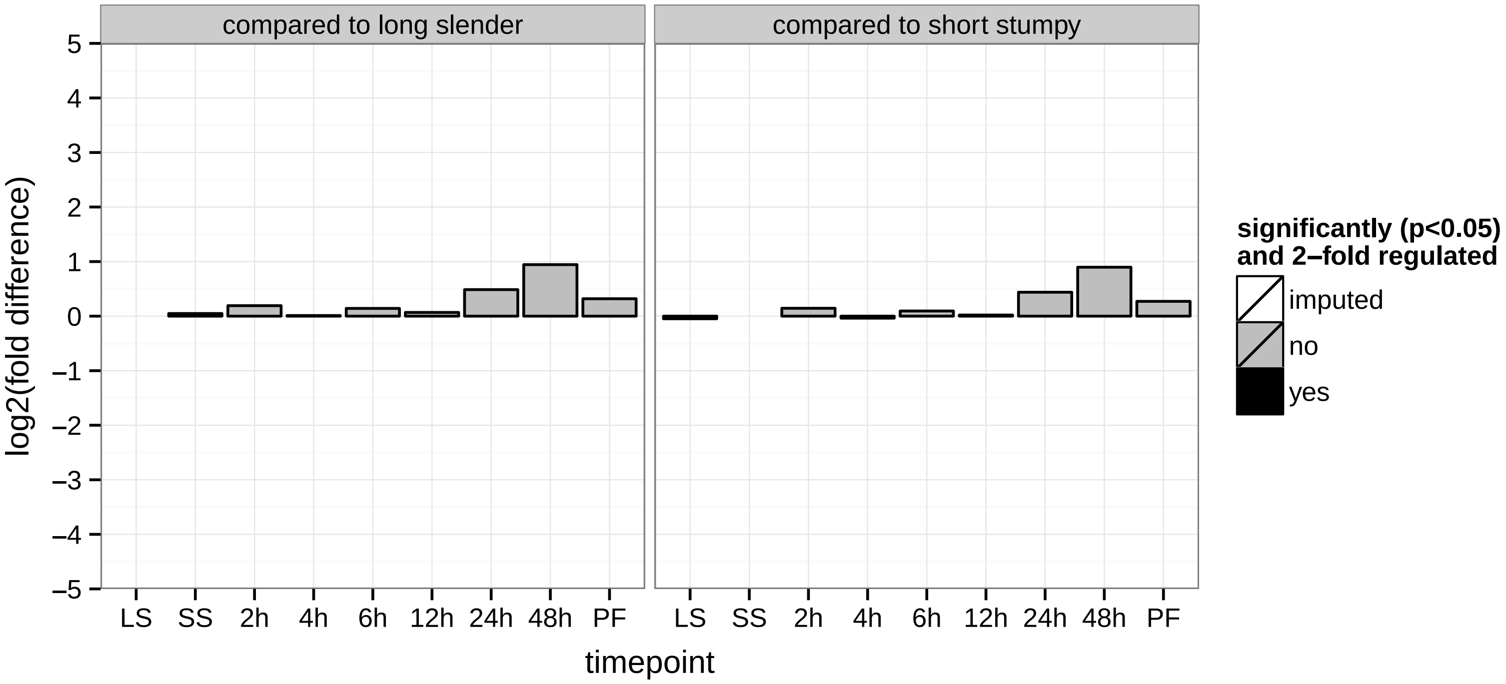
DNA–directed RNA polymerase III largest subunit, putative, DNA–directed RNA polymerase III subunit C1, DNA–directed RN
Tb927.10.2780
AGOF: null, DNA binding, DNA–directed RNA polymerase activity, ribonucleoside binding, zinc ion binding
AGOC: null, nucleus
AGOP: null, transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA–dependent

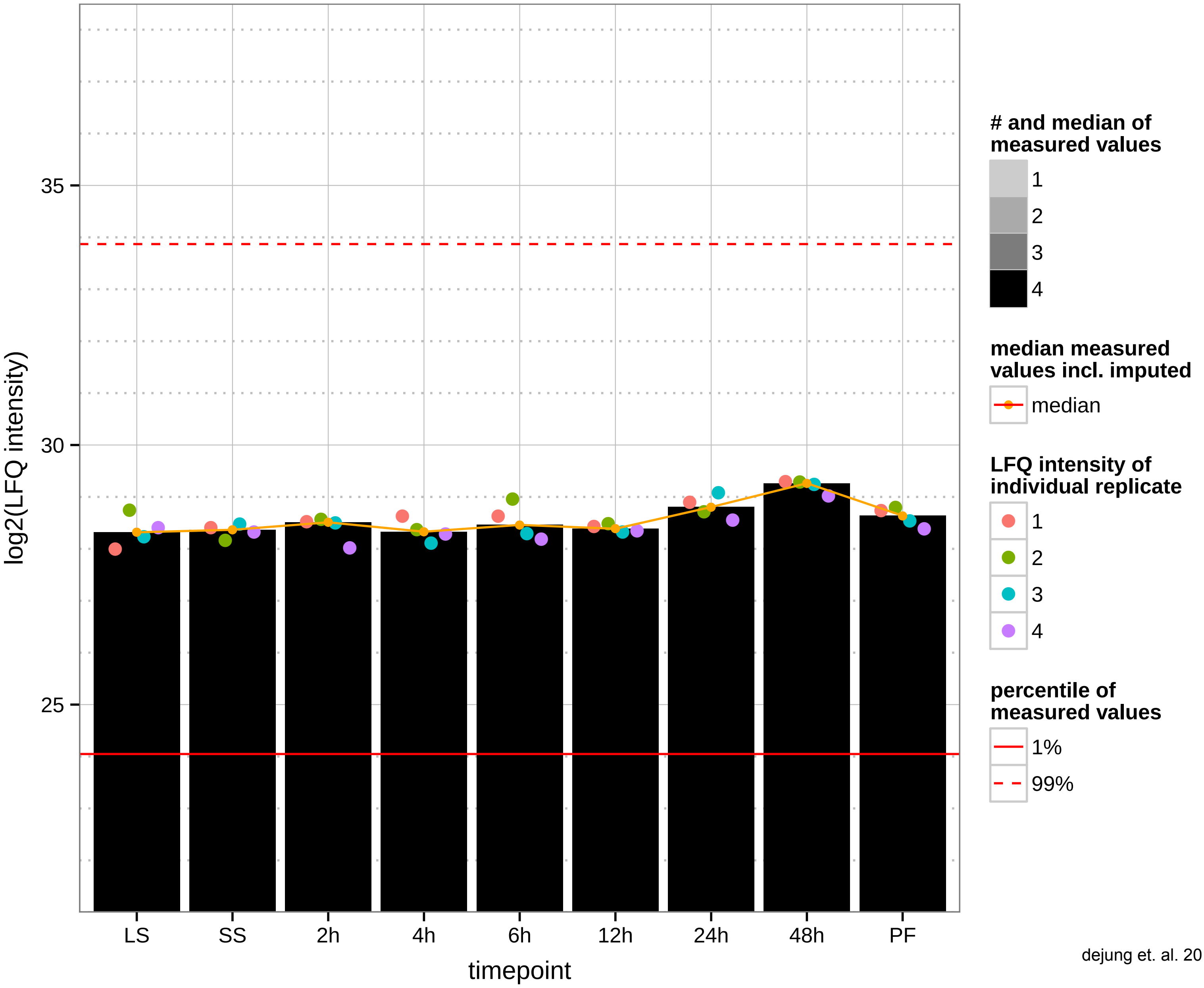




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.2810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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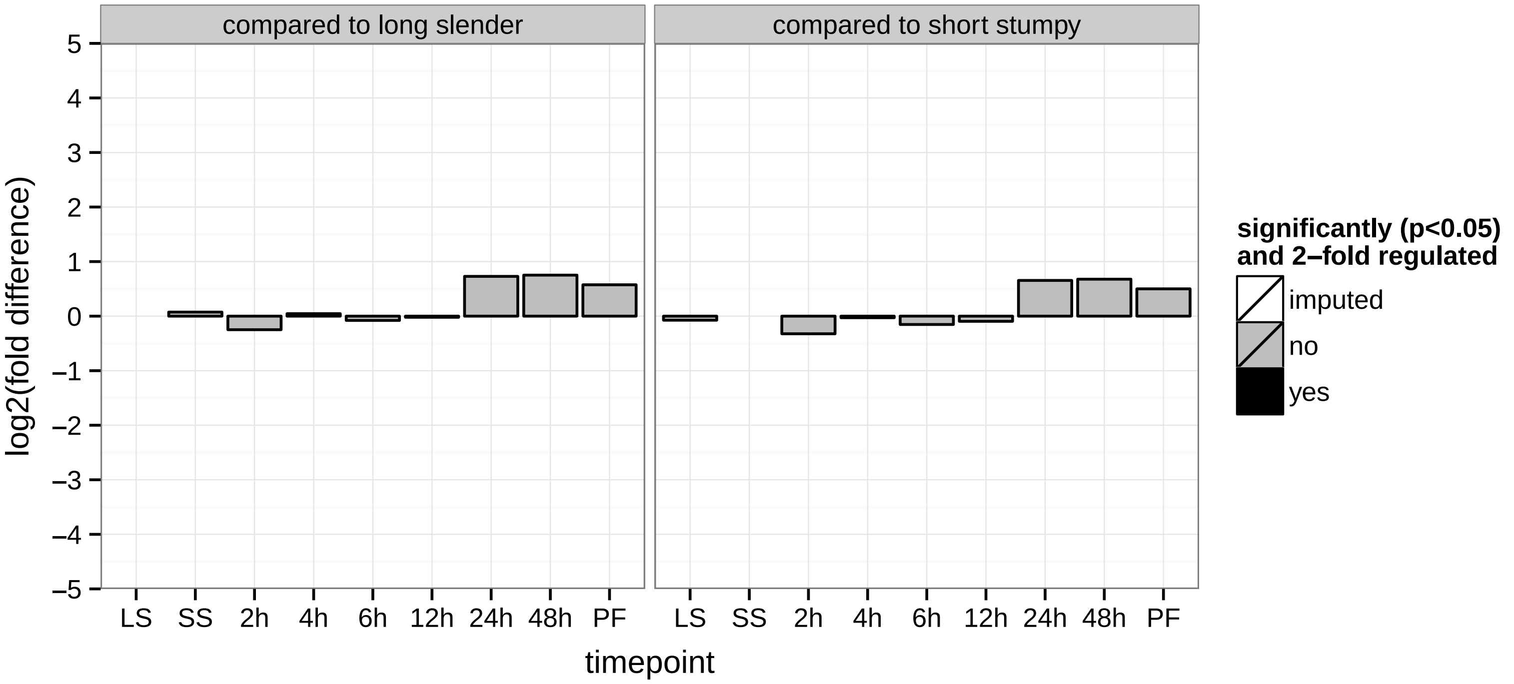
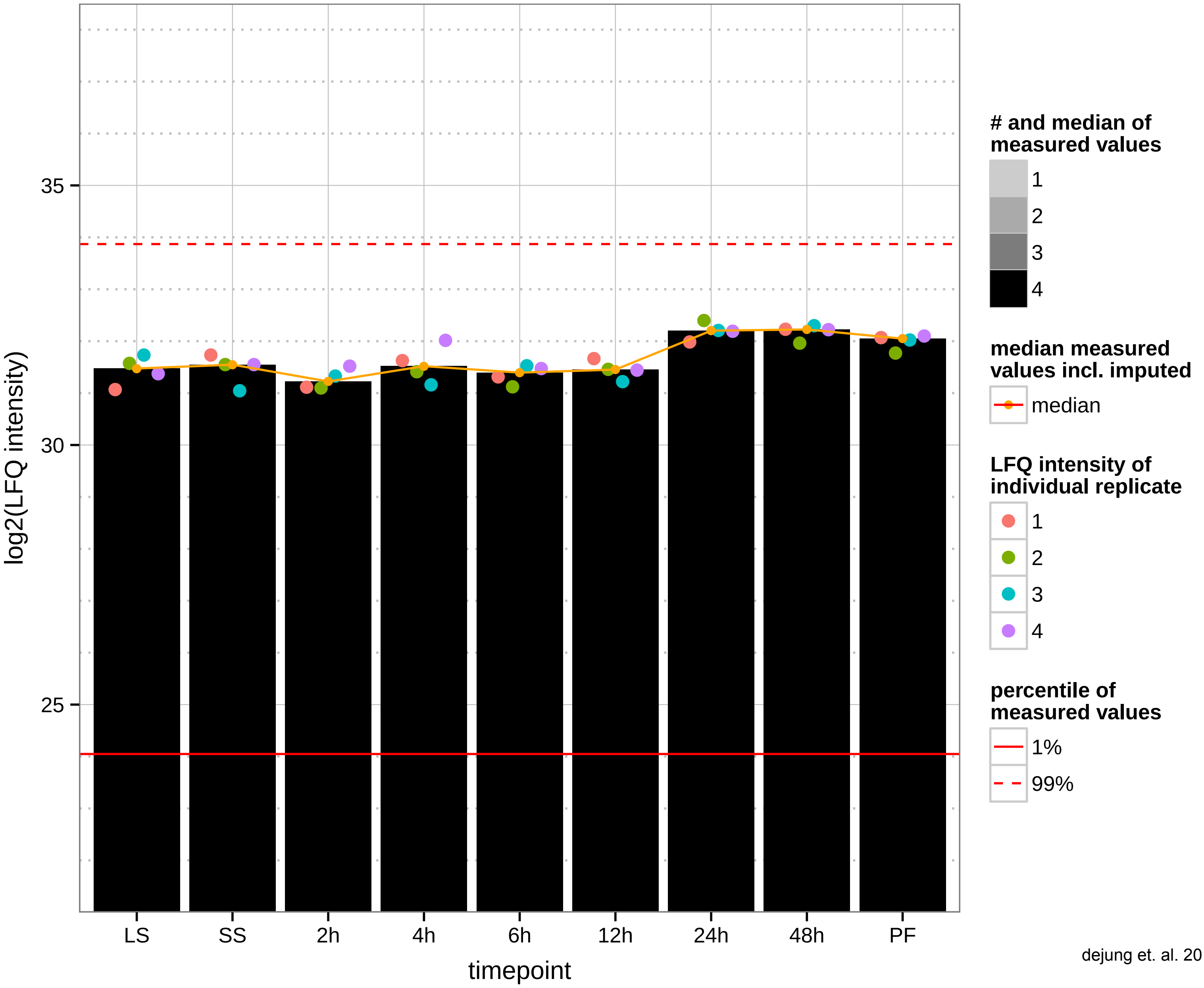
ribosomal protein S25, putative, 40S ribosomal protein S25
Tb927.3.1370;Tb927.10.2840
AGOF: structural constituent of ribosome, null
AGOC: ribosome, null
AGOP: translation, null
PGOF: null
PGOC: null
PGOP: null





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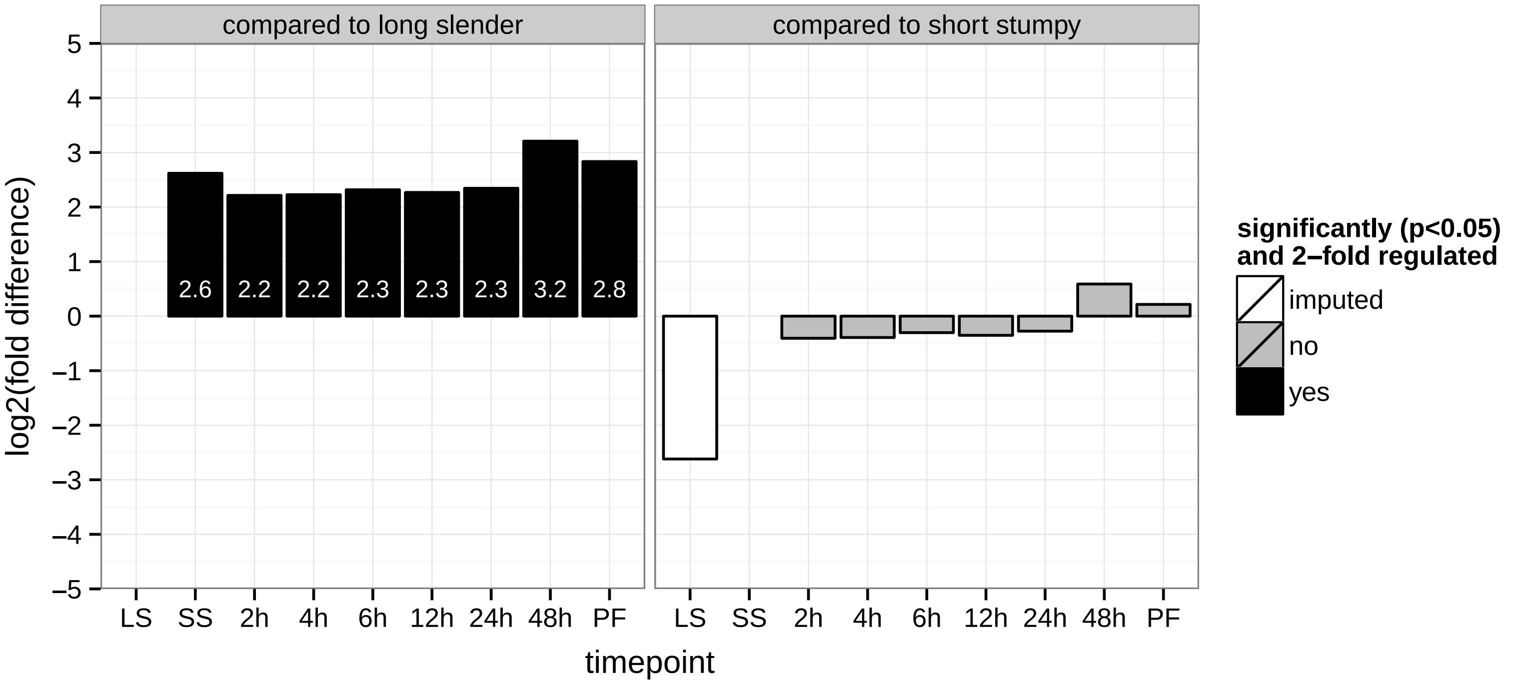
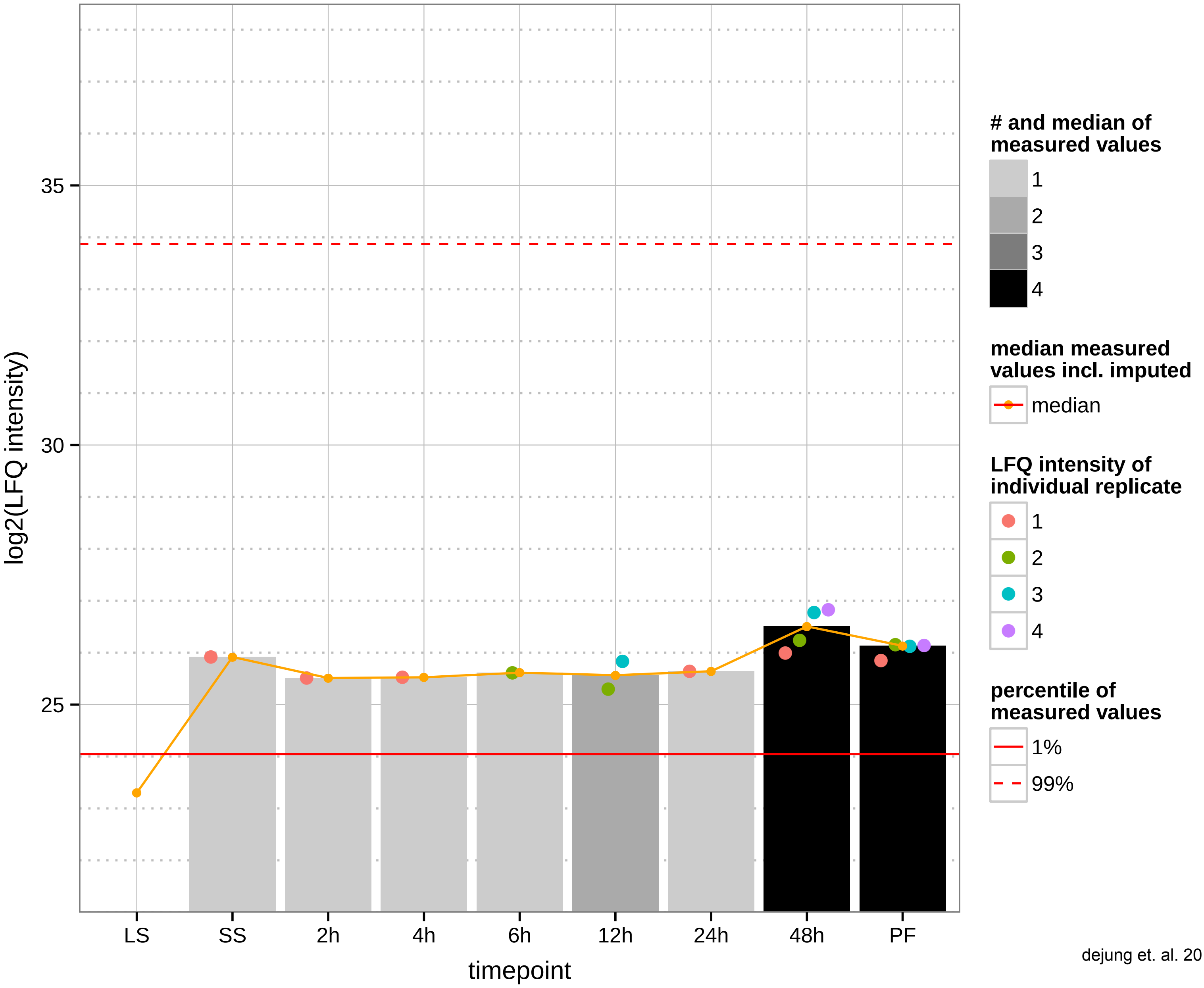
hypothetical protein, conserved
Tb927.10.2860
AGOF: null
AGOC: bacterial–type flagellum basal body
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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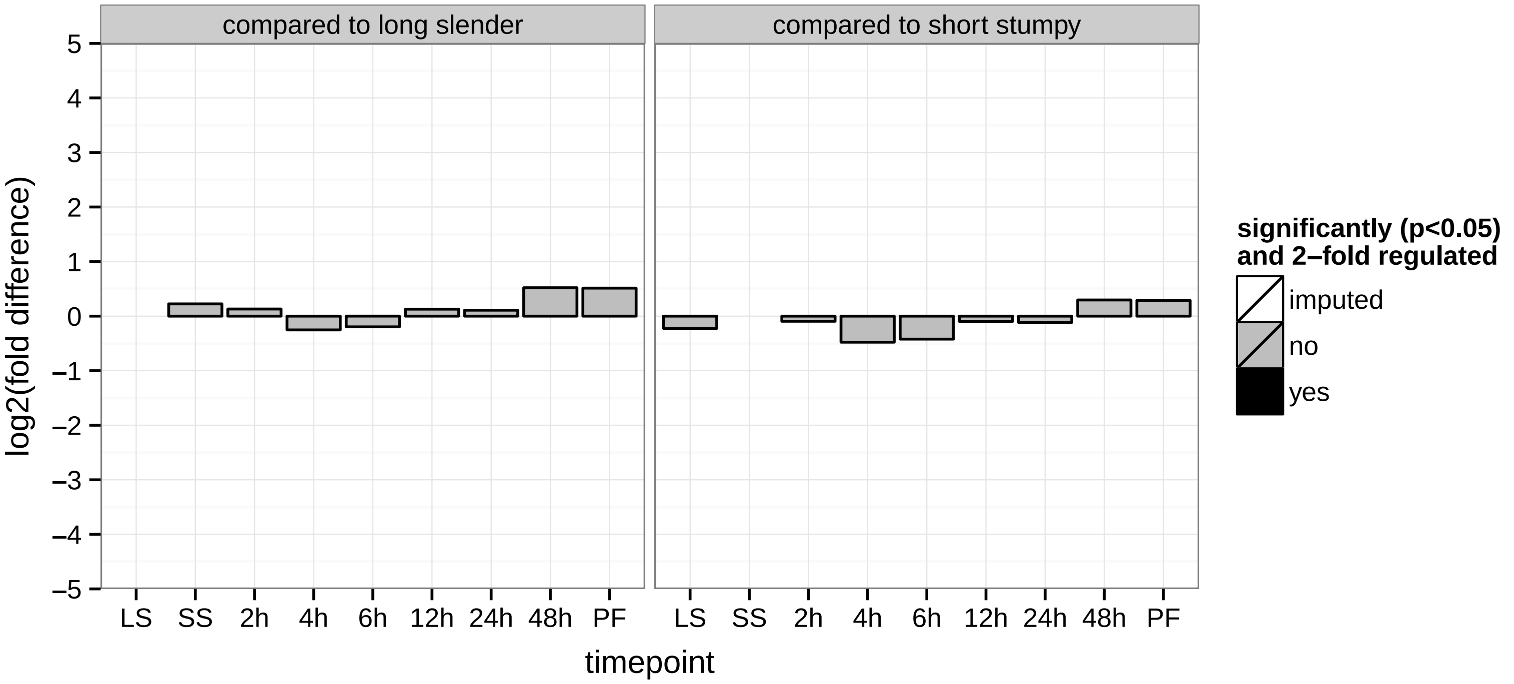
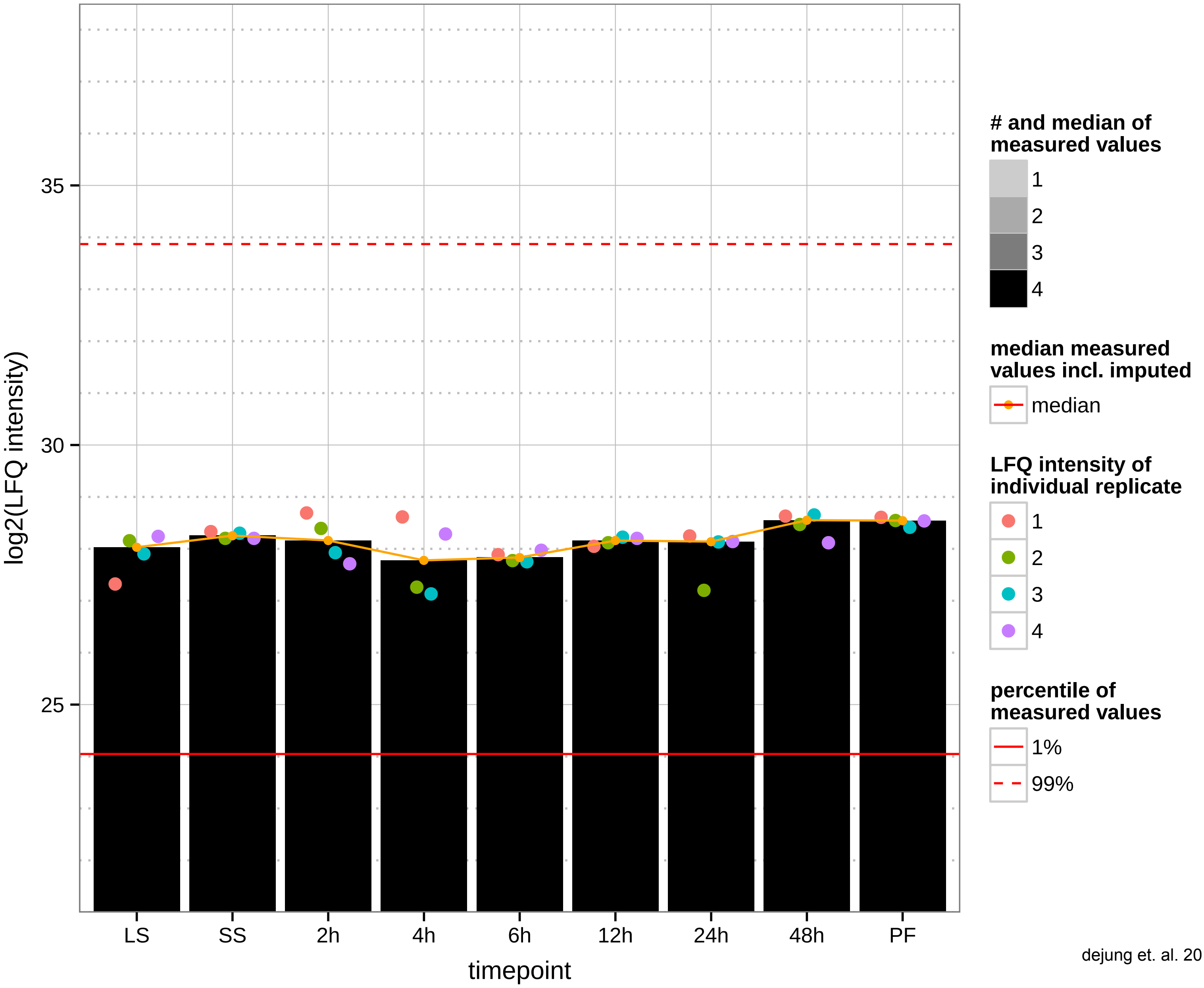
calcium channel protein, putative
Tb927.10.2880
AGOF: ion channel activity
AGOC: null
AGOP: ion transport
PGOF: ion channel activity
PGOC: membrane
PGOP: ion transport, transmembrane transport





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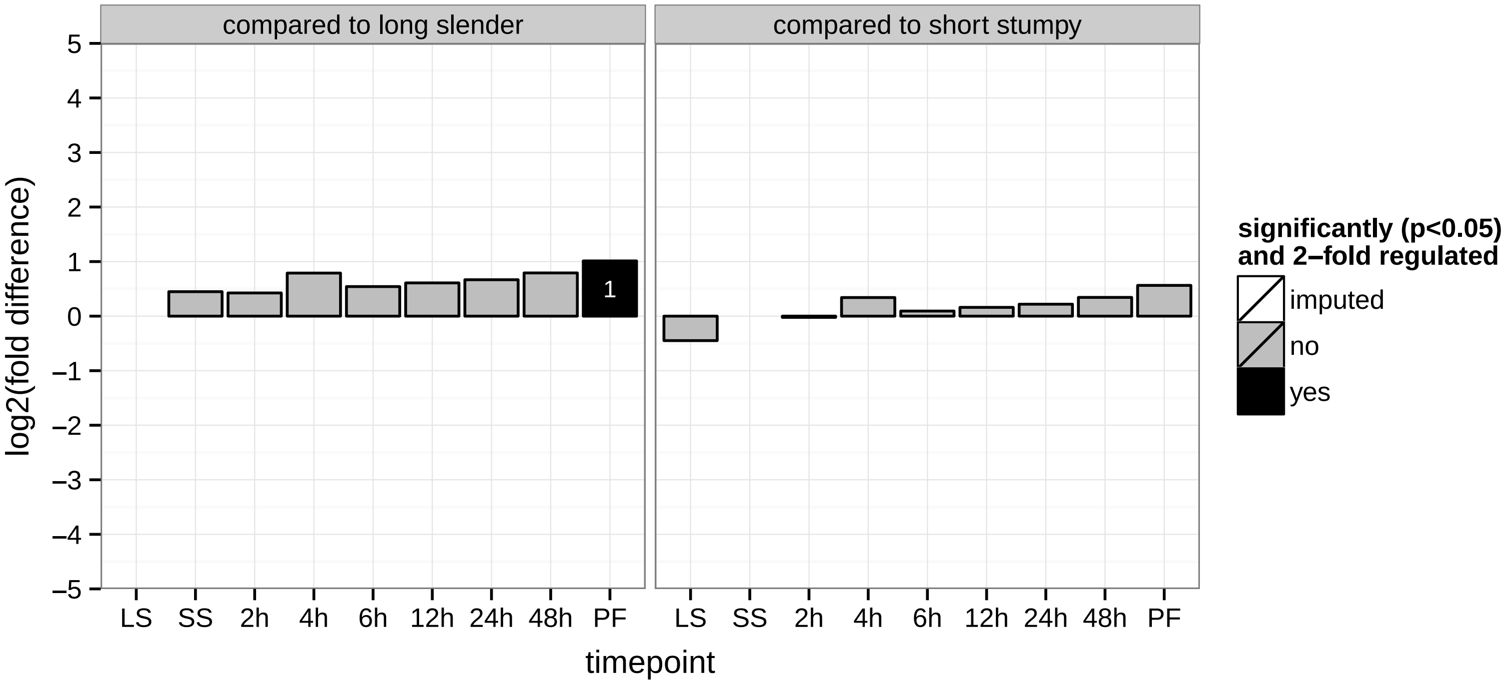
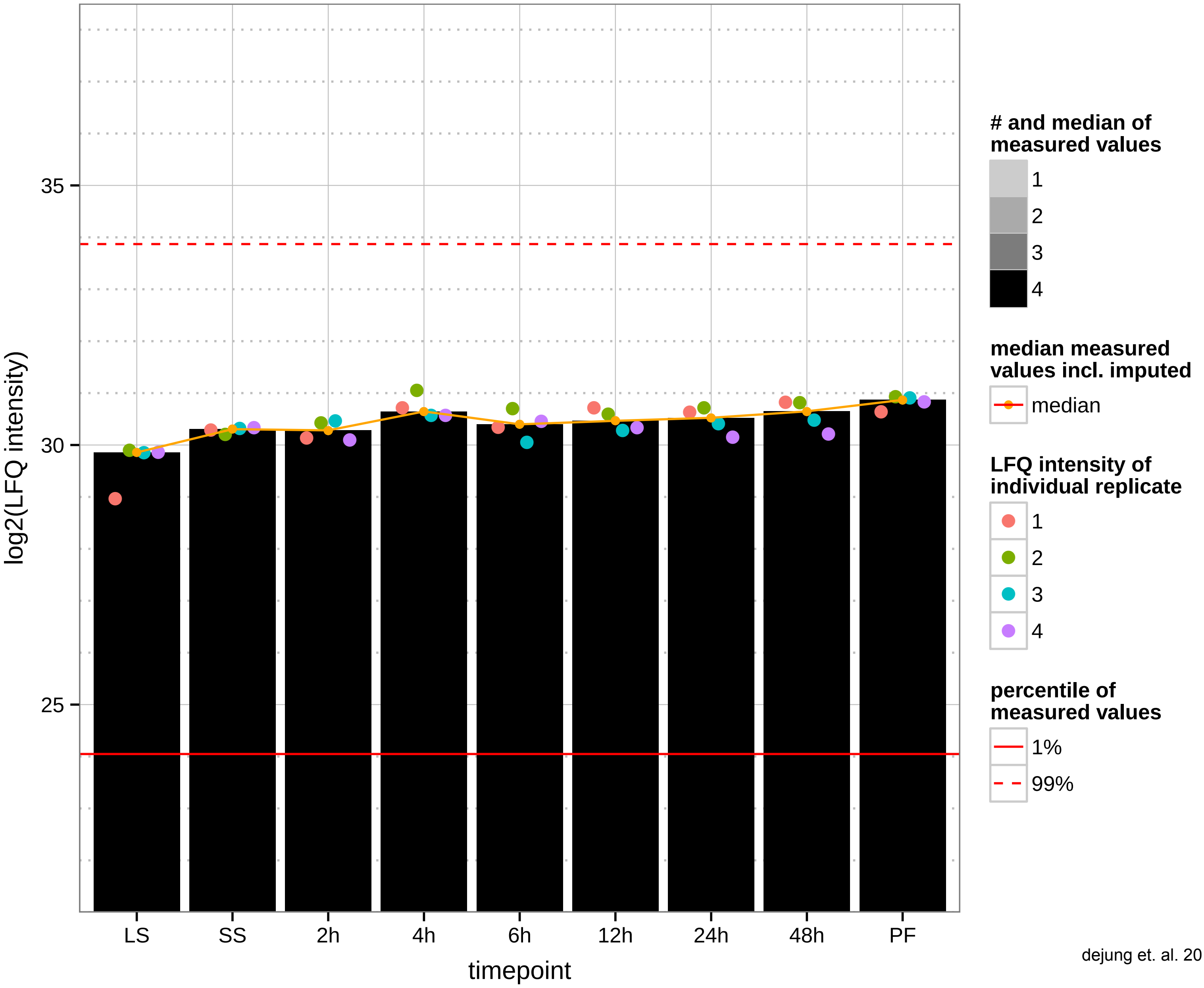
proteasome alpha 2 subunit, putative
Tb927.10.290
AGOF: endopeptidase activity, threonine–type endopeptidase activity
AGOC: proteasome core complex
AGOP: ubiquitin–dependent protein catabolic process
PGOF: endopeptidase activity, threonine–type endopeptidase activity
PGOC: proteasome core complex, proteasome core complex, alpha–subunit complex
PGOP: proteolysis involved in cellular protein catabolic process, ubiquitin–dependent protein catabolic process





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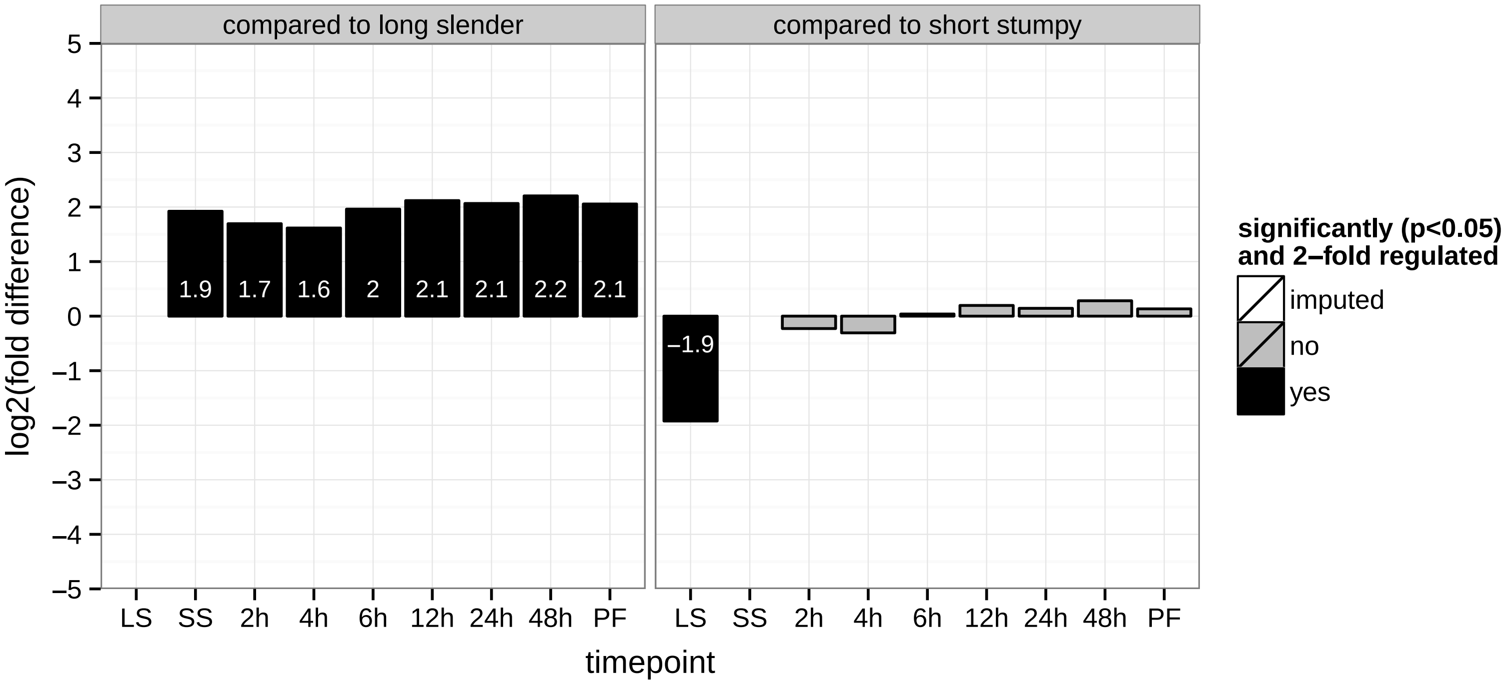
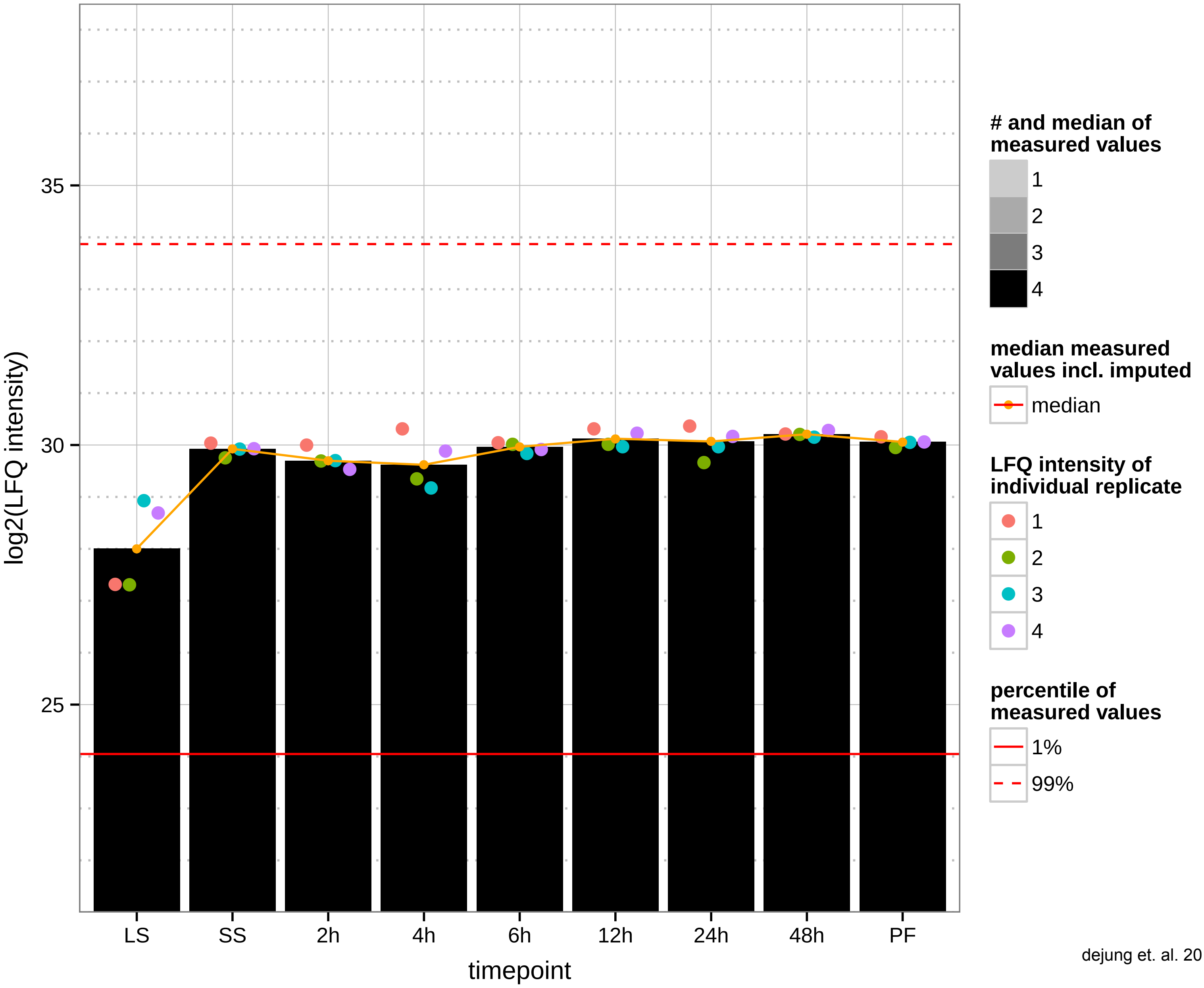
importin beta–1 subunit, putative
Tb927.10.2900;Tb11.v5.0837
AGOF: null, protein transporter activity
AGOC: null, cytoplasm, nuclear pore, nucleus
AGOP: null, intracellular protein transport, nuclear import, protein import into nucleus, docking
PGOF: binding, protein transporter activity
PGOC: null
PGOP: intracellular protein transport





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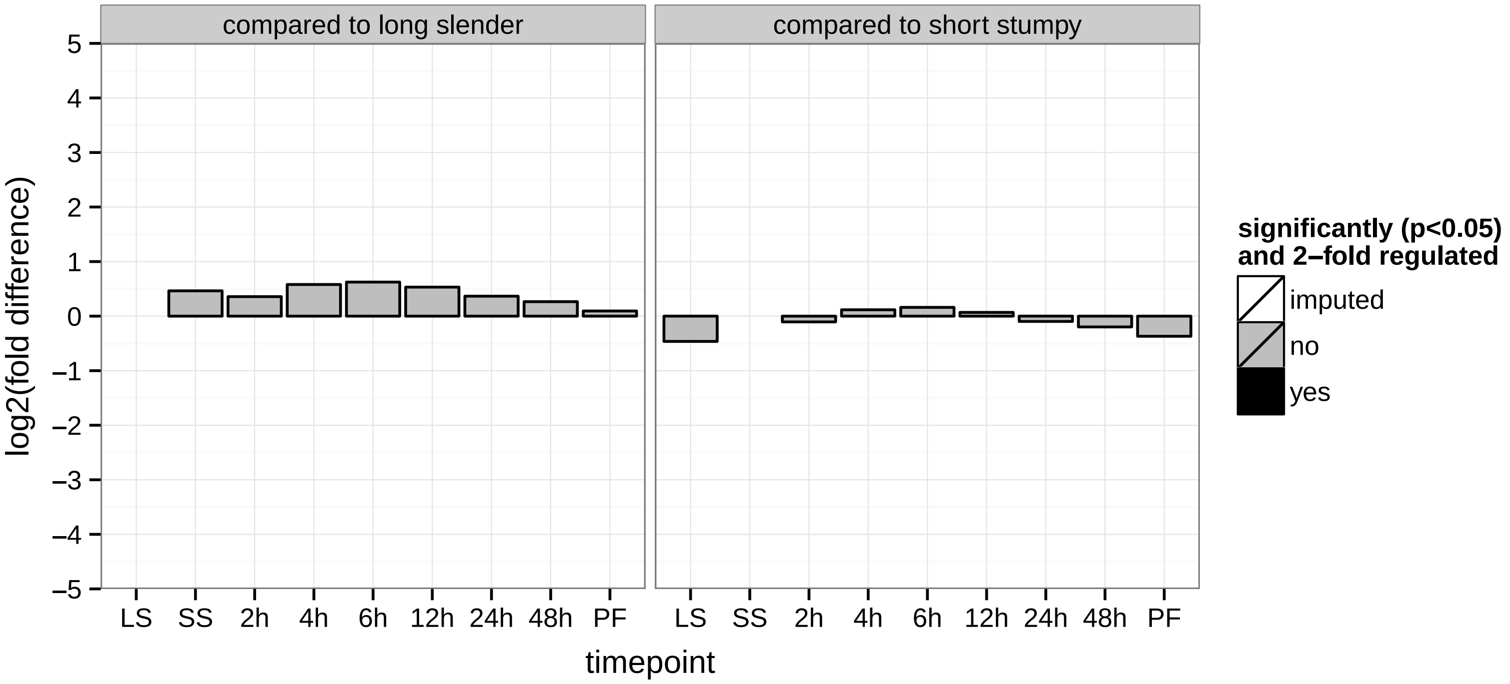
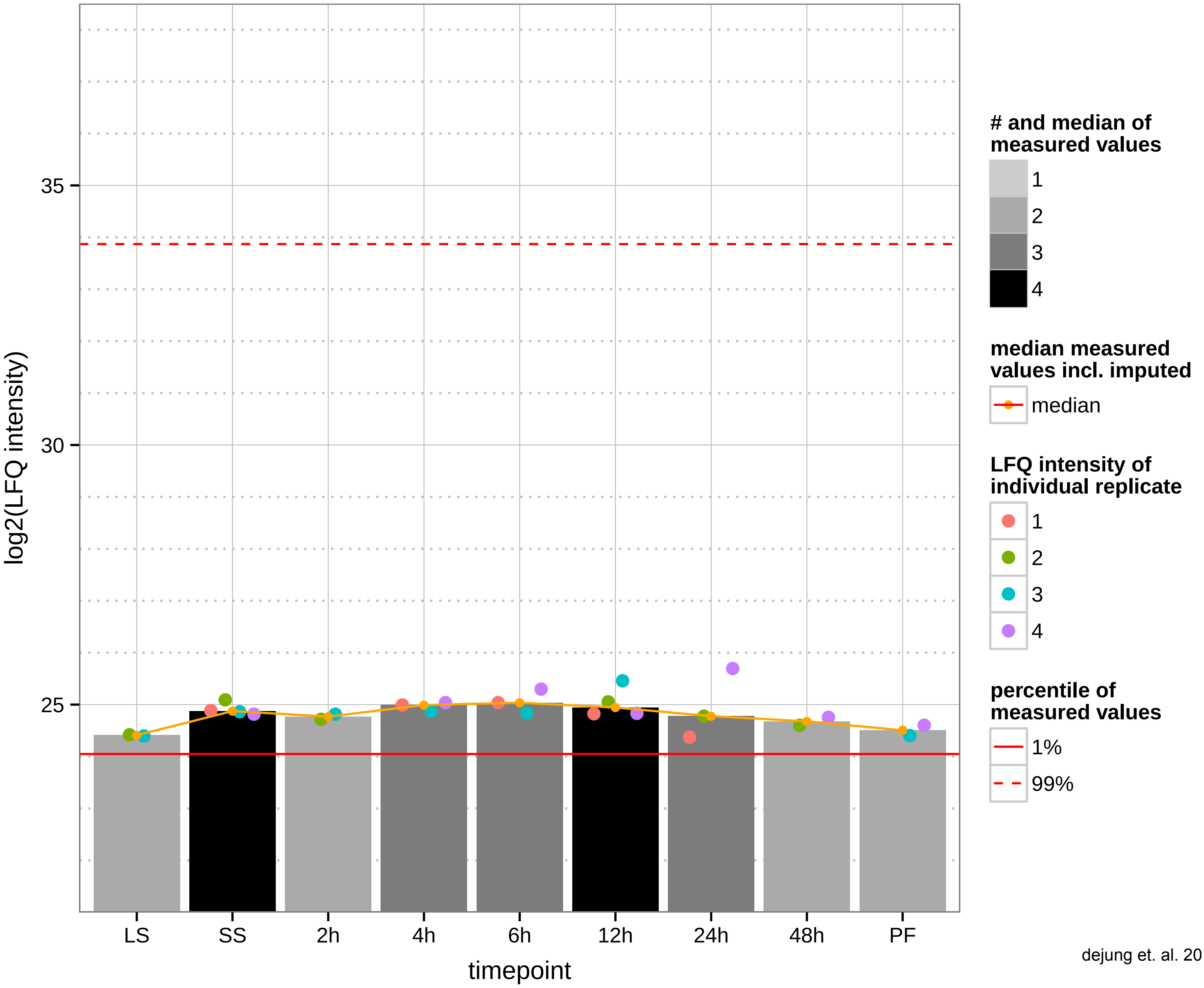
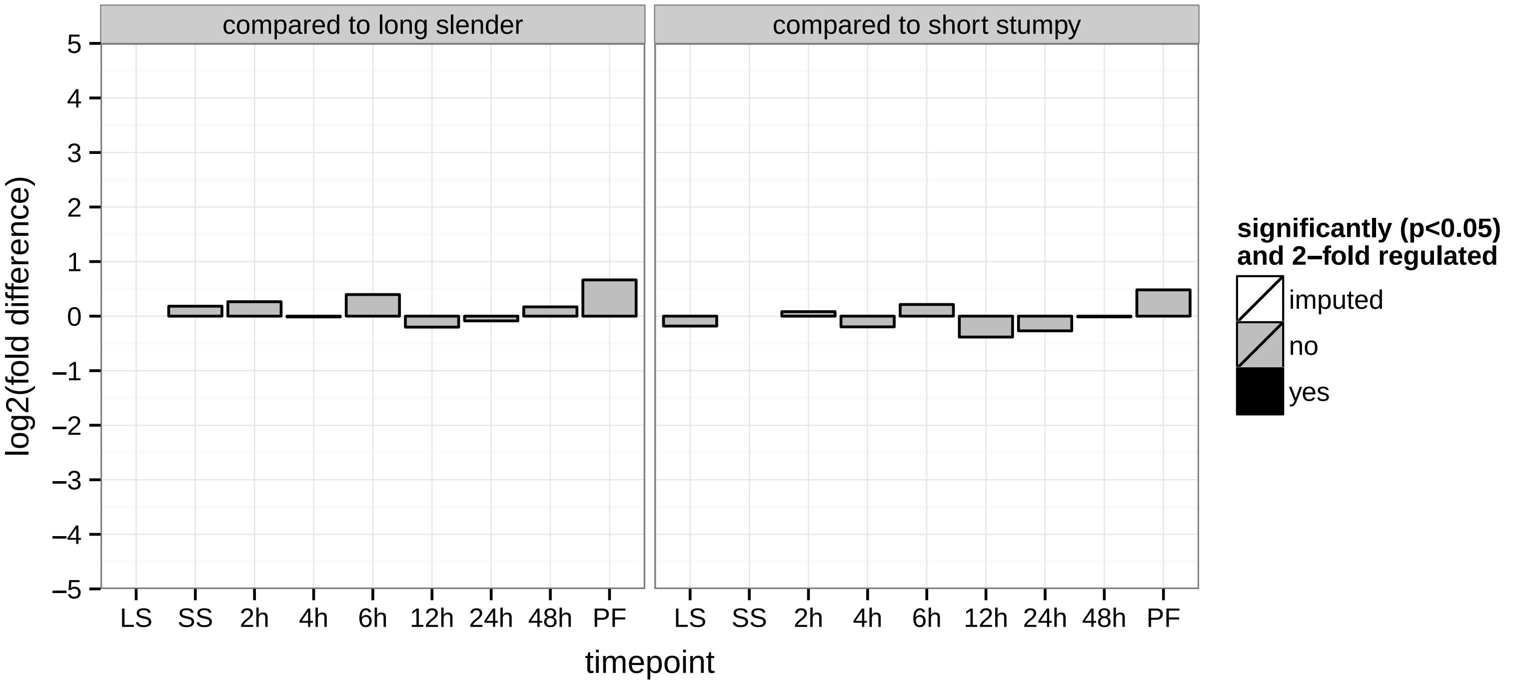
splicing factor PTSR1 interacting protein (TSR1IP)
Tb927.10.2910
AGOF: RNA binding
AGOC: nucleus
AGOP: nuclear mRNA splicing, via spliceosome
PGOF: null
PGOC: null
PGOP: null

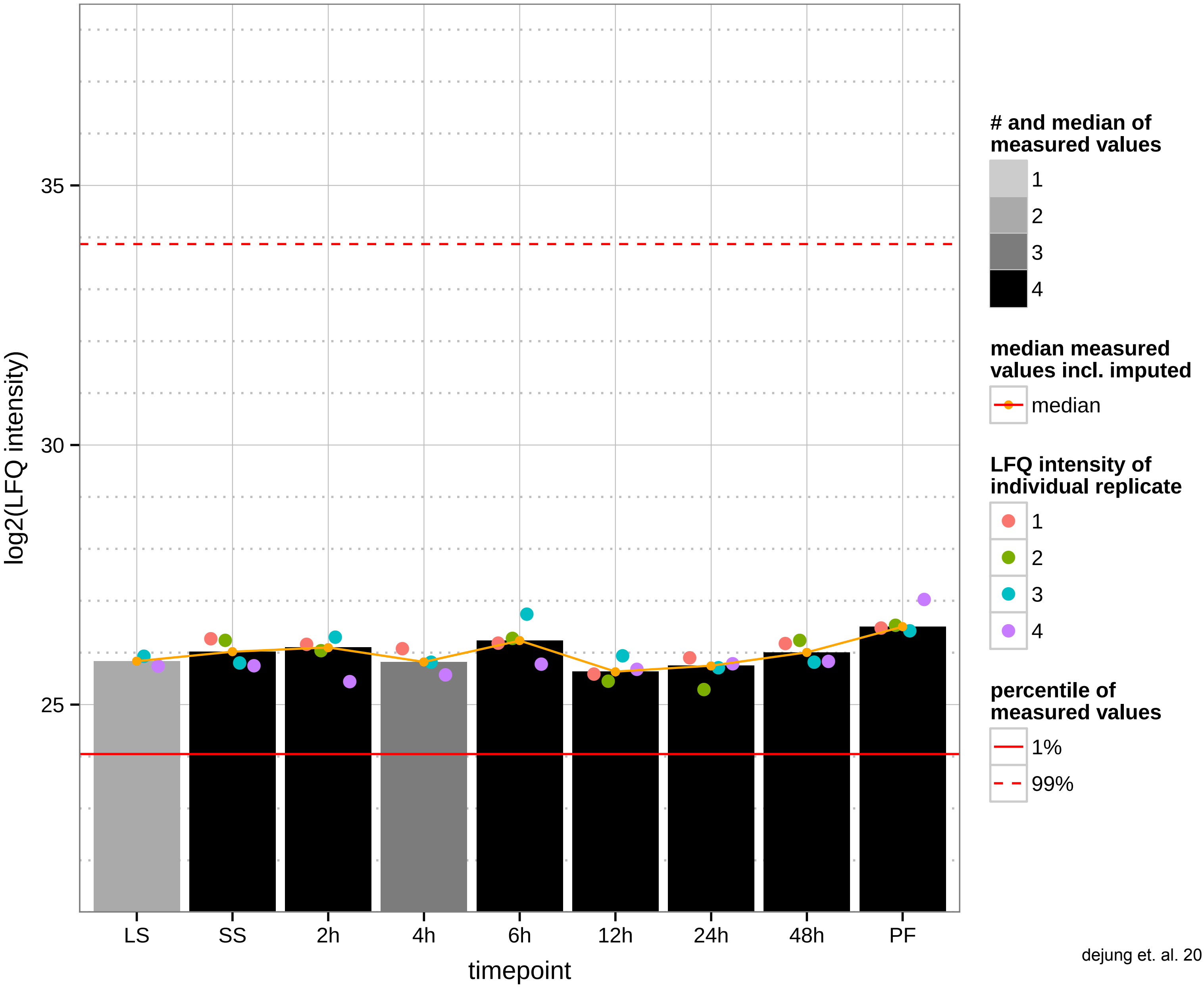




dejung et. al. 2015

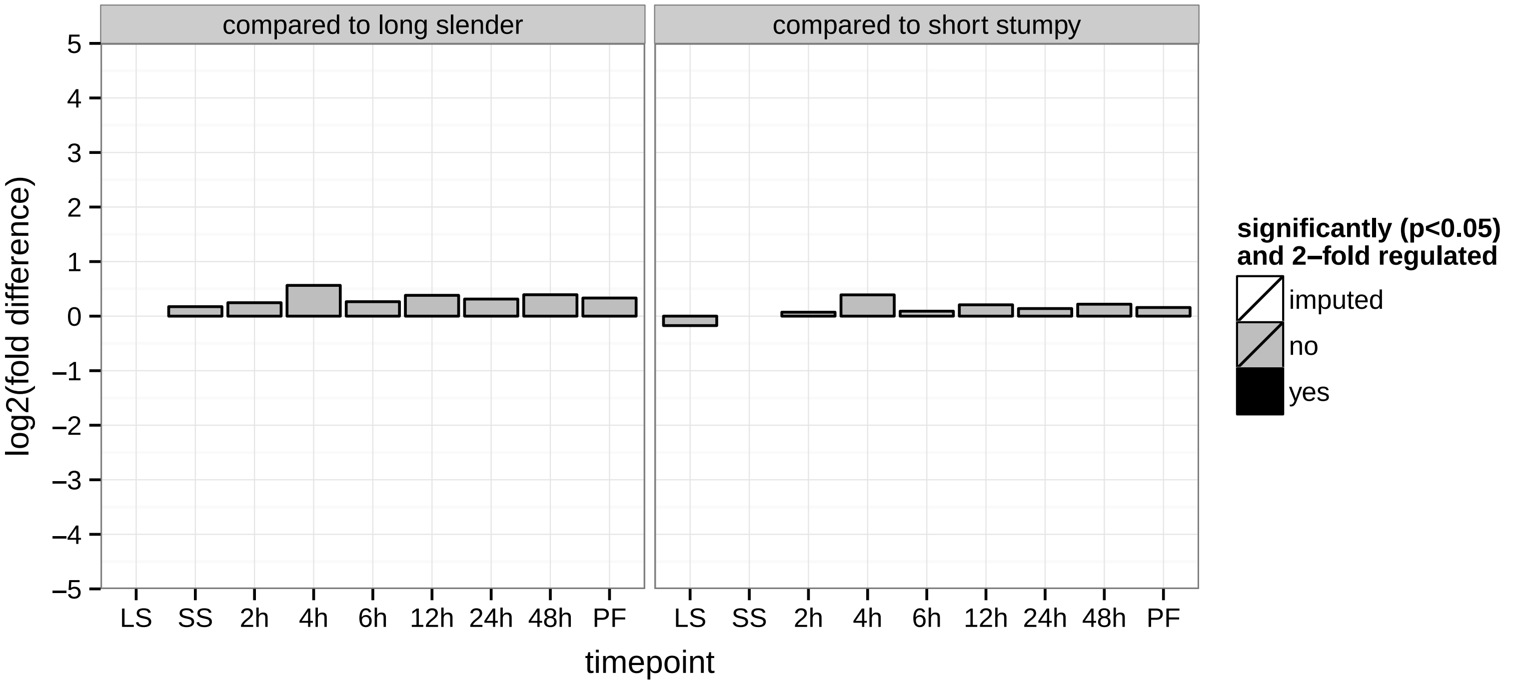
hypothetical protein, conserved
Tb927.10.2950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

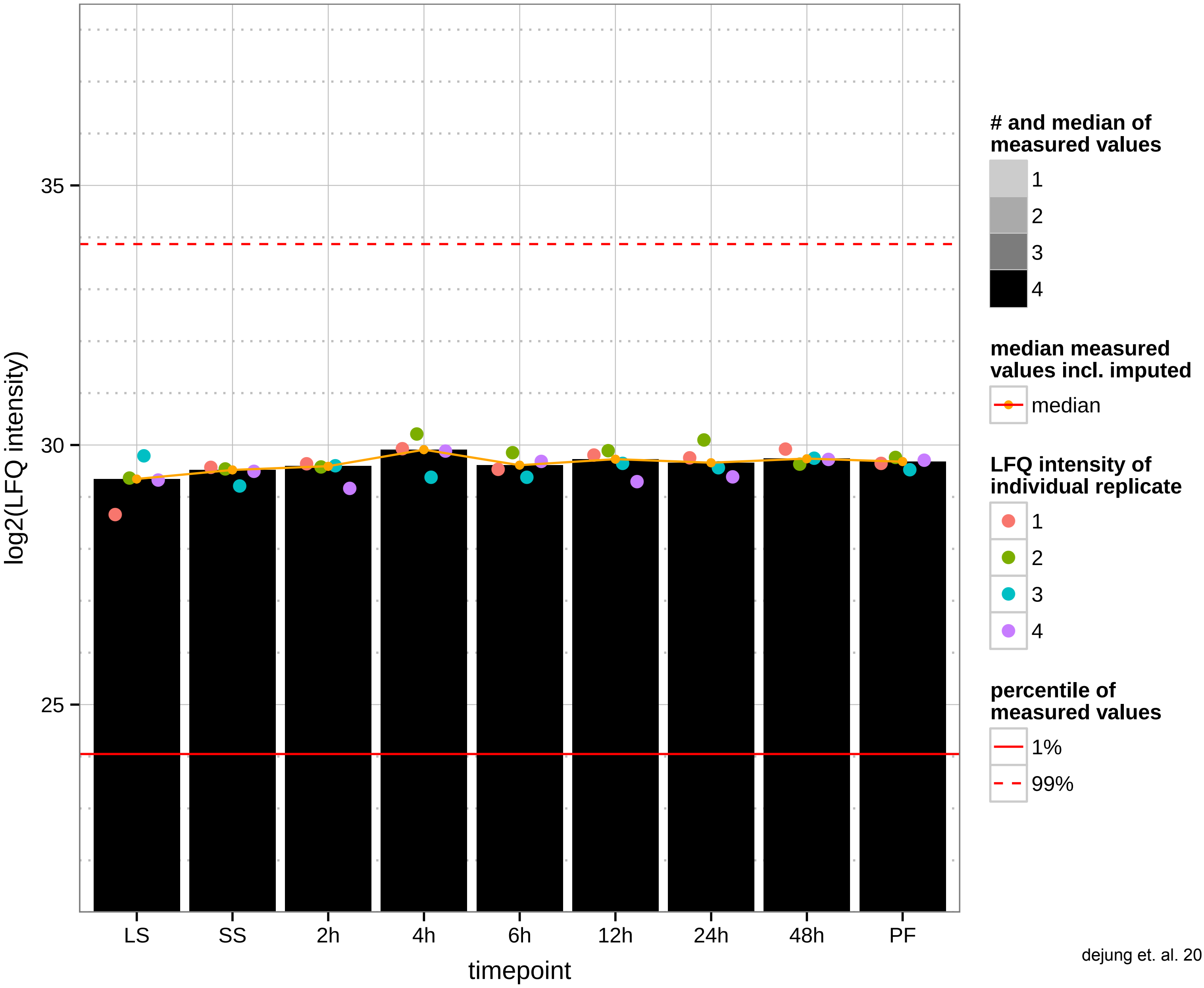




dejung et. al. 2015

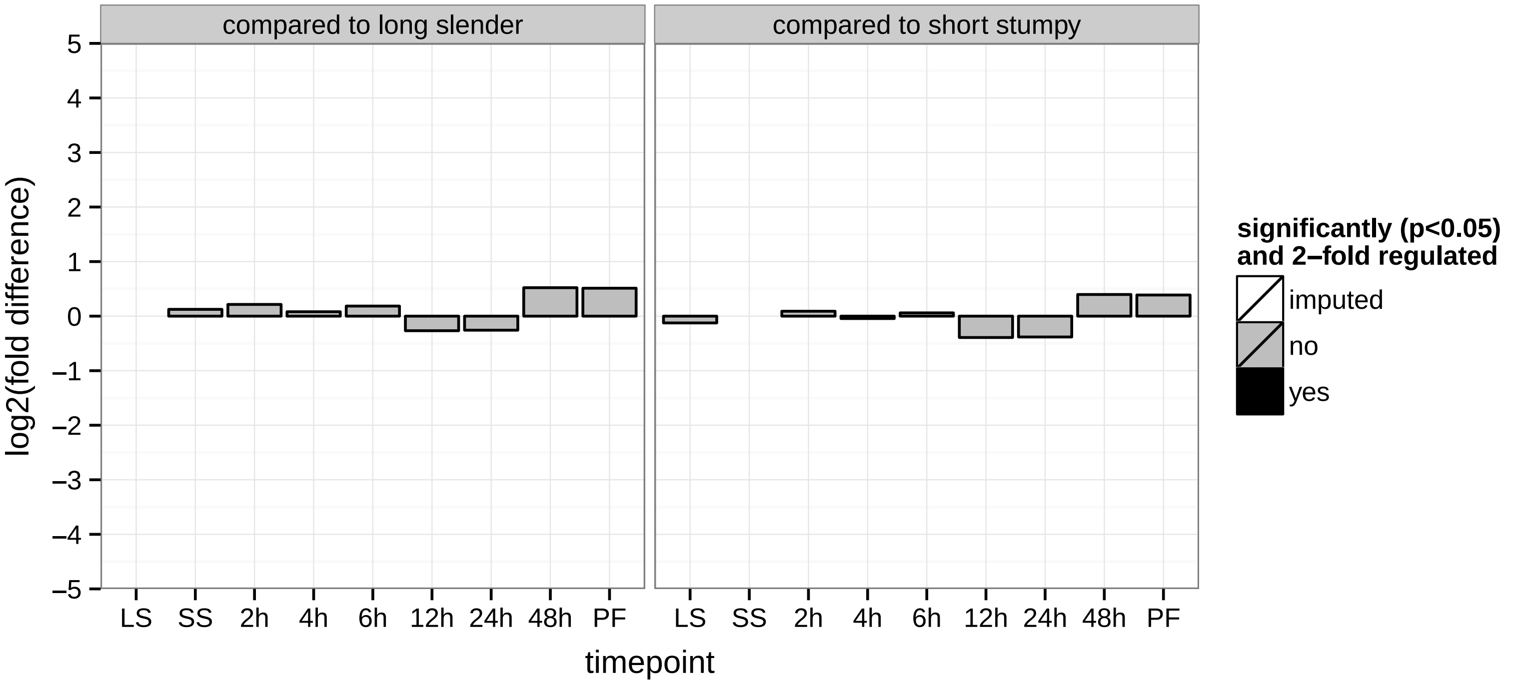
proteasome regulatory non–ATPase subunit 11, Metallo–peptidase, Clan MP, Family M67, 19S proteasome regulatory subuni
Tb927.10.3030;Tb927.10.2980
AGOF: null, endopeptidase activity
AGOC: proteasome regulatory particle
AGOP: cell growth, ubiquitin–dependent protein catabolic process
PGOF: protein binding
PGOC: null
PGOP: null

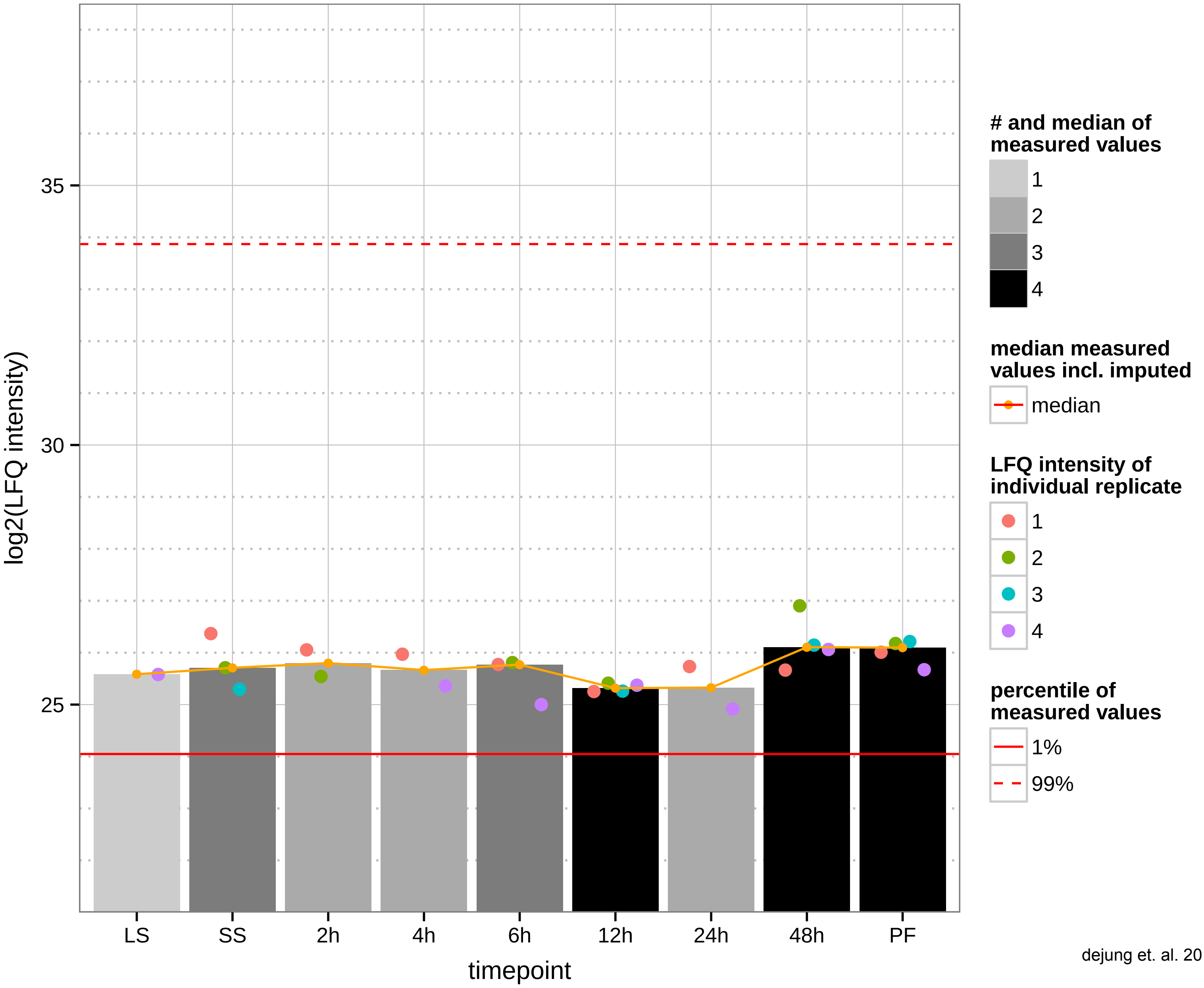




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.3010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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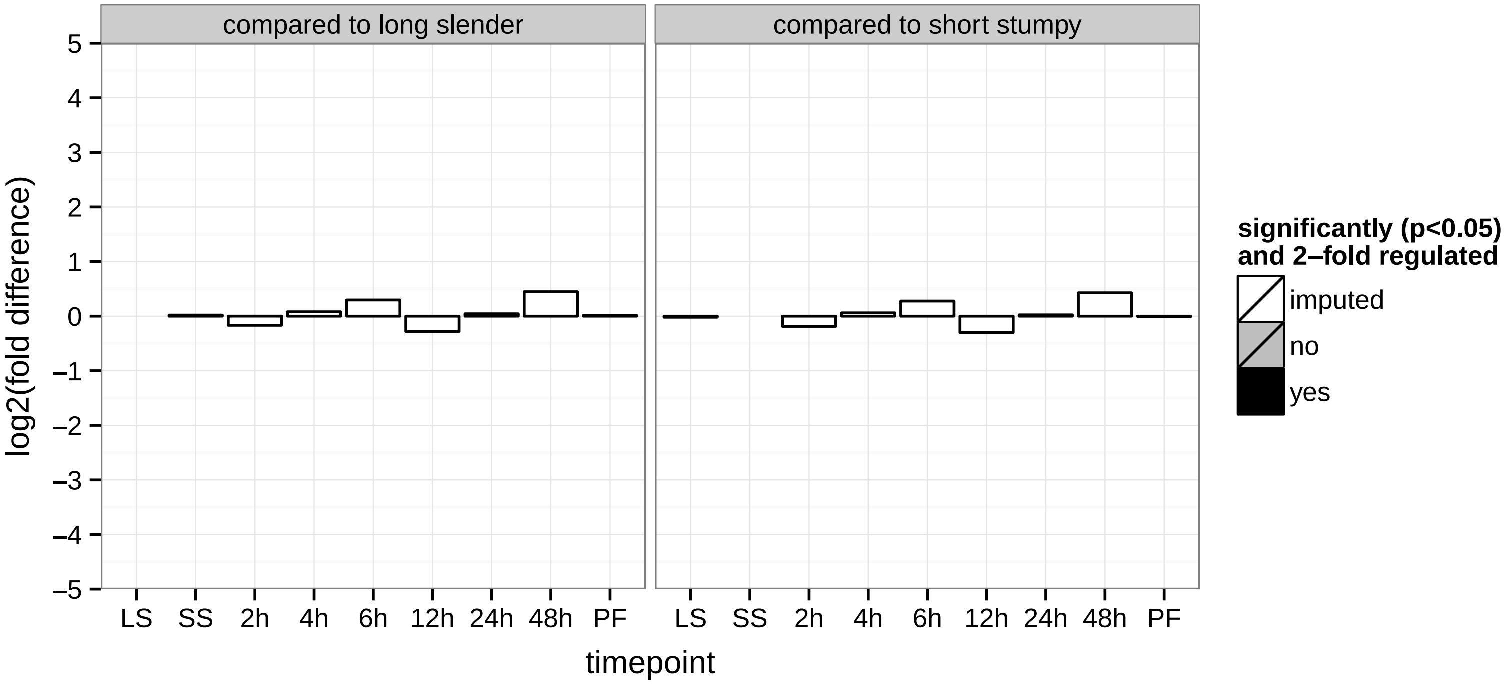
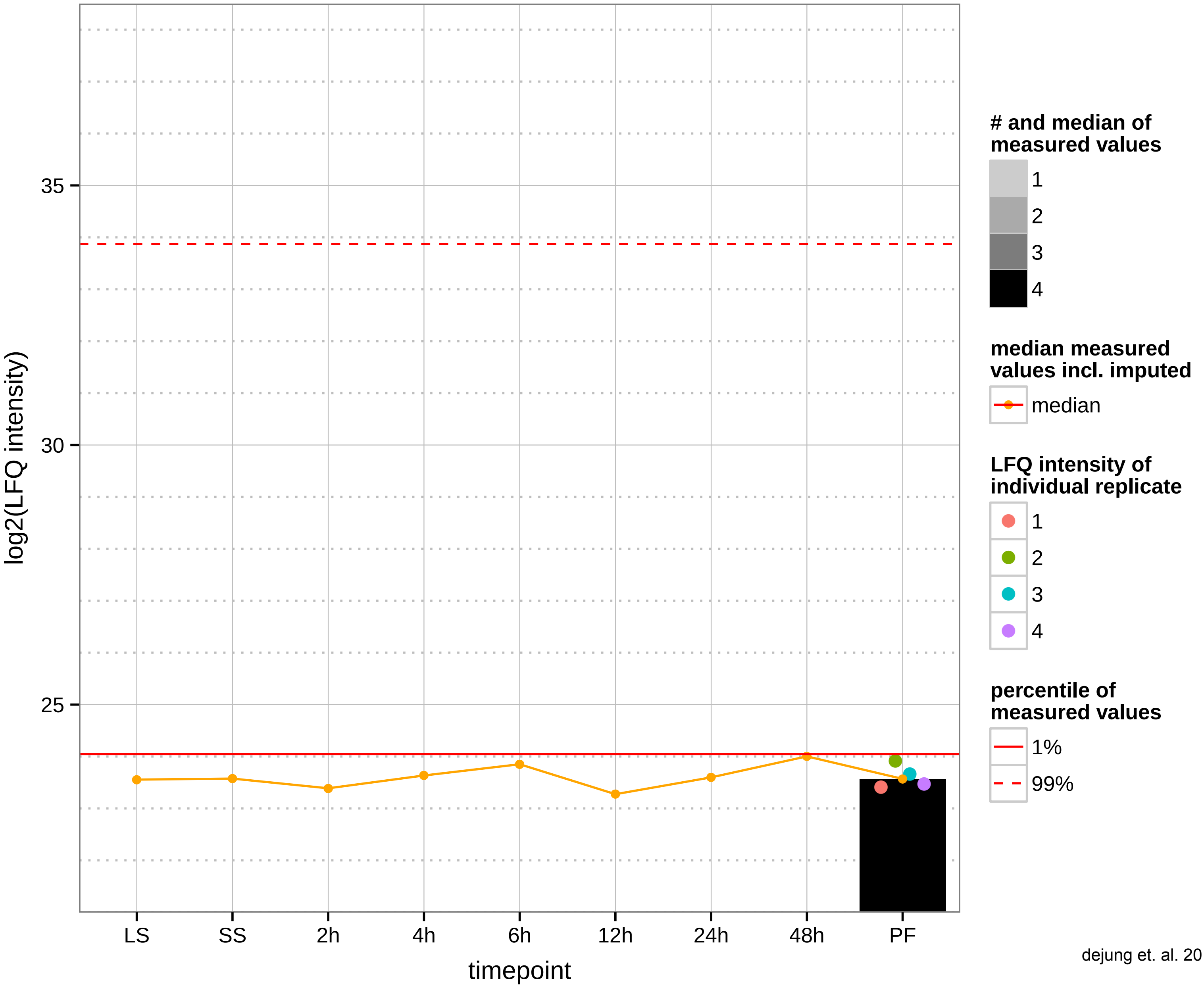
hypothetical protein, conserved
Tb927.10.3070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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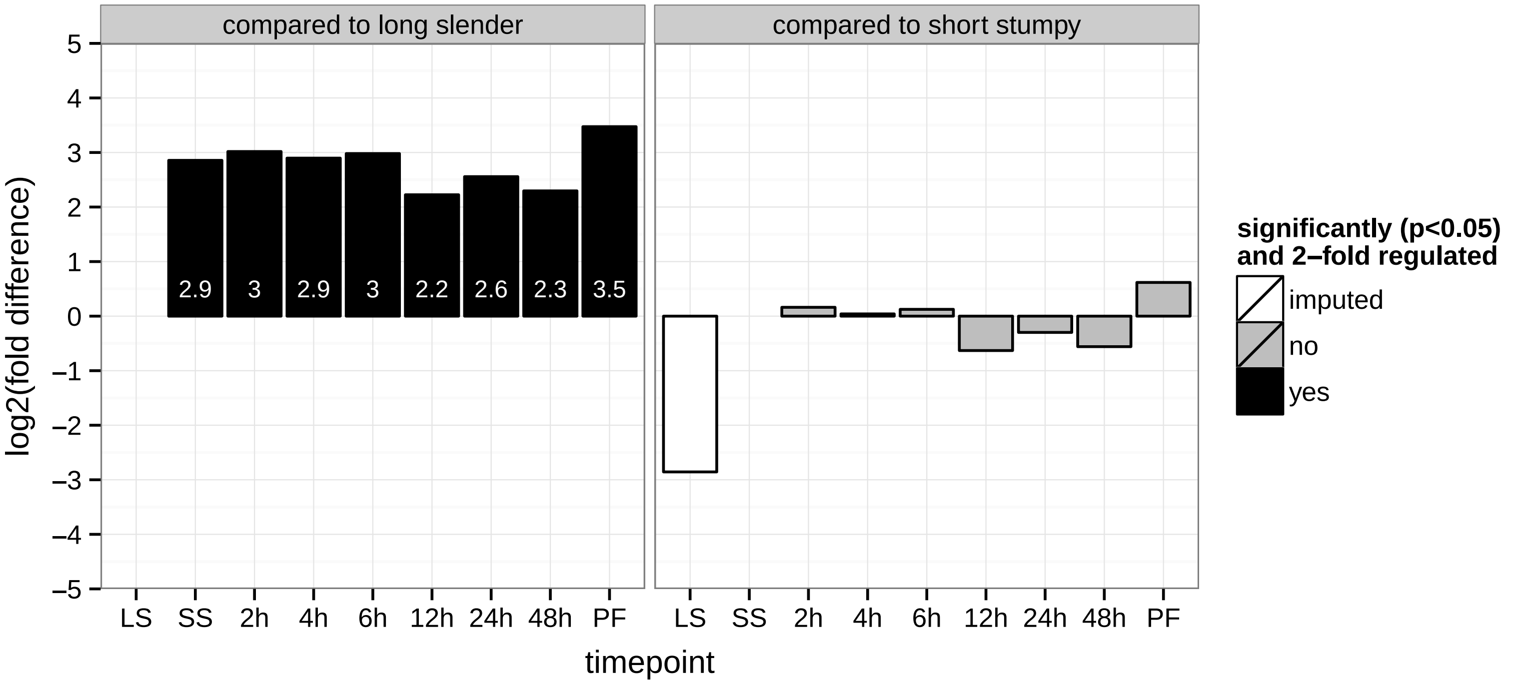
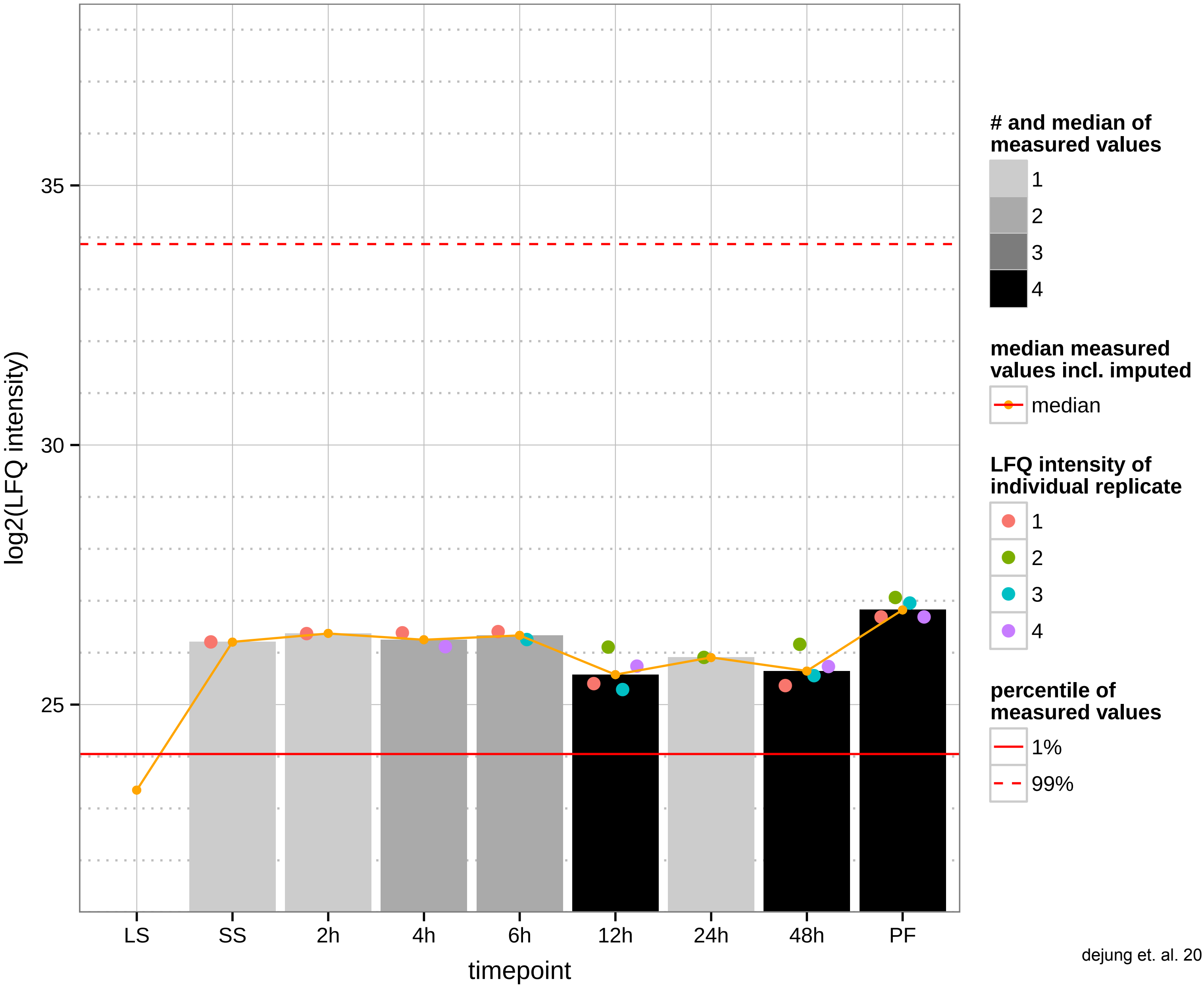
methionine biosynthetic protein, putative
Tb927.10.3080
AGOF: null
AGOC: mitochondrial inner membrane
AGOP: null
PGOF: transferase activity
PGOC: null
PGOP: null





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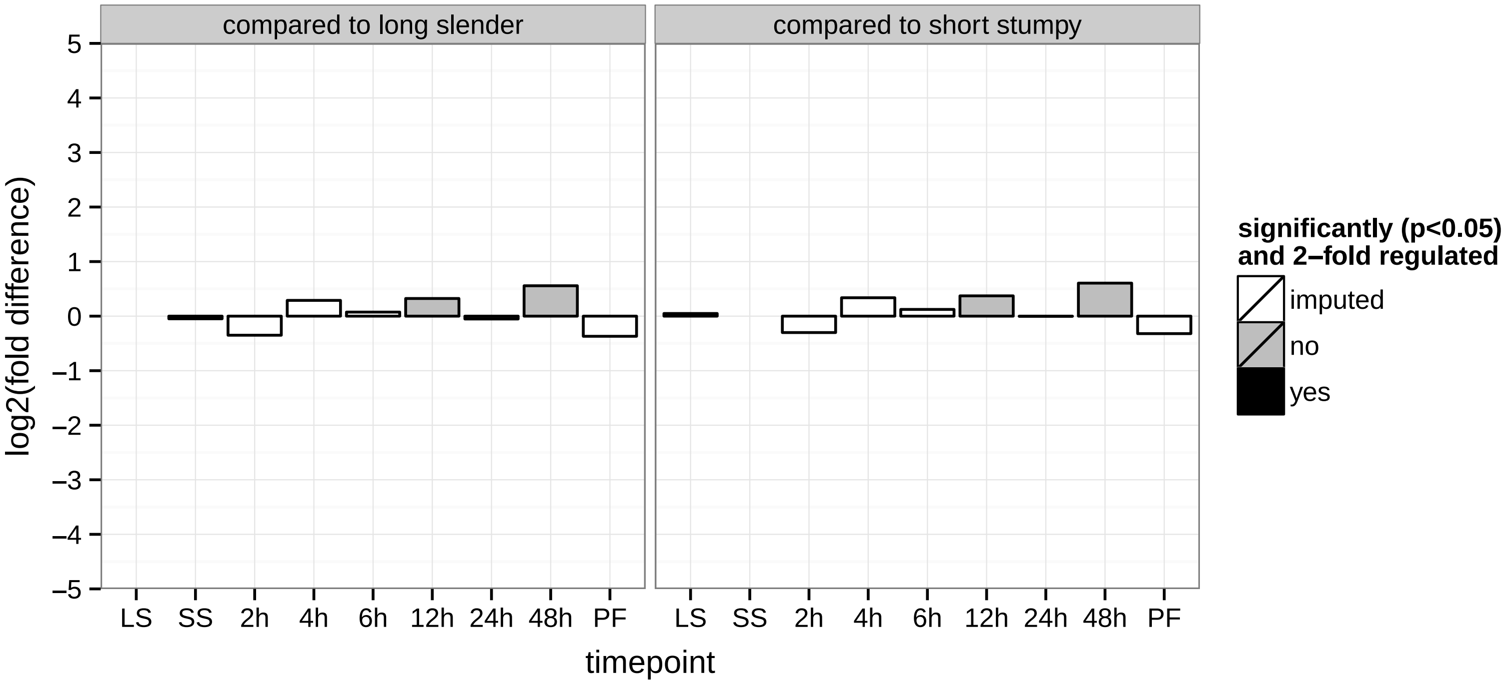
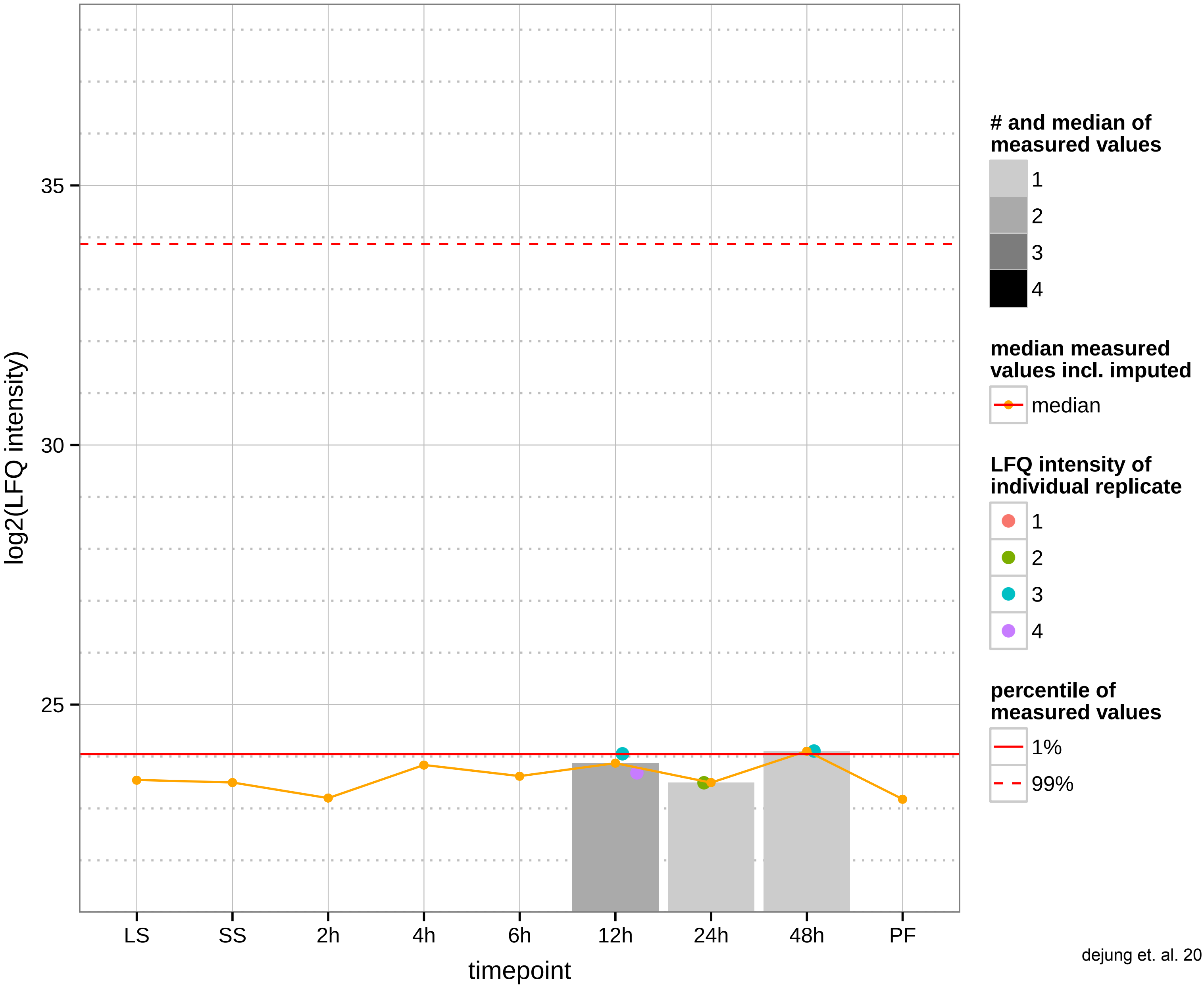
hypothetical protein, conserved
Tb927.10.3090
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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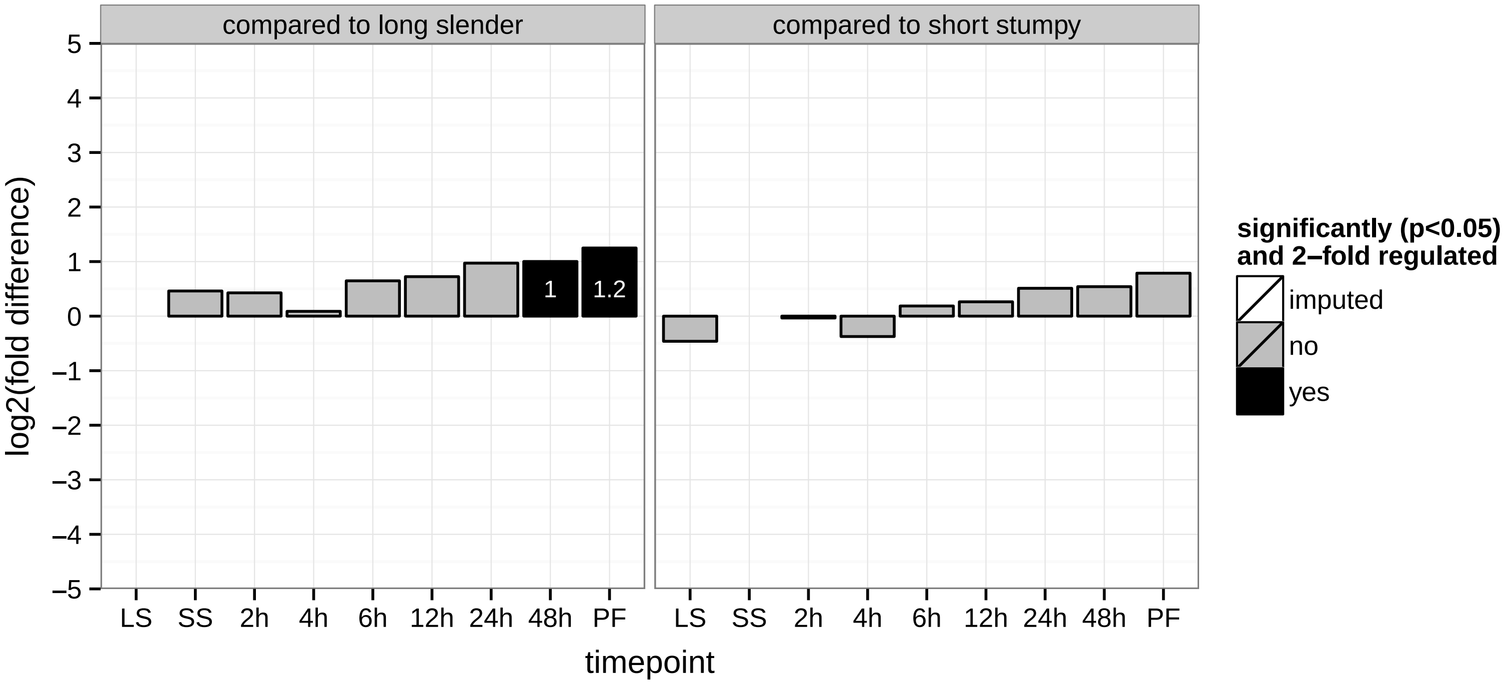
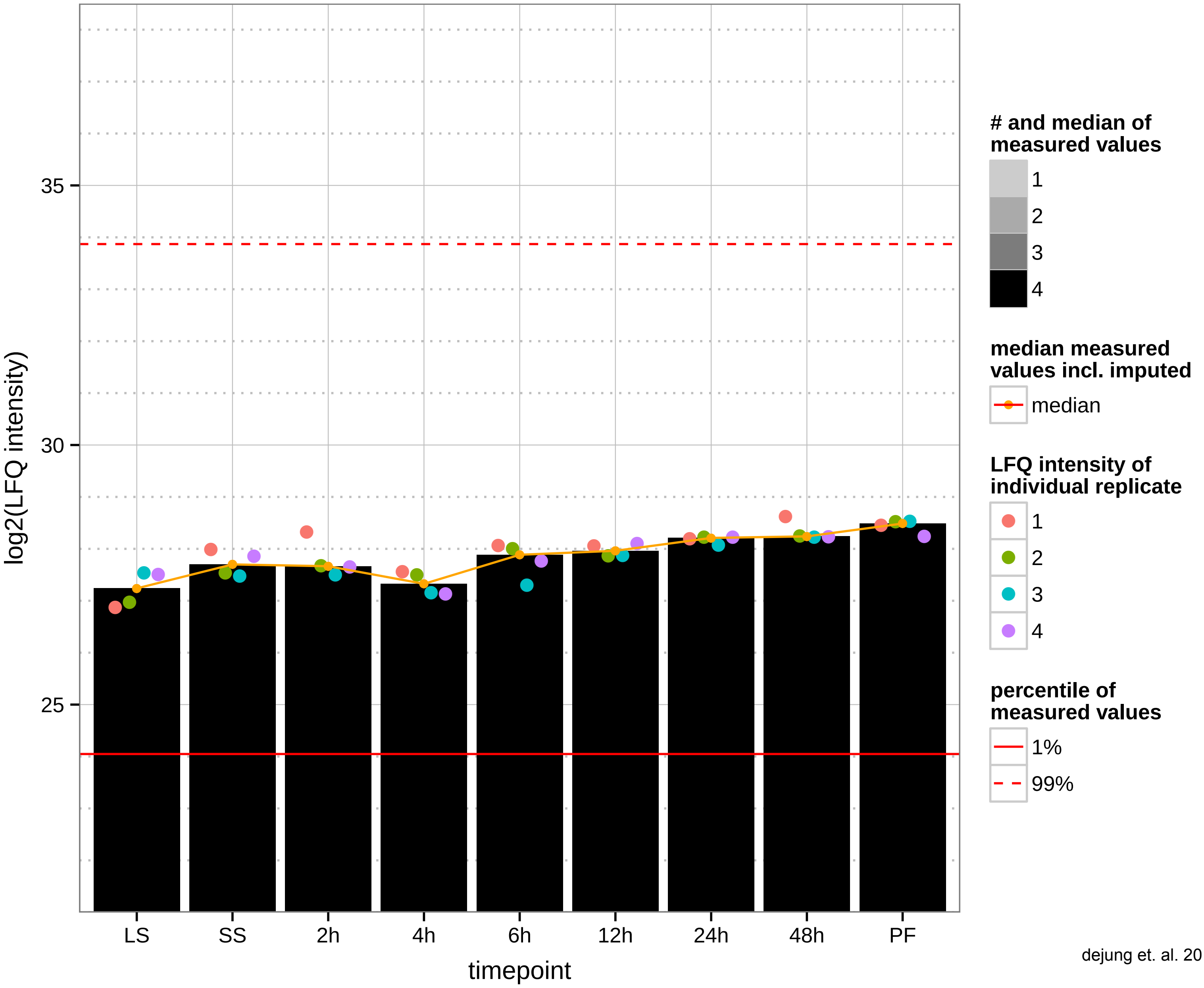
N–acetyltransferase, putative
Tb927.10.3150
AGOF: N–acetyltransferase activity
AGOC: null
AGOP: metabolic process
PGOF: N–acetyltransferase activity
PGOC: null
PGOP: null





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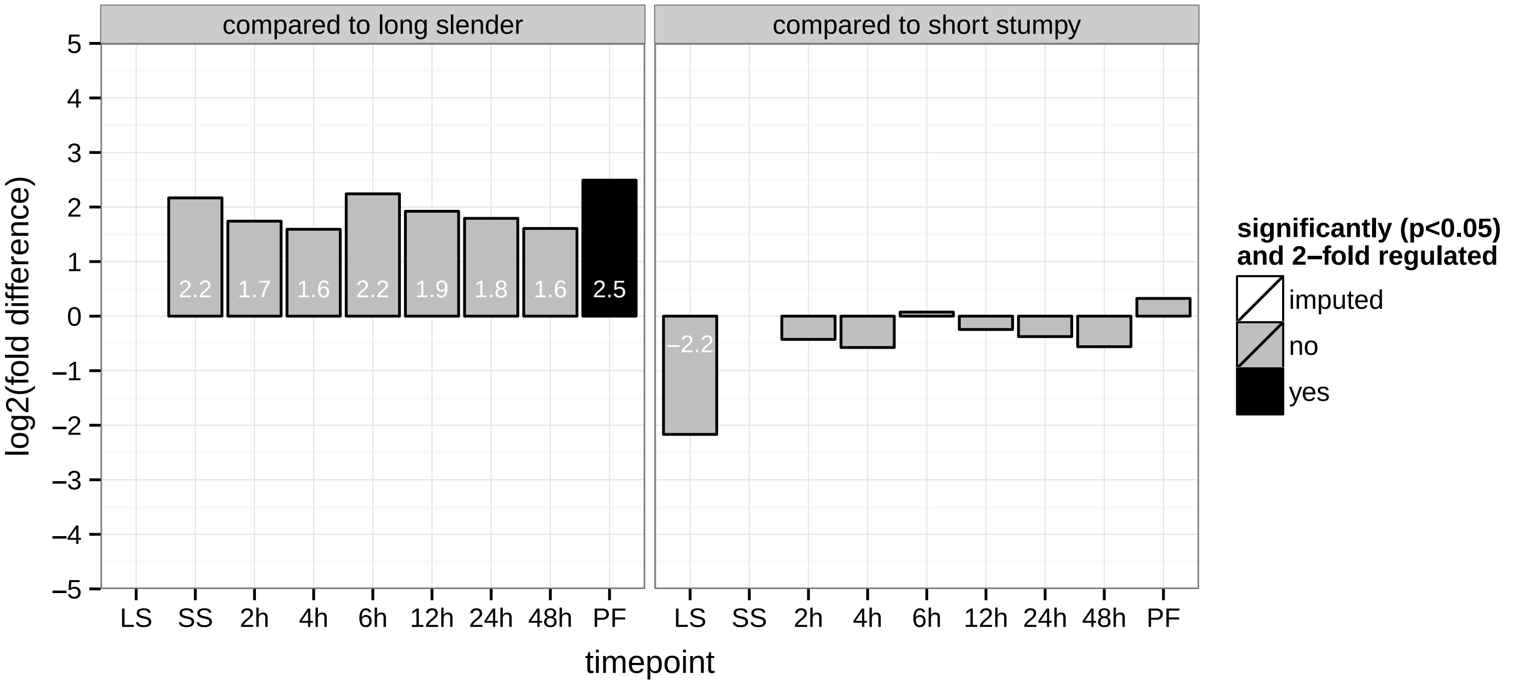
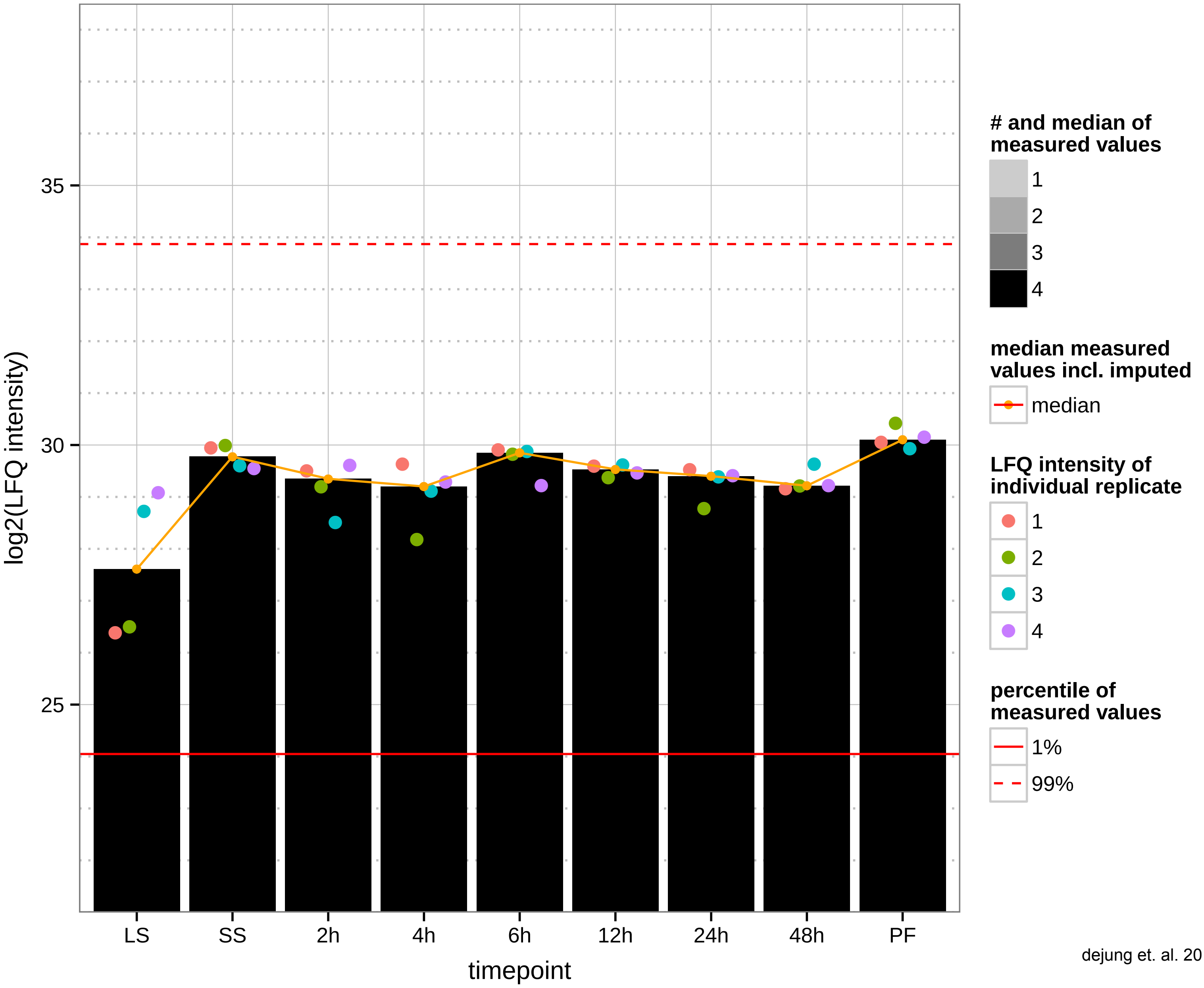
U2 splicing auxiliary factor, putative (U2AF35)
Tb927.10.3200
AGOF: RNA binding, zinc ion binding
AGOC: nuclear speck, nucleus
AGOP: RNA splicing, RNA splicing, via transesterification reactions, mRNA processing
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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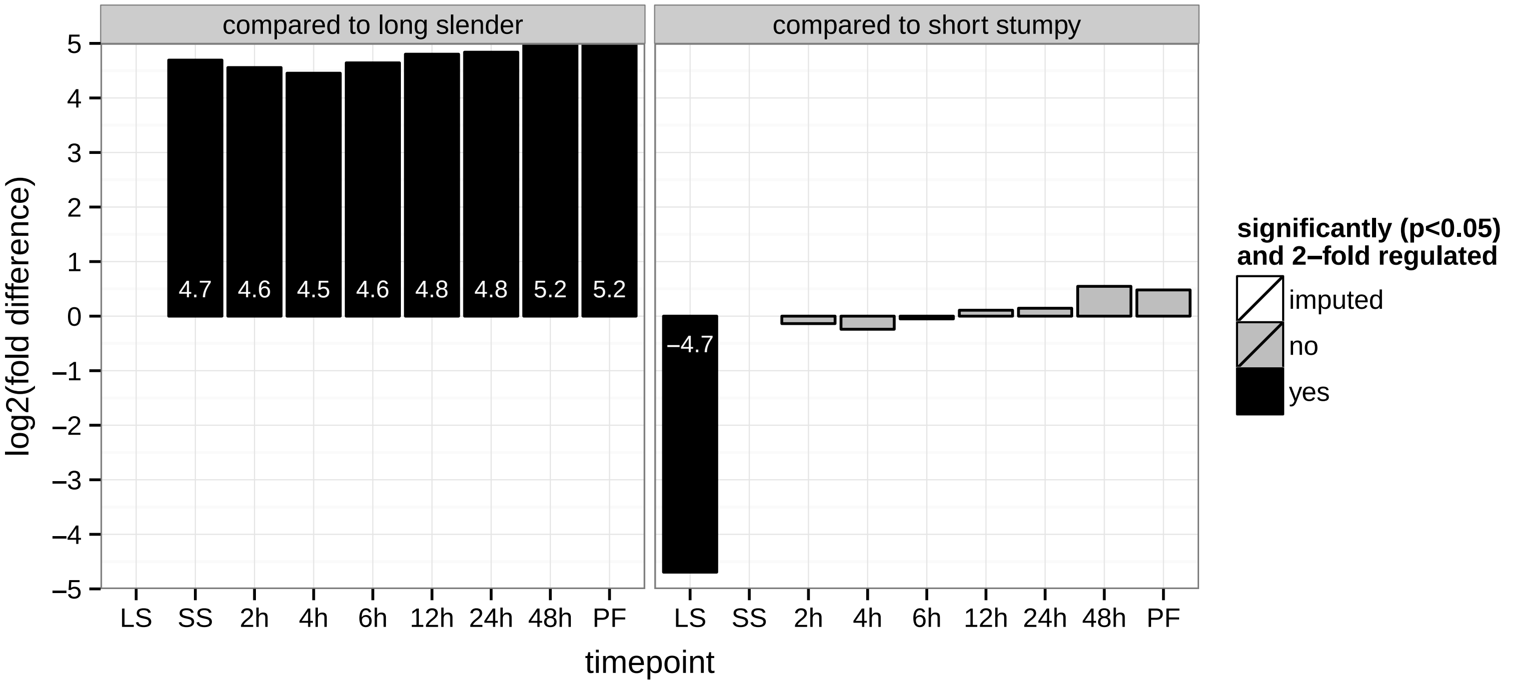
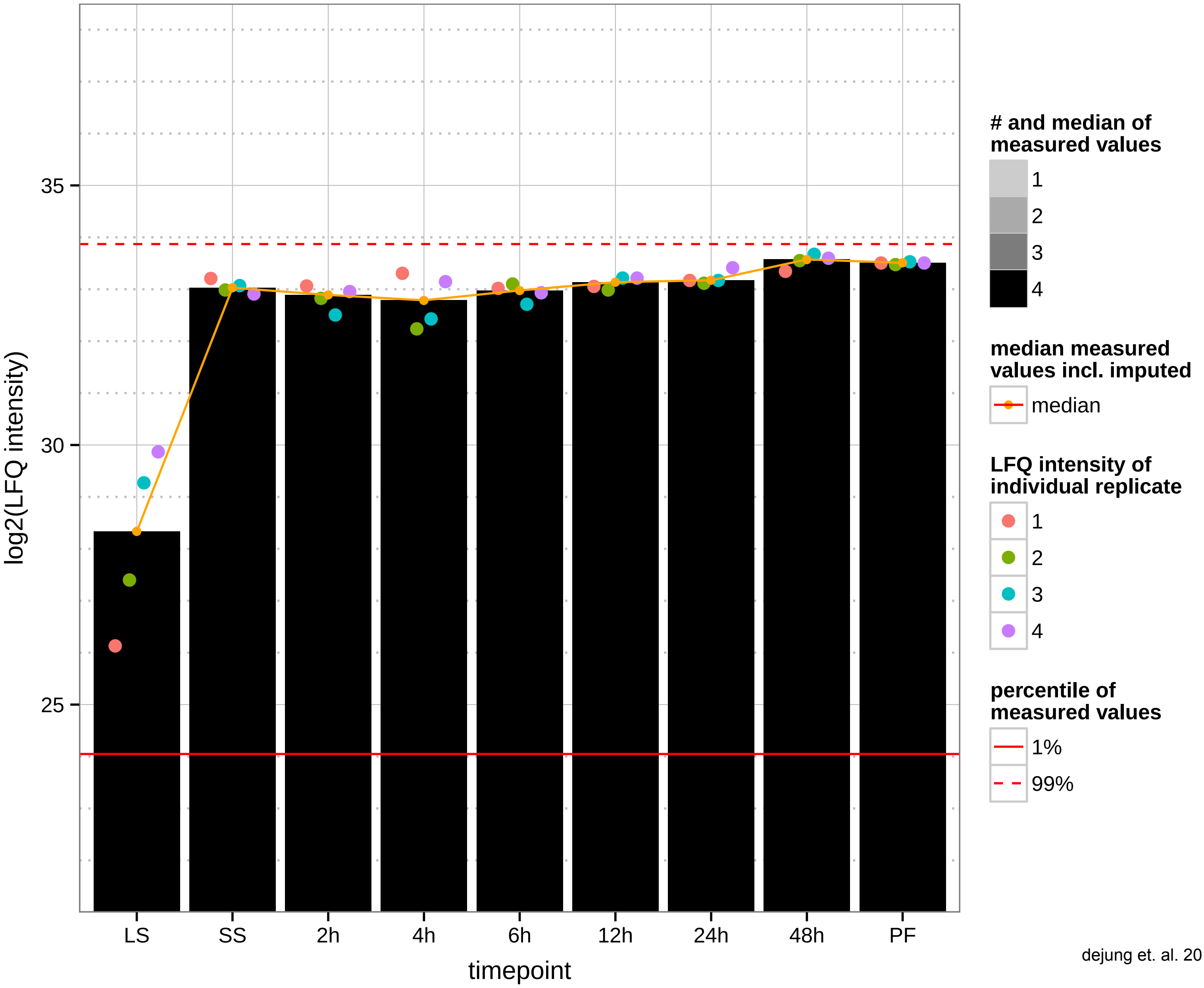
delta–1–pyrroline–5–carboxylate dehydrogenase, putative
Tb927.10.3210
AGOF: 1–pyrroline–5–carboxylate dehydrogenase activity, 3–chloroallyl aldehyde dehydrogenase activity
AGOC: mitochondrial matrix, mitochondrion
AGOP: oxidation–reduction process, proline biosynthetic process, proline catabolic process
PGOF: 1–pyrroline–5–carboxylate dehydrogenase activity, oxidoreductase activity
PGOC: mitochondrial matrix
PGOP: metabolic process, oxidation–reduction process, proline biosynthetic process





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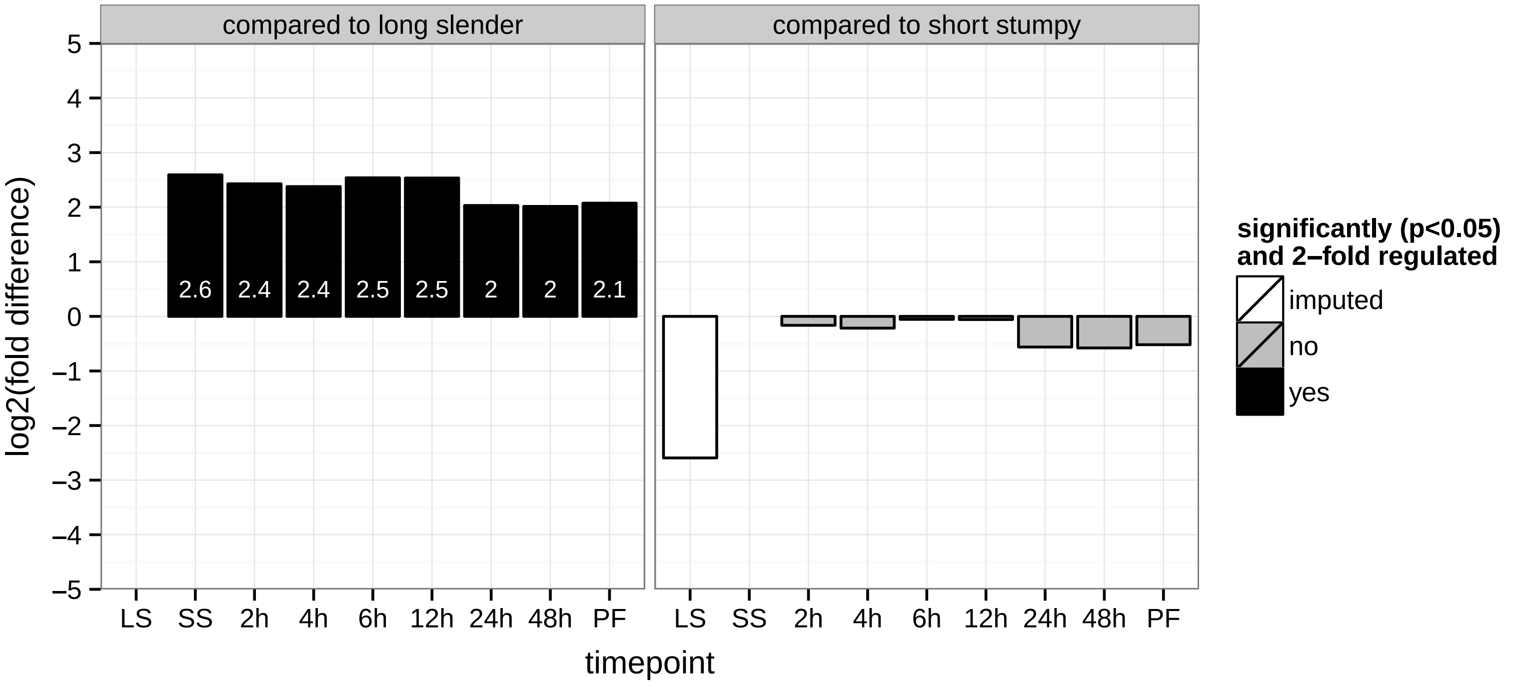
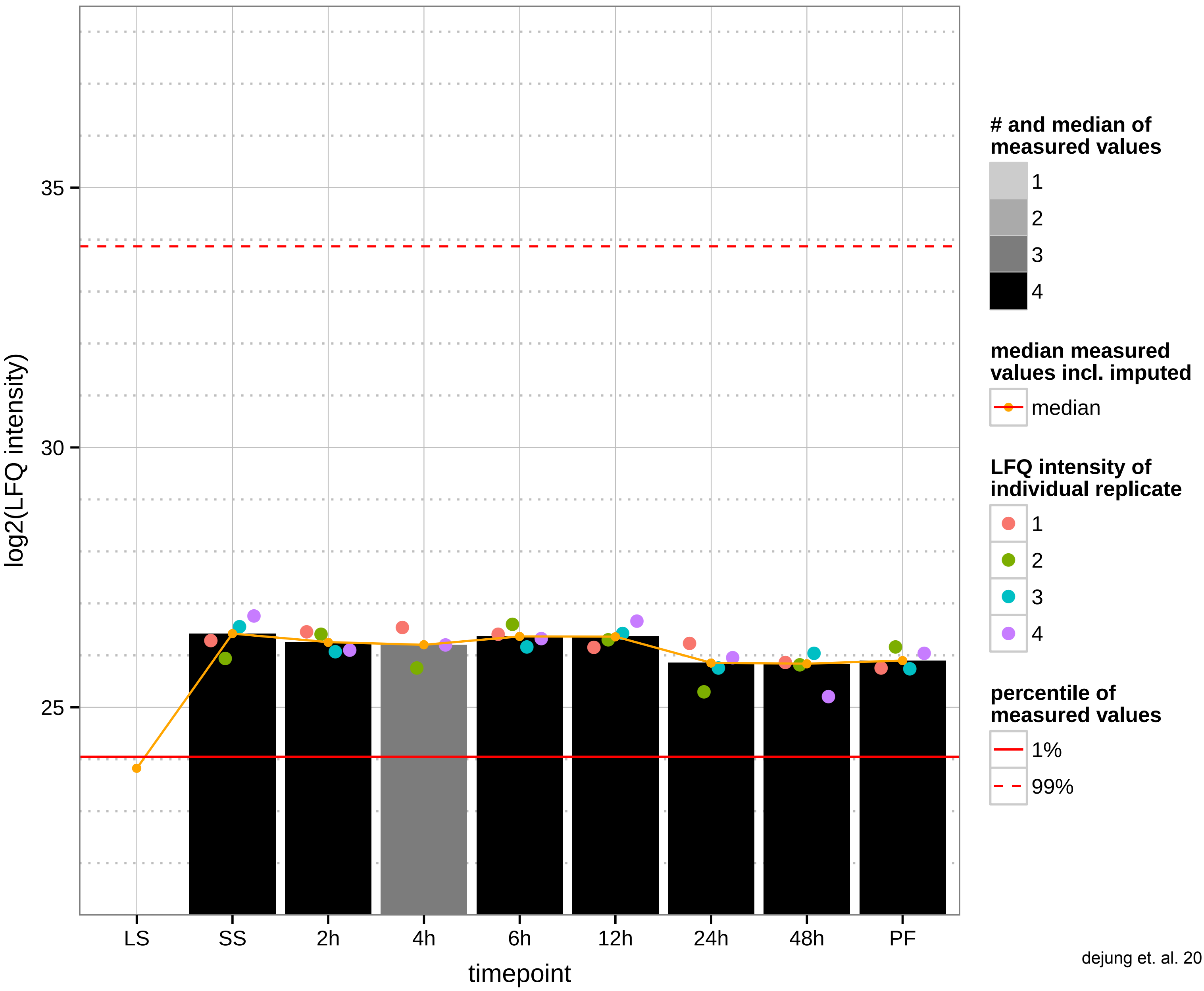
hypothetical protein, conserved
Tb927.10.330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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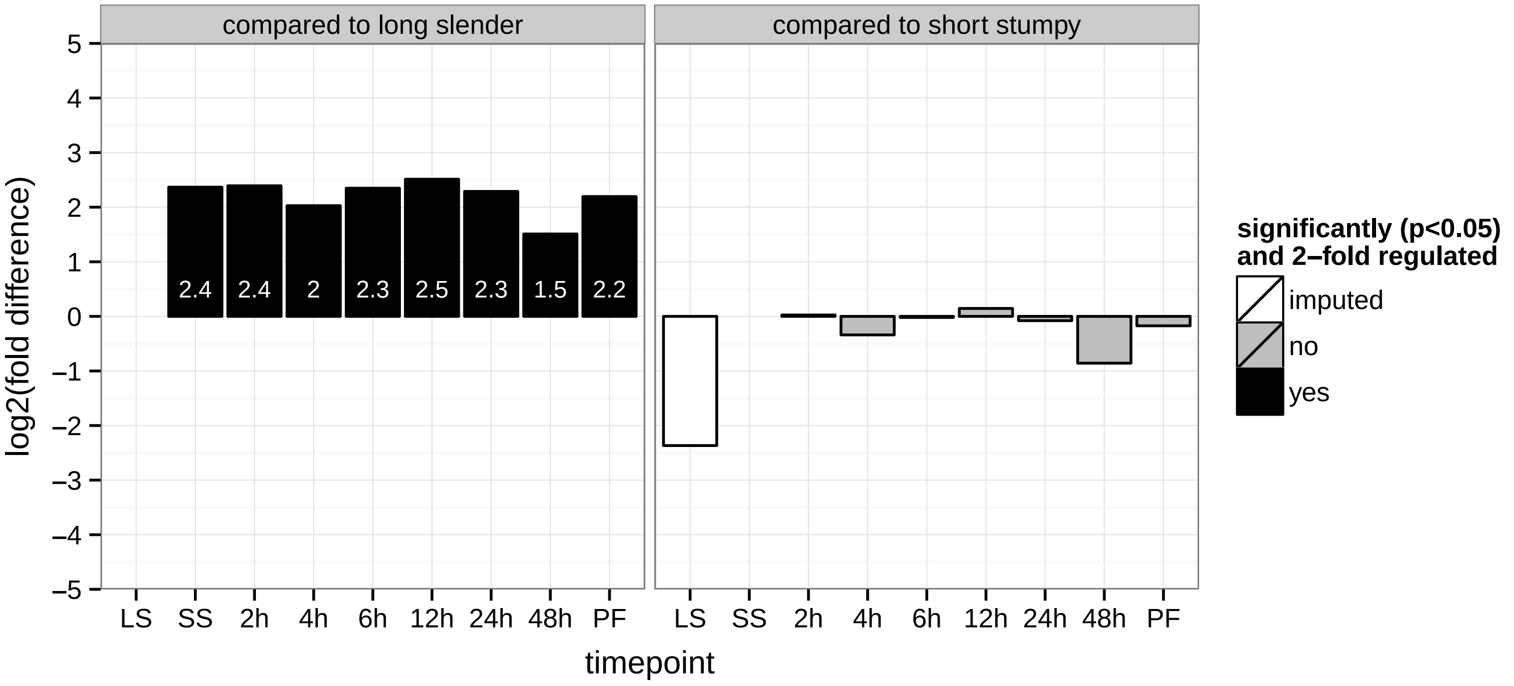
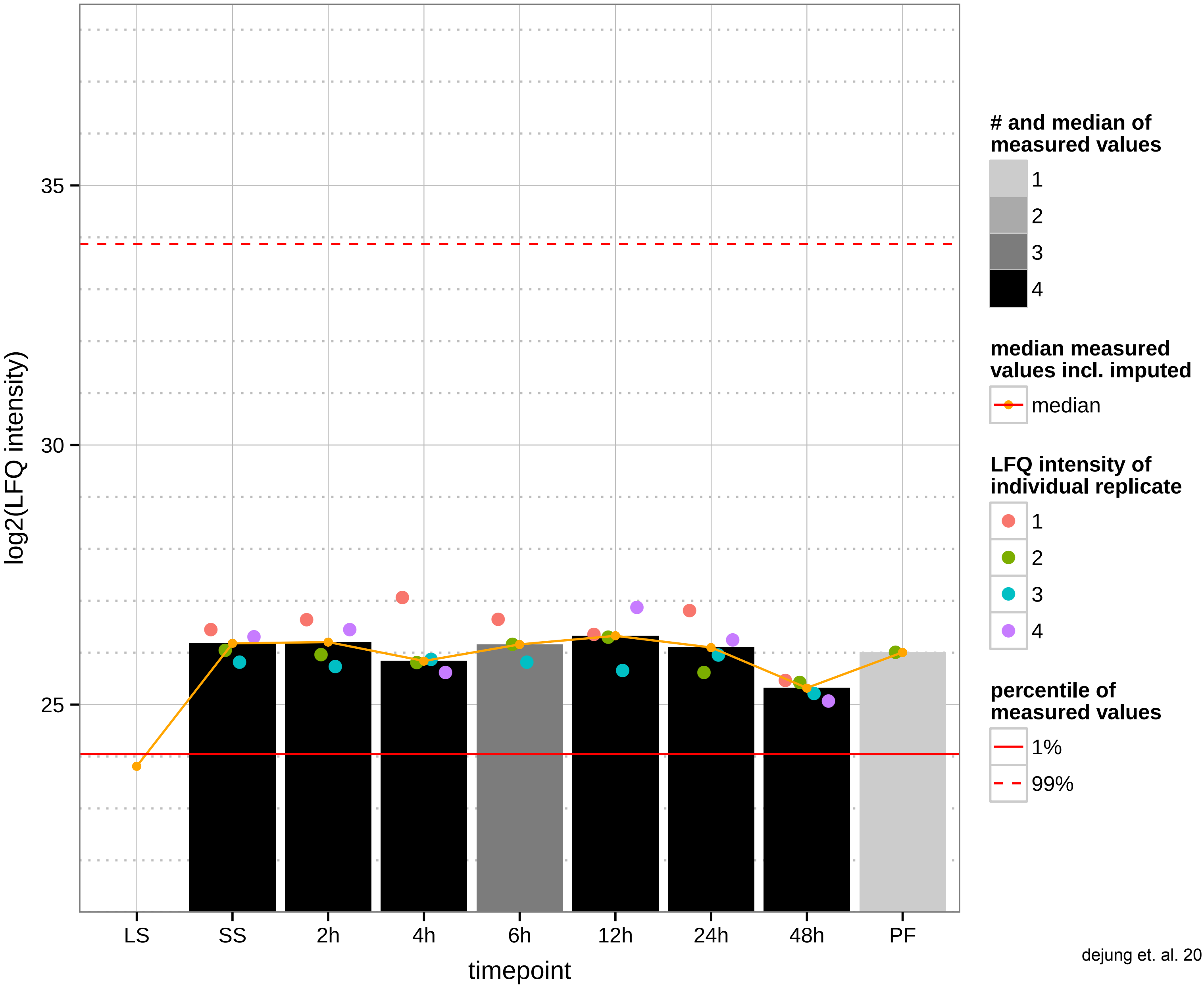
hypothetical protein, conserved, predicted TLD domain protein
Tb927.10.3390;Tb11.v5.0724
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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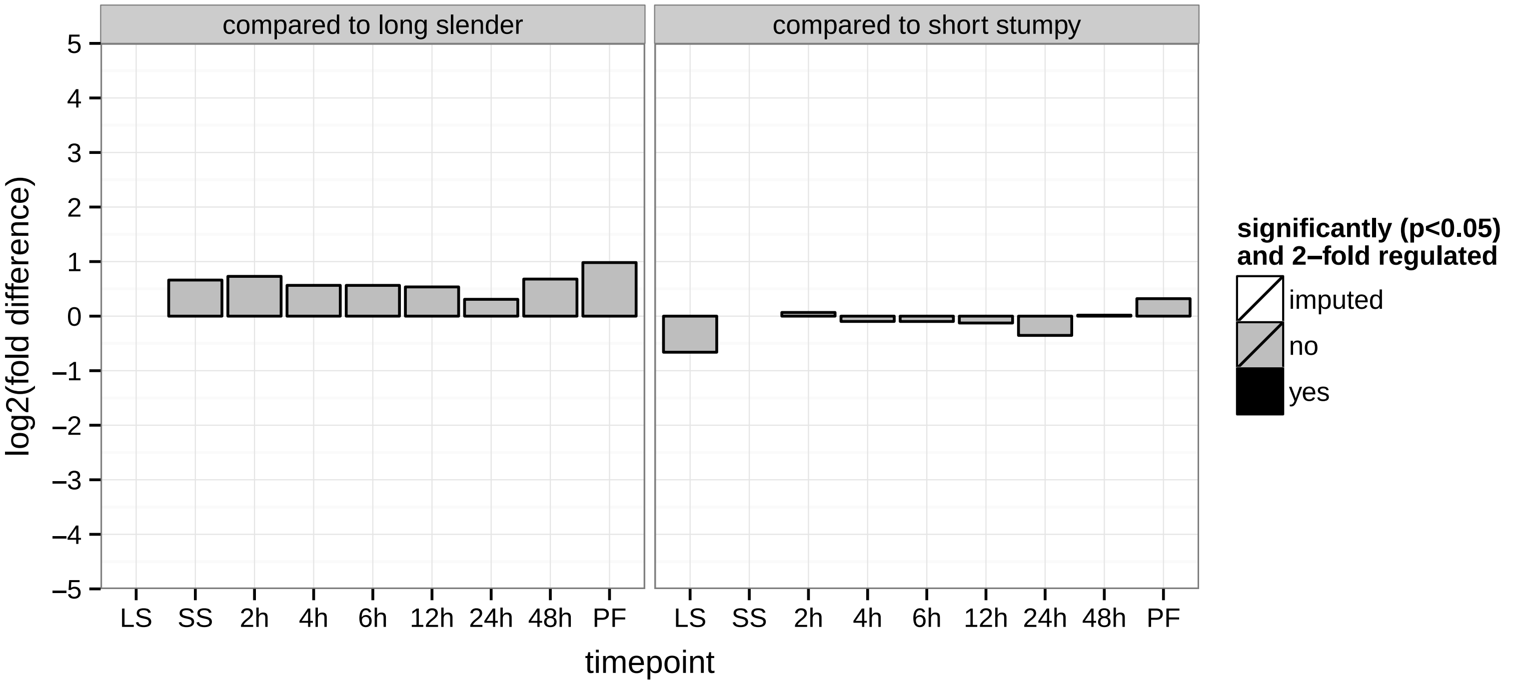
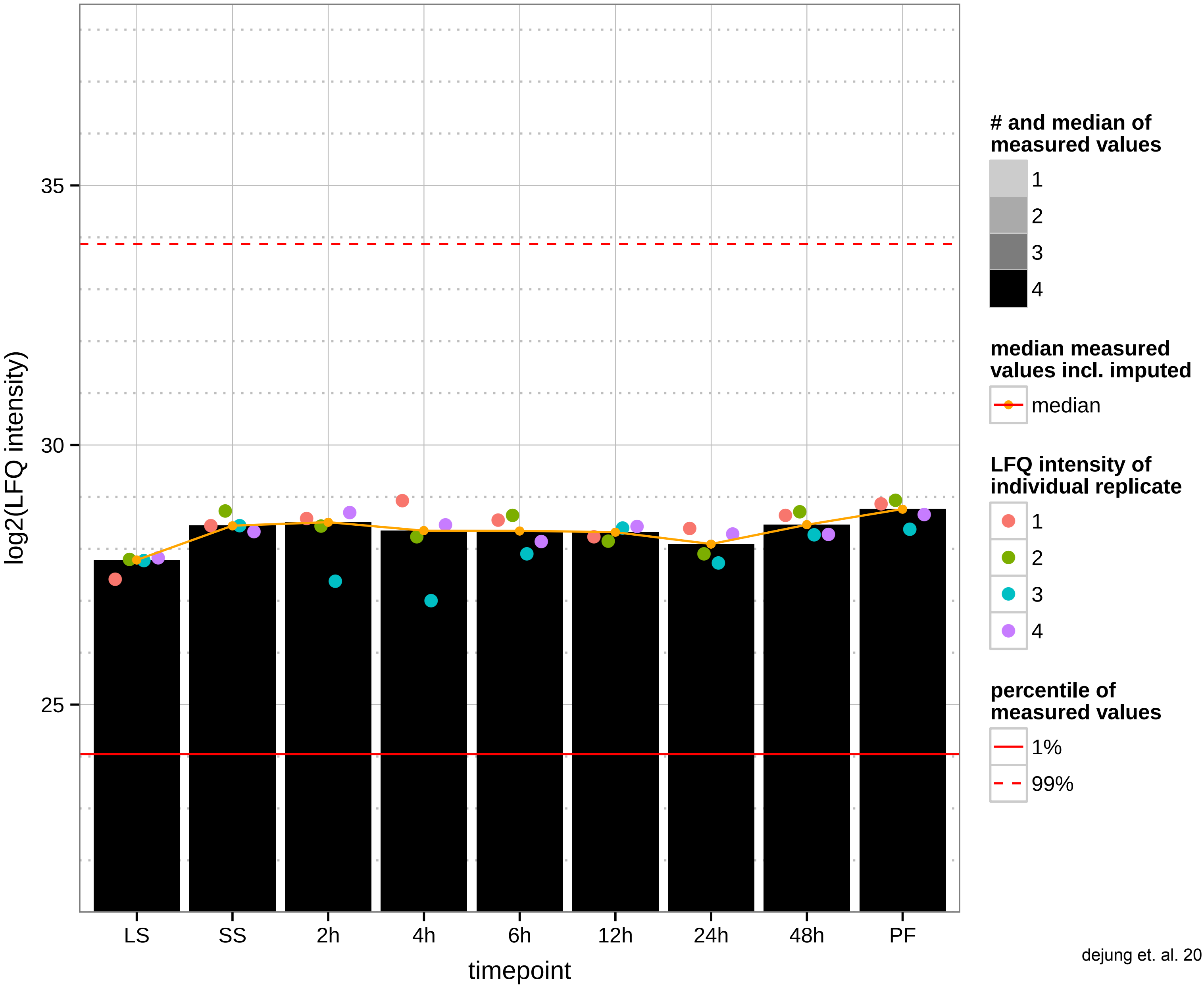
RNA–binding protein, putative (RBSR4)
Tb927.10.3500
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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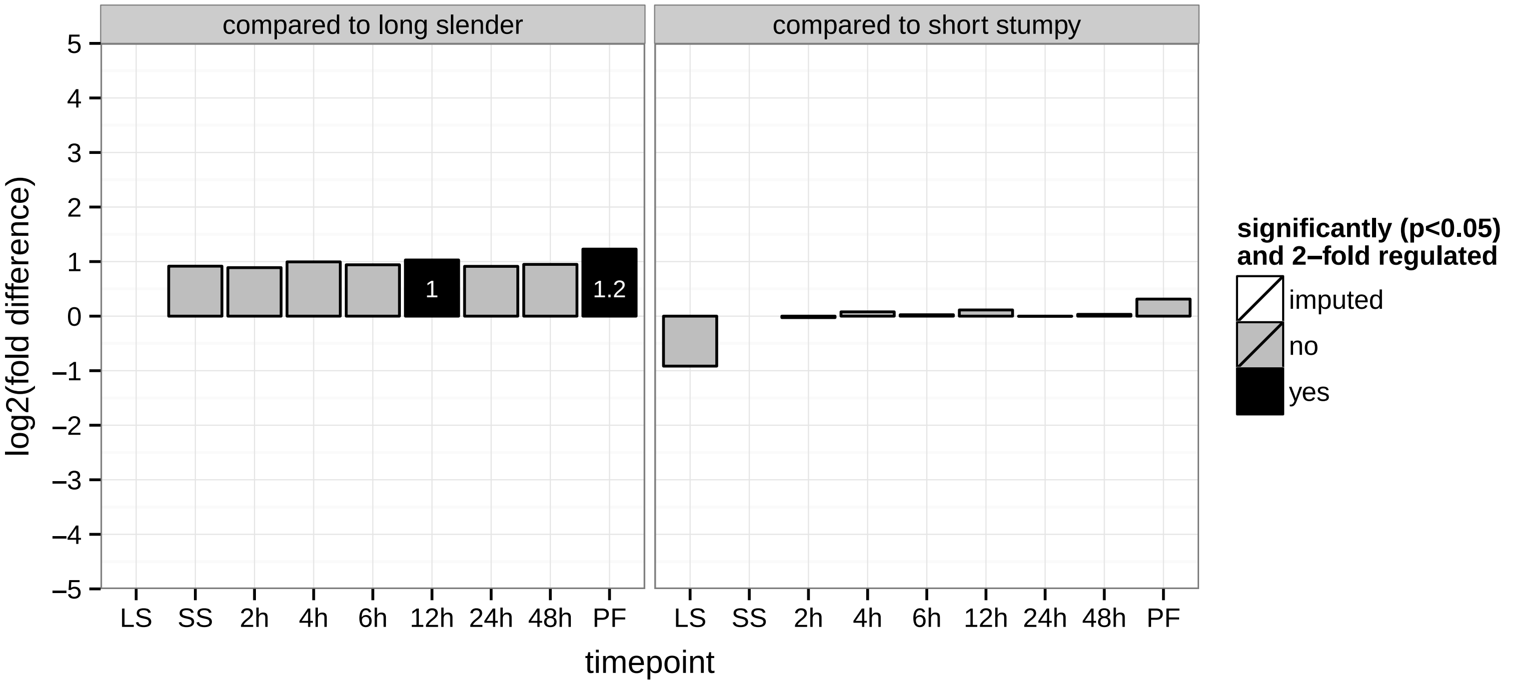
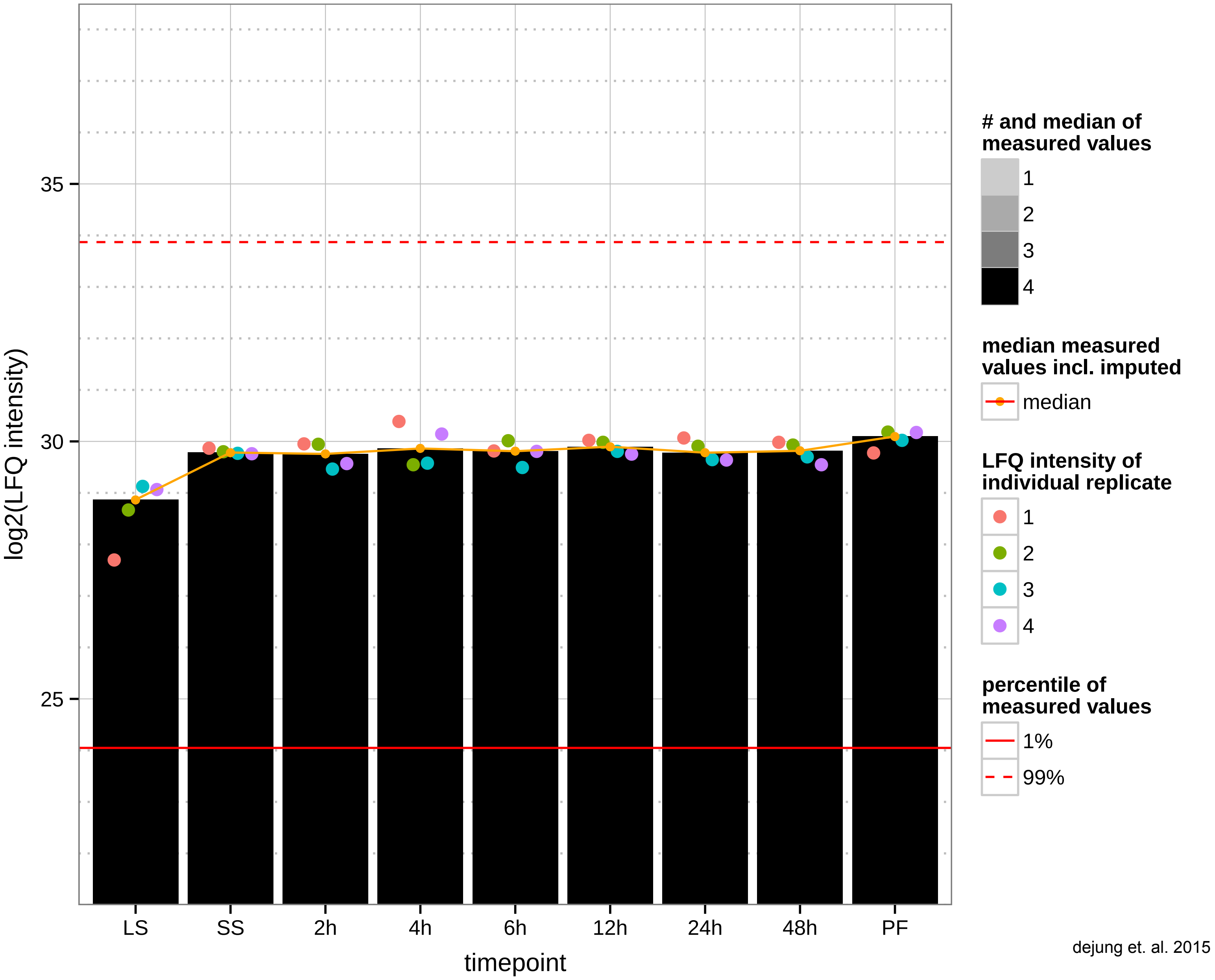
protease regulatory ATPase subunit 4 (RPT4)
Tb927.10.3520
AGOF: ATP binding, ATPase activity
AGOC: cytoplasm, nucleus, proteasome regulatory particle
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ATP binding, hydrolase activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: cytoplasm
PGOP: protein catabolic process





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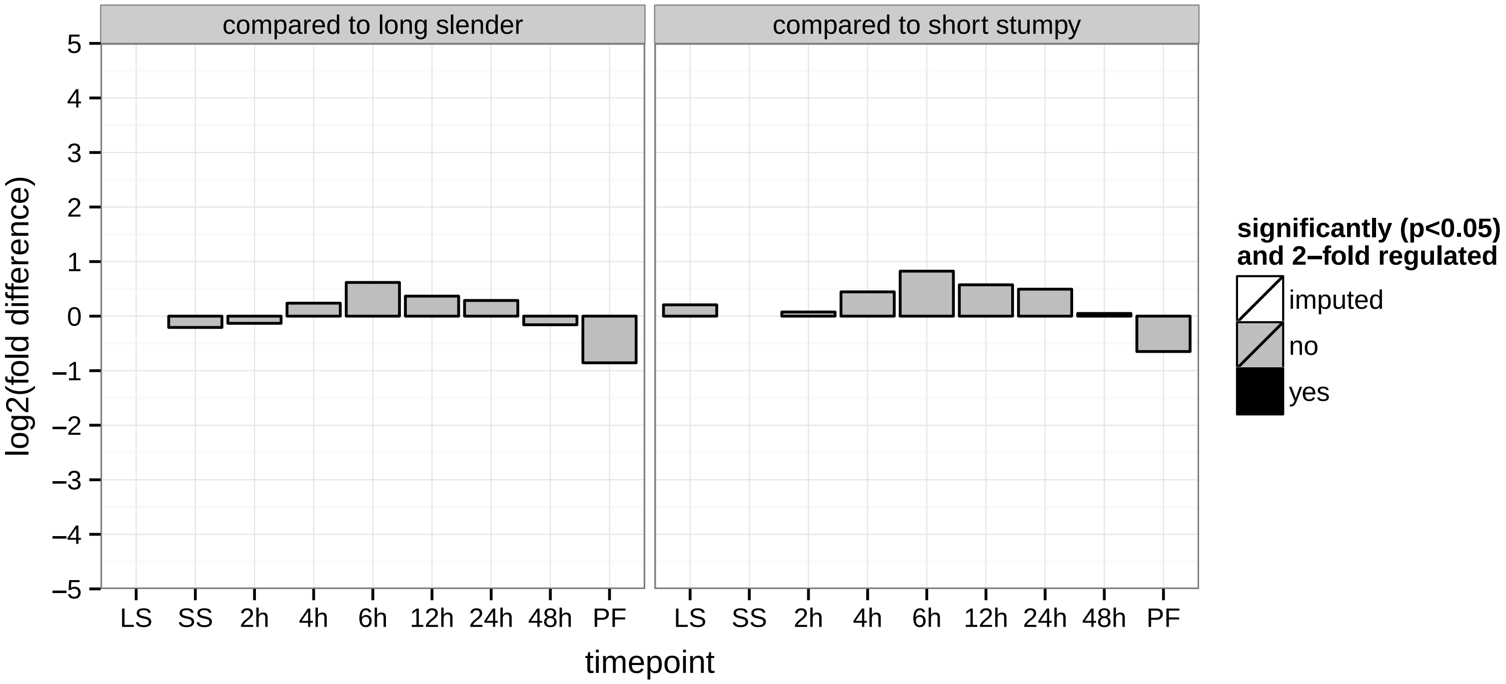
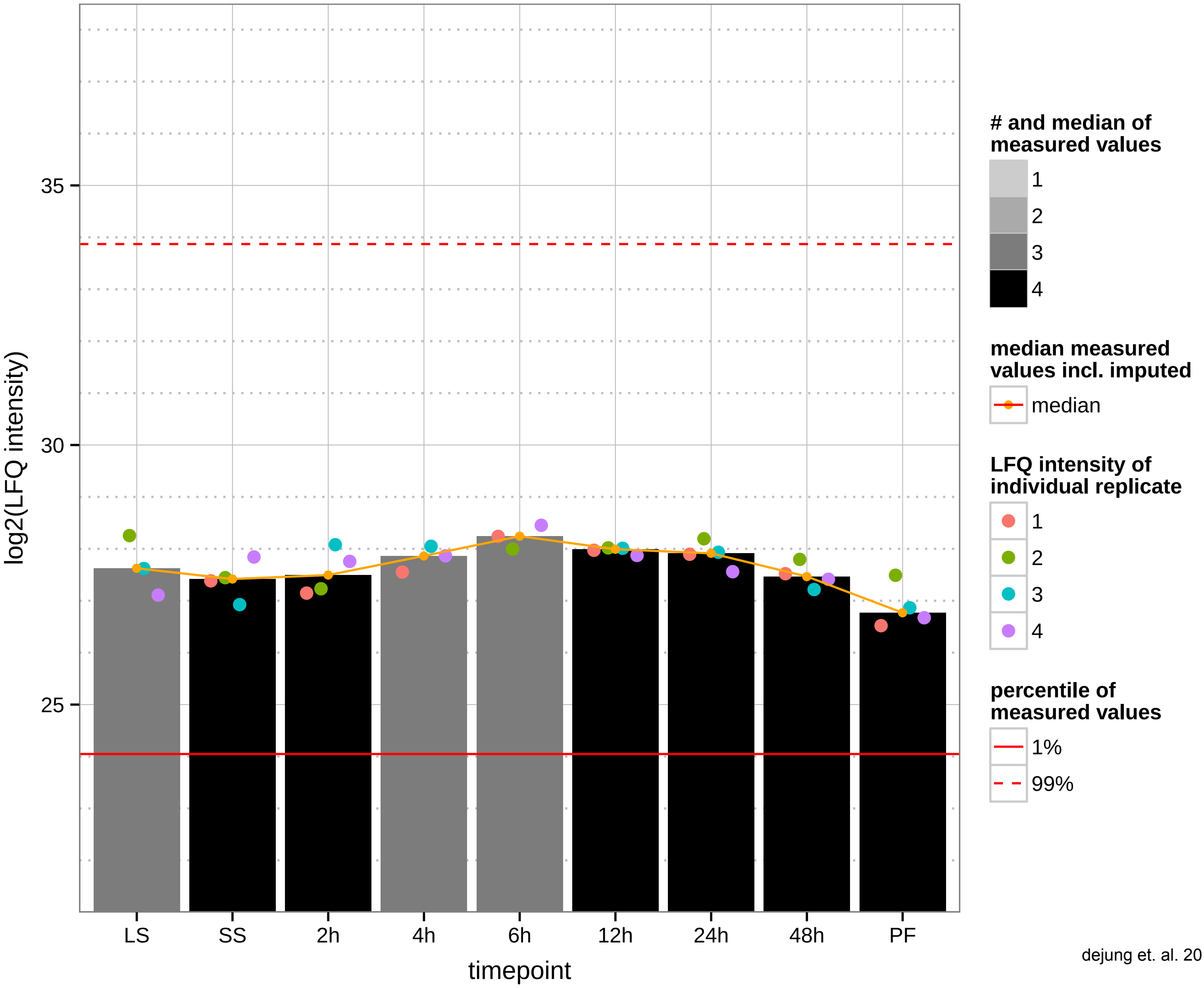
hypothetical protein, conserved
Tb927.10.3540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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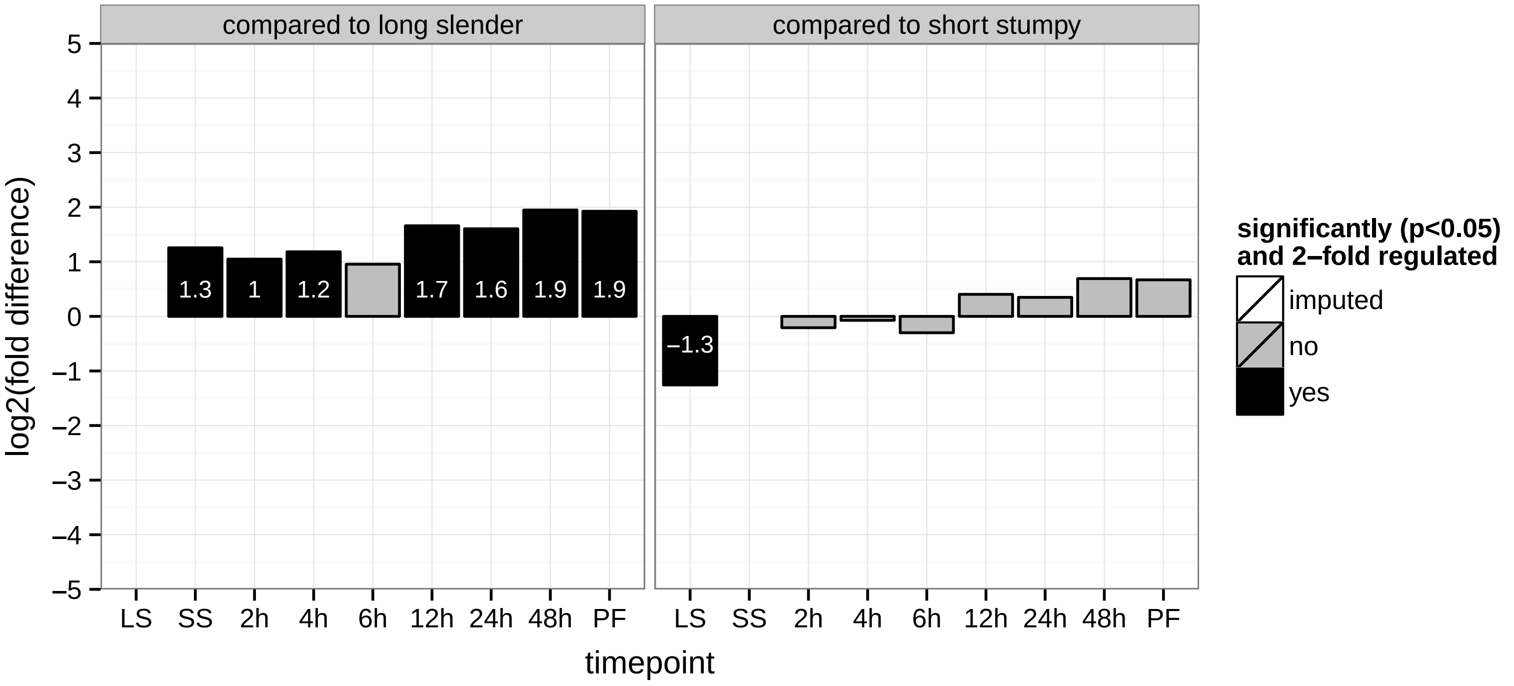
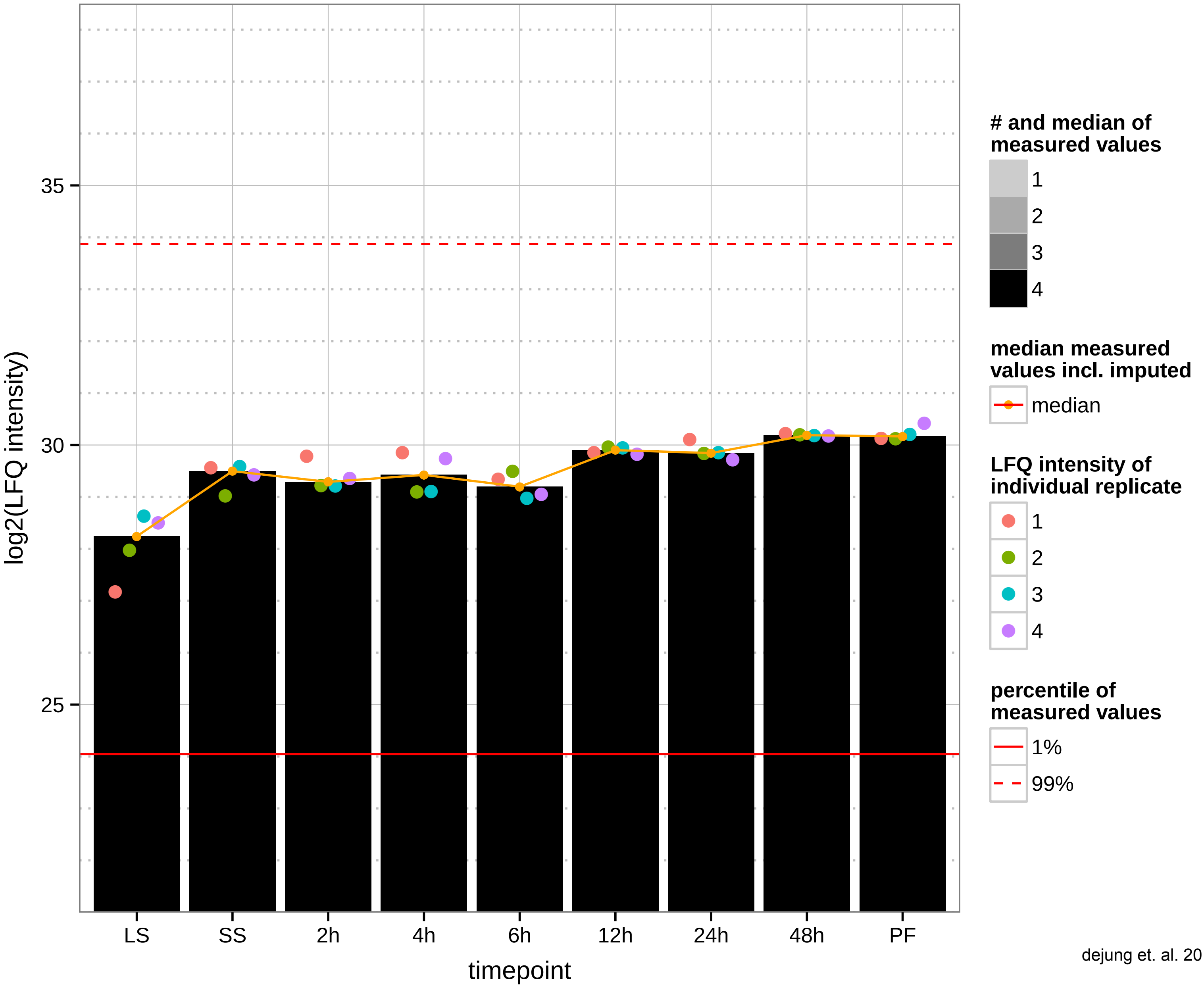
arginine N–methyltransferase, putative
Tb927.10.3560
AGOF: histone–arginine N–methyltransferase activity
AGOC: histone methyltransferase complex
AGOP: histone methylation
PGOF: null
PGOC: null
PGOP: null





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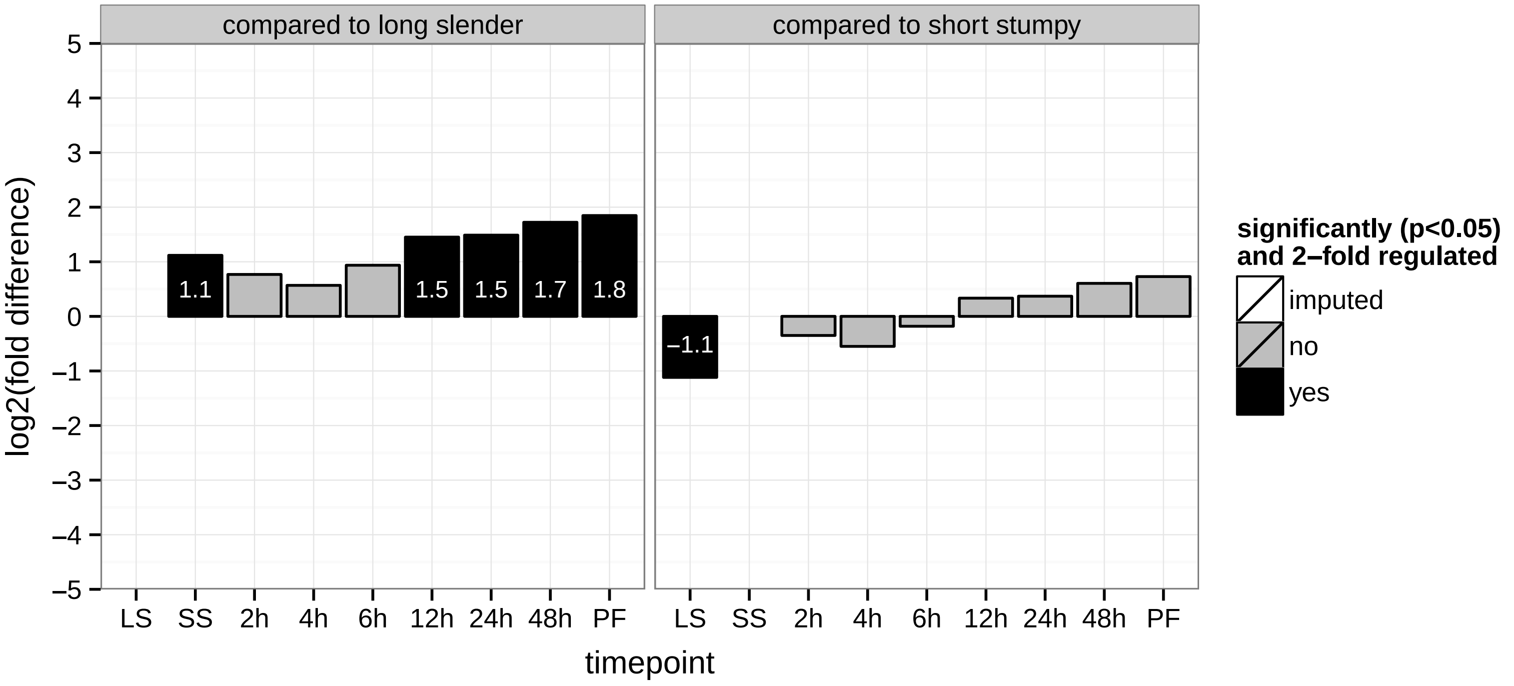
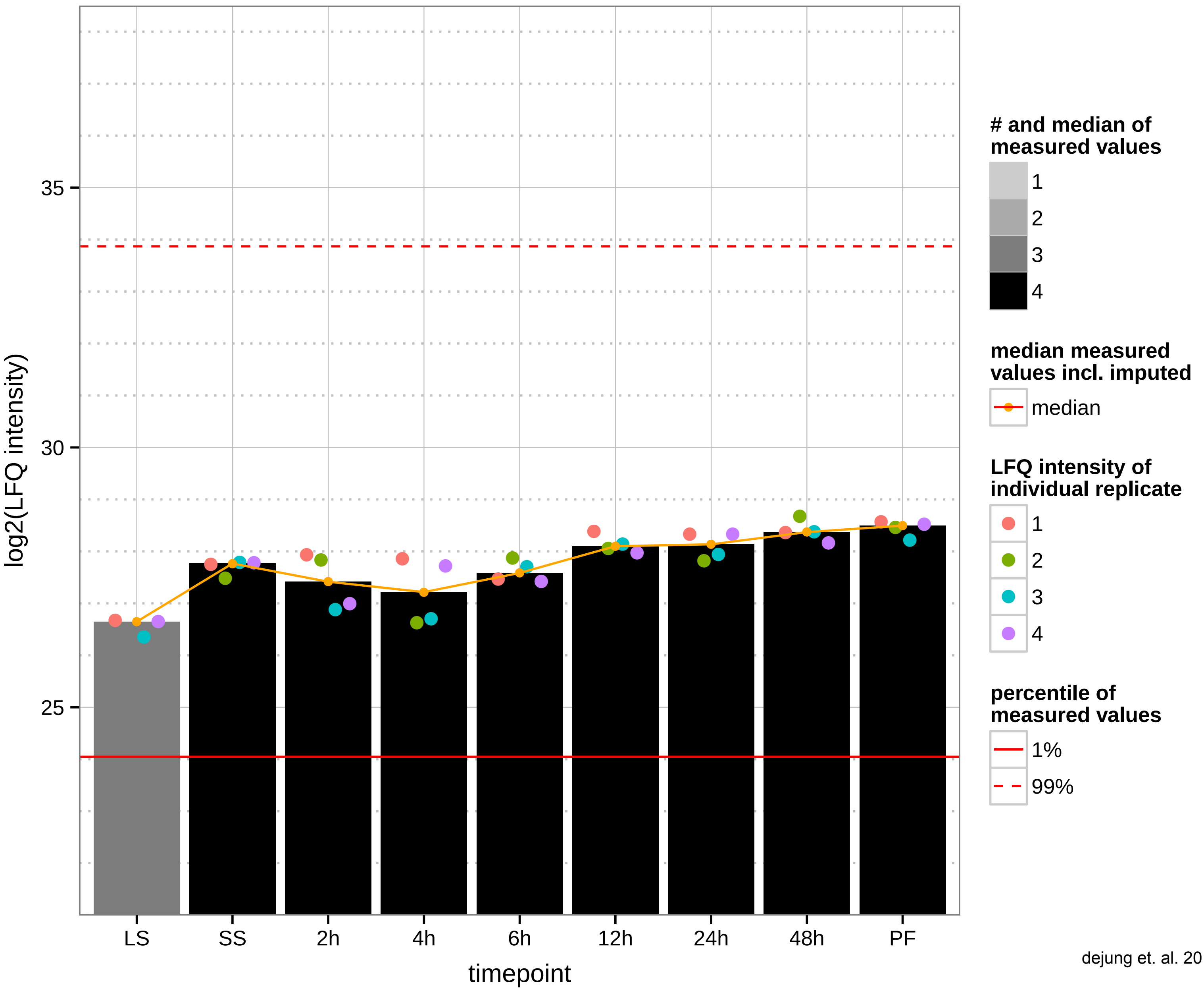
RNA–editing complex protein, putative, RNA editing exonuclease 2, RNA editing 3' exouridylylase, RNA–editing complex prot
Tb927.10.3570
AGOF: null
AGOC: null, mitochondrial mRNA editing complex, mitochondrion
AGOP: null, RNA modification
PGOF: null
PGOC: null
PGOP: null





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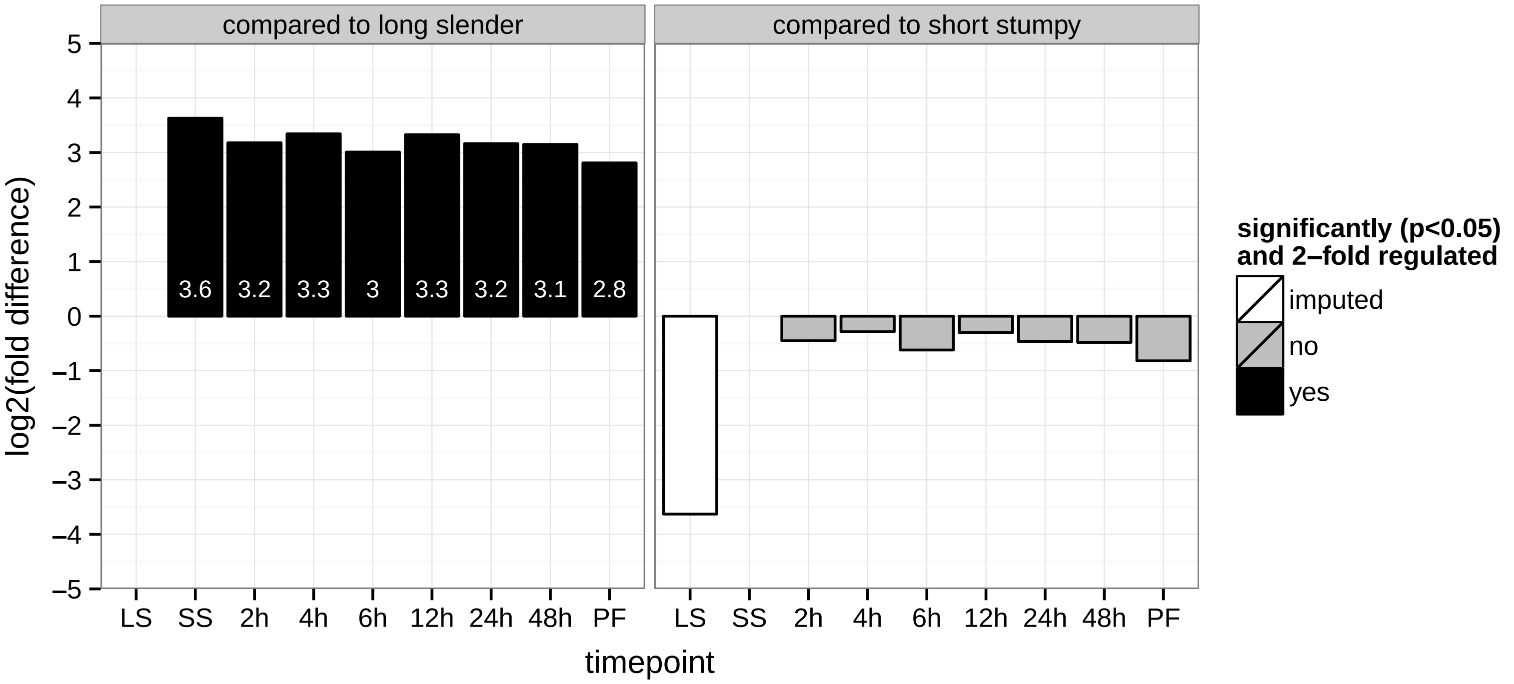
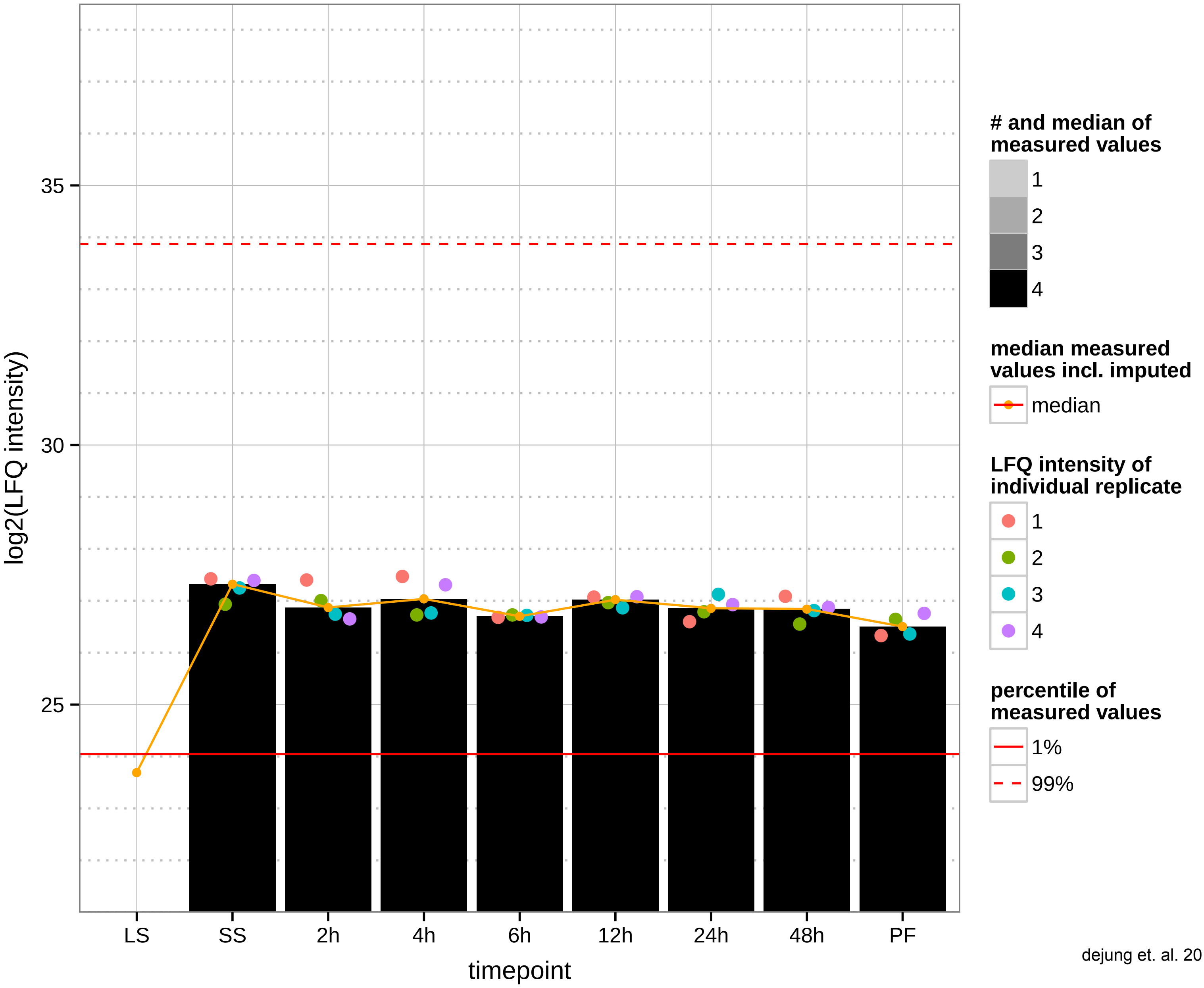
hypothetical protein, conserved
Tb927.10.3590
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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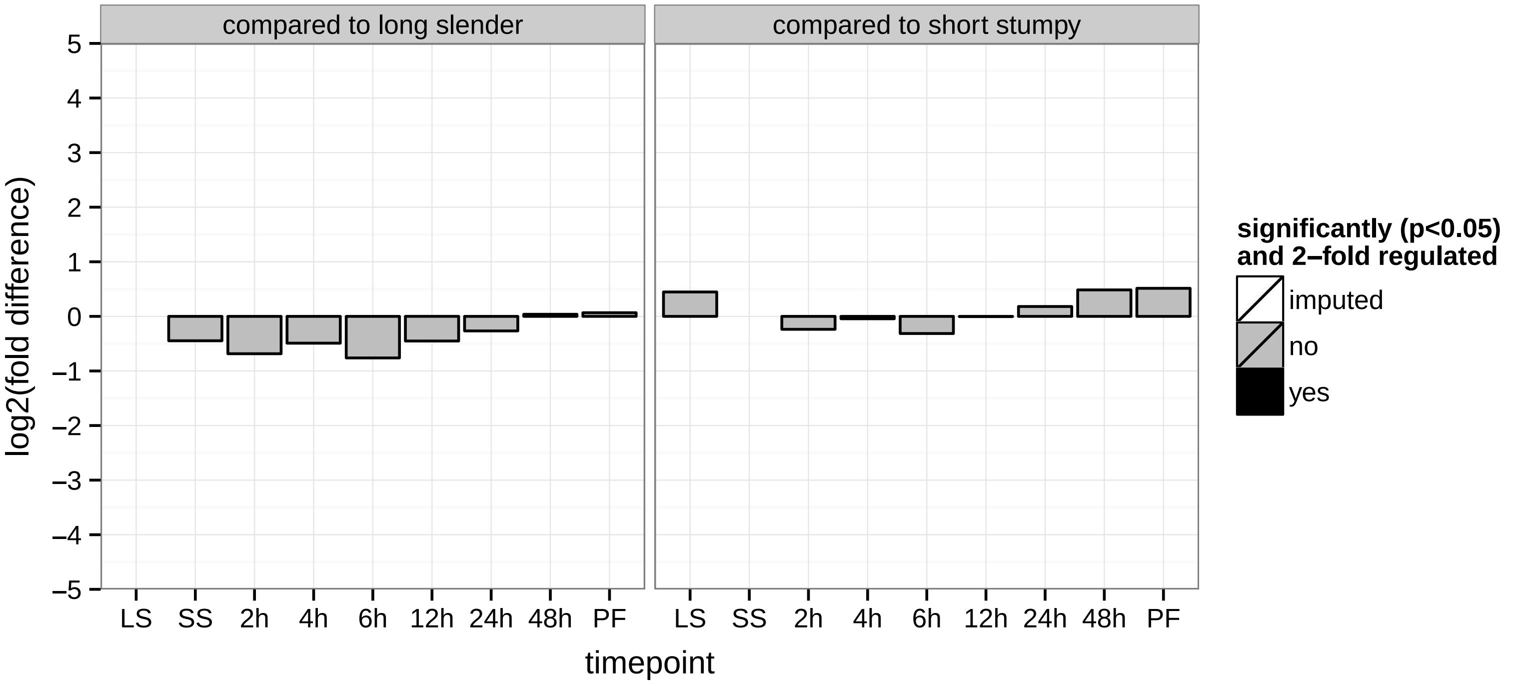
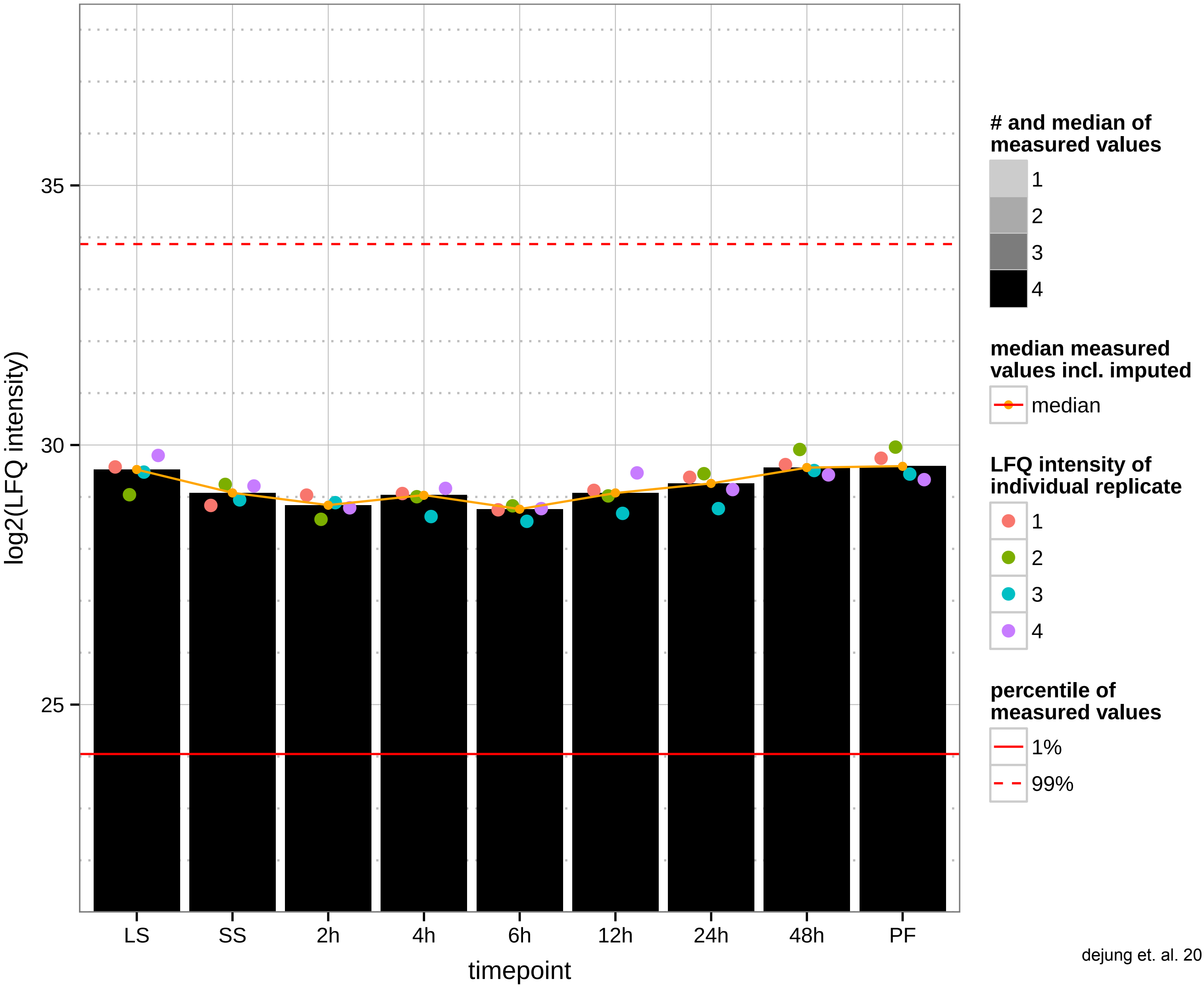
hypothetical protein, conserved
Tb927.10.3640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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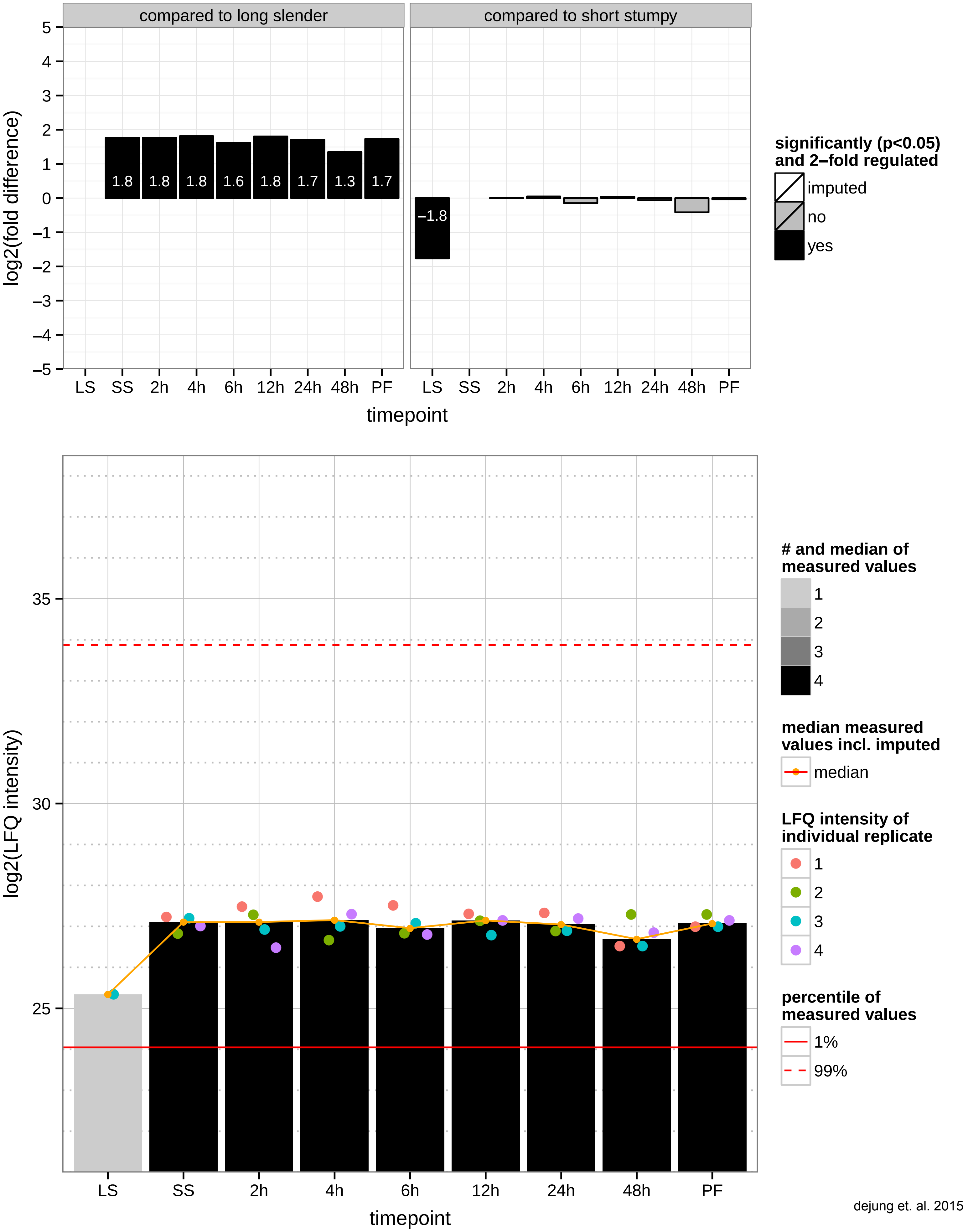
predicted CBS domain protein
Tb927.10.3700
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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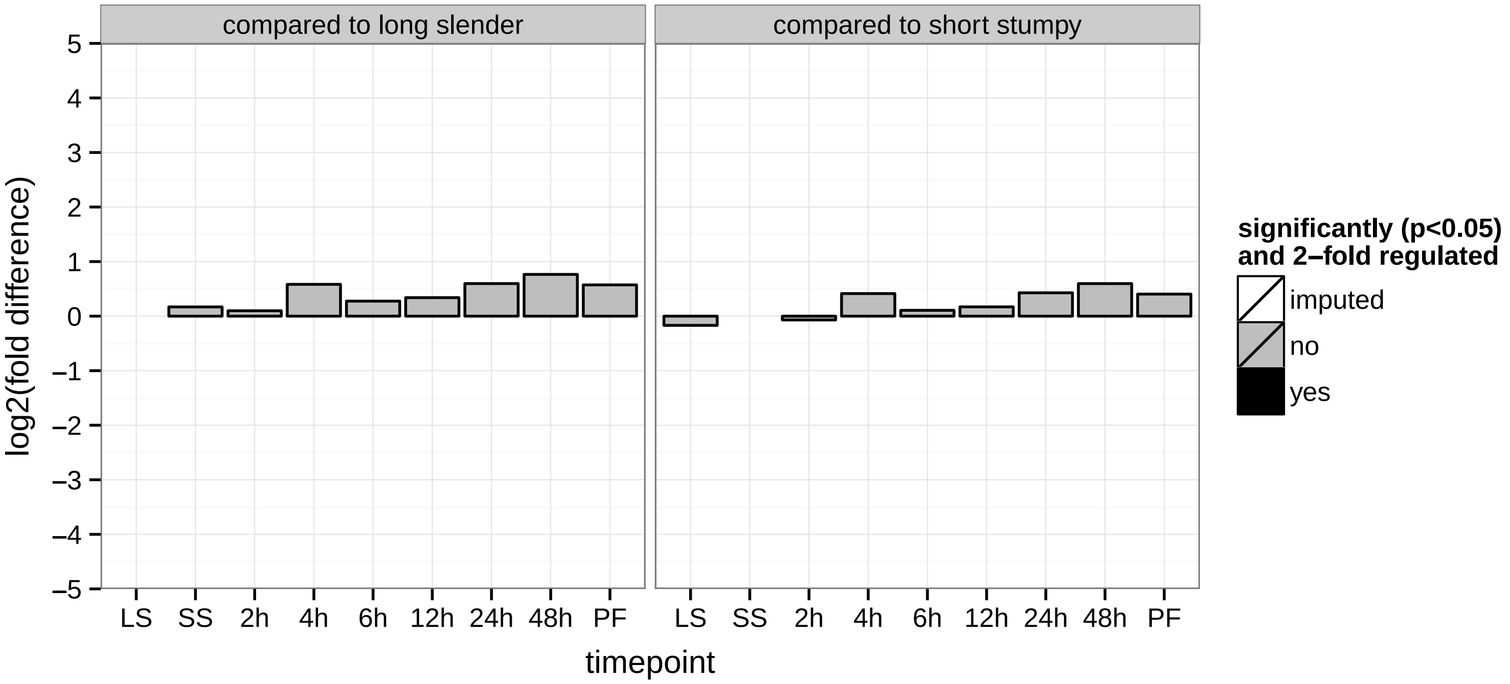
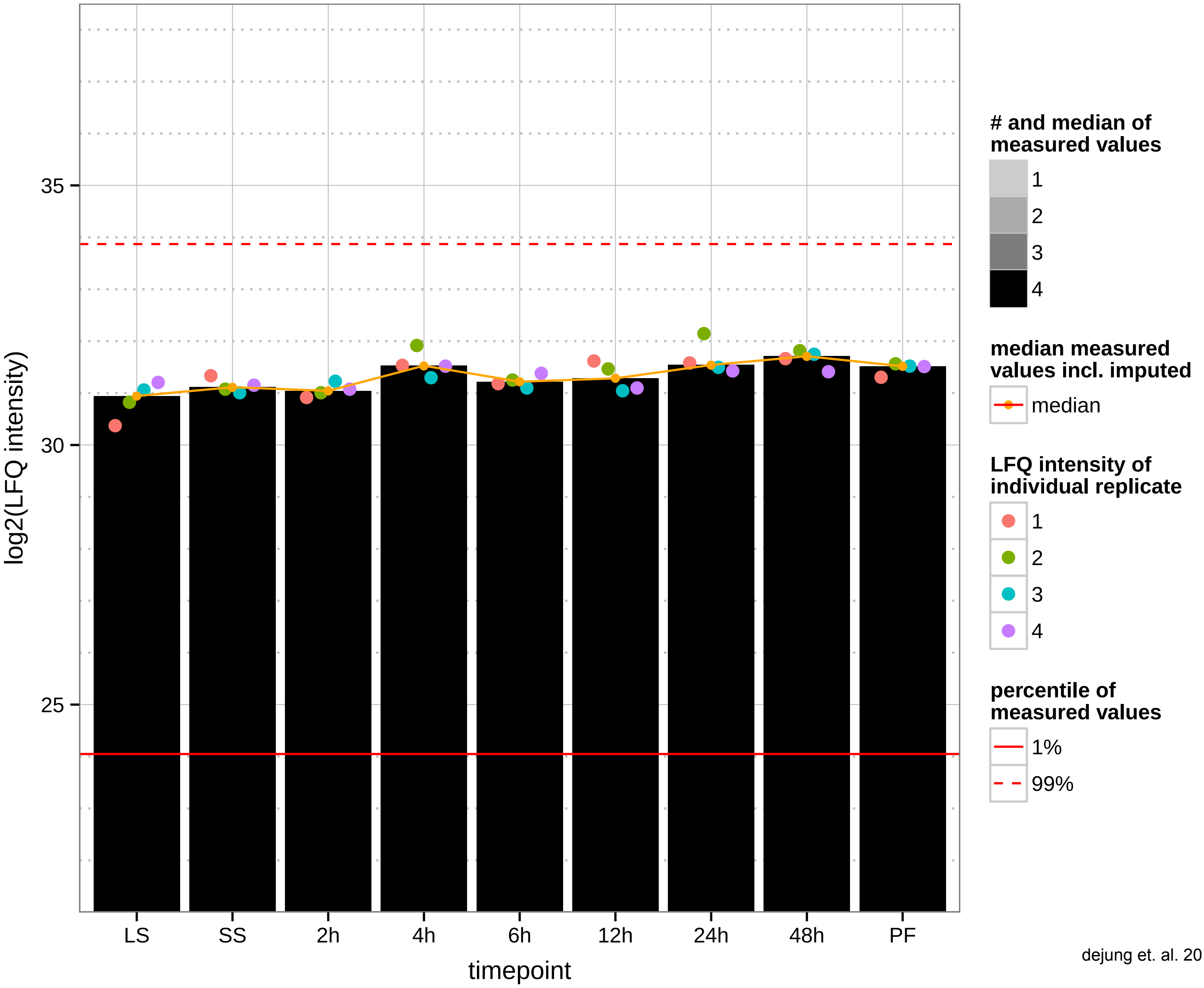
proteasome activator protein pa26, putative, proteasome activator protein PA26 (pa26)
Tb927.10.3710;Tb11.v5.0761
AGOF: null
AGOC: null, proteasome activator complex
AGOP: null, proteolysis, regulation of proteasomal protein catabolic process
PGOF: null
PGOC: proteasome activator complex
PGOP: null





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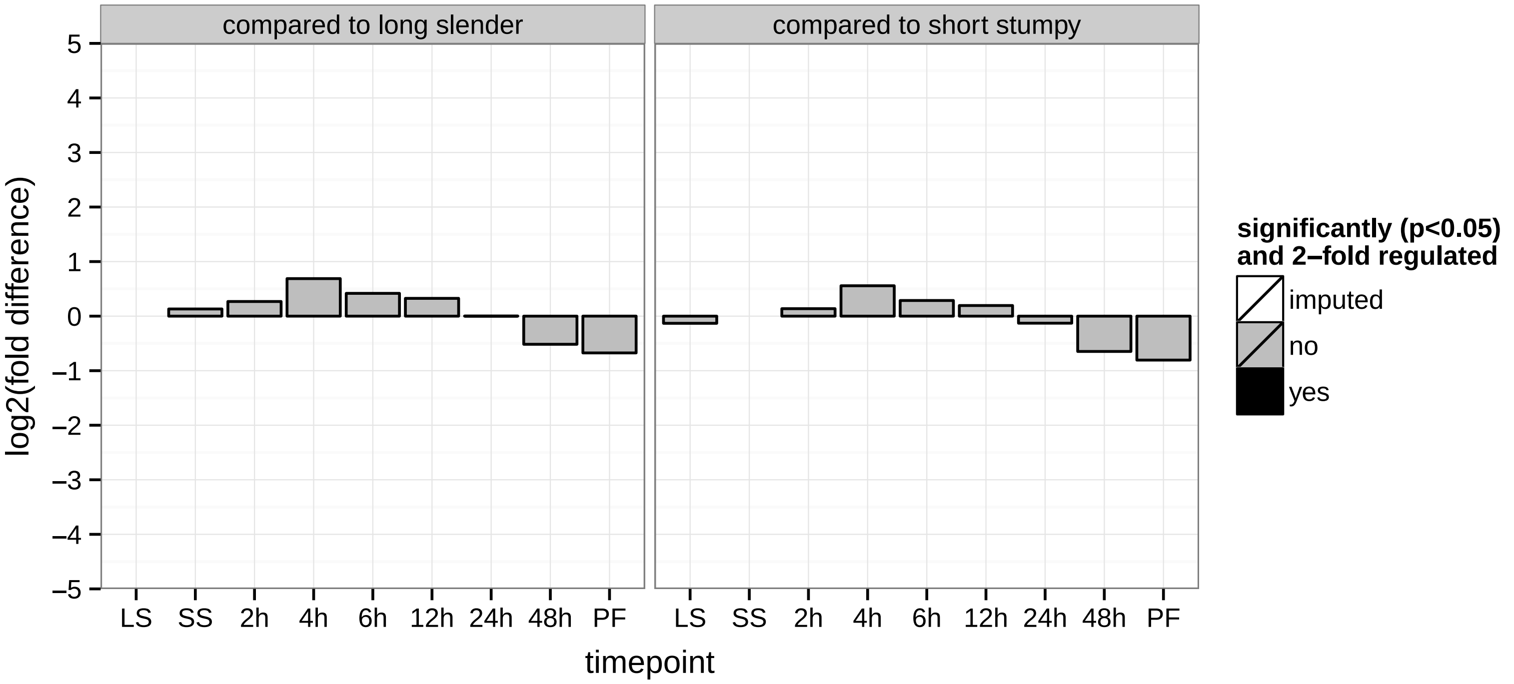
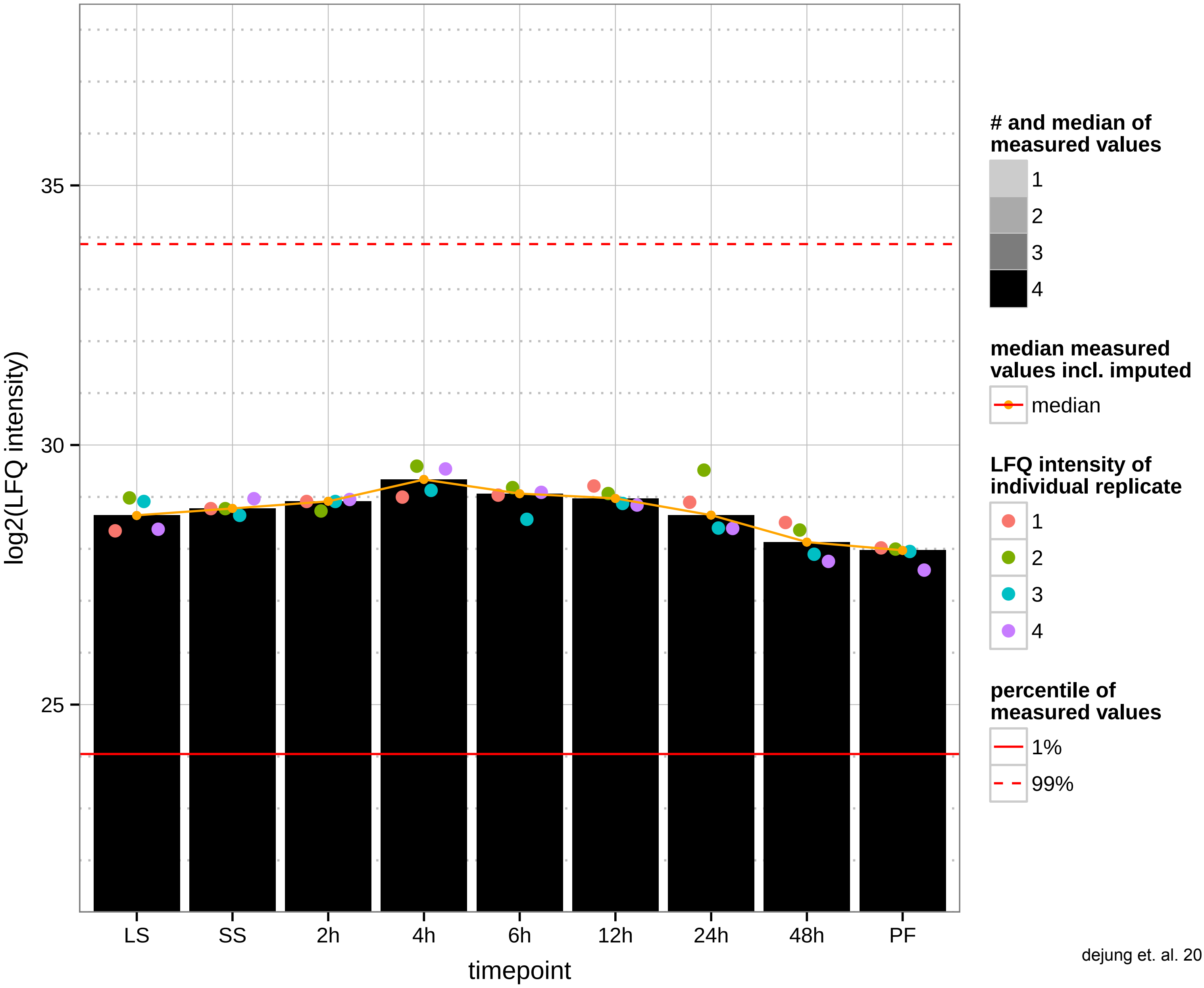
vacuolar ATP synthase subunit d, putative
Tb927.10.3760
AGOF: hydrogen–exporting ATPase activity, phosphorylative mechanism, proton–transporting ATPase activity, rotational mech
AGOC: proton–transporting two–sector ATPase complex, catalytic domain, vacuolar proton–transporting V–type ATPase com
AGOP: ATP hydrolysis coupled proton transport, ATP synthesis coupled proton transport
PGOF: ATPase activity, coupled to transmembrane movement of substances
PGOC: null
PGOP: null





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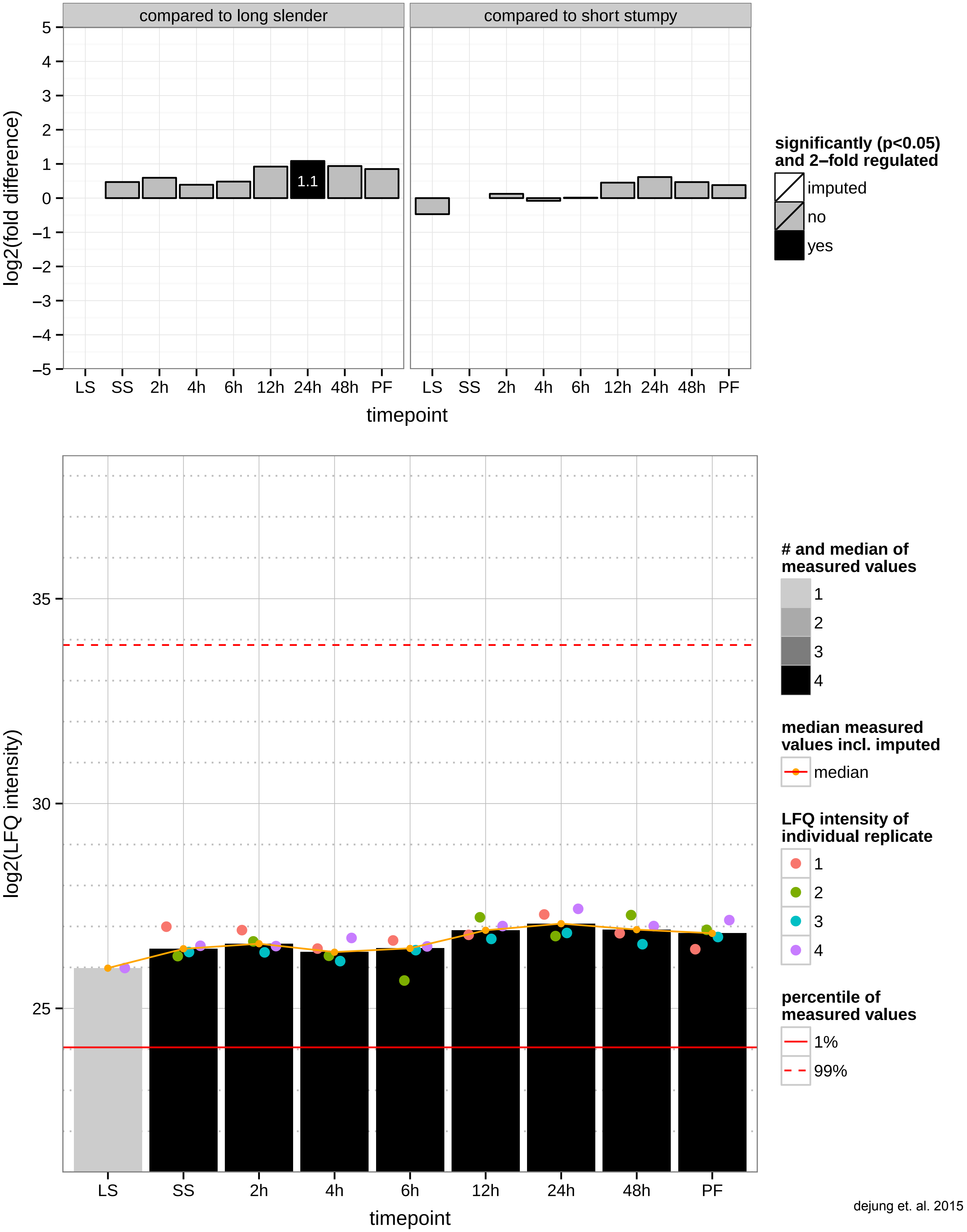
predicted TPR repeat protein
Tb927.10.3770
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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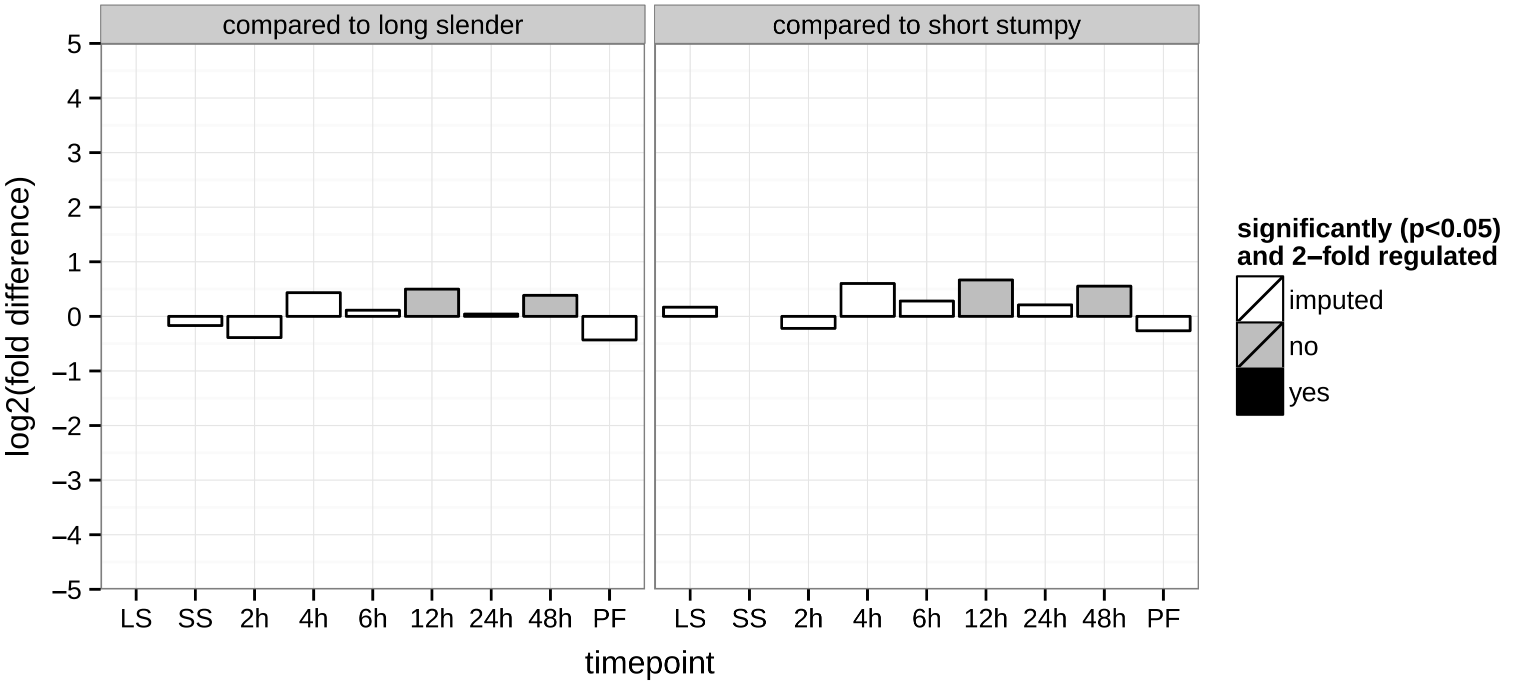
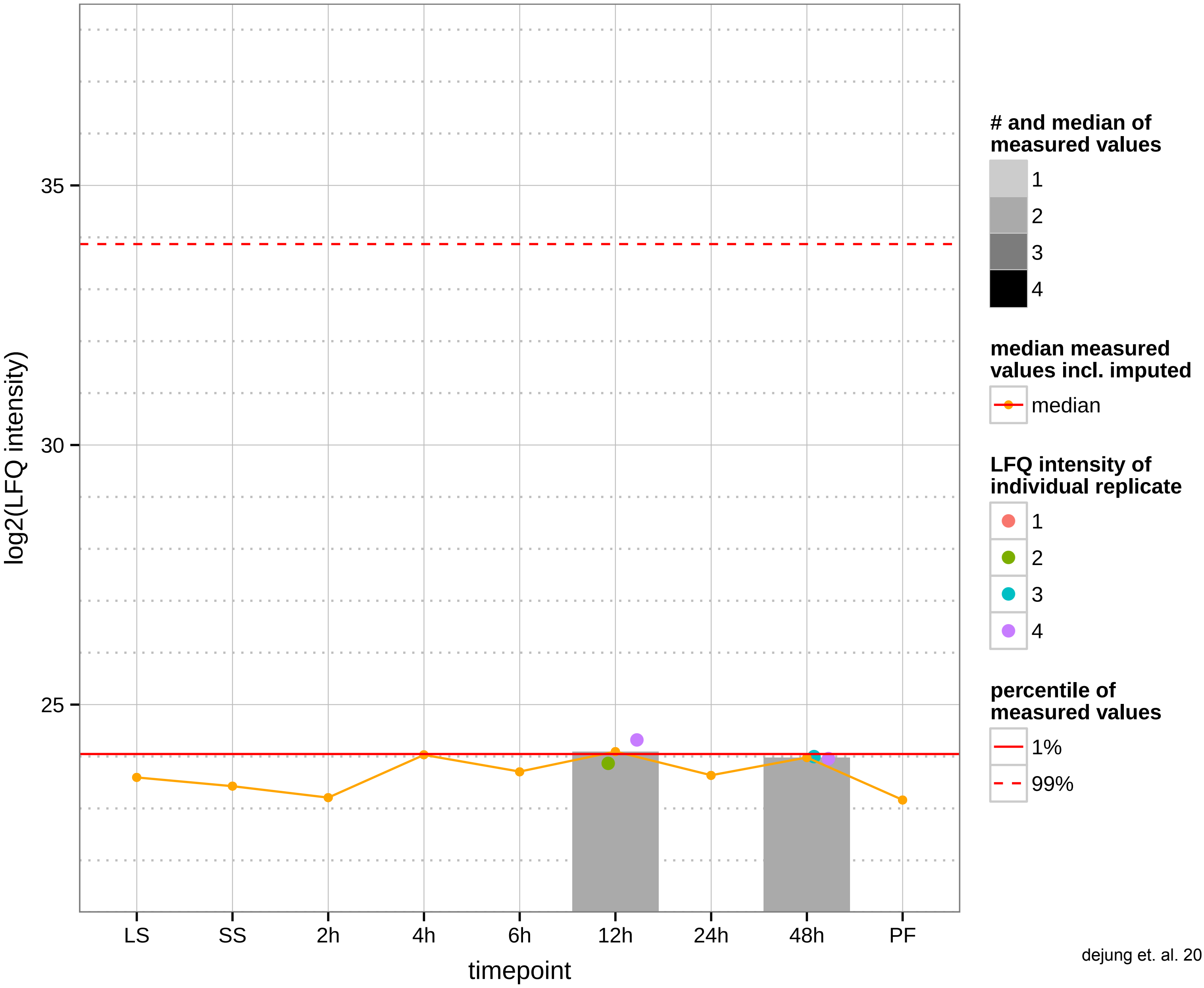
hypothetical protein, conserved
Tb927.10.3820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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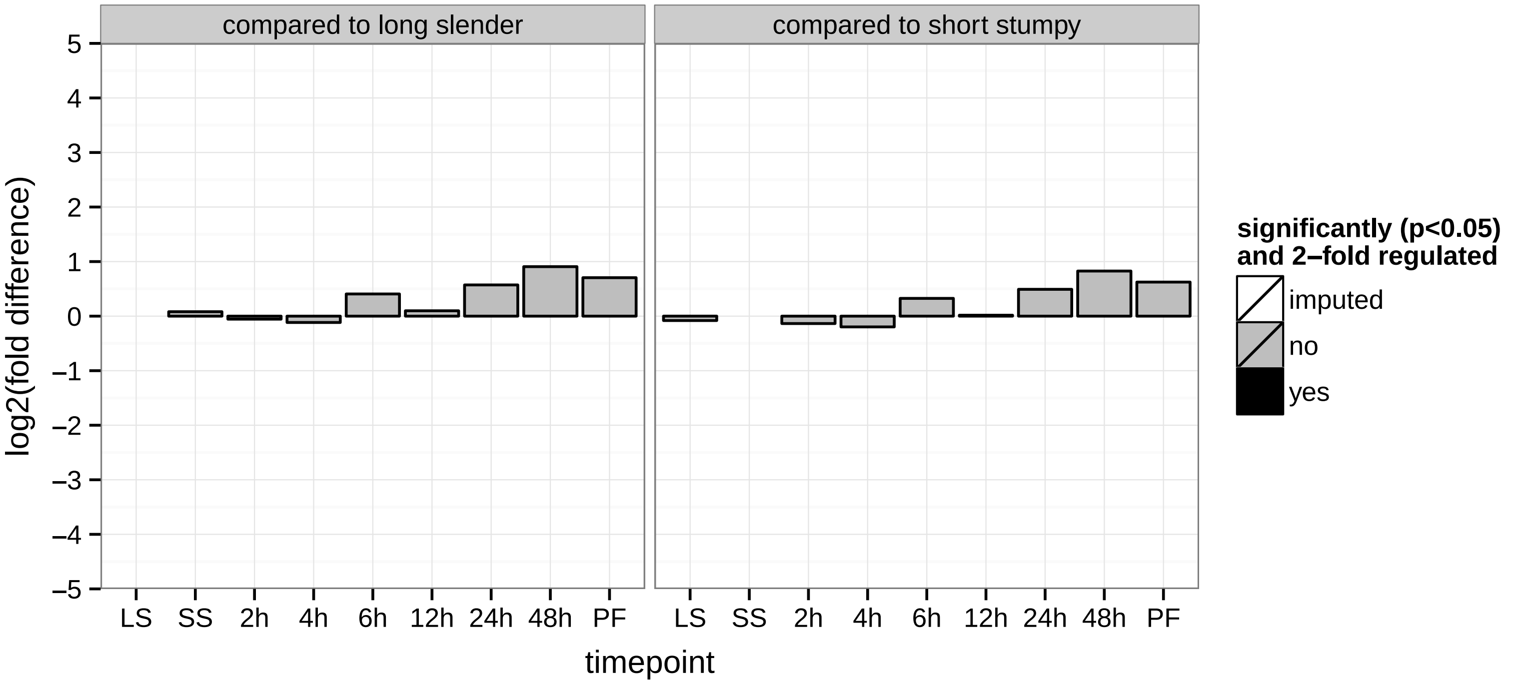
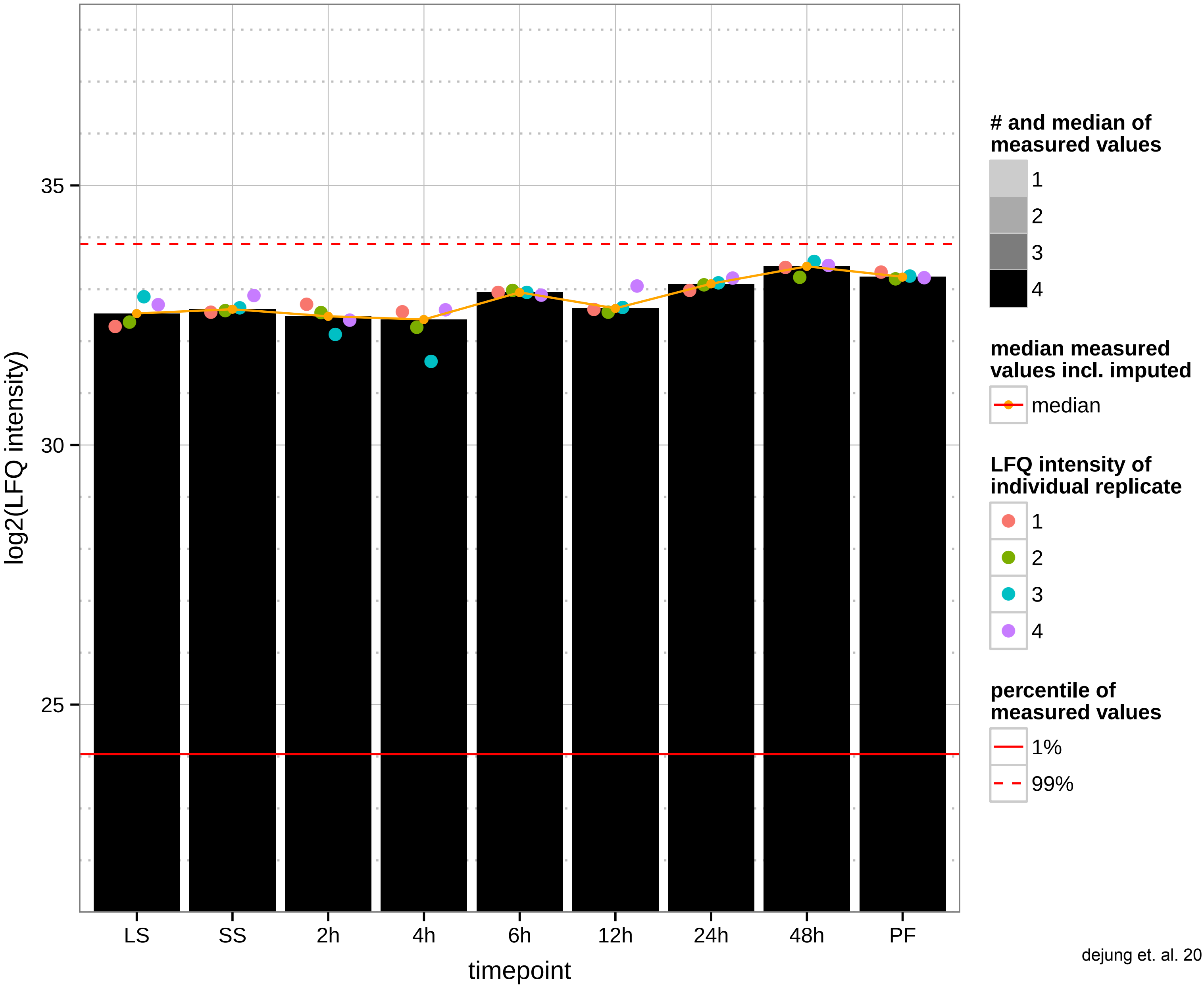
60S ribosomal protein L18a, putative, ribosomal protein L18
Tb927.11.14130;Tb927.10.3840
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: ribosome
PGOP: translation





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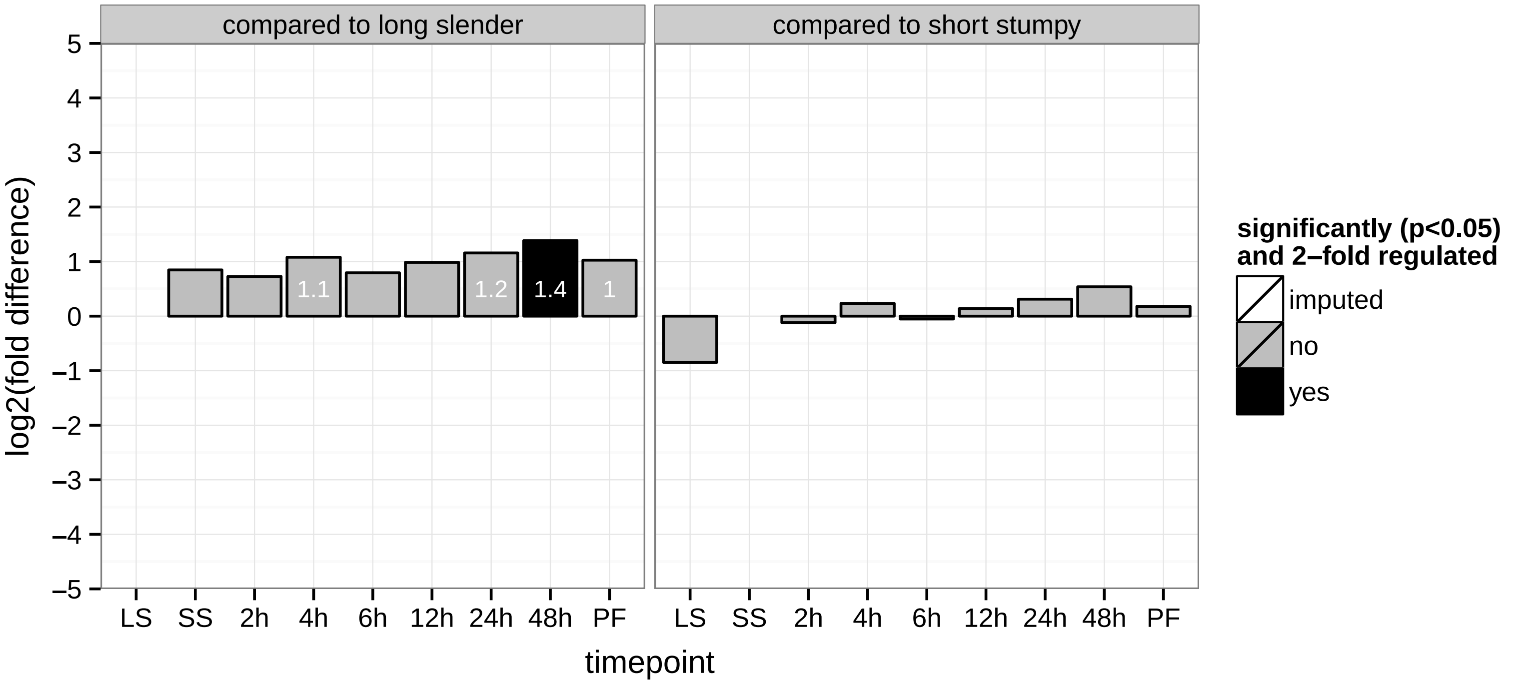
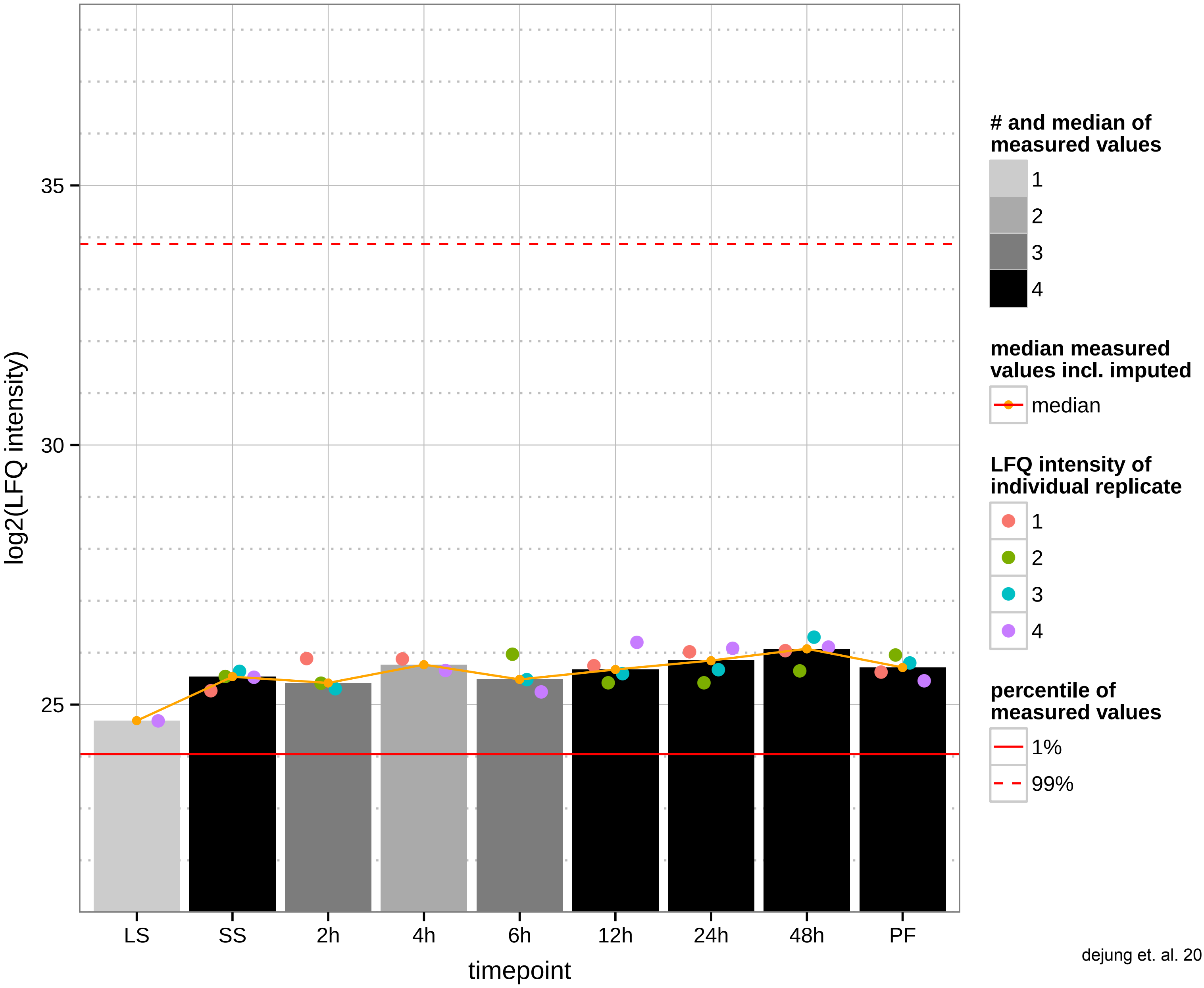
hypothetical protein, conserved
Tb927.10.3950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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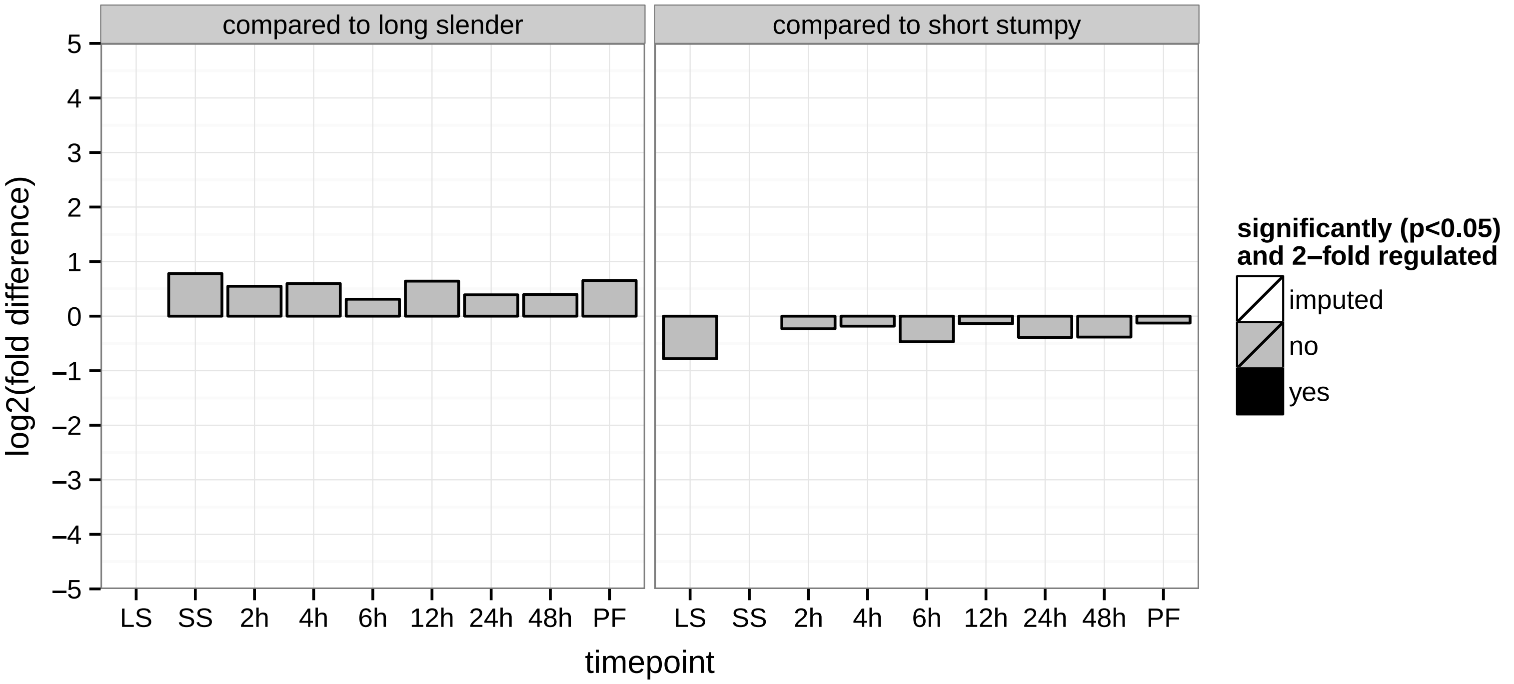
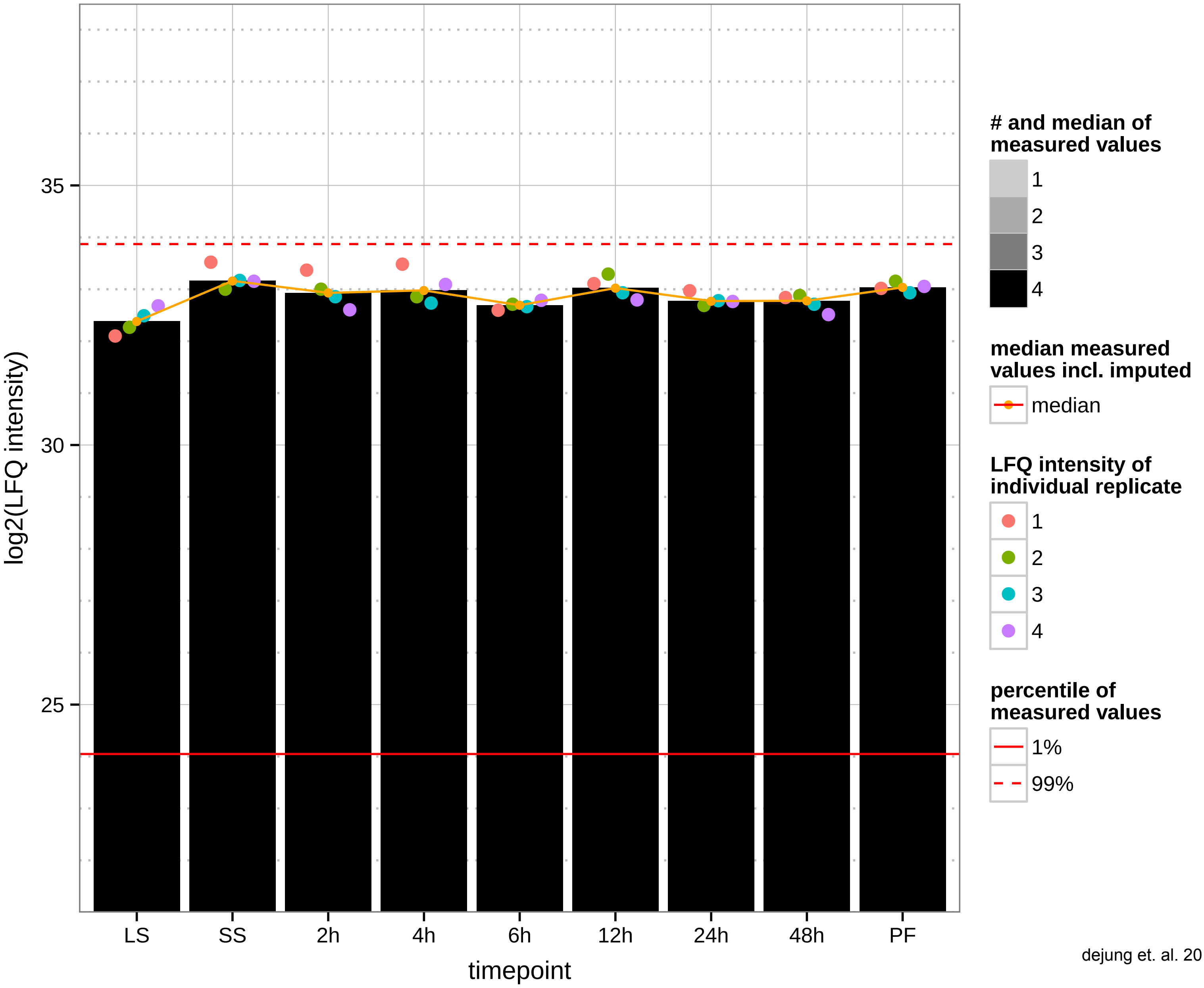
DHH1 (DHH1)
Tb927.10.3990
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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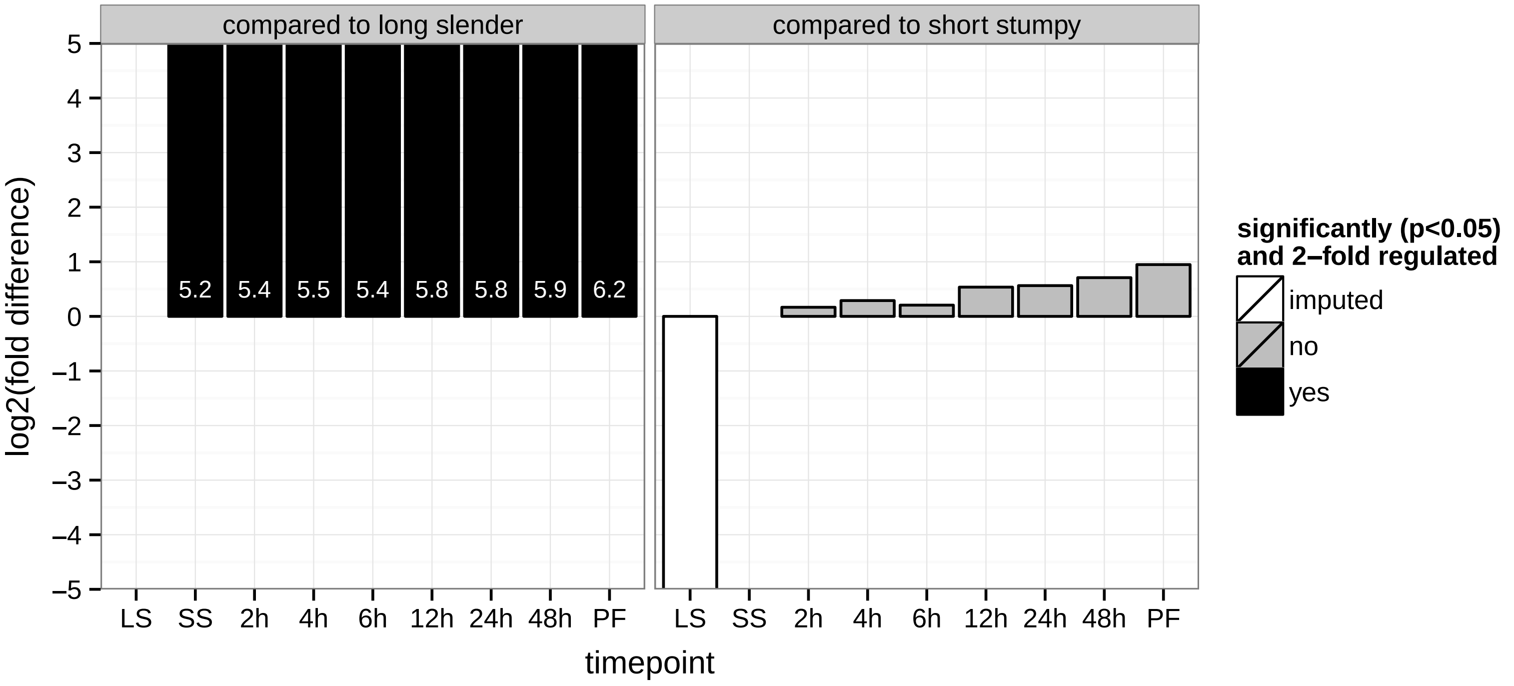
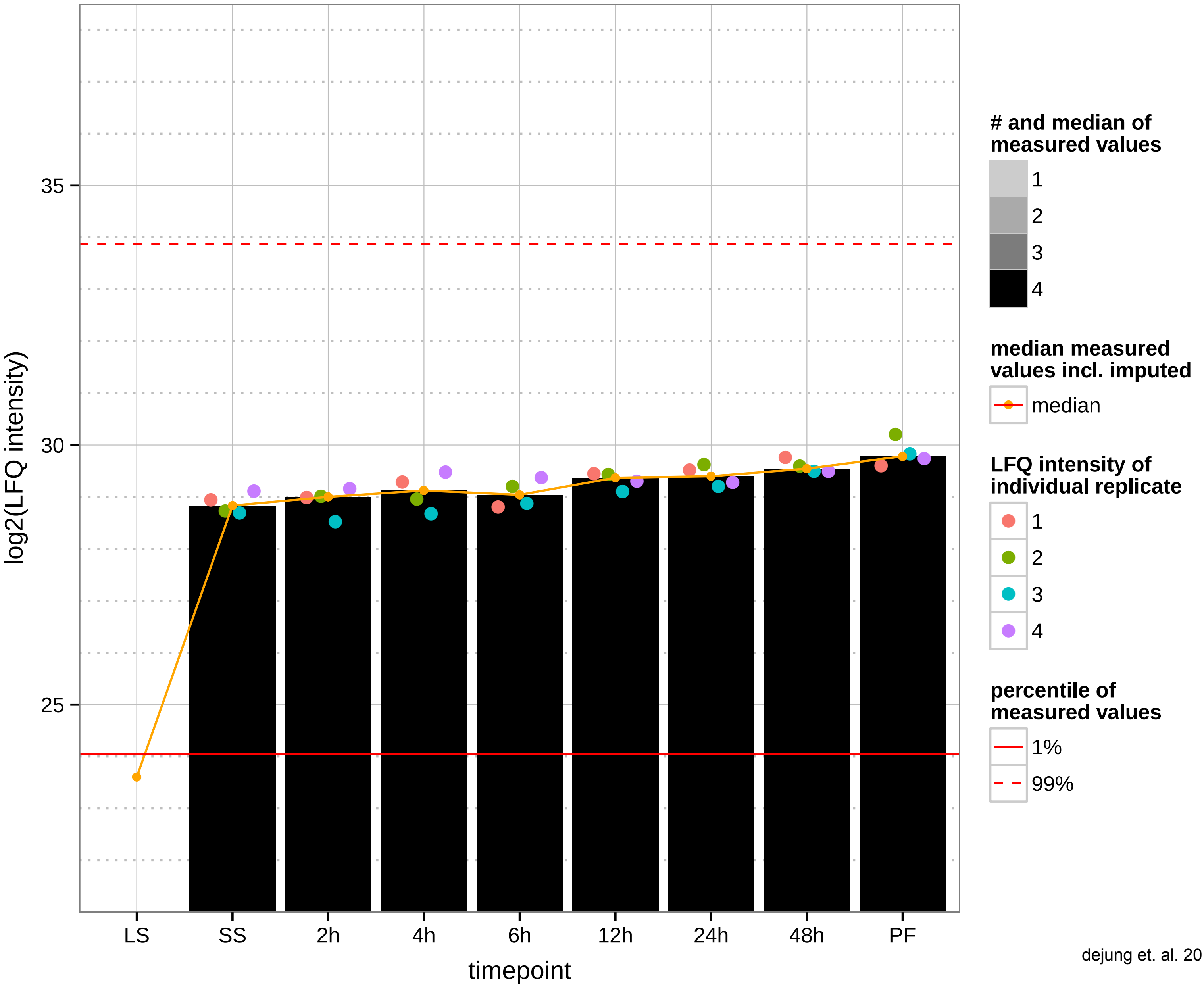
methylglutaconyl–CoA hydratase, mitochondrial precursor, putative
Tb927.10.4000
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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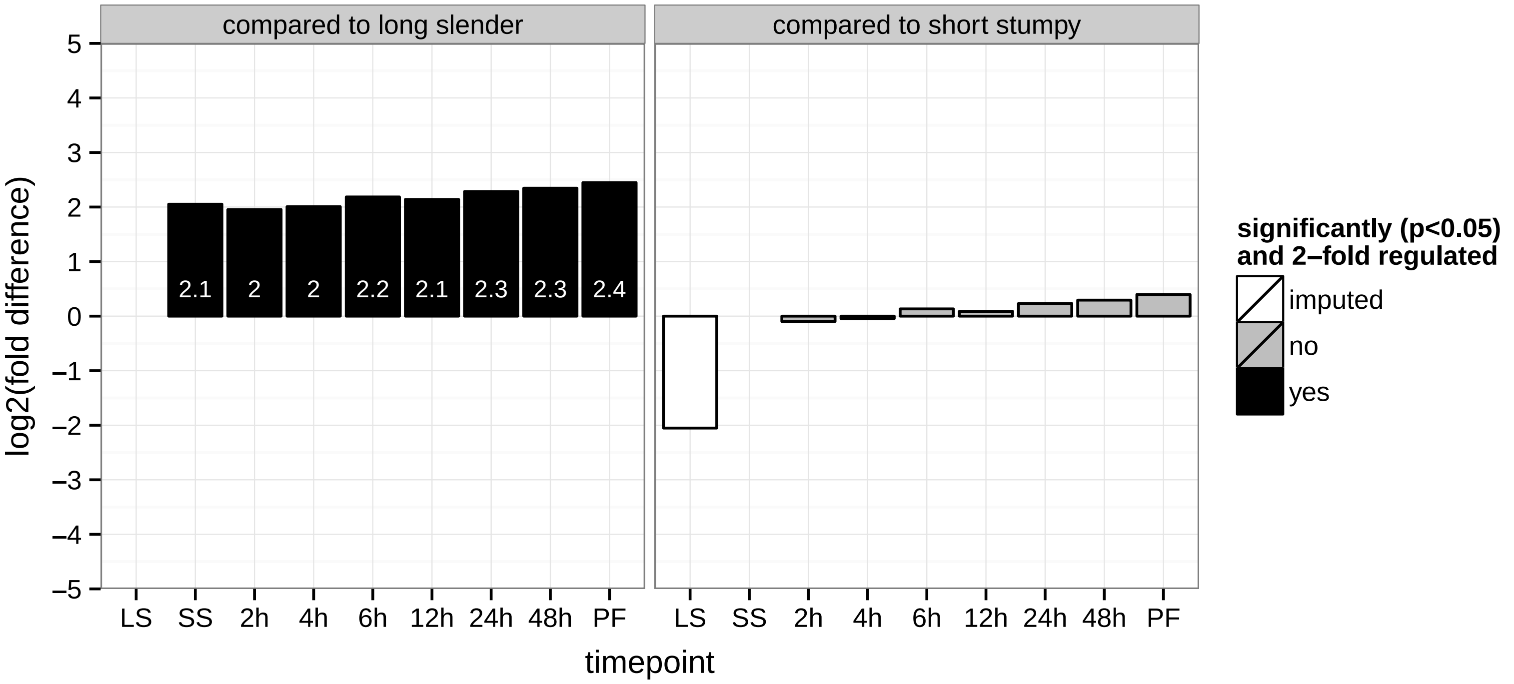
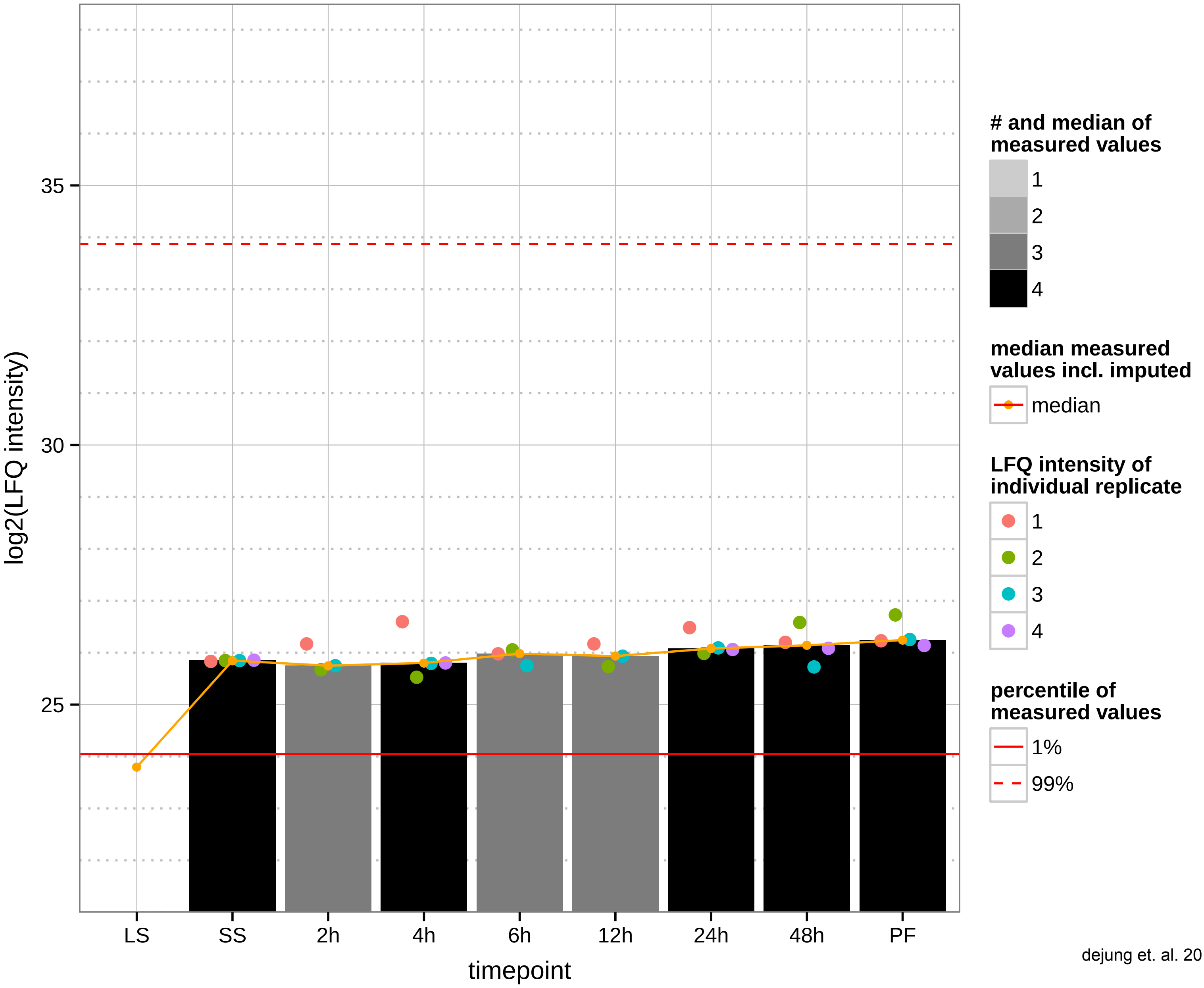
hypothetical protein, conserved
Tb927.10.4010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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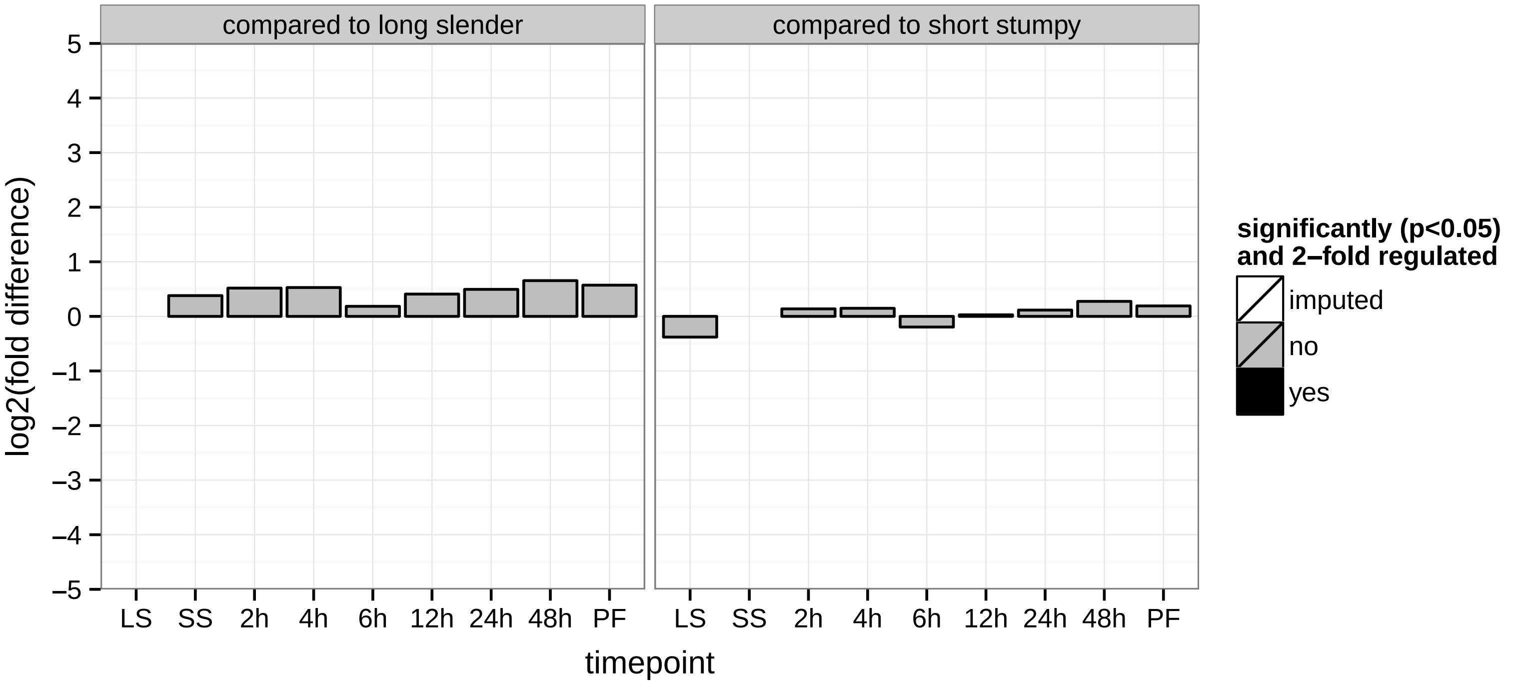
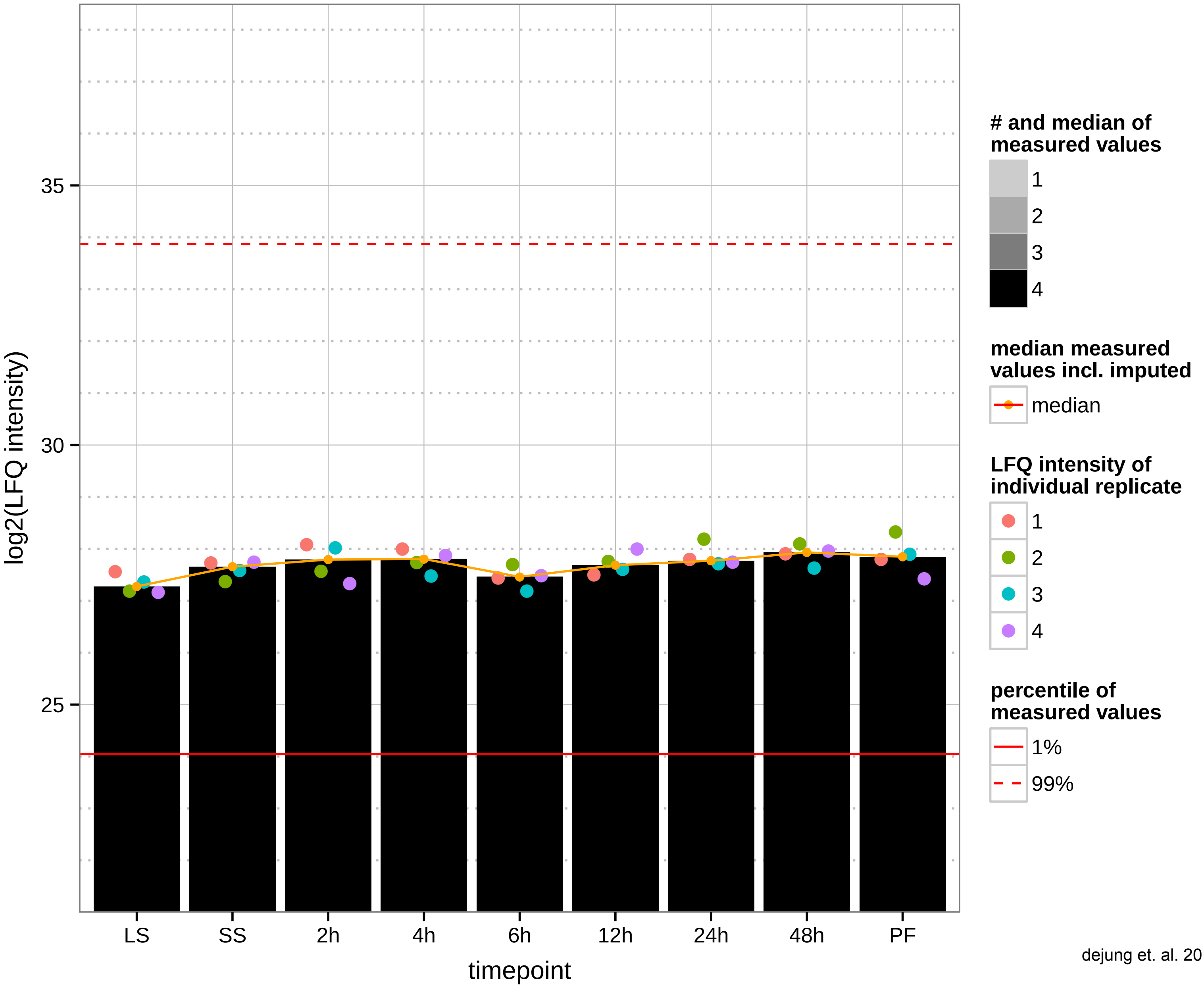
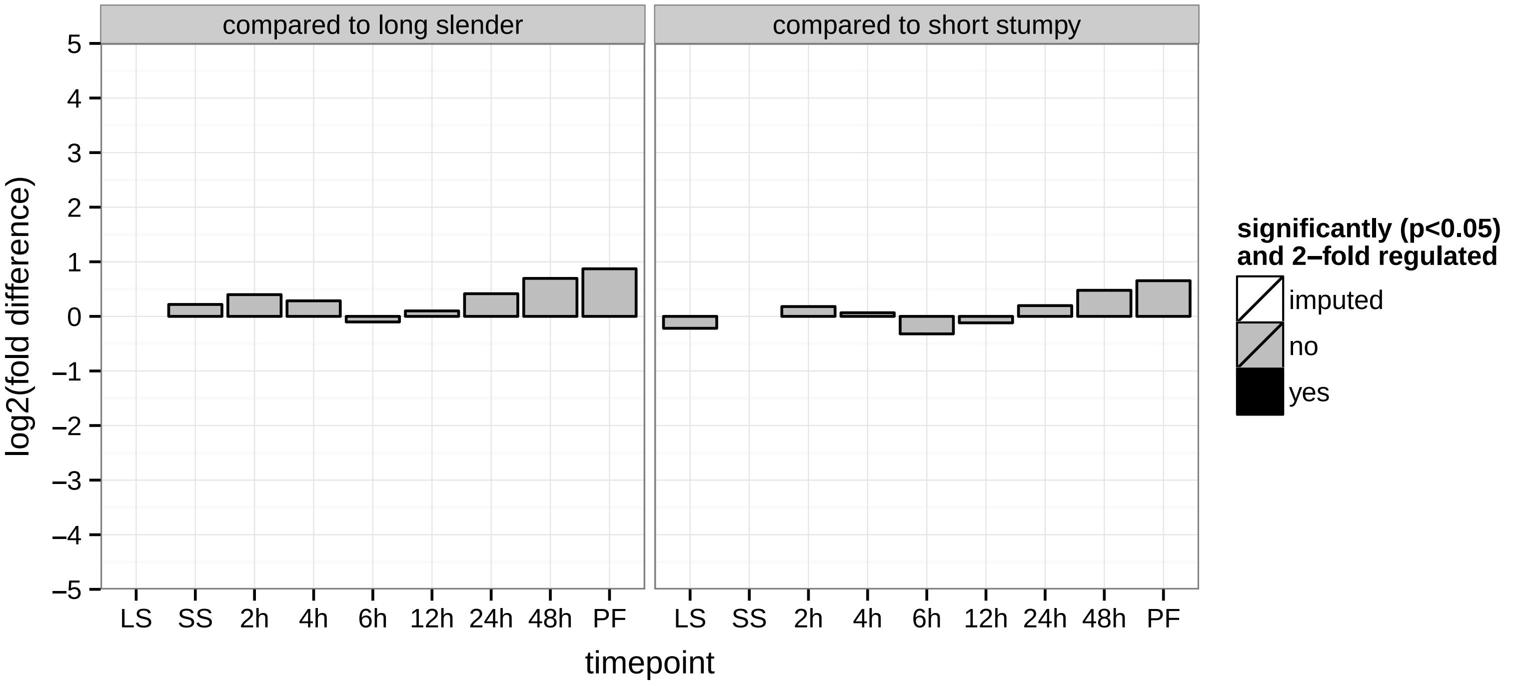
3–keto–dihydrosphingosine reductase
Tb927.10.4040
AGOF: 3–dehydrosphinganine reductase activity
AGOC: endoplasmic reticulum membrane
AGOP: fatty acid biosynthetic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process

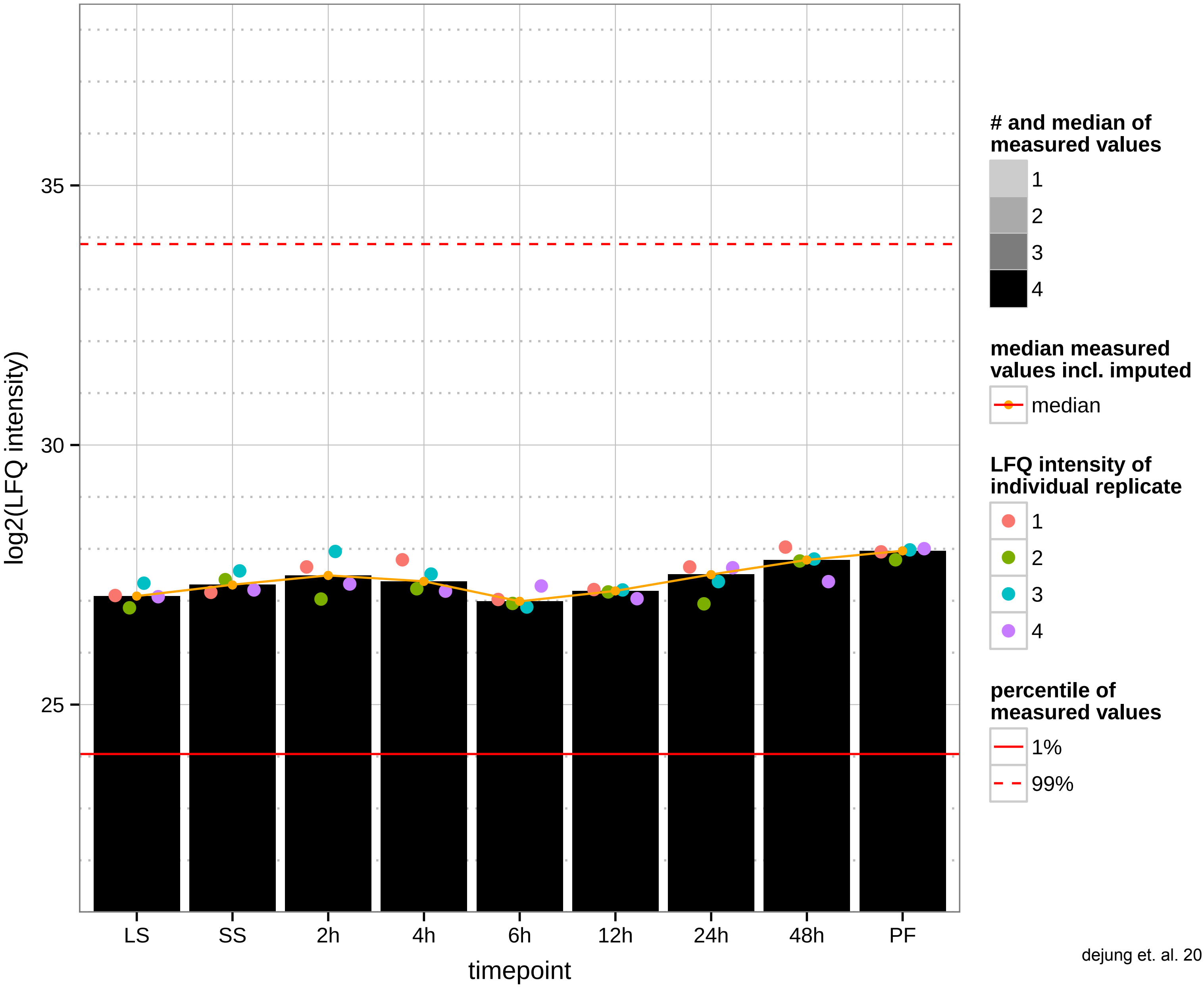




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.4060
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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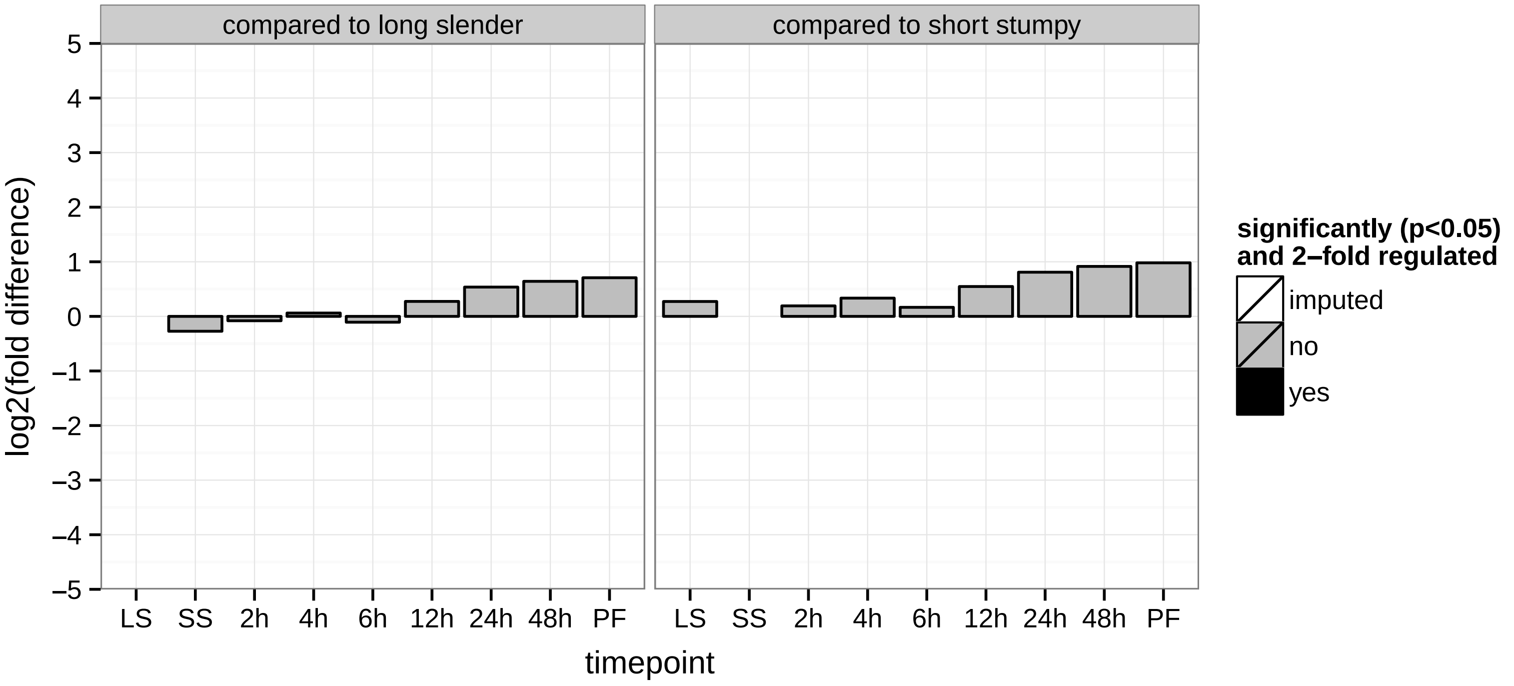
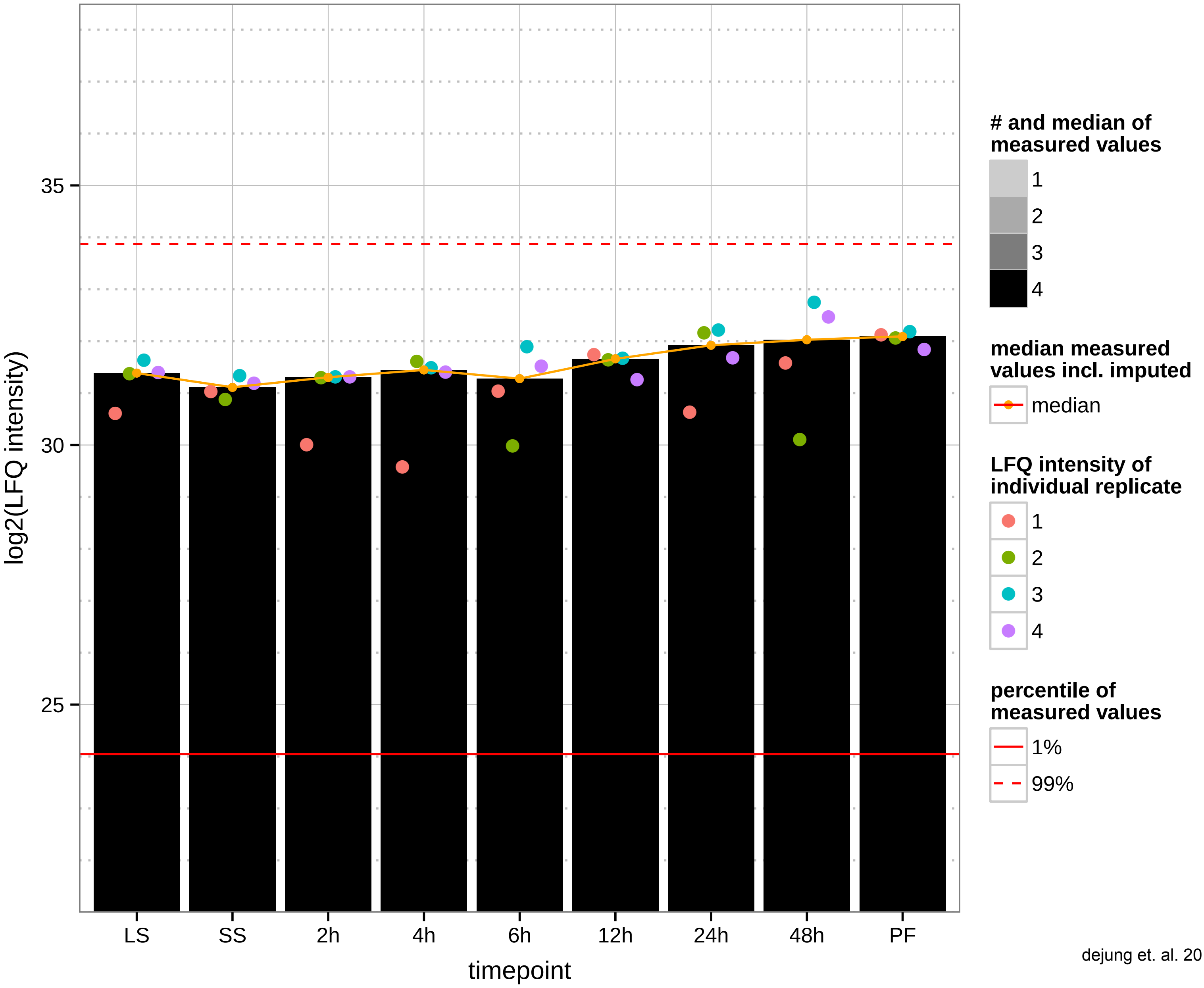
60S ribosomal protein L30 (RPL30)
Tb927.10.4120;Tb927.10.4110
AGOF: structural constituent of ribosome
AGOC: ribosome, intracellular, ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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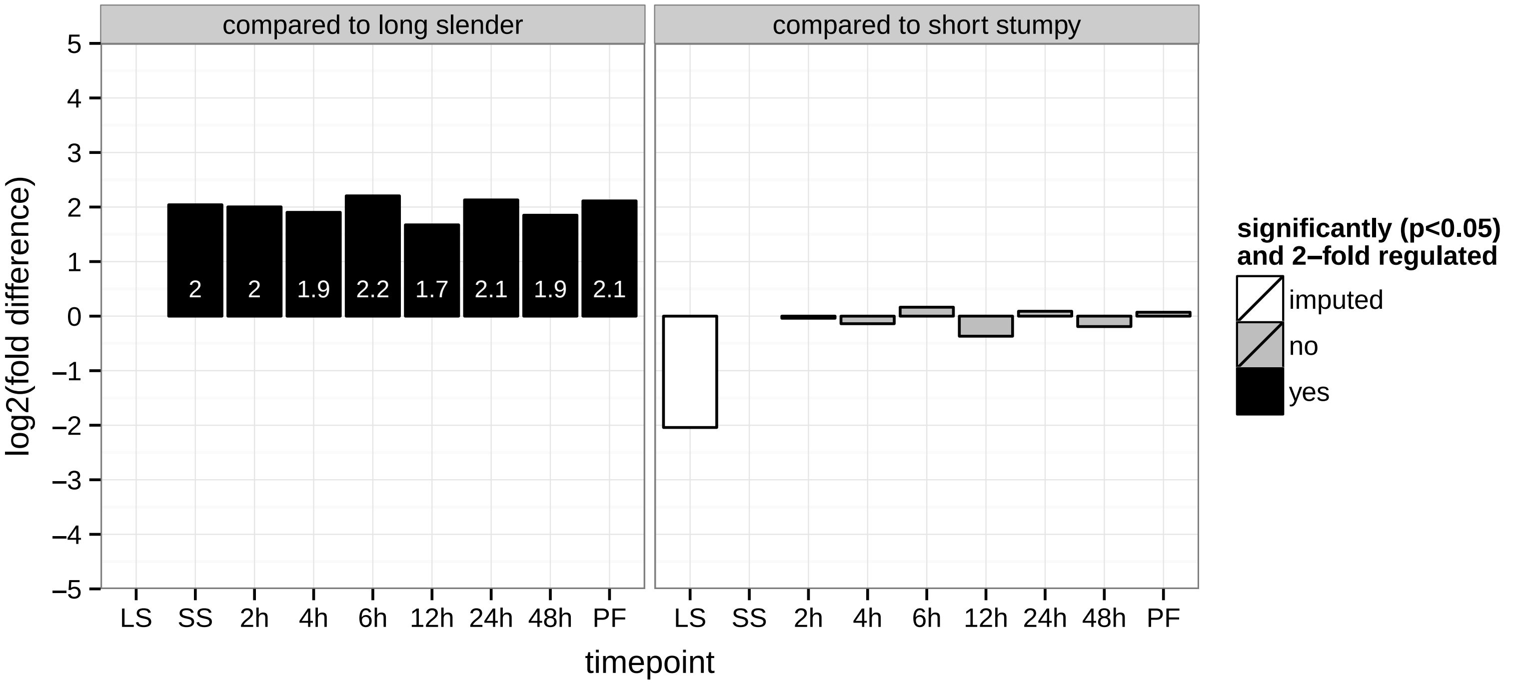
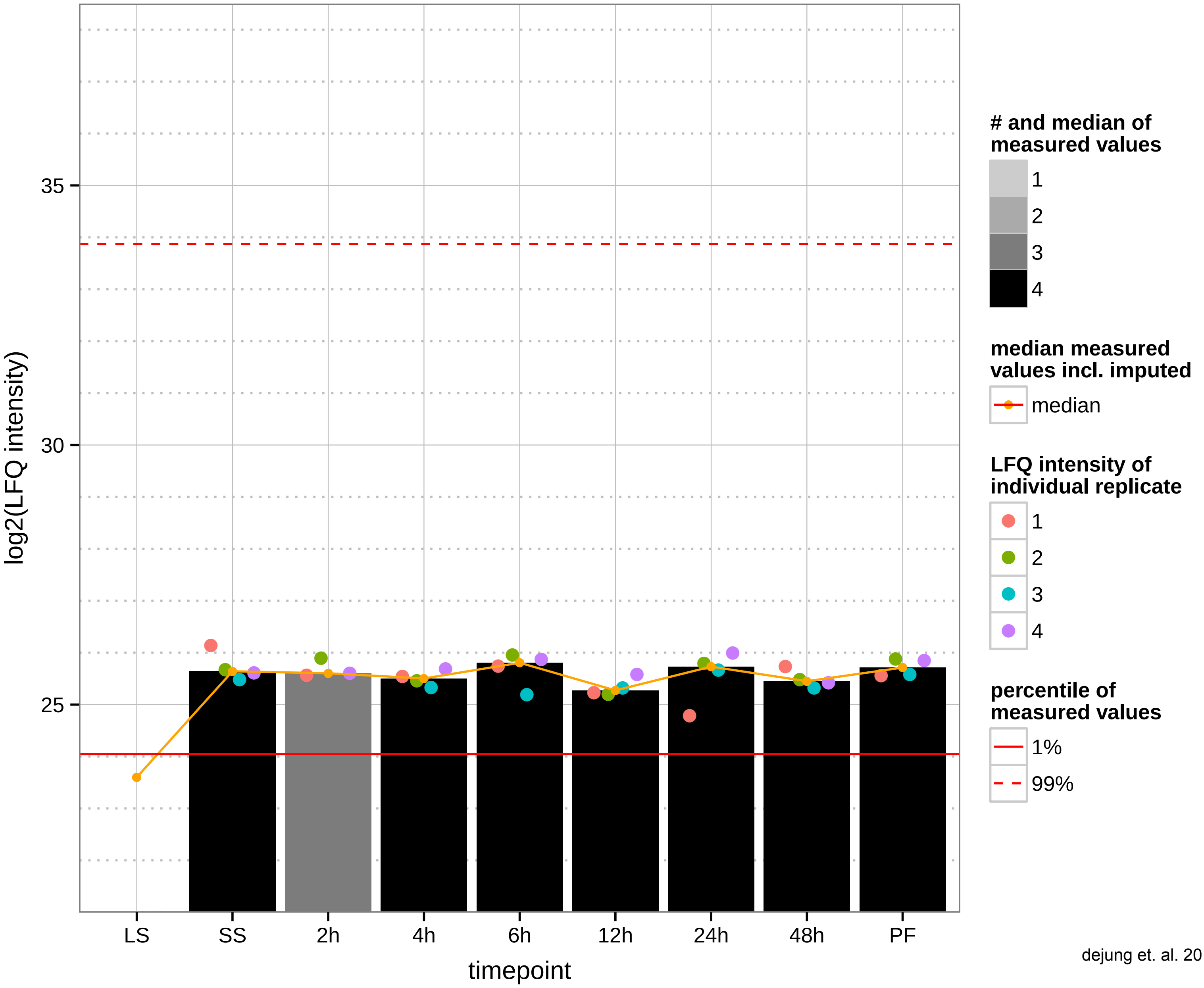
ADP–ribosylation factor–like 2, arl2 (ARL2)
Tb927.10.4250
AGOF: null
AGOC: cytoplasm, intracellular
AGOP: cytokinesis, intracellular protein transport, small GTPase mediated signal transduction
PGOF: GTP binding
PGOC: intracellular
PGOP: intracellular protein transport, small GTPase mediated signal transduction





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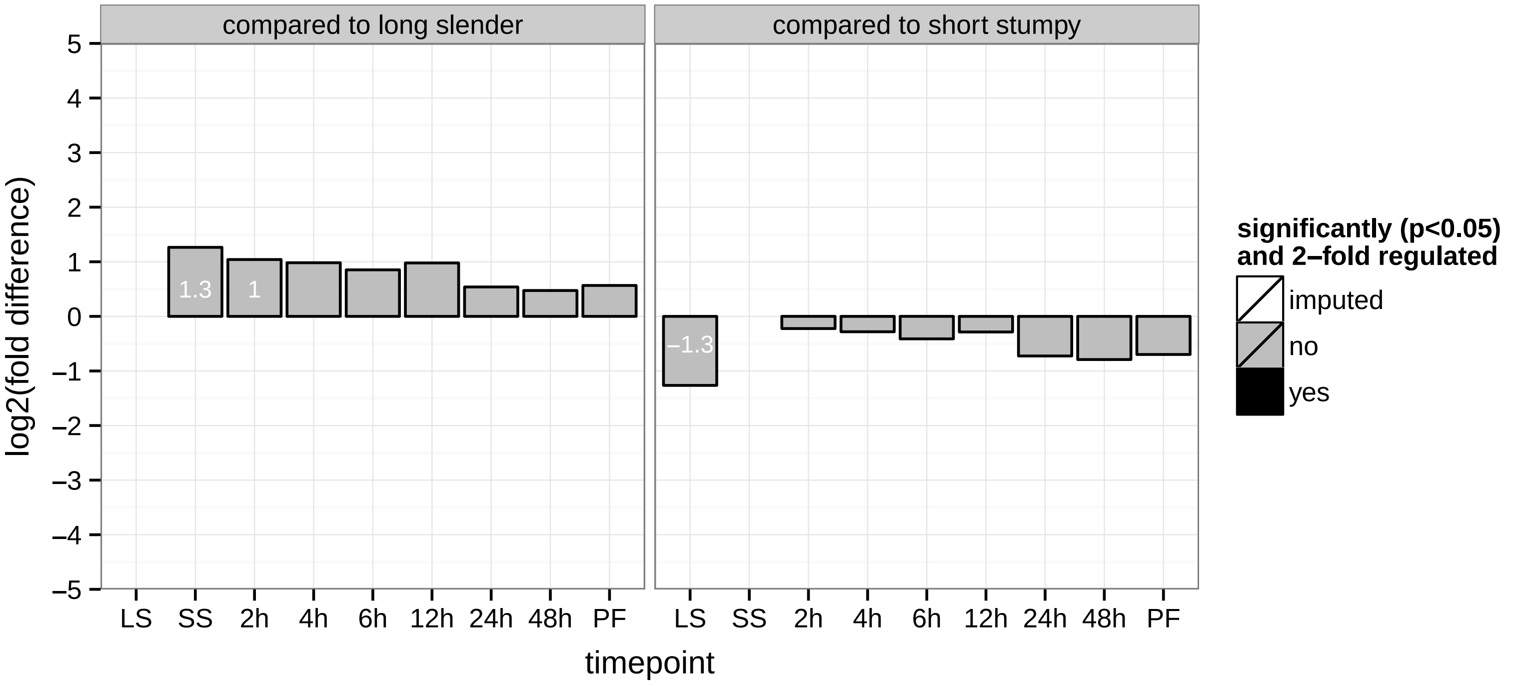
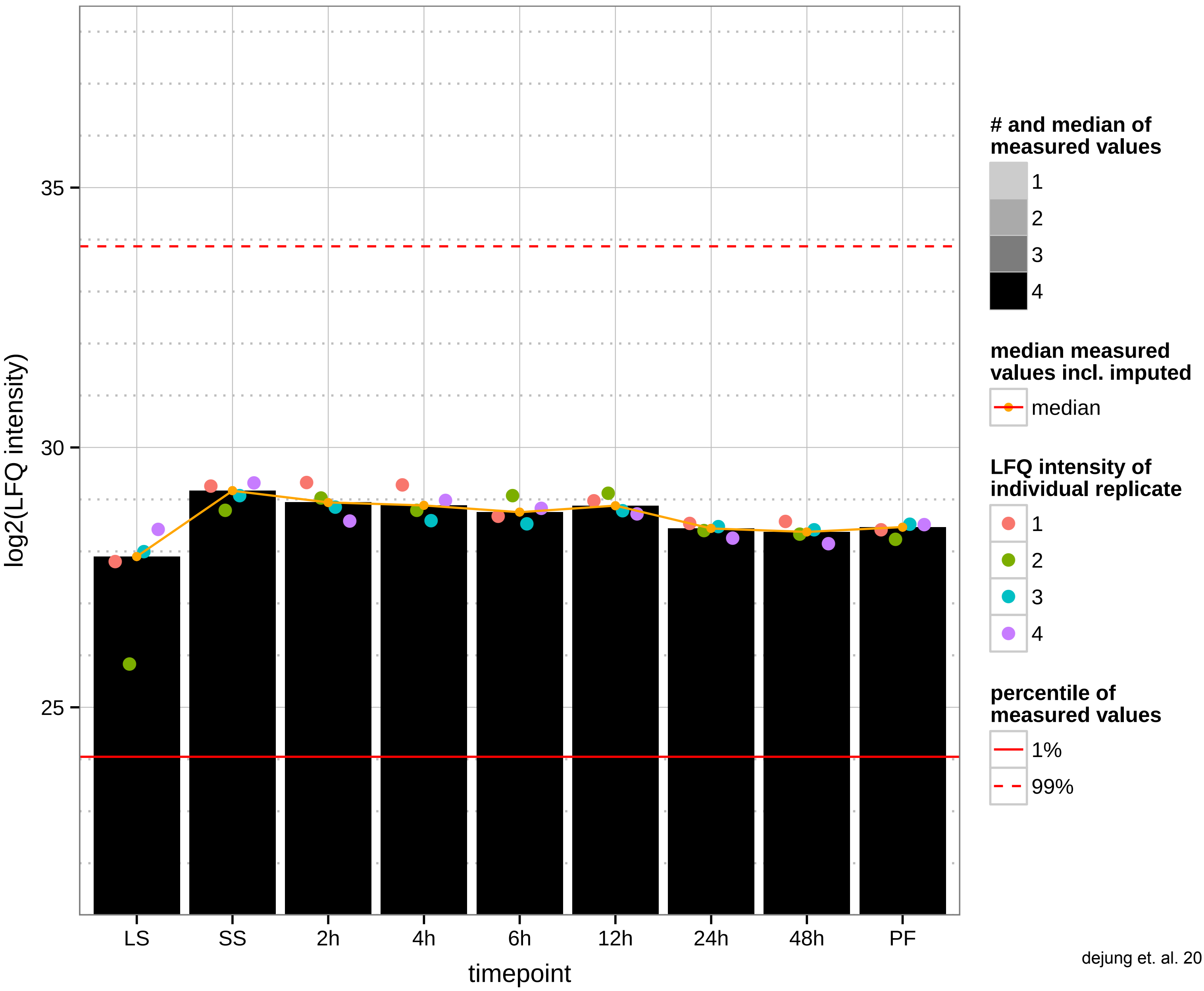
dolicholphosphate−mannose synthase, putative (DPMS)
Tb927.10.4610
AGOF: dolichyl−phosphate beta−D−mannosyltransferase activity
AGOC: null
AGOP: GPI anchor biosynthetic process
PGOF: null
PGOC: null
PGOP: null





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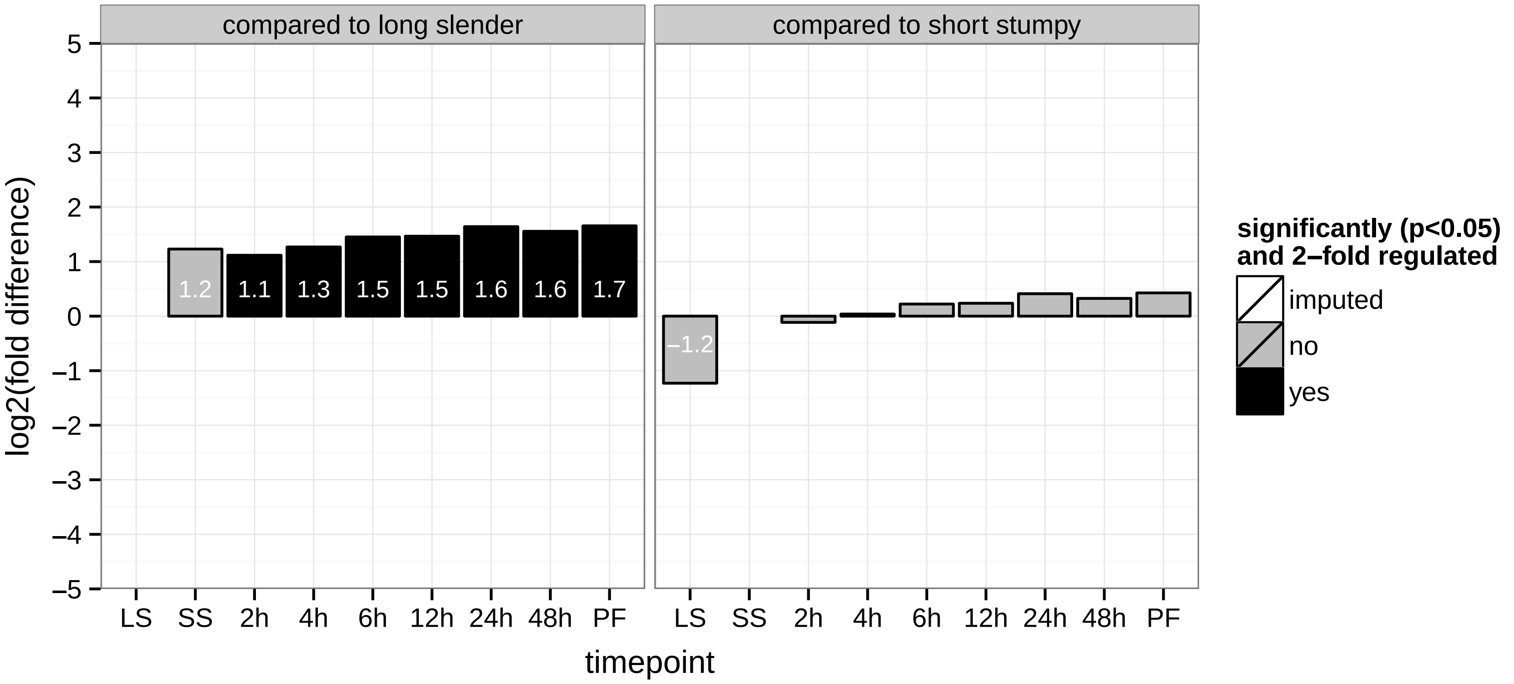
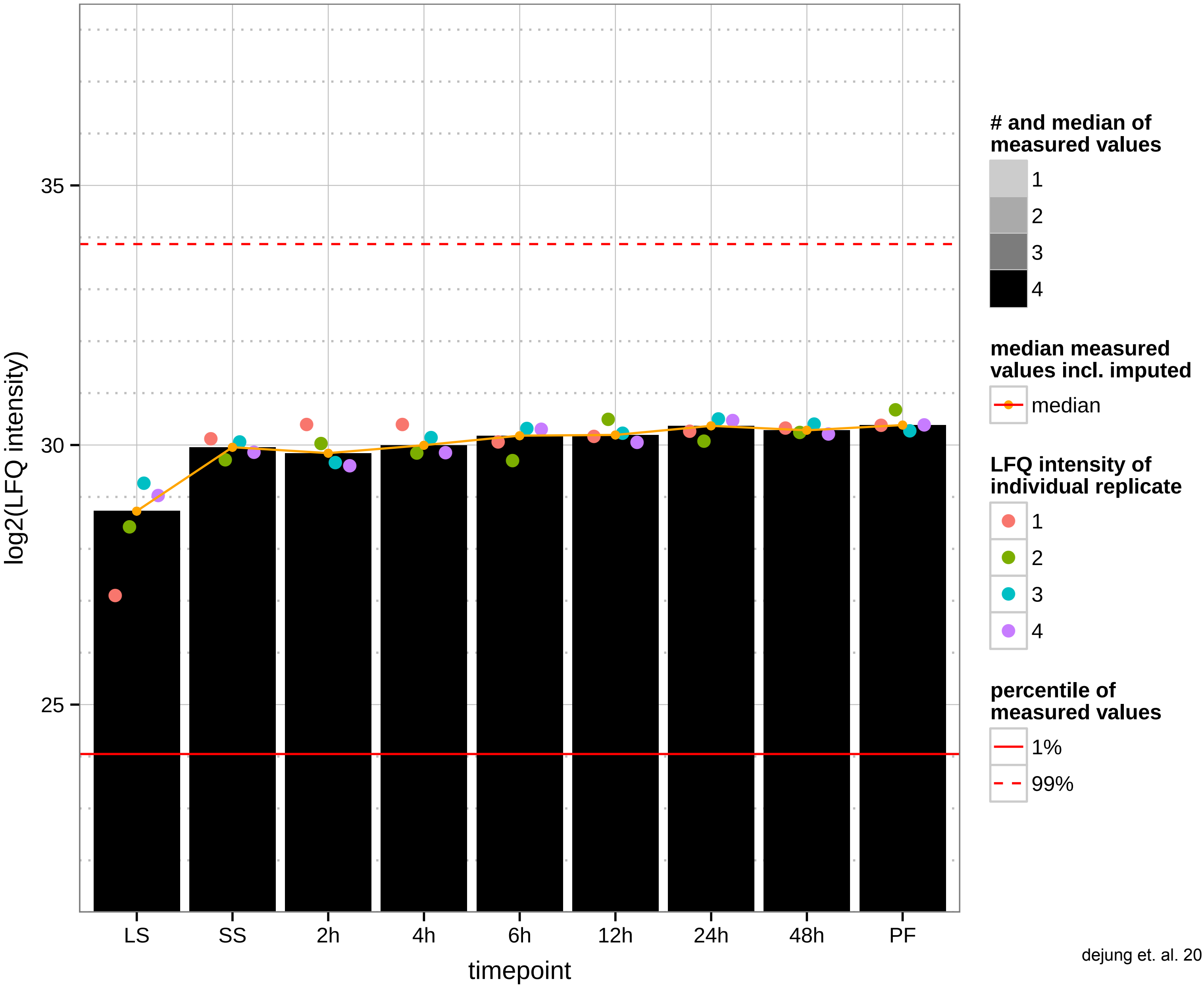
eukaryotic translation initiation factor 3 subunit L, putative (EIF3L)
Tb927.10.4640
AGOF: translation initiation factor activity
AGOC: eukaryotic translation initiation factor 3 complex
AGOP: translational initiation
PGOF: null
PGOC: null
PGOP: null





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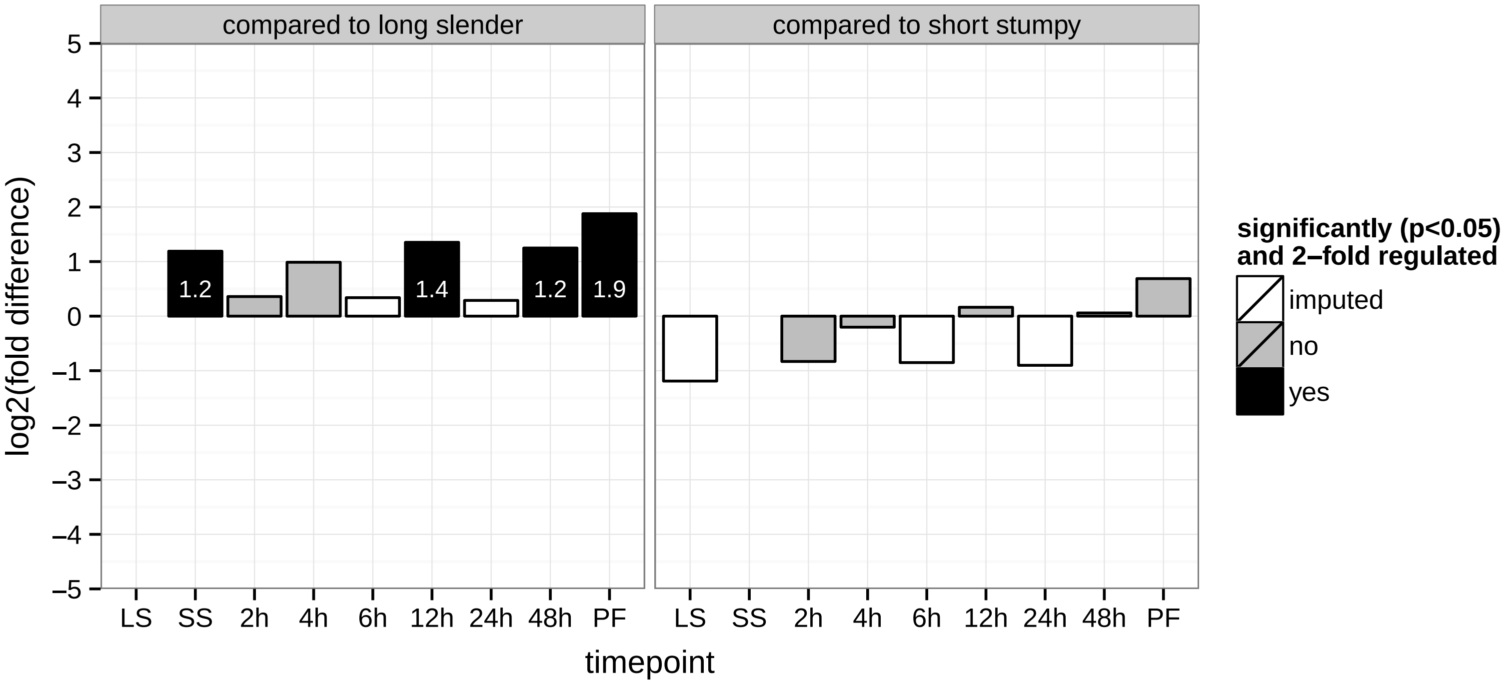
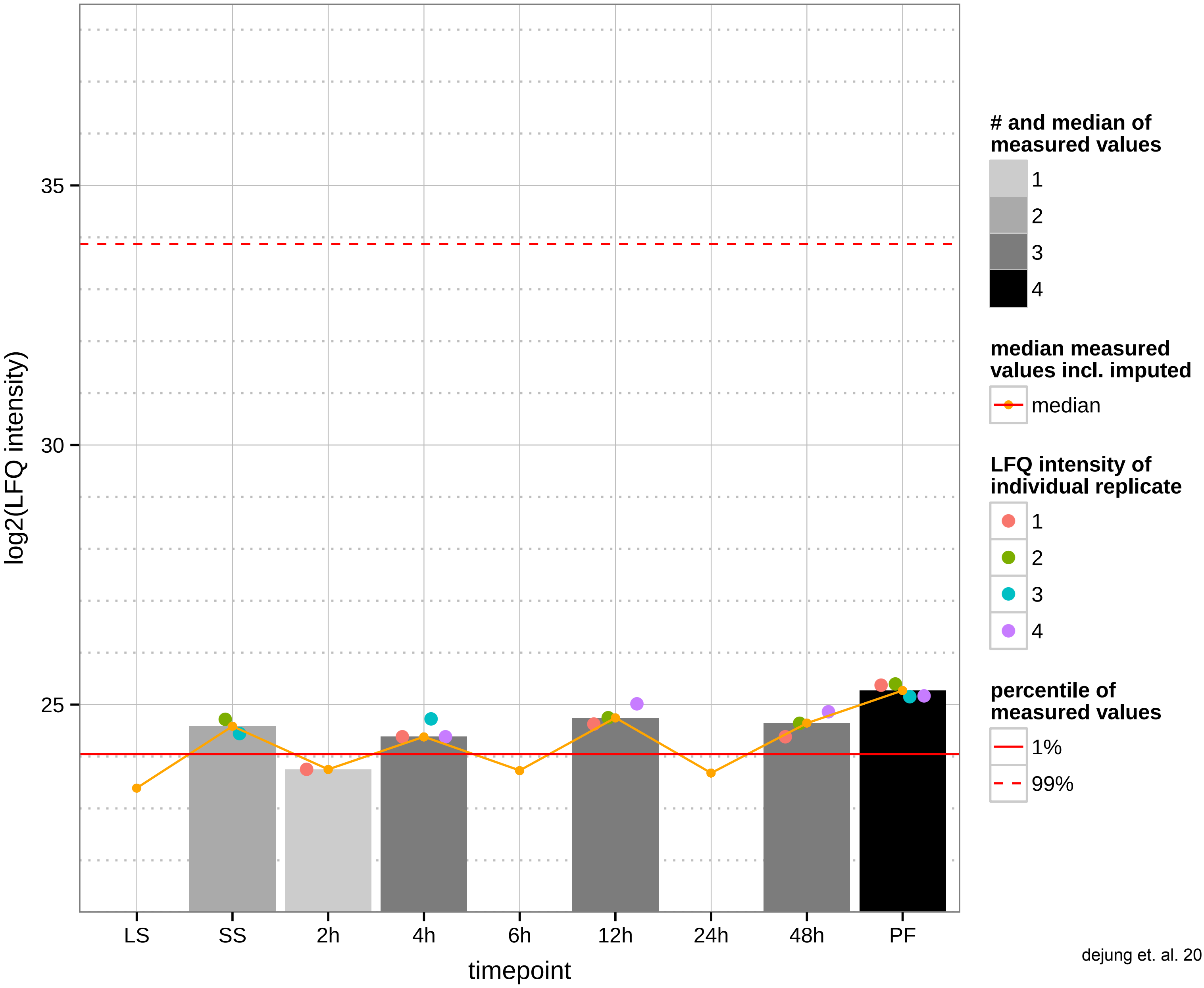
hypothetical protein, conserved
Tb927.10.4660
AGOF: null
AGOC: null
AGOP: transcription, DNA–dependent
PGOF: null
PGOC: null
PGOP: transcription, DNA–dependent





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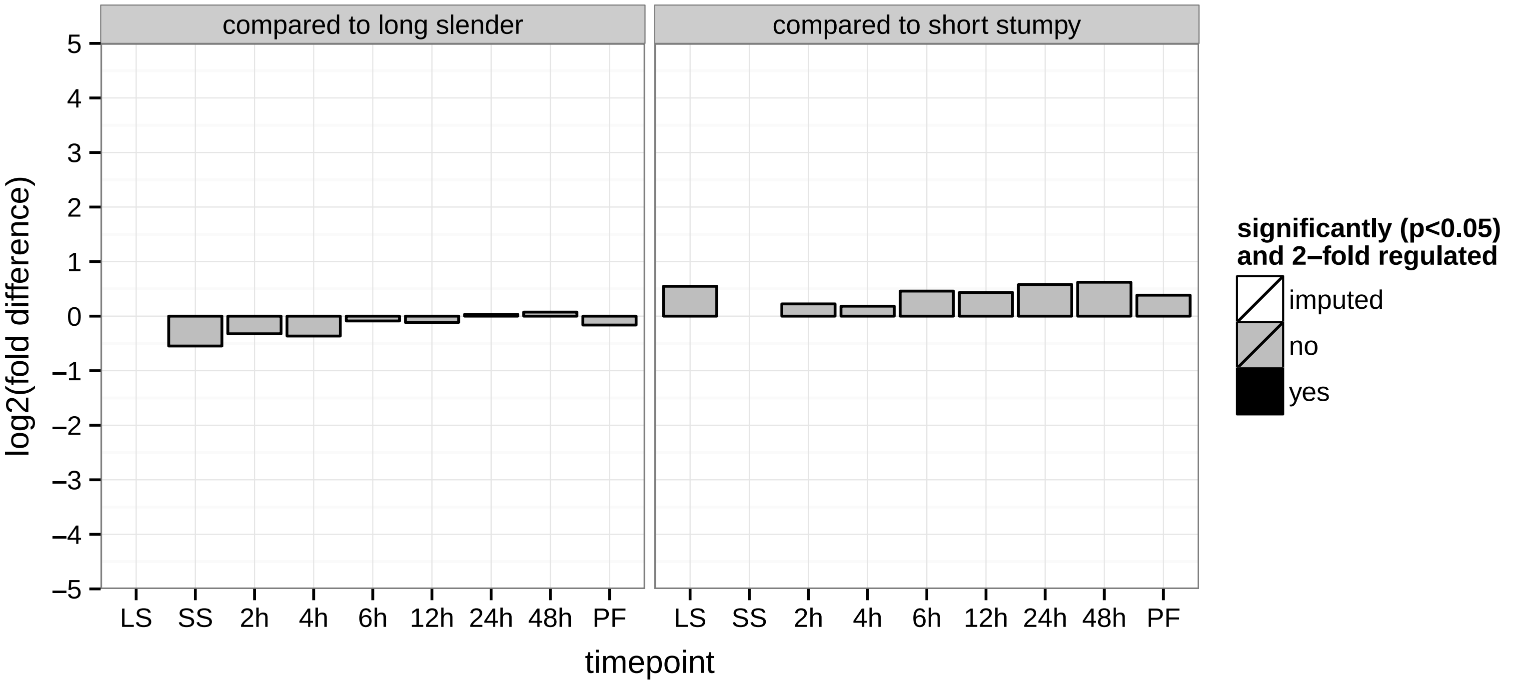
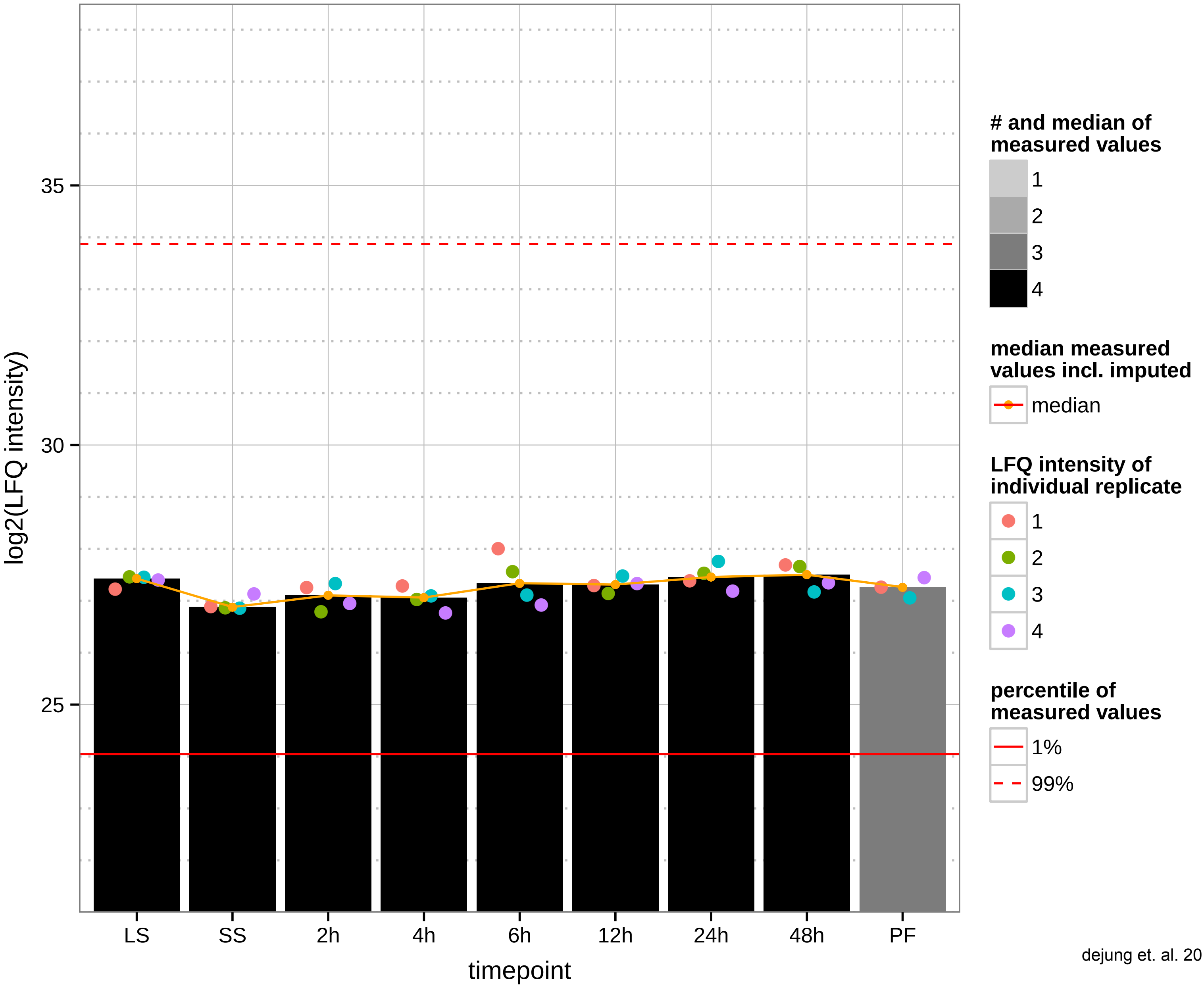
dynein light chain, putative
Tb927.10.4690
AGOF: microtubule motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based process
PGOF: null
PGOC: microtubule associated complex
PGOP: microtubule–based process





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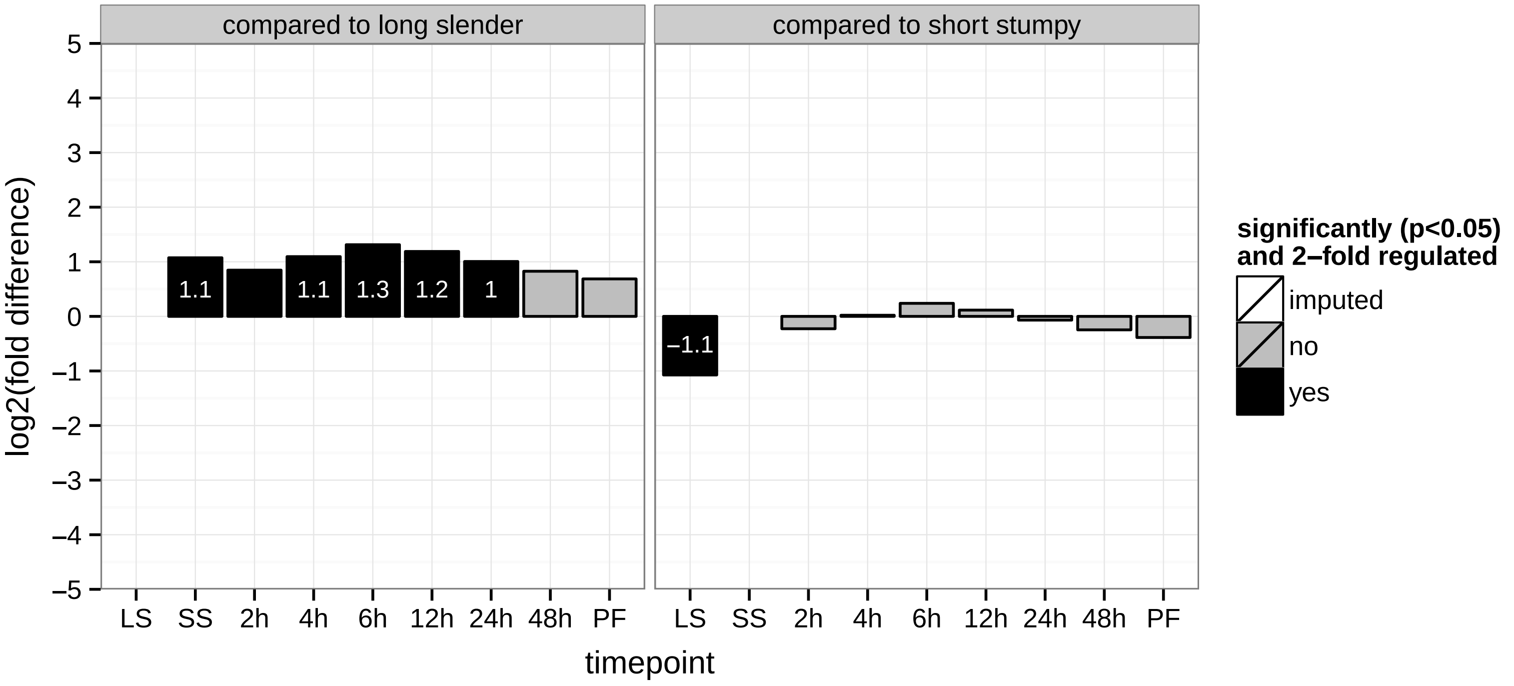
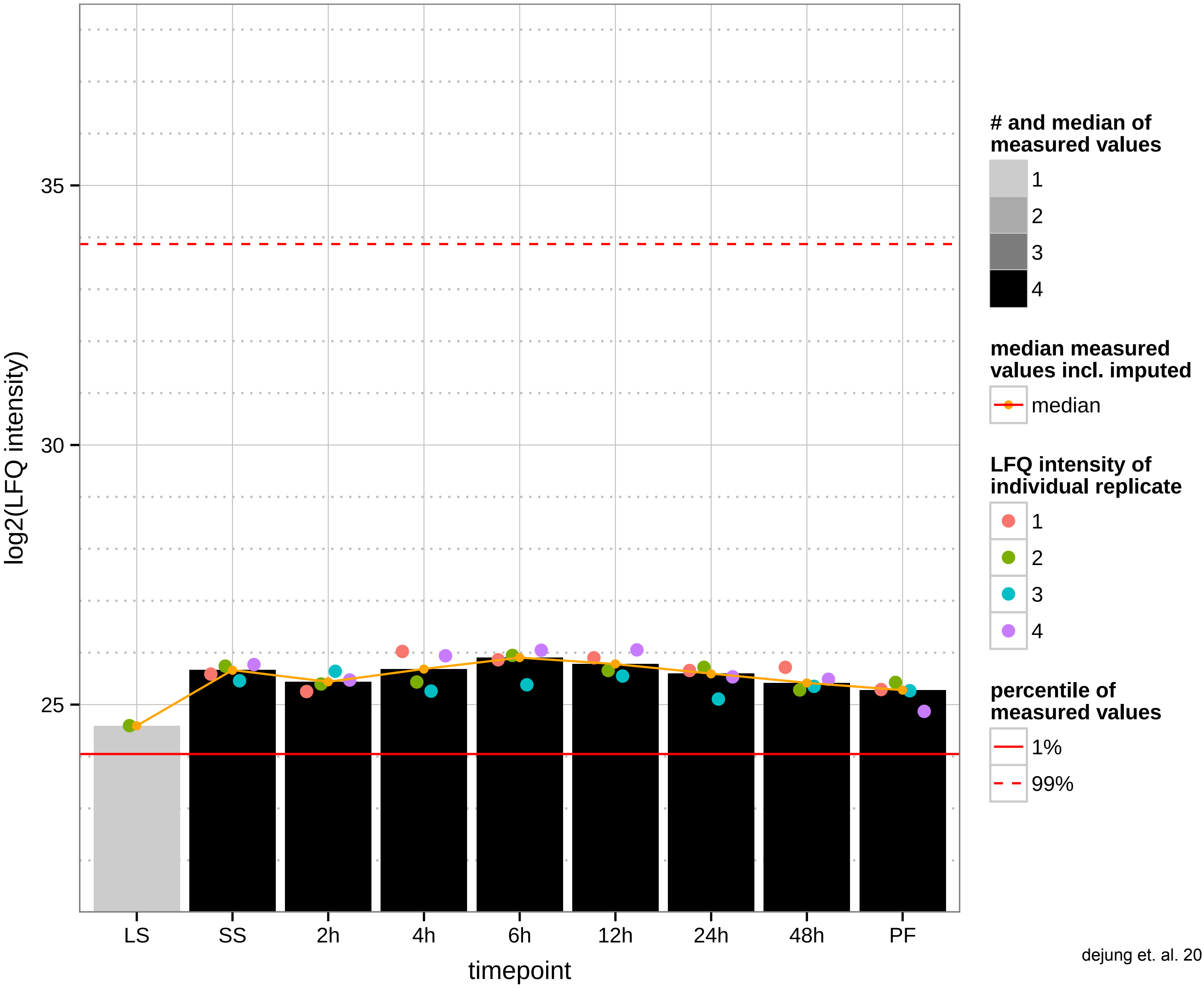
dolicholphosphate–mannose synthase, putative
Tb927.10.4700
AGOF: dolichyl–phosphate beta–D–mannosyltransferase activity
AGOC: endoplasmic reticulum membrane
AGOP: dolichol–linked oligosaccharide biosynthetic process
PGOF: null
PGOC: null
PGOP: null





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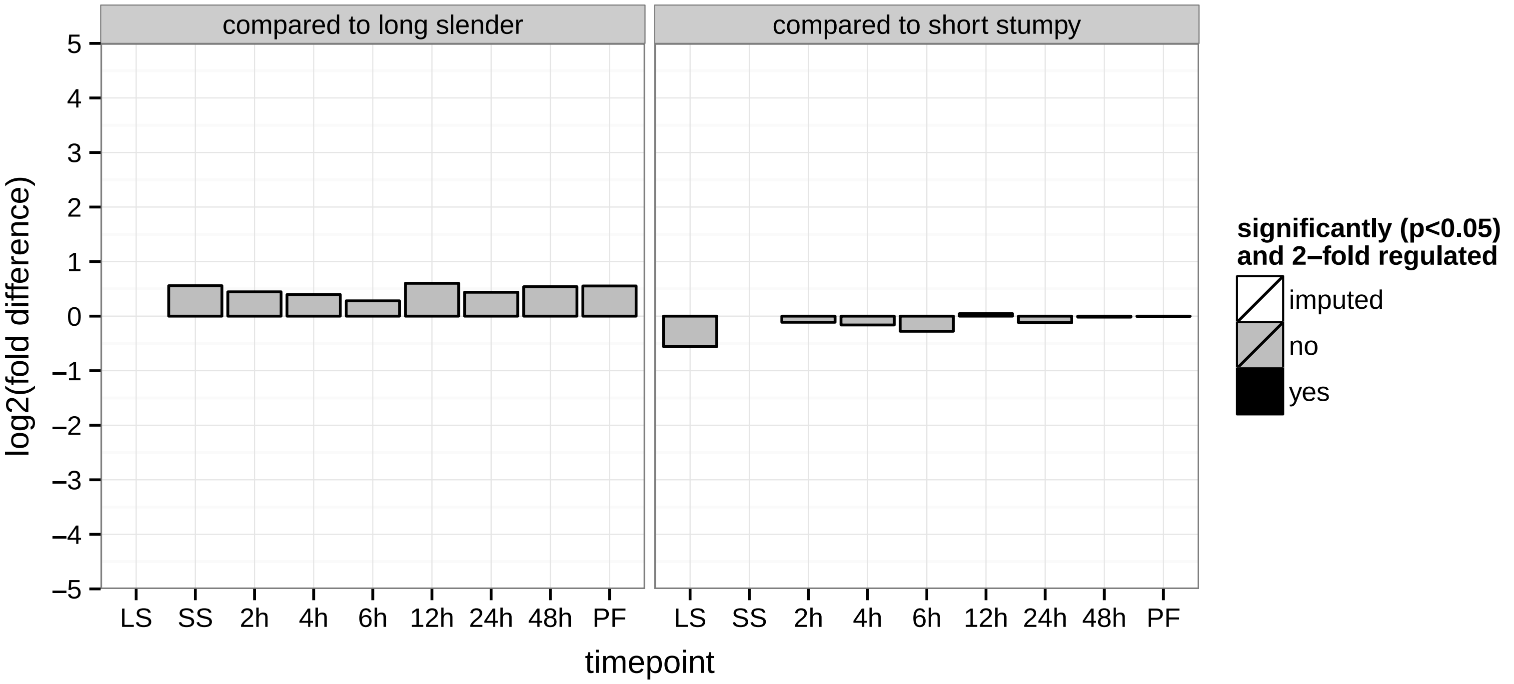
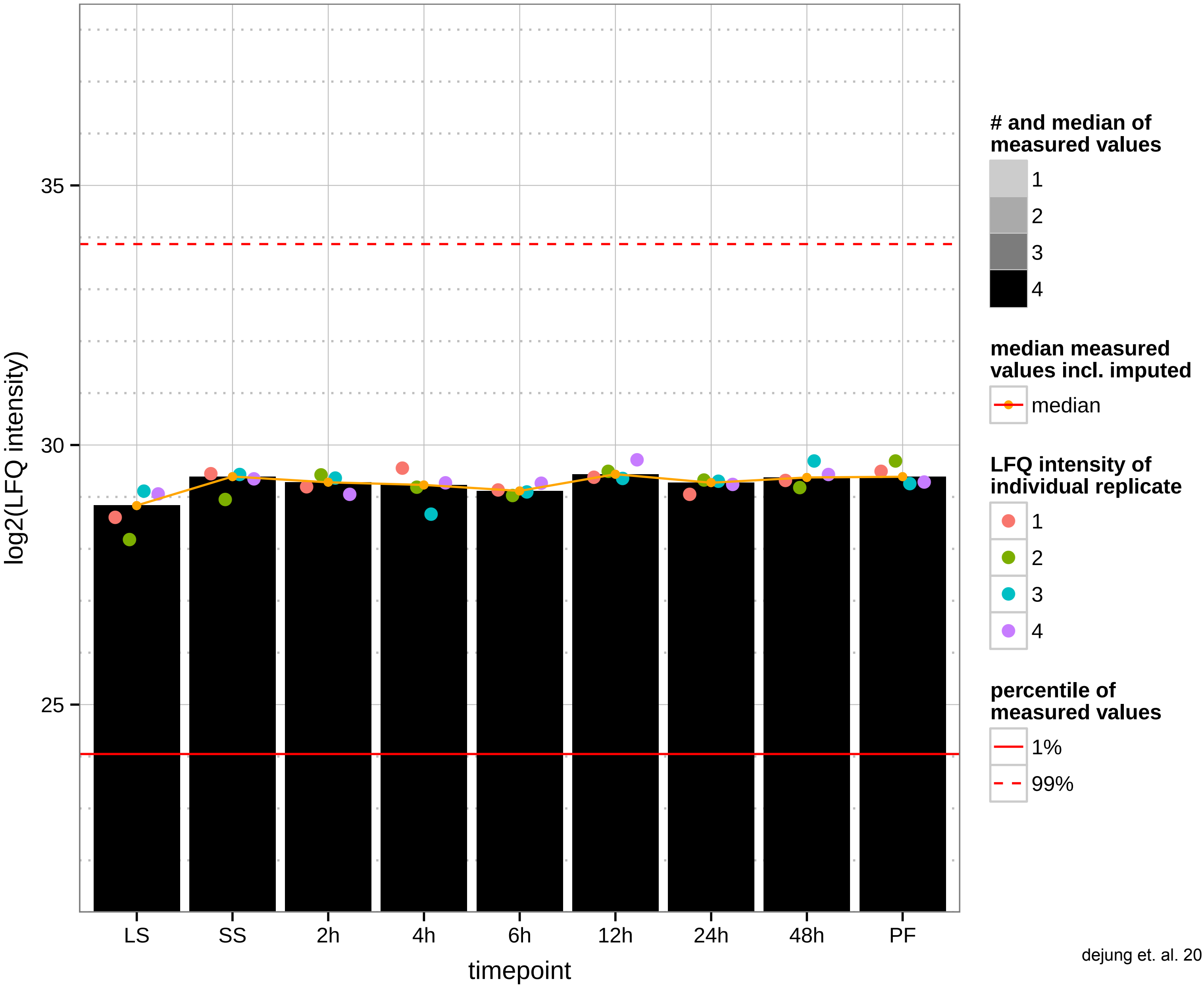
proteasome beta 2 subunit, putative, 20S proteasome subunit
Tb927.10.4710
AGOF: endopeptidase activity, threonine−type endopeptidase activity
AGOC: proteasome core complex, proteasome core complex, beta−subunit complex
AGOP: ubiquitin−dependent protein catabolic process
PGOF: threonine−type endopeptidase activity
PGOC: proteasome core complex
PGOP: proteolysis involved in cellular protein catabolic process





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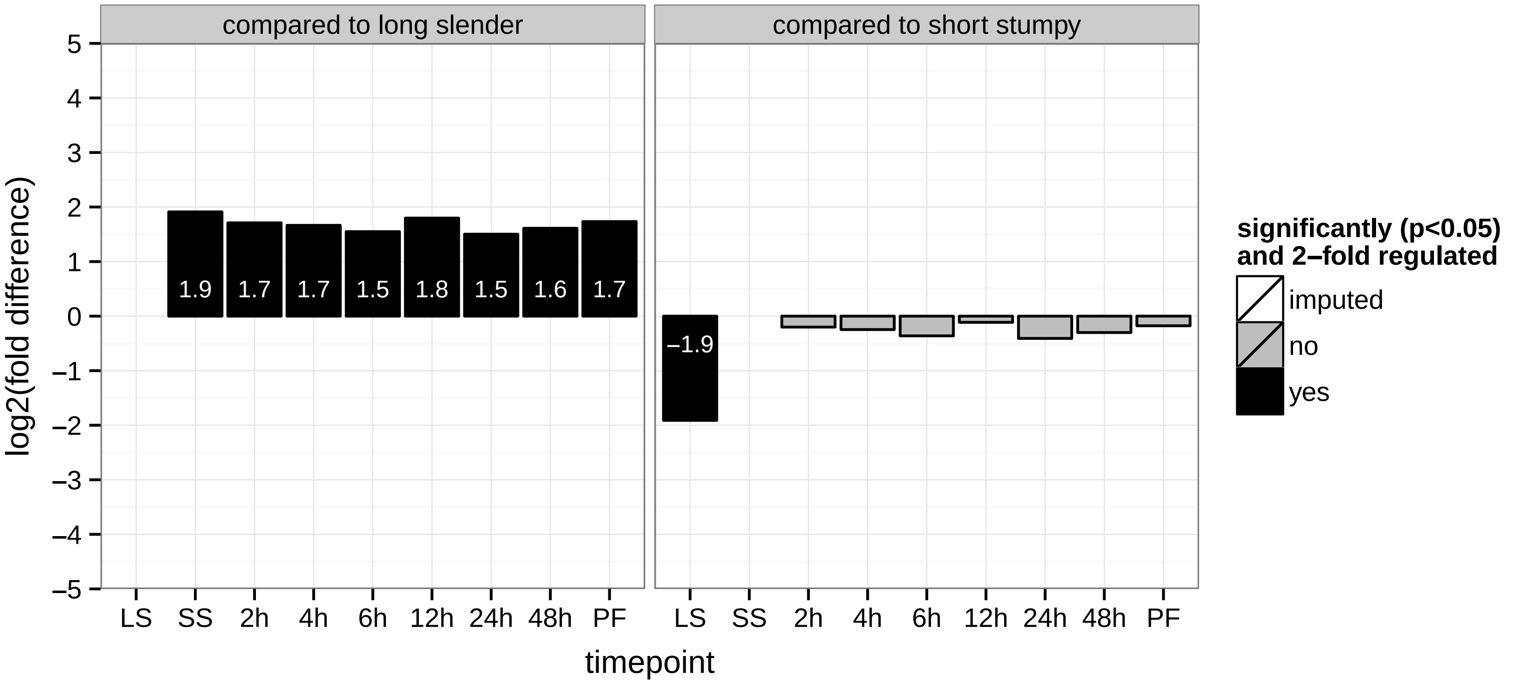
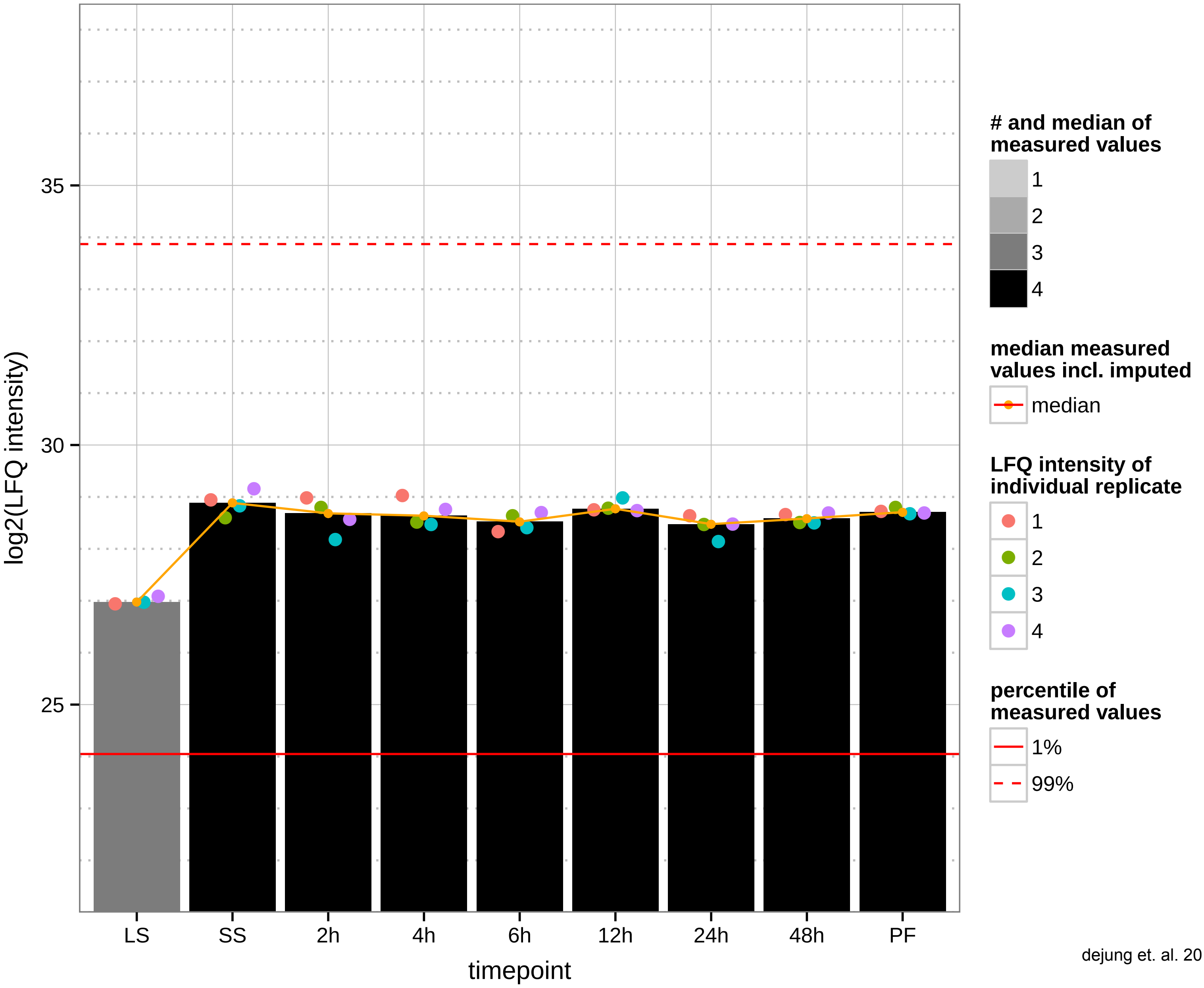
hypothetical protein, conserved
Tb927.10.4850
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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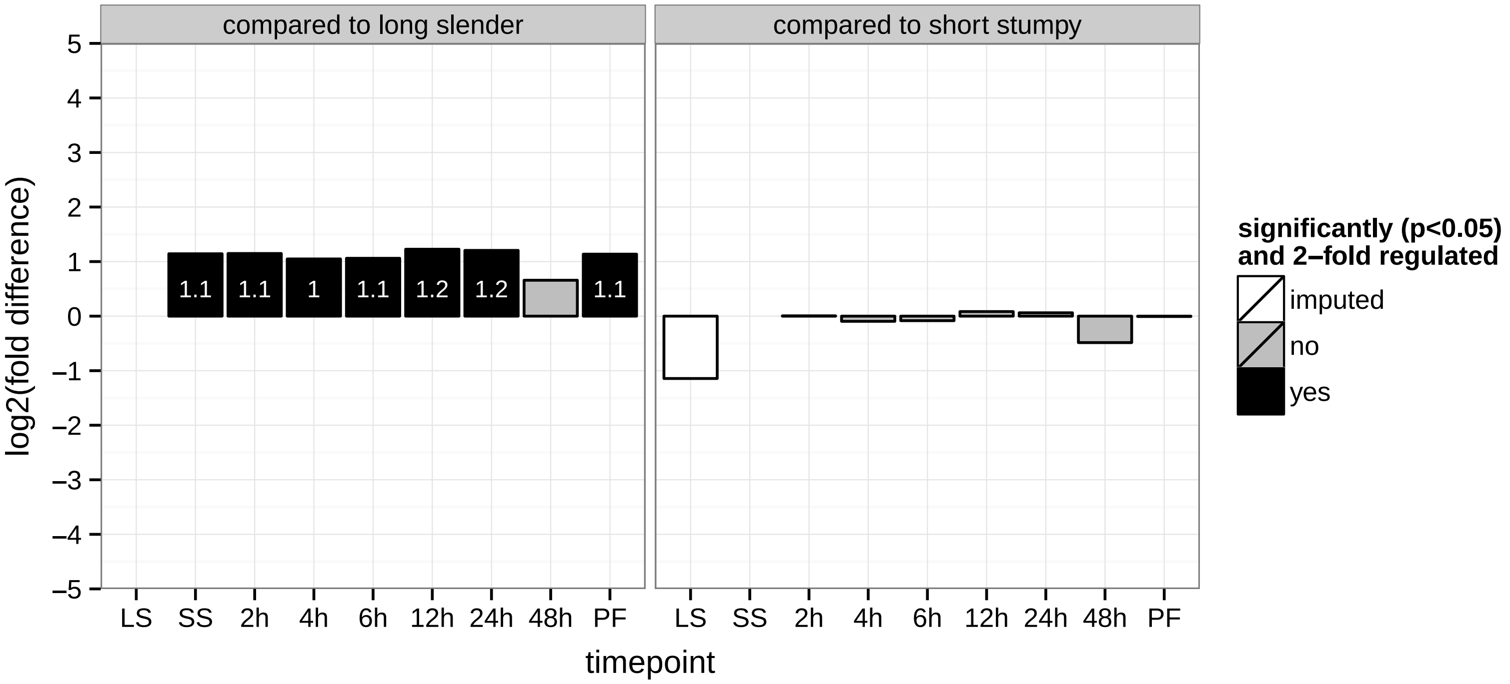
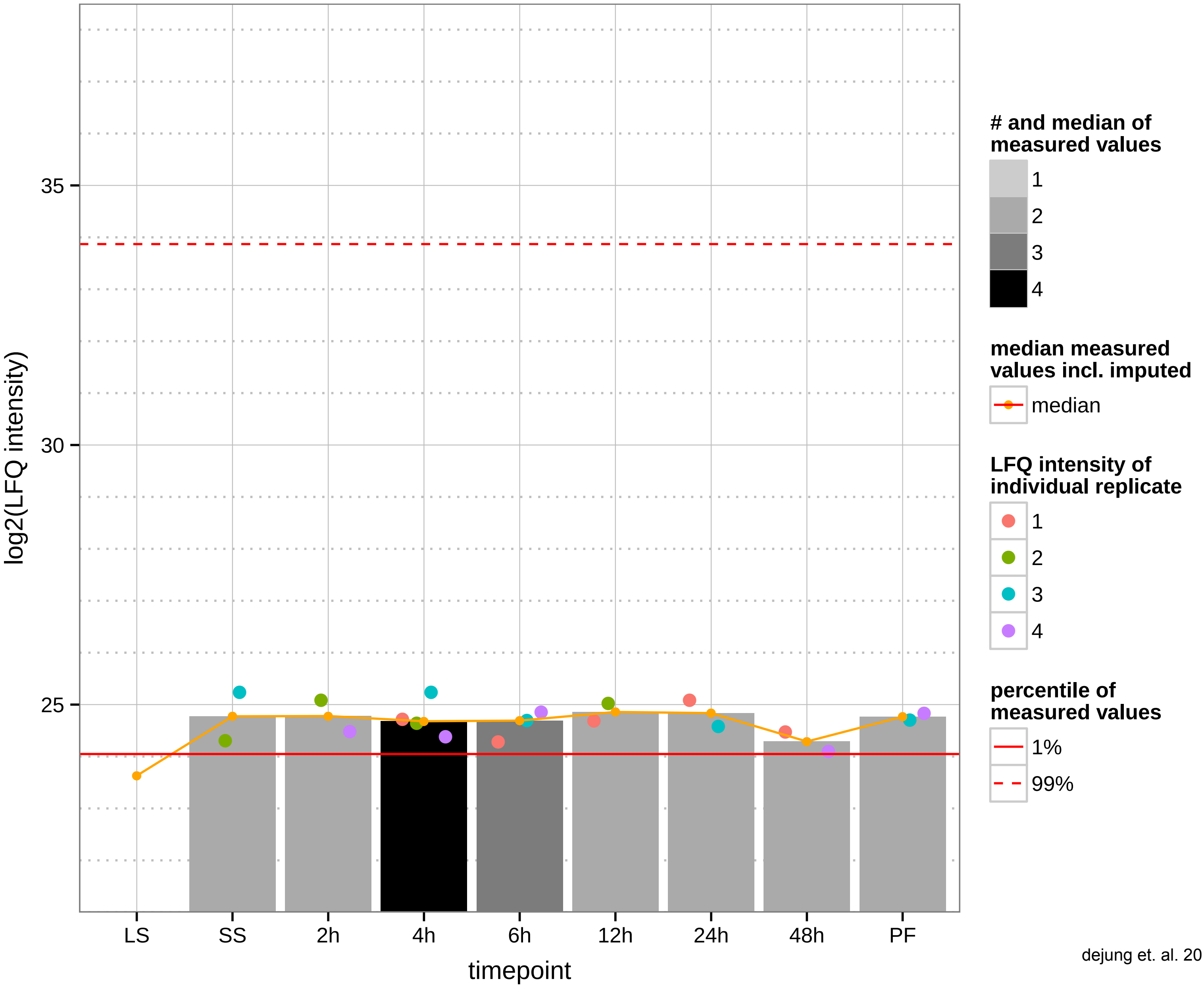
protein phosphatase 2C, putative
Tb927.10.4930
AGOF: phosphatase activity
AGOC: protein serine/threonine phosphatase complex
AGOP: dephosphorylation
PGOF: catalytic activity
PGOC: null
PGOP: null





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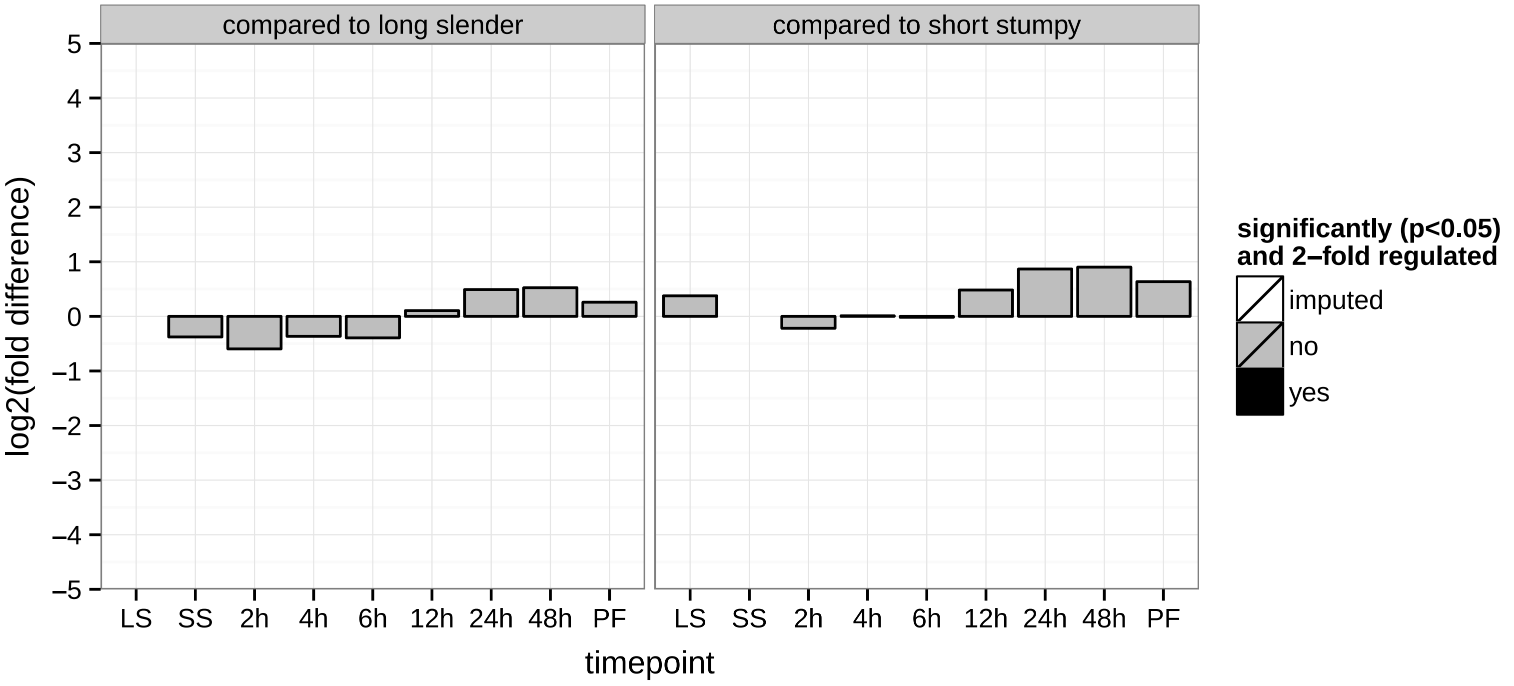
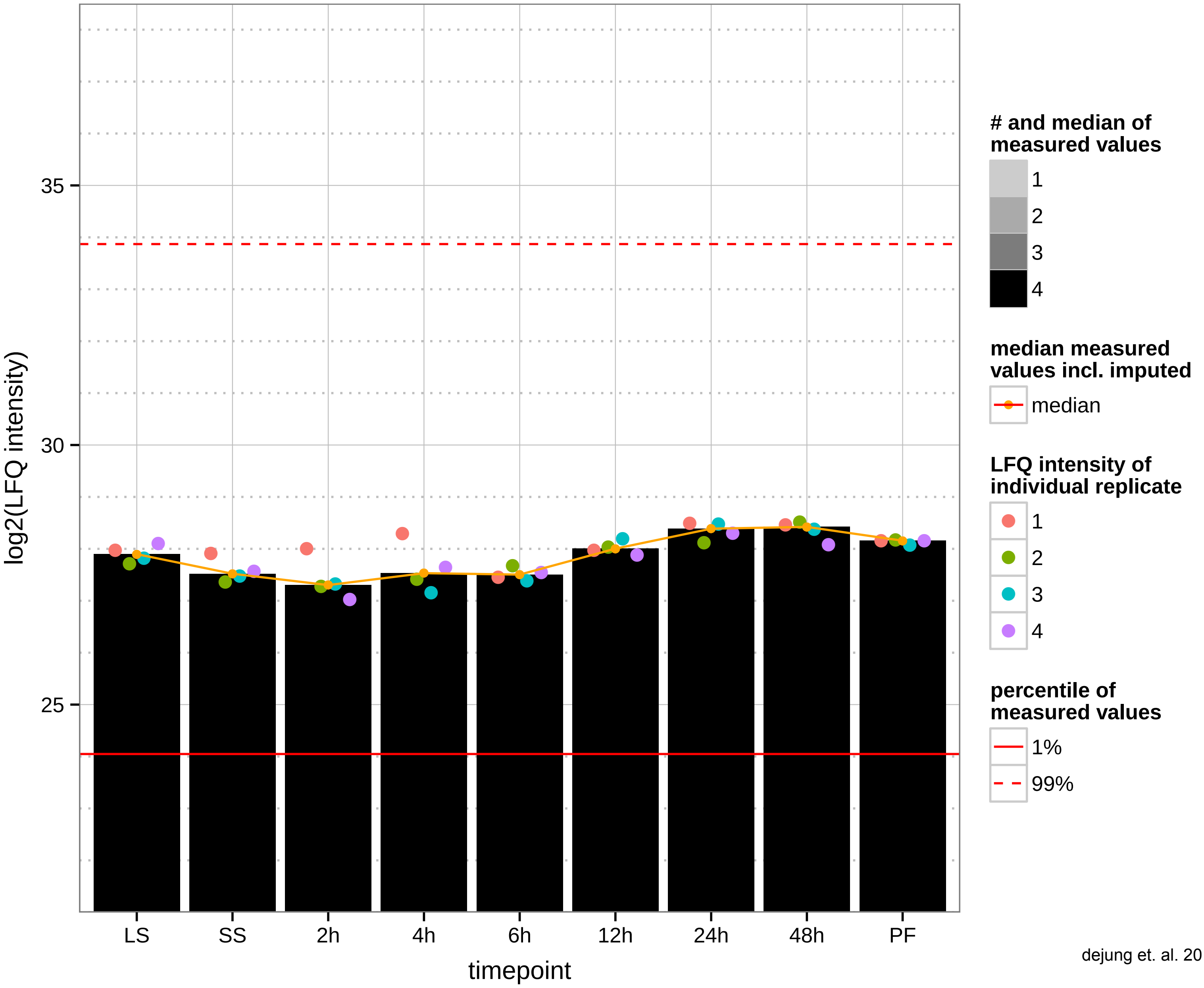
serine/threonine protein kinase, putative, Nuclear Dbf2–related kinase (PK50)
Tb927.10.4940;Tb11.v5.0596
AGOF: null, ATP binding, protein kinase activity, protein tyrosine kinase activity
AGOC: null, cytosol, kinetoplast
AGOP: null, cytokinesis, growth, protein phosphorylation, regulation of cell cycle
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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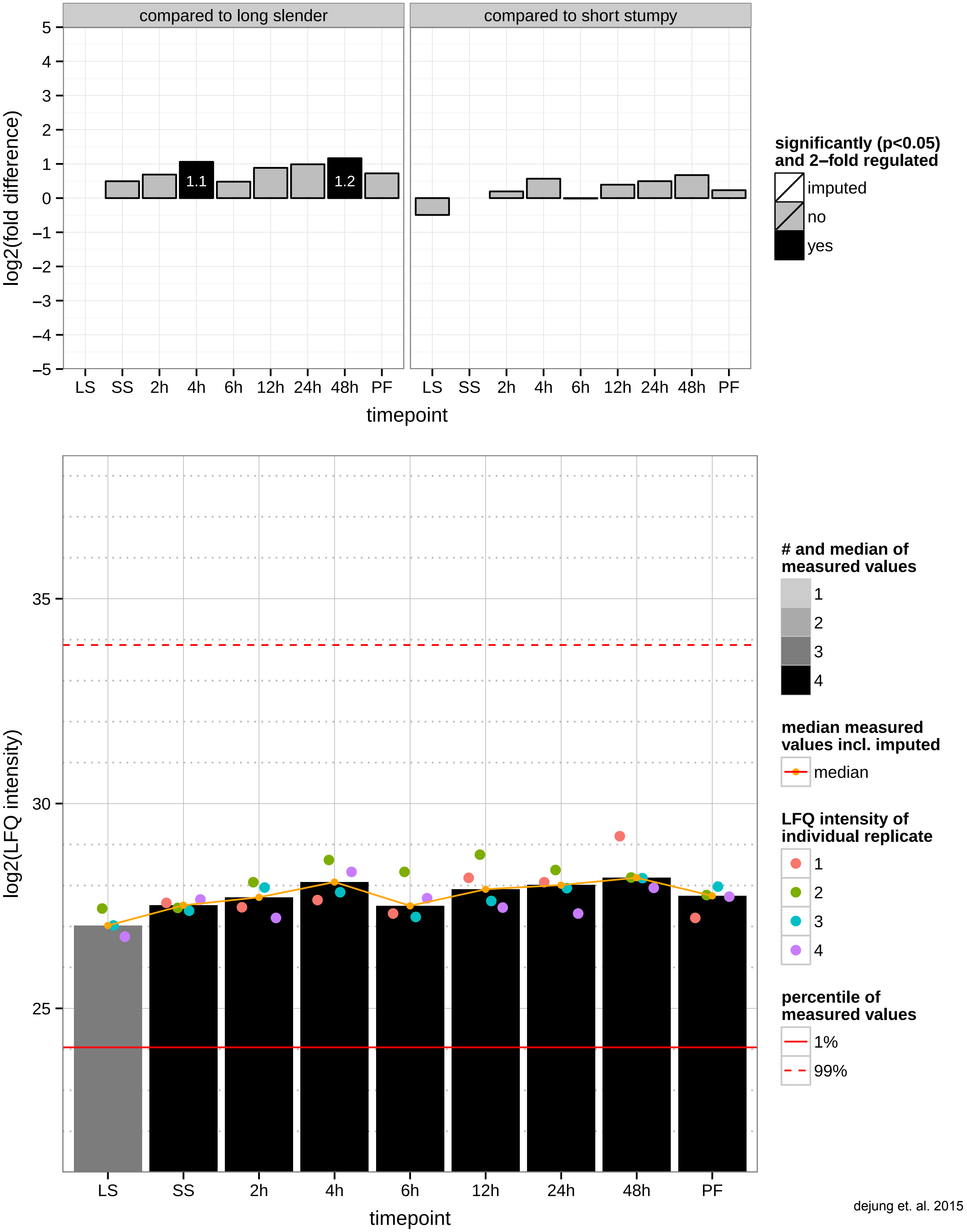
ubiquitin–like protein DSK2, putative (DSK2)
Tb927.10.4980
AGOF: protein binding, bridging
AGOC: null
AGOP: DNA replication, chromosome organization, chromosome segregation
PGOF: protein binding
PGOC: null
PGOP: null



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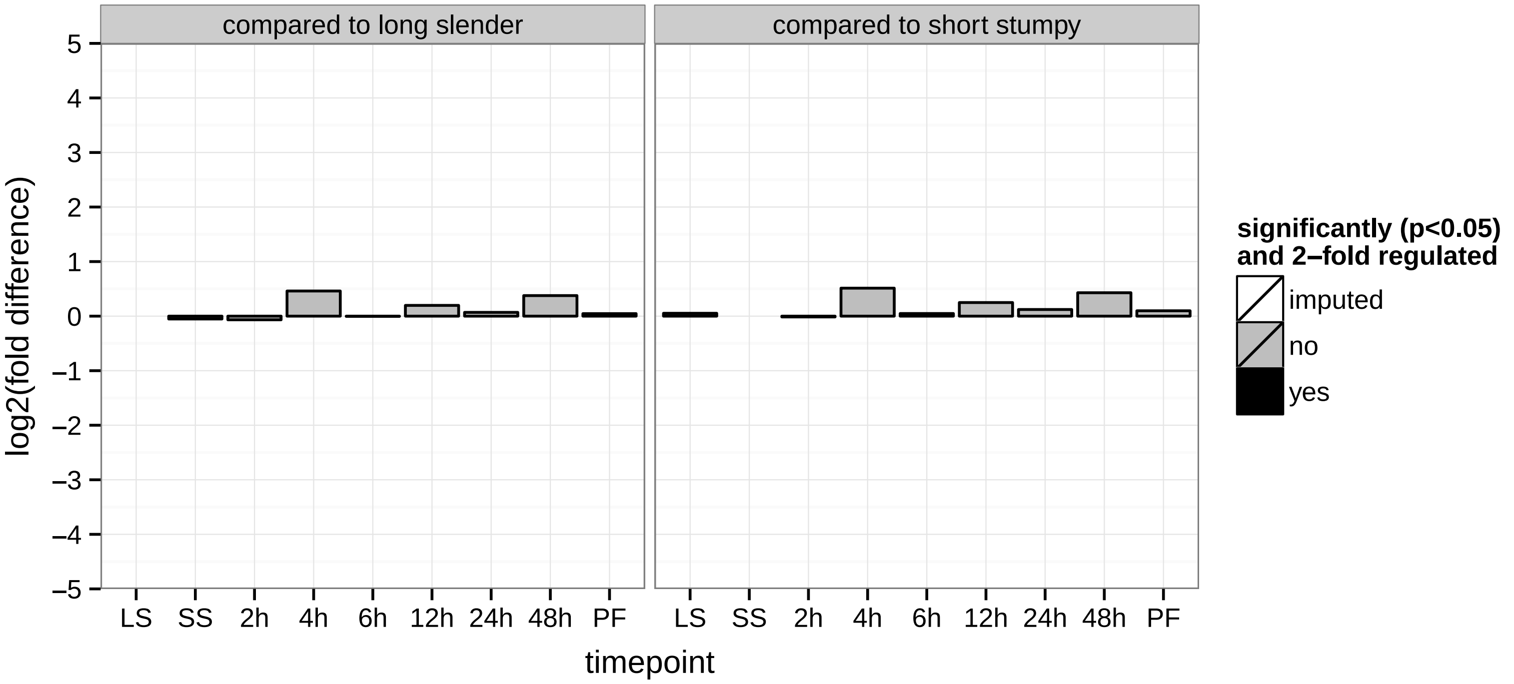
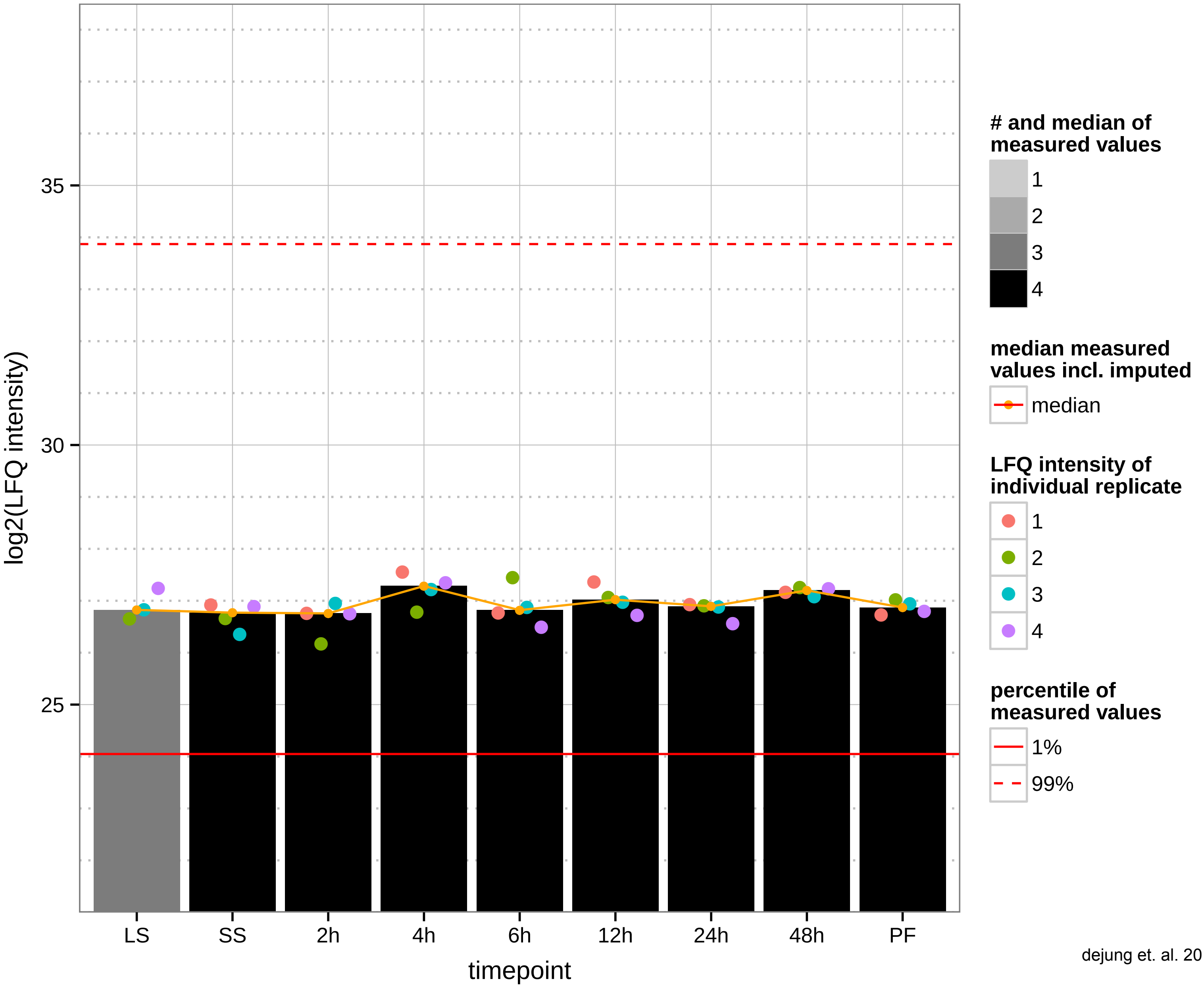
ADP–ribosylation factor–like protein, putative, ADP–ribosylation factor
Tb927.10.5230
AGOF: null, GTP binding
AGOC: null, intracellular
AGOP: null, intracellular protein transport, protein transport, small GTPase mediated signal transduction
PGOF: GTP binding, cAMP–dependent protein kinase regulator activity
PGOC: intracellular
PGOP: small GTPase mediated signal transduction, intracellular protein transport, signal transduction, small GTPase mediate





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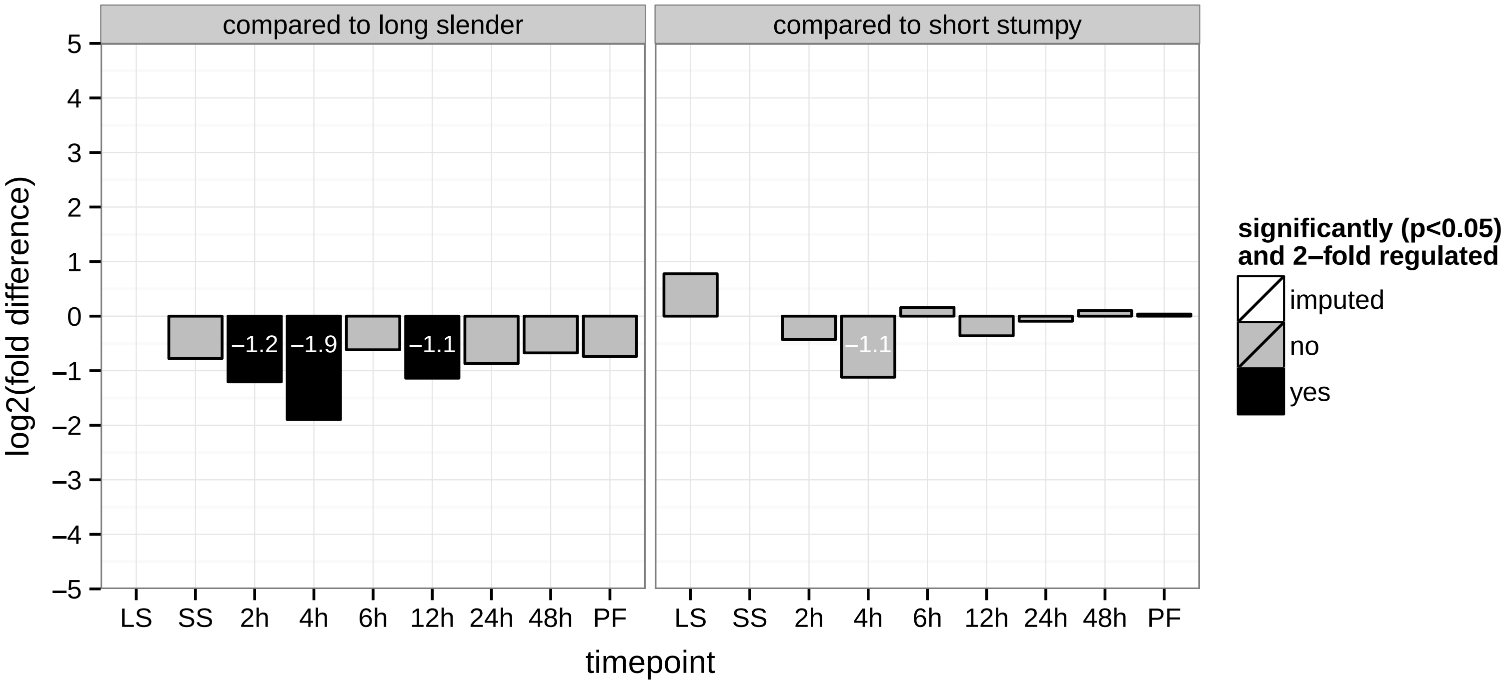
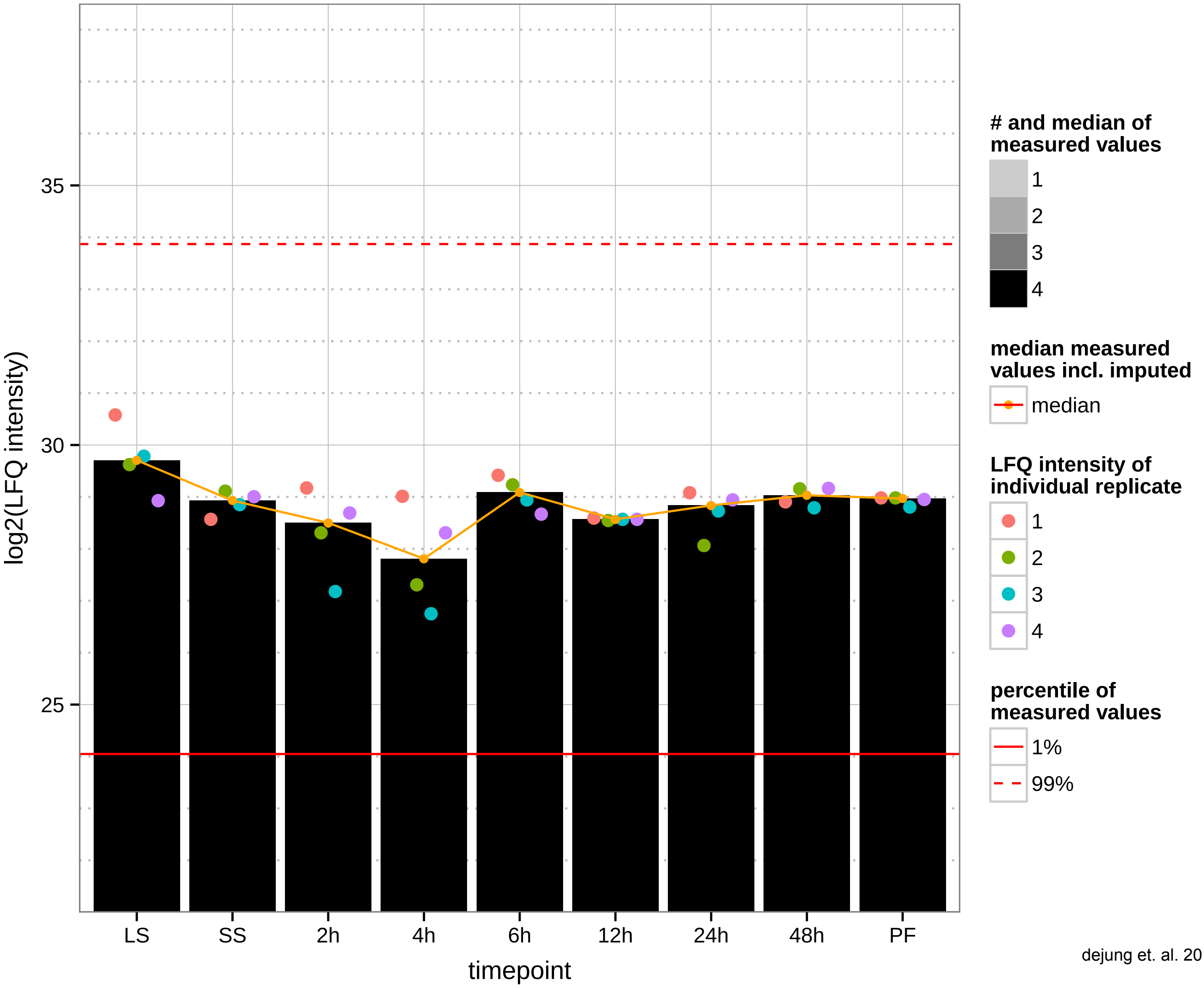
dynein heavy chain, putative
Tb927.10.5350;Tb11.v5.0242
AGOF: null, ATP binding, ATPase activity, microtubule motor activity
AGOC: null, dynein complex
AGOP: null, microtubule–based movement
PGOF: microtubule motor activity, null
PGOC: dynein complex, null
PGOP: microtubule–based movement, null





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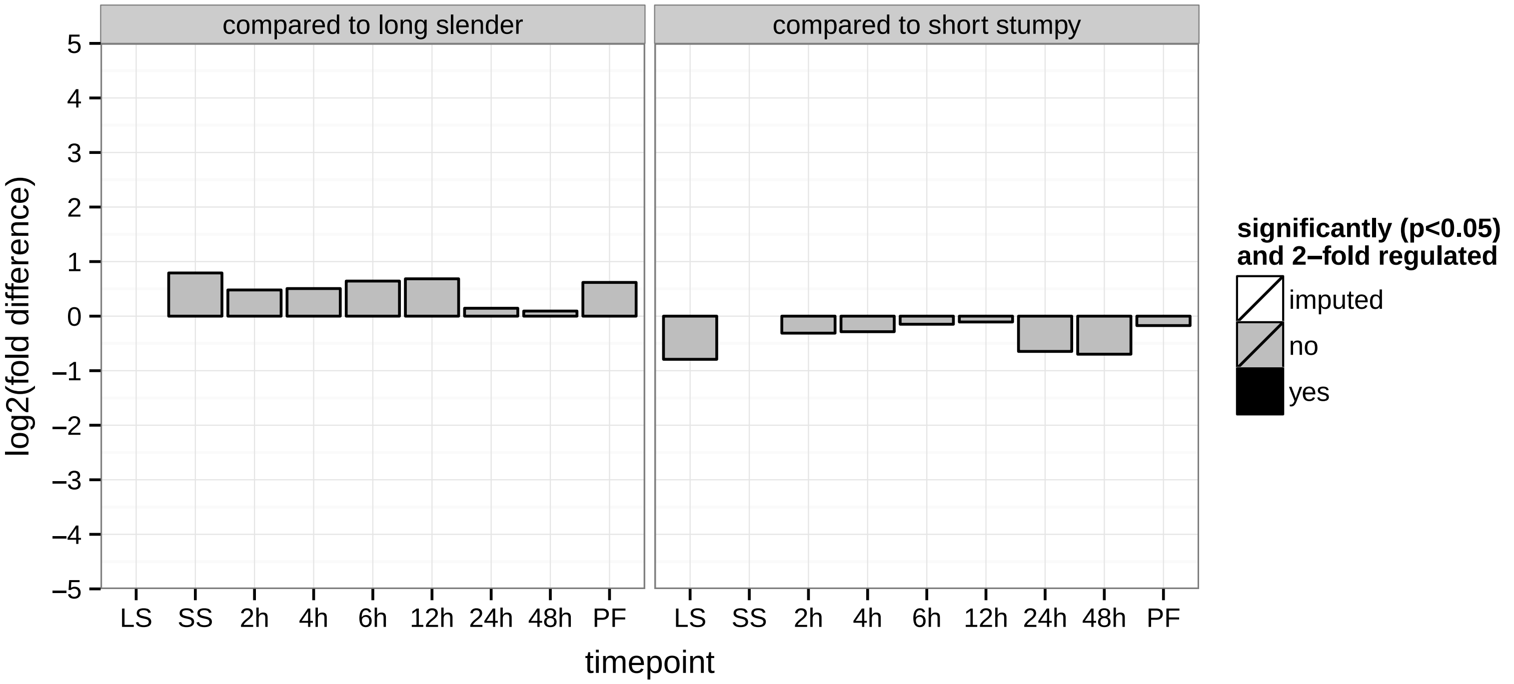
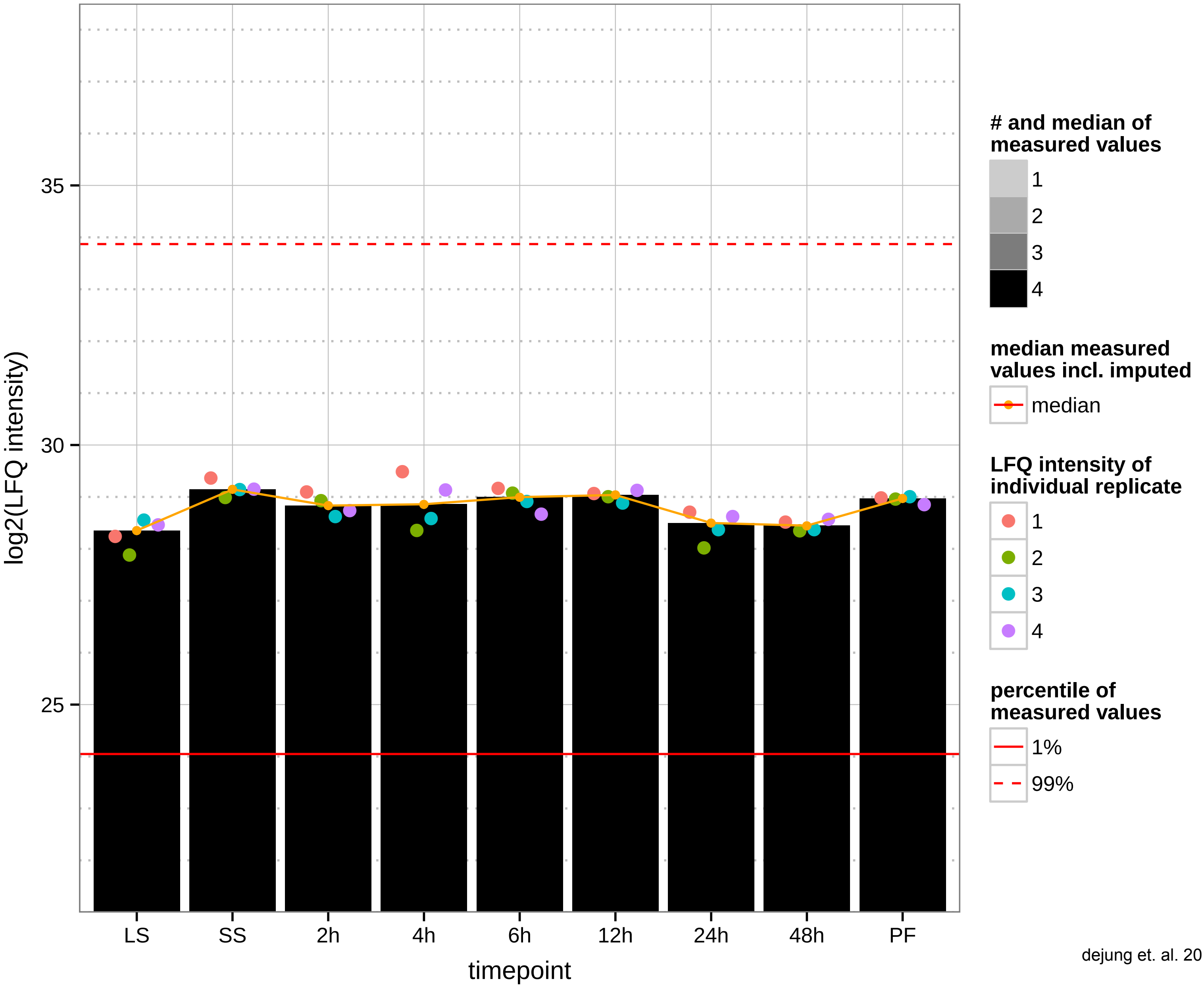
hypothetical protein, conserved, intraflagellar transport protein IFT122, putative
Tb927.10.5380;Tb11.v5.0337
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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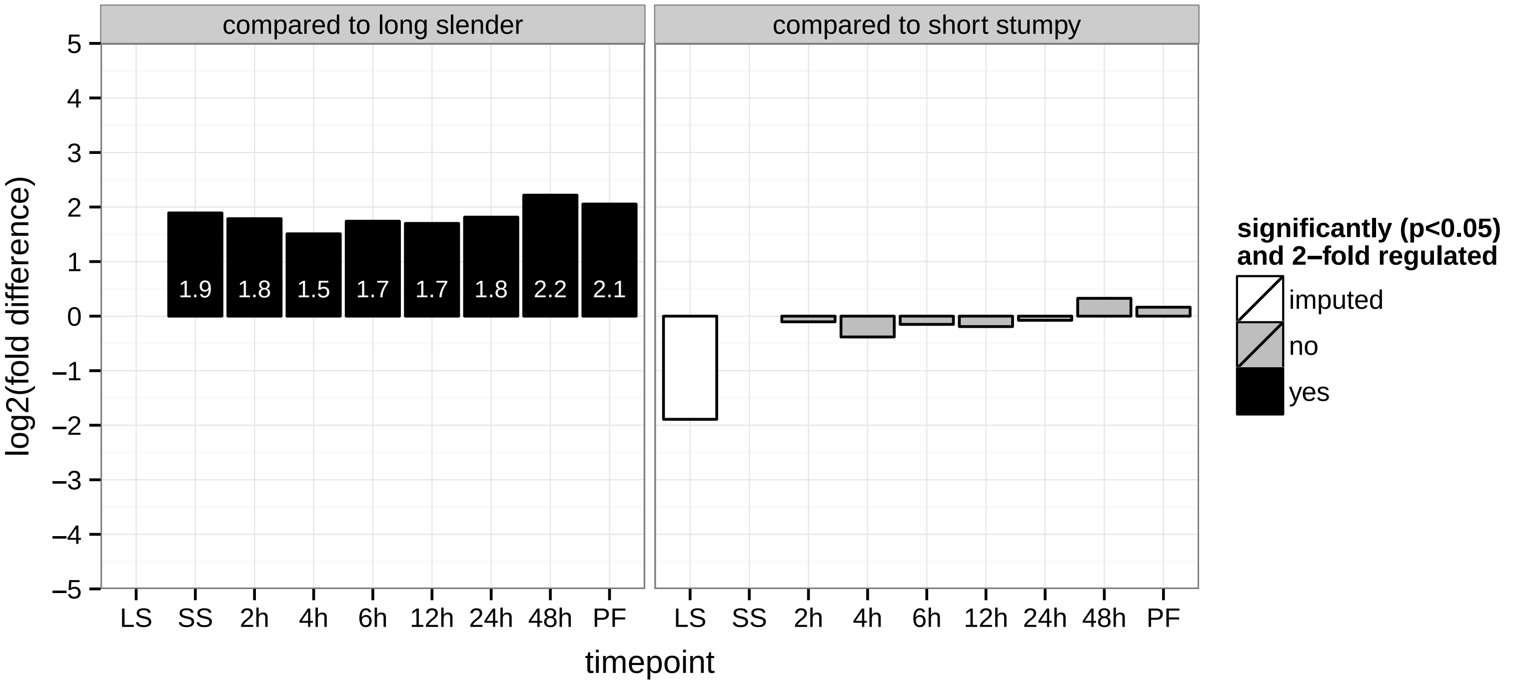
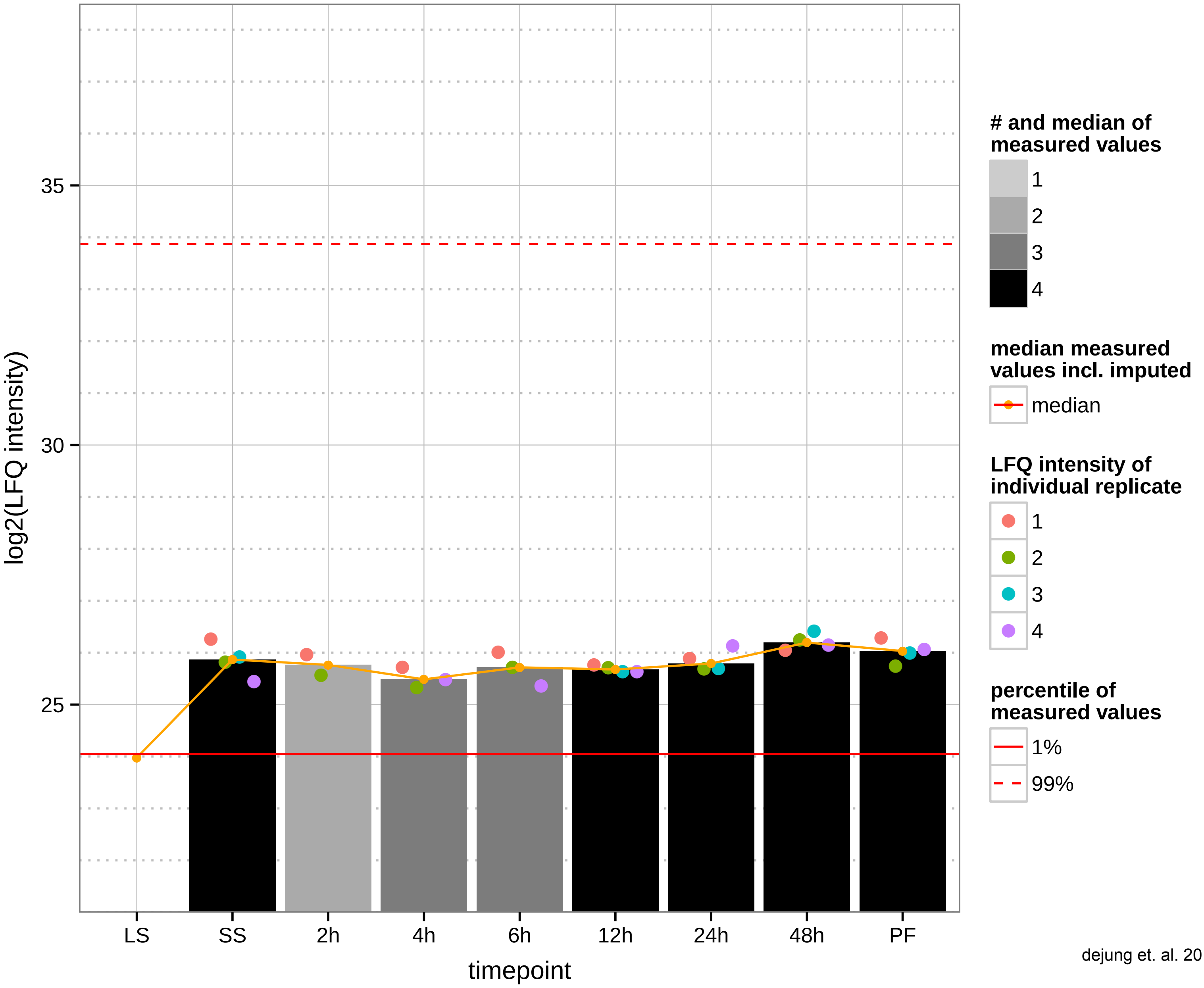
hypothetical protein, conserved
Tb927.10.5430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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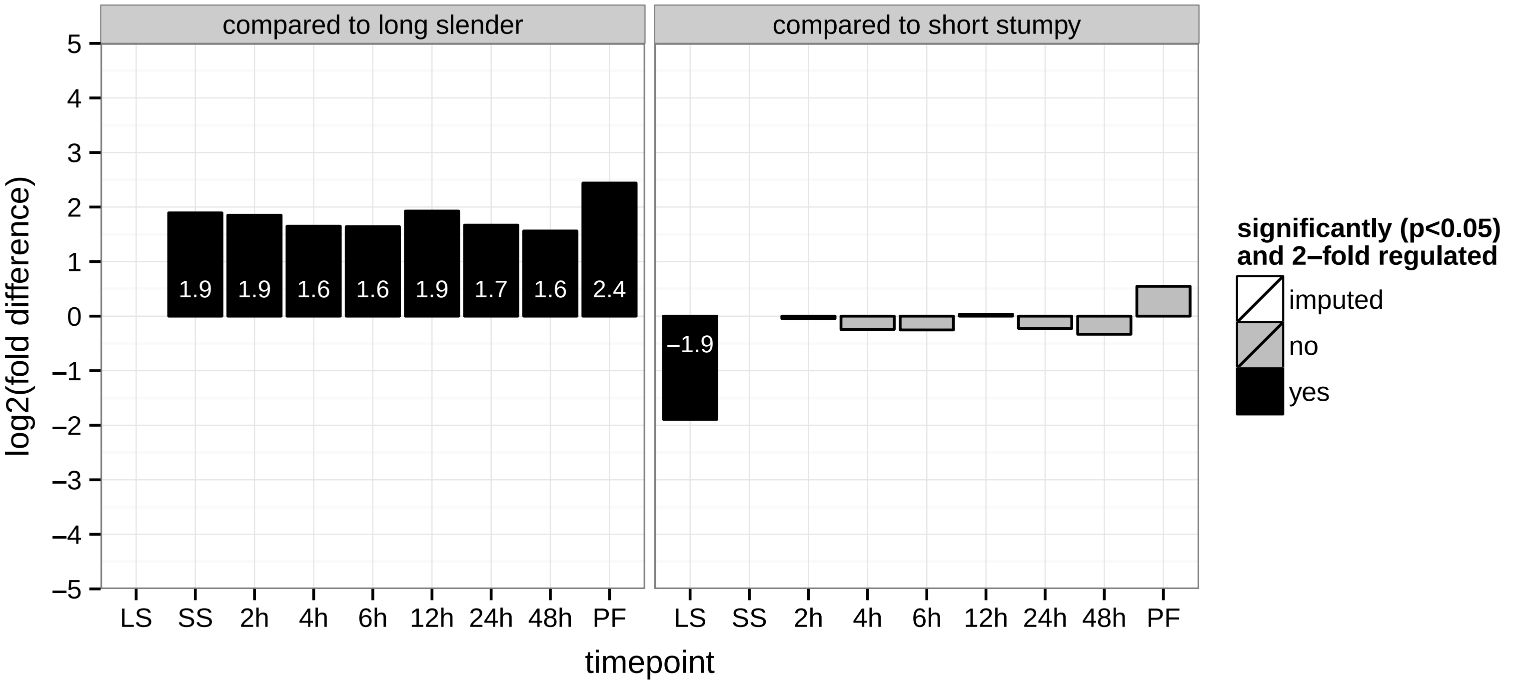
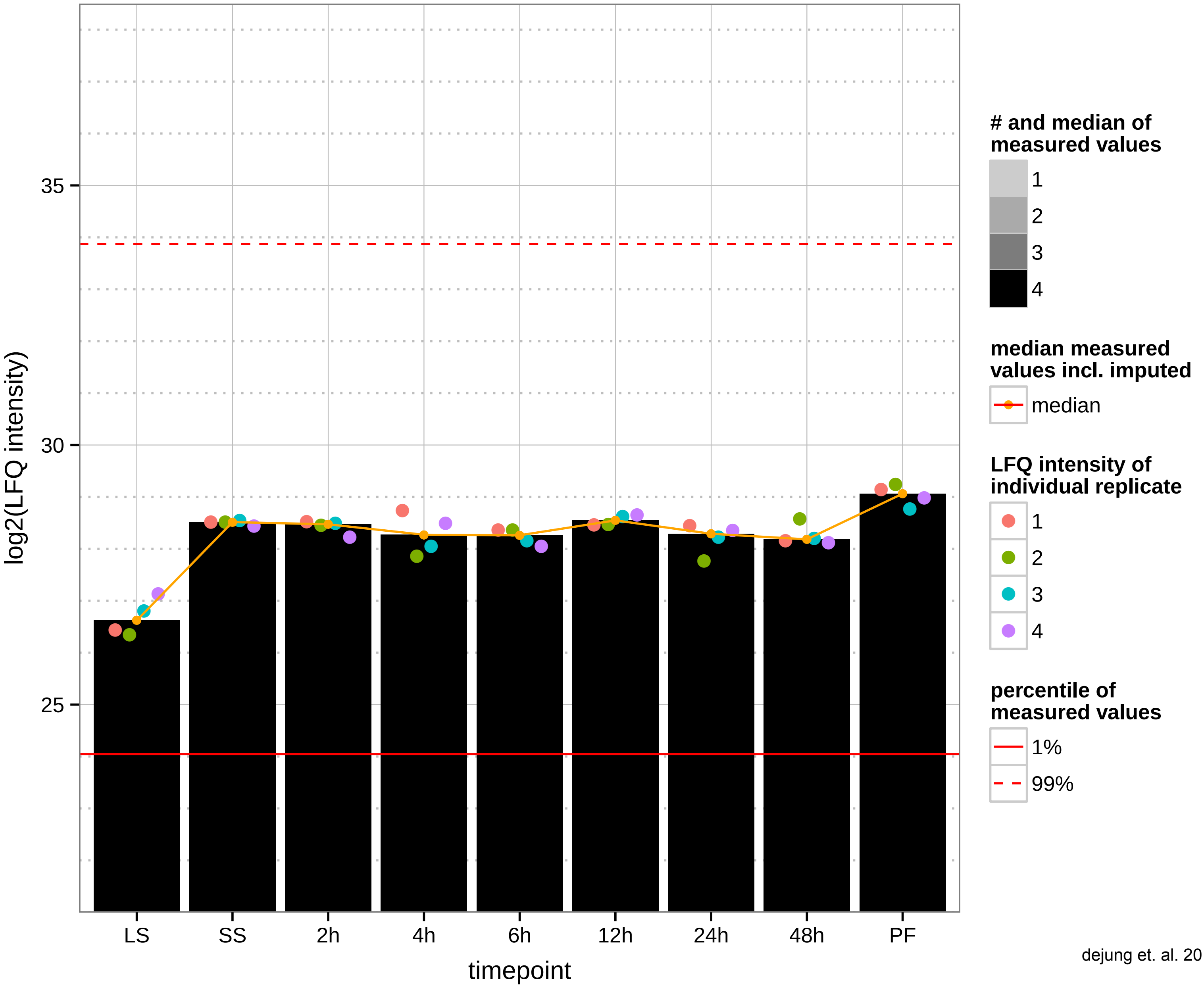
nucleoplasmin–like protein (NLP) (nlp)
Tb927.10.5450
AGOF: DNA binding
AGOC: nucleus
AGOP: chromatin remodeling, negative regulation of transcription, DNA–dependent, positive regulation of transcription, regula
PGOF: binding
PGOC: null
PGOP: null





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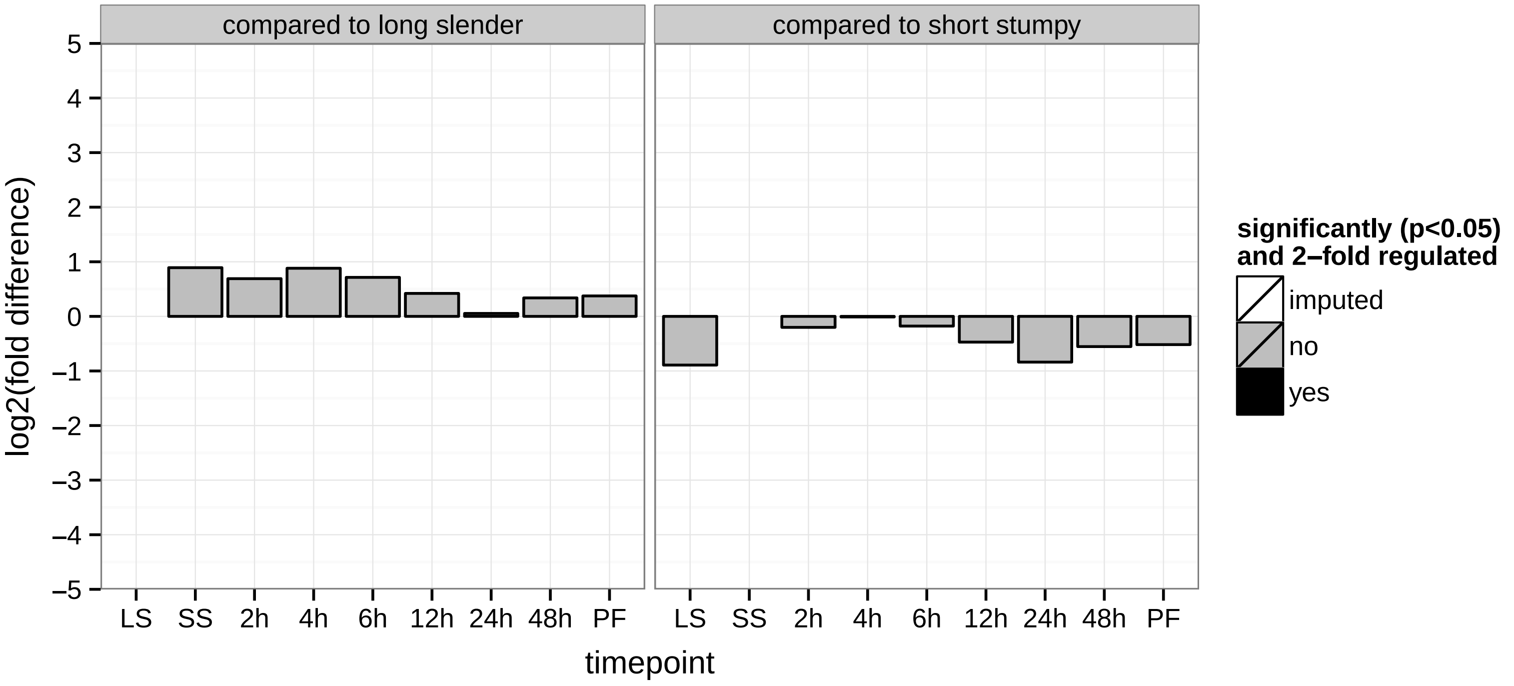
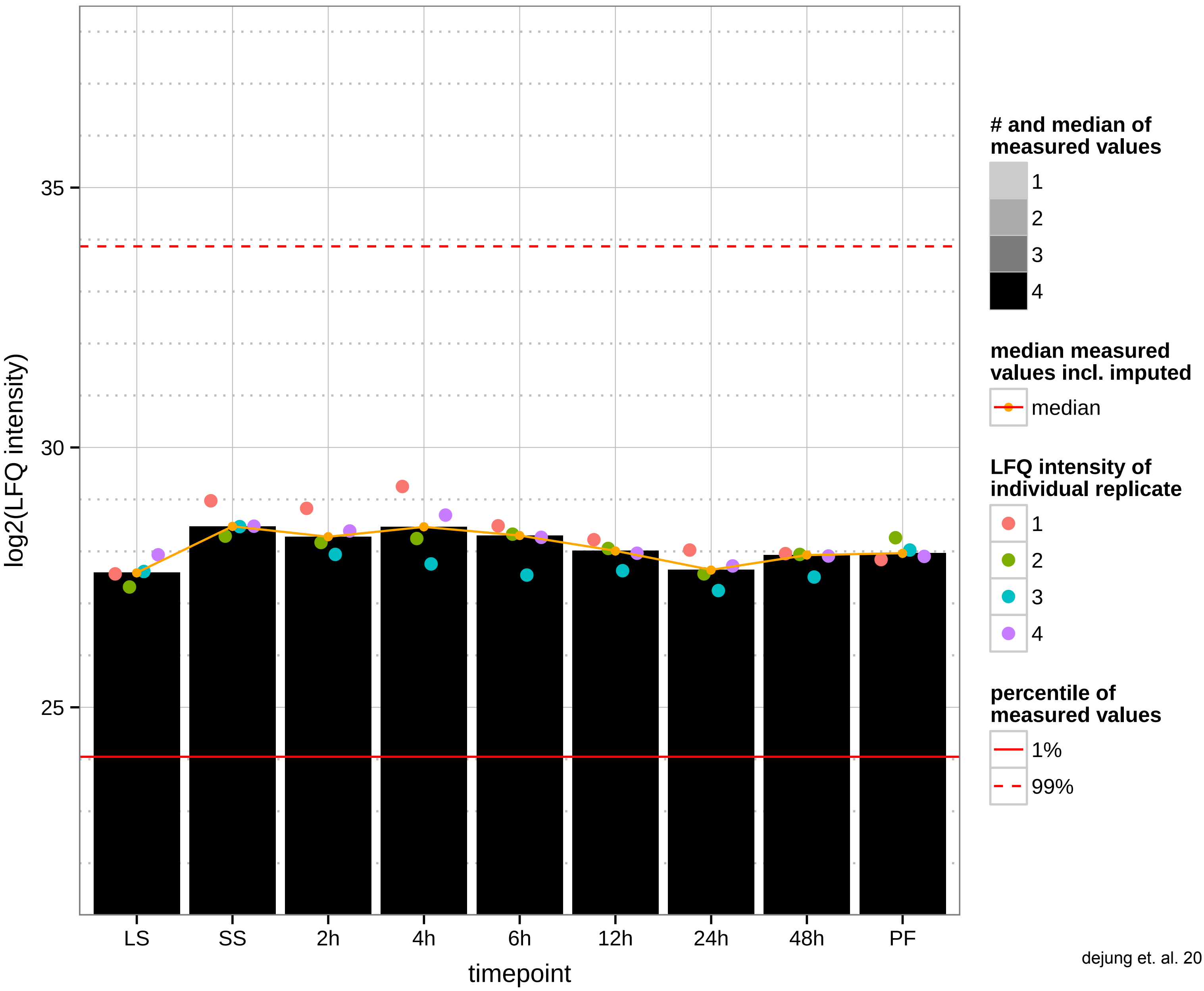
hypothetical protein, conserved
Tb927.10.5520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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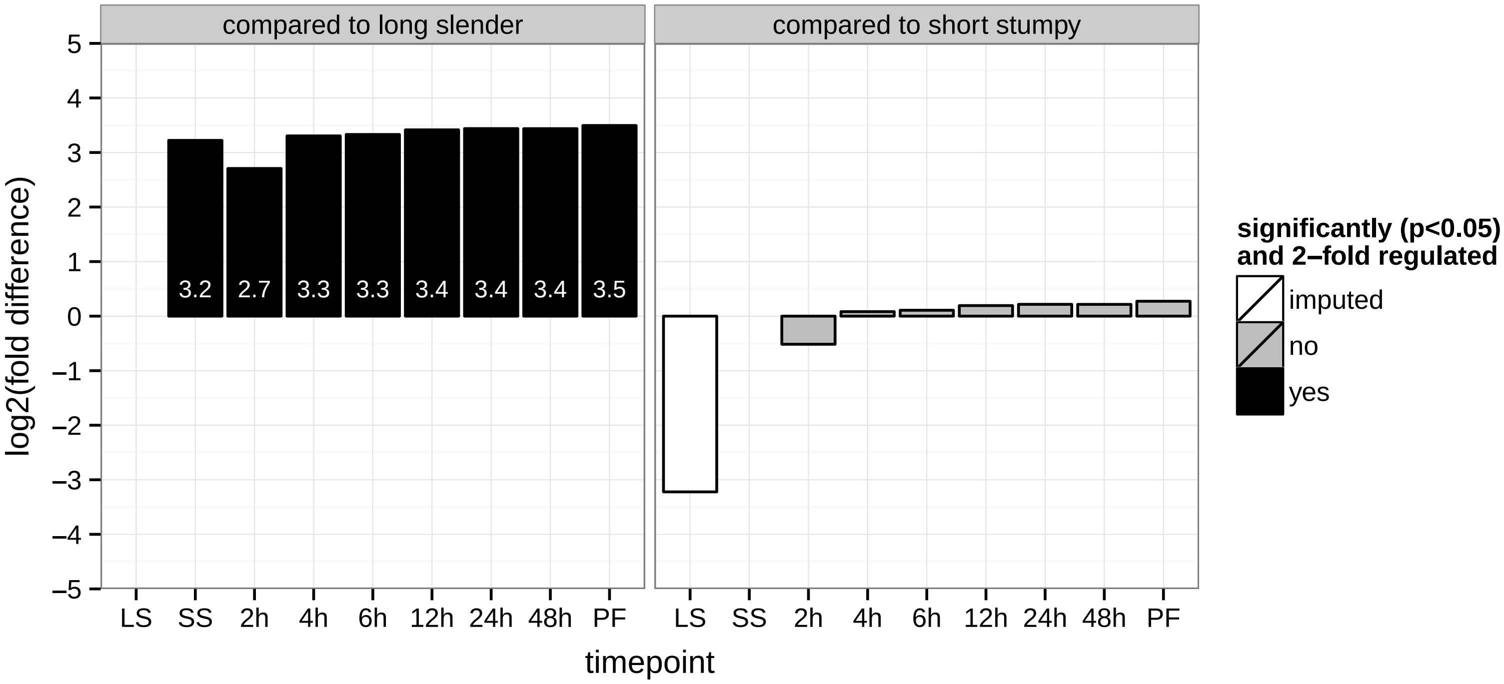
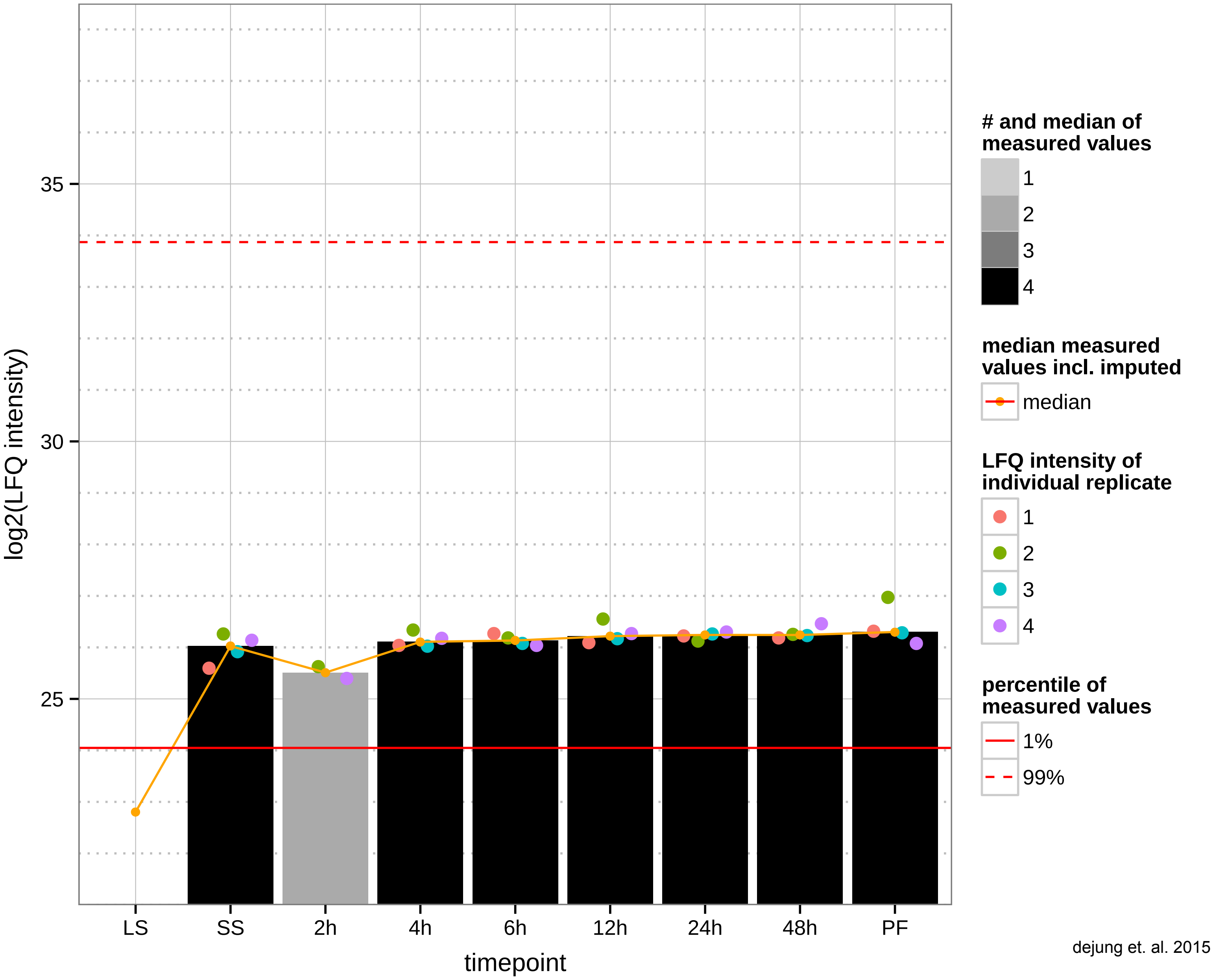
hypothetical protein, conserved
Tb927.10.5540
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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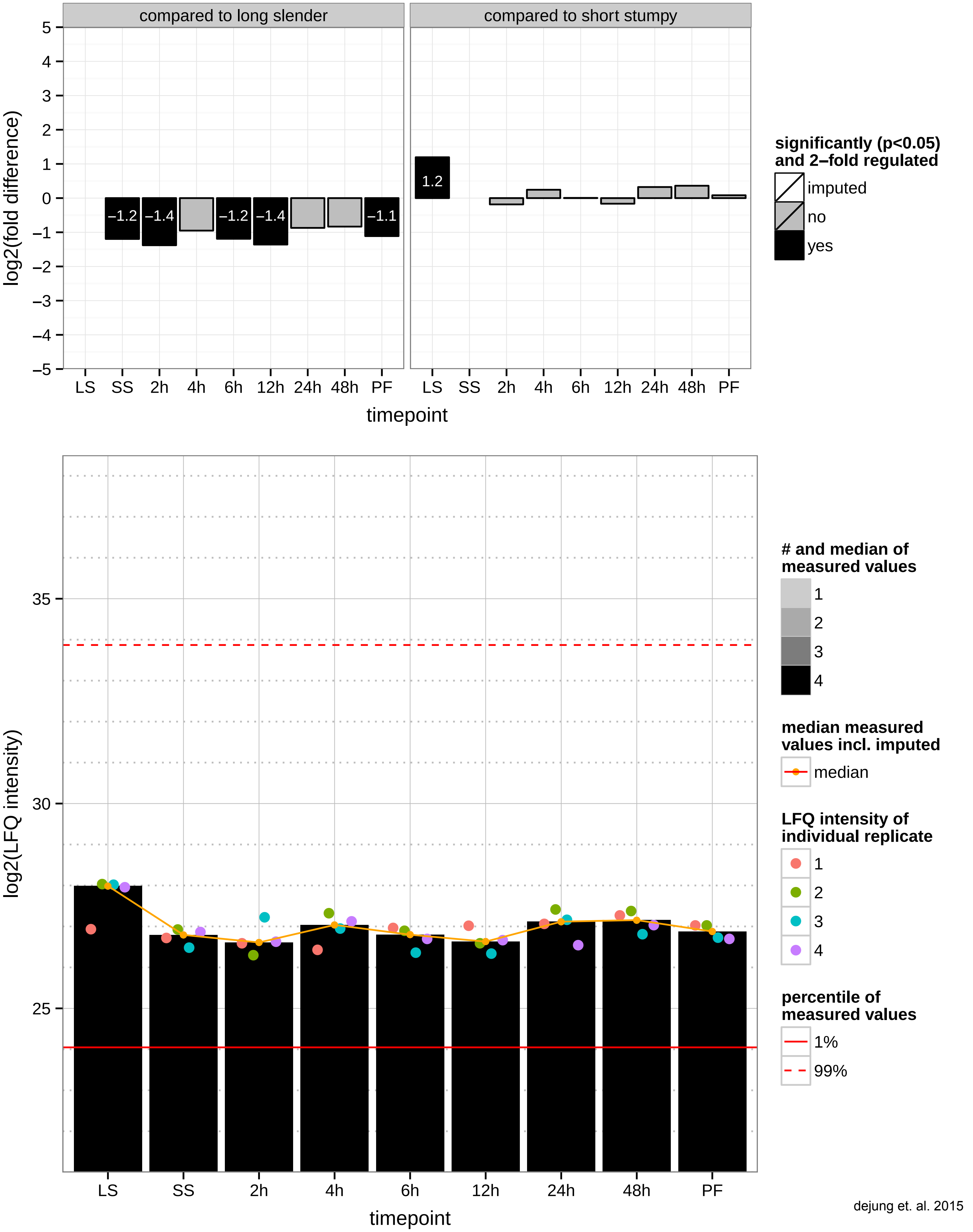
hypothetical protein, conserved
Tb927.10.5630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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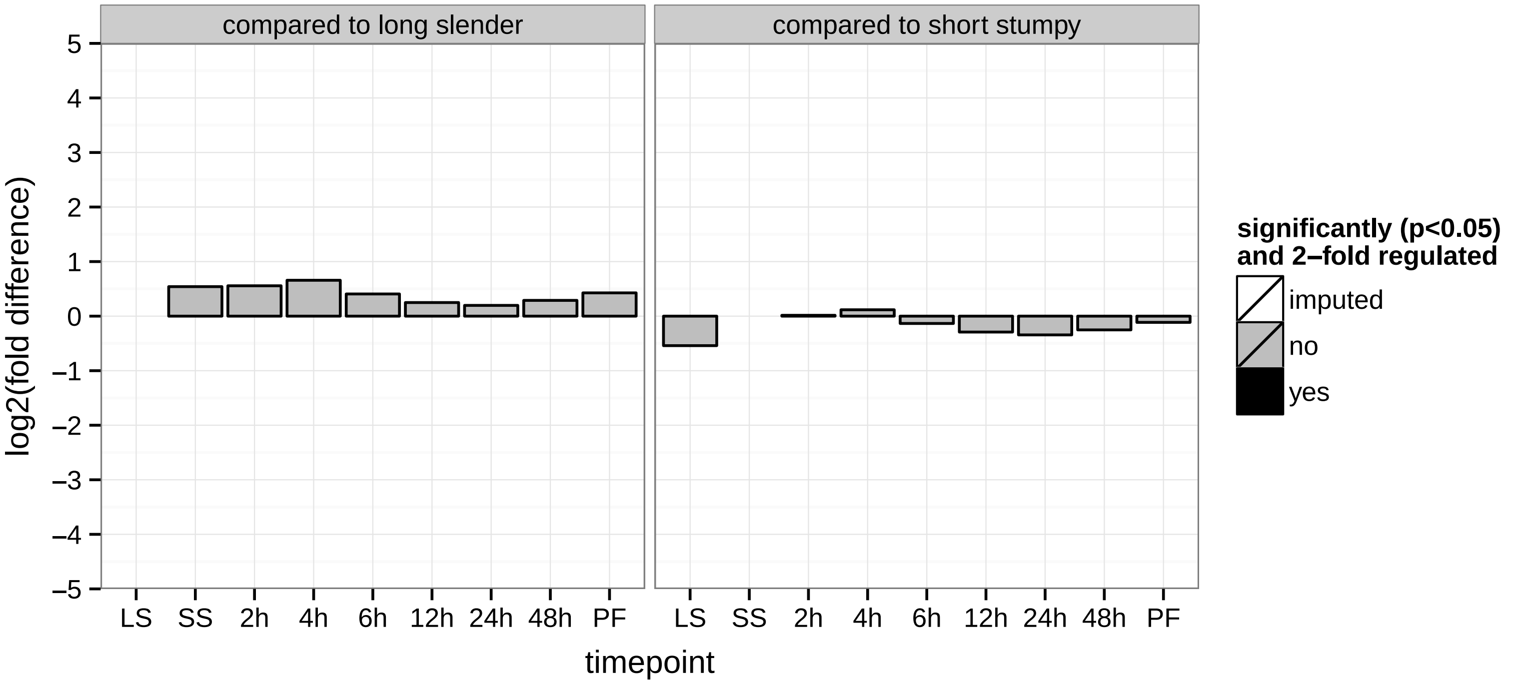
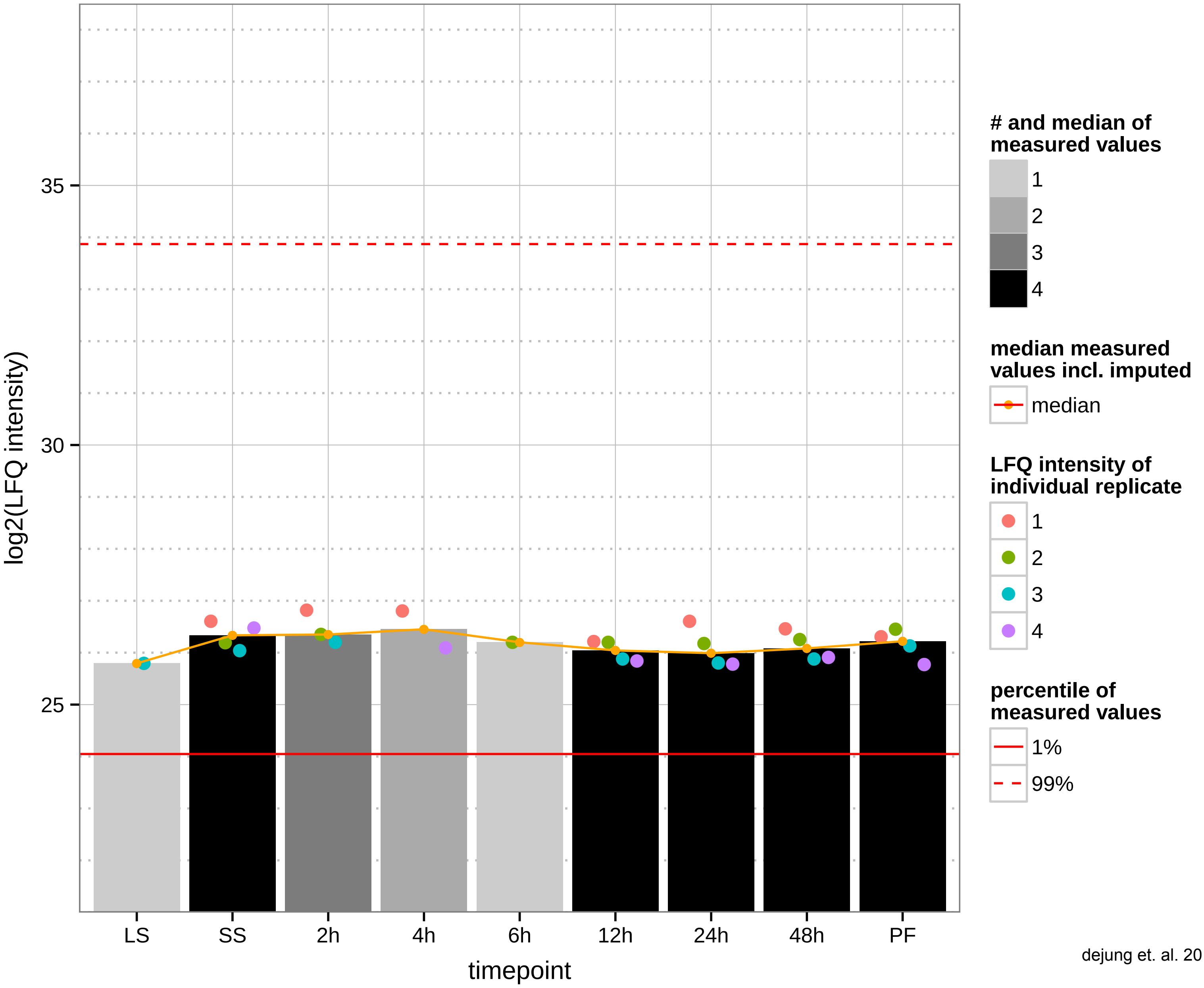
hypothetical protein, conserved
Tb927.10.5640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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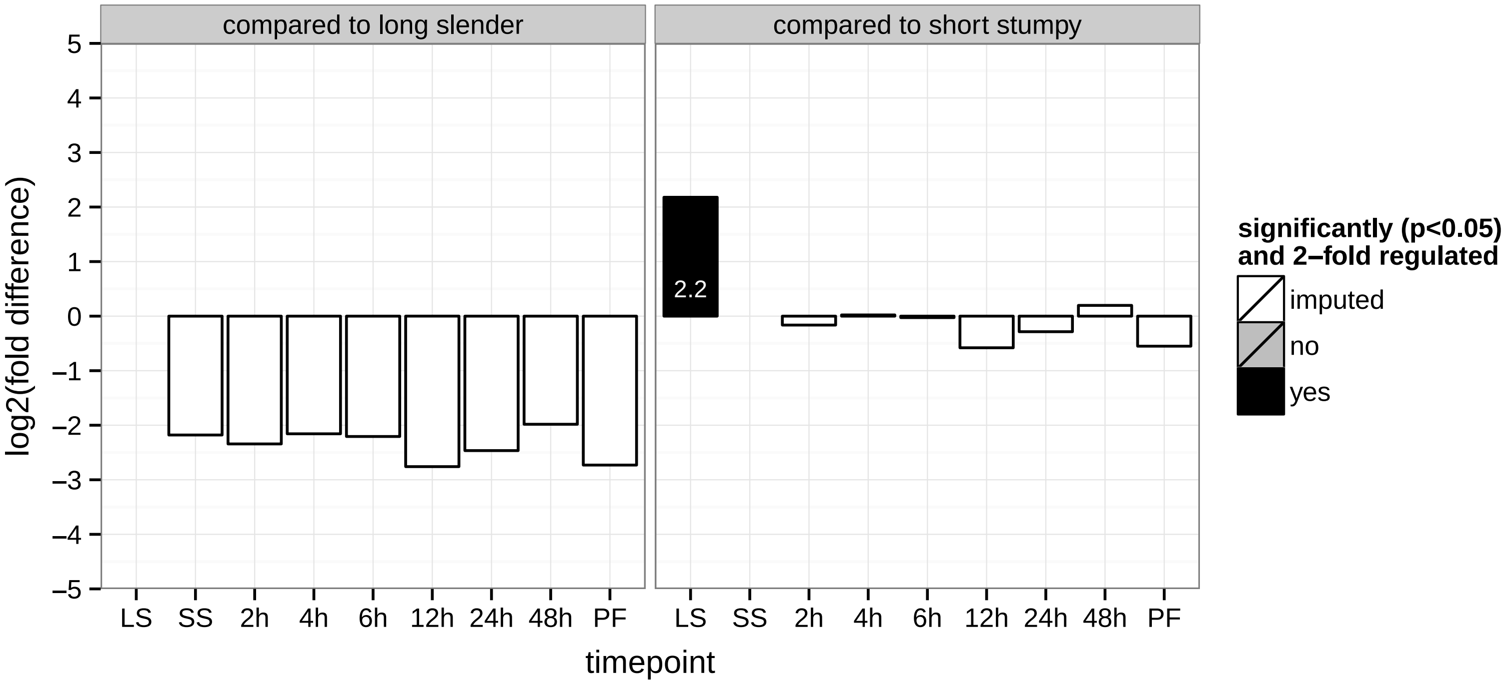
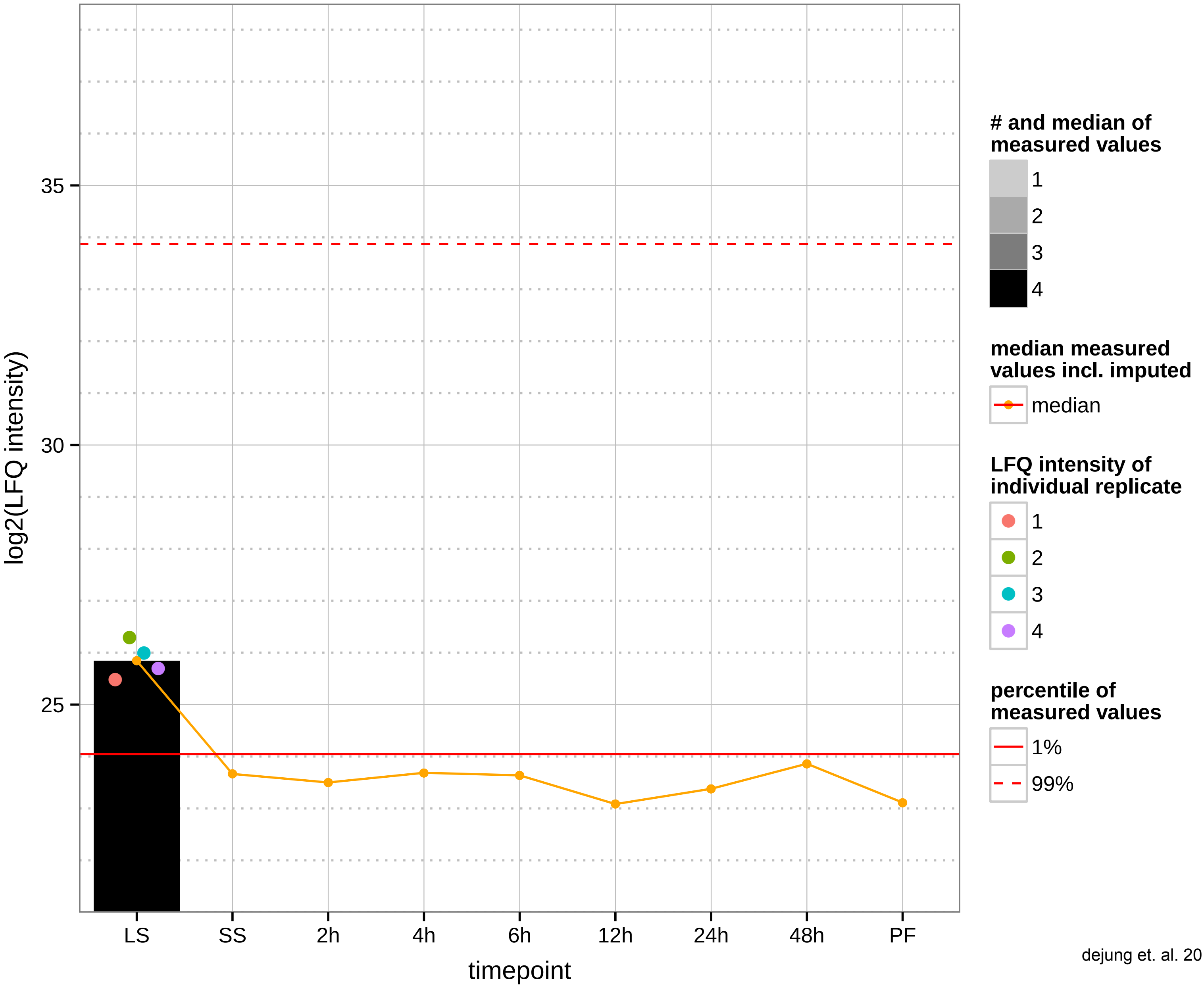
procyclin–associated gene 1 (PAG1) protein, putative
Tb927.10.5680
AGOF: null
AGOC: null
AGOP: evasion or tolerance of host immune response
PGOF: null
PGOC: null
PGOP: evasion or tolerance of host immune response





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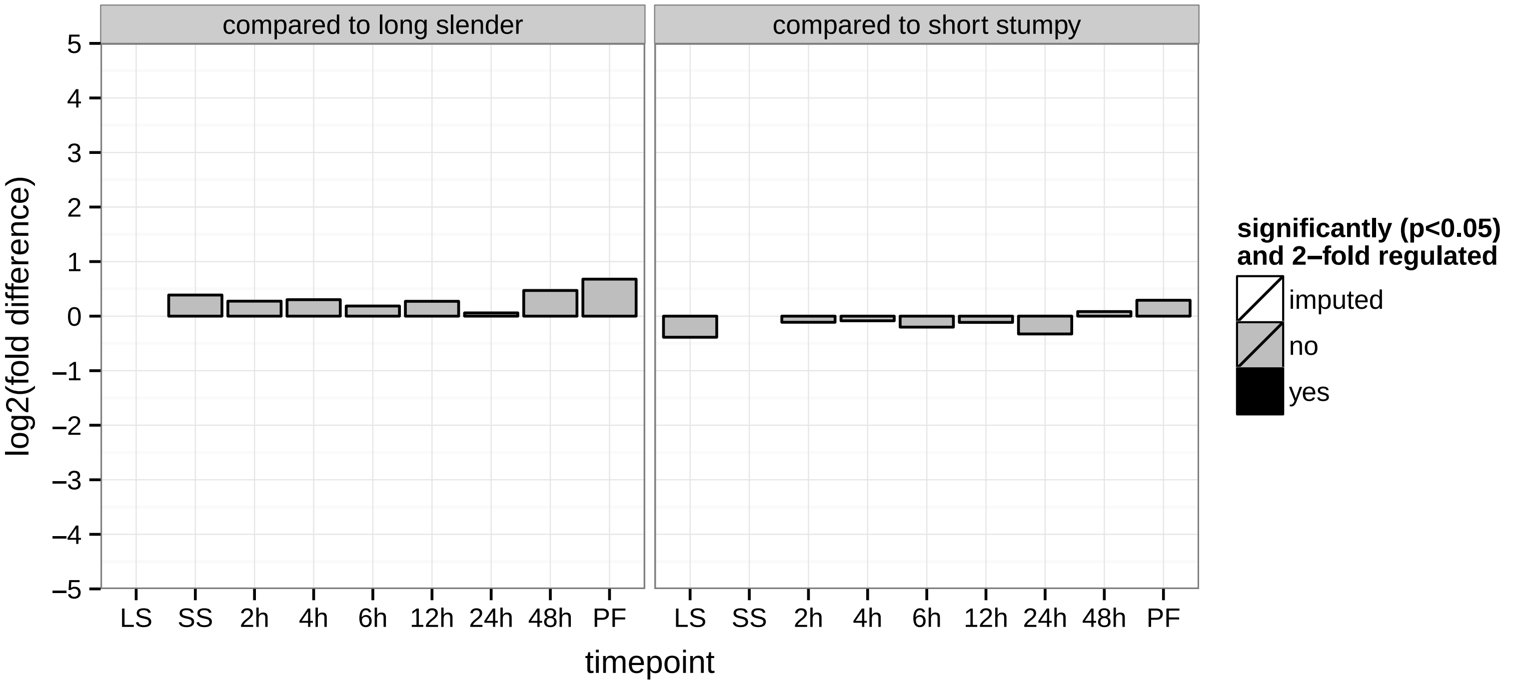
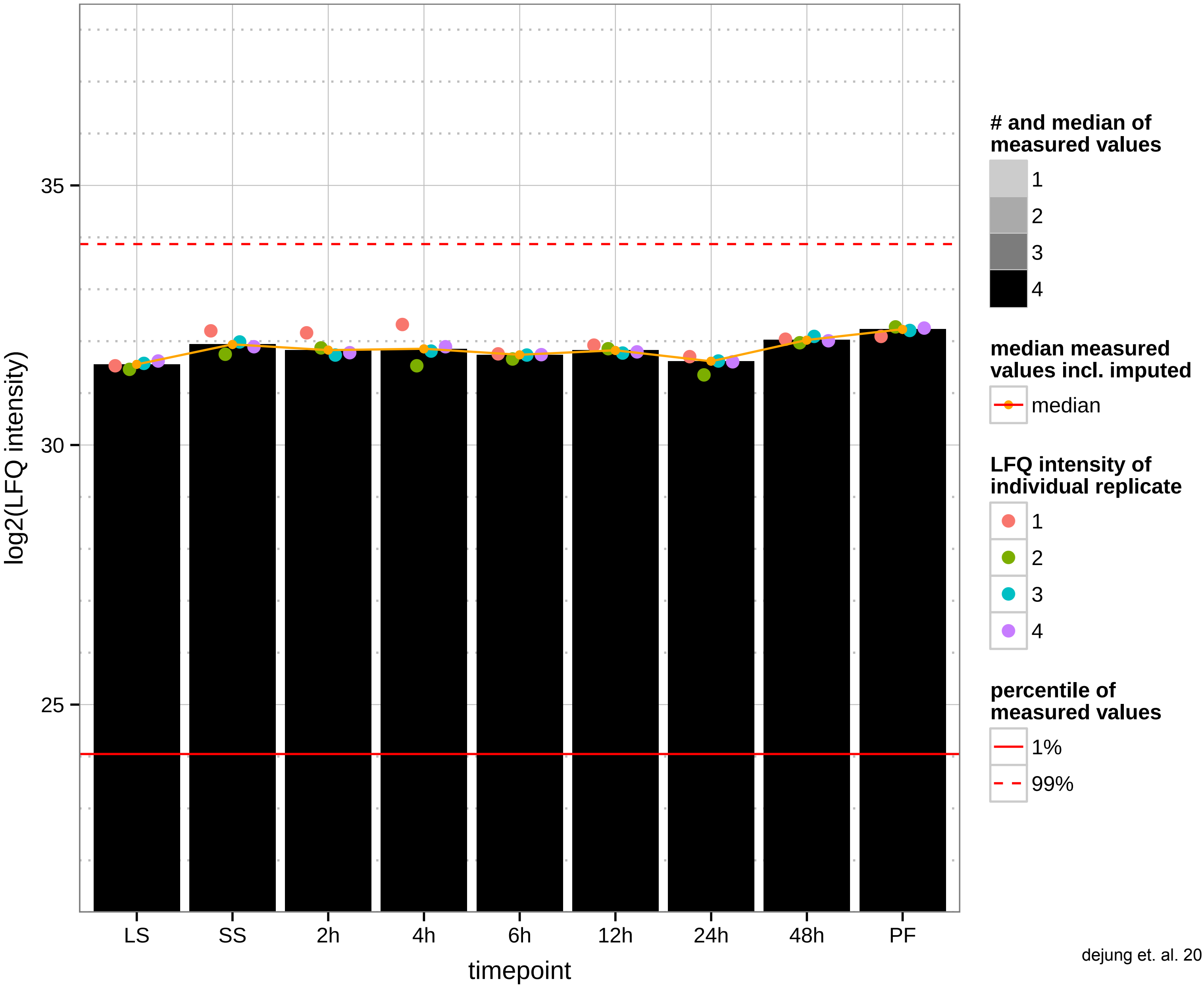
valosin–containing protein homolog, Transitional endoplasmic reticulum ATPase, putative (VCP)
Tb927.10.5770
AGOF: ATP binding, ATPase activity
AGOC: cytoplasm, membrane
AGOP: biological_process
PGOF: ATP binding, hydrolase activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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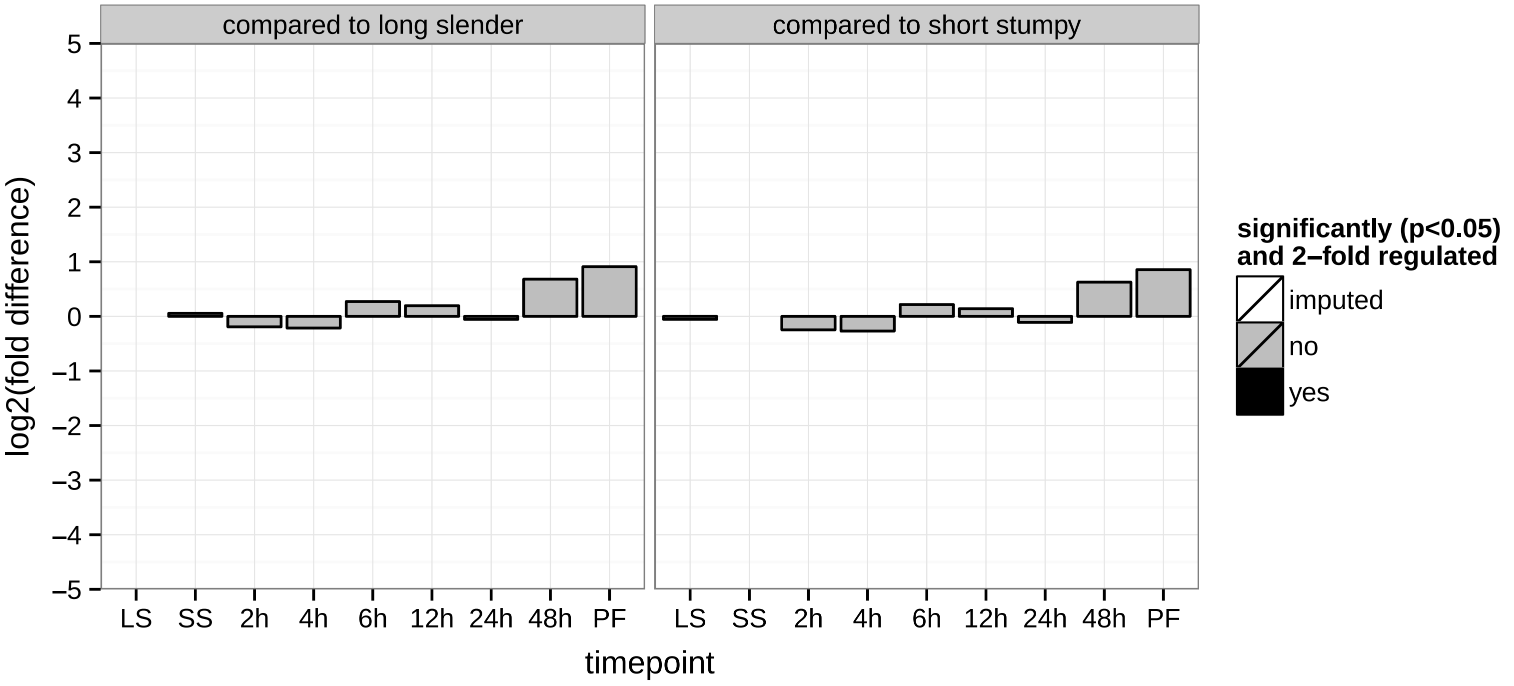
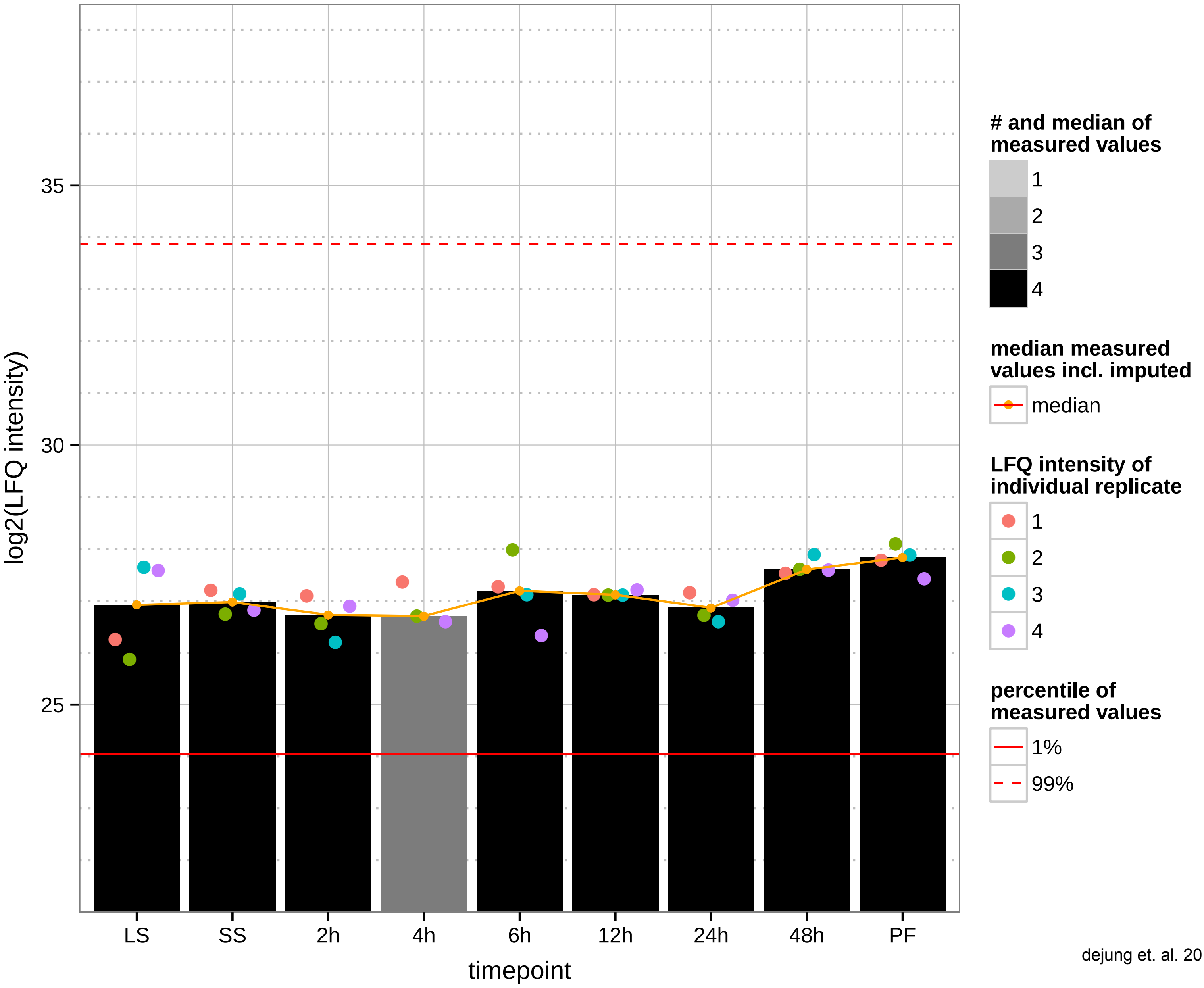
hypothetical protein, conserved
Tb927.10.5790
AGOF: catalytic activity
AGOC: null
AGOP: null
PGOF: binding, catalytic activity, protein binding
PGOC: null
PGOP: null





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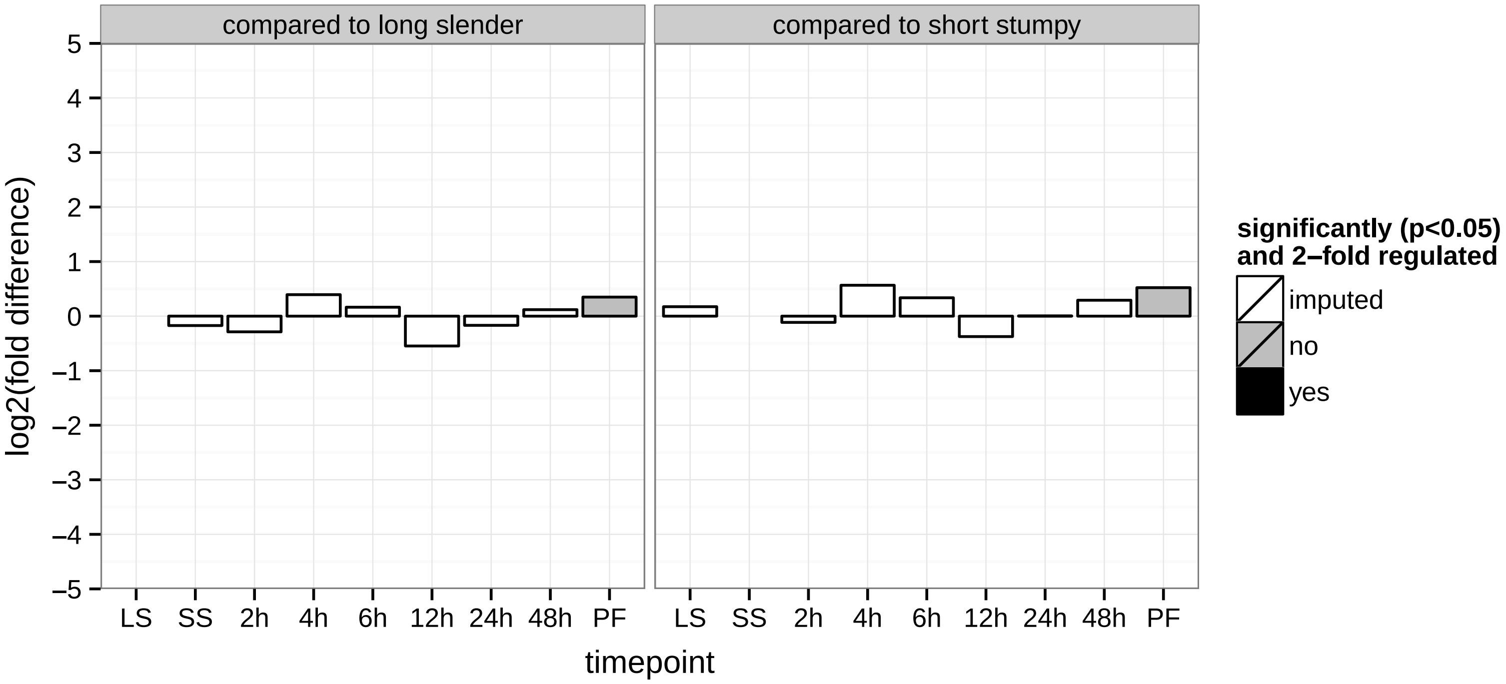
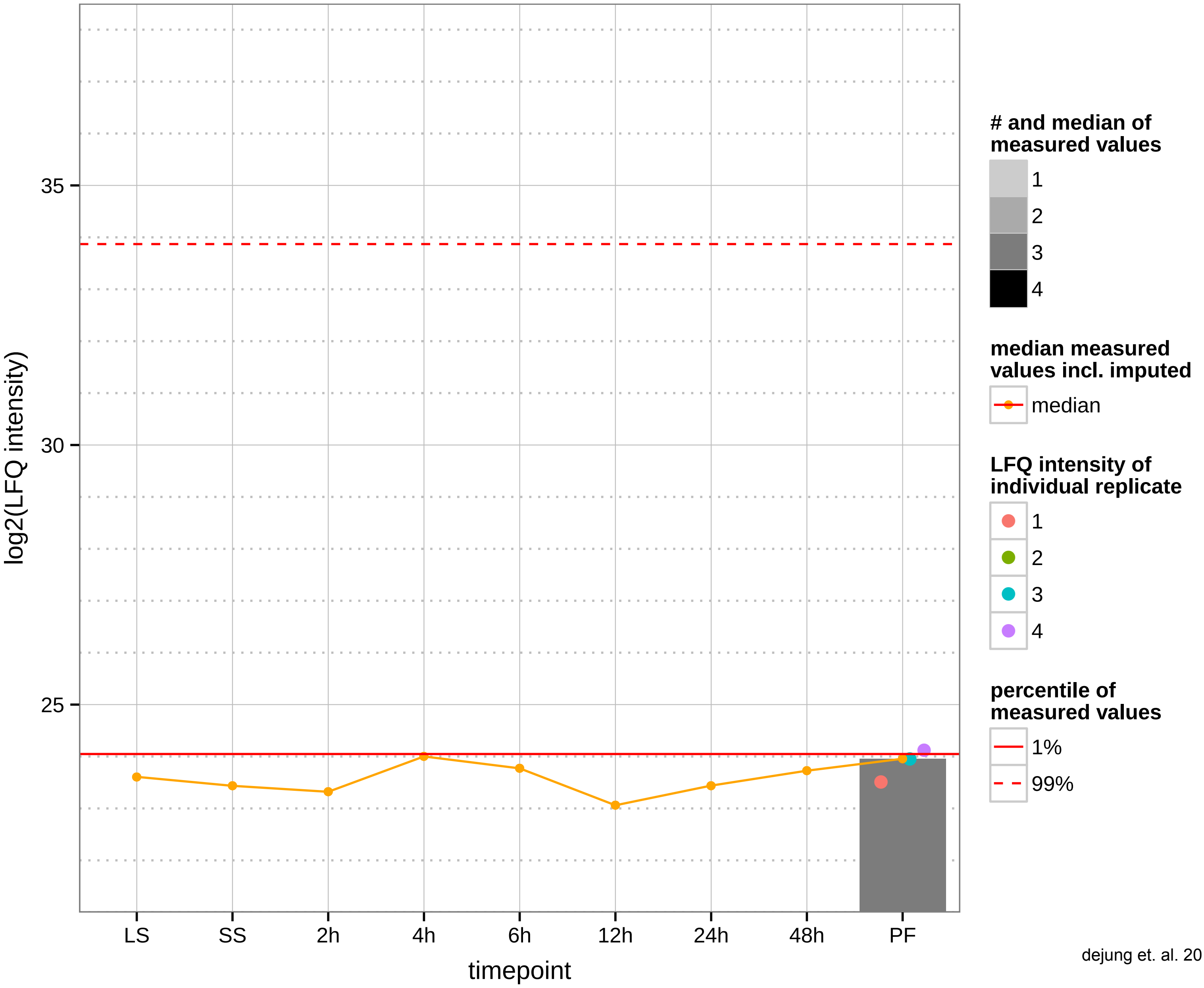
hypothetical protein, conserved
Tb927.10.5830
AGOF: zinc ion binding
AGOC: intracellular
AGOP: null
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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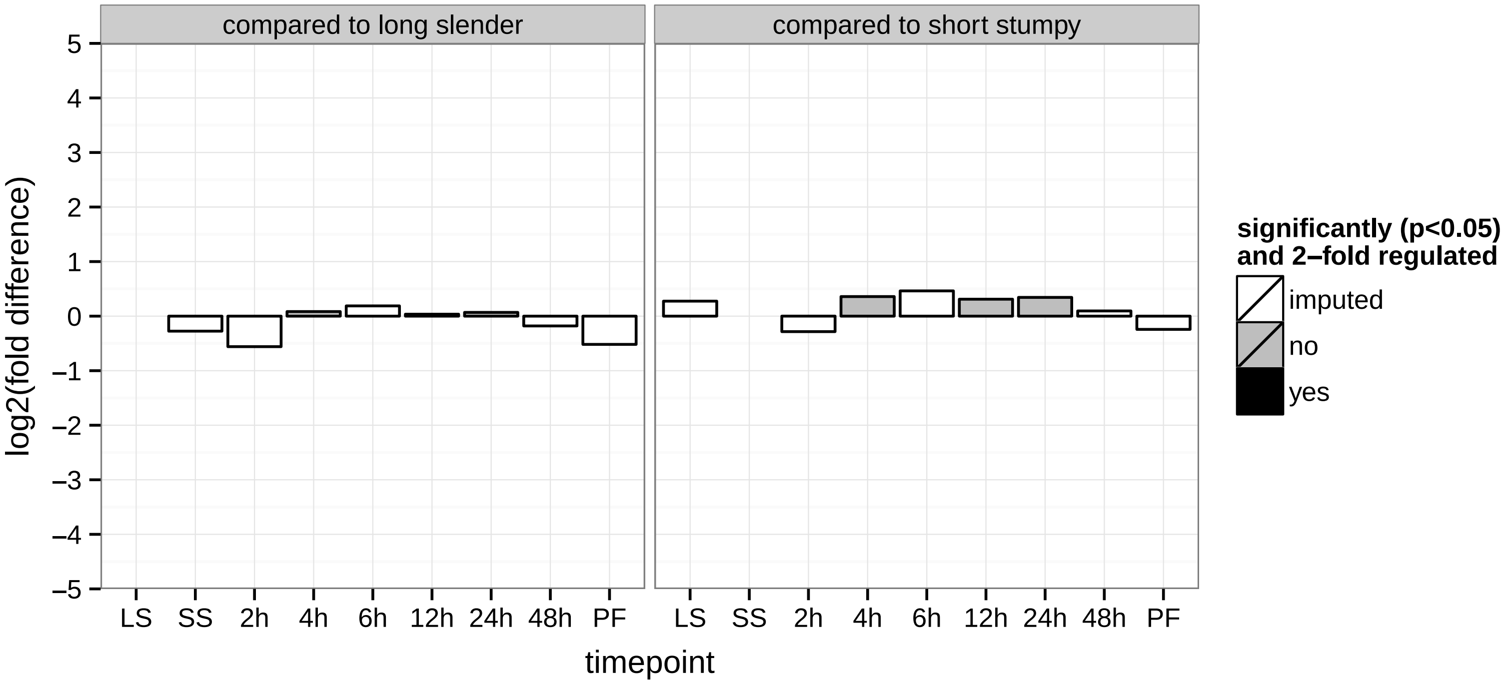
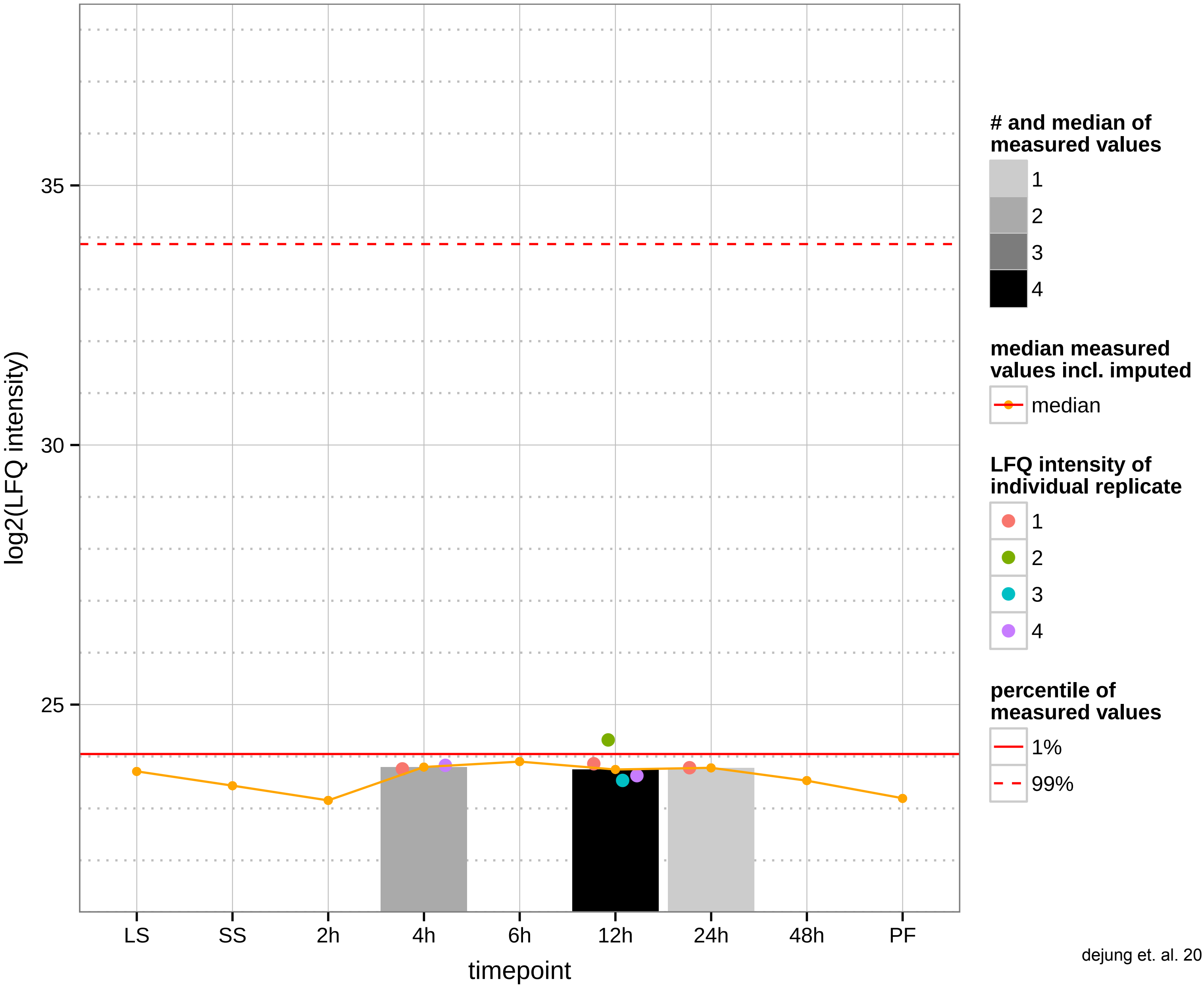
hypothetical protein, conserved
Tb927.10.5900
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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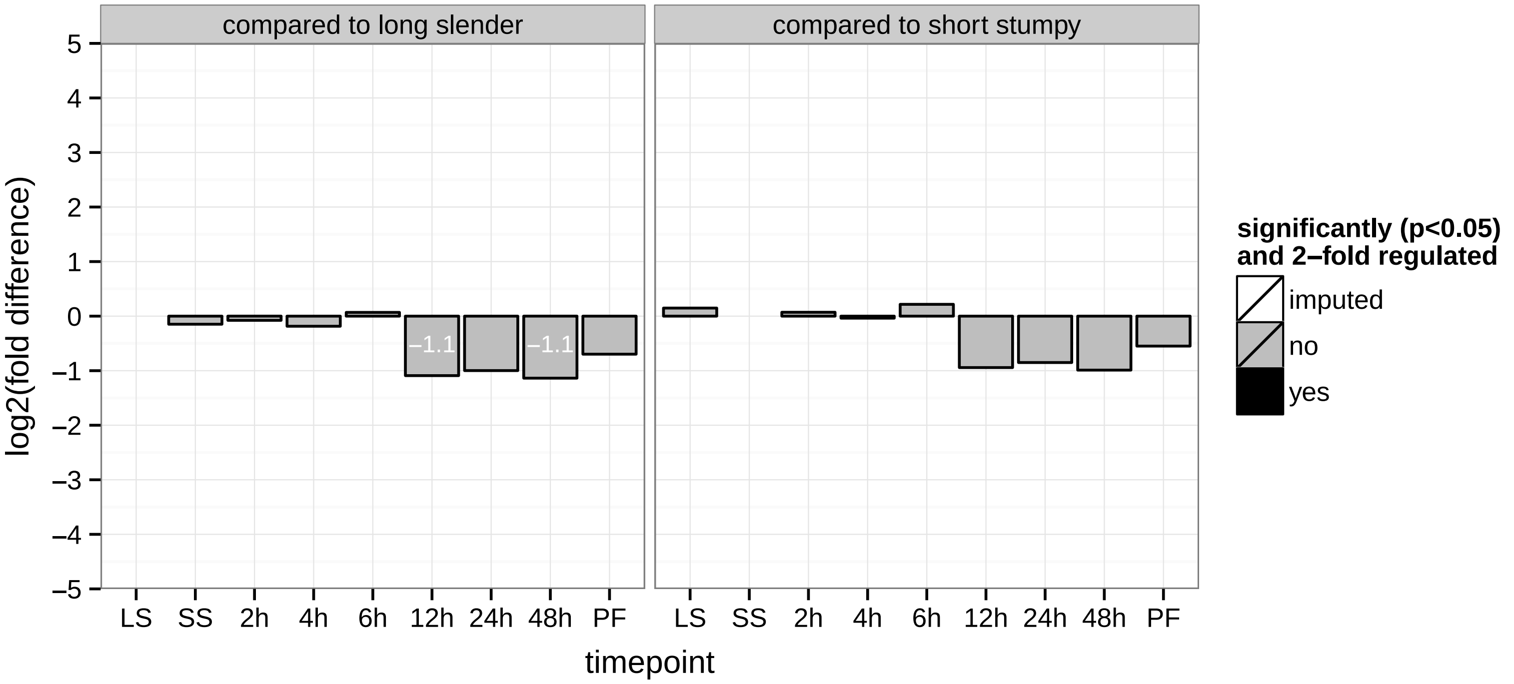
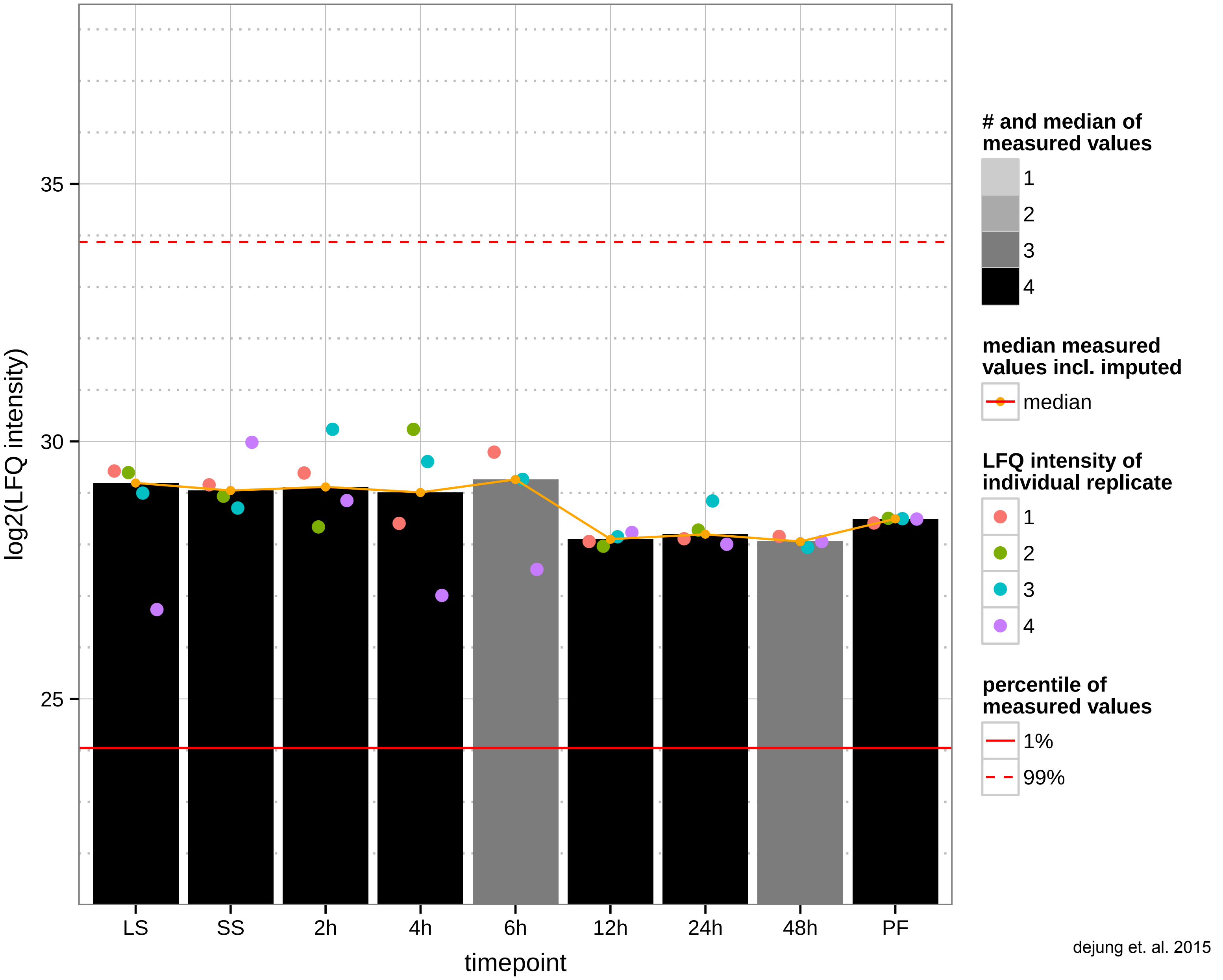
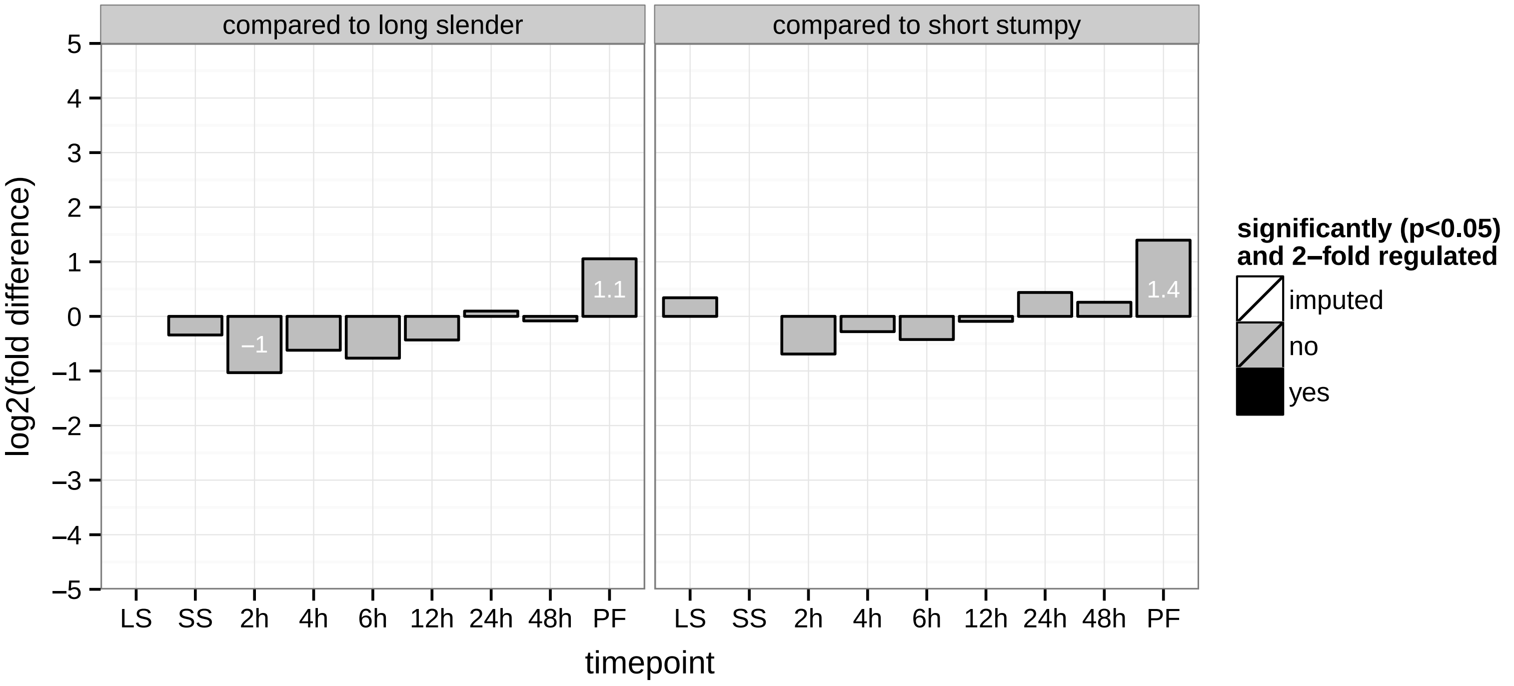
leucine−rich repeat protein (LRRP), putative
Tb927.10.5980
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

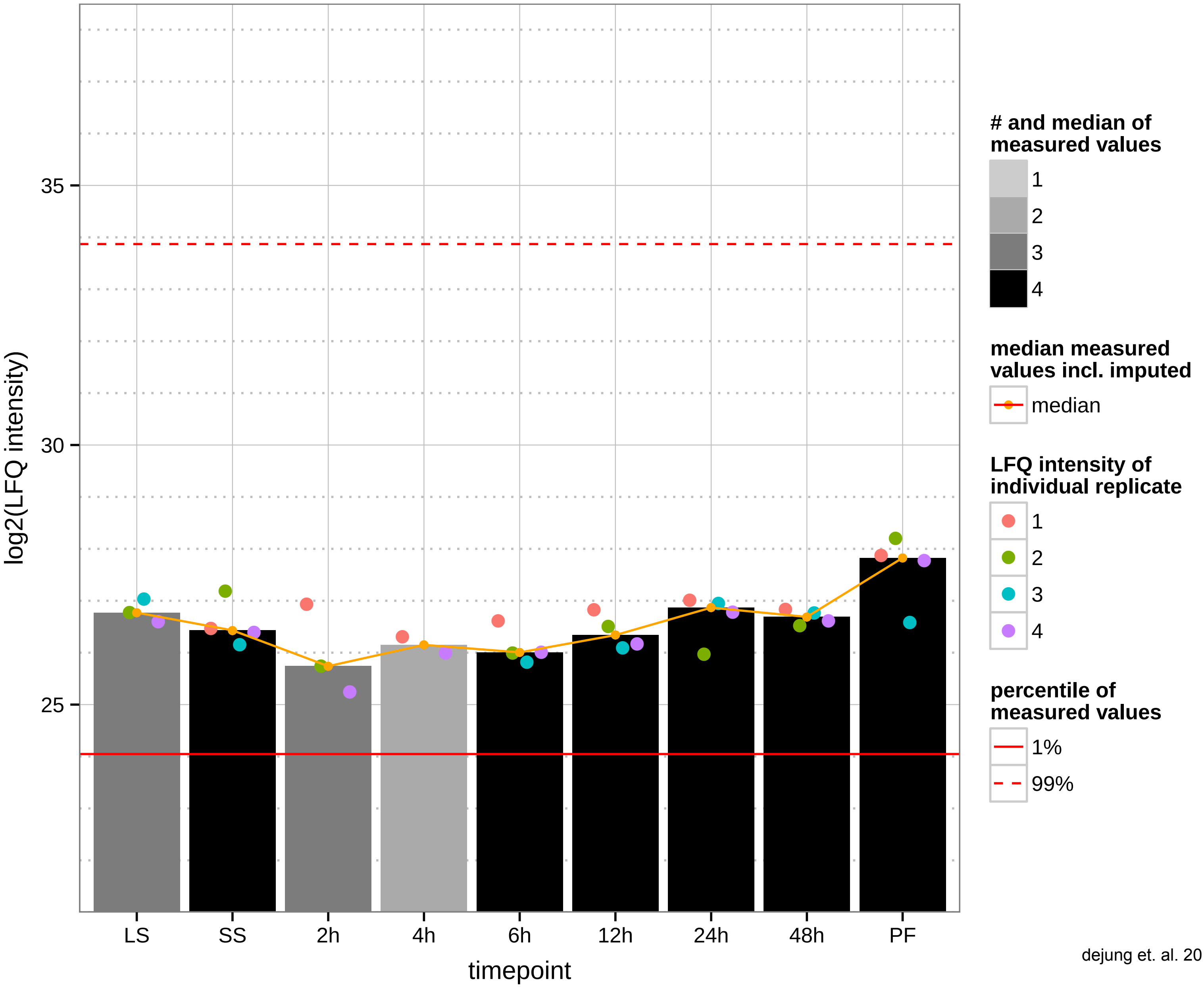




dejung et. al. 2015

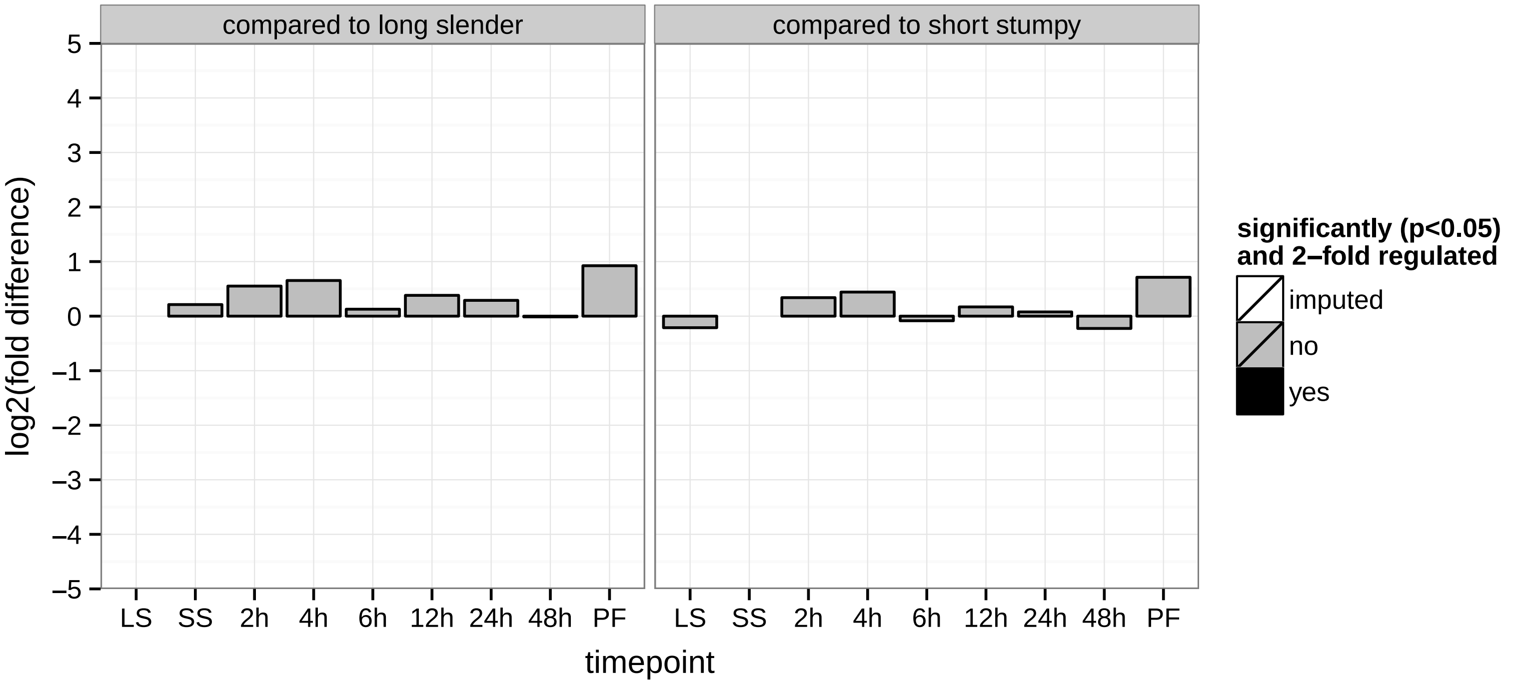
hypothetical protein, conserved
Tb927.10.6010
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

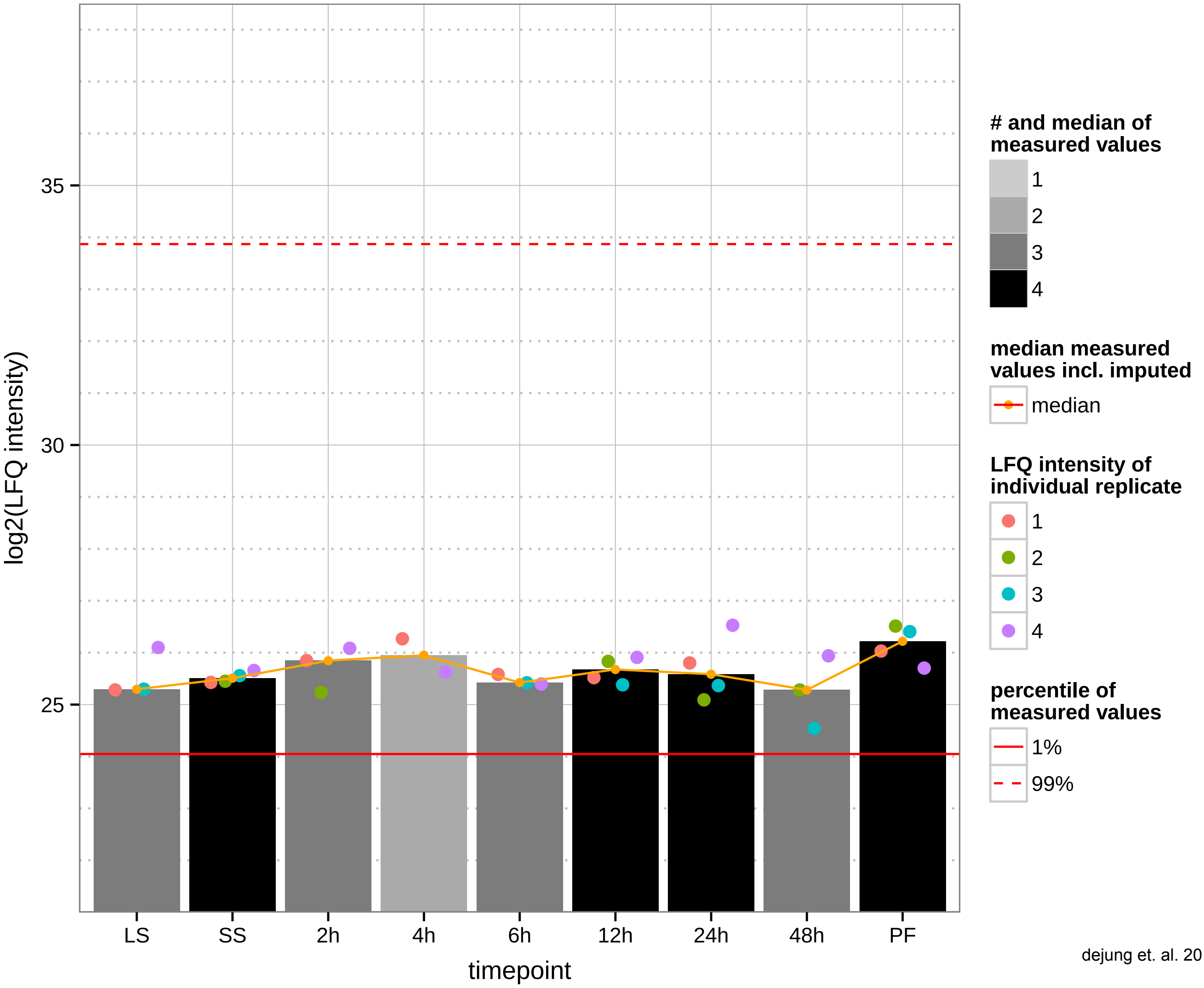




dejung et. al. 2015

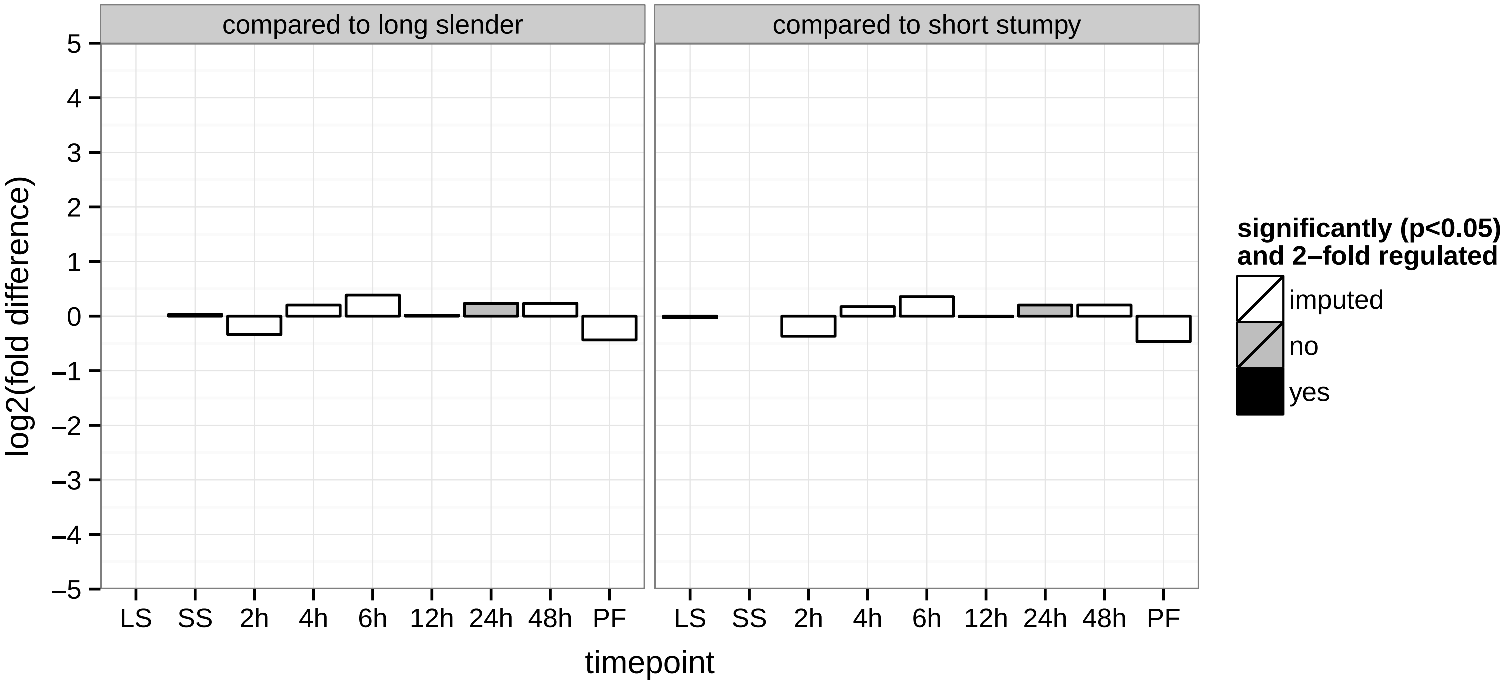
hypothetical protein, conserved
Tb927.10.6160
AGOF: null
AGOC: cis–Golgi network, membrane
AGOP: intracellular protein transport
PGOF: null
PGOC: cis–Golgi network, membrane
PGOP: intracellular protein transport

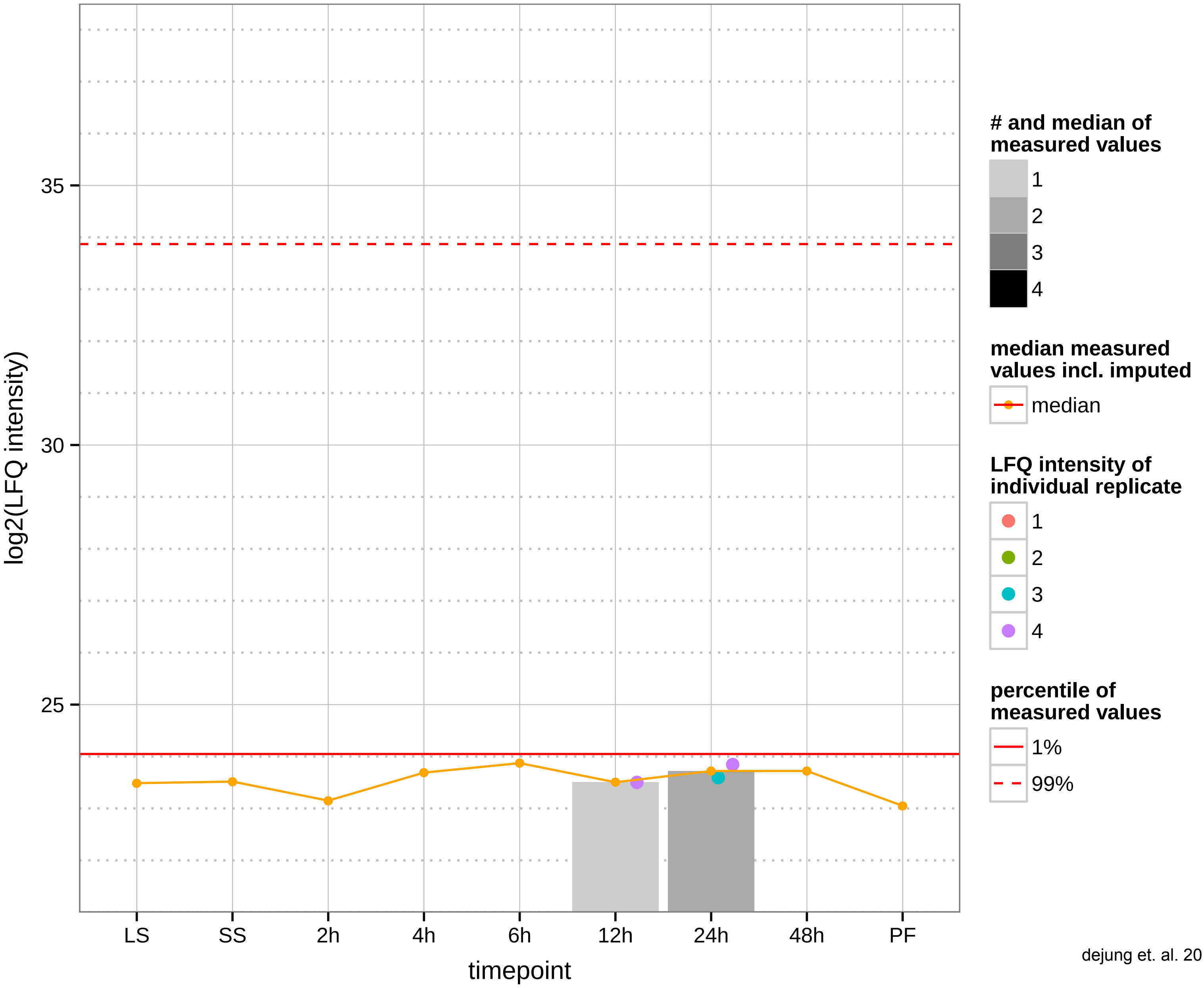




dejung et. al. 2015

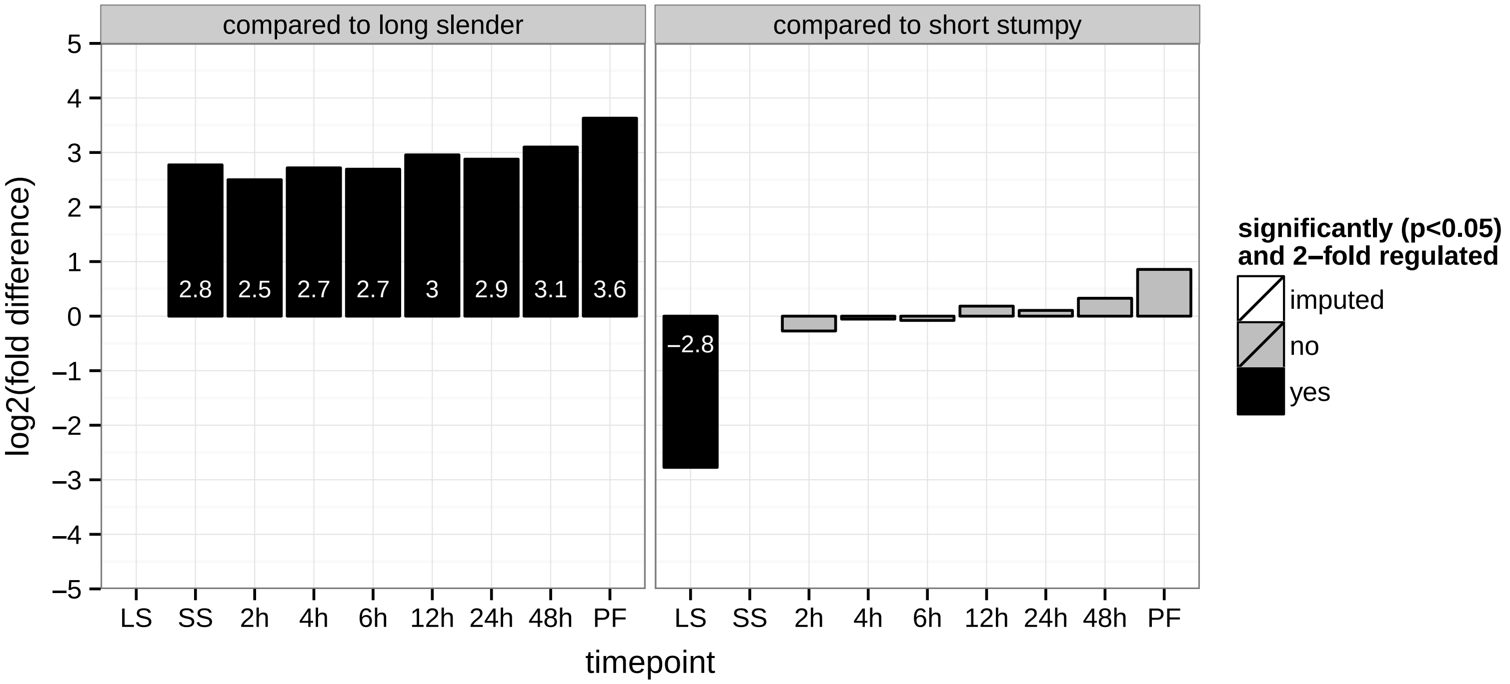
hypothetical protein, conserved
Tb927.10.6170
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

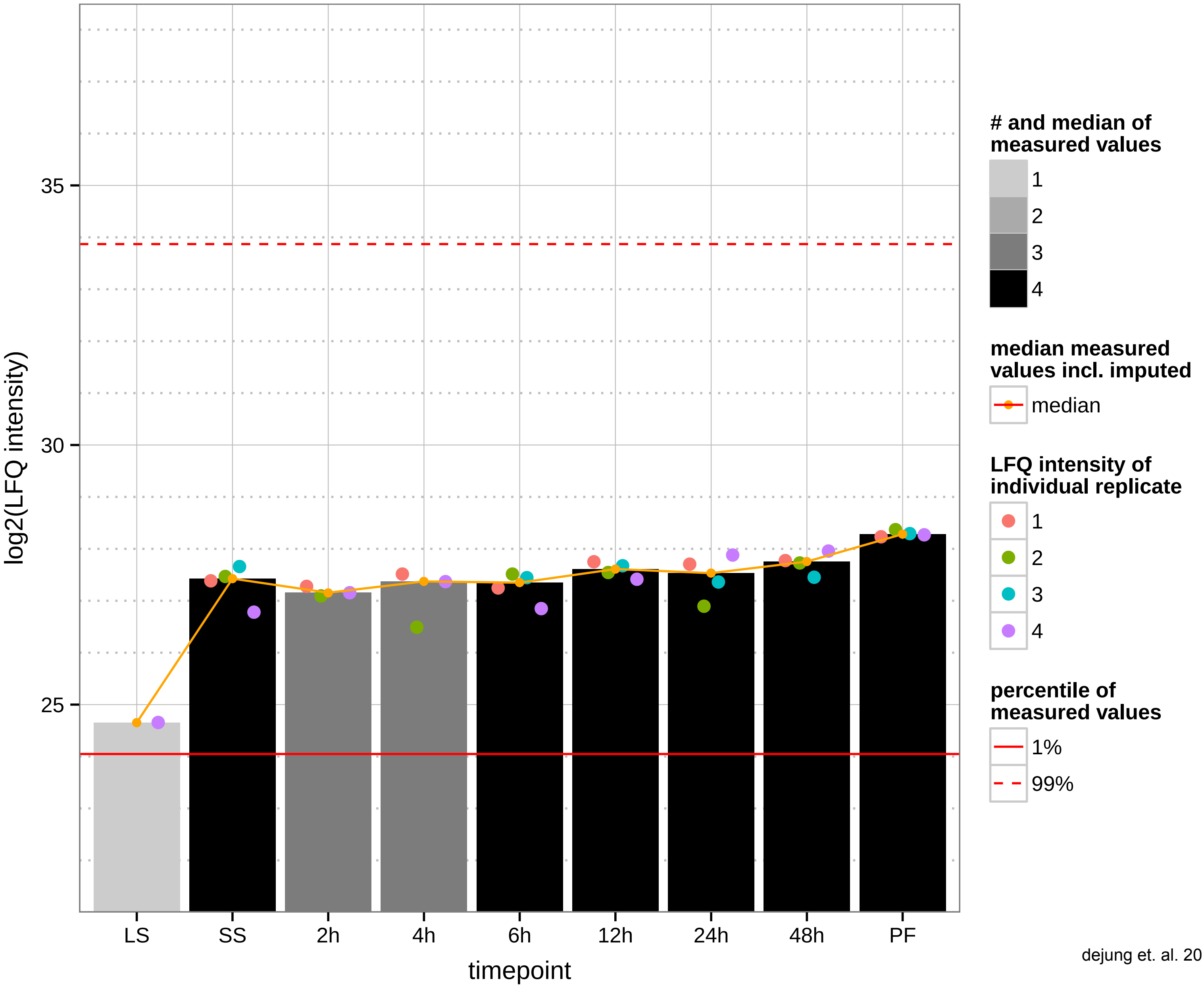




dejung et. al. 2015

5'–3' exoribonuclease 2, putative (XRND)
Tb927.10.6220
AGOF: exonuclease activity, nucleic acid binding
AGOC: intracellular, nucleus
AGOP: RNA processing
PGOF: exonuclease activity, nucleic acid binding
PGOC: intracellular
PGOP: null





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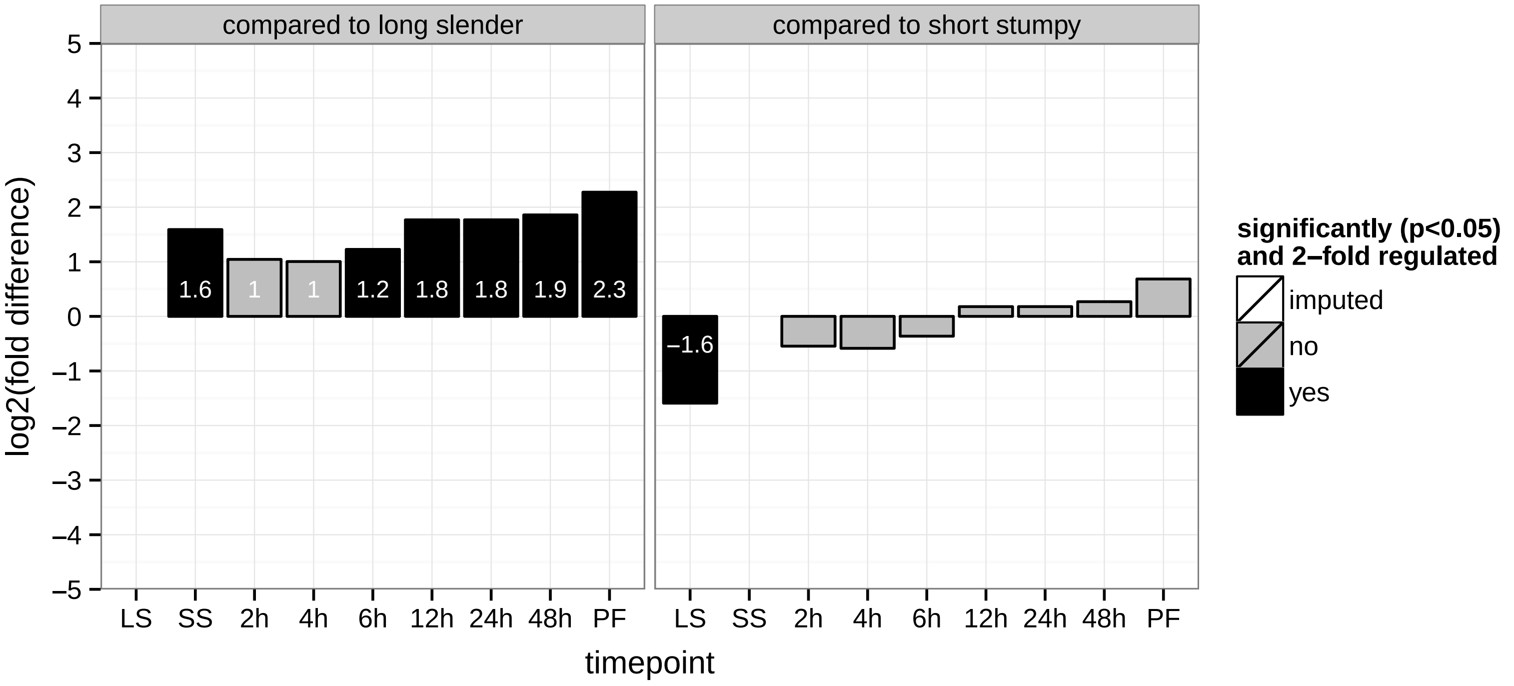
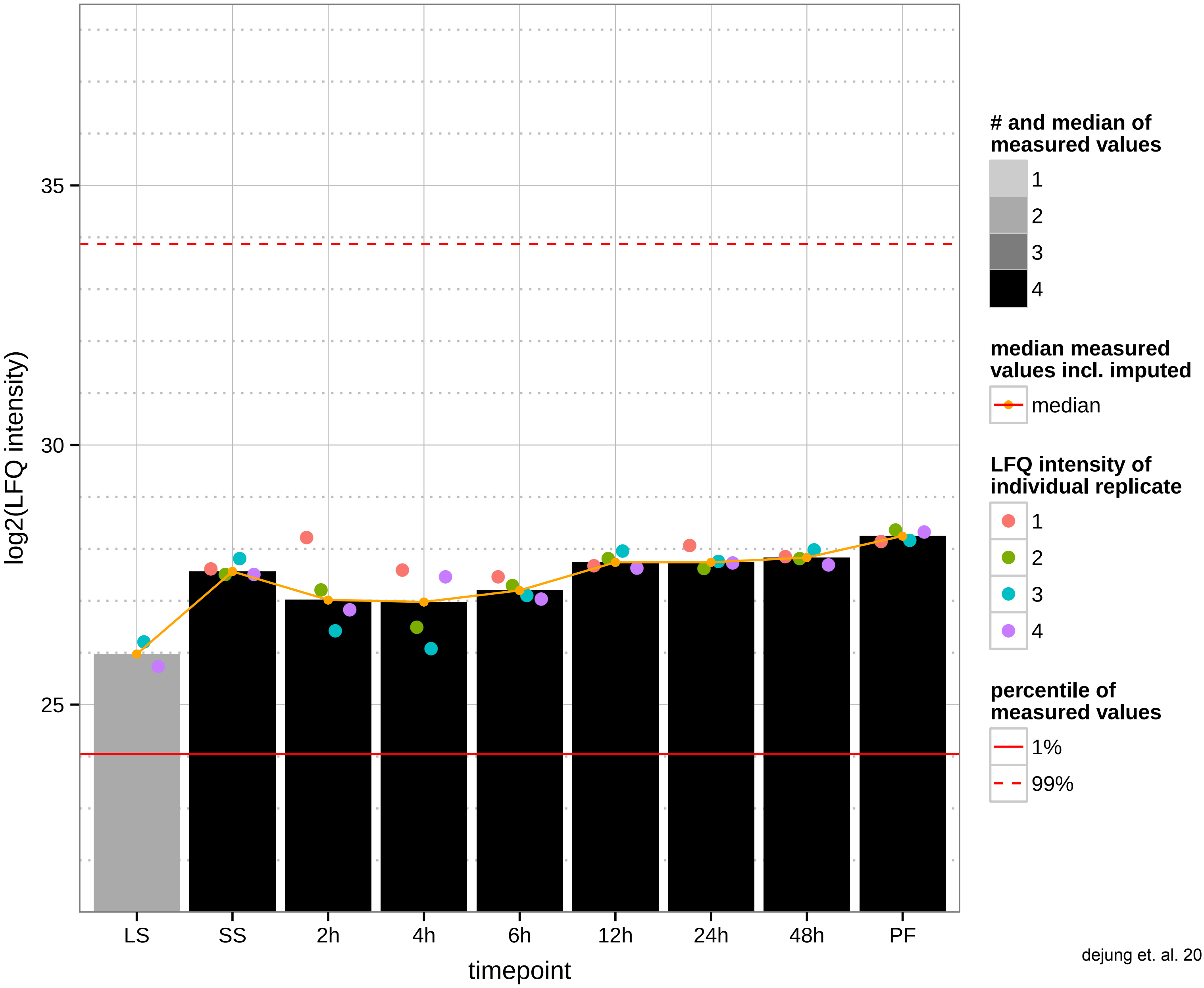
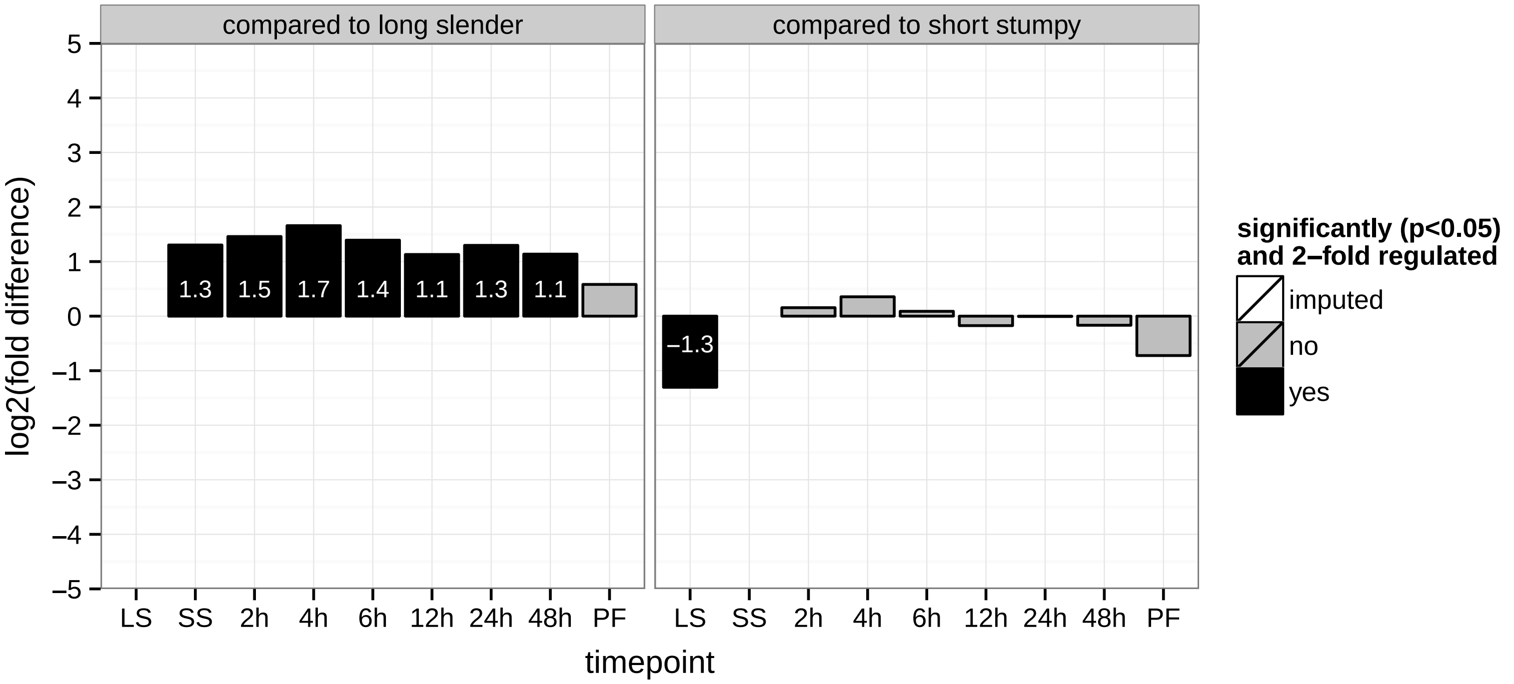
ATP−dependent DEAD/H RNA helicase, putative
Tb927.10.6260;Tb11.v5.0279
AGOF: null, ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: null, nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null

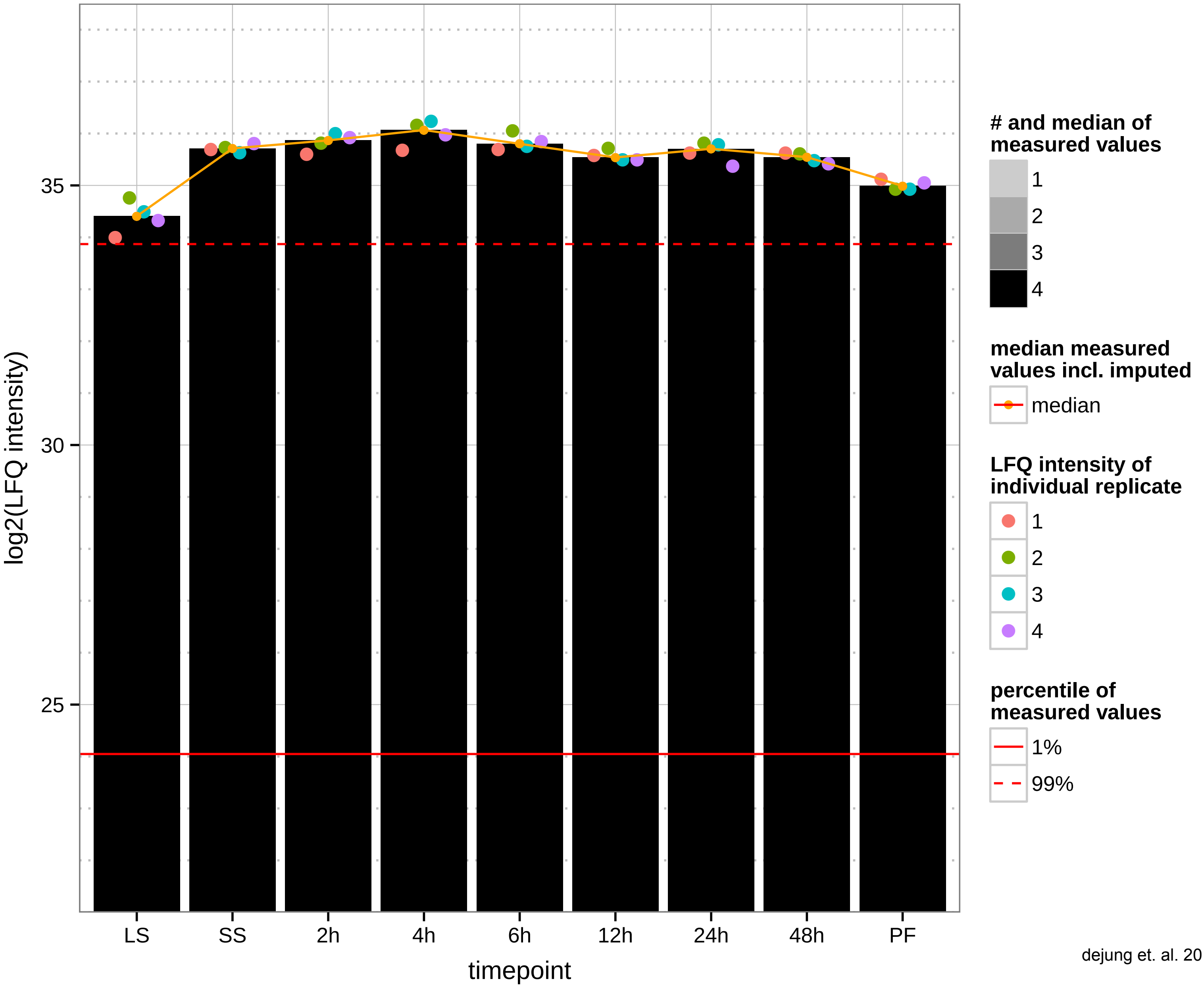




dejung et. al. 2015

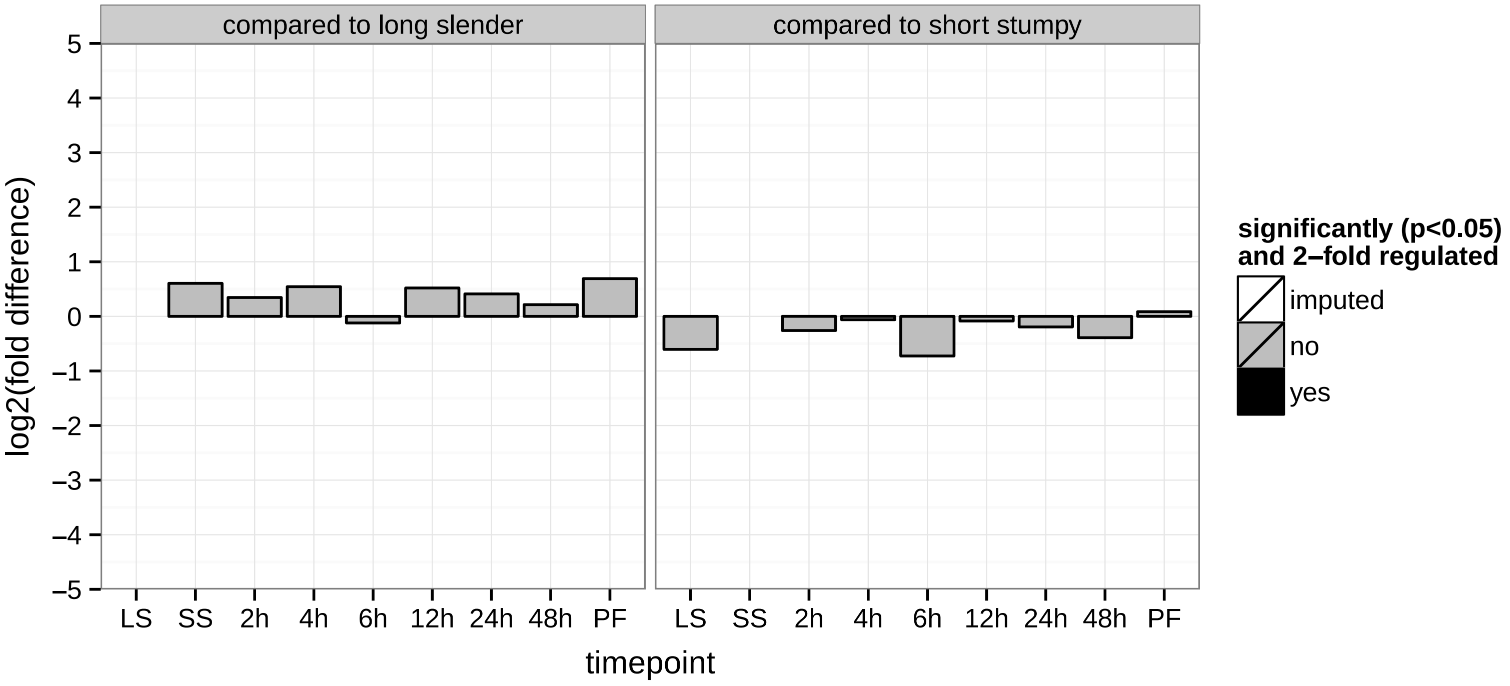
chaperonin HSP60, mitochondrial precursor (HSP60)
Tb927.10.6510;Tb927.10.6400
AGOF: ATP binding, unfolded protein binding
AGOC: mitochondrion
AGOP: protein complex assembly, protein folding, protein import into mitochondrial matrix
PGOF: ATP binding
PGOC: cytoplasm
PGOP: cellular protein metabolic process, protein refolding

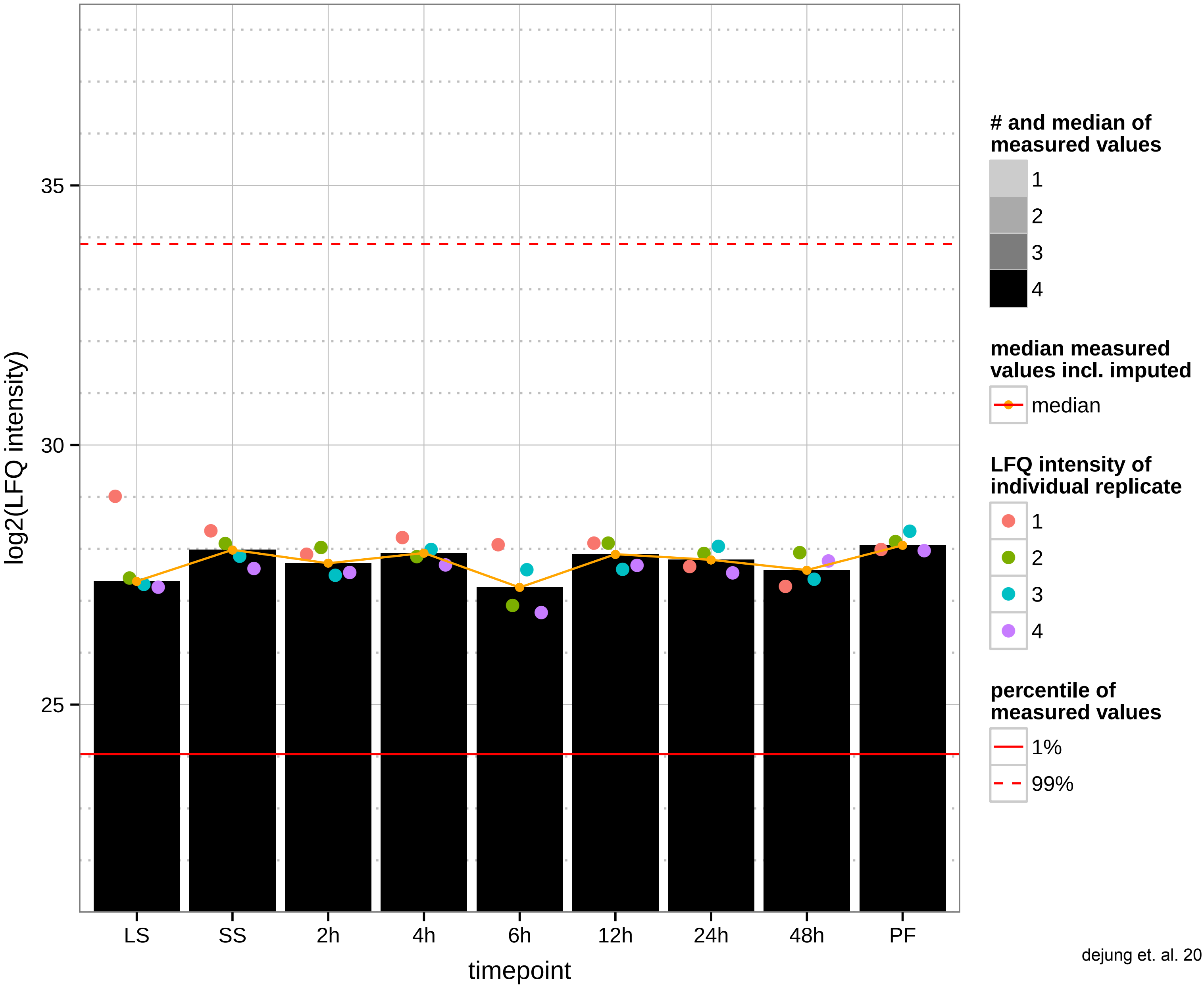




dejung et. al. 2015

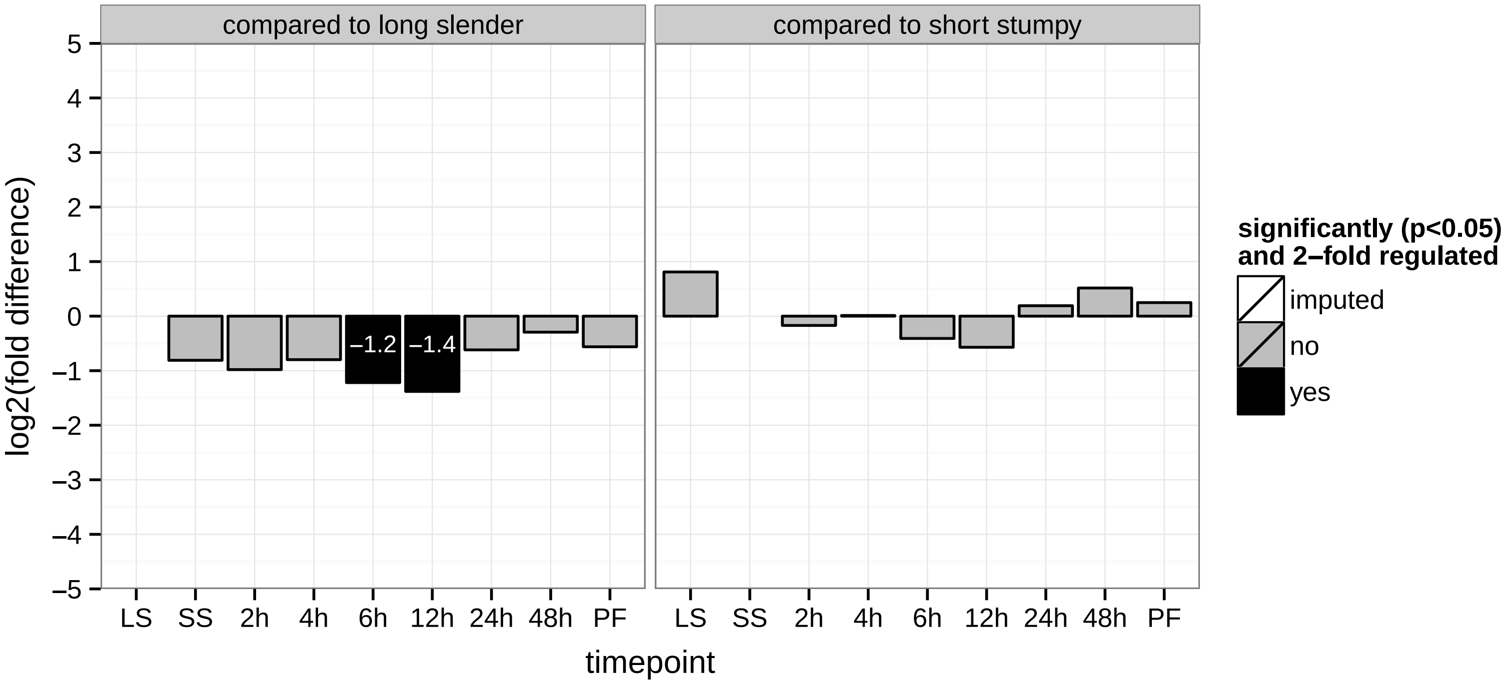
phosphomannomutase, putative
Tb927.10.6440
AGOF: phosphomannomutase activity
AGOC: cytoplasm
AGOP: mannose biosynthetic process
PGOF: catalytic activity, phosphomannomutase activity
PGOC: cytoplasm
PGOP: mannose biosynthetic process, metabolic process

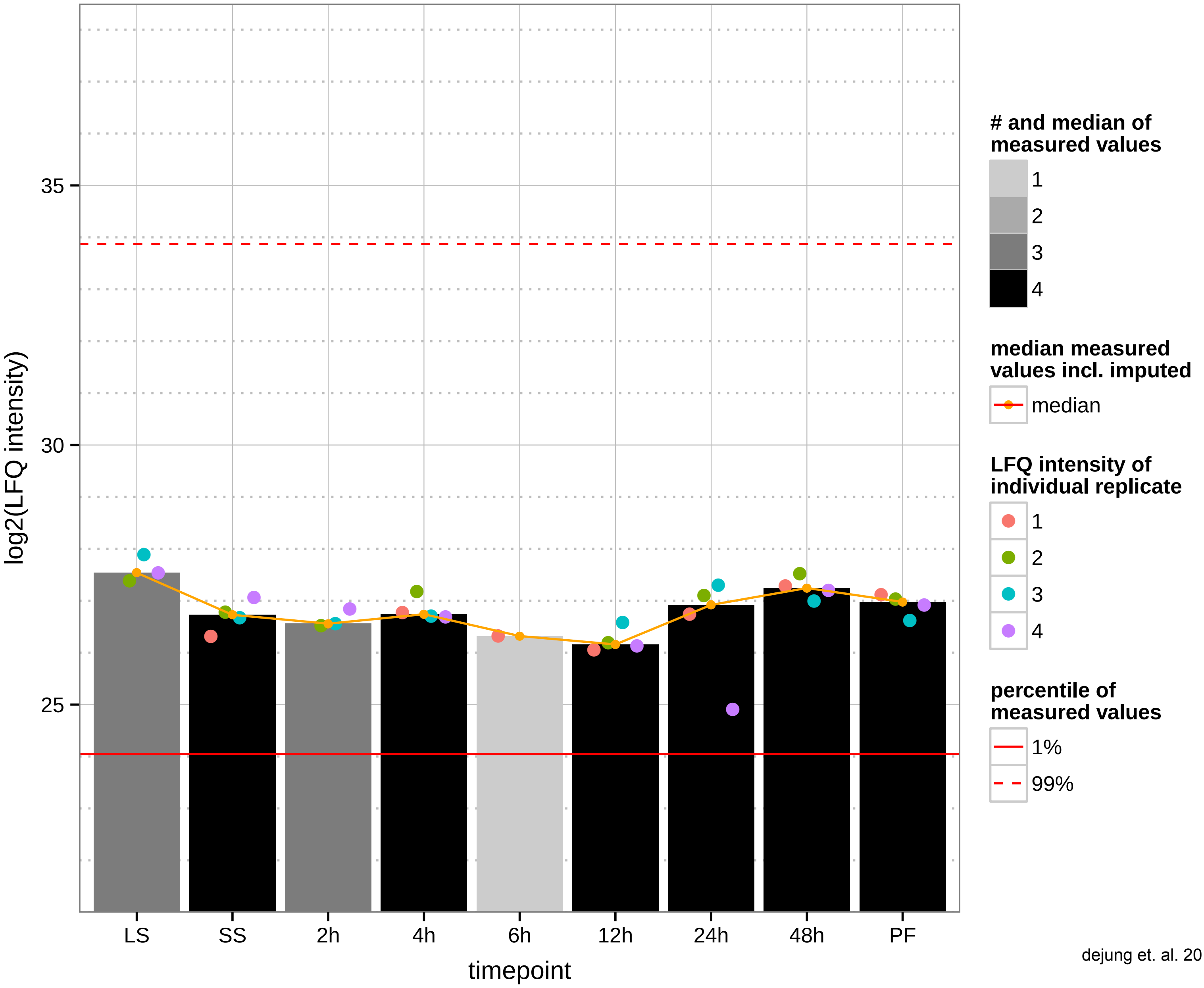




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.6490
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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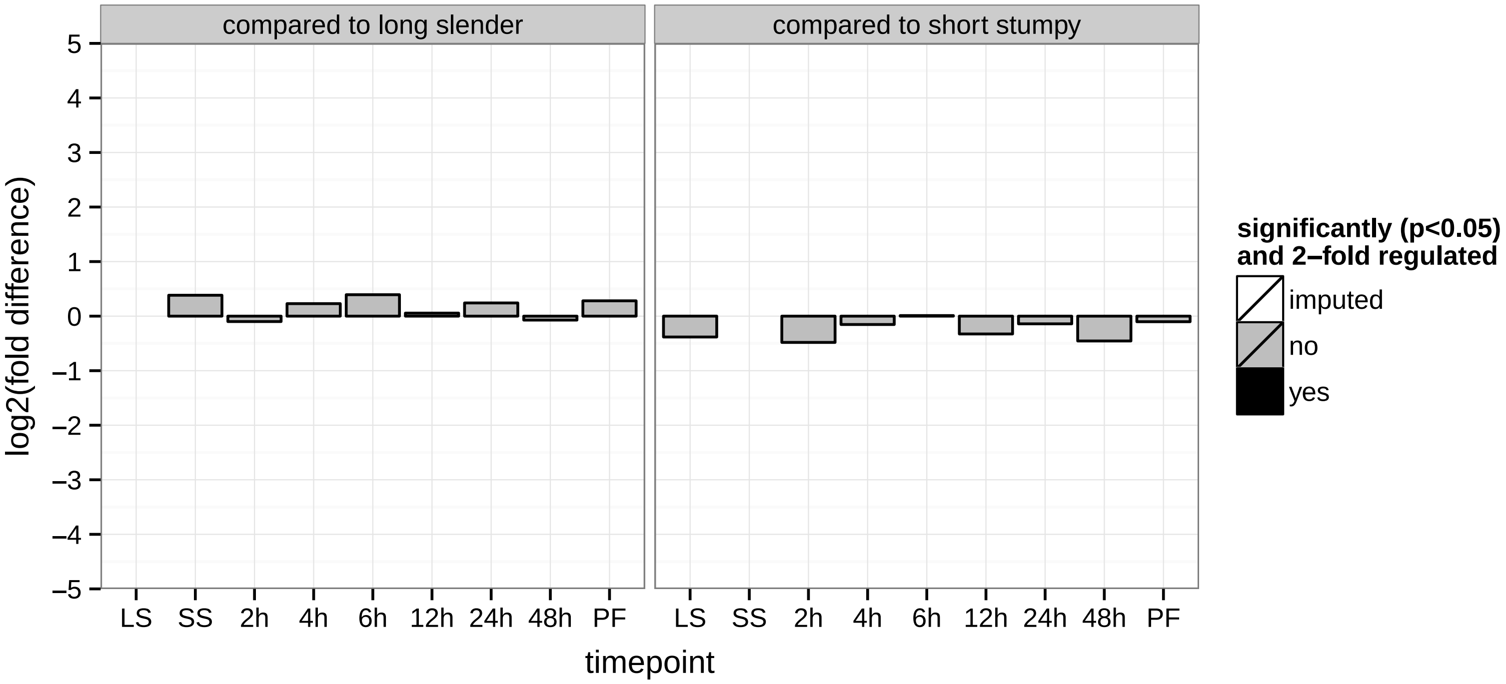
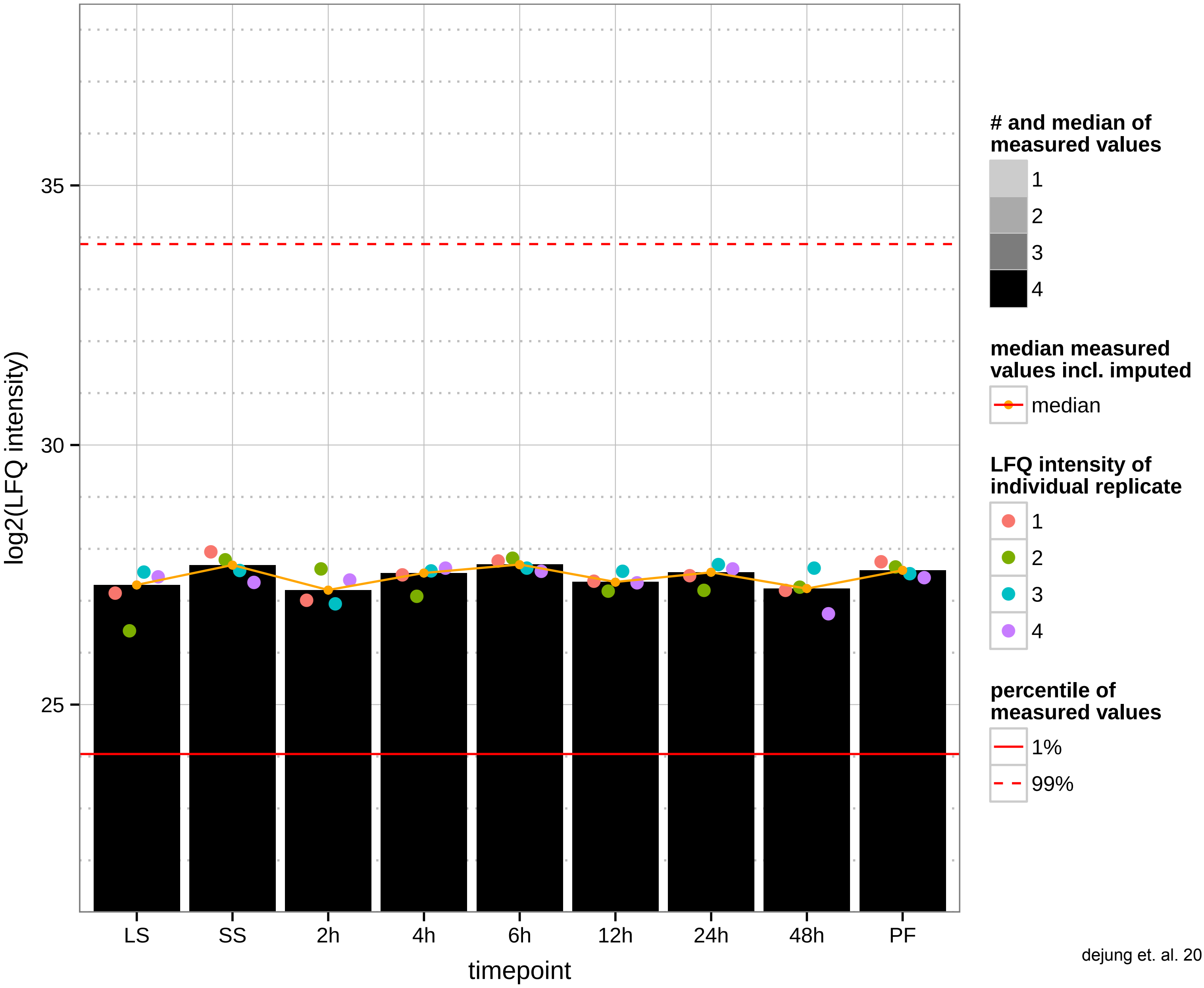
TAX−2
Tb927.10.650
AGOF: heme binding
AGOC: cilium part
AGOP: ciliary or flagellar motility
PGOF: heme binding
PGOC: null
PGOP: null





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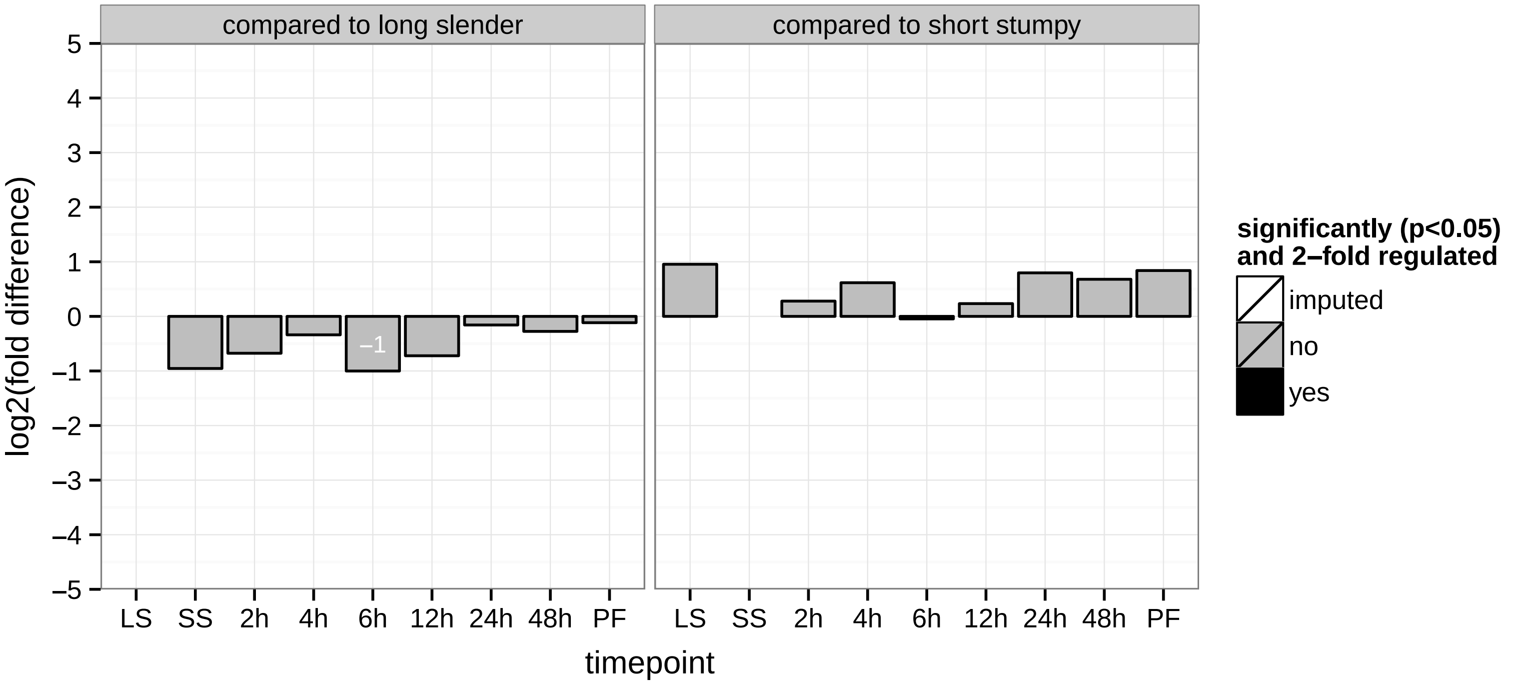
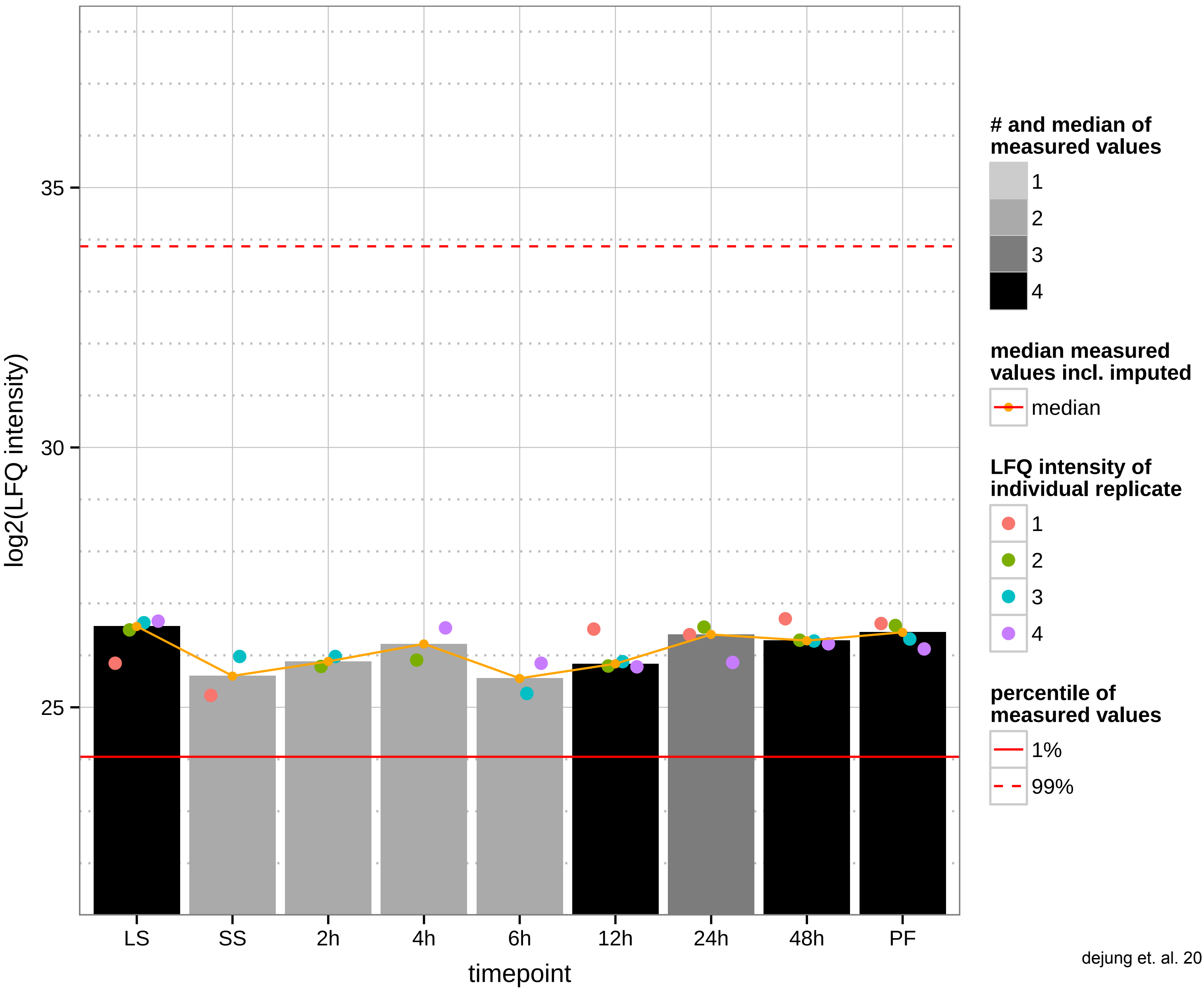
chaperone protein DNAj, putative
Tb927.10.6610
AGOF: heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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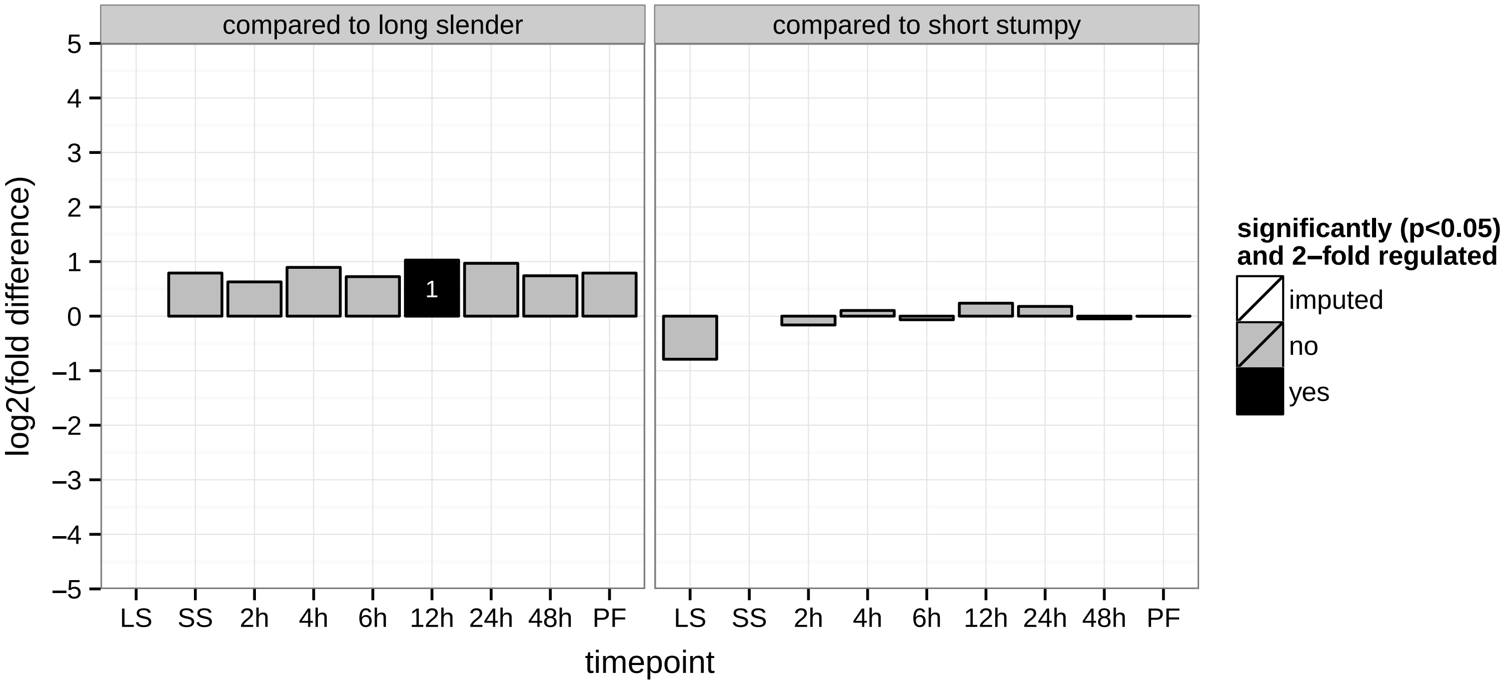
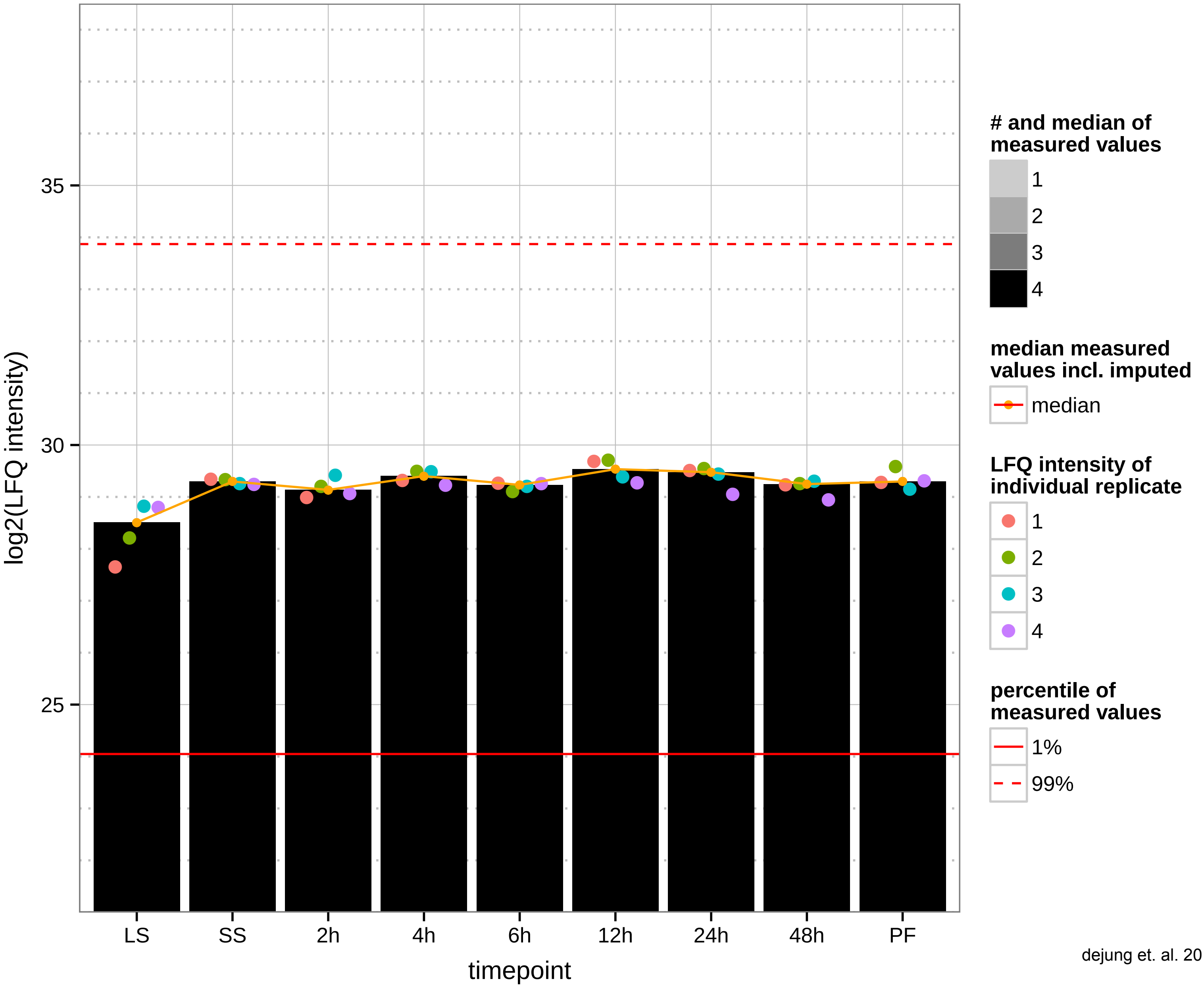
COP−coated vesicle membrane protein erv25 precursor, putative, ER−−golgi transport protein erv25 precursor
Tb927.10.6640
AGOF: null
AGOC: integral to membrane
AGOP: transport
PGOF: null
PGOC: integral to membrane
PGOP: transport





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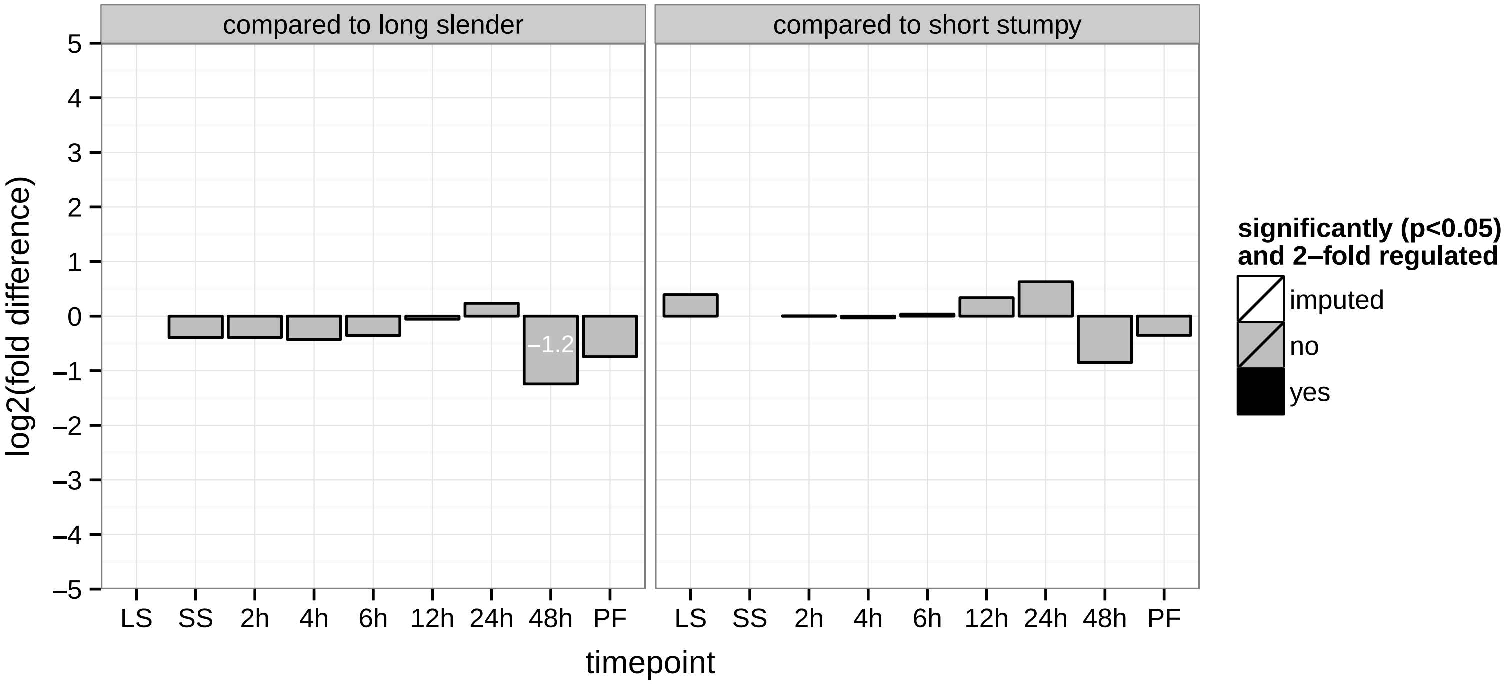
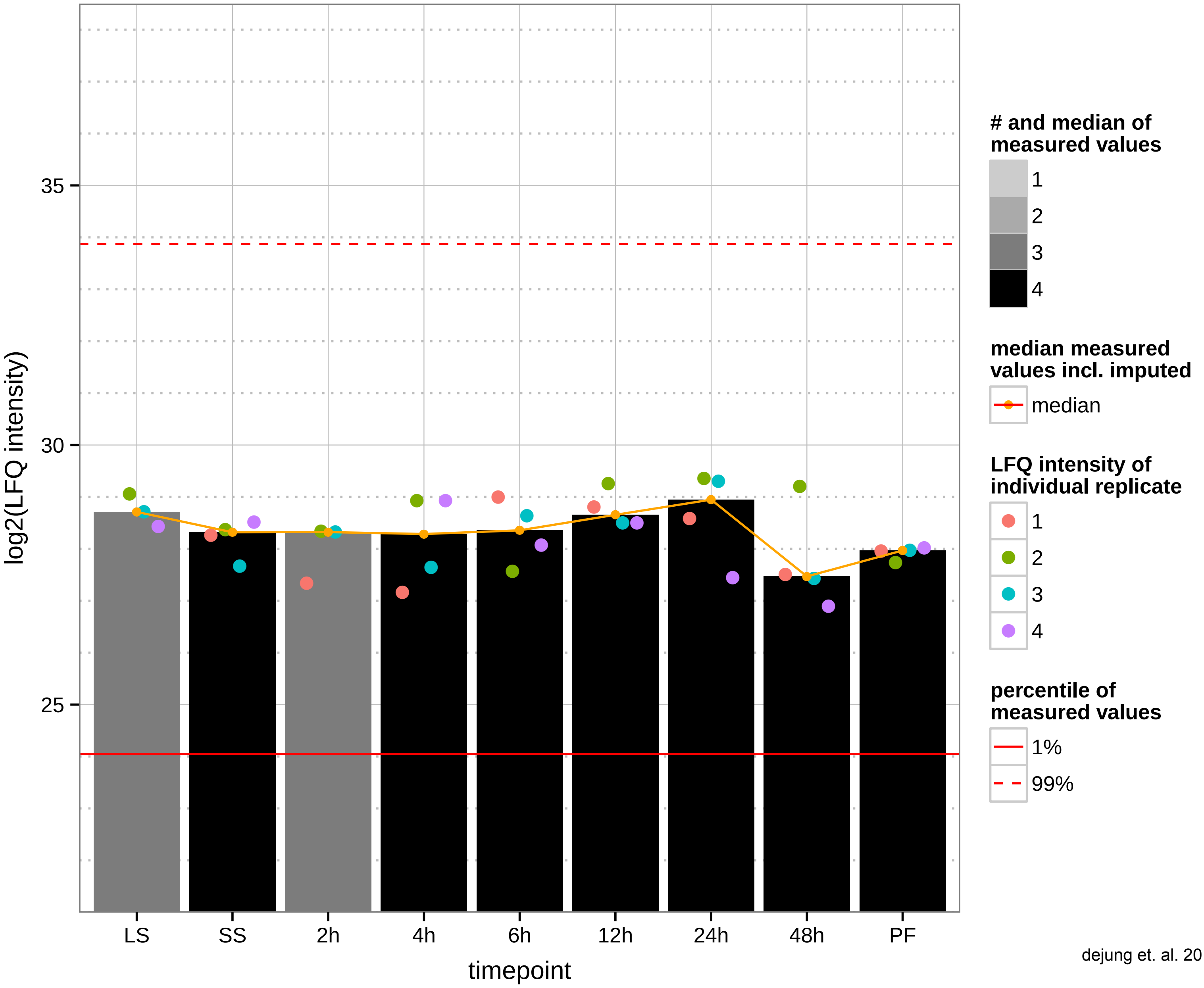
dynein light chain, putative
Tb927.10.6670
AGOF: microtubule motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based process
PGOF: null
PGOC: microtubule associated complex
PGOP: microtubule–based process





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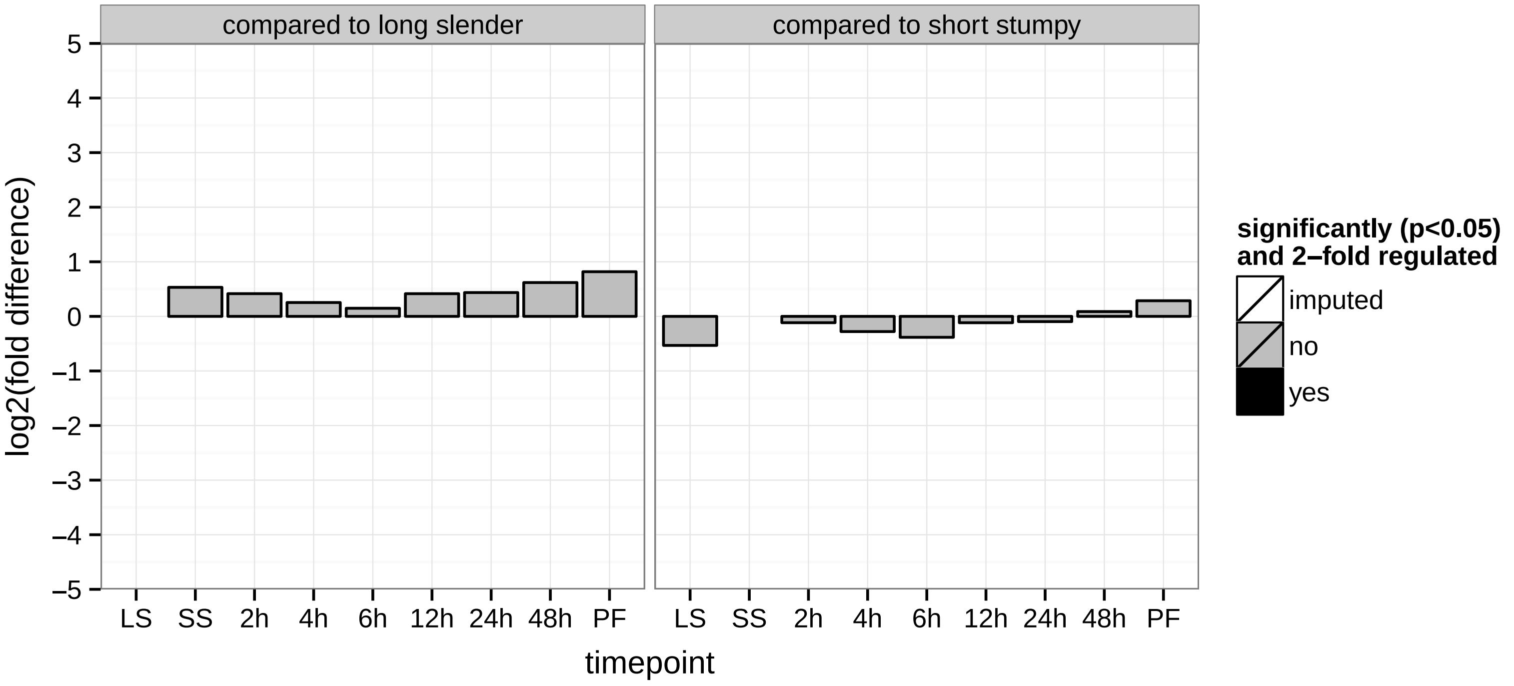
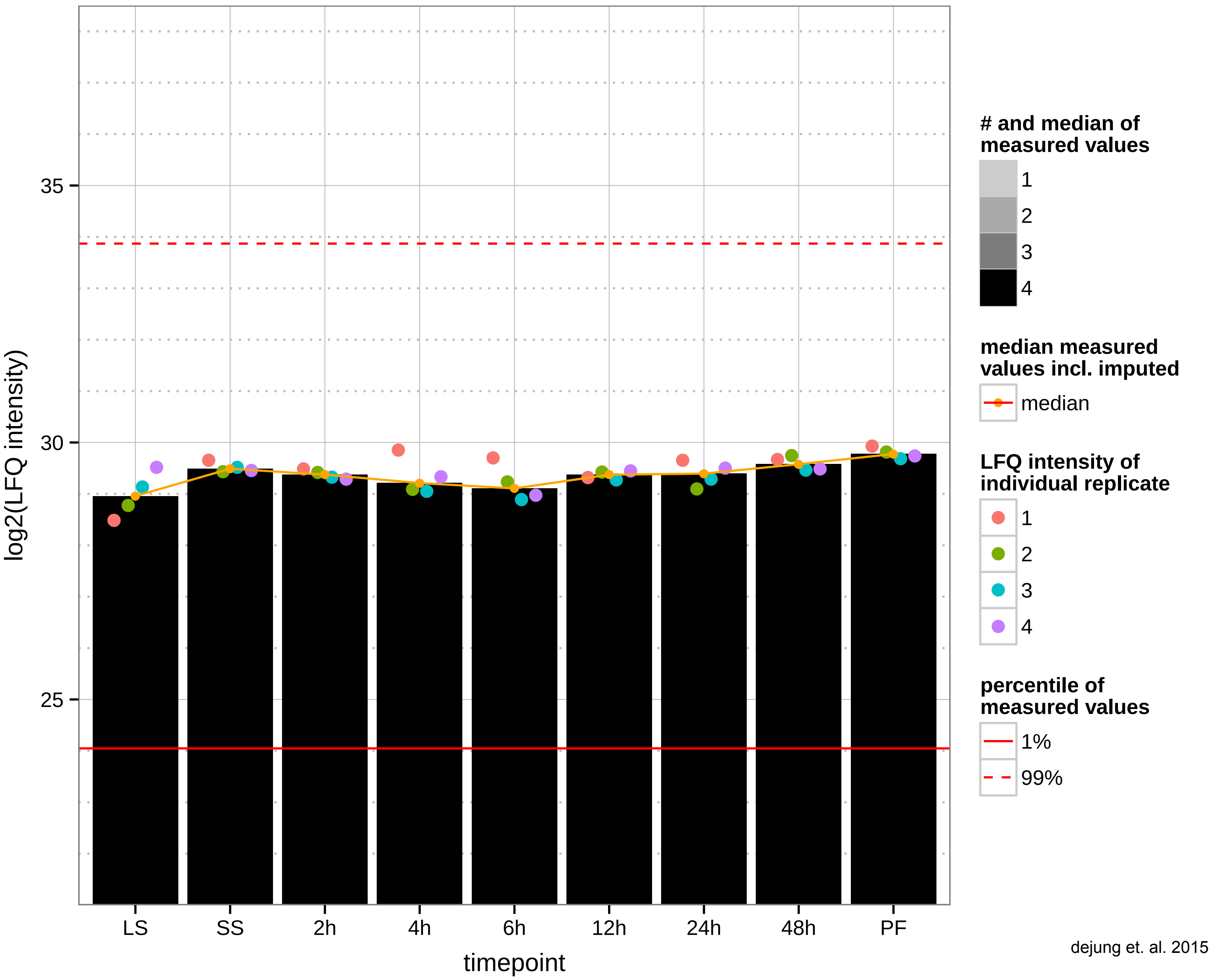
developmentally regulated GTP–binding protein, putative
Tb927.10.6800
AGOF: GTP binding
AGOC: cytoplasm, intracellular
AGOP: cellular process
PGOF: GTP binding
PGOC: null
PGOP: null





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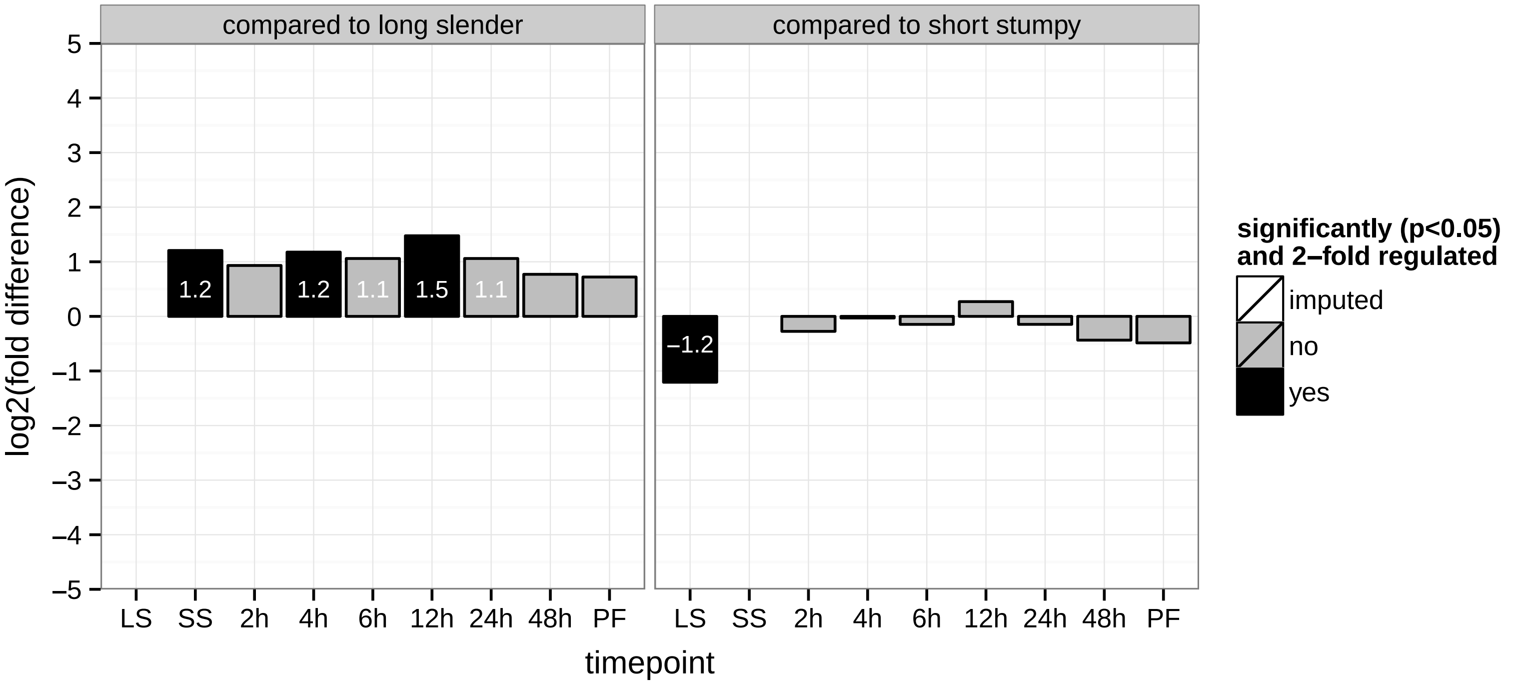
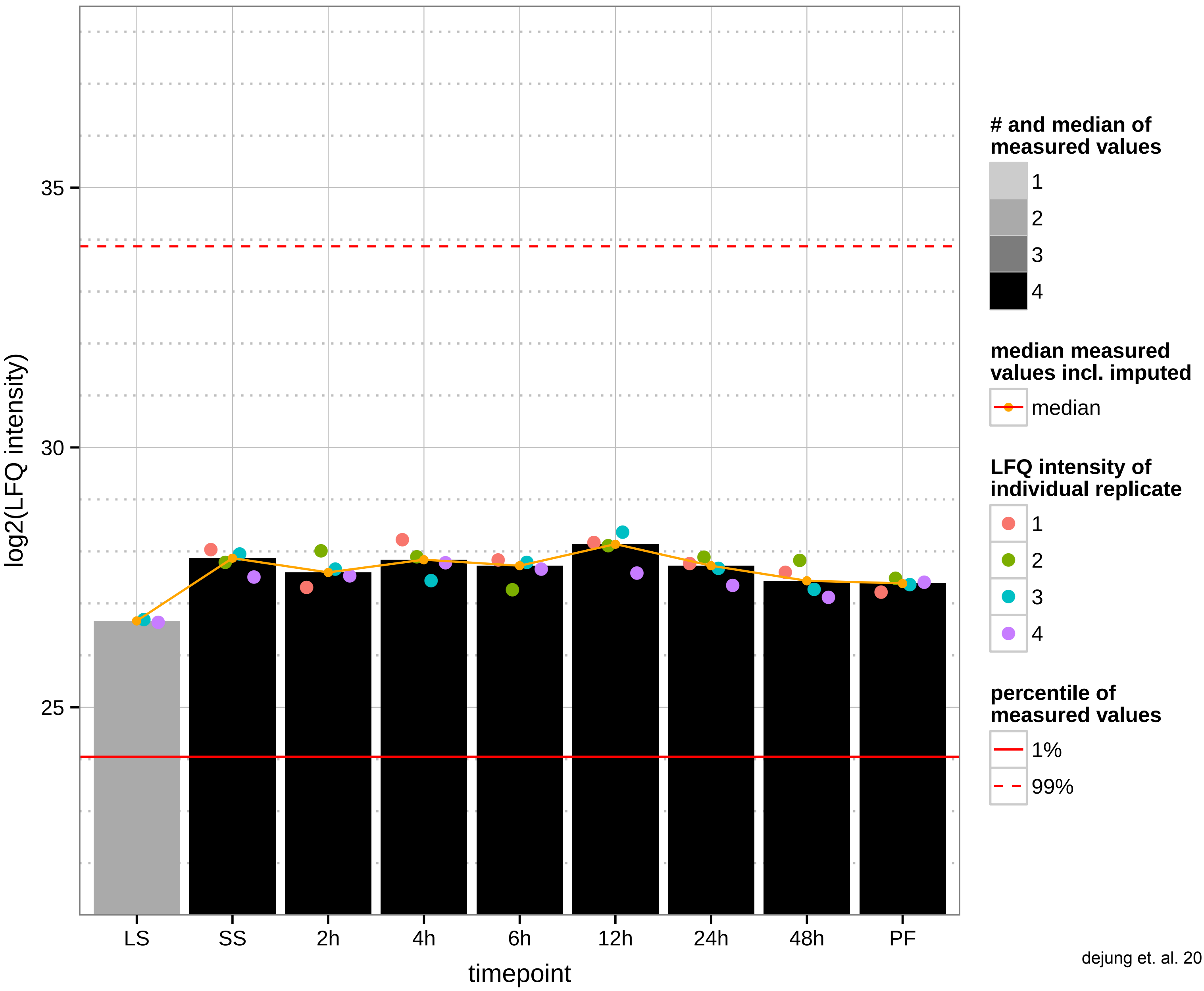
guanylate kinase, putative
Tb927.10.6810
AGOF: null
AGOC: null
AGOP: nucleobase−containing small molecule interconversion
PGOF: protein binding
PGOC: null
PGOP: null





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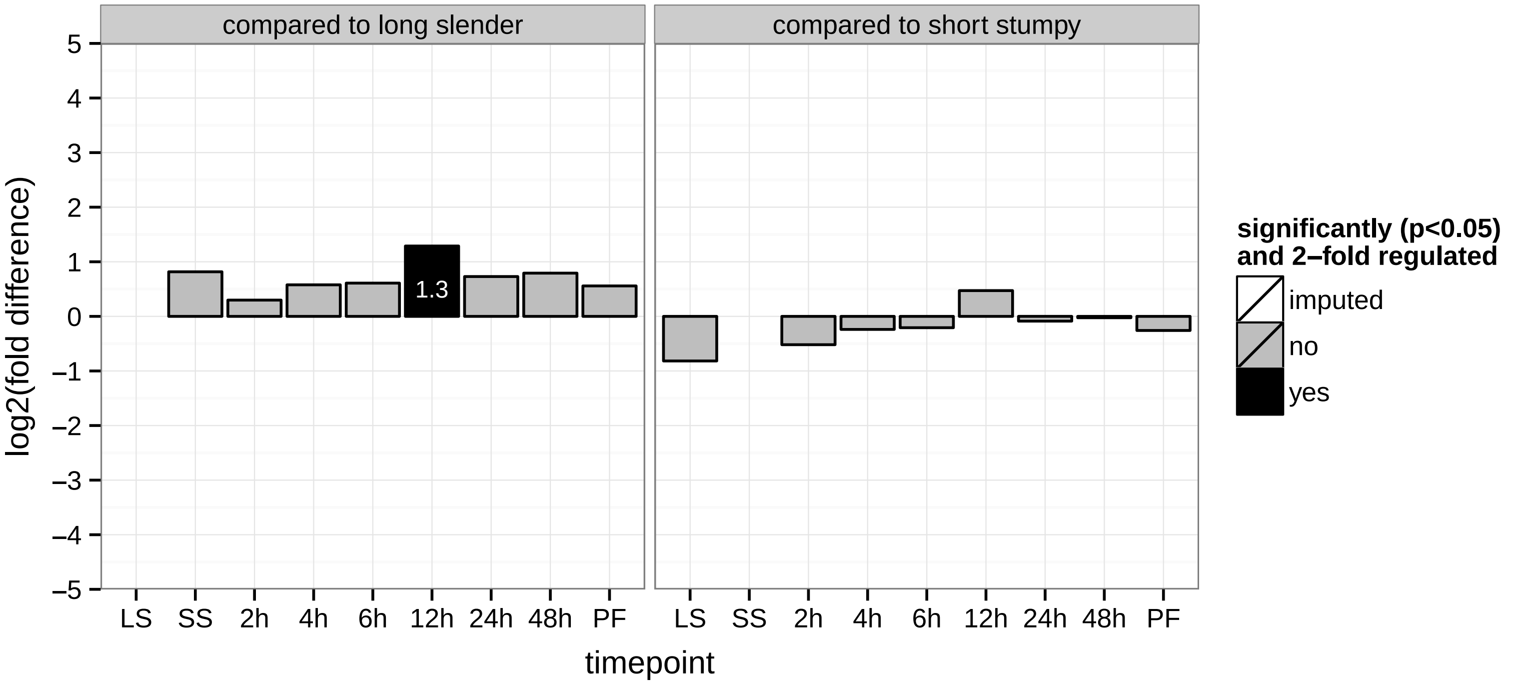
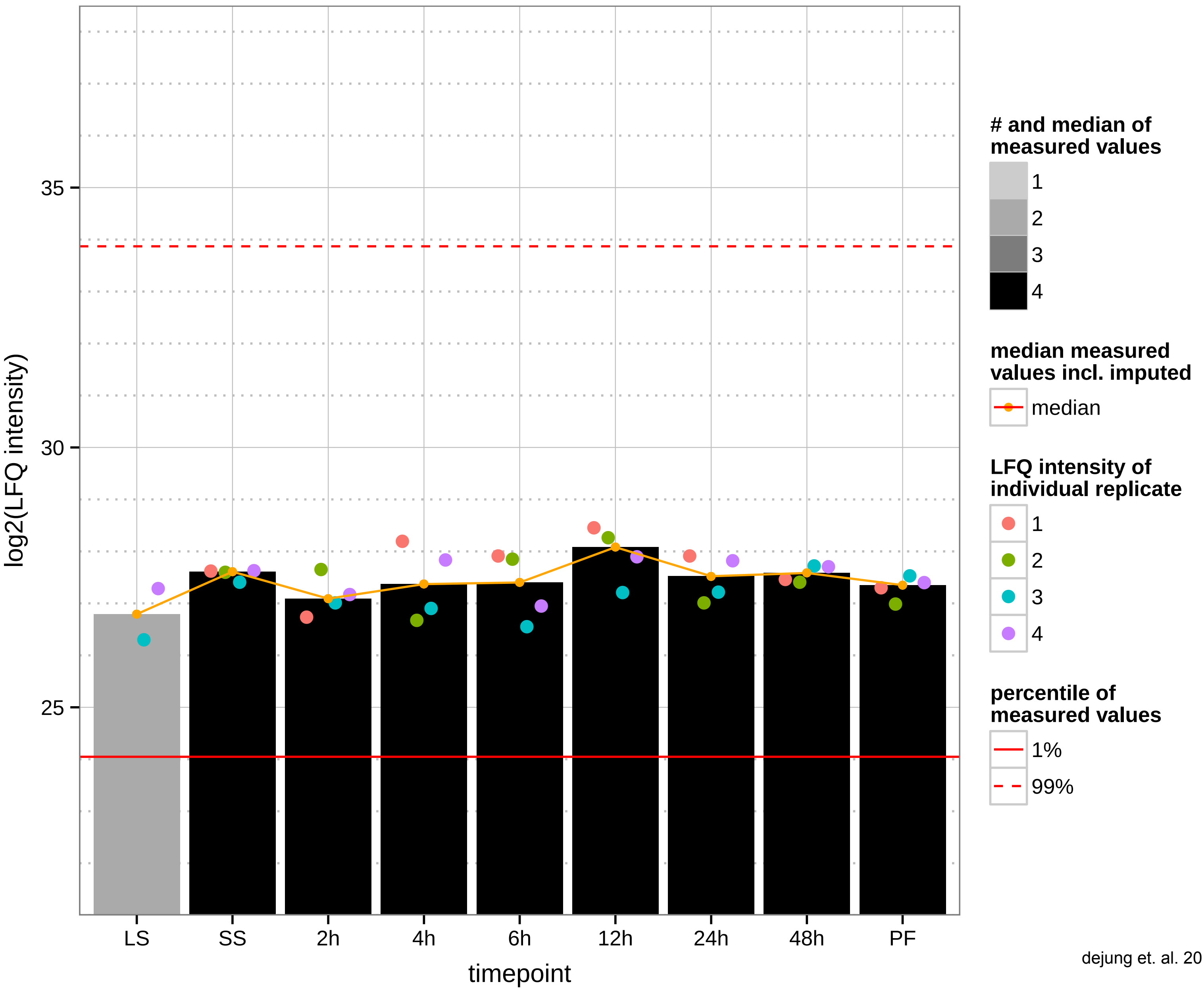
hypothetical protein, conserved
Tb927.10.6820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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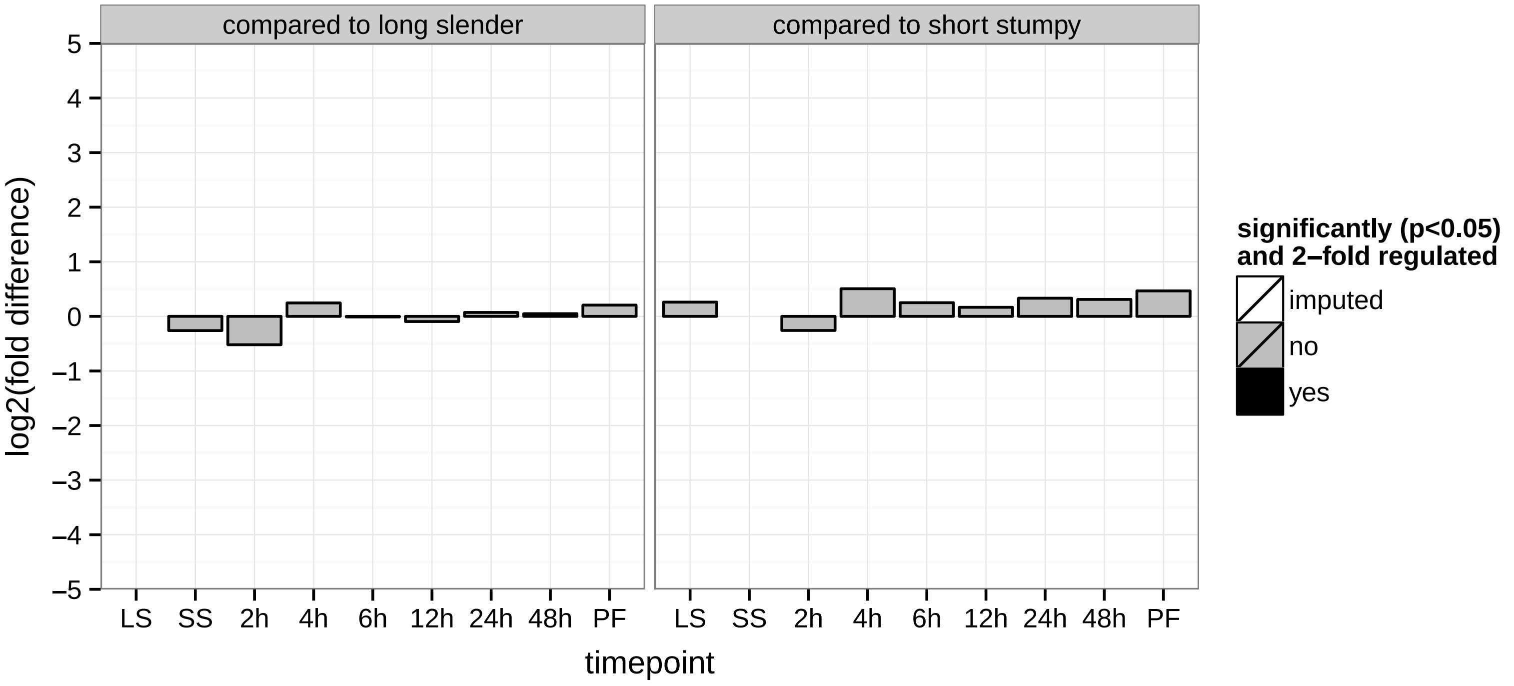
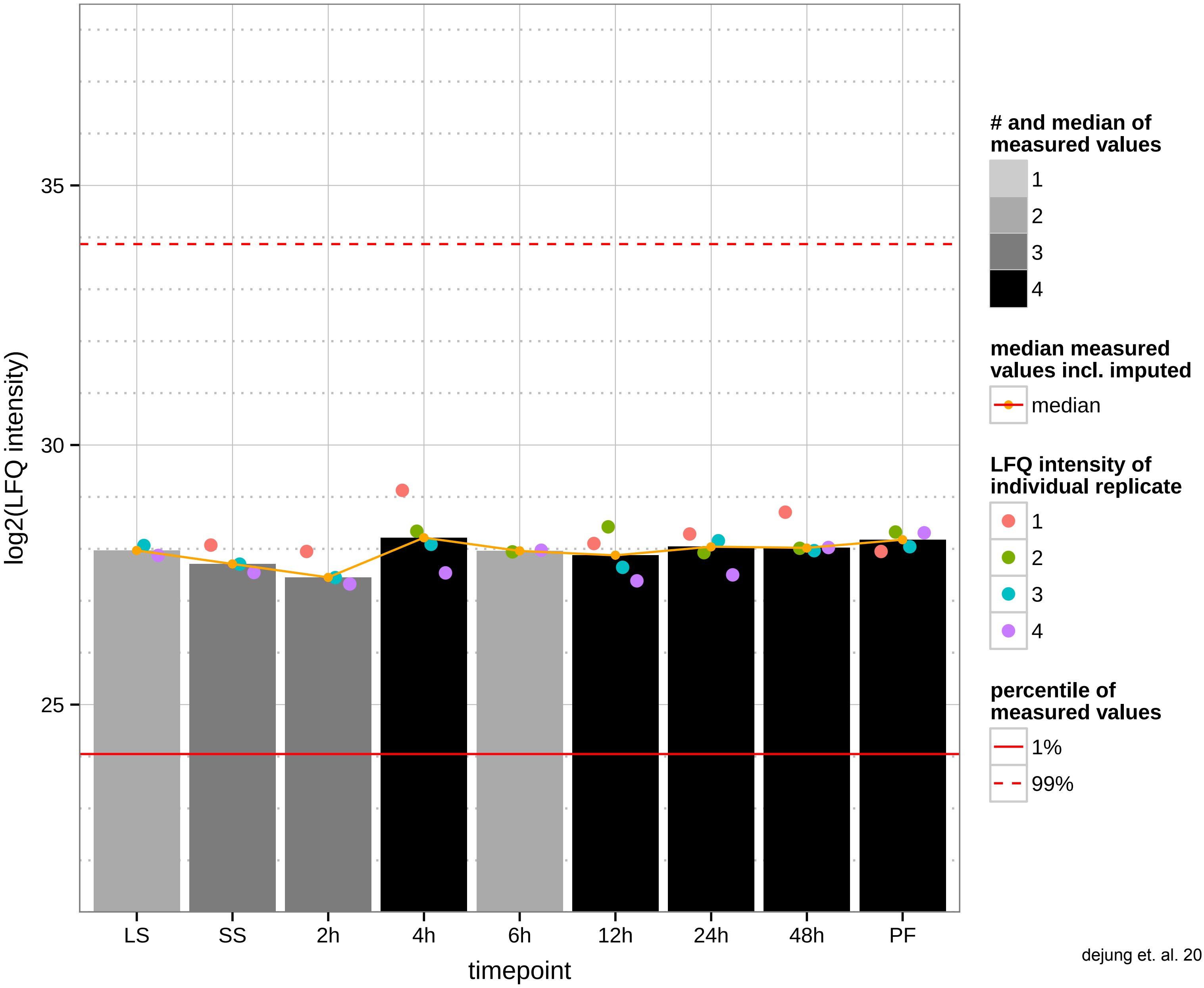
hypothetical protein, conserved
Tb927.10.6840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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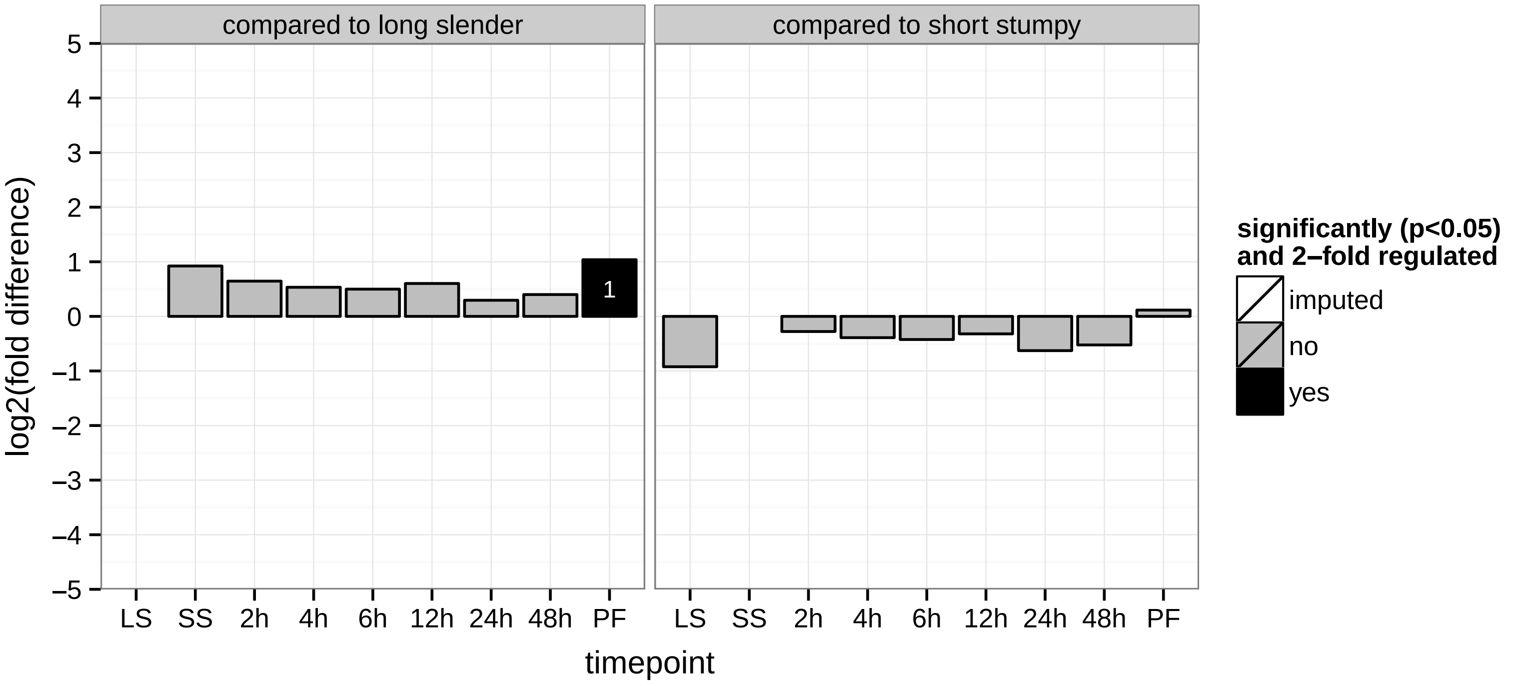
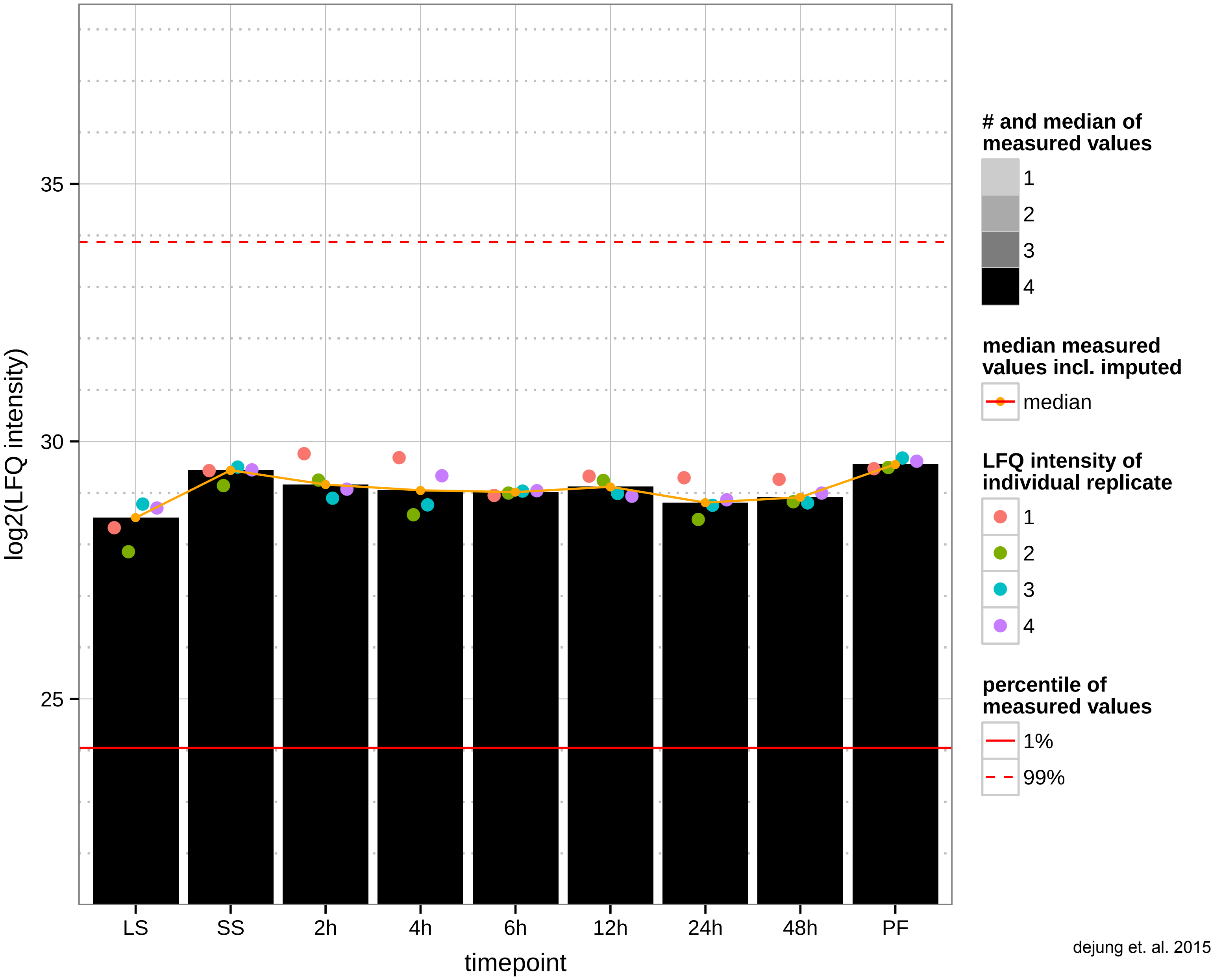
Dipeptidyl–peptidase 8–like, putative, dipeptidyl–peptidase 8–like serine peptidase, serine peptidase, Clan SC, Family S9B
Tb927.10.6970;Tb927.10.6940
AGOF: serine–type peptidase activity
AGOC: membrane
AGOP: proteolysis
PGOF: serine–type peptidase activity
PGOC: membrane
PGOP: proteolysis





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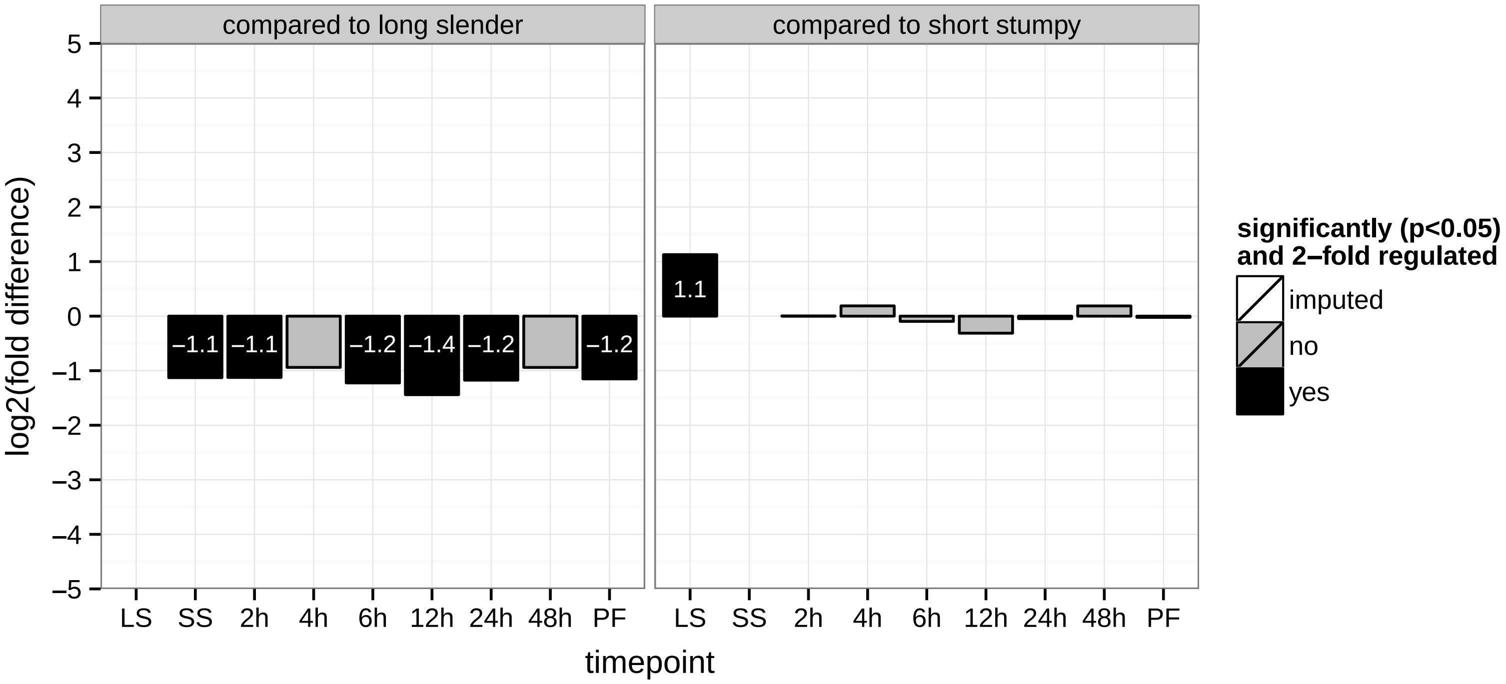
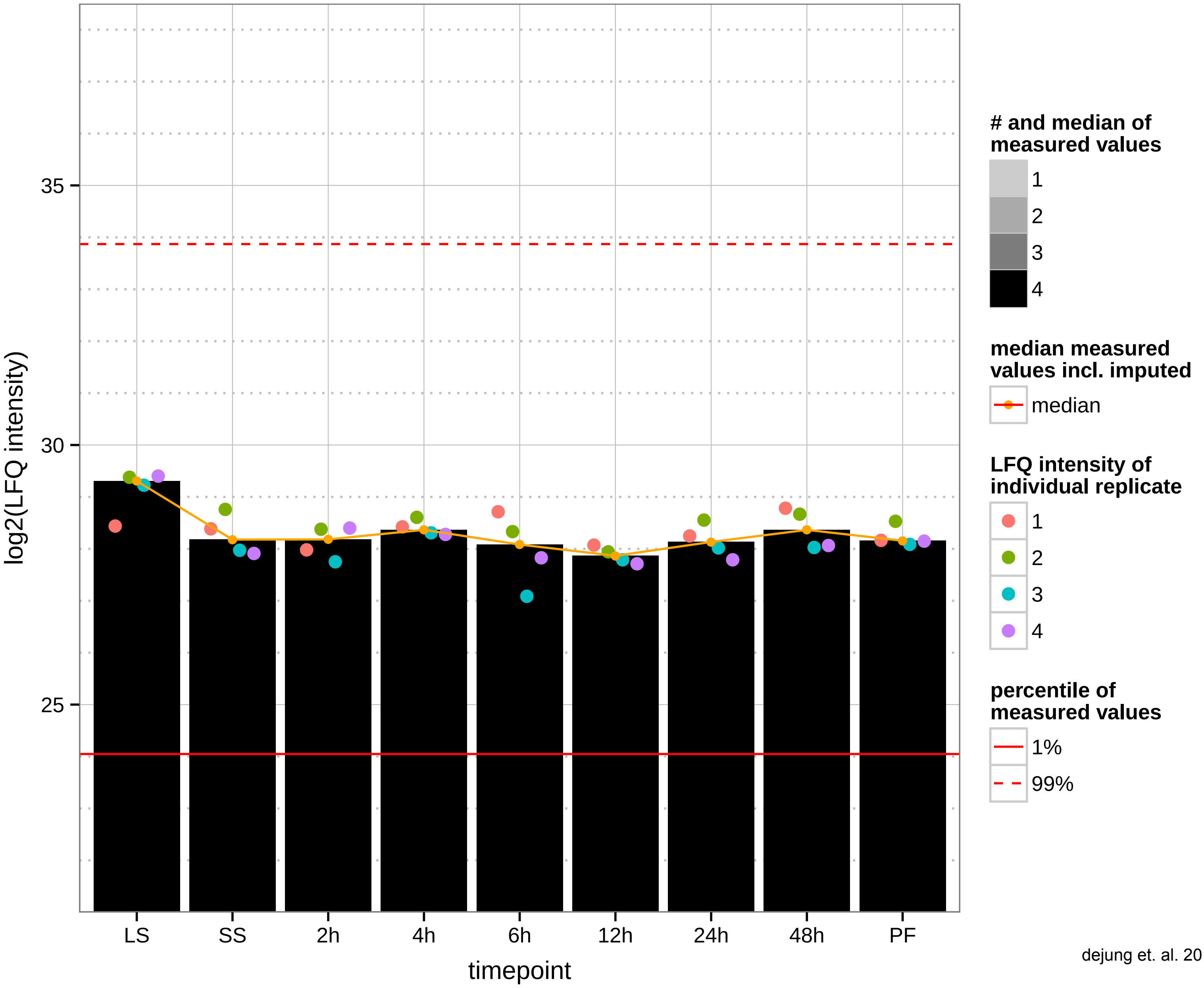
hypothetical protein, conserved
Tb927.10.6960
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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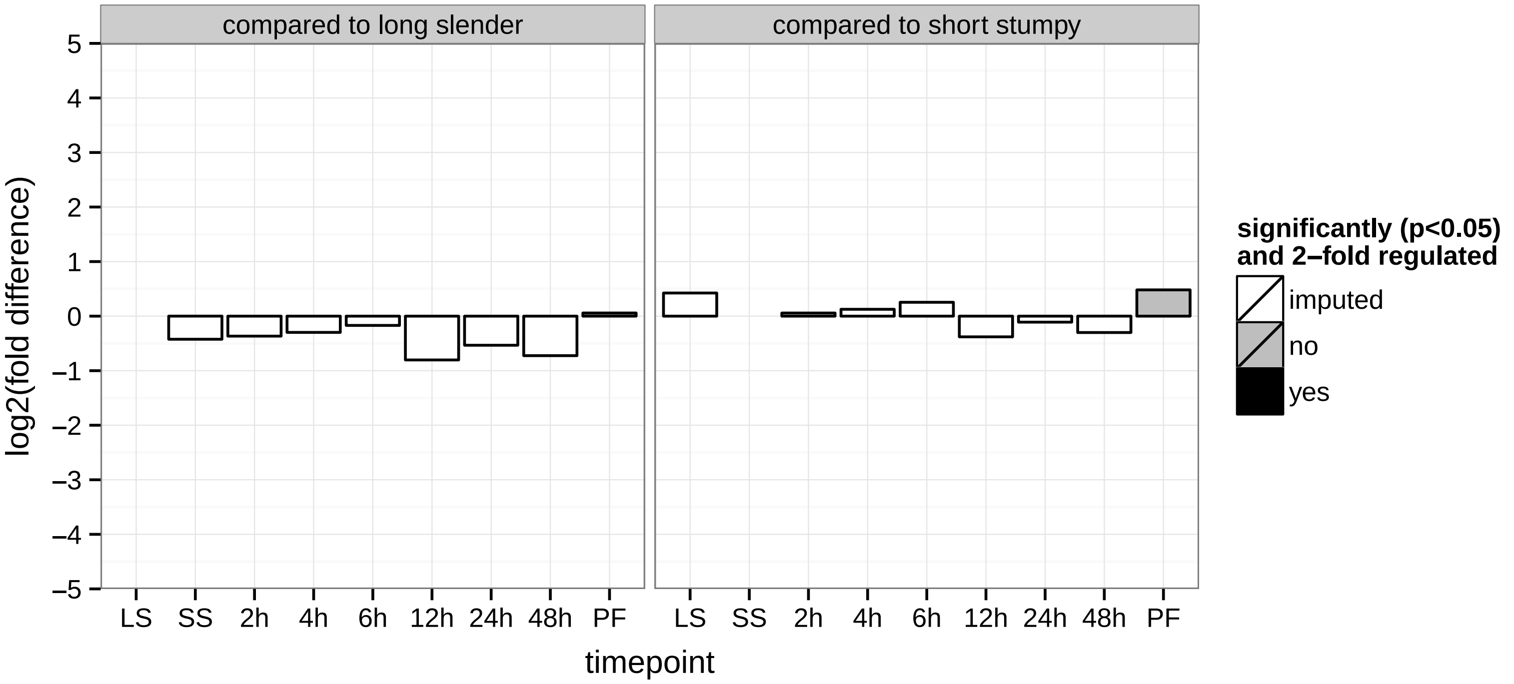
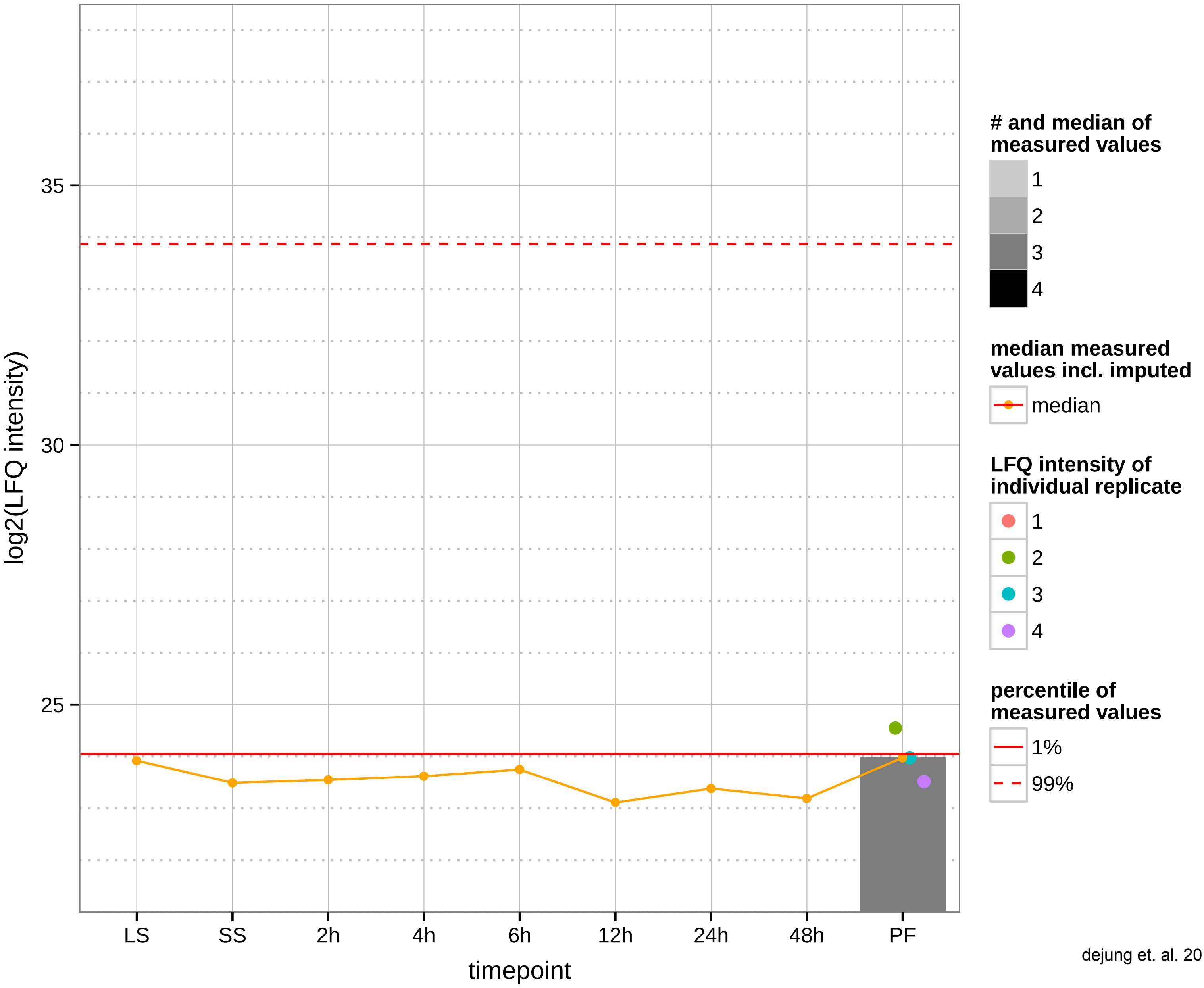
hypothetical protein, conserved
Tb927.10.700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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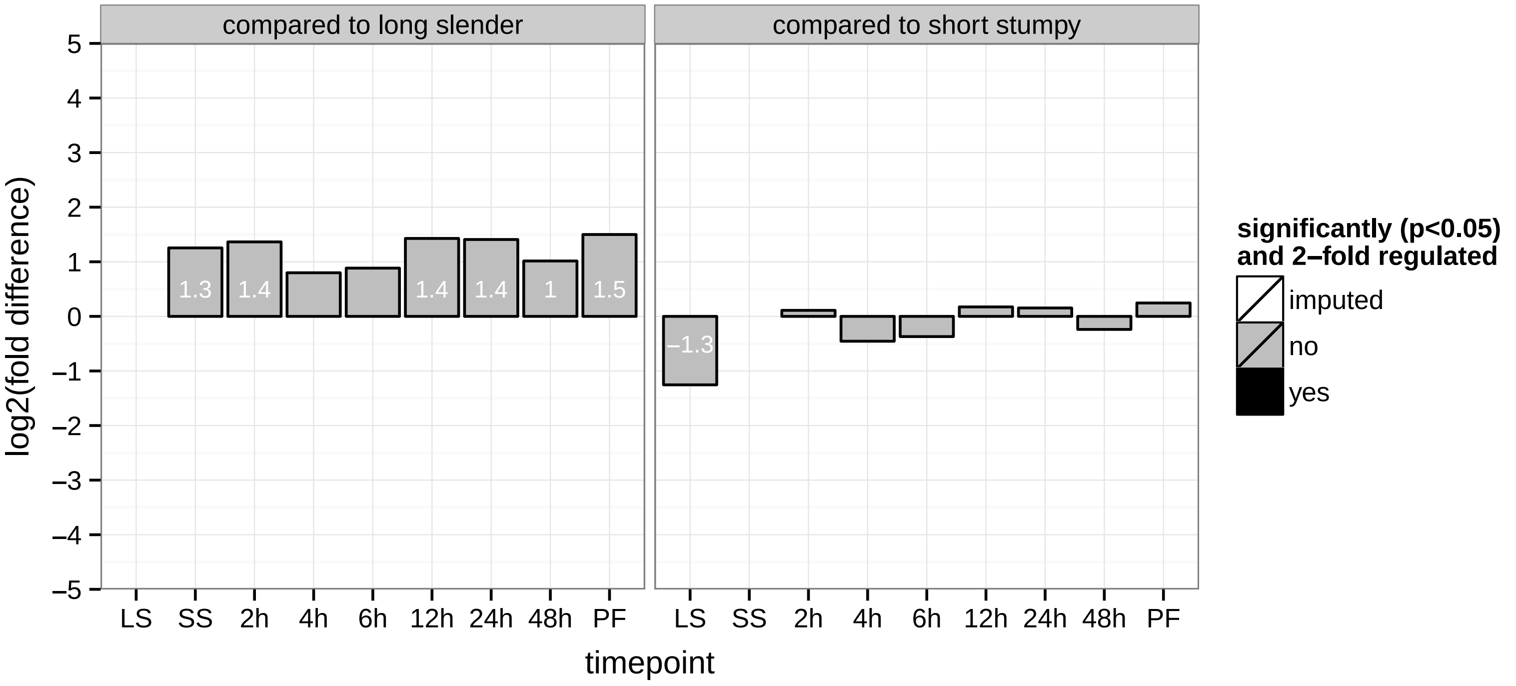
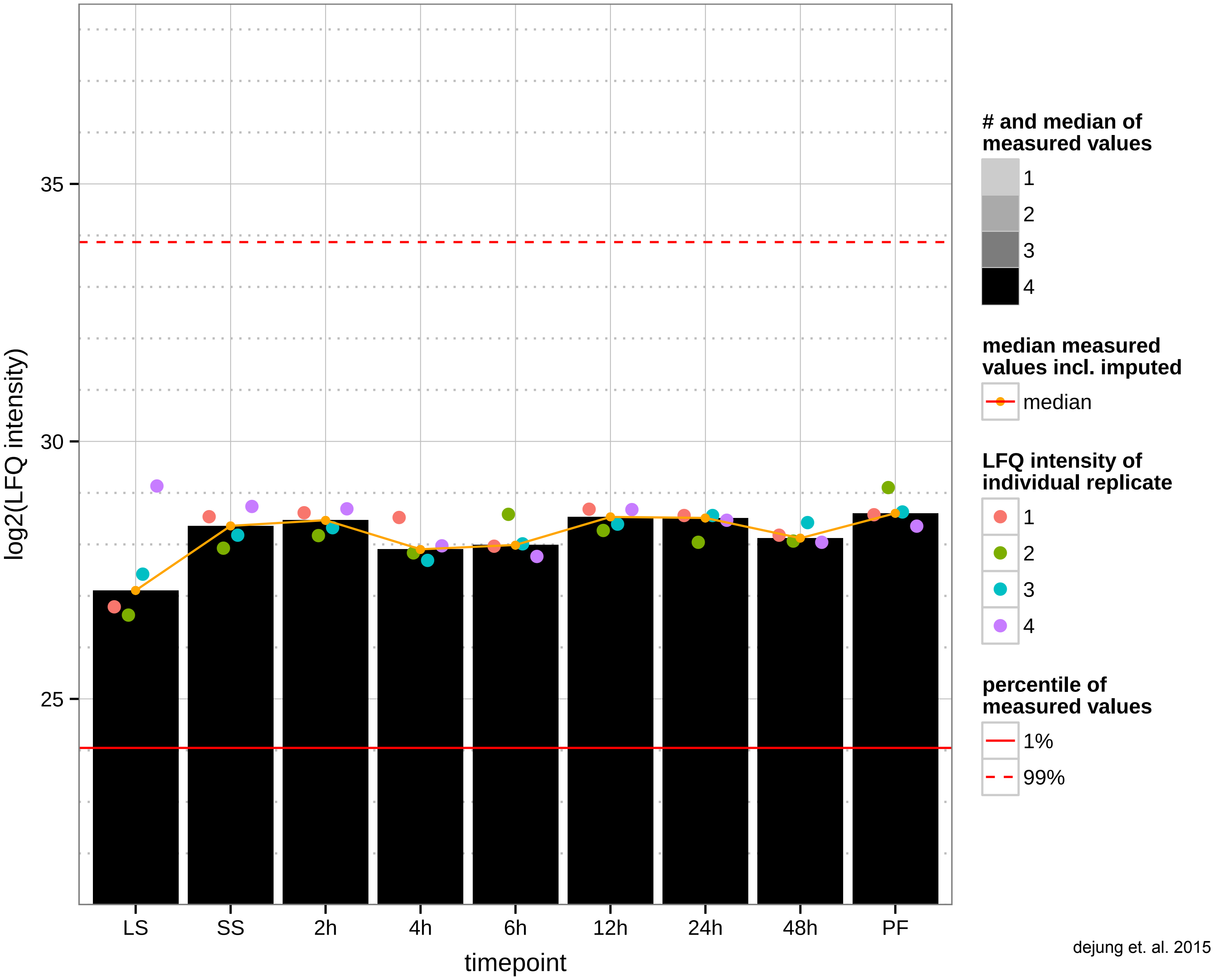
acid phosphatase, putative
Tb927.10.7020
AGOF: acid phosphatase activity
AGOC: null
AGOP: null
PGOF: acid phosphatase activity
PGOC: null
PGOP: null





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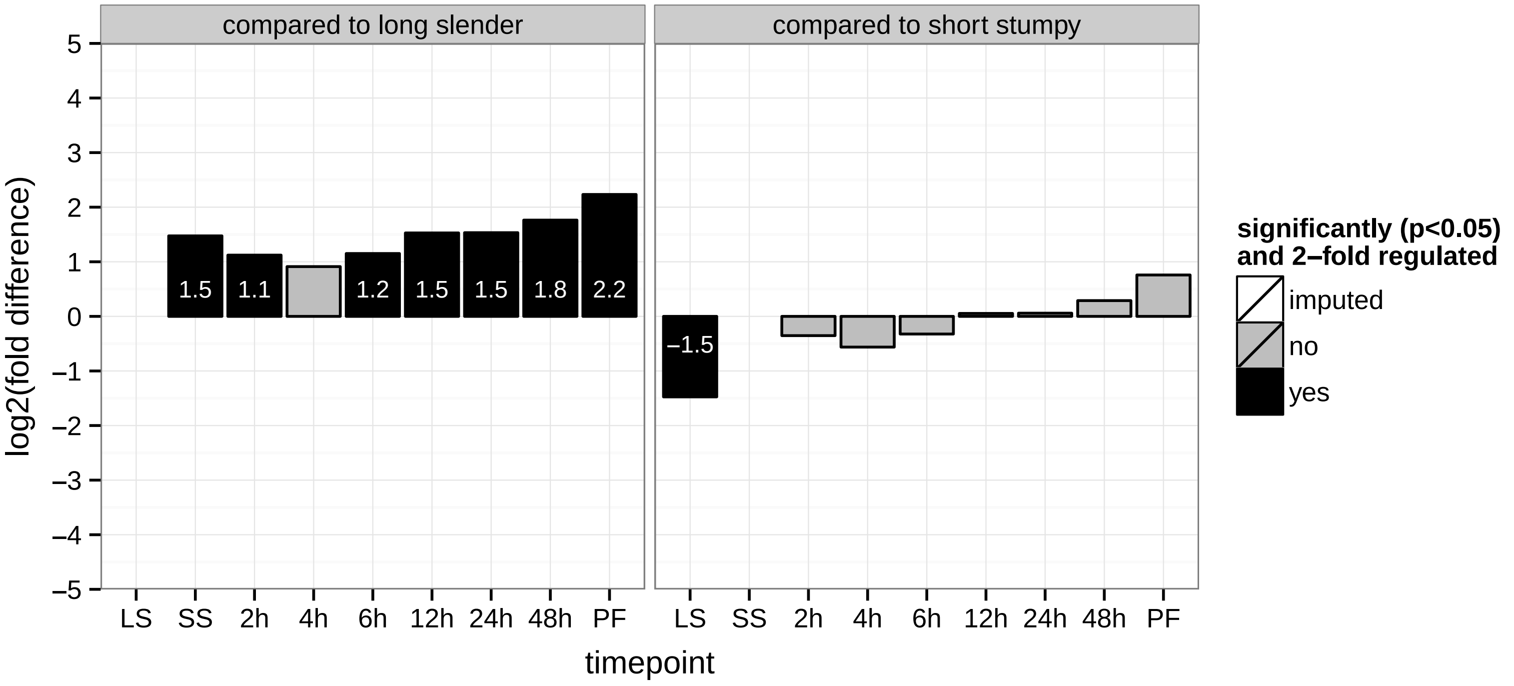
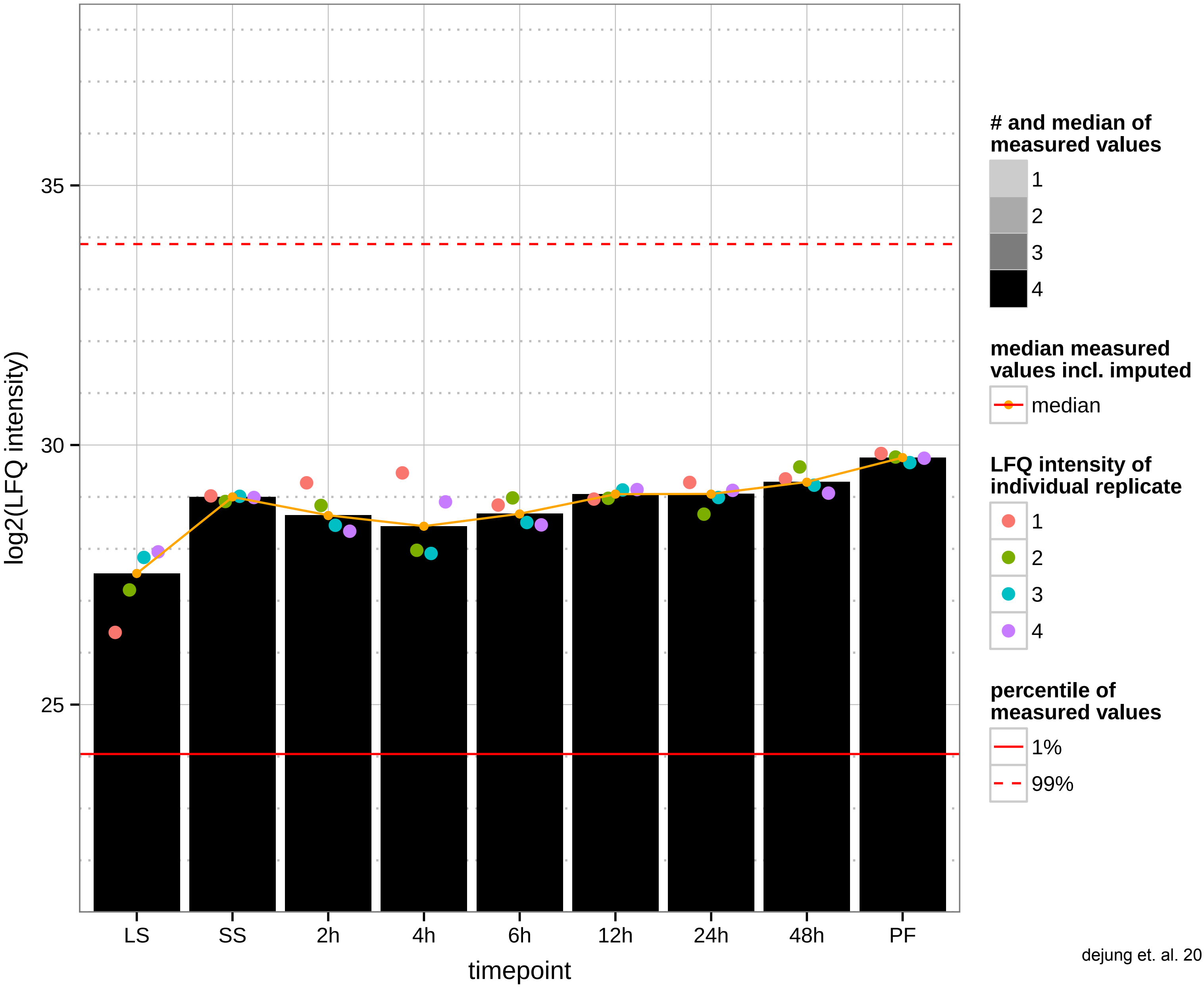
nucleoporin interacting component (NUP93), putative
Tb927.10.7060
AGOF: null
AGOC: nuclear pore
AGOP: transport
PGOF: null
PGOC: nuclear pore
PGOP: transport





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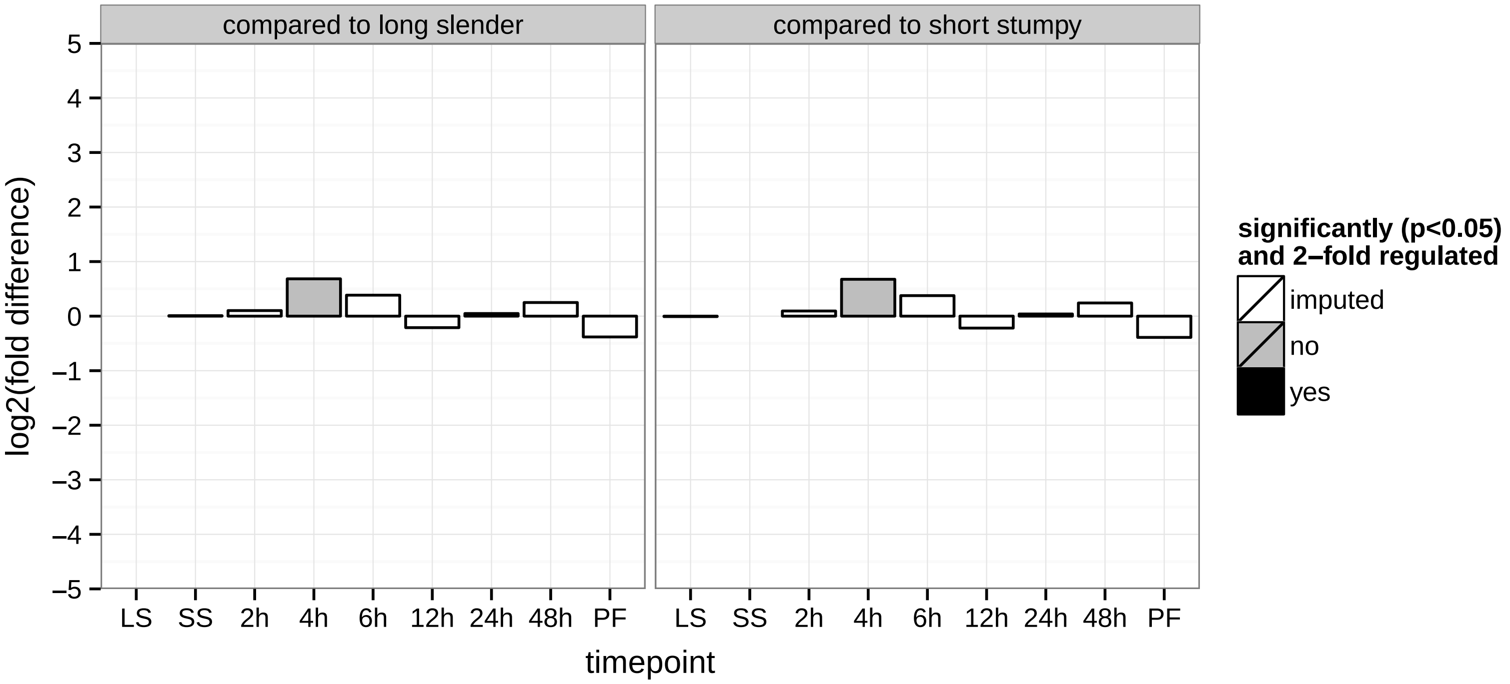
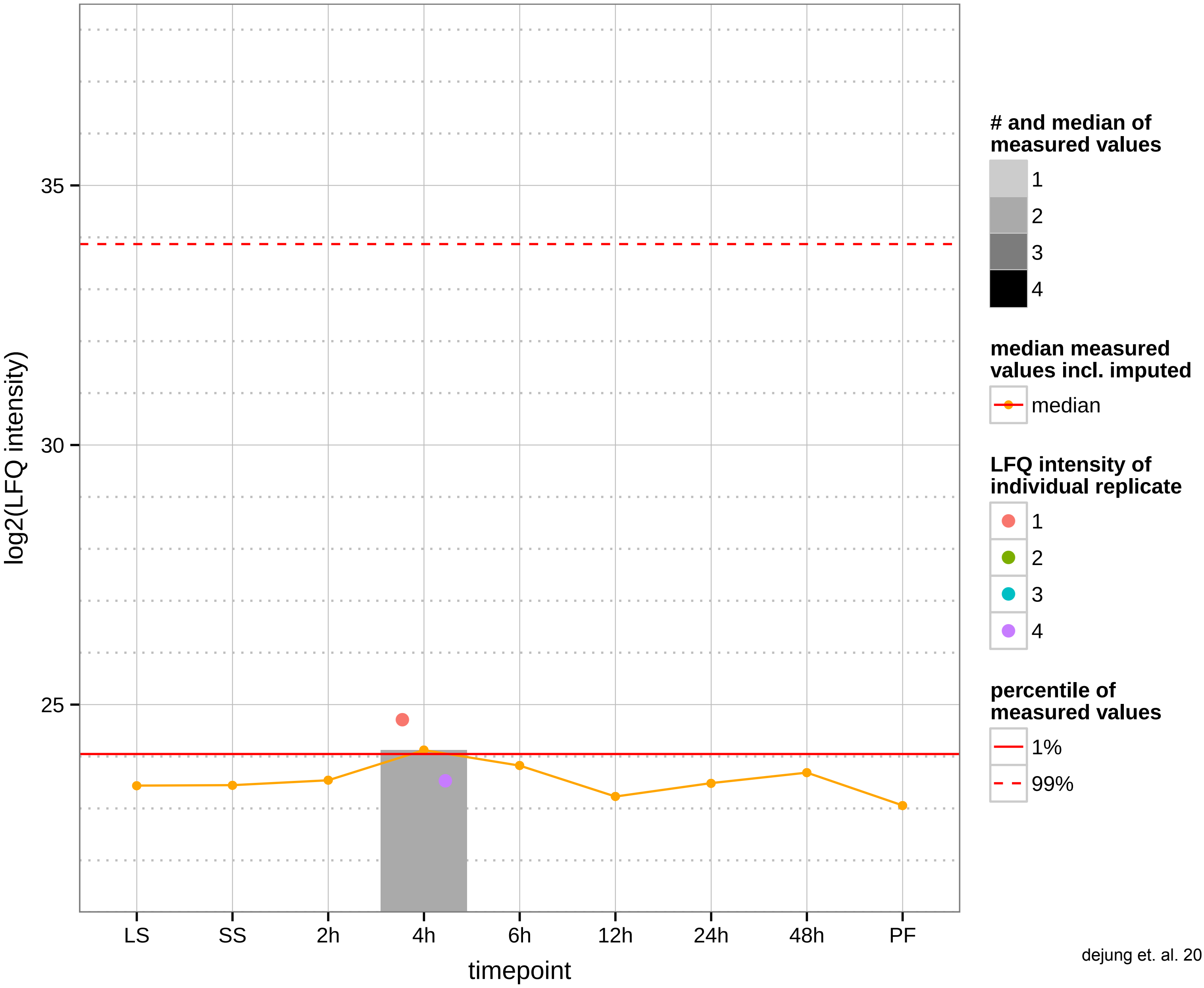
ATP−dependent DEAD/H RNA helicase, putative, RNA helicase
Tb927.10.7080
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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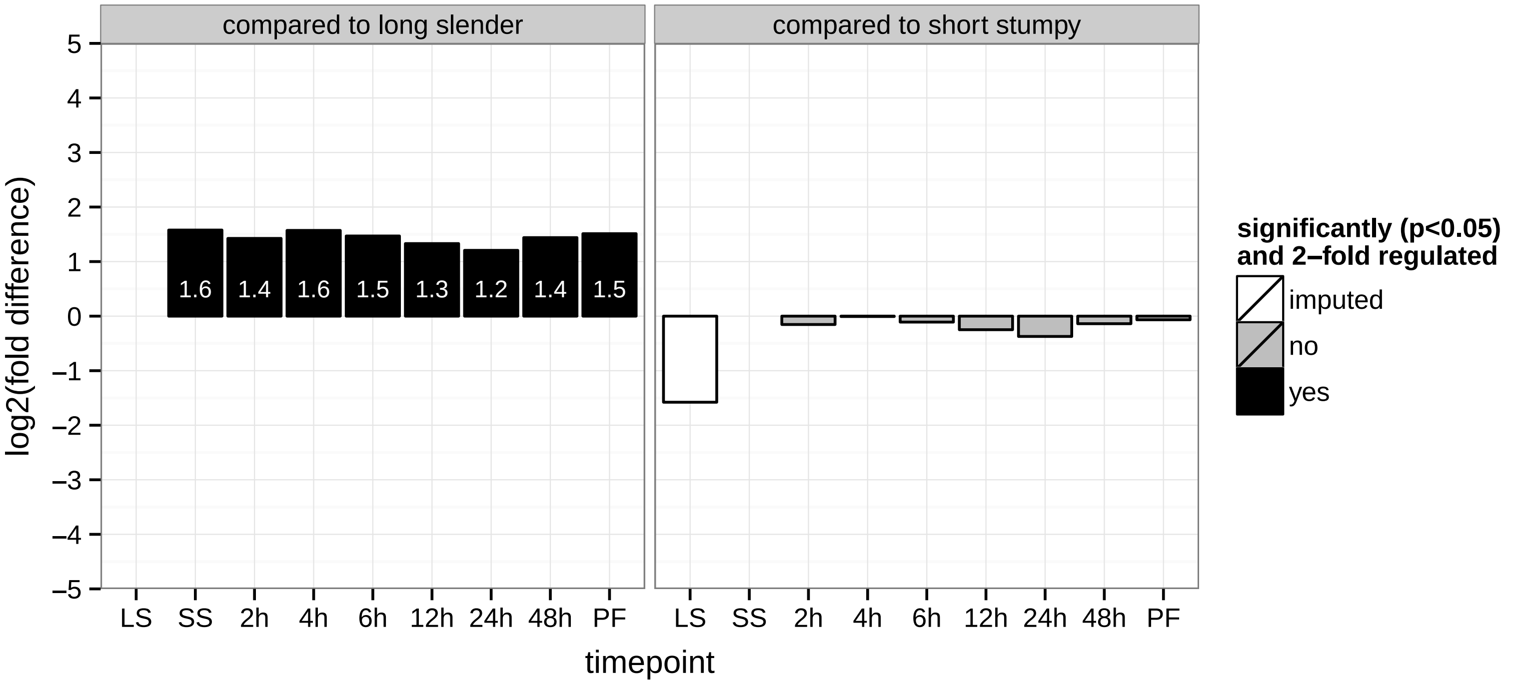
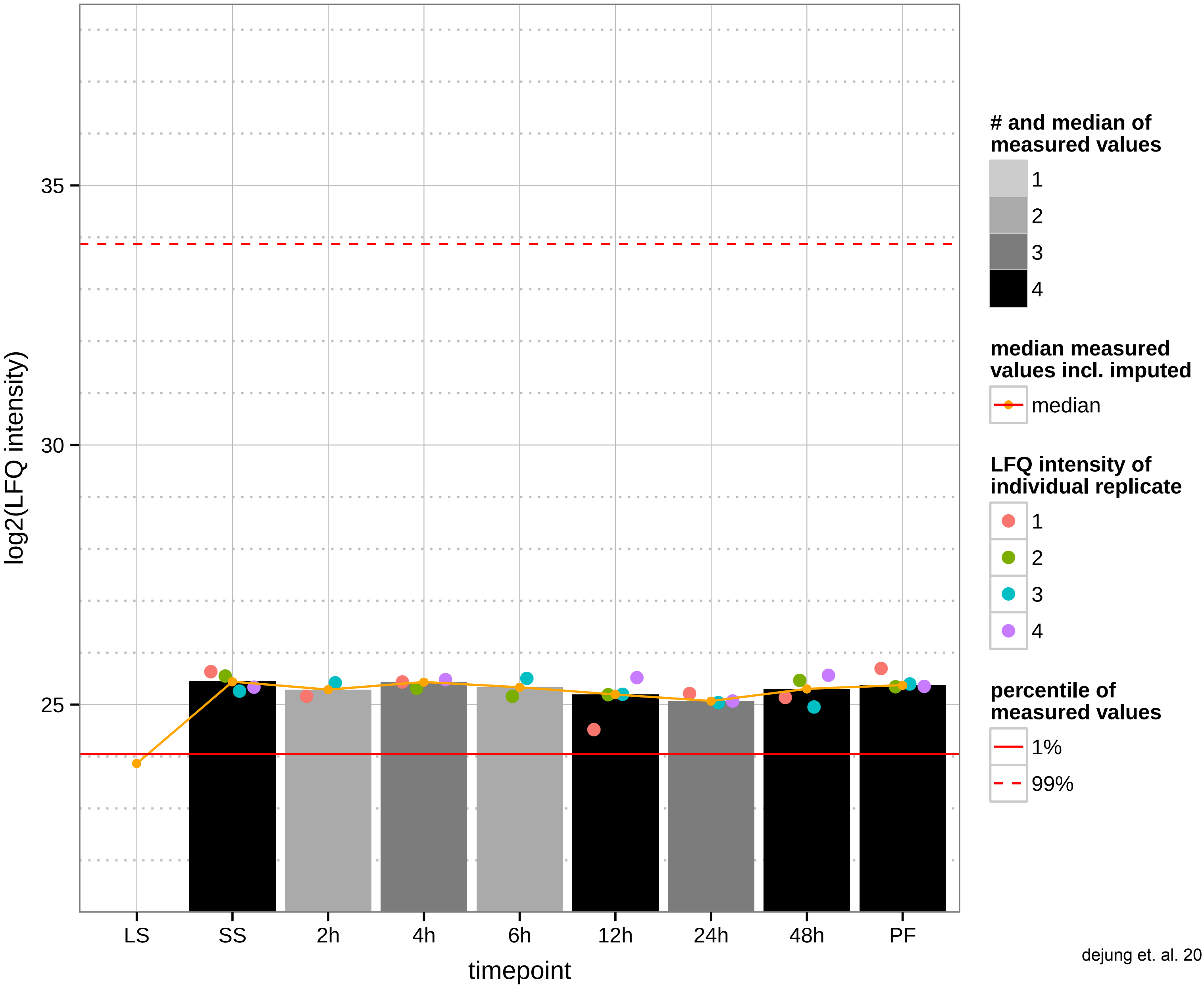
hypothetical protein, conserved
Tb927.10.7120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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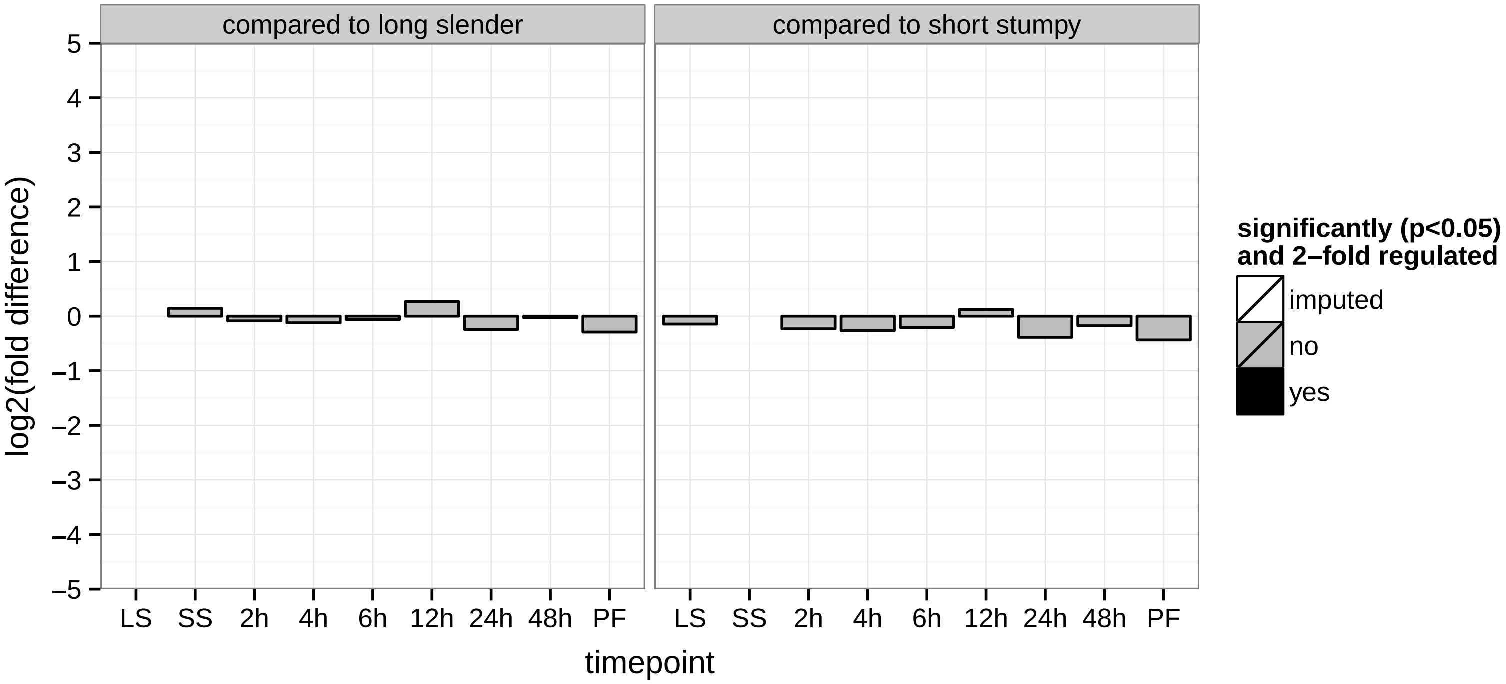
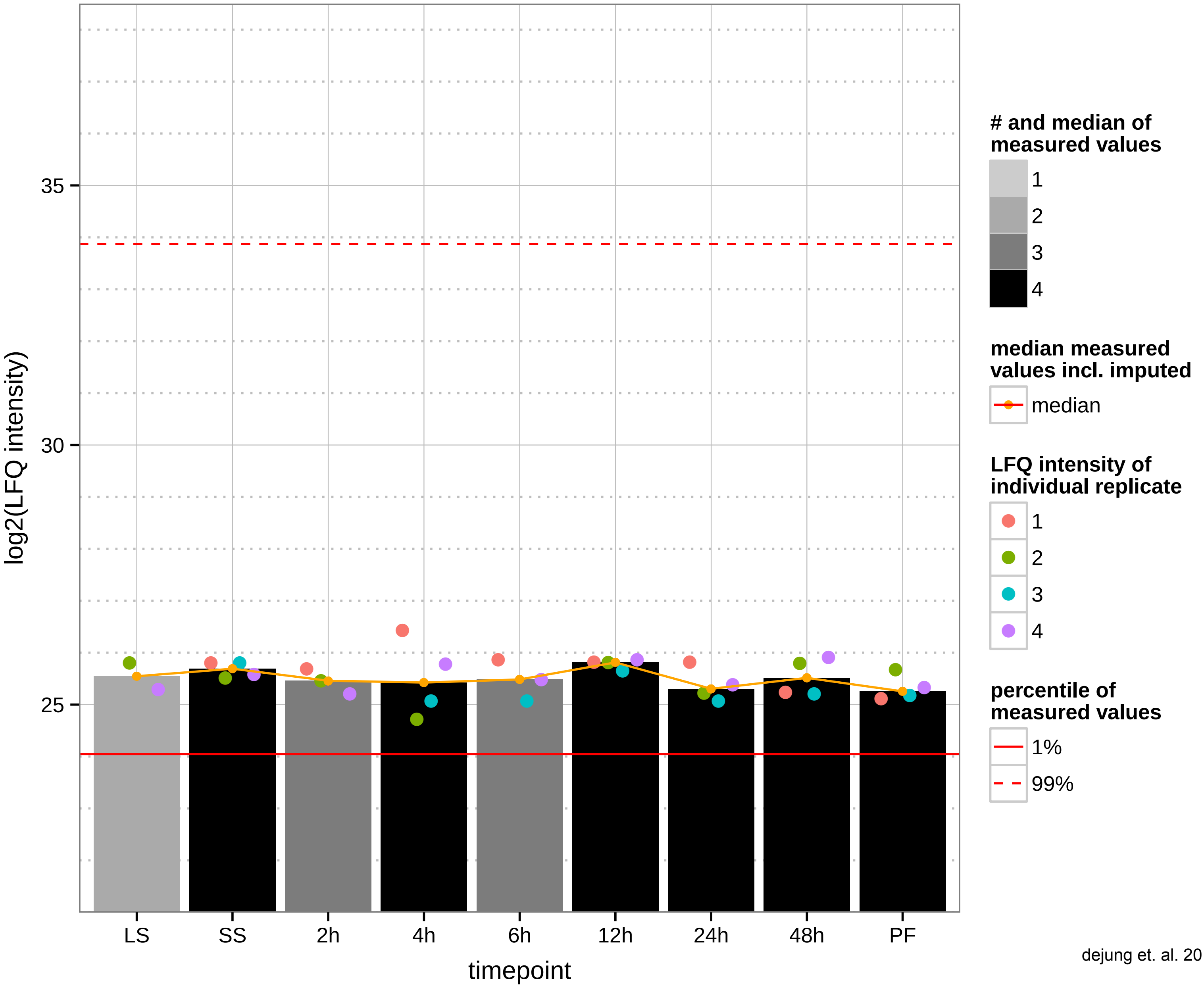
hypothetical protein, conserved
Tb927.10.7130
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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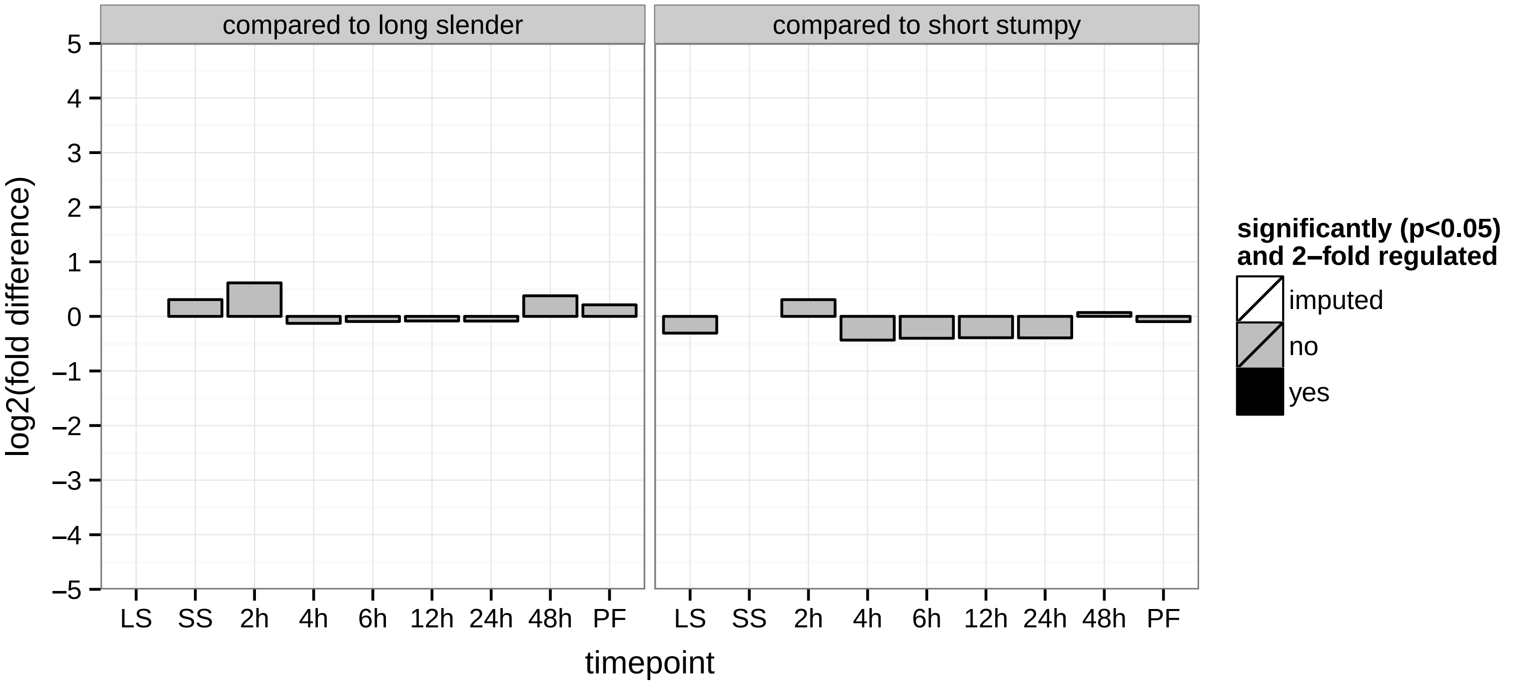
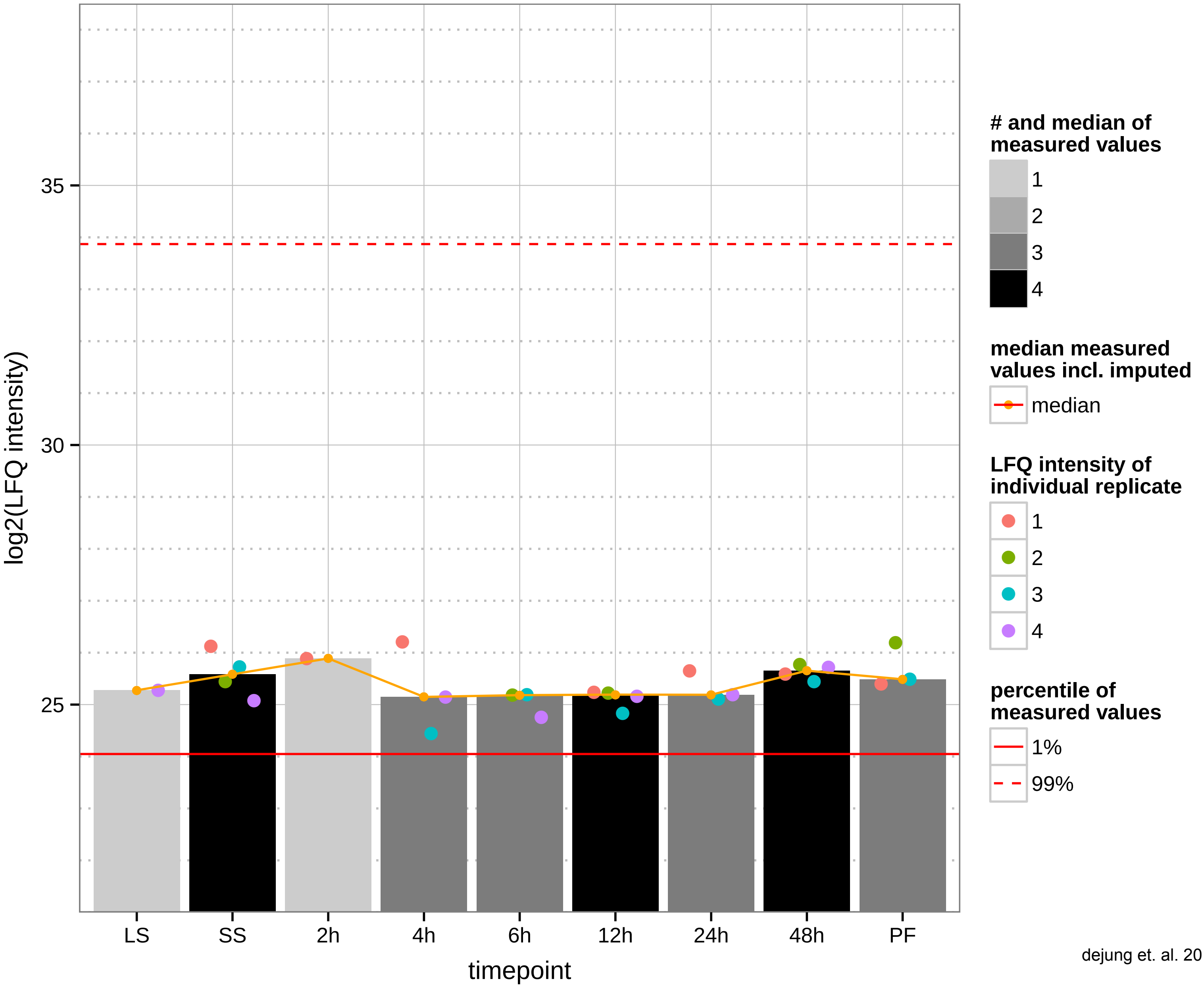
hypothetical protein, conserved
Tb927.10.7200
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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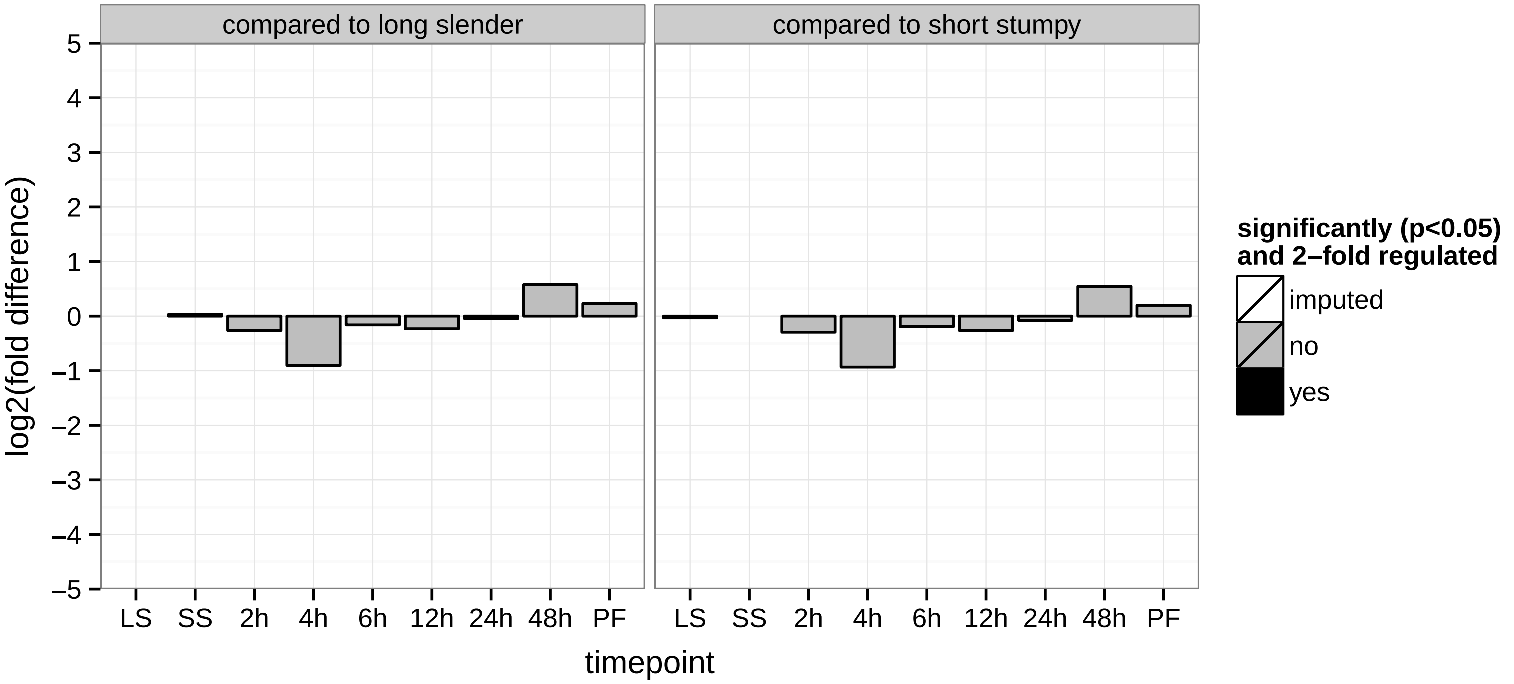
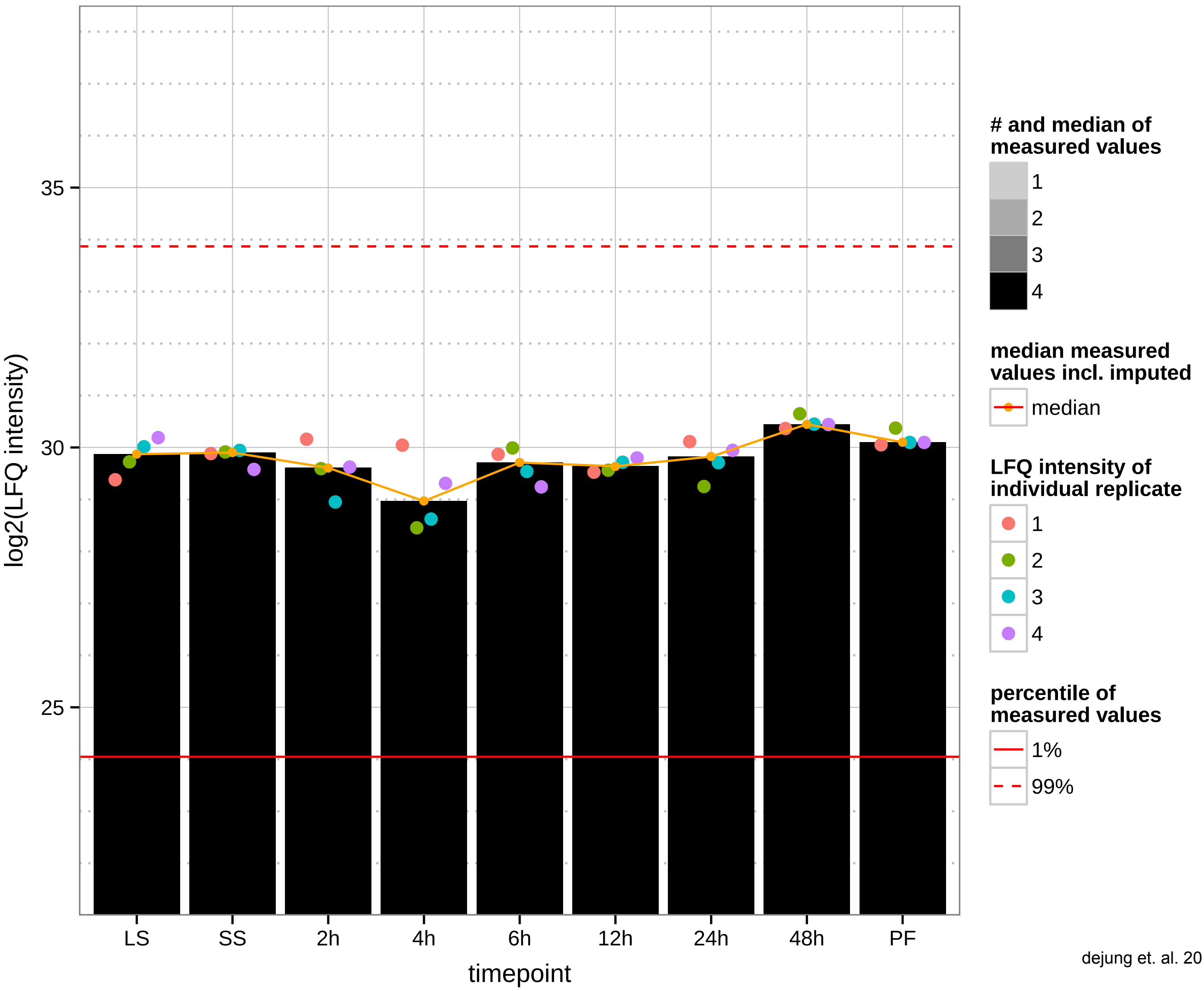
hypothetical protein, conserved
Tb927.10.7230
AGOF: null, ATP binding, nucleoside diphosphate kinase activity
AGOC: null
AGOP: null, CTP biosynthetic process, GTP biosynthetic process, UTP biosynthetic process, oxidation–reduction process
PGOF: ATP binding, nucleoside diphosphate kinase activity
PGOC: null
PGOP: CTP biosynthetic process, GTP biosynthetic process, UTP biosynthetic process, nucleoside diphosphate phosphoryla





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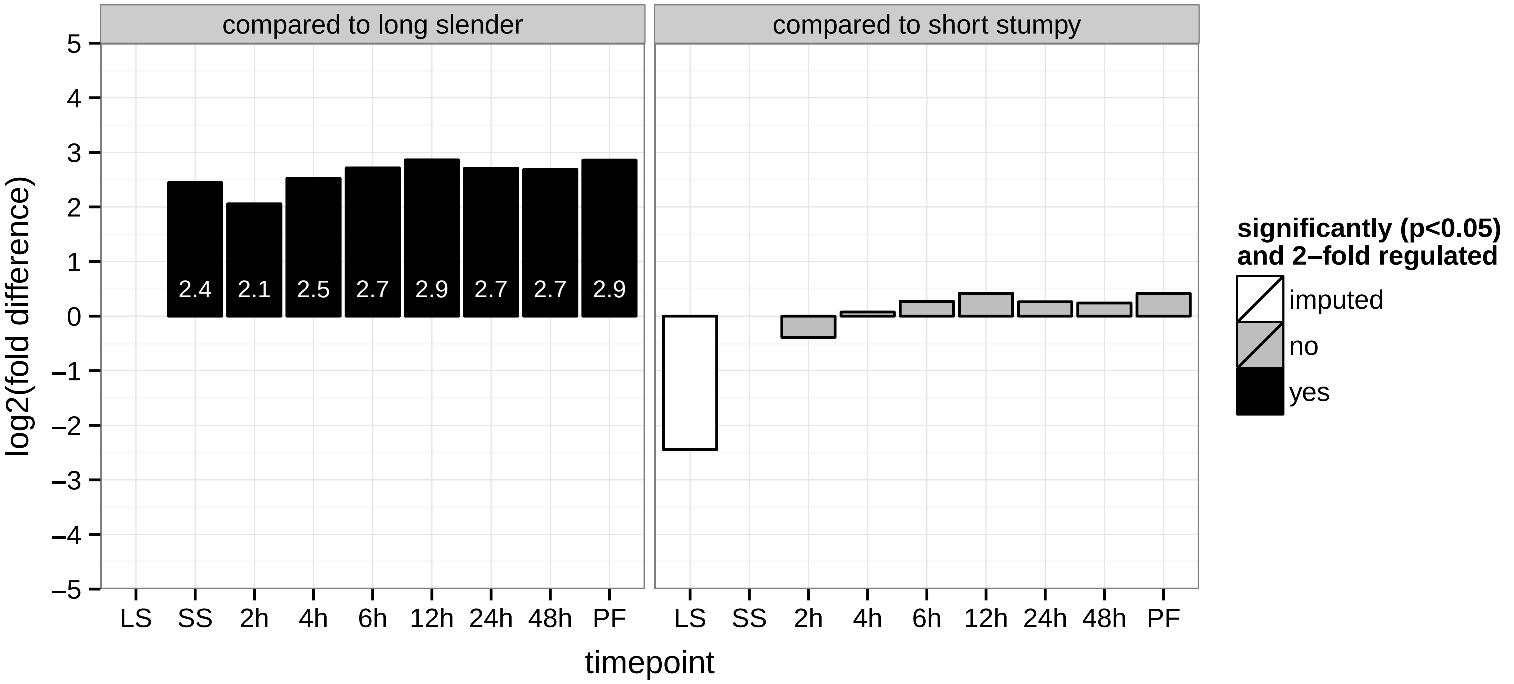
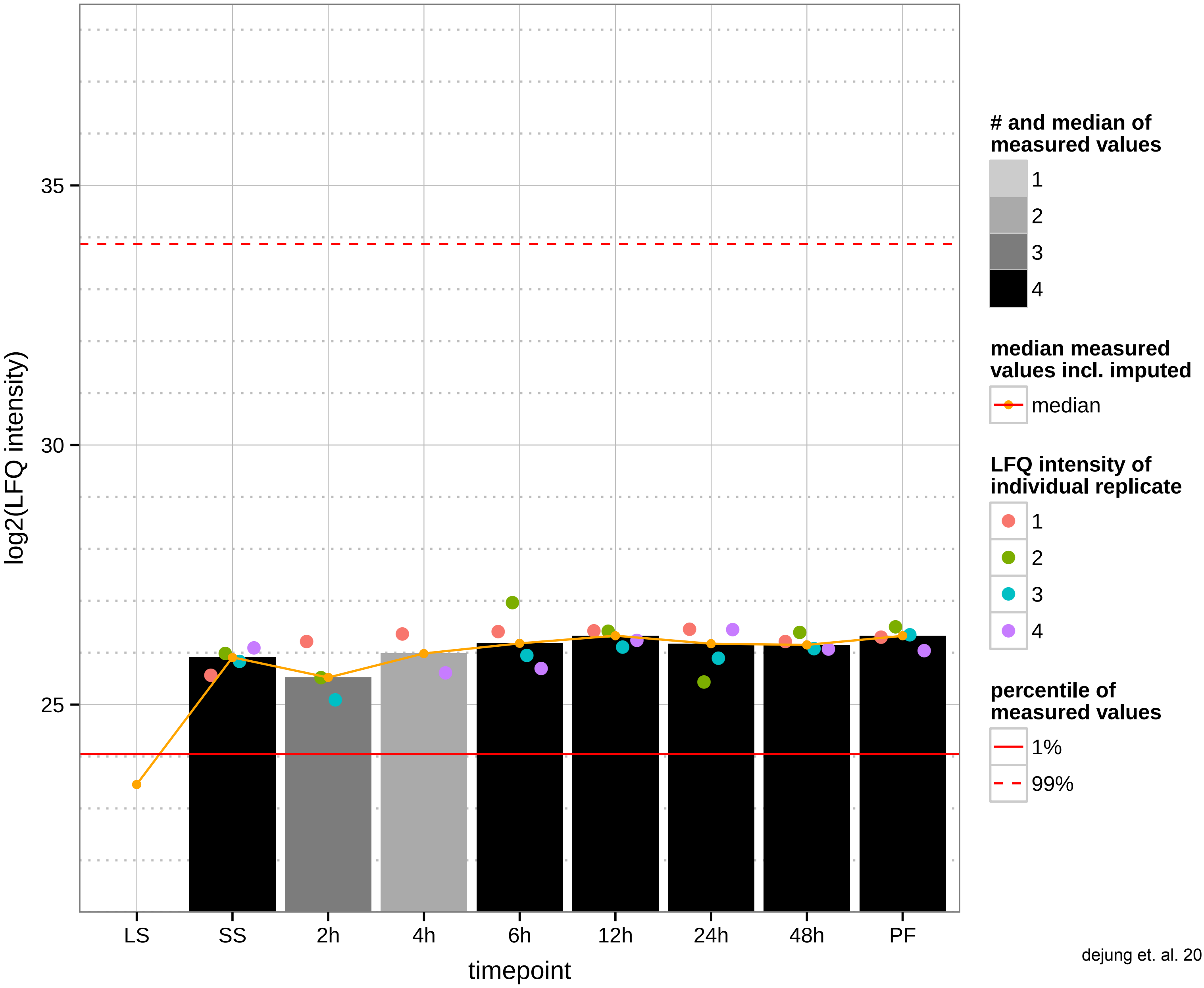
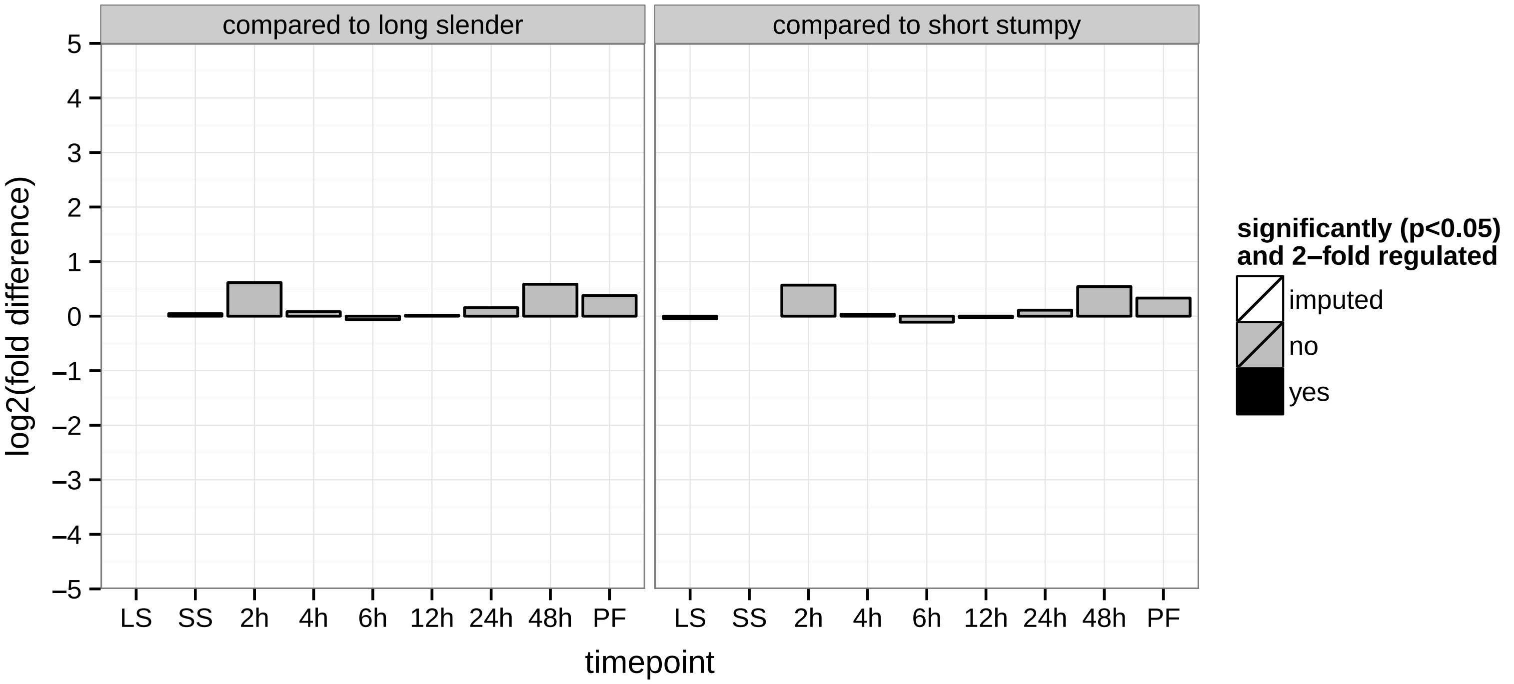
pre–mRNA splicing factor ATP–dependent RNA helicase, putative, RNA helicase
Tb927.10.7280
AGOF: ATP binding, ATP–dependent RNA helicase activity, nucleic acid binding
AGOC: spliceosomal complex
AGOP: RNA splicing, RNA splicing, via transesterification reactions
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null

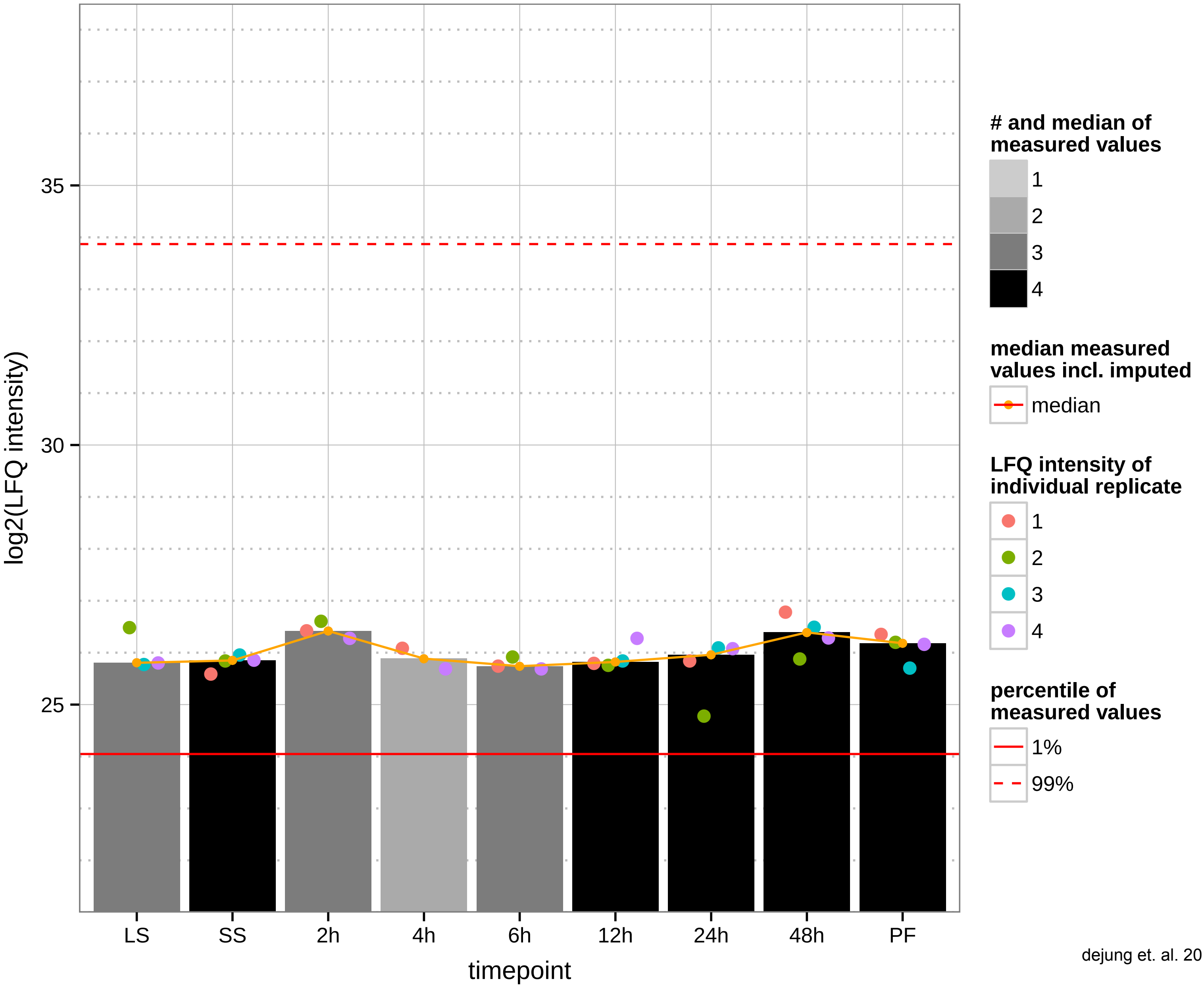




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.7350
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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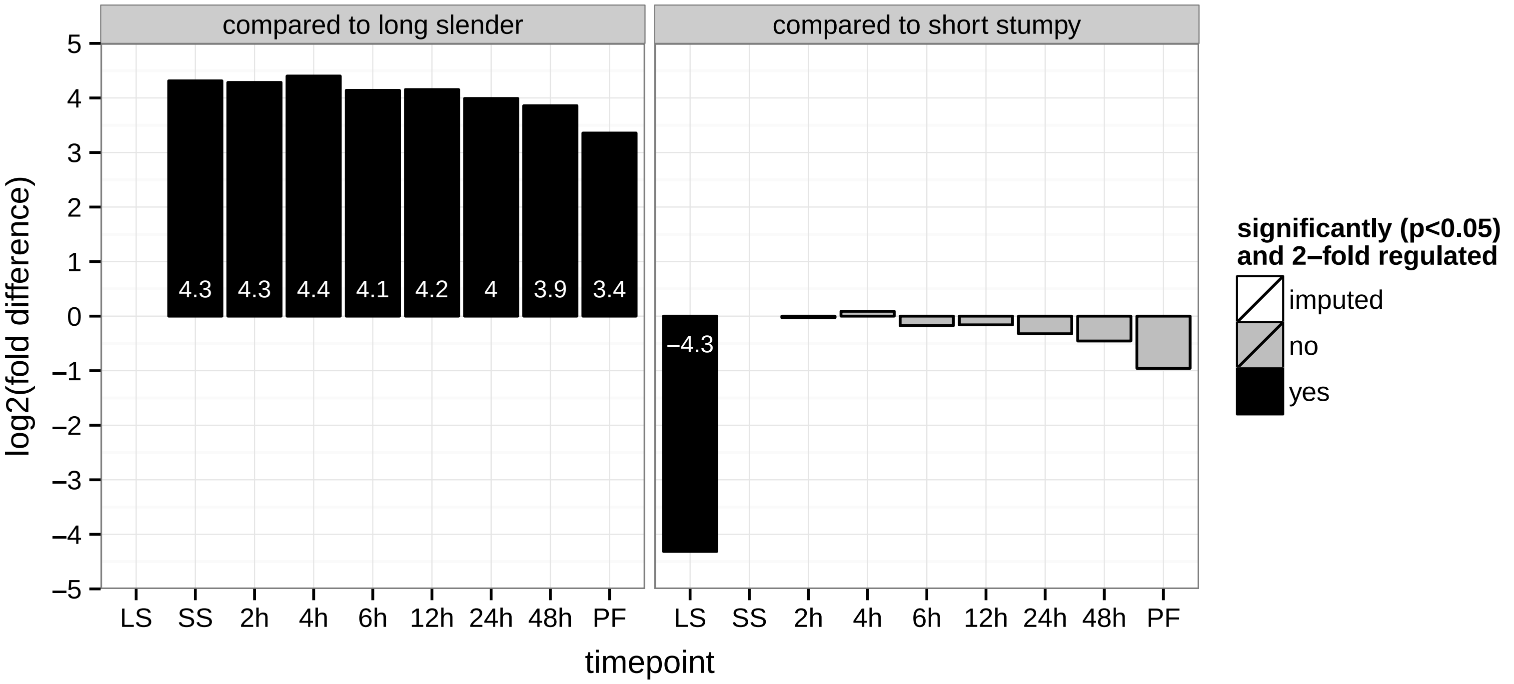
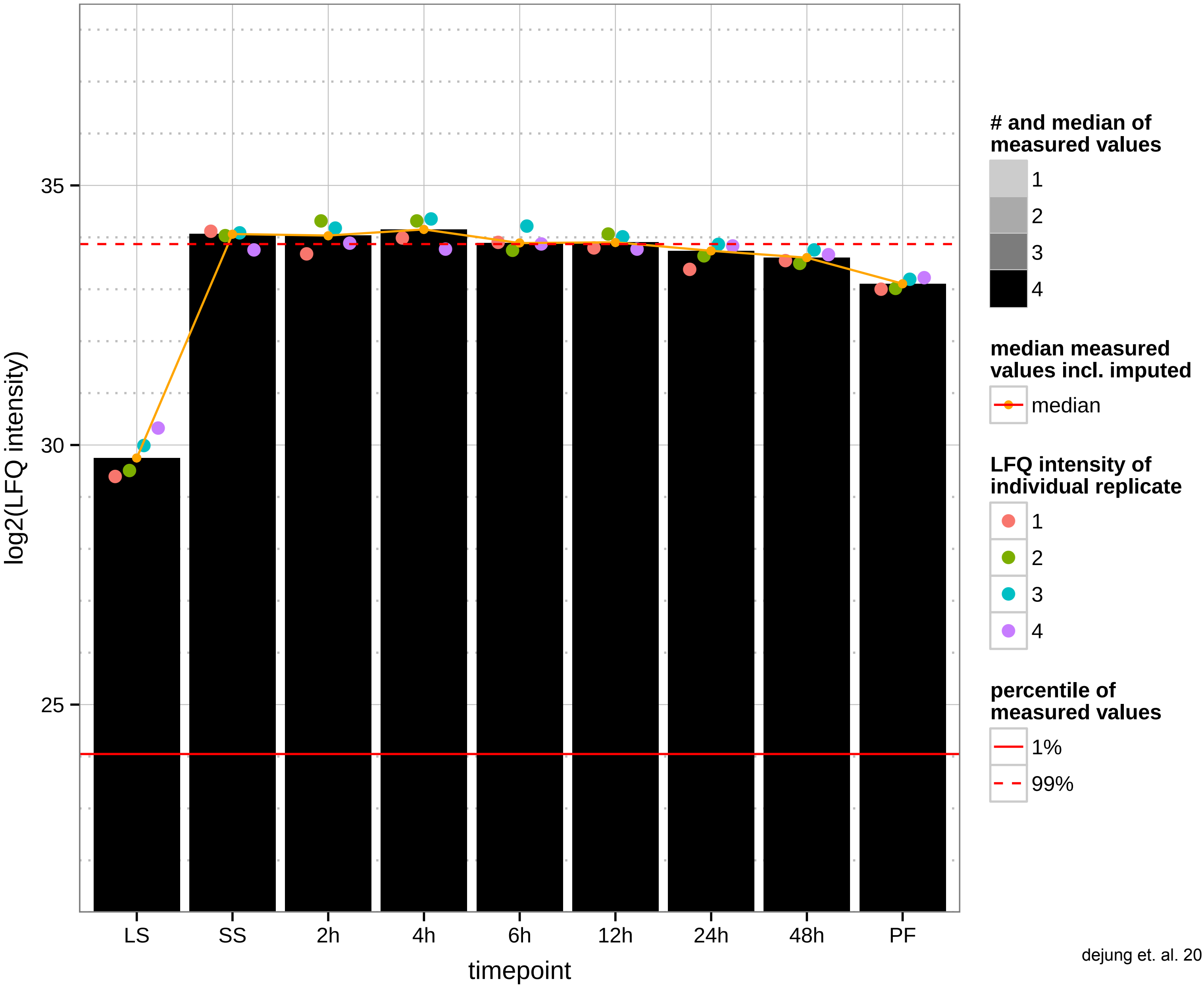
succinyl–CoA ligase [GDP–forming] beta–chain, putative
Tb927.10.7410
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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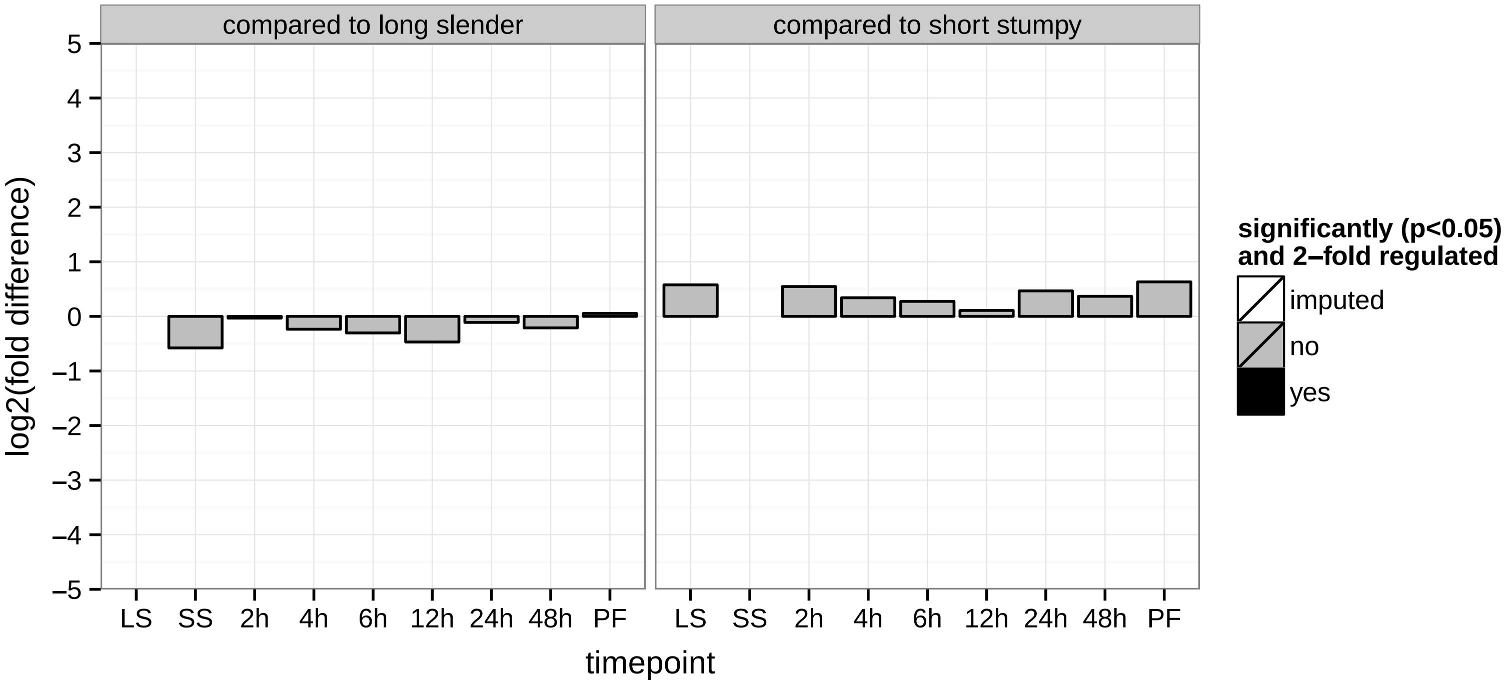
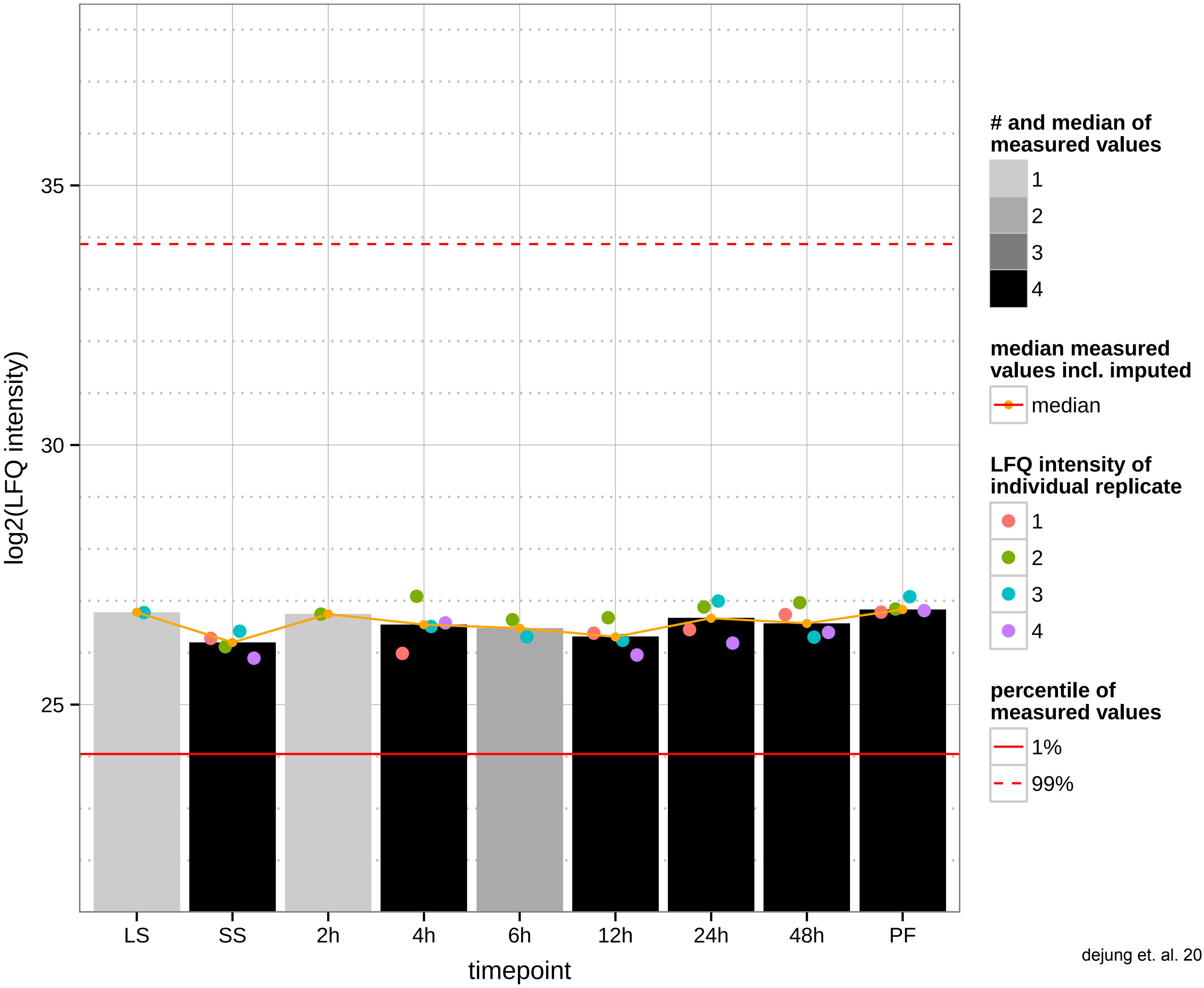
bromodomain factor 2 protein, putative
Tb927.10.7420
AGOF: histone binding
AGOC: nucleus
AGOP: chromatin remodeling, histone modification
PGOF: protein binding
PGOC: null
PGOP: null





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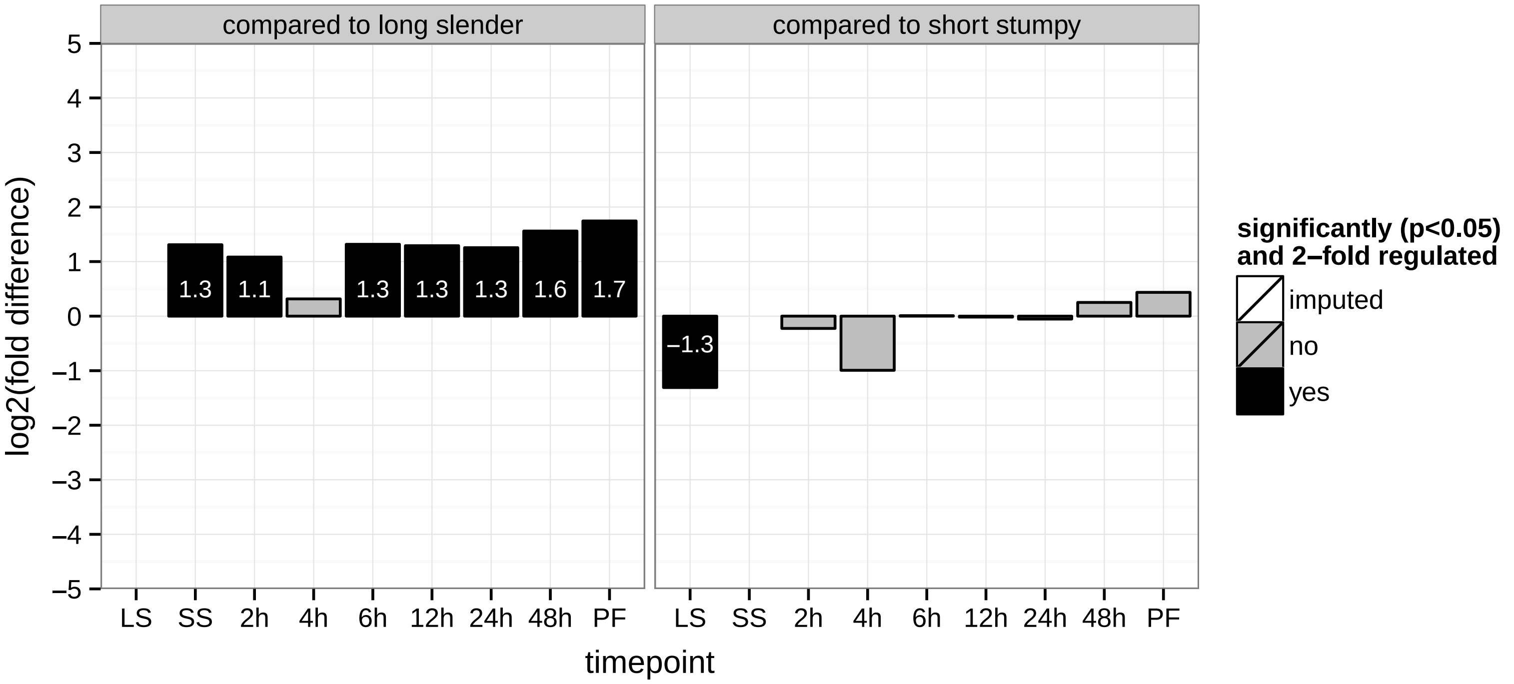
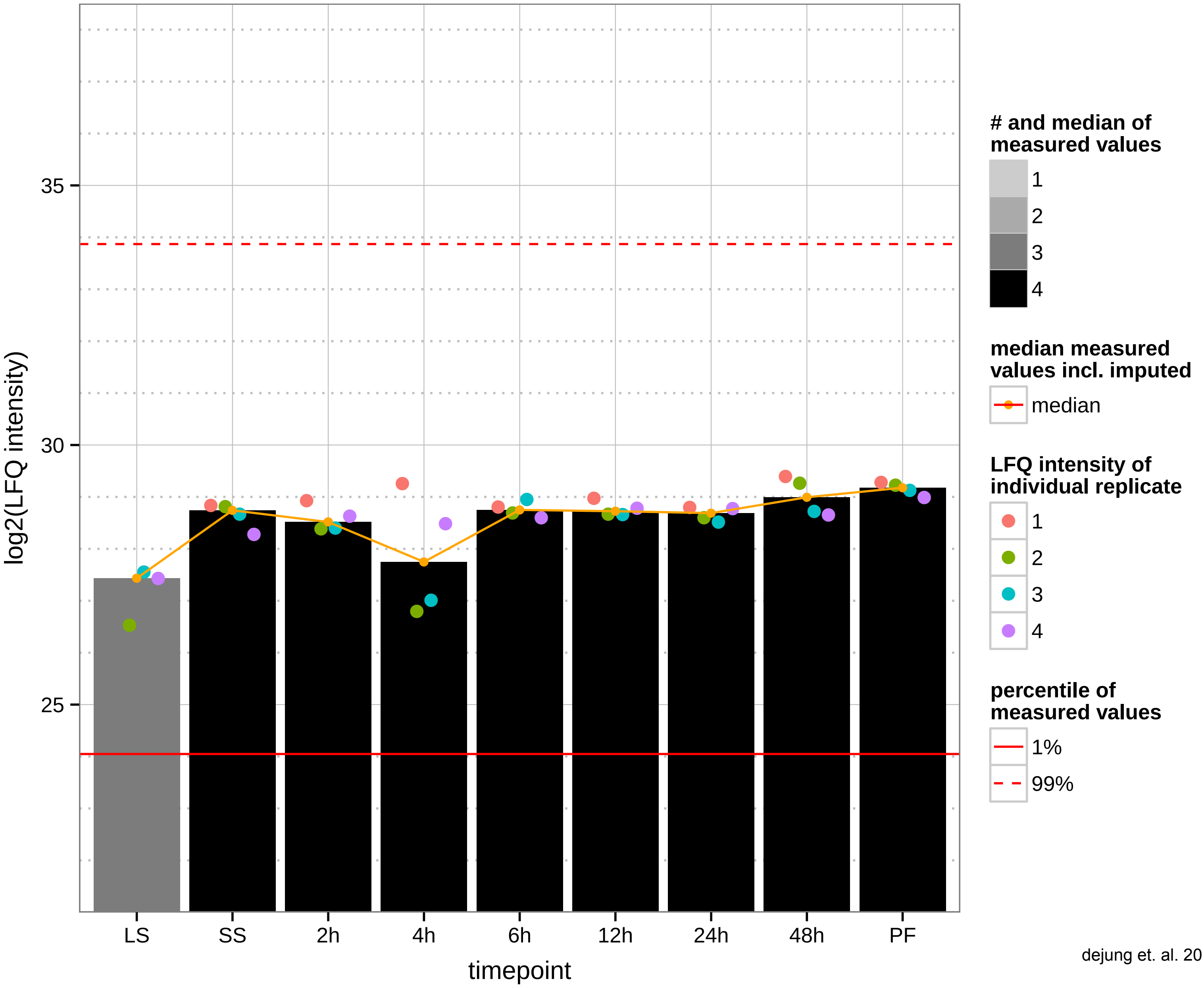
MTR4, ATP–dependent DEAD/H RNA helicase (MTR4)
Tb927.10.7440
AGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
AGOC: nucleus
AGOP: rRNA processing
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, hydrolase activity, acting on acid anhydrides, in phosp
PGOC: null
PGOP: null





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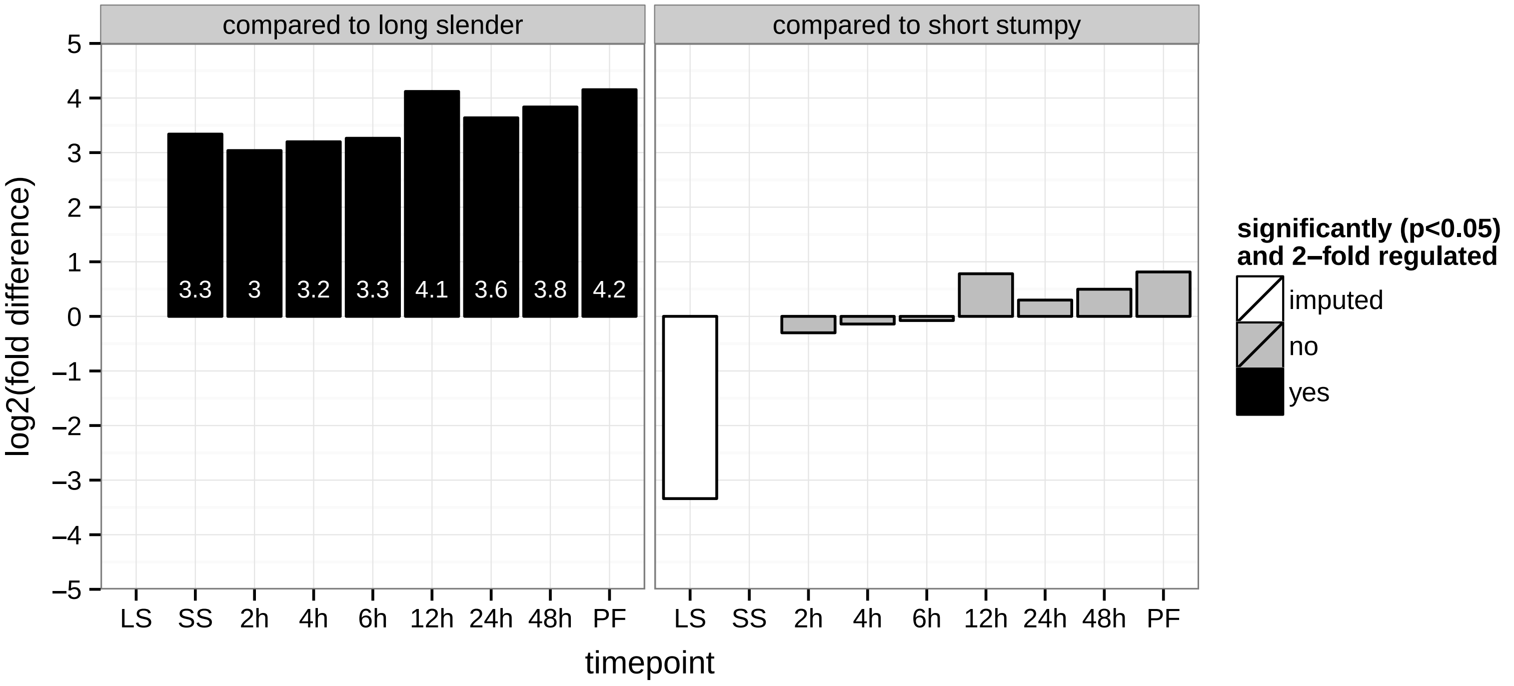
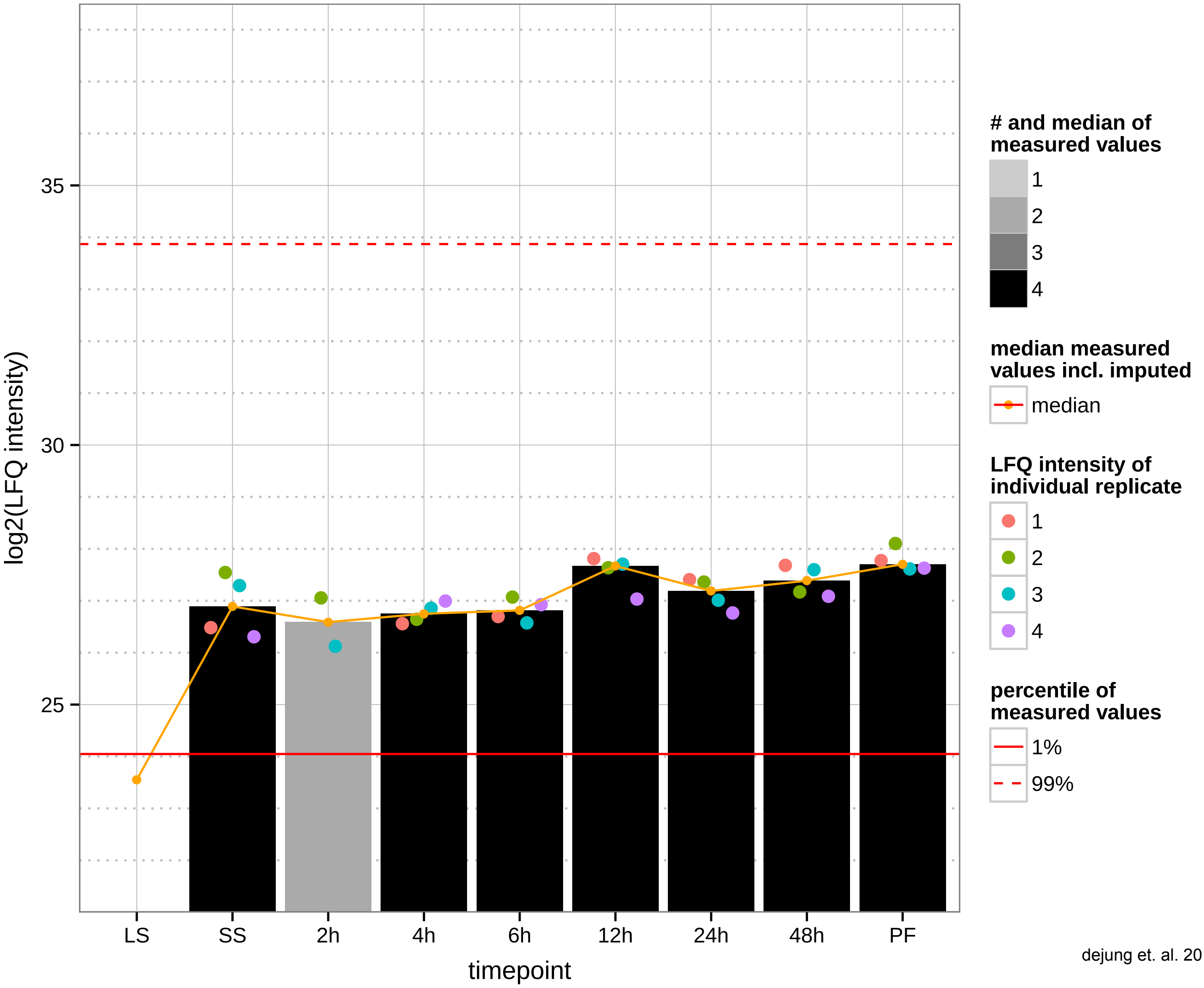
exosome complex exonuclease RRP41A, Rrp41p homologue (RRP41A)
Tb927.10.7450
AGOF: 3'−5'−exoribonuclease activity, RNA binding
AGOC: null
AGOP: RNA processing, rRNA processing
PGOF: null
PGOC: null
PGOP: null





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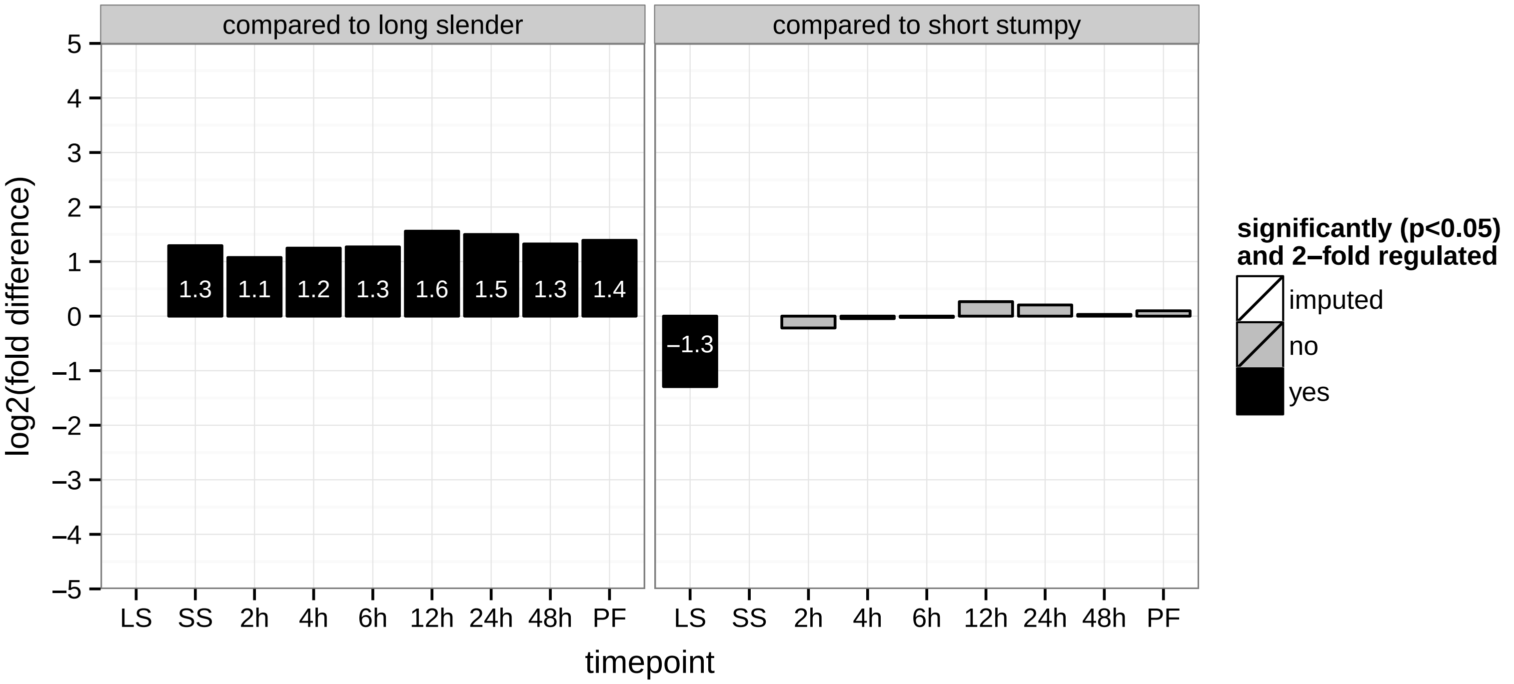
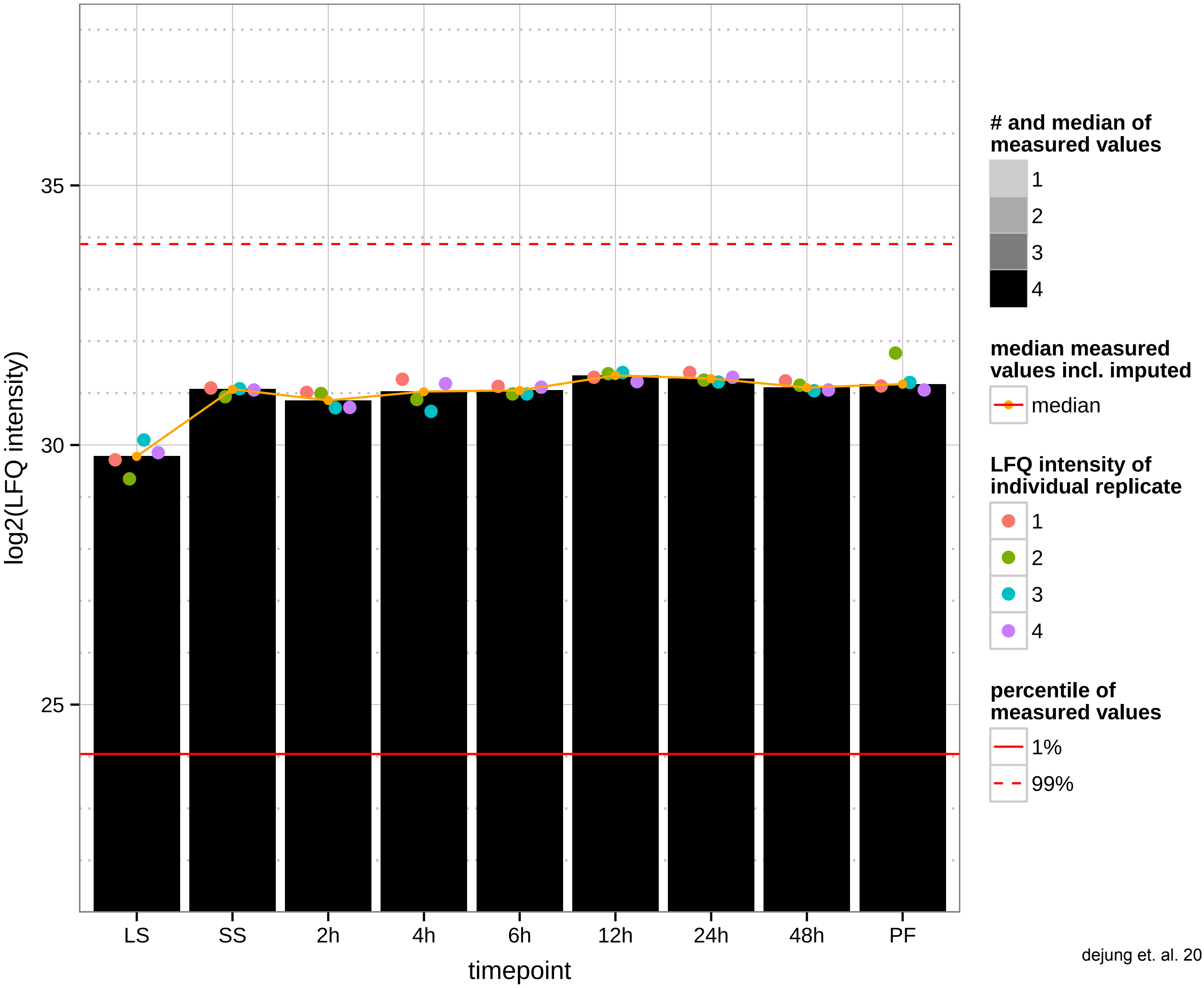
fibrillarin (NOP1)
Tb927.10.7500
AGOF: RNA binding, rRNA 2'–O–ribose methylation guide activity
AGOC: box C/D snoRNP complex, nucleus
AGOP: rRNA processing
PGOF: RNA binding, methyltransferase activity
PGOC: null
PGOP: rRNA processing, tRNA processing





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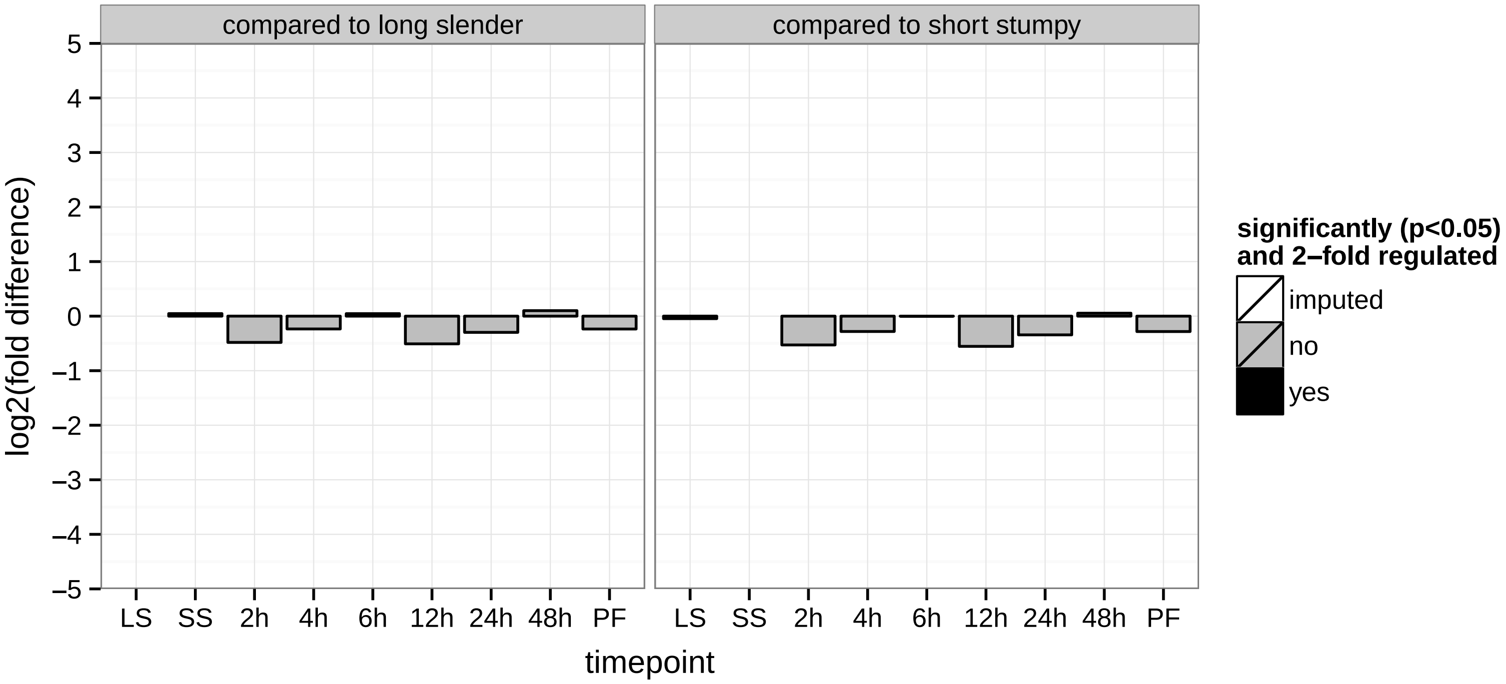
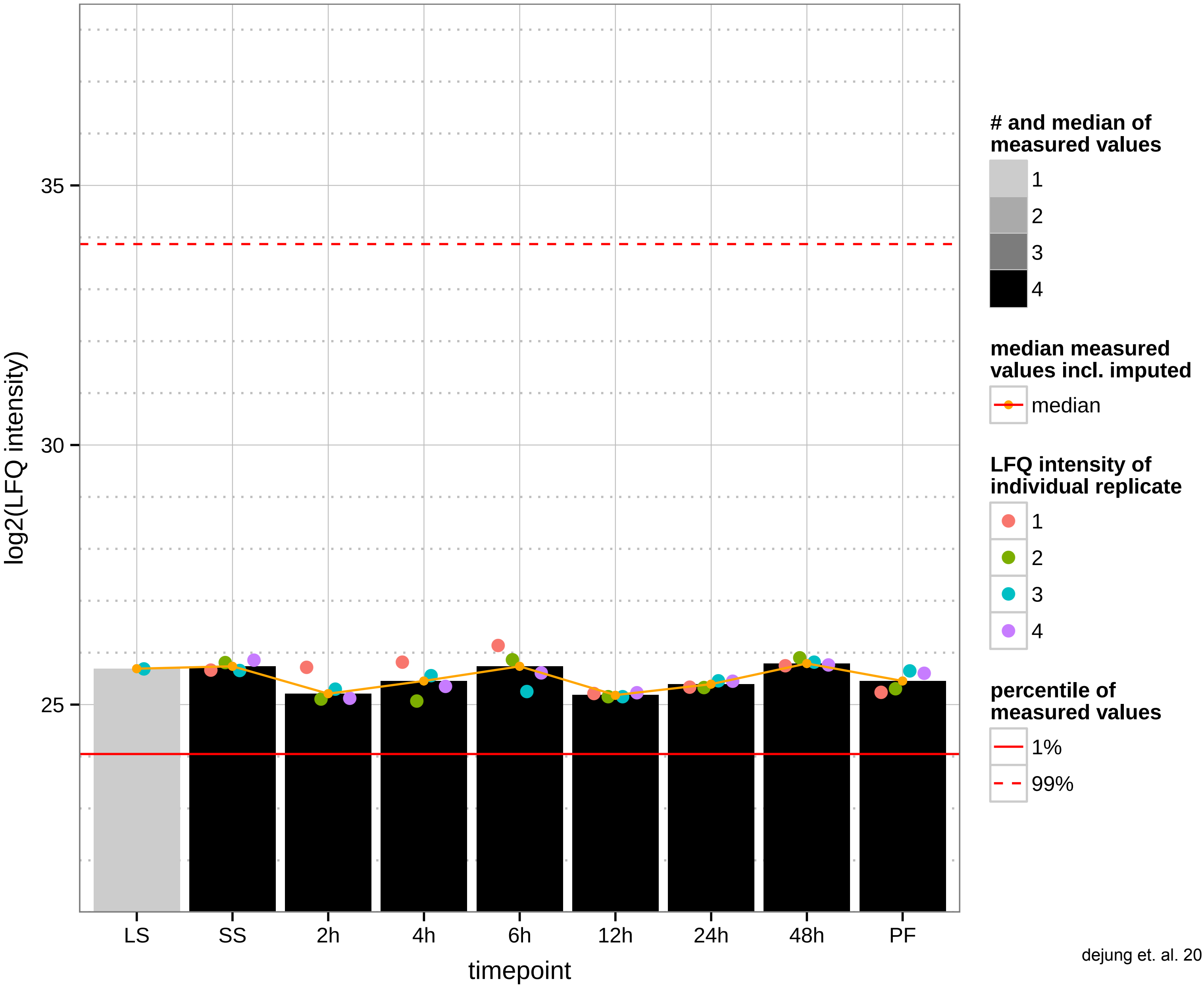
chromatin binding protein, putative
Tb927.10.7510
AGOF: Ran GTPase binding, chromatin binding
AGOC: null
AGOP: chromosome organization
PGOF: null
PGOC: null
PGOP: null





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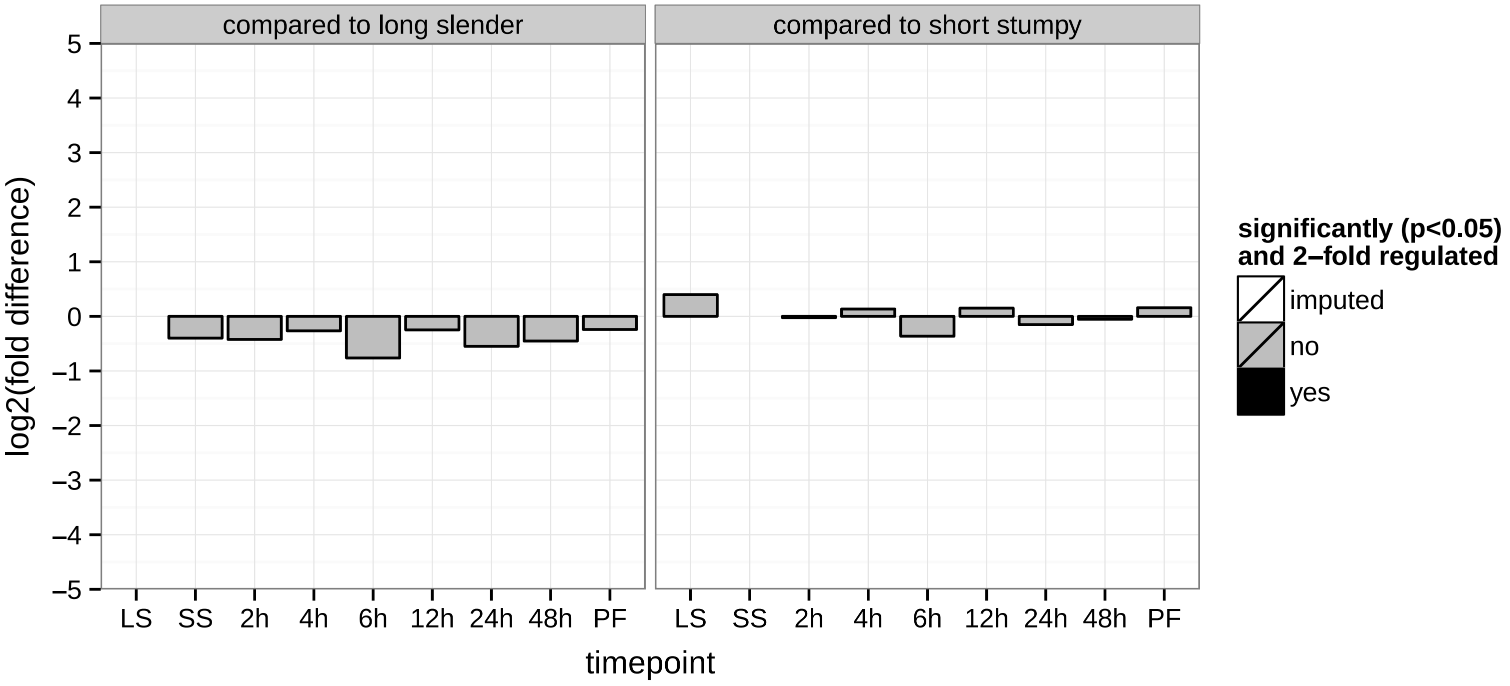
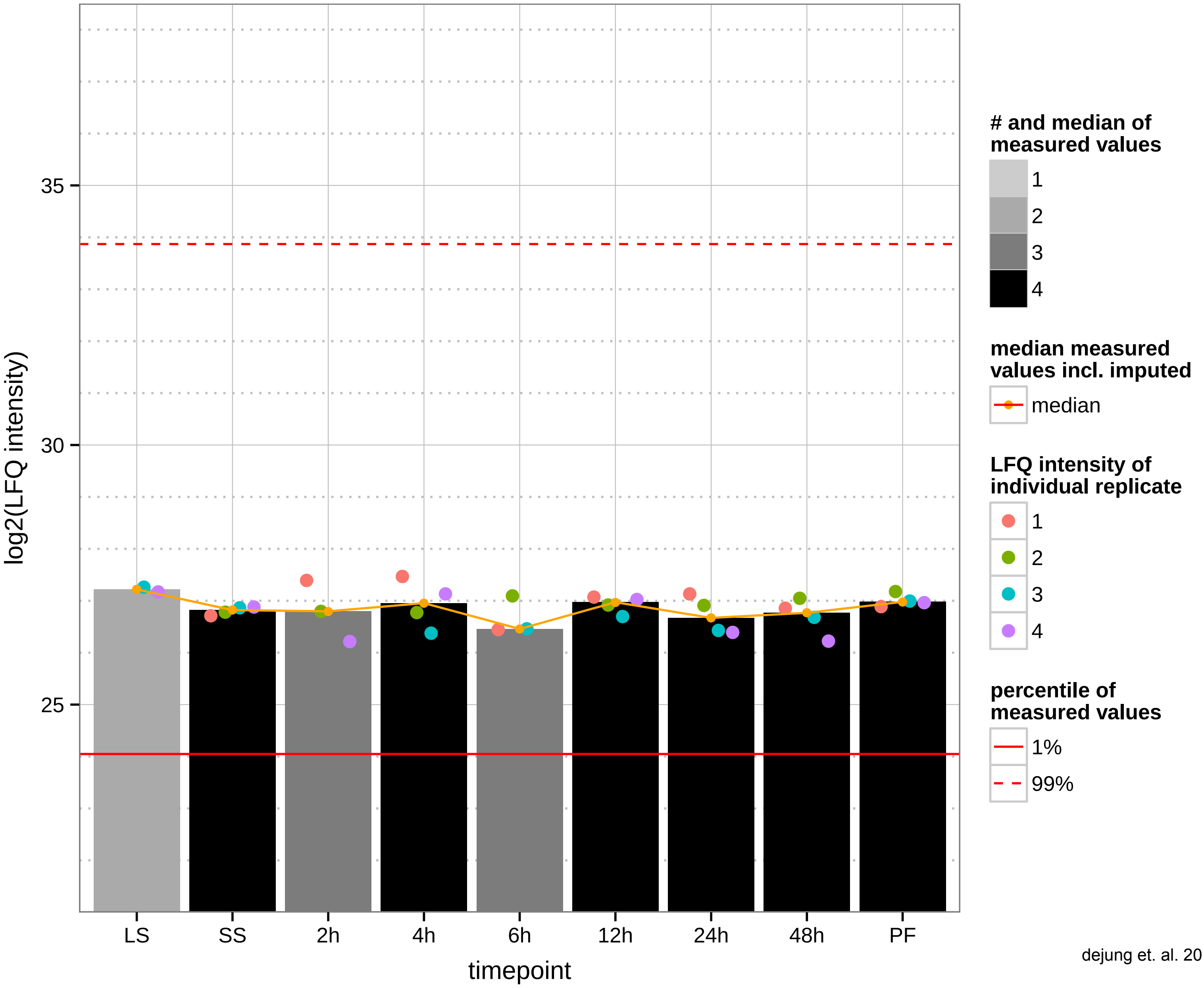
hypothetical protein, conserved
Tb927.10.7550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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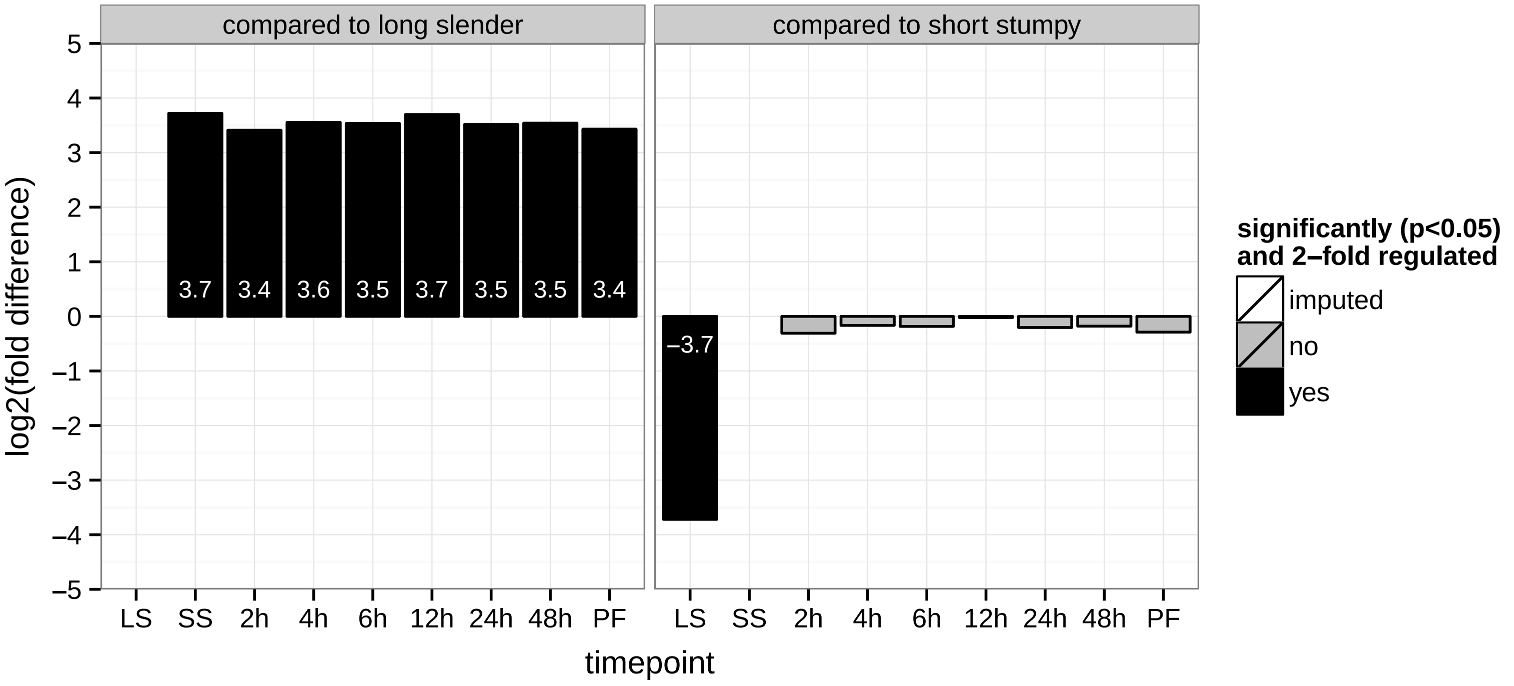
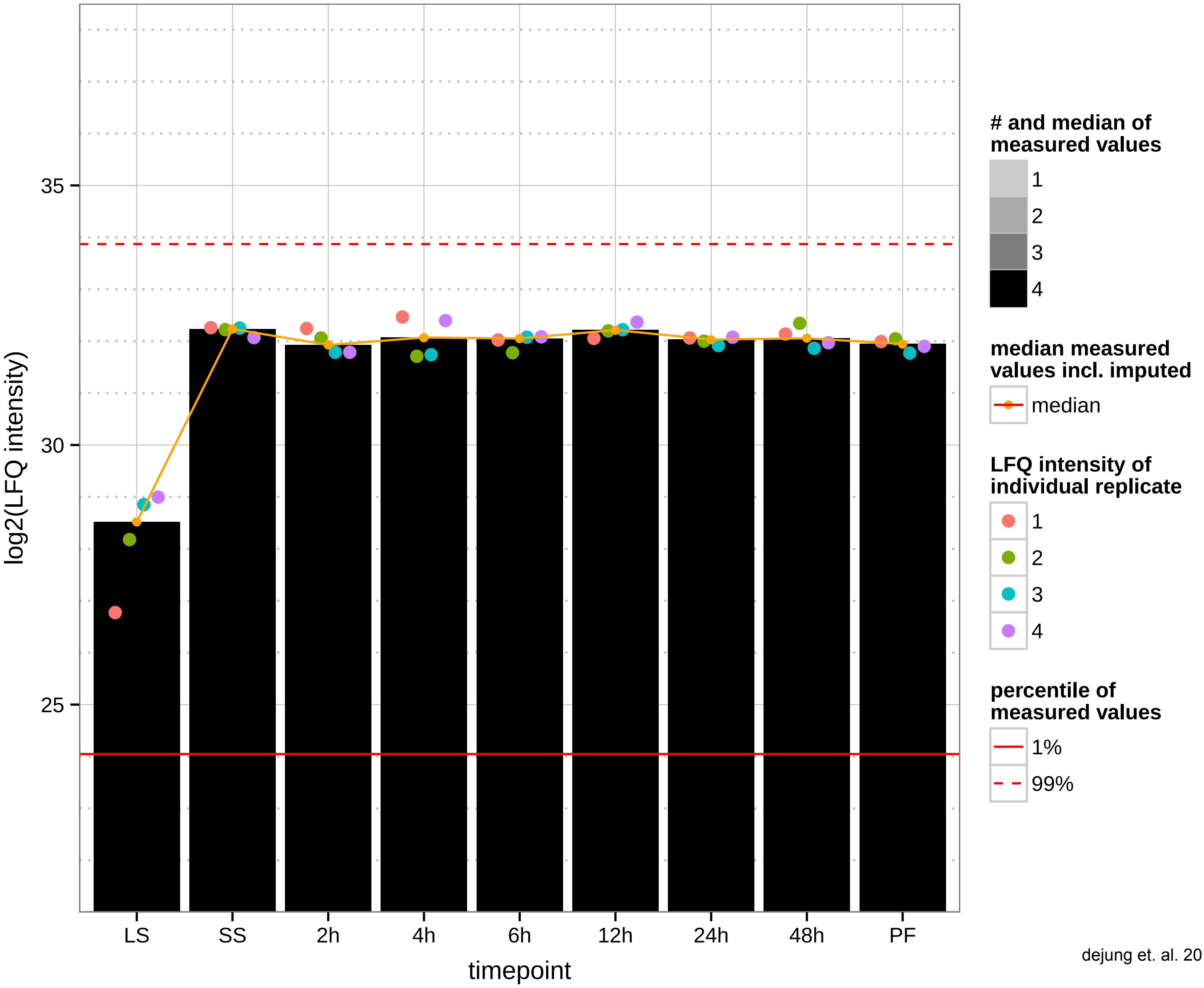
dihydrolipoamide acetyltransferase precursor, putative, dihydrolipoamide acetyltransferase E2 subunit
Tb927.10.7570
AGOF: null, dihydrolipoyllysine–residue acetyltransferase activity, pyruvate dehydrogenase activity
AGOC: null, mitochondrial pyruvate dehydrogenase complex, mitochondrion
AGOP: null, acetyl–CoA biosynthetic process from pyruvate
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: metabolic process





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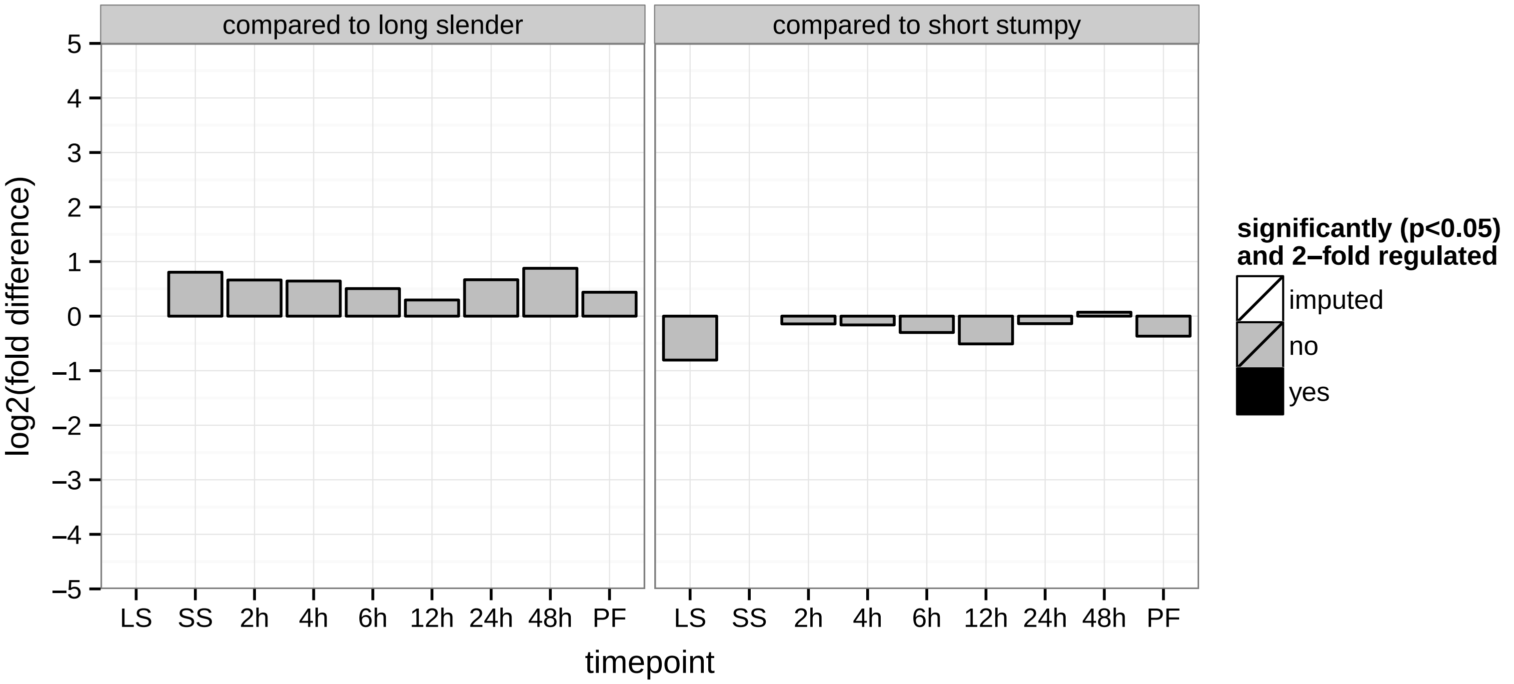
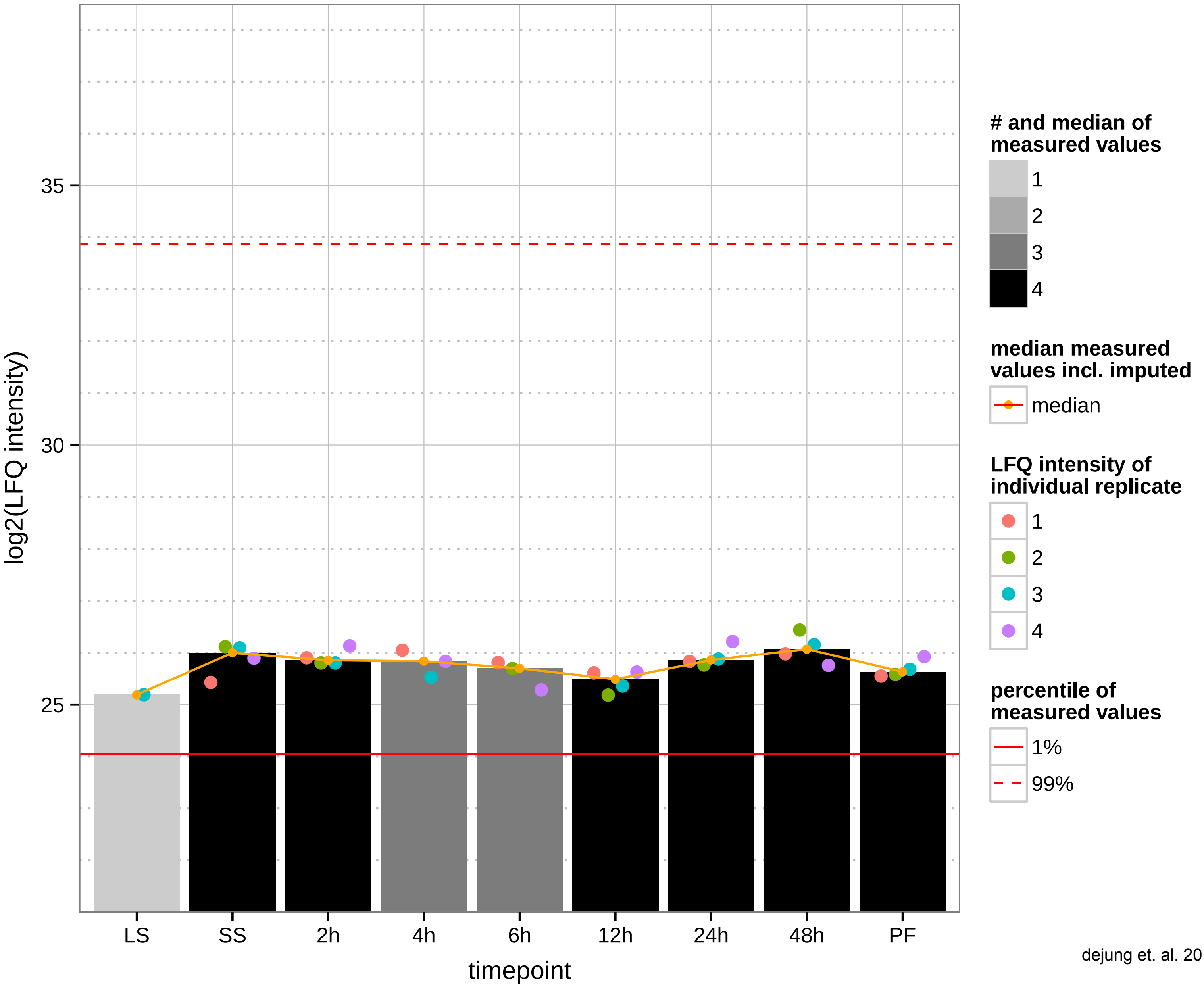
hypothetical protein, conserved
Tb927.10.7580
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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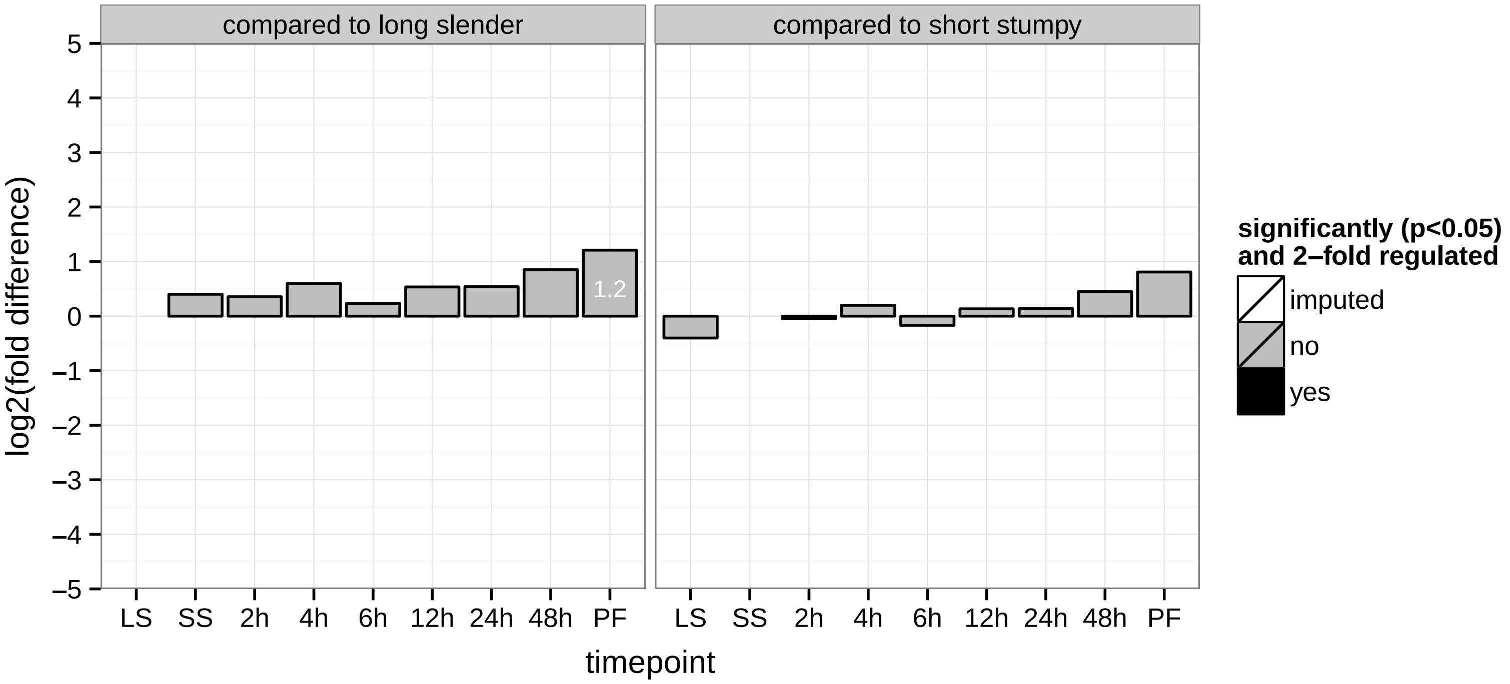
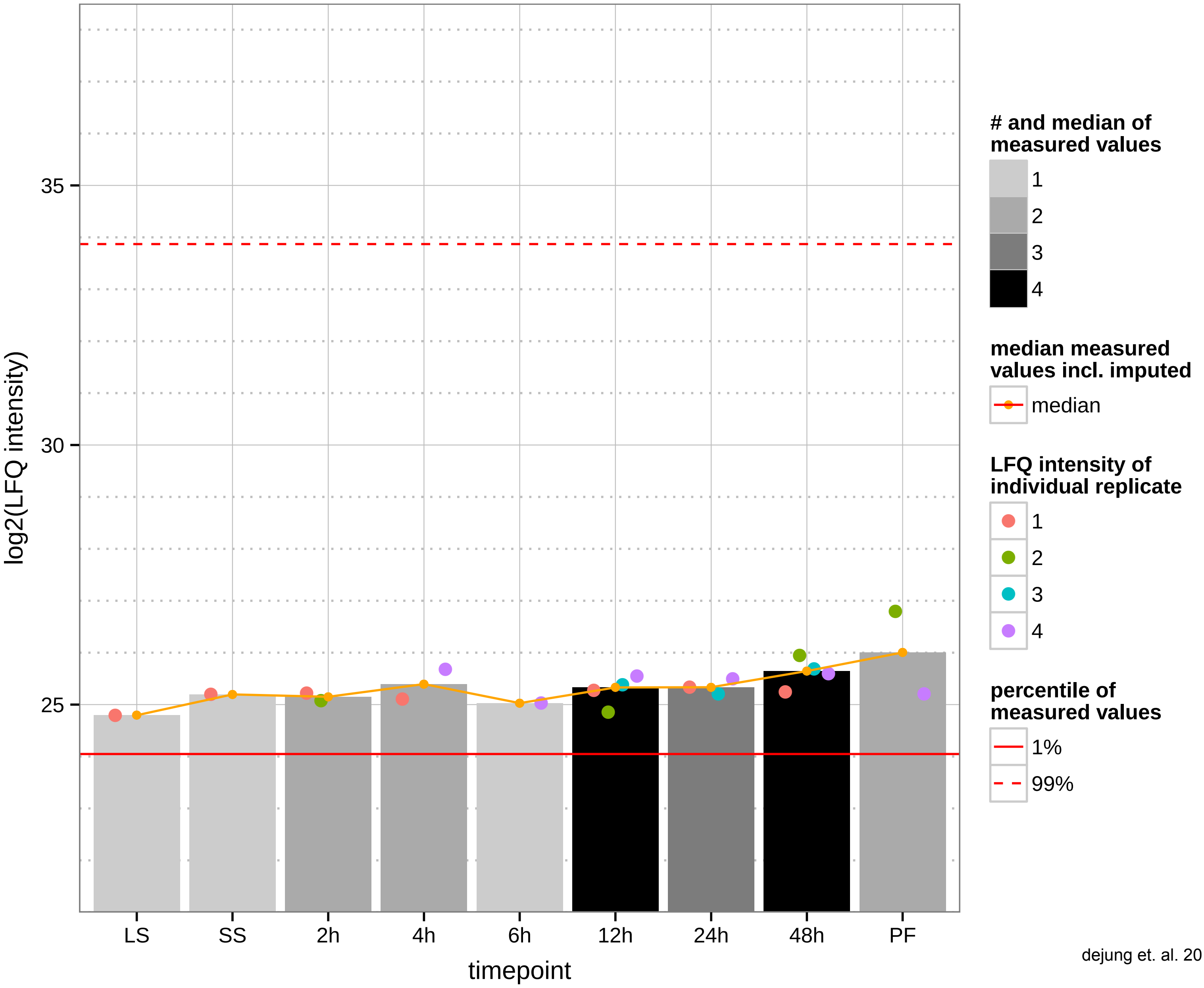
hypothetical protein, conserved
Tb927.10.7610
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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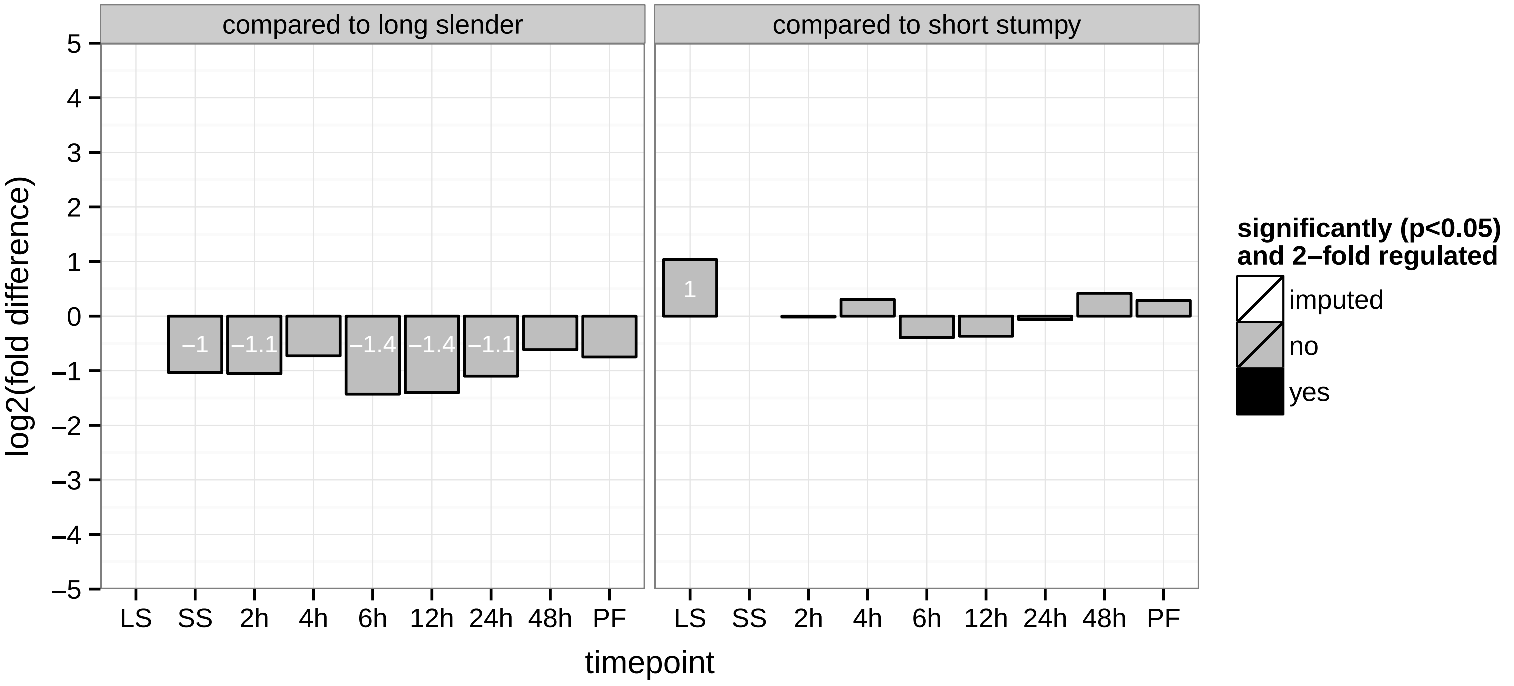
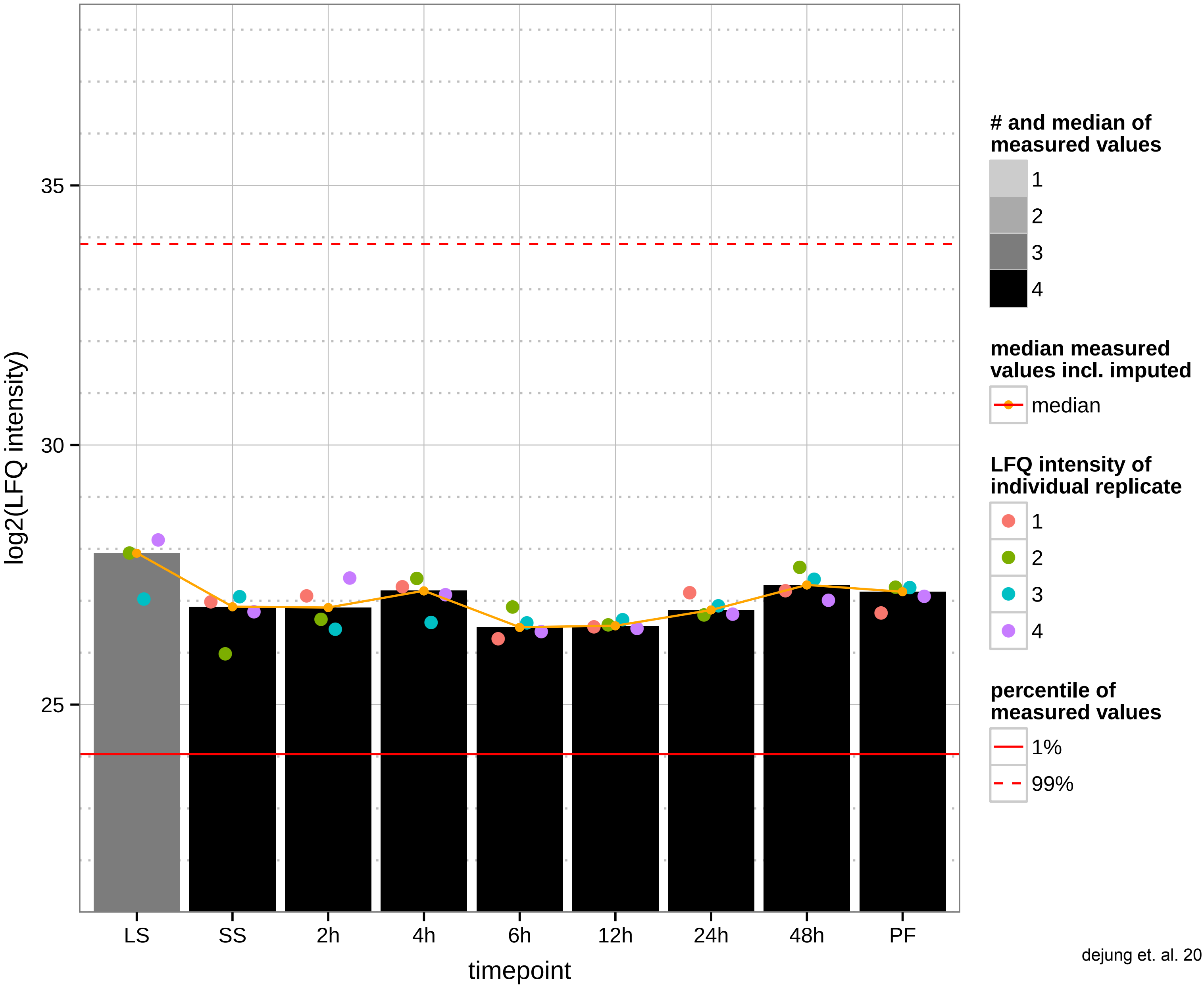
transportin2– like protein
Tb927.10.7630
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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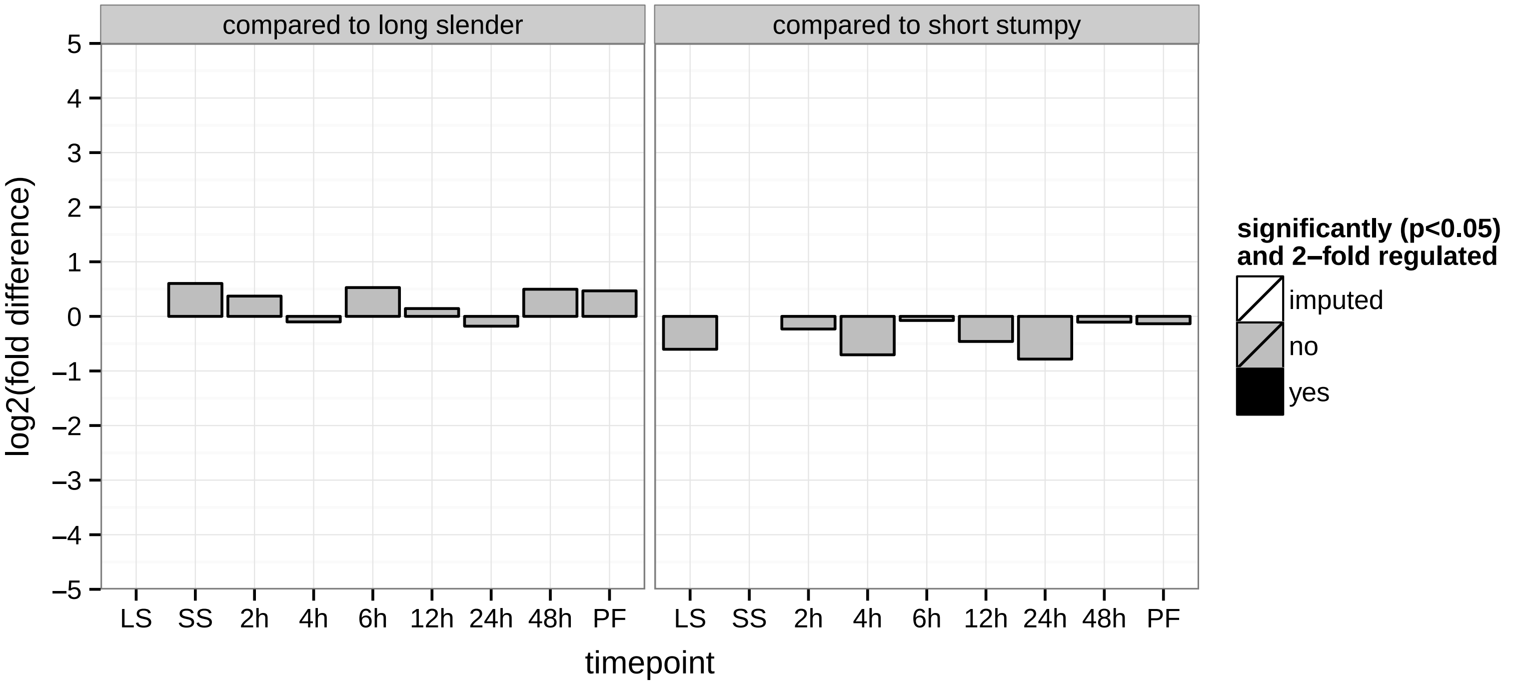
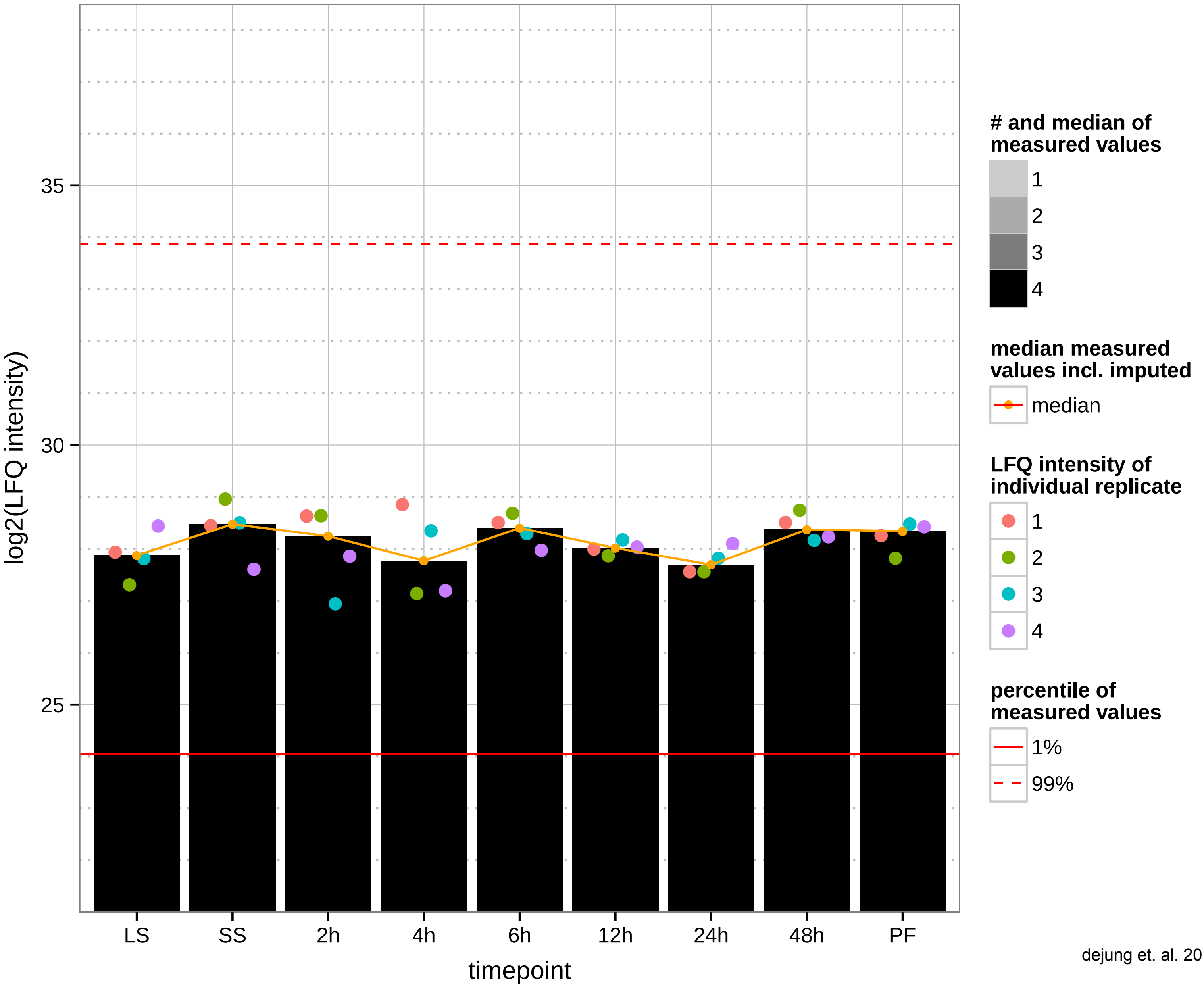
rib72 protein– like protein
Tb927.10.7690
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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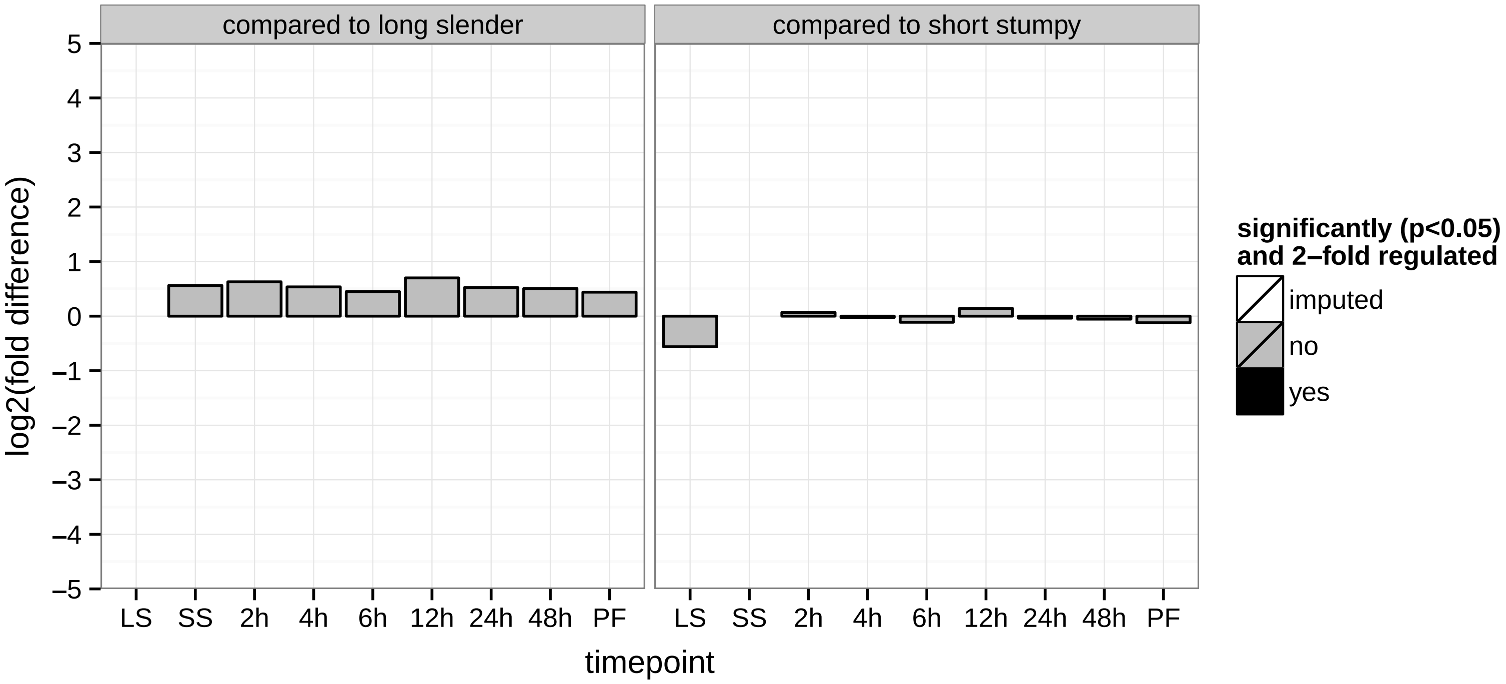
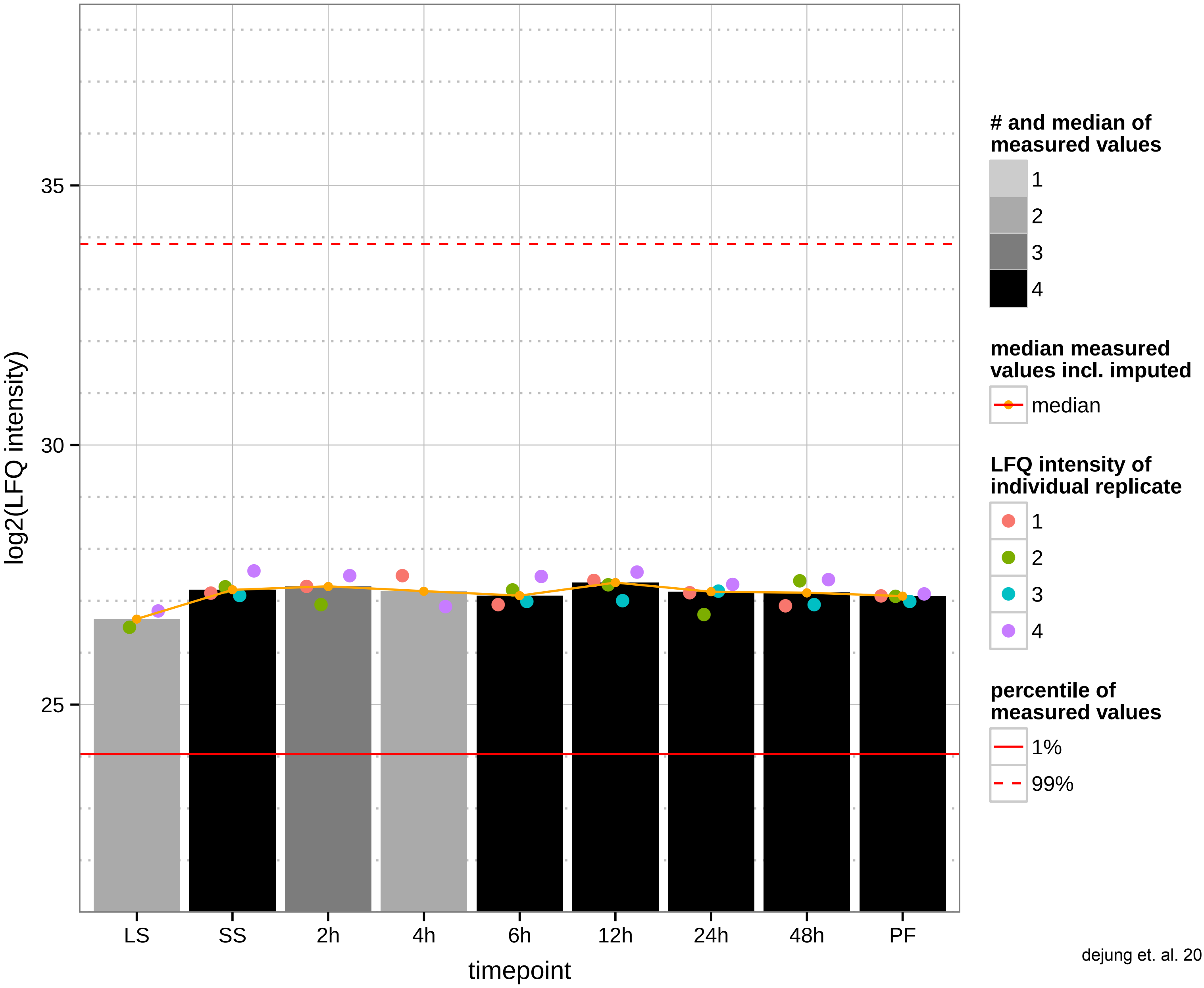
protein transport protein SEC23 (SEC23.2)
Tb927.10.7740
AGOF: protein binding, zinc ion binding
AGOC: COPII vesicle coat
AGOP: ER to Golgi vesicle–mediated transport, intracellular protein transport
PGOF: zinc ion binding
PGOC: COPII vesicle coat
PGOP: ER to Golgi vesicle–mediated transport, intracellular protein transport





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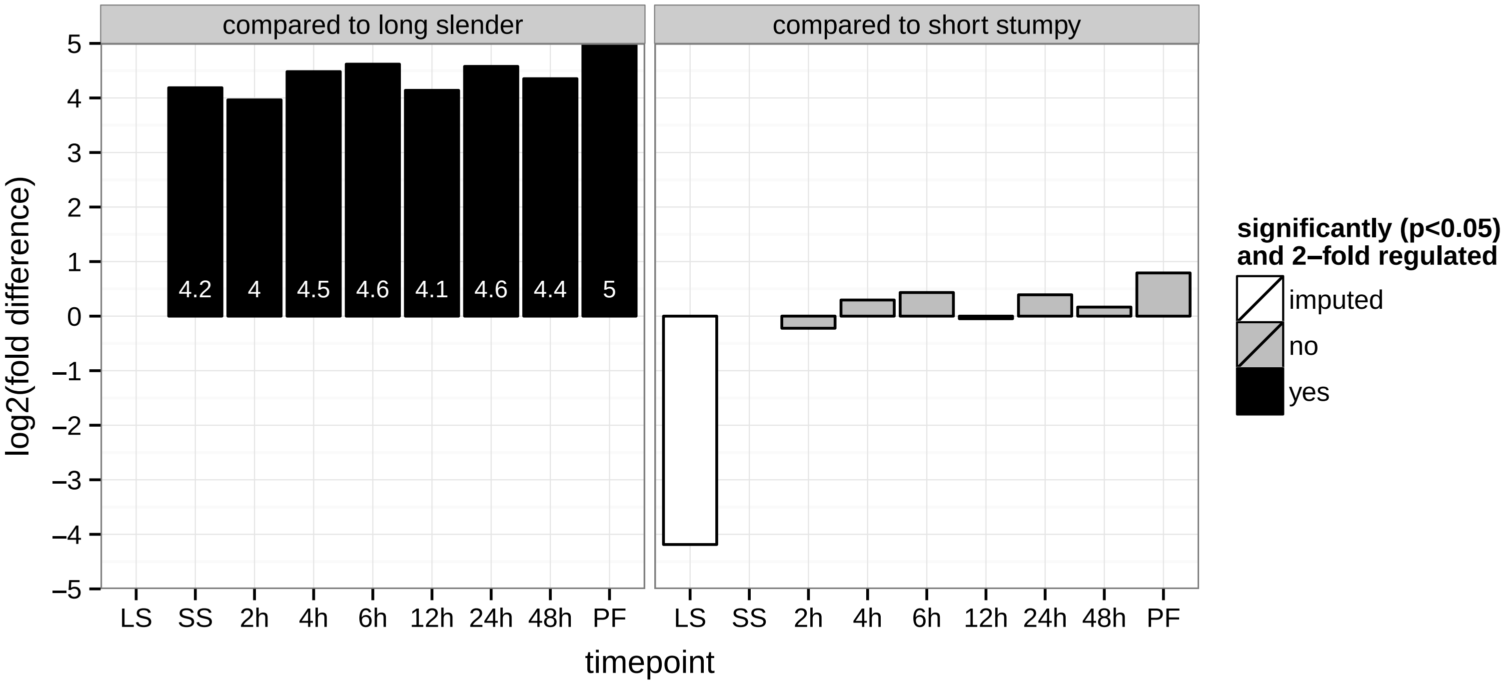
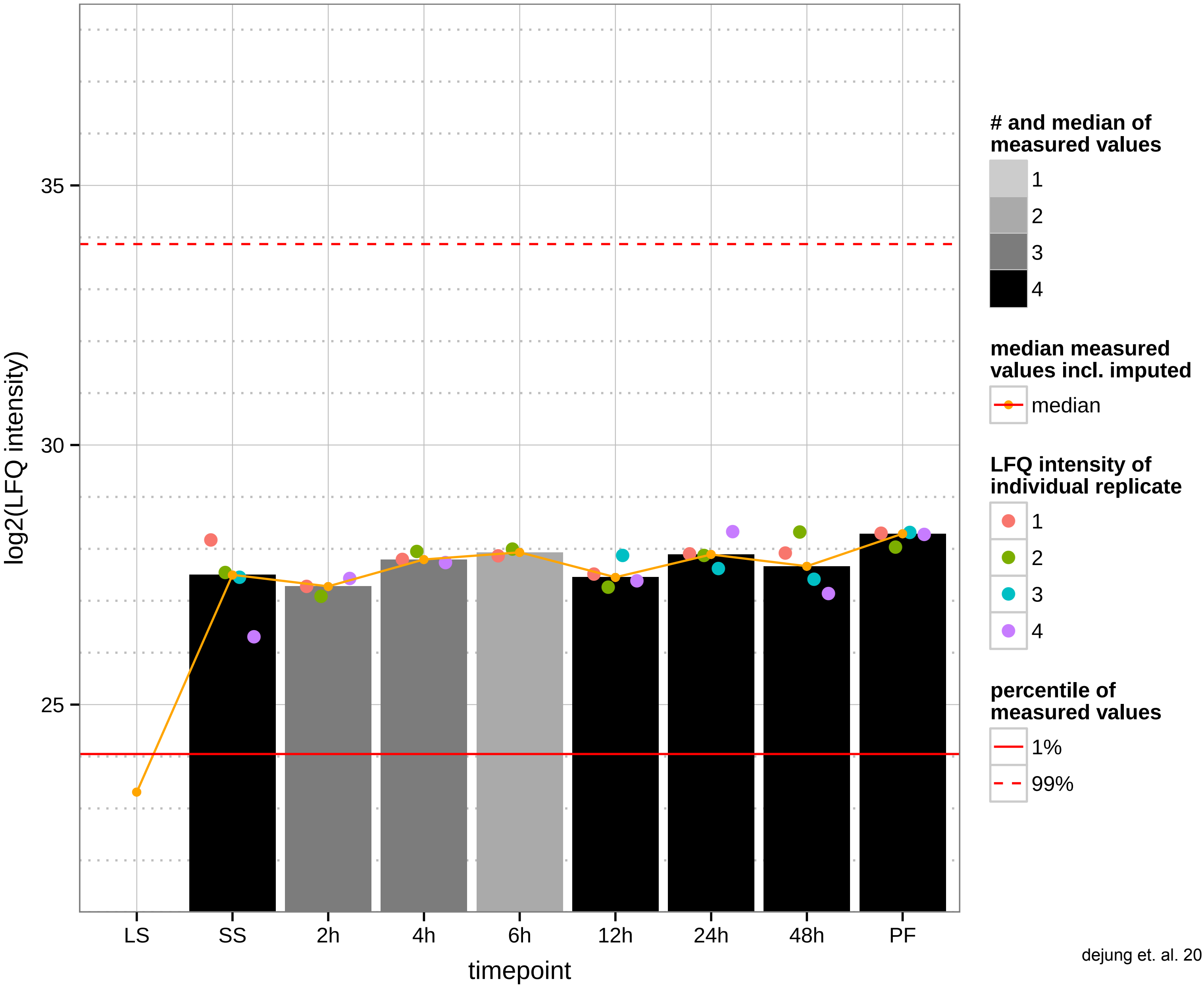
ubiquitin fusion degradation protein, putative
Tb927.10.7790
AGOF: null
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: null
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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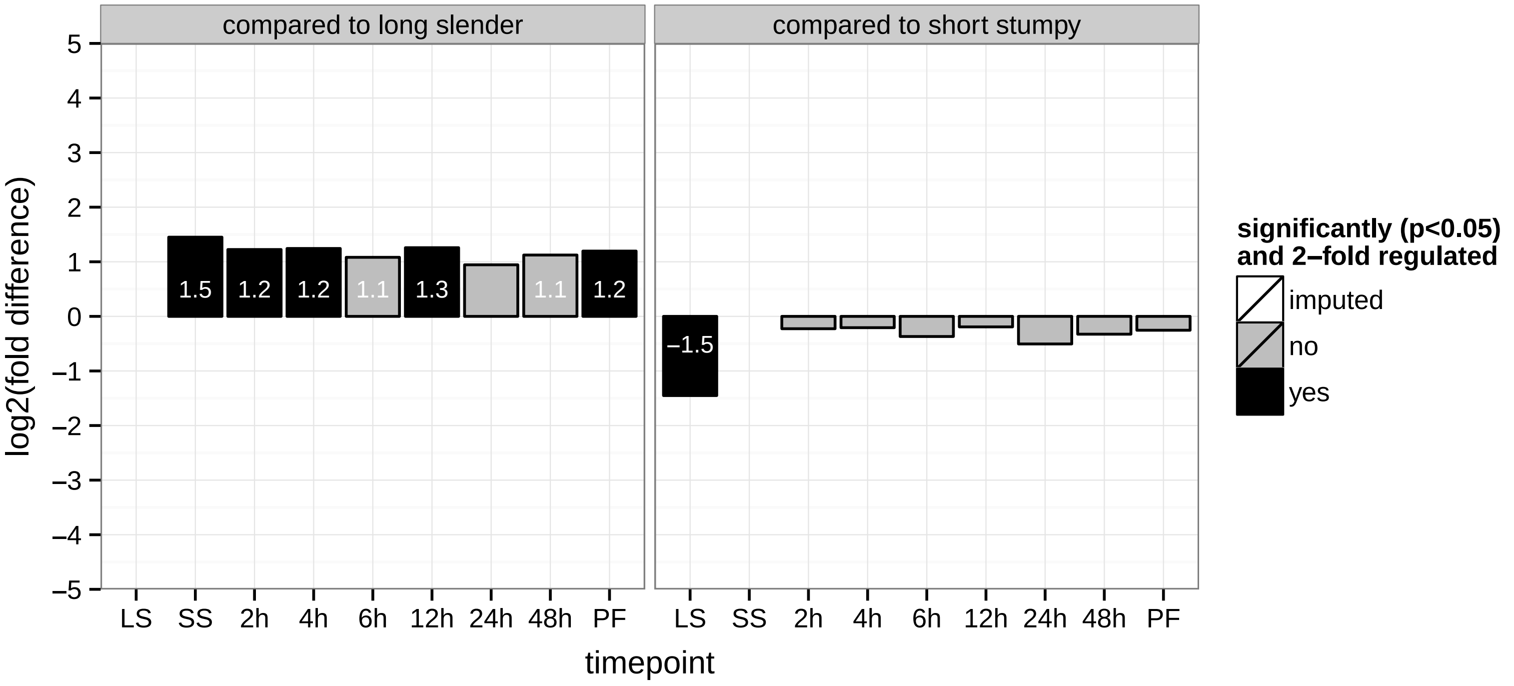
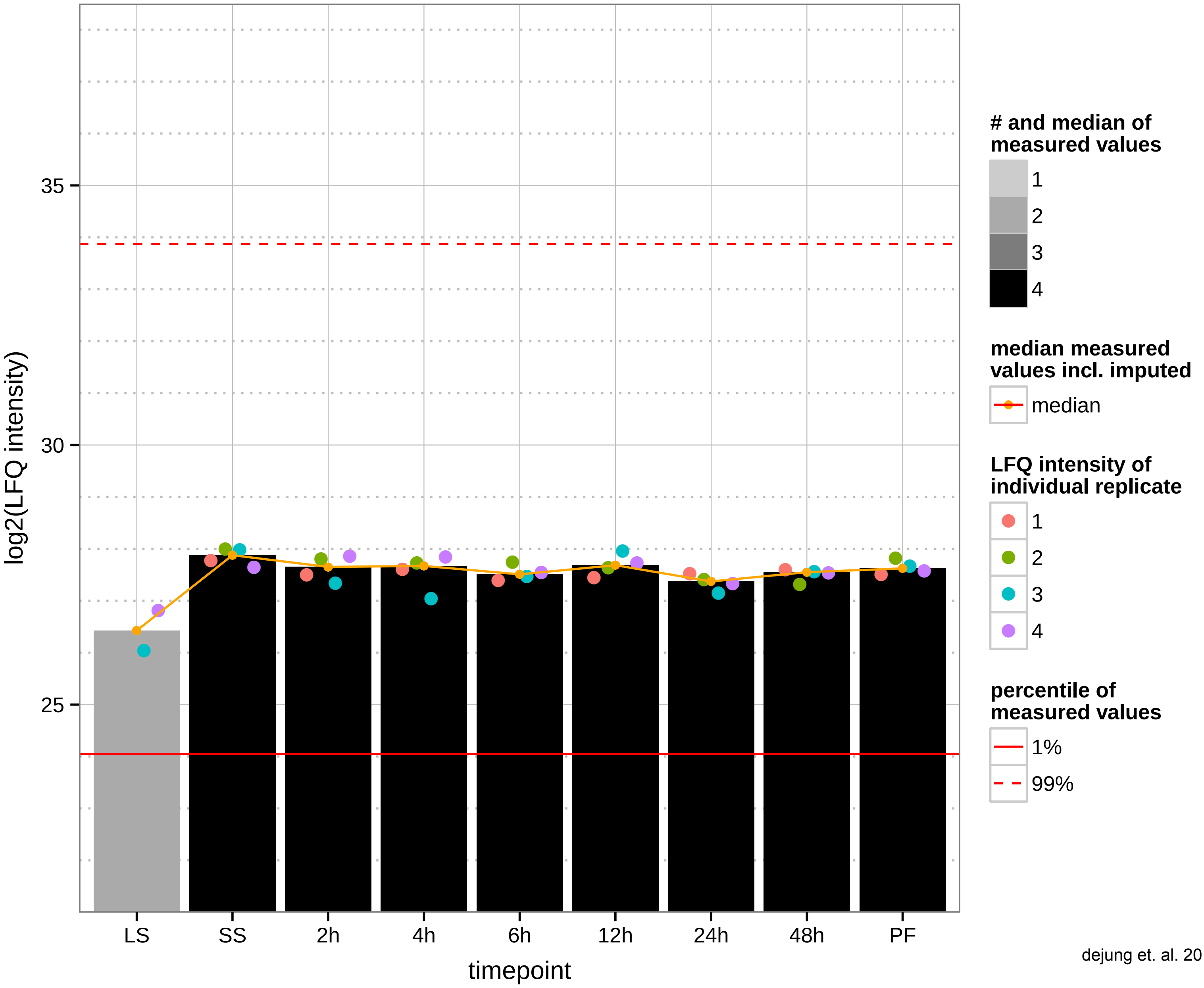
hypothetical protein, conserved
Tb927.10.7810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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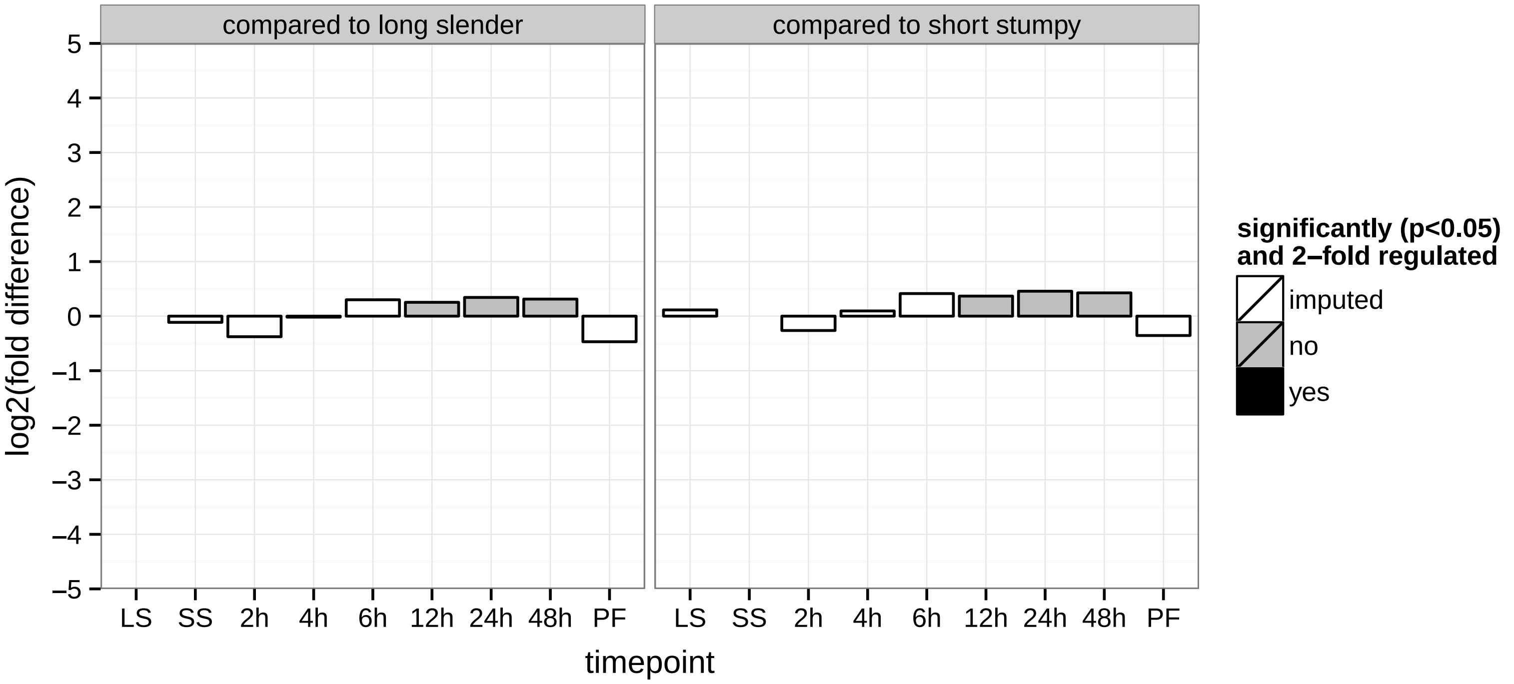
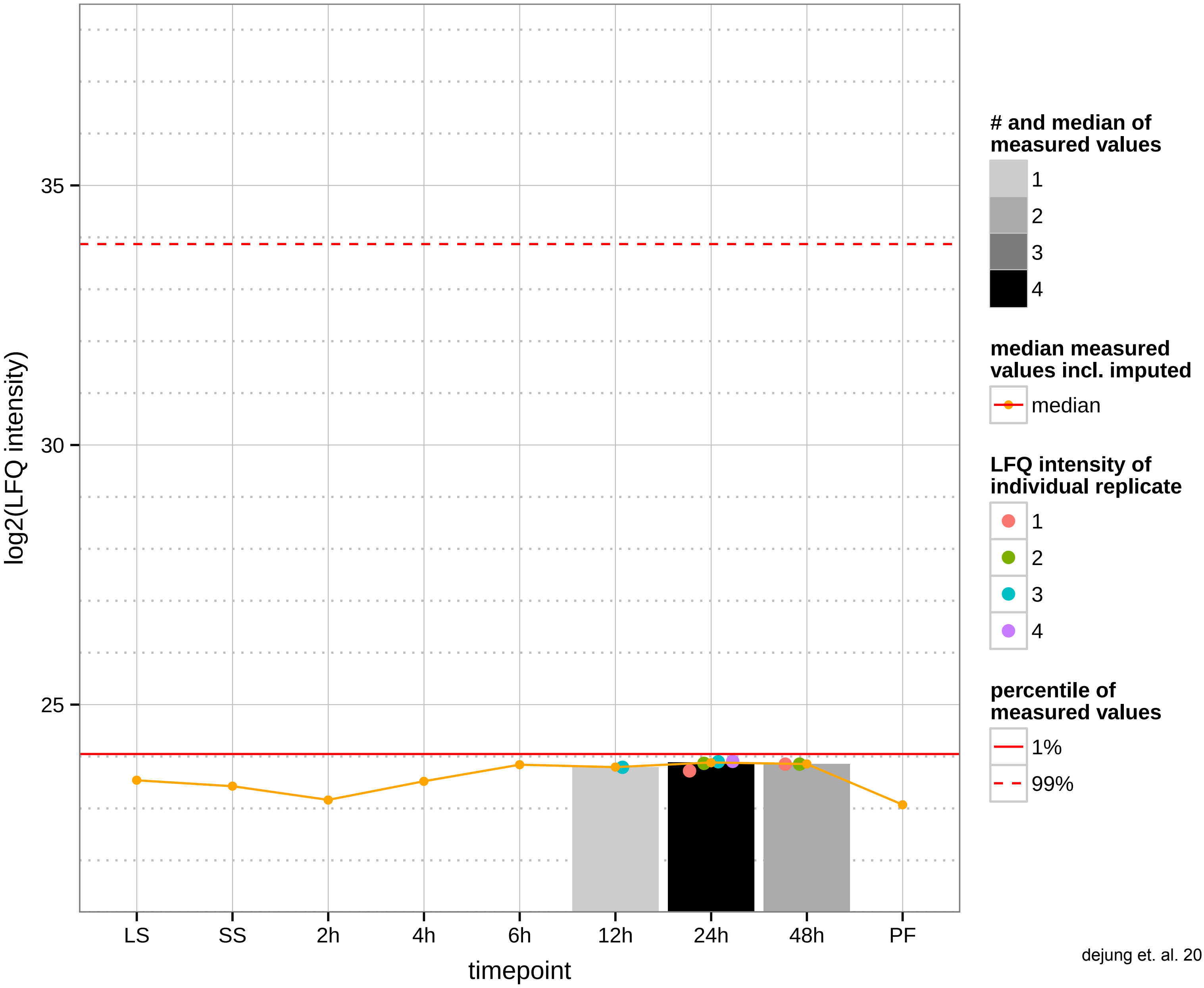
hypothetical protein, conserved
Tb927.10.7870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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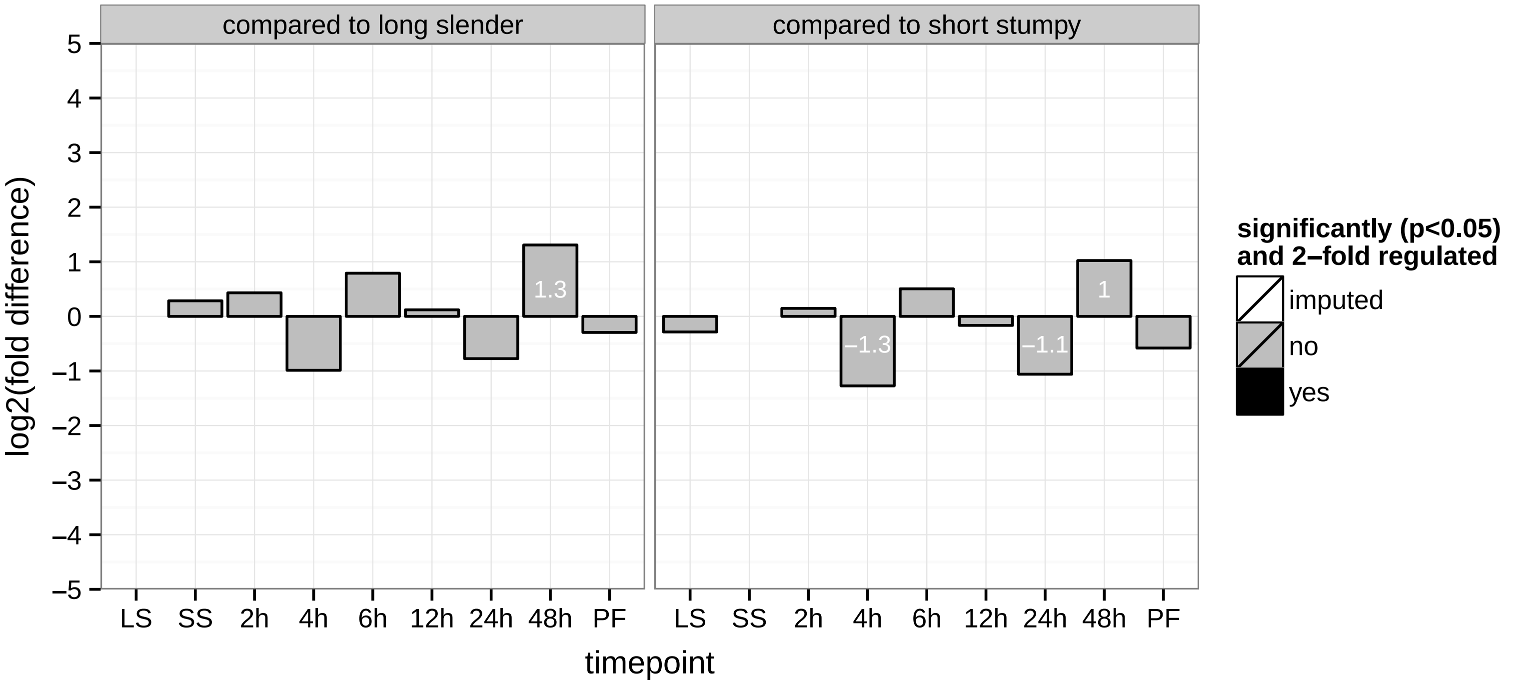
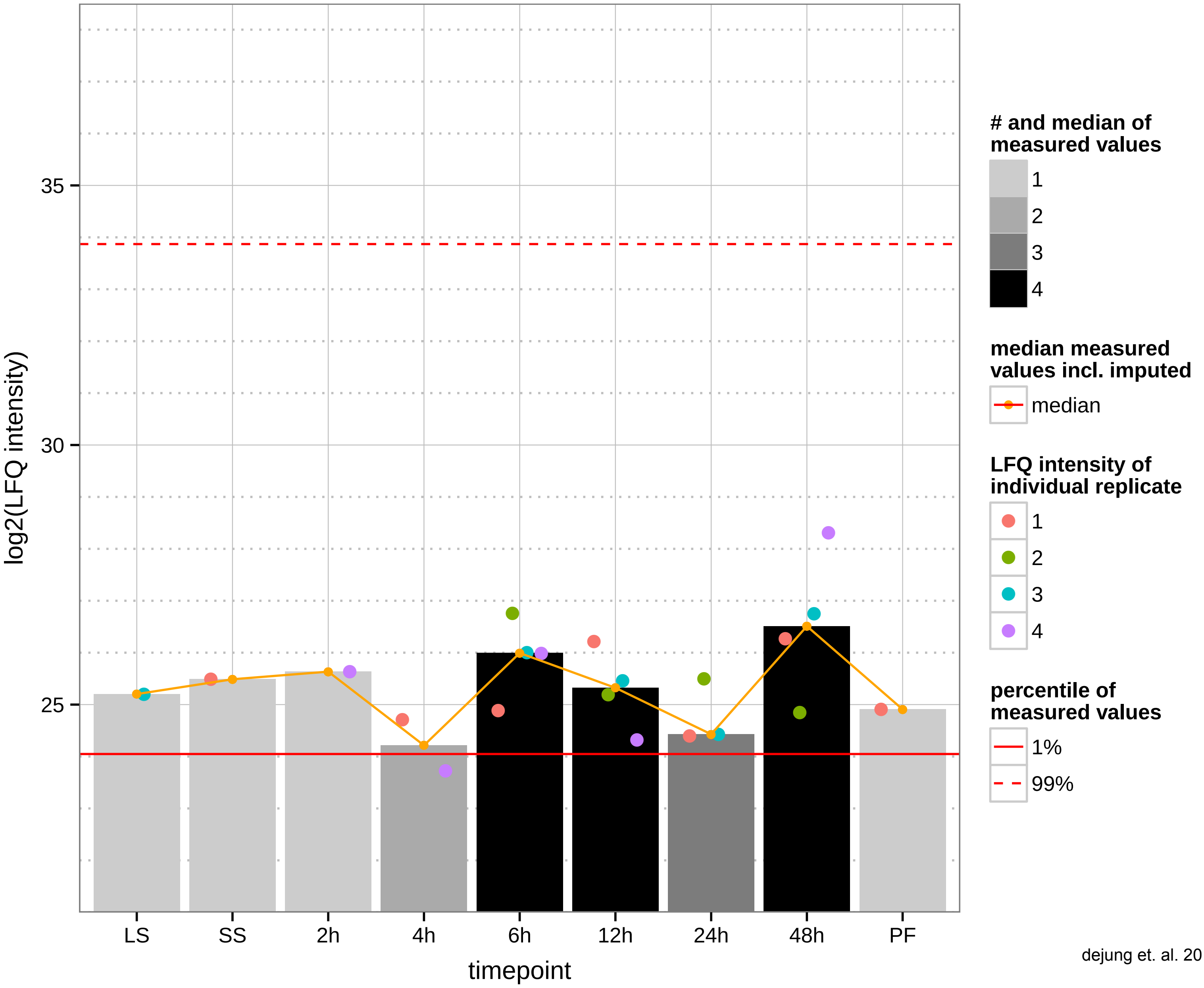
hypothetical protein, conserved
Tb927.10.7880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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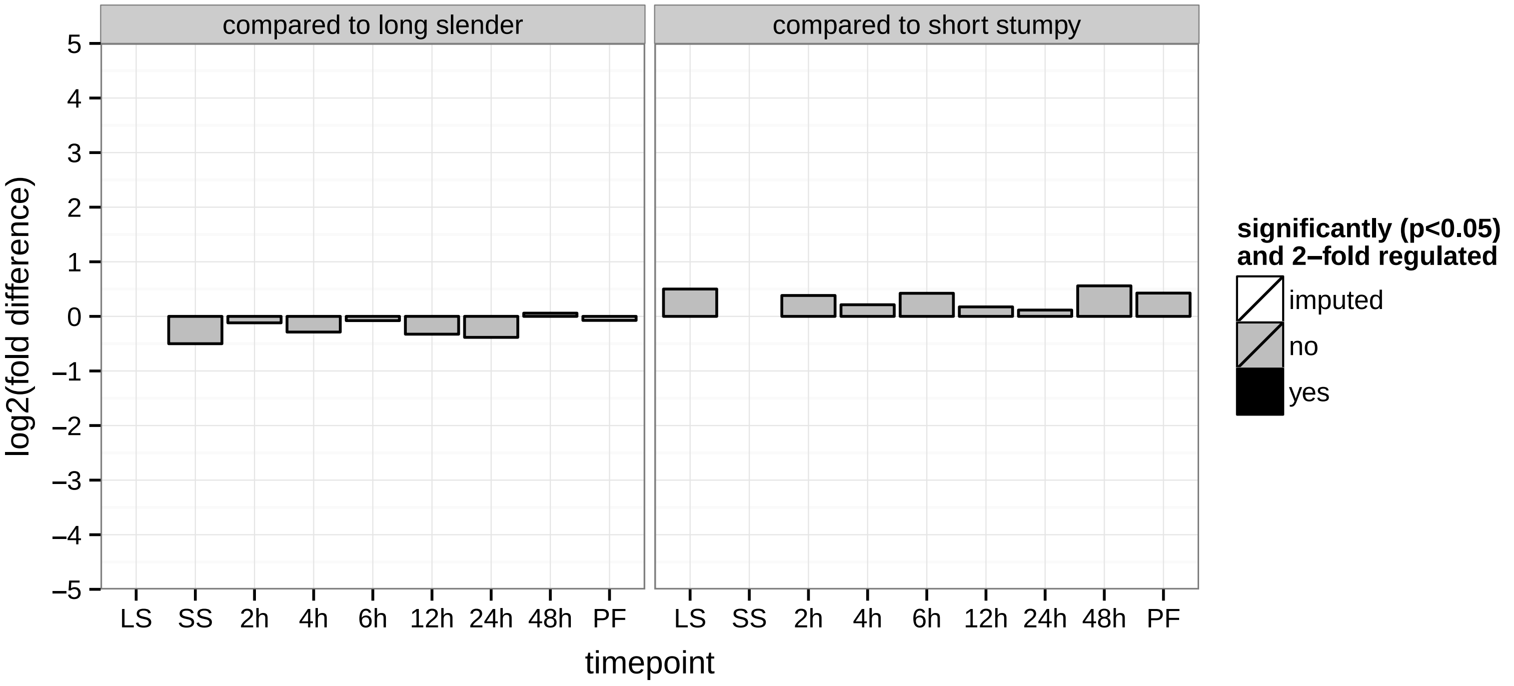
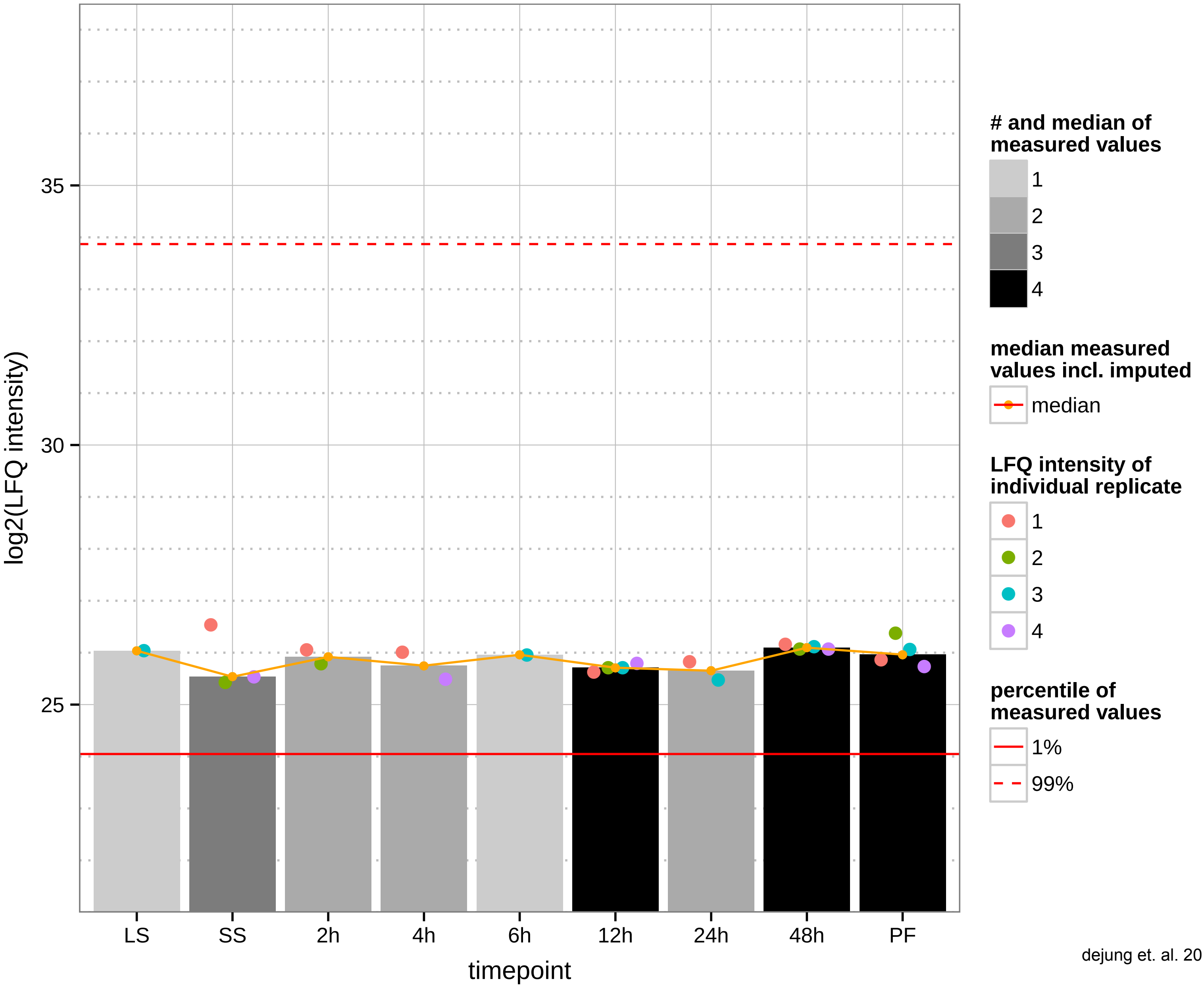
hypothetical protein, conserved
Tb927.10.7920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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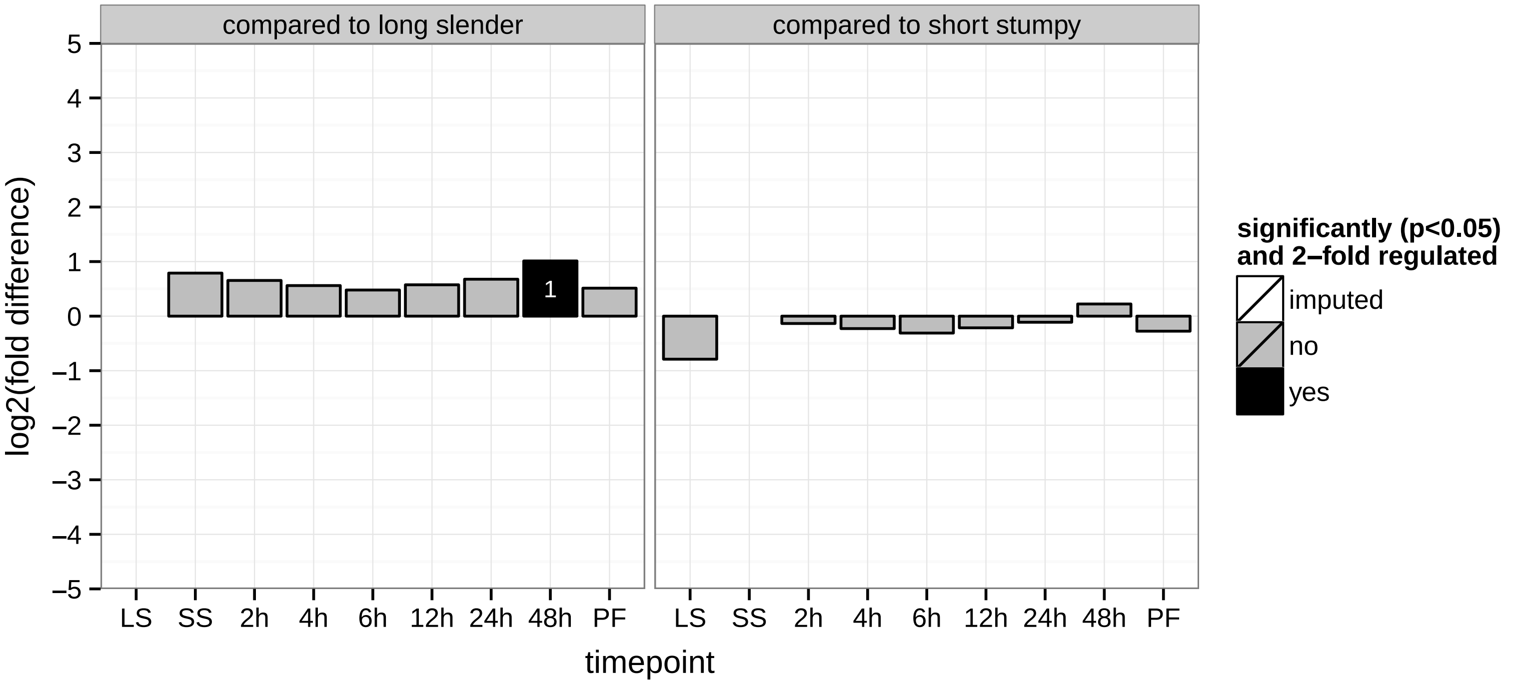
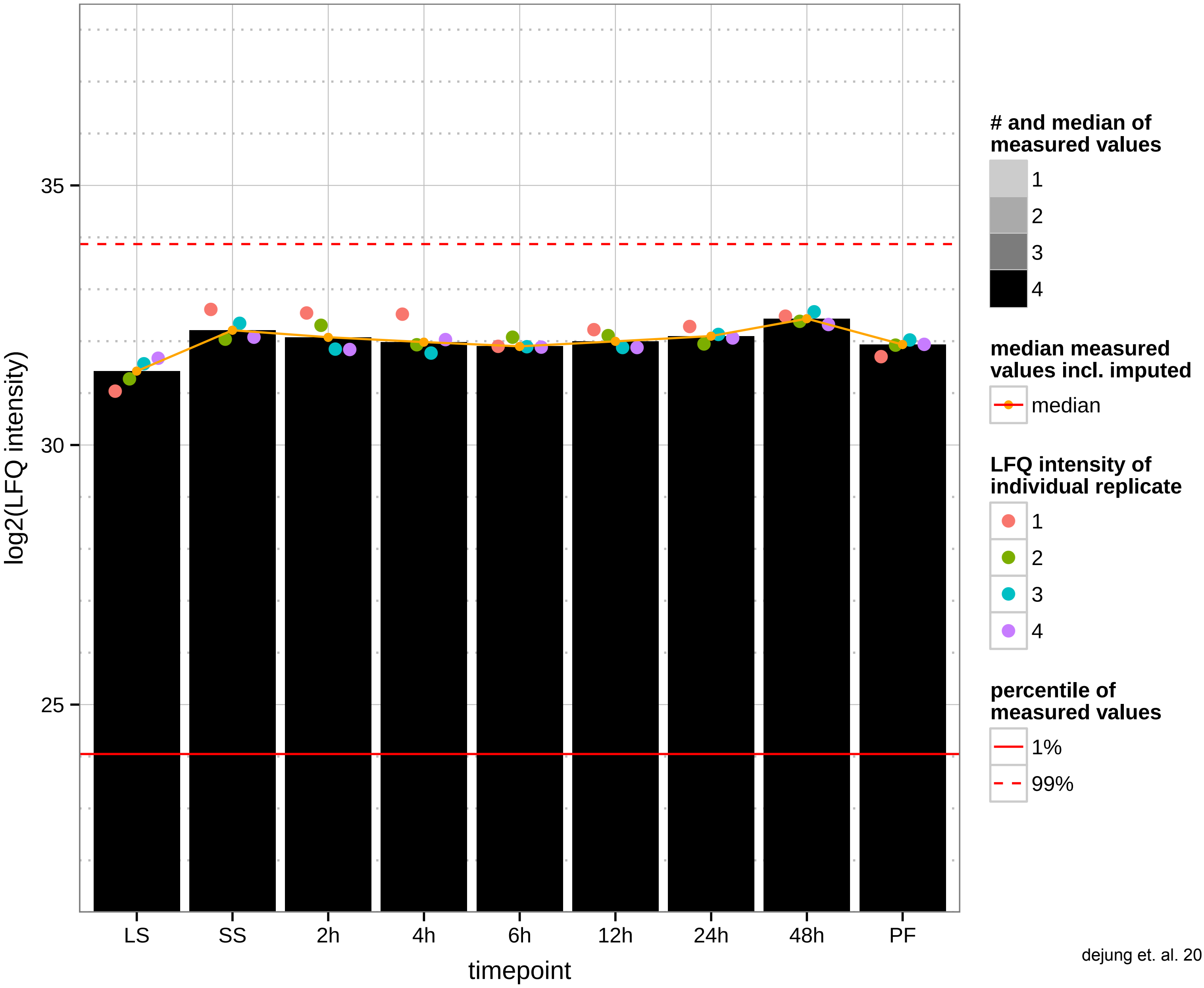
2, 3–bisphosphoglycerate–independent phosphoglycerate mutase (PGAM)
Tb927.10.7930
AGOF: 2, 3–bisphosphoglycerate–independent phosphoglycerate mutase activity, manganese ion binding
AGOC: cytoplasm, cytosol
AGOP: gluconeogenesis, glycolysis
PGOF: catalytic activity, manganese ion binding, metal ion binding, phosphoglycerate mutase activity
PGOC: cytoplasm
PGOP: glucose catabolic process, metabolic process





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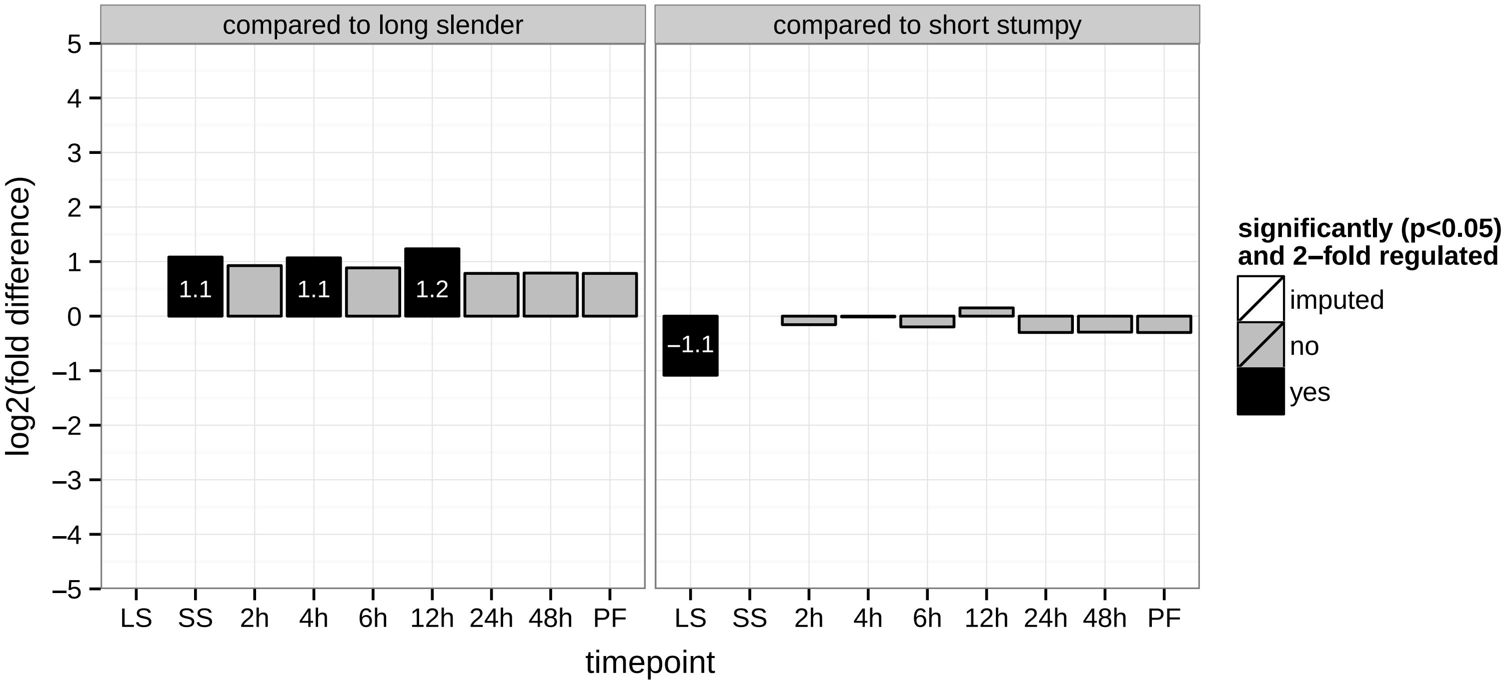
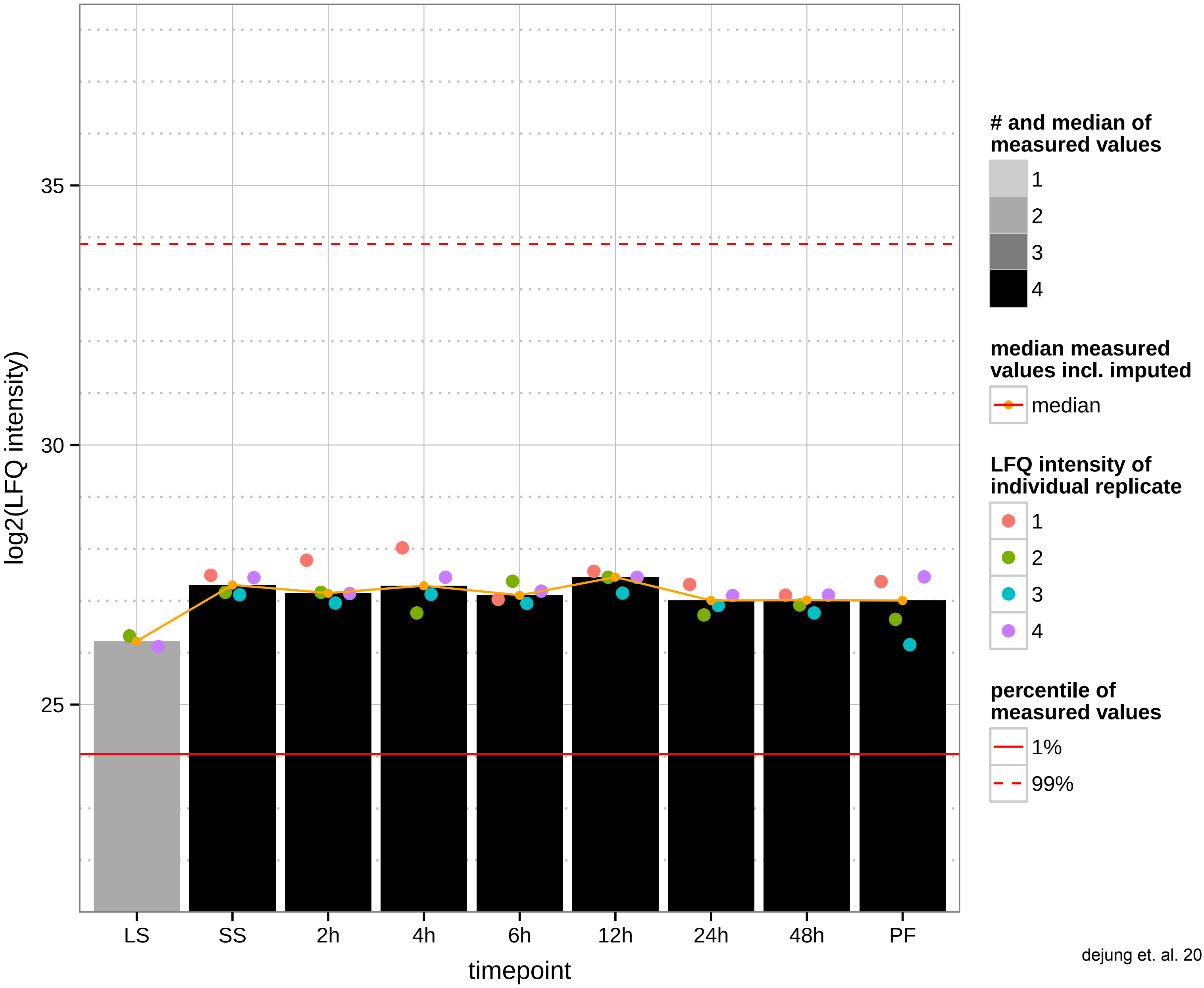
methyltransferase, putative
Tb927.10.7940
AGOF: nucleic acid binding, rRNA methyltransferase activity
AGOC: null
AGOP: RNA methylation
PGOF: methyltransferase activity, nucleic acid binding
PGOC: null
PGOP: methylation





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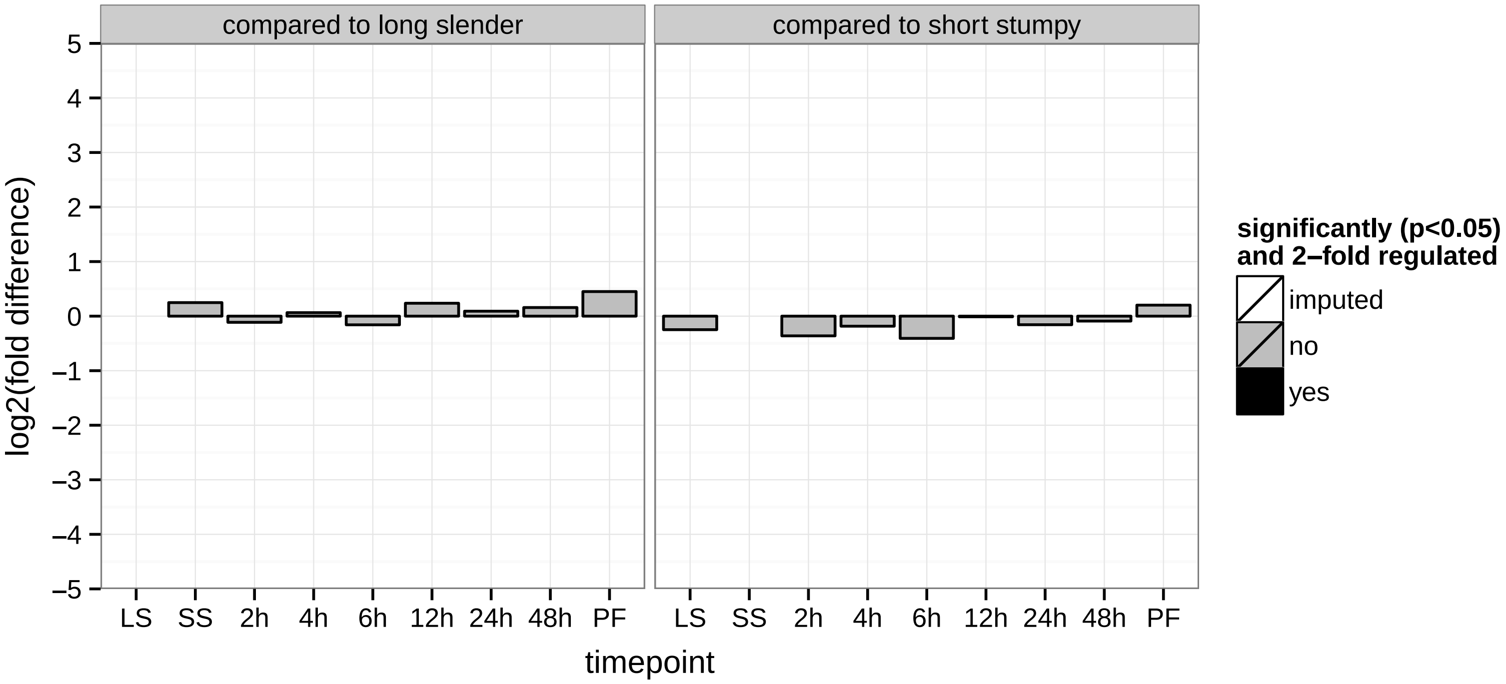
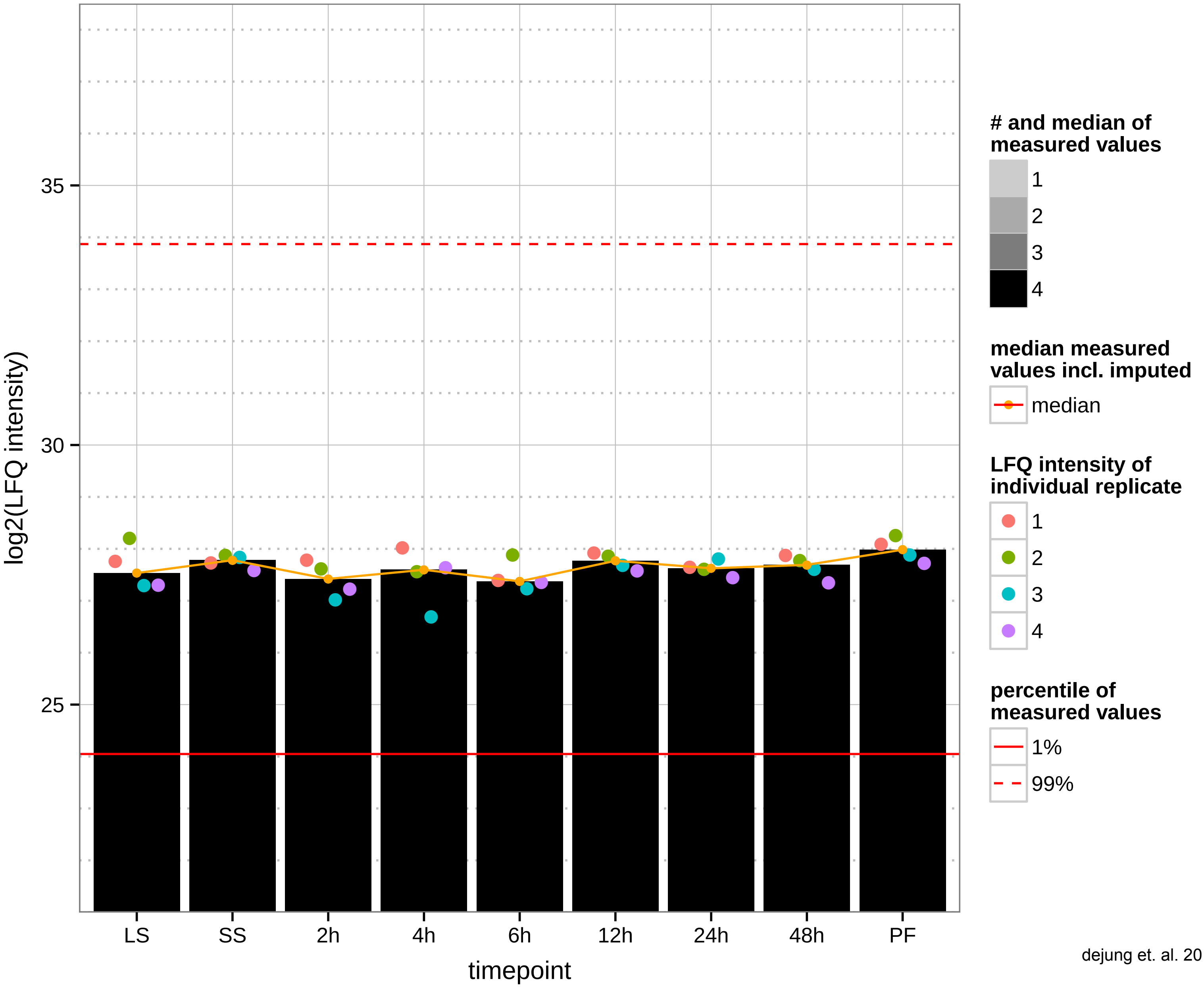
replication factor C, subunit 5, putative, ATPase
Tb927.10.7990
AGOF: DNA binding, nucleoside–triphosphatase activity, nucleotide binding
AGOC: nucleus
AGOP: DNA replication
PGOF: DNA binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: DNA replication





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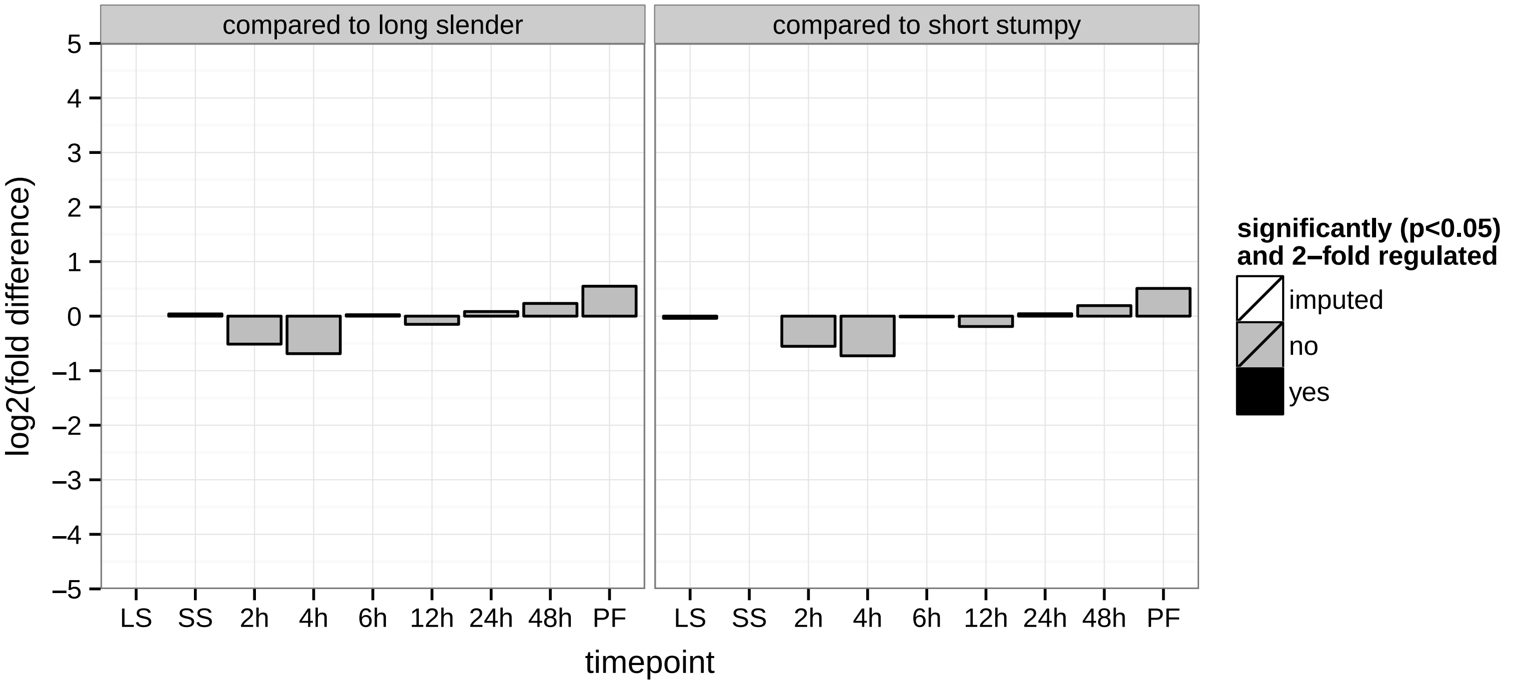
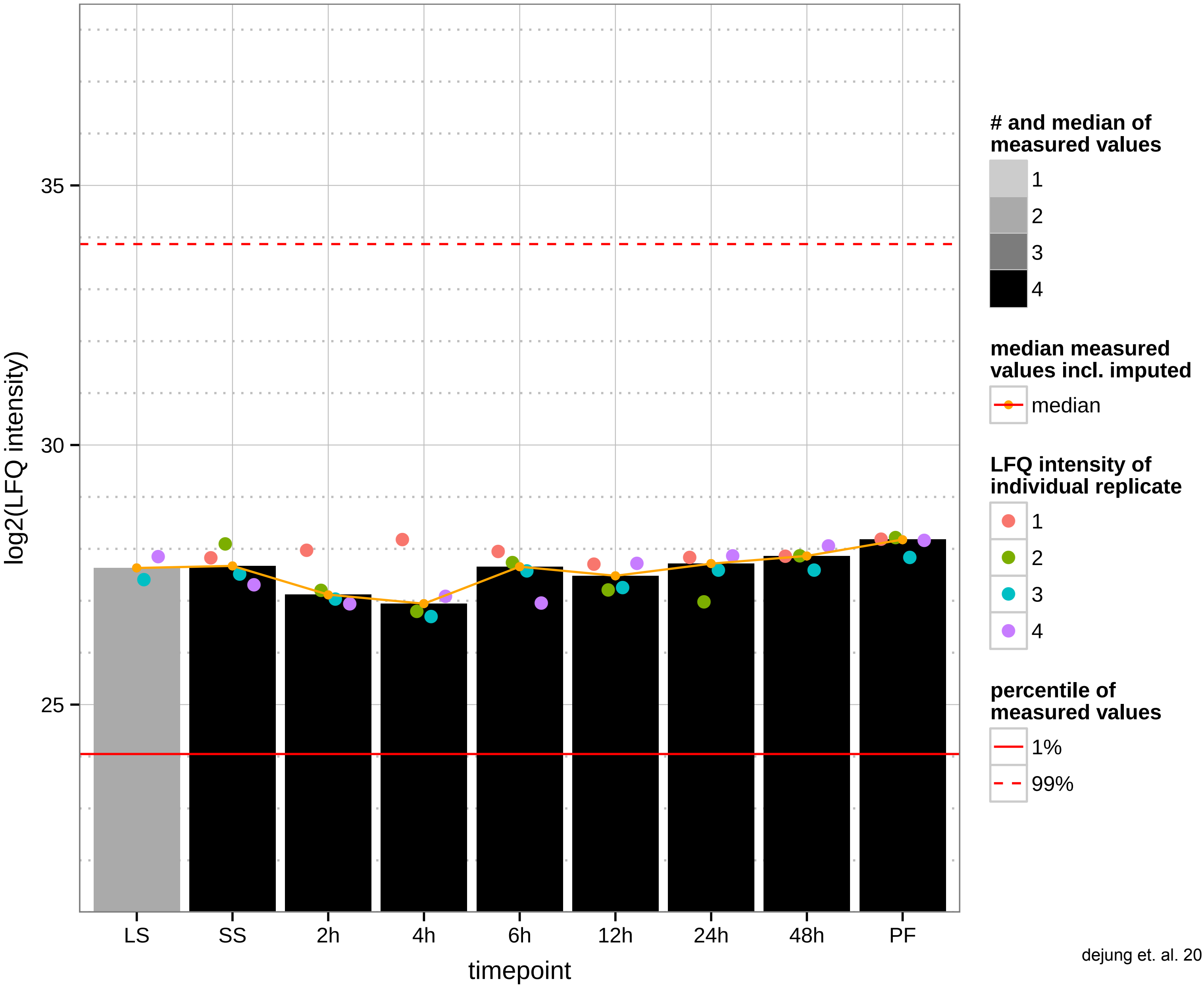
hypothetical protein, conserved
Tb927.10.8000
AGOF: null
AGOC: null
AGOP: null
PGOF: adenylate kinase activity
PGOC: null
PGOP: null





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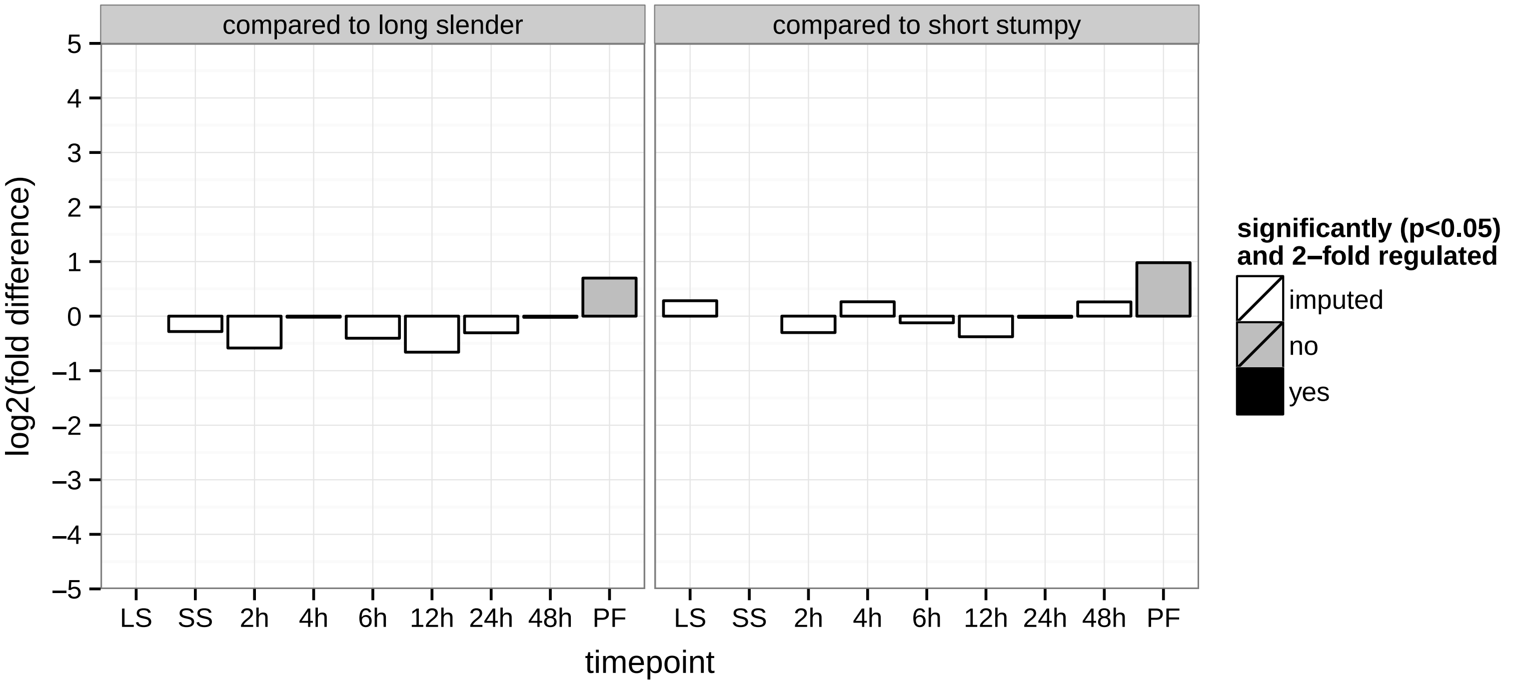
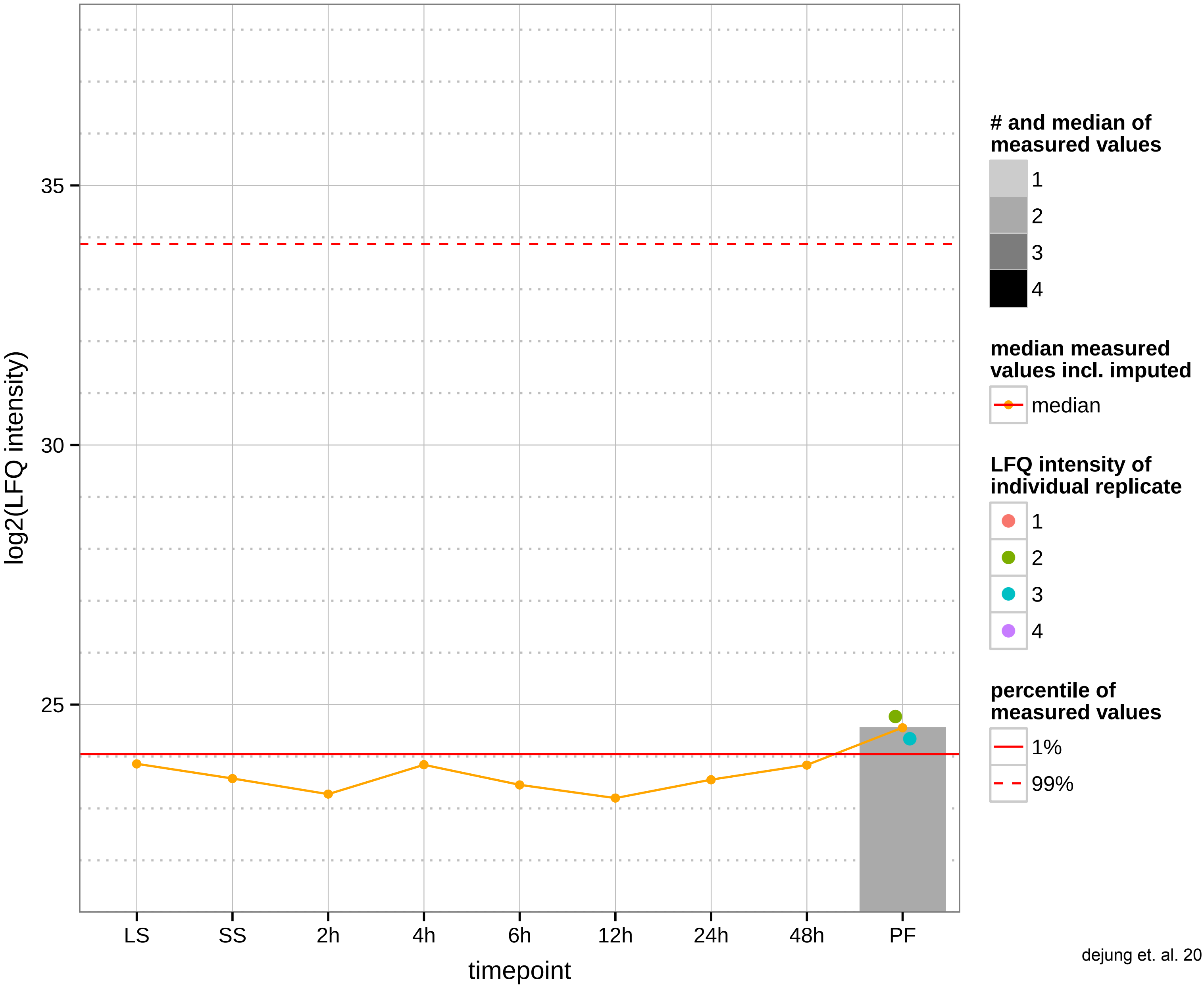
hypothetical protein, conserved
Tb927.10.8010
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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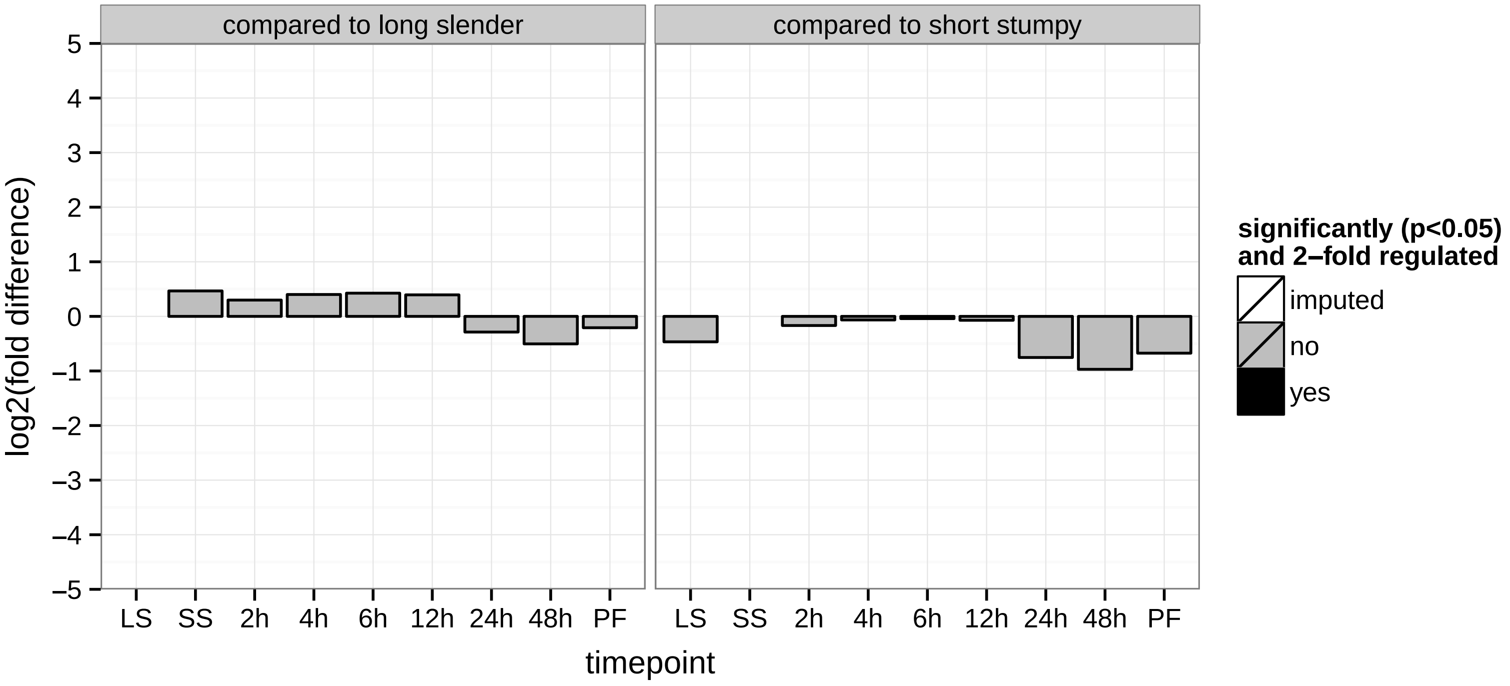
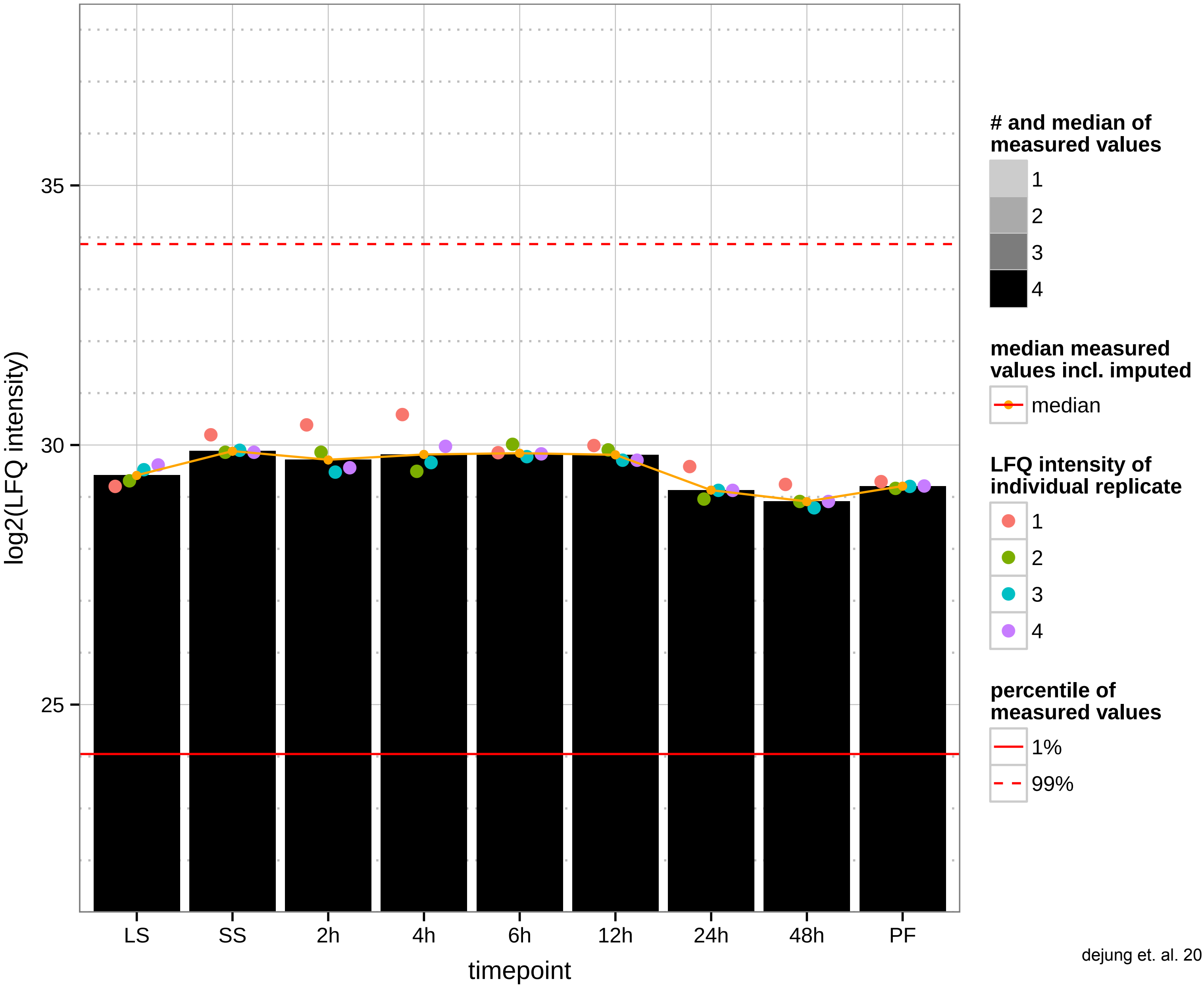
adaptin complex 1 subunit, putative, beta–adaptin, fragment (BAD1)
Tb927.10.8040
AGOF: protein transporter activity
AGOC: Golgi apparatus, clathrin coat of trans–Golgi network vesicle, coated pit, trans–Golgi network
AGOP: intracellular protein transport, vesicle–mediated transport
PGOF: binding, protein transporter activity
PGOC: membrane coat
PGOP: intracellular protein transport, protein transport, vesicle–mediated transport





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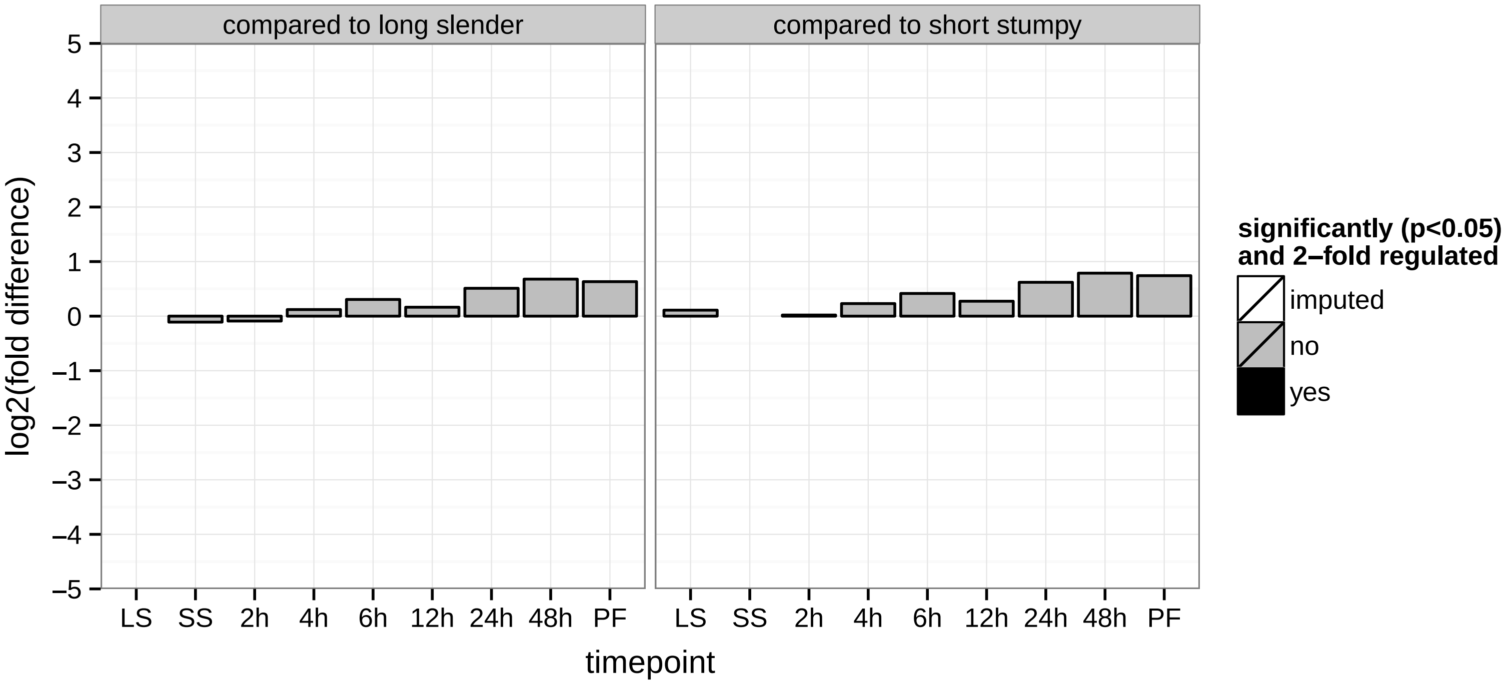
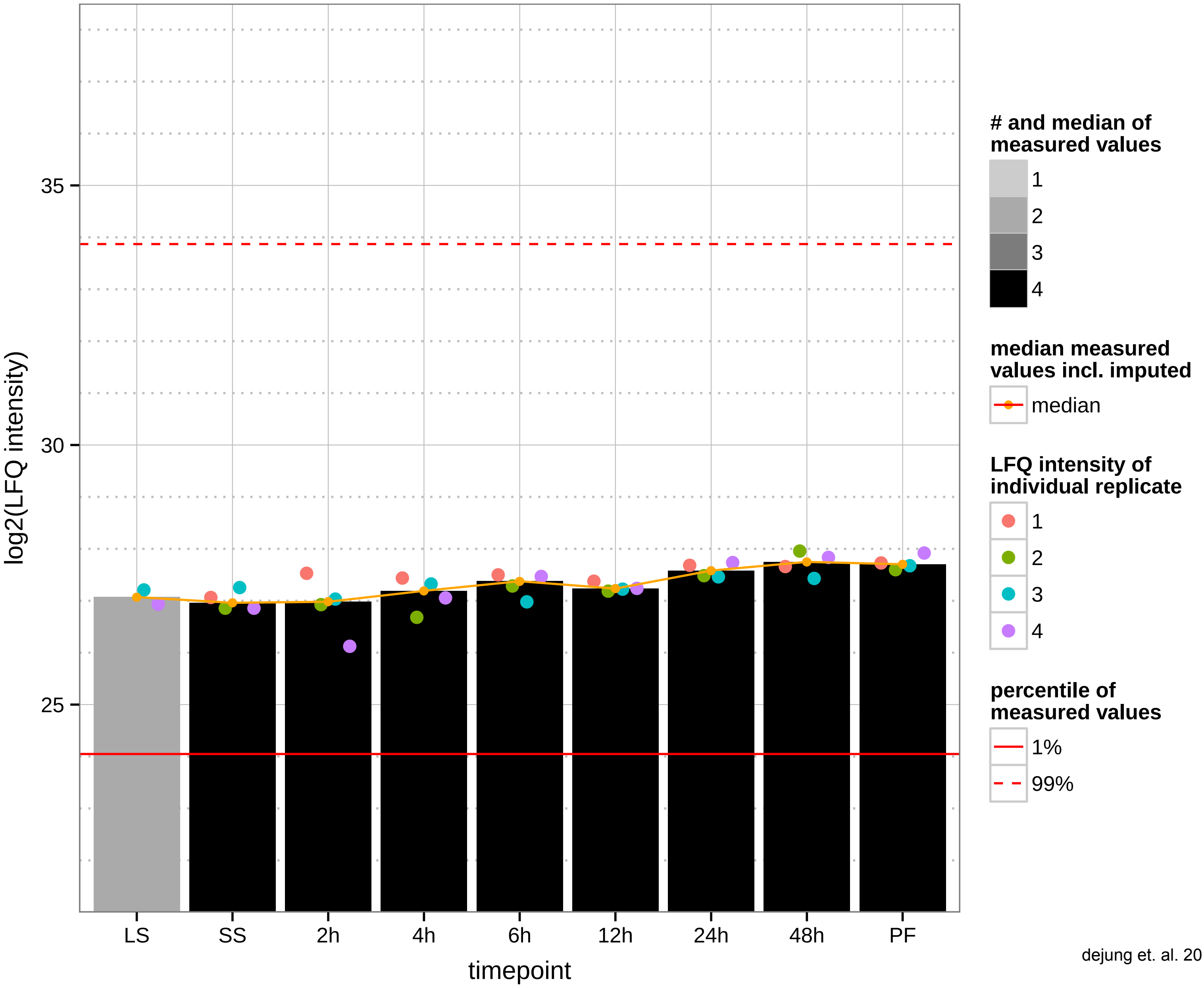
hypothetical protein, conserved
Tb927.10.8060
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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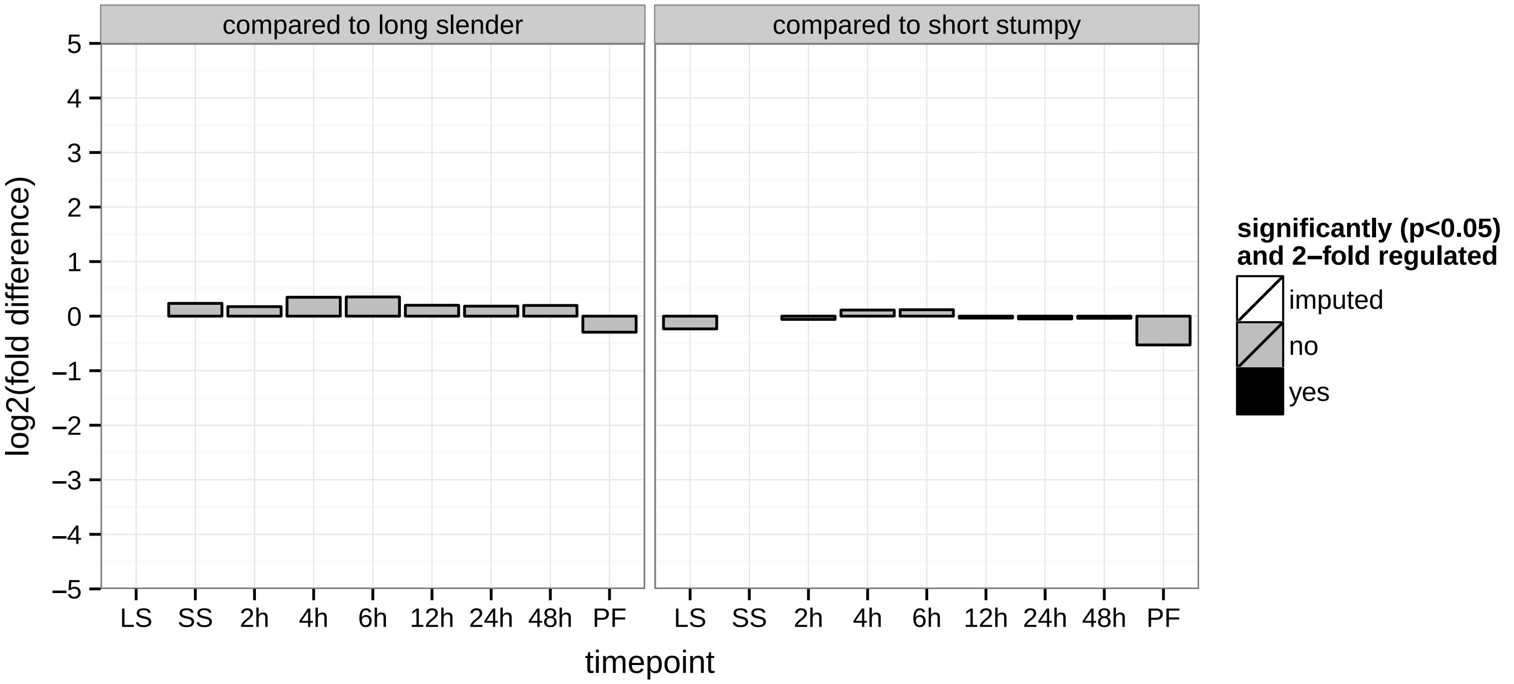
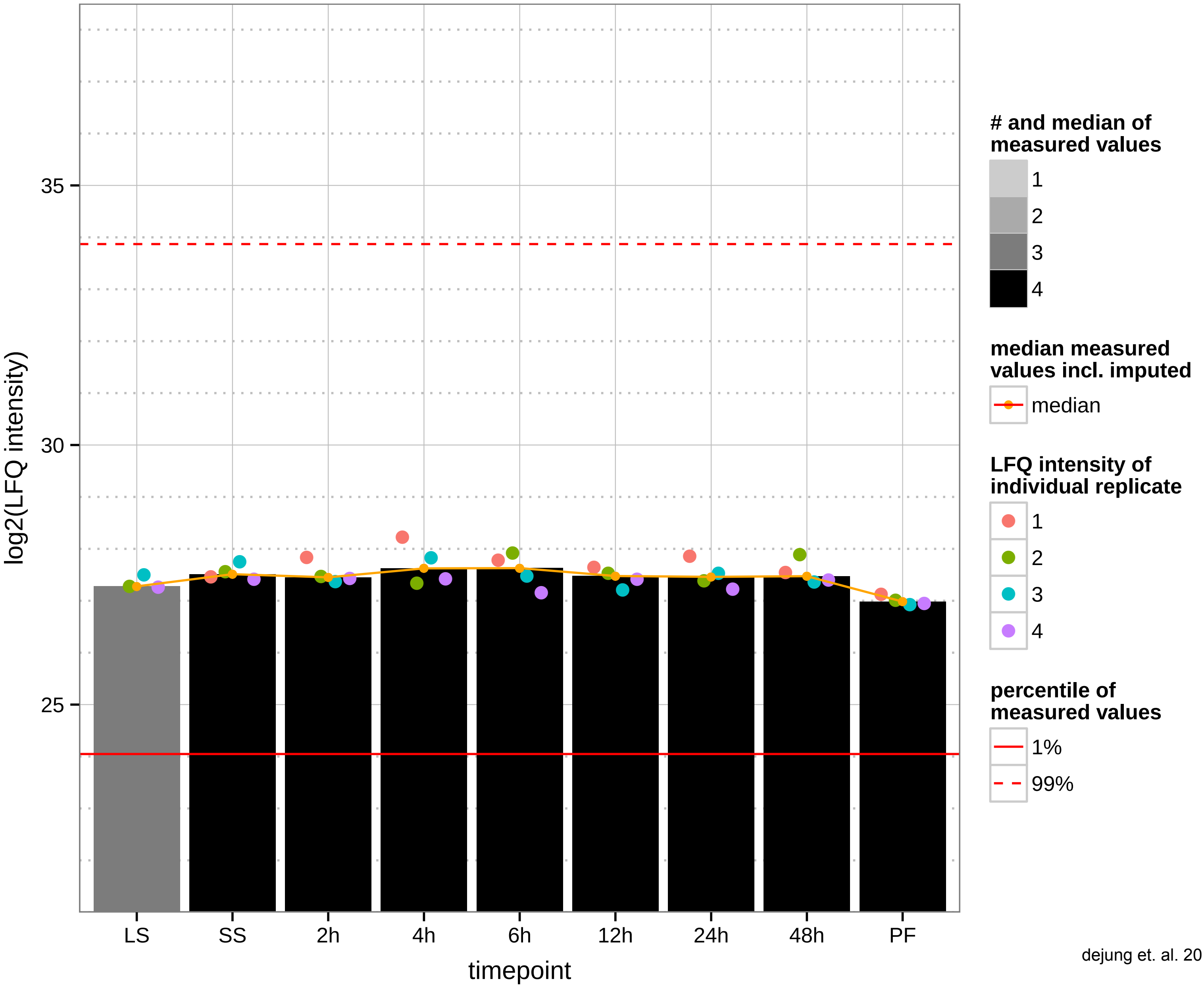
hypothetical protein, conserved
Tb927.10.8080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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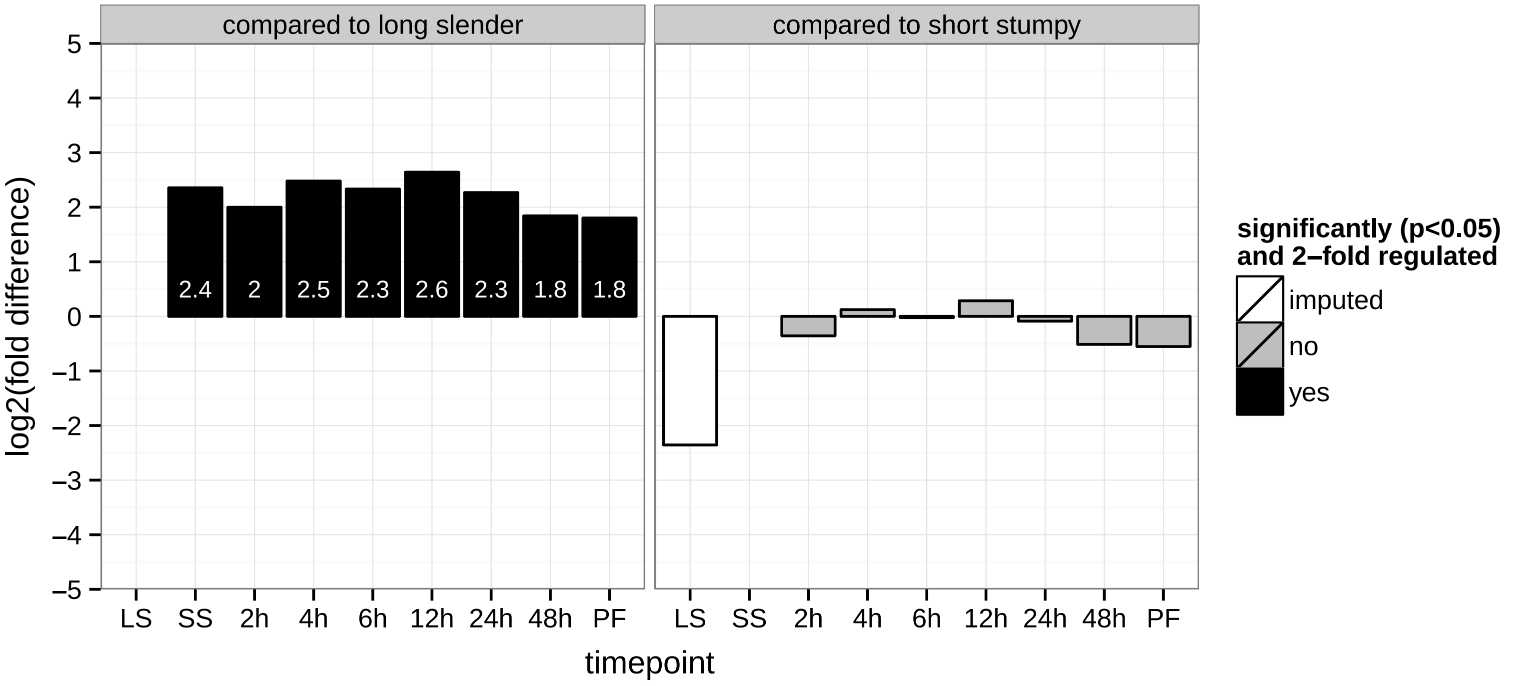
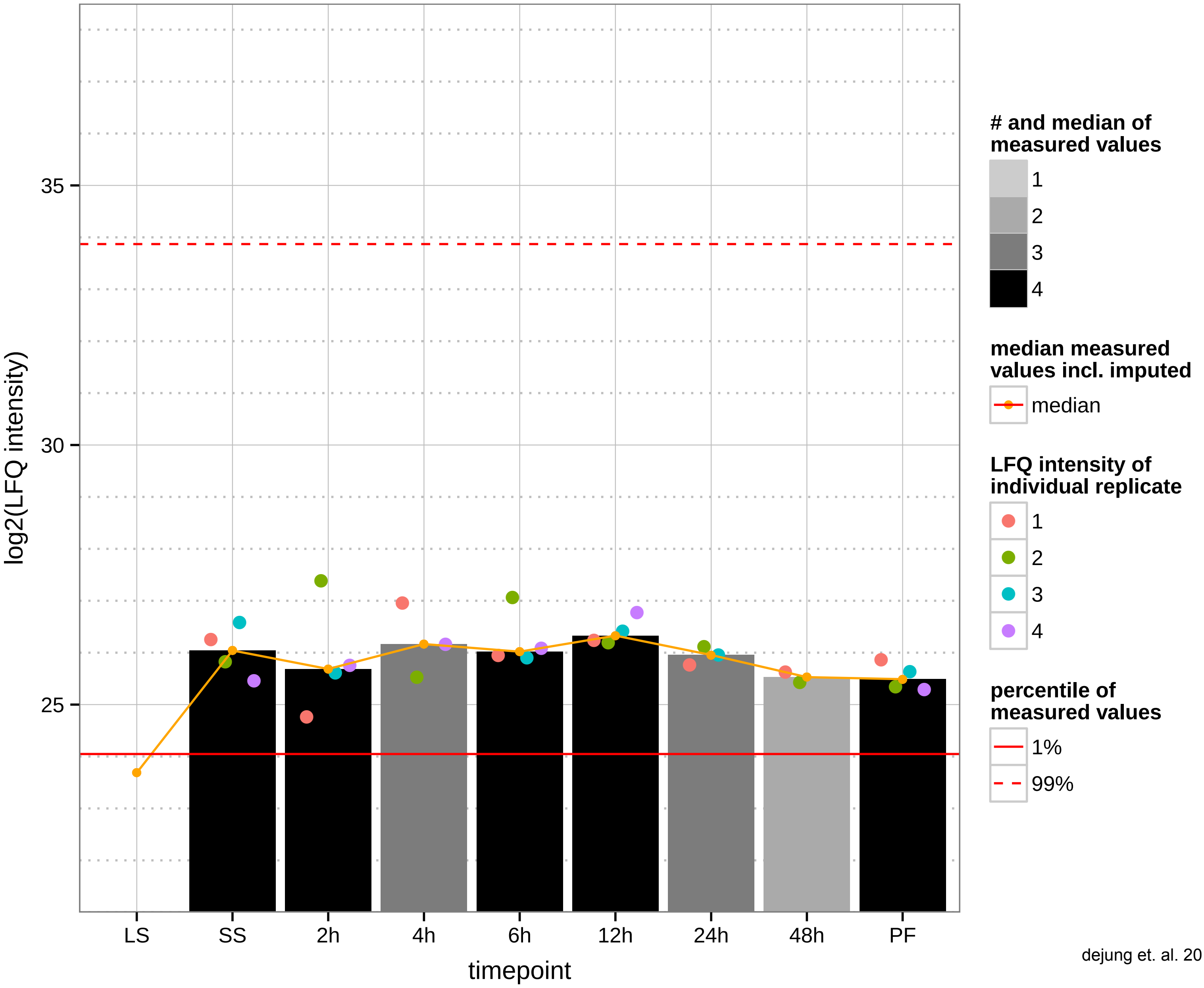
hypothetical protein, conserved
Tb927.10.8090
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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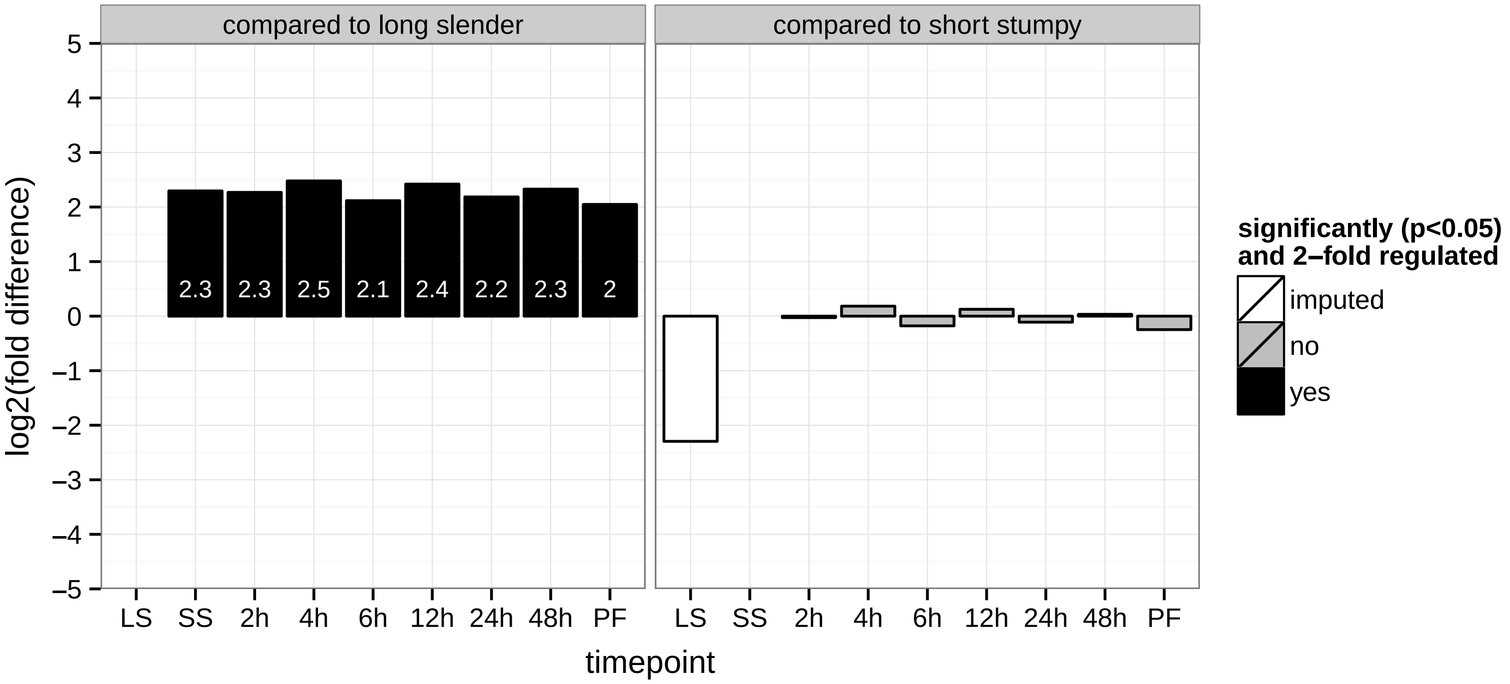
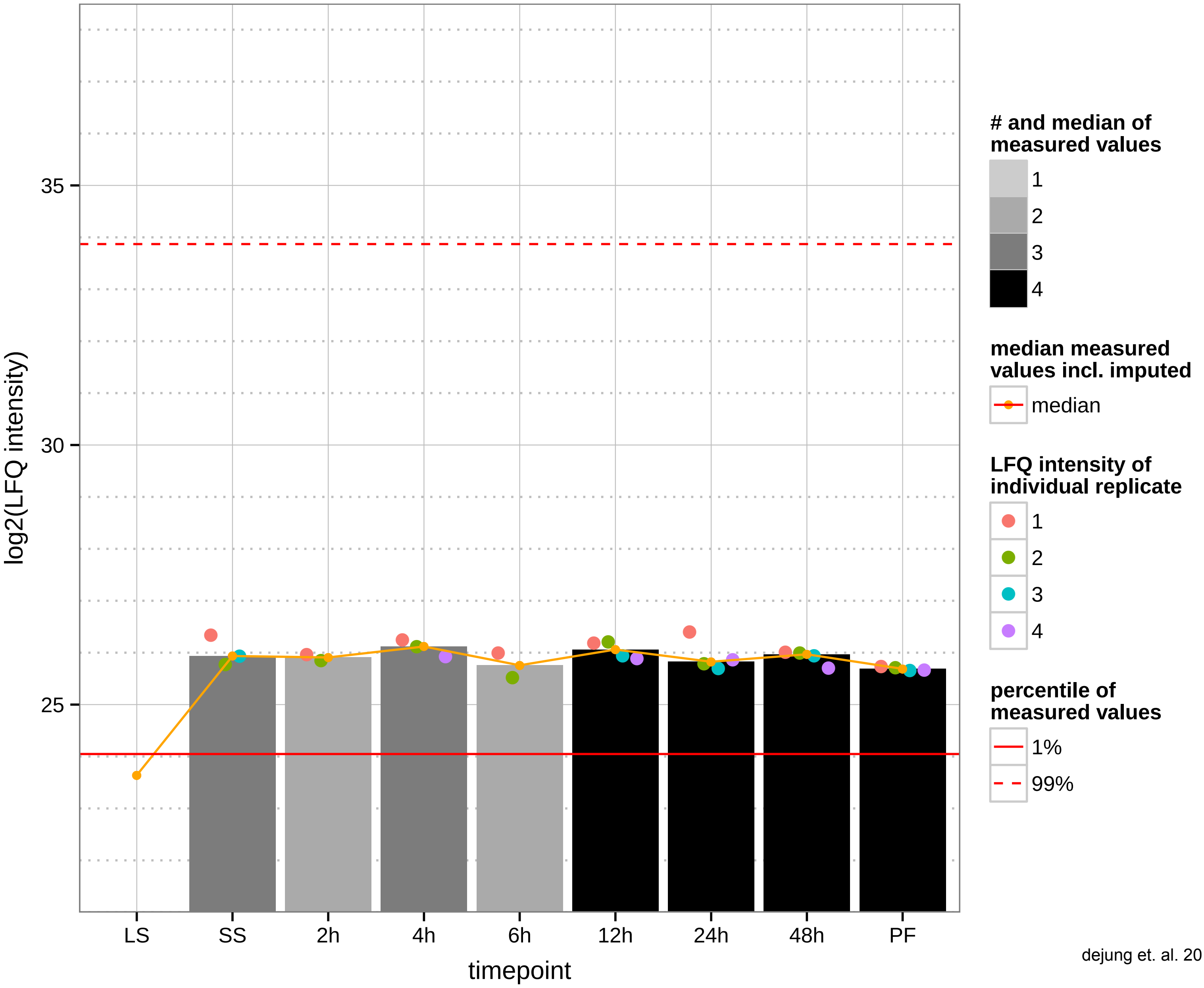
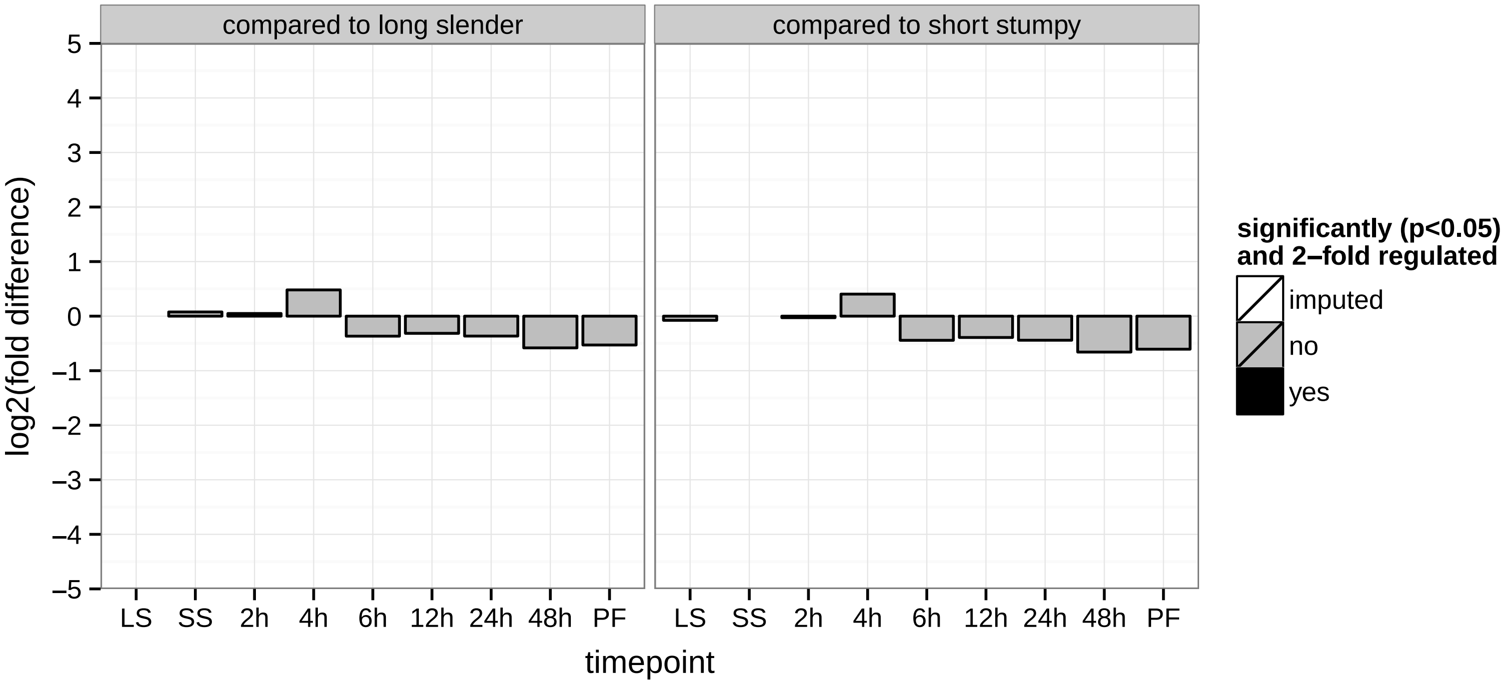
hypothetical protein, conserved
Tb927.10.810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

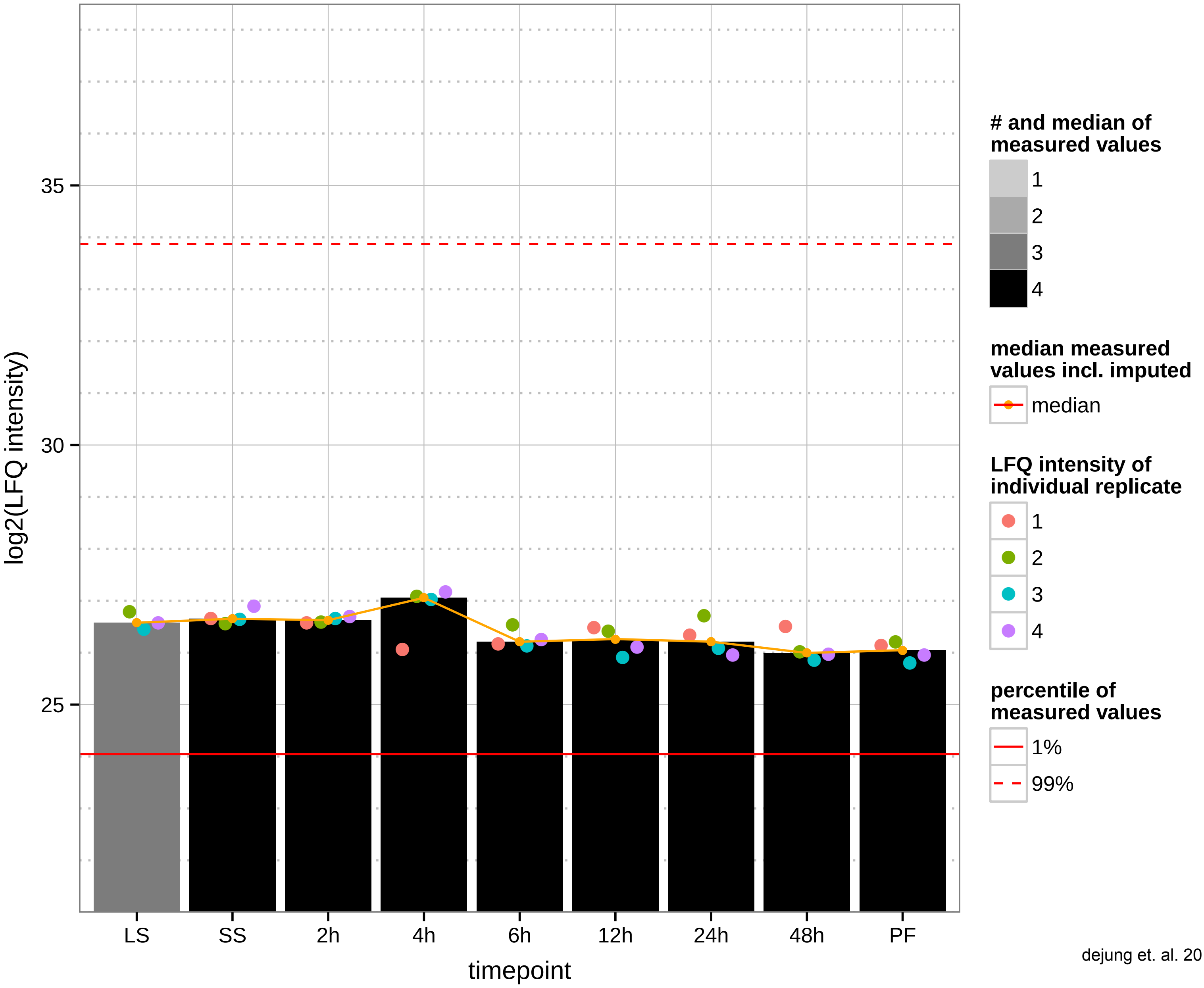




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.8110
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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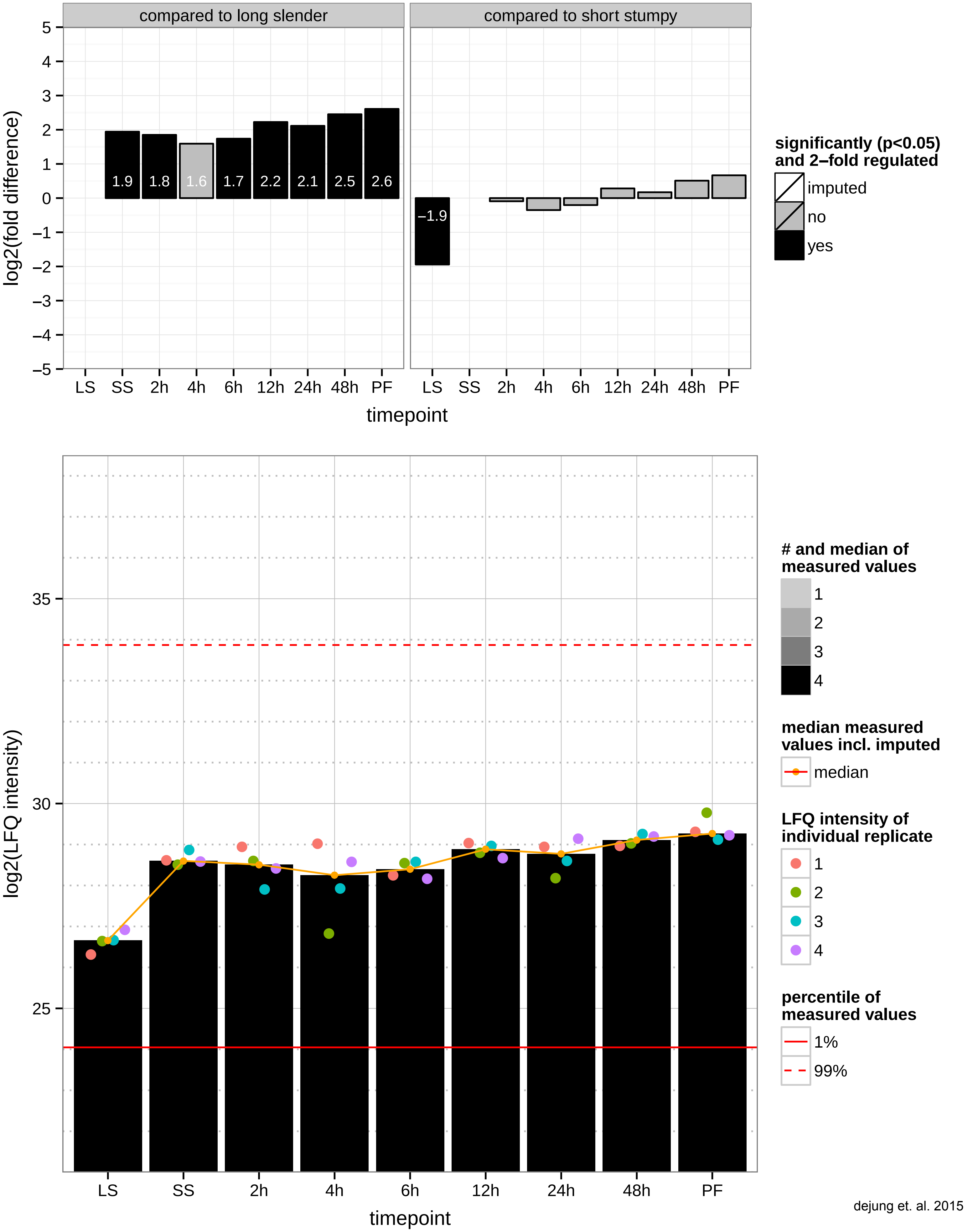
nuclear pore complex protein (NUP155), putative, nucleoporin
Tb927.10.8170
AGOF: structural constituent of nuclear pore
AGOC: nuclear pore
AGOP: nucleocytoplasmic transport
PGOF: null
PGOC: null
PGOP: null



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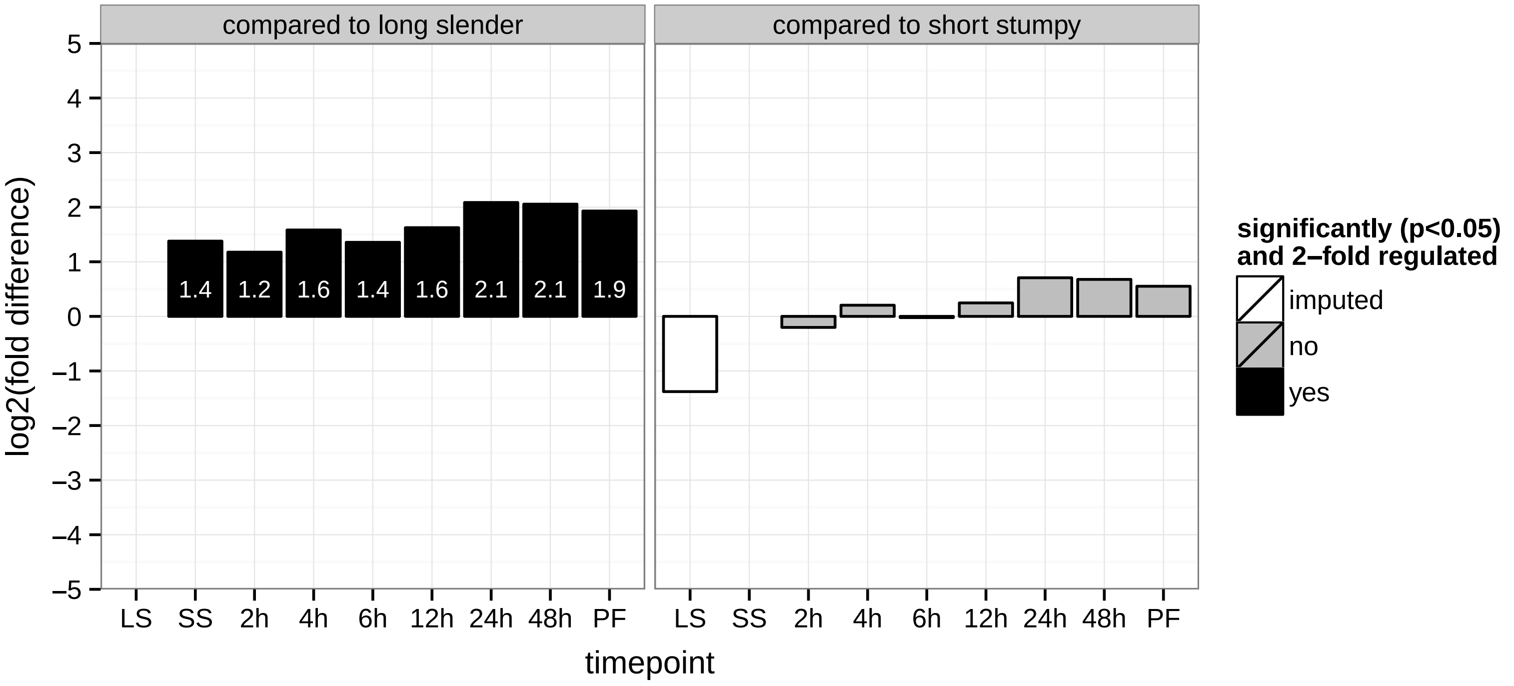
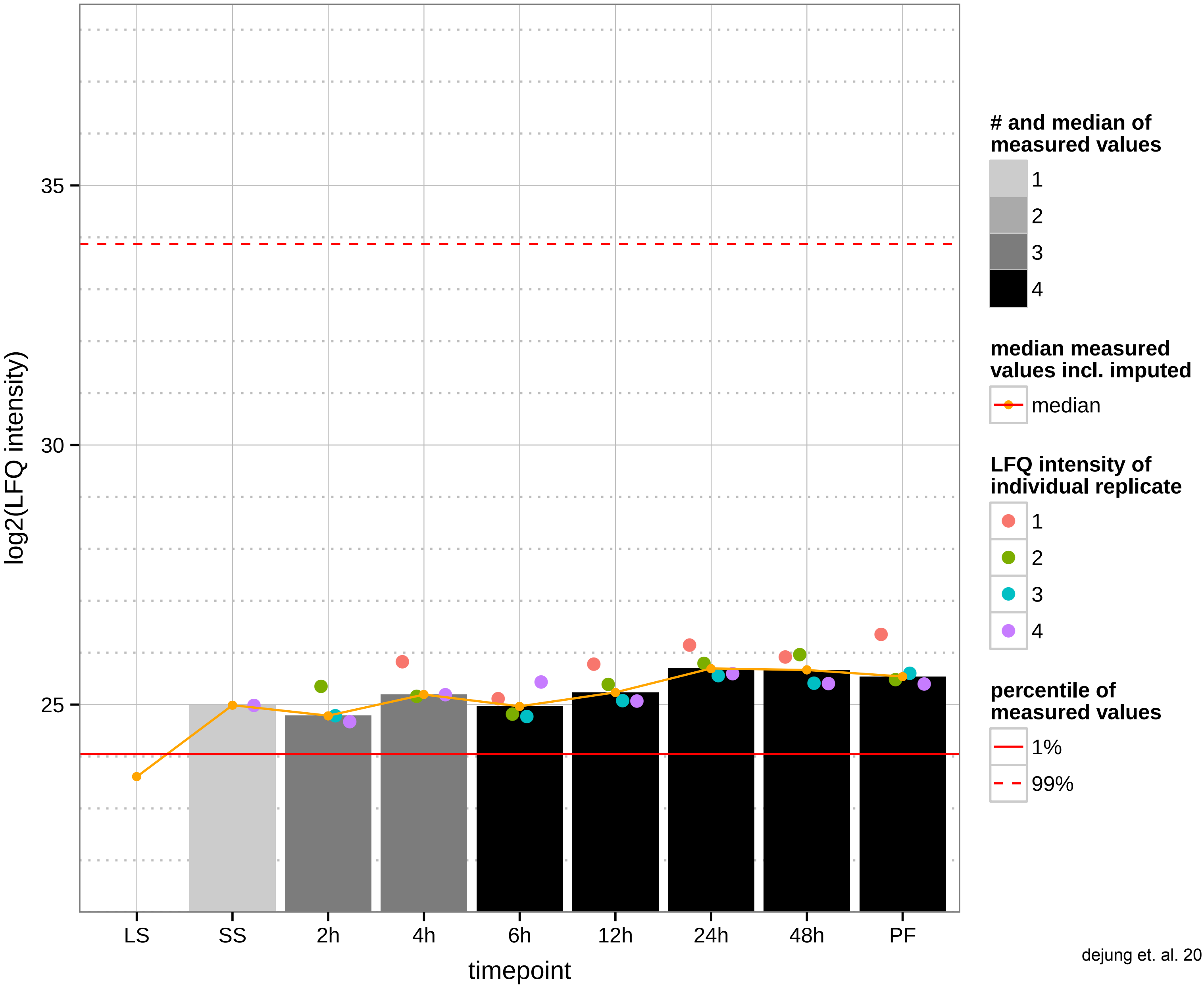
KREPA2, RNA–editing complex protein (KREPA2)
Tb927.10.8210
AGOF: zinc ion binding
AGOC: intracellular, mRNA editing complex, mitochondrial mRNA editing complex, mitochondrion
AGOP: mRNA modification
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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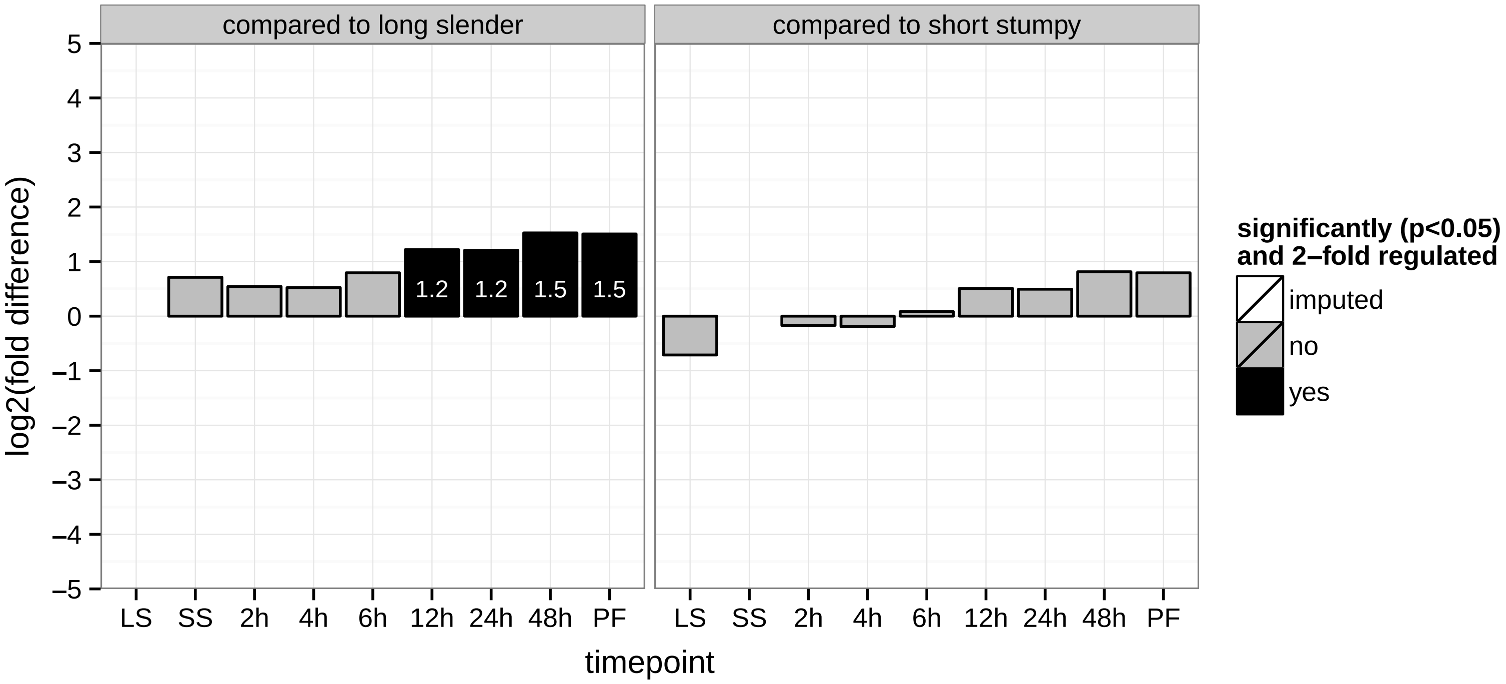
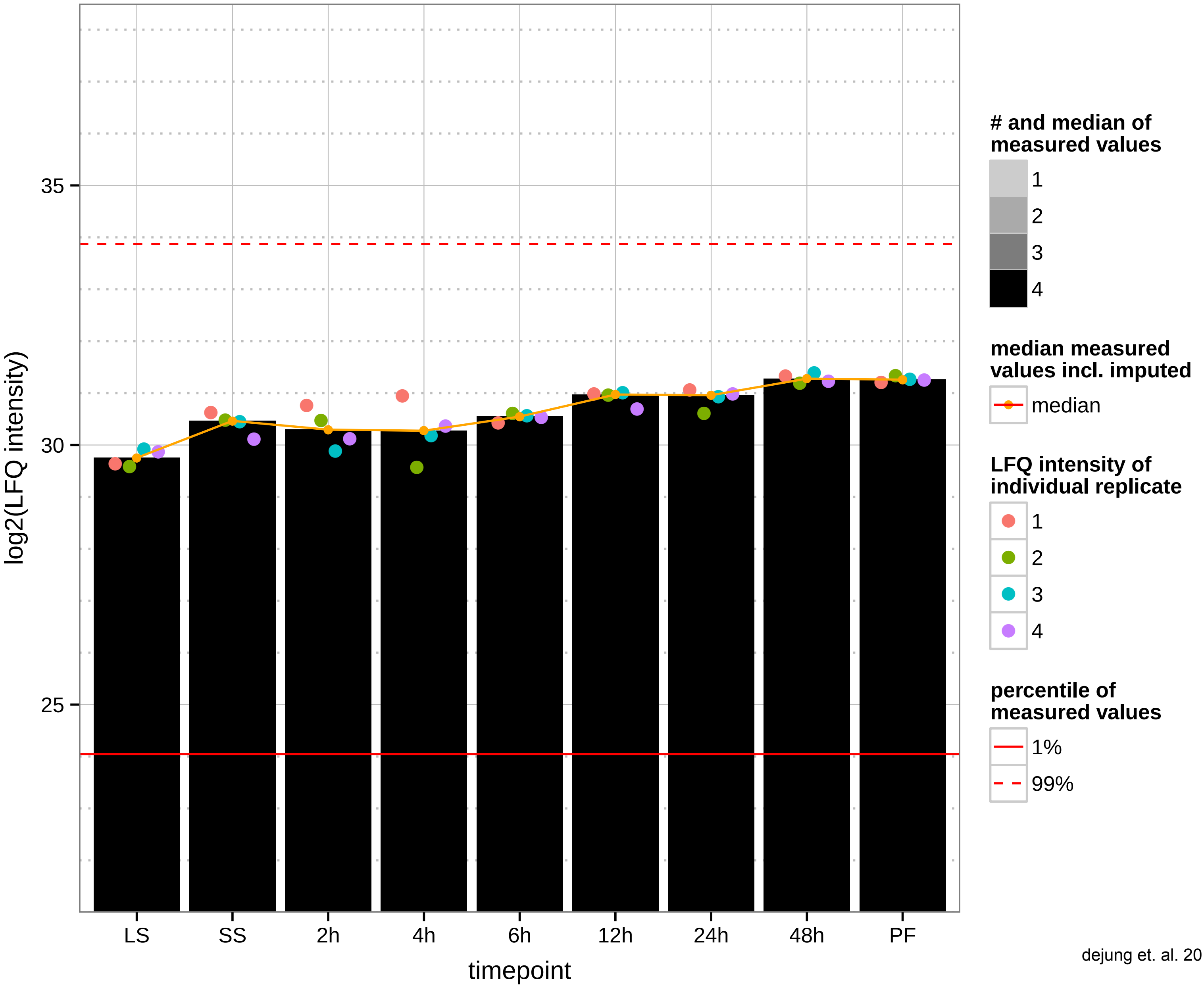
eukaryotic translation initiation factor 3 subunit 8, putative
Tb927.10.8290;Tb927.10.8270;Tb11.v5.0877
AGOF: null, ribosomal small subunit binding, translation initiation factor activity
AGOC: null, eukaryotic translation initiation factor 3 complex
AGOP: null, translational initiation
PGOF: translation initiation factor activity
PGOC: eukaryotic translation initiation factor 3 complex
PGOP: translational initiation





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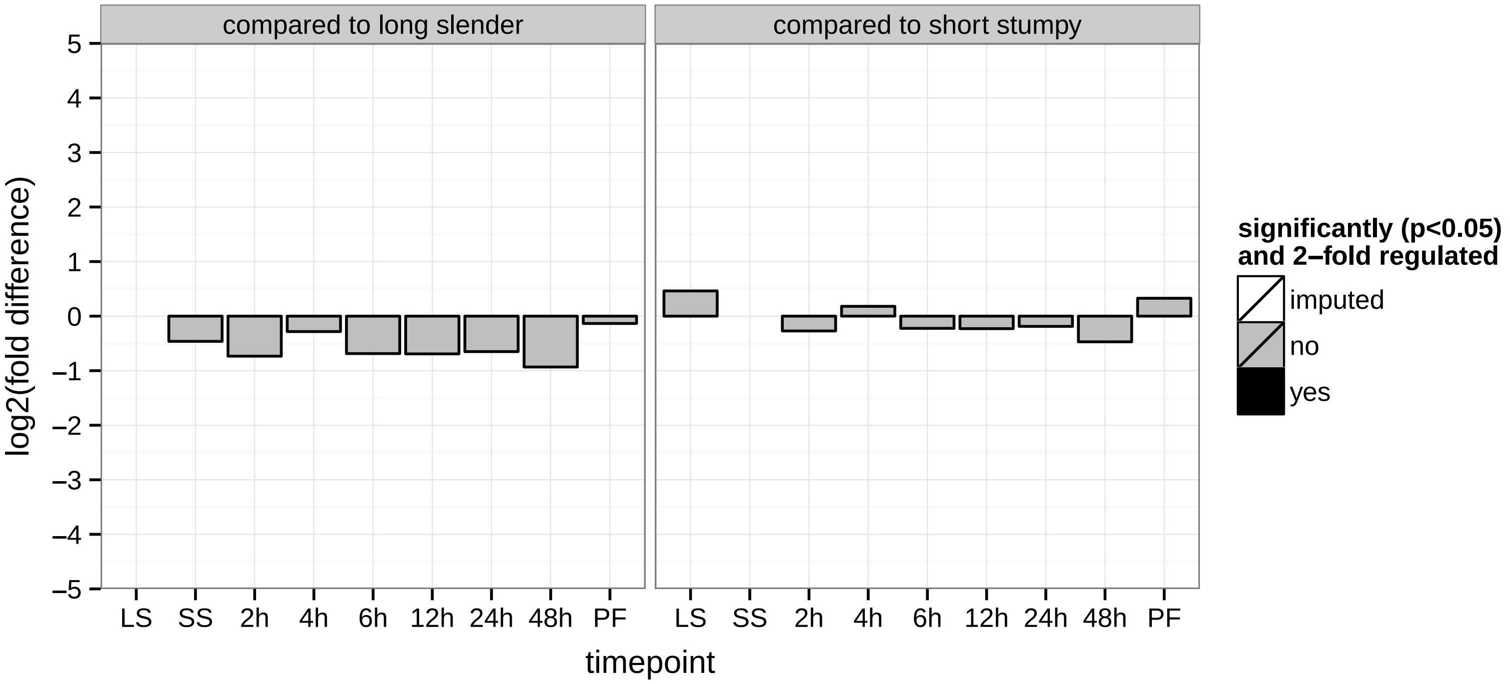
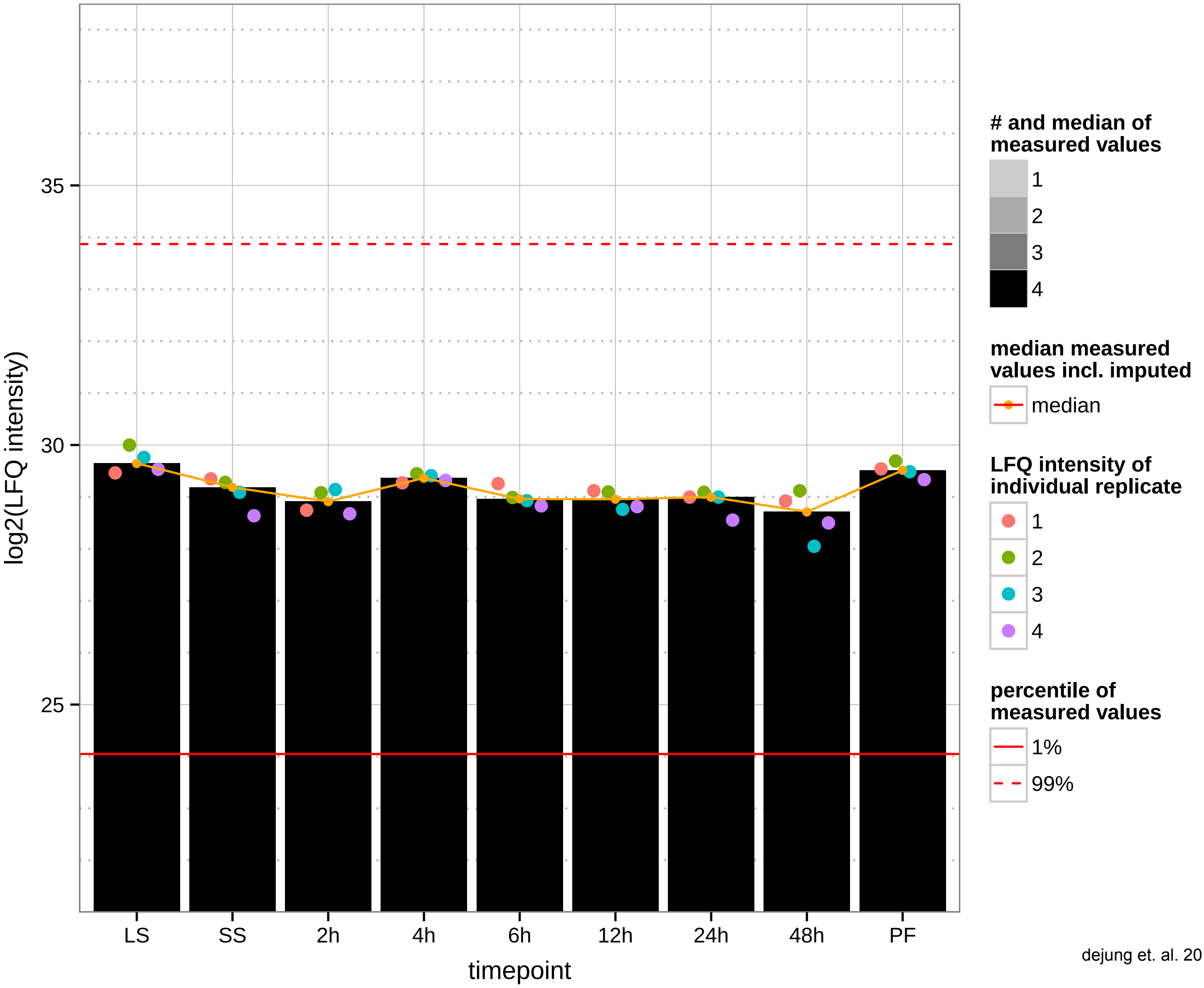
adenylate kinase, putative
Tb927.10.830
AGOF: ATP binding, adenylate kinase activity
AGOC: cytosol, glycosome
AGOP: nucleobase–containing compound metabolic process
PGOF: ATP binding, adenylate kinase activity, cAMP–dependent protein kinase regulator activity, nucleobase–containing com
PGOC: null
PGOP: nucleobase–containing compound metabolic process, nucleotide phosphorylation, signal transduction





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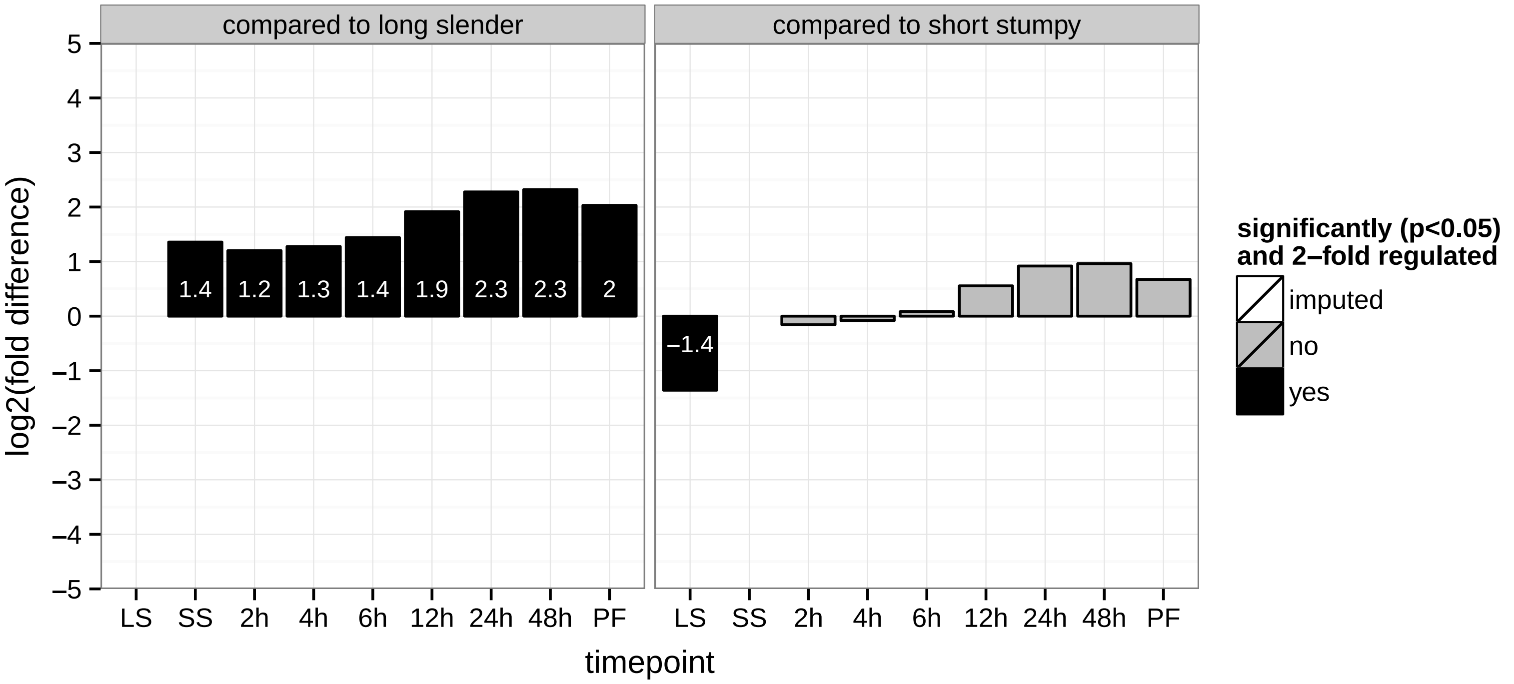
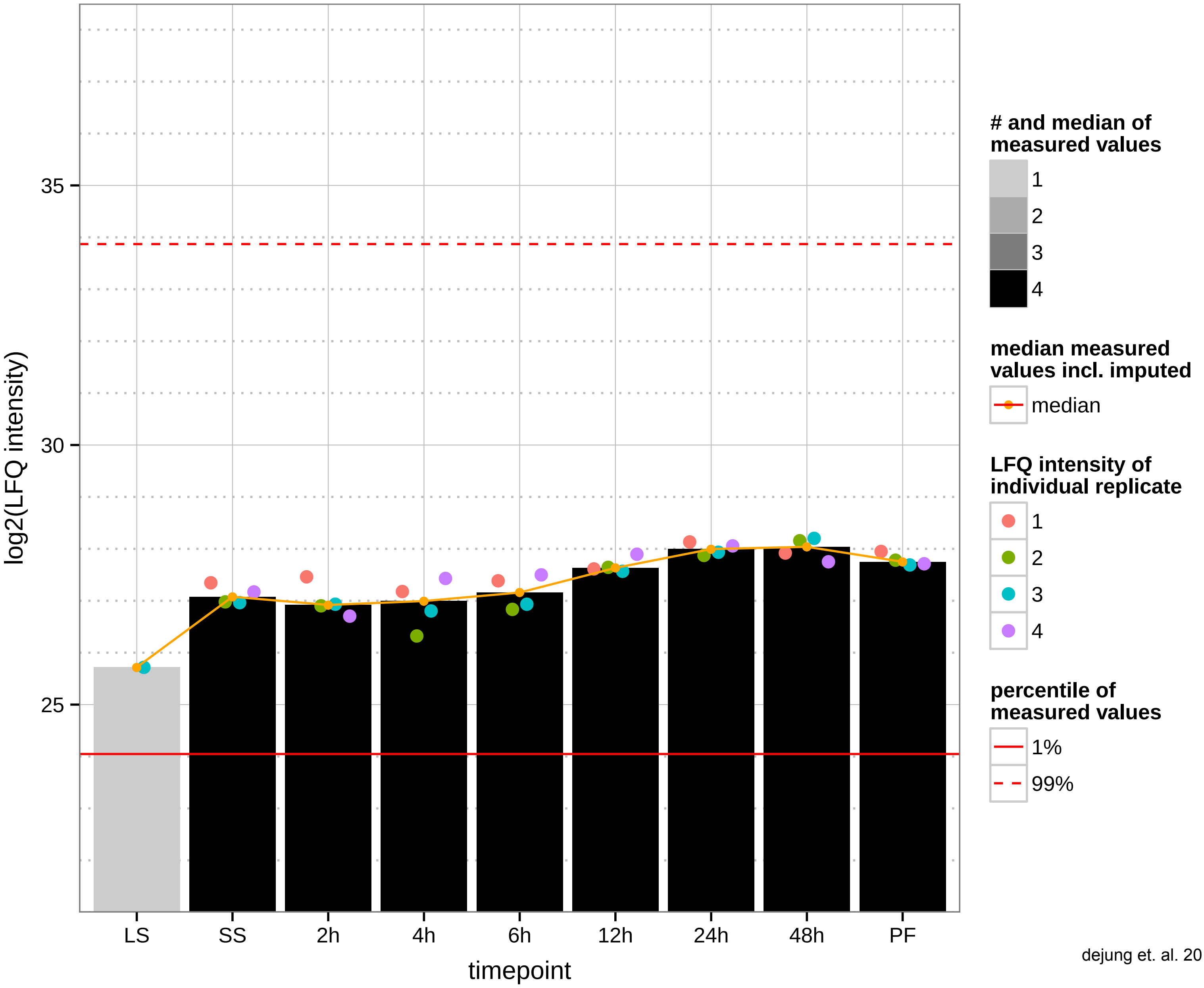
hypothetical protein, conserved
Tb927.10.8410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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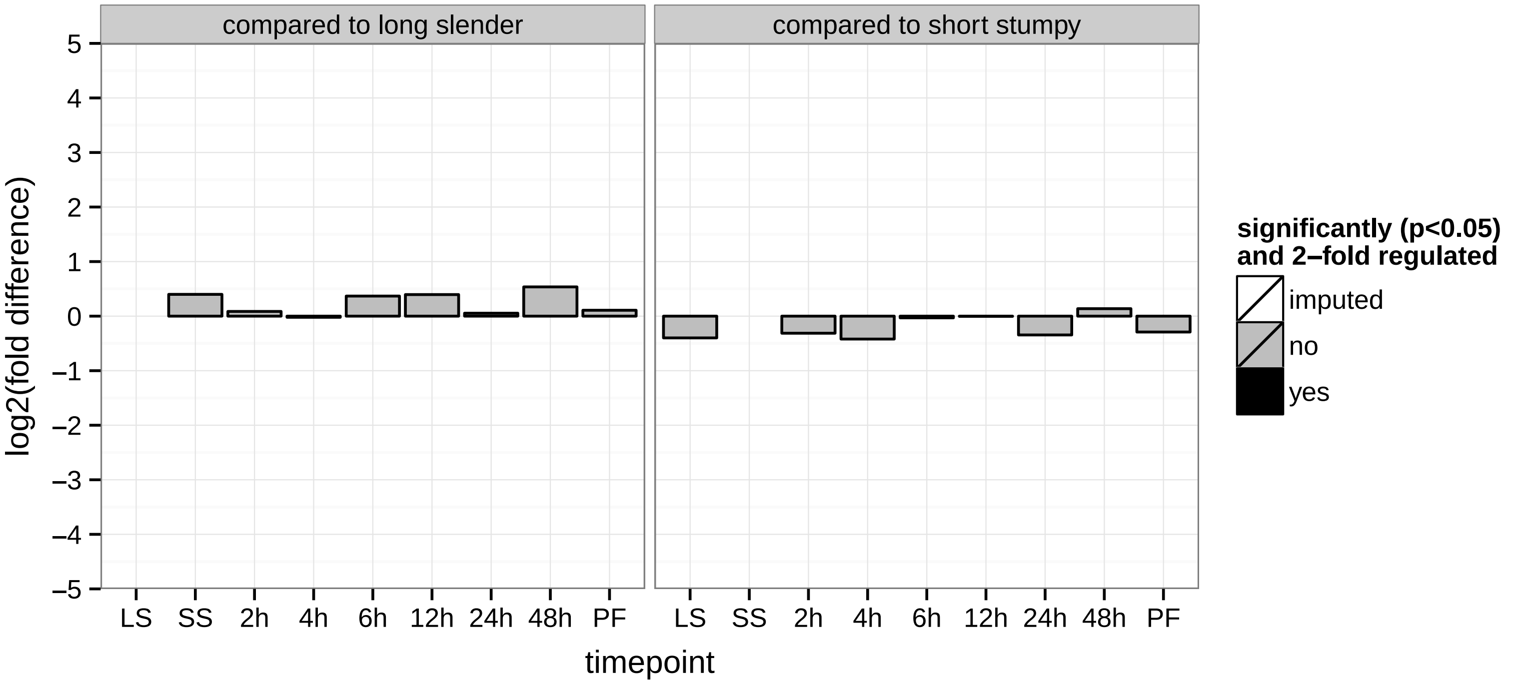
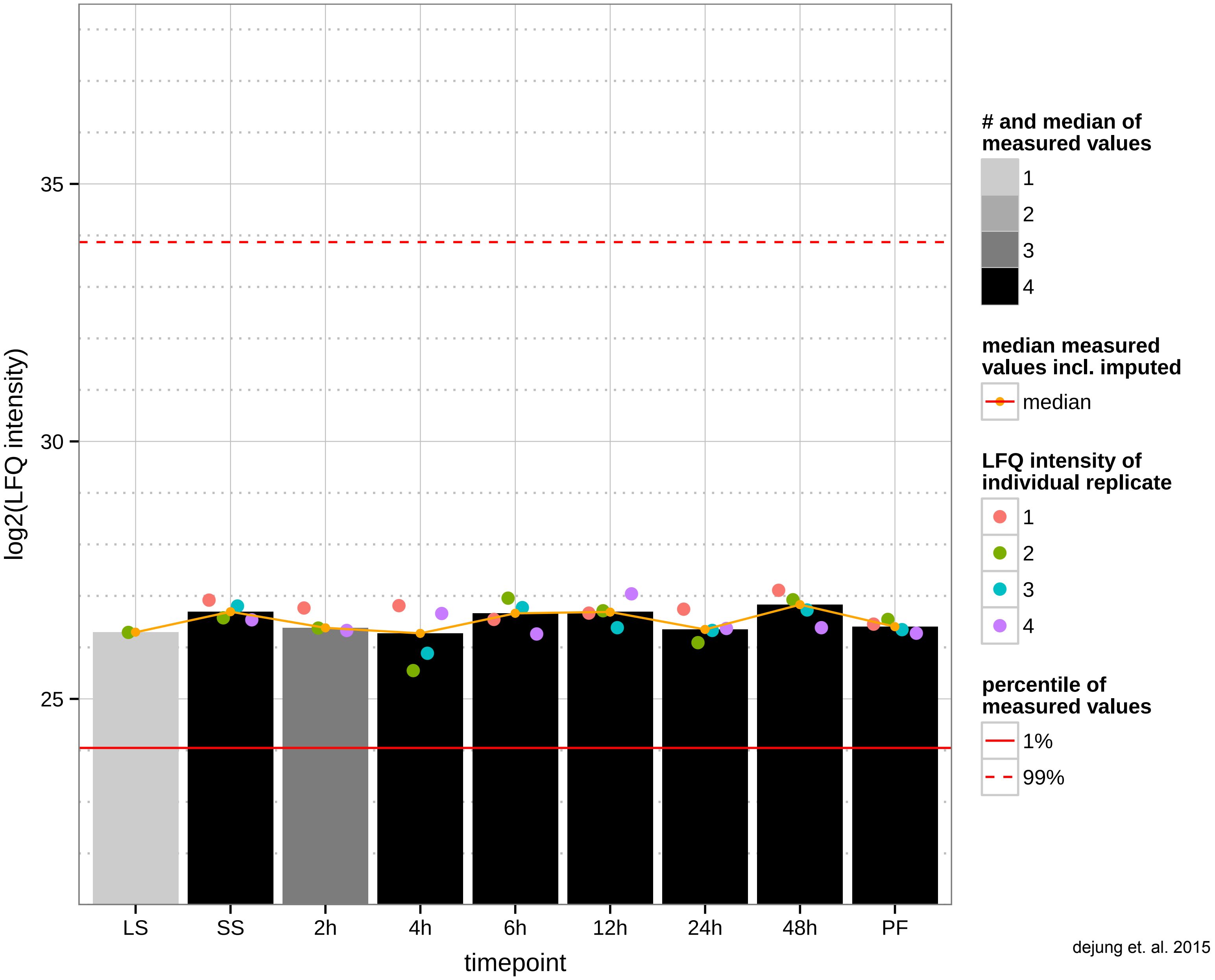
target of rapamycin (TOR) kinase 1 (TOR1)
Tb927.10.8420
AGOF: phosphotransferase activity, alcohol group as acceptor
AGOC: null
AGOP: growth, intracellular signal transduction
PGOF: binding, phosphotransferase activity, alcohol group as acceptor, protein binding, transferase activity, transferring phosp
PGOC: null
PGOP: null





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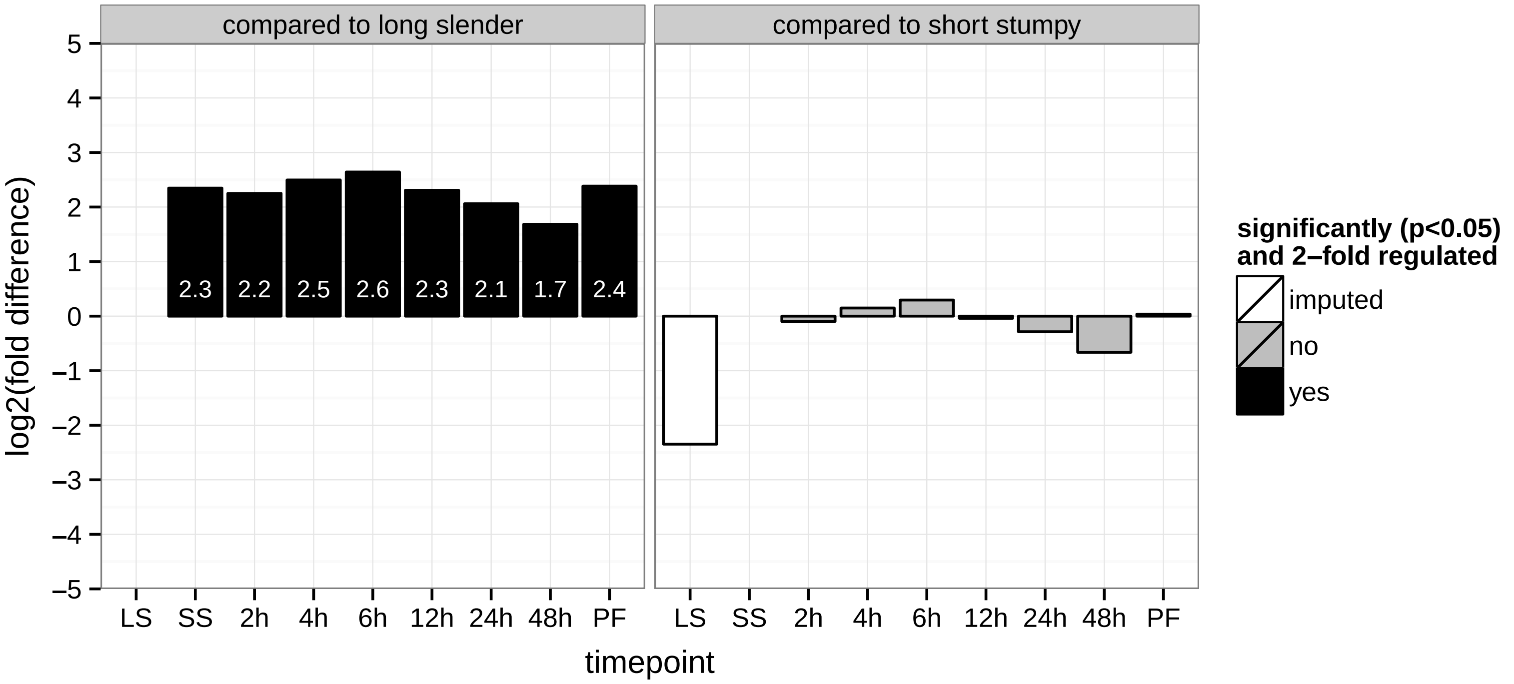
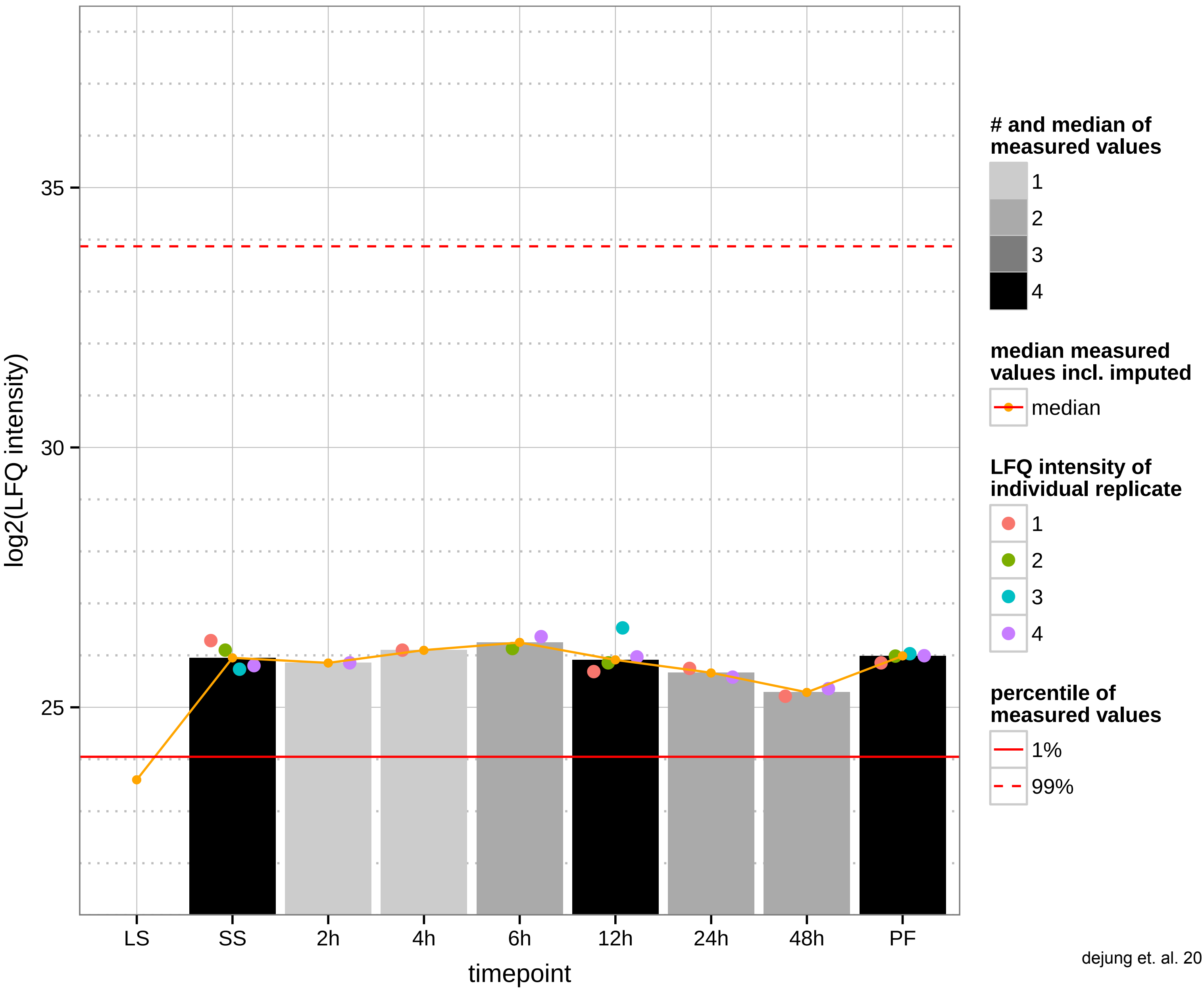
hypothetical protein, conserved
Tb927.10.850
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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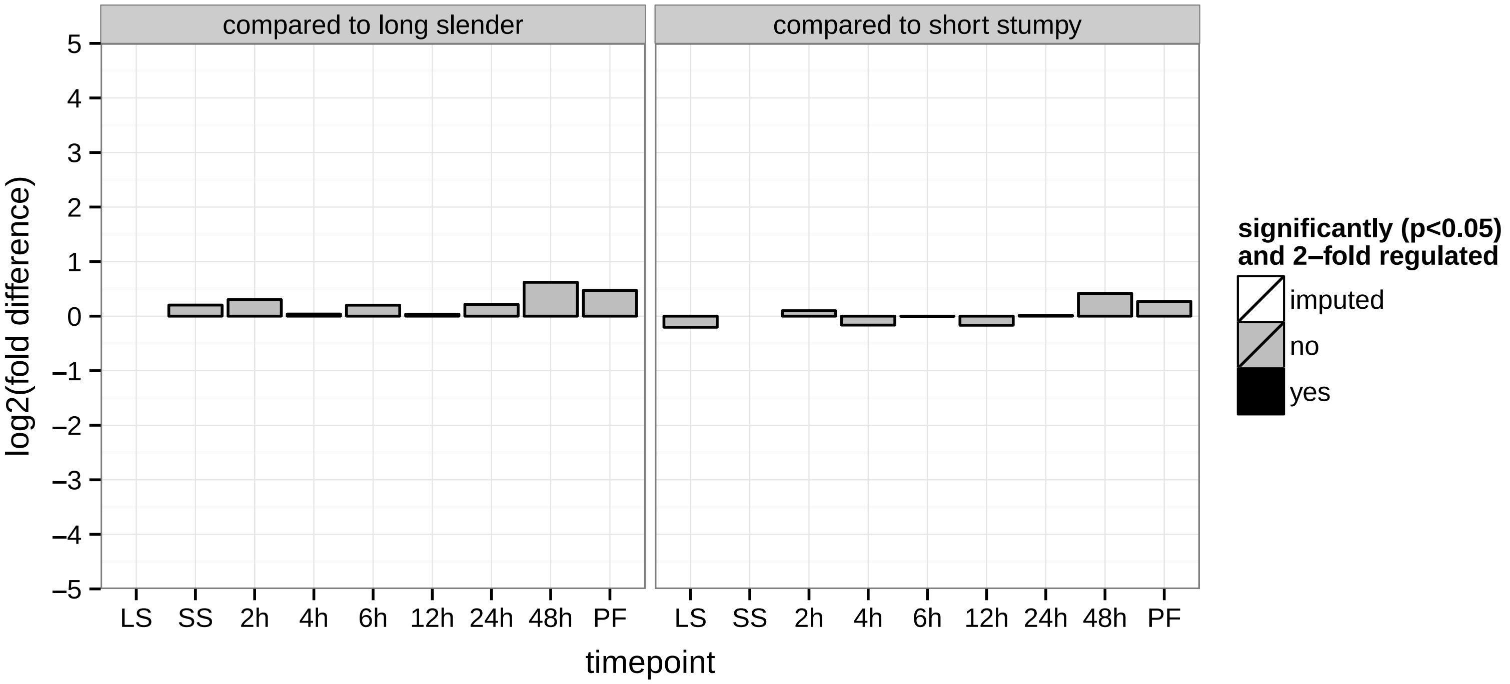
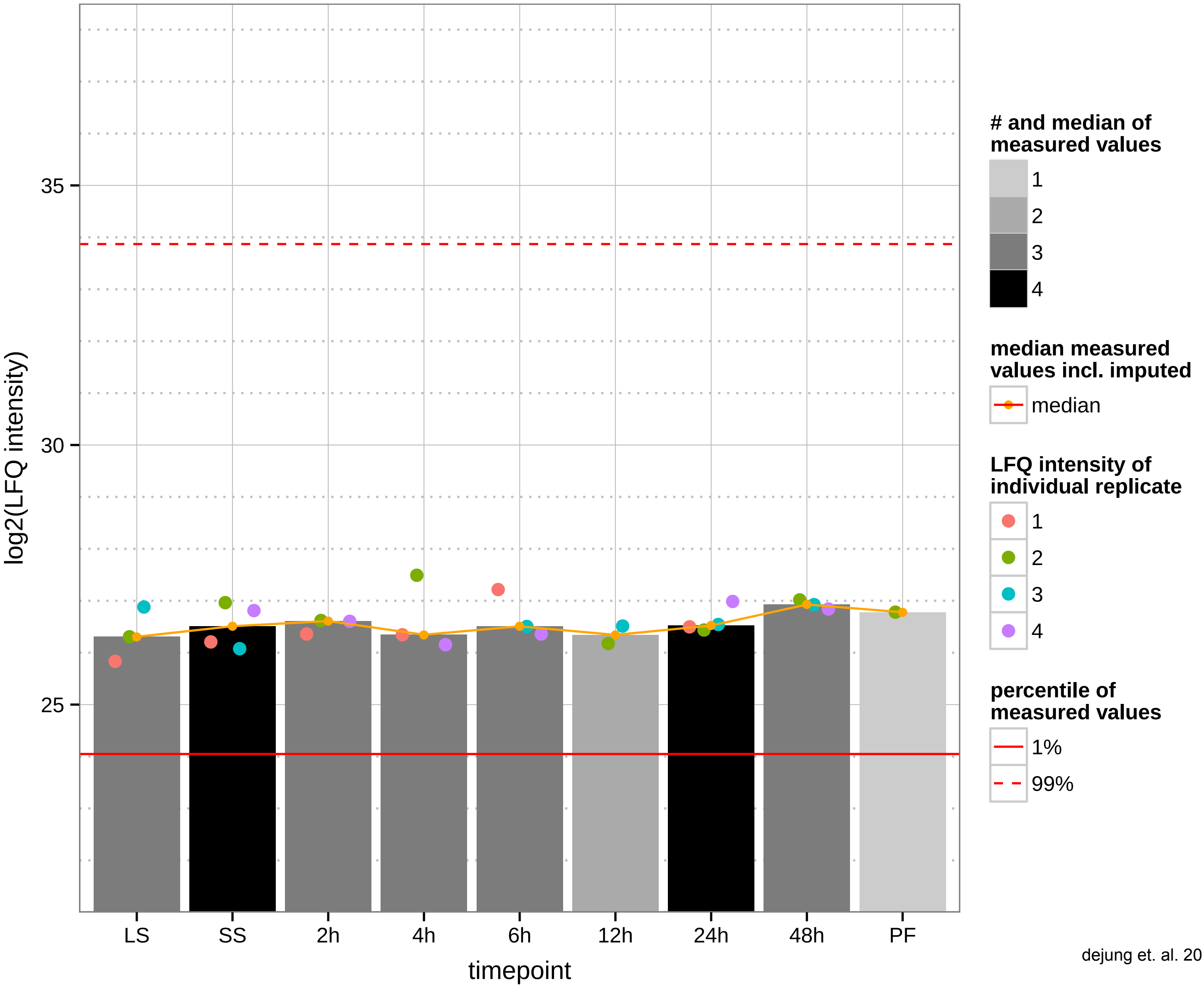
flagellum transition zone component, putative, flagellum transition zone component (FTZC)
Tb927.10.8590
AGOF: null
AGOC: null, axoneme
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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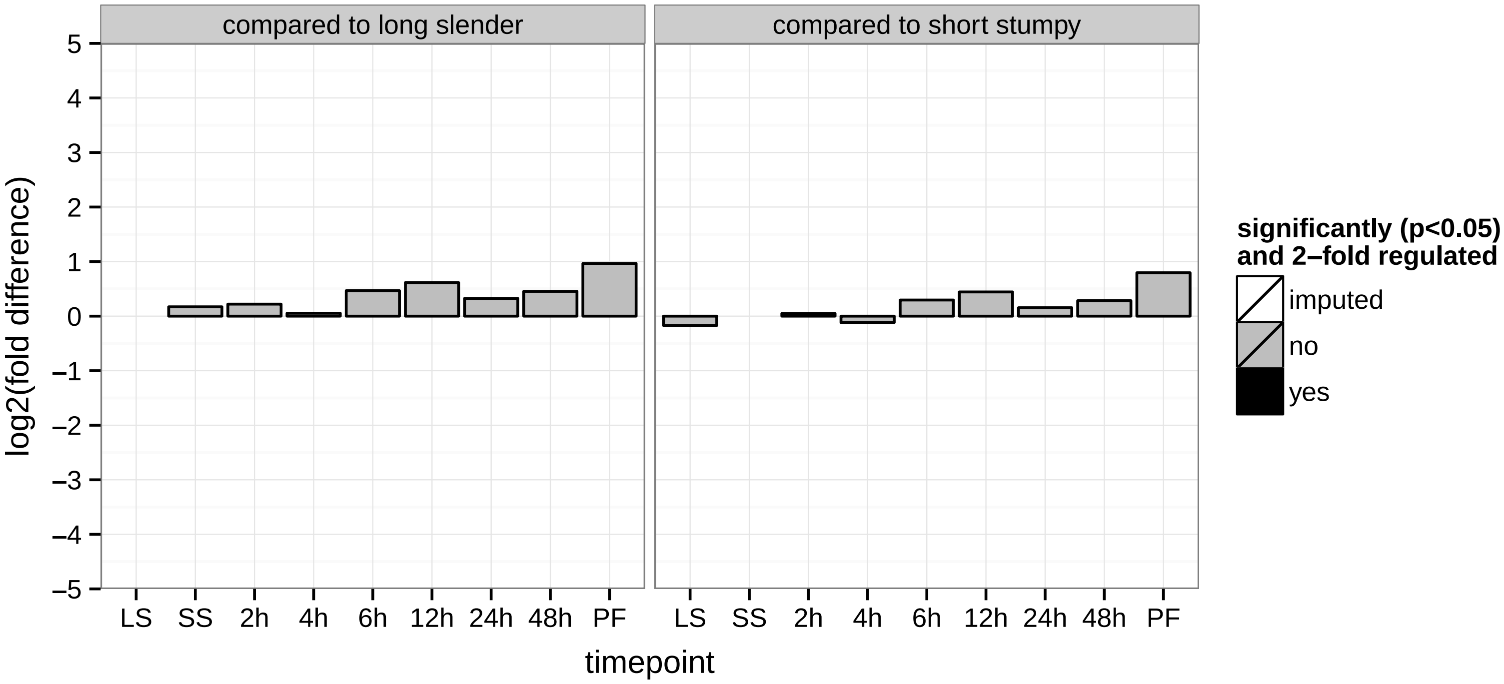
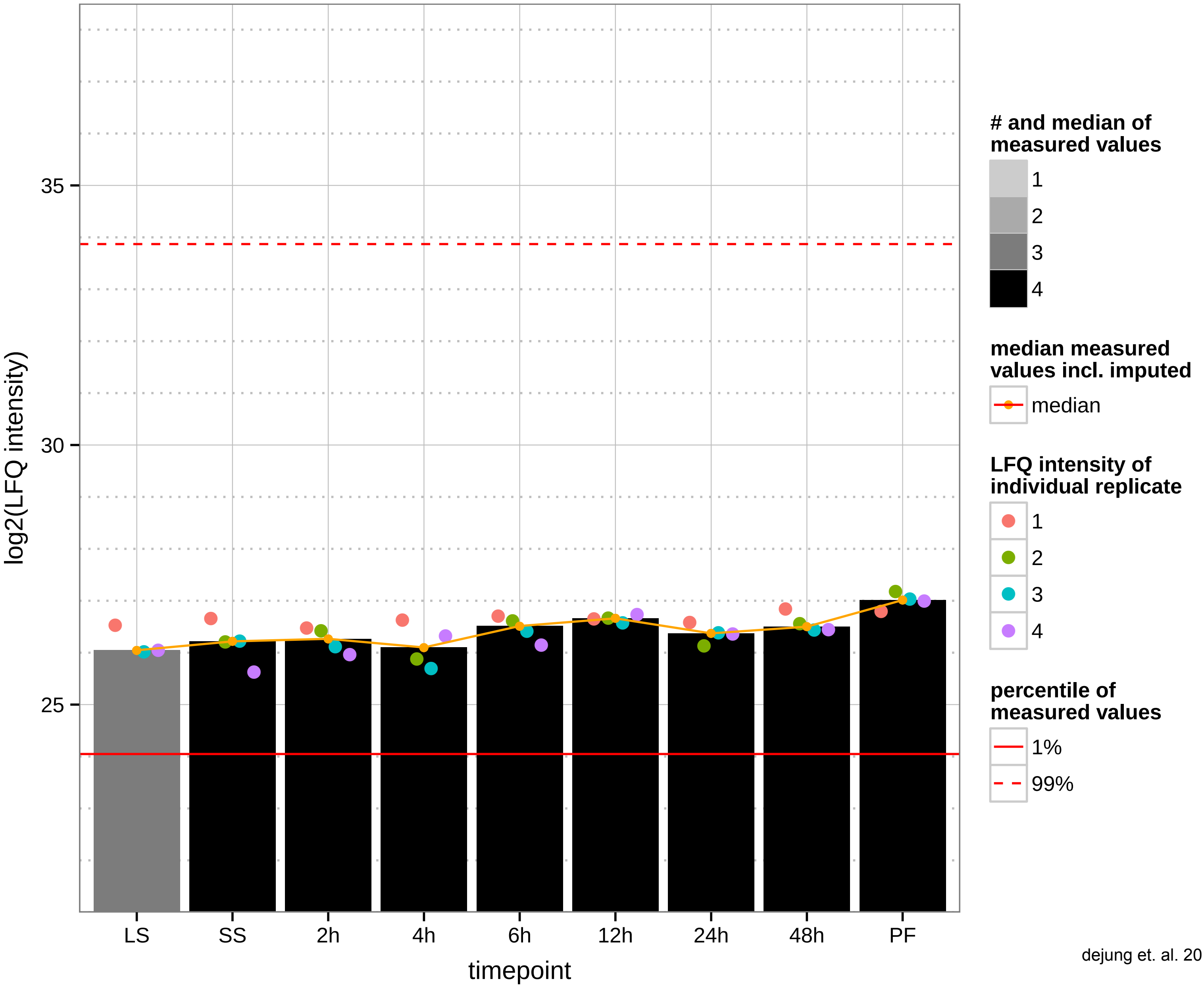
hypothetical protein, conserved
Tb927.10.8640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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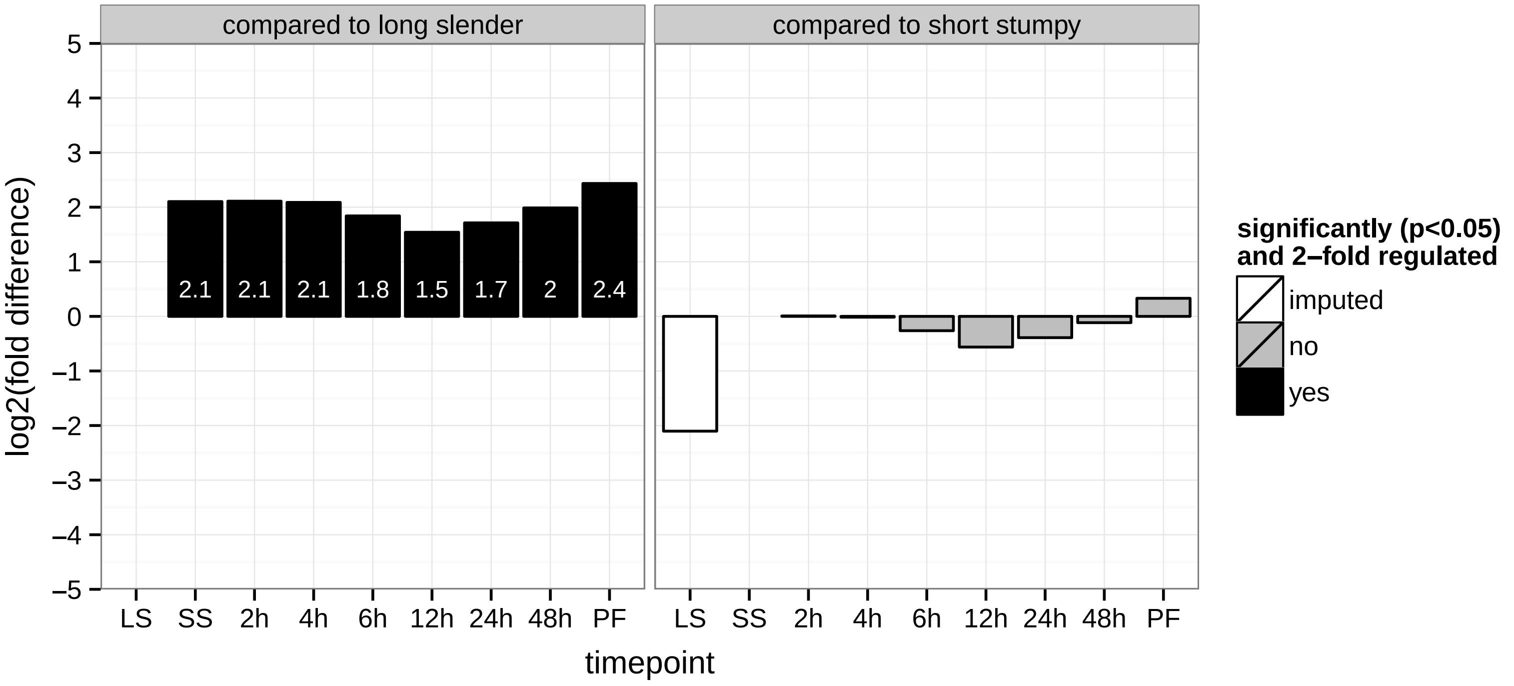
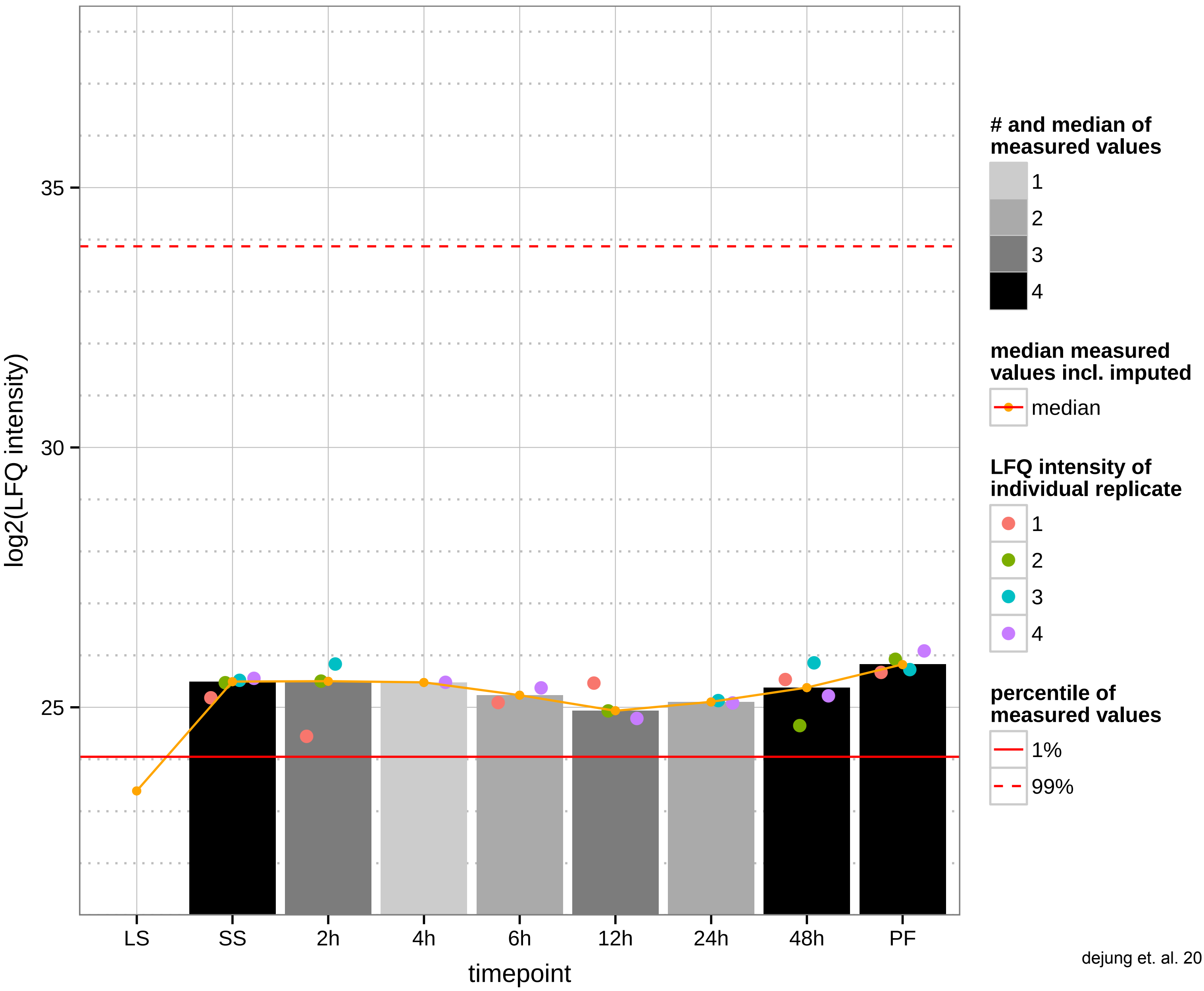
hypothetical protein, conserved
Tb927.10.8660
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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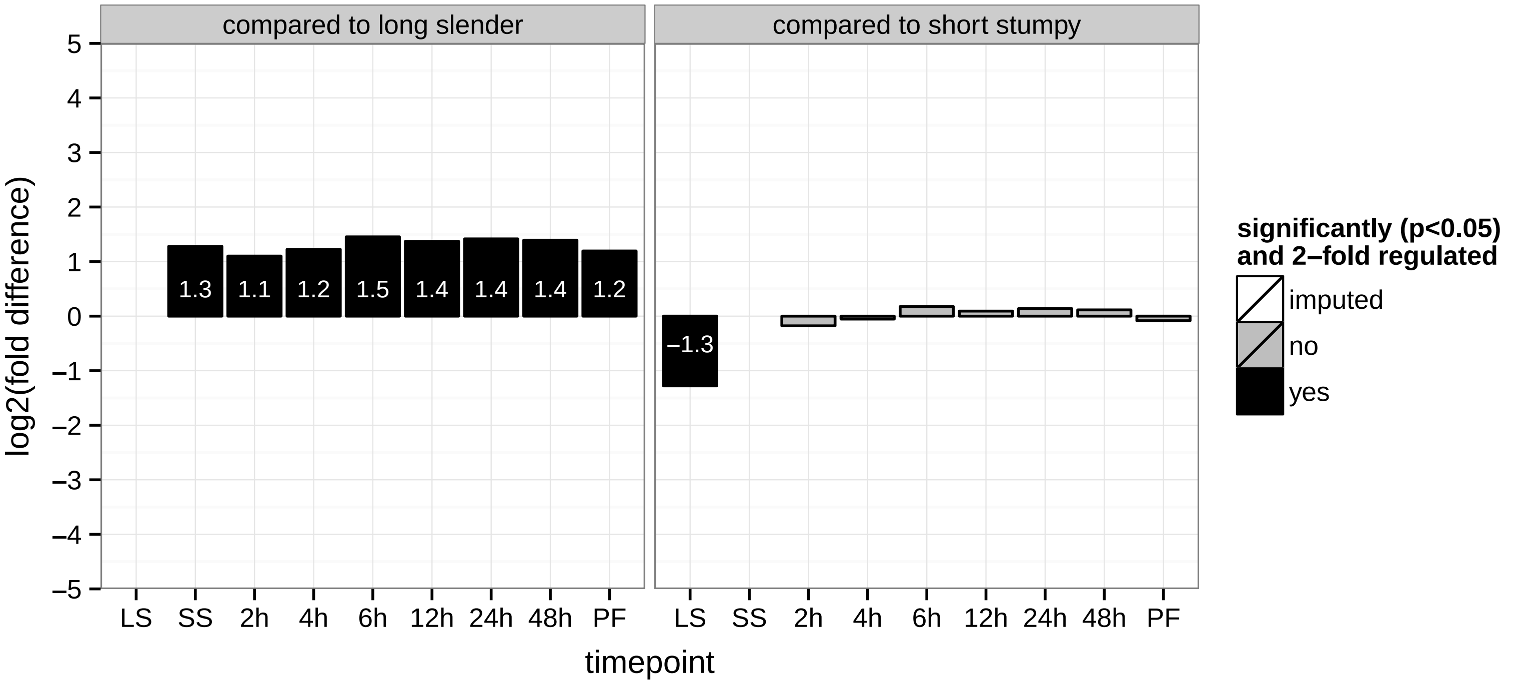
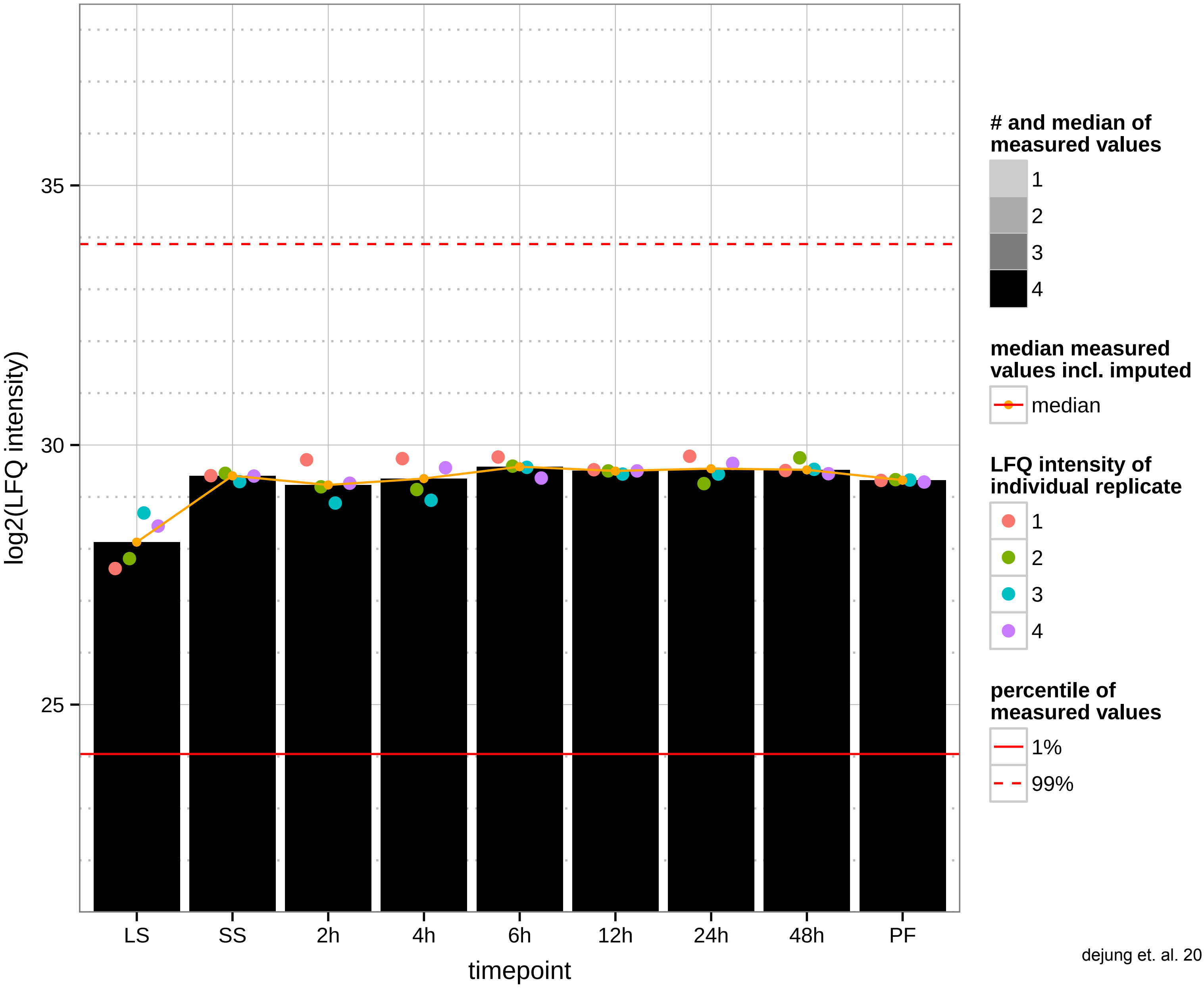
CCR4–NOT transcription complex subunit 10, putative
Tb927.10.8720
AGOF: null
AGOC: cytoplasm
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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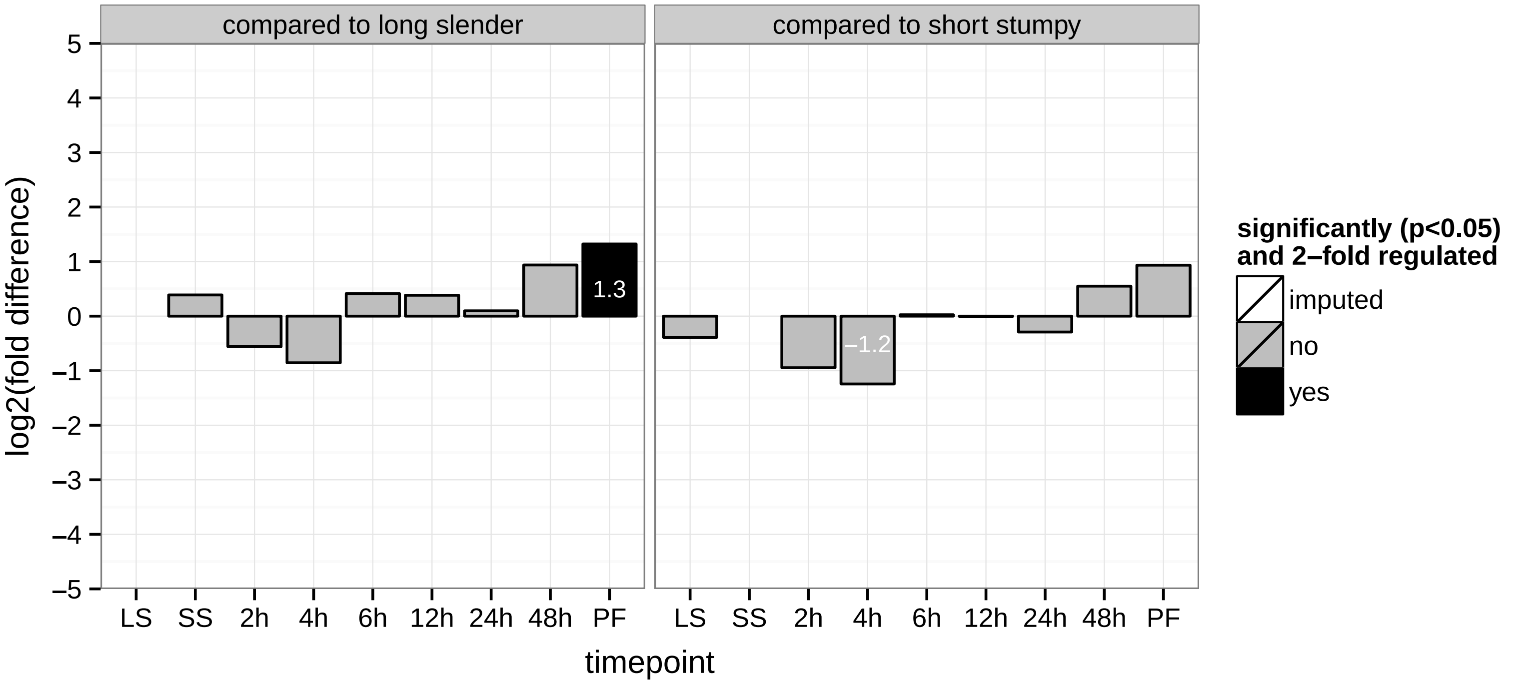
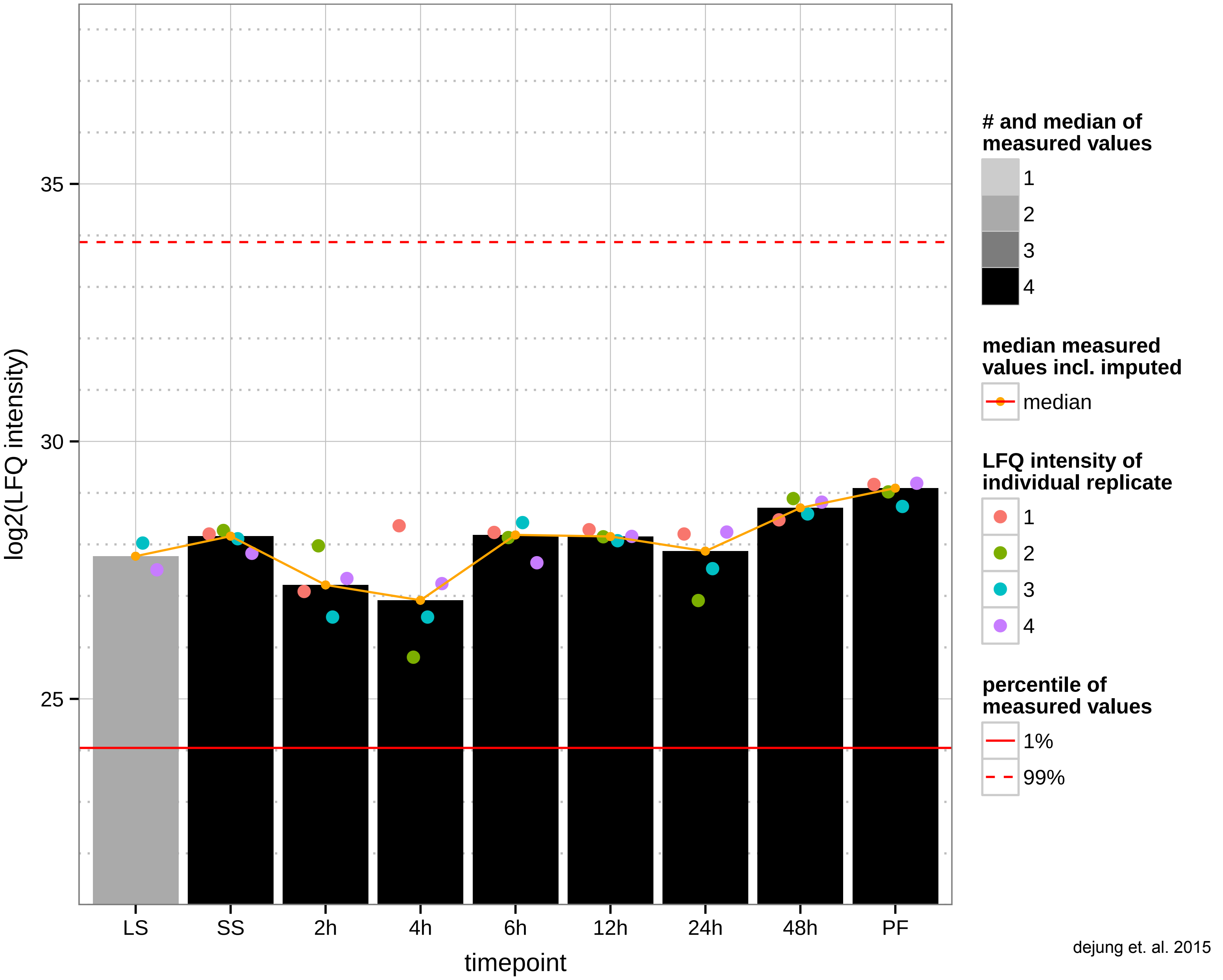
hypothetical protein, conserved
Tb927.10.8780
AGOF: ATP binding, nucleobase–containing compound kinase activity
AGOC: null
AGOP: nucleobase–containing compound metabolic process
PGOF: null
PGOC: null
PGOP: null





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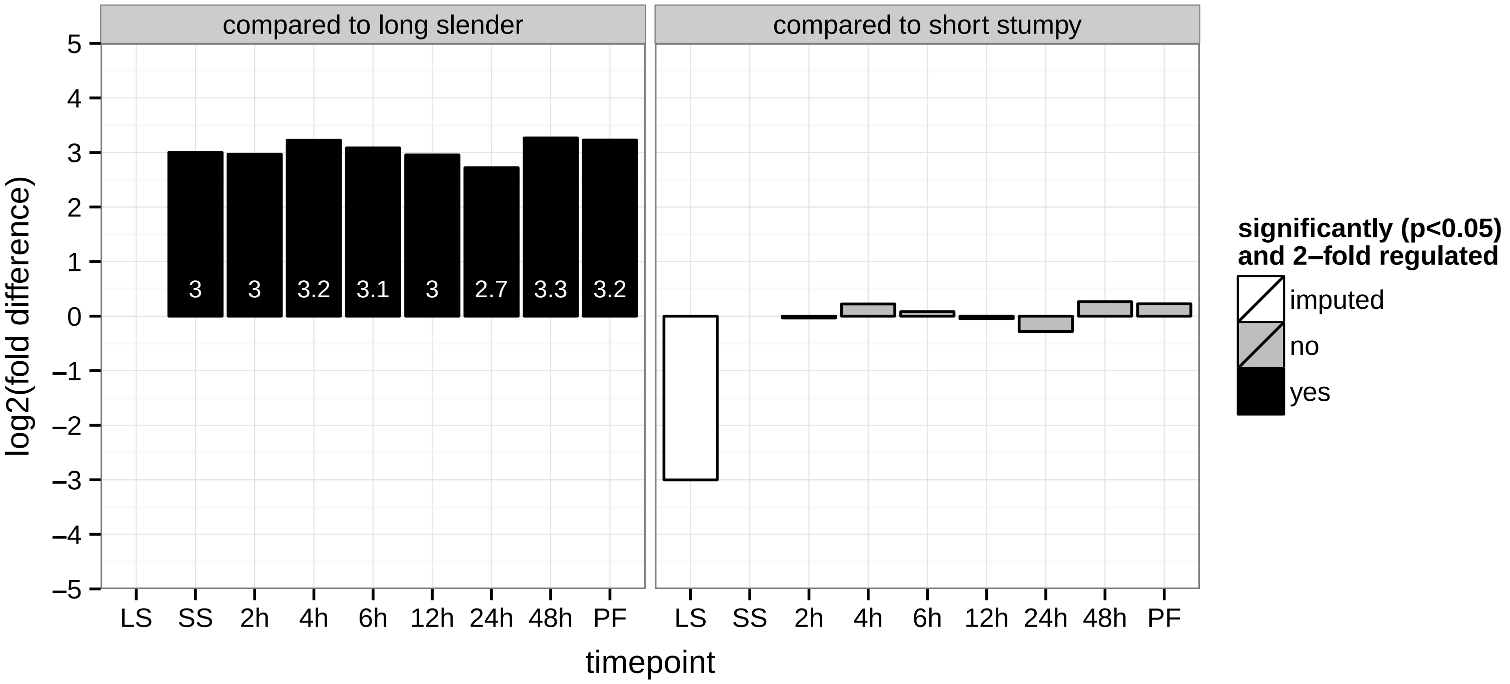
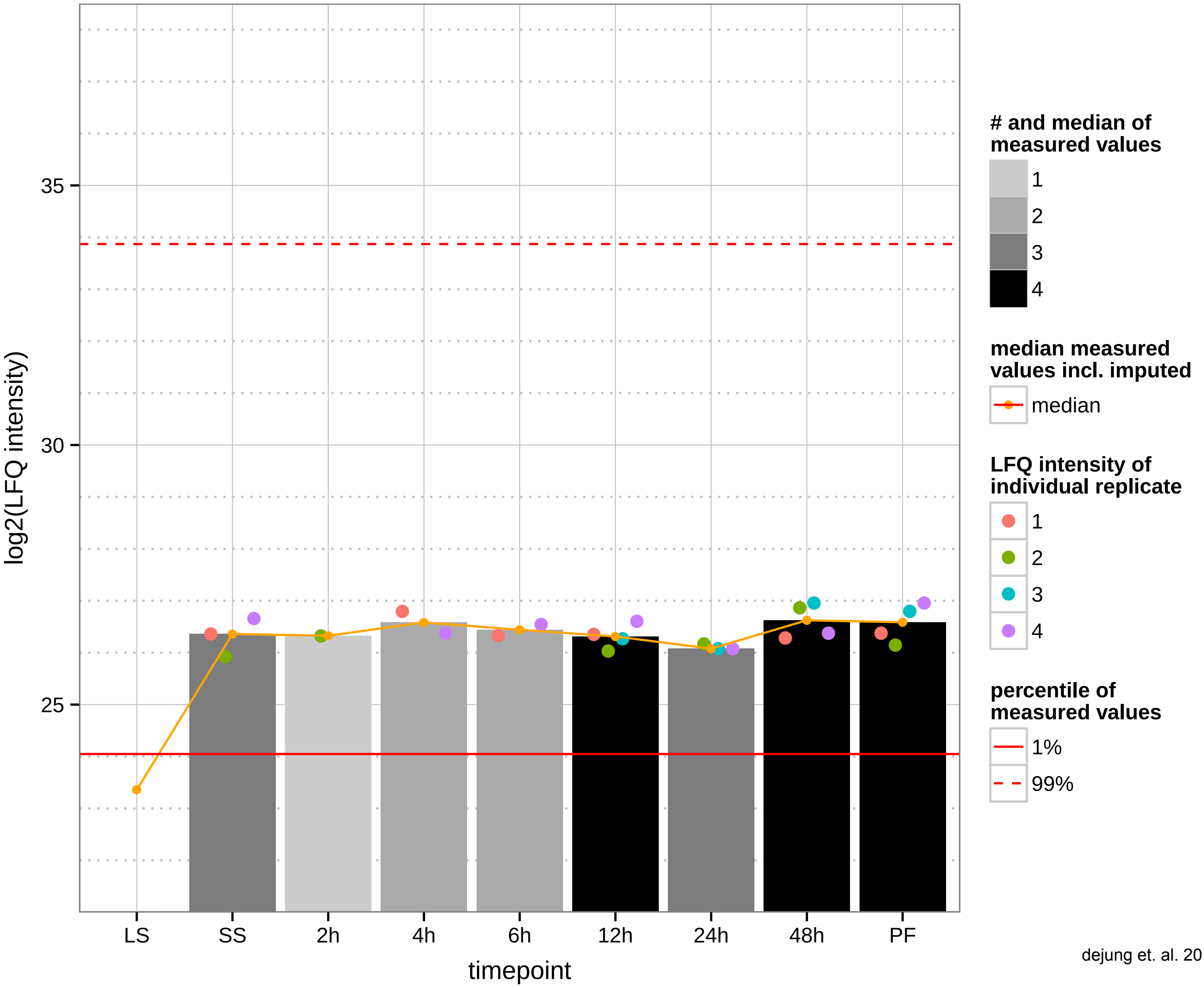
hypothetical protein, conserved
Tb927.10.8790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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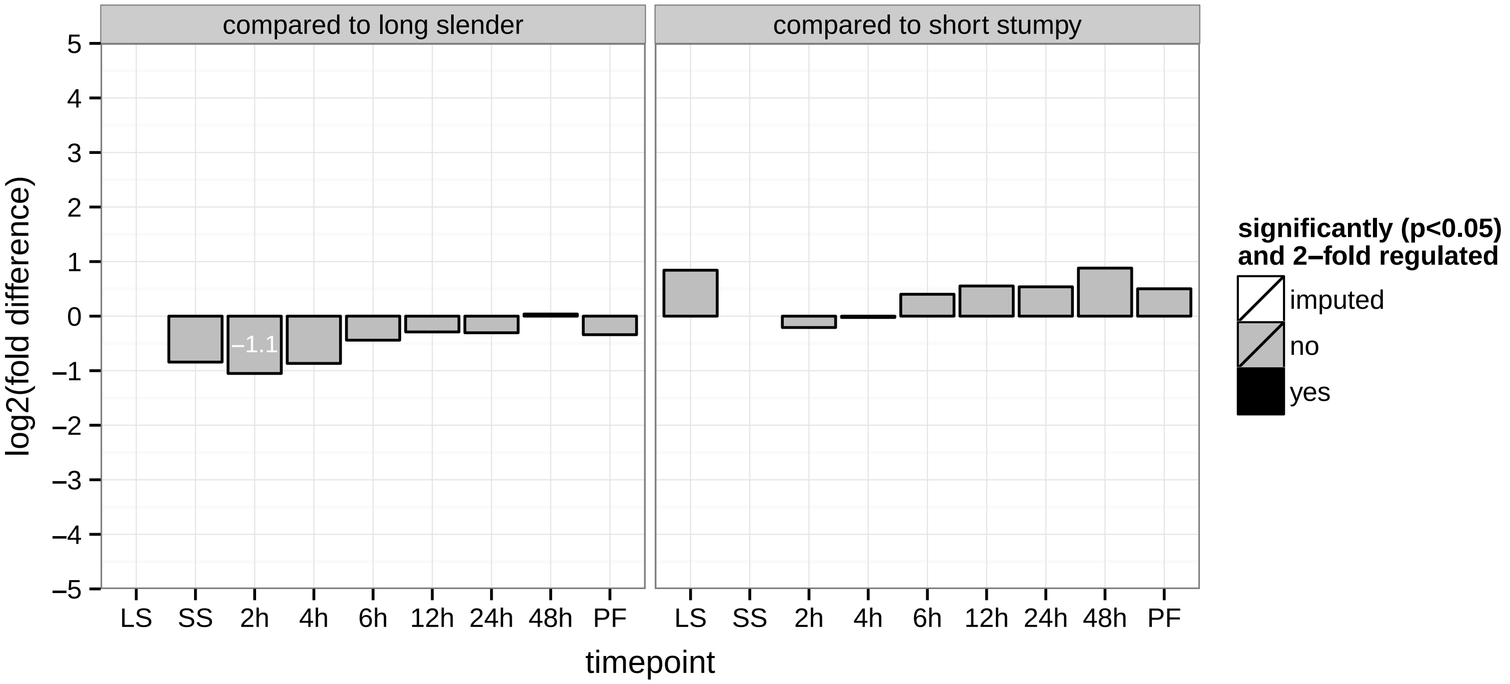
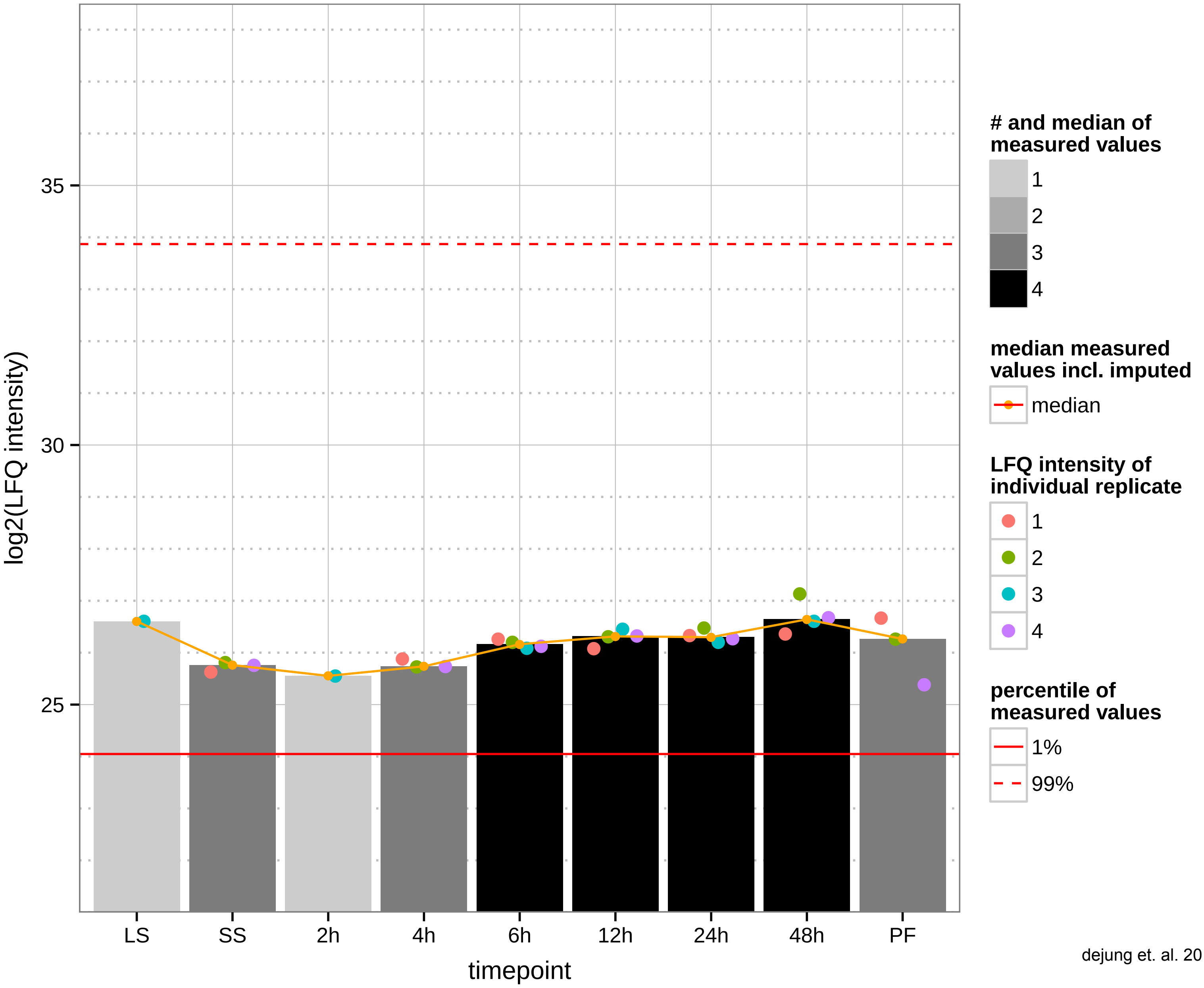
hypothetical protein, conserved
Tb927.10.8820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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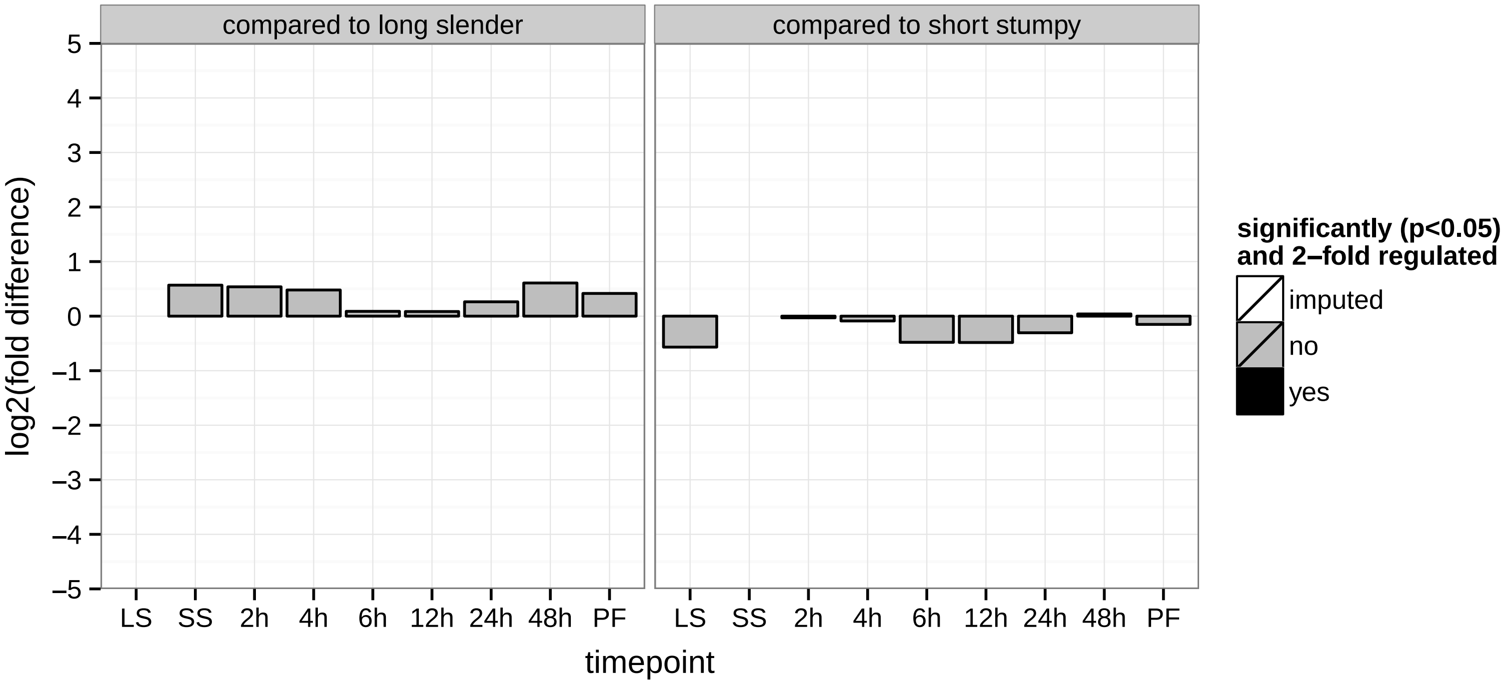
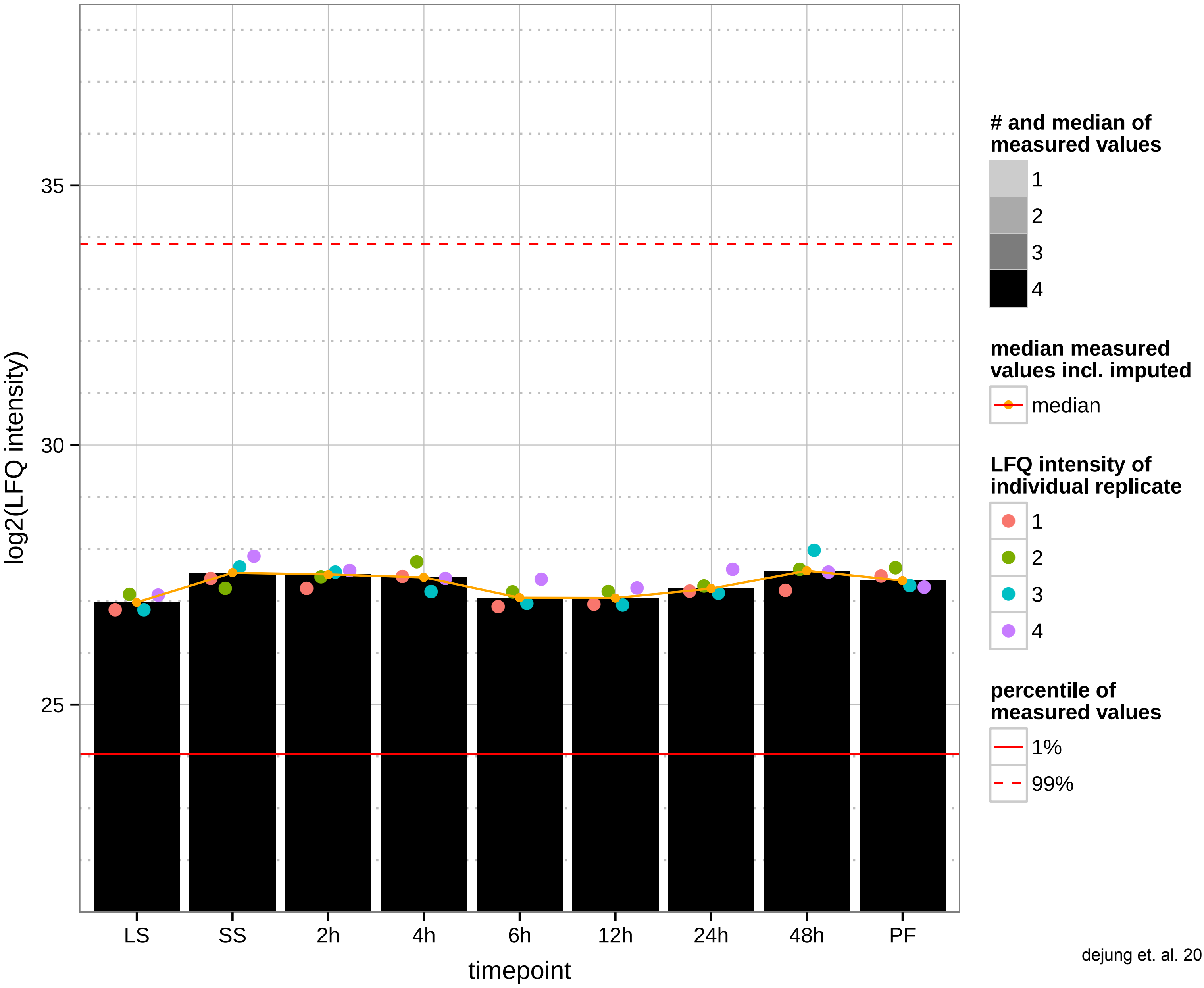
hypothetical protein, conserved
Tb927.10.8830
AGOF: heat shock protein binding
AGOC: null
AGOP: null
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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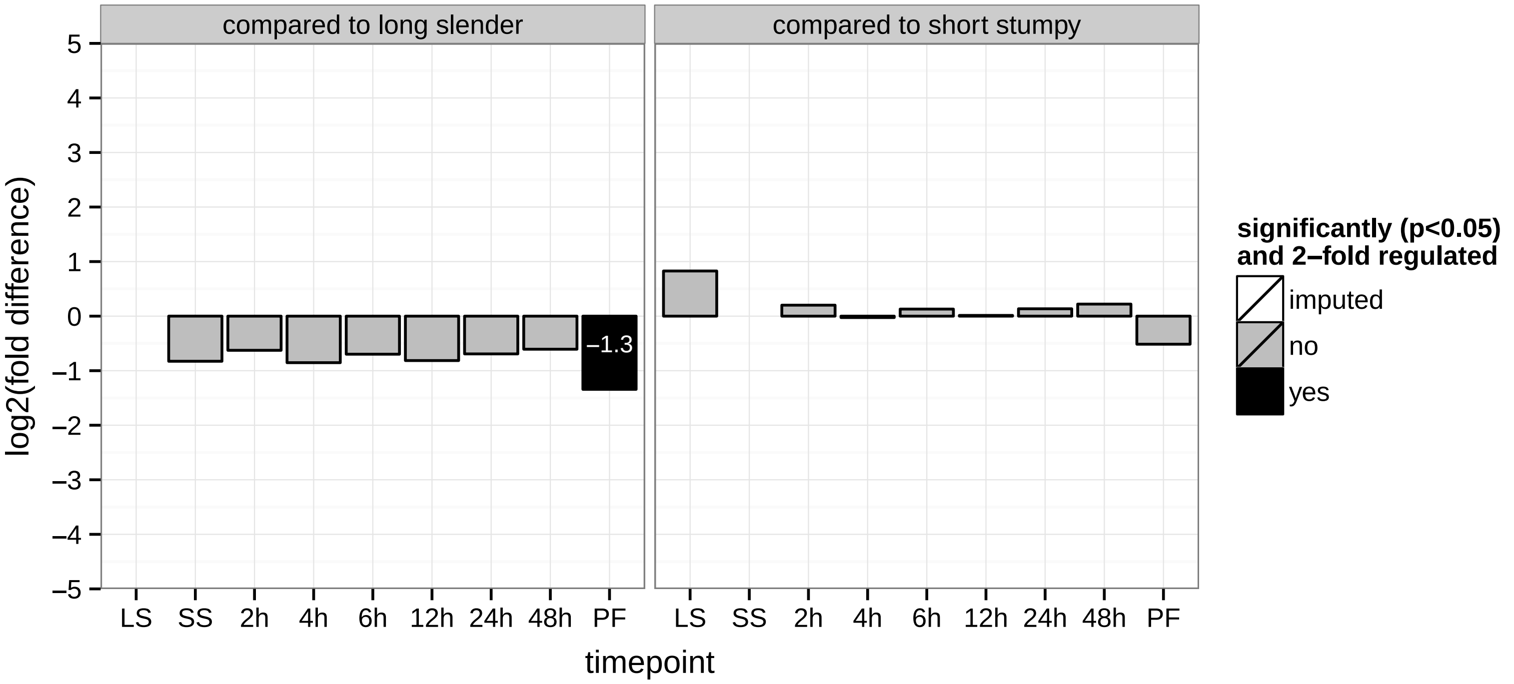
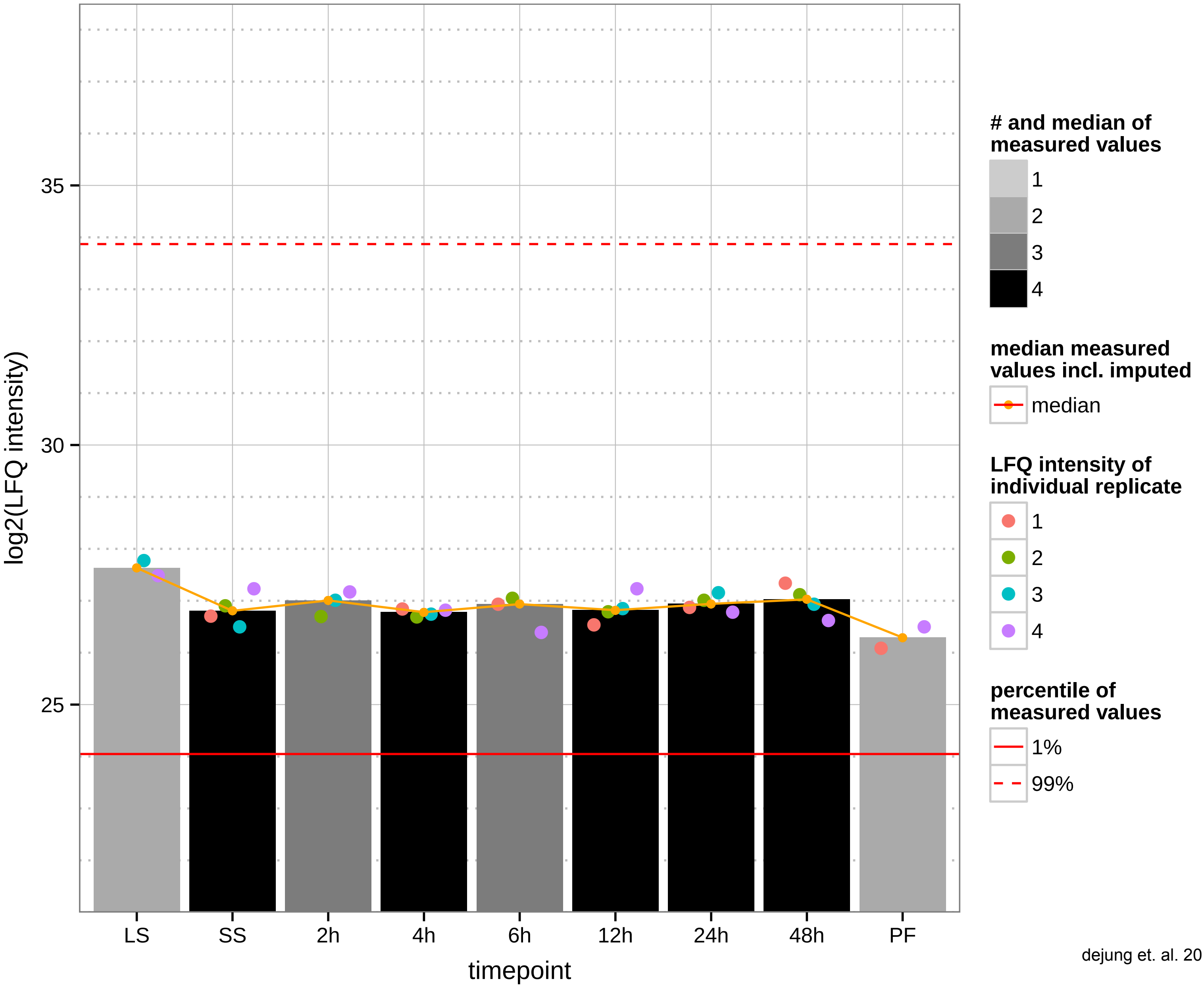
kinetoplast DNA–associated protein, putative
Tb927.10.8890
AGOF: DNA binding
AGOC: kinetoplast, mitochondrion
AGOP: DNA packaging
PGOF: protein binding
PGOC: null
PGOP: null





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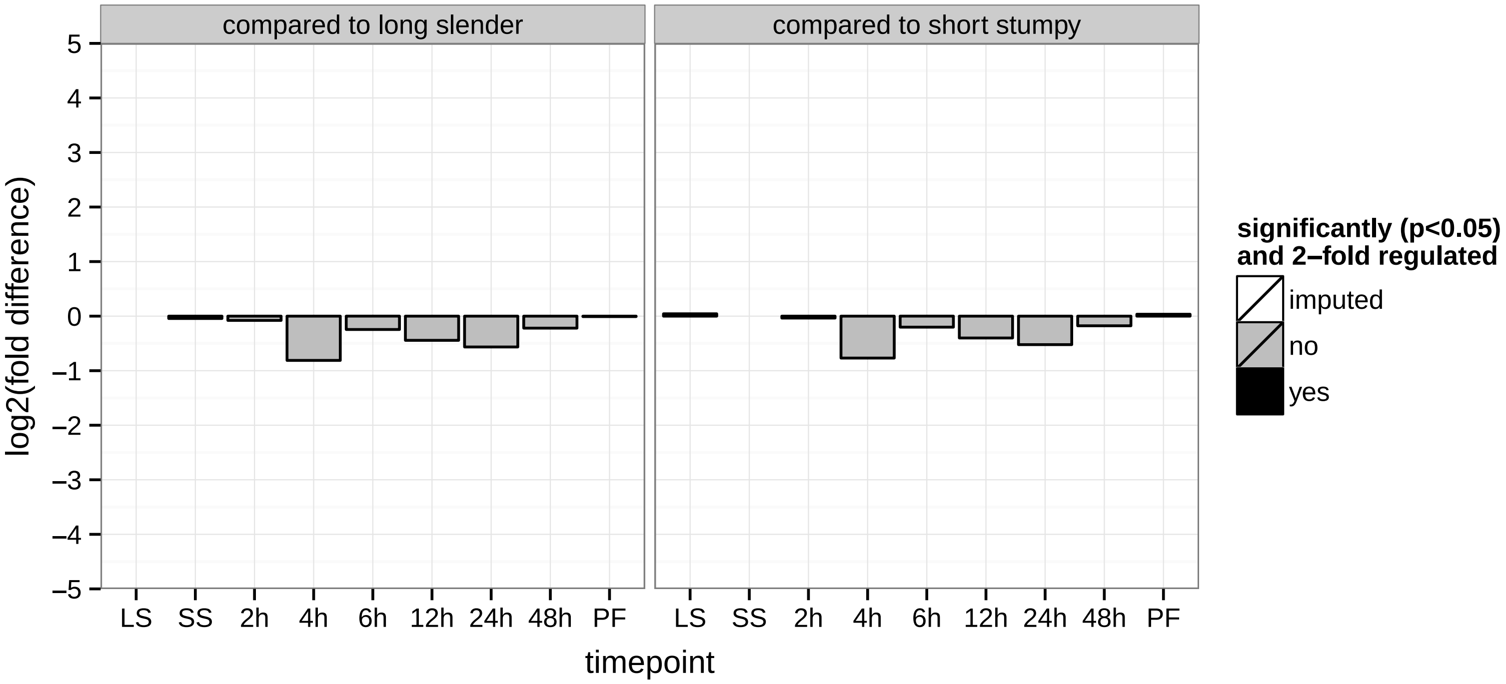
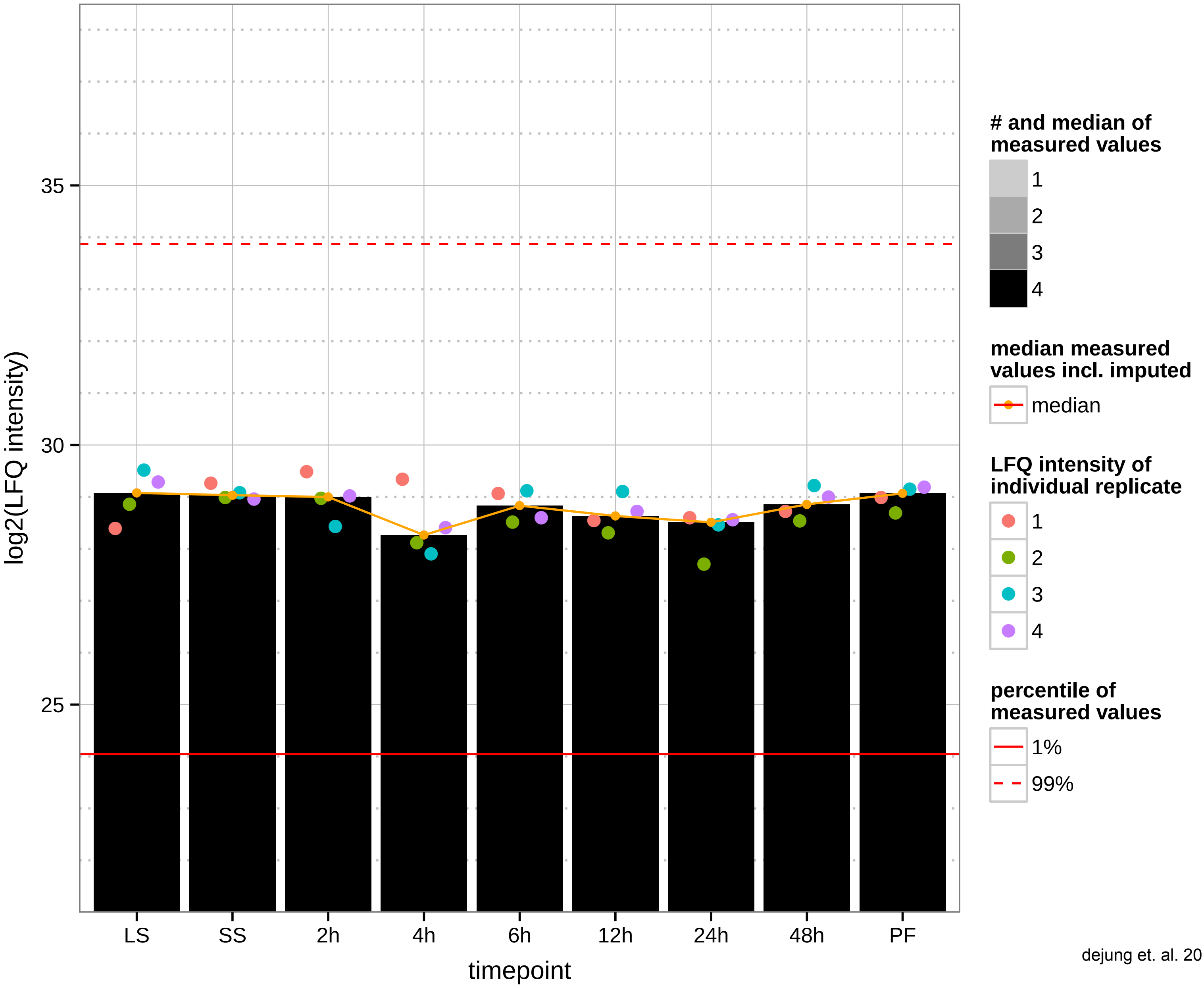
paraflagellar rod component, putative (PFC18)
Tb927.10.8930
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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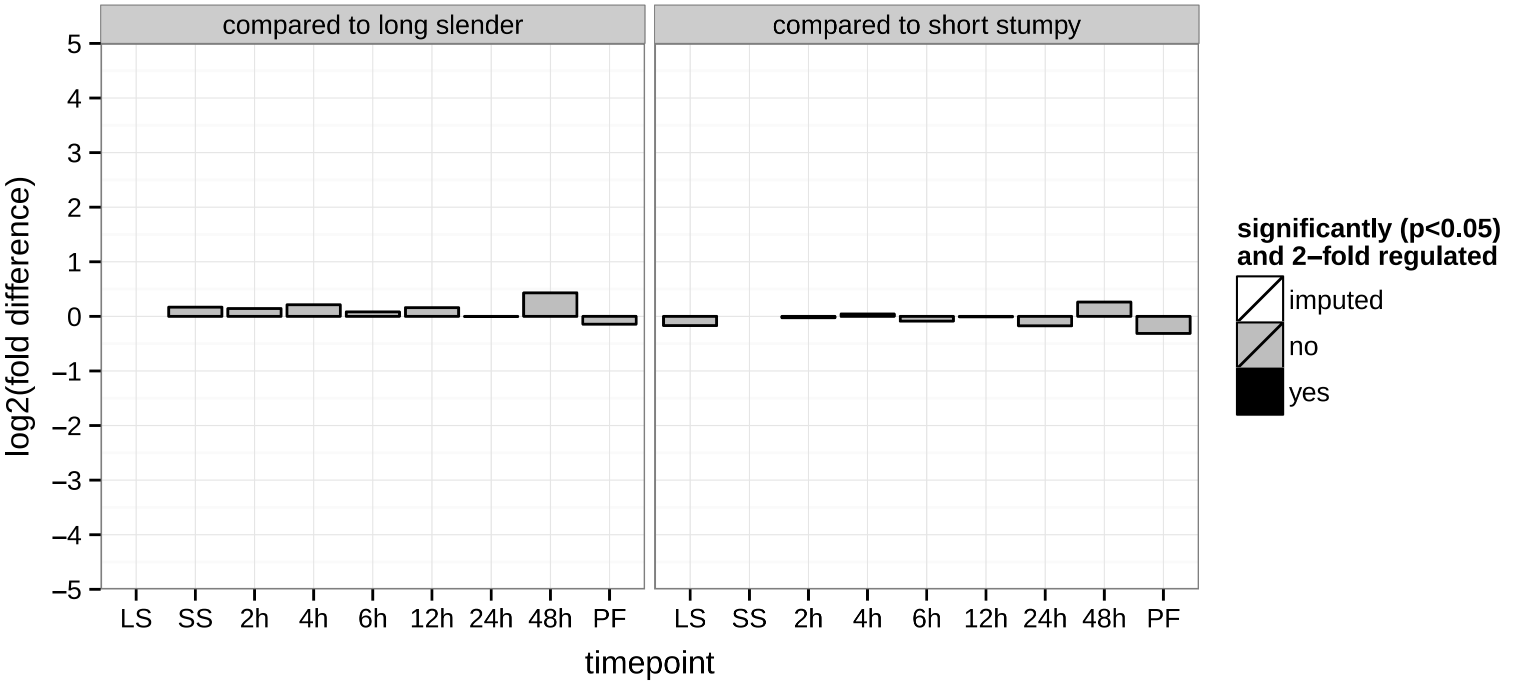
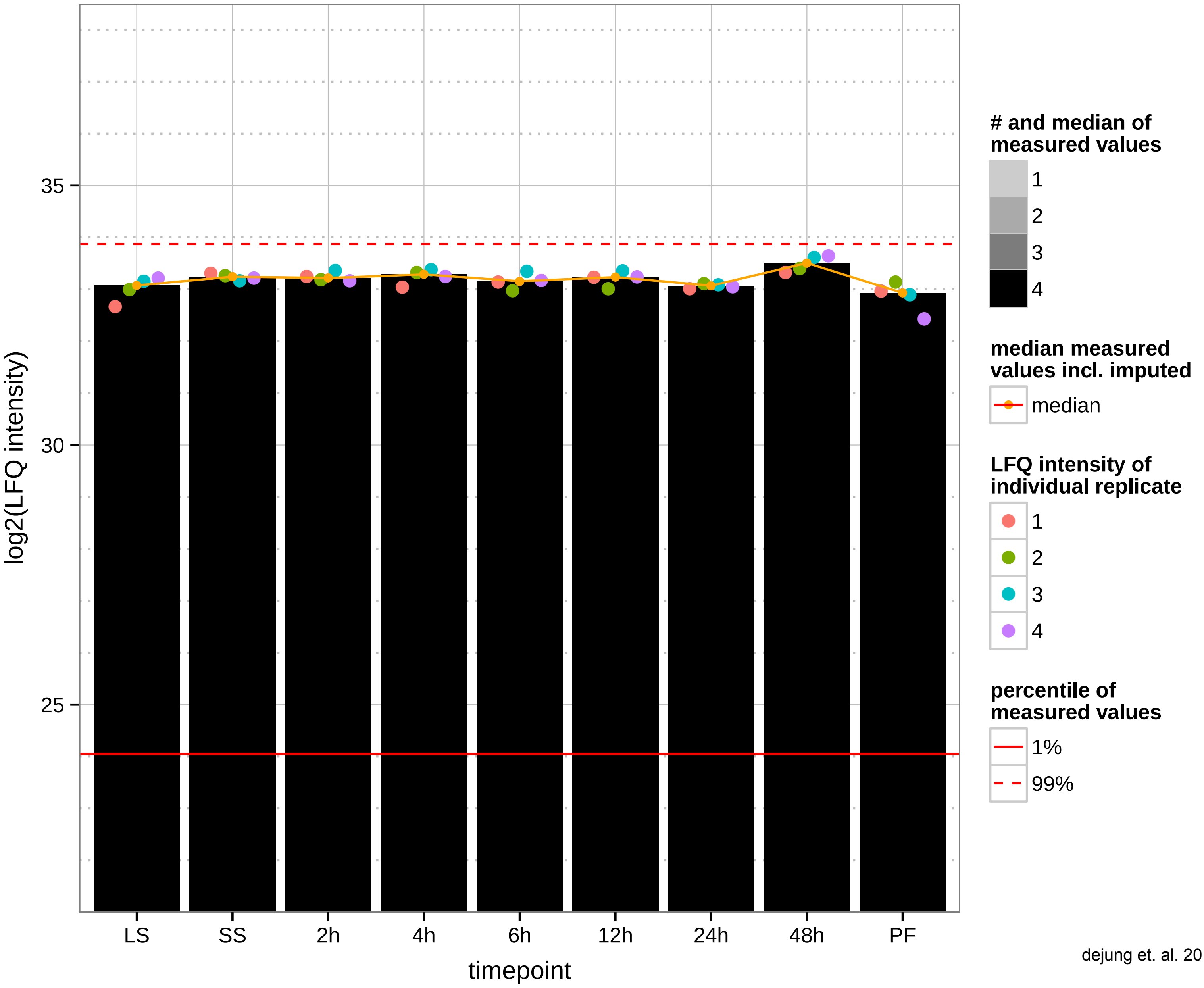
flagellum targeting protein kharon1, putative (KH1)
Tb927.10.8940
AGOF: null
AGOC: flagellar pocket
AGOP: pathogenesis, protein targeting
PGOF: null
PGOC: null
PGOP: null





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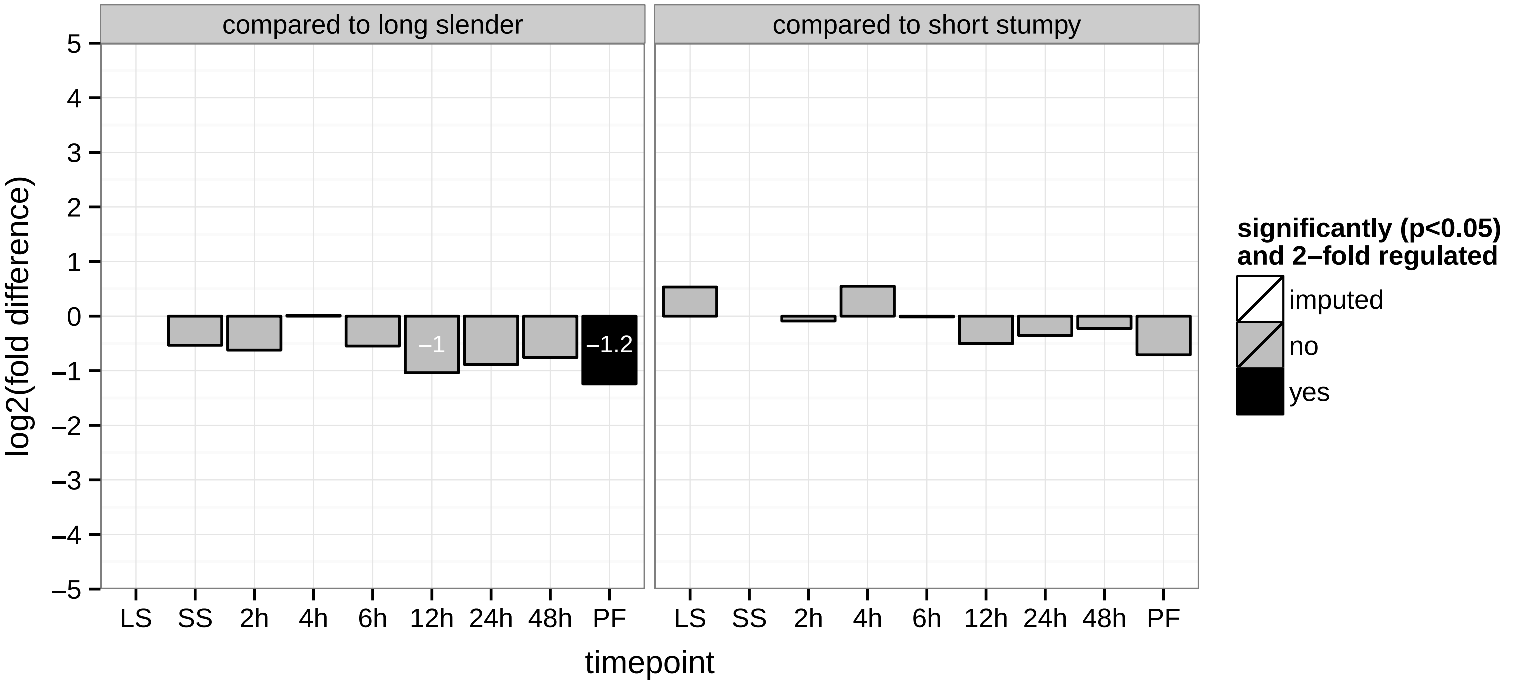
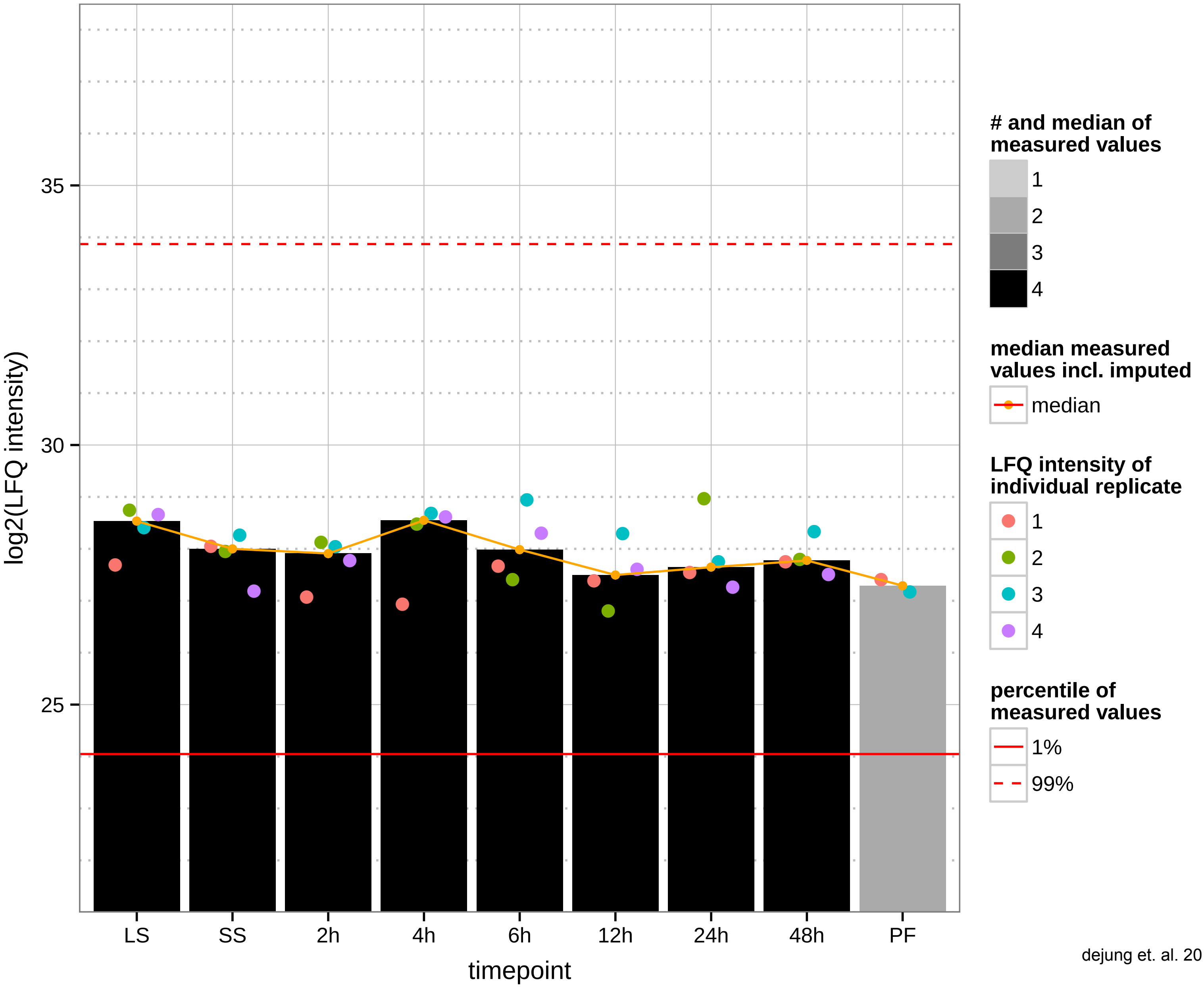
kinetoplast DNA–associated protein, putative
Tb927.10.8950;Tb927.10.8970
AGOF: DNA binding
AGOC: kinetoplast, mitochondrion
AGOP: DNA packaging
PGOF: null
PGOC: null
PGOP: null





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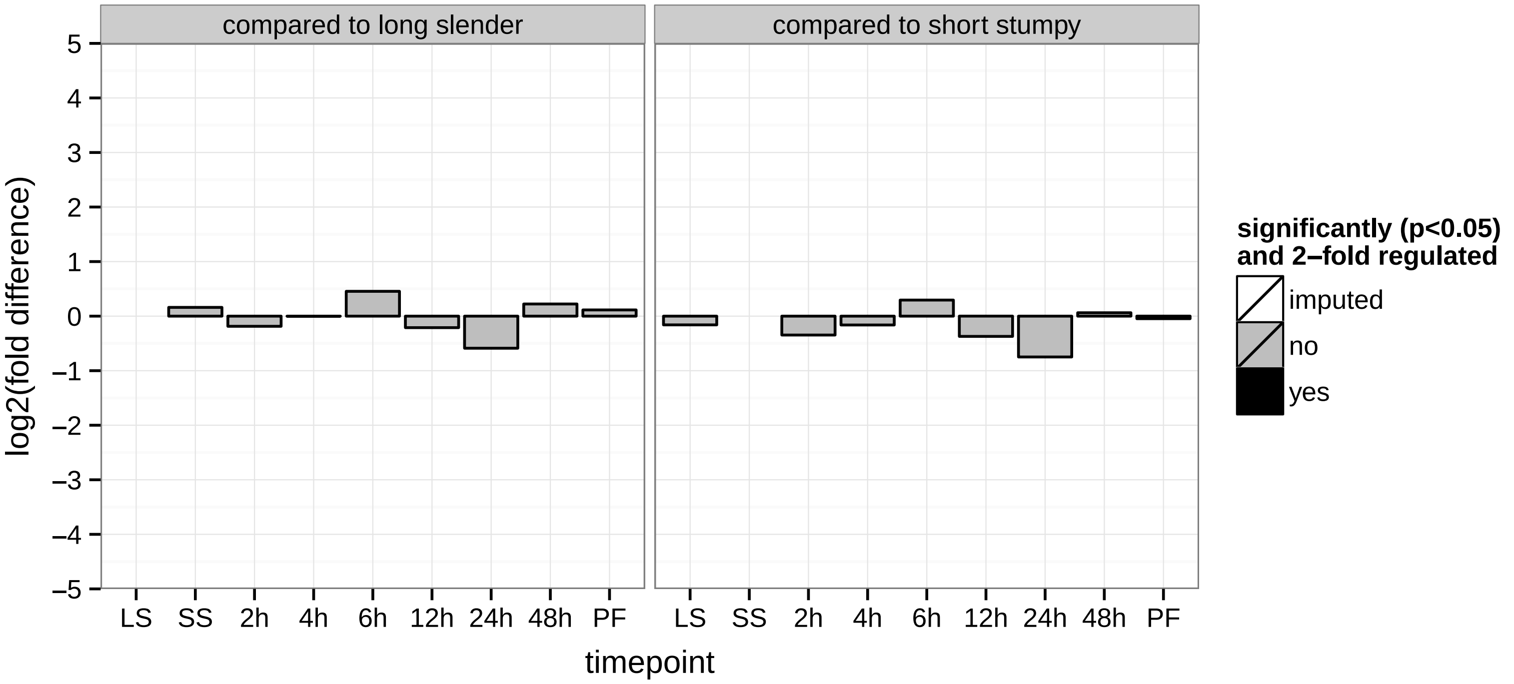
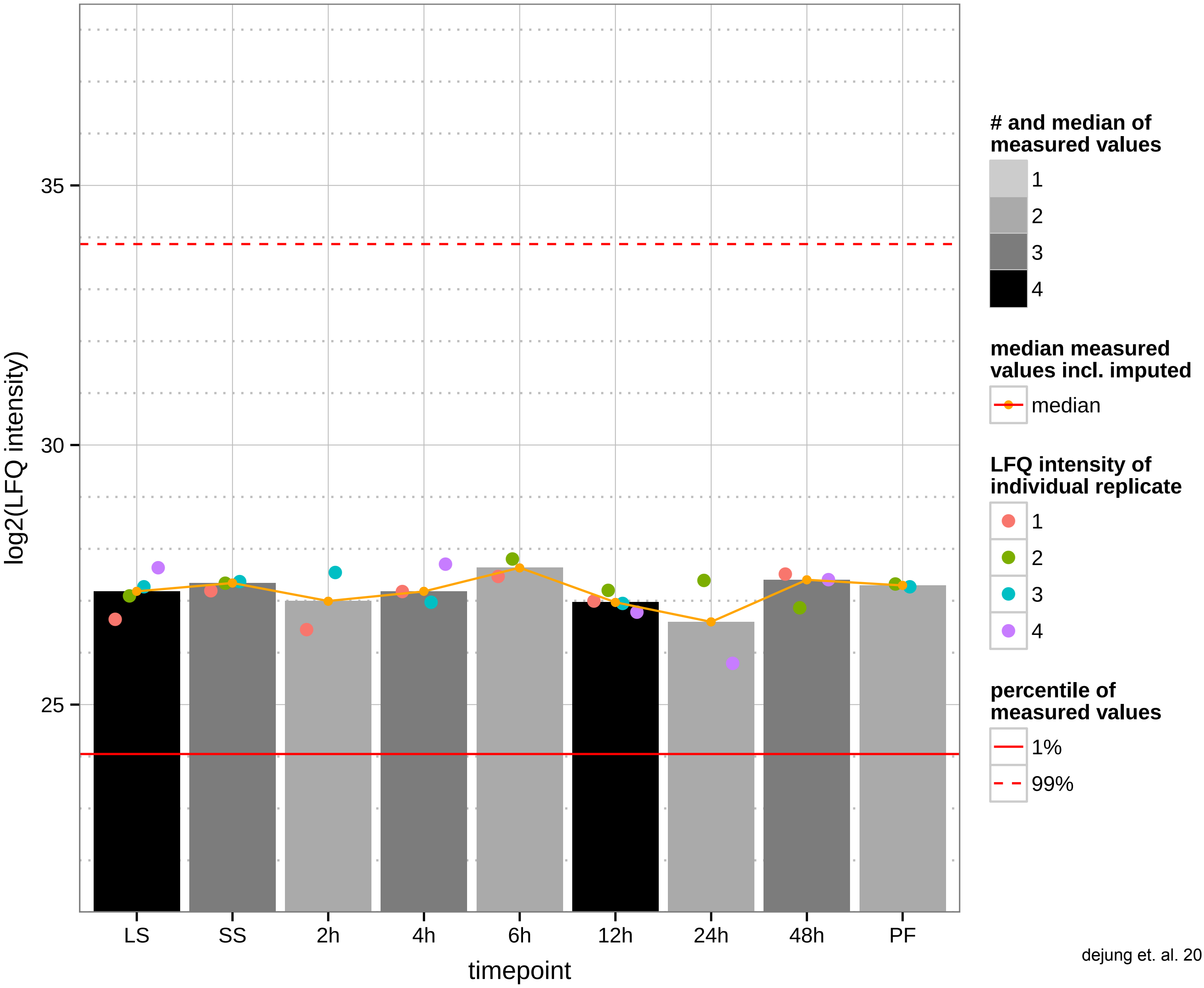
hypothetical protein, conserved
Tb927.10.8960
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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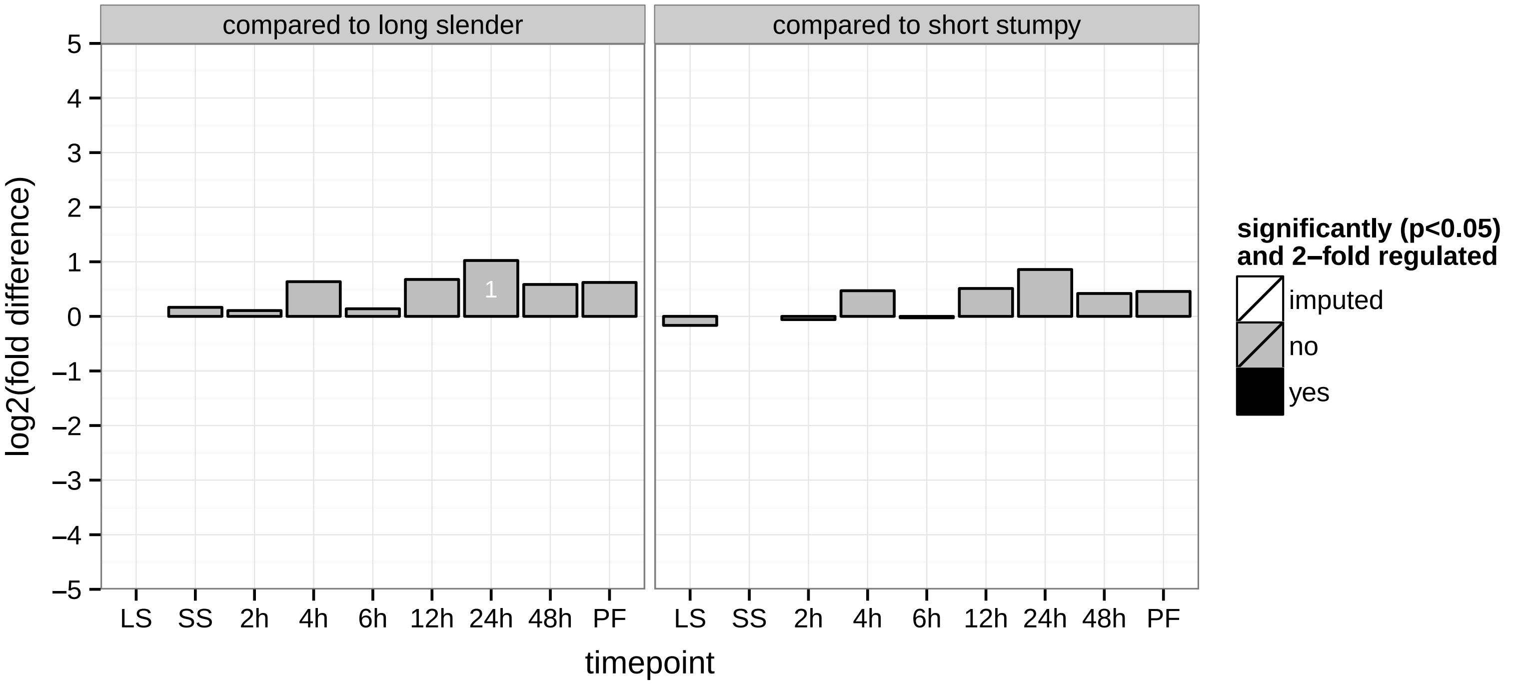
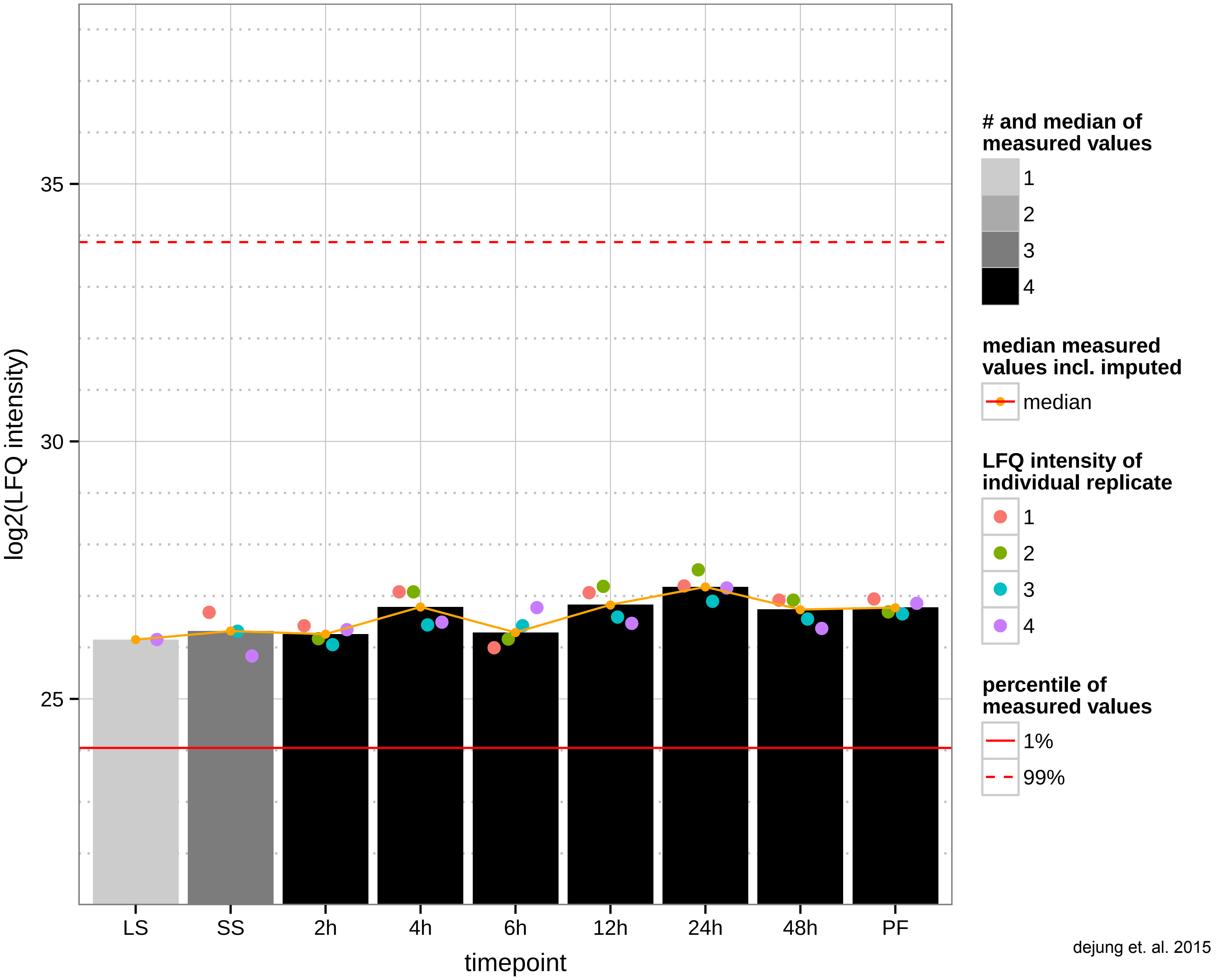
hypothetical protein, conserved
Tb927.10.9020
AGOF: null, translation initiation factor activity
AGOC: null
AGOP: null, regulation of translational initiation, translational initiation
PGOF: null, translation initiation factor activity
PGOC: null
PGOP: null, regulation of translational initiation, translational initiation





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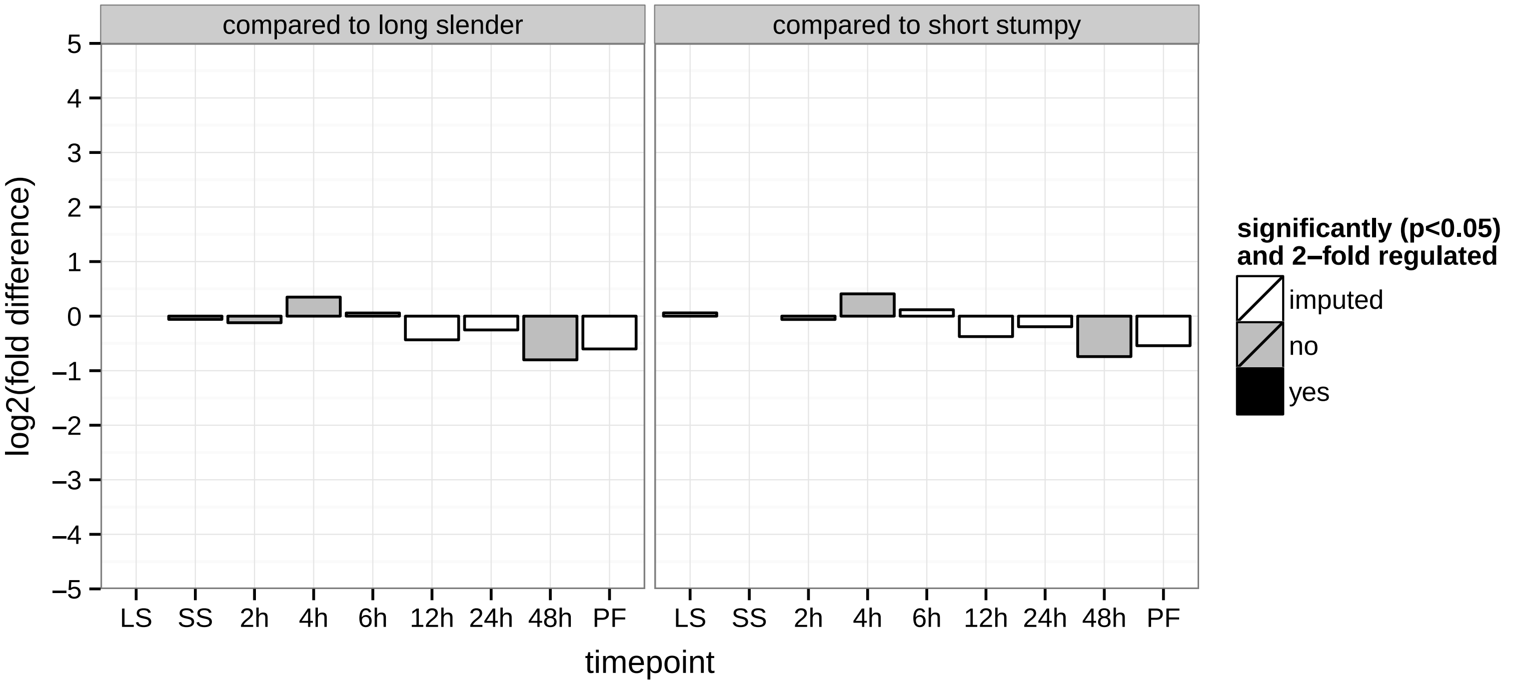
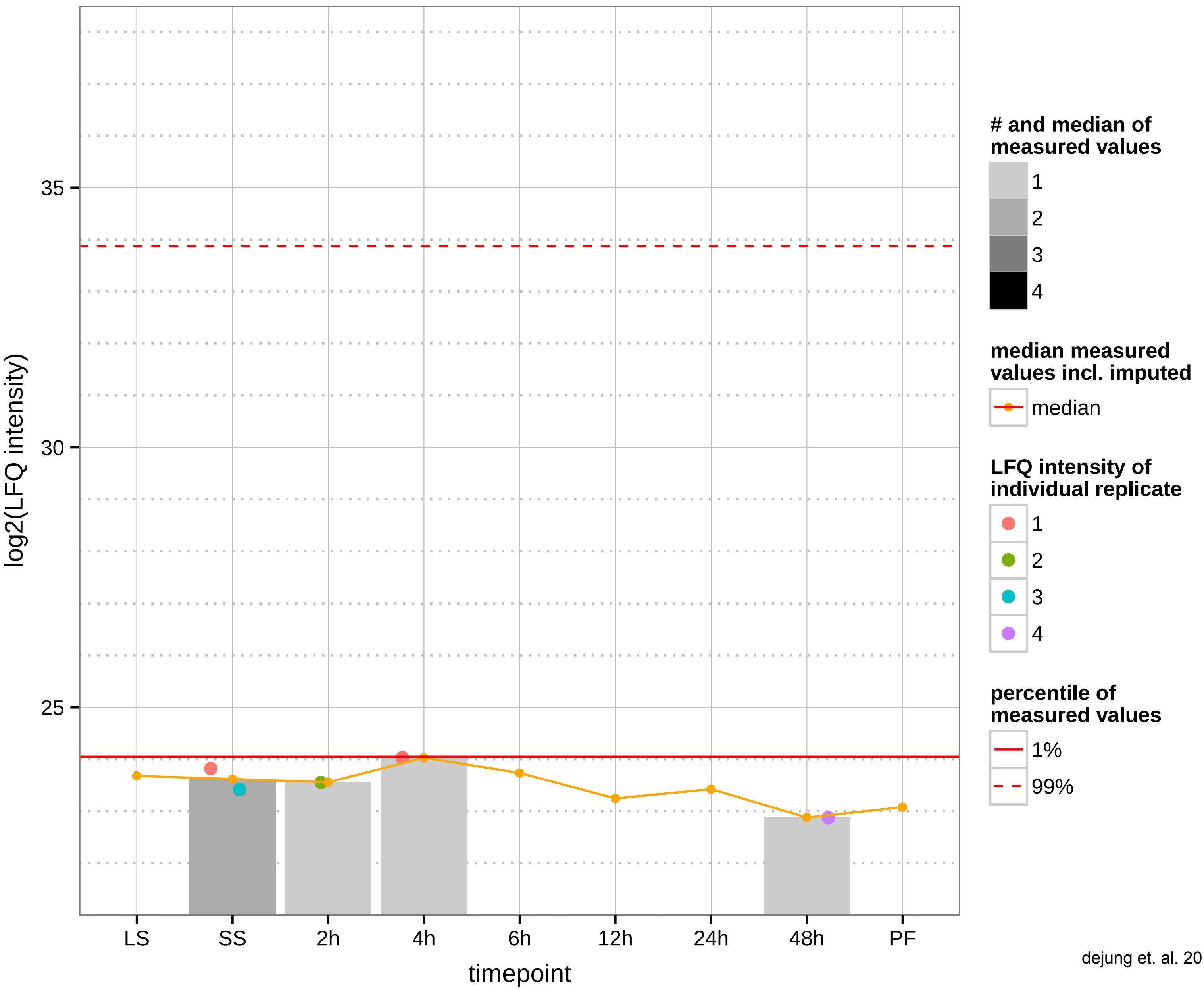
hypothetical protein, conserved
Tb927.10.9040
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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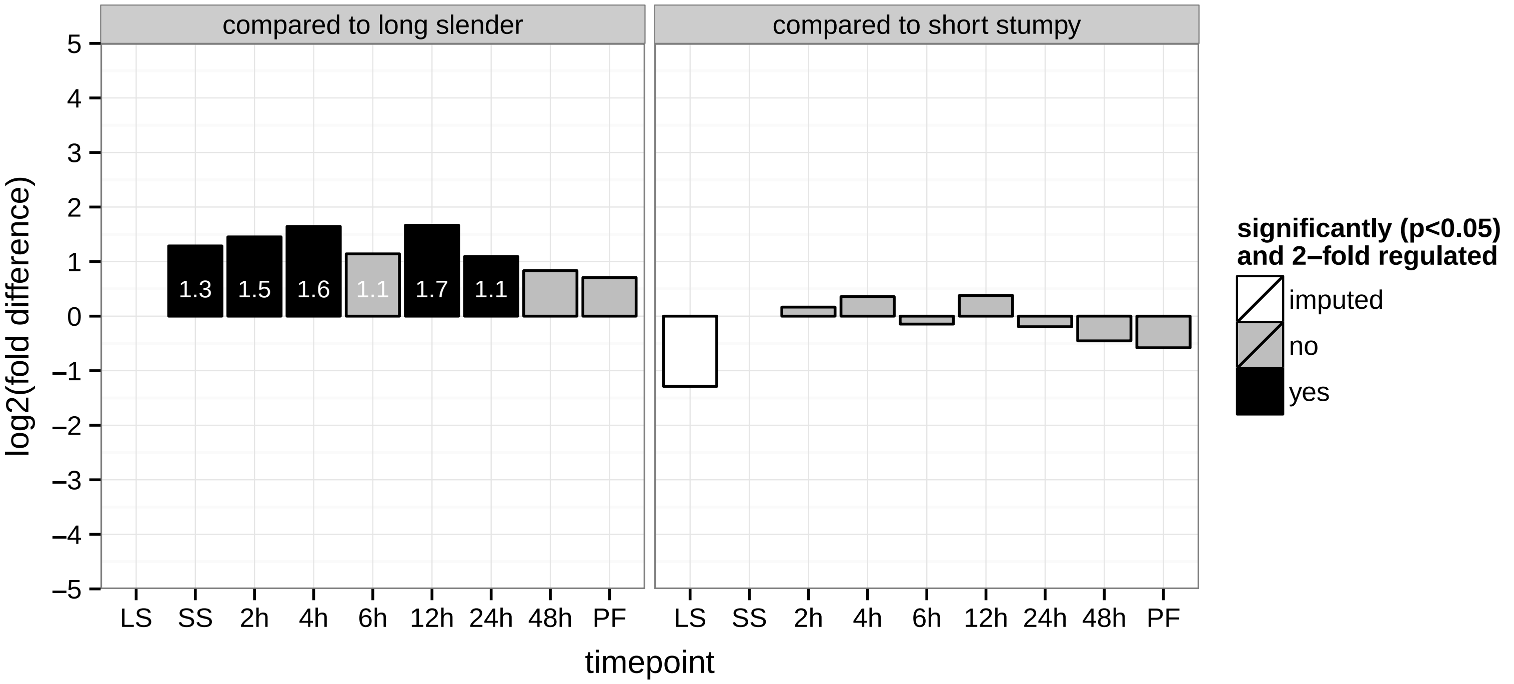
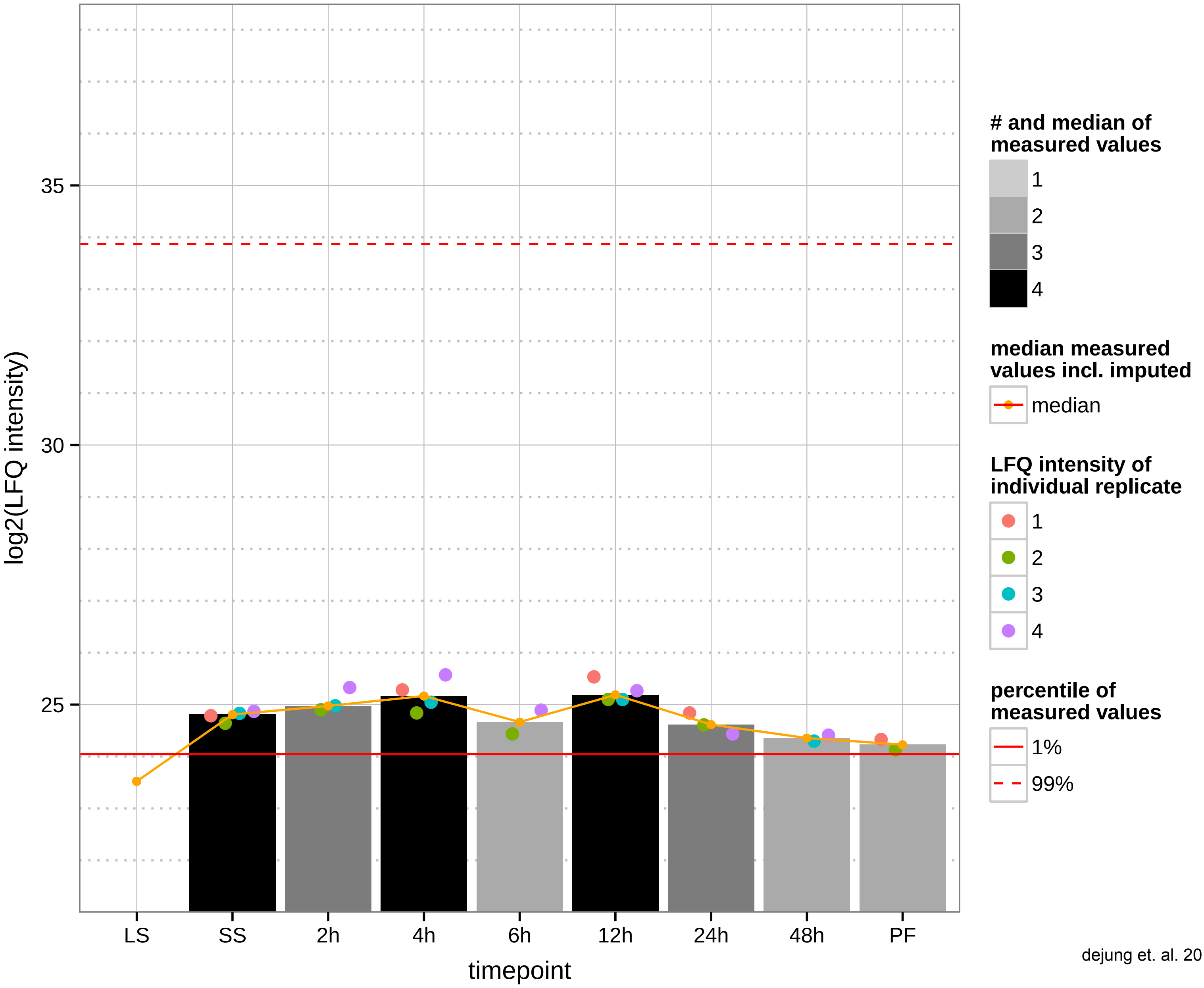
hypothetical protein, conserved
Tb927.10.9090
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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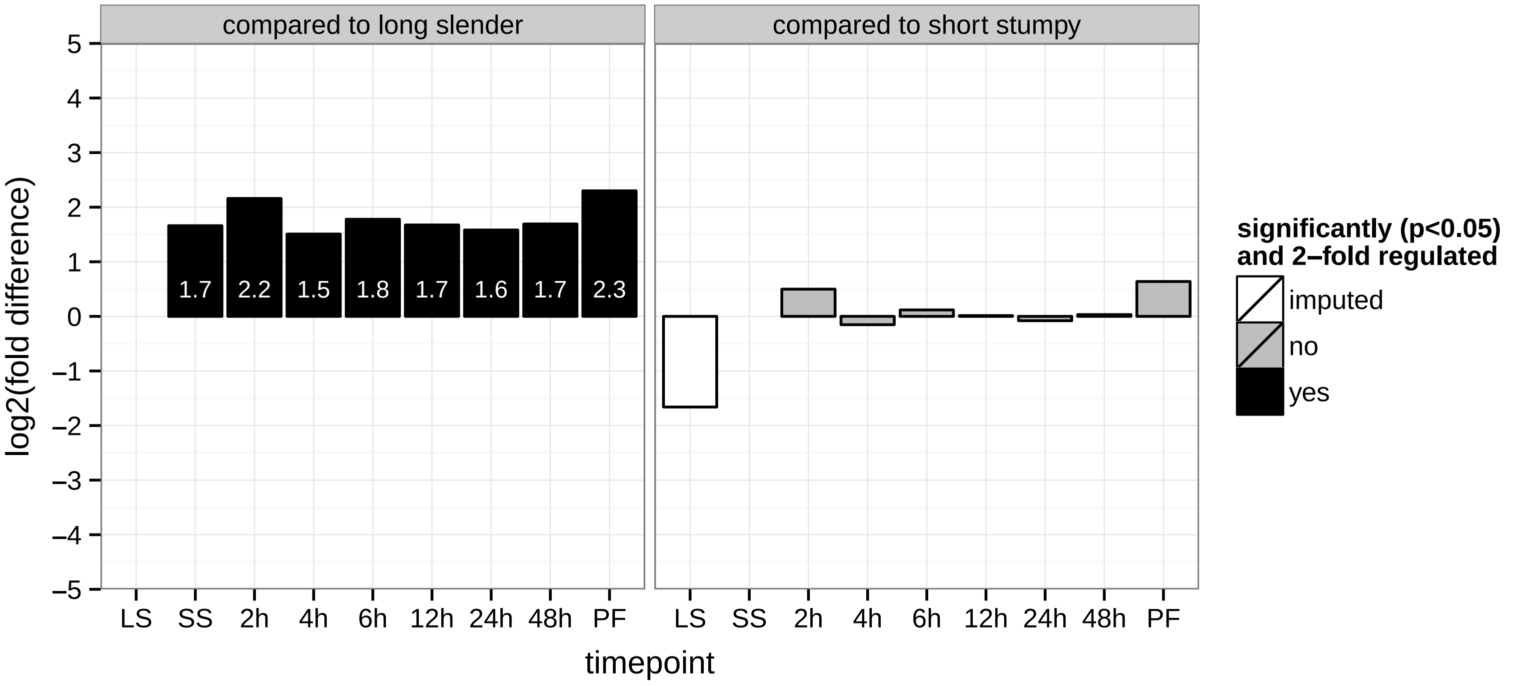
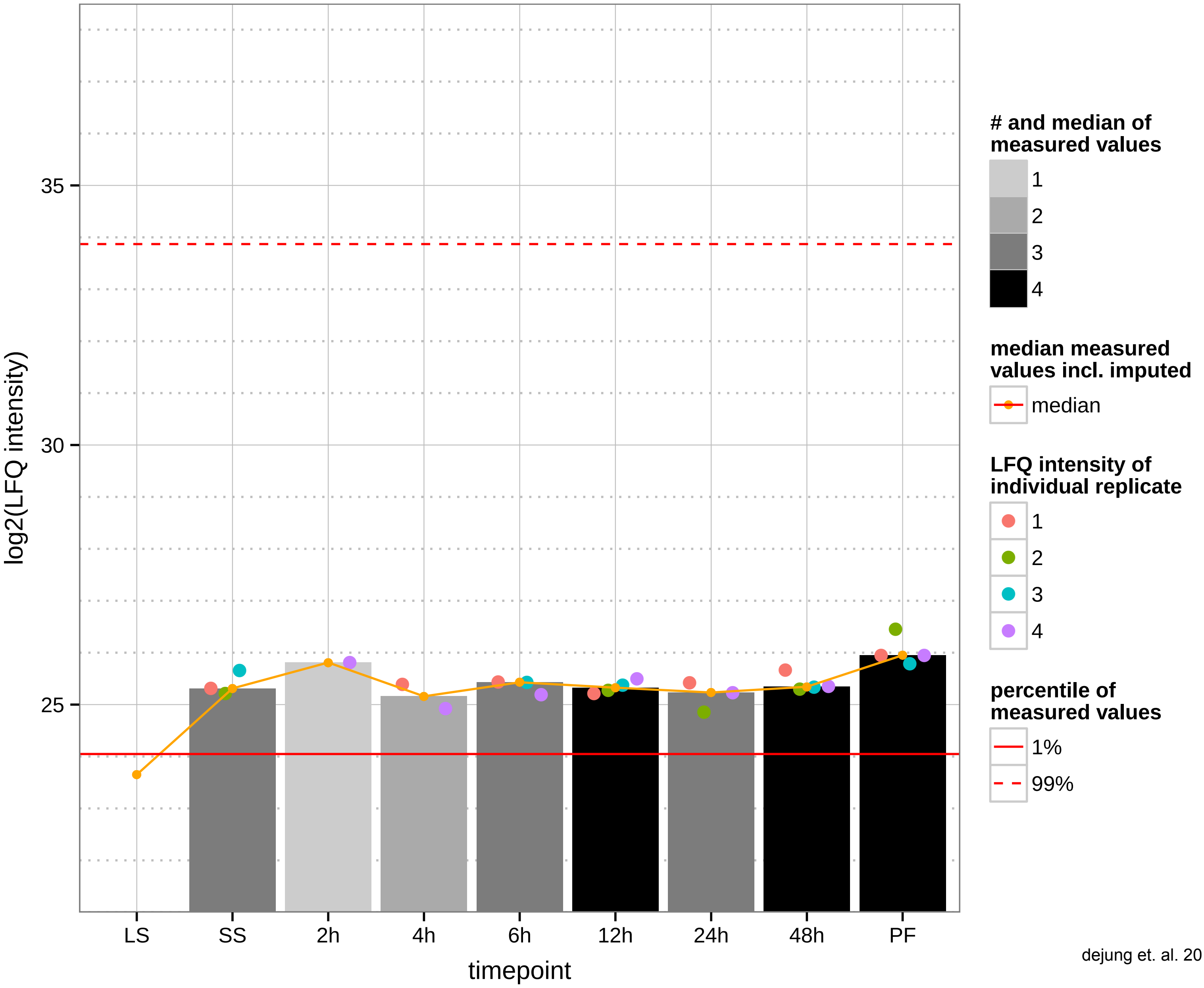
pre−mRNA splicing factor ATP−dependent RNA helicase, putative
Tb927.10.9130
AGOF: ATP binding, ATP−dependent RNA helicase activity, nucleic acid binding
AGOC: spliceosomal complex
AGOP: RNA splicing, RNA splicing, via transesterification reactions
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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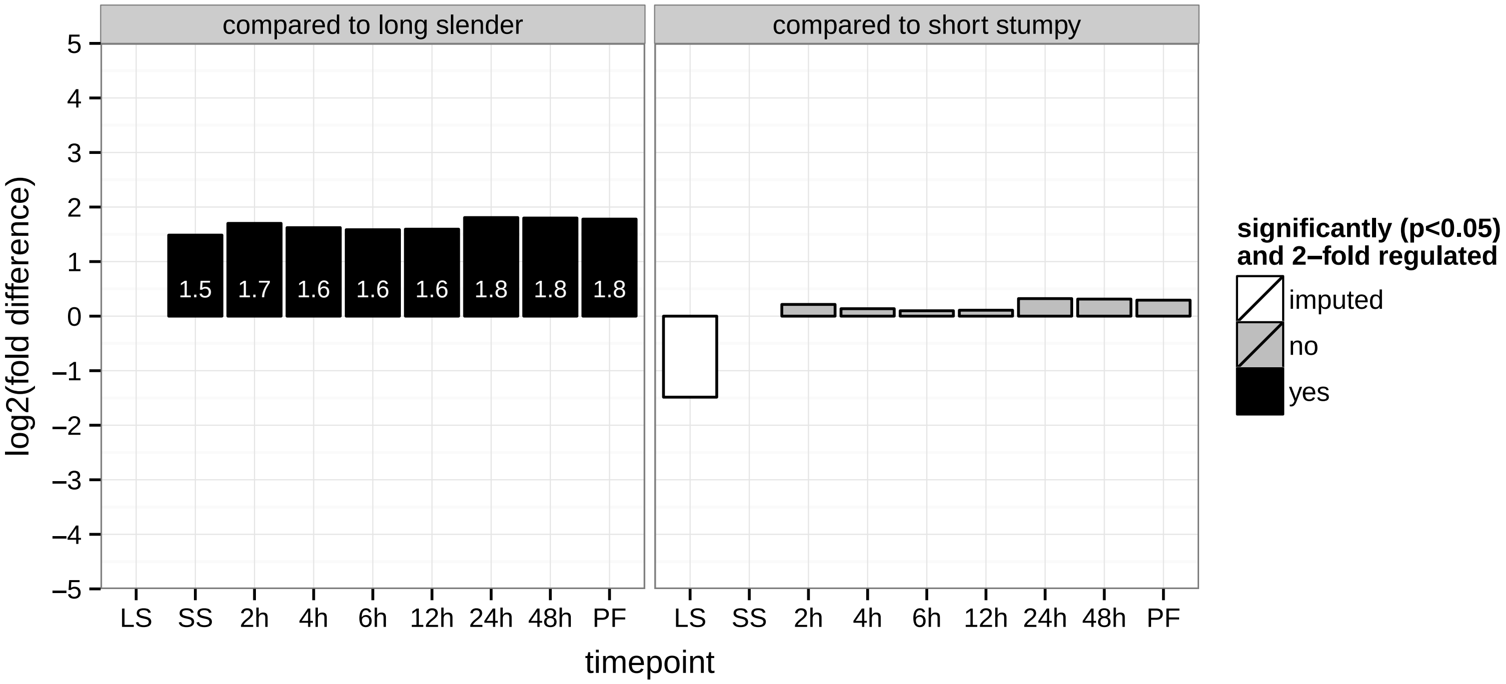
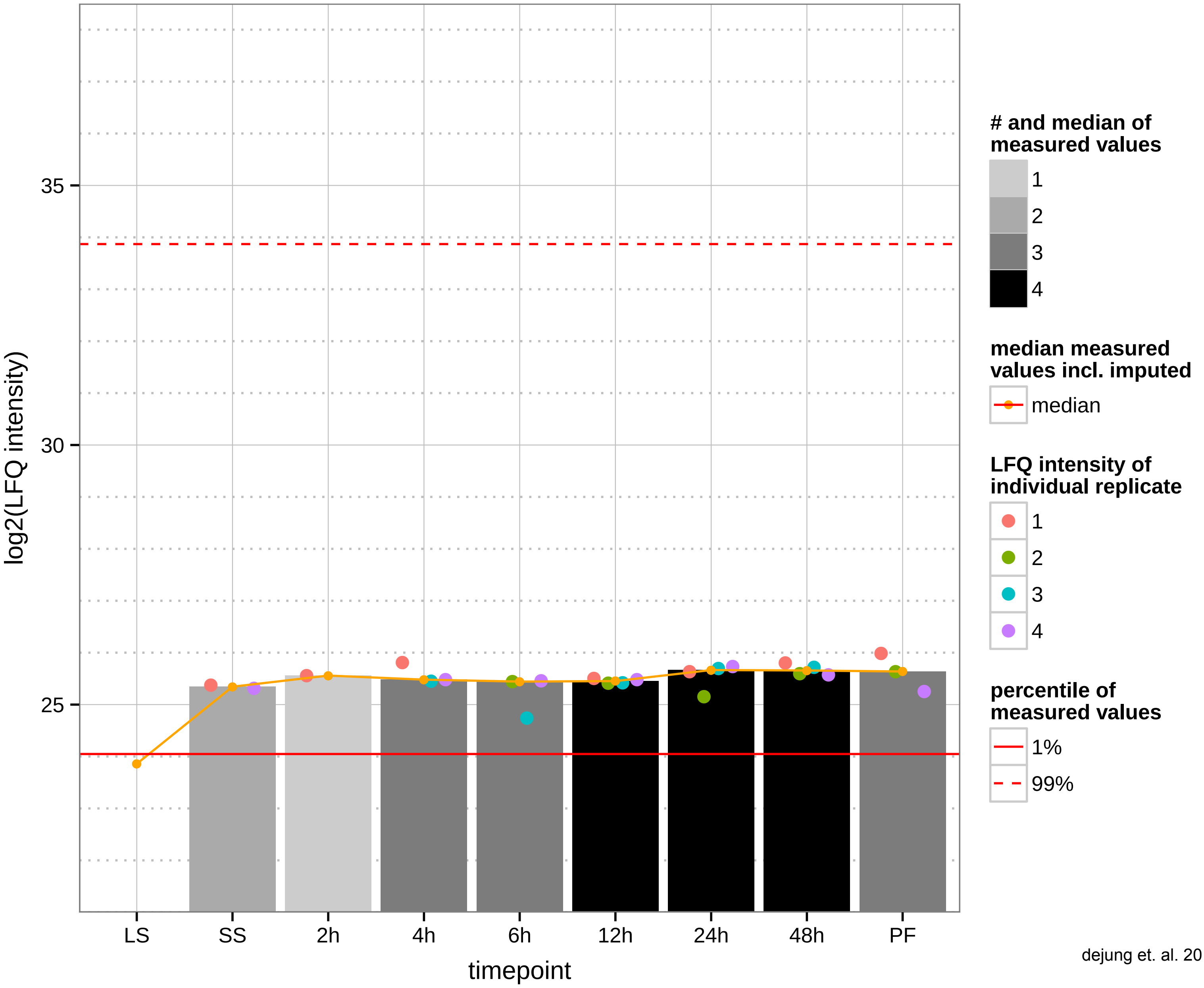
hypothetical protein, conserved
Tb927.10.9140
AGOF: oxidoreductase activity
AGOC: mitochondrion
AGOP: null
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation−reduction process





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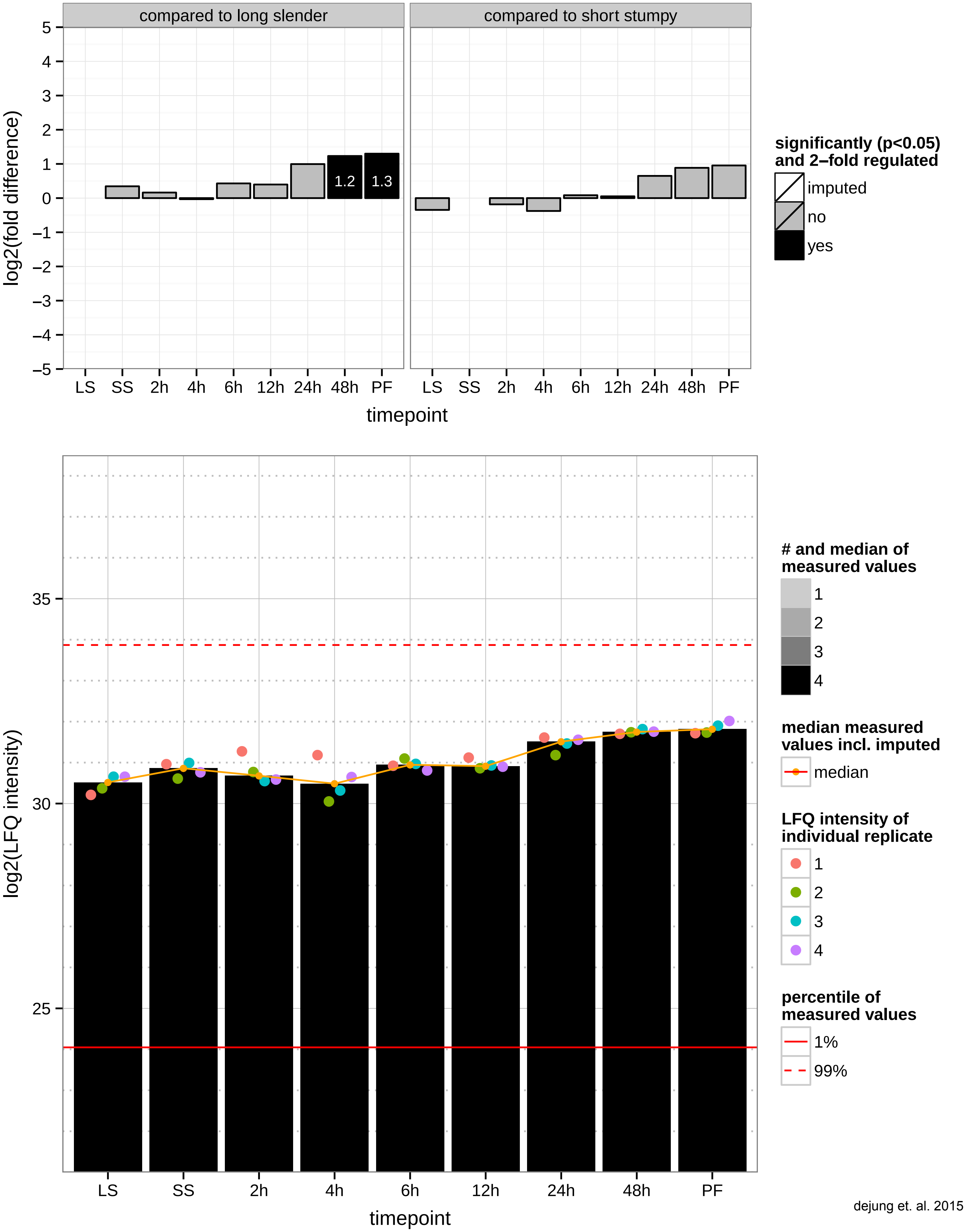
isoleucyl–tRNA synthetase, putative (IleRS)
Tb927.10.9190
AGOF: ATP binding, isoleucine–tRNA ligase activity, zinc ion binding
AGOC: cytoplasm, mitochondrion
AGOP: isoleucyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA editing activity, aminoacyl–tRNA ligase activity, isoleucine–tRNA ligase activity, nucleoti
PGOC: cytoplasm
PGOP: isoleucyl–tRNA aminoacylation, tRNA aminoacylation for protein translation



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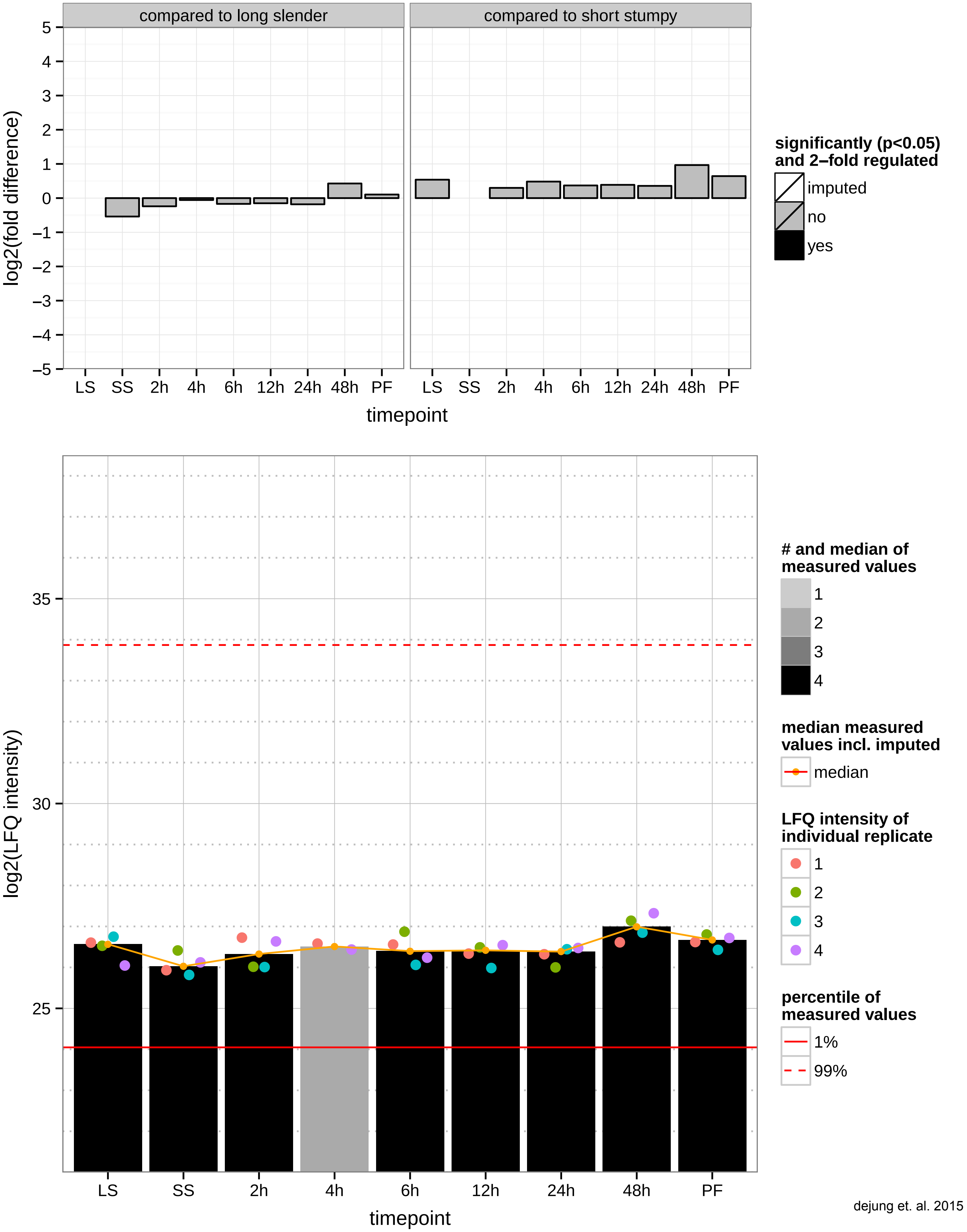
hypothetical protein, conserved
Tb927.10.9240
AGOF: null
AGOC: cytoplasm
AGOP: pathogenesis, regulation of protein secretion
PGOF: null
PGOC: cytoplasm
PGOP: pathogenesis, regulation of protein secretion



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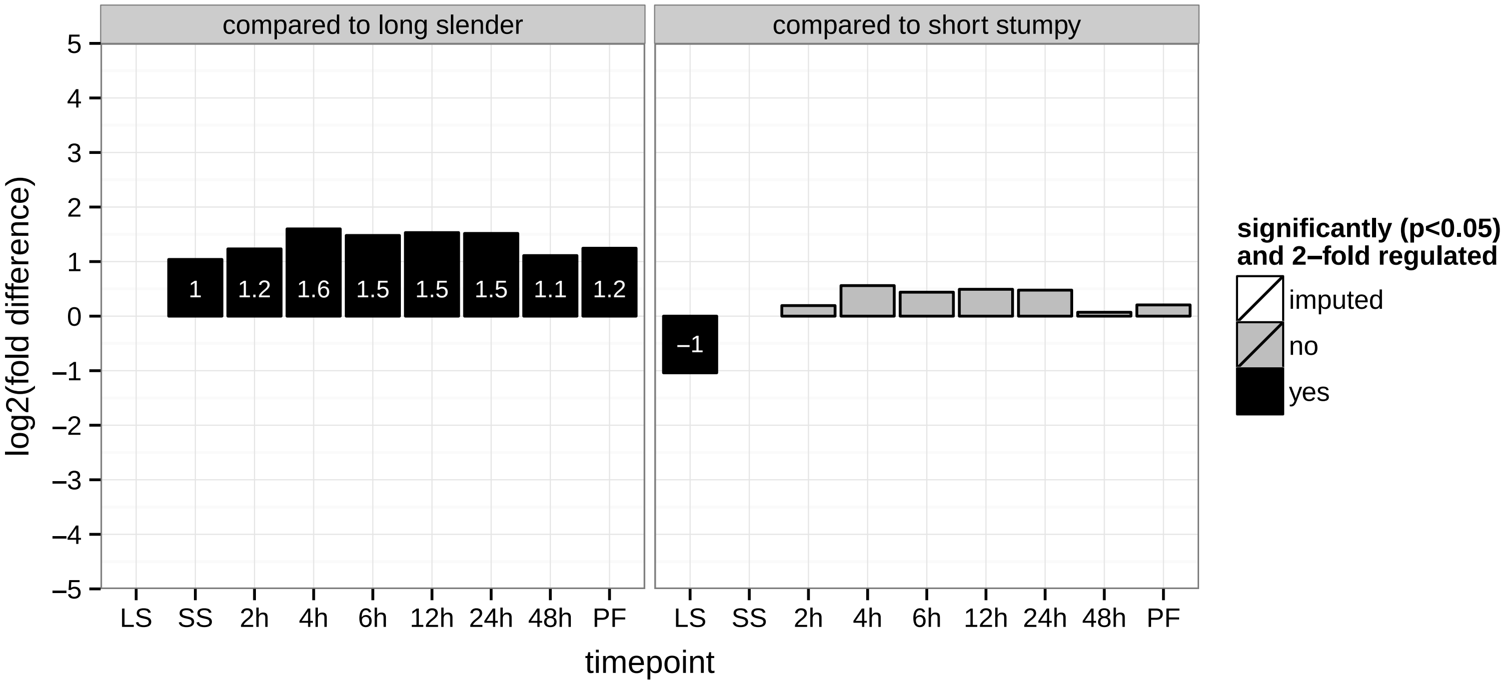
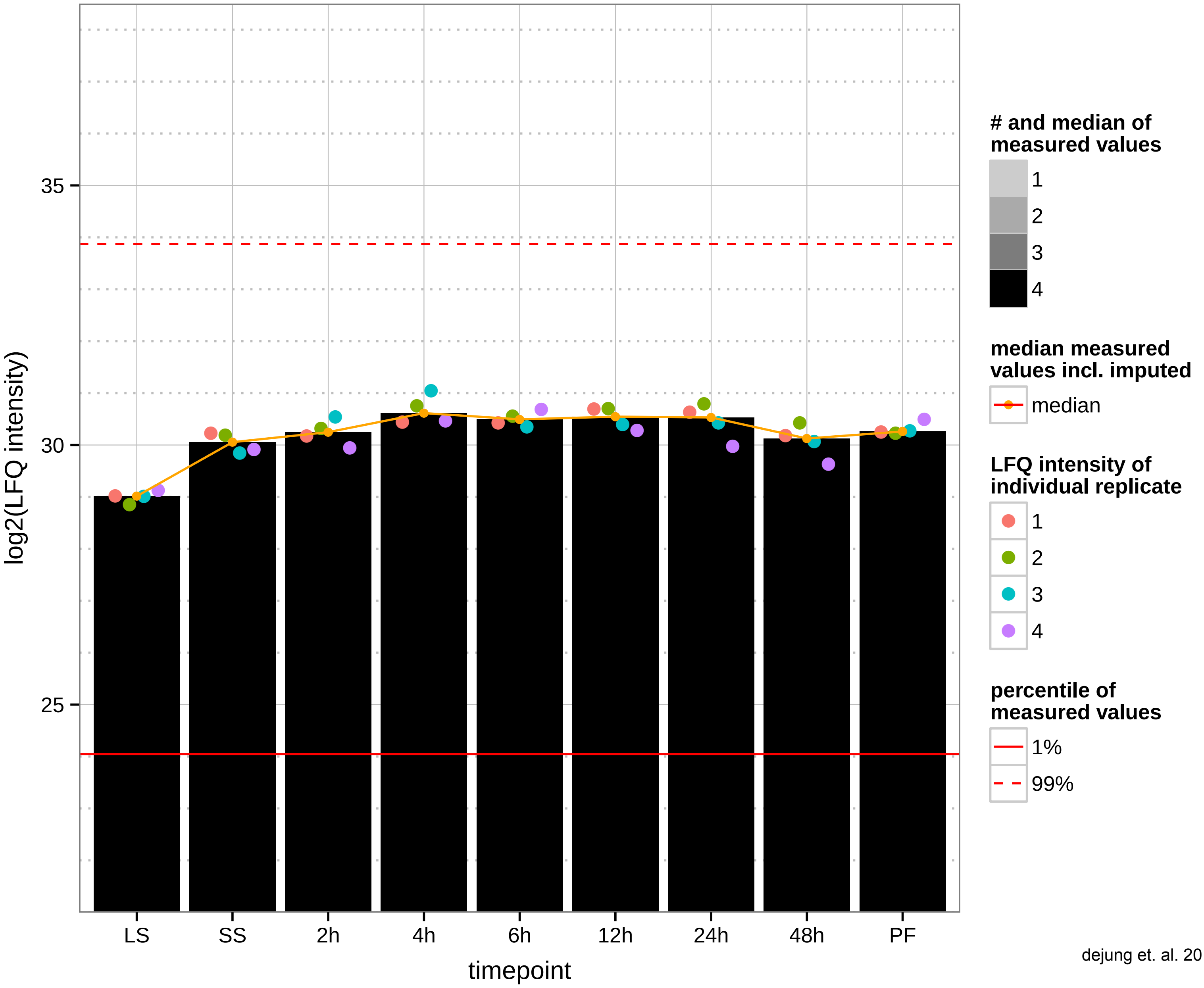
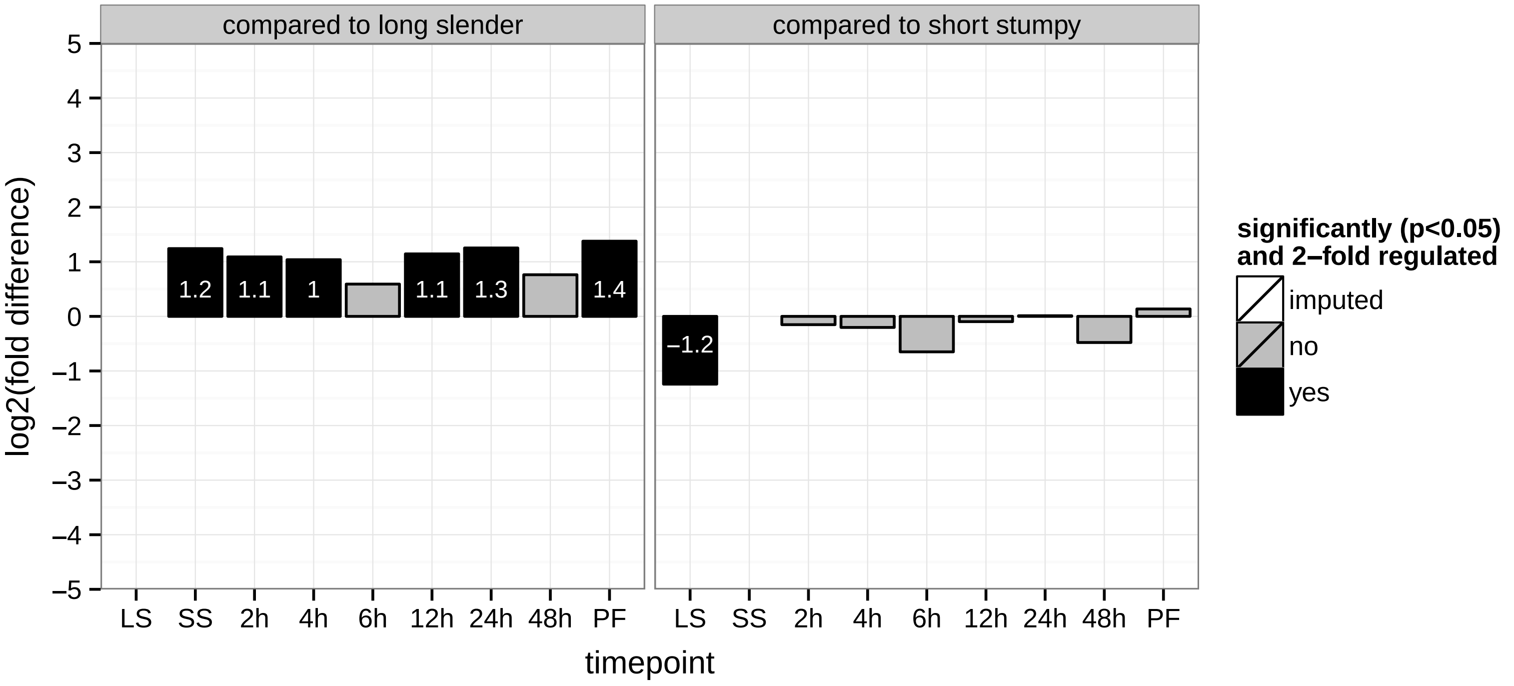
G–actin binding protein, putative, CAP/Srv2p
Tb927.10.9250
AGOF: actin binding
AGOC: null
AGOP: activation of adenylate cyclase activity, cytoskeleton organization
PGOF: actin binding
PGOC: null
PGOP: cytoskeleton organization

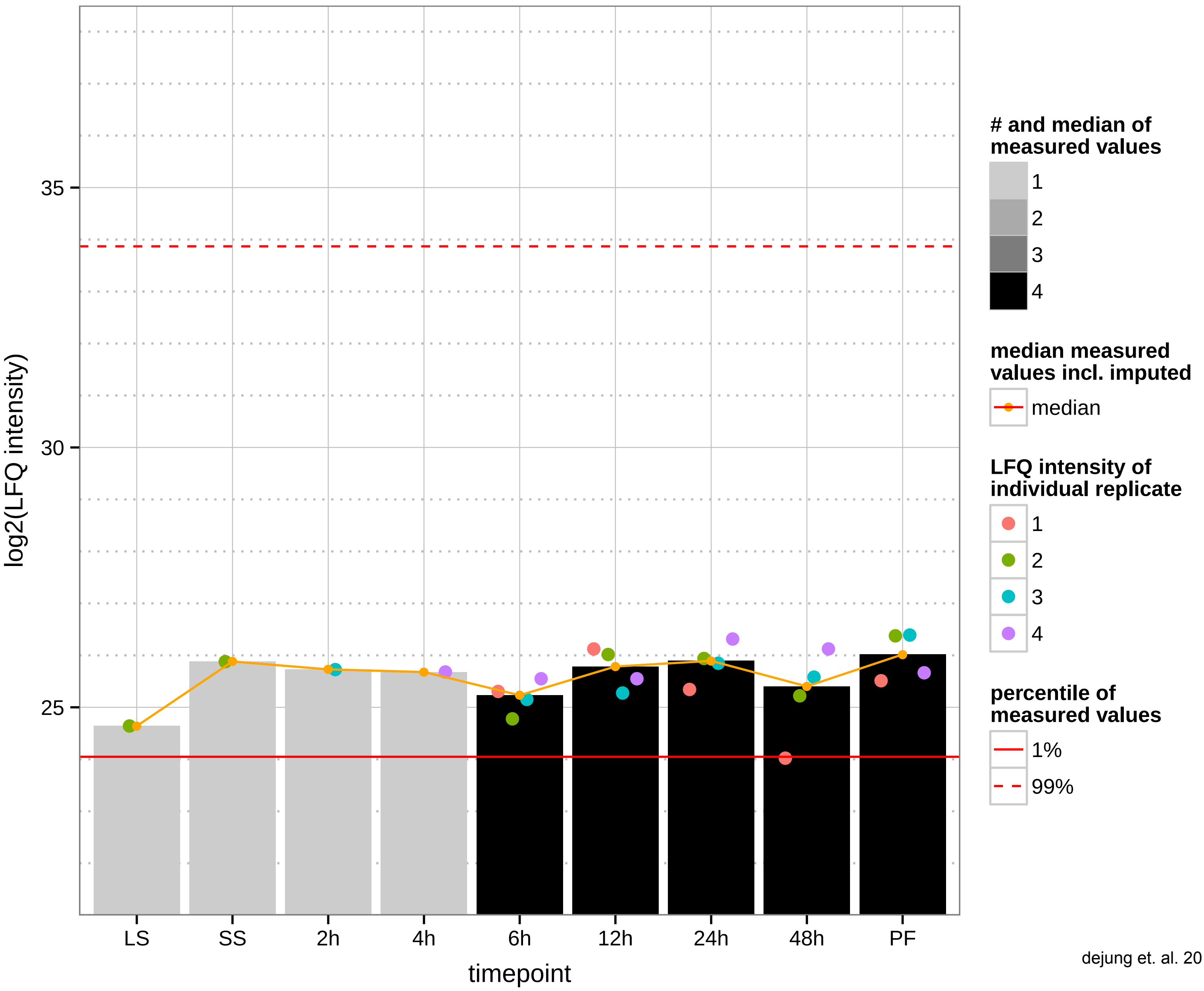




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.9260
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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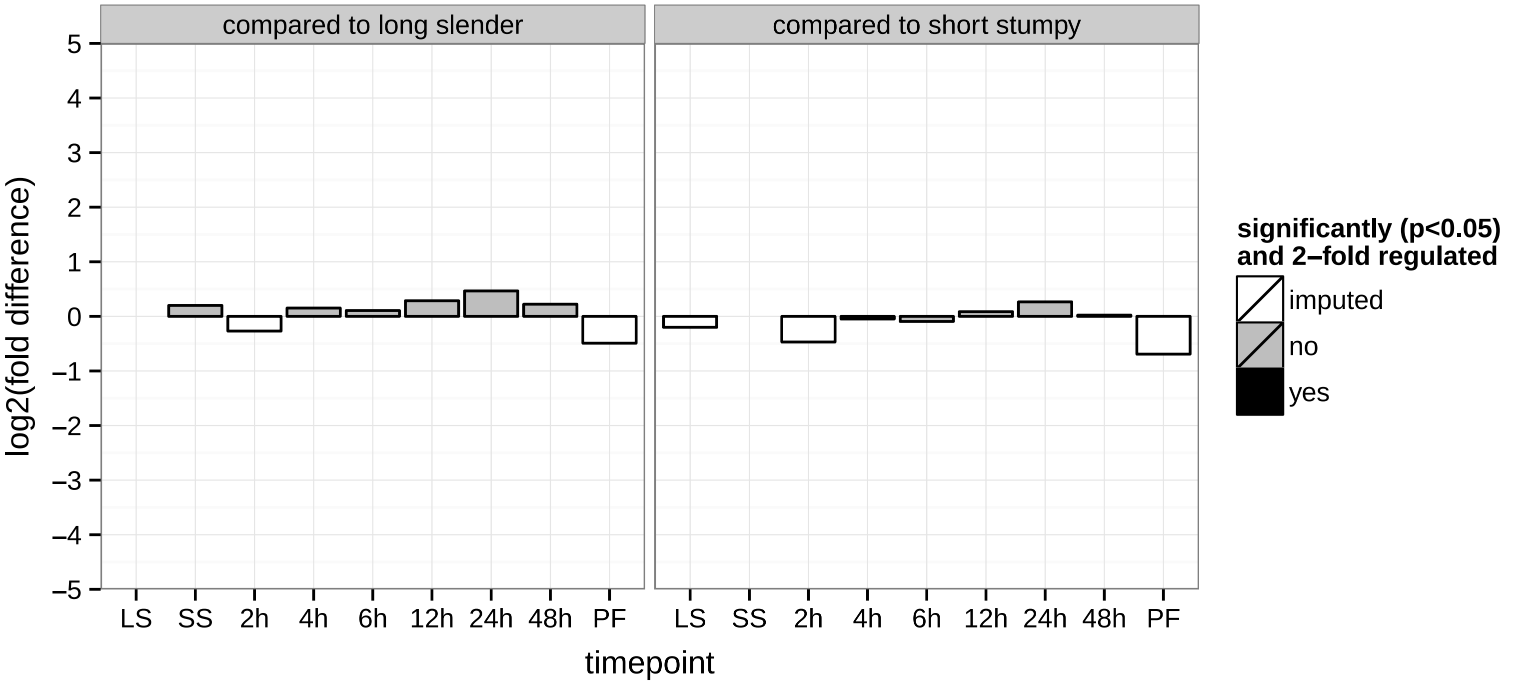
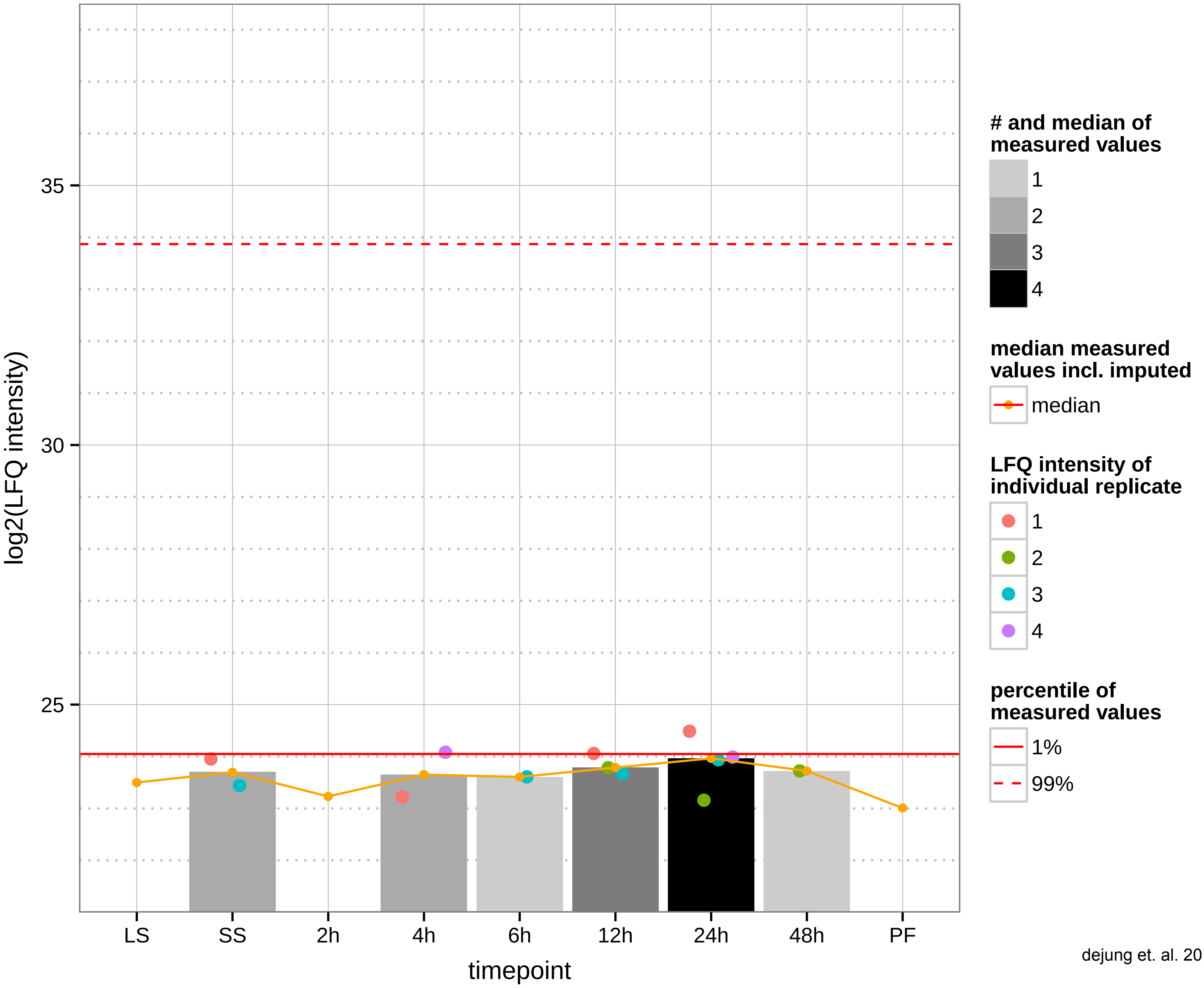
hypothetical protein, conserved
Tb927.10.9390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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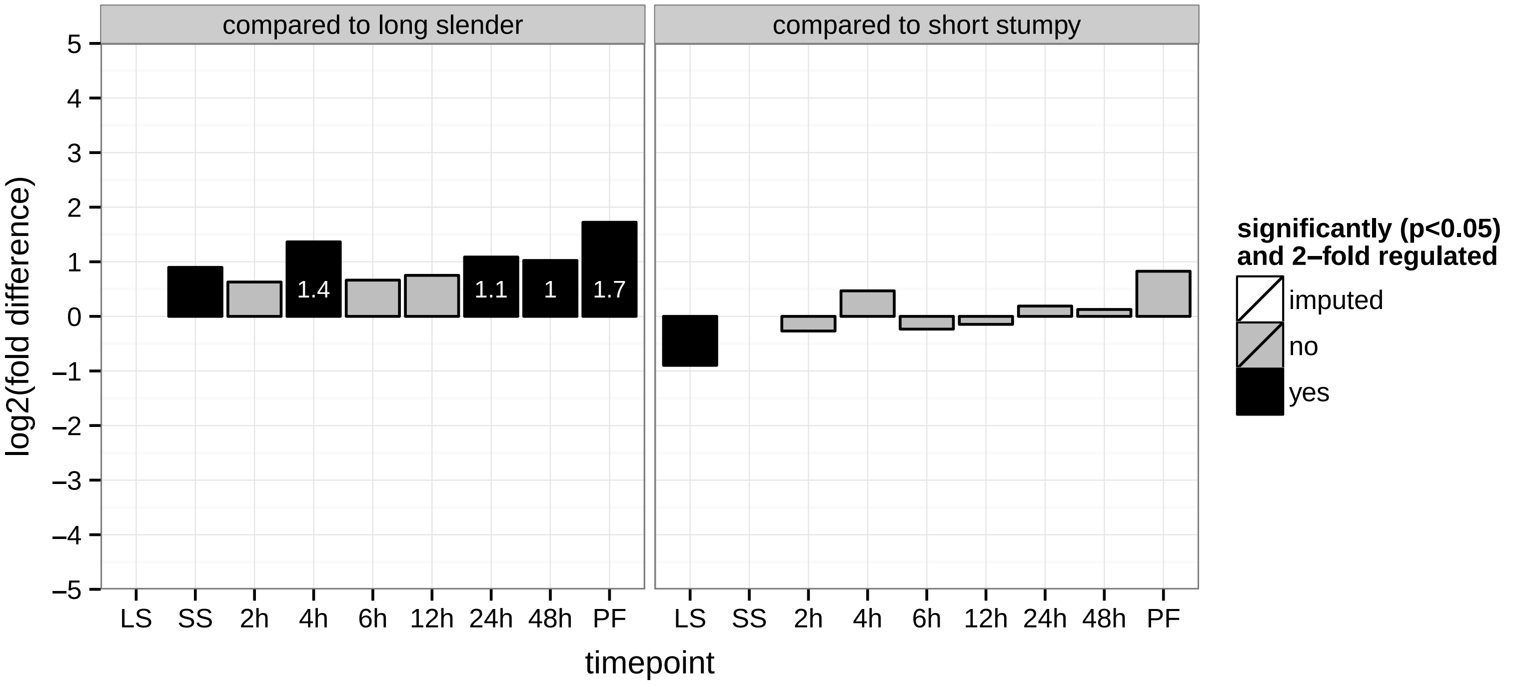
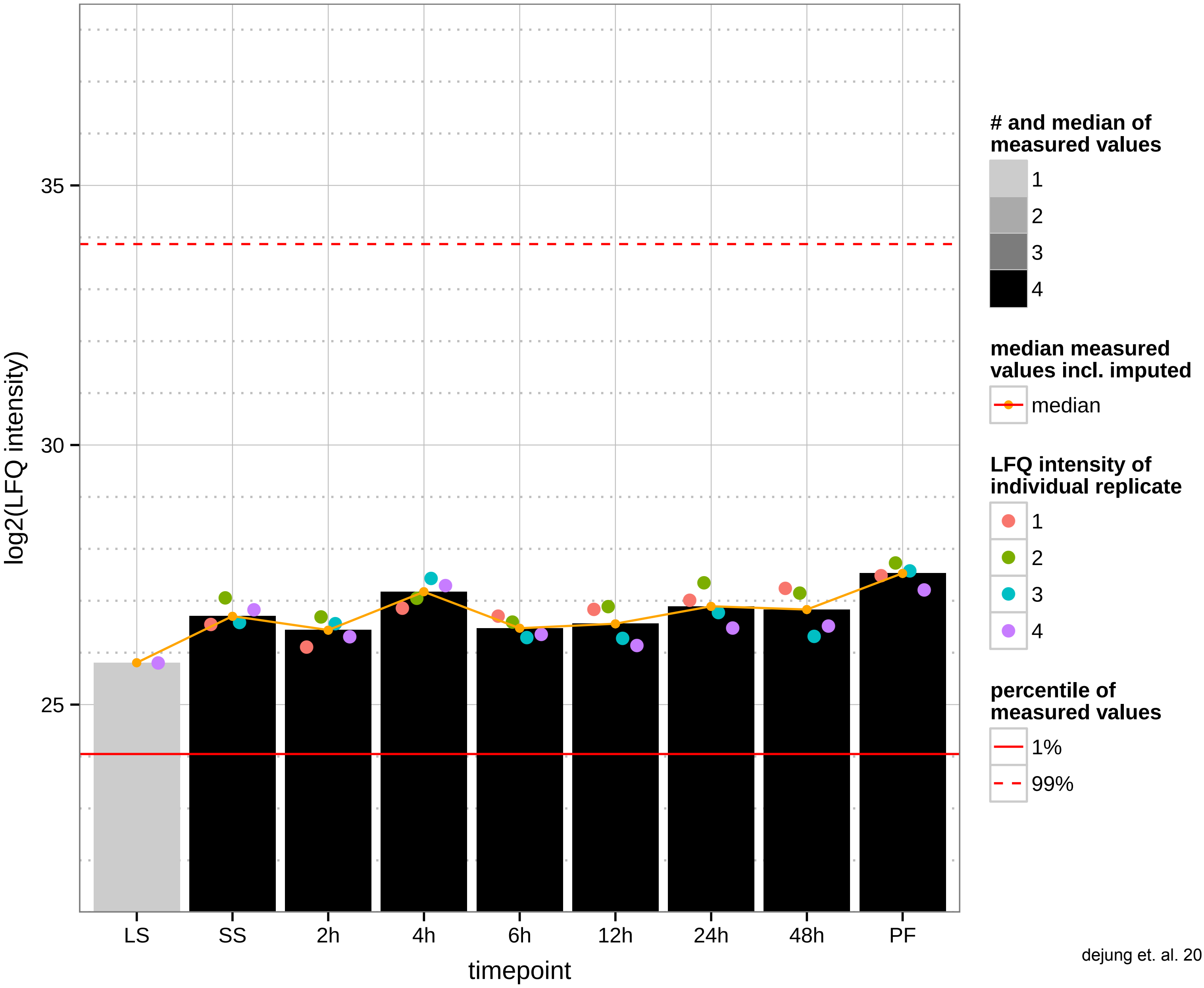
branch point binding protein, putative
Tb927.10.9400
AGOF: transcription corepressor activity
AGOC: nucleus
AGOP: spliceosomal complex assembly
PGOF: null
PGOC: null
PGOP: null





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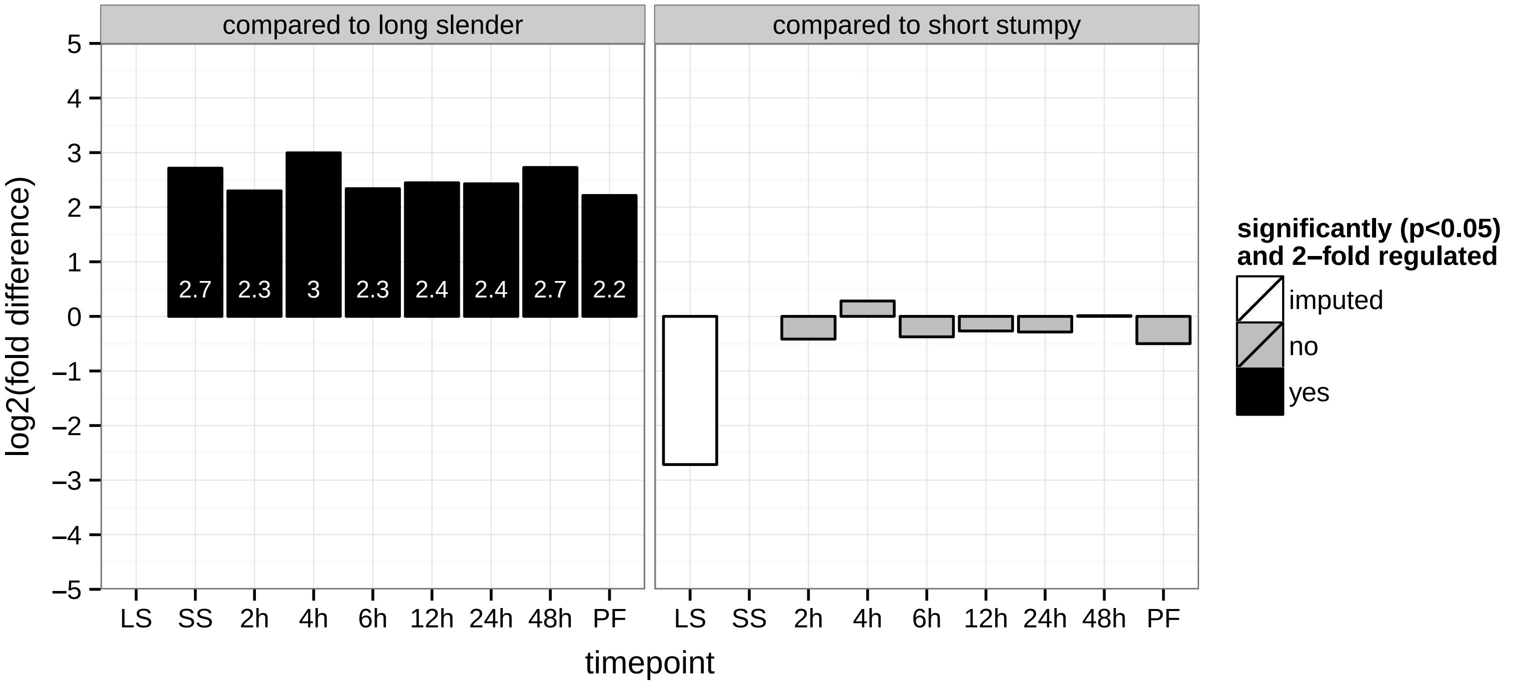
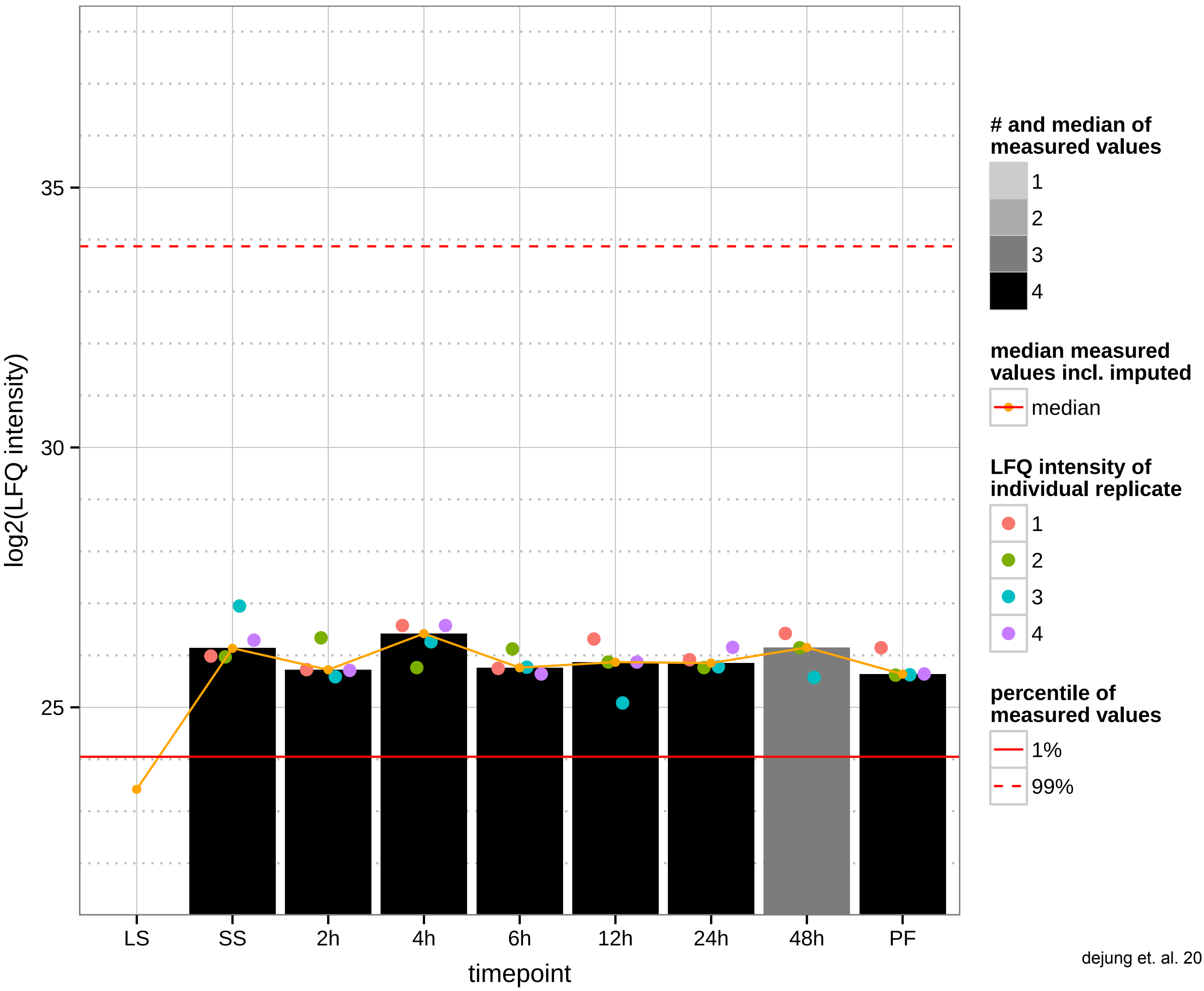
selenophosphate synthetase, putative (SPS2)
Tb927.10.9410
AGOF: ATP binding, selenide, water dikinase activity
AGOC: null
AGOP: tRNA aminoacylation for protein translation
PGOF: ATP binding, catalytic activity, selenide, water dikinase activity
PGOC: null
PGOP: null





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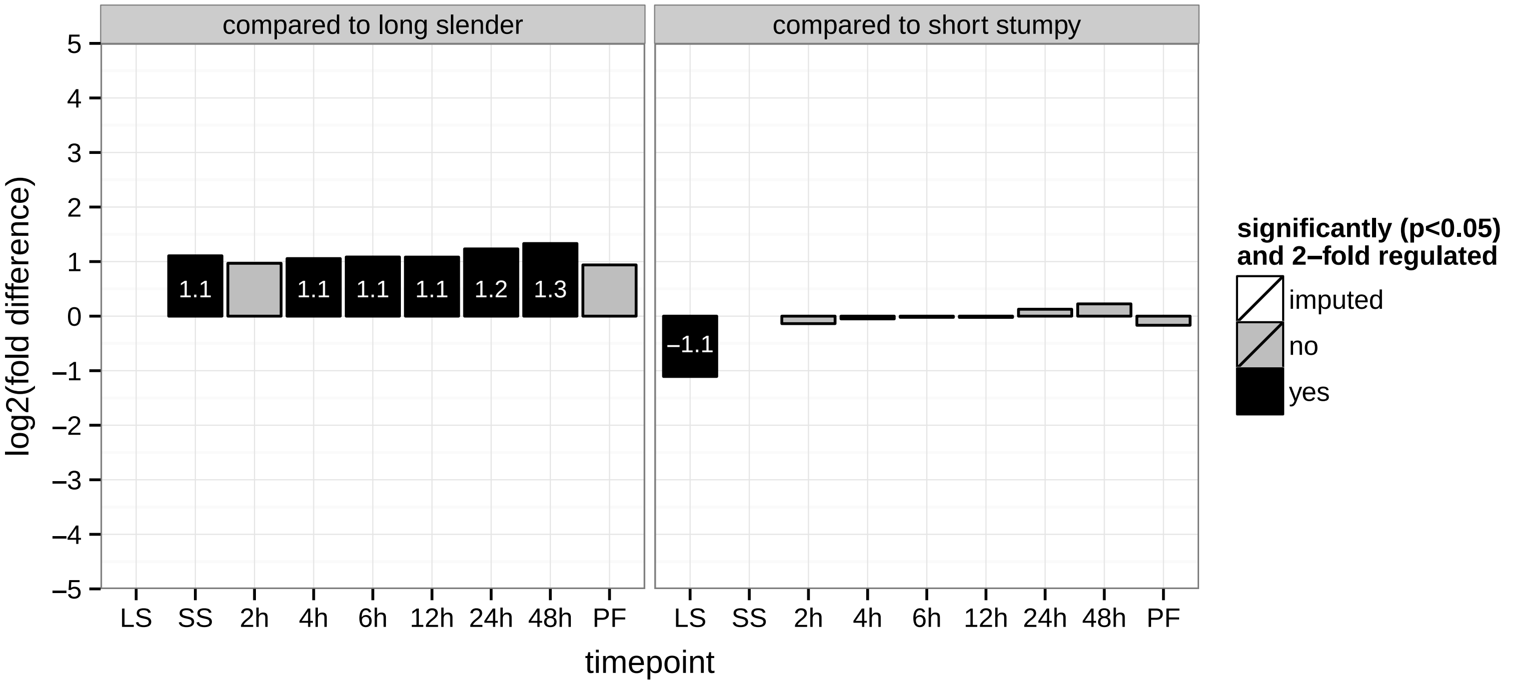
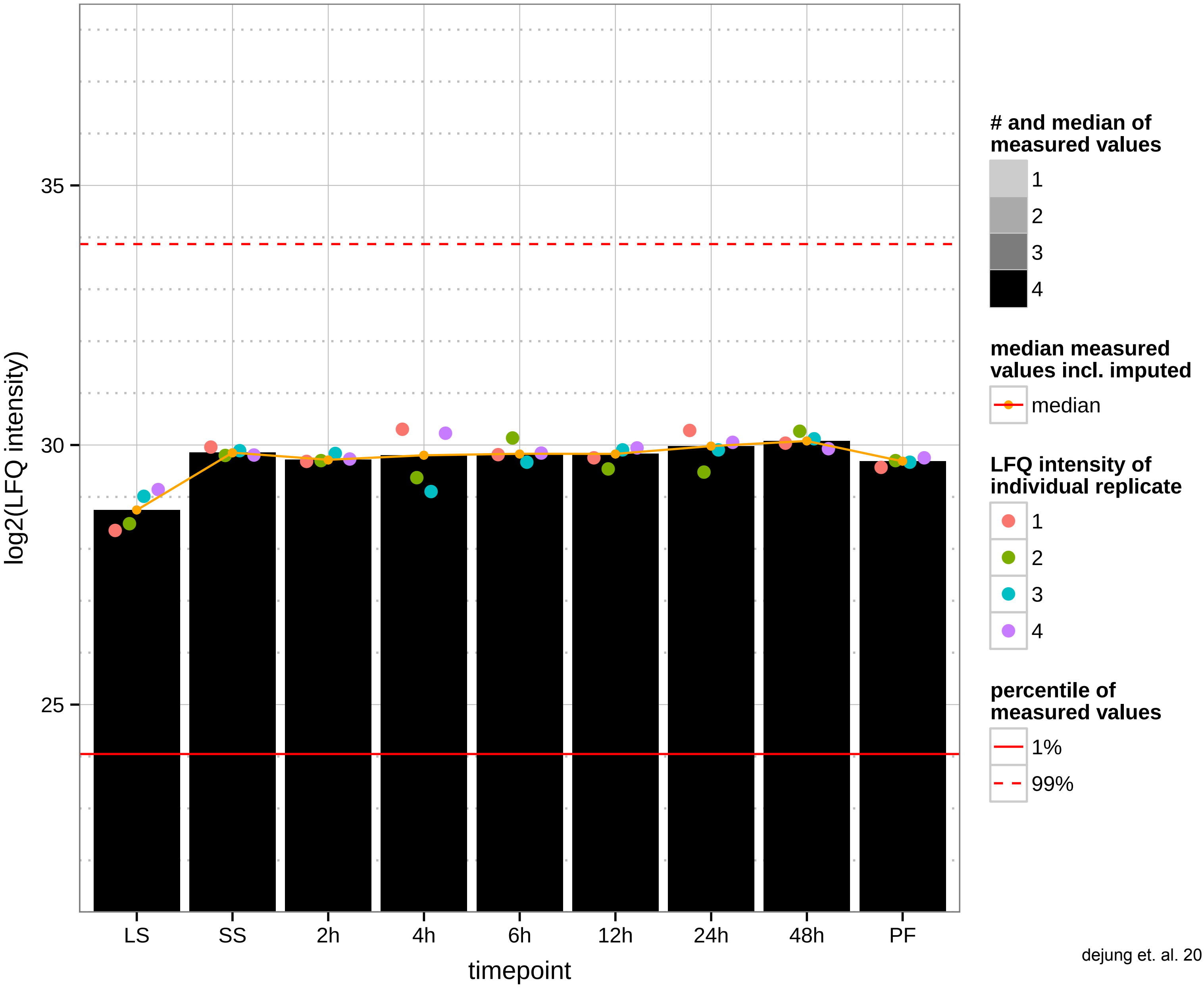
phosphoribosylpyrophosphate synthetase, putative (PRS)
Tb927.10.9430
AGOF: ATP binding, magnesium ion binding, ribose phosphate diphosphokinase activity
AGOC: null
AGOP: nucleoside metabolic process, purine ribonucleotide biosynthetic process
PGOF: magnesium ion binding, ribose phosphate diphosphokinase activity
PGOC: null
PGOP: nucleoside metabolic process, nucleotide biosynthetic process





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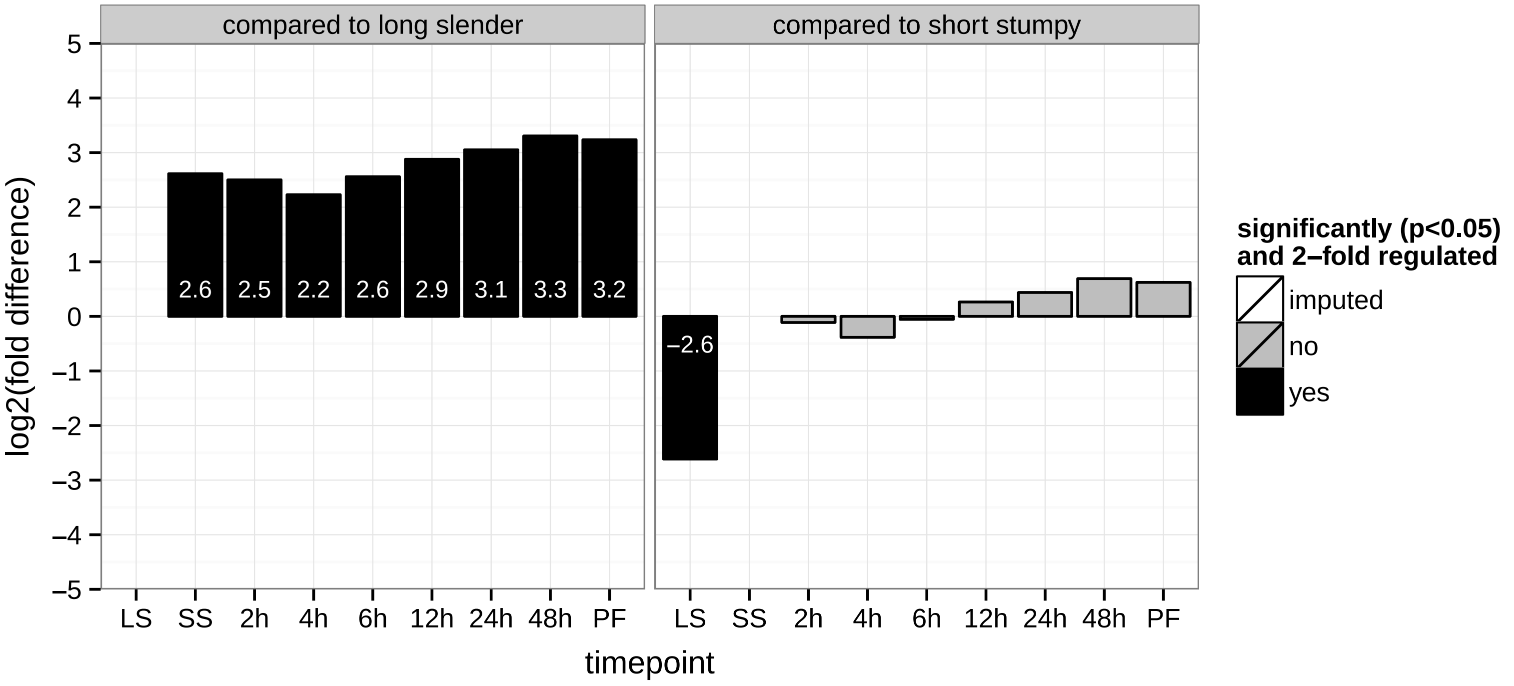
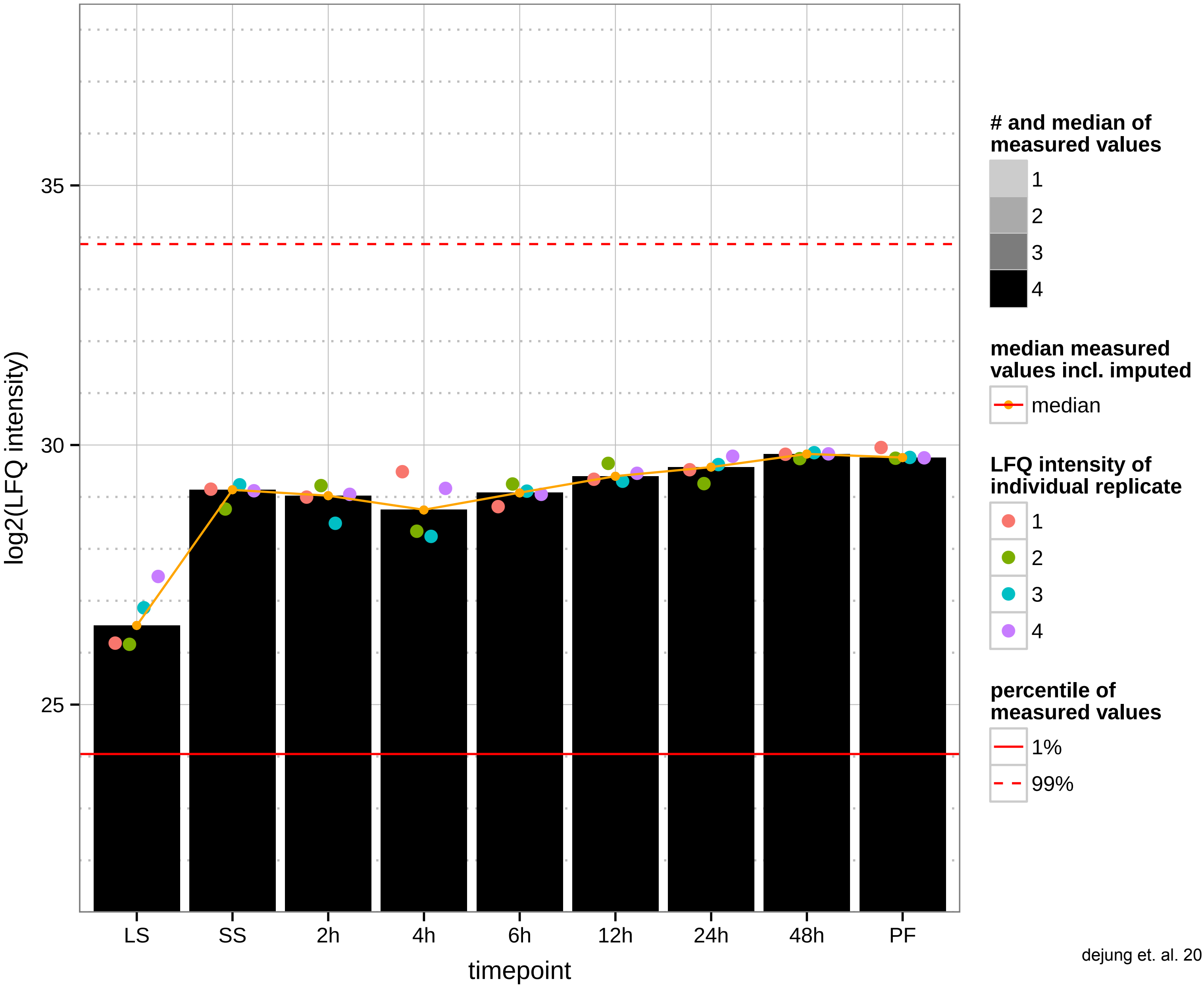
NADH dehydrogenase (54 NDH2)
Tb927.10.9440
AGOF: NADH dehydrogenase (ubiquinone) activity
AGOC: mitochondrion
AGOP: mitochondrial electron transport, NADH to ubiquinone
PGOF: flavin adenine dinucleotide binding, oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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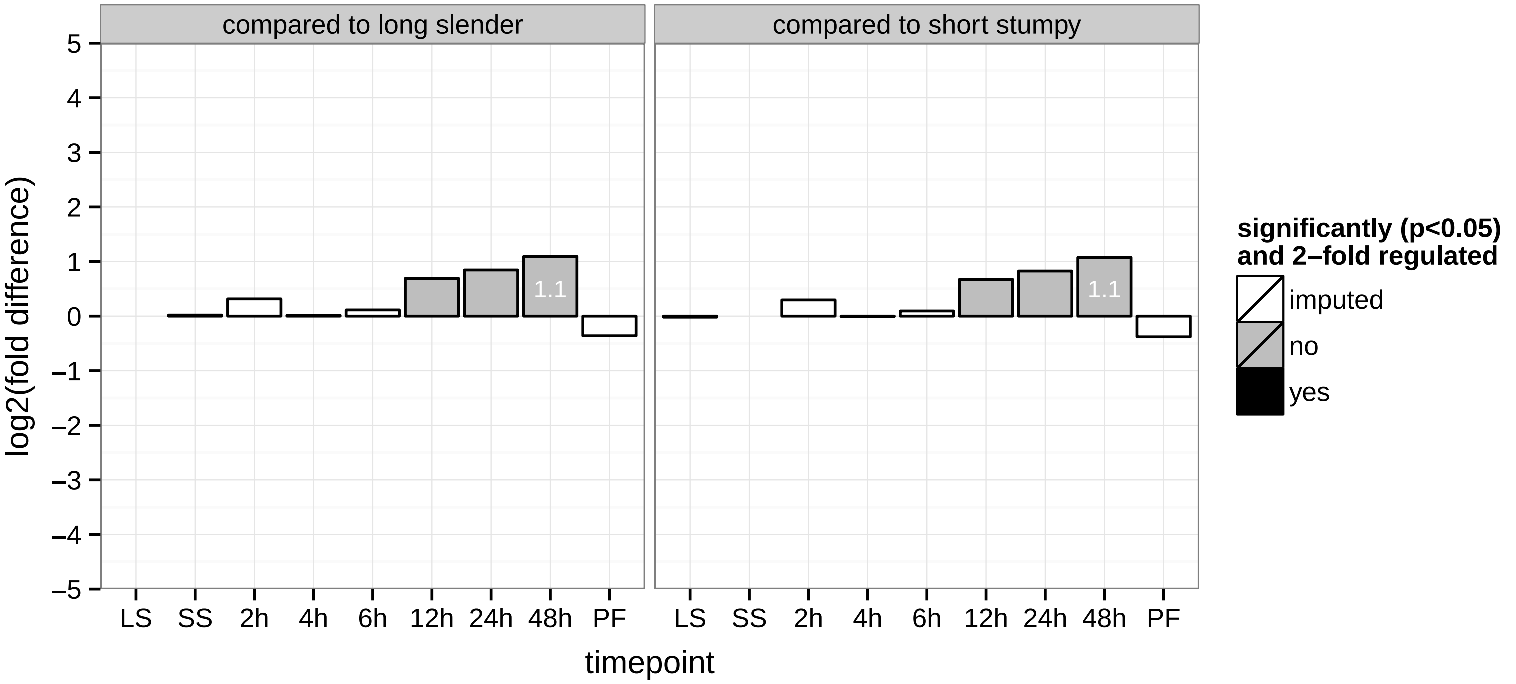
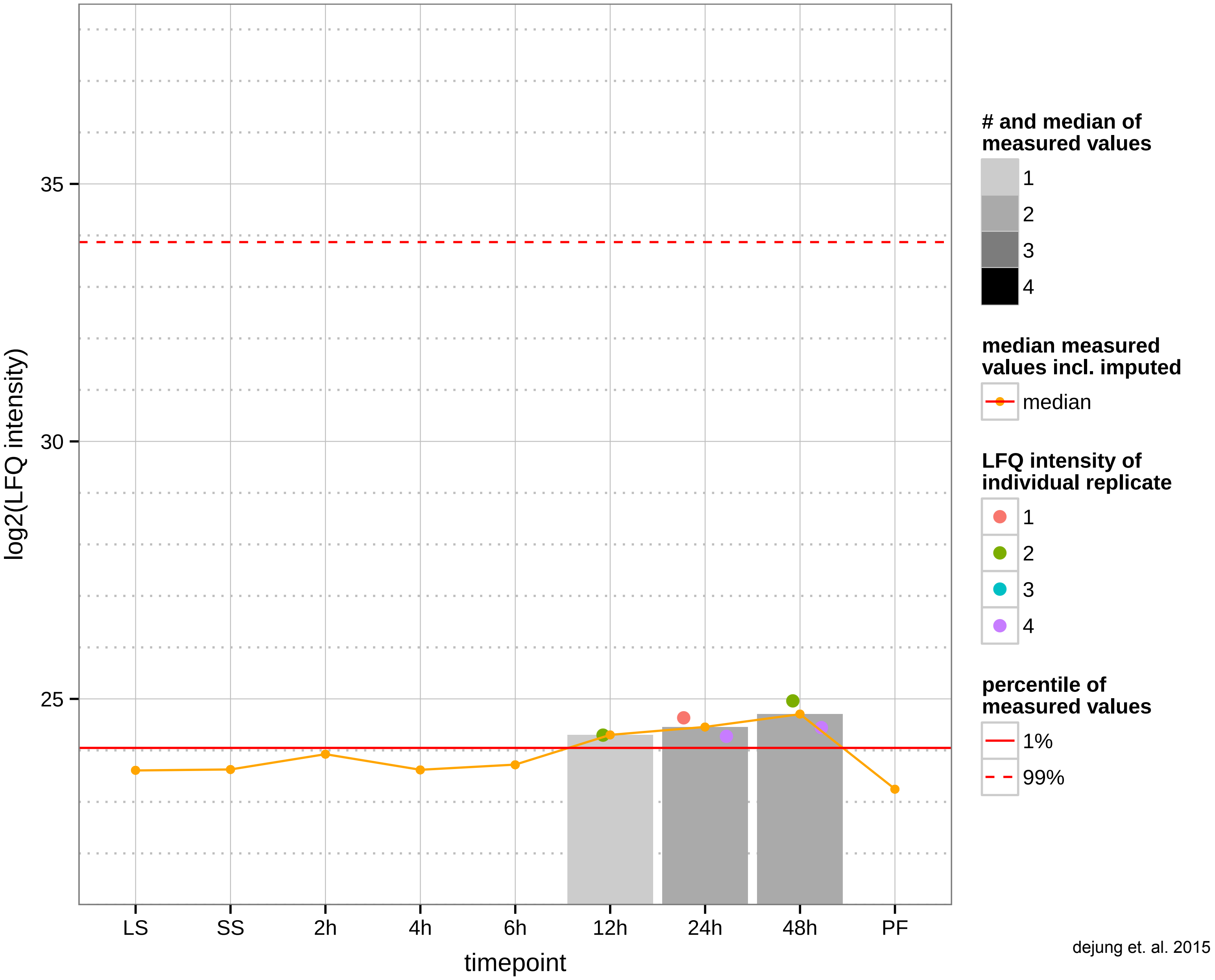
oxidoreductase, putative
Tb927.10.9560
AGOF: alcohol dehydrogenase activity, zinc–dependent, oxidoreductase activity, zinc ion binding
AGOC: null
AGOP: metabolic process, oxidation–reduction process
PGOF: oxidoreductase activity, transferase activity, transferring acyl groups other than amino–acyl groups, zinc ion binding
PGOC: null
PGOP: oxidation–reduction process





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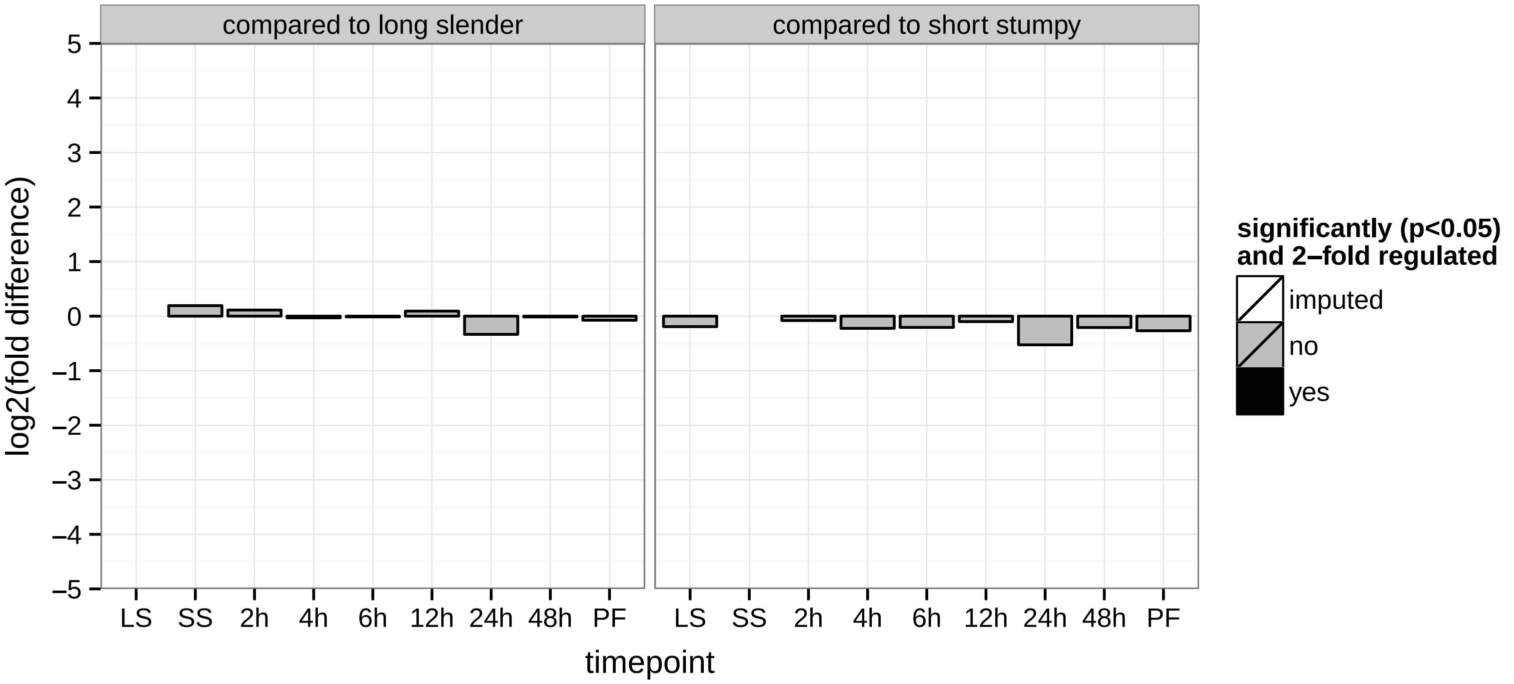
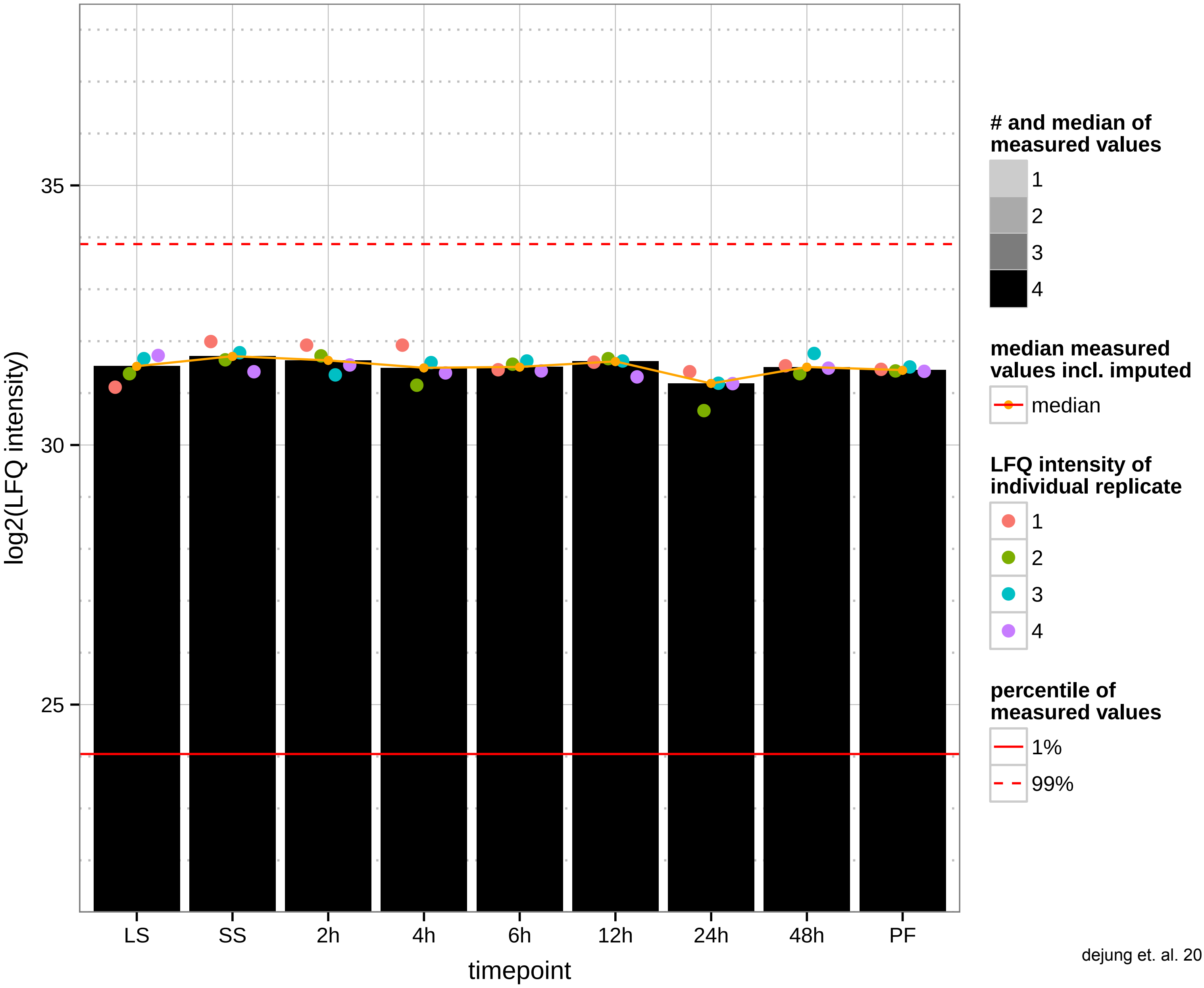
hypothetical protein, conserved, paraflagellar rod component, putative (PFC14)
Tb927.10.9570
AGOF: null
AGOC: null
AGOP: null
PGOF: null, protein binding
PGOC: null
PGOP: null





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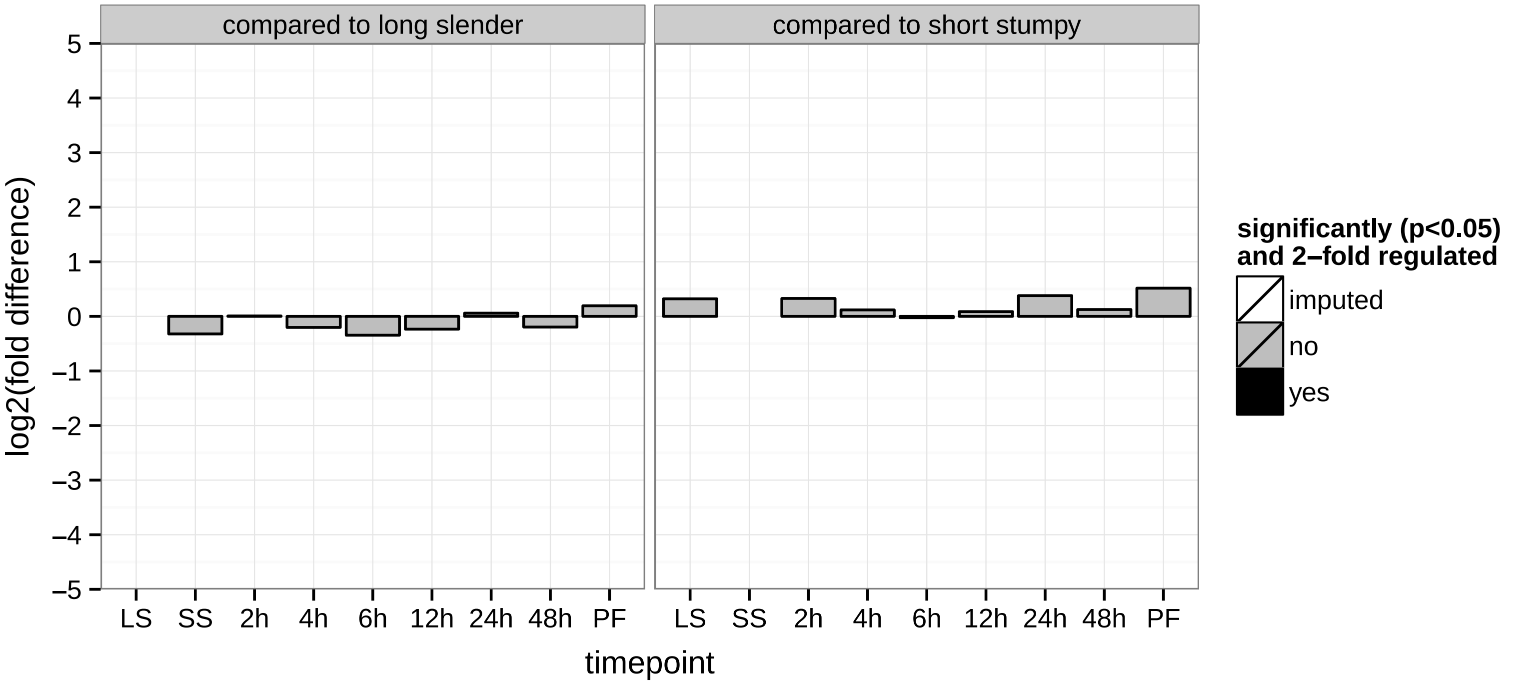
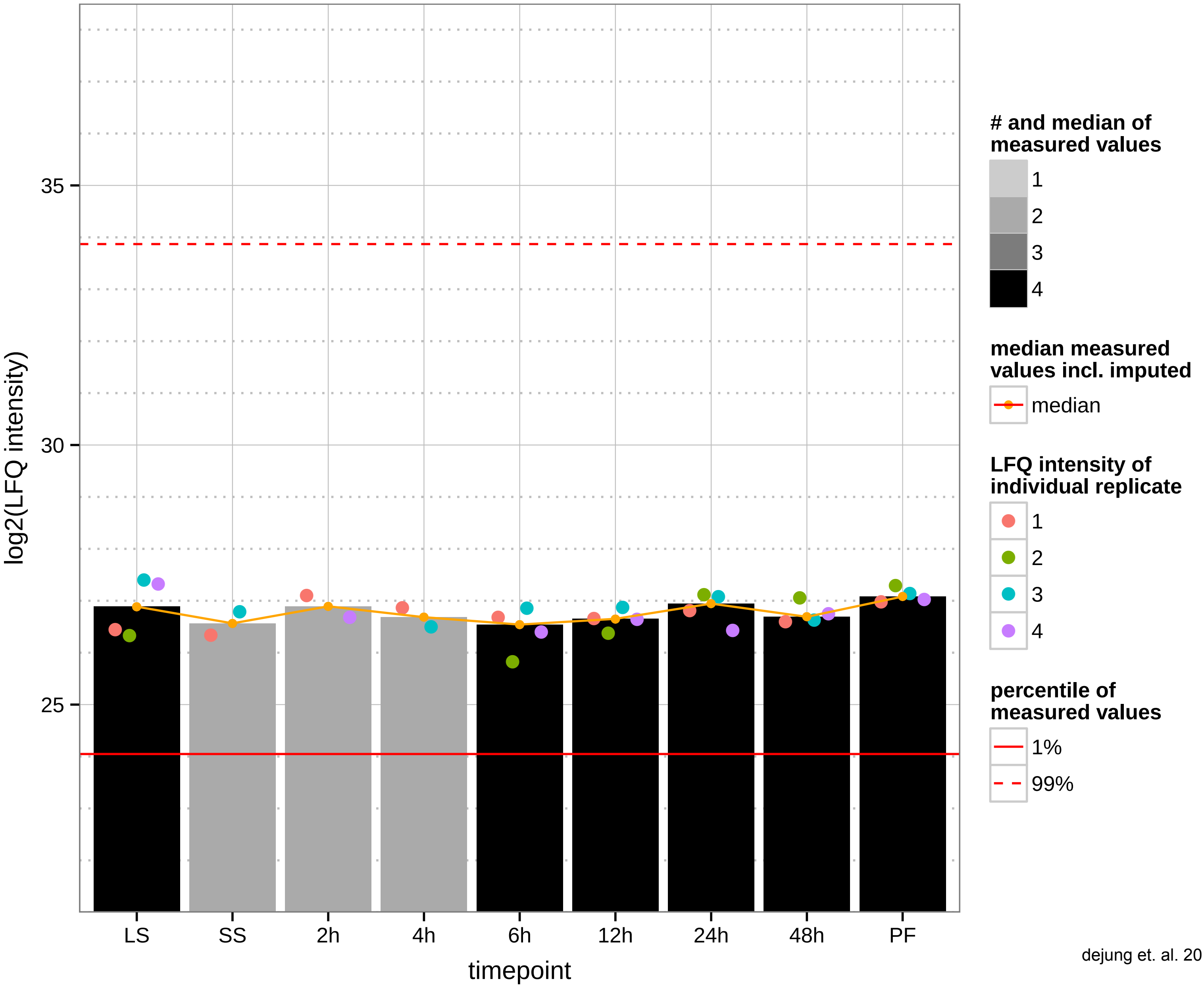
hypothetical protein, conserved
Tb927.10.9640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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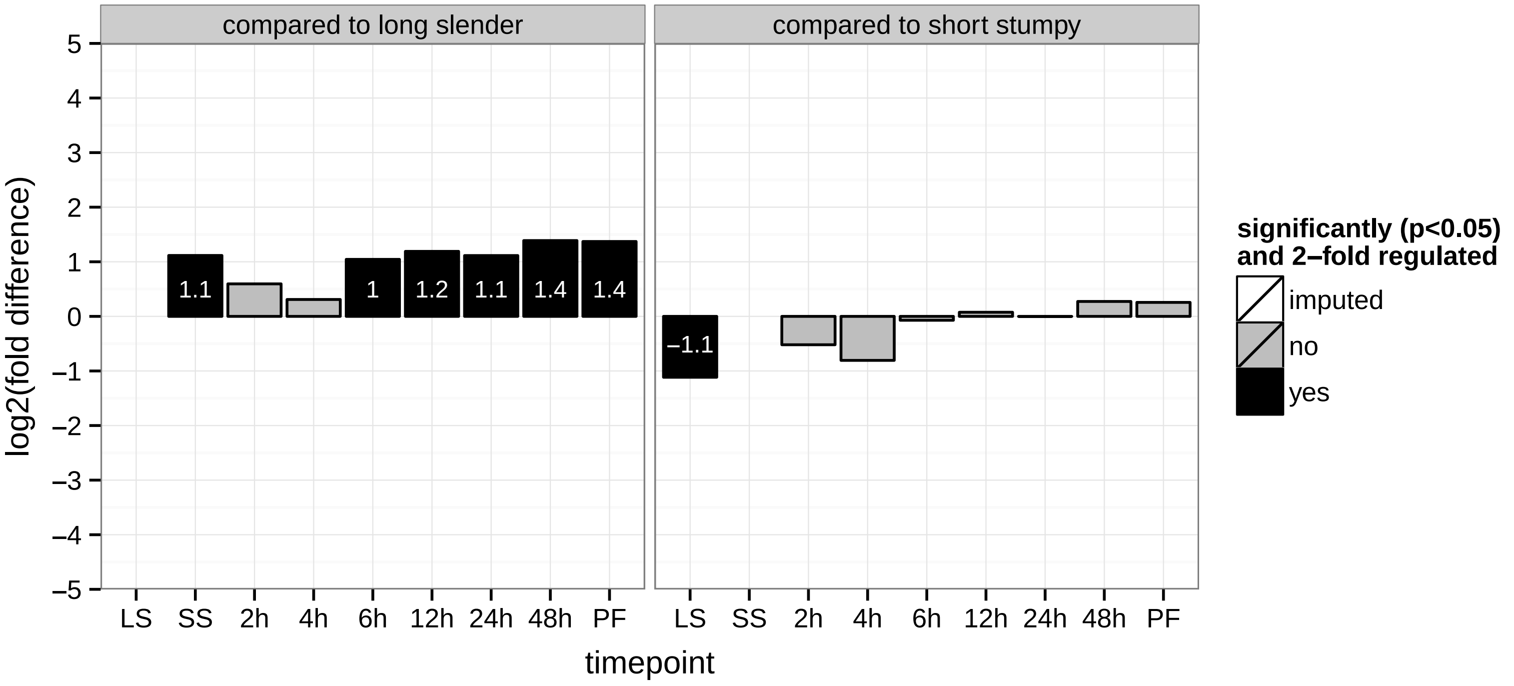
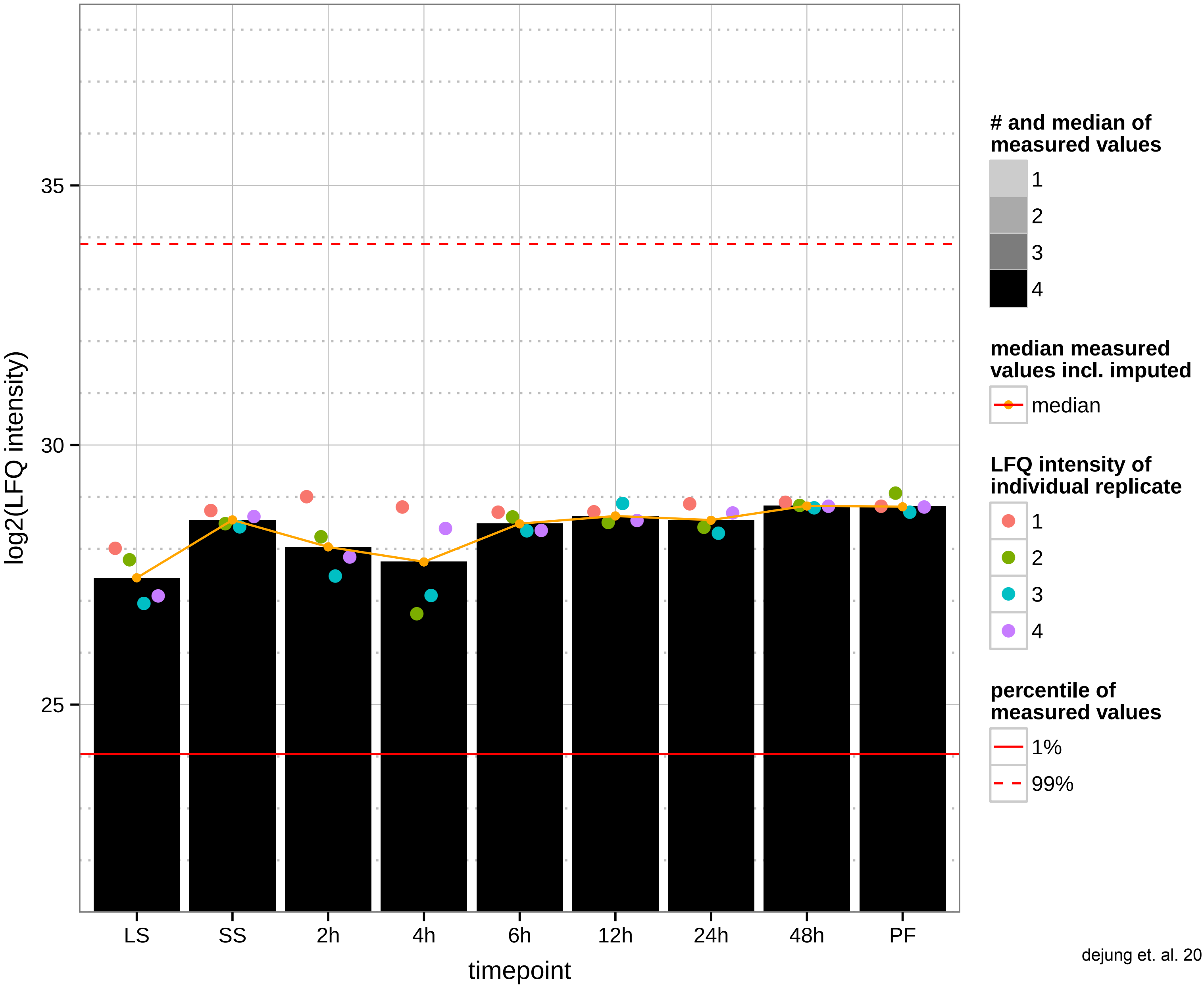
hypothetical protein, conserved
Tb927.10.9650;Tb11.v5.0399
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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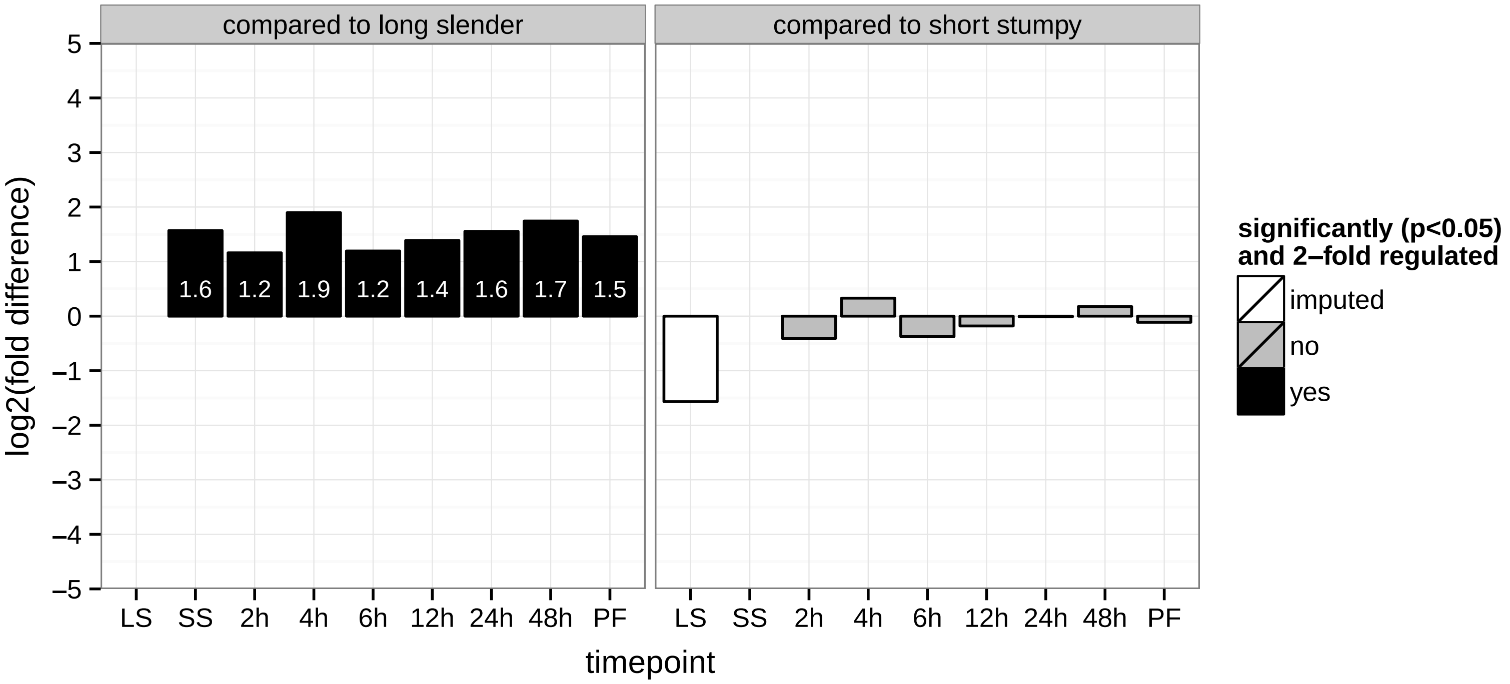
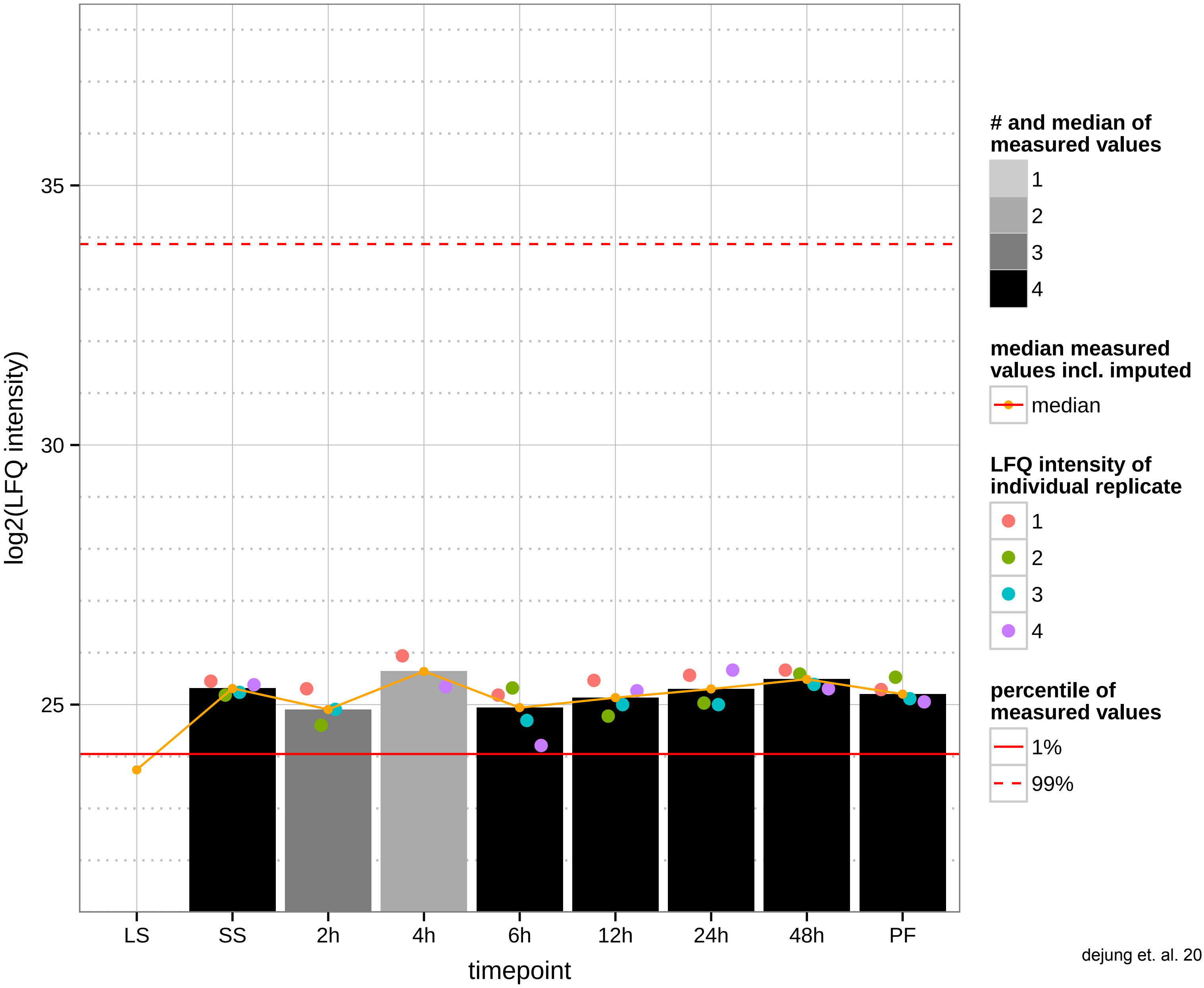
hypothetical protein, conserved
Tb927.10.9660;Tb11.v5.0735
AGOF: null
AGOC: null, intracellular
AGOP: null, RNA processing
PGOF: null
PGOC: intracellular
PGOP: RNA processing





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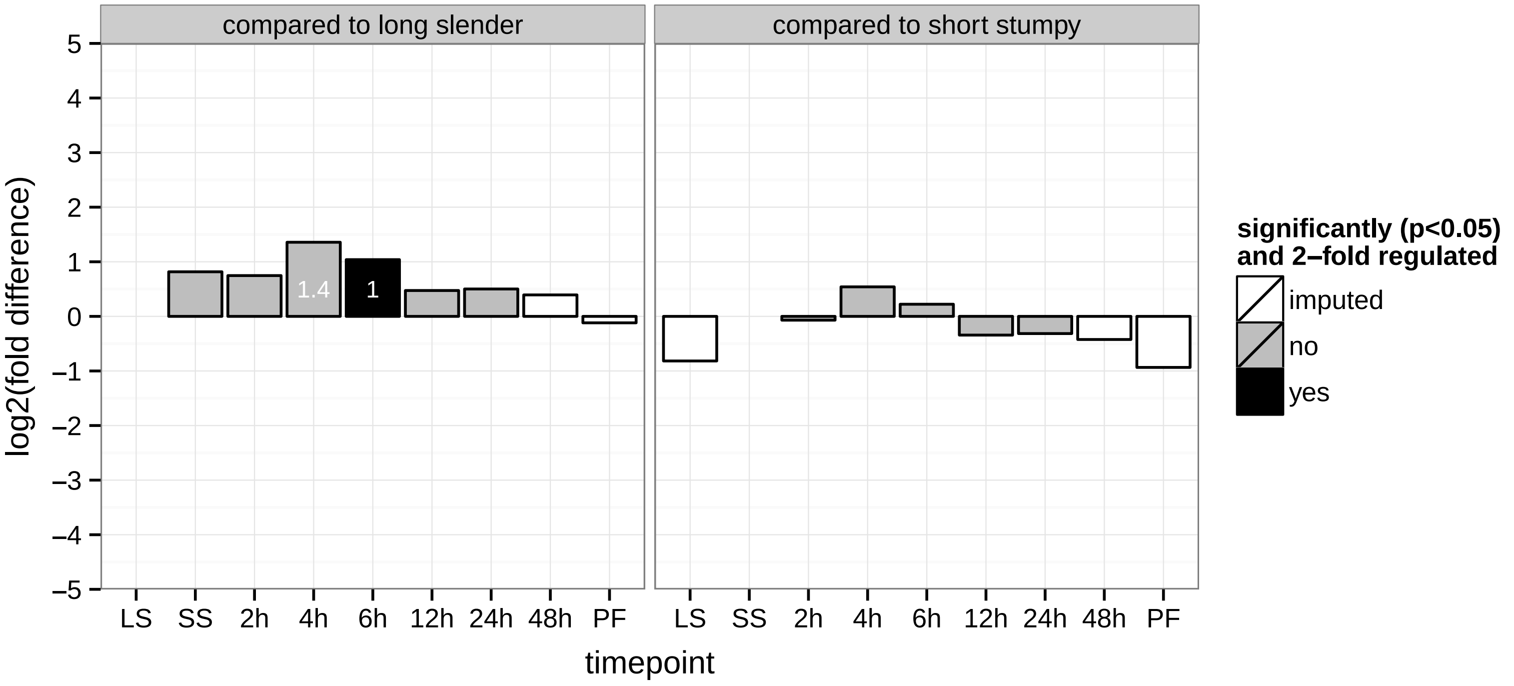
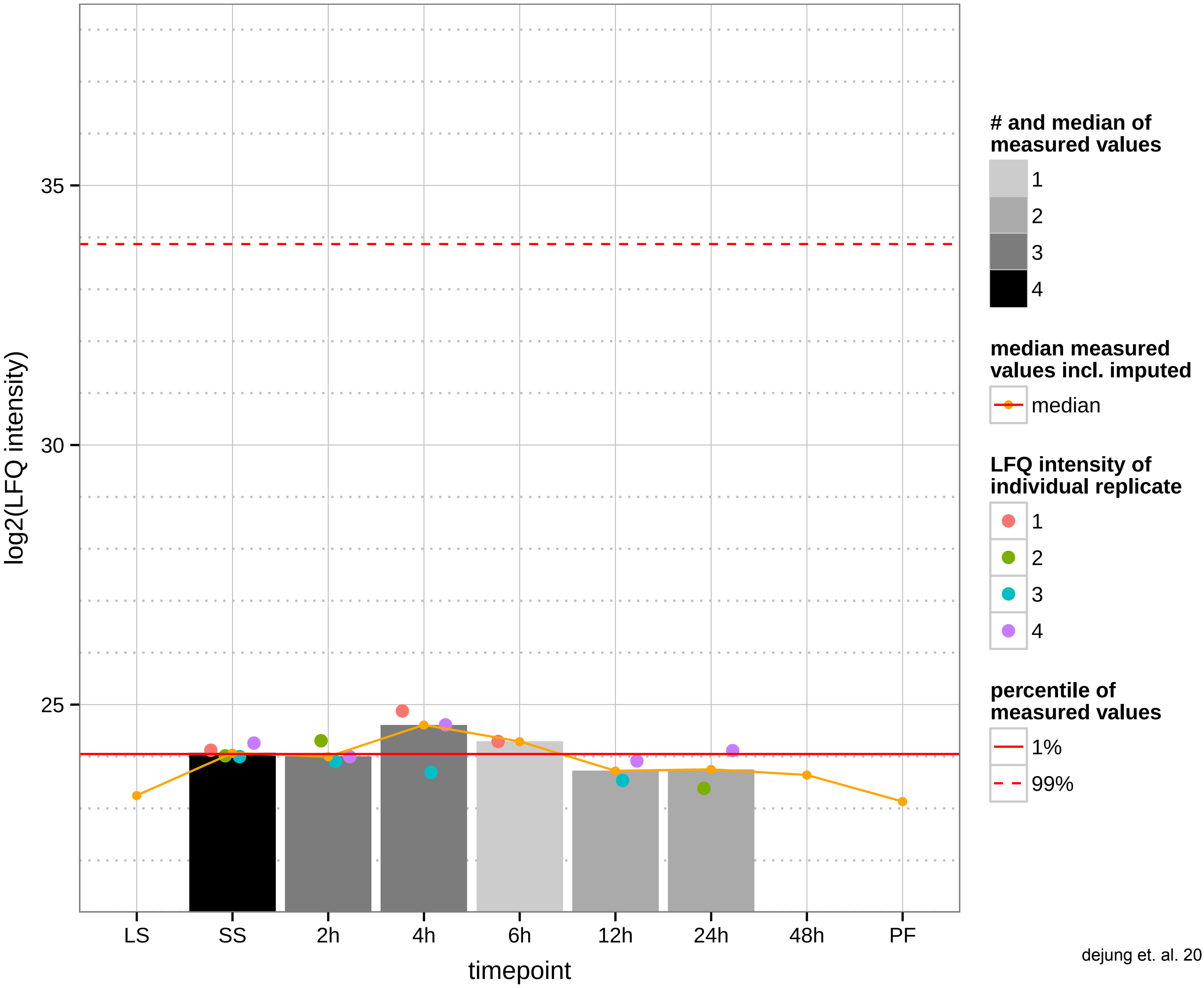
hypothetical protein, conserved
Tb927.10.9680
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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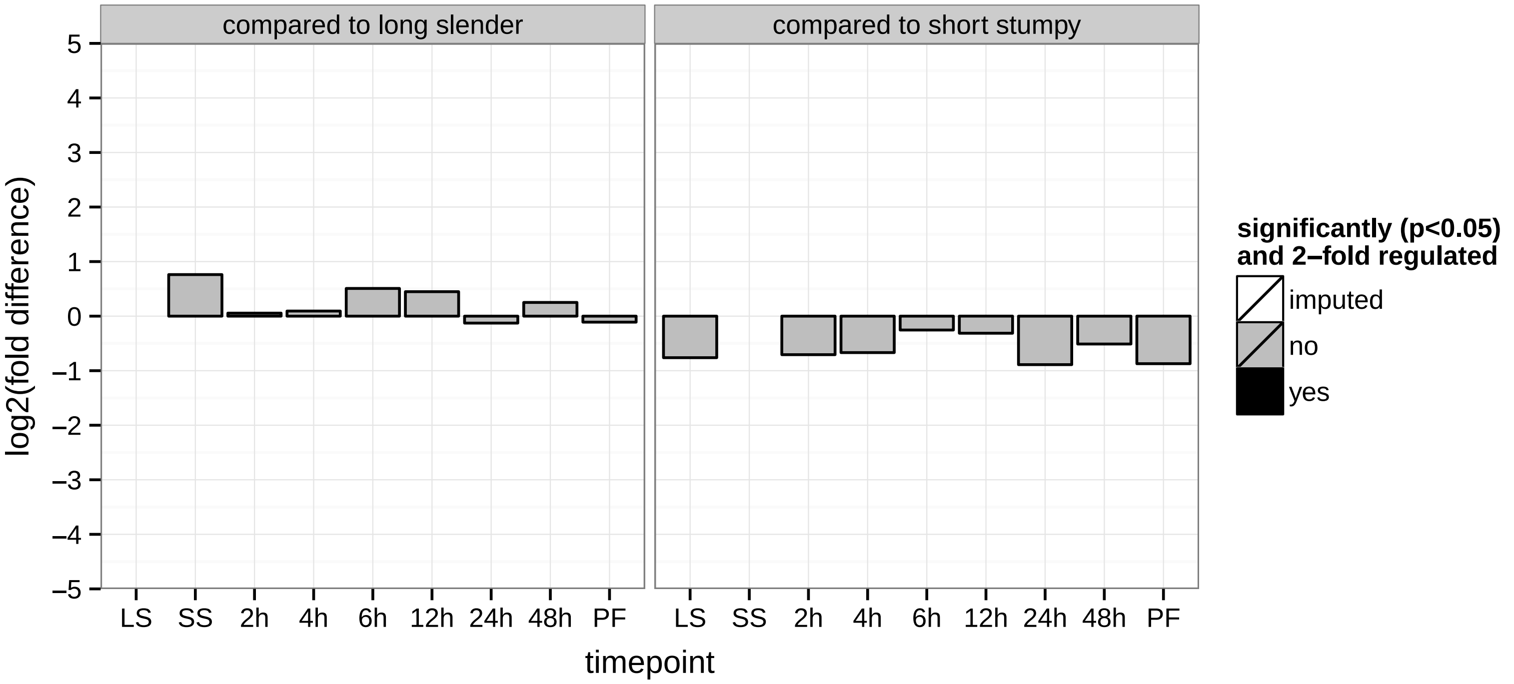
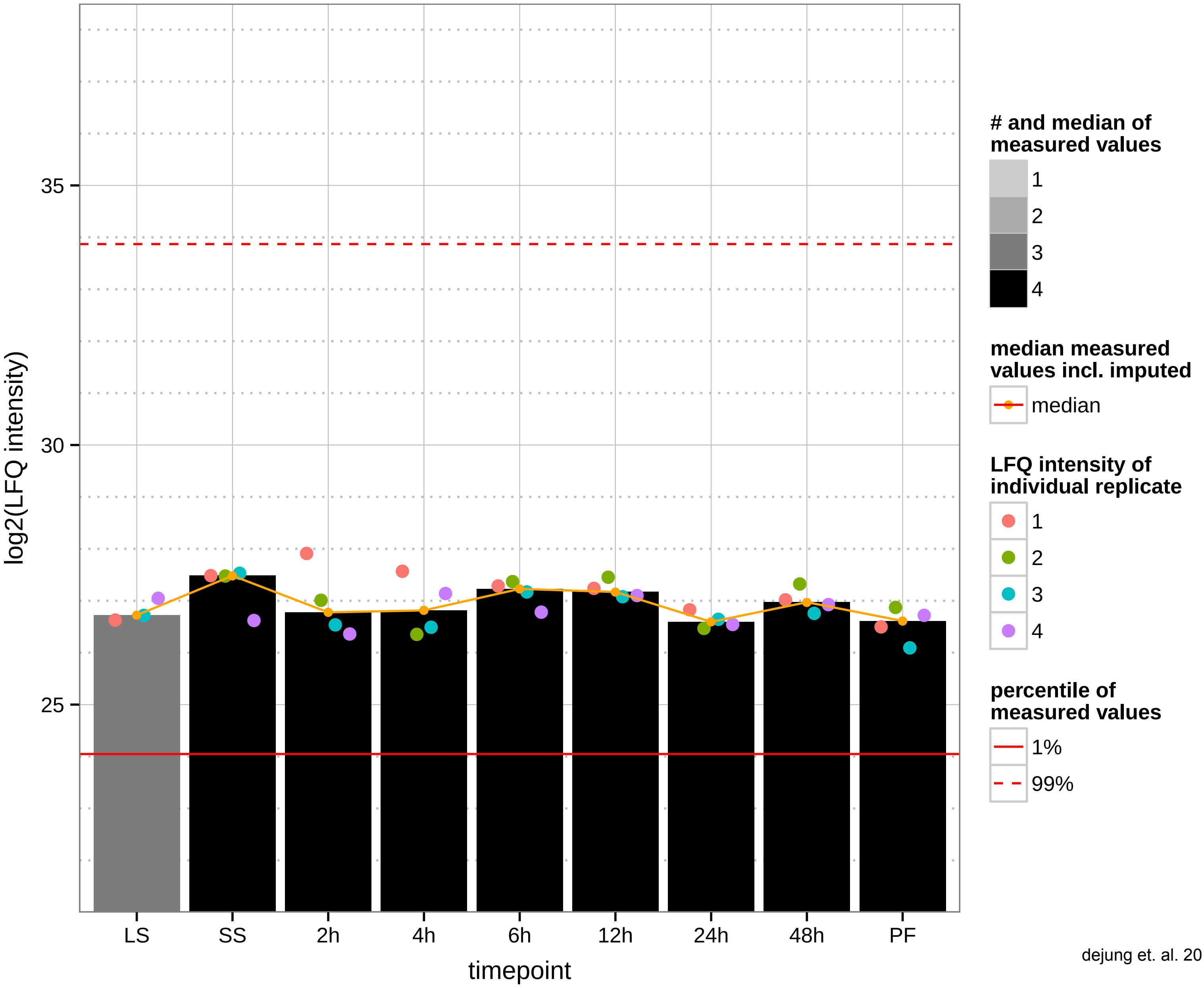
hypothetical protein, conserved, predicted C2 domain protein
Tb927.10.9700
AGOF: null
AGOC: null
AGOP: null
PGOF: null, protein binding
PGOC: null
PGOP: null





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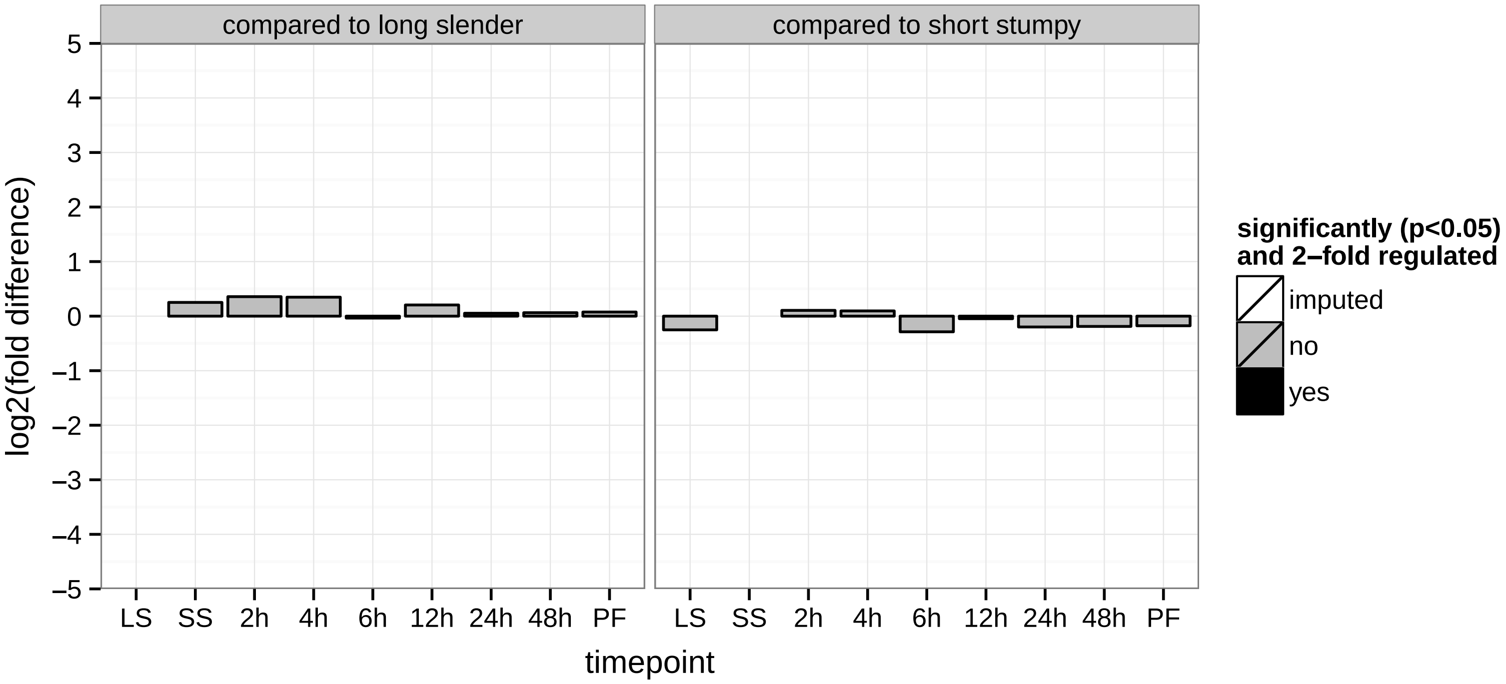
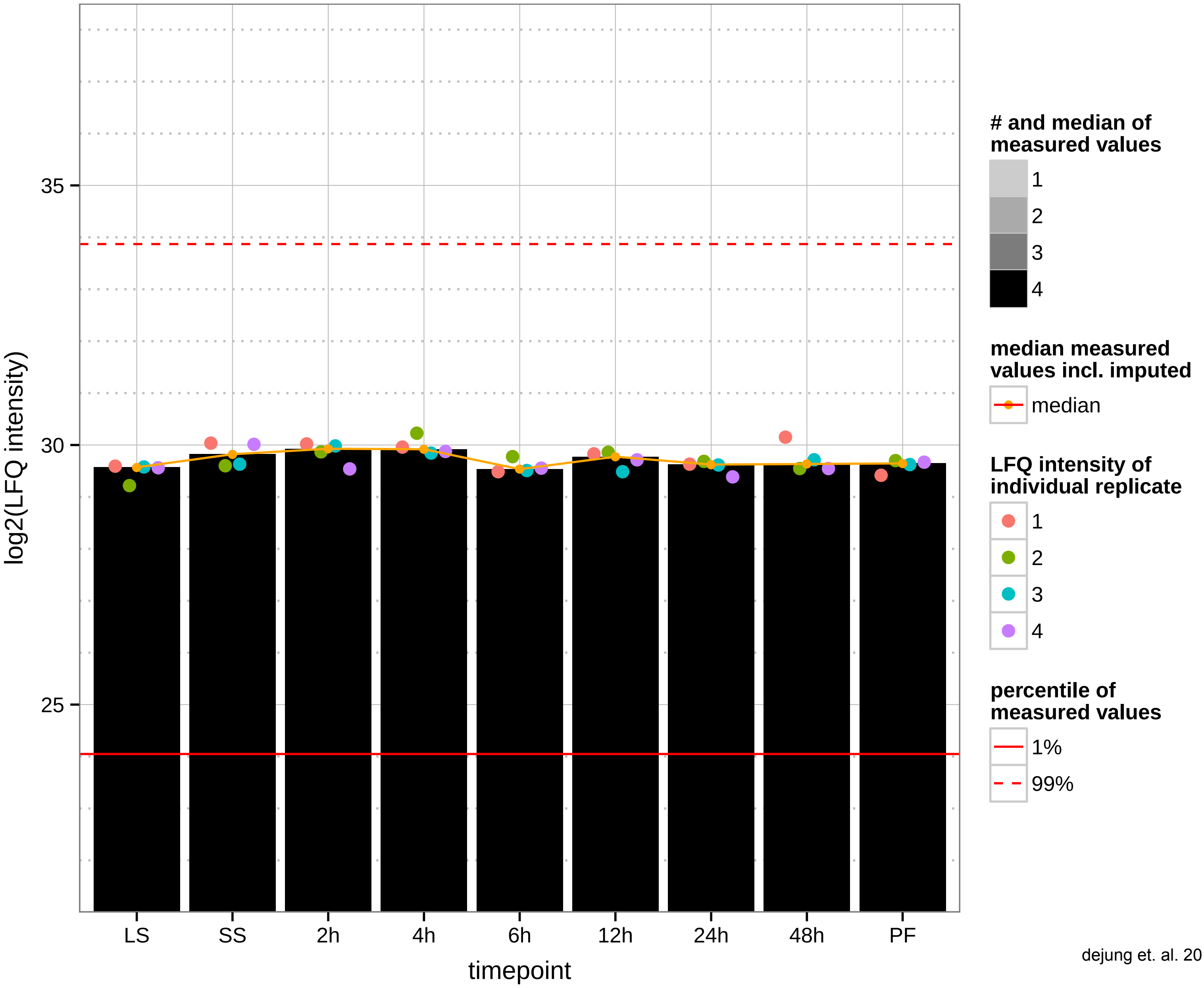
proteasome regulatory ATPase subunit 6, 19S proteasome regulatory subunit (RPT6)
Tb927.10.9740
AGOF: ATP binding, nucleoside–triphosphatase activity
AGOC: cytoplasm, nucleus, proteasome regulatory particle
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ATP binding, hydrolase activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: cytoplasm
PGOP: protein catabolic process





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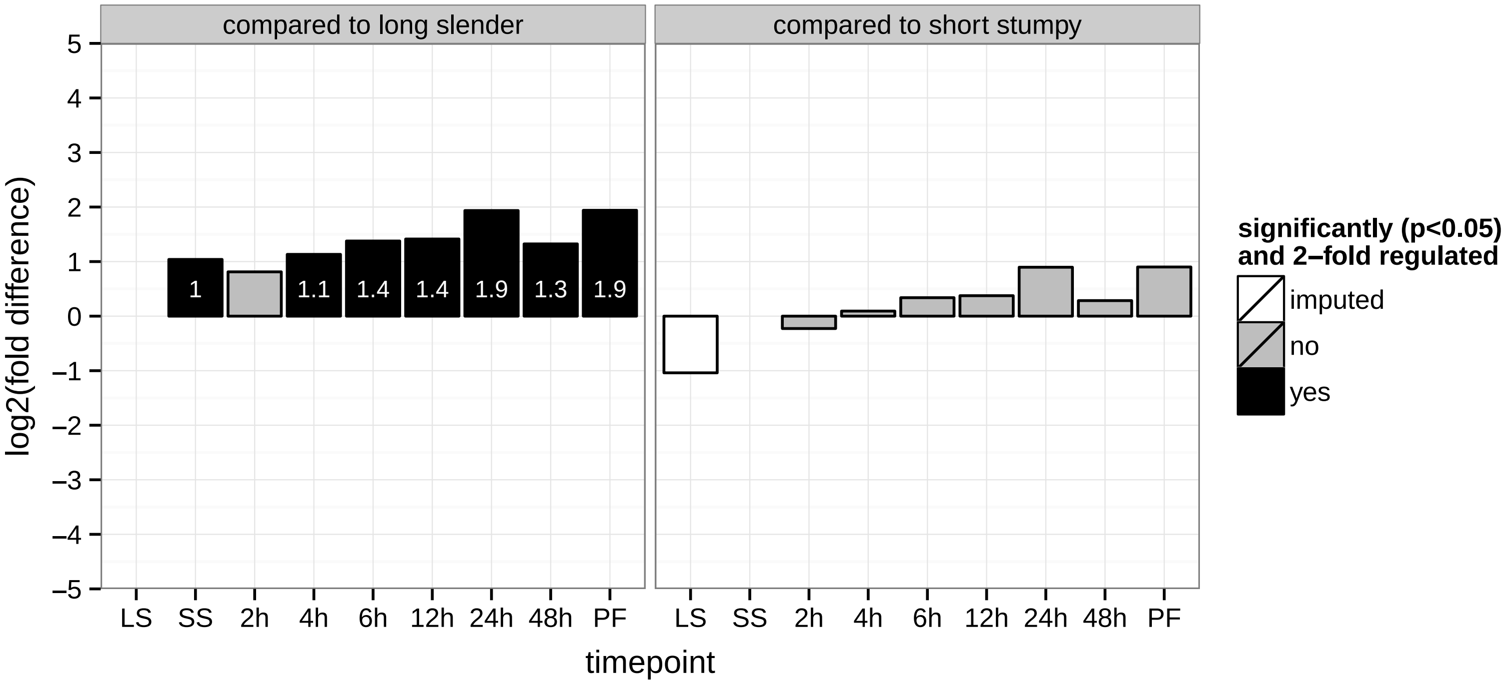
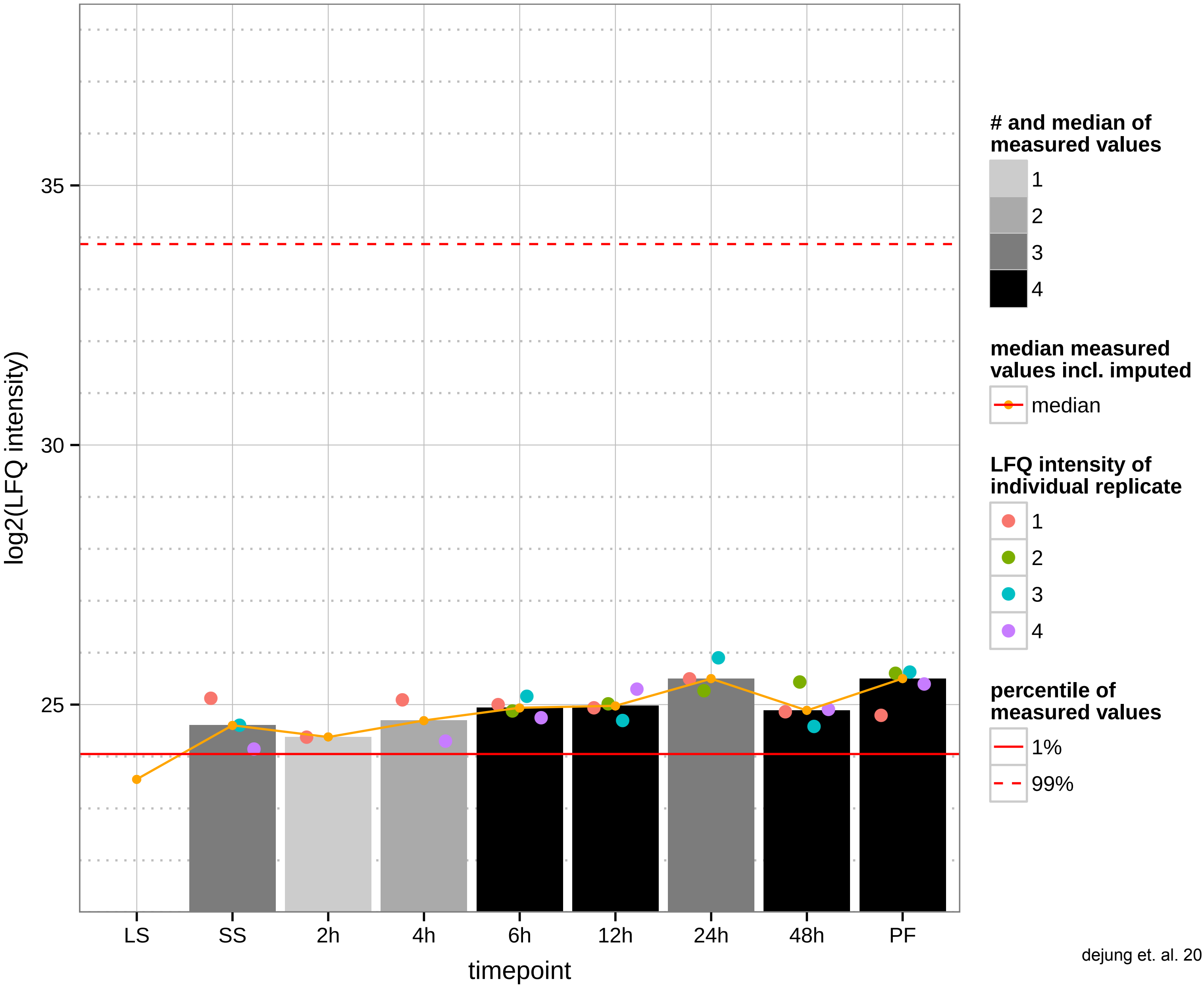
alternative oxidase
Tb927.10.9760
AGOF: null
AGOC: mitochondrial envelope, mitochondrion
AGOP: respiratory gaseous exchange
PGOF: null
PGOC: mitochondrial envelope
PGOP: oxidation–reduction process, respiratory gaseous exchange





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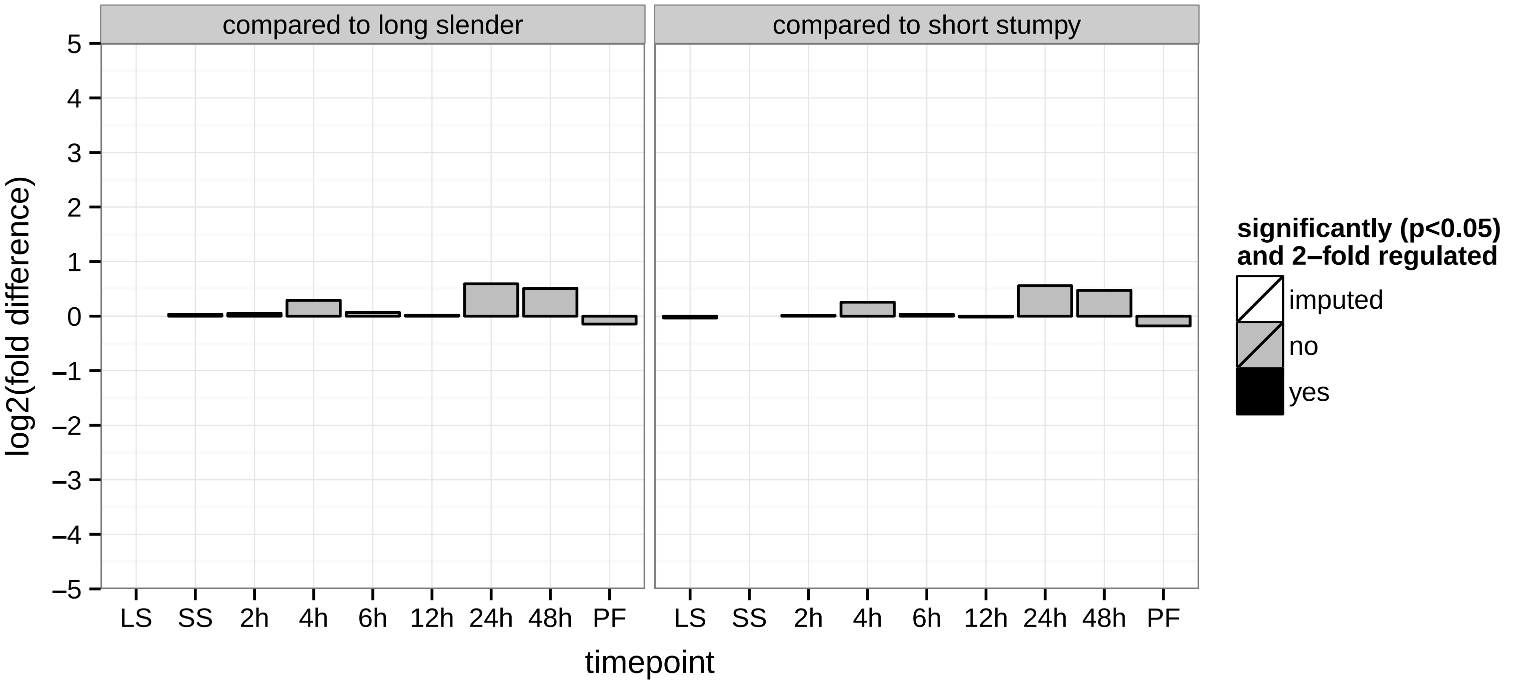
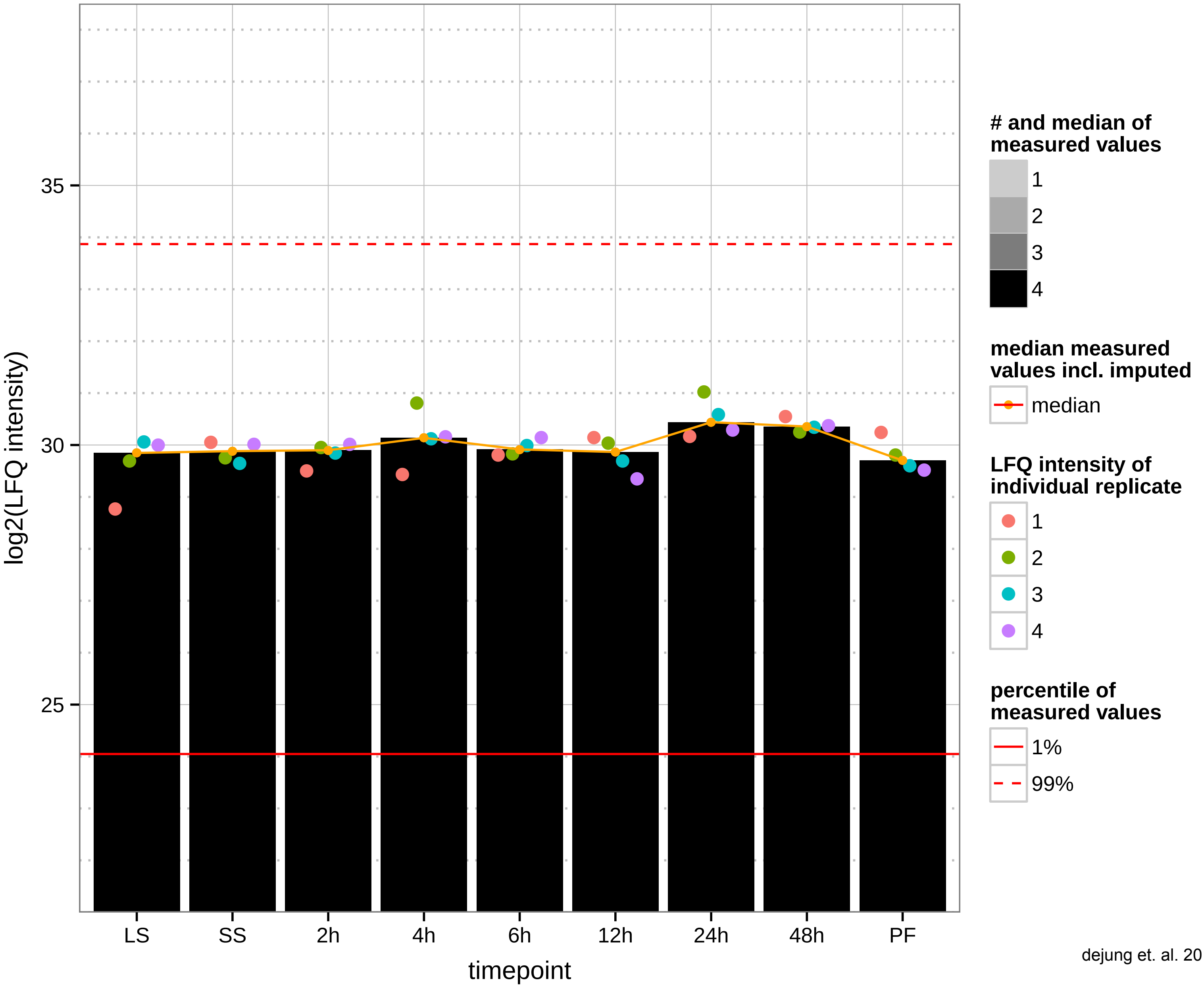
60S ribosomal protein L22
Tb927.10.9800
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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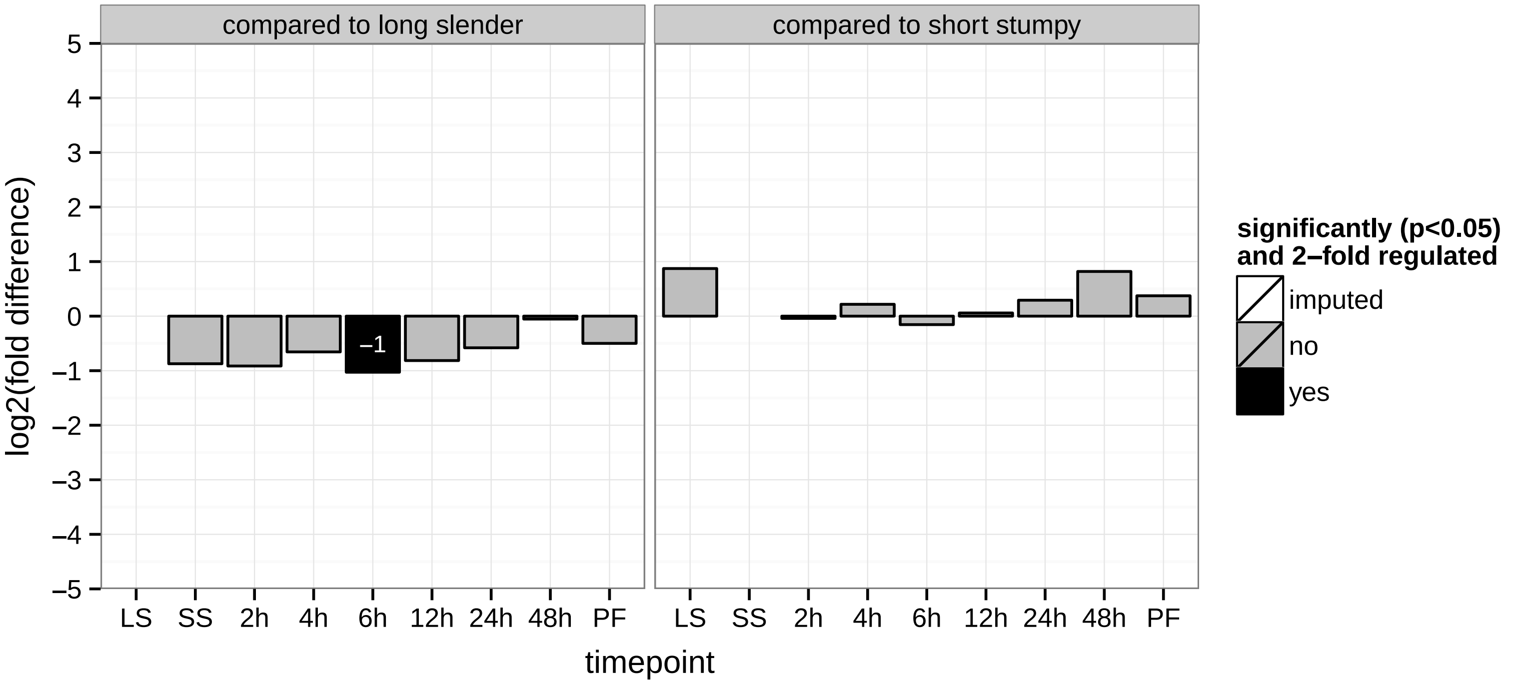
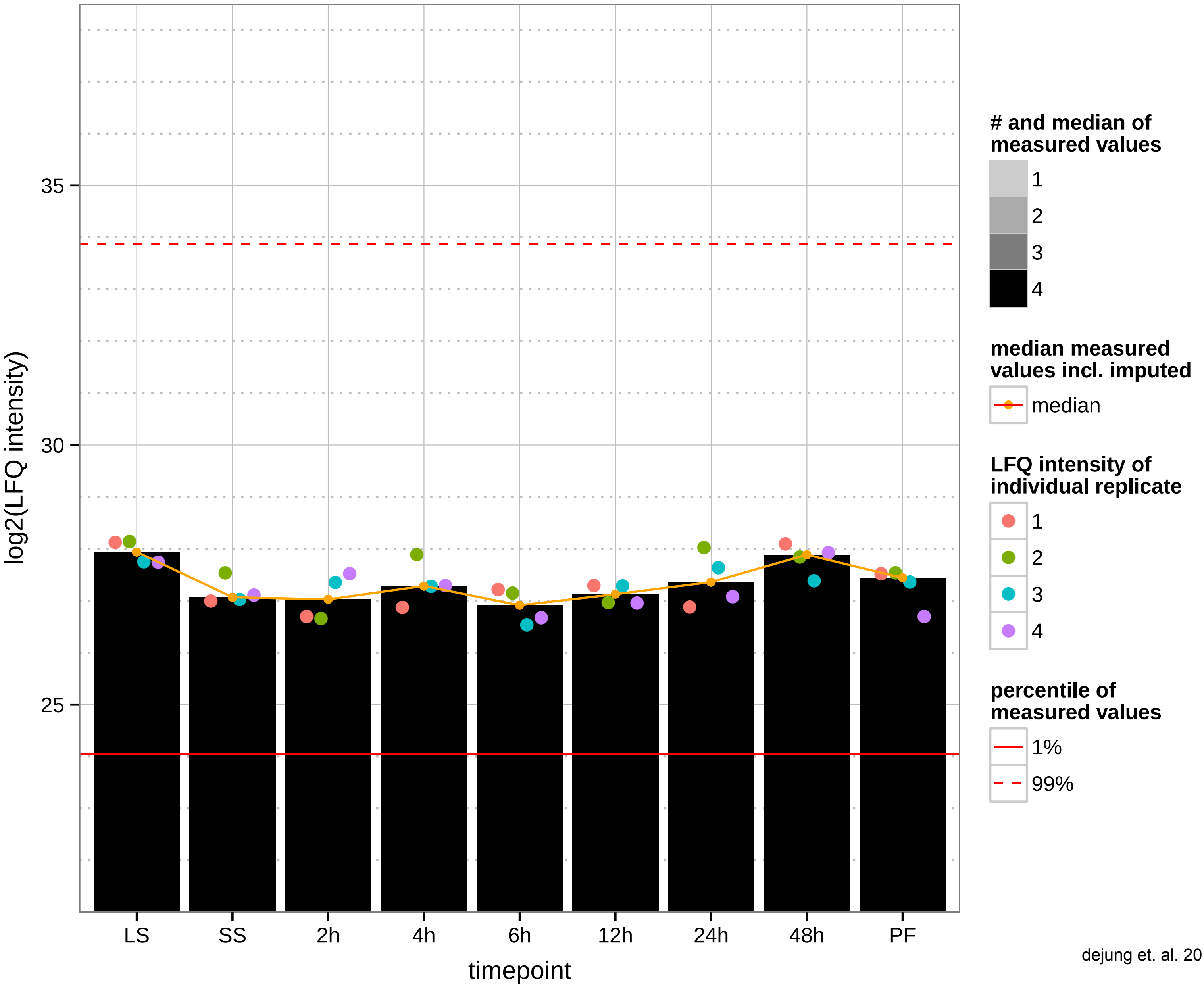
chaperone protein DNAj, putative
Tb927.10.9840
AGOF: heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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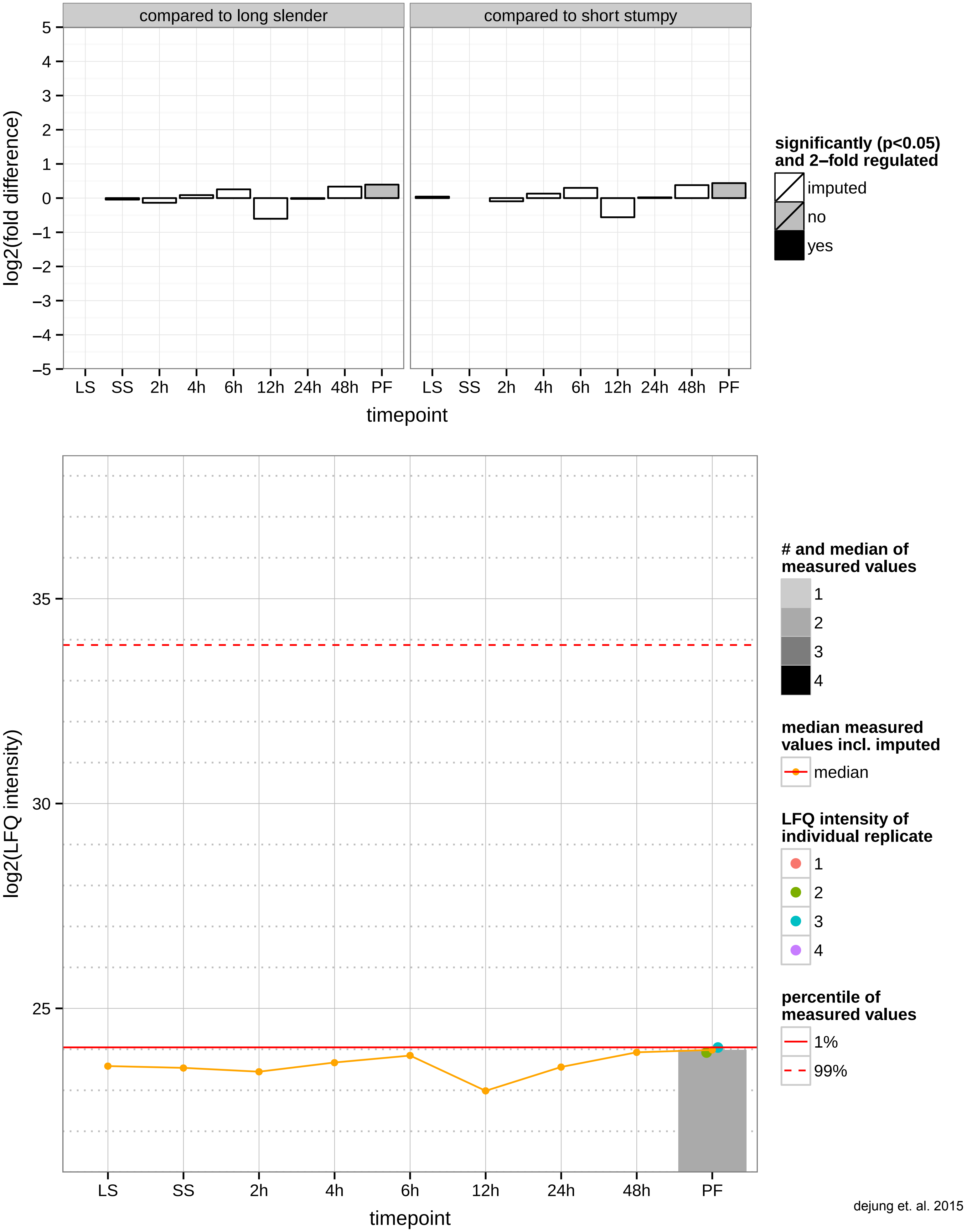
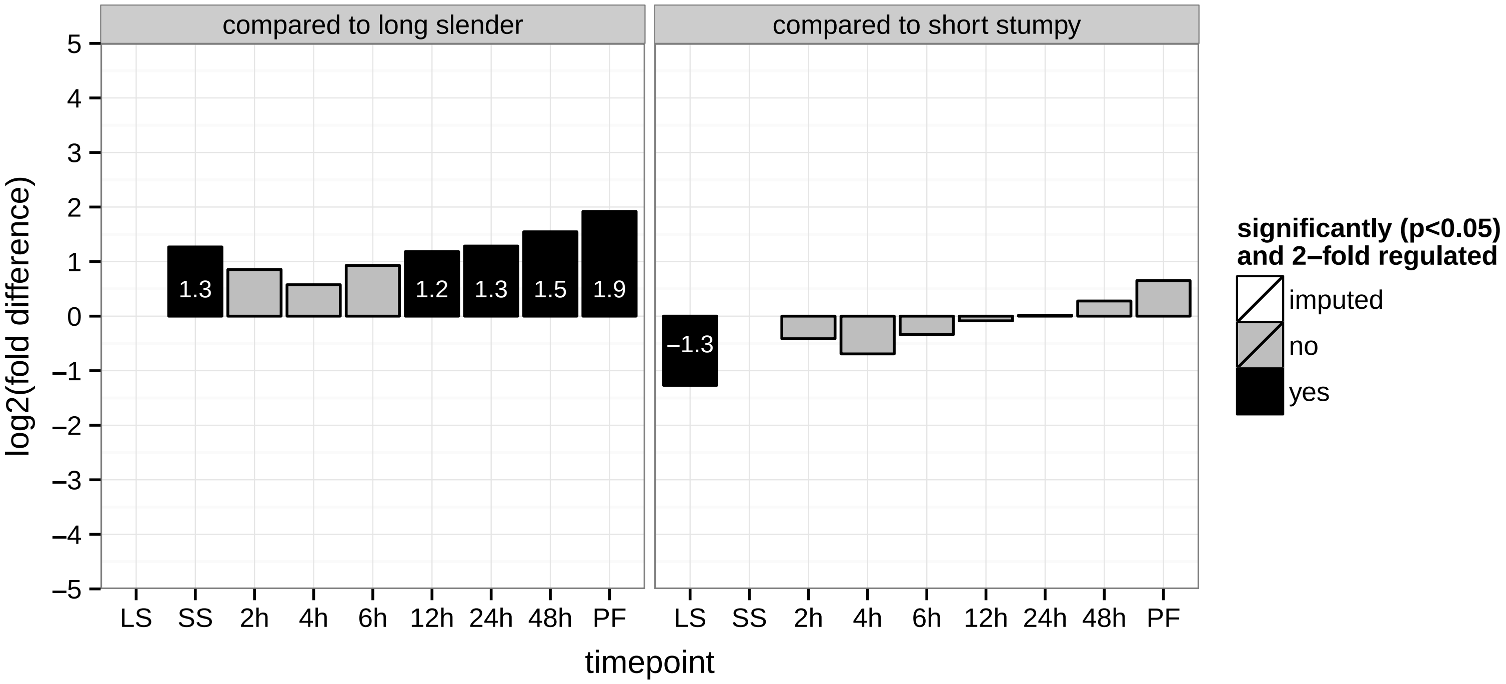
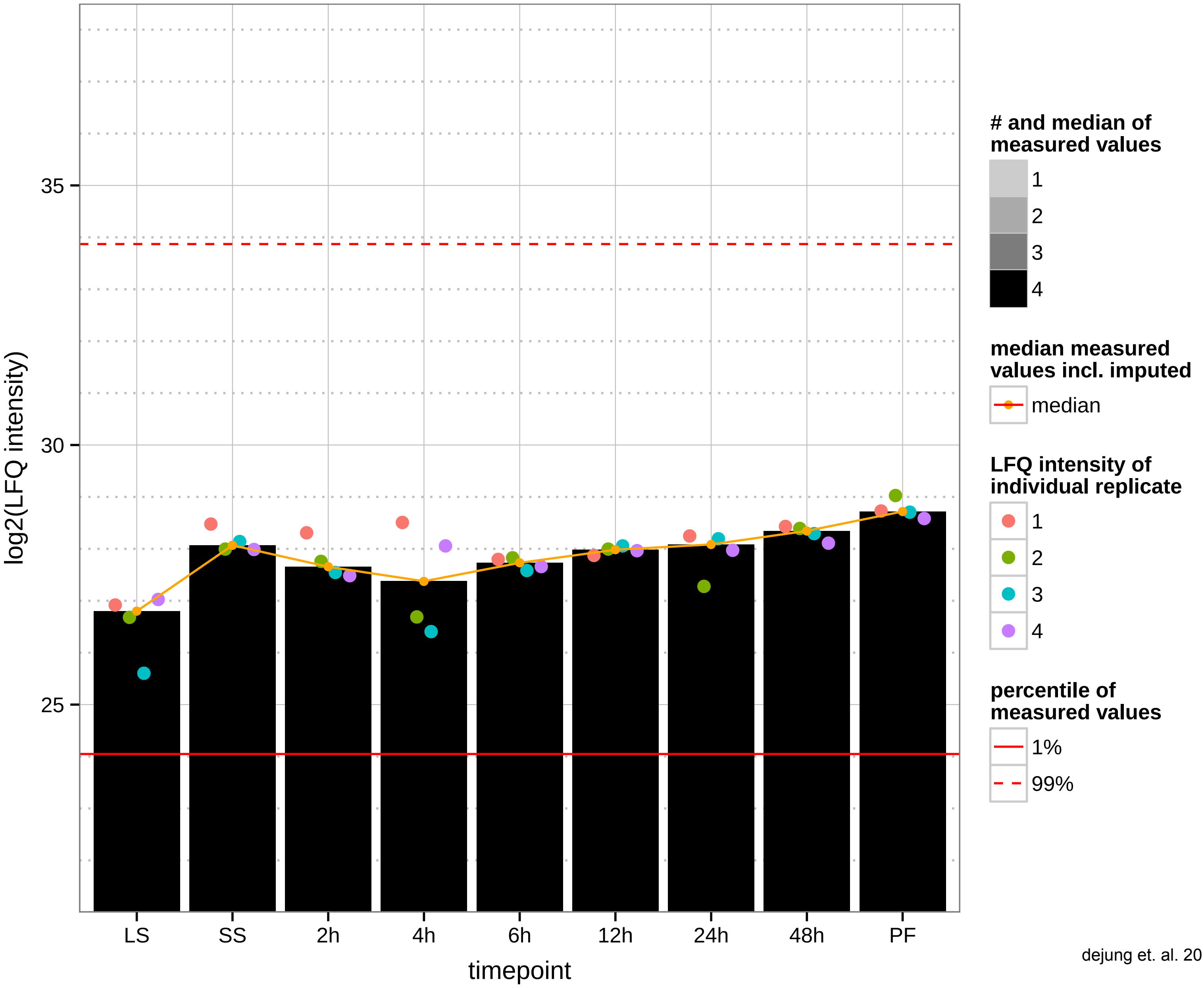
Mitochondrial N(5)–glutamine methyltransferase MTQ1, putative
Tb927.10.9860
AGOF: S–adenosylmethionine–dependent methyltransferase activity, protein methyltransferase activity
AGOC: mitochondrion
AGOP: protein methylation, translational readthrough
PGOF: protein methyltransferase activity
PGOC: null
PGOP: protein methylation



hypothetical protein, conserved
Tb927.10.9890
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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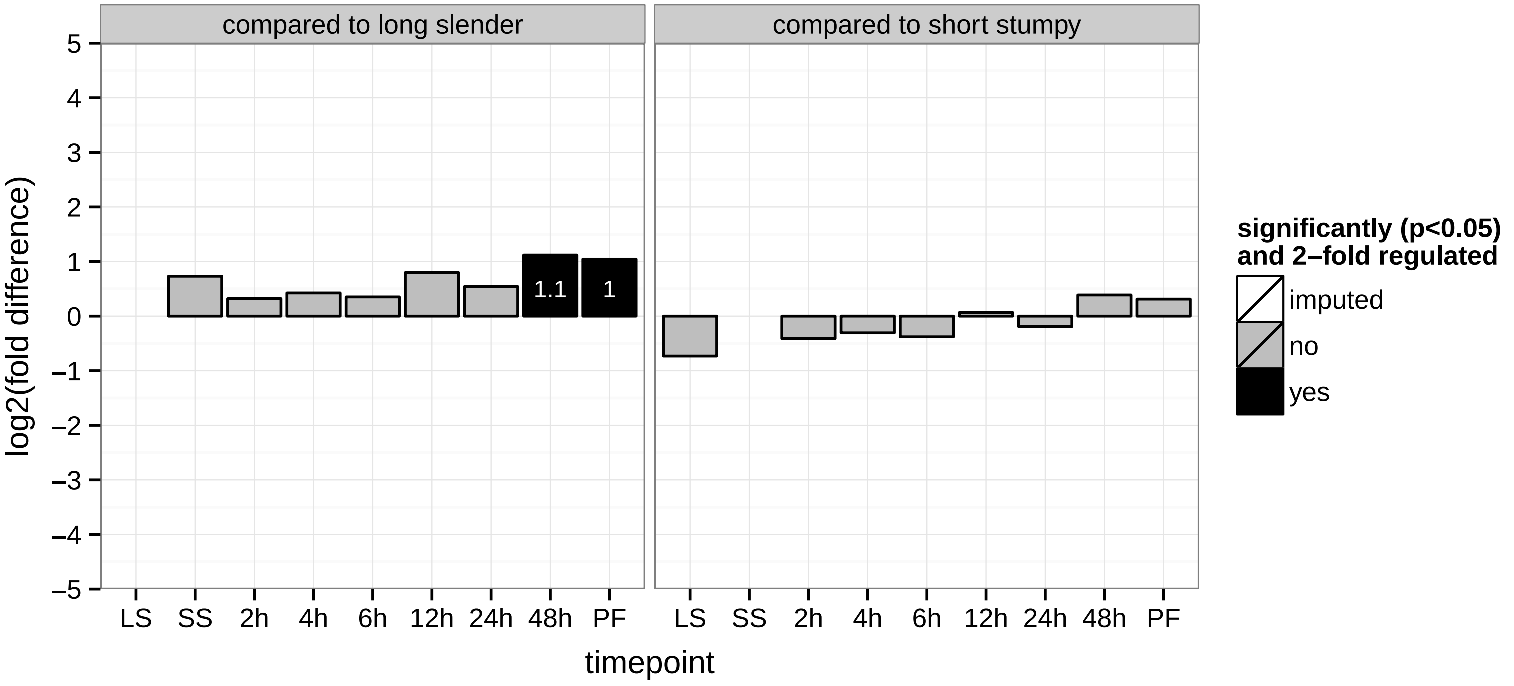
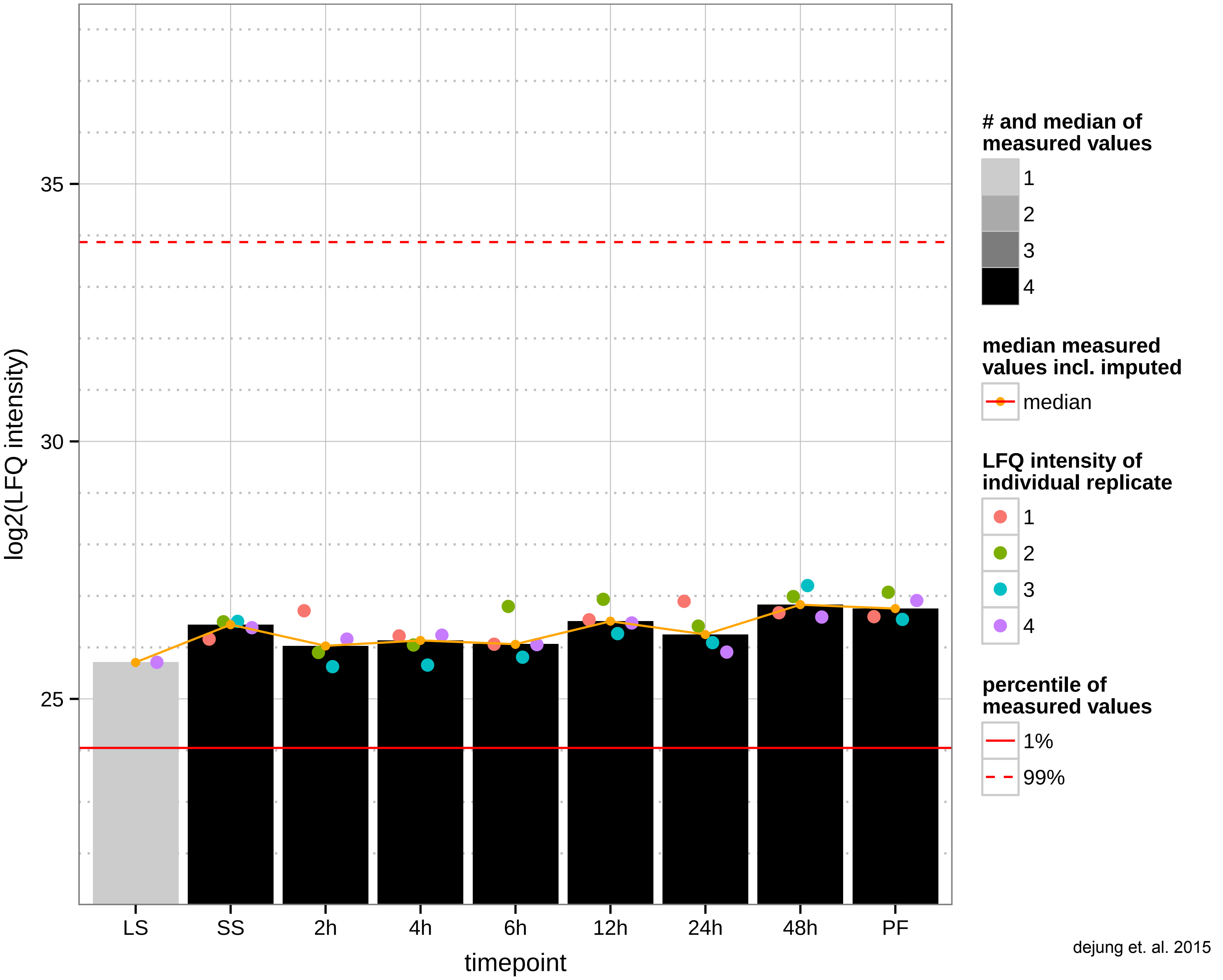
ABC1 protein, putative
Tb927.10.9900
AGOF: protein kinase activity
AGOC: null
AGOP: null
PGOF: transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: null





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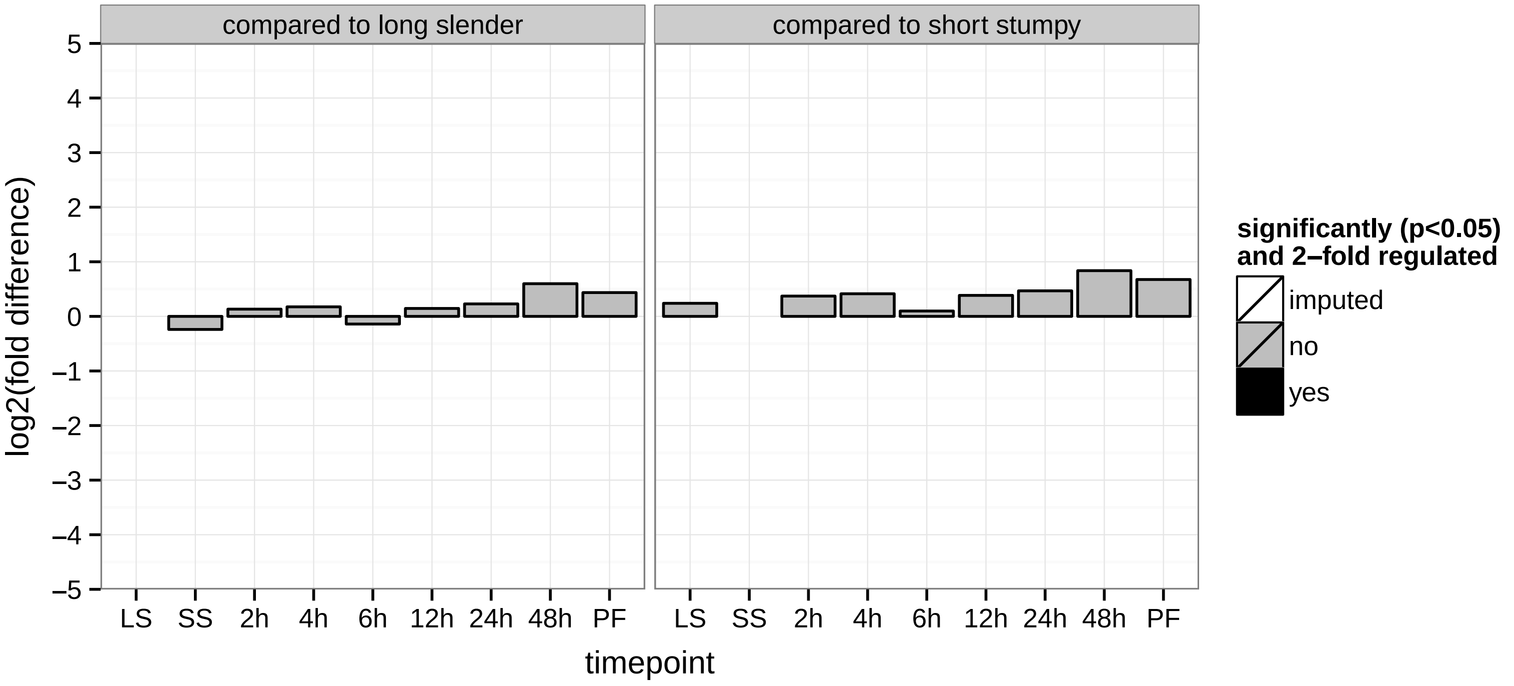
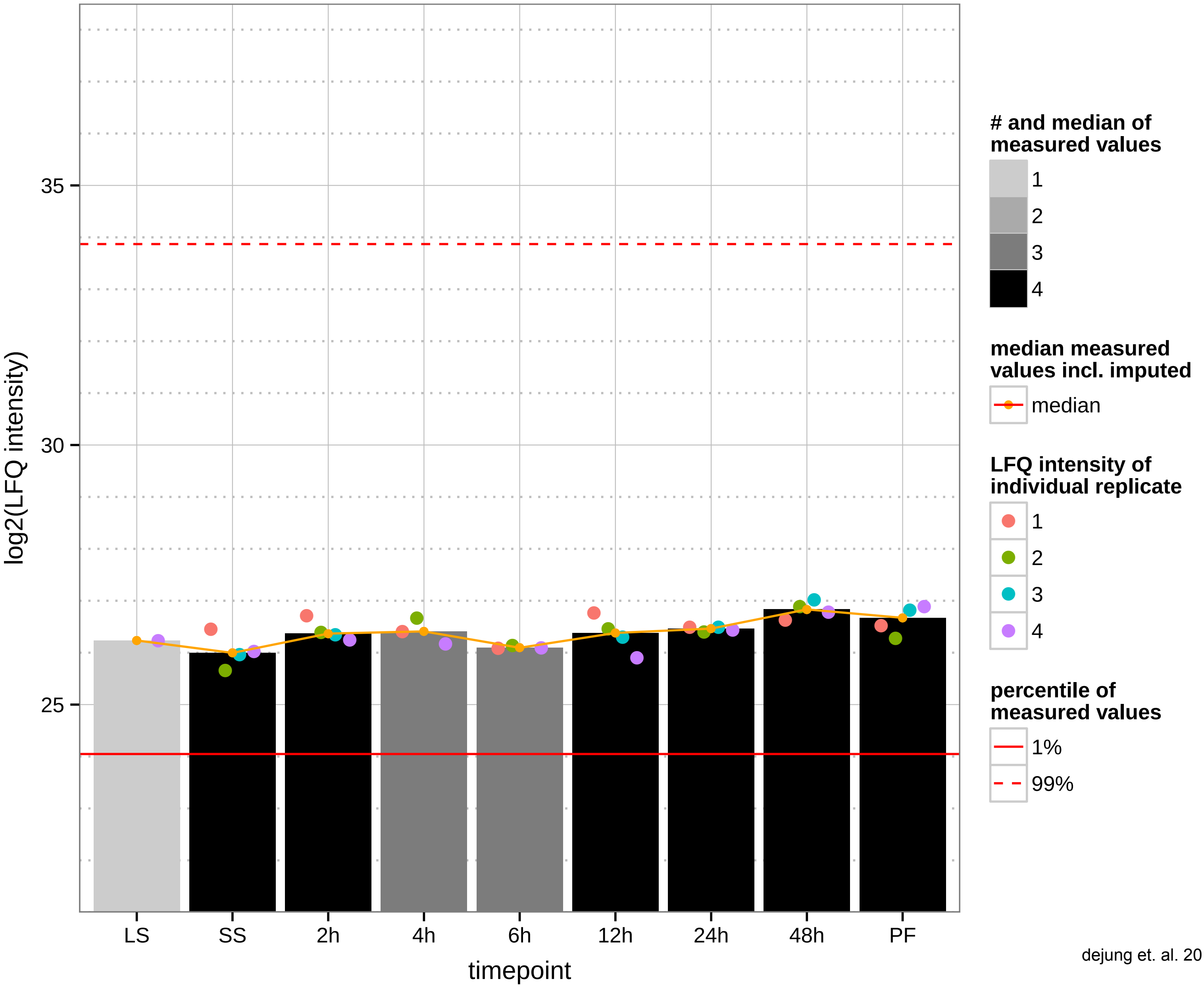
hypothetical protein, conserved
Tb927.10.9910
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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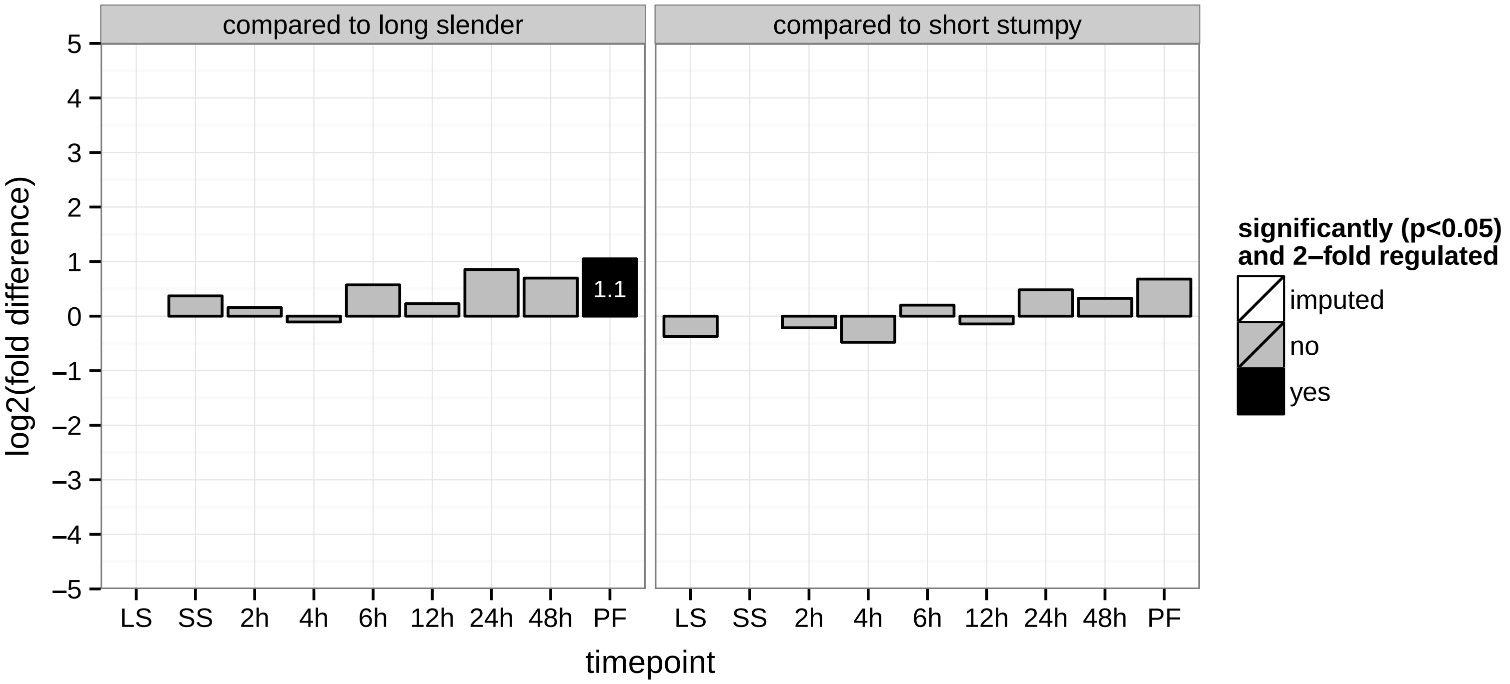
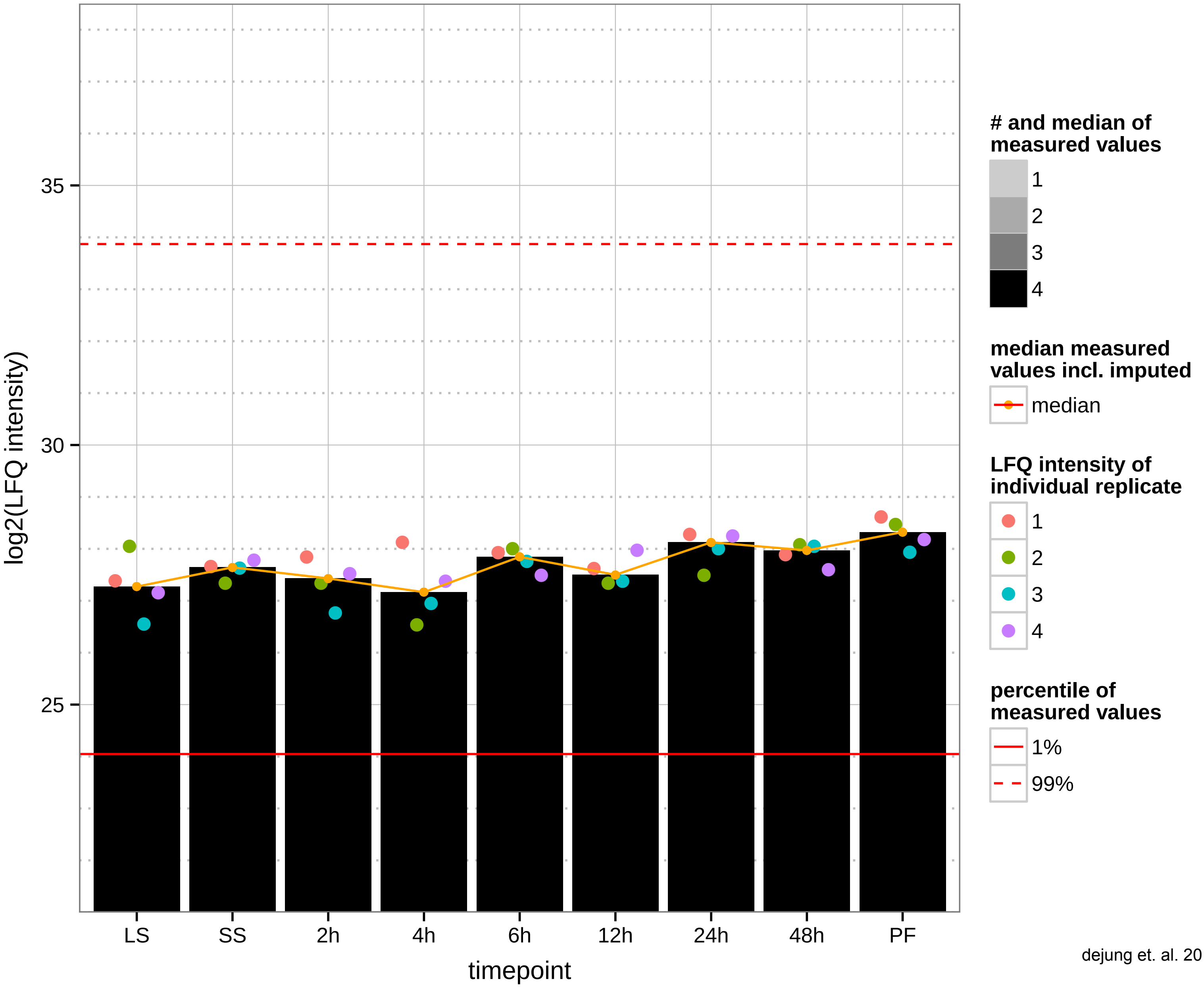
hypothetical protein, conserved
Tb927.10.9970
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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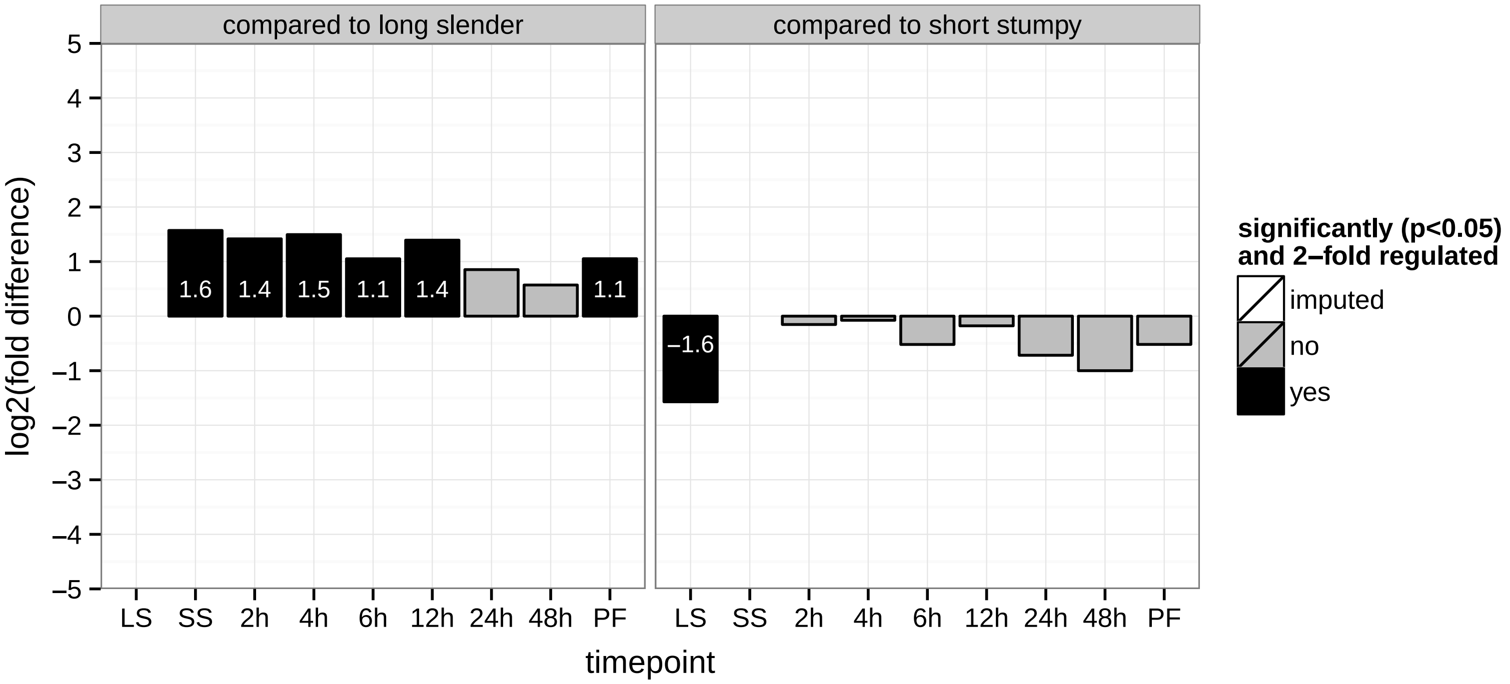
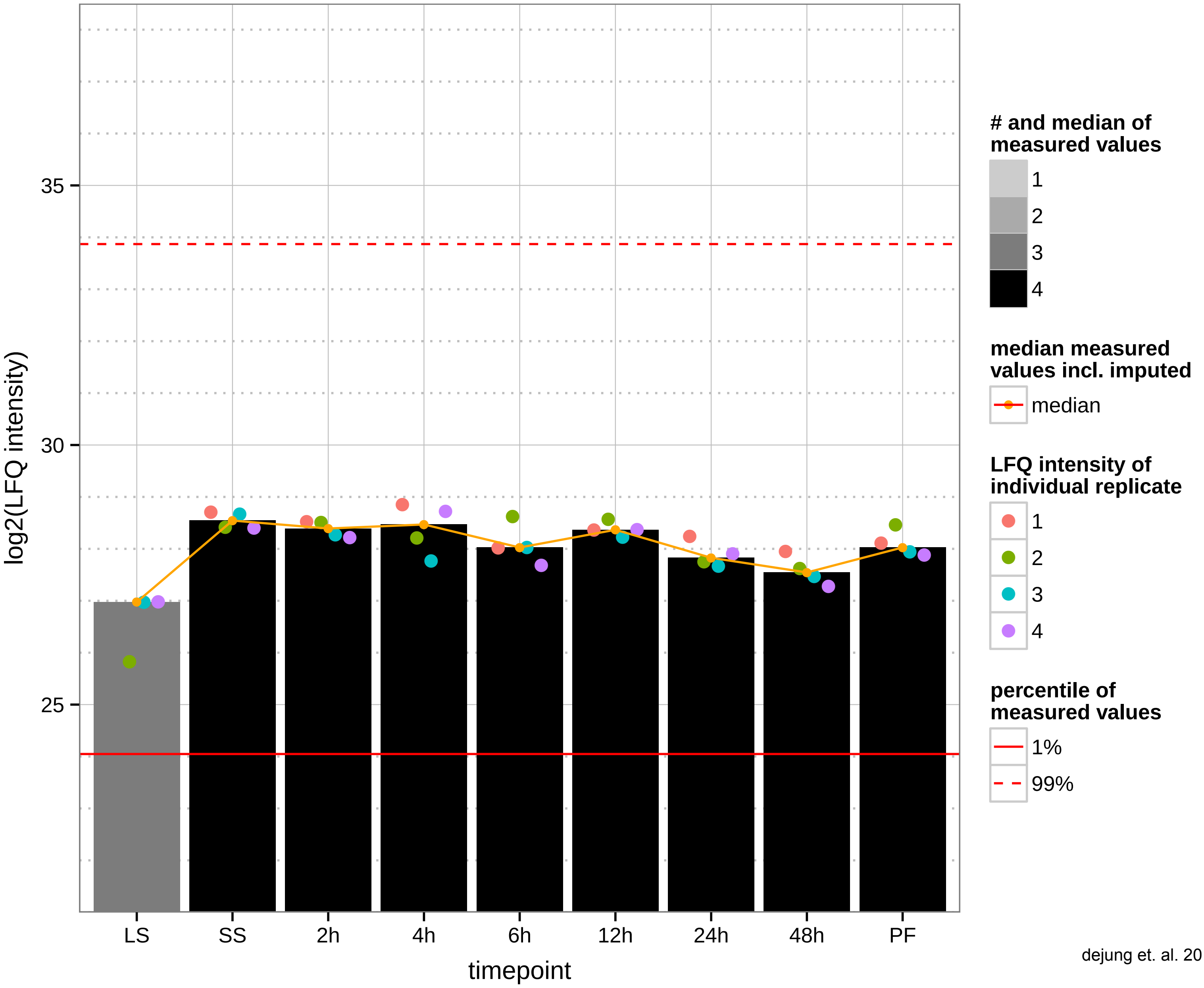
short–chain dehydrogenase, putative
Tb927.11.10020
AGOF: oxidoreductase activity
AGOC: integral to membrane
AGOP: metabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process





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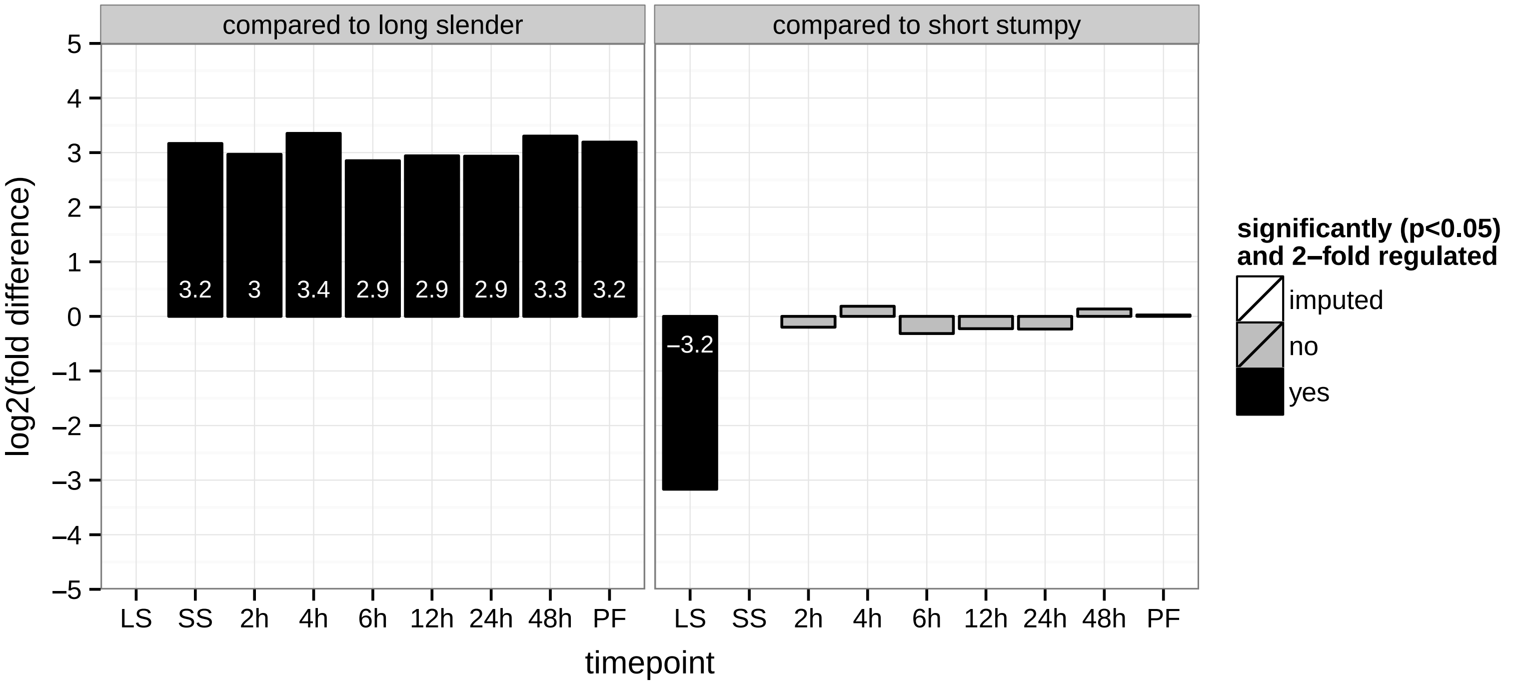
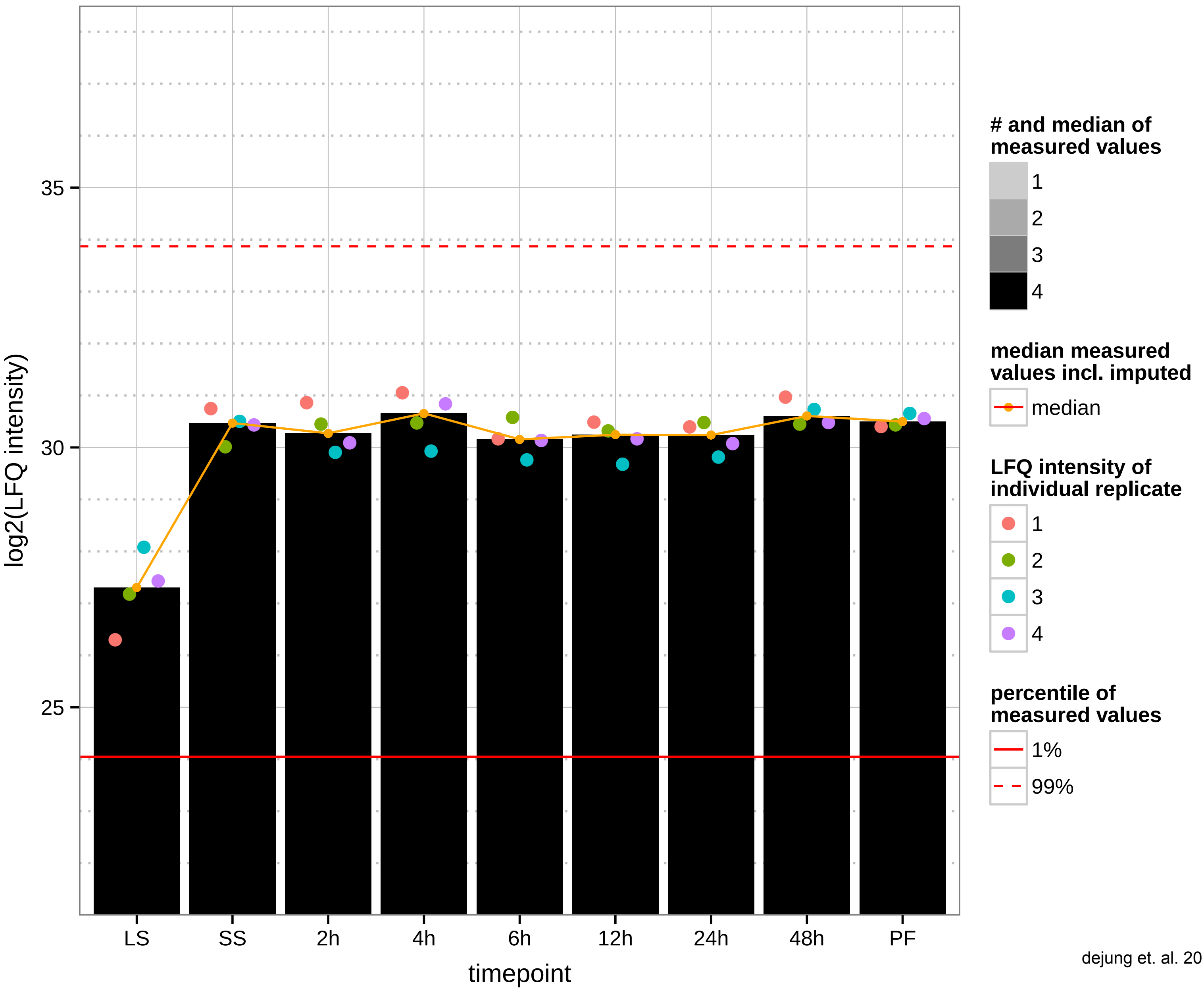
Biotin-–acetyl–CoA–carboxylase ligase, putative, biotin-–protein ligase
Tb927.11.10060
AGOF: biotin–[acetyl–CoA–carboxylase] ligase activity
AGOC: null
AGOP: biotin biosynthetic process, cellular protein modification process
PGOF: biotin–[acetyl–CoA–carboxylase] ligase activity, catalytic activity
PGOC: null
PGOP: cellular protein modification process





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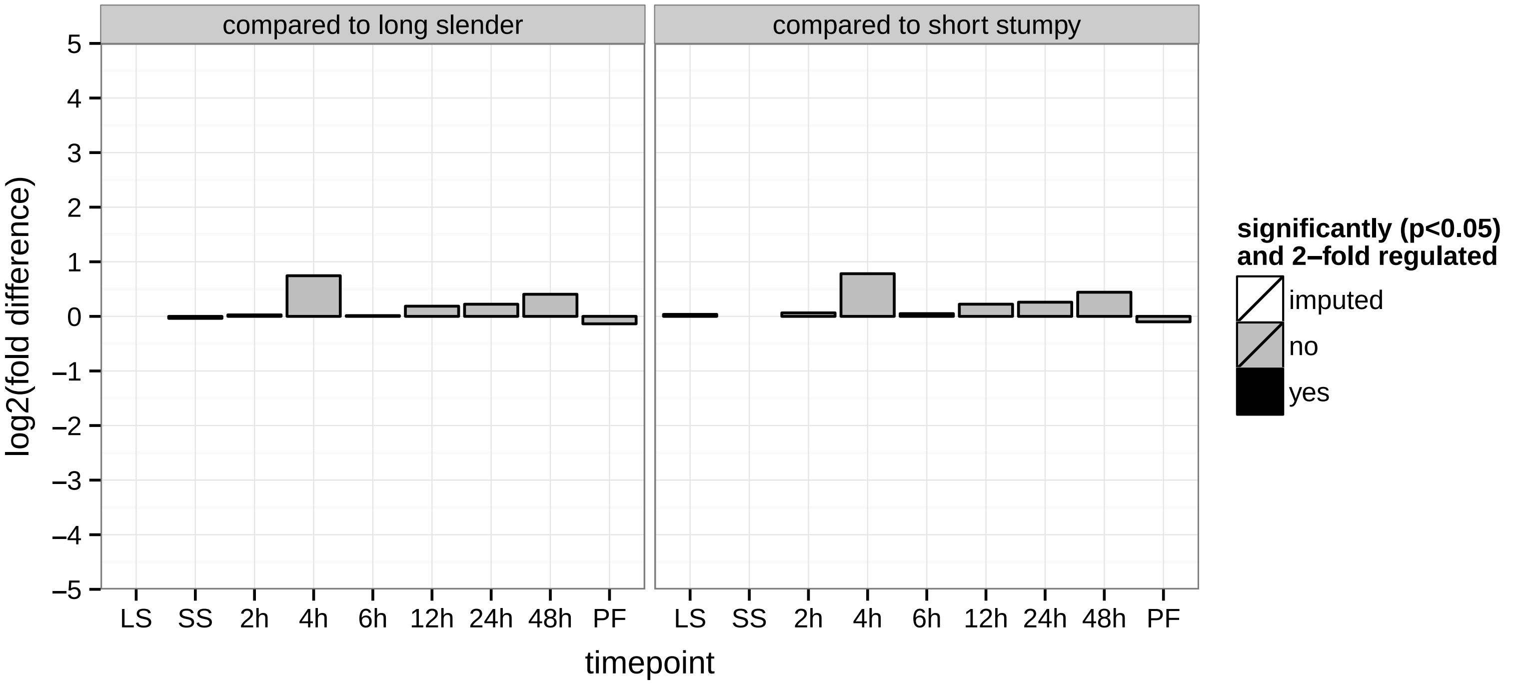
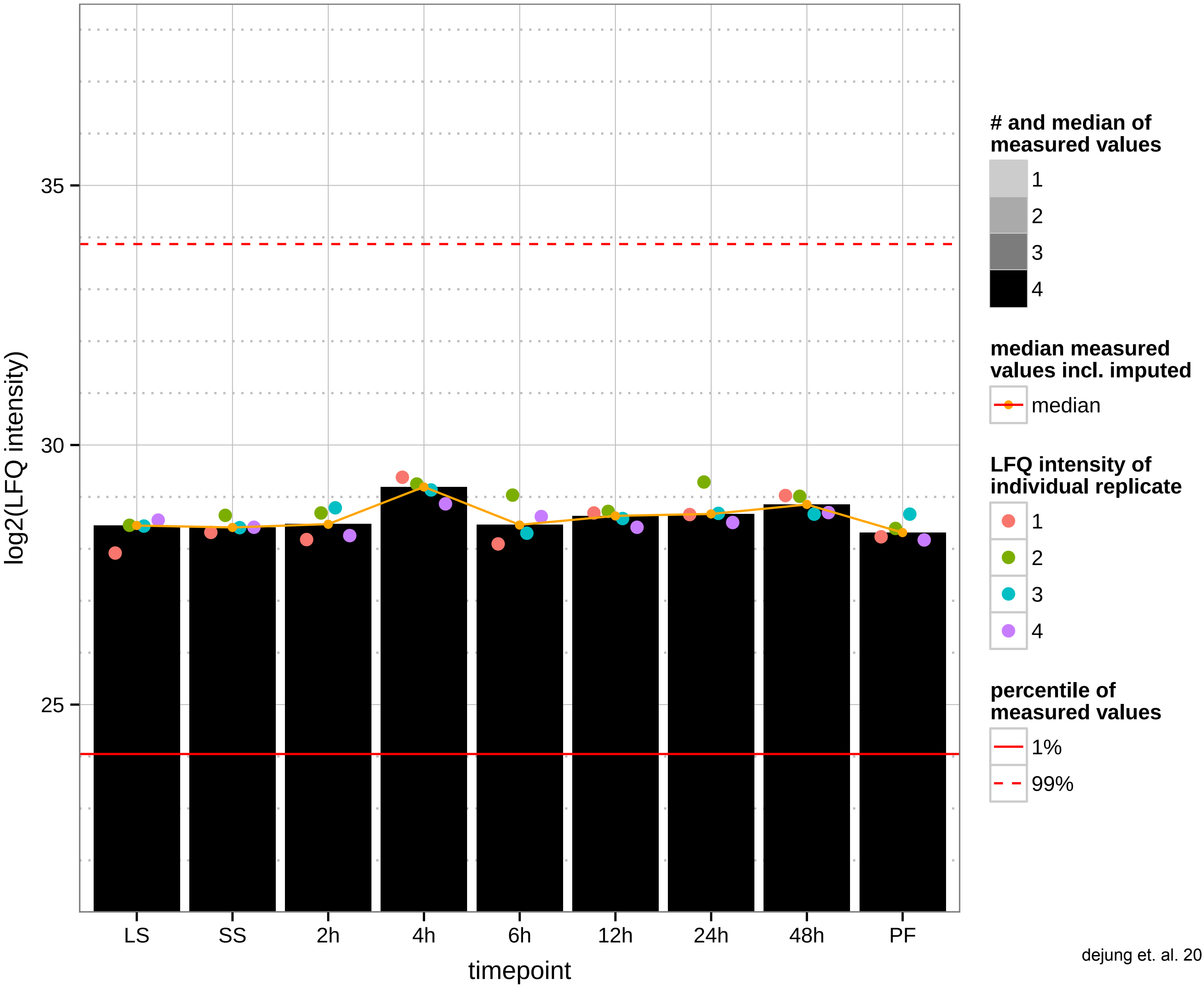
hypothetical protein, conserved
Tb927.11.10070
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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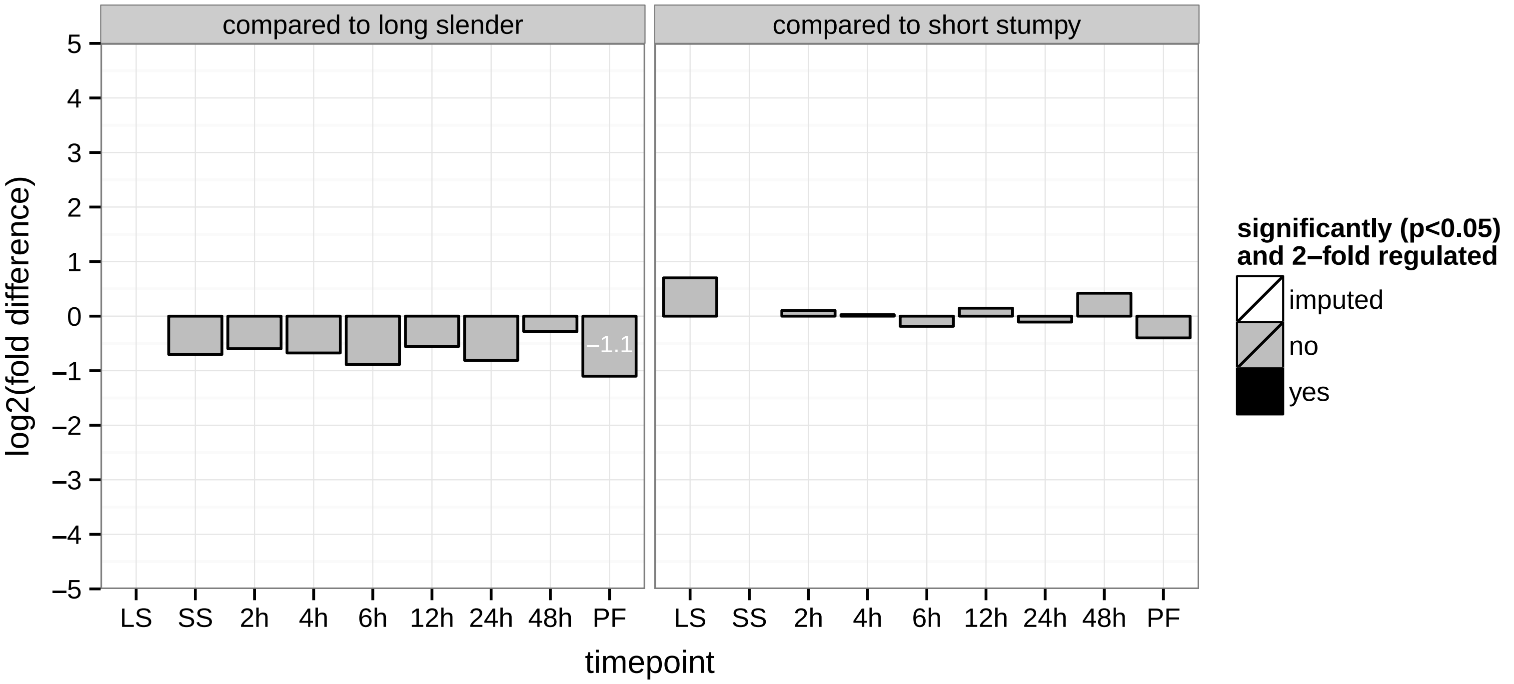
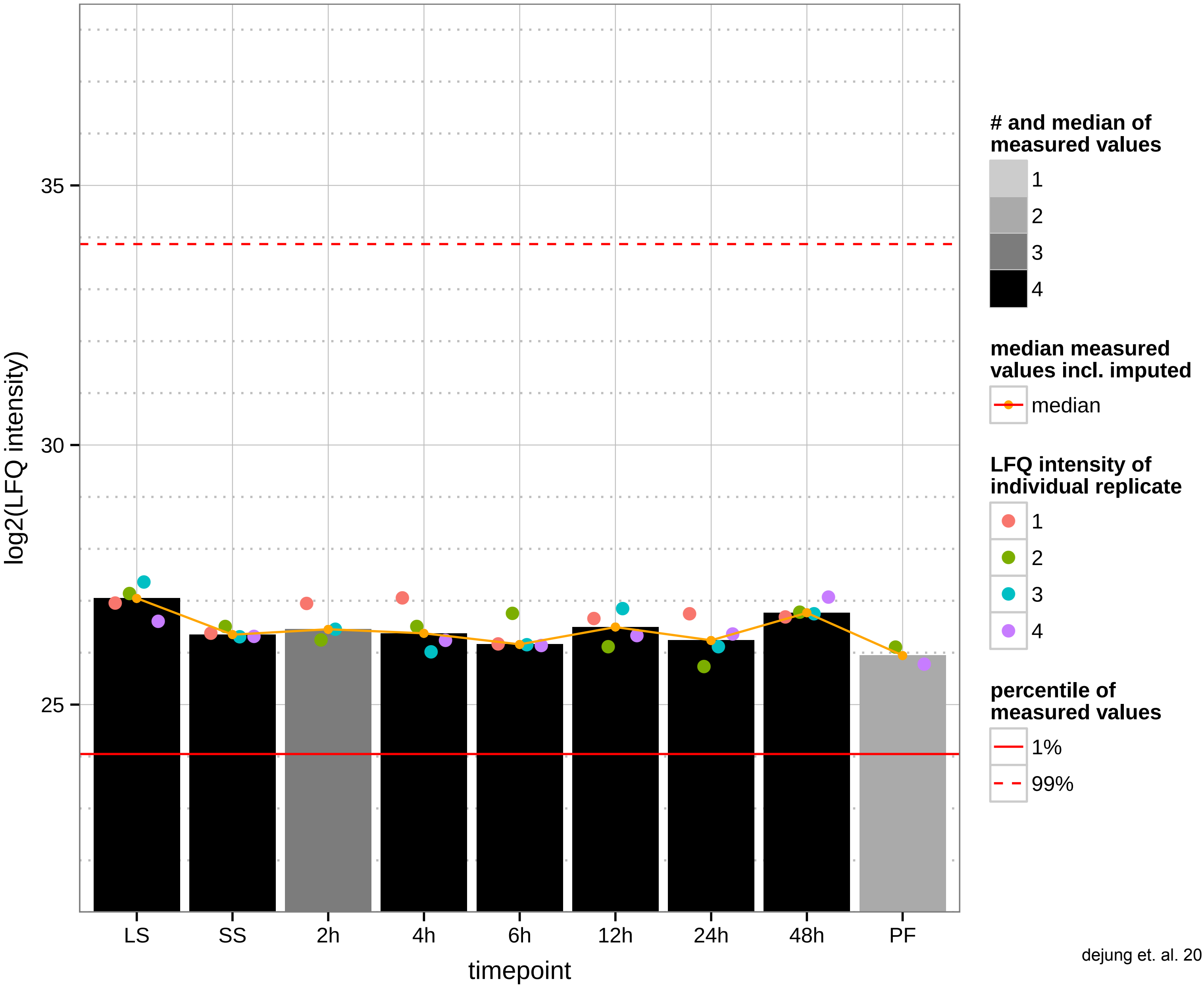
hypothetical protein, conserved
Tb927.11.10090
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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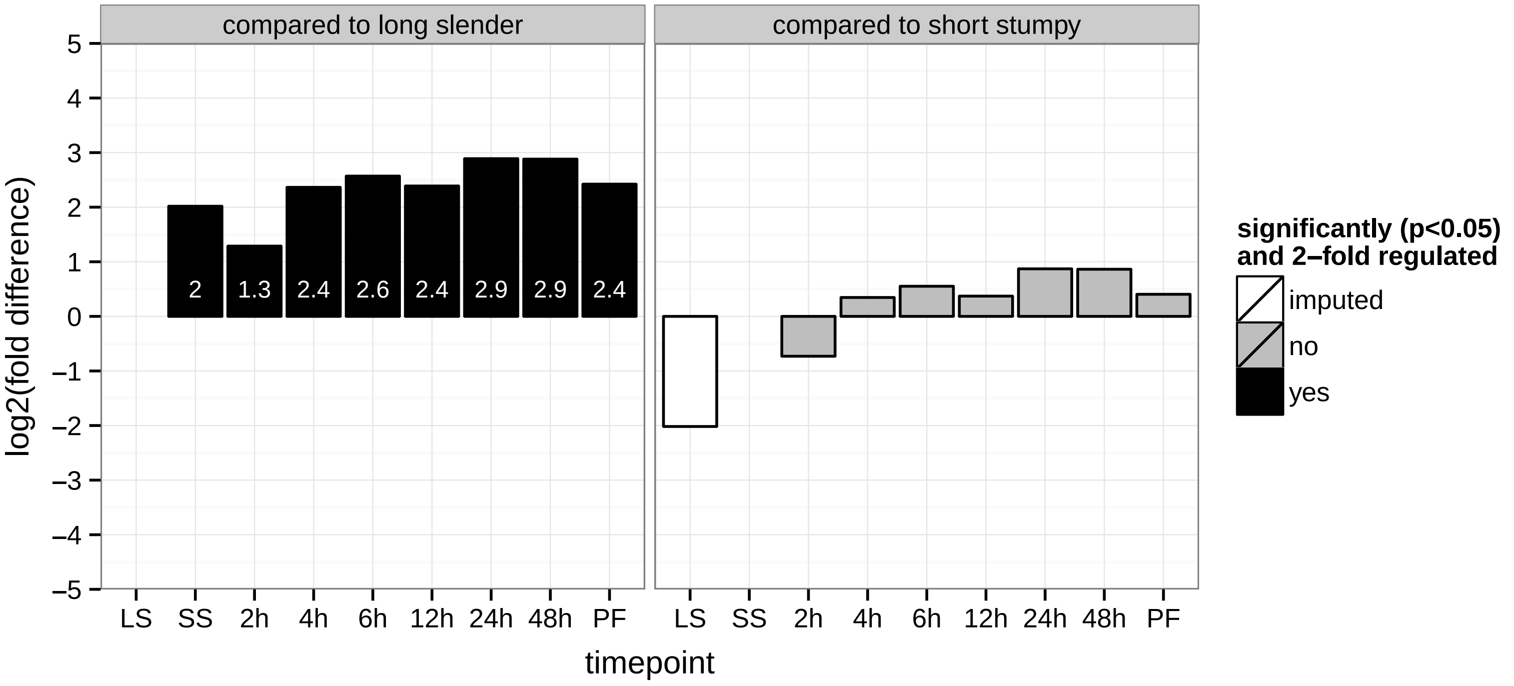
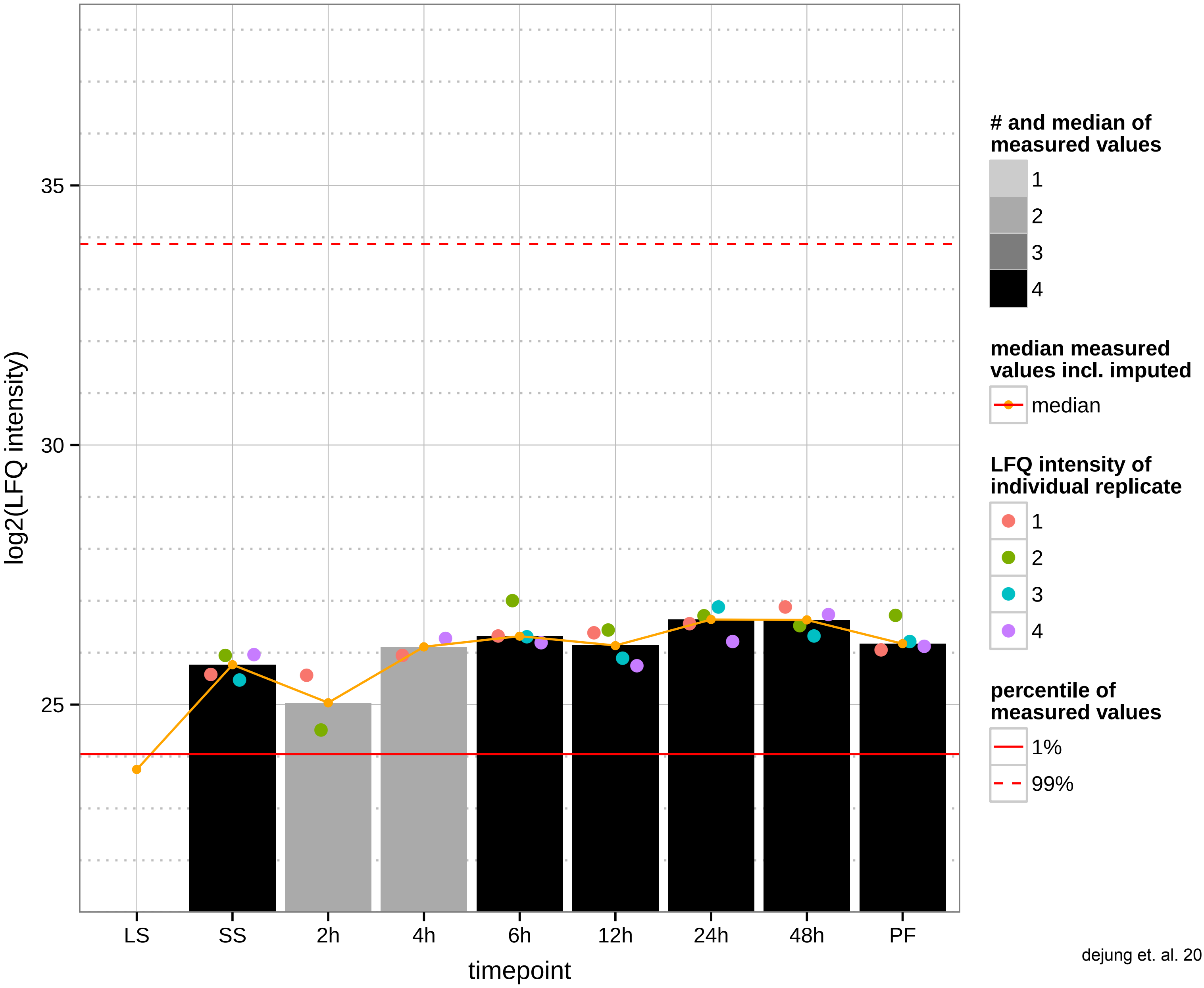
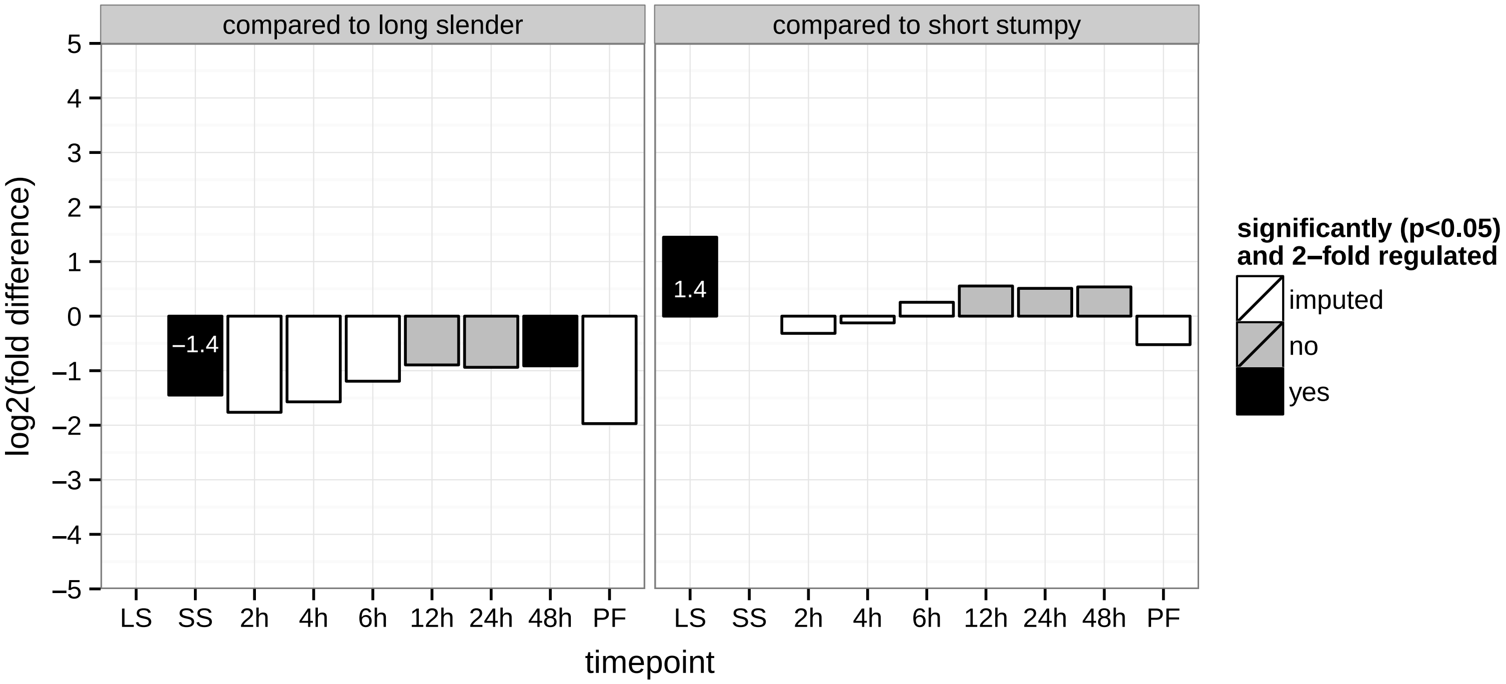
chaperone protein DNAj, putative
Tb927.11.1010
AGOF: heat shock protein binding, unfolded protein binding
AGOC: integral to membrane, mitochondrial inner membrane, mitochondrion
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null

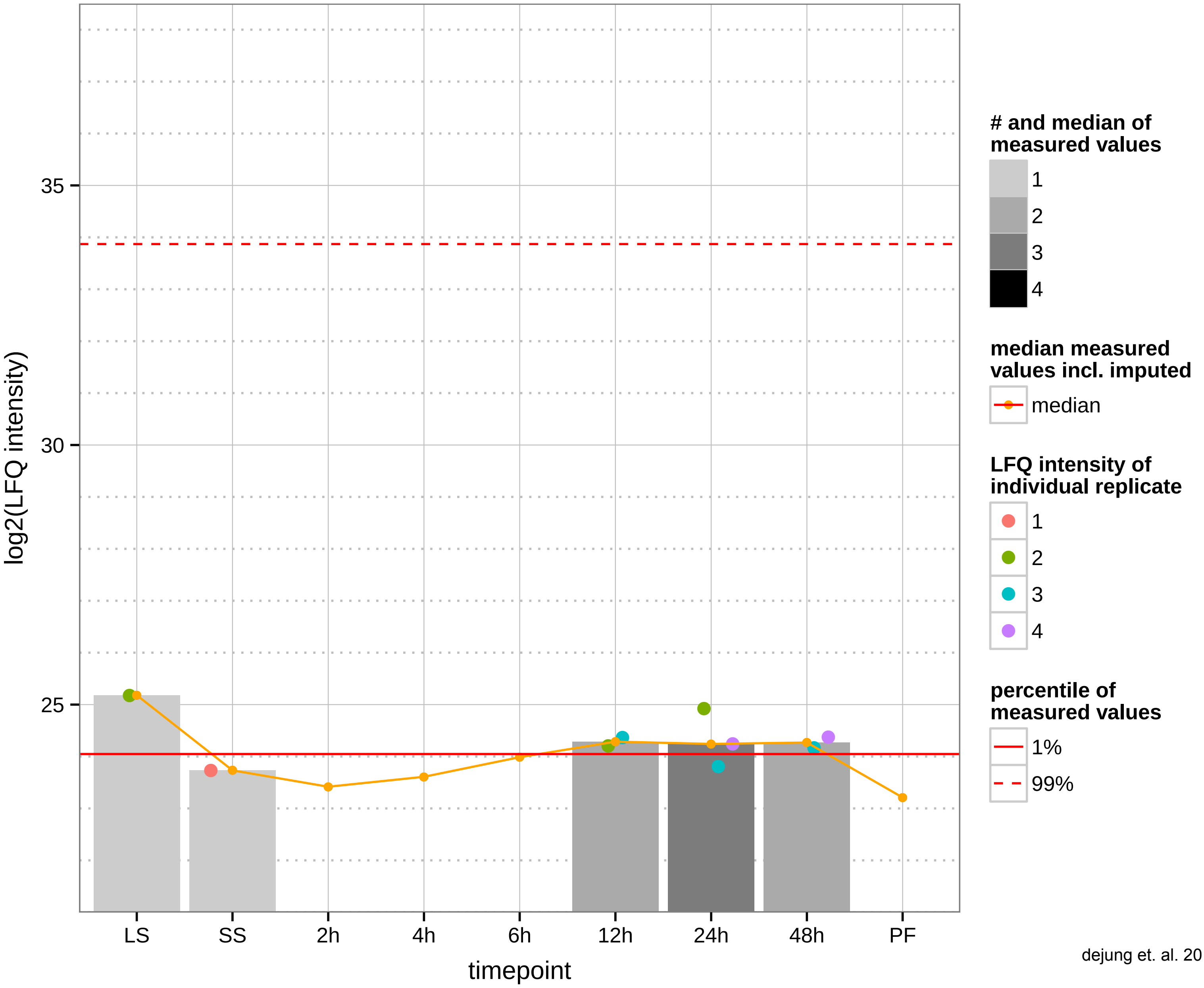




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.10130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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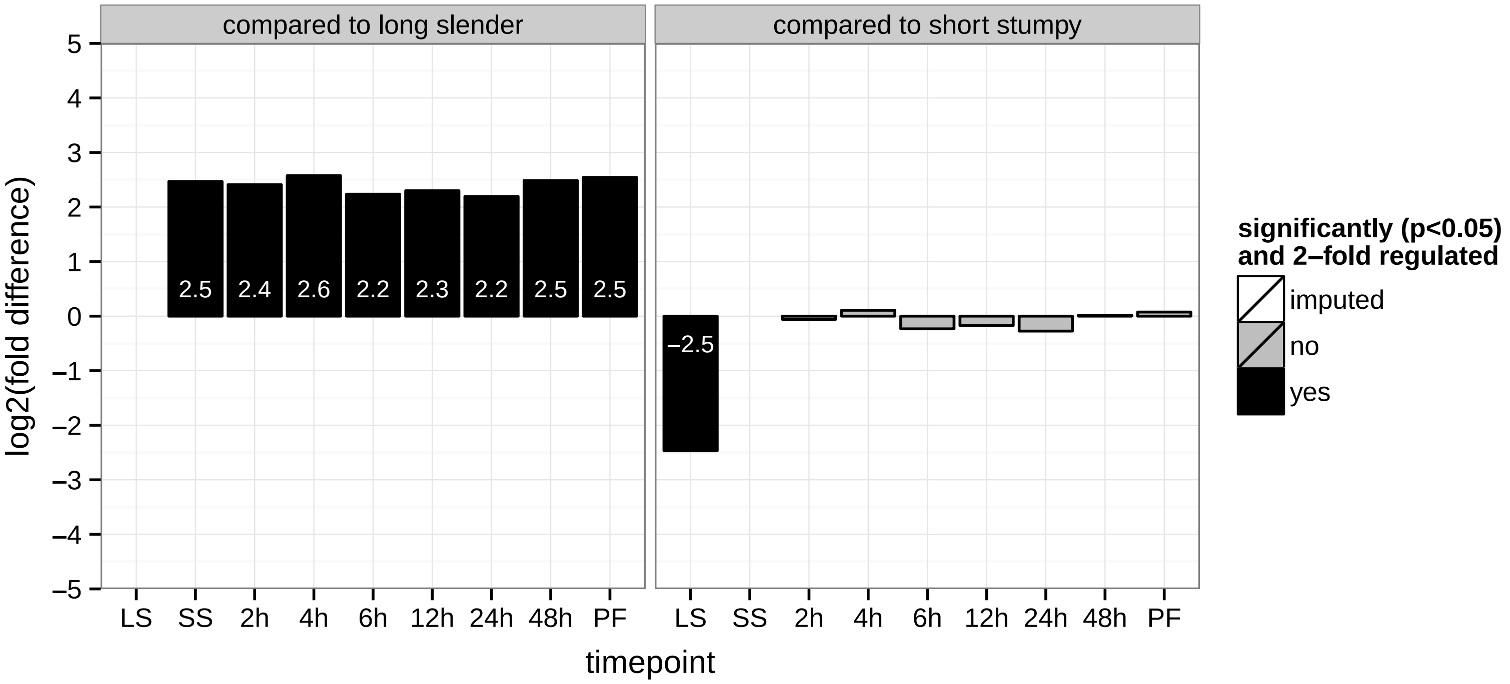
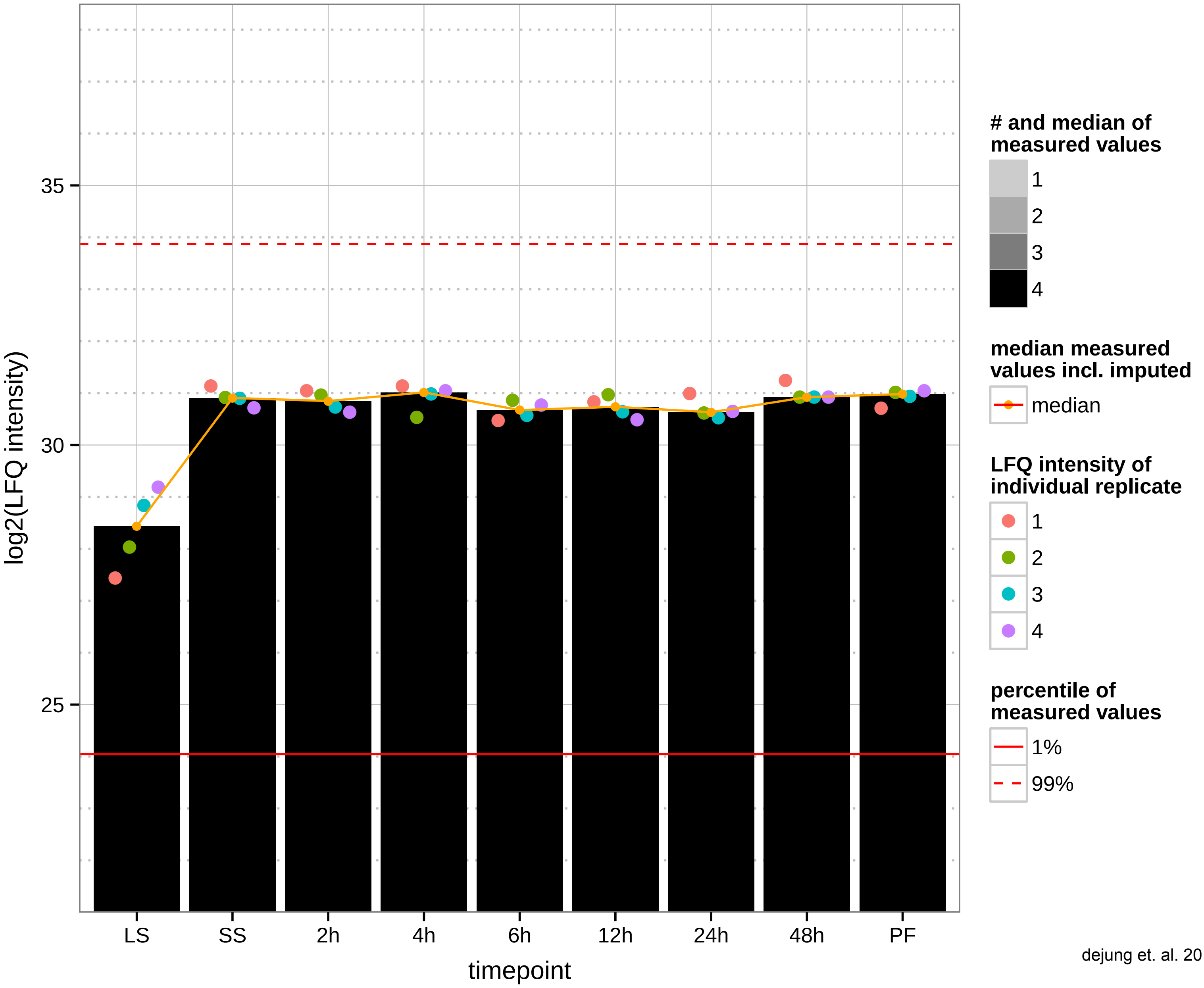
ribokinase, putative
Tb927.11.1020
AGOF: ribokinase activity
AGOC: null
AGOP: D–ribose metabolic process
PGOF: null
PGOC: null
PGOP: null





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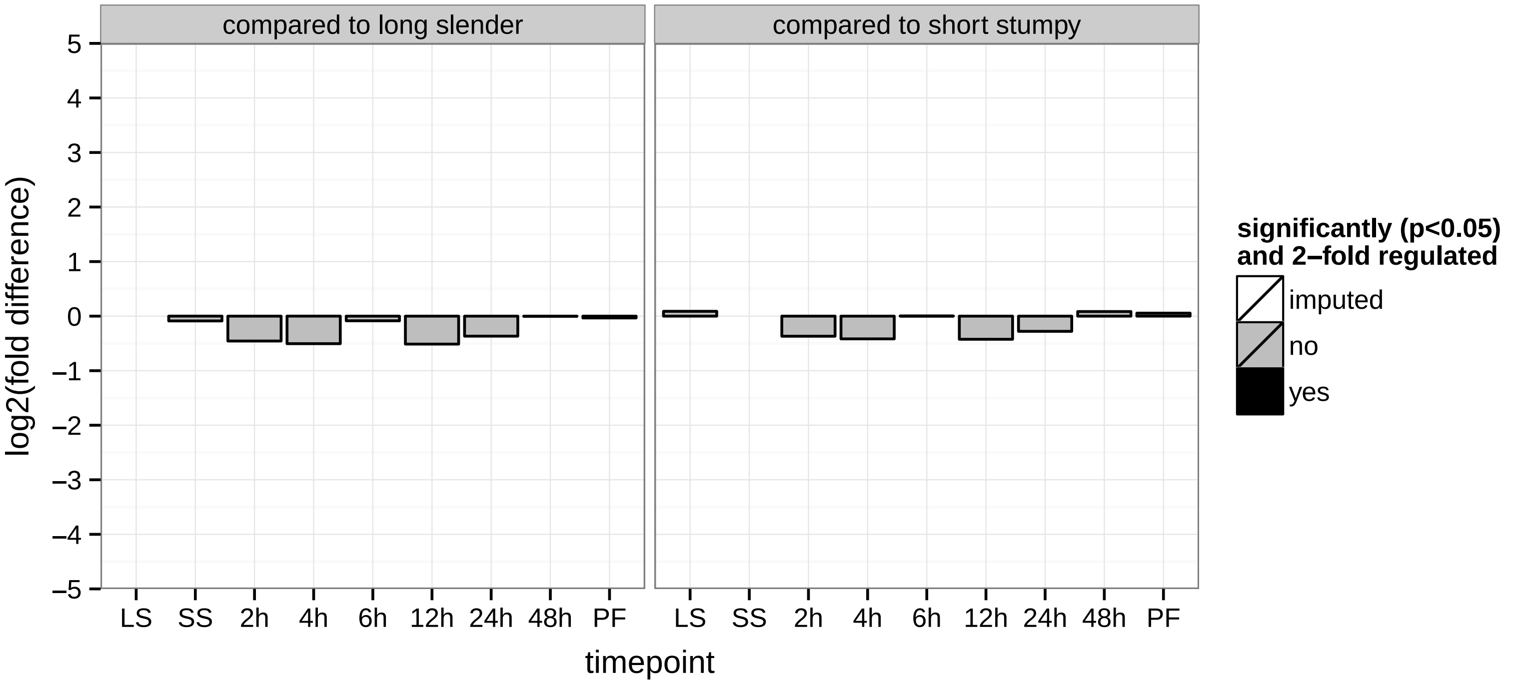
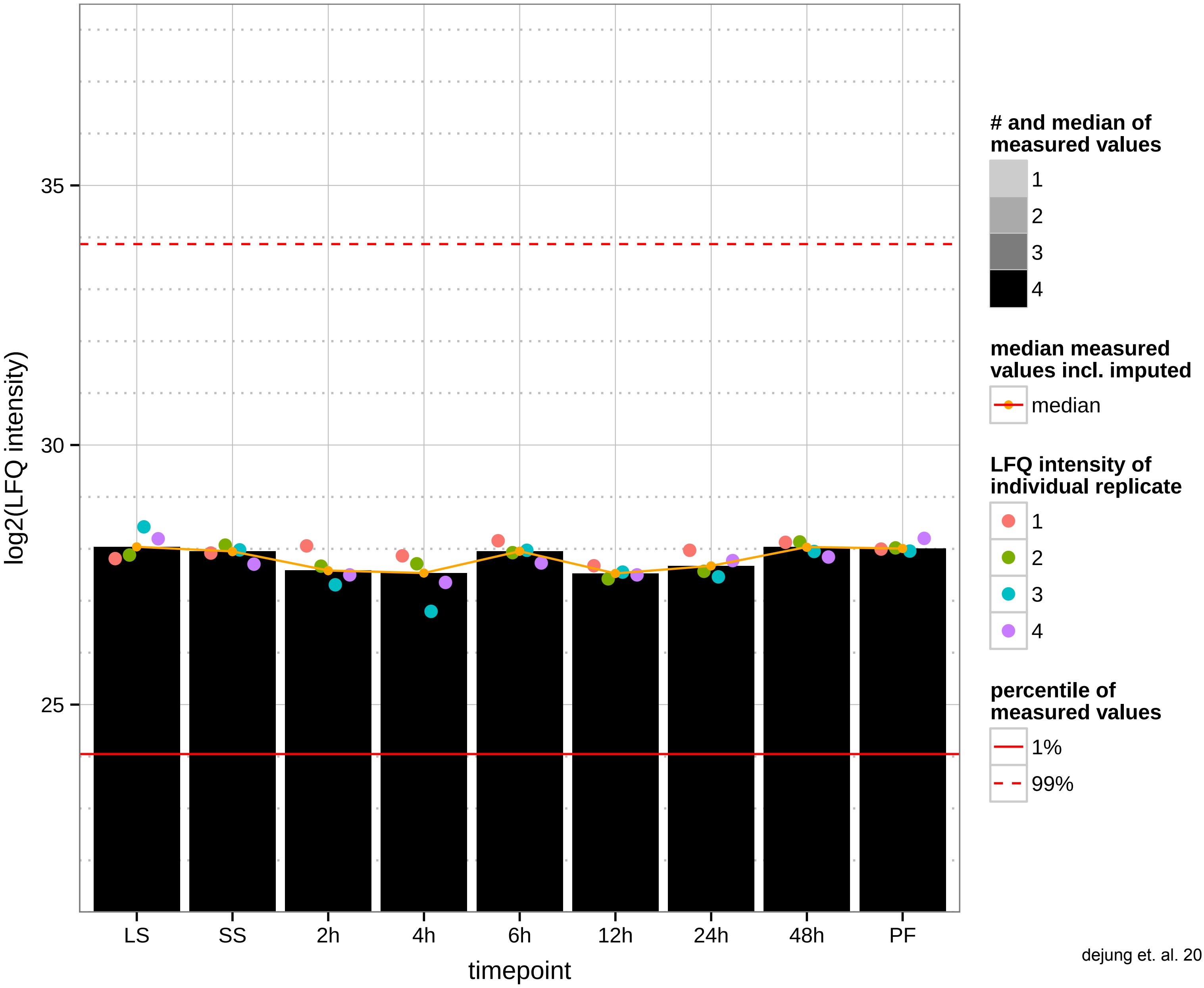
hypothetical protein, conserved
Tb927.11.10200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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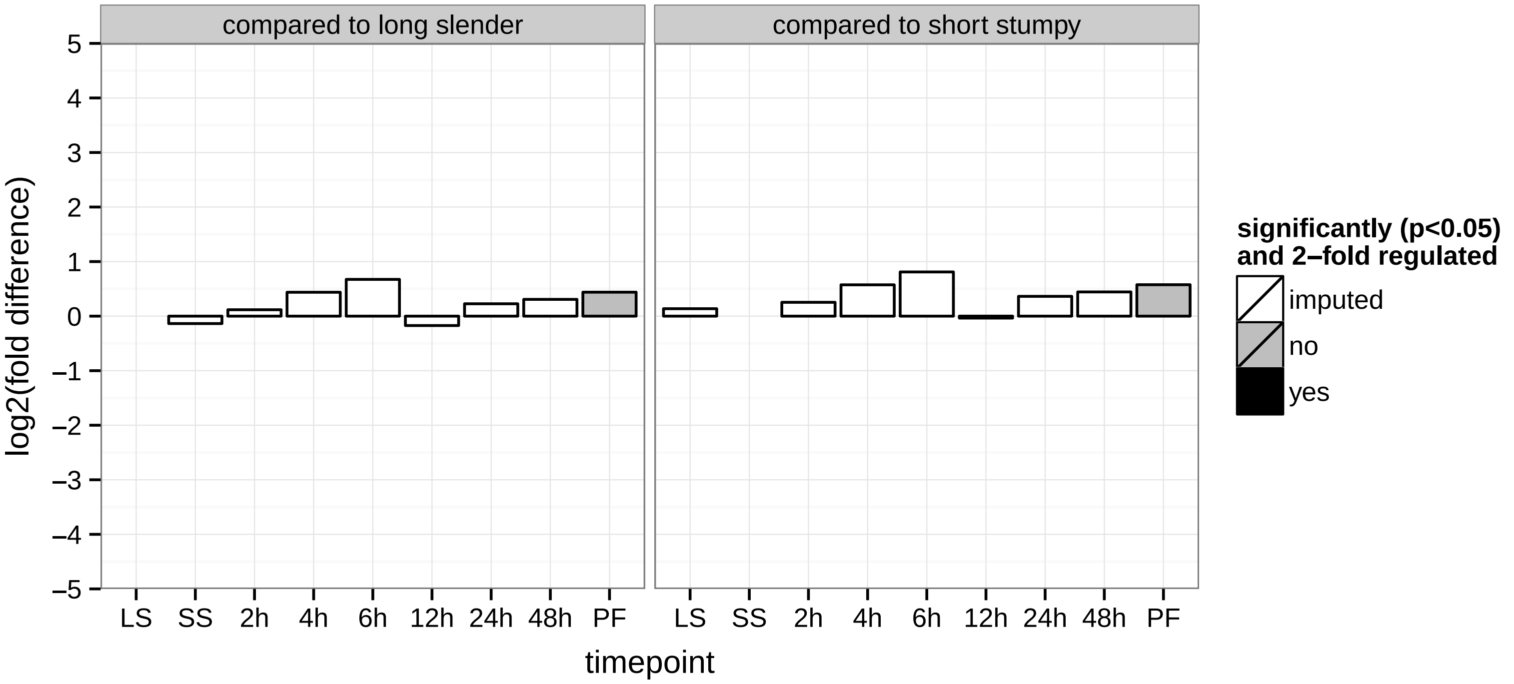
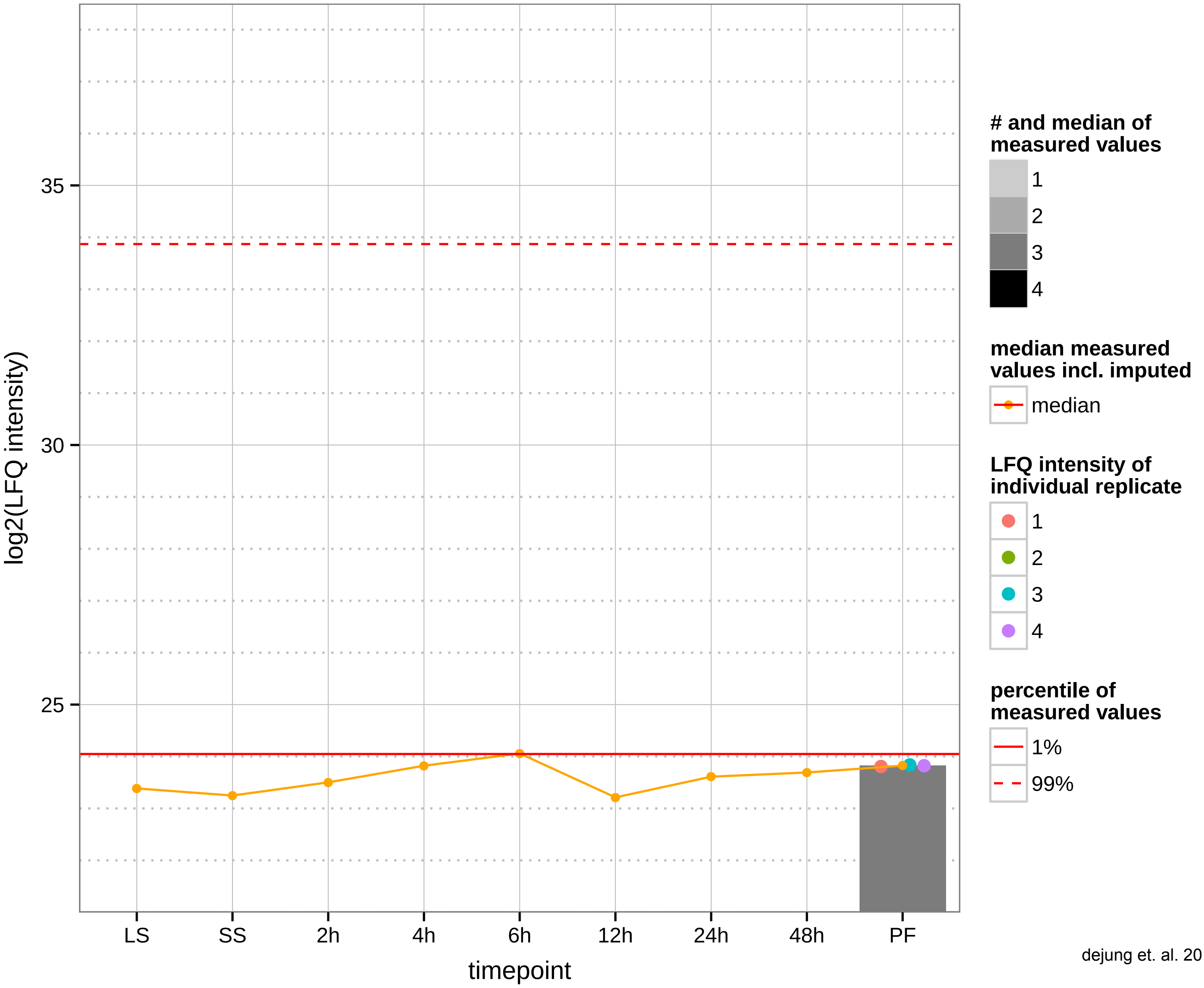
kinetoplastid kinetochore protein 7 (kkt7)
Tb927.11.1030
AGOF: null
AGOC: kinetochore
AGOP: chromosome segregation
PGOF: null
PGOC: null
PGOP: null





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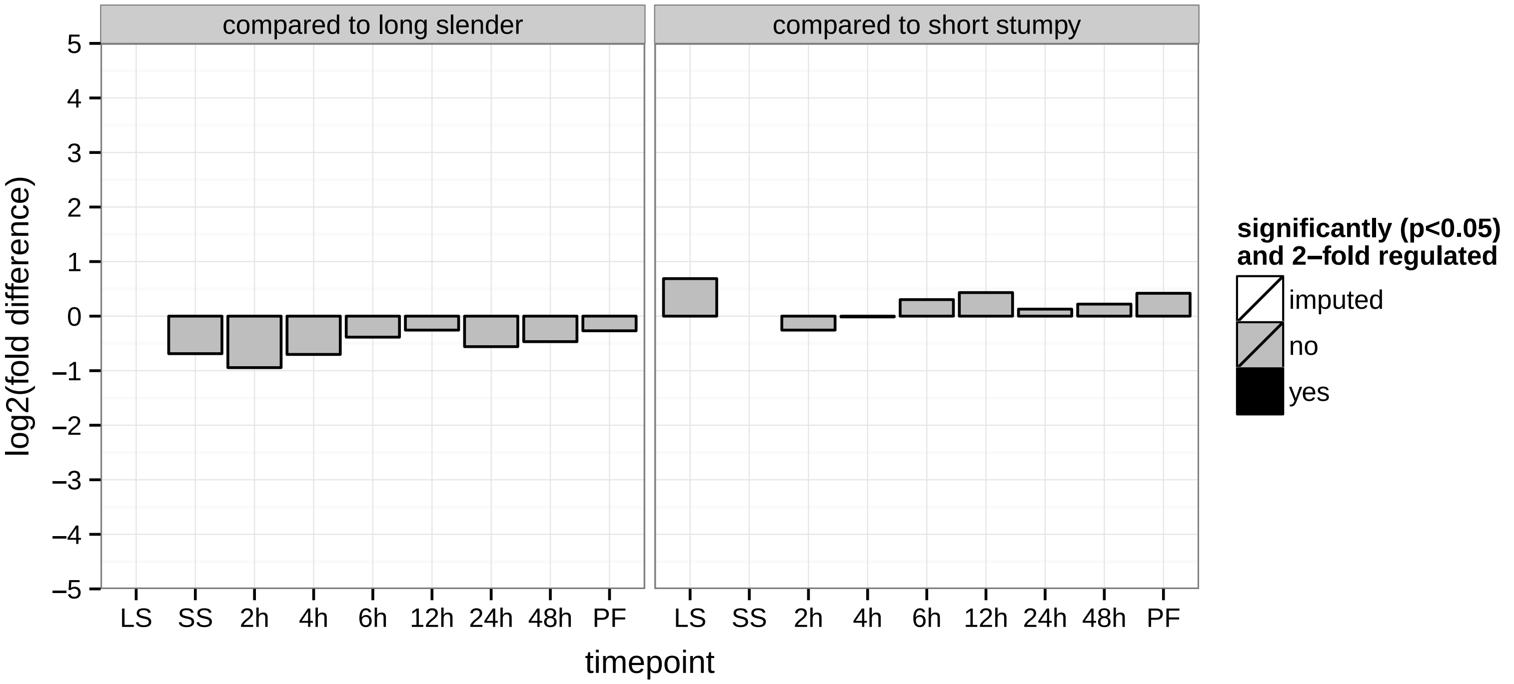
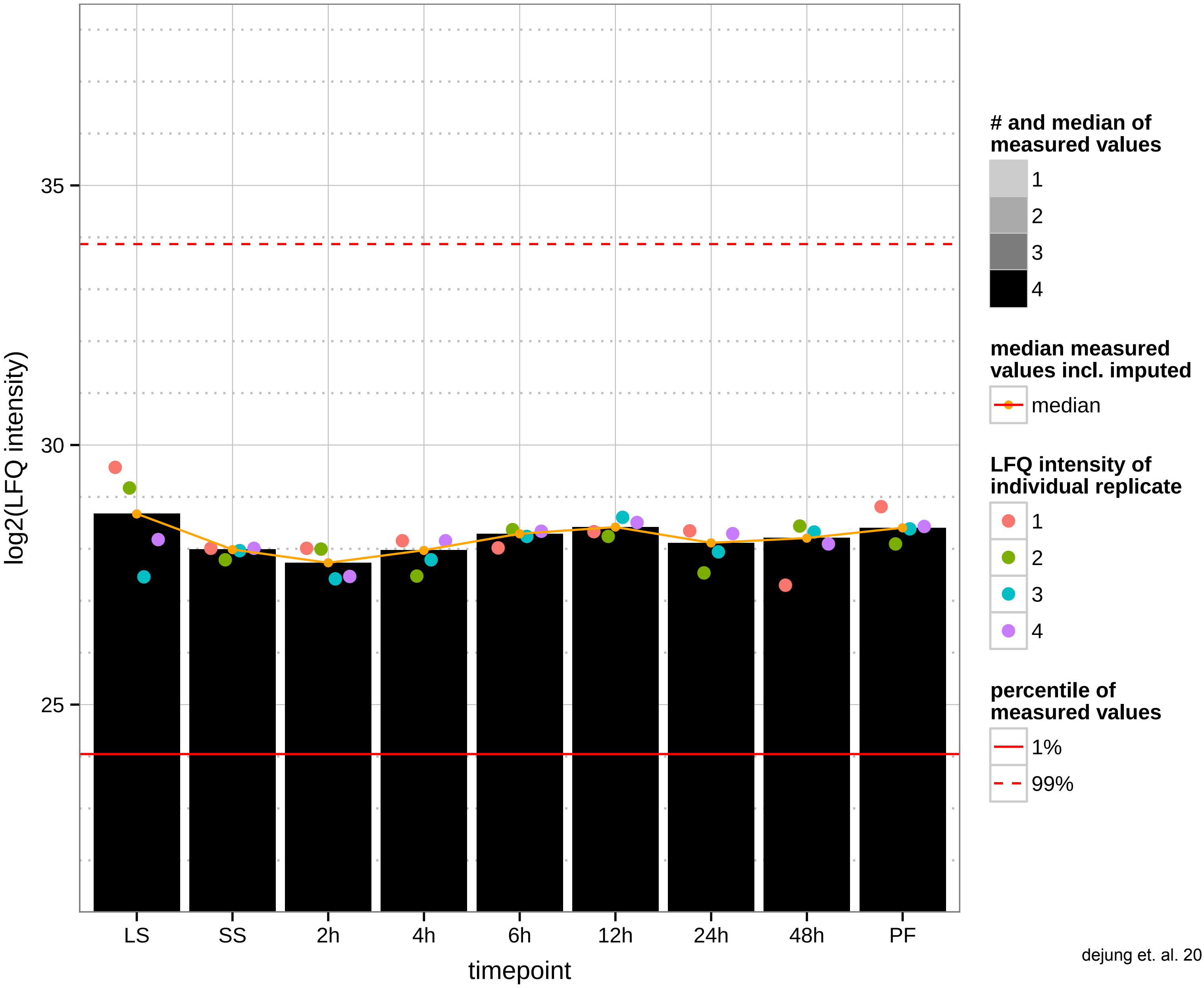
hypothetical protein, conserved
Tb927.11.10330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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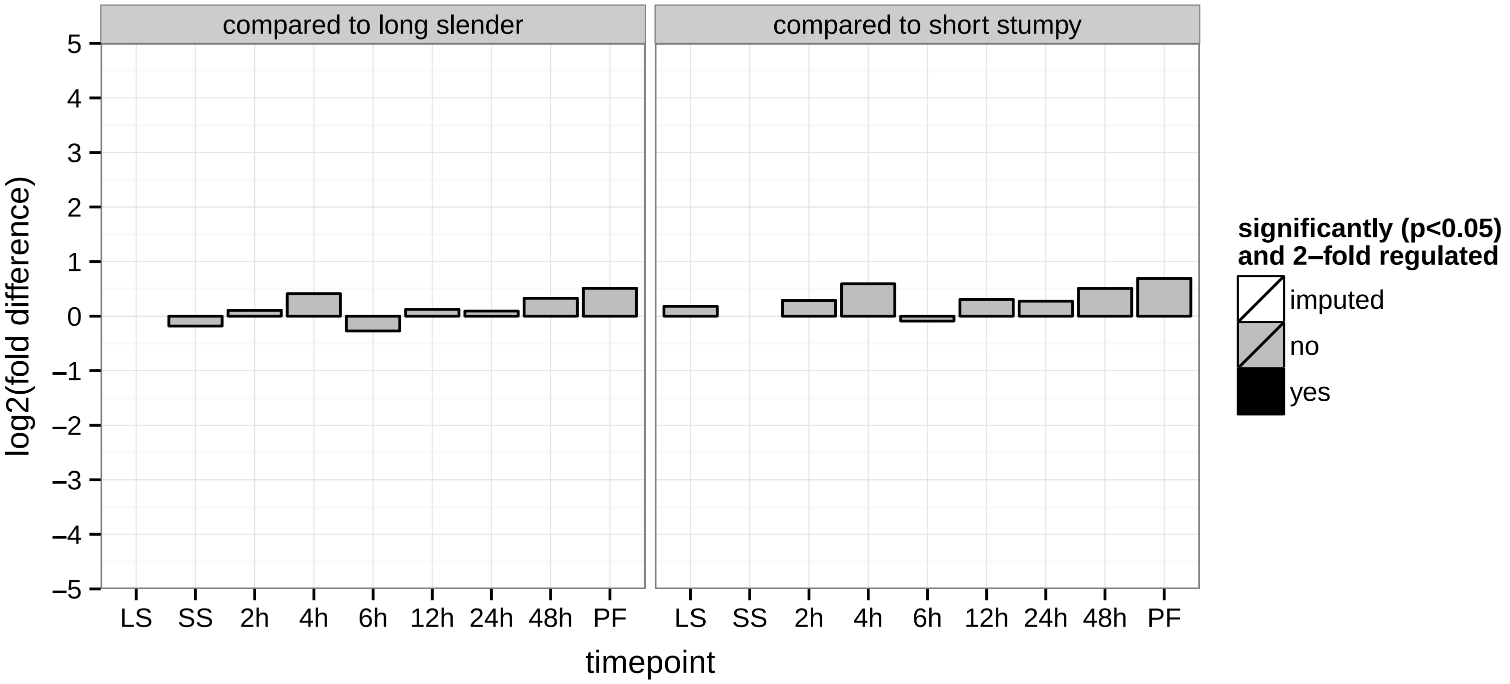
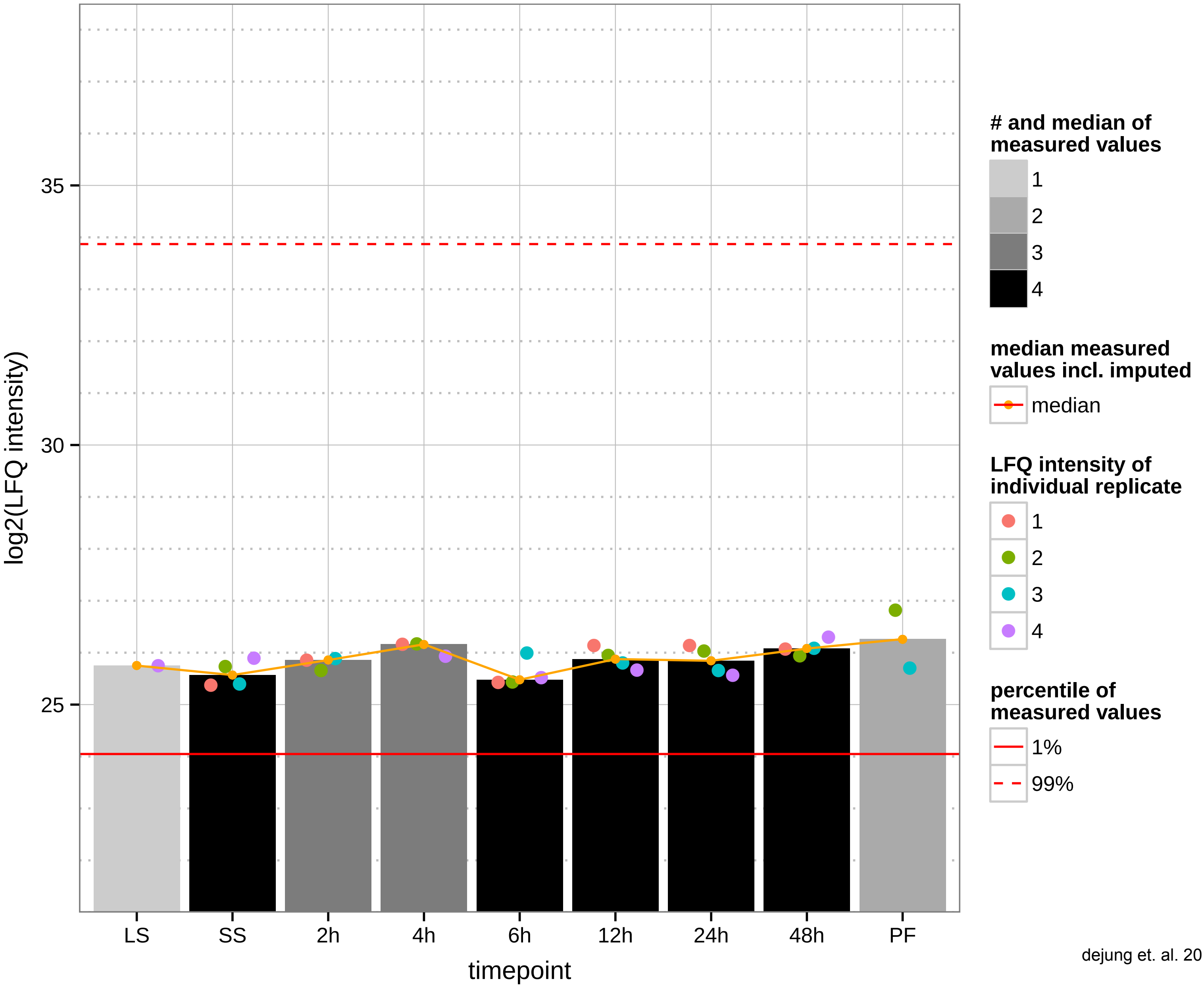
Serine/threonine−protein phosphatase PGAM5, mitochondrial, putative, phosphoglycerate mutase family member 5, putative
Tb927.11.10340
AGOF: phosphoprotein phosphatase activity, protein serine/threonine kinase activator activity
AGOC: null
AGOP: regulation of mitochondrion organization
PGOF: null
PGOC: null
PGOP: null





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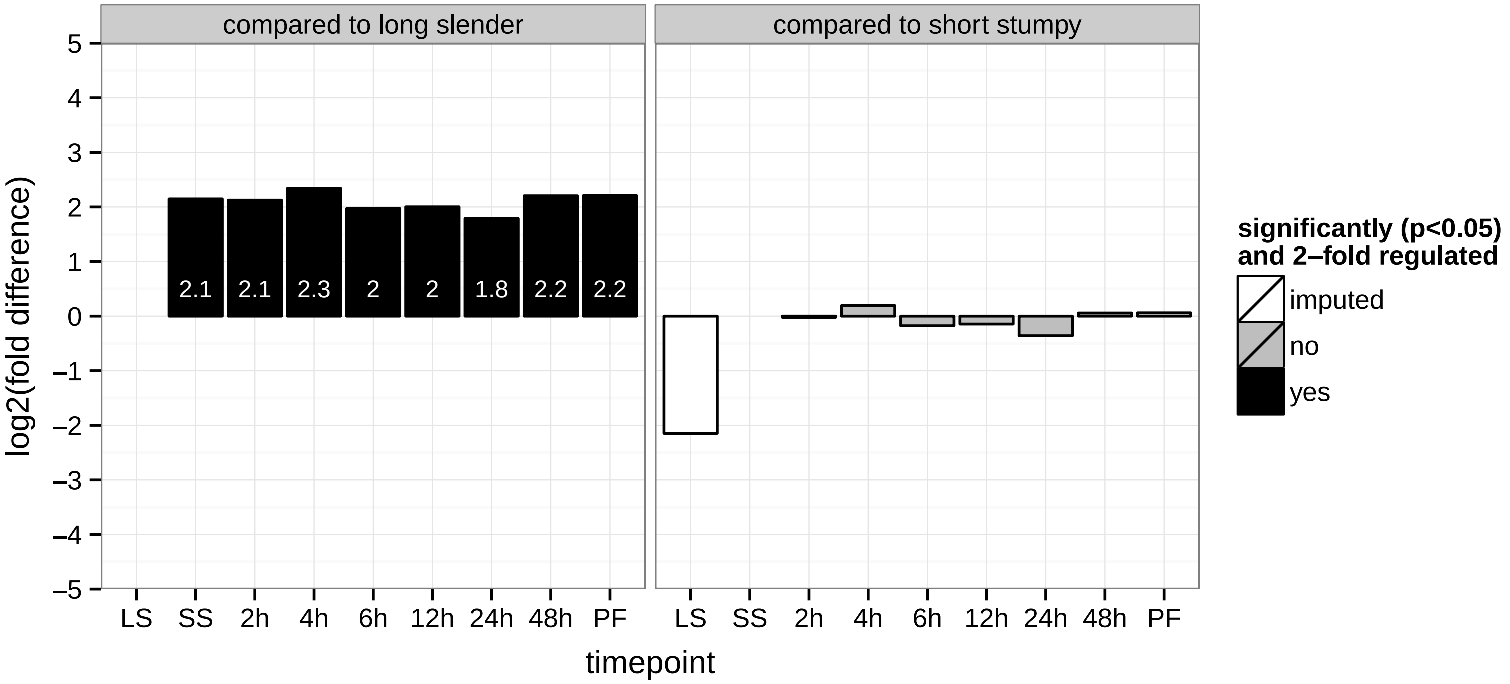
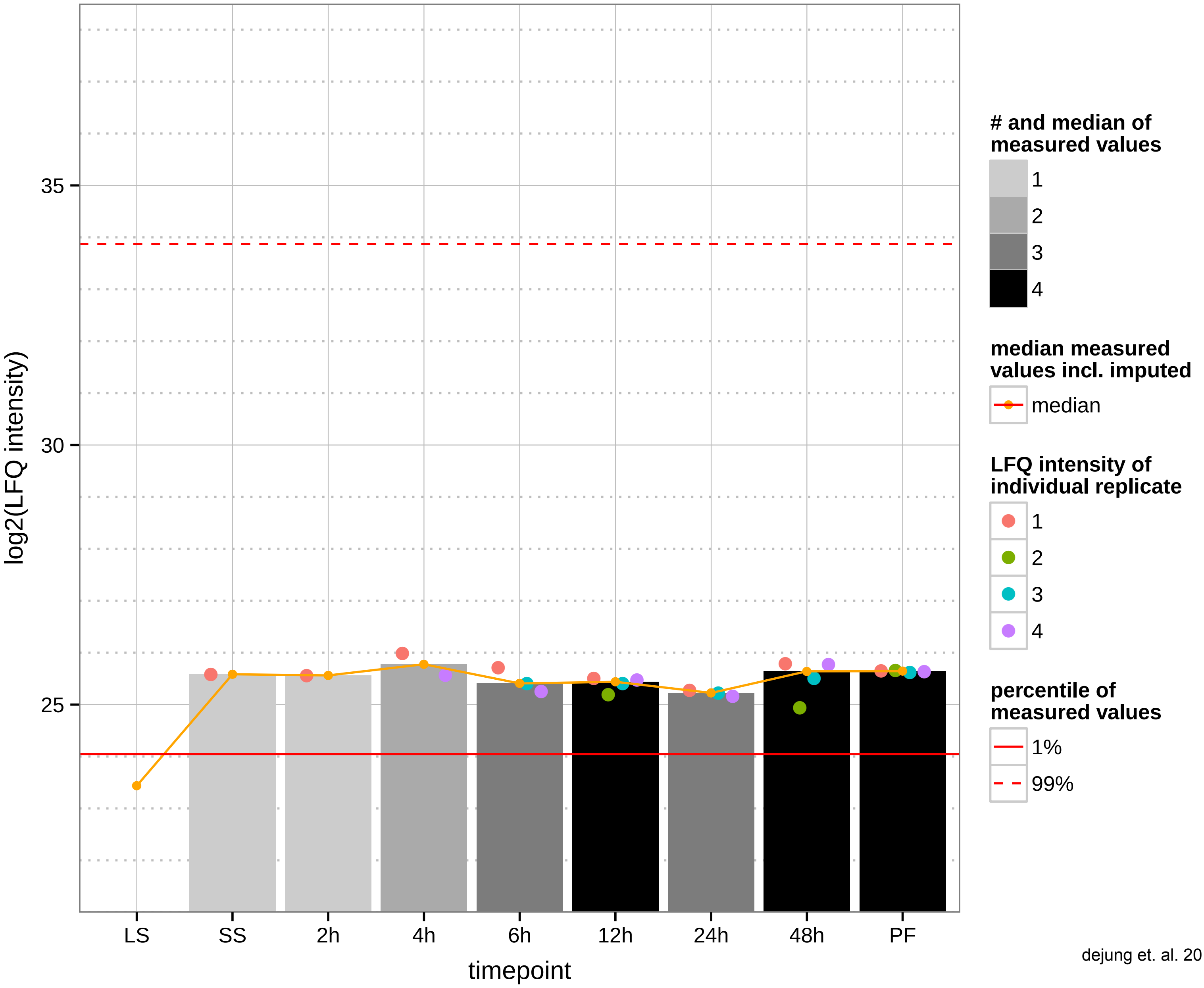
hypothetical protein, conserved
Tb927.11.10380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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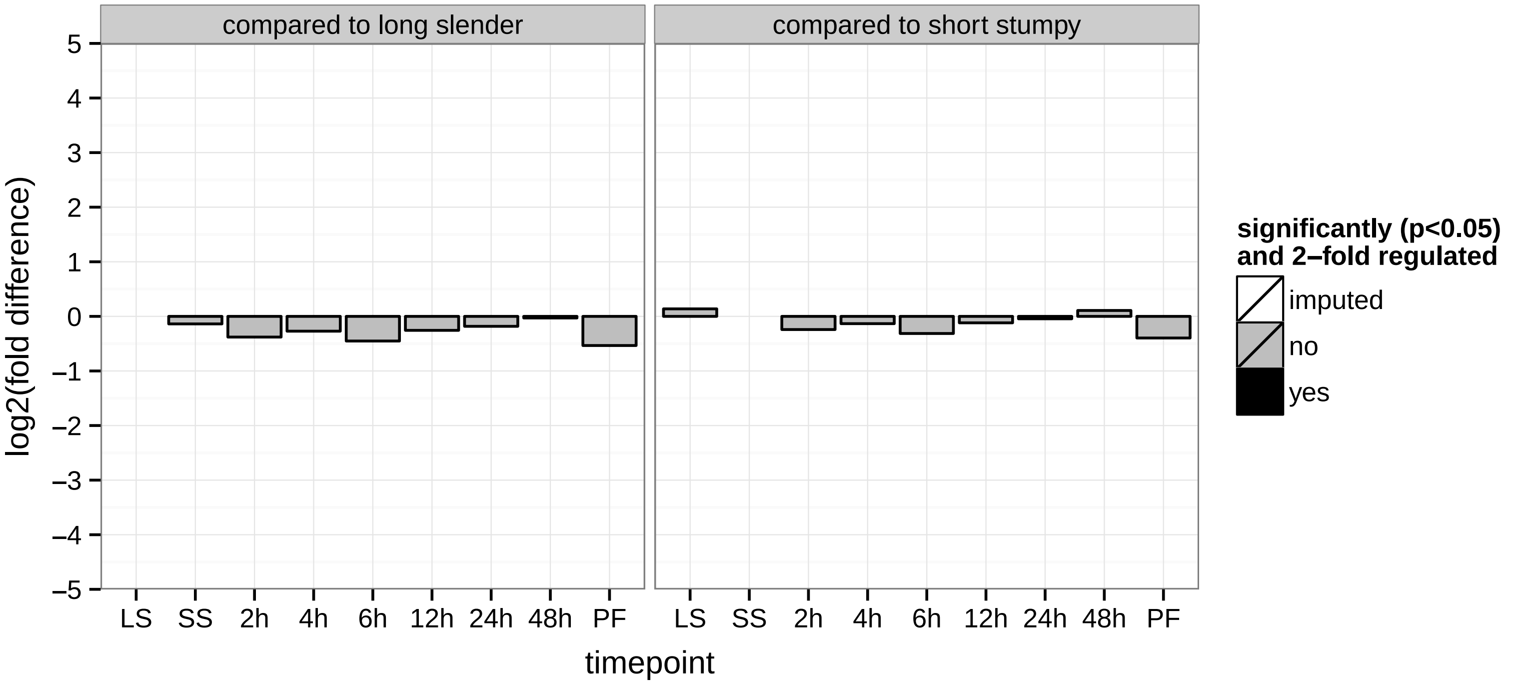
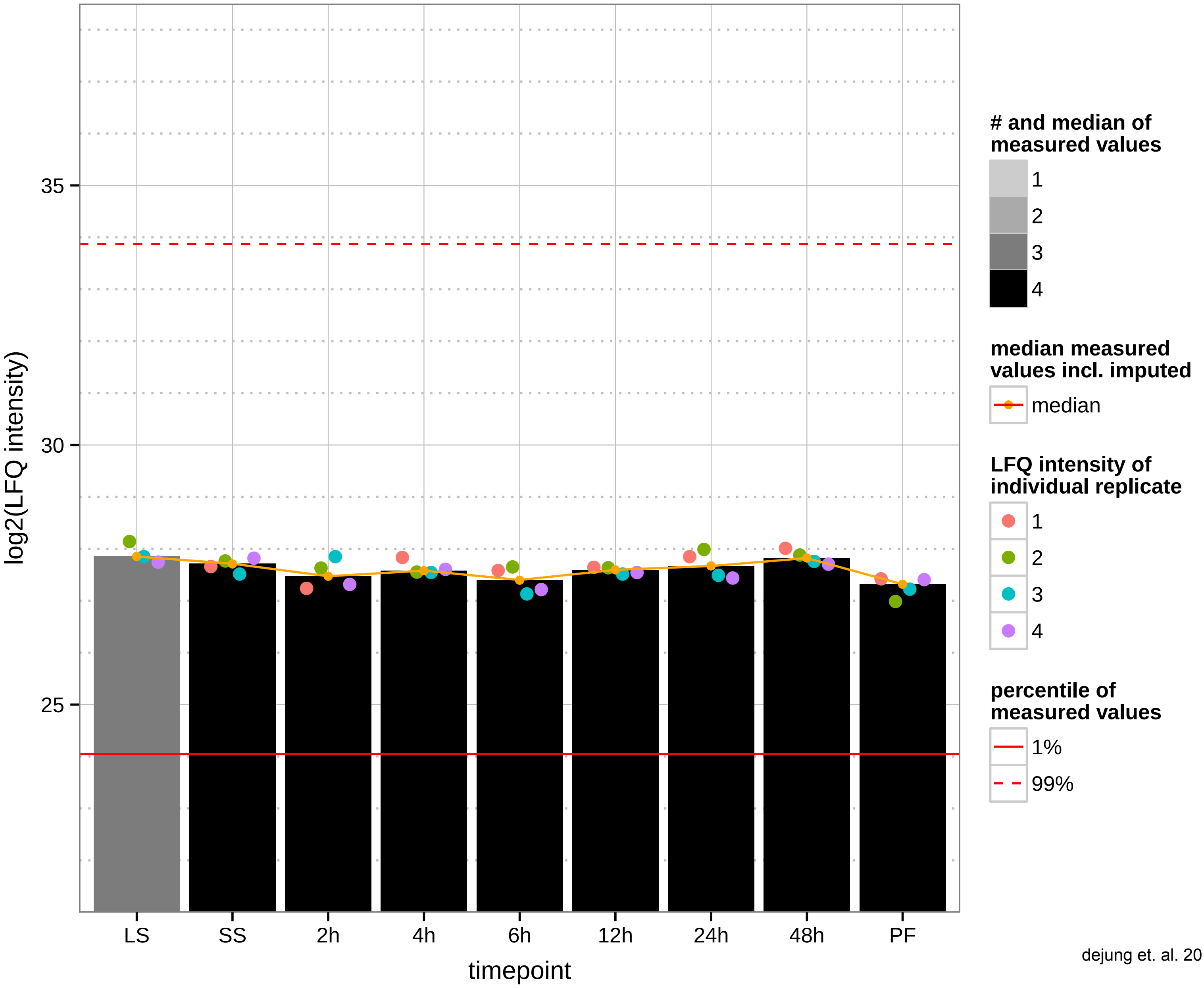
hypothetical protein, conserved
Tb927.11.10430
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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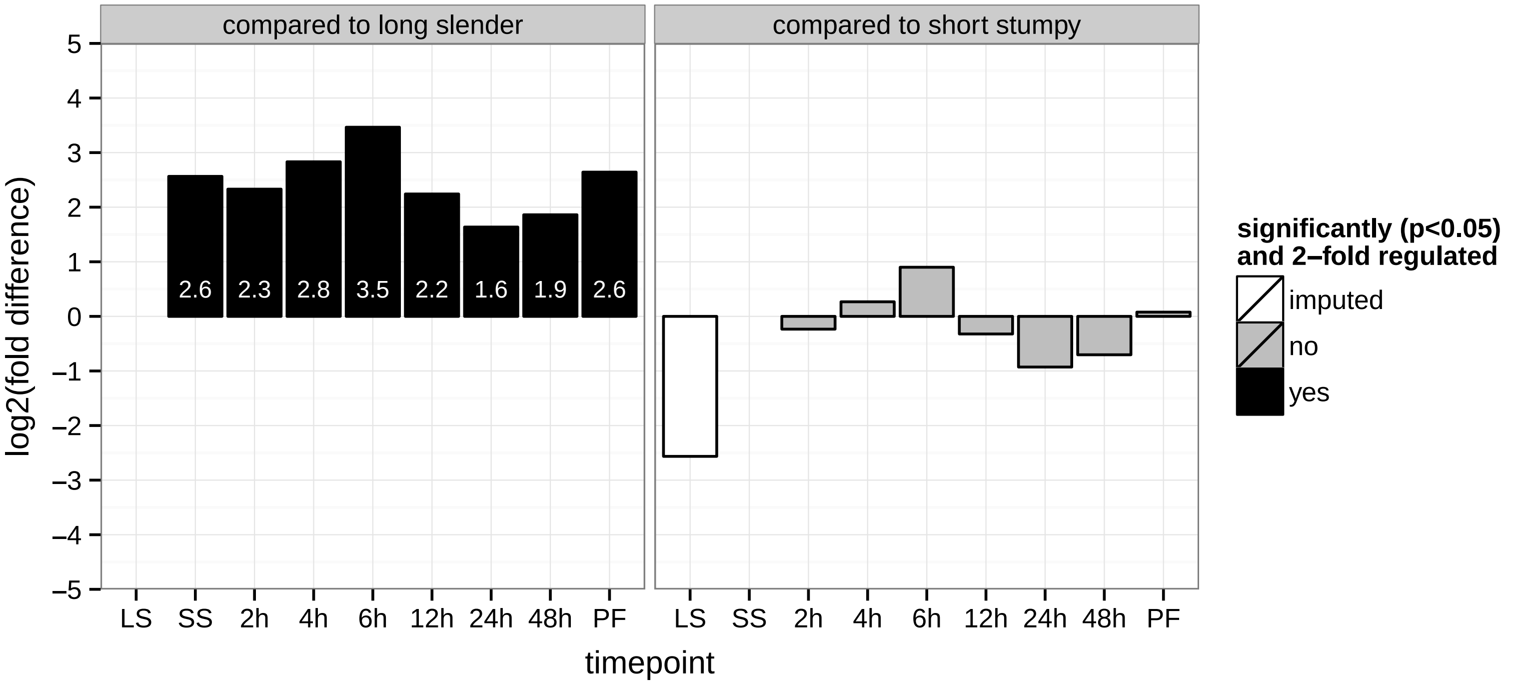
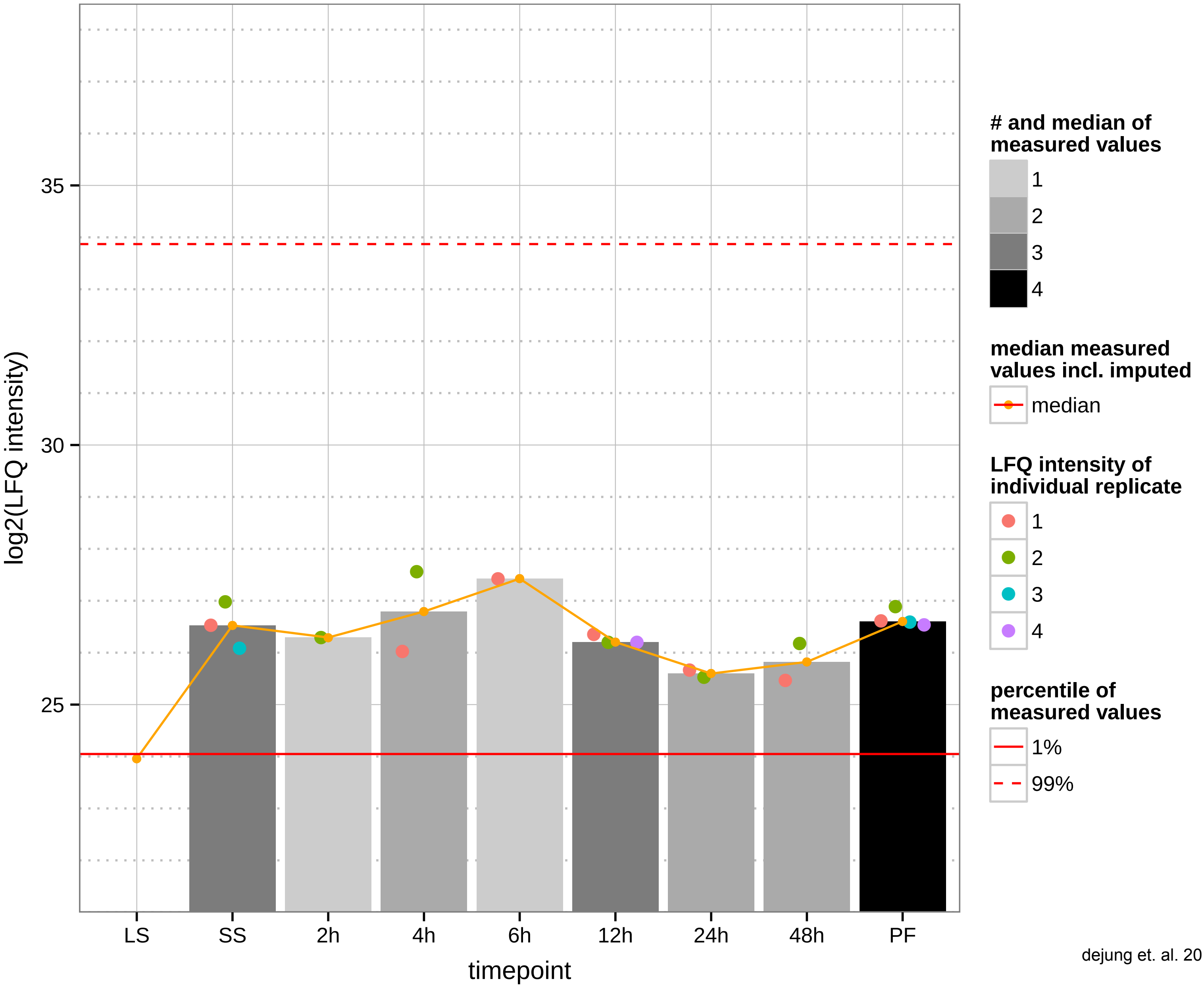
UDP–N–acetylglucosamine–dolichyl–phosphate N–acetylglucosaminephosphotransferase, putative
Tb927.11.10450
AGOF: UDP–N–acetylglucosamine–dolichyl–phosphate N–acetylglucosaminephosphotransferase activity
AGOC: integral to membrane
AGOP: dolichol–linked oligosaccharide biosynthetic process
PGOF: phospho–N–acetylmuramoyl–pentapeptide–transferase activity
PGOC: integral to membrane
PGOP: null





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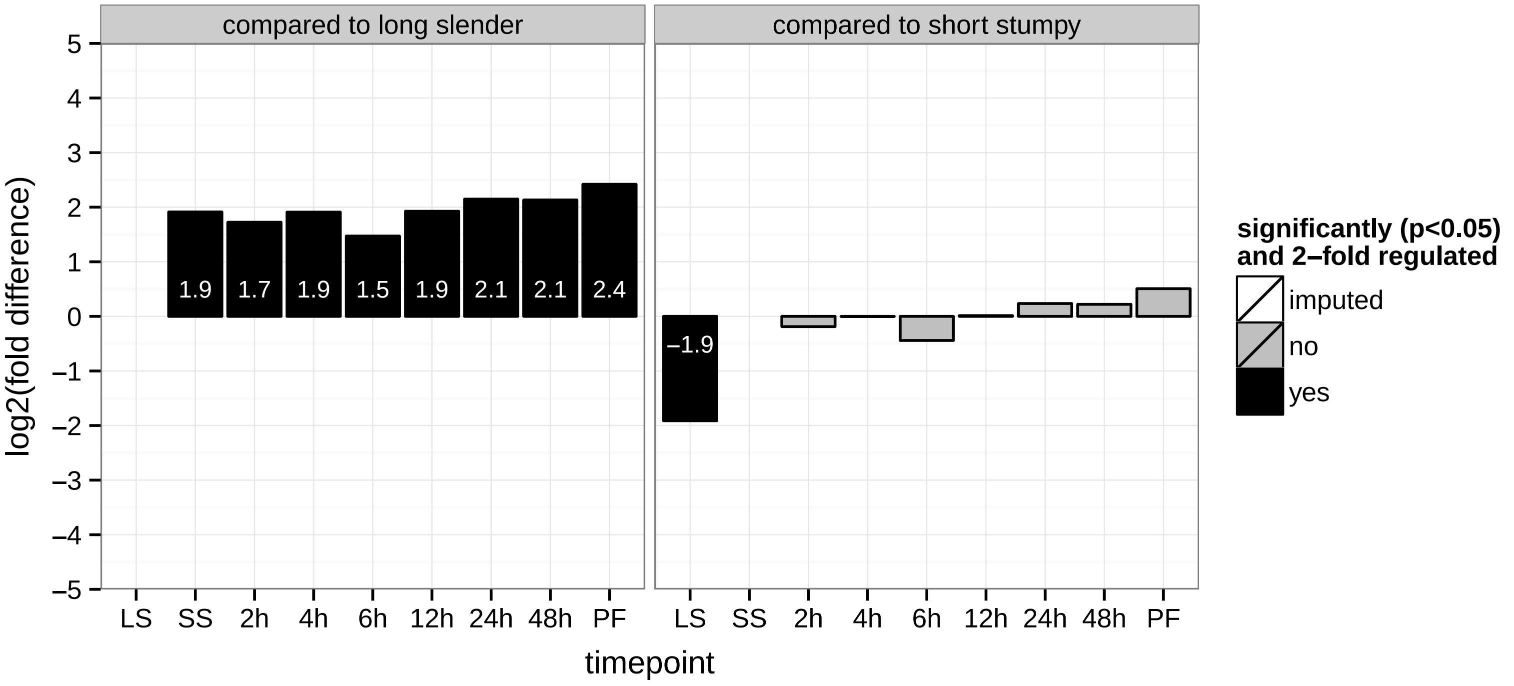
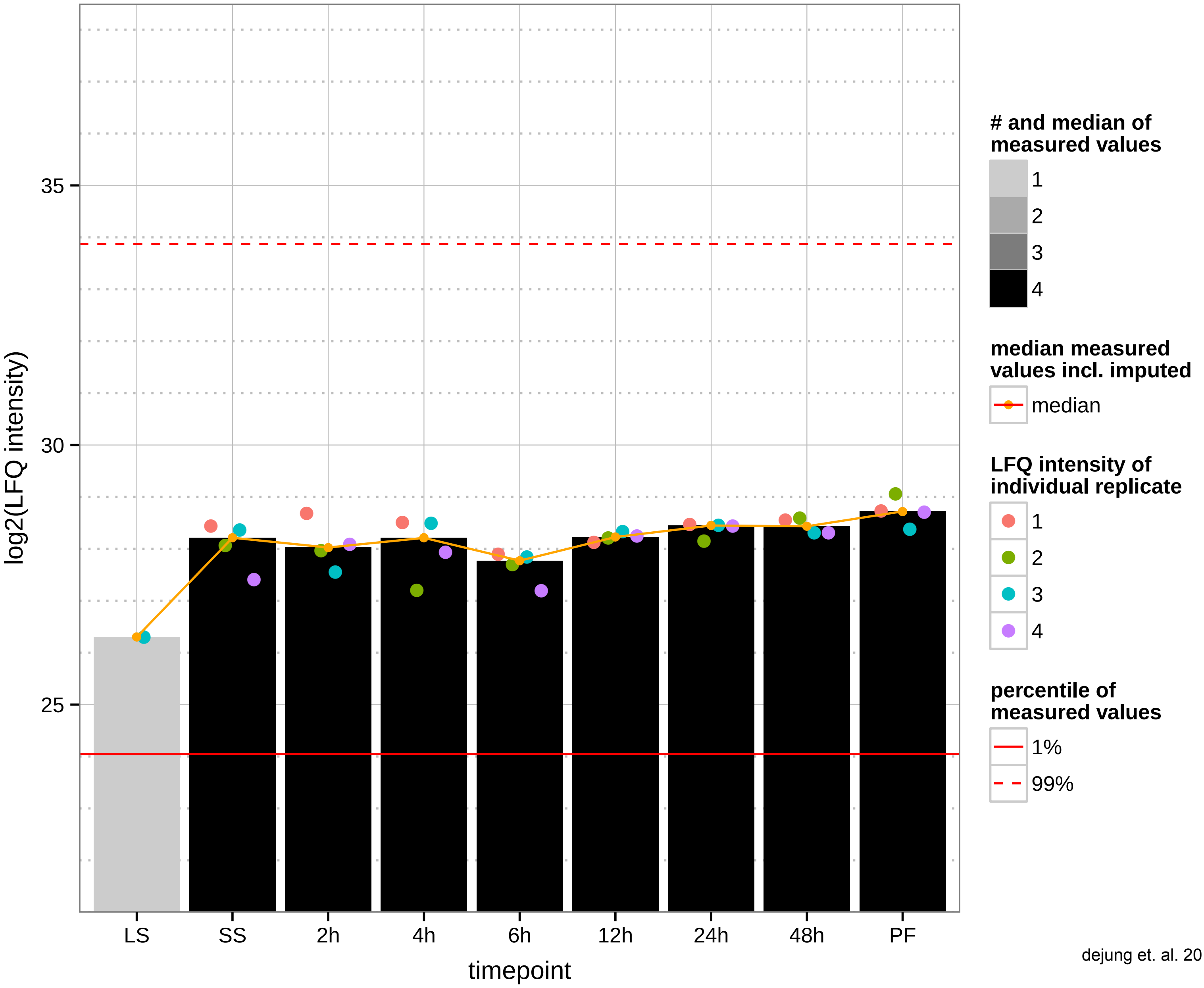
hypothetical protein, conserved
Tb927.11.10480
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: small–subunit processome
PGOP: rRNA processing





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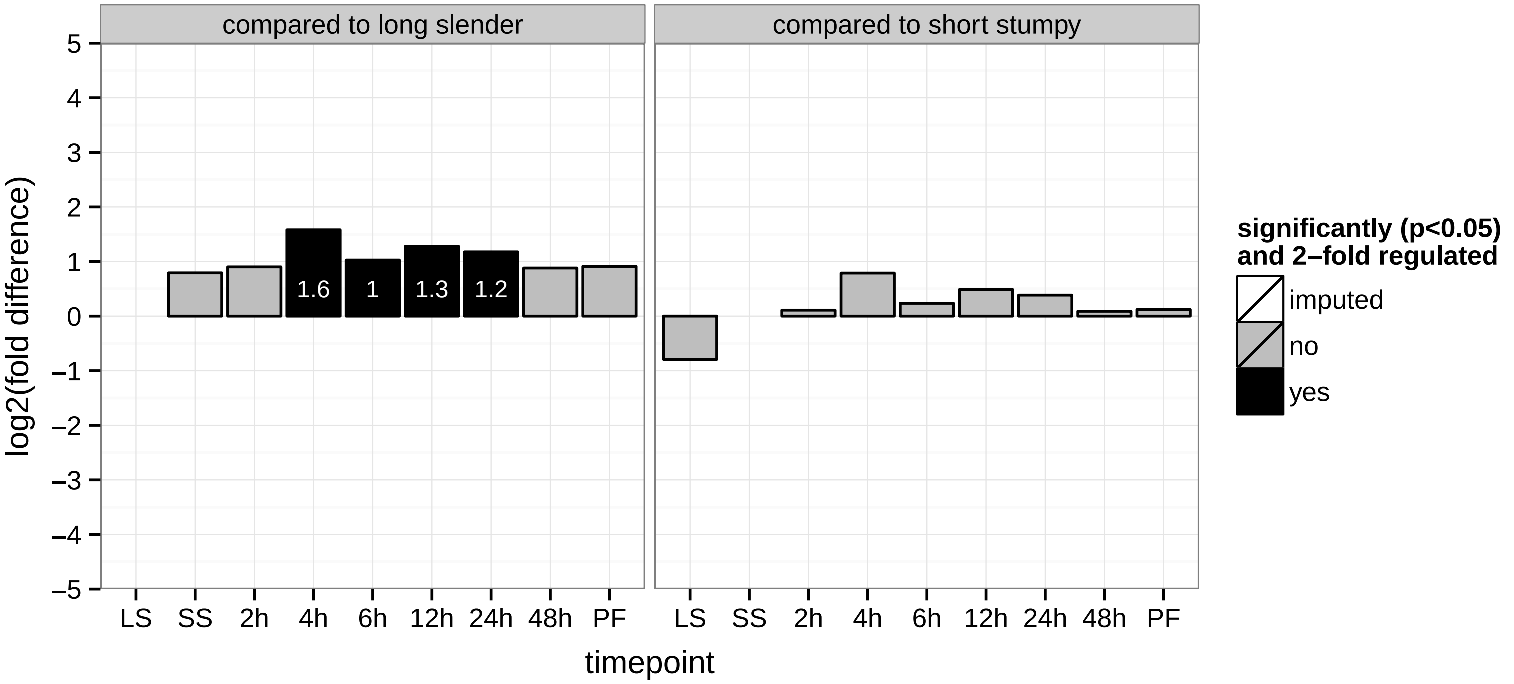
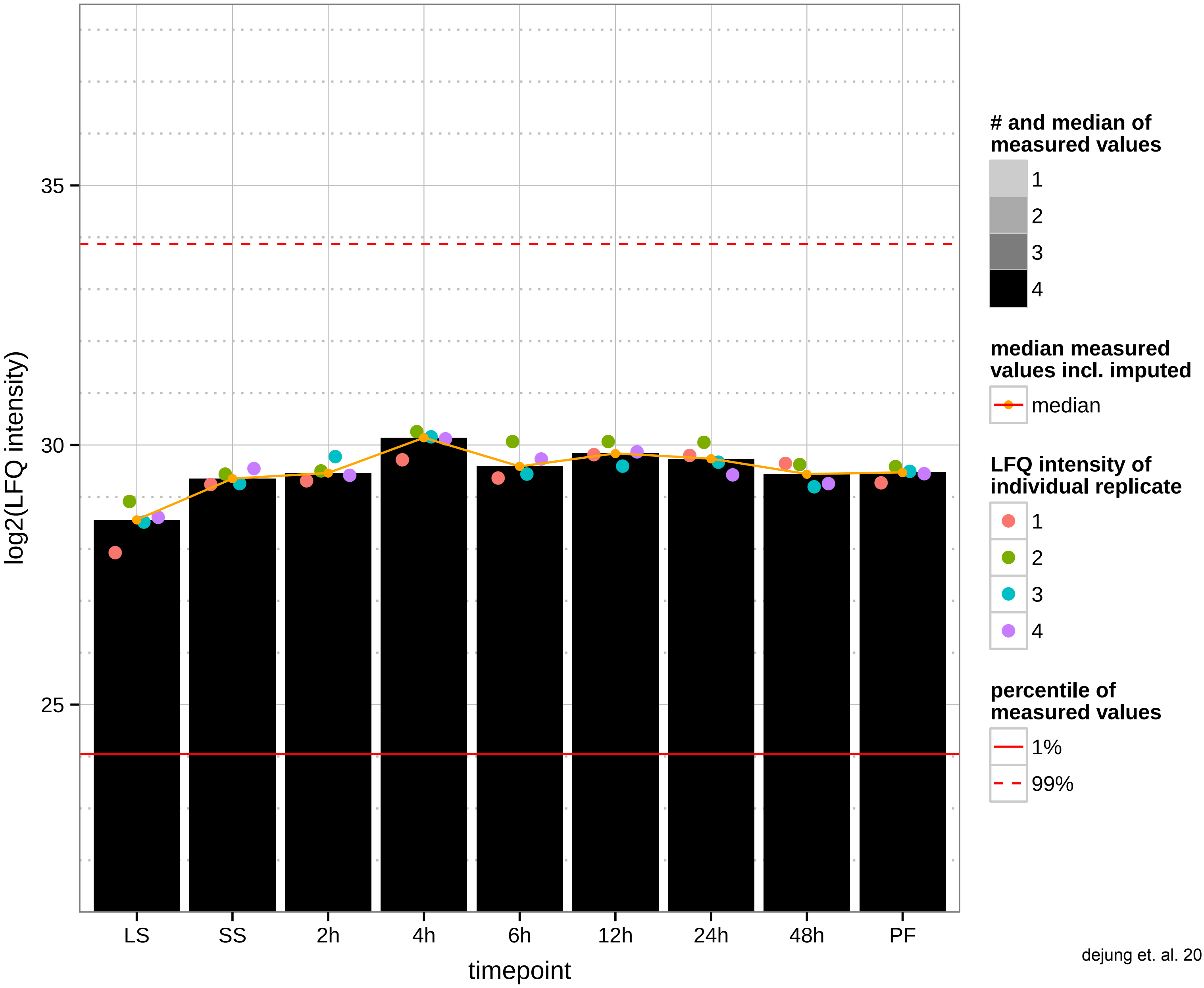
ubiquinone biosynthesis methyltransferase, putative
Tb927.11.10510
AGOF: 2–polyprenyl–6–methoxy–1, 4–benzoquinone methyltransferase activity
AGOC: mitochondrion
AGOP: coenzyme biosynthetic process, ubiquinone metabolic process
PGOF: methyltransferase activity
PGOC: null
PGOP: null





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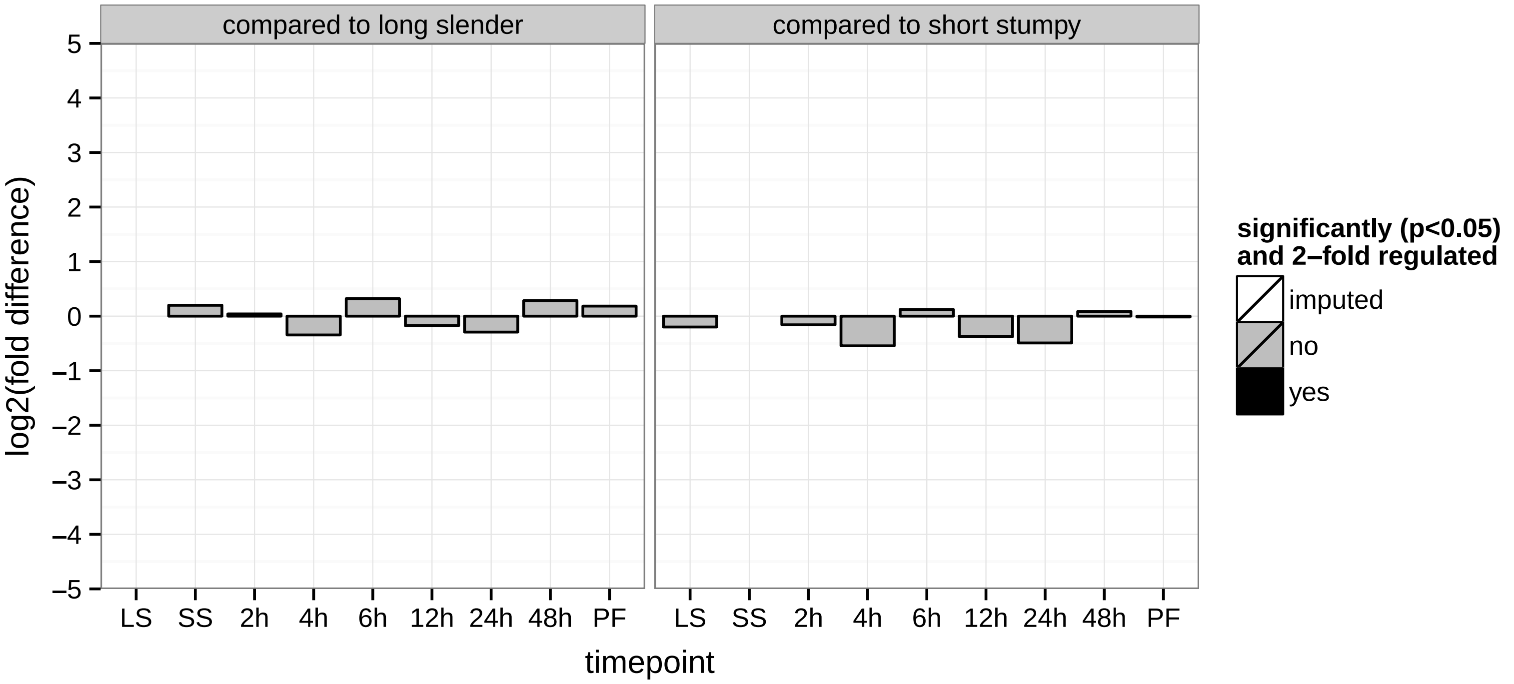
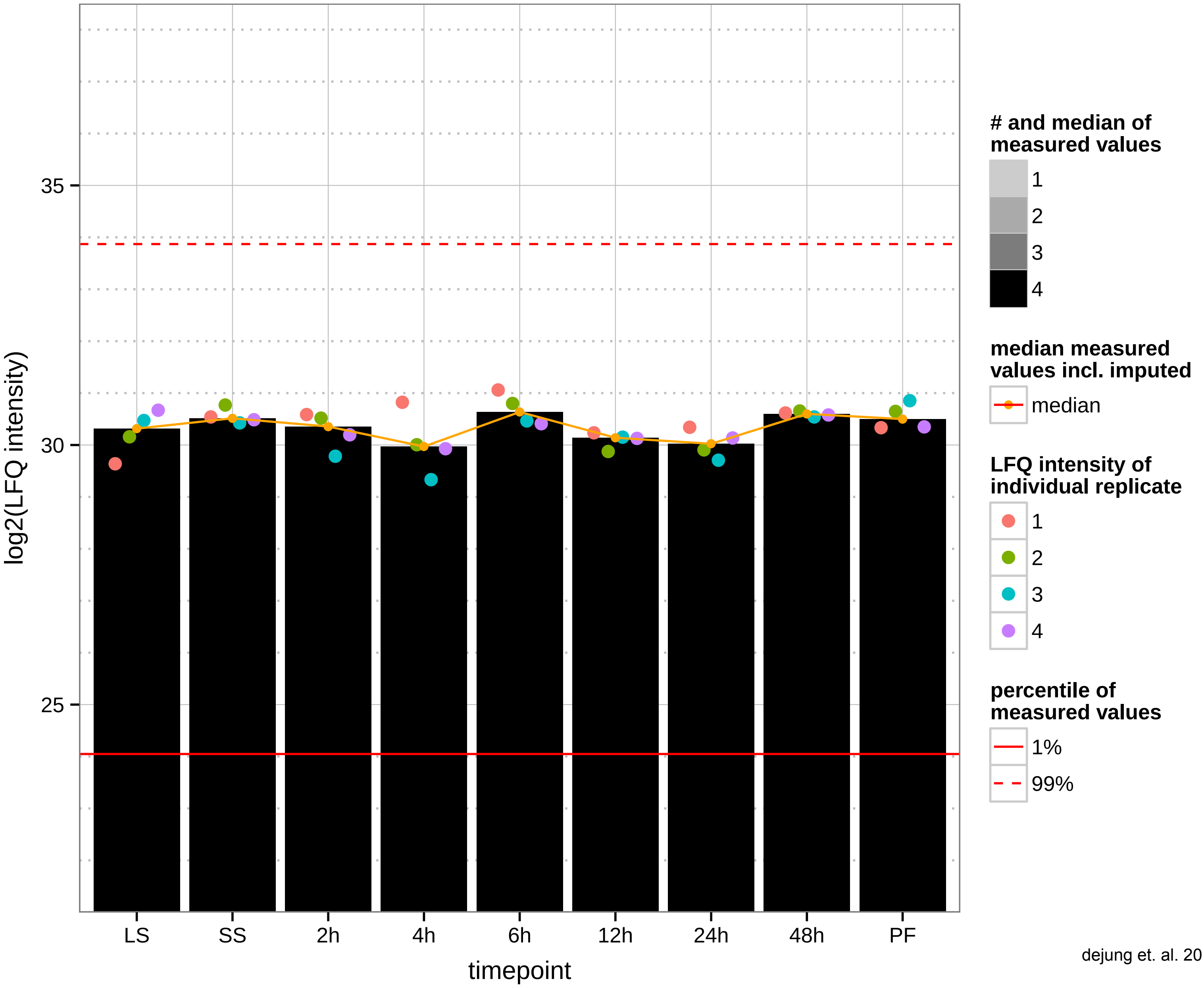
hypothetical protein, conserved
Tb927.11.10540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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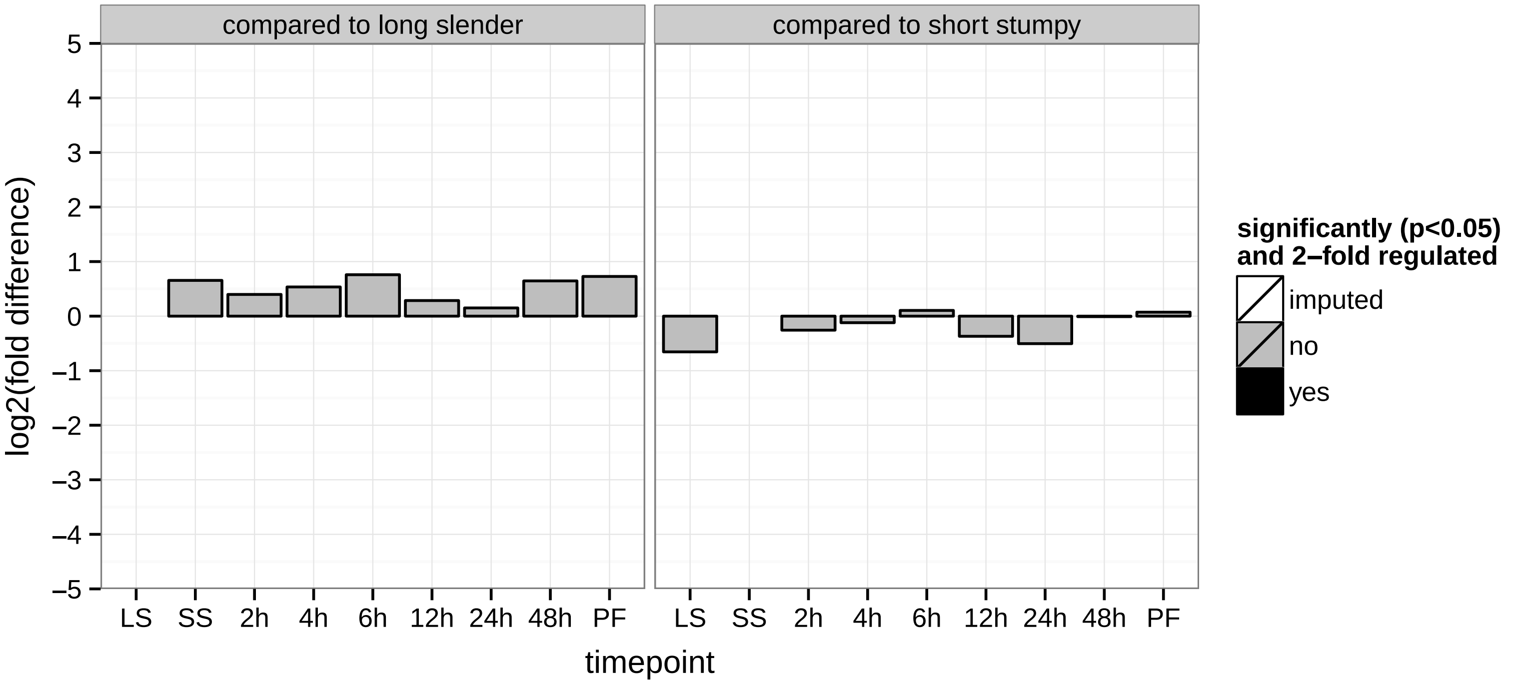
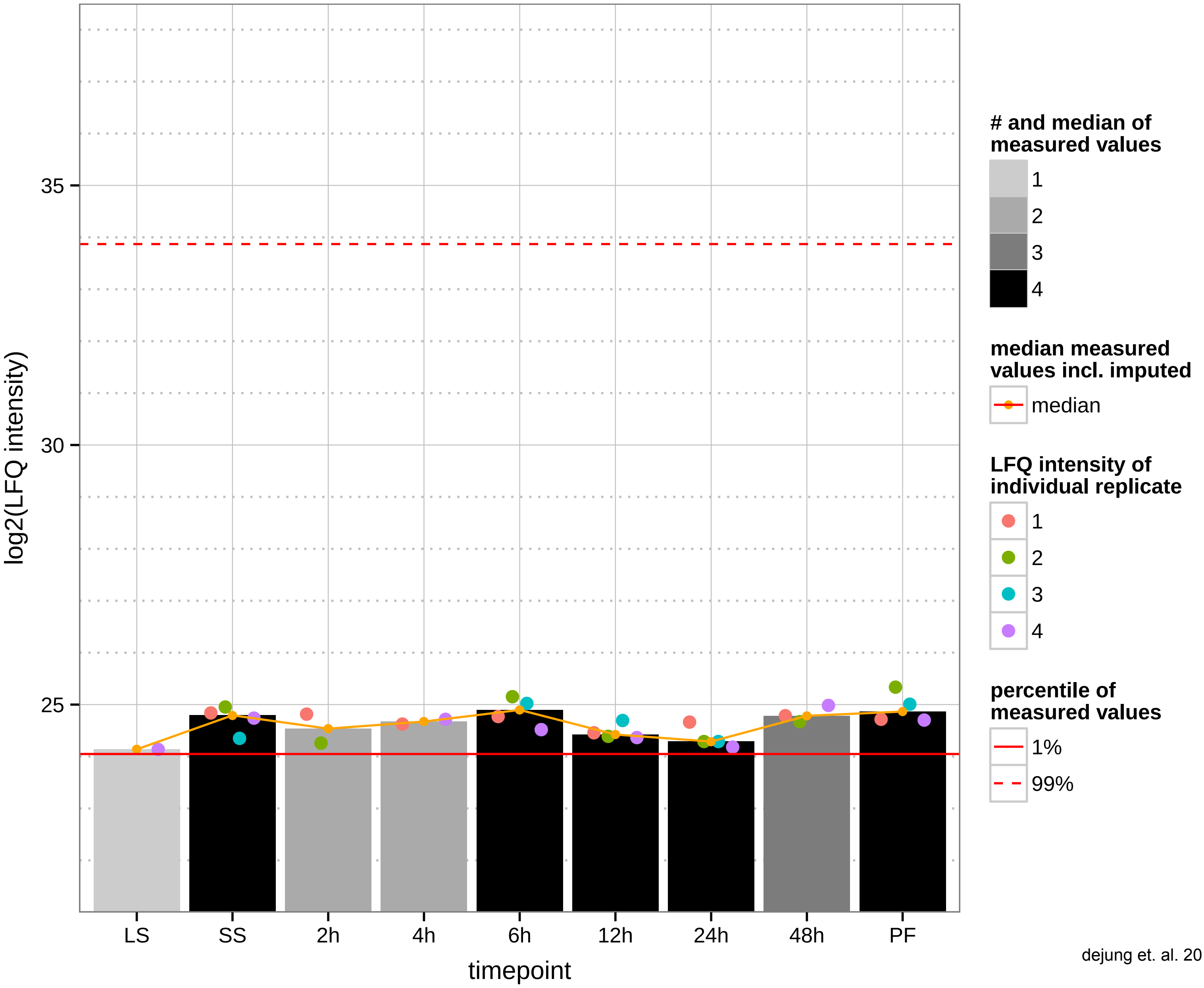
hypothetical protein, conserved
Tb927.11.10580
AGOF: null
AGOC: membrane
AGOP: Golgi organization, protein transport
PGOF: null
PGOC: null
PGOP: null





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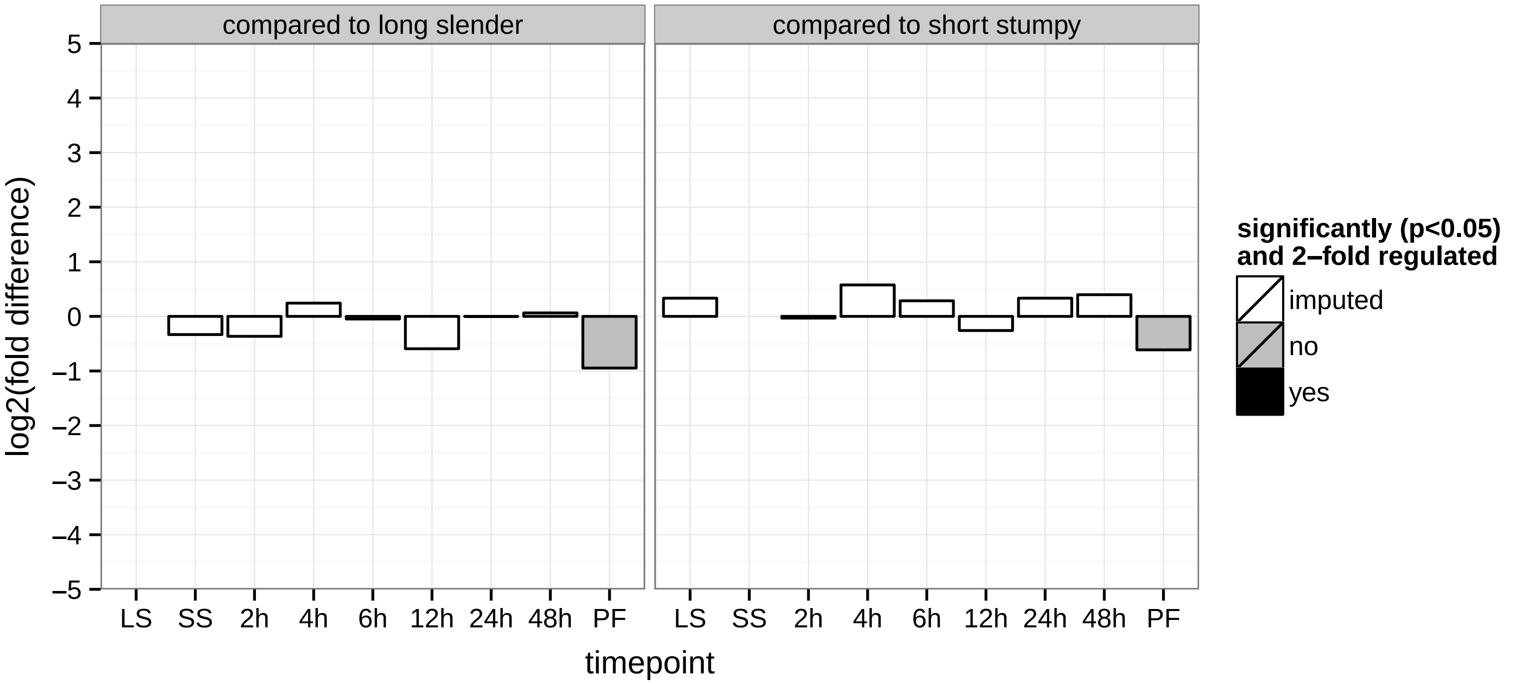
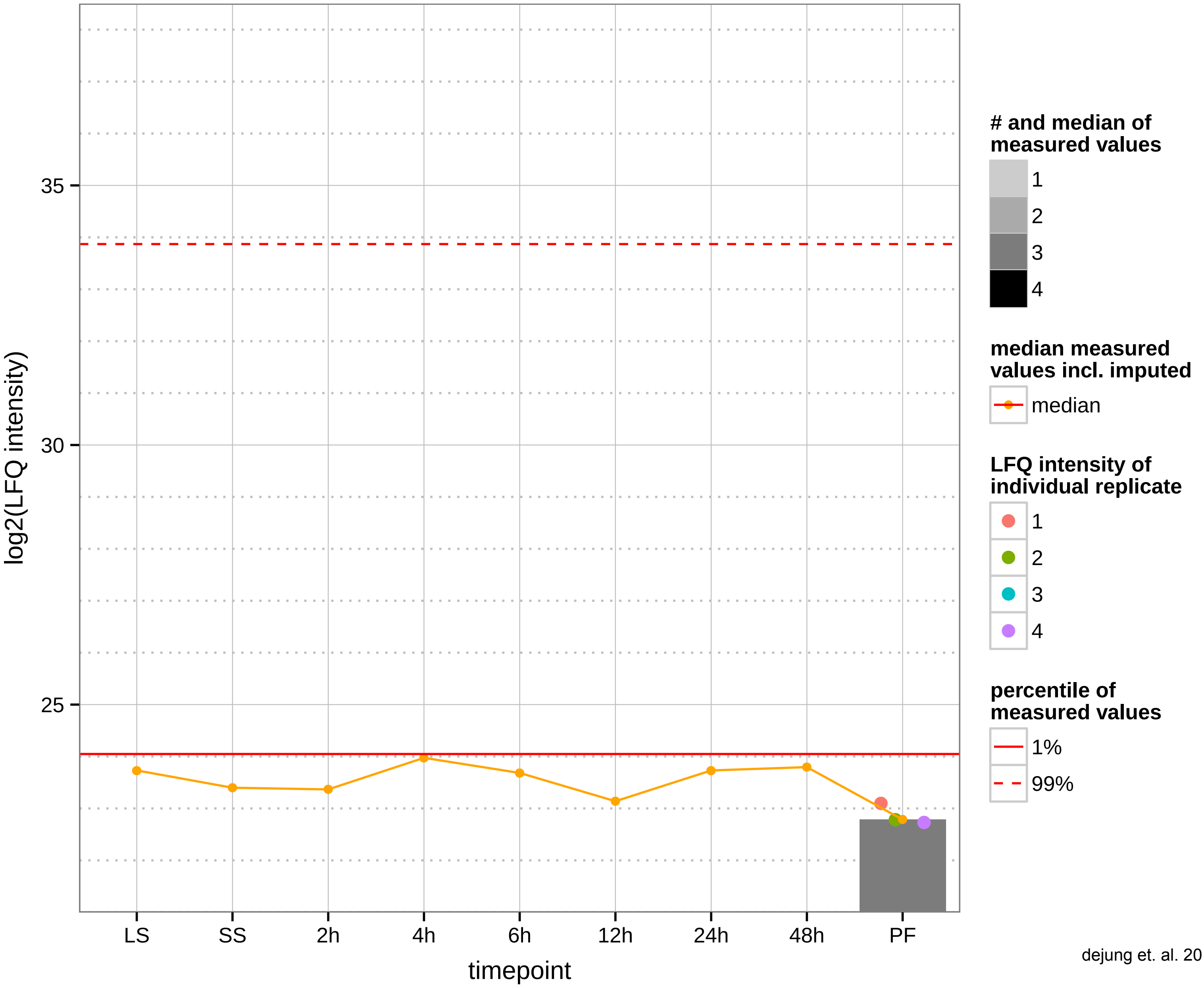
hypothetical protein, conserved
Tb927.11.10720
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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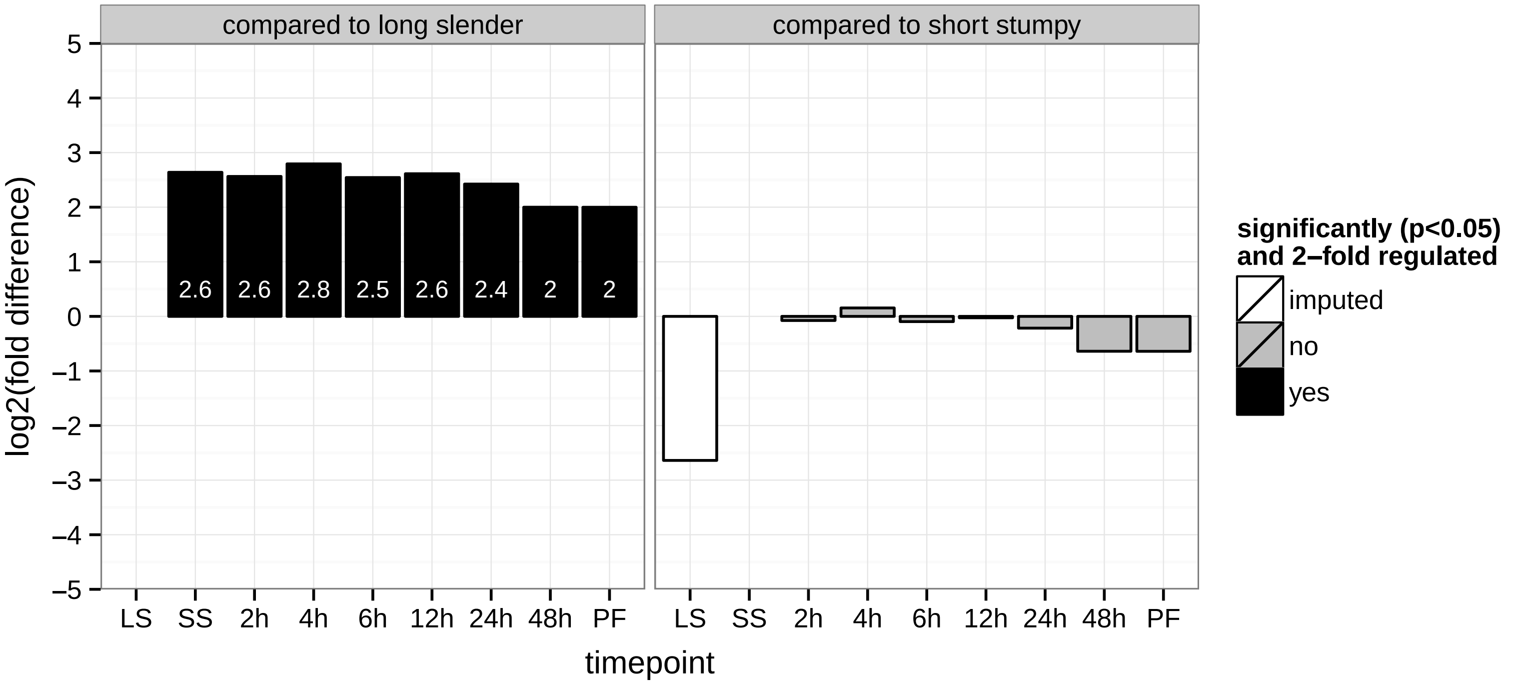
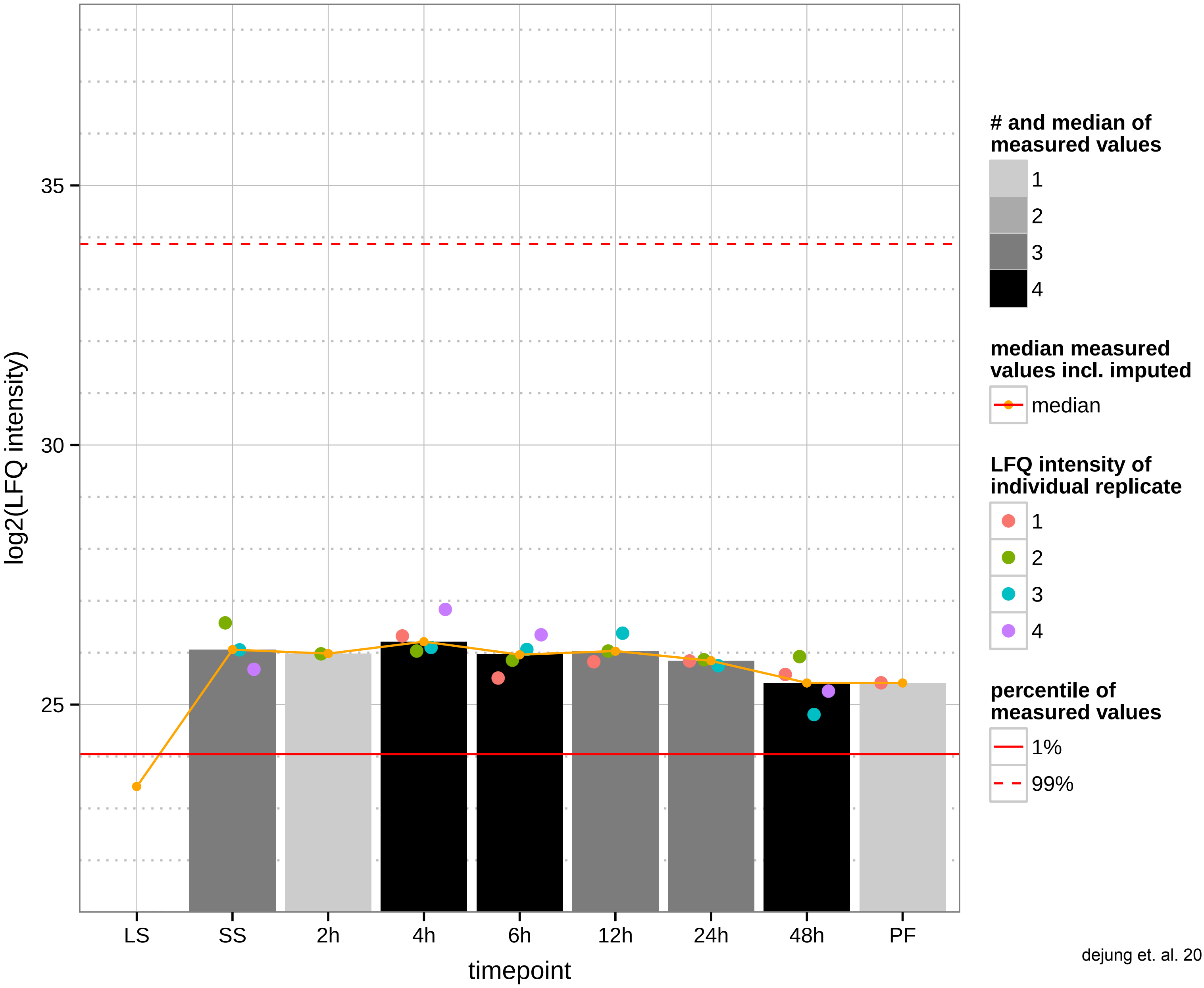
vacuolar sorting–associated protein–like, putative
Tb927.11.10740
AGOF: null
AGOC: endosome
AGOP: protein targeting to vacuole
PGOF: null
PGOC: null
PGOP: null





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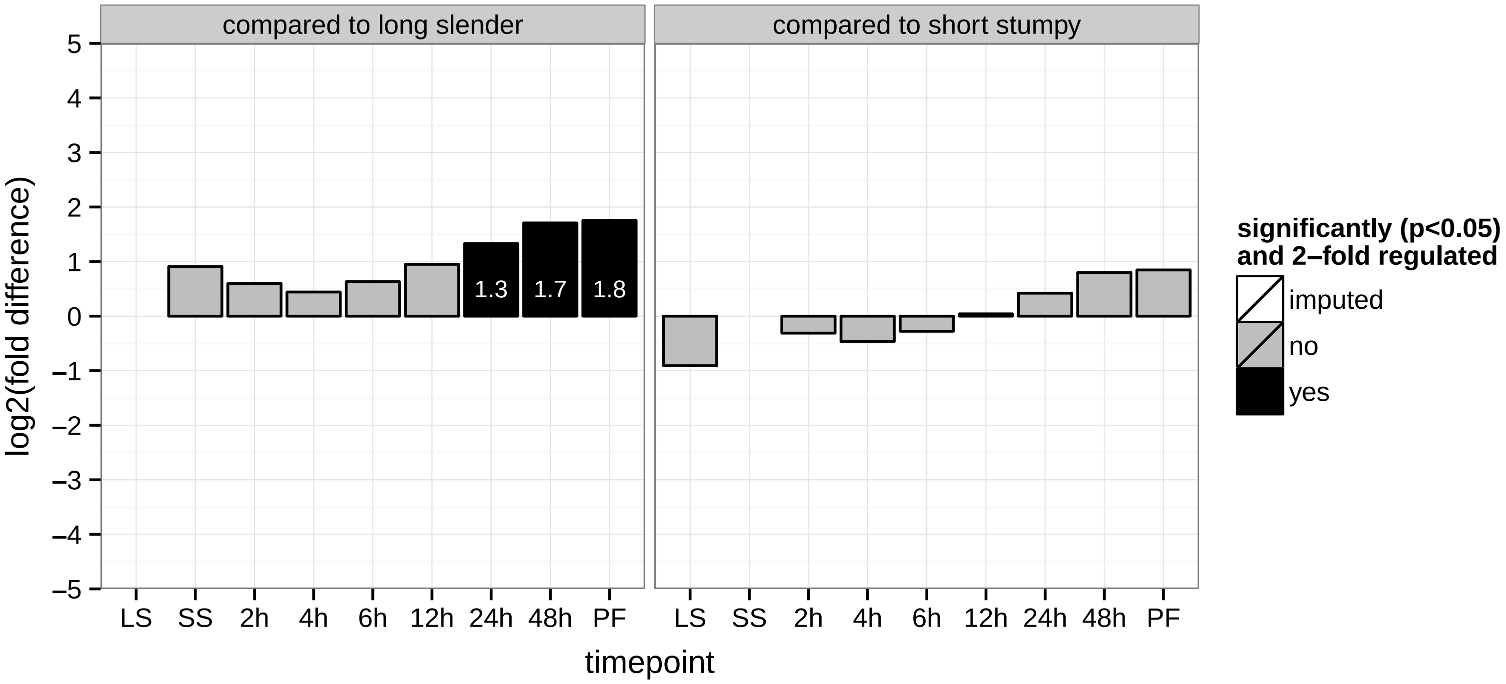
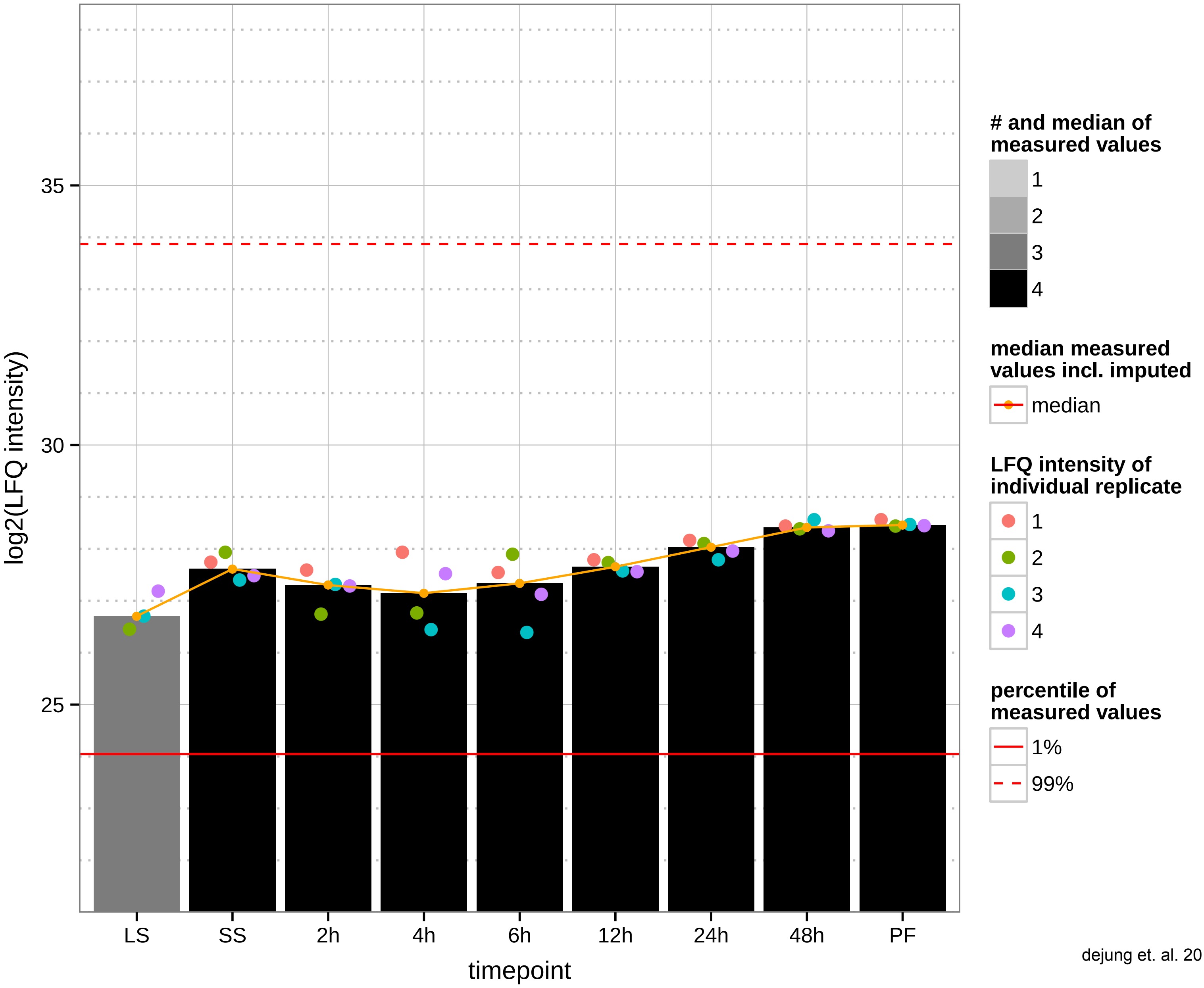
hypothetical protein, conserved
Tb927.11.10780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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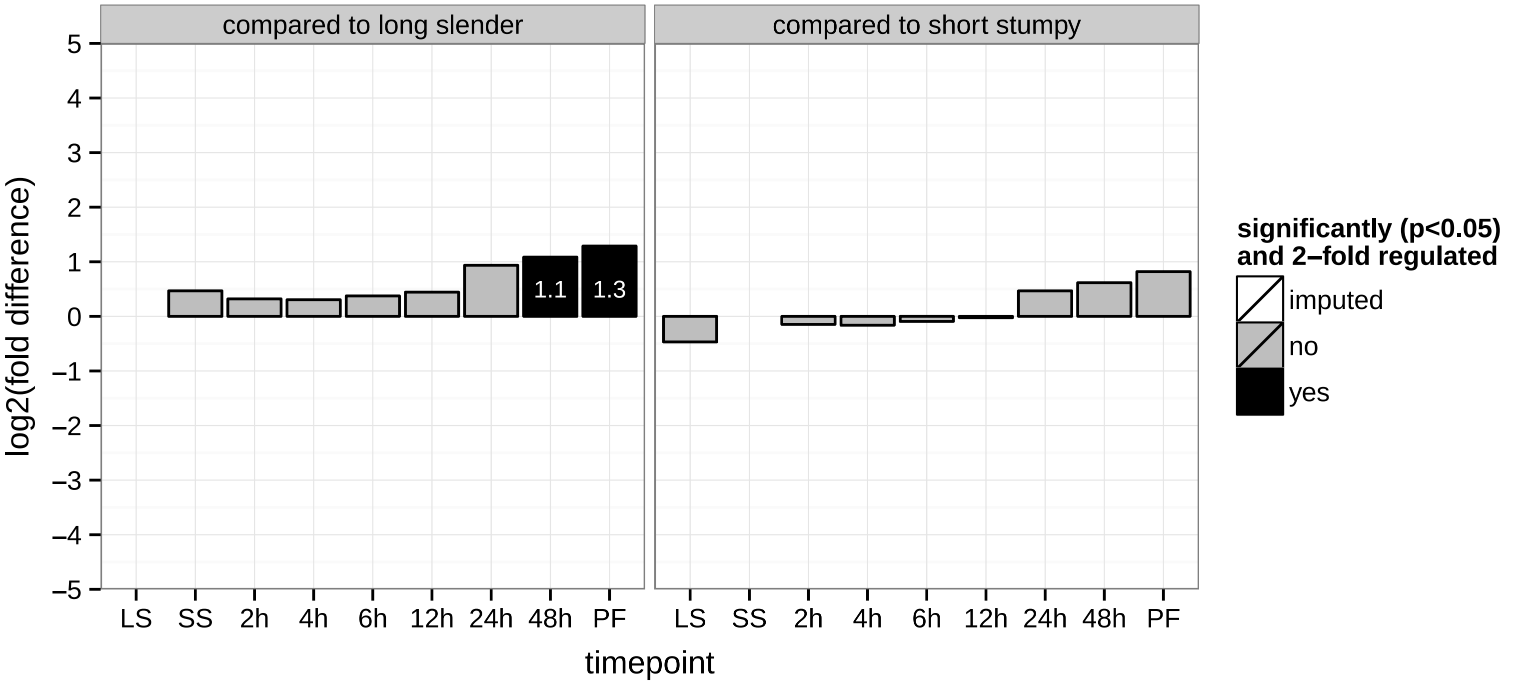
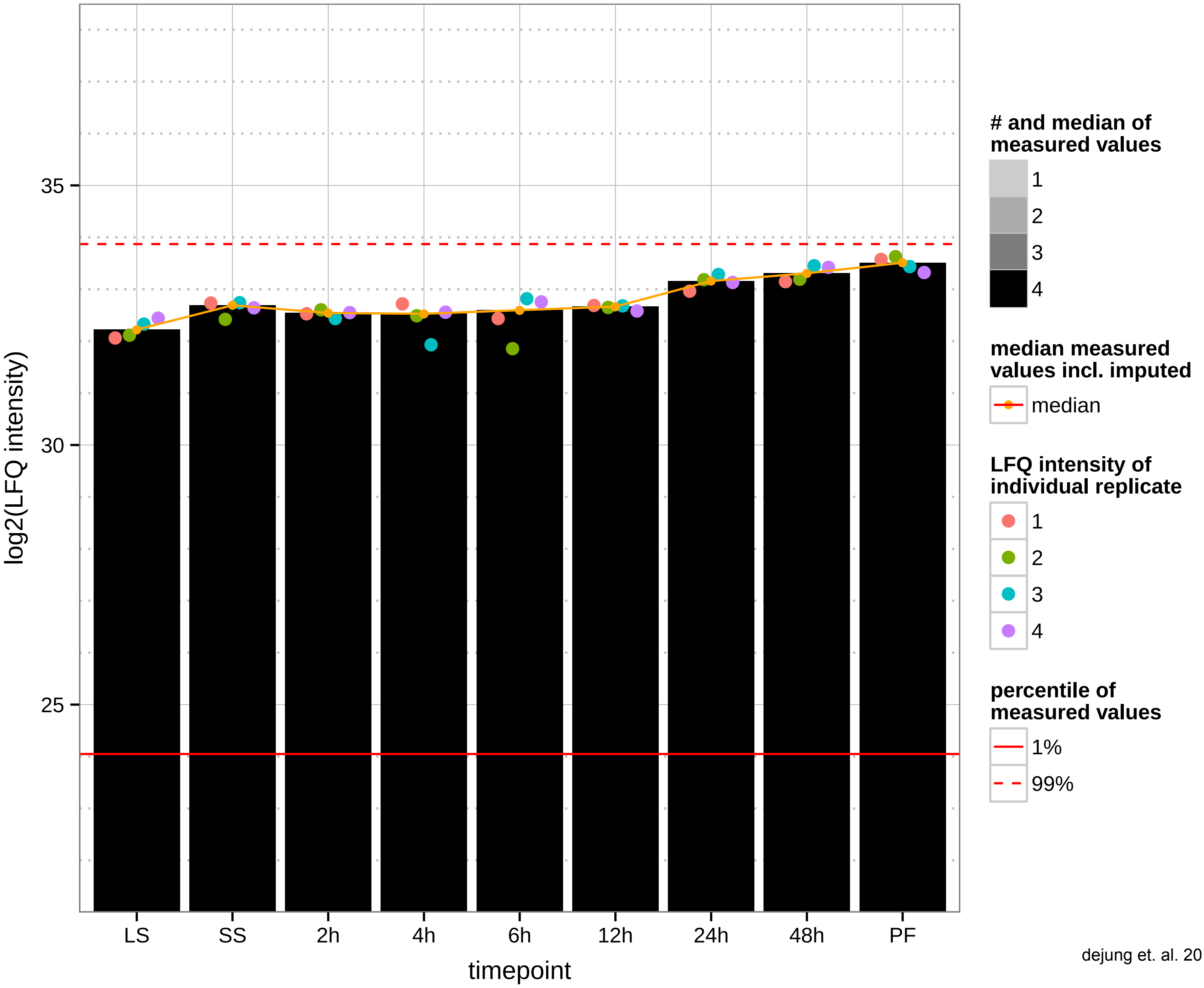
40S ribosomal protein SA, putative
Tb927.11.10910;Tb927.11.10790
AGOF: structural constituent of ribosome
AGOC: intracellular, organellar small ribosomal subunit, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome, small ribosomal subunit
PGOP: translation





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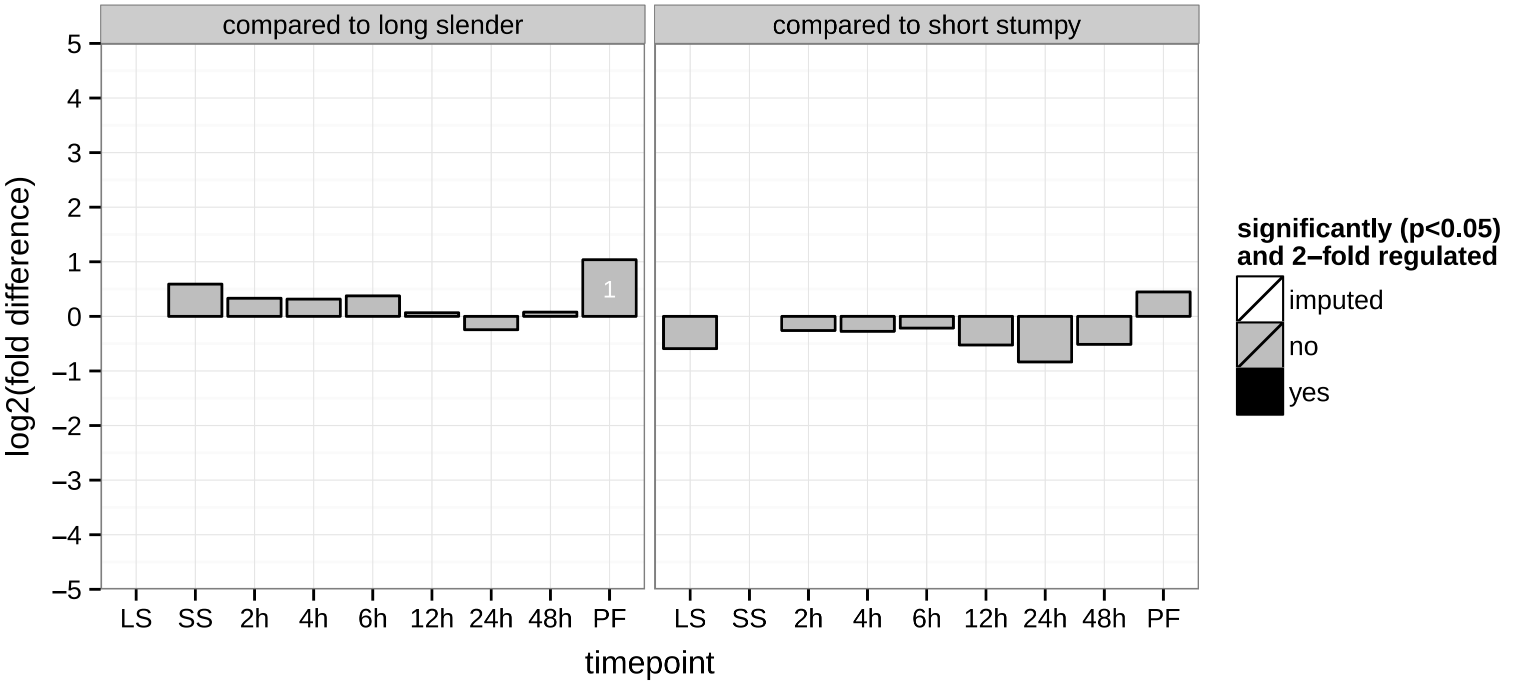
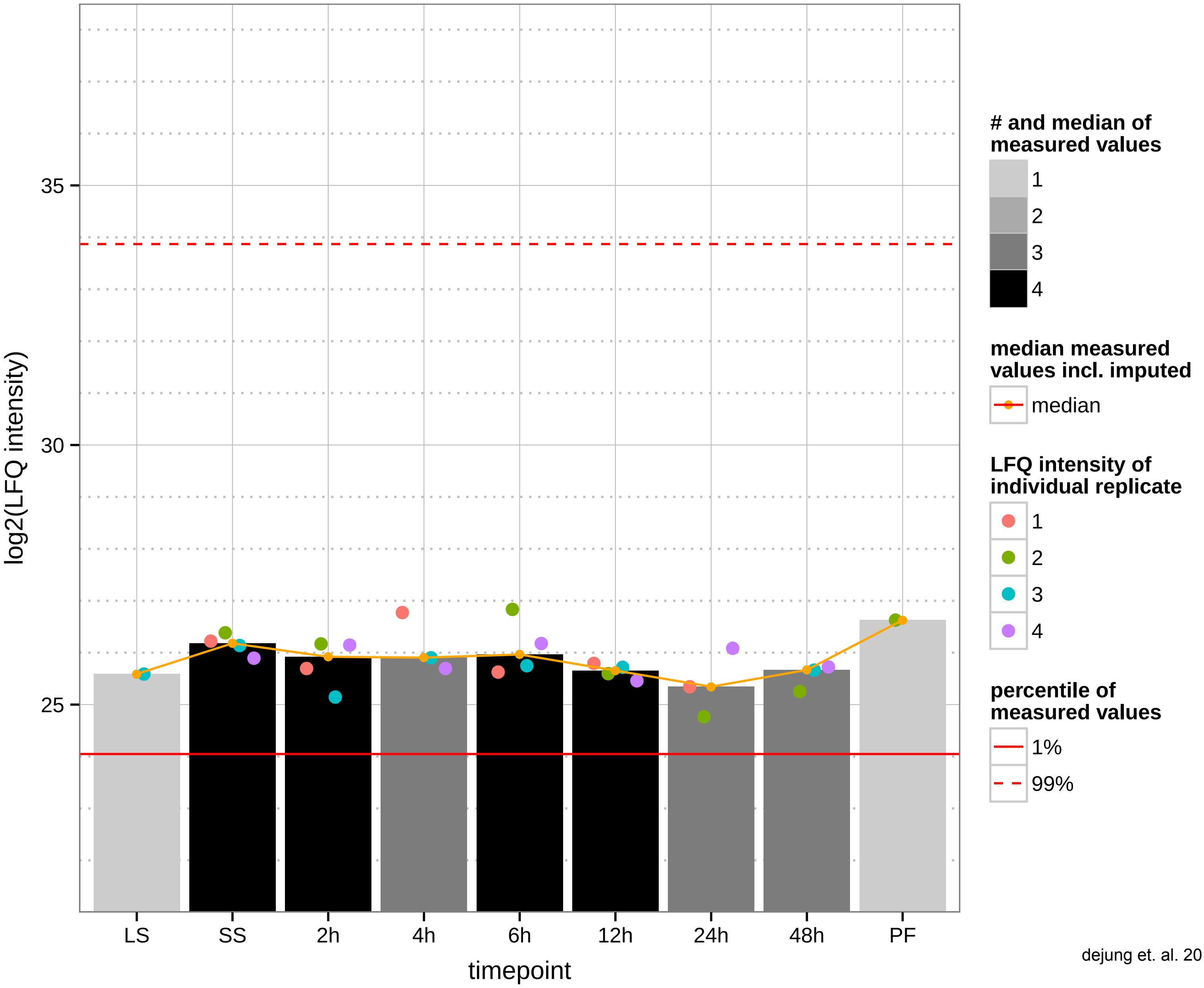
hypothetical protein, conserved
Tb927.11.1080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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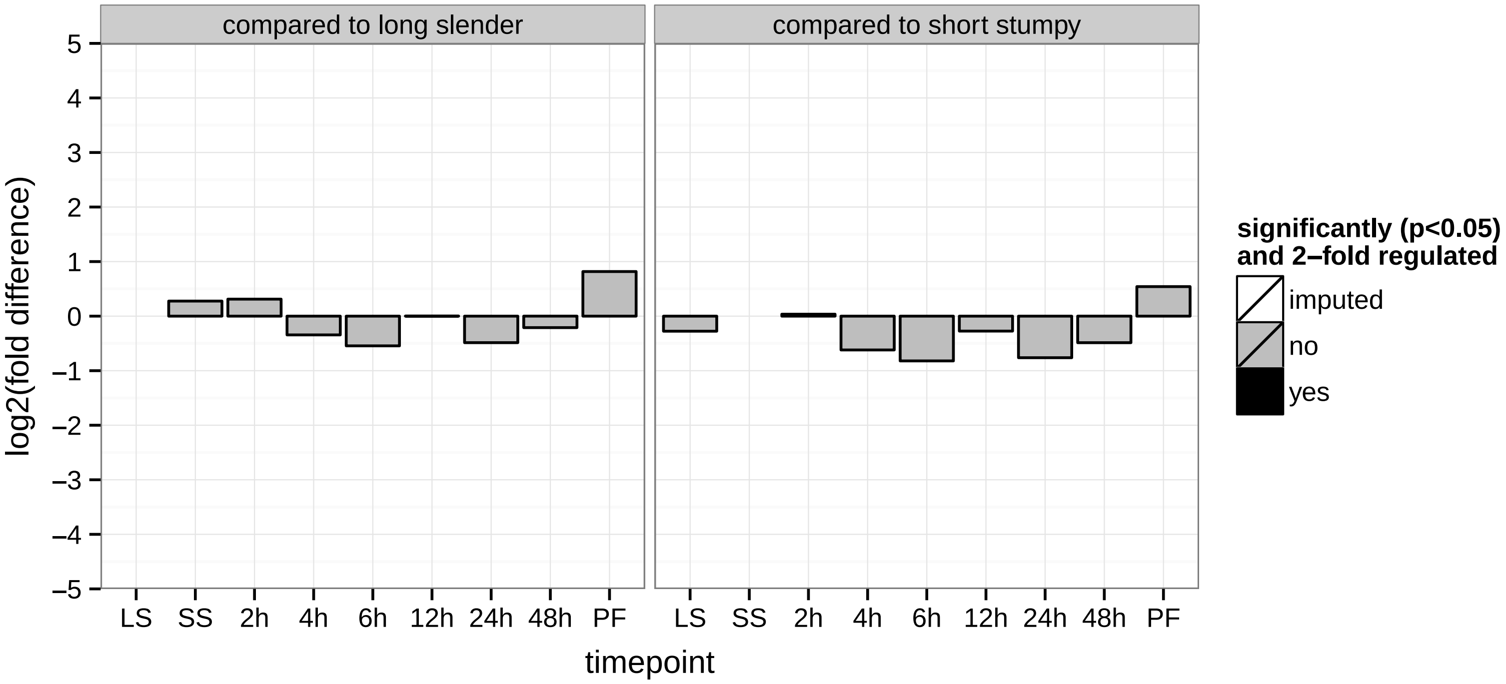
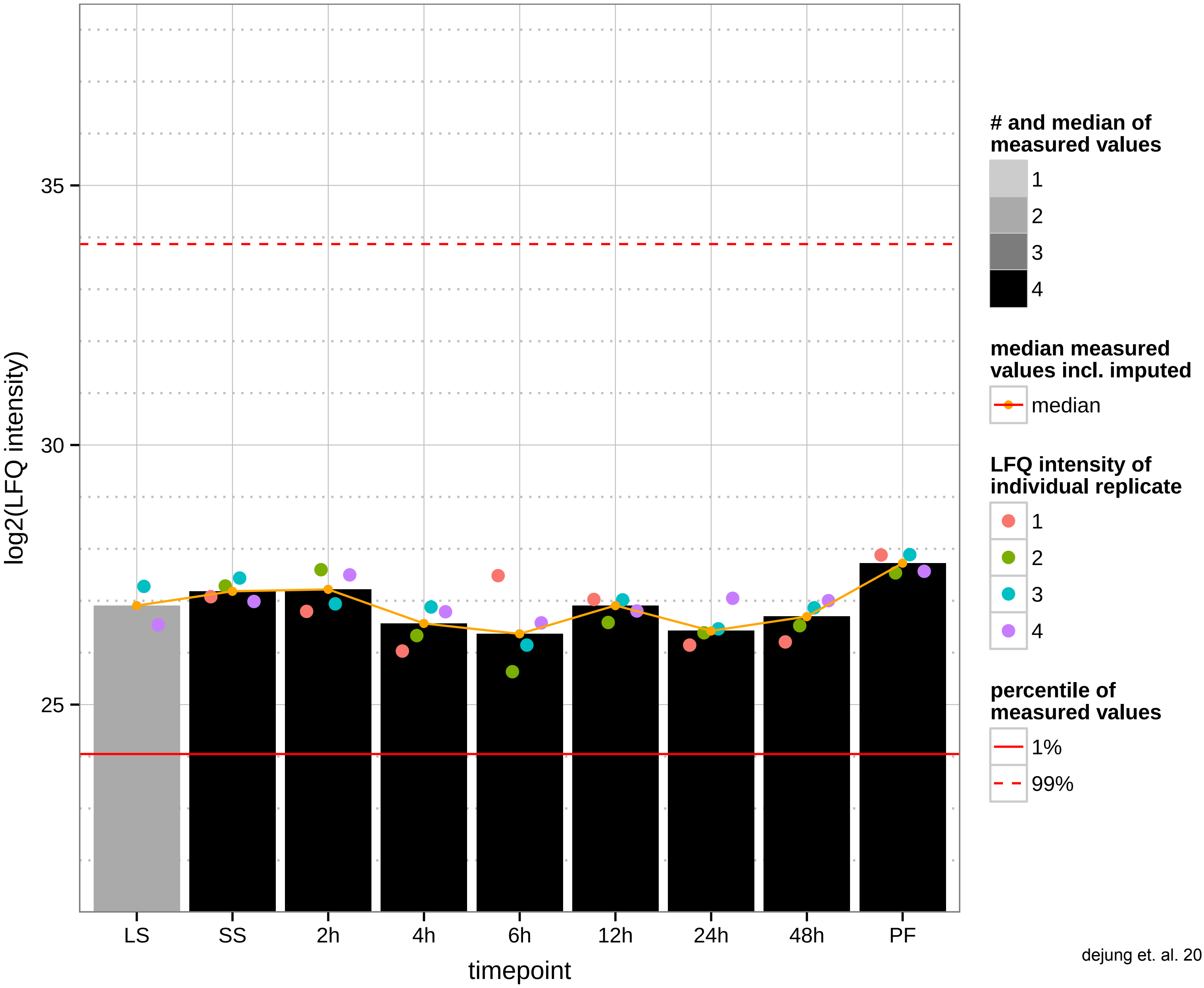
hypothetical protein, conserved
Tb927.11.10800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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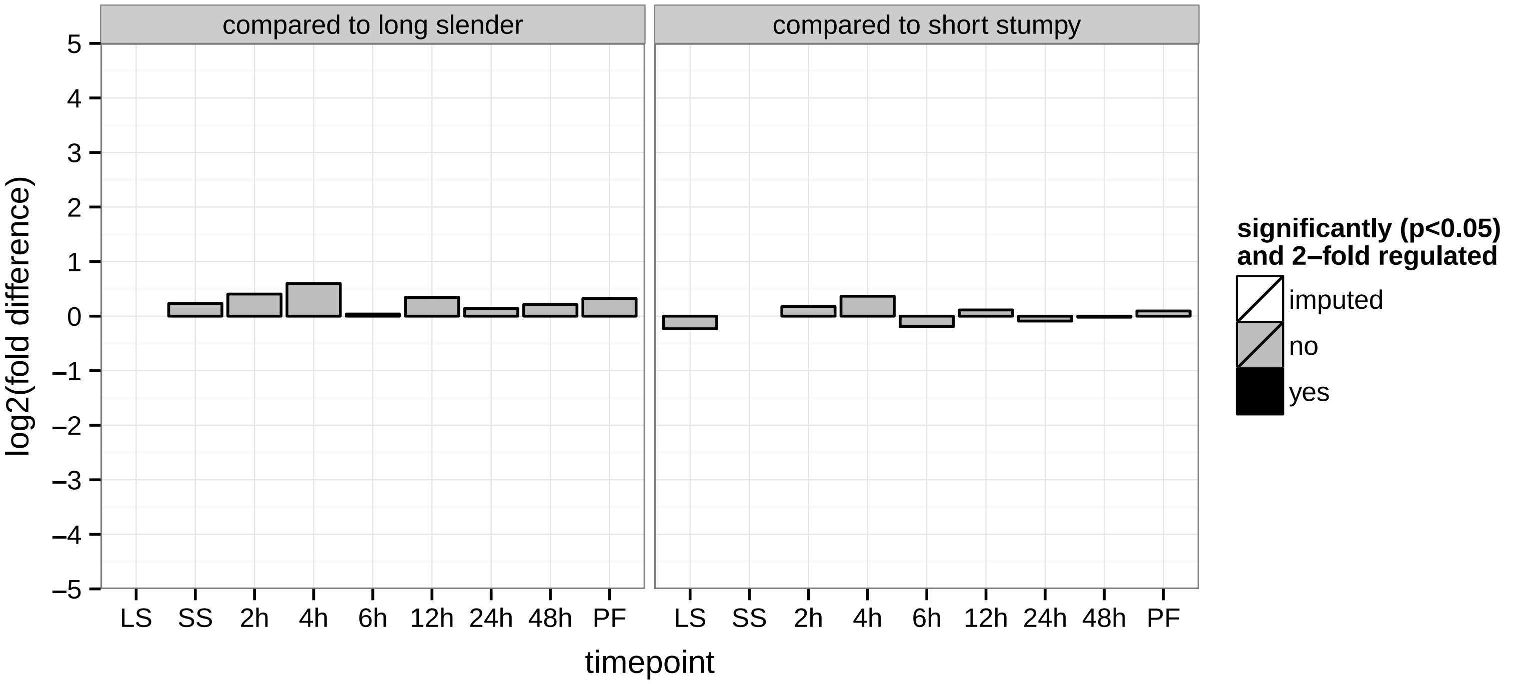
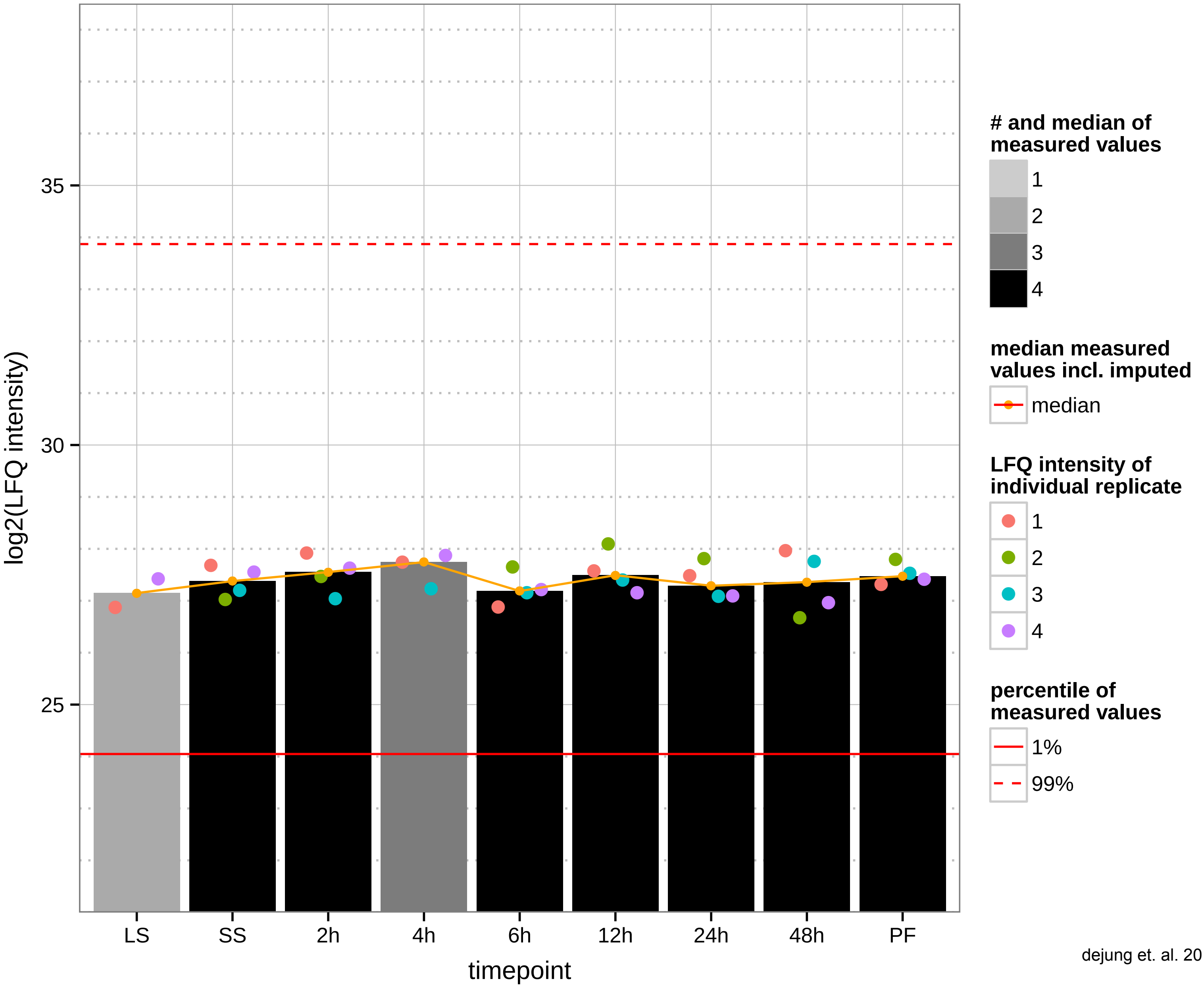
protein kinase ck2 regulatory subunit, putative, casein kinase II beta chain
Tb927.11.10820
AGOF: protein kinase regulator activity
AGOC: protein kinase CK2 complex
AGOP: null
PGOF: protein kinase regulator activity
PGOC: protein kinase CK2 complex
PGOP: null





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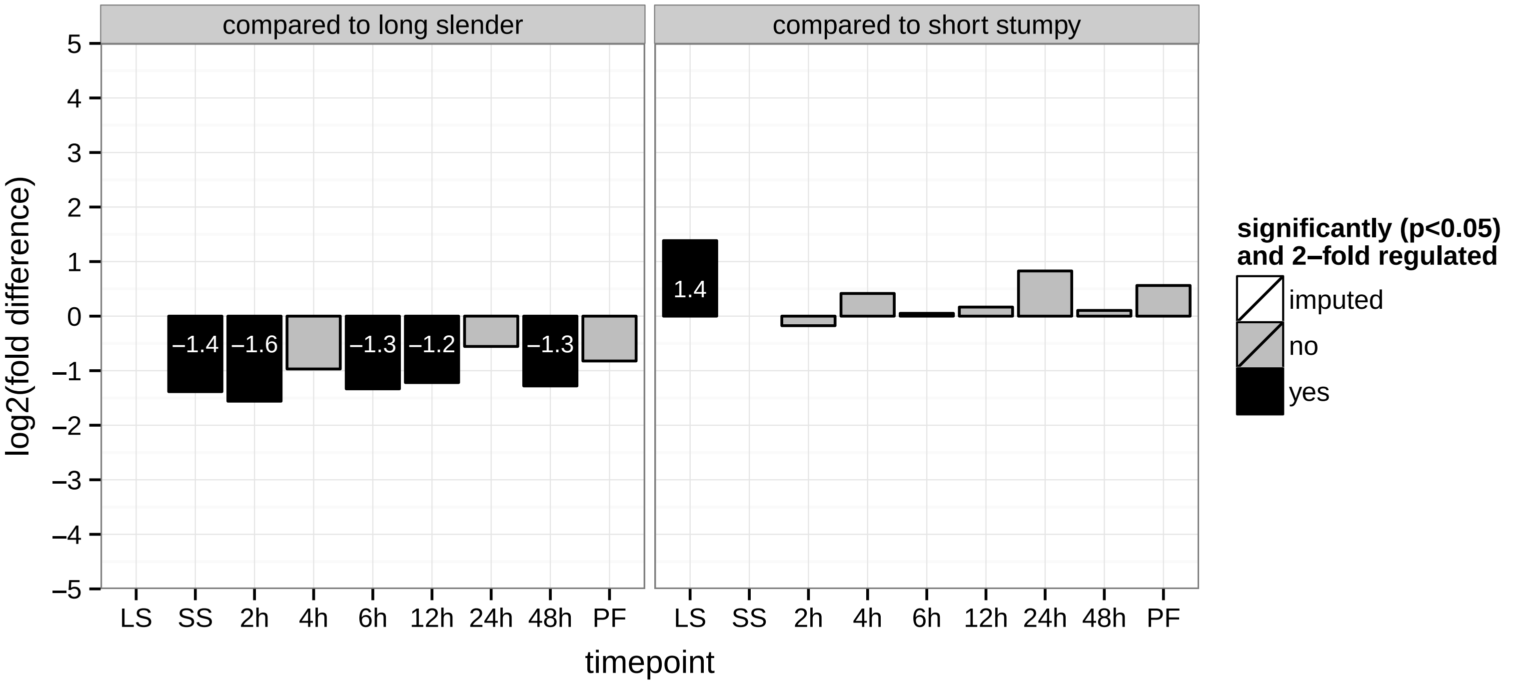
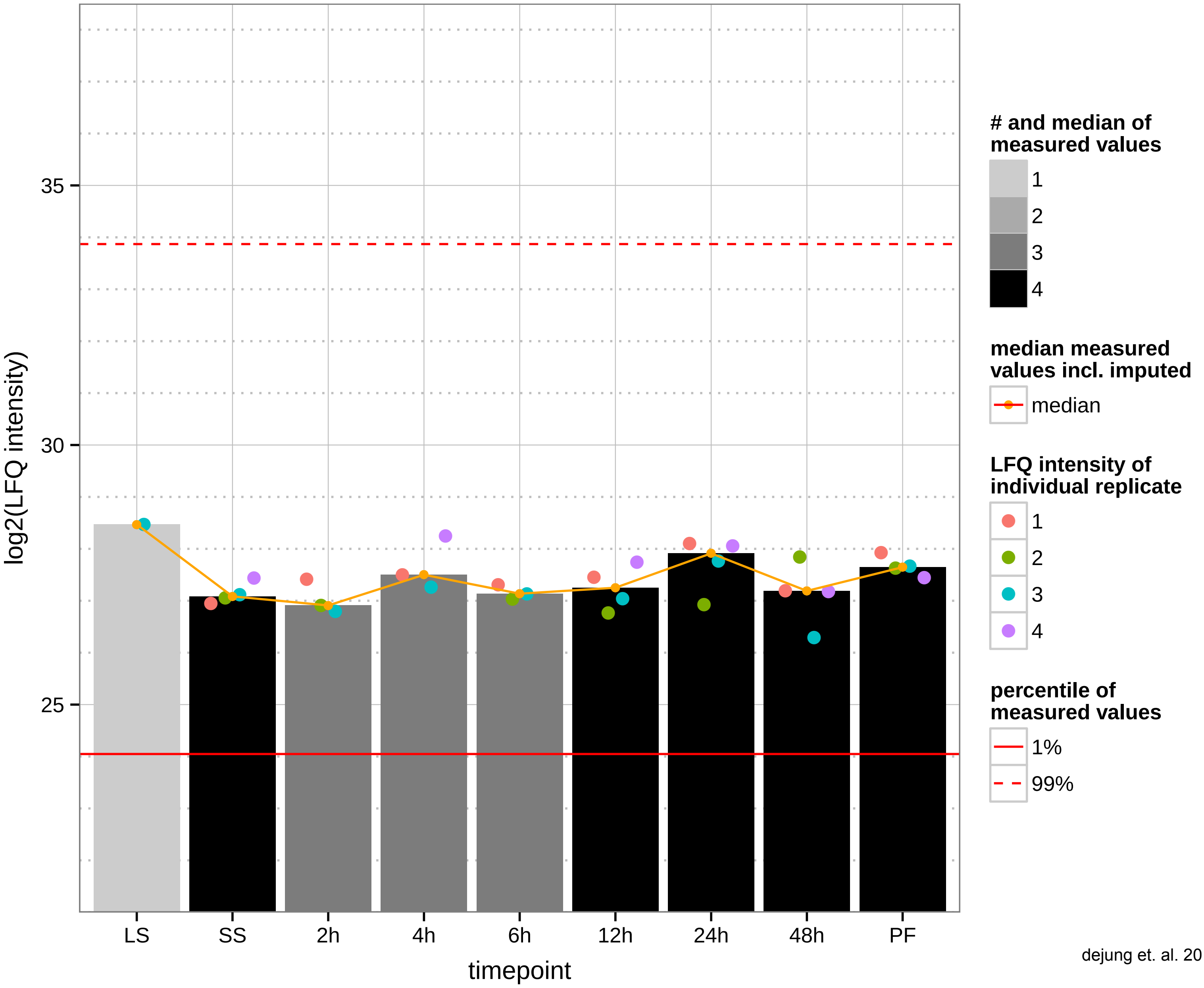
hypothetical protein, conserved
Tb927.11.10840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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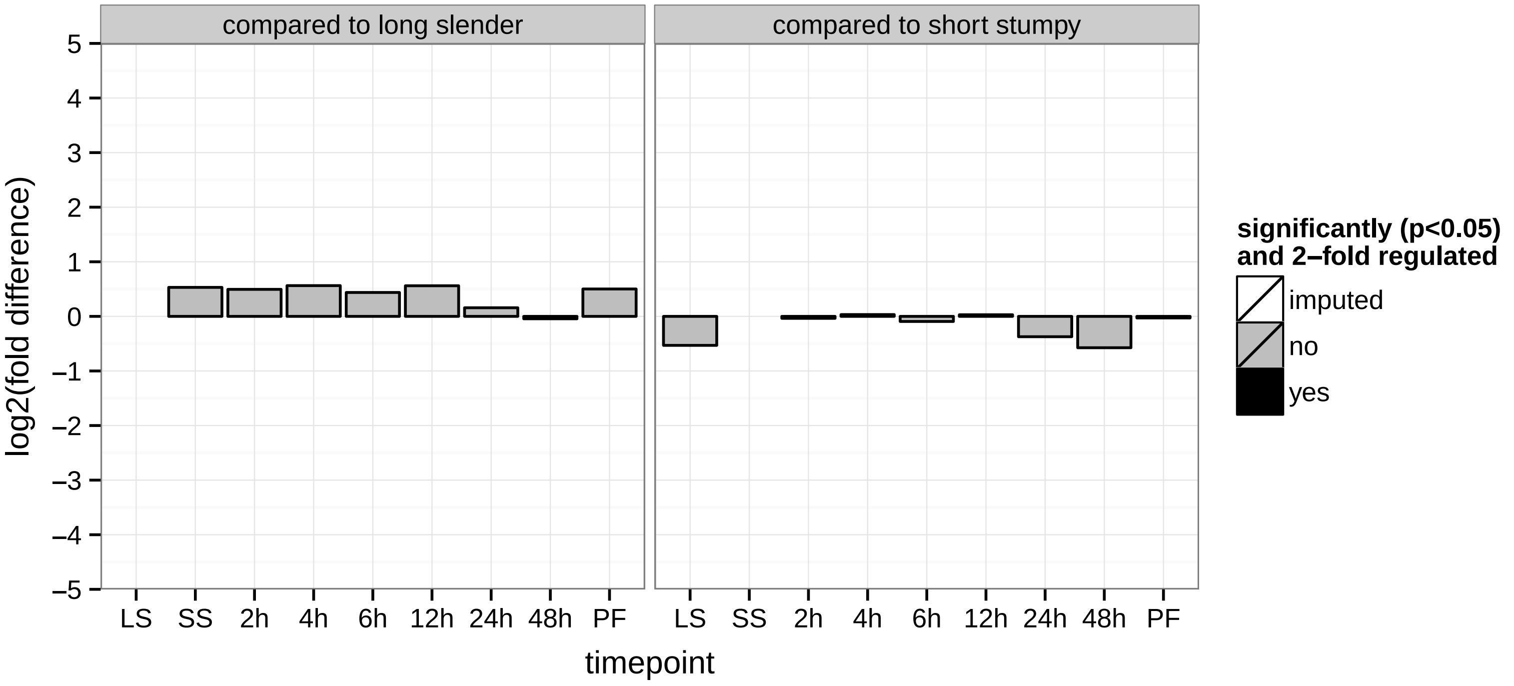
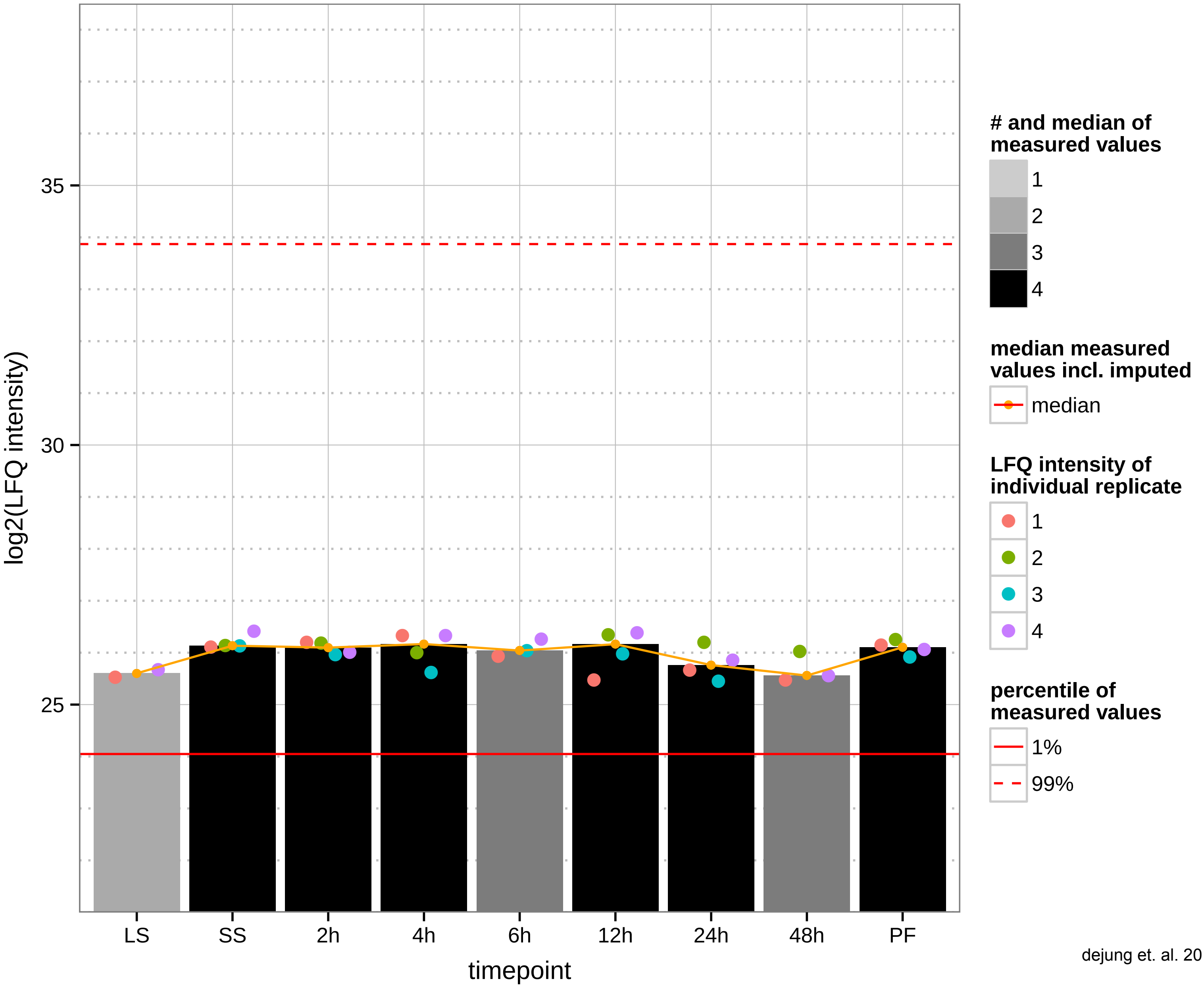
32 kDa ER–associated protein (ERAP32)
Tb927.11.10870
AGOF: null
AGOC: endoplasmic reticulum
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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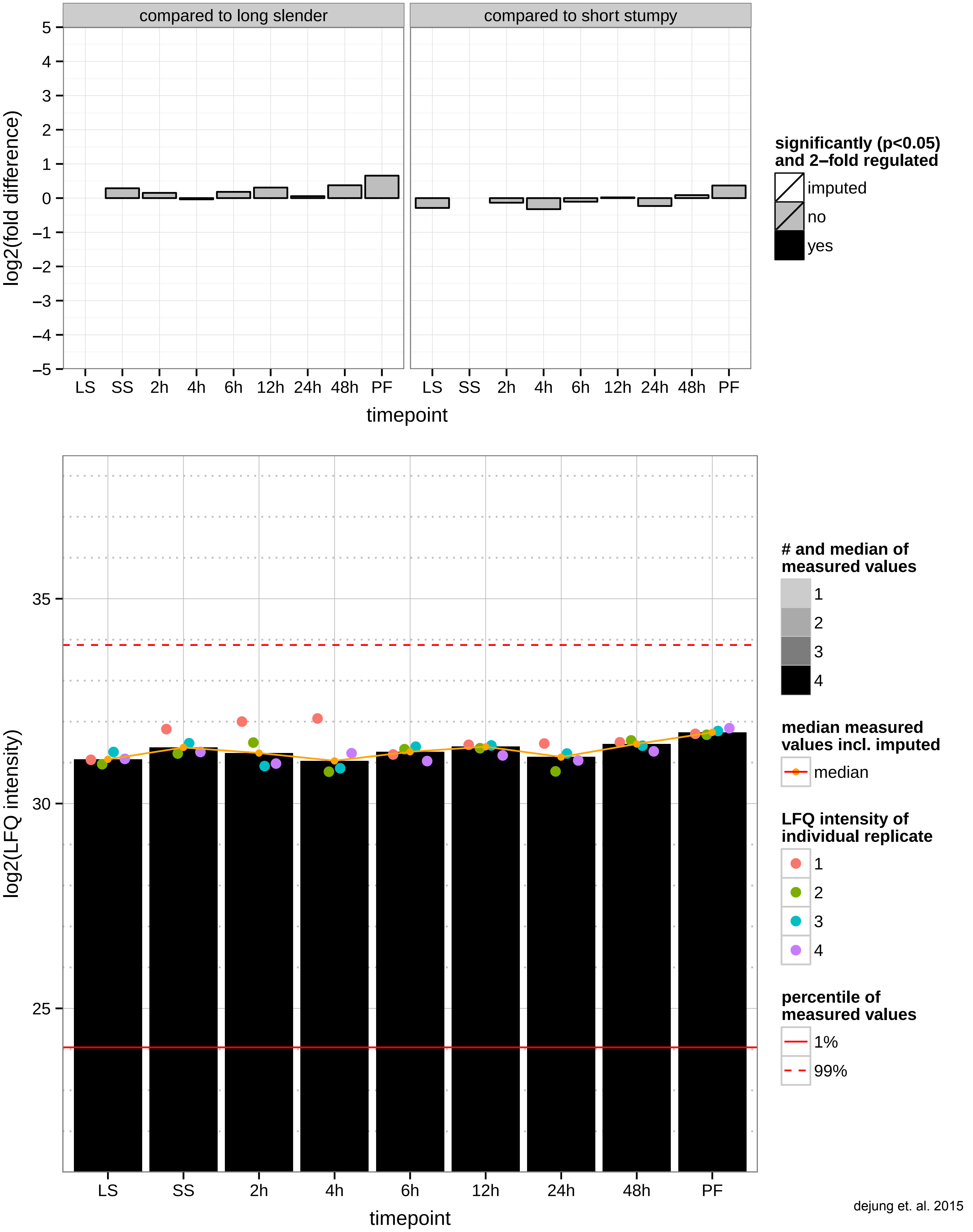
calpain–like protein, putative, cytoskeleton assocociated protein, calpain, cysteine peptidase, Clan CA, family C2
Tb927.11.1090
AGOF: calcium–dependent cysteine–type endopeptidase activity
AGOC: intracellular, cytoplasm
AGOP: proteolysis
PGOF: calcium–dependent cysteine–type endopeptidase activity, null
PGOC: intracellular, null
PGOP: proteolysis, null



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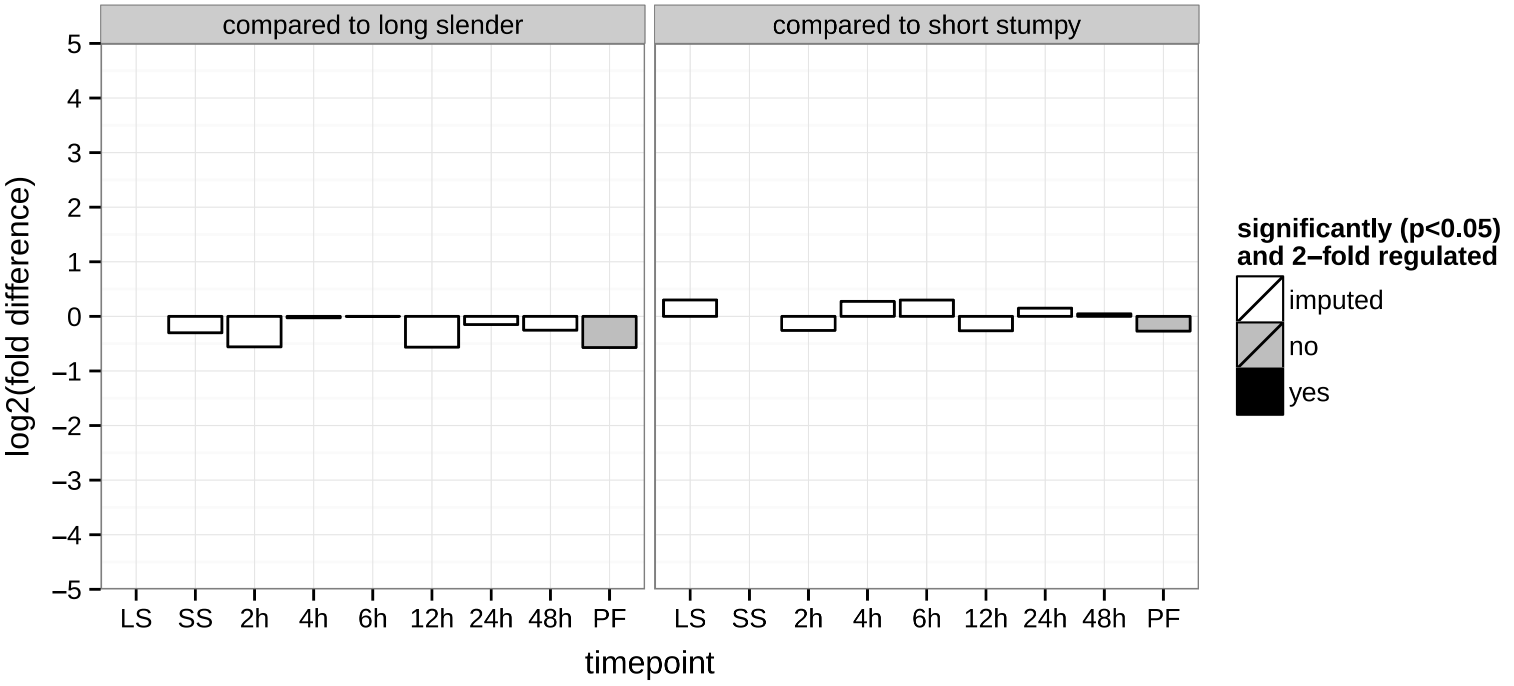
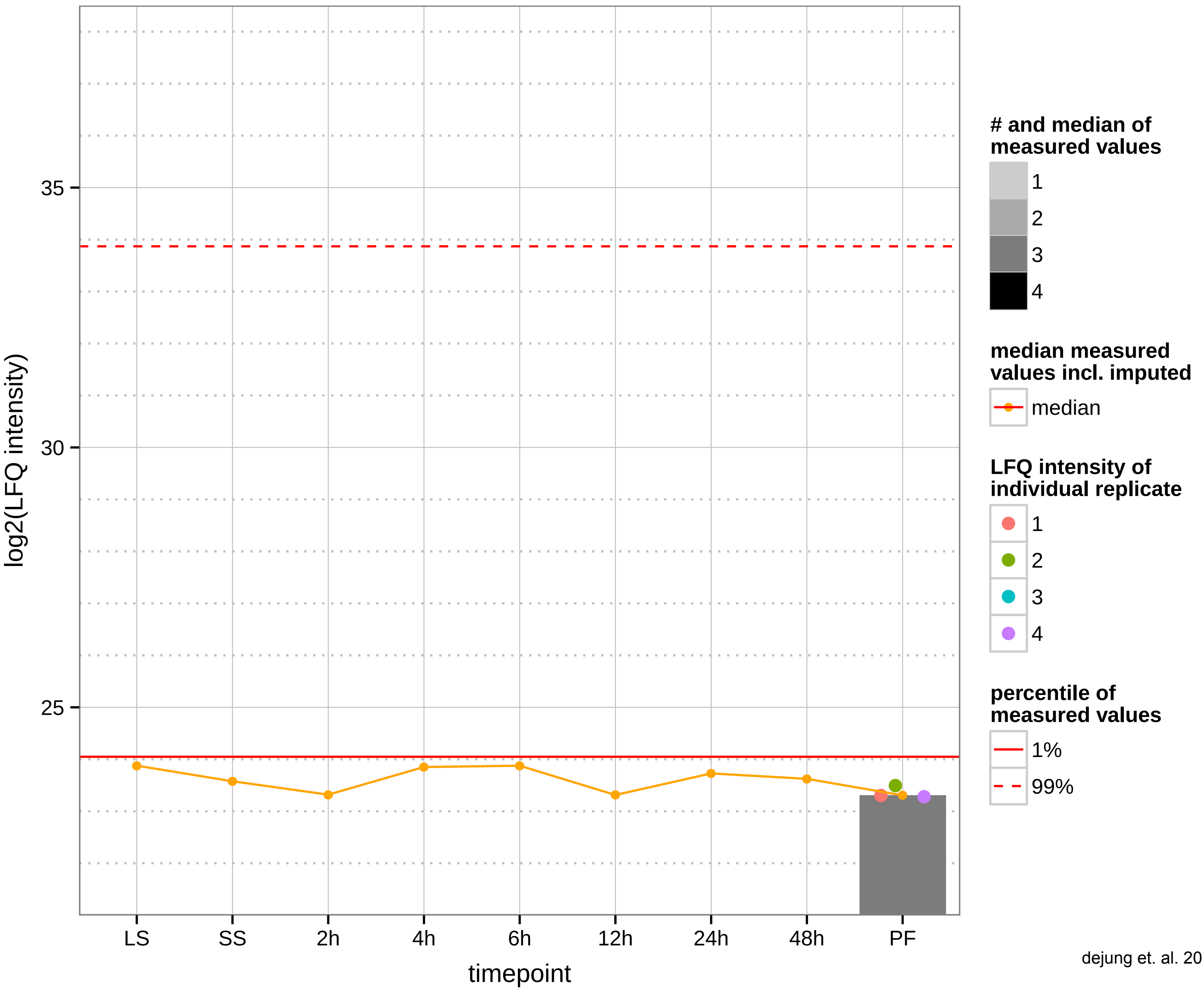
delta tubulin, tubulin delta chain (TUBD1)
Tb927.11.10930
AGOF: GTP binding, structural molecule activity
AGOC: microtubule, protein complex
AGOP: cell growth, microtubule–based movement, protein polymerization
PGOF: null
PGOC: protein complex
PGOP: protein polymerization





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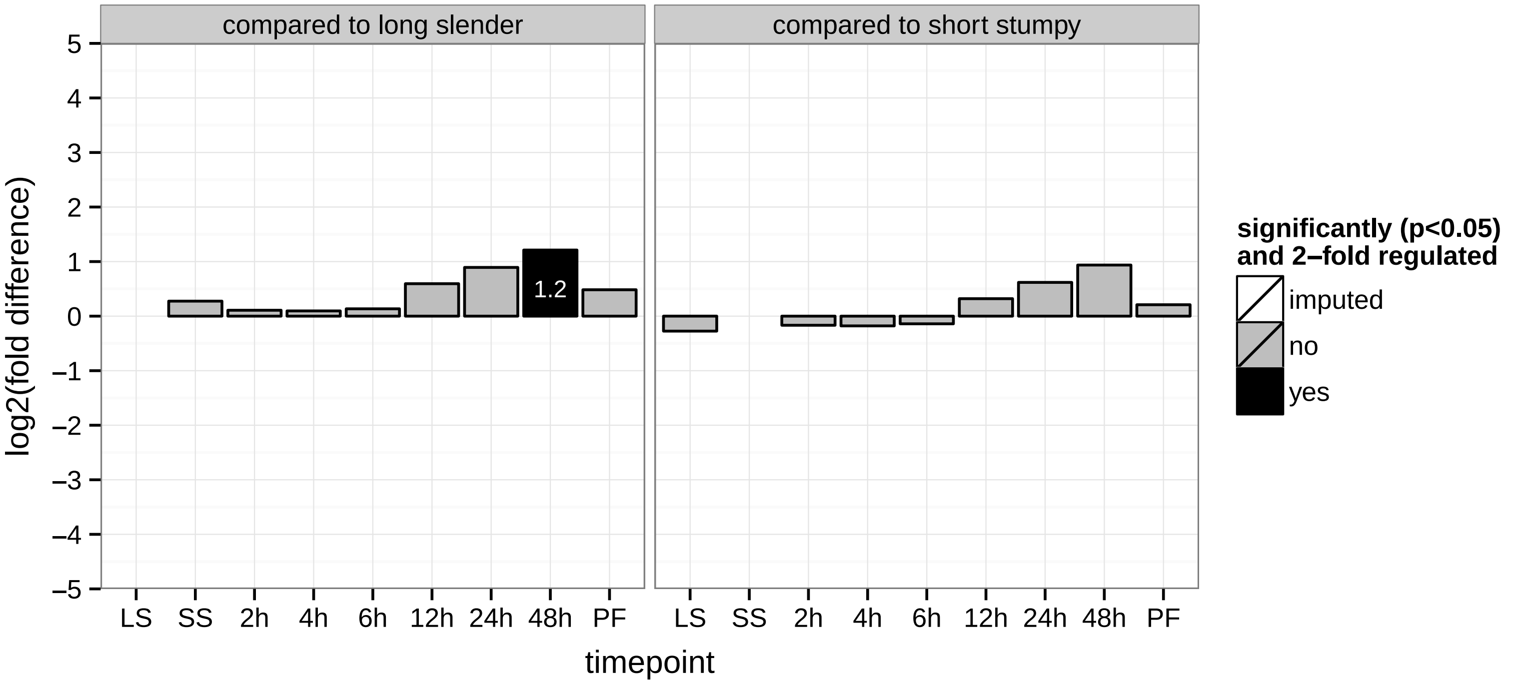
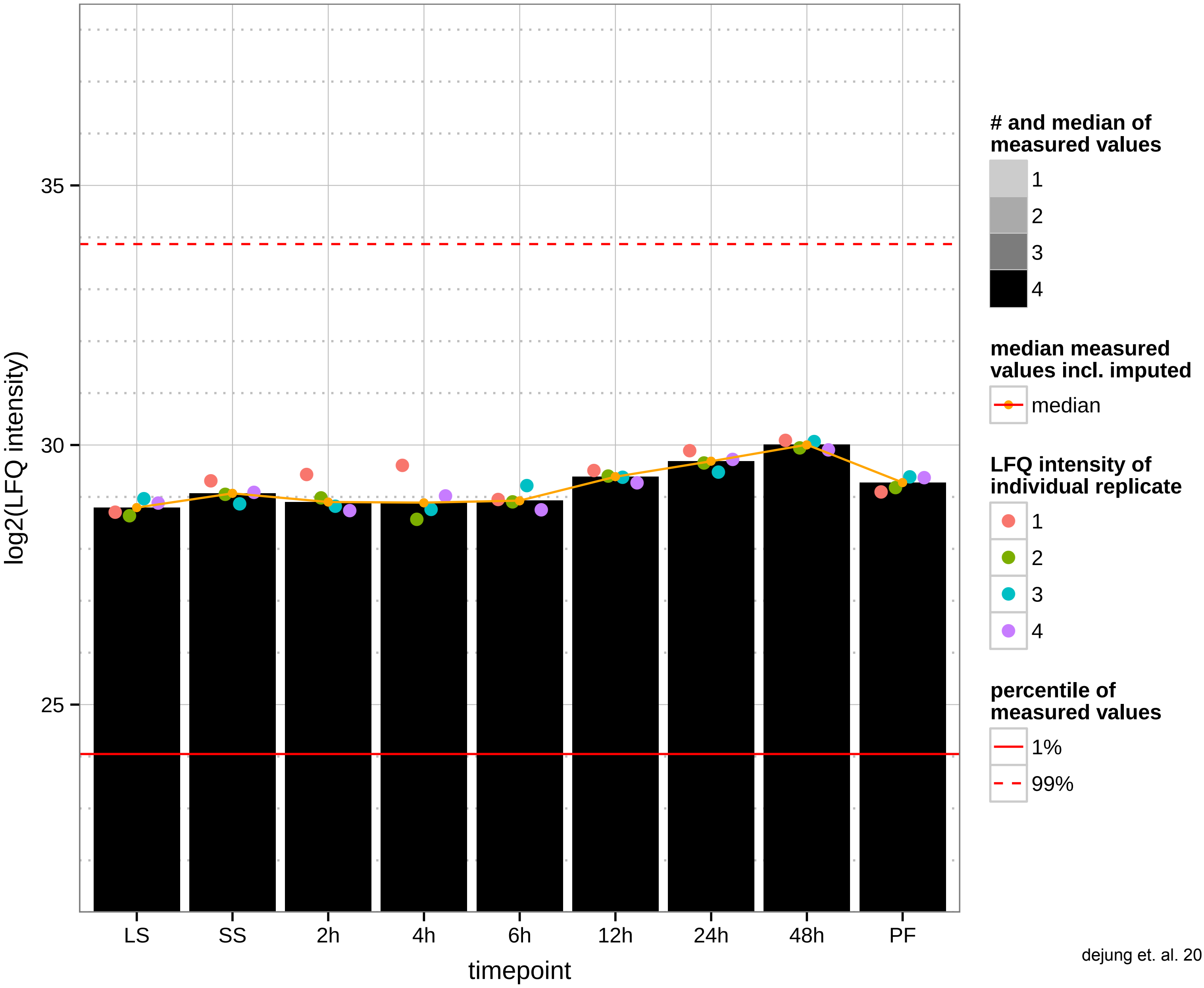
translation initiation factor 2 subunit, putative
Tb927.11.10990
AGOF: GTP binding, translation initiation factor activity
AGOC: eukaryotic translation initiation factor 2B complex
AGOP: cellular biosynthetic process, translational initiation
PGOF: null
PGOC: null
PGOP: cellular biosynthetic process, cellular metabolic process





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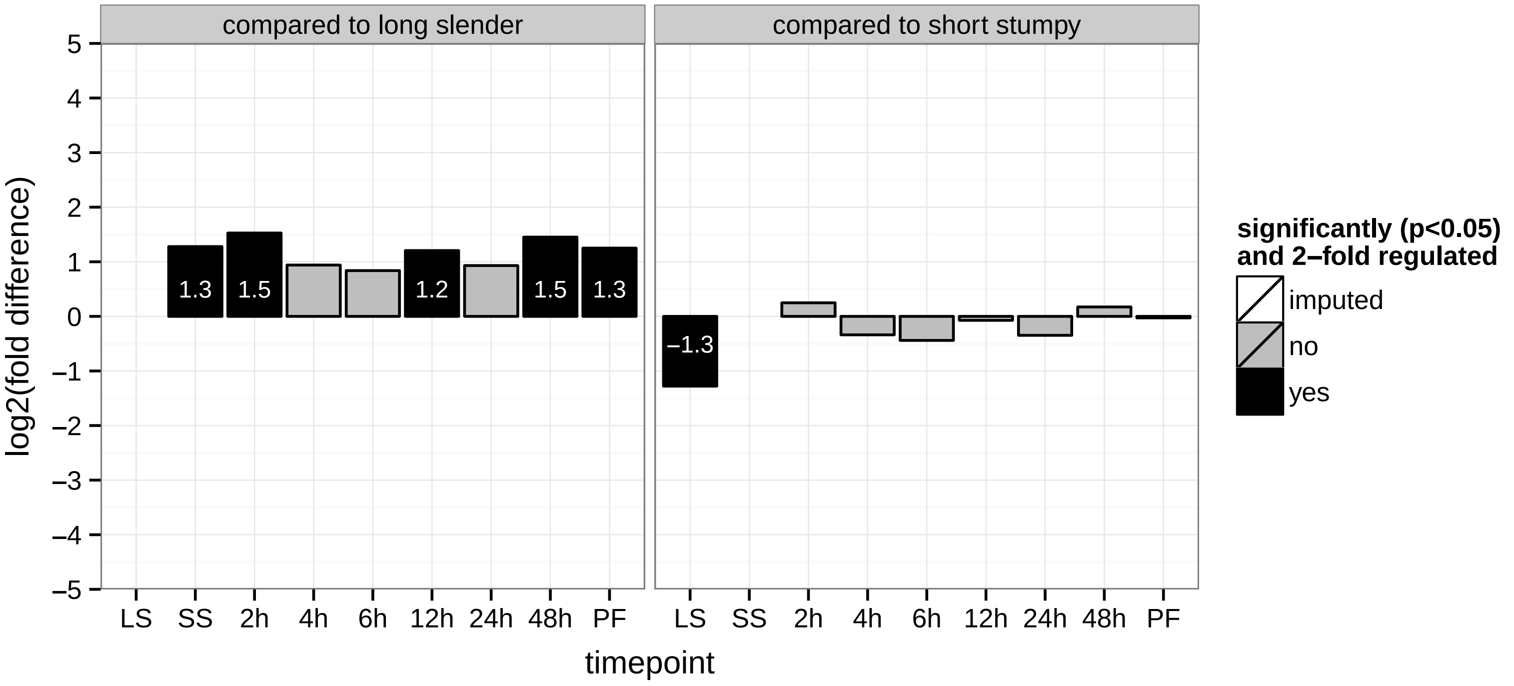
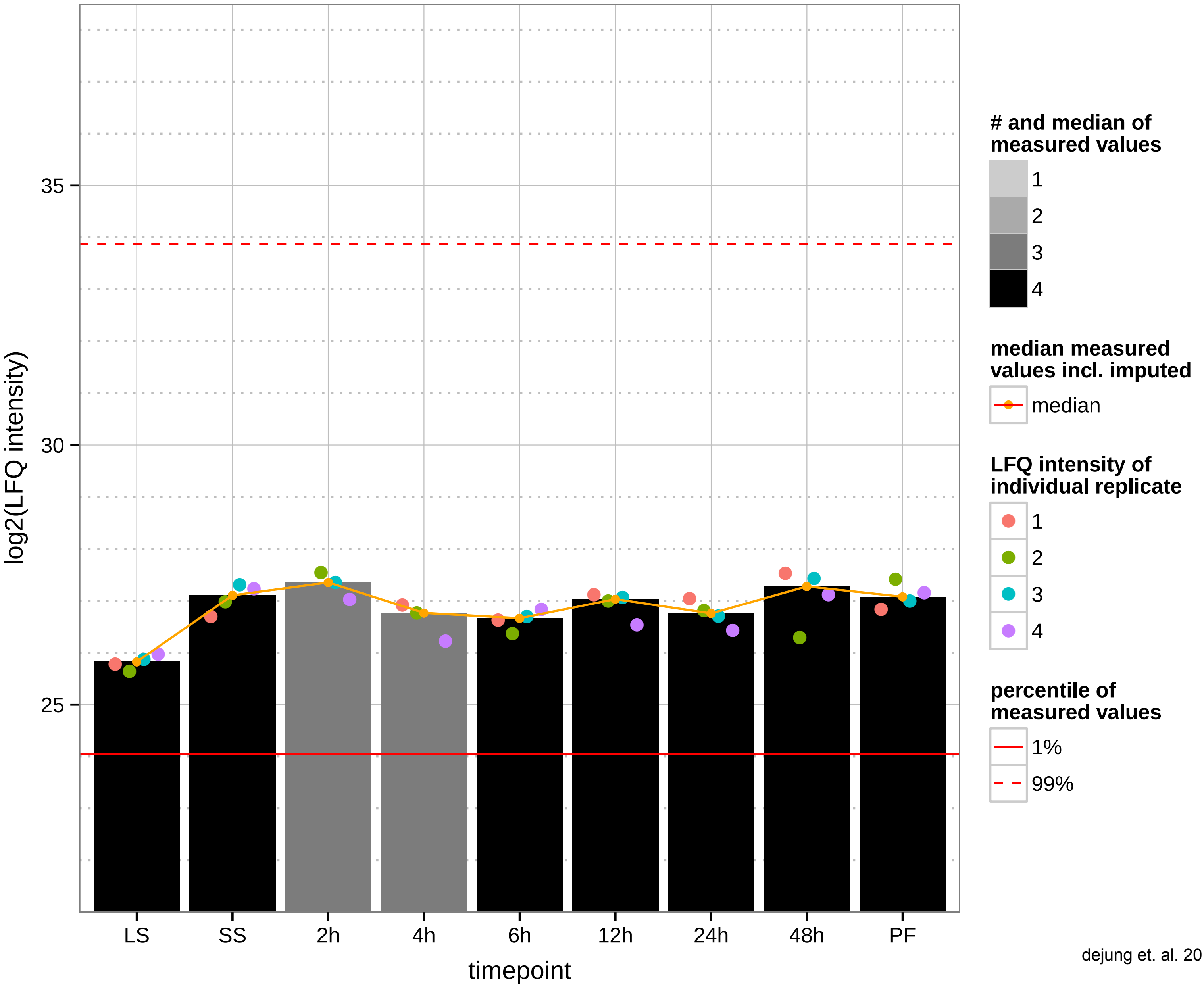
hypothetical protein, conserved
Tb927.11.11000
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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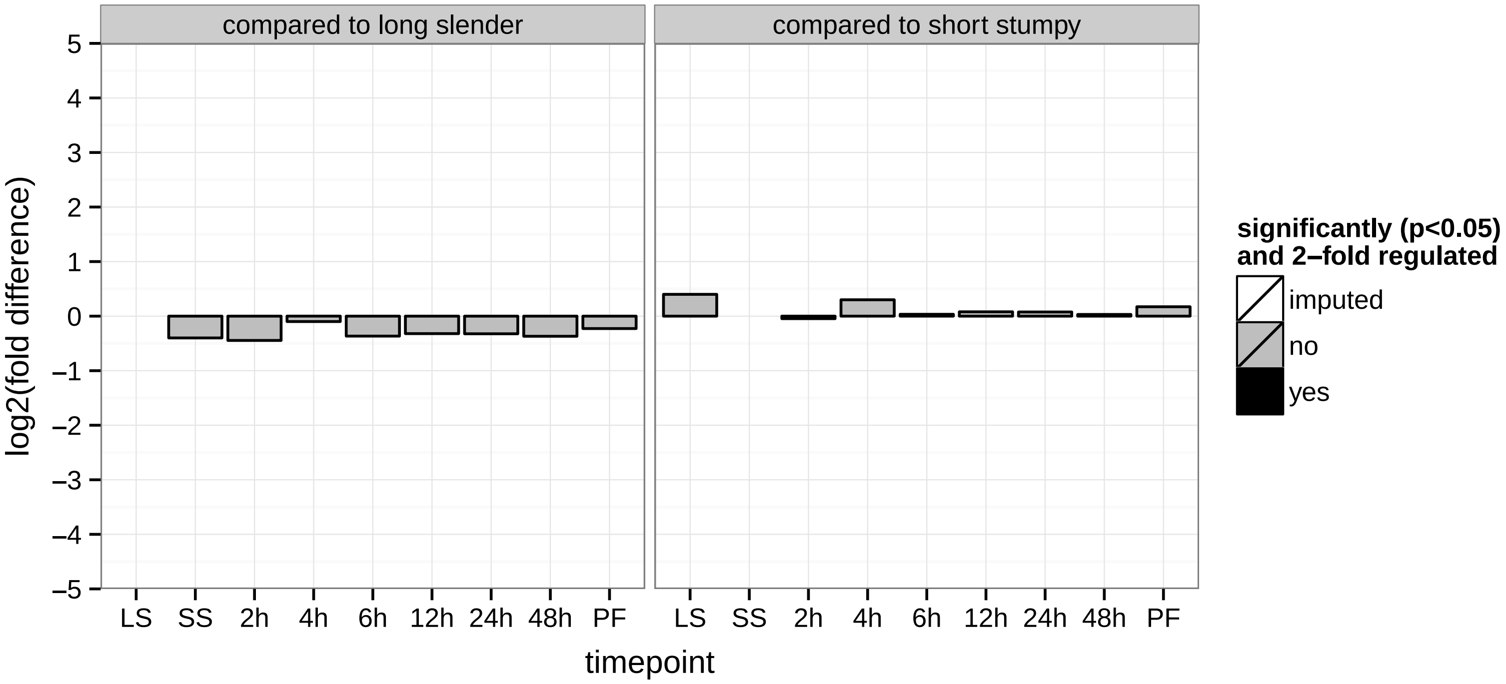
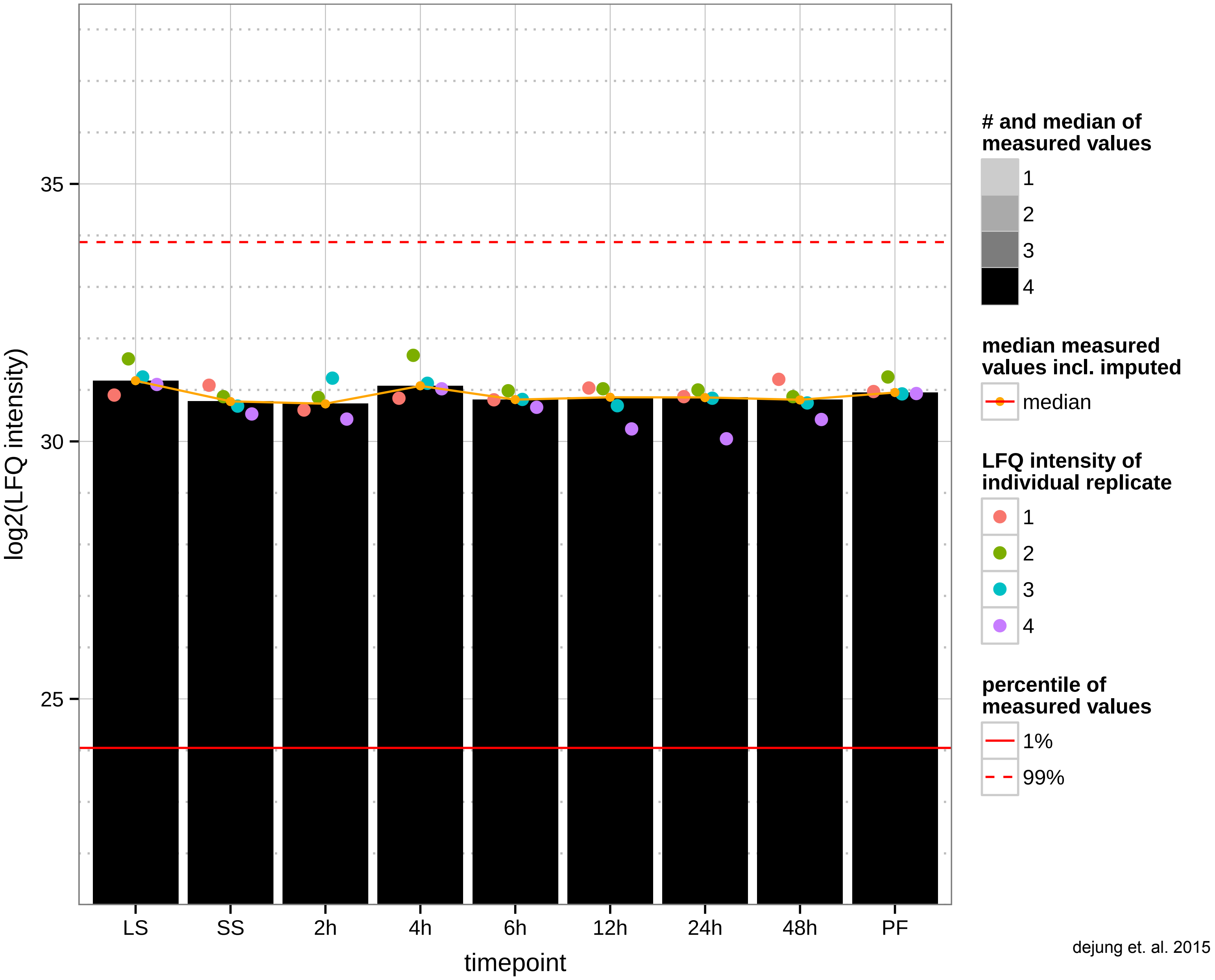
hypothetical protein, conserved
Tb927.11.11010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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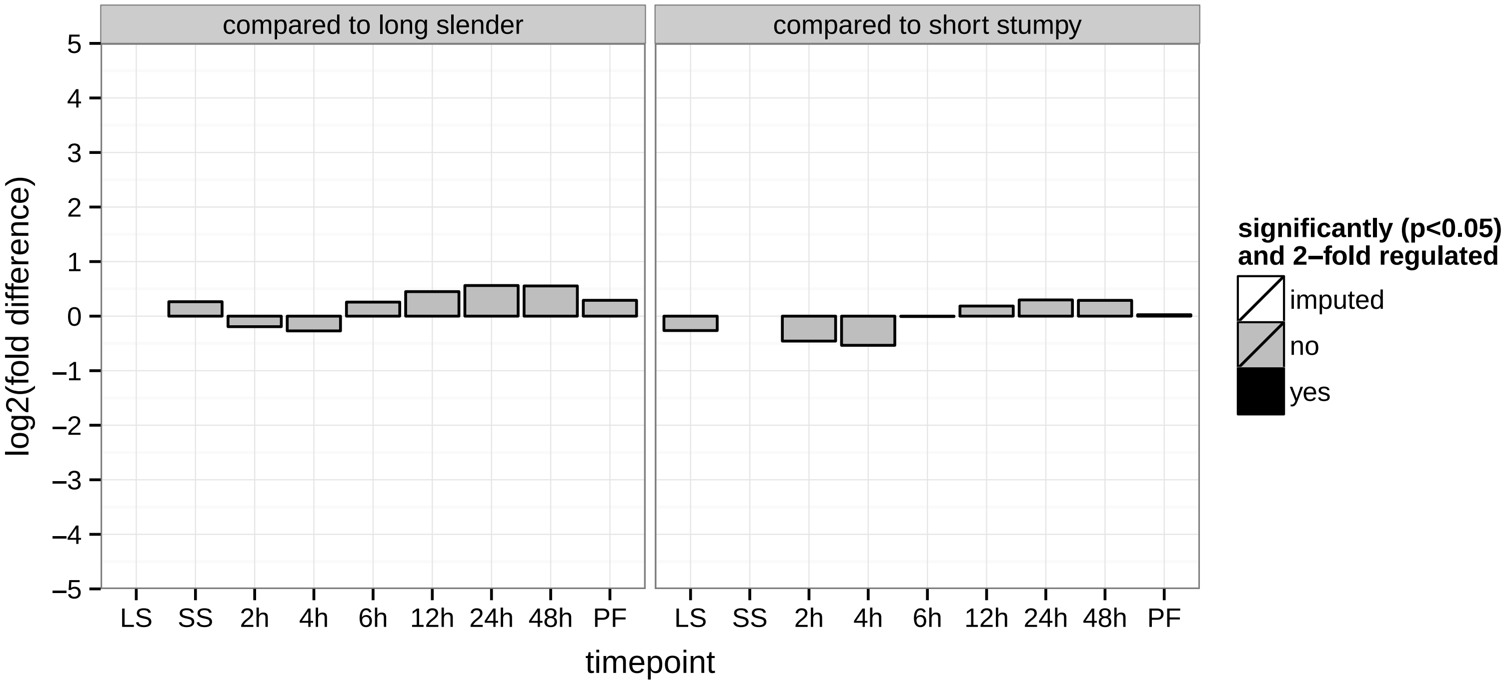
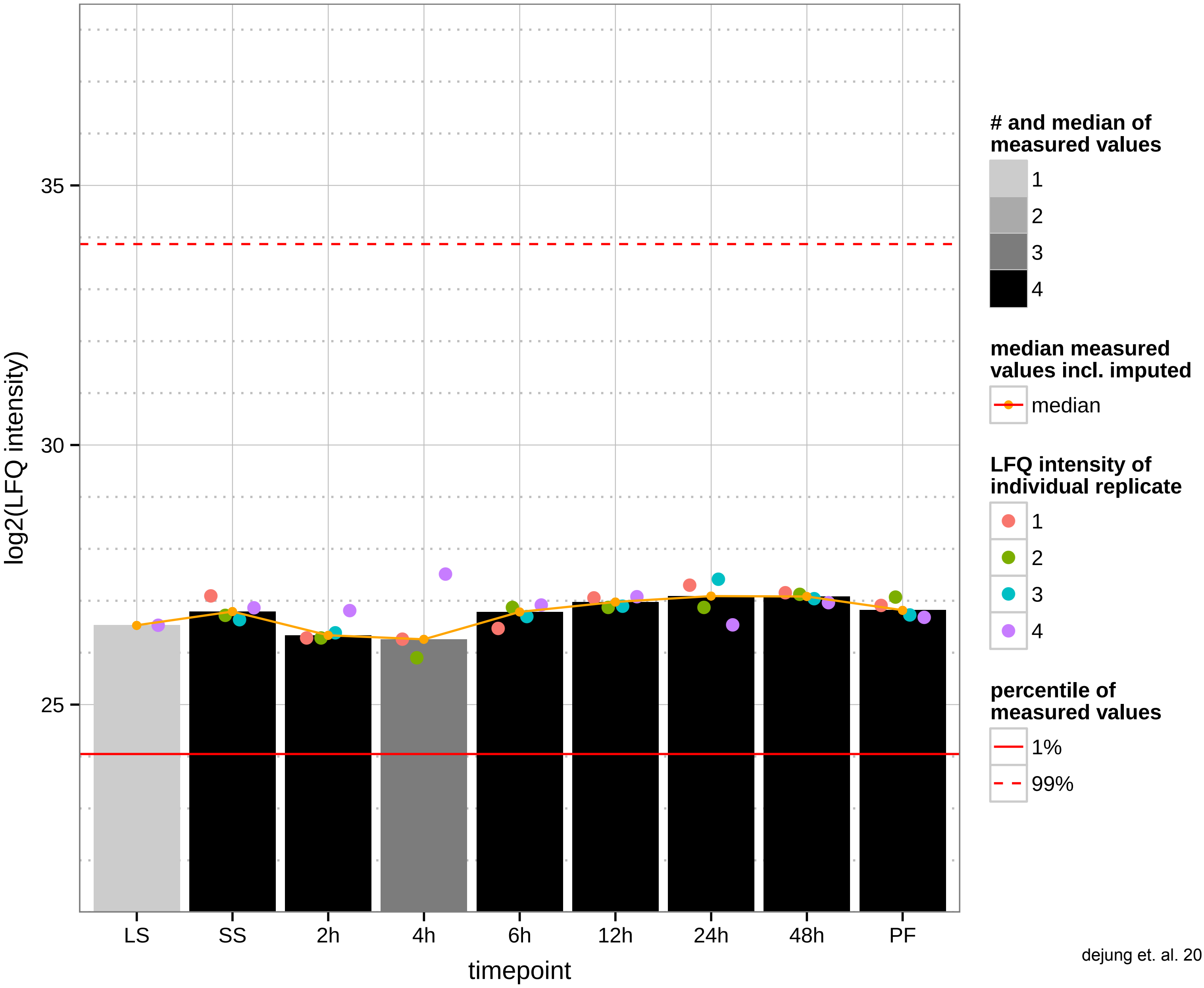
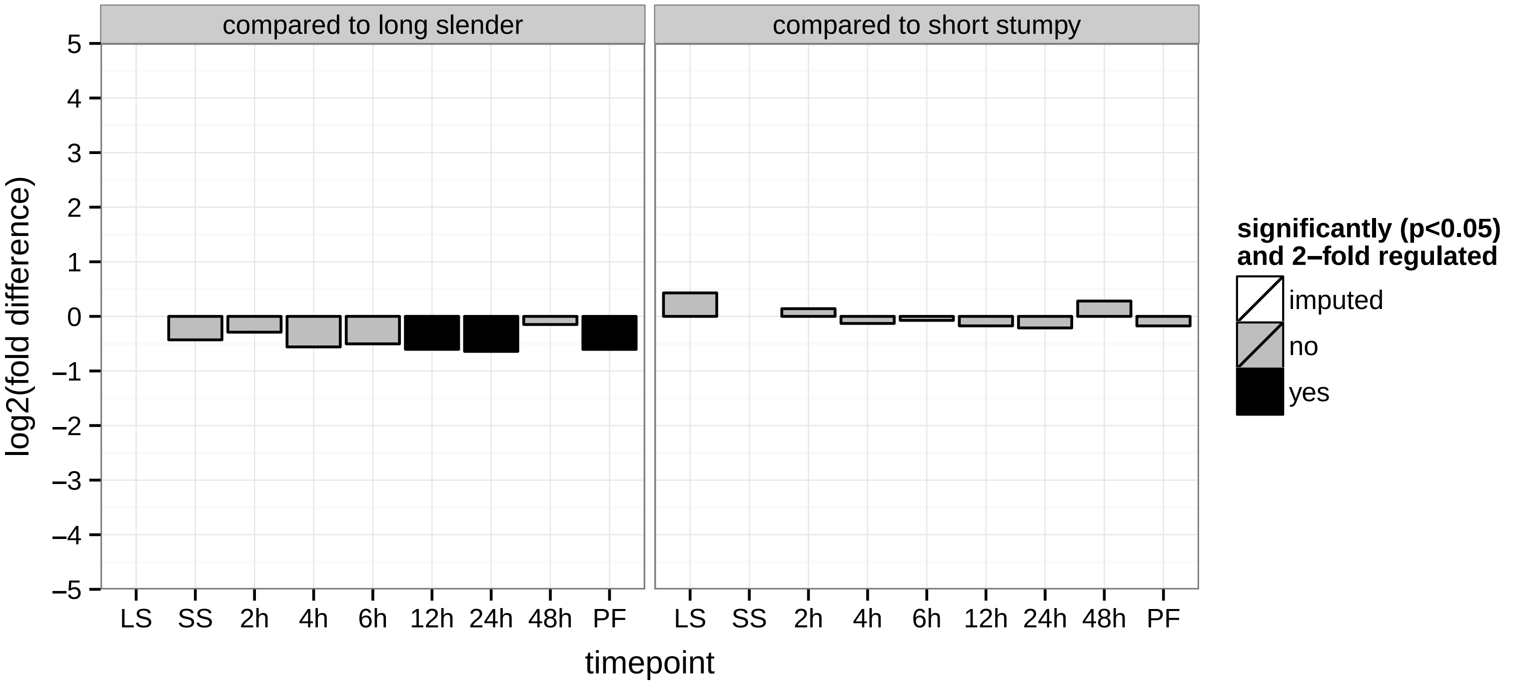
Nucleoporin (TbNup140)
Tb927.11.11090
AGOF: null
AGOC: nuclear pore
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

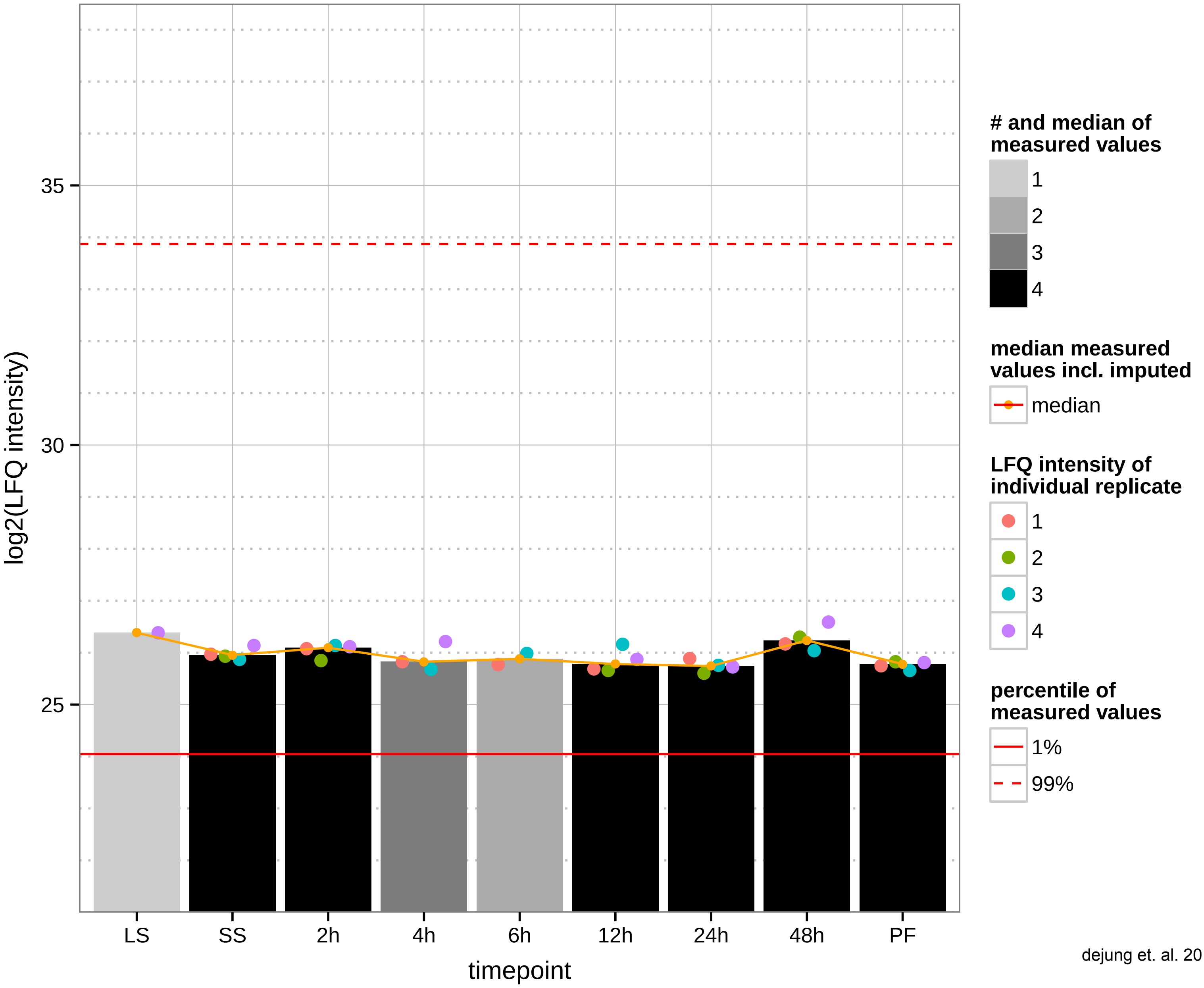




dejung et. al. 2015

calpain–like cysteine peptidase, putative, calpain
Tb927.11.1110
AGOF: null, calcium–dependent cysteine–type endopeptidase activity
AGOC: null, intracellular
AGOP: null, proteolysis
PGOF: null, calcium–dependent cysteine–type endopeptidase activity
PGOC: null, intracellular
PGOP: null, proteolysis





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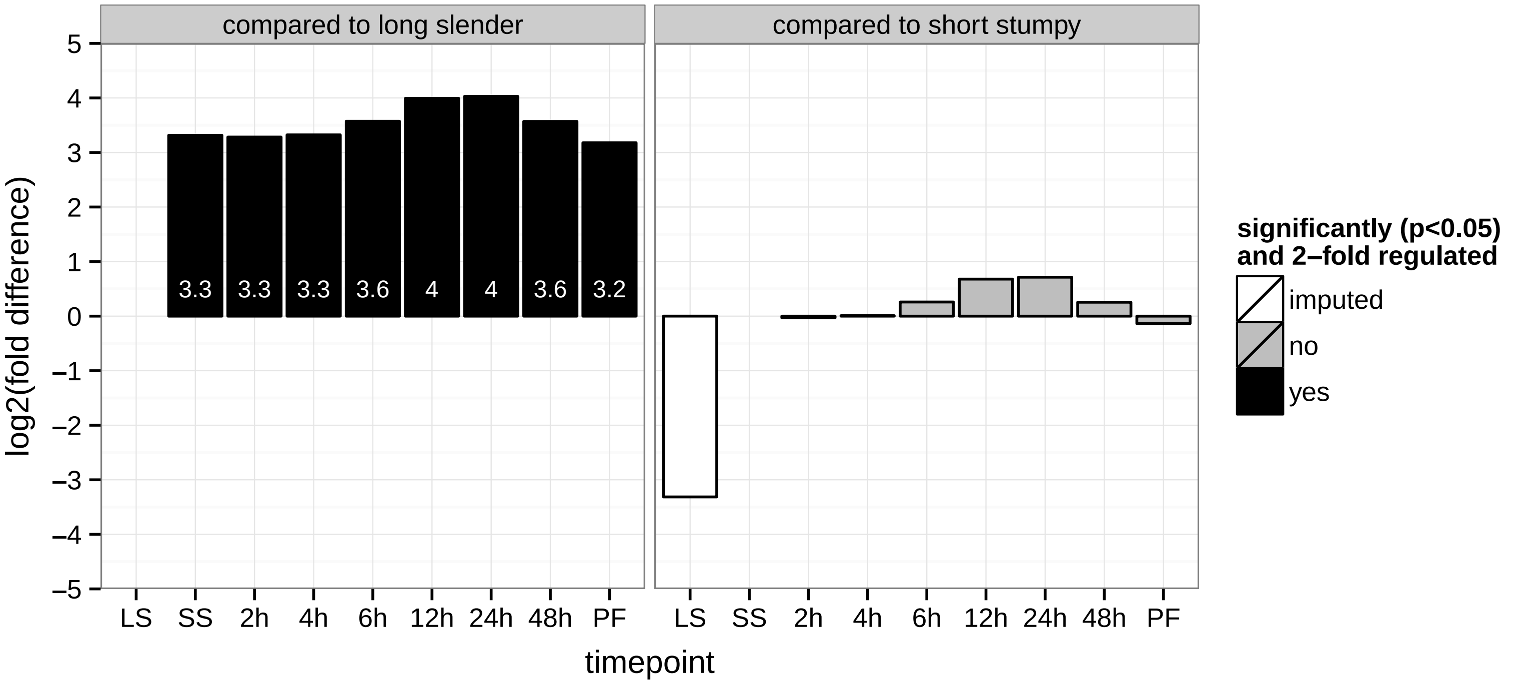
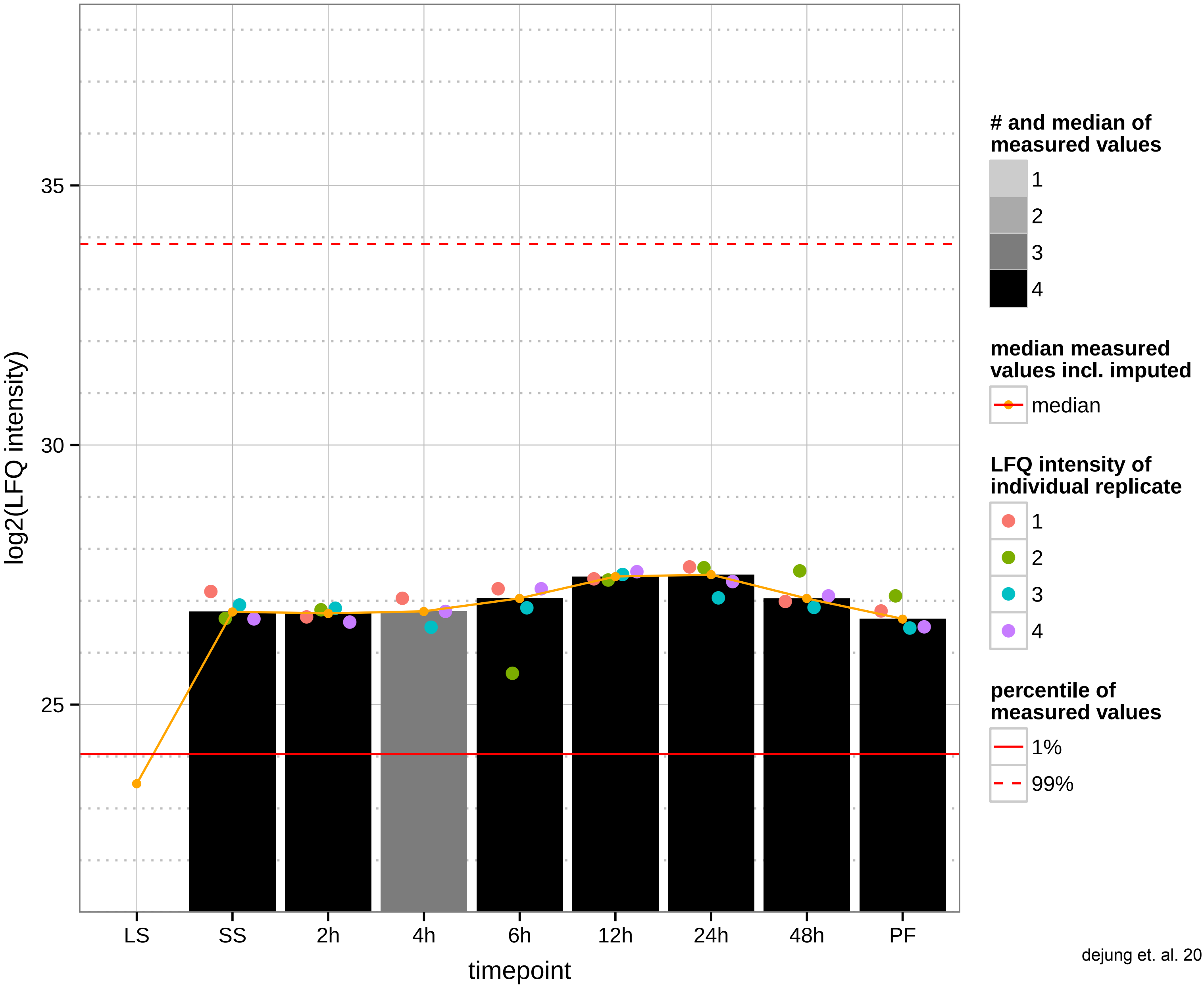
U5 snRNP–specific 40 kDa protein
Tb927.11.11150
AGOF: pre–mRNA 5'–splice site binding
AGOC: cytosol, nucleus
AGOP: RNA splicing
PGOF: protein binding
PGOC: null
PGOP: null





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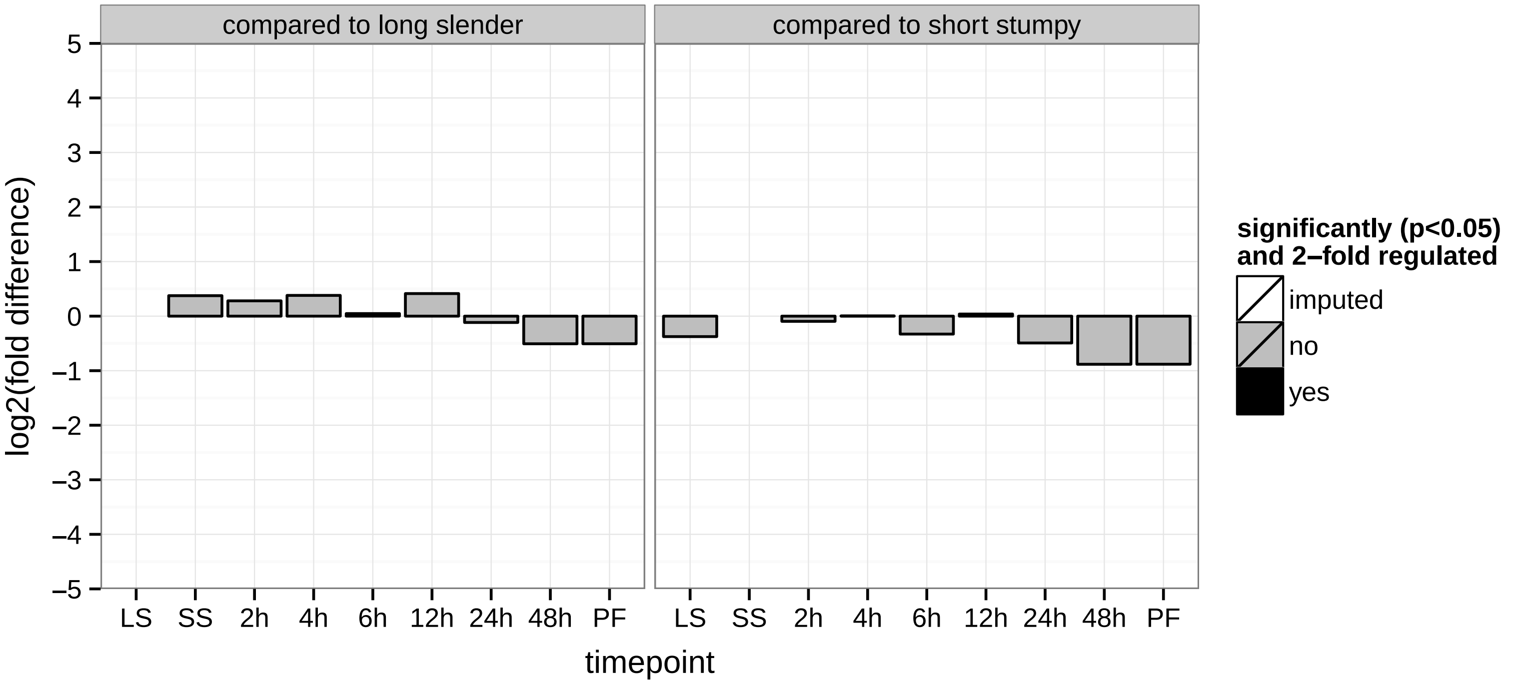
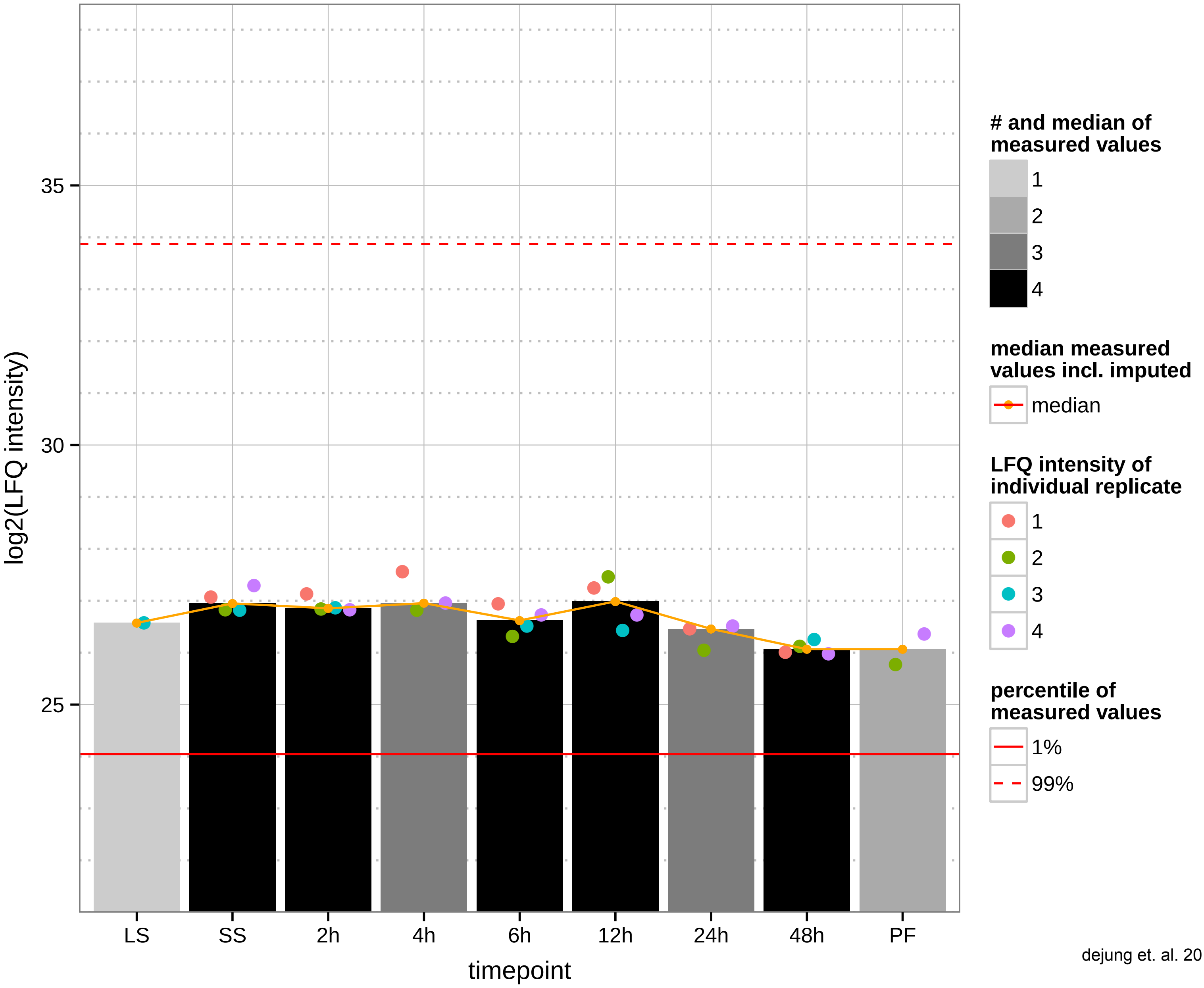
phosphate transporter, putative
Tb927.11.11160
AGOF: citrate transmembrane transporter activity
AGOC: contractile vacuole, integral to membrane
AGOP: citrate transport
PGOF: transporter activity
PGOC: membrane
PGOP: sodium ion transport, transmembrane transport





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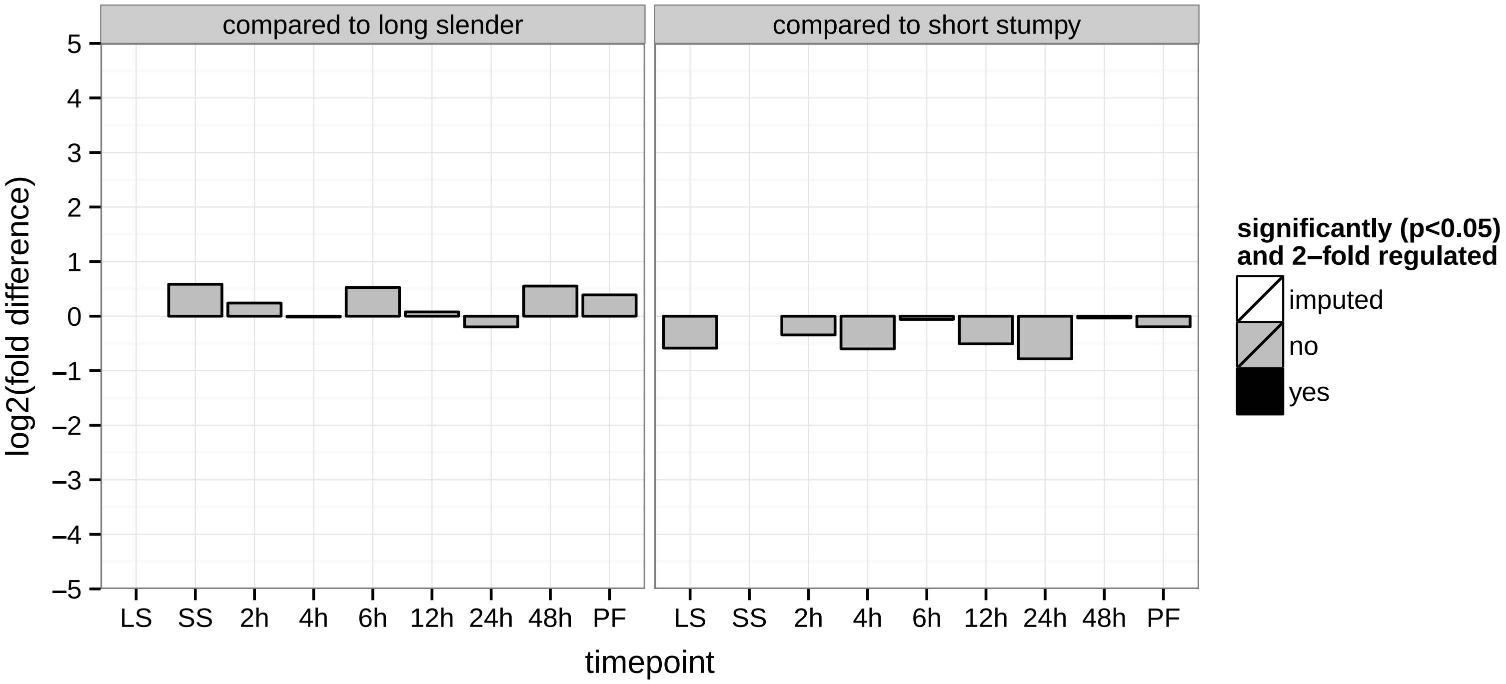
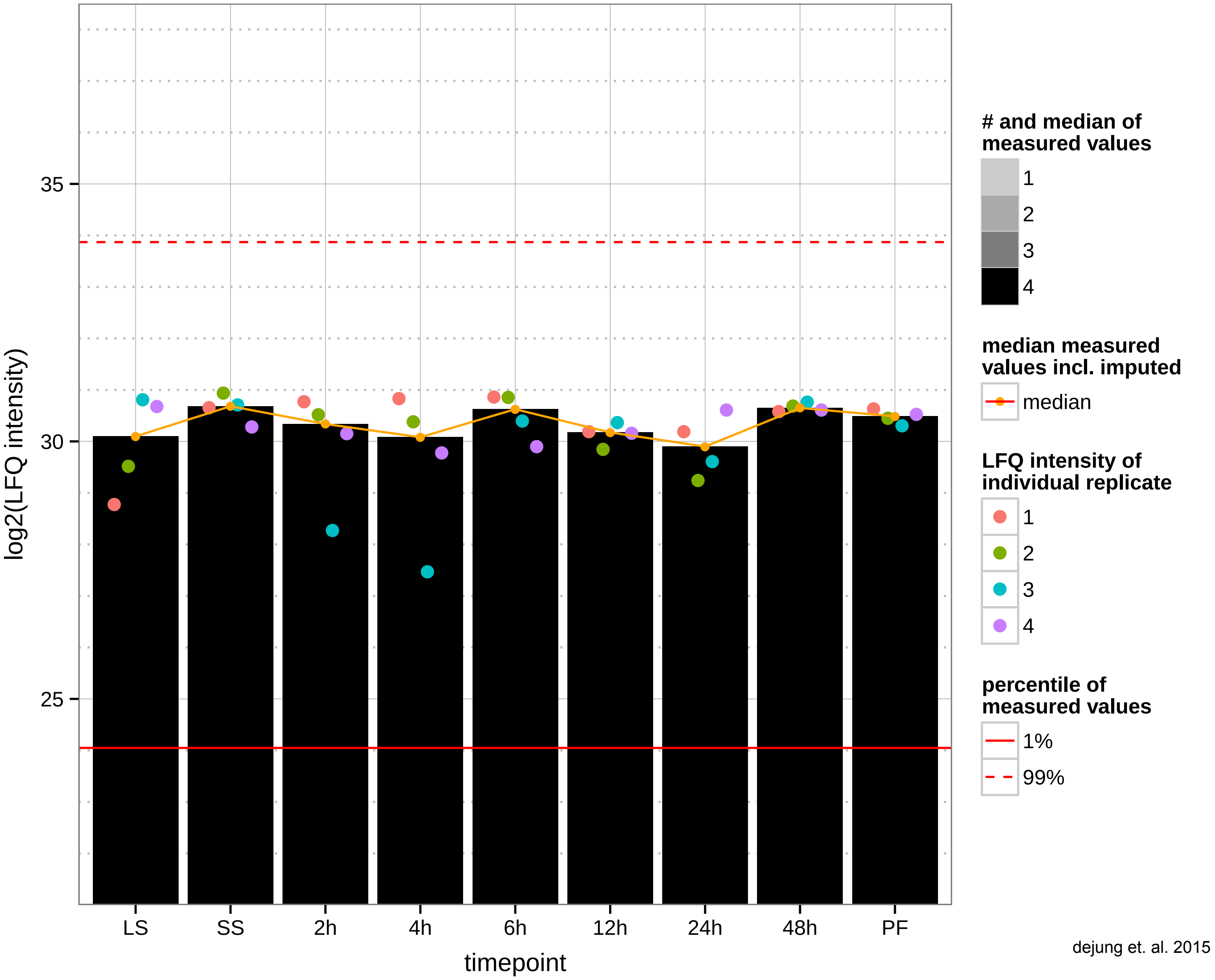
dynein heavy chain, putative
Tb927.11.11220
AGOF: ATP binding, ATPase activity, microtubule motor activity
AGOC: dynein complex
AGOP: microtubule–based movement
PGOF: ATP binding, ATPase activity, microtubule motor activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: dynein complex
PGOP: microtubule–based movement





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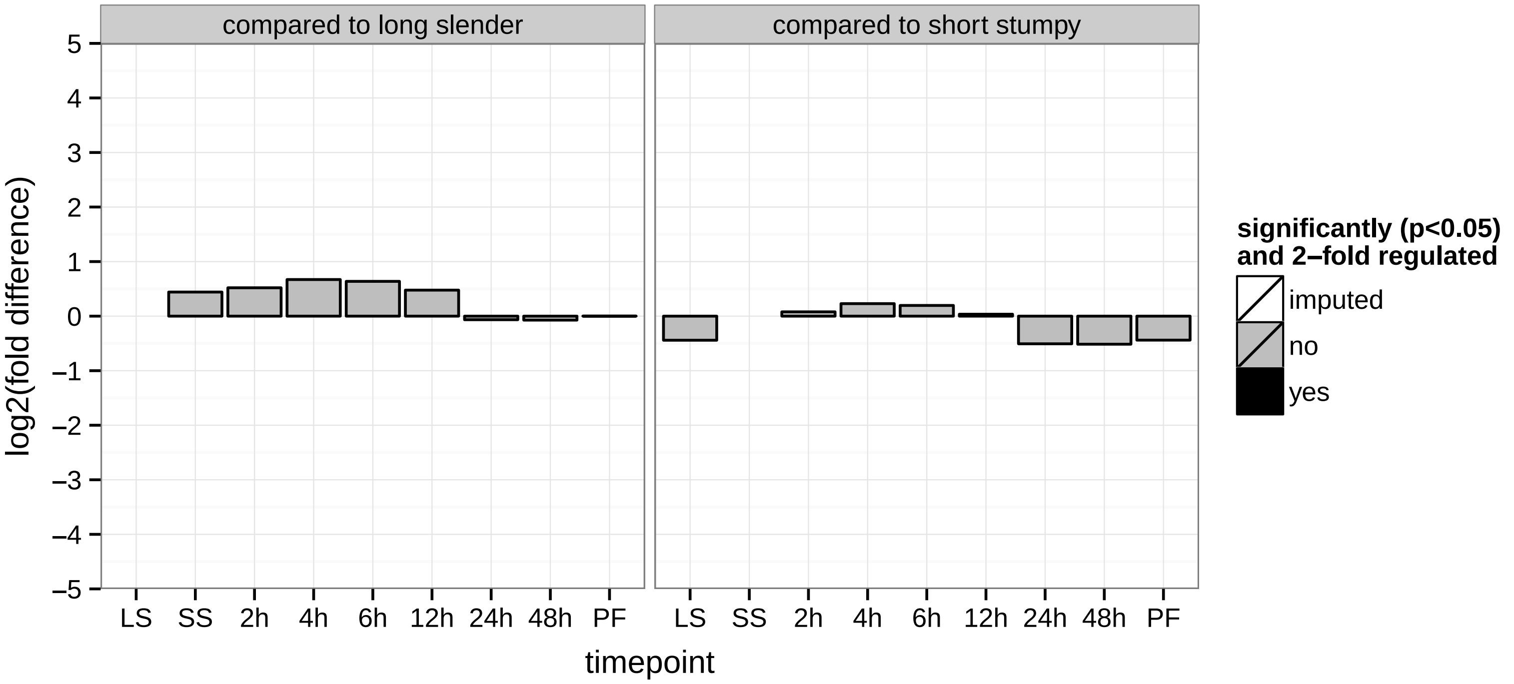
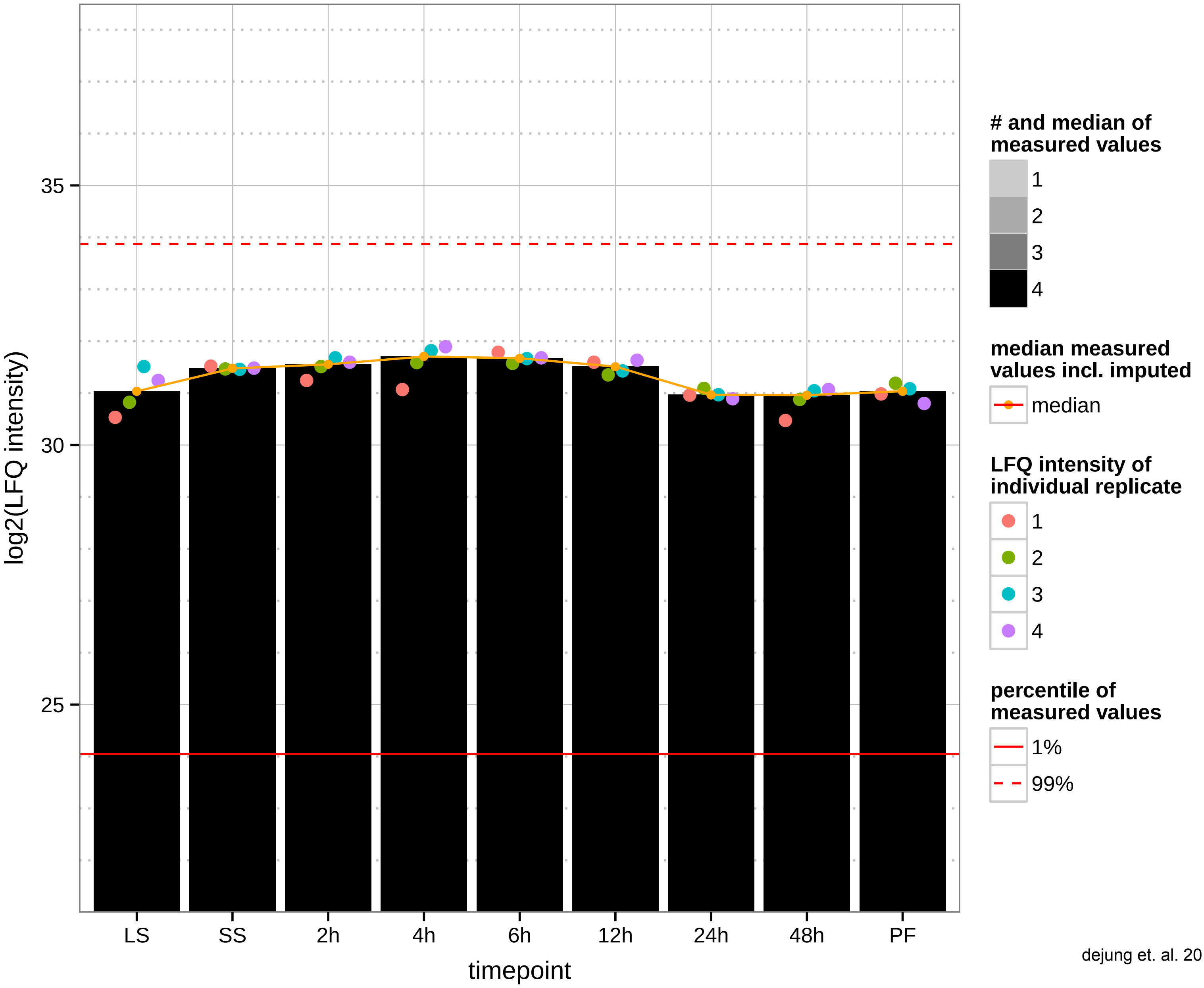
cytosolic malate dehydrogenase (cMDH)
Tb927.11.11250
AGOF: L−malate dehydrogenase activity, malate dehydrogenase activity
AGOC: cytoplasm
AGOP: glycolysis, malate metabolic process, oxidation−reduction process
PGOF: L−malate dehydrogenase activity, catalytic activity, malate dehydrogenase activity, oxidoreductase activity, acting on th
PGOC: null
PGOP: carbohydrate metabolic process, cellular carbohydrate metabolic process, malate metabolic process, oxidation−reduct





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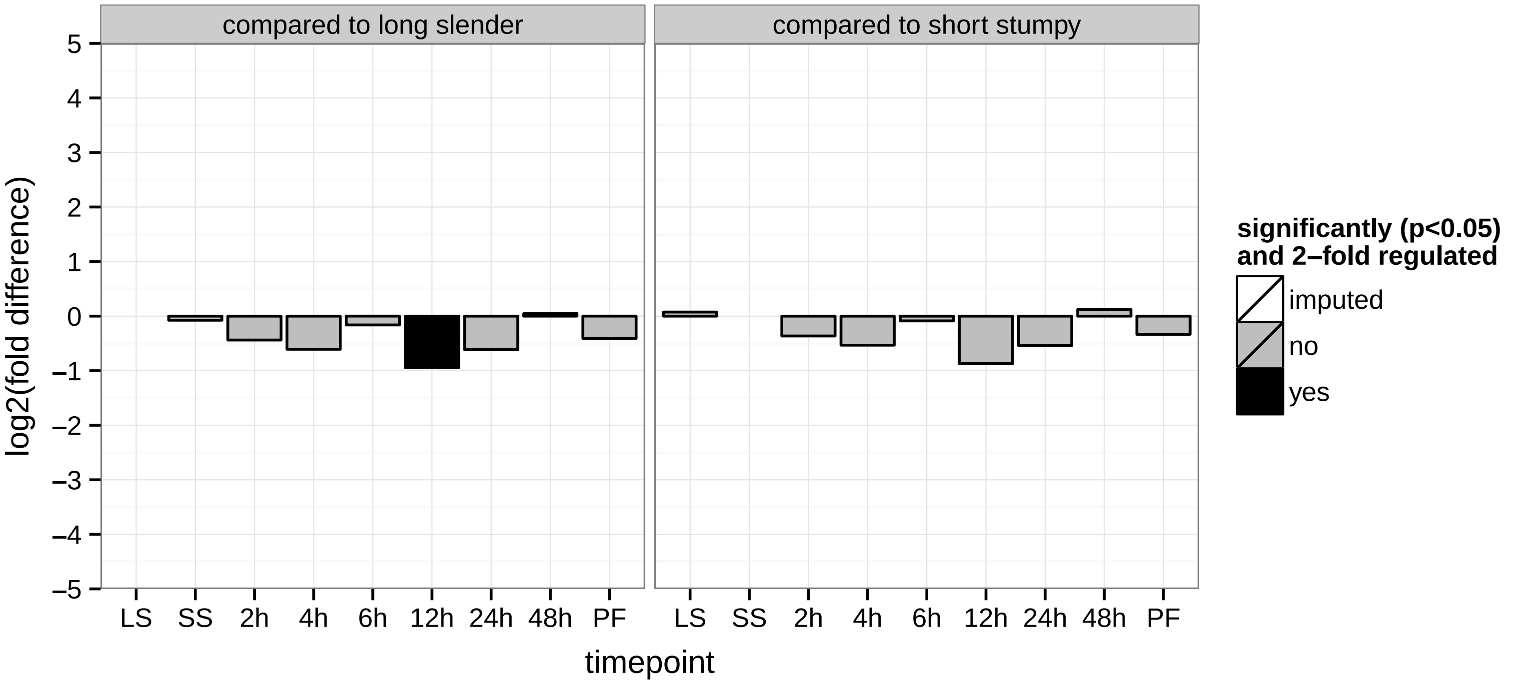
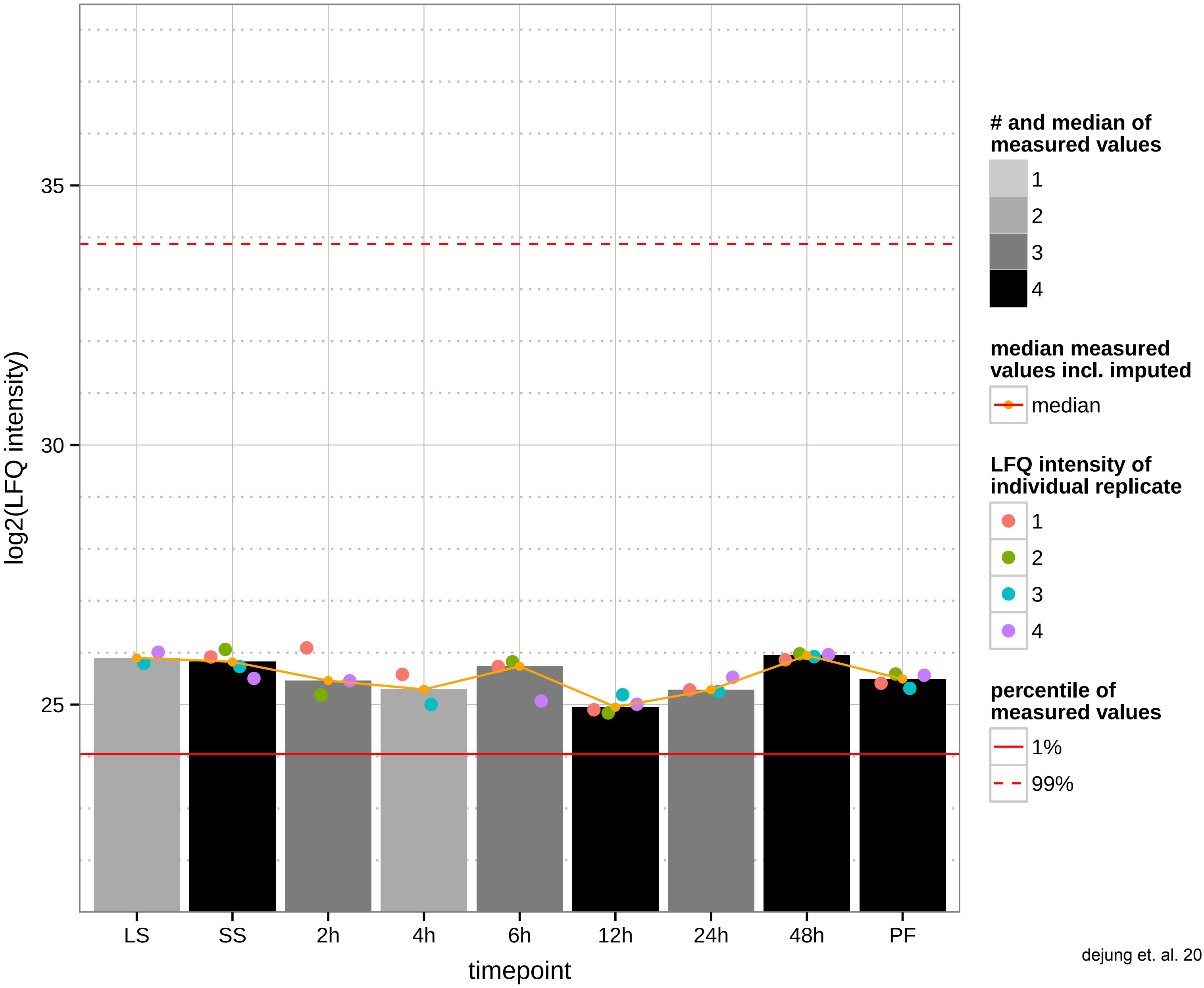
hypothetical protein, conserved
Tb927.11.11280
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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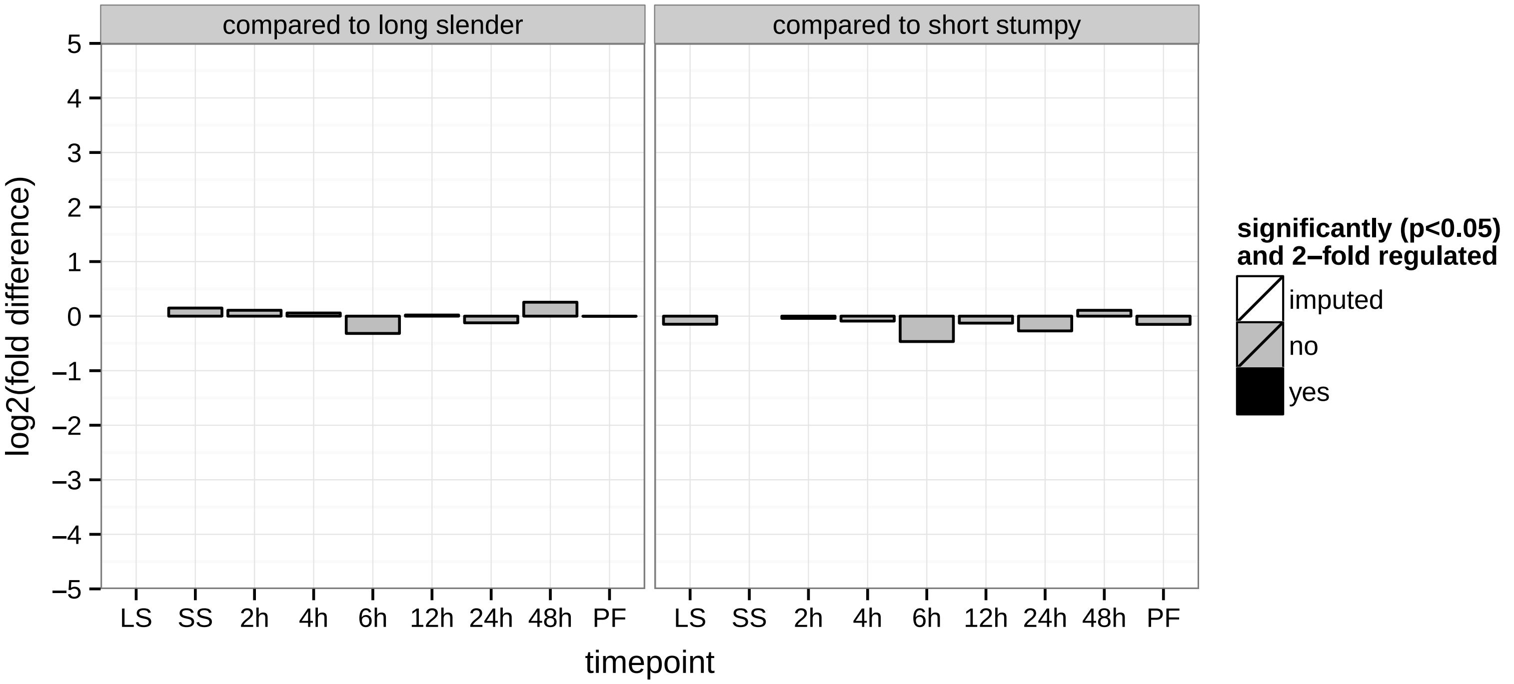
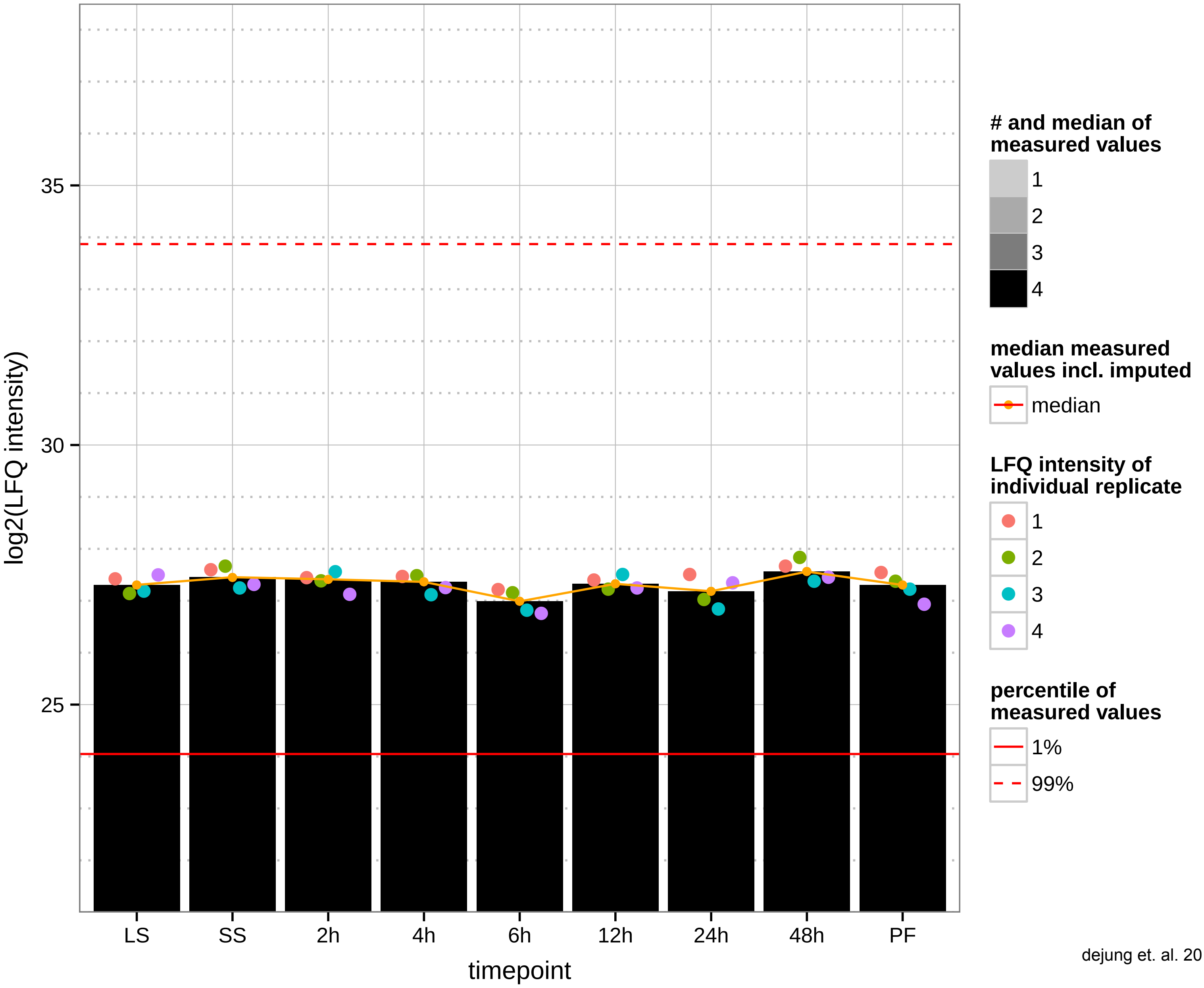
heat shock protein 70, putative
Tb927.11.11290
AGOF: ATP binding
AGOC: null
AGOP: protein folding
PGOF: null
PGOC: null
PGOP: null





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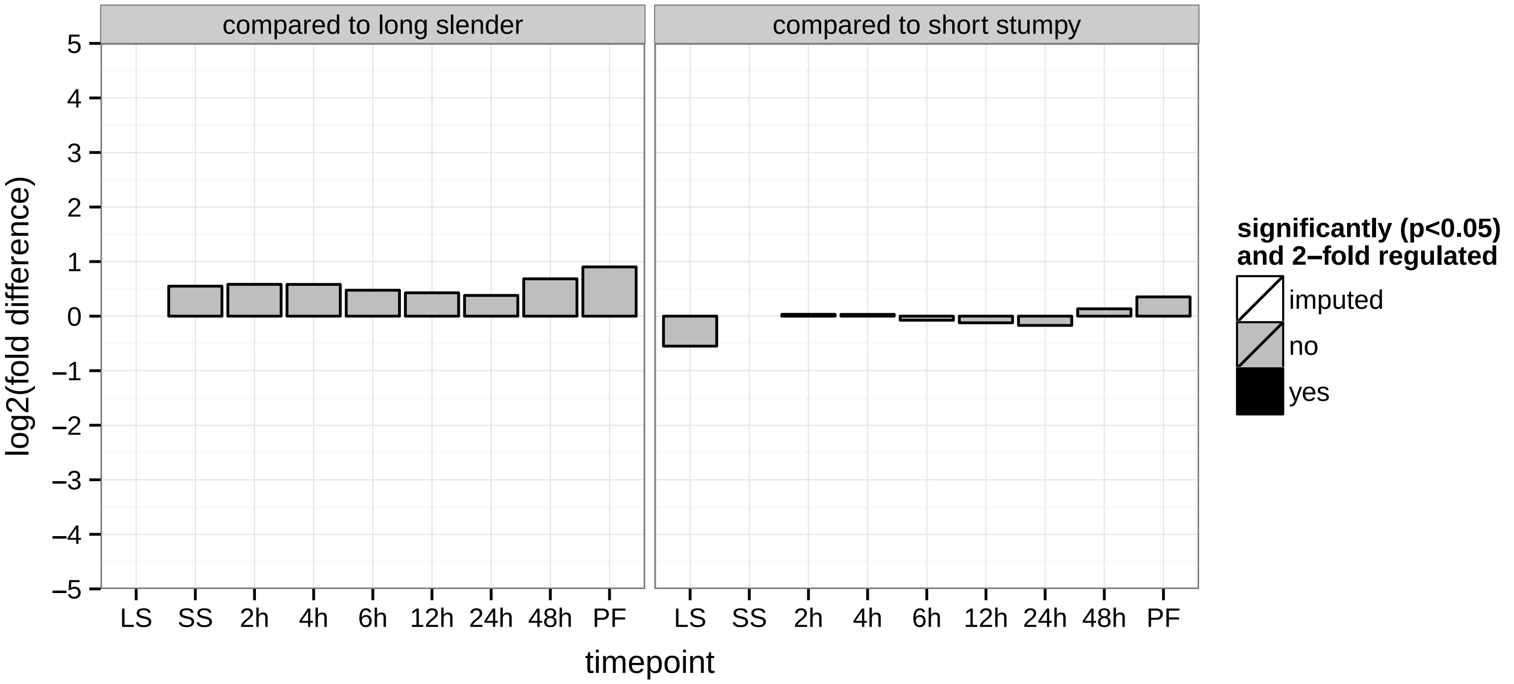
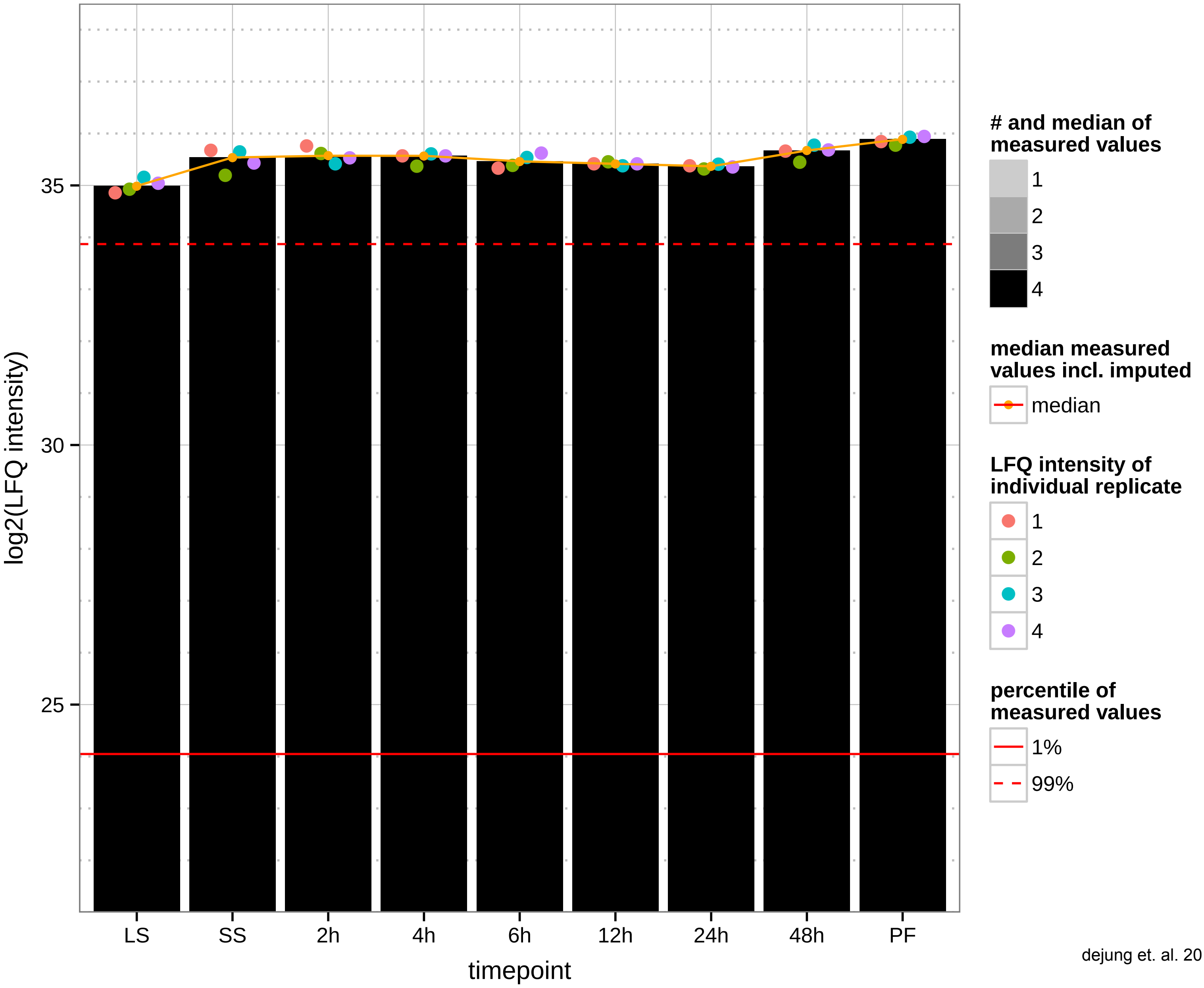
heat shock protein 70 (hsp70), putative, heat shock protein 70
Tb927.11.11330;Tb11.v5.1035
AGOF: null, ATP binding
AGOC: null
AGOP: null, protein folding
PGOF: null
PGOC: null
PGOP: null





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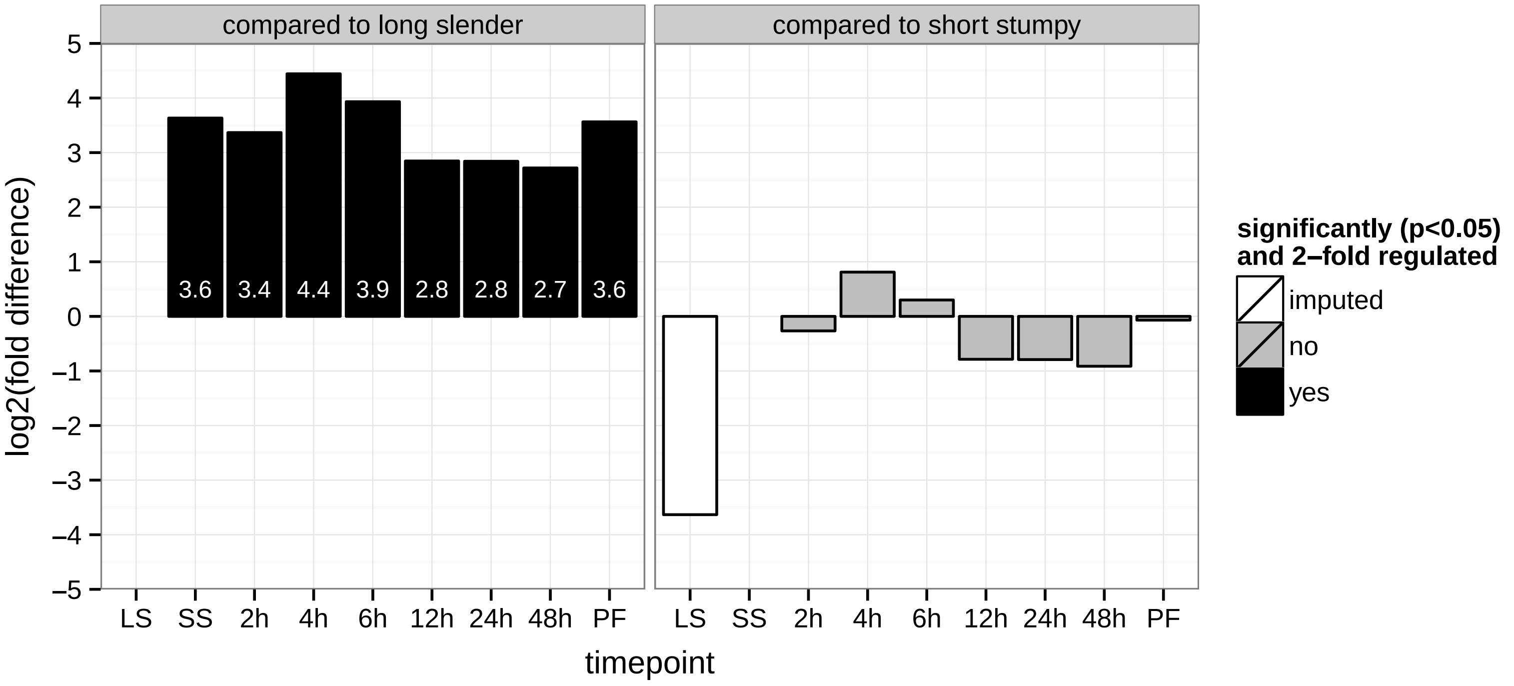
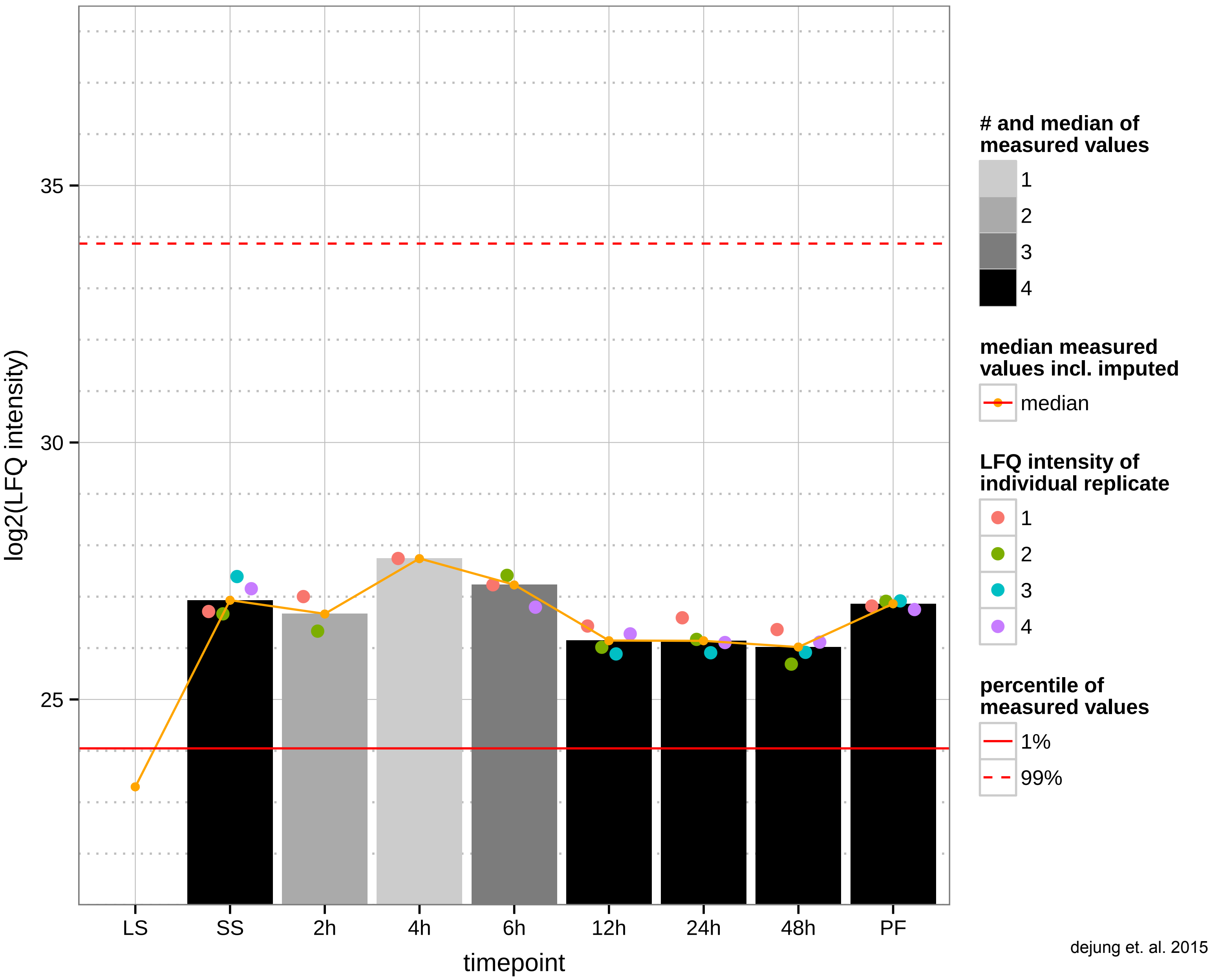
gamma−tubulin complex subunit, putative, spindle pole body component alp6
Tb927.11.11340
AGOF: null
AGOC: null, integral to membrane, microtubule organizing center, spindle pole
AGOP: null, microtubule cytoskeleton organization
PGOF: null
PGOC: microtubule organizing center, spindle pole
PGOP: microtubule cytoskeleton organization





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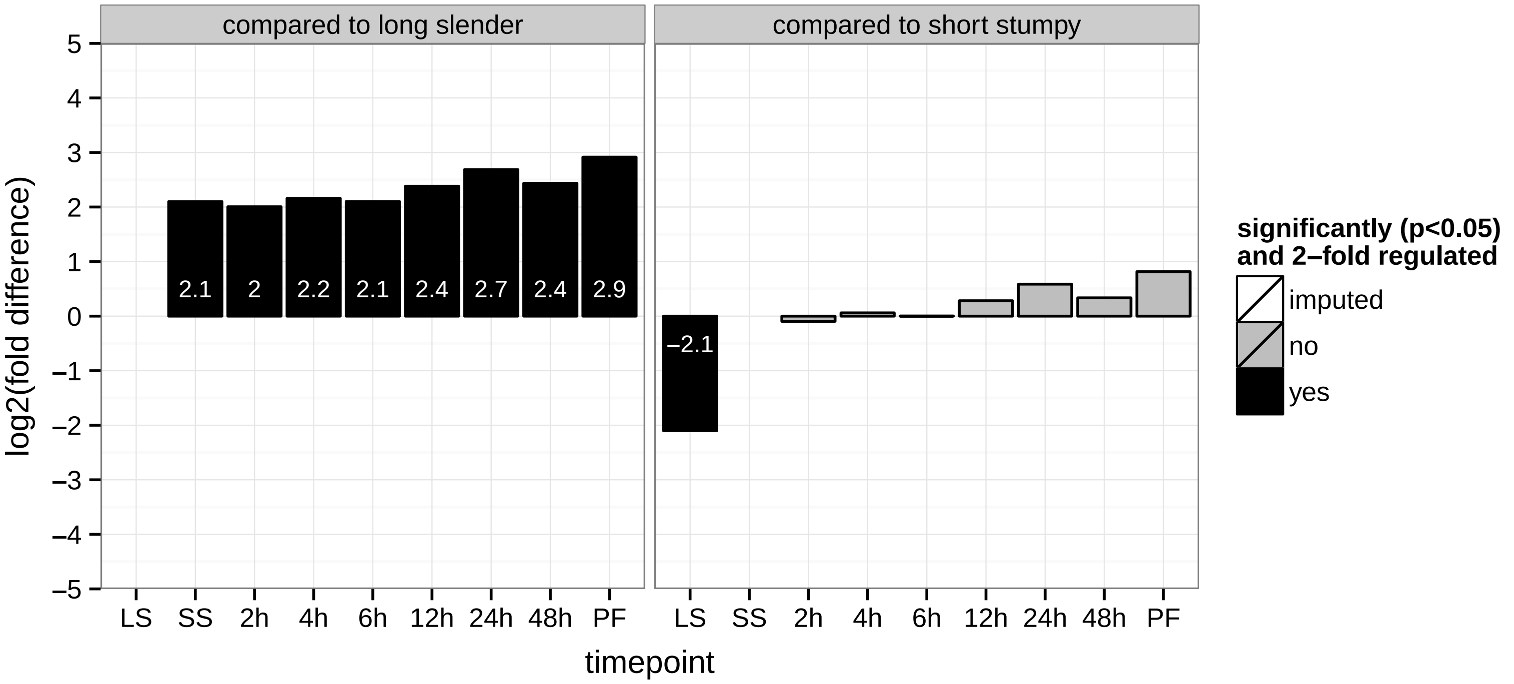
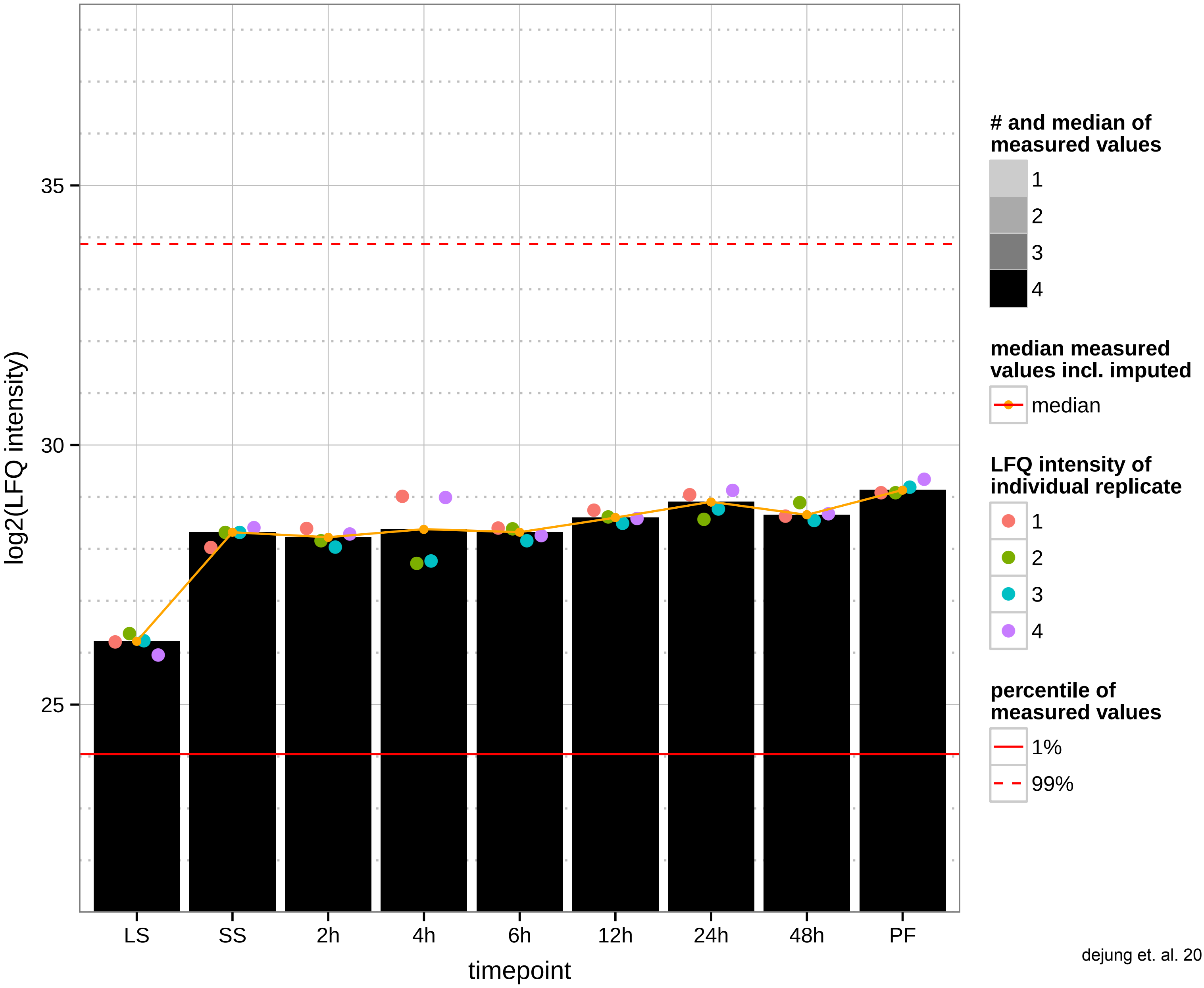
hypothetical protein, conserved
Tb927.11.11380
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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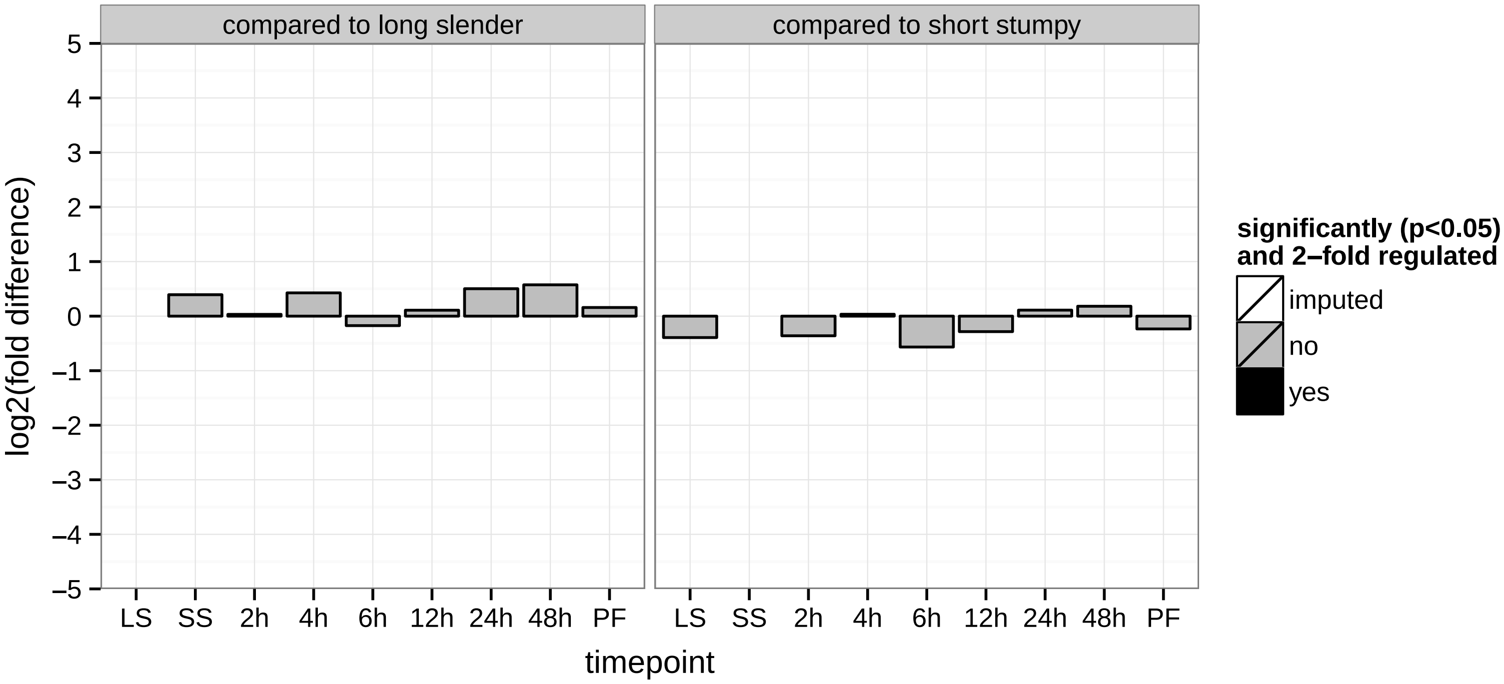
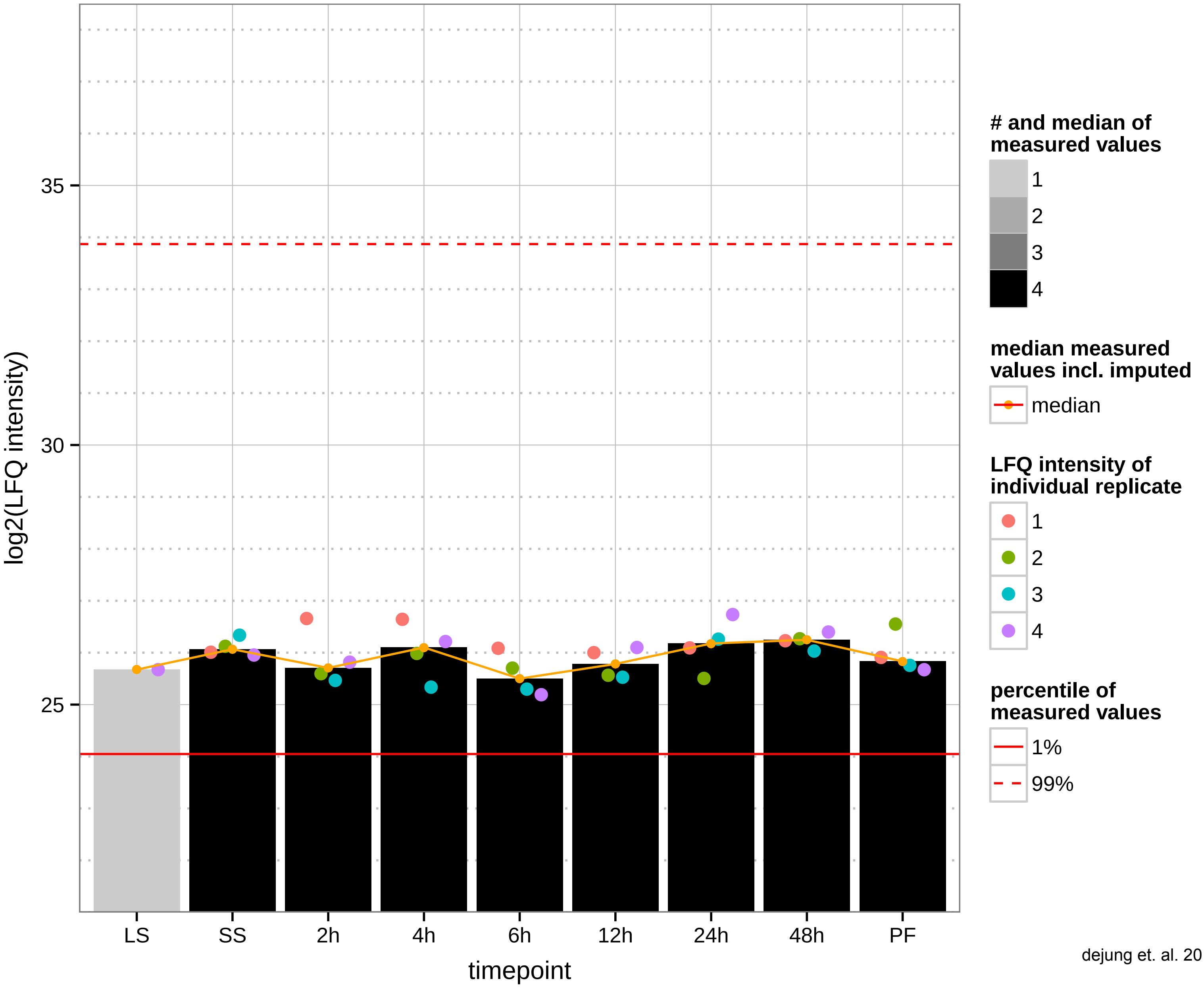
cullin 1, putative
Tb927.11.11430
AGOF: ubiquitin protein ligase binding
AGOC: cullin–RING ubiquitin ligase complex
AGOP: cell proliferation, ubiquitin–dependent protein catabolic process
PGOF: ubiquitin protein ligase binding
PGOC: cullin–RING ubiquitin ligase complex
PGOP: ubiquitin–dependent protein catabolic process





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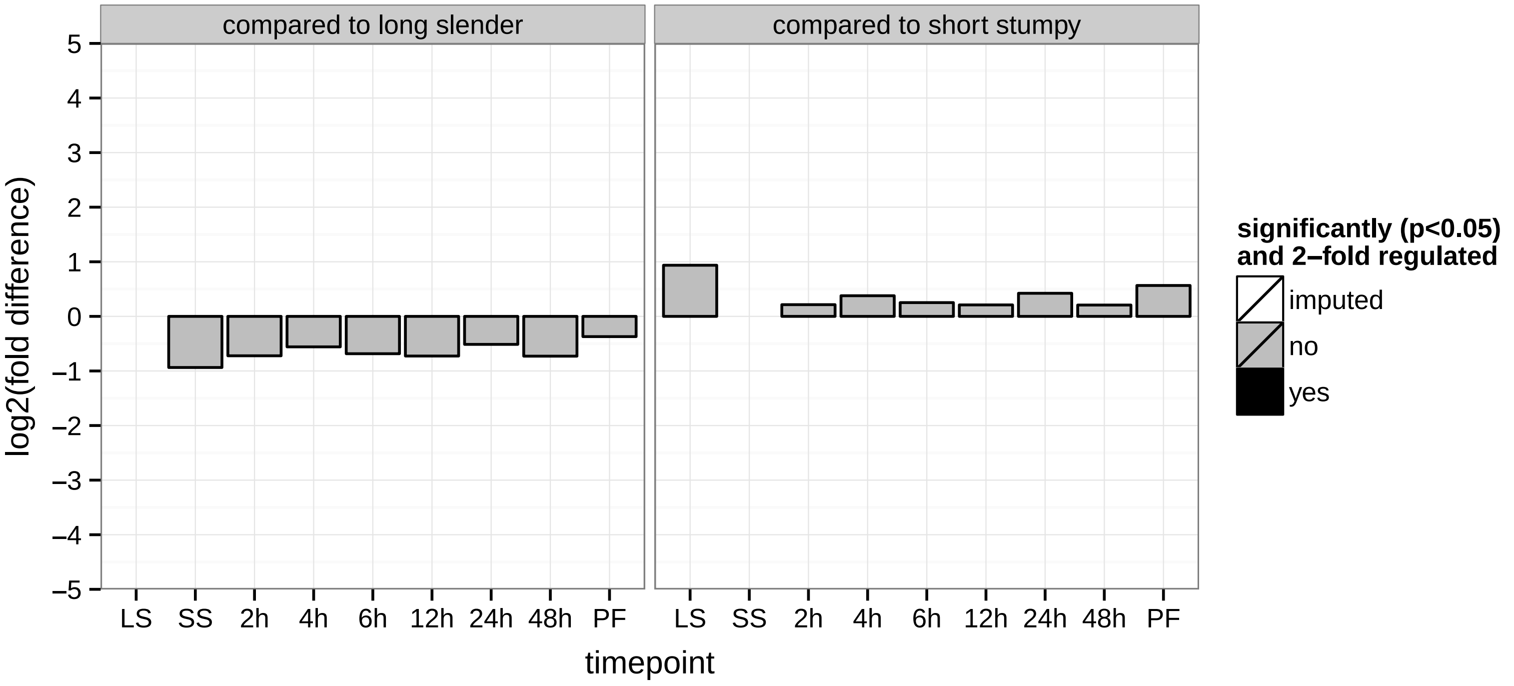
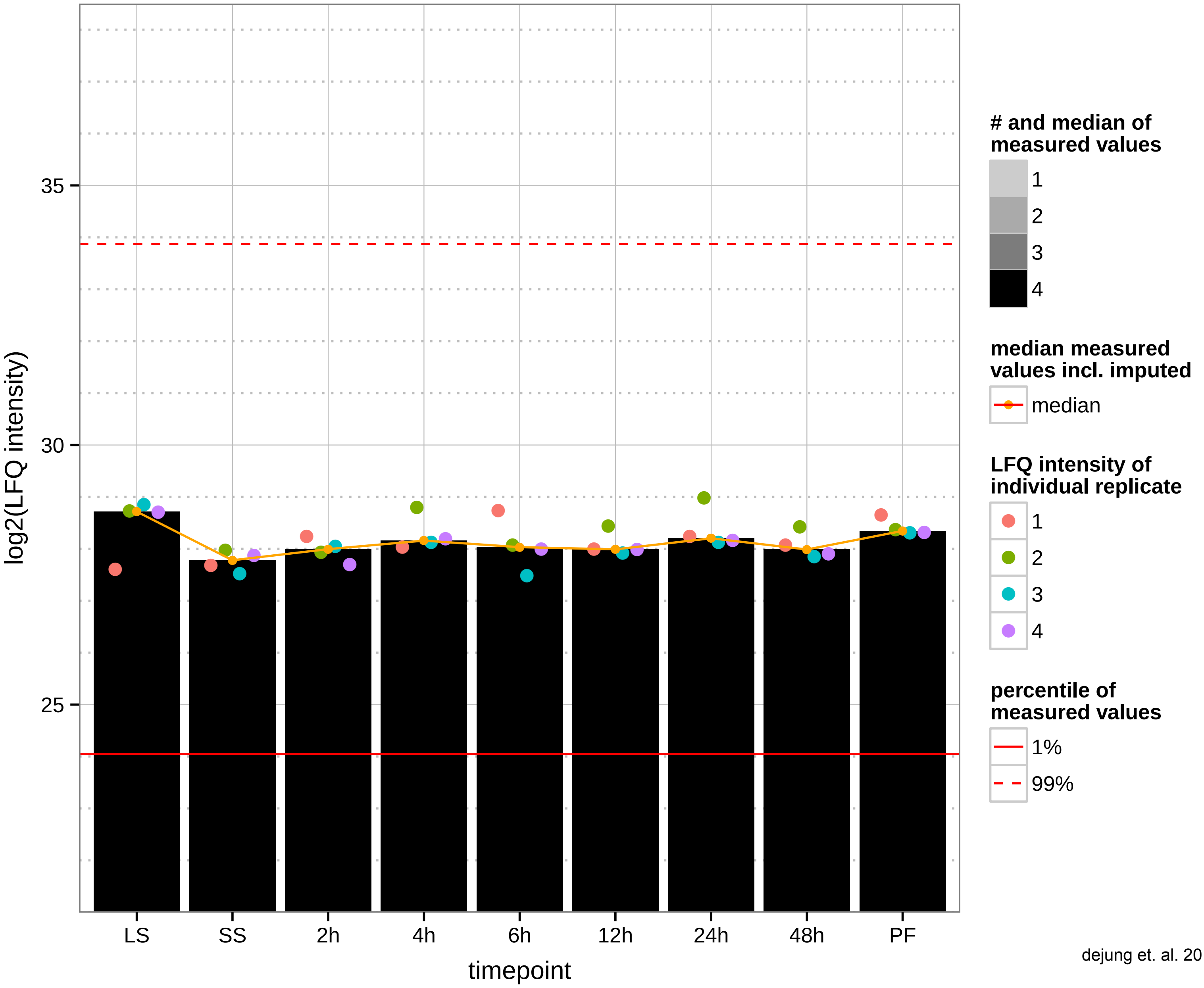
radial spoke protein RSP3, putative
Tb927.11.1150
AGOF: null
AGOC: radial spoke
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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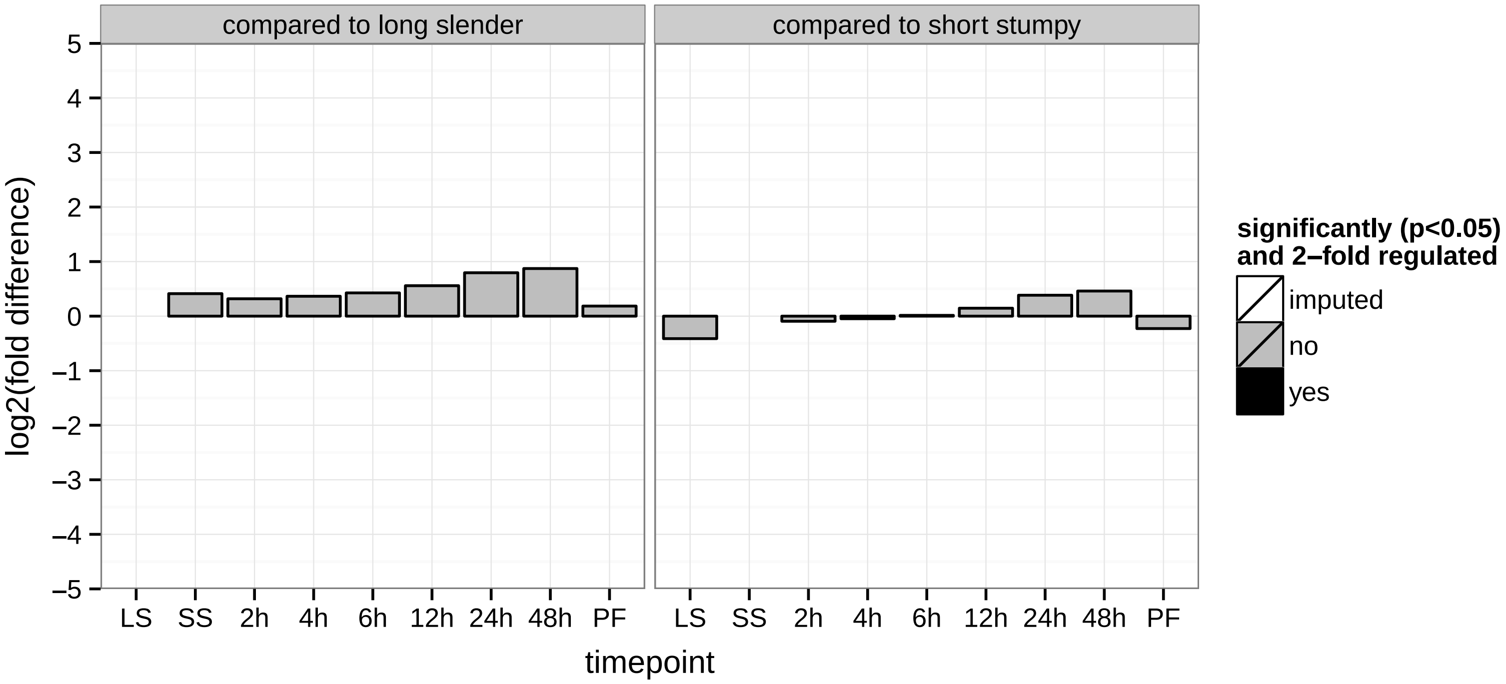
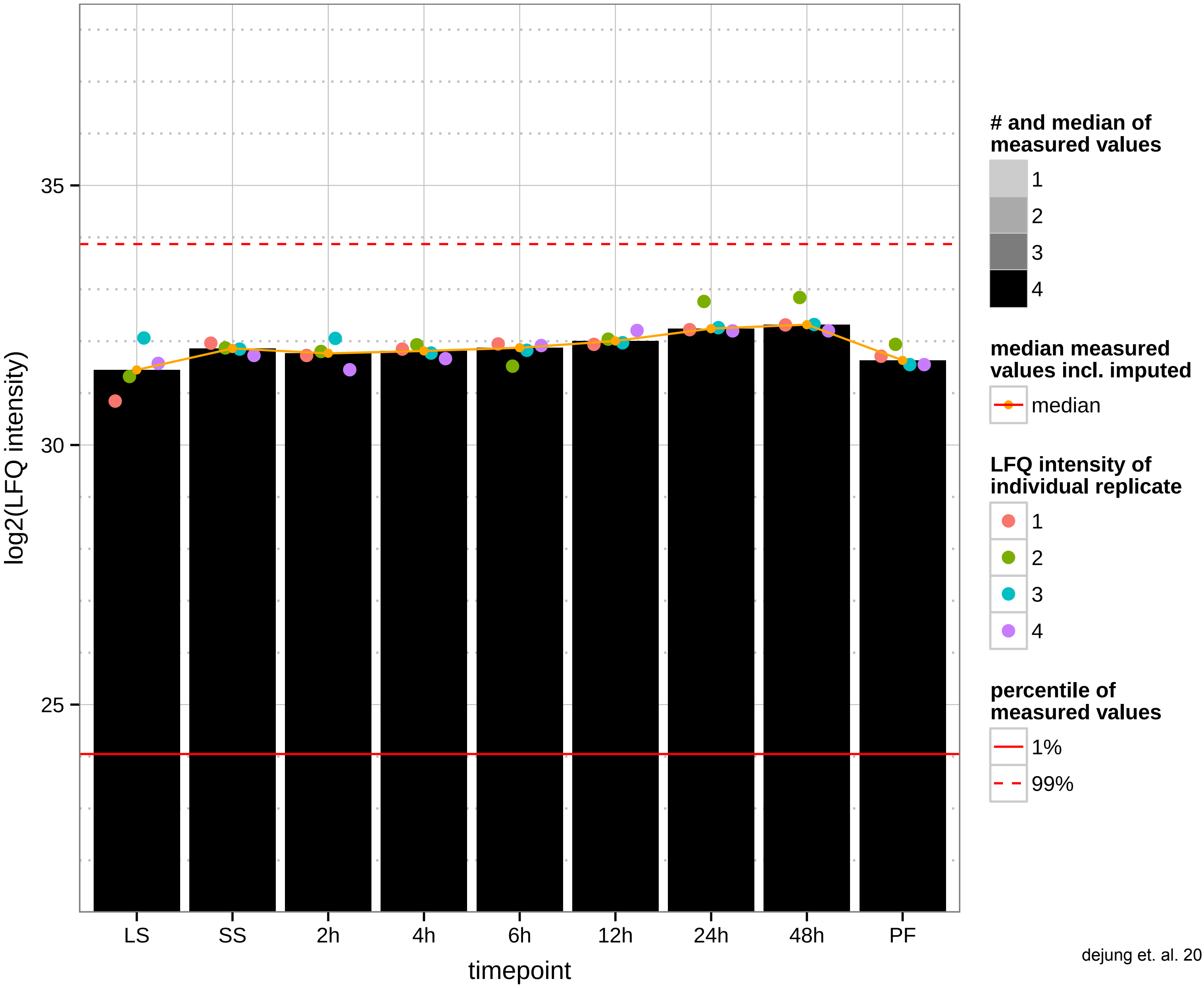
glycosomal membrane protein (PEX11)
Tb927.11.11520
AGOF: null
AGOC: endoplasmic reticulum, glycosome membrane
AGOP: peroxisome fission
PGOF: null
PGOC: integral to peroxisomal membrane
PGOP: peroxisome fission





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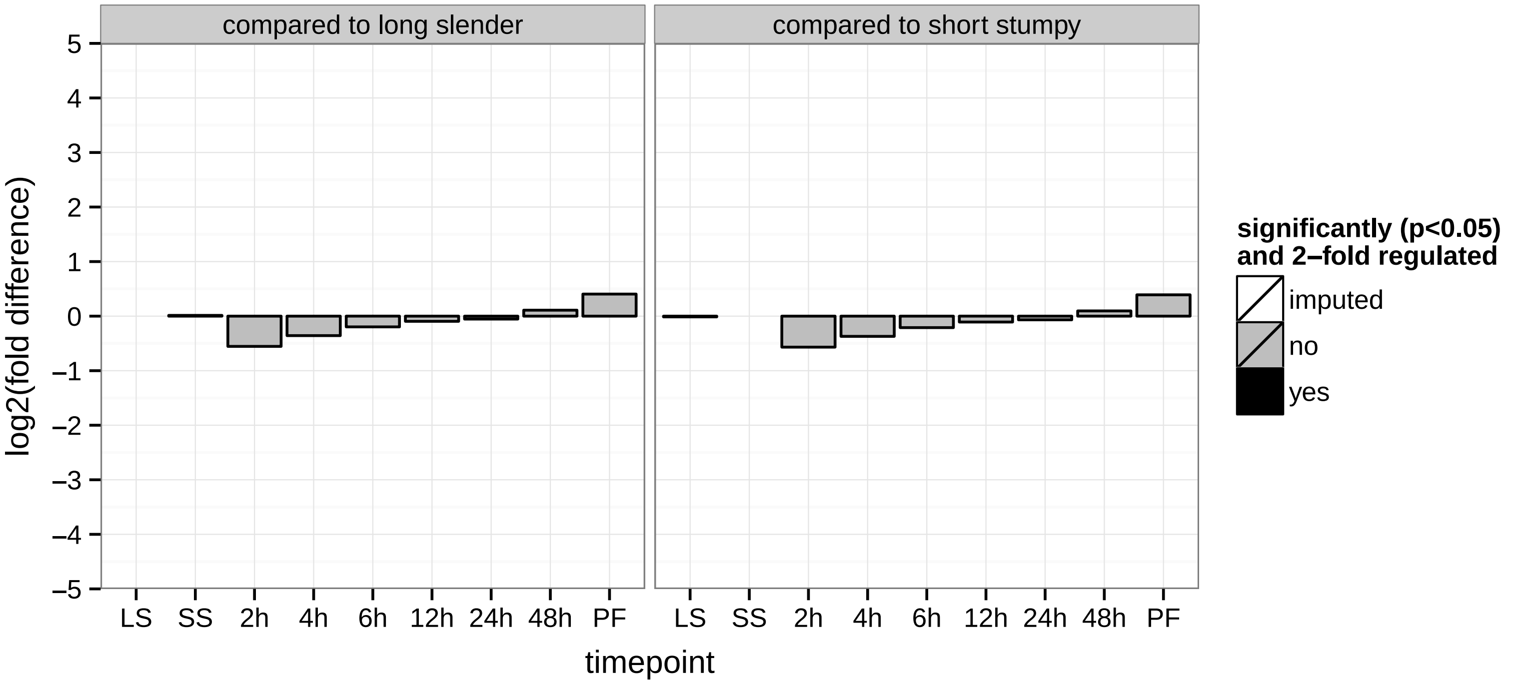
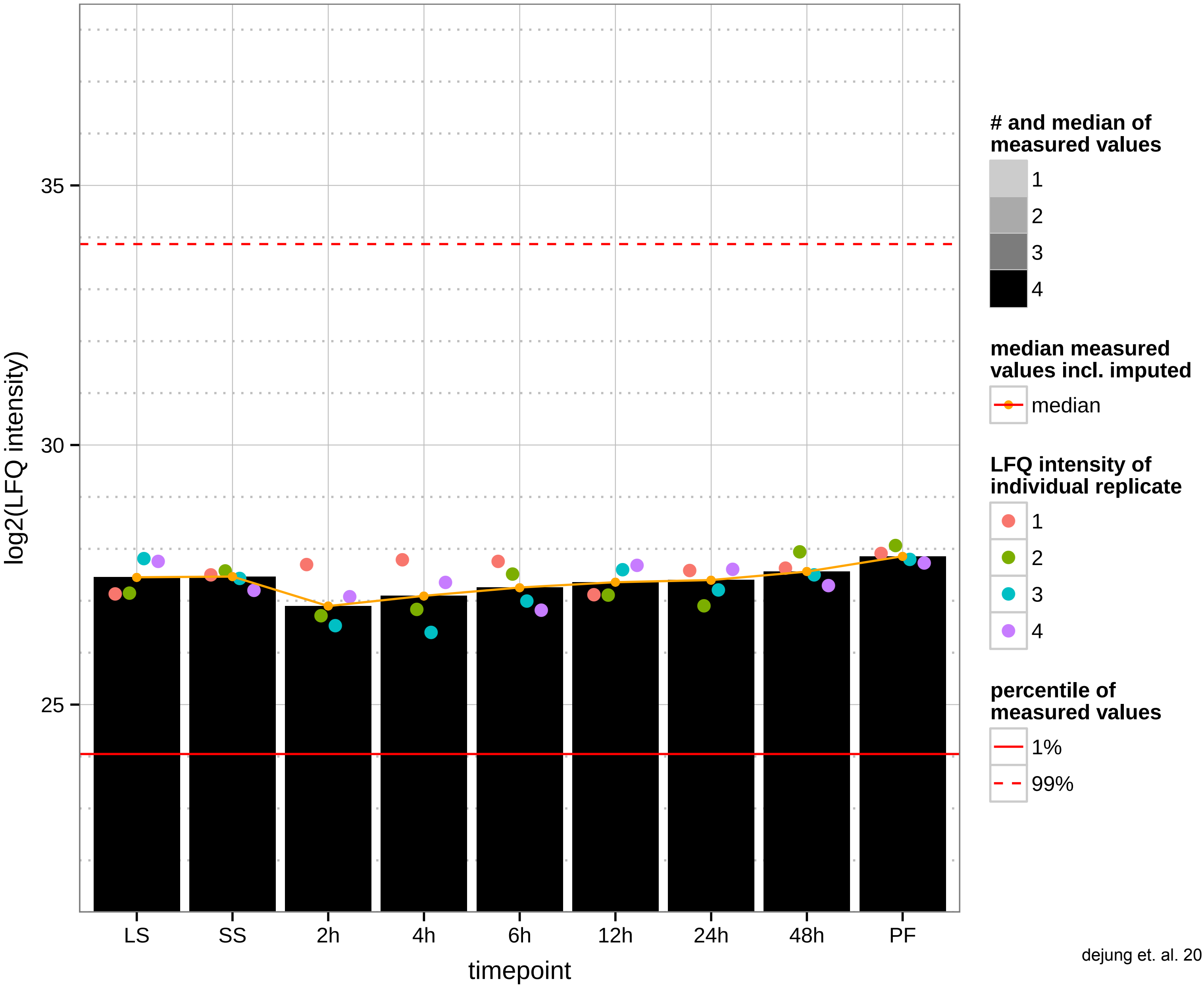
unspecified product, DNA topoisomerase II, putative
Tb927.11.11550;Tb927.11.11540
AGOF: null, ATP binding, DNA topoisomerase (ATP–hydrolyzing) activity
AGOC: null, chromosome
AGOP: null, DNA topological change
PGOF: ATP binding, DNA binding, DNA topoisomerase (ATP–hydrolyzing) activity
PGOC: chromosome
PGOP: DNA topological change





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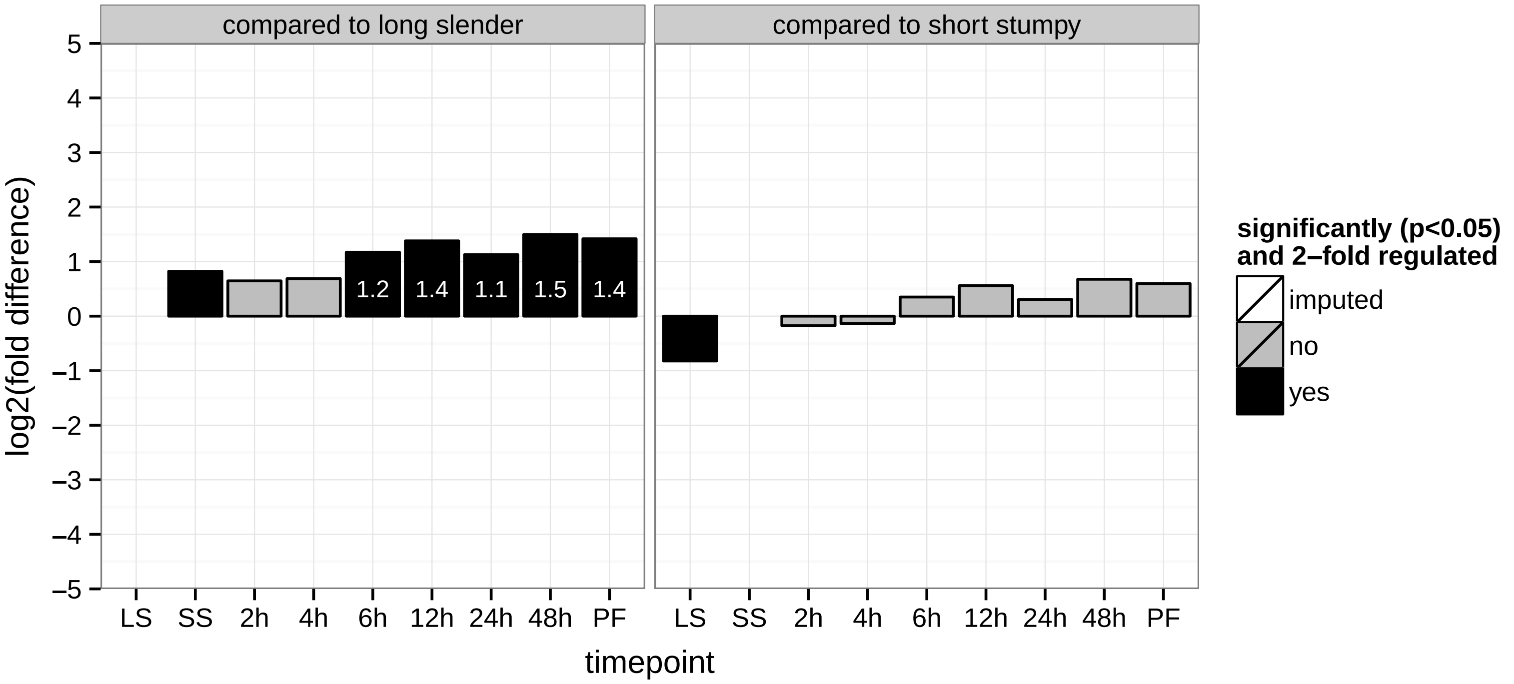
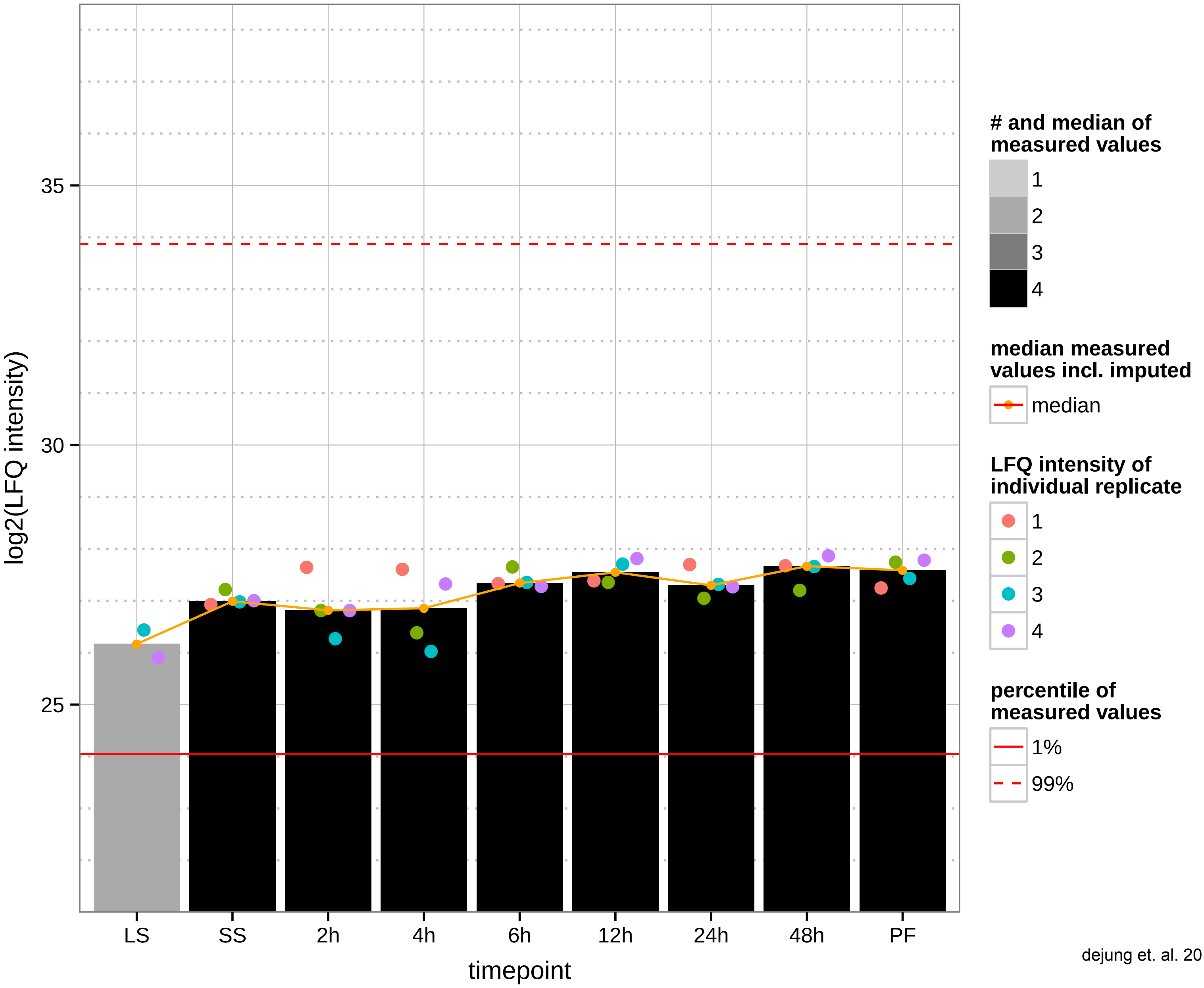
Translation initiation factor eIF−2B subunit epsilon, putative, eIF−2B GDP−GTP exchange factor subunit epsilon (EIF2BE)
Tb927.11.11570
AGOF: null
AGOC: null
AGOP: null
PGOF: transferase activity
PGOC: null
PGOP: null





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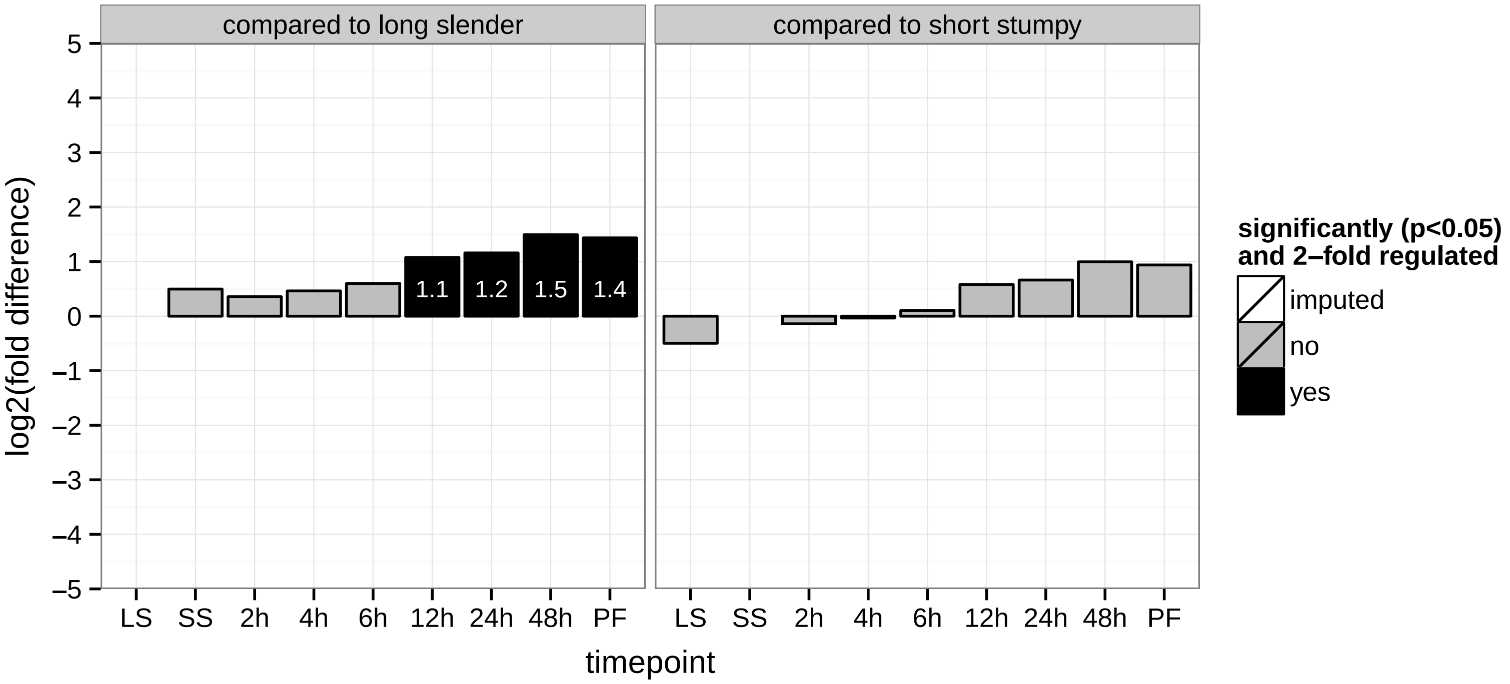
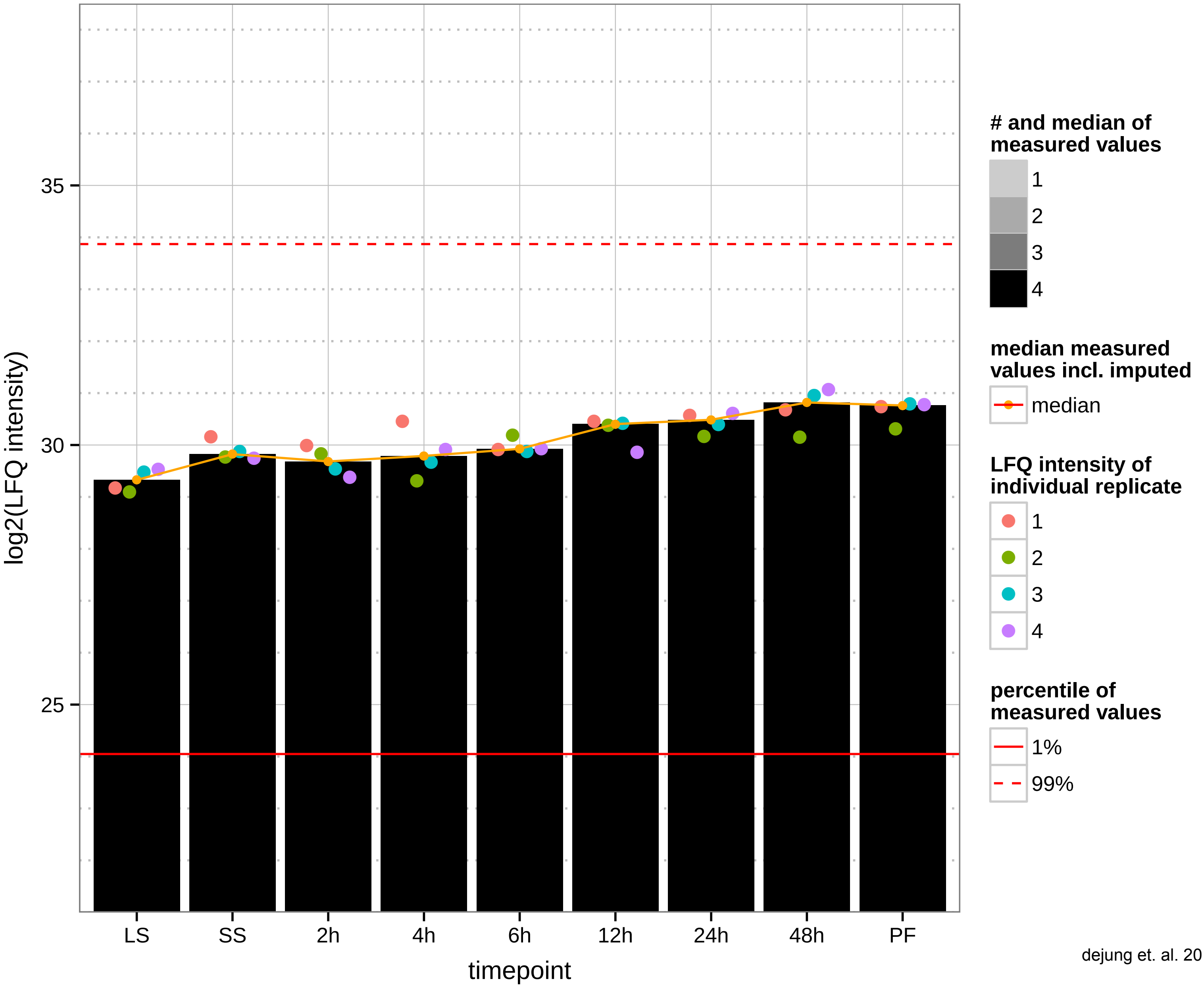
eukaryotic translation initiation factor, putative
Tb927.11.11590
AGOF: translation initiation factor activity
AGOC: eukaryotic translation initiation factor 3 complex
AGOP: translational initiation
PGOF: protein binding
PGOC: null
PGOP: null





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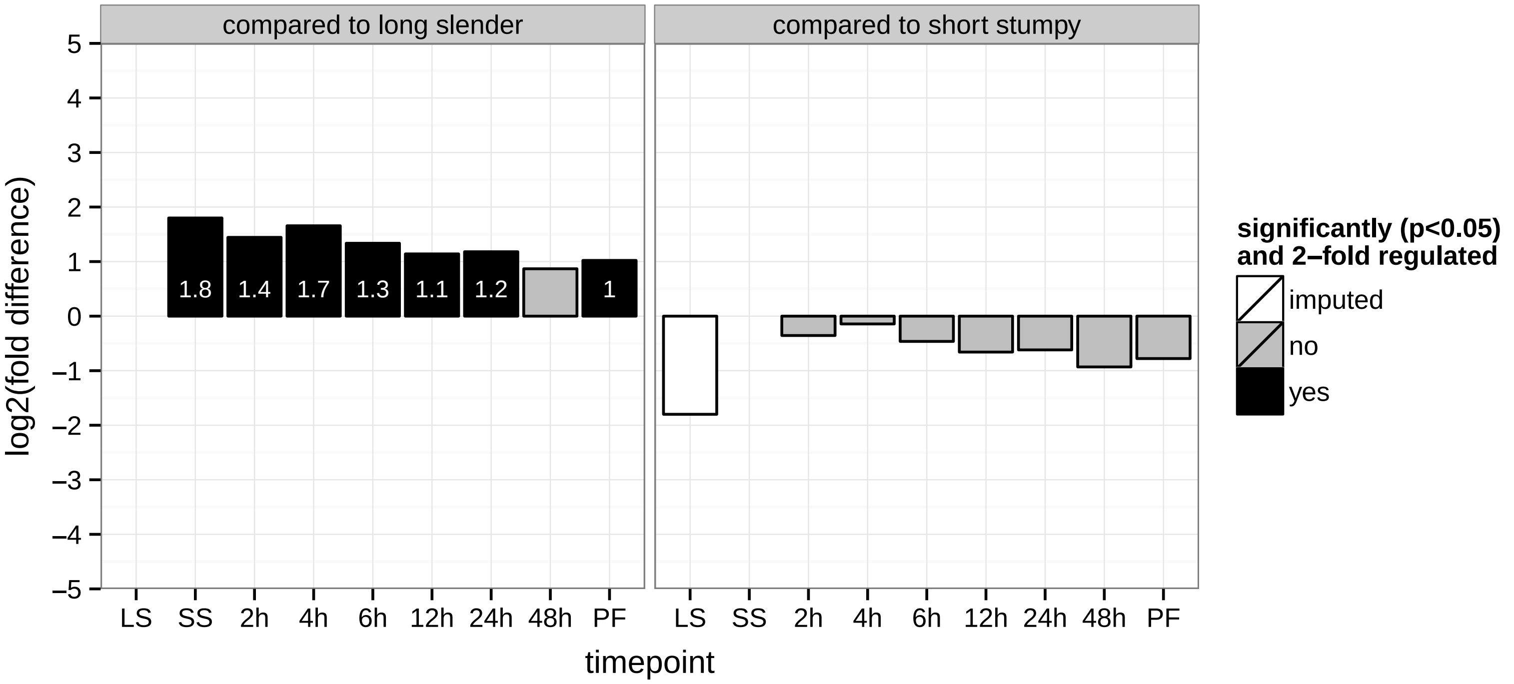
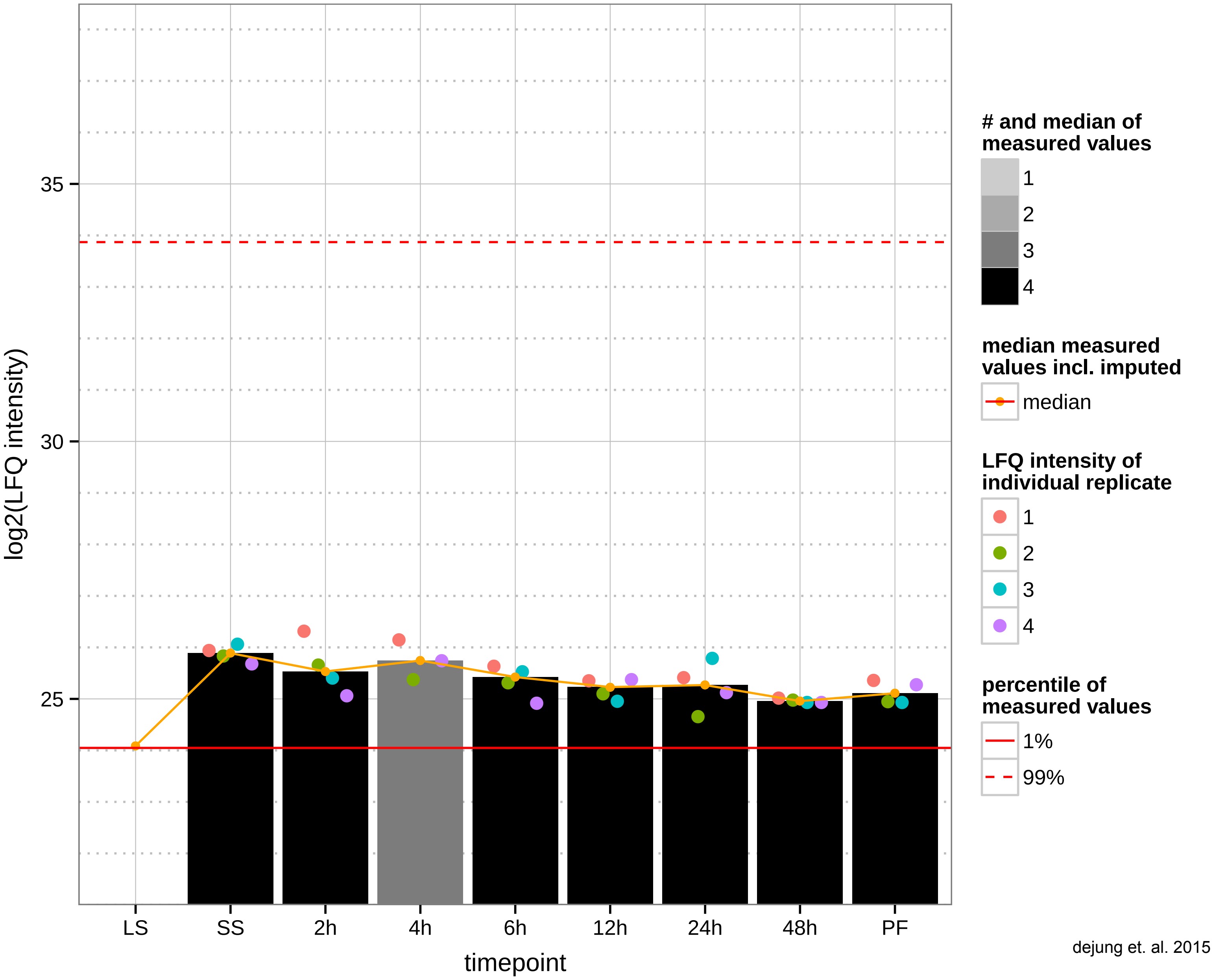
hypothetical protein, conserved
Tb927.11.1160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: intracellular protein transport, vesicle−mediated transport





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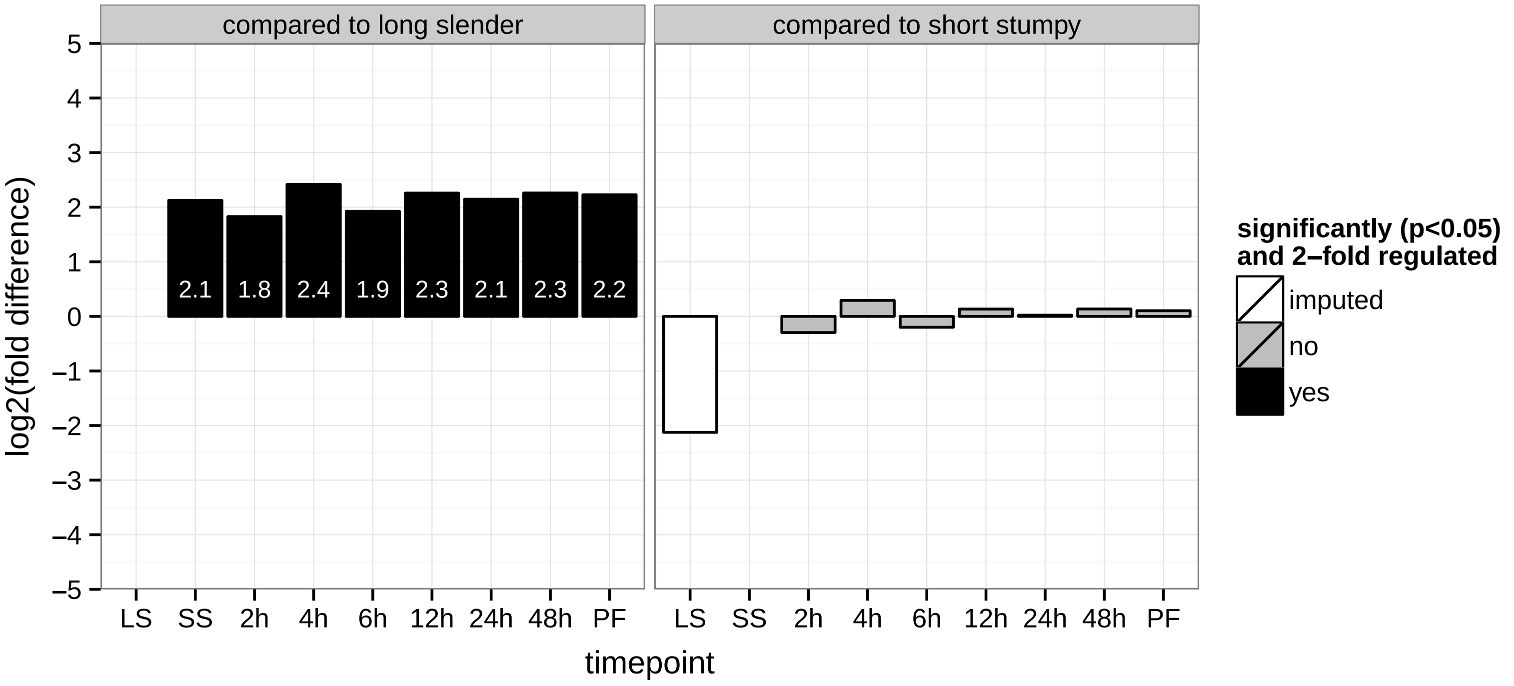
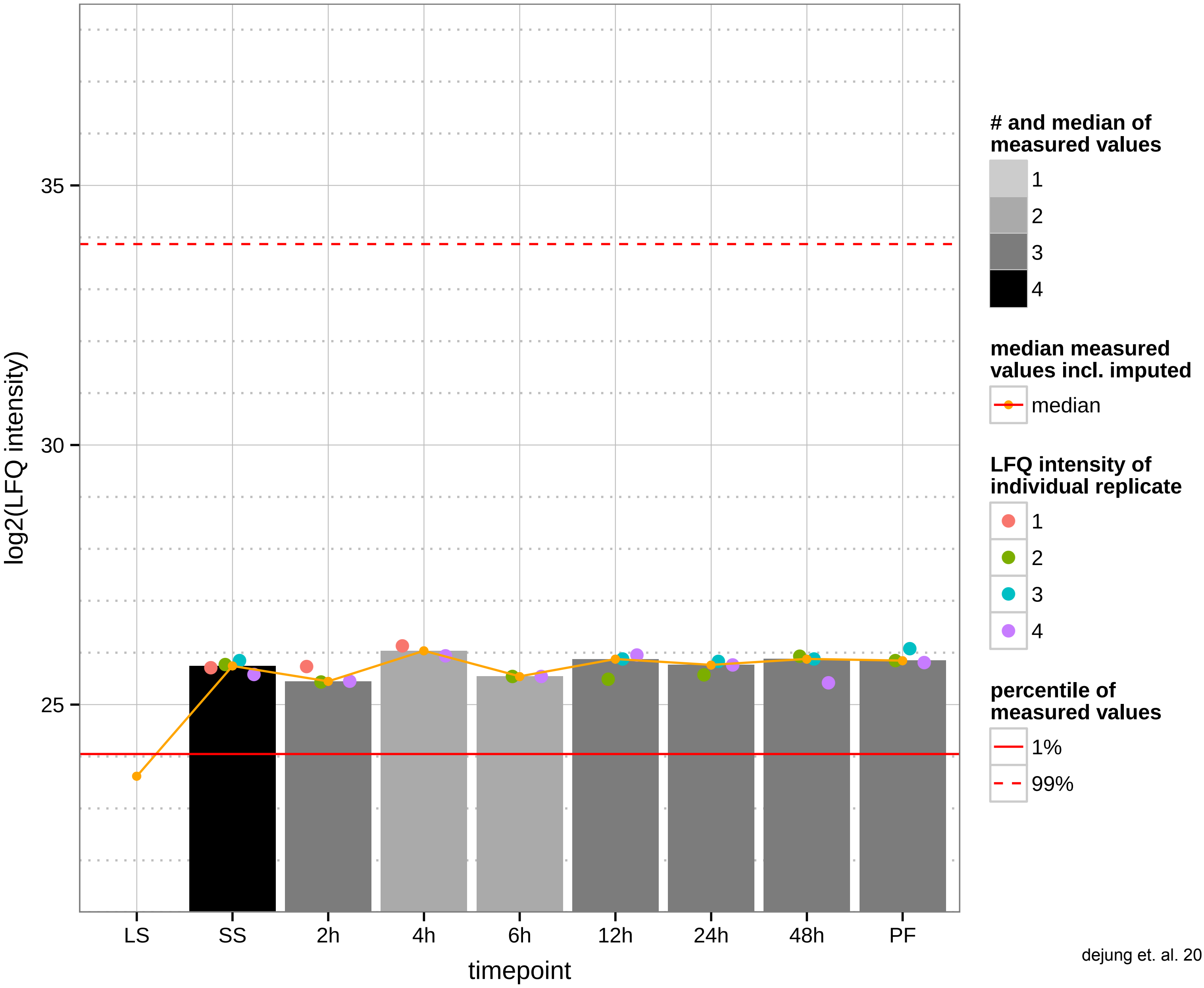
conserved protein
Tb927.11.11660
AGOF: tRNA (adenine–N1–)–methyltransferase activity
AGOC: null
AGOP: tRNA methylation
PGOF: tRNA (adenine–N1–)–methyltransferase activity
PGOC: tRNA (m1A) methyltransferase complex
PGOP: tRNA methylation





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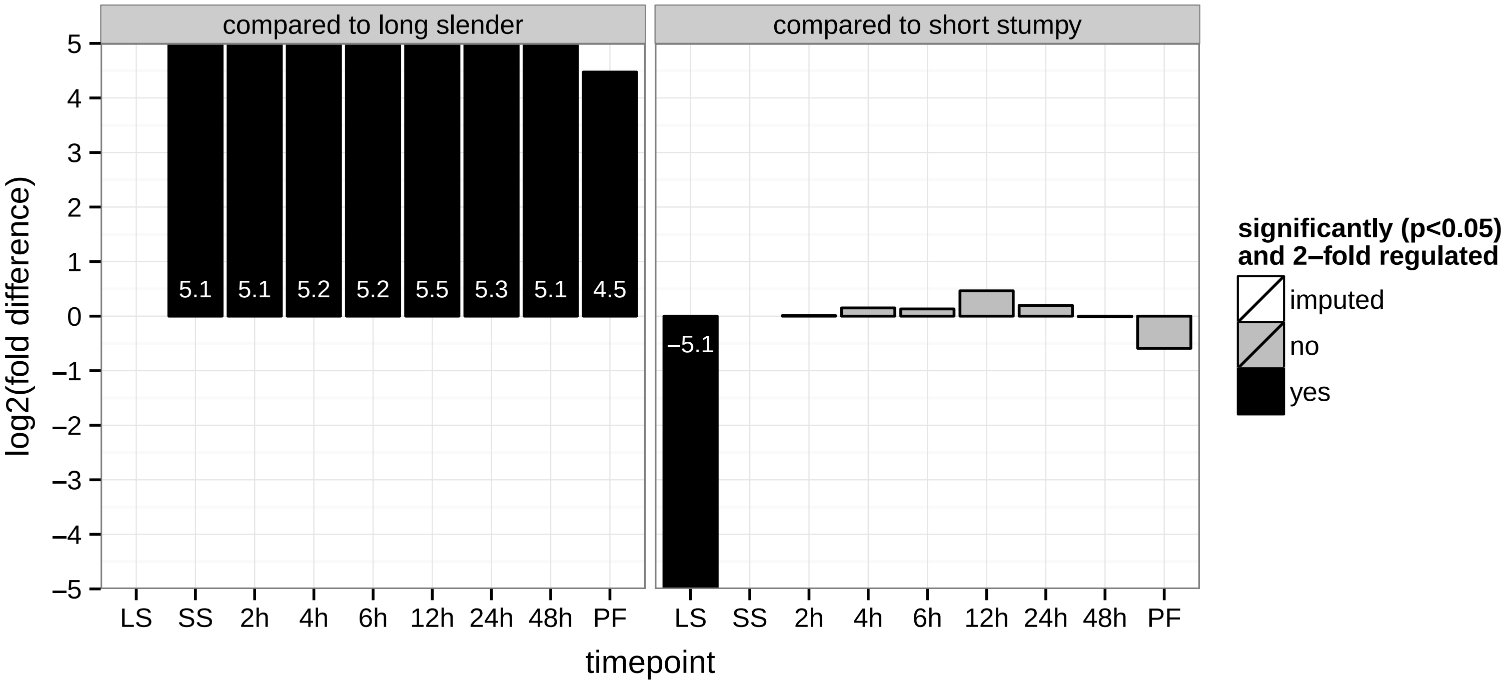
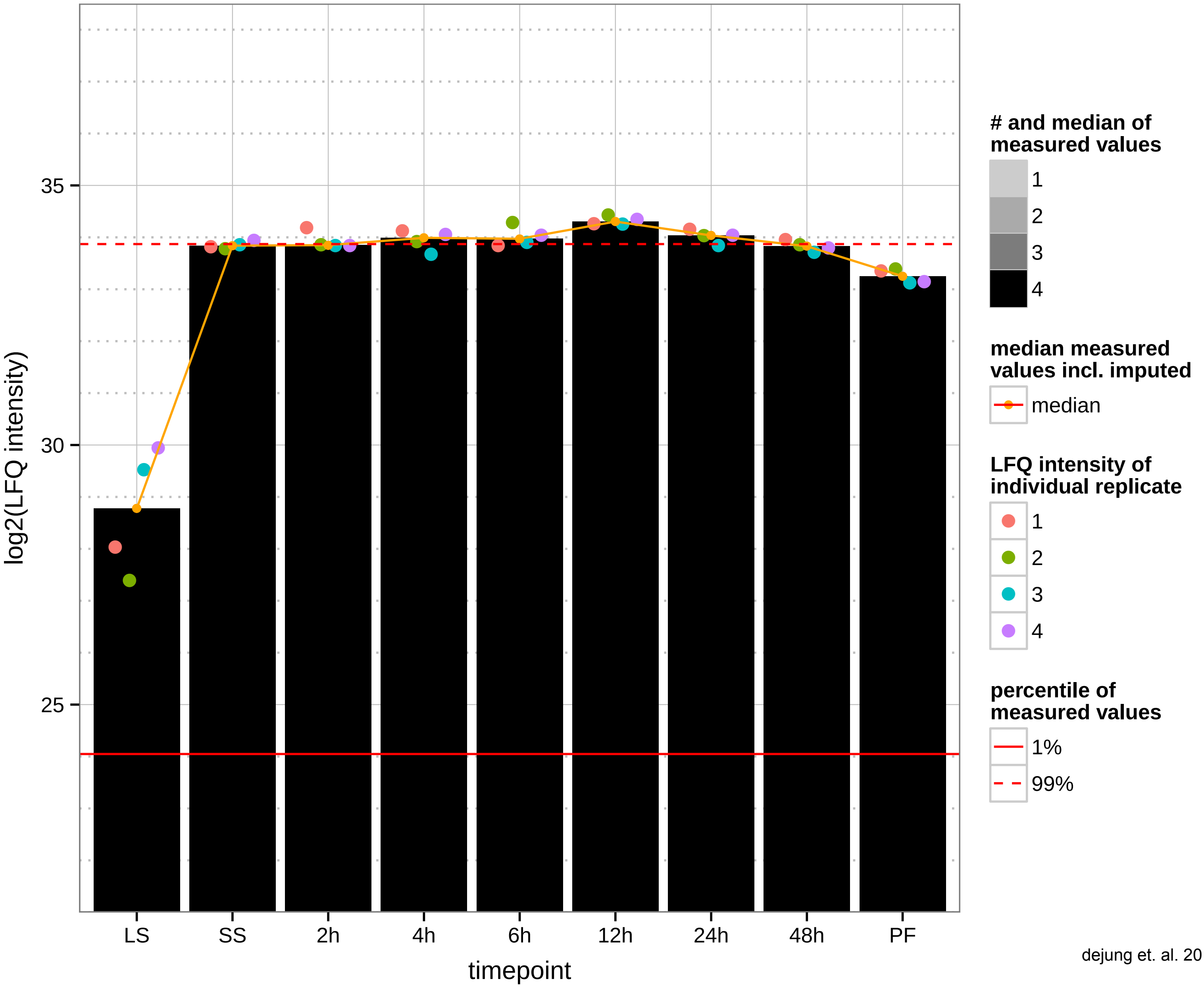
2–oxoglutarate dehydrogenase E2 component, putative
Tb927.11.11680
AGOF: dihydrolipoyllysine–residue succinyltransferase activity
AGOC: mitochondrion, oxoglutarate dehydrogenase complex
AGOP: tricarboxylic acid cycle
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: metabolic process





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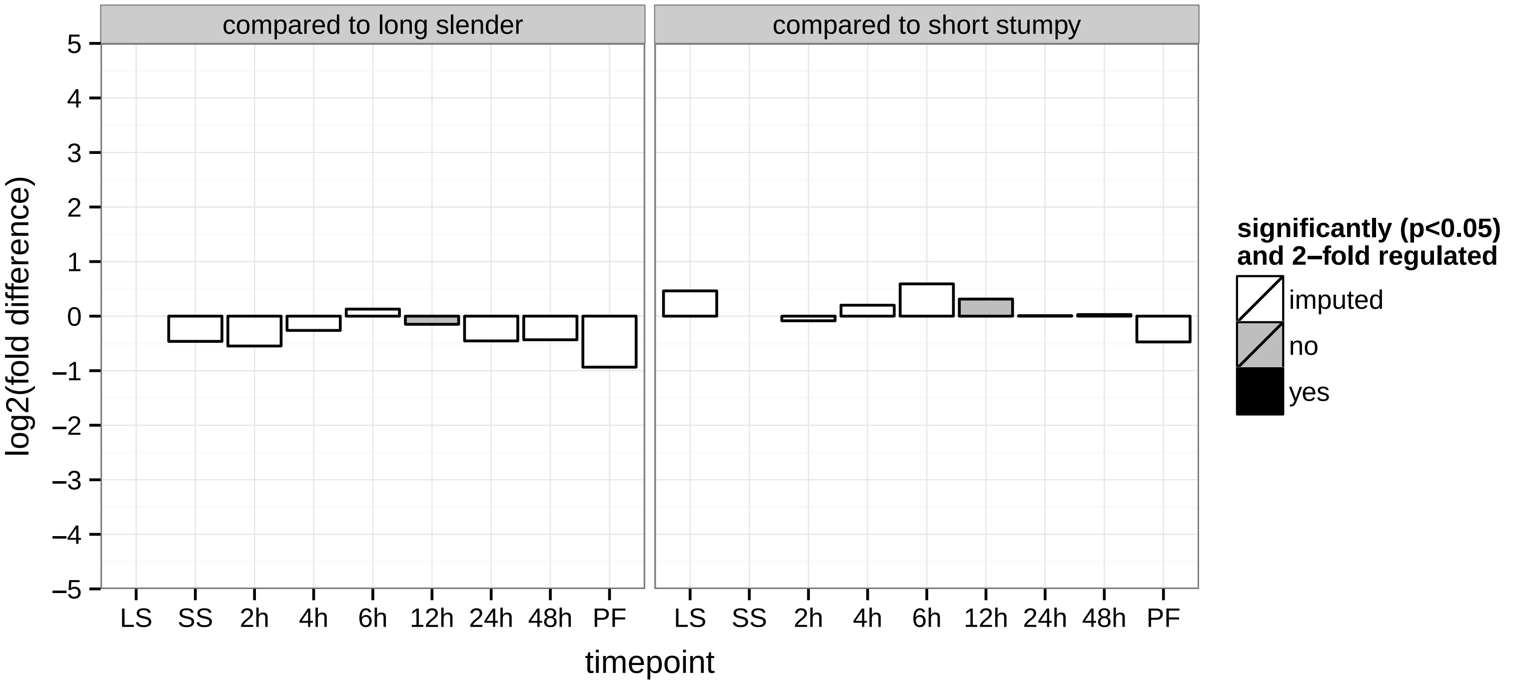
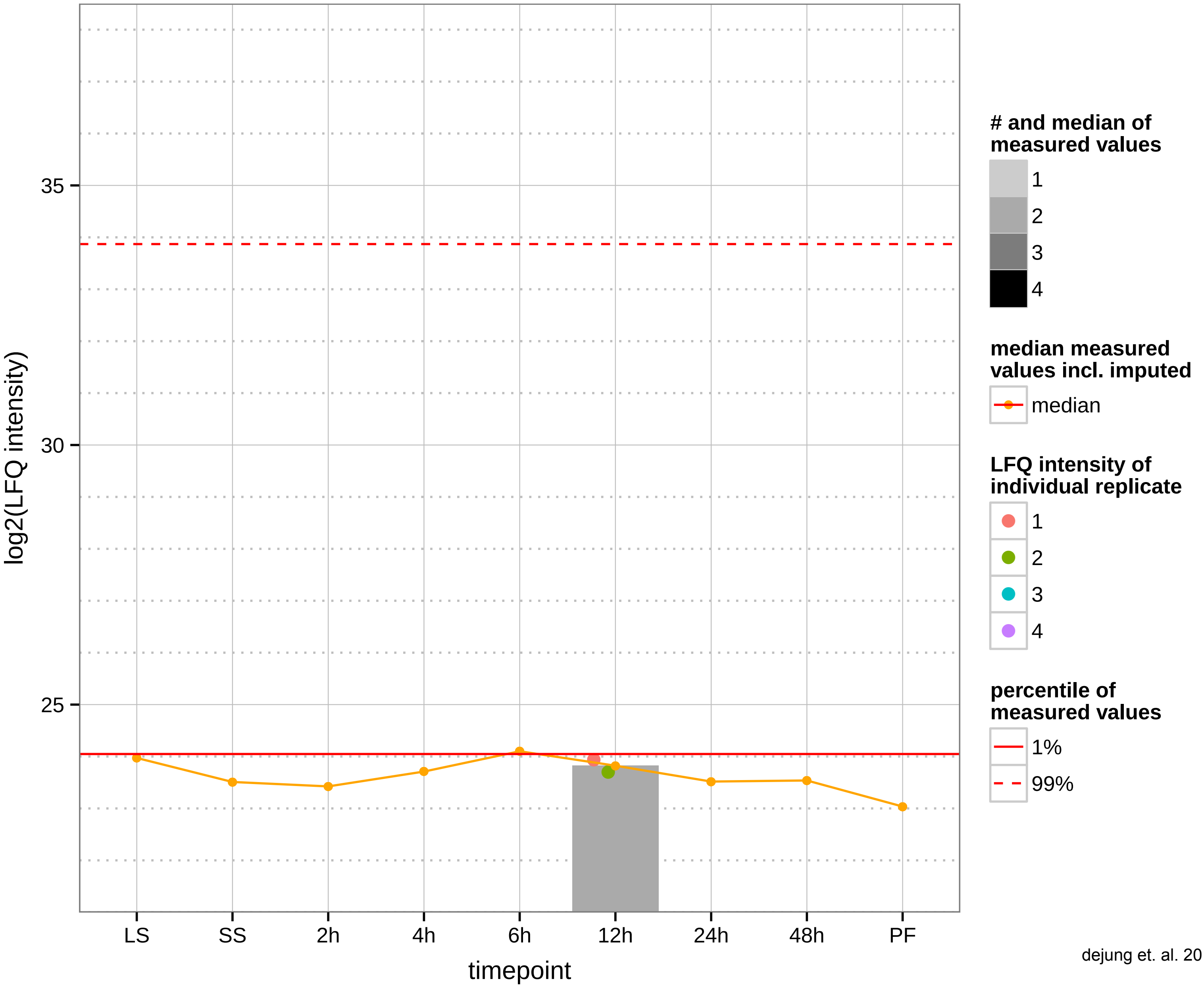
hypothetical protein, conserved
Tb927.11.1170
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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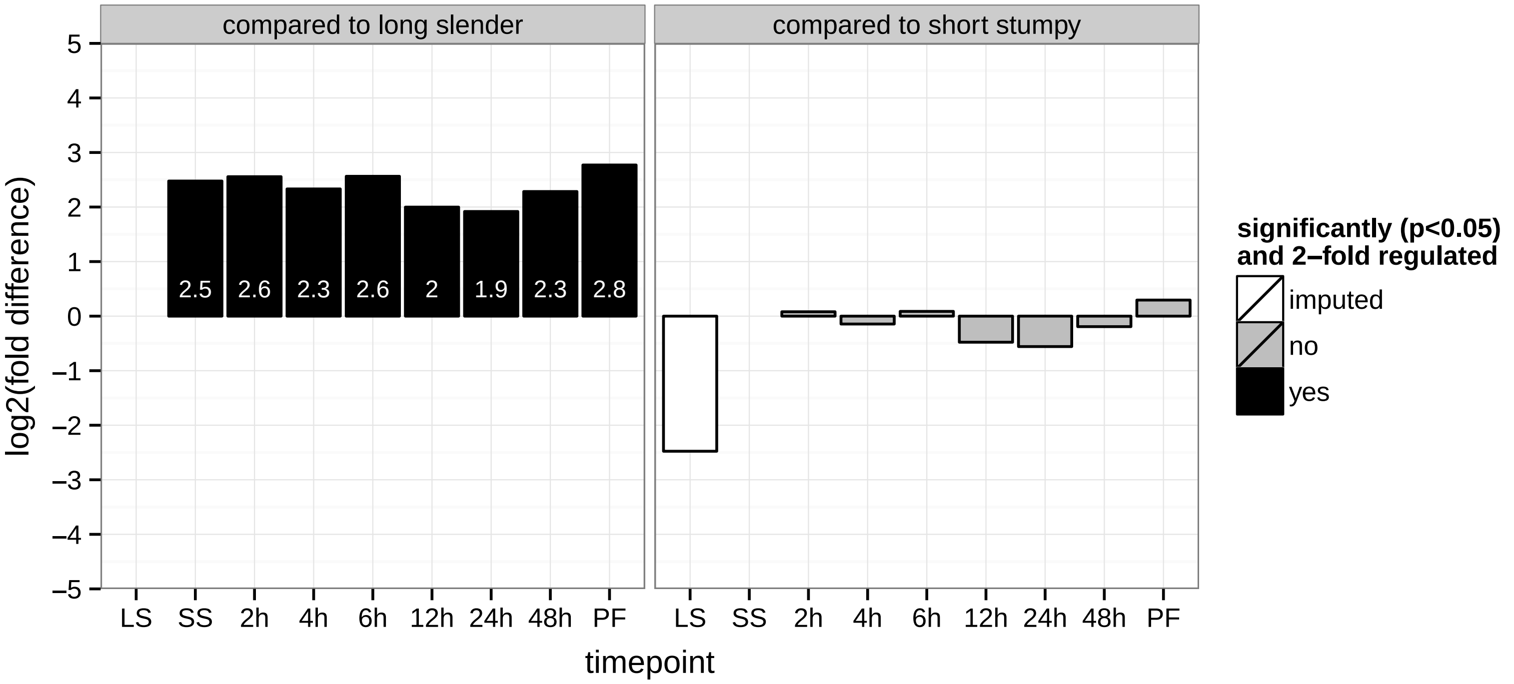
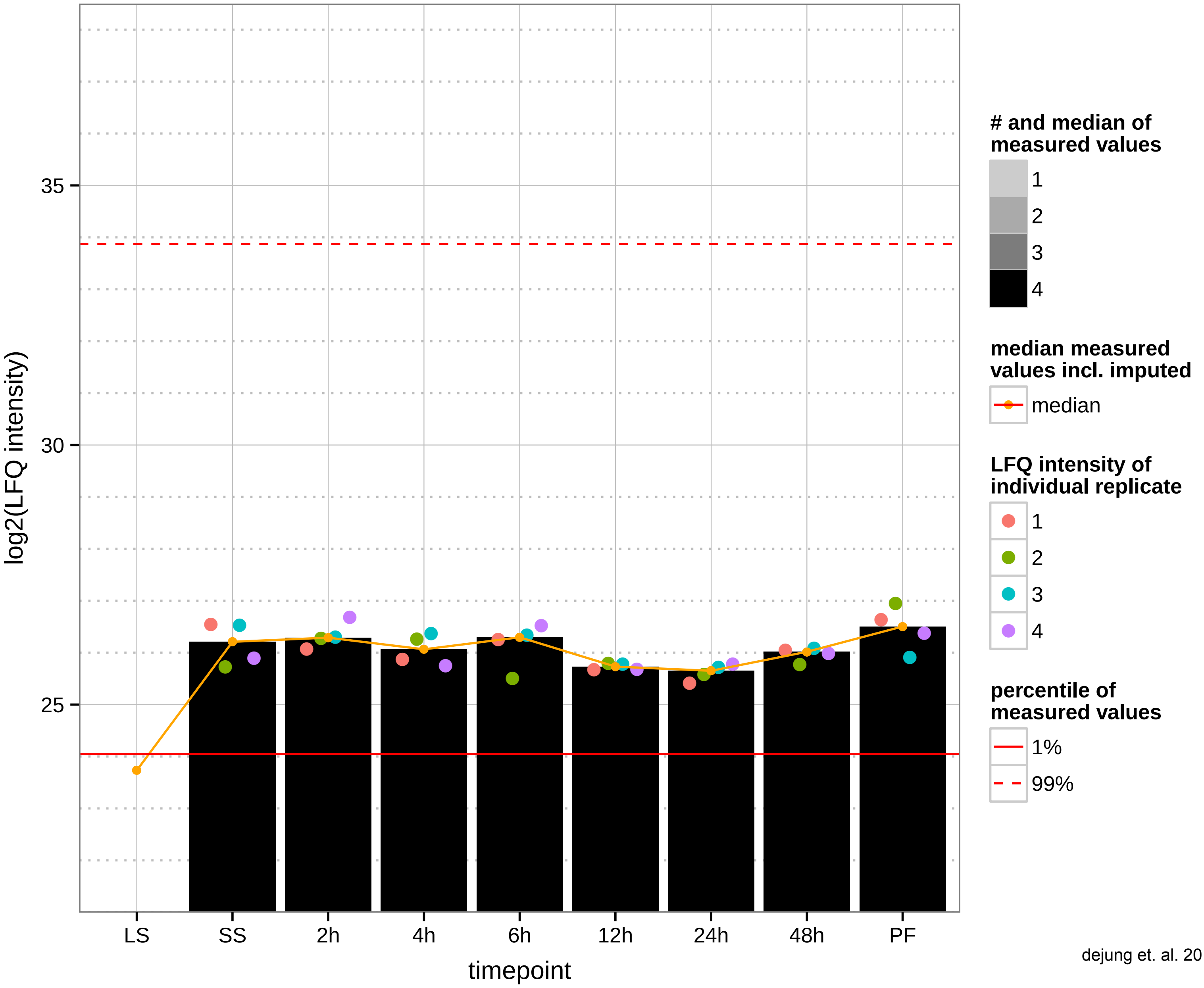
hypothetical protein, conserved
Tb927.11.11700
AGOF: transferase activity
AGOC: null
AGOP: null
PGOF: nucleotidyltransferase activity, transferase activity
PGOC: null
PGOP: biosynthetic process





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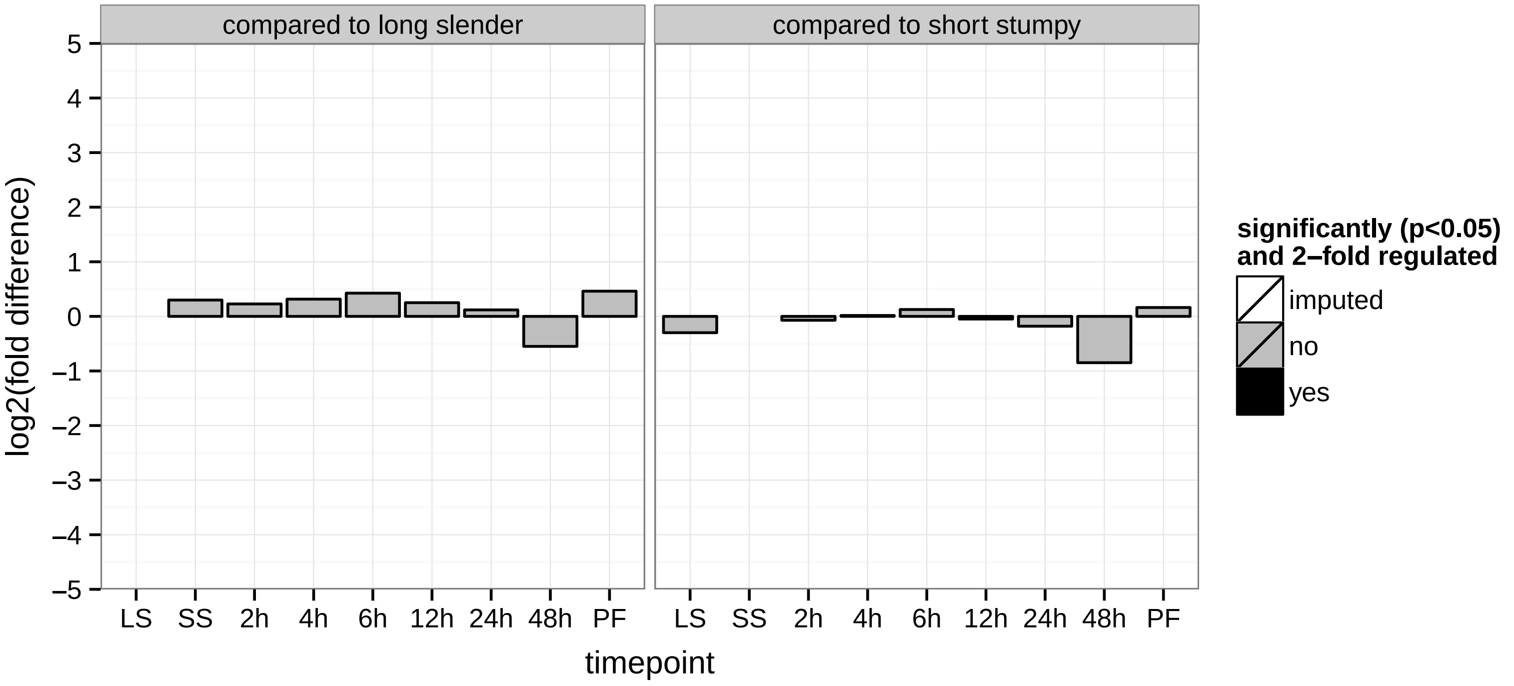
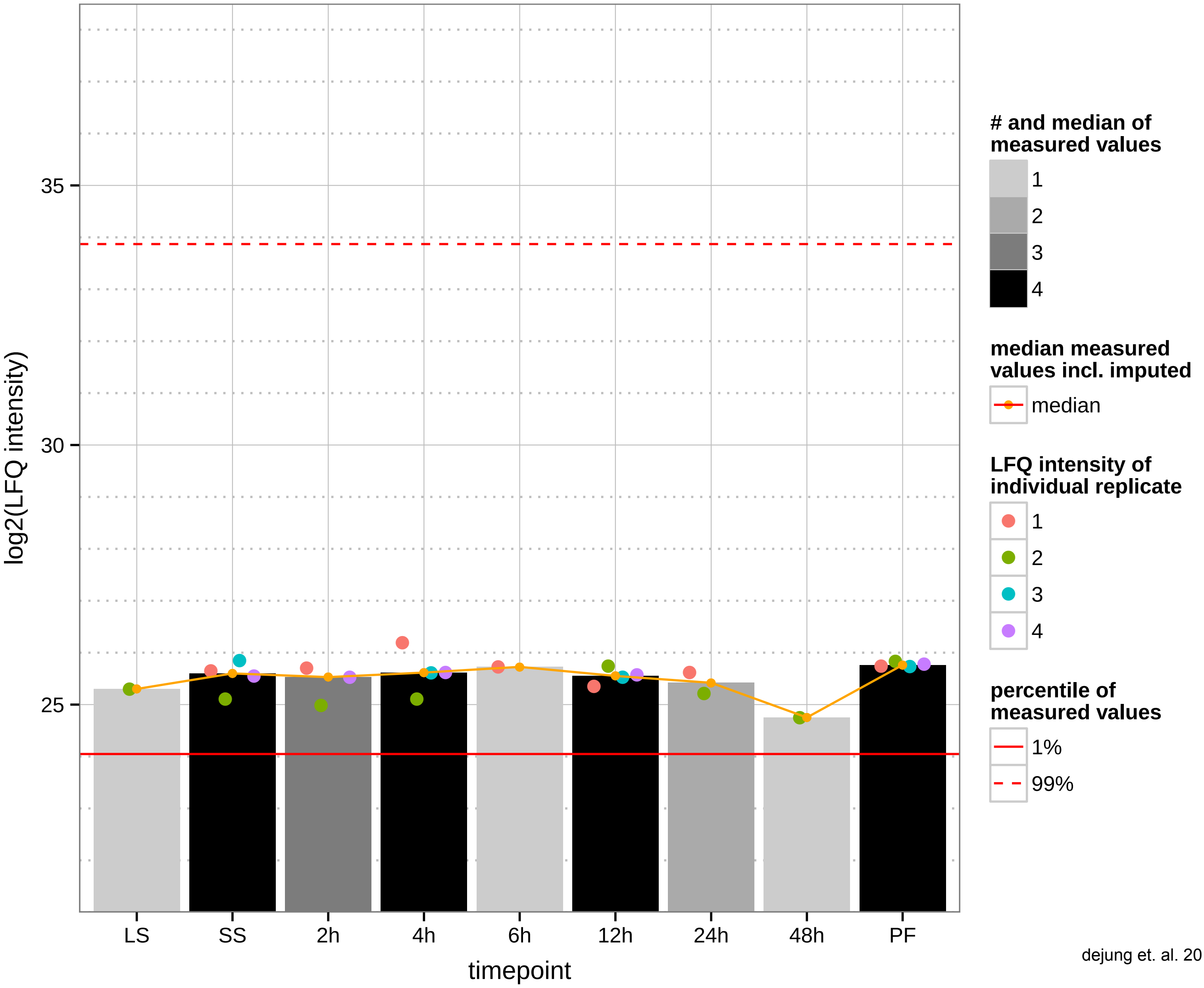
FG−GAP repeat protein, putative, intergrin alpha chain protein
Tb927.11.11720
AGOF: null
AGOC: integral to membrane, integrin complex
AGOP: cell−matrix adhesion
PGOF: null
PGOC: null
PGOP: null





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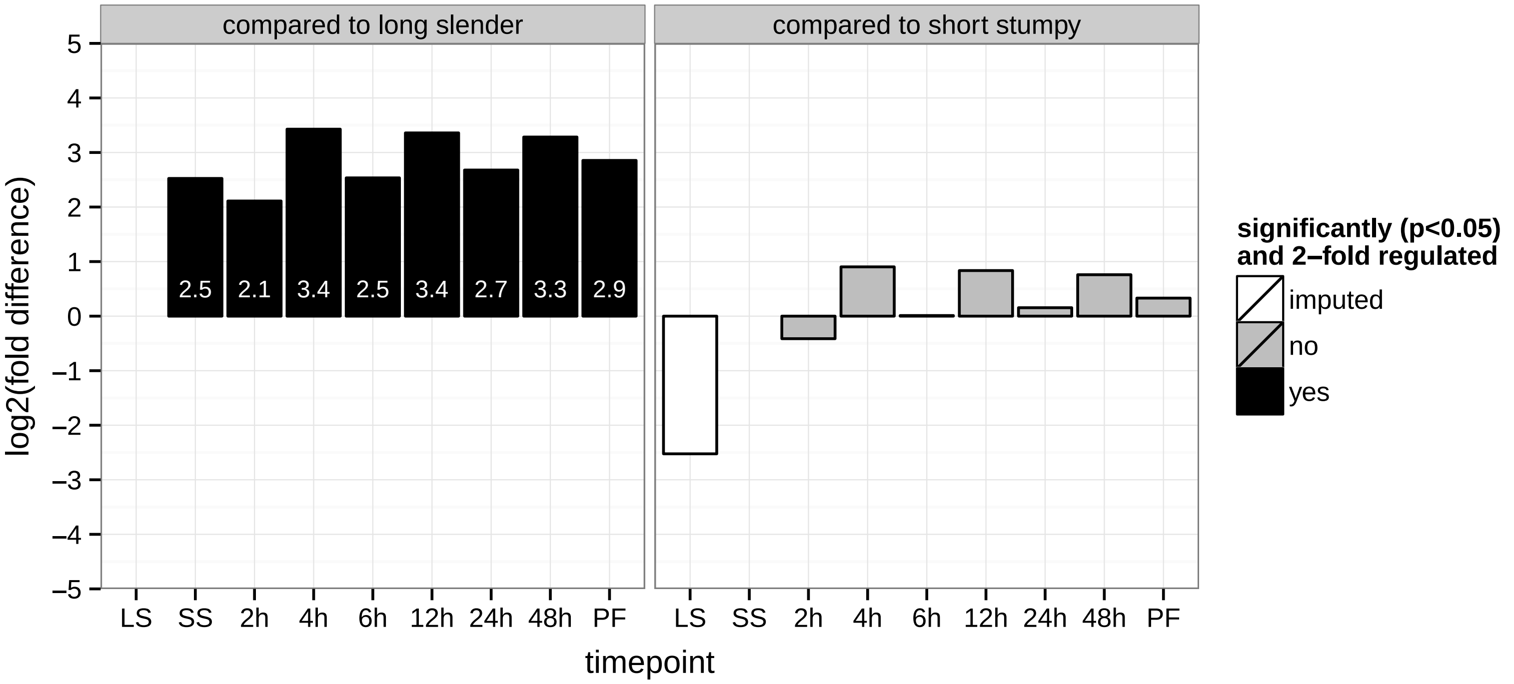
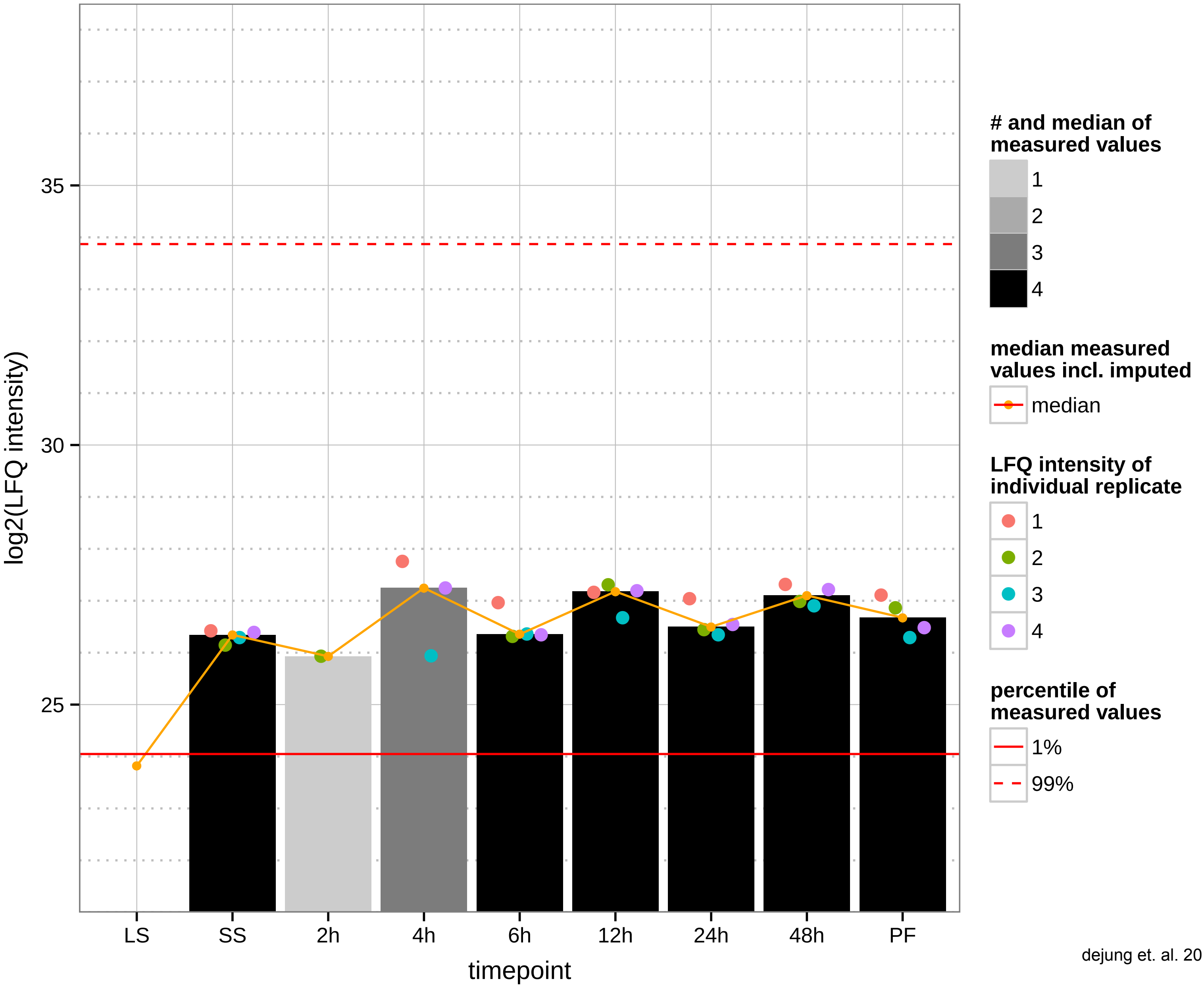
MRP protein, putative
Tb927.11.11730
AGOF: nucleotide binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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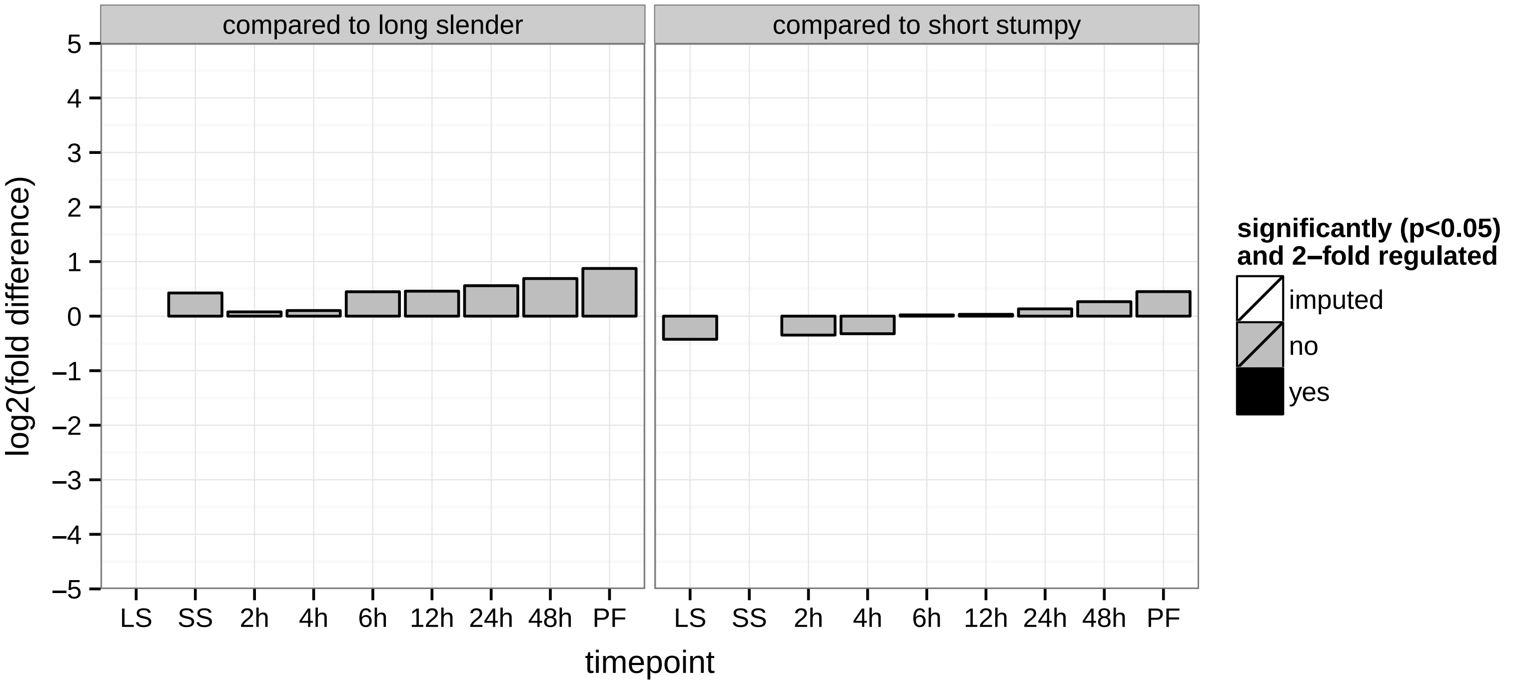
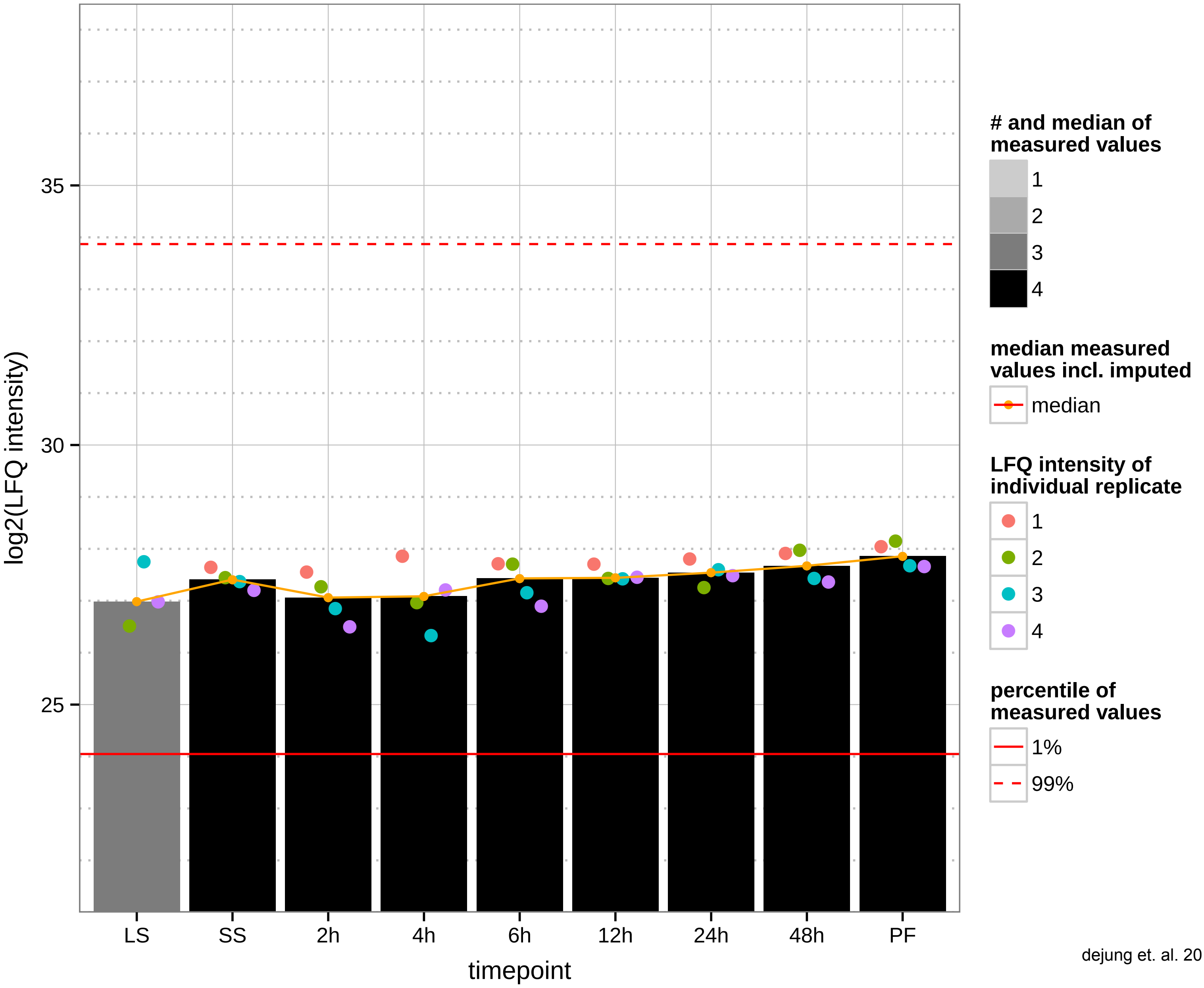
NA, splicing factor 3B subunit 1, putative
Tb927.11.11850
AGOF: NA, null
AGOC: NA, null
AGOP: NA, null
PGOF: NA, binding, protein binding
PGOC: NA, null
PGOP: NA, null





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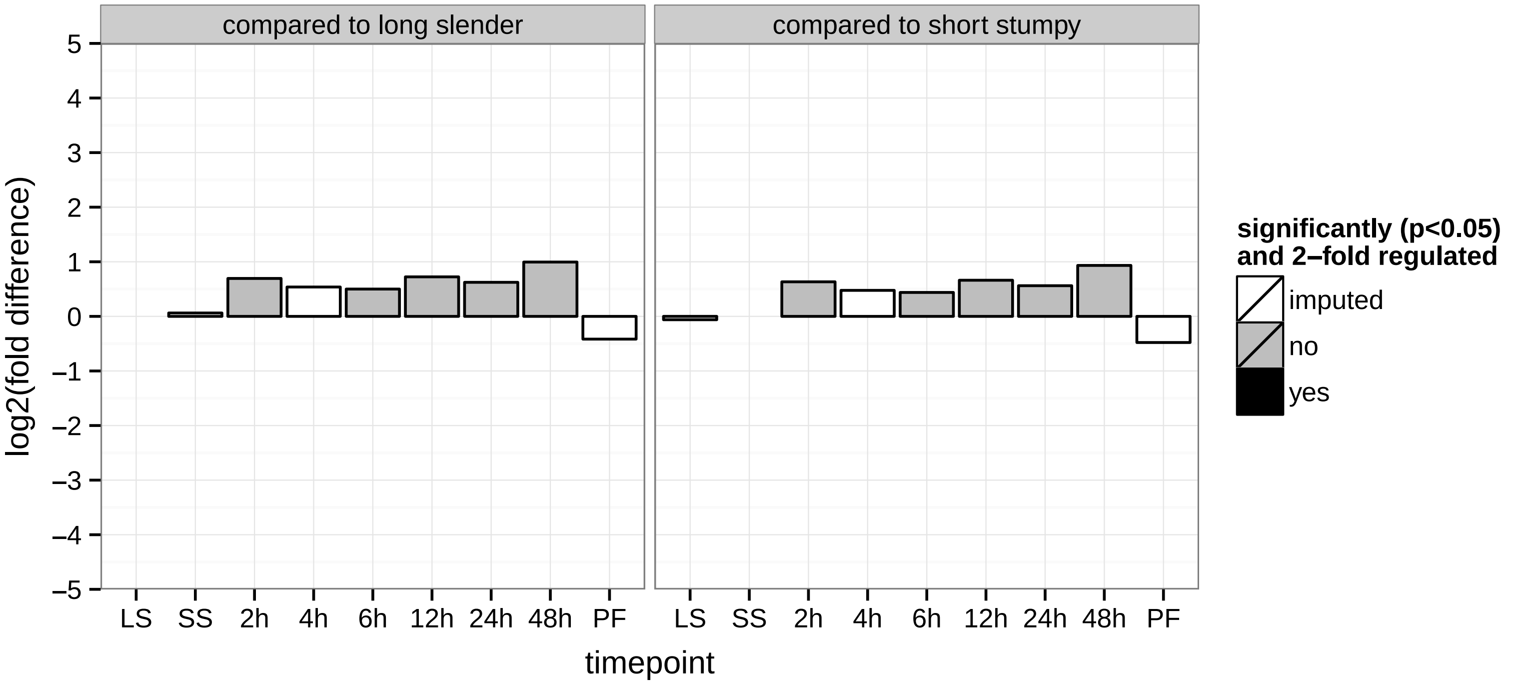
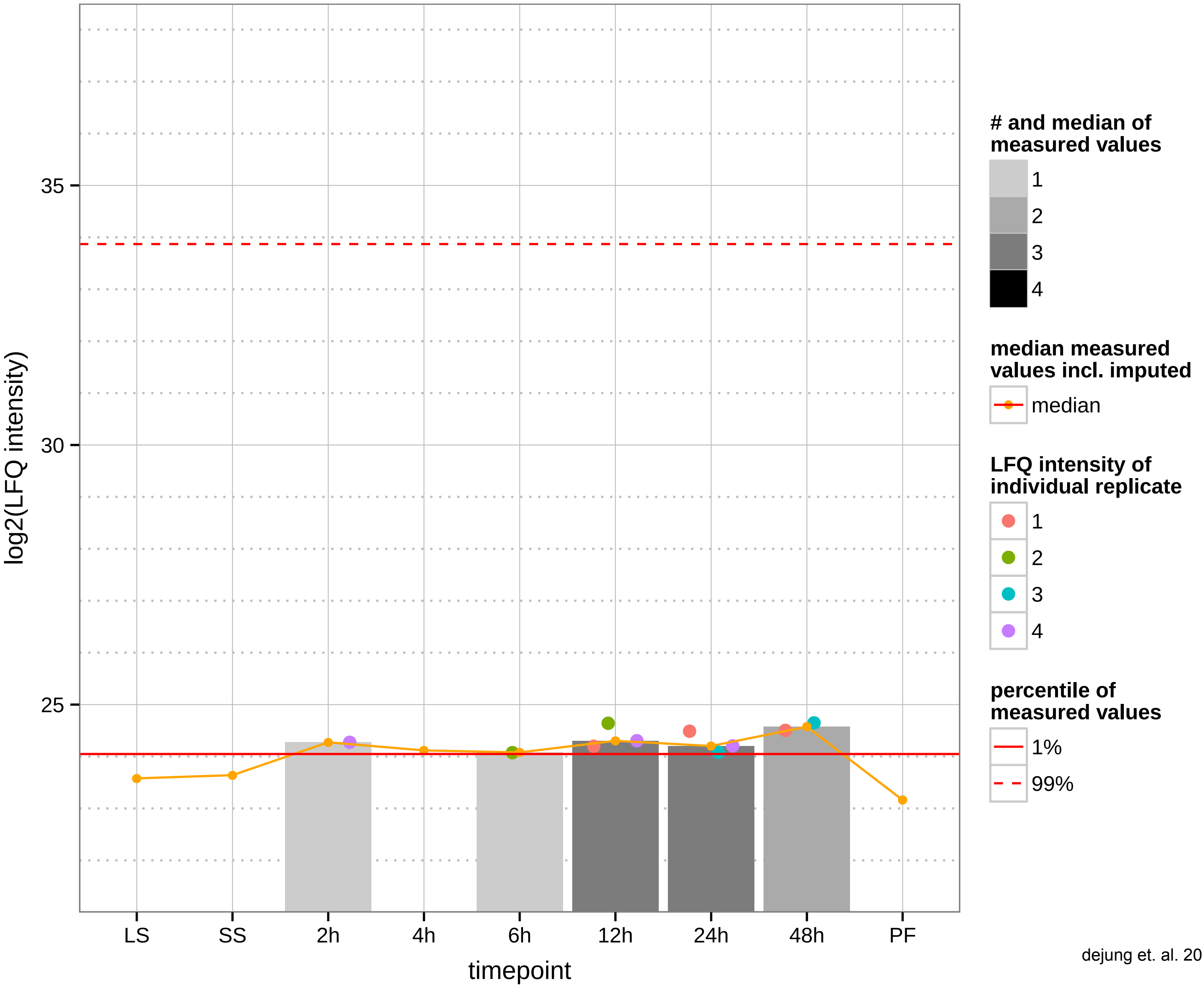
hypothetical protein, conserved
Tb927.11.11870
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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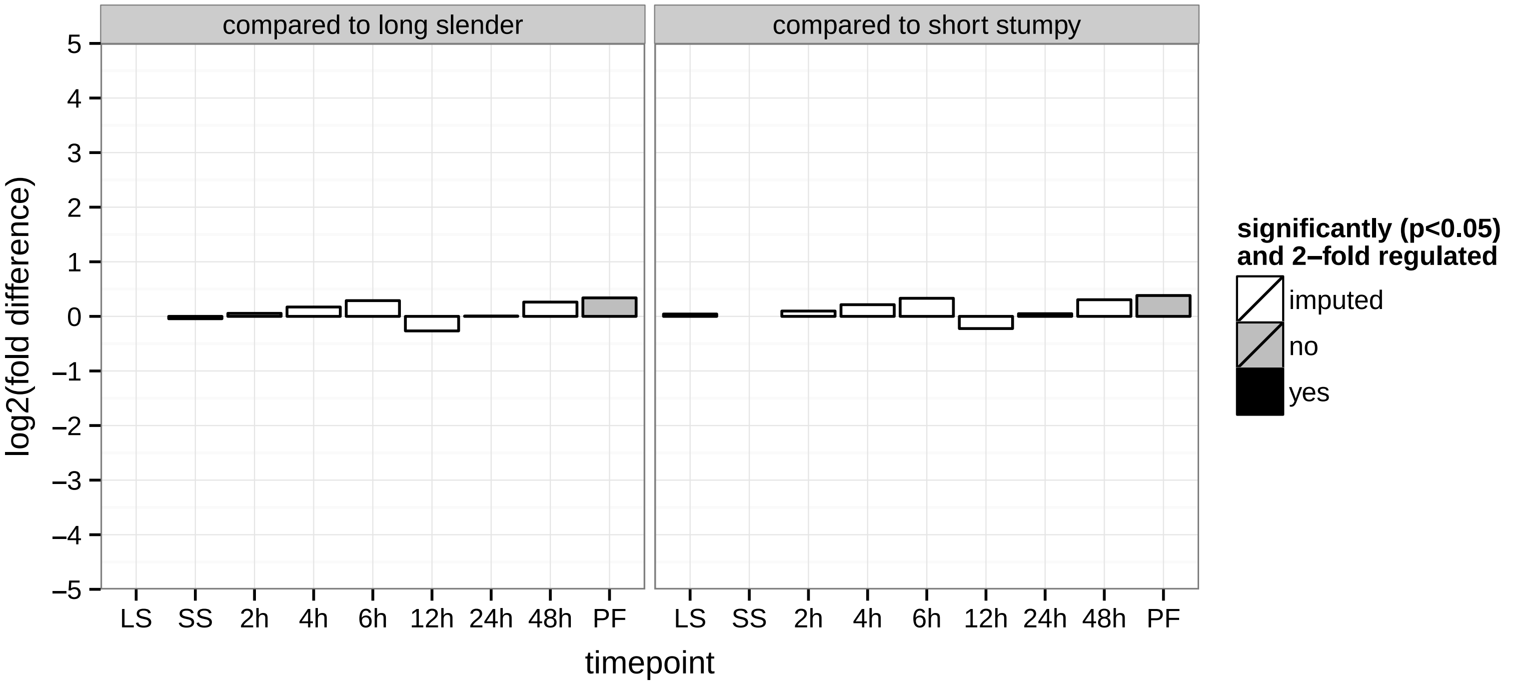
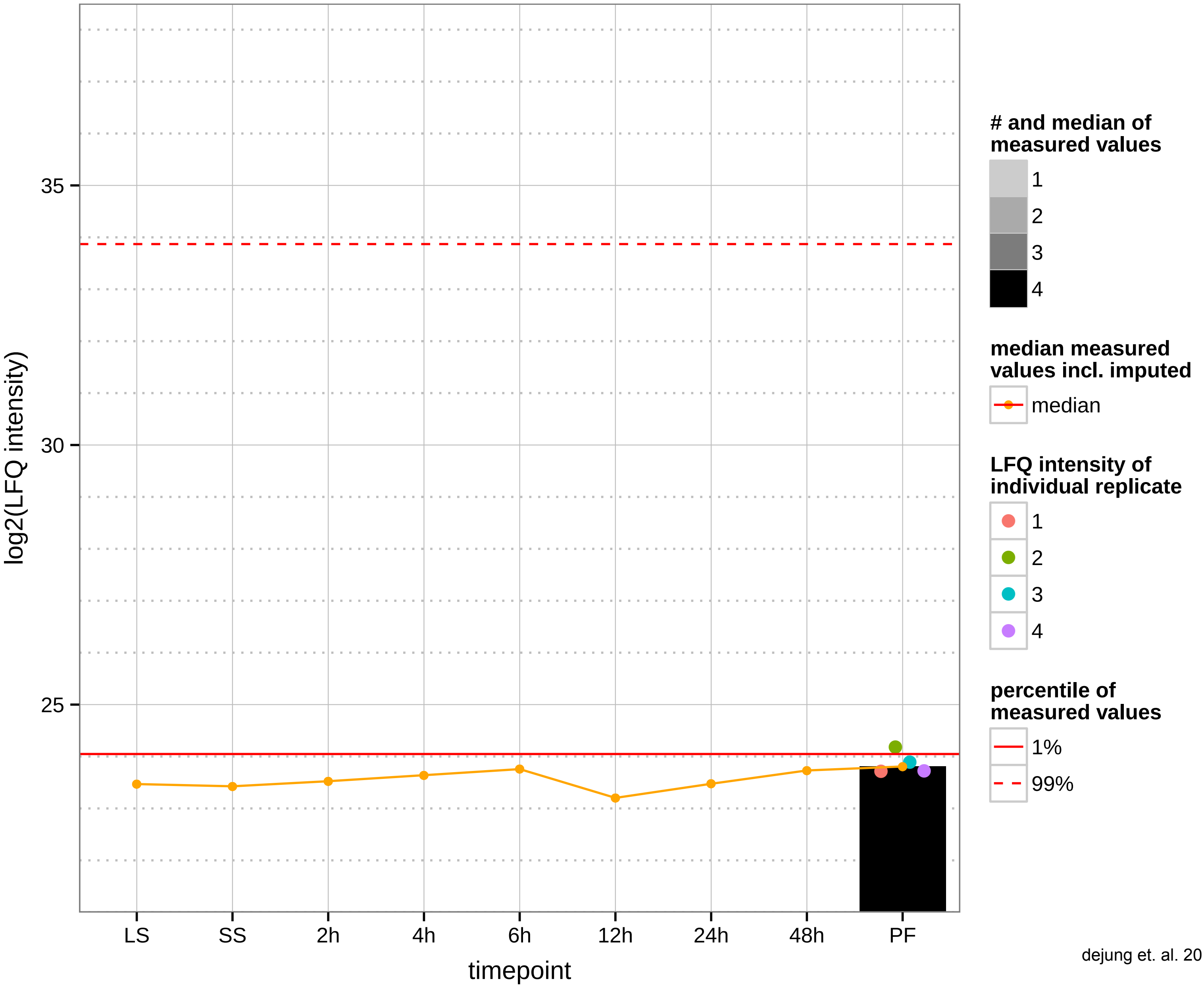
conserved protein
Tb927.11.11880
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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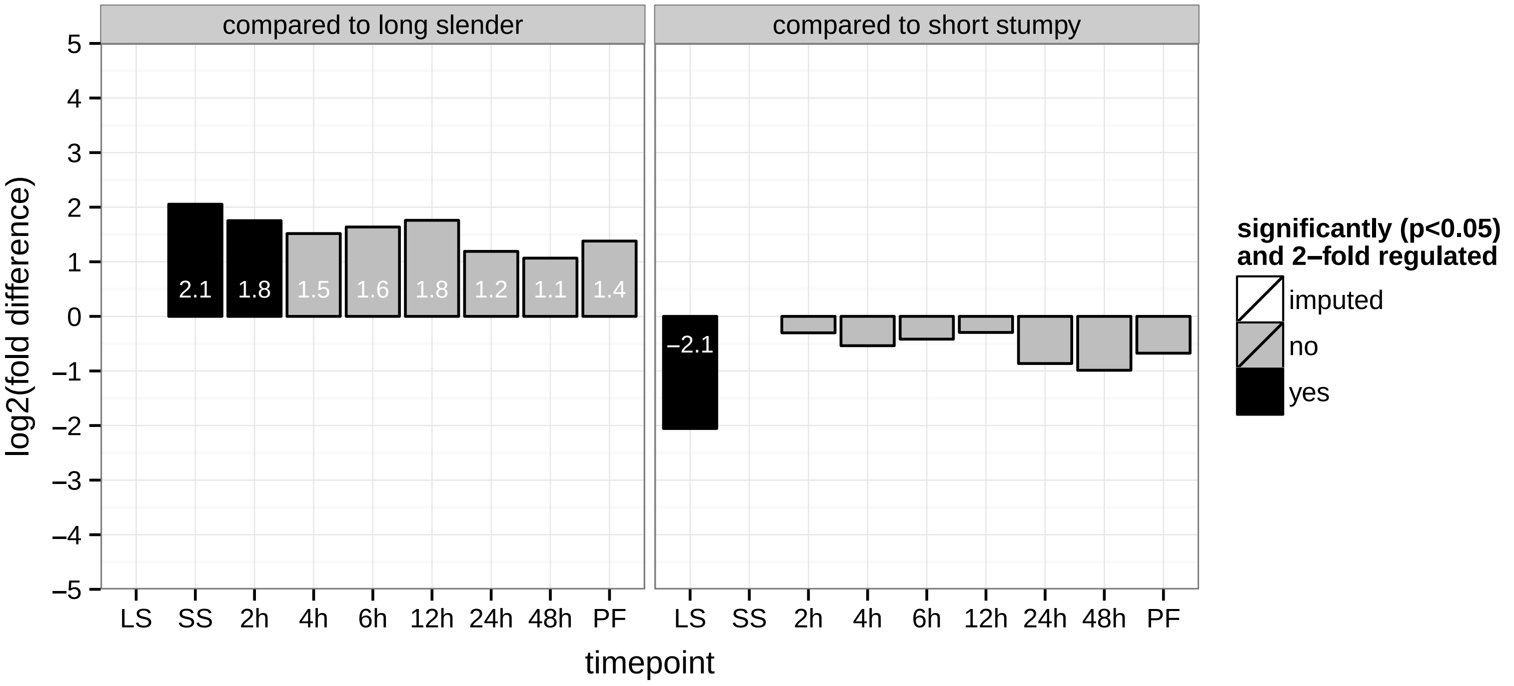
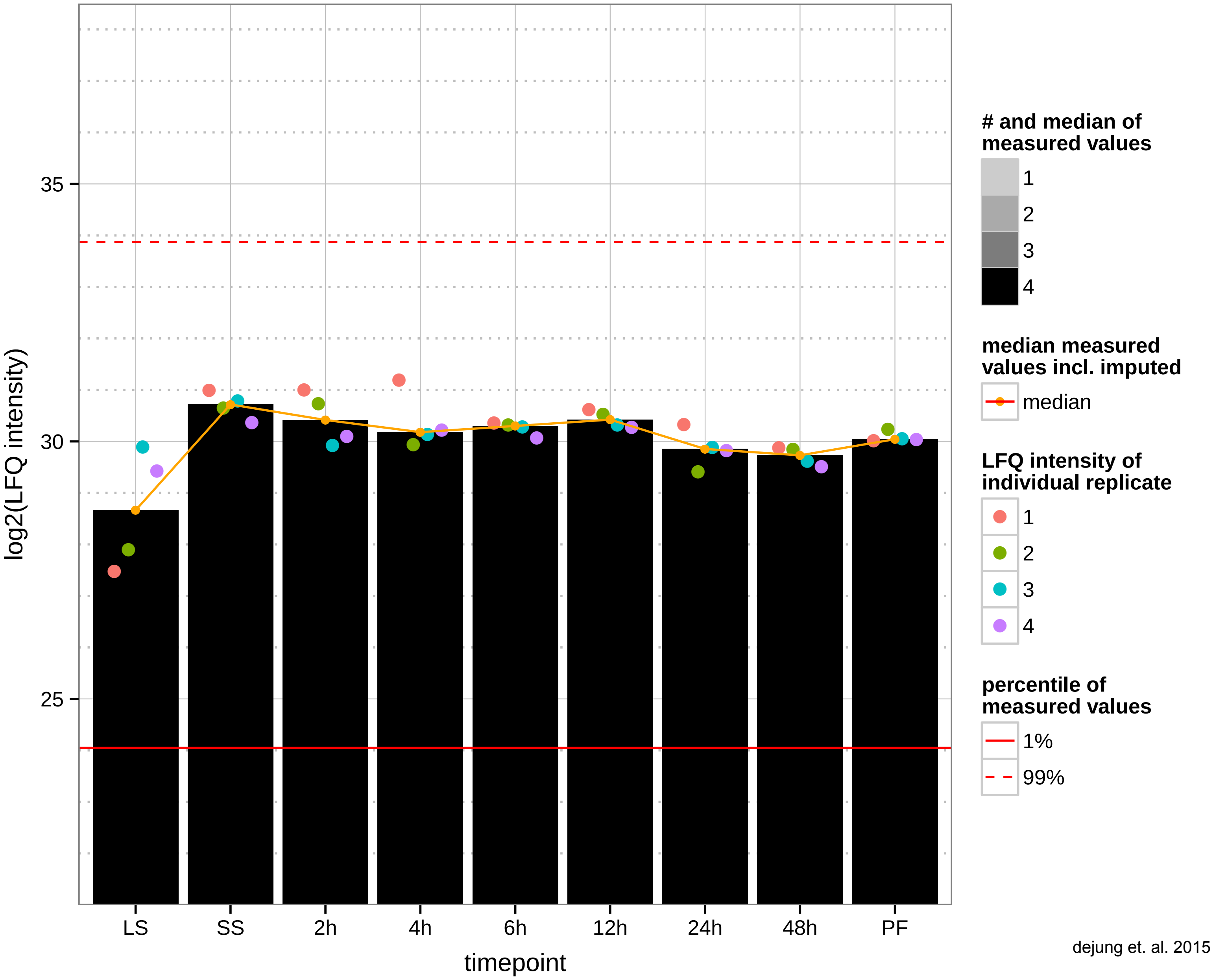
coatomer gamma subunit, putative, cytosolic coat protein, putative (TbCoatomerGamma)
Tb927.11.11900
AGOF: structural molecule activity
AGOC: COPI vesicle coat, Golgi–associated vesicle
AGOP: intracellular protein transport, retrograde vesicle–mediated transport, Golgi to ER
PGOF: binding, structural molecule activity
PGOC: Golgi–associated vesicle, membrane coat
PGOP: intracellular protein transport, vesicle–mediated transport





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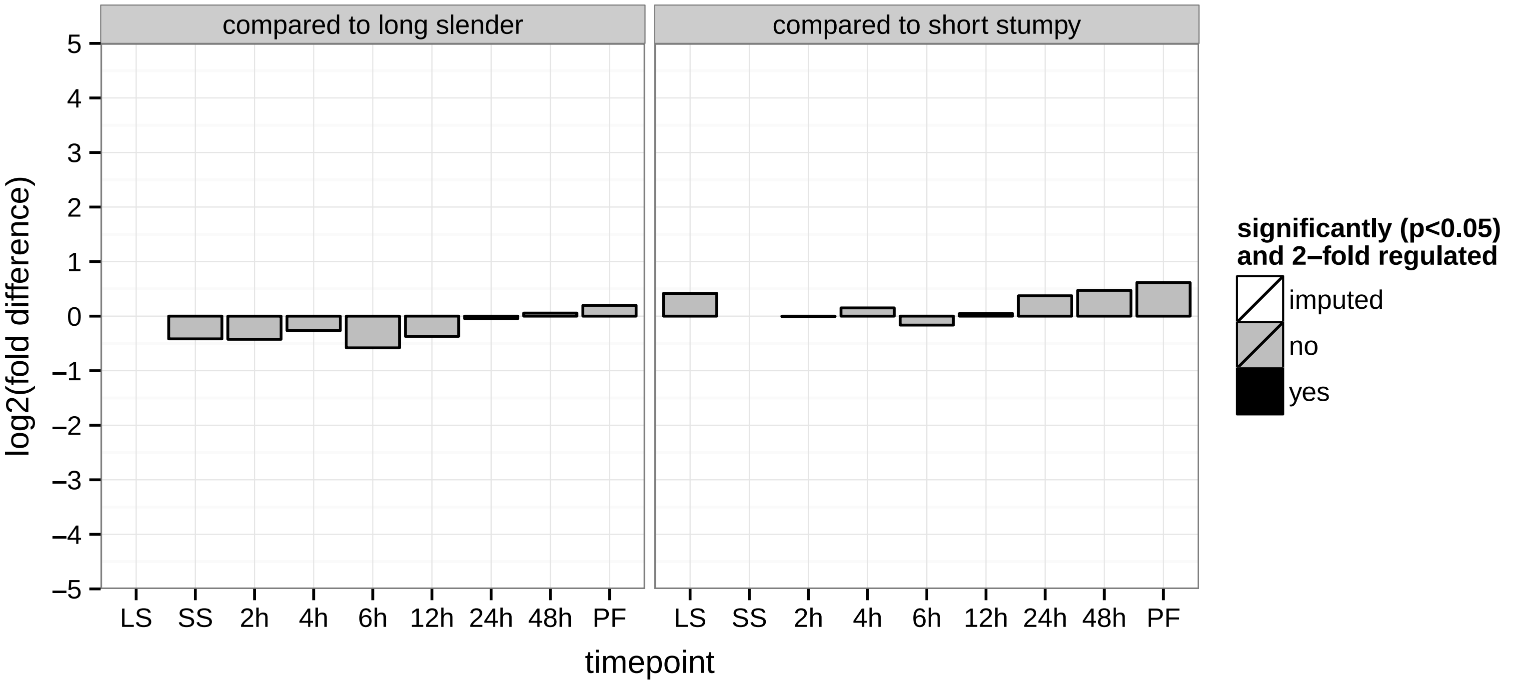
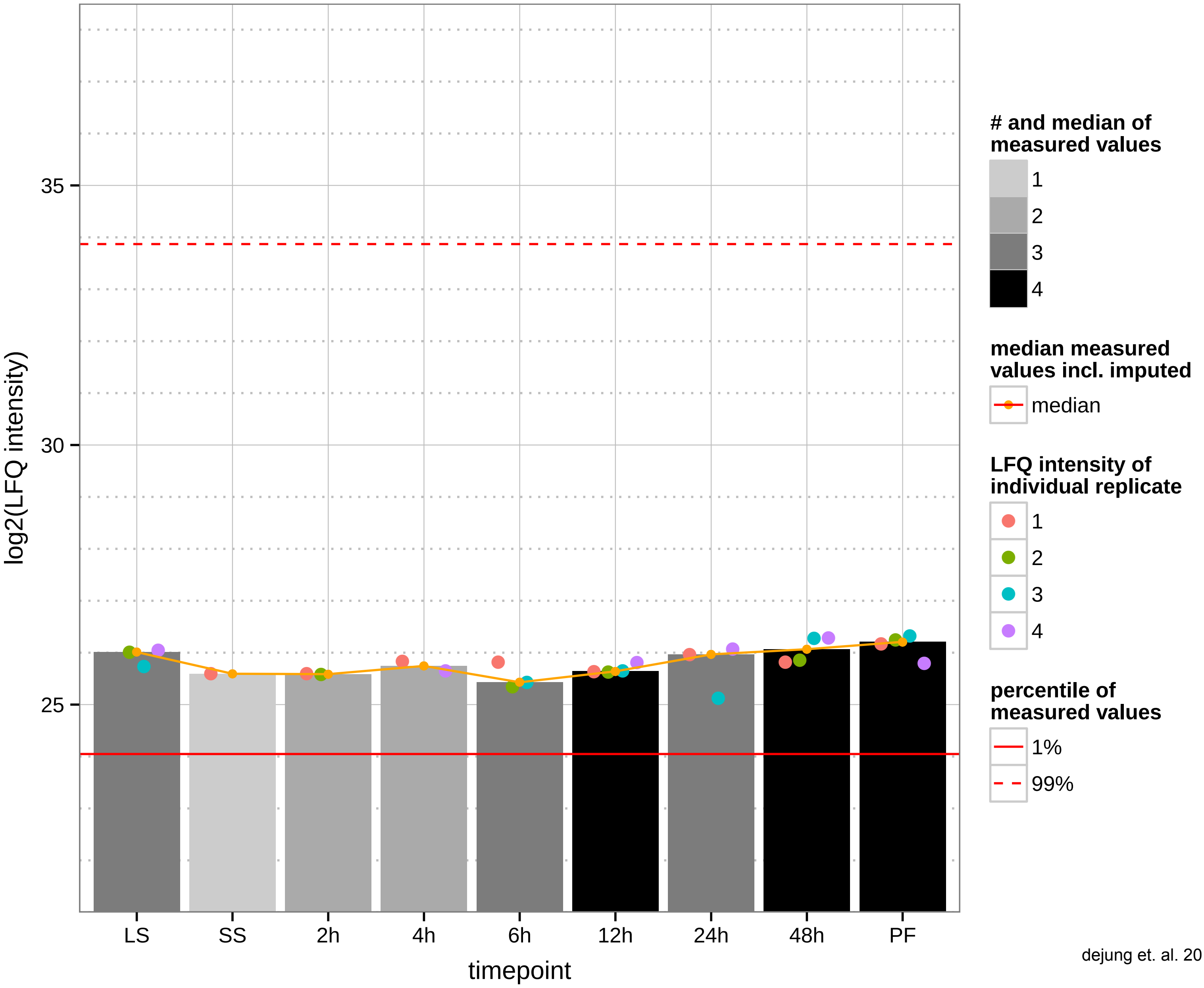
hypothetical protein, conserved
Tb927.11.1210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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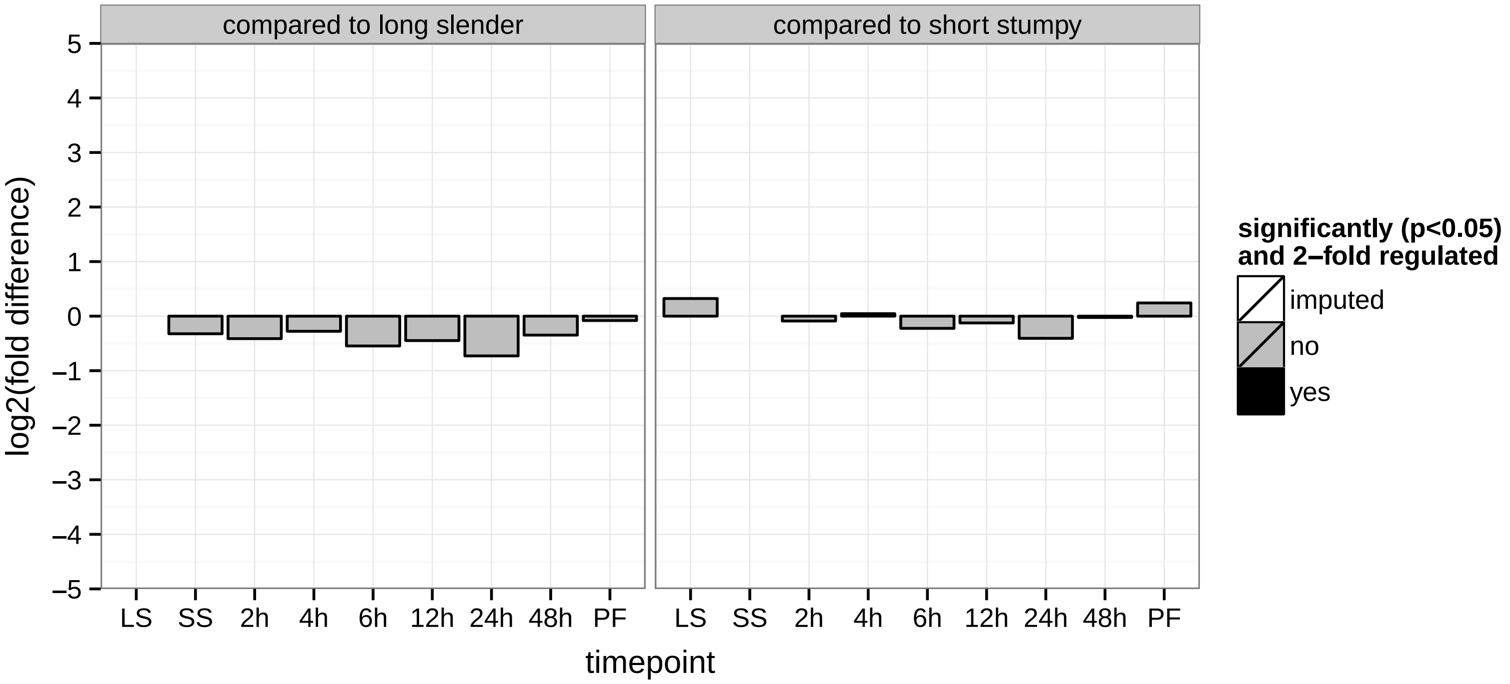
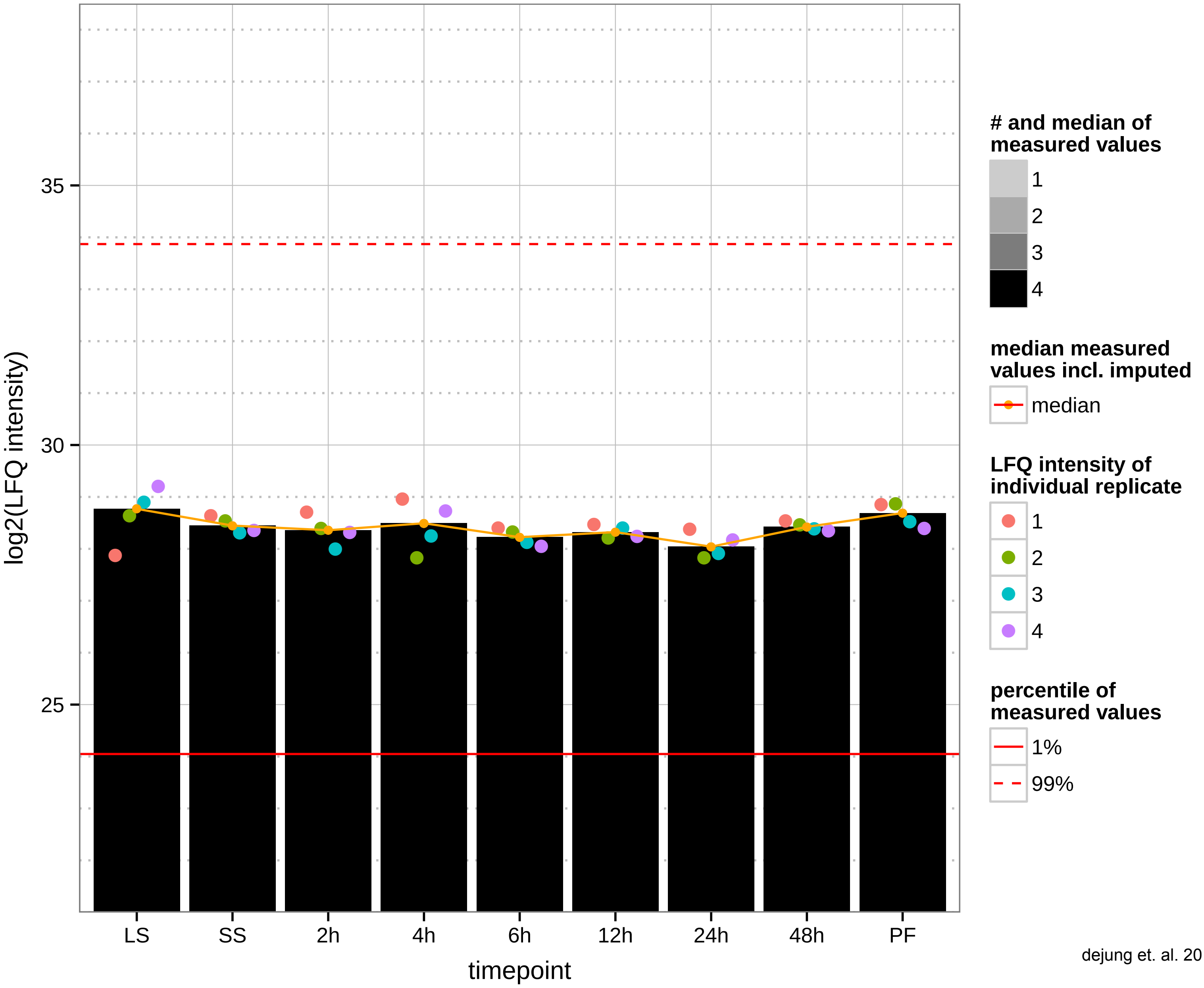
hypothetical protein, conserved
Tb927.11.12210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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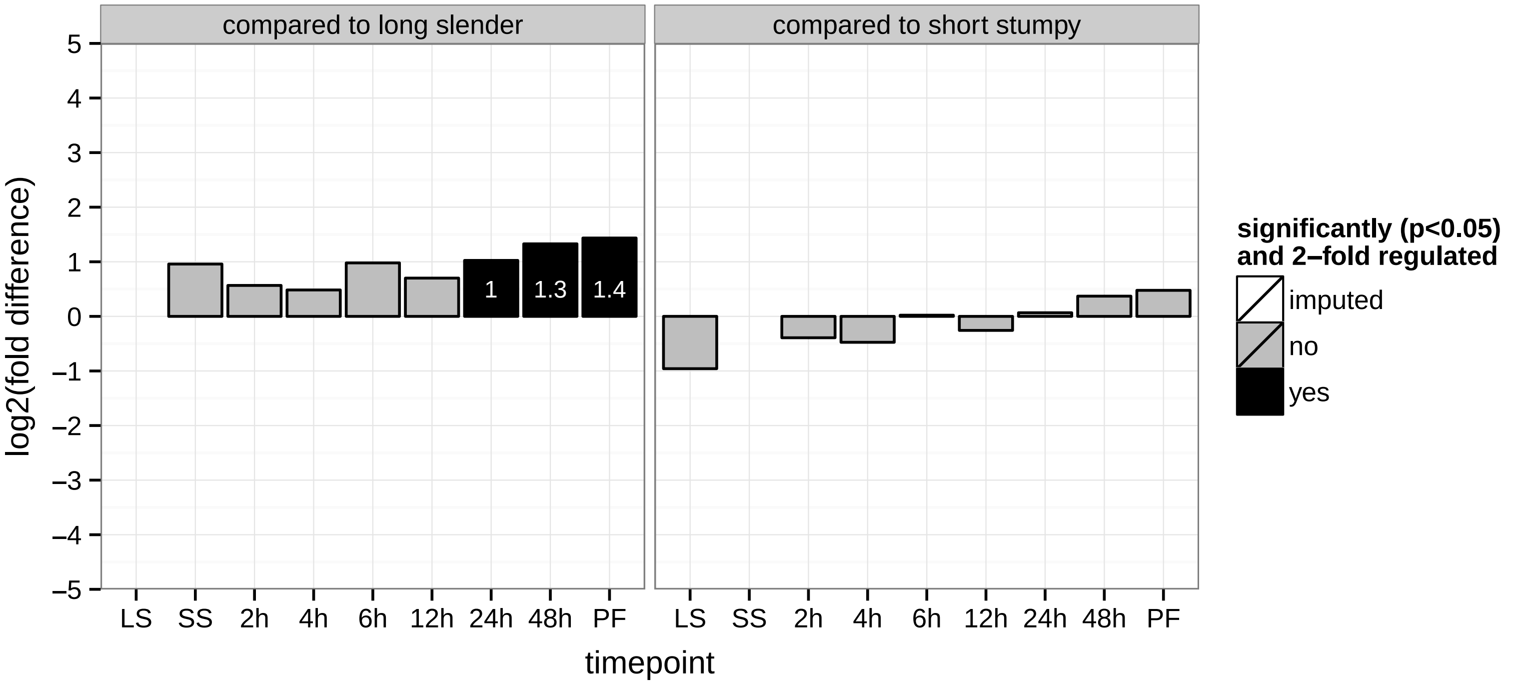
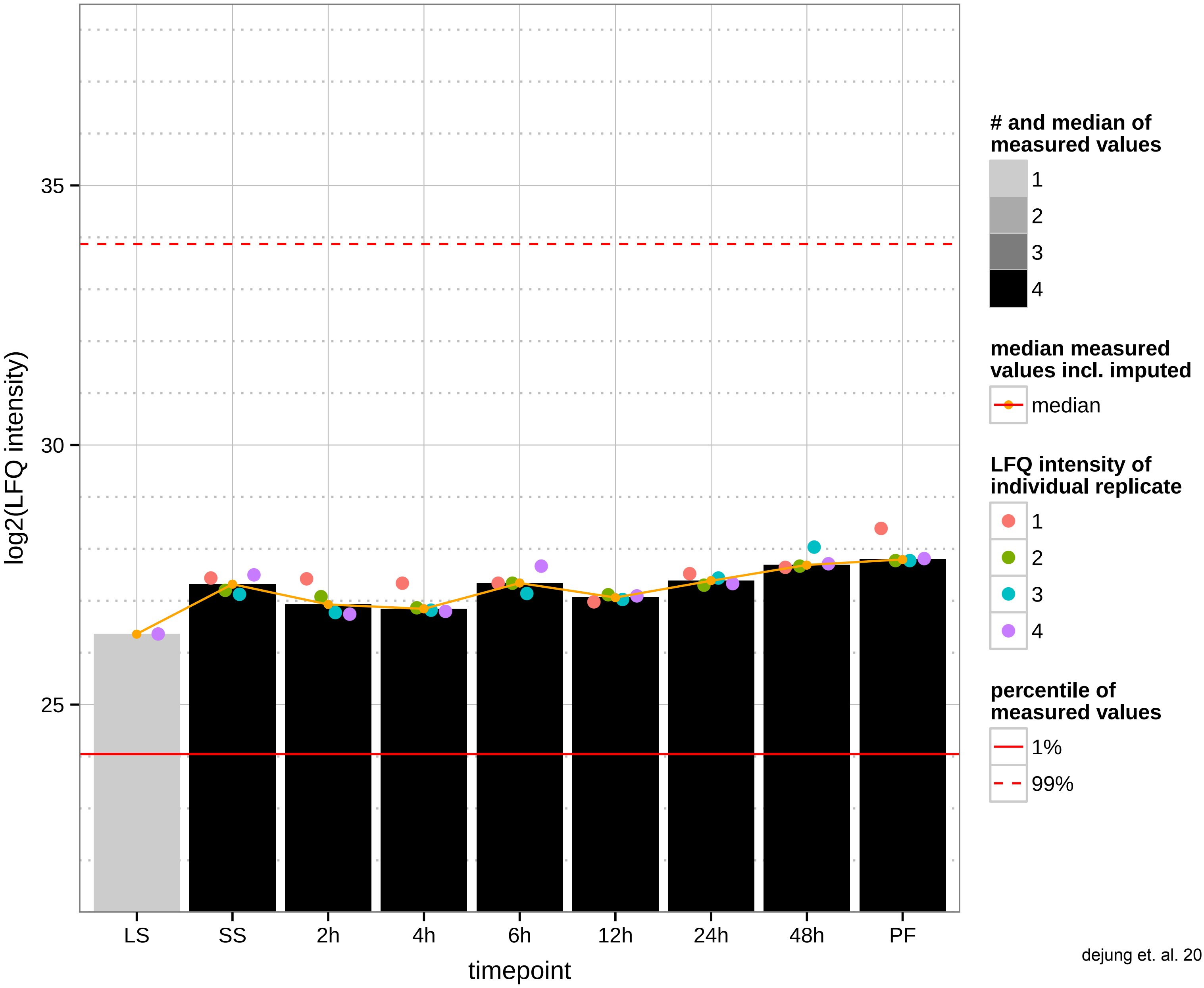
catalytic subunit of the vacuolar transporter chaperone 4
Tb927.11.12220
AGOF: metal ion binding
AGOC: vacuolar transporter chaperone complex
AGOP: polyphosphate biosynthetic process
PGOF: null
PGOC: null
PGOP: null





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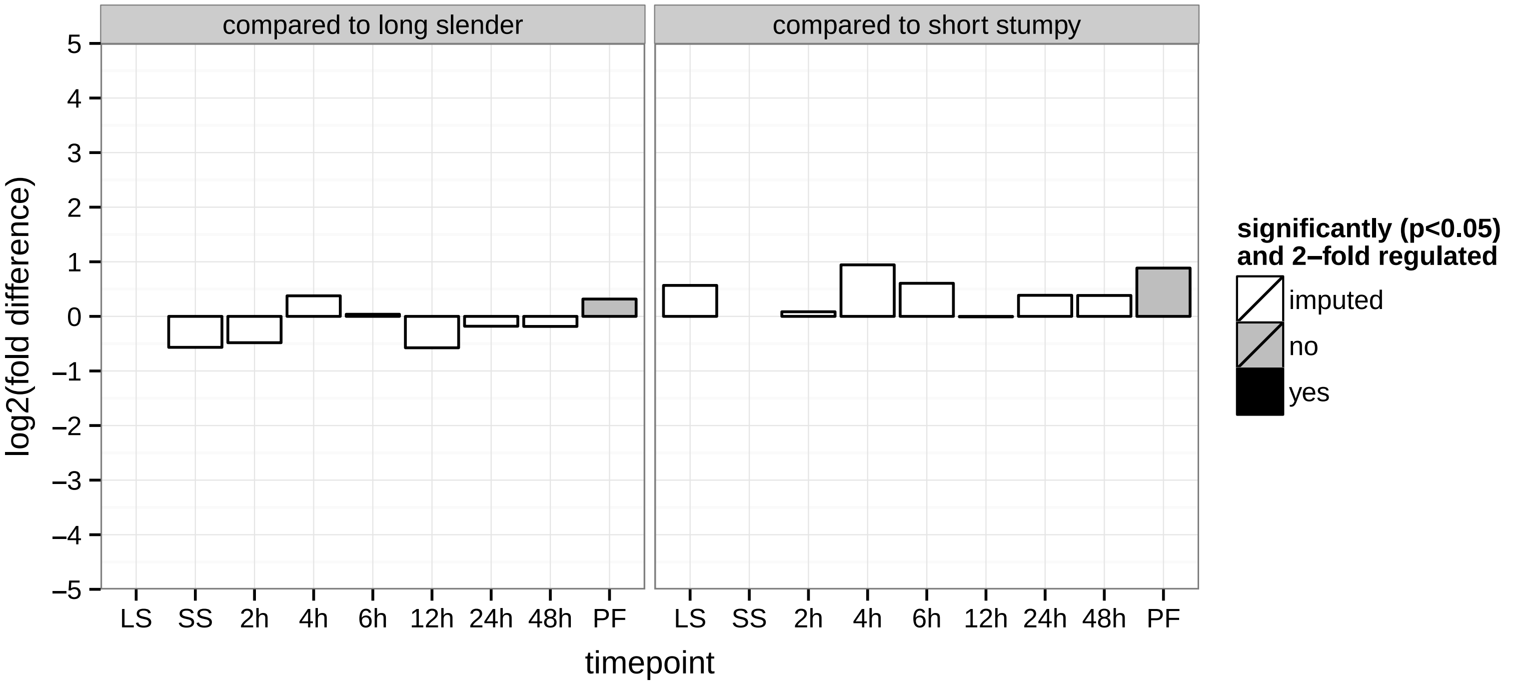
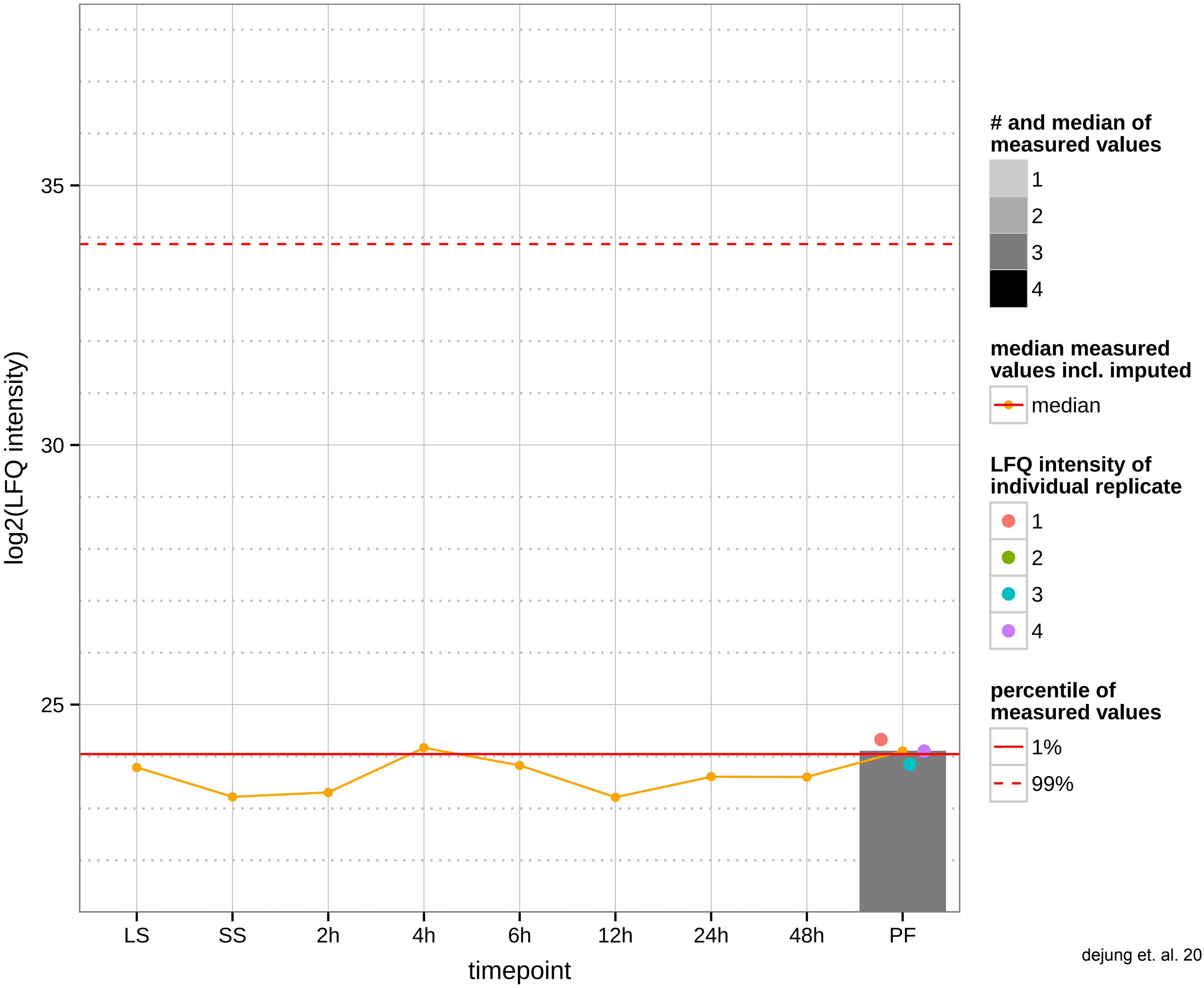
hypothetical protein, conserved
Tb927.11.12260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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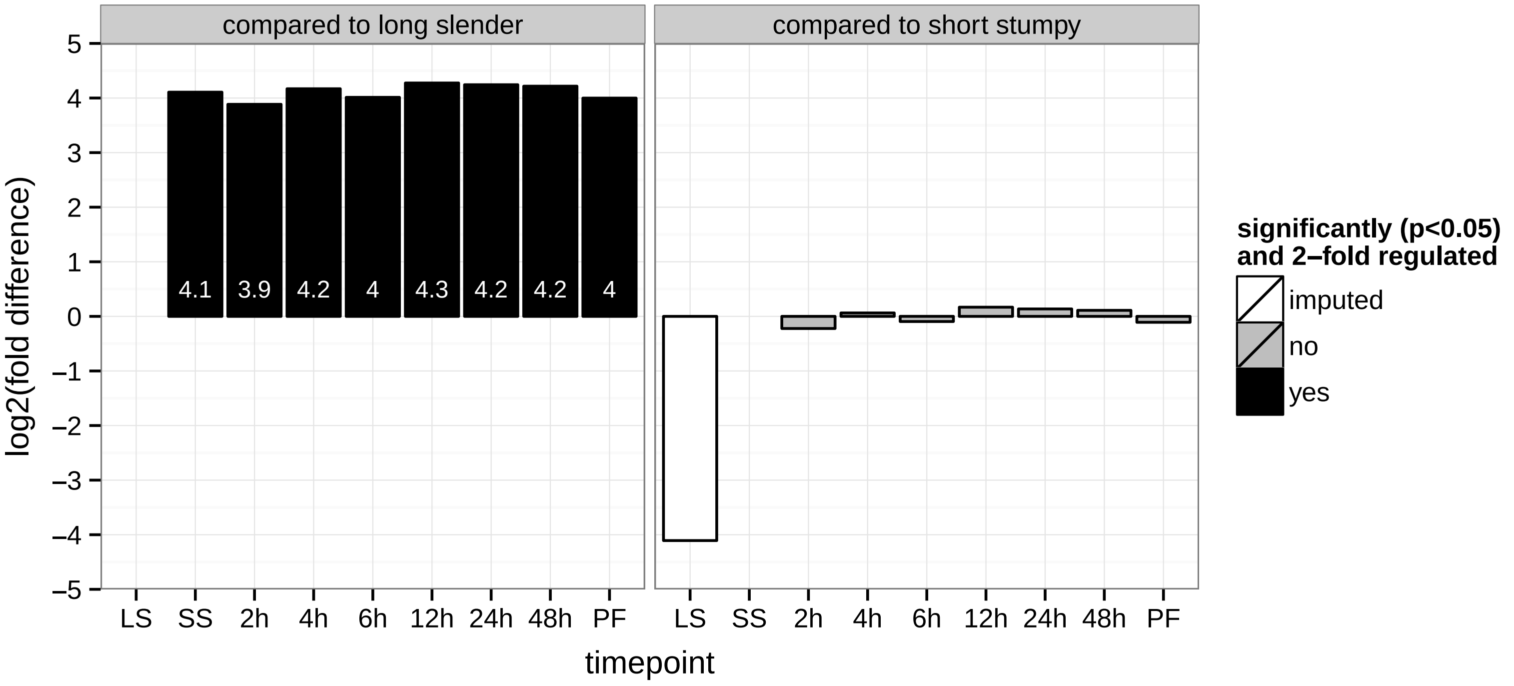
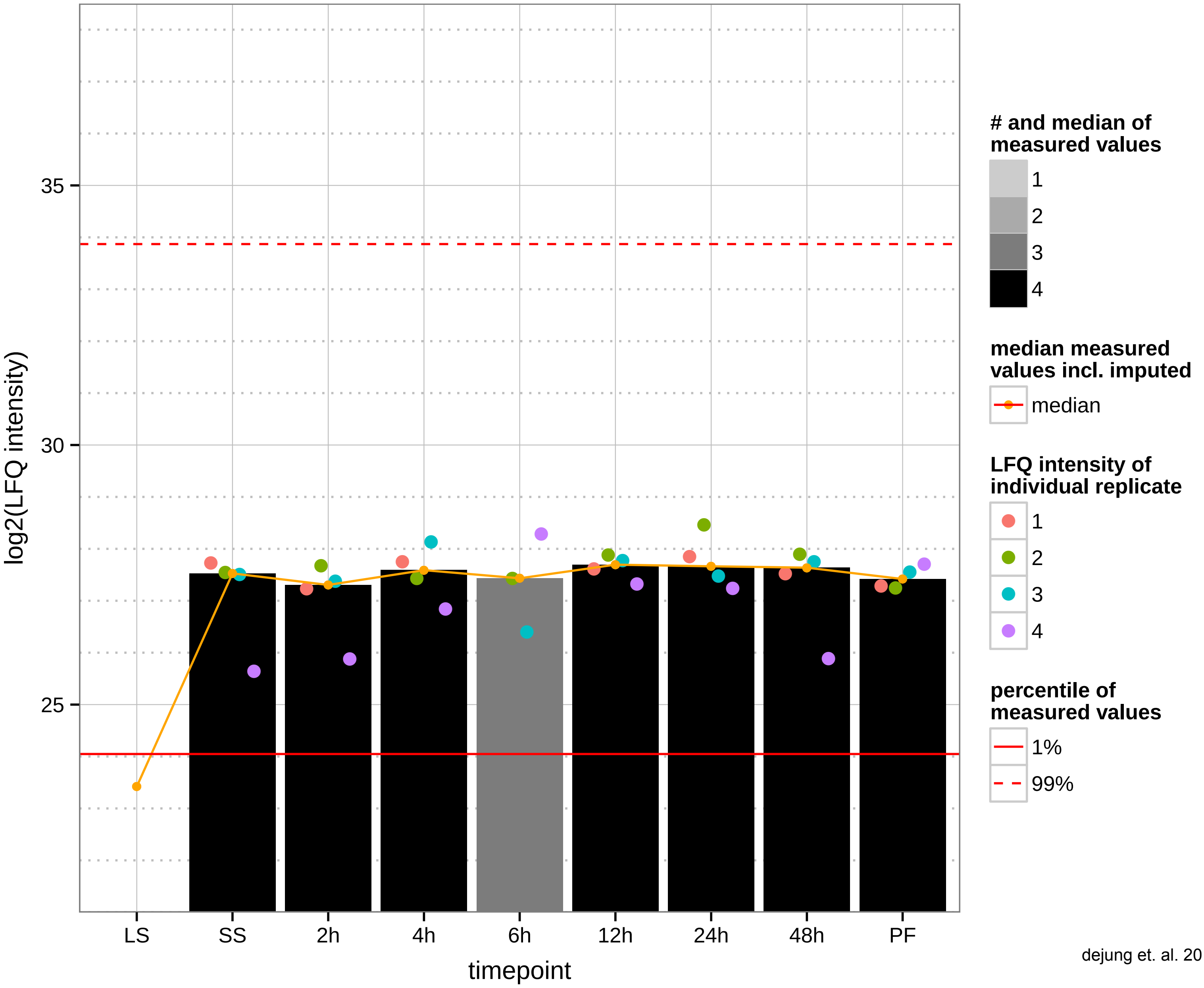
hypothetical protein, conserved
Tb927.11.12380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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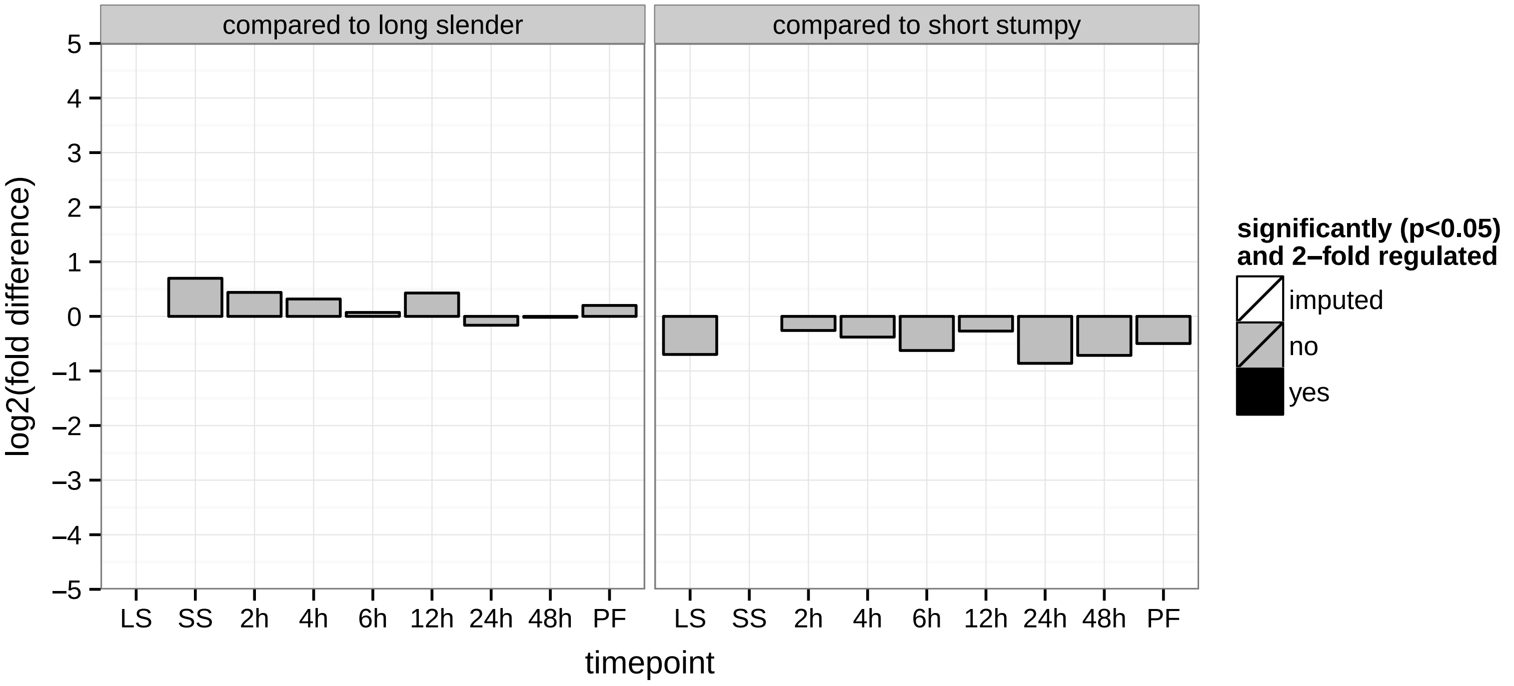
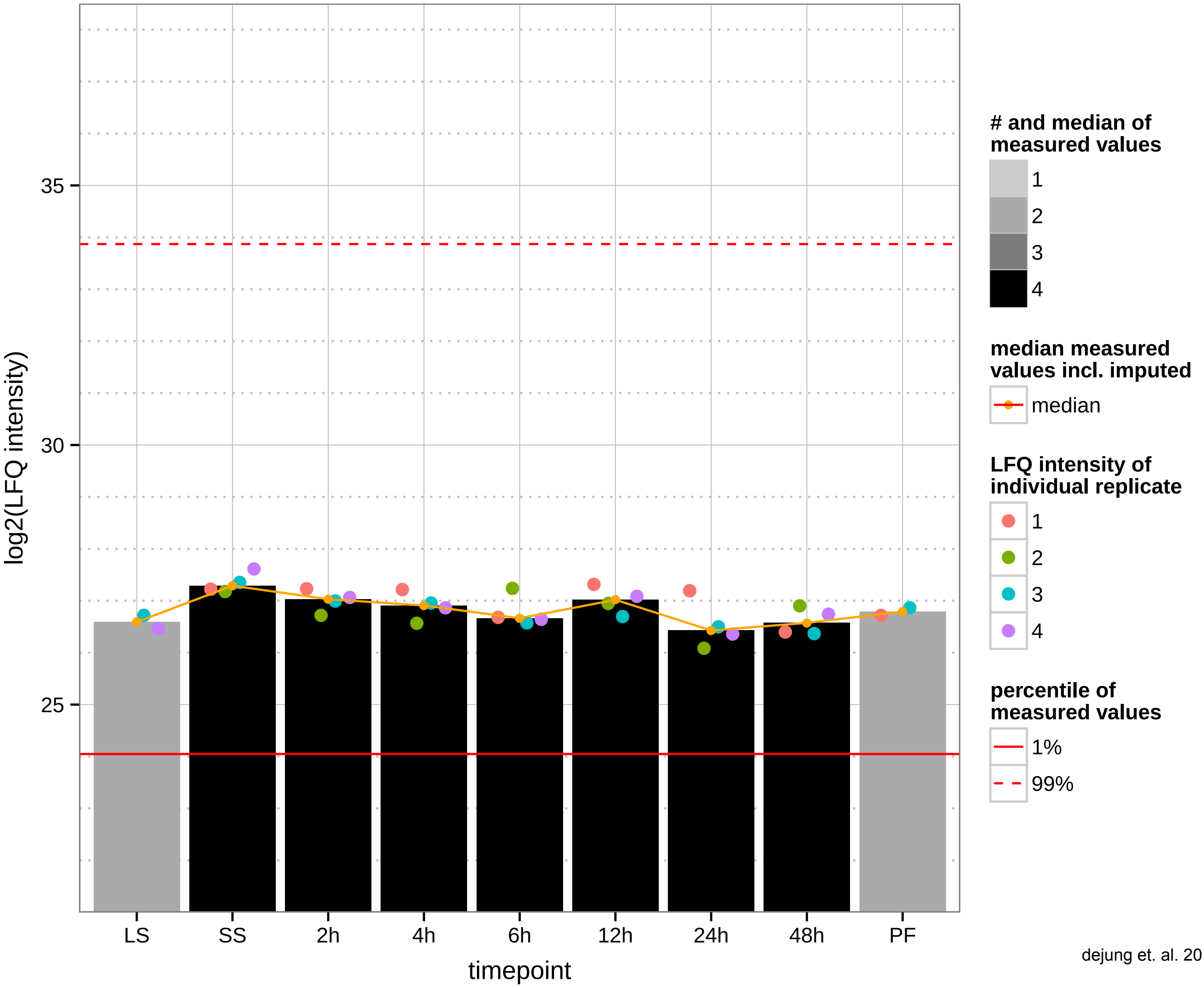
hypothetical protein, conserved
Tb927.11.12470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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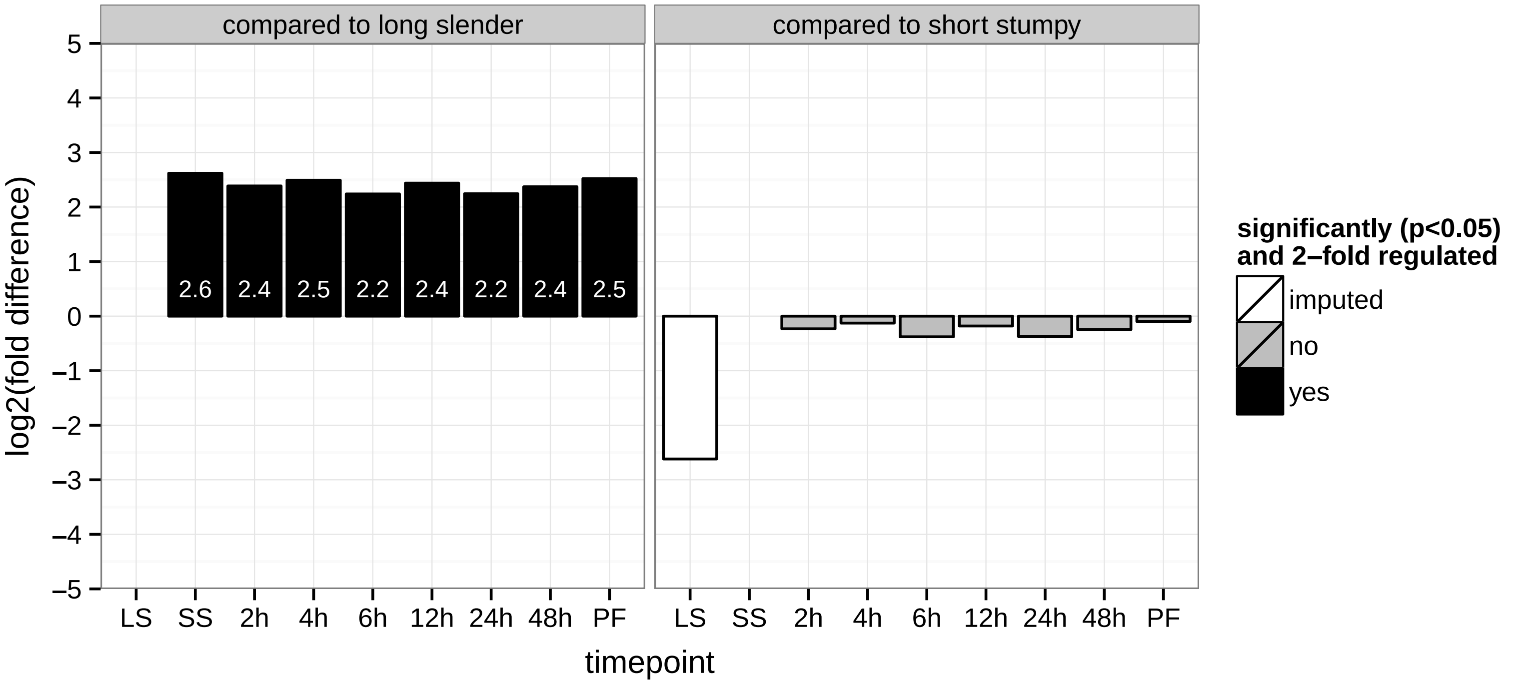
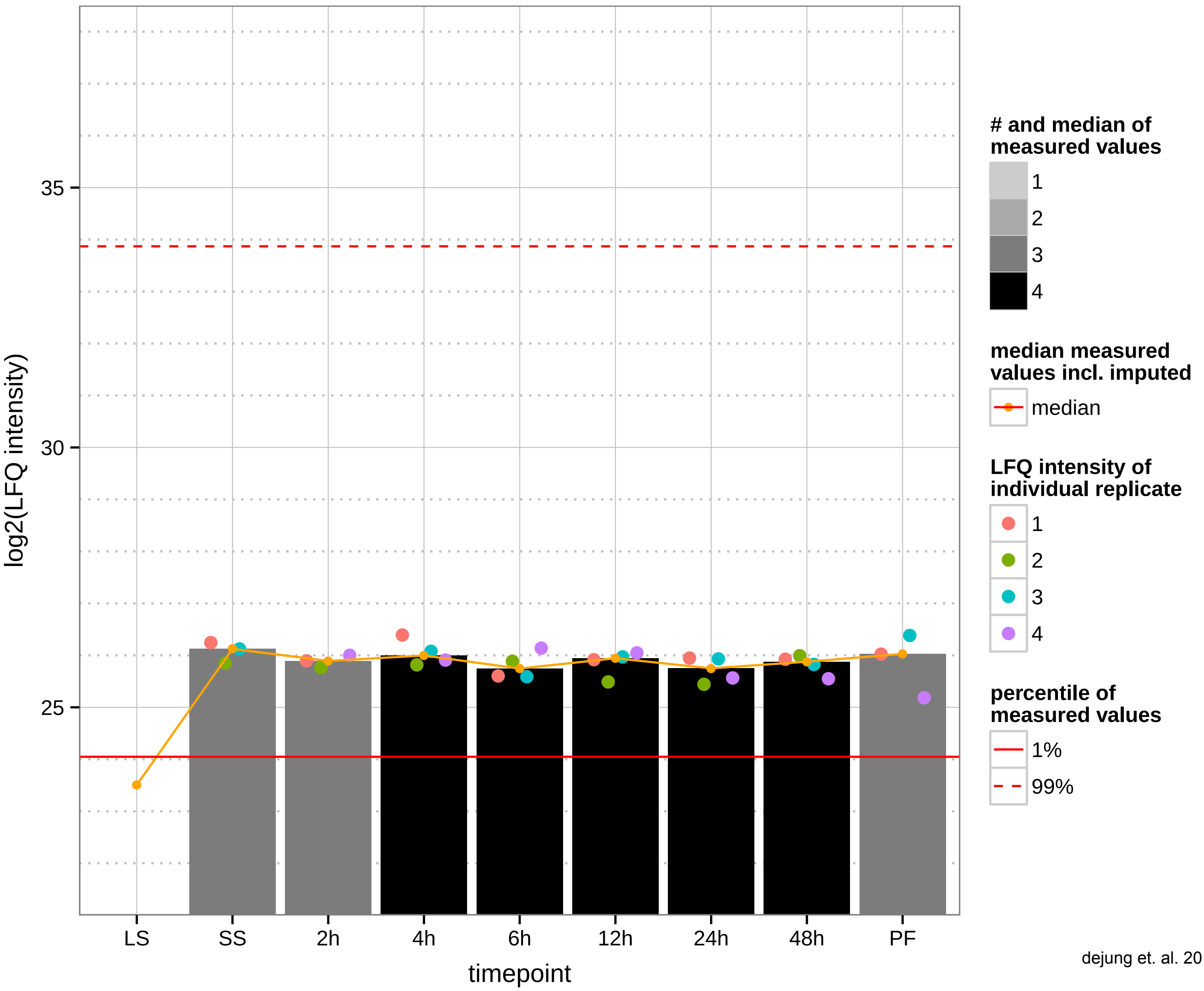
kinetoplastid−specific phospho−protein phosphatase, putative
Tb927.11.12480
AGOF: hydrolase activity, protein serine/threonine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: hydrolase activity
PGOC: null
PGOP: null





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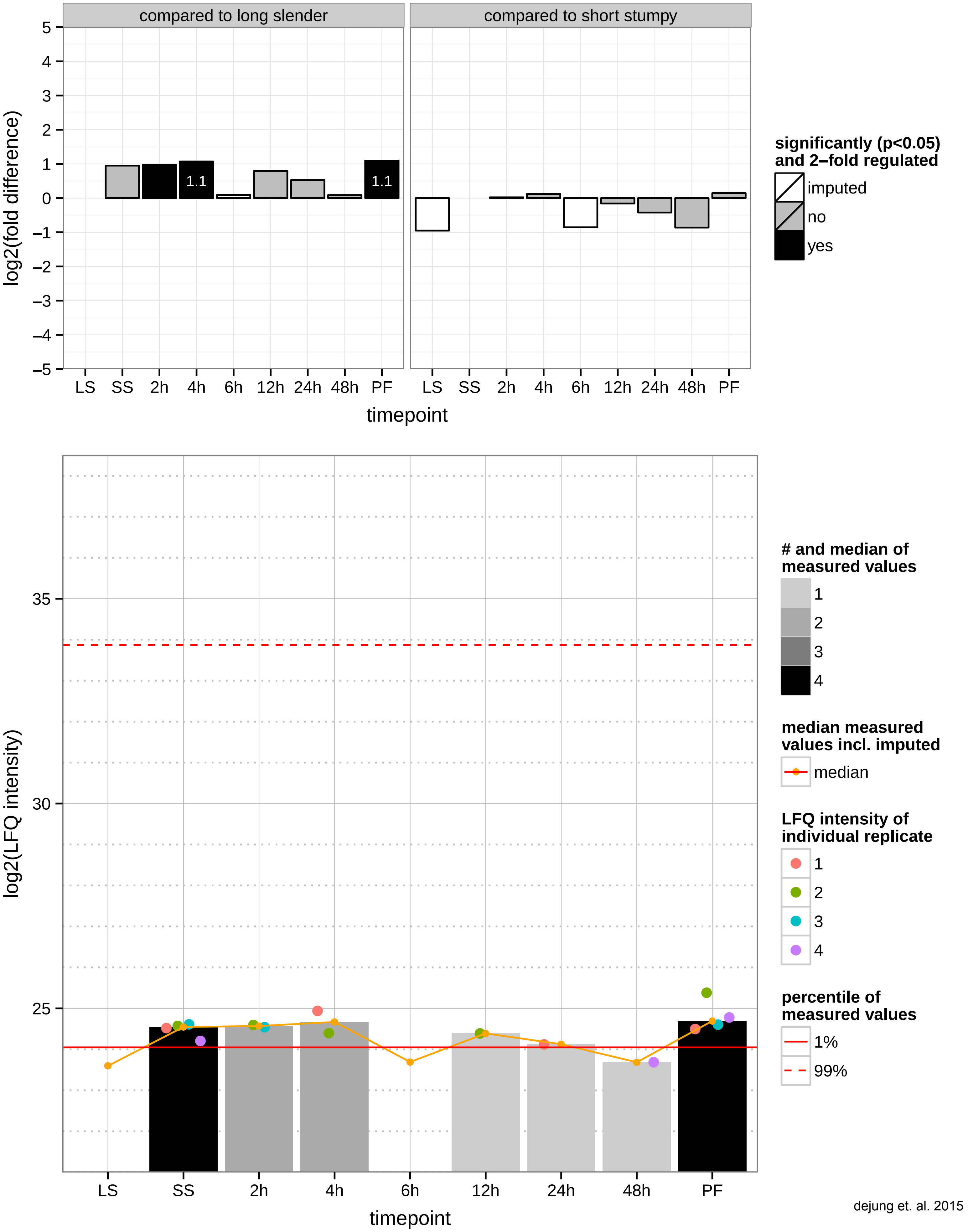
hypothetical protein, conserved
Tb927.11.12490
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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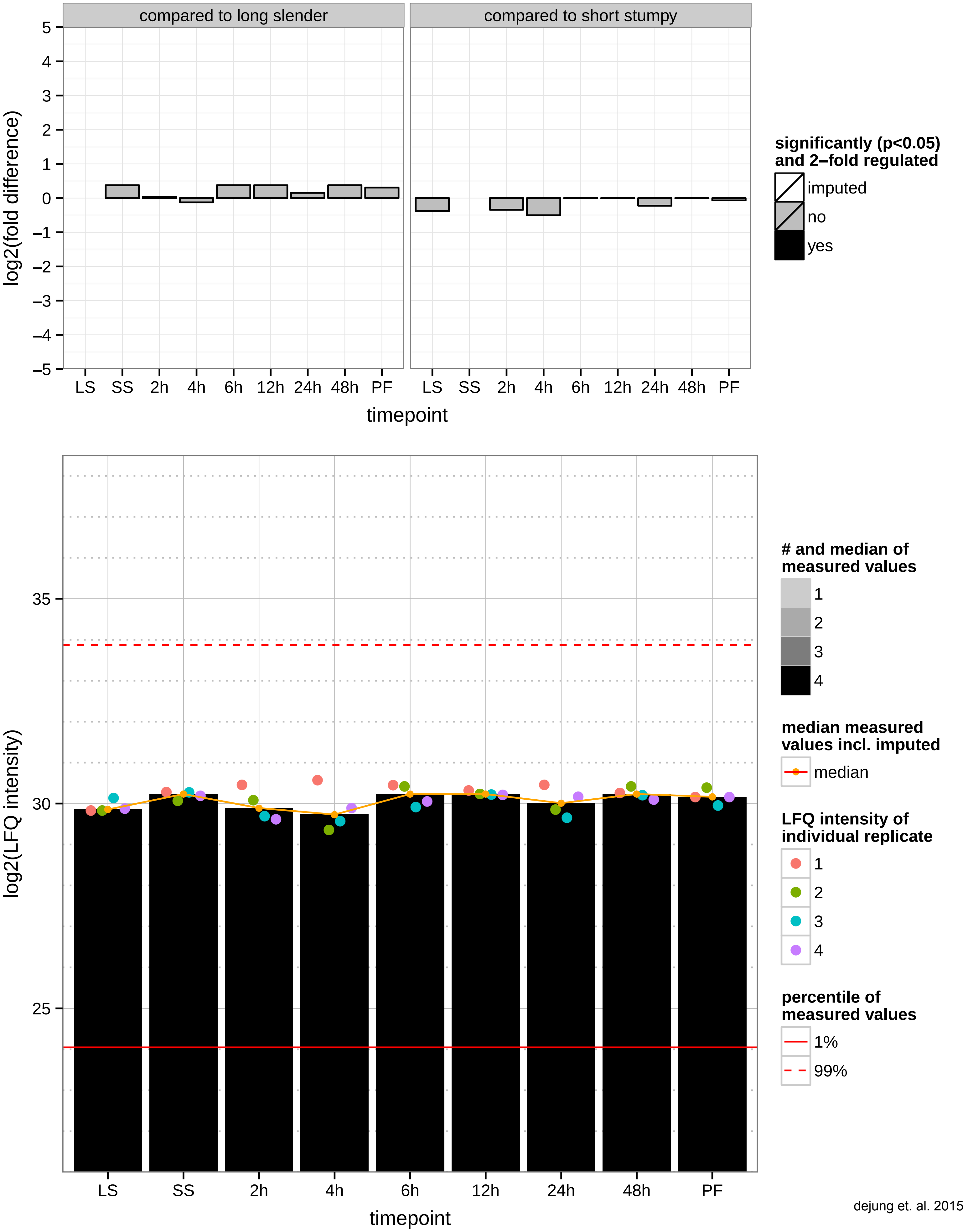
hypothetical protein, conserved
Tb927.11.12530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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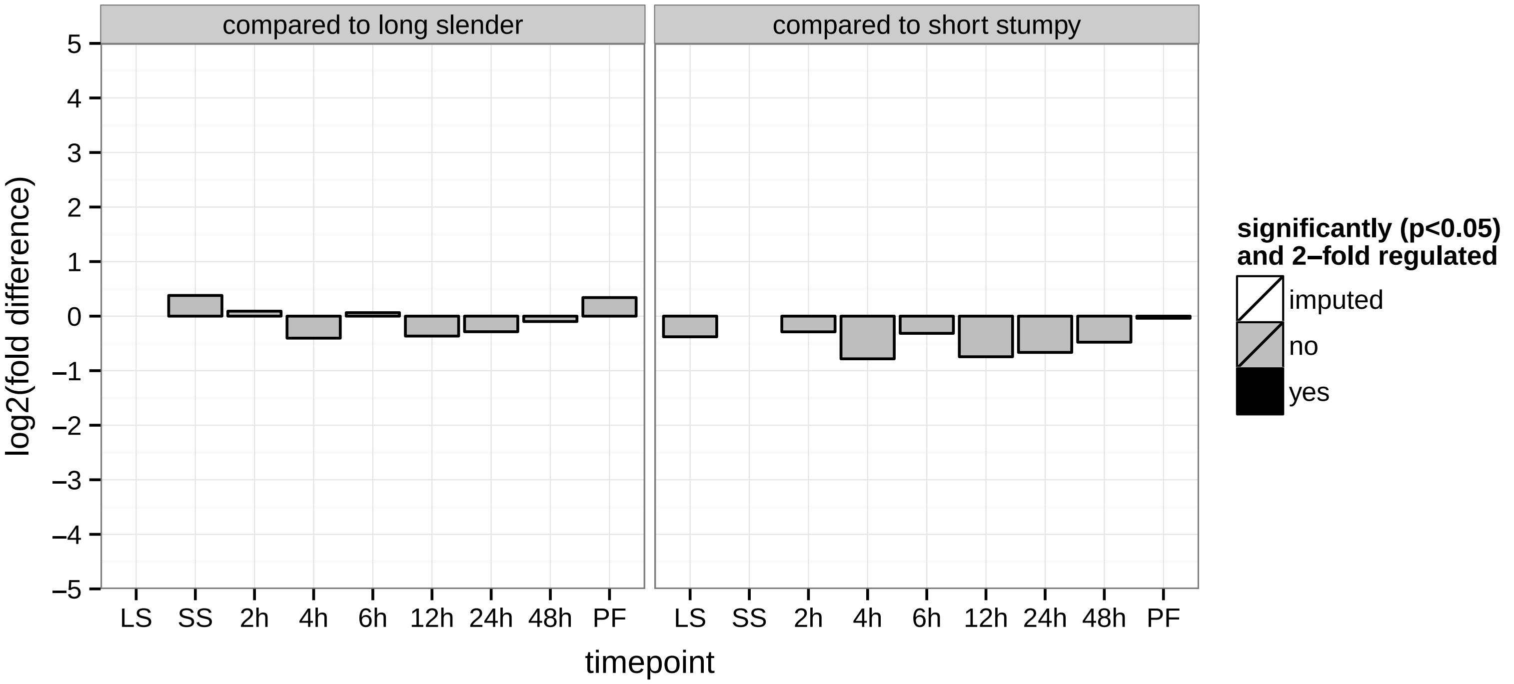
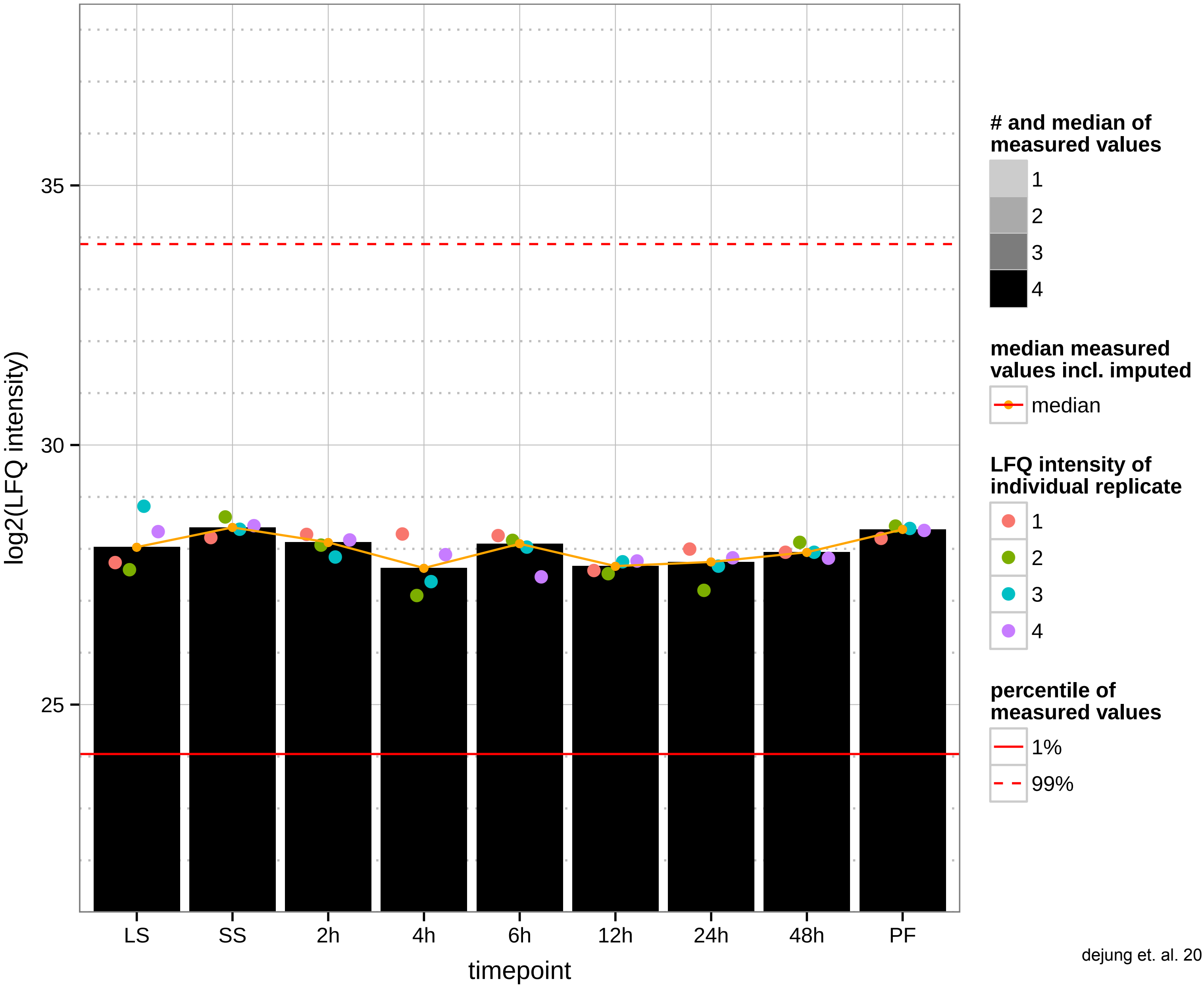
leucine−rich repeat protein (LRRP), putative
Tb927.11.12540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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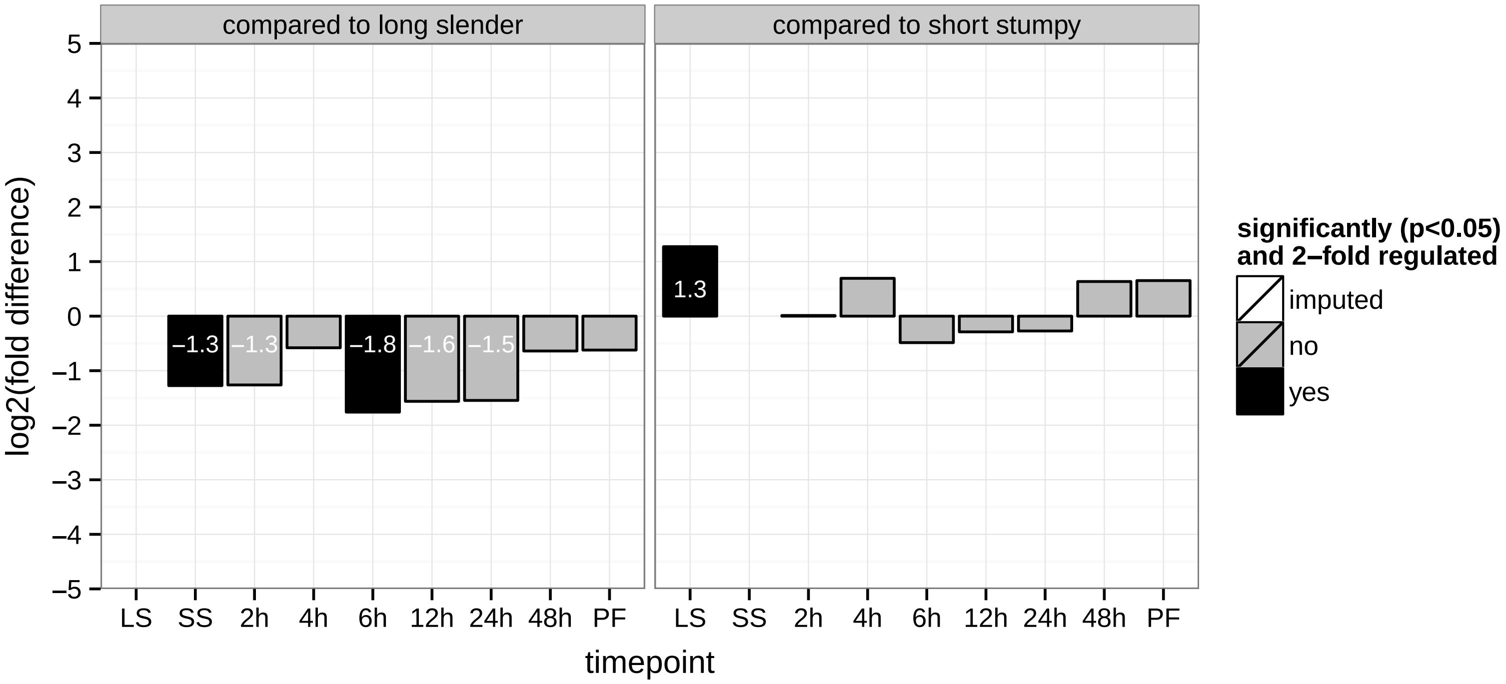
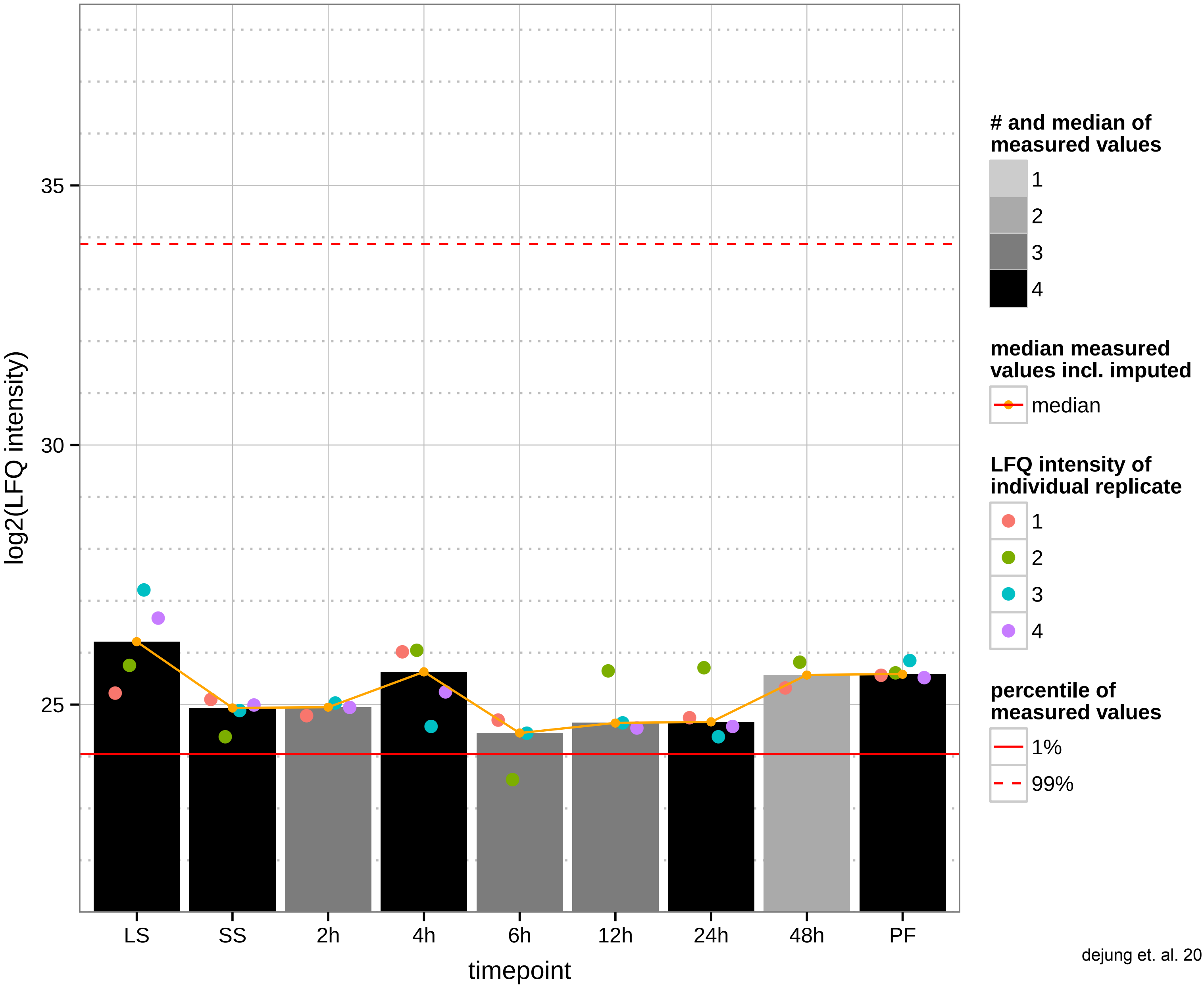
hypothetical protein, conserved
Tb927.11.12590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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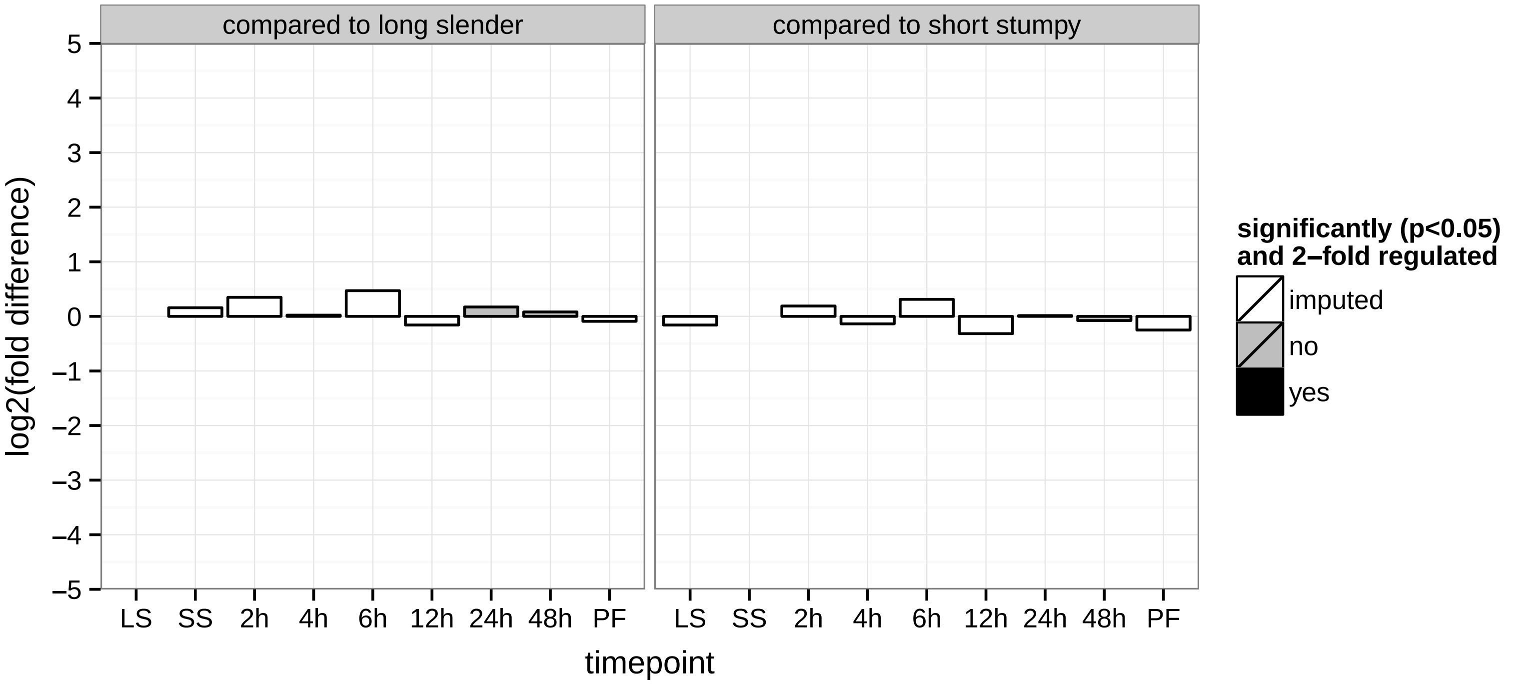
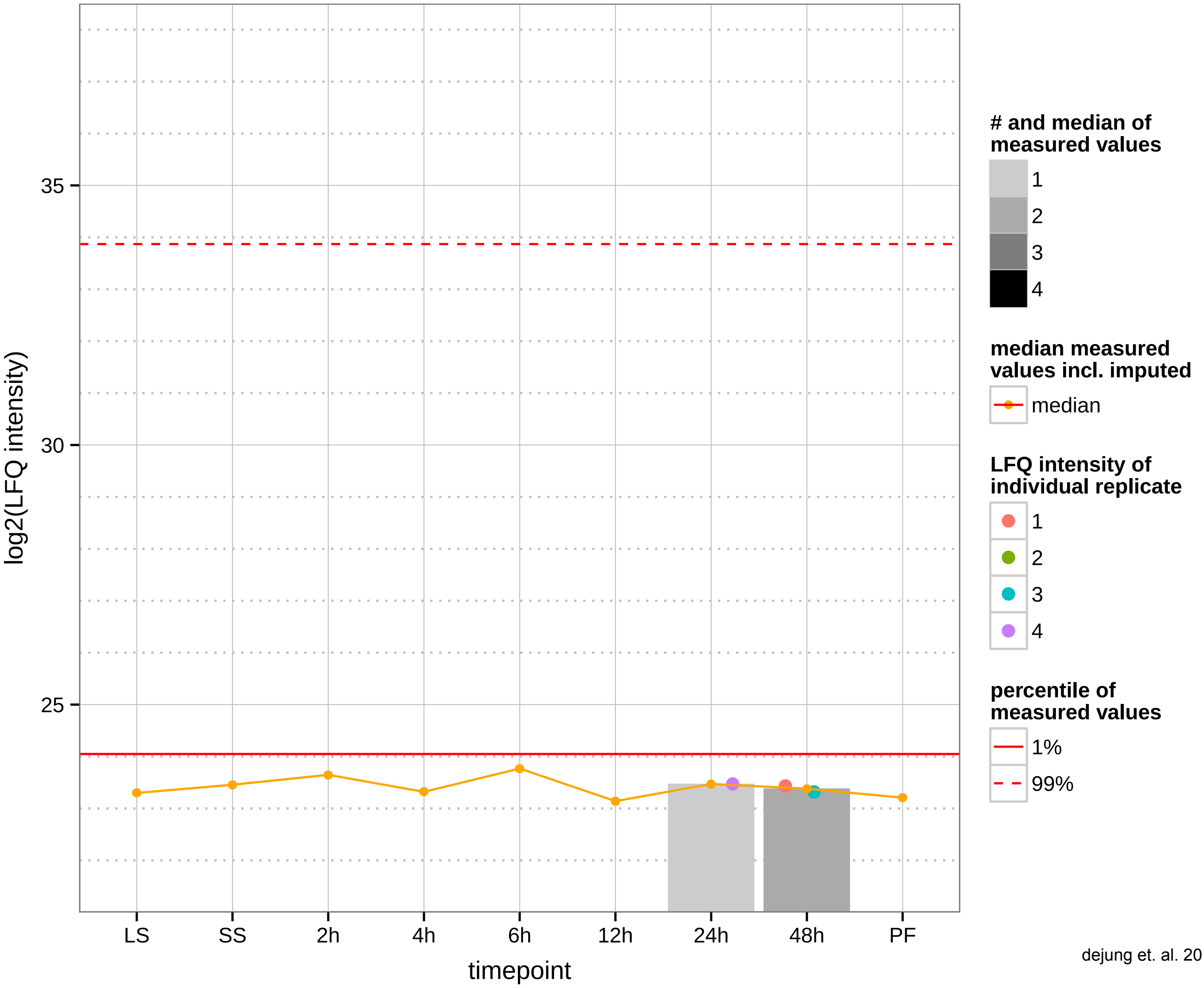
hypothetical protein, conserved
Tb927.11.12630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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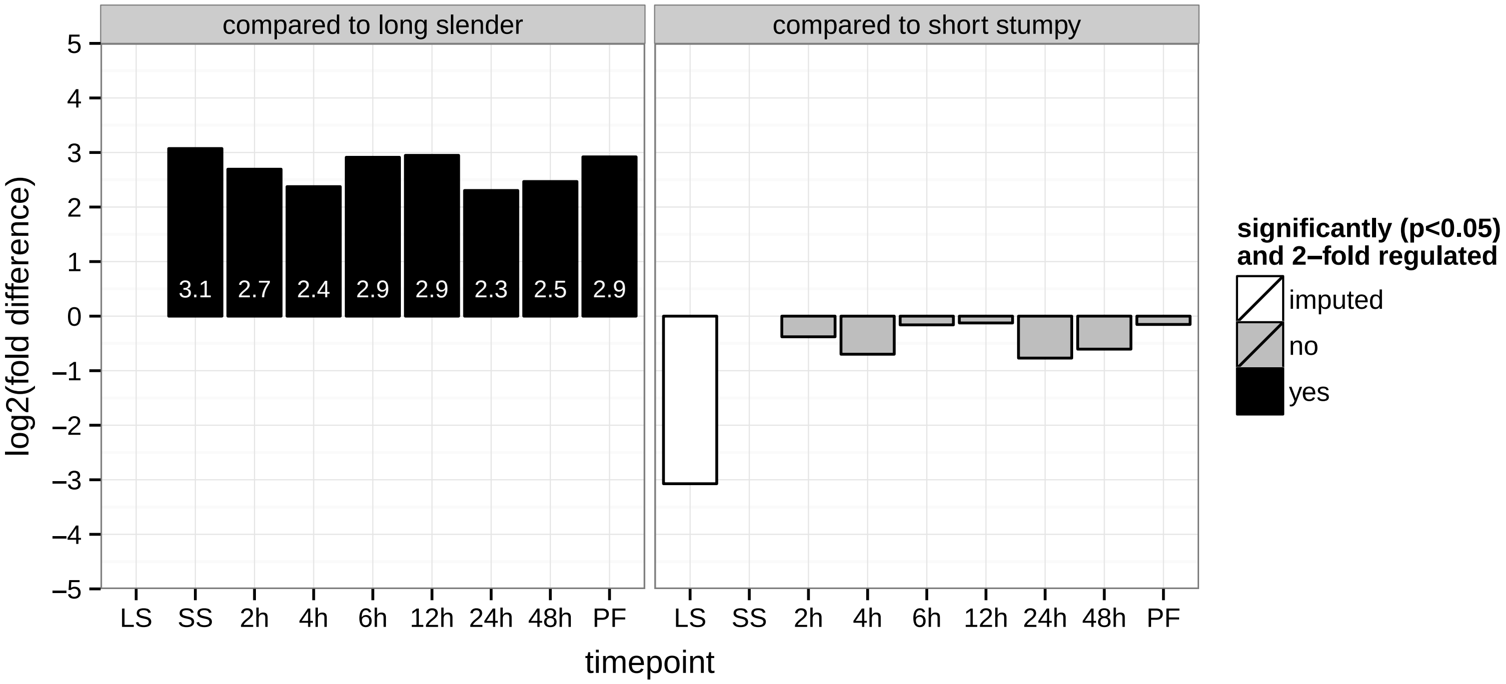
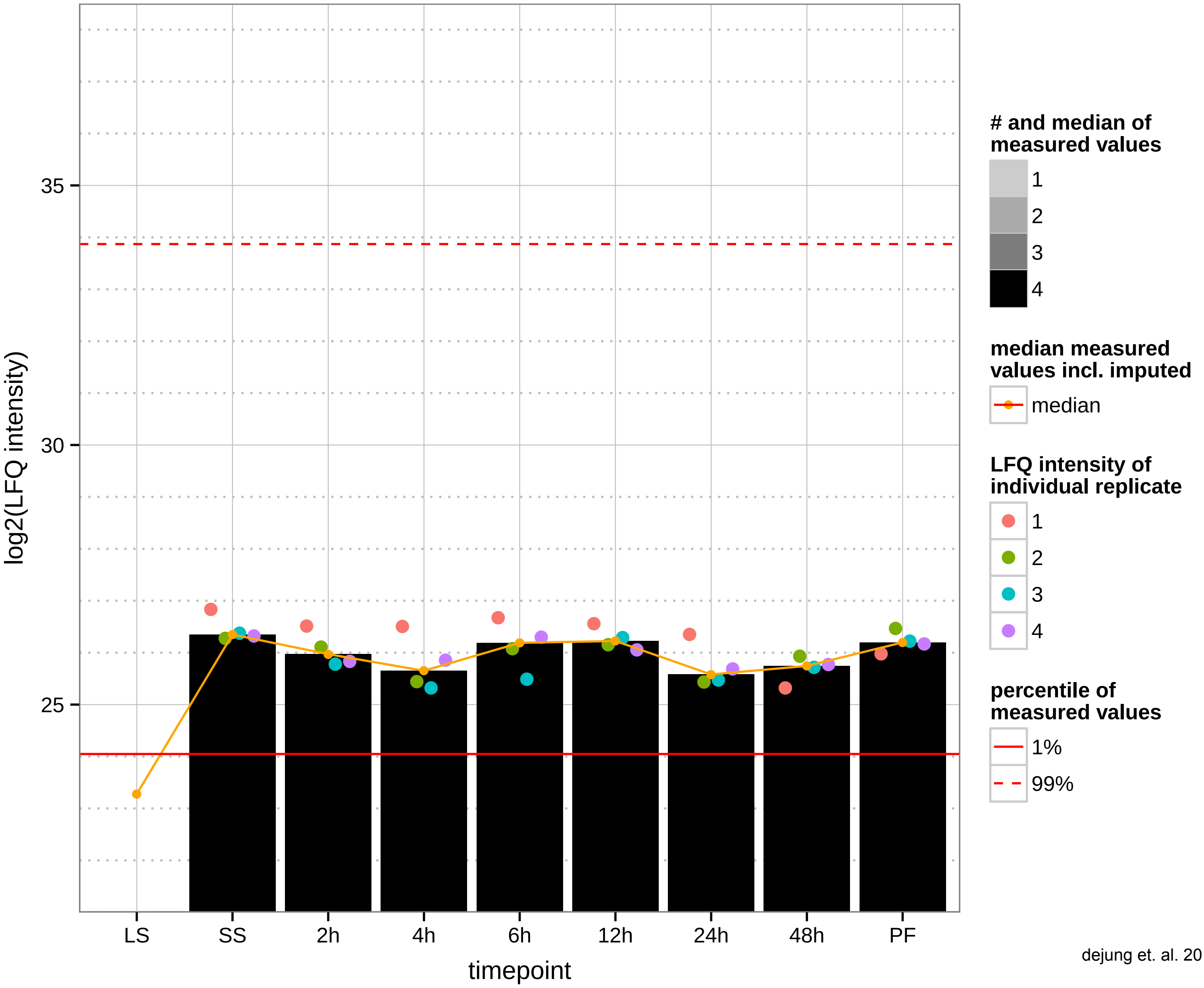
hypothetical protein, conserved
Tb927.11.12640
AGOF: null
AGOC: null
AGOP: null
PGOF: Rho guanyl–nucleotide exchange factor activity, phospholipid binding, protein binding
PGOC: intracellular
PGOP: regulation of Rho protein signal transduction





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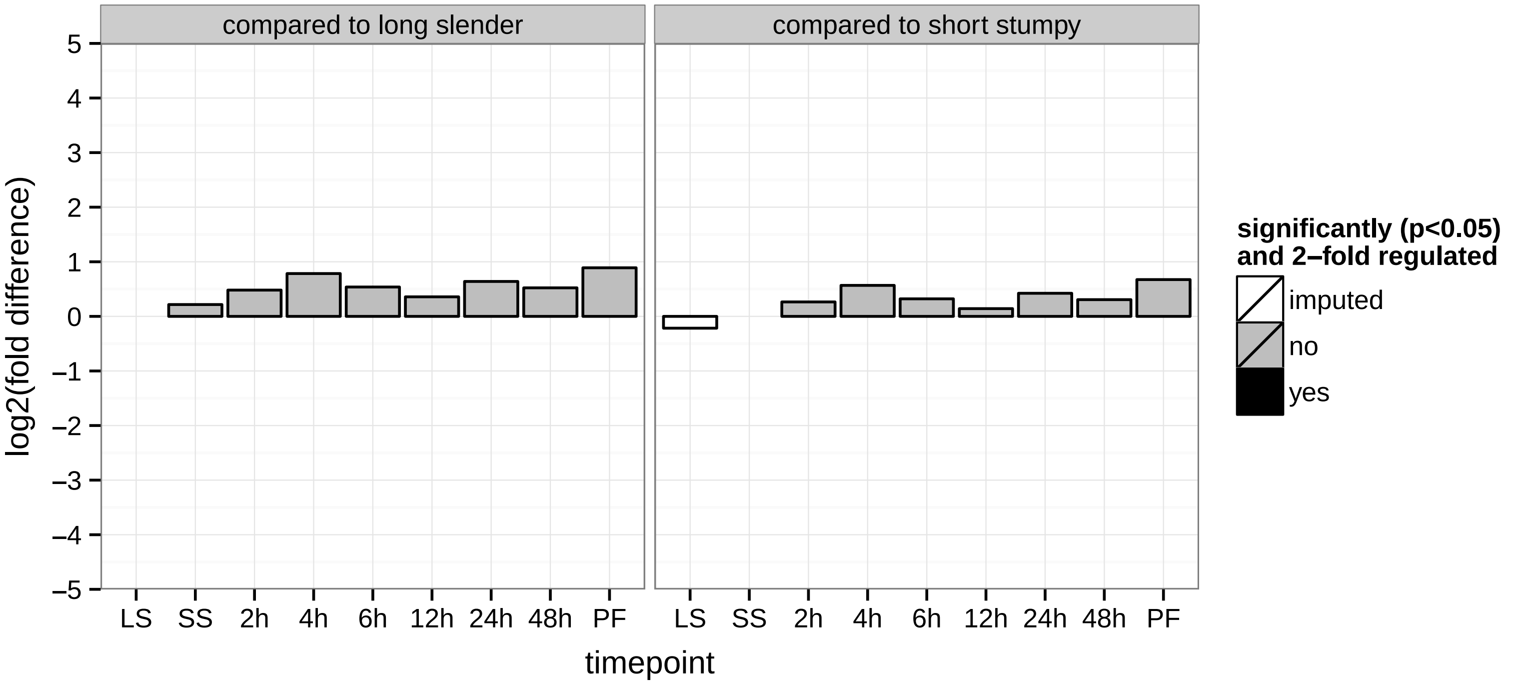
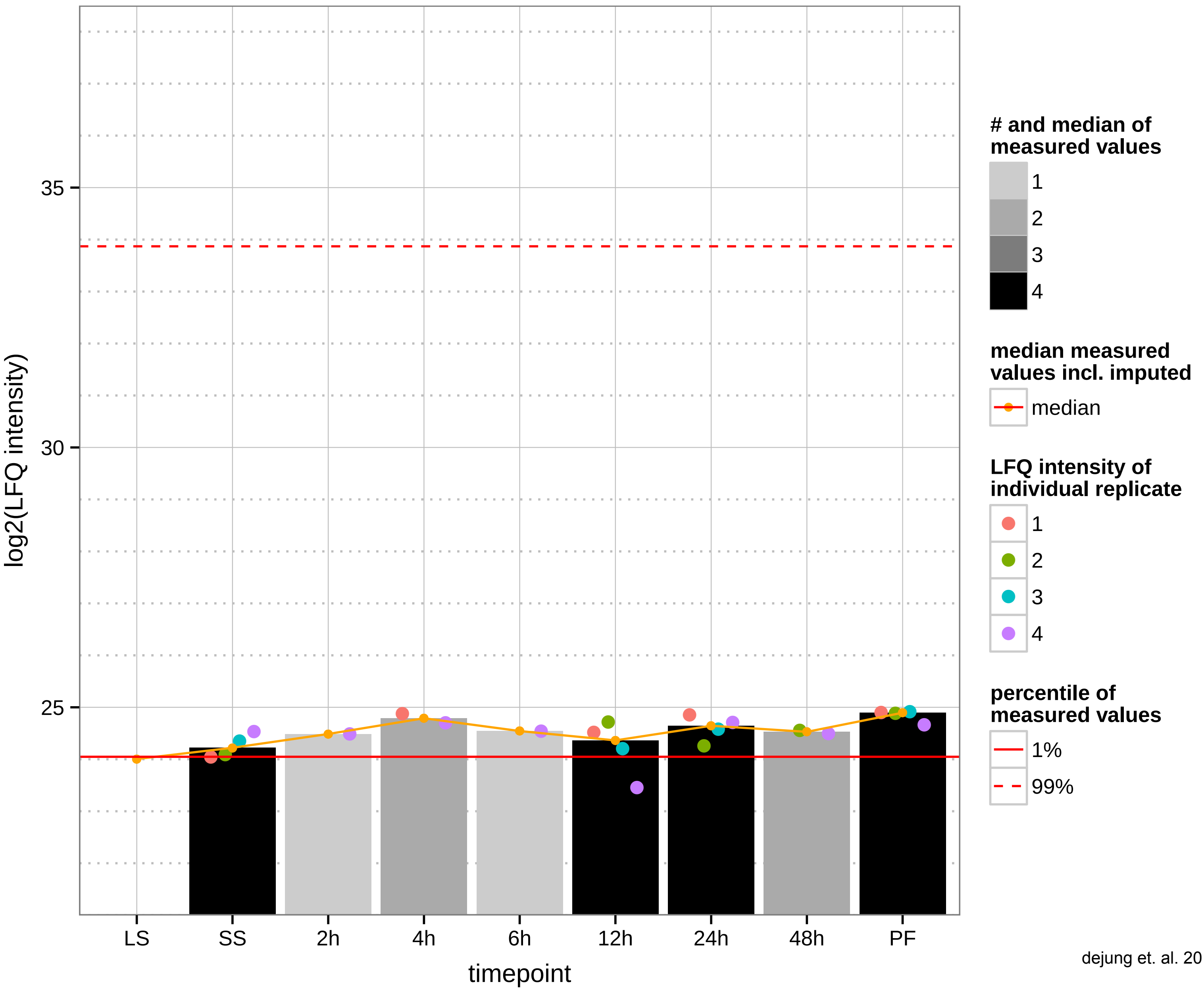
hypothetical protein, conserved
Tb927.11.12910
AGOF: null
AGOC: null
AGOP: null
PGOF: unfolded protein binding
PGOC: prefoldin complex
PGOP: protein folding





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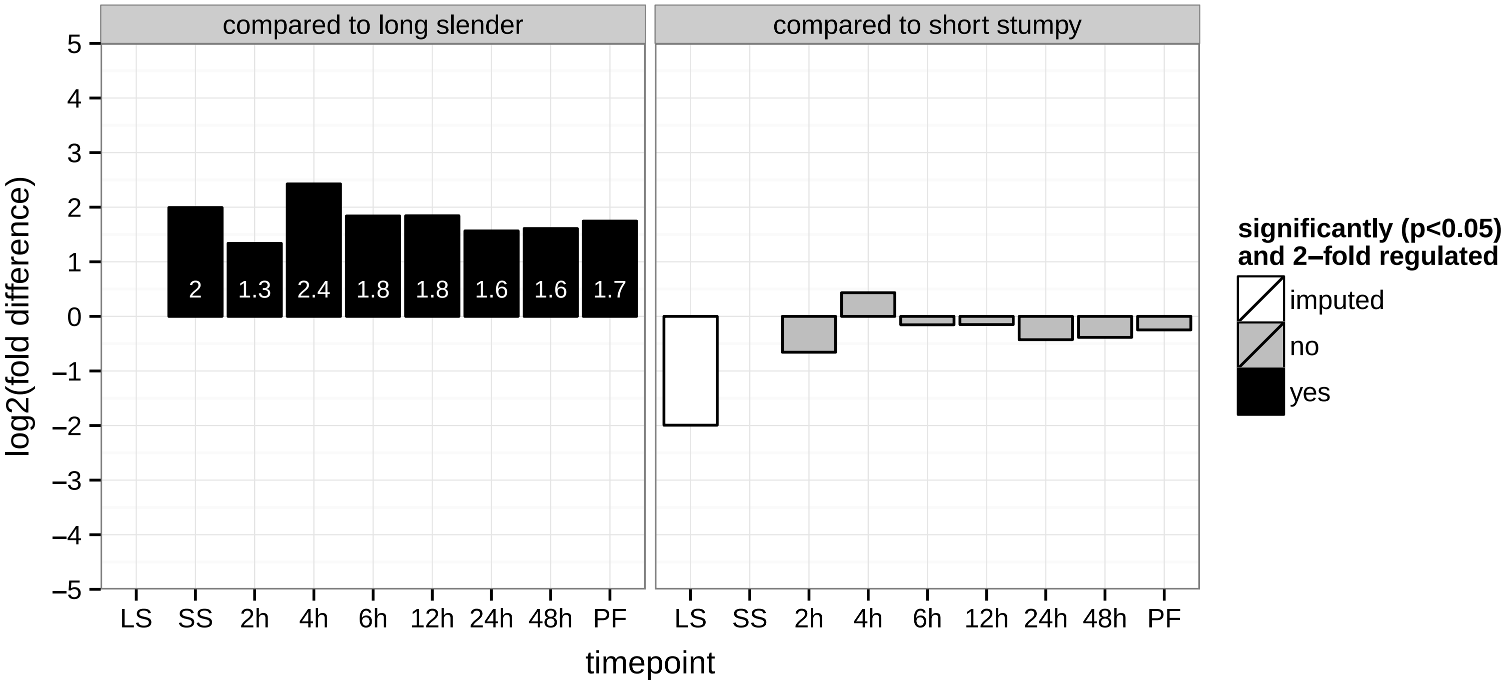
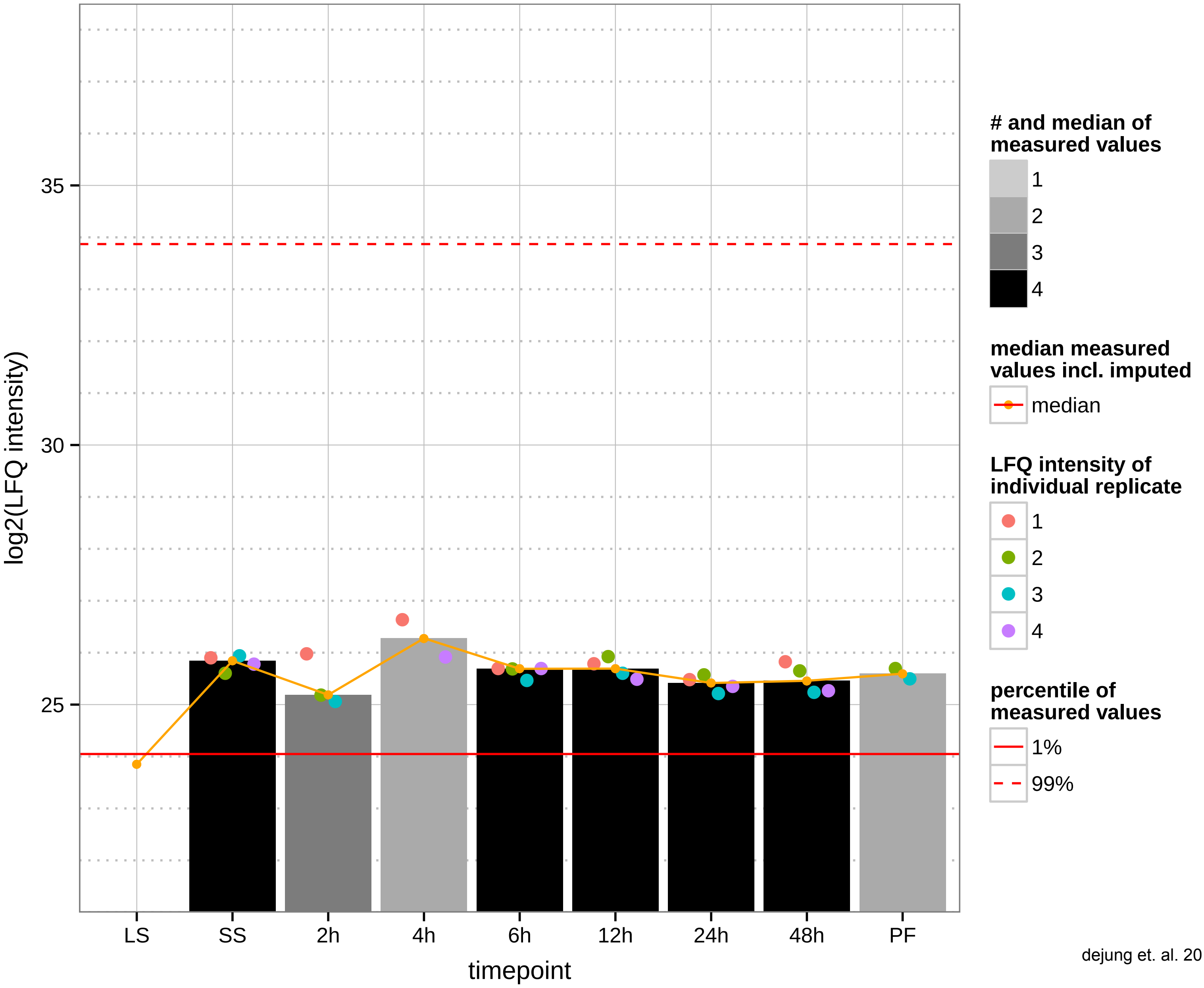
hypothetical protein, conserved
Tb927.11.12920
AGOF: ATP binding, nucleoside−triphosphatase activity
AGOC: null
AGOP: null
PGOF: nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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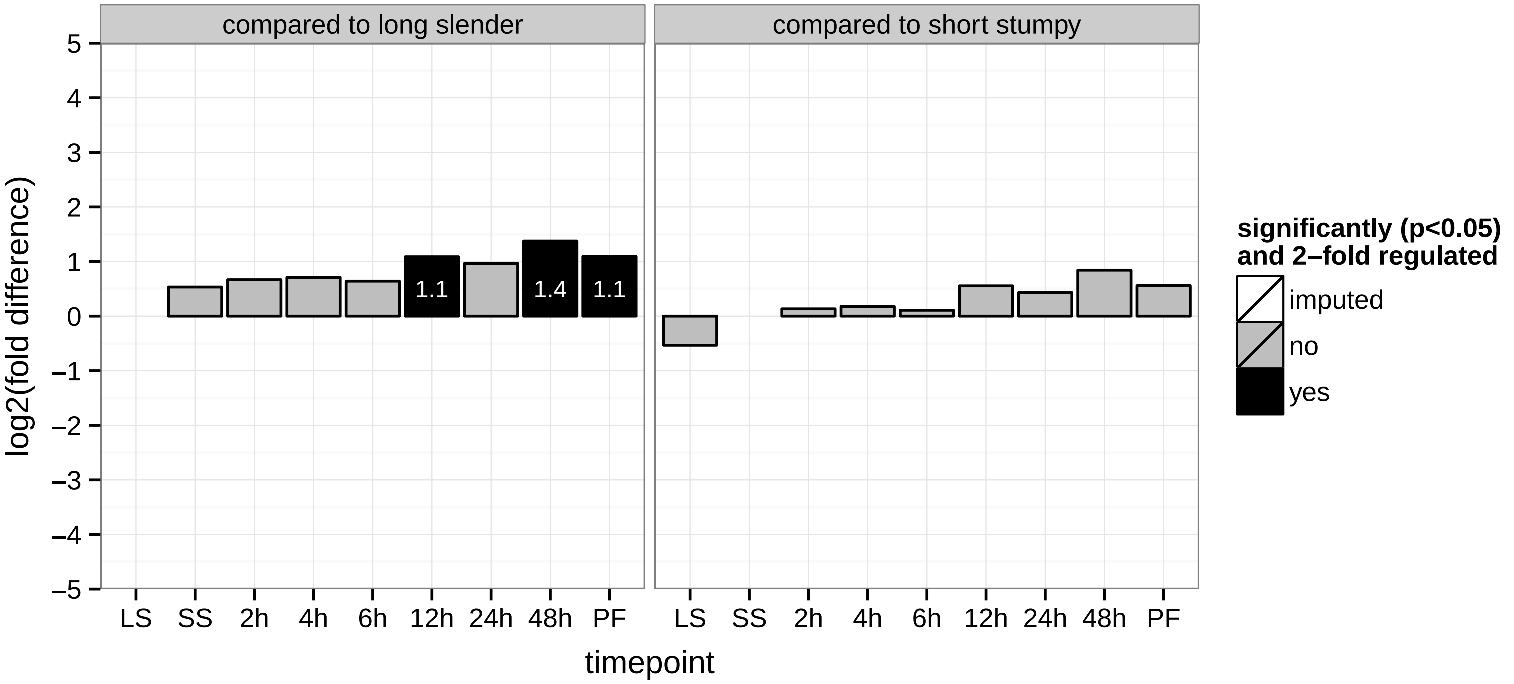
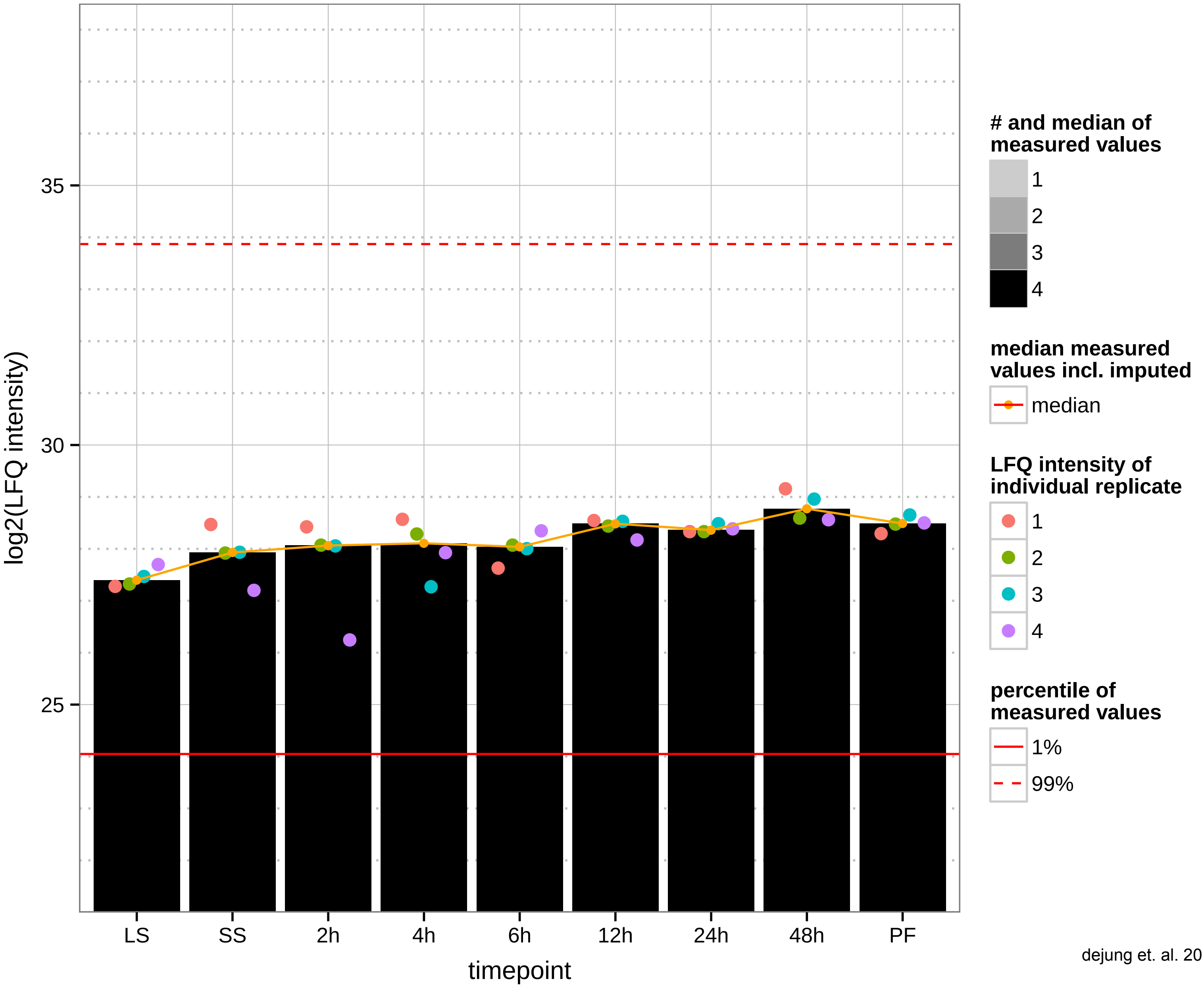
hypothetical protein, conserved
Tb927.11.12940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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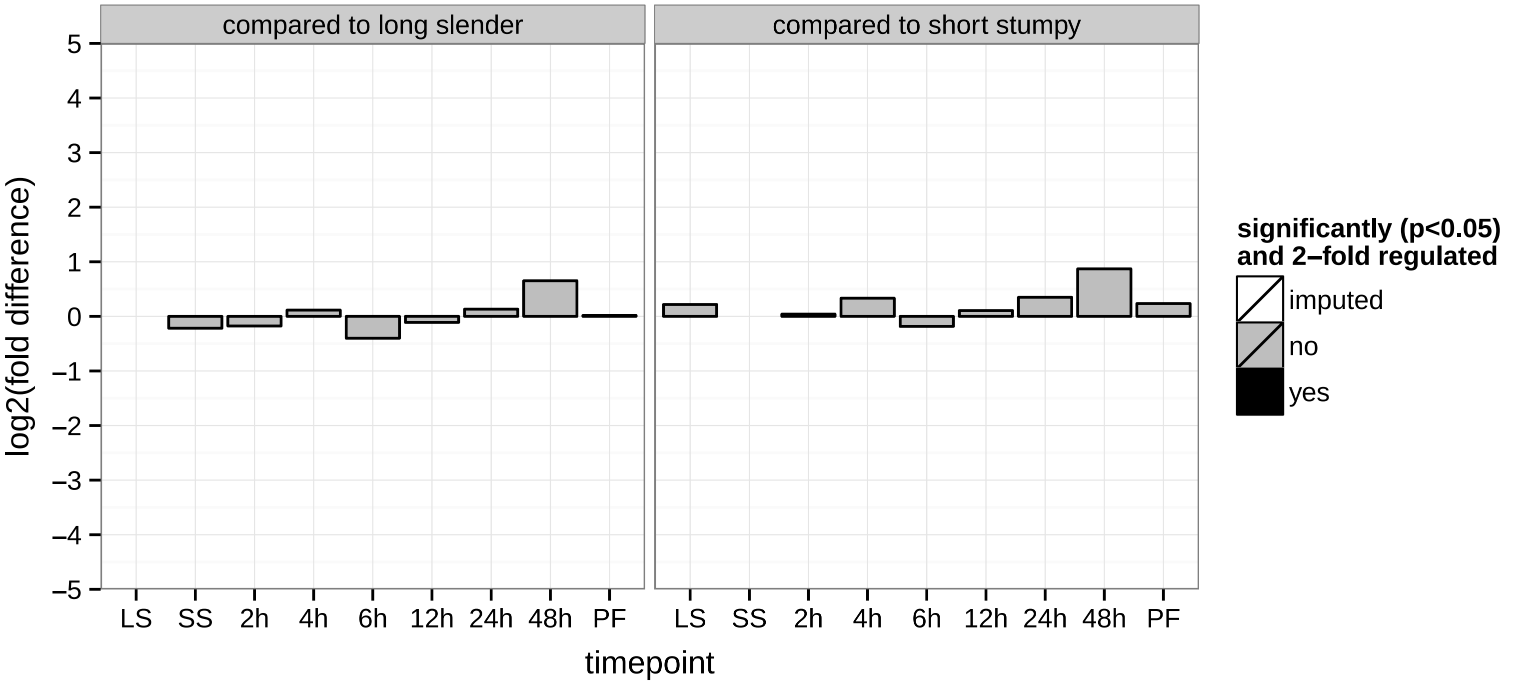
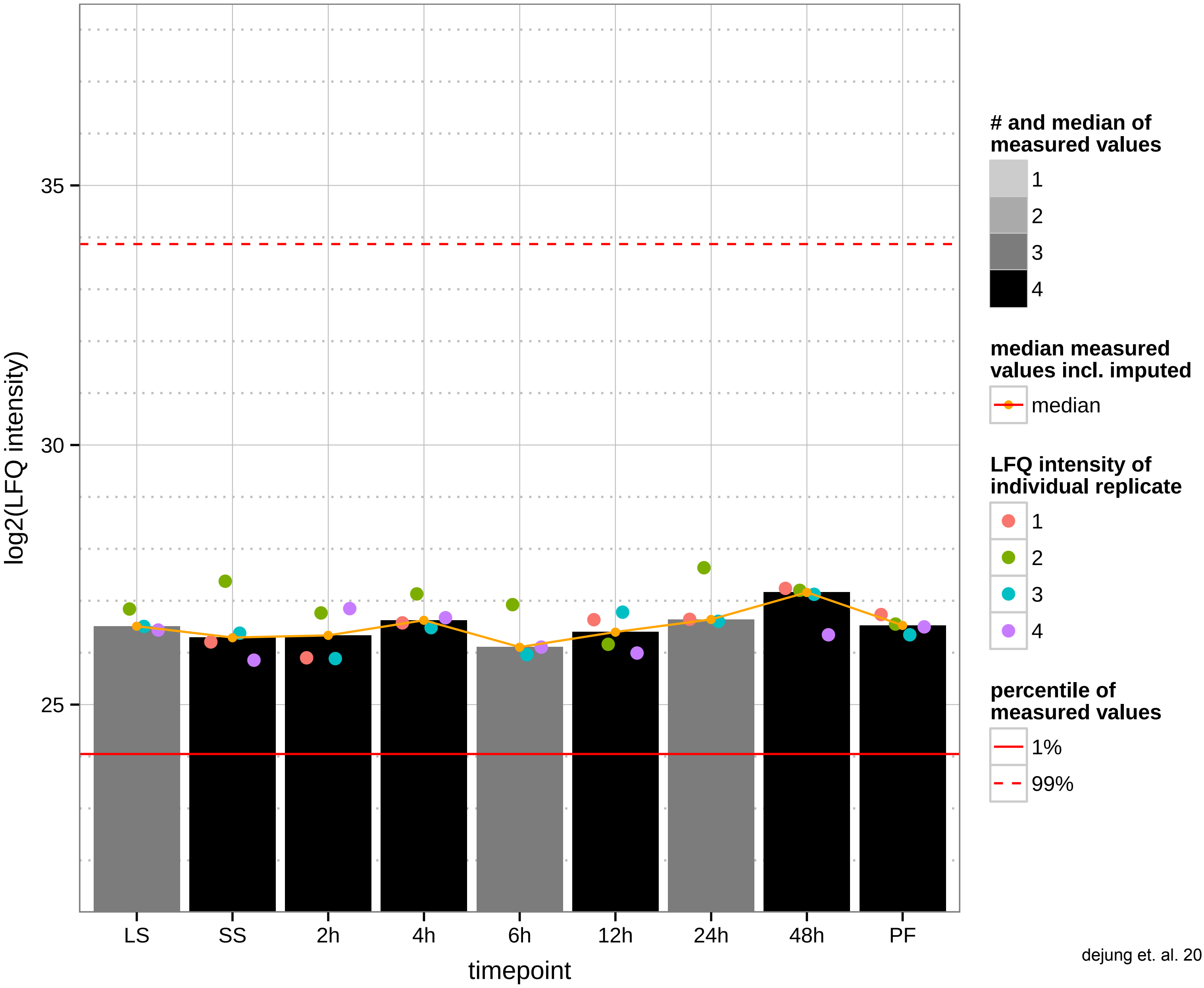
hypothetical protein
Tb927.11.13010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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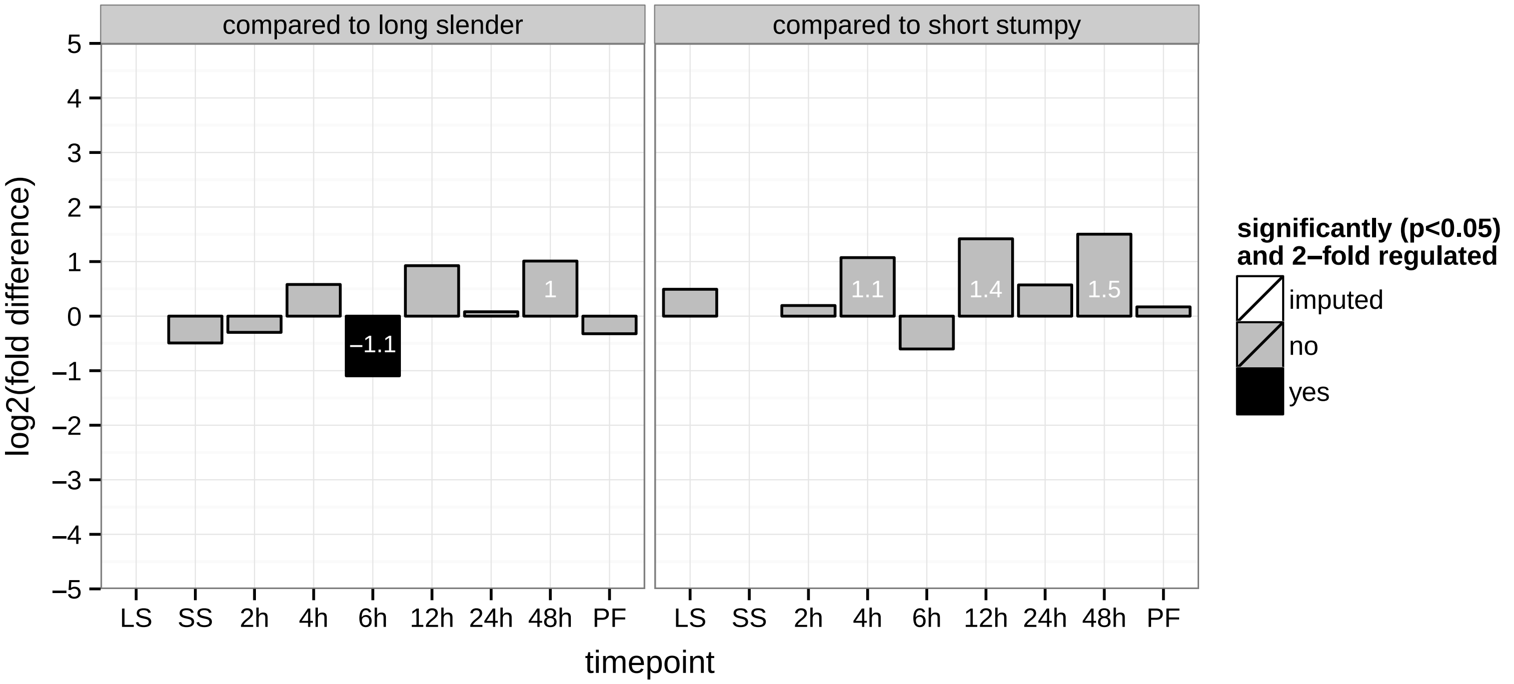
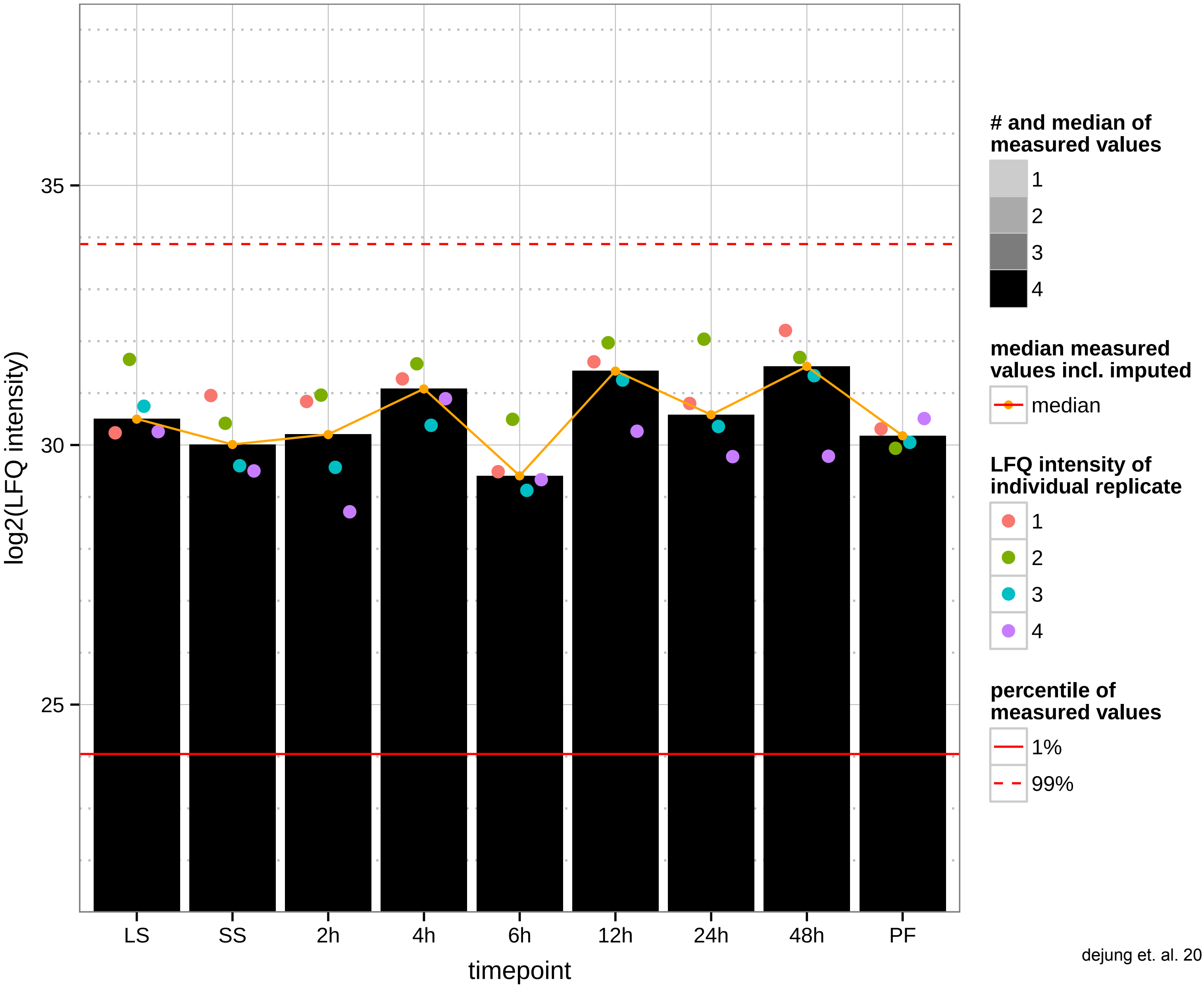
calmodulin
Tb927.11.13050;Tb927.11.13040;Tb927.11.13030;Tb927.11.13020
AGOF: calcium ion binding
AGOC: cilium, contractile vacuole, cytosol
AGOP: null
PGOF: null, calcium ion binding
PGOC: null
PGOP: null





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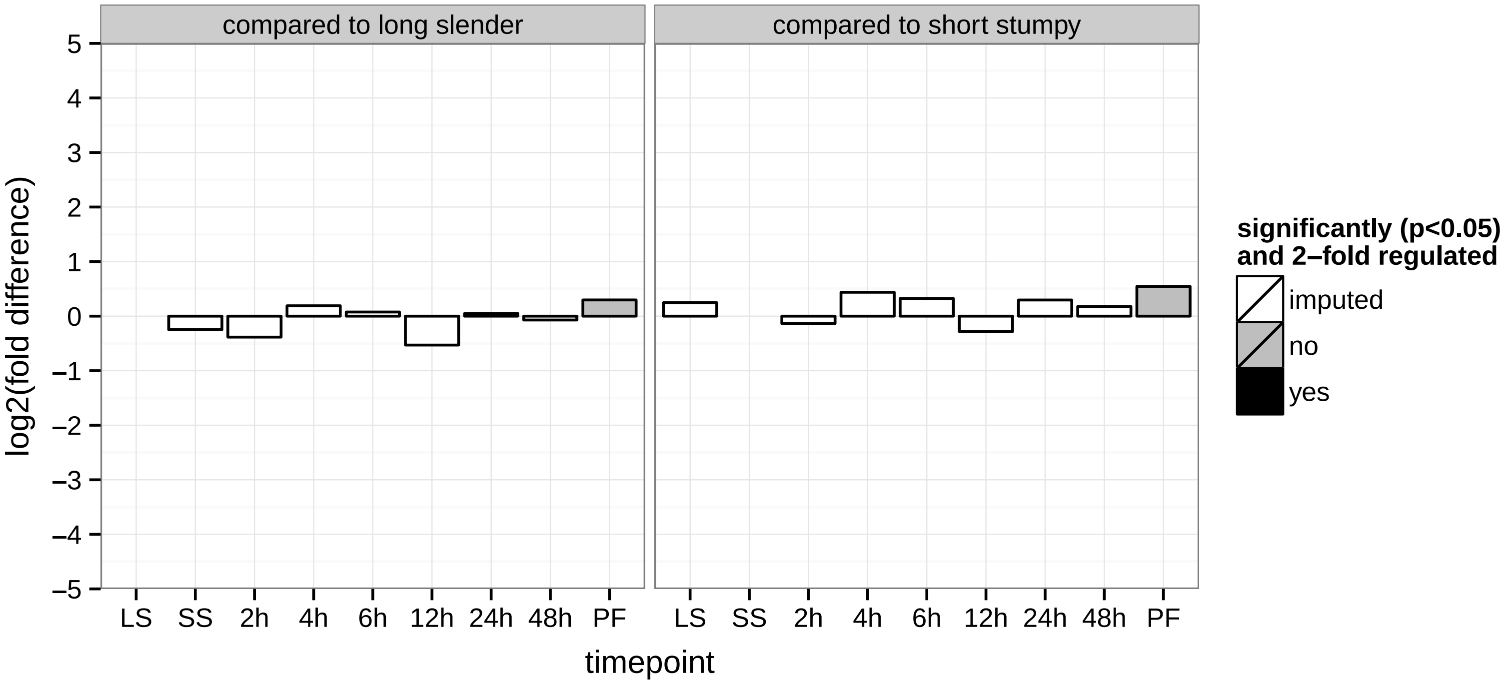
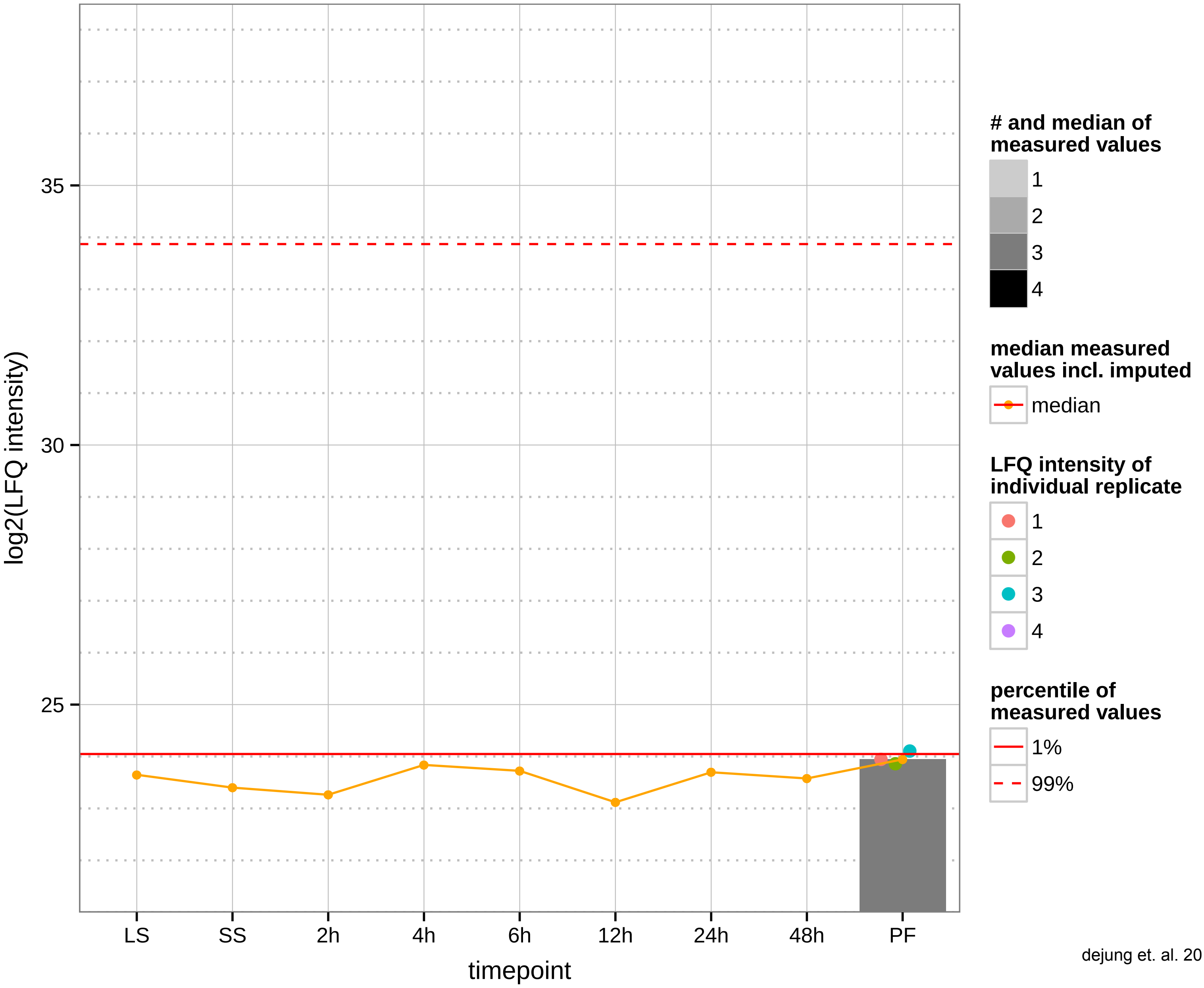
hypothetical protein, conserved
Tb927.11.13070
AGOF: null
AGOC: null
AGOP: null
PGOF: transferase activity, transferase activity, transferring selenium–containing groups
PGOC: null
PGOP: null





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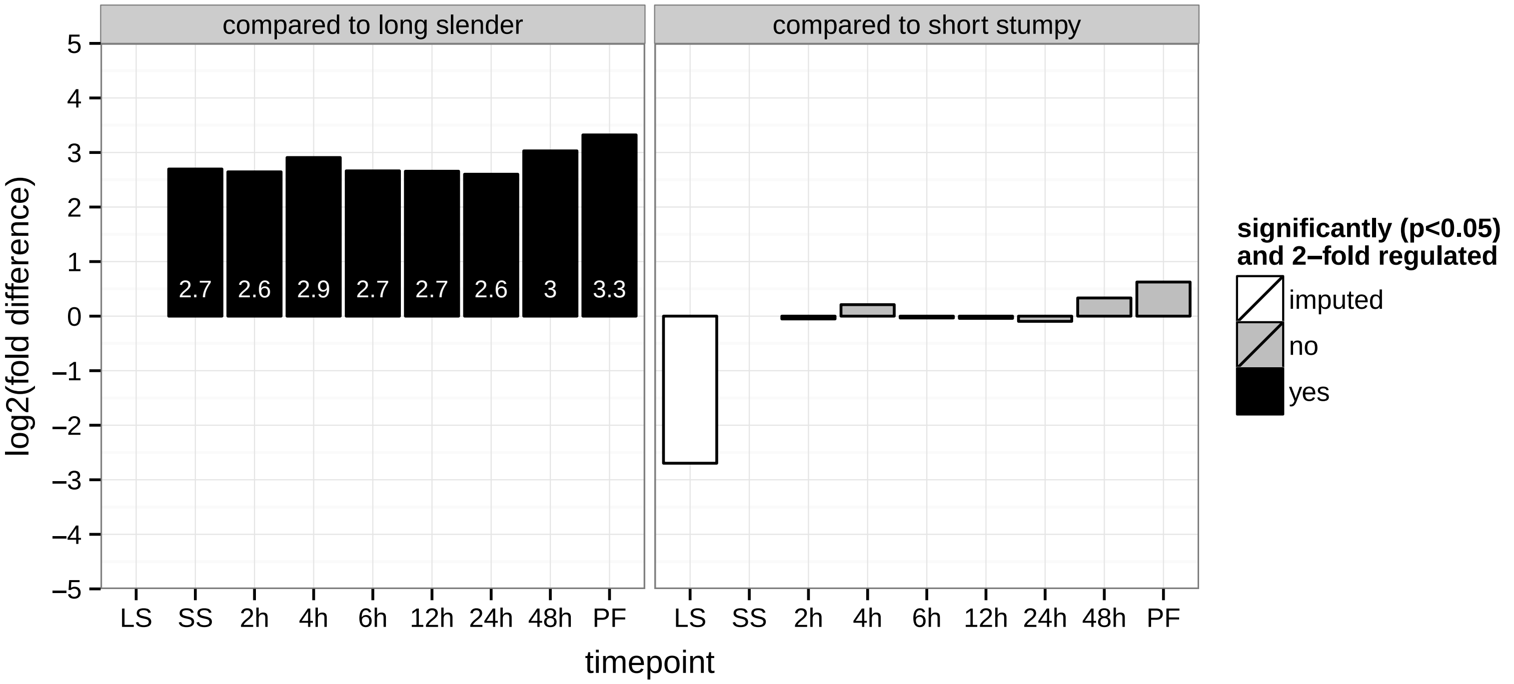
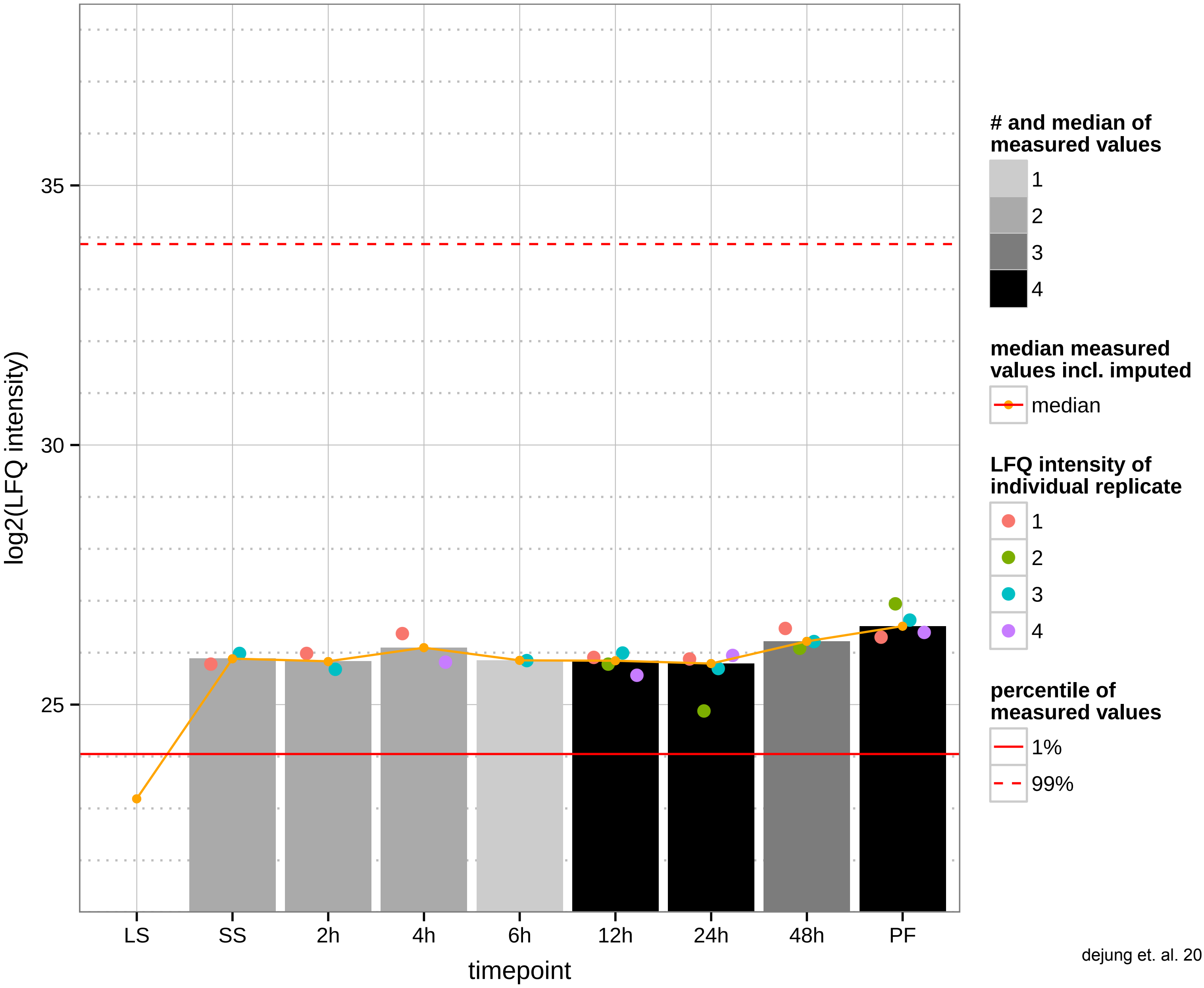
hypothetical protein, conserved
Tb927.11.13080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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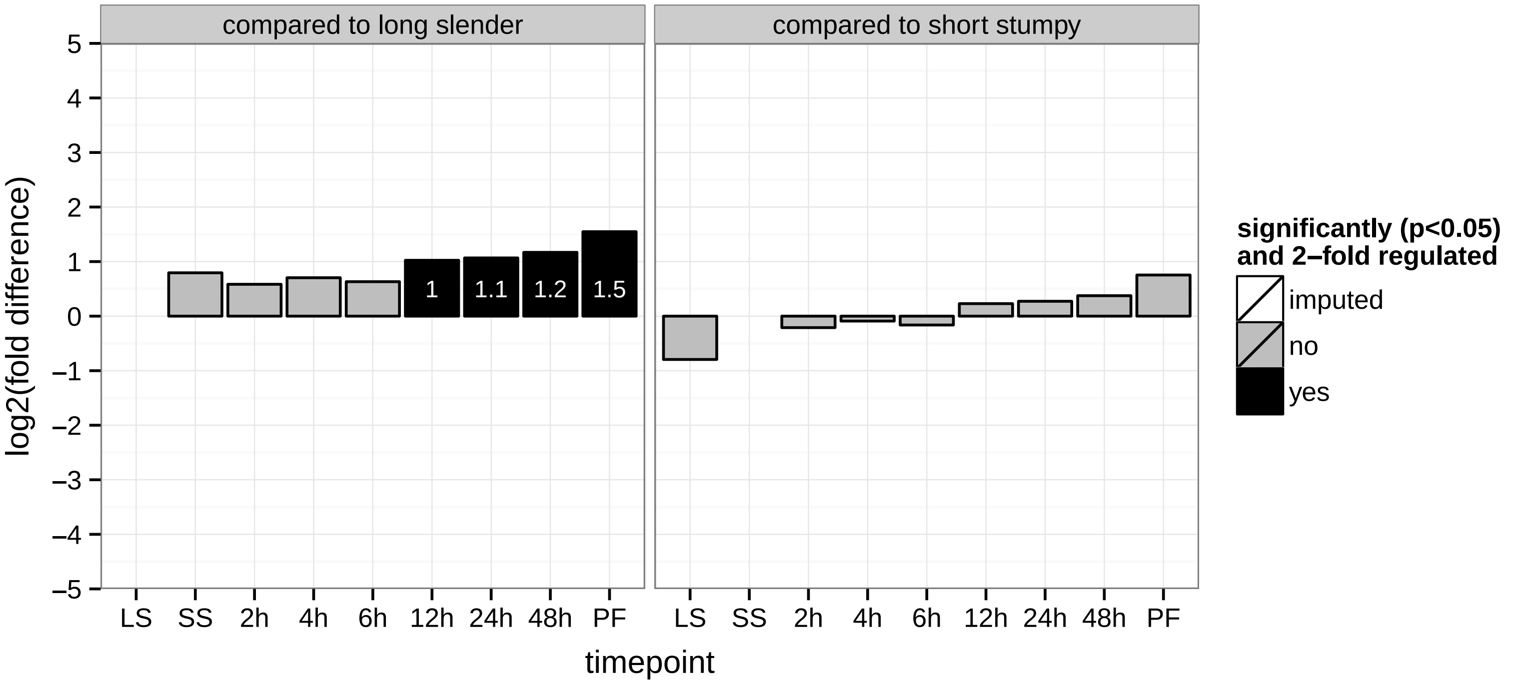
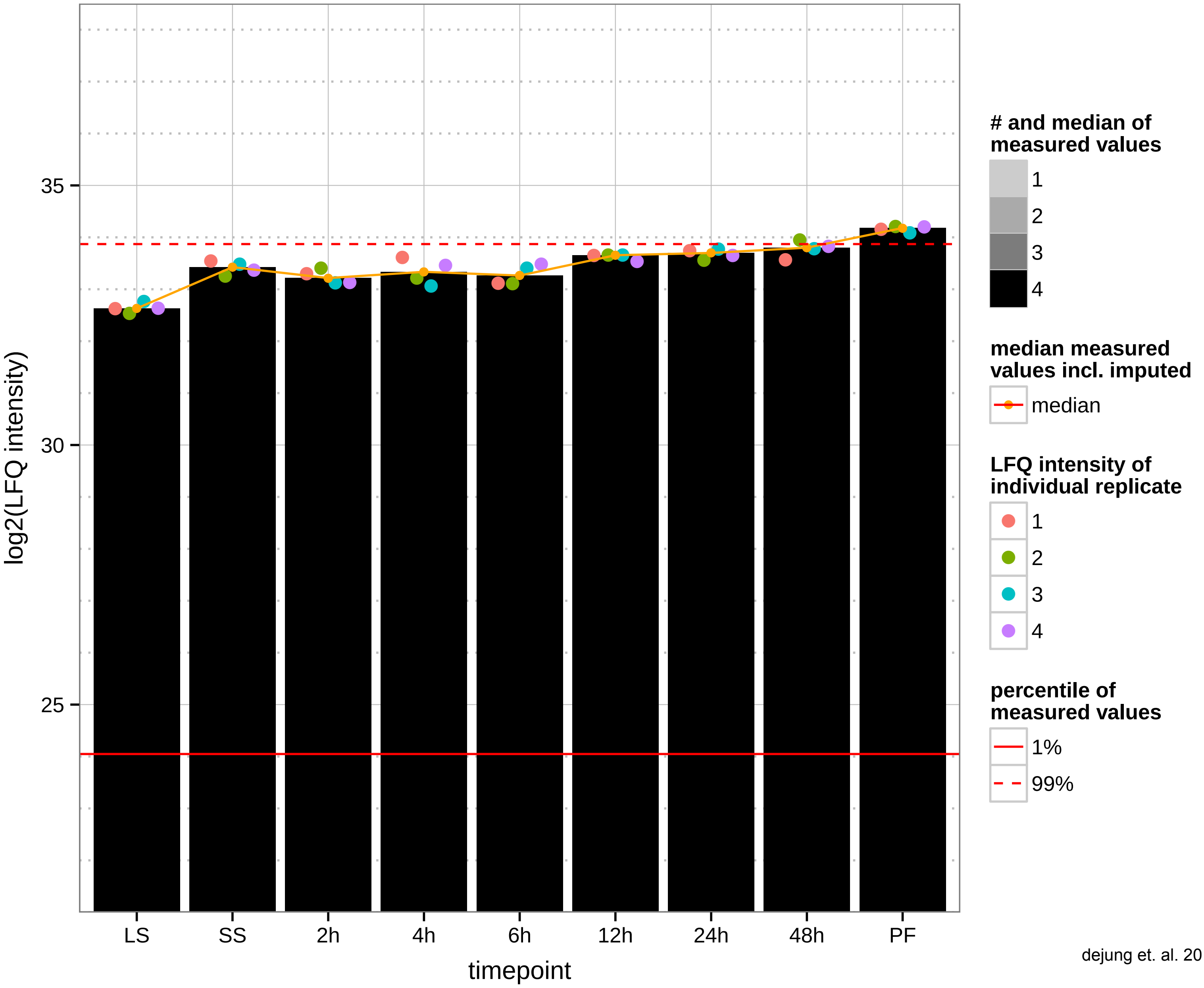
elongation factor 1 gamma, putative
Tb927.11.13190;Tb927.11.13090
AGOF: translation elongation factor activity
AGOC: eukaryotic translation elongation factor 1 complex
AGOP: translational elongation
PGOF: protein binding, translation elongation factor activity
PGOC: eukaryotic translation elongation factor 1 complex
PGOP: translational elongation





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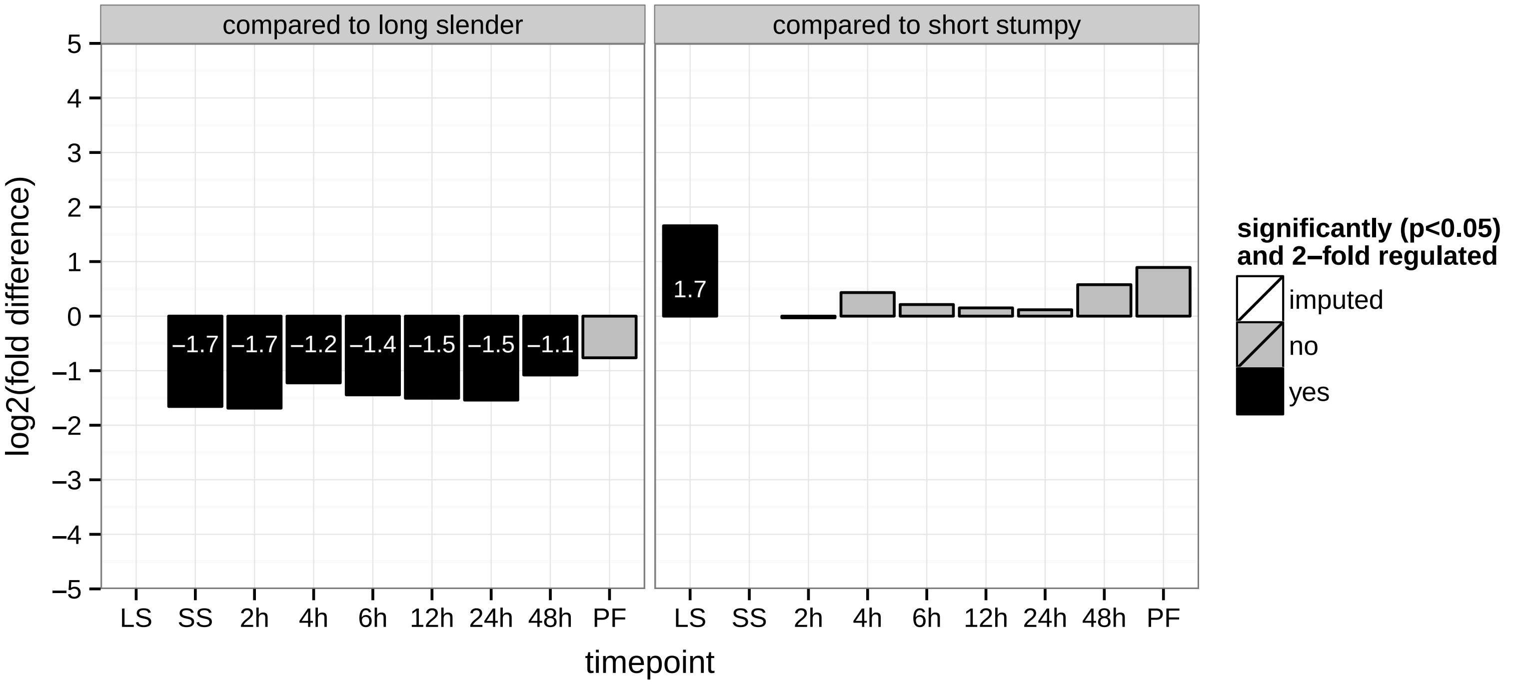
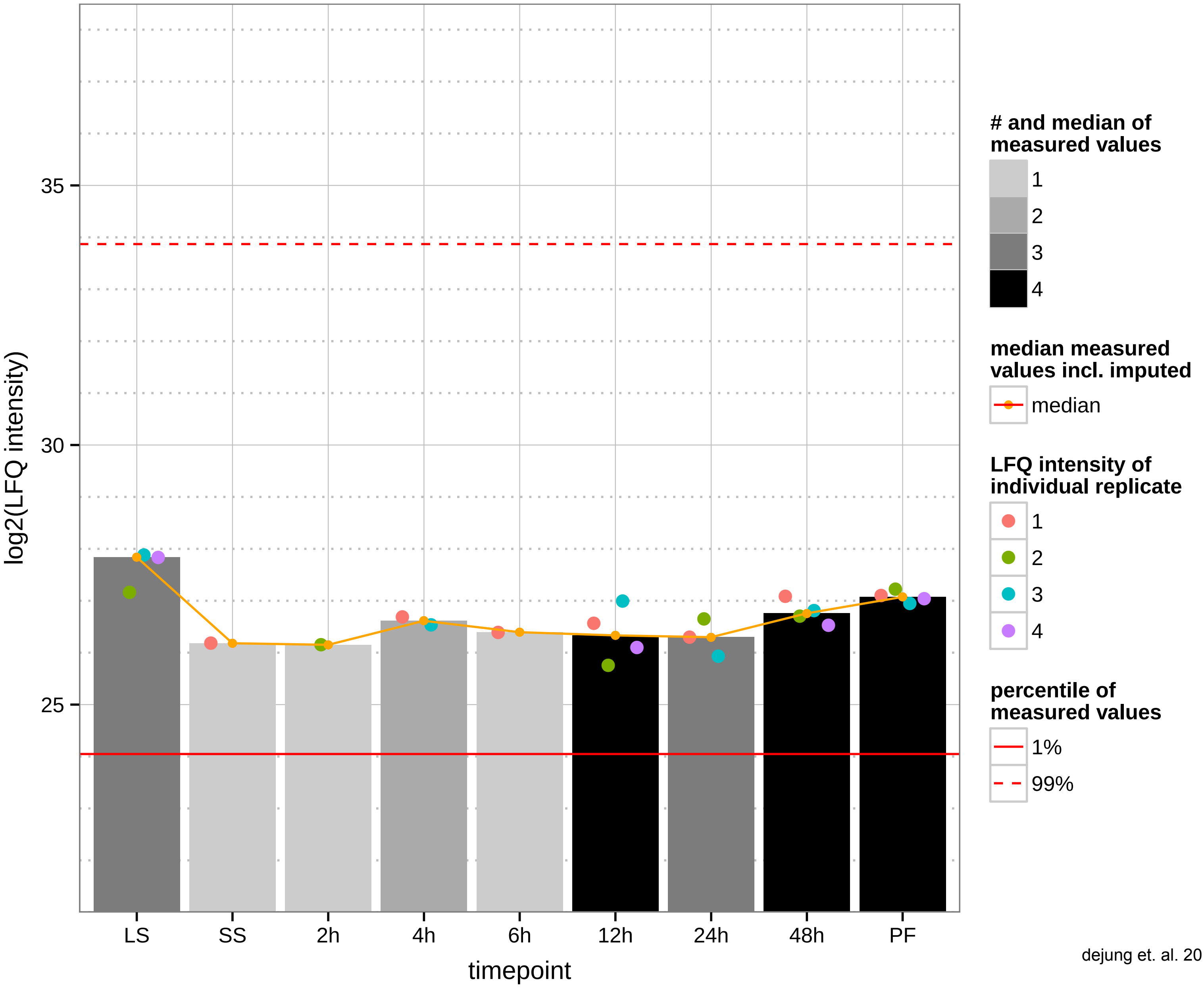
hypothetical protein, conserved
Tb927.11.13270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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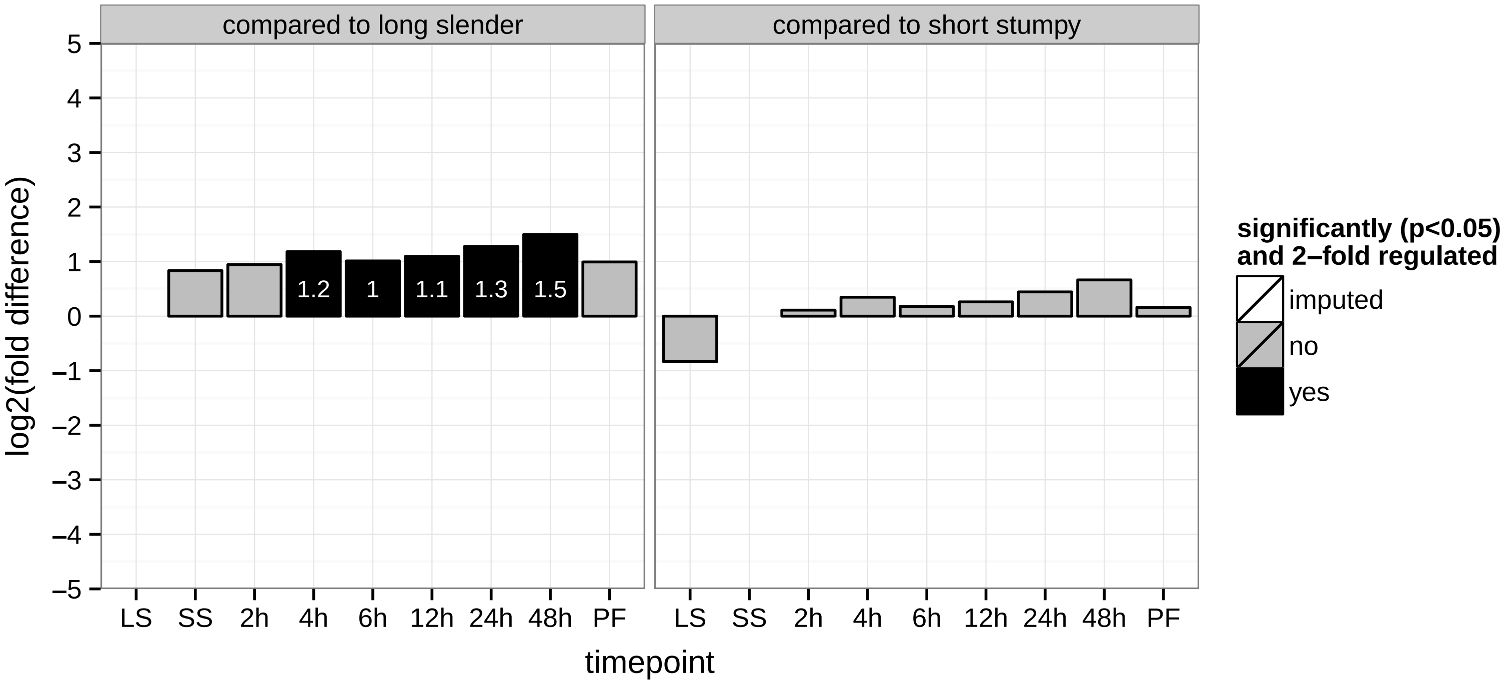
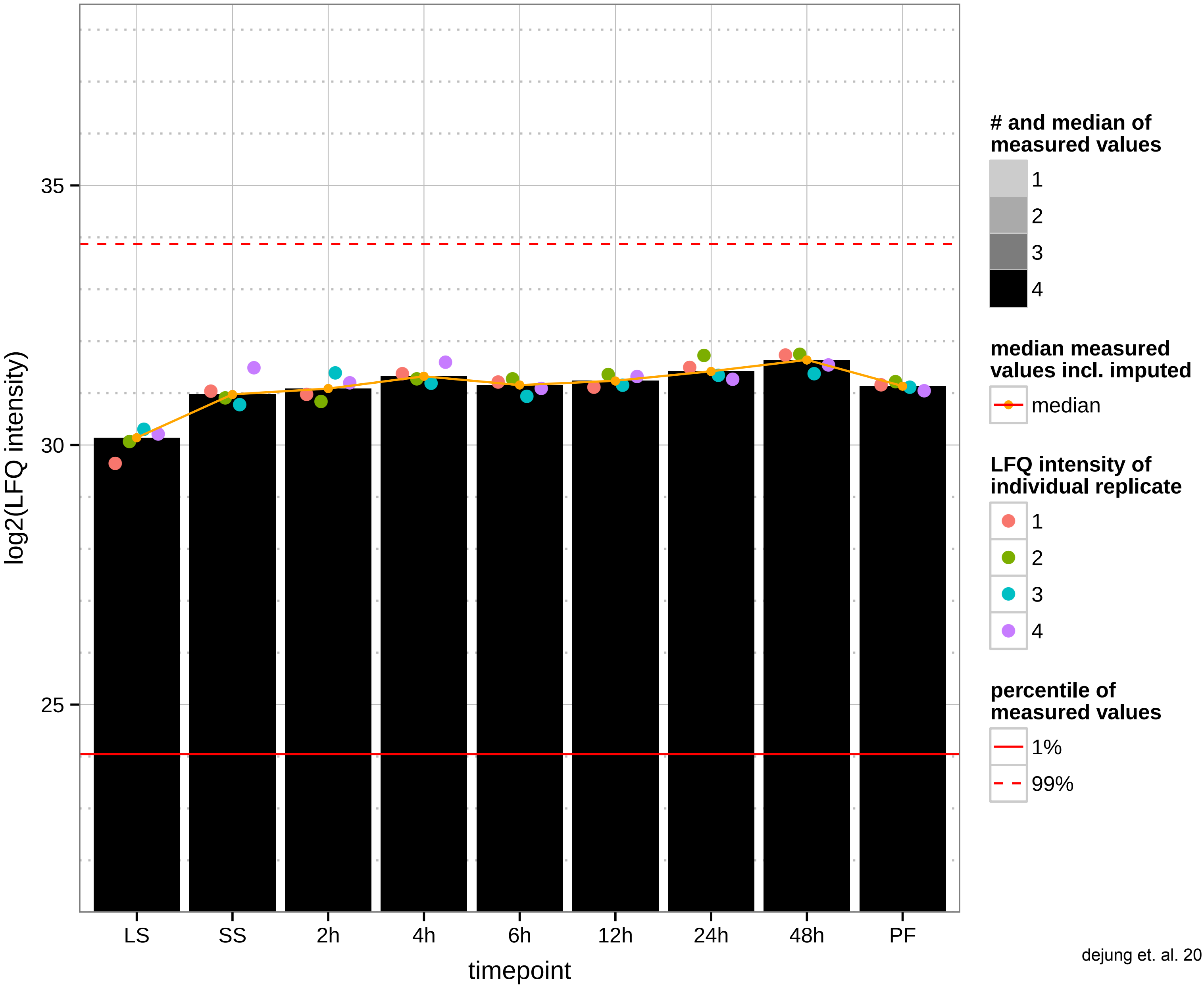
mitochondrial RNA binding protein 2 (GBP25)
Tb927.11.13280
AGOF: RNA binding
AGOC: mitochondrion
AGOP: RNA modification
PGOF: DNA binding
PGOC: null
PGOP: regulation of transcription, DNA–dependent





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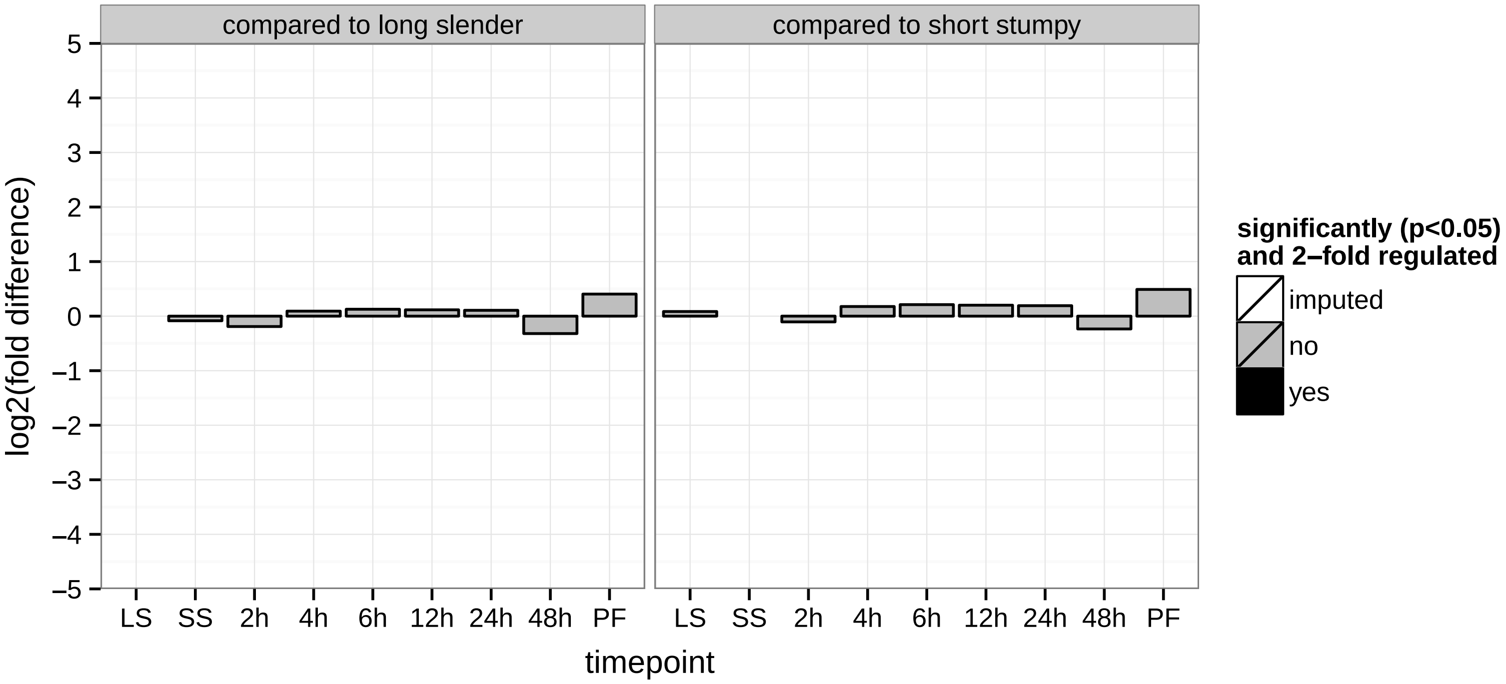
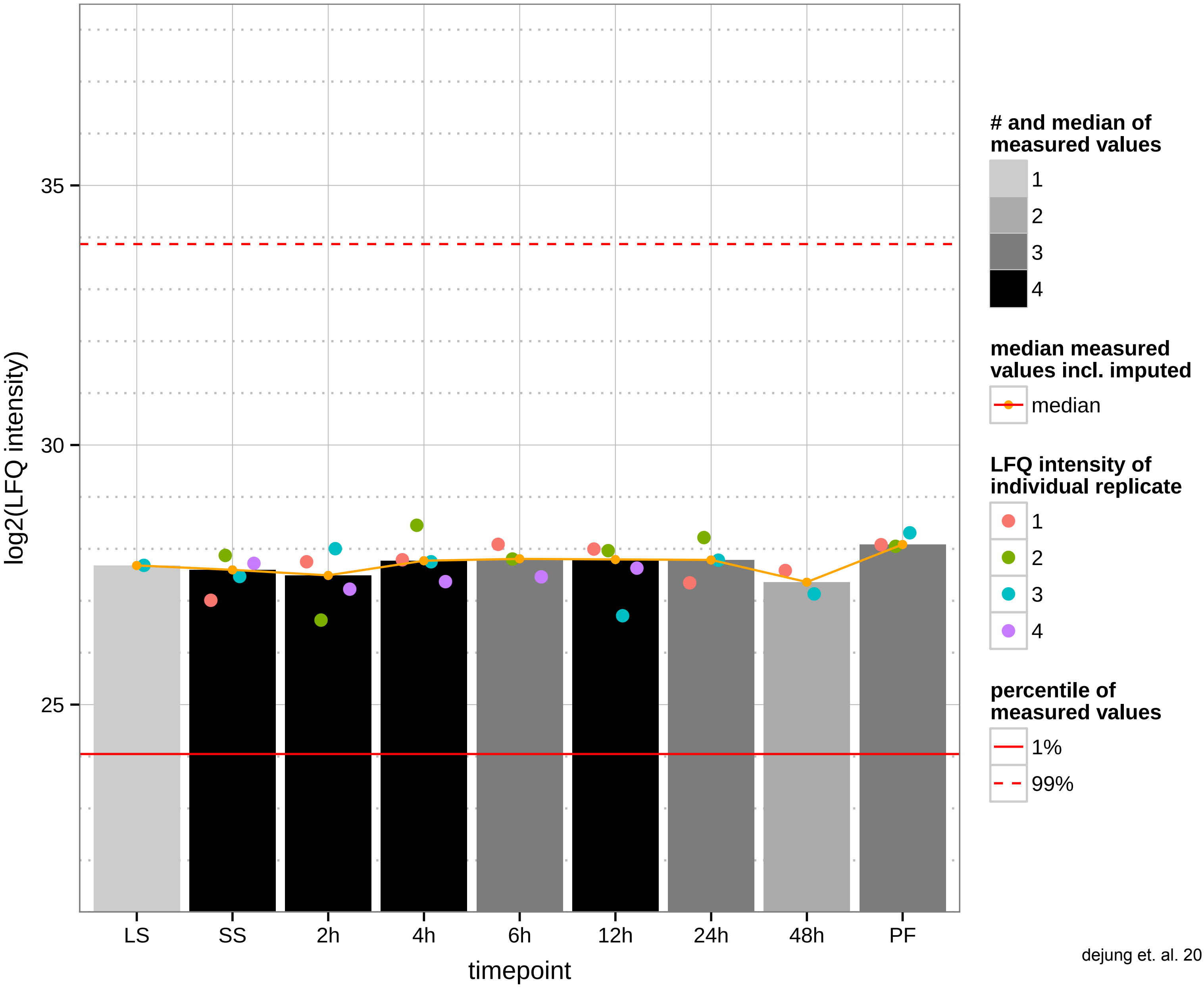
hypothetical protein, conserved
Tb927.11.1330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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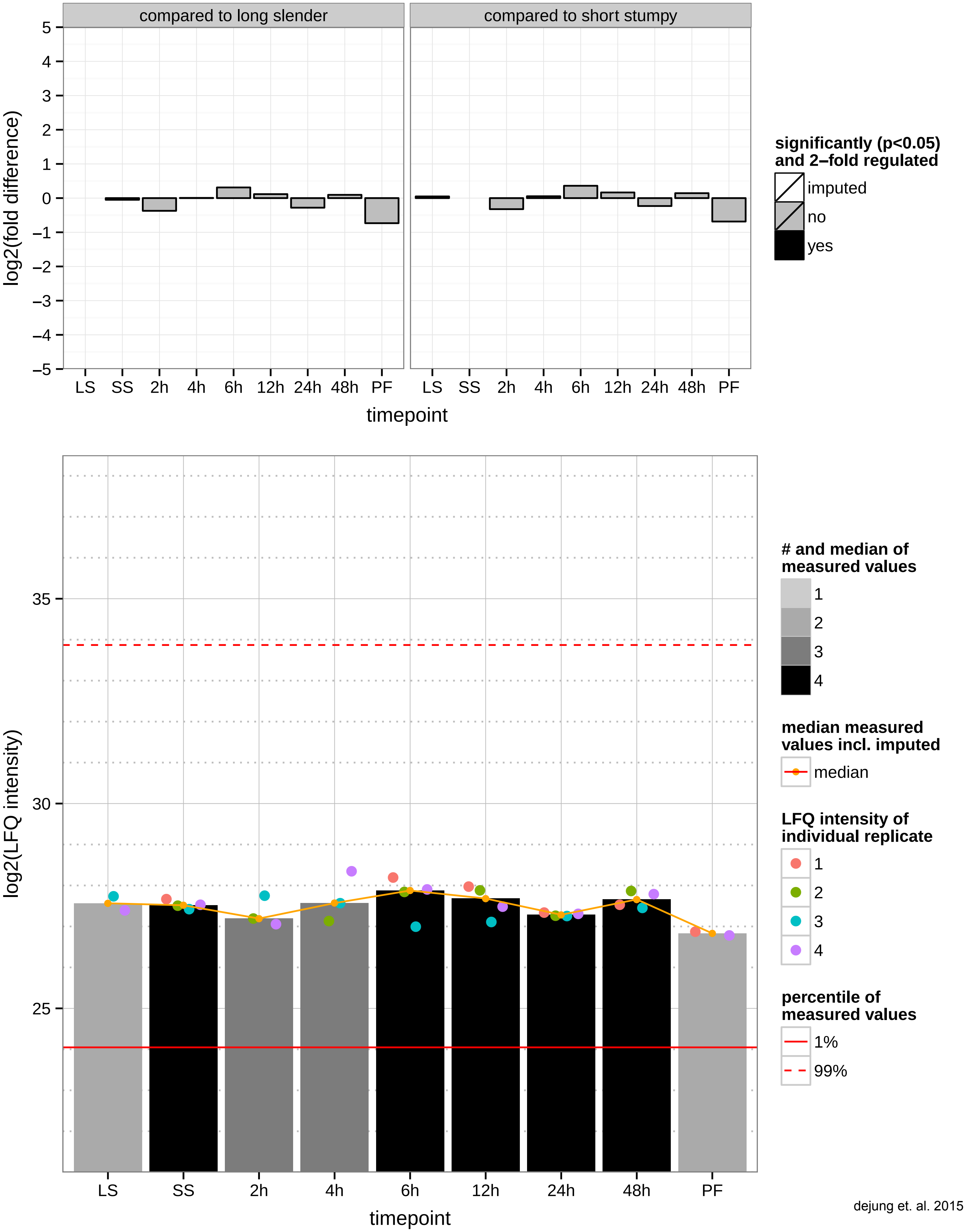
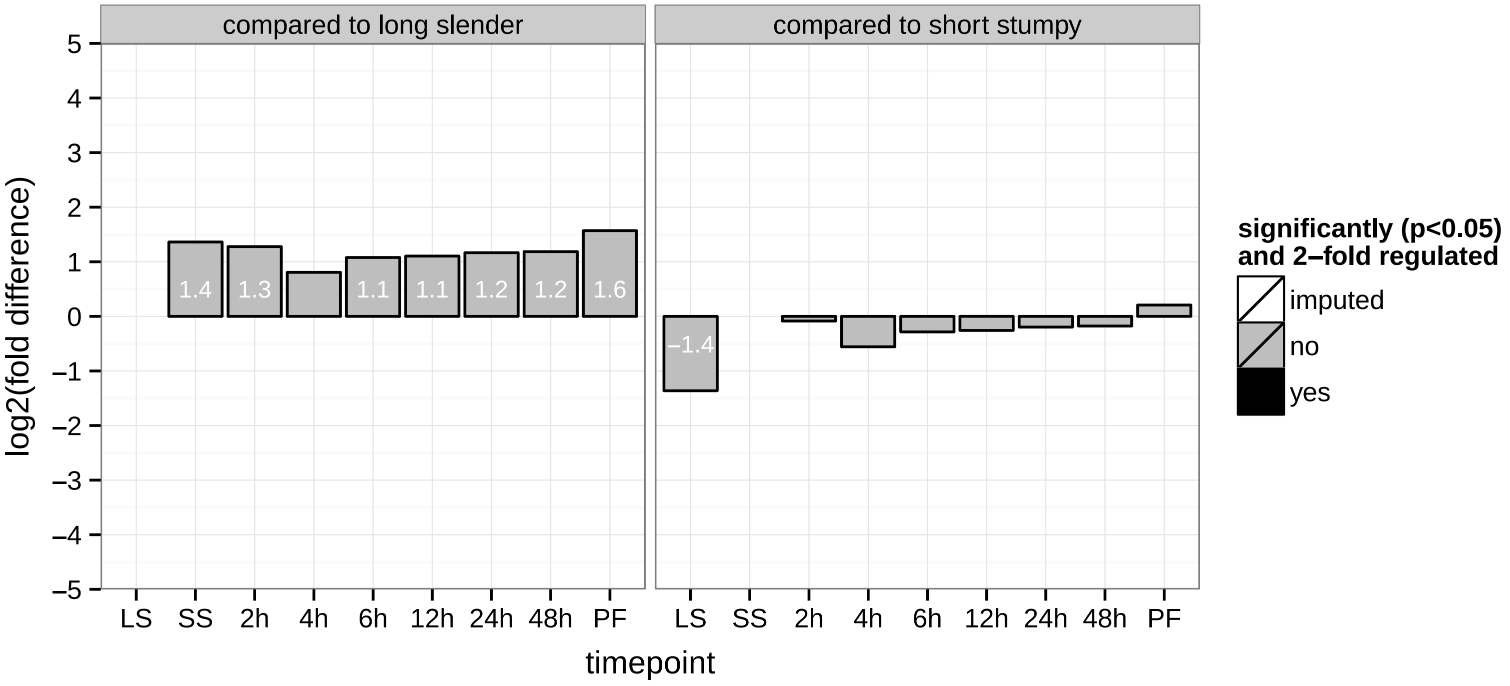
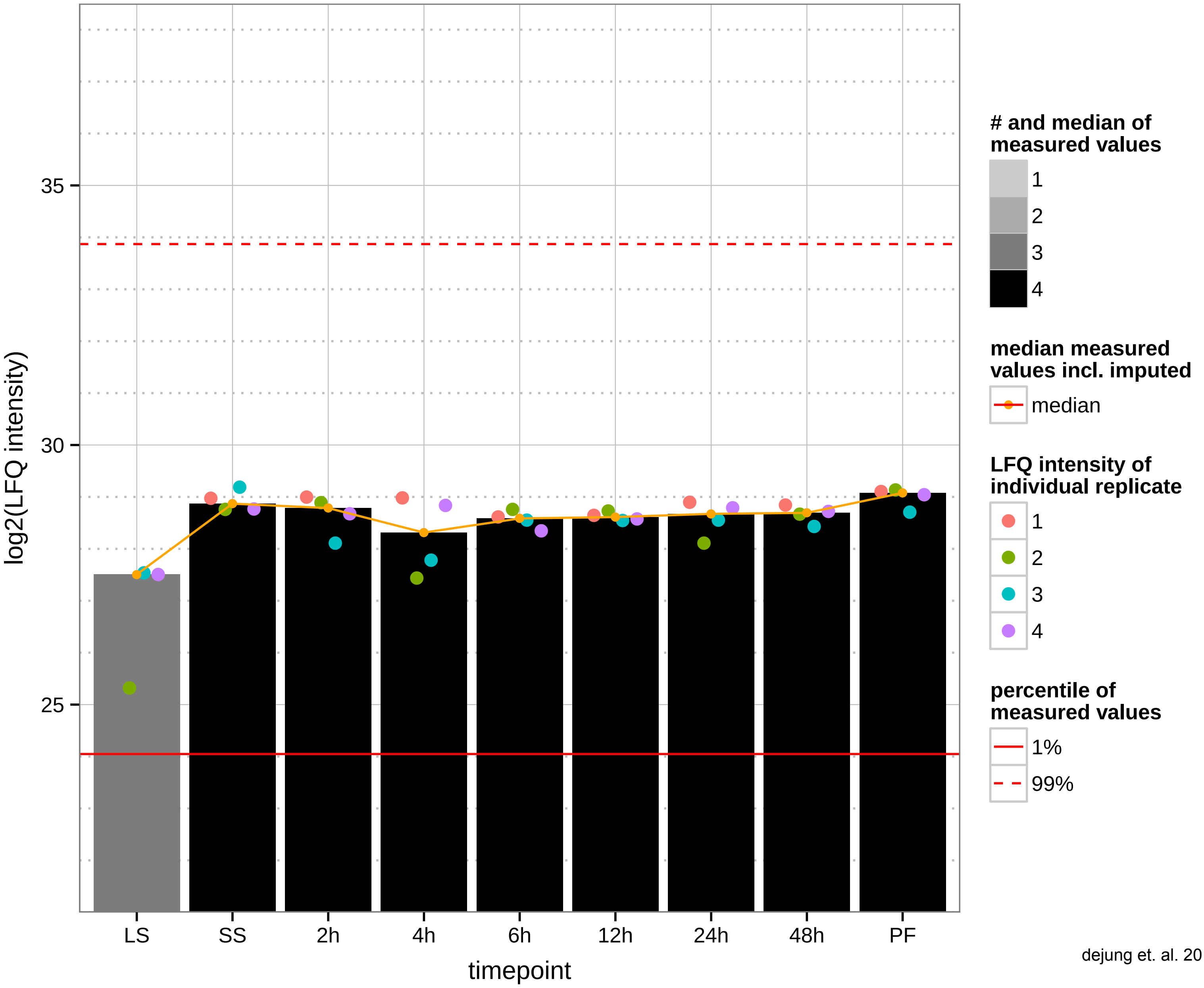
hypothetical protein, conserved
Tb927.11.13300
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



AAA ATPase, putative
Tb927.11.13360
AGOF: ATP binding, ATPase activity
AGOC: null
AGOP: protein metabolic process
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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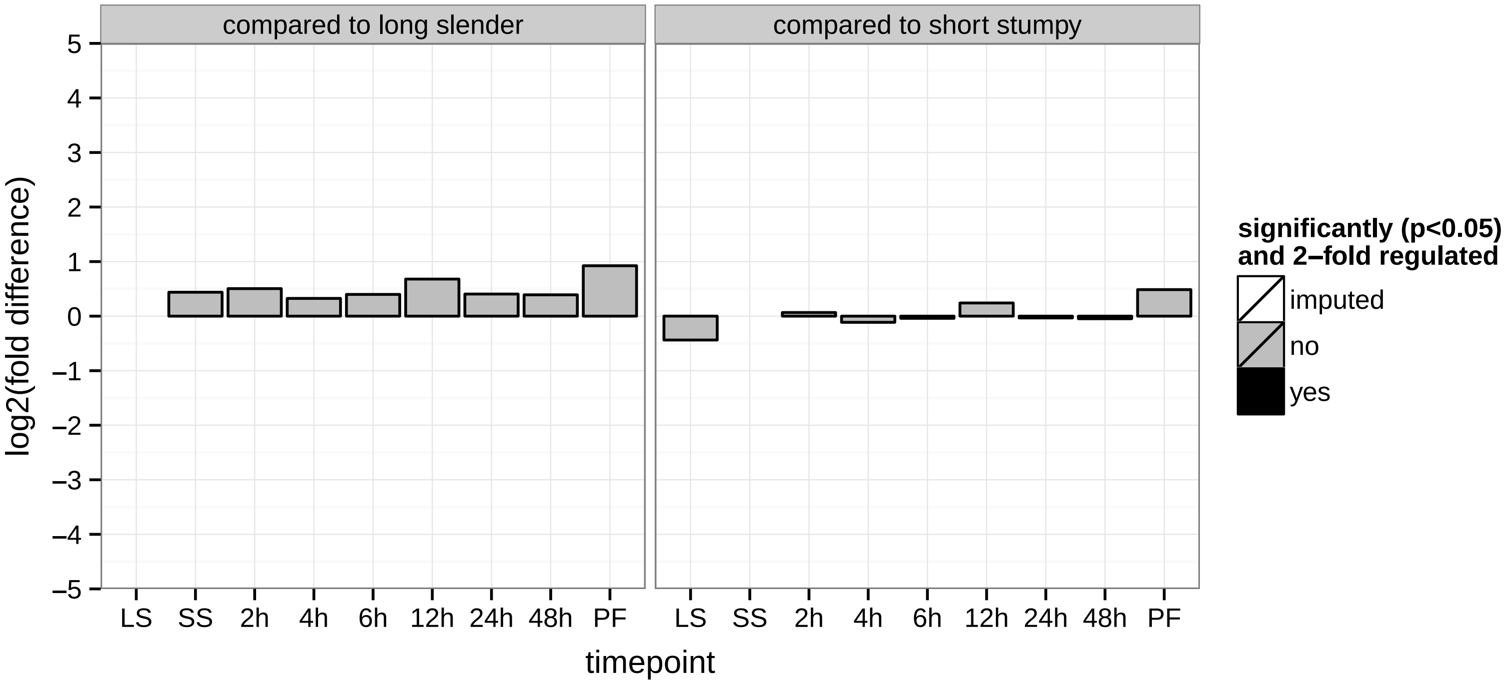
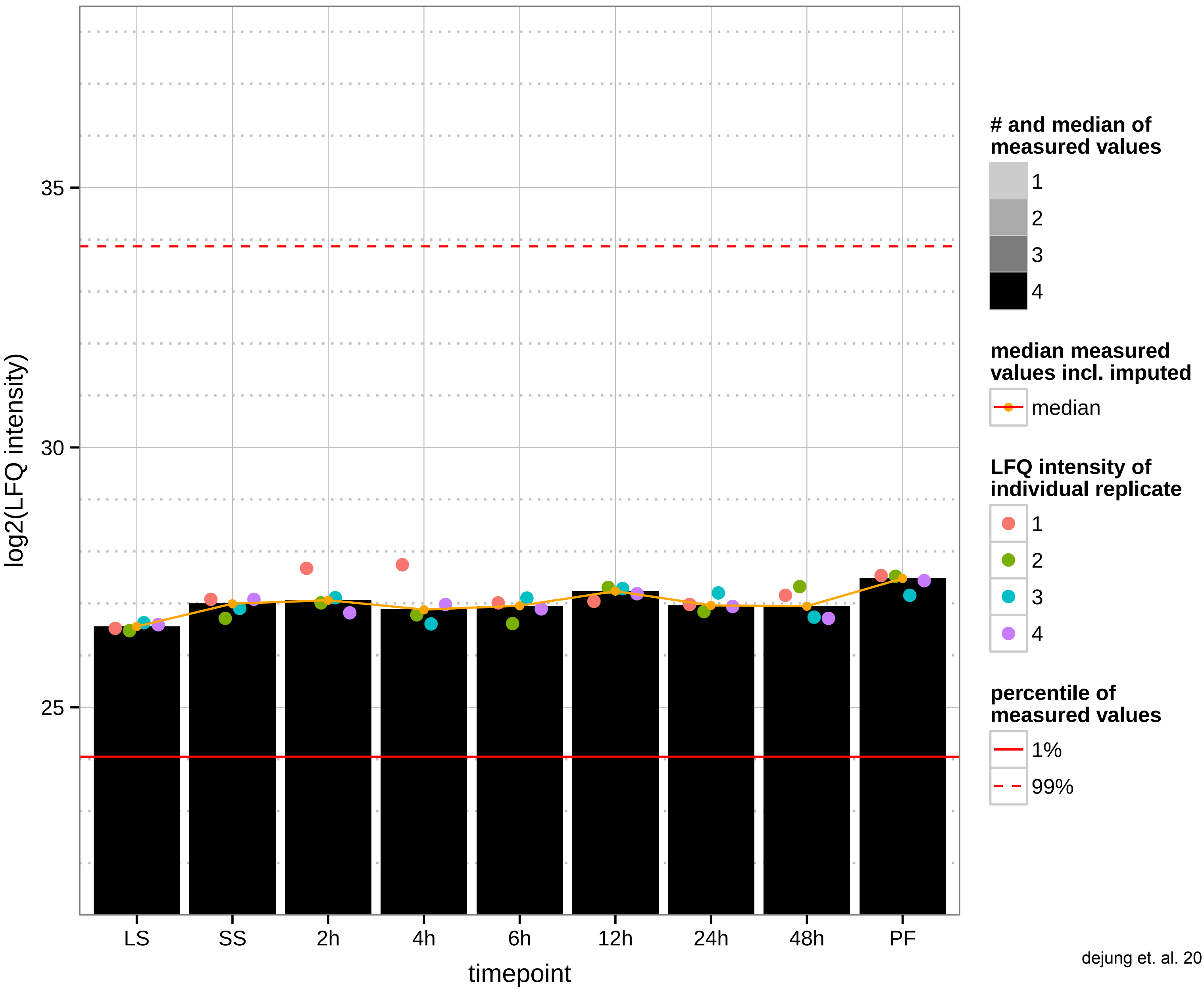
hypothetical protein, conserved
Tb927.11.13400
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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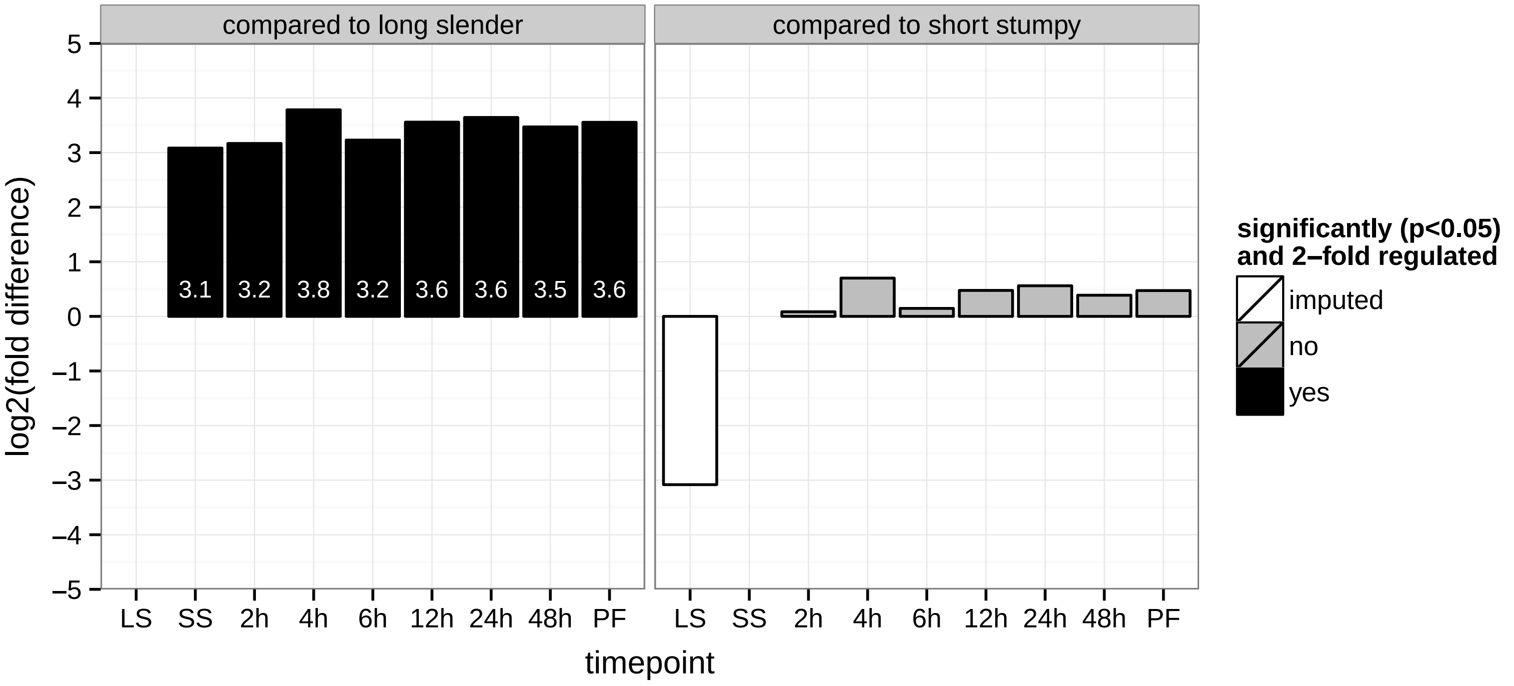
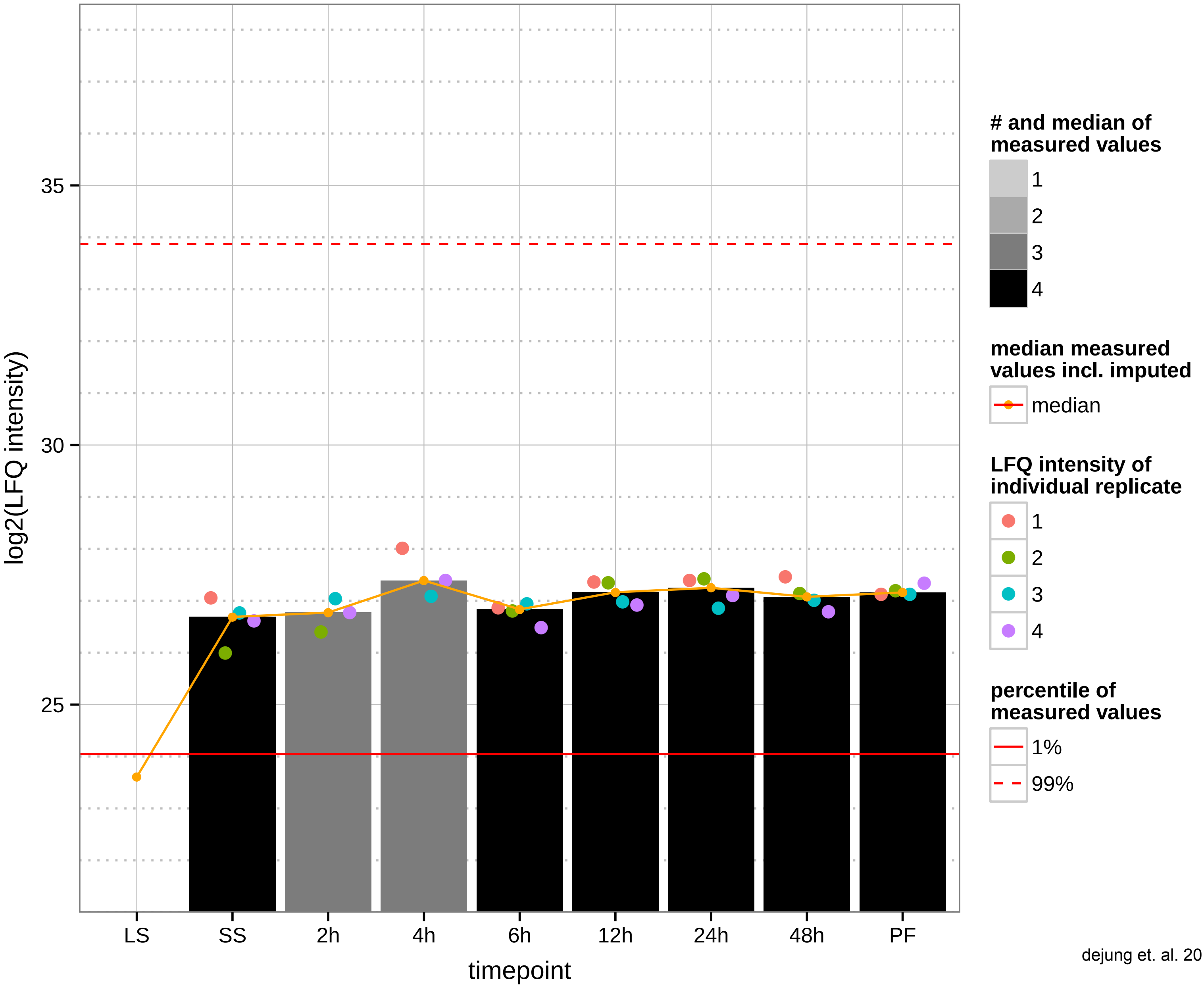
hypothetical protein, conserved
Tb927.11.13470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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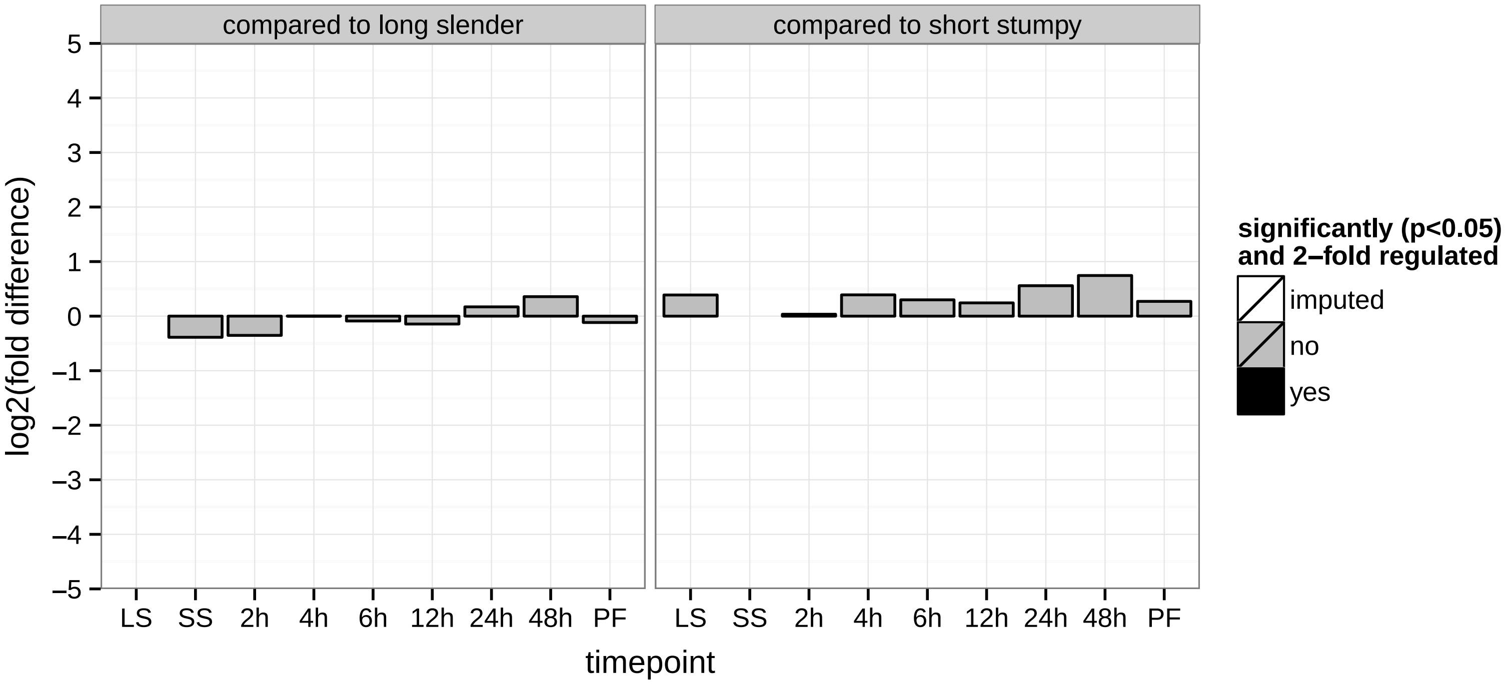
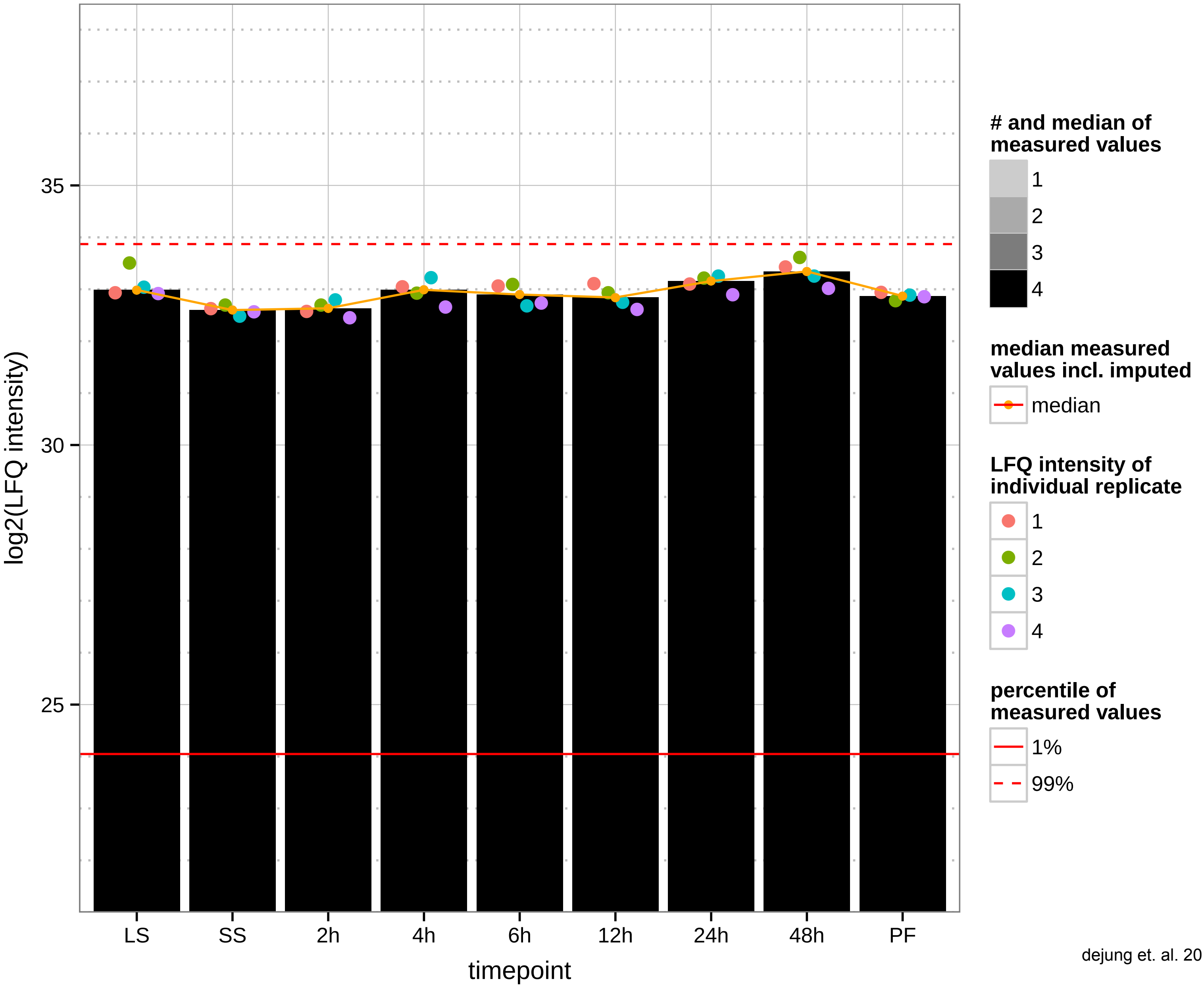
par1
Tb927.11.13500
AGOF: calmodulin binding
AGOC: motile cilium
AGOP: null
PGOF: calmodulin binding
PGOC: microtubule–based flagellum
PGOP: null





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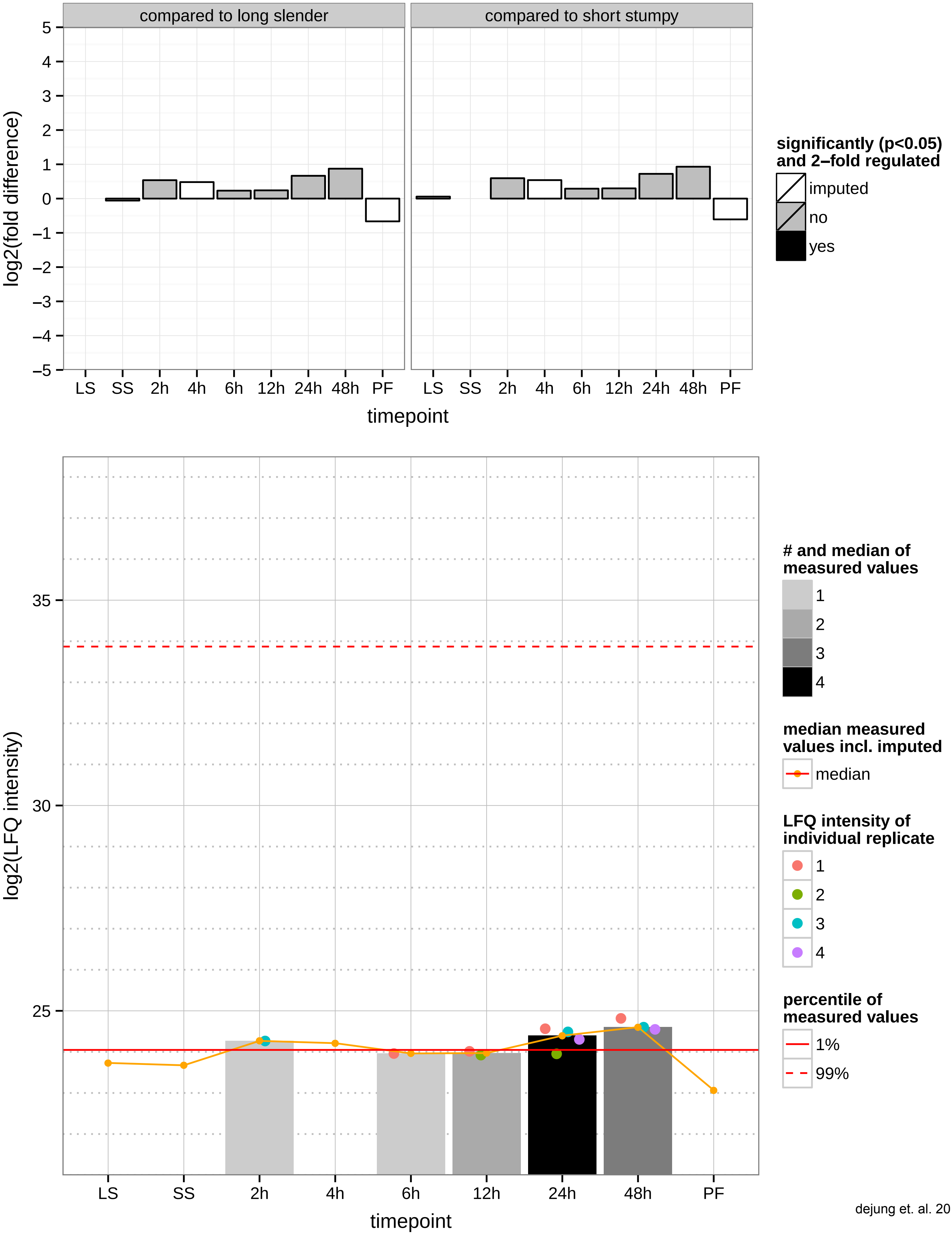
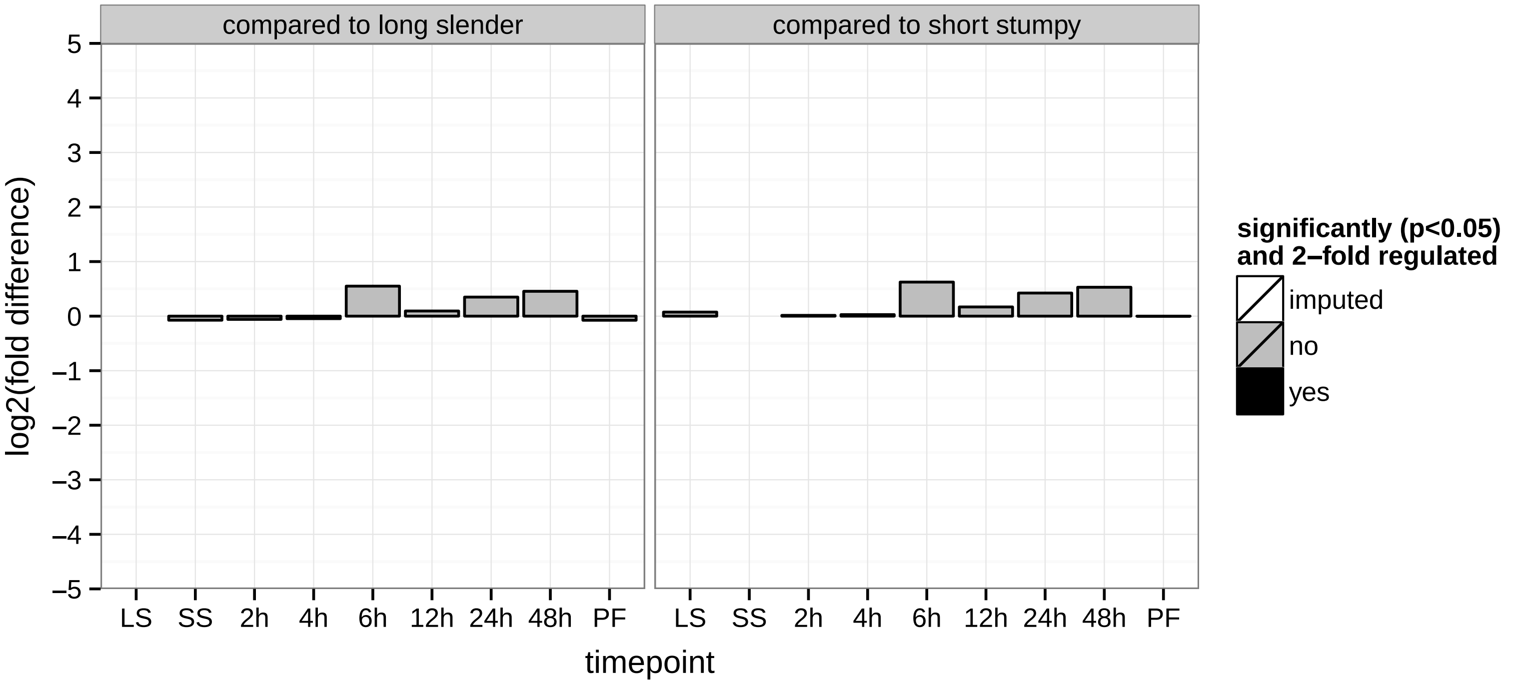
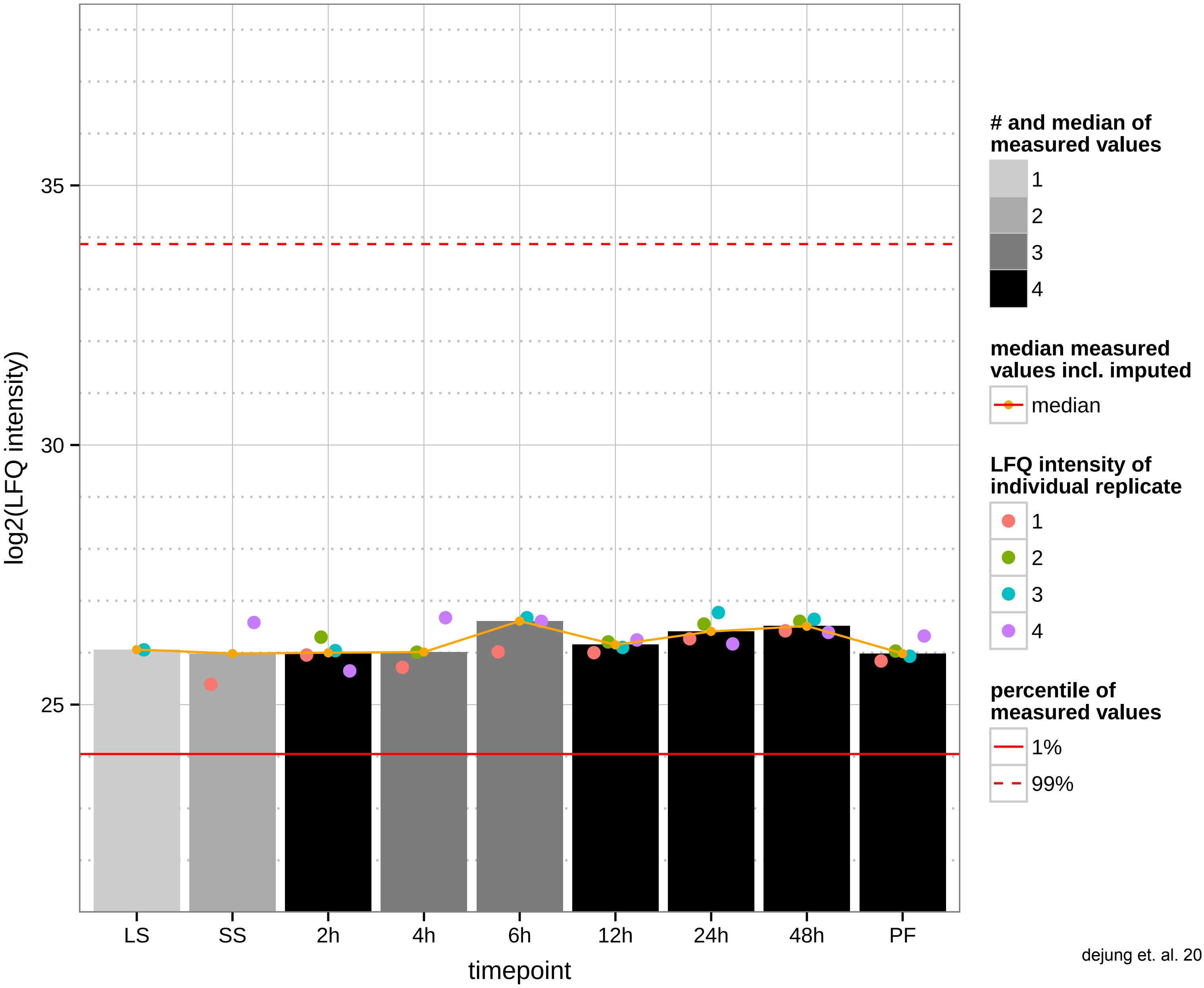
hypothetical protein, conserved
Tb927.11.13540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015

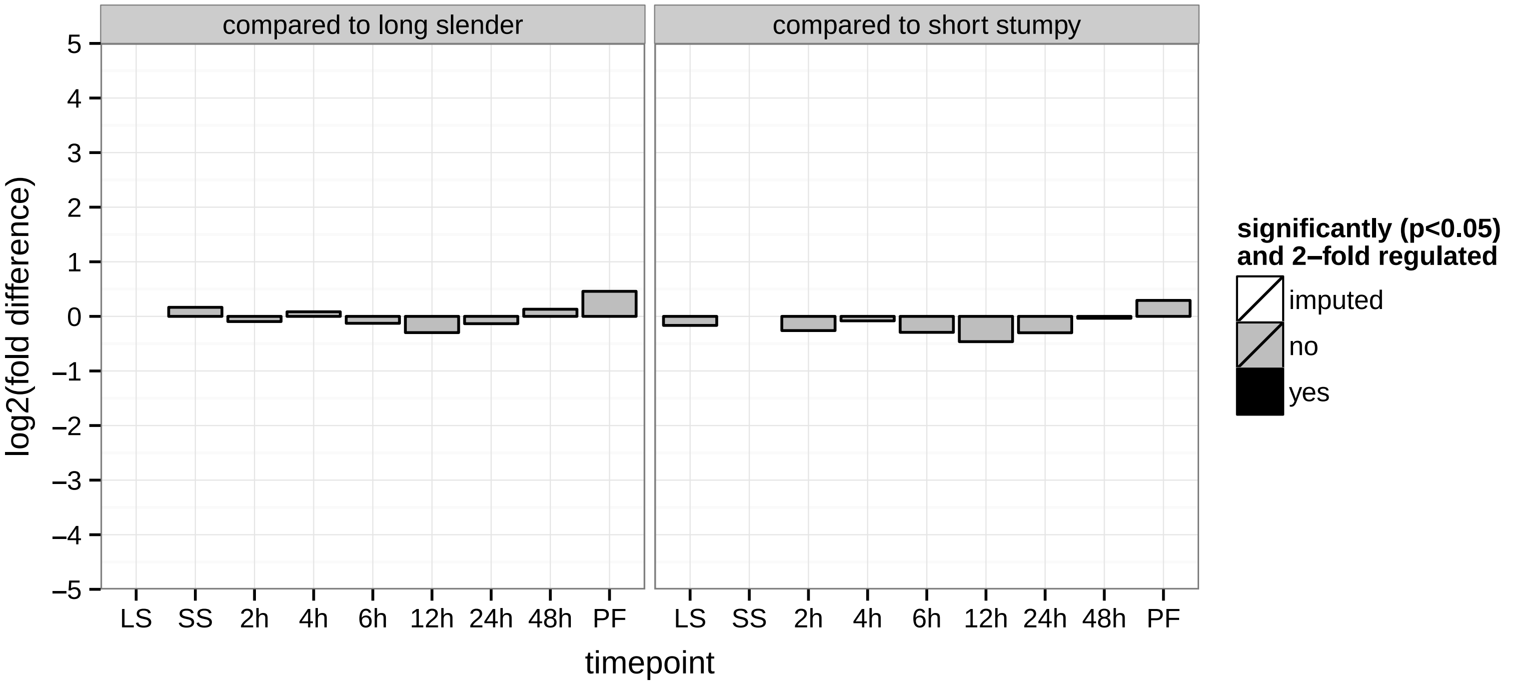
ubiquinone biosynthesis protein–like protein
Tb927.11.13580
AGOF: null
AGOC: integral to membrane, mitochondrion
AGOP: ubiquinone biosynthetic process
PGOF: null
PGOC: null
PGOP: ubiquinone biosynthetic process

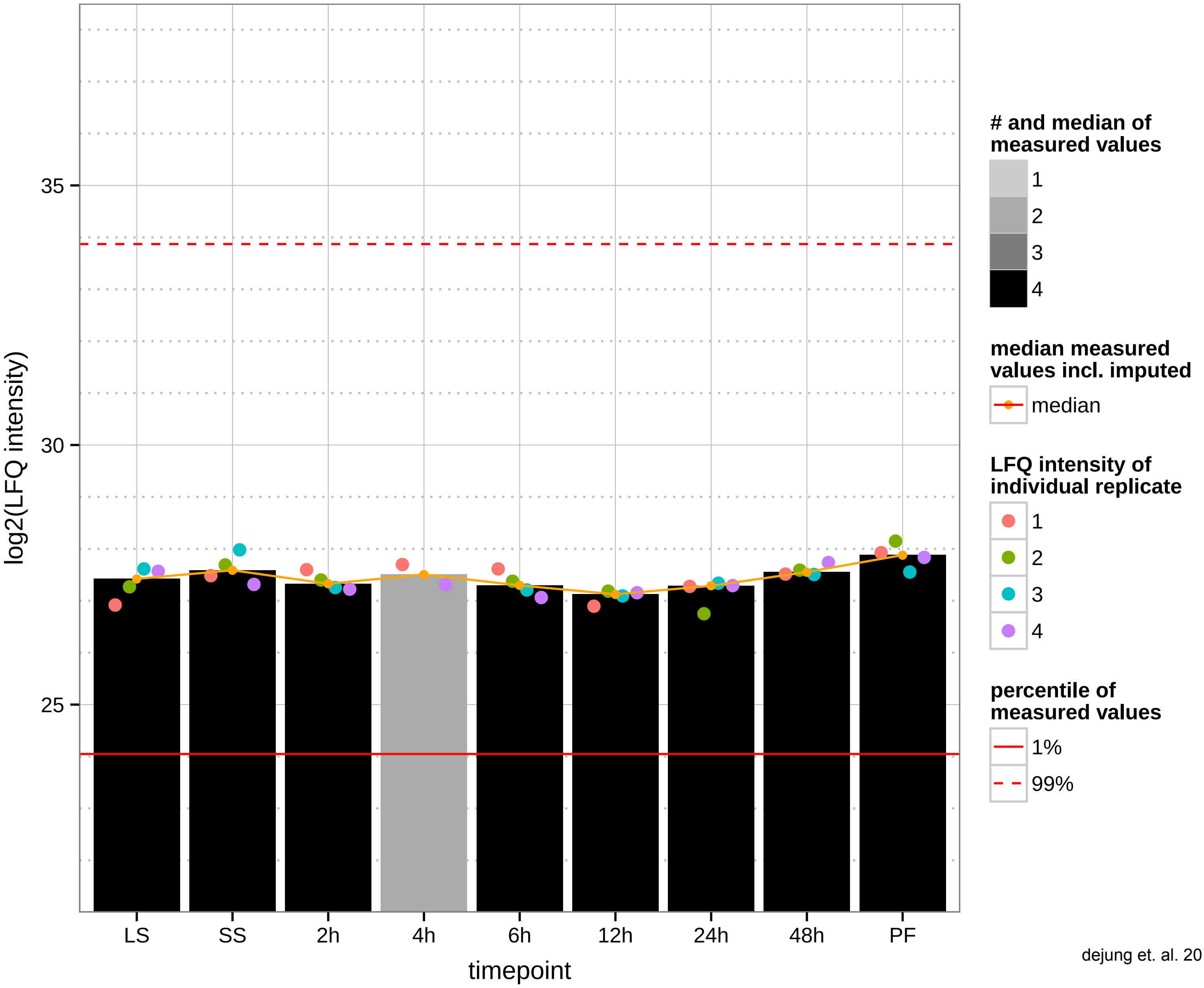




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.13670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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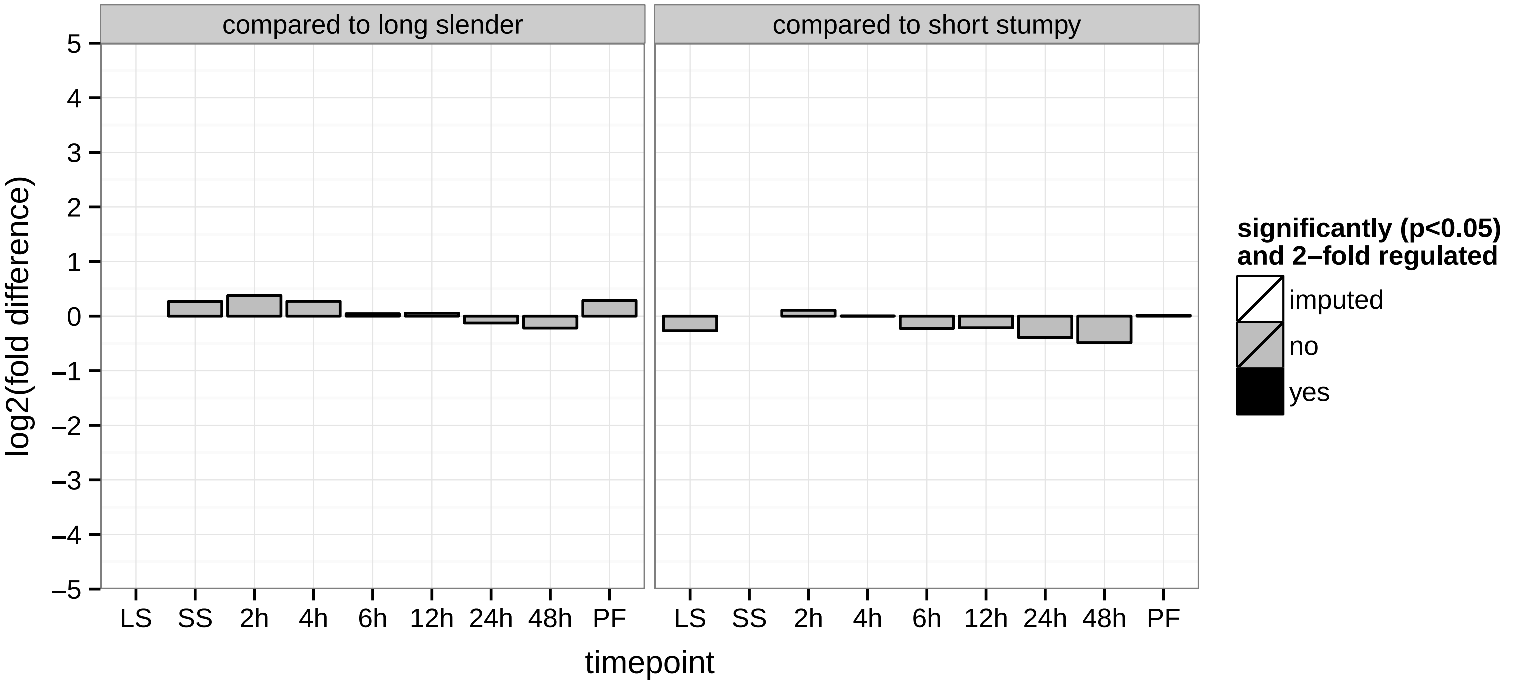
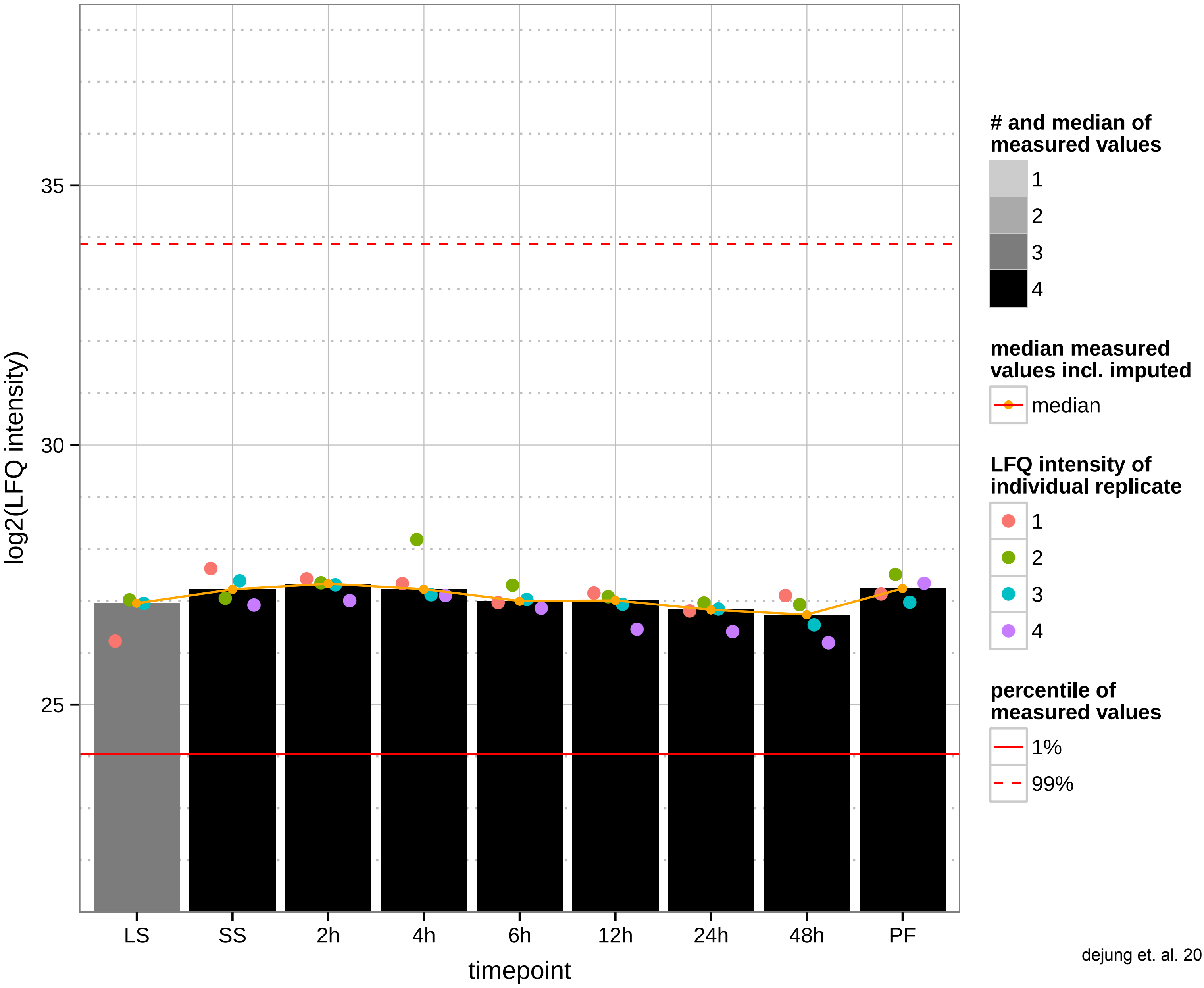
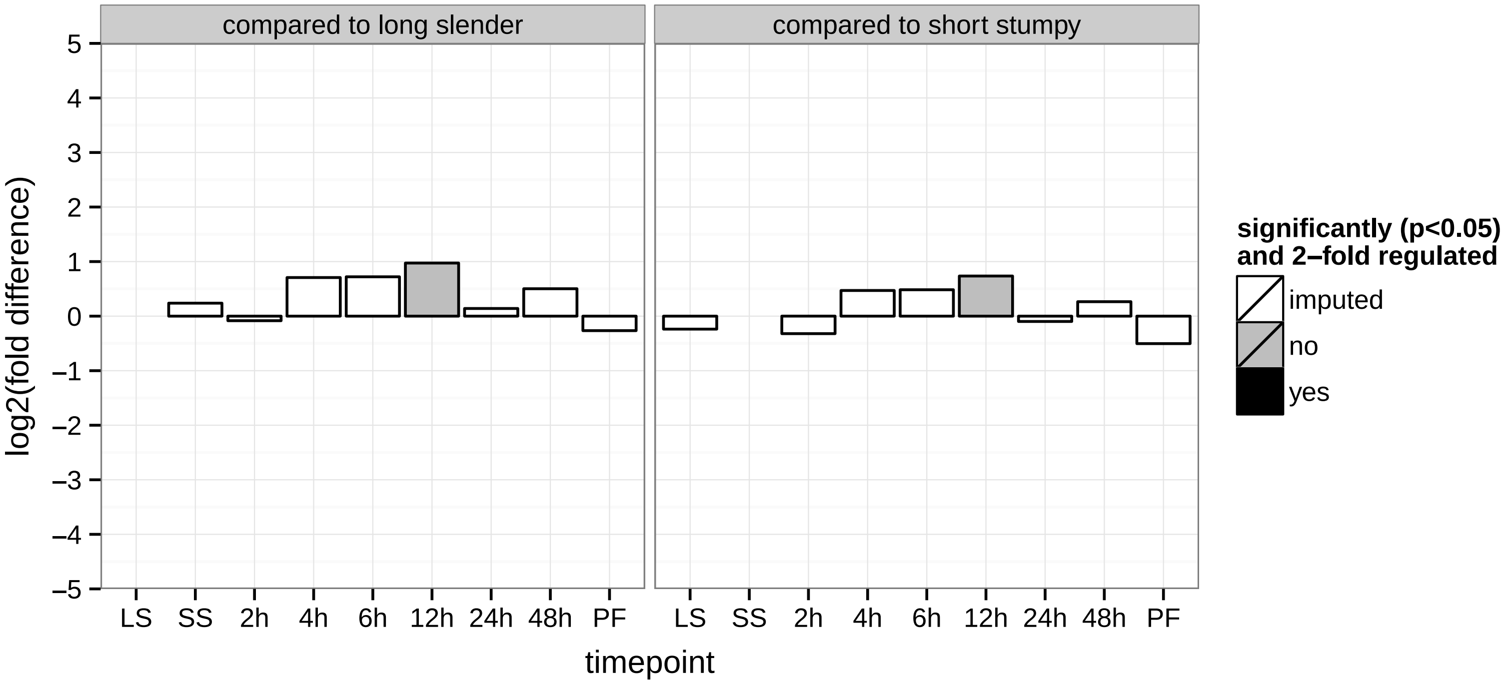
Ras−related protein Rab4 (RAB4)
Tb927.11.13750
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti

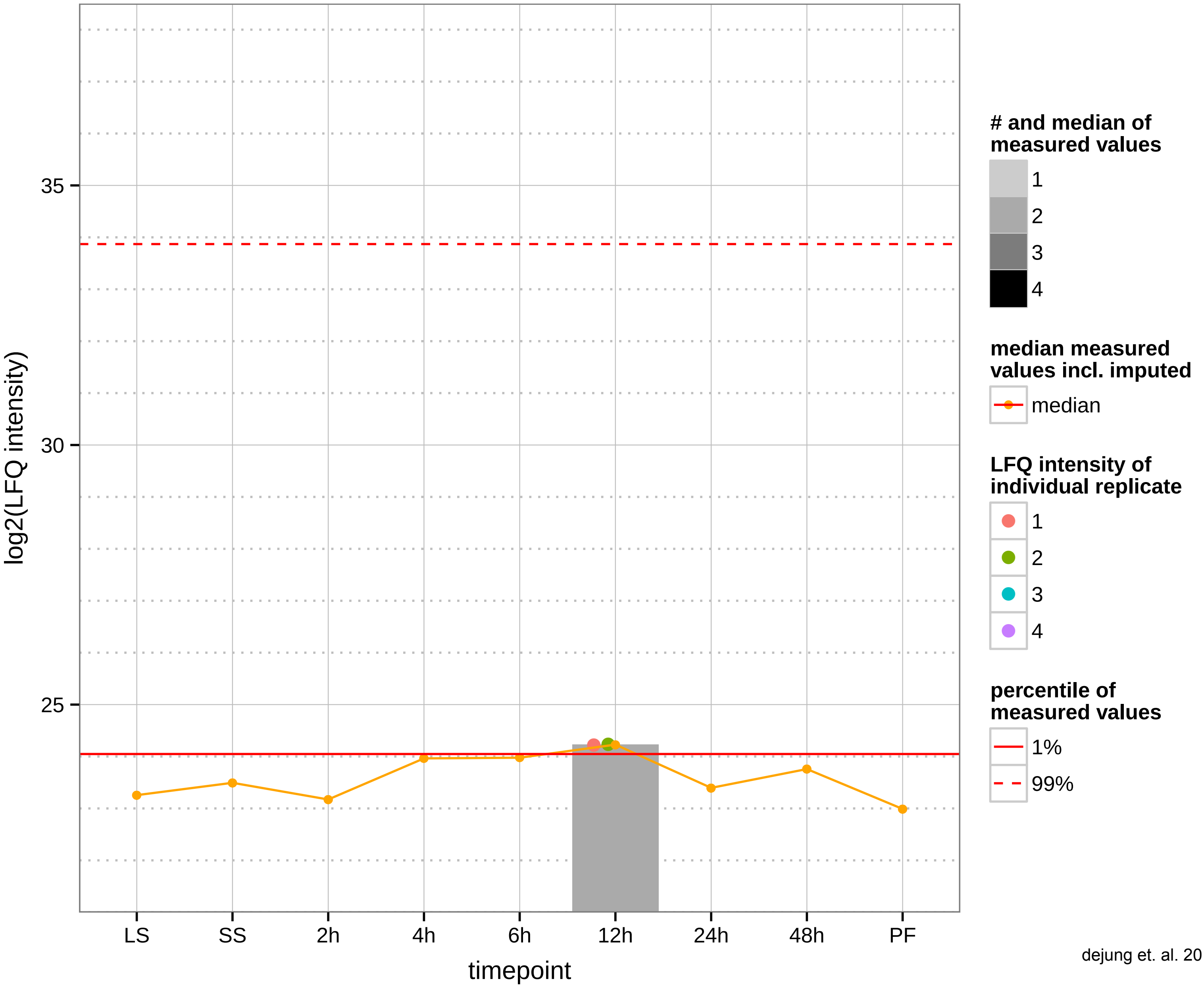




dejung et. al. 2015

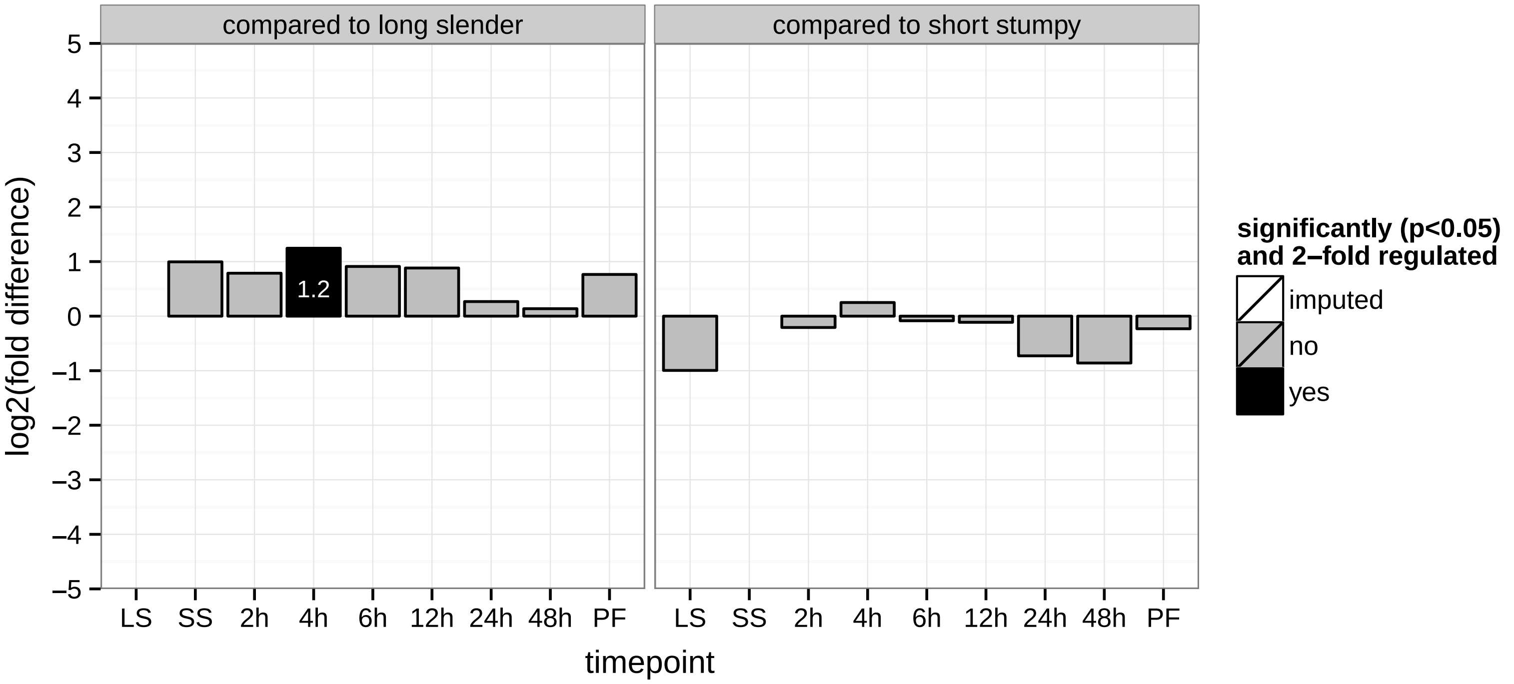
hypothetical protein, conserved
Tb927.11.13770
AGOF: null
AGOC: membrane
AGOP: null
PGOF: null
PGOC: membrane
PGOP: null

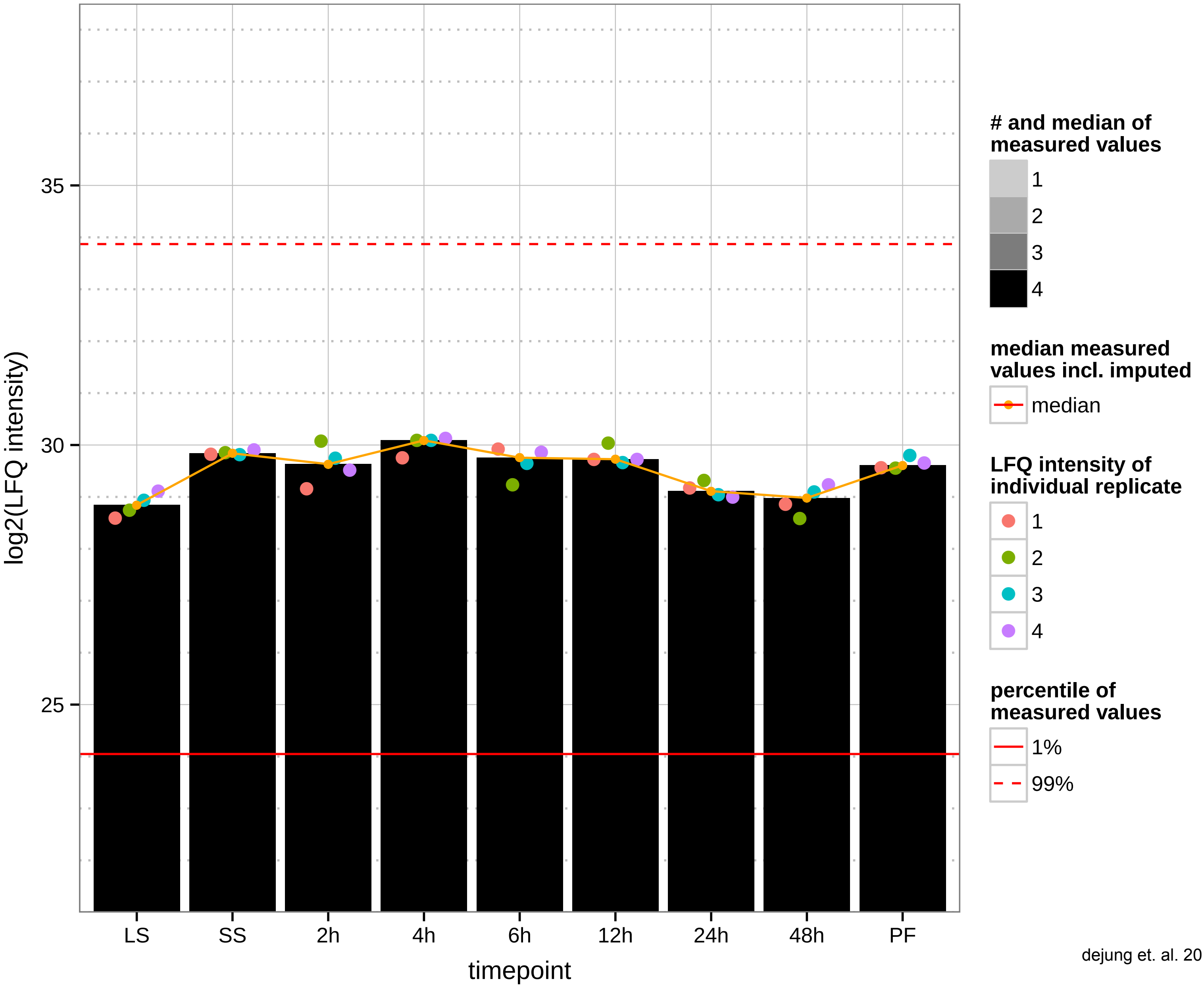




dejung et. al. 2015

profilin
Tb927.11.13780
AGOF: actin binding
AGOC: null
AGOP: actin cytoskeleton organization, cytoskeleton organization
PGOF: actin binding
PGOC: actin cytoskeleton
PGOP: cytoskeleton organization





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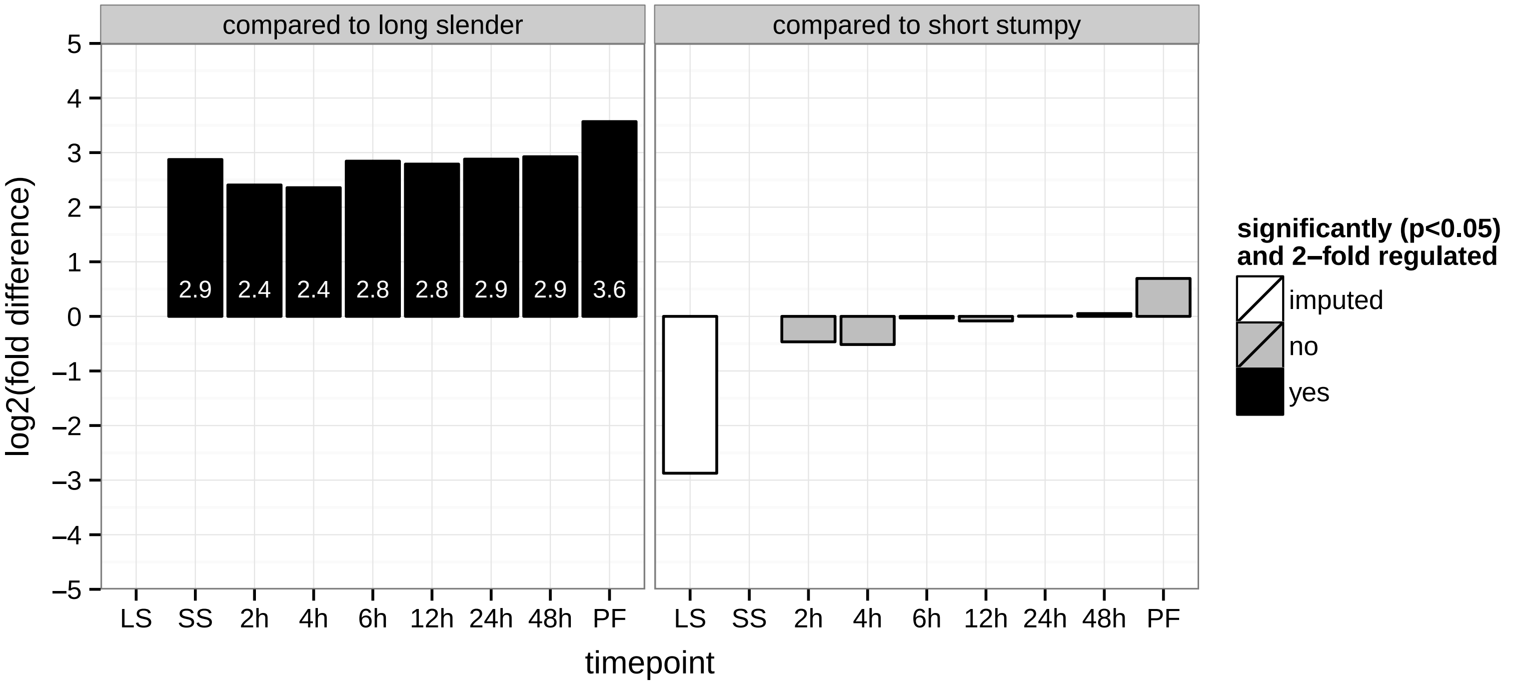
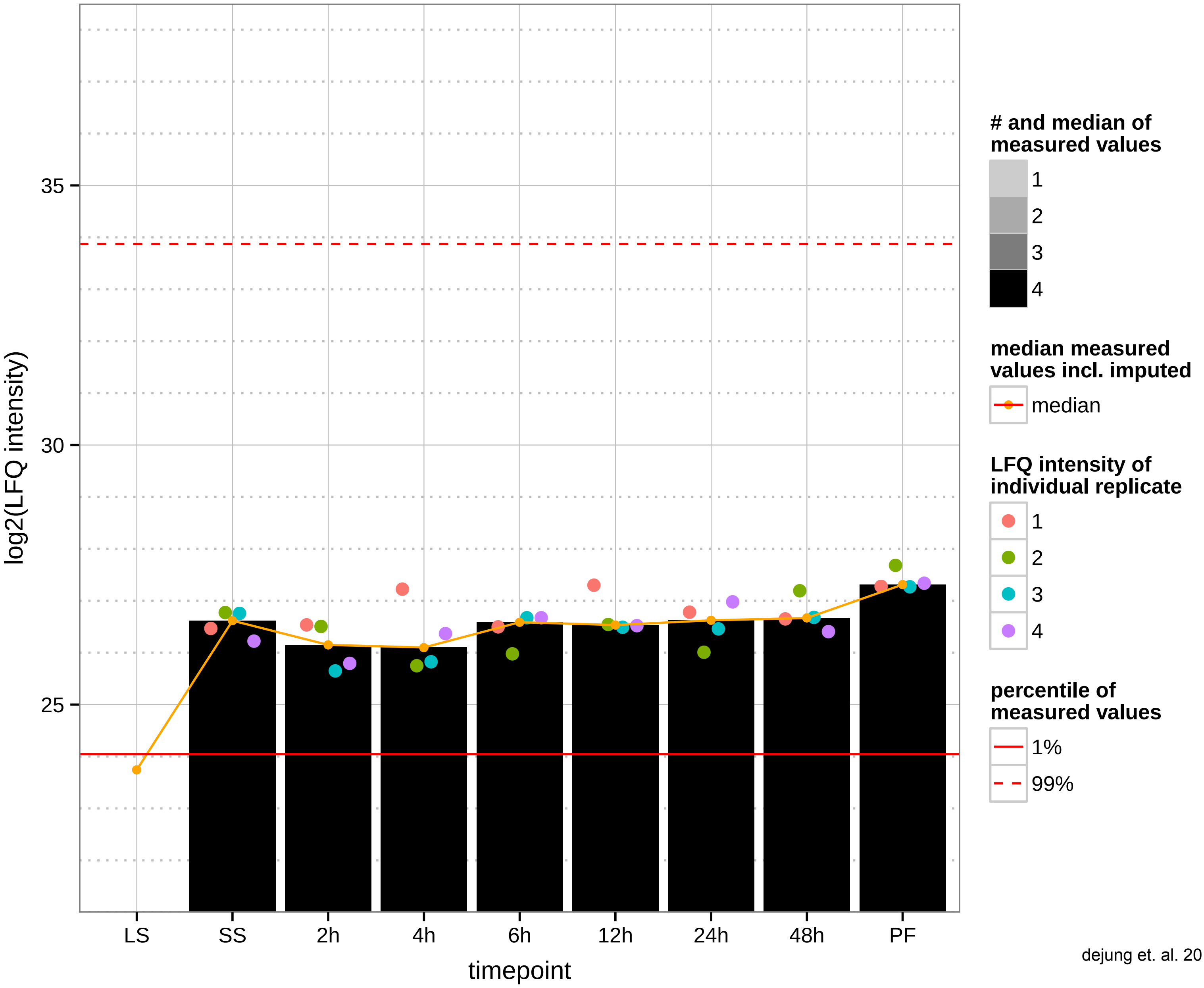
ATP−dependent DEAD/H RNA helicase, putative, ATP− dependent RNA helicase
Tb927.11.13810
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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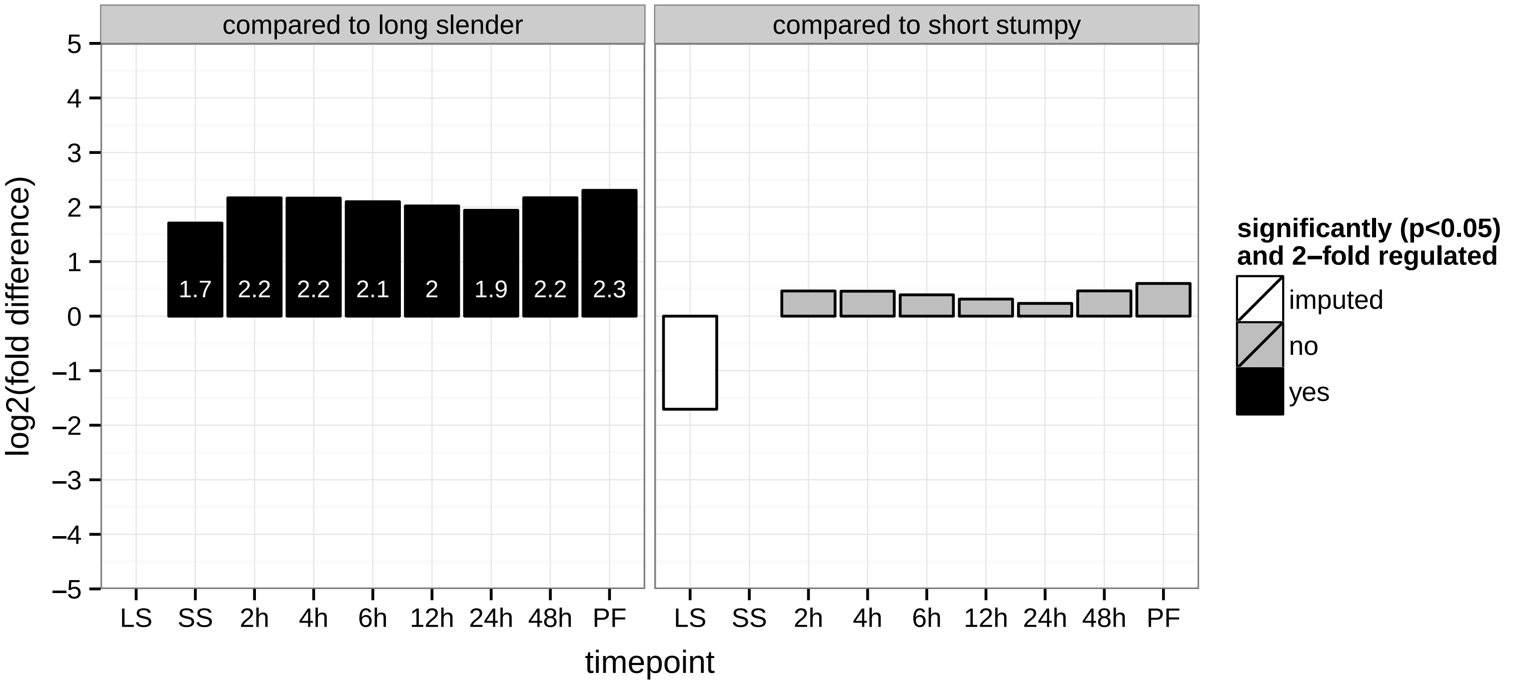
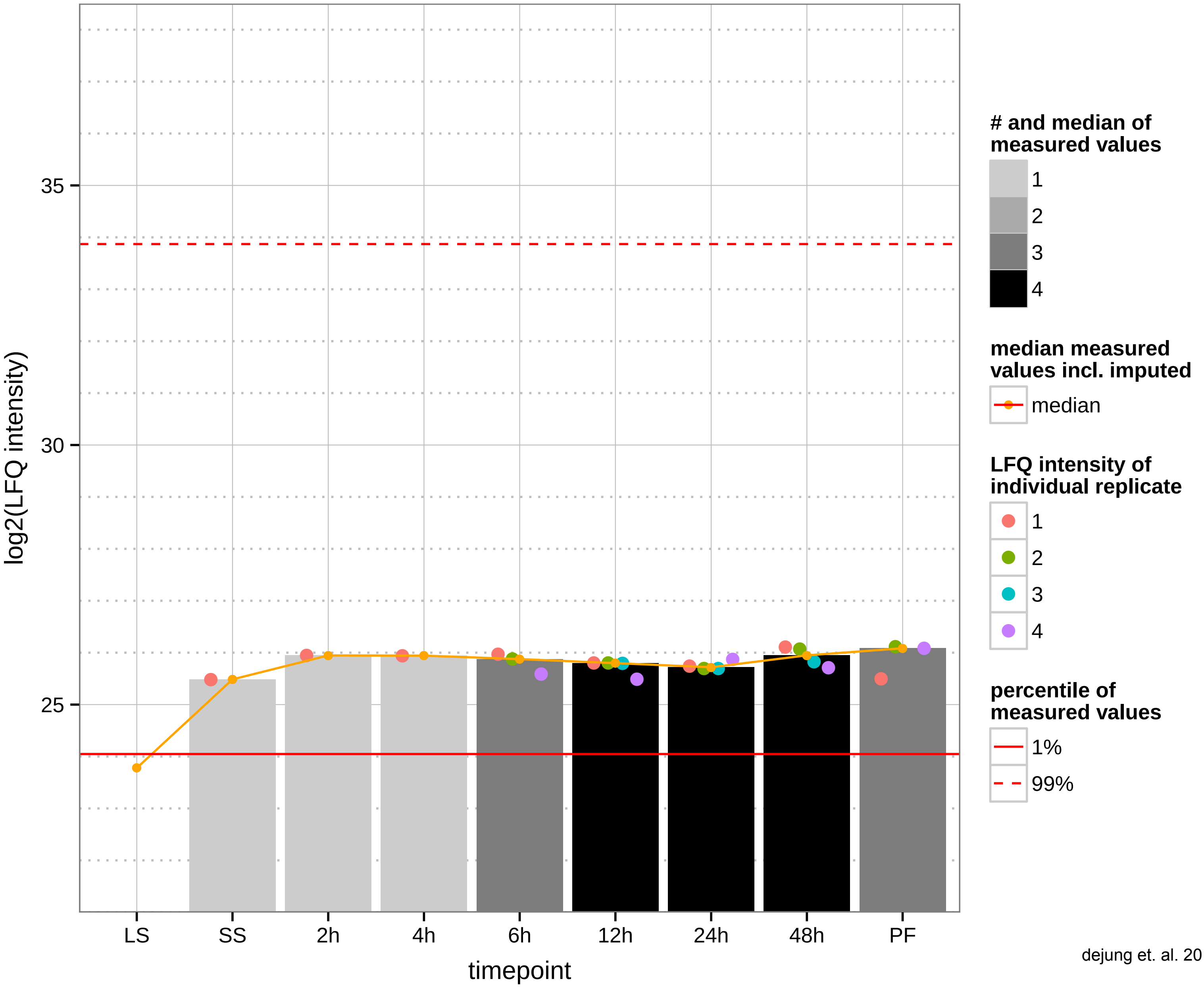
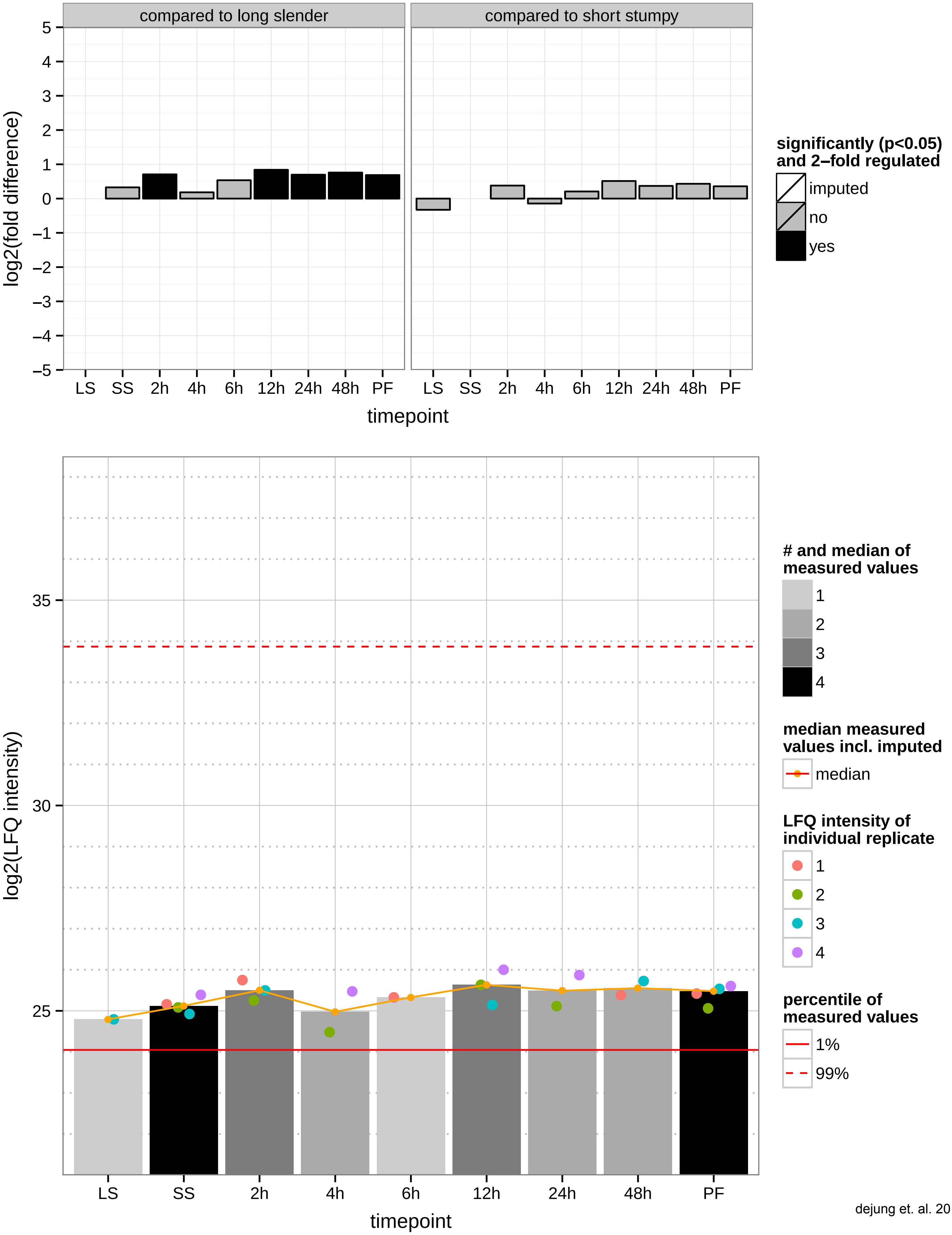
hypothetical protein, conserved
Tb927.11.13820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.13860
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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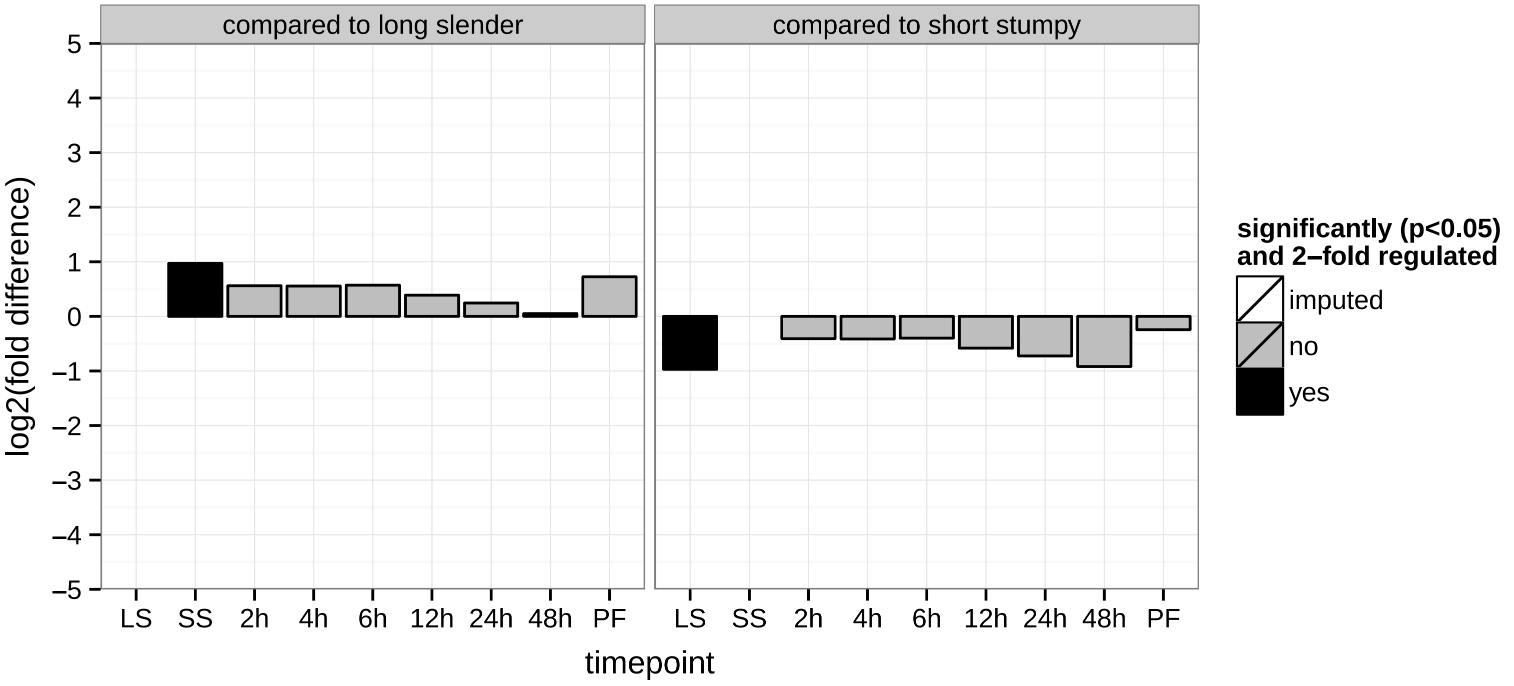
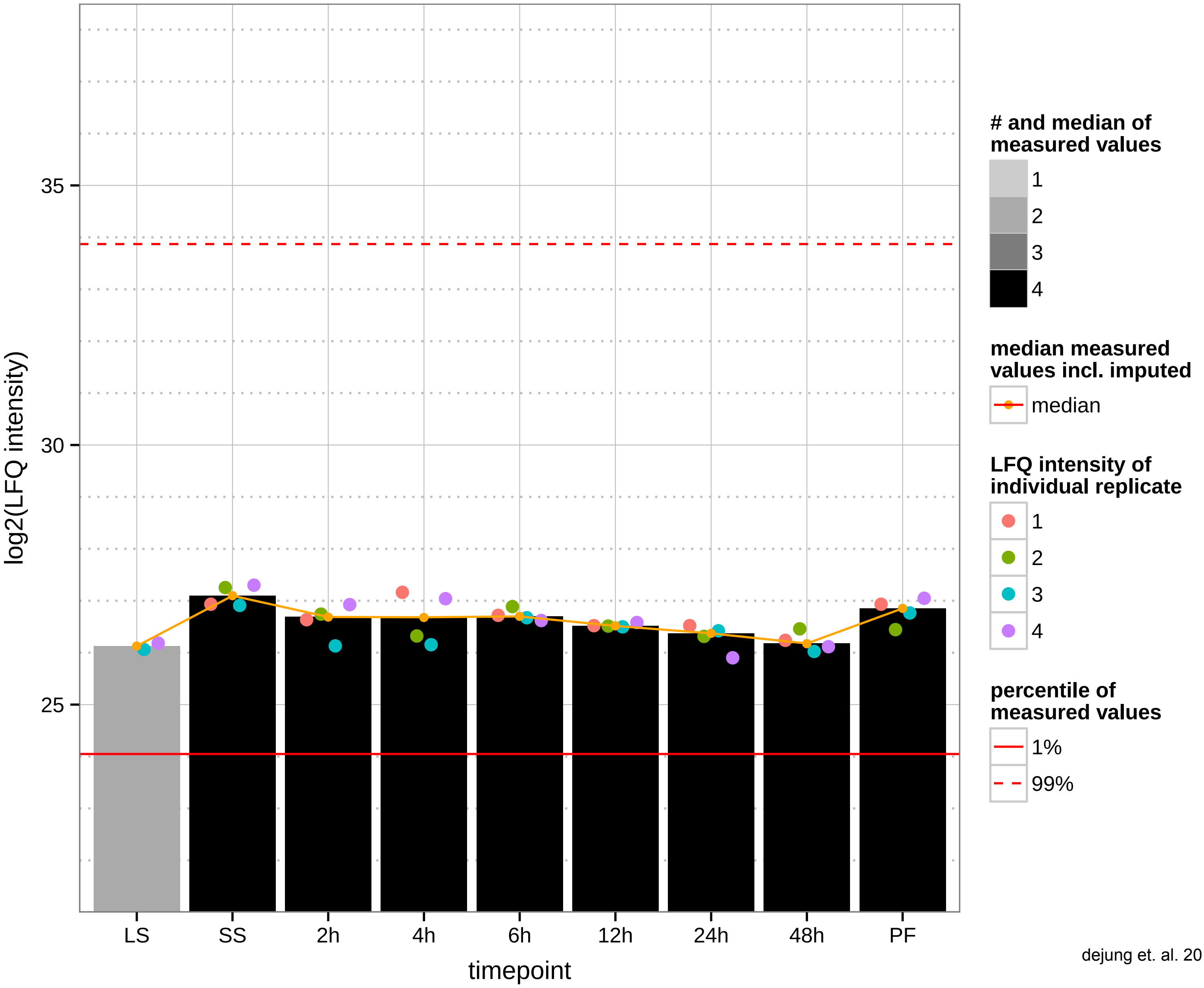
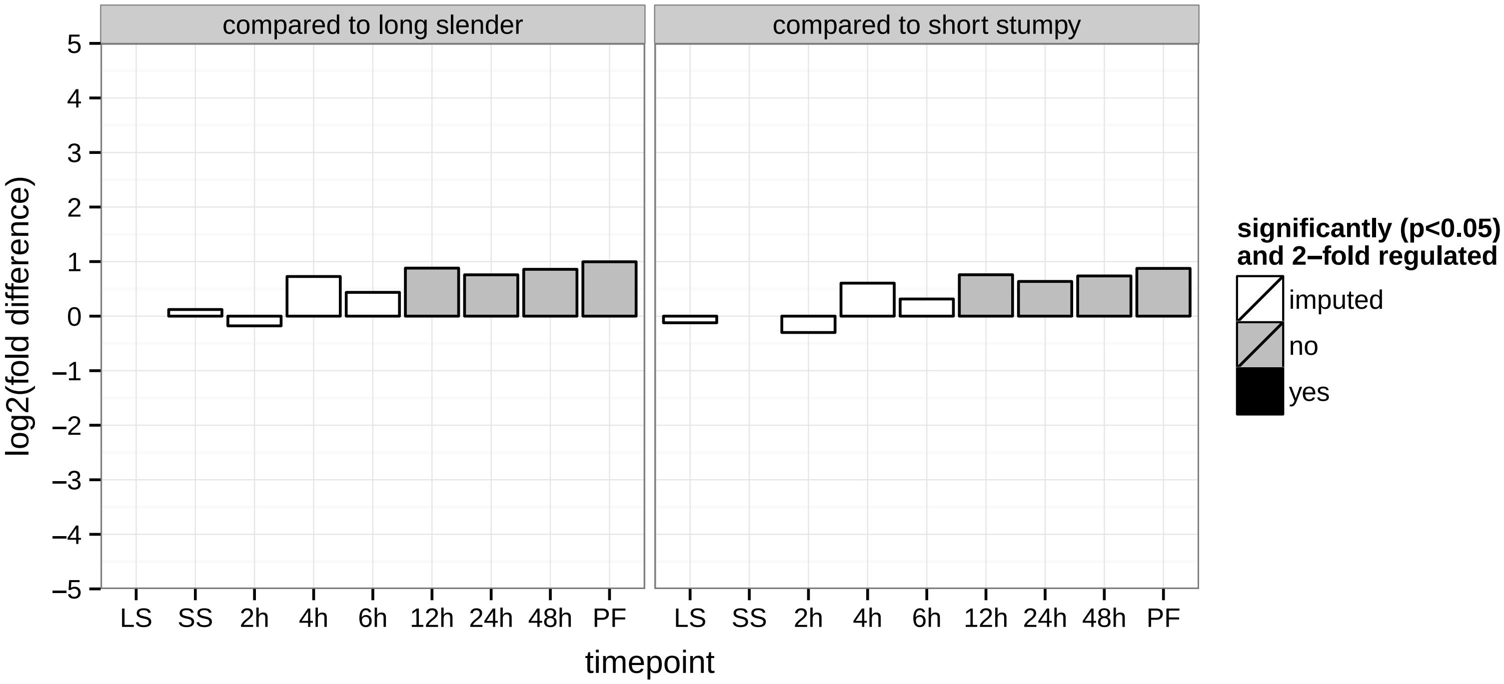
class I transcription factor A, subunit 1 (CITFA−1)
Tb927.11.1390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

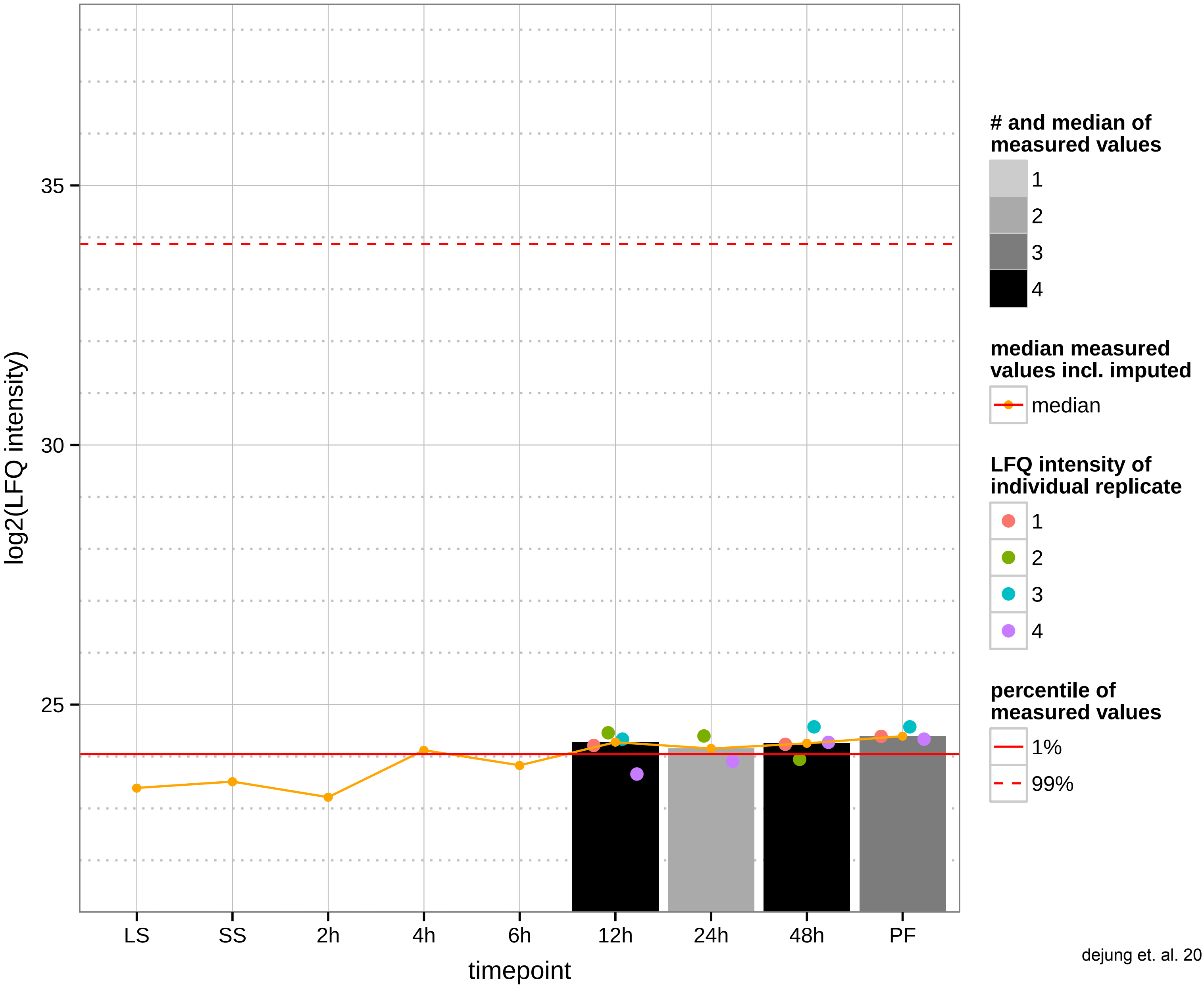




dejung et. al. 2015

centrin, putative
Tb927.11.13900
AGOF: calcium ion binding
AGOC: cilium basal body
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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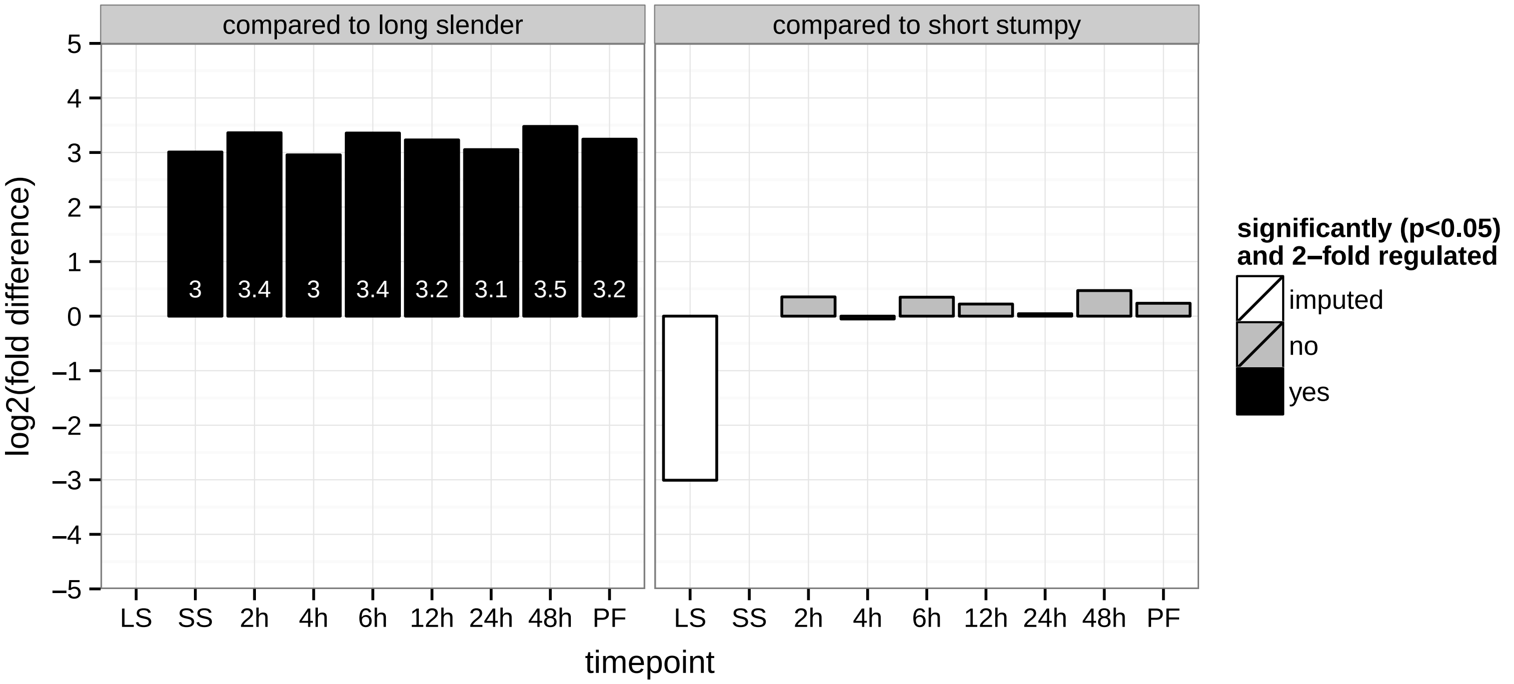
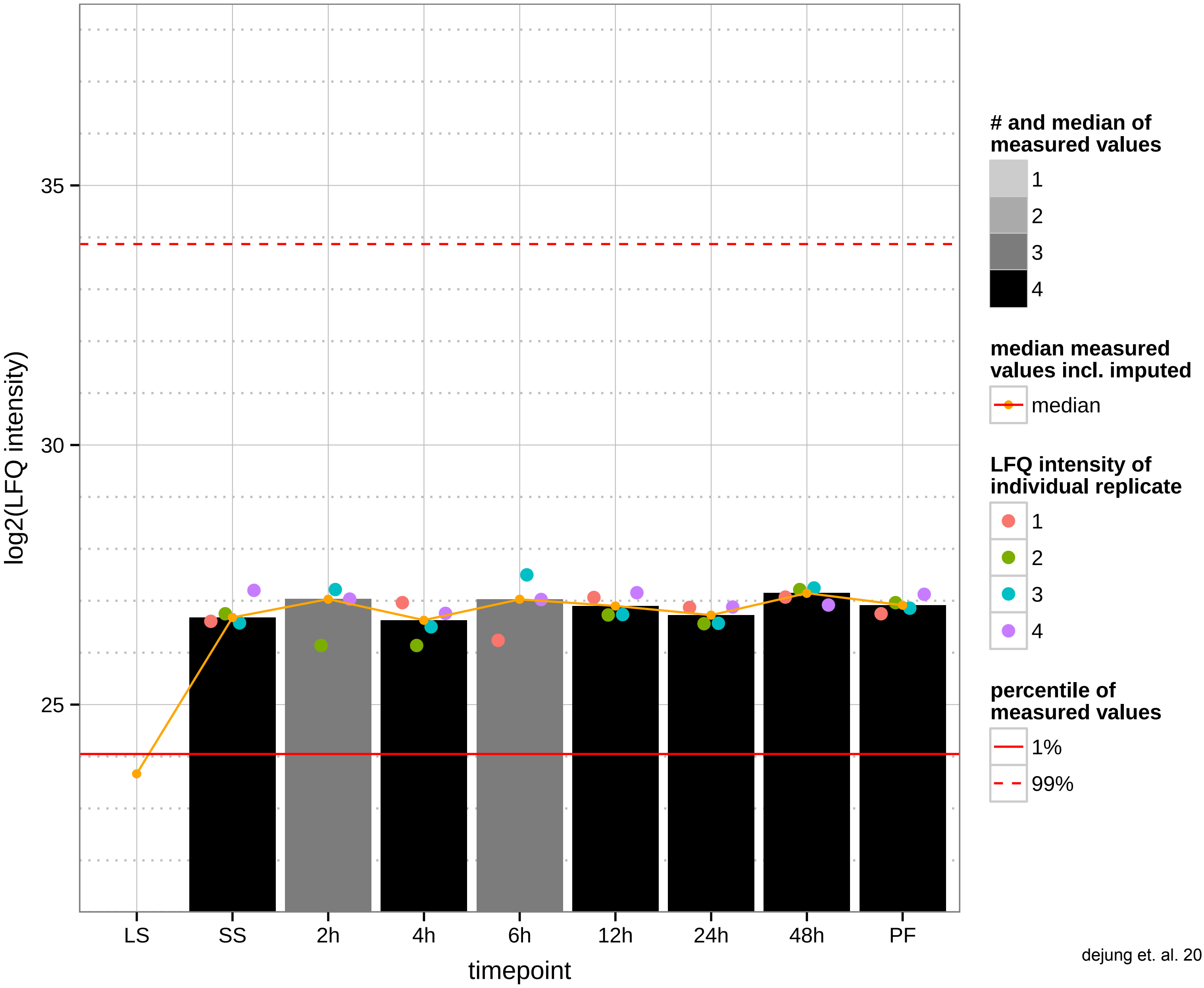
hypothetical protein, conserved
Tb927.11.1400
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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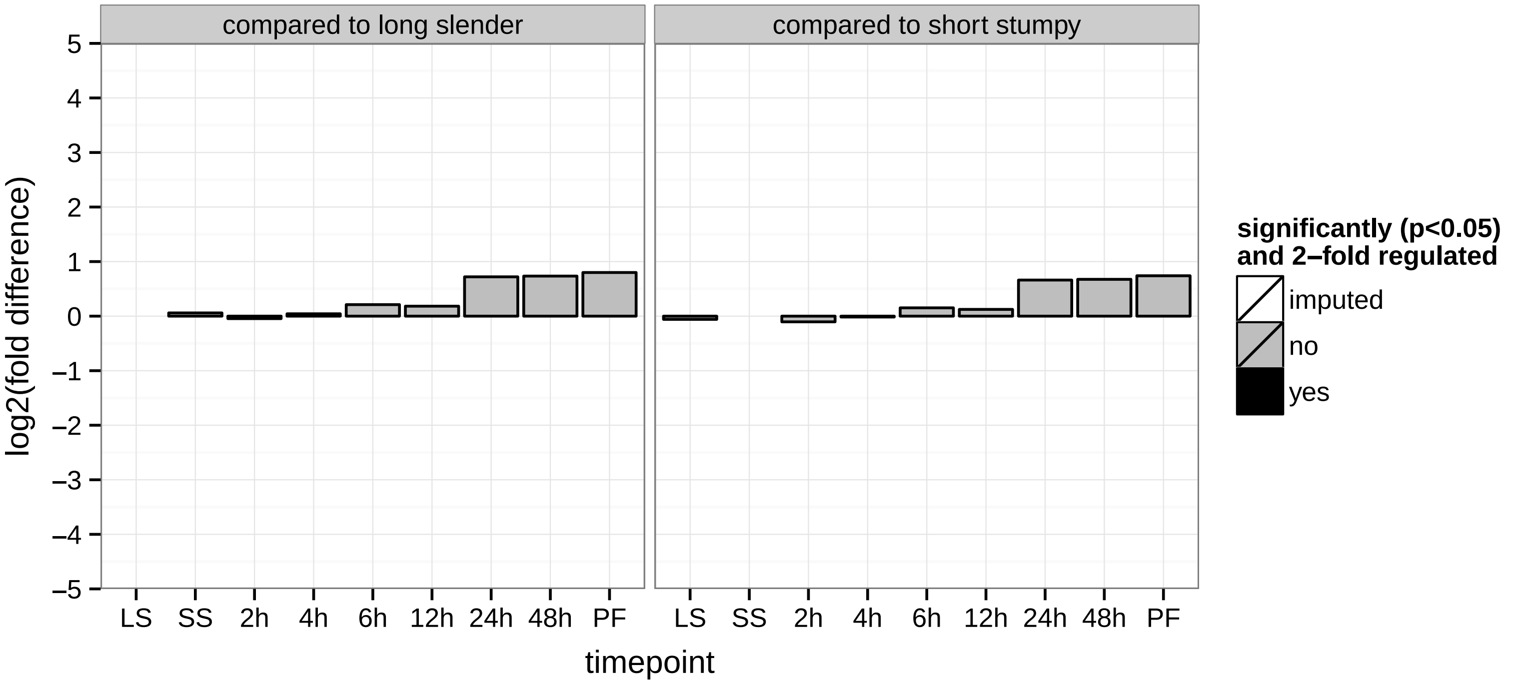
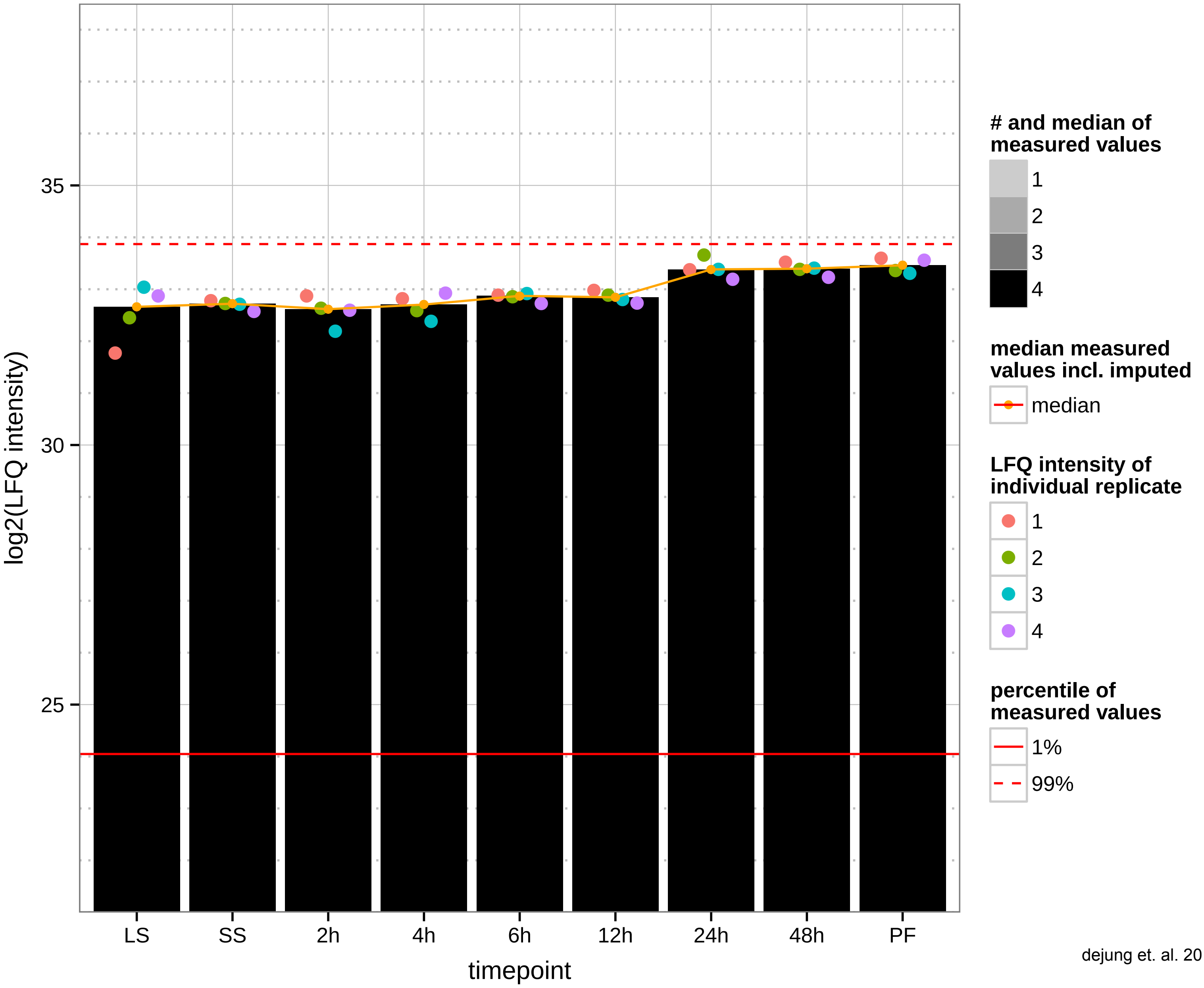
NRBD1, p34 (NRBD1), RNA–binding protein (NRBD2)
Tb927.11.14020;Tb927.11.14000
AGOF: RNA binding, protein binding
AGOC: nucleus
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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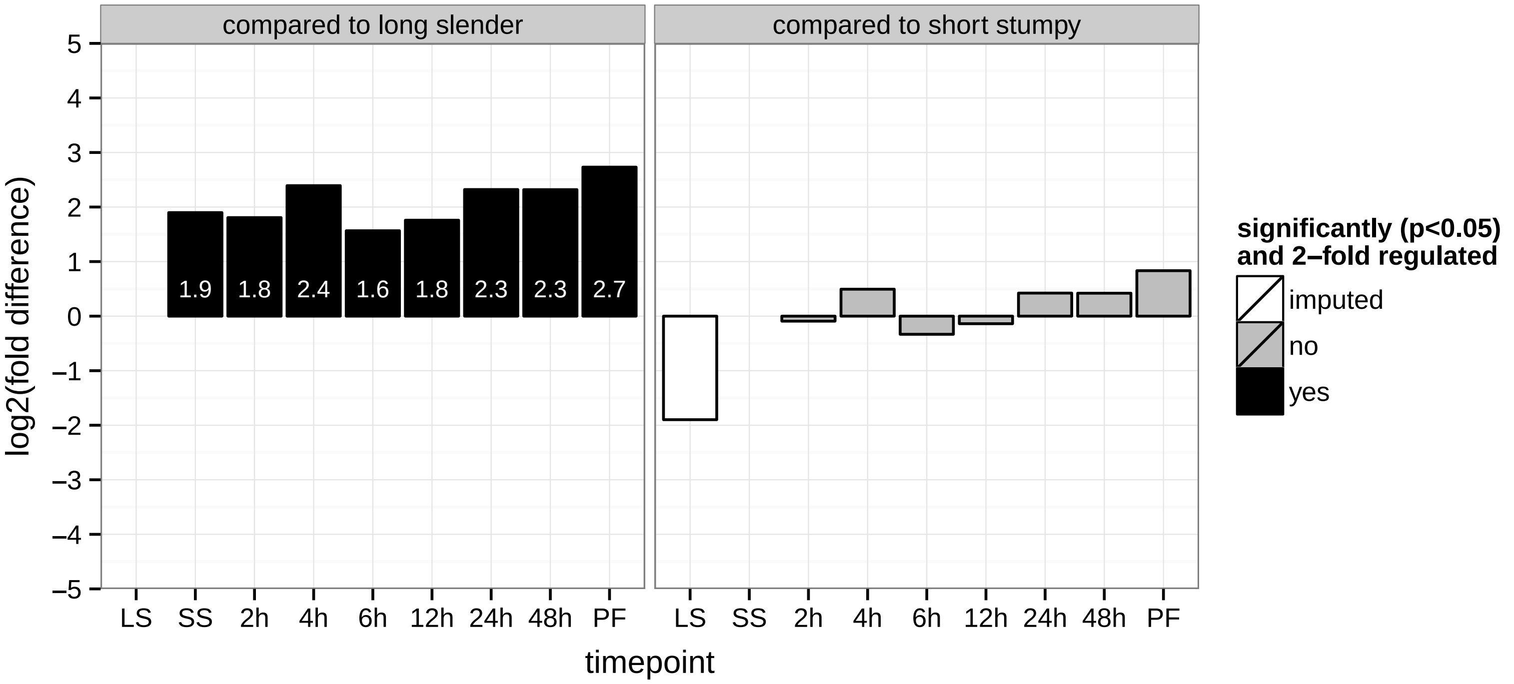
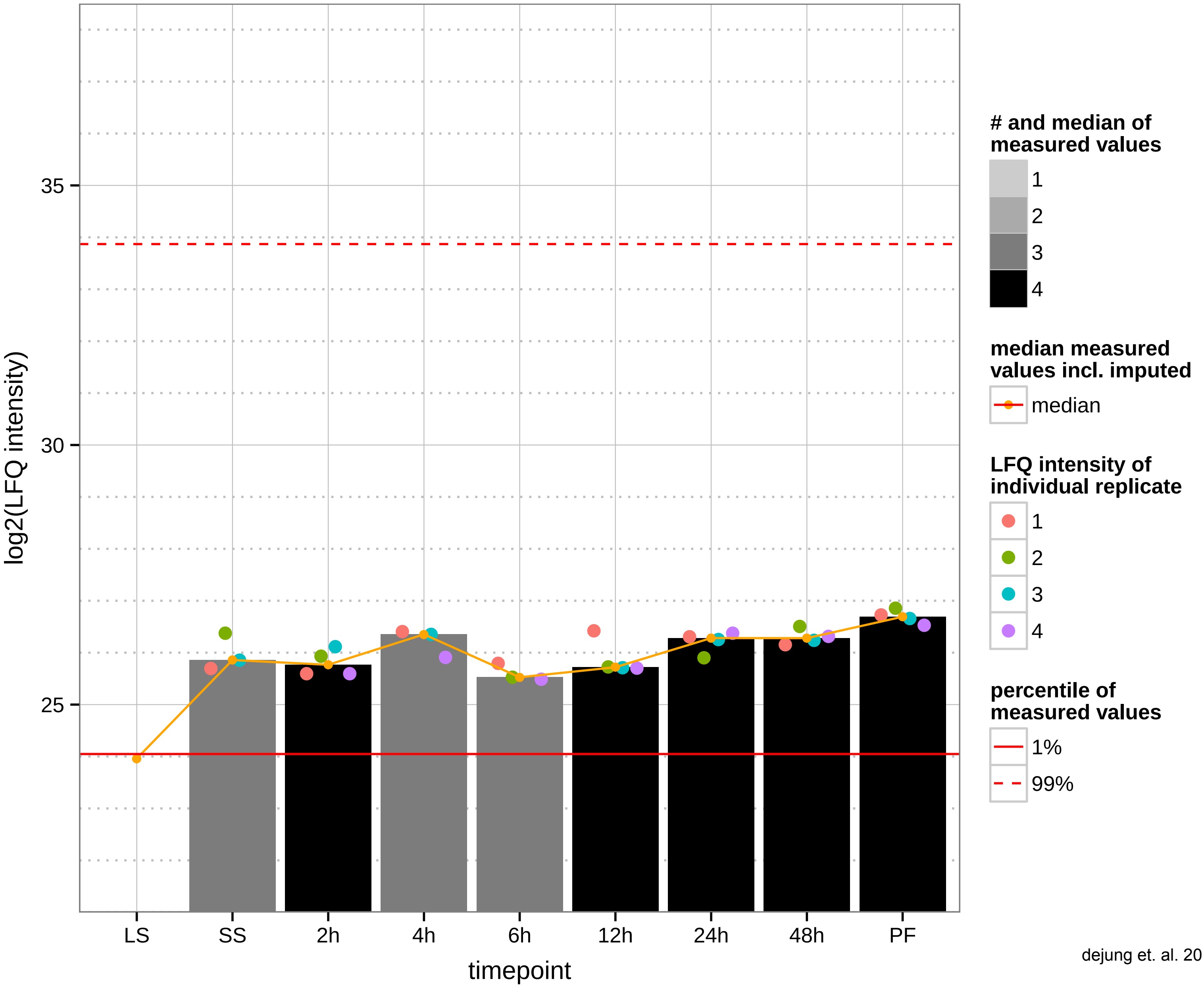
cyclin 2, G1 cyclin (CYC2)
Tb927.11.14080
AGOF: cyclin binding, cyclin–dependent protein kinase regulator activity, protein binding
AGOC: cyclin–dependent protein kinase holoenzyme complex
AGOP: cell cycle
PGOF: protein kinase binding
PGOC: null
PGOP: regulation of cyclin–dependent protein kinase activity





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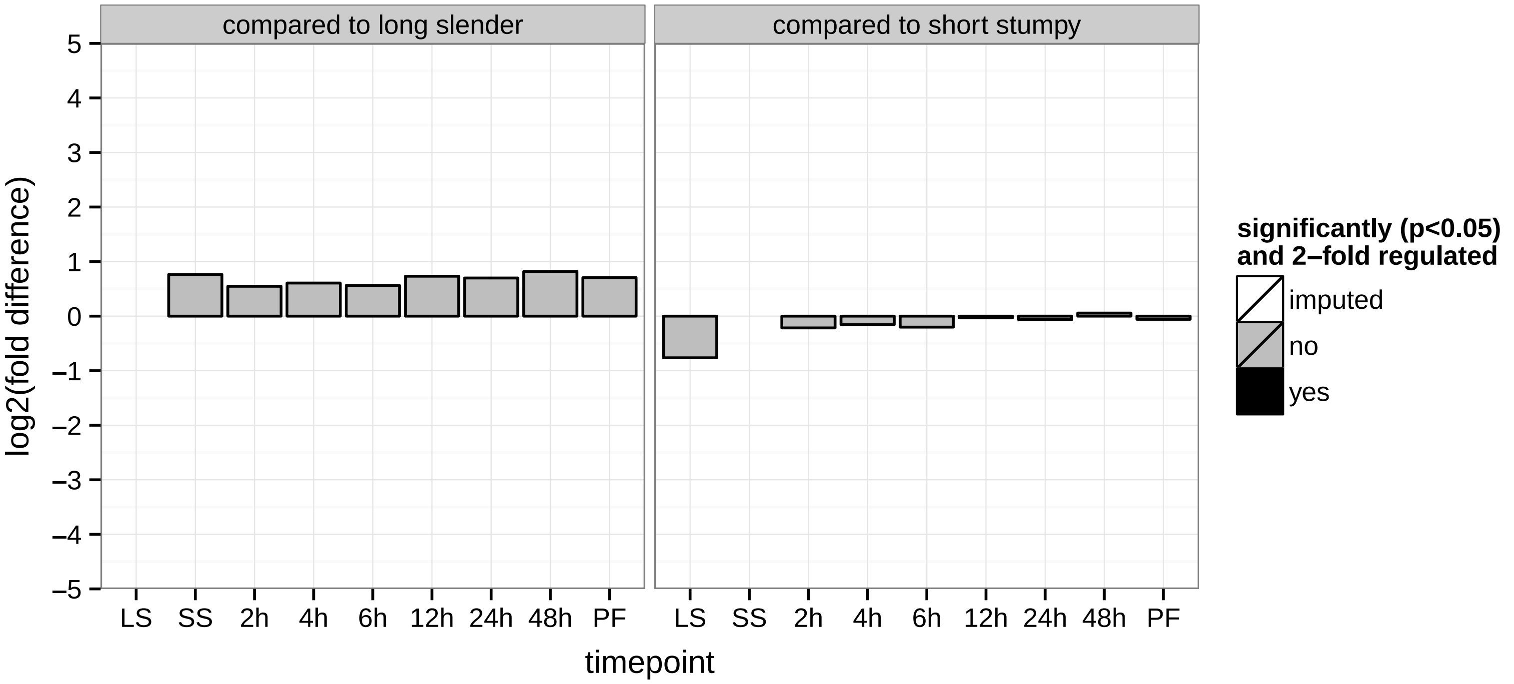
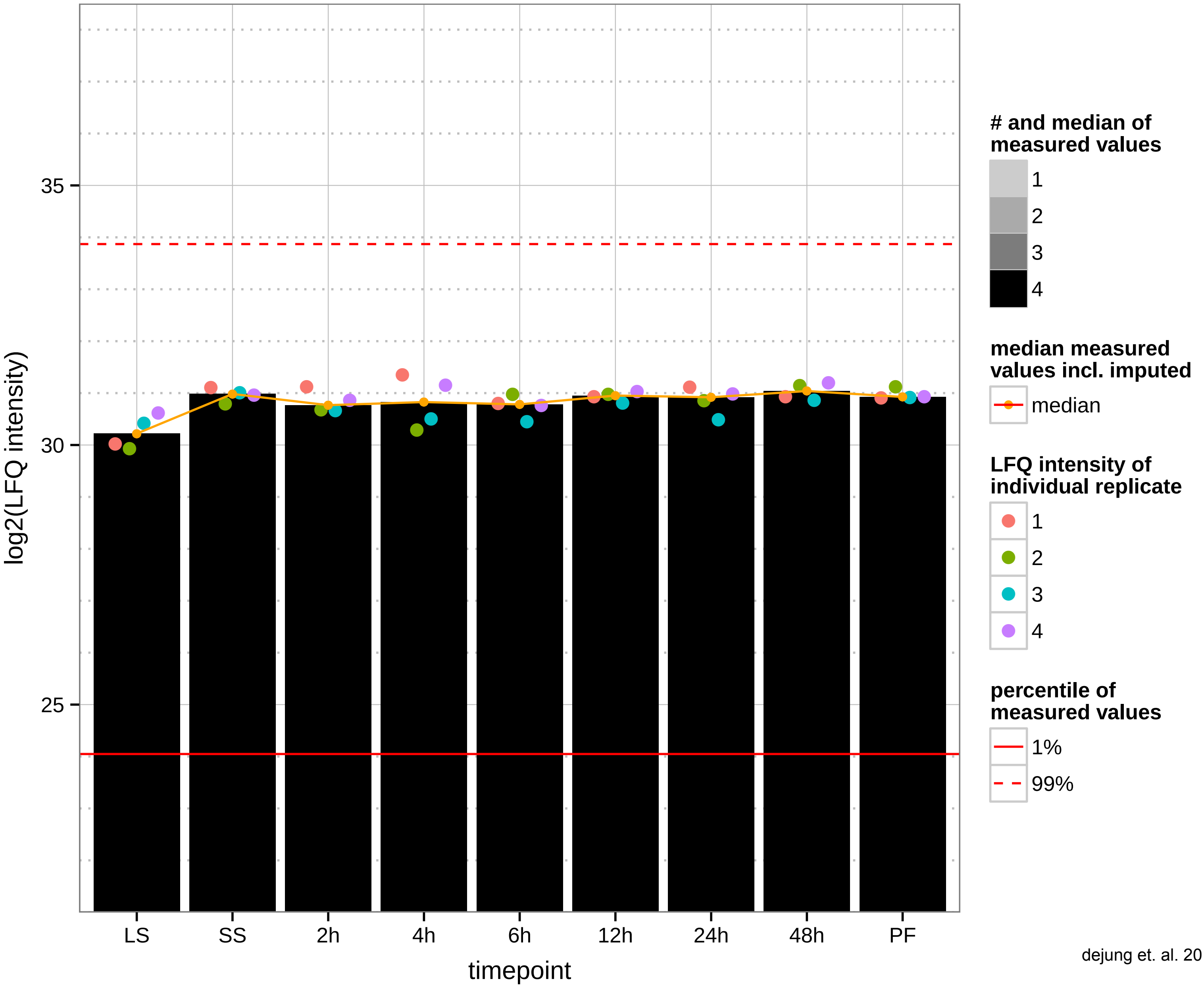
hypothetical protein, conserved
Tb927.11.14090
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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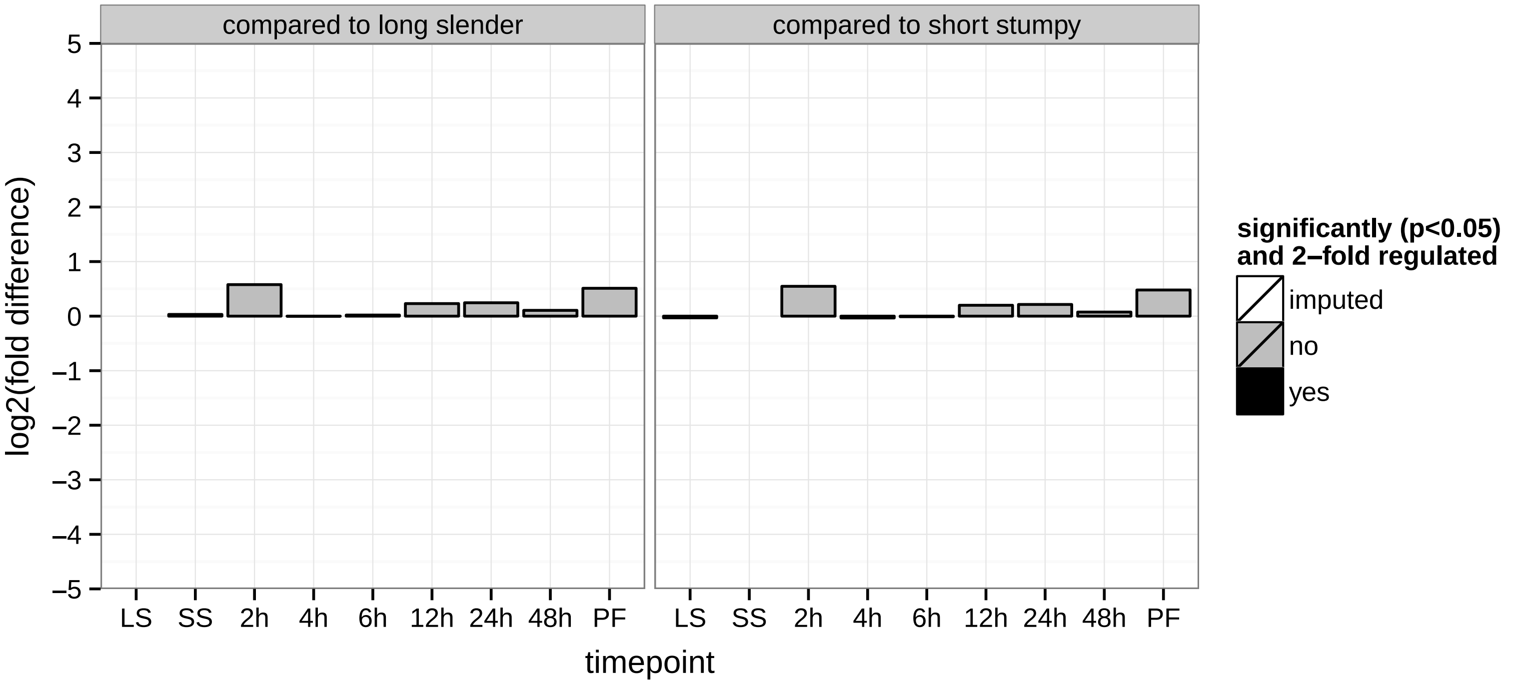
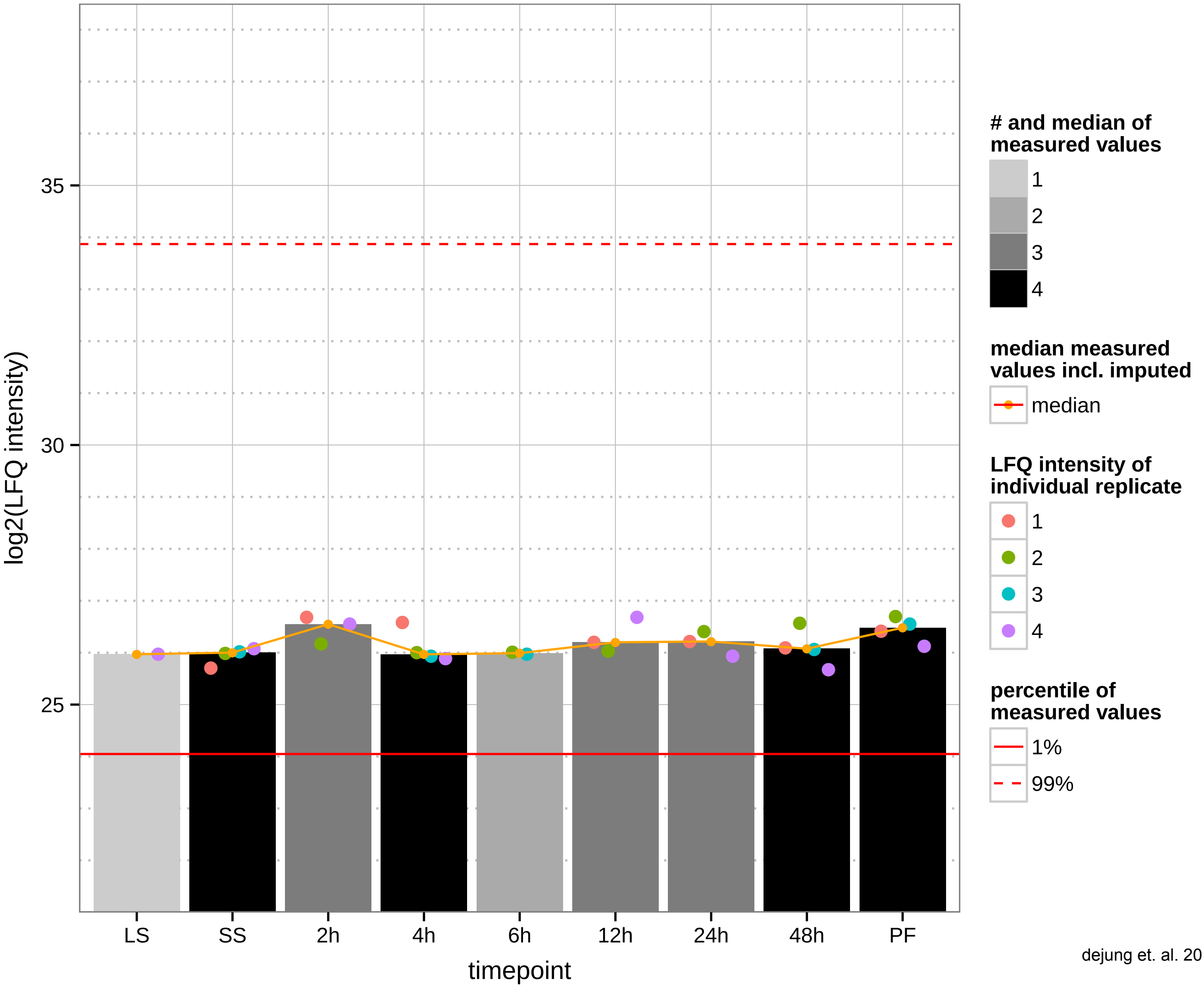
class I transcription factor A, subunit 3 (CITFA–3)
Tb927.11.1410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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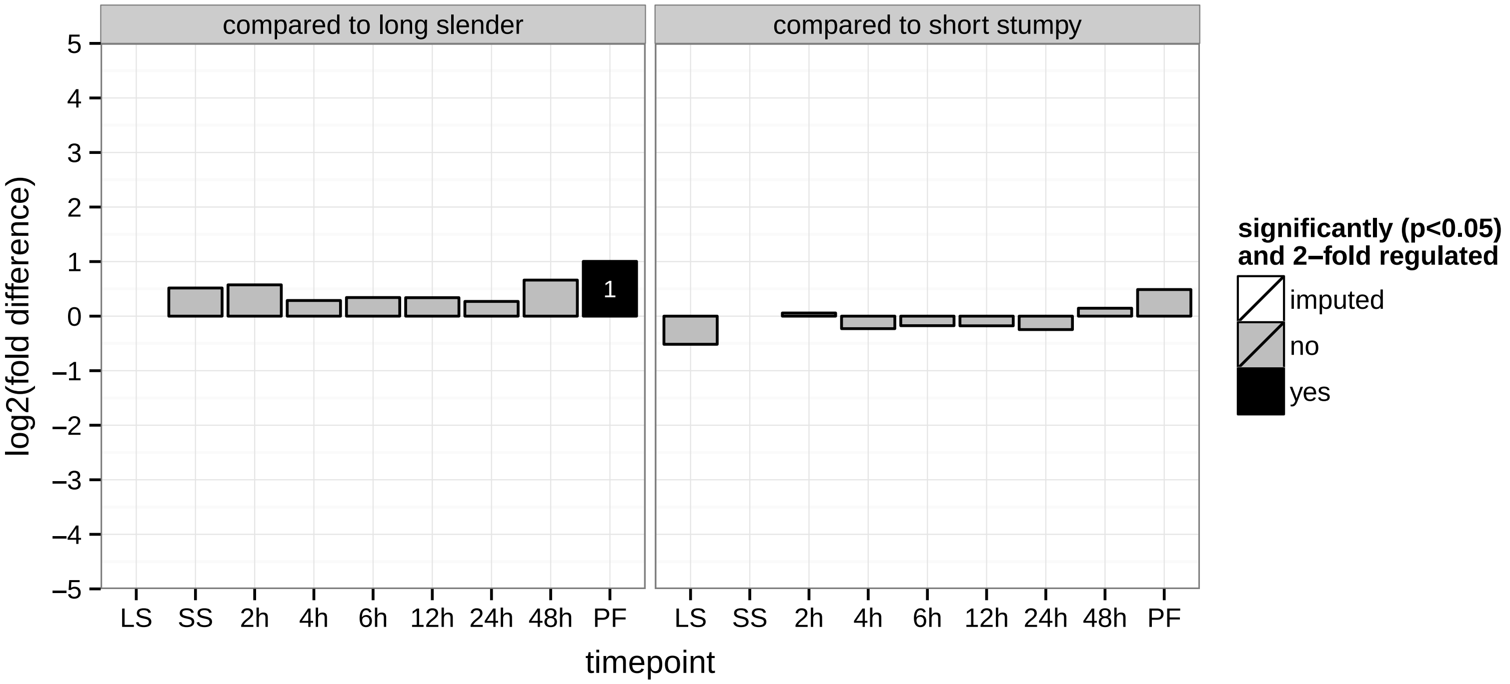
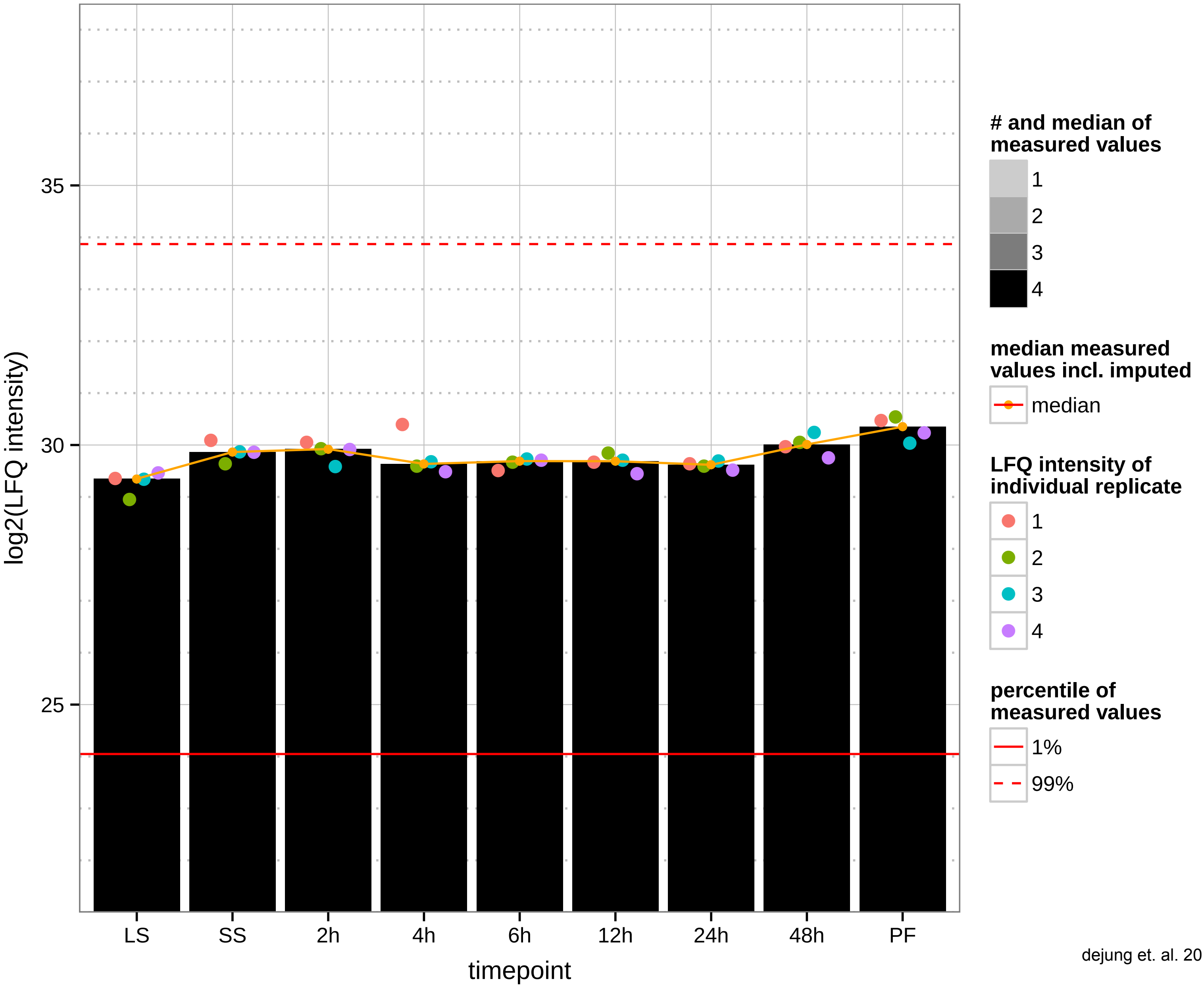
DRBD4 (DRBD4)
Tb927.11.14100
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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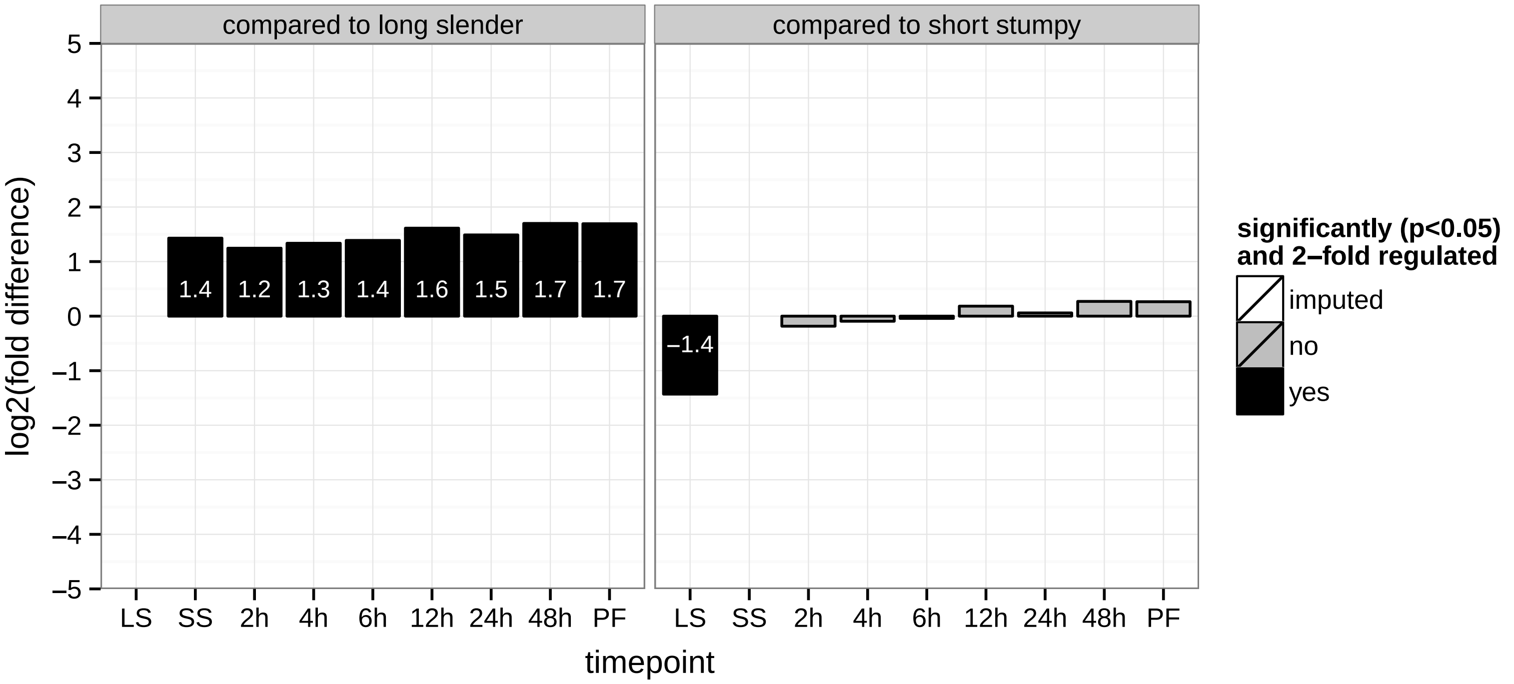
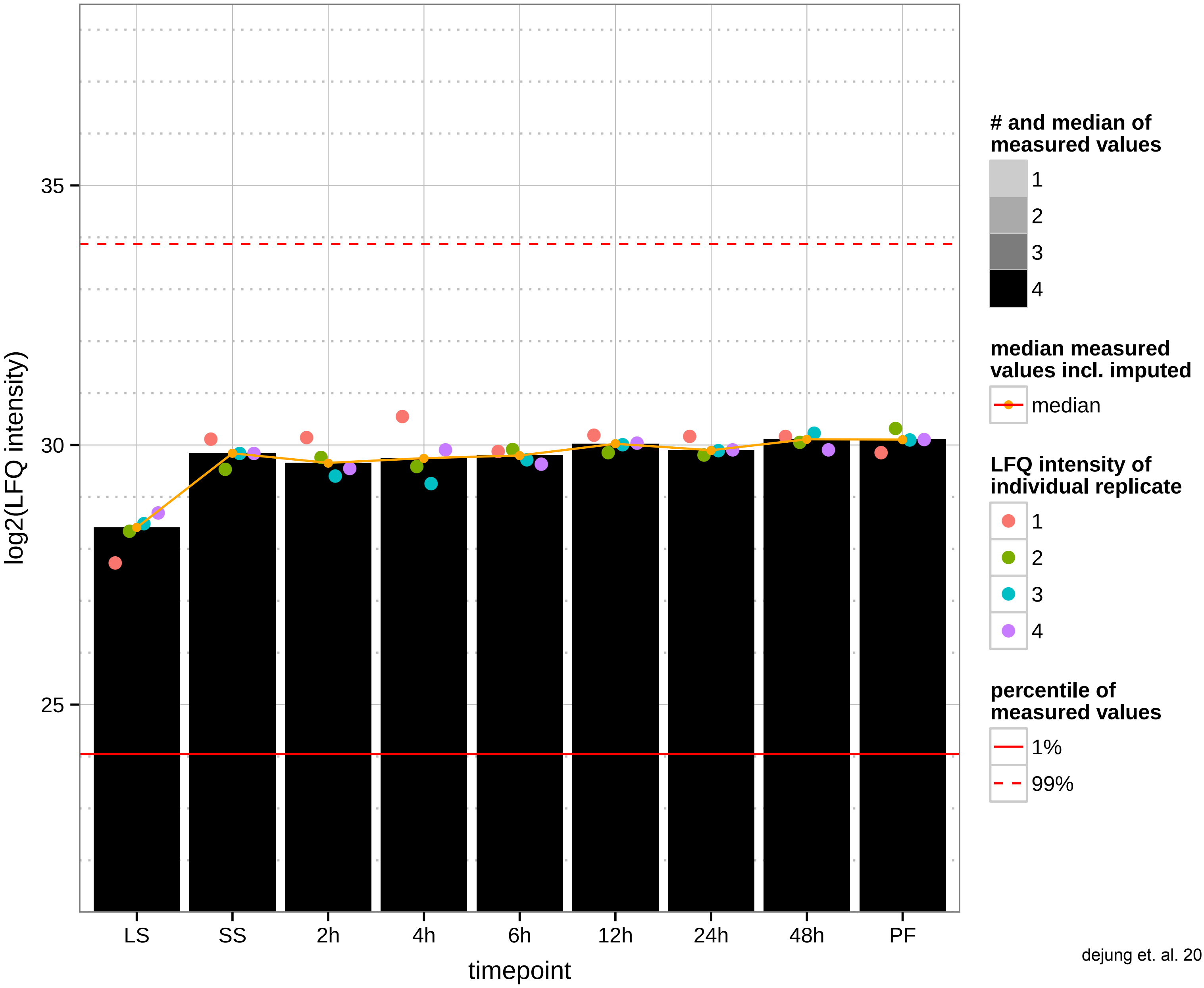
phenylalanyl–tRNA synthetase alpha chain, putative
Tb927.11.14120
AGOF: ATP binding, phenylalanine–tRNA ligase activity, tRNA binding
AGOC: cytoplasm
AGOP: phenylalanyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, nucleotide binding, phenylalanine–tRNA ligase activity, tRNA binding
PGOC: cytoplasm
PGOP: phenylalanyl–tRNA aminoacylation, tRNA aminoacylation, tRNA aminoacylation for protein translation





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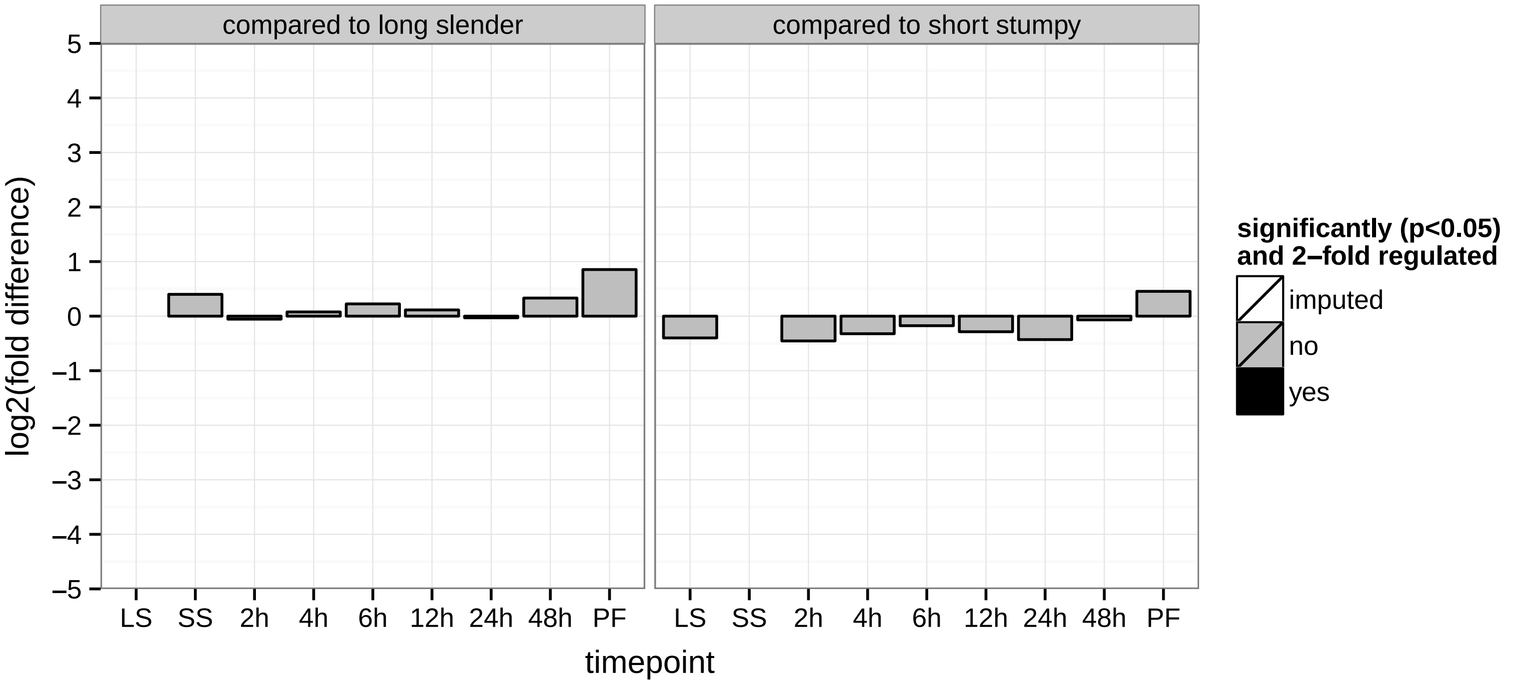
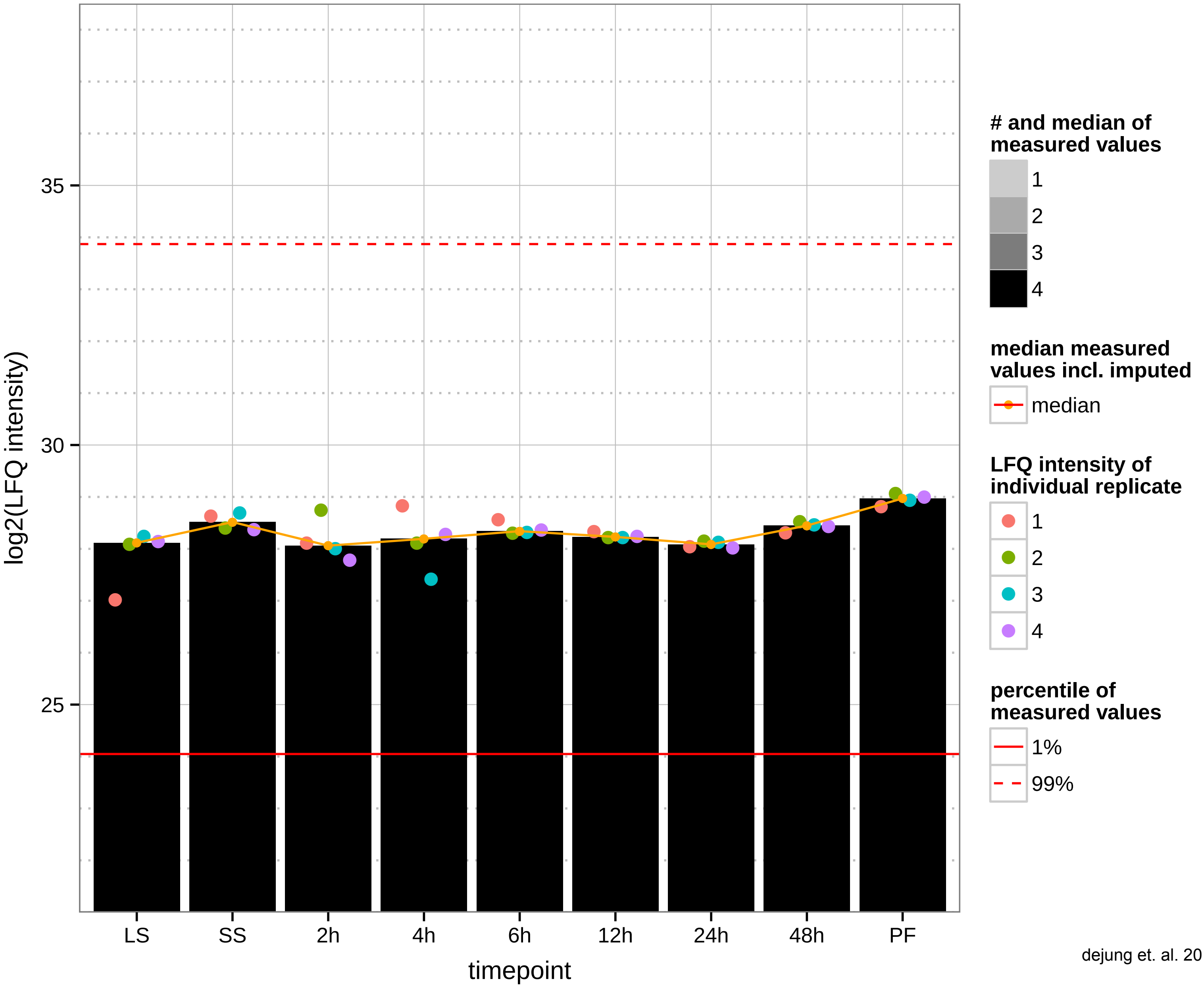
ethanolamine–phosphate cytidylyltransferase (TbECT)
Tb927.11.14140
AGOF: ethanolamine–phosphate cytidylyltransferase activity, nucleotidyltransferase activity
AGOC: cytosol
AGOP: ethanolamine biosynthetic process, phosphatidylethanolamine biosynthetic process, phospholipid biosynthetic proces
PGOF: catalytic activity, nucleotidyltransferase activity
PGOC: null
PGOP: biosynthetic process





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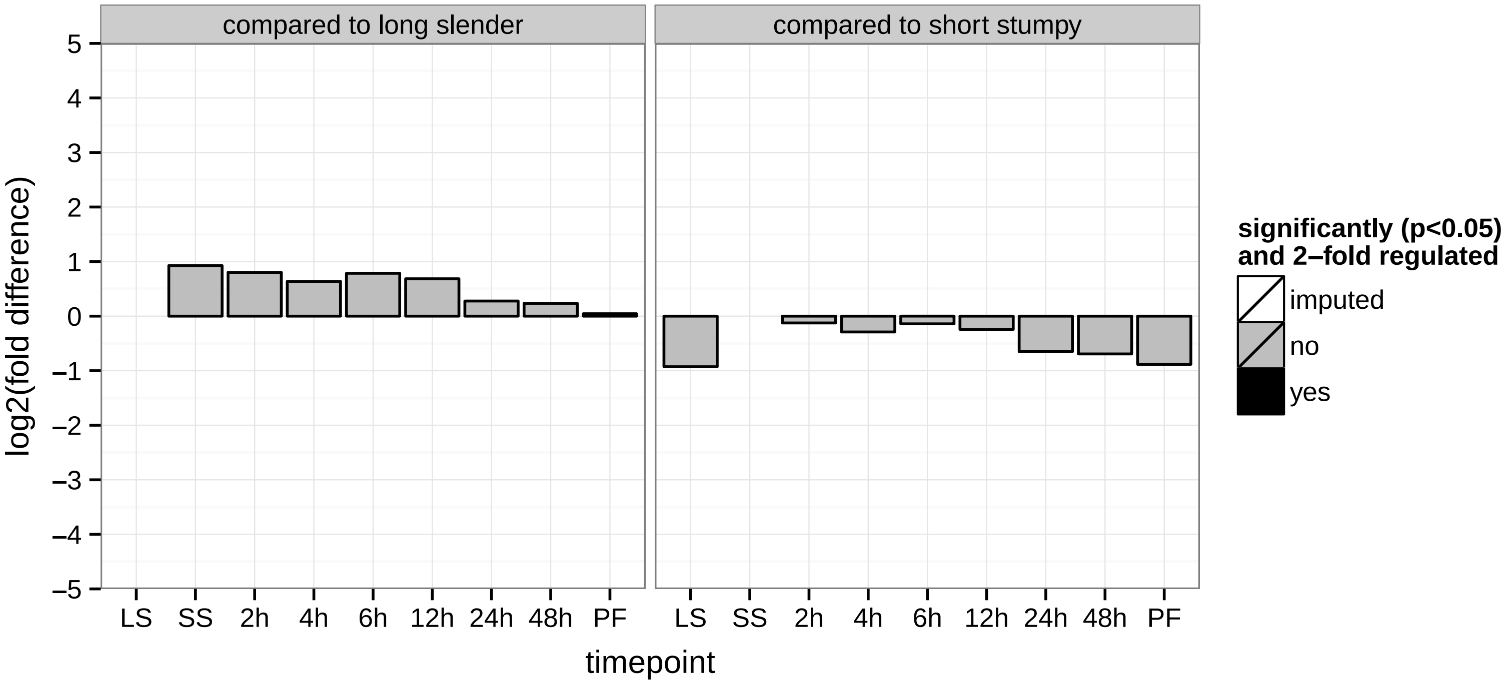
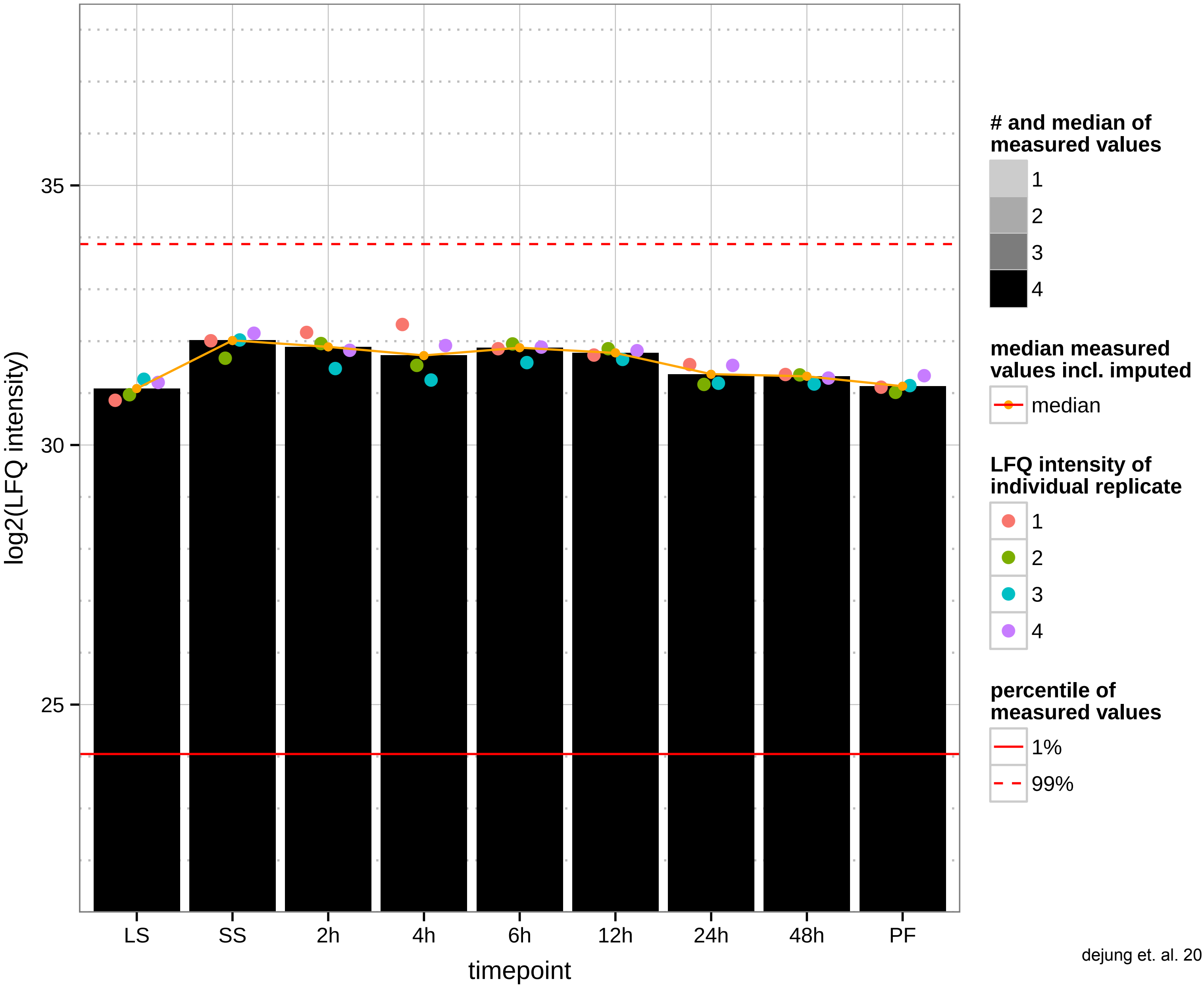
hypothetical protein, conserved
Tb927.11.14190
AGOF: hydrolase activity, acting on ester bonds, nucleic acid binding
AGOC: RNA–induced silencing complex
AGOP: RNA interference
PGOF: hydrolase activity, acting on ester bonds, nucleic acid binding
PGOC: RNA–induced silencing complex
PGOP: gene silencing by RNA





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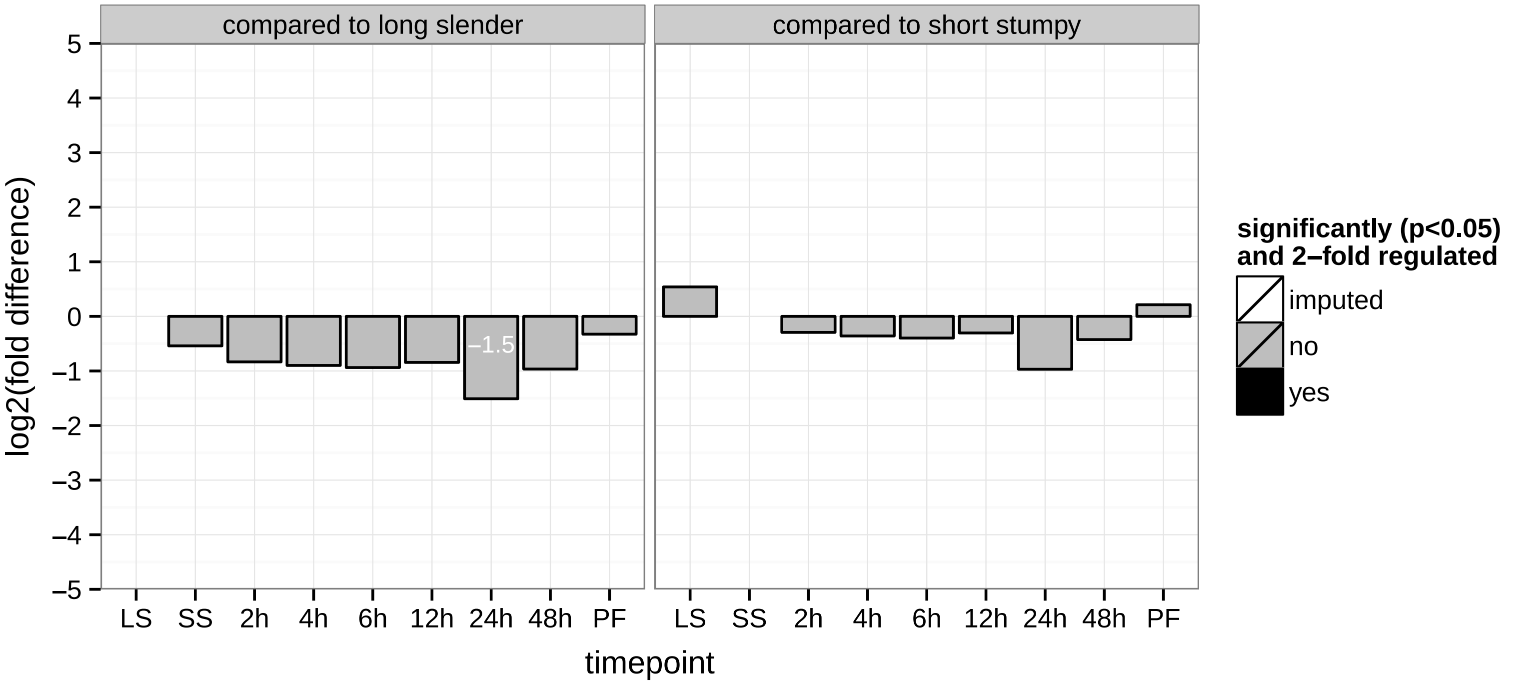
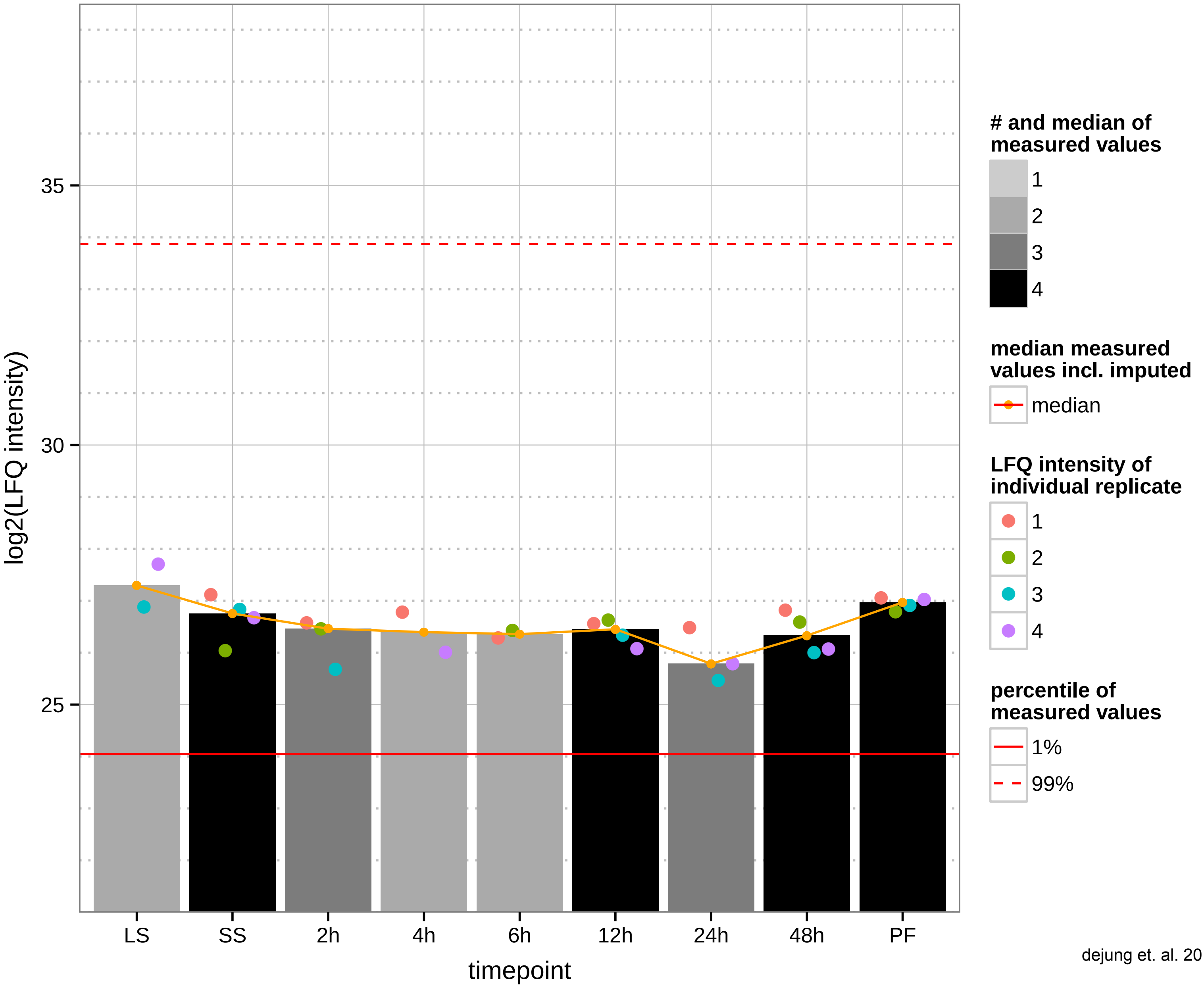
hypothetical protein, conserved
Tb927.11.1420
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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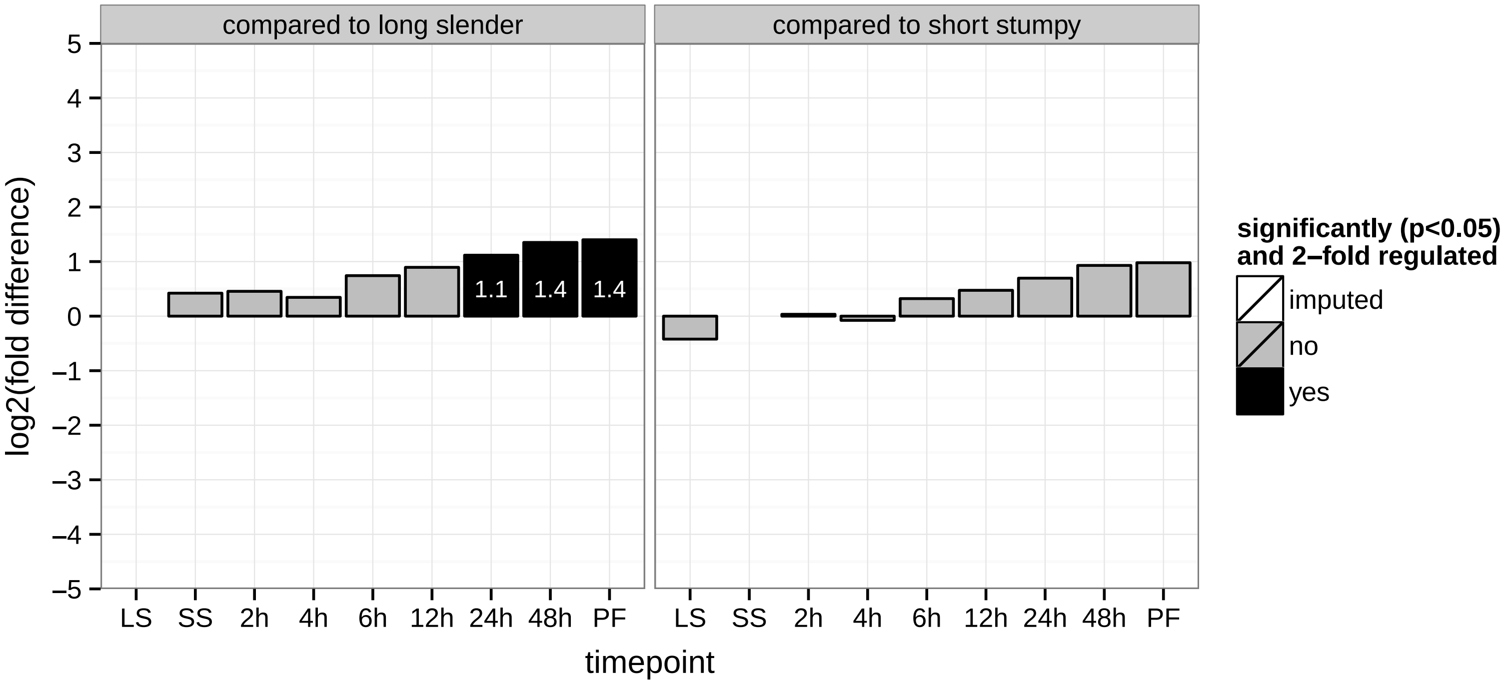
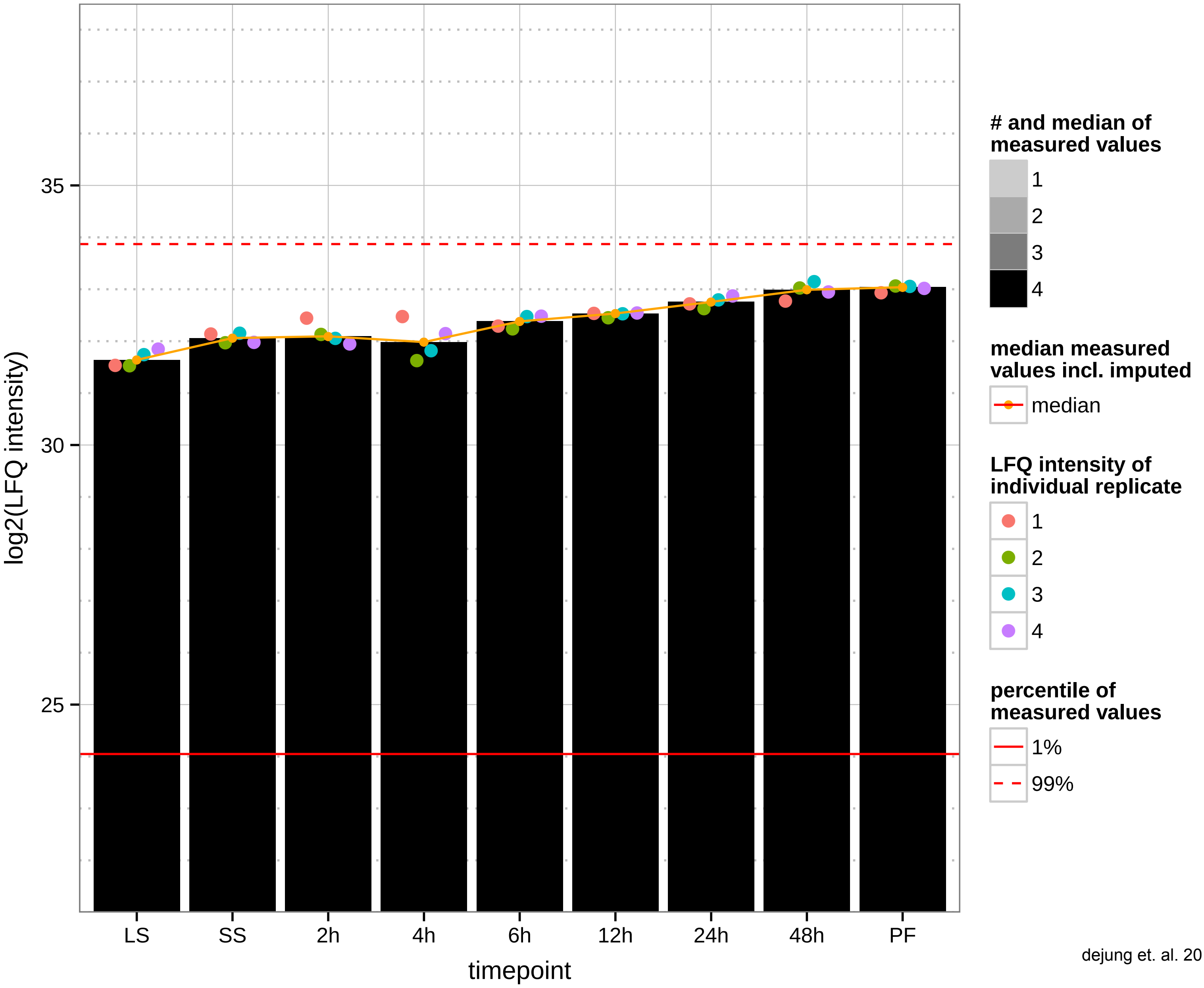
T–complex protein 1, epsilon subunit, putative (TCP–1–epsilon)
Tb927.11.14250
AGOF: ATP binding, unfolded protein binding
AGOC: chaperonin–containing T–complex
AGOP: cellular protein metabolic process, regulation of cell cycle
PGOF: ATP binding, unfolded protein binding
PGOC: null
PGOP: cellular protein metabolic process, protein folding





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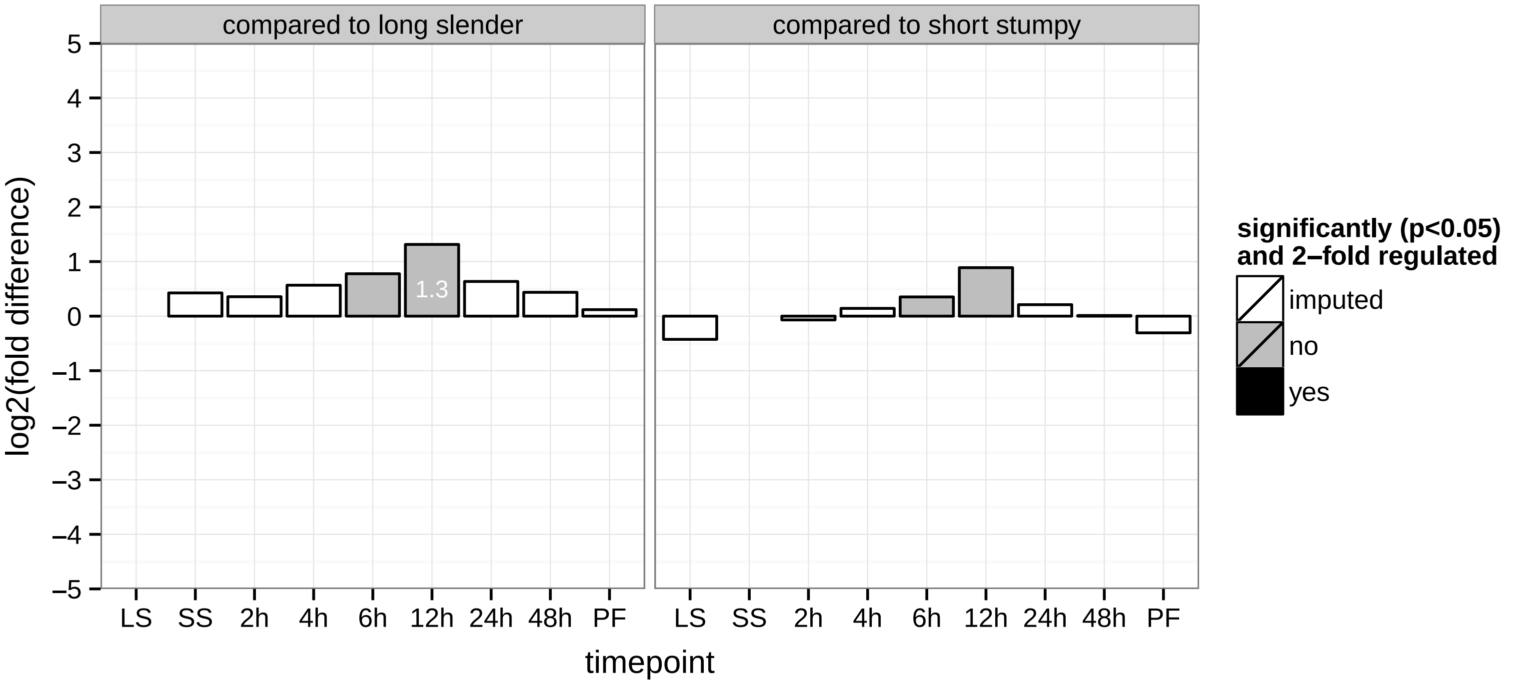
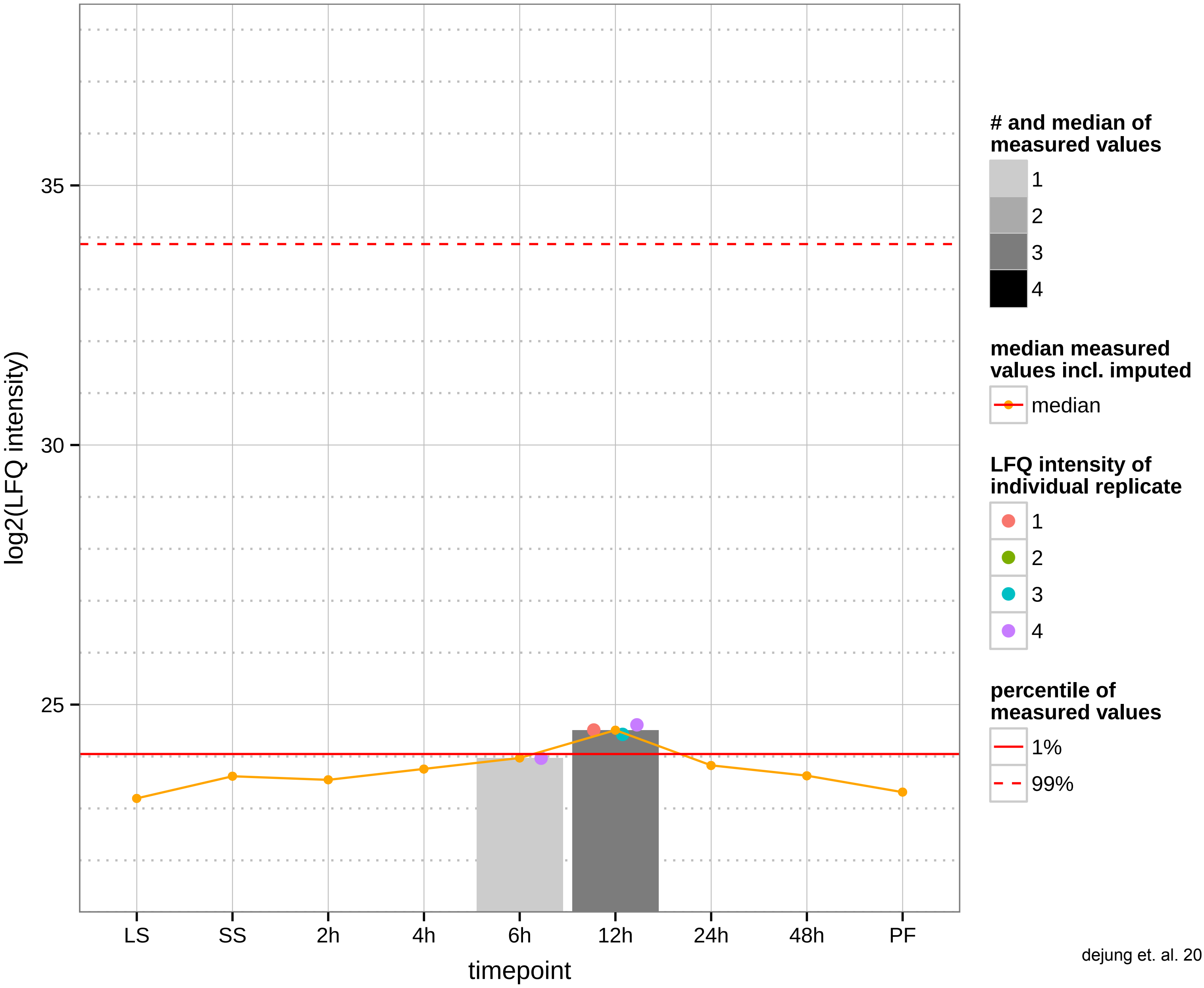
septum formation protein MAF homologue, putative
Tb927.11.14280
AGOF: null
AGOC: cytoplasm
AGOP: barrier septum assembly
PGOF: null
PGOC: cytoplasm
PGOP: null





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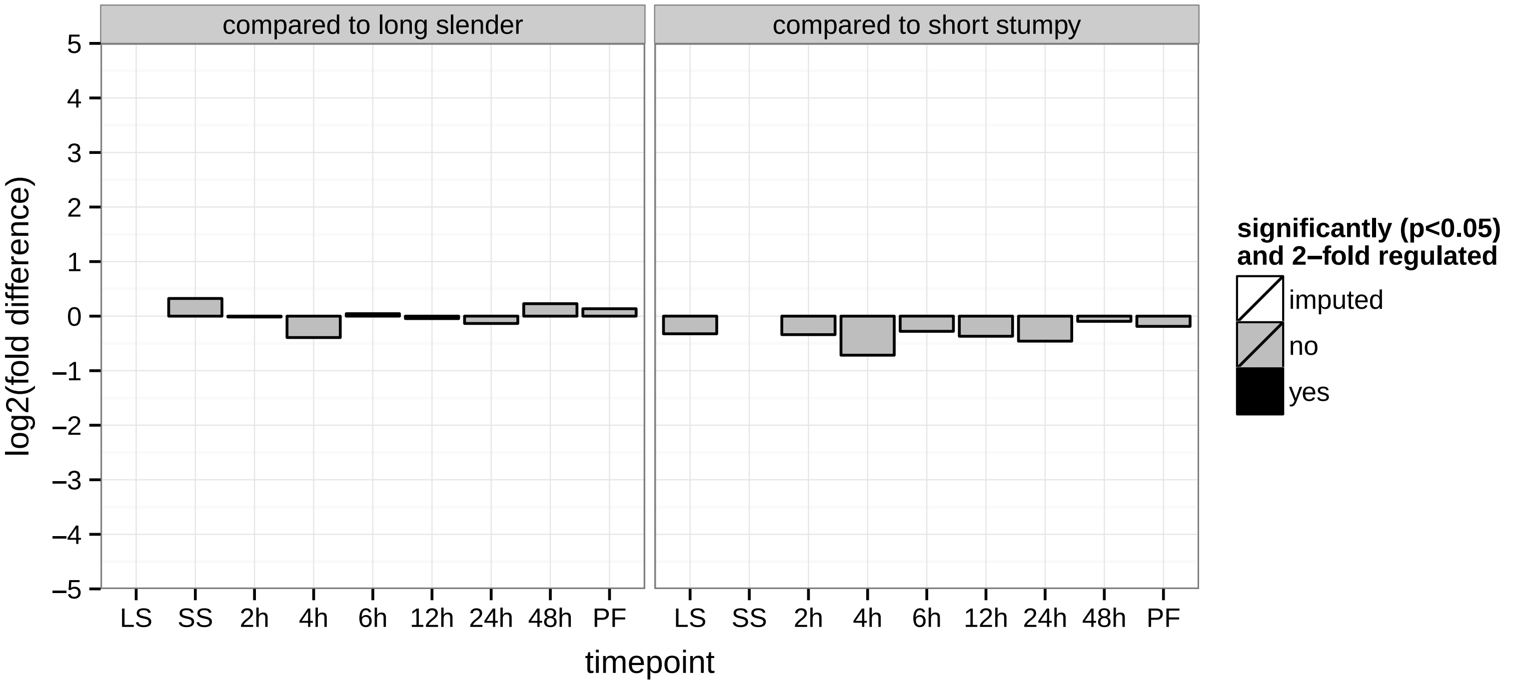
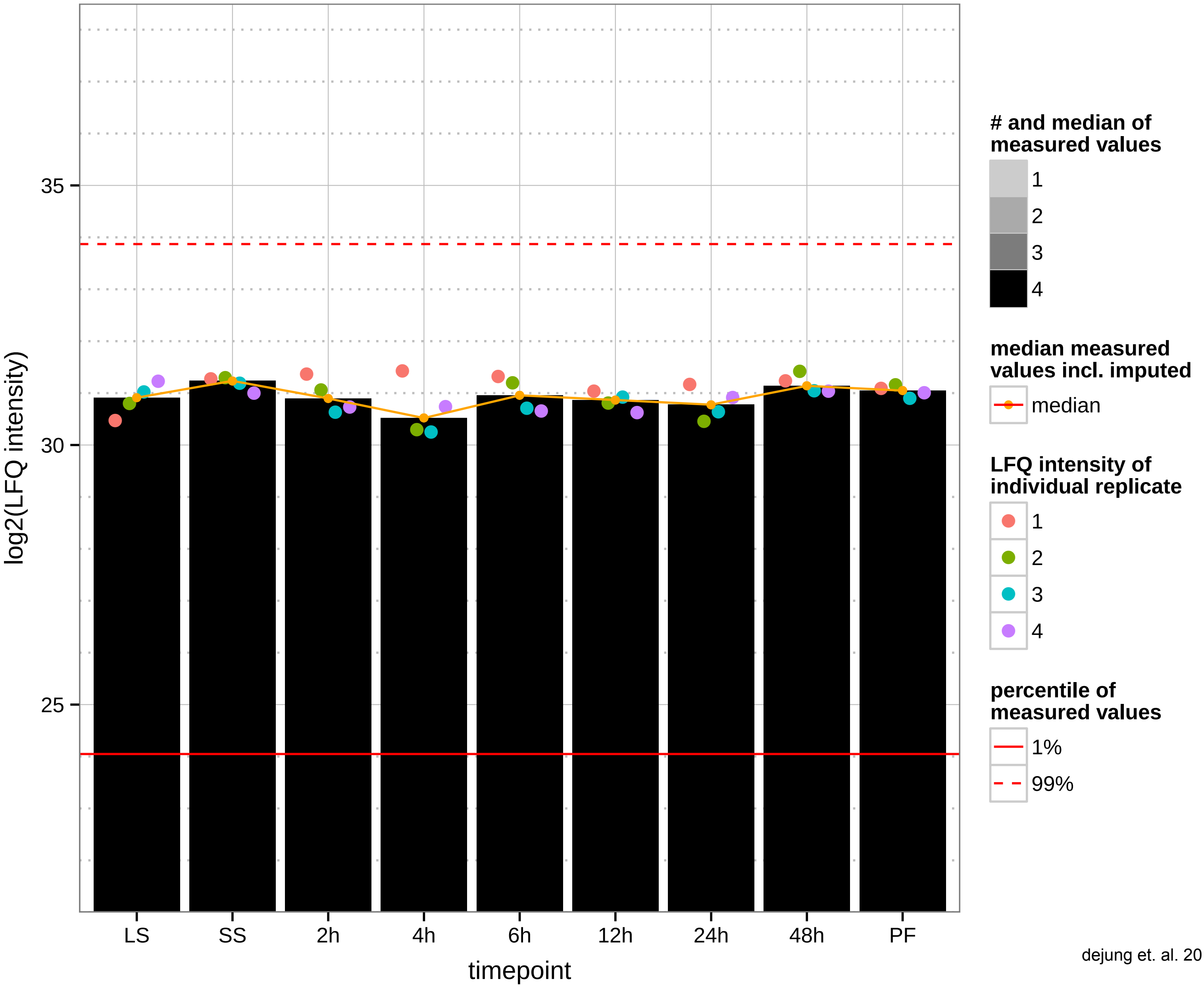
hypothetical protein, conserved
Tb927.11.1430
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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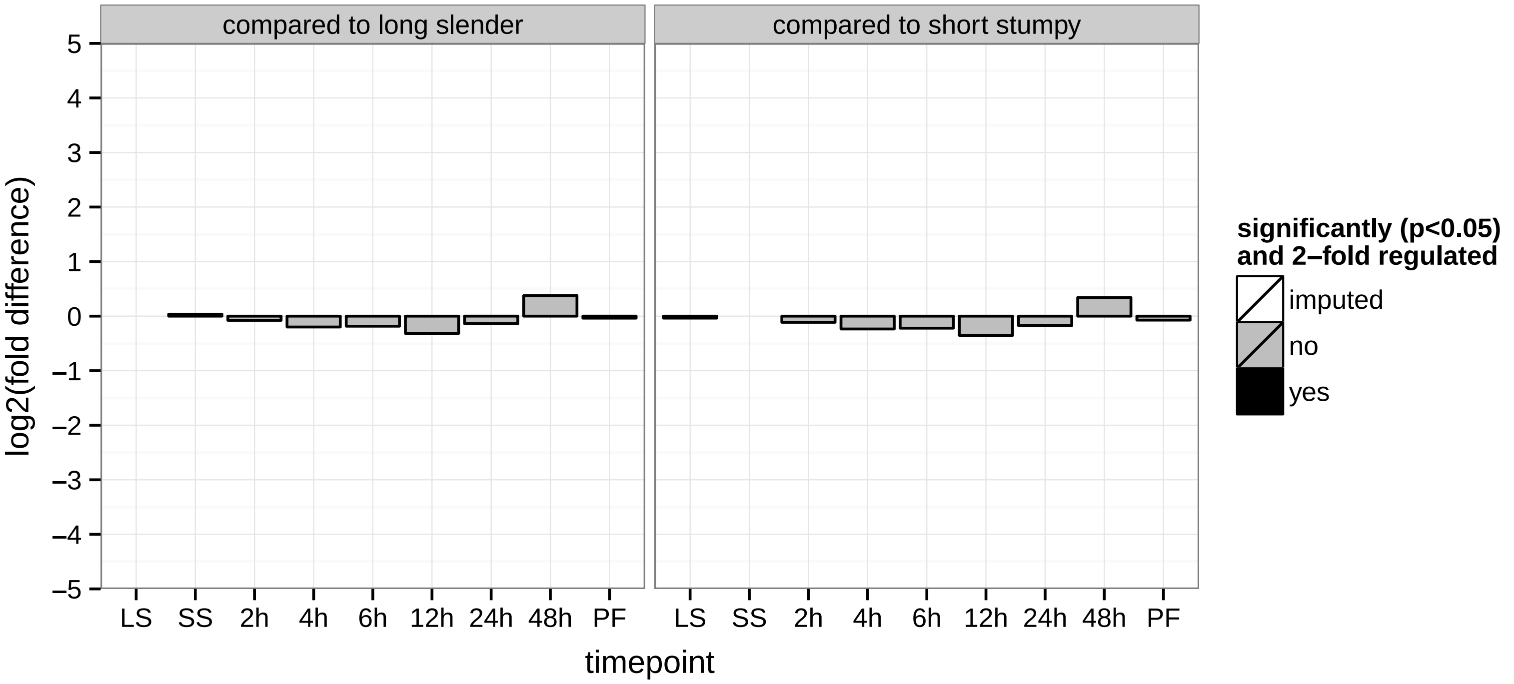
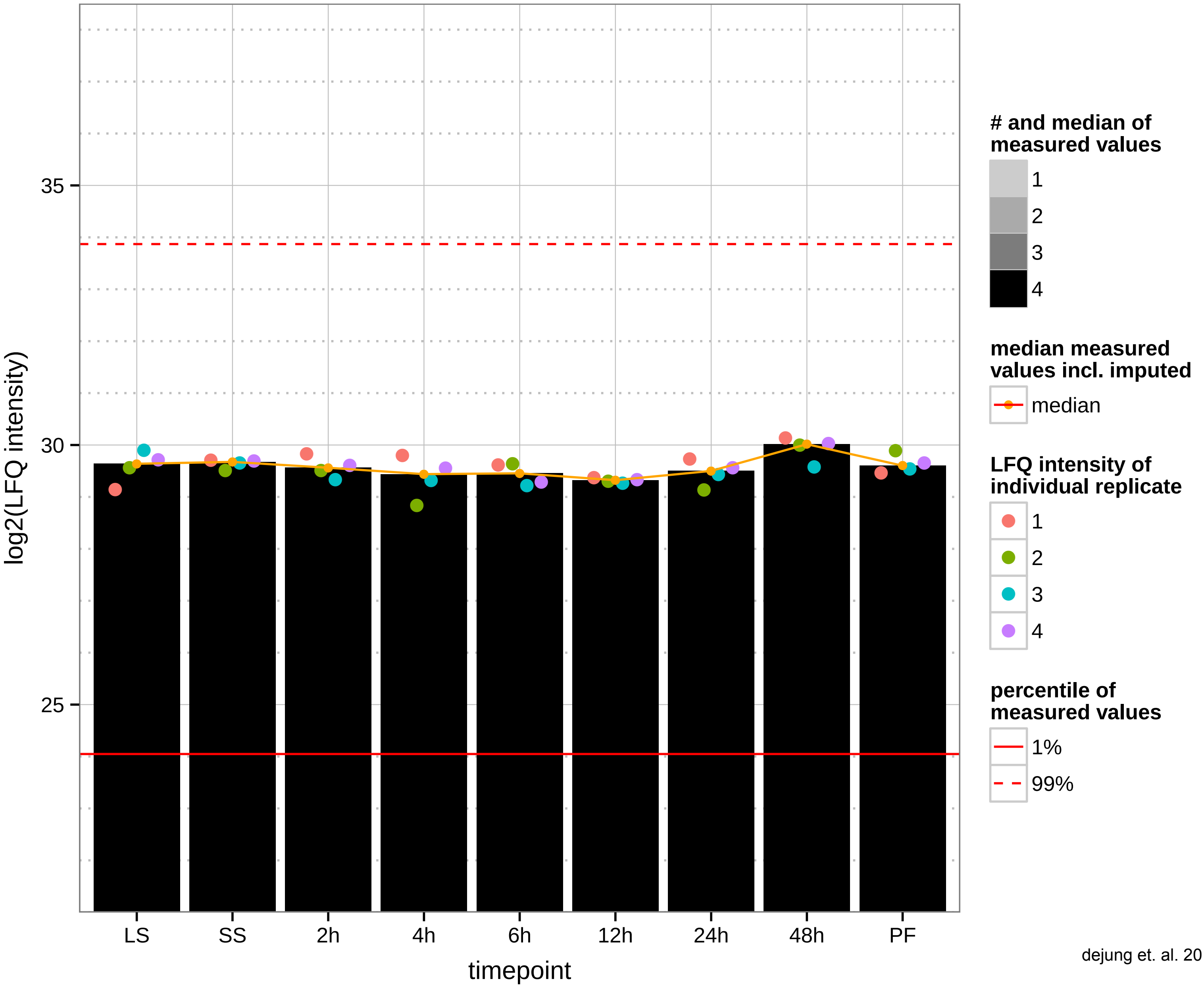
dynein intermediate chain IC70, putative
Tb927.11.14300
AGOF: microtubule motor activity, motor activity
AGOC: dynein complex
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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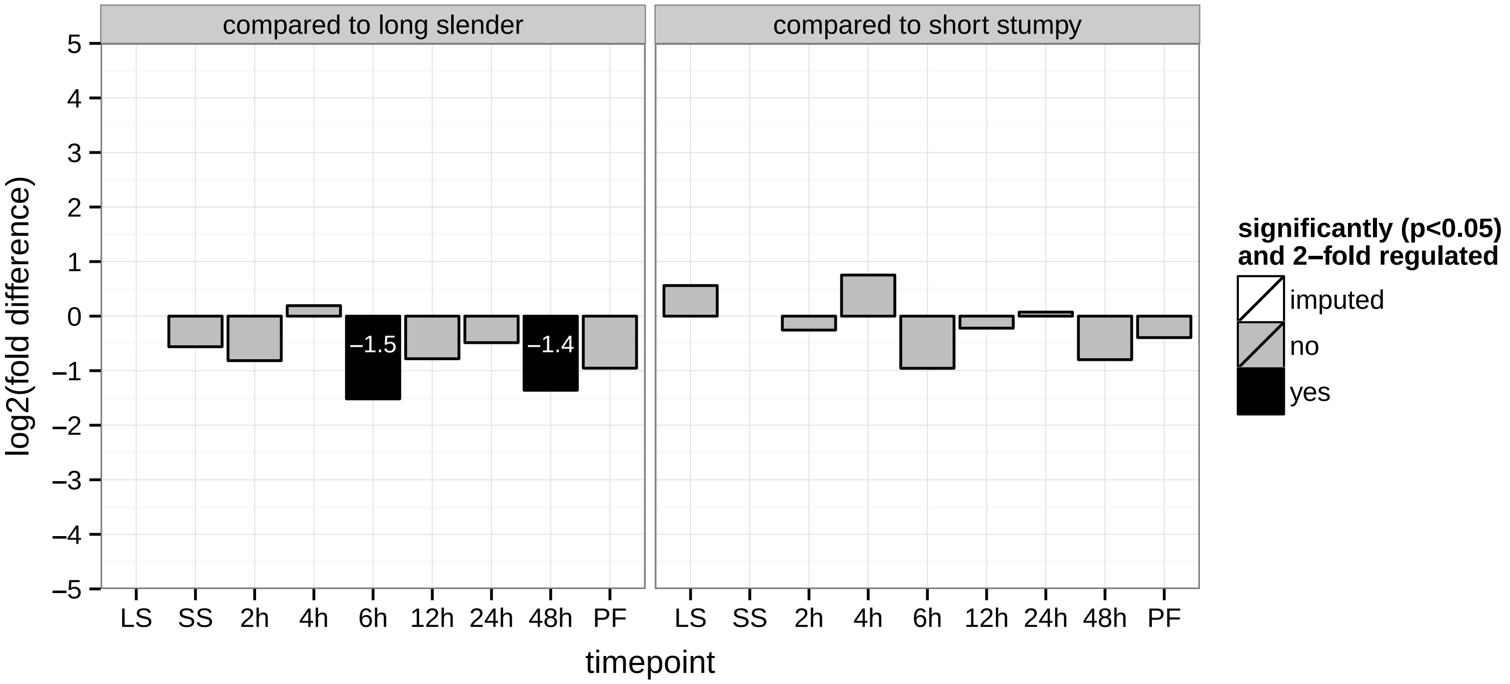
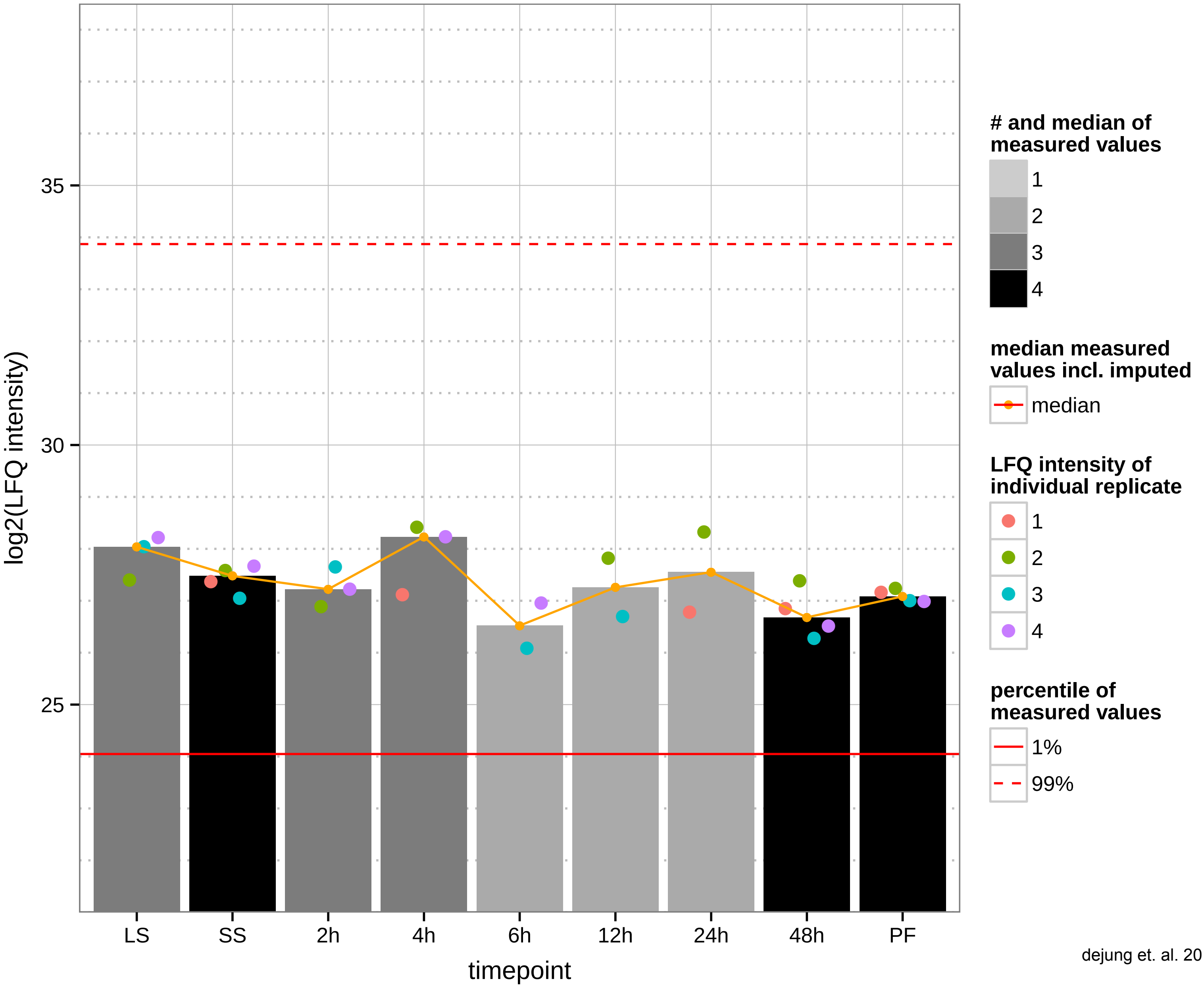
small nuclear ribonucleoprotein Sm–G (Sm–G)
Tb927.11.14310
AGOF: null
AGOC: nucleus, small nucleolar ribonucleoprotein complex
AGOP: RNA splicing, RNA splicing, via transesterification reactions, nuclear mRNA trans splicing, SL addition
PGOF: null
PGOC: null
PGOP: null





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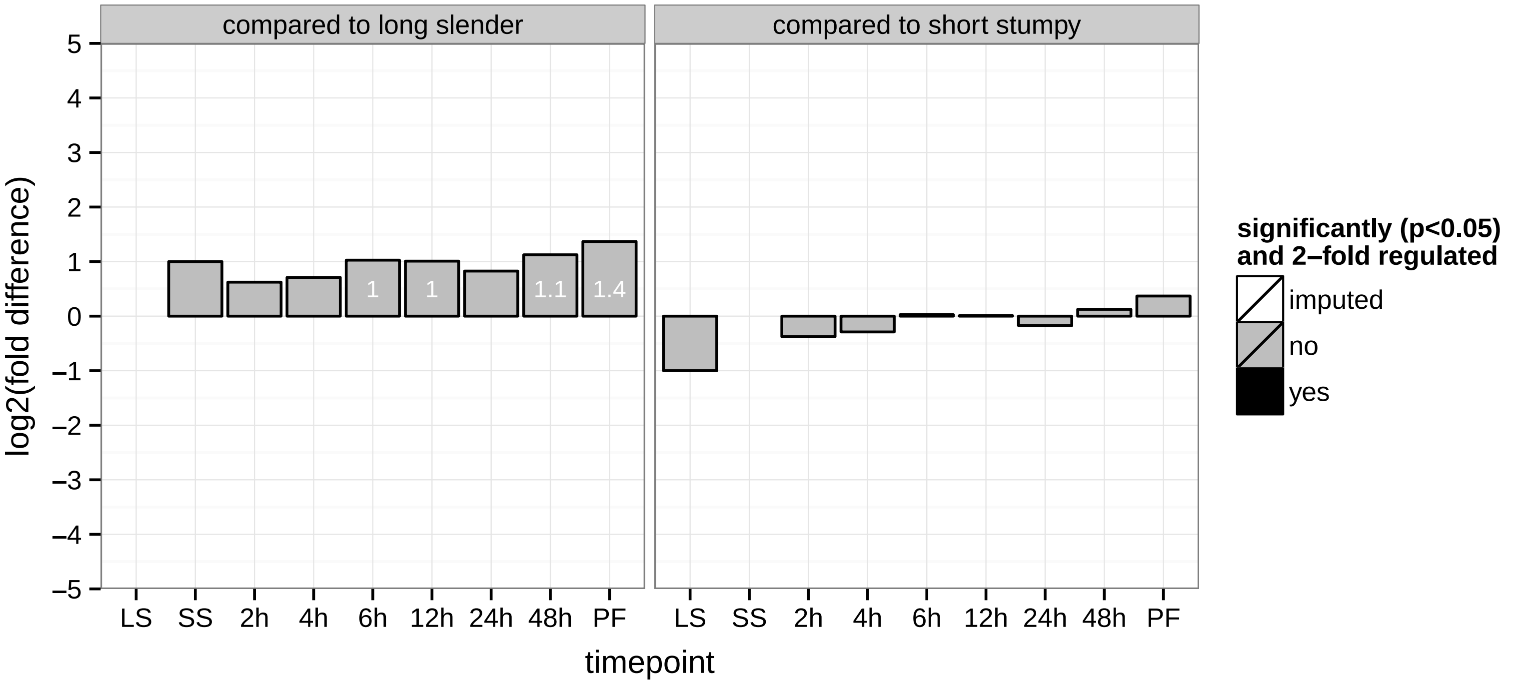
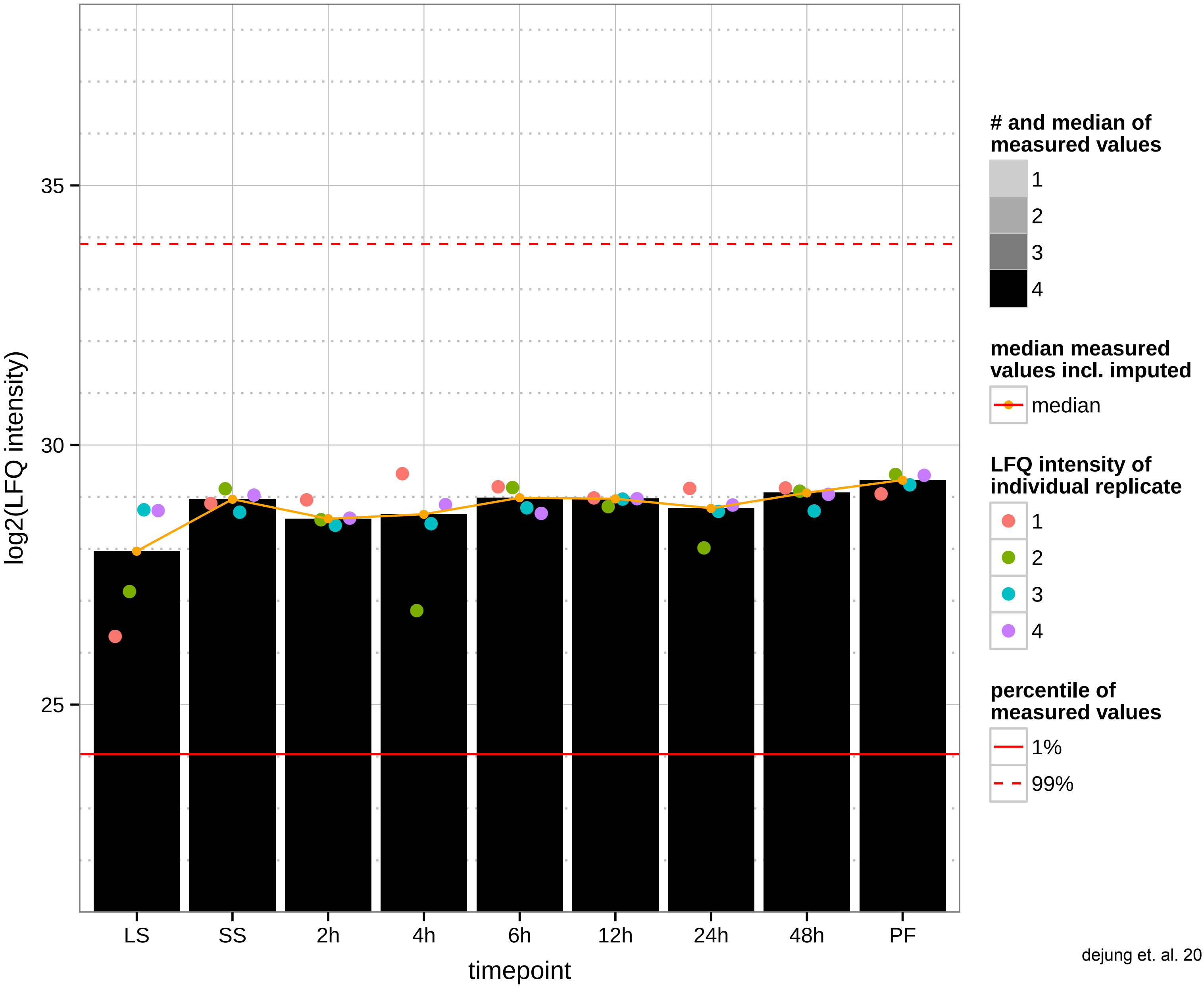
hypothetical protein, conserved
Tb927.11.14330
AGOF: acid–amino acid ligase activity, zinc ion binding
AGOC: intracellular
AGOP: cellular protein modification process
PGOF: acid–amino acid ligase activity, binding, zinc ion binding
PGOC: intracellular
PGOP: cellular protein modification process





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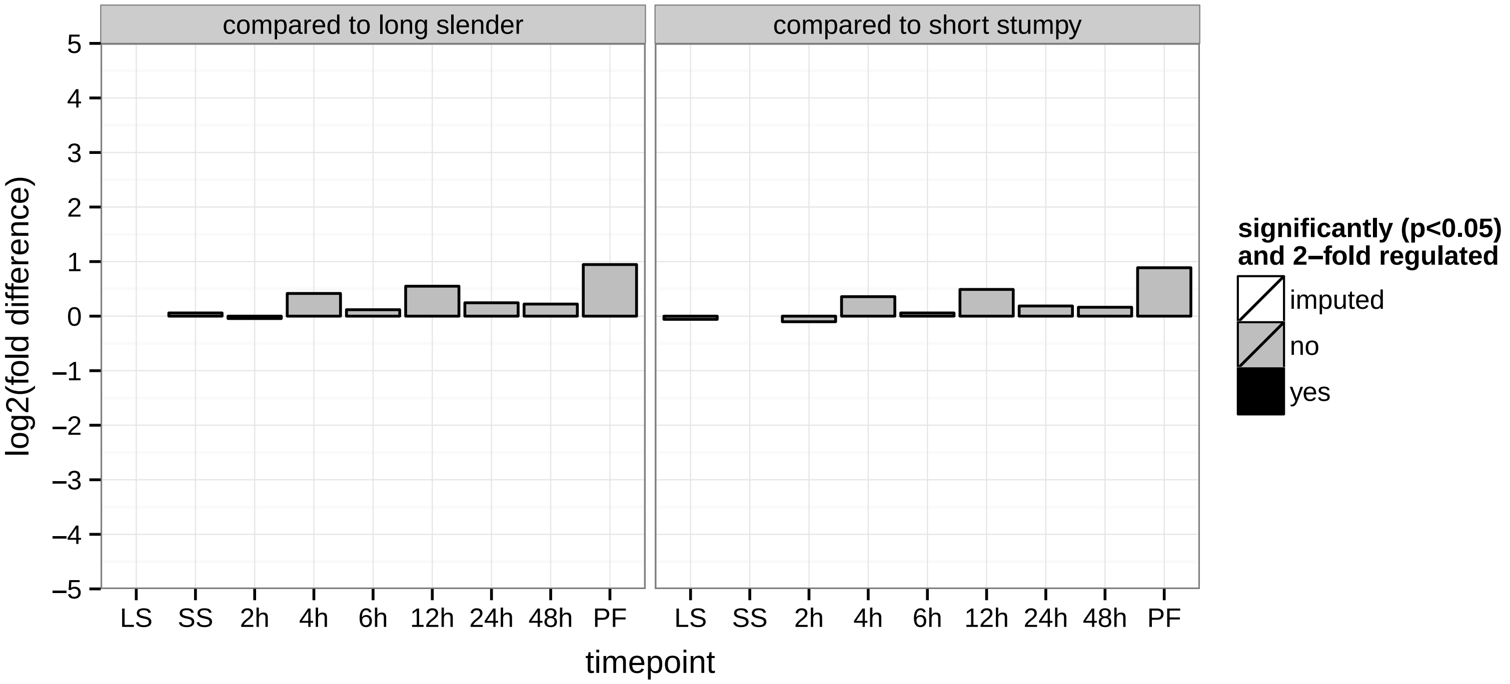
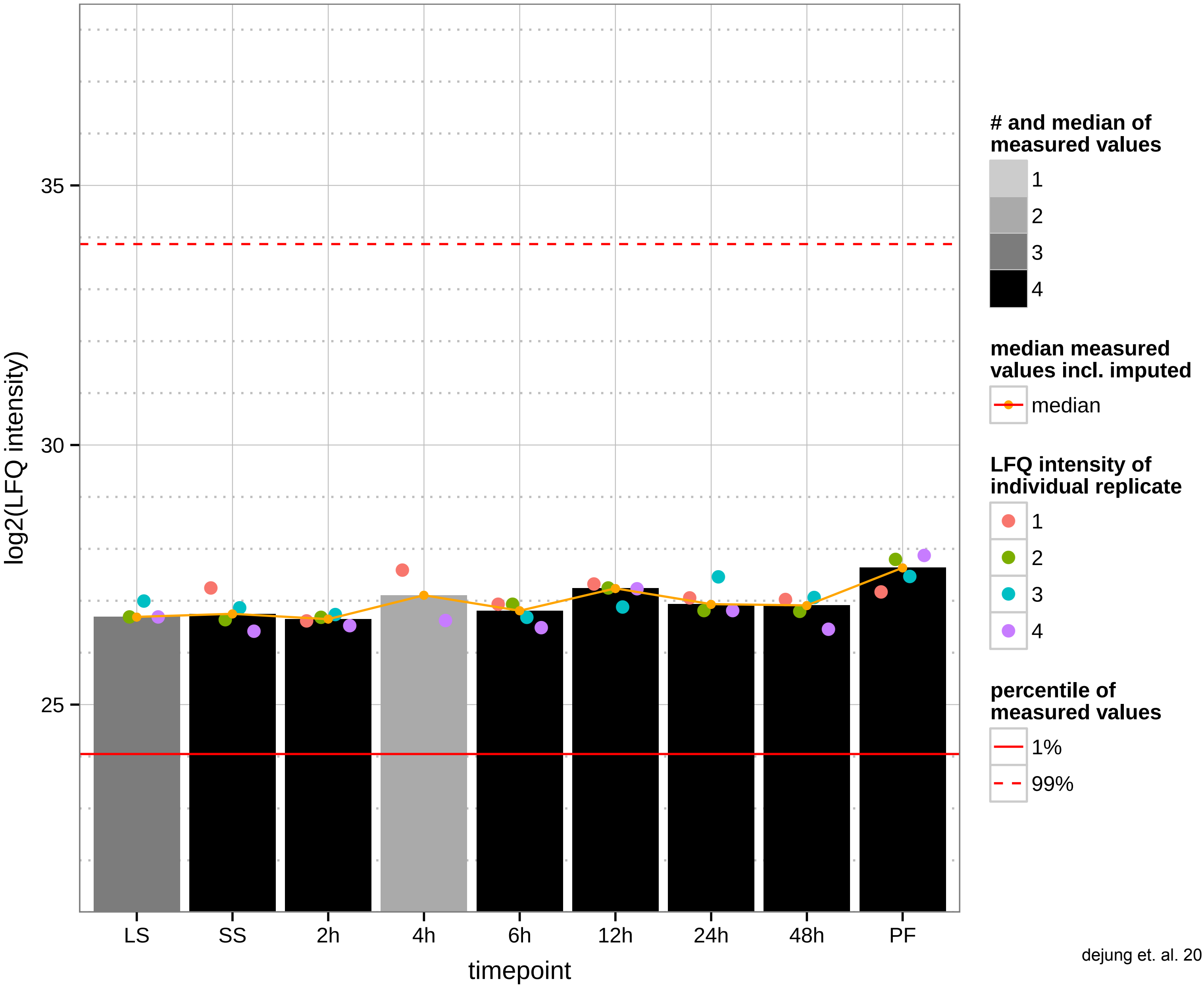
exportin 1 (XPO1)
Tb927.11.14340
AGOF: protein transporter activity
AGOC: cytoplasm, nuclear pore, nucleus
AGOP: intracellular protein transport, nuclear export, protein import into nucleus, docking
PGOF: binding, protein transporter activity
PGOC: null
PGOP: intracellular protein transport





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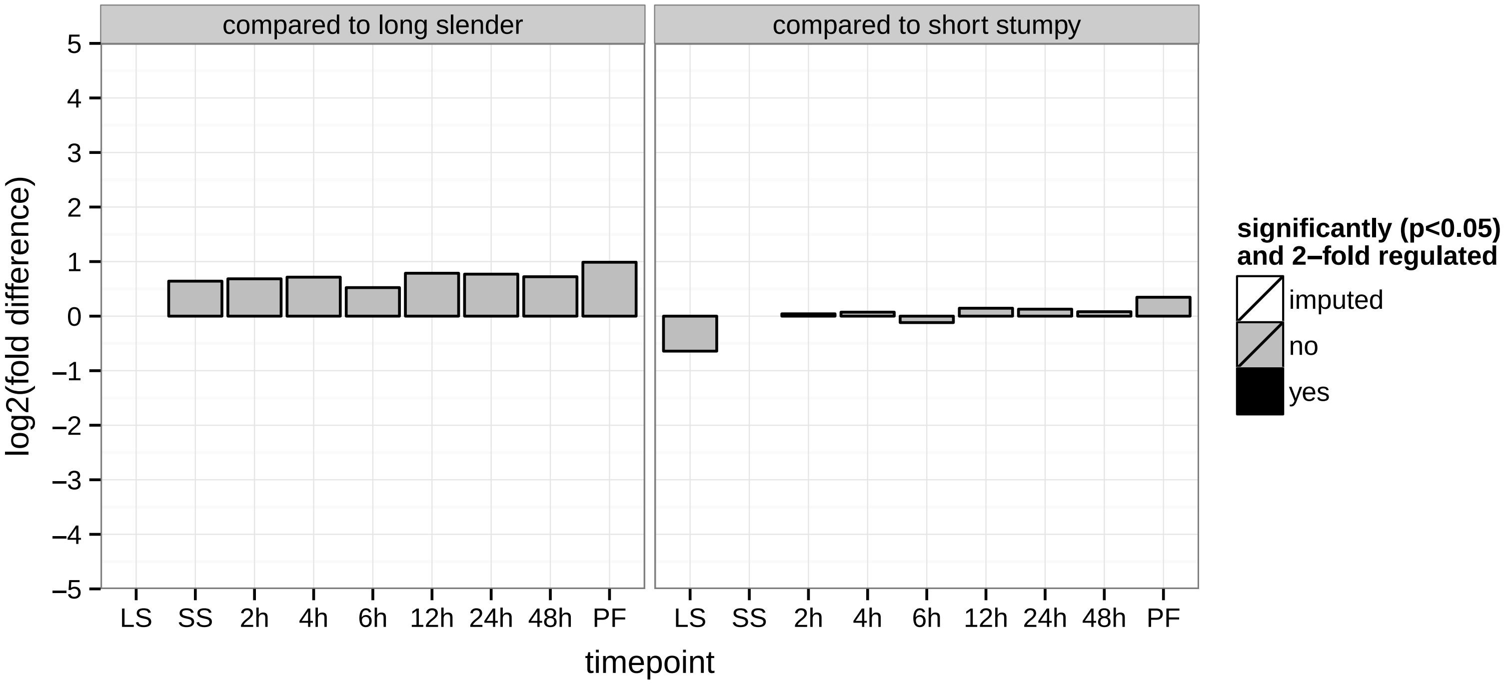
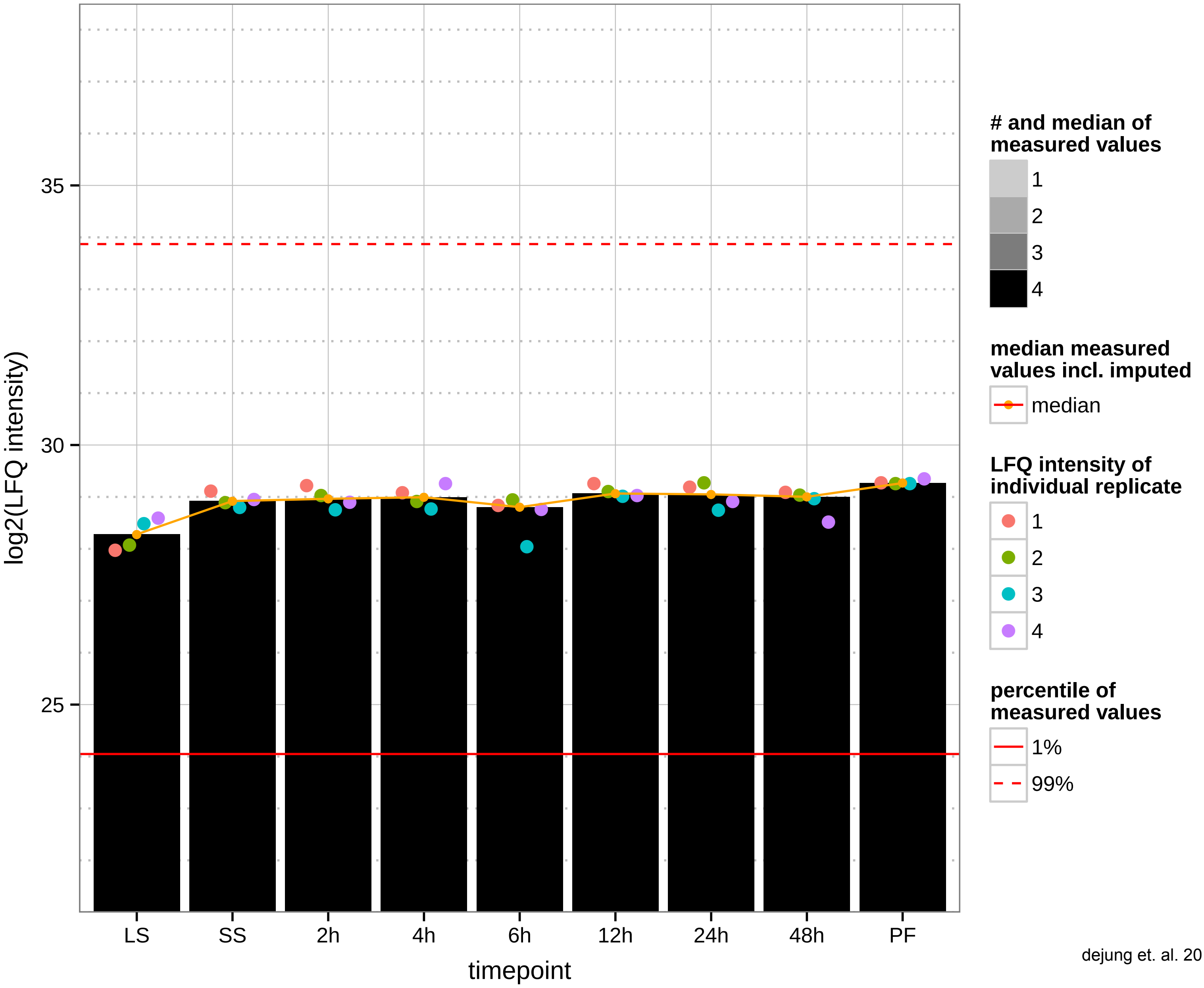
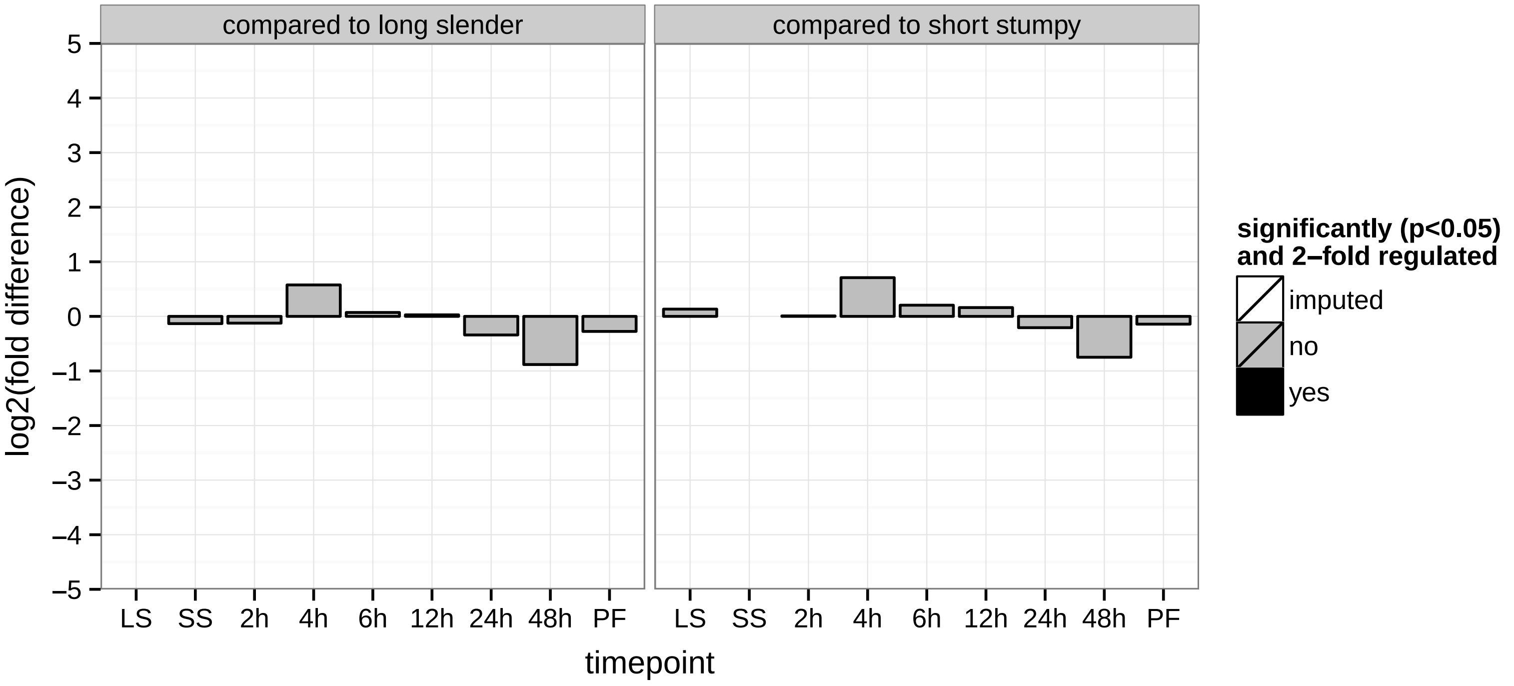
proteasome regulatory non–ATP–ase subunit
Tb927.11.14430
AGOF: endopeptidase activity
AGOC: proteasome regulatory particle
AGOP: proteolysis
PGOF: null
PGOC: null
PGOP: null

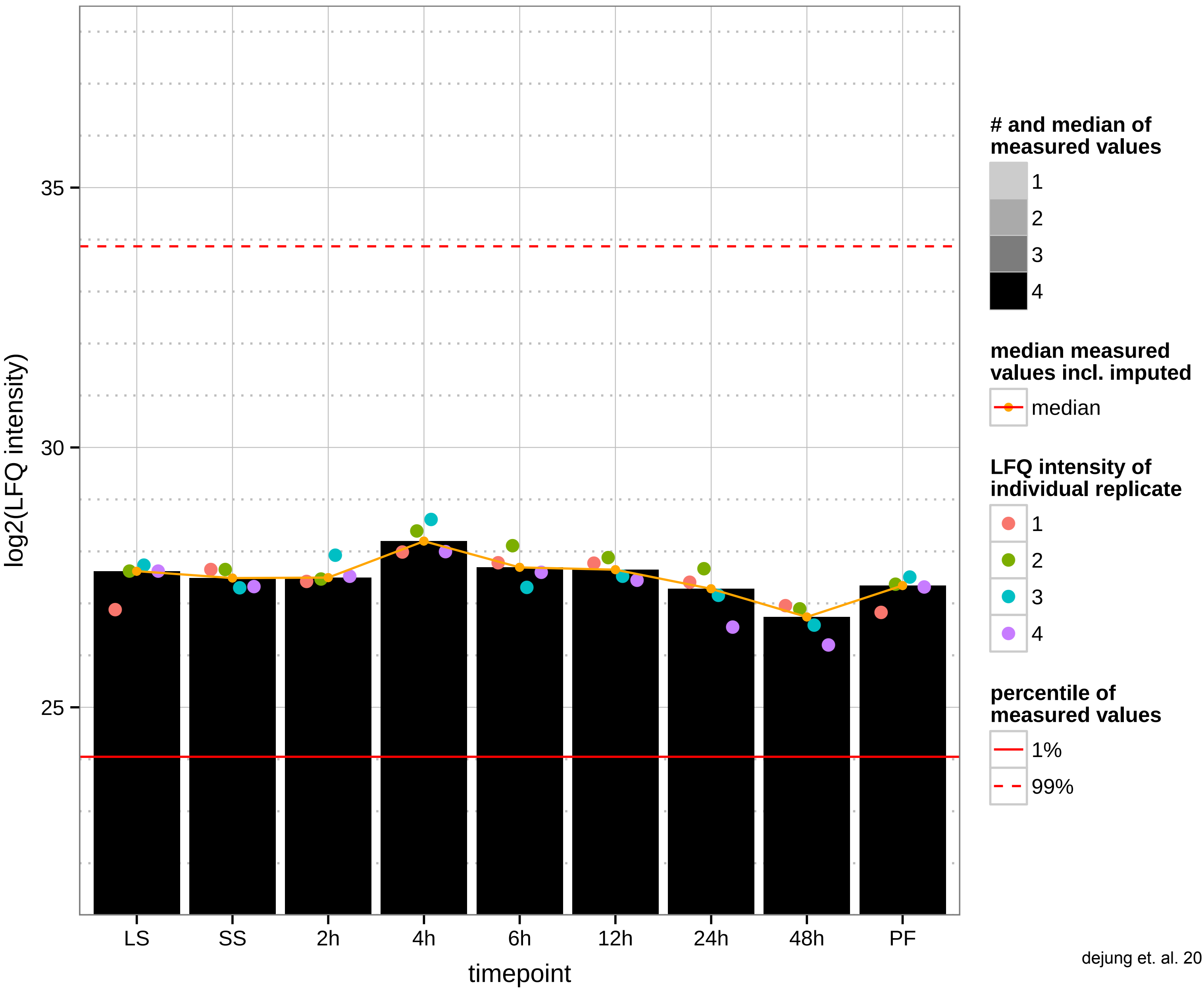




dejung et. al. 2015

ADP–ribosylation factor GTPase activating protein 1, putative
Tb927.11.14460
AGOF: ARF GTPase activator activity, DNA binding, zinc ion binding
AGOC: nucleus
AGOP: regulation of ARF GTPase activity
PGOF: ARF GTPase activator activity, zinc ion binding
PGOC: null
PGOP: regulation of ARF GTPase activity





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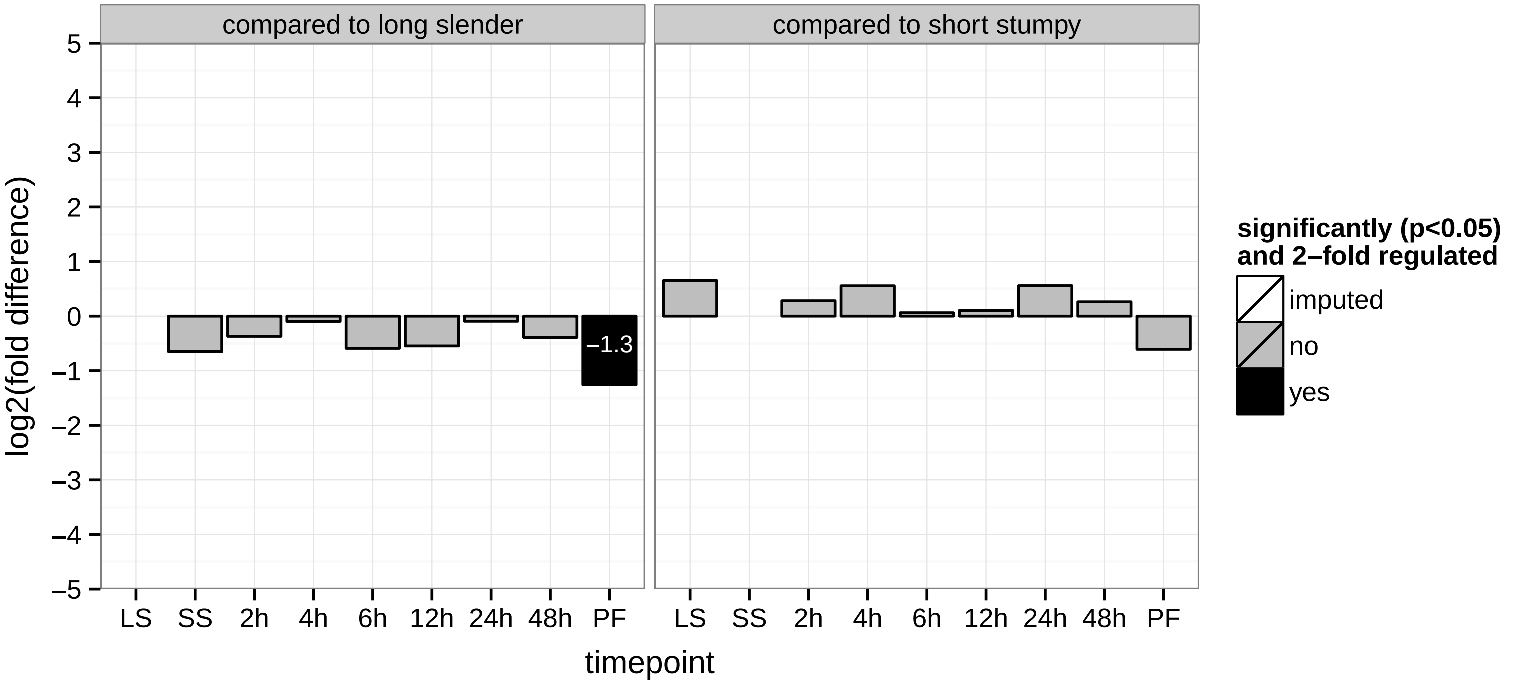
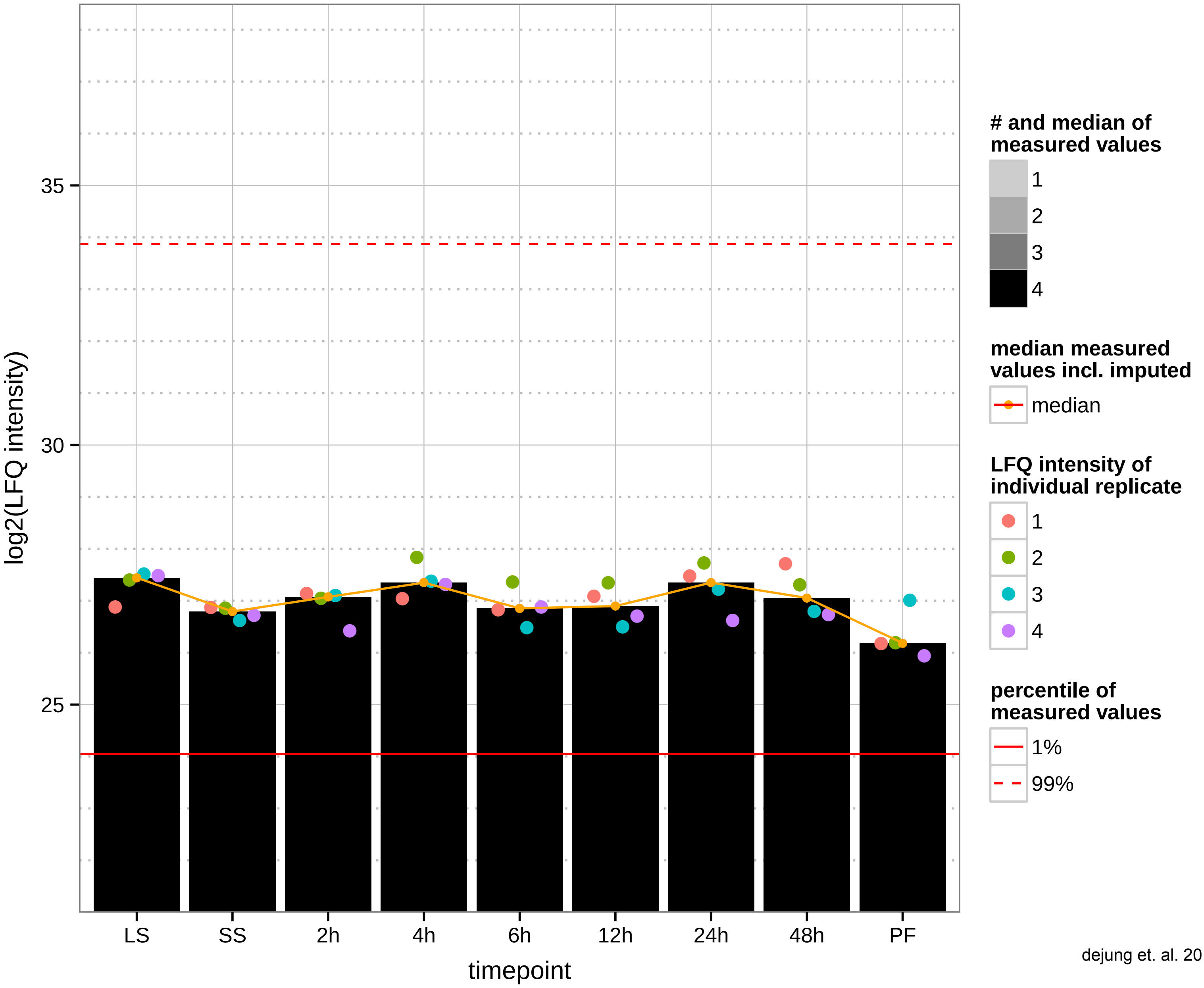
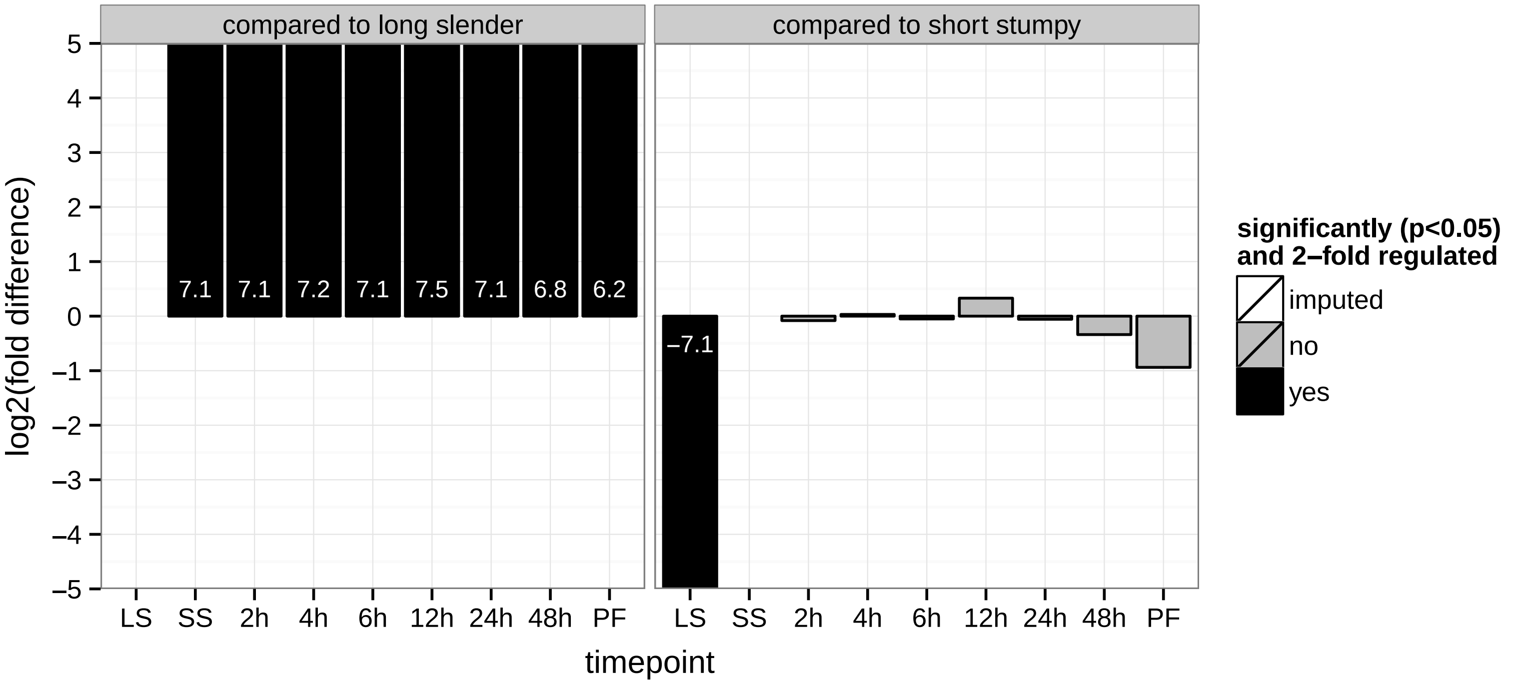
RNA polymerase subunit, putative (RPB7)
Tb927.11.14490
AGOF: DNA−directed RNA polymerase activity
AGOC: null
AGOP: transcription, DNA−dependent
PGOF: DNA−directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA−dependent

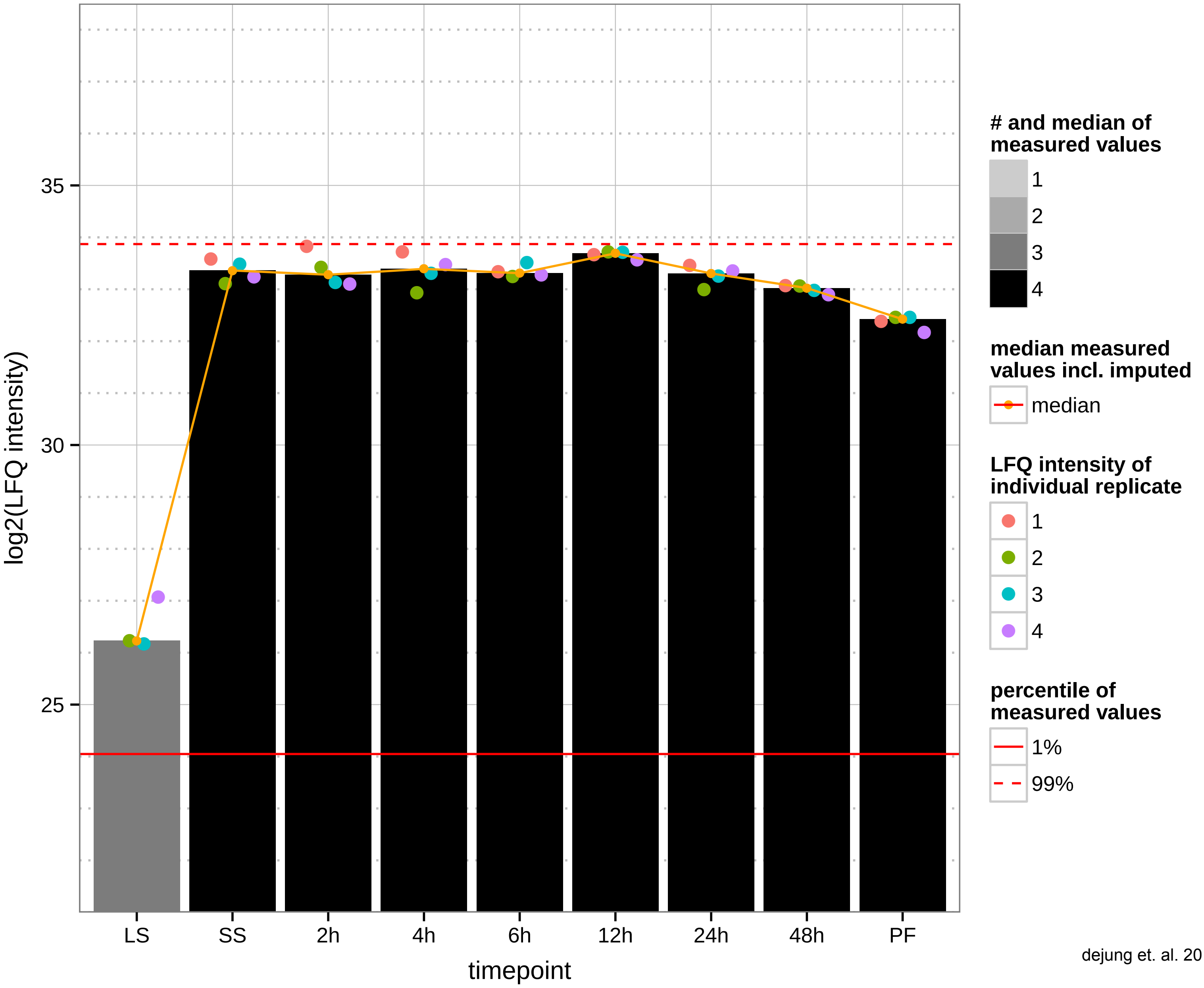




dejung et. al. 2015

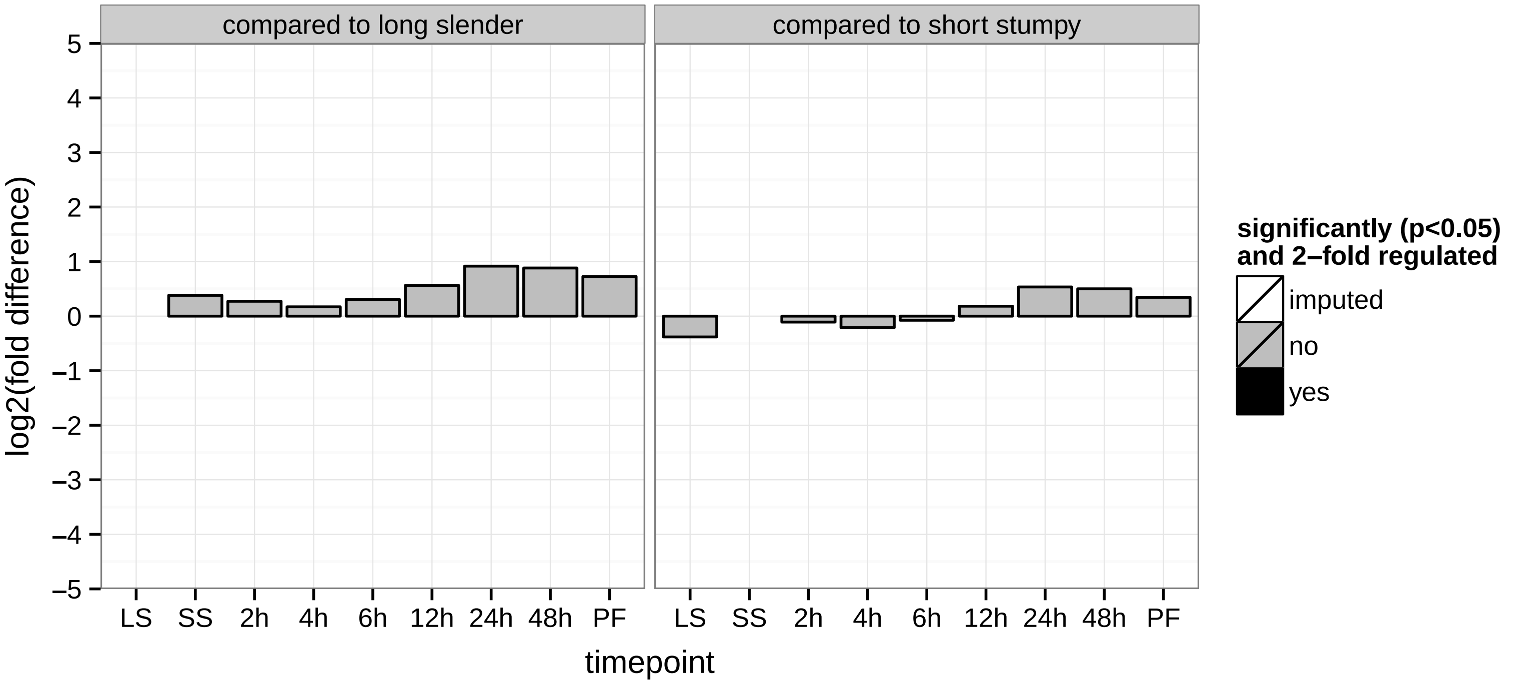
2–oxoglutarate dehydrogenase E1 component, putative
Tb927.11.1450
AGOF: oxoglutarate dehydrogenase (succinyl–transferring) activity, thiamine pyrophosphate binding
AGOC: mitochondrion, oxoglutarate dehydrogenase complex
AGOP: glycolysis, lysine catabolic process, tricarboxylic acid cycle, tryptophan metabolic process
PGOF: oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, oxoglutarate dehydrogen
PGOC: null
PGOP: metabolic process, oxidation–reduction process, tricarboxylic acid cycle

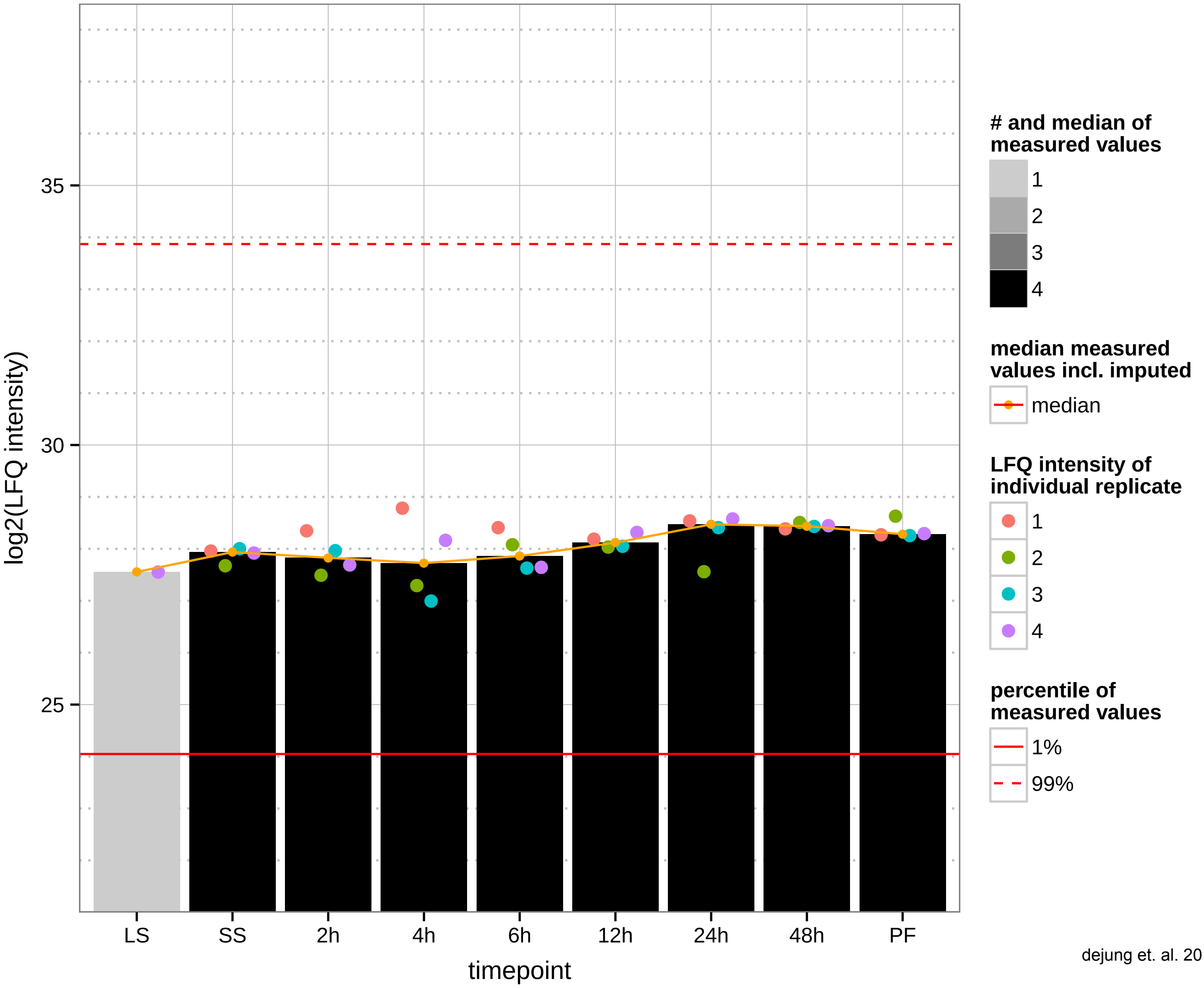




dejung et. al. 2015

cleavage and polyadenylation specificity factor–like protein, putative
Tb927.11.14560
AGOF: nucleic acid binding
AGOC: nucleus
AGOP: mRNA cleavage, mRNA polyadenylation
PGOF: nucleic acid binding
PGOC: nucleus
PGOP: null





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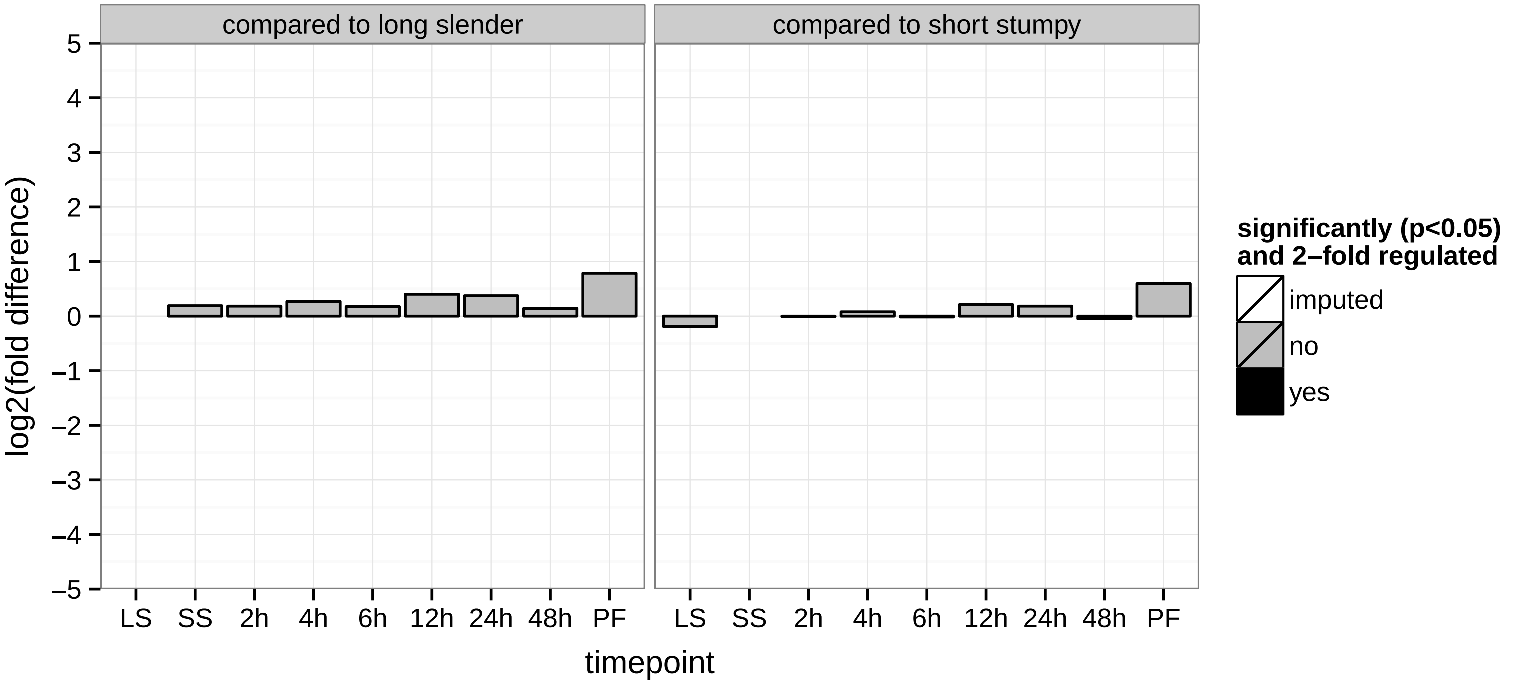
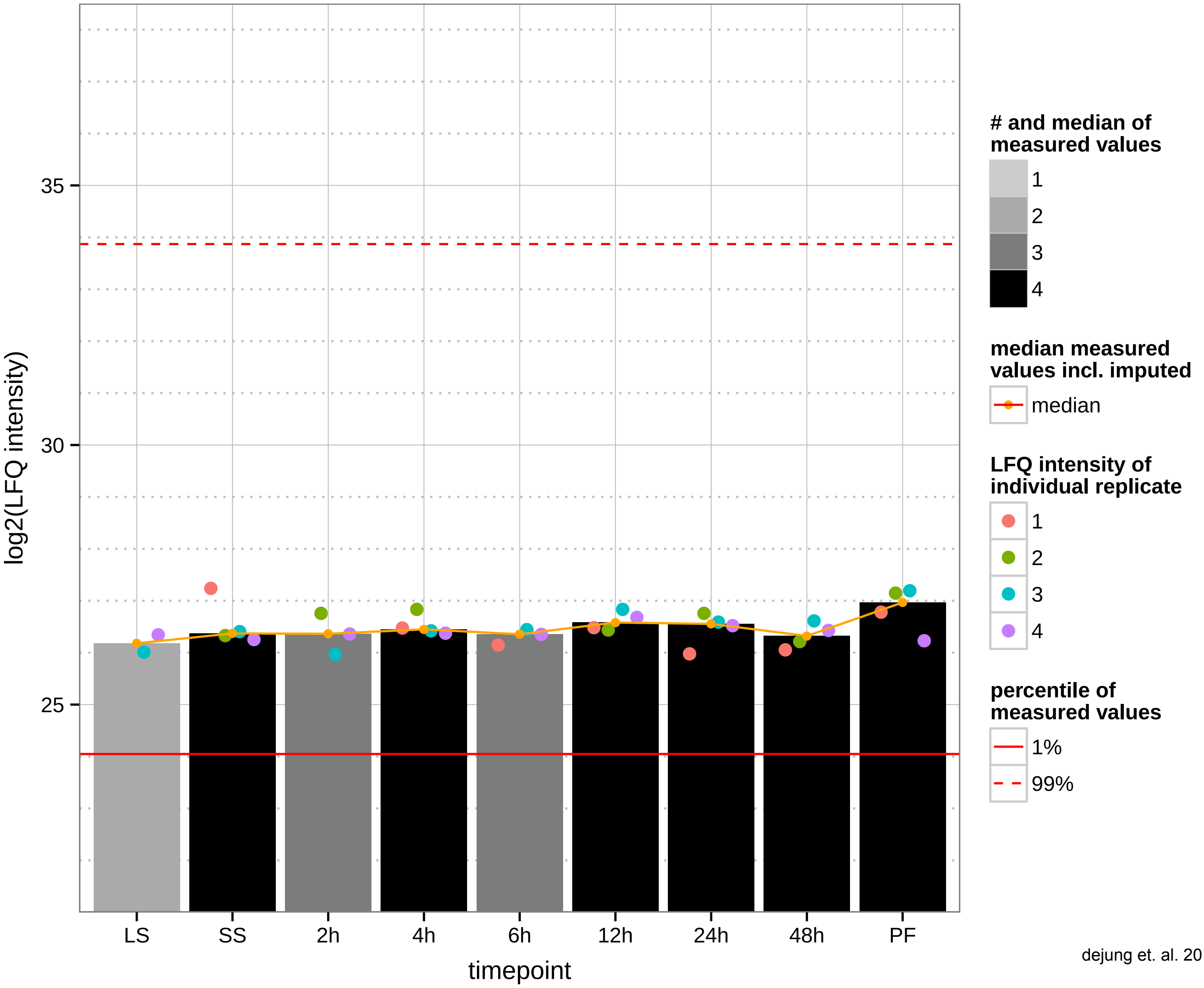
NAD+ synthase, putative
Tb927.11.14870
AGOF: ATP binding, NAD+ synthase (glutamine−hydrolyzing) activity
AGOC: null
AGOP: NAD biosynthetic process
PGOF: ATP binding, NAD+ synthase (glutamine−hydrolyzing) activity
PGOC: null
PGOP: NAD biosynthetic process





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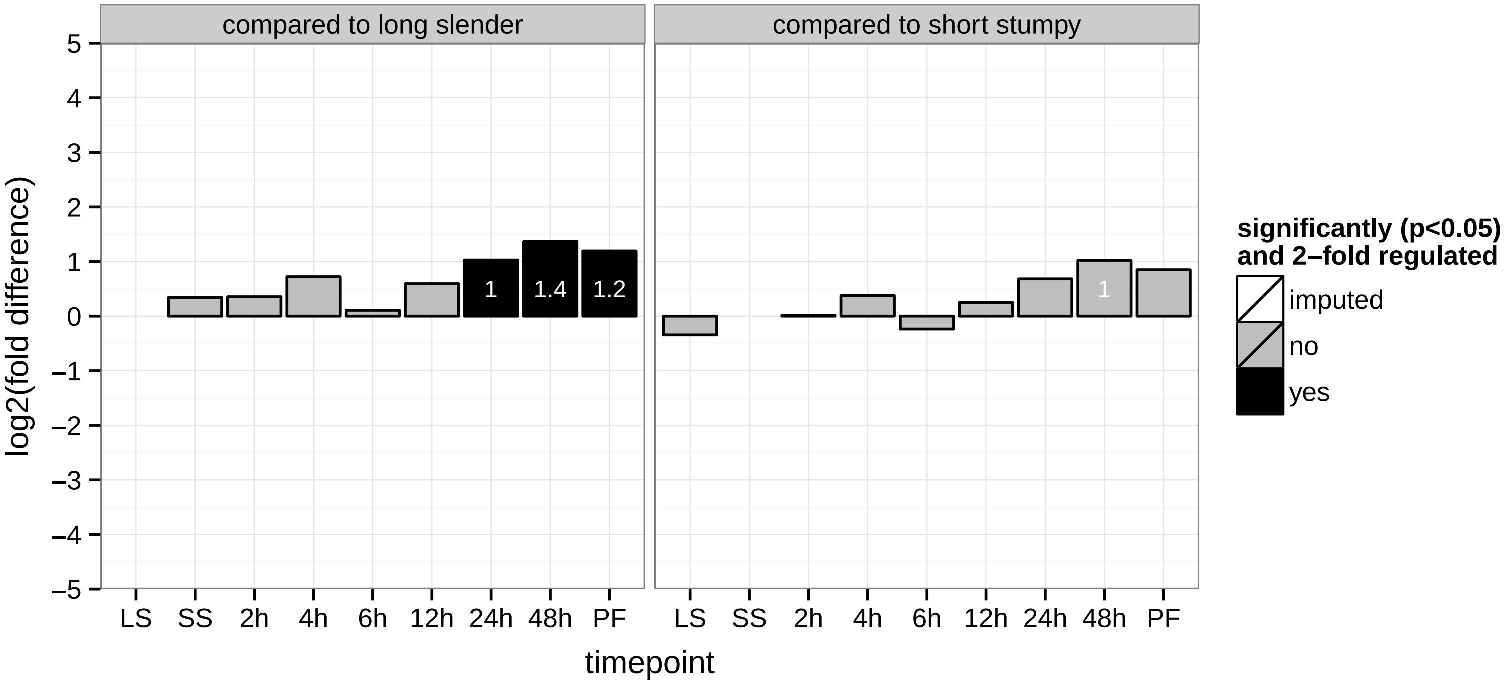
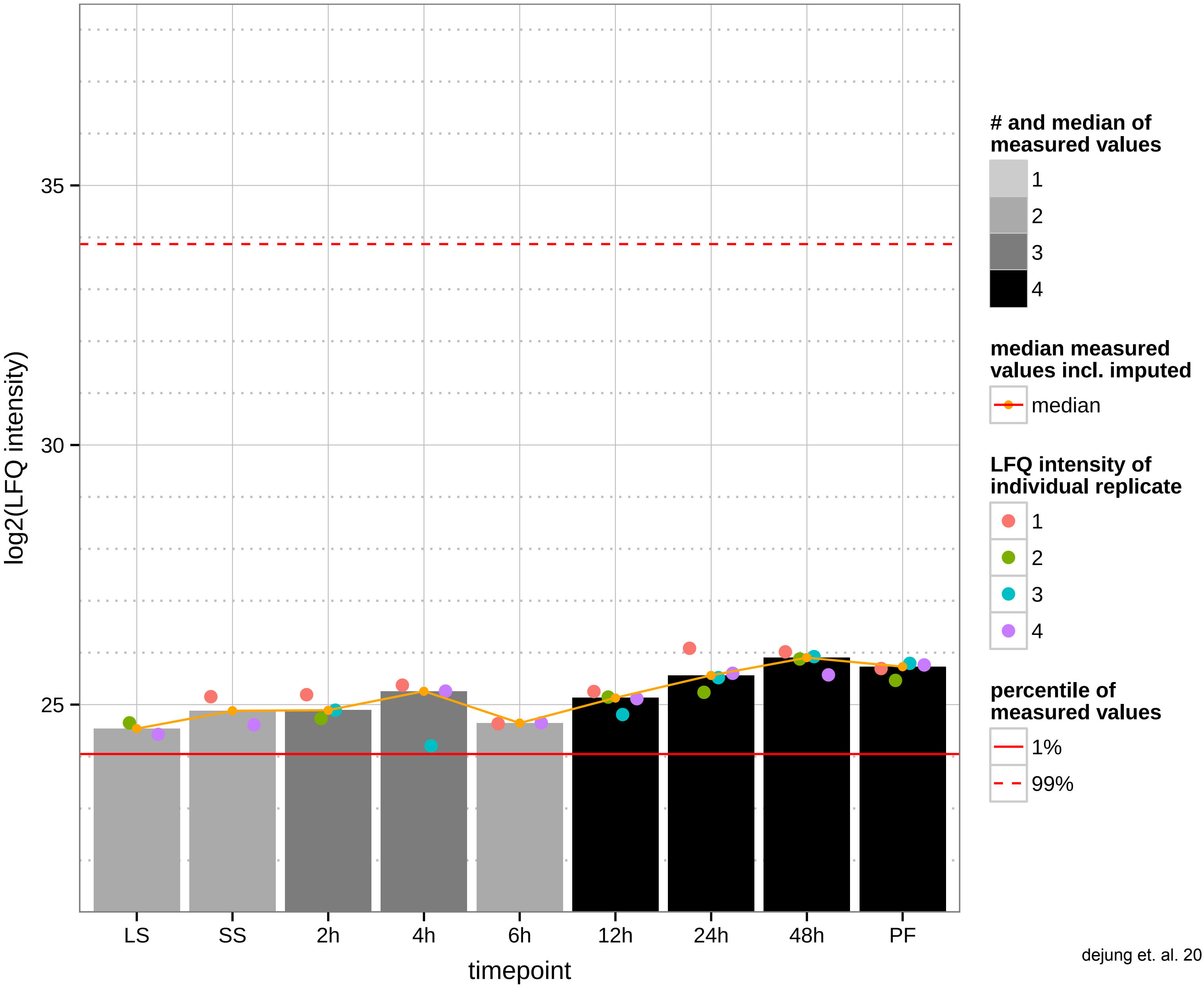
hypothetical protein, conserved
Tb927.11.14890
AGOF: DNA binding, DNA−directed DNA polymerase activity
AGOC: nucleus
AGOP: DNA replication
PGOF: DNA binding, DNA−directed DNA polymerase activity
PGOC: null
PGOP: DNA replication





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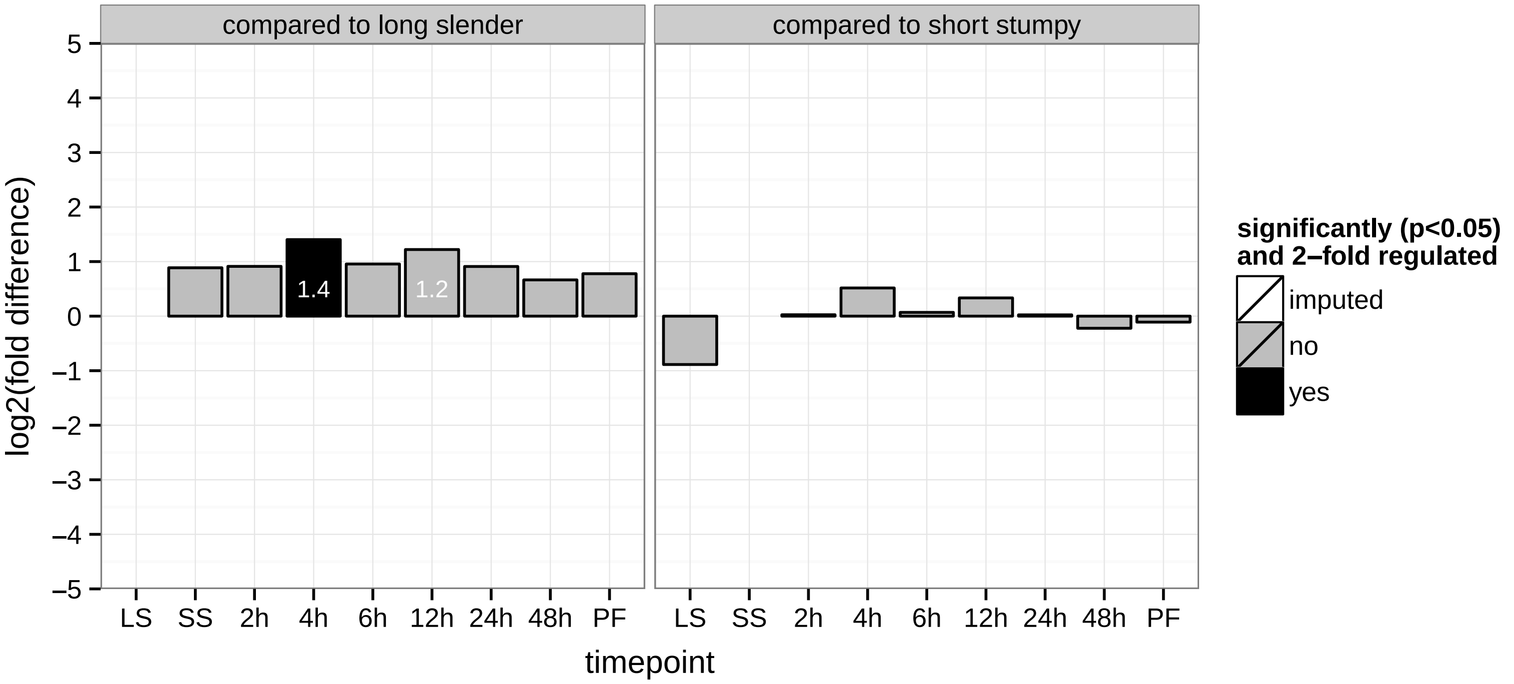
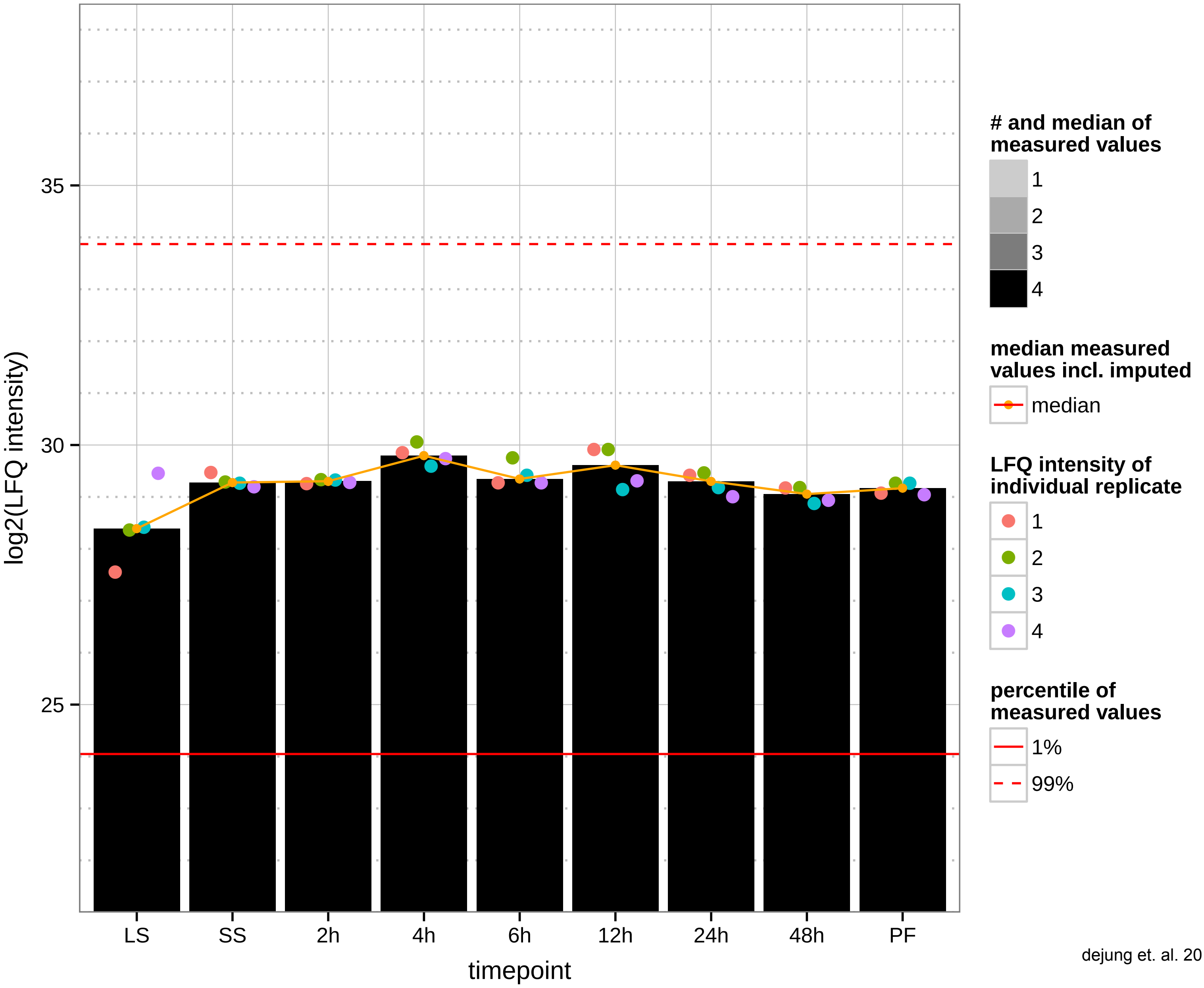
coatomer epsilon subunit, putative, cytosolic coat protein
Tb927.11.14900
AGOF: protein transporter activity, structural molecule activity
AGOC: COPI vesicle coat, cytoplasm, membrane
AGOP: intracellular protein transport, retrograde vesicle–mediated transport, Golgi to ER
PGOF: structural molecule activity
PGOC: COPI vesicle coat
PGOP: retrograde vesicle–mediated transport, Golgi to ER





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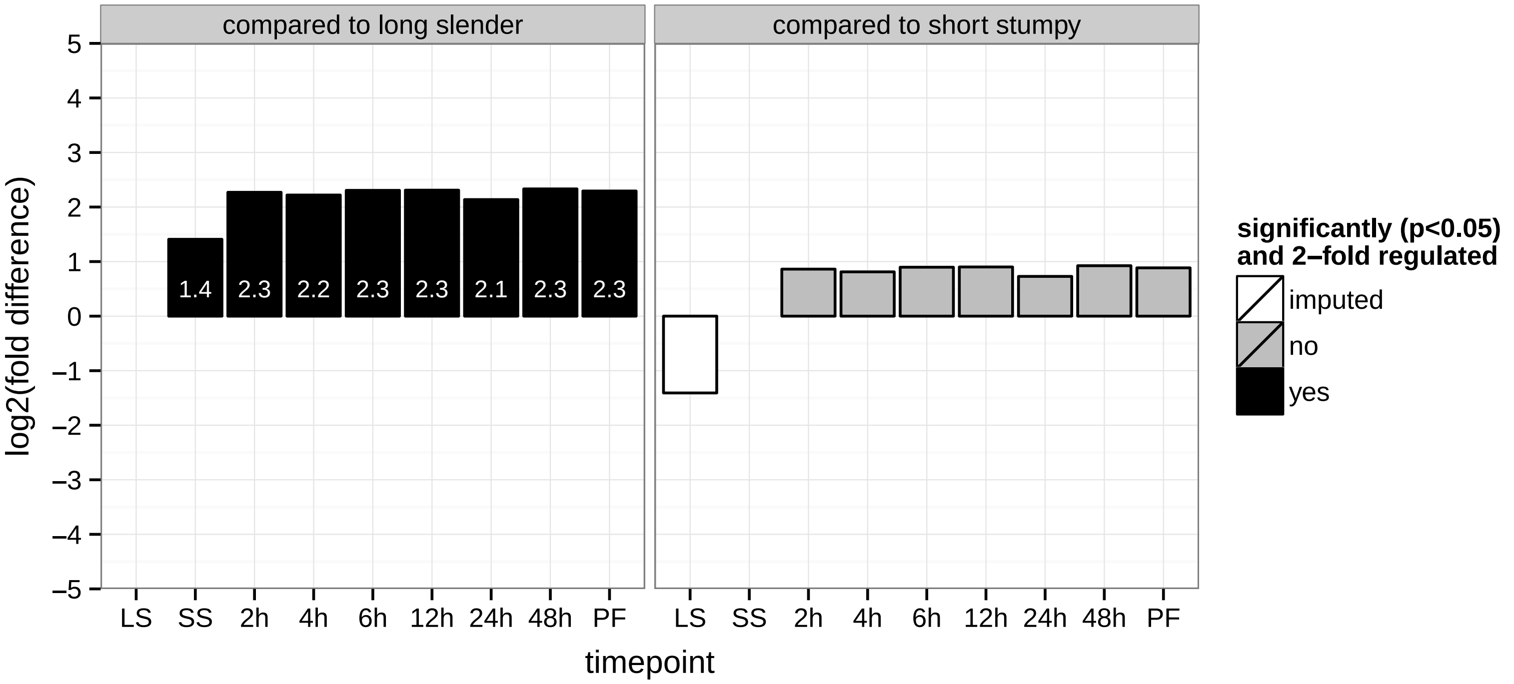
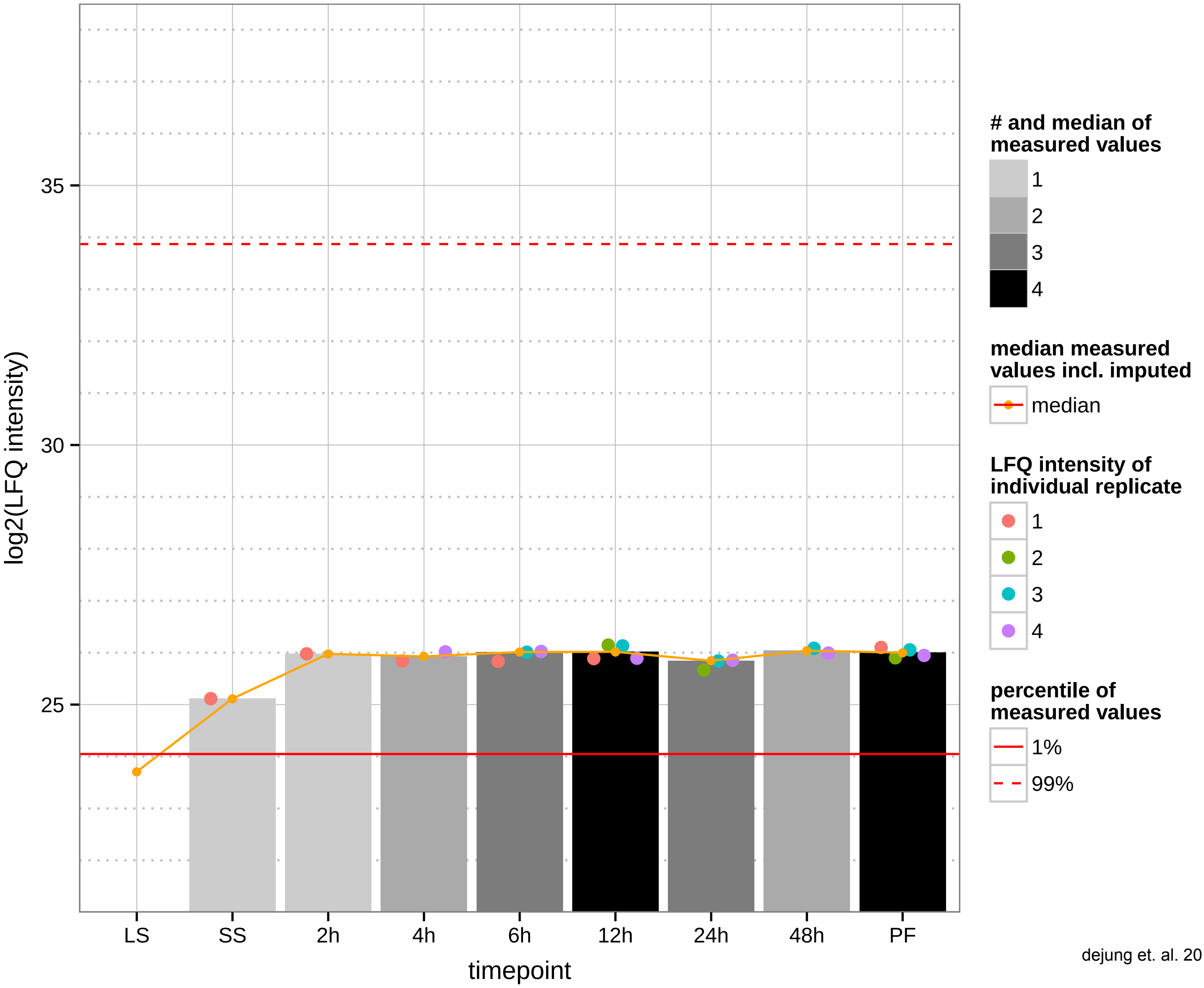
protein phosphatase 2C, putative
Tb927.11.14910
AGOF: phosphatase activity
AGOC: integral to membrane
AGOP: dephosphorylation
PGOF: catalytic activity
PGOC: null
PGOP: null





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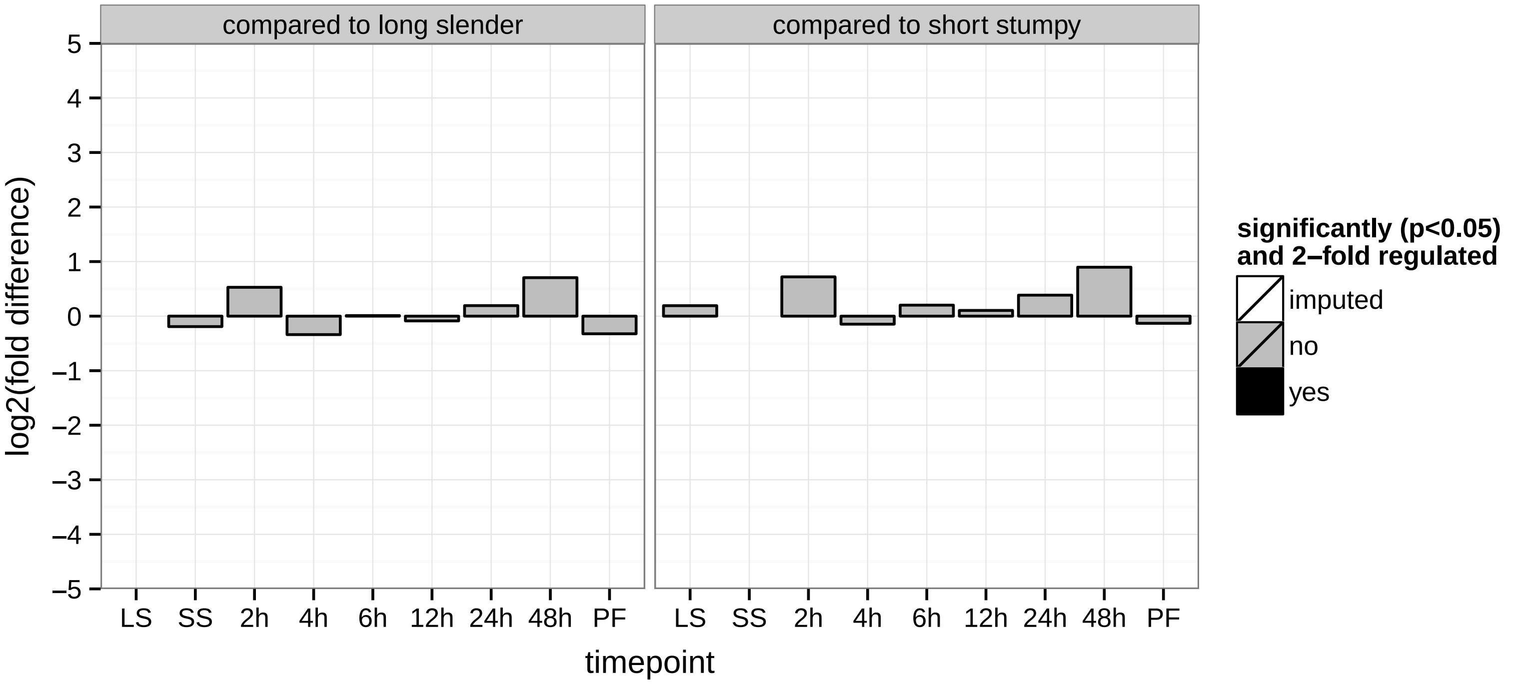
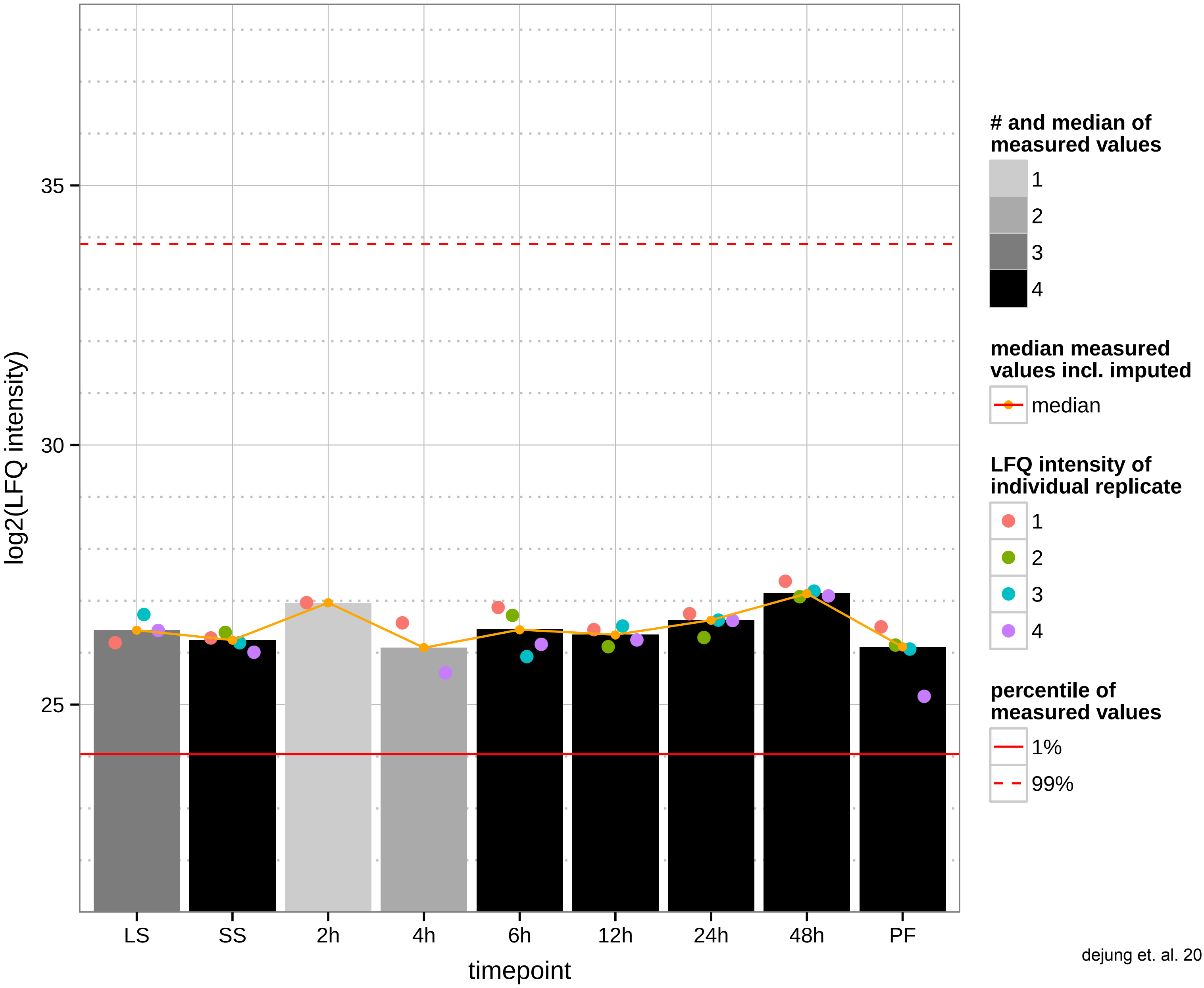
hypothetical protein, conserved
Tb927.11.14970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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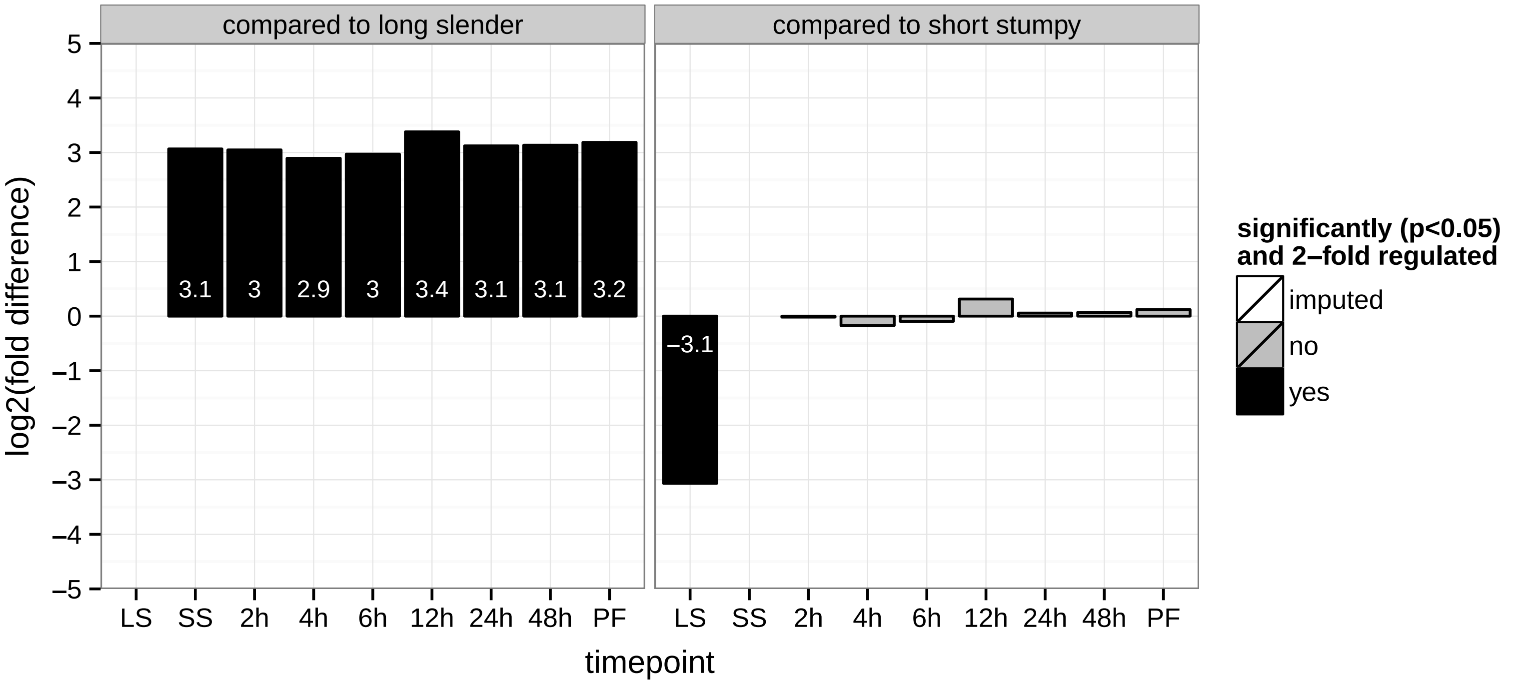
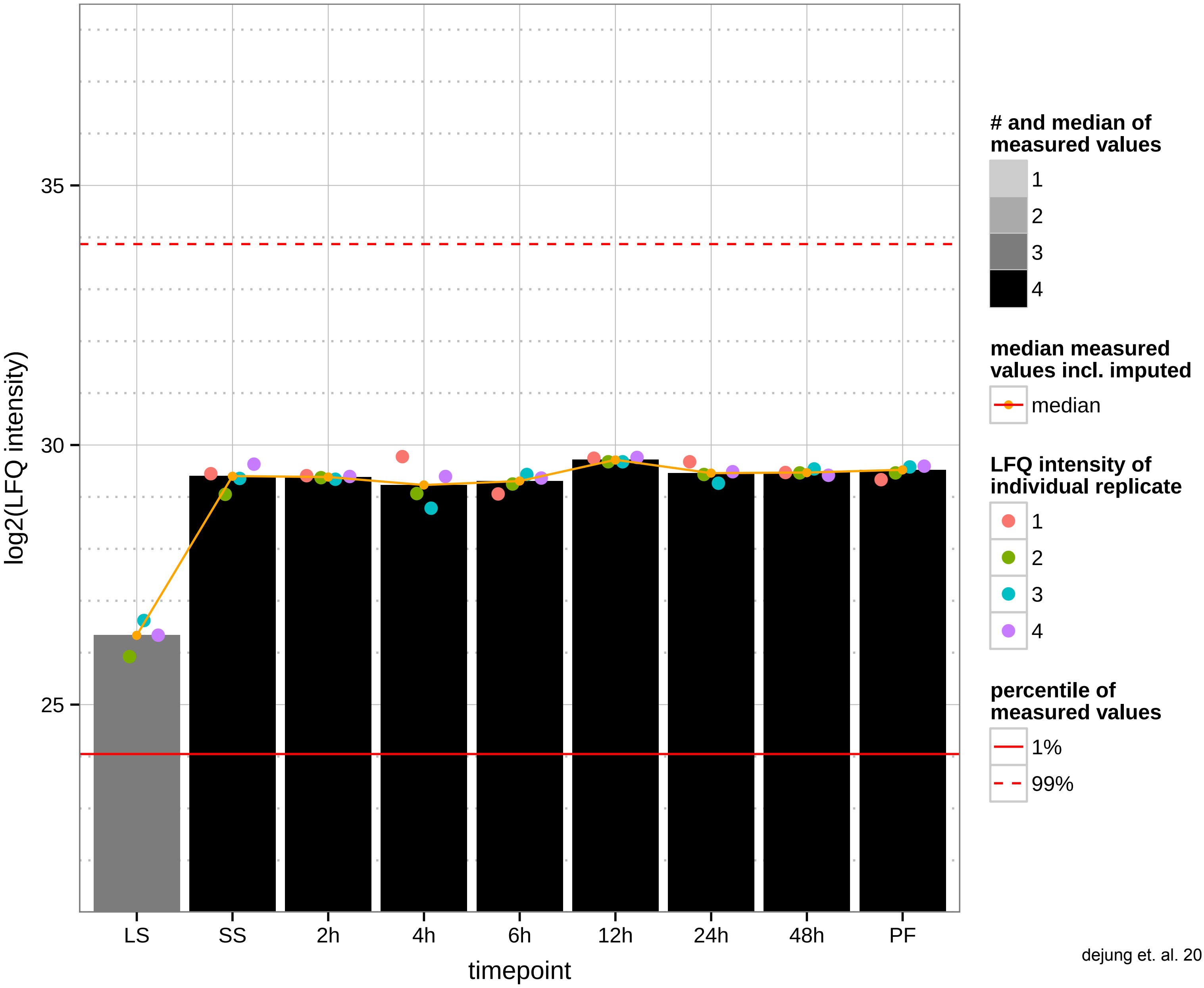
chaperonin HSP60, mitochondrial precursor, putative, heat shock protein 60 (Cpn60)
Tb927.11.15040
AGOF: ATP binding, unfolded protein binding
AGOC: mitochondrion
AGOP: protein complex assembly, protein folding
PGOF: ATP binding
PGOC: cytoplasm
PGOP: cellular protein metabolic process, protein refolding





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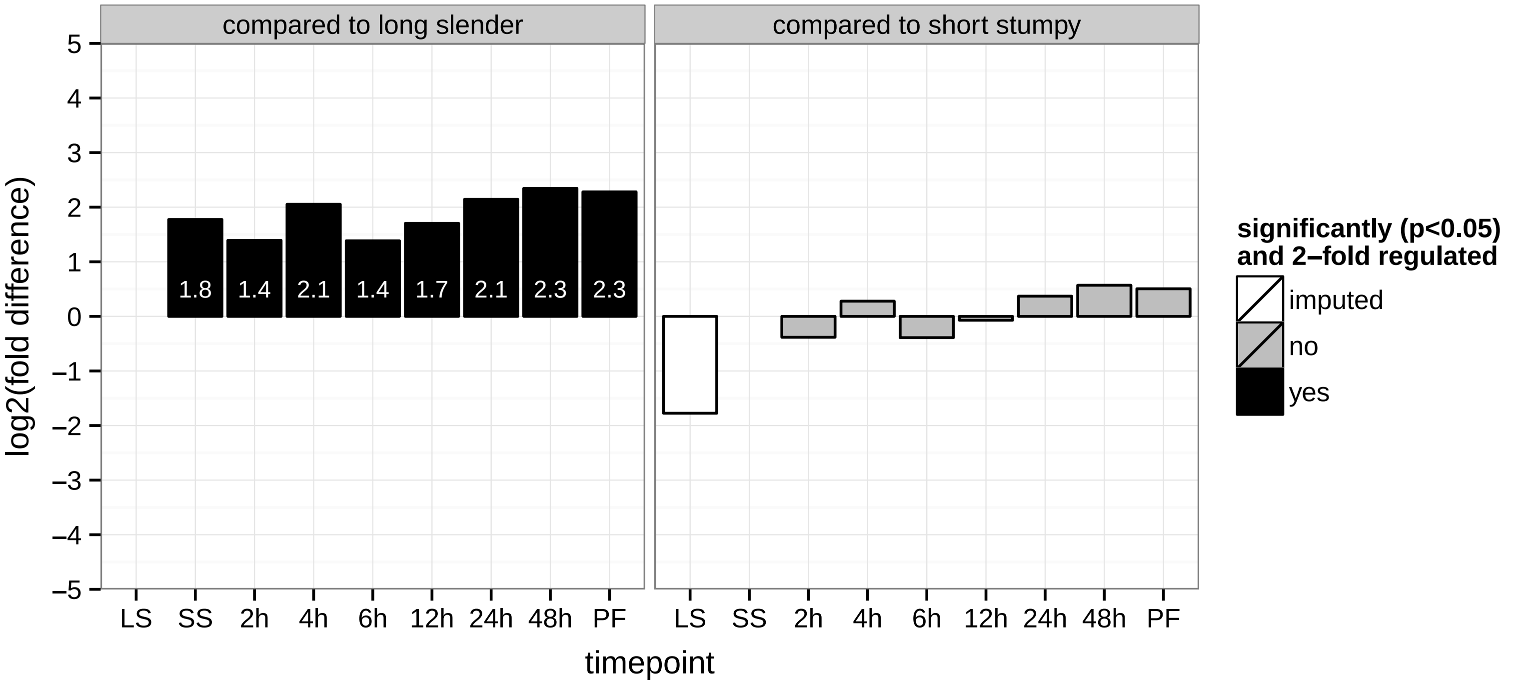
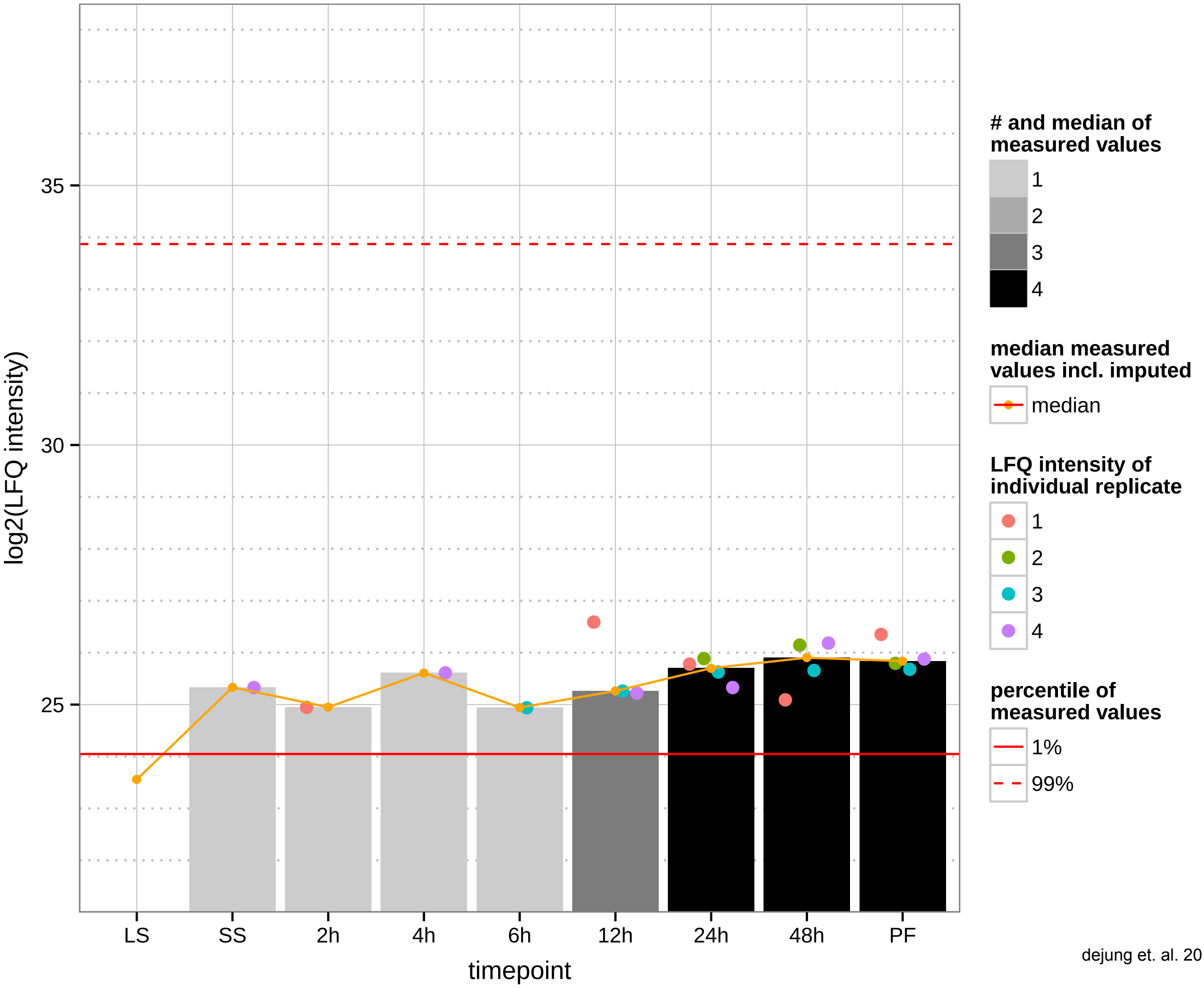
hypothetical protein, conserved
Tb927.11.15070
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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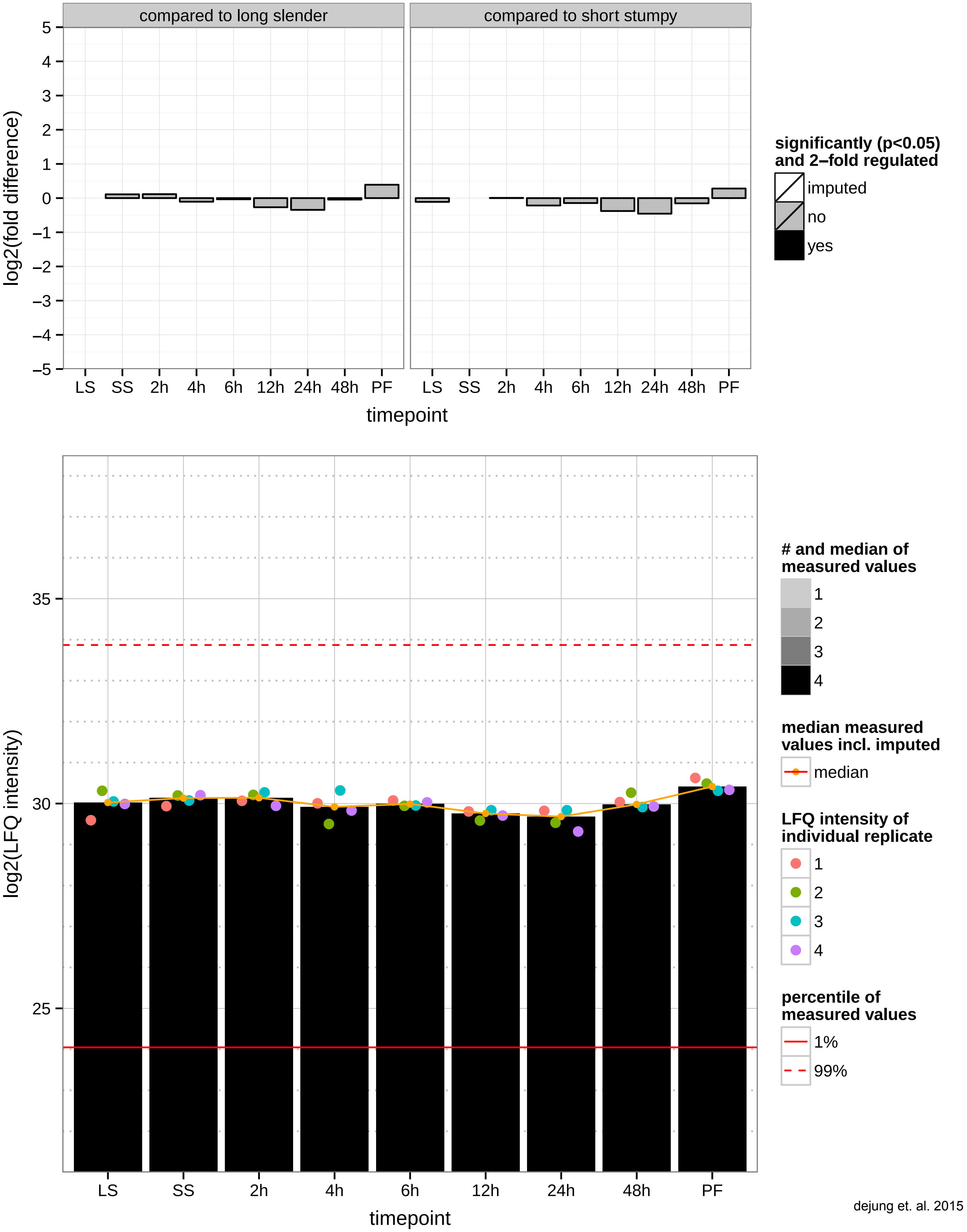
Tb5.20
Tb927.11.15100
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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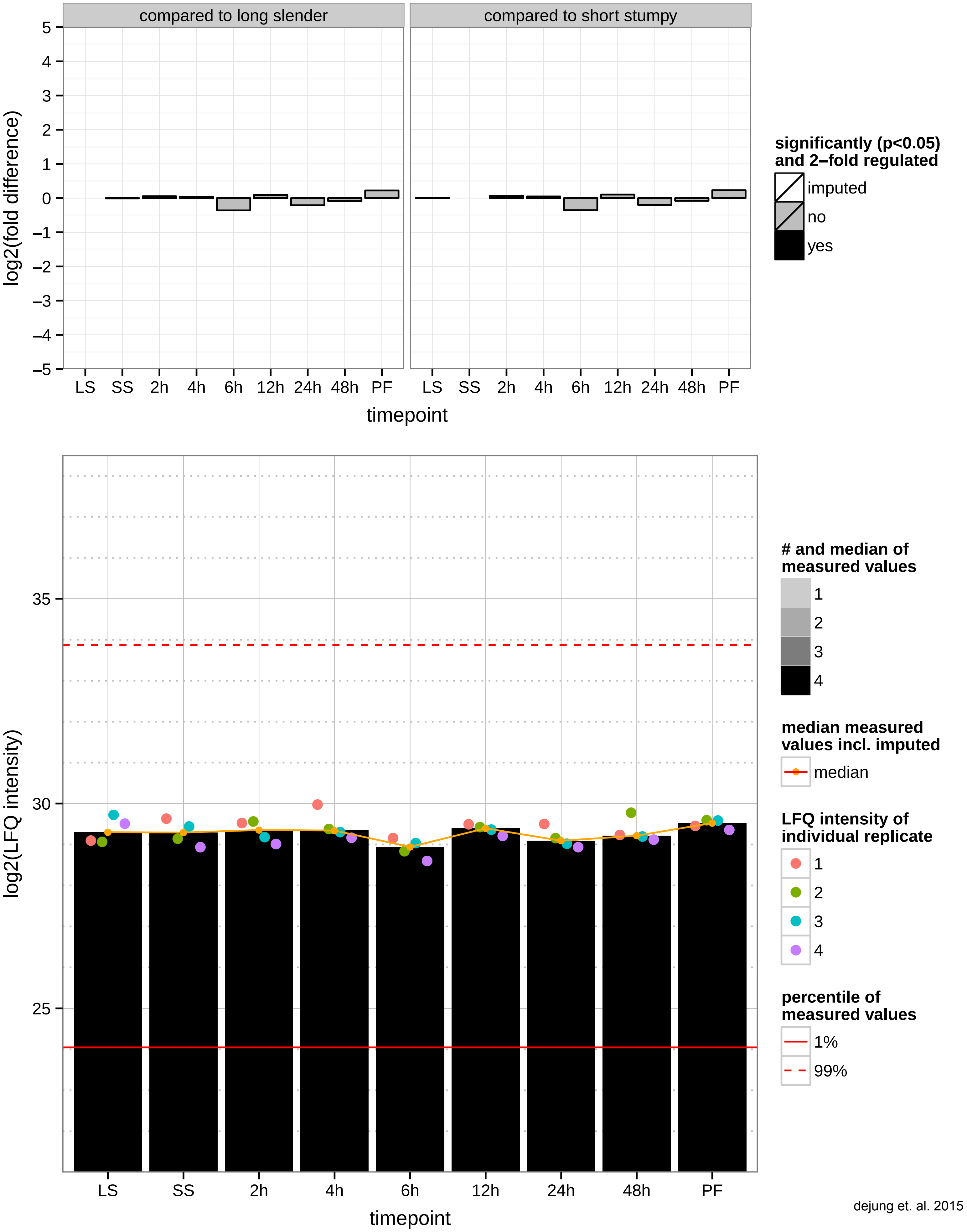
chaperone protein DNAj, putative, heat shock protein−like protein
Tb927.11.15130
AGOF: heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding, unfolded protein binding
PGOC: null
PGOP: protein folding



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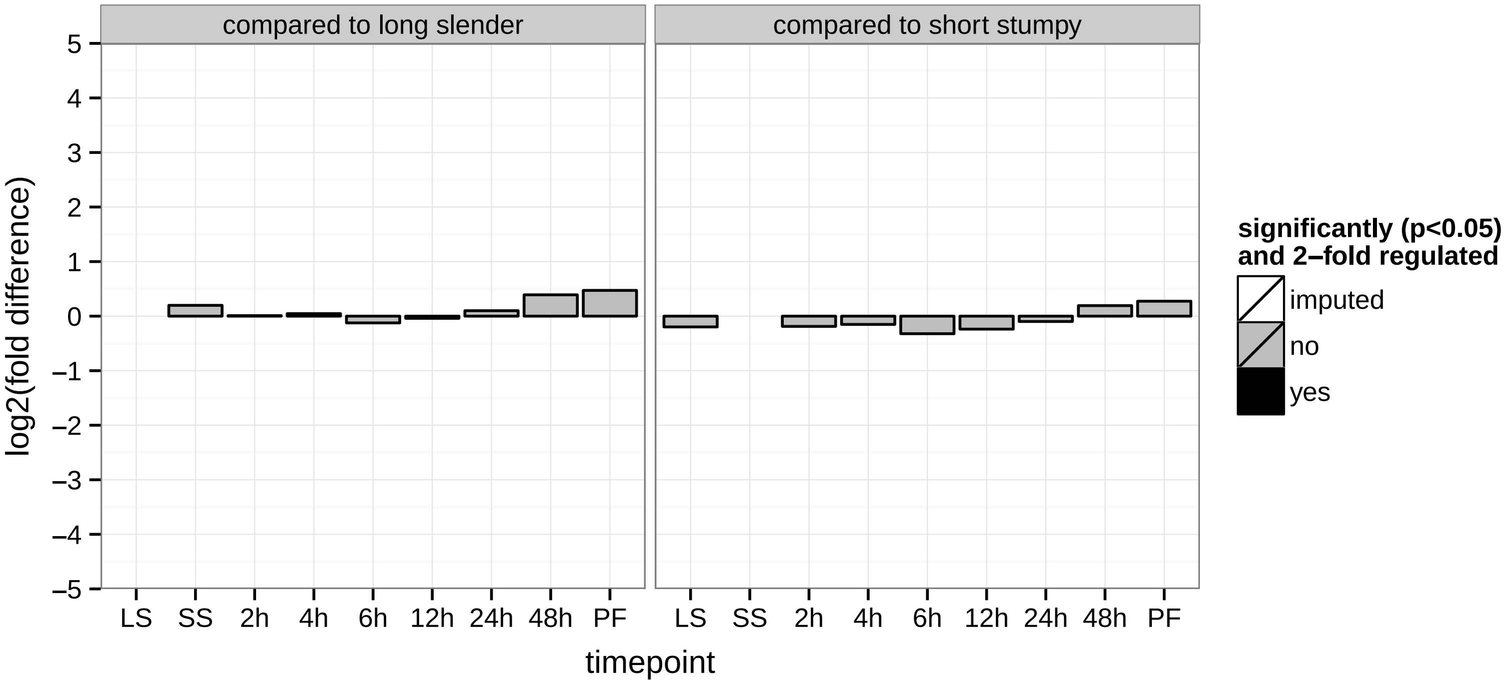
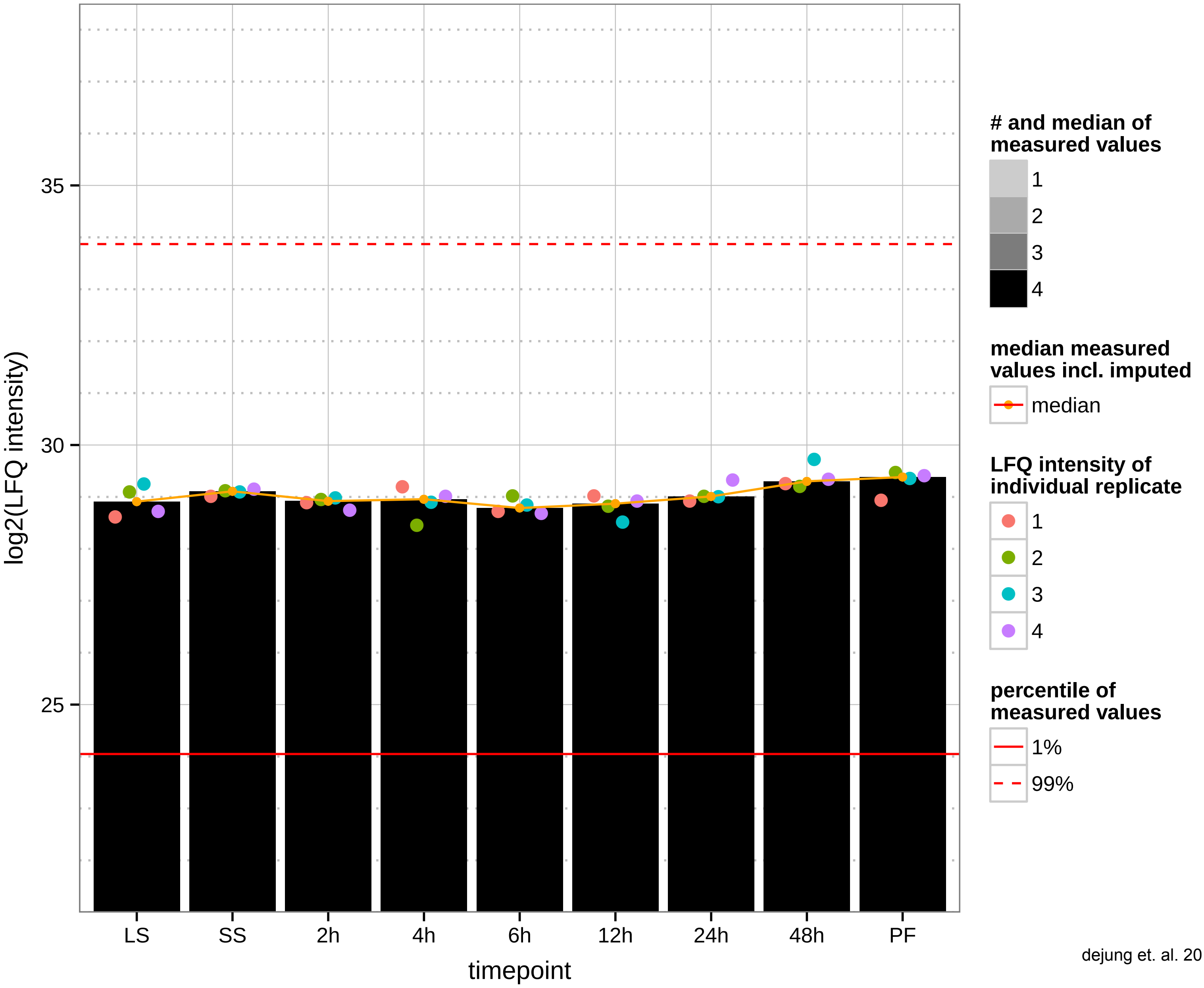
1–acyl–sn–glycerol–3–phosphate acyltransferase, putative
Tb927.11.15150
AGOF: 1–acylglycerol–3–phosphate O–acyltransferase activity
AGOC: integral to membrane
AGOP: metabolic process
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: metabolic process





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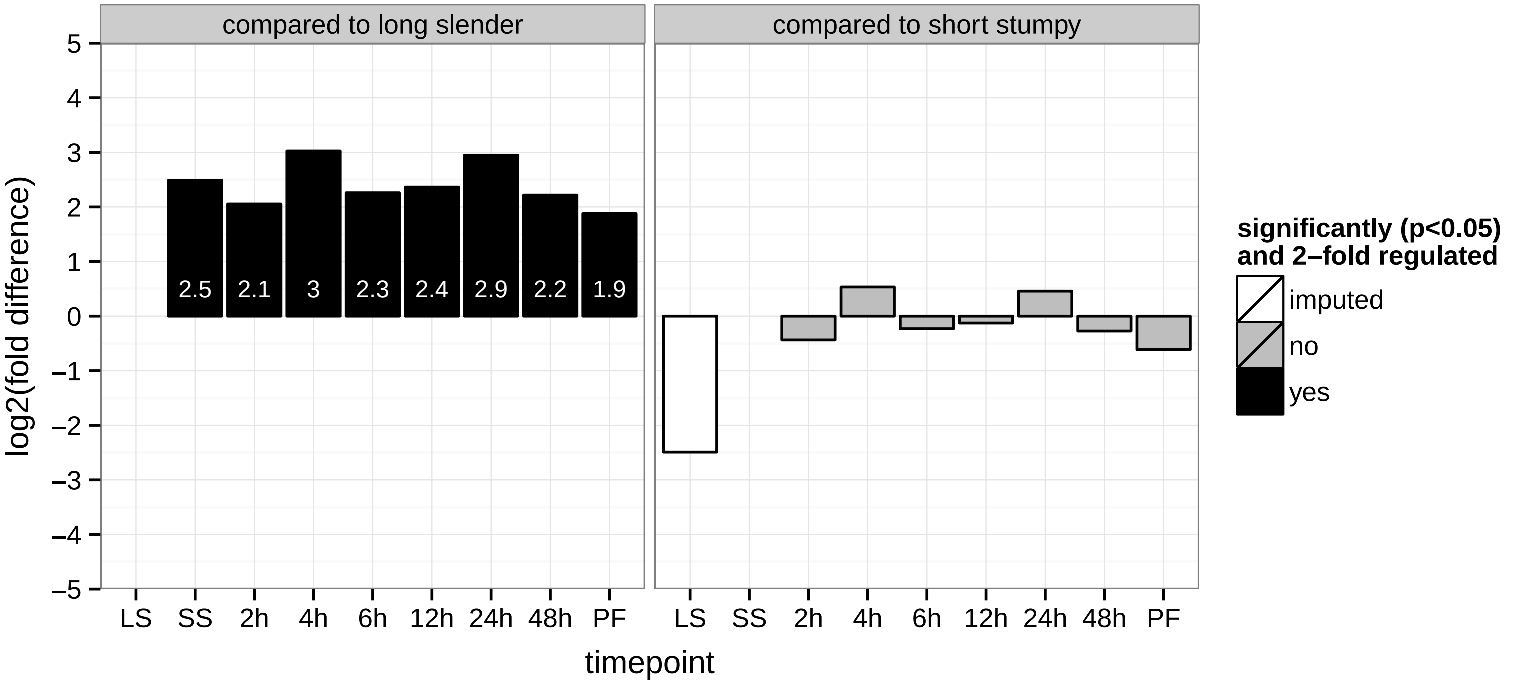
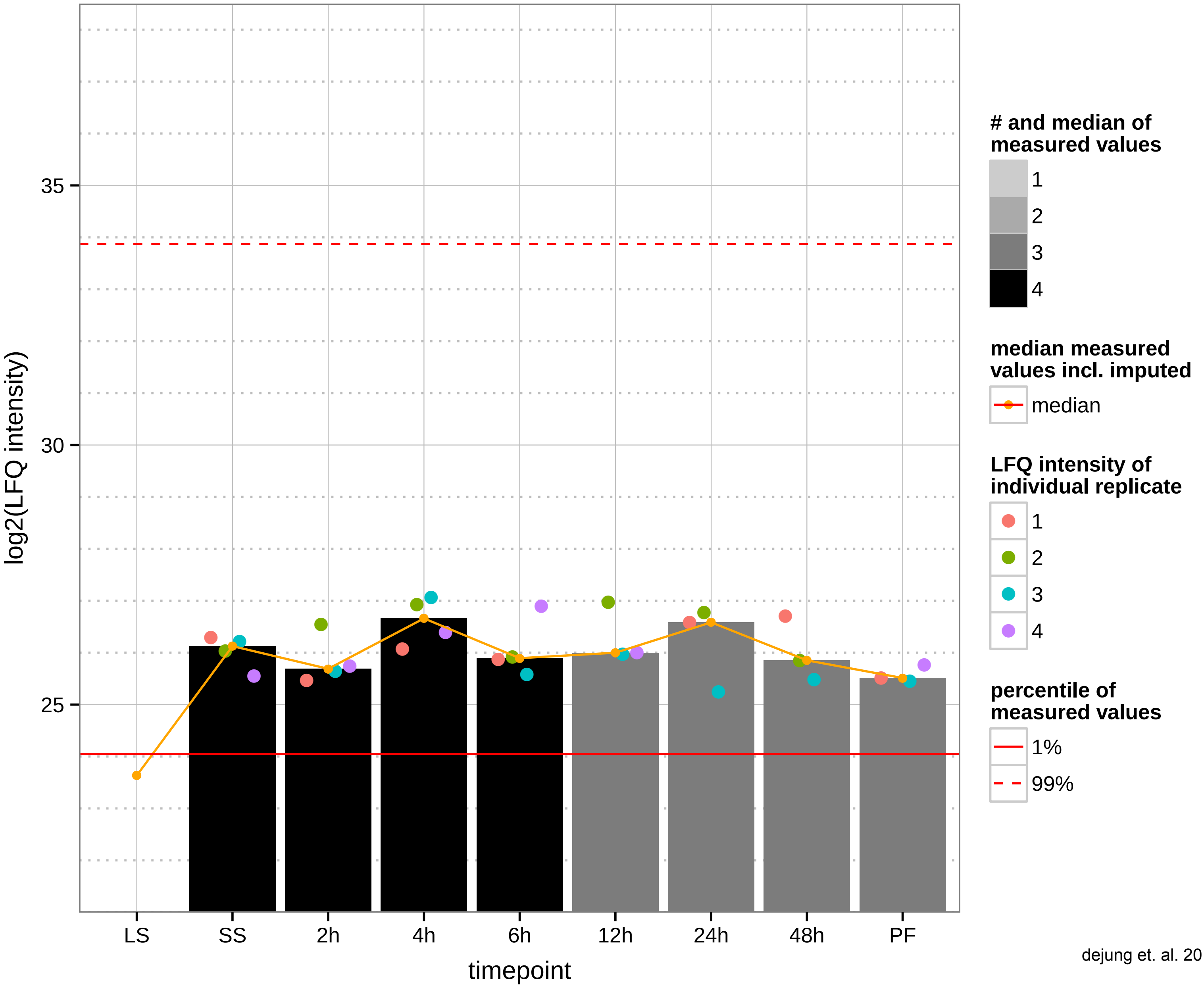
hypothetical protein, conserved
Tb927.11.15180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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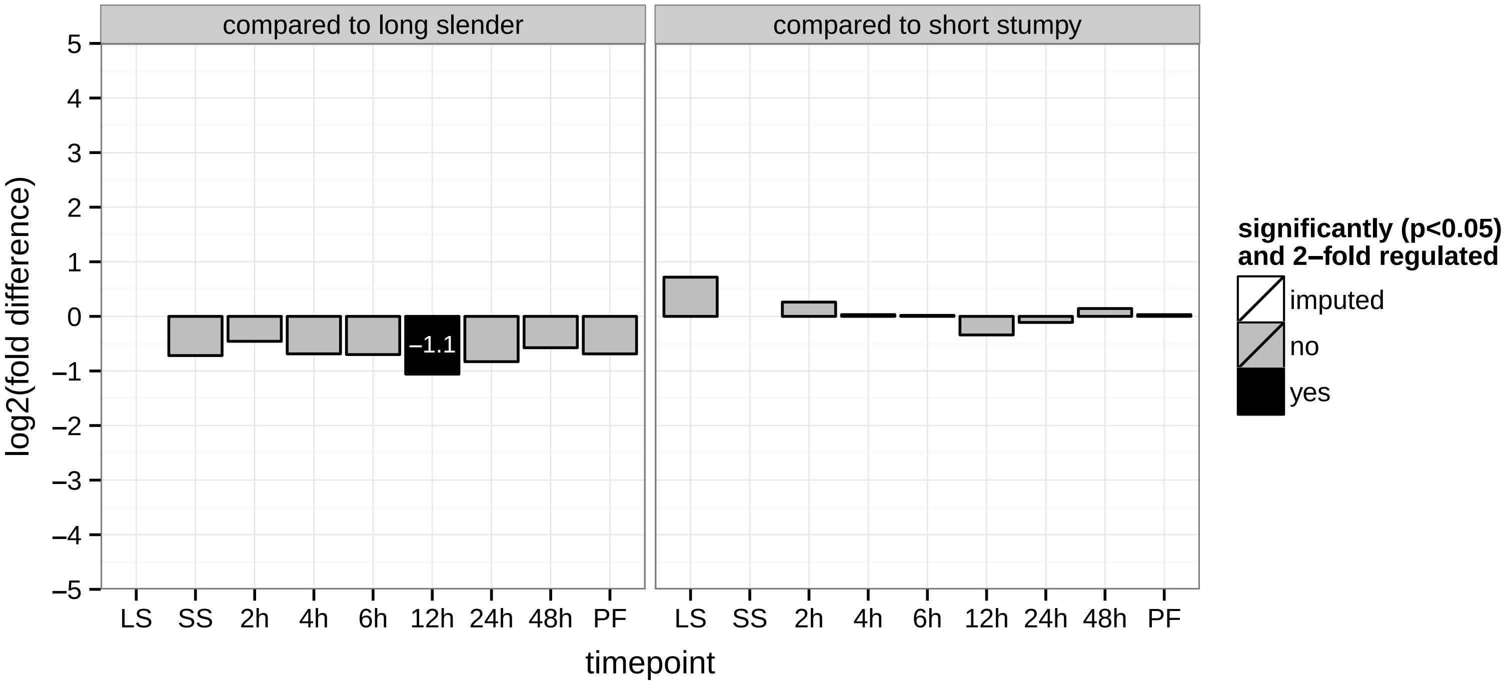
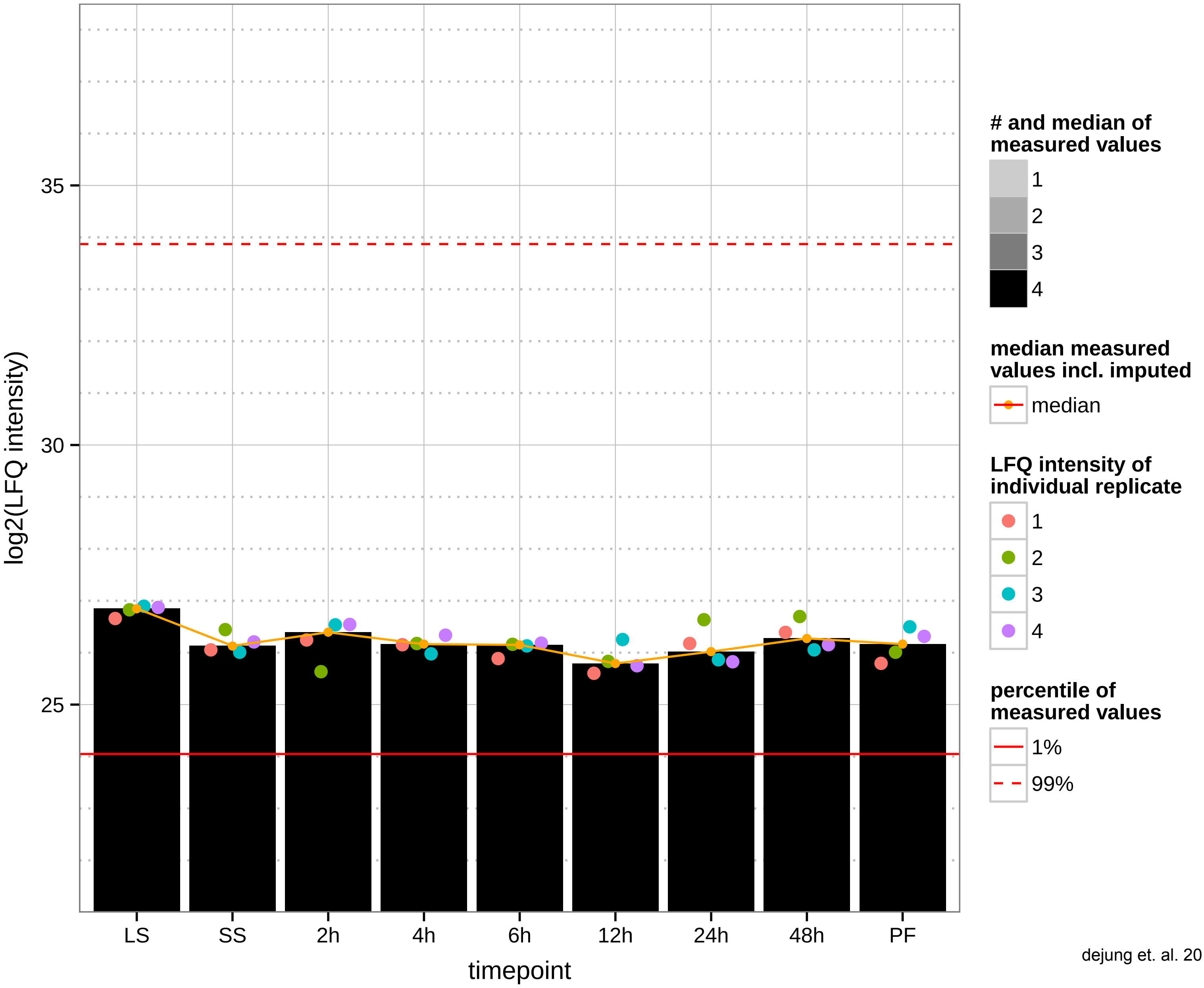
hypothetical protein, conserved
Tb927.11.15190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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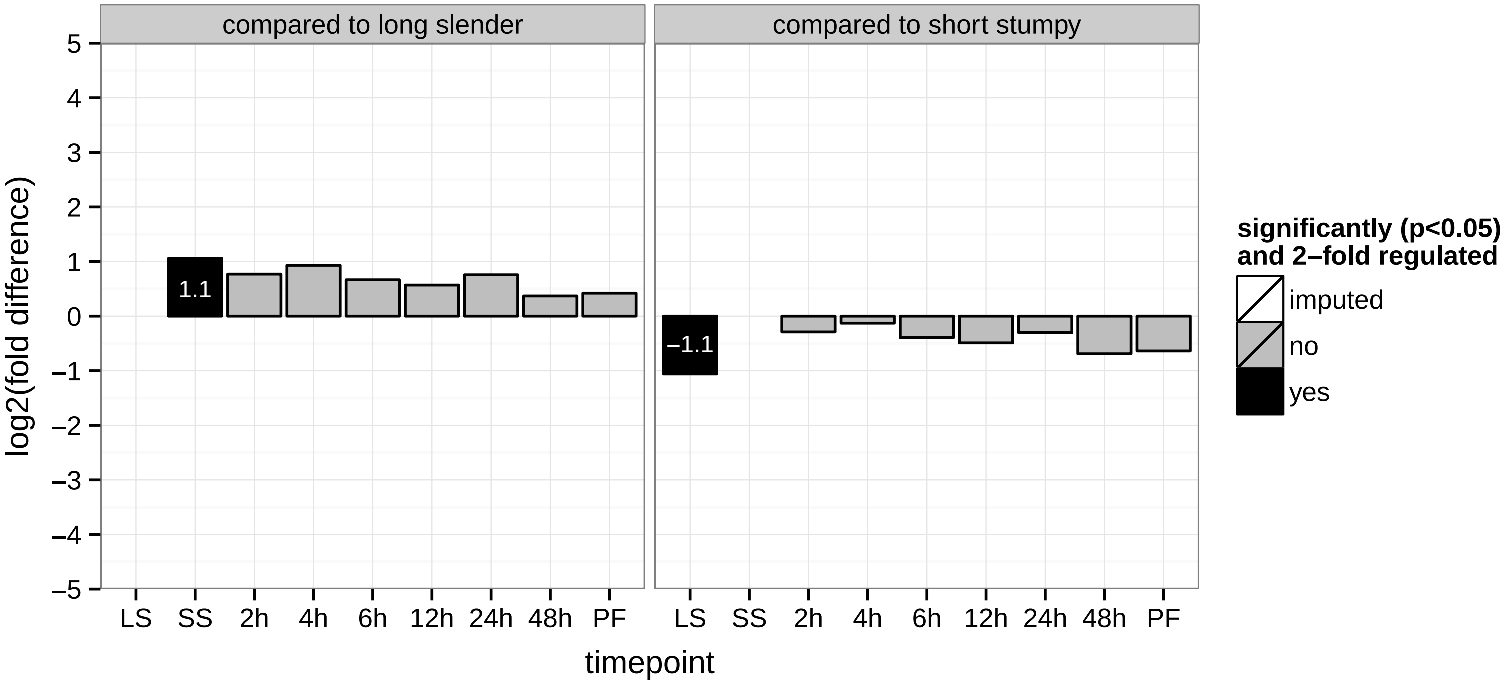
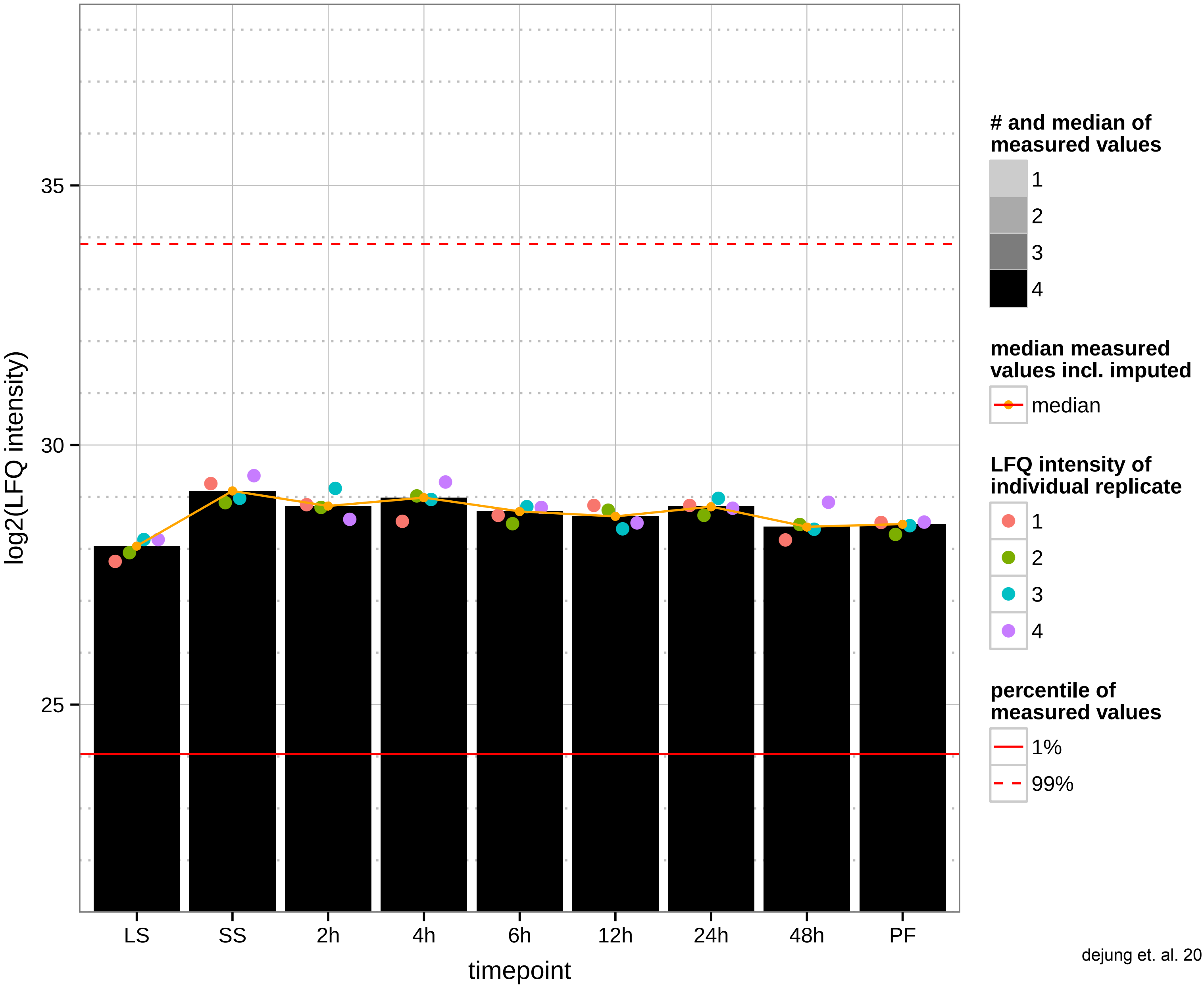
cytosolic coat protein, putative
Tb927.11.15230
AGOF: protein transmembrane transporter activity
AGOC: ER to Golgi transport vesicle membrane, integral to membrane
AGOP: ER to Golgi vesicle–mediated transport
PGOF: null
PGOC: integral to membrane
PGOP: transport





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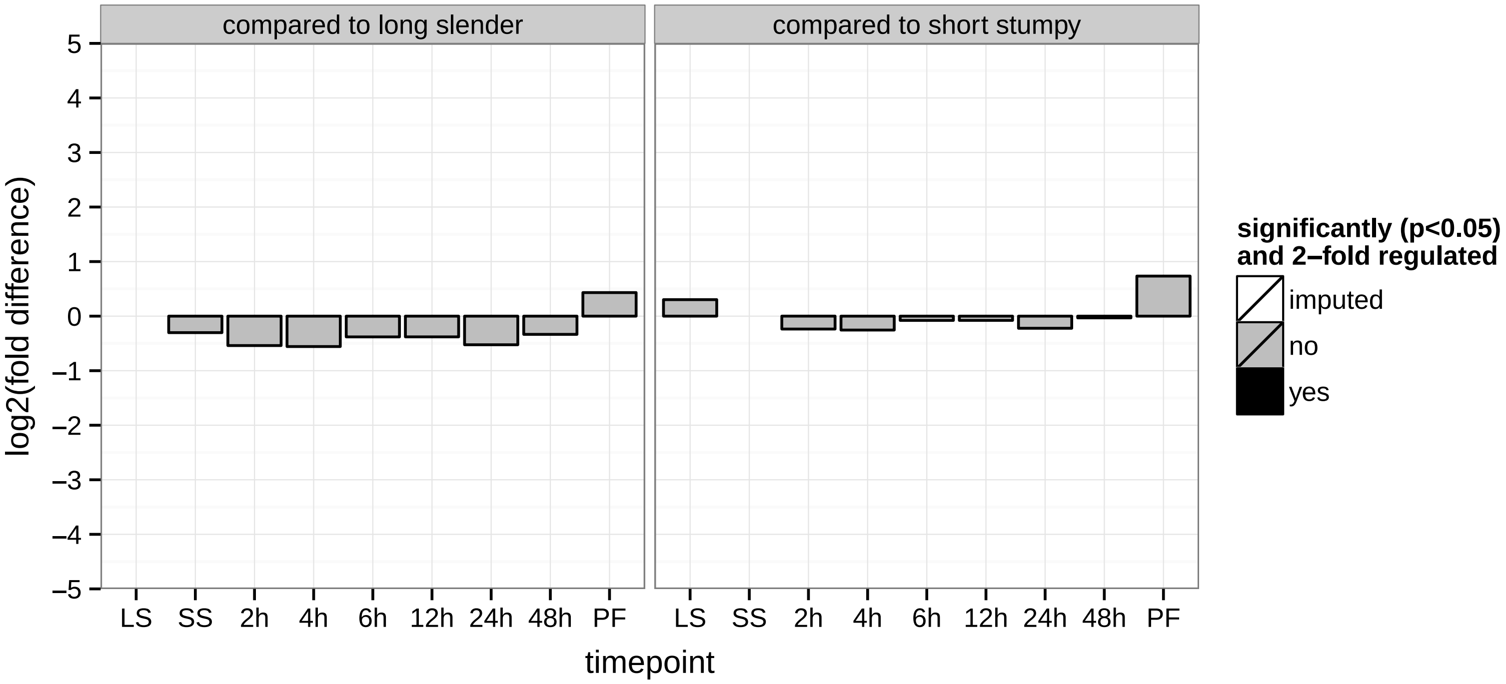
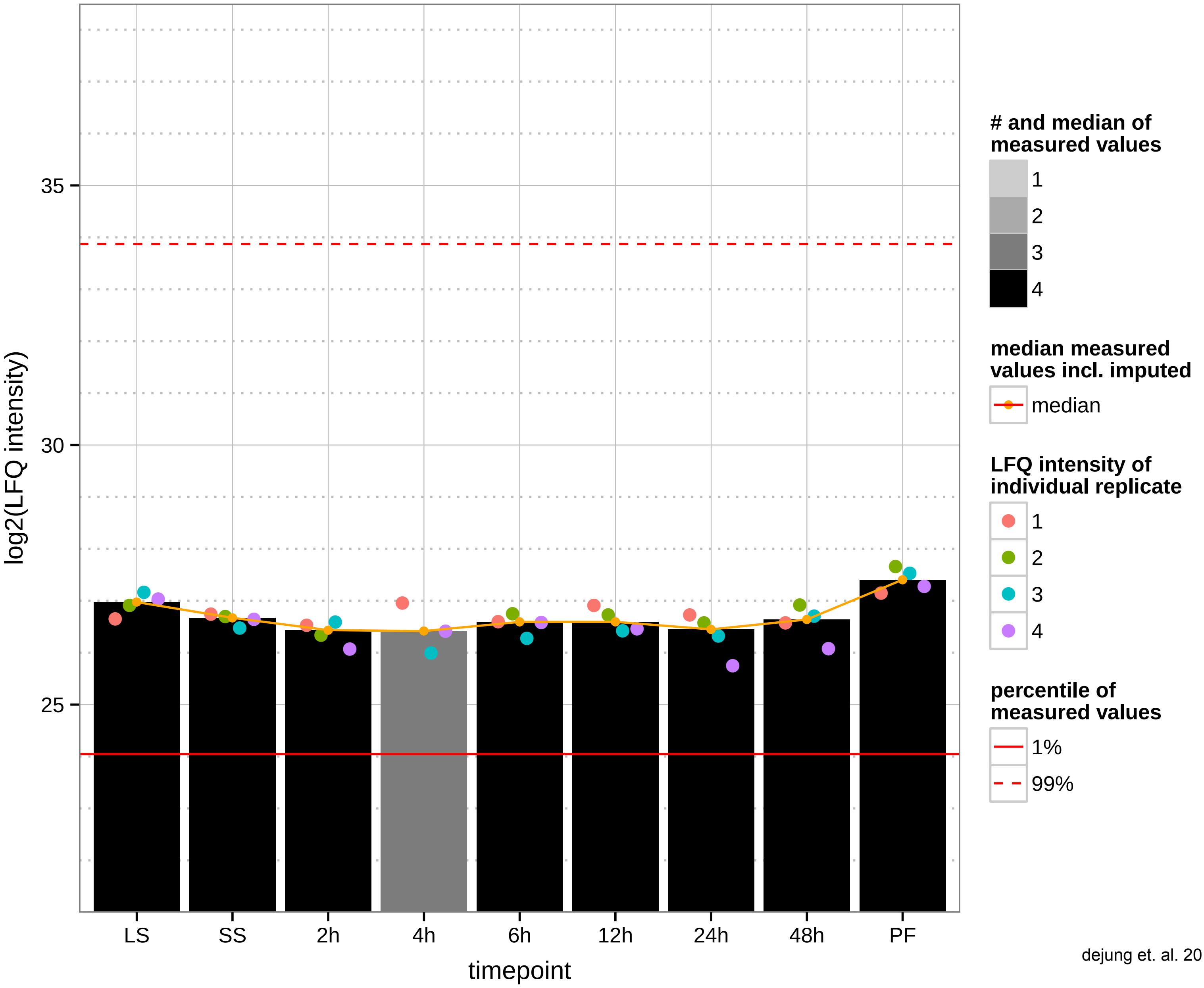
hypothetical protein, conserved
Tb927.11.15270
AGOF: nucleotidyltransferase activity
AGOC: null
AGOP: biosynthetic process
PGOF: nucleotidyltransferase activity
PGOC: null
PGOP: biosynthetic process





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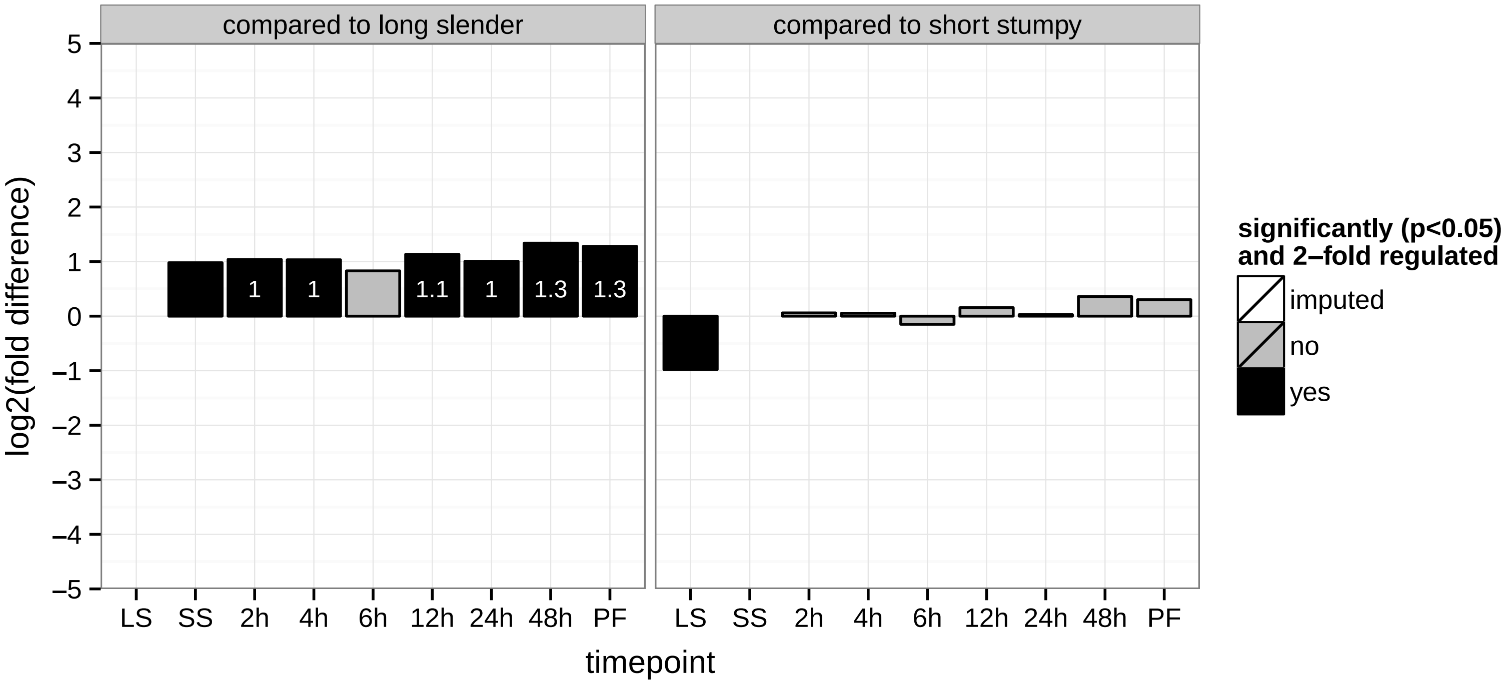
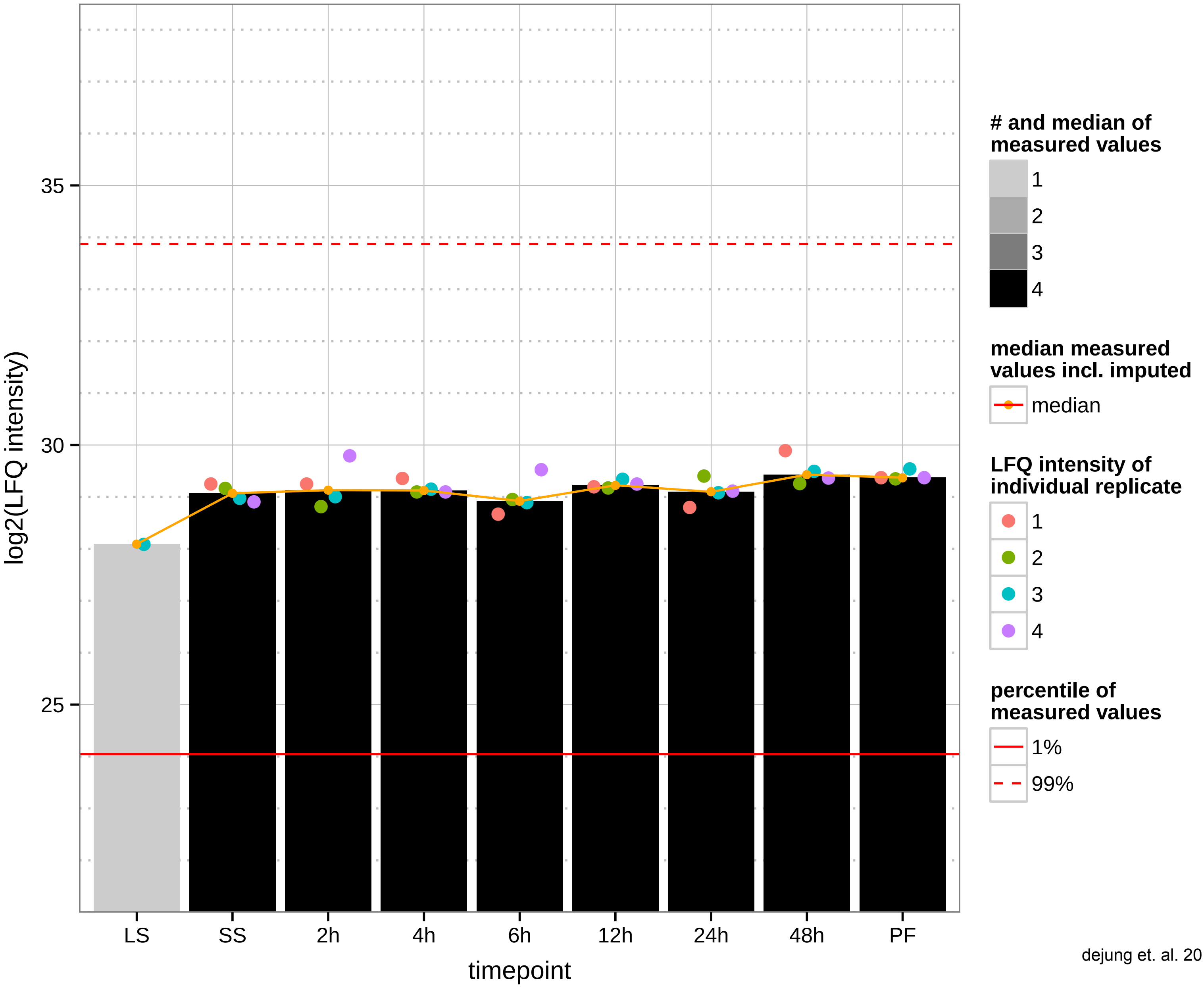
isovaleryl–coA dehydrogenase, putative
Tb927.11.1540
AGOF: acyl–CoA dehydrogenase activity, oxidoreductase activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: acyl–CoA dehydrogenase activity, oxidoreductase activity, acting on the CH–CH group of donors
PGOC: null
PGOP: metabolic process, oxidation–reduction process





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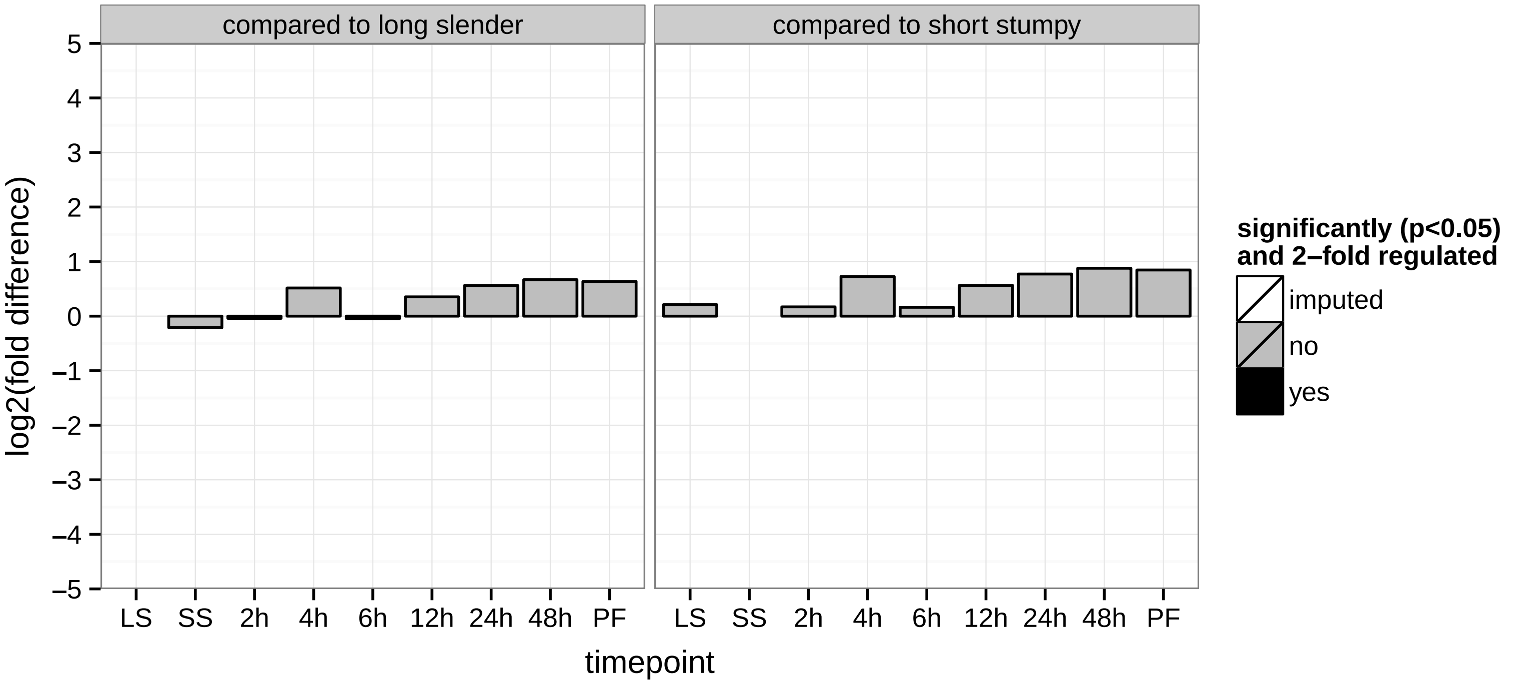
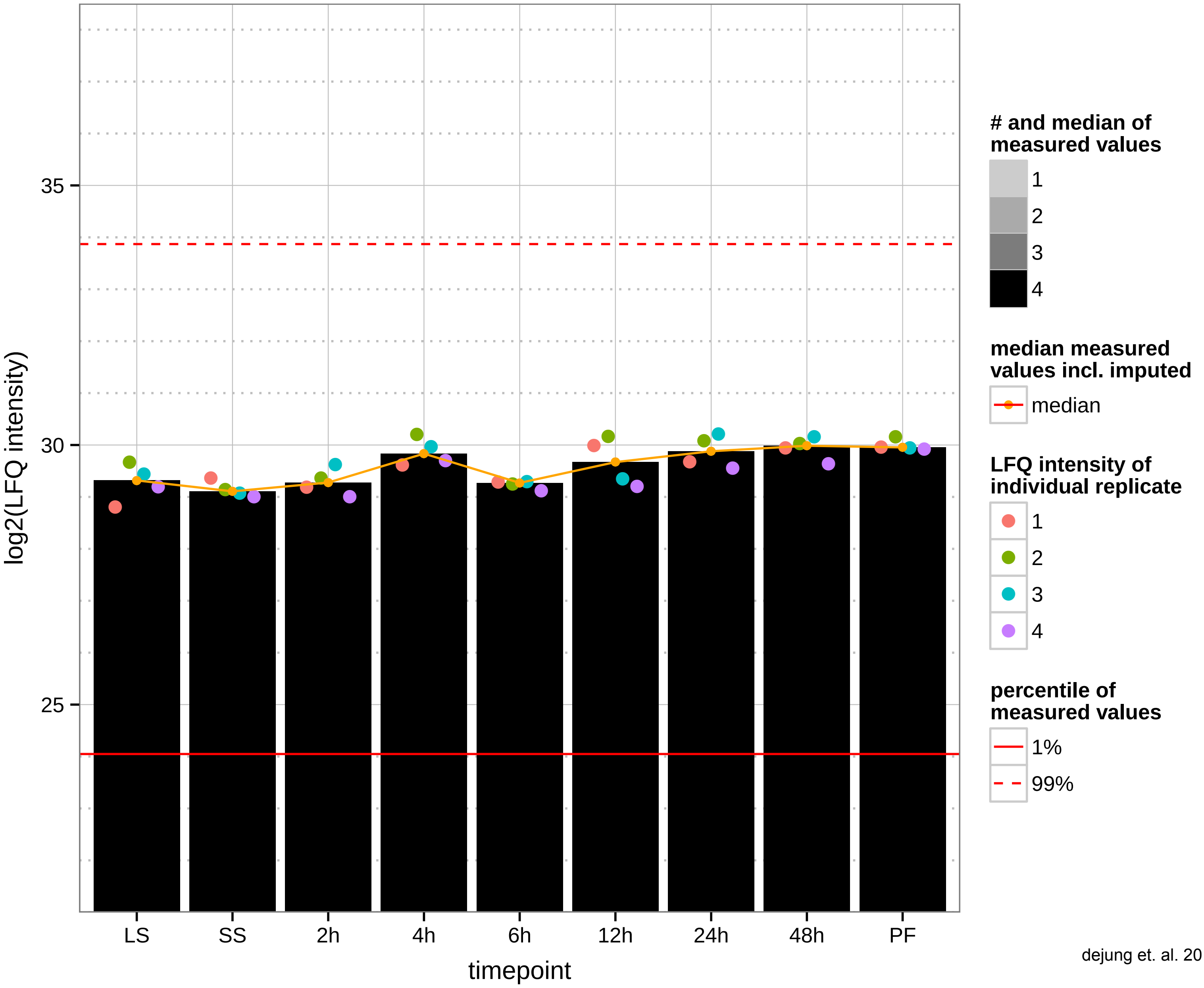
hypothetical protein, conserved
Tb927.11.15420
AGOF: translation initiation factor activity
AGOC: nucleus
AGOP: translational initiation
PGOF: binding
PGOC: null
PGOP: null





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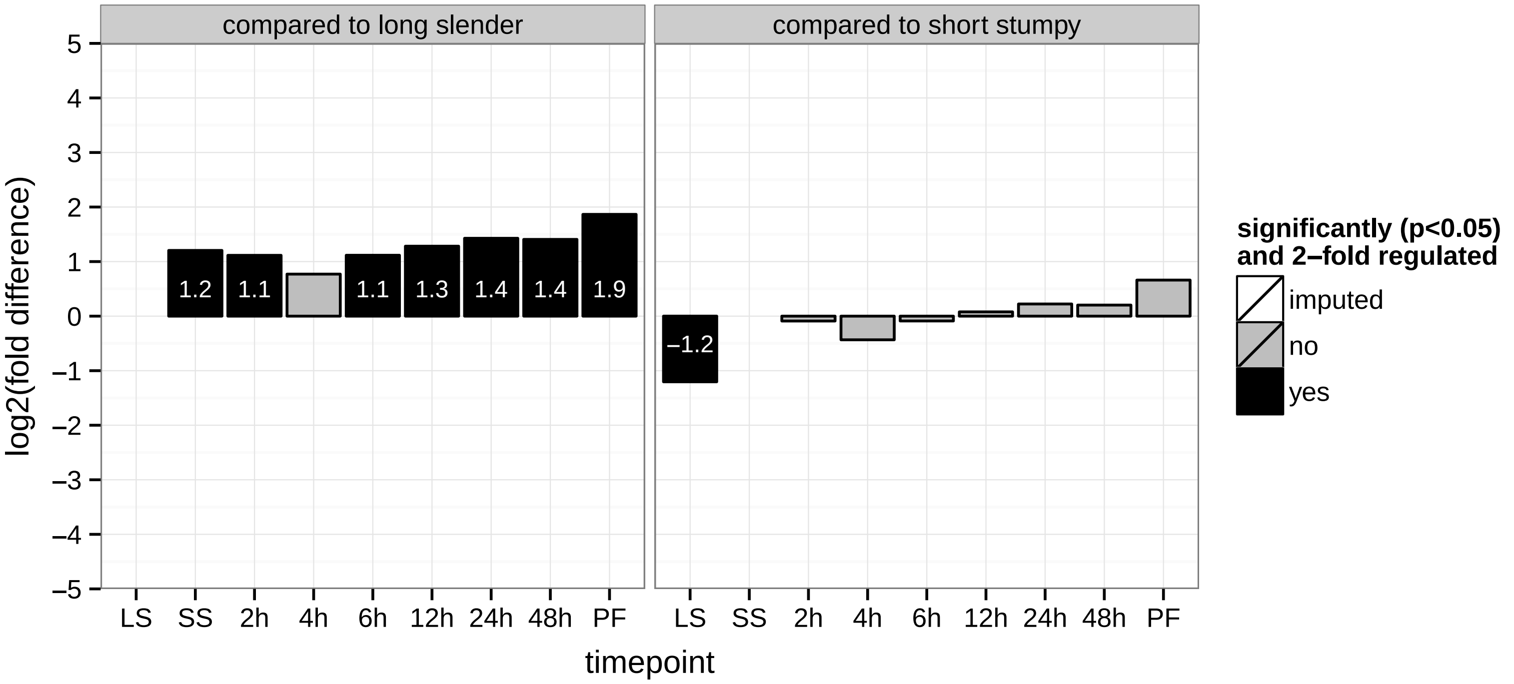
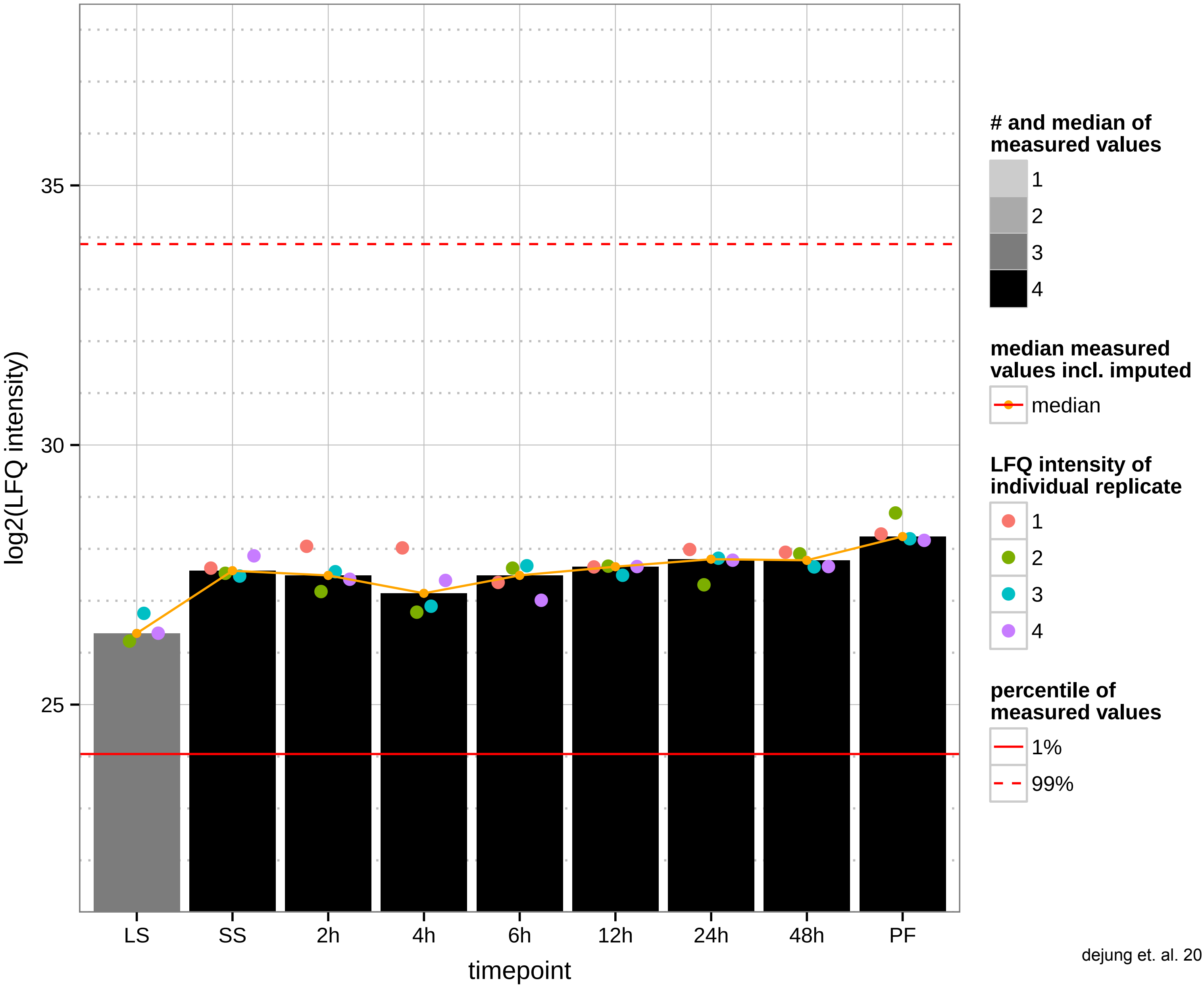
U5 small nuclear ribonucleoprotein component, putative, U5 snrnp–specific protein
Tb927.11.15430
AGOF: GTP binding, GTPase activity
AGOC: nucleus
AGOP: translation
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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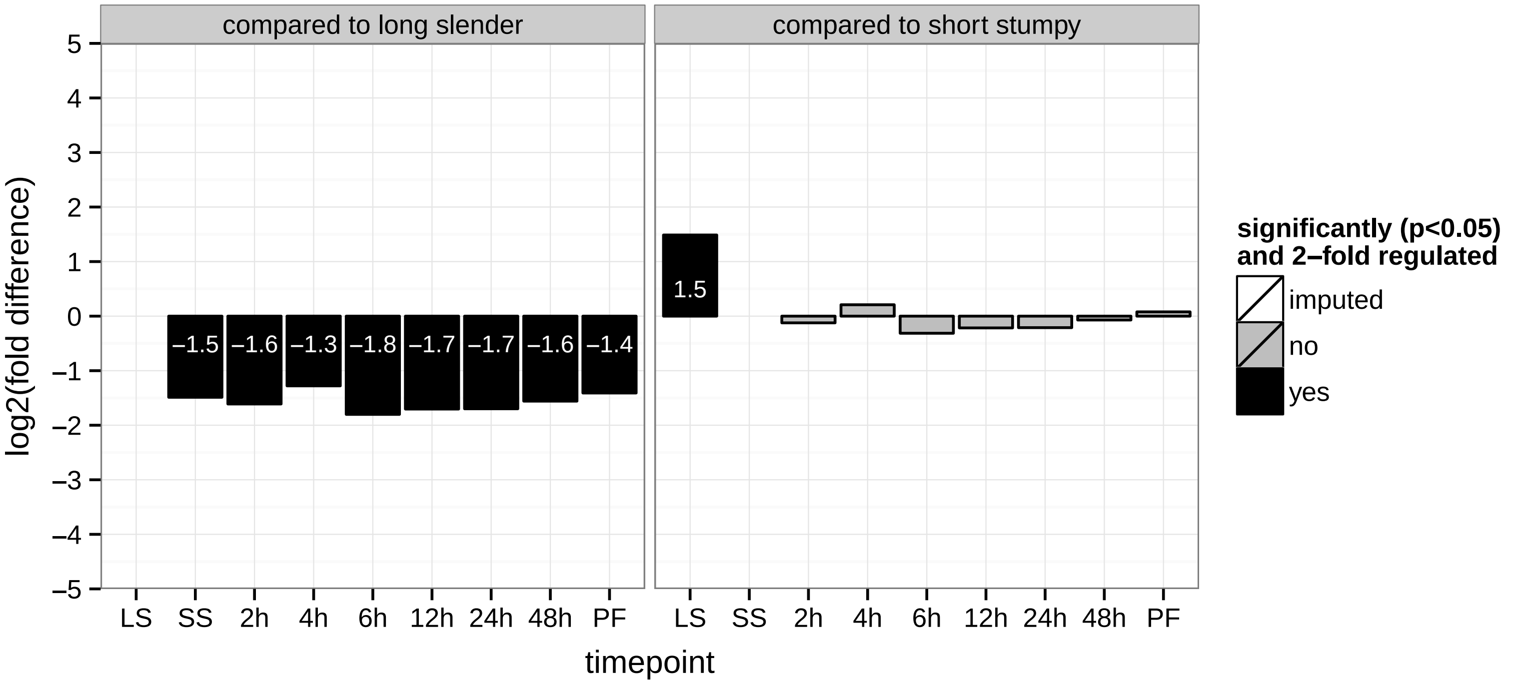
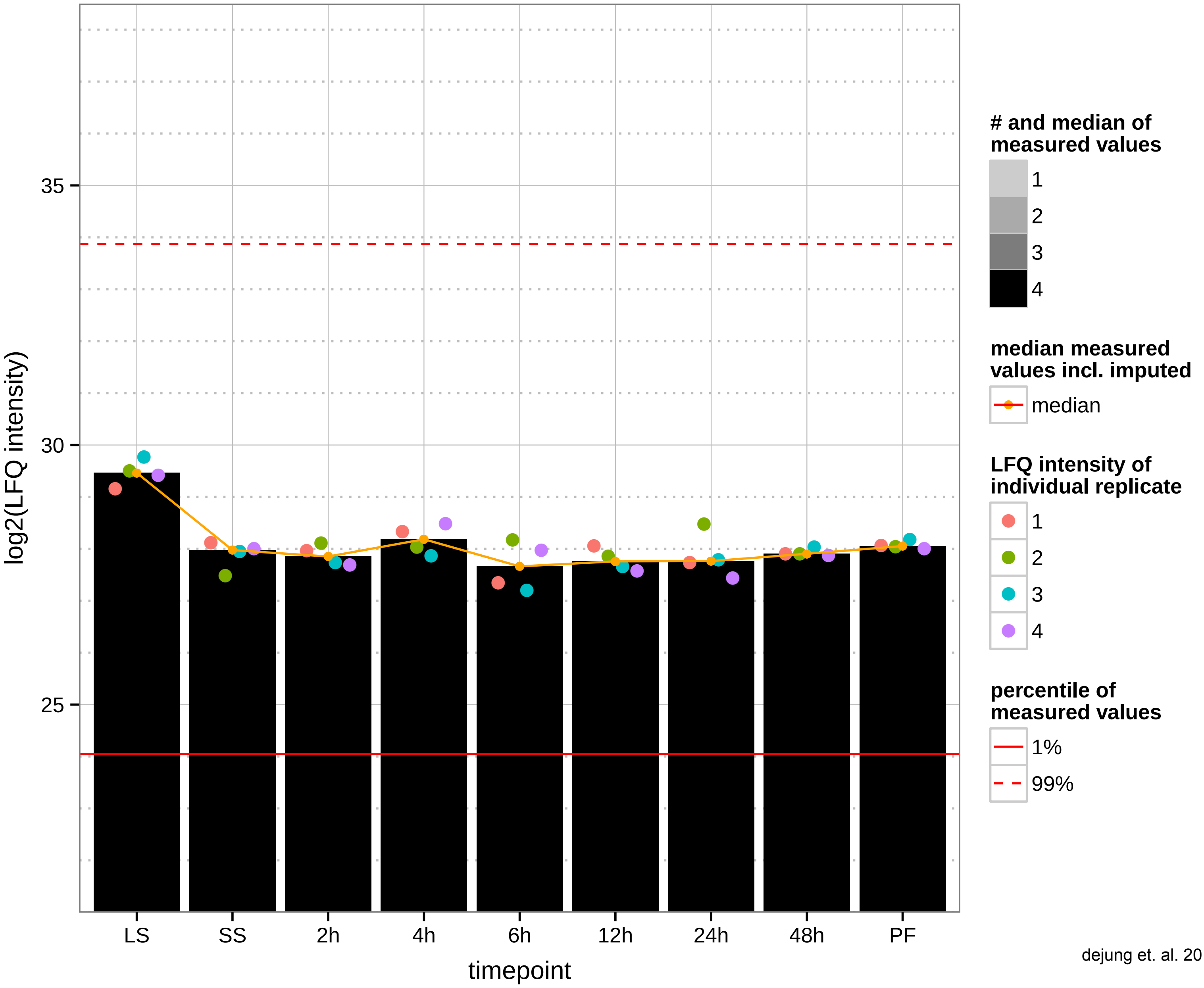
heat shock protein Hsp20, putative
Tb927.11.15480
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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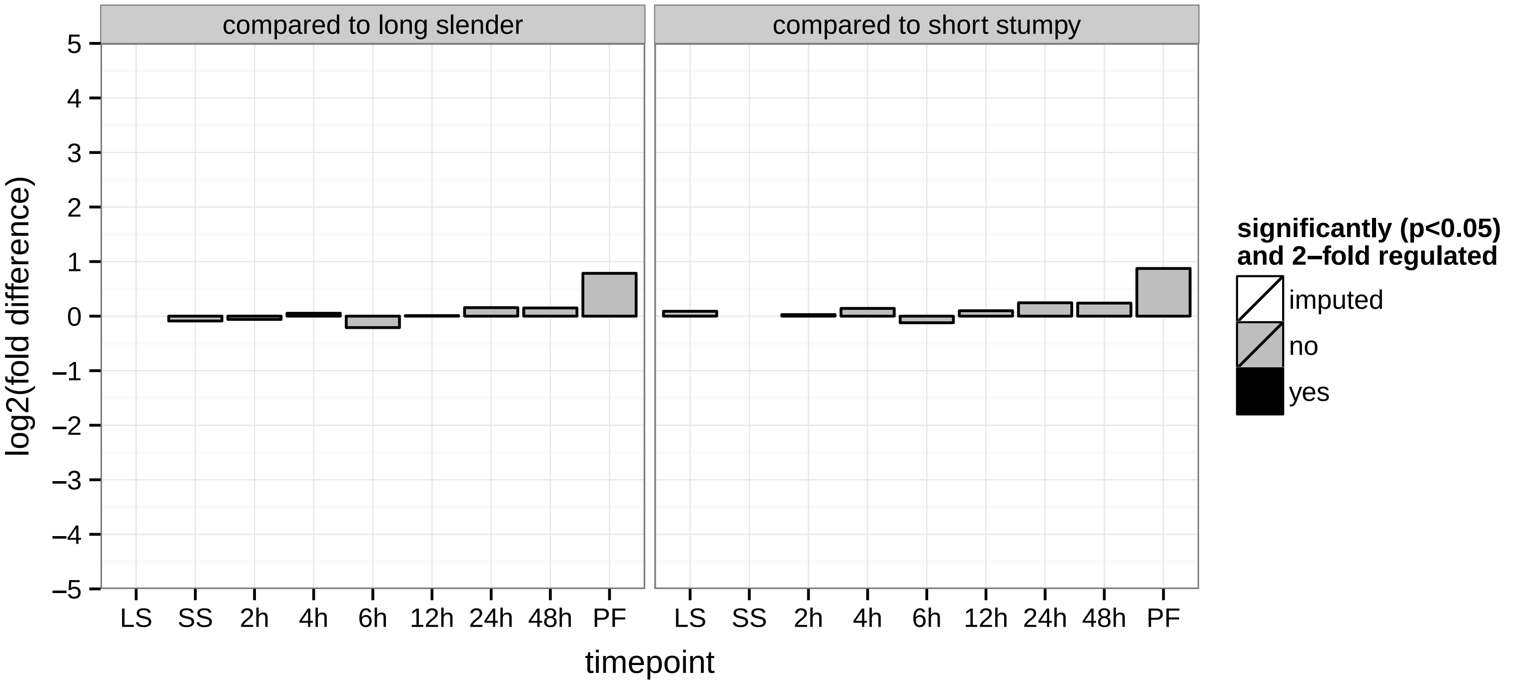
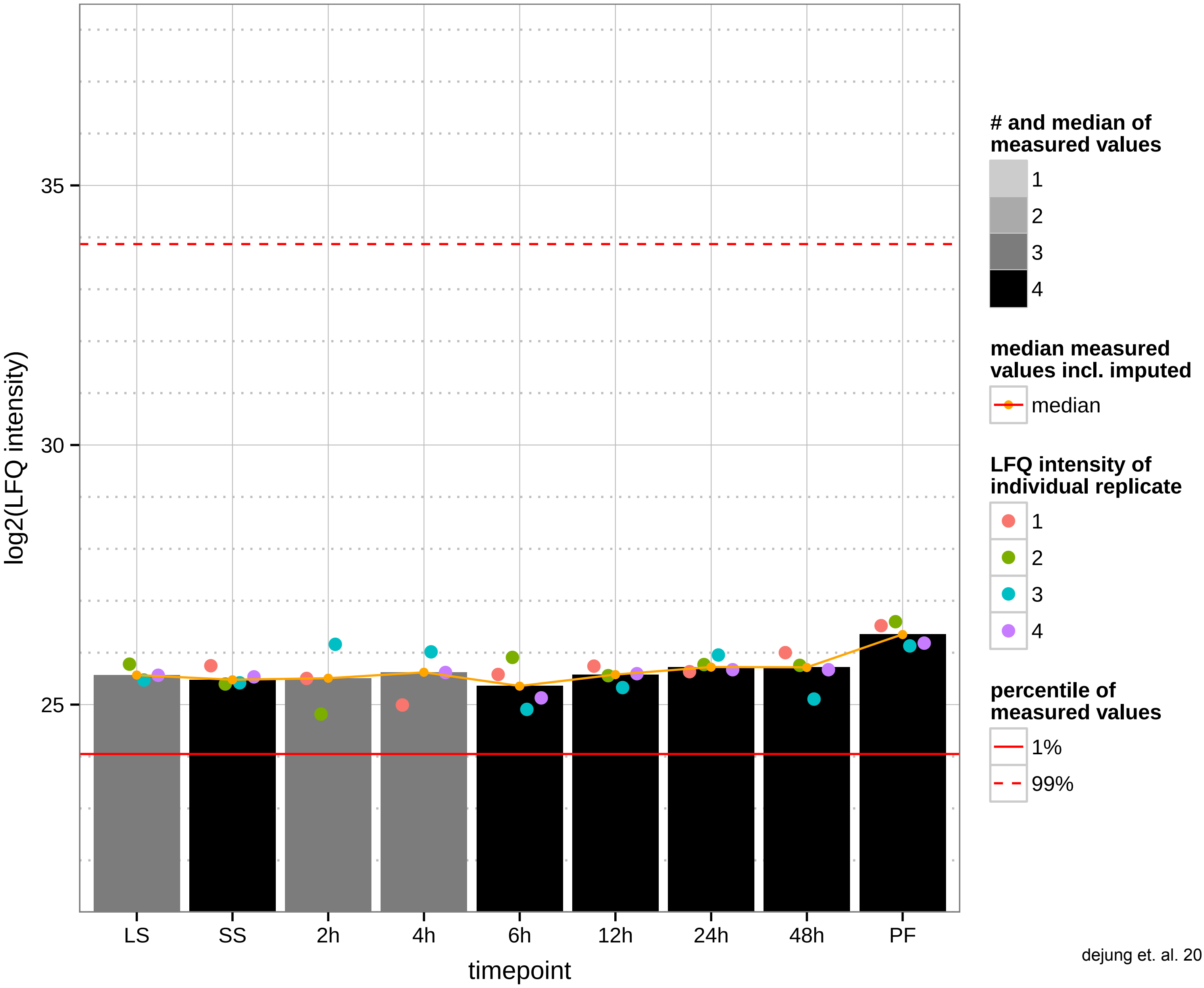
Nucleoporin (TbNup53a)
Tb927.11.15560
AGOF: structural constituent of nuclear pore
AGOC: nuclear pore
AGOP: null
PGOF: structural constituent of nuclear pore
PGOC: nuclear pore
PGOP: null





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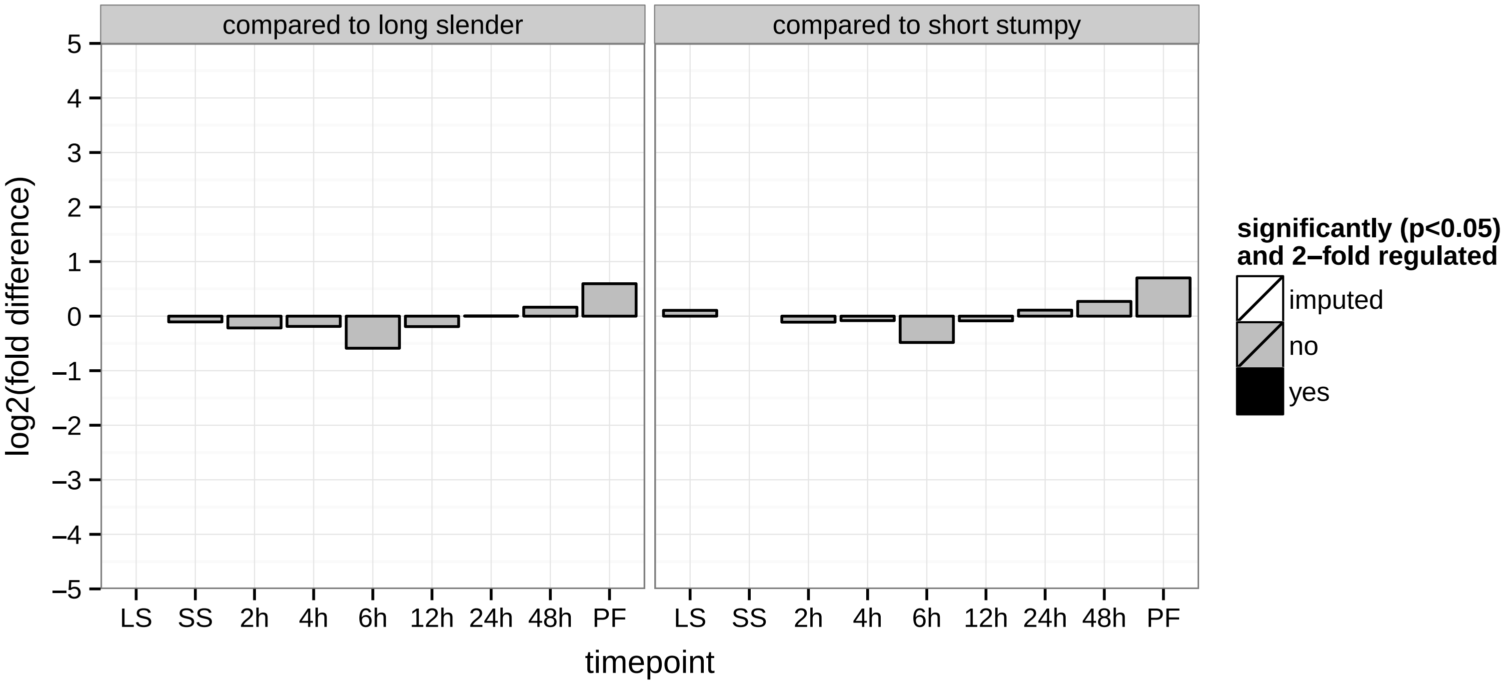
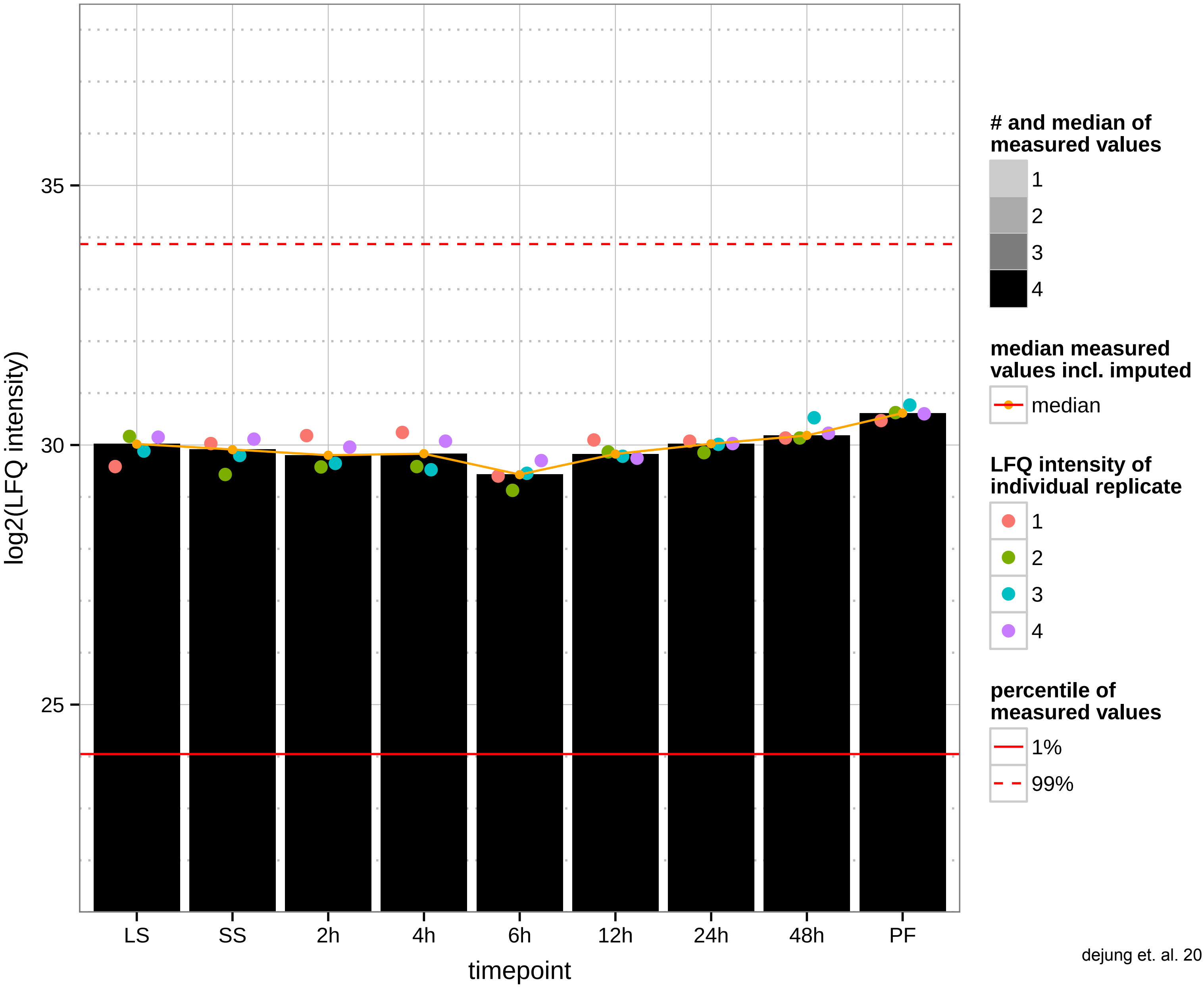
1, 2–Dihydroxy–3–keto–5–methylthiopentene dioxygenase, putative
Tb927.11.1560
AGOF: dioxygenase activity, metal ion binding
AGOC: cytosol
AGOP: L–methionine salvage from methylthioadenosine
PGOF: acireductone dioxygenase [iron(II)–requiring] activity
PGOC: null
PGOP: oxidation–reduction process





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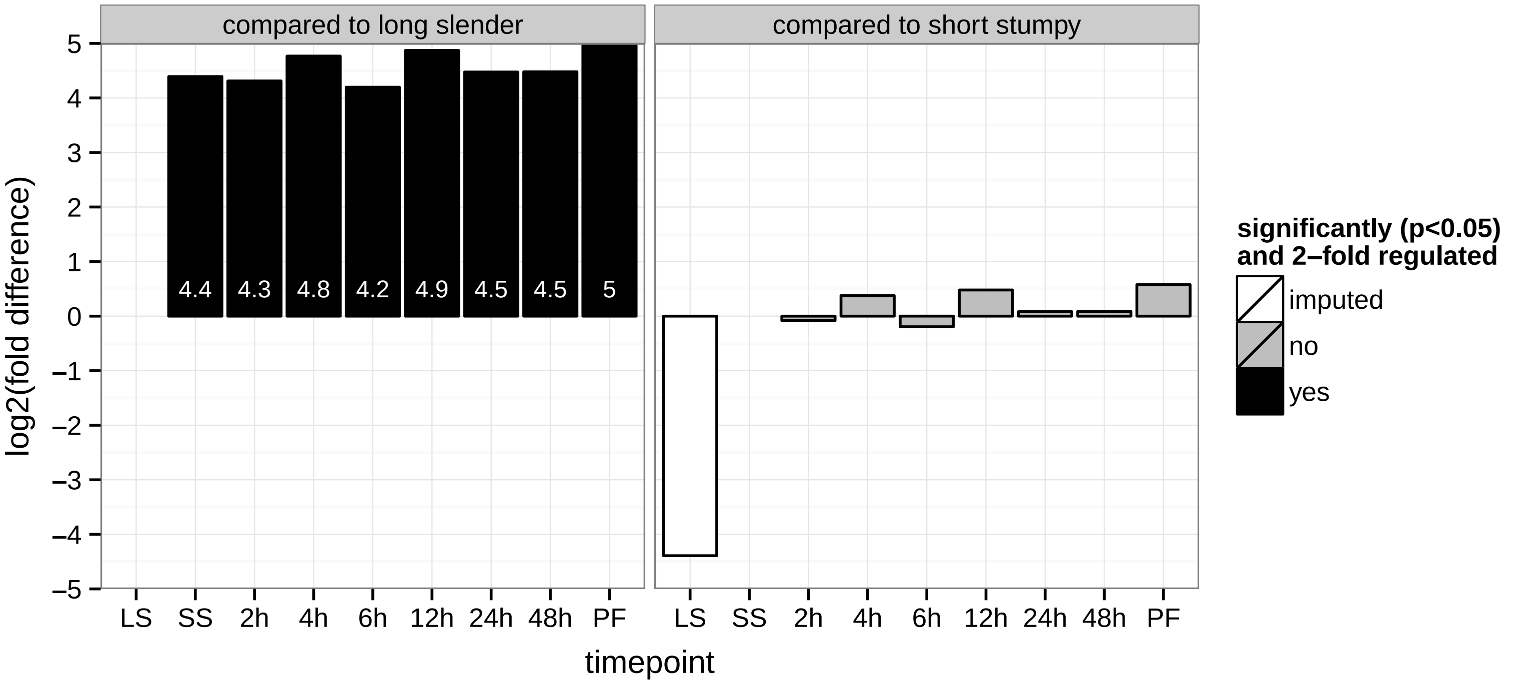
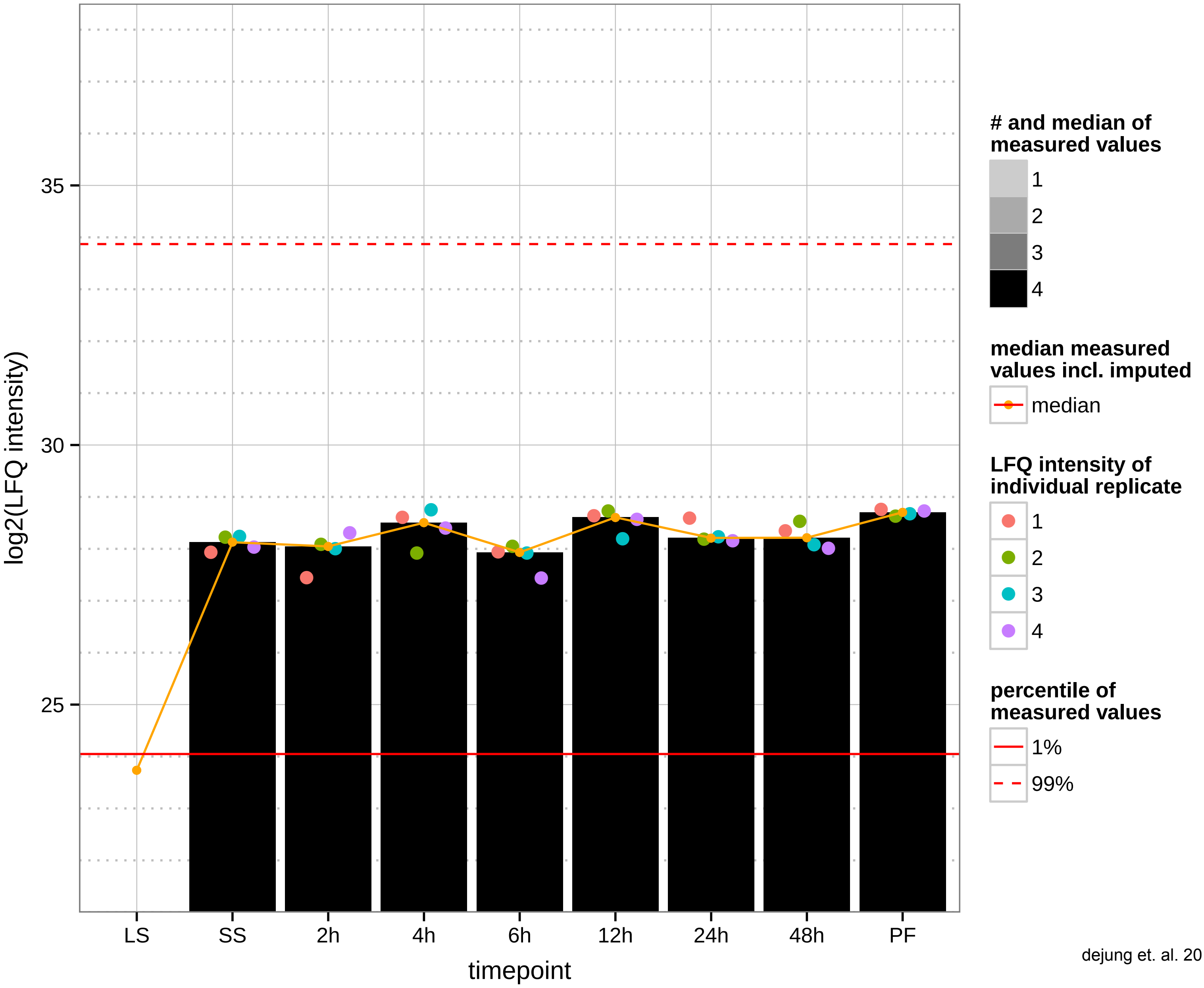
mitochondrial RNA binding complex 1 subunit, NUDIX hydrolase, putative (MERS1)
Tb927.11.15640
AGOF: RNA binding, hydrolase activity
AGOC: mitochondrion
AGOP: cytidine to uridine editing, mRNA stabilization
PGOF: hydrolase activity
PGOC: null
PGOP: null





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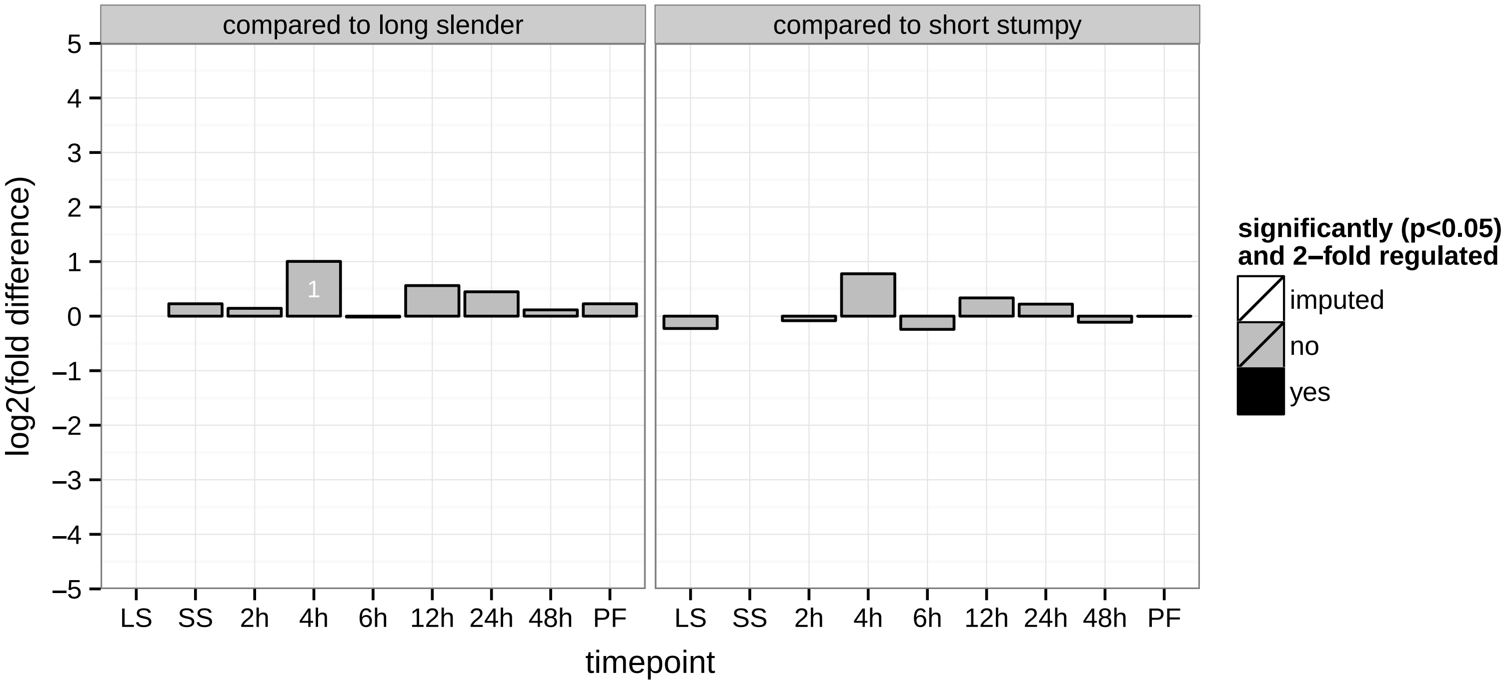
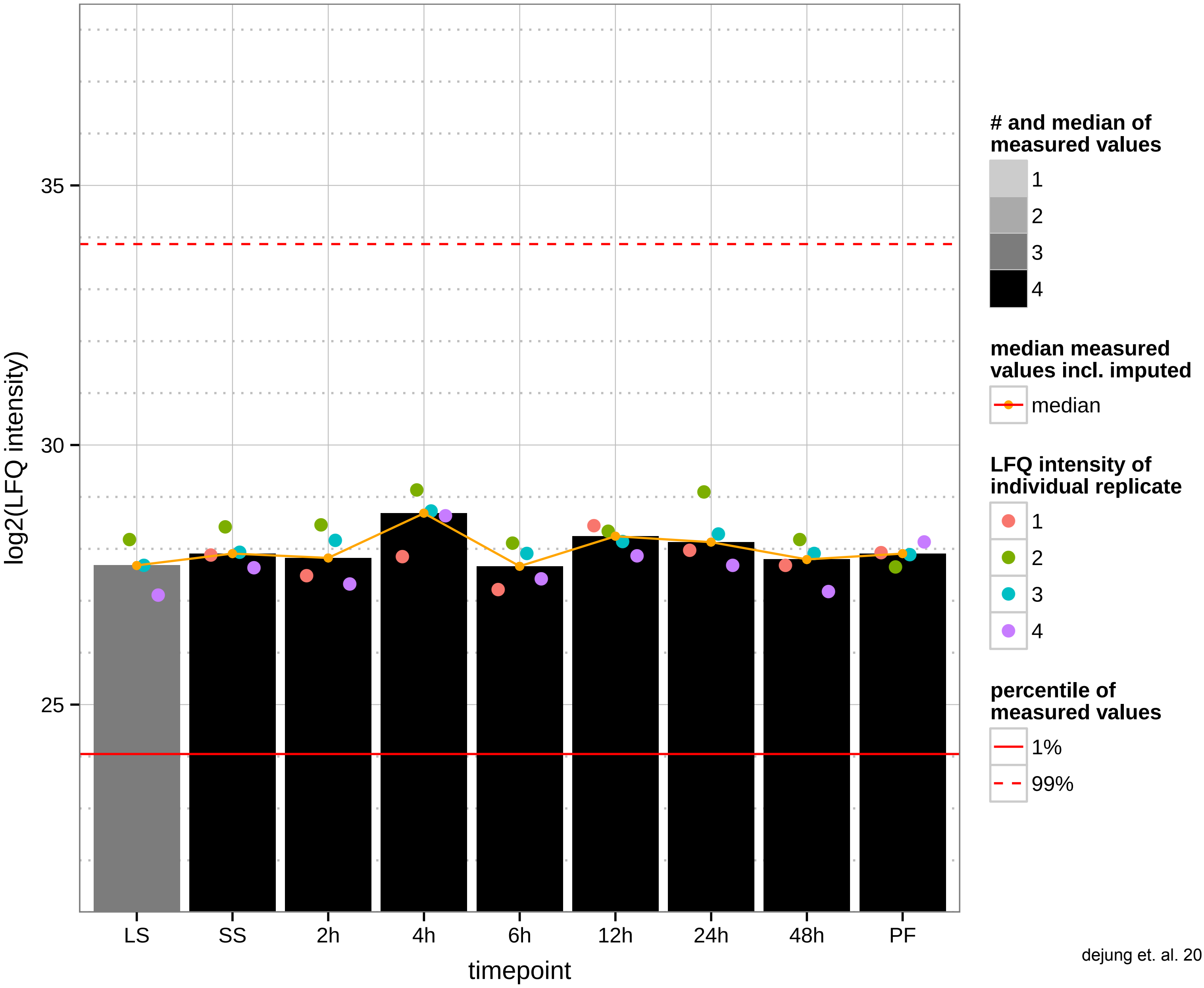
hypothetical protein, conserved
Tb927.11.15680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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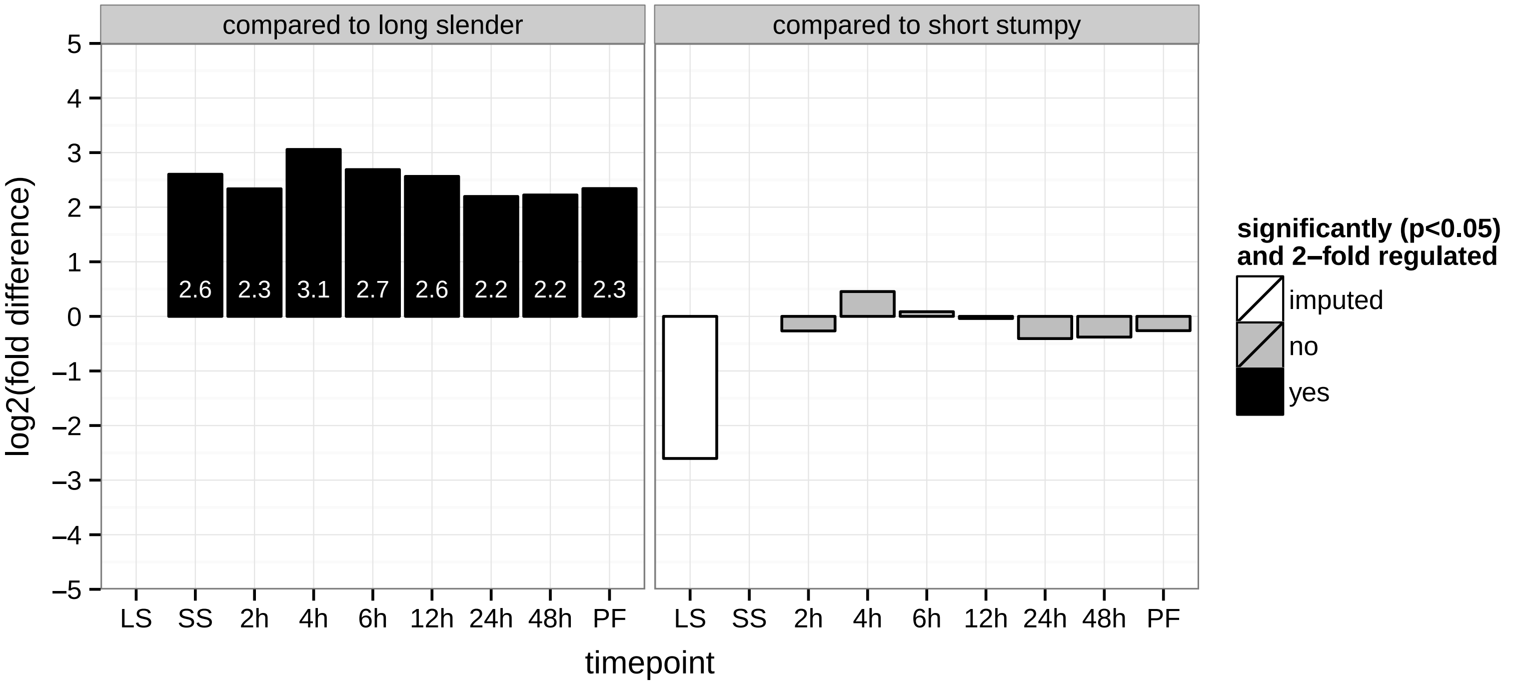
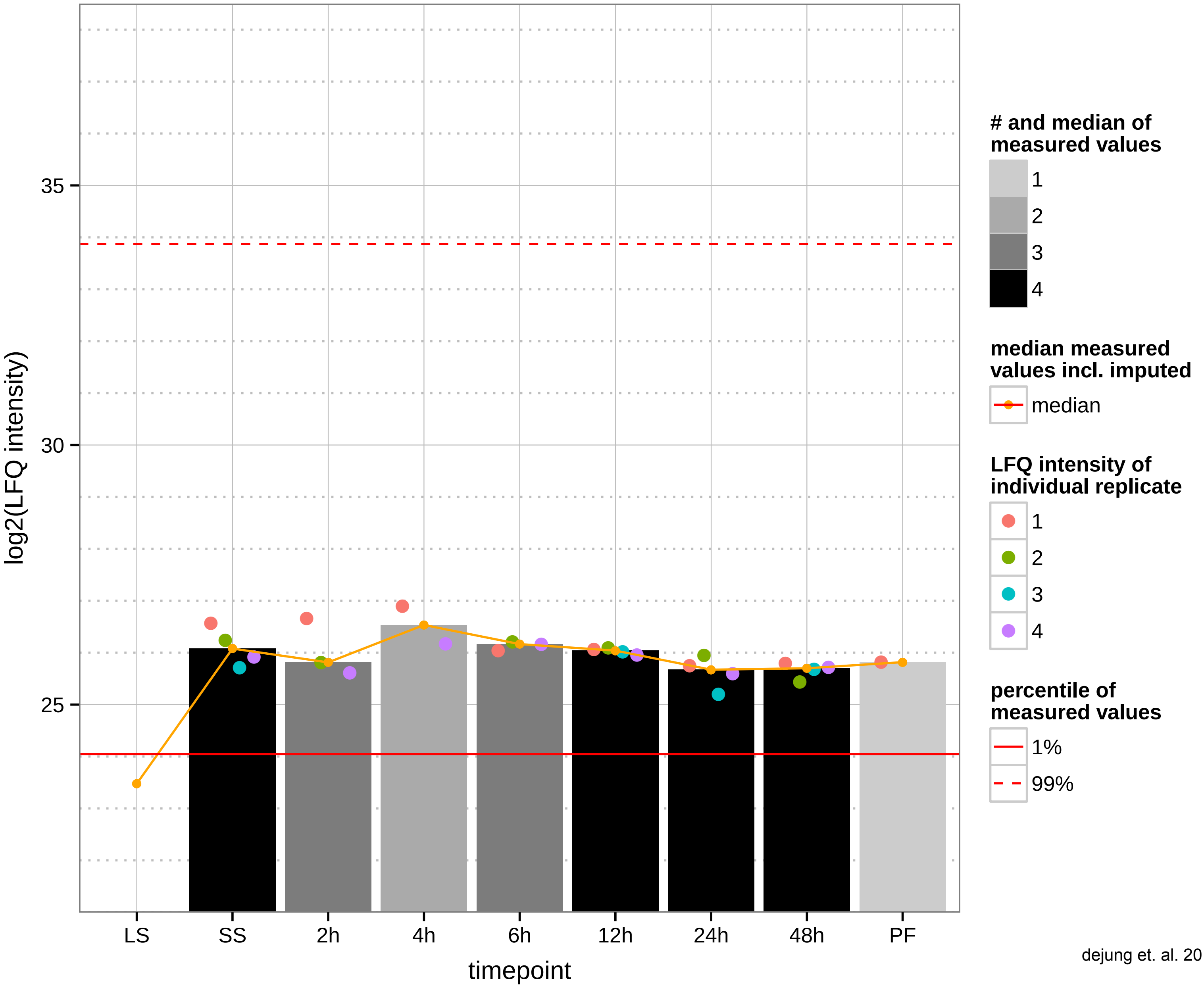
U5 snRNP–associated 102 kDa protein, putative
Tb927.11.15690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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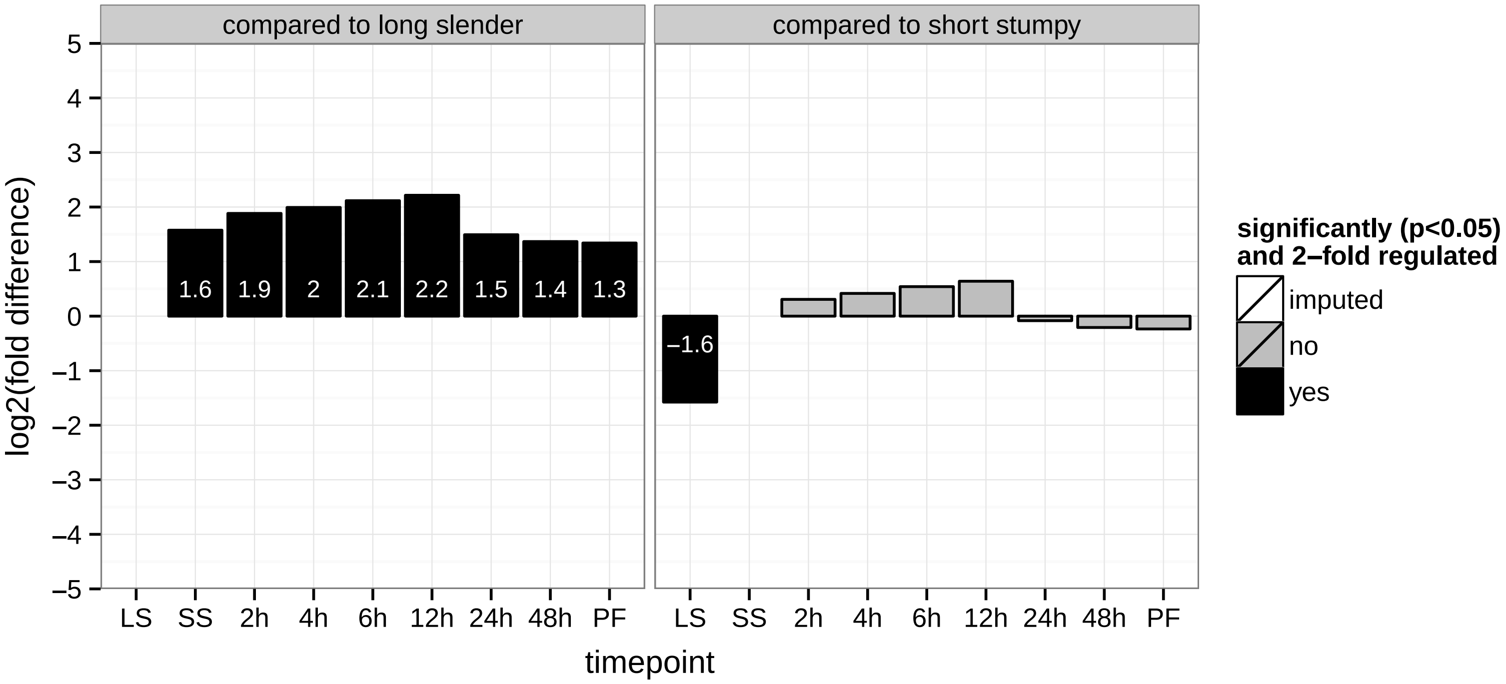
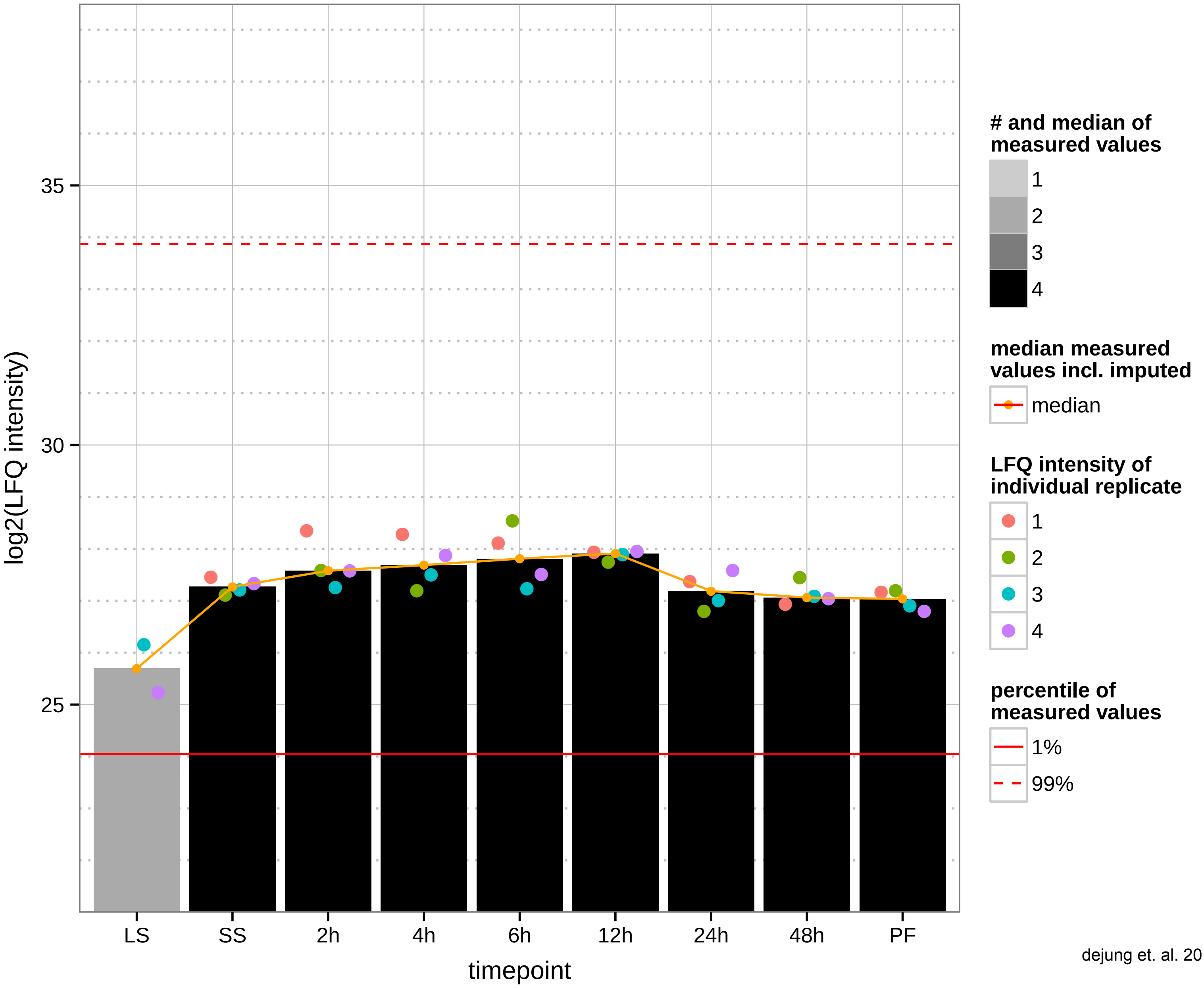
hypothetical protein, conserved
Tb927.11.15730
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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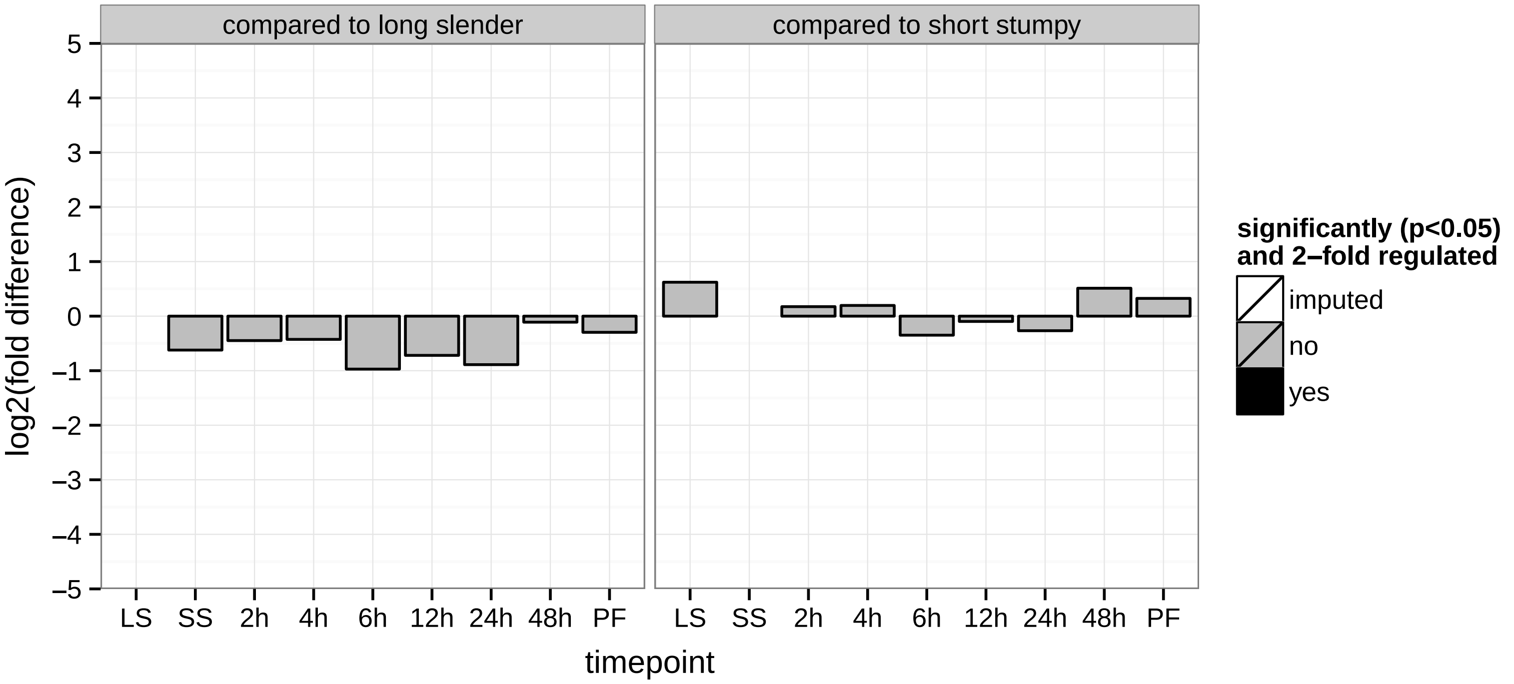
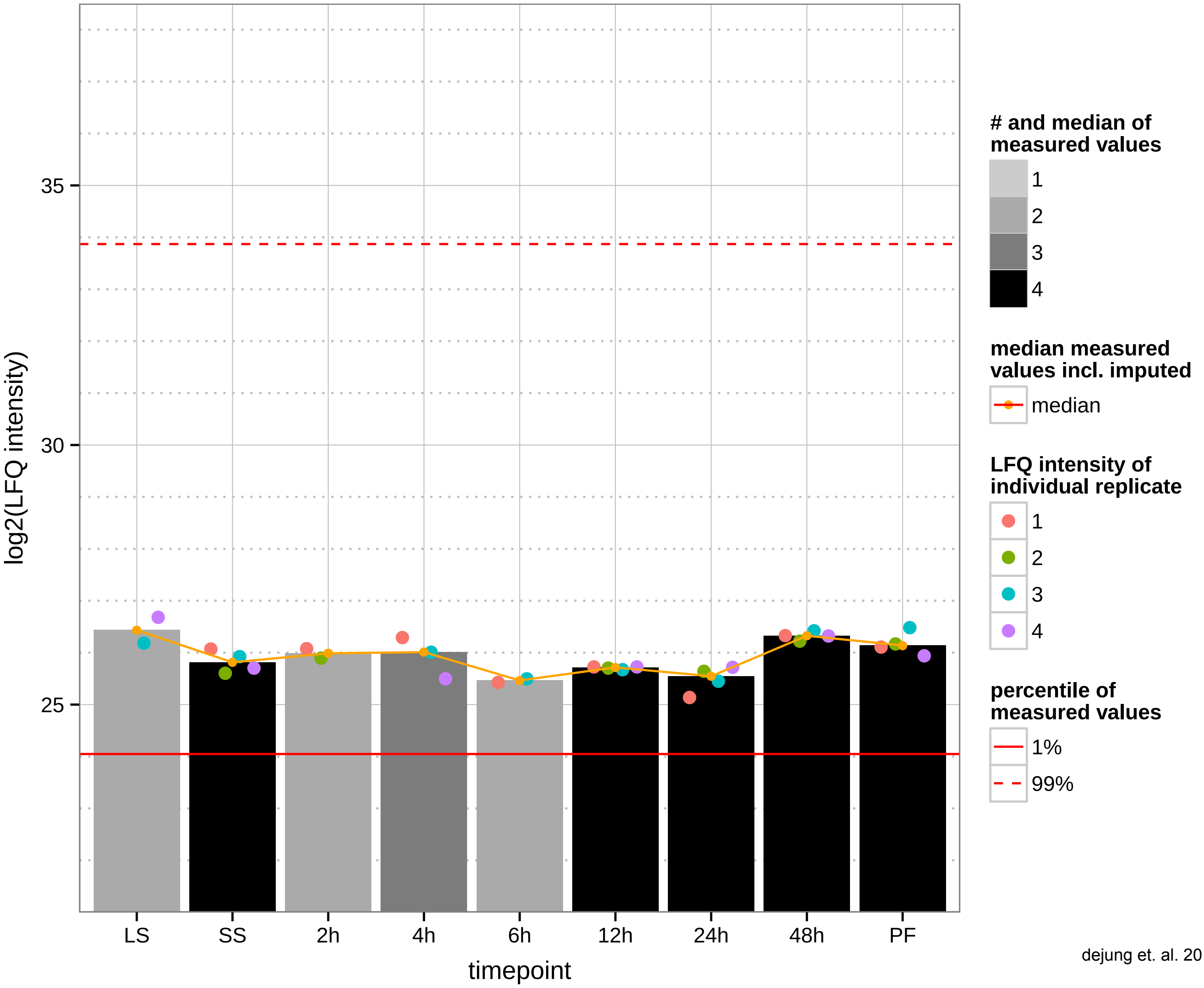
AMP deaminase, putative
Tb927.11.15750
AGOF: AMP deaminase activity
AGOC: null
AGOP: generation of precursor metabolites and energy, purine ribonucleoside monophosphate biosynthetic process
PGOF: deaminase activity
PGOC: null
PGOP: purine ribonucleoside monophosphate biosynthetic process





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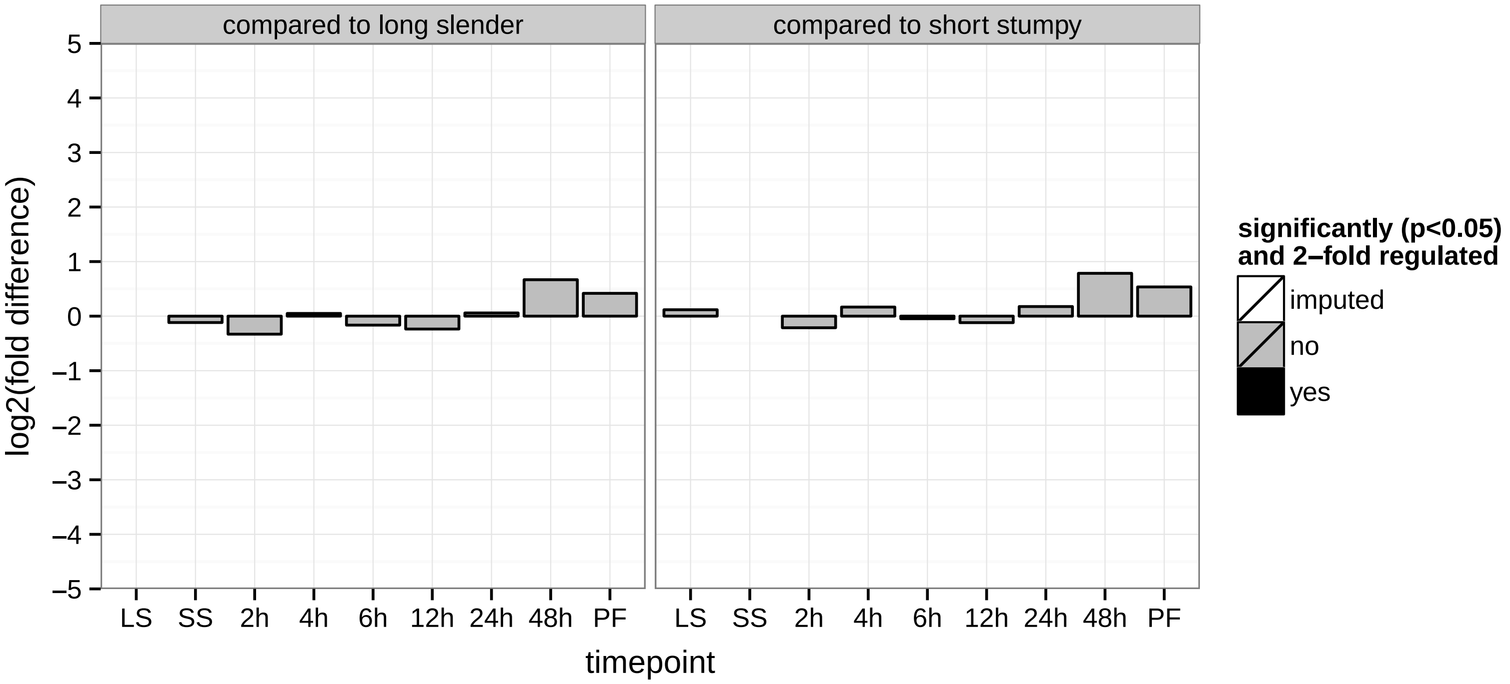
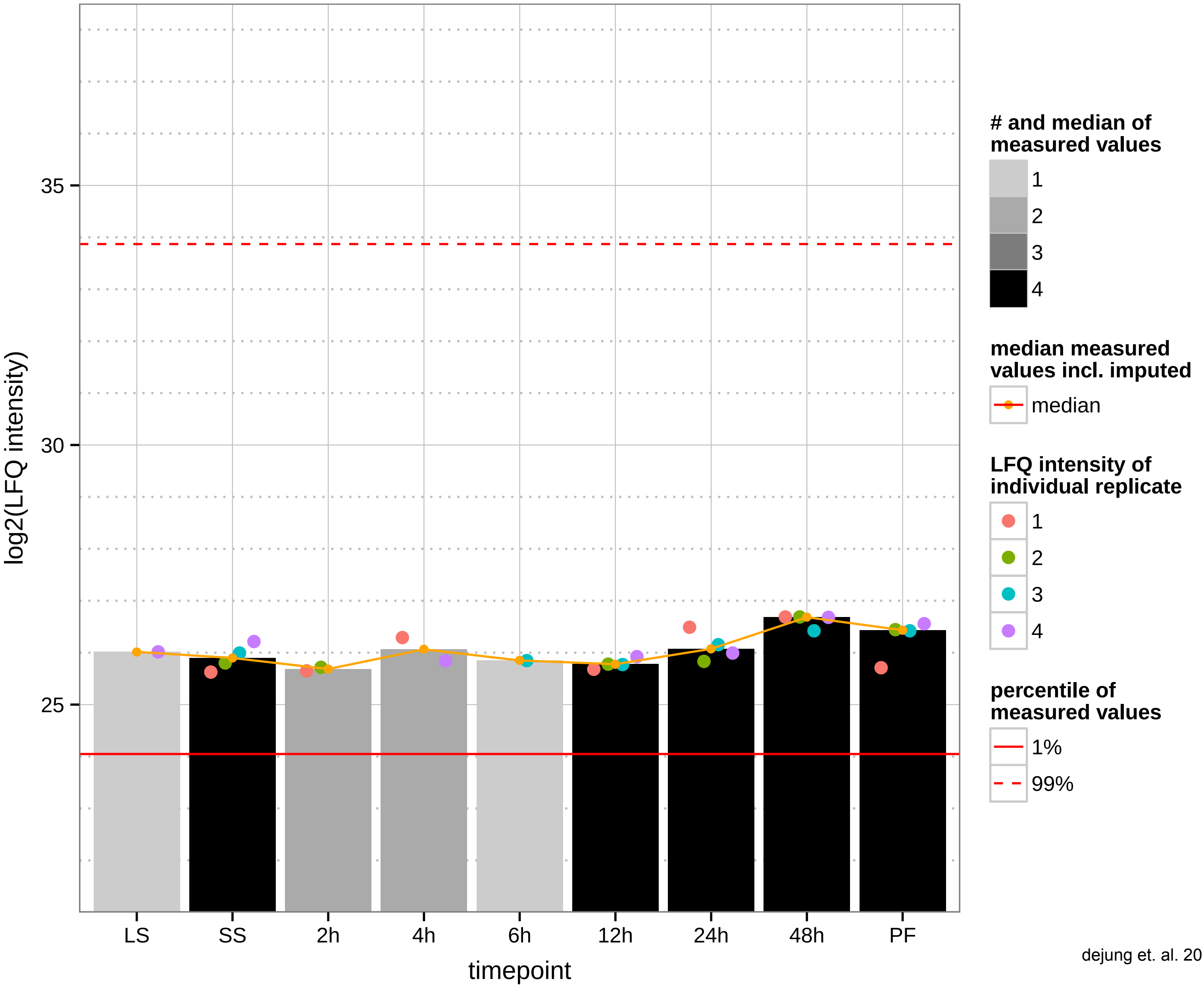
variant surface glycoprotein (VSG), putative, RNA methyltransferase
Tb927.11.15830;Tb11.v5.0683
AGOF: null, RNA binding, RNA methyltransferase activity
AGOC: null
AGOP: null, RNA processing, tRNA methylation
PGOF: RNA binding, RNA methyltransferase activity
PGOC: null
PGOP: RNA processing





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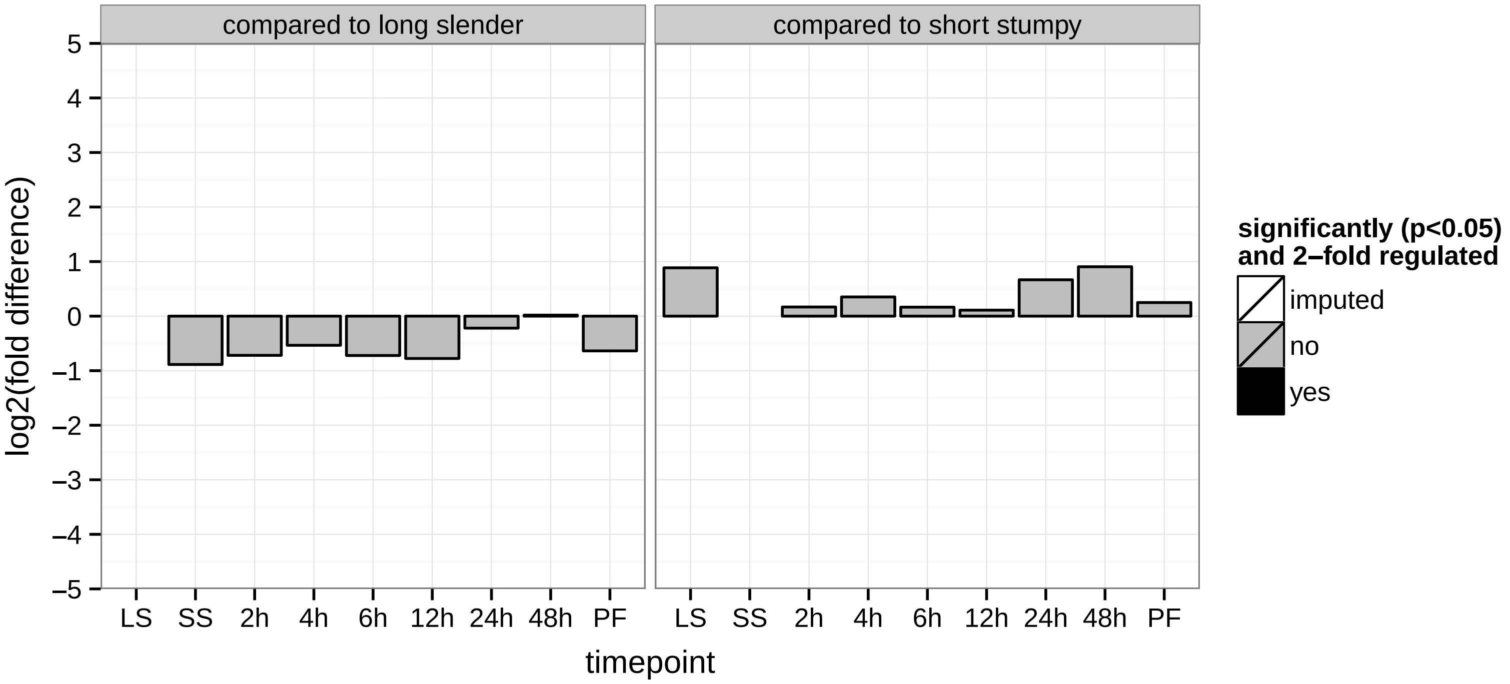
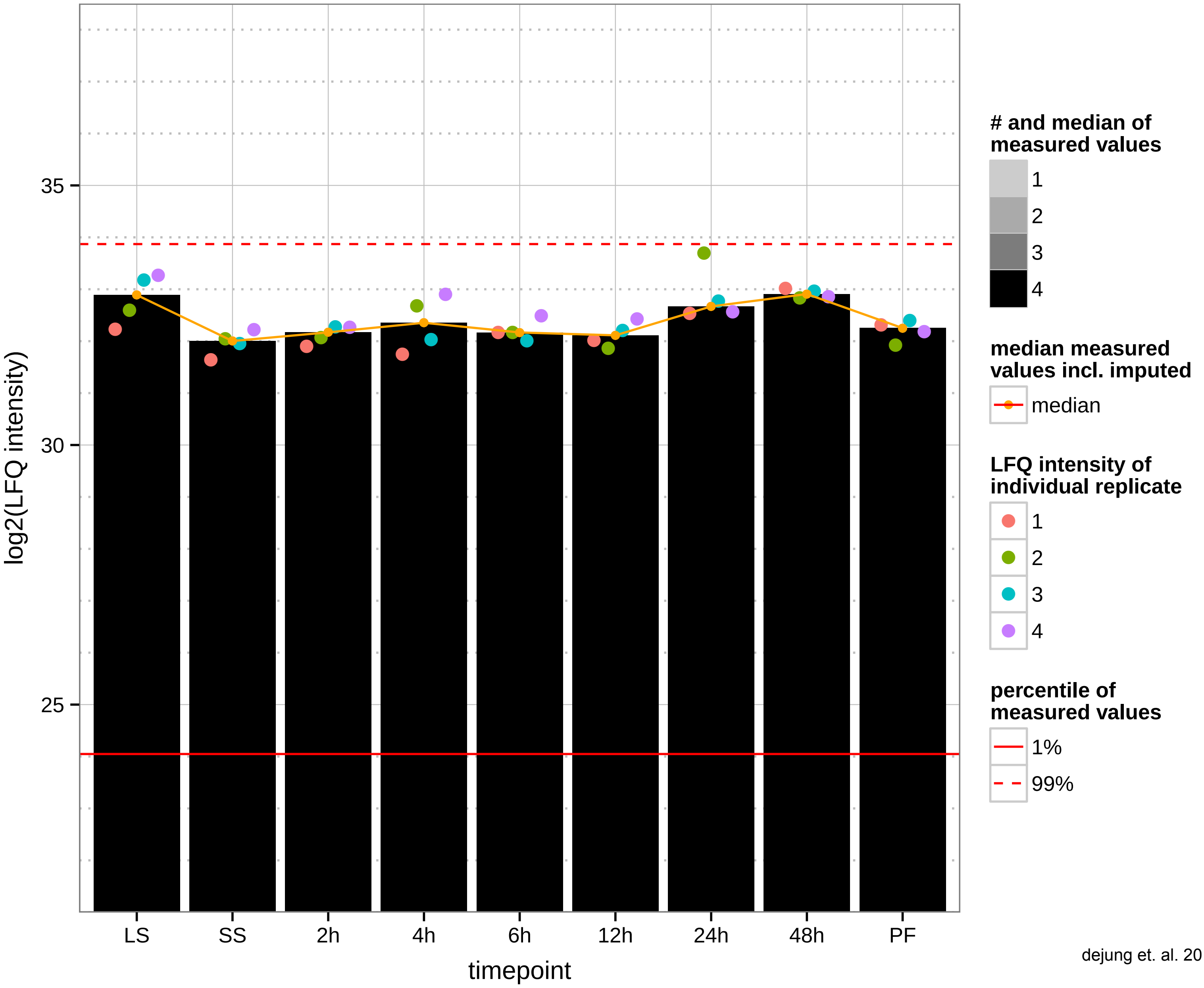
60S ribosomal protein L27, putative
Tb927.11.15900;Tb927.11.15880
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome, null
PGOC: intracellular, ribosome, null
PGOP: translation, null





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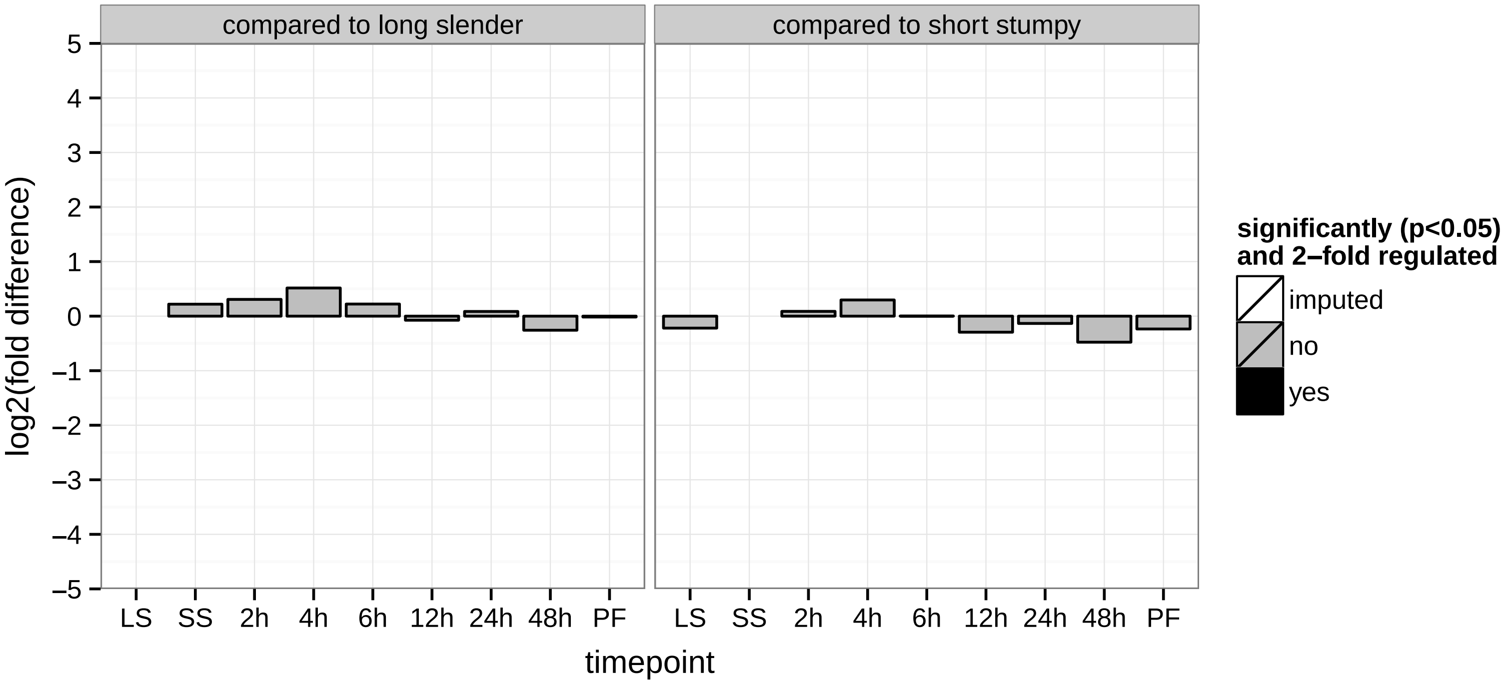
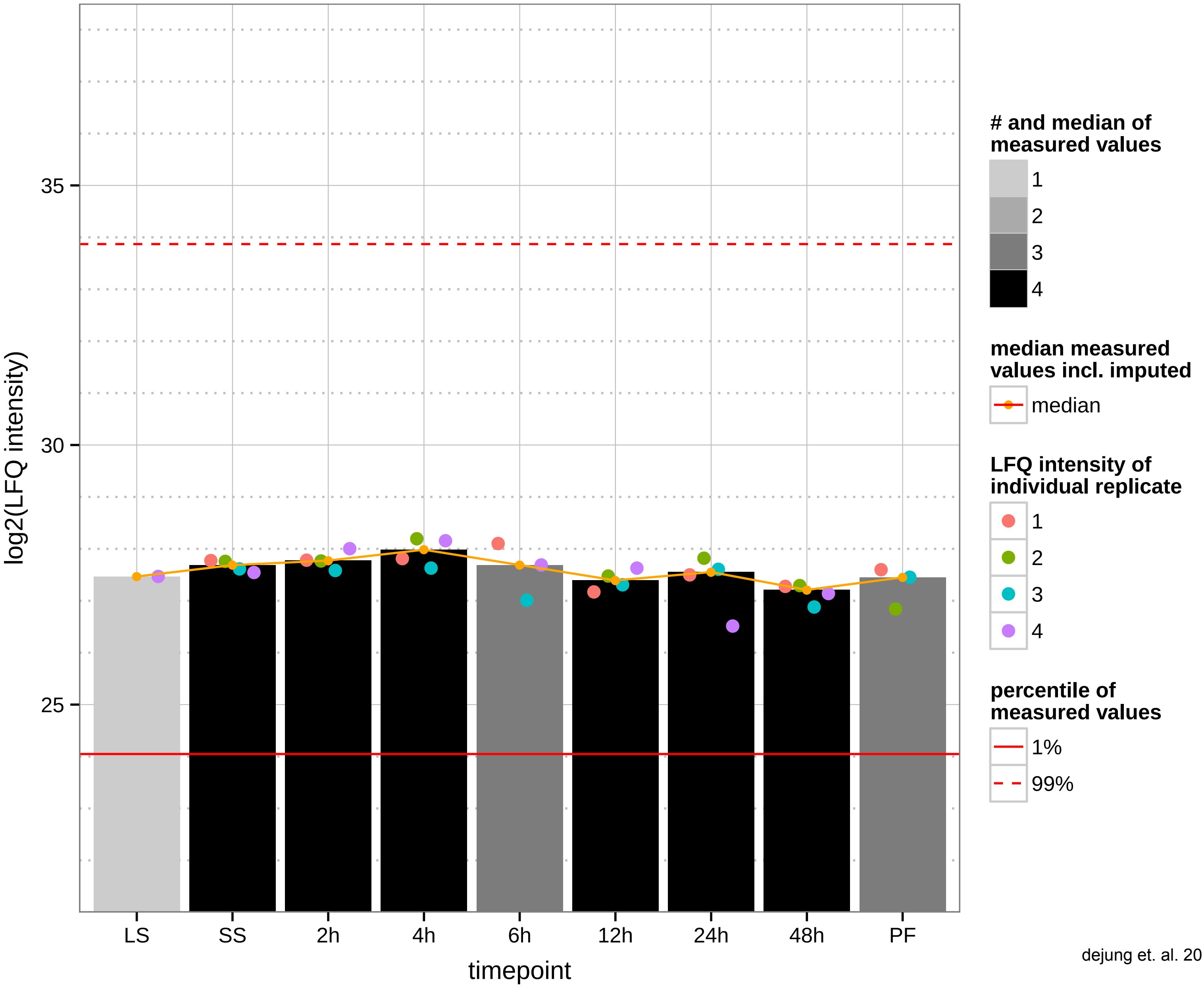
hypothetical protein, conserved
Tb927.11.15930
AGOF: null
AGOC: cis–Golgi network
AGOP: ER to Golgi vesicle–mediated transport
PGOF: null
PGOC: cis–Golgi network
PGOP: ER to Golgi vesicle–mediated transport, transport





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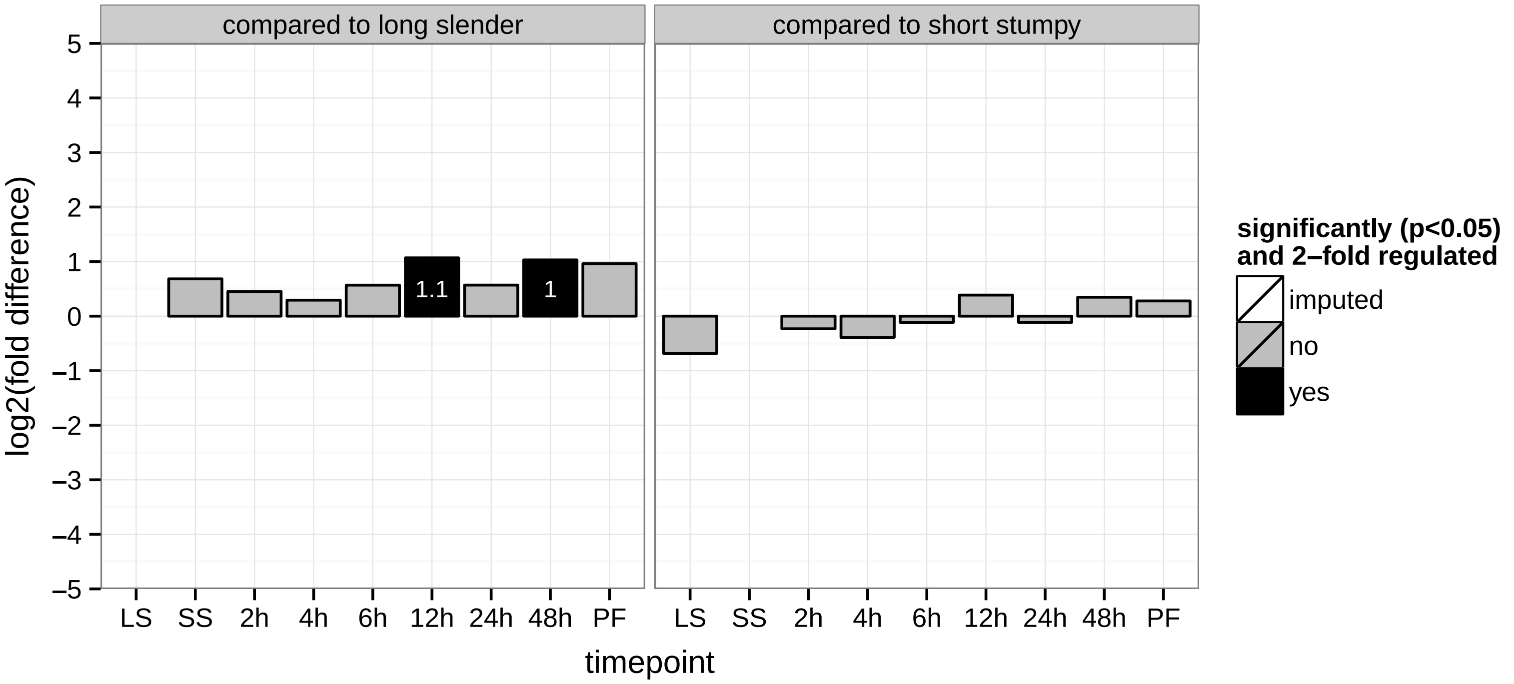
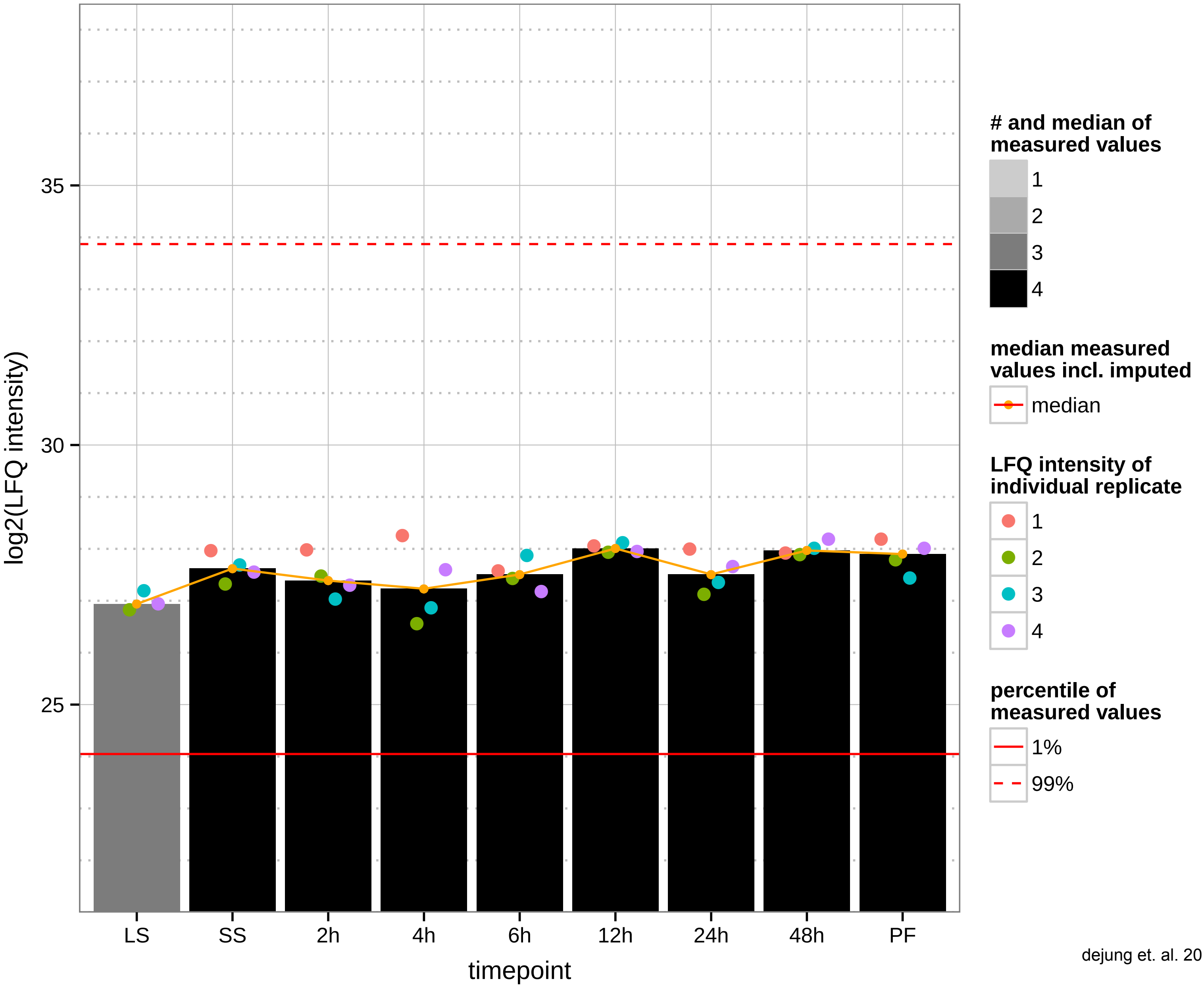
nucleoporin Nup109 (TbNup109)
Tb927.11.15990
AGOF: null
AGOC: nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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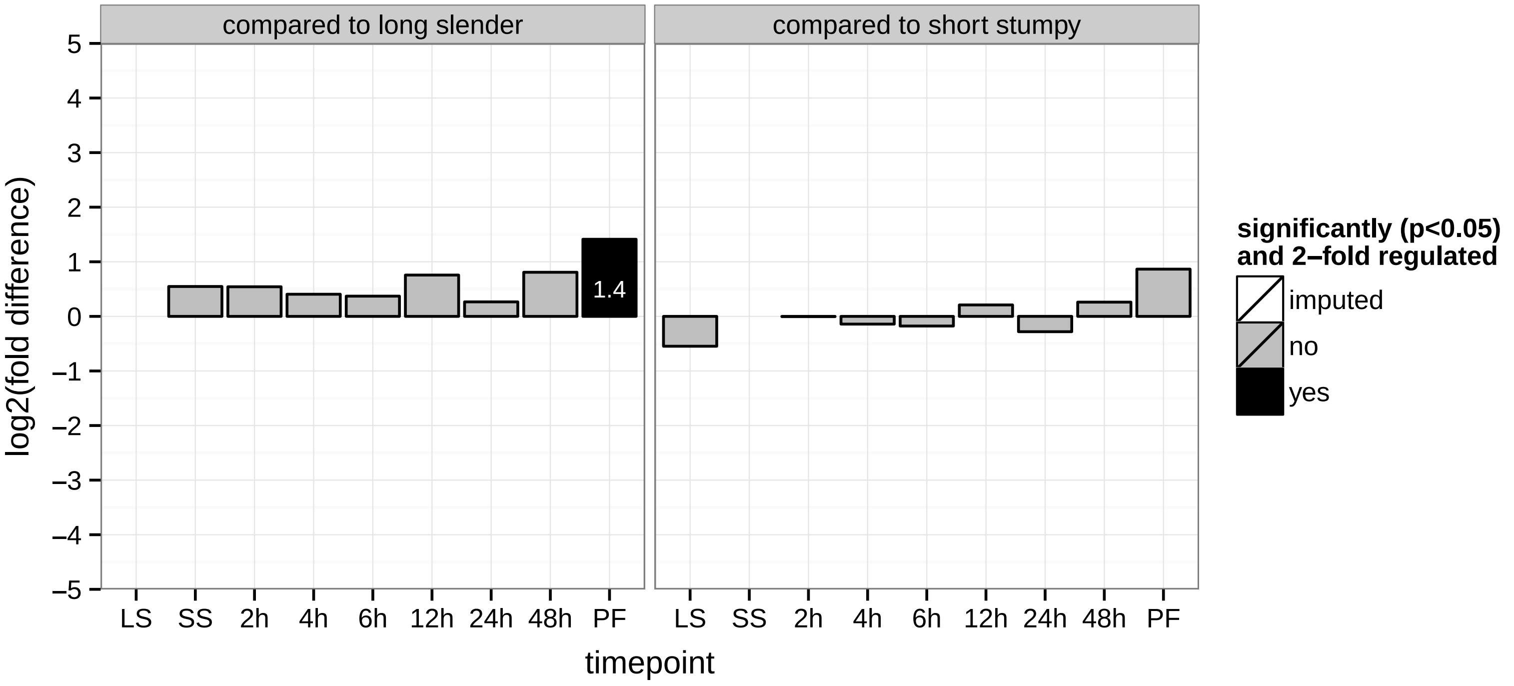
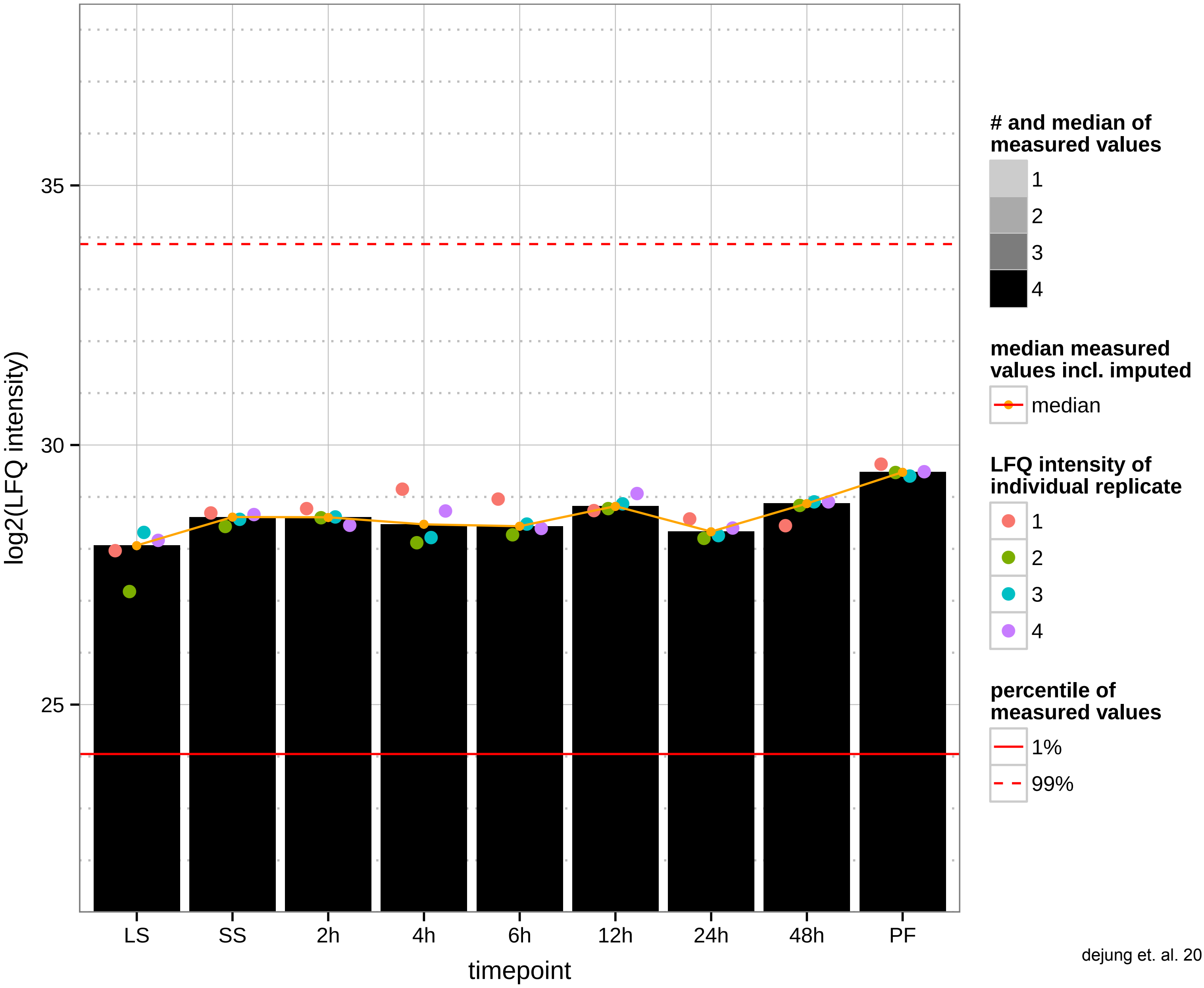
proteasome regulatory non–ATP–ase subunit 7 (RPN7)
Tb927.11.16030
AGOF: endopeptidase activity
AGOC: proteasome regulatory particle
AGOP: ubiquitin–dependent protein catabolic process
PGOF: protein binding
PGOC: null
PGOP: null





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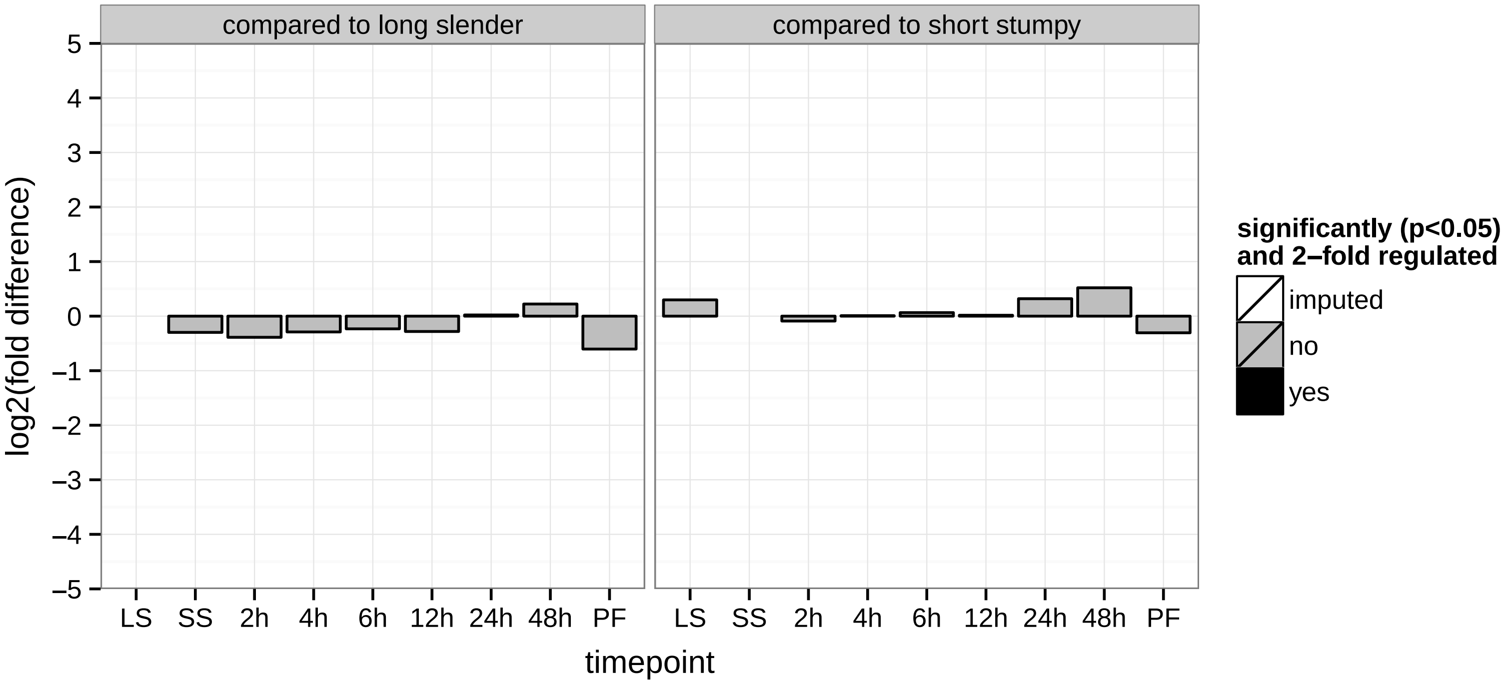
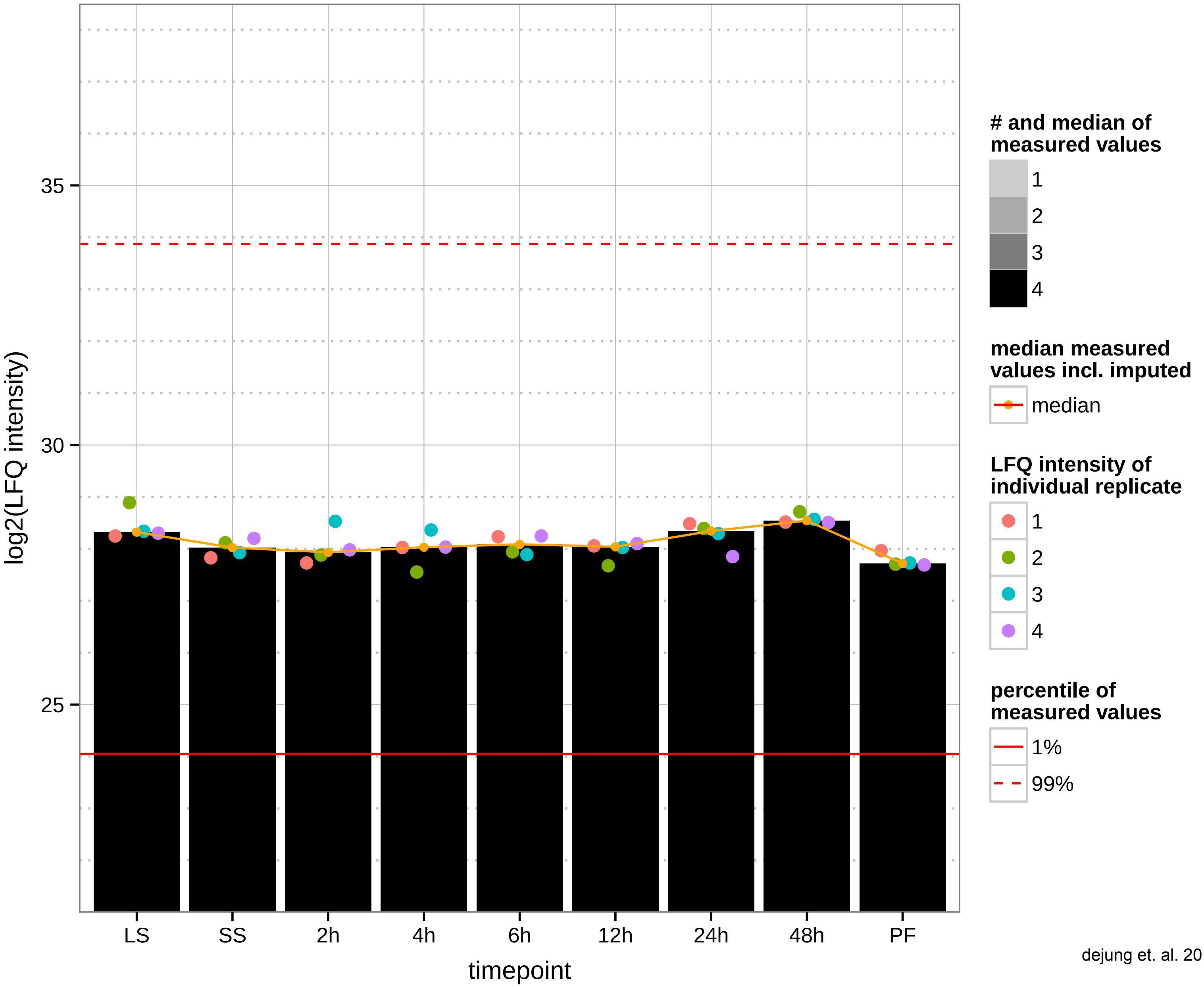
outer dynein arm docking complex, putative (DC2)
Tb927.11.16090
AGOF: null
AGOC: axonemal dynein complex
AGOP: axonemal dynein complex assembly
PGOF: null
PGOC: null
PGOP: null





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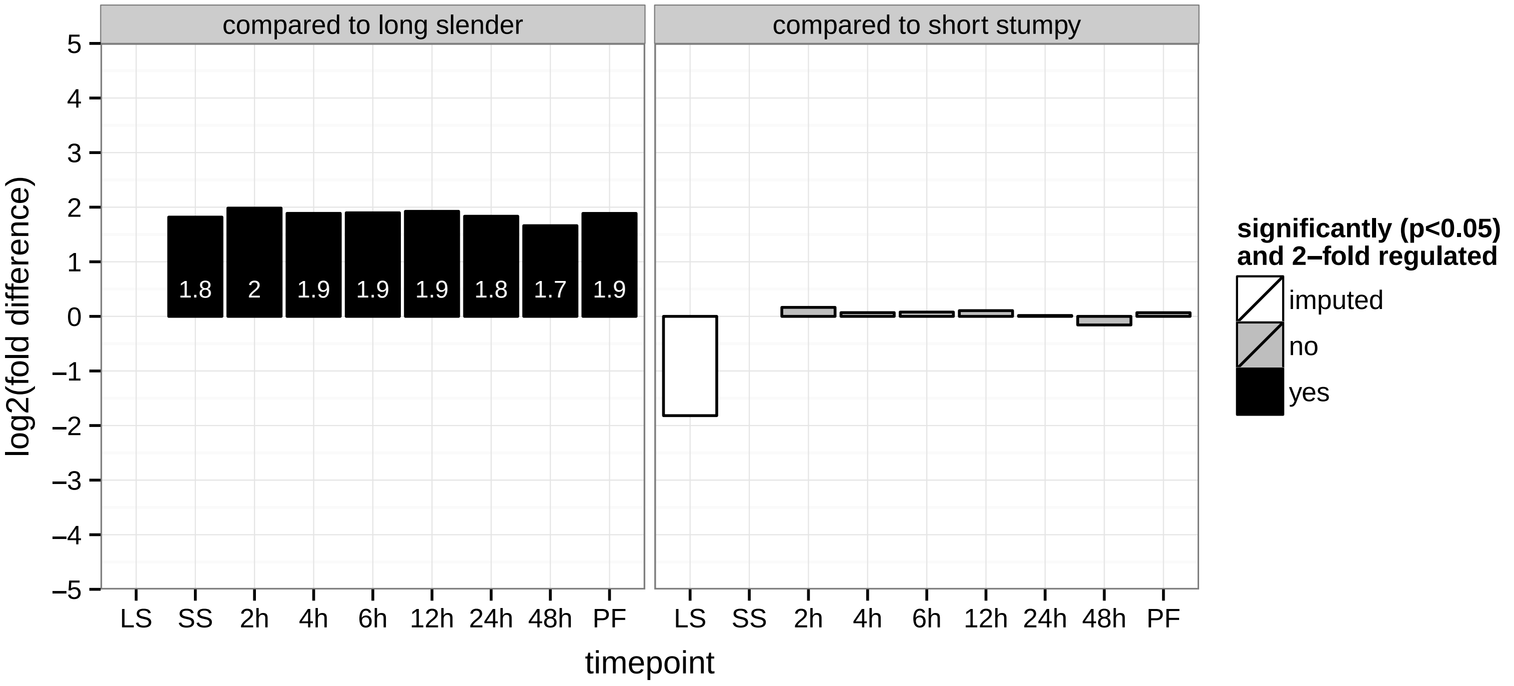
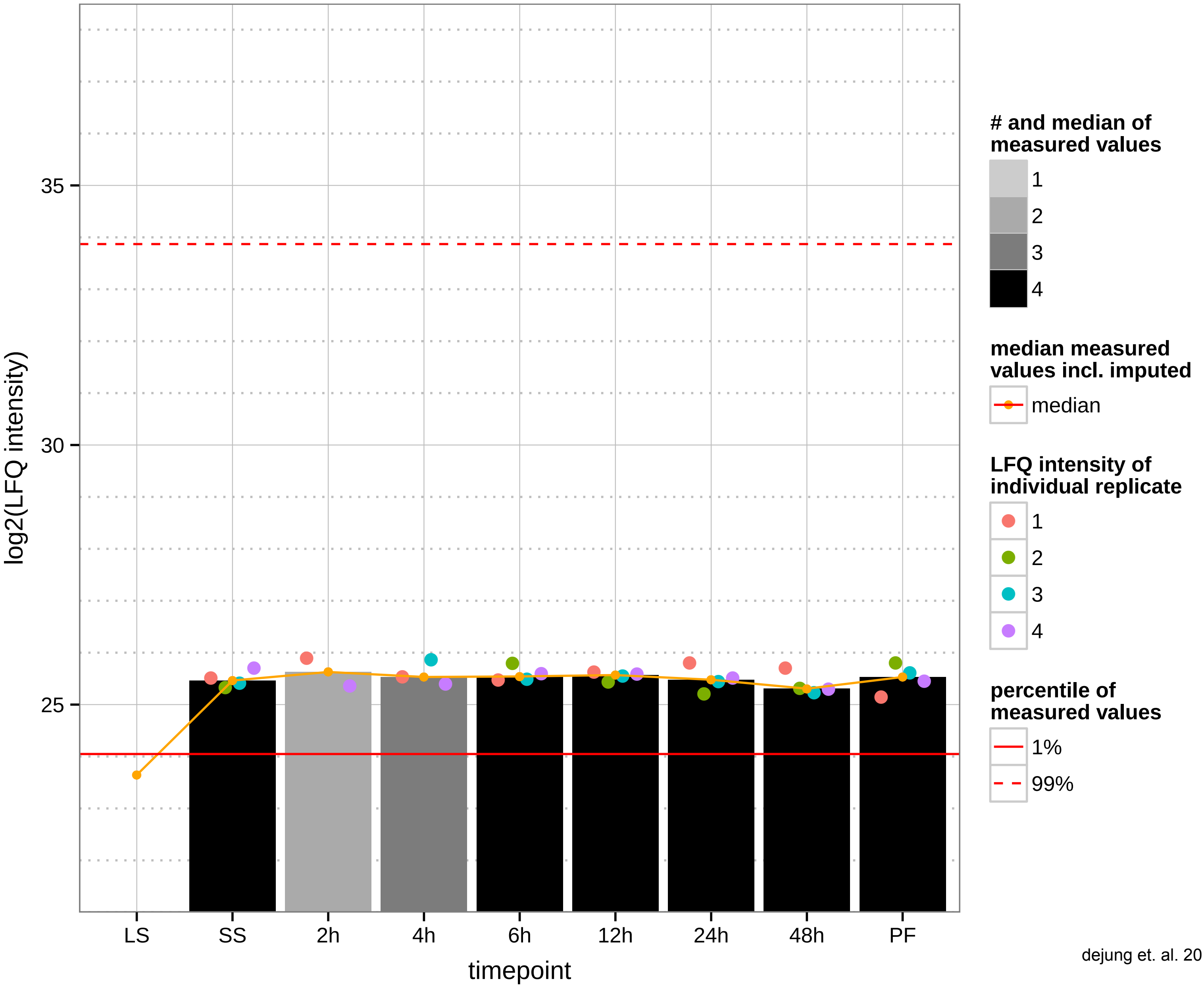
ubiquitin carboxyl–terminal hydrolase, putative
Tb927.11.16100
AGOF: cysteine–type endopeptidase activity, ubiquitin thiolesterase activity
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ubiquitin thiolesterase activity
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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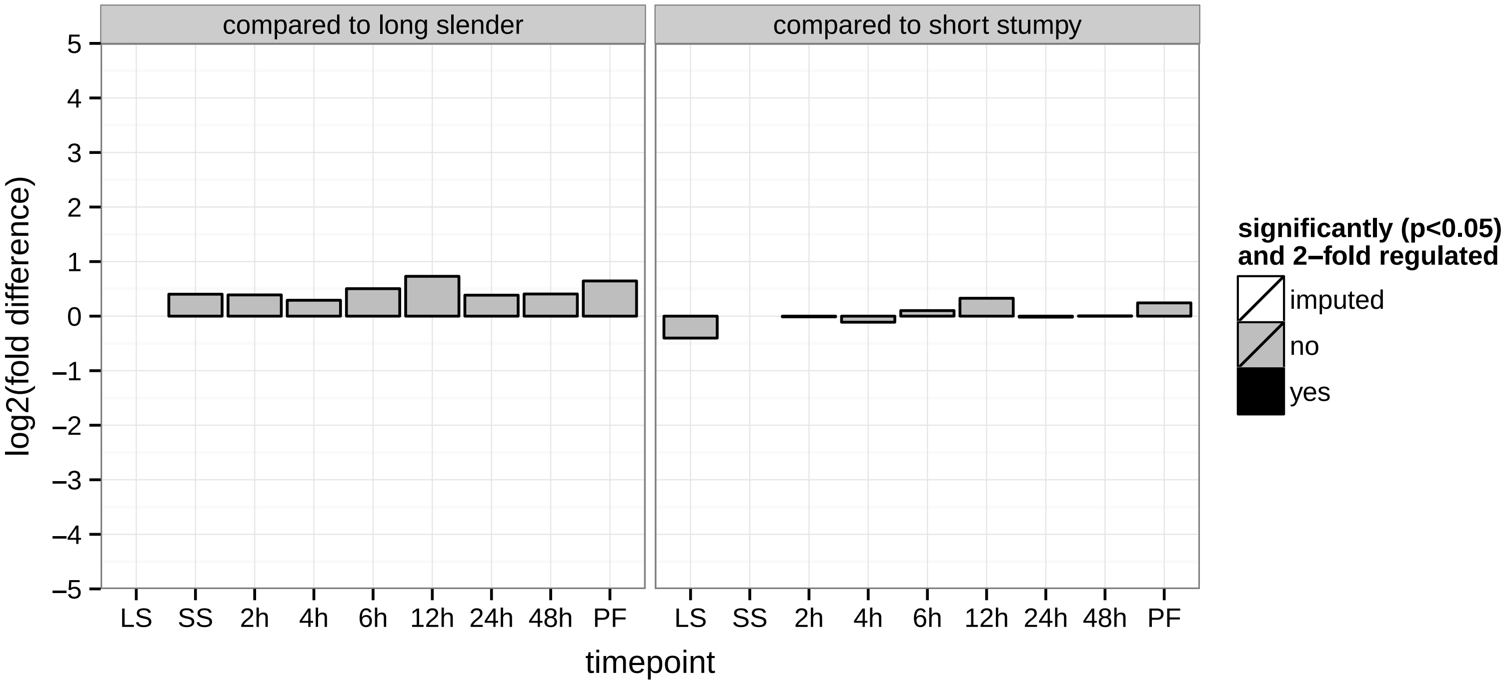
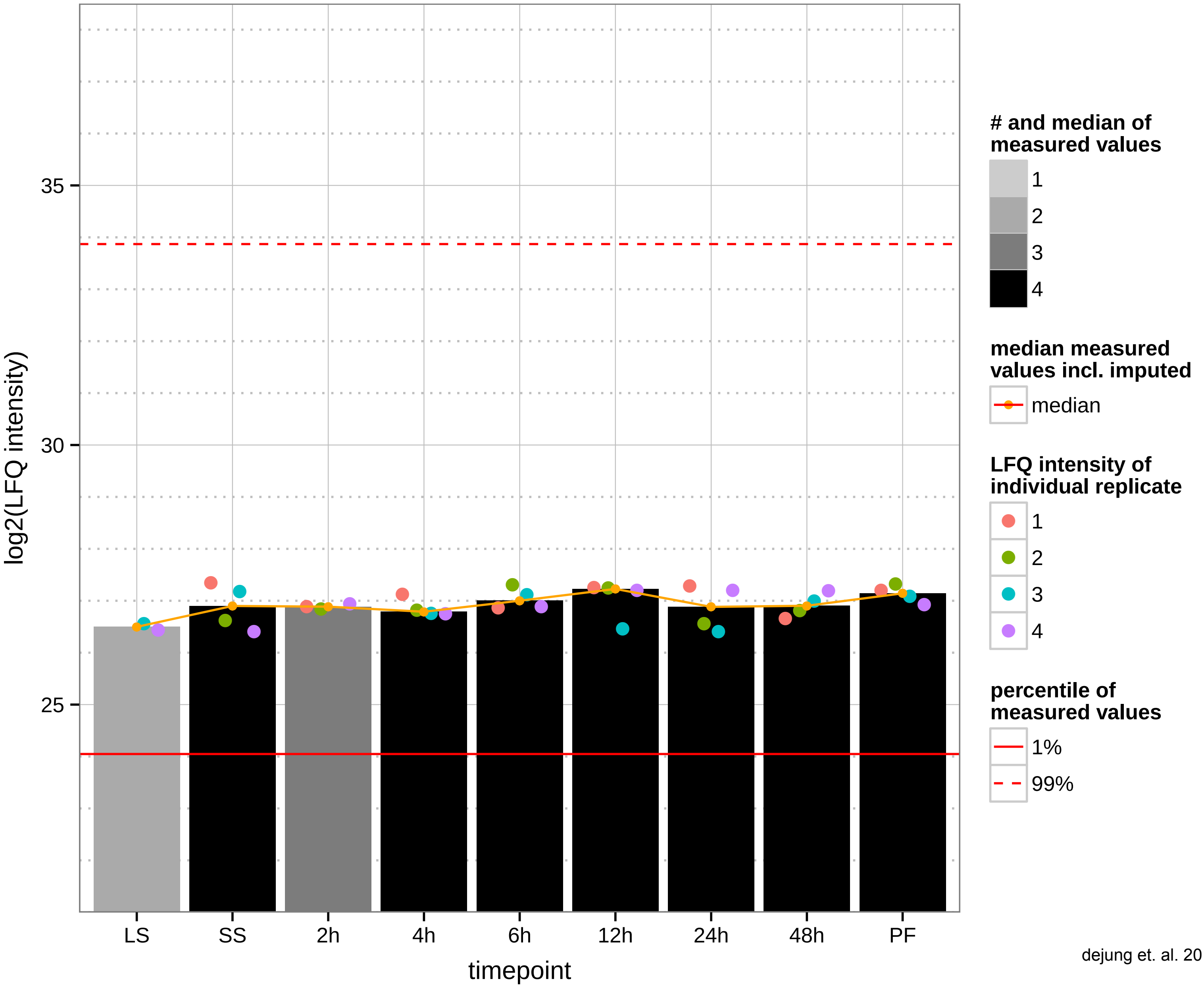
integrin alpha chain protein, putative, FG−GAP repeat protein
Tb927.11.16110
AGOF: null
AGOC: integral to membrane, integrin complex
AGOP: cell−matrix adhesion
PGOF: null
PGOC: null
PGOP: null





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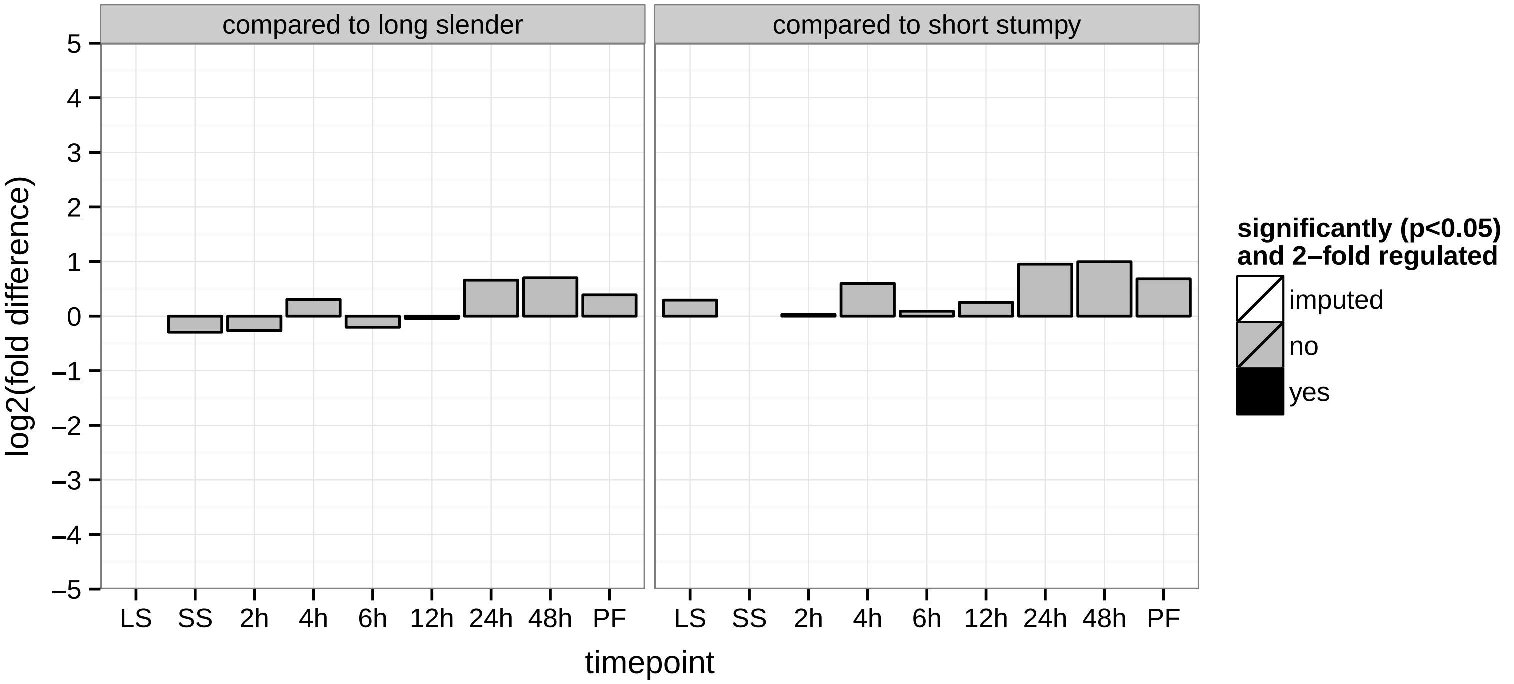
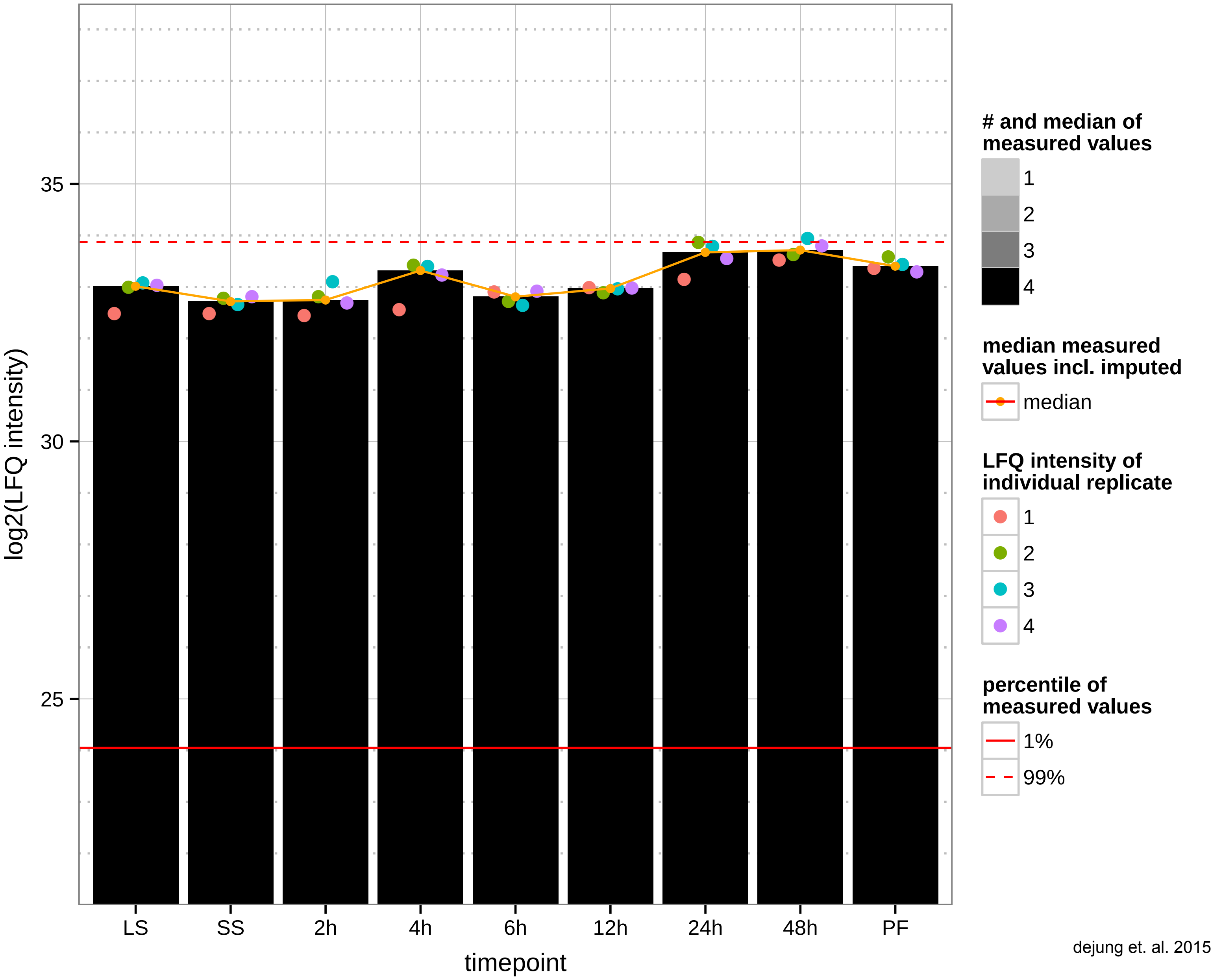
nucleoside diphosphate kinase (NDPK)
Tb927.11.16130
AGOF: ATP binding, nucleoside diphosphate kinase activity
AGOC: nucleus
AGOP: CTP biosynthetic process, GTP biosynthetic process, UTP biosynthetic process
PGOF: ATP binding, nucleoside diphosphate kinase activity
PGOC: null
PGOP: CTP biosynthetic process, GTP biosynthetic process, UTP biosynthetic process, nucleoside diphosphate phosphoryla





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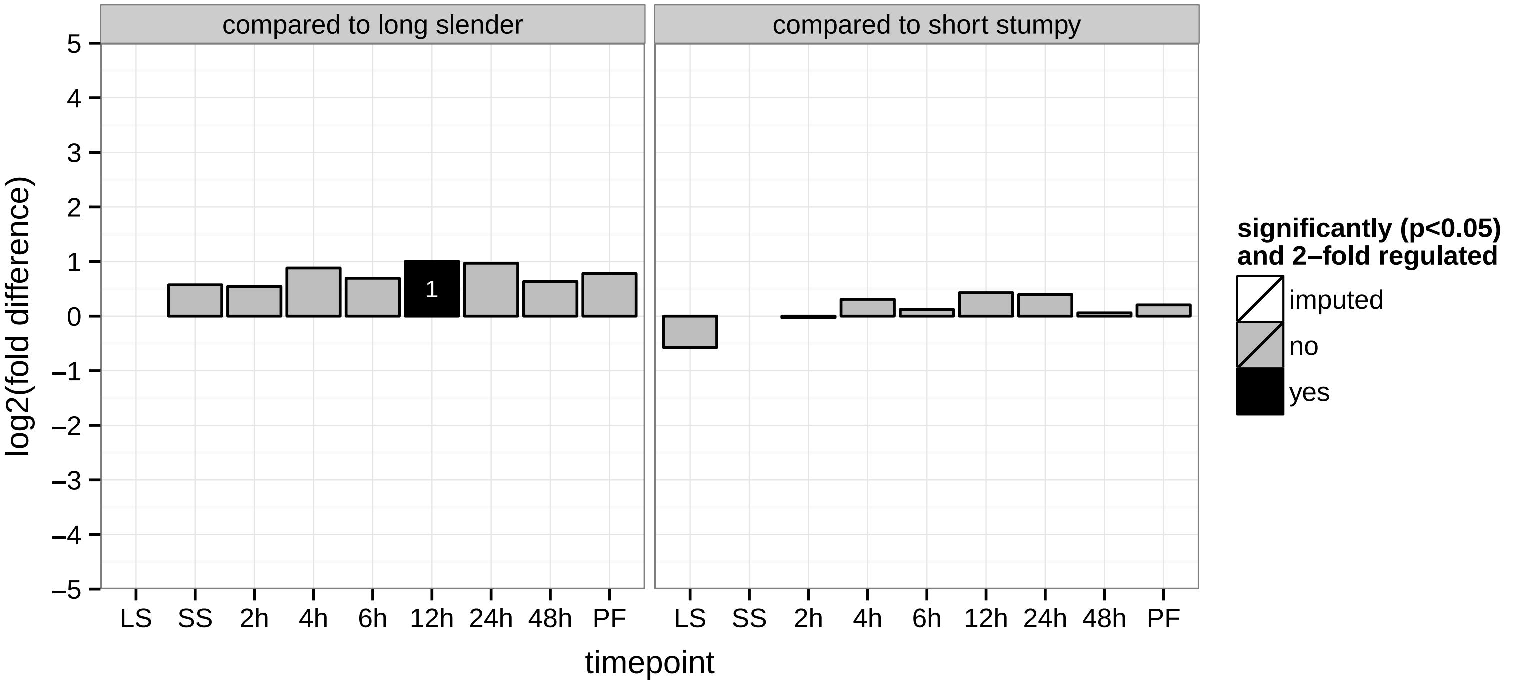
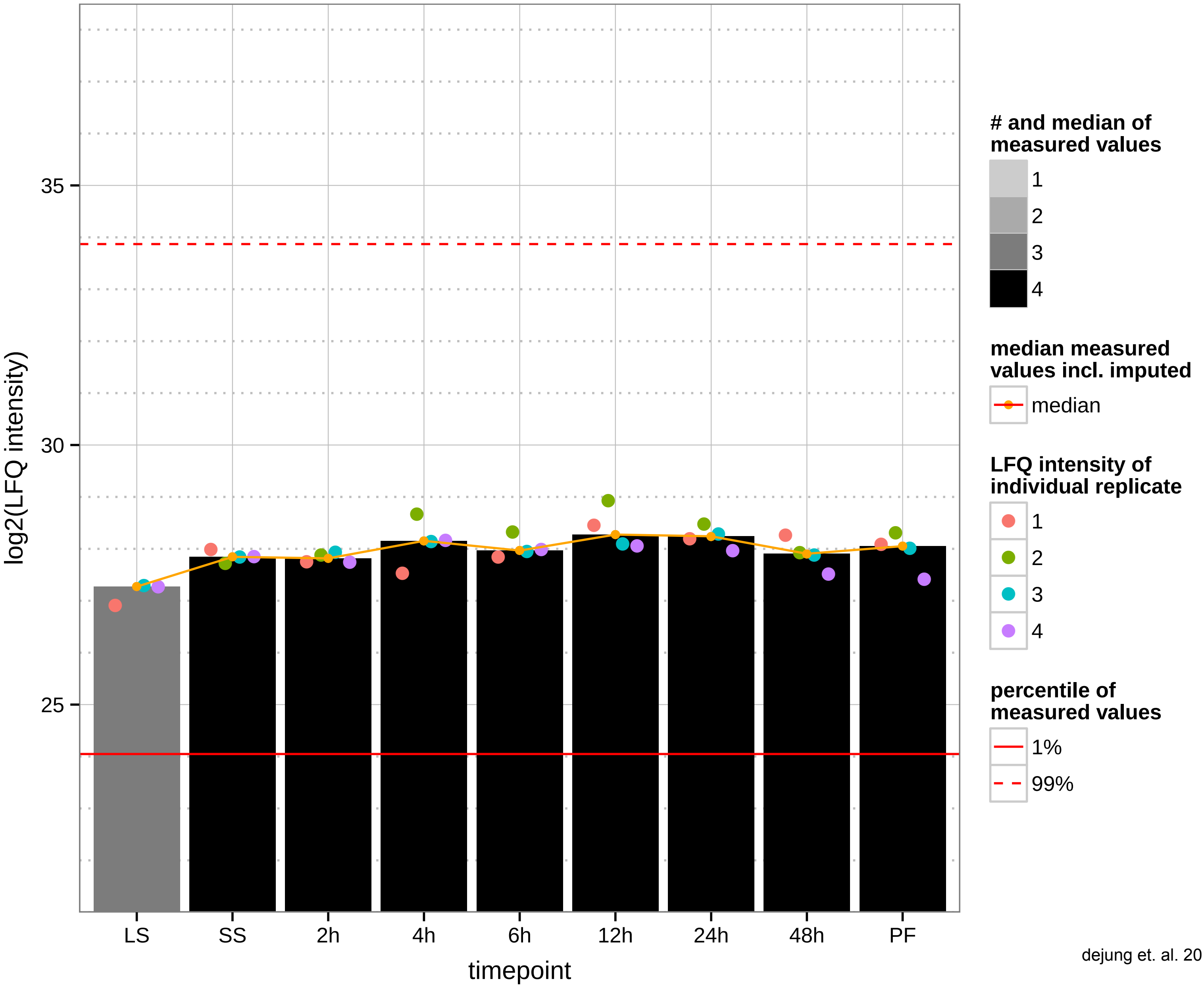
hypothetical protein, conserved
Tb927.11.1620
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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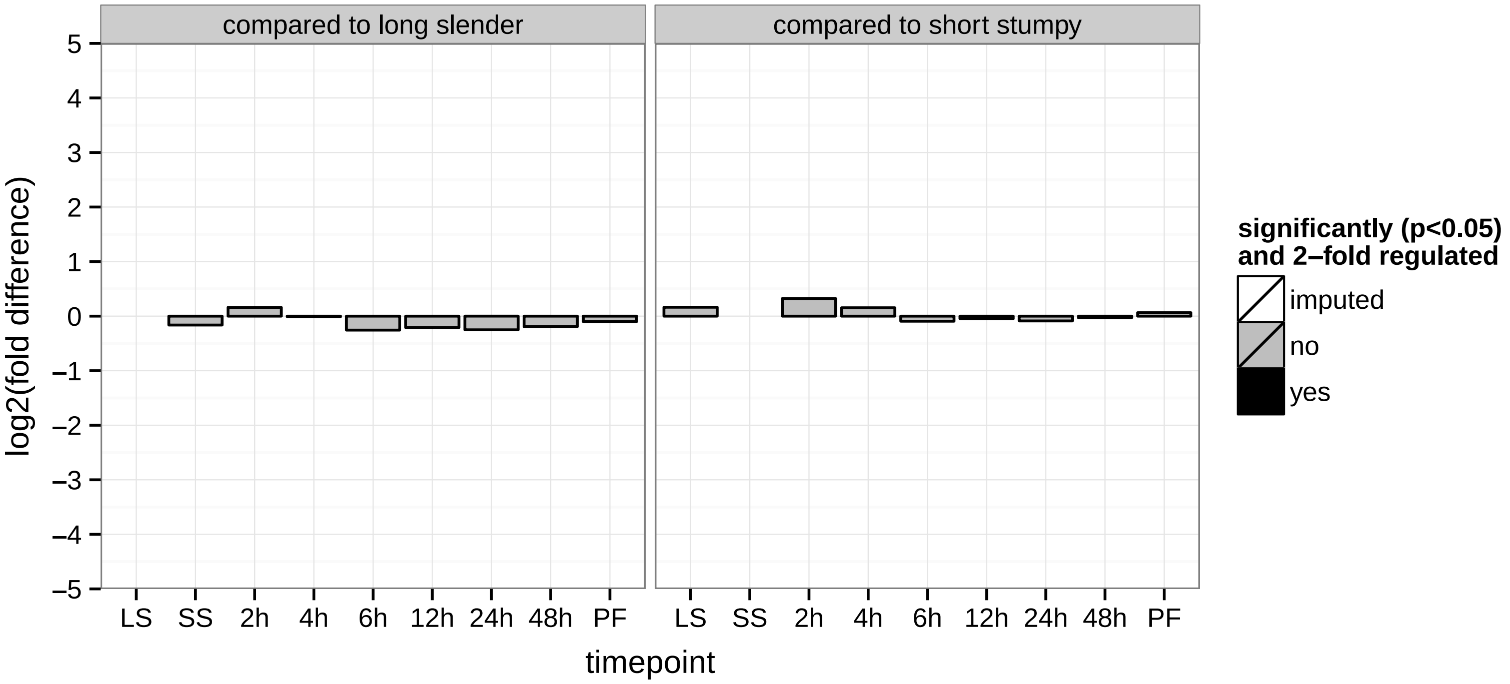
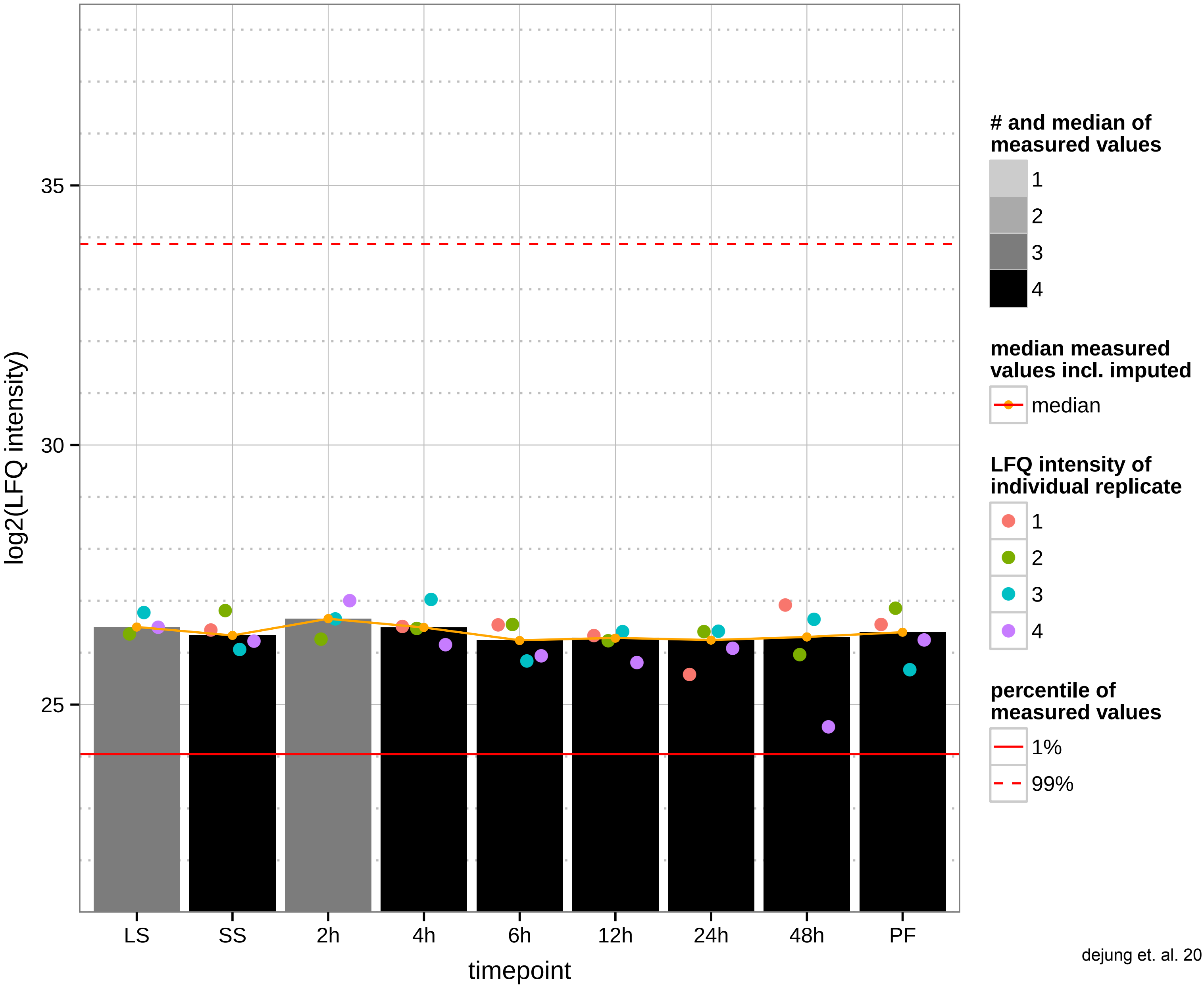
hypothetical protein, conserved
Tb927.11.16350
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: membrane
PGOP: intracellular signal transduction





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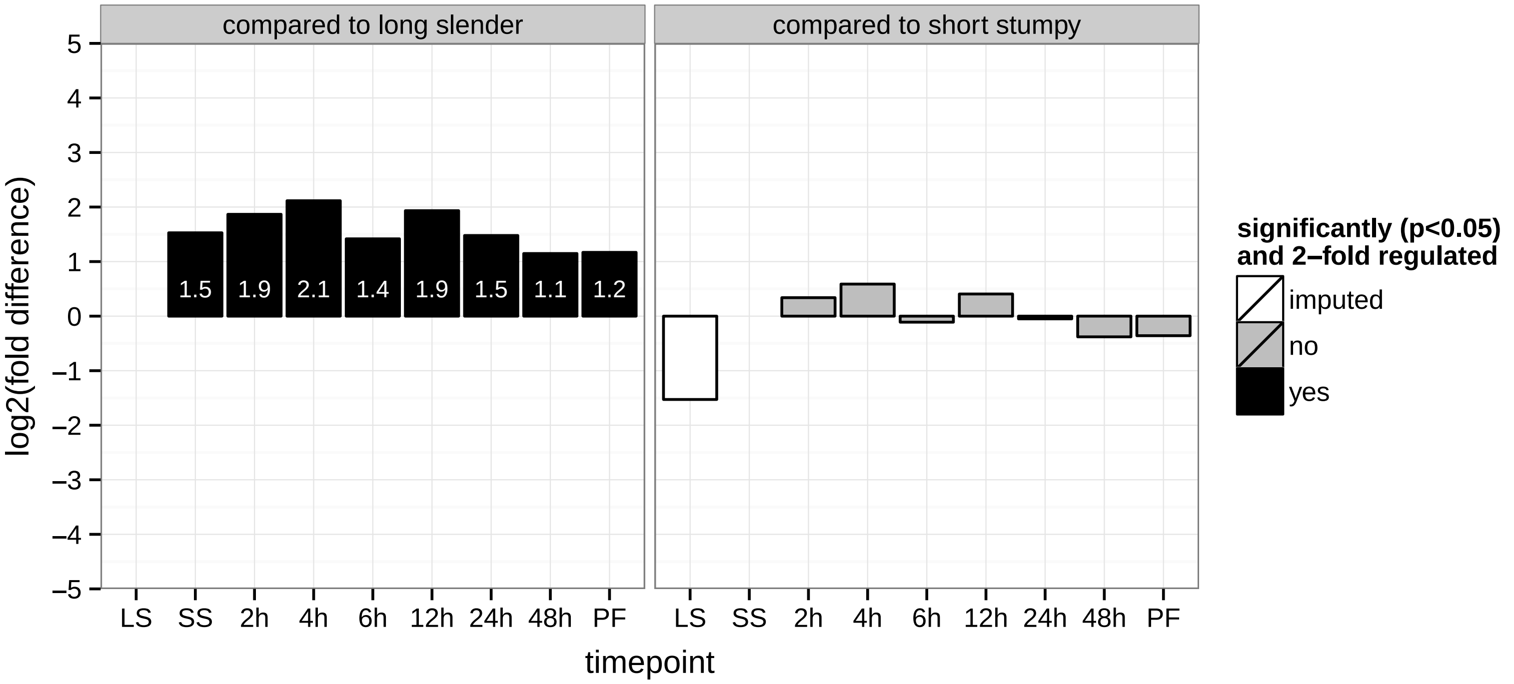
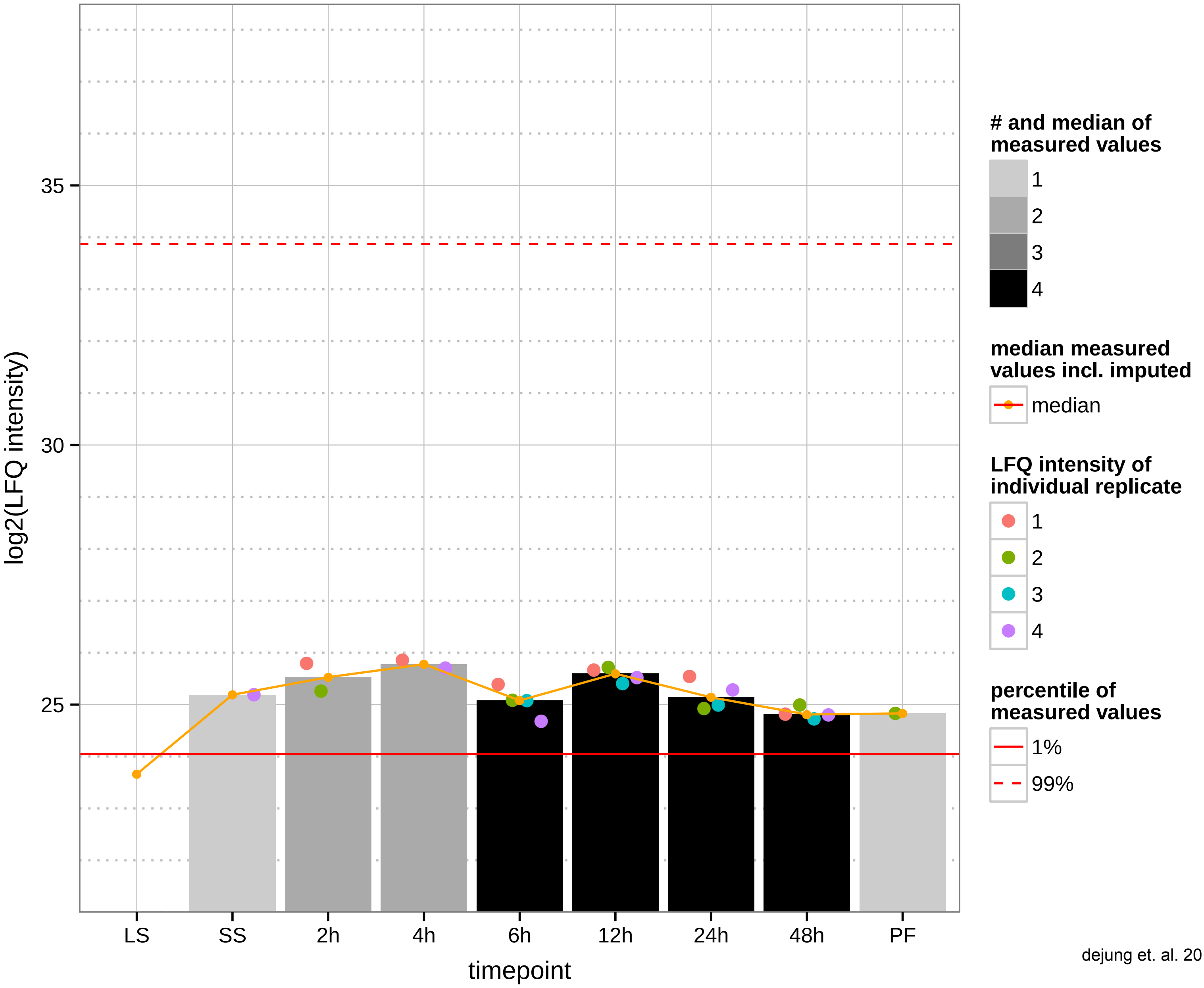
hypothetical protein, conserved
Tb927.11.16370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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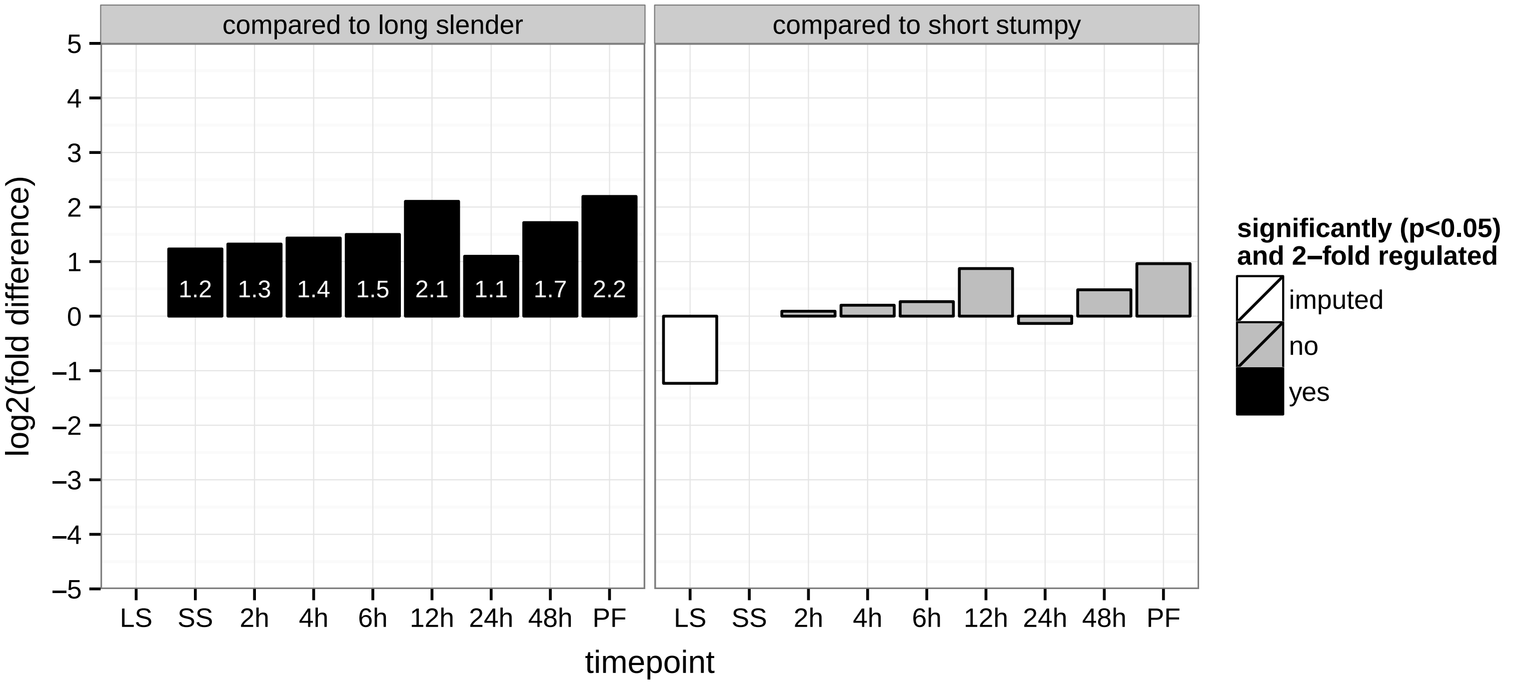
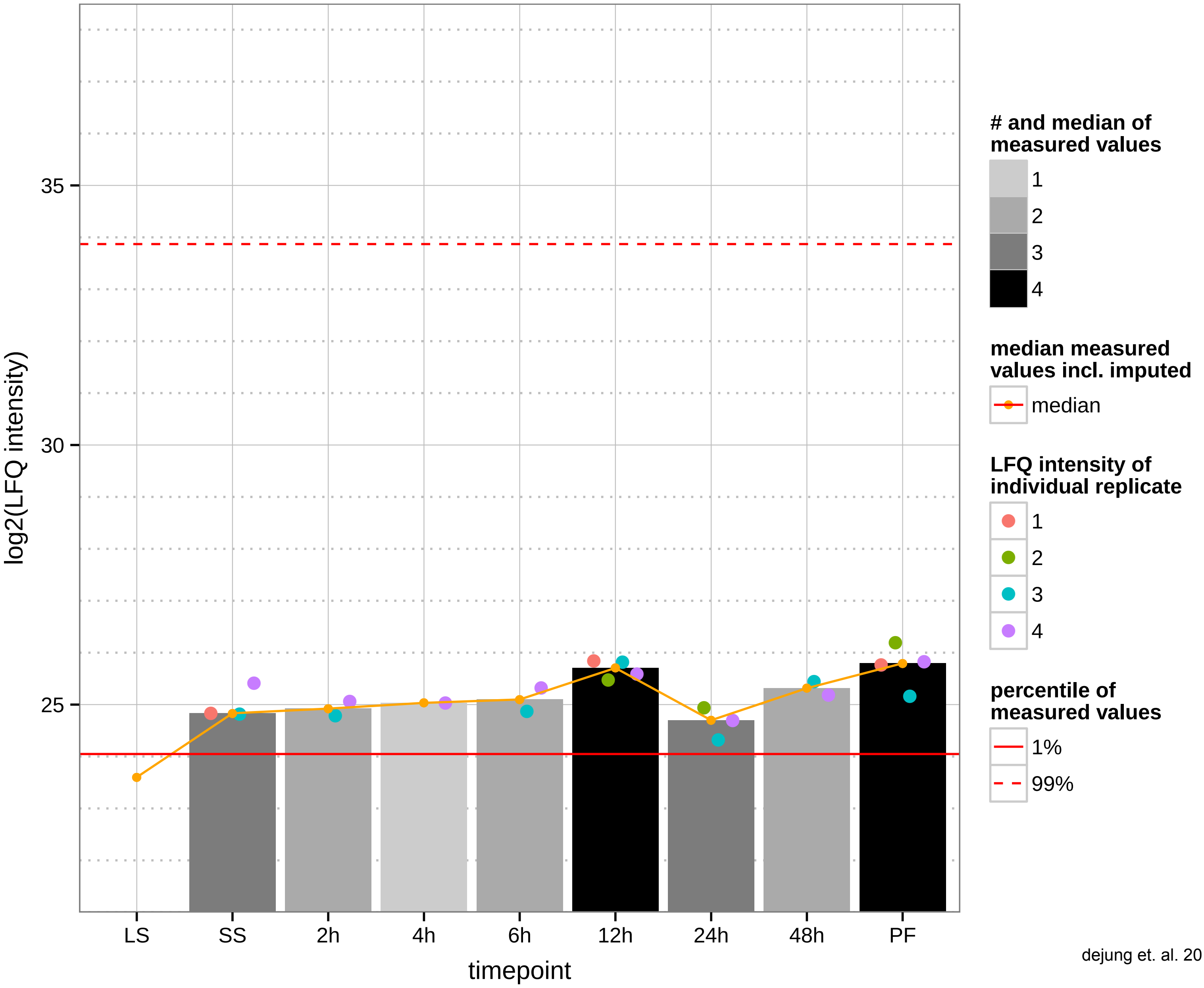
hypothetical protein, conserved
Tb927.11.16380
AGOF: null
AGOC: mitochondrion
AGOP: protein folding
PGOF: protein binding
PGOC: null
PGOP: null





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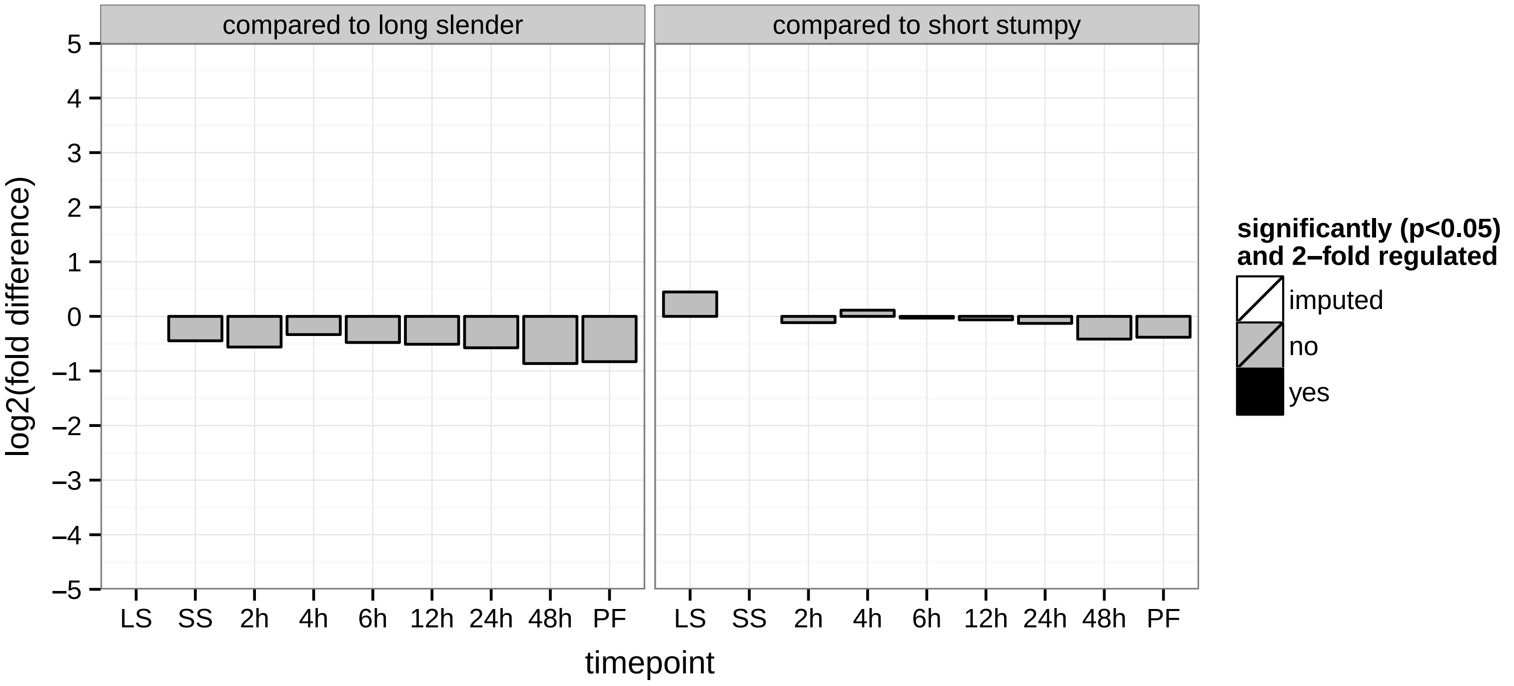
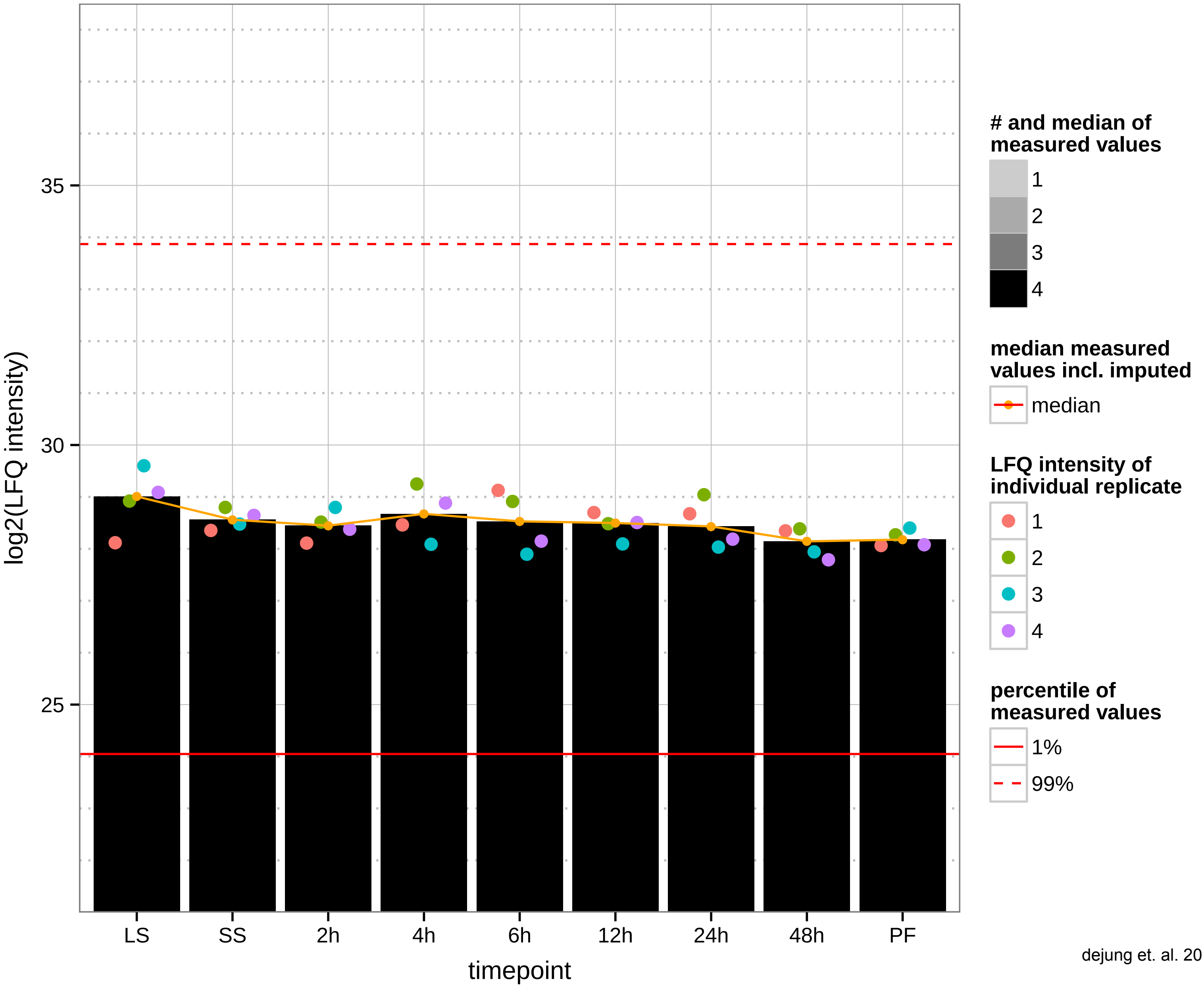
kinetoplast–associated protein 3, putative (KAP3)
Tb927.11.16400
AGOF: DNA binding
AGOC: kinetoplast, mitochondrial matrix, mitochondrion
AGOP: DNA metabolic process, DNA packaging
PGOF: null
PGOC: null
PGOP: null





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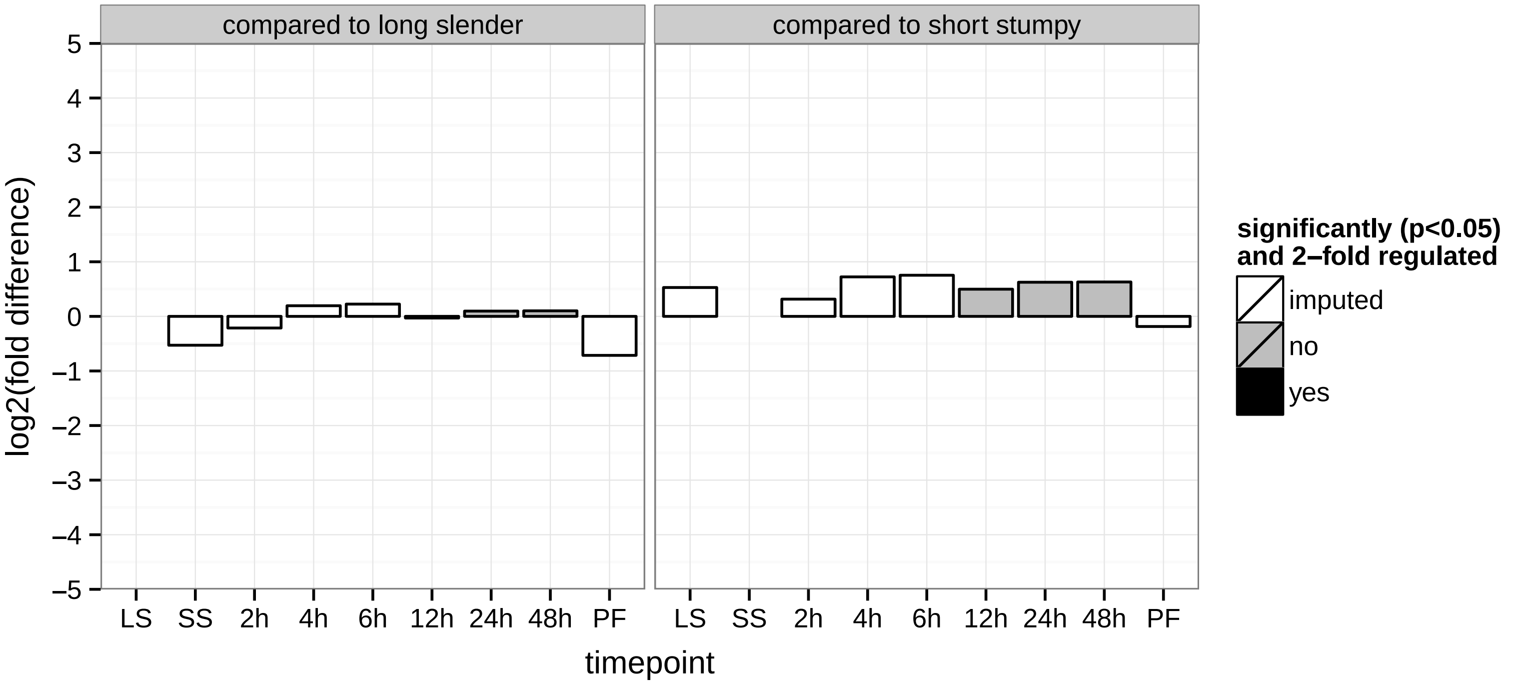
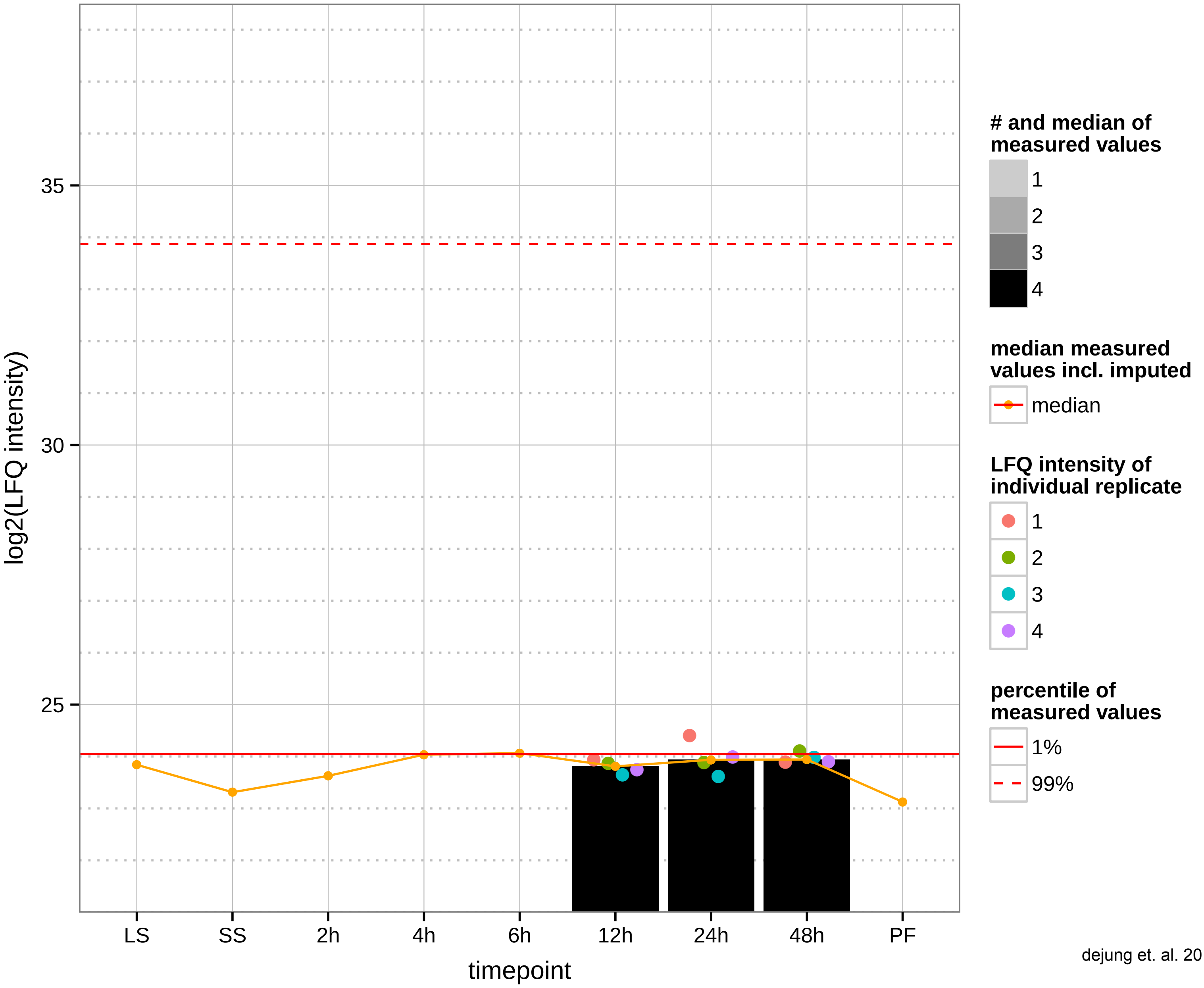
hypothetical protein, conserved
Tb927.11.16460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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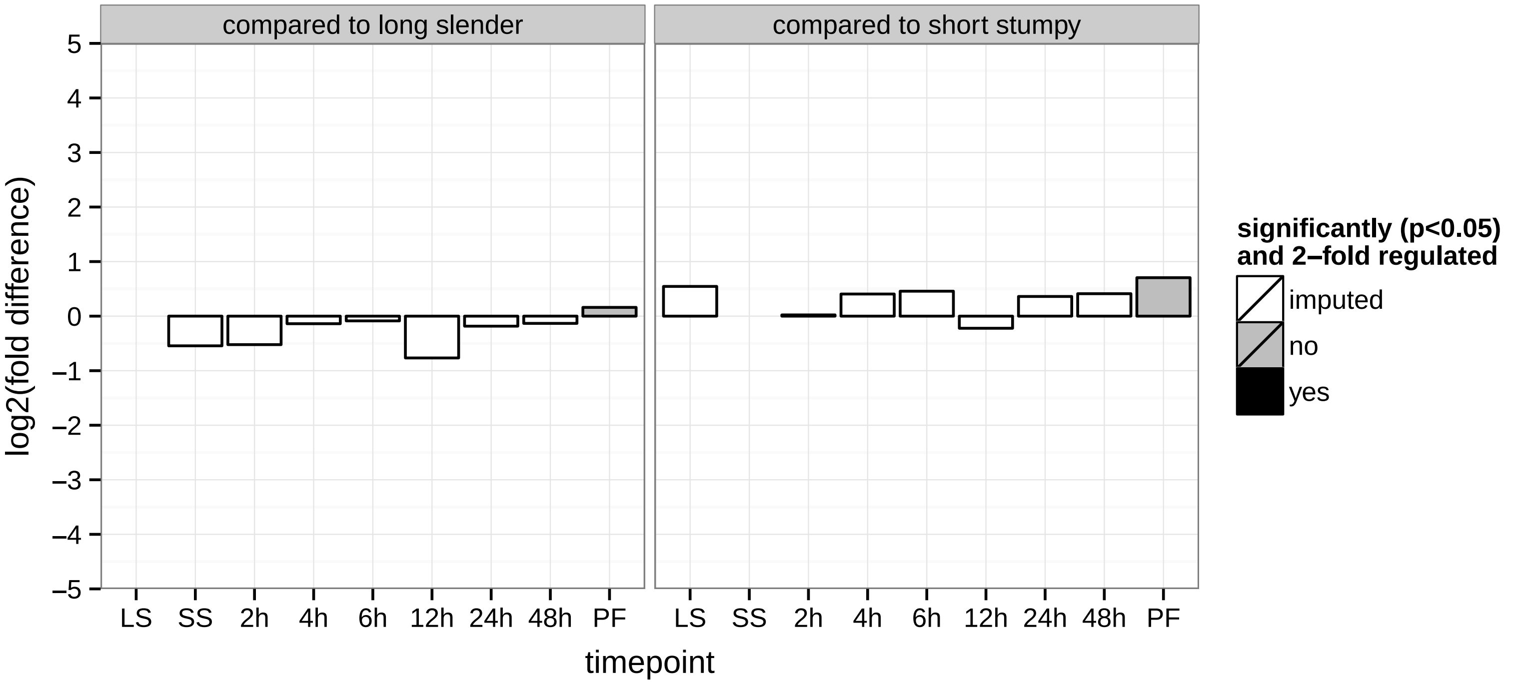
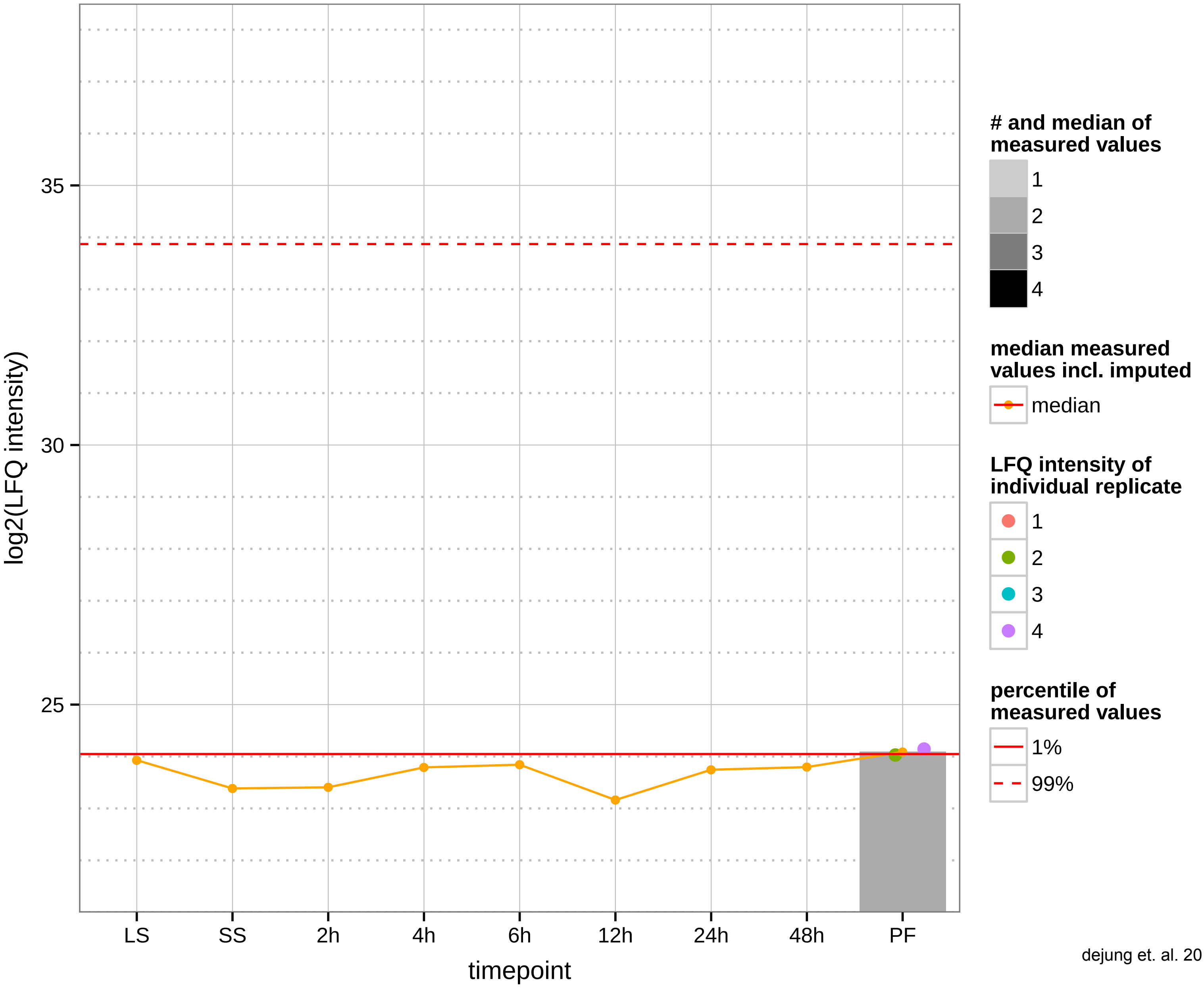
hypothetical protein, conserved
Tb927.11.16470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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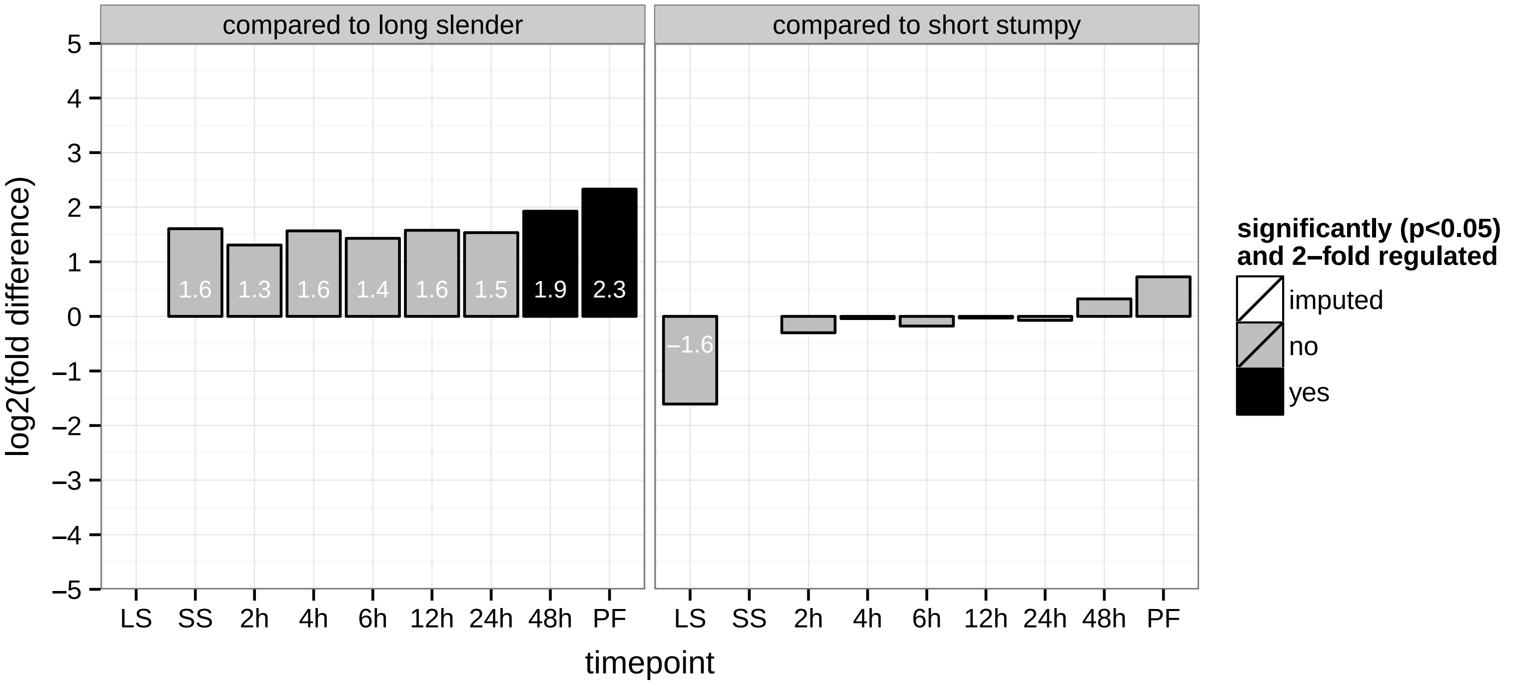
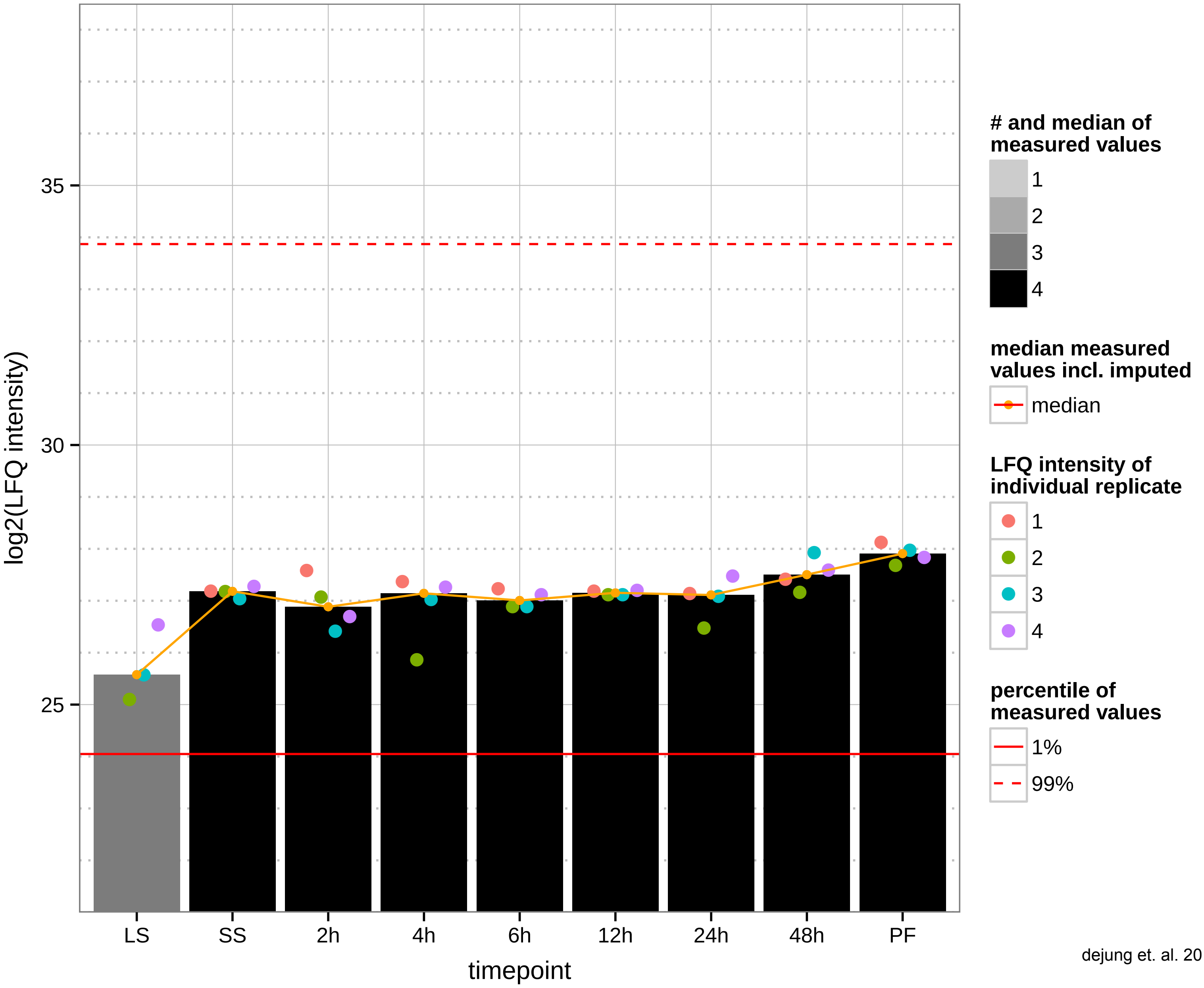
vesicular transport protein (CDC48 homologue), putative
Tb927.11.1660
AGOF: ATP binding, ATPase activity
AGOC: null
AGOP: regulation of transcription, DNA−dependent, two−component signal transduction system (phosphorelay)
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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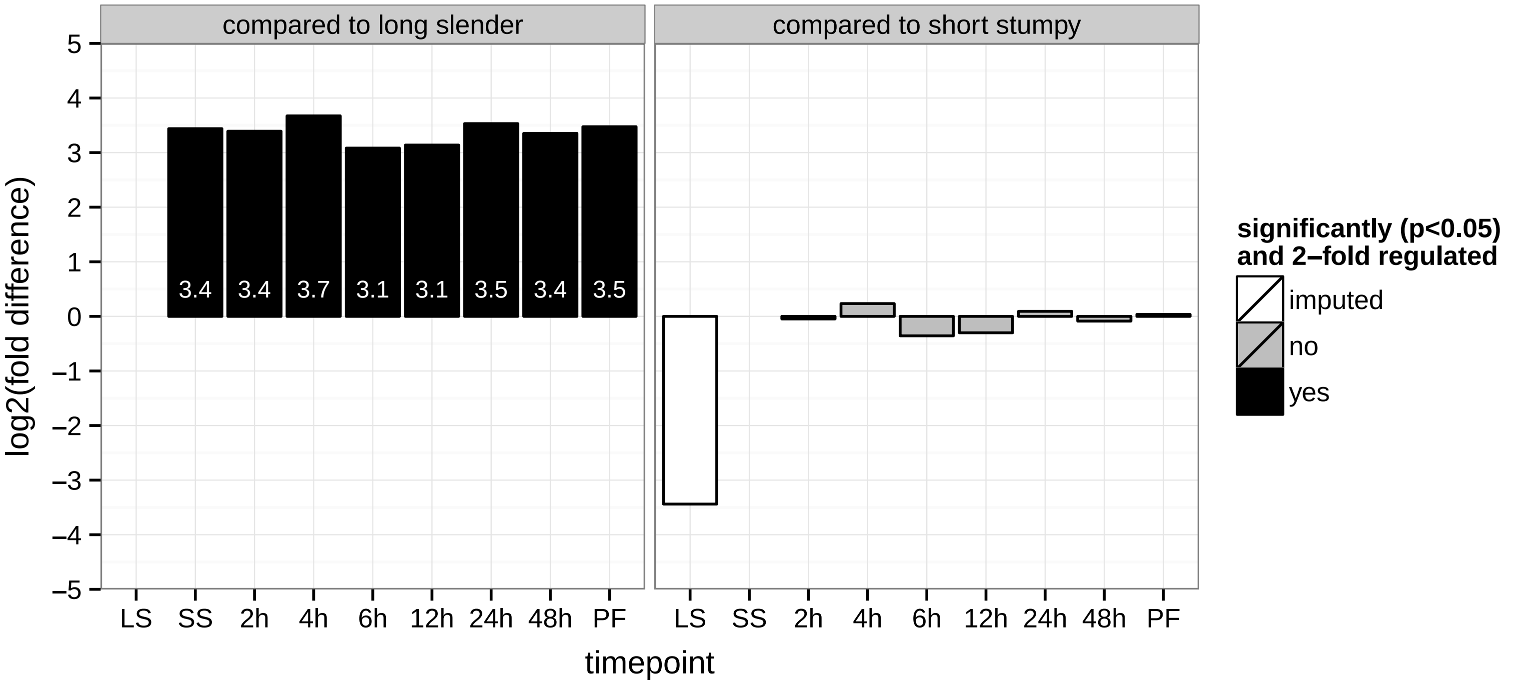
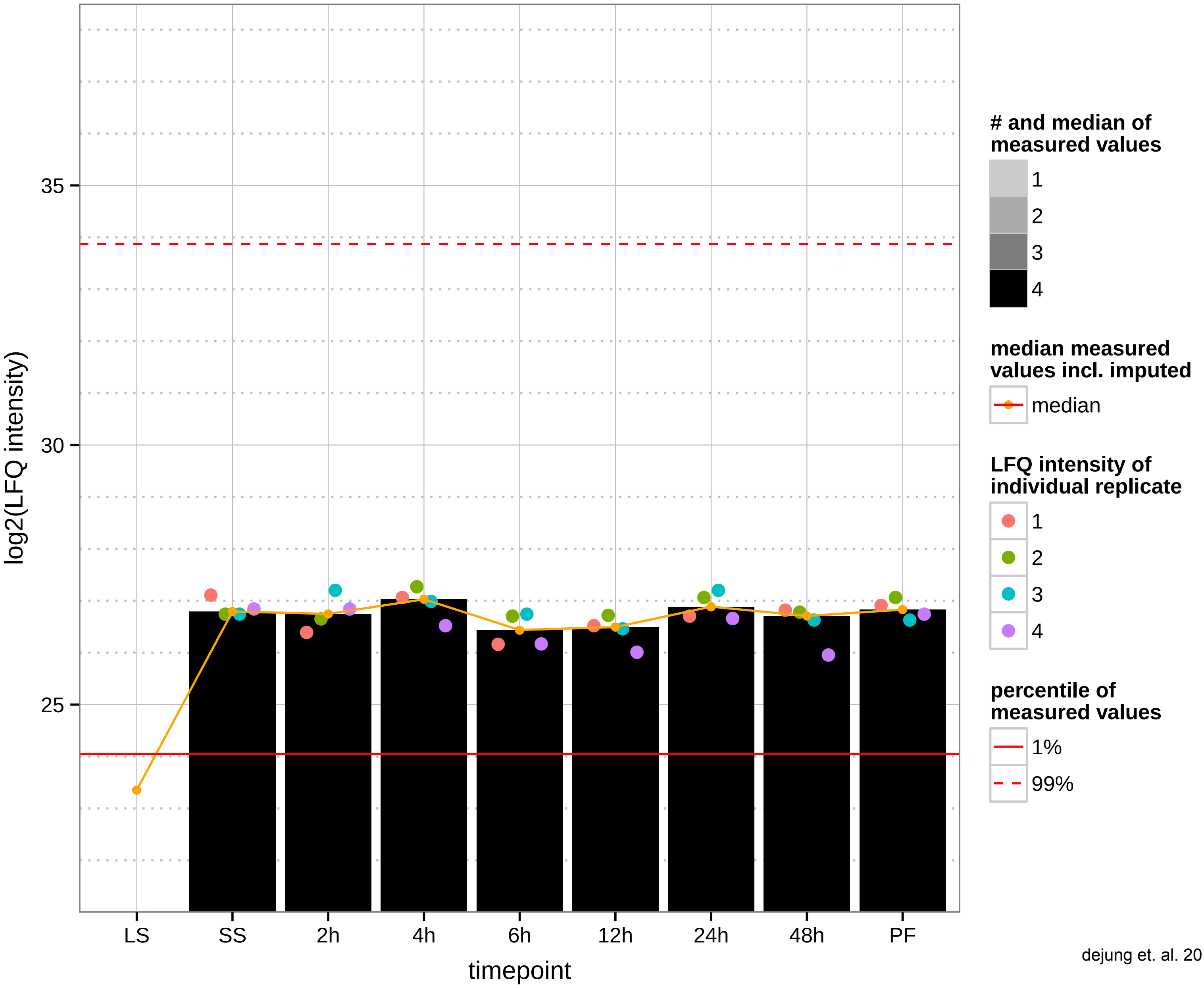
exosome–associated protein 2 (EAP2)
Tb927.11.16600
AGOF: 3'–5'–exoribonuclease activity, RNA binding
AGOC: cytoplasmic exosome (RNase complex), nuclear exosome (RNase complex)
AGOP: RNA processing, rRNA processing
PGOF: null
PGOC: null
PGOP: null





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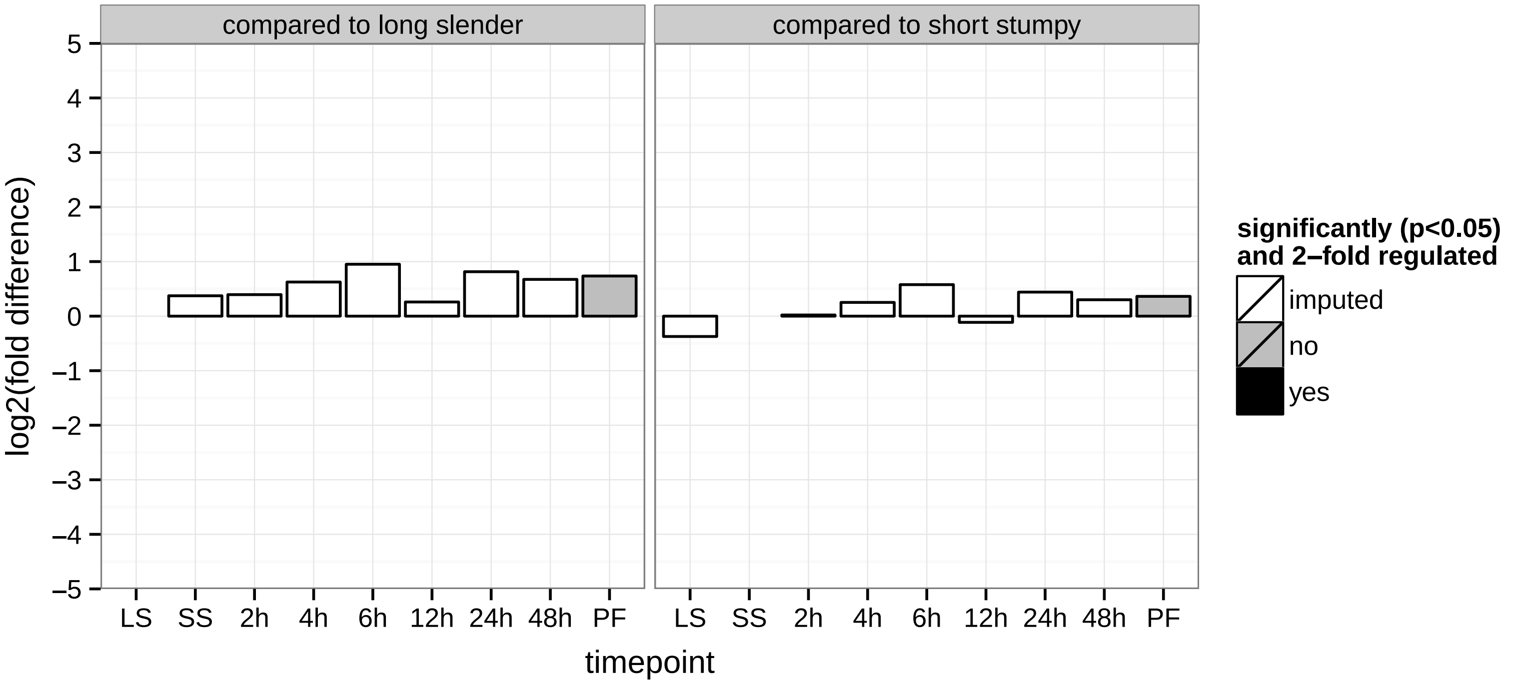
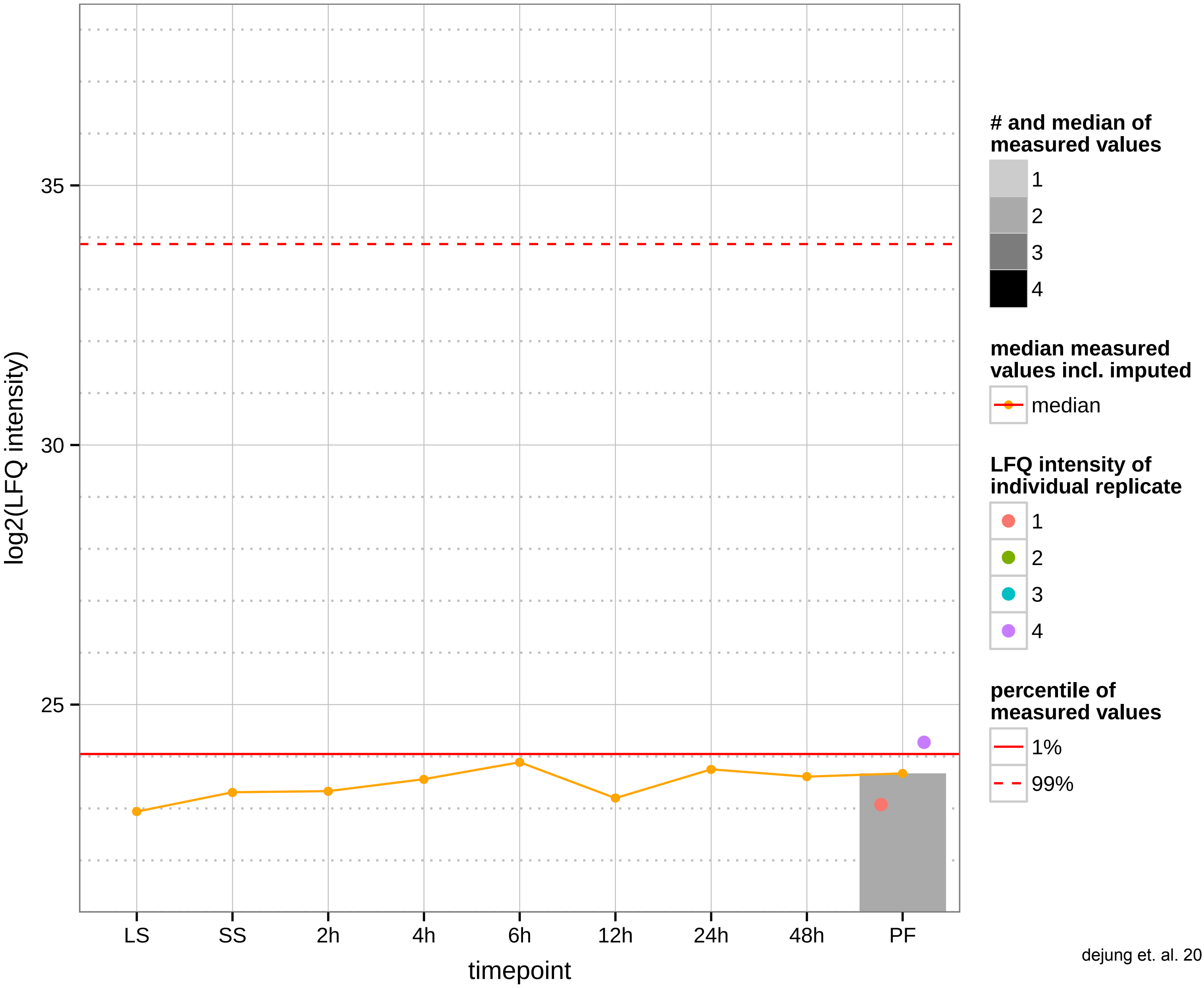
hypothetical protein, conserved
Tb927.11.16630
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: integral to membrane
PGOP: transmembrane transport





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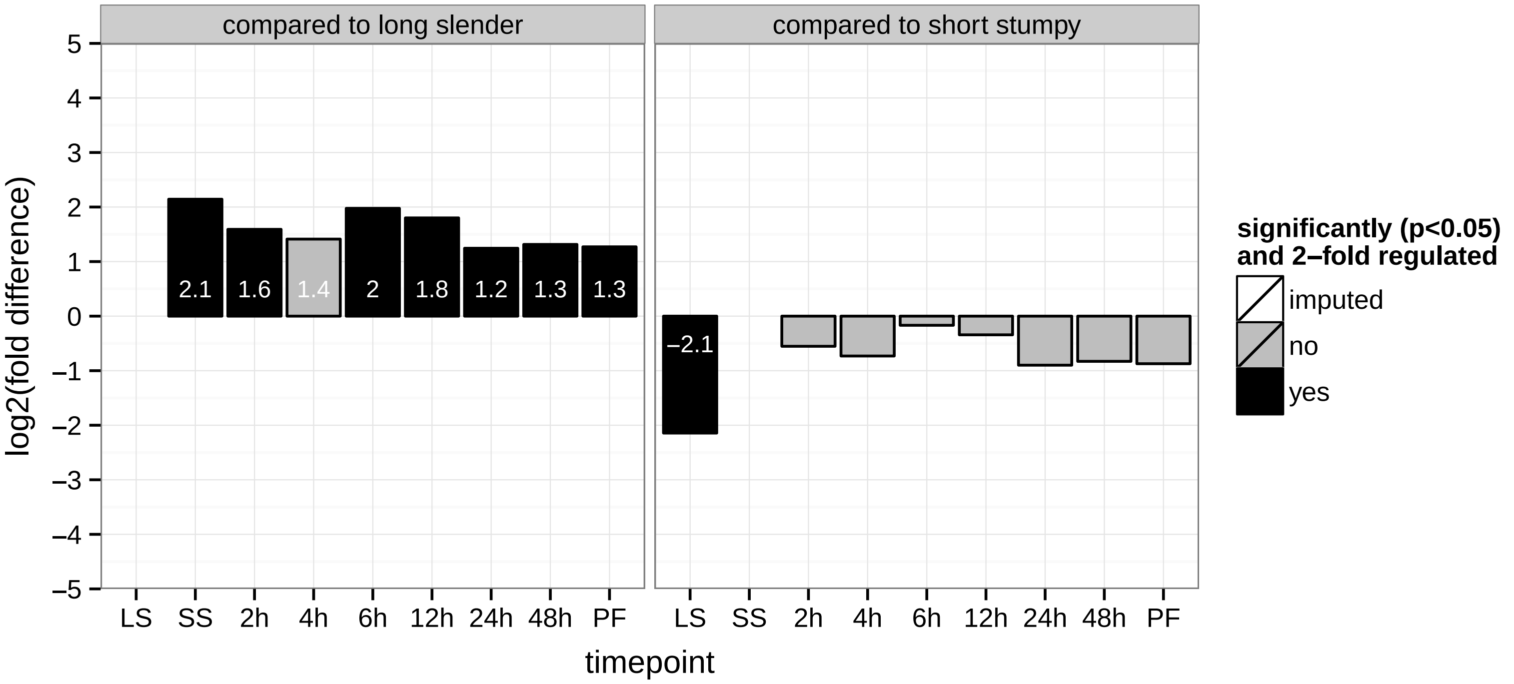
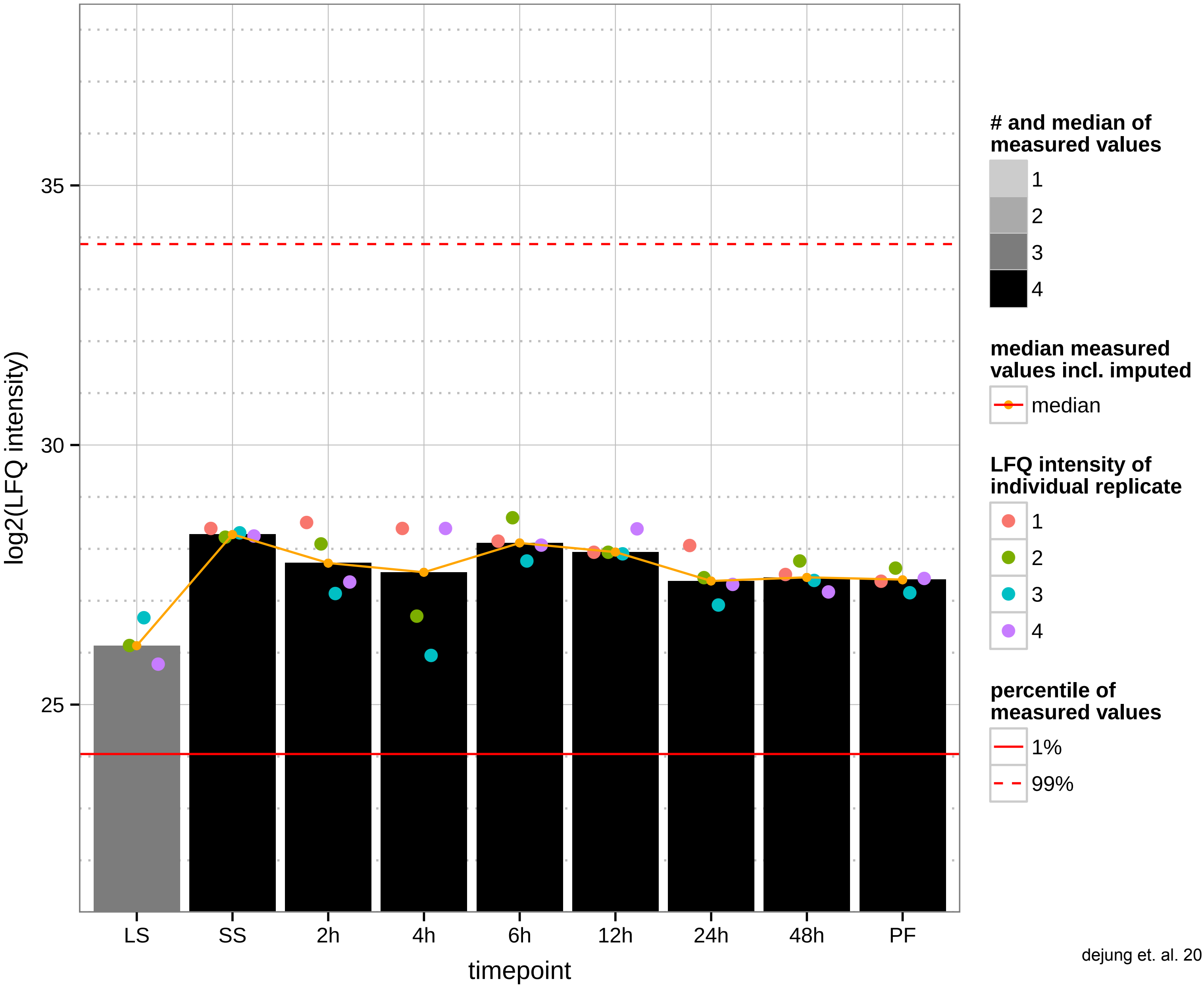
hypothetical protein, conserved
Tb927.11.16660
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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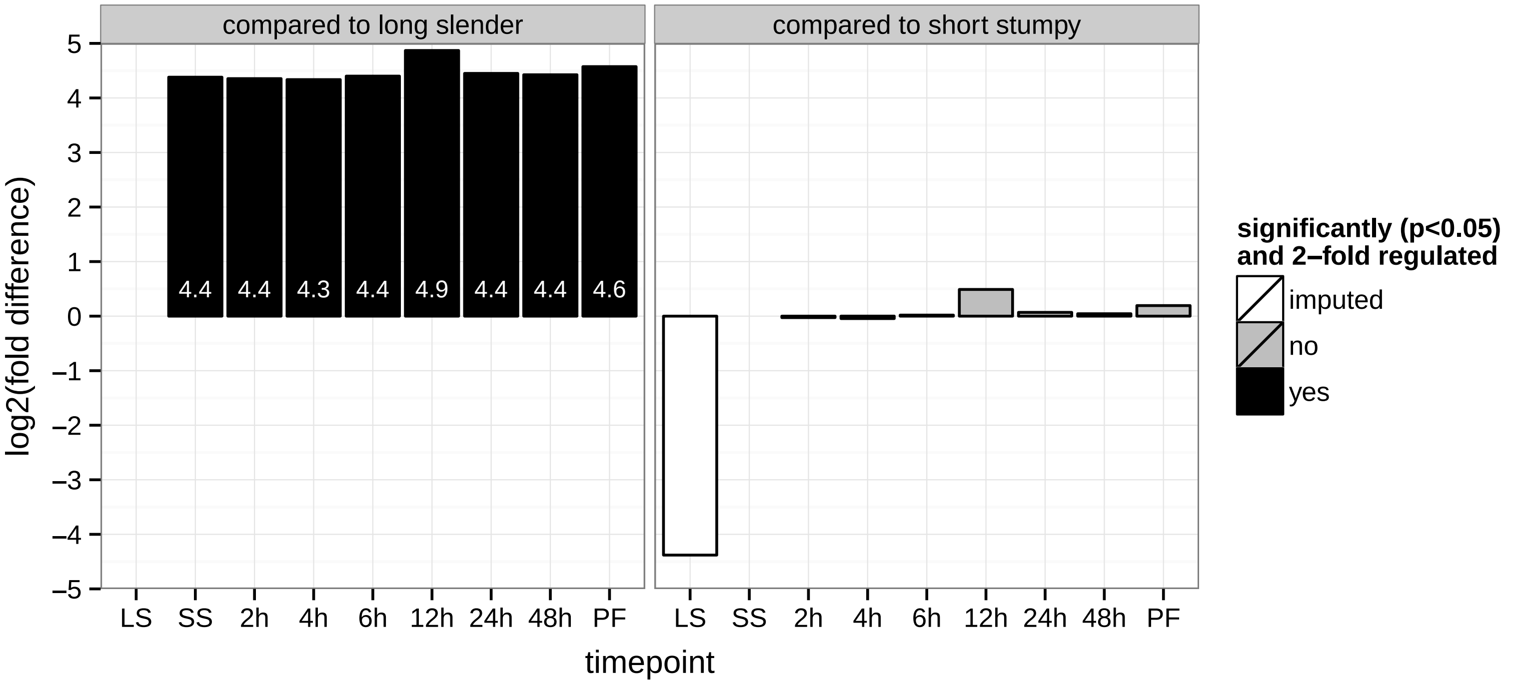
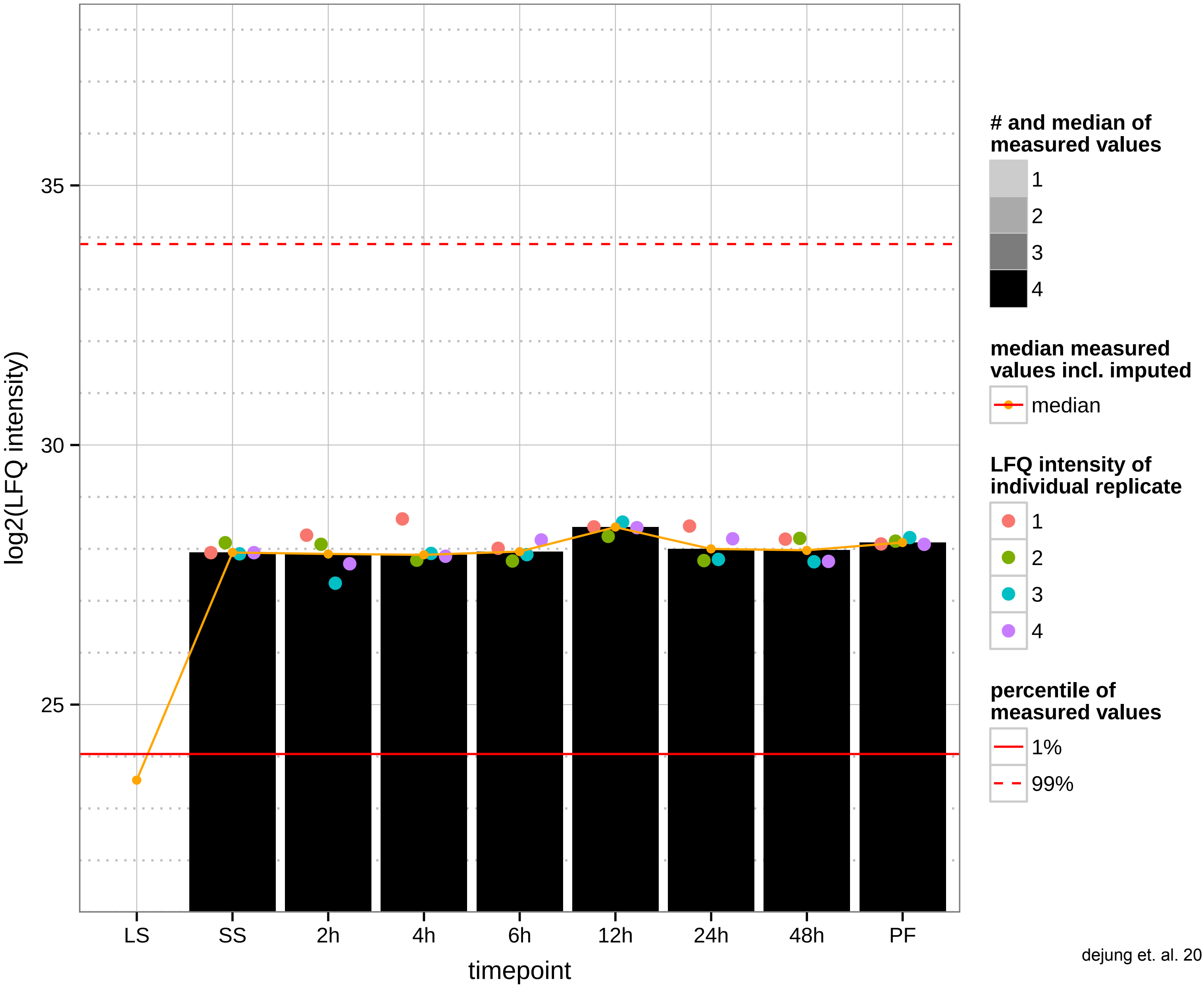
cysteine desulfurase
Tb927.11.1670
AGOF: cysteine desulfurase activity, transaminase activity
AGOC: mitochondrion
AGOP: iron-sulfur cluster assembly, protein complex assembly, sulfur amino acid metabolic process, tRNA wobble position ur
PGOF: null
PGOC: null
PGOP: metabolic process





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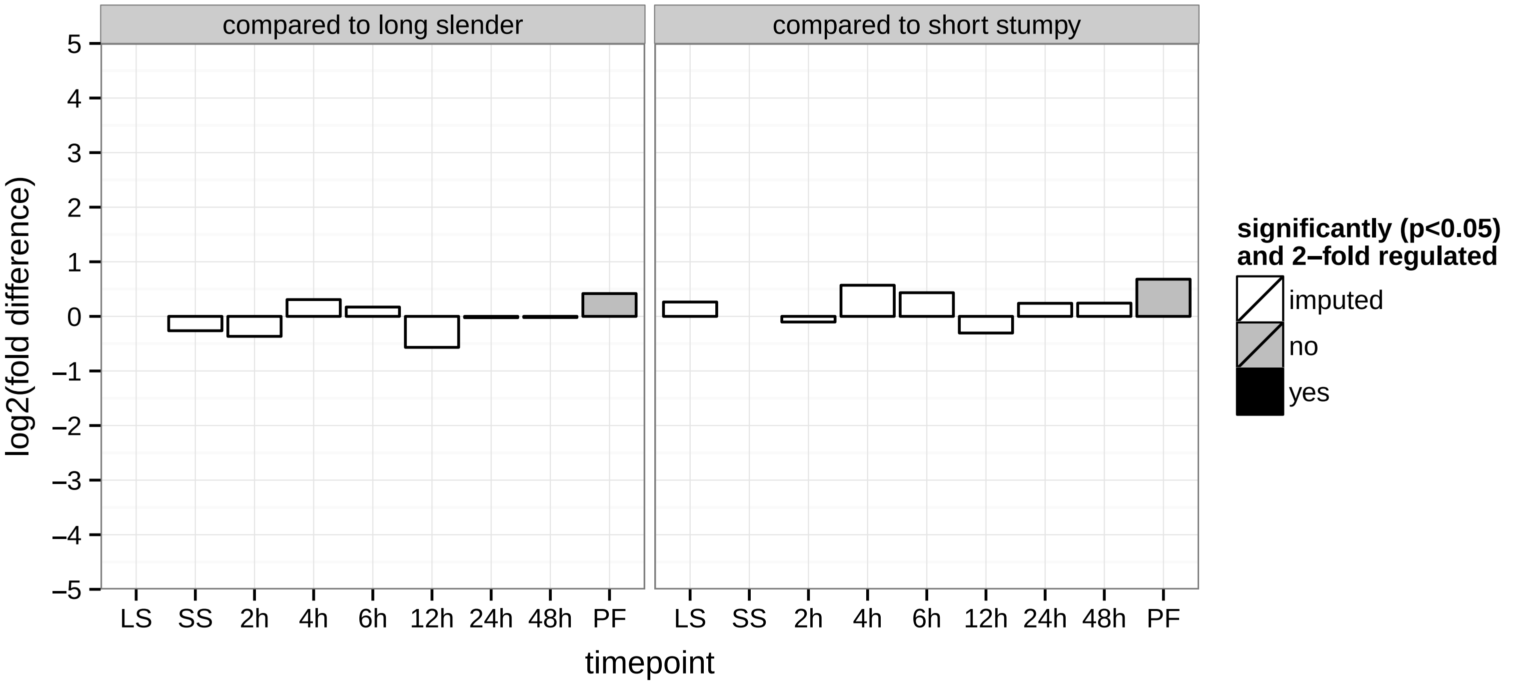
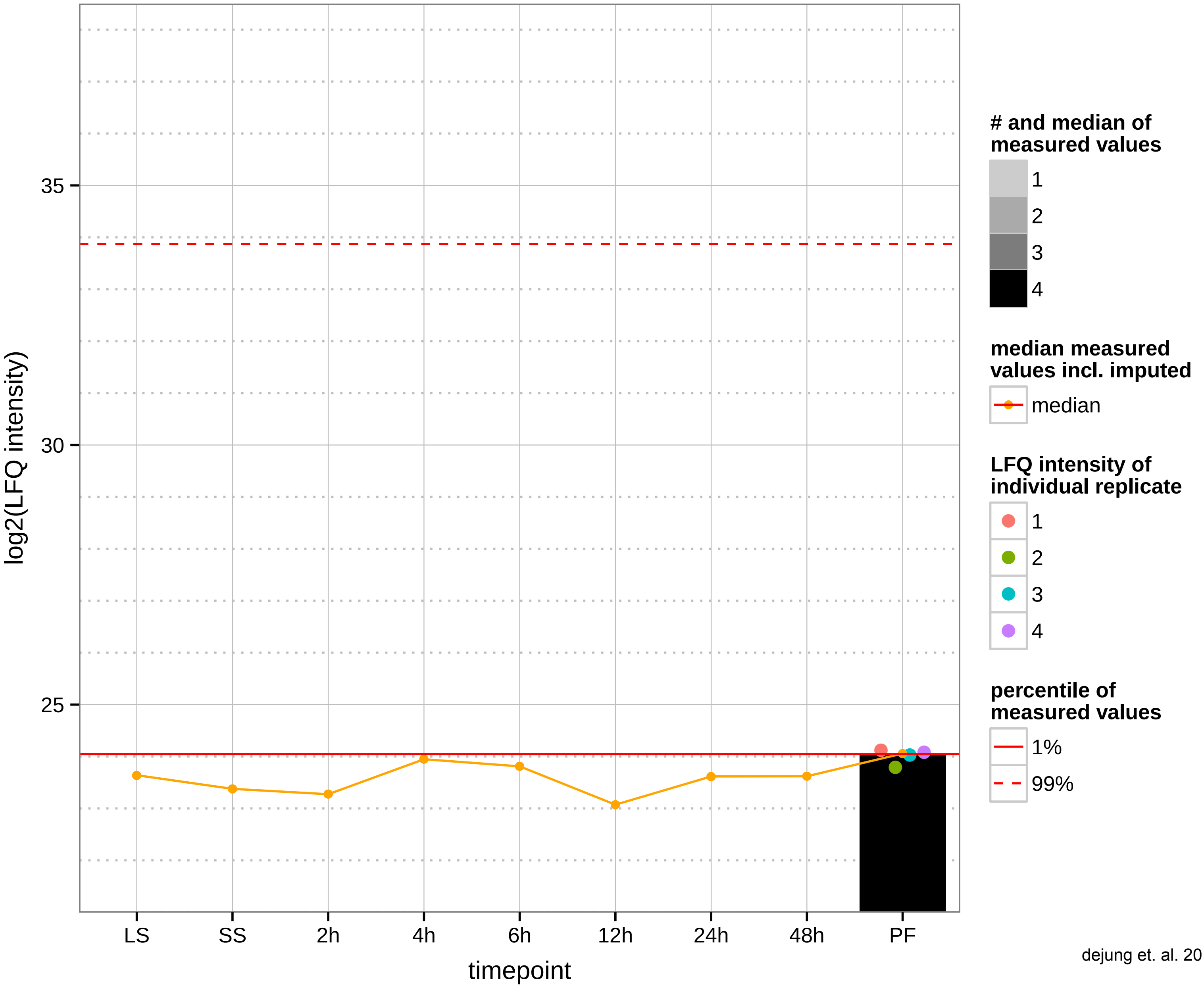
hypothetical protein, conserved
Tb927.11.16700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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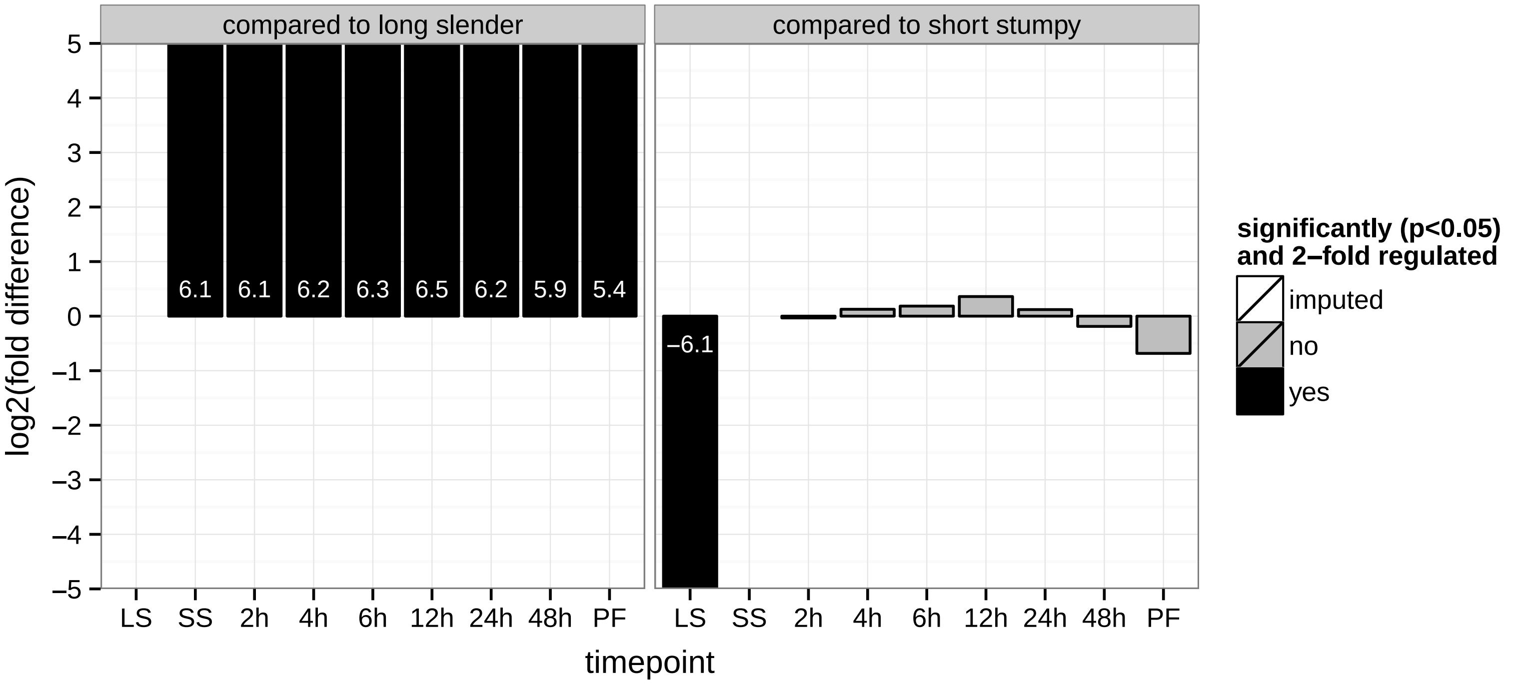
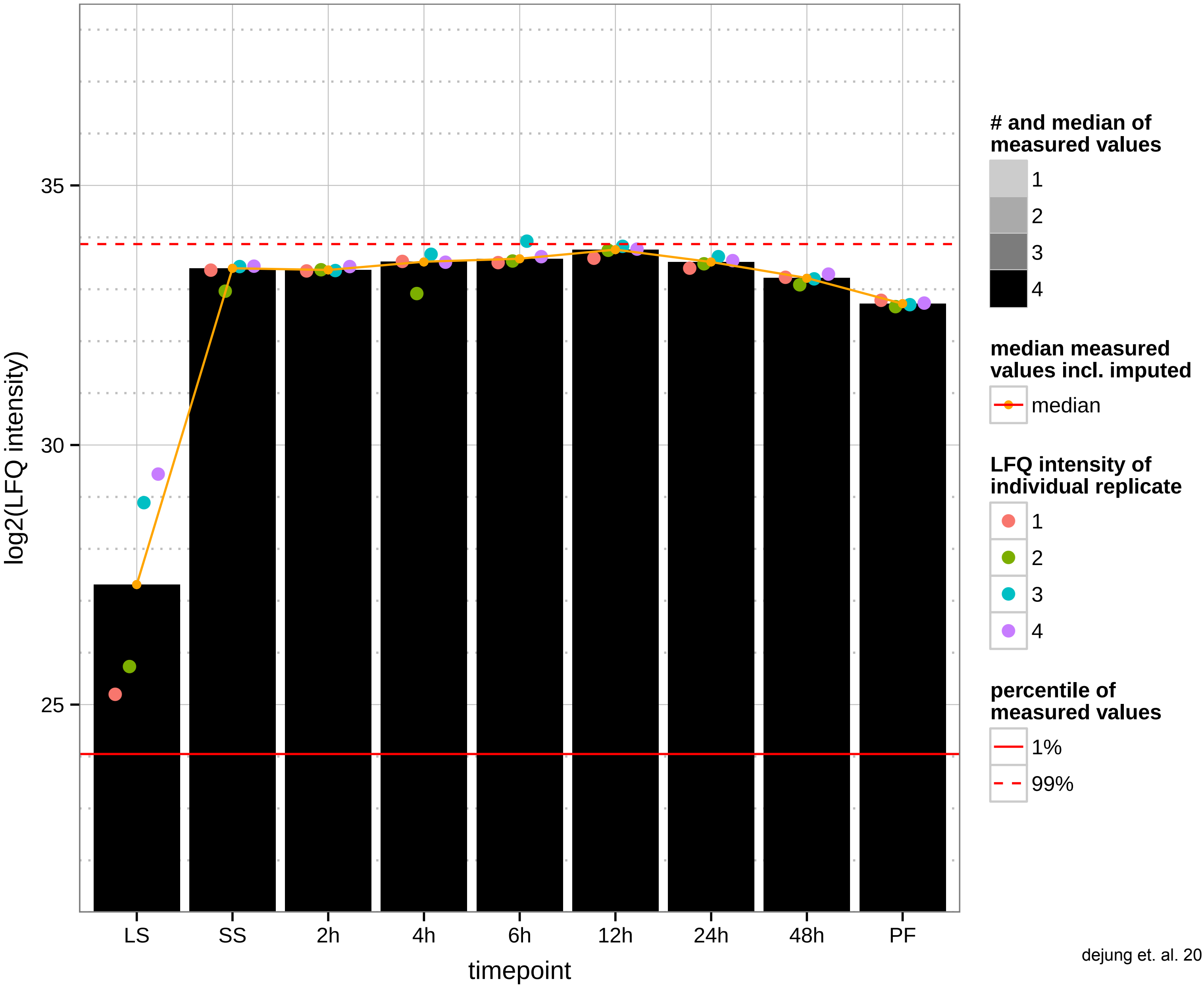
dihydrolipoyl dehydrogenase (GCVL−2)
Tb927.11.16730
AGOF: dihydrolipoyl dehydrogenase activity, disulfide oxidoreductase activity, flavin adenine dinucleotide binding
AGOC: cytoplasm, mitochondrial inner membrane, mitochondrion
AGOP: cell redox homeostasis, oxidation−reduction process
PGOF: dihydrolipoyl dehydrogenase activity, flavin adenine dinucleotide binding, oxidoreductase activity
PGOC: cytoplasm
PGOP: cell redox homeostasis, oxidation−reduction process





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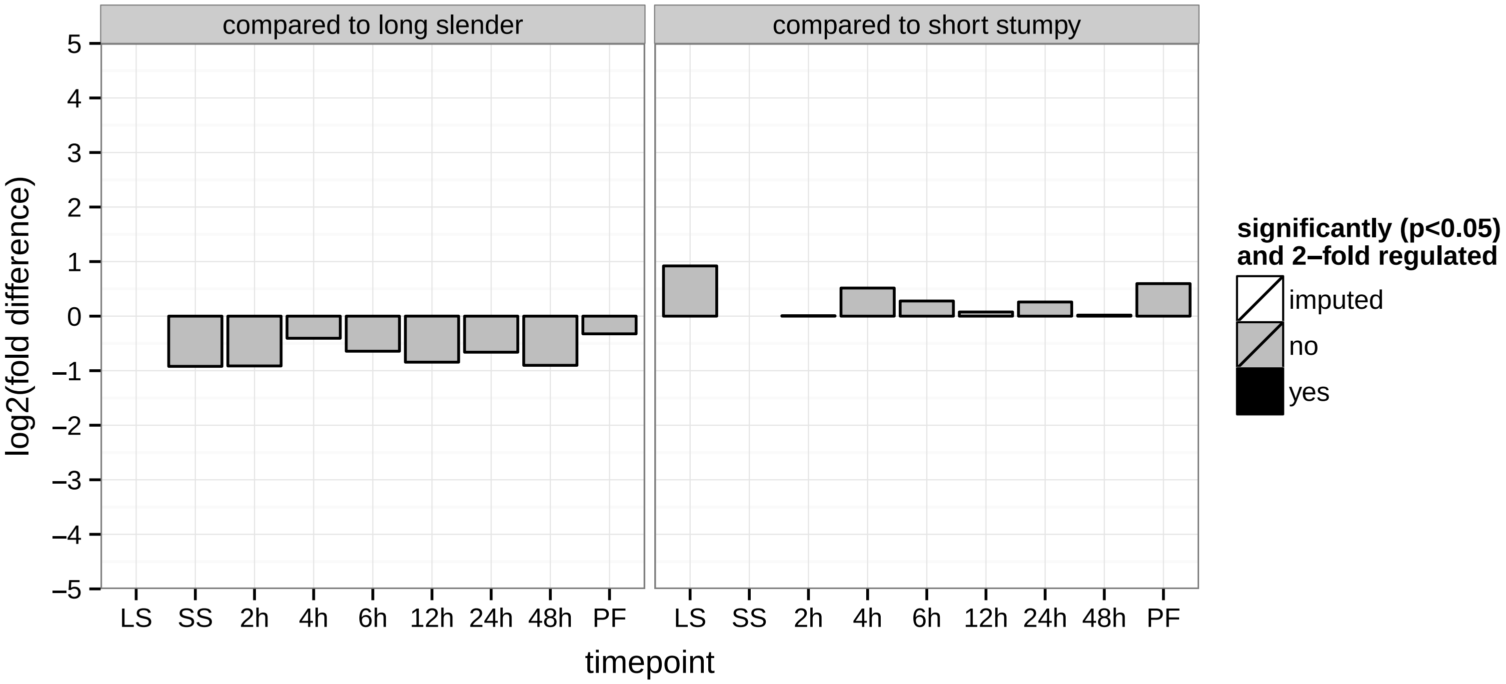
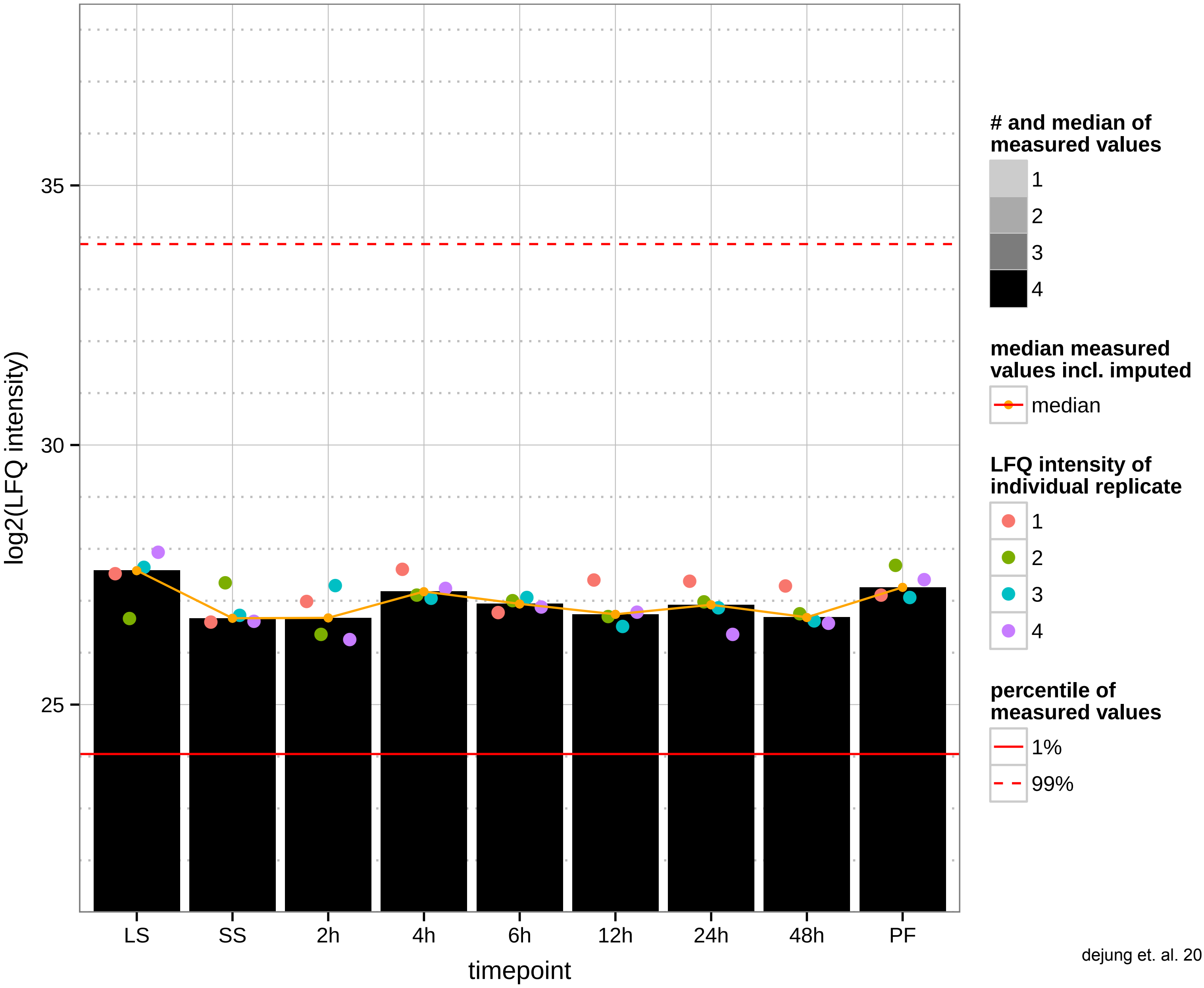
chaperone protein DNAj, putative
Tb927.11.16740
AGOF: chaperone binding, heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding, unfolded protein binding
PGOC: null
PGOP: protein folding





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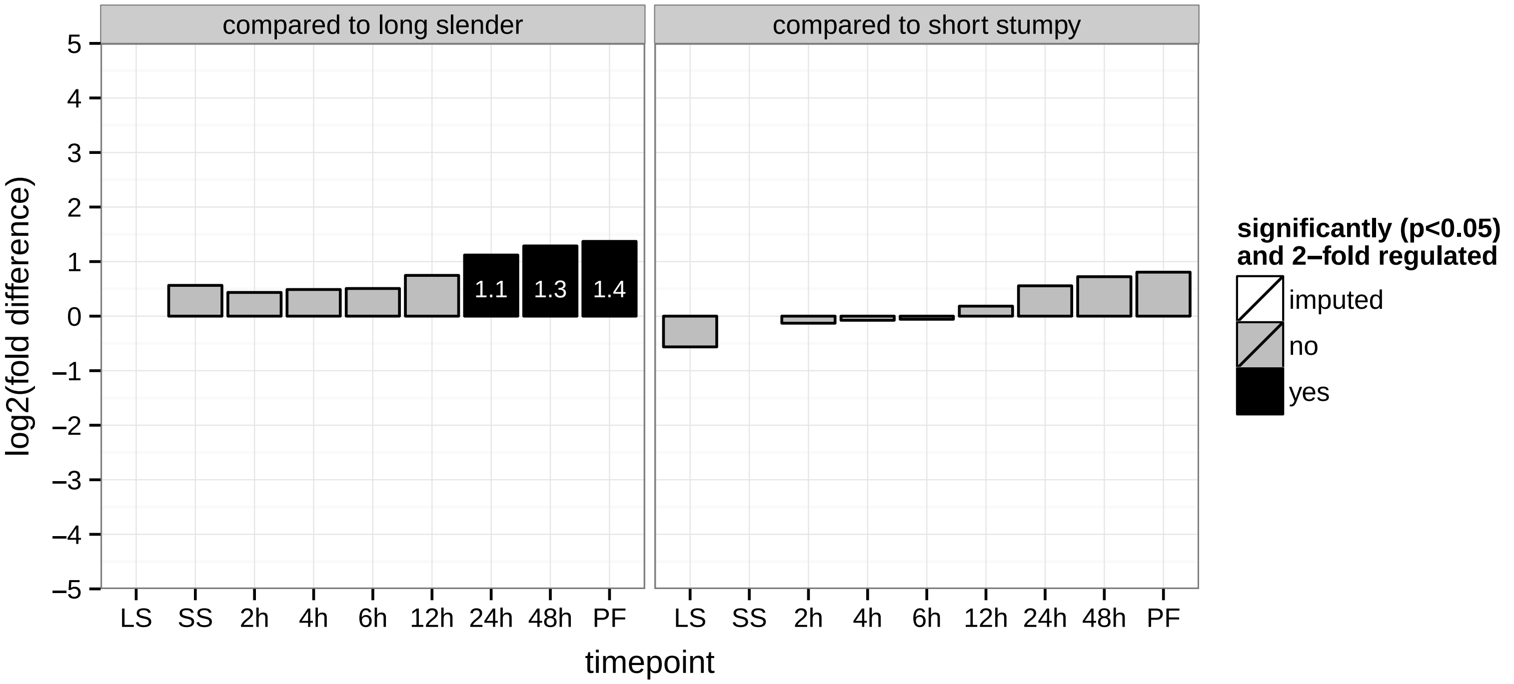
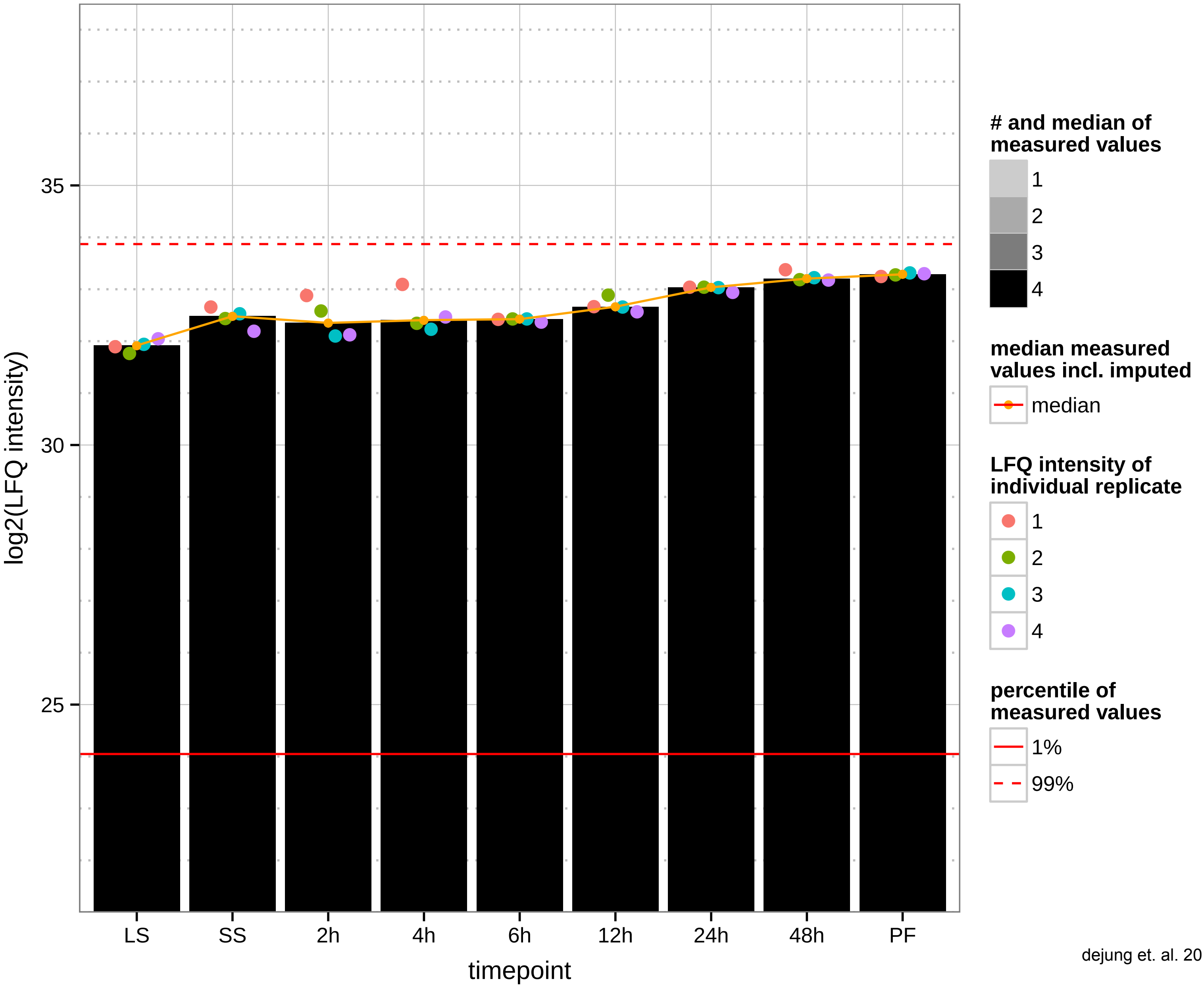
T–complex protein 1, alpha subunit, putative (TCP–1–alpha)
Tb927.11.16760
AGOF: ATP binding, unfolded protein binding
AGOC: chaperonin–containing T–complex
AGOP: protein folding, regulation of cell cycle
PGOF: ATP binding
PGOC: null
PGOP: cellular protein metabolic process





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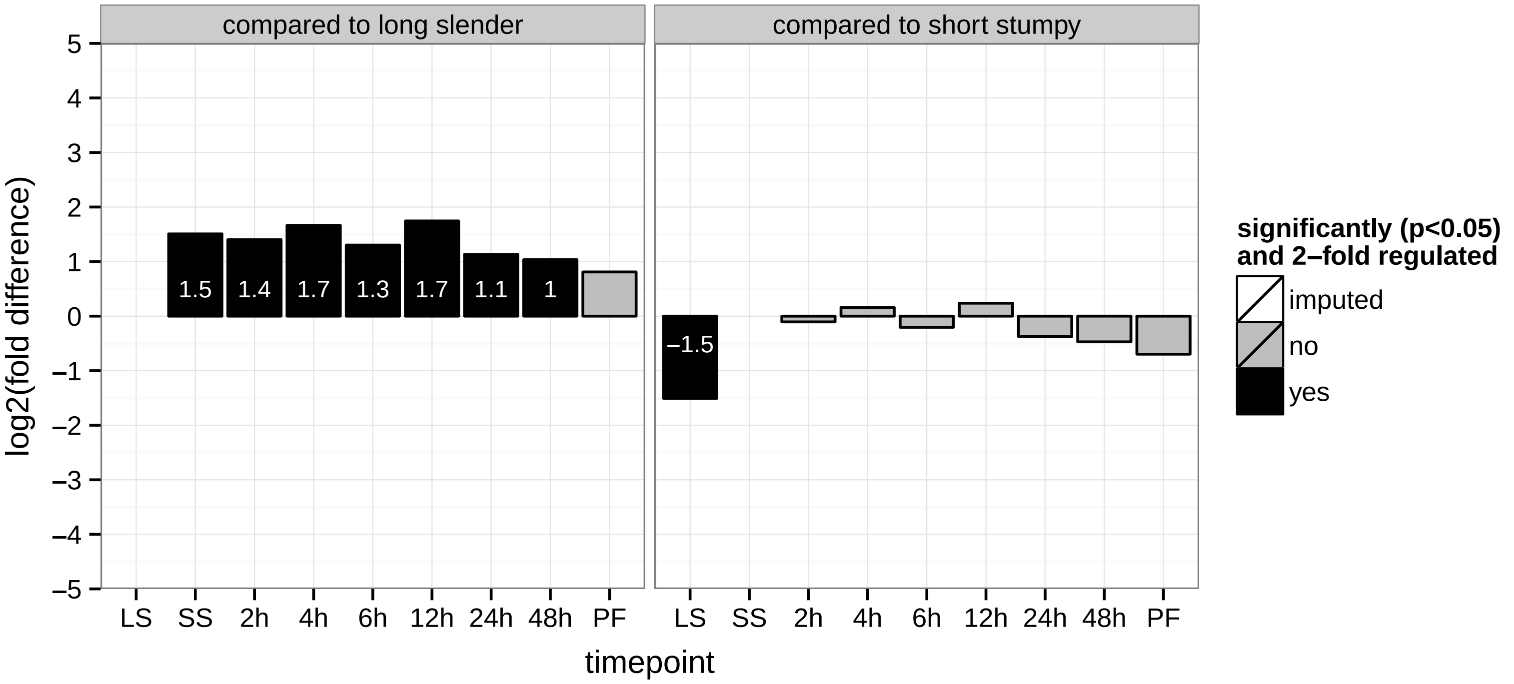
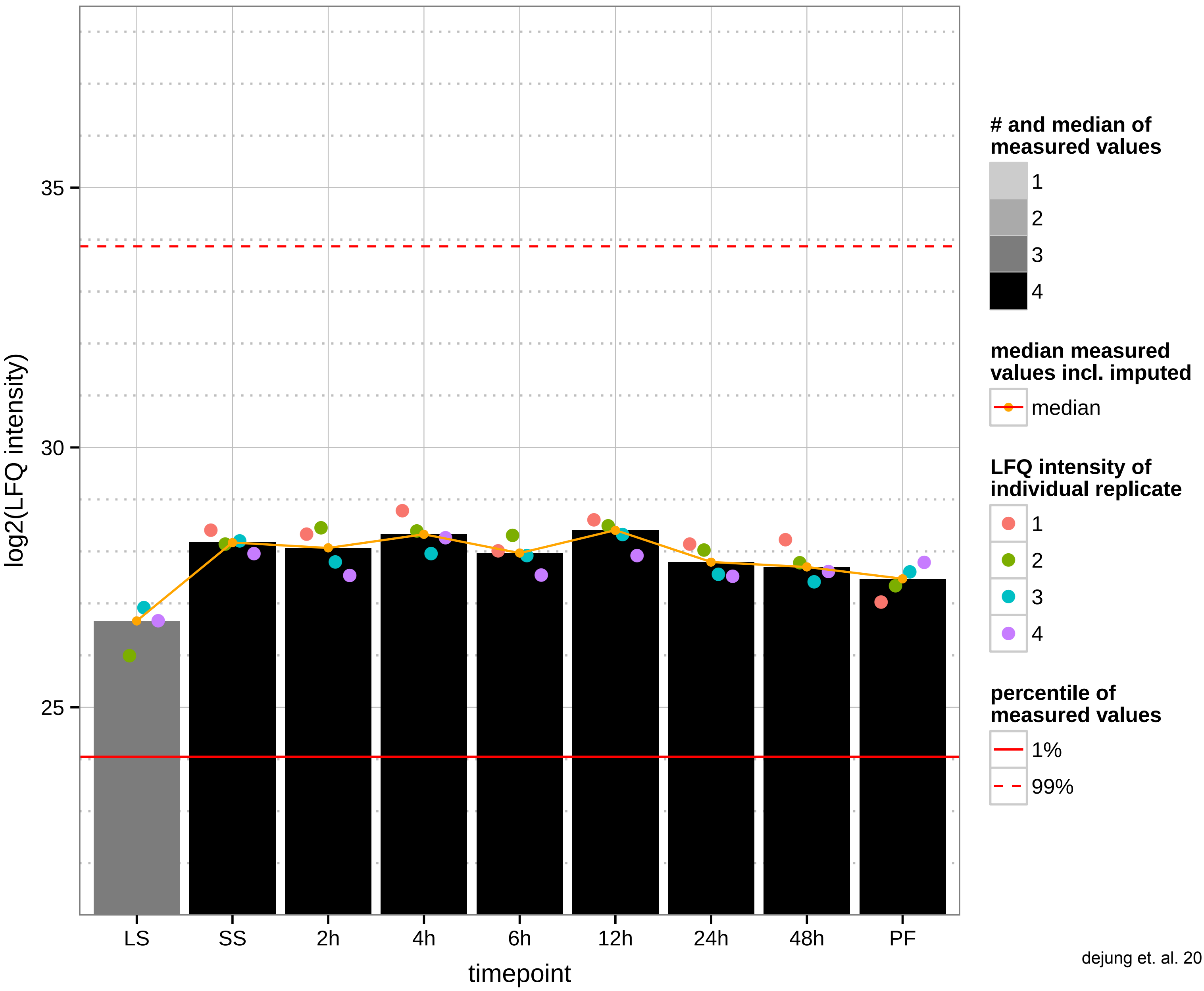
glucosamine–6–phosphate isomerase, putative
Tb927.11.16770
AGOF: glucosamine–6–phosphate deaminase activity
AGOC: null
AGOP: N–acetylglucosamine catabolic process, carbohydrate metabolic process
PGOF: glucosamine–6–phosphate deaminase activity
PGOC: null
PGOP: N–acetylglucosamine metabolic process, carbohydrate metabolic process





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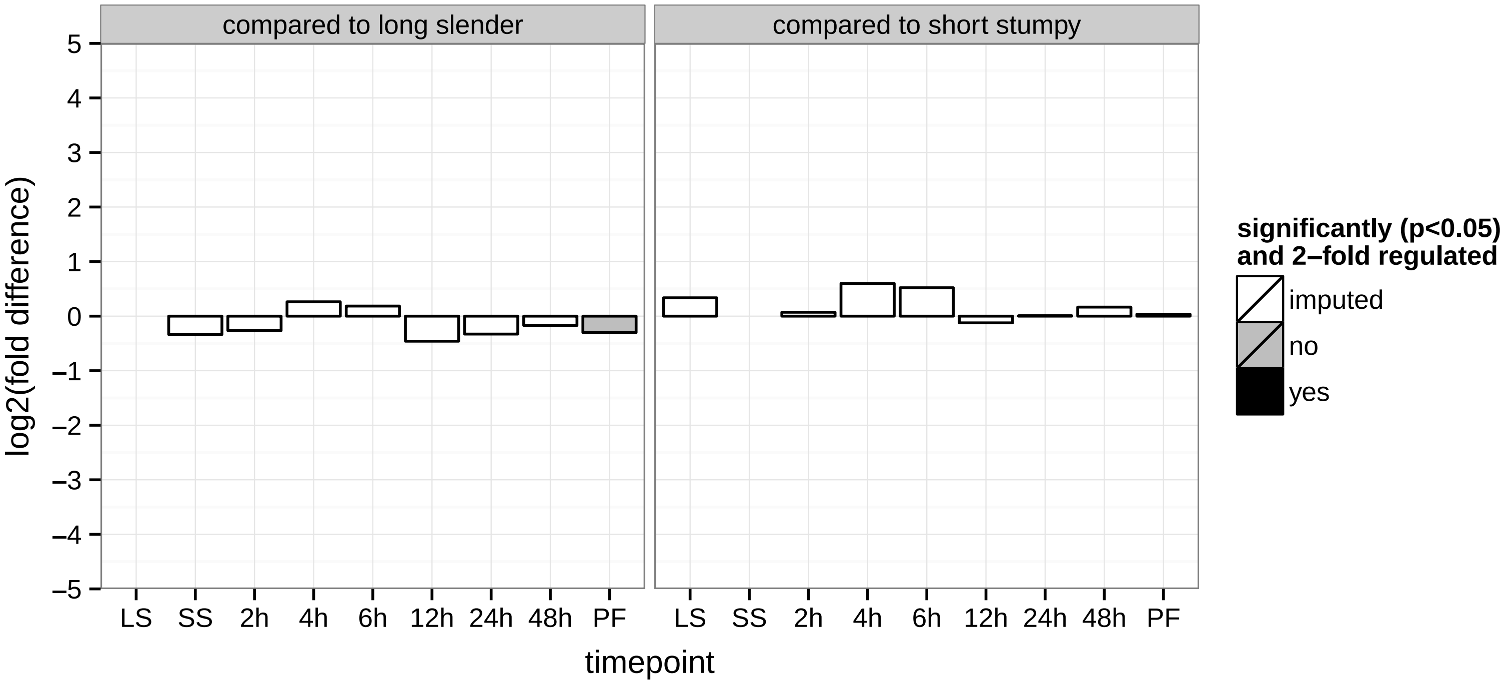
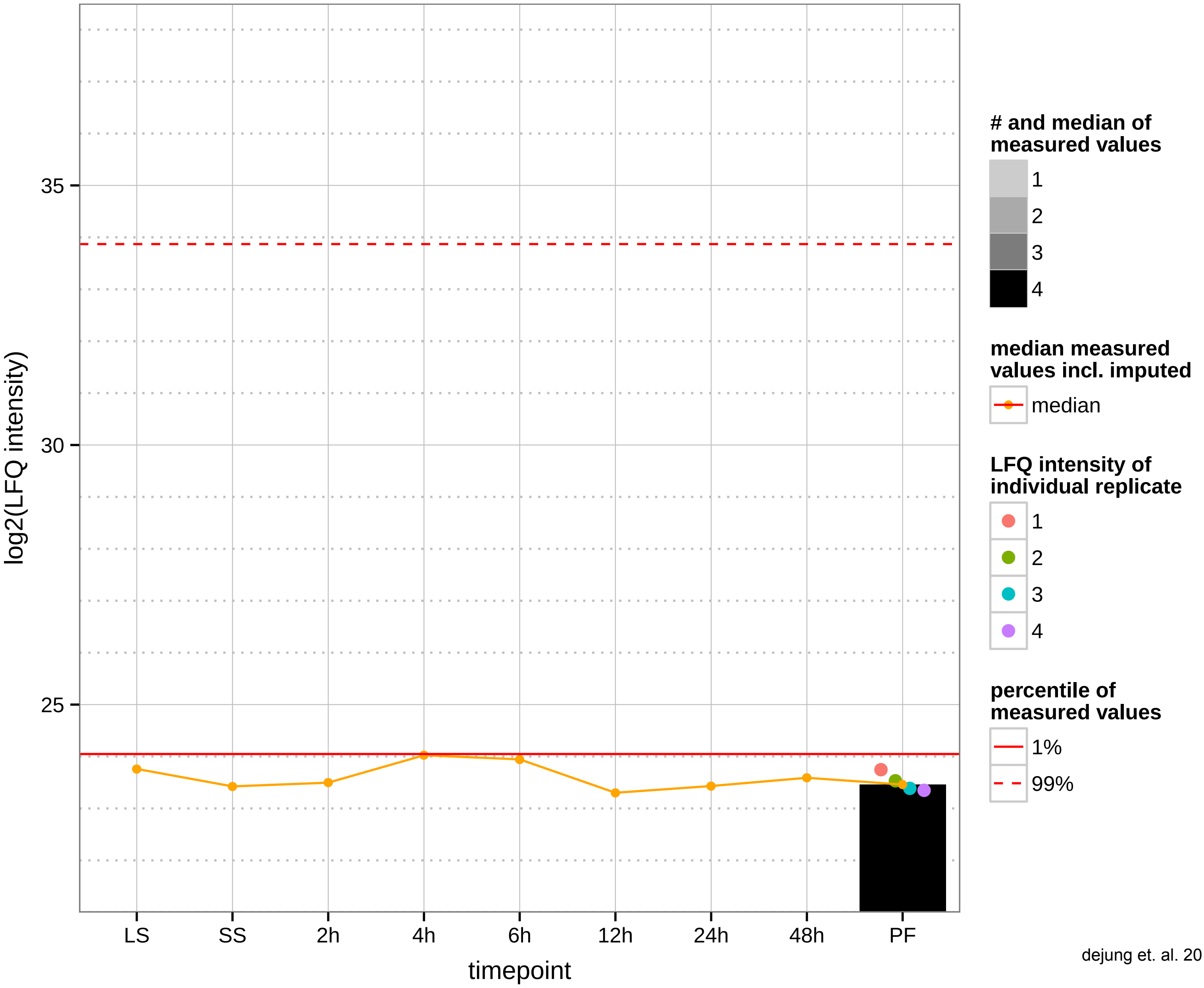
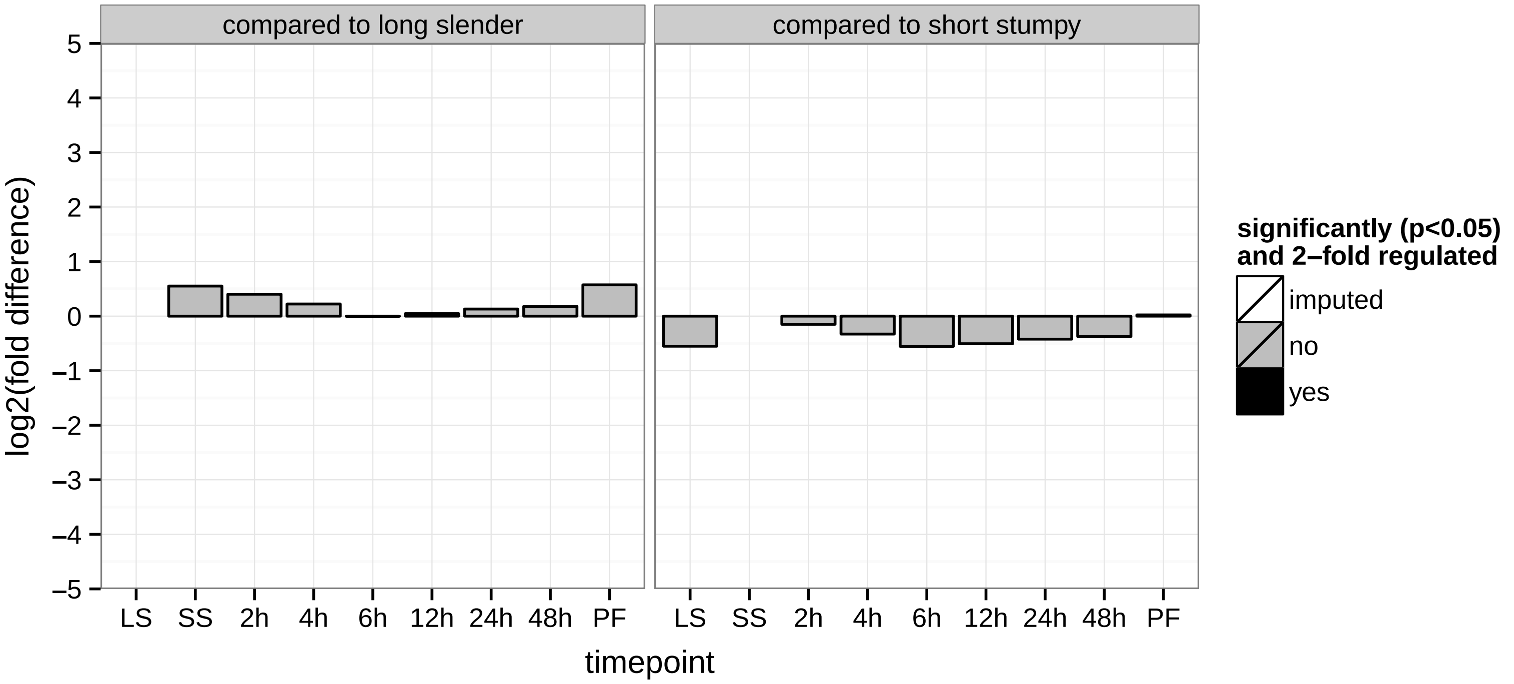
mitogen–activated protein kinase (ECK1)
Tb927.11.16790
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

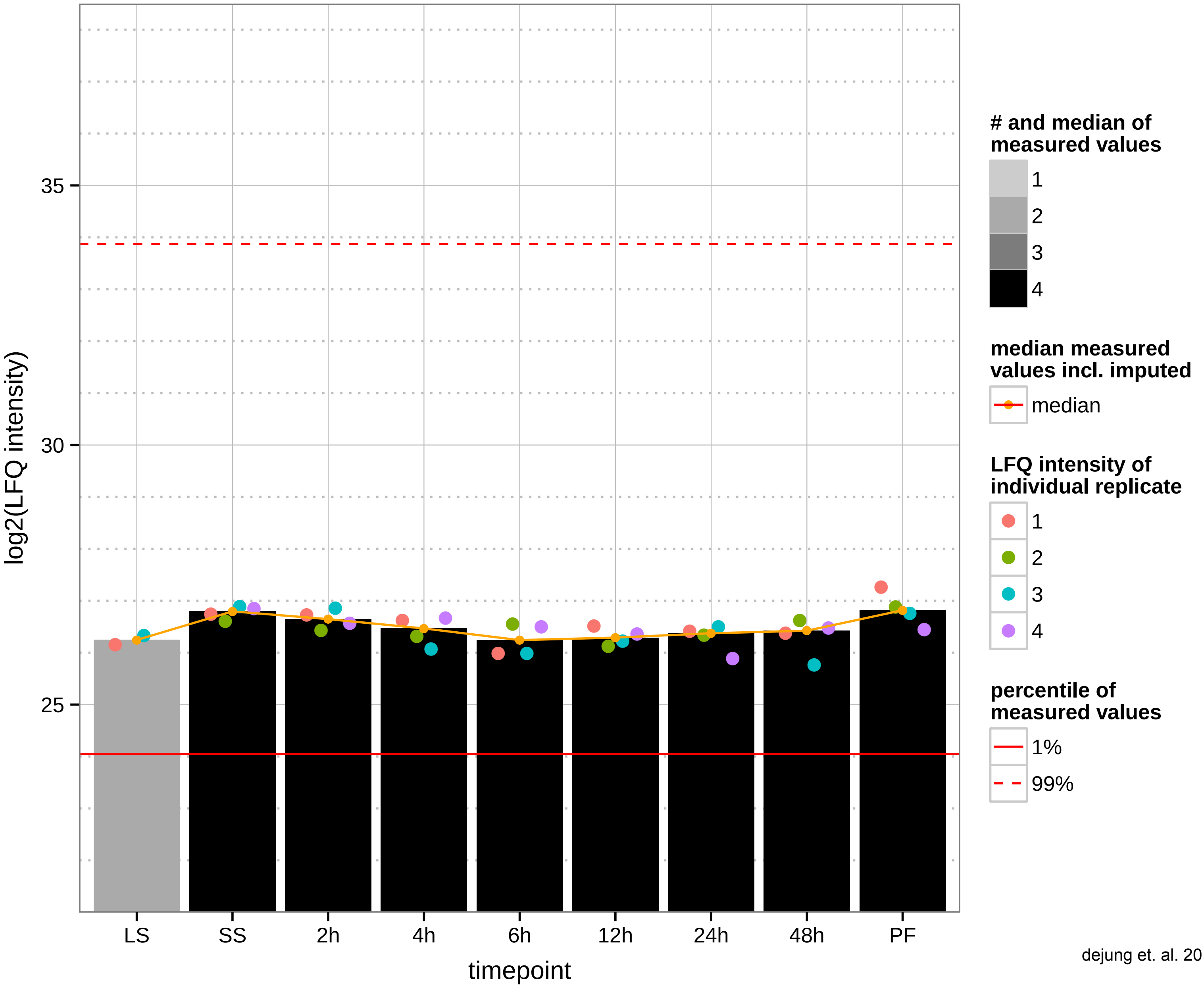




dejung et. al. 2015

vesicular–fusion protein SEC18, putative
Tb927.11.1680
AGOF: ATP binding, nucleoside–triphosphatase activity
AGOC: null
AGOP: ER to Golgi vesicle–mediated transport, Golgi vesicle transport, vesicle–mediated transport
PGOF: ATP binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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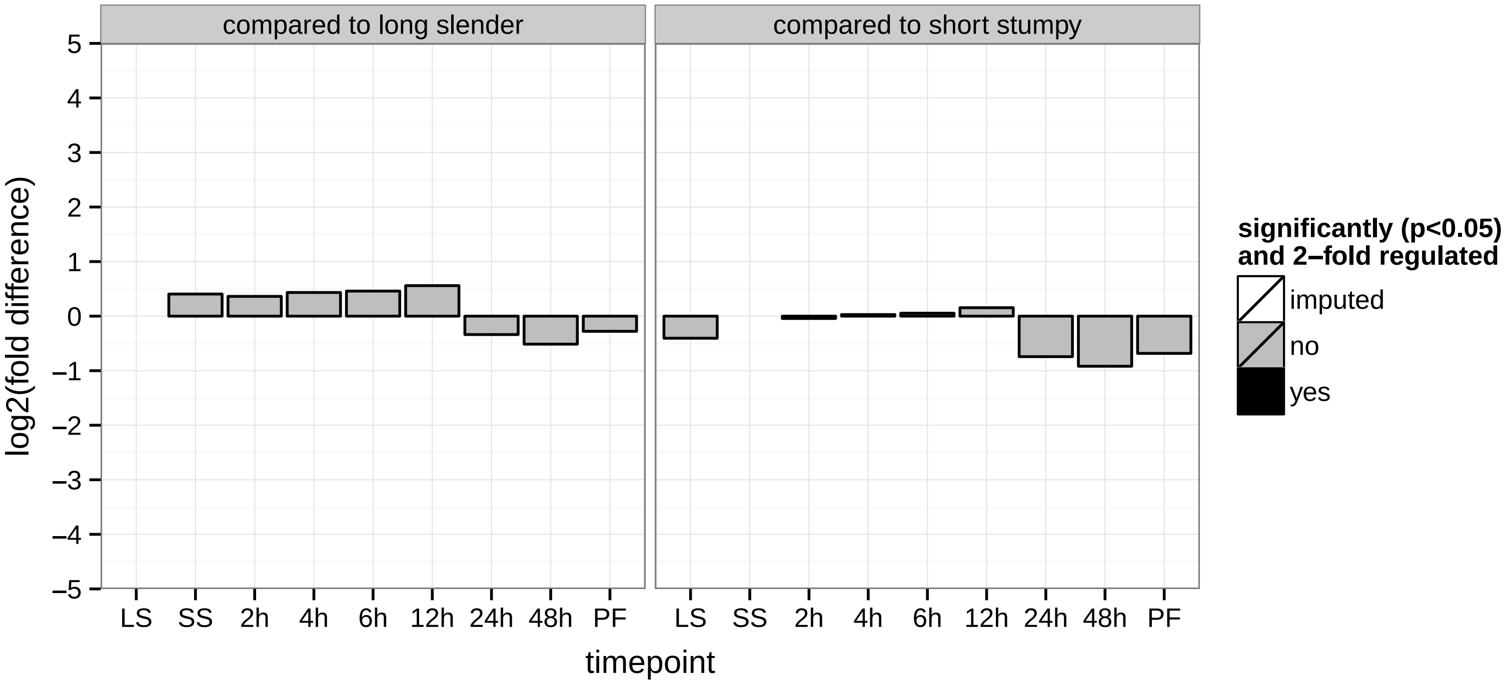
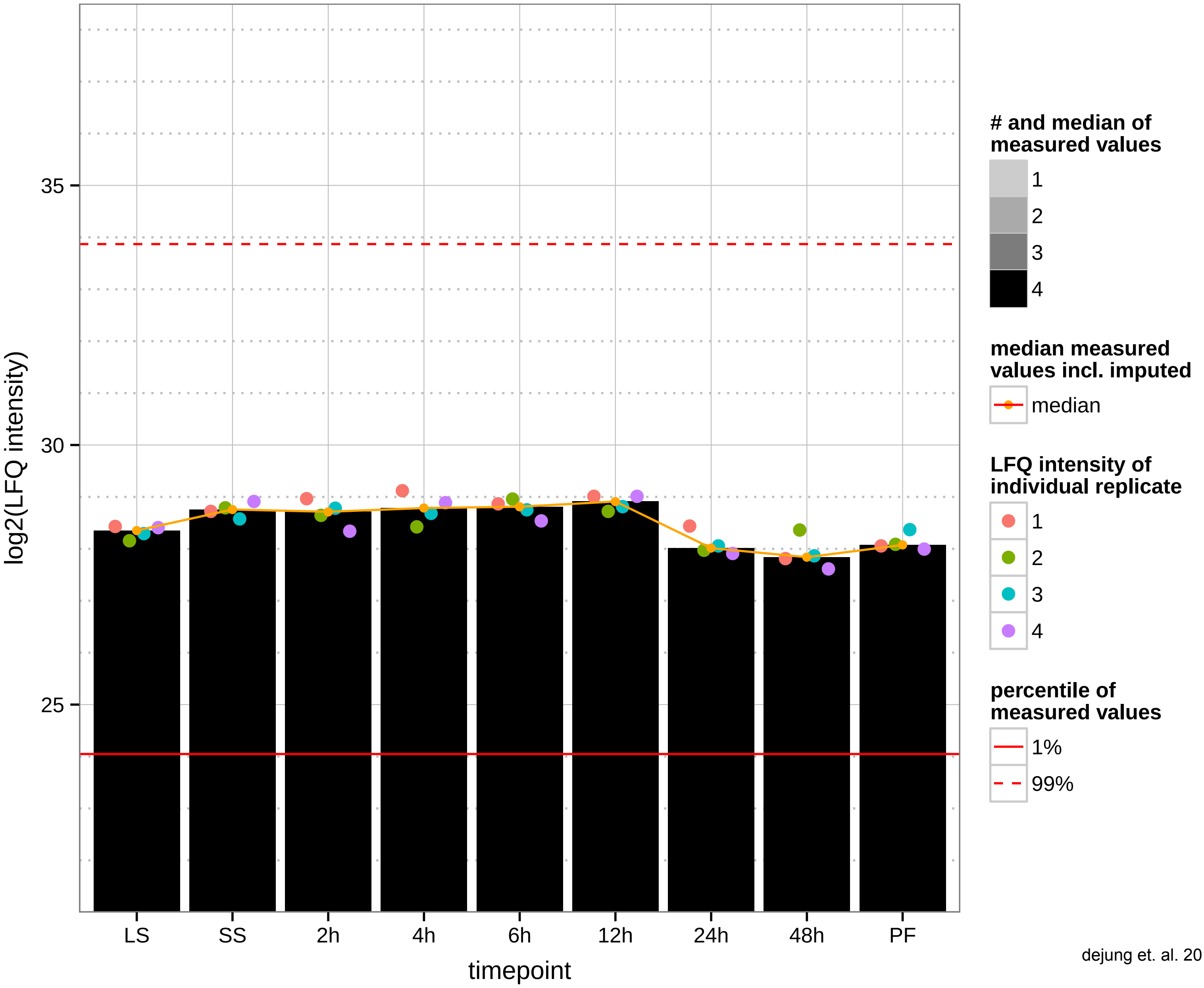
dynein light intermediate chain D1bLIC, putative
Tb927.11.16810
AGOF: null
AGOC: null
AGOP: null
PGOF: GTP binding
PGOC: intracellular
PGOP: small GTPase mediated signal transduction





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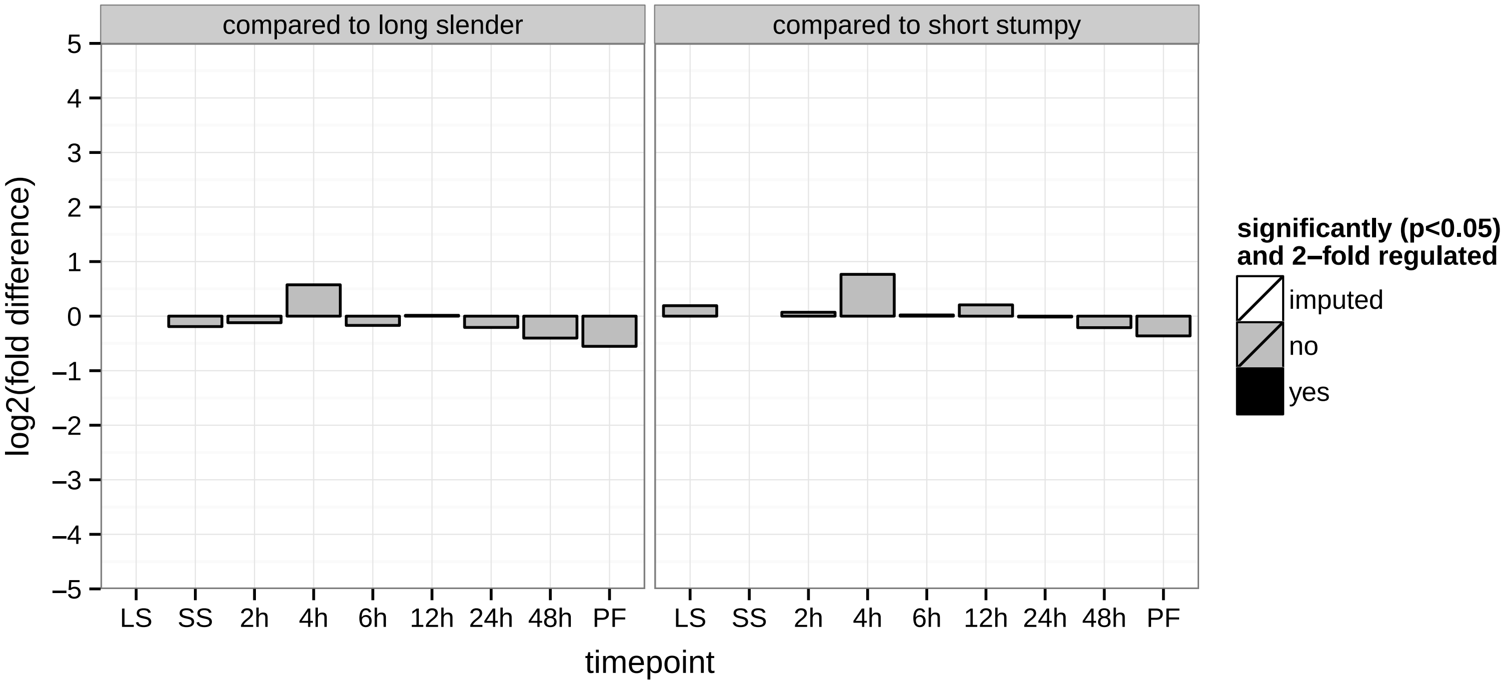
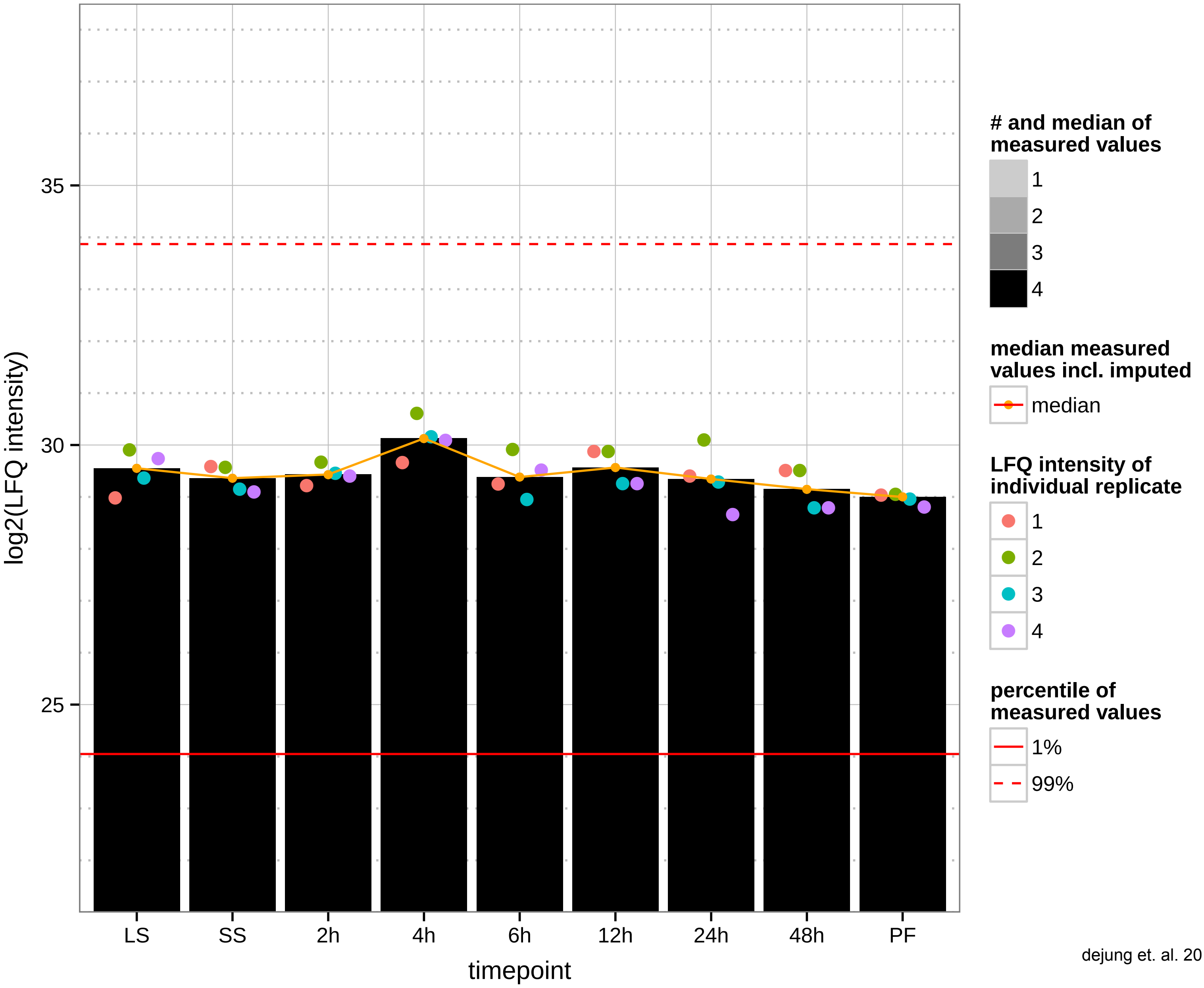
Rab–like 5, small G protein (RABL5)
Tb927.11.16830
AGOF: GTP binding
AGOC: null
AGOP: cilium assembly
PGOF: GTP binding
PGOC: intracellular
PGOP: small GTPase mediated signal transduction





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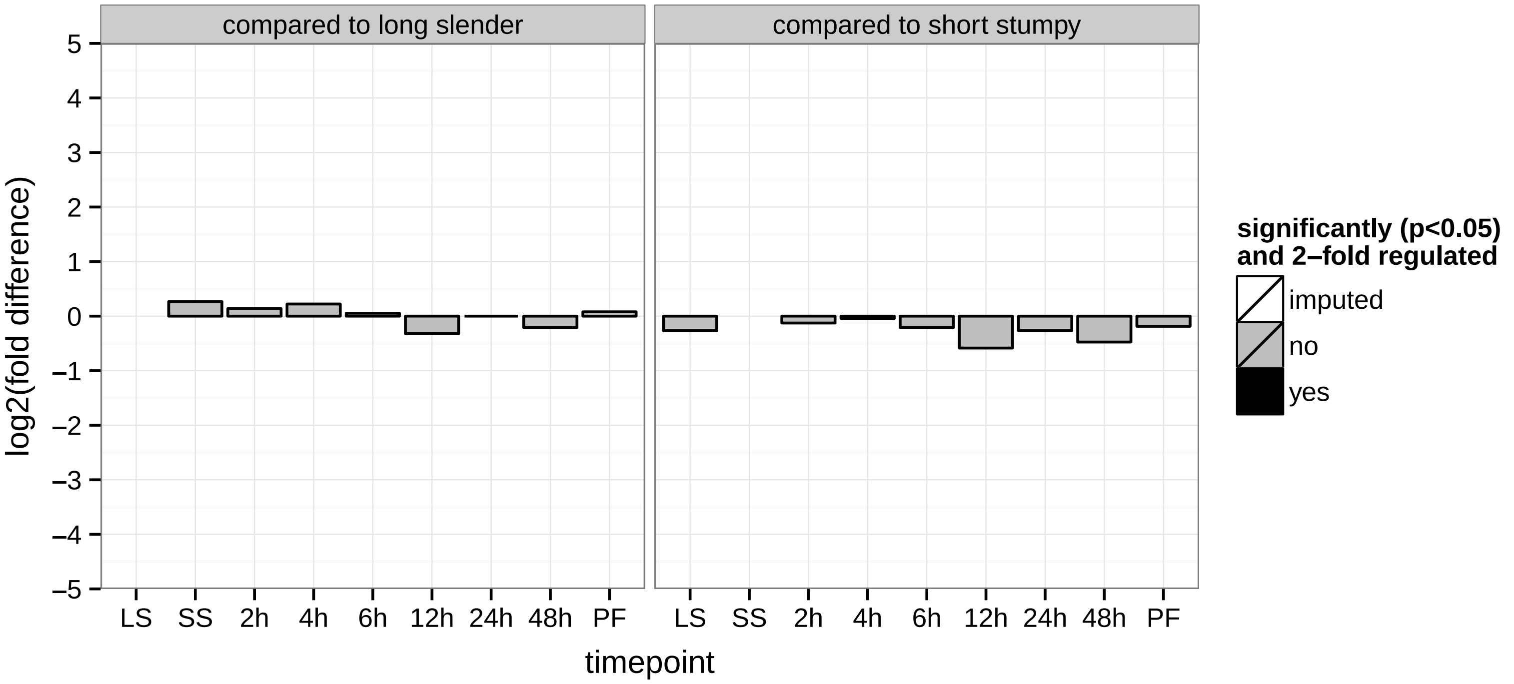
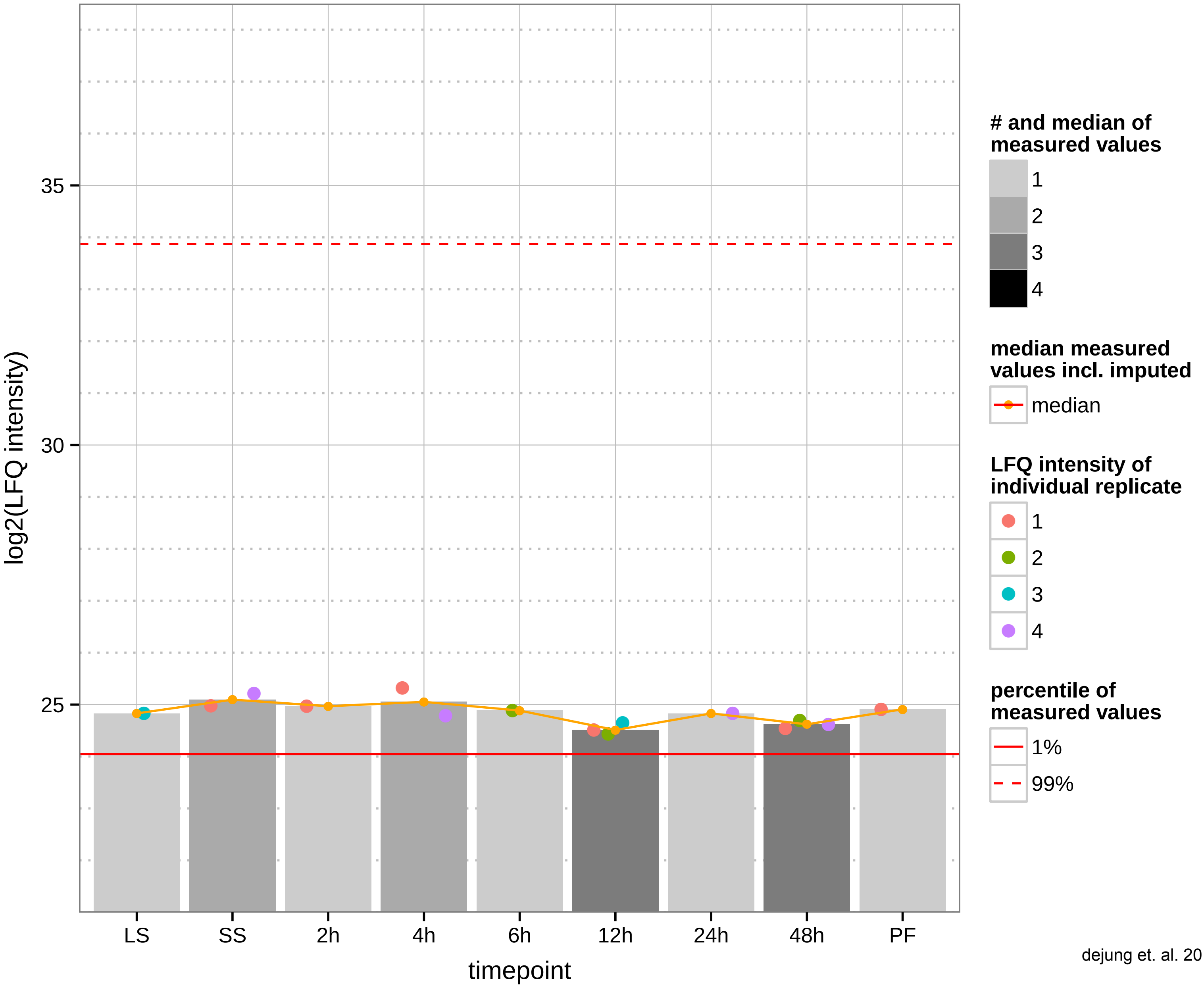
hypothetical protein, conserved
Tb927.11.16850
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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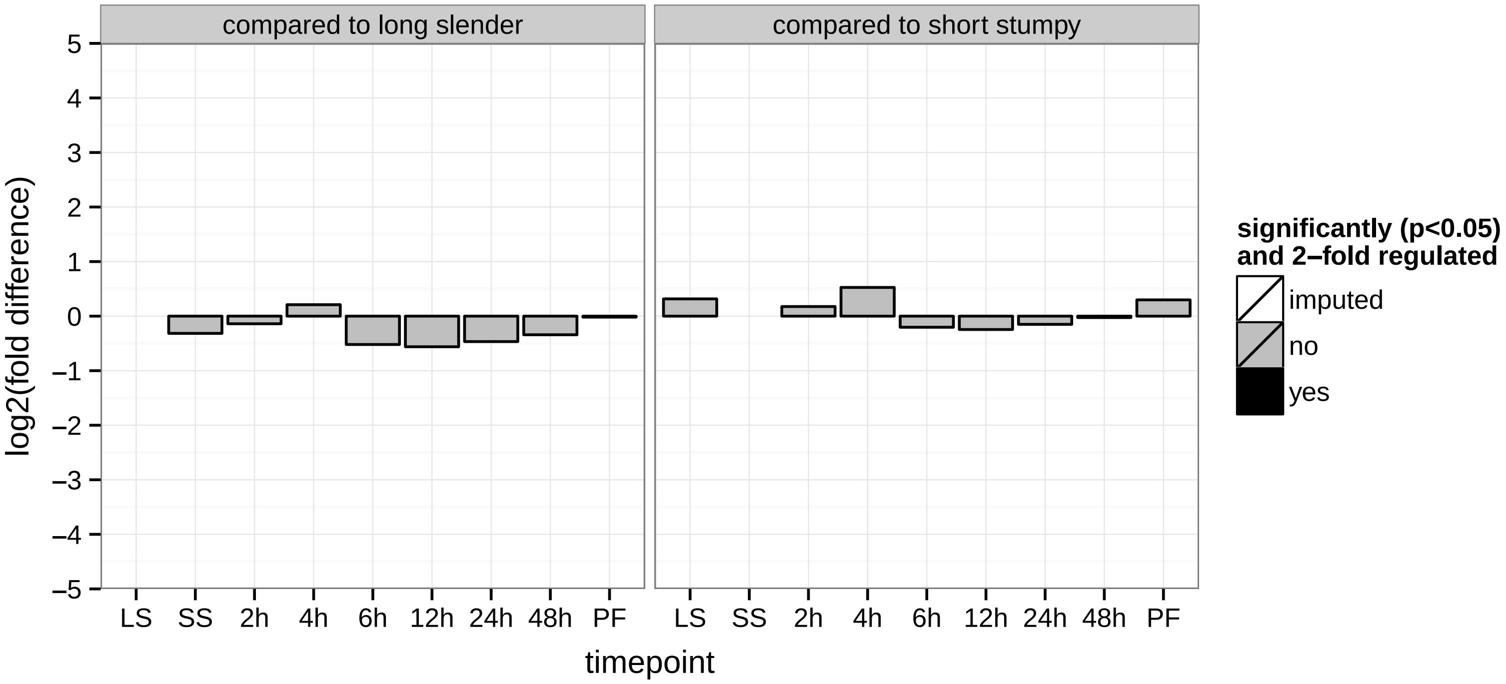
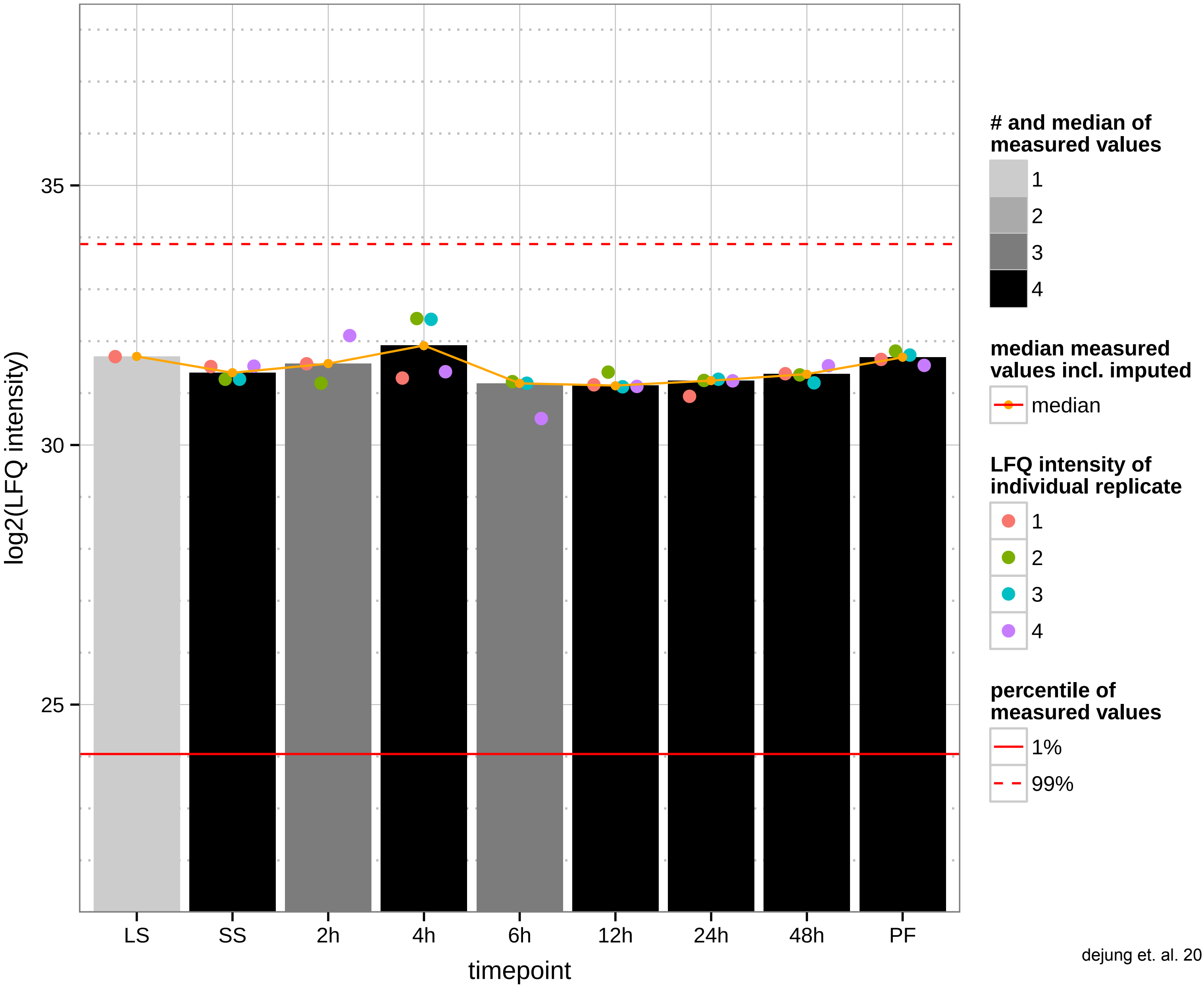
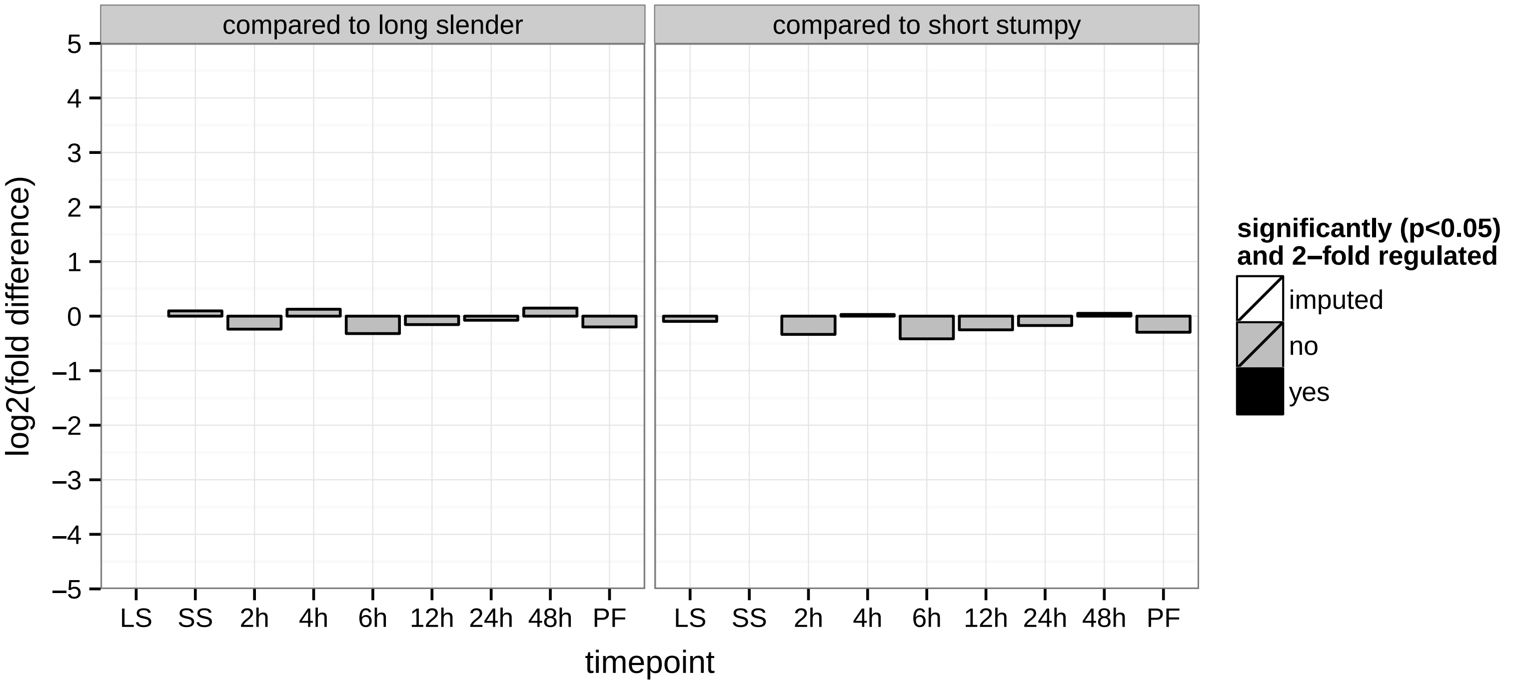
mitochondrial RNA binding protein (MRB8620)
Tb927.11.16860
AGOF: RNA binding
AGOC: mitochondrion
AGOP: RNA metabolic process
PGOF: null
PGOC: null
PGOP: null

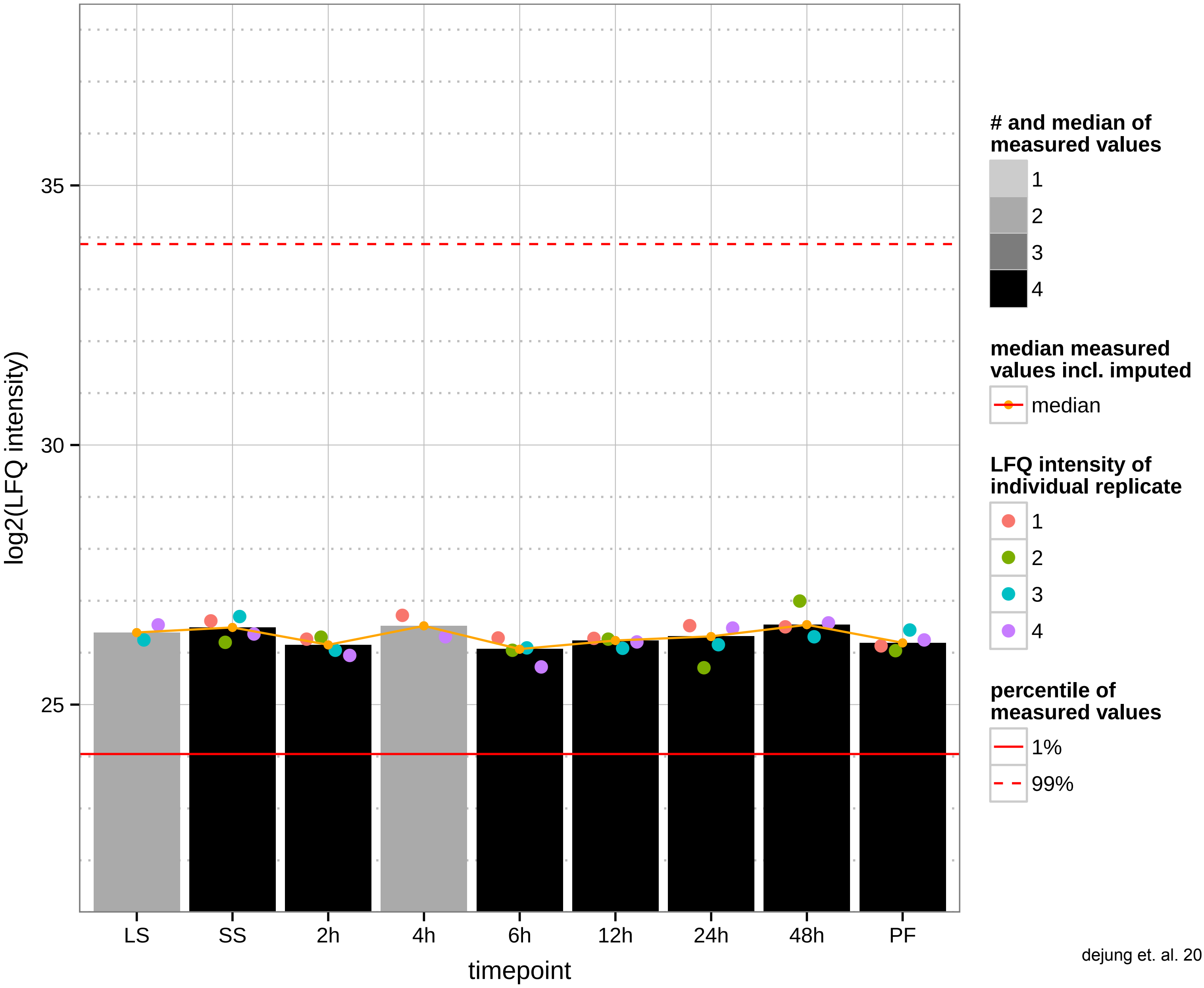




dejung et. al. 2015

leucine–rich repeat protein (LRRP), putative
Tb927.11.16880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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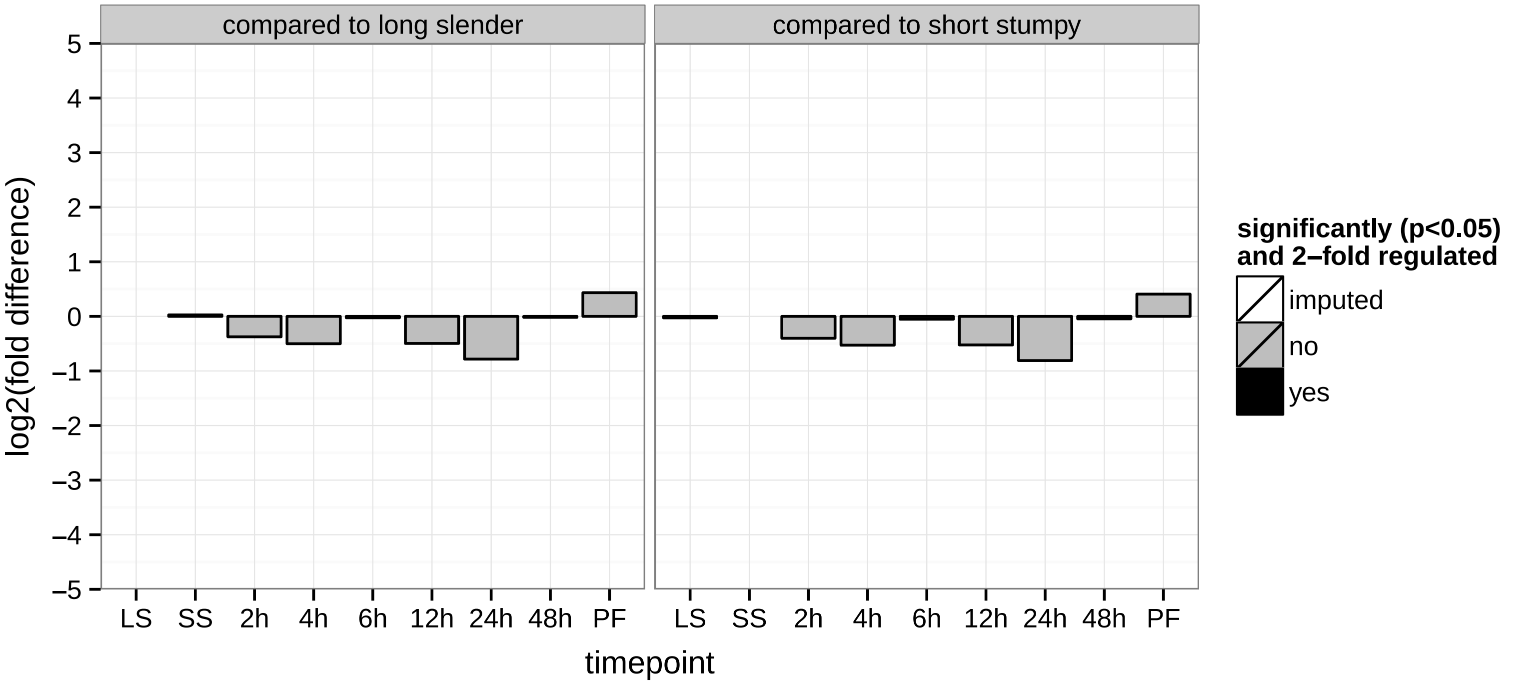
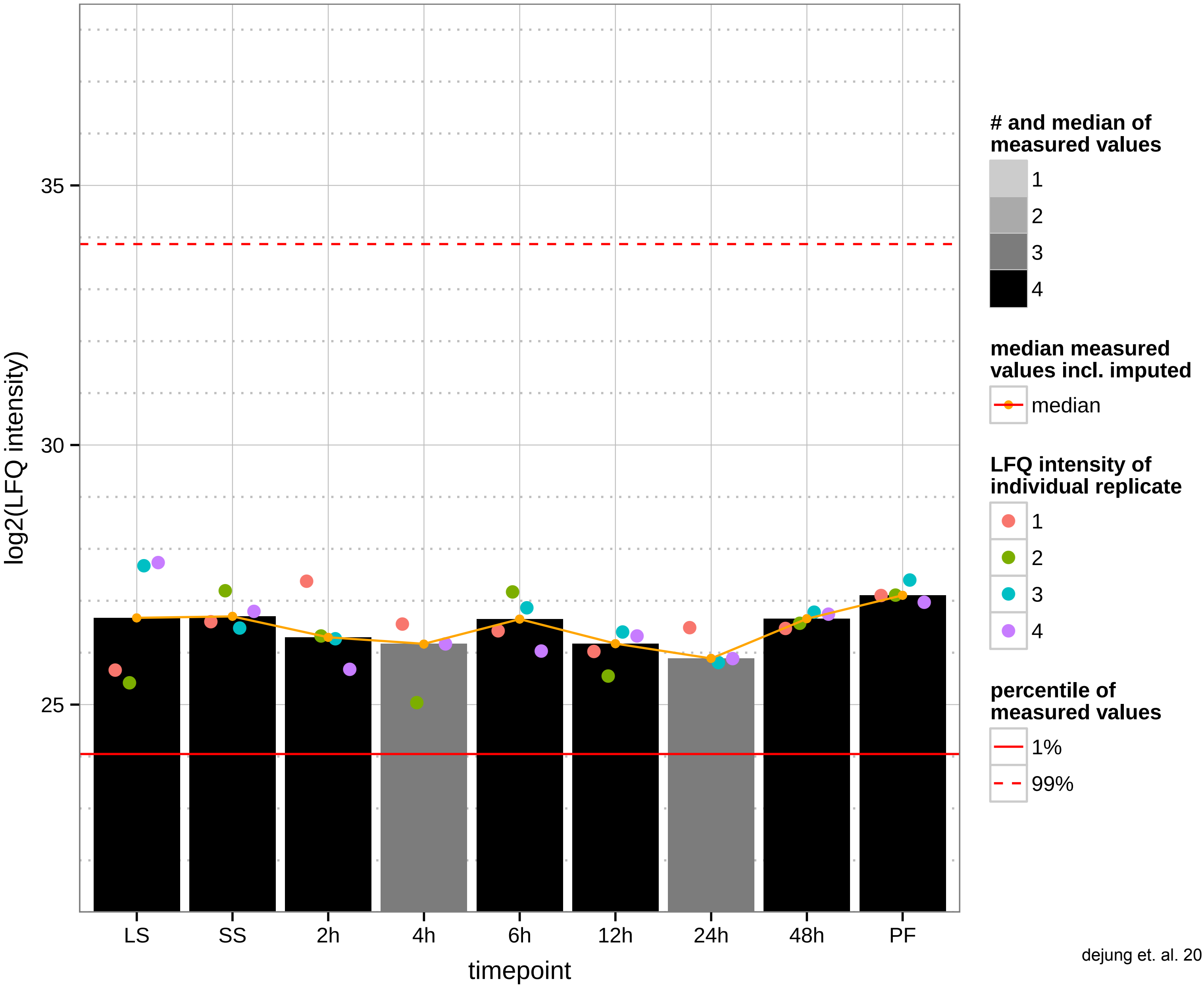
hypothetical protein, conserved
Tb927.11.16890
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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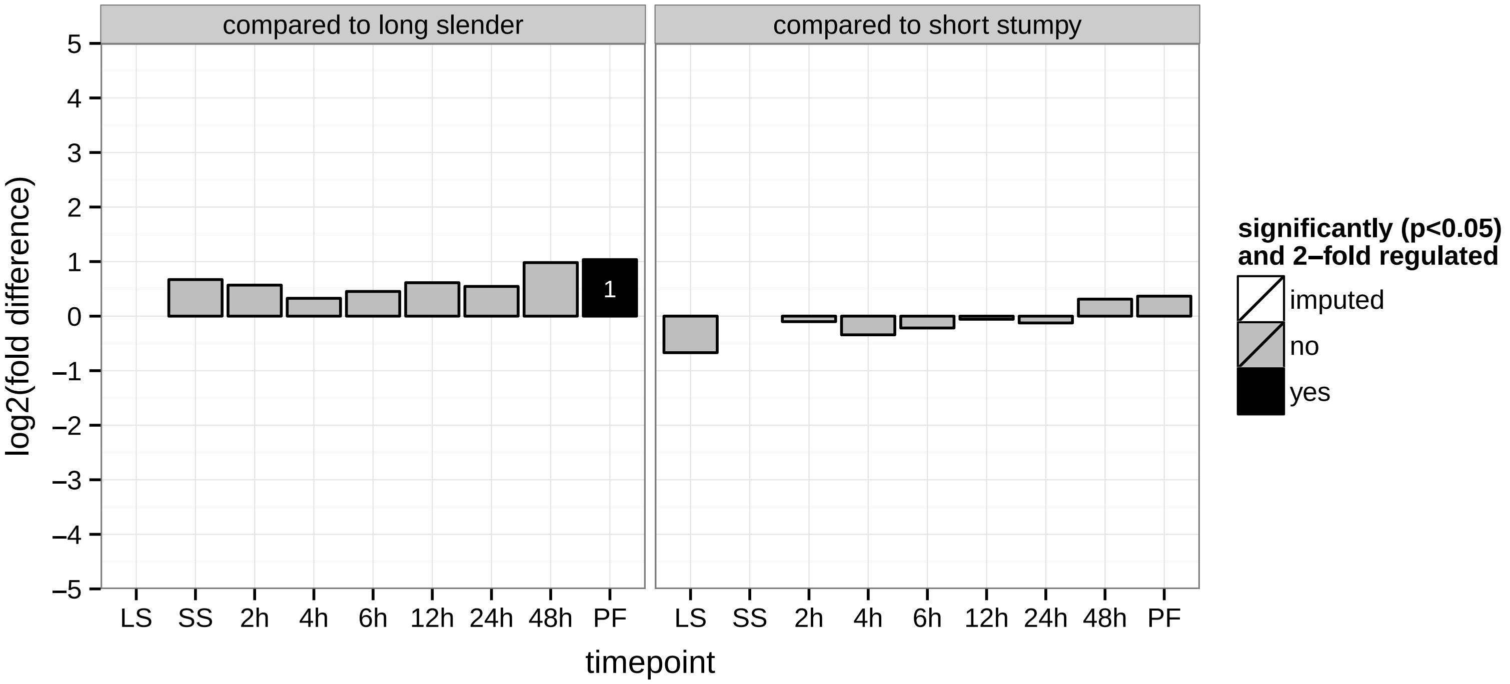
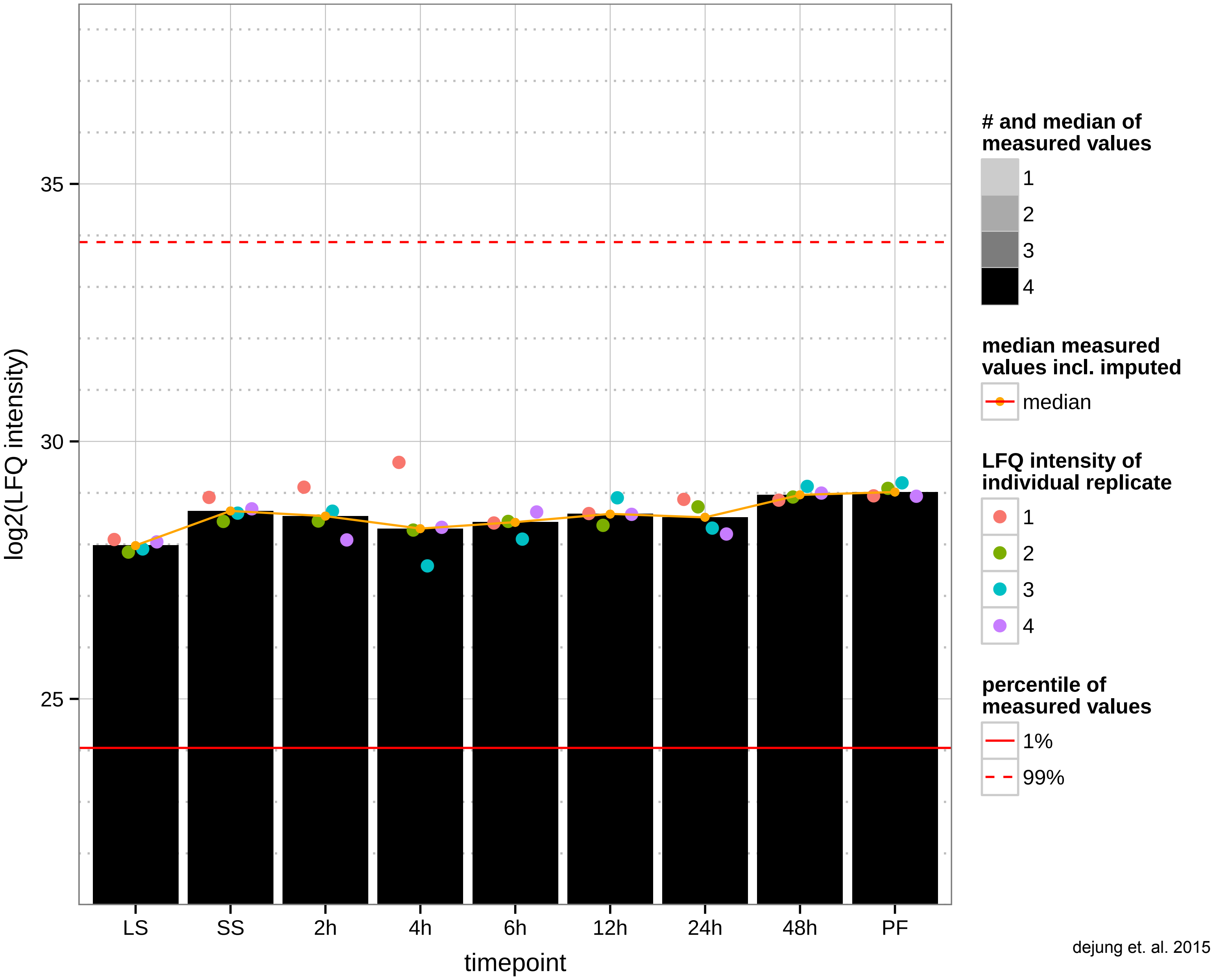
protein phosphatase 4, putative
Tb927.11.16970
AGOF: phosphoric ester hydrolase activity, protein serine/threonine phosphatase activity
AGOC: protein phosphatase type 2A complex
AGOP: phosphate−containing compound metabolic process
PGOF: hydrolase activity
PGOC: null
PGOP: null





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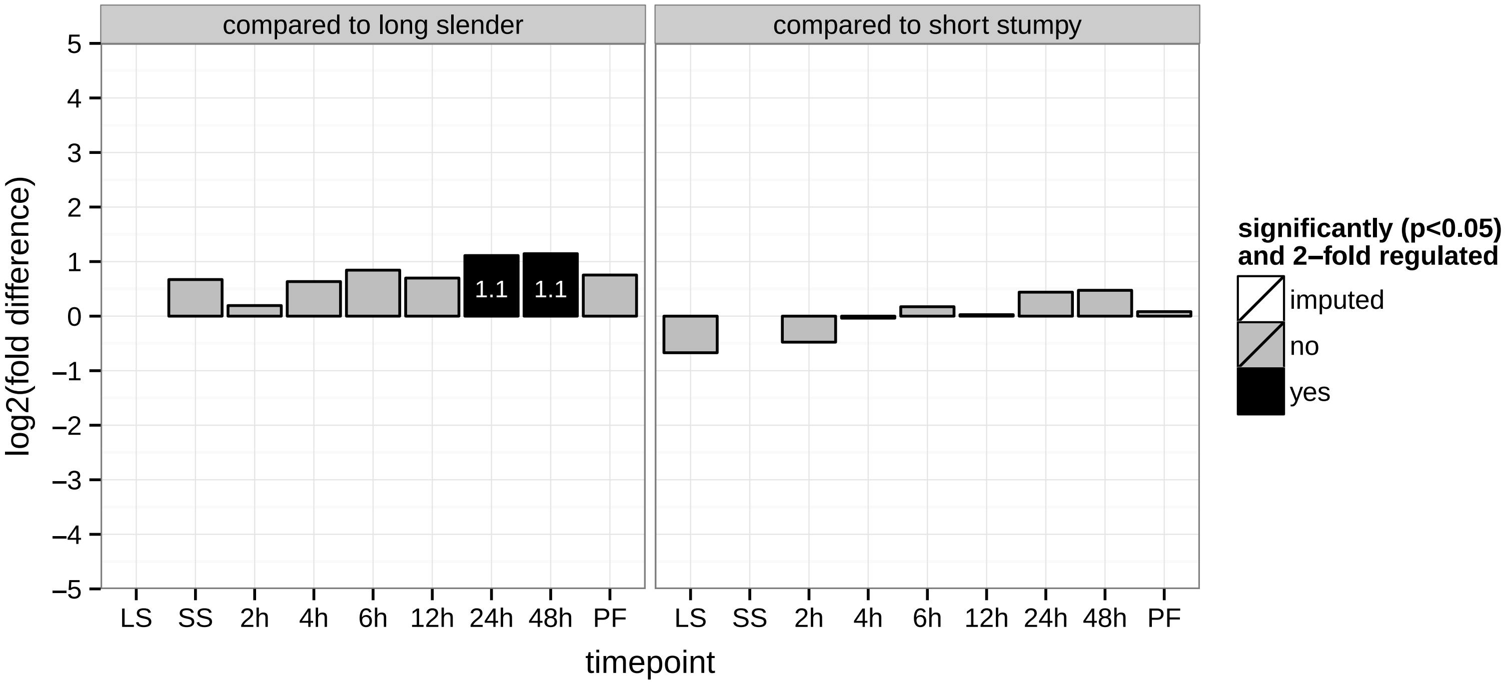
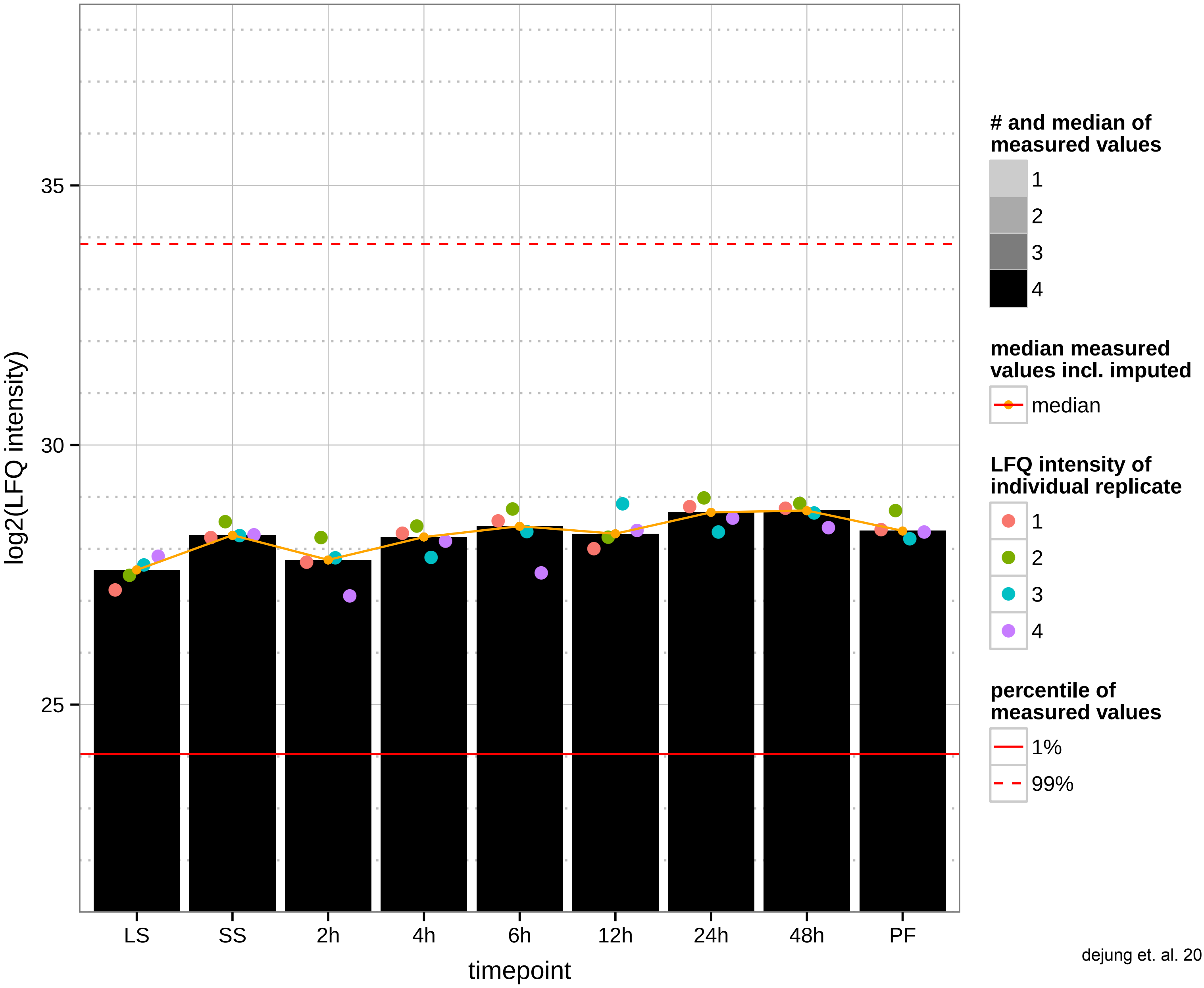
hypothetical protein, conserved
Tb927.11.1700
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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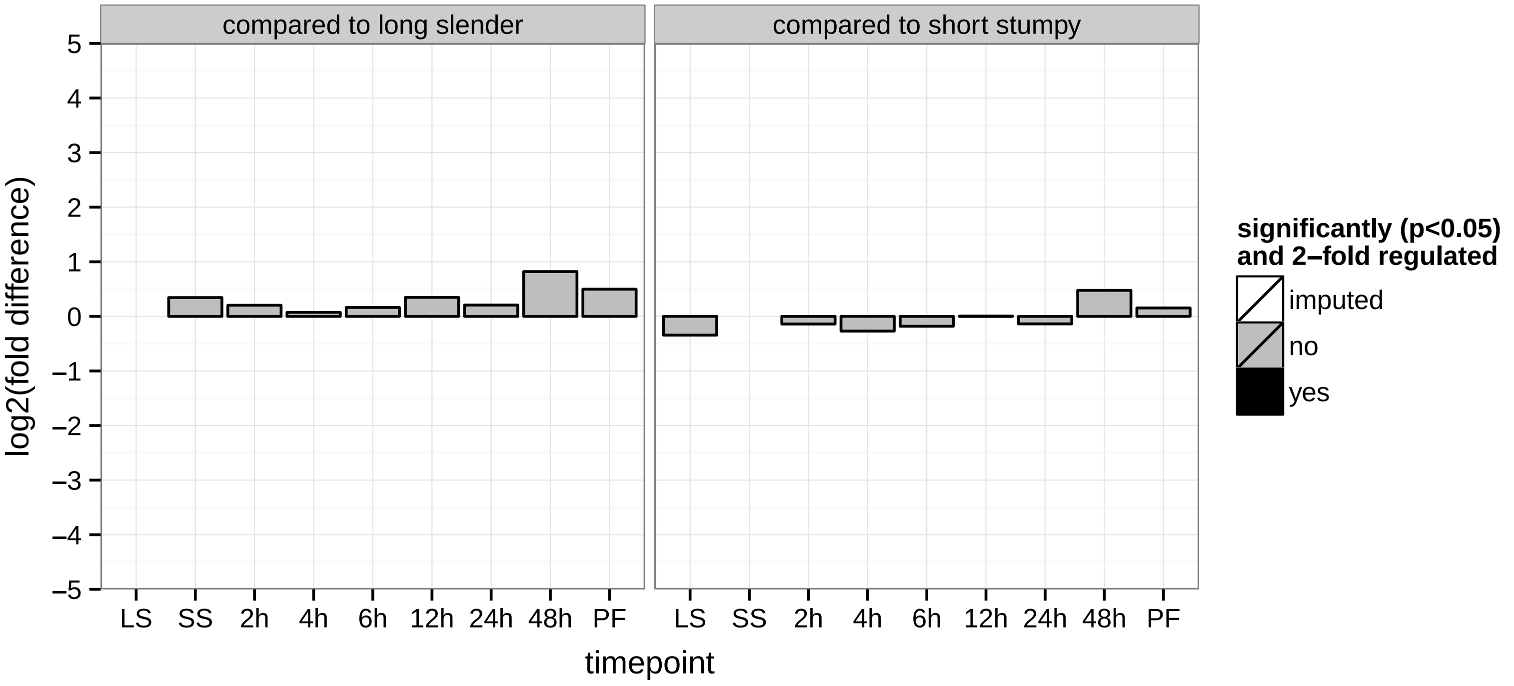
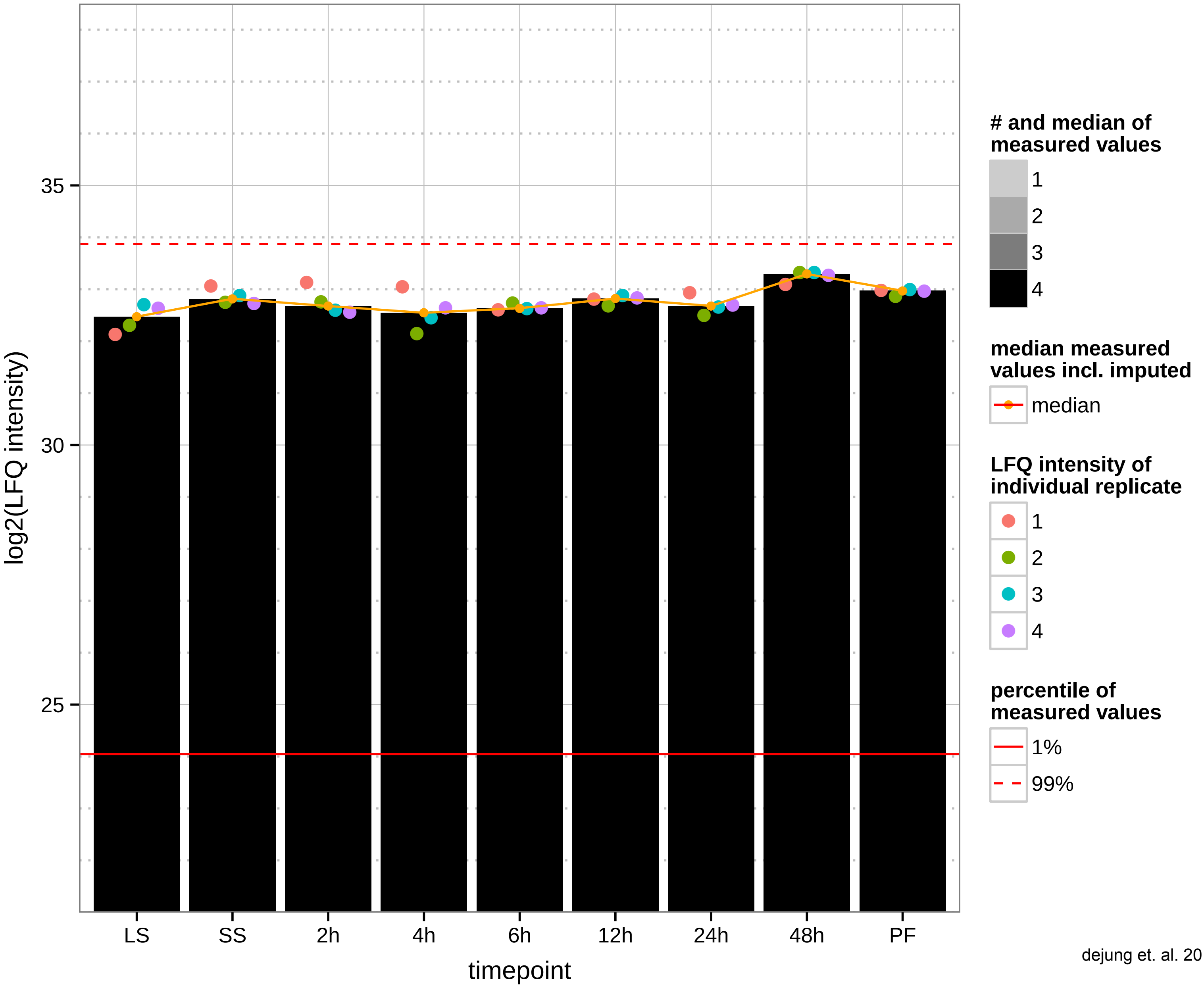
hypothetical protein, conserved, leucine−rich repeat protein (LRRP), putative
Tb927.11.17000;Tb11.v5.0404
AGOF: null
AGOC: null
AGOP: null
PGOF: null, protein binding
PGOC: null
PGOP: null





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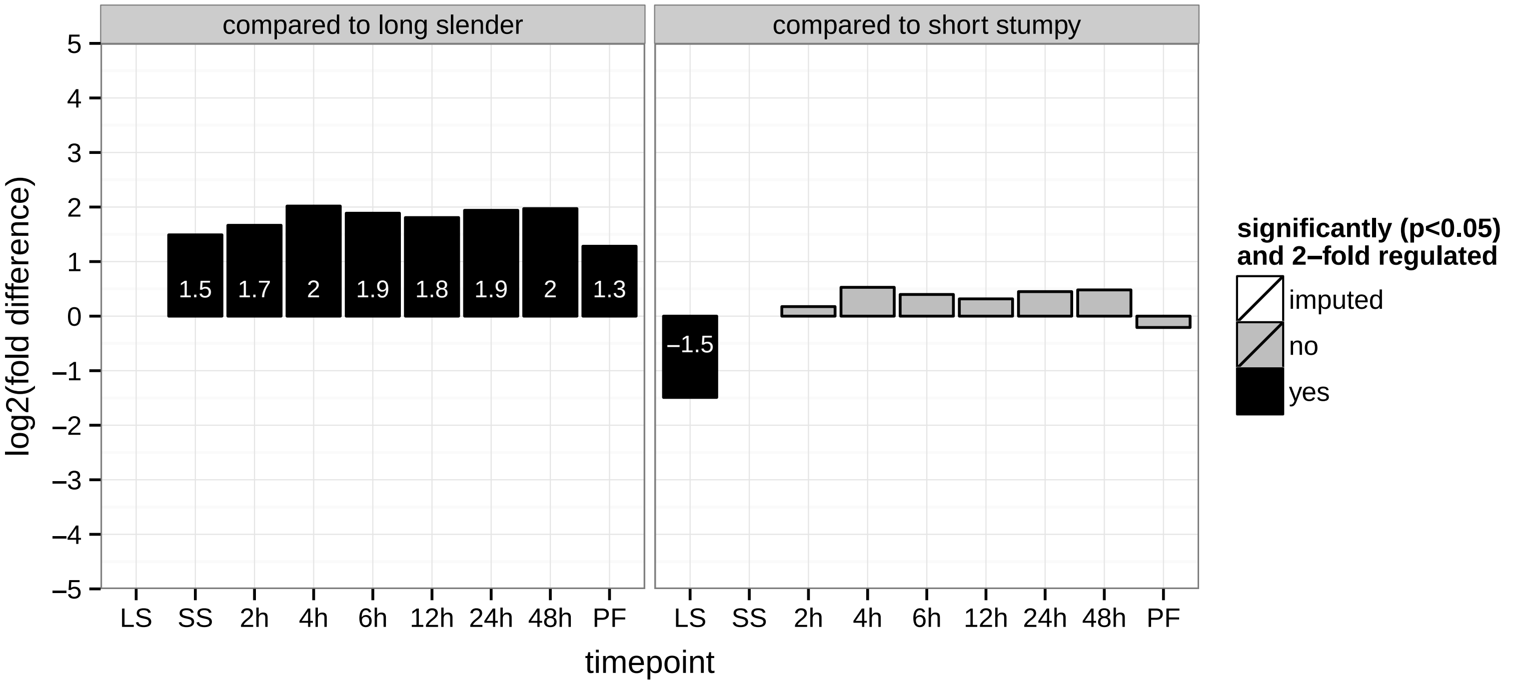
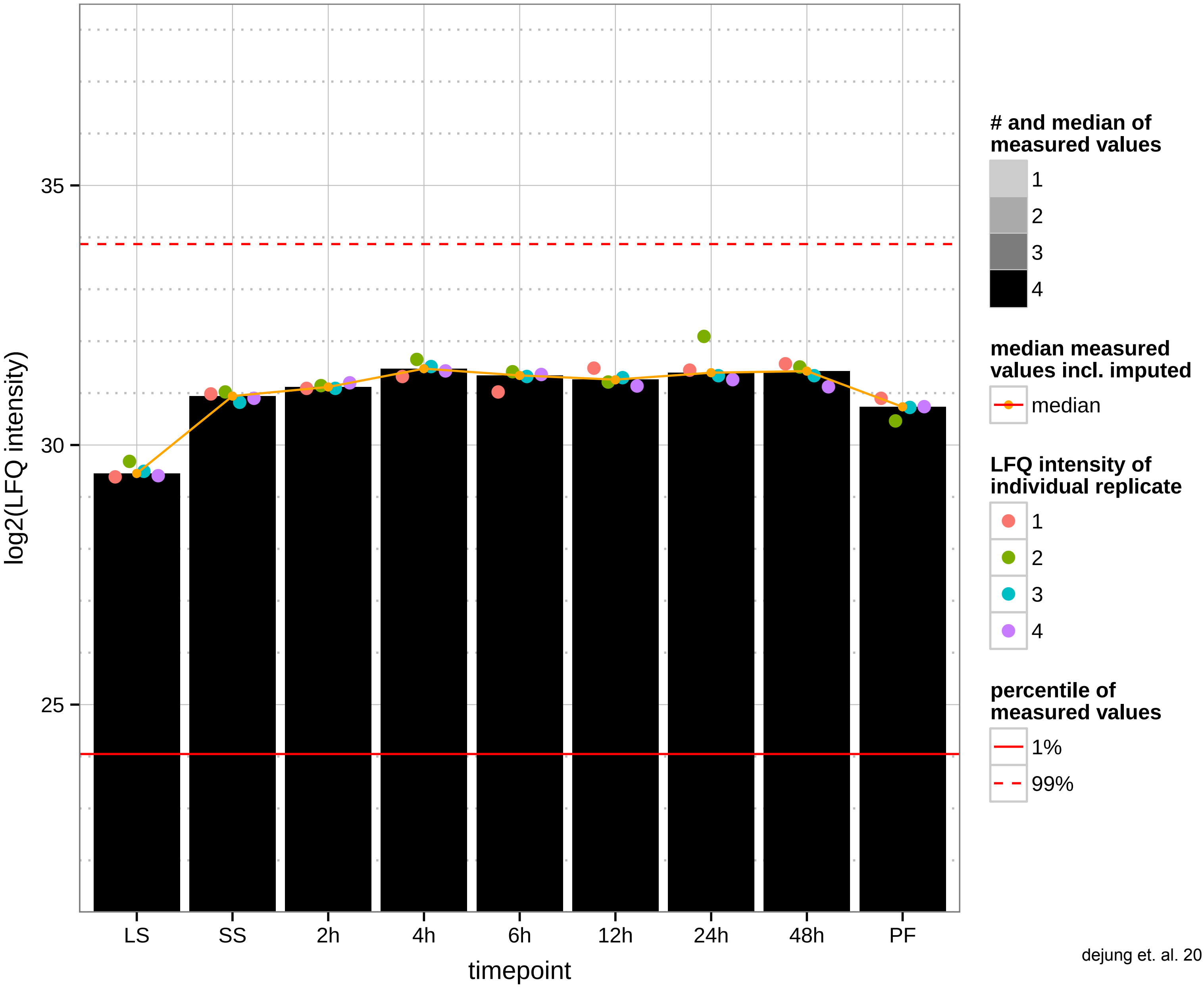
mitochondrial RNA binding protein 1, gBP21, MRP1 (GBP21)
Tb927.11.1710
AGOF: RNA binding
AGOC: mitochondrion
AGOP: mRNA modification
PGOF: DNA binding
PGOC: null
PGOP: regulation of transcription, DNA–dependent





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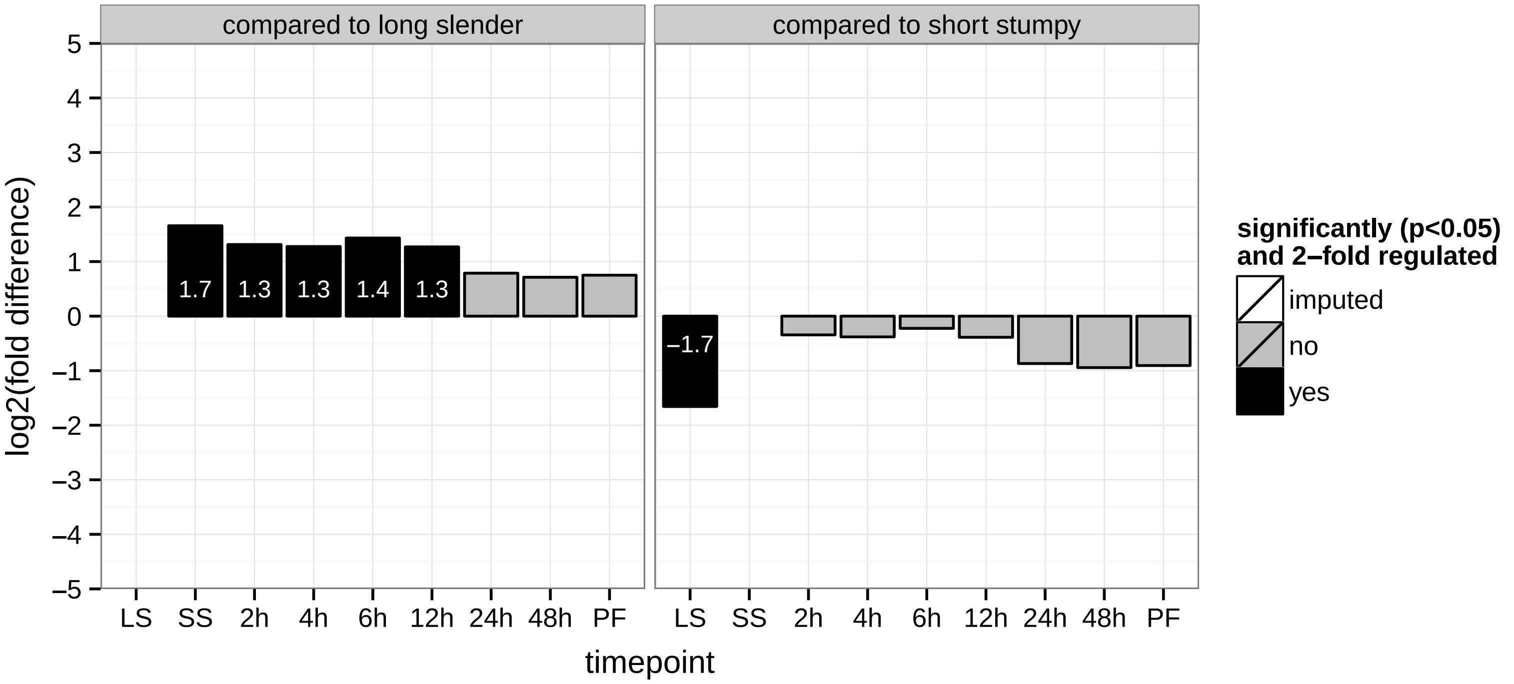
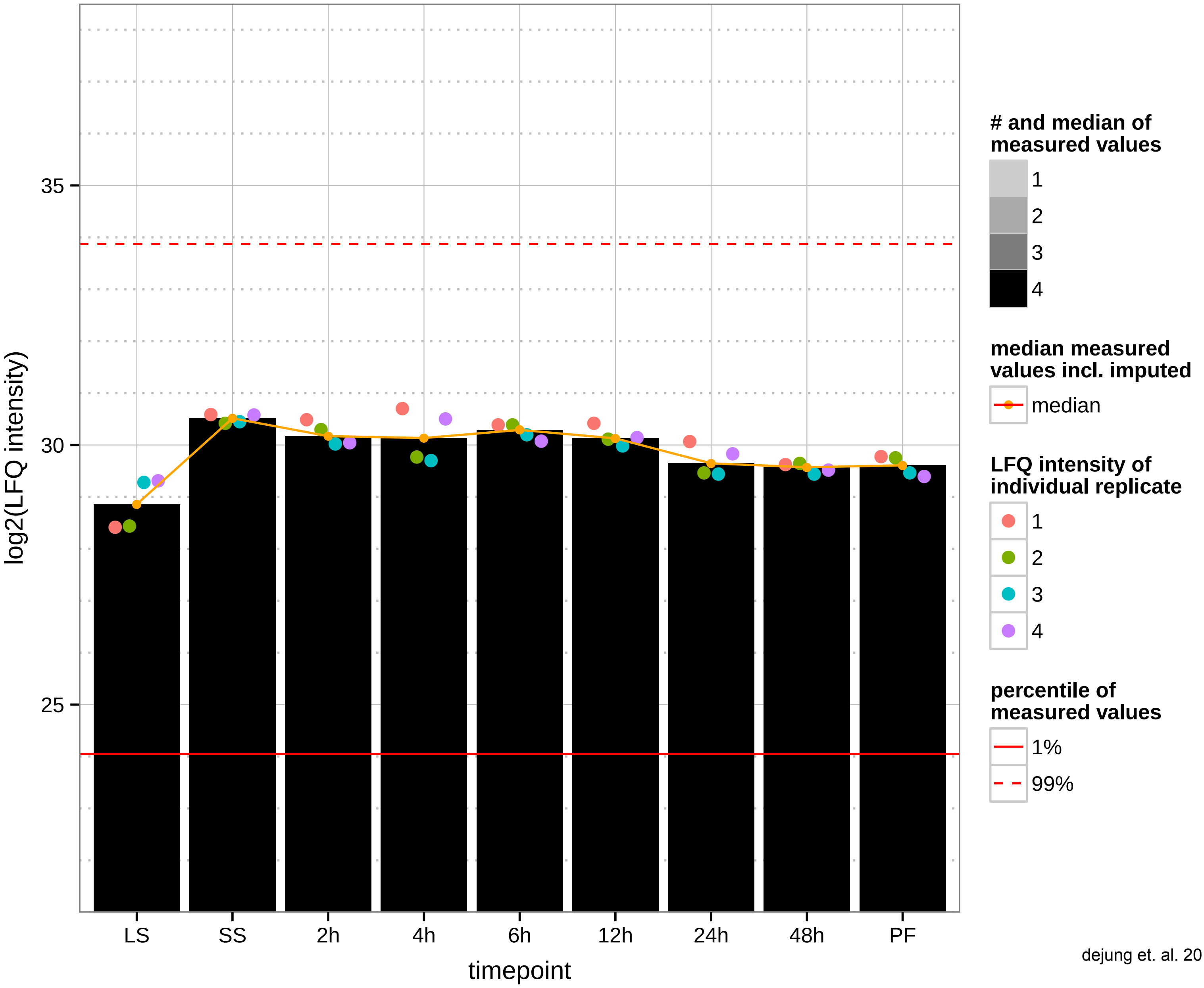
intraflagellar transport protein IFT88 (IFT88)
Tb927.11.1740
AGOF: null
AGOC: motile cilium
AGOP: cilium assembly, establishment of cell polarity, regulation of cell size
PGOF: protein binding
PGOC: null
PGOP: null





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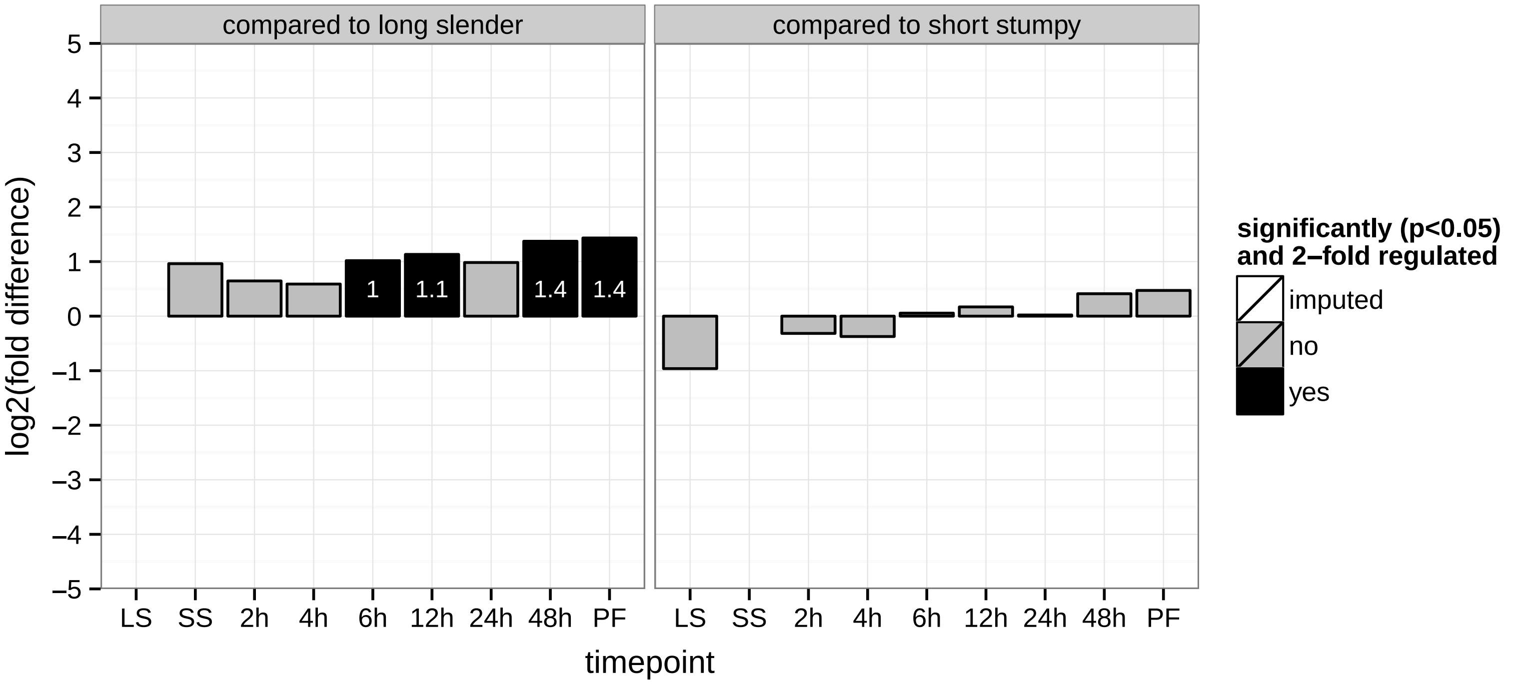
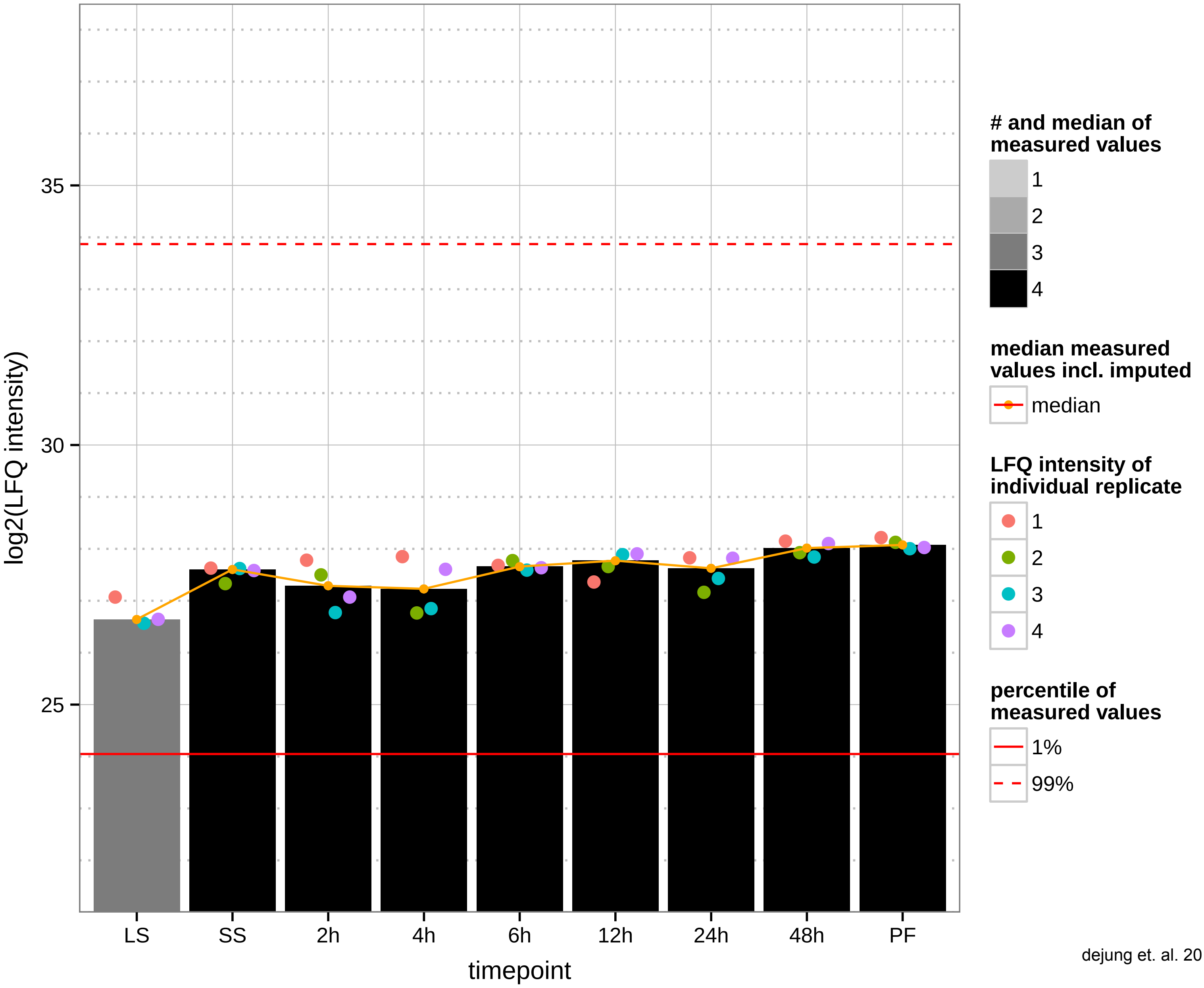
hypothetical protein, conserved (pseudogene), translation initiation factor eIF2B delta subunit, putative, eIF−2B GDP−GTP exc
Tb927.11.1820;Tb11.1400
AGOF: null, GTP binding, translation initiation factor activity
AGOC: null, eukaryotic translation initiation factor 2B complex
AGOP: cellular metabolic process, regulation of translation, translational initiation
PGOF: null
PGOC: null
PGOP: cellular metabolic process





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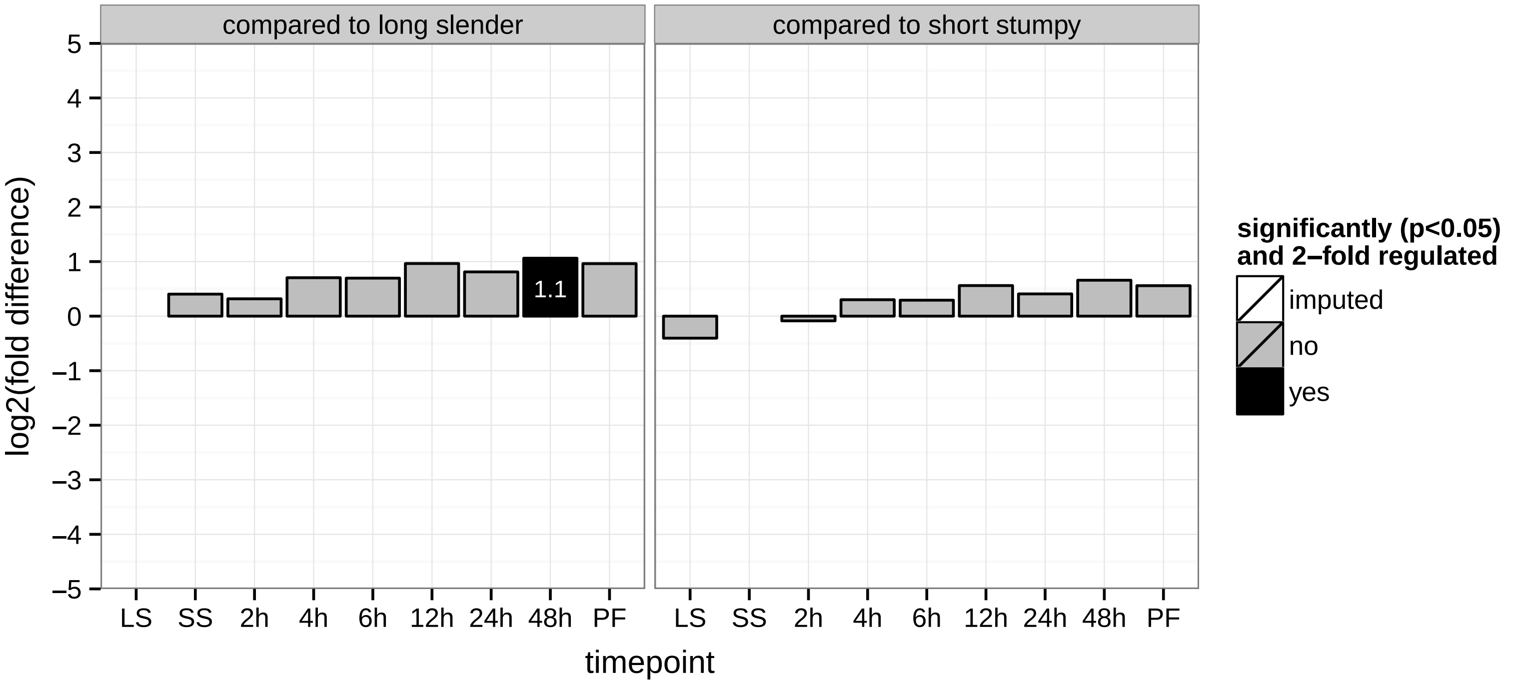
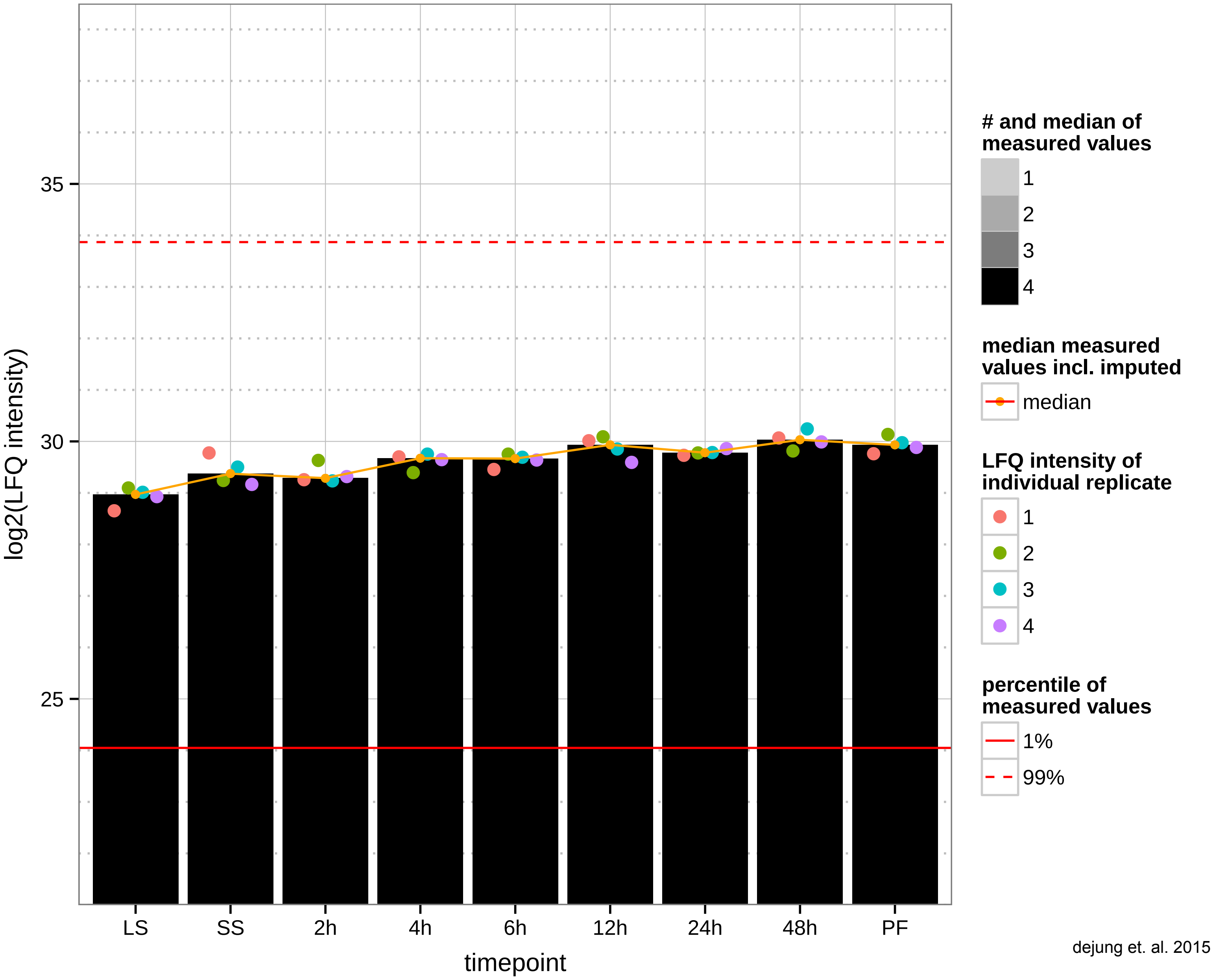
hypothetical protein, conserved
Tb927.11.1890
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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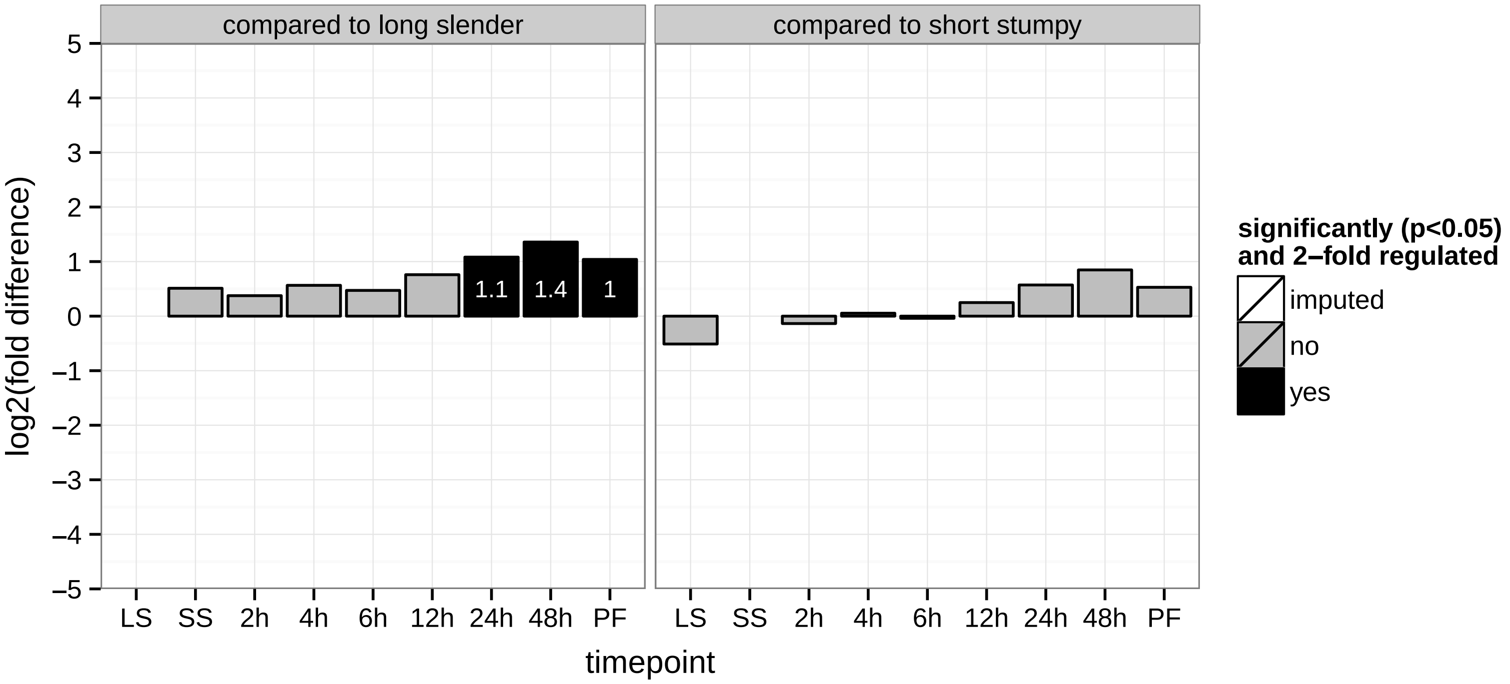
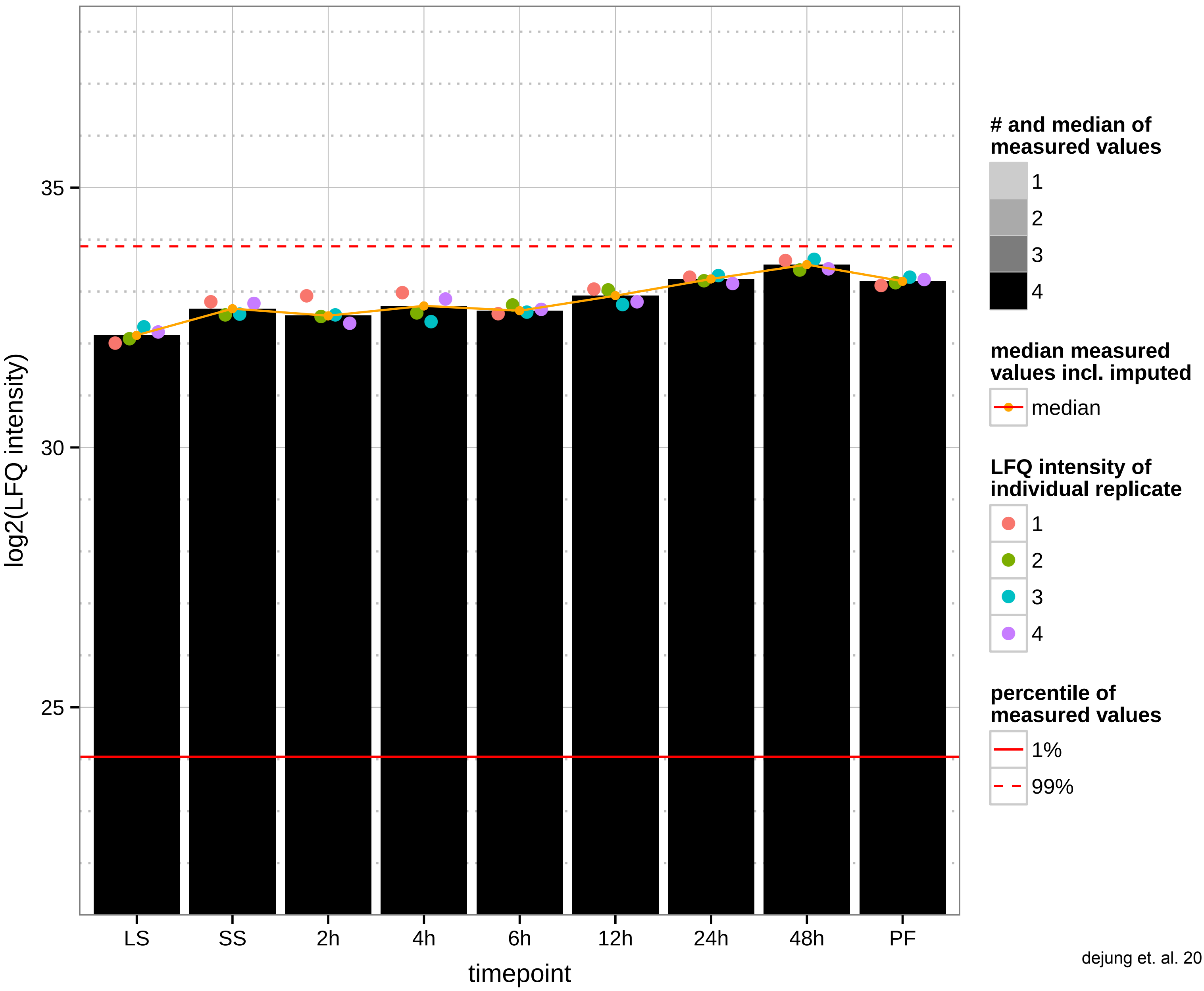
T–complex protein 1, beta subunit, putative
Tb927.11.1900
AGOF: ATP binding, unfolded protein binding
AGOC: chaperonin–containing T–complex
AGOP: protein folding, regulation of cell cycle
PGOF: ATP binding, unfolded protein binding
PGOC: null
PGOP: cellular protein metabolic process, protein folding





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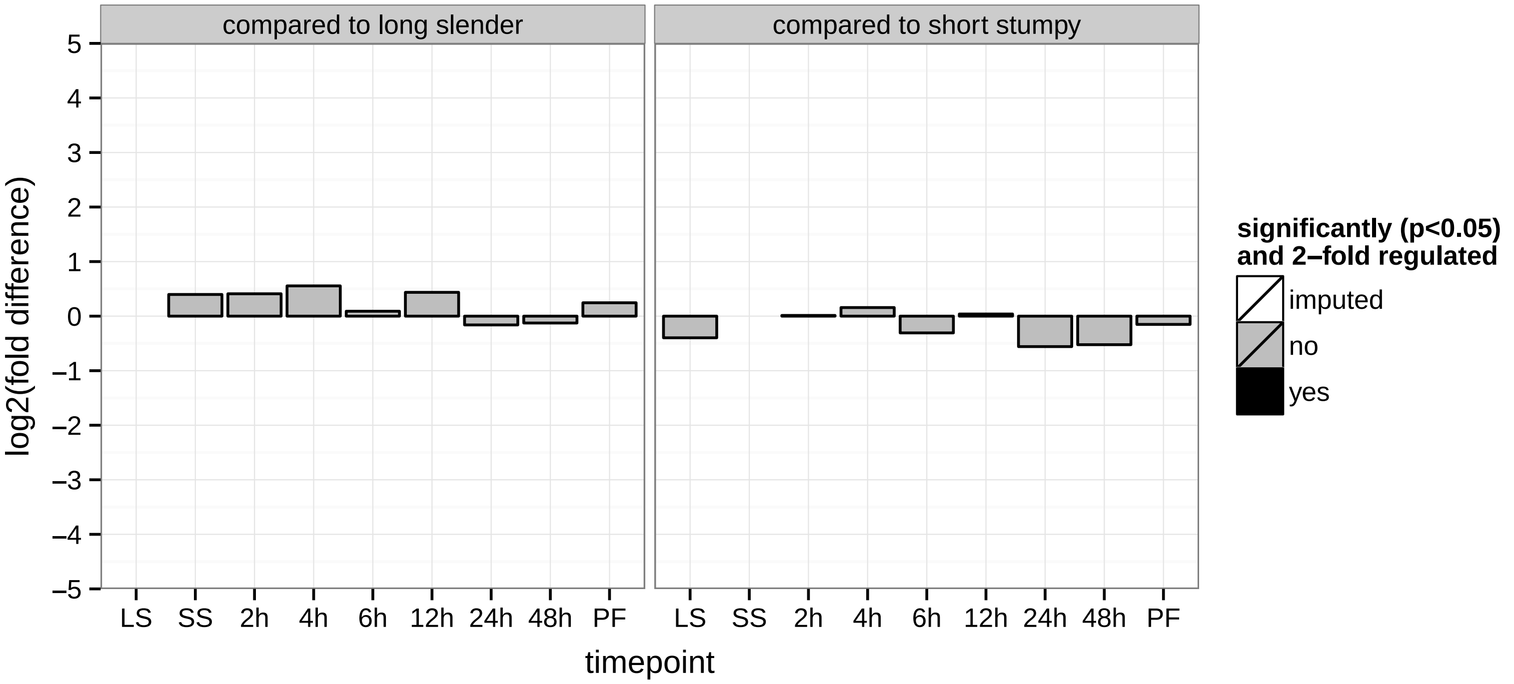
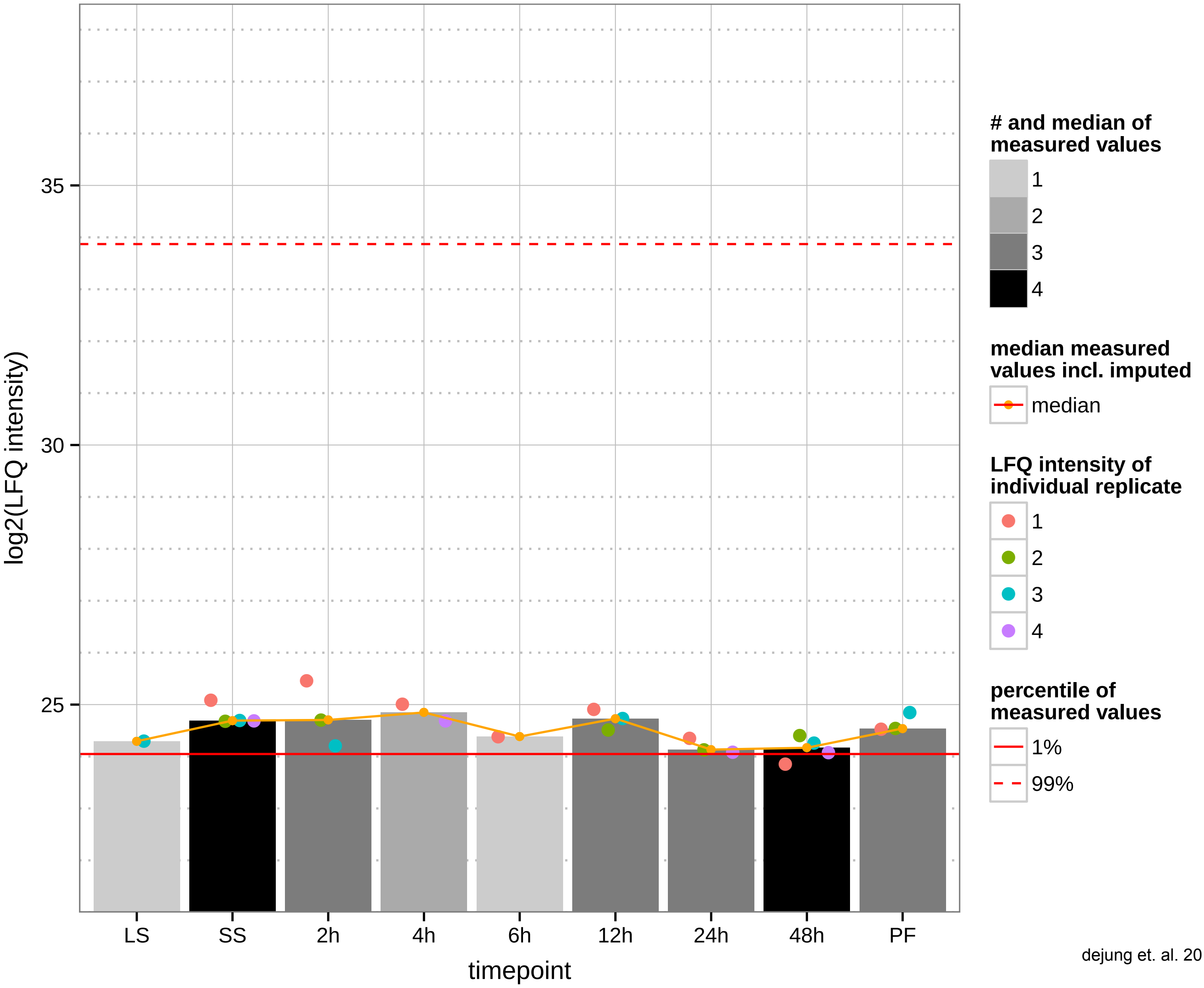
ubiquitin carboxyl–terminal hydrolase, putative, cysteine peptidase, Clan CA, family C19
Tb927.11.1930
AGOF: cysteine–type endopeptidase activity, ubiquitin thiolesterase activity
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ubiquitin thiolesterase activity
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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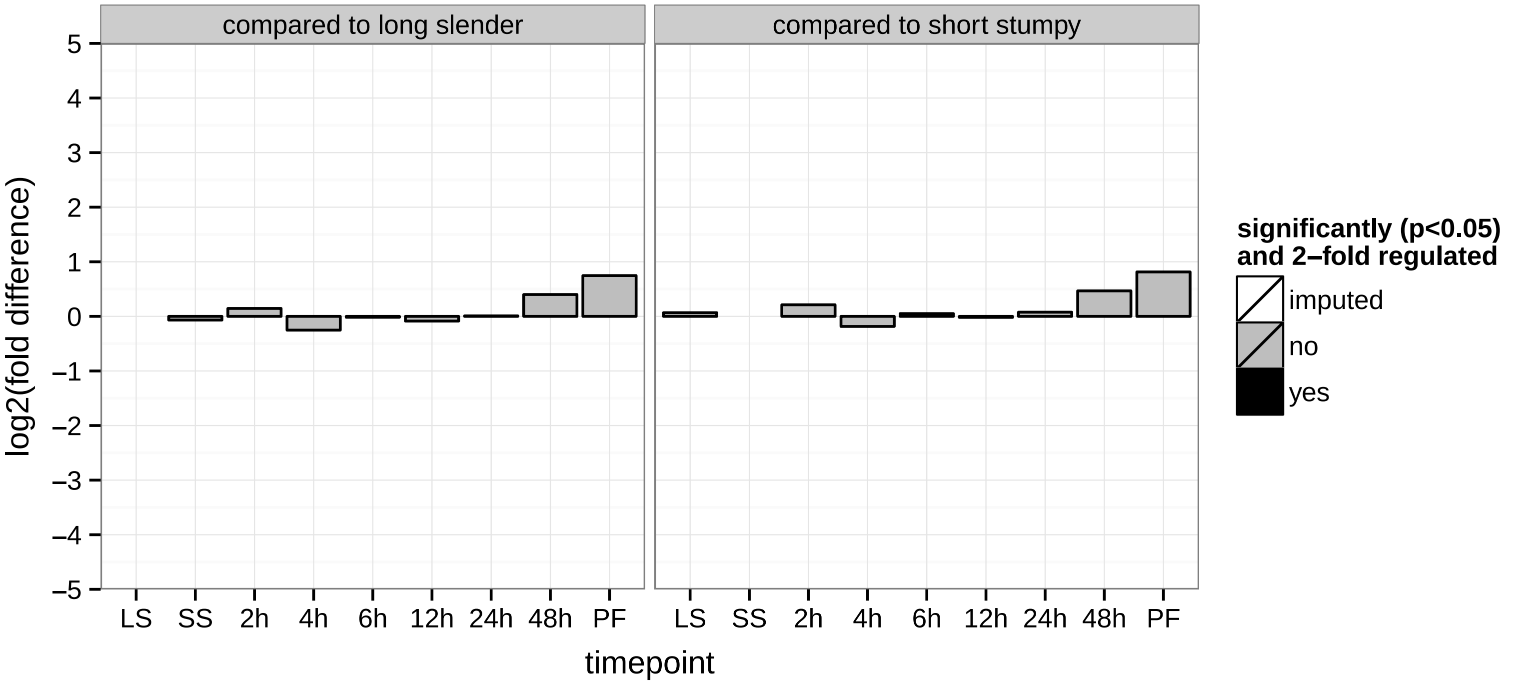
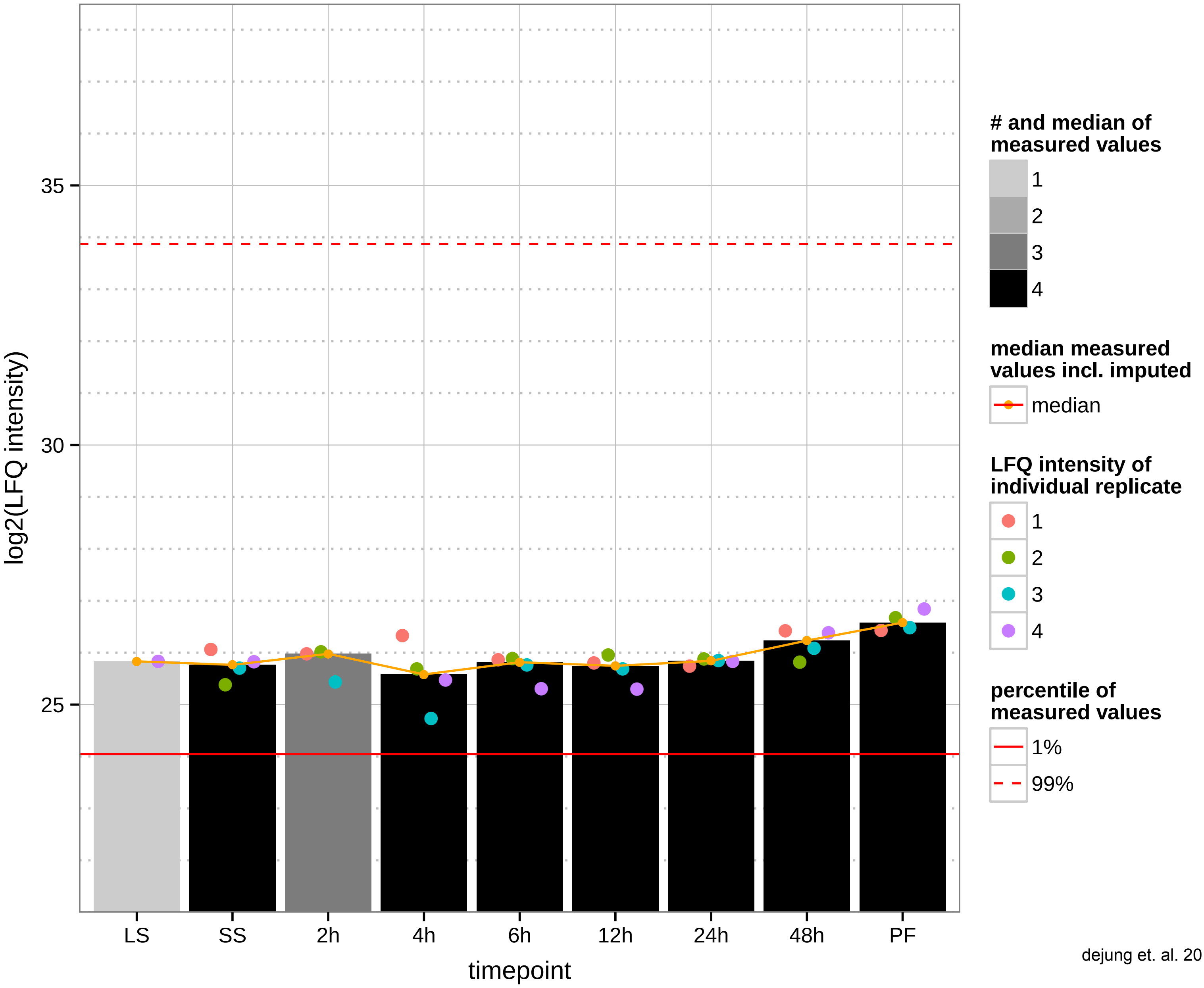
leucine–rich repeat protein (LRRP), putative
Tb927.11.1960
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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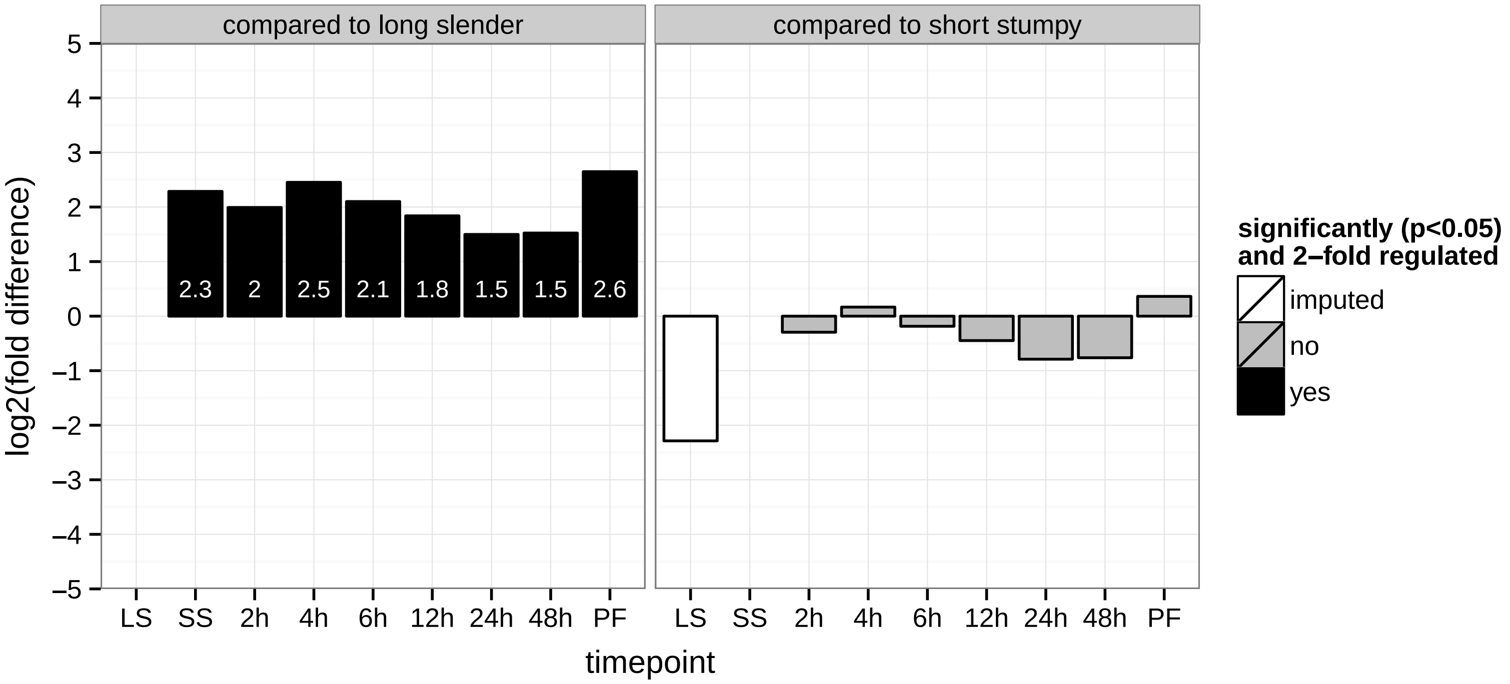
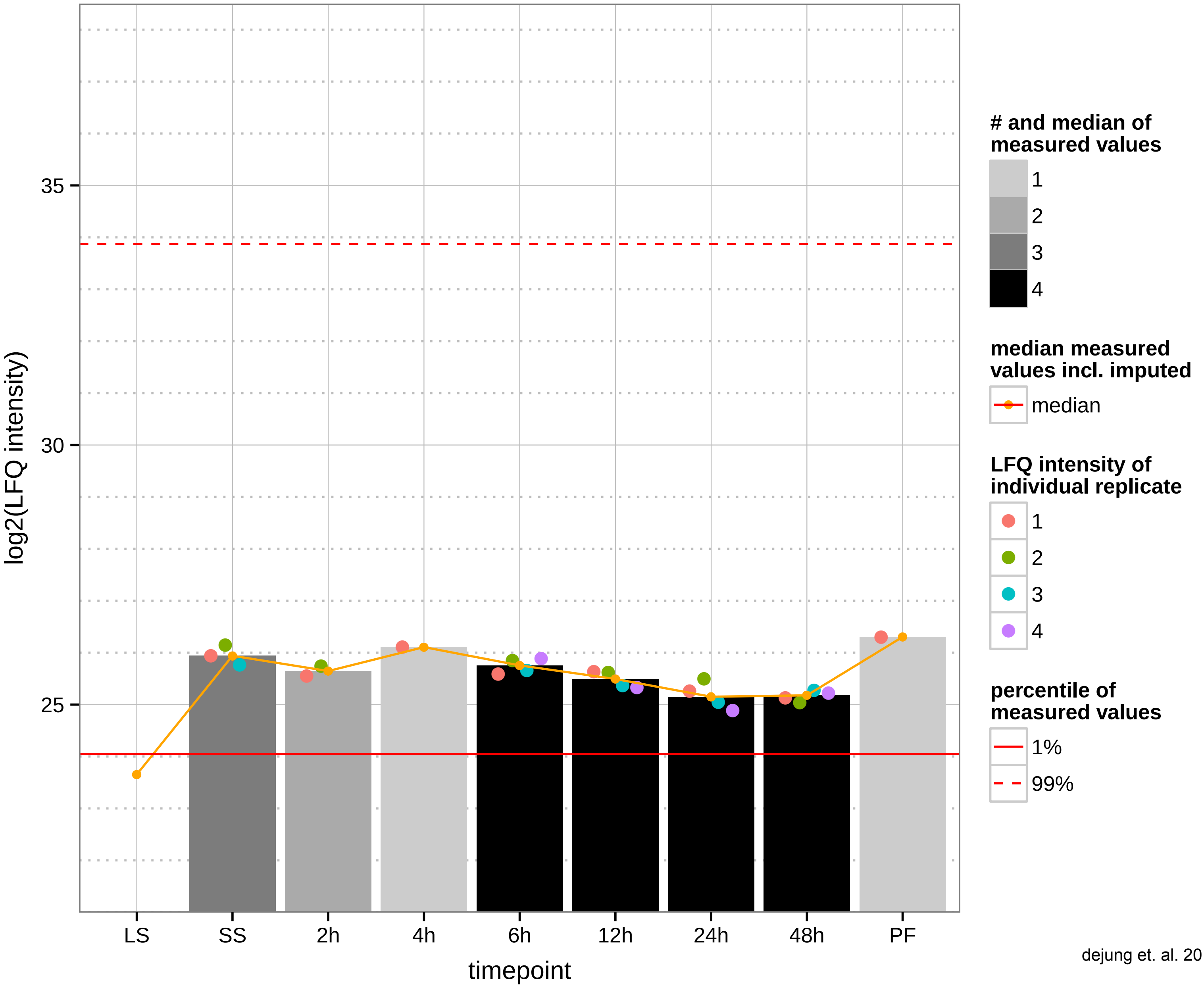
hypothetical protein, conserved
Tb927.11.2030
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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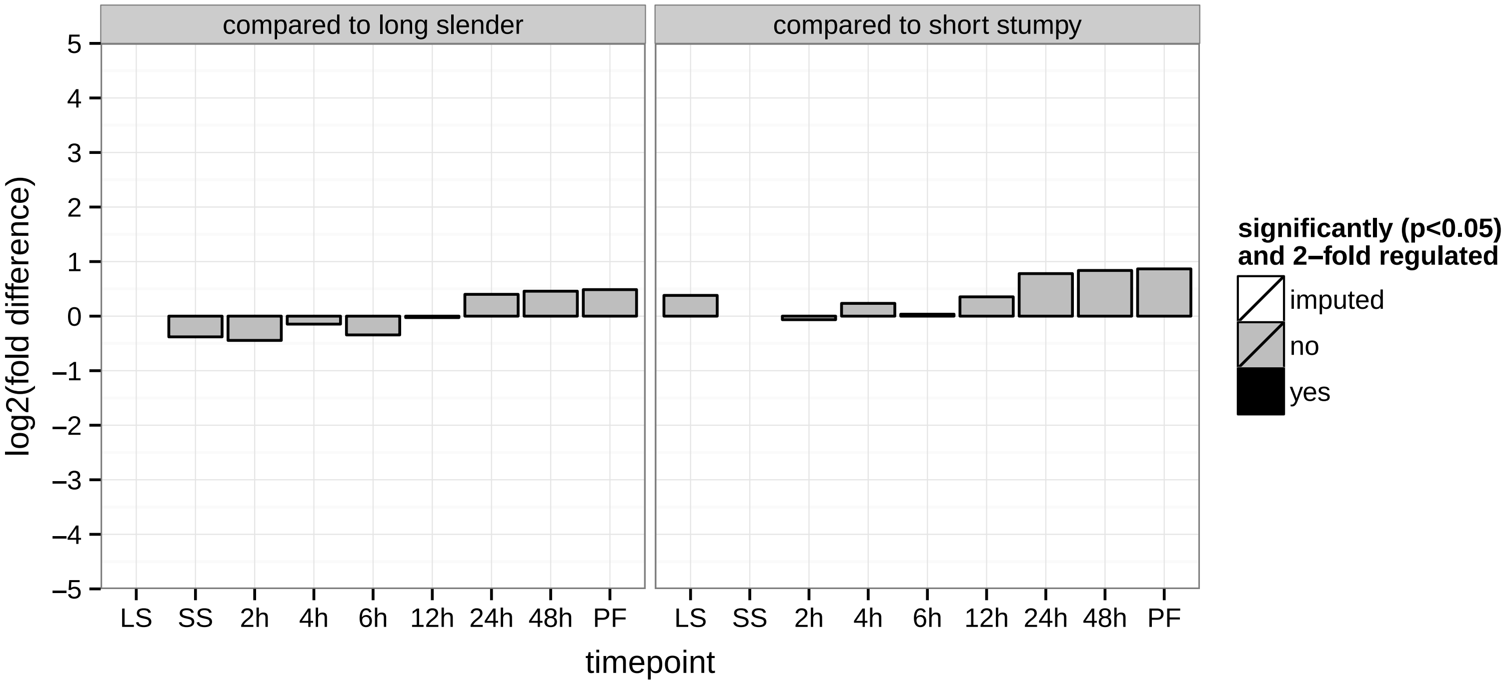
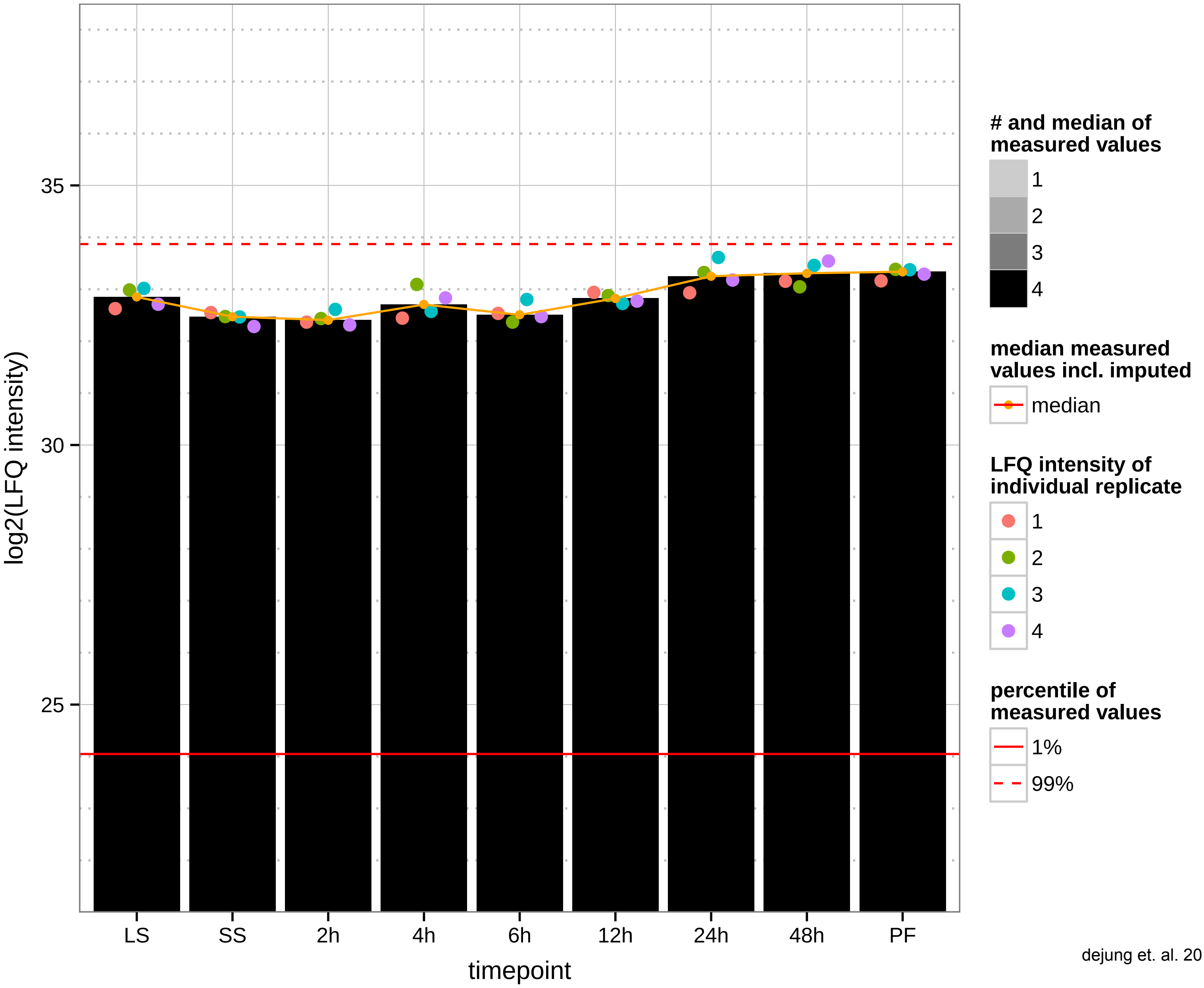
60S acidic ribosomal subunit protein, putative
Tb927.11.2060;Tb927.11.2050
AGOF: structural constituent of ribosome
AGOC: intracellular, large ribosomal subunit, ribosome
AGOP: ribosome biogenesis, translation, translational elongation
PGOF: null, structural constituent of ribosome
PGOC: null, intracellular, ribosome
PGOP: null, ribosome biogenesis, translational elongation





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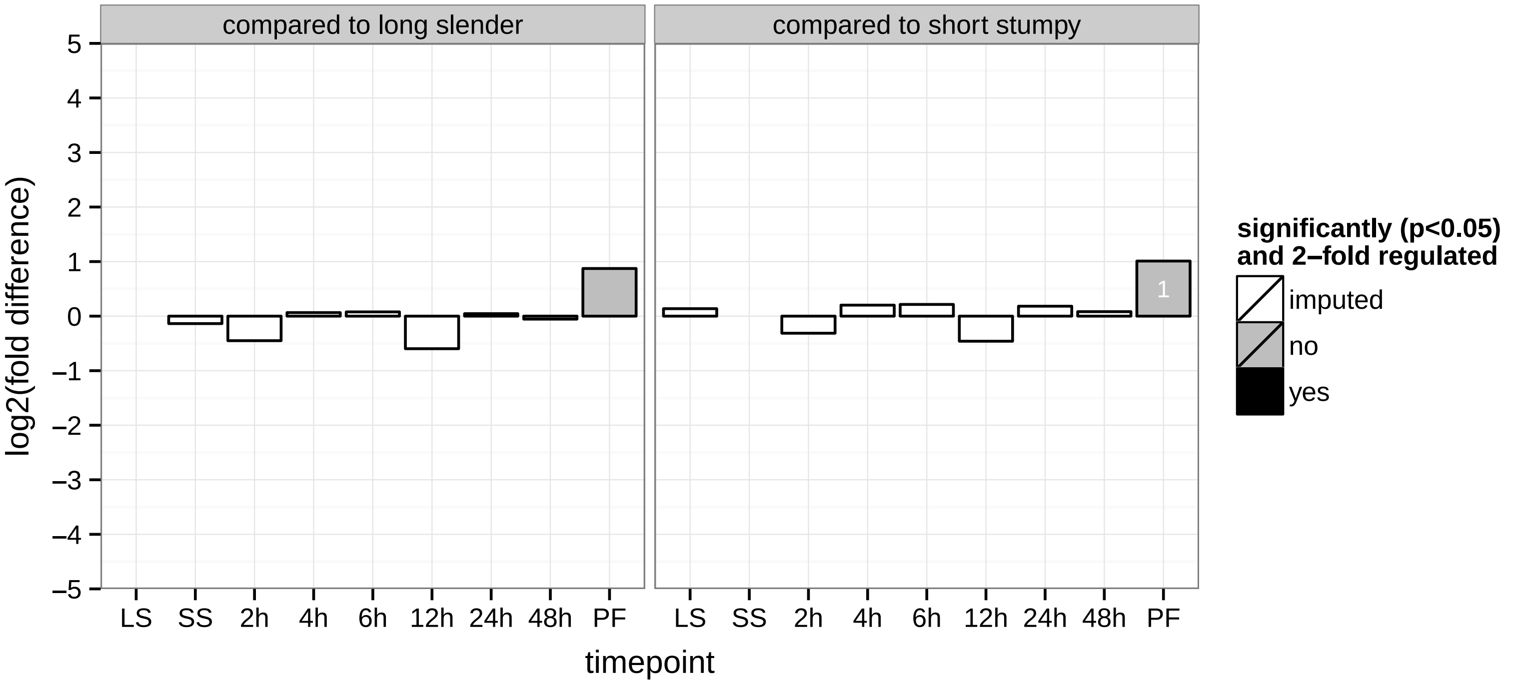
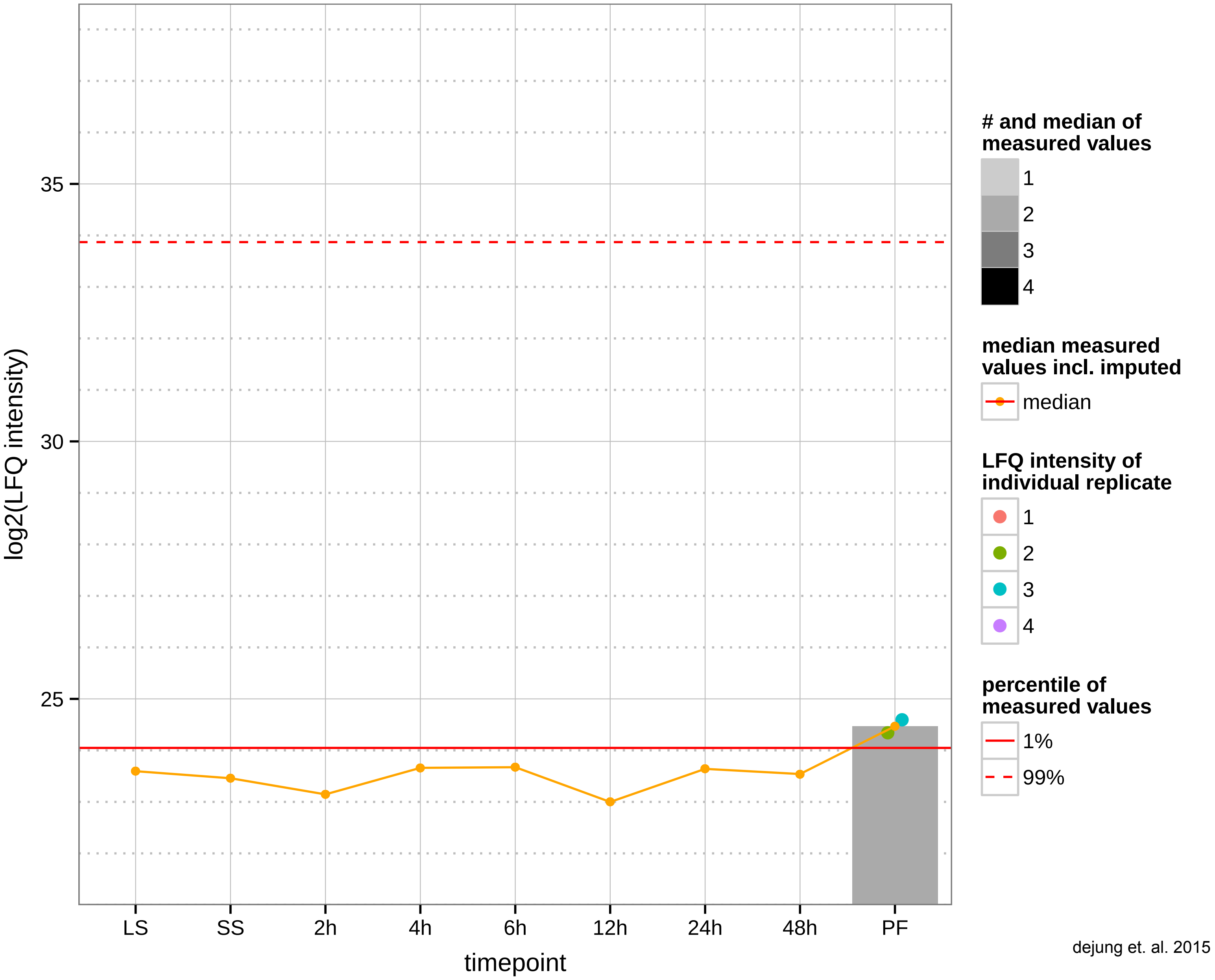
hypothetical protein, conserved
Tb927.11.2080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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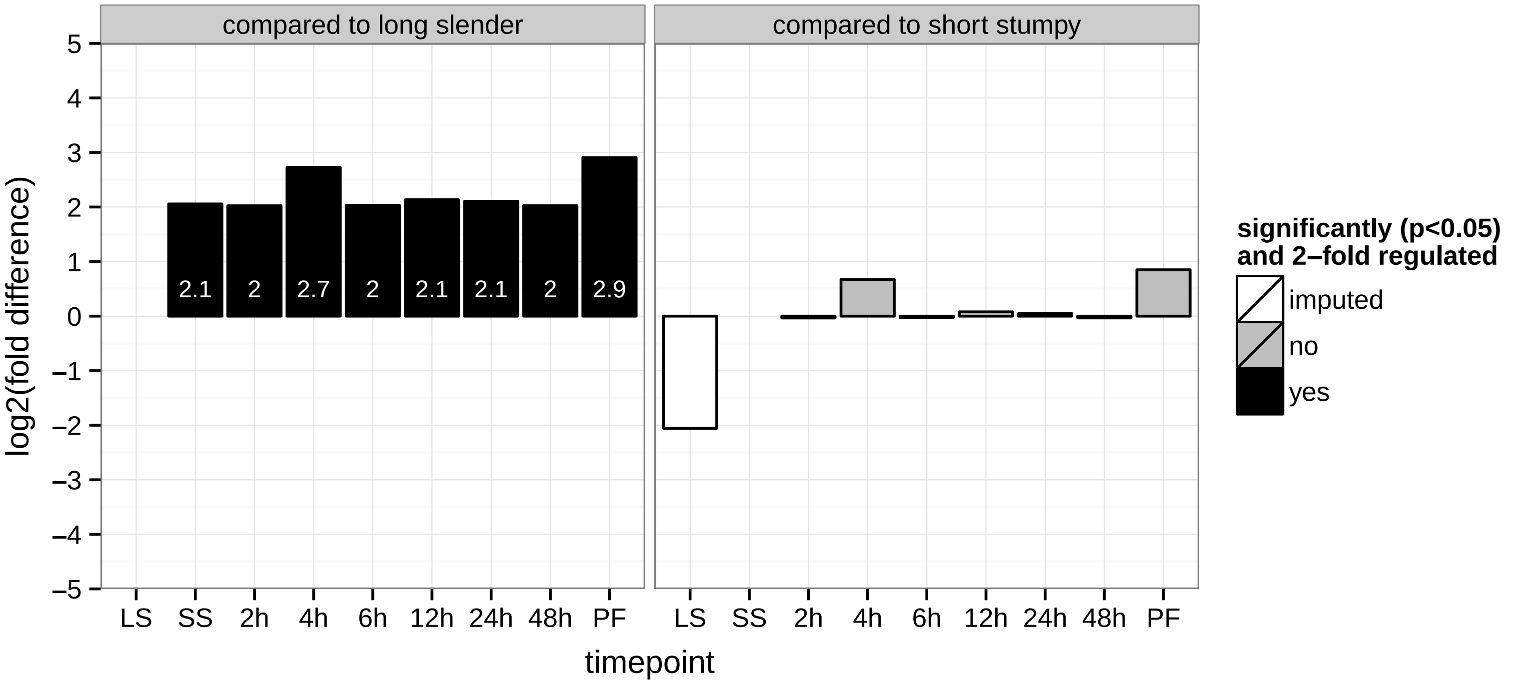
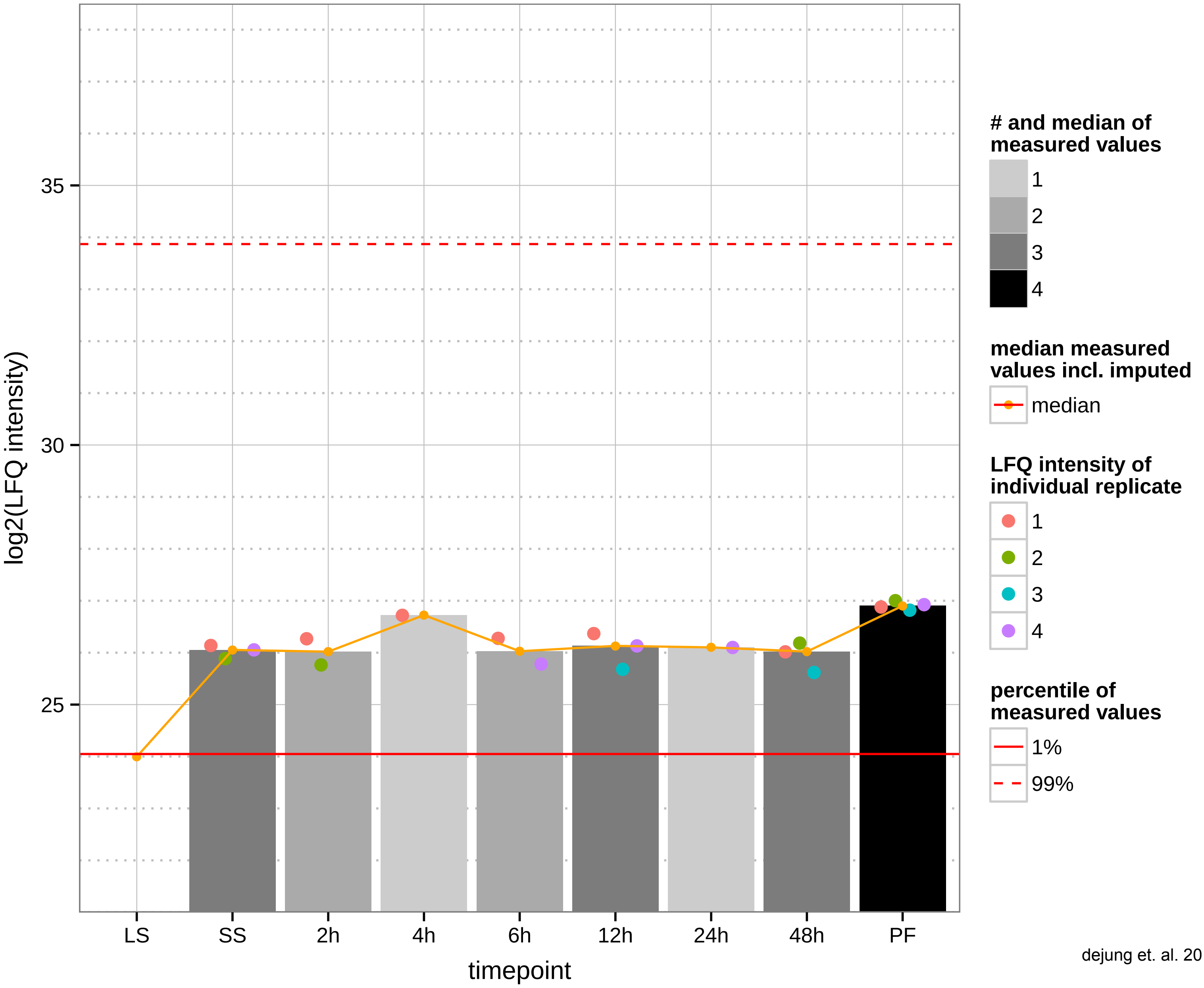
choline kinase (EK1)
Tb927.11.2090
AGOF: ethanolamine kinase activity
AGOC: cytosol
AGOP: phosphatidylethanolamine biosynthetic process
PGOF: phosphotransferase activity, alcohol group as acceptor, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: null





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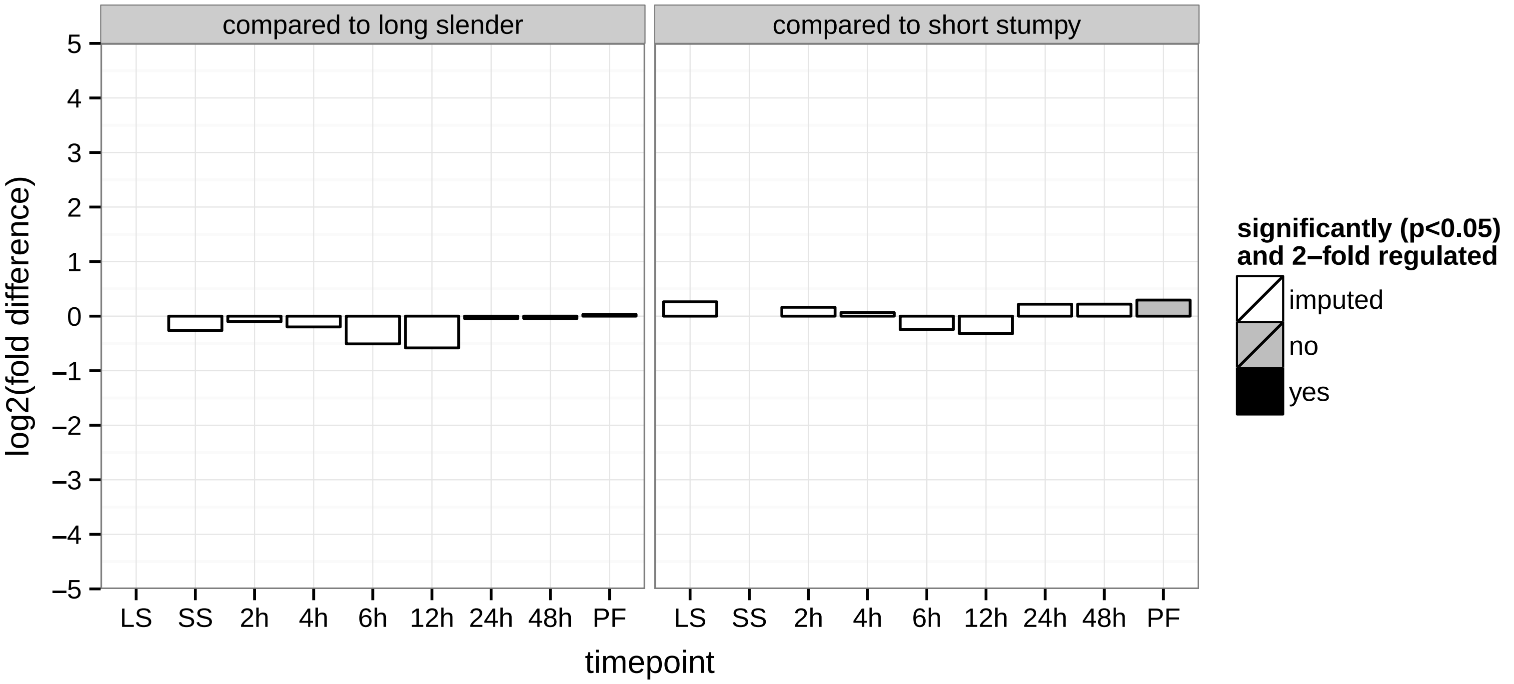
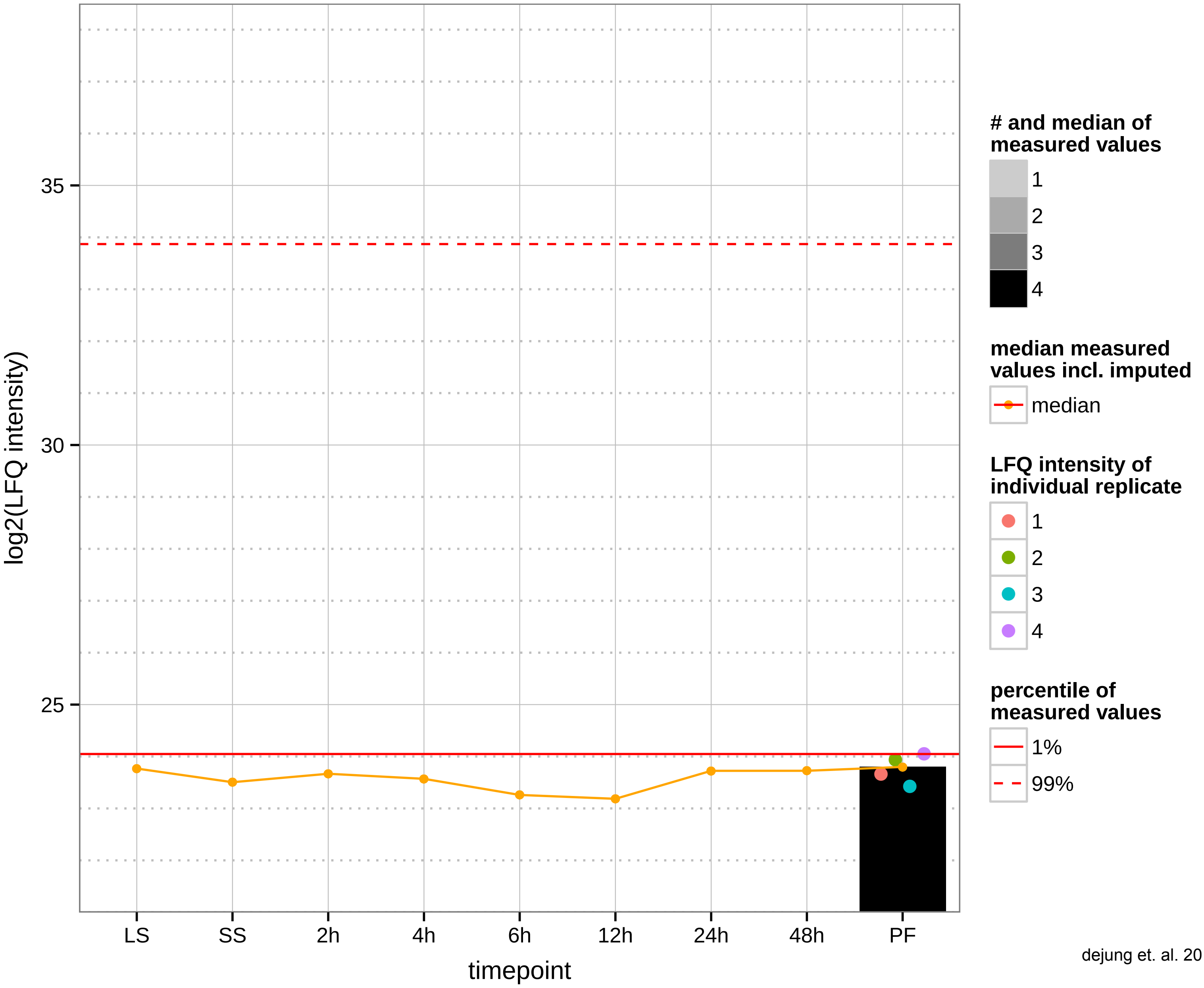
hypothetical protein, conserved
Tb927.11.210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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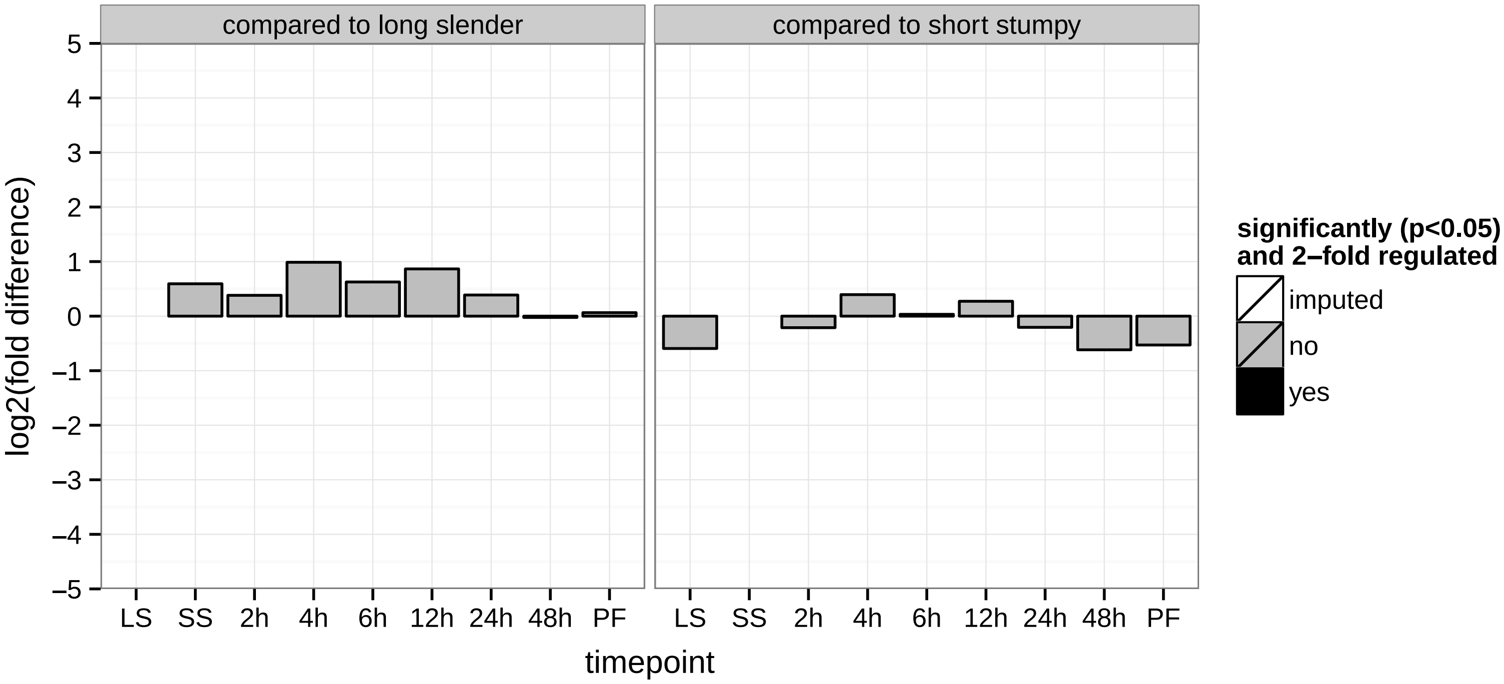
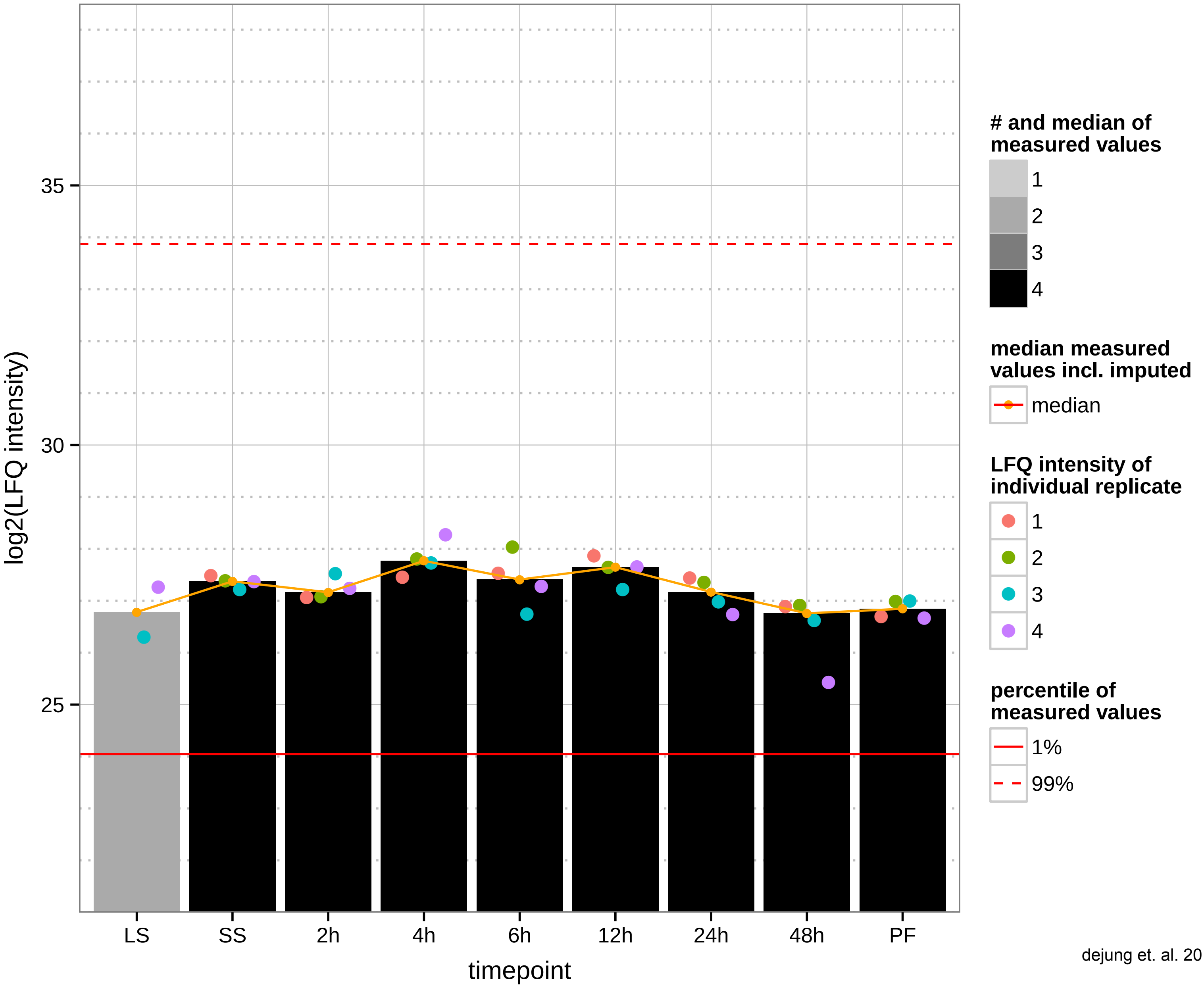
hypothetical protein, conserved
Tb927.11.2110
AGOF: null
AGOC: null
AGOP: protein transport
PGOF: null
PGOC: null
PGOP: protein transport





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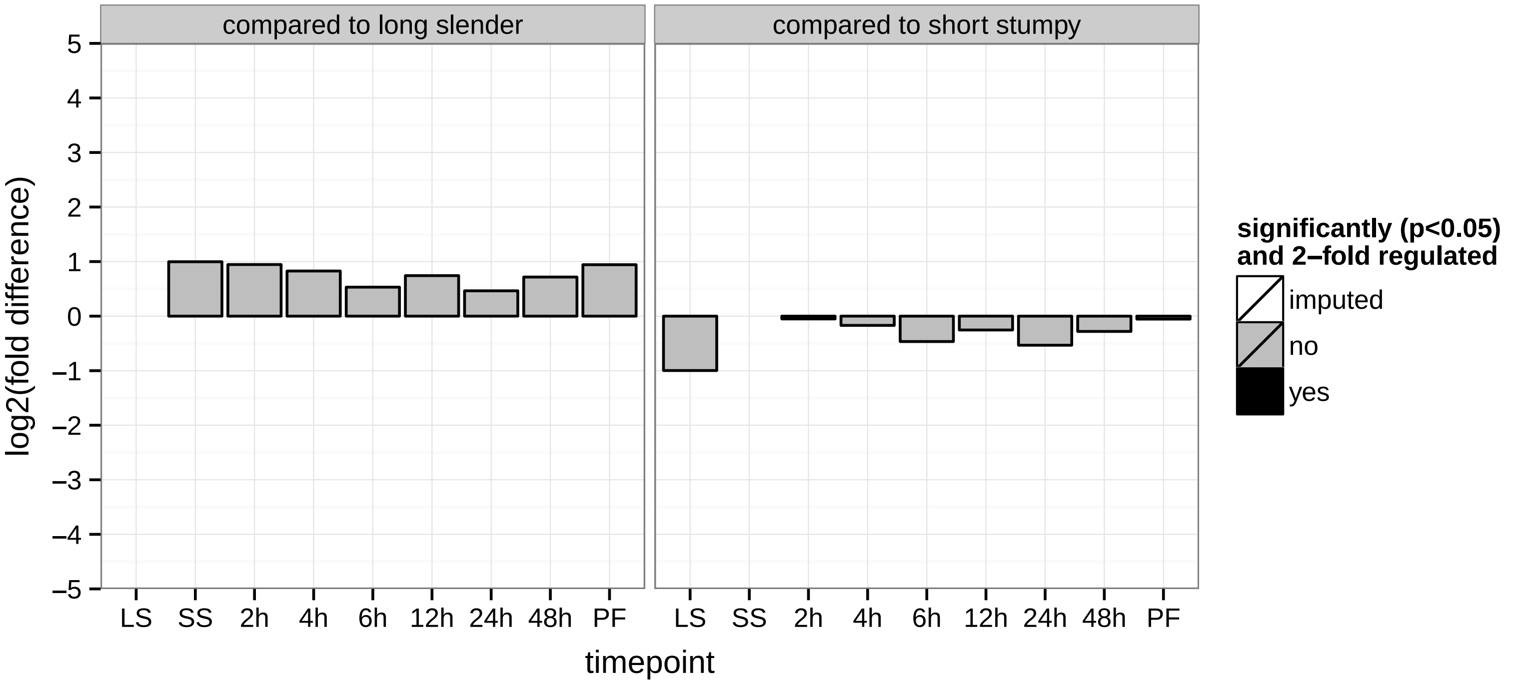
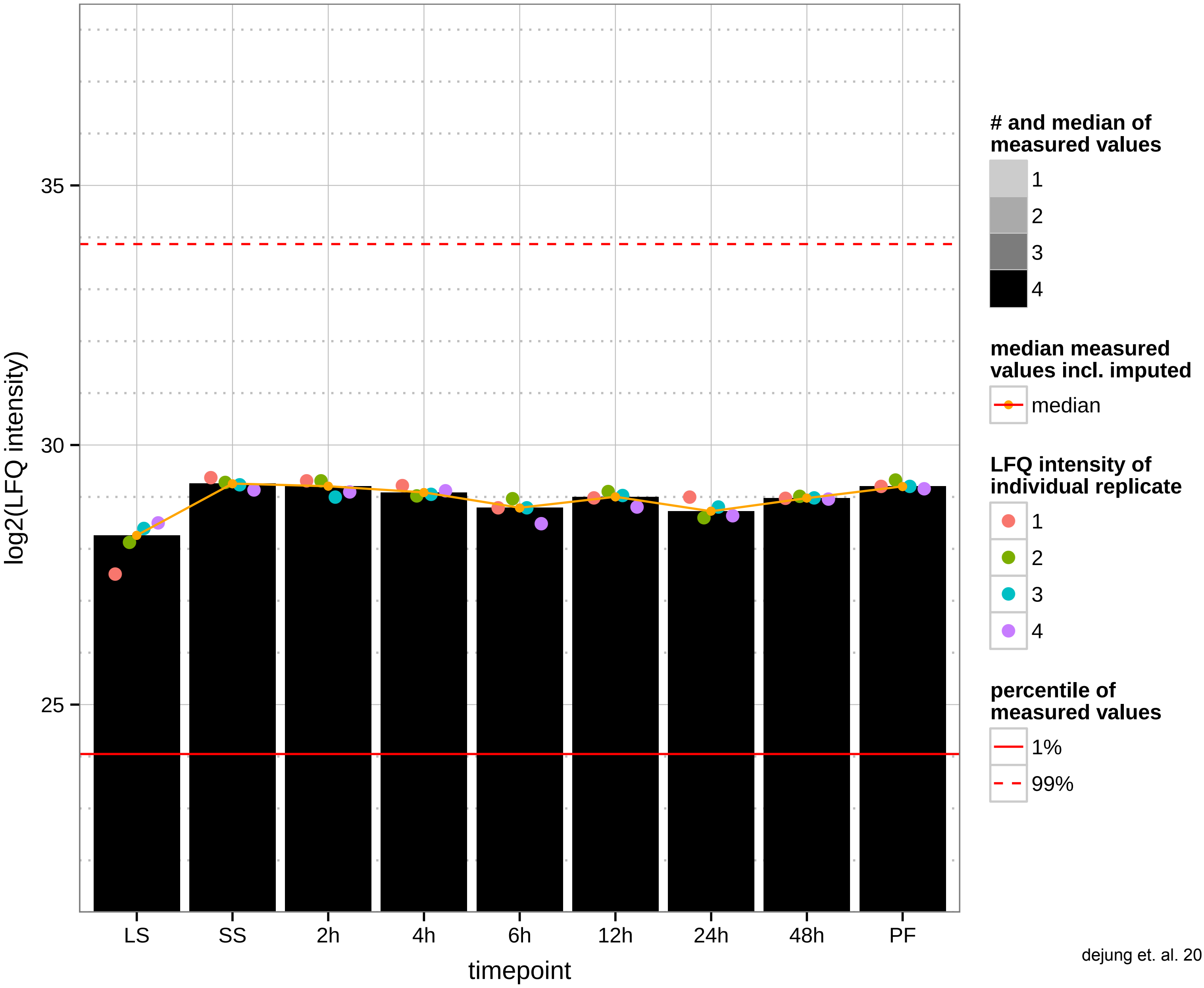
proteasome regulatory non–ATP–ase subunit 3 (RPN3)
Tb927.11.2130
AGOF: endopeptidase activity, enzyme regulator activity
AGOC: proteasome complex, proteasome regulatory particle
AGOP: regulation of protein catabolic process, ubiquitin–dependent protein catabolic process
PGOF: enzyme regulator activity, protein binding
PGOC: proteasome complex
PGOP: regulation of protein catabolic process





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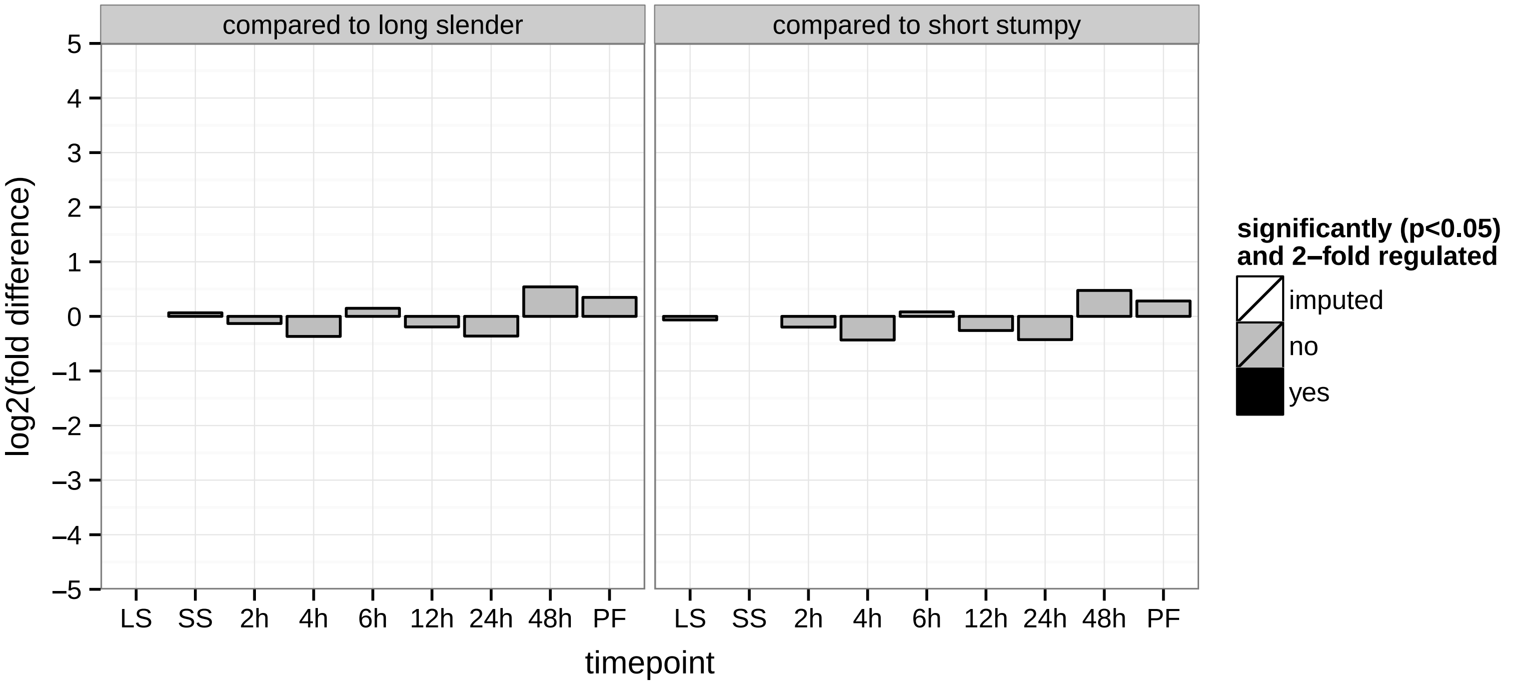
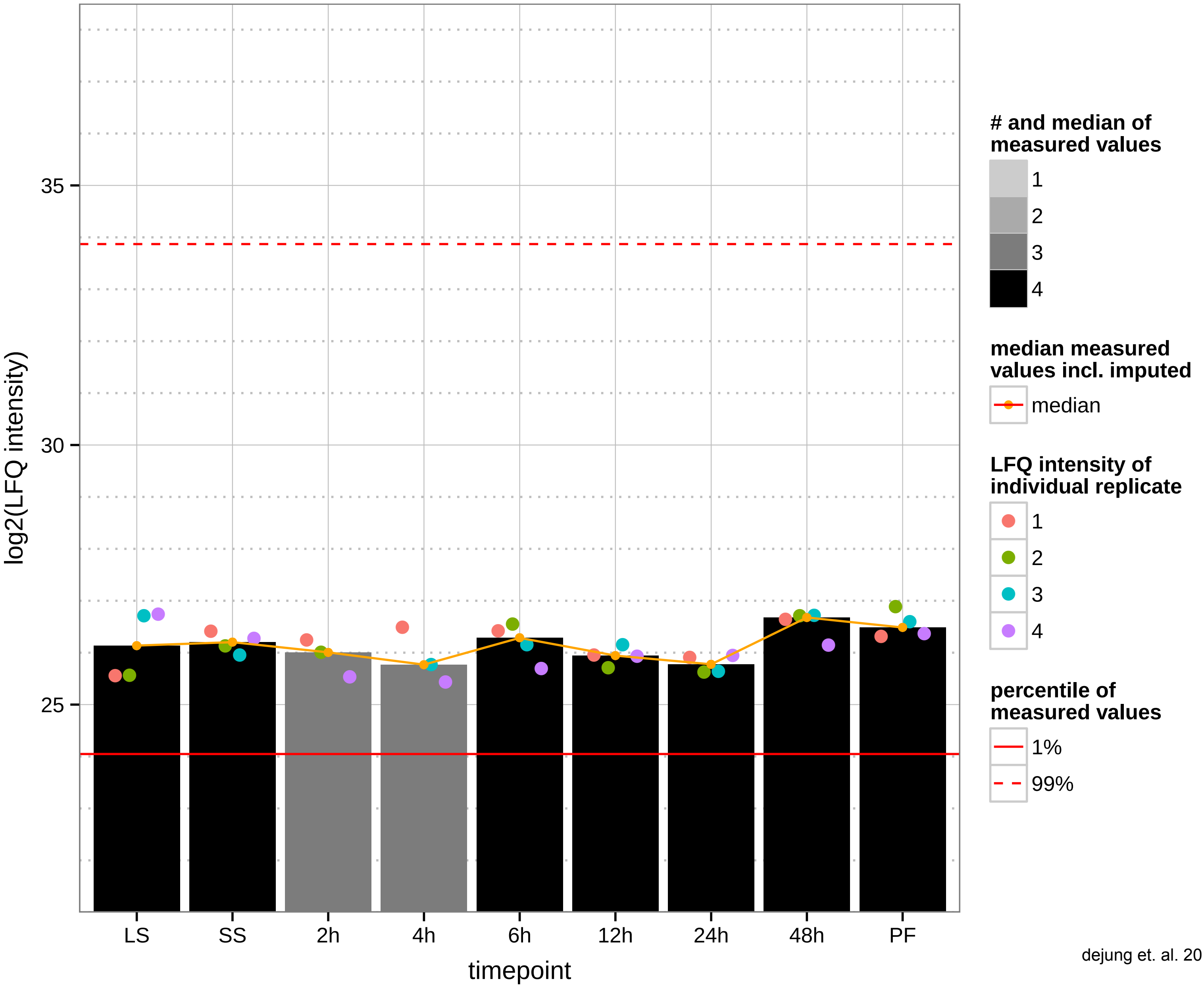
hypothetical protein, conserved
Tb927.11.2140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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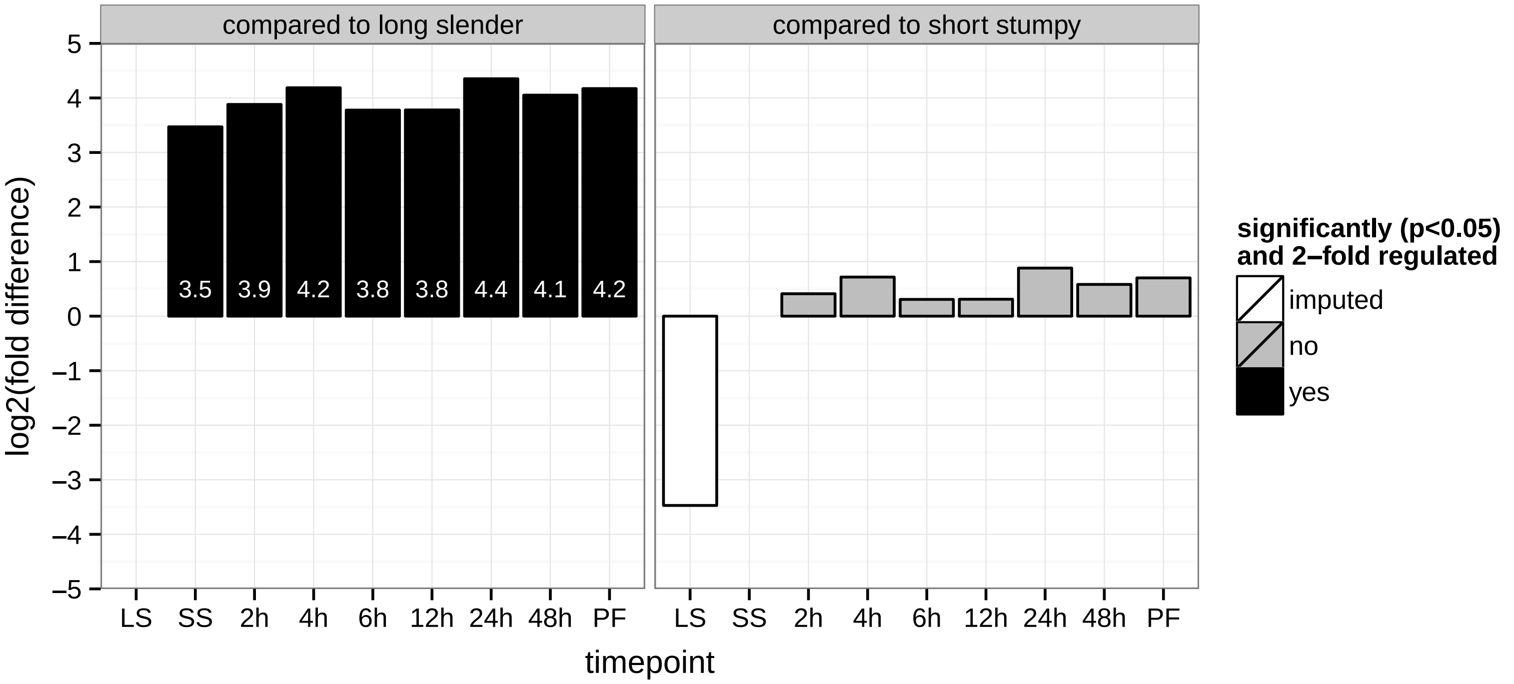
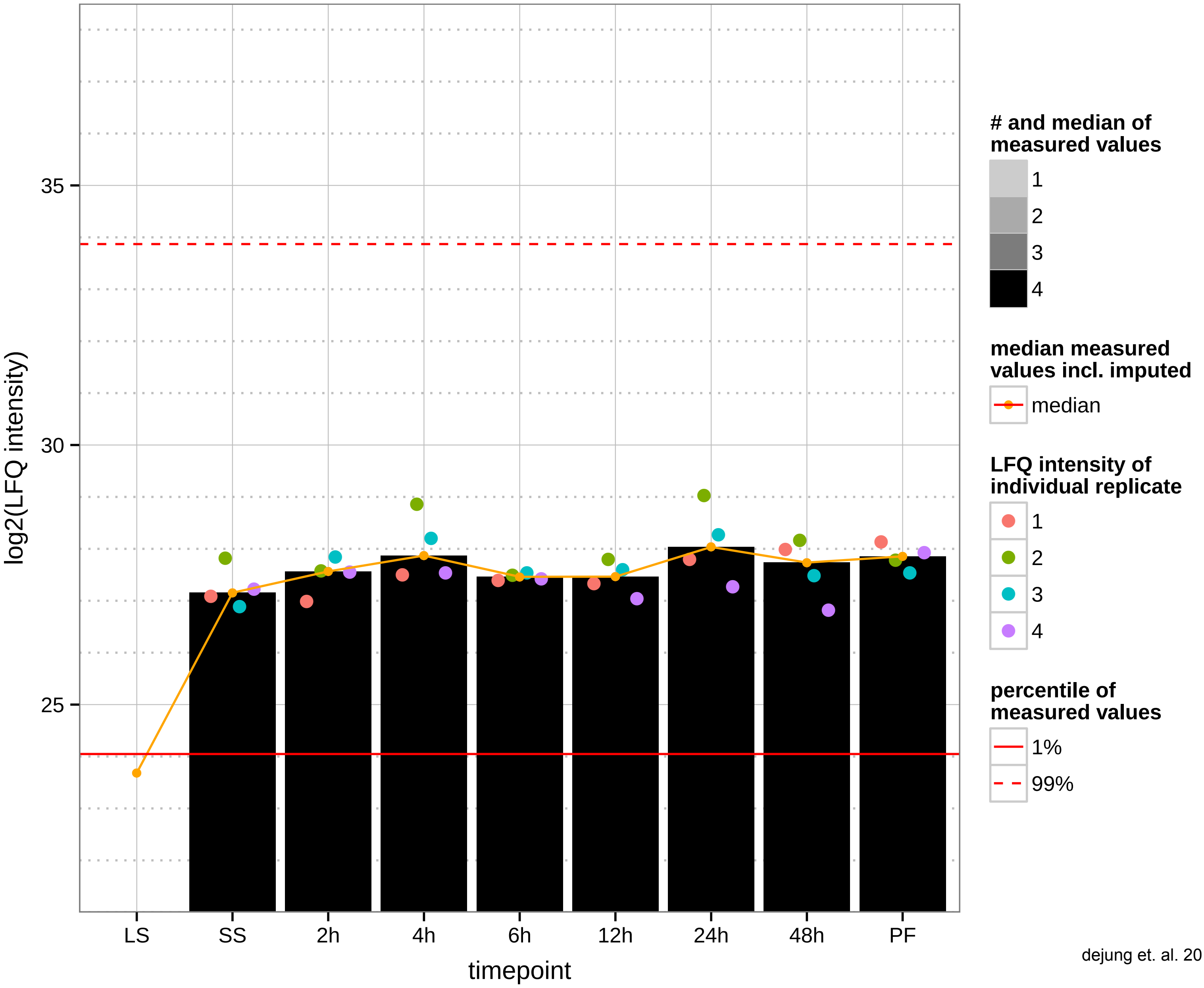
hypothetical protein, conserved
Tb927.11.2190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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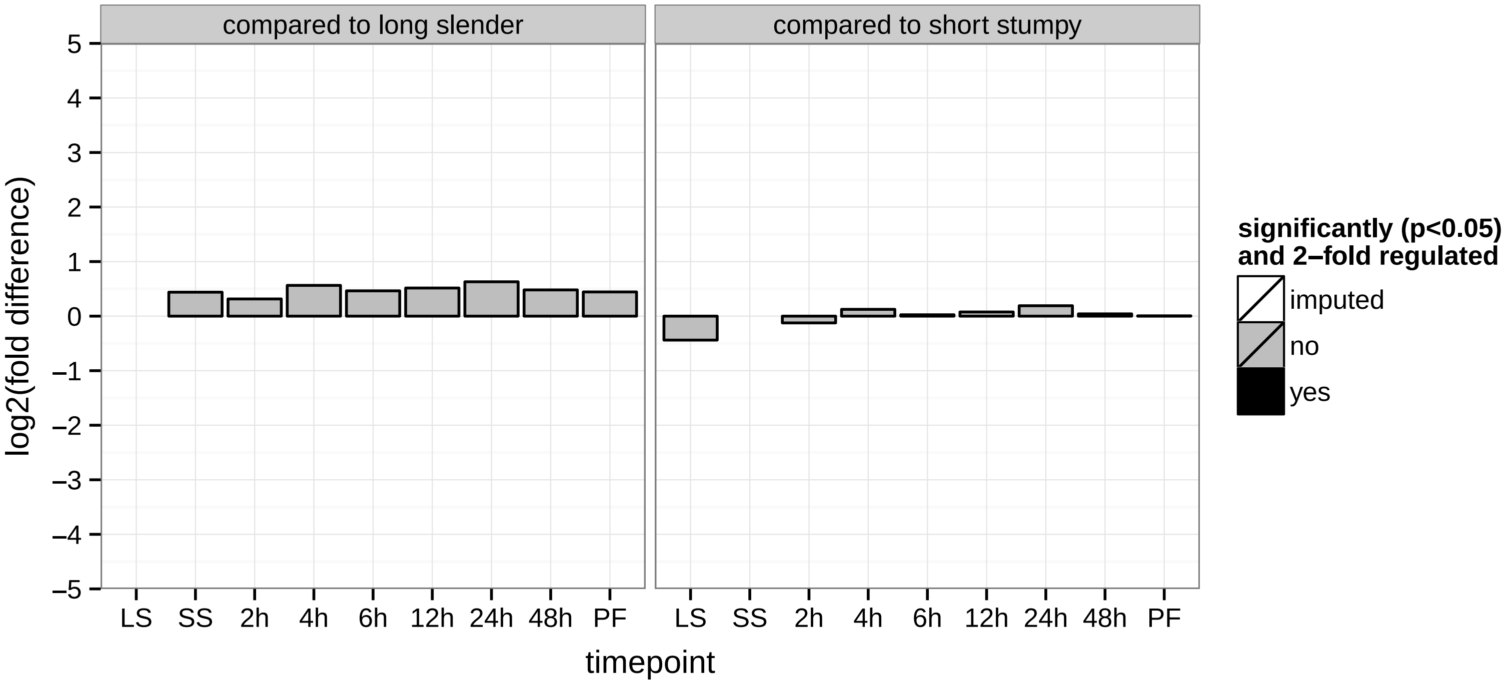
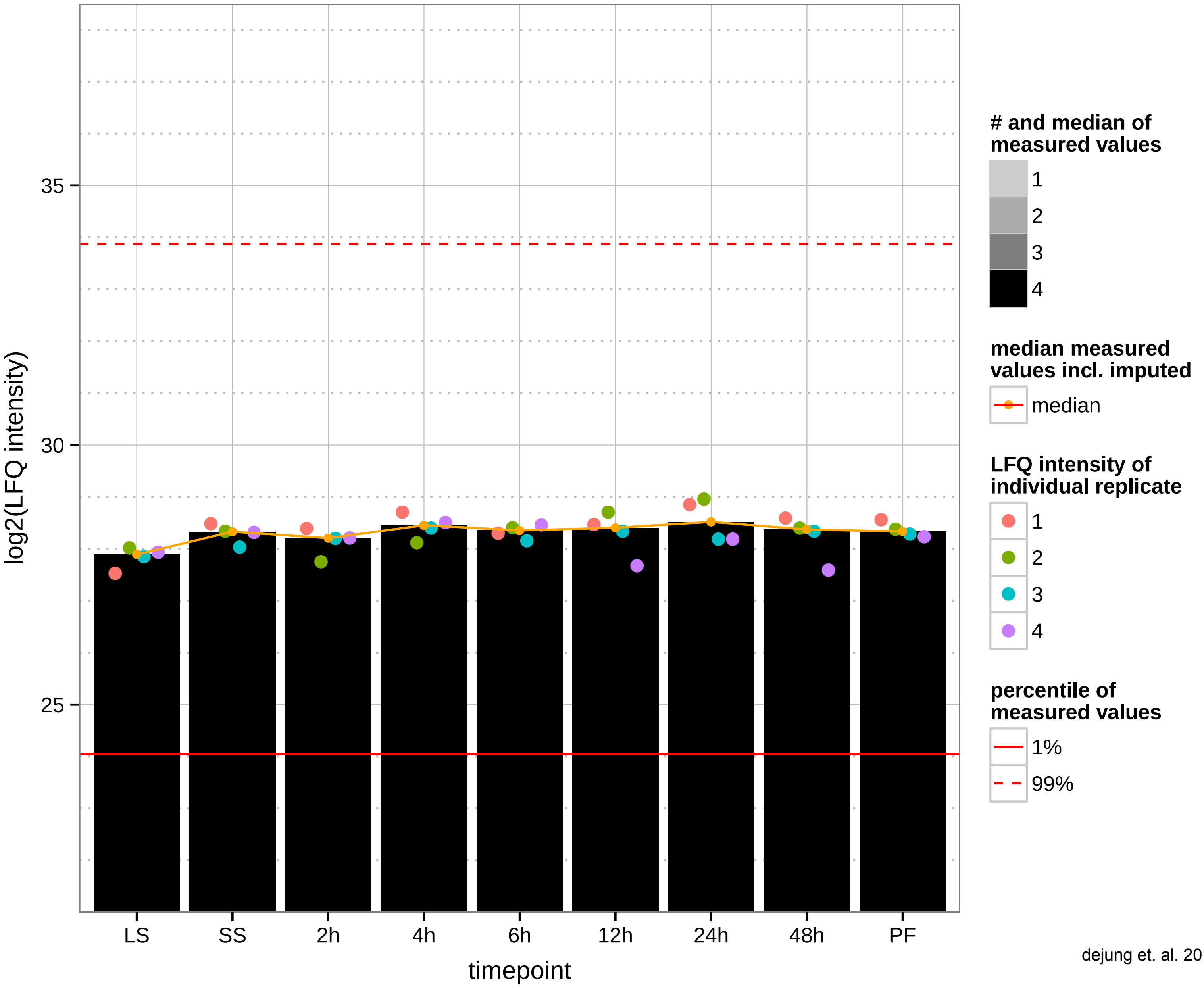
eukaryotic translation initiation factor 4e, putative (eIF4E)
Tb927.11.2260
AGOF: RNA binding, translation initiation factor activity
AGOC: cytoplasm
AGOP: translational initiation
PGOF: RNA binding, translation initiation factor activity
PGOC: cytoplasm
PGOP: translational initiation





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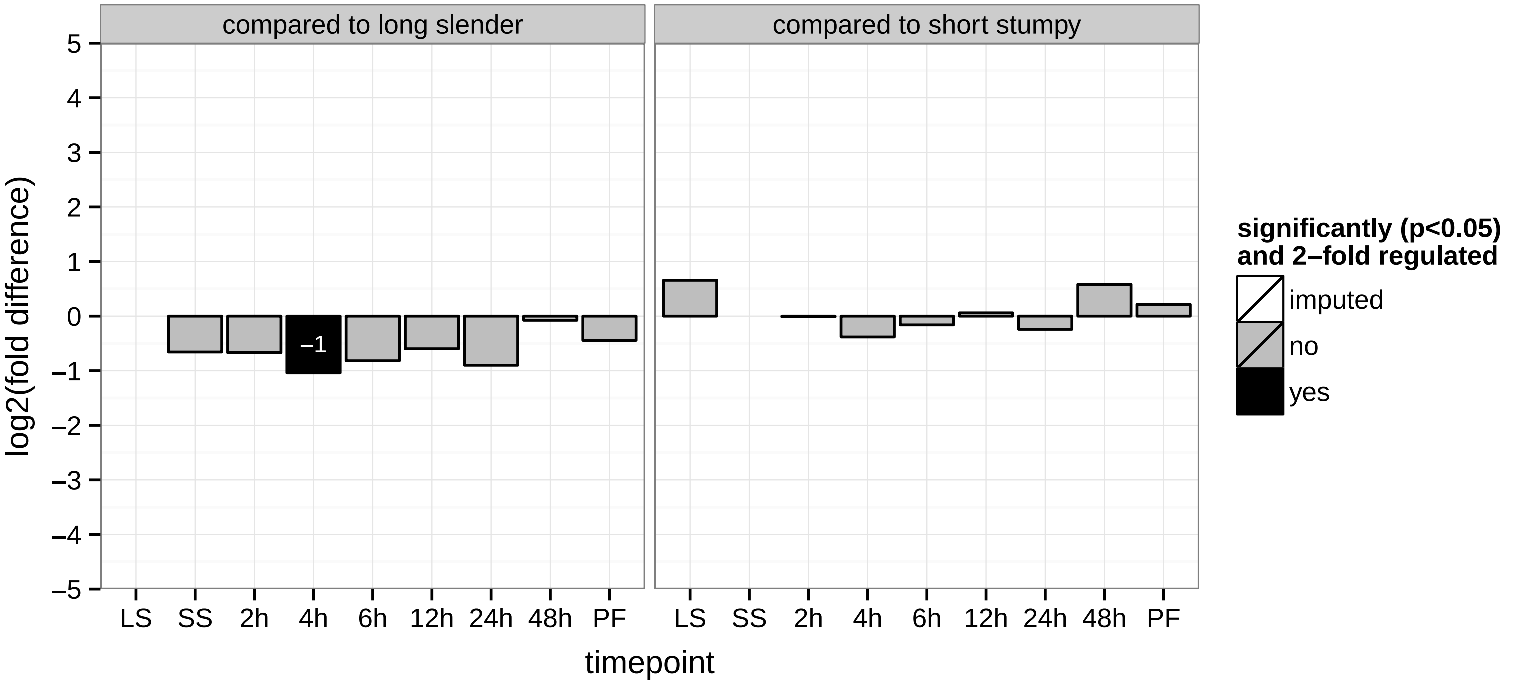
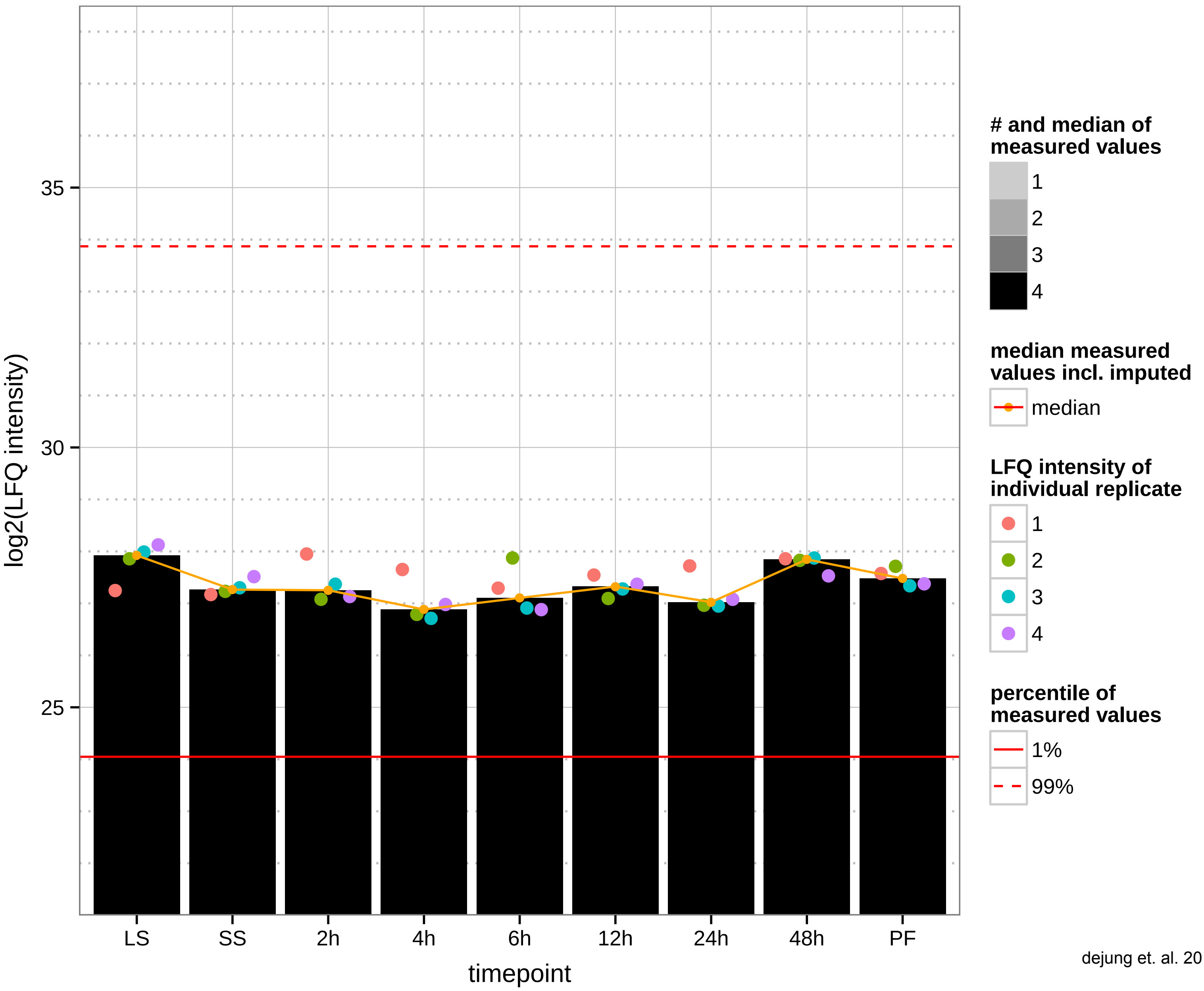
dynein intermediate chain IC140 (IDA7), putative
Tb927.11.2270
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null





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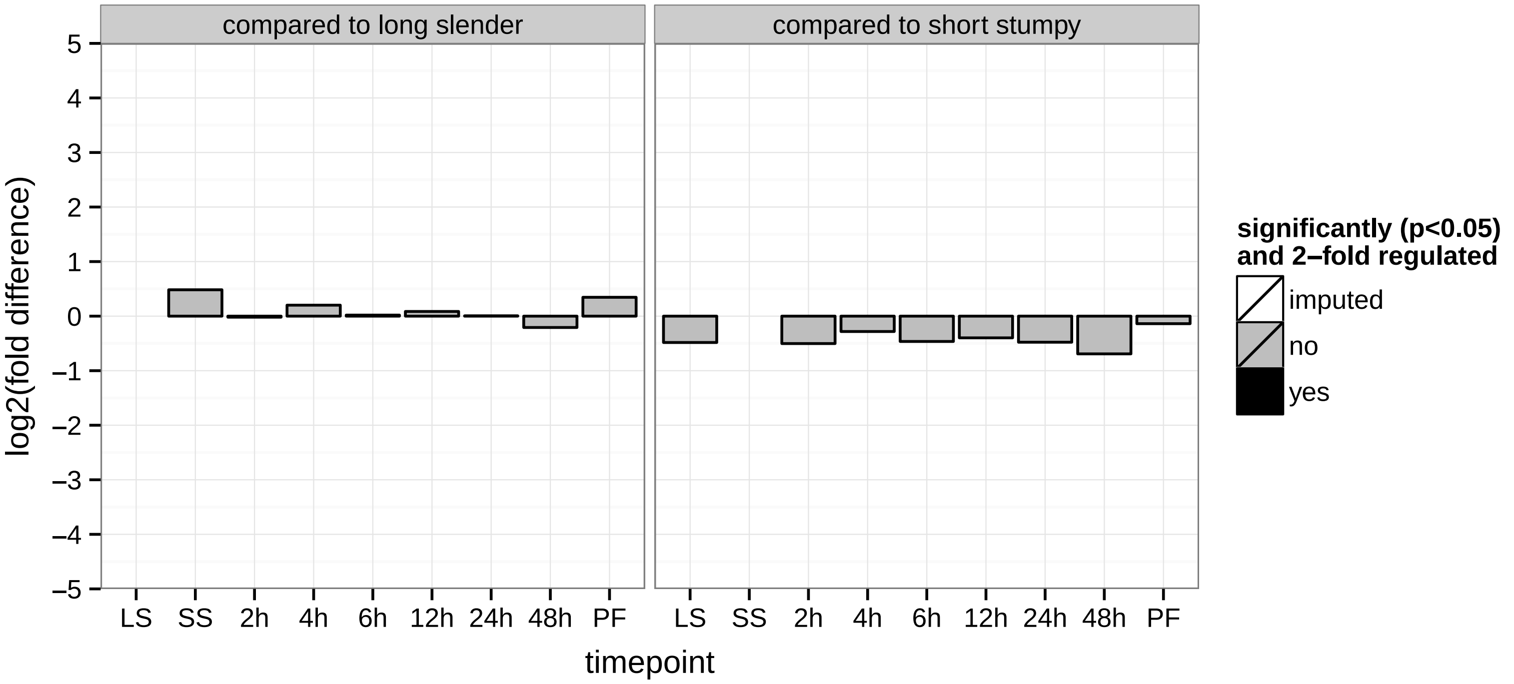
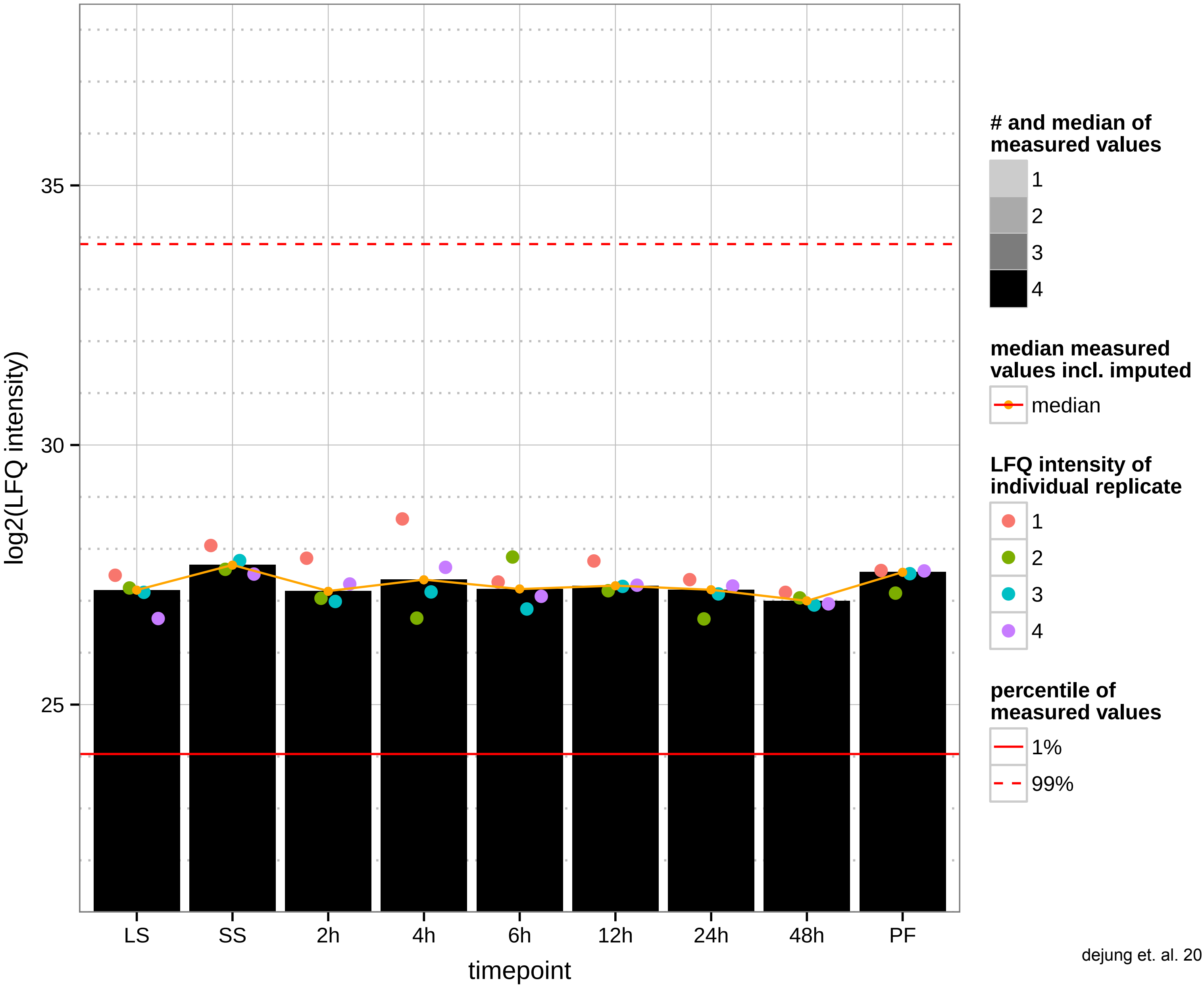
hypothetical protein, conserved
Tb927.11.2280
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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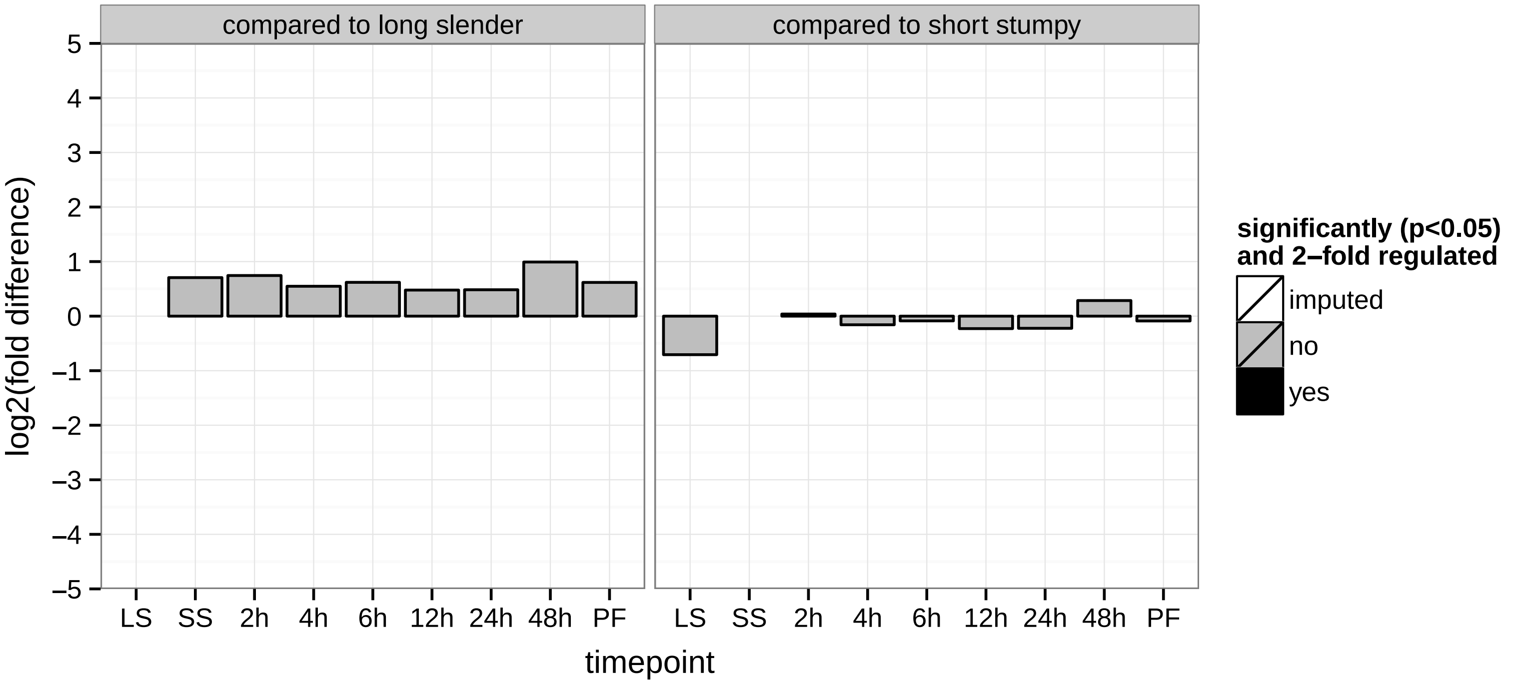
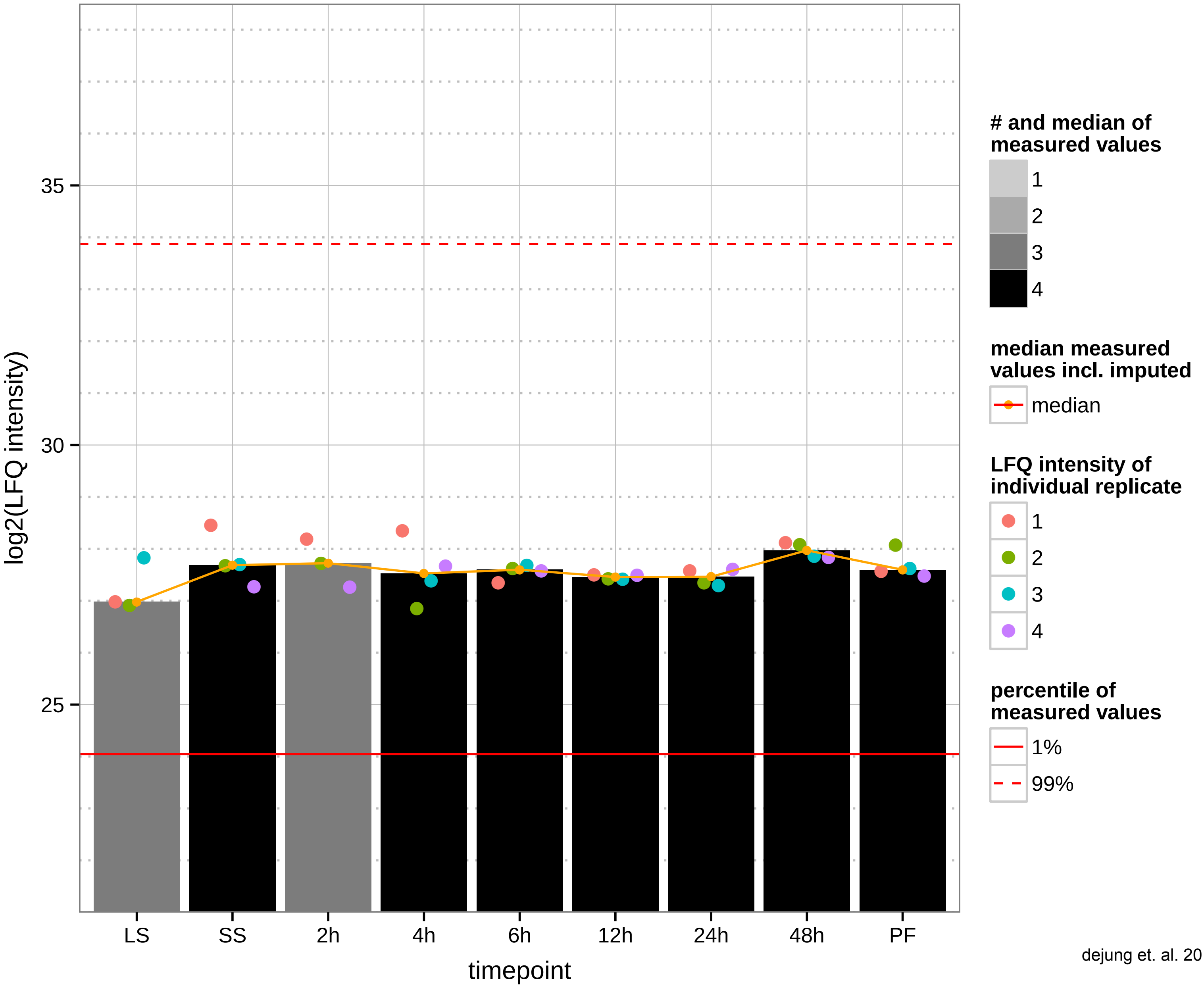
cleavage and polyadenylation specificity factor, putative
Tb927.11.230
AGOF: mRNA 3'–UTR binding
AGOC: mRNA cleavage and polyadenylation specificity factor complex
AGOP: mRNA cleavage, mRNA polyadenylation
PGOF: null
PGOC: null
PGOP: null





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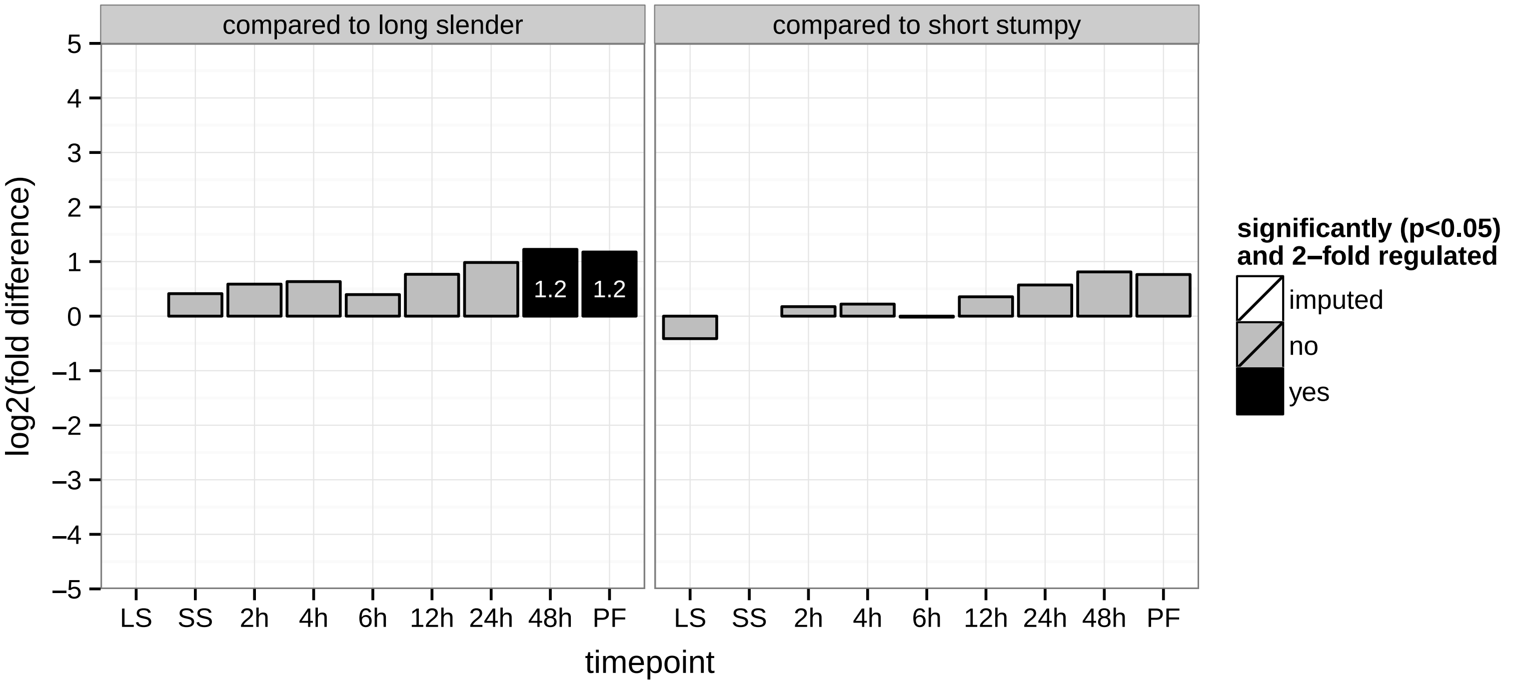
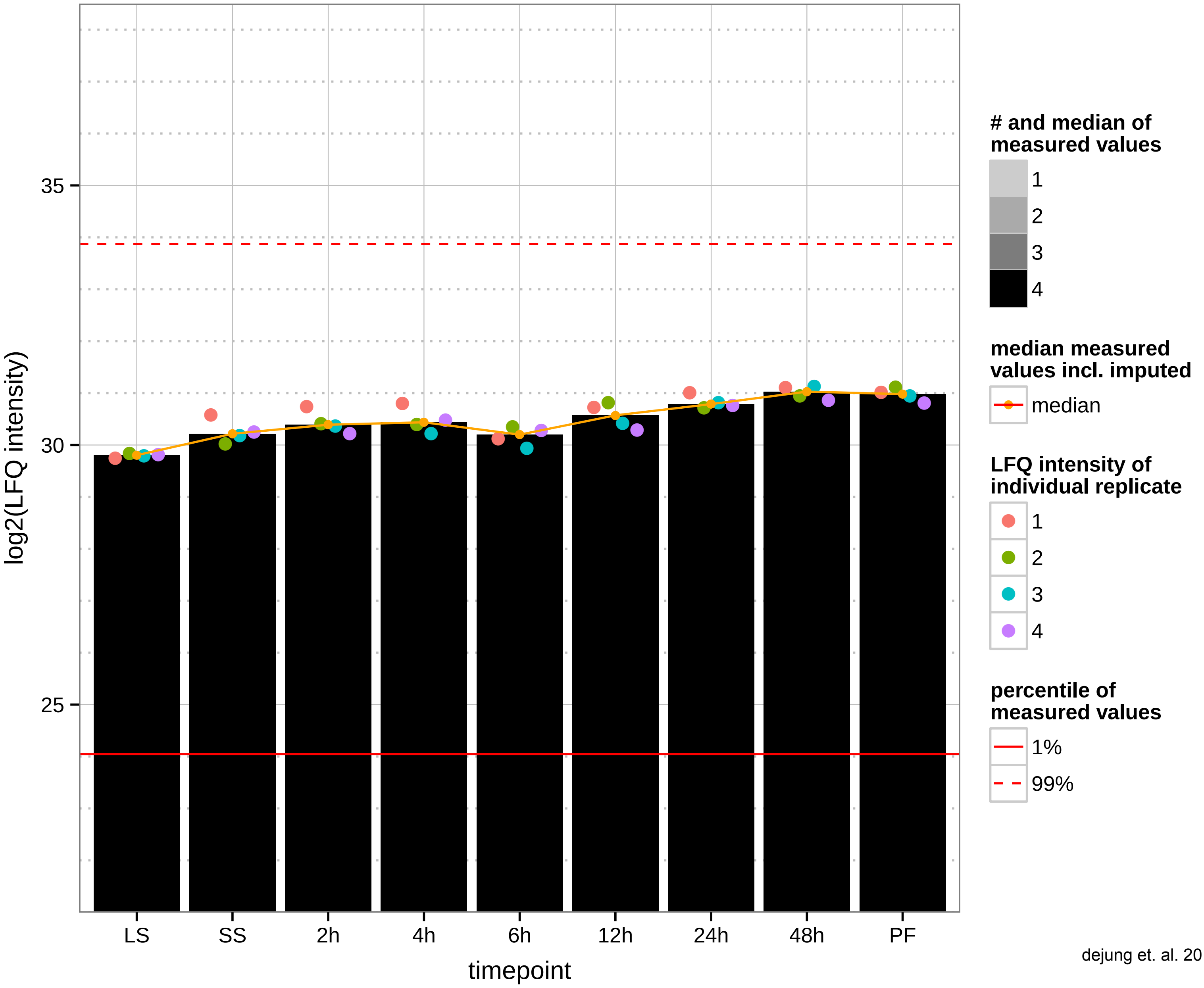
eukaryotic peptide chain release factor subunit 1, putative (ERF1)
Tb927.11.2300
AGOF: translation release factor activity, translation release factor activity, codon specific
AGOC: null
AGOP: translation, translational termination
PGOF: translation release factor activity, codon specific
PGOC: cytoplasm
PGOP: translational termination





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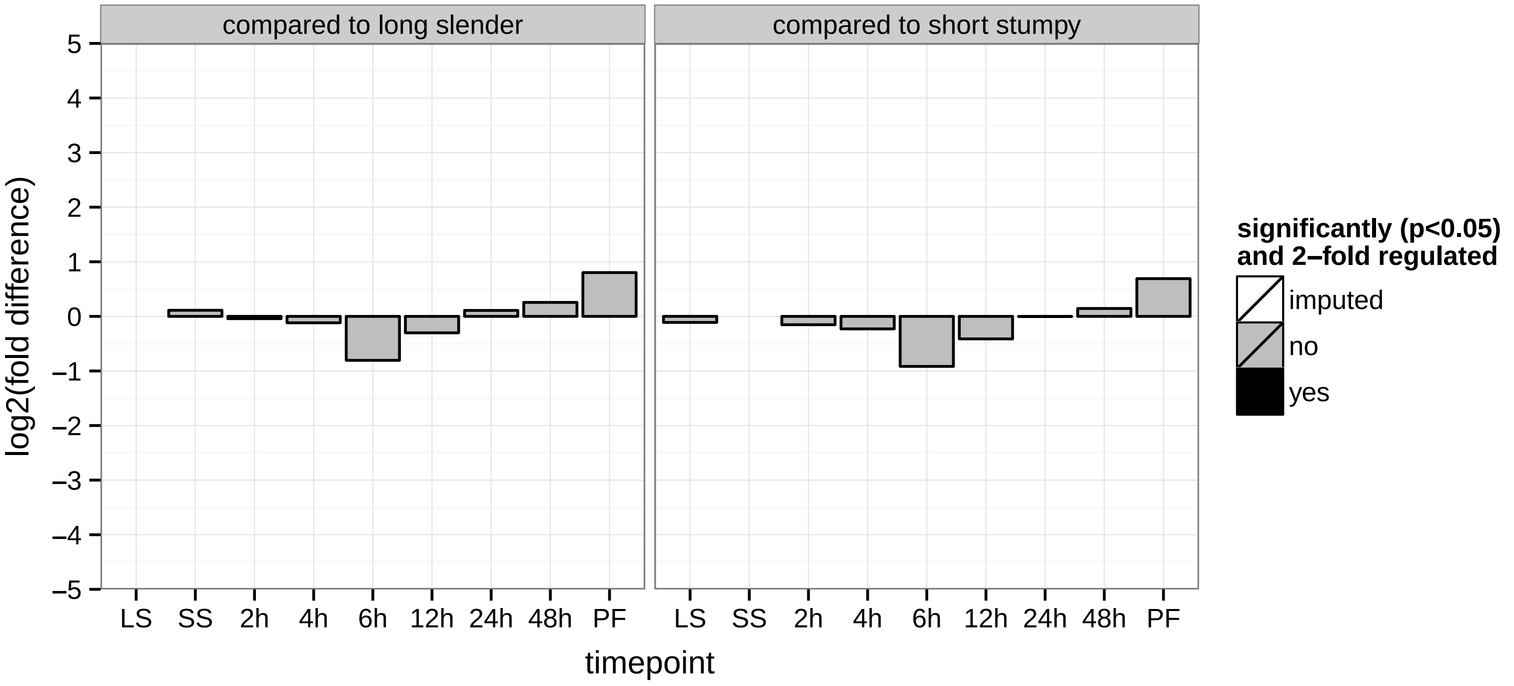
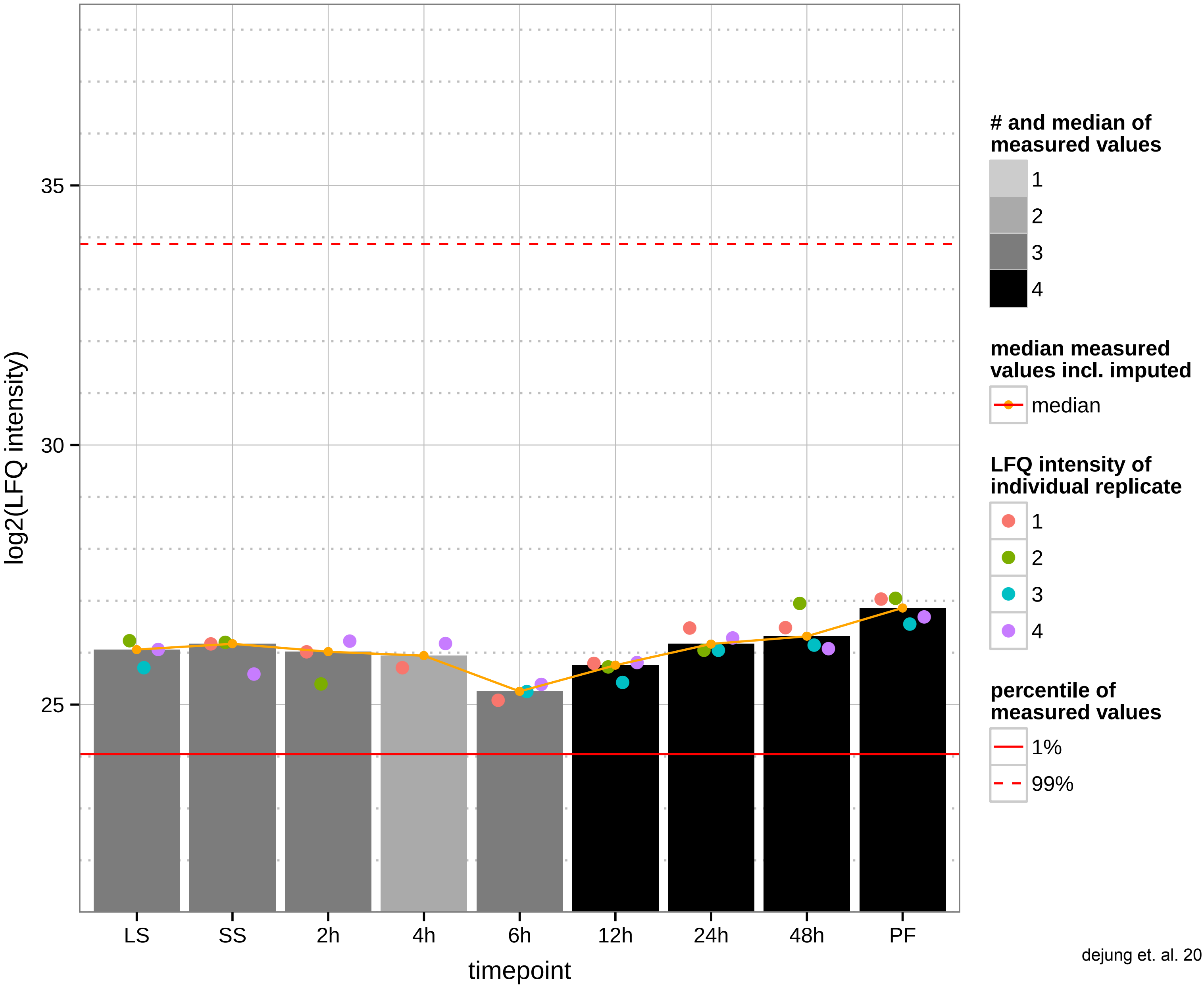
hypothetical protein, conserved
Tb927.11.2340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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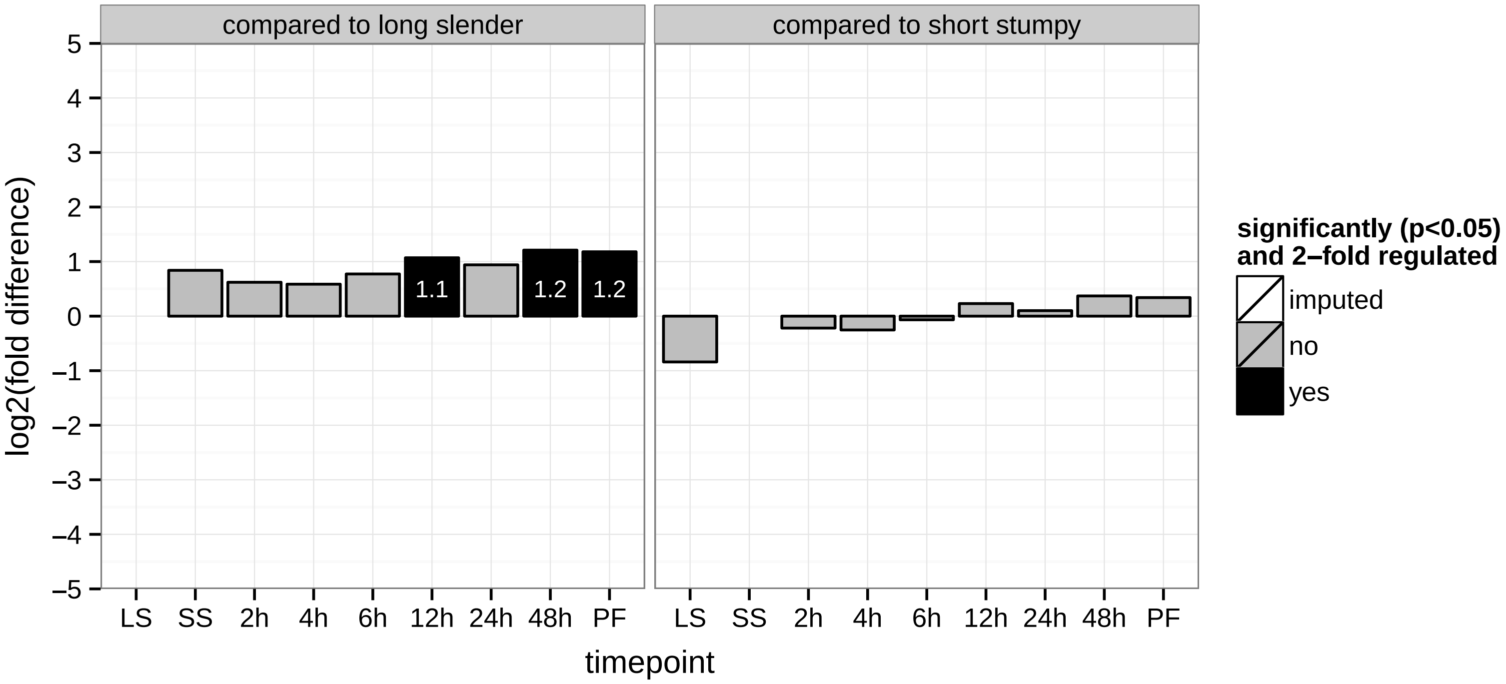
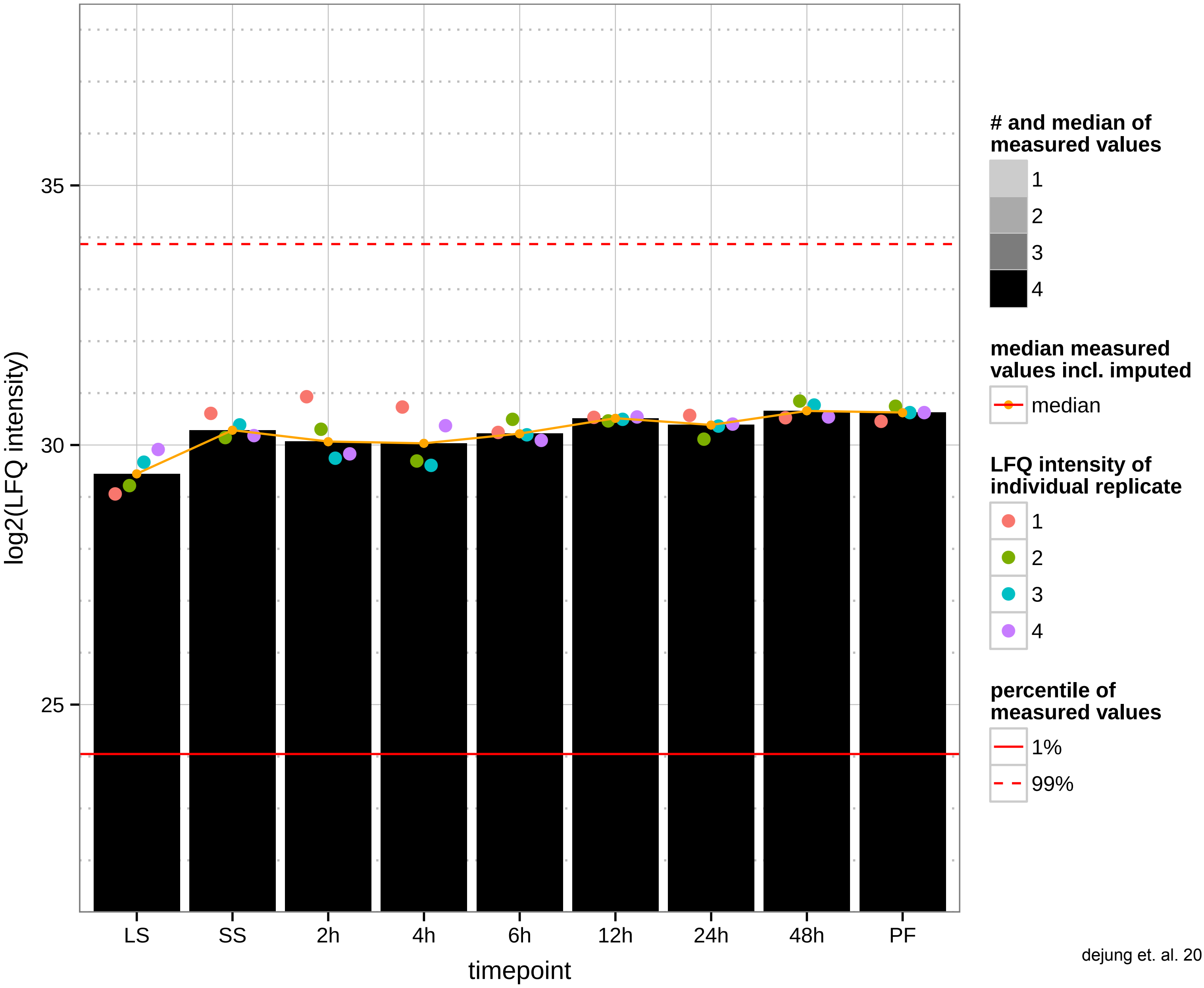
phenylalanyl–tRNA synthetase (beta subunit), putative
Tb927.11.2360
AGOF: ATP binding, RNA binding, magnesium ion binding, phenylalanine–tRNA ligase activity
AGOC: cytoplasm, phenylalanine–tRNA ligase complex
AGOP: phenylalanyl–tRNA aminoacylation, translation
PGOF: ATP binding, RNA binding, magnesium ion binding, nucleotide binding, phenylalanine–tRNA ligase activity
PGOC: cytoplasm
PGOP: phenylalanyl–tRNA aminoacylation





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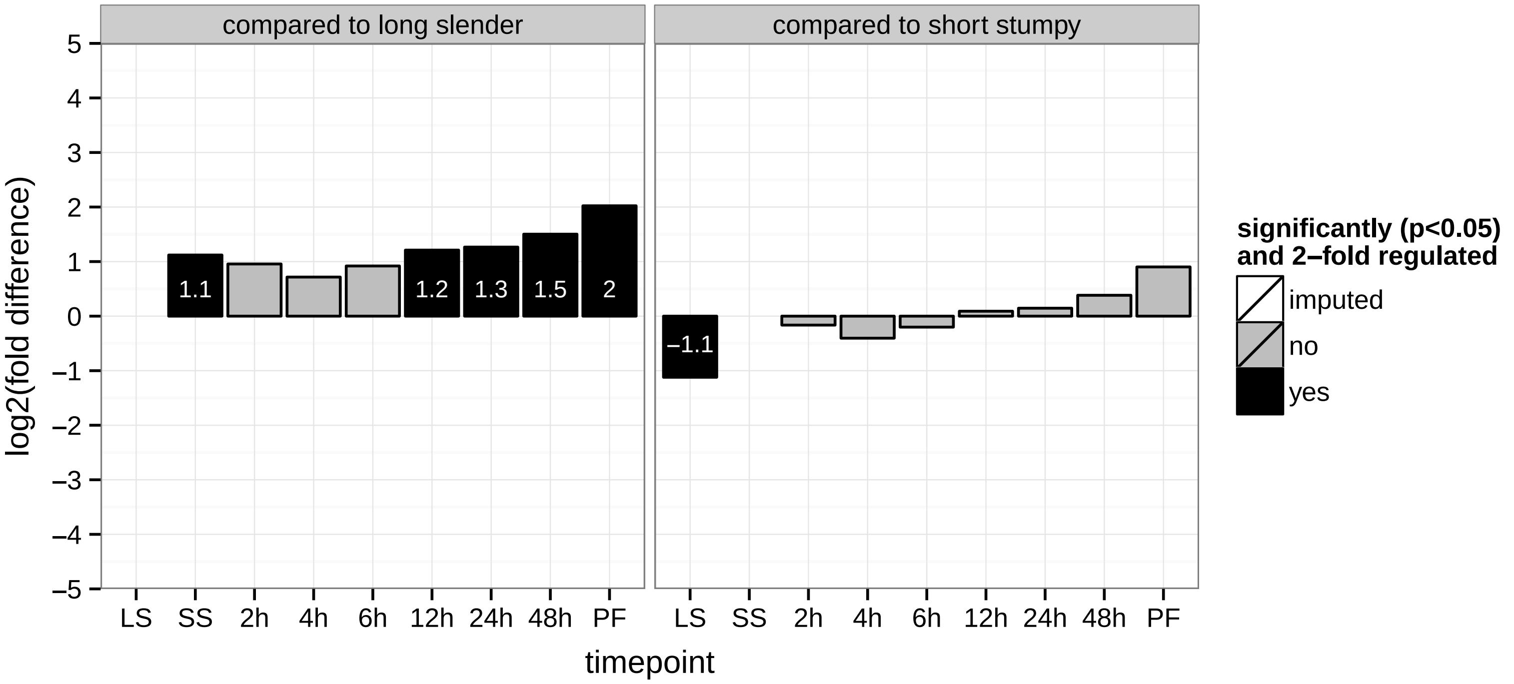
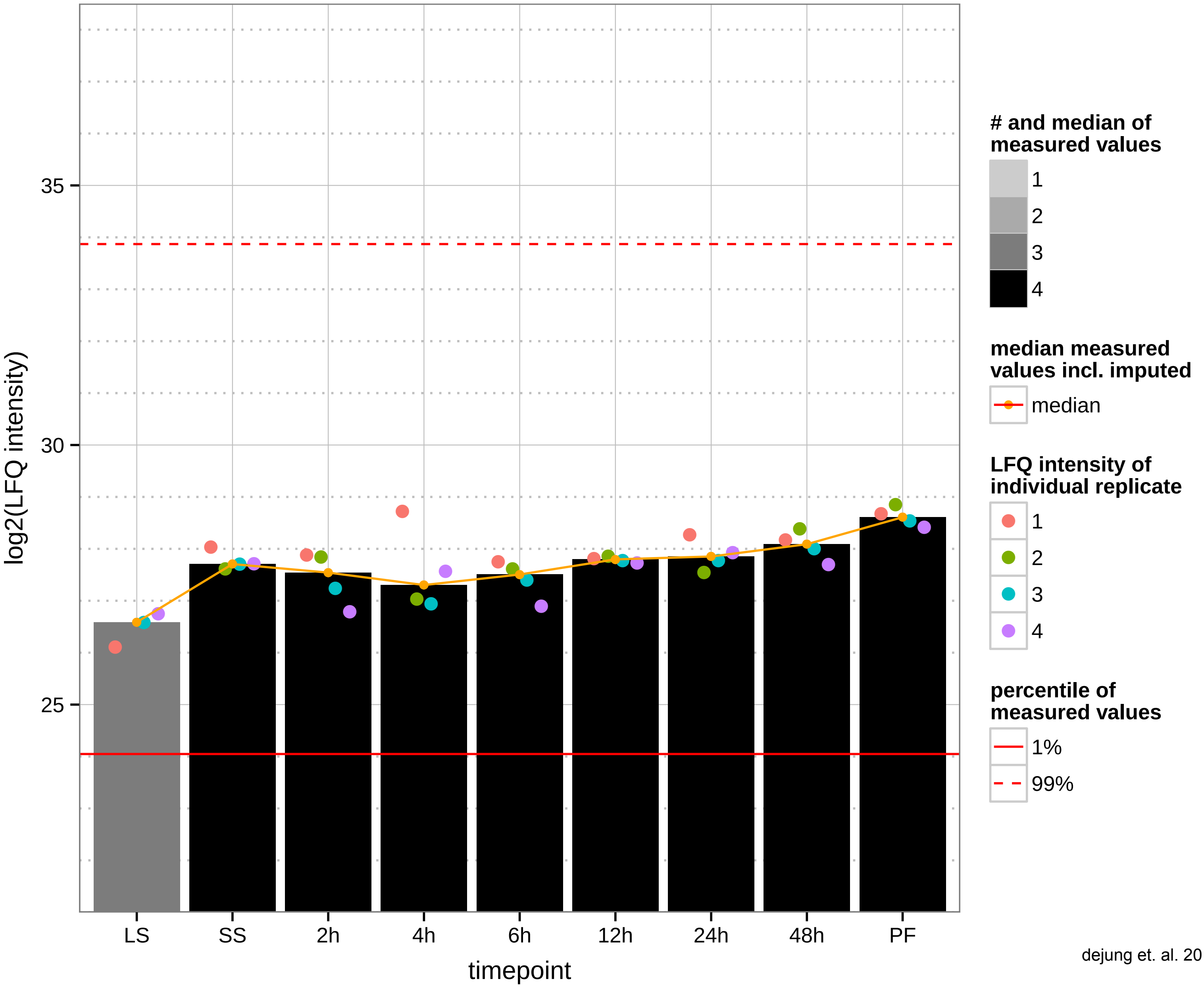
hypothetical protein, conserved
Tb927.11.2370
AGOF: RNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, protein binding, zinc ion binding
PGOC: null
PGOP: null





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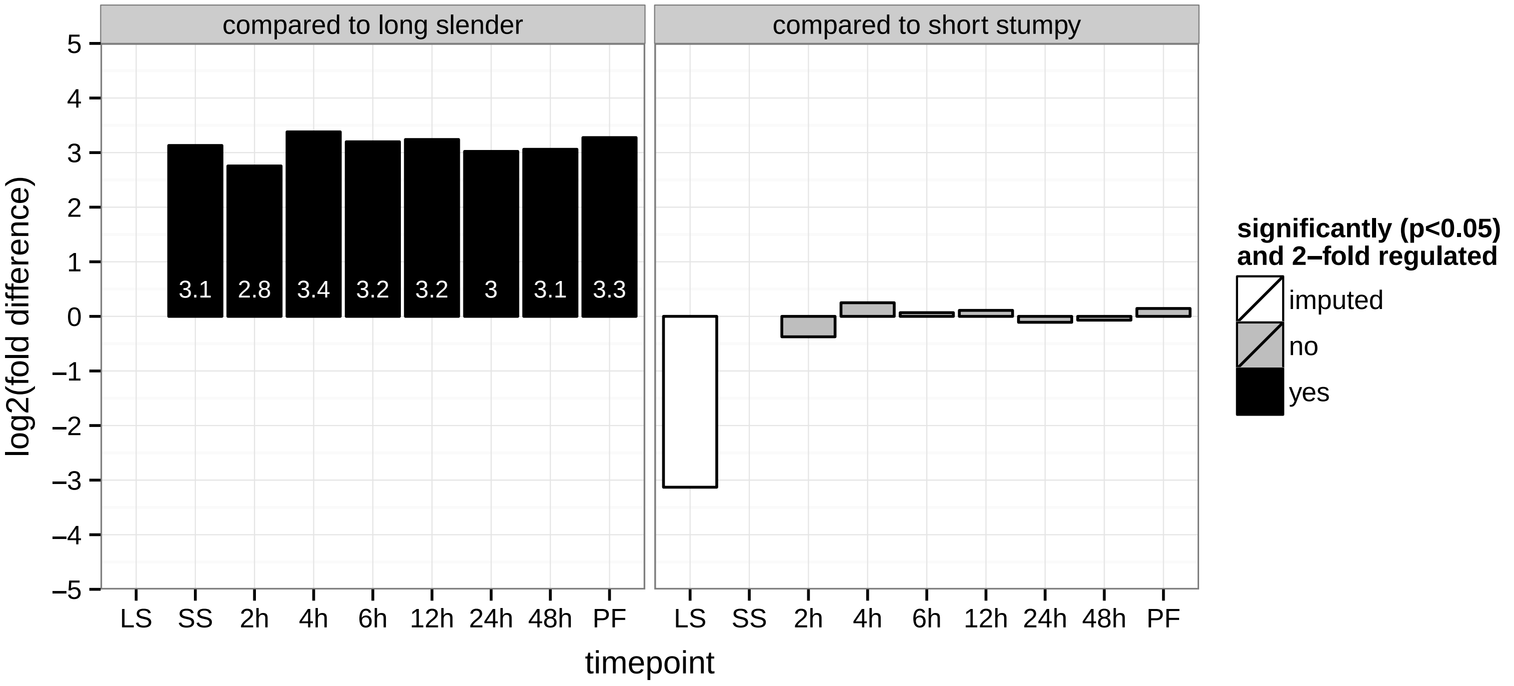
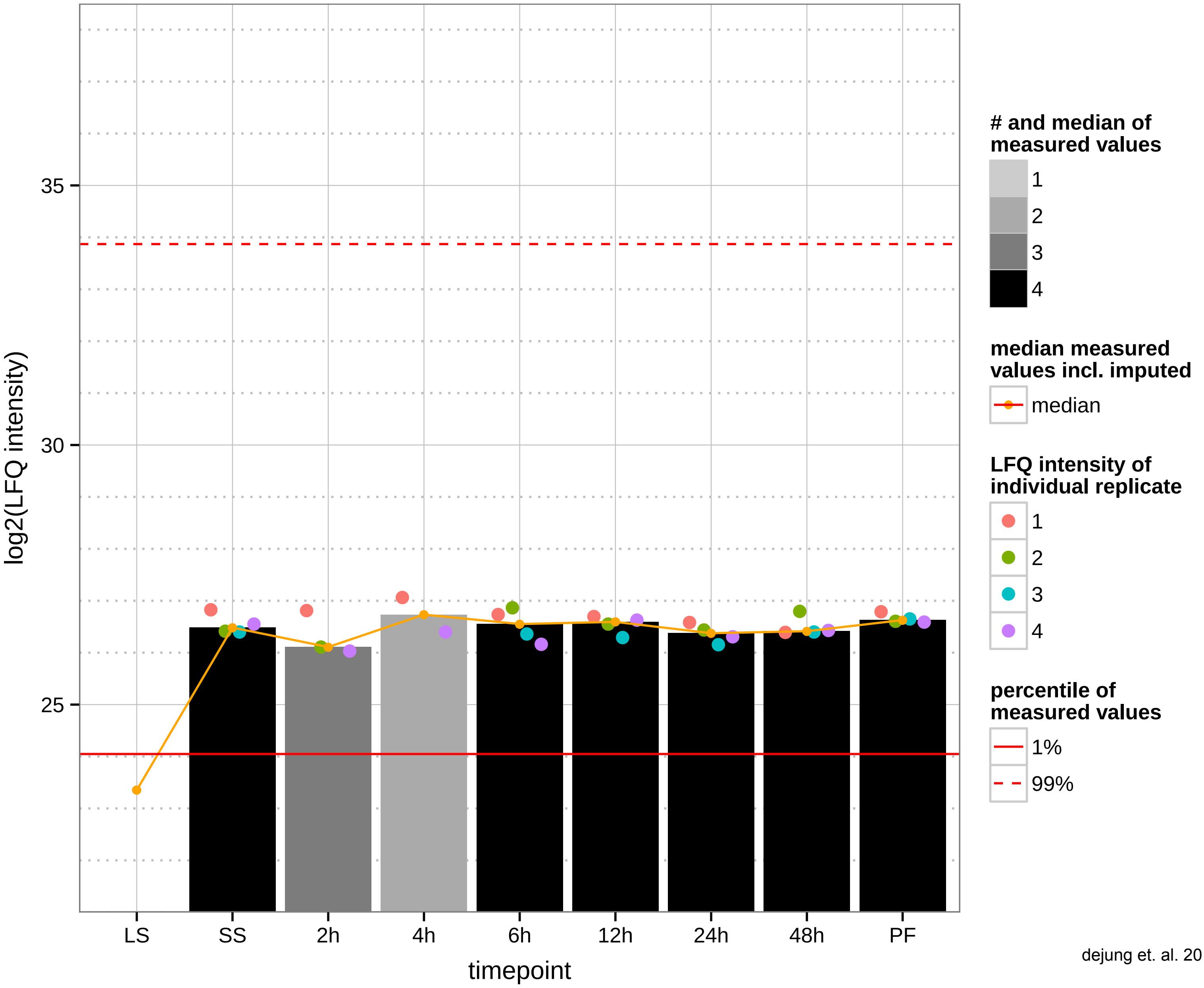
phosphoglycerate kinase, putative
Tb927.11.2380
AGOF: phosphoglycerate kinase activity
AGOC: integral to membrane
AGOP: glycolysis
PGOF: phosphoglycerate kinase activity
PGOC: null
PGOP: glycolysis





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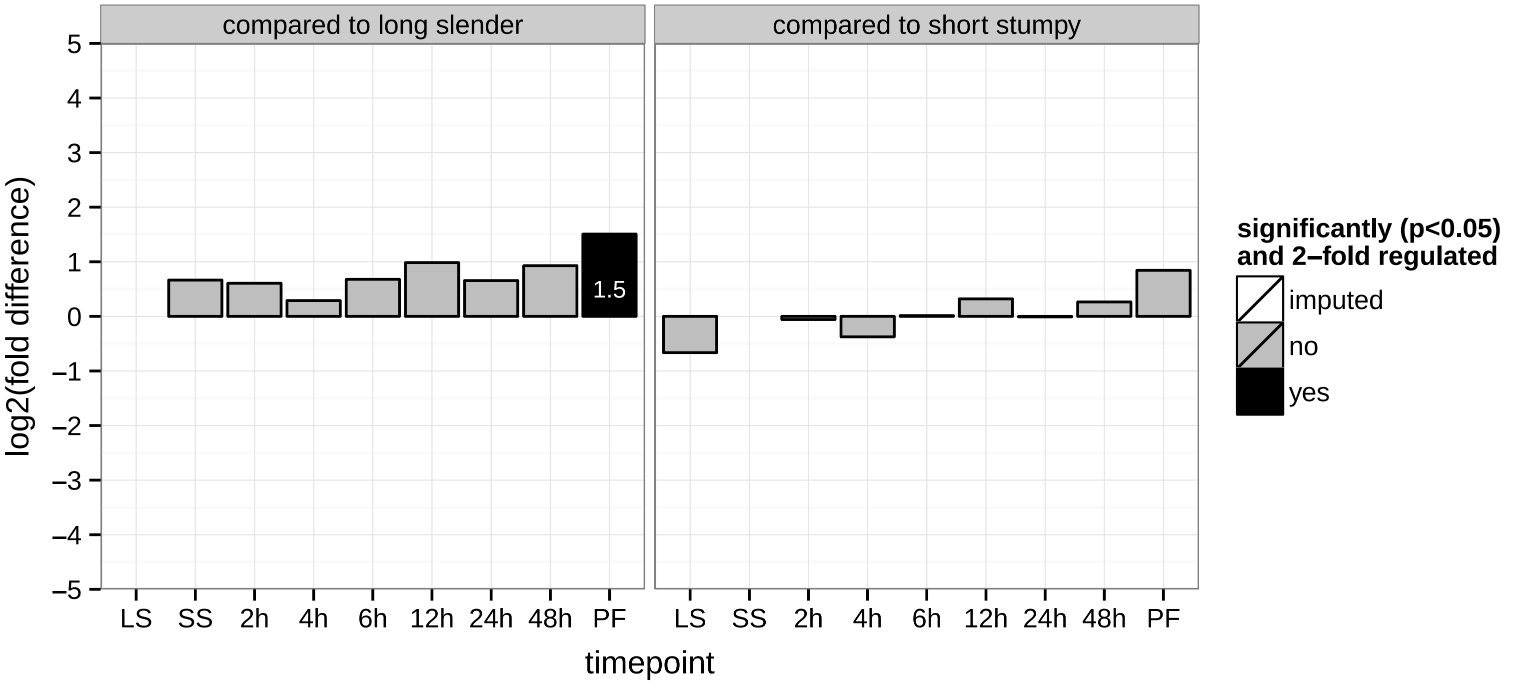
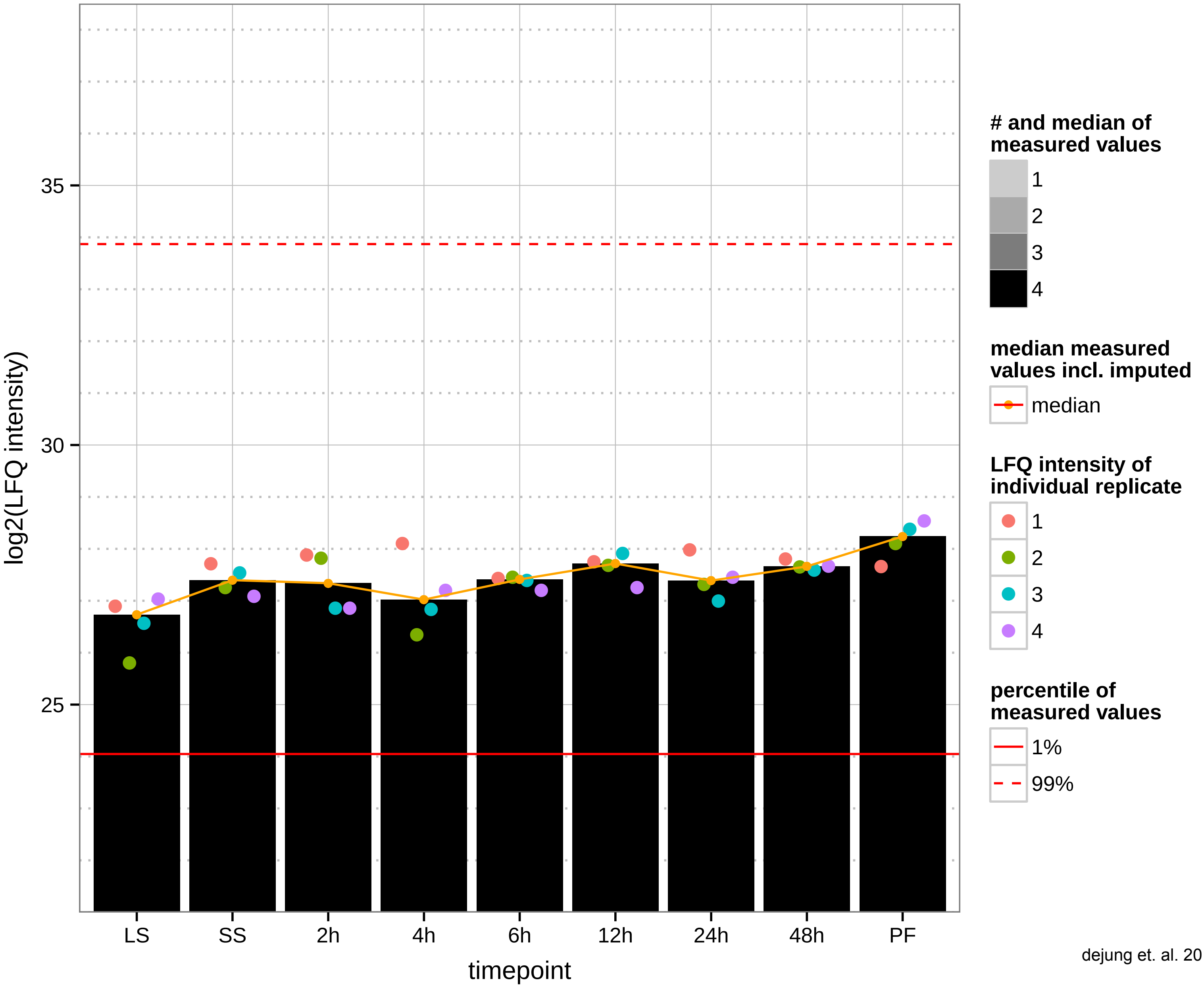
UDP−N−acetylglucosamine pyrophosphorylase, putative
Tb927.11.2520
AGOF: nucleotidyltransferase activity
AGOC: null
AGOP: UDP−glucose metabolic process
PGOF: nucleotidyltransferase activity
PGOC: null
PGOP: metabolic process





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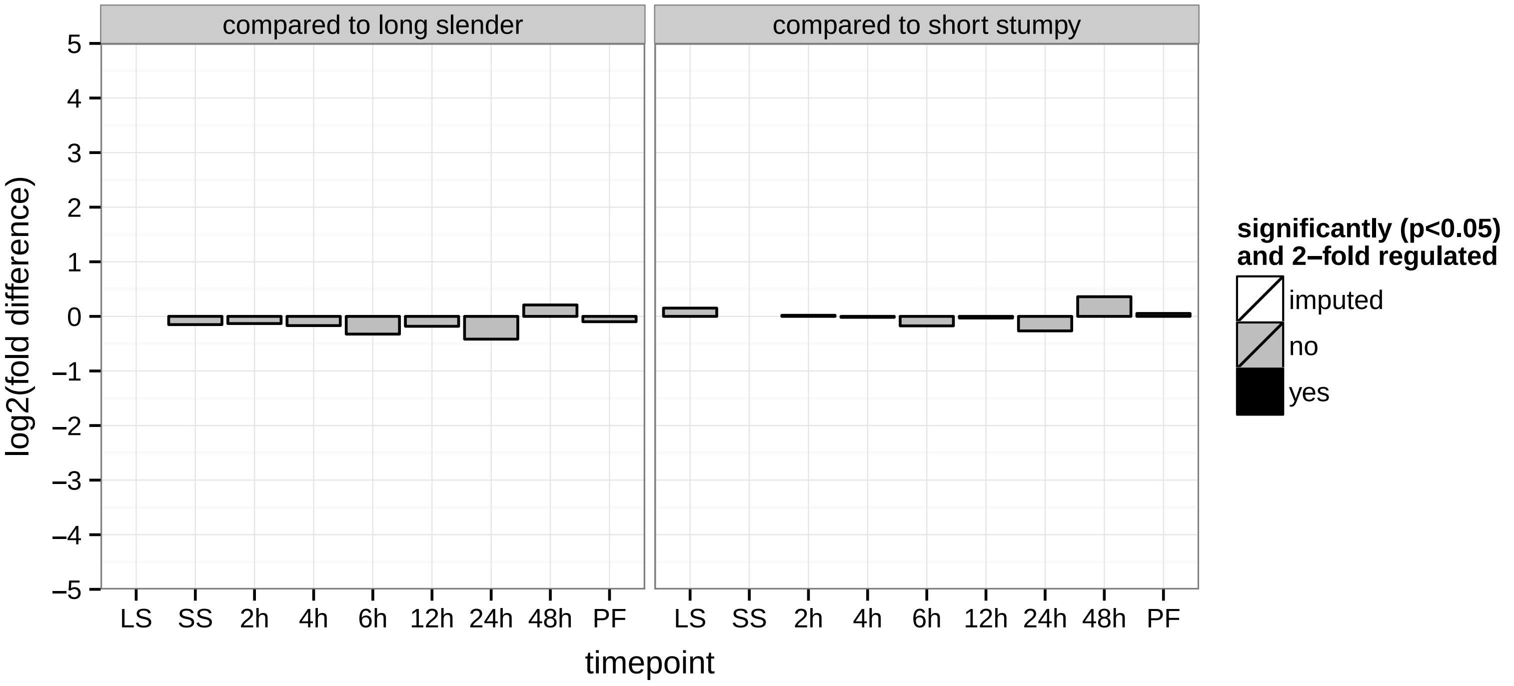
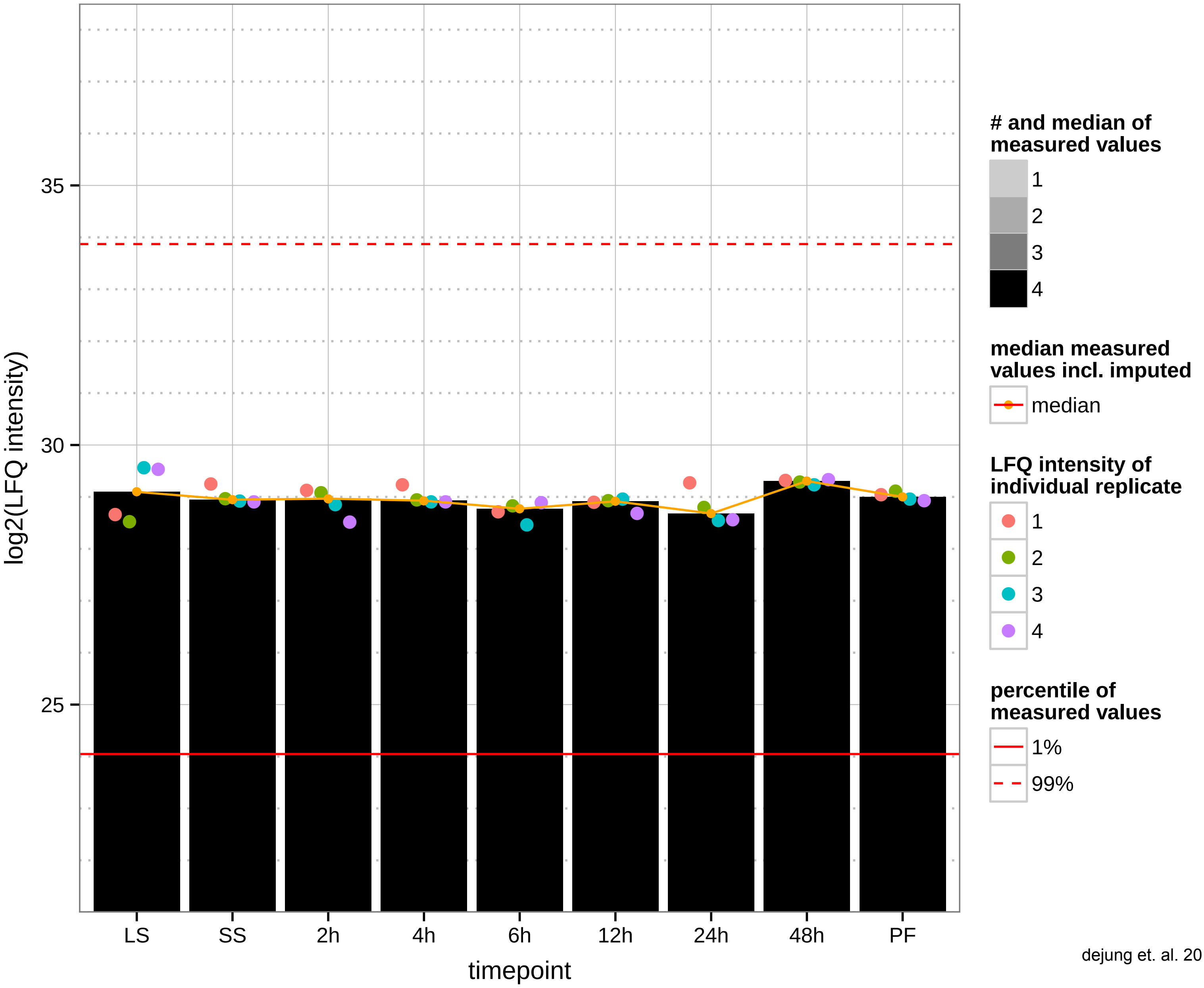
hypothetical protein, conserved
Tb927.11.2540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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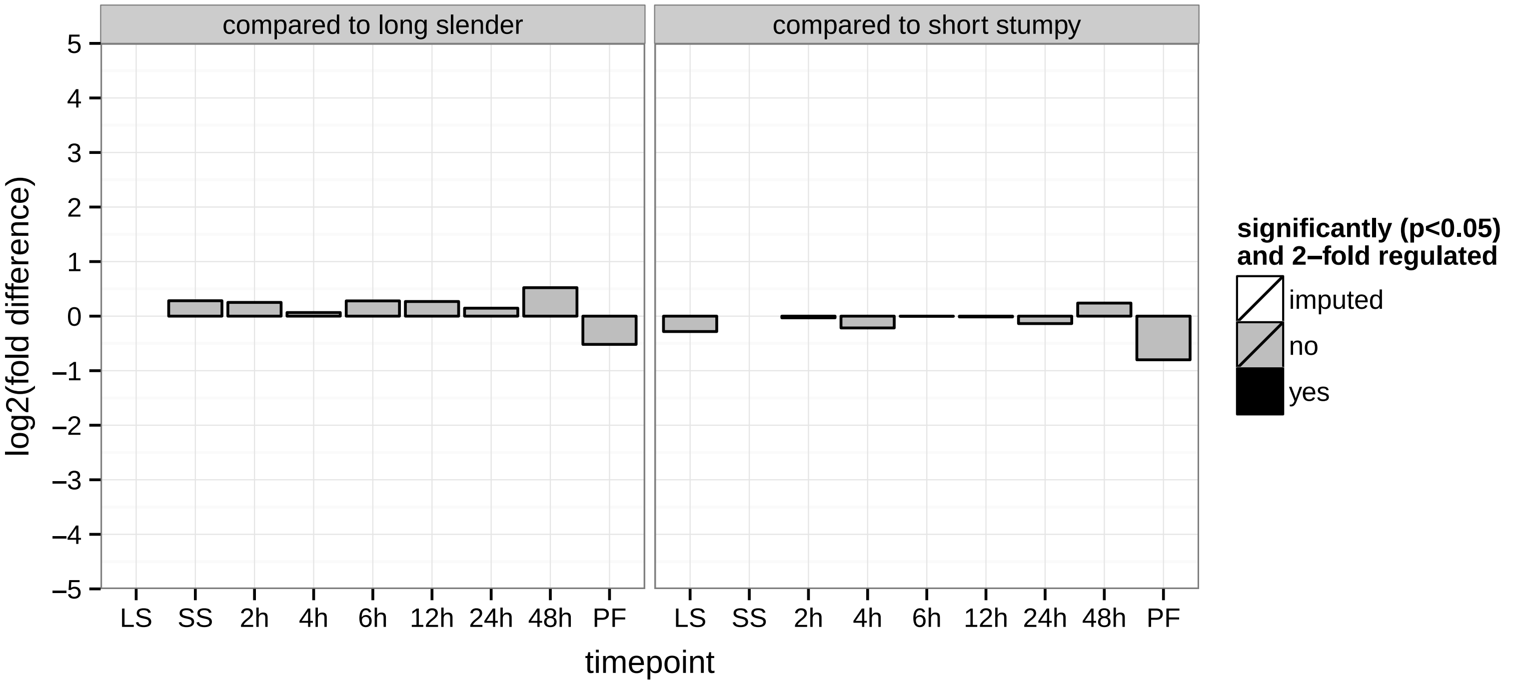
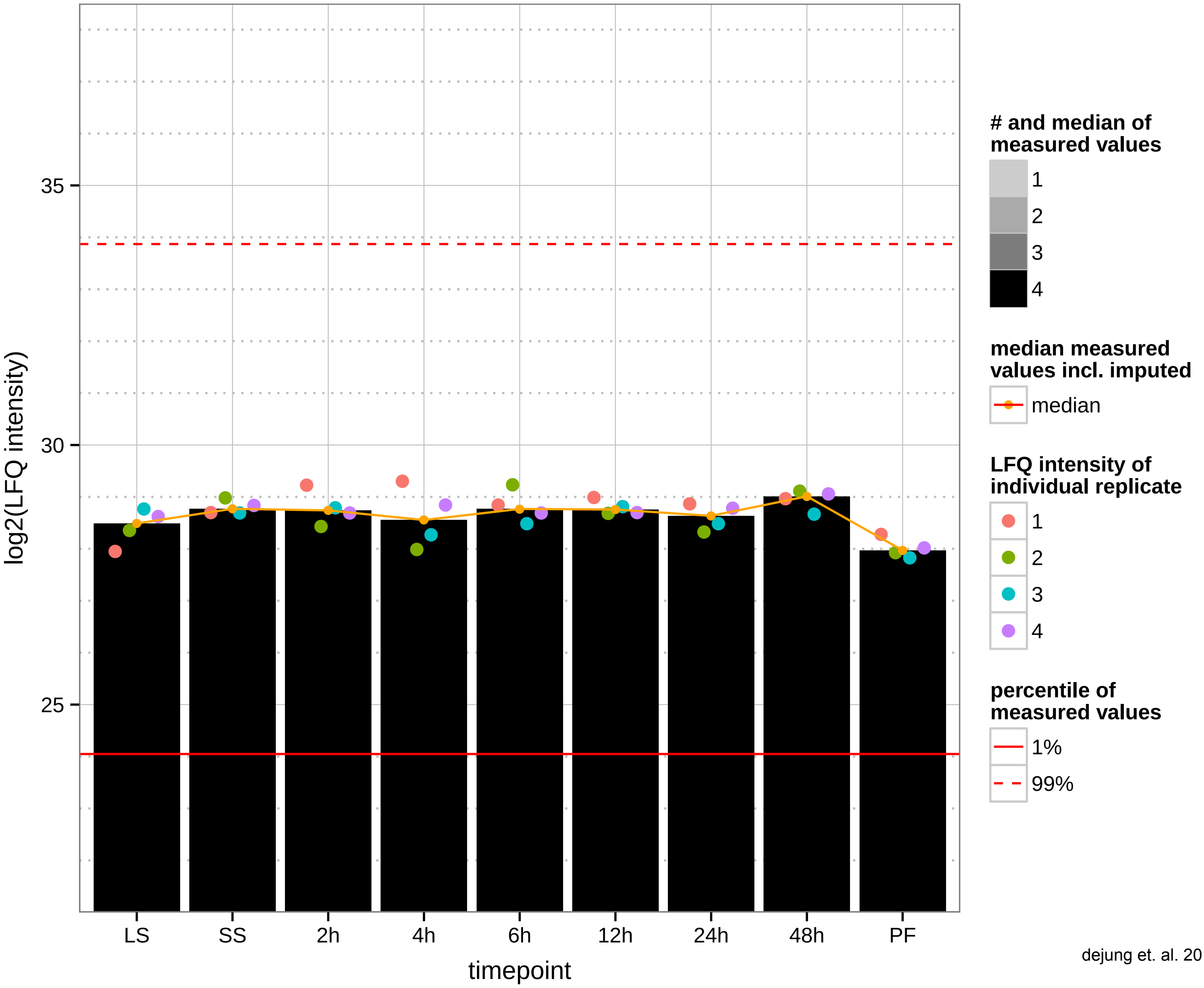
hypothetical protein, conserved
Tb927.11.2570
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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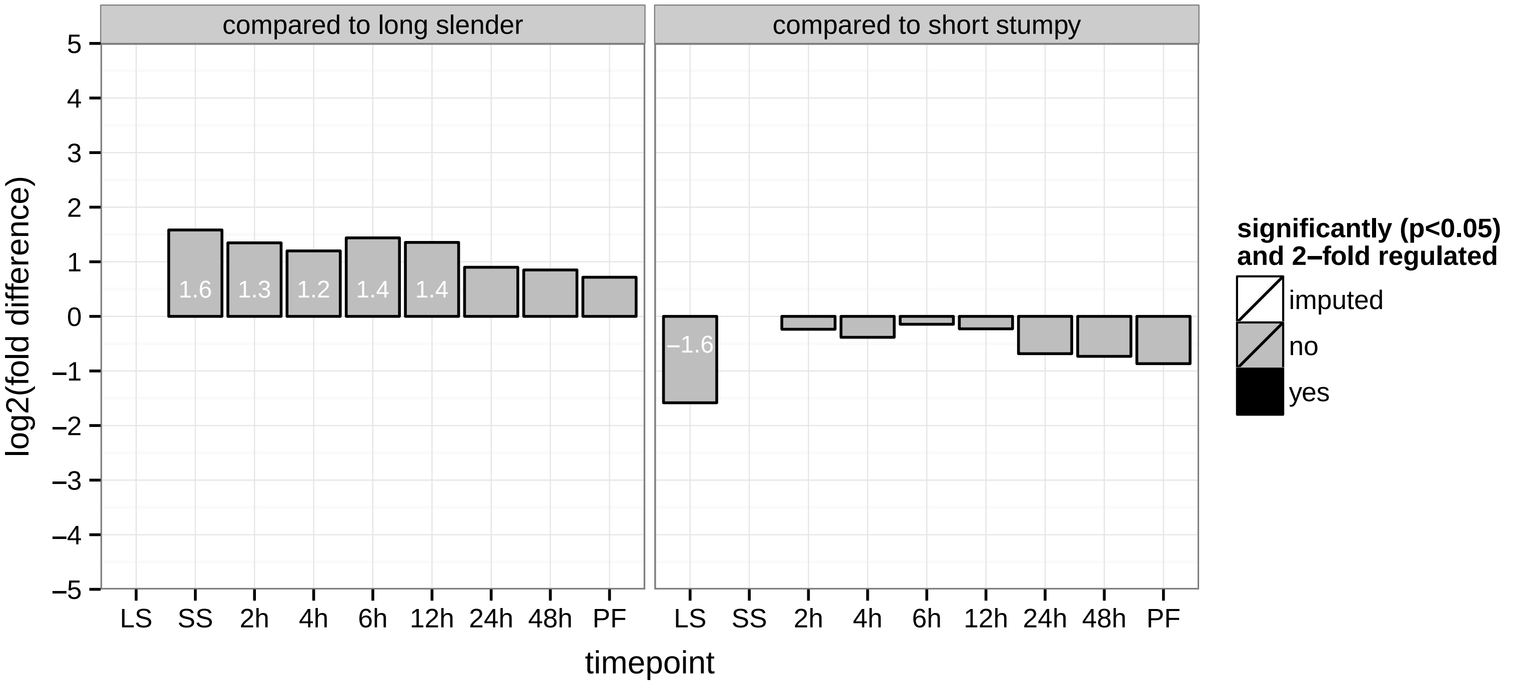
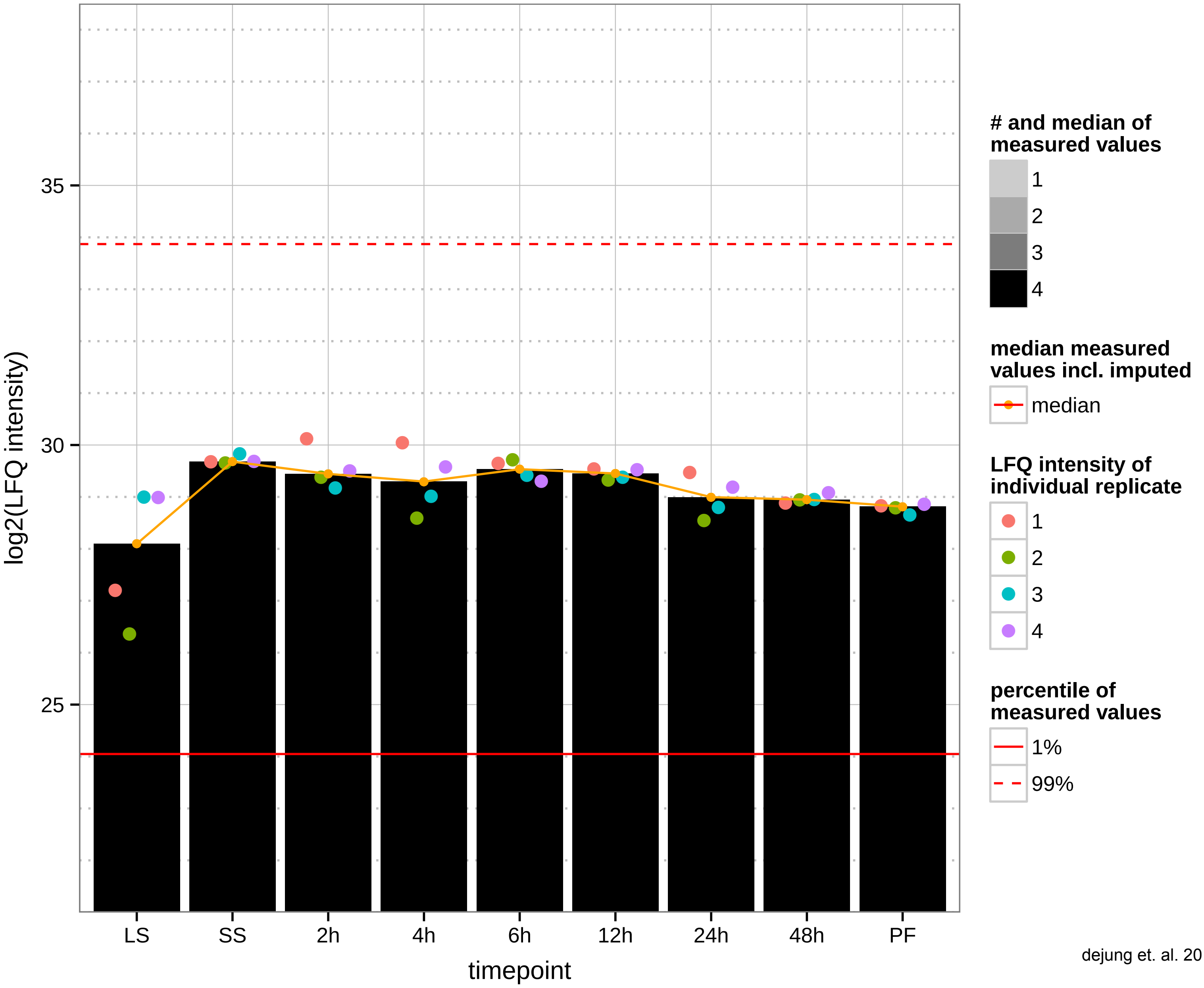
predicted WD40 repeat protein (PIFTF6)
Tb927.11.260
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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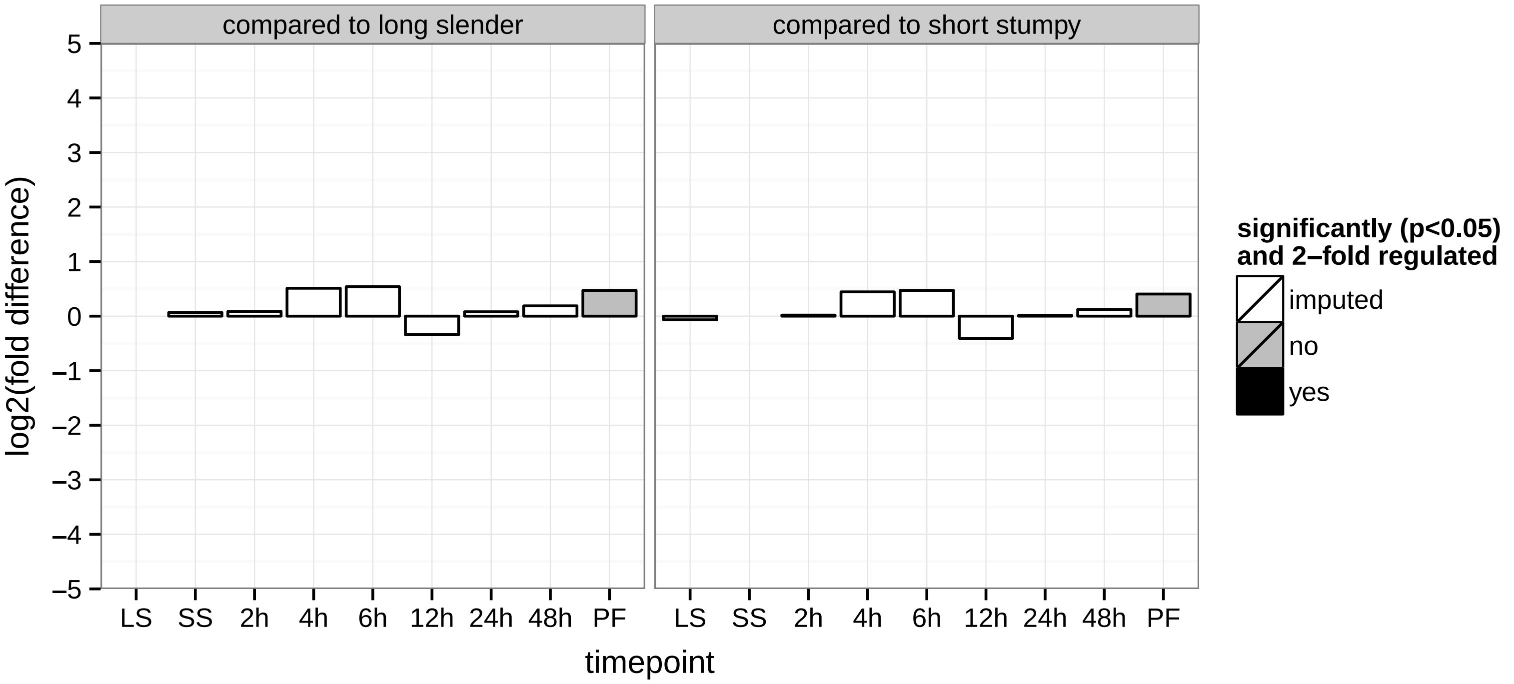
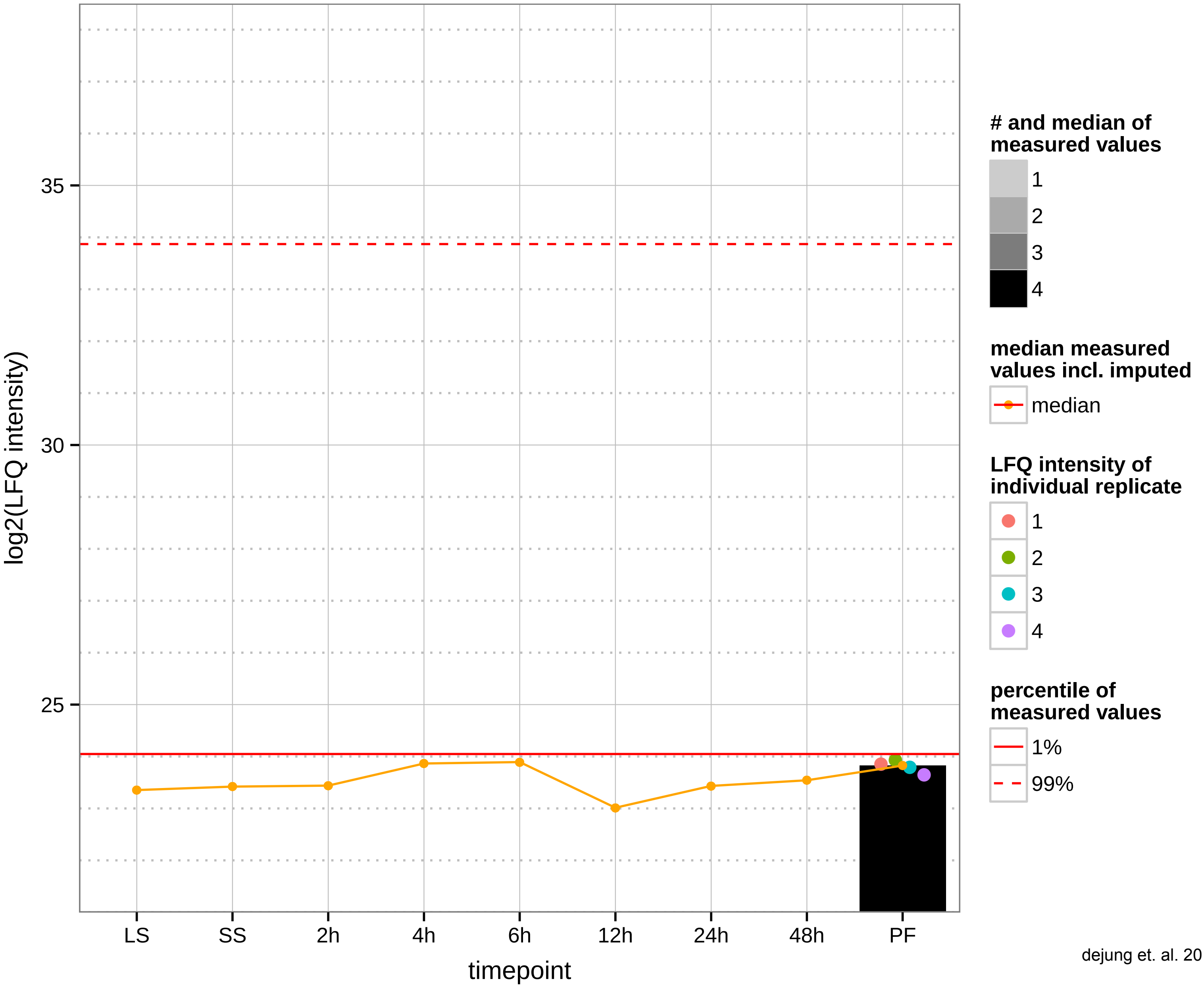
hypothetical protein, conserved
Tb927.11.2600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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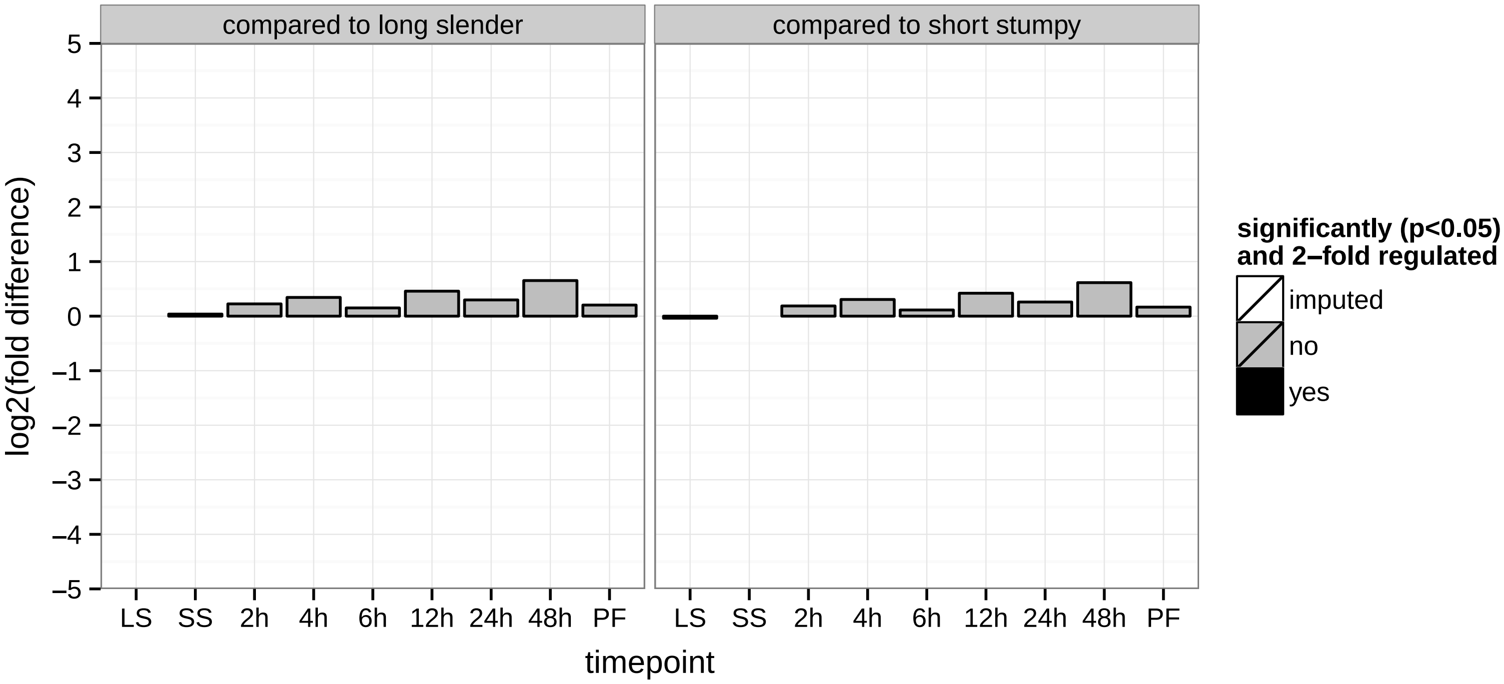
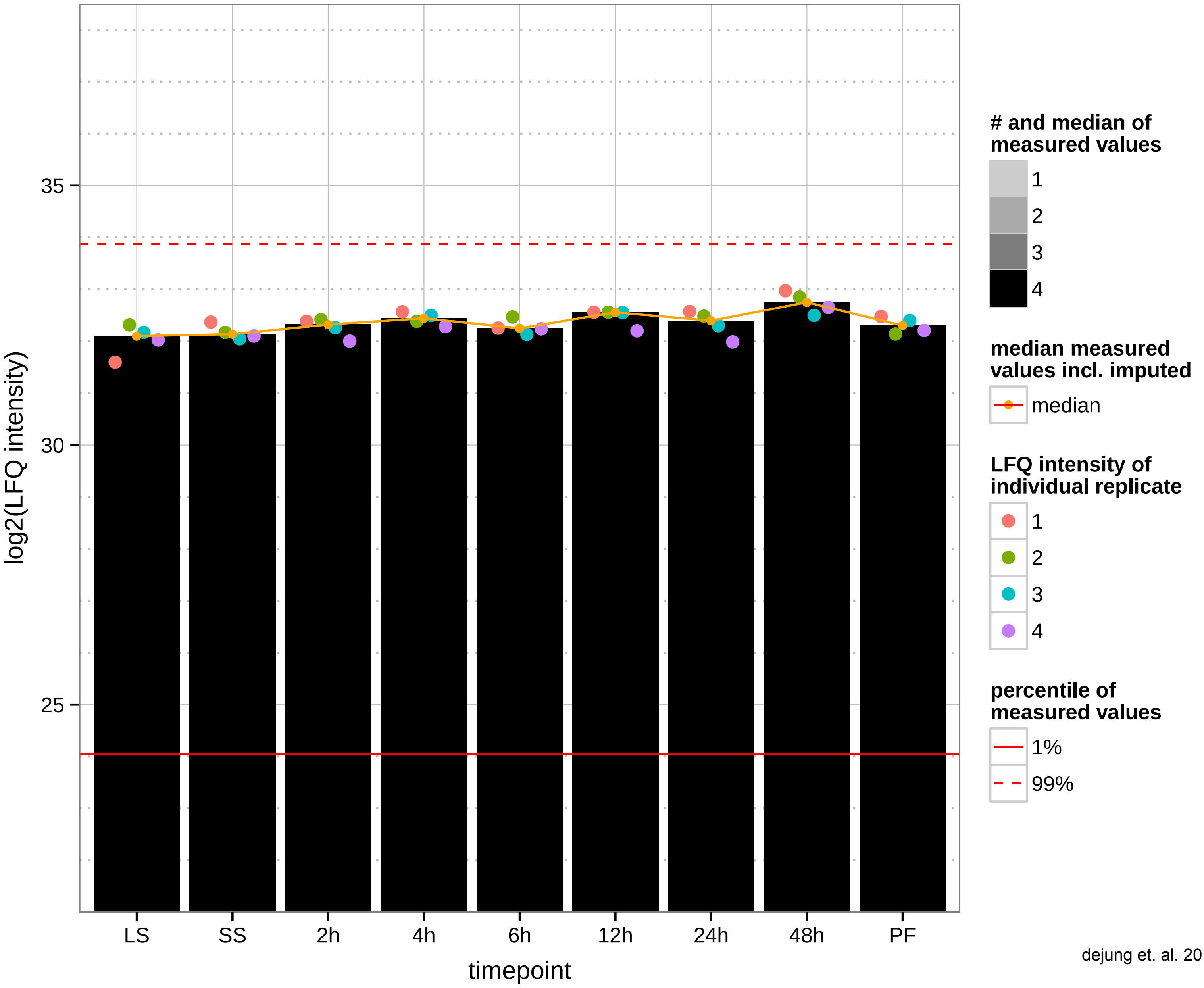
hypothetical protein, conserved
Tb927.11.2610
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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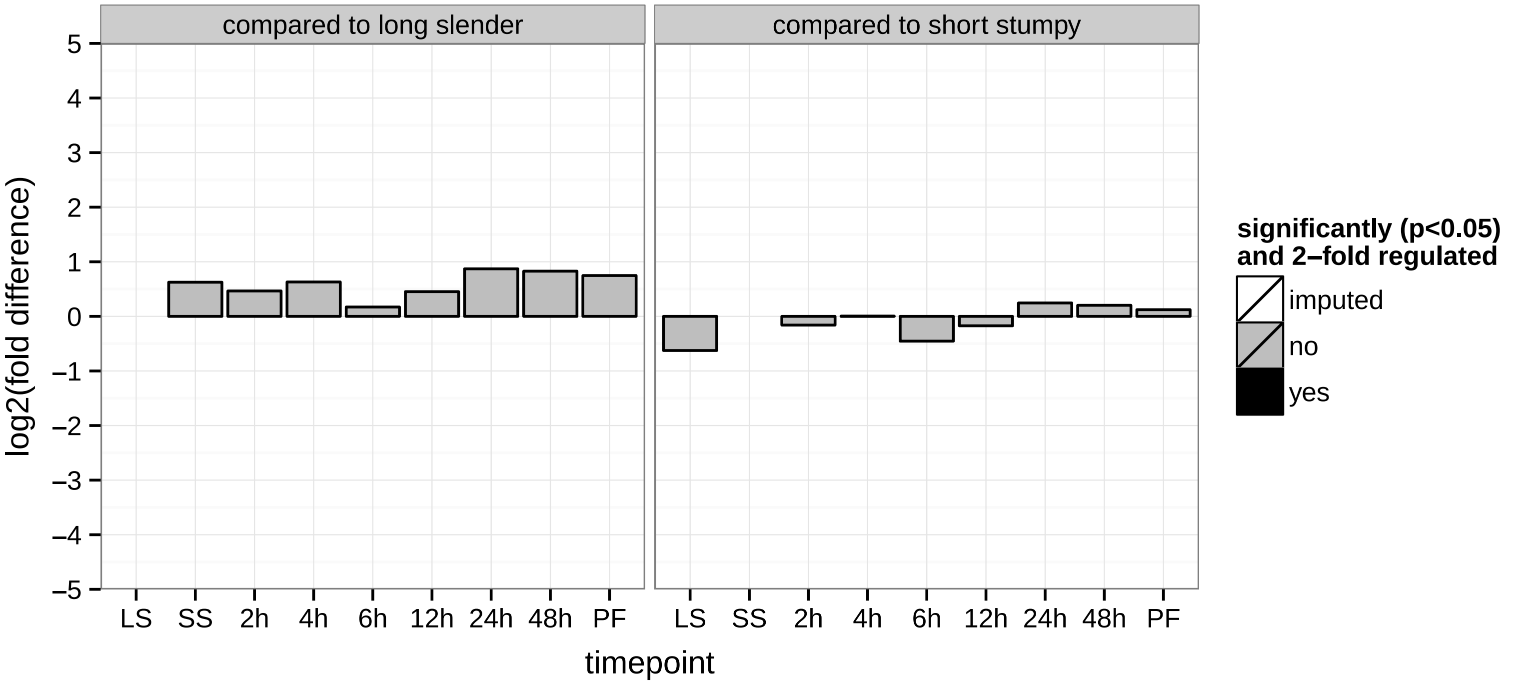
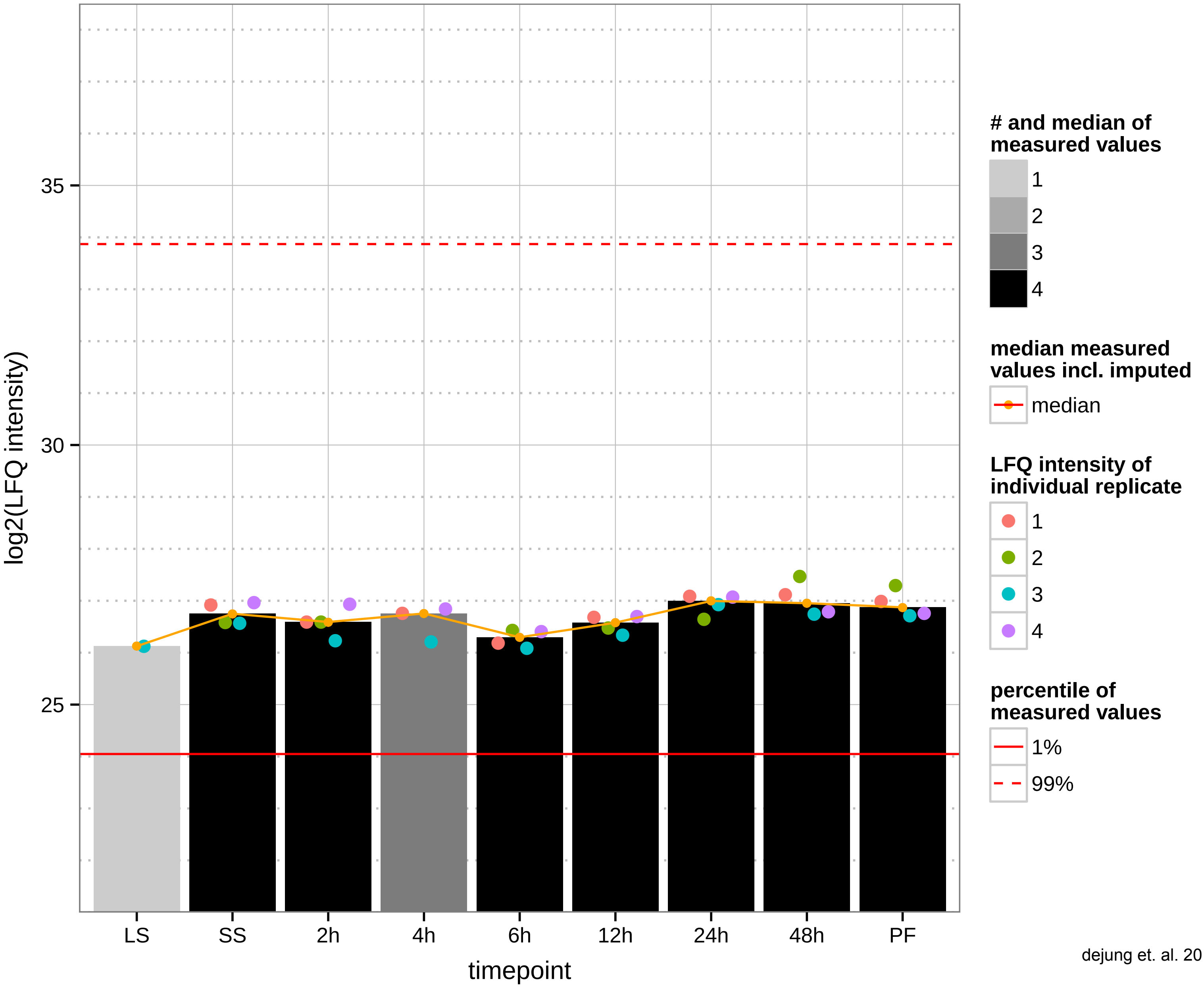
hypothetical protein, conserved
Tb927.11.2620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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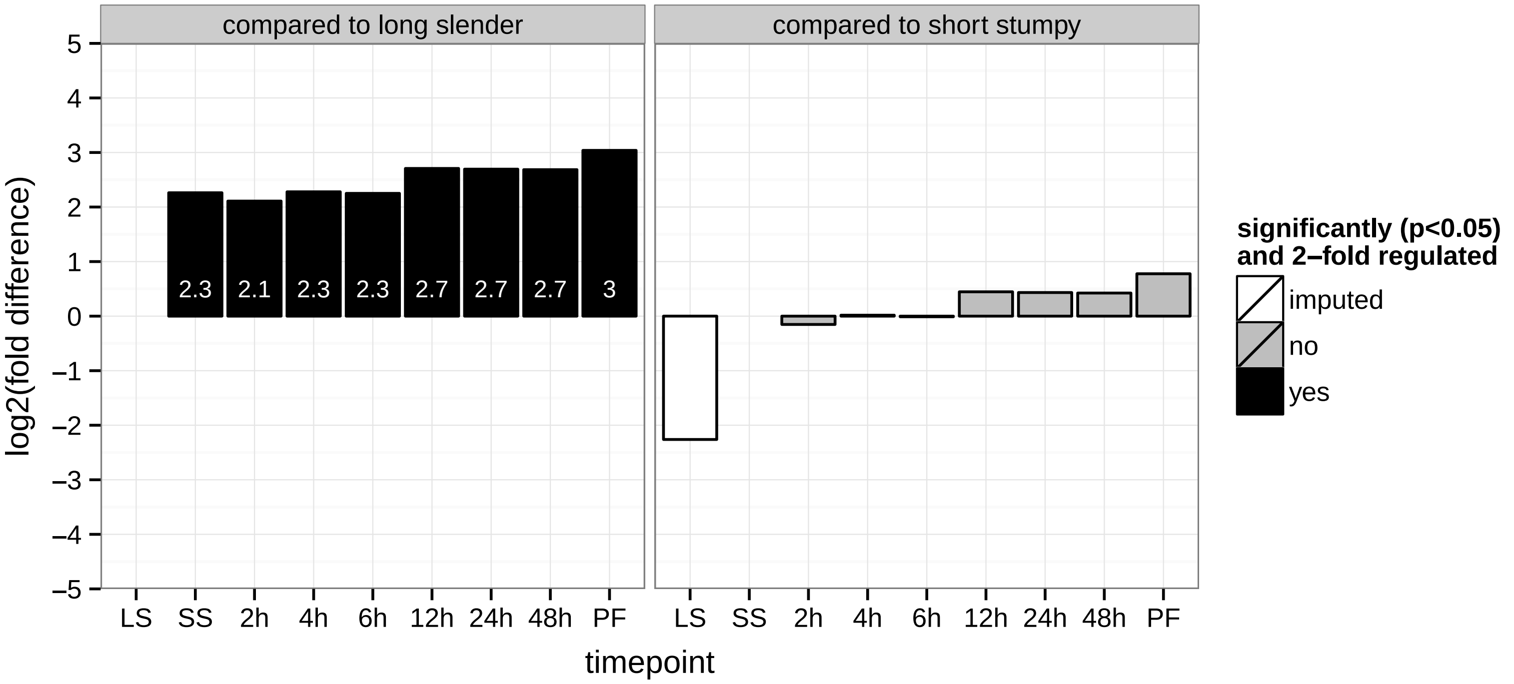
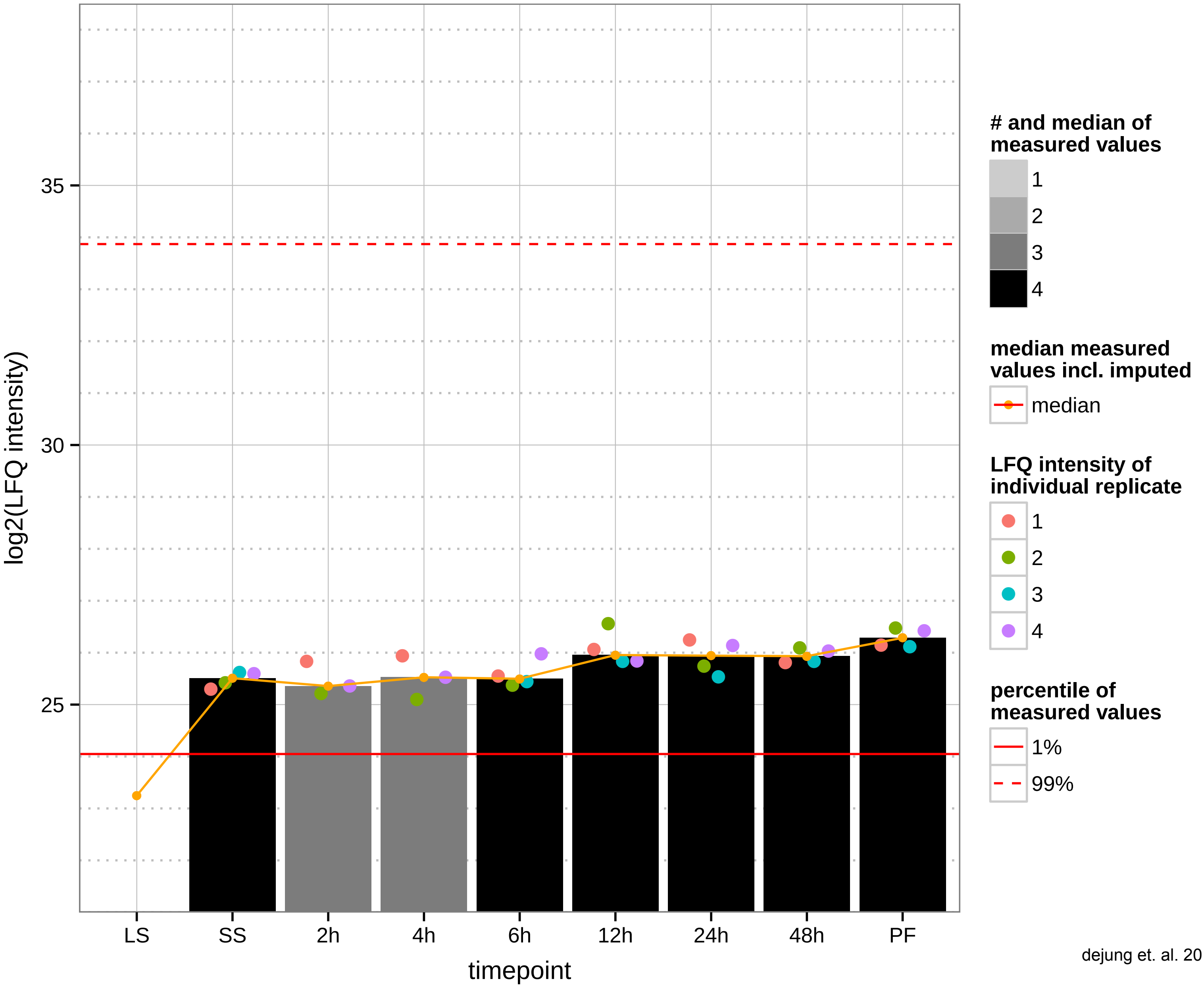
ras–like small GTPase, putative (TbNST)
Tb927.11.2640
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: null
PGOF: GTP binding
PGOC: null
PGOP: null





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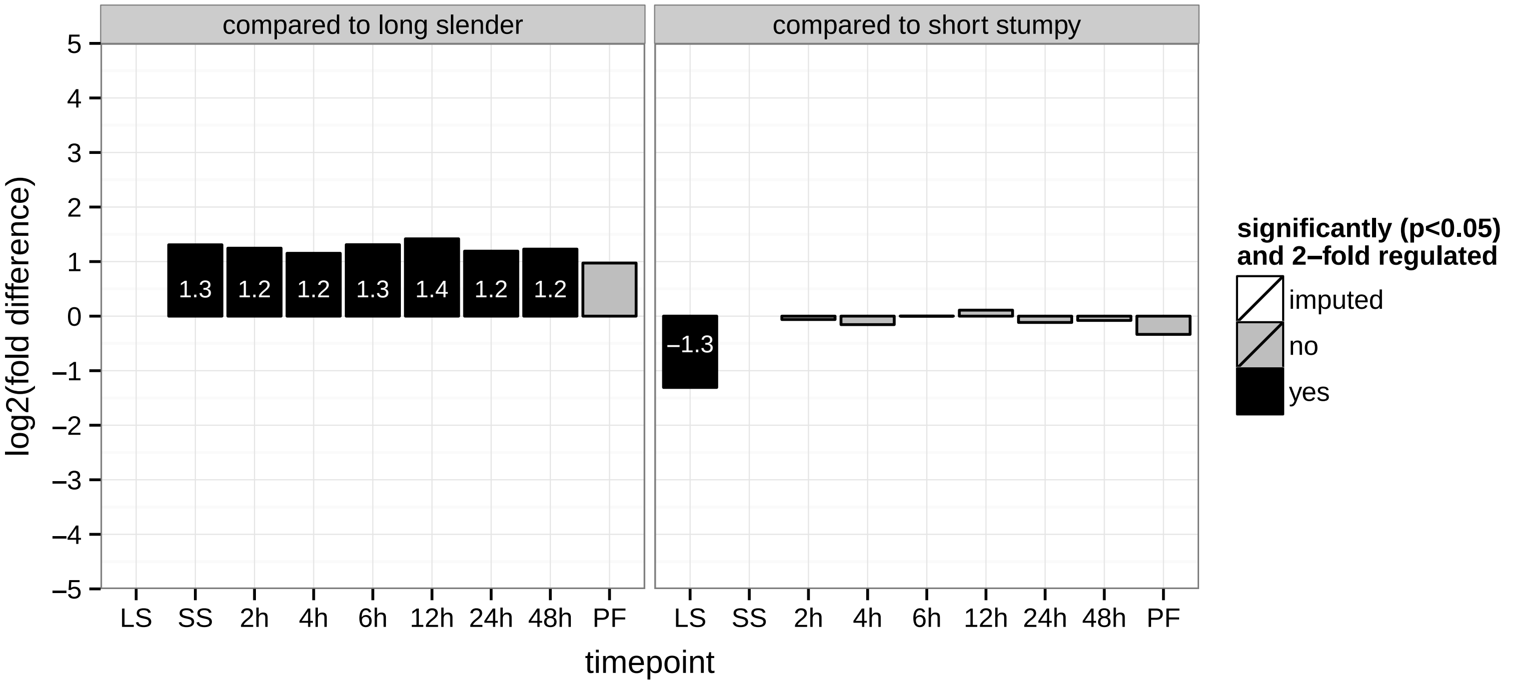
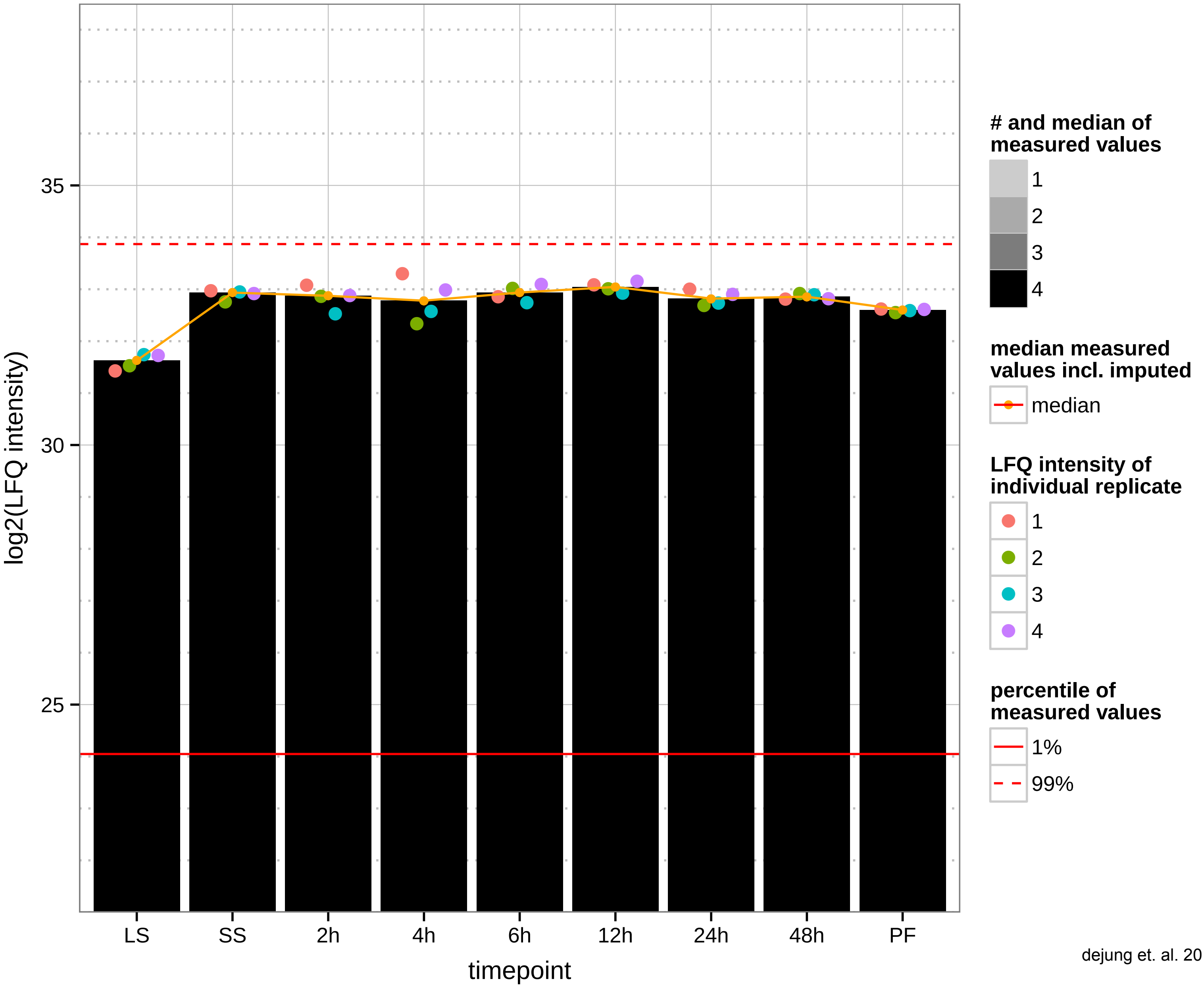
heat shock protein 84, putative
Tb927.11.2650
AGOF: ATP binding, ATPase activity, coupled, unfolded protein binding
AGOC: mitochondrion
AGOP: protein folding, response to stress
PGOF: ATP binding, unfolded protein binding
PGOC: null
PGOP: protein folding, response to stress





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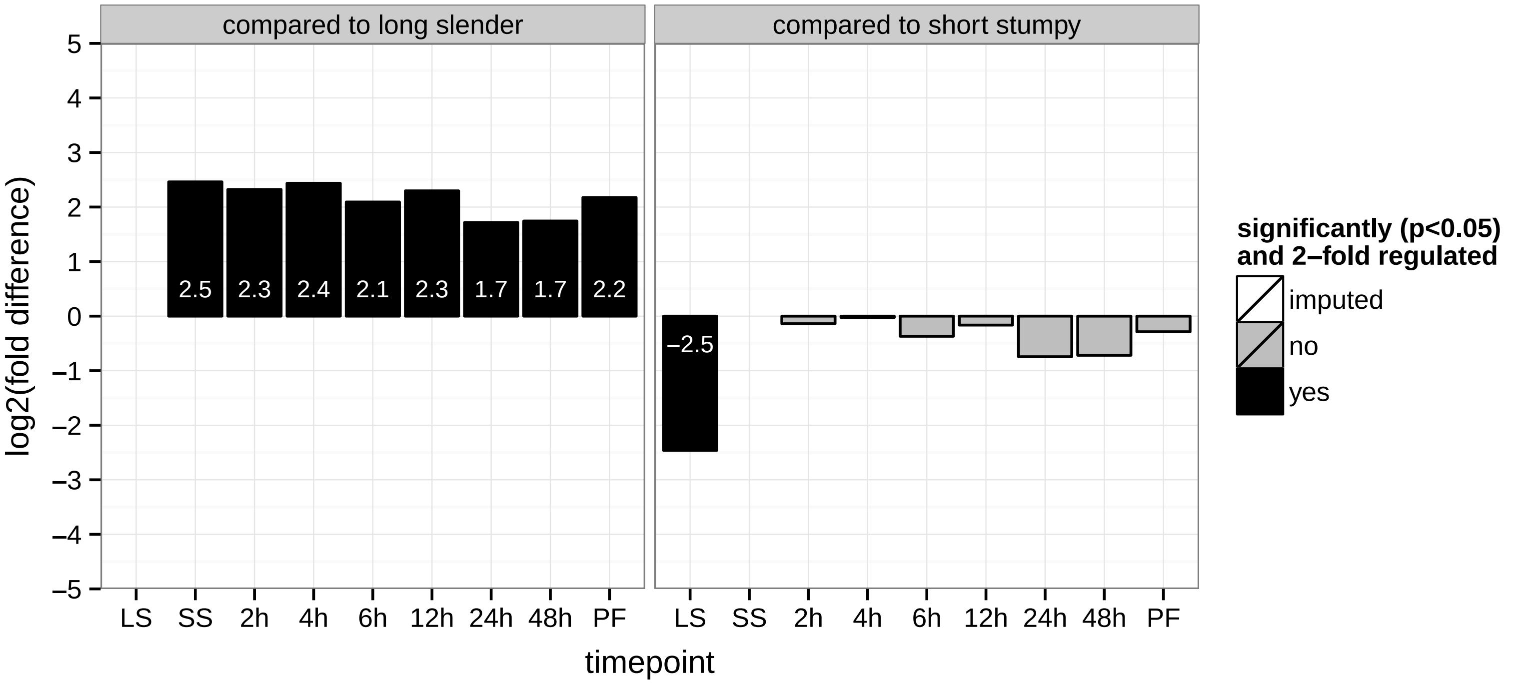
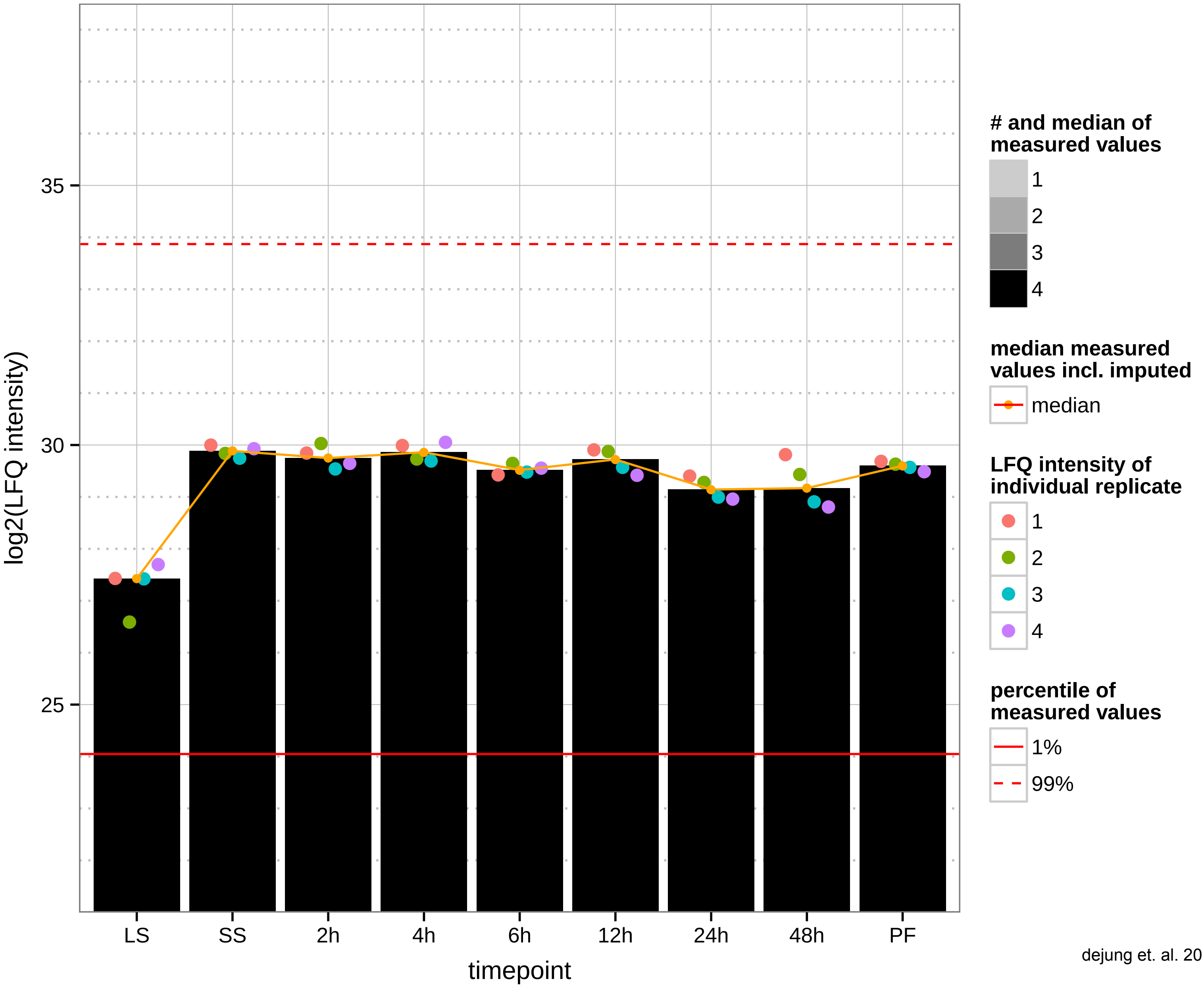
Nucleoporin (TbNup59)
Tb927.11.2670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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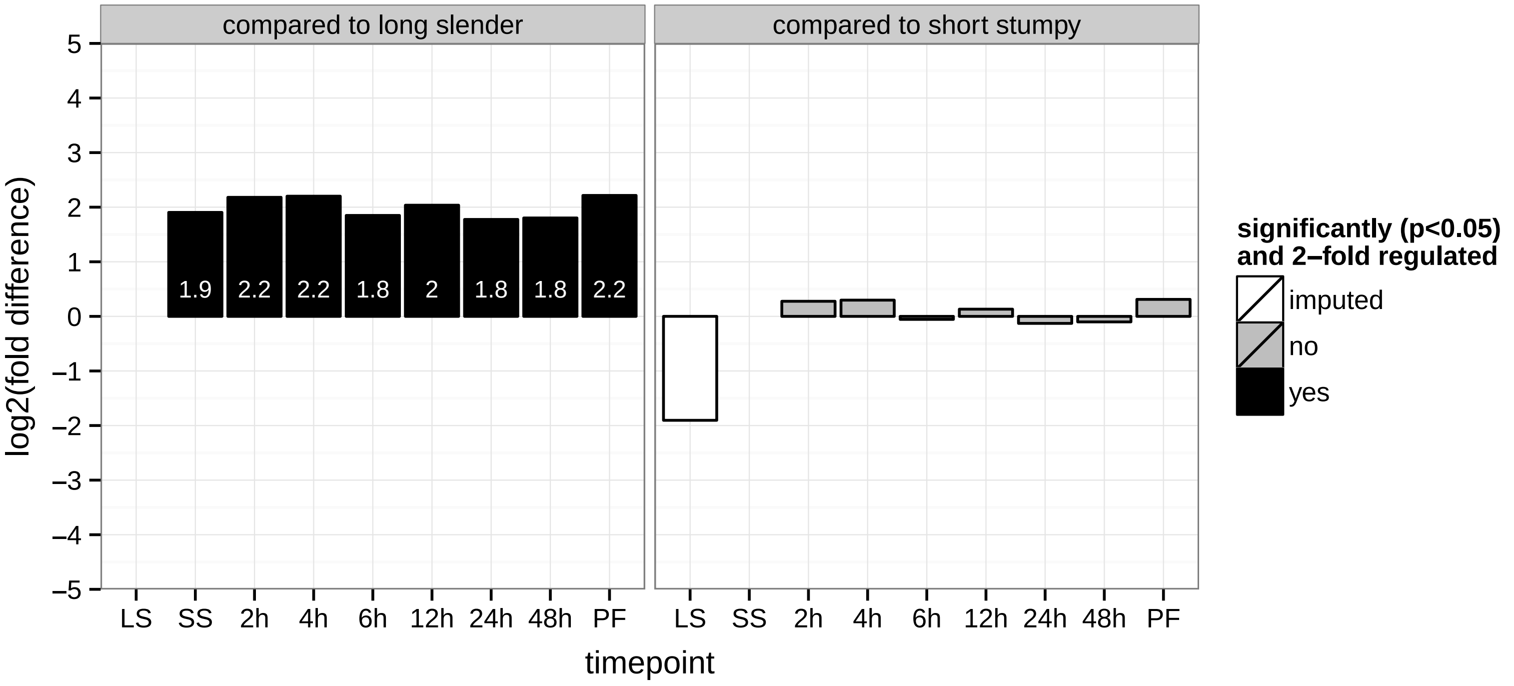
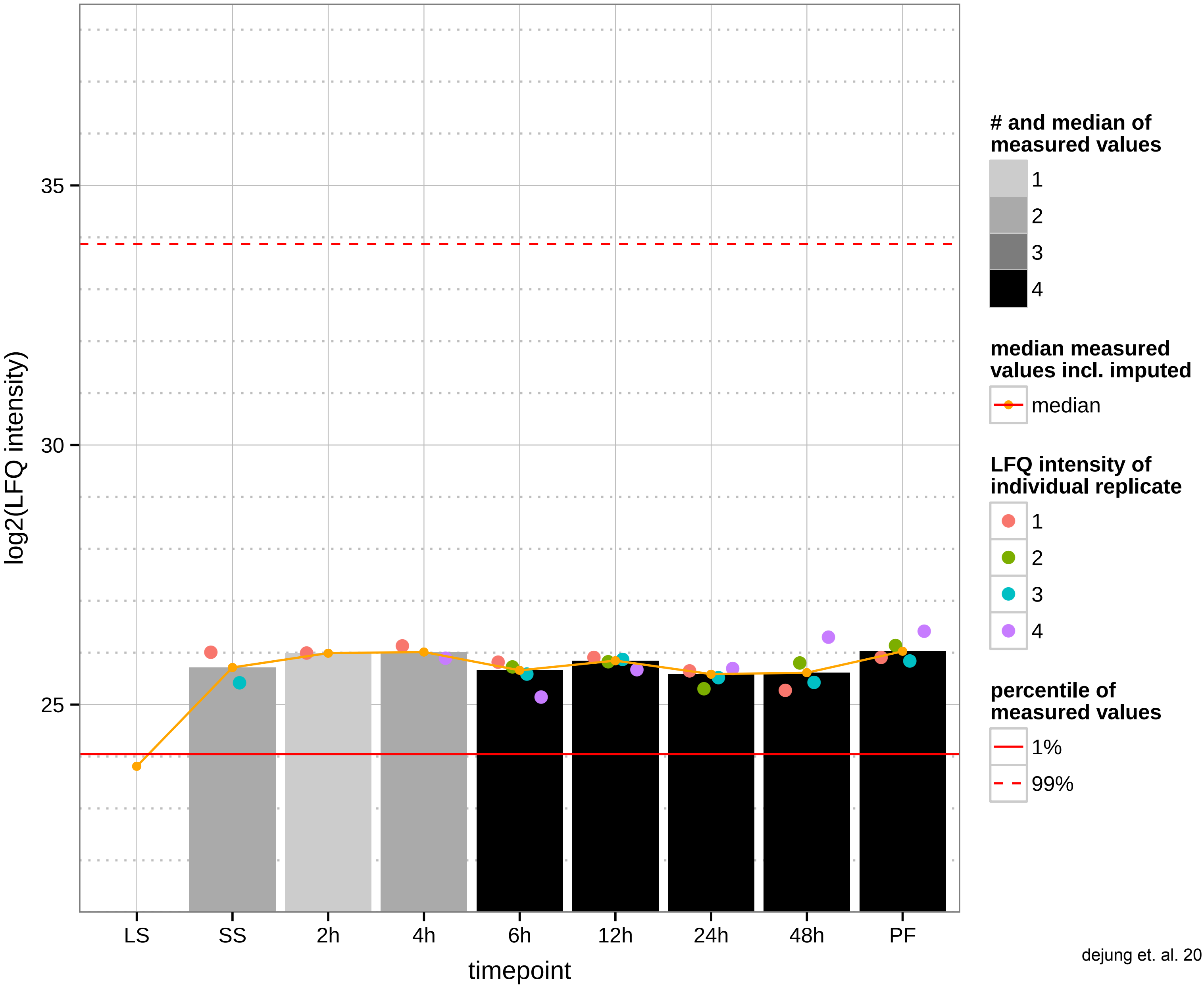
hypothetical protein, conserved
Tb927.11.2740
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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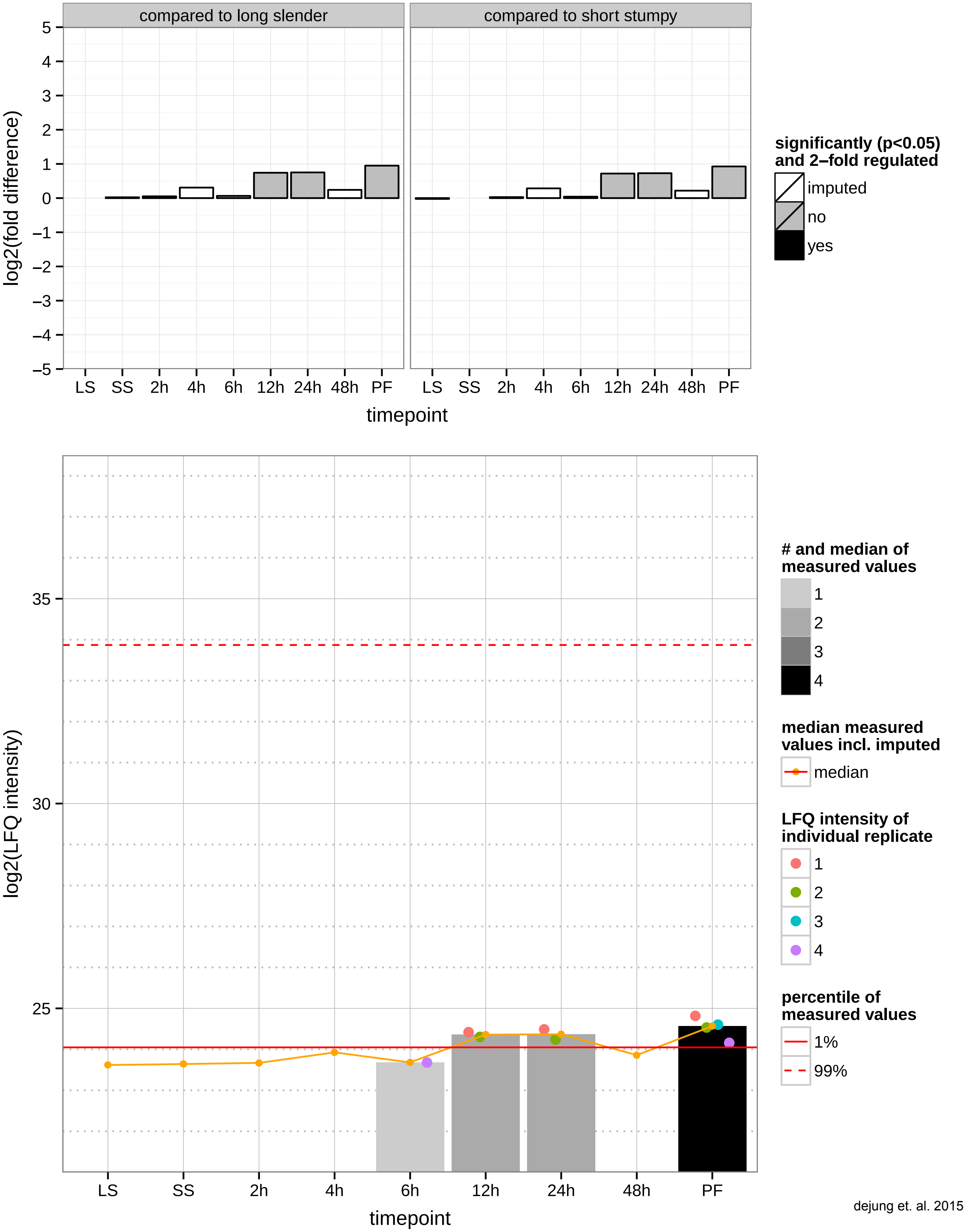
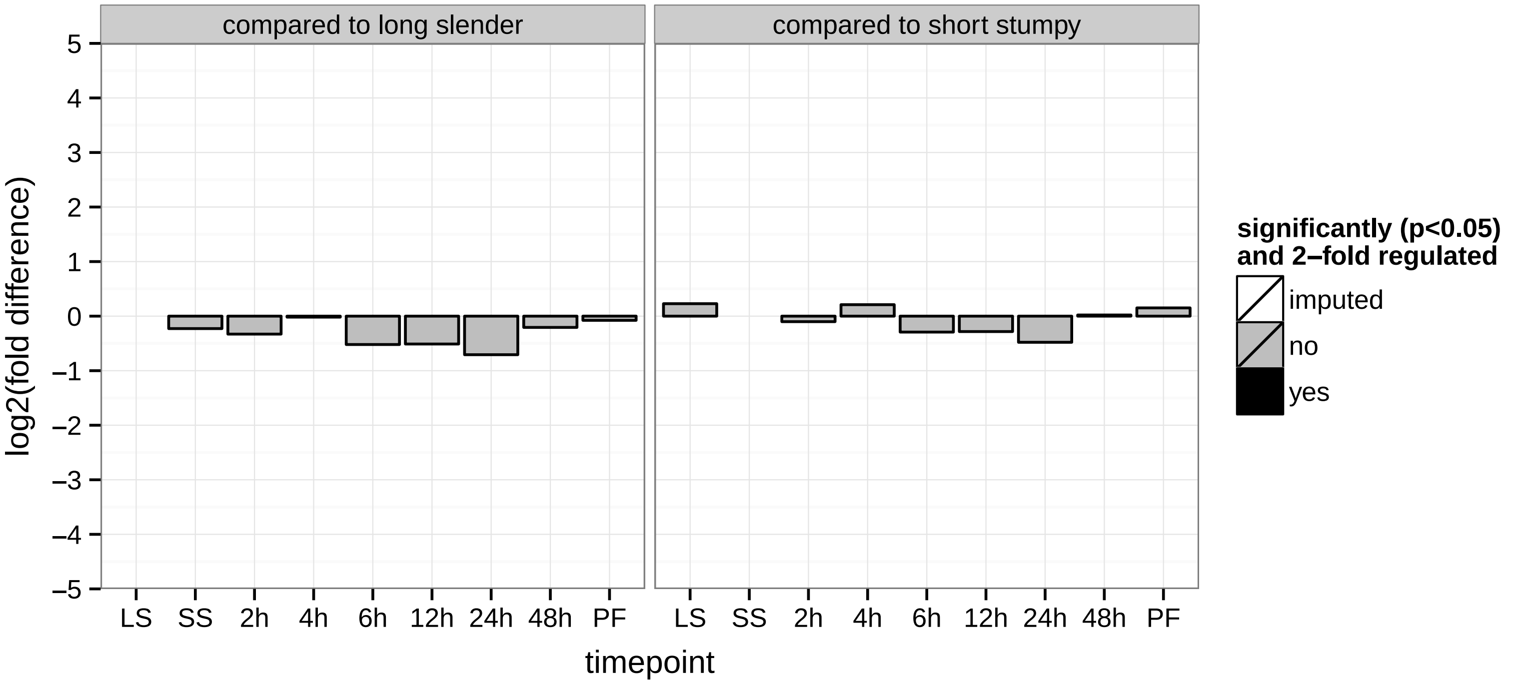
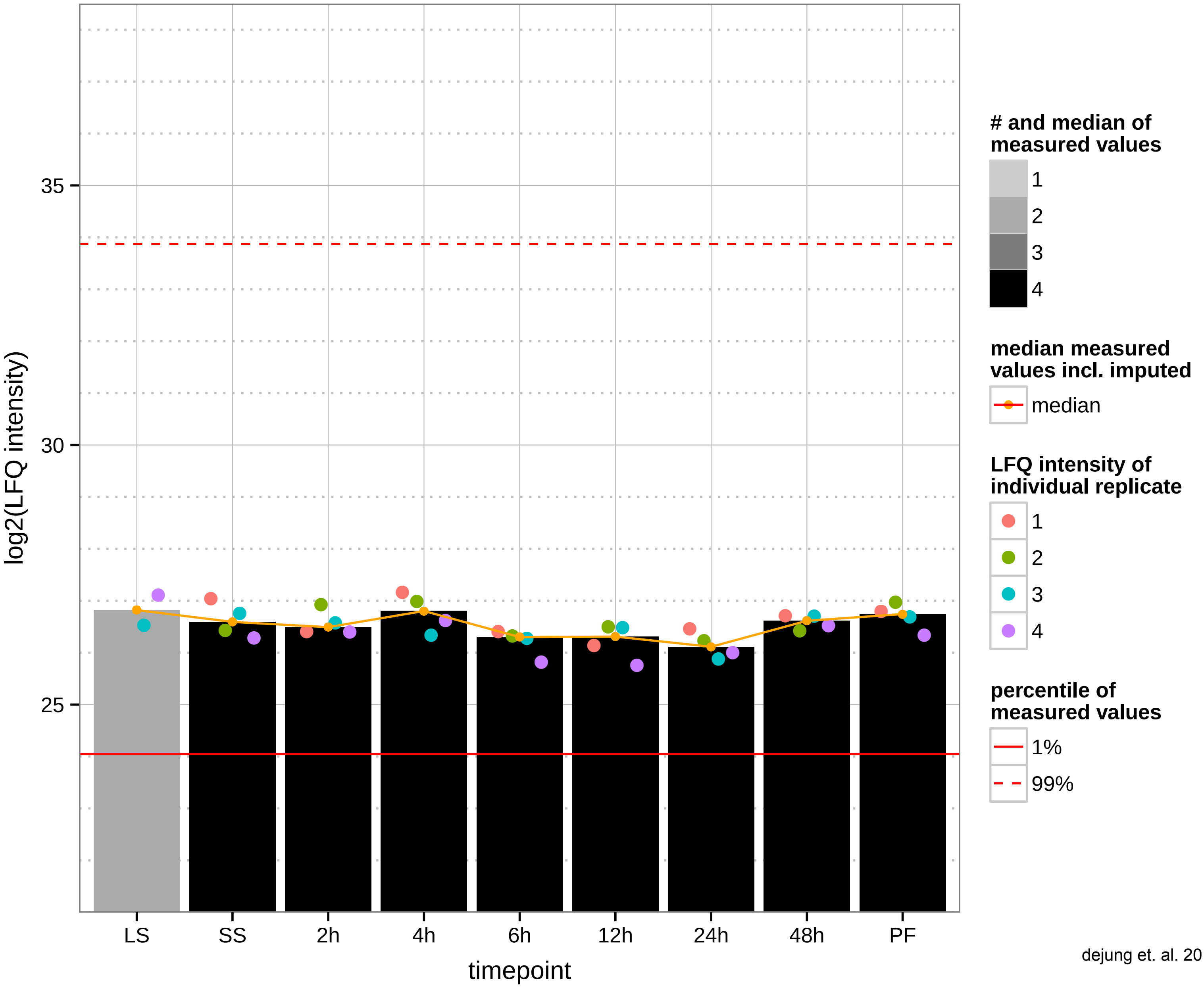
hypothetical protein, conserved
Tb927.11.2760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



hypothetical protein, conserved
Tb927.11.2770
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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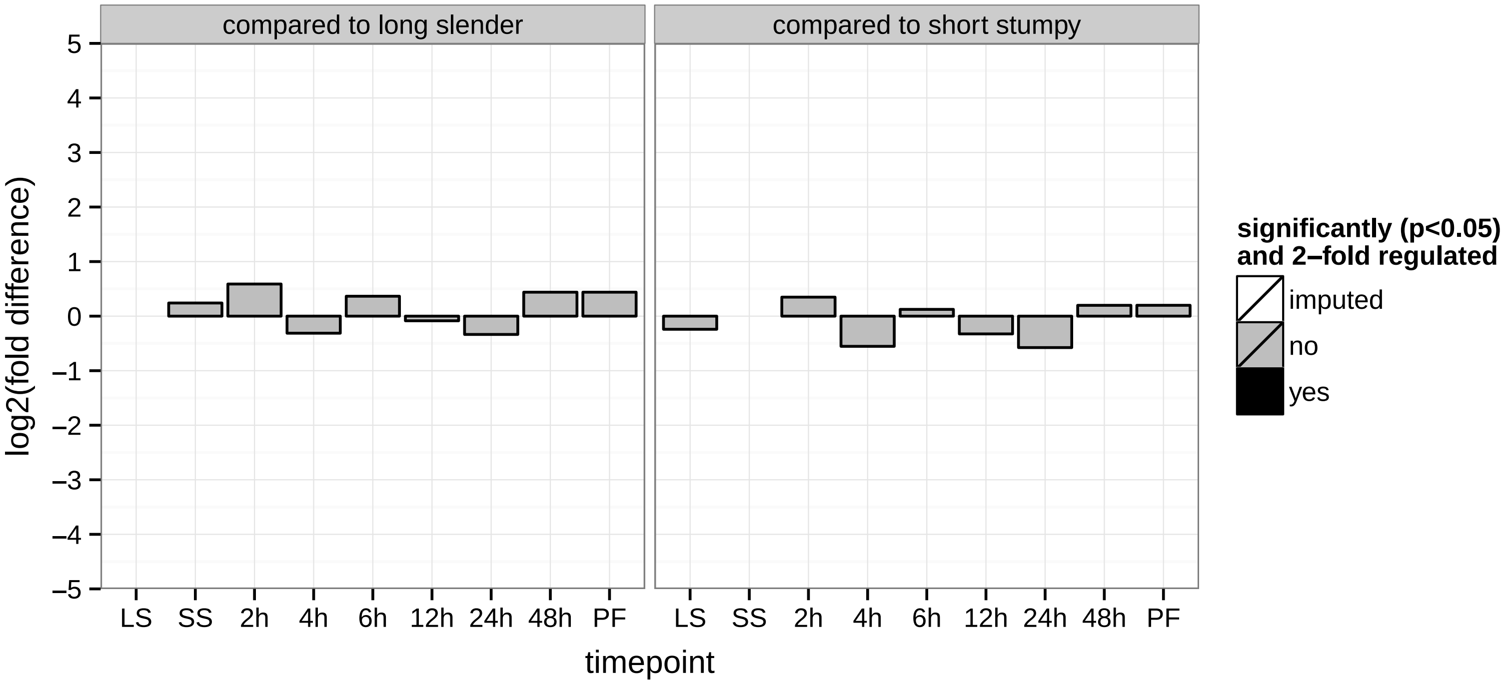
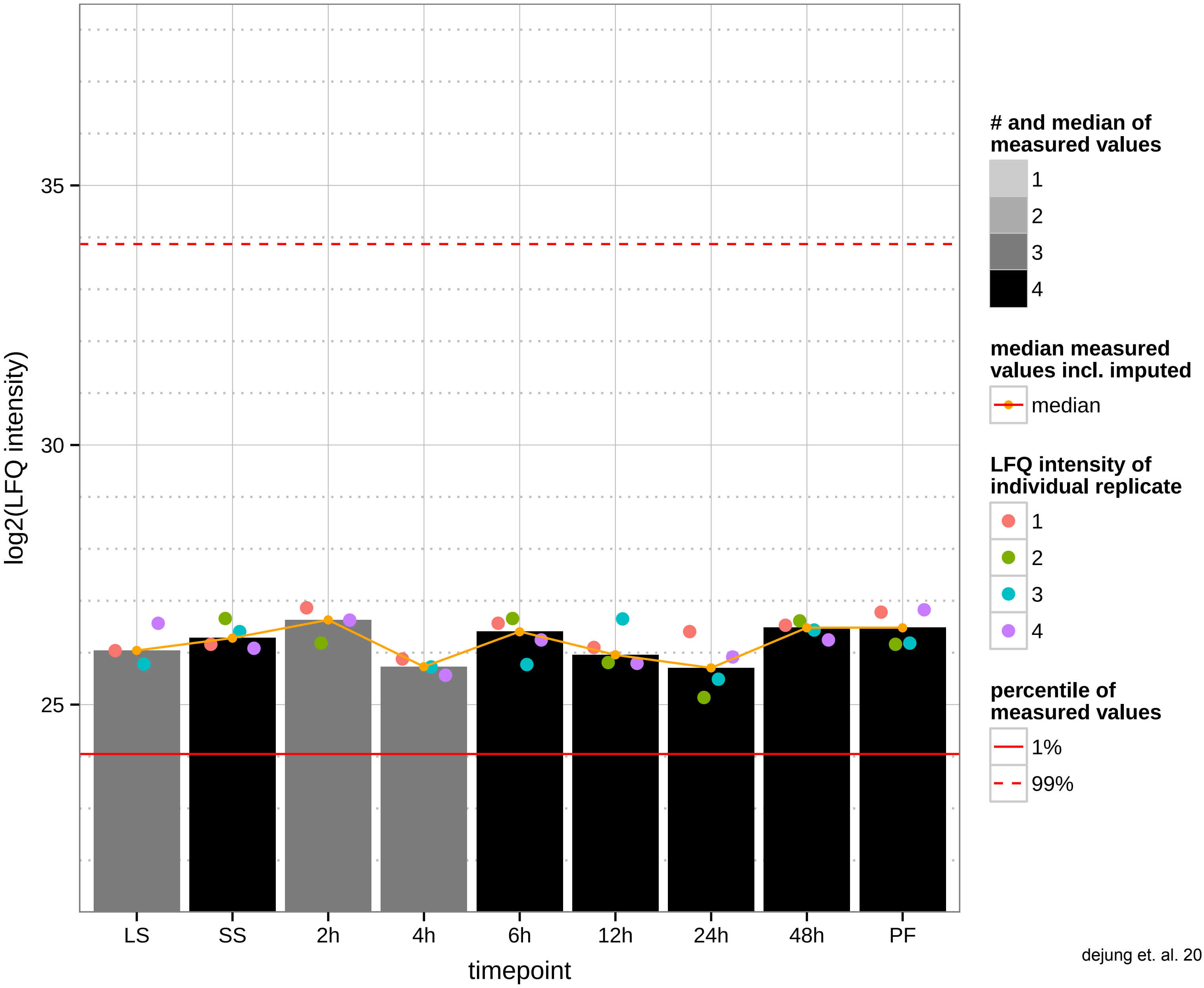
hypothetical protein, conserved
Tb927.11.2790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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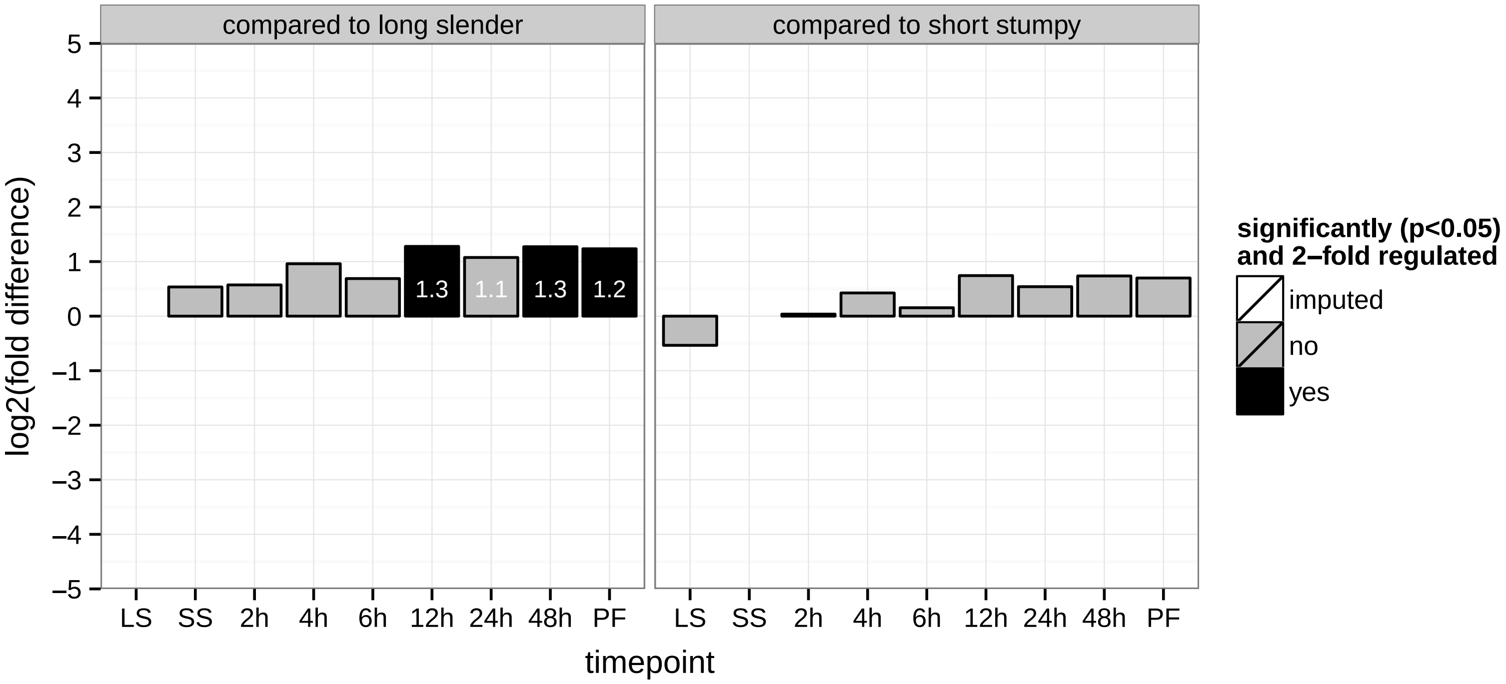
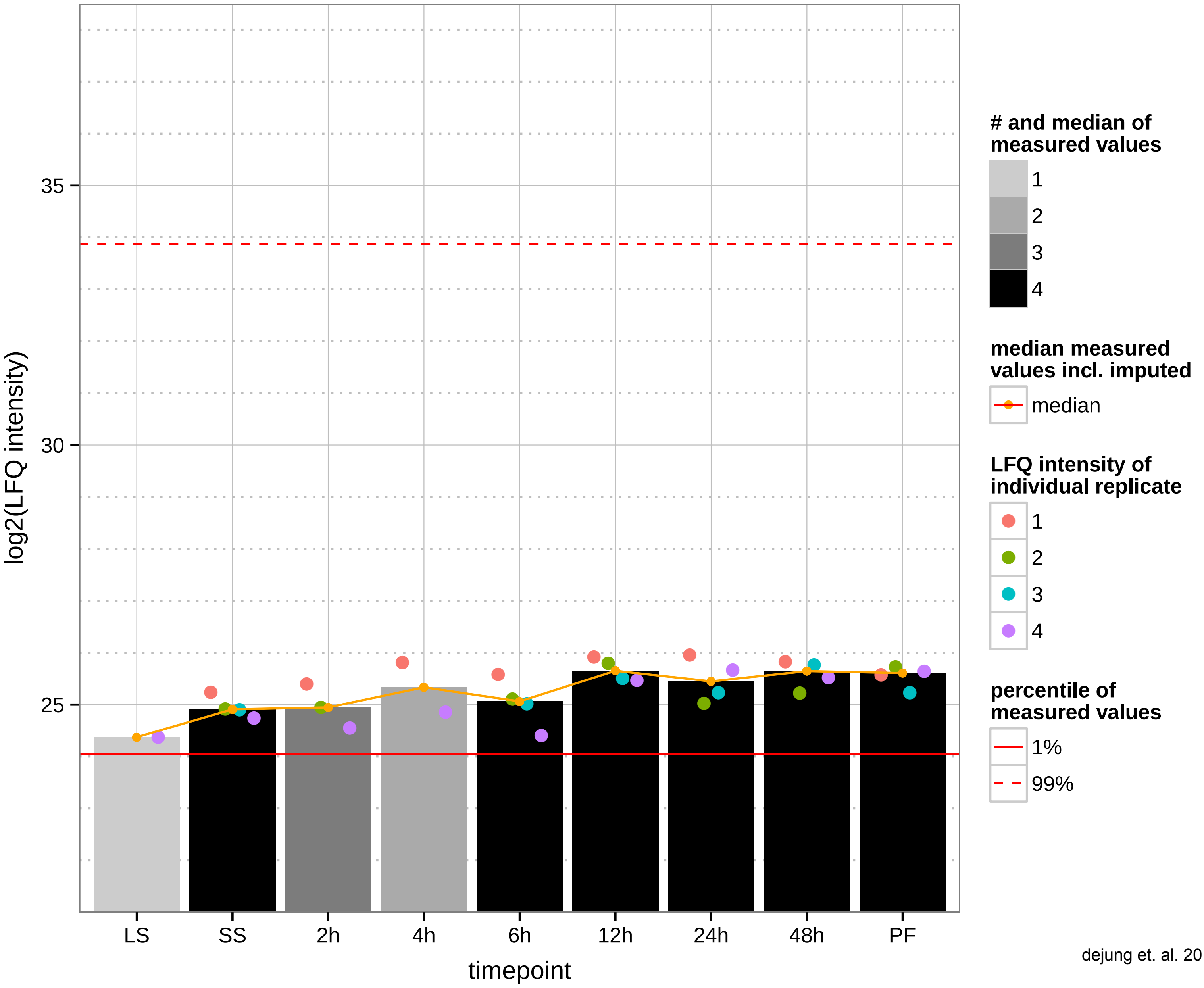
hypothetical protein, conserved
Tb927.11.280
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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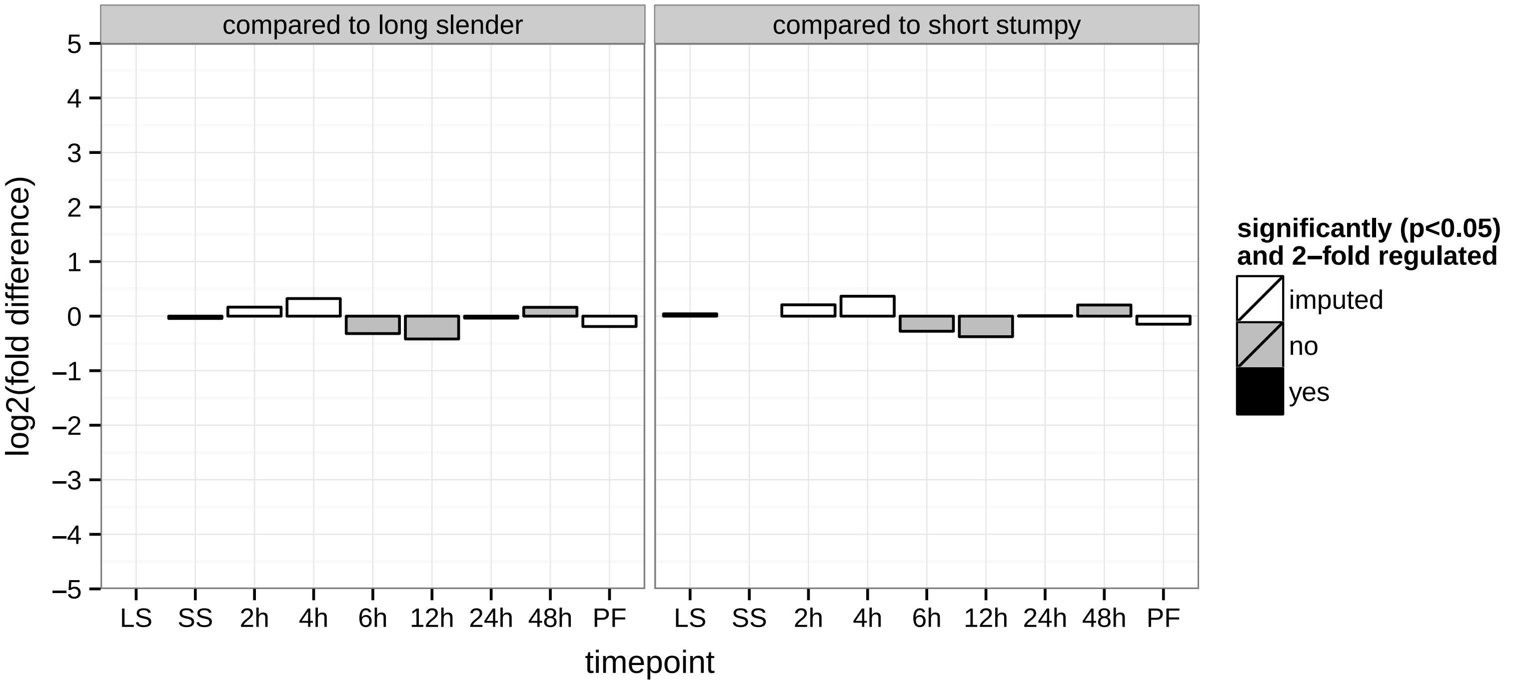
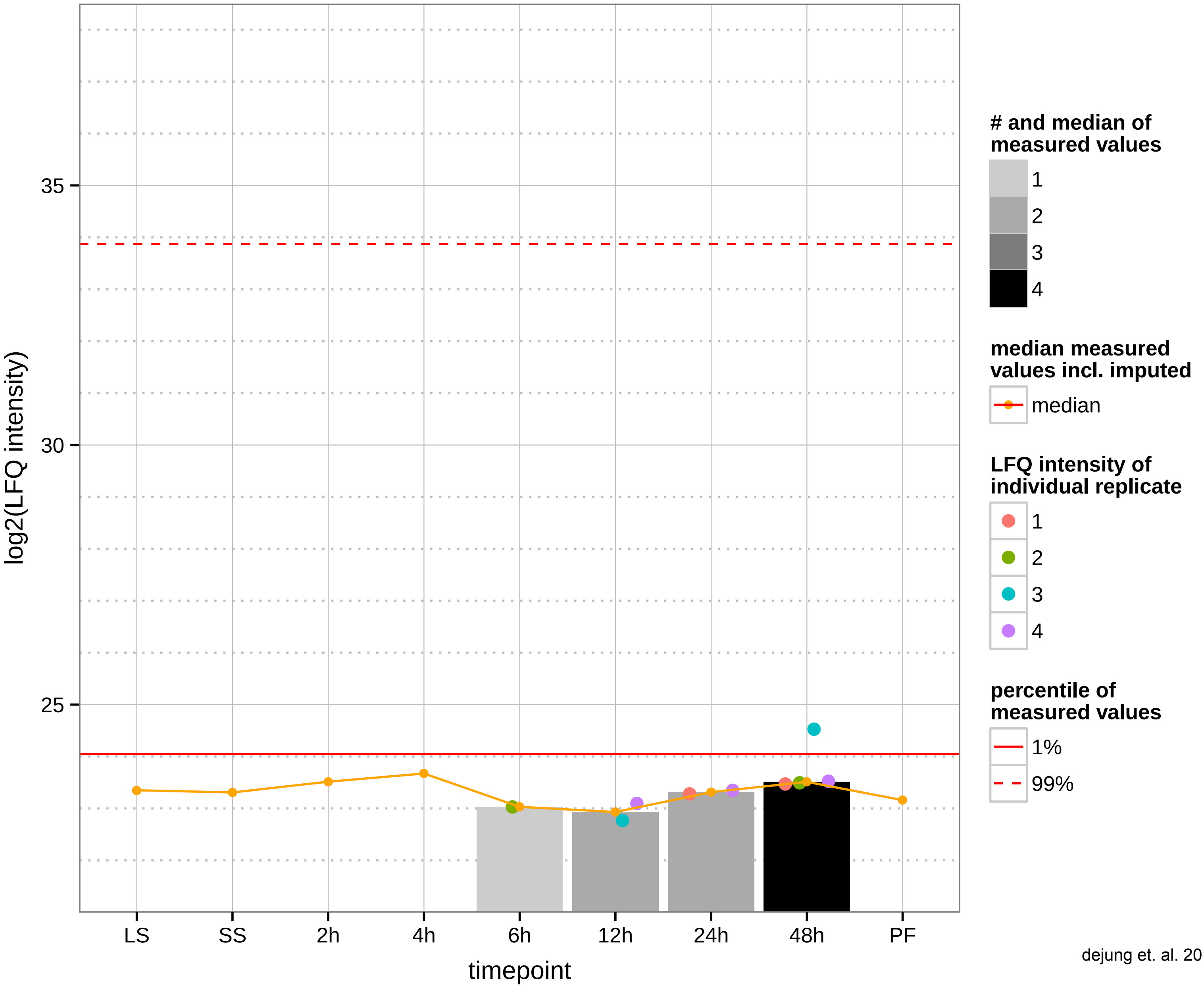
kinesin, putative (KIN–A)
Tb927.11.2880
AGOF: ATP binding, microtubule motor activity, motor activity, protein binding
AGOC: chromosome passenger complex, kinesin complex, microtubule associated complex, nucleus, spindle midzone
AGOP: chromosome segregation, cytokinesis, microtubule–based movement, spindle assembly
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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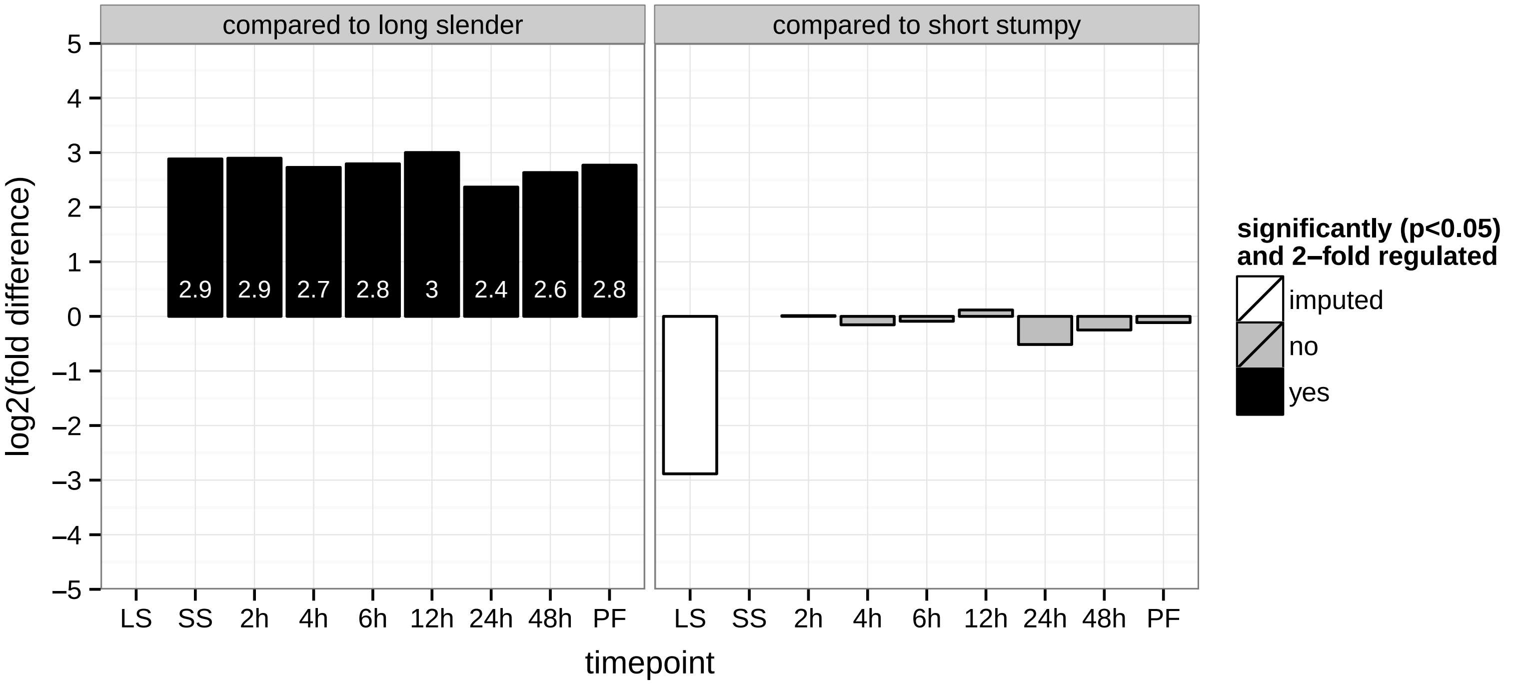
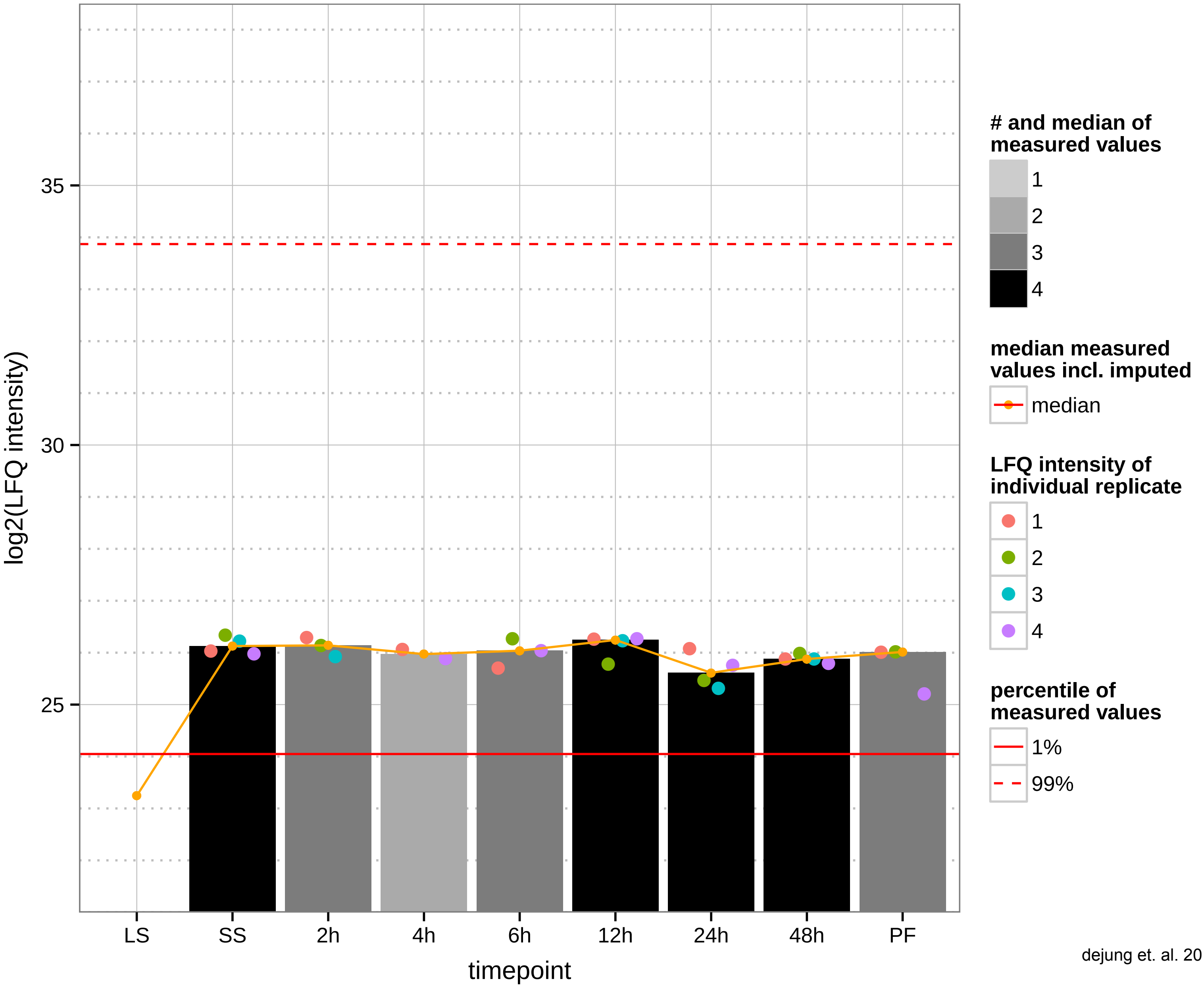
phosphoglycerate mutase, putative (iPGAM)
Tb927.11.2910
AGOF: cobalt ion binding, phosphoglycerate mutase activity
AGOC: mitochondrion
AGOP: glycolysis
PGOF: null
PGOC: null
PGOP: null





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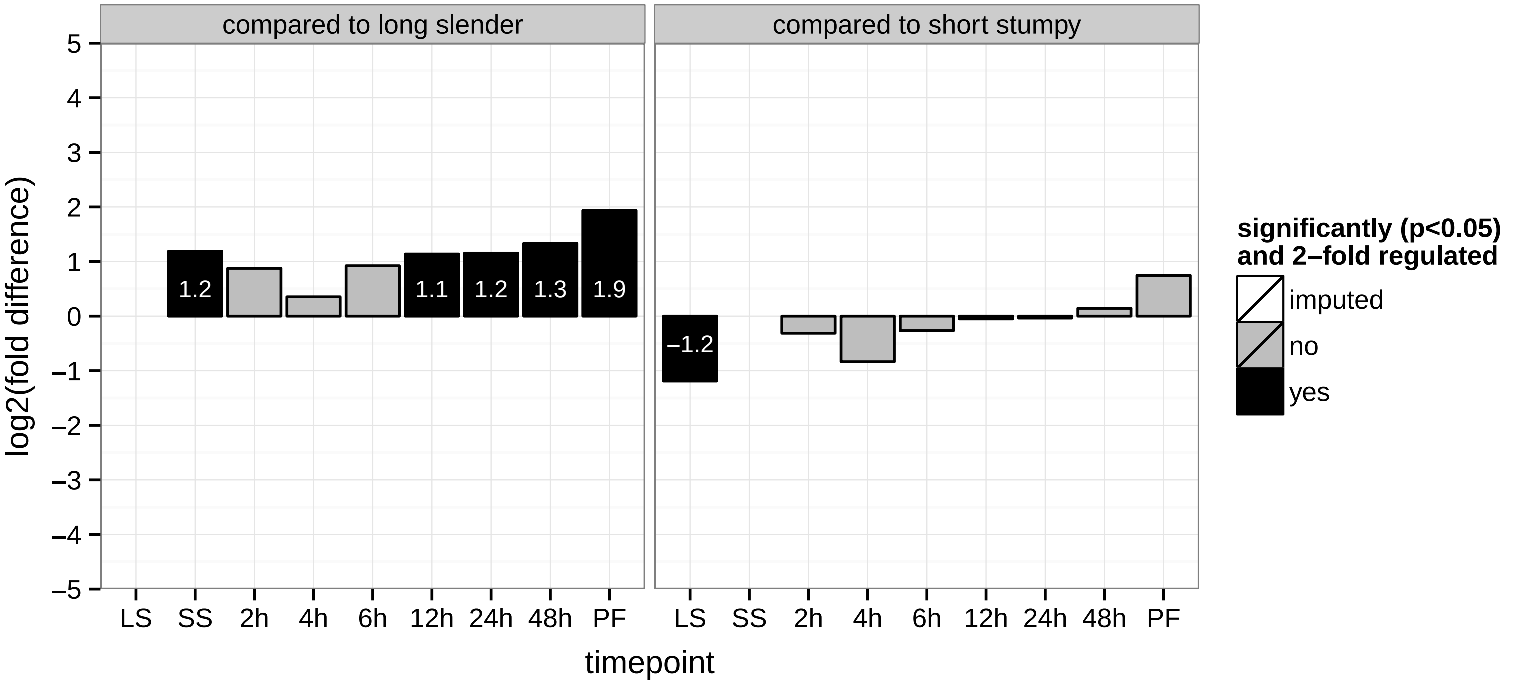
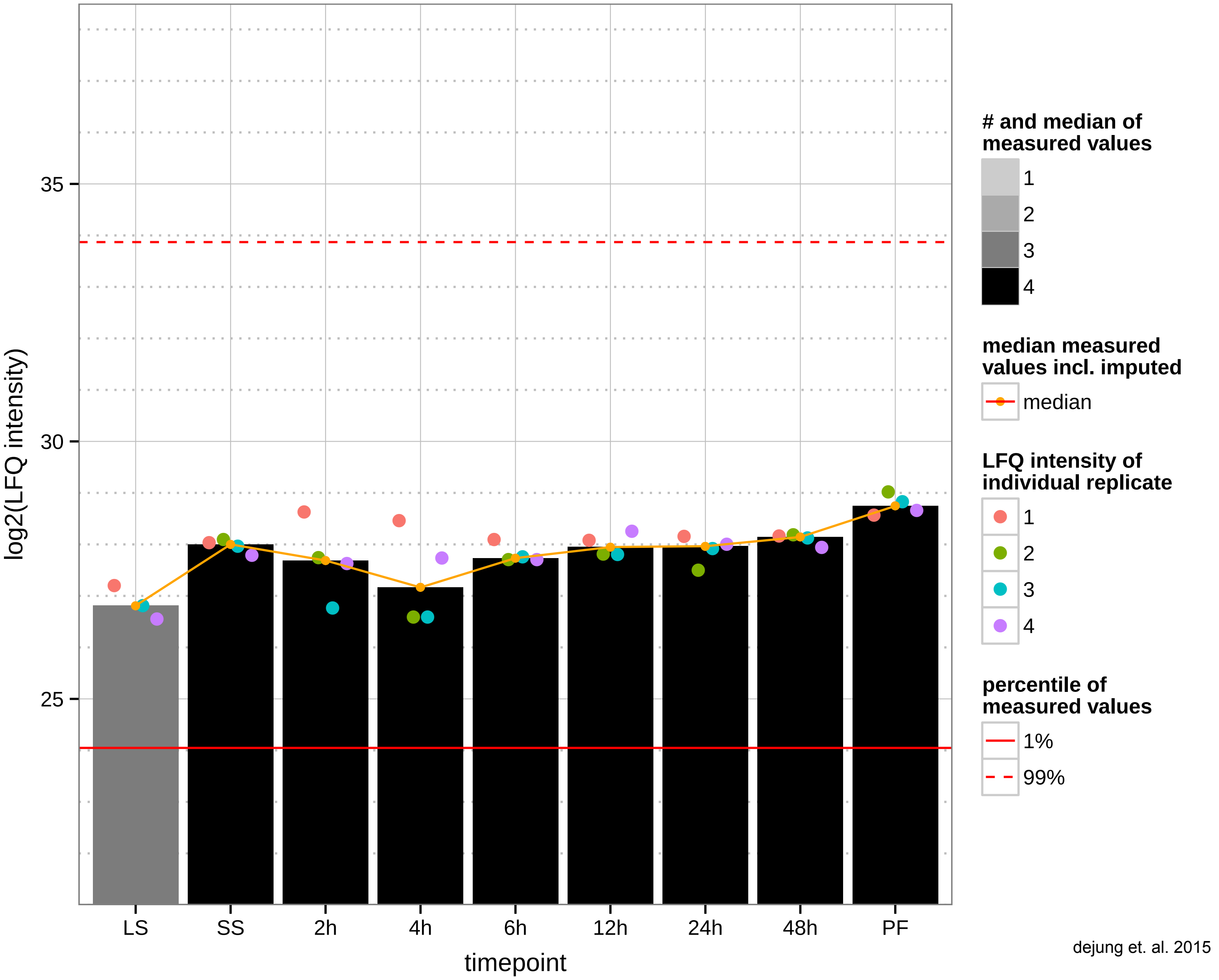
Nucleoporin (TbNup89)
Tb927.11.2950
AGOF: null
AGOC: nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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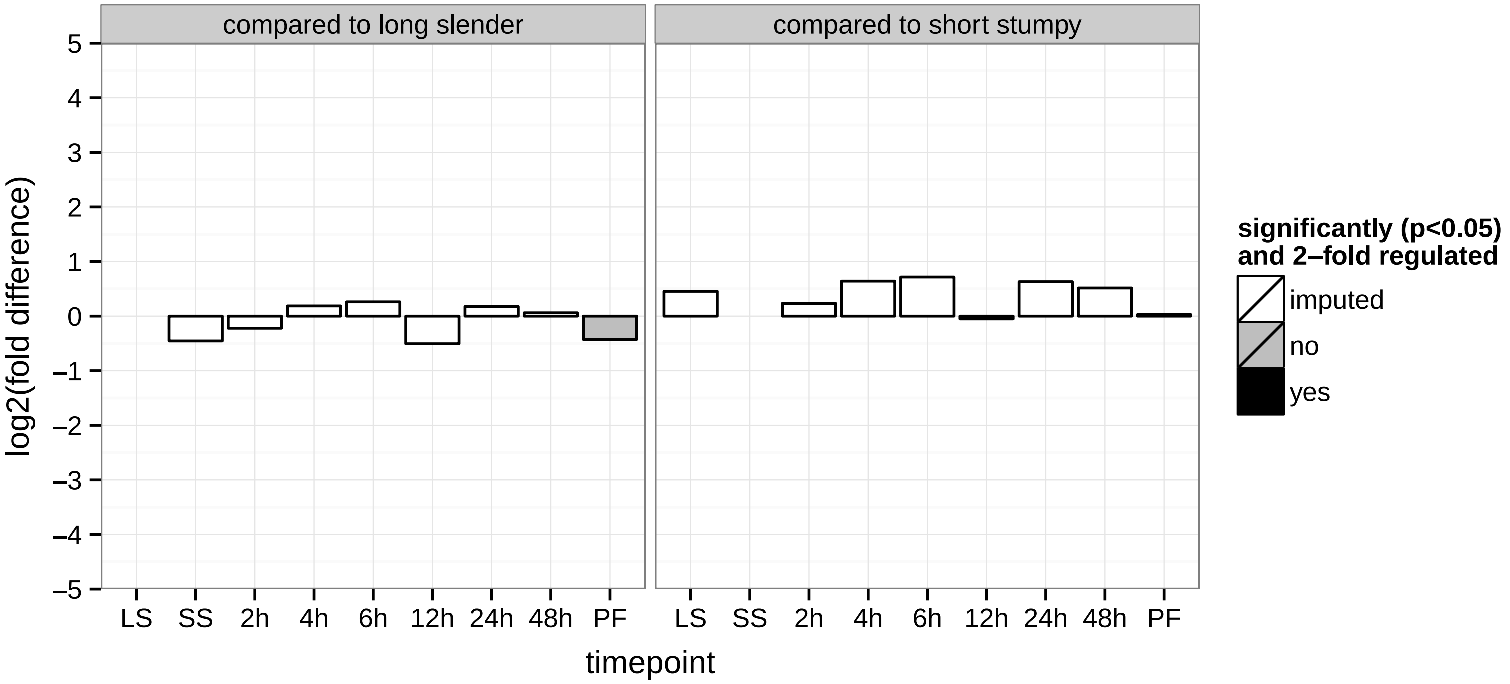
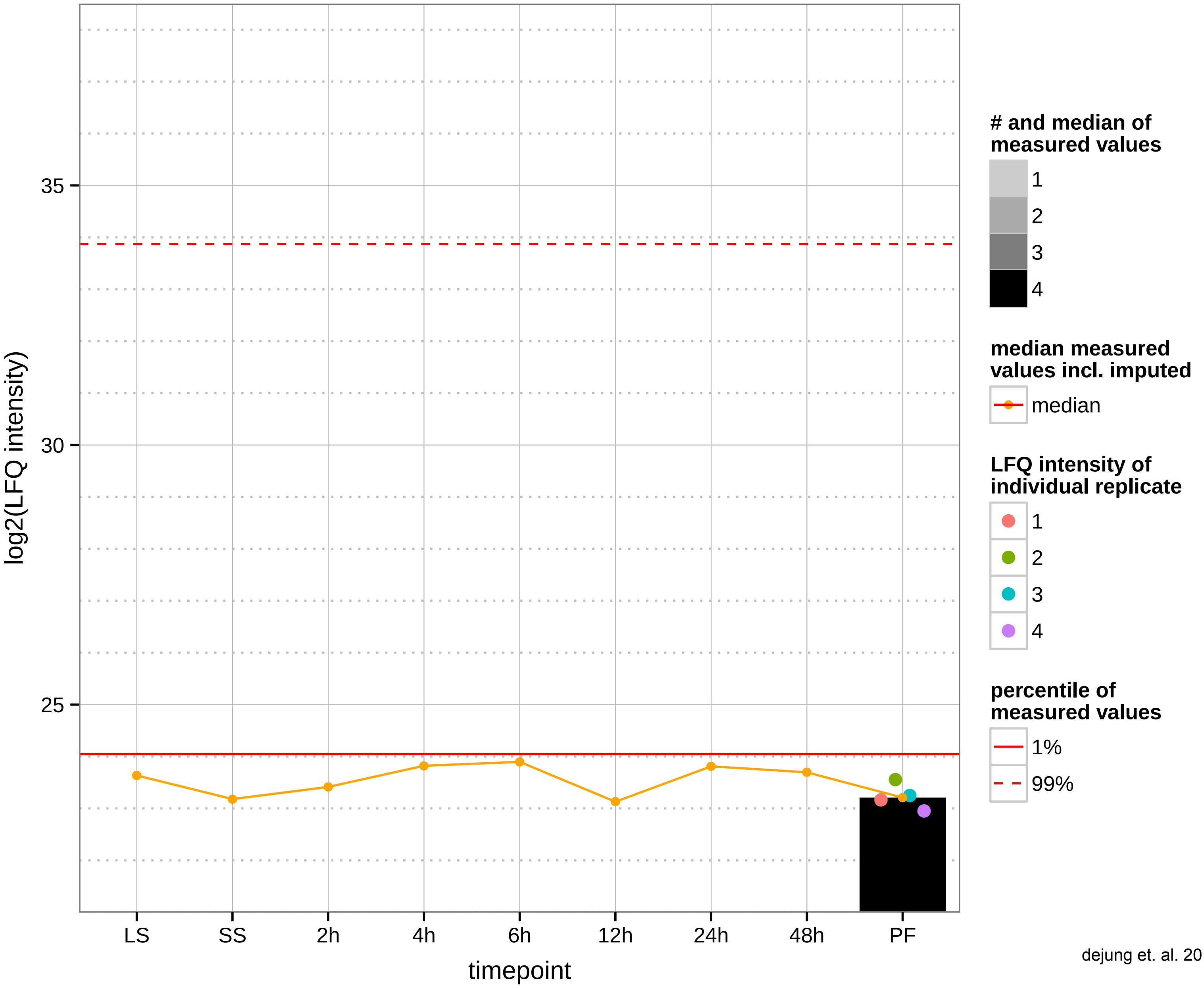
hypothetical protein, conserved
Tb927.11.2970
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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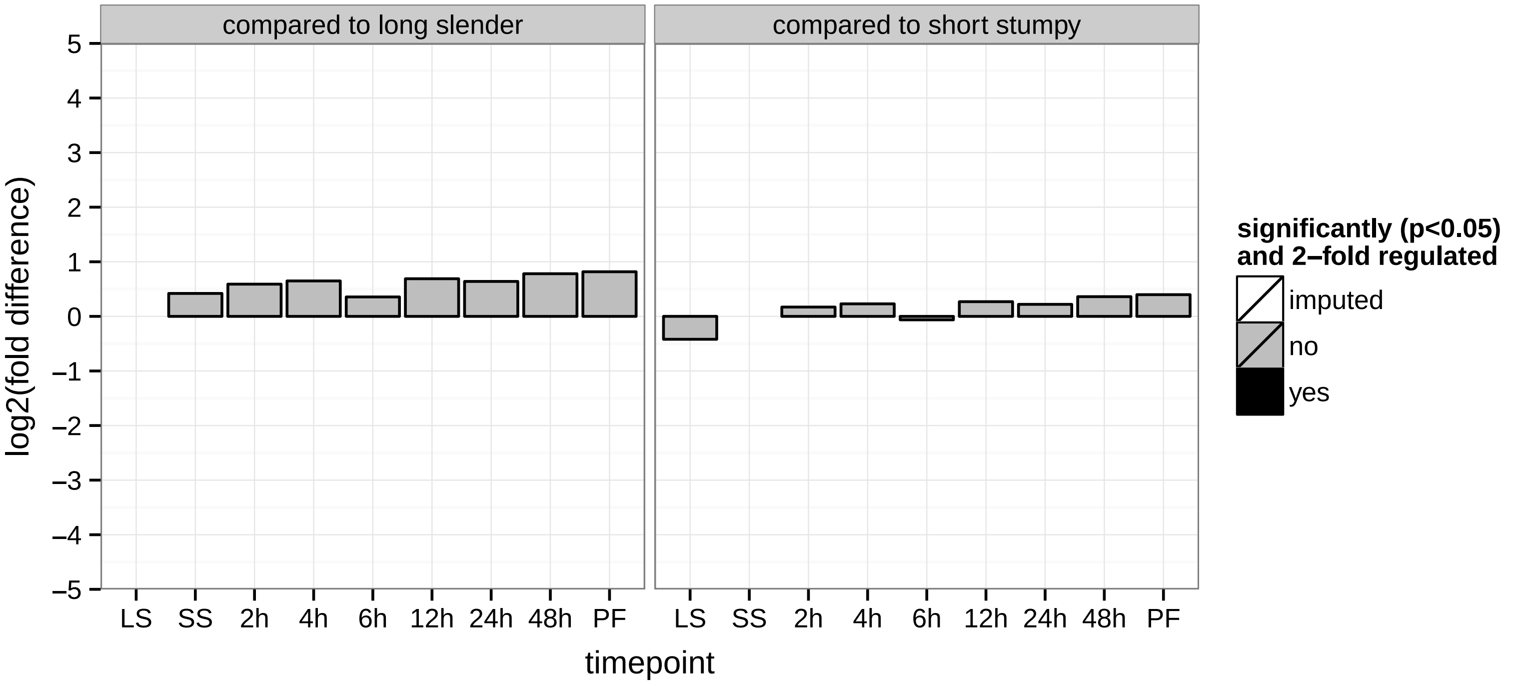
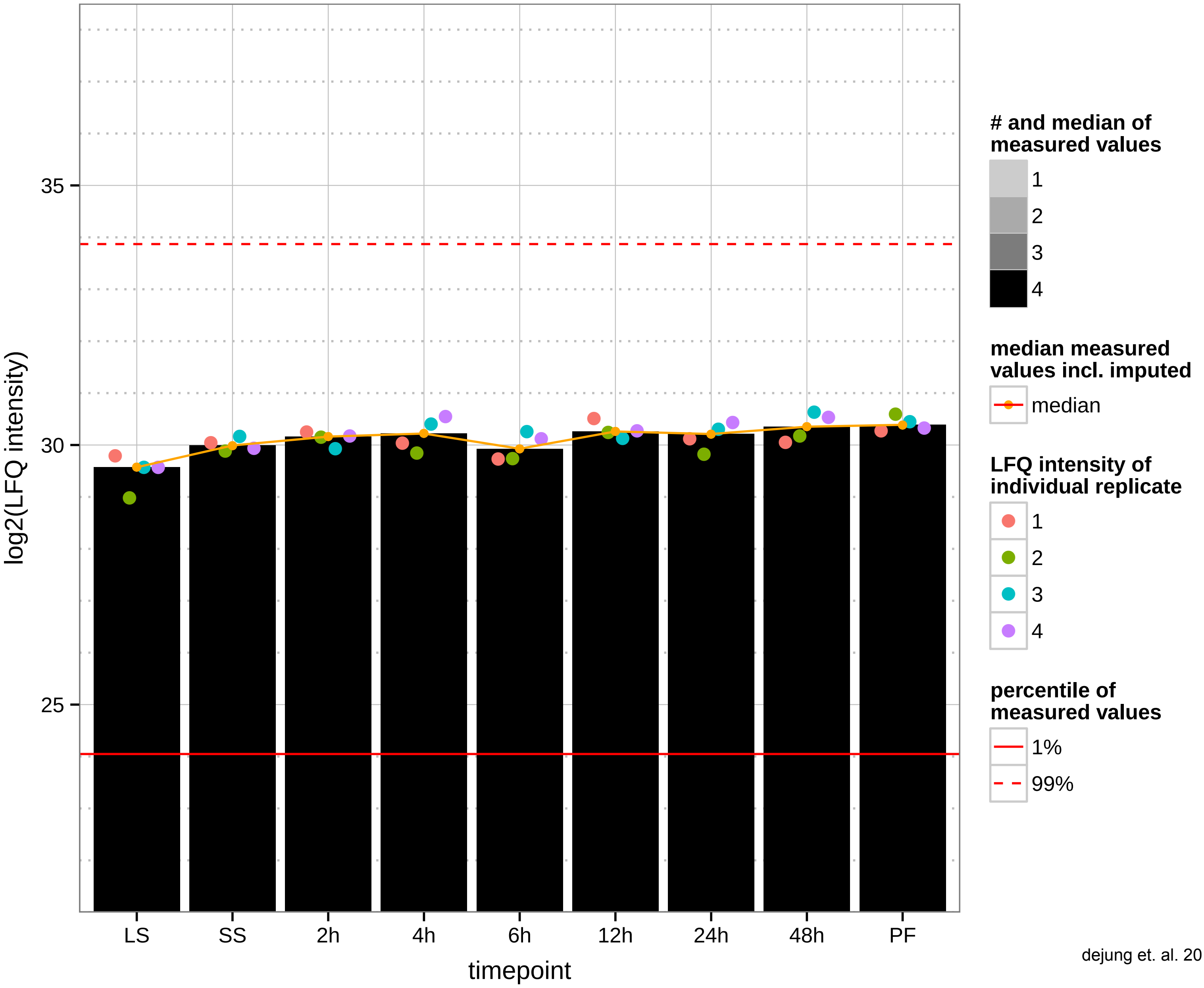
phosphoribosylpyrophosphate synthetase, putative (PRS)
Tb927.11.3030
AGOF: ATP binding, magnesium ion binding, ribose phosphate diphosphokinase activity
AGOC: integral to membrane
AGOP: nucleoside metabolic process, purine ribonucleotide biosynthetic process
PGOF: magnesium ion binding, ribose phosphate diphosphokinase activity
PGOC: null
PGOP: nucleoside metabolic process, nucleotide biosynthetic process





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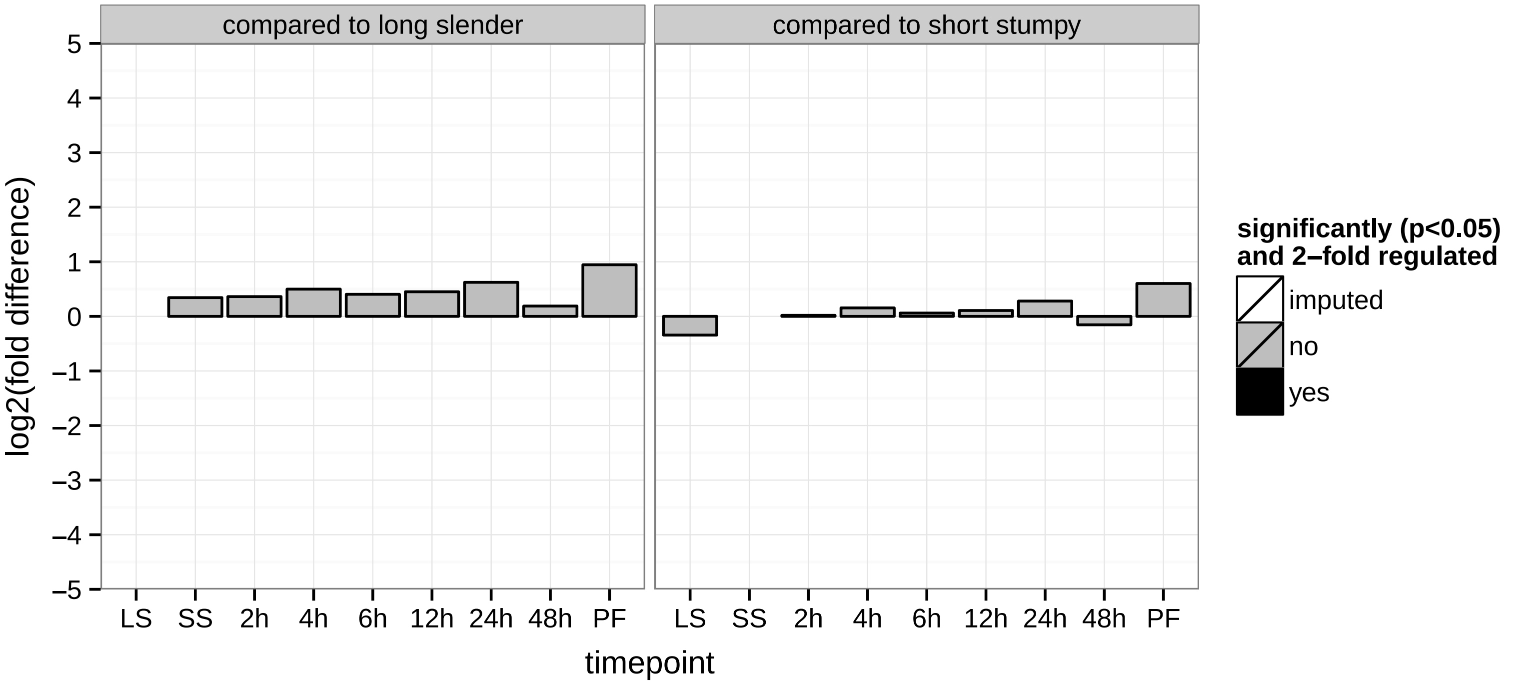
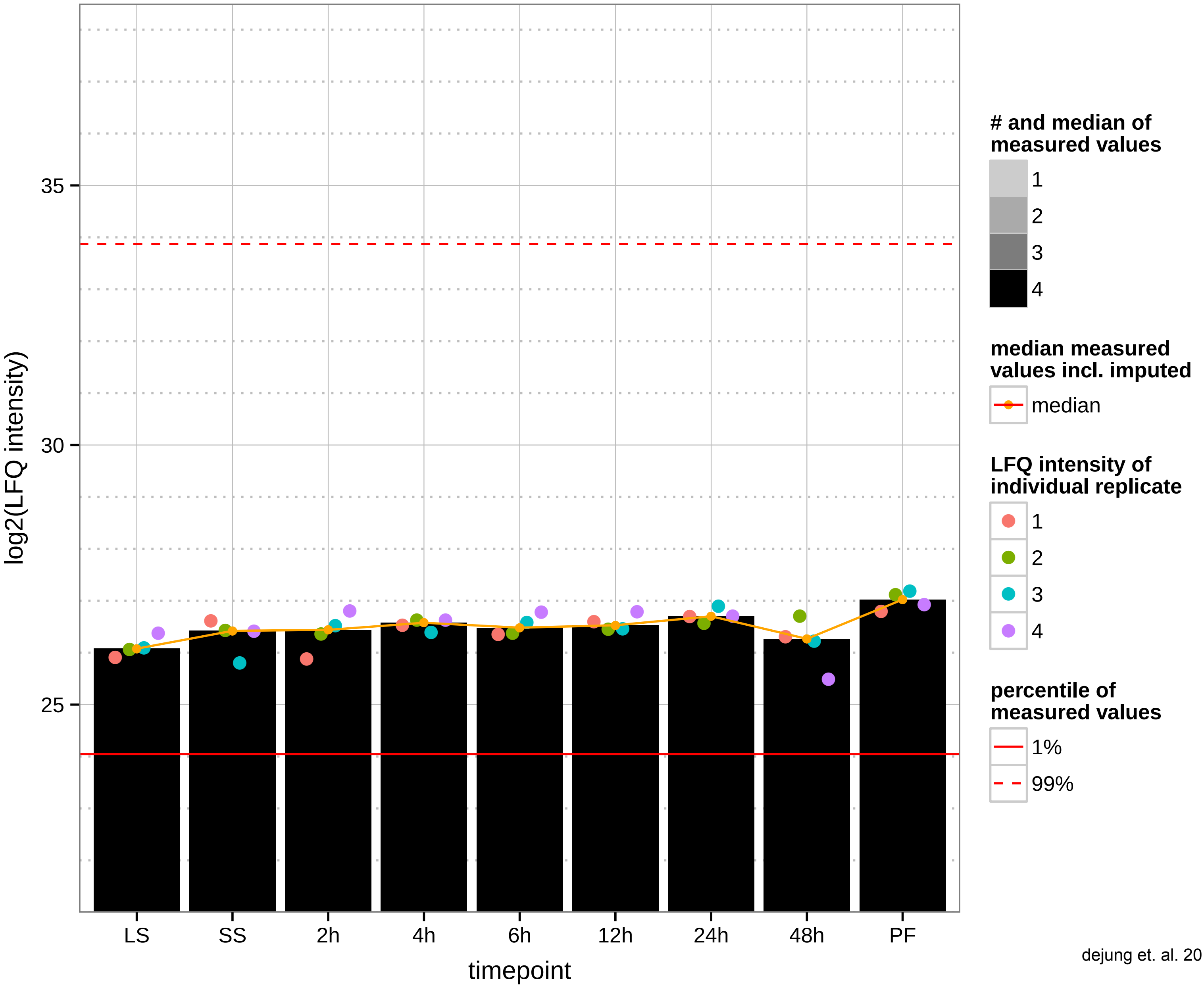
hypothetical protein, conserved
Tb927.11.3160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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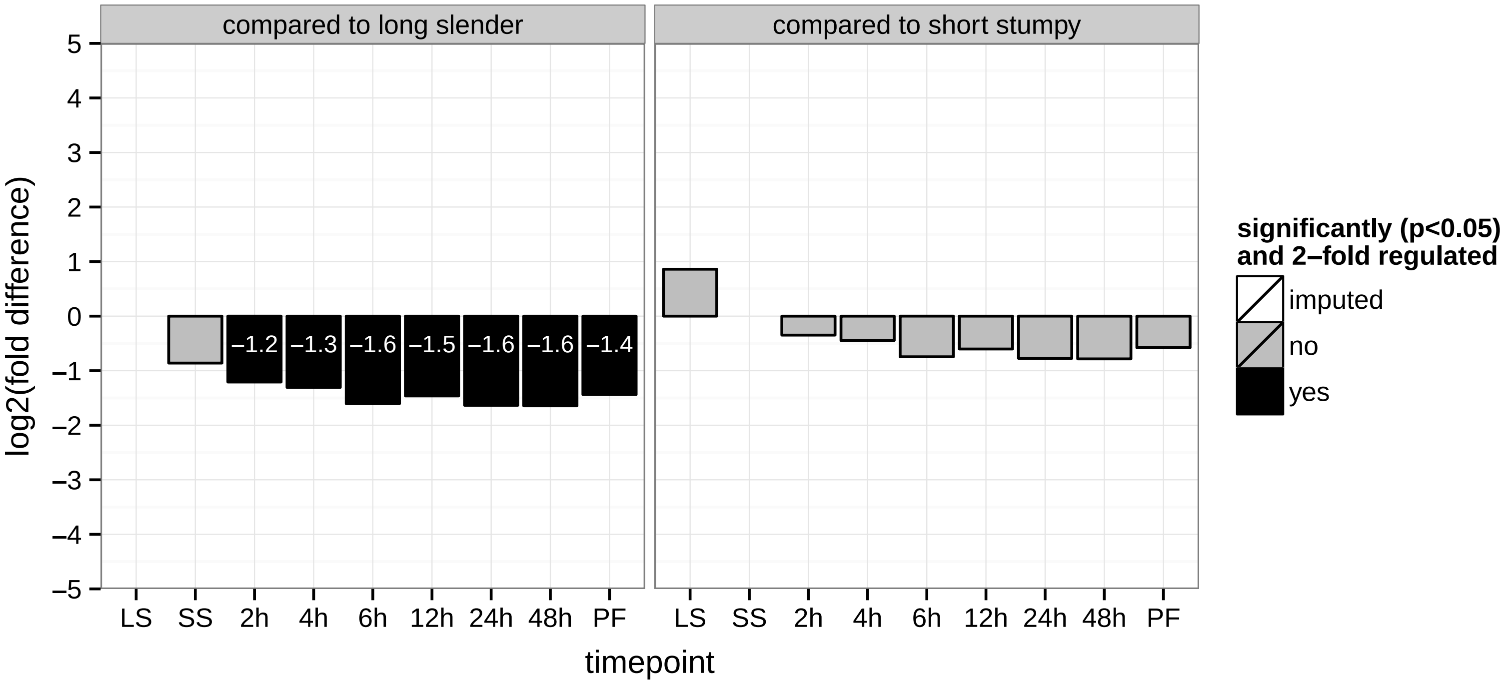
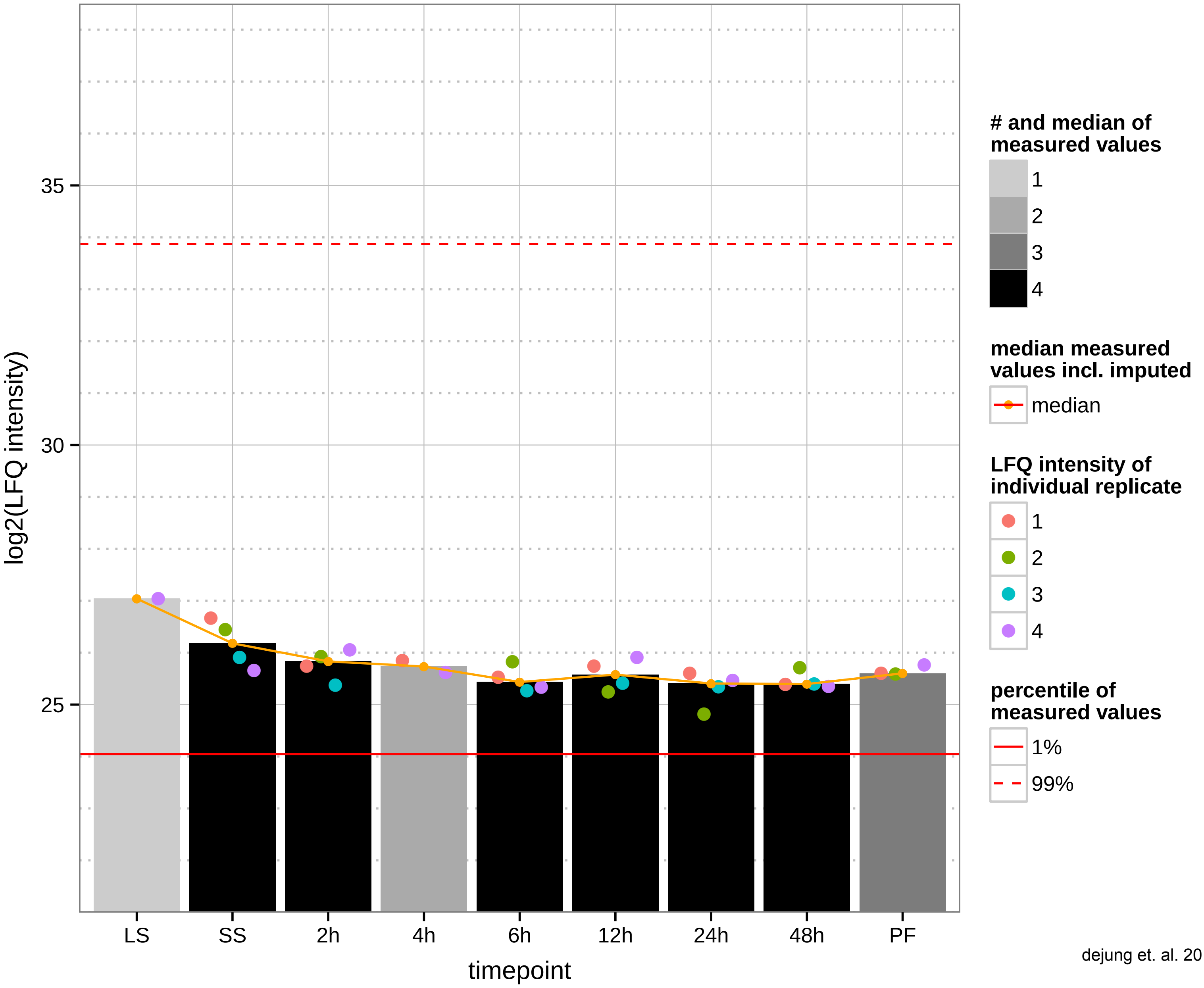
hypothetical protein, conserved
Tb927.11.3190
AGOF: null
AGOC: null
AGOP: null
PGOF: binding, protein binding
PGOC: null
PGOP: null





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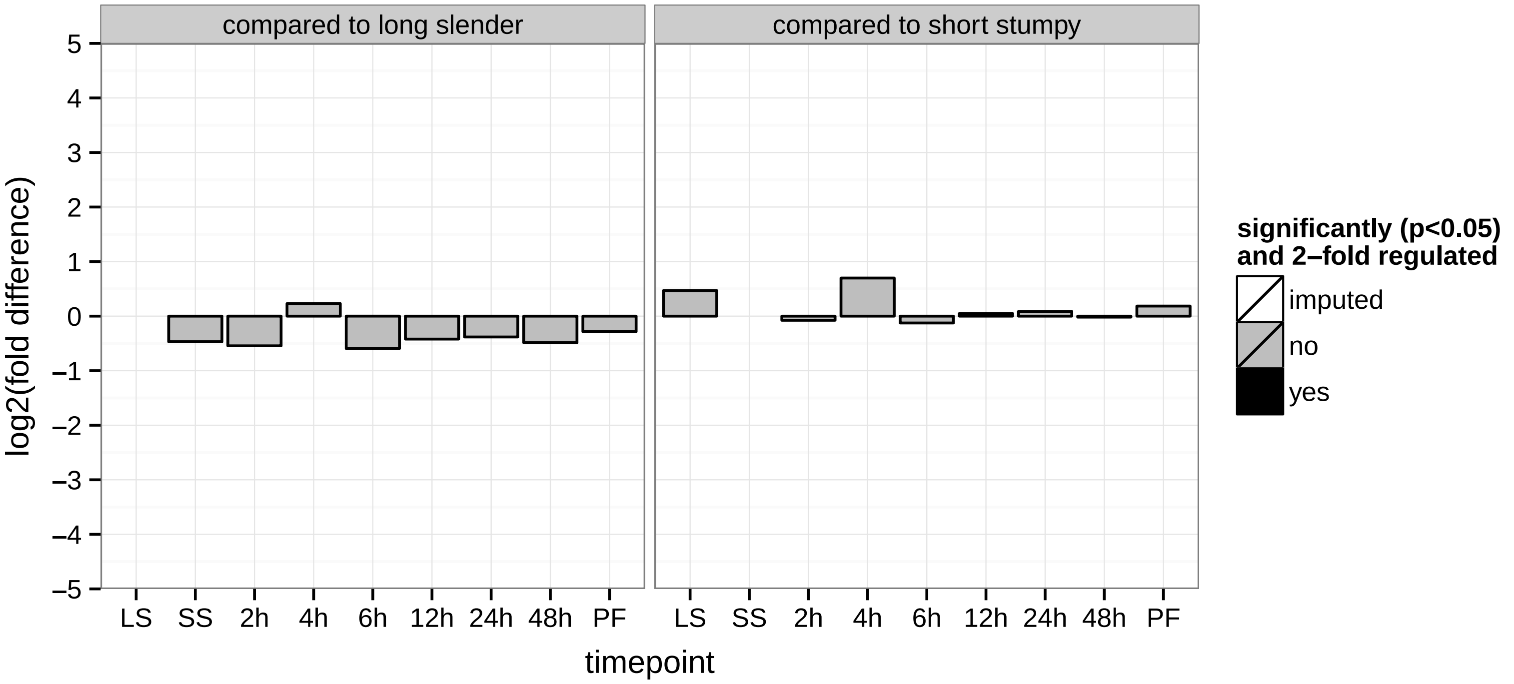
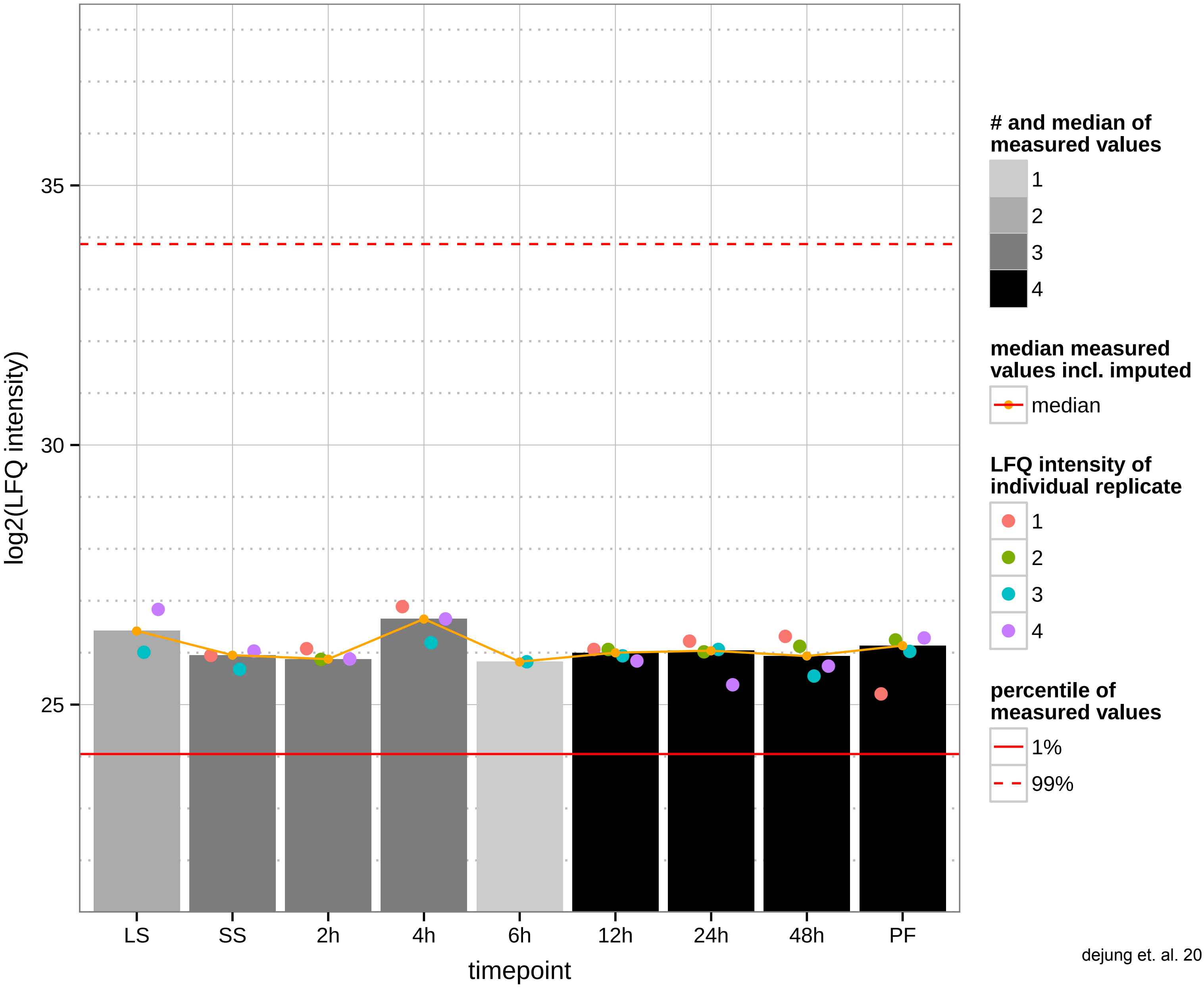
dynein light chain 1, putative
Tb927.11.320
AGOF: microtubule motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based process
PGOF: null
PGOC: microtubule associated complex
PGOP: microtubule–based process





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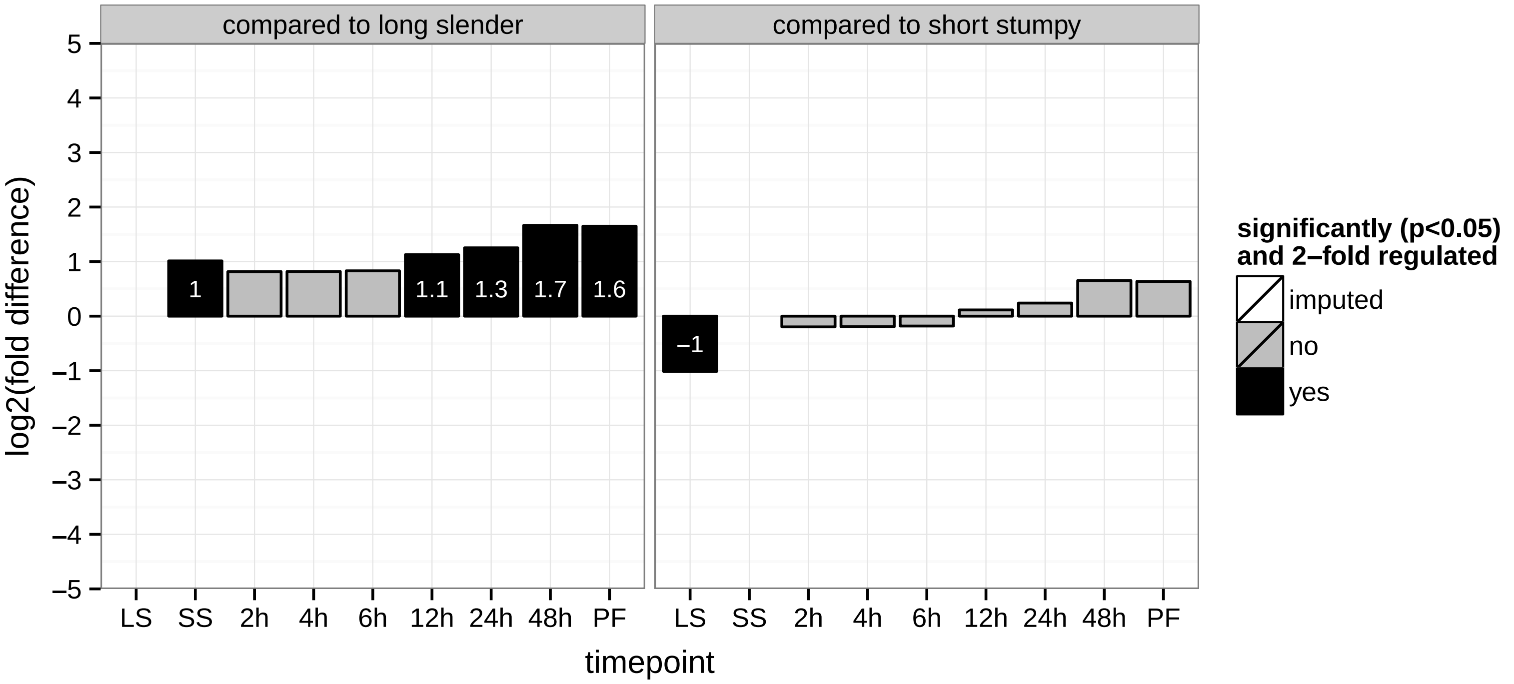
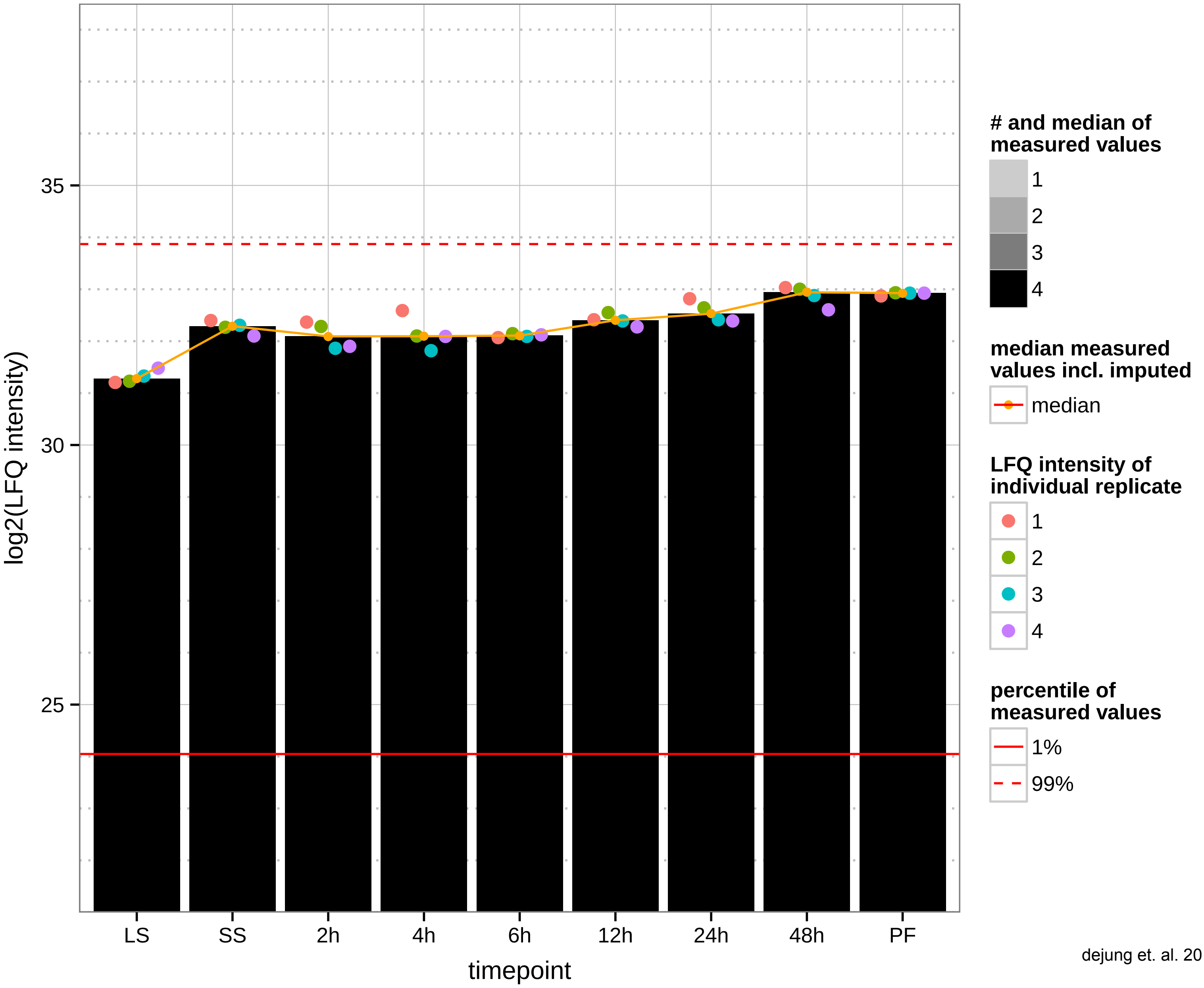
T−complex protein 1, zeta subunit, putative (TCP−1−zeta)
Tb927.11.3240
AGOF: ATP binding, unfolded protein binding
AGOC: chaperonin−containing T−complex
AGOP: protein folding, regulation of cell cycle
PGOF: ATP binding, unfolded protein binding
PGOC: null
PGOP: cellular protein metabolic process, protein folding





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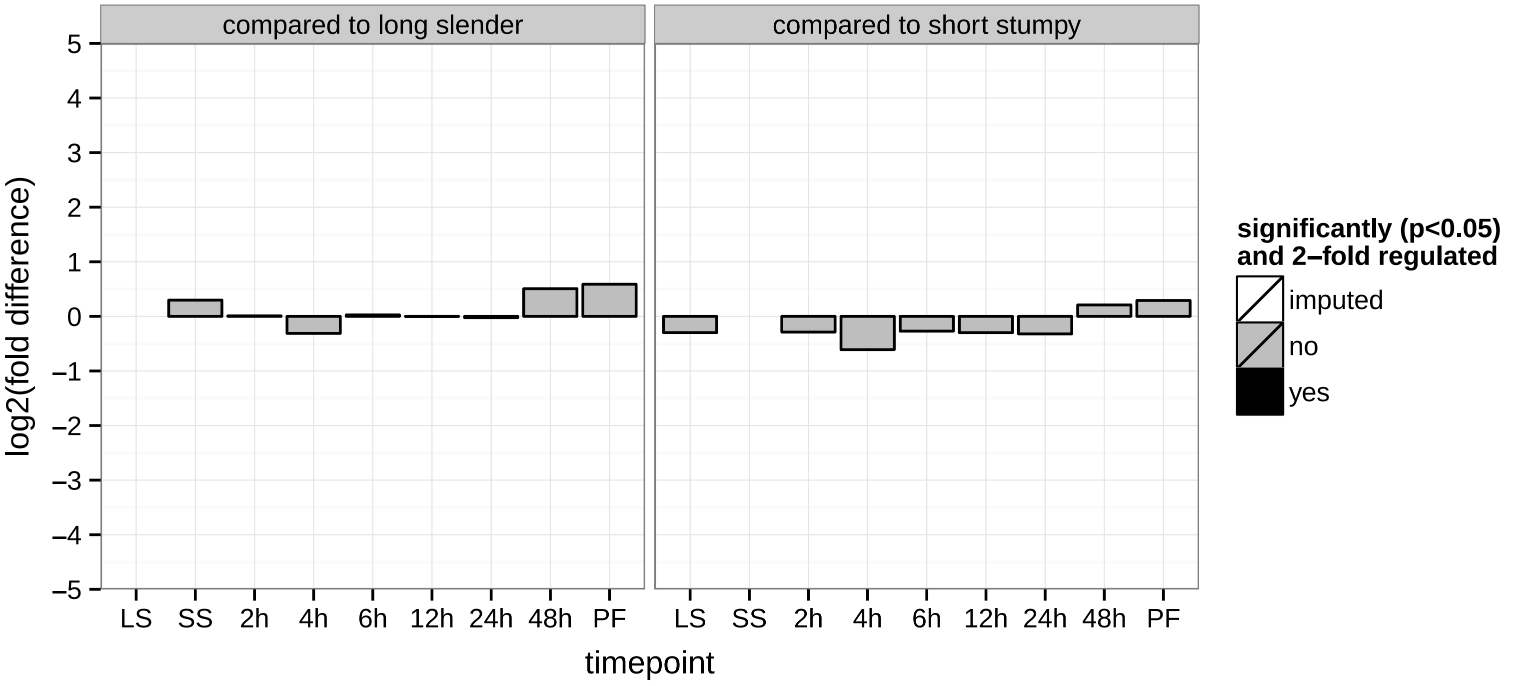
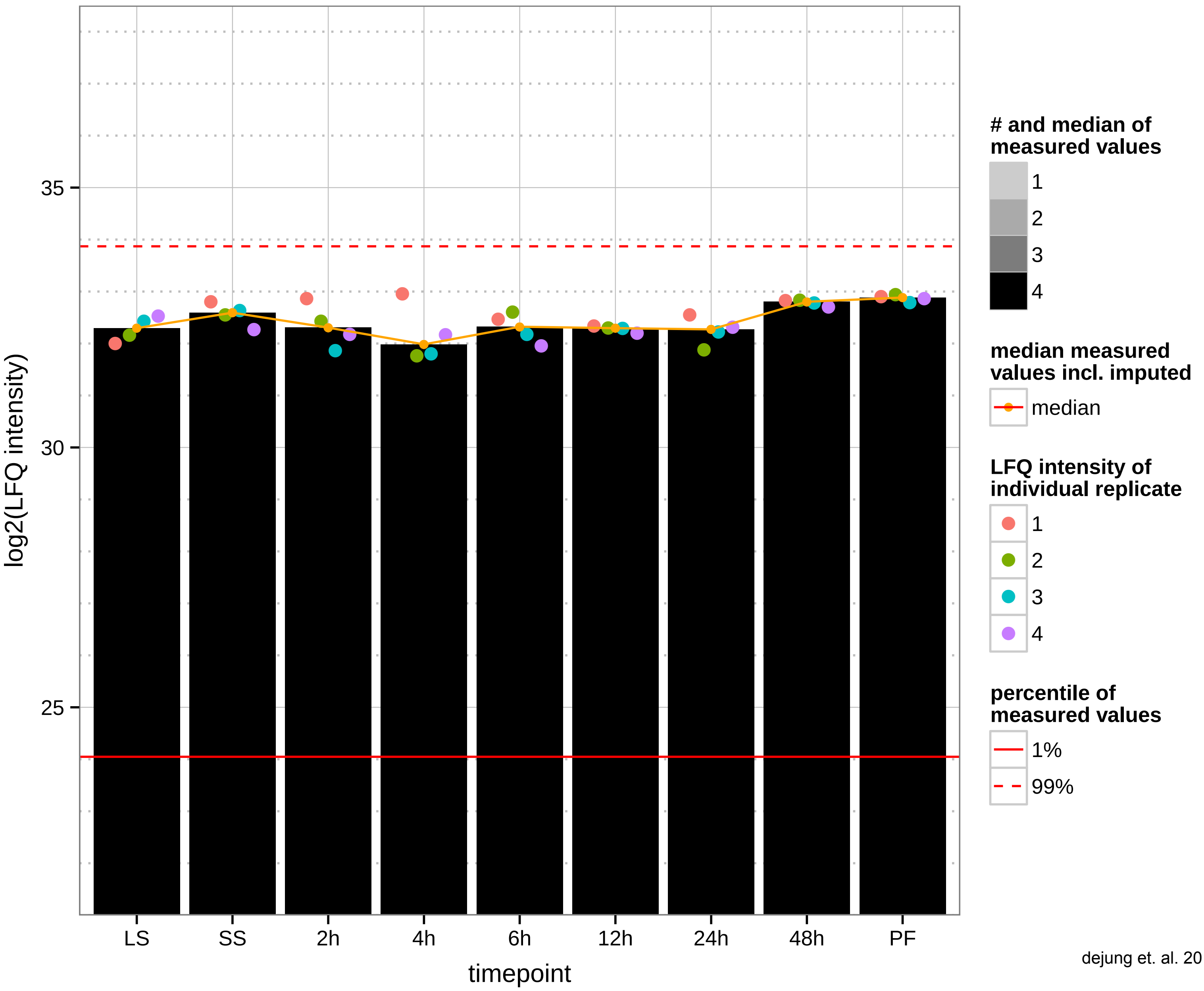
dynein heavy chain, putative
Tb927.11.3250
AGOF: ATP binding, ATPase activity, microtubule motor activity
AGOC: dynein complex
AGOP: microtubule–based movement
PGOF: ATP binding, ATPase activity, microtubule motor activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: dynein complex
PGOP: microtubule–based movement





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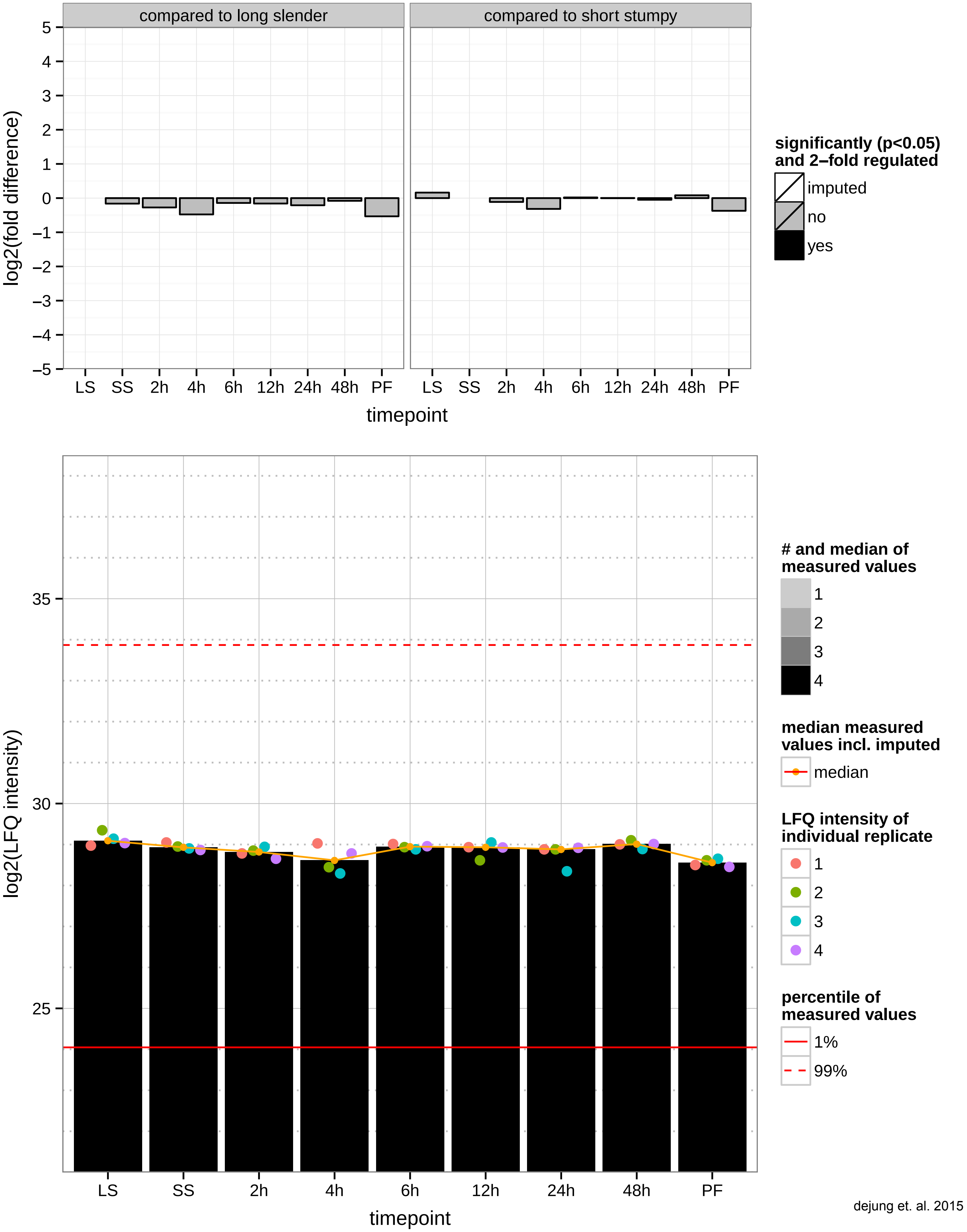
hypothetical protein, conserved
Tb927.11.3300
AGOF: null
AGOC: mitochondrial membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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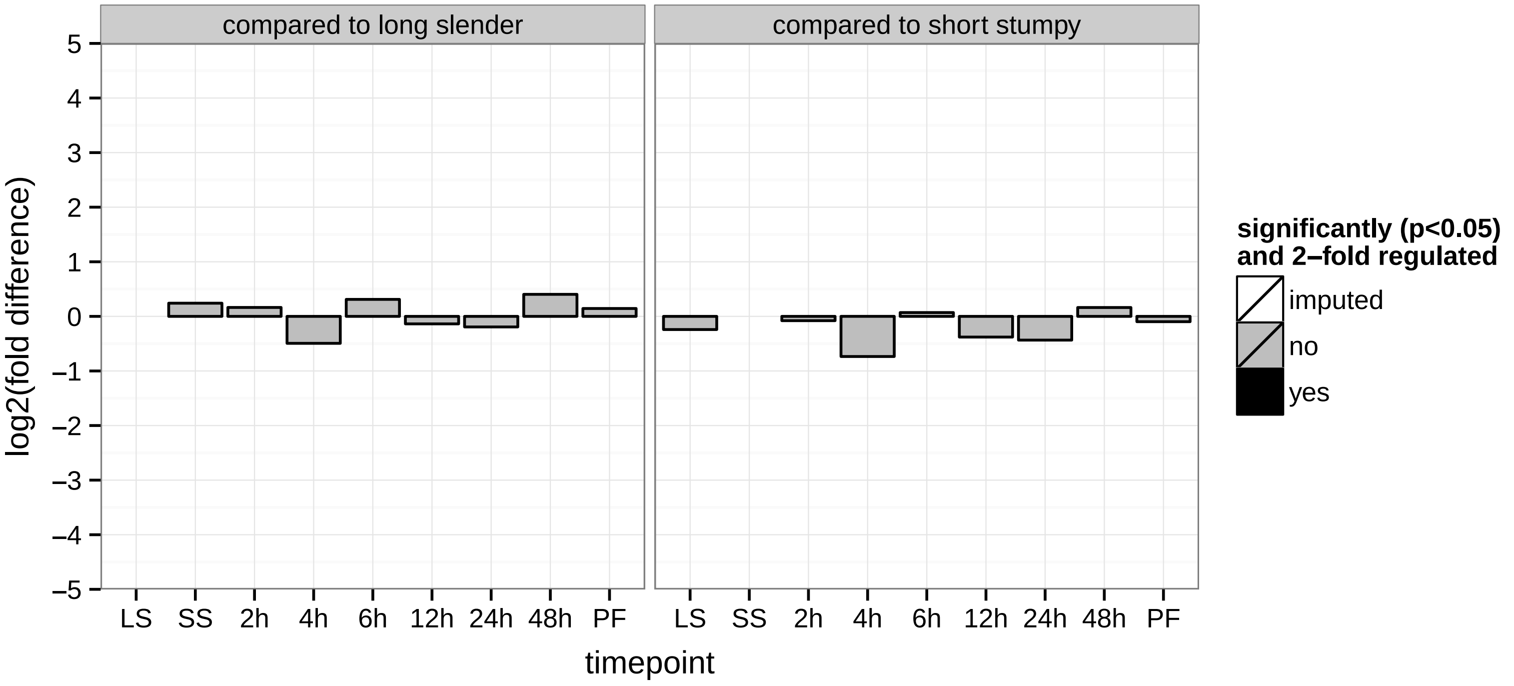
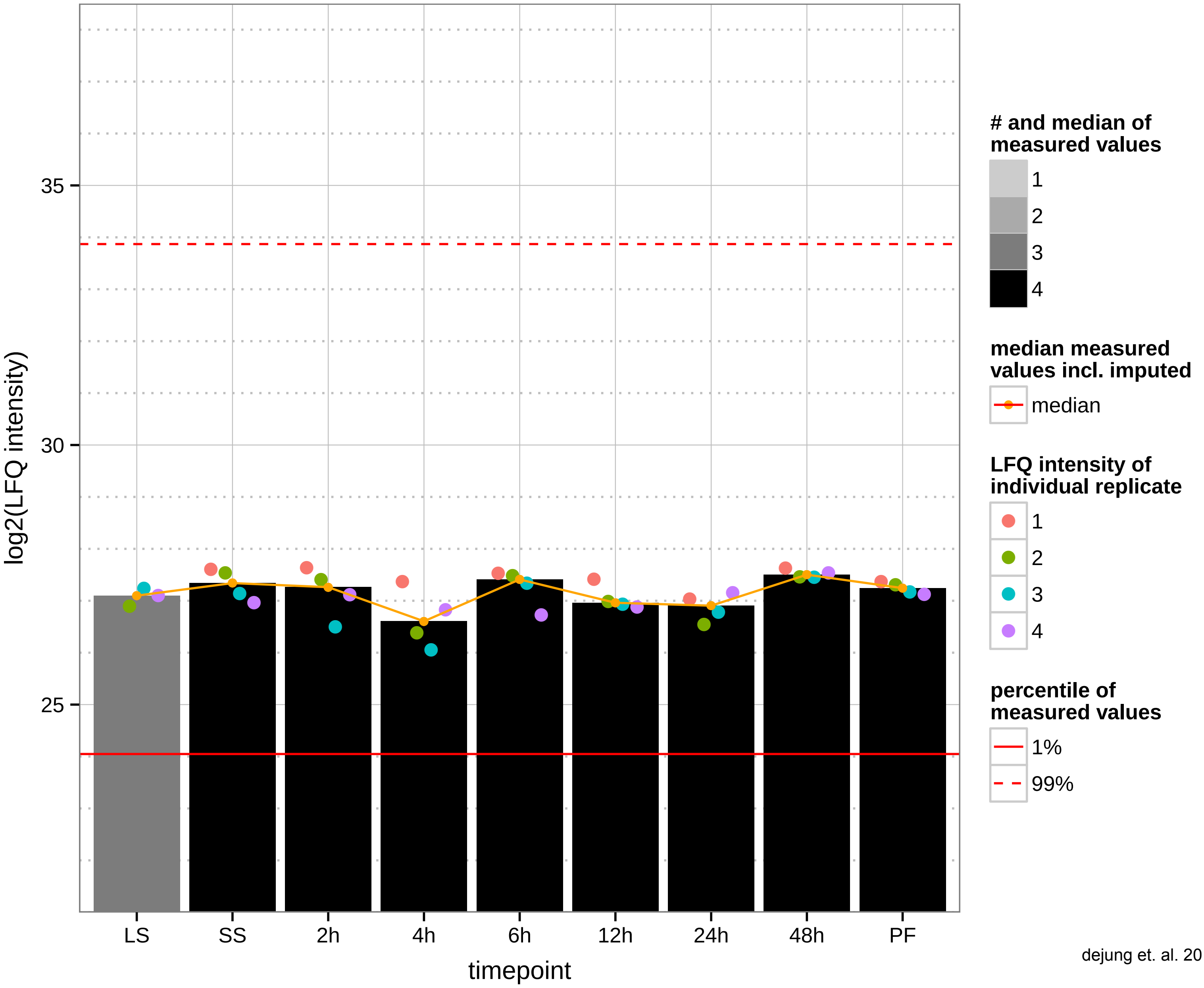
hypothetical protein, conserved
Tb927.11.3360
AGOF: ATP binding
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: ATP binding, protein binding
PGOC: null
PGOP: null





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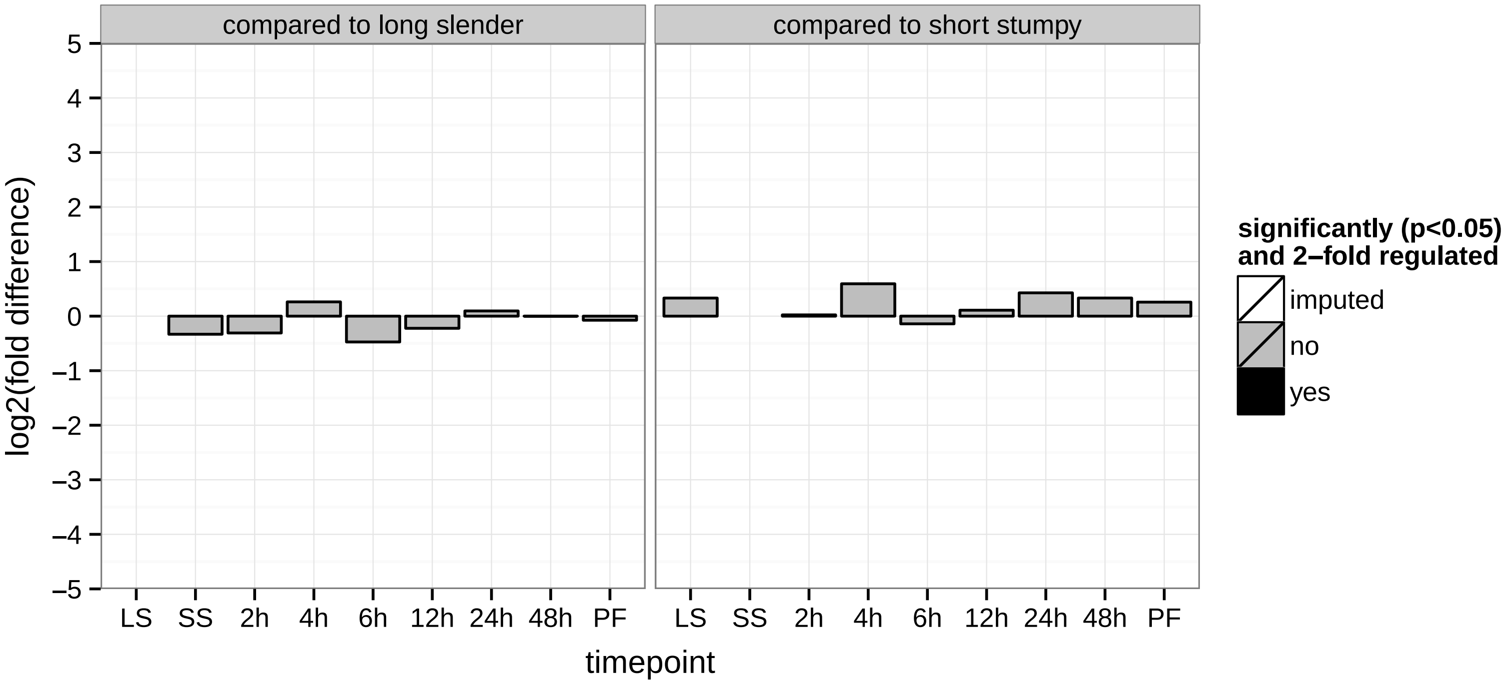
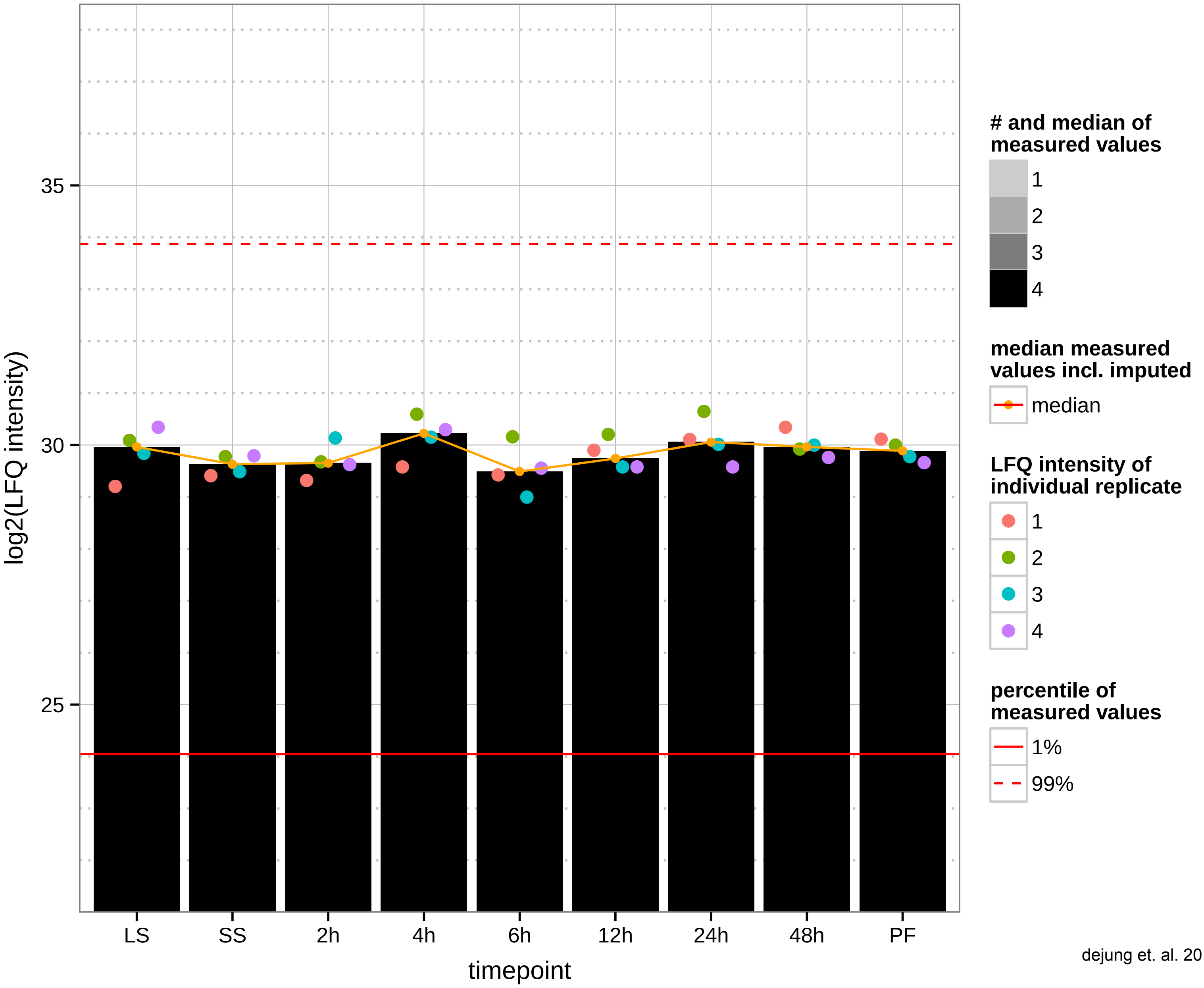
Ran–binding protein 1, putative
Tb927.11.3380
AGOF: GDP–dissociation inhibitor activity
AGOC: cytoplasm, nucleus
AGOP: nuclear transport
PGOF: null
PGOC: null
PGOP: intracellular transport





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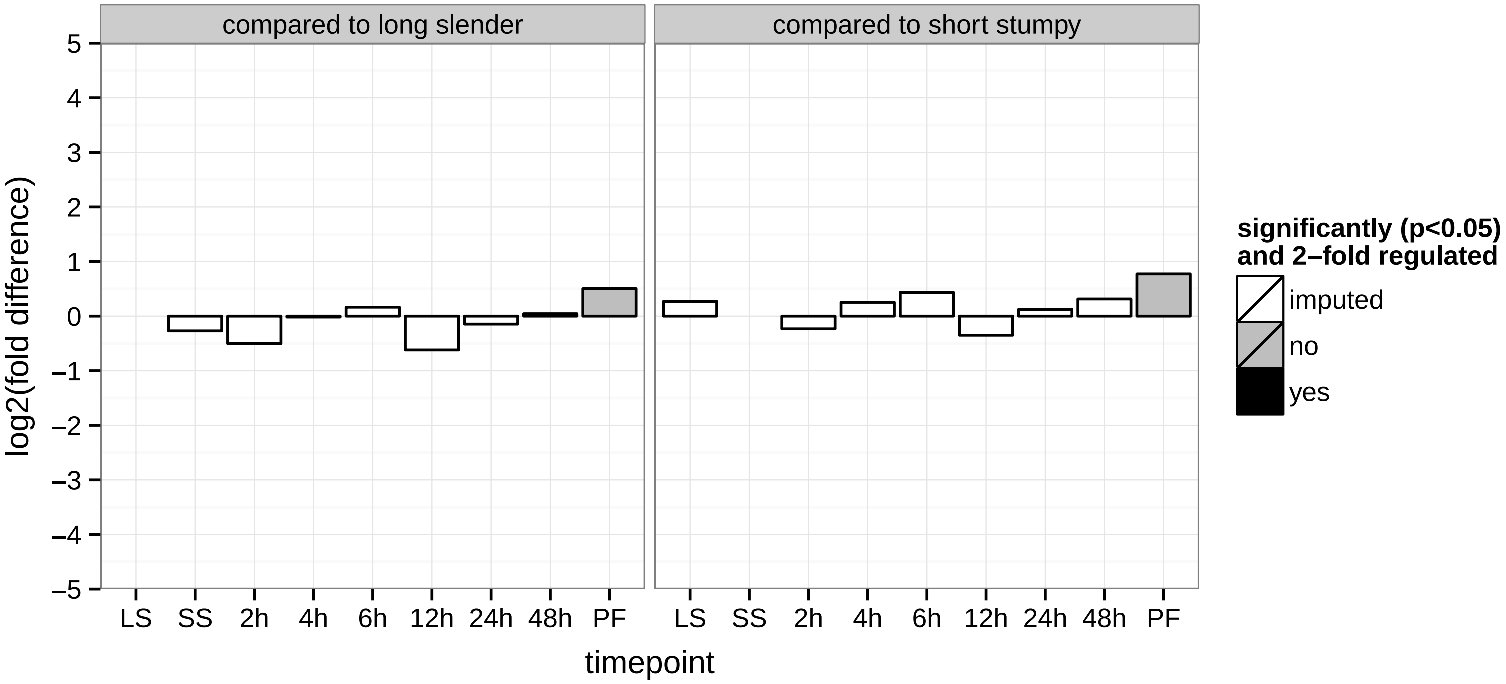
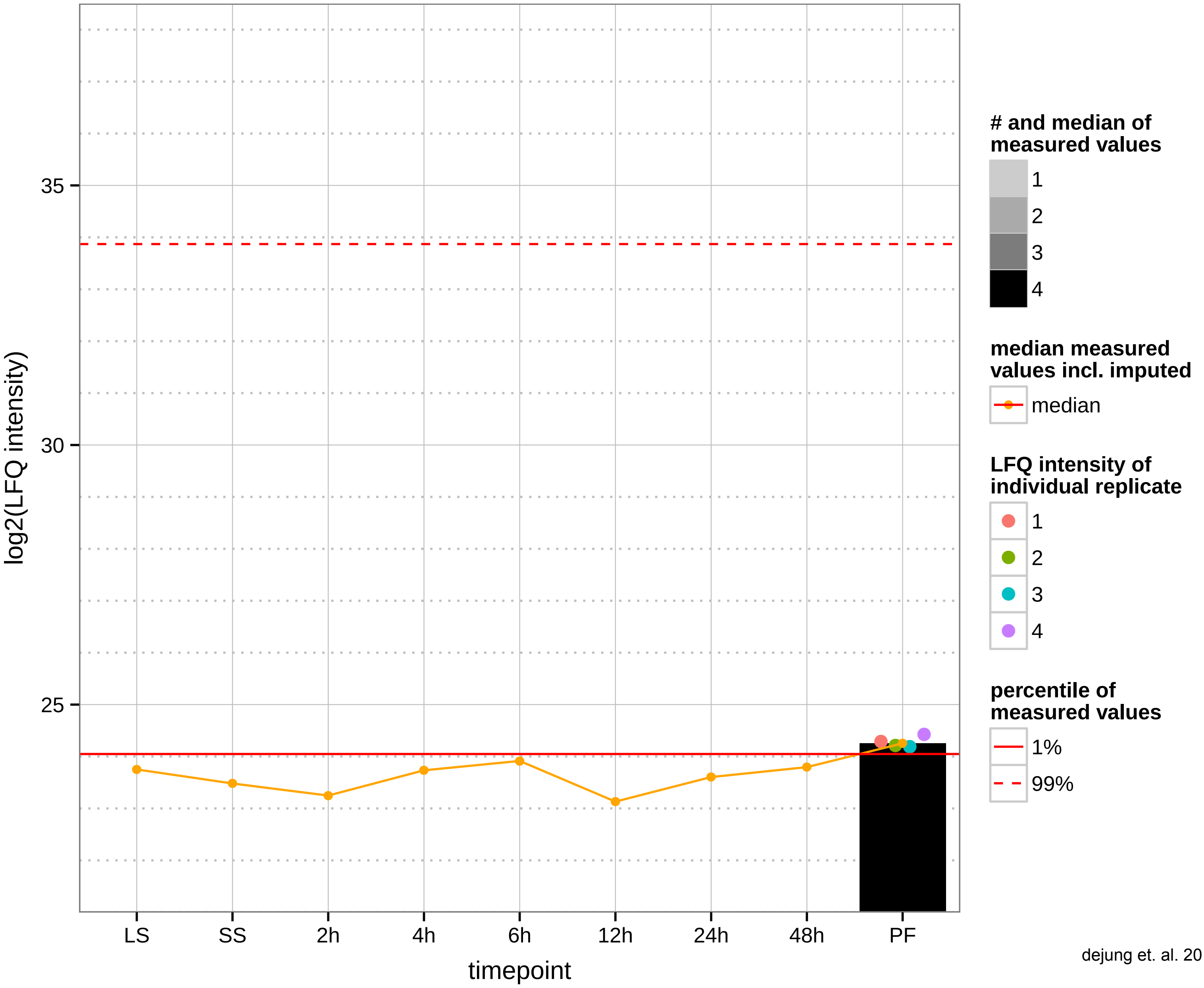
hypothetical protein, conserved
Tb927.11.3390
AGOF: acid–amino acid ligase activity
AGOC: intracellular
AGOP: cellular protein modification process
PGOF: acid–amino acid ligase activity, protein binding
PGOC: intracellular
PGOP: cellular protein modification process





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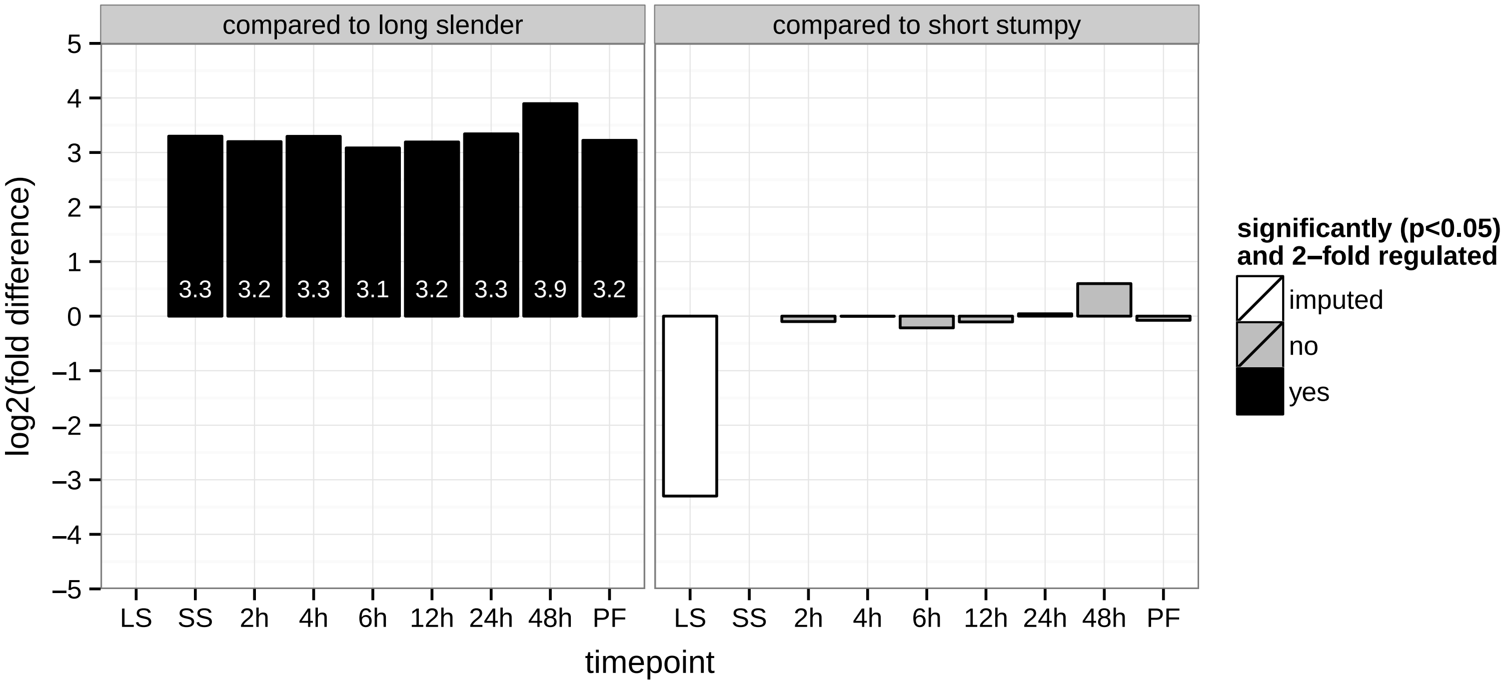
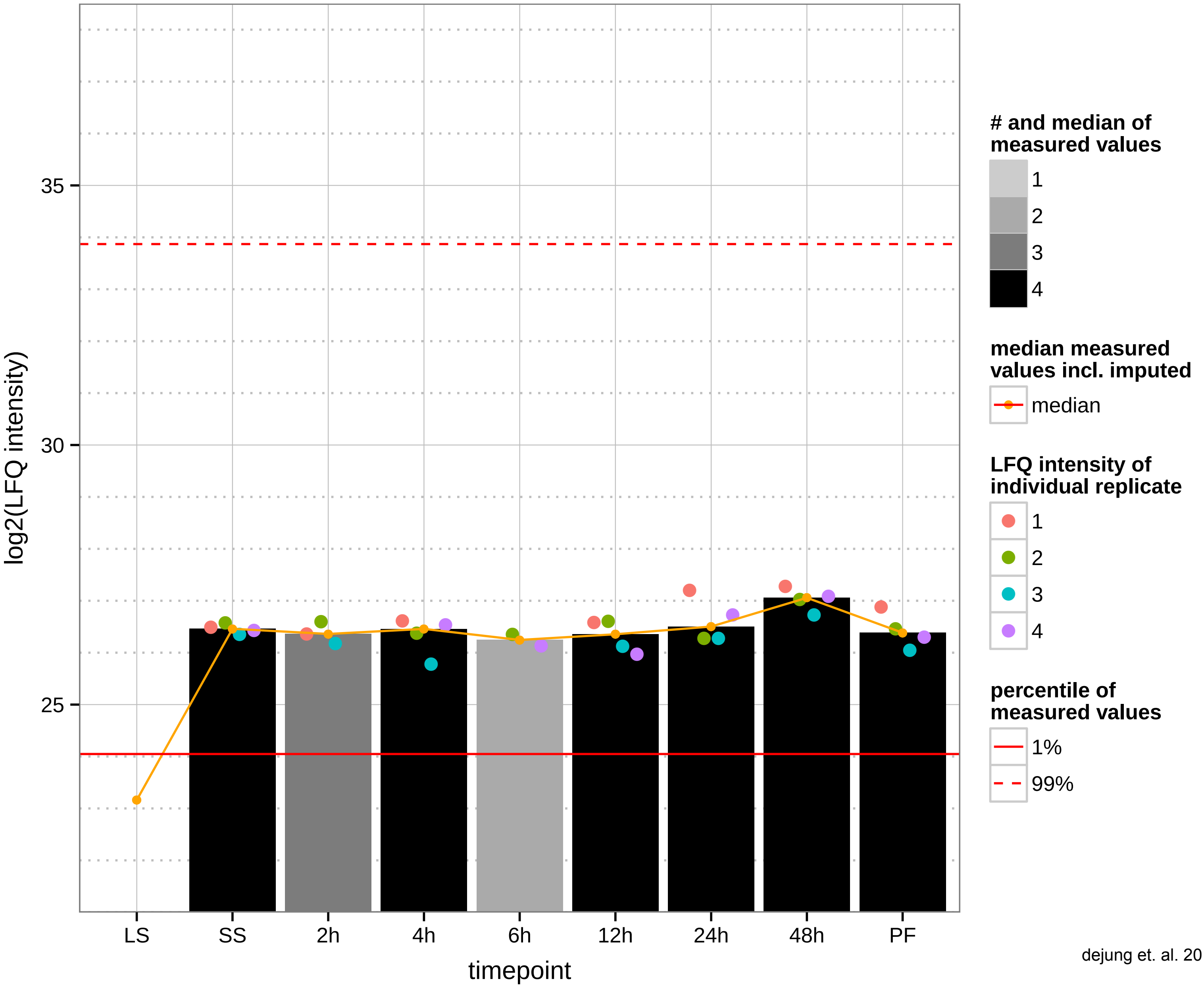
hypothetical protein, conserved
Tb927.11.3480
AGOF: null
AGOC: null
AGOP: null
PGOF: DNA–directed RNA polymerase activity
PGOC: nucleus
PGOP: transcription, DNA–dependent





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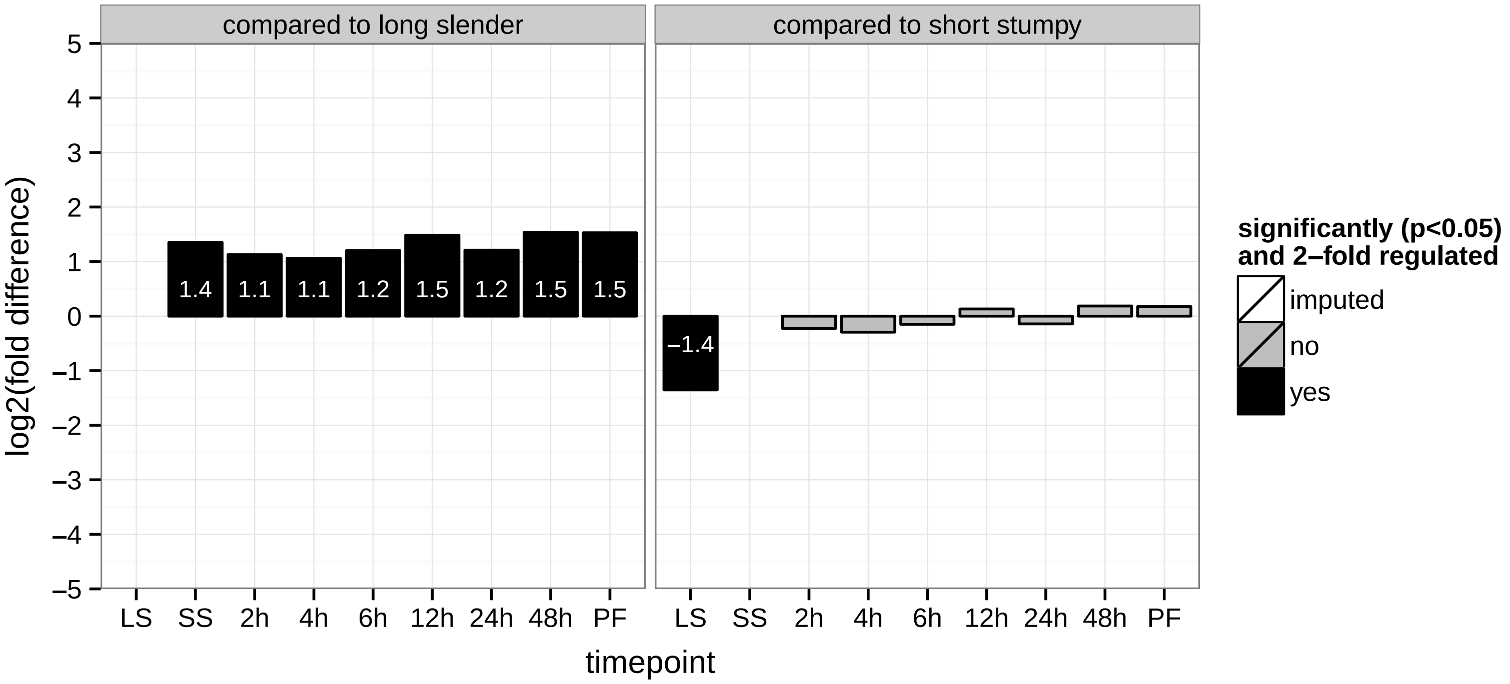
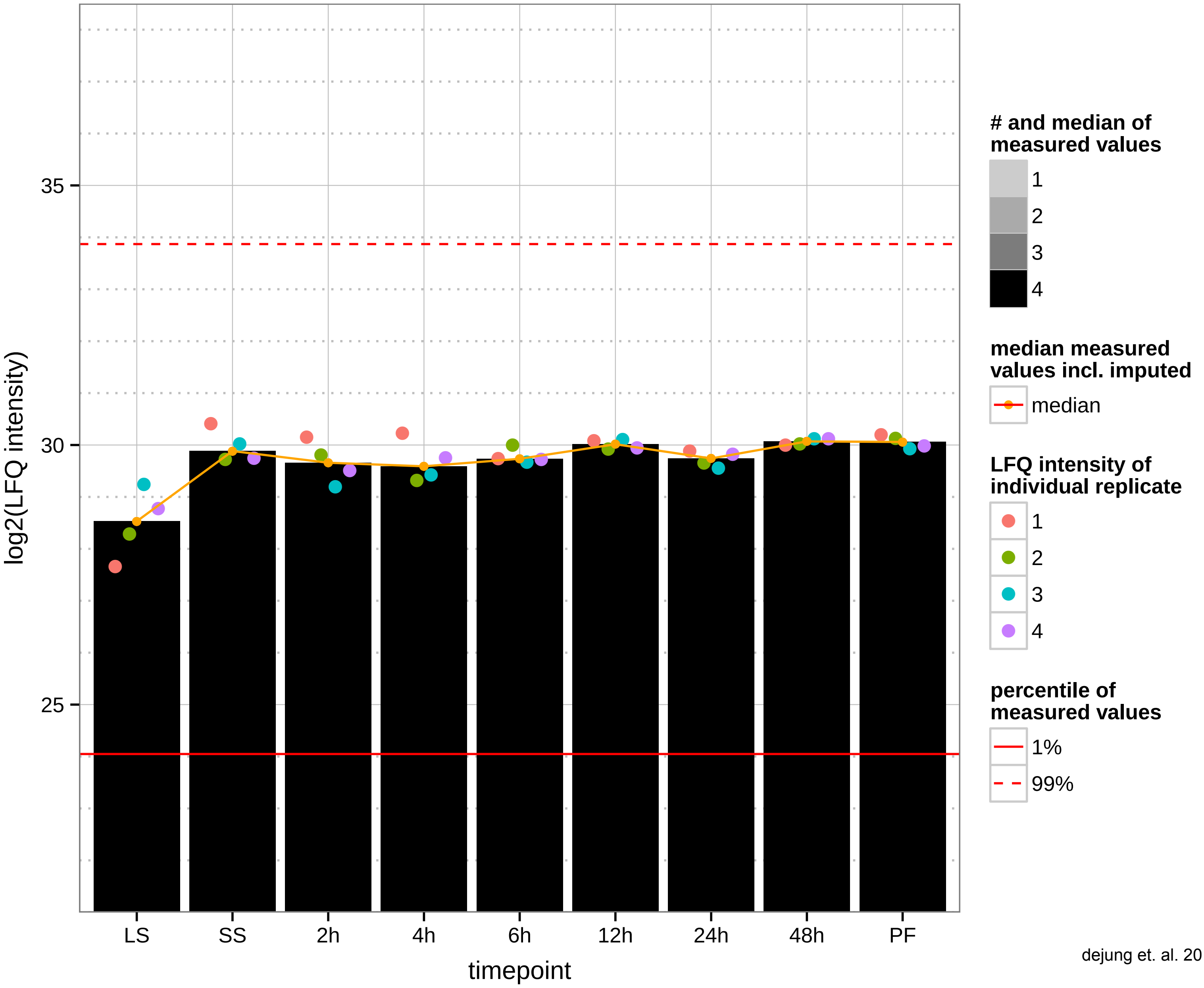
hypothetical protein, conserved
Tb927.11.3490
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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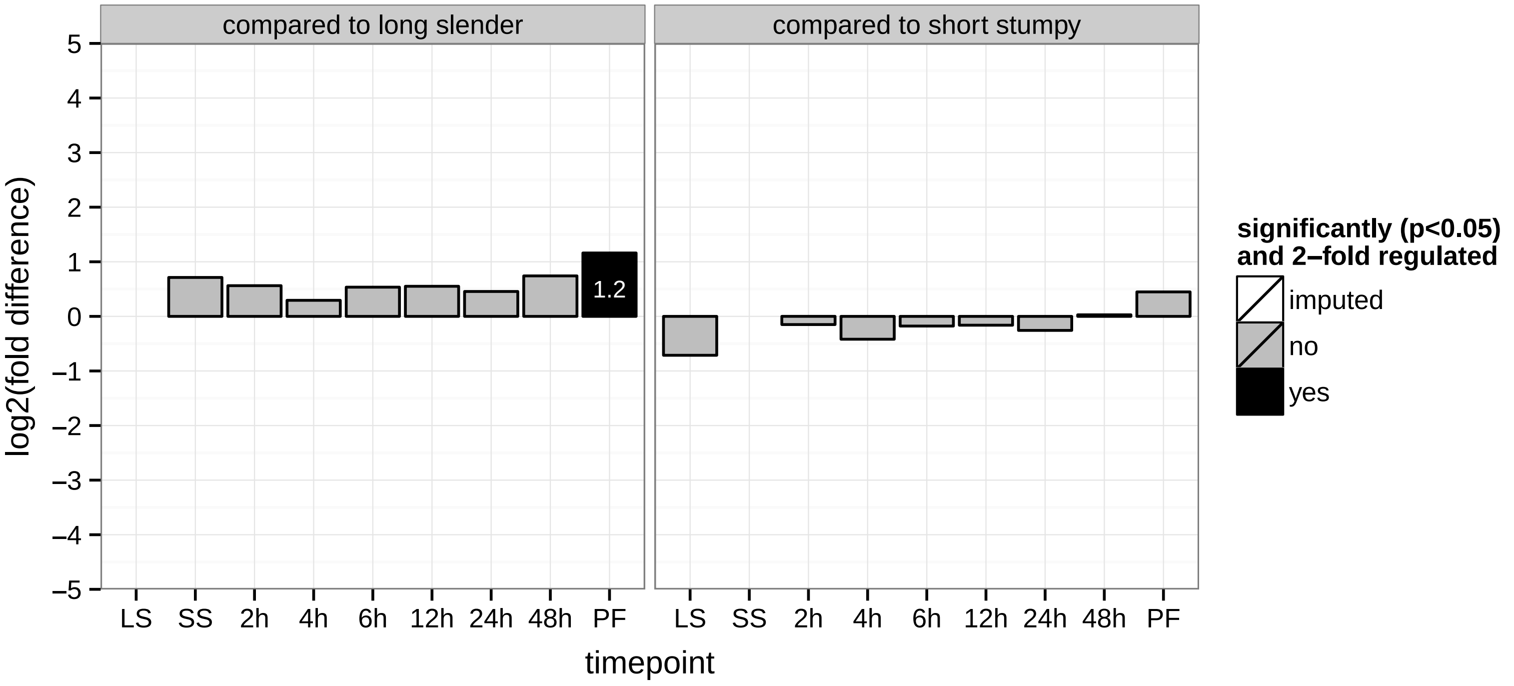
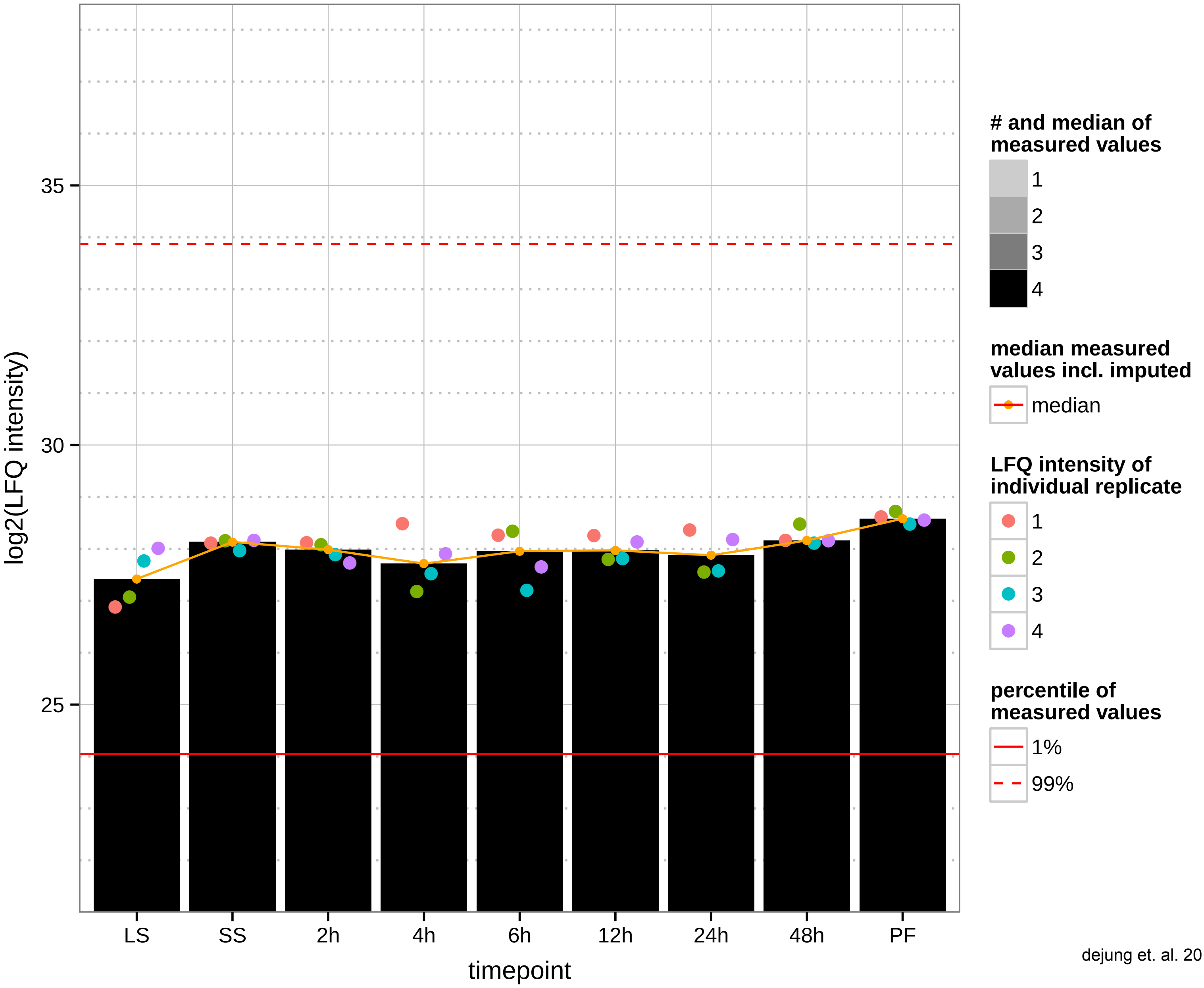
hypothetical protein, conserved
Tb927.11.3500
AGOF: catalytic activity
AGOC: null
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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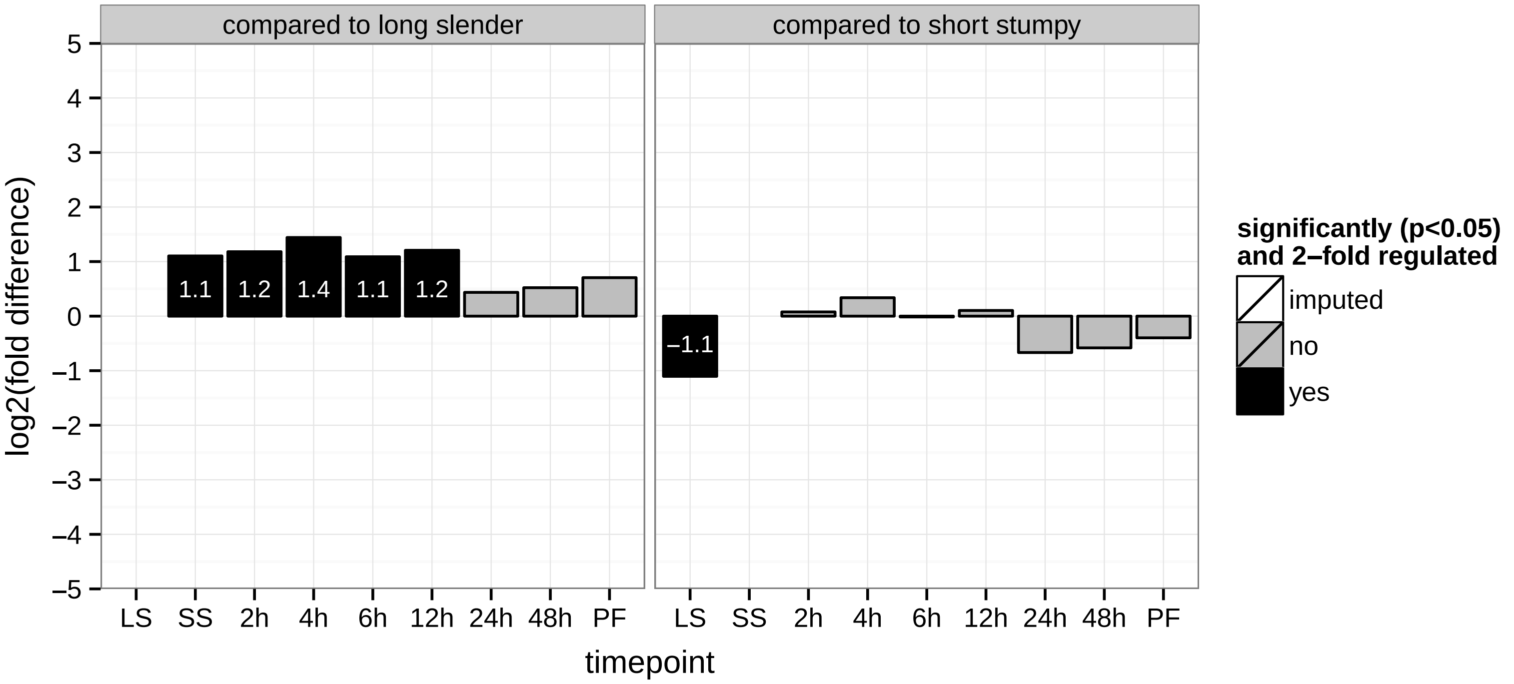
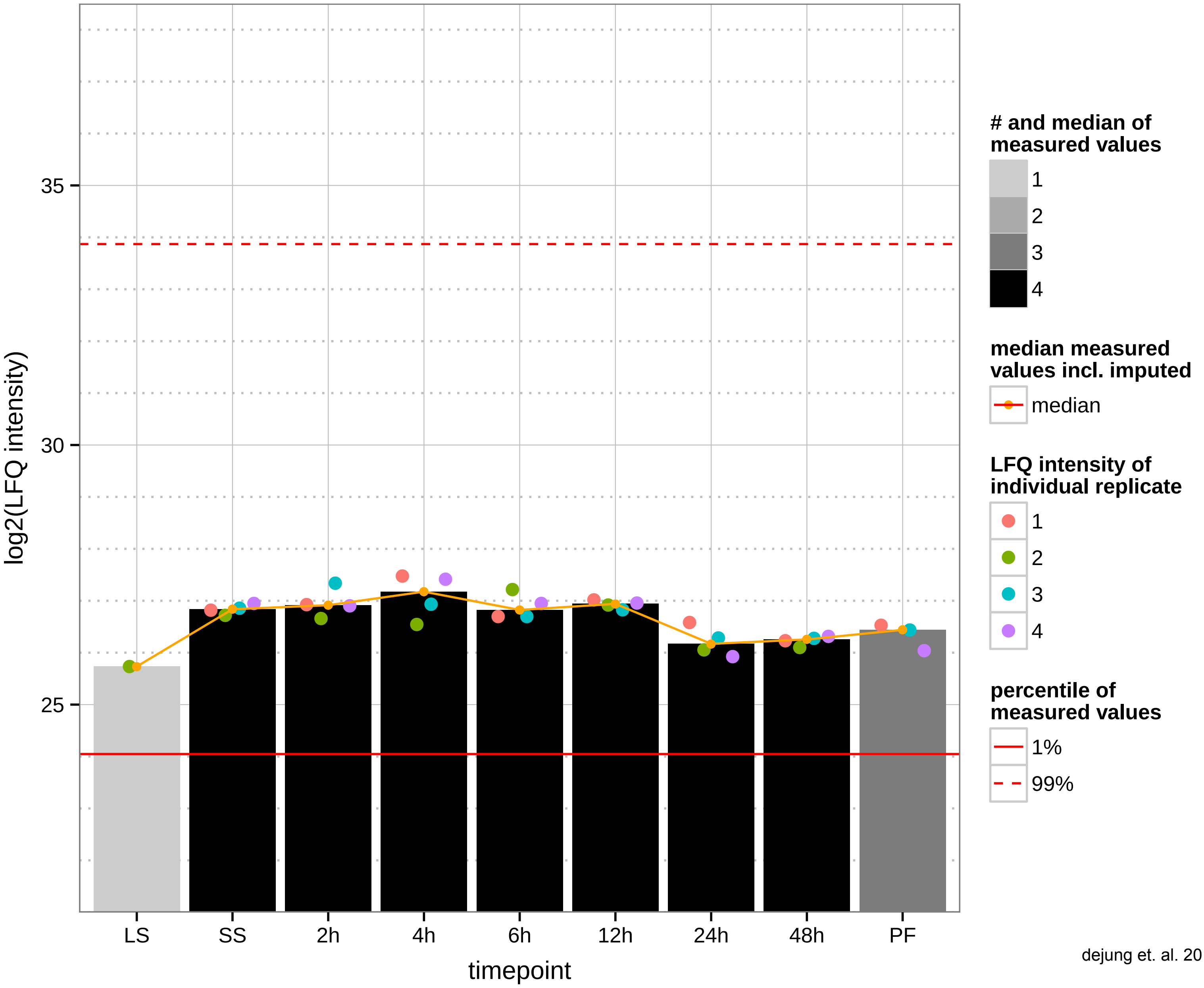
hypothetical protein, conserved
Tb927.11.3510
AGOF: null
AGOC: null
AGOP: protein folding
PGOF: null
PGOC: null
PGOP: protein folding





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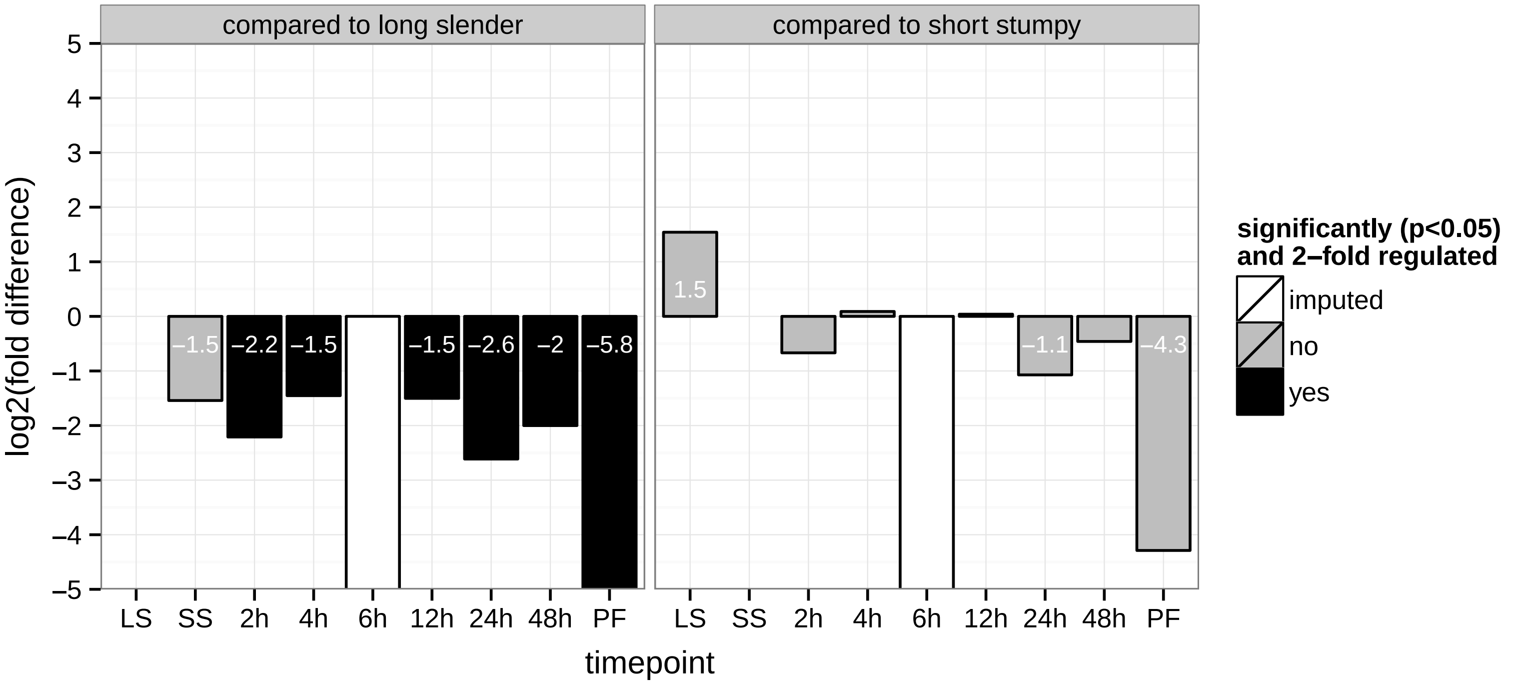
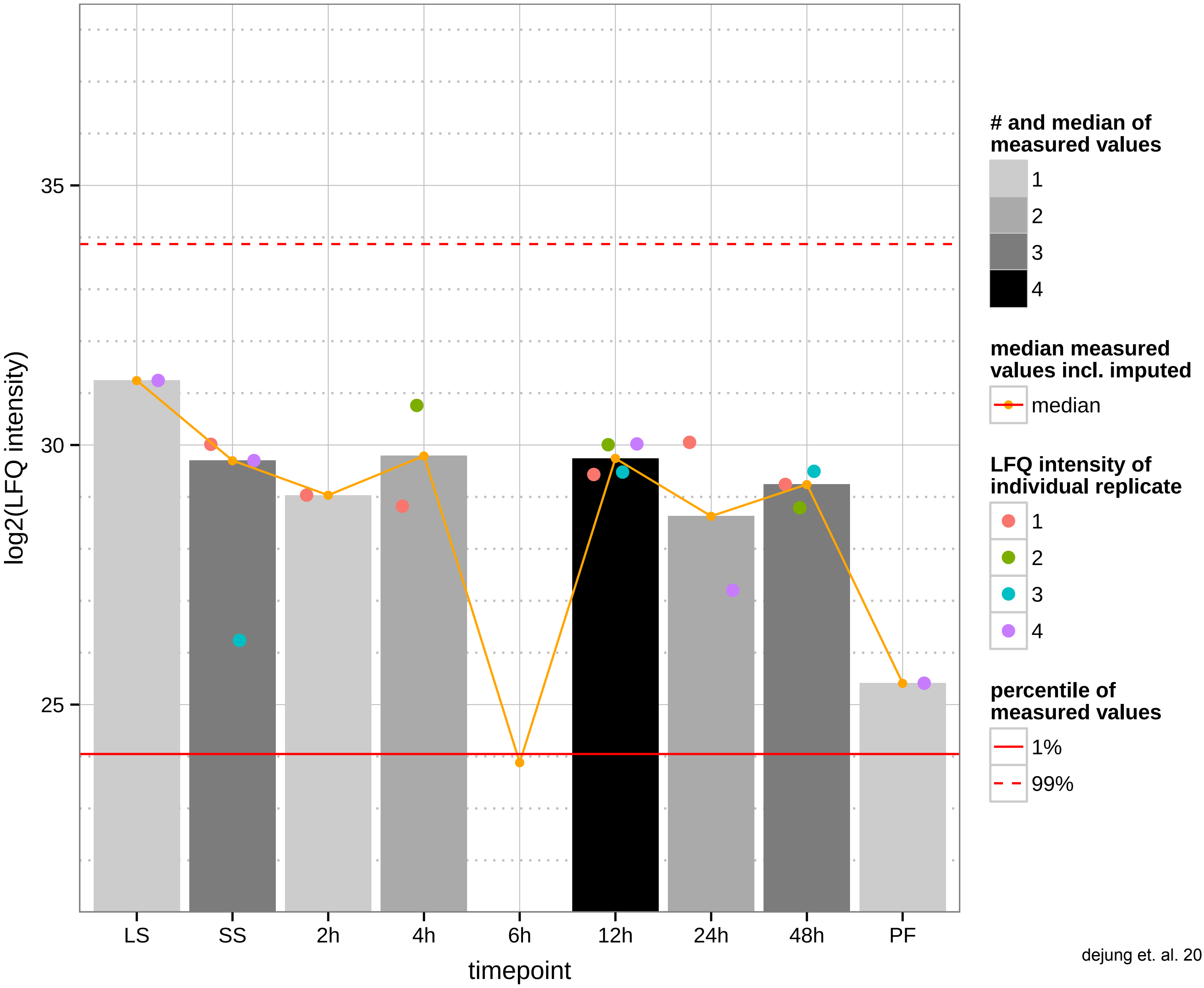
hypothetical protein, conserved
Tb927.11.3540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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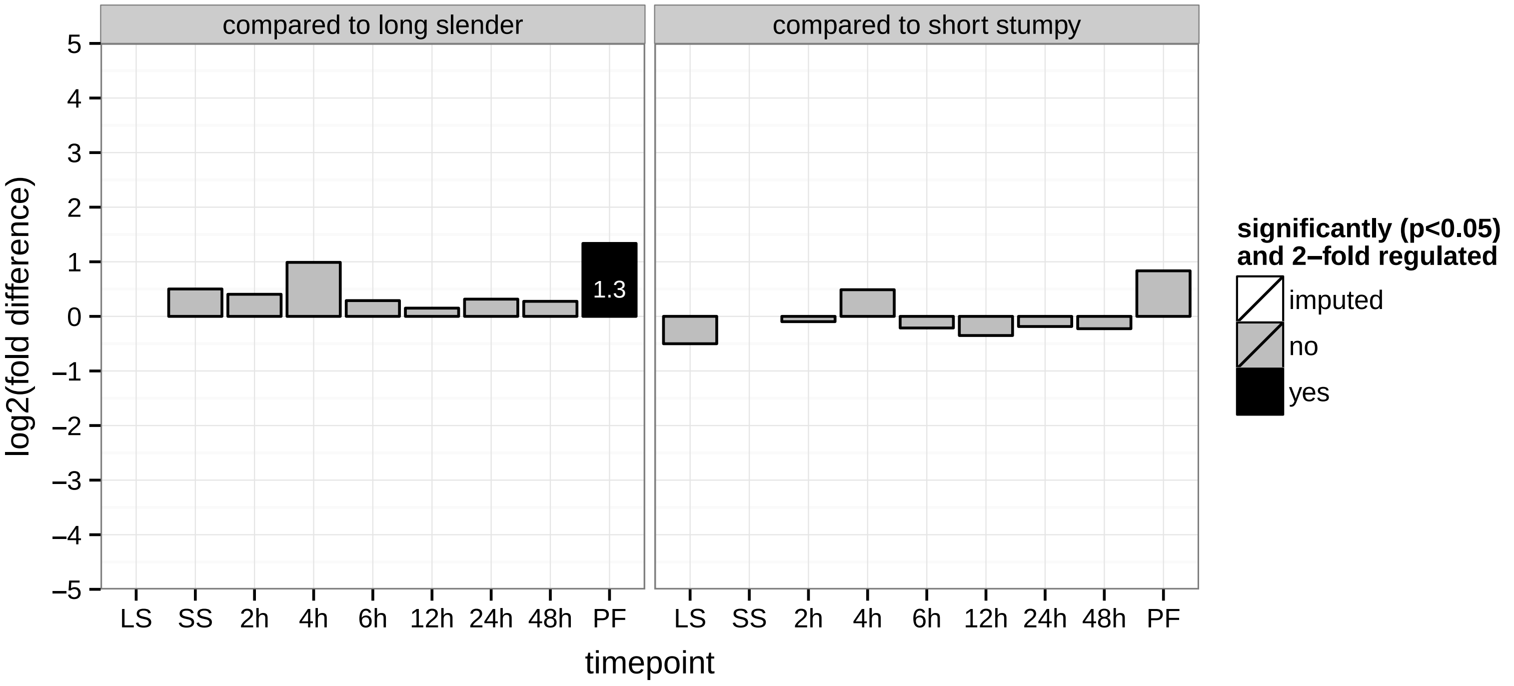
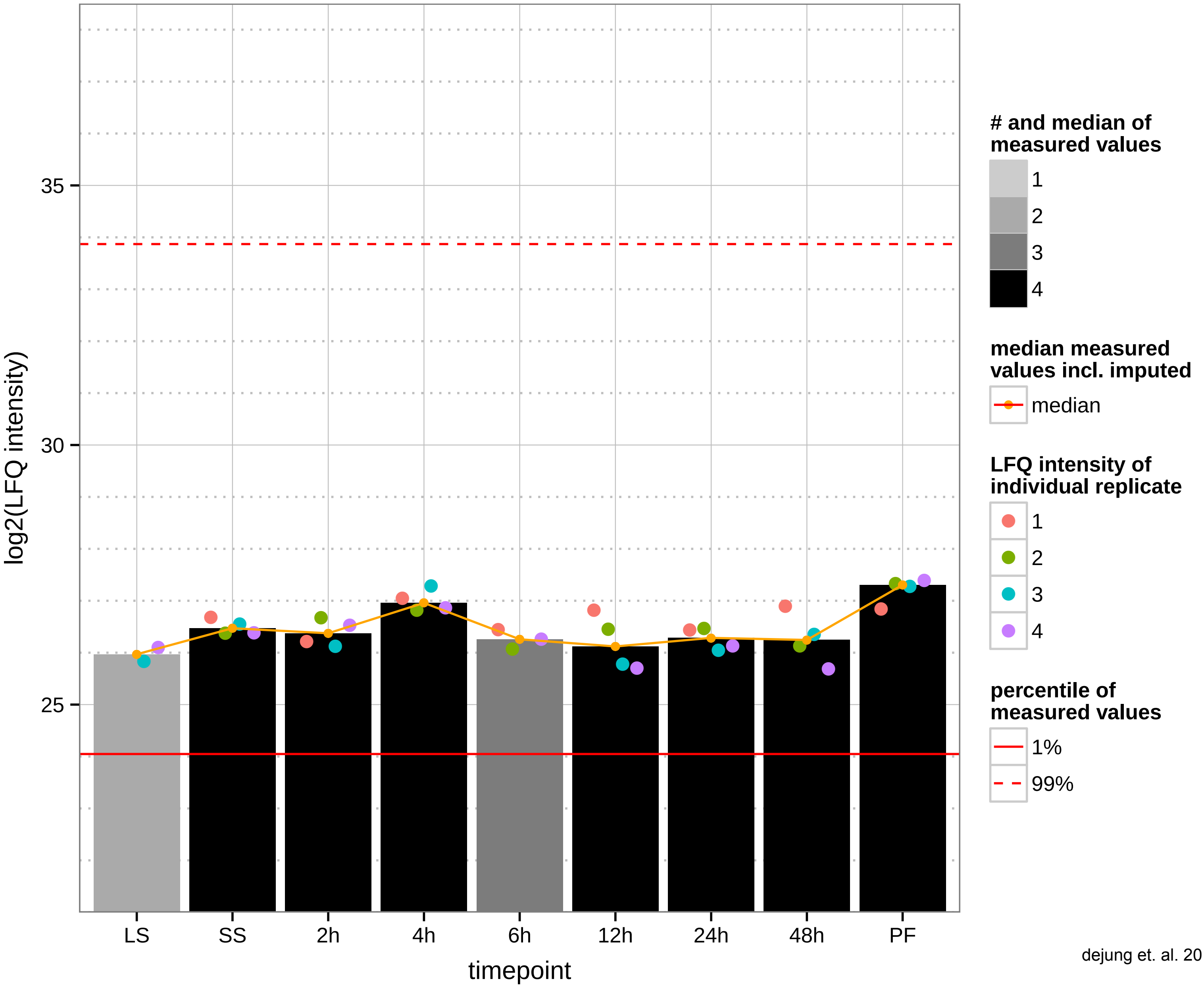
XPA–interacting protein, putative
Tb927.11.3550
AGOF: GTP binding, nucleoside–triphosphatase activity
AGOC: null
AGOP: small GTPase mediated signal transduction
PGOF: nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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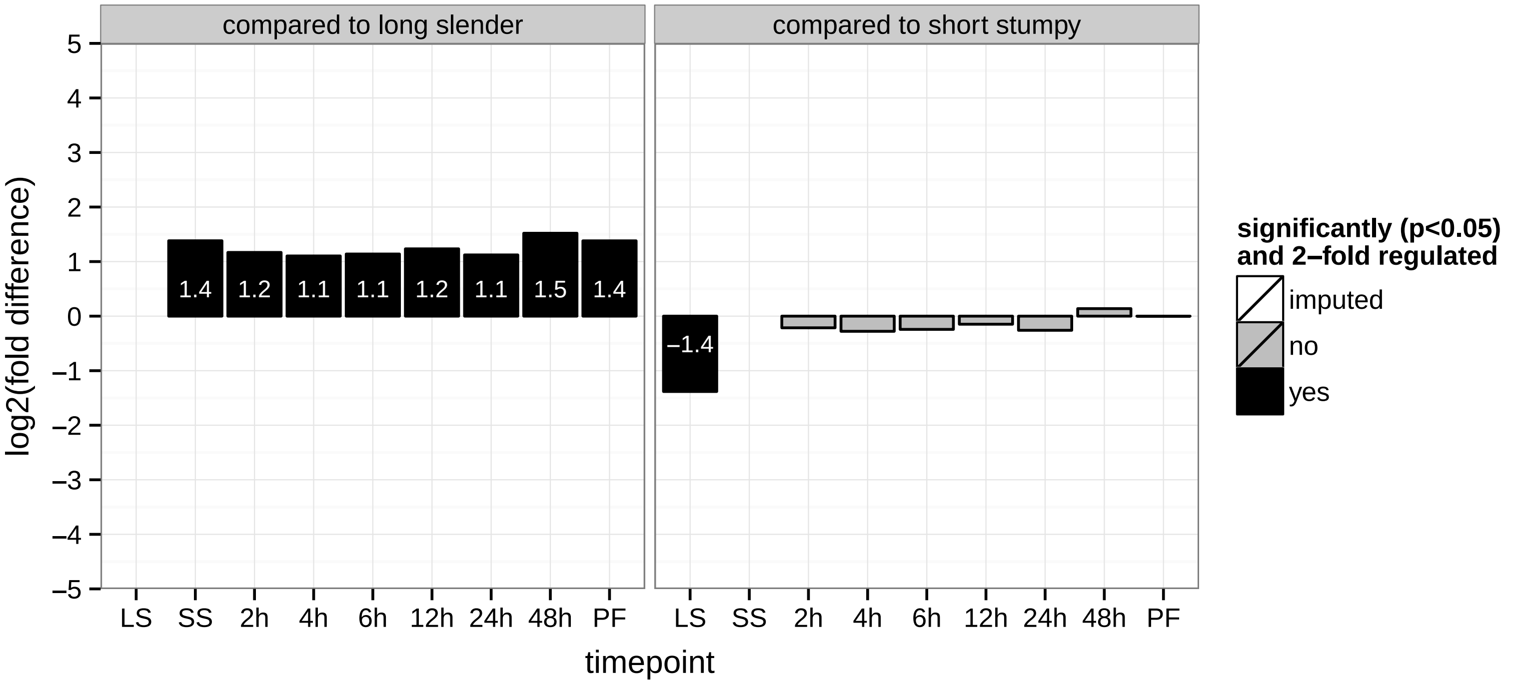
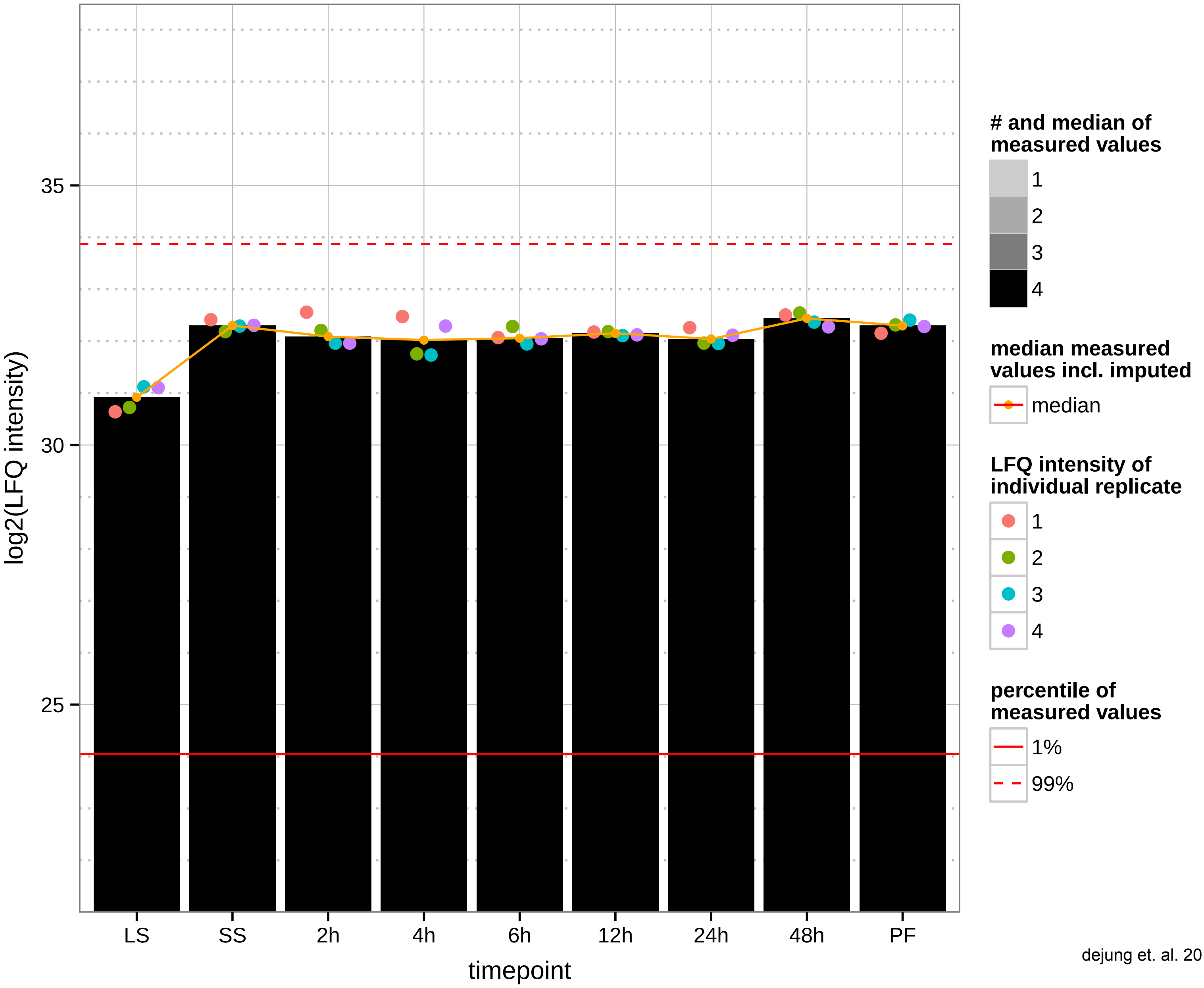
aminopeptidase, putative, metallo–peptidase, Clan MA(E) Family M1
Tb927.11.3570
AGOF: metalloexopeptidase activity, metallopeptidase activity, zinc ion binding
AGOC: null
AGOP: proteolysis
PGOF: metallopeptidase activity, zinc ion binding
PGOC: null
PGOP: null





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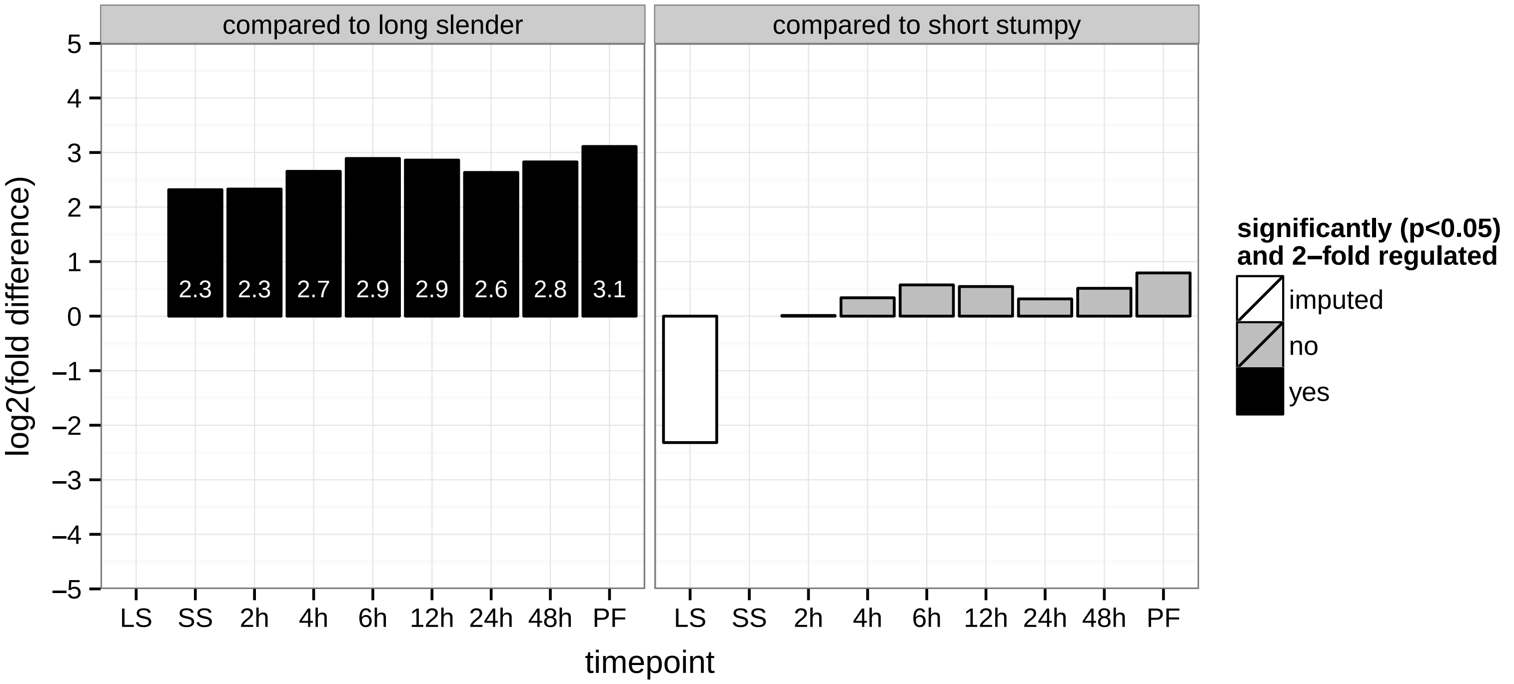
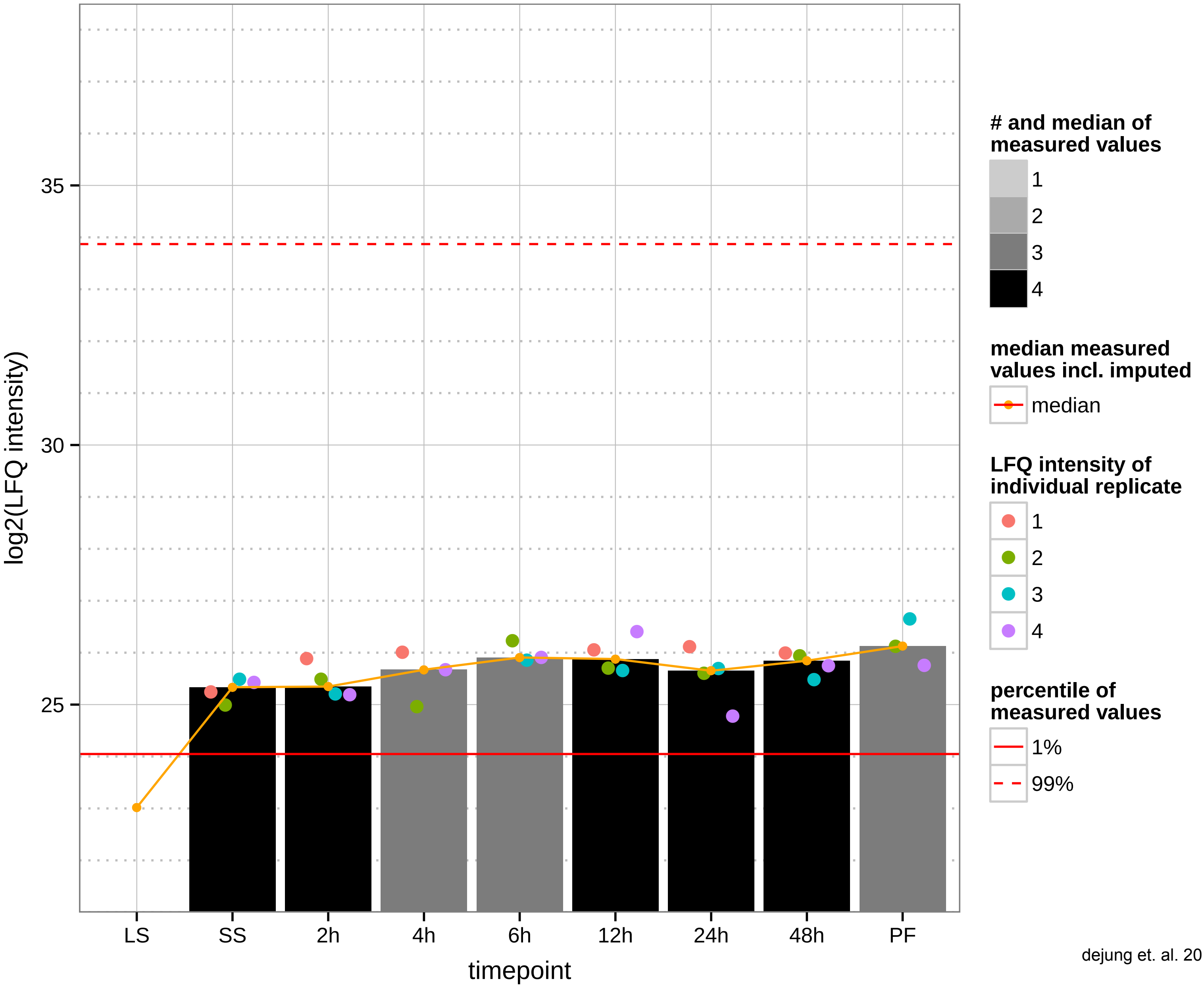
hypothetical protein, conserved
Tb927.11.3580
AGOF: ATP binding, thiamine diphosphokinase activity
AGOC: null
AGOP: thiamine diphosphate biosynthetic process
PGOF: ATP binding, thiamine diphosphokinase activity
PGOC: null
PGOP: thiamine diphosphate biosynthetic process





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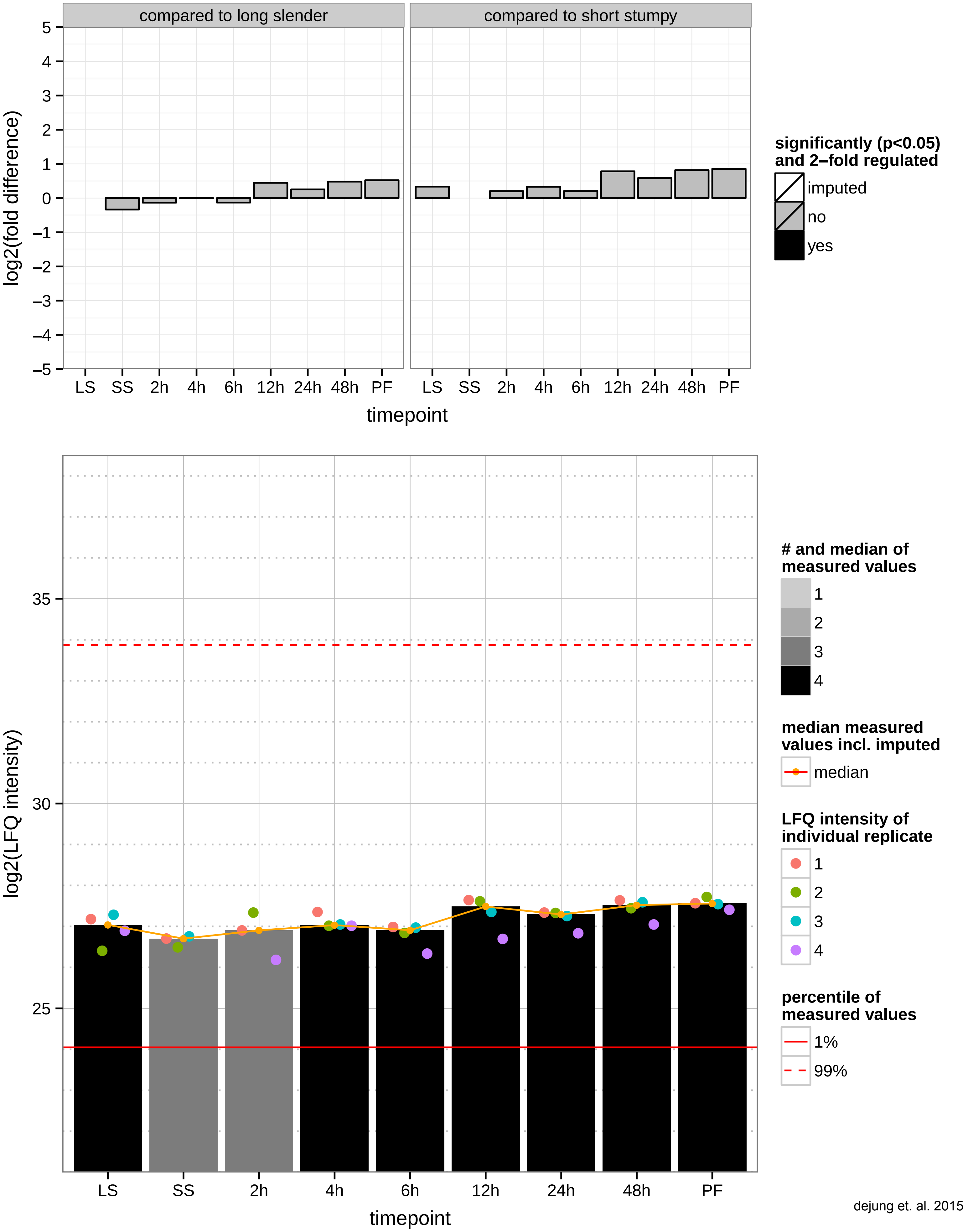
Dynein light chain Tctex–type, putative
Tb927.11.3660
AGOF: microtubule motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based process
PGOF: null
PGOC: null
PGOP: null



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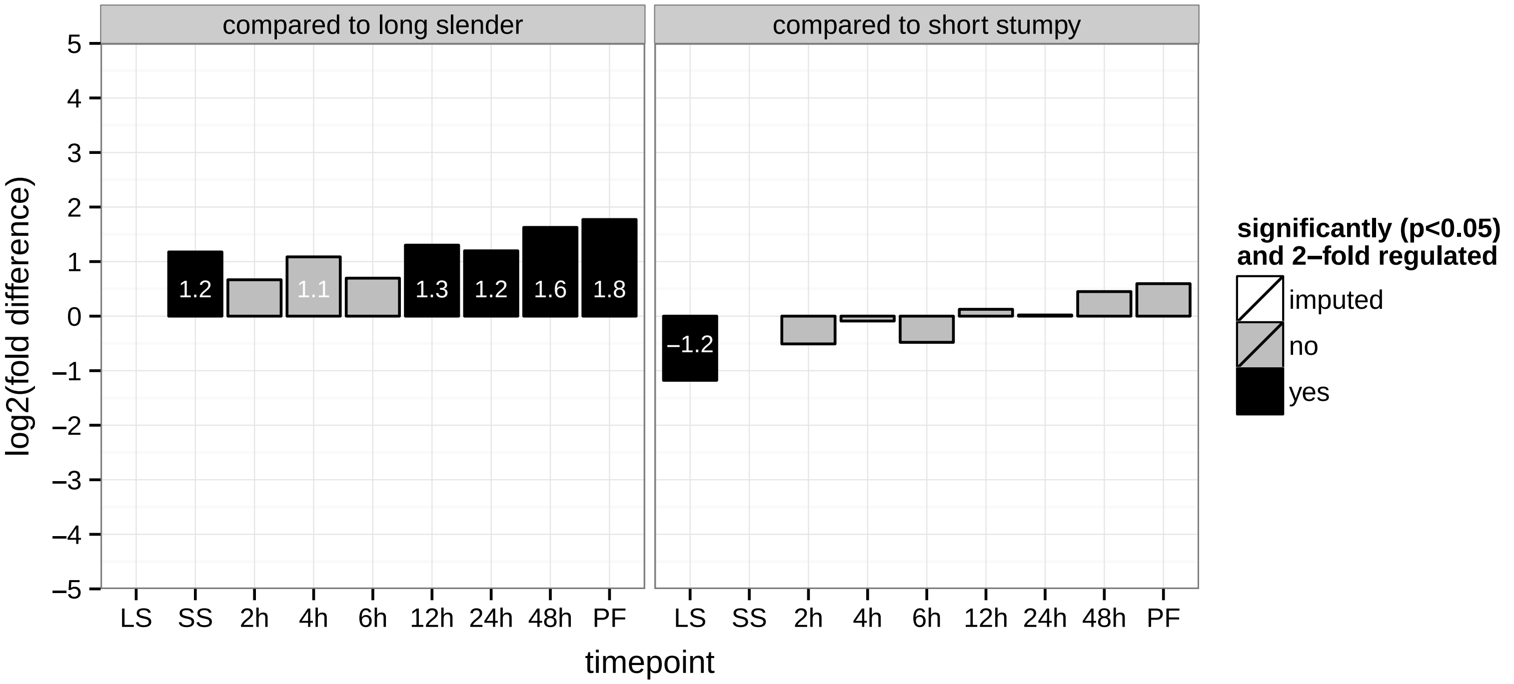
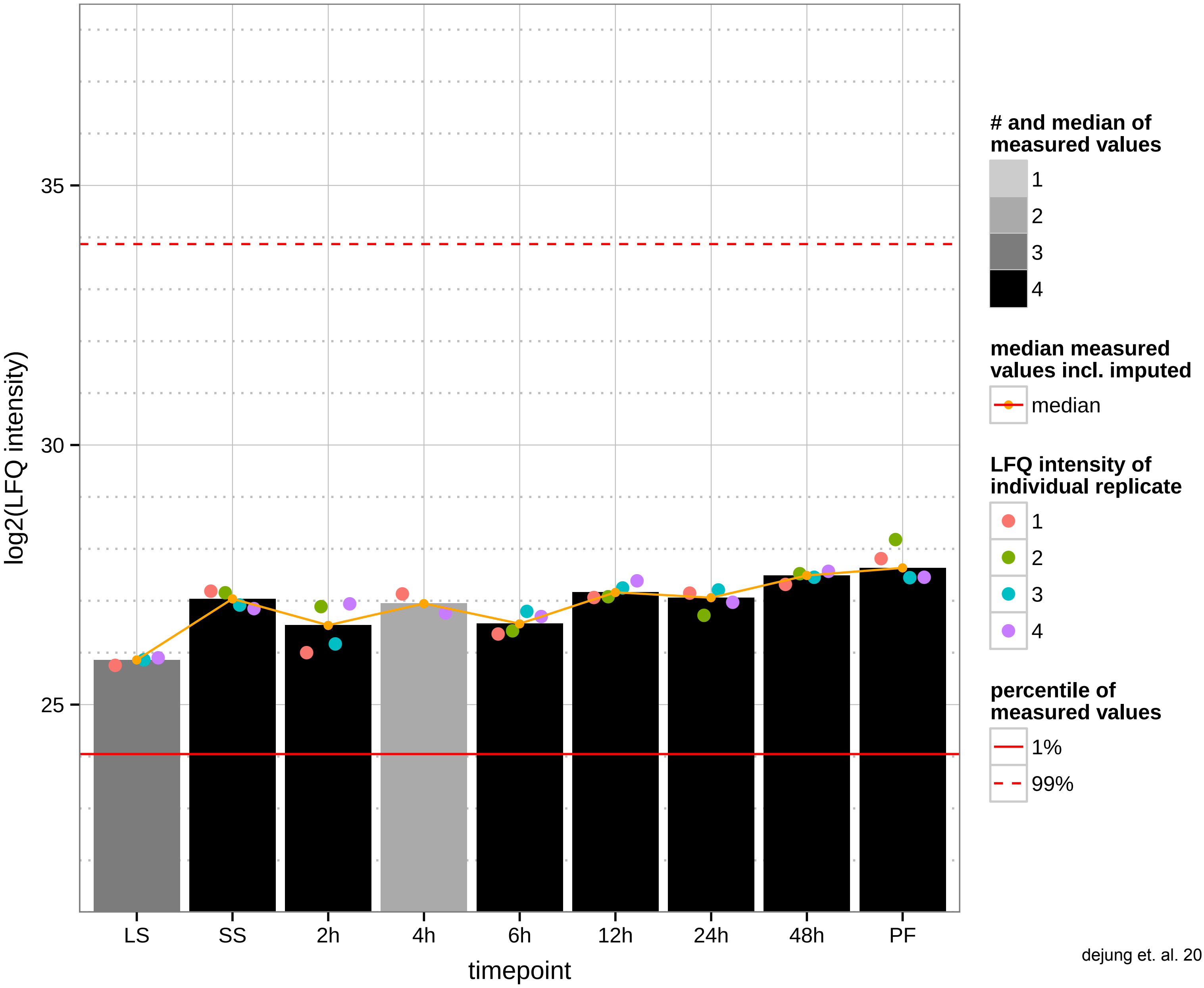
repressor activator protein 1 (RAP1)
Tb927.11.370
AGOF: null
AGOC: nuclear chromosome, telomeric region, nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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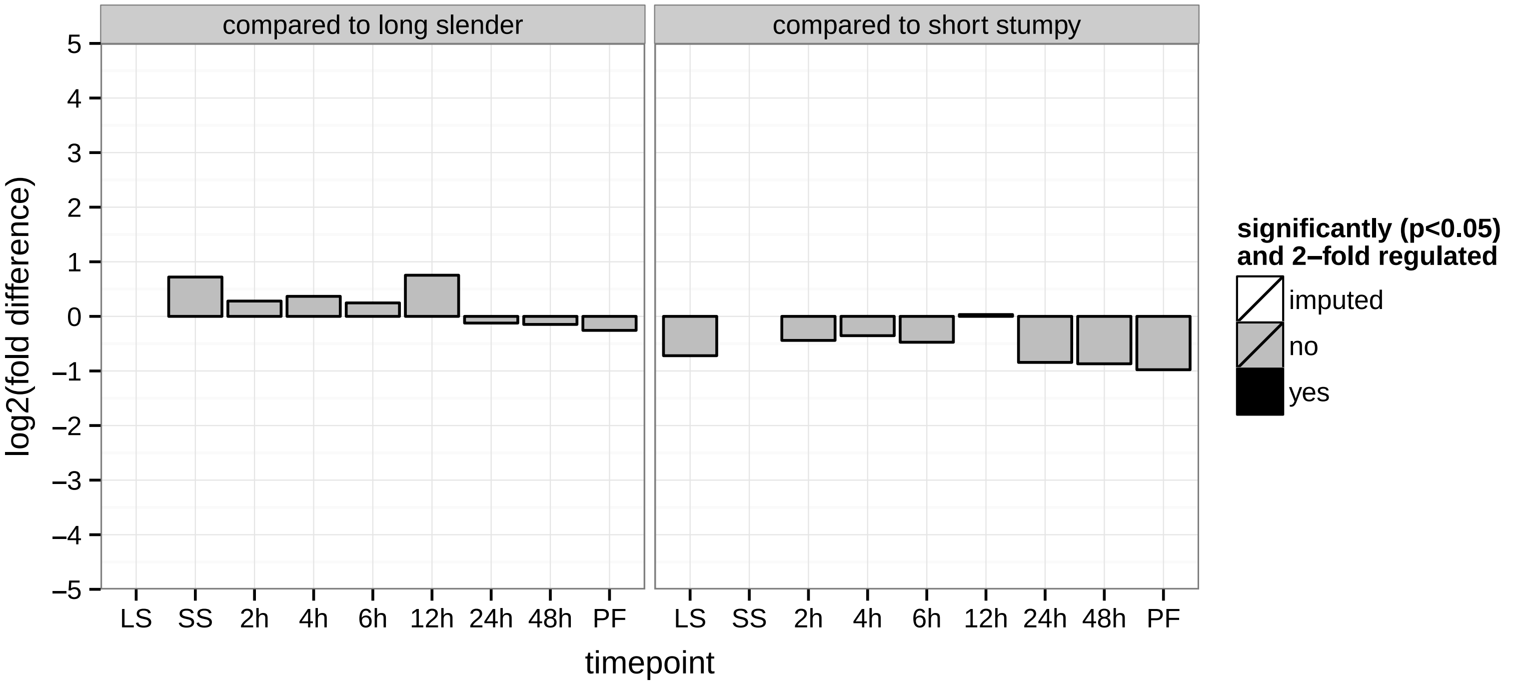
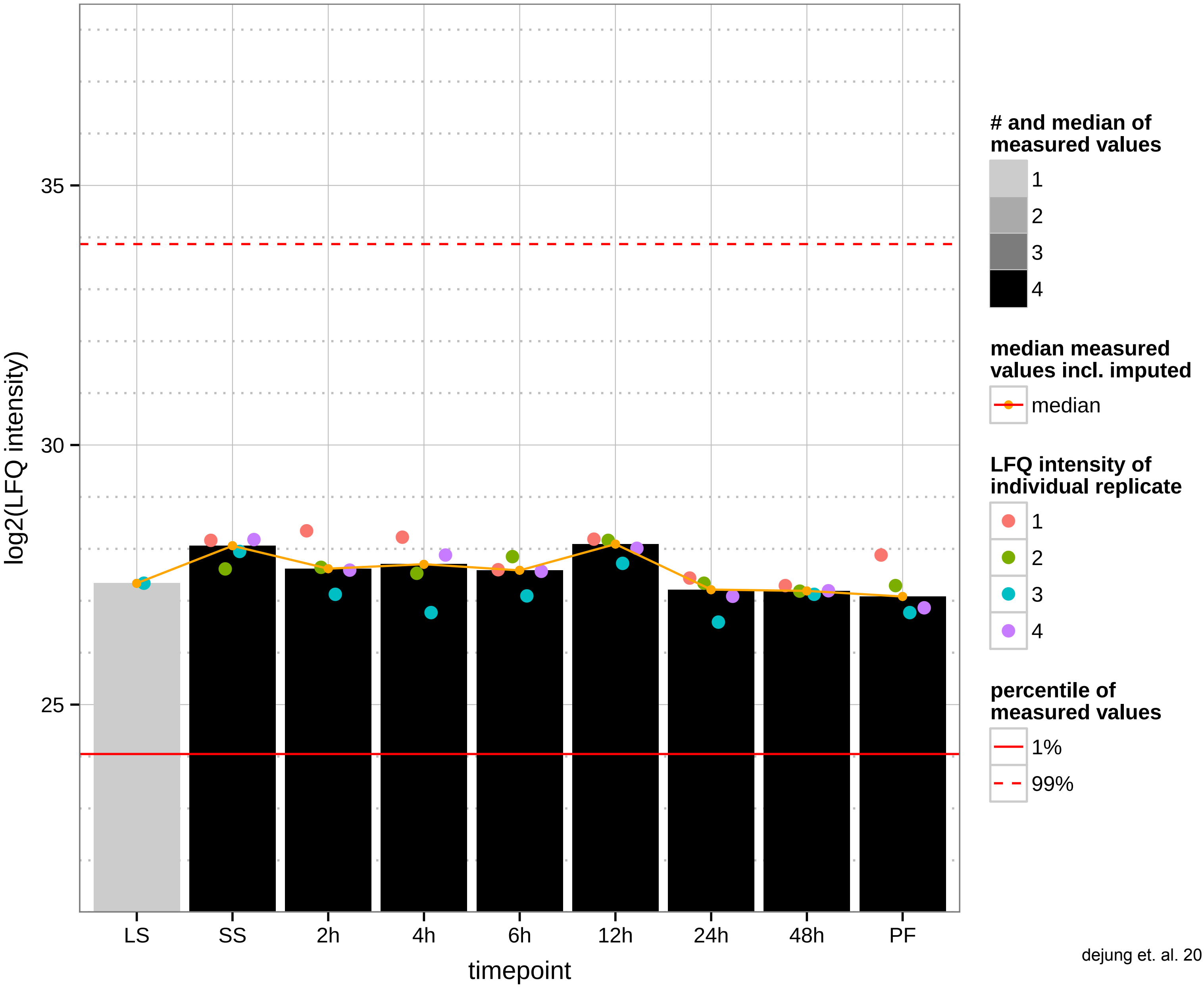
hypothetical protein, conserved
Tb927.11.3700
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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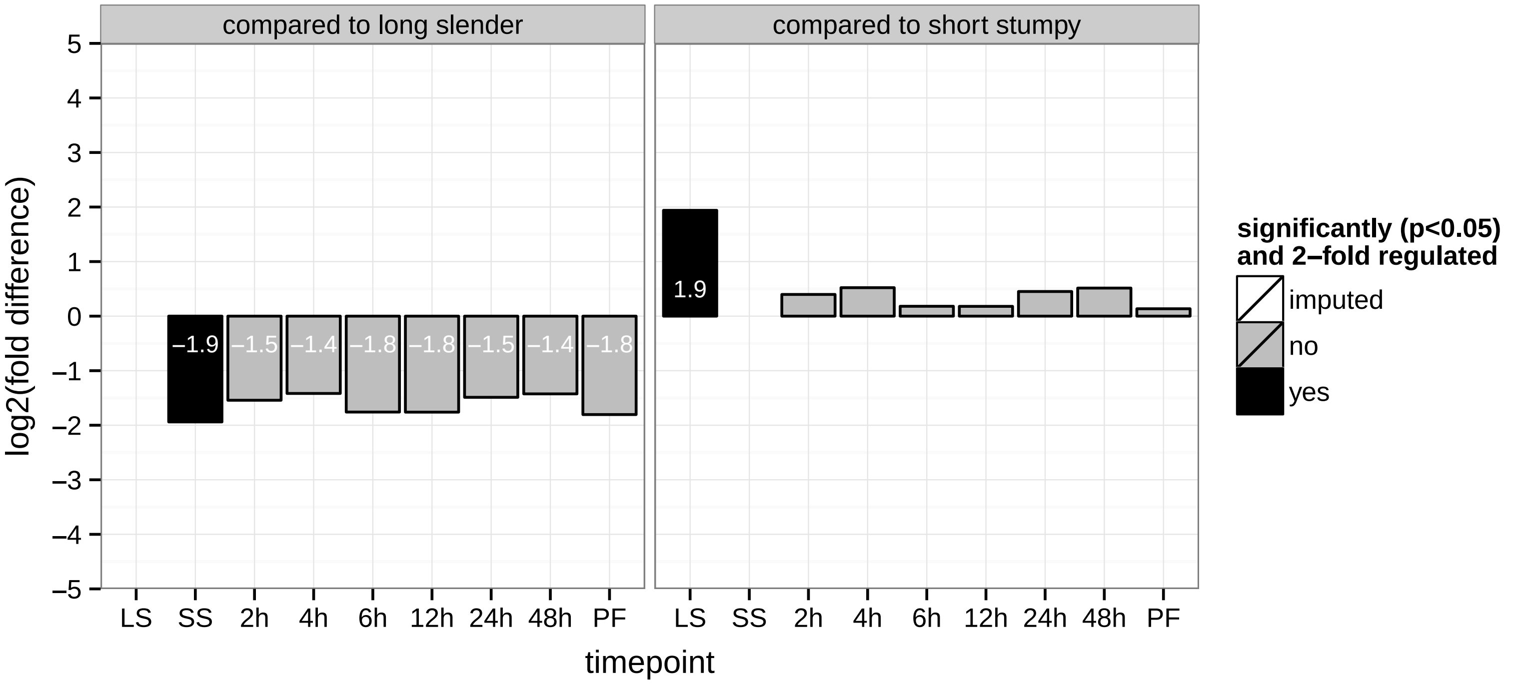
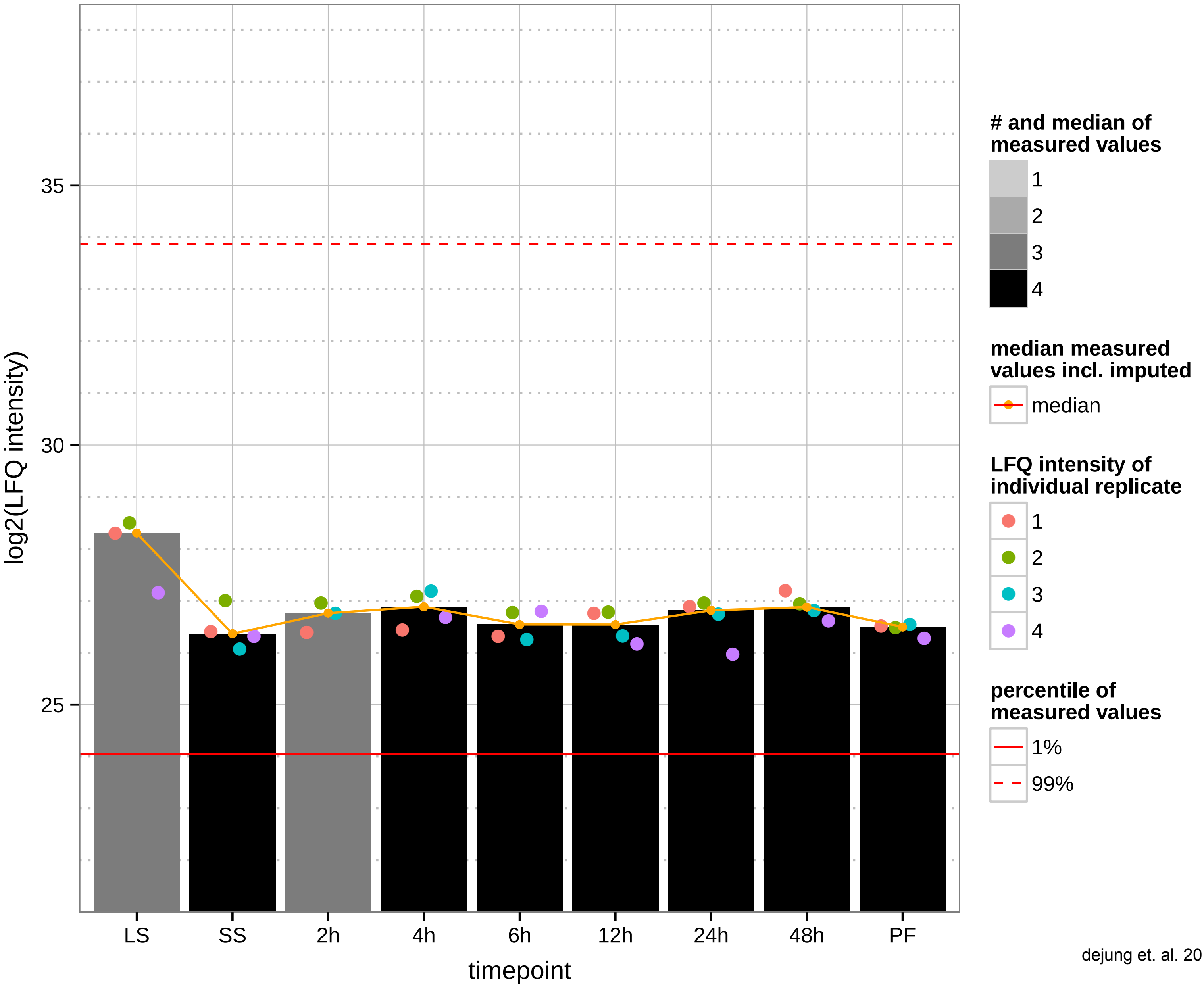
hypothetical protein, conserved
Tb927.11.3710
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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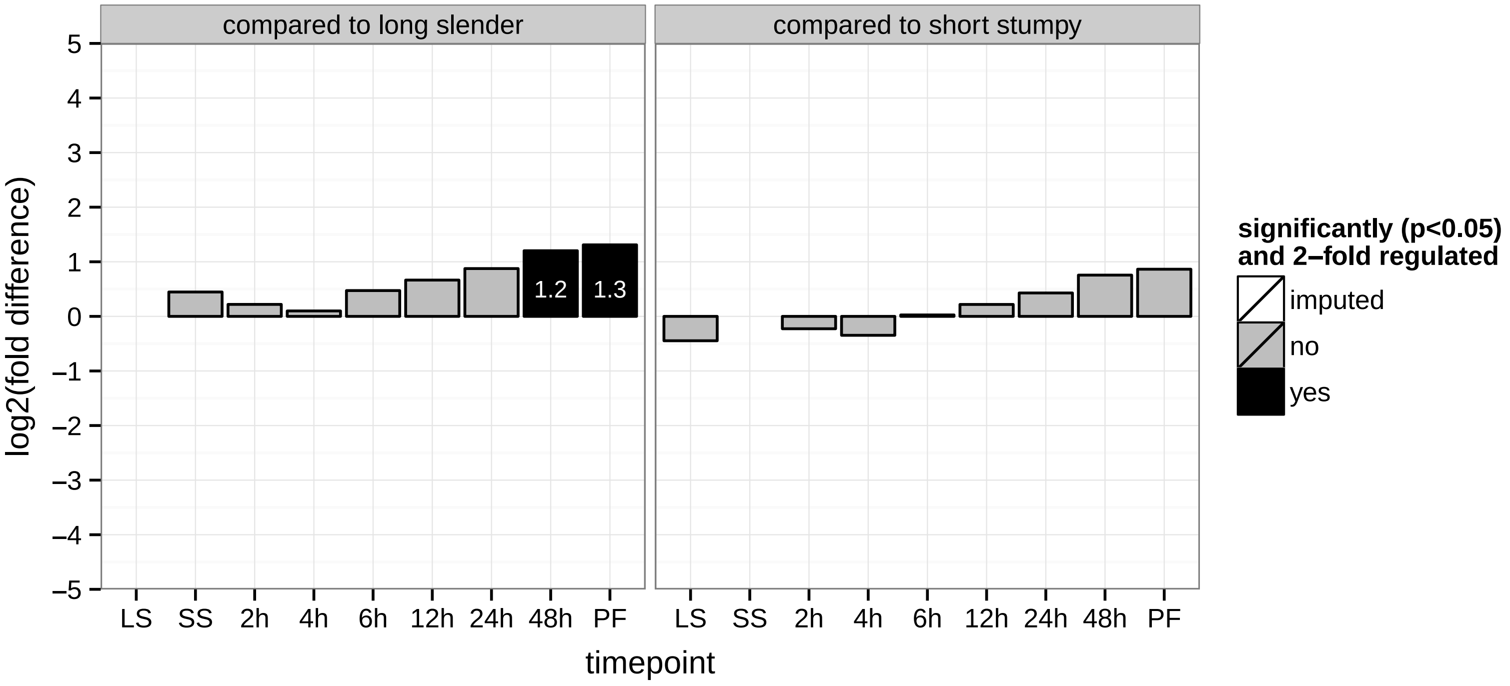
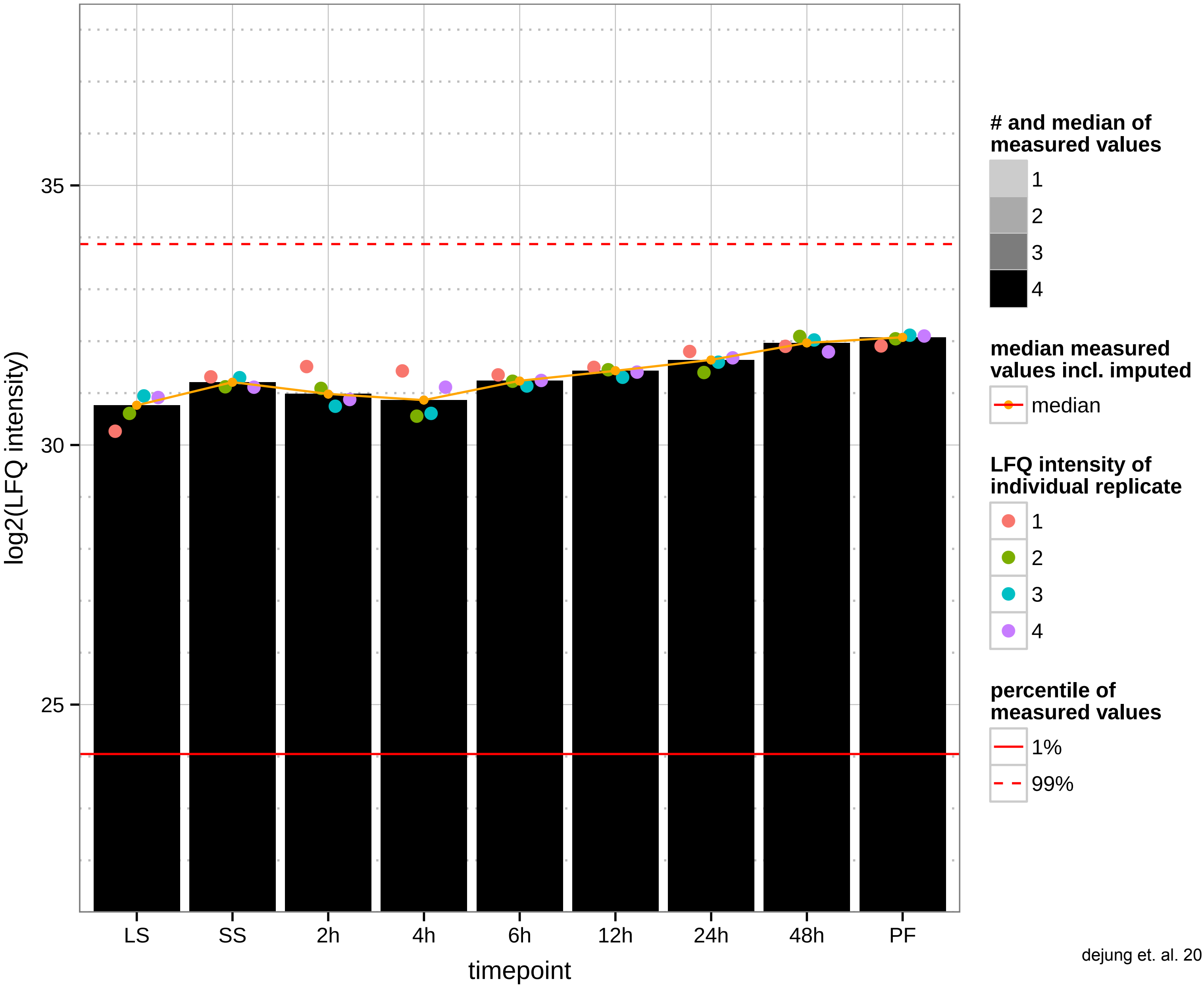
leucyl–tRNA synthetase, putative (LeuRS)
Tb927.11.3730
AGOF: ATP binding, leucine–tRNA ligase activity
AGOC: cytoplasm
AGOP: leucyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA editing activity, aminoacyl–tRNA ligase activity, leucine–tRNA ligase activity, nucleotide
PGOC: cytoplasm
PGOP: leucyl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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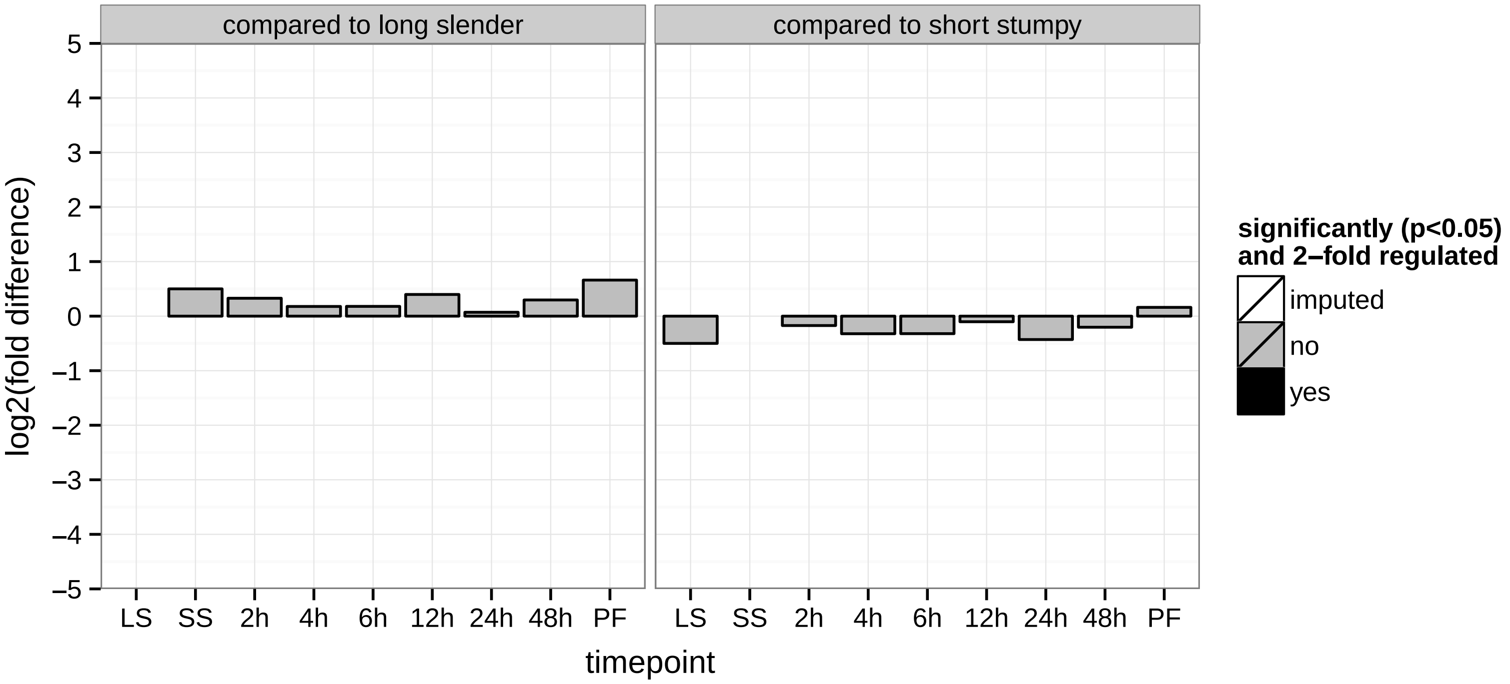
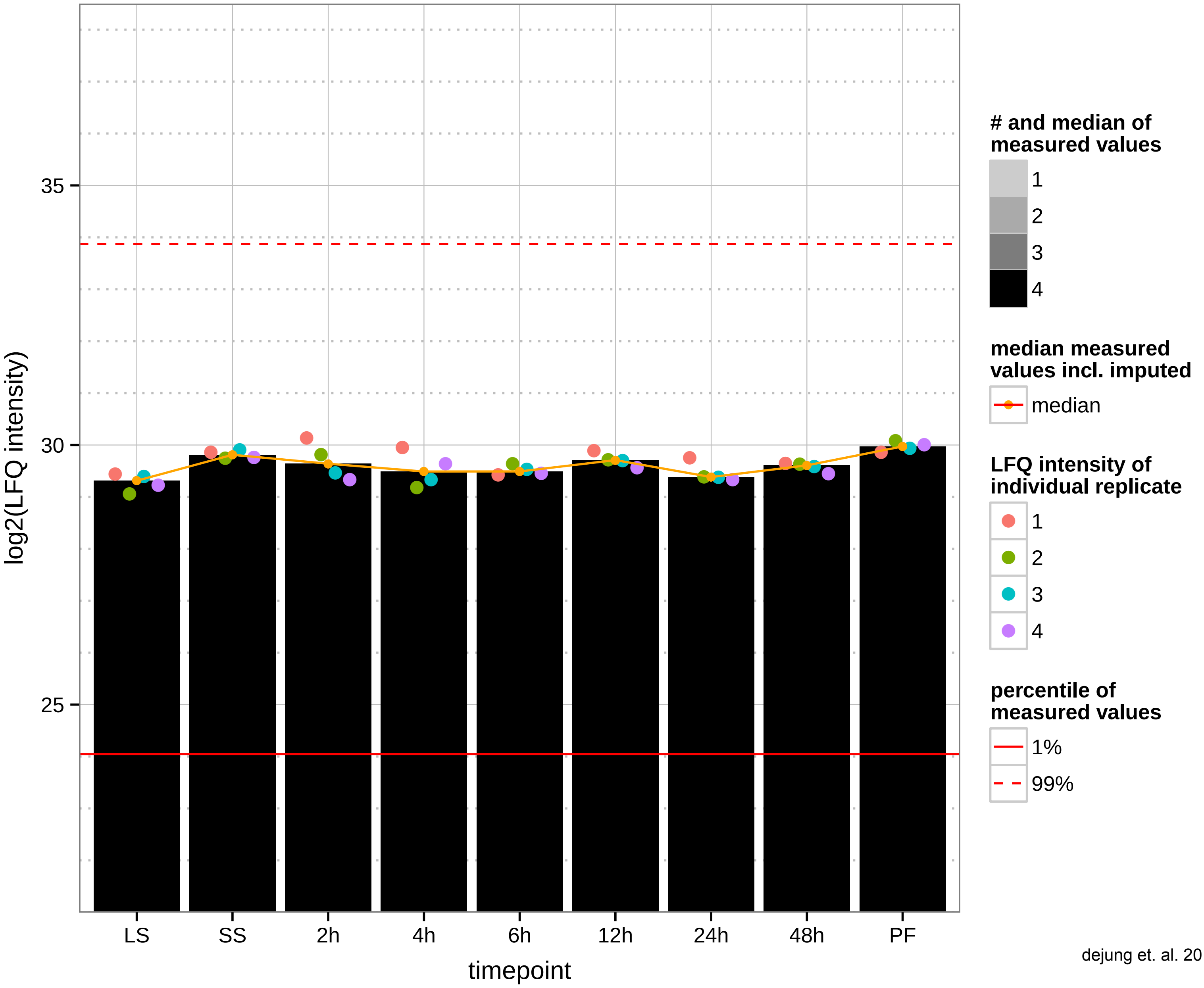
proteasome regulatory ATPase subunit 2 (RPT2)
Tb927.11.3740
AGOF: ATP binding, ATPase activity
AGOC: cytoplasm, nucleus, proteasome regulatory particle
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ATP binding, hydrolase activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: cytoplasm
PGOP: protein catabolic process





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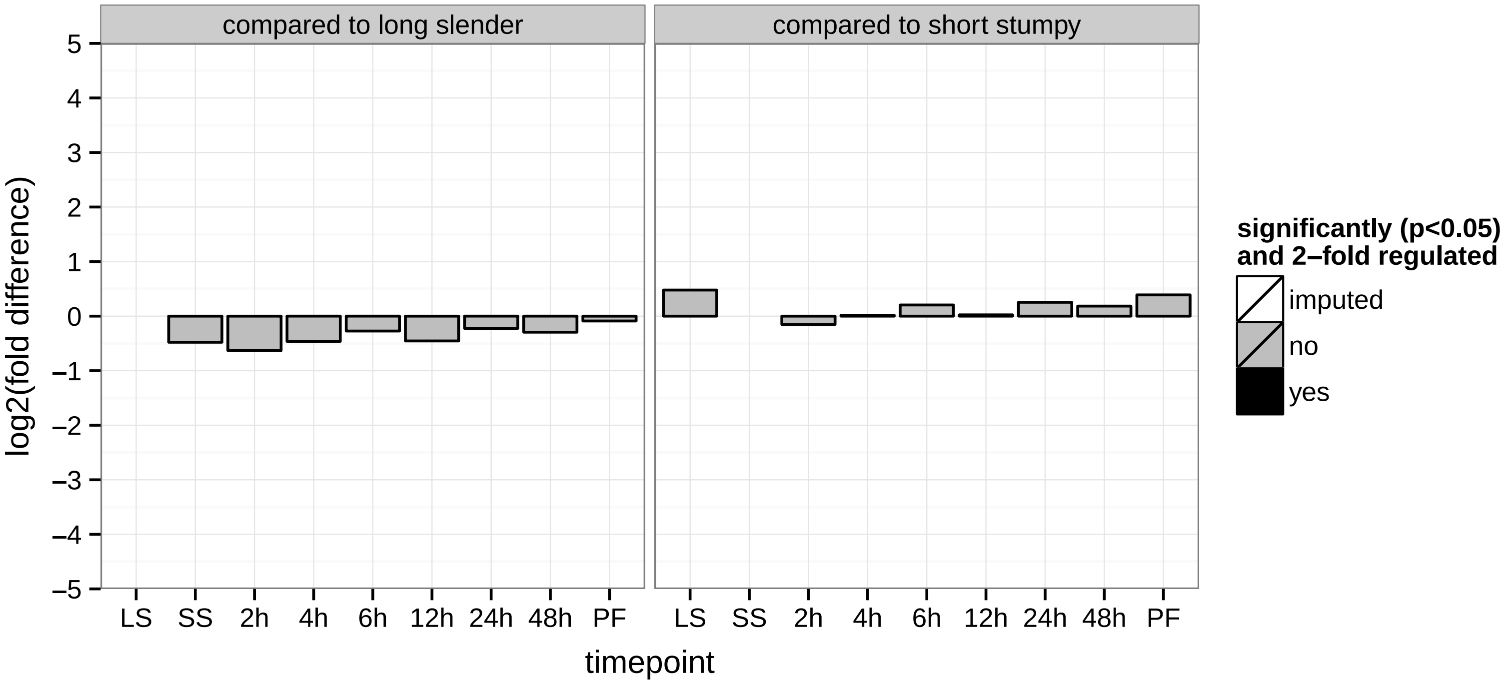
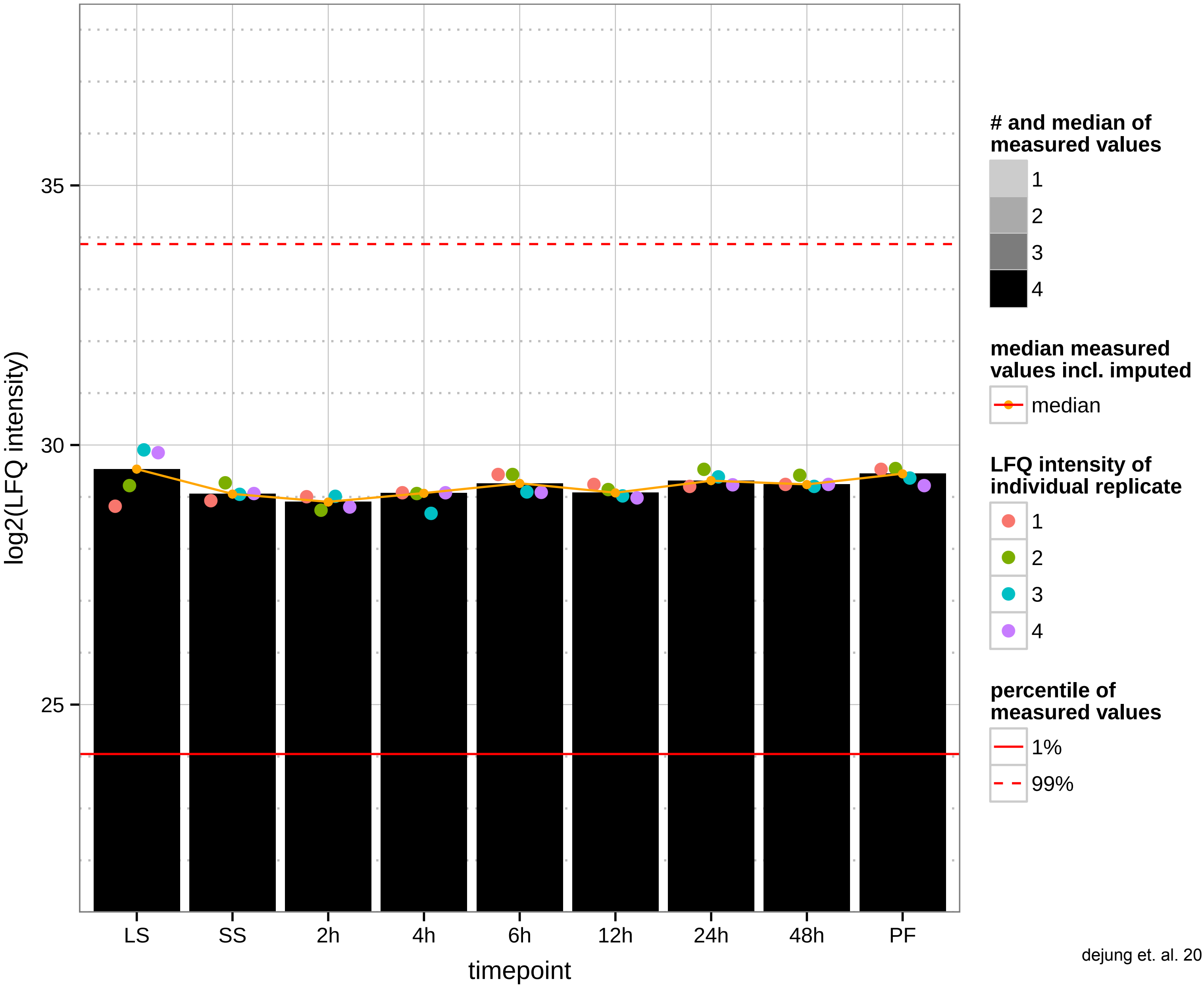
hypothetical protein, conserved
Tb927.11.3770
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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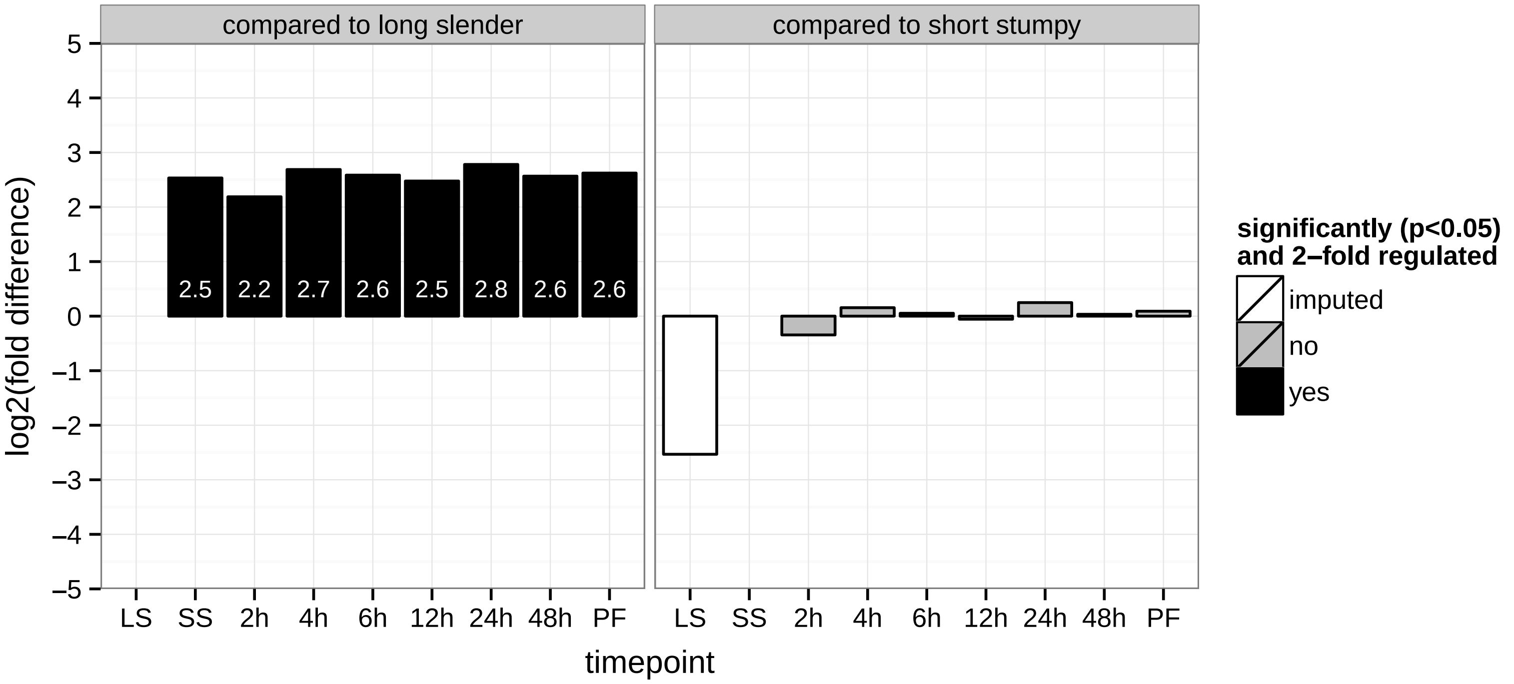
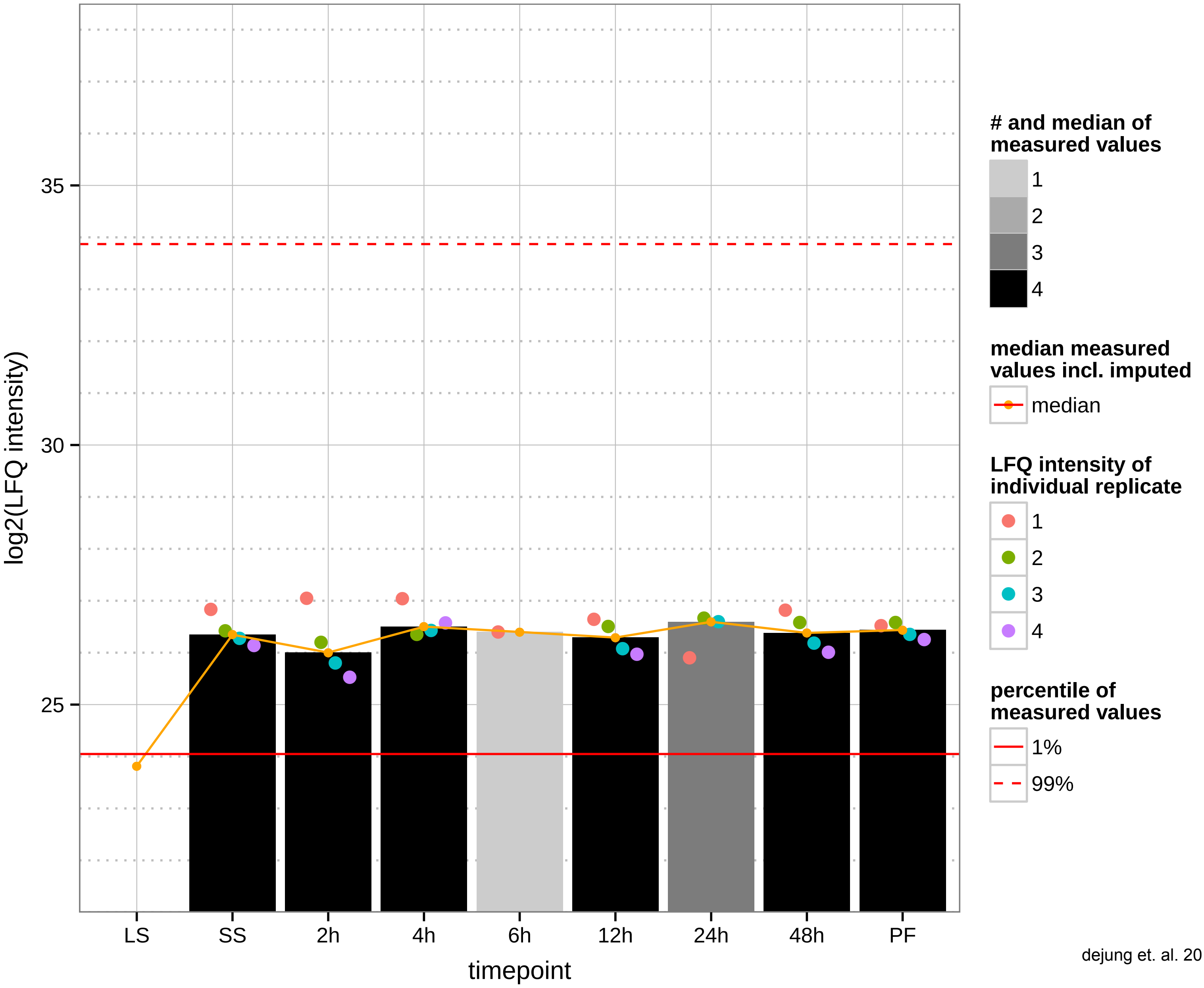
hypothetical protein, conserved
Tb927.11.3790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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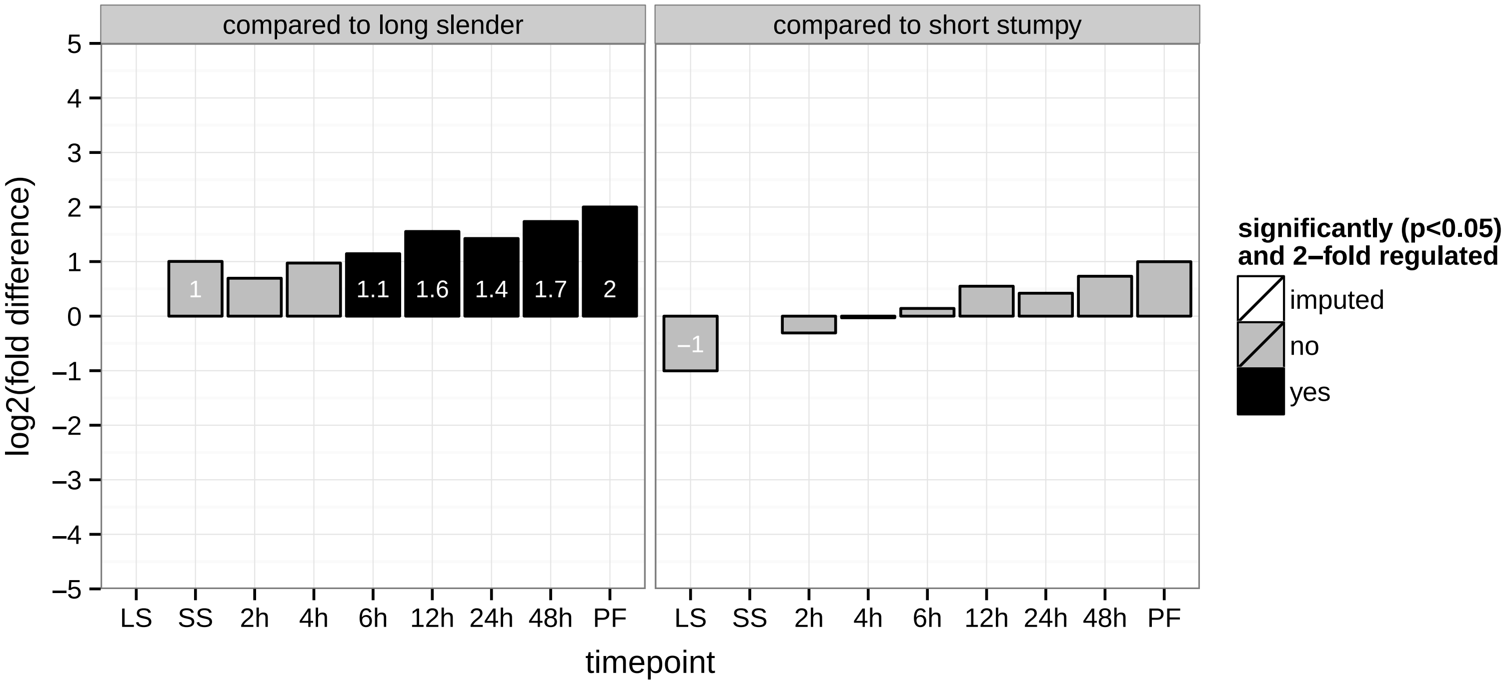
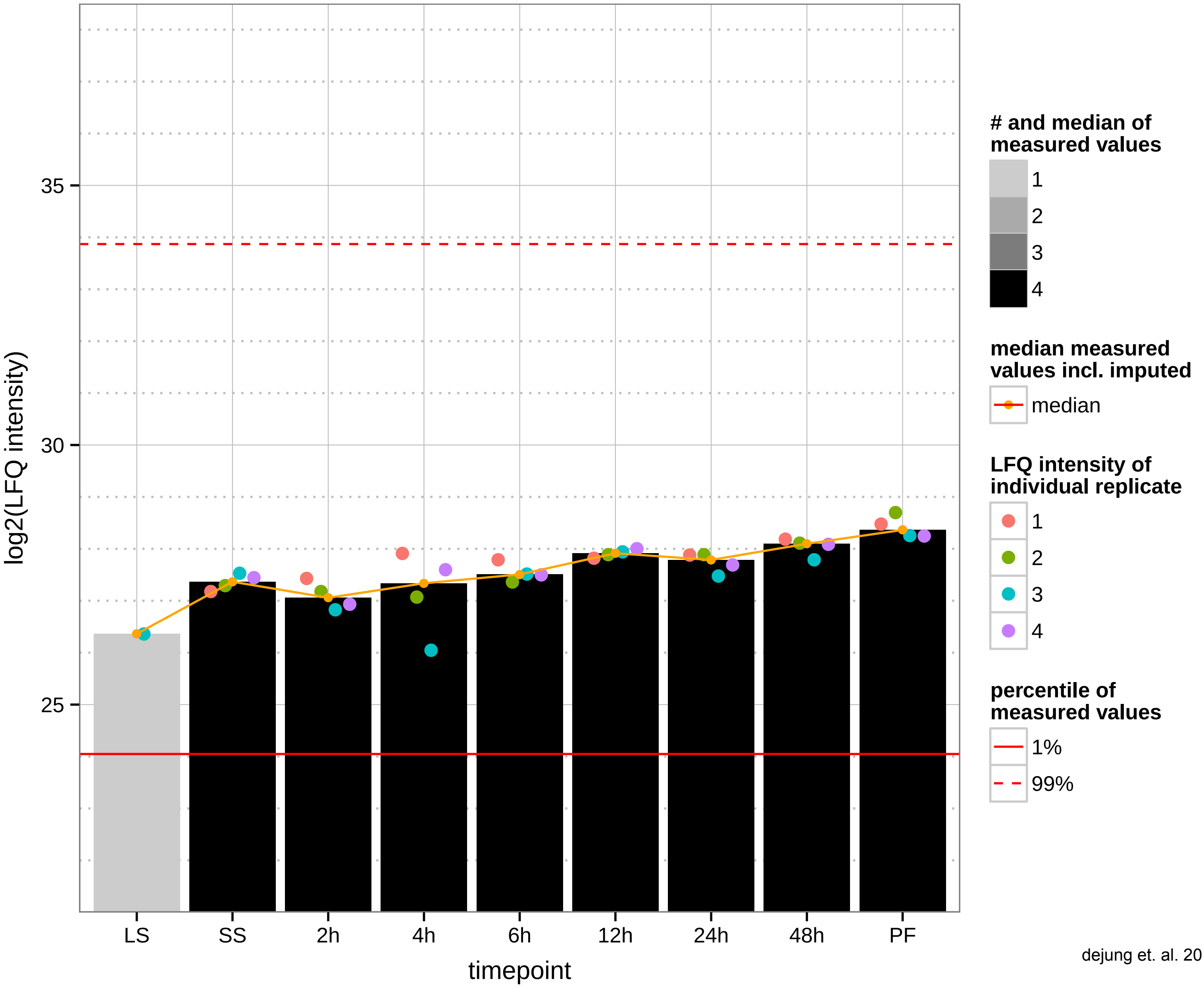
hypothetical protein, conserved
Tb927.11.3830
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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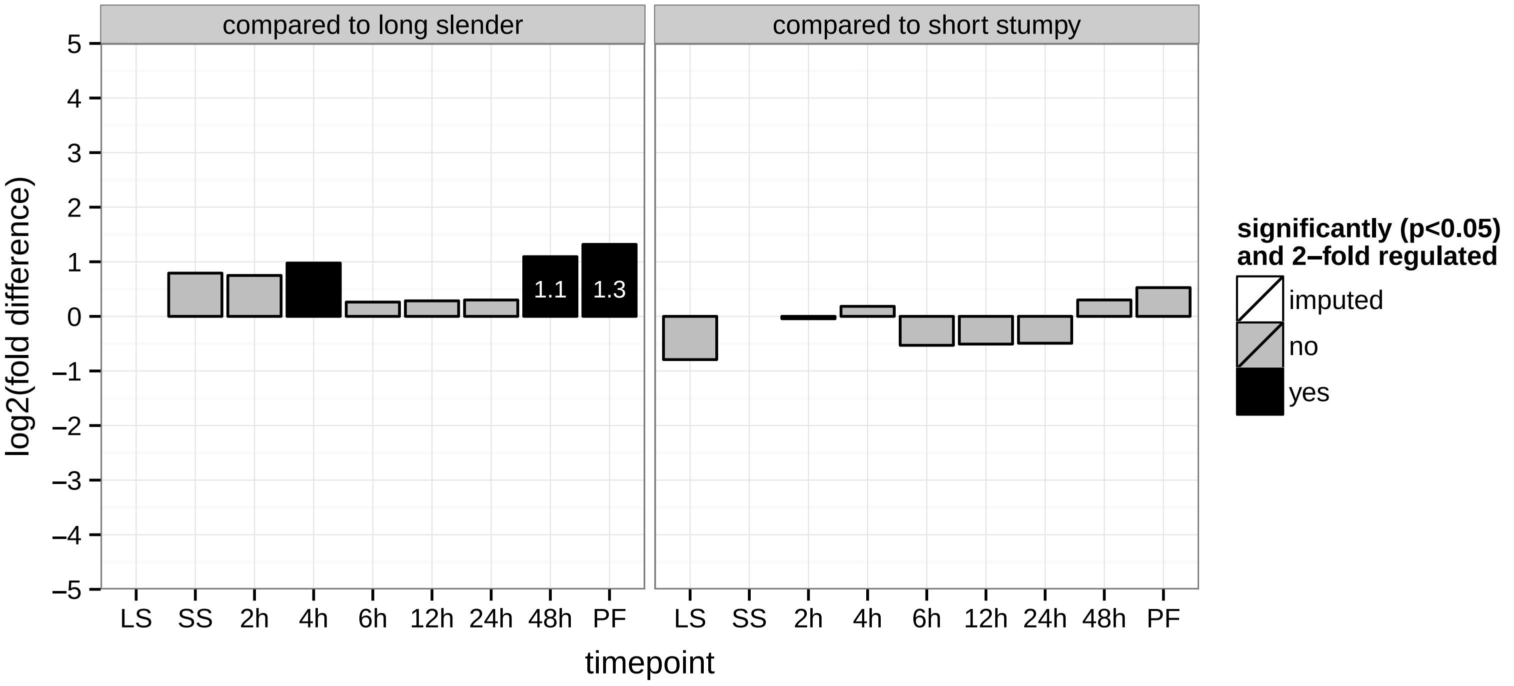
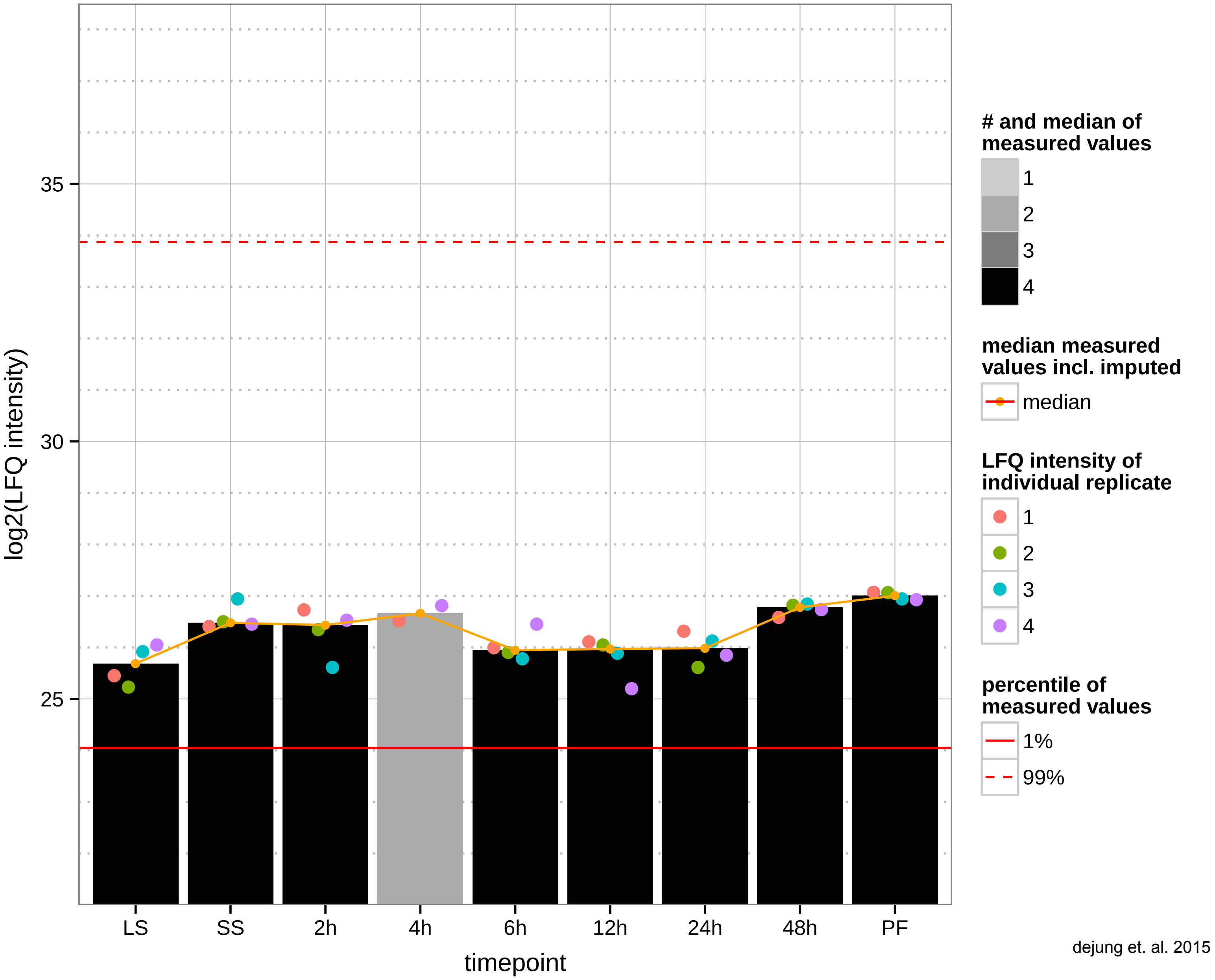
actin, putative (TRYPARP)
Tb927.11.3880
AGOF: structural constituent of cytoskeleton
AGOC: actin cytoskeleton
AGOP: cytoskeleton organization
PGOF: null
PGOC: null
PGOP: null





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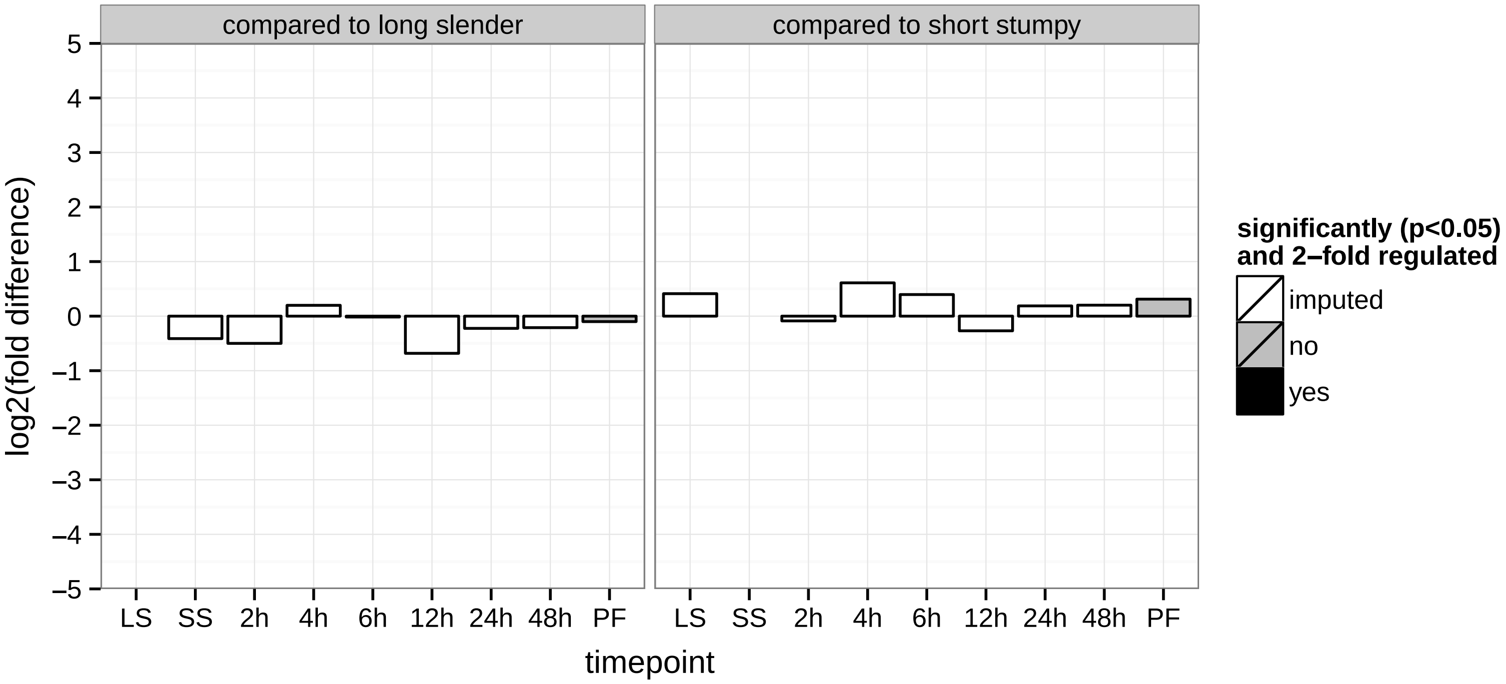
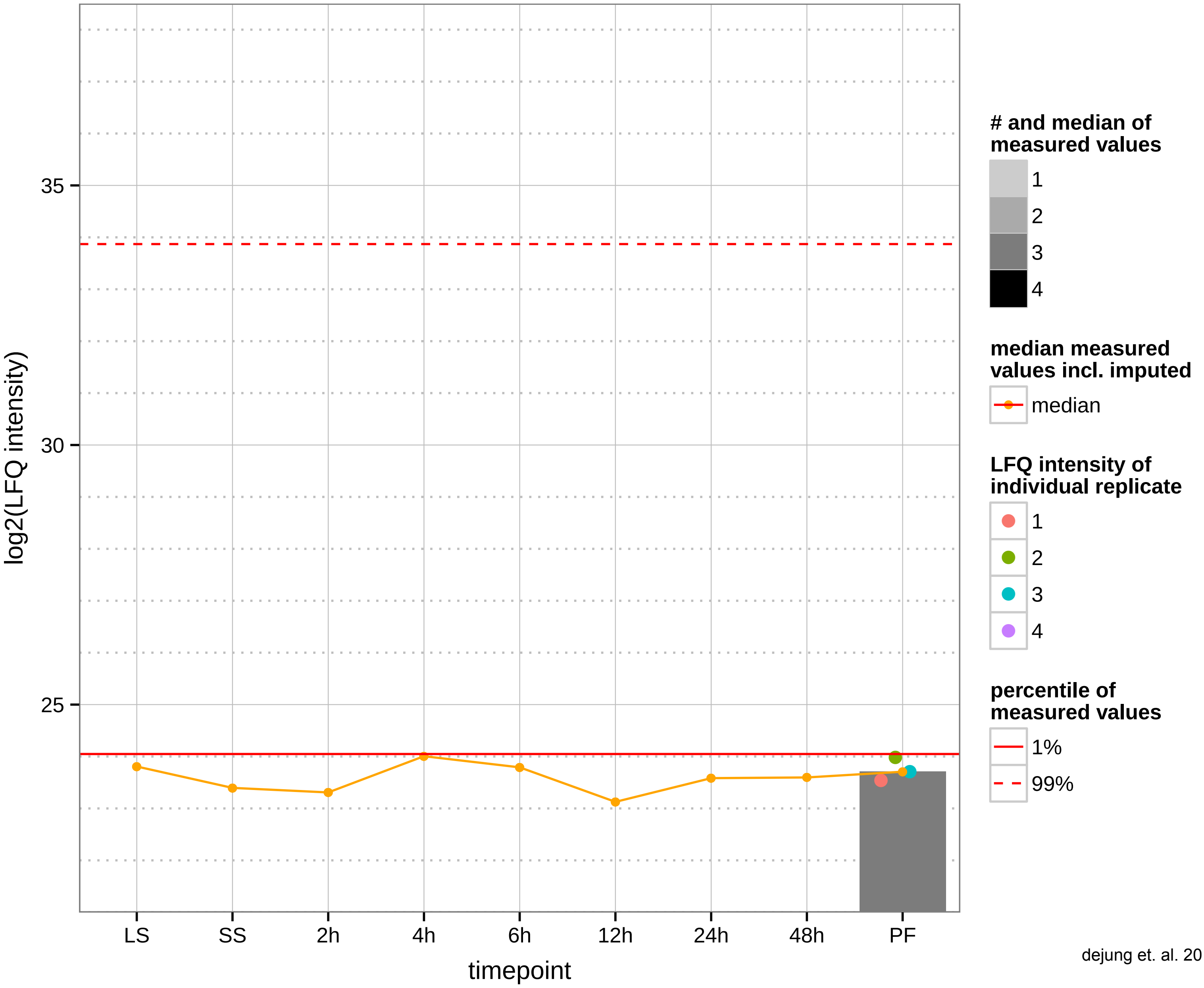
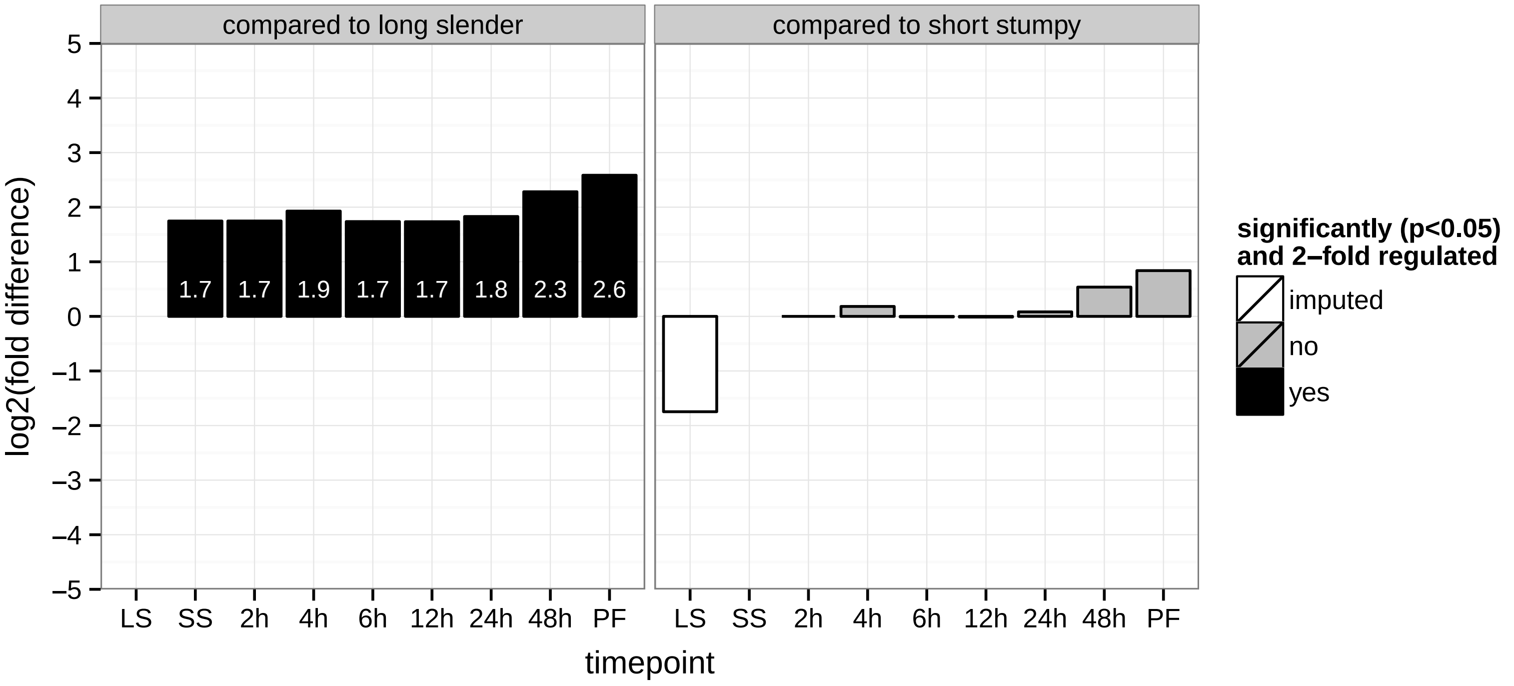
hypothetical protein, conserved
Tb927.11.3910
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

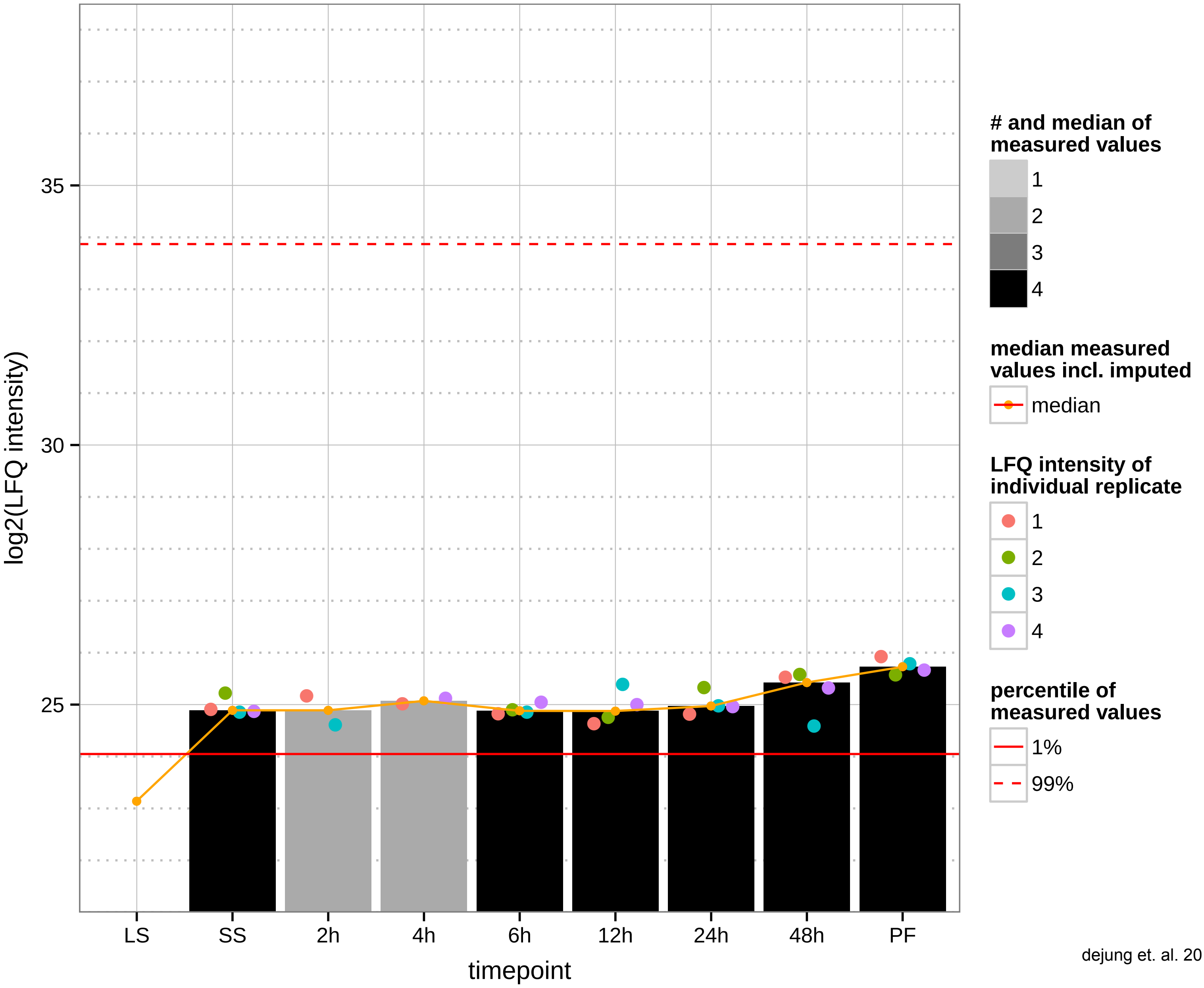




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.3940
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: metabolic process





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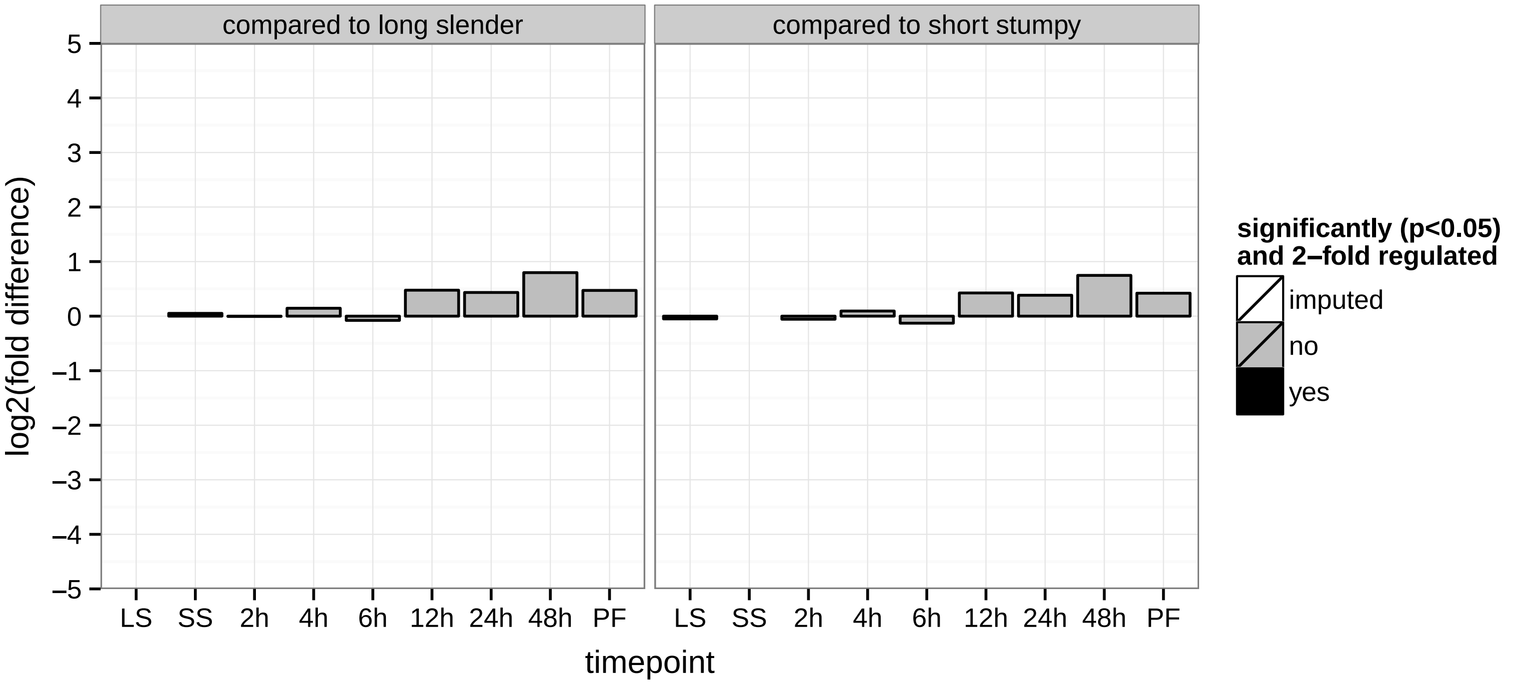
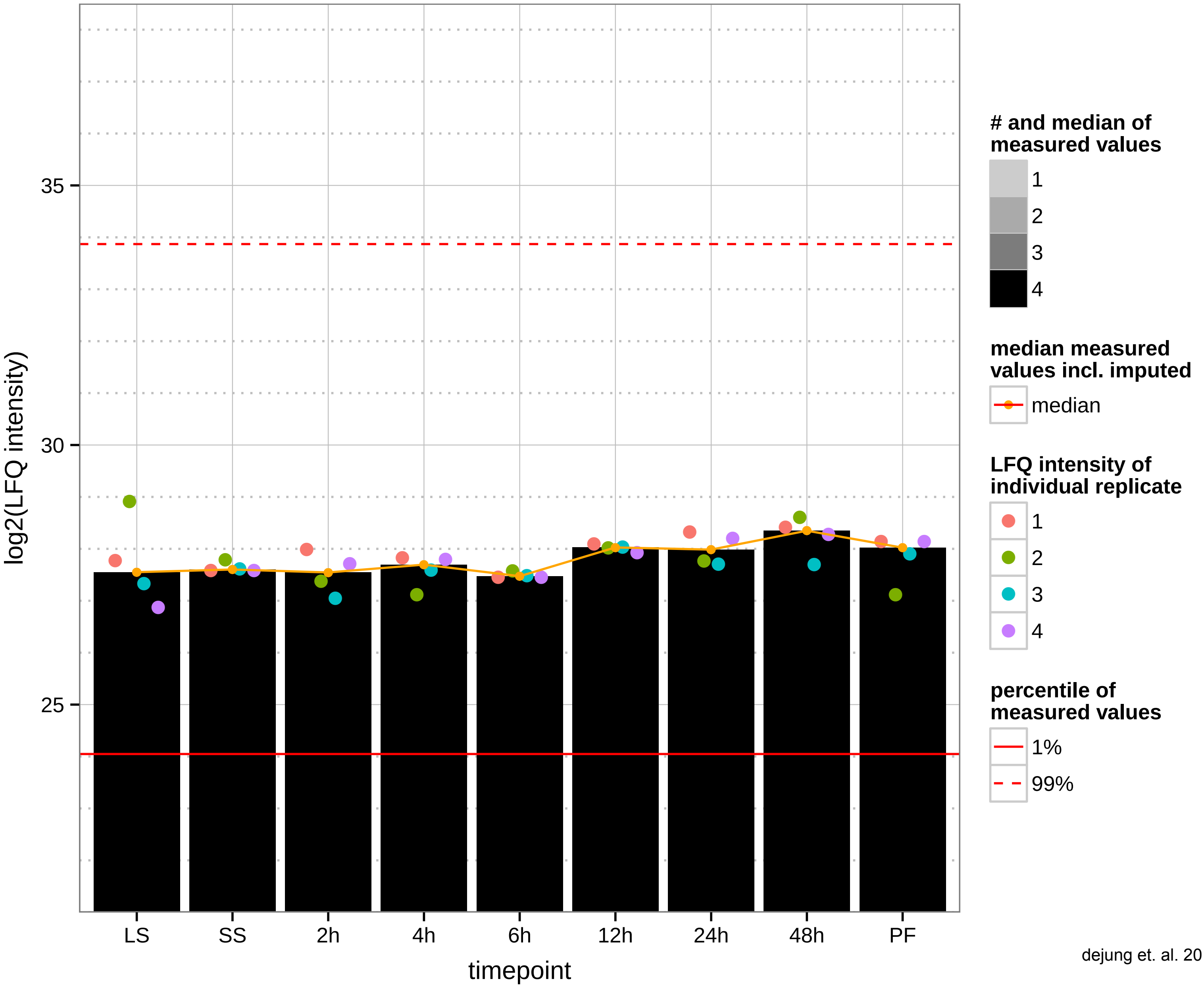
hypothetical protein, conserved
Tb927.11.3970
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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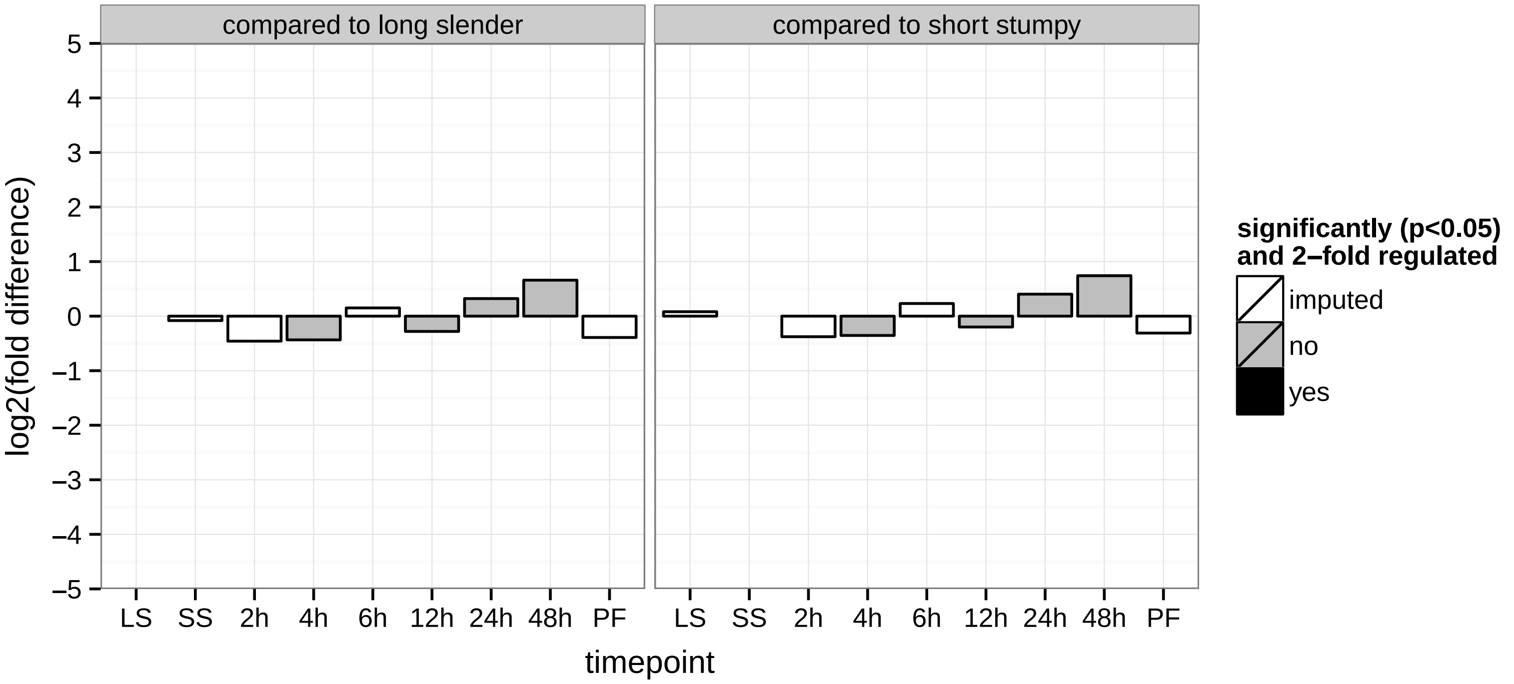
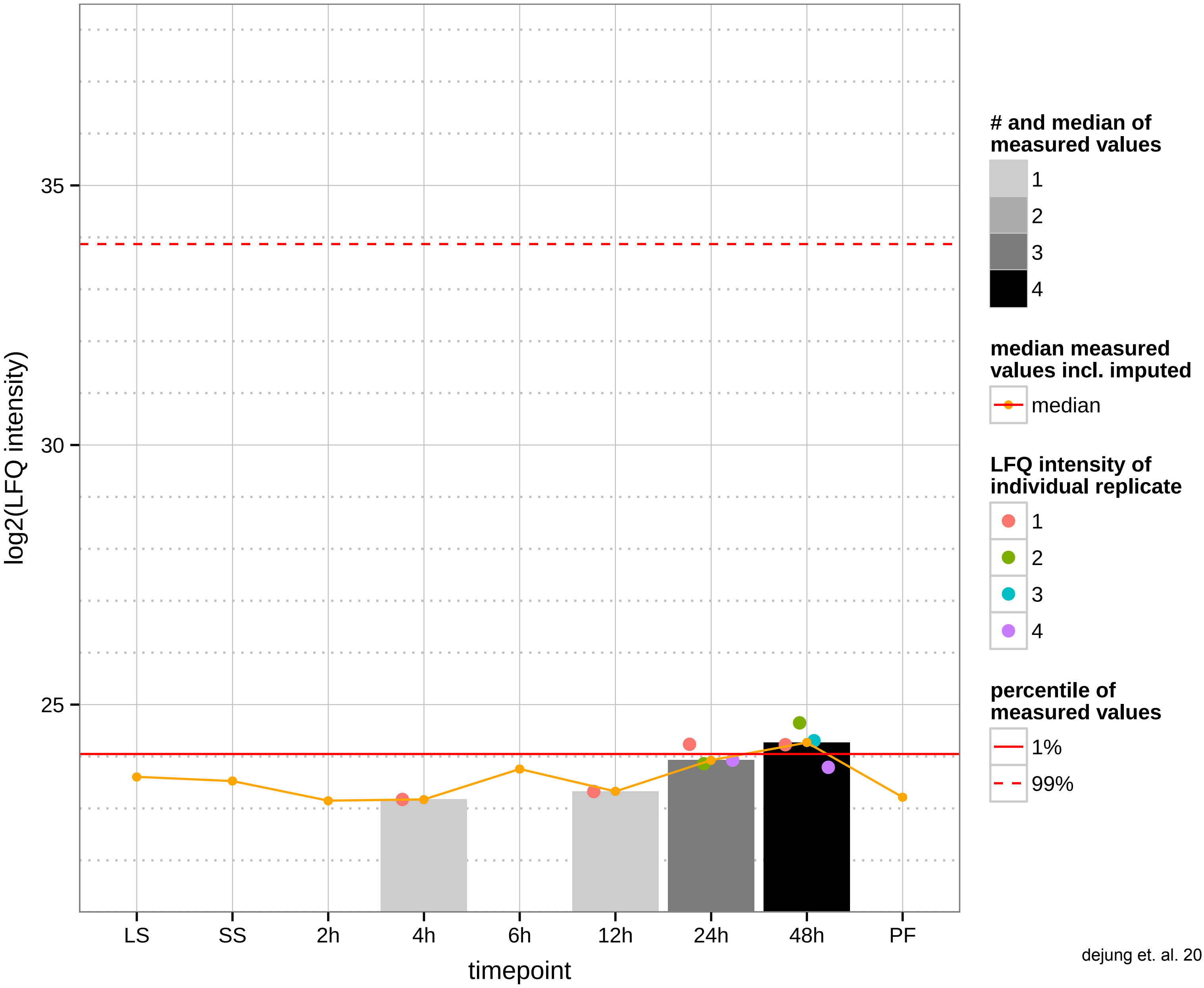
hypothetical protein, conserved
Tb927.11.400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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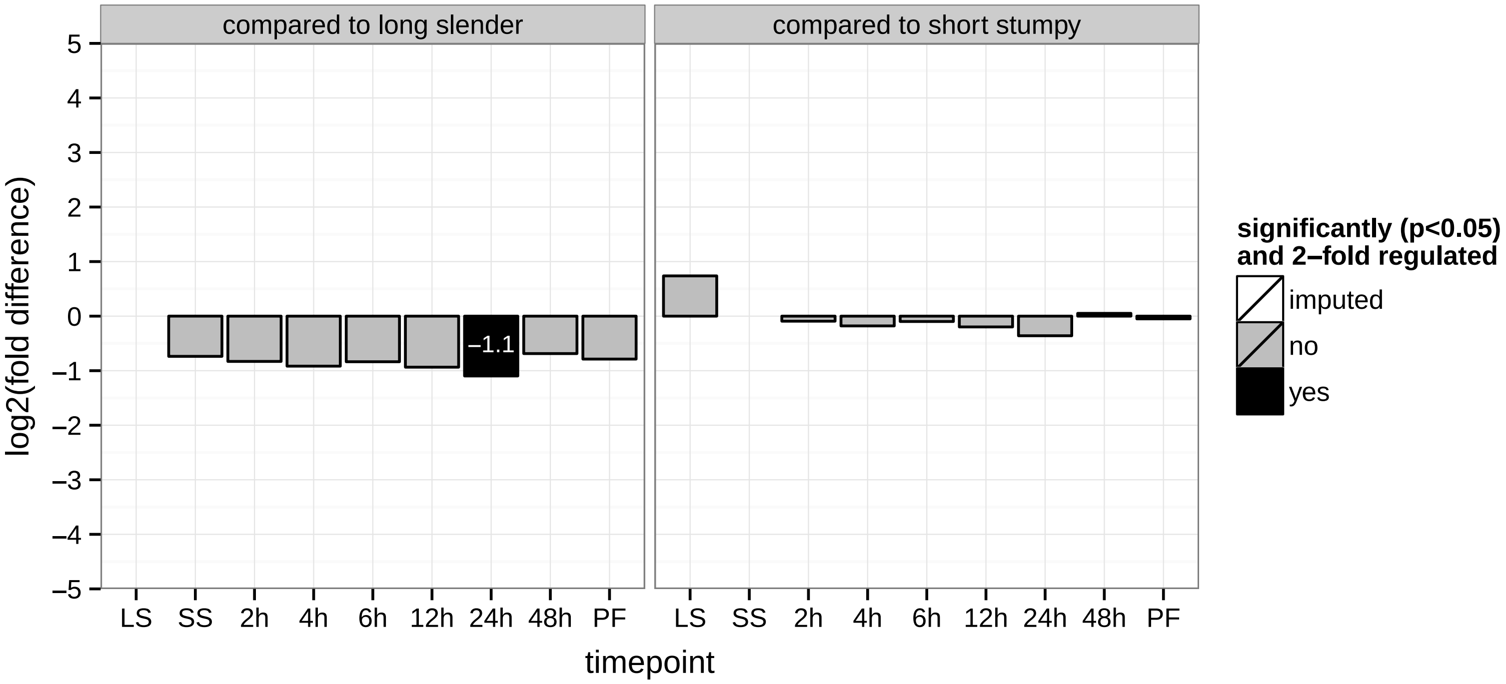
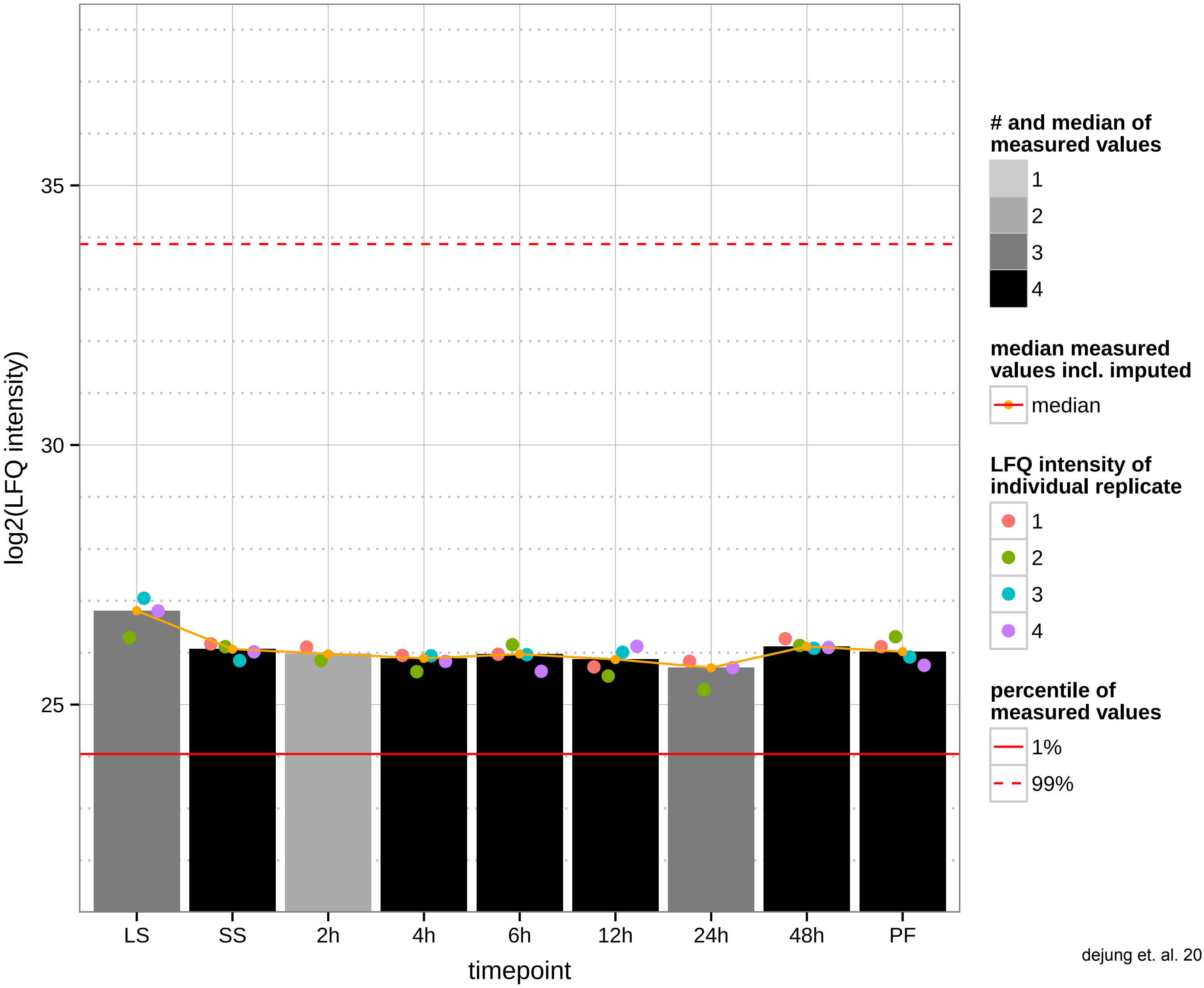
hypothetical protein, conserved
Tb927.11.4000
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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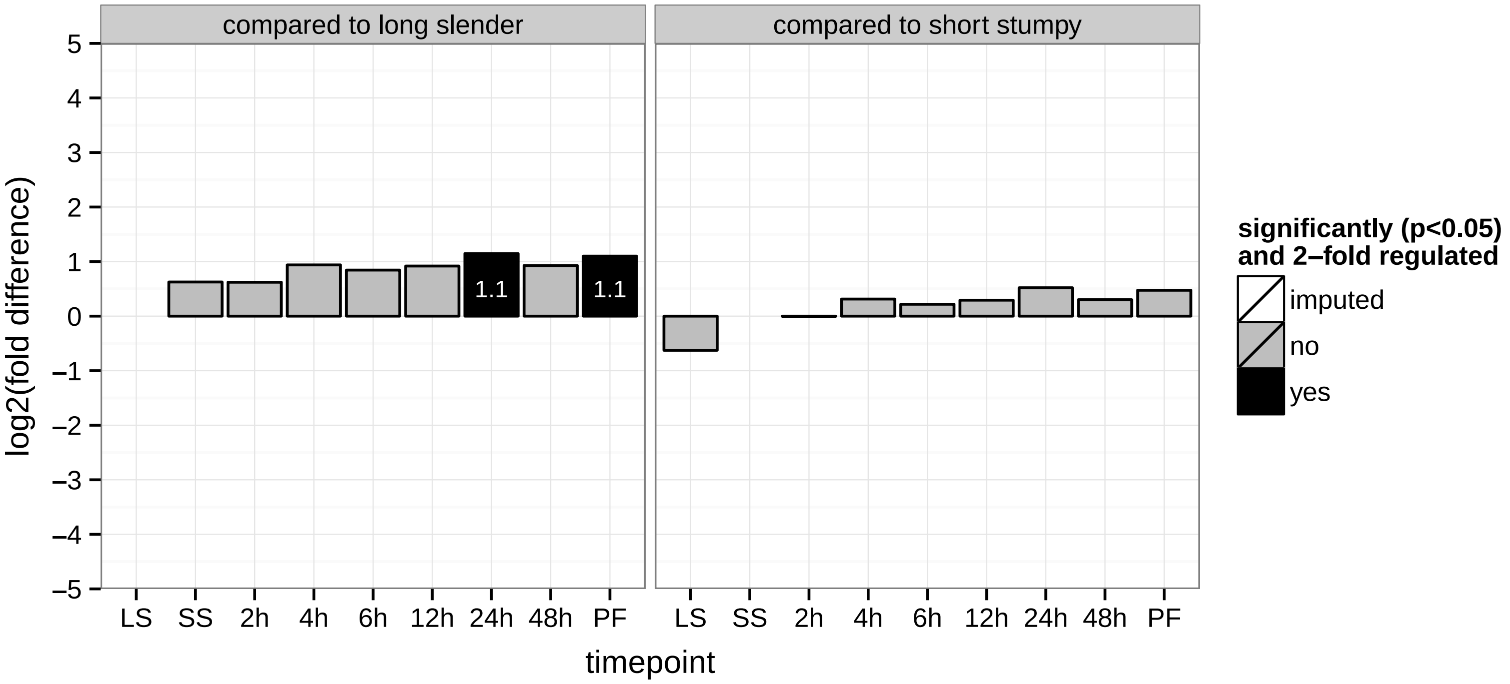
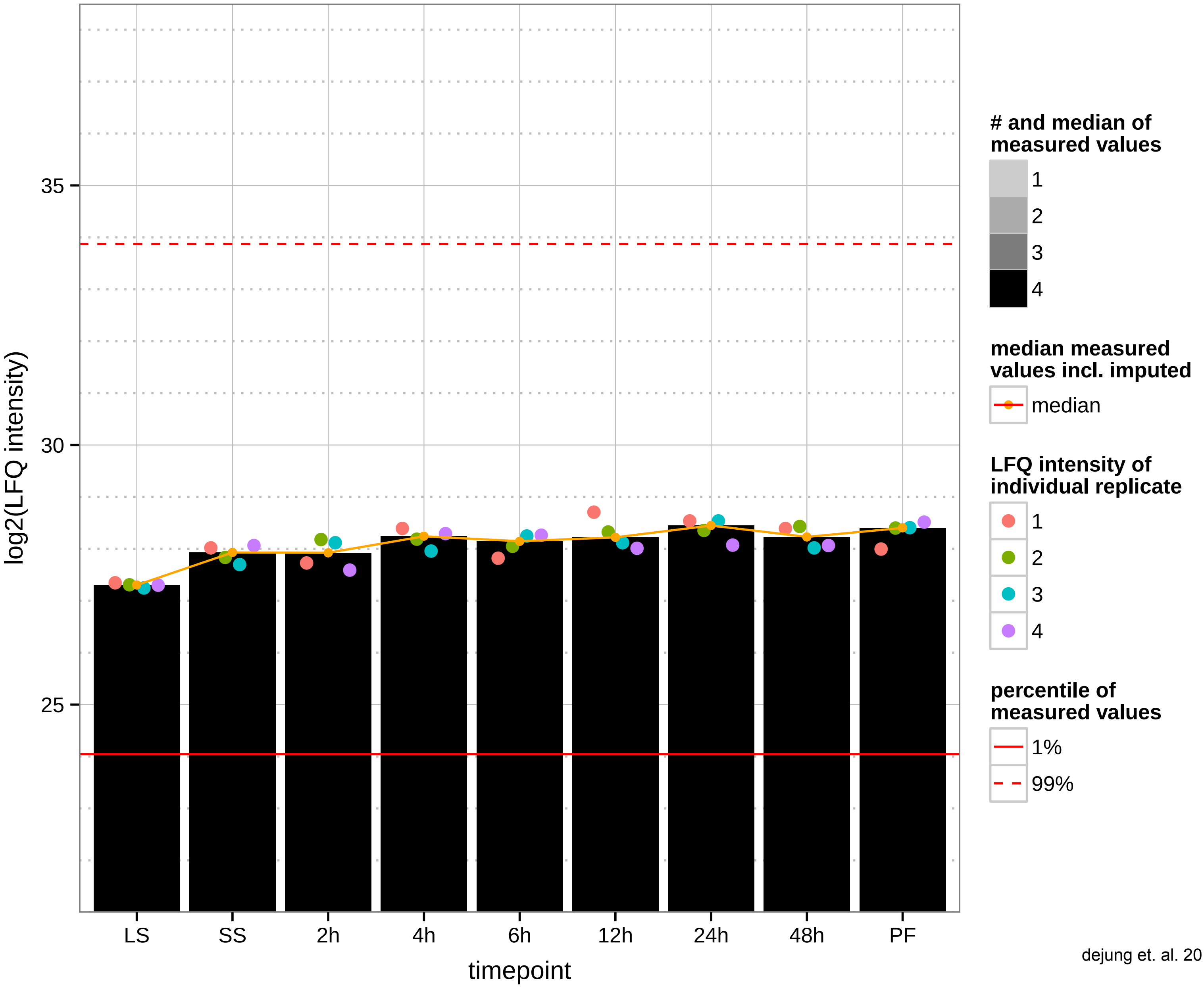
ubiquitin–like protein, putative
Tb927.11.4130
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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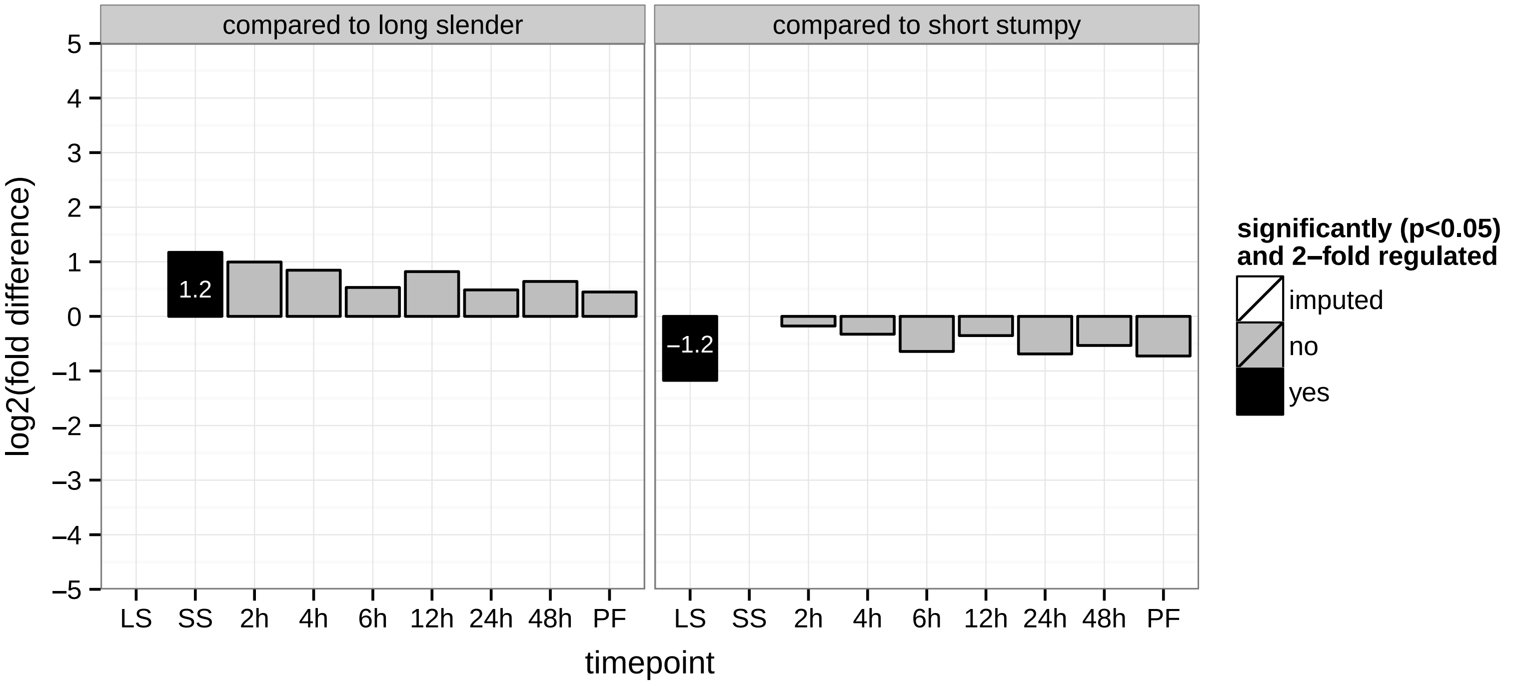
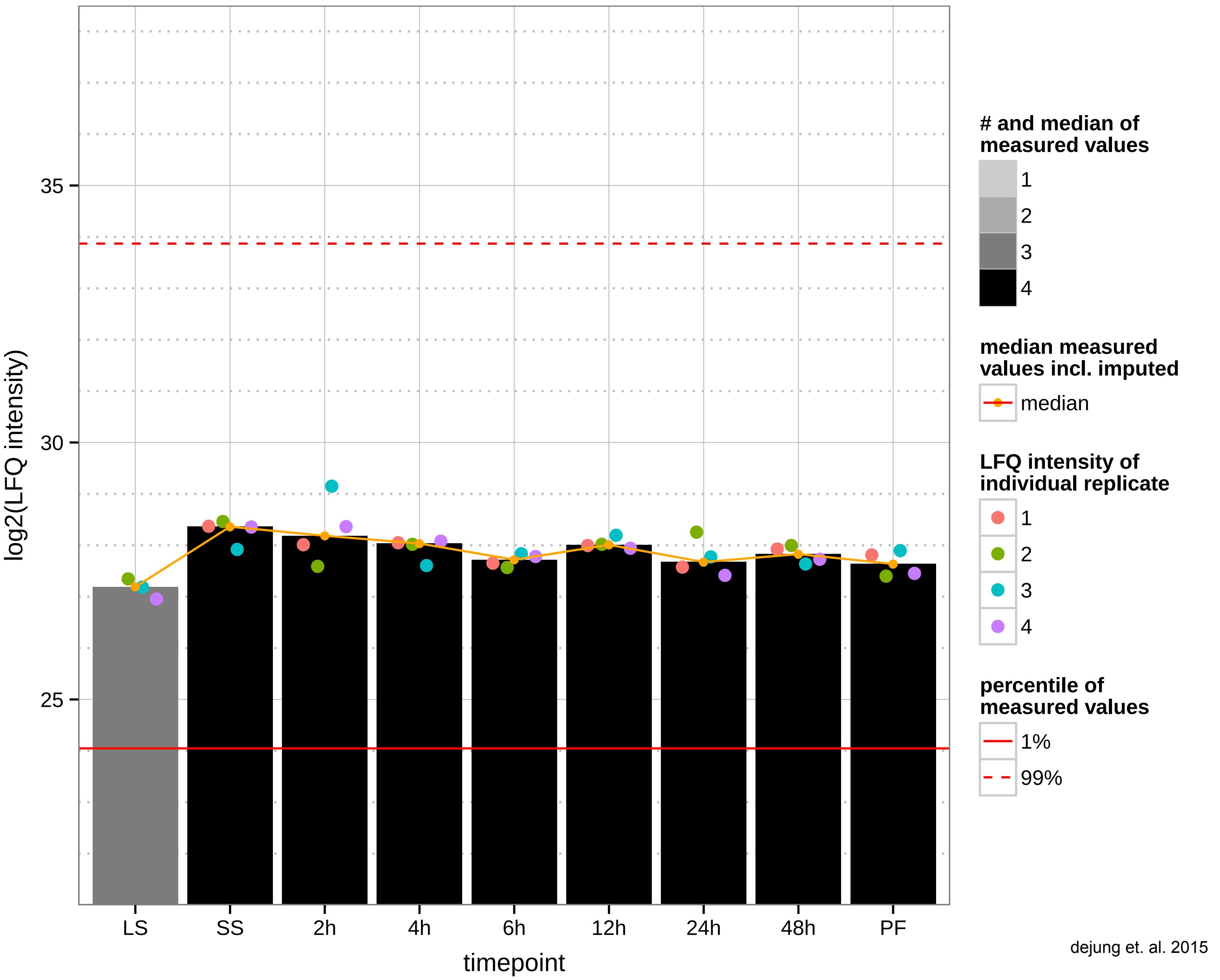
lectin, putative, mannose−specific lectin
Tb927.11.4200
AGOF: mannose binding
AGOC: integral to membrane, membrane
AGOP: protein secretion
PGOF: null
PGOC: membrane
PGOP: null





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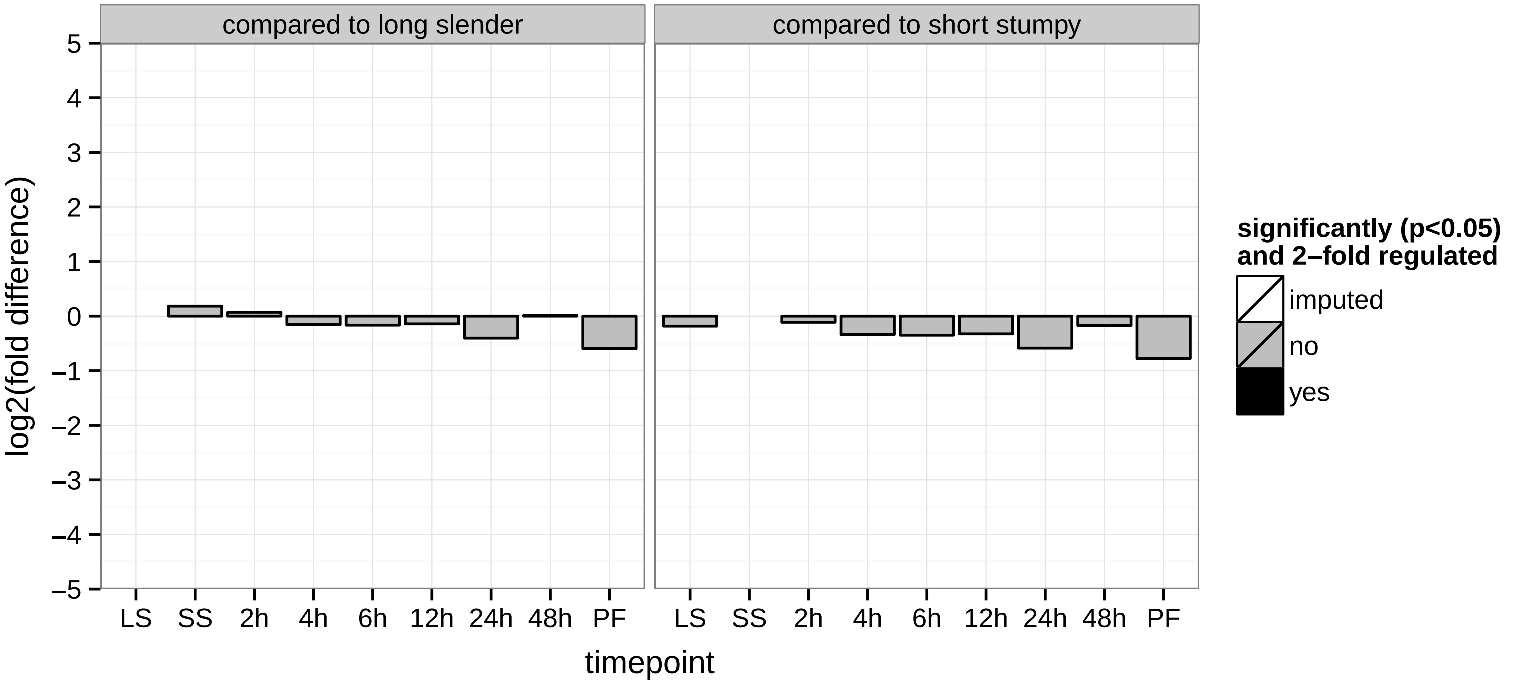
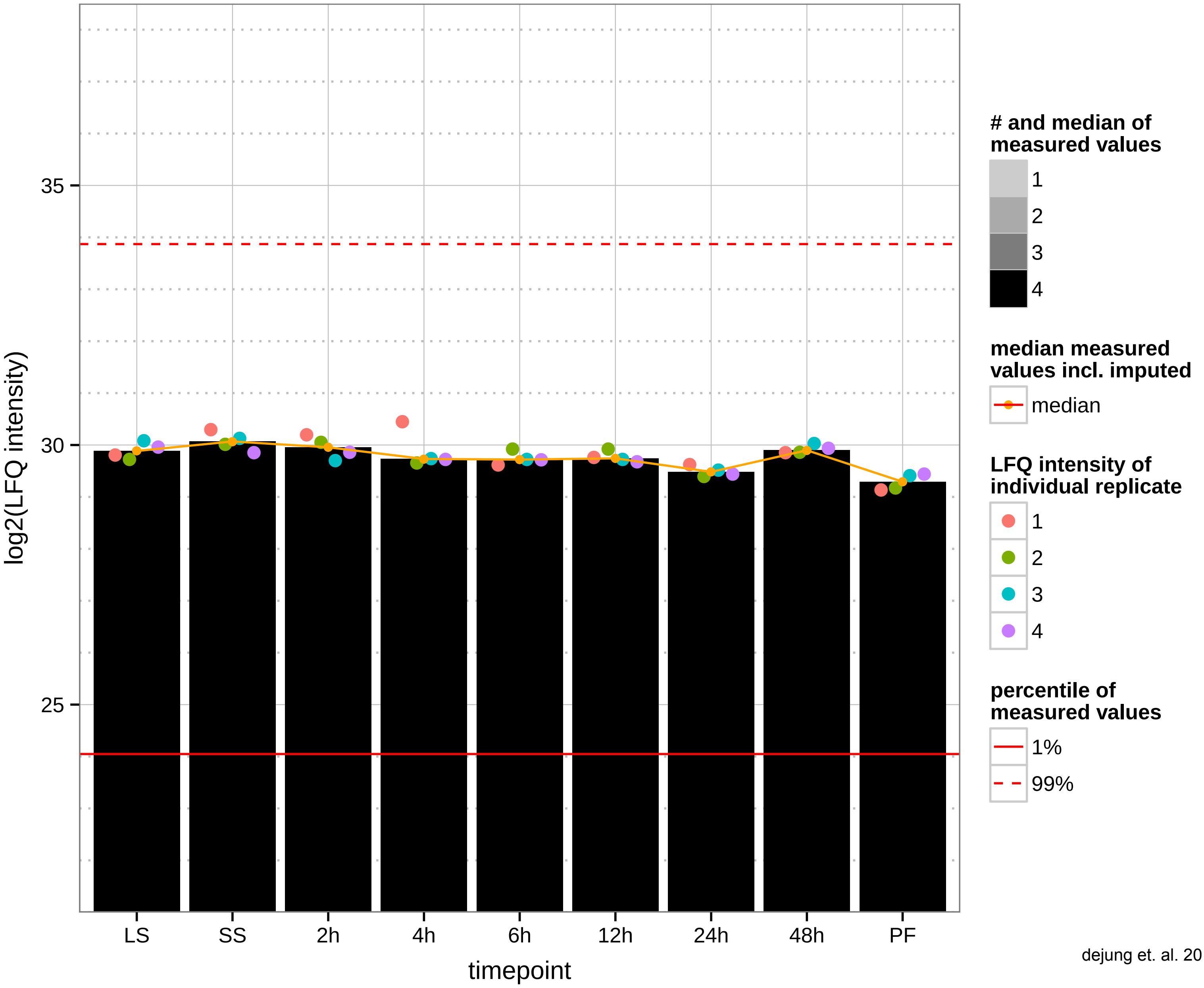
hypothetical protein, conserved
Tb927.11.4210
AGOF: ubiquitin–protein ligase activity
AGOC: ubiquitin ligase complex
AGOP: protein ubiquitination
PGOF: binding, ubiquitin–protein ligase activity
PGOC: ubiquitin ligase complex
PGOP: protein ubiquitination





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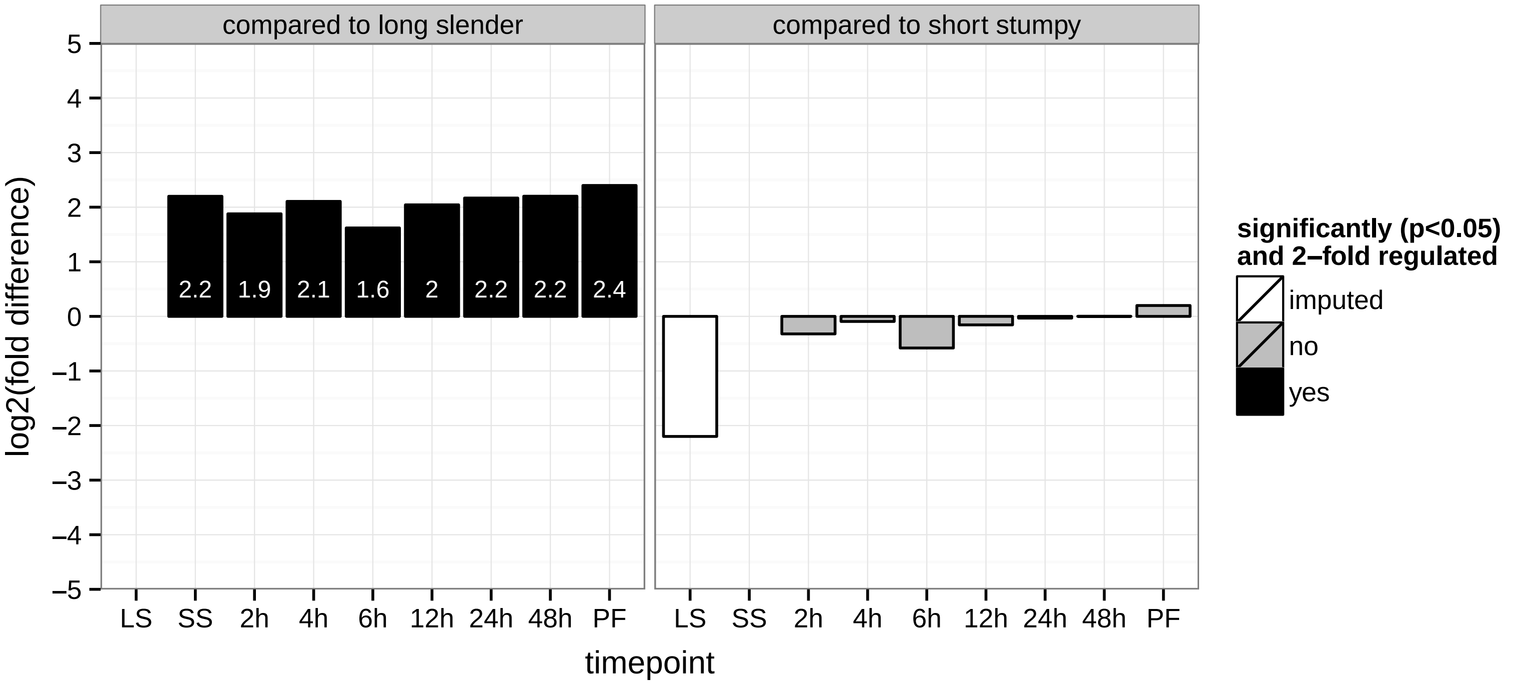
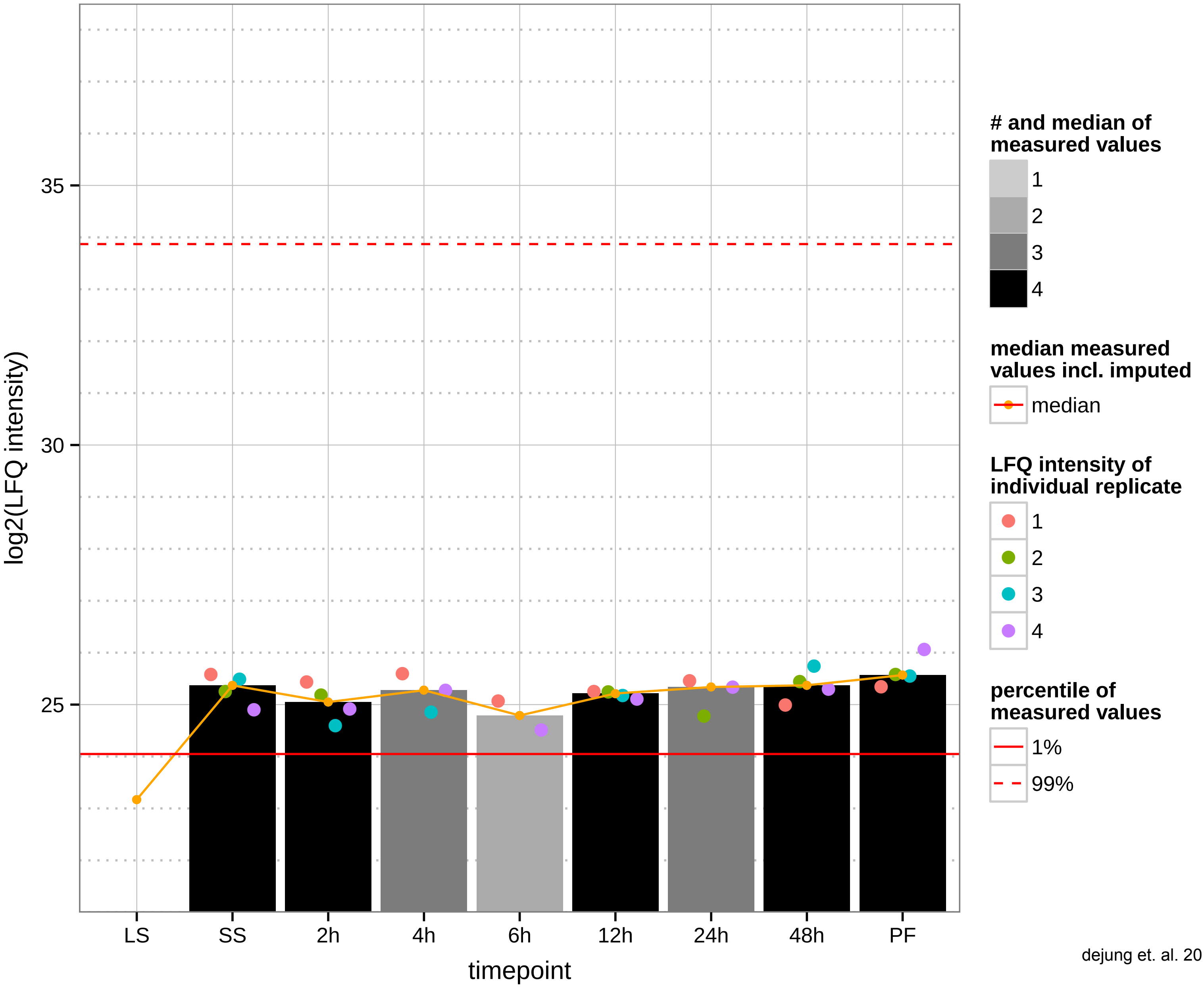
hypothetical protein, conserved
Tb927.11.4230
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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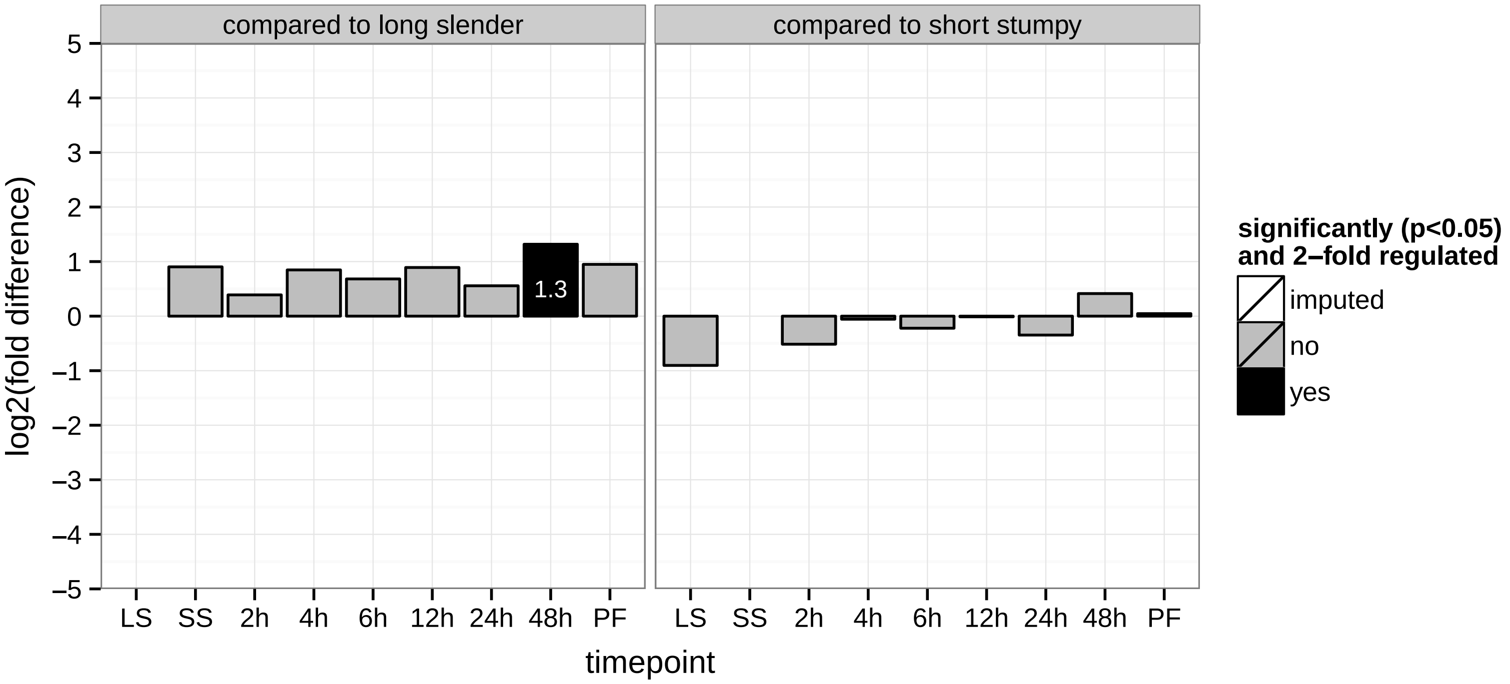
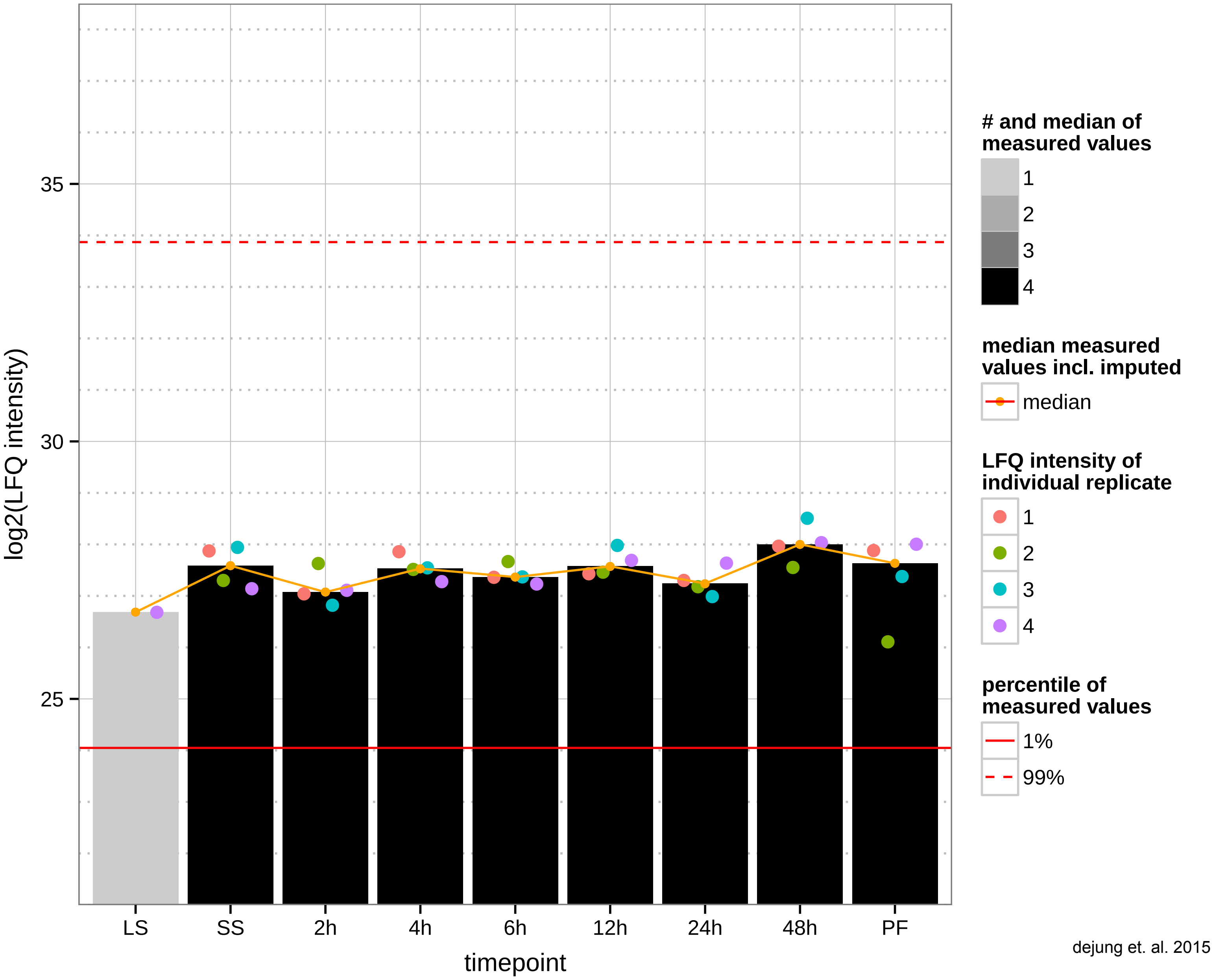
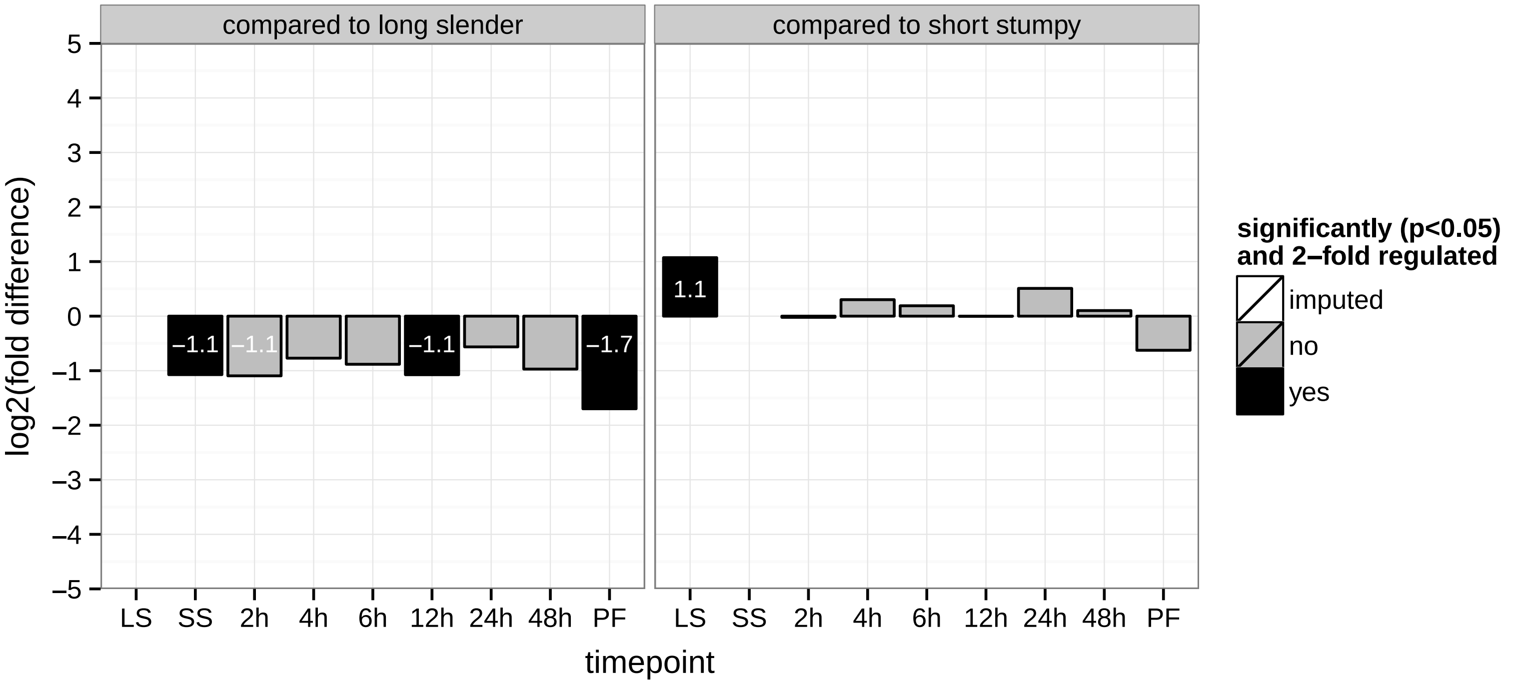
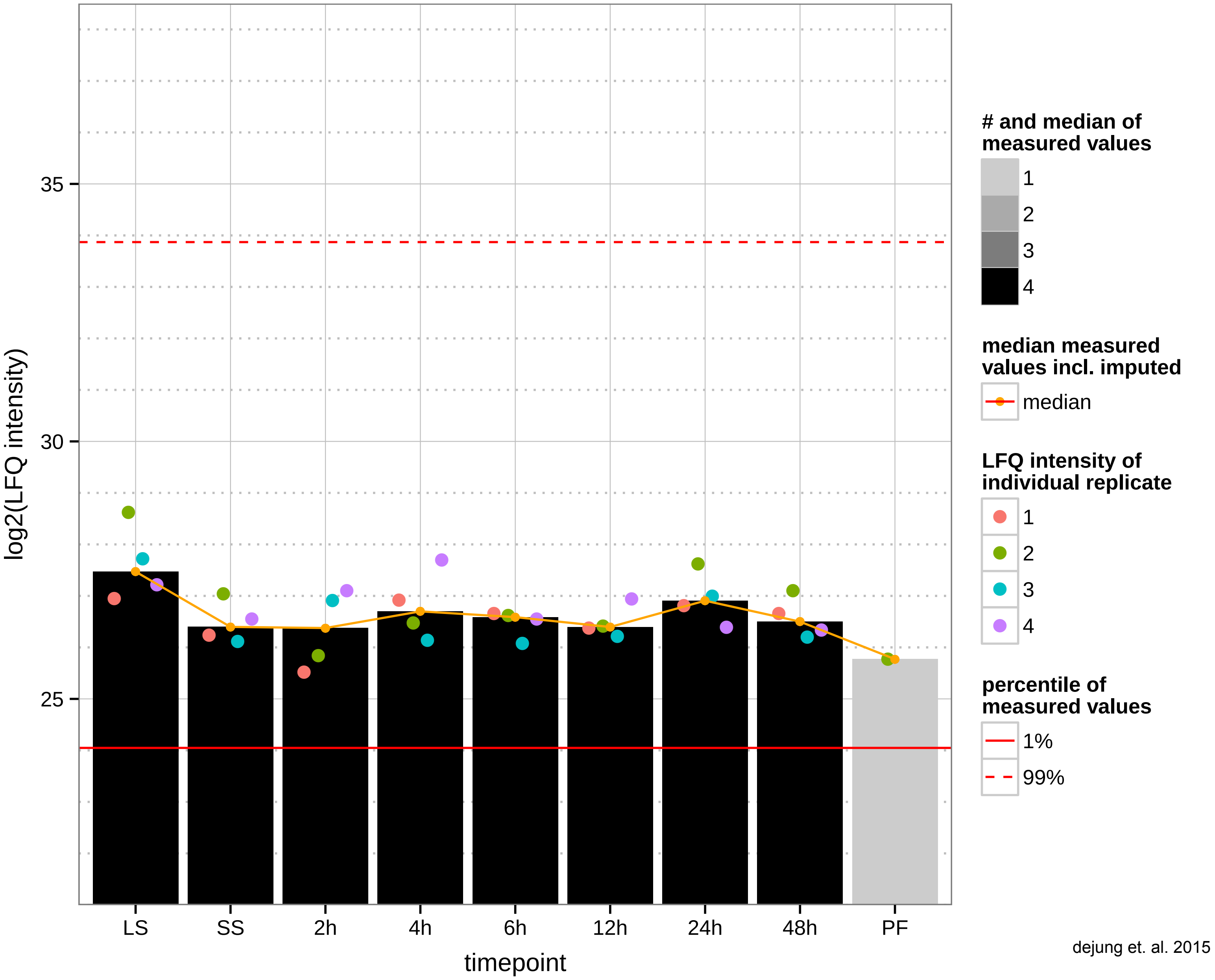
hypothetical protein, conserved
Tb927.11.4280
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





40S ribosomal protein S12 (RPS12)
Tb927.11.4290
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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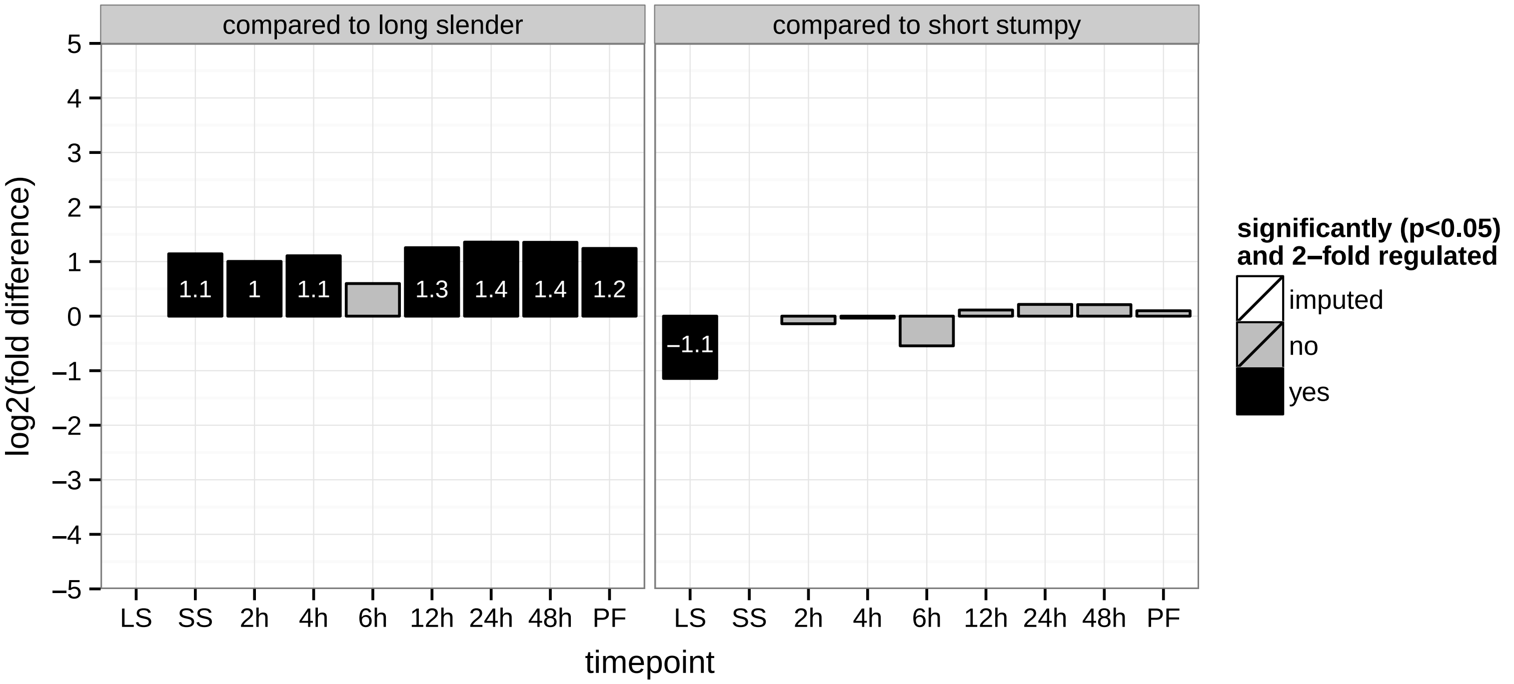
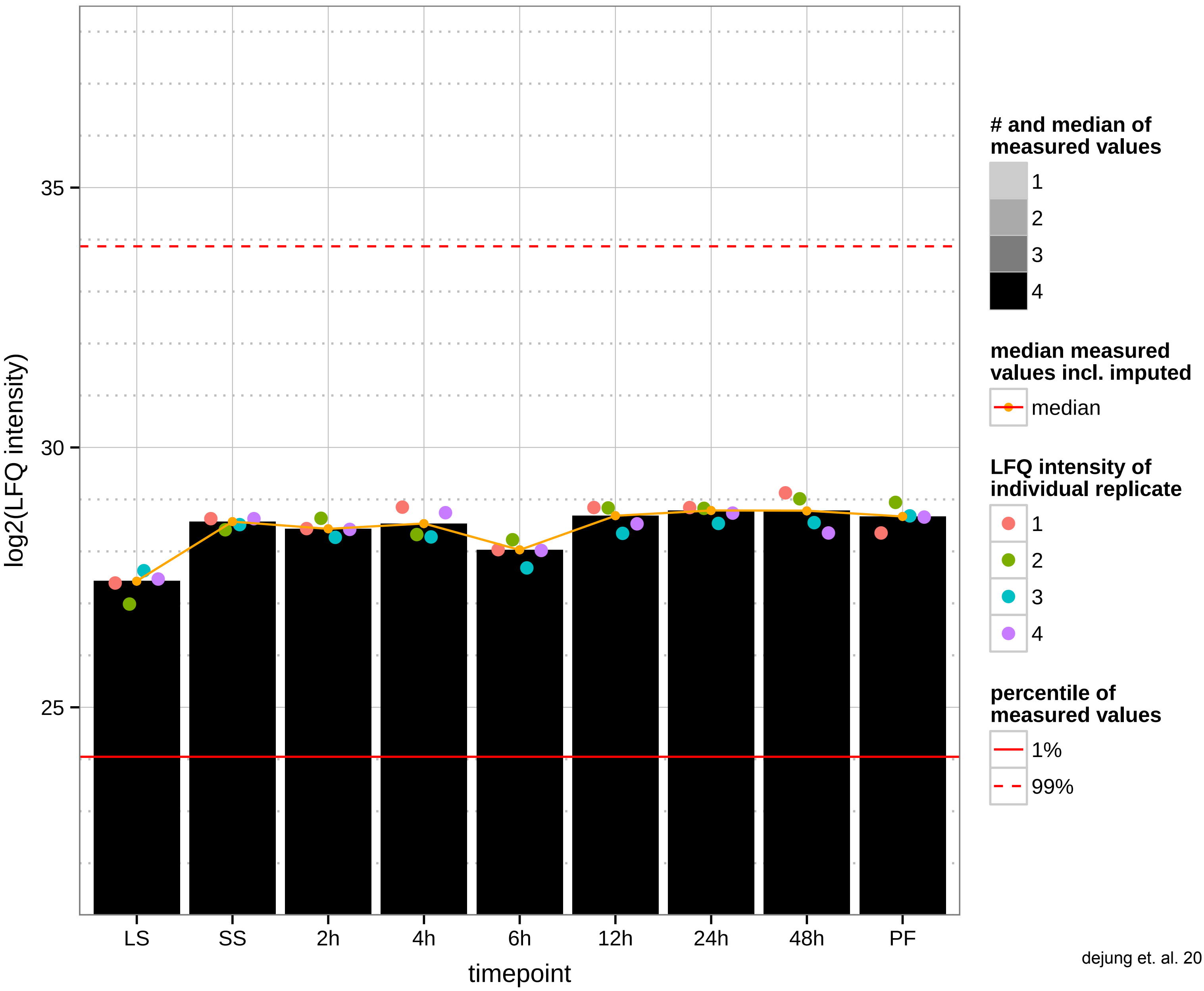
hypothetical protein, conserved
Tb927.11.4320
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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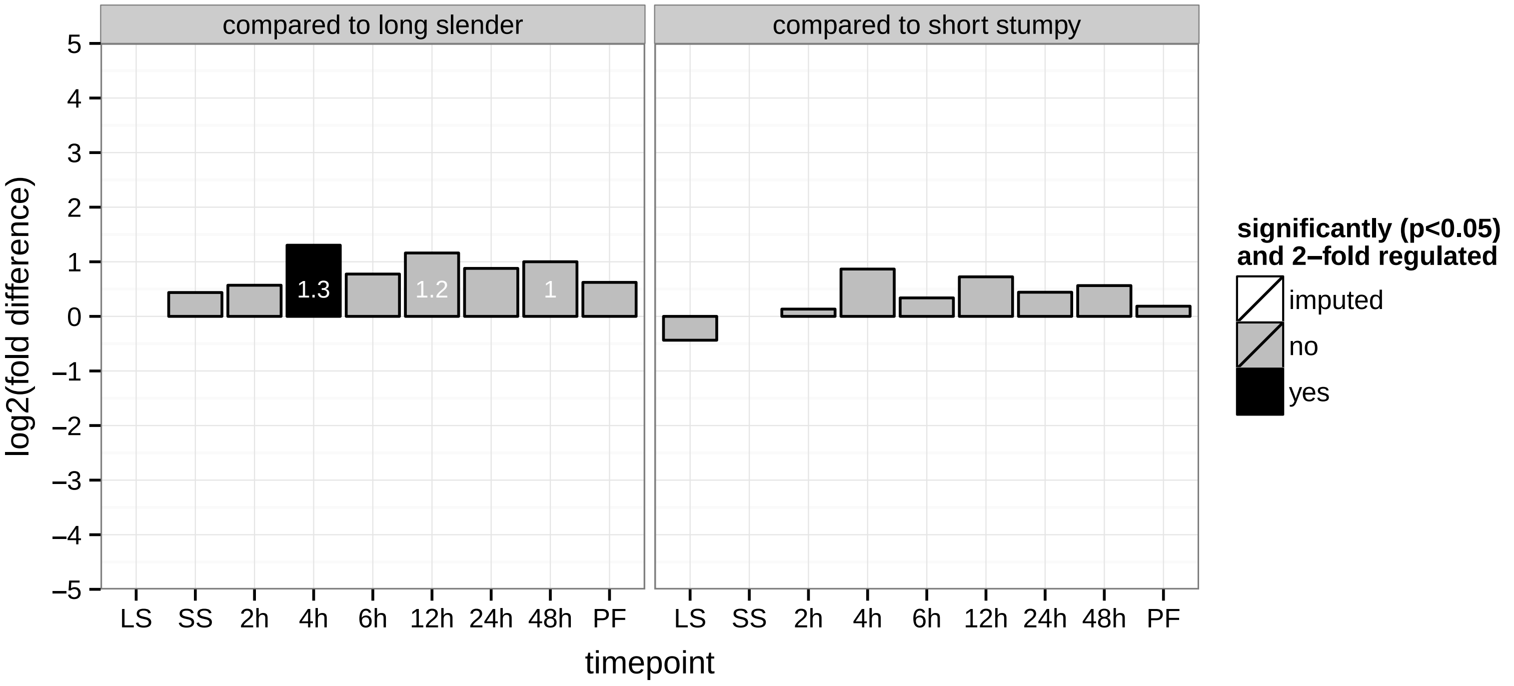
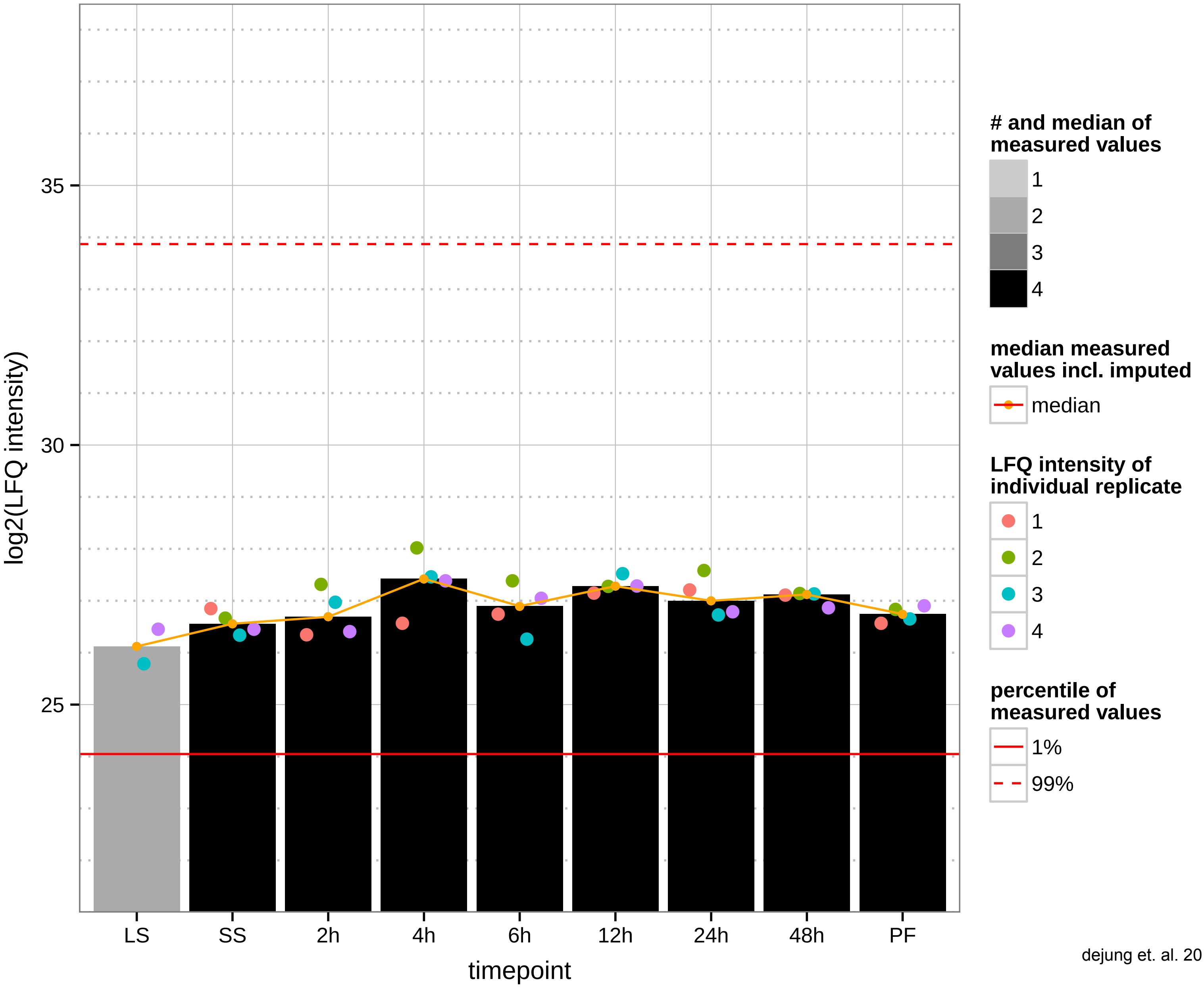
hypothetical protein, conserved
Tb927.11.4360
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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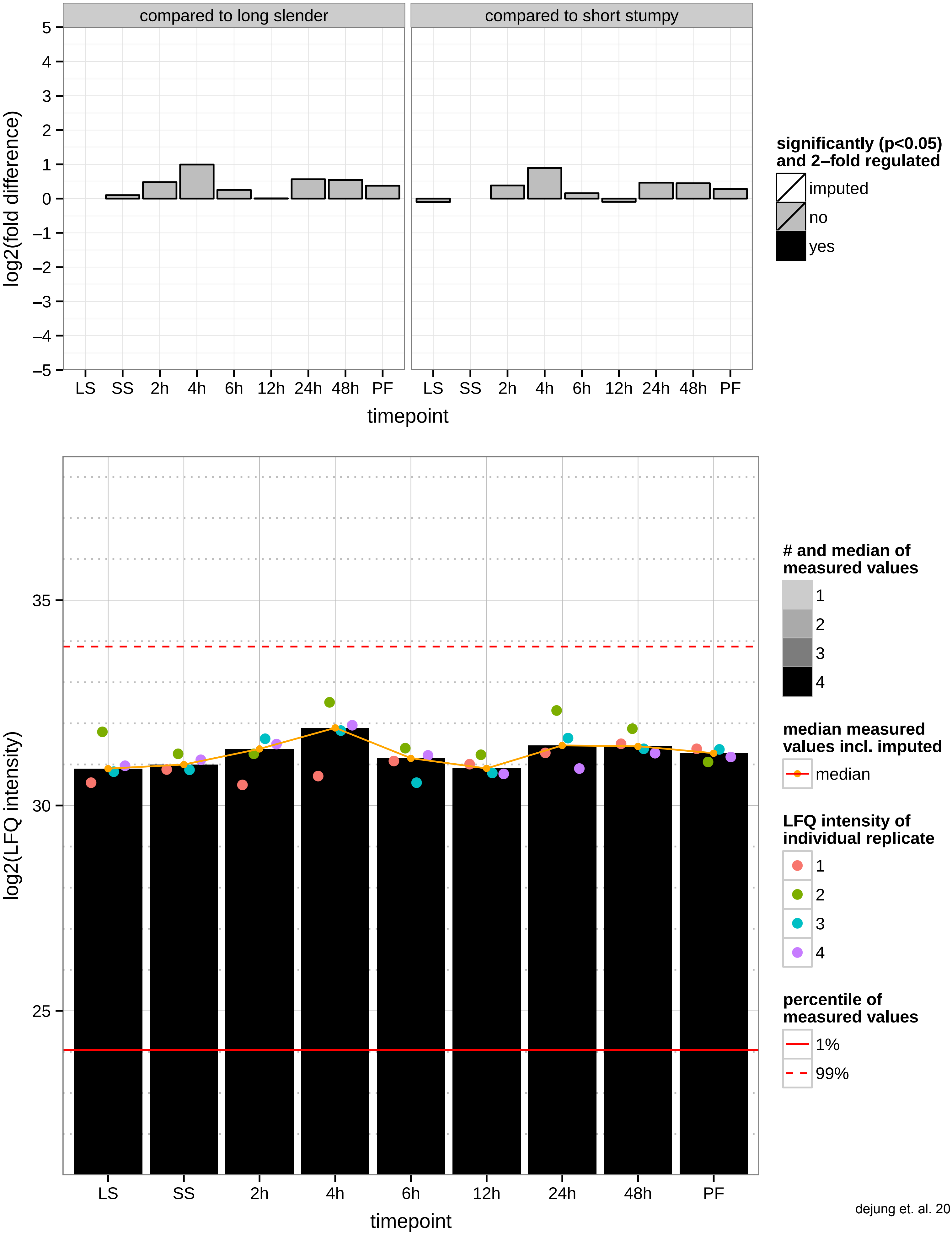
ALBA–Domain Protein (ALBA2)
Tb927.11.4450
AGOF: nucleic acid binding
AGOC: cytoplasm, cytoplasmic stress granule
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null



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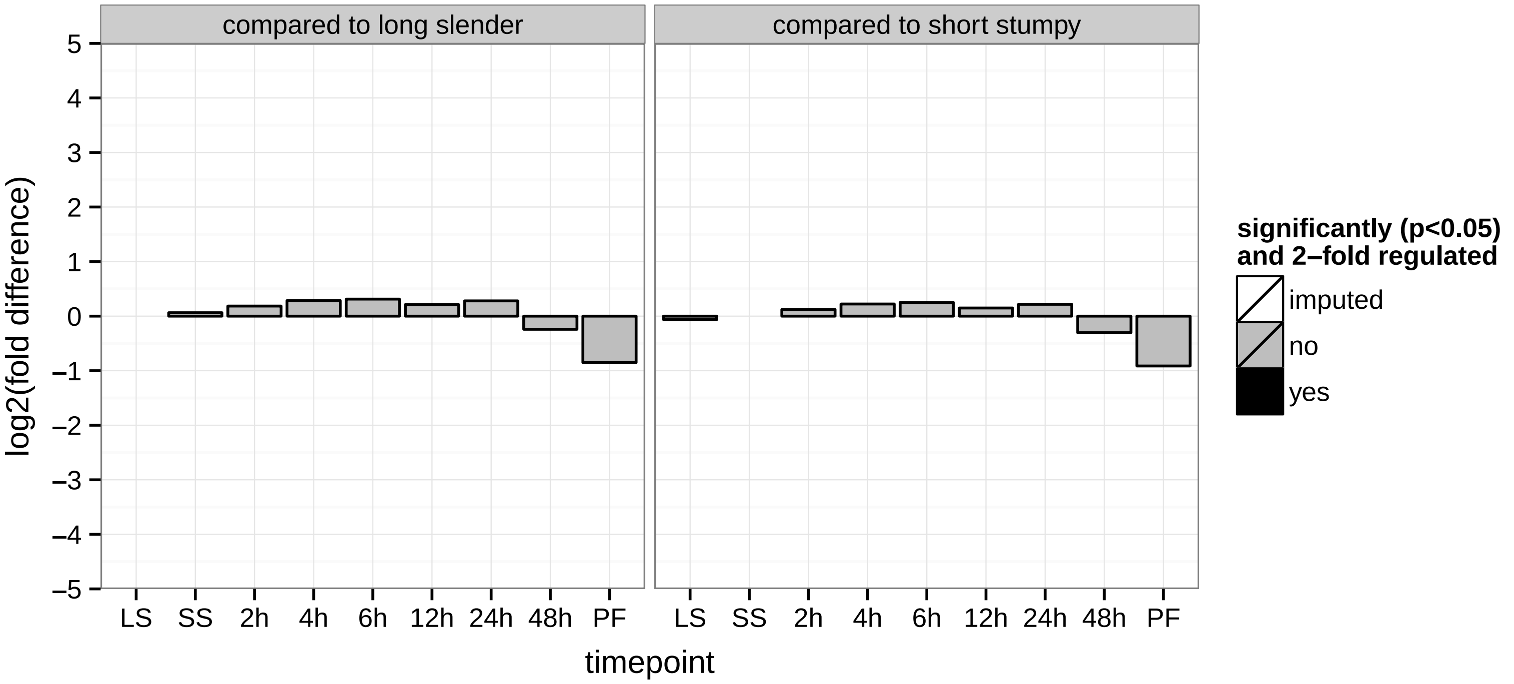
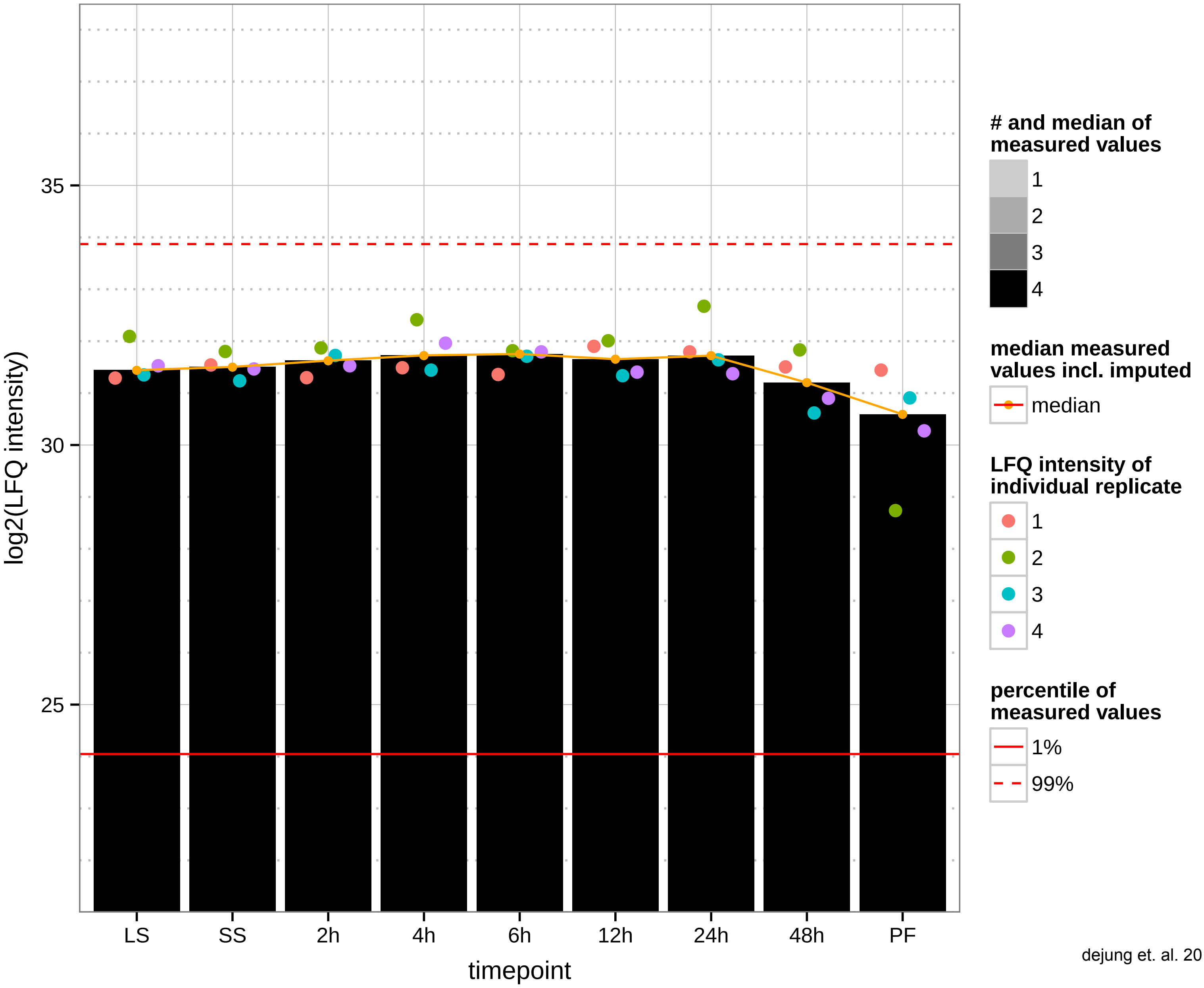
ALBA–Domain Protein (ALBA1)
Tb927.11.4460
AGOF: nucleic acid binding
AGOC: cytoplasm, cytoplasmic stress granule
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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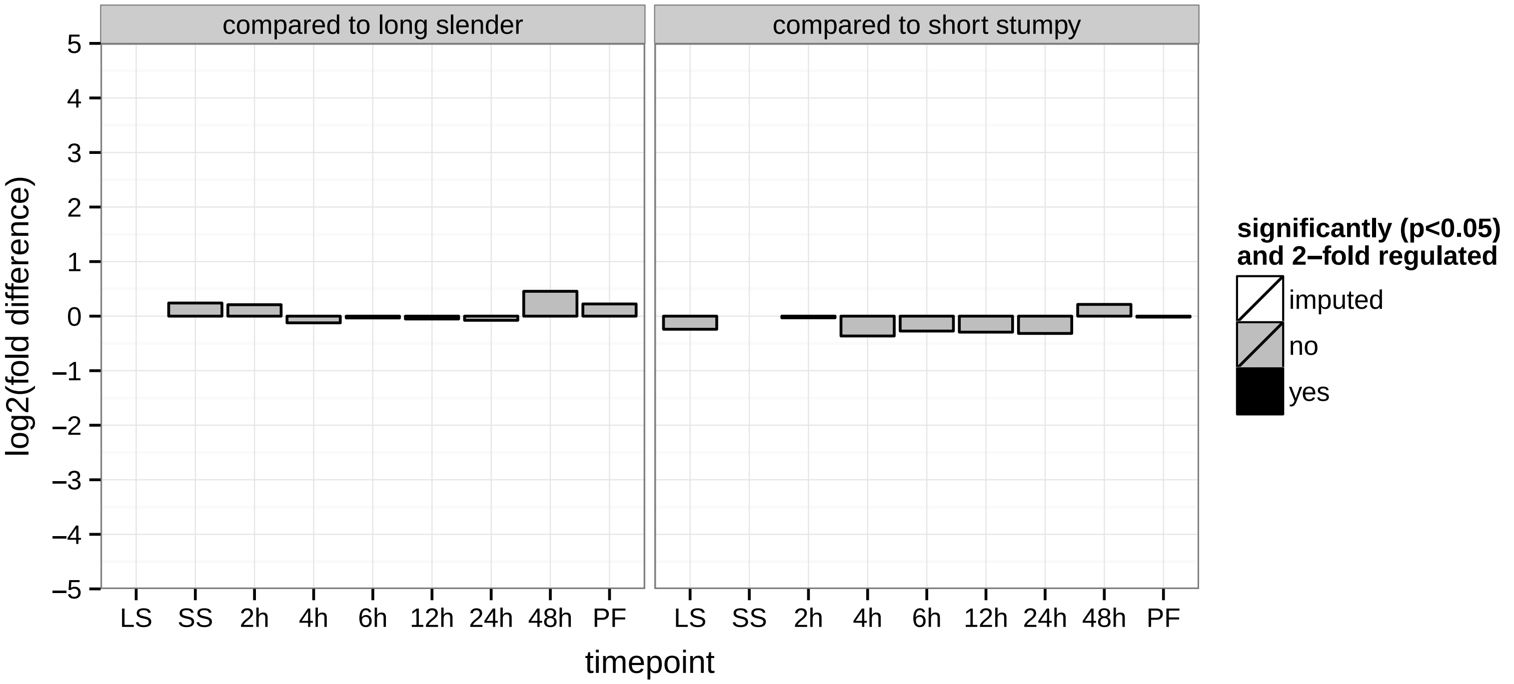
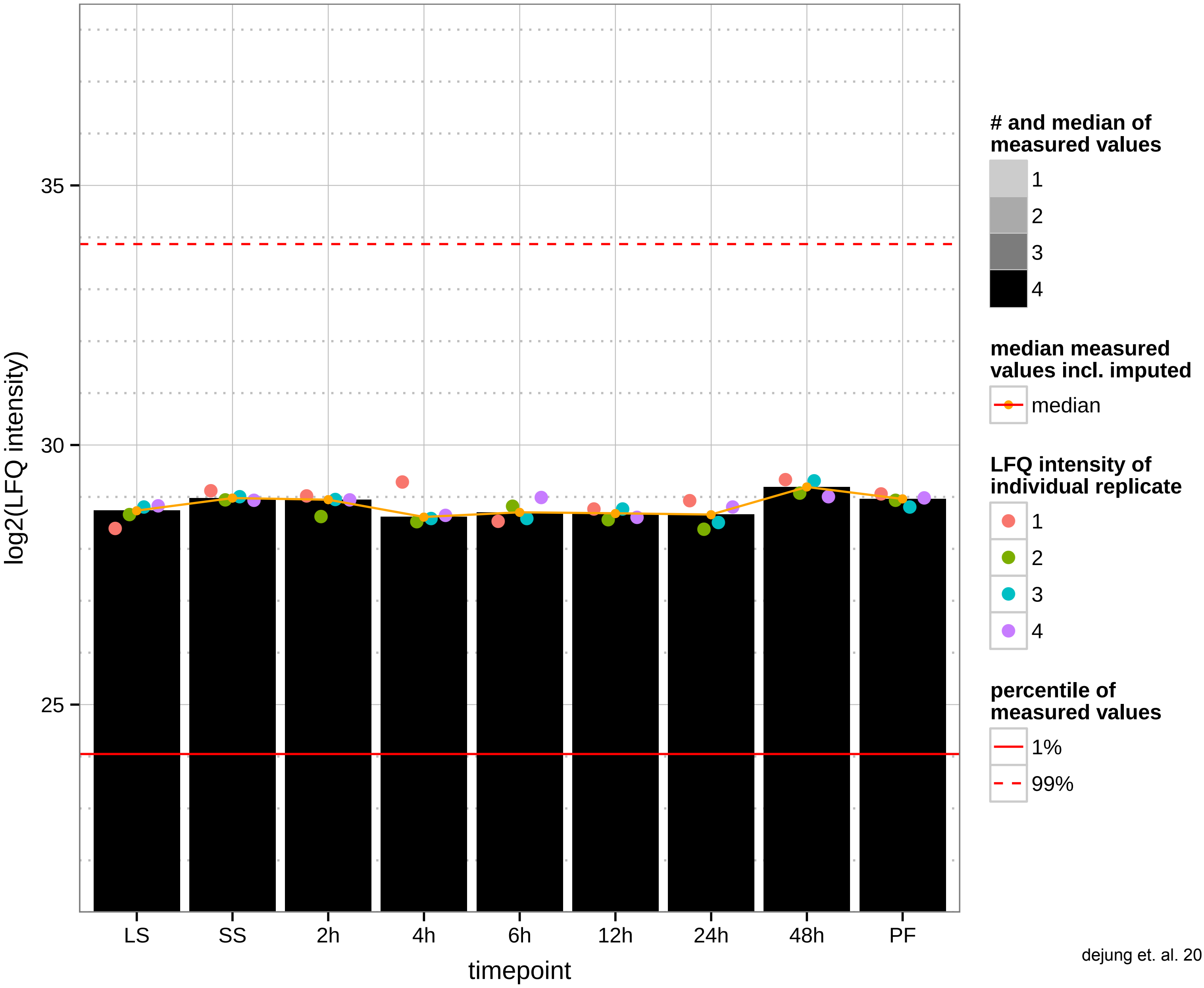
radial spoke protein RSP4/6, putative
Tb927.11.4480
AGOF: null
AGOC: radial spoke
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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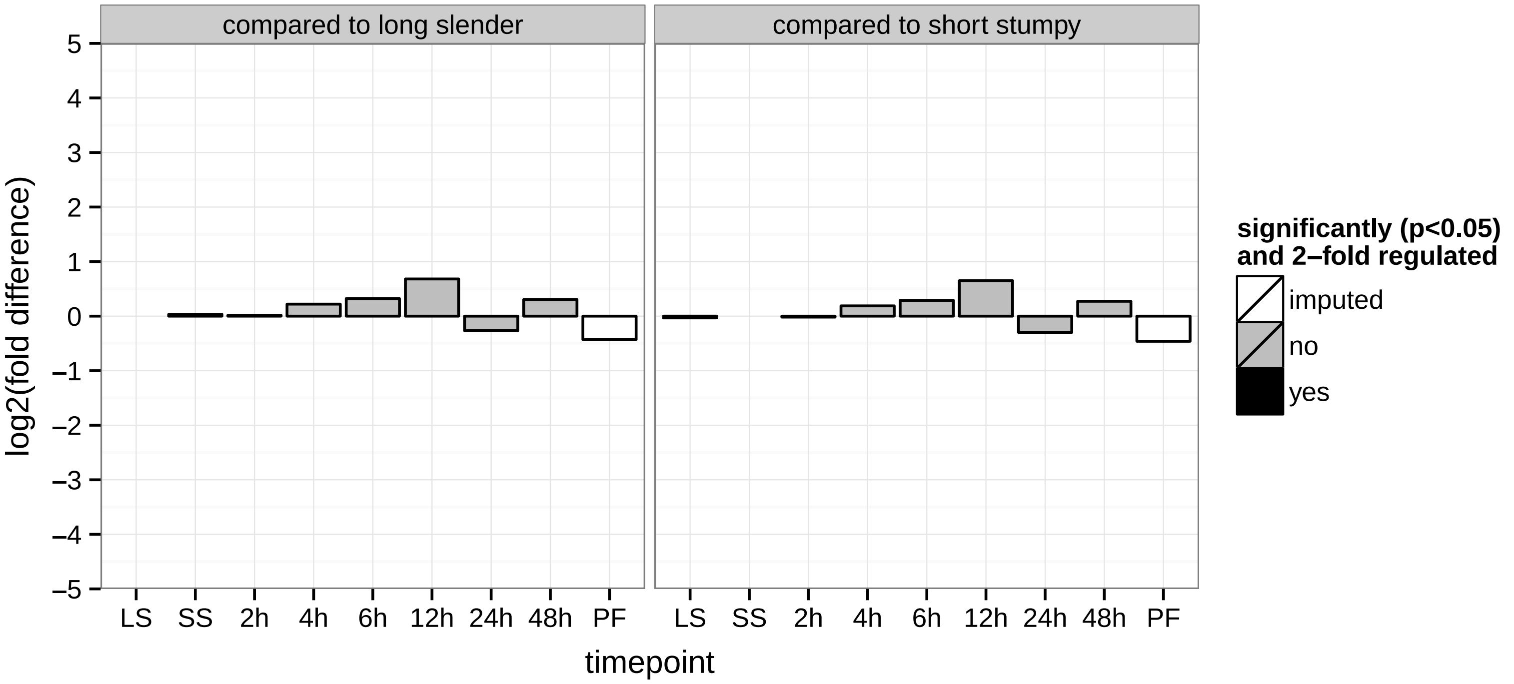
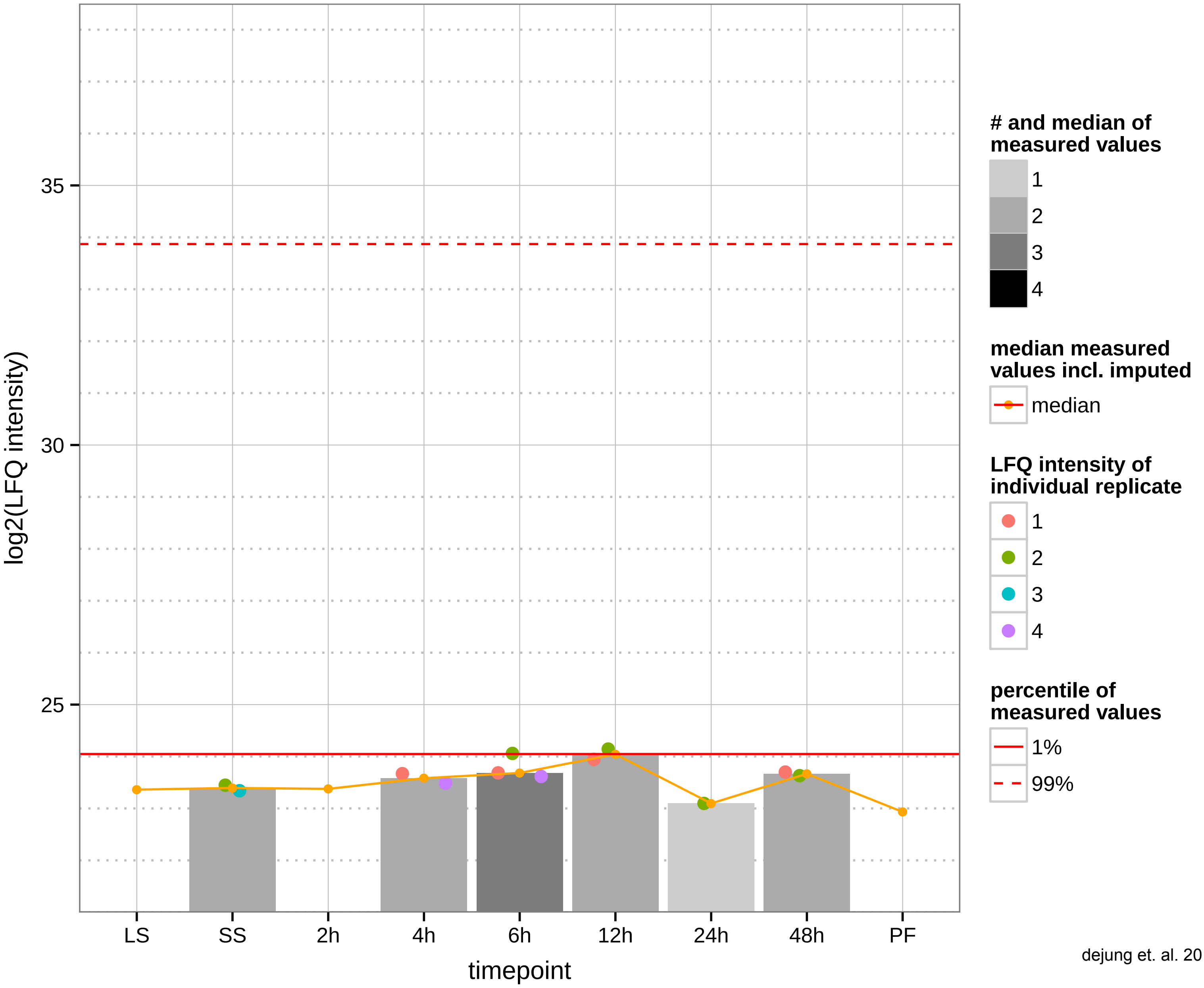
hypothetical protein, conserved
Tb927.11.450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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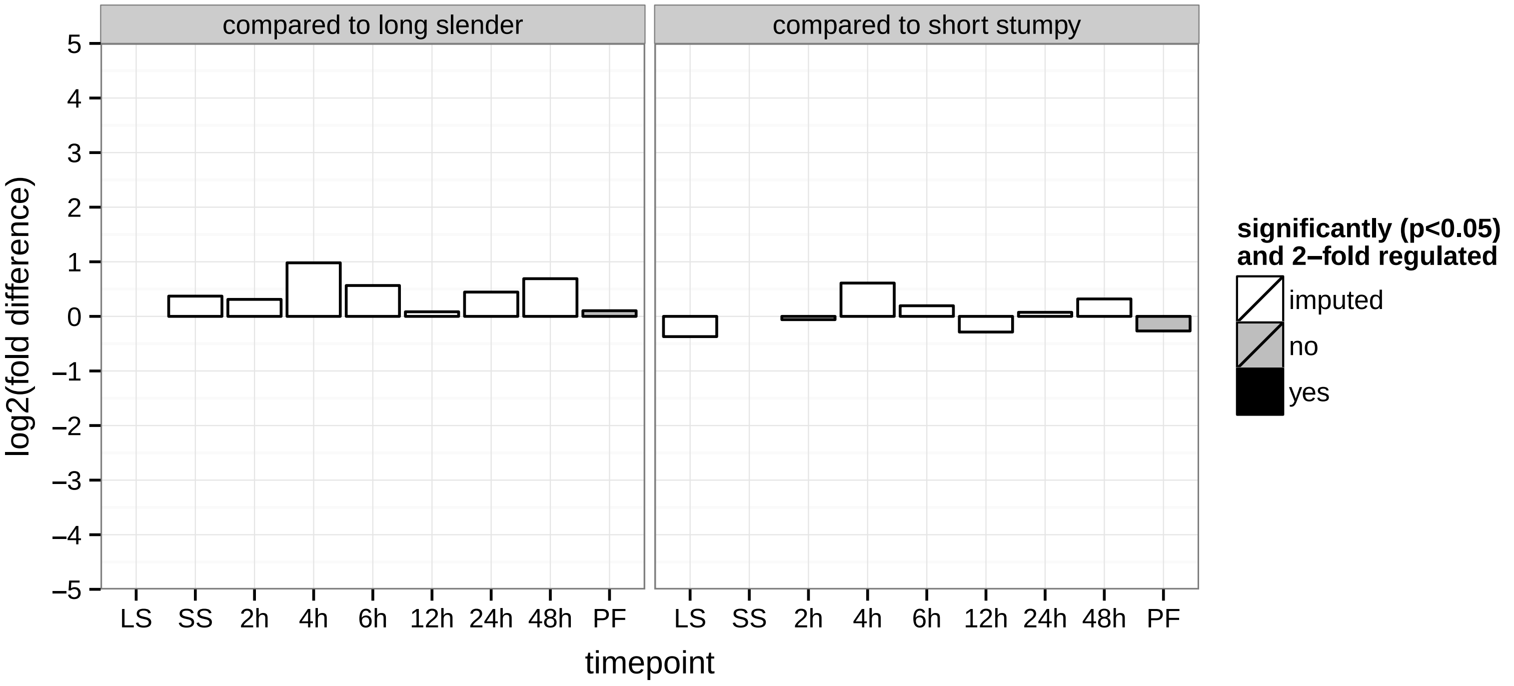
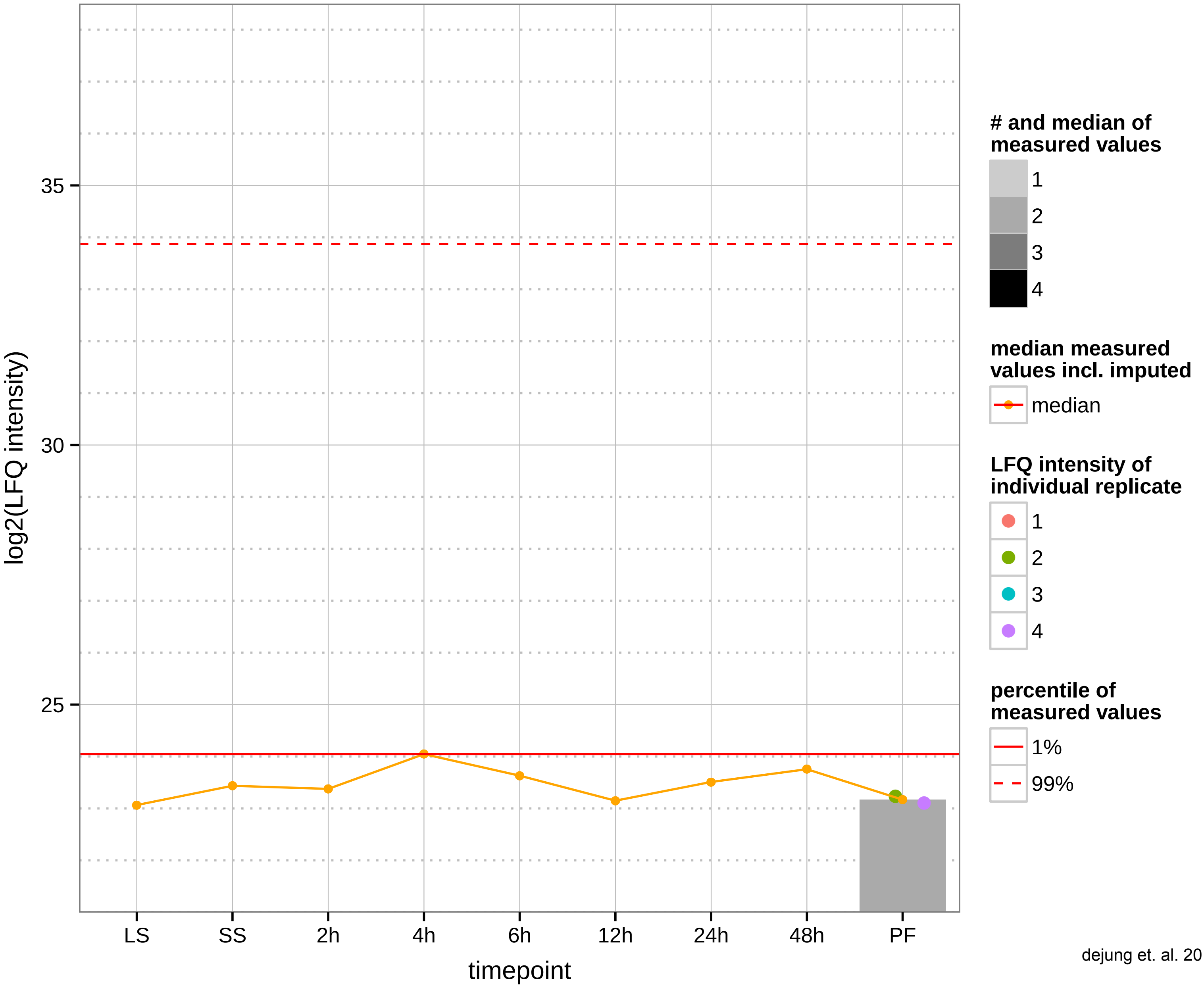
hypothetical protein, conserved
Tb927.11.4510
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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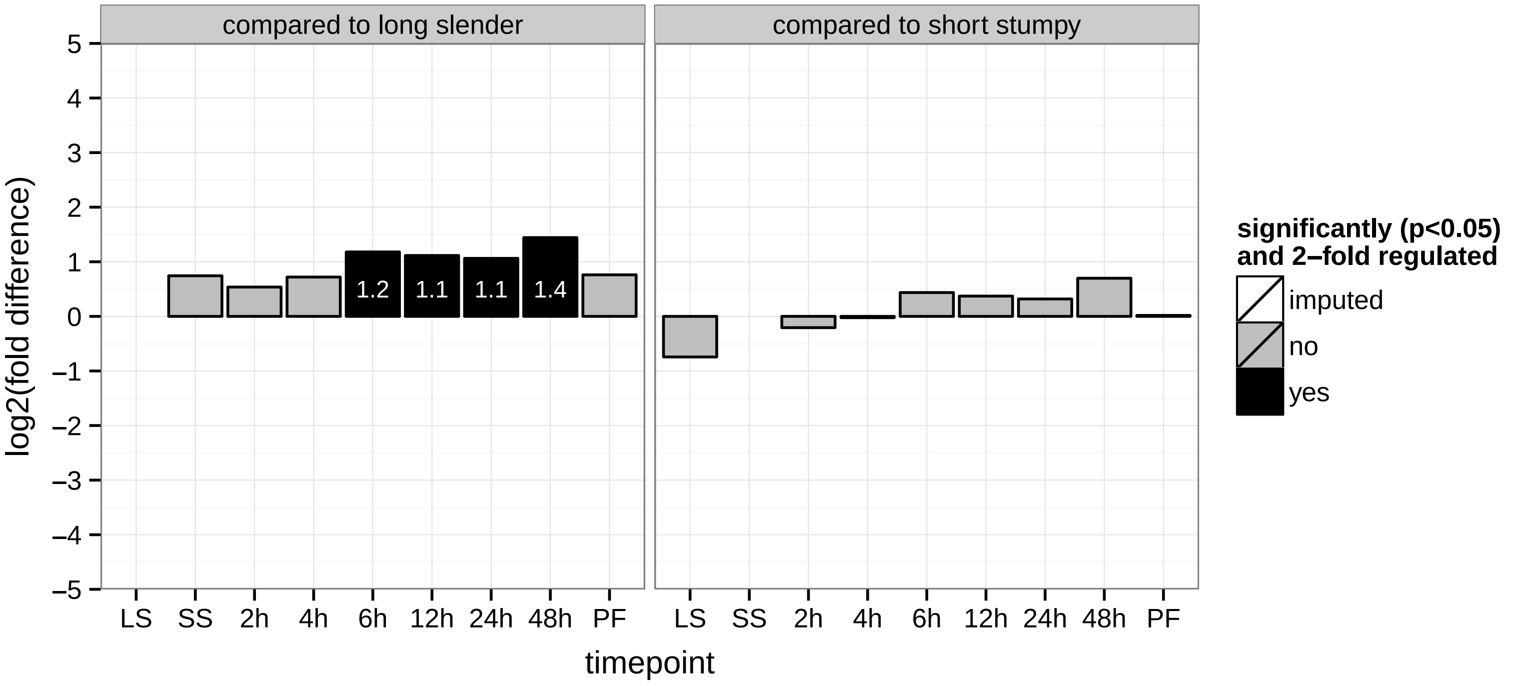
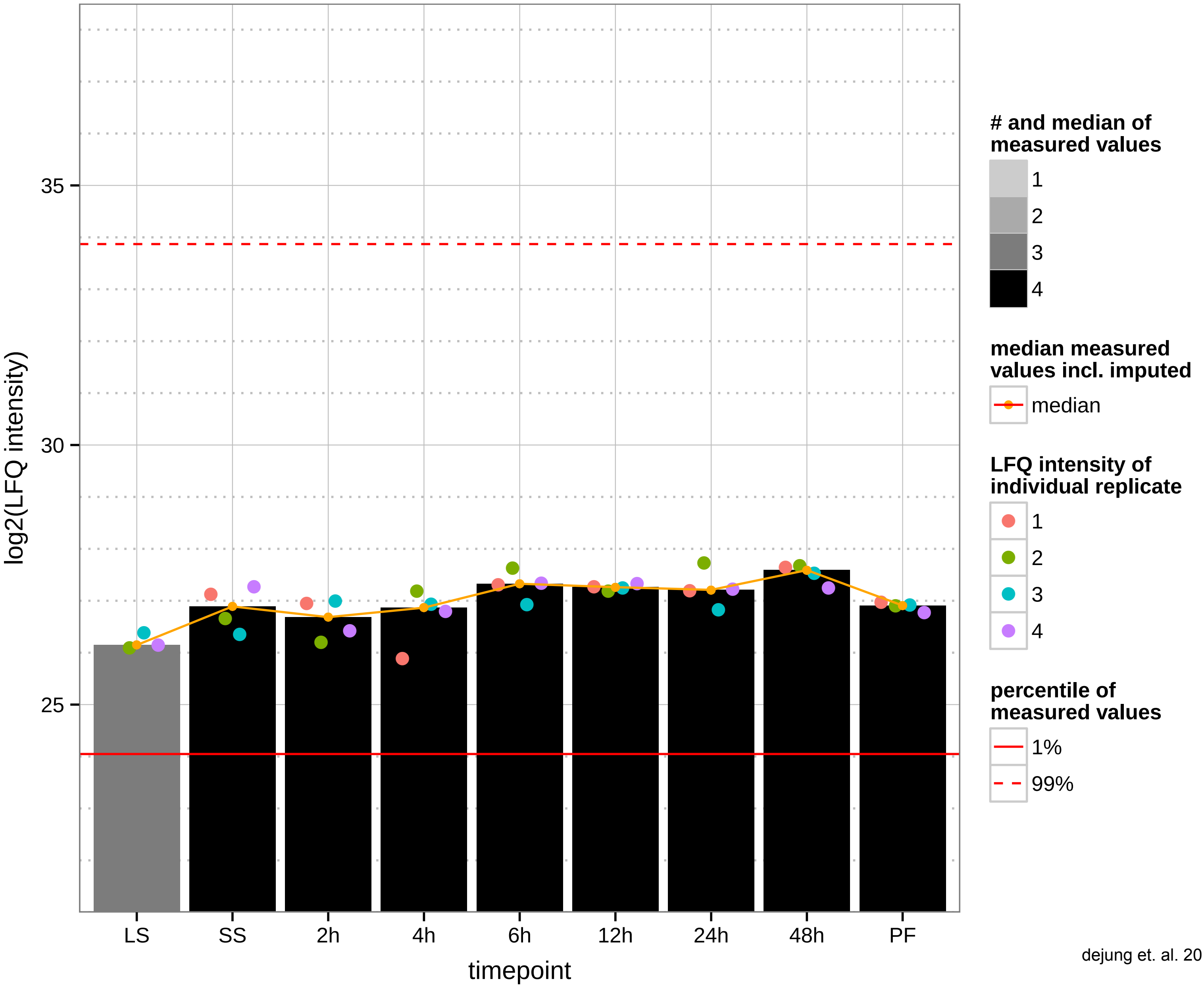
hypothetical protein, conserved
Tb927.11.4810
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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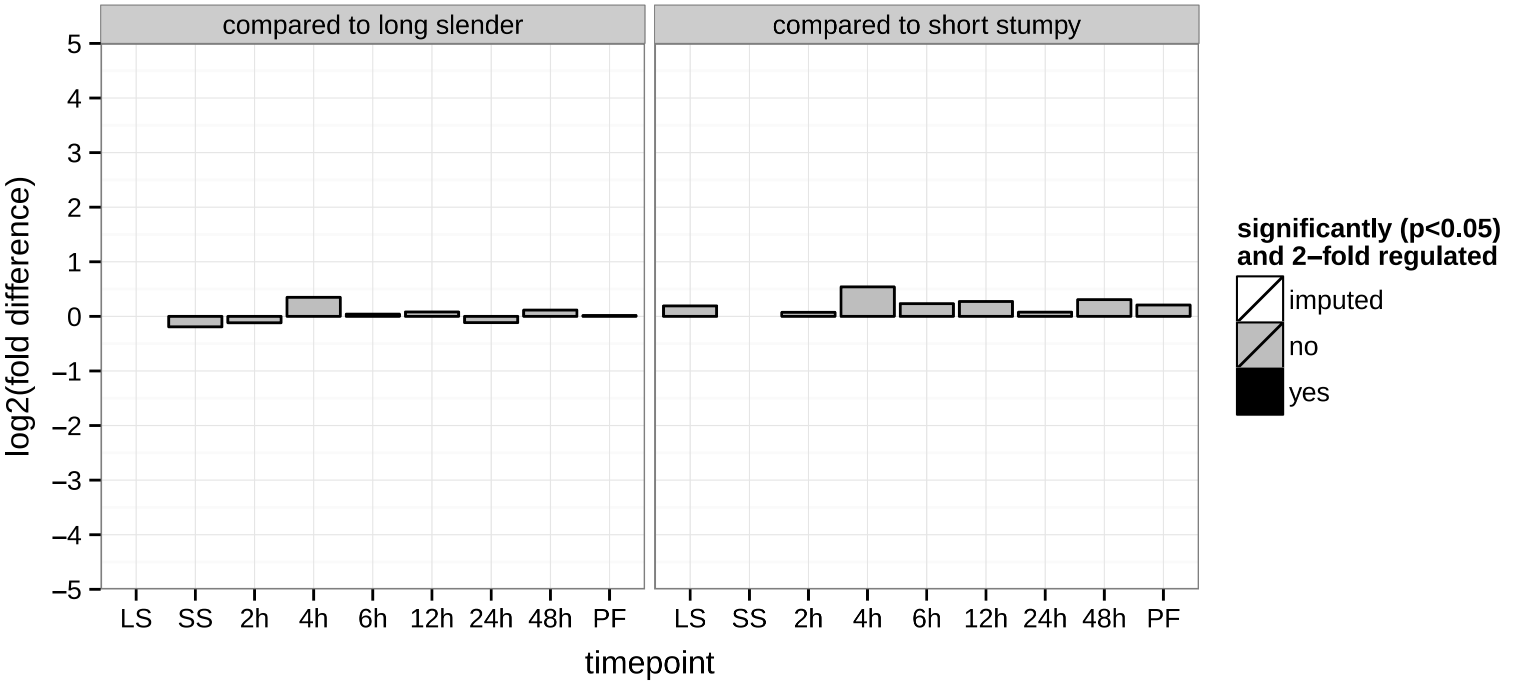
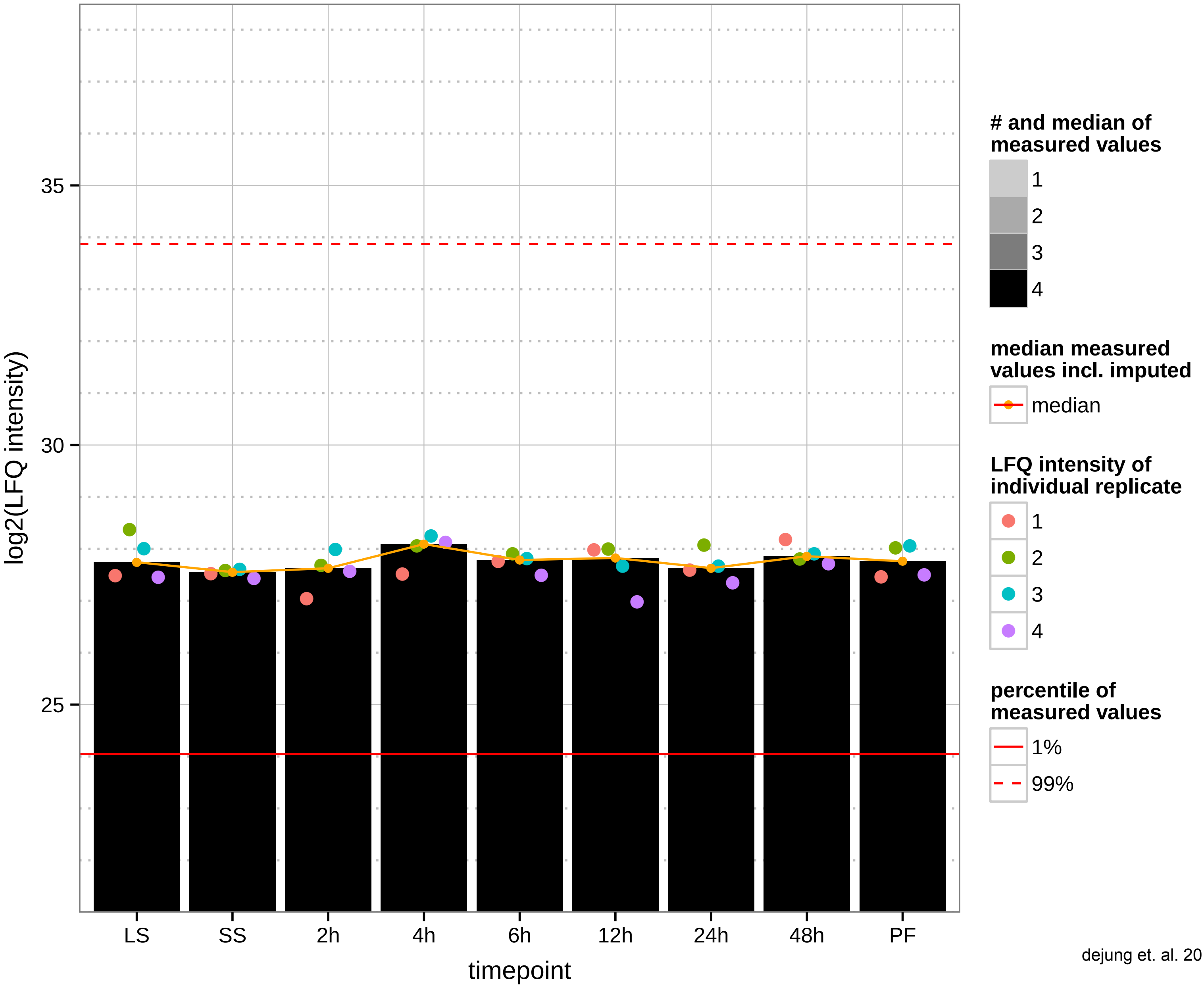
hypothetical protein, conserved
Tb927.11.4880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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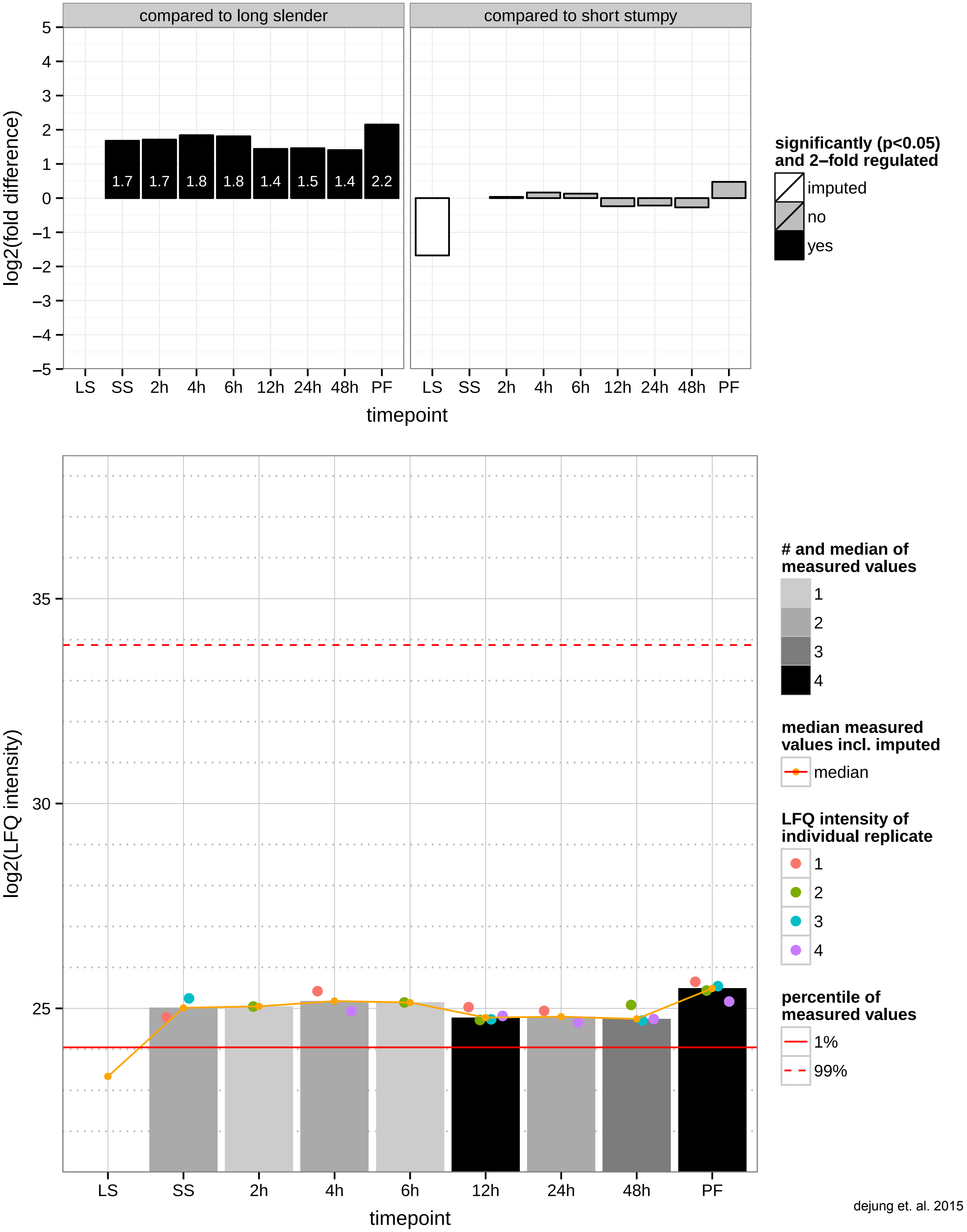
hypothetical protein, conserved
Tb927.11.4890
AGOF: mRNA (nucleoside−2'−O−)−methyltransferase activity
AGOC: null
AGOP: 7−methylguanosine mRNA capping
PGOF: null
PGOC: null
PGOP: null



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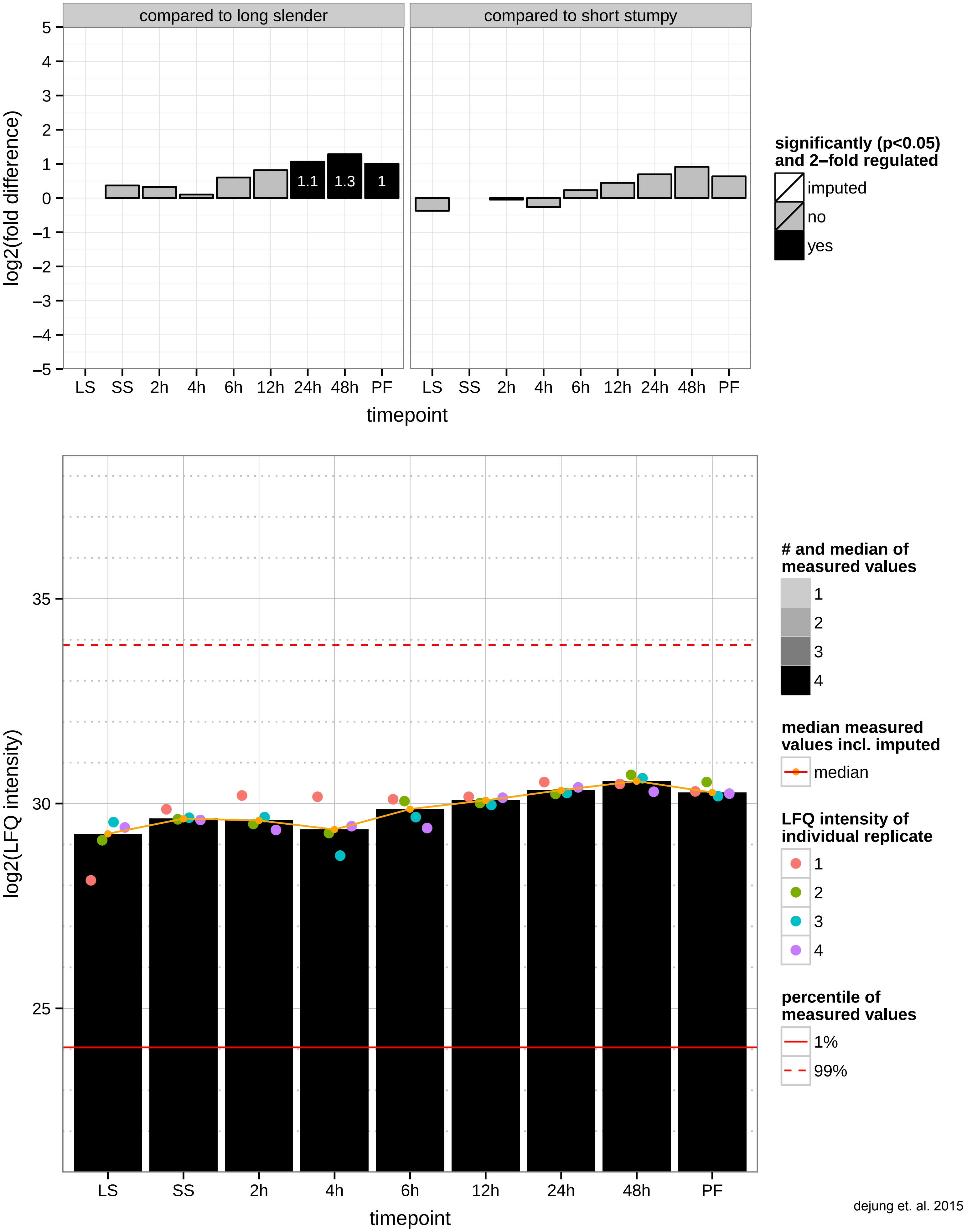
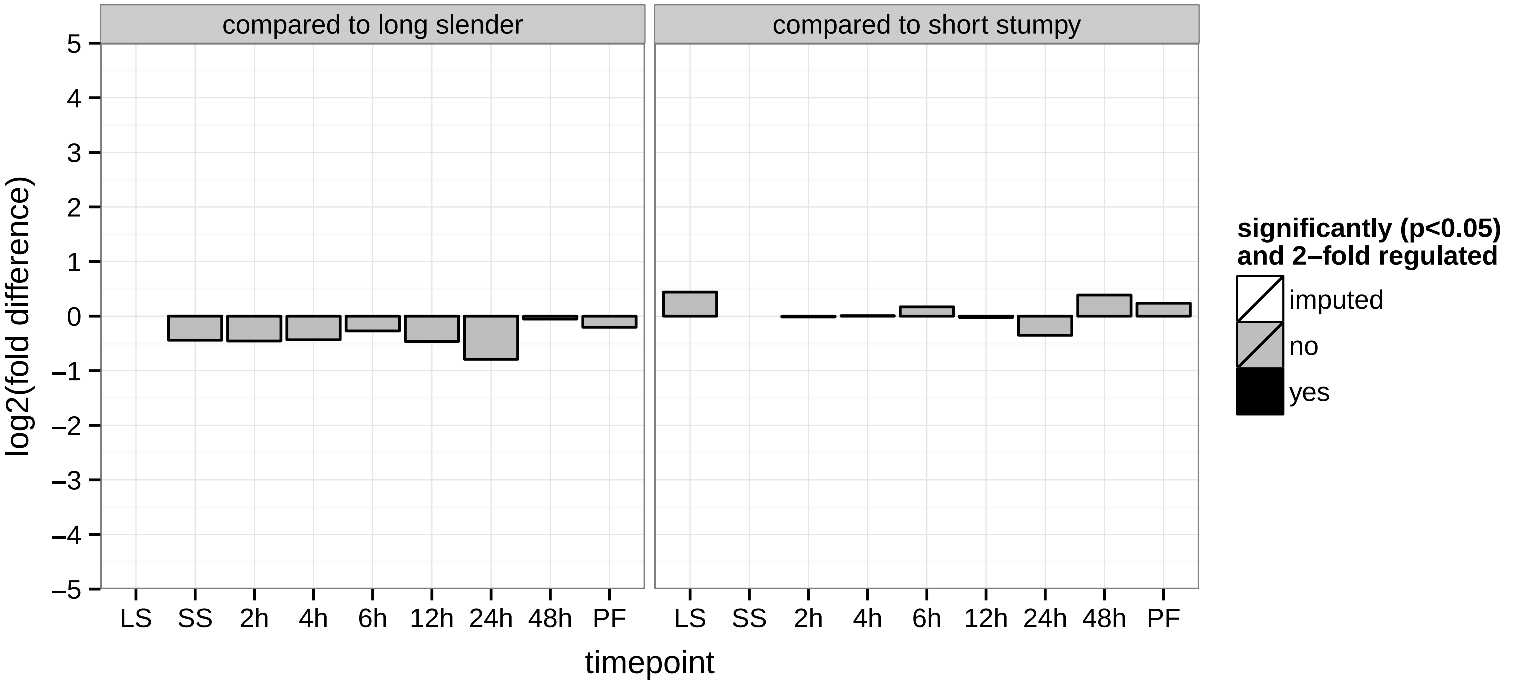
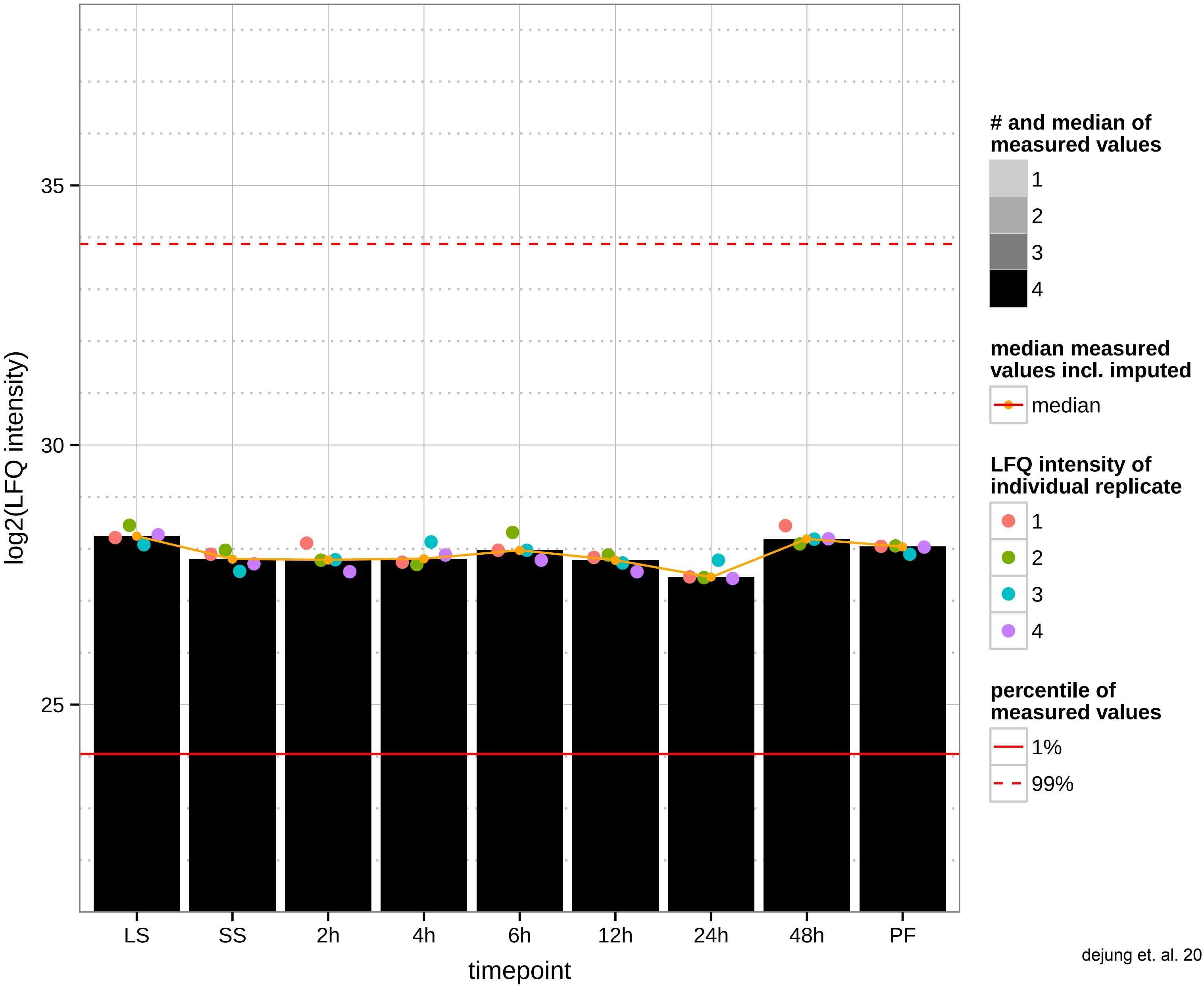
guanine nucleotide−binding beta subunit−like protein, G−protein (beta)−like protein, beta transducin−like protein
Tb927.11.4900
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



hypothetical protein, conserved
Tb927.11.4920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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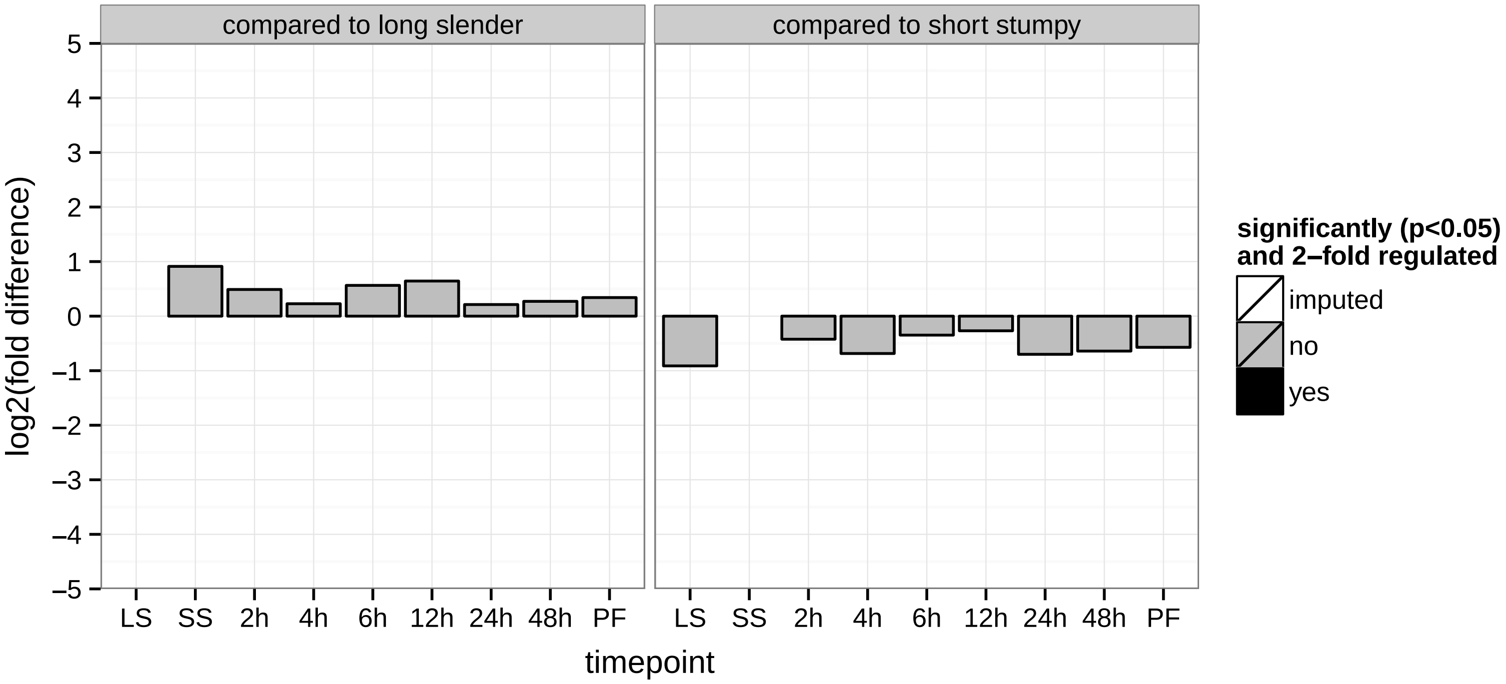
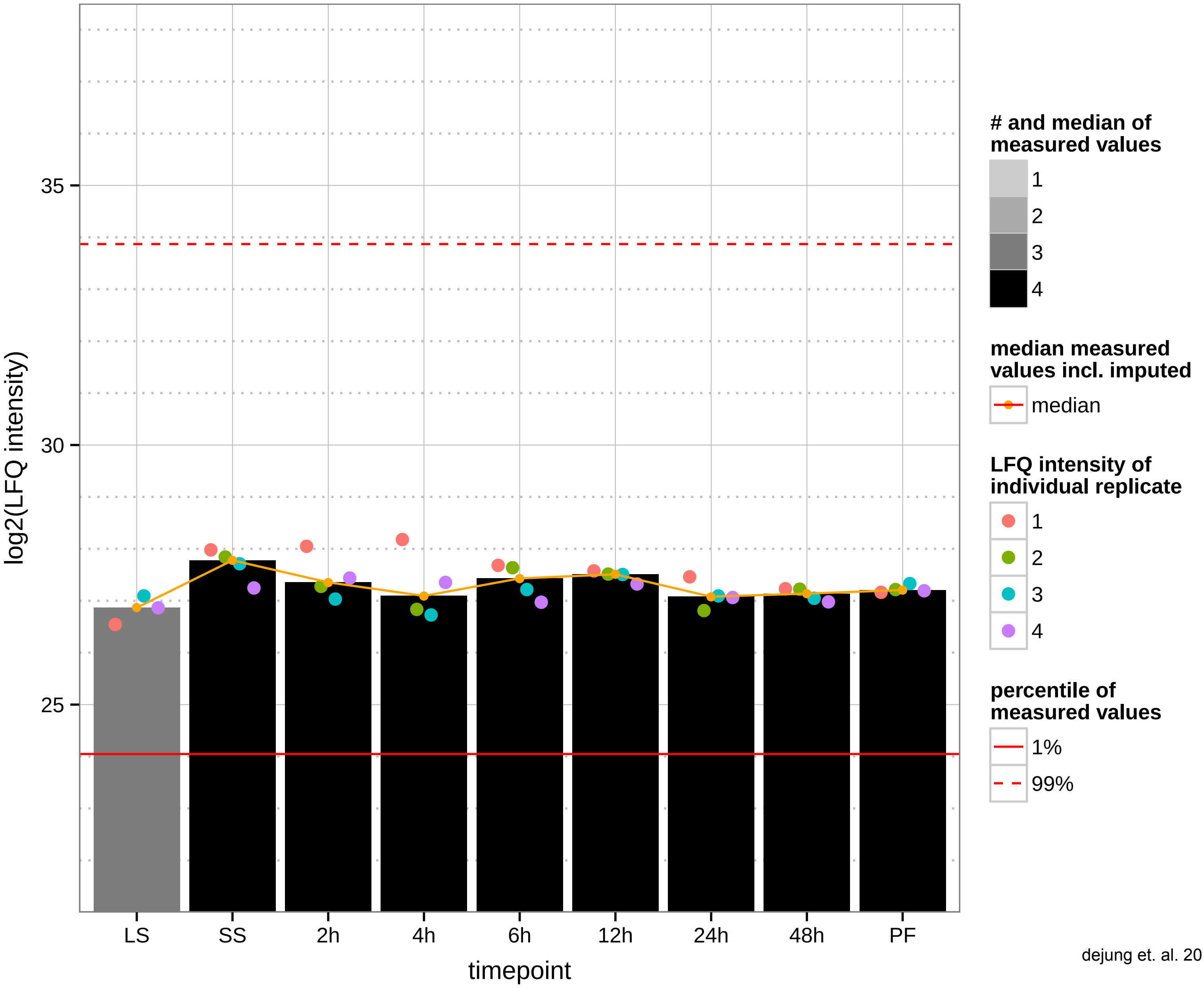
hypothetical protein, conserved
Tb927.11.4950
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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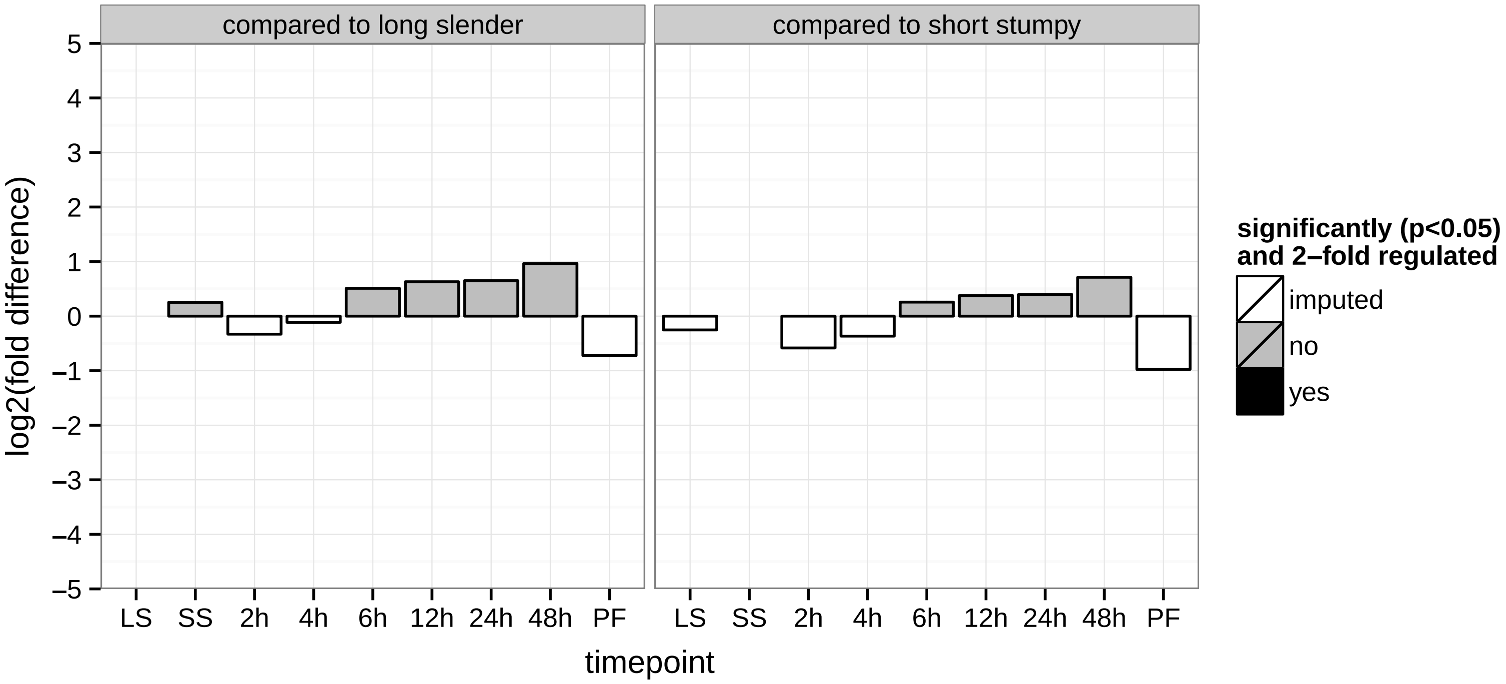
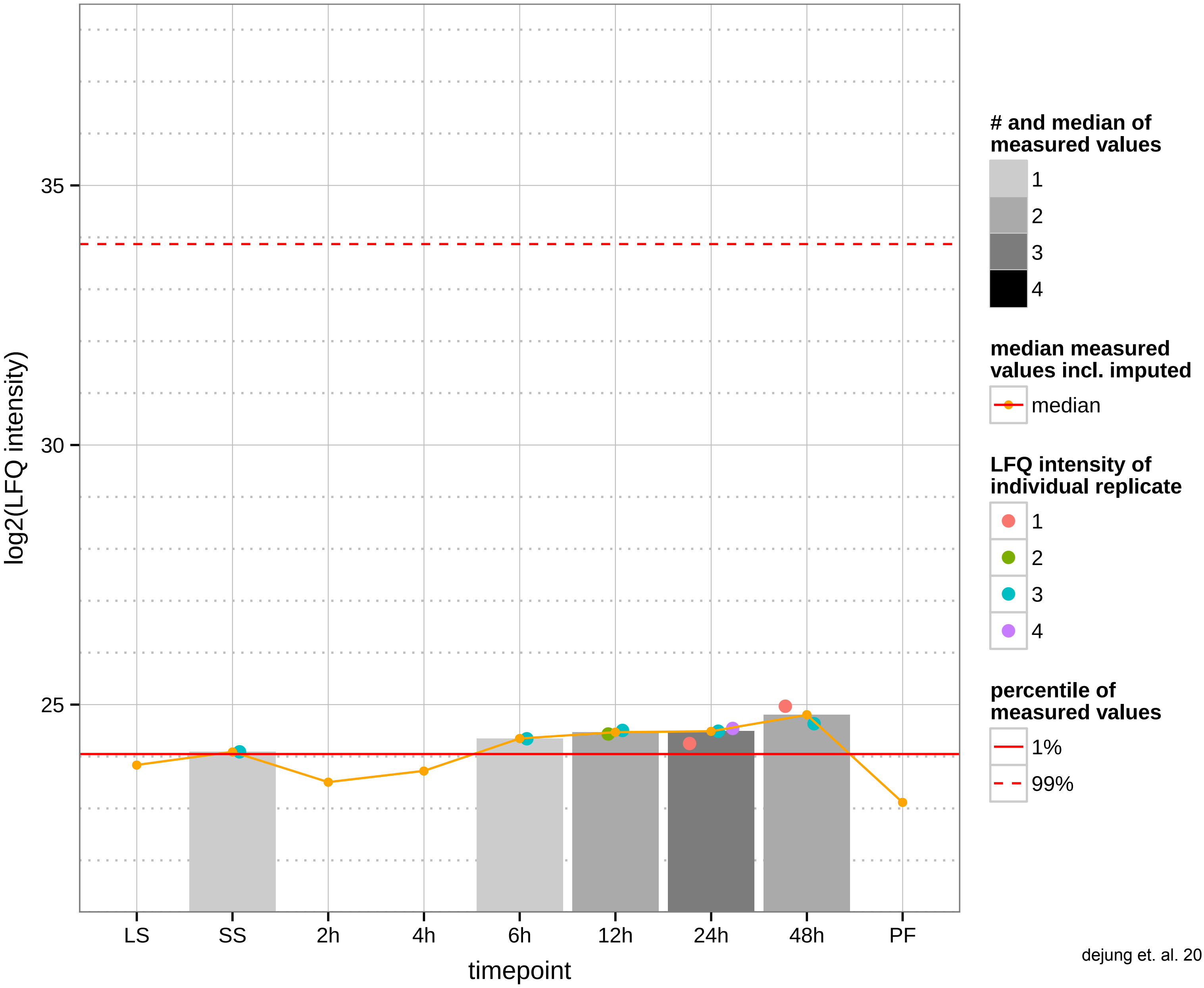
predicted WD40 repeat protein
Tb927.11.4970
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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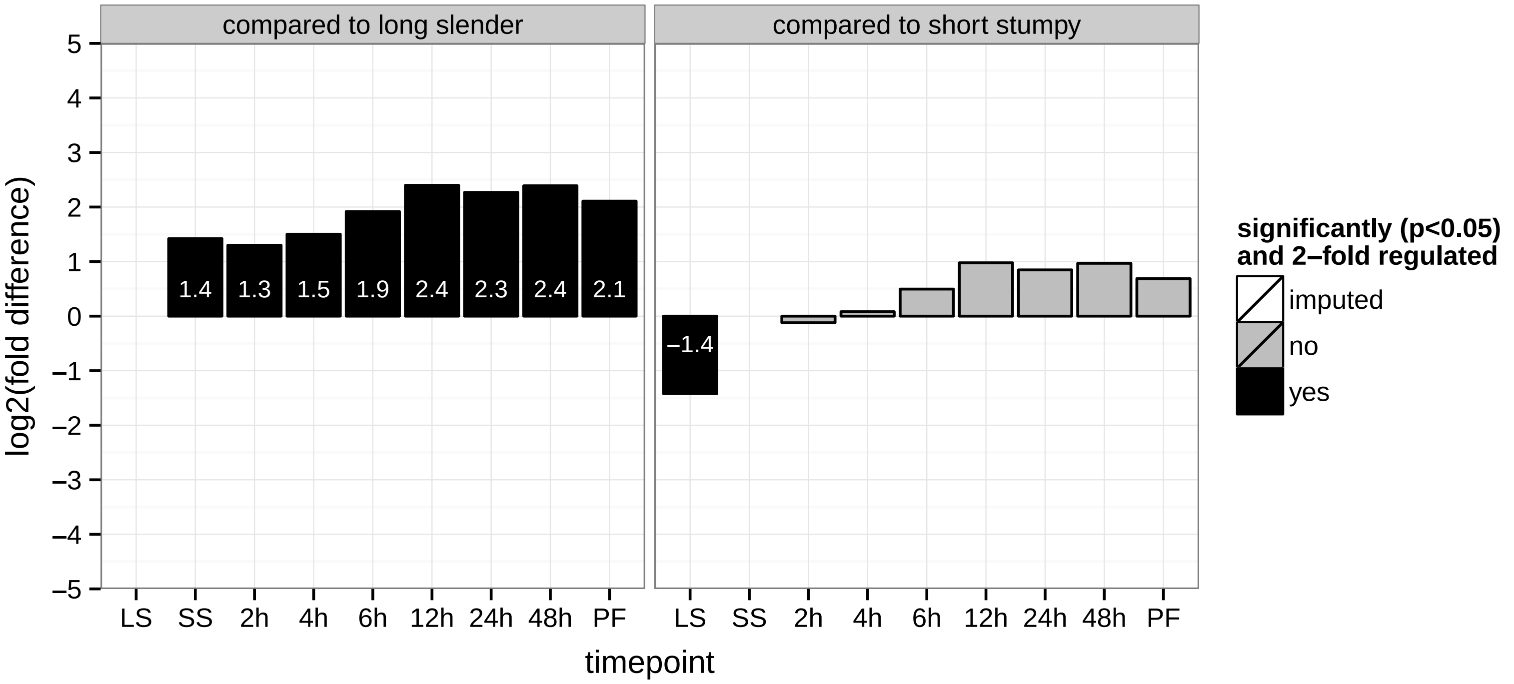
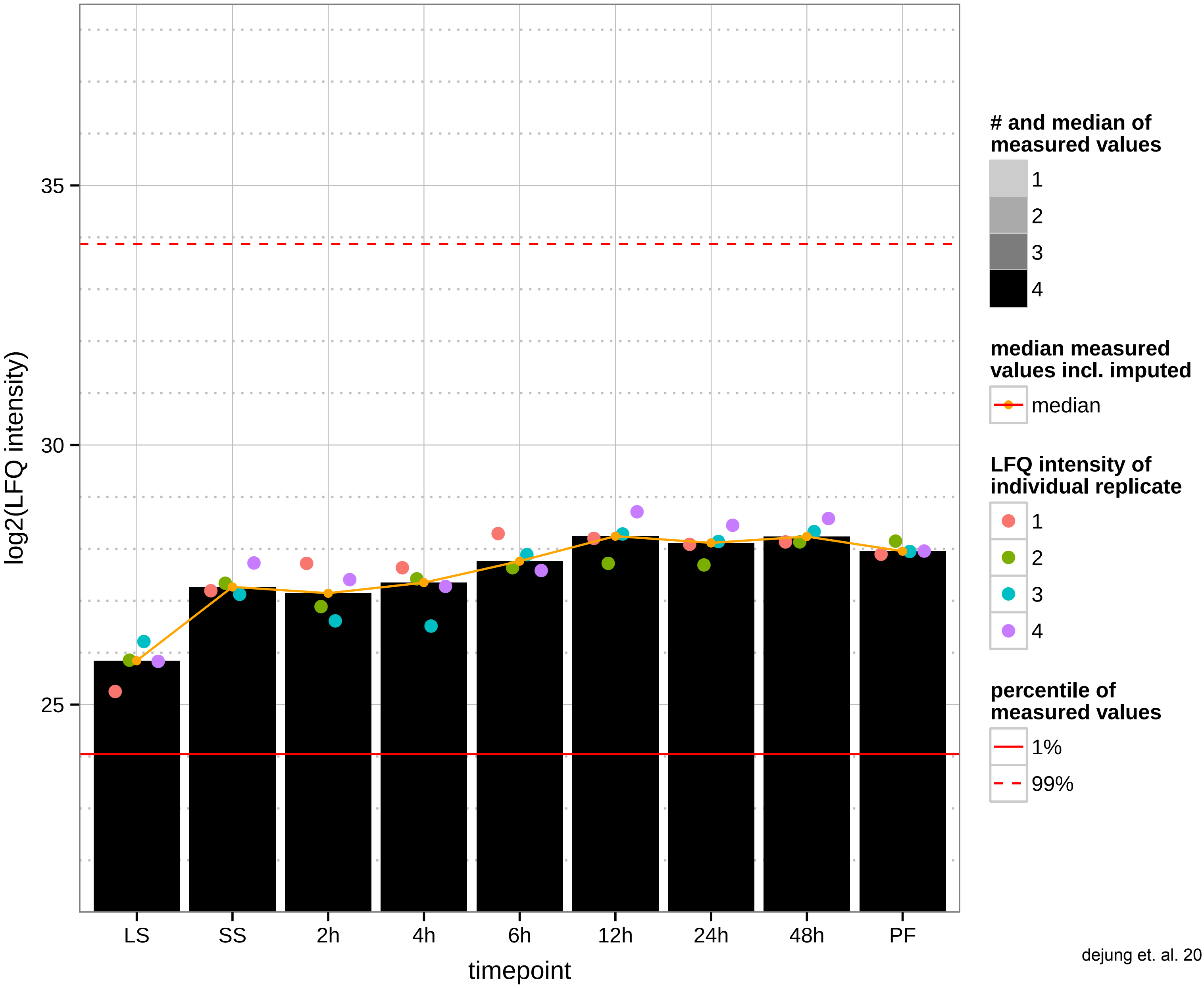
ATP−dependent DEAD/H RNA helicase, putative, ATP− dependent RNA helicase
Tb927.11.4980
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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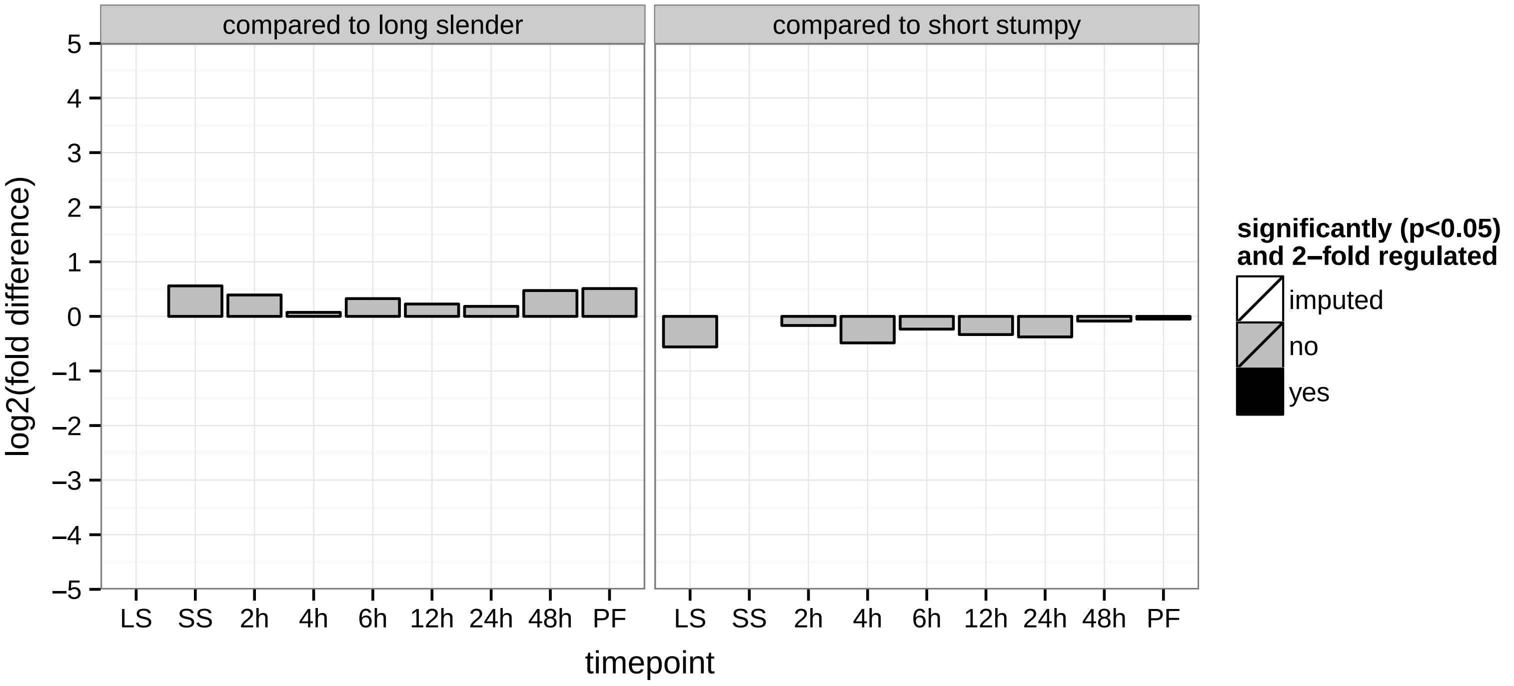
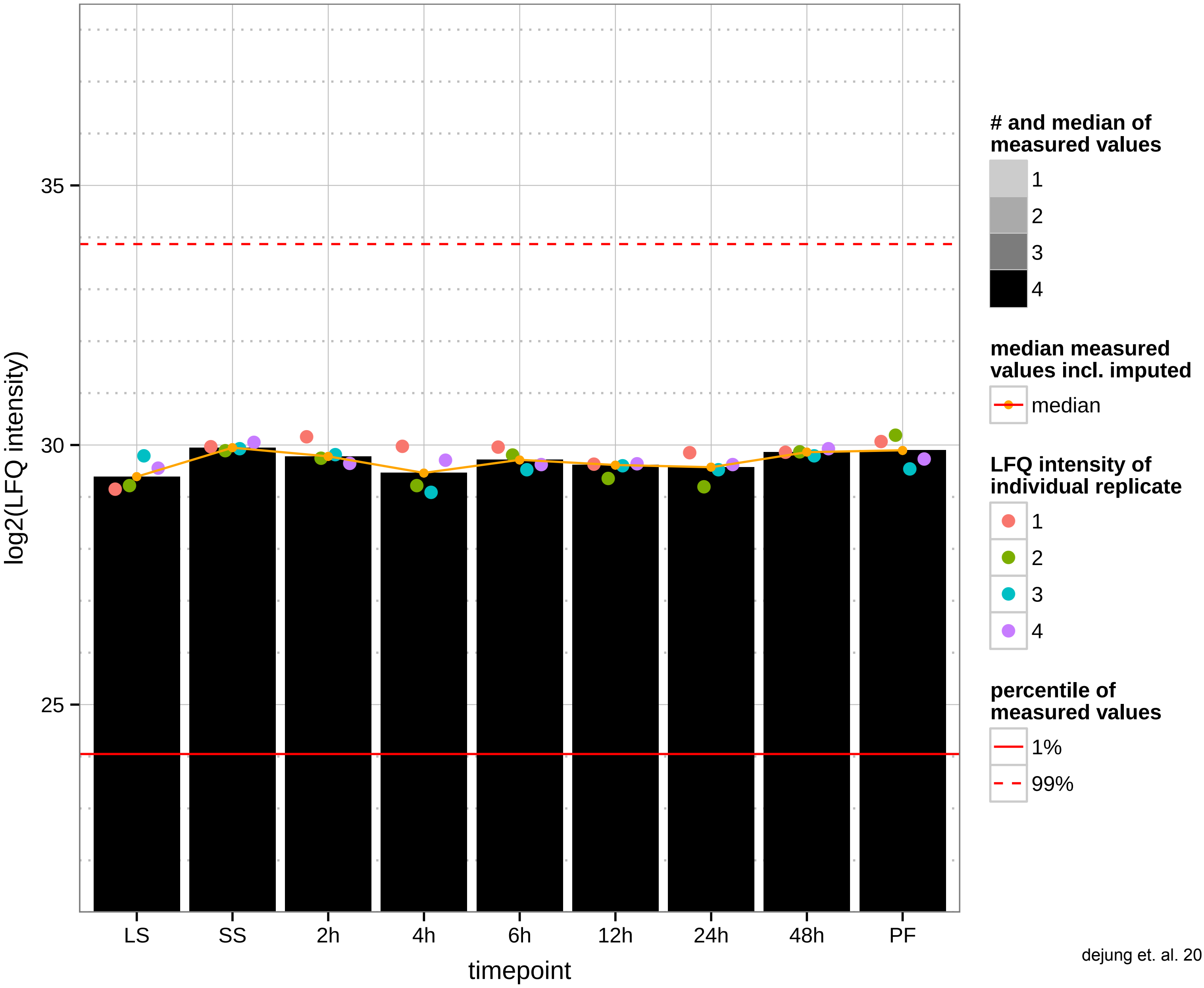
dynein intermediate chain IC78, putative
Tb927.11.5000
AGOF: motor activity
AGOC: cytoskeleton, dynein complex
AGOP: microtubule–based movement
PGOF: protein binding
PGOC: null
PGOP: null





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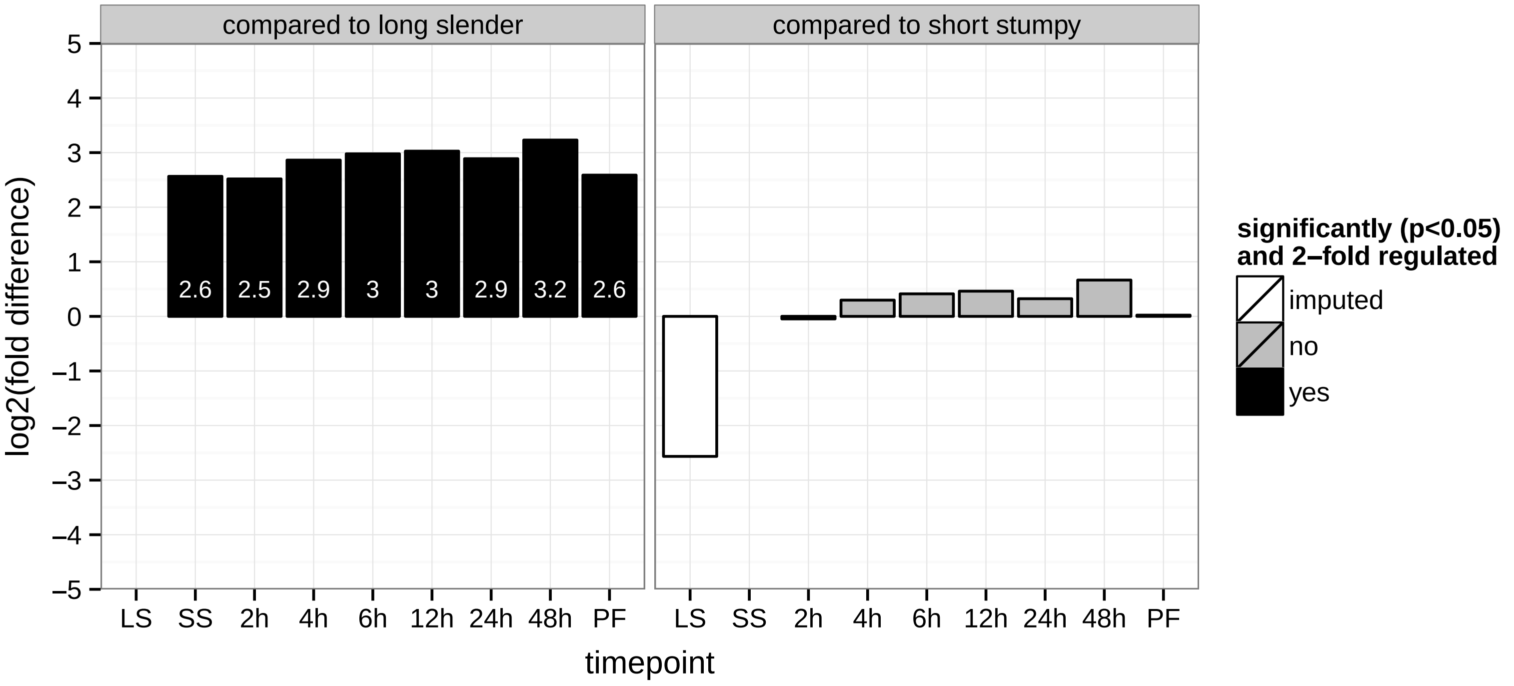
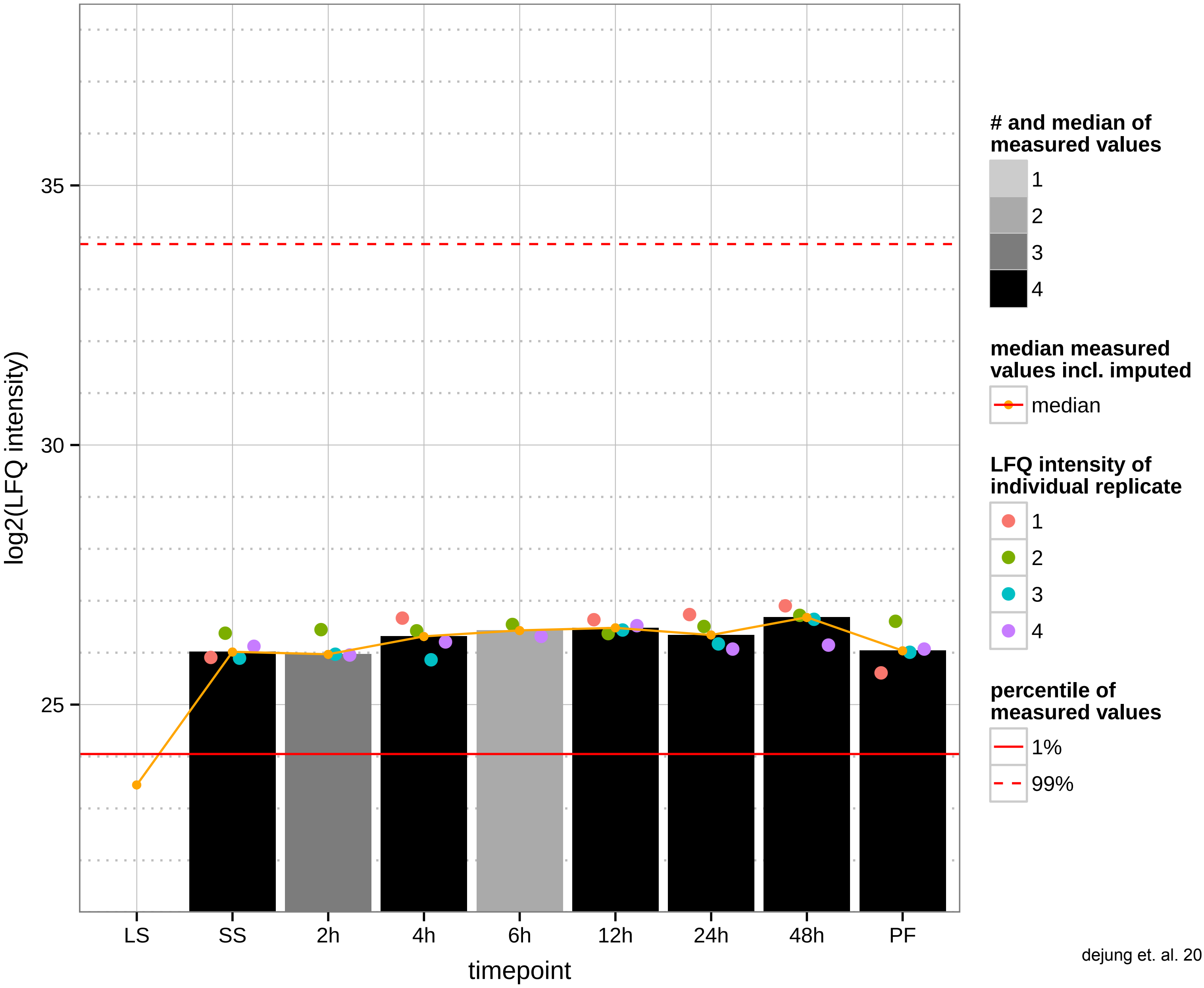
hypothetical protein, conserved
Tb927.11.5030
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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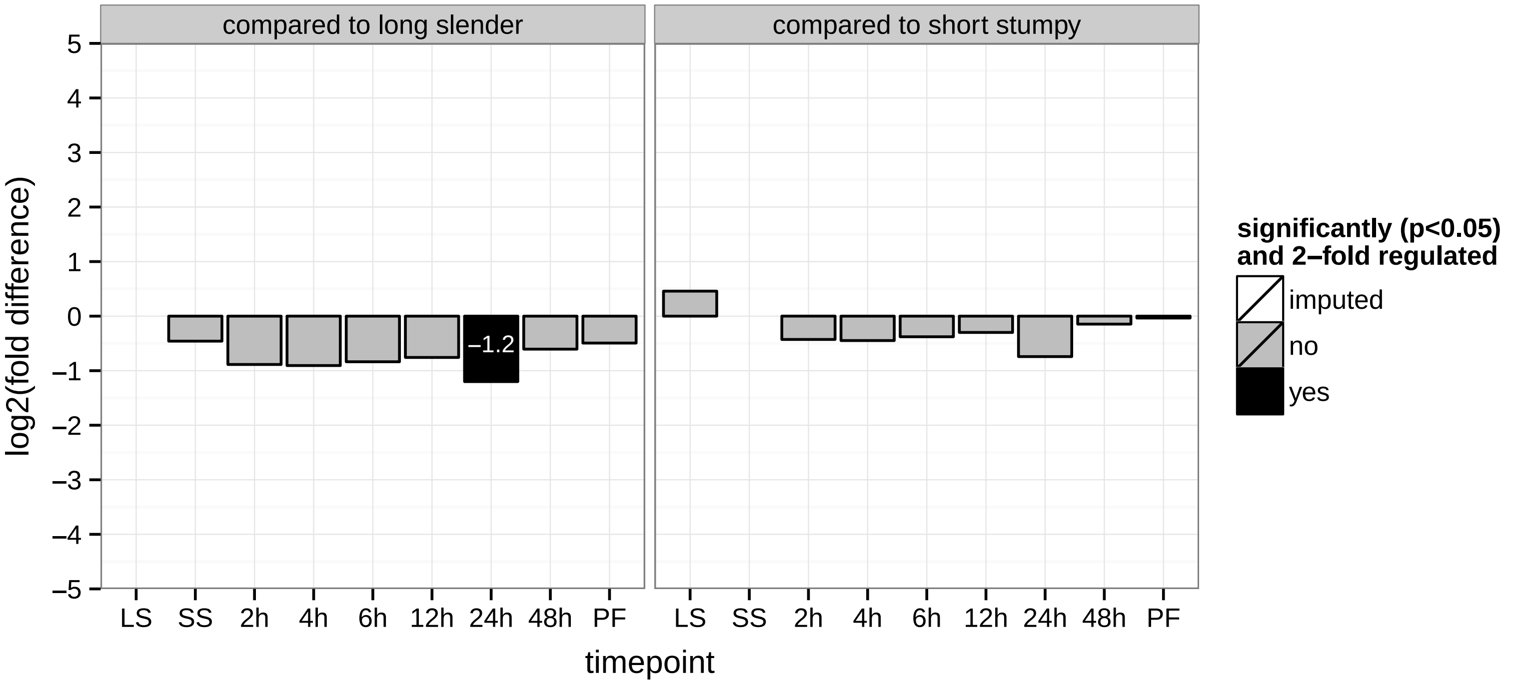
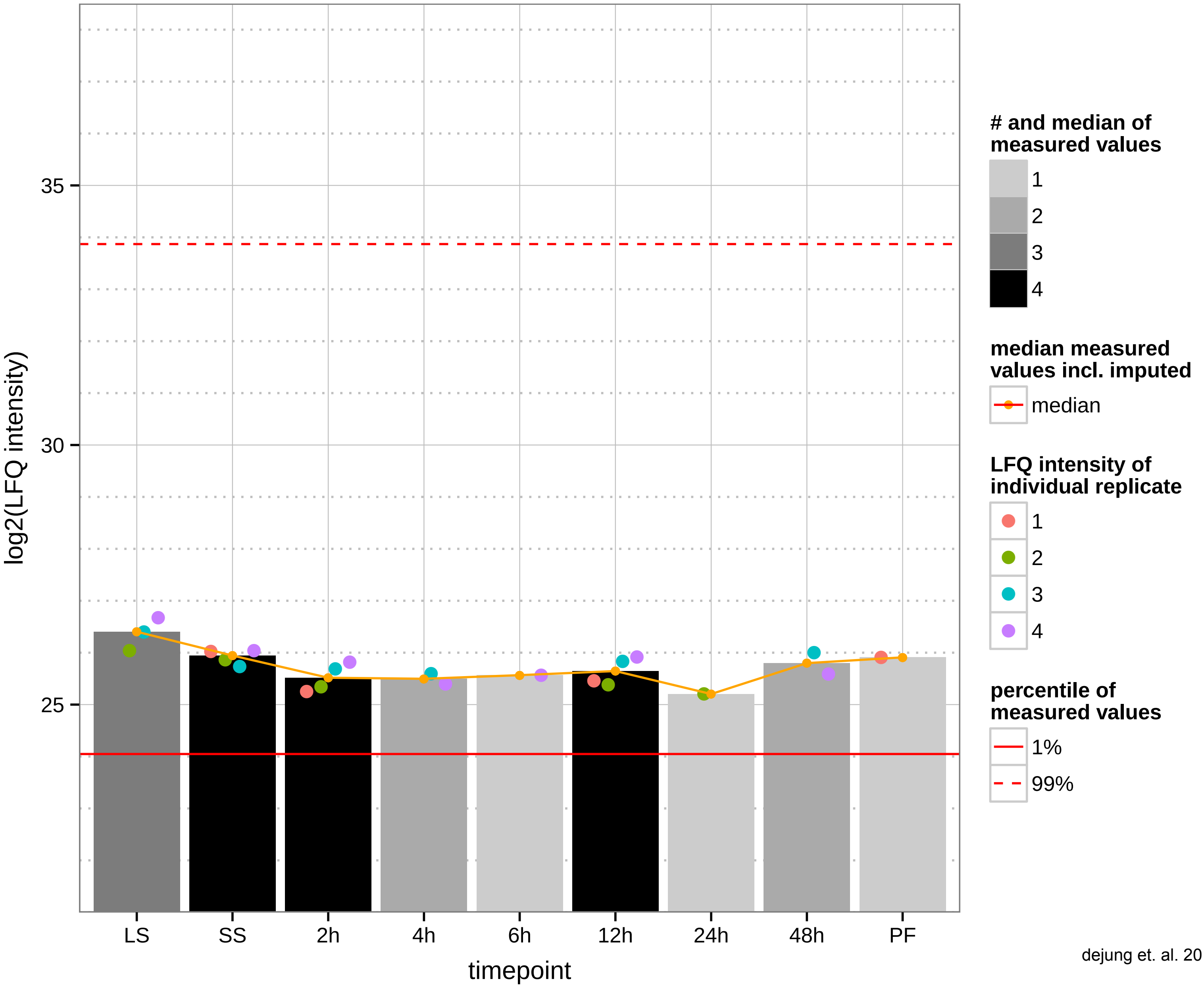
leucine–rich repeat protein (LRRP), putative
Tb927.11.5040
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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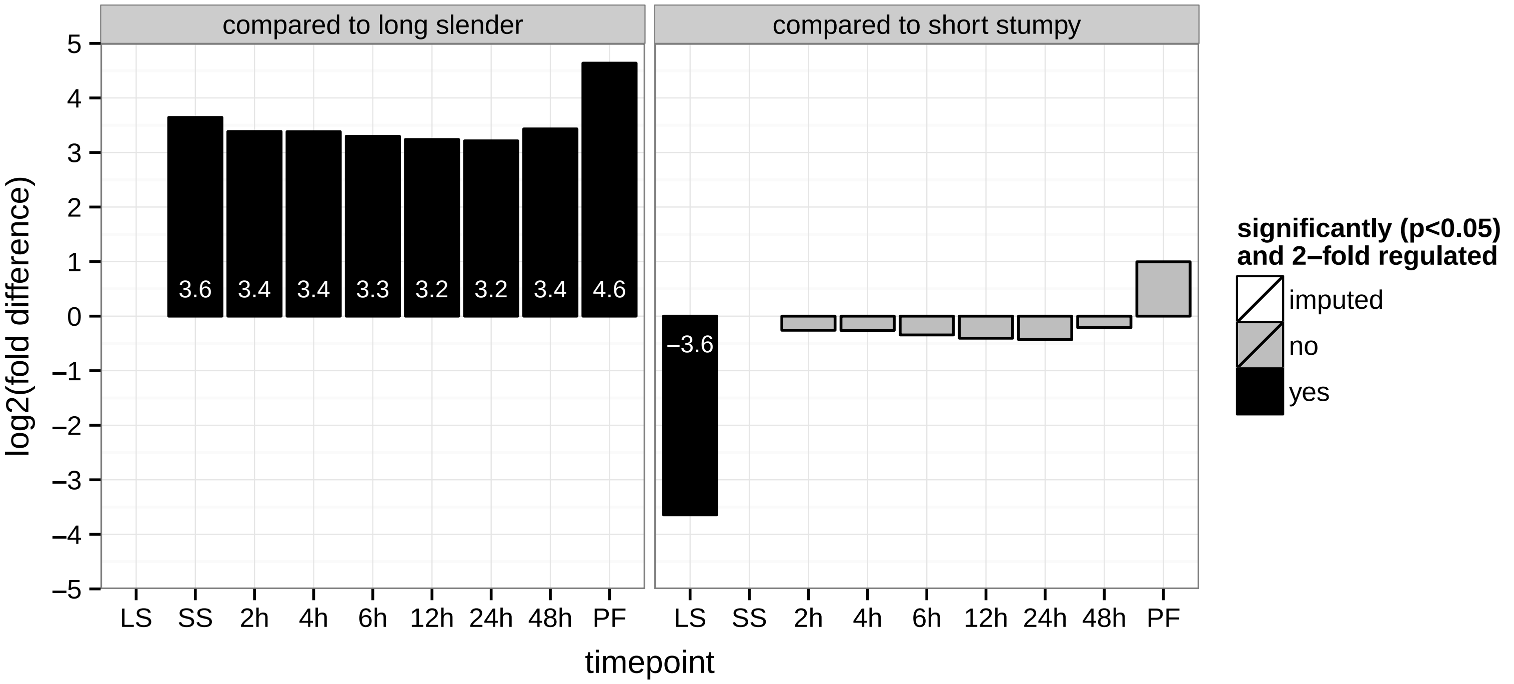
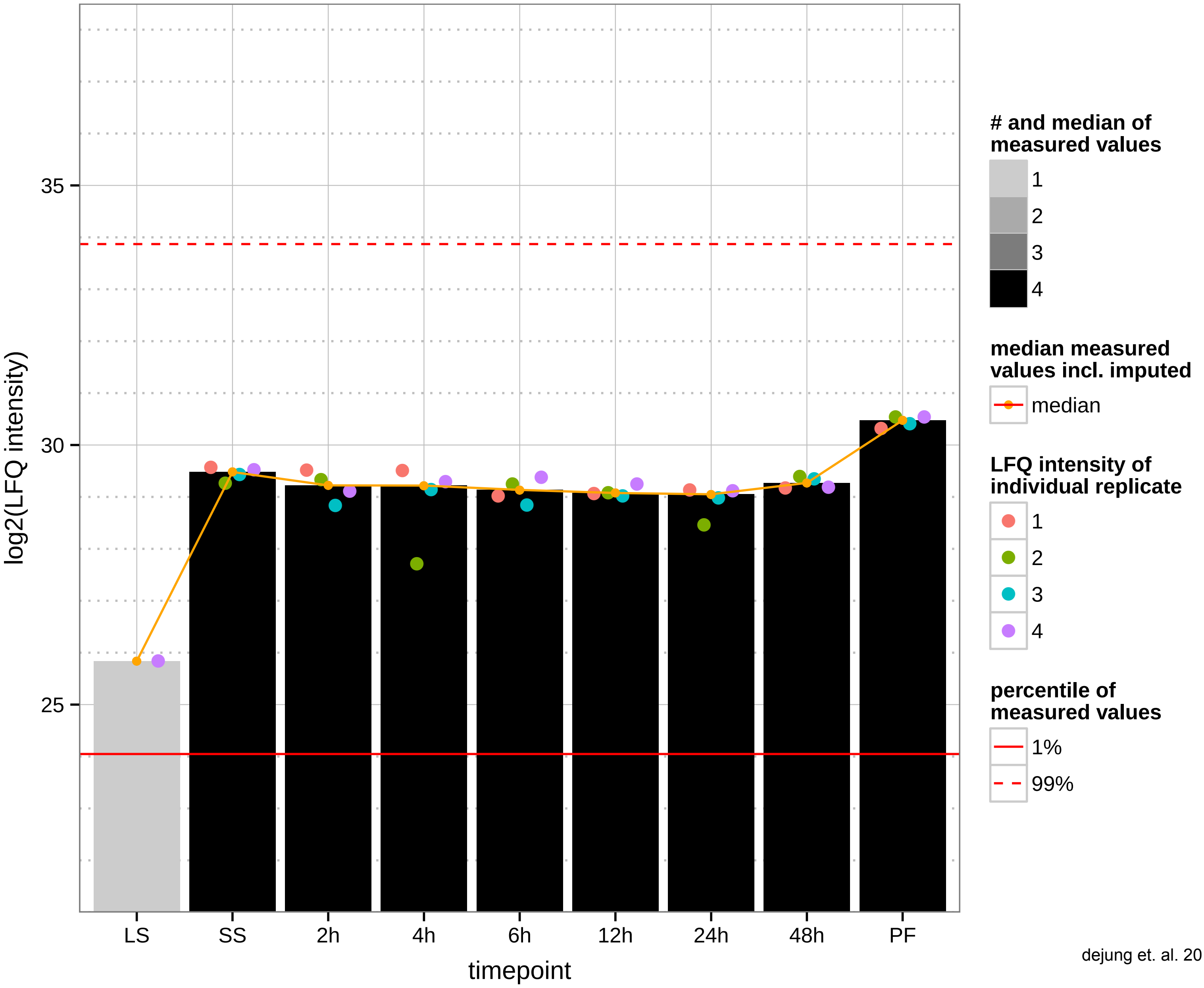
fumarate hydratase, class I (FHm)
Tb927.11.5050
AGOF: fumarate hydratase activity
AGOC: mitochondrion
AGOP: fumarate metabolic process, generation of precursor metabolites and energy
PGOF: fumarate hydratase activity, hydro–lyase activity, lyase activity
PGOC: null
PGOP: generation of precursor metabolites and energy





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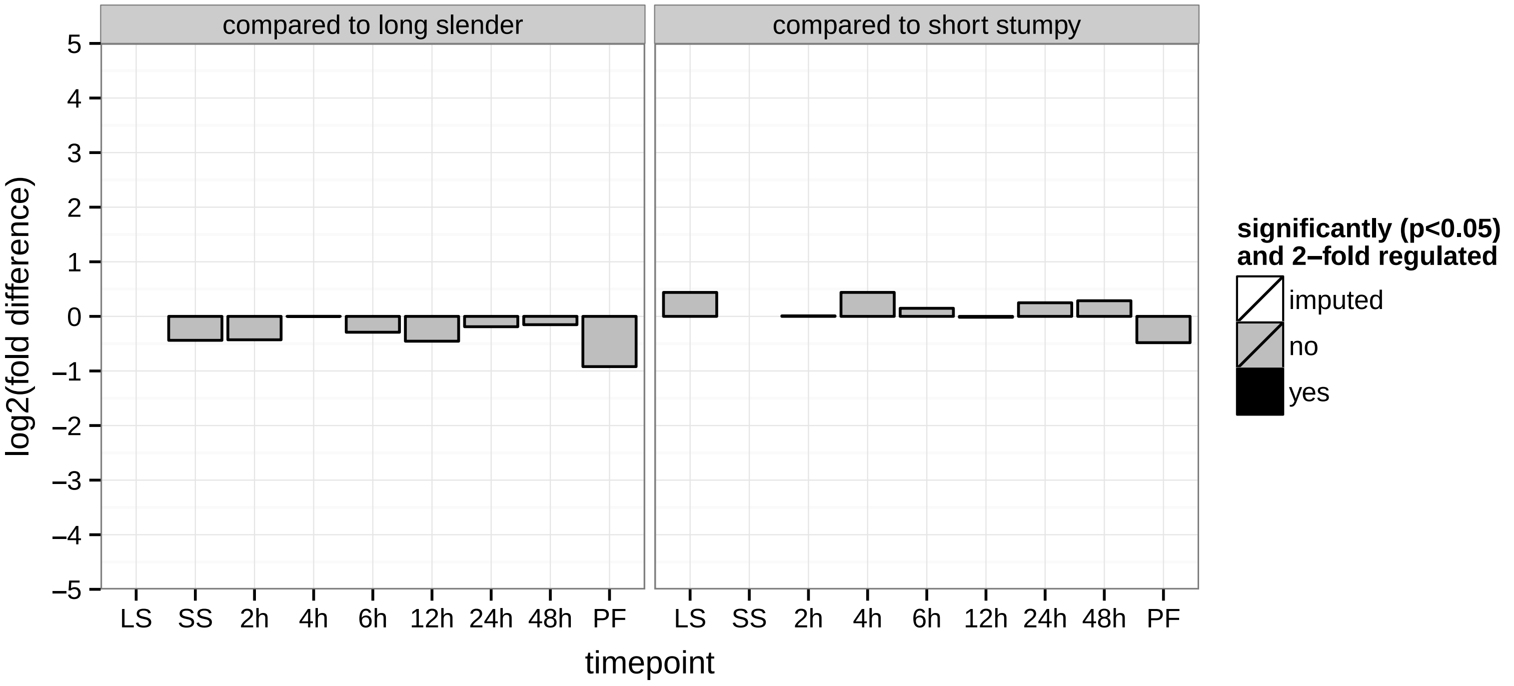
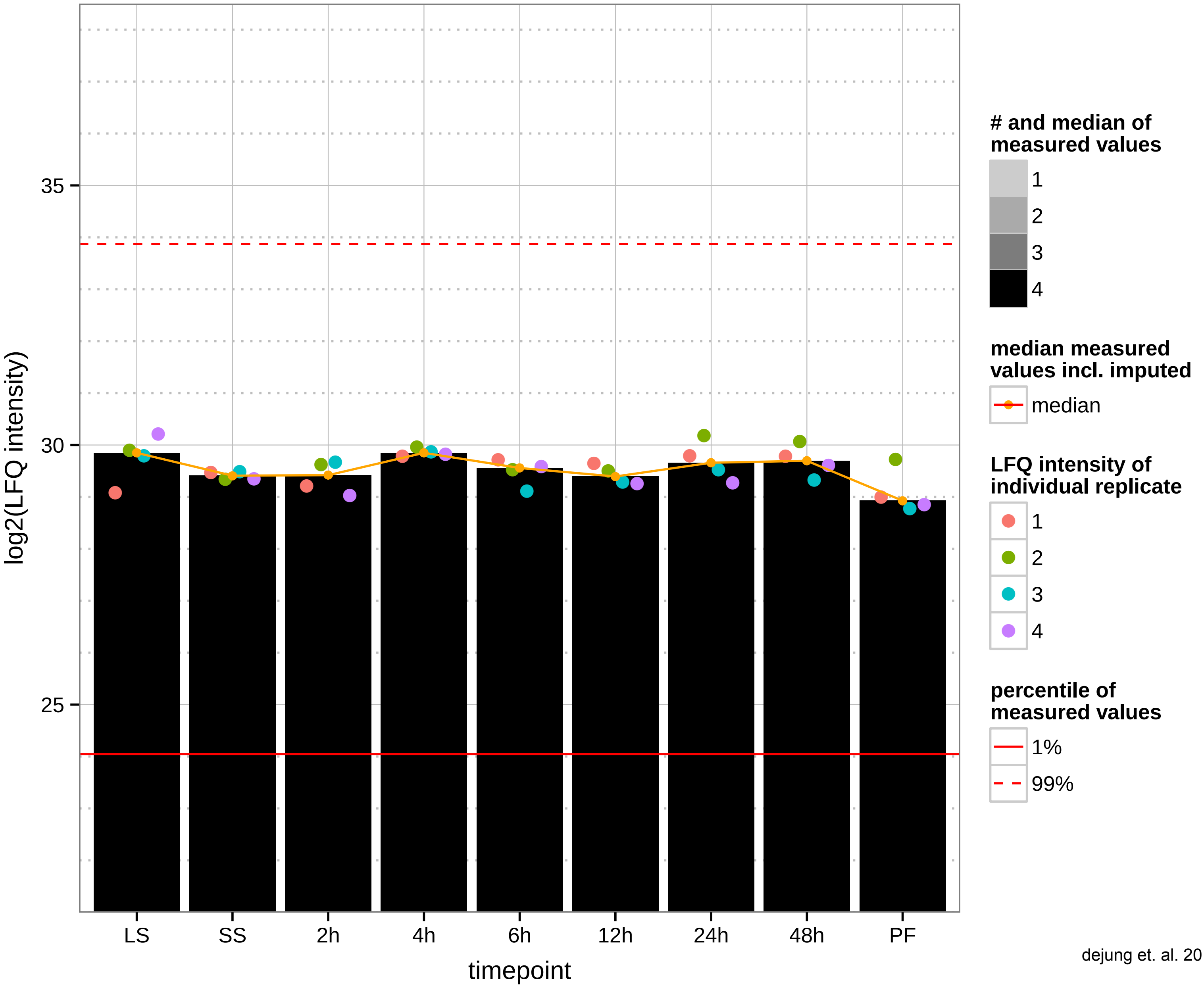
hypothetical protein, conserved
Tb927.11.5230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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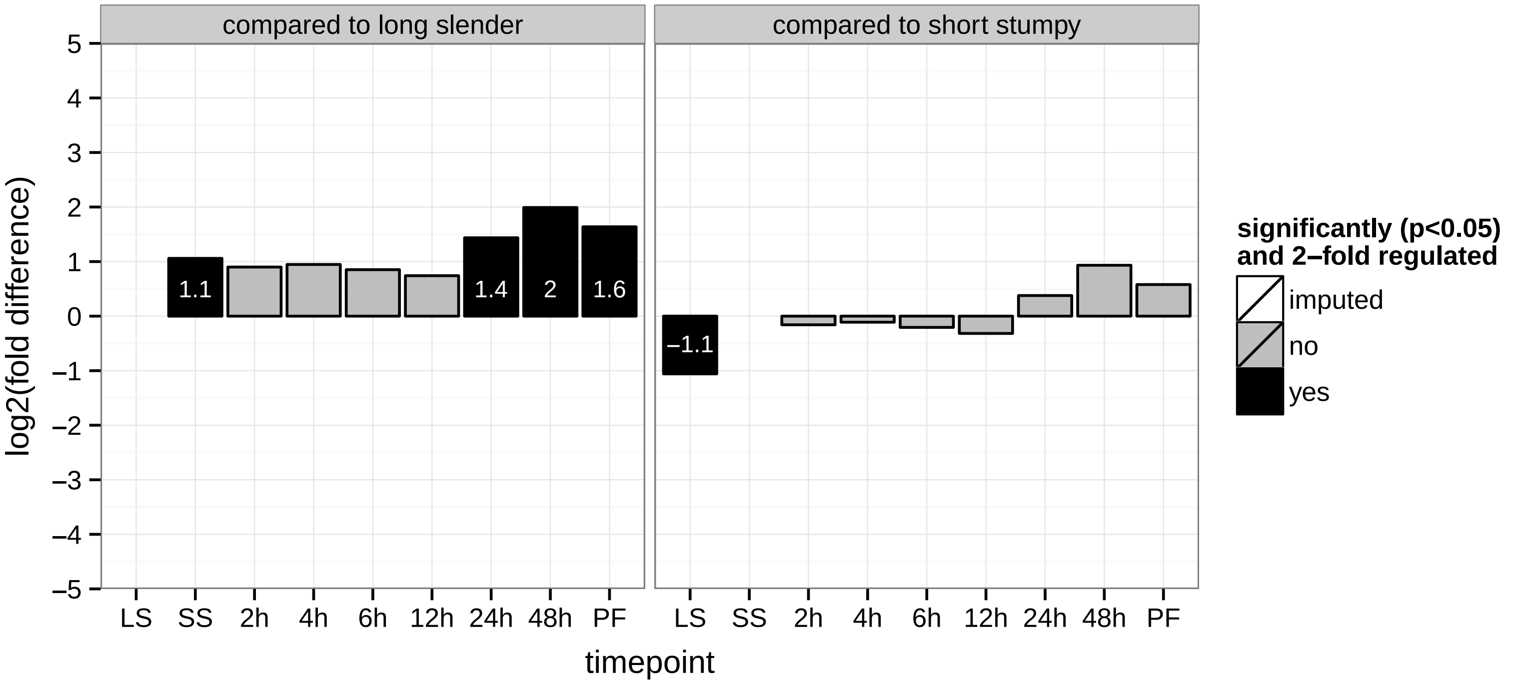
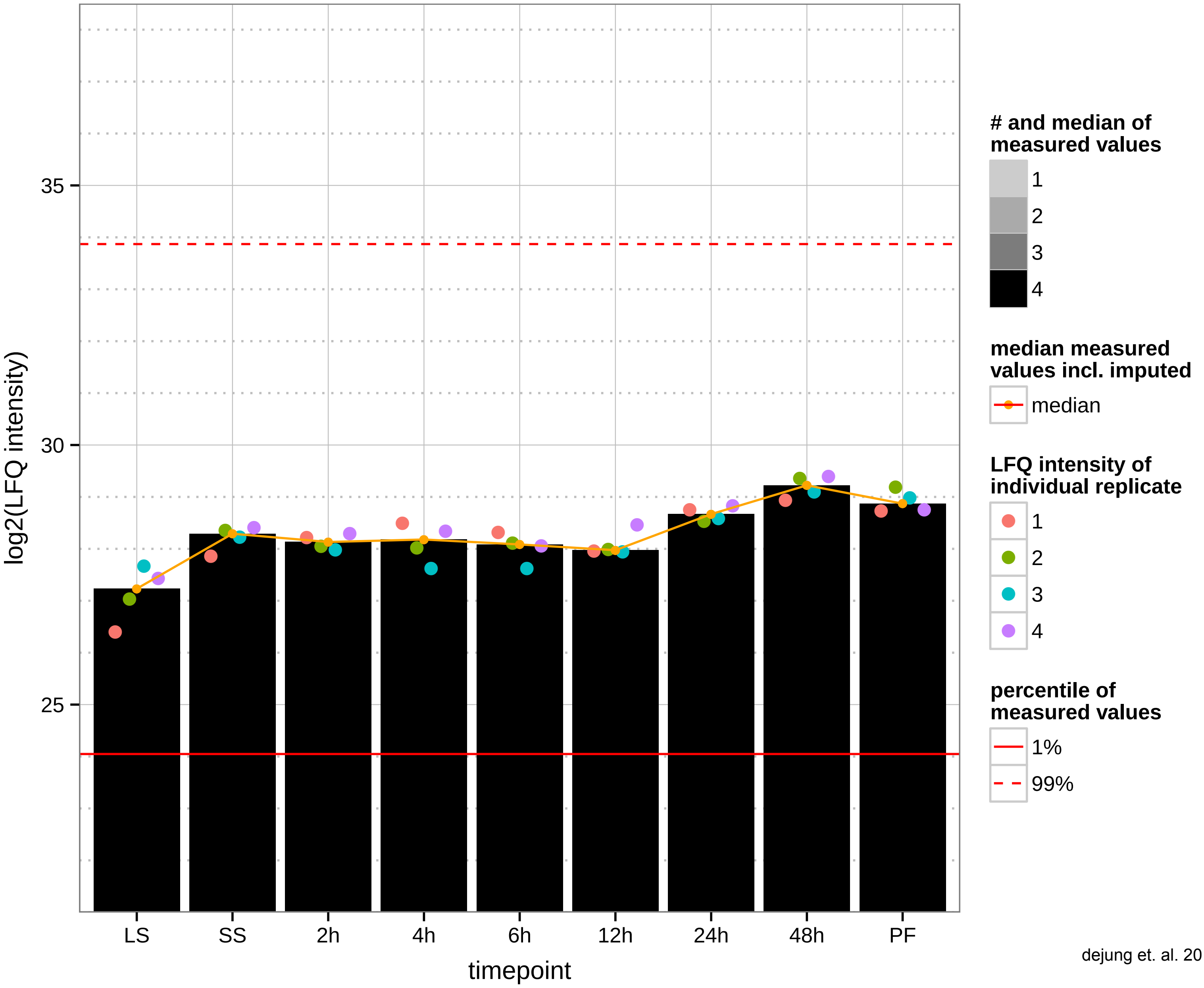
mitochondrial carrier protein (MCP9)
Tb927.11.5290
AGOF: null
AGOC: integral to membrane, membrane, mitochondrial inner membrane, mitochondrion
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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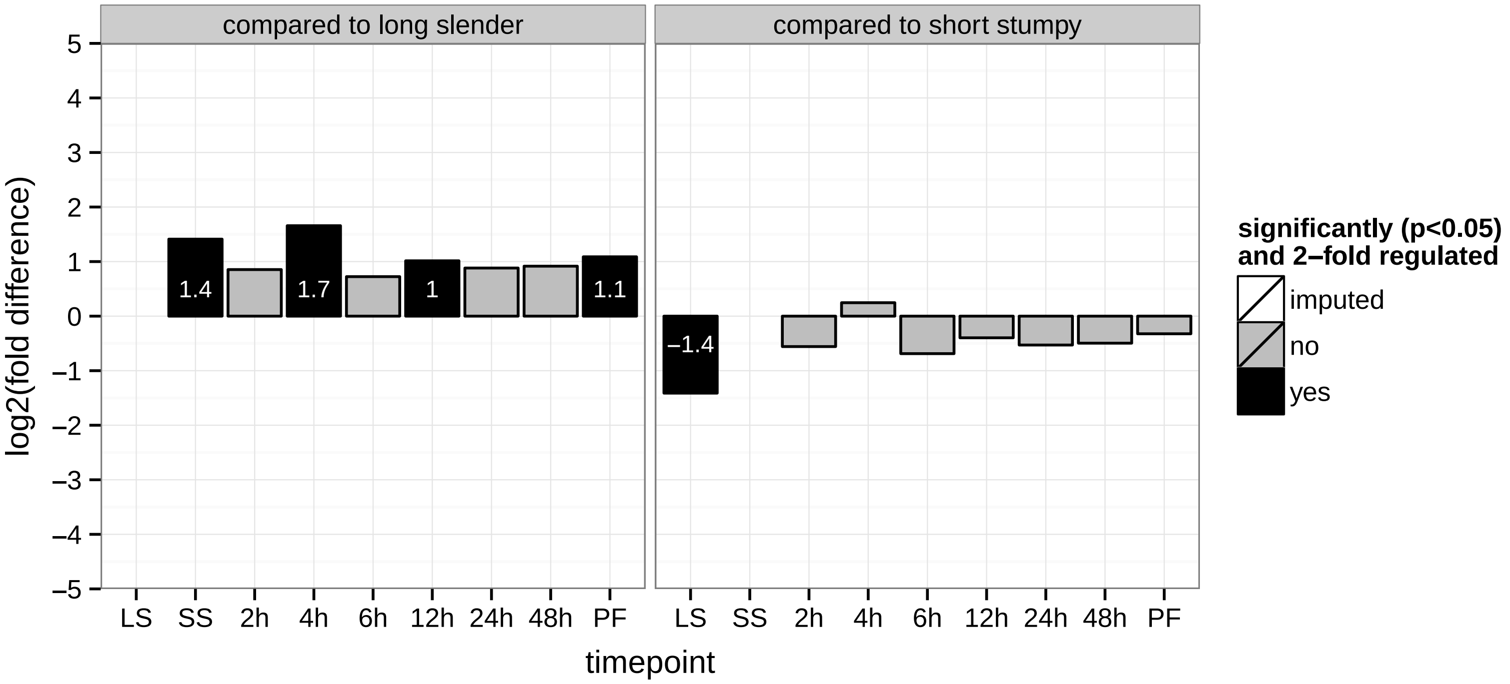
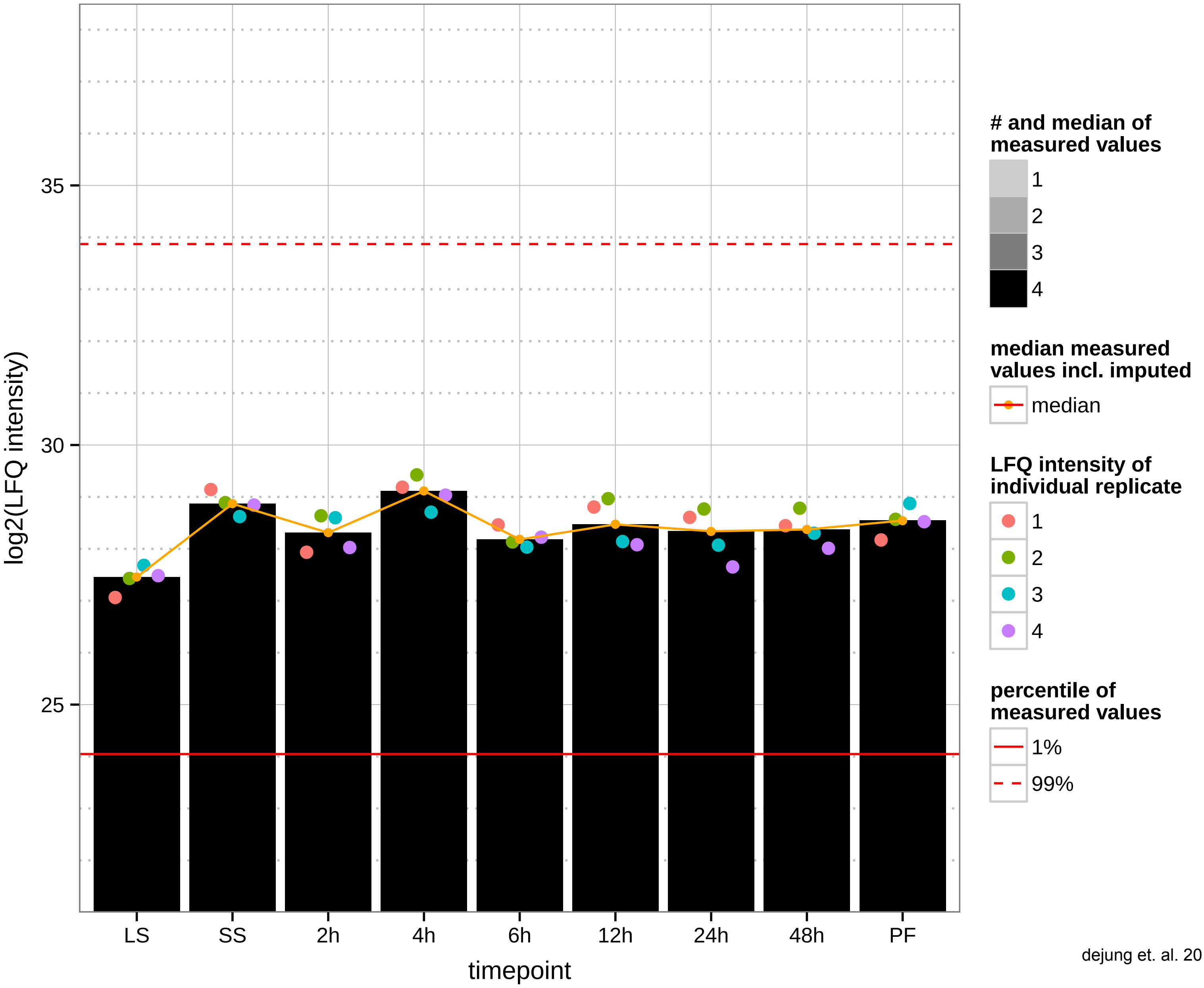
RNA–binding protein, putative (RBP3)
Tb927.11.530
AGOF: RNA binding
AGOC: cytoplasm
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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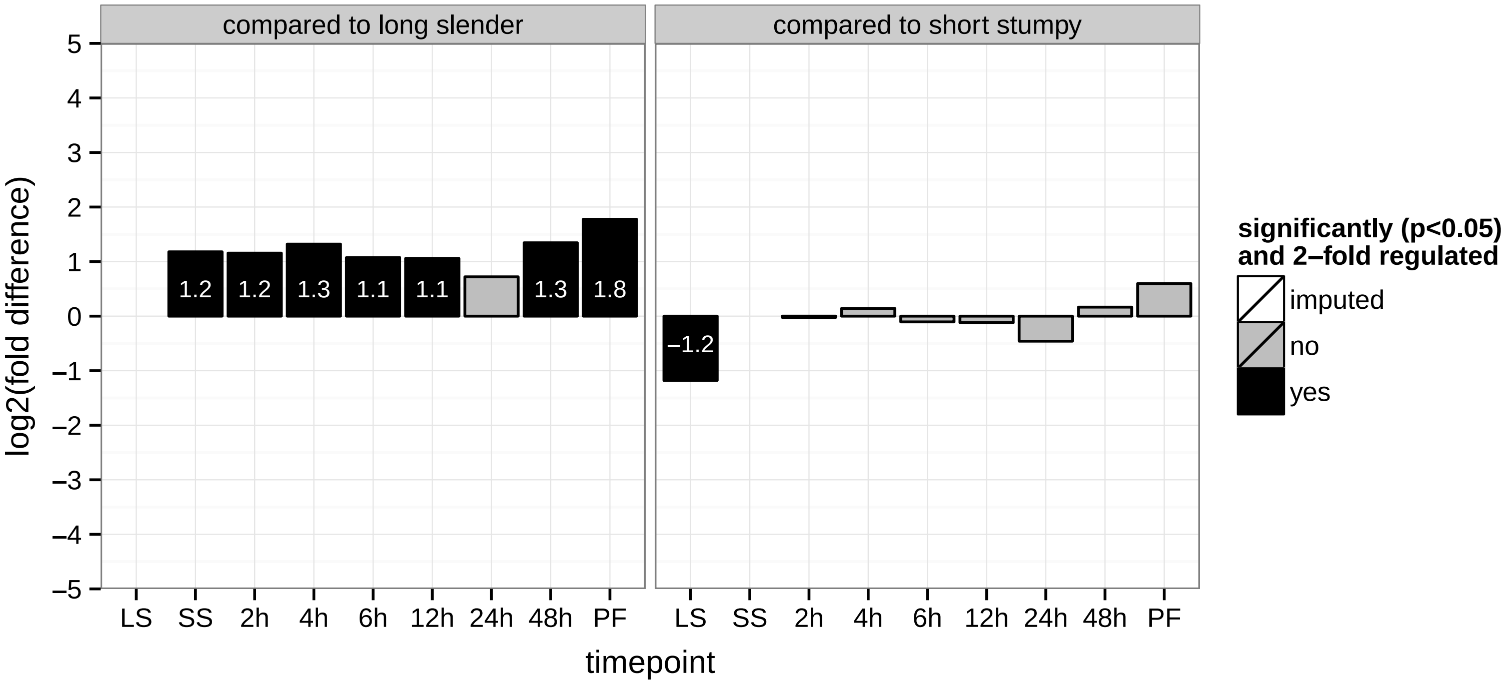
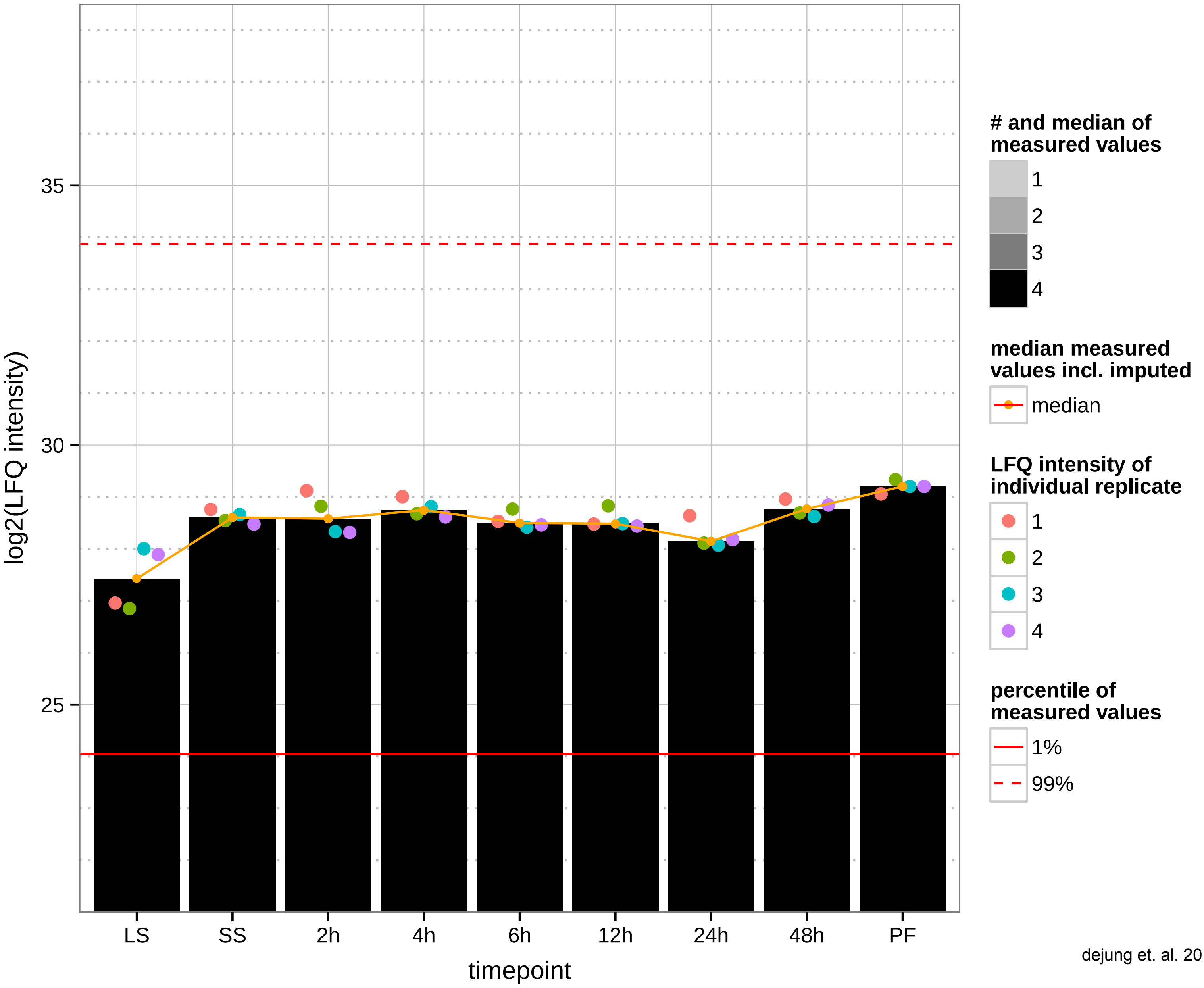
kinesin, putative, mitotic centromere–associated kinesin, putative (Kif13–3)
Tb927.11.5300
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: cell part, kinesin complex, microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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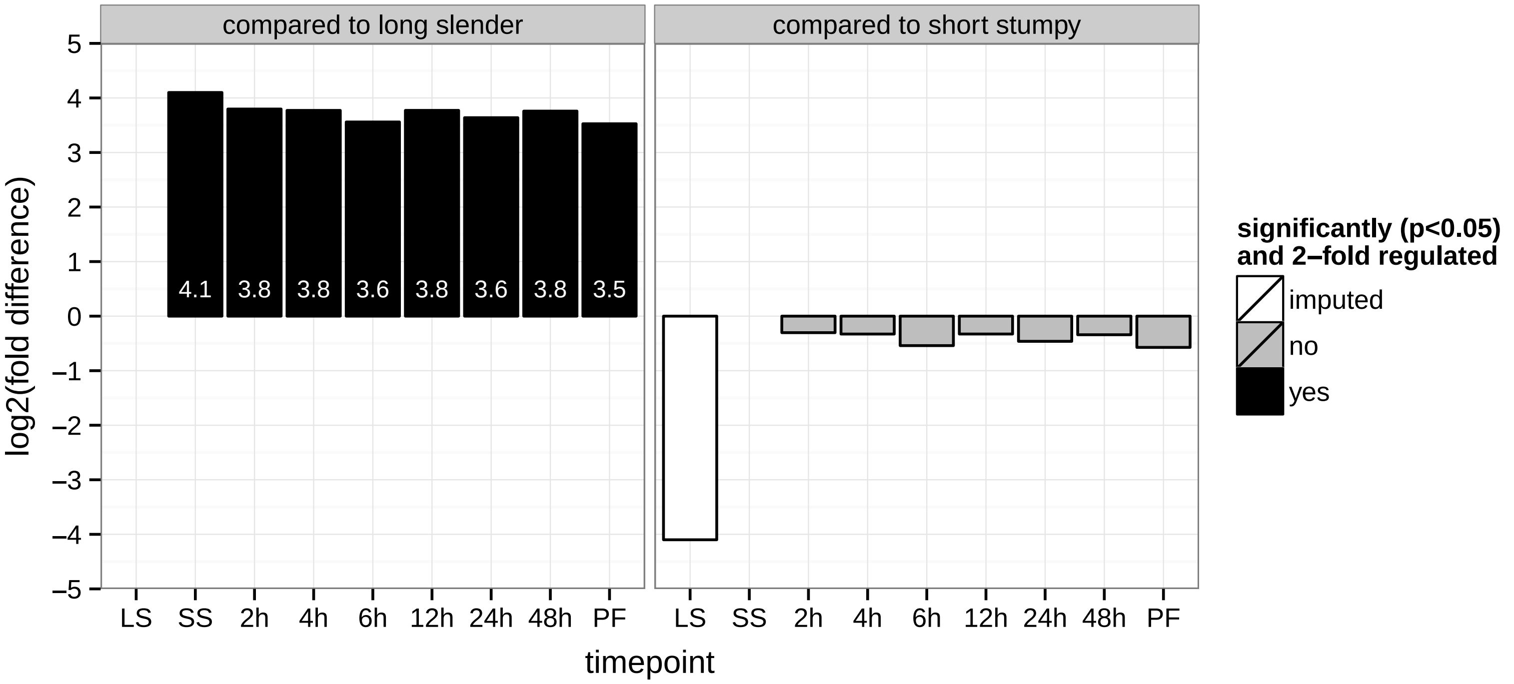
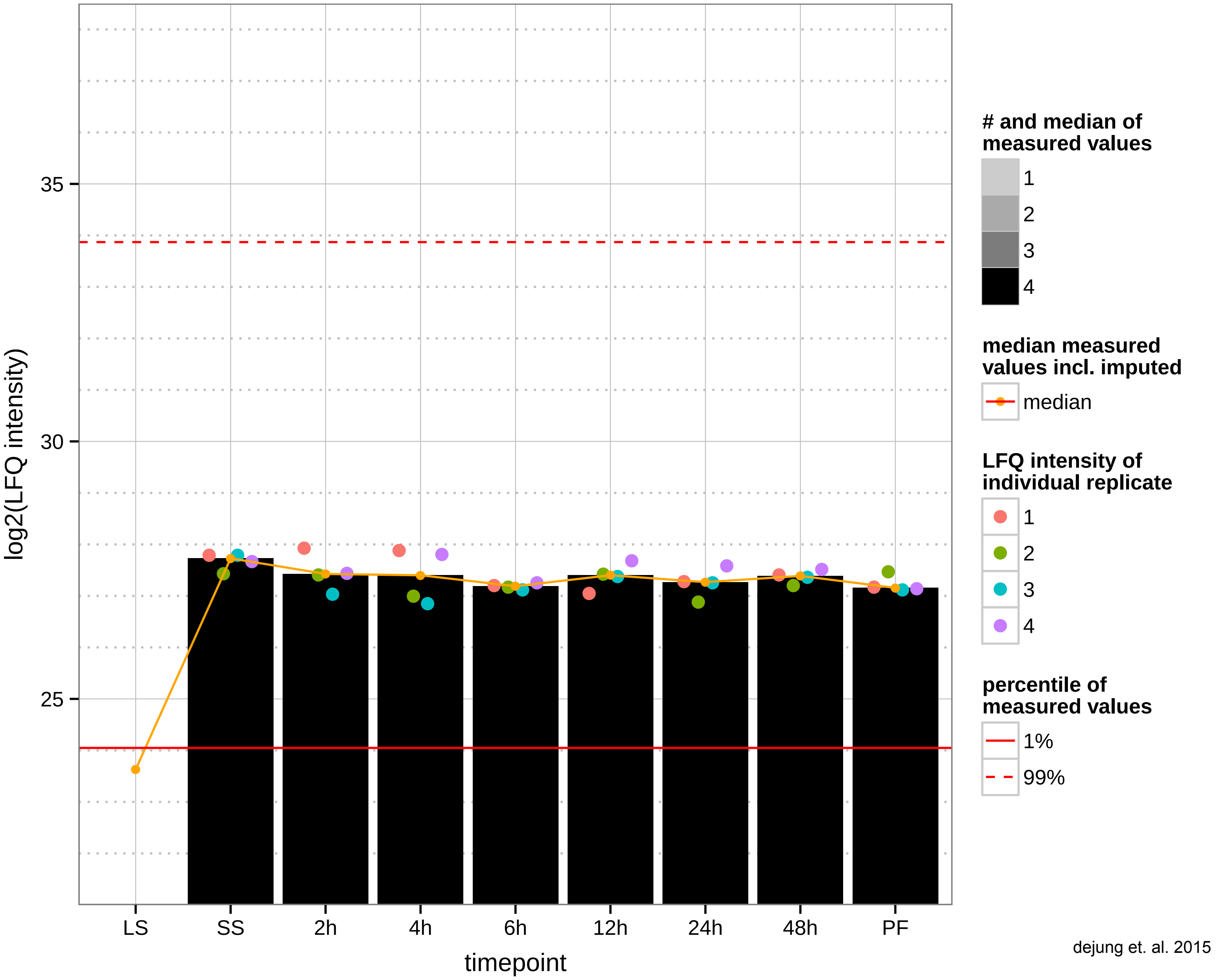
ABC transporter, putative (ABCB10)
Tb927.11.540
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances
AGOC: ATP−binding cassette (ABC) transporter complex, integral to membrane, mitochondrial inner membrane
AGOP: transport
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances, nucleoside−triphosphatase activity
PGOC: integral to membrane
PGOP: transmembrane transport, transport





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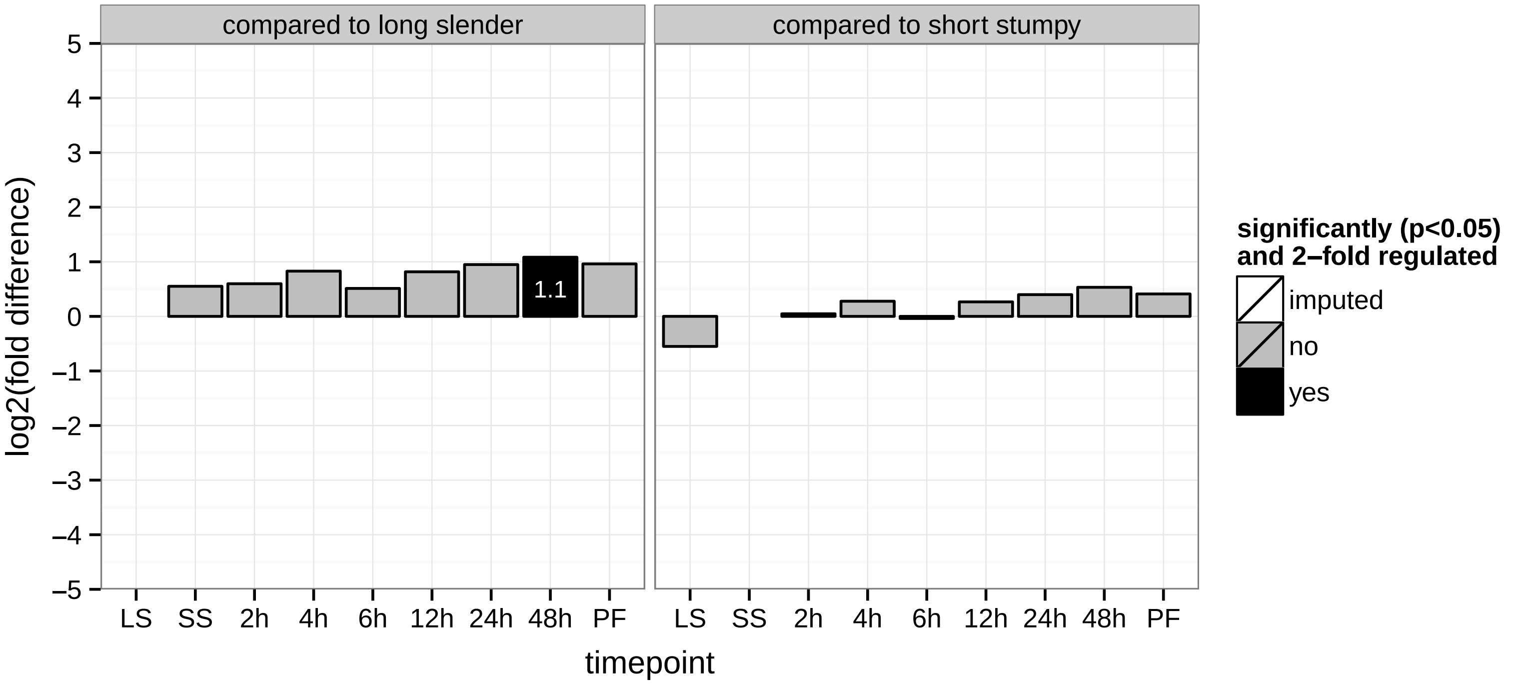
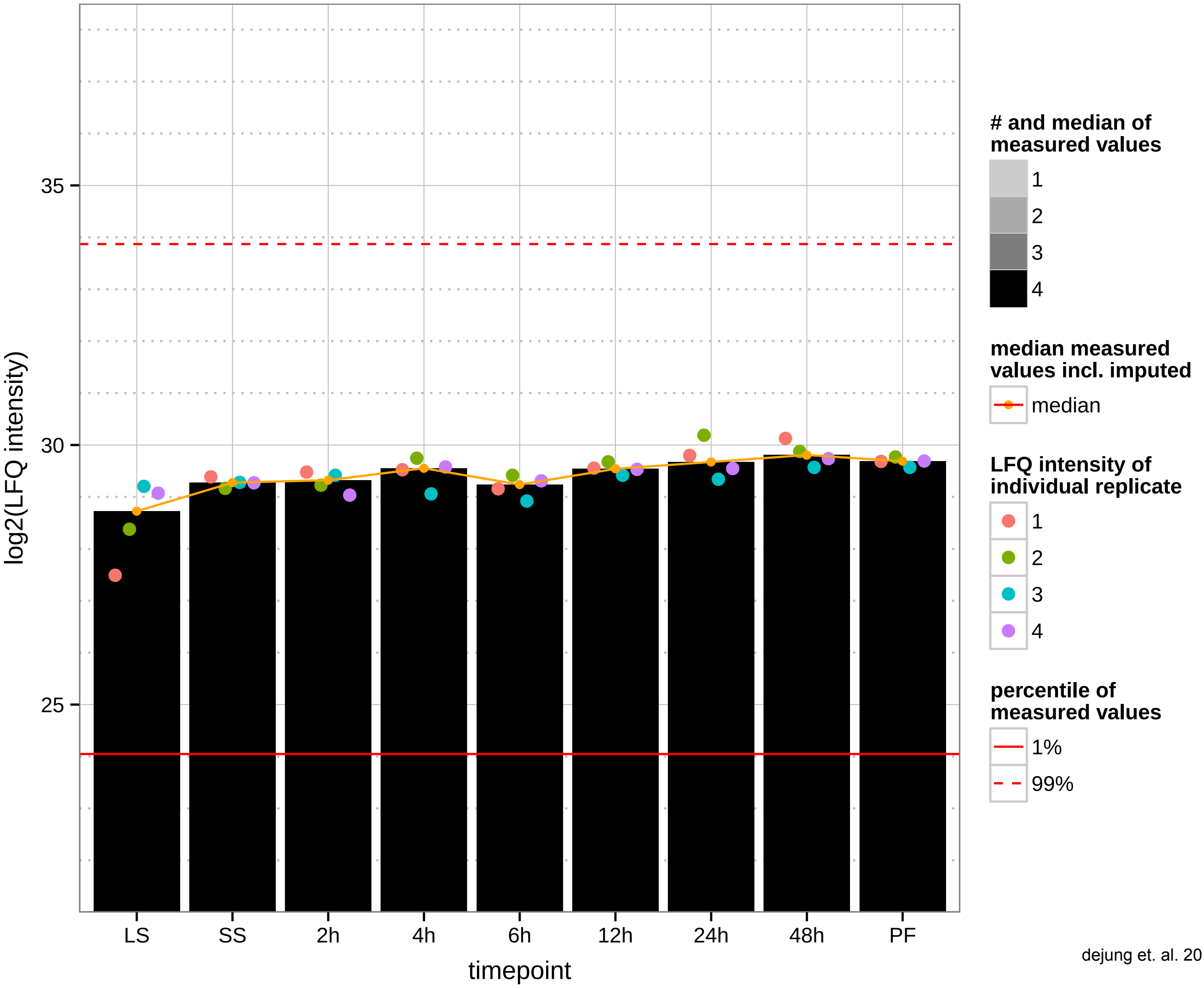
signal recognition particle 54 kDa (SRP54)
Tb927.11.5400
AGOF: 7S RNA binding, GTP binding, GTPase activity, RNA binding
AGOC: signal recognition particle, endoplasmic reticulum targeting
AGOP: SRP–dependent cotranslational protein targeting to membrane, protein targeting
PGOF: 7S RNA binding, GTP binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: signal recognition particle
PGOP: SRP–dependent cotranslational protein targeting to membrane





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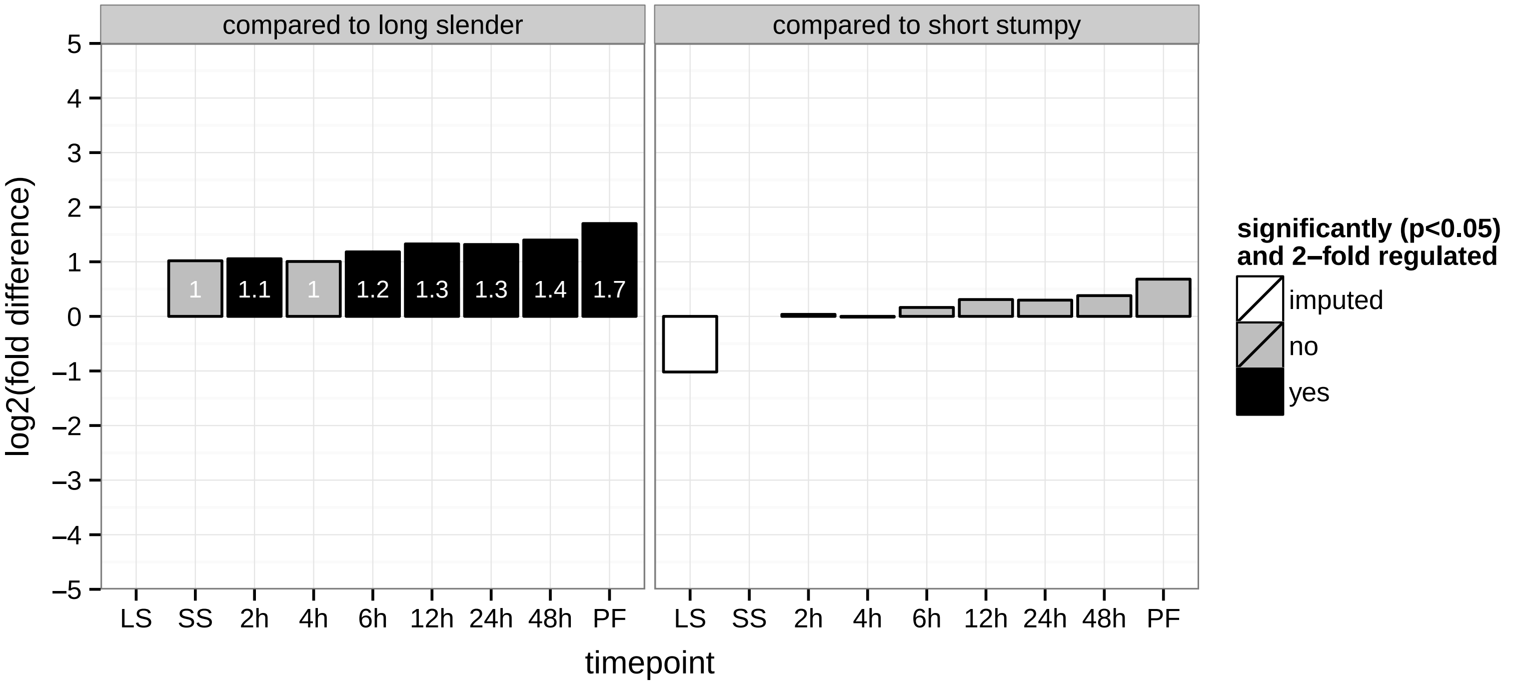
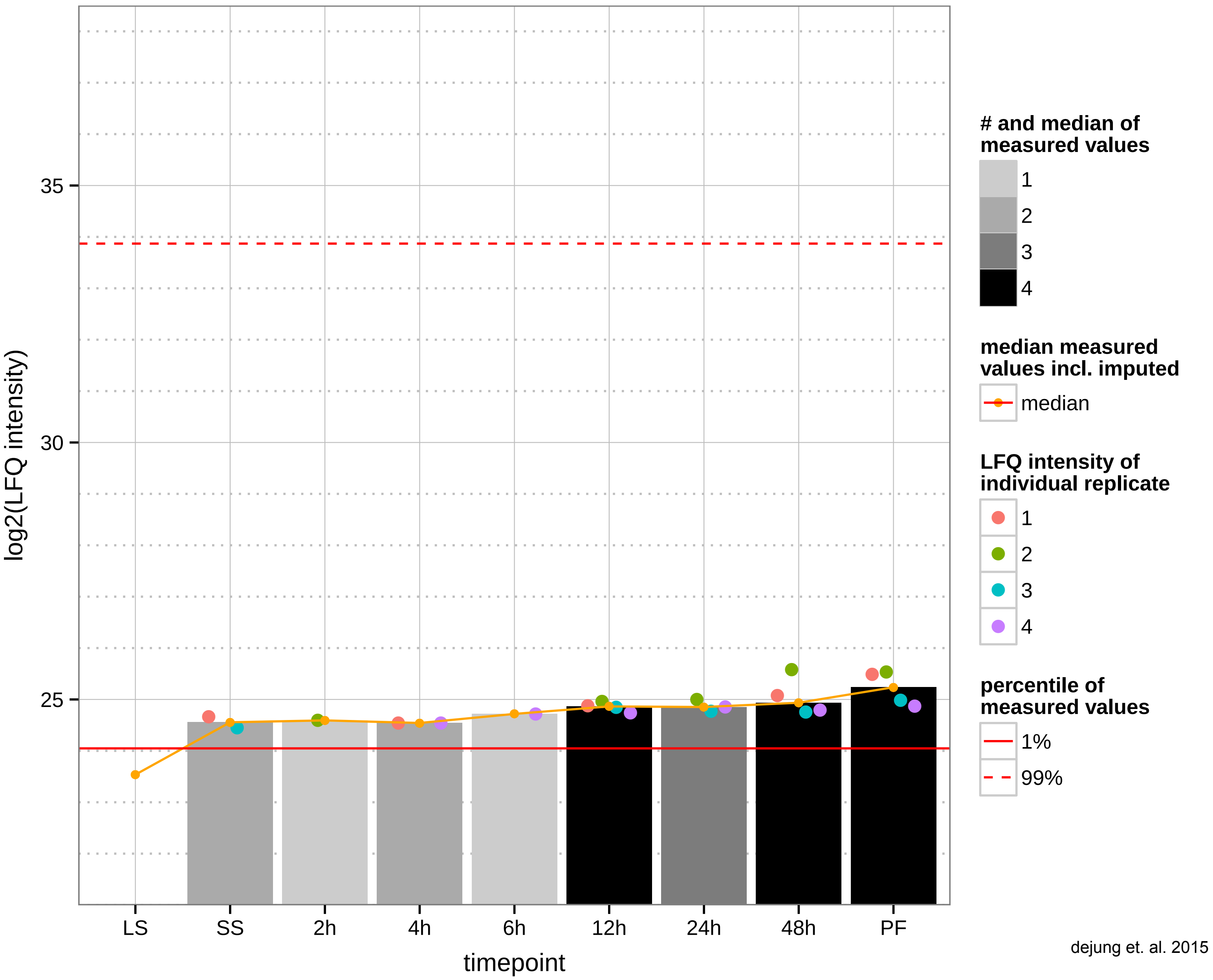
hypothetical protein, conserved
Tb927.11.5420
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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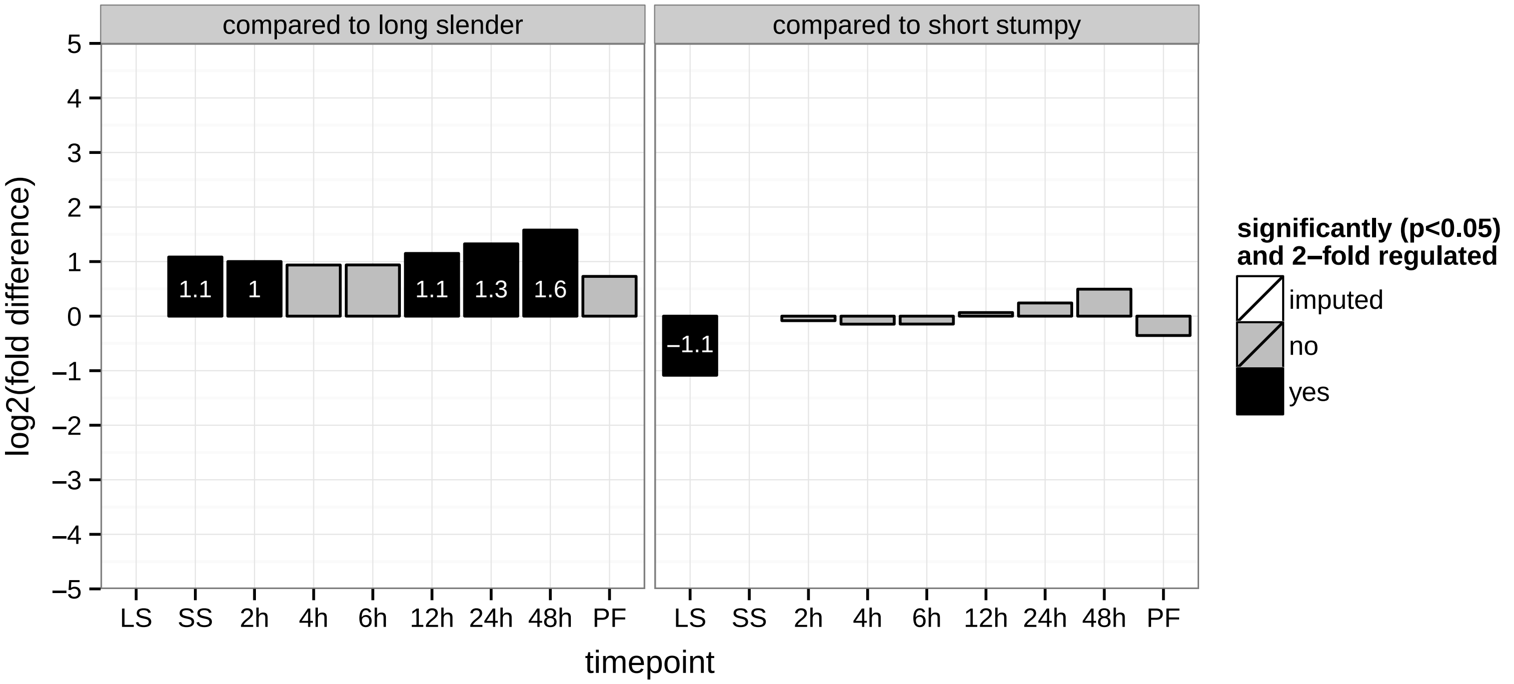
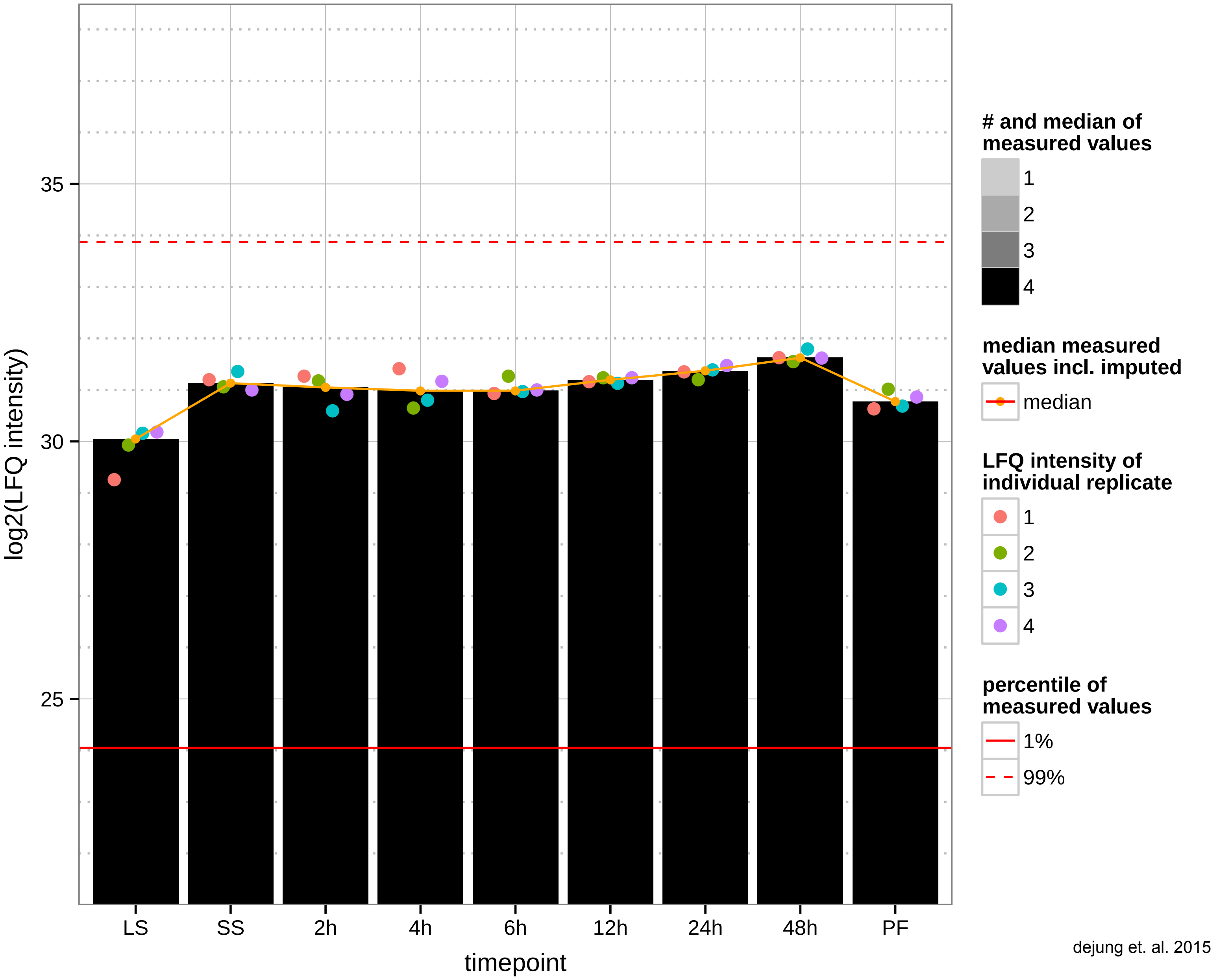
malic enzyme
Tb927.11.5450
AGOF: NAD binding, NADP+ binding, malic enzyme activity, oxidoreductase activity, acting on the CH–OH group of donors, N
AGOC: mitochondrion
AGOP: malate metabolic process
PGOF: NAD binding, malate dehydrogenase (oxaloacetate–decarboxylating) activity, malic enzyme activity, oxidoreductase ac
PGOC: null
PGOP: malate metabolic process, oxidation–reduction process





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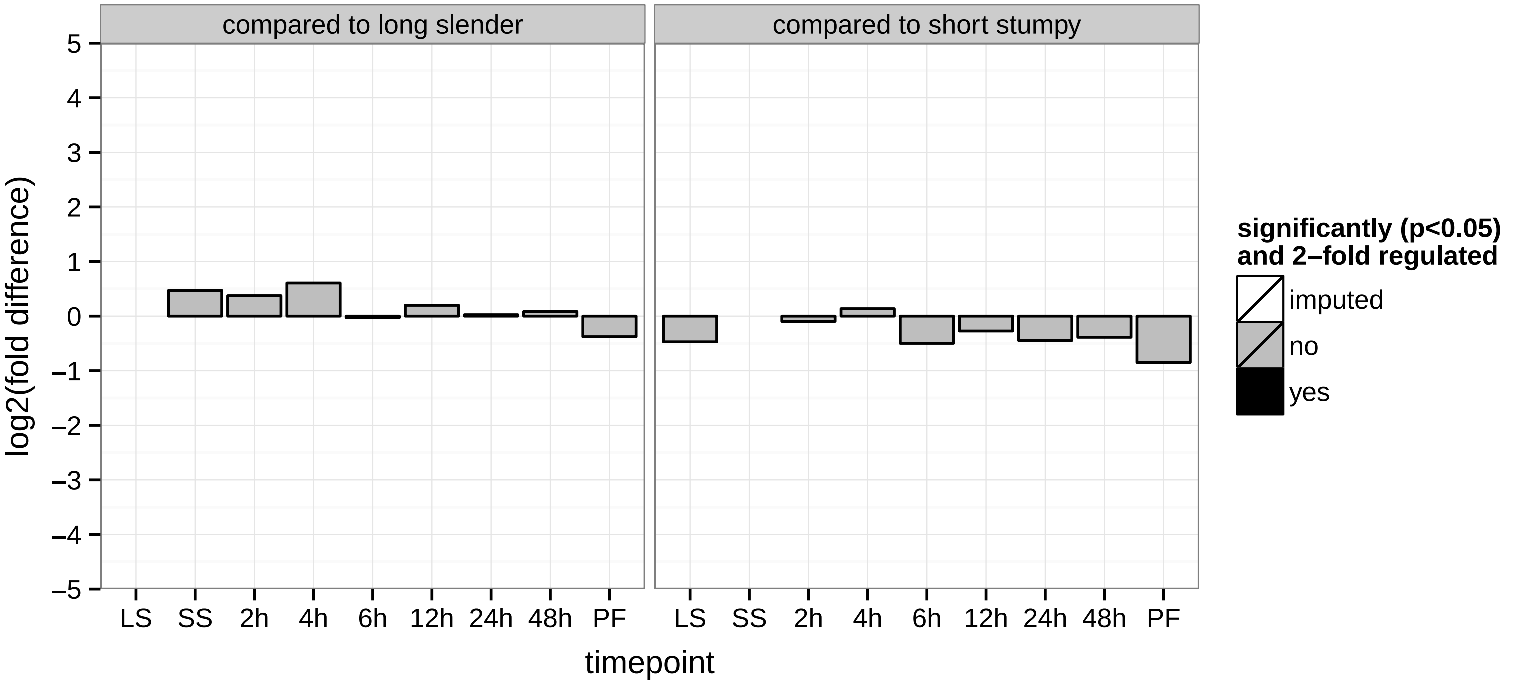
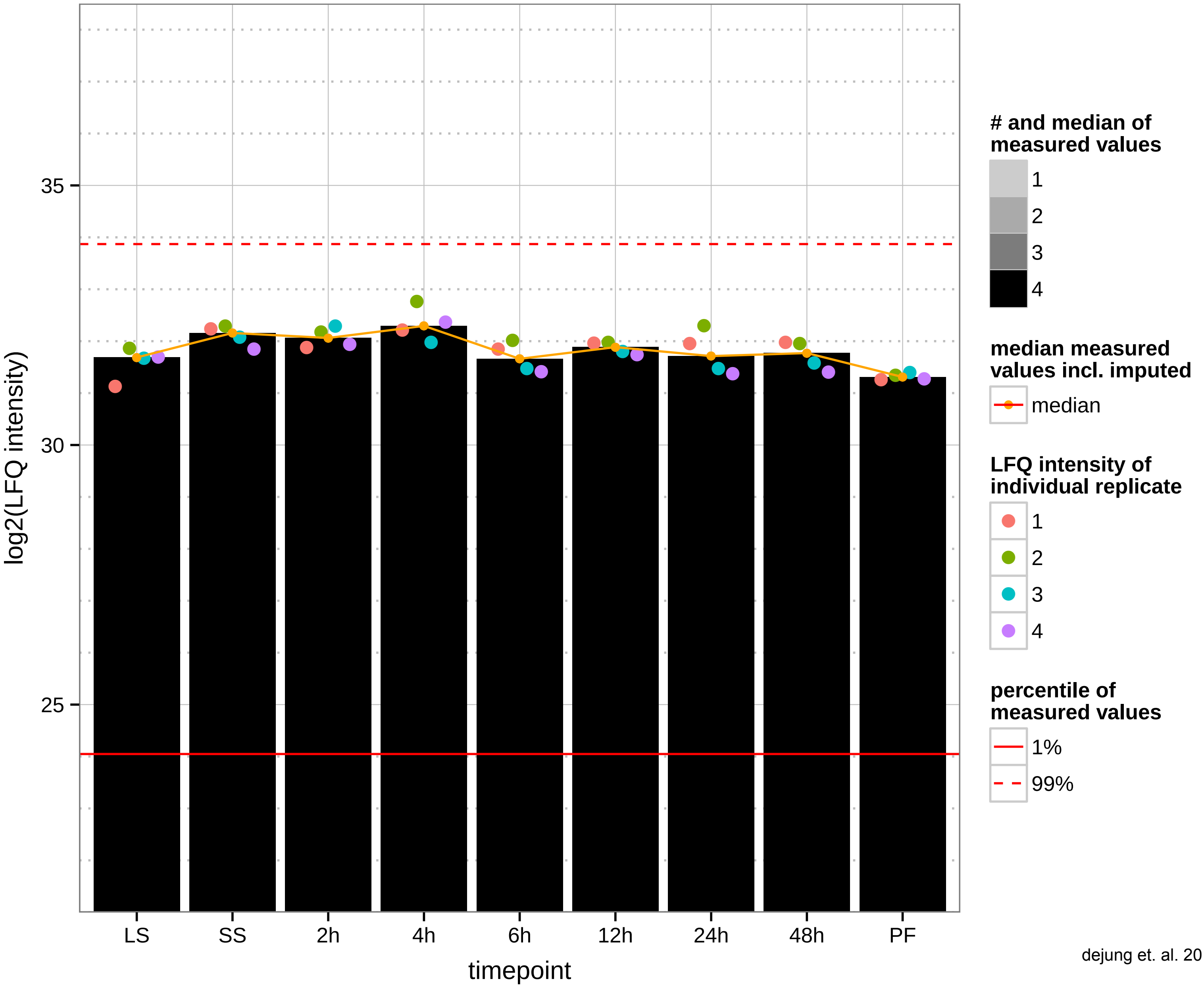
hypothetical protein SCD6.10
Tb927.11.550
AGOF: null
AGOC: cytoplasm
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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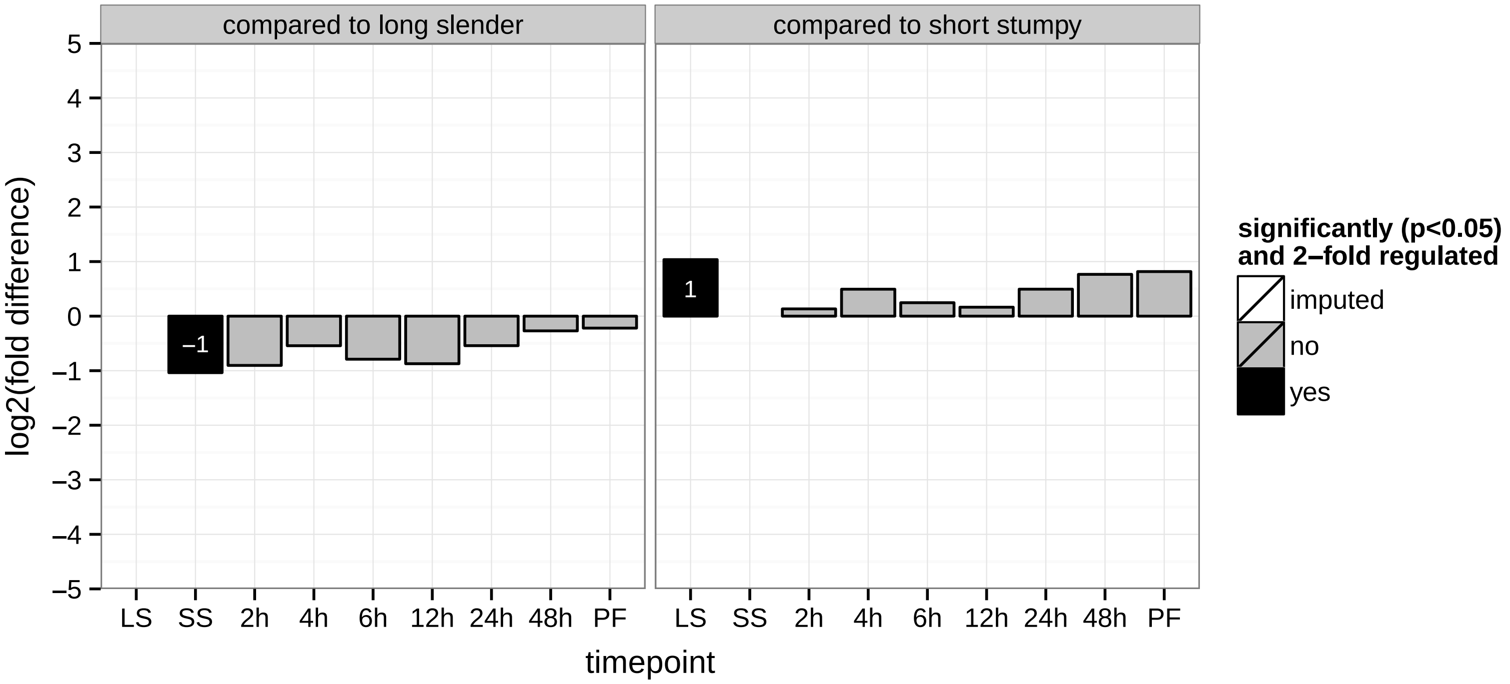
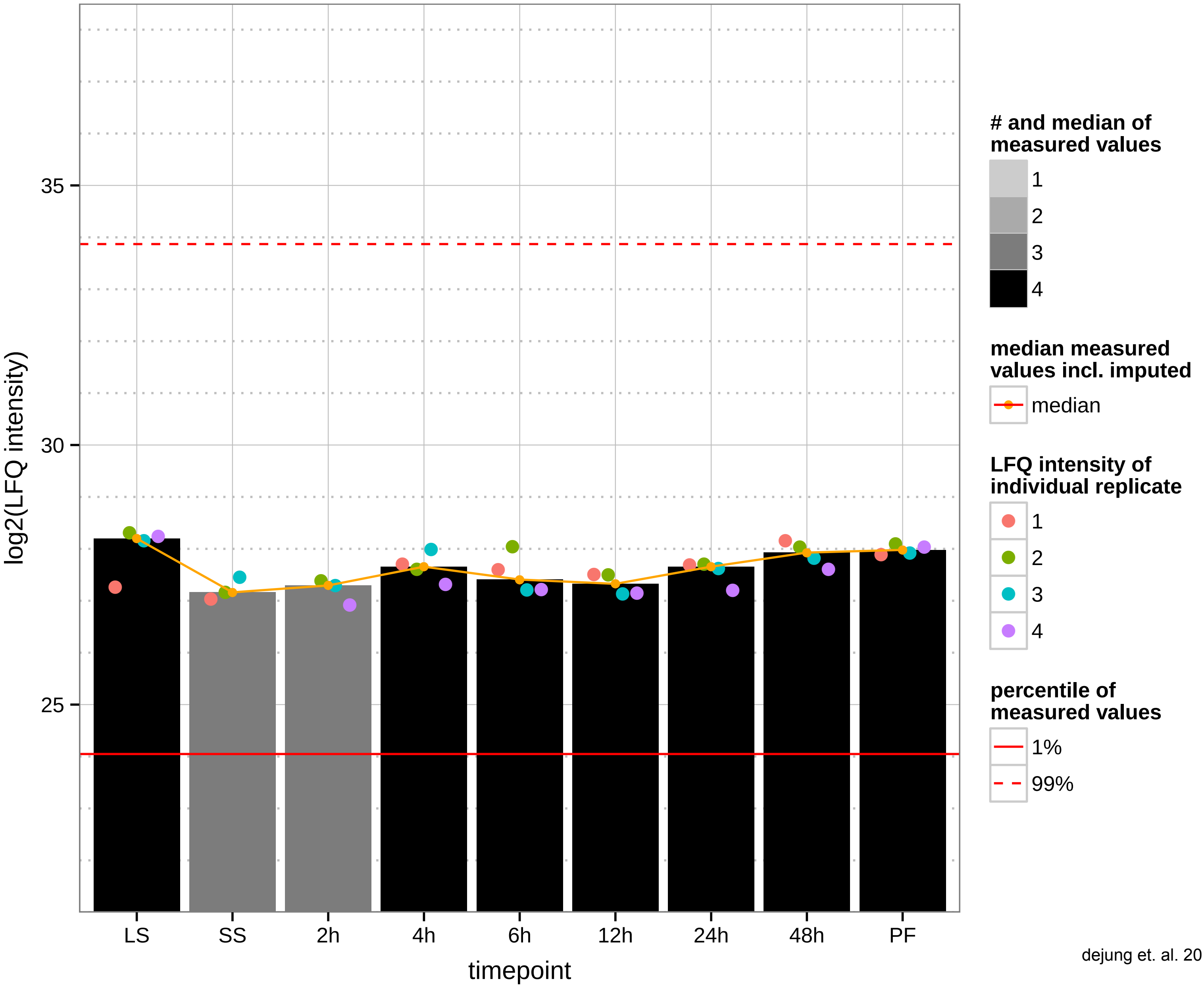
dynein light chain p28, axonemal, putative
Tb927.11.5510
AGOF: microtubule motor activity
AGOC: axonemal dynein complex
AGOP: cellular component movement
PGOF: null
PGOC: null
PGOP: null





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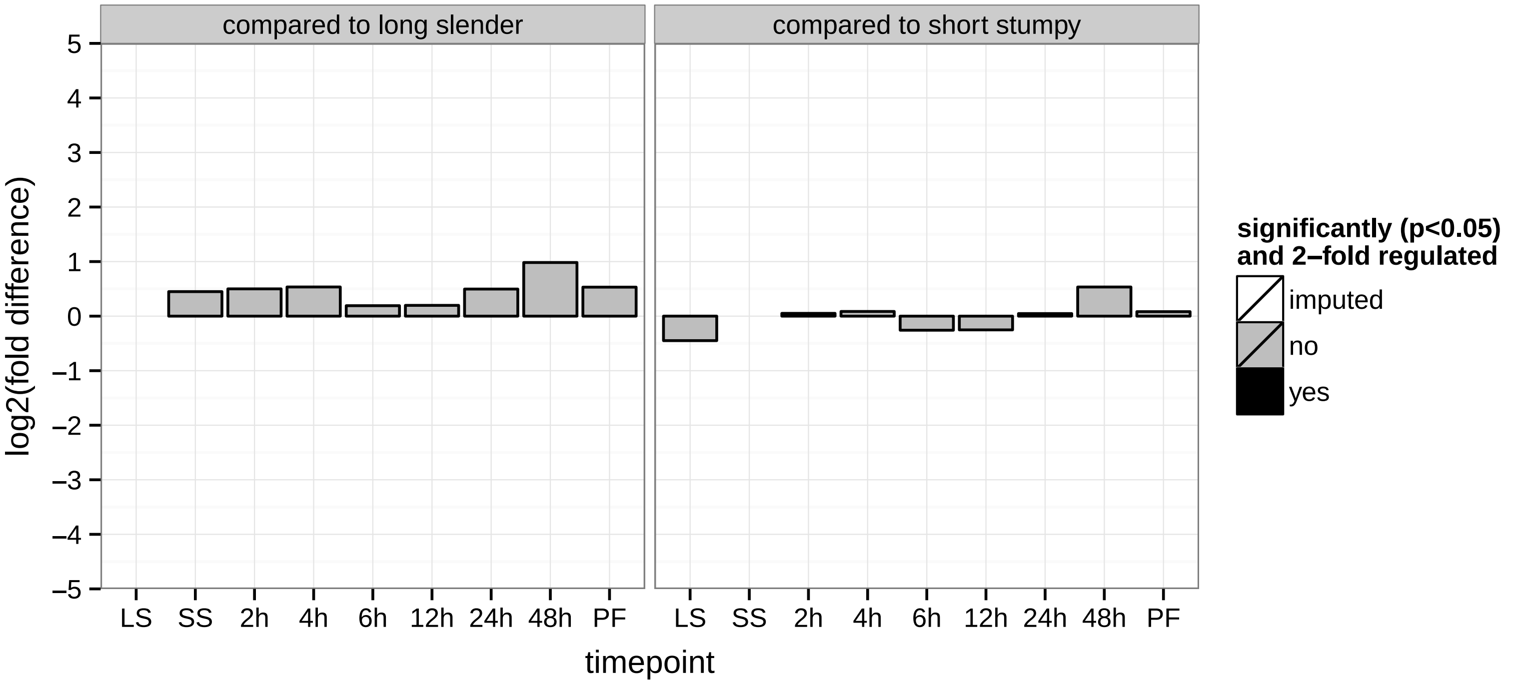
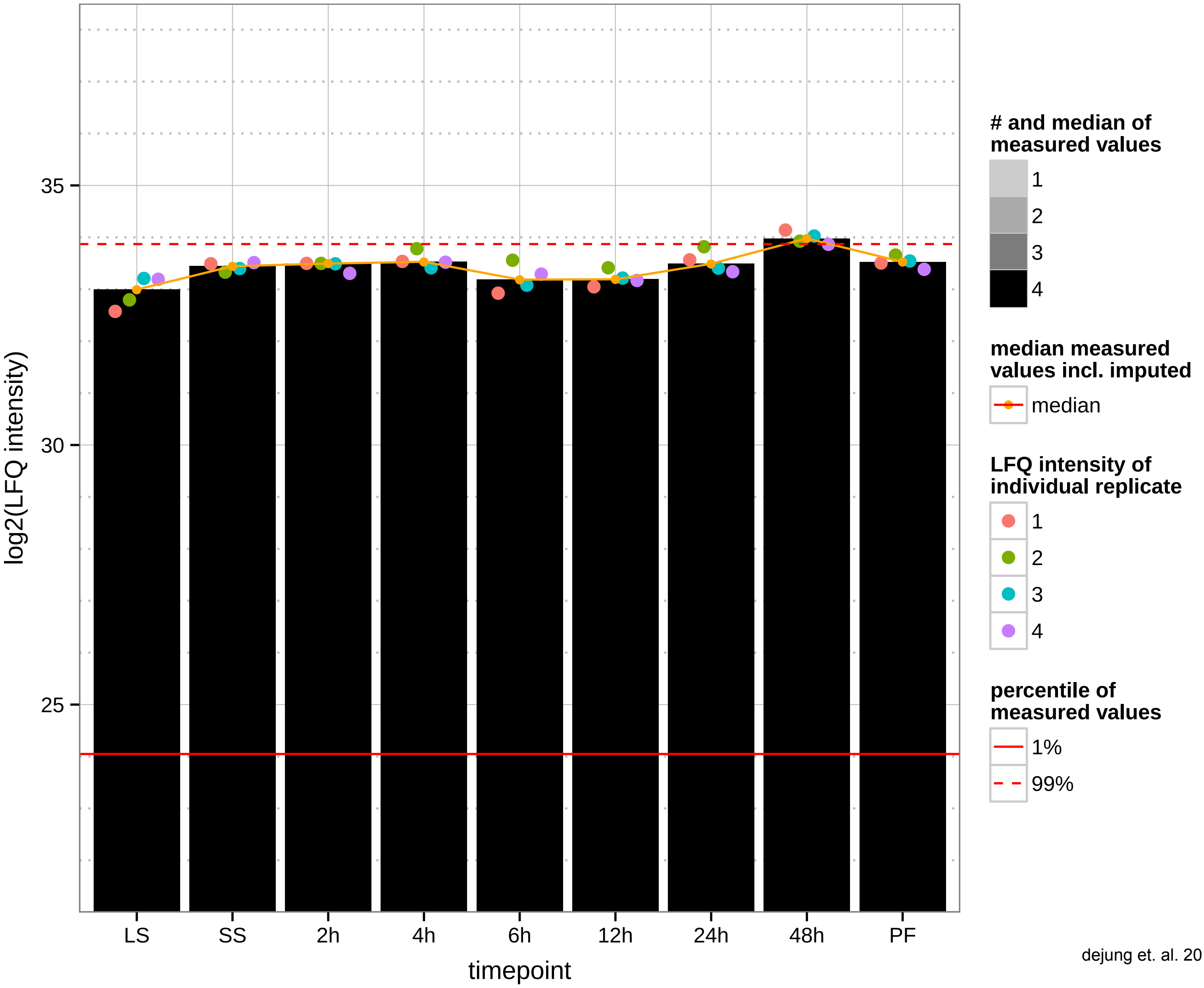
triosephosphate isomerase (TIM)
Tb927.11.5520
AGOF: triose−phosphate isomerase activity
AGOC: glycosome
AGOP: glycolysis
PGOF: triose−phosphate isomerase activity
PGOC: null
PGOP: metabolic process





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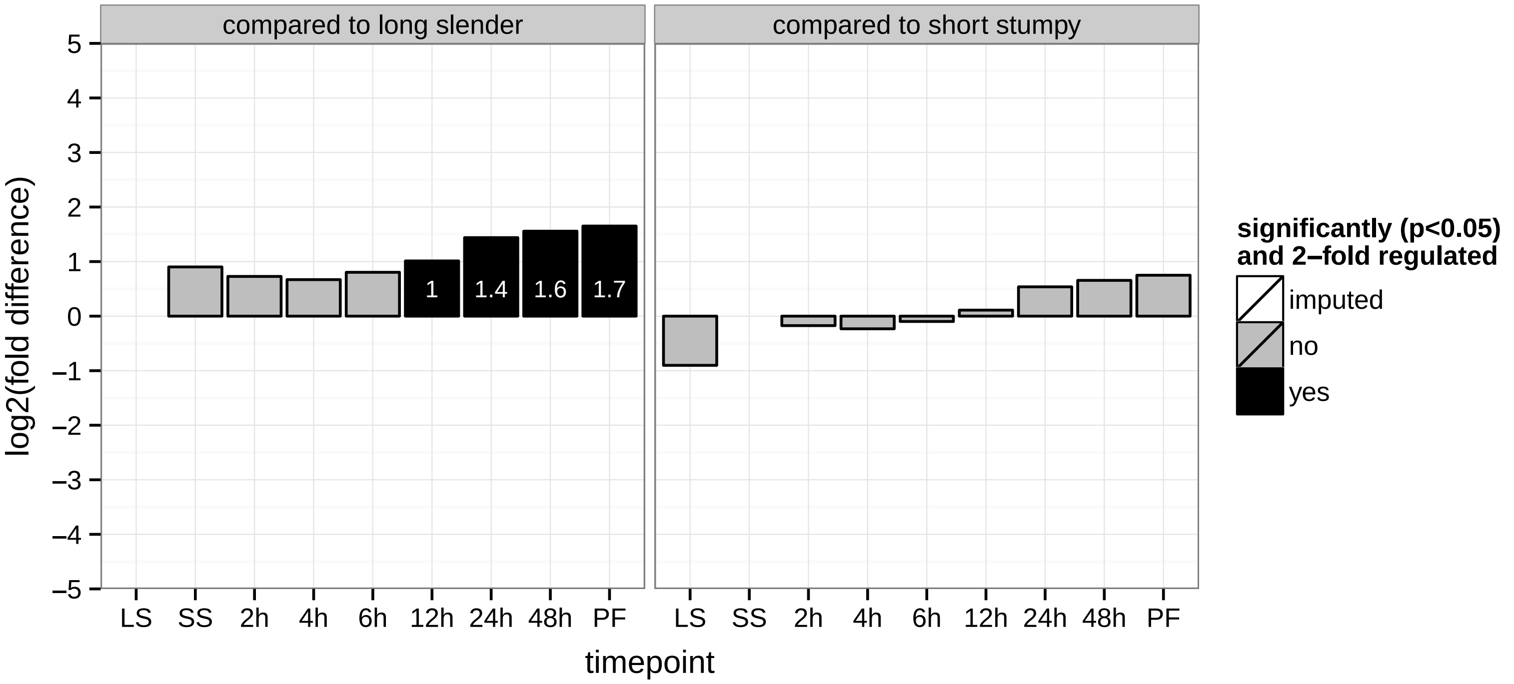
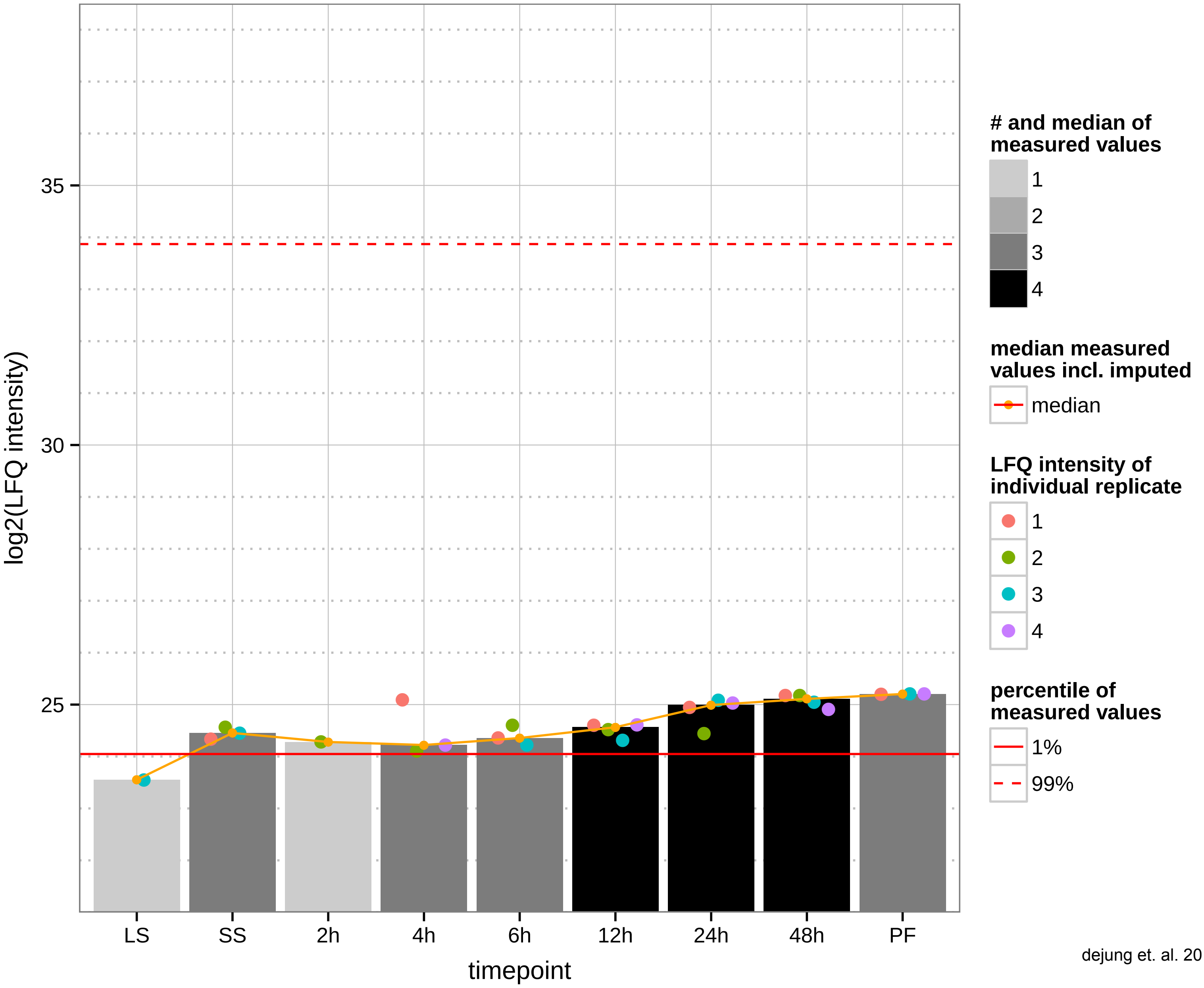
hypothetical protein, conserved
Tb927.11.5590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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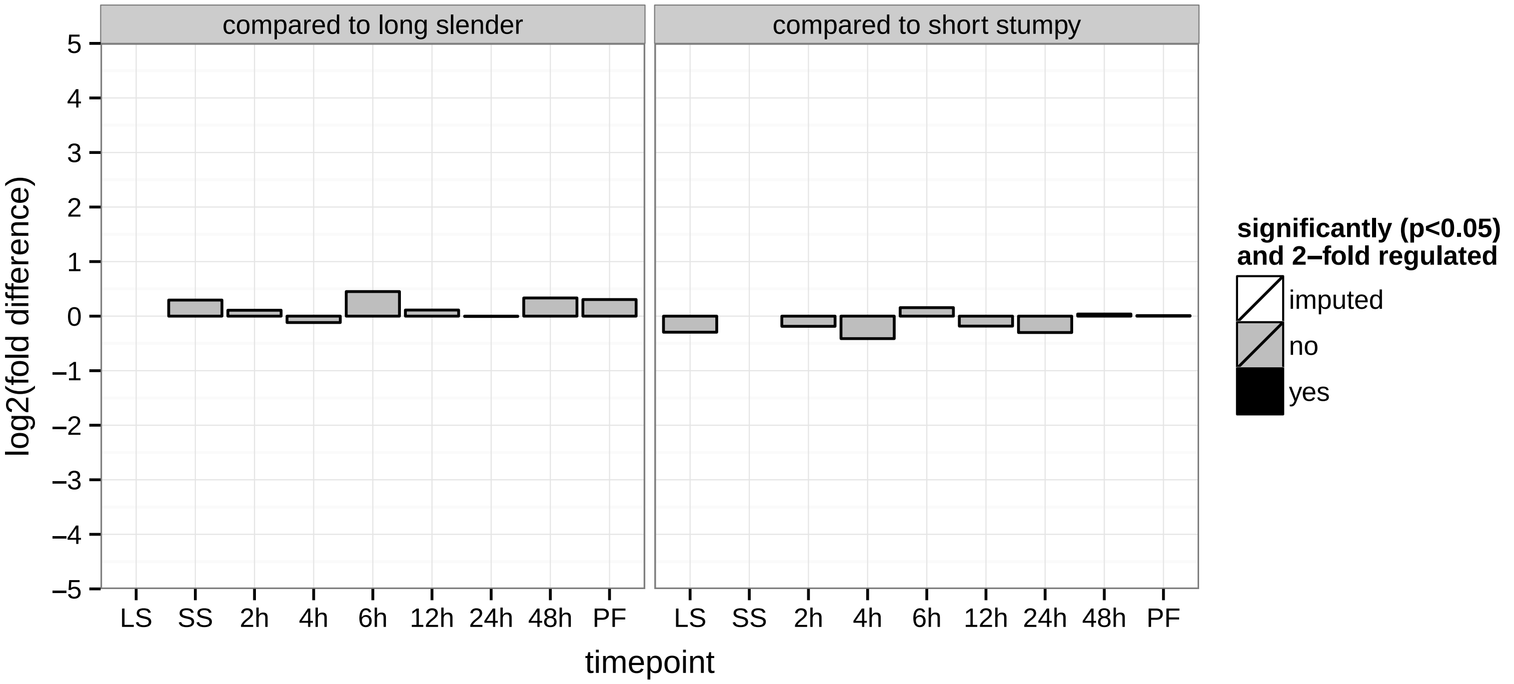
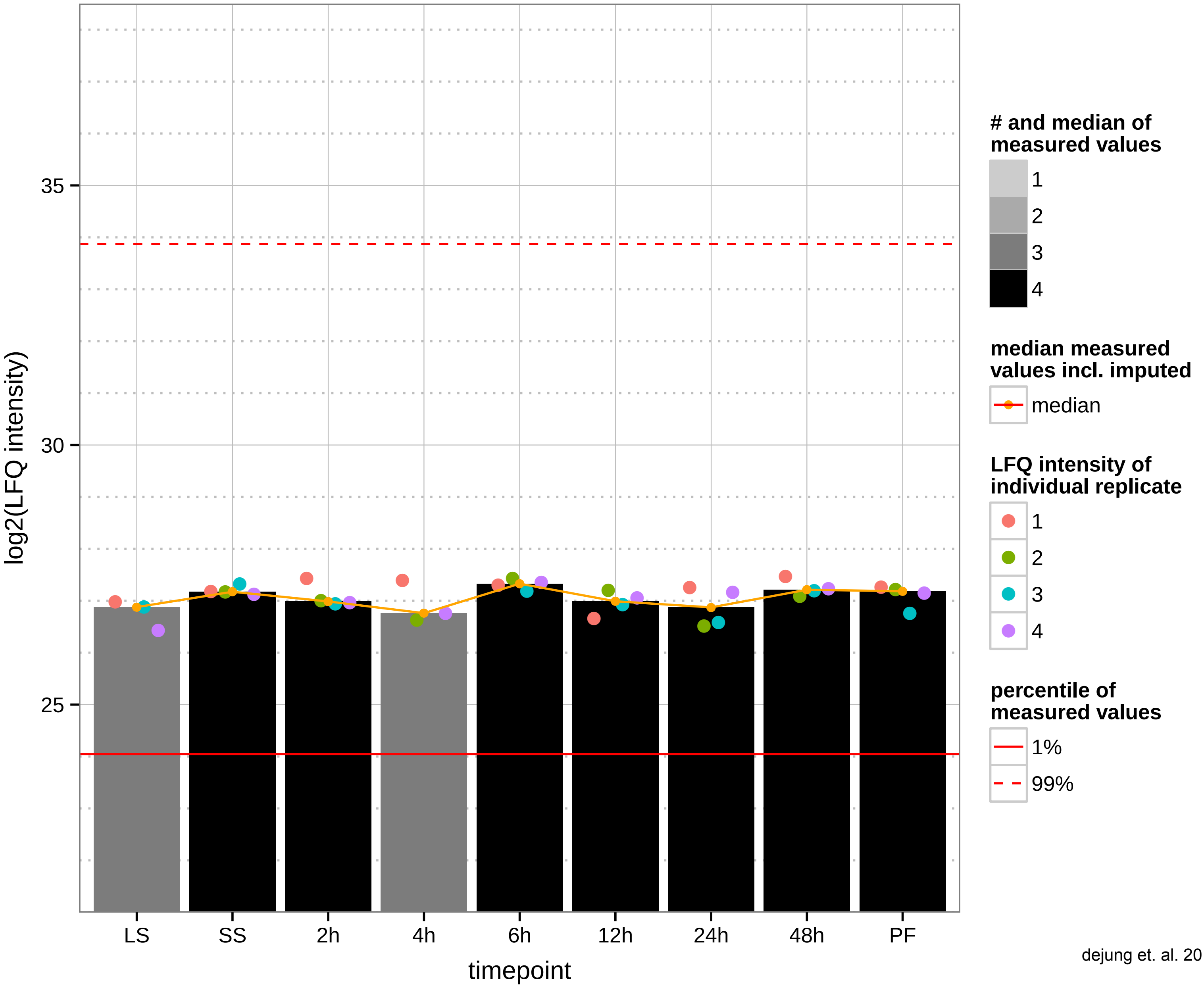
replication factor C, subunit 1, putative, replication factor C large subunit
Tb927.11.5650
AGOF: ATP binding, ATP−dependent peptidase activity, DNA binding, DNA clamp loader activity, serine−type endopeptidase a
AGOC: DNA replication factor C complex
AGOP: DNA replication, proteolysis
PGOF: ATP binding, DNA binding, DNA clamp loader activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: DNA replication factor C complex
PGOP: DNA replication





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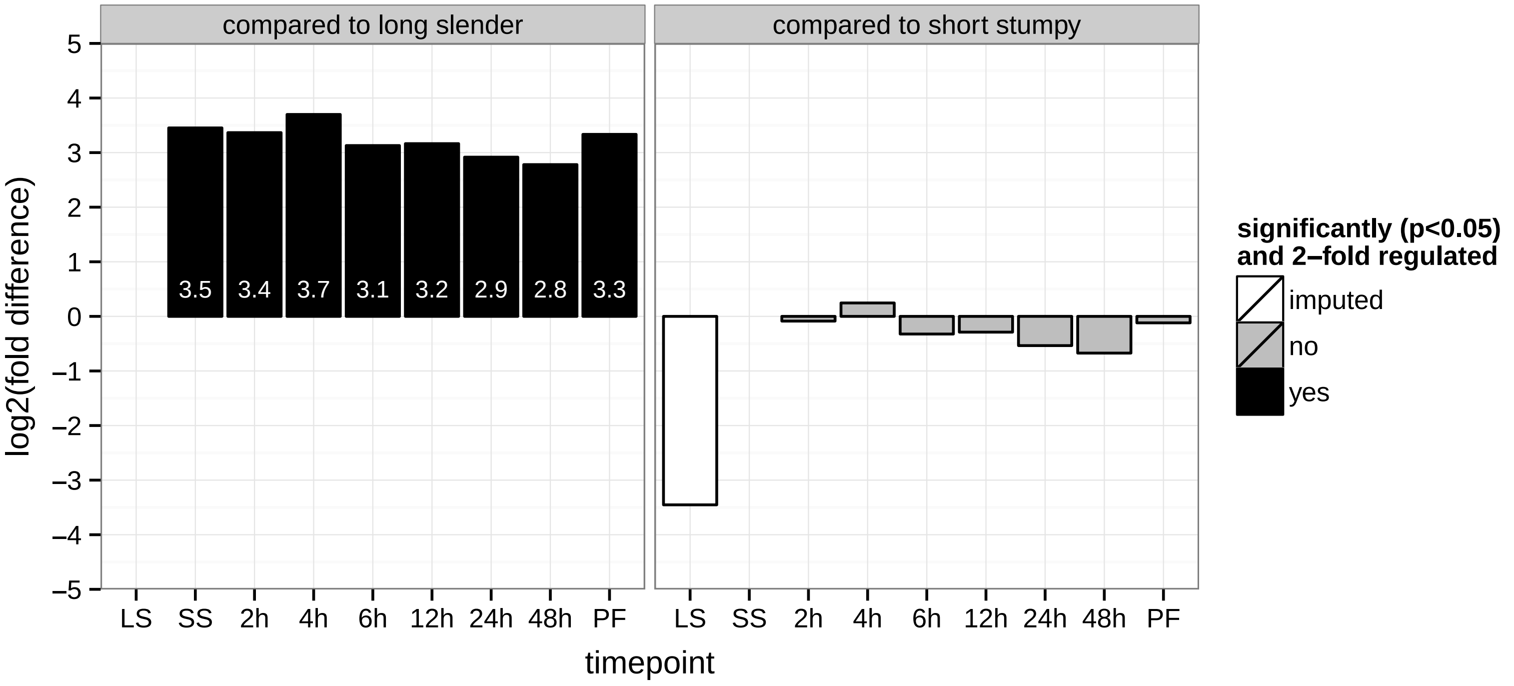
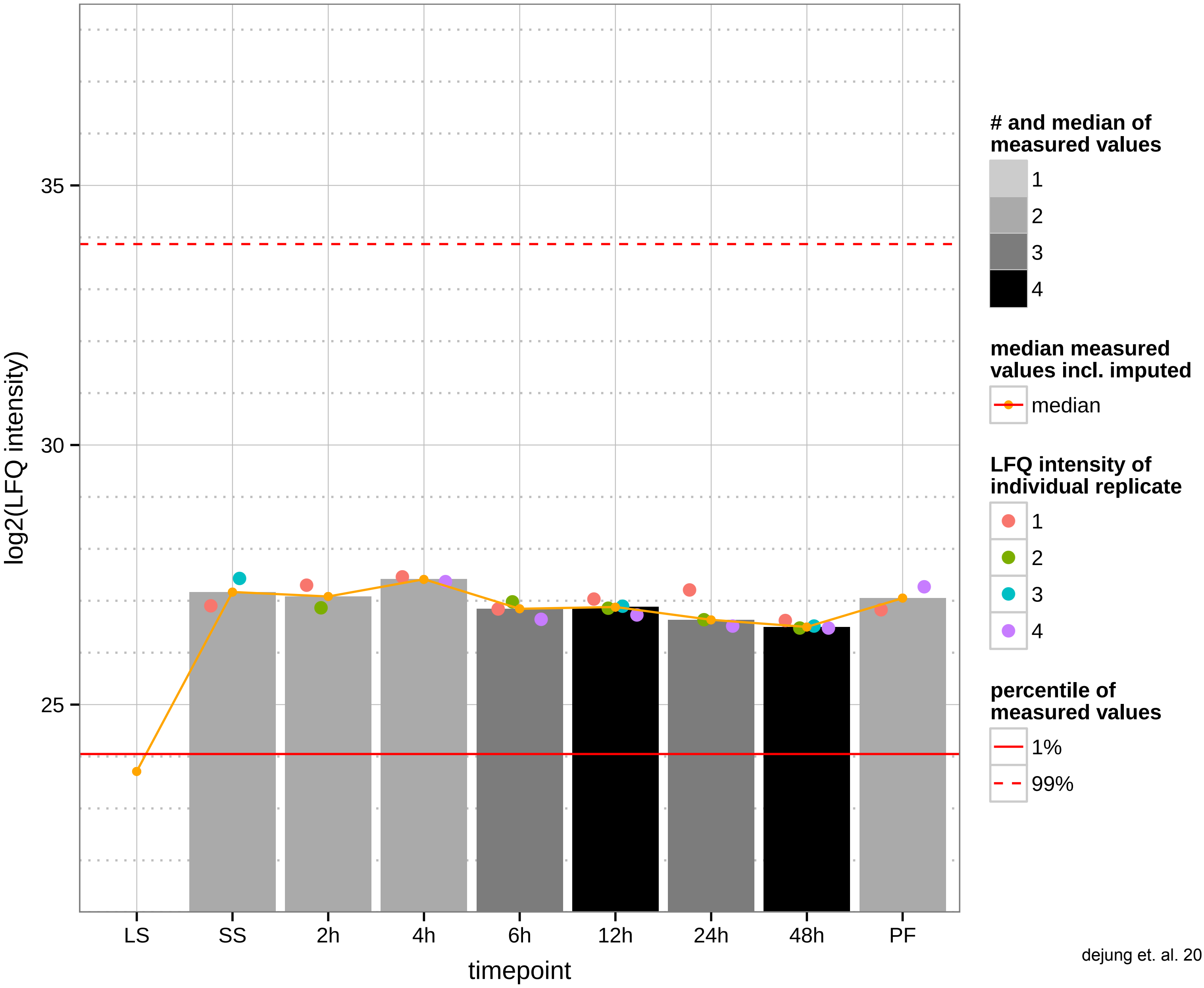
hypothetical protein, conserved
Tb927.11.5700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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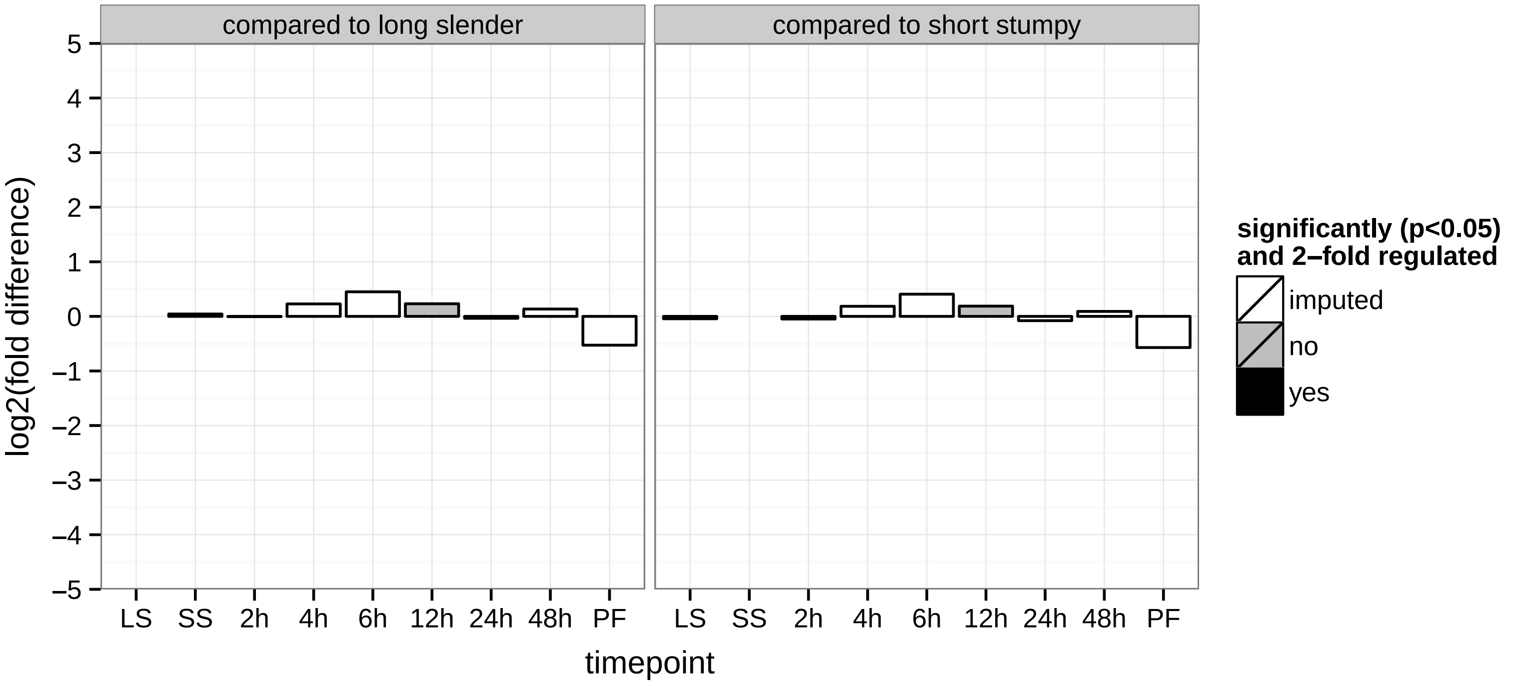
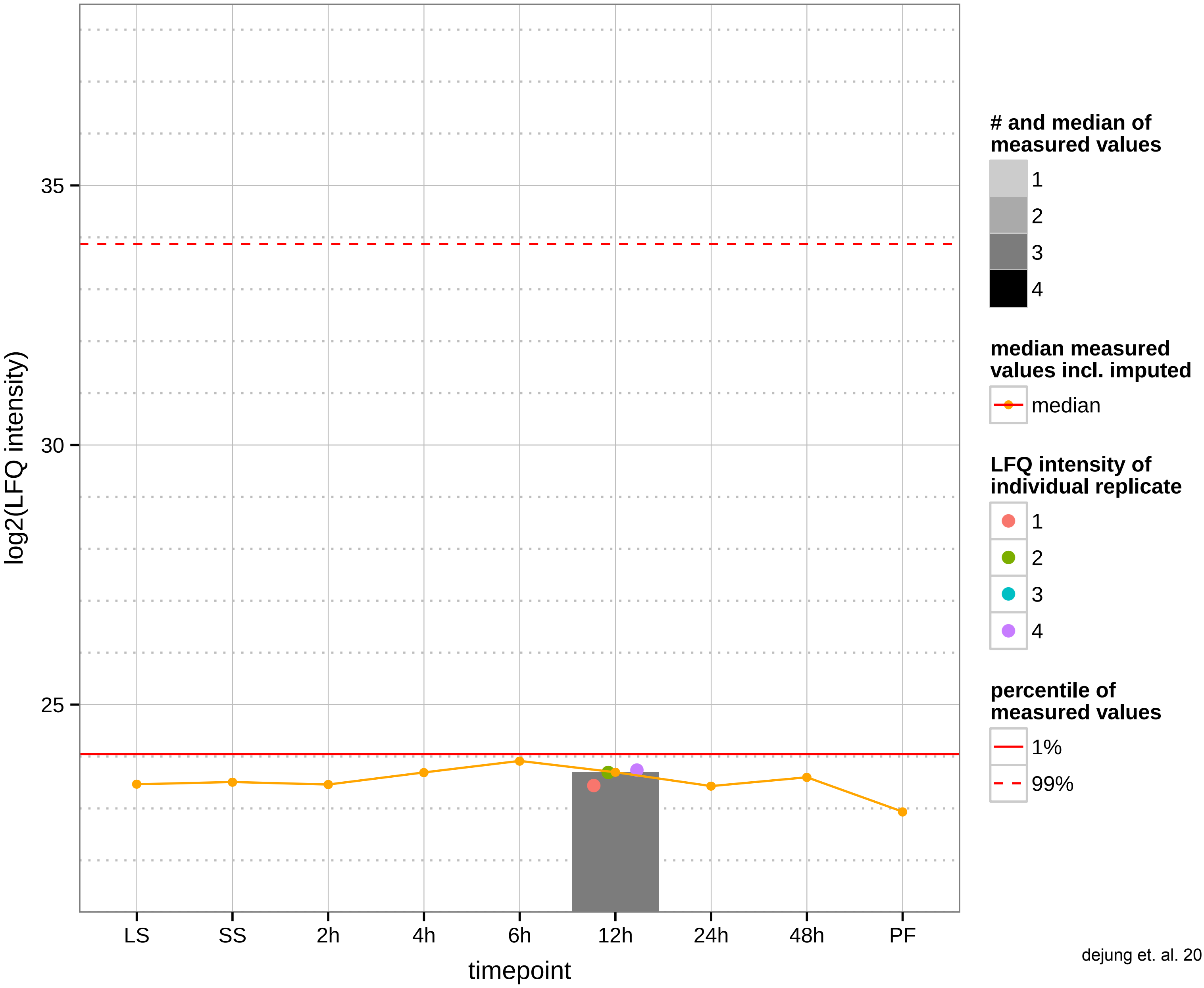
pre–mRNA splicing factor, putative, ATP– dependent RNA helicase
Tb927.11.5730
AGOF: ATP binding, ATP–dependent RNA helicase activity, nucleic acid binding
AGOC: null
AGOP: RNA splicing, RNA splicing, via transesterification reactions, nuclear mRNA splicing, via spliceosome
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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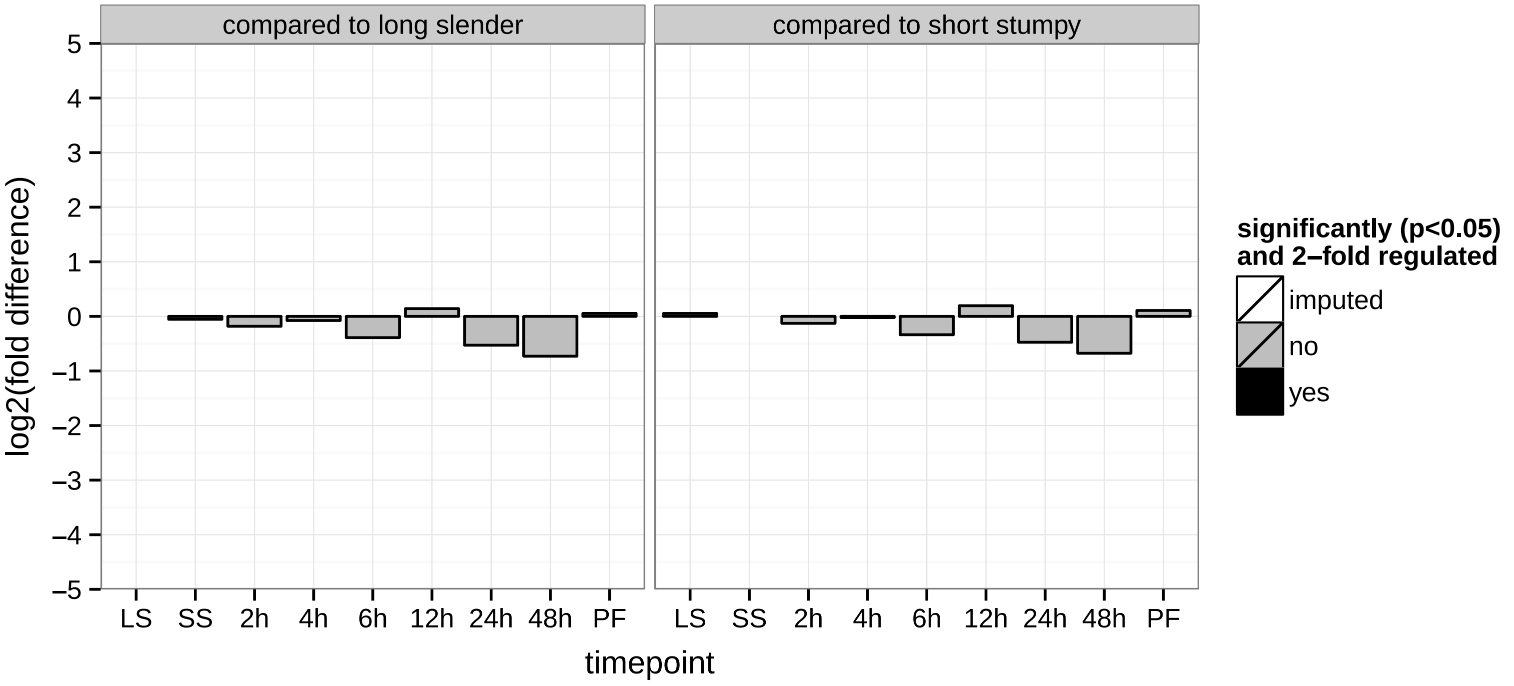
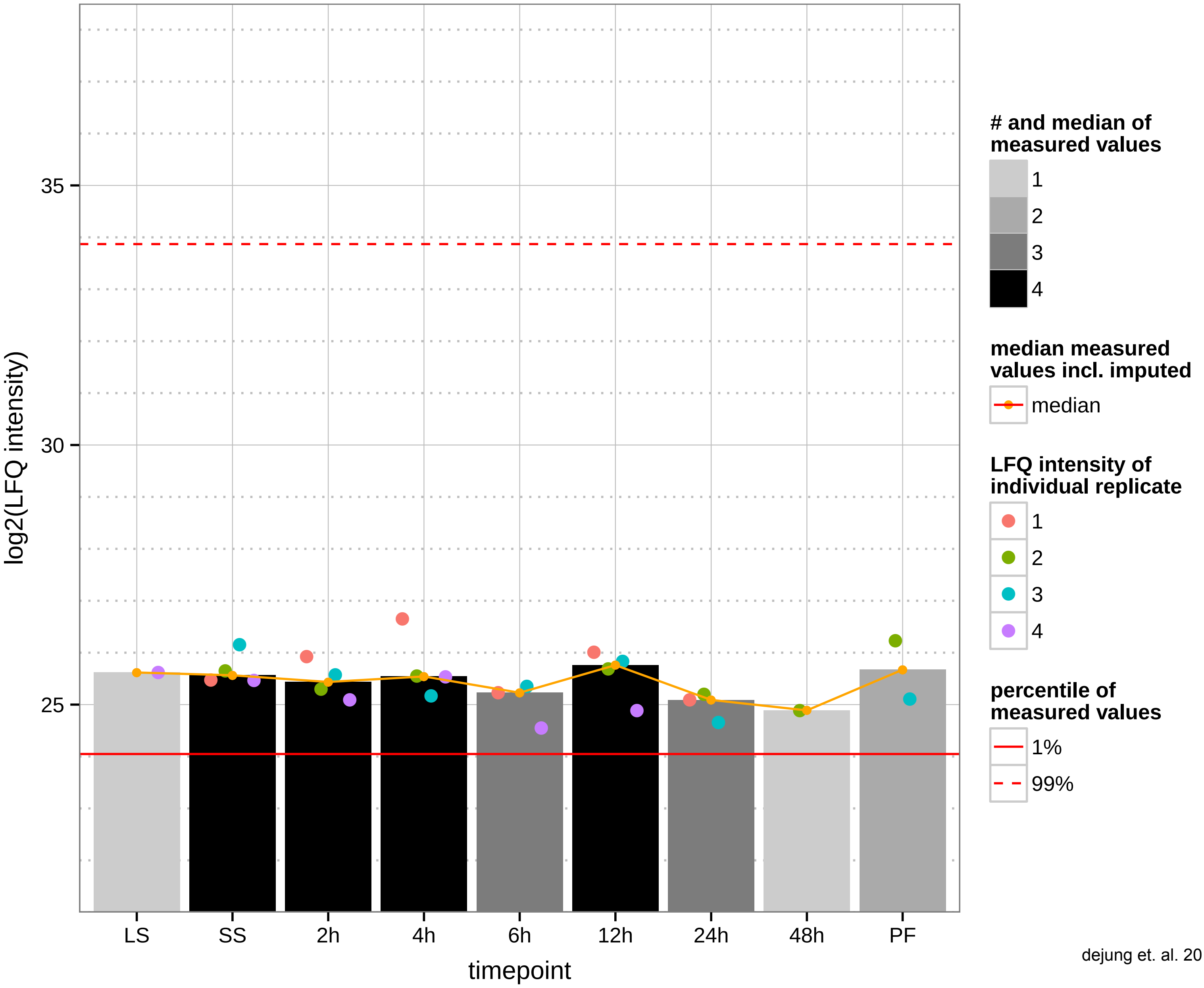
hypothetical protein, conserved
Tb927.11.5890
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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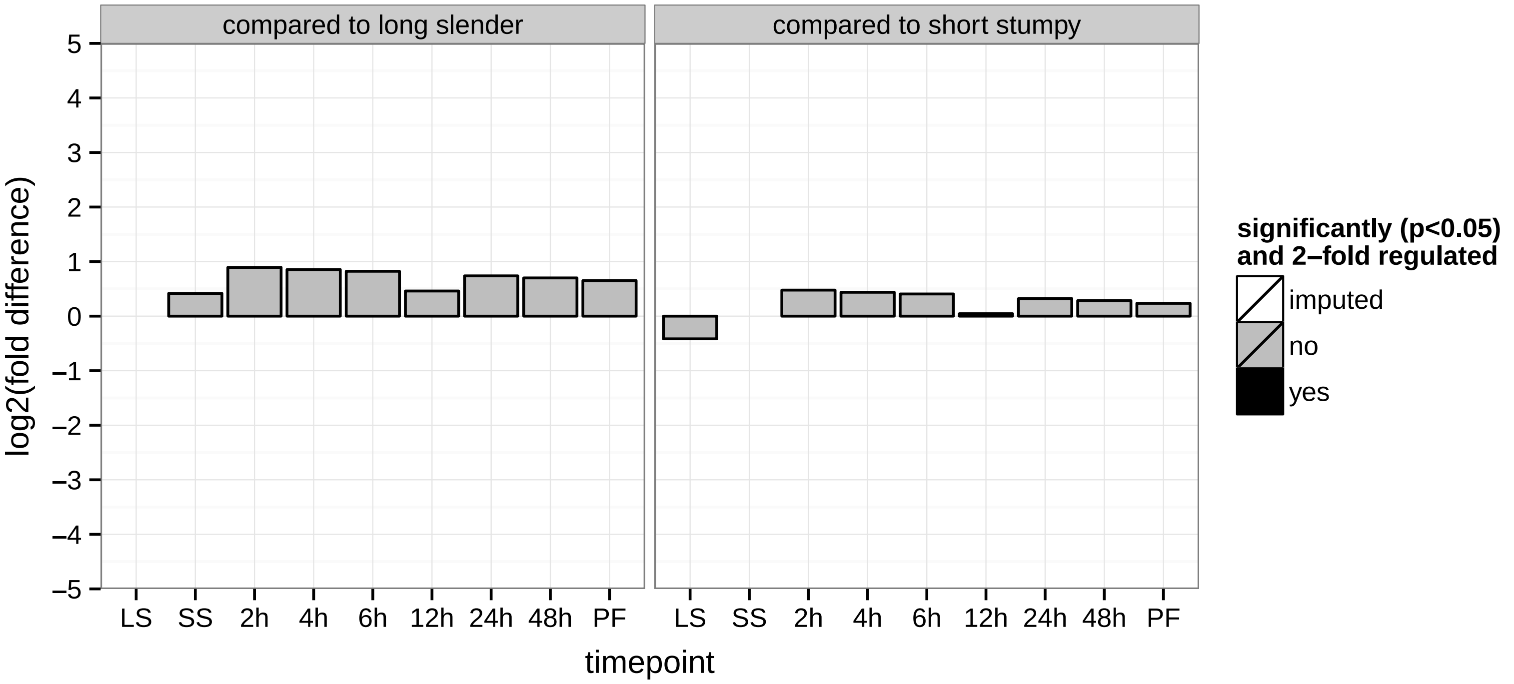
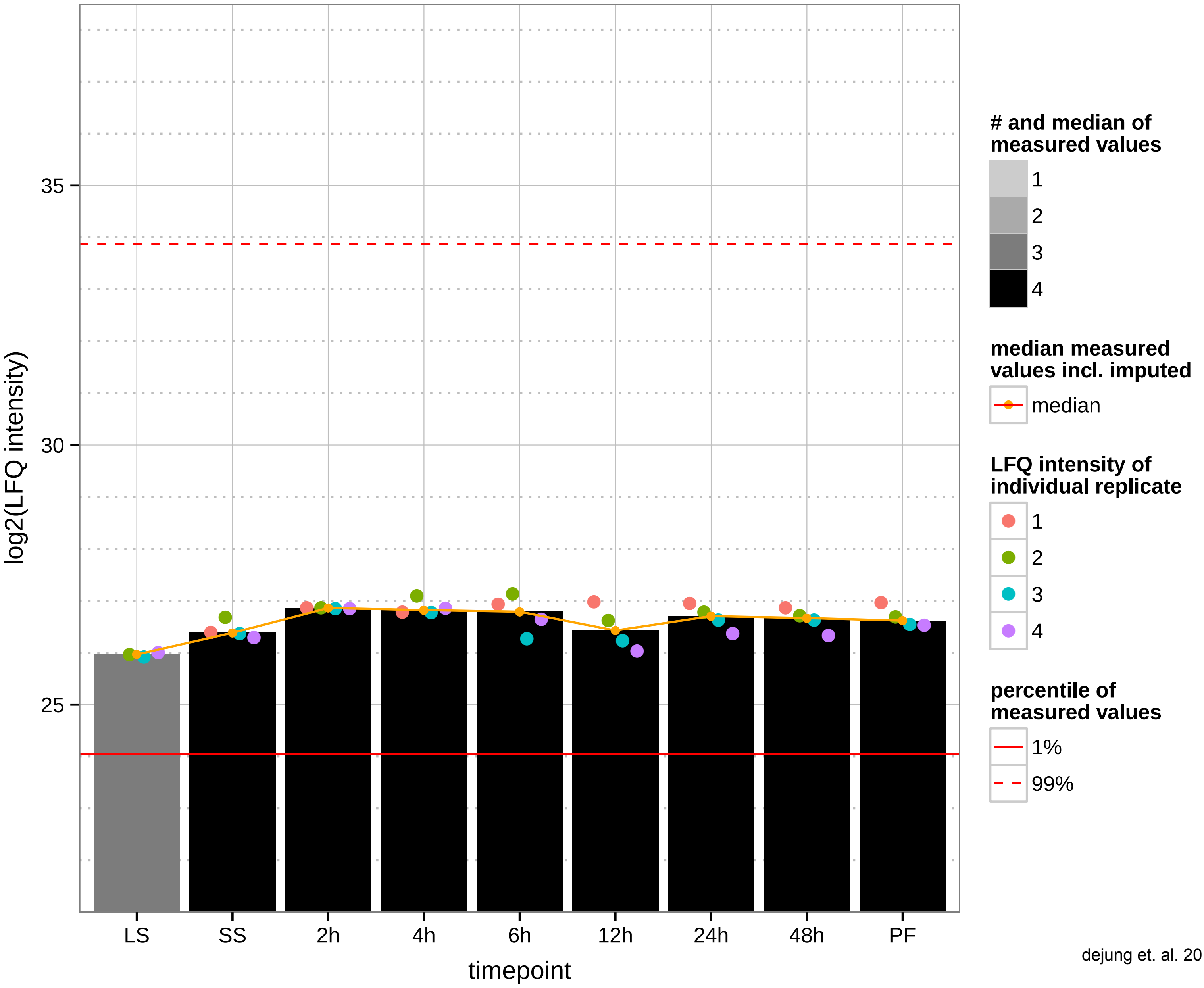
conserved protein, unknown function
Tb927.11.6010
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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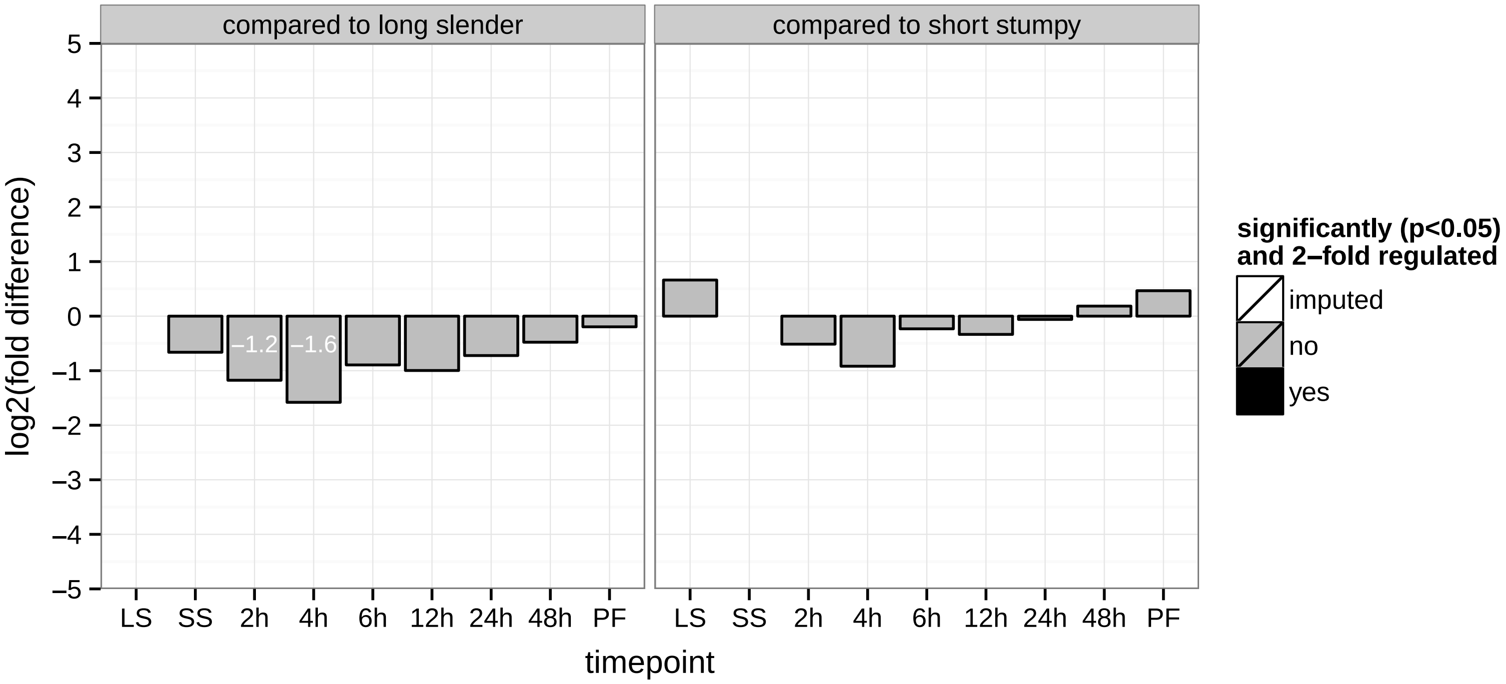
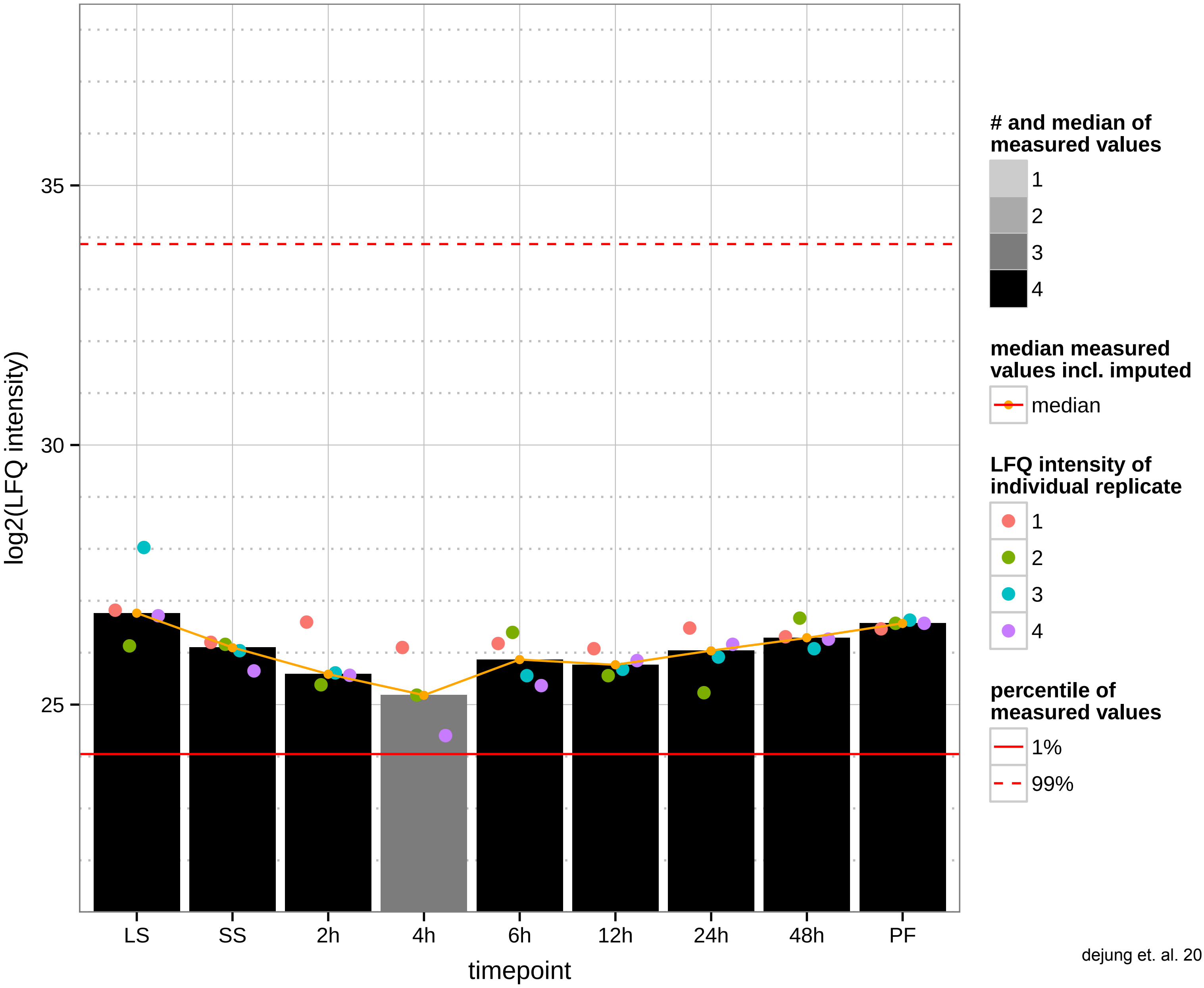
hypothetical protein, conserved
Tb927.11.6050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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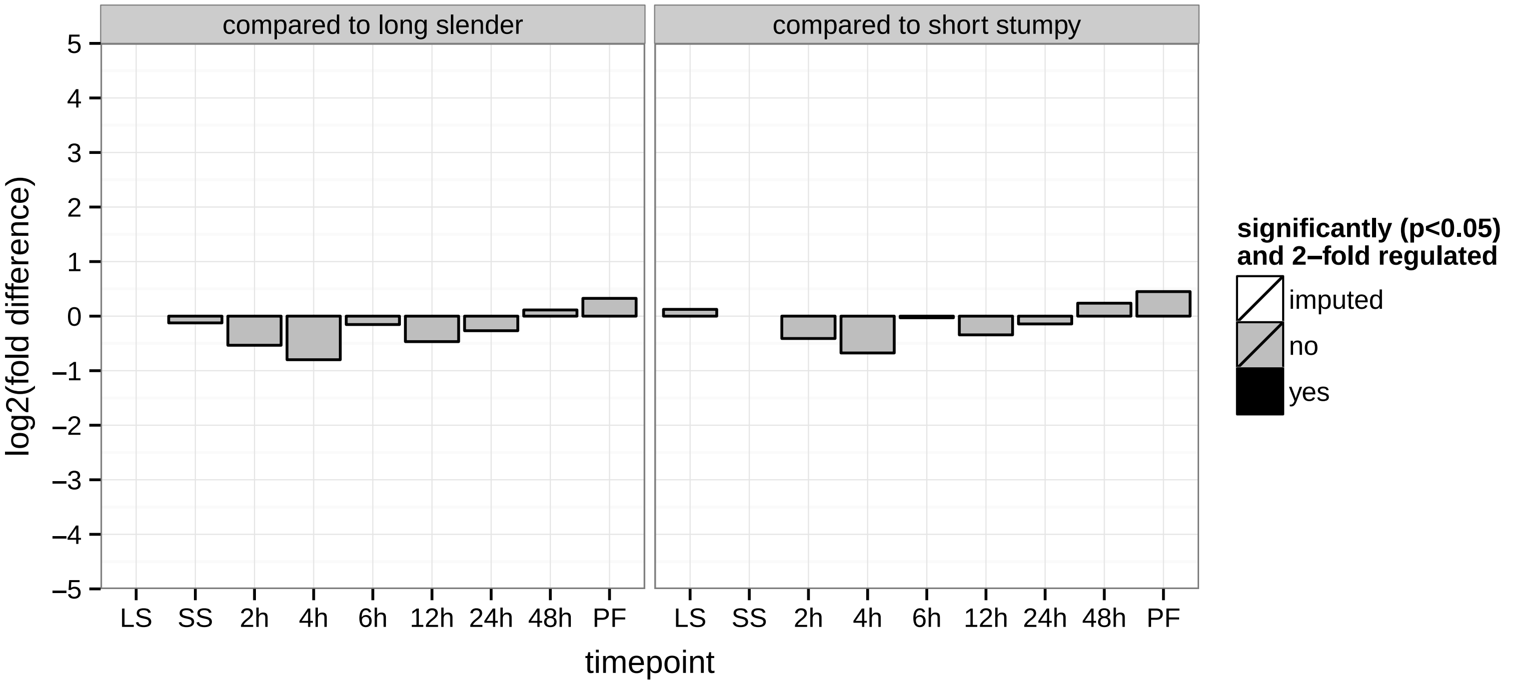
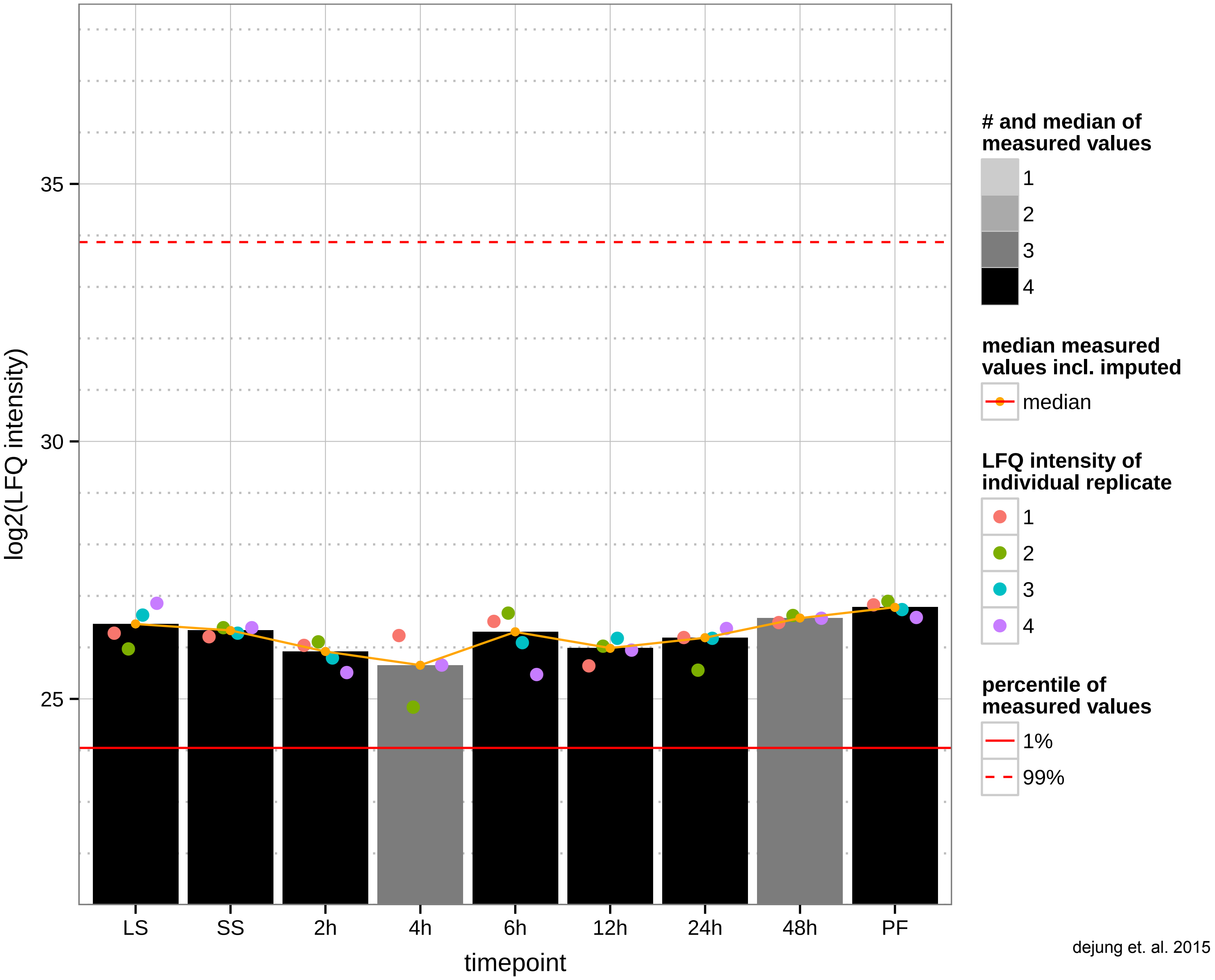
hypothetical protein, conserved
Tb927.11.6070
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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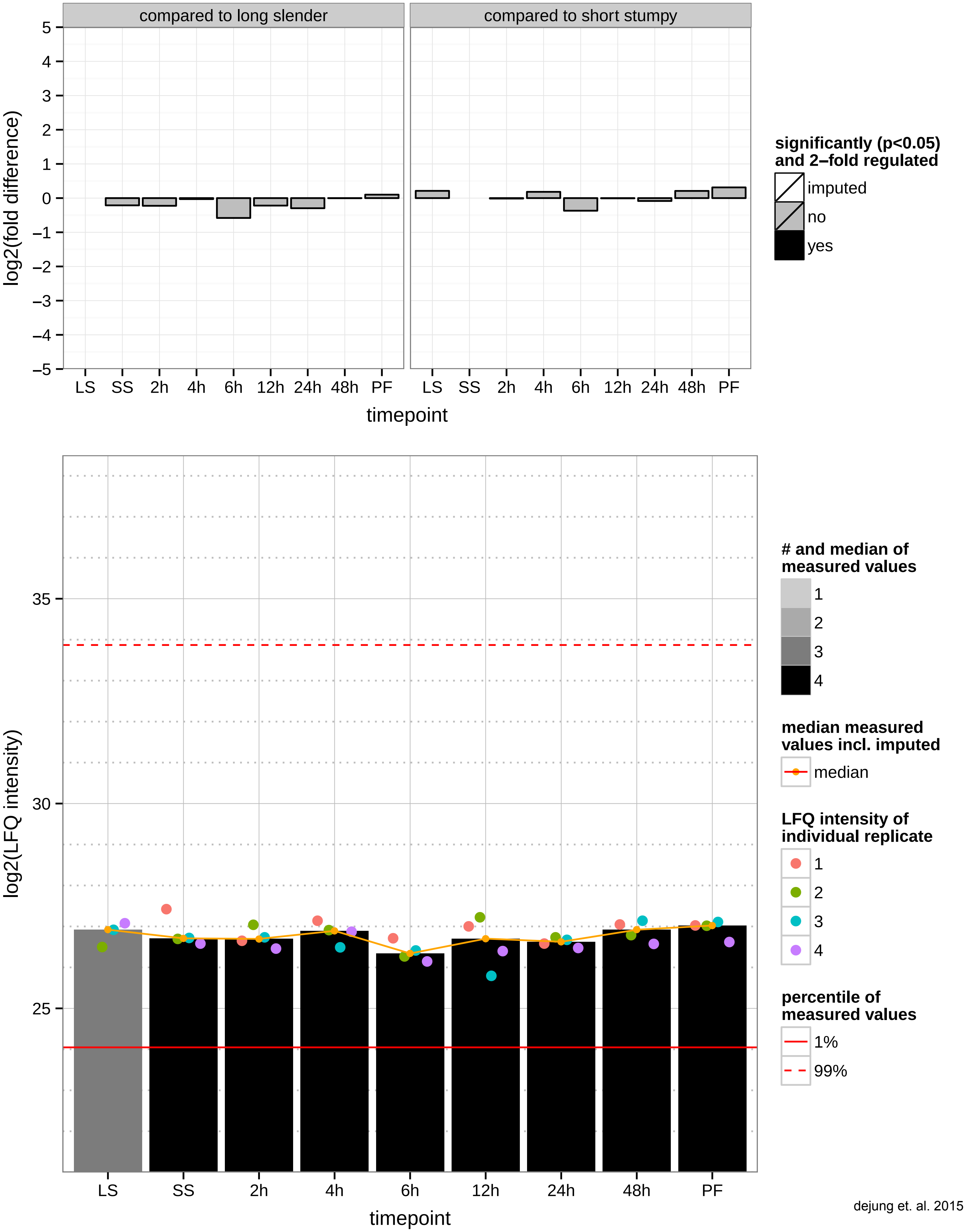
hypothetical protein, conserved
Tb927.11.610
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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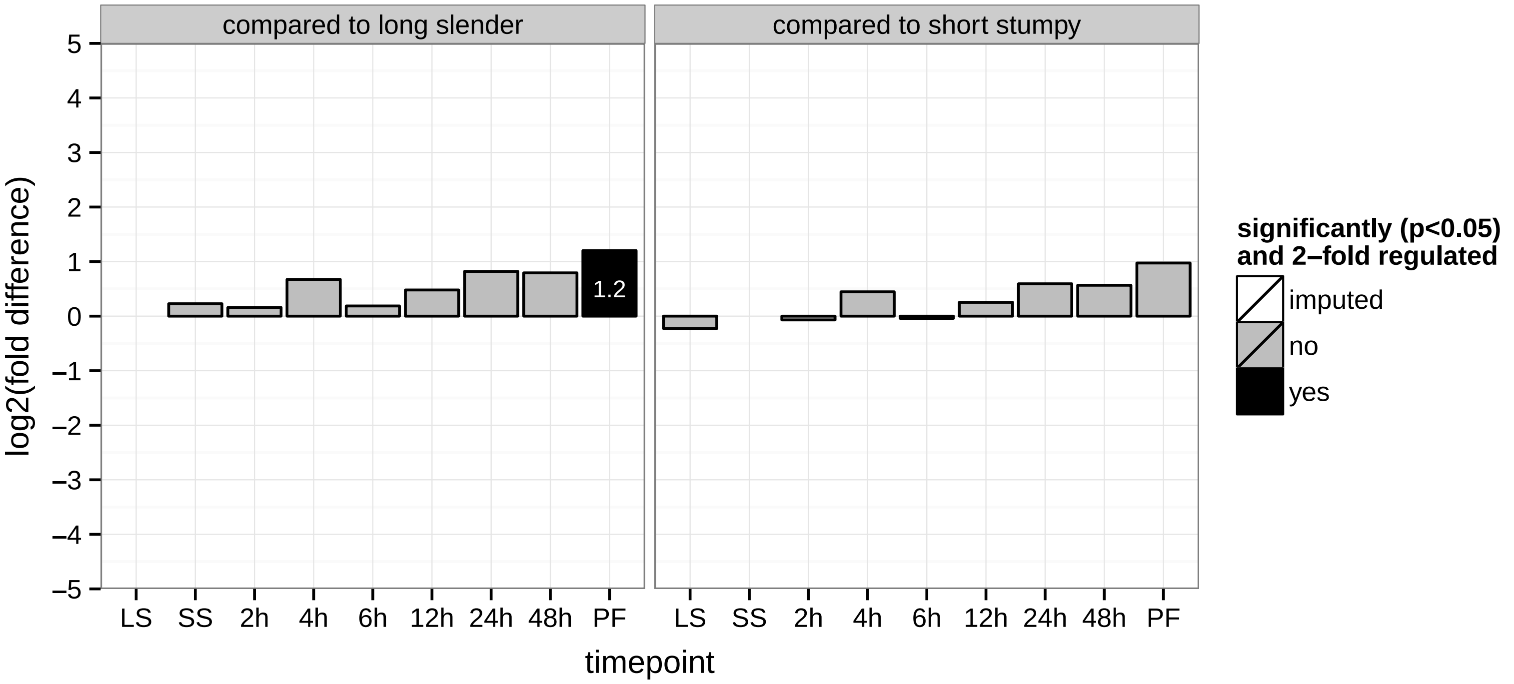
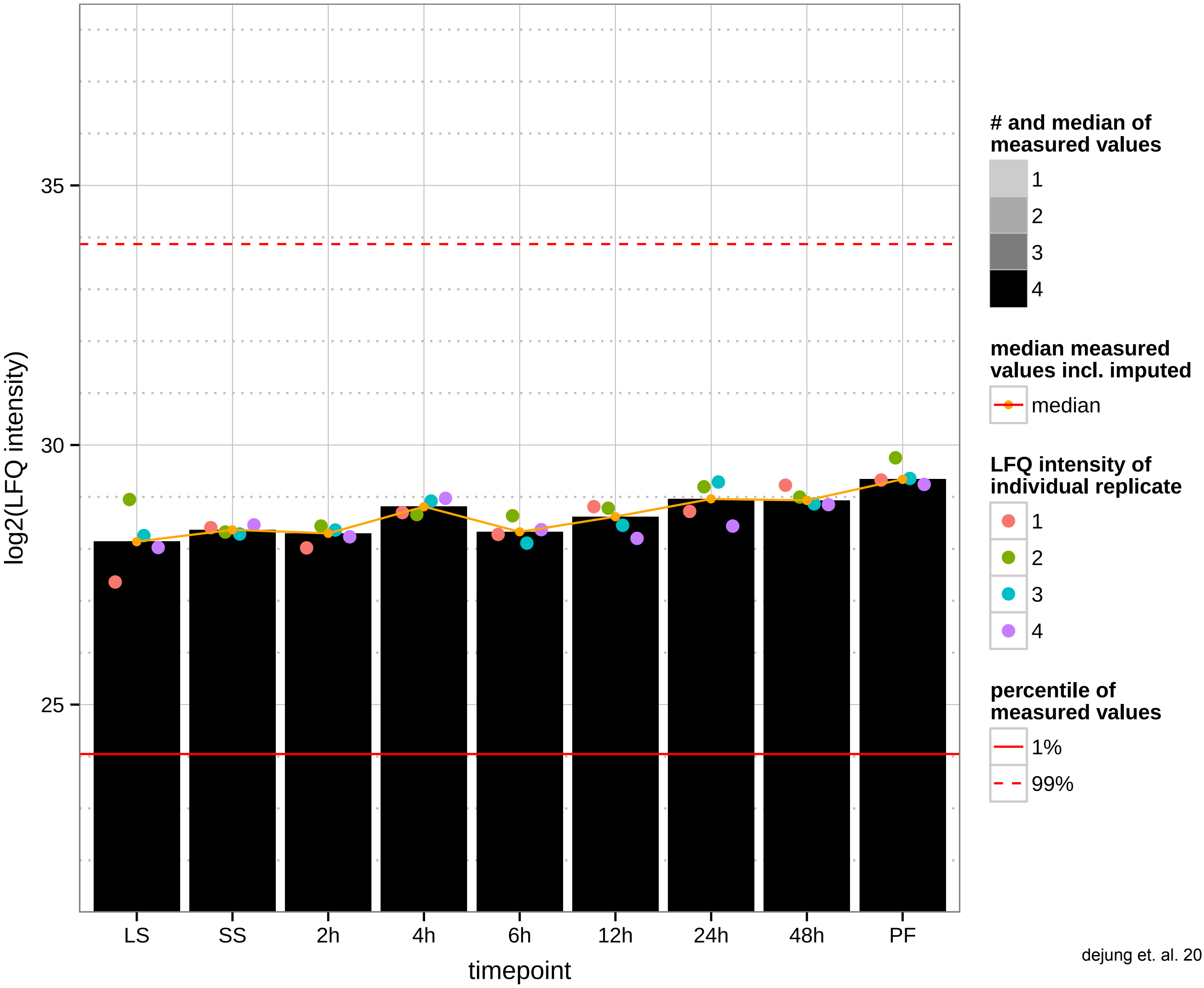
SKP1–like protein
Tb927.11.6130
AGOF: null
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: null
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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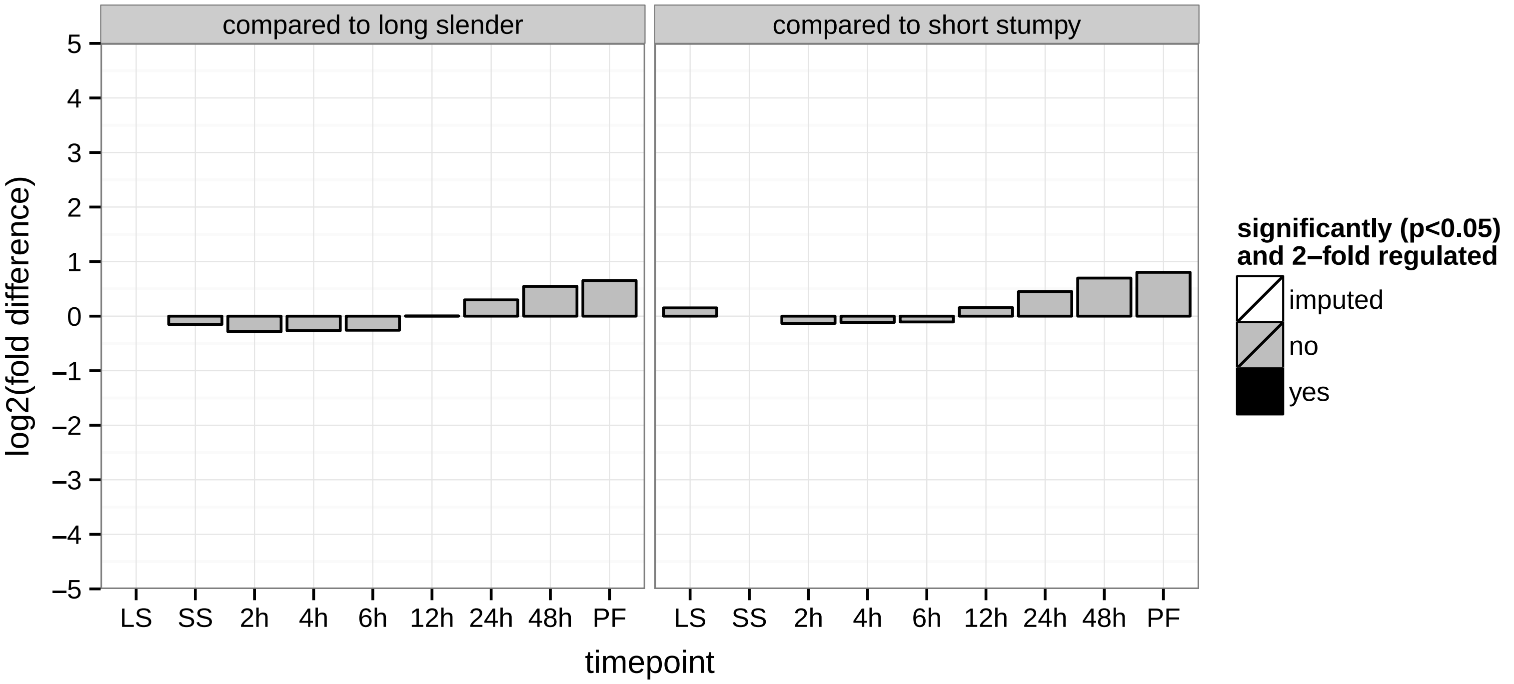
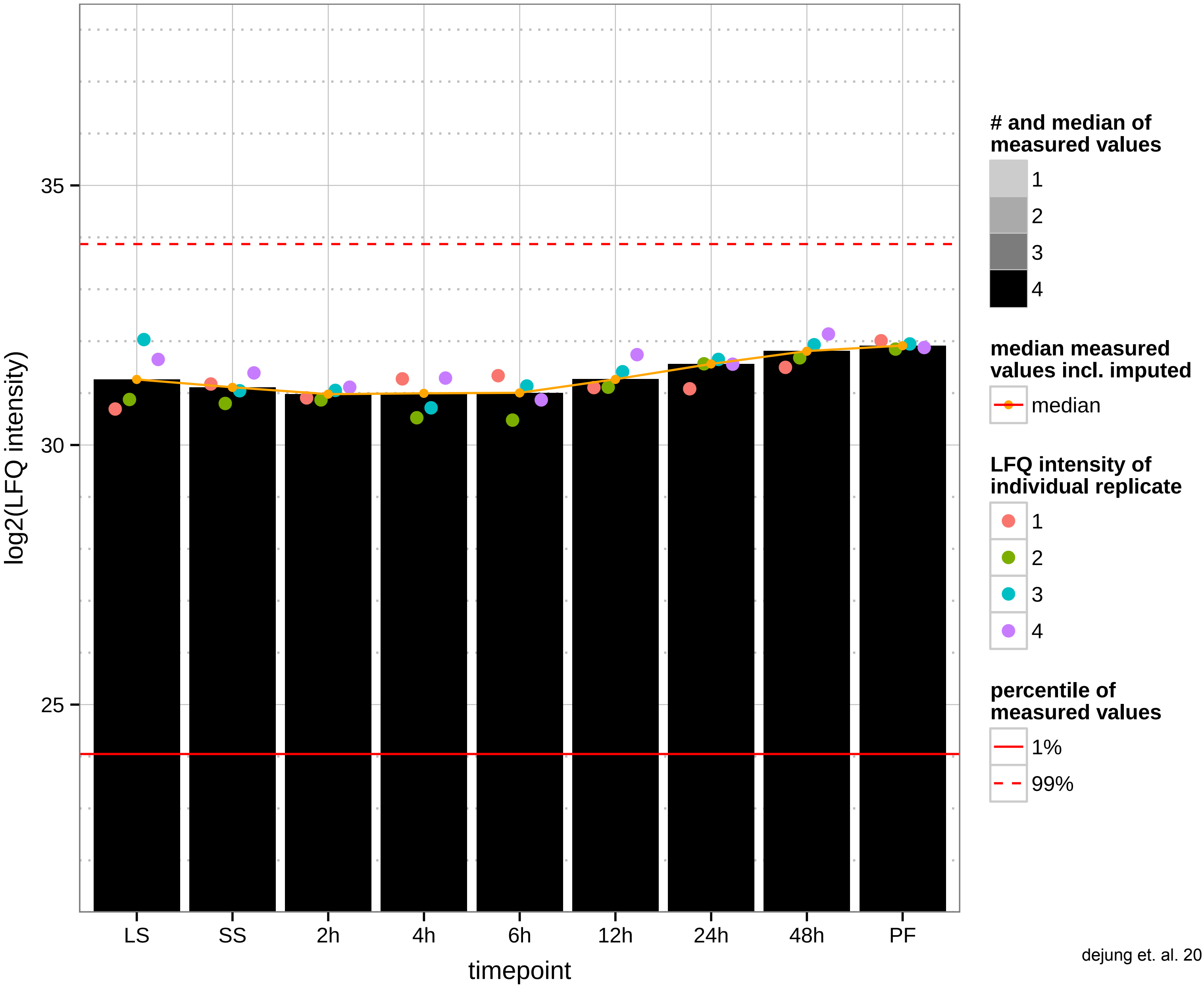
40S ribosomal protein S15A, putative
Tb927.11.6140;Tb927.3.4360
AGOF: structural constituent of ribosome
AGOC: intracellular, organellar small ribosomal subunit, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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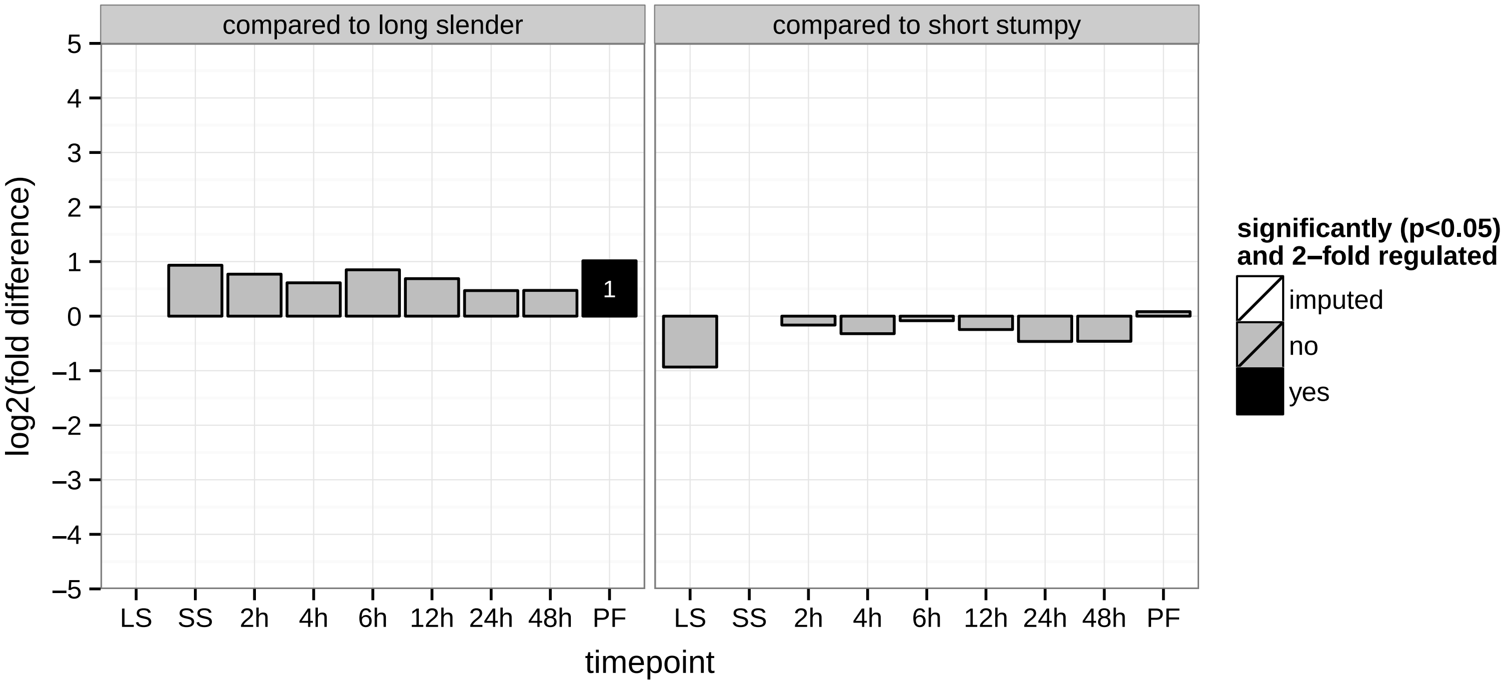
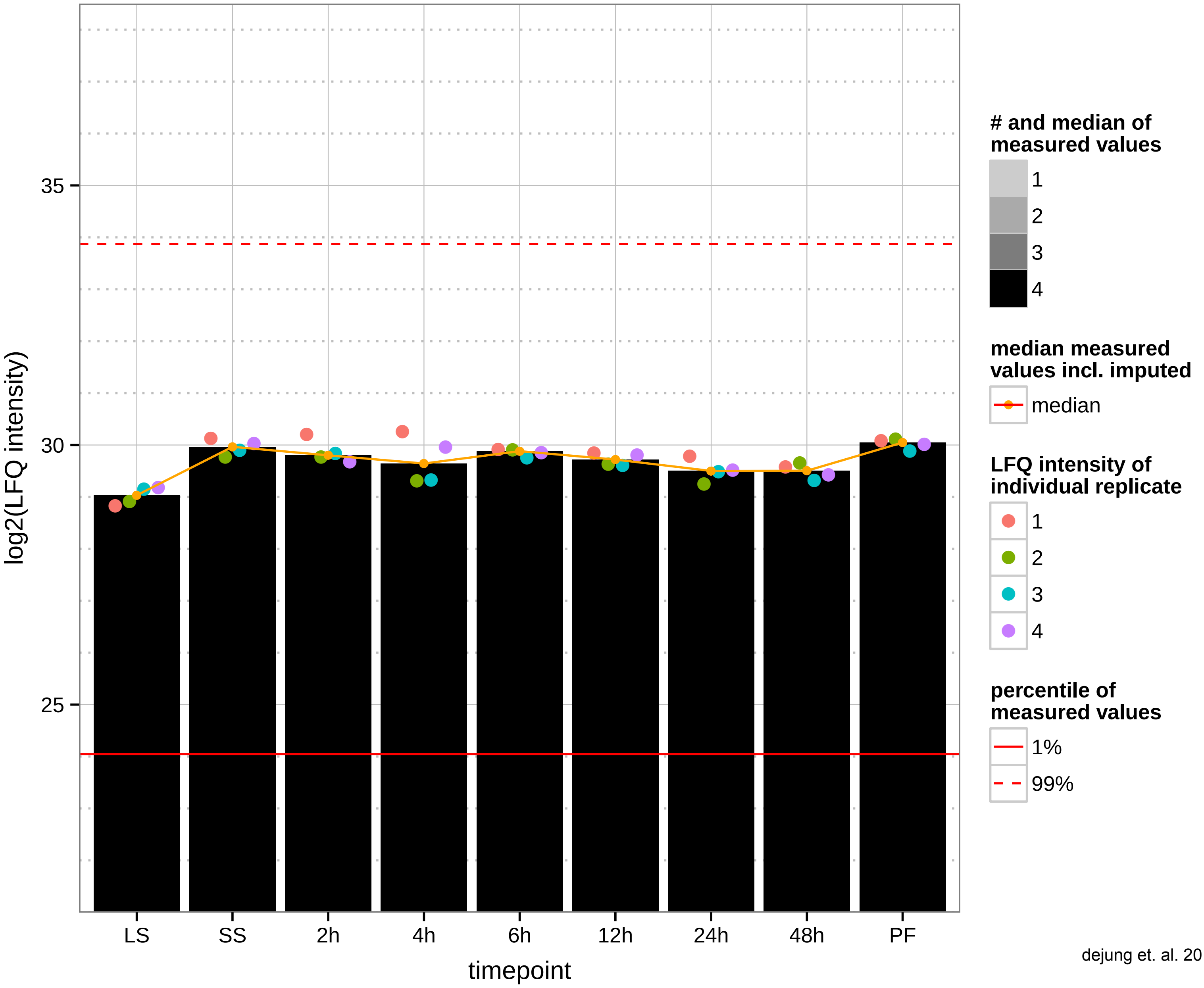
protein transport protein SEC31, putative, cytosolic coat protein
Tb927.11.6170
AGOF: null
AGOC: null
AGOP: transport
PGOF: protein binding
PGOC: null
PGOP: null





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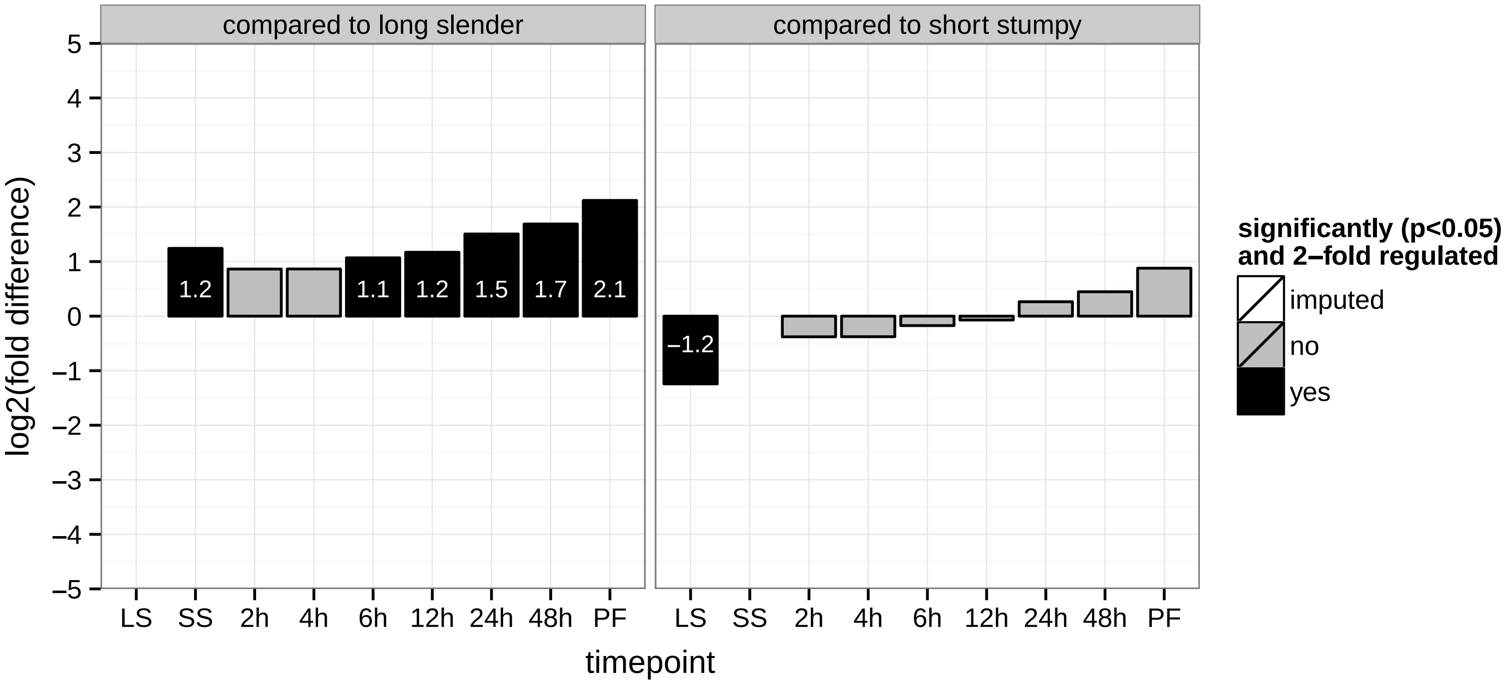
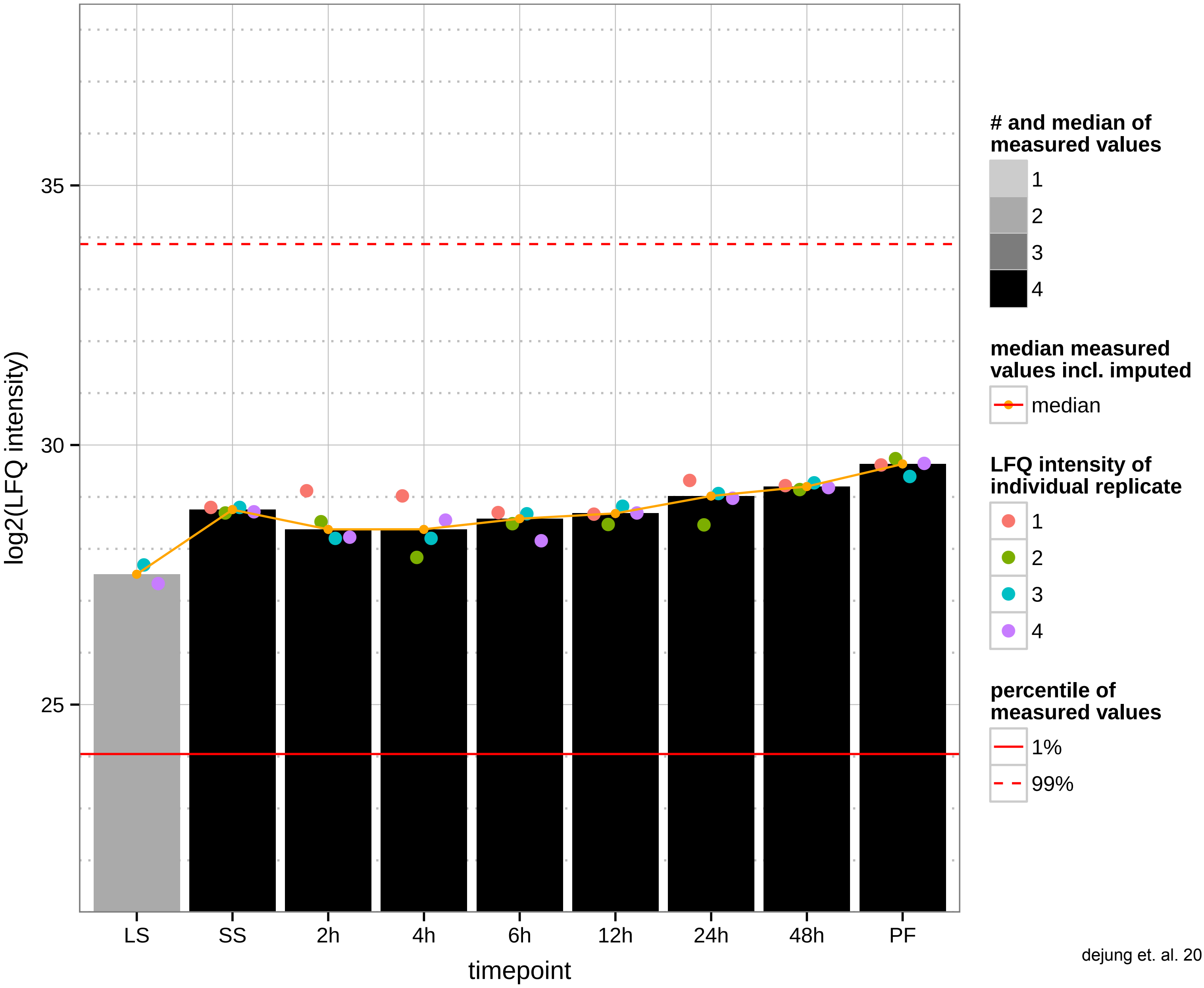
RNA polymerase I second largest subunit (RPA135)
Tb927.11.630
AGOF: DNA binding, DNA−directed RNA polymerase activity, ribonucleoside binding
AGOC: nucleus
AGOP: transcription, DNA−dependent
PGOF: DNA binding, DNA−directed RNA polymerase activity
PGOC: nucleus
PGOP: transcription, DNA−dependent





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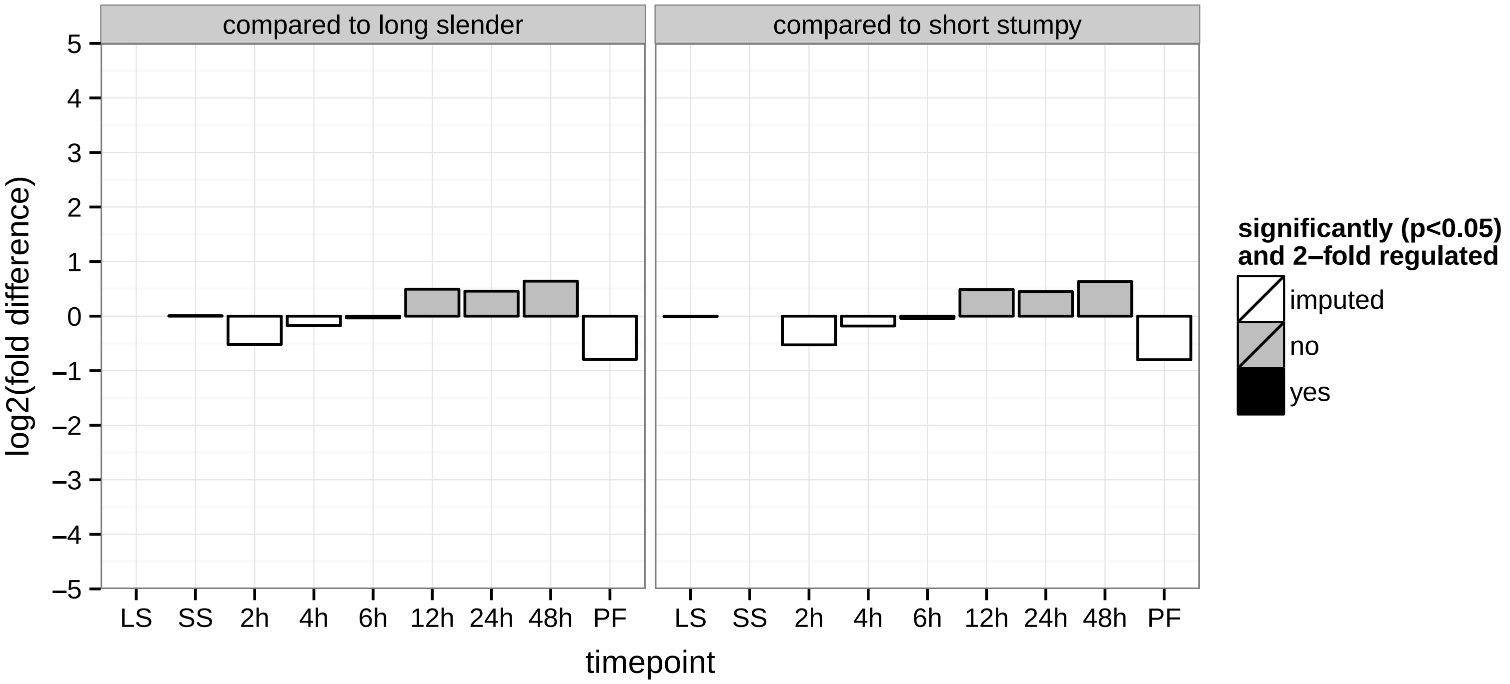
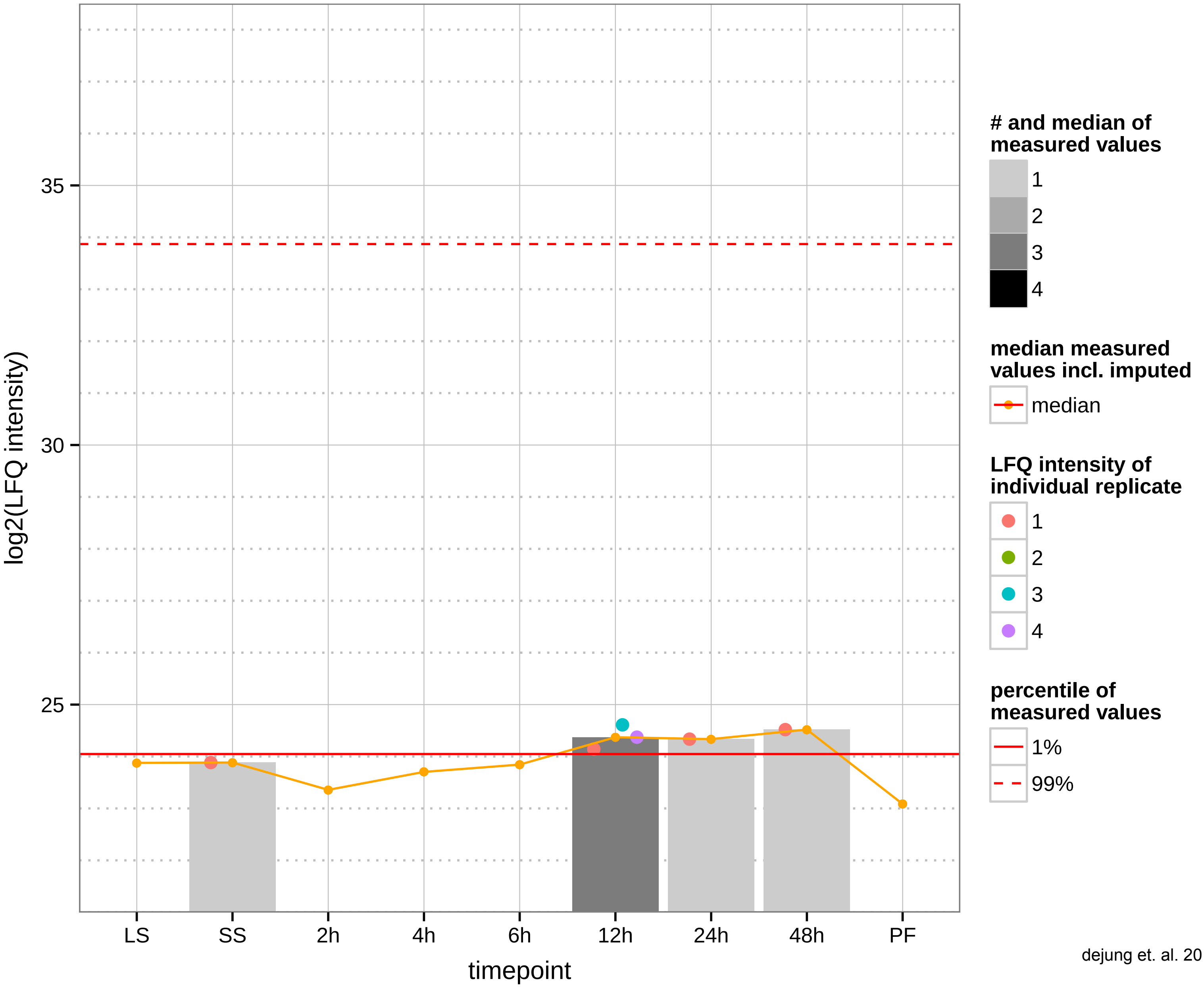
hypothetical protein, conserved
Tb927.11.6310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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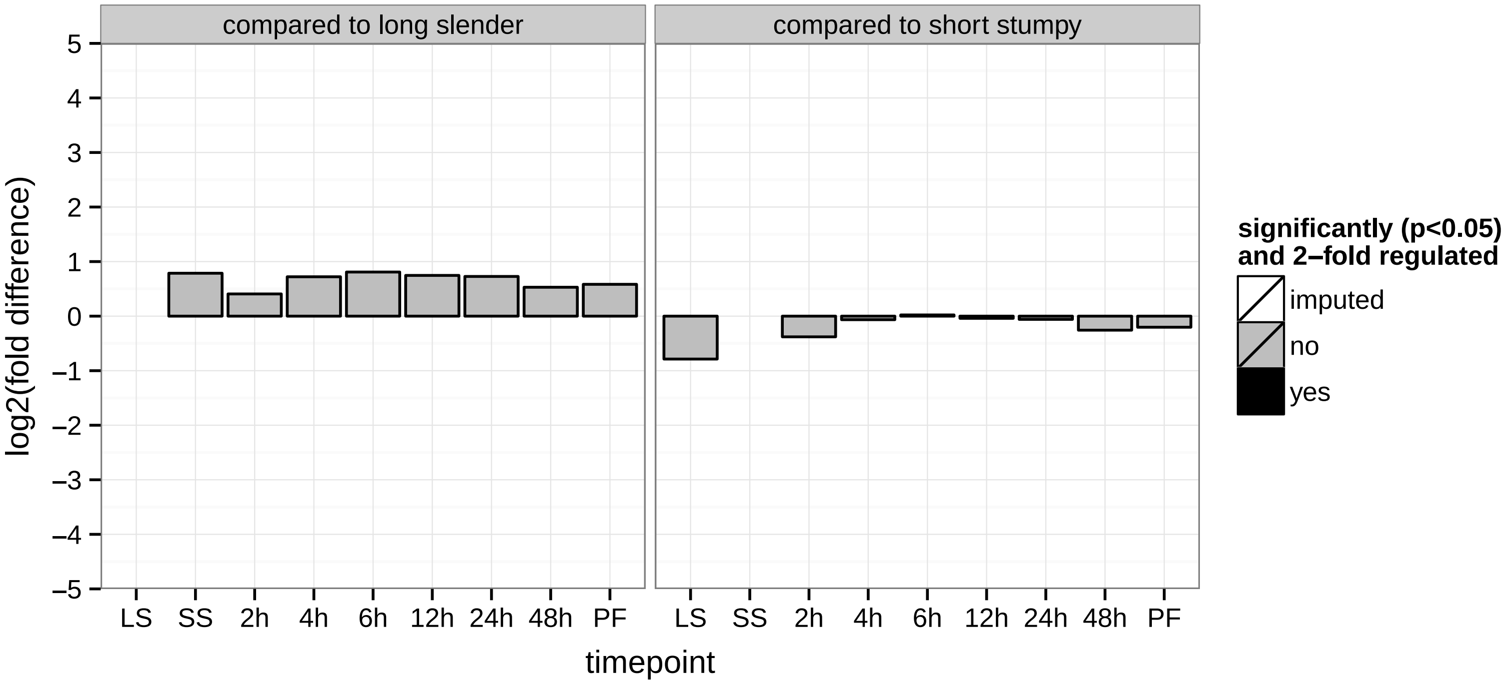
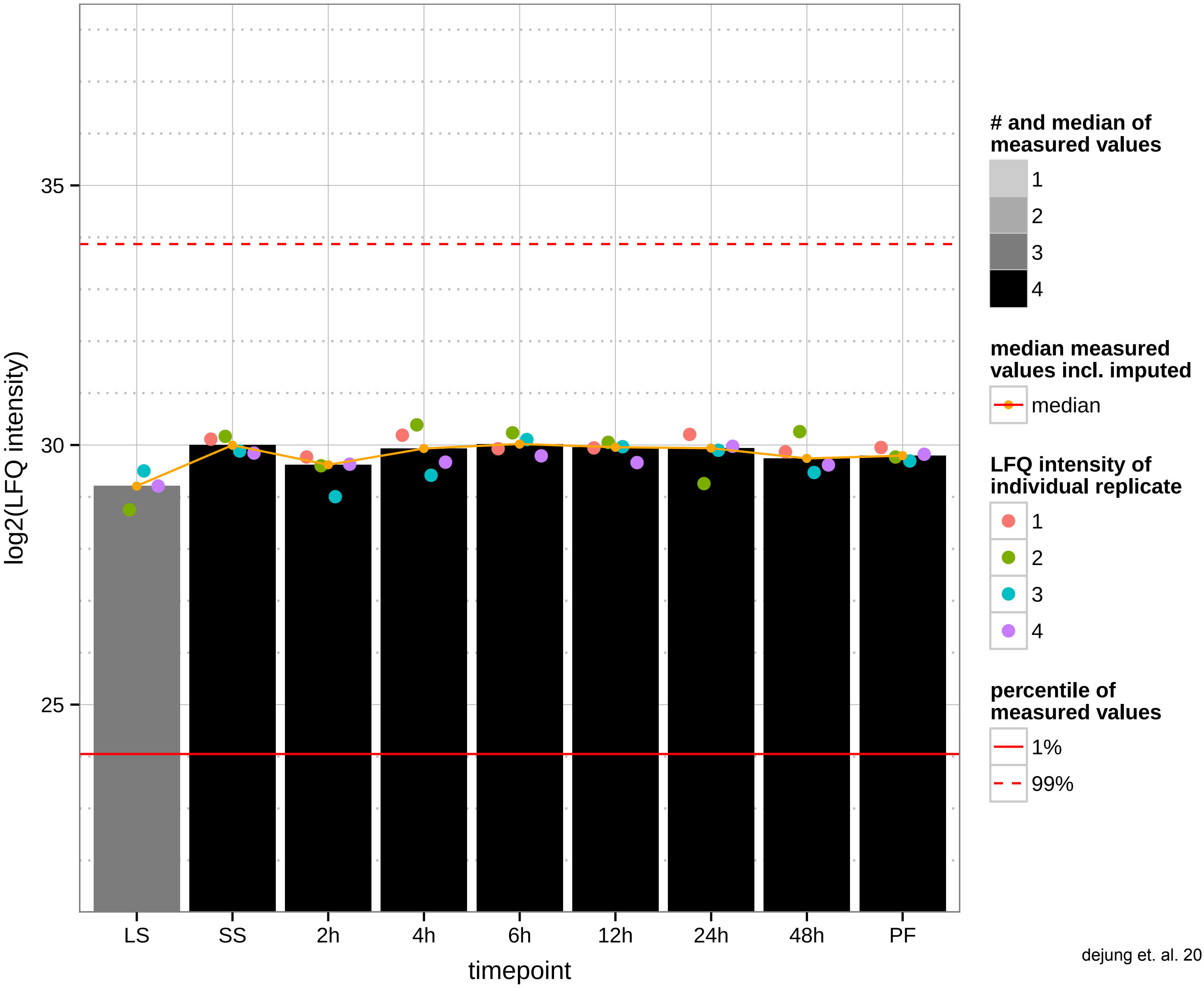
MRB1–associated protein, zinc finger ccch and cchc domain–containing protein
Tb927.11.6320
AGOF: null
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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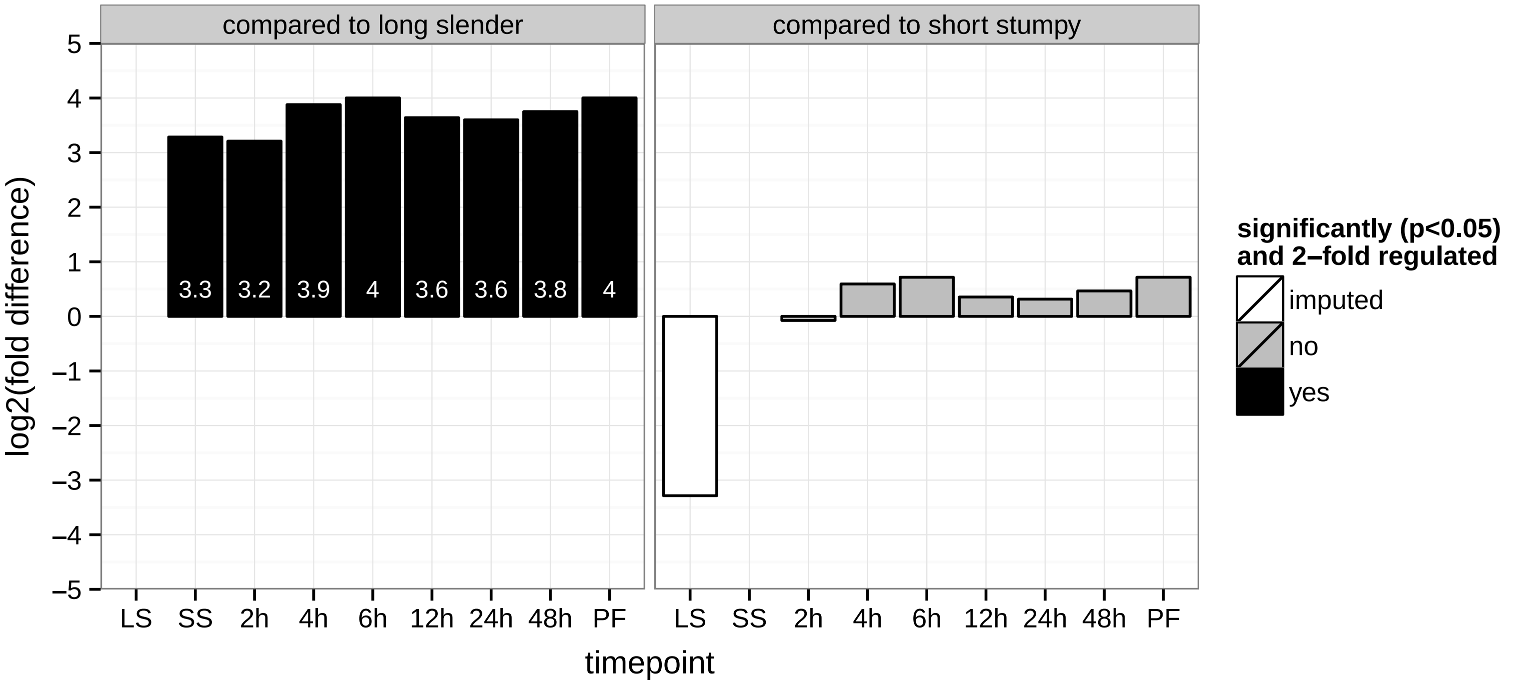
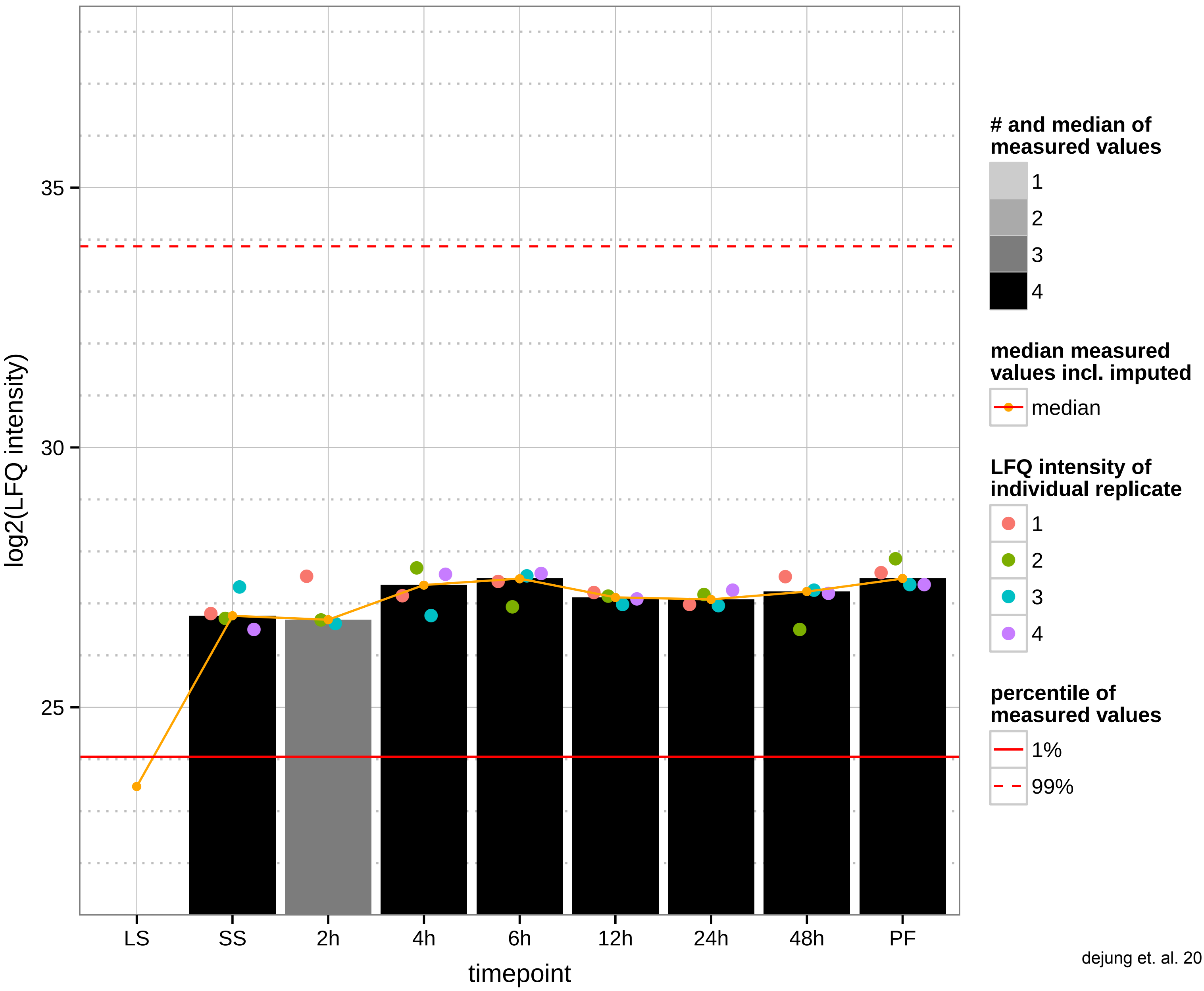
60S ribosomal protein L24, putative
Tb927.11.6360
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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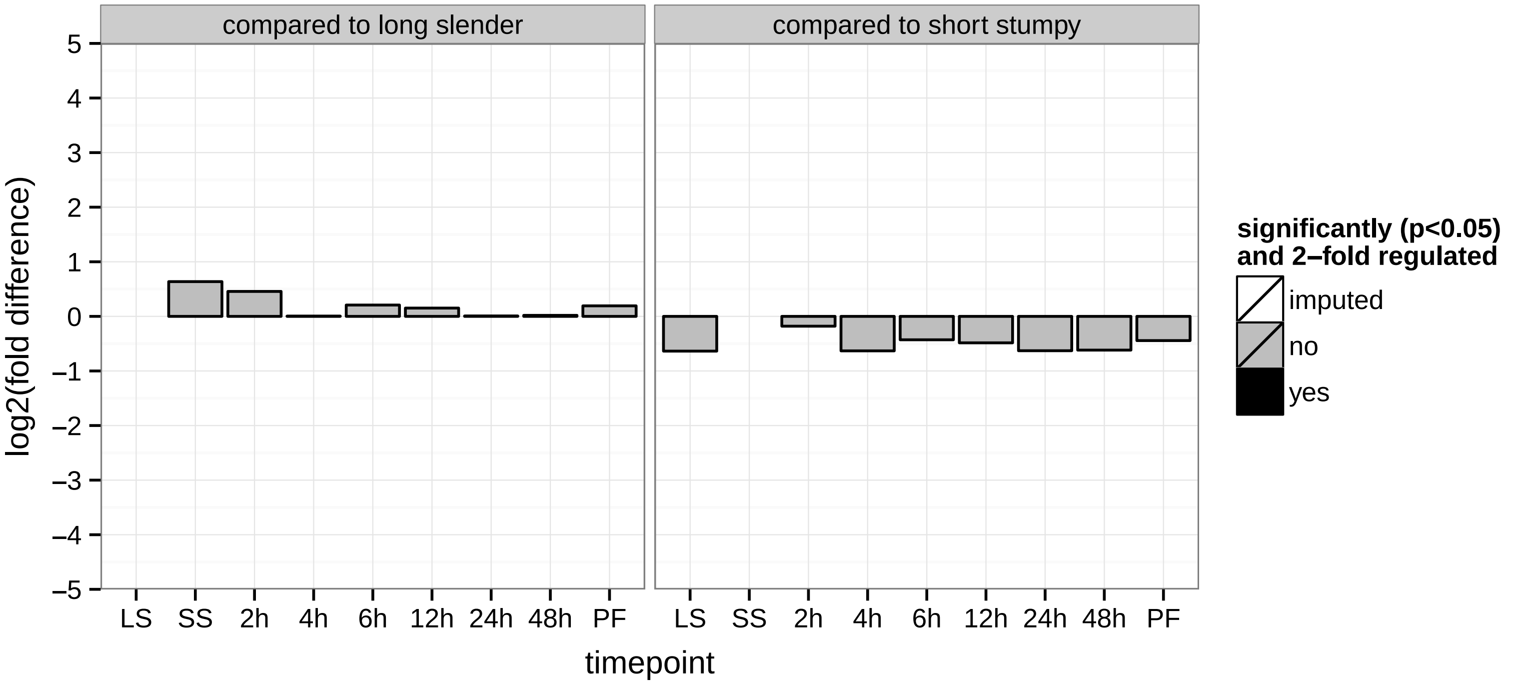
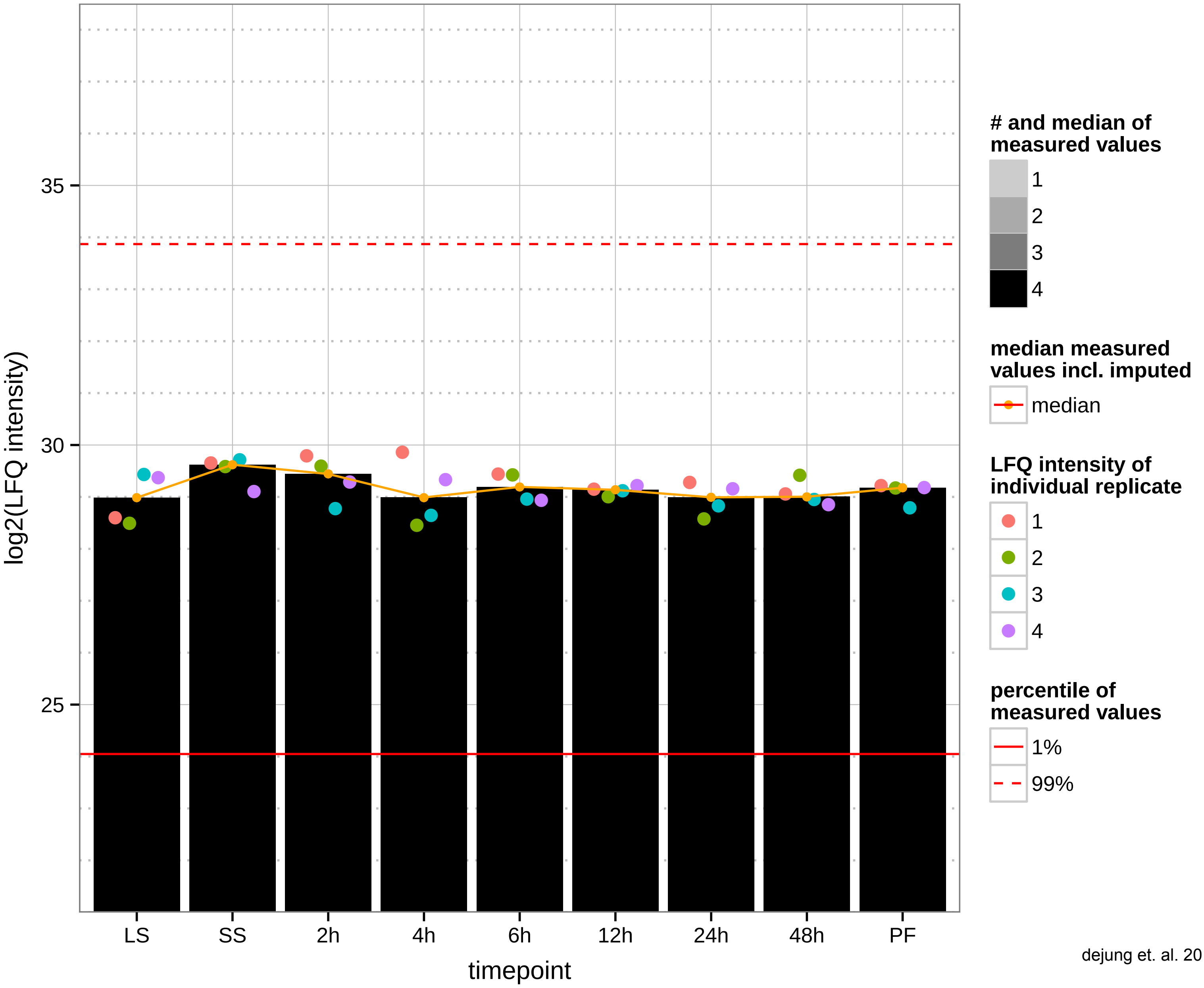
leucine−rich repeat protein (LRRP), putative
Tb927.11.6370
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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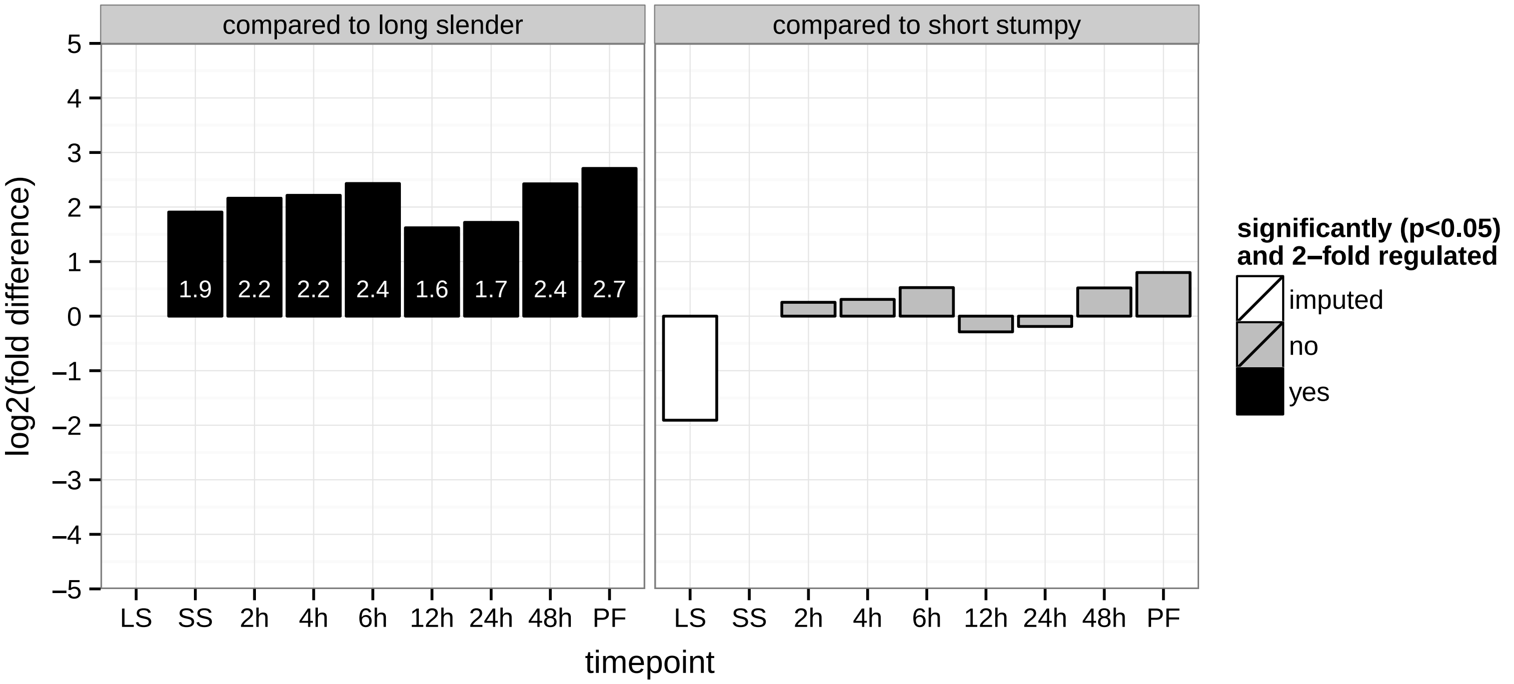
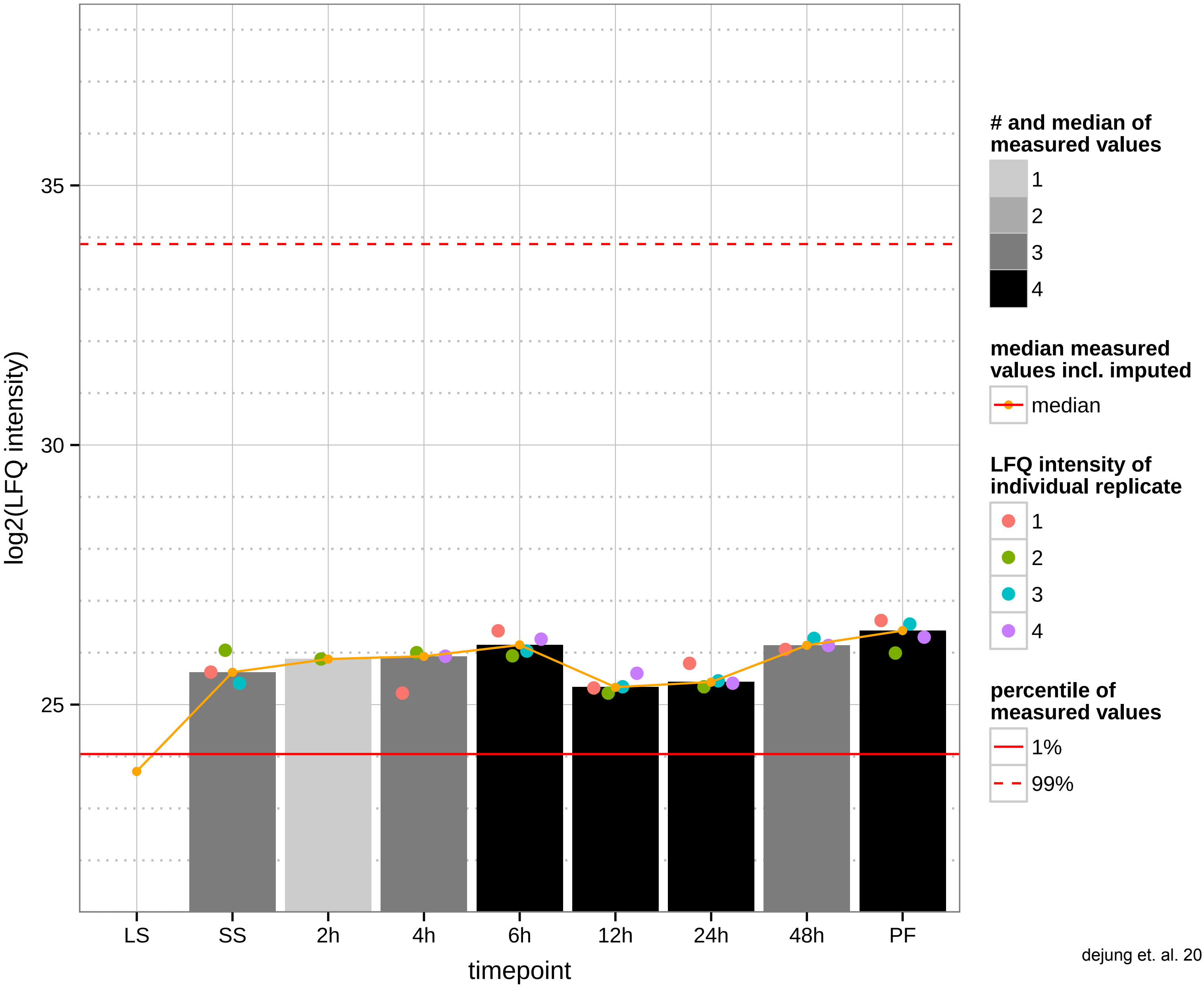
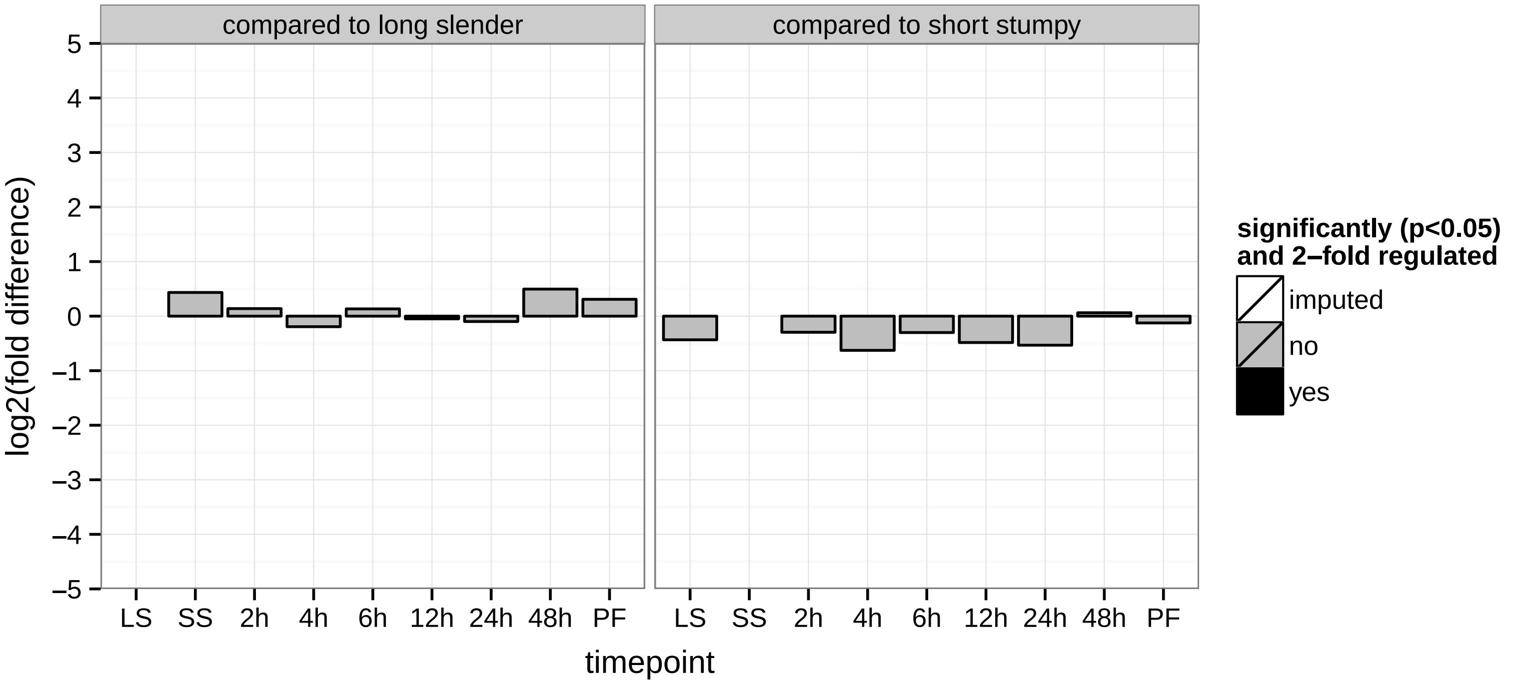
kinesin, putative
Tb927.11.6400
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: kinesin complex, microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement

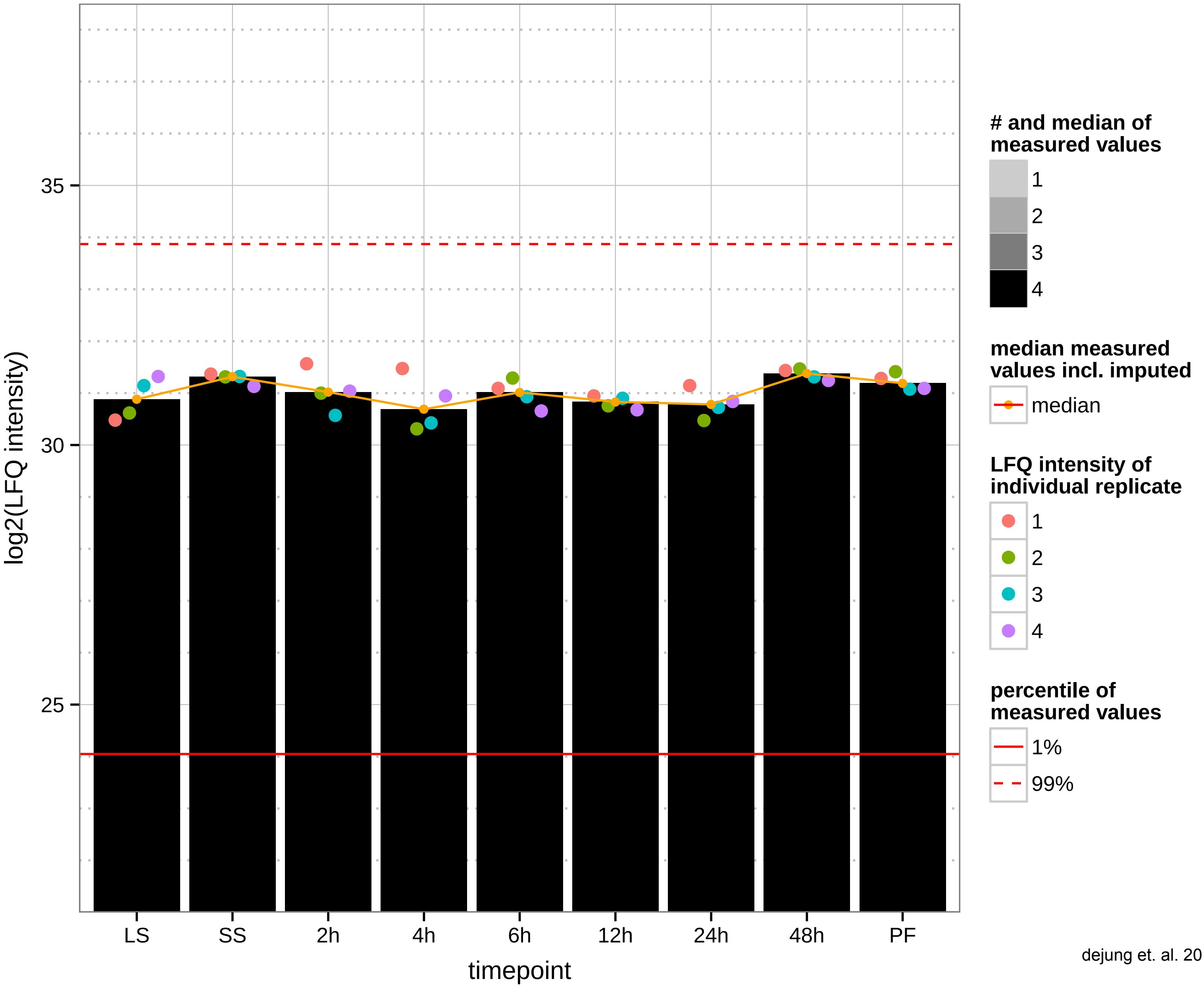




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.6460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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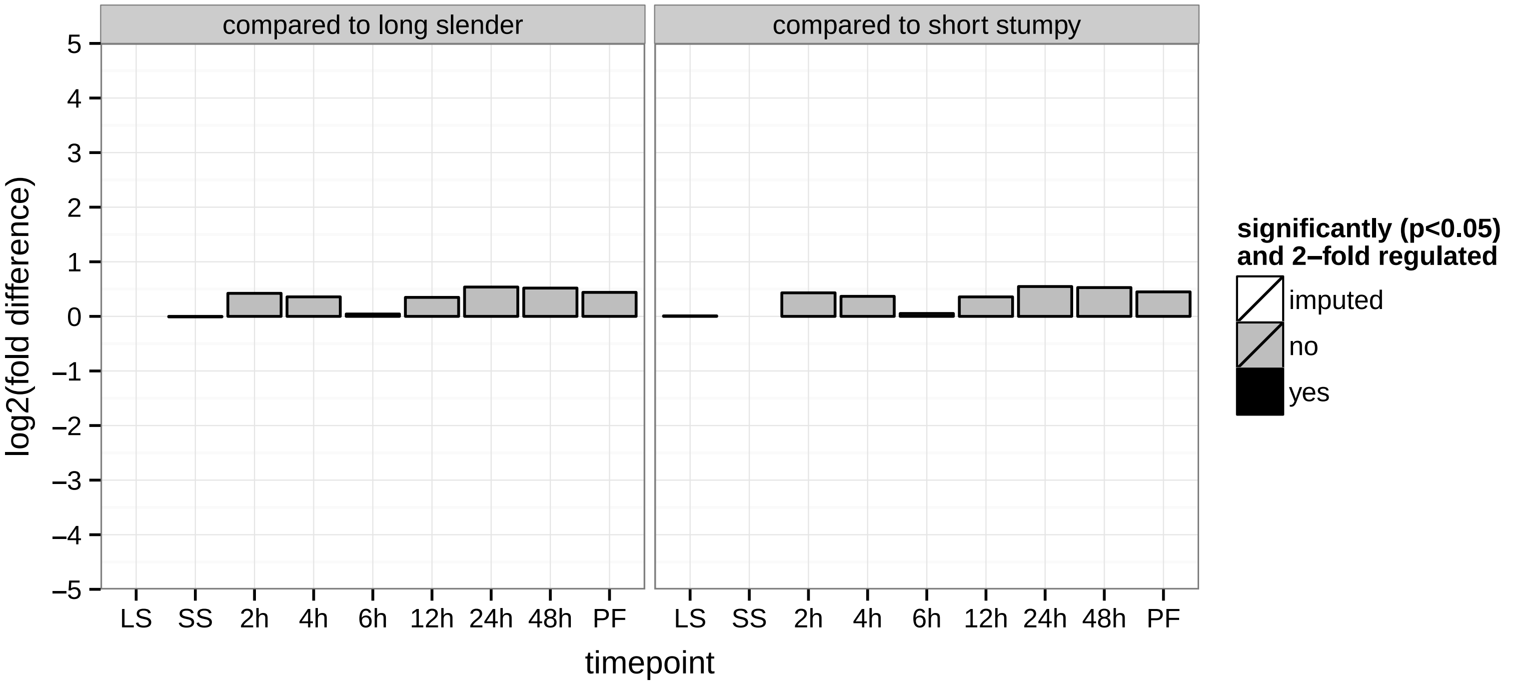
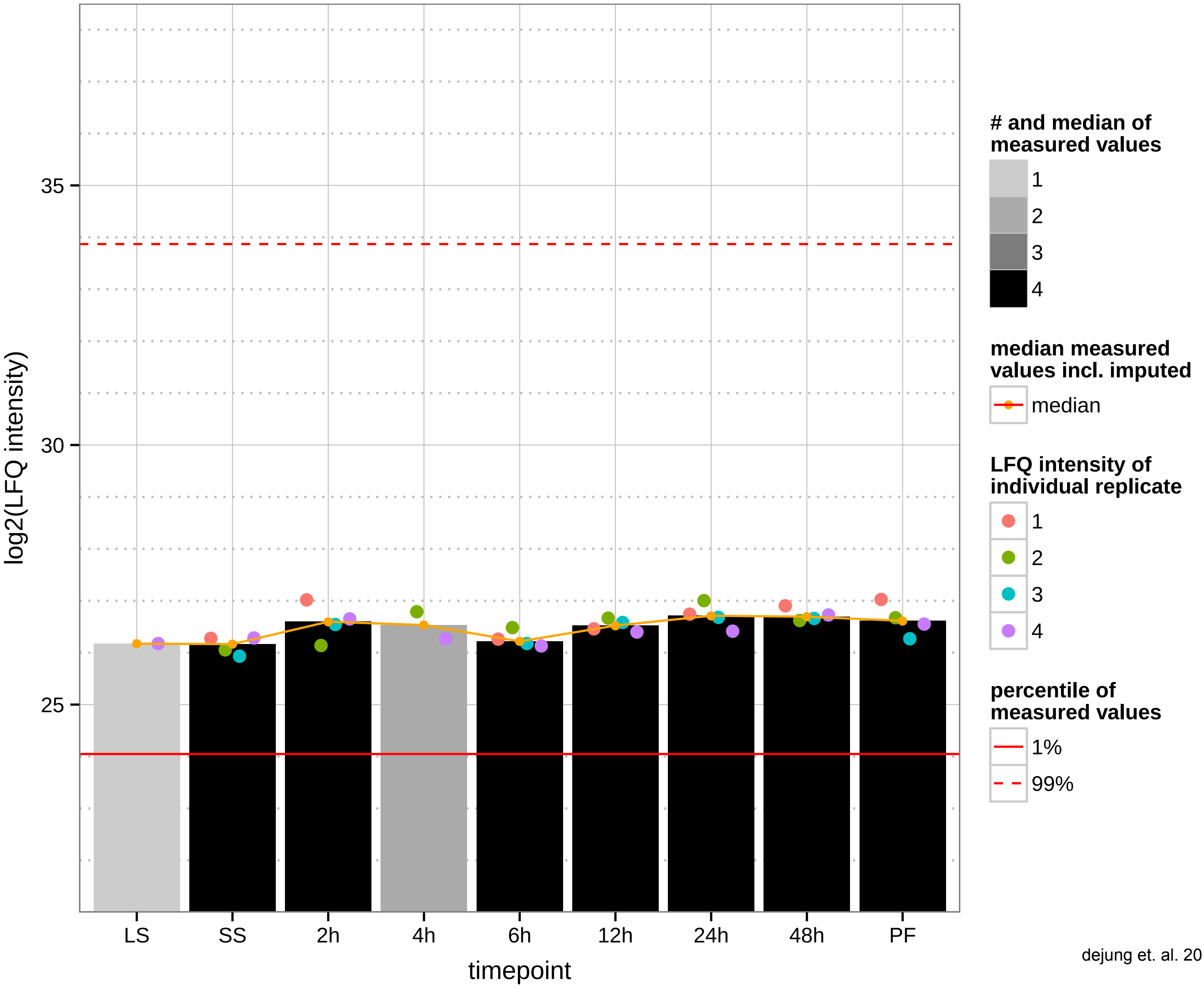
hypothetical protein, conserved
Tb927.11.6470
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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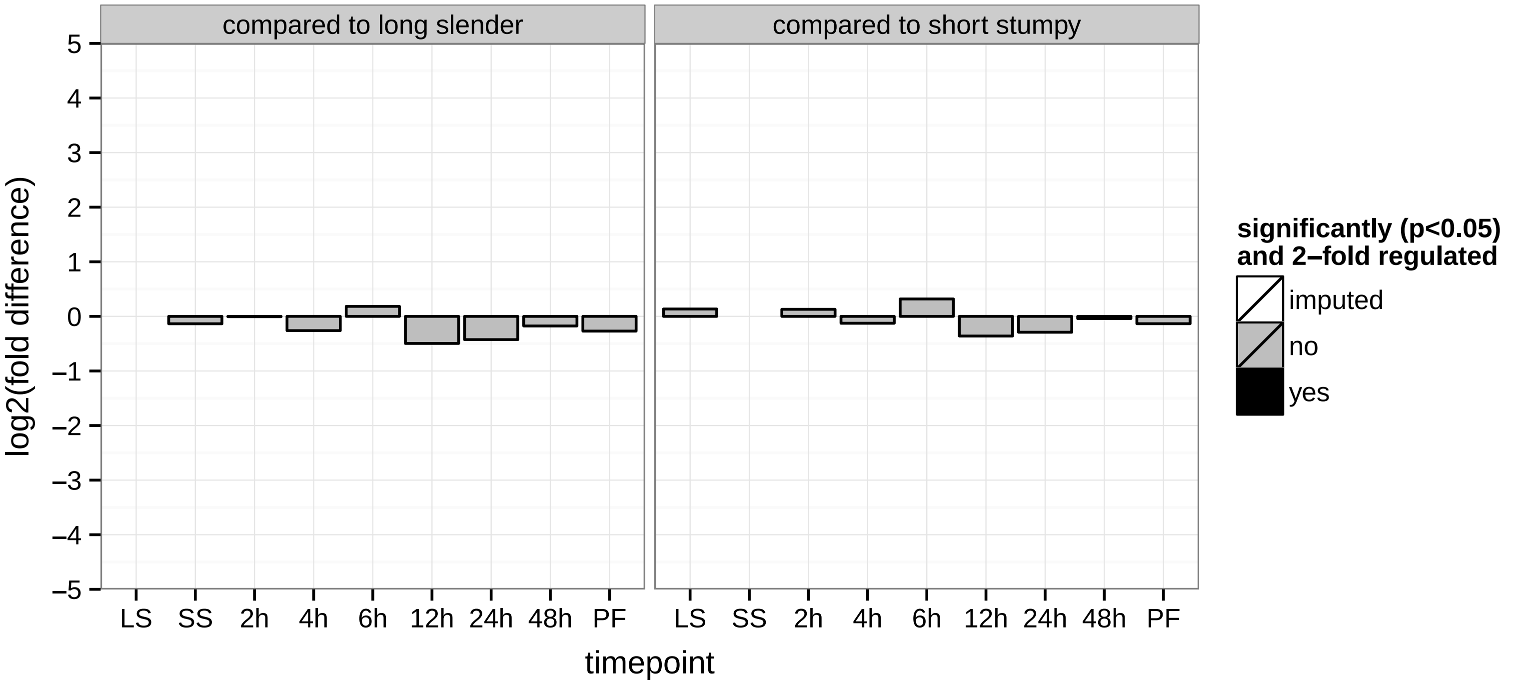
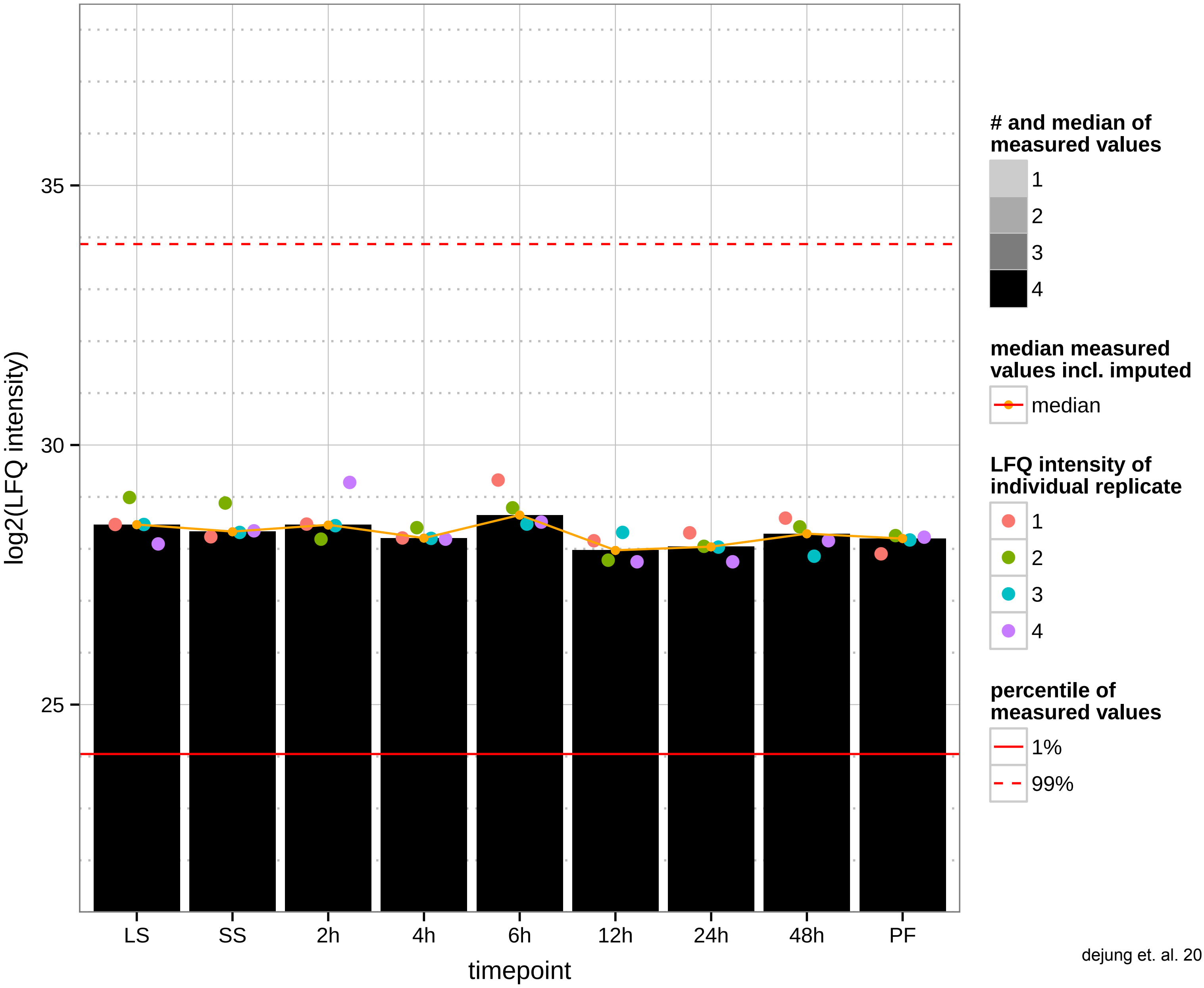
hypothetical protein, conserved
Tb927.11.6530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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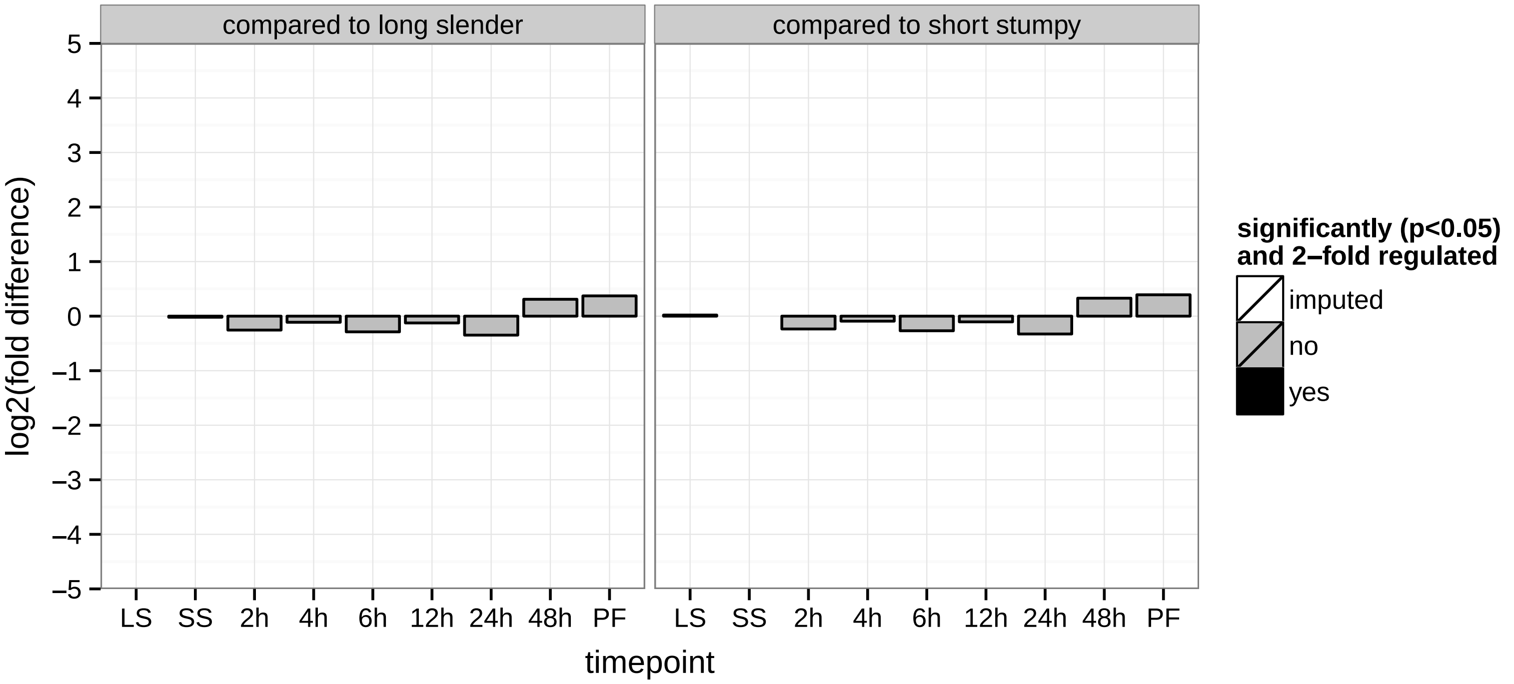
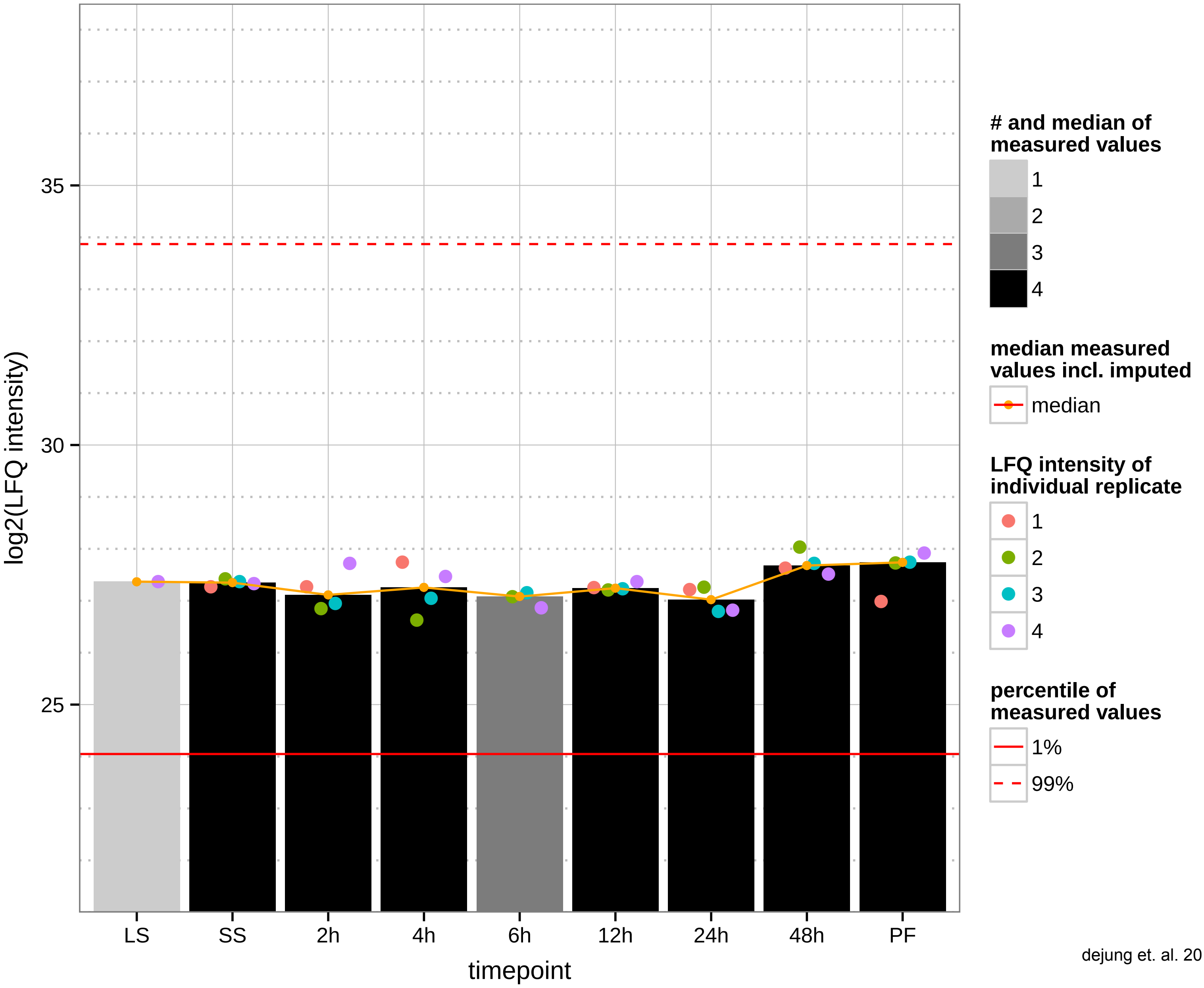
hypothetical protein, conserved
Tb927.11.6600
AGOF: null
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, quorum sensing involved in interaction with ho
PGOF: null
PGOC: null
PGOP: null





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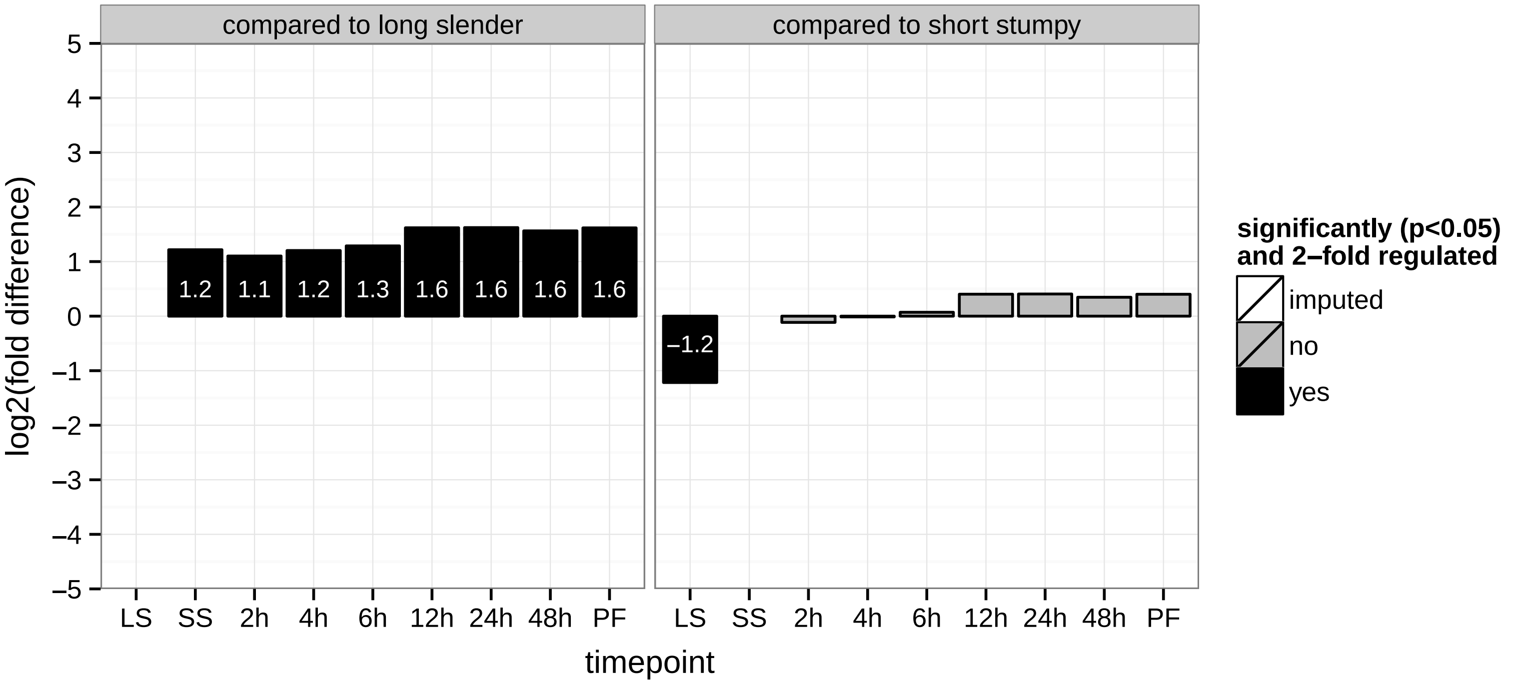
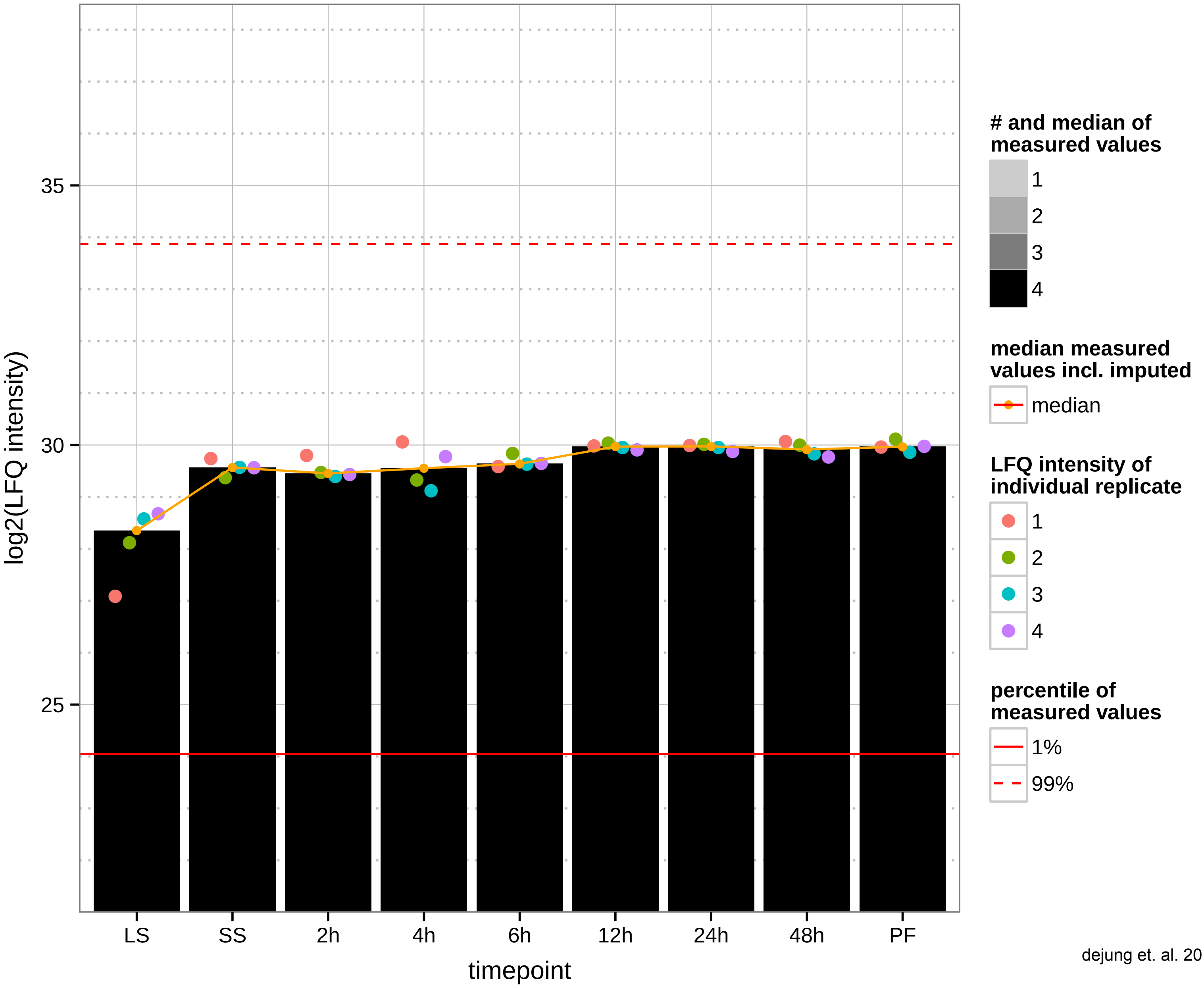
hypothetical protein, conserved
Tb927.11.6610
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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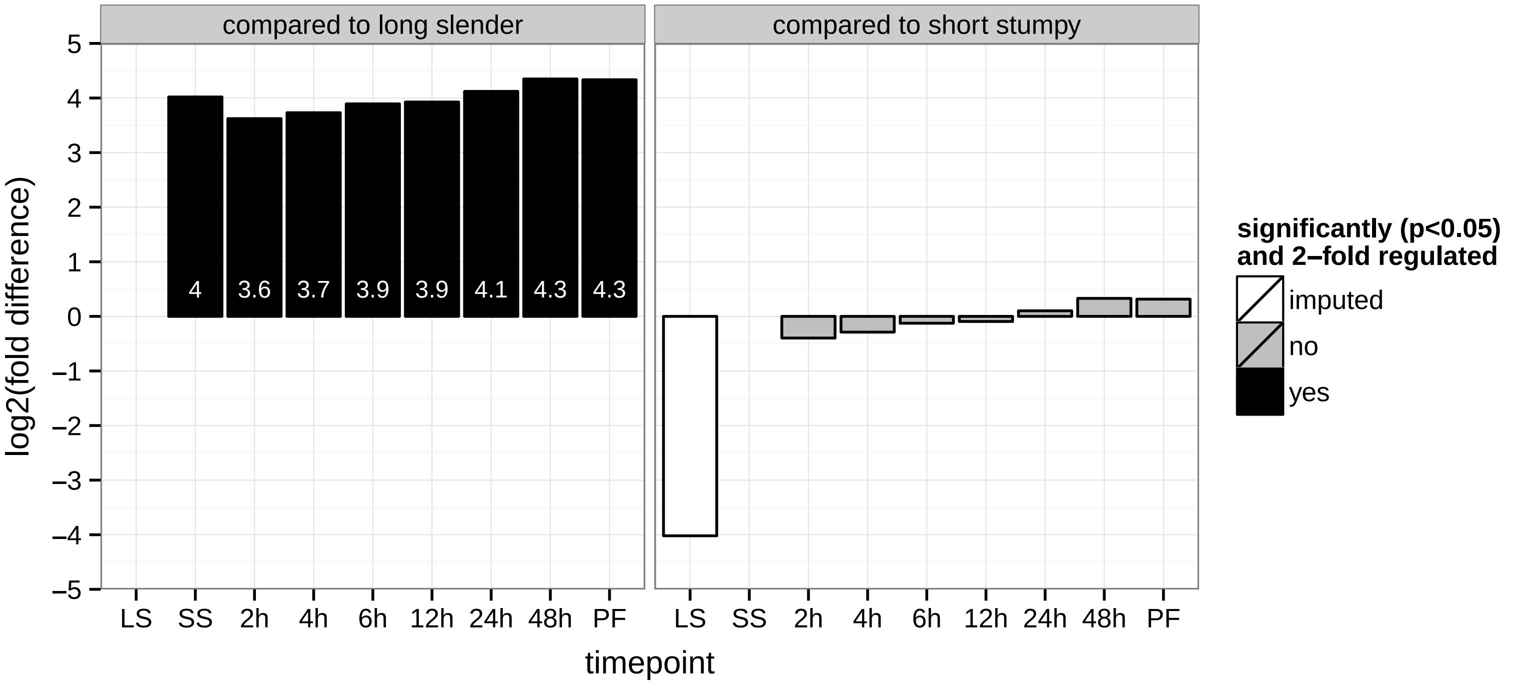
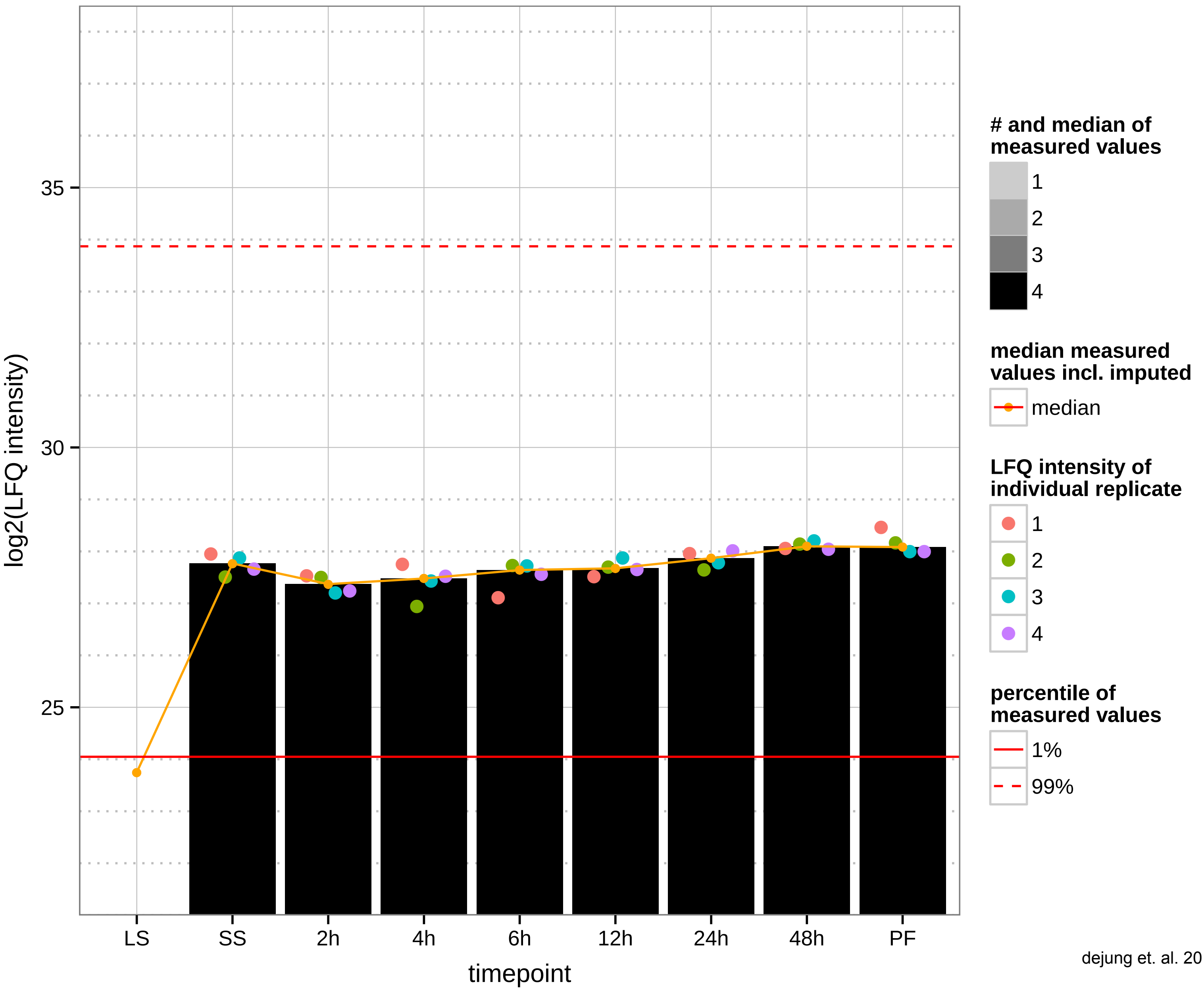
3–methylcrotonoyl–CoA carboxylase beta subunit, putative
Tb927.11.6630
AGOF: methylcrotonoyl–CoA carboxylase activity
AGOC: mitochondrion
AGOP: null
PGOF: ligase activity
PGOC: null
PGOP: null





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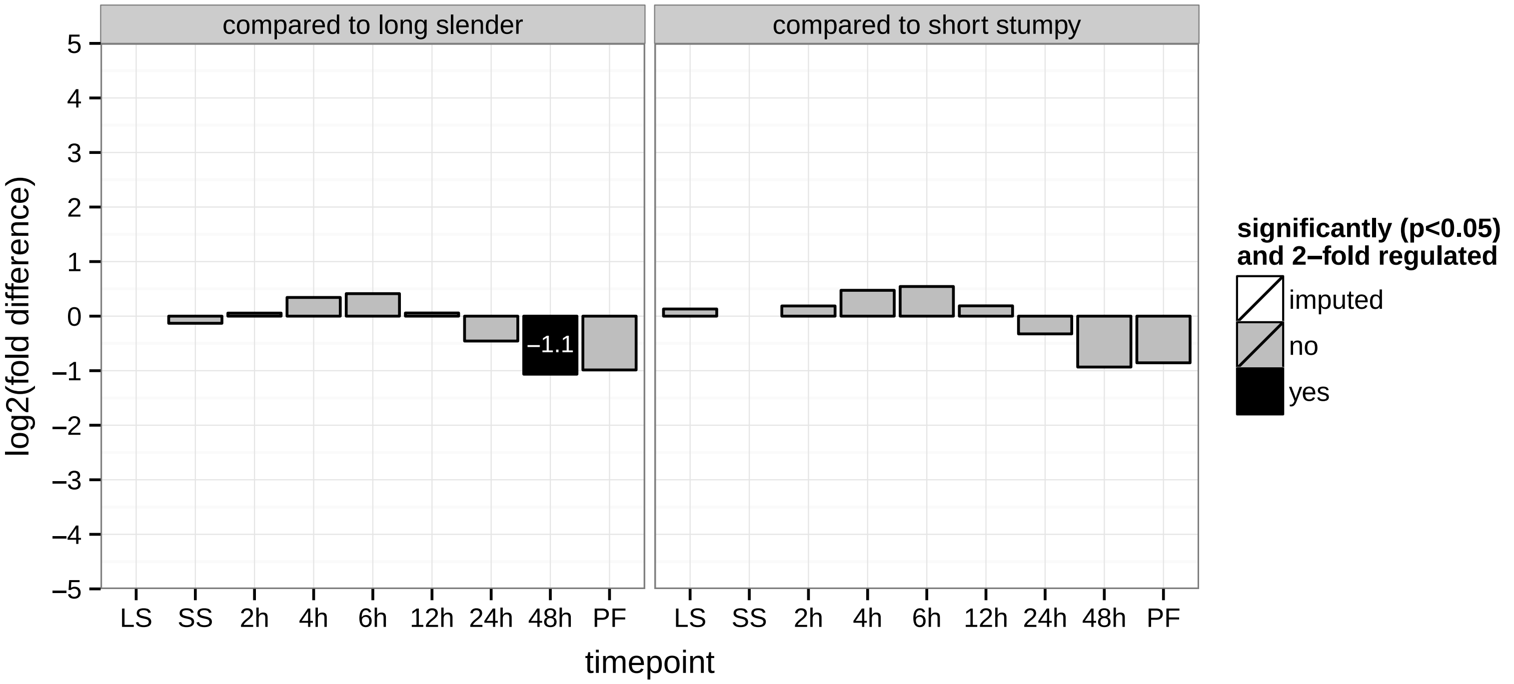
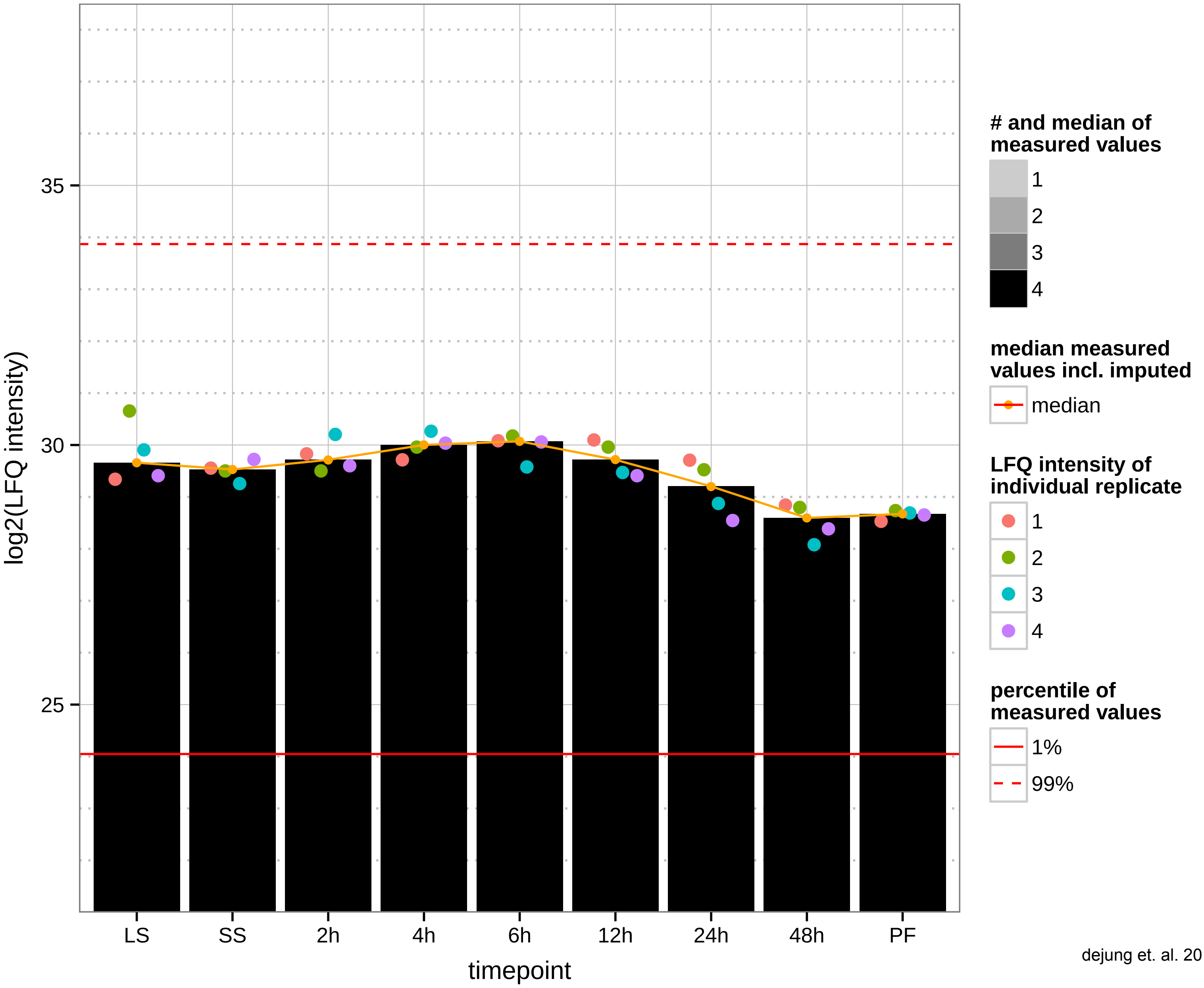
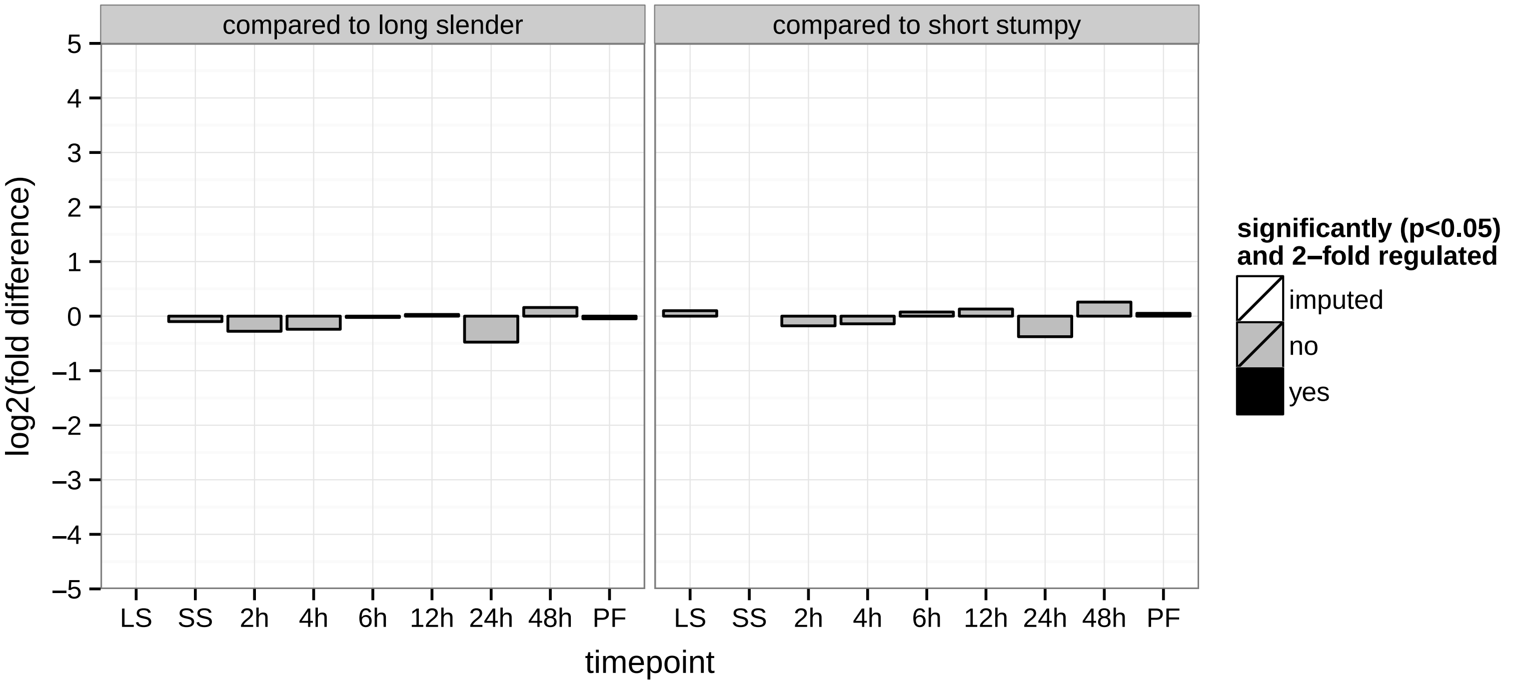
epsin, putative, chrXI additional, unordered contigs, epsinR
Tb927.11.670;Tb11.0890
AGOF: null, clathrin binding
AGOC: null, clathrin coat of coated pit, cytosol, endosome membrane, flagellar pocket
AGOP: null, receptor–mediated endocytosis
PGOF: null
PGOC: null
PGOP: null

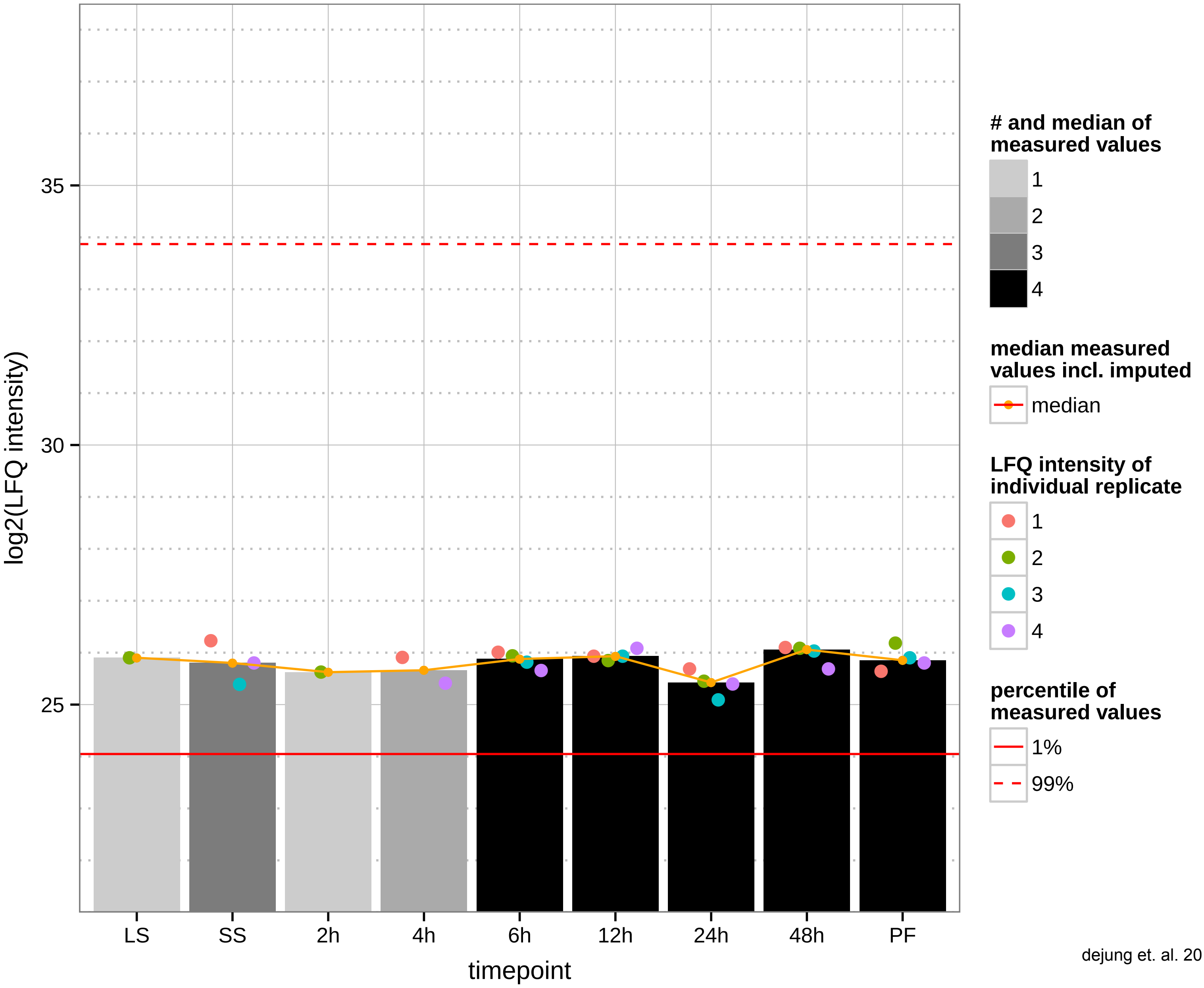




dejung et. al. 2015

predicted tetratricopeptide repeat (TPR) protein
Tb927.11.6710
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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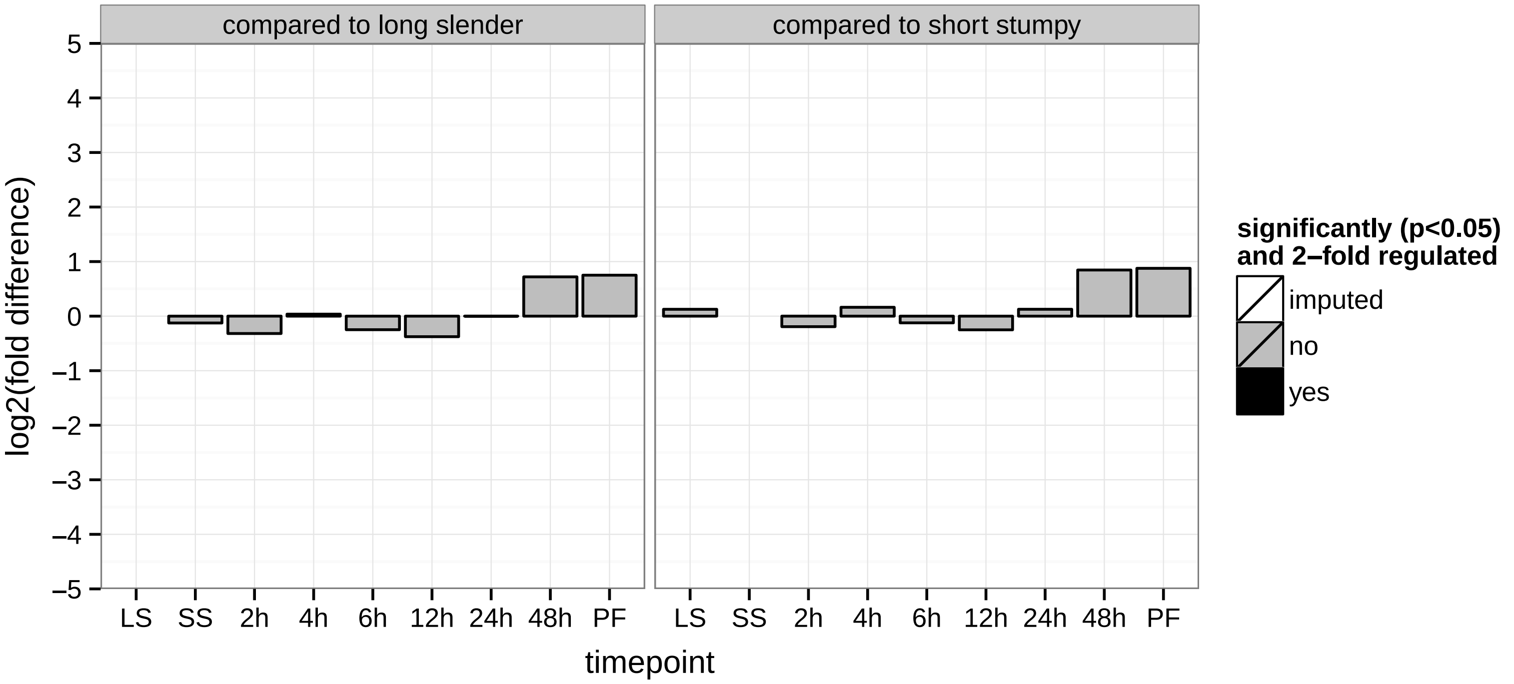
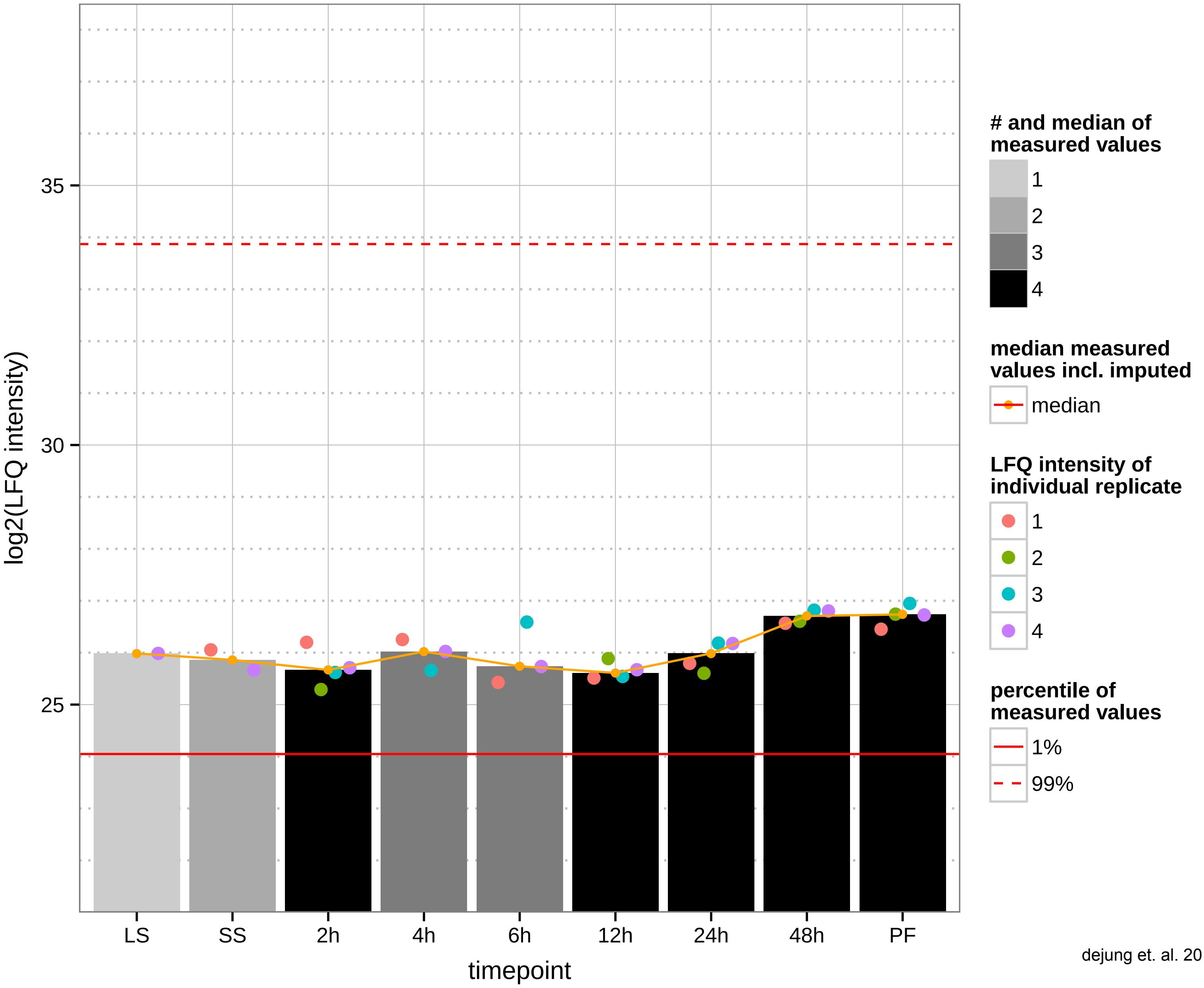
chromatin binding protein, putative, regulator of chromatin condensation, putative (RCC1)
Tb927.11.6780
AGOF: Ran GTPase binding, chromatin binding
AGOC: null
AGOP: chromosome organization
PGOF: null
PGOC: null
PGOP: null





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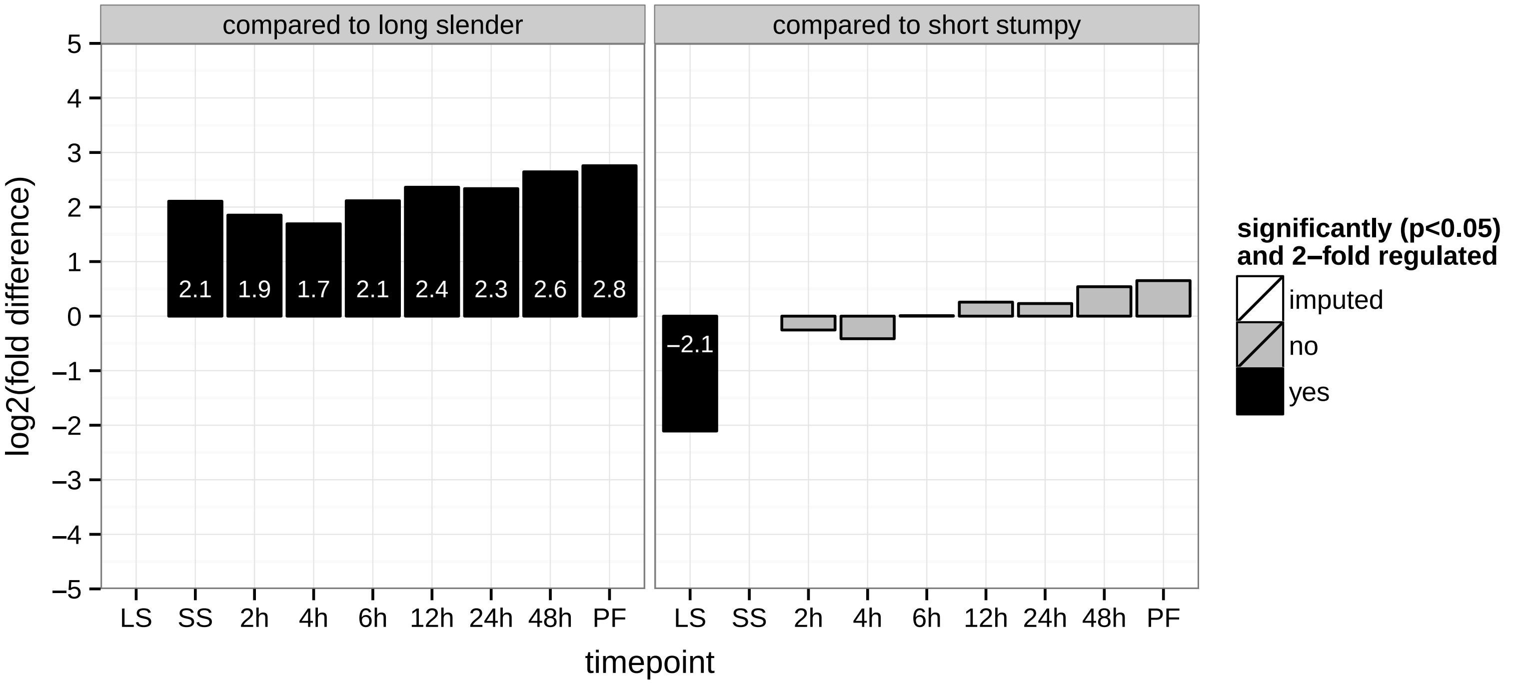
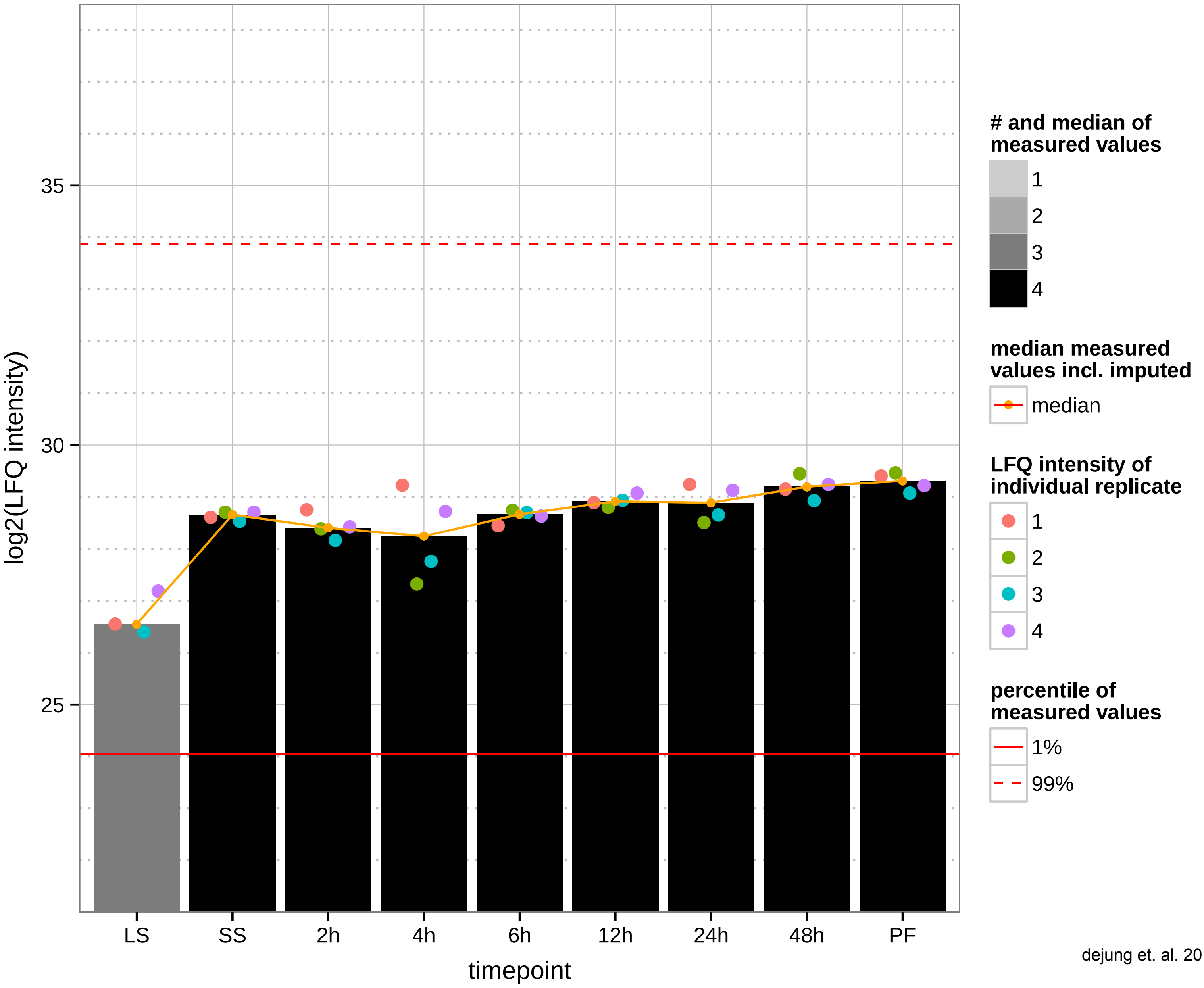
predicted WD40 repeat protein
Tb927.11.6790
AGOF: null
AGOC: nucleus
AGOP: rRNA processing
PGOF: protein binding
PGOC: null
PGOP: rRNA processing, regulation of cell cycle





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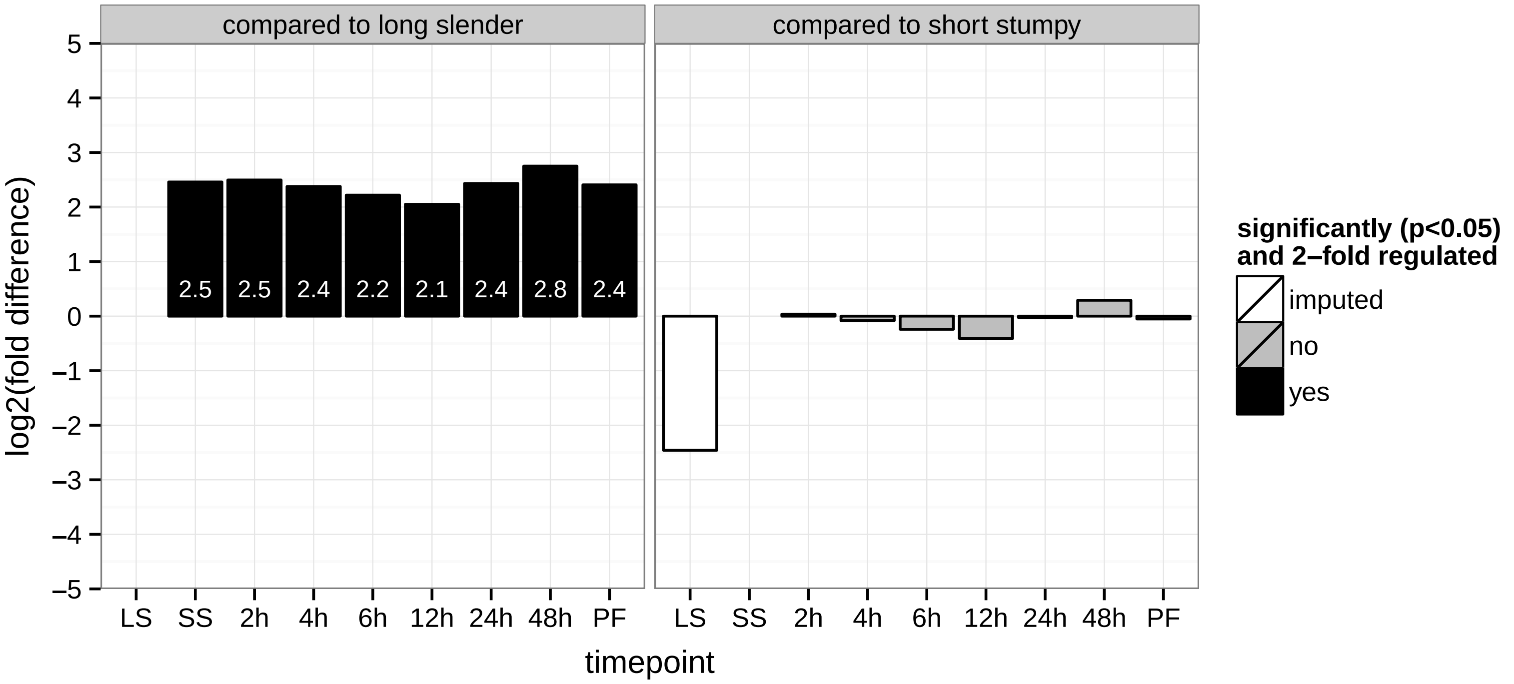
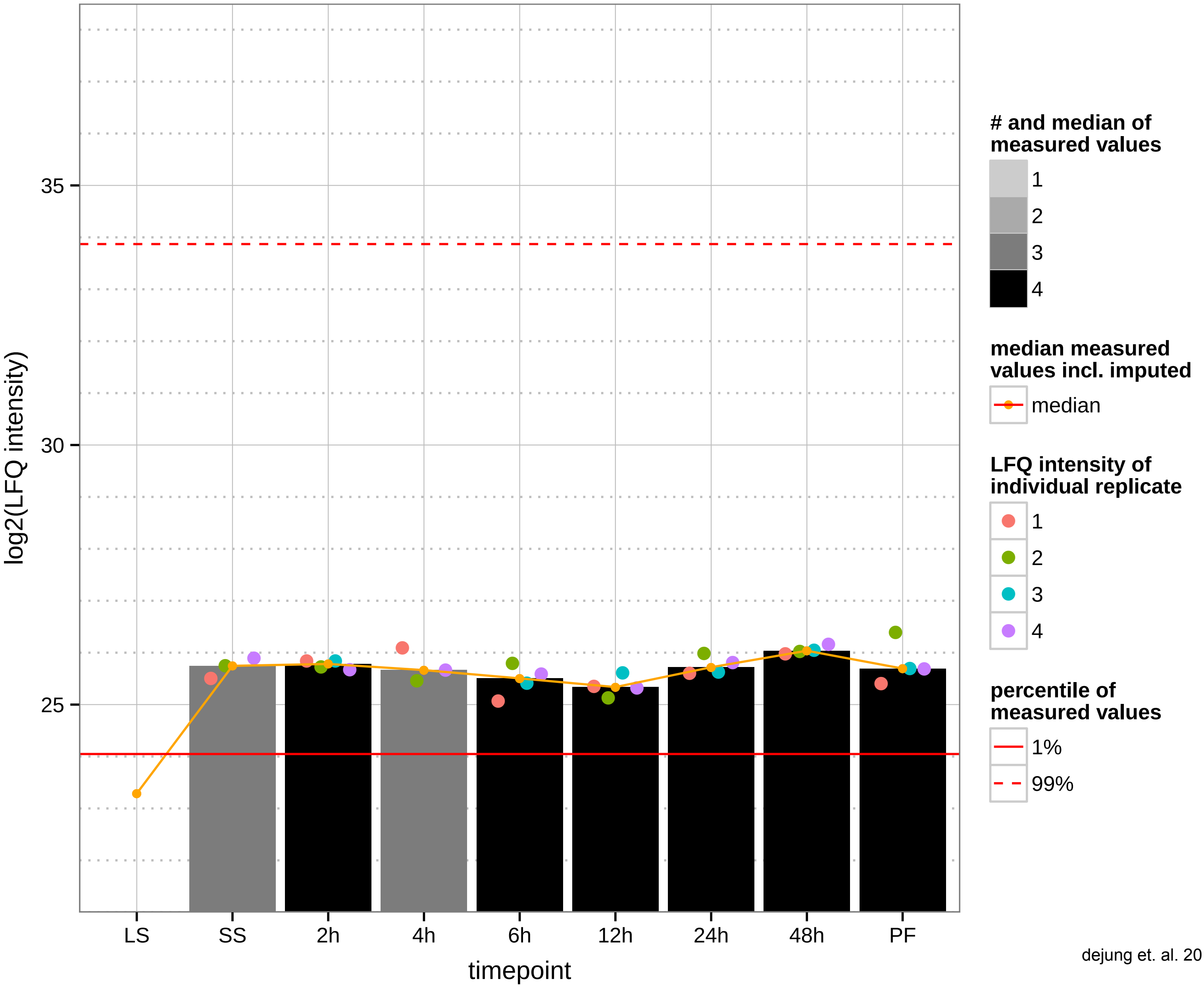
hypothetical protein, conserved
Tb927.11.6820;Tb11.v5.0900
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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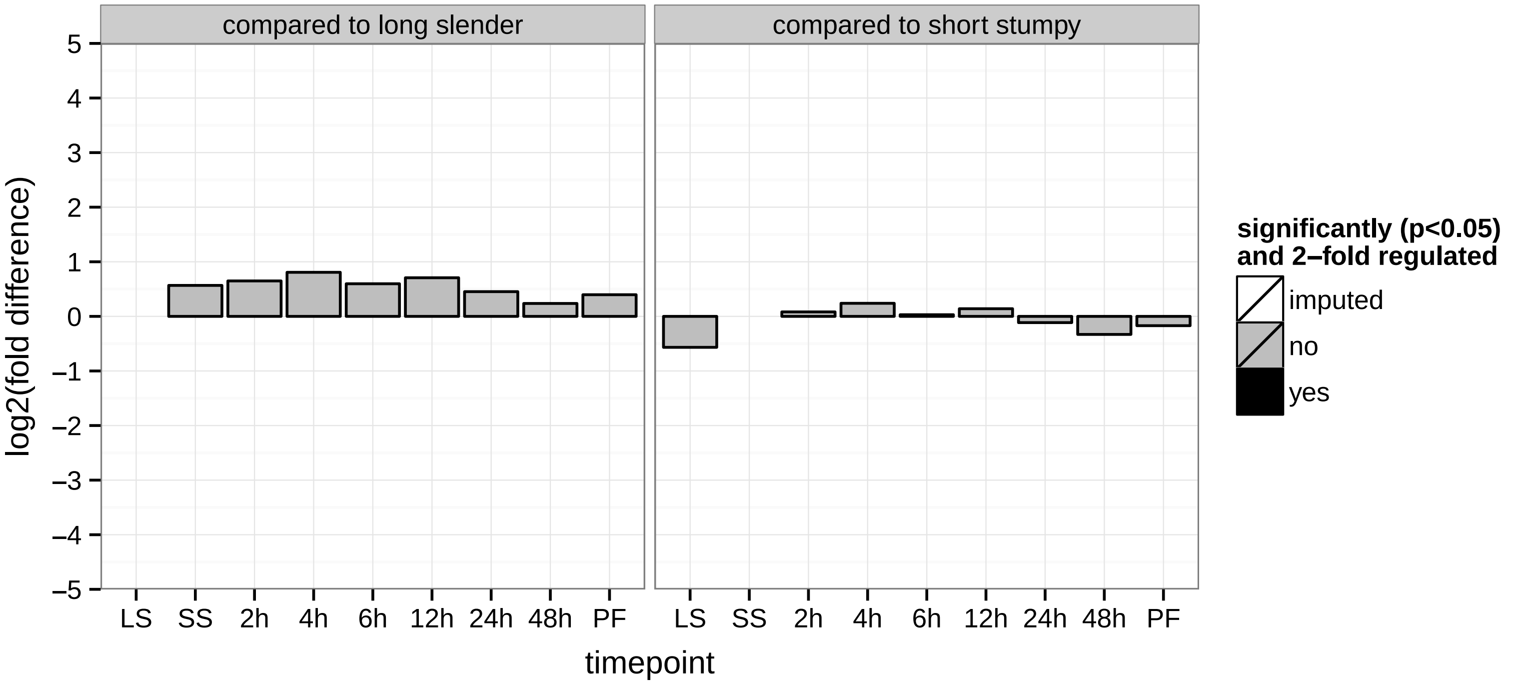
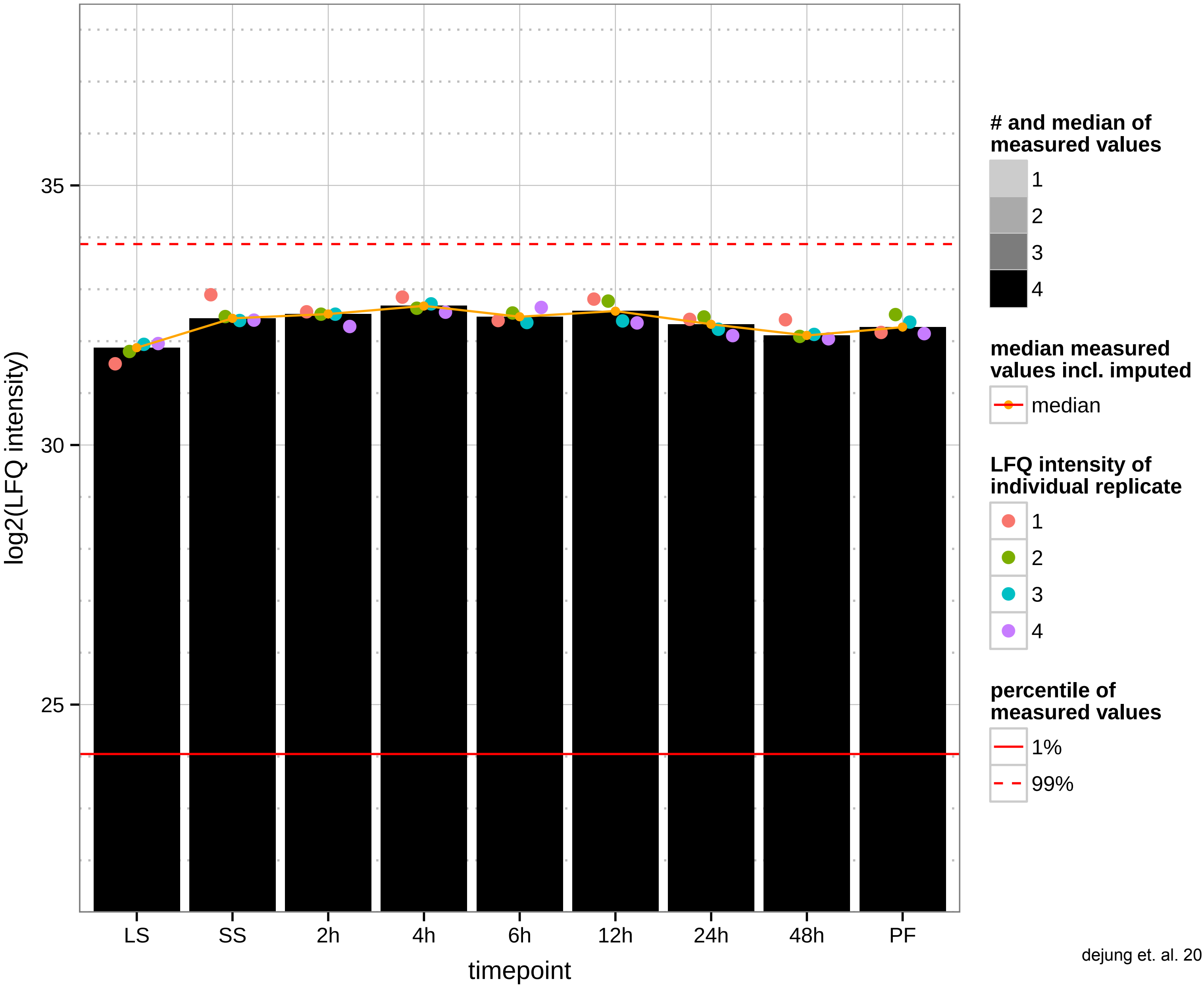
14–3–3 protein
Tb927.11.6870
AGOF: protein binding, protein domain specific binding, protein phosphorylated amino acid binding
AGOC: eukaryotic translation initiation factor 4F complex, nucleus
AGOP: DNA damage checkpoint, endocytosis, regulation of mitosis
PGOF: protein domain specific binding
PGOC: null
PGOP: null





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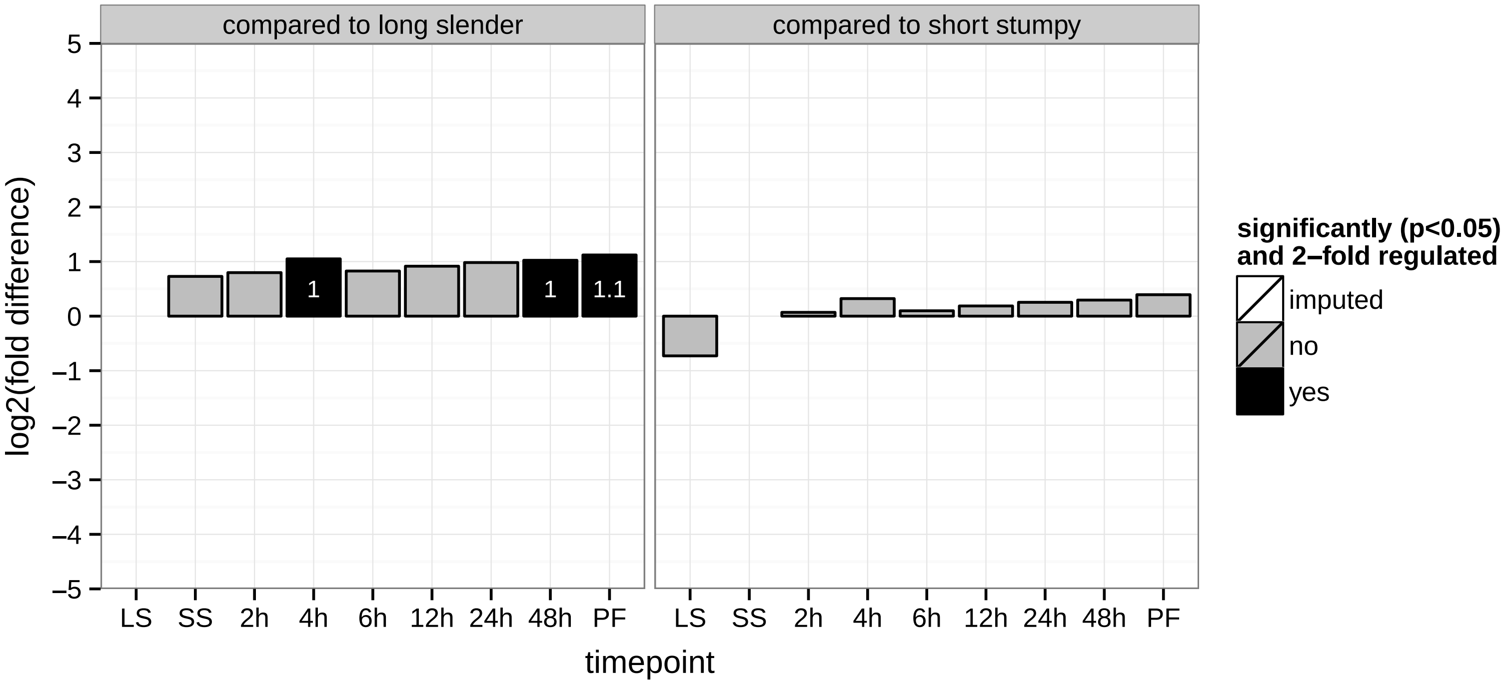
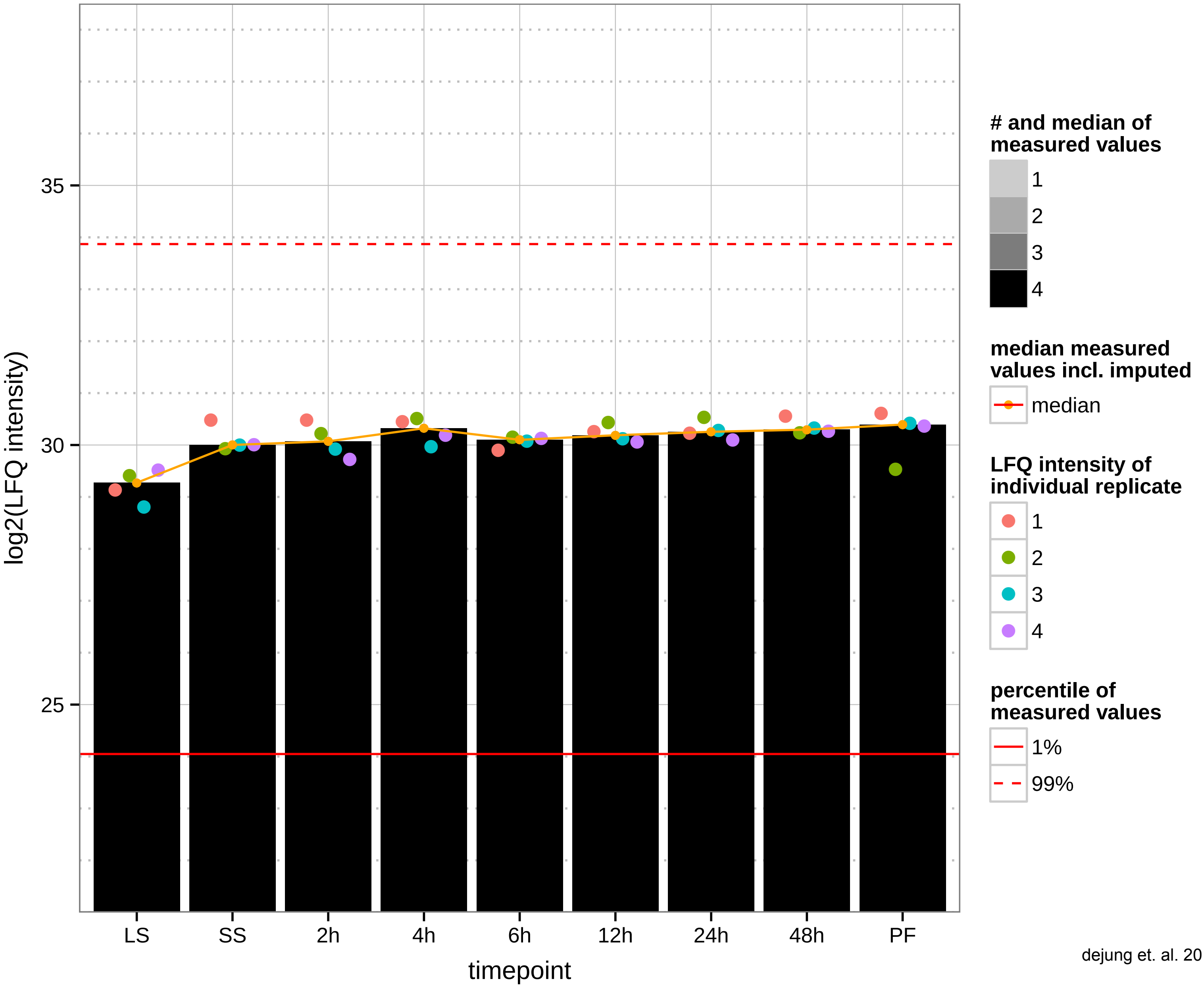
proteasome alpha 7 subunit, putative (PSA4)
Tb927.11.7020
AGOF: threonine–type endopeptidase activity
AGOC: cytosol, nucleus, proteasome core complex
AGOP: ubiquitin–dependent protein catabolic process
PGOF: endopeptidase activity, threonine–type endopeptidase activity
PGOC: proteasome core complex, proteasome core complex, alpha–subunit complex
PGOP: proteolysis involved in cellular protein catabolic process, ubiquitin–dependent protein catabolic process





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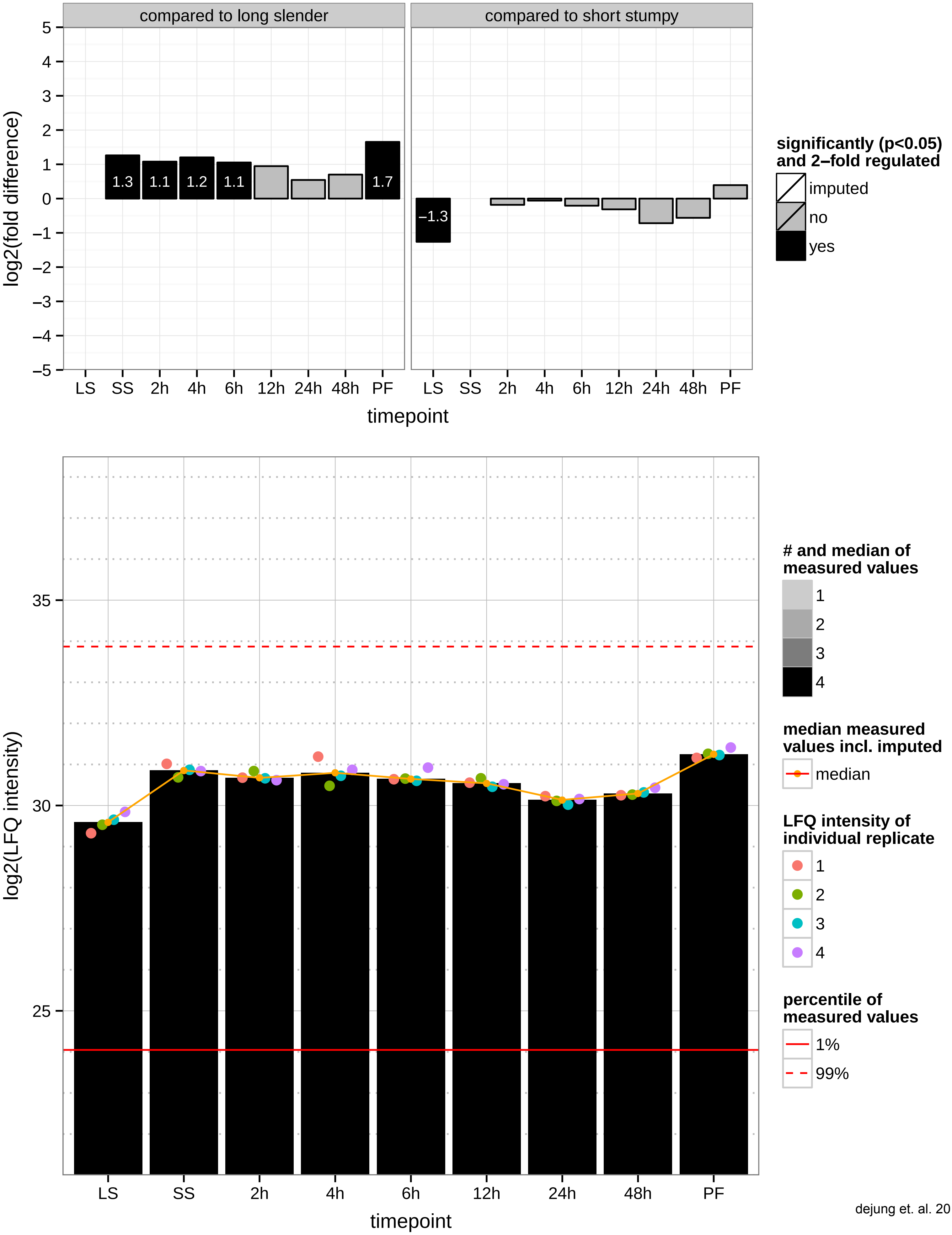
acidocalcisomal pyrophosphatase
Tb927.11.7060
AGOF: inorganic diphosphatase activity, magnesium ion binding, pyrophosphatase activity
AGOC: cytoplasm, membrane
AGOP: metabolic process, phosphate−containing compound metabolic process
PGOF: inorganic diphosphatase activity, magnesium ion binding
PGOC: cytoplasm
PGOP: phosphate−containing compound metabolic process



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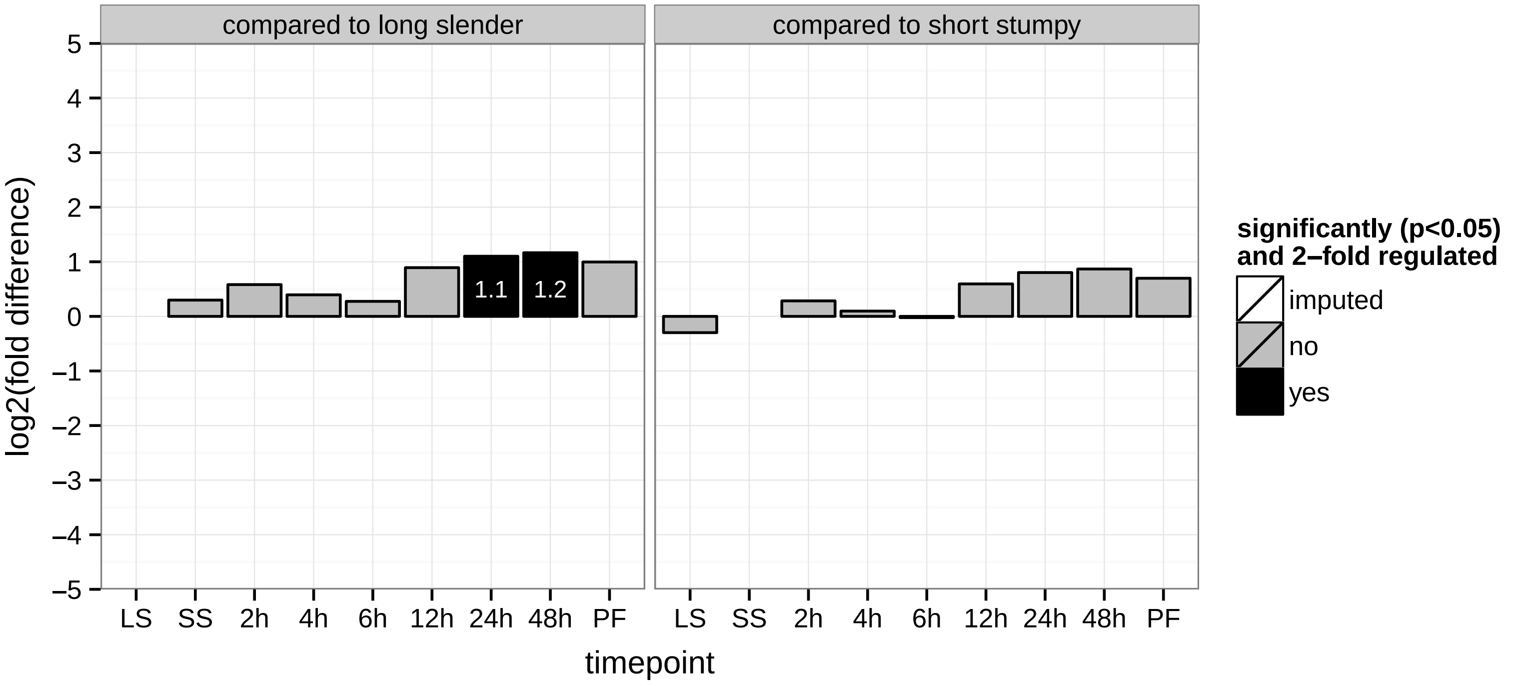
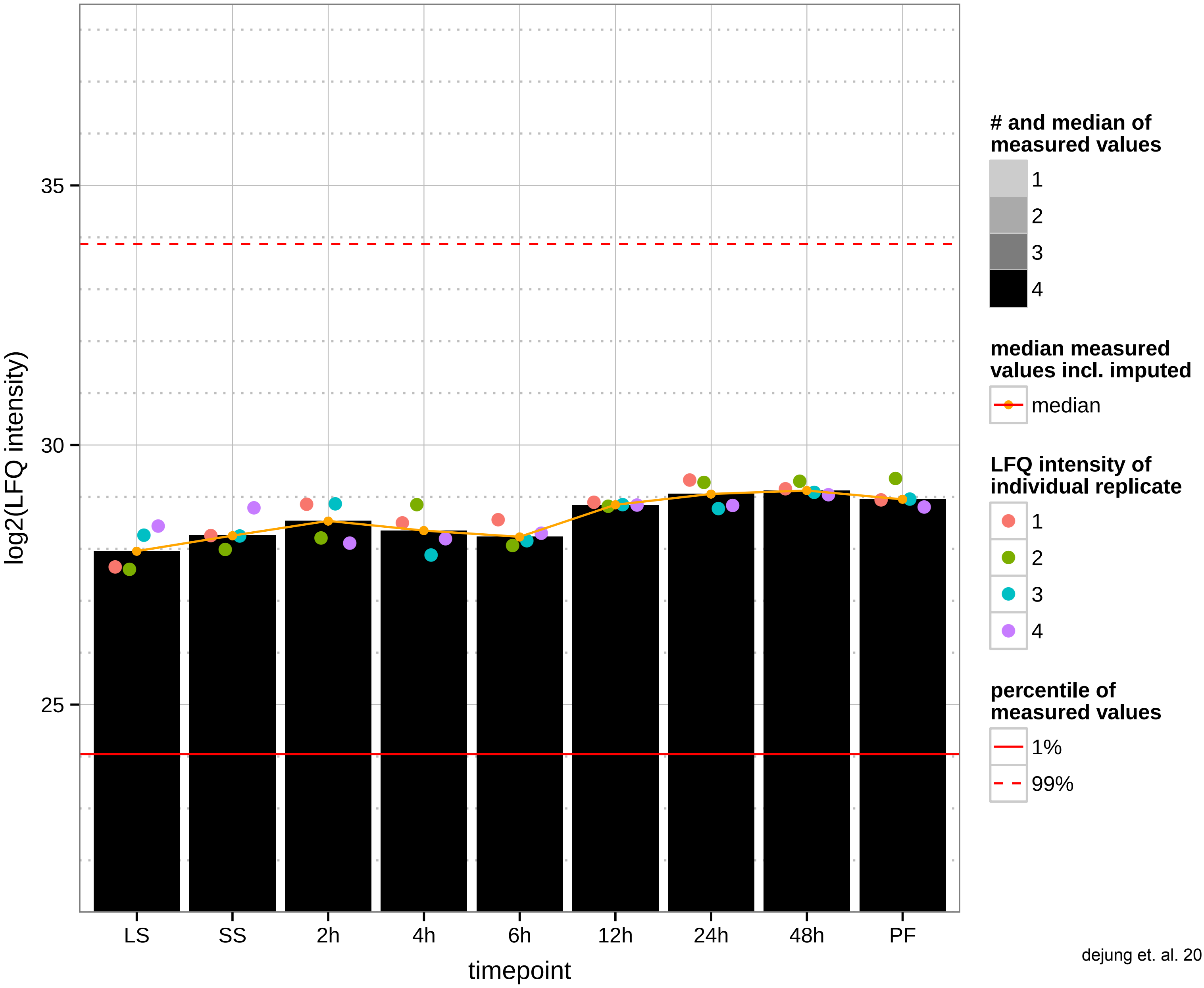
cytoplasmic translation machinery associated protein, putative
Tb927.11.7100
AGOF: RNA binding
AGOC: cytosol, ribosome
AGOP: ribosome biogenesis
PGOF: RNA binding
PGOC: null
PGOP: null





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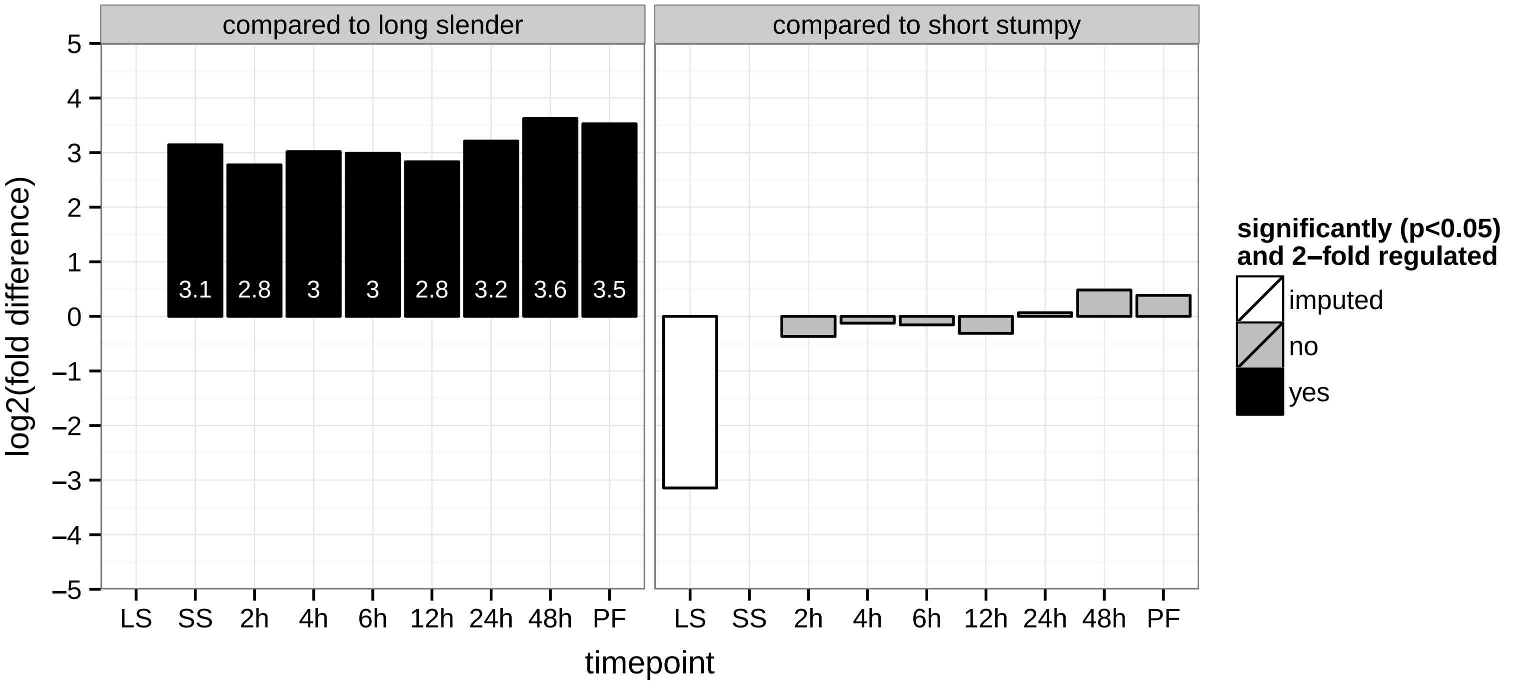
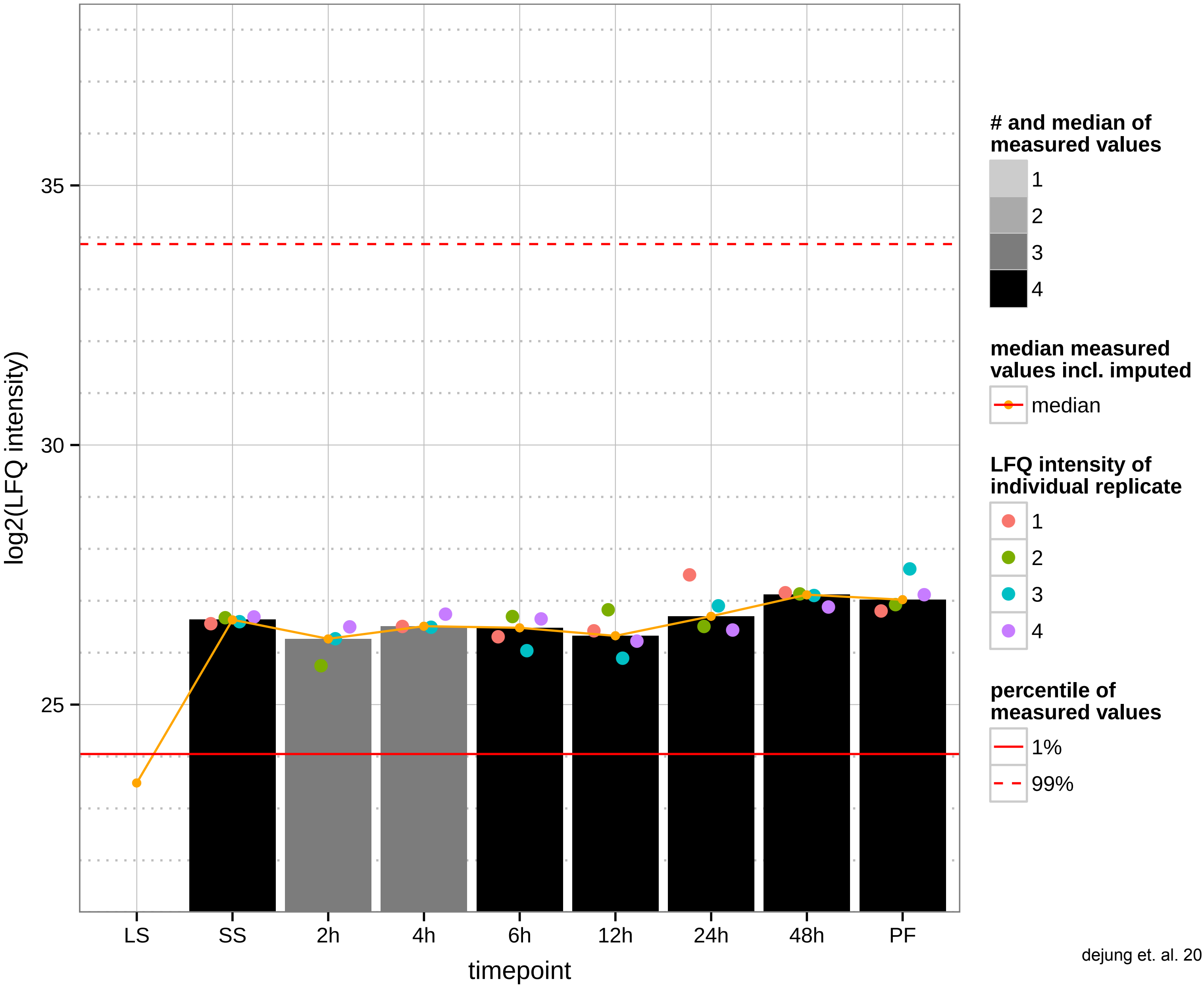
cell cycle sequence binding phosphoprotein (RBP45), putative
Tb927.11.7140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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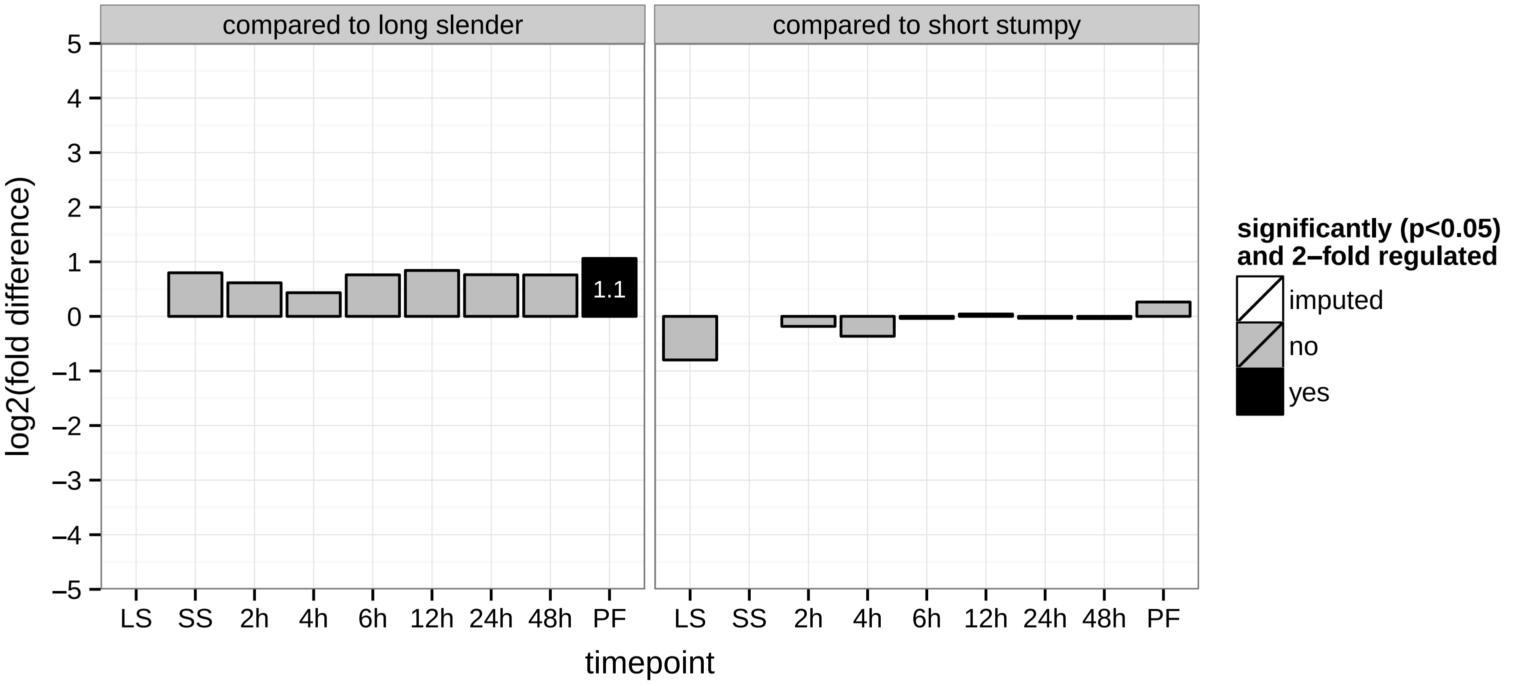
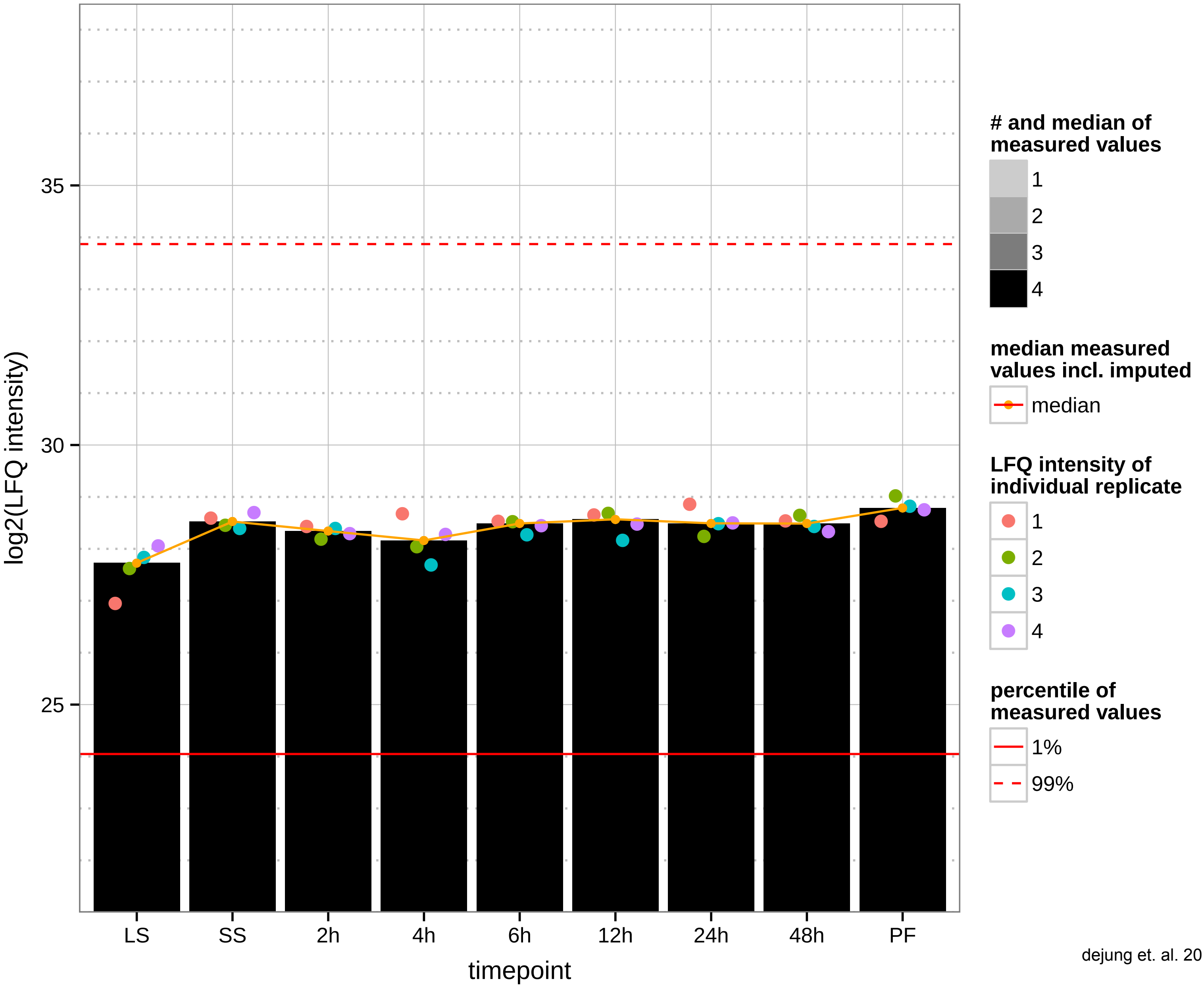
NGG1 interacting factor 3–like
Tb927.11.7150
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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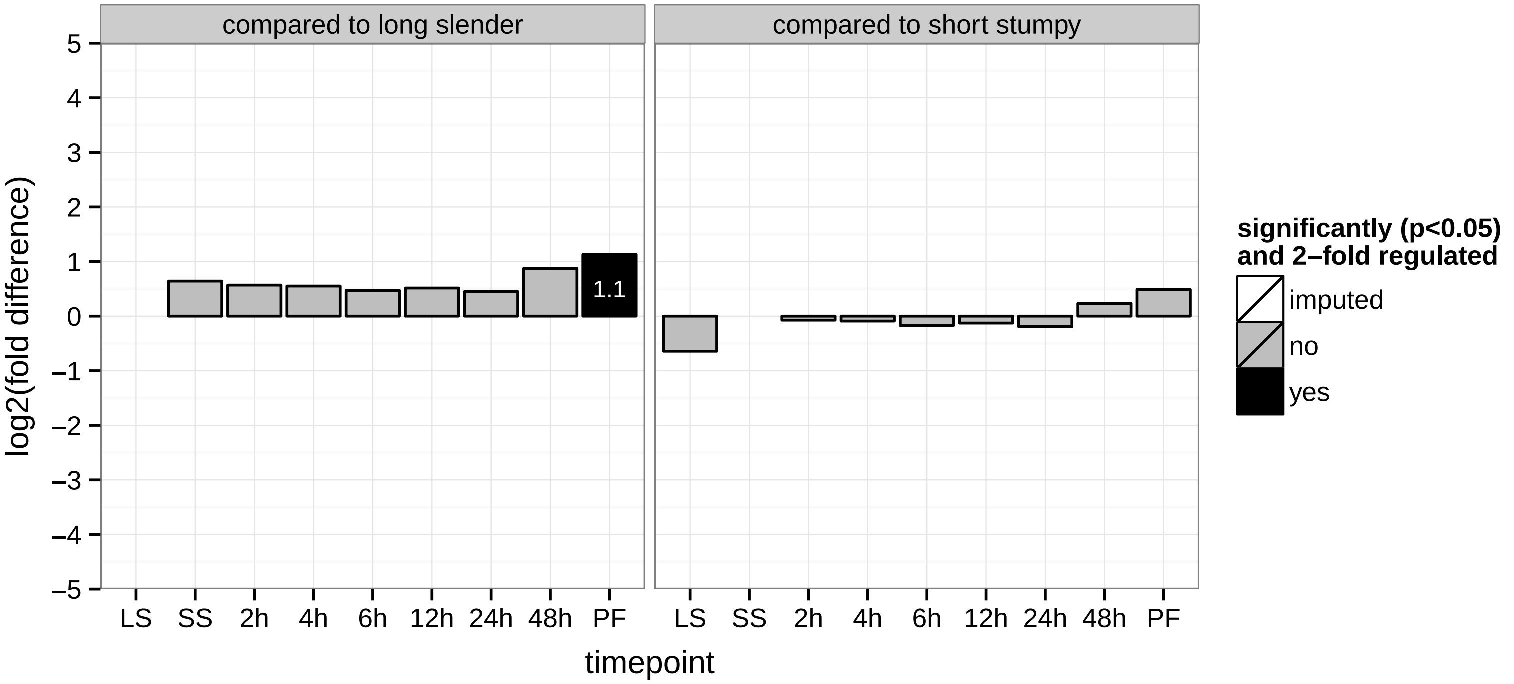
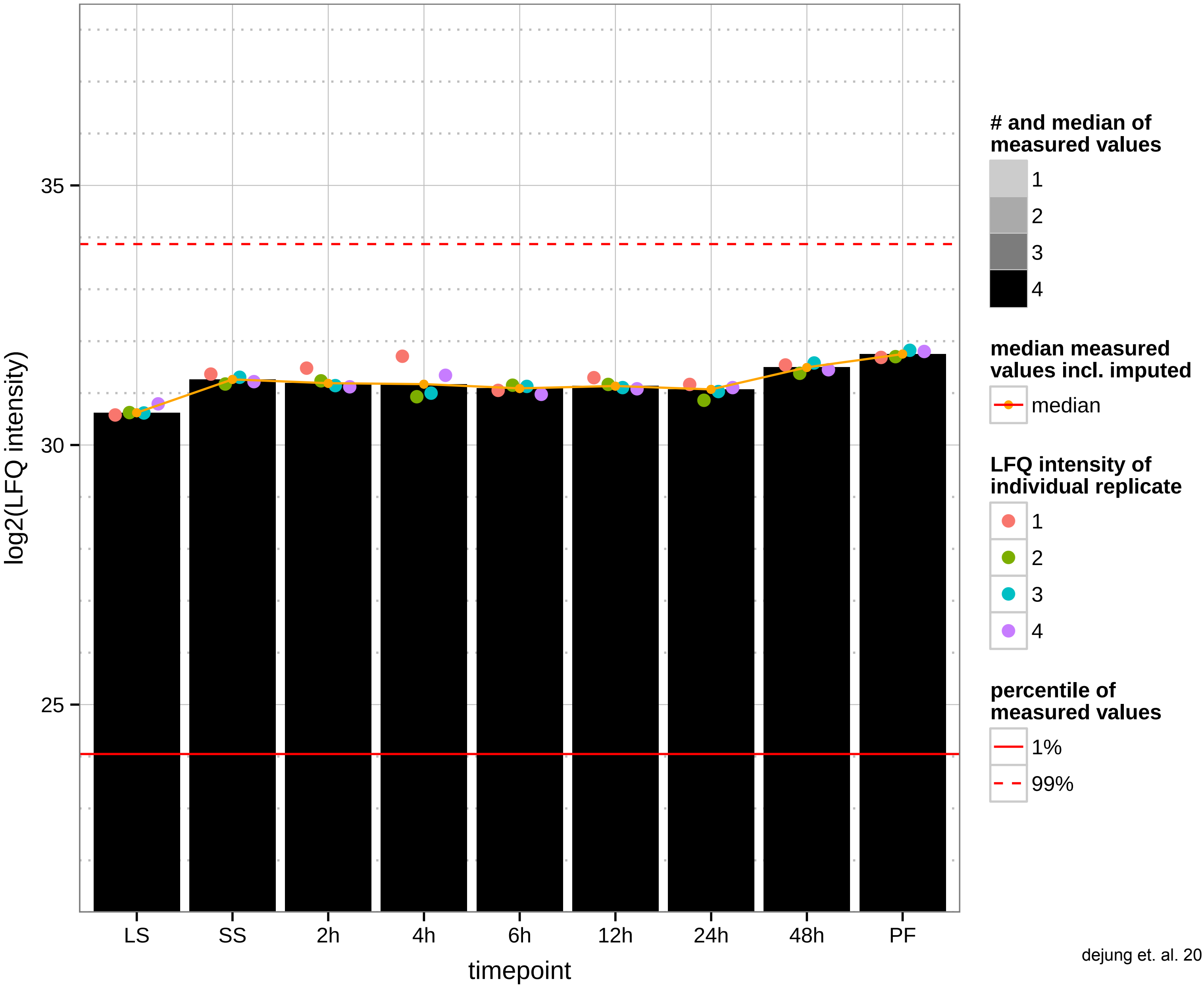
seryl–tRNA synthetase
Tb927.11.7170
AGOF: ATP binding, serine–tRNA ligase activity
AGOC: cytoplasm, cytosol, mitochondrion
AGOP: seryl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, nucleotide binding, serine–tRNA ligase activity
PGOC: cytoplasm
PGOP: seryl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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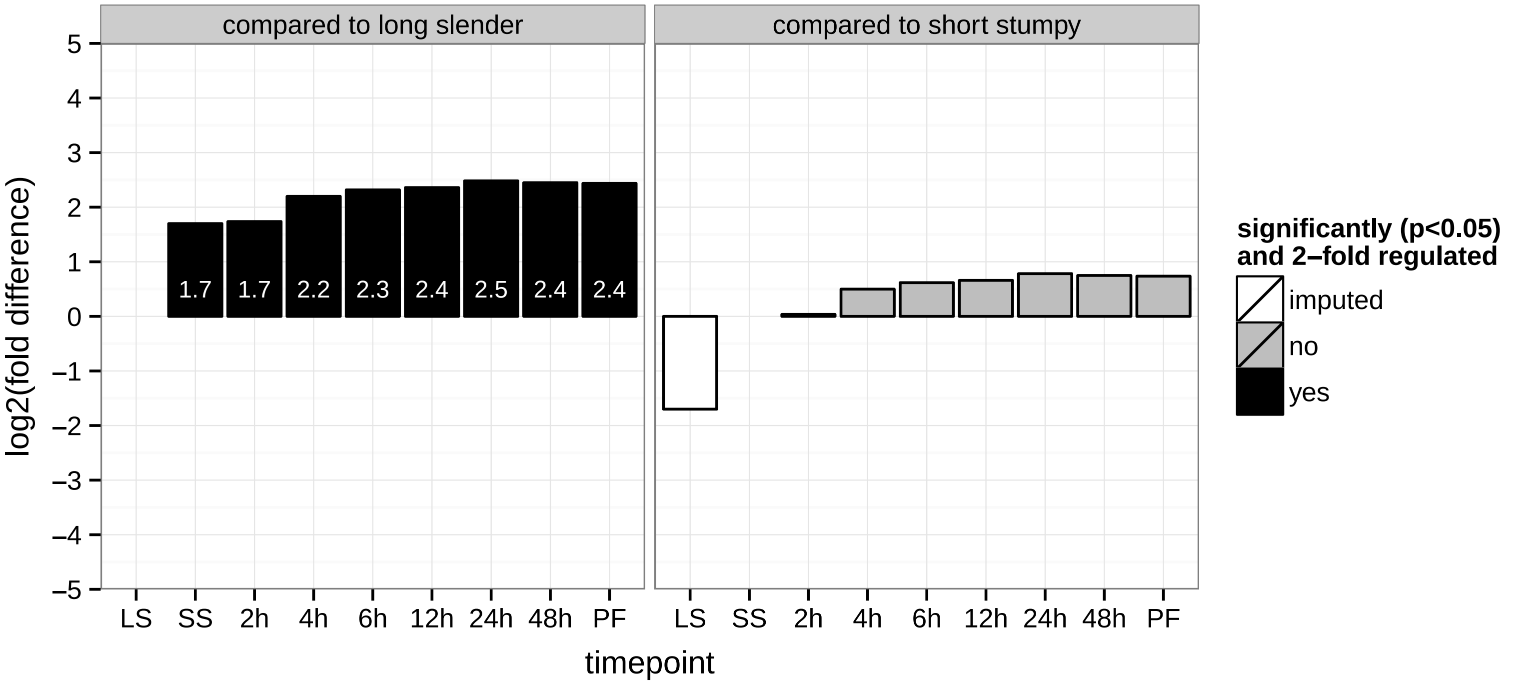
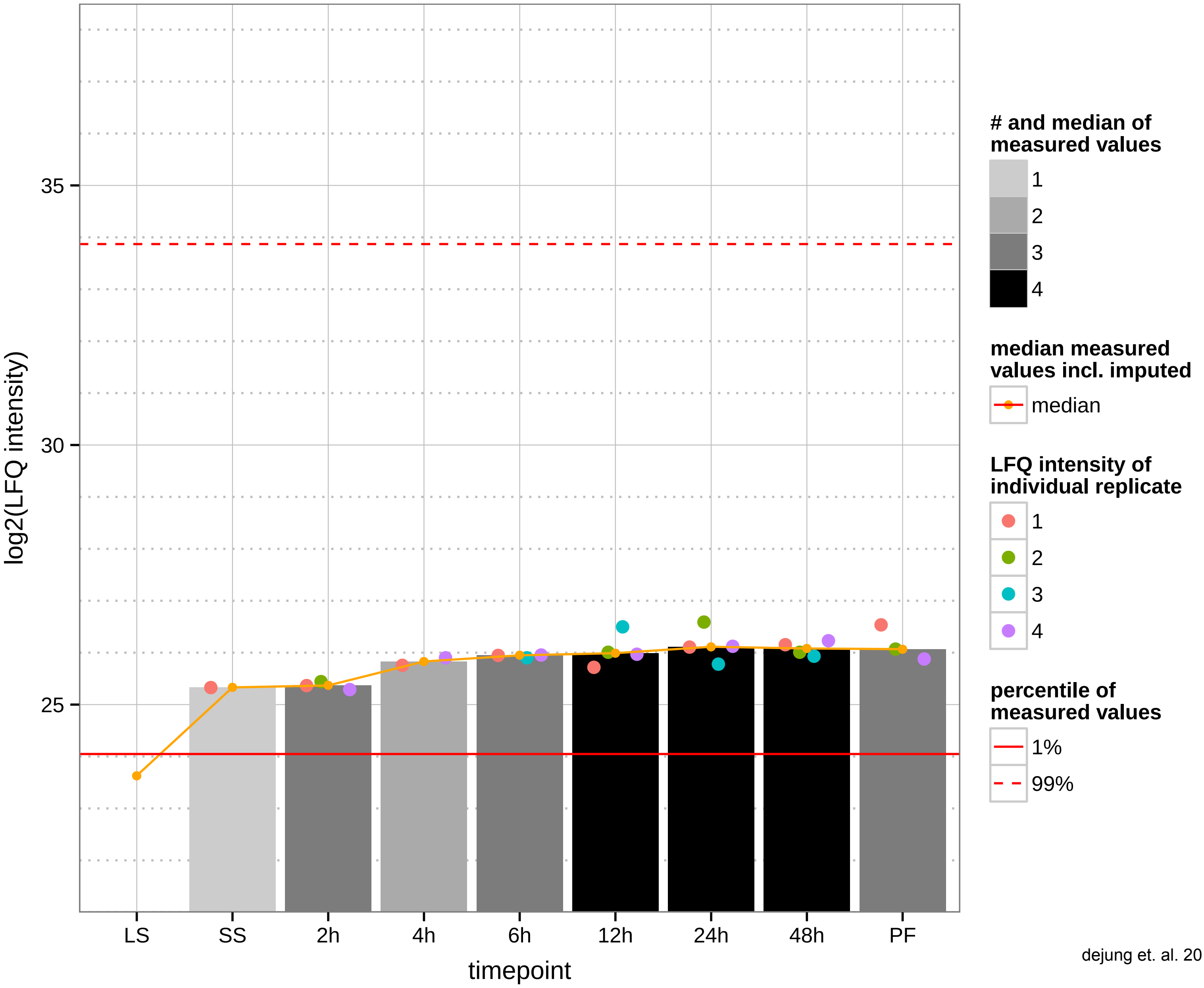
hypothetical protein
Tb927.11.7190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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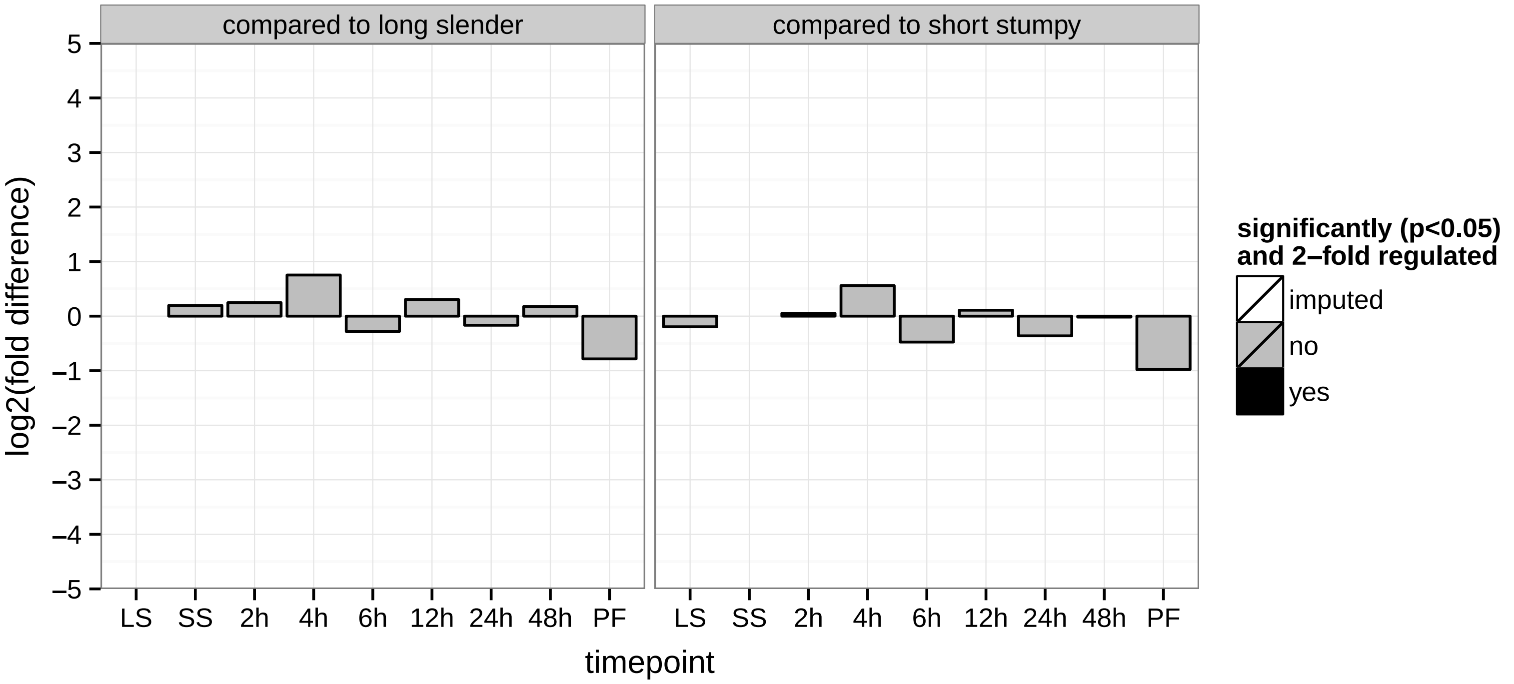
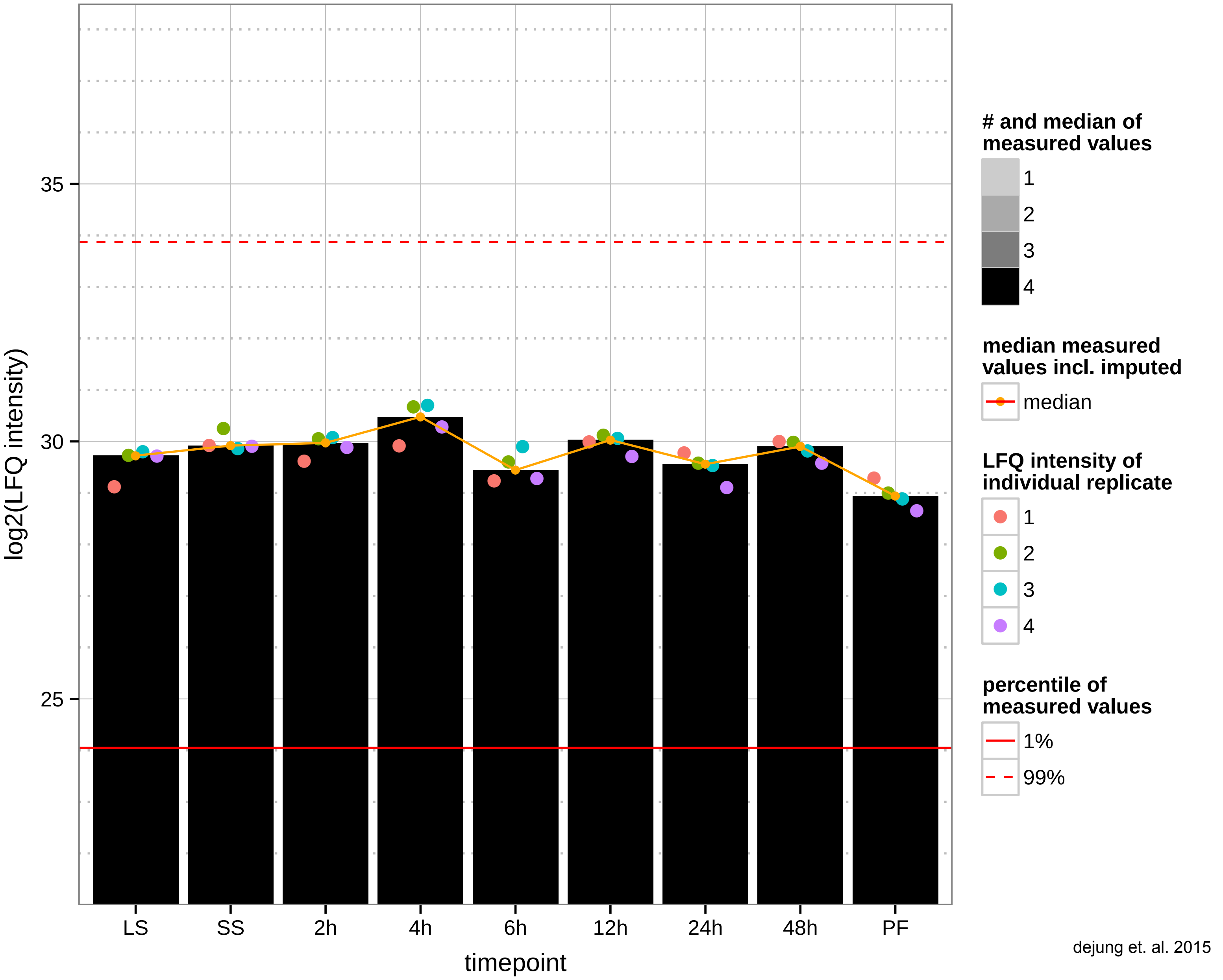
hypothetical protein, chrXI additional, unordered contigs, conserved
Tb927.11.720;Tb11.0840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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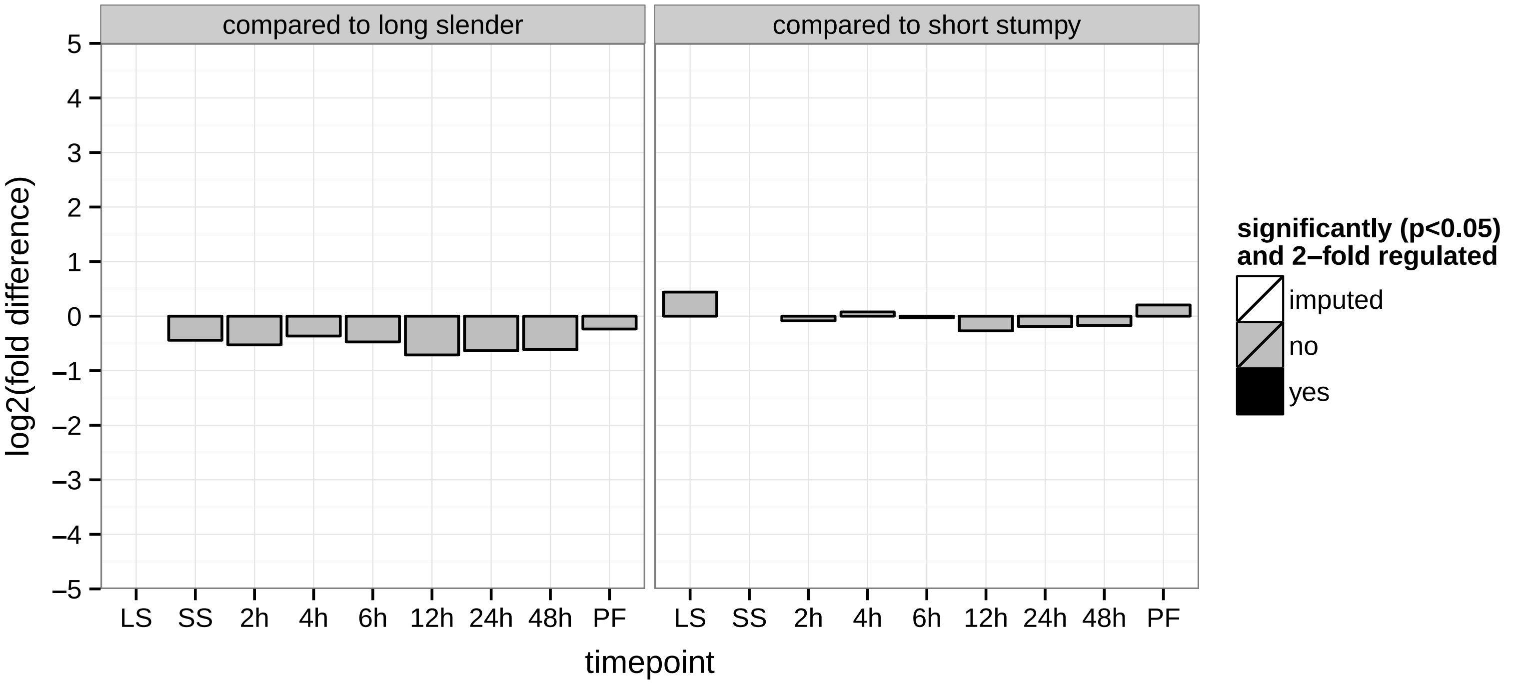
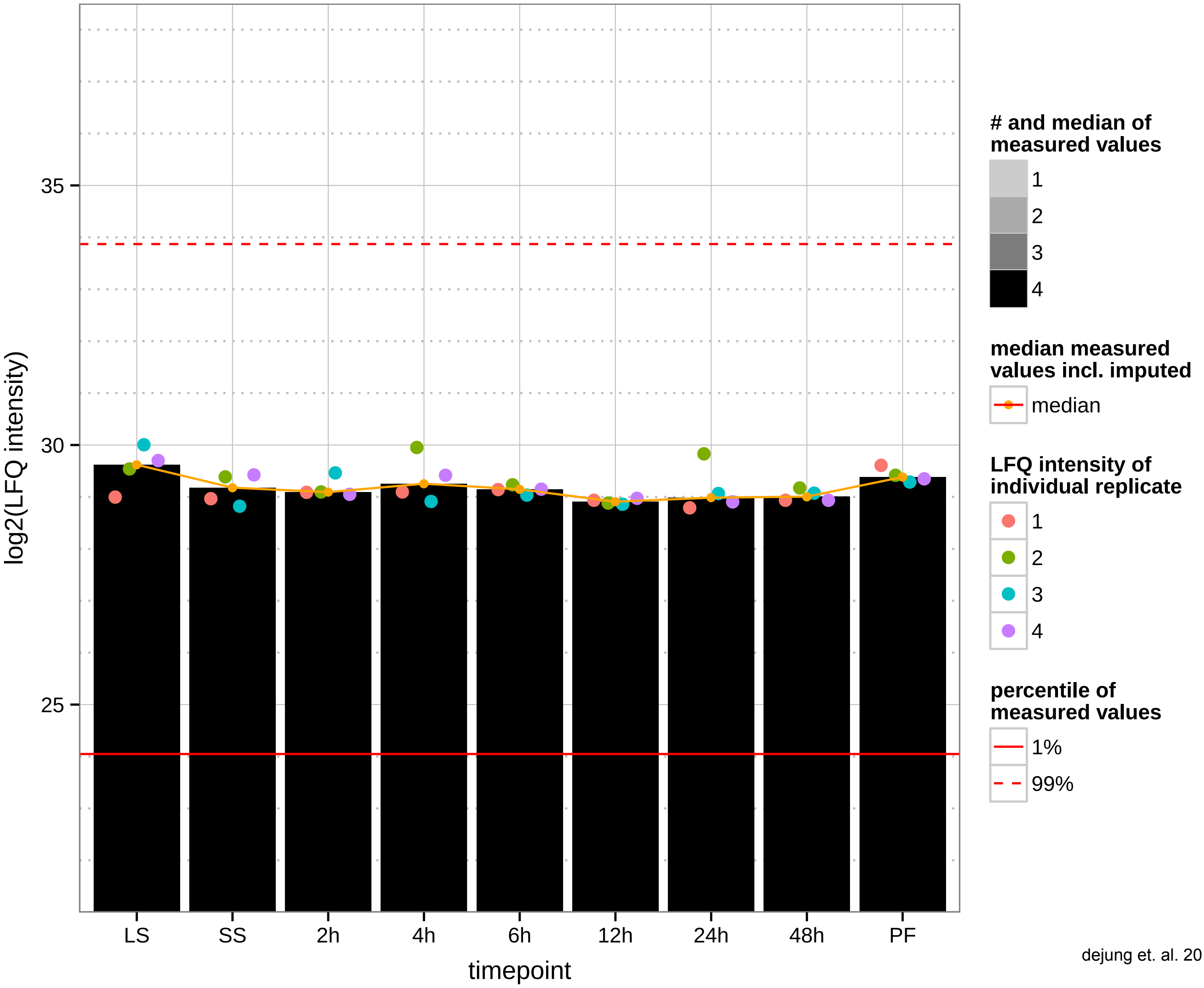
histone H2B variant, putative (H2BVAR)
Tb927.11.7350
AGOF: DNA binding
AGOC: nucleosome, nucleus
AGOP: DNA replication, nucleosome assembly
PGOF: DNA binding
PGOC: nucleosome, nucleus
PGOP: nucleosome assembly





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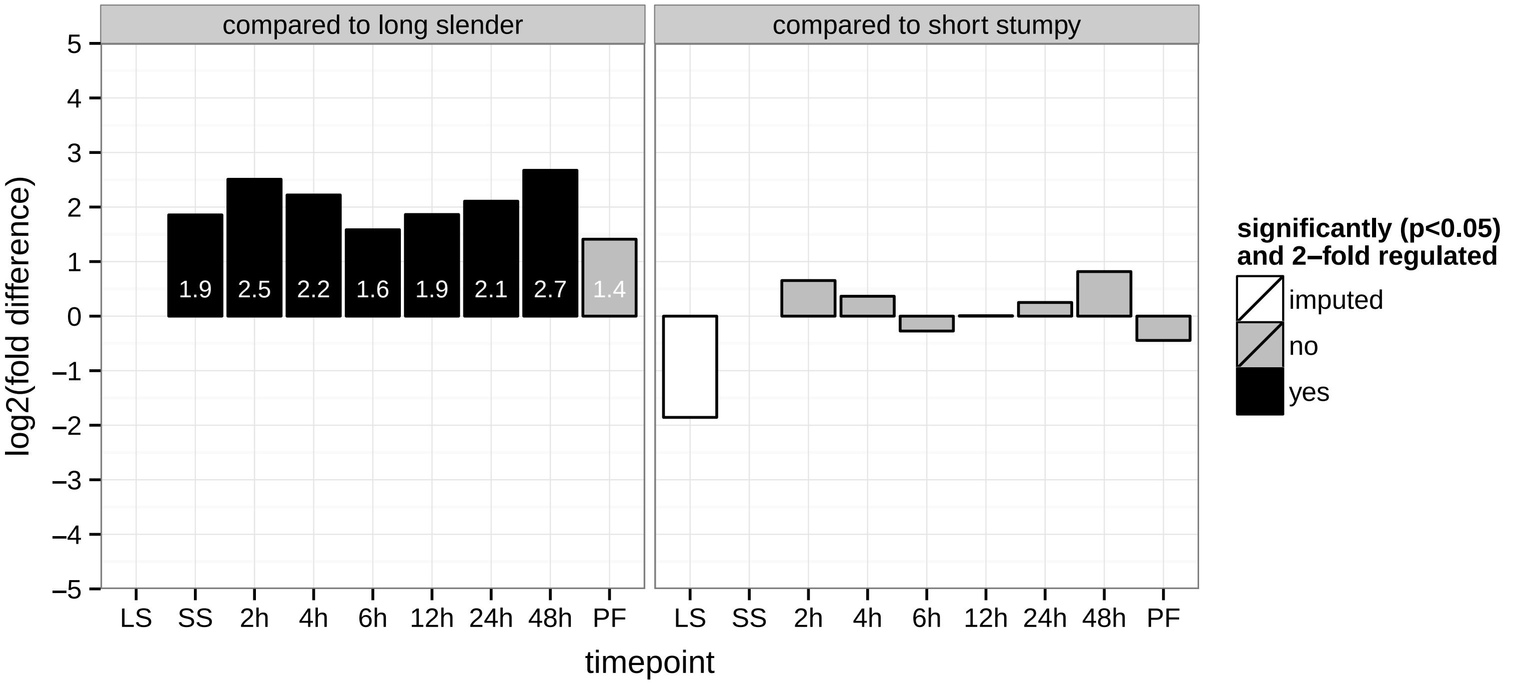
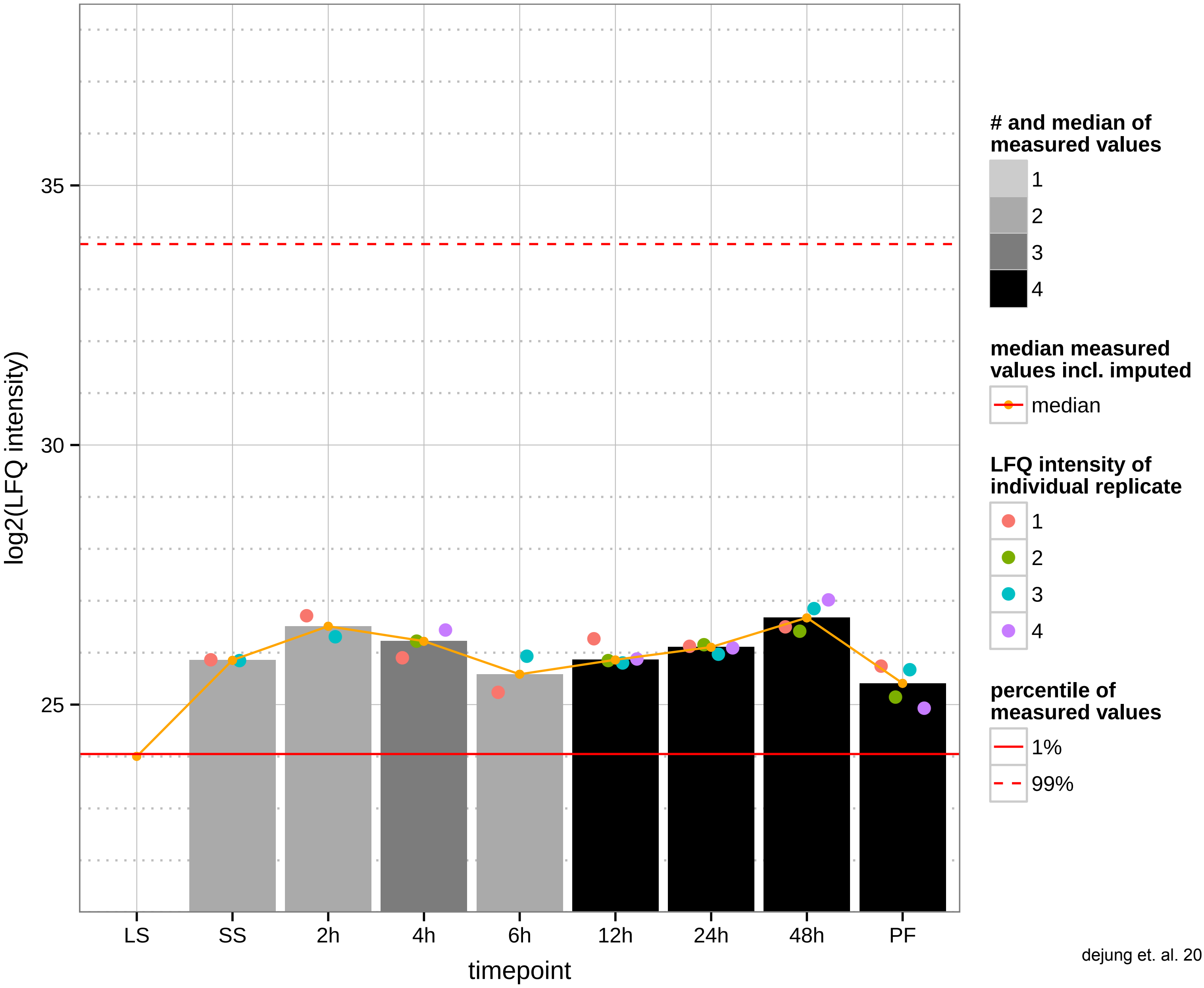
hypothetical protein, conserved
Tb927.11.7390
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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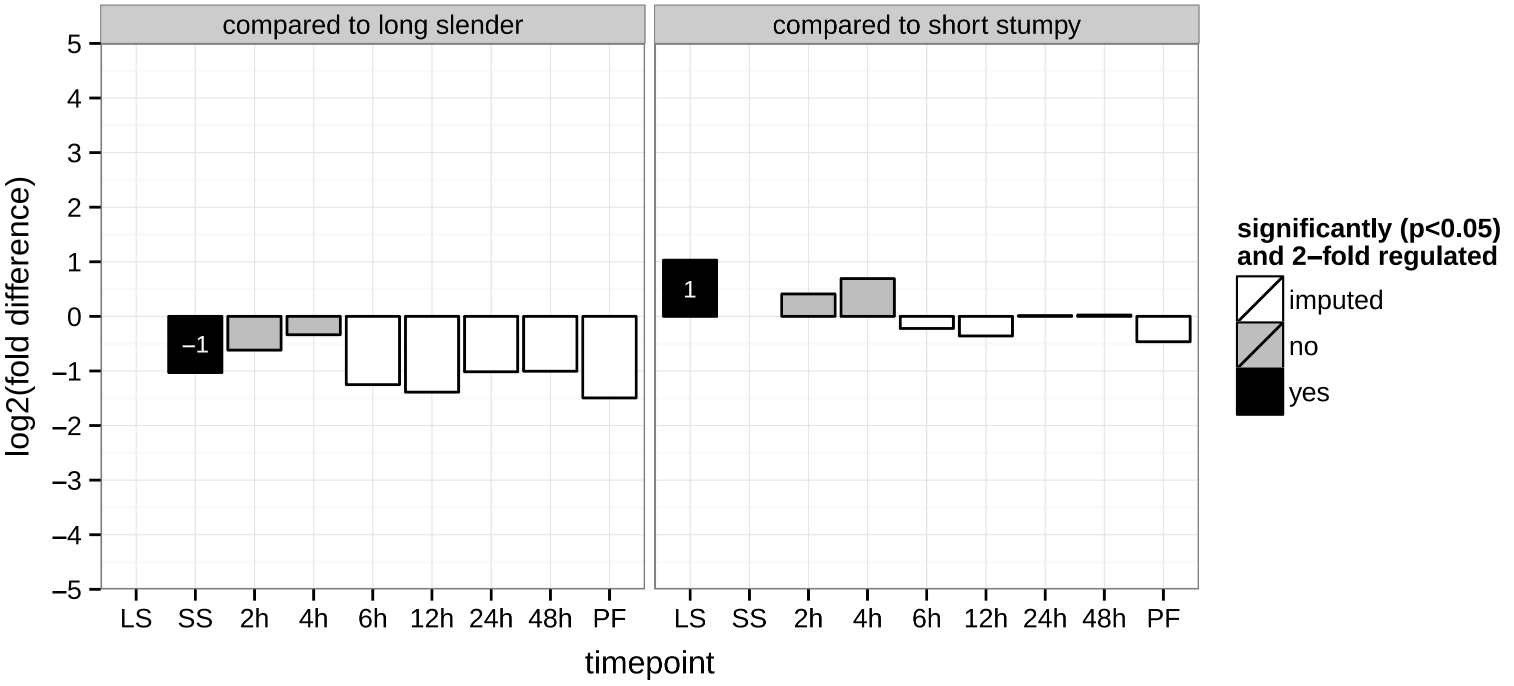
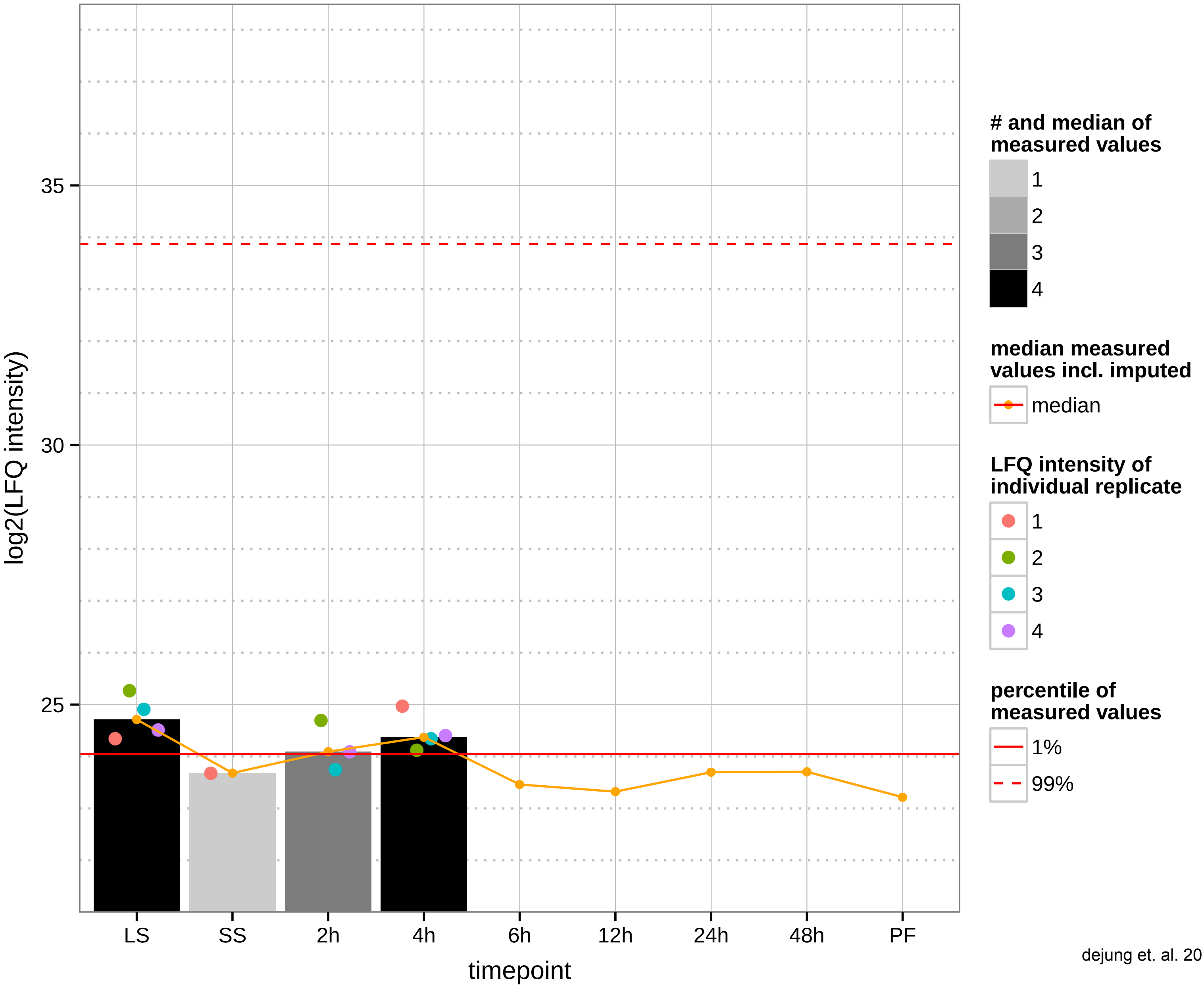
hypothetical protein, conserved
Tb927.11.7430
AGOF: null
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: null
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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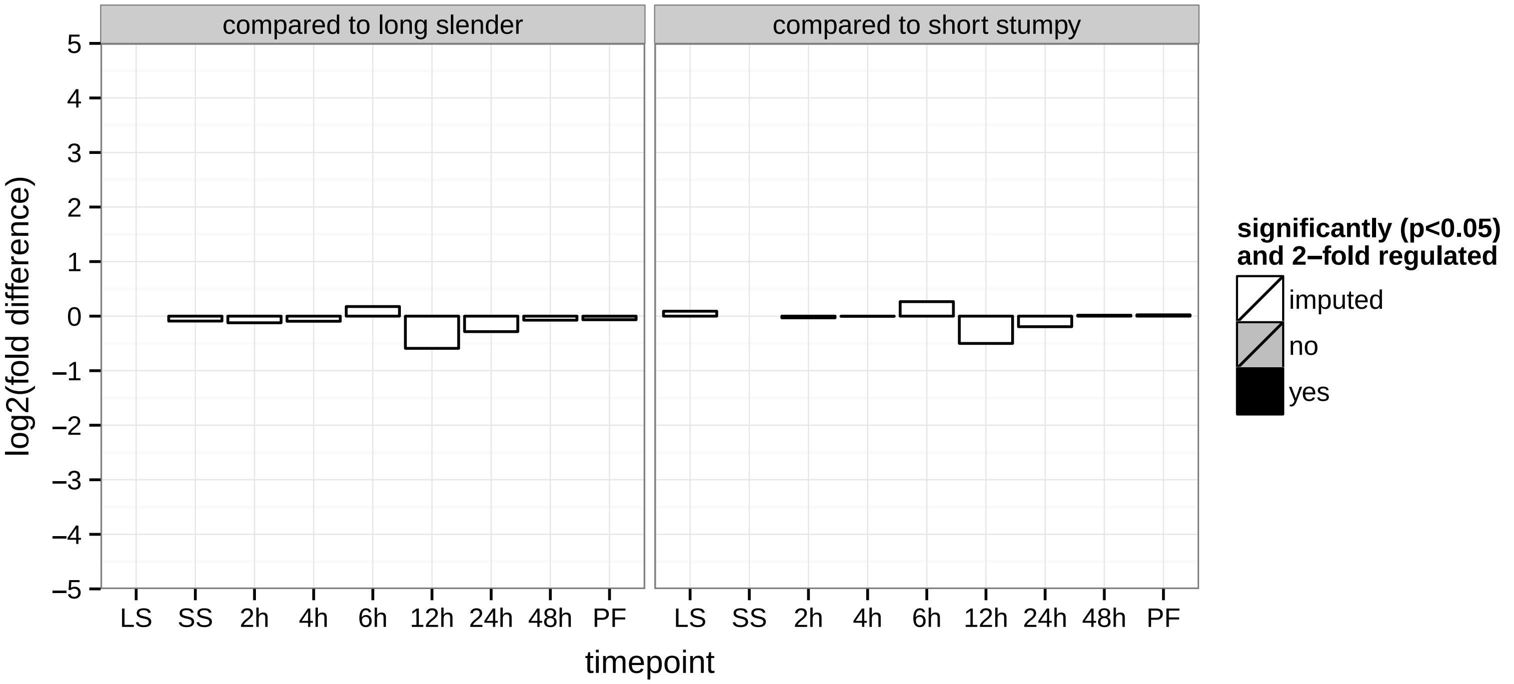
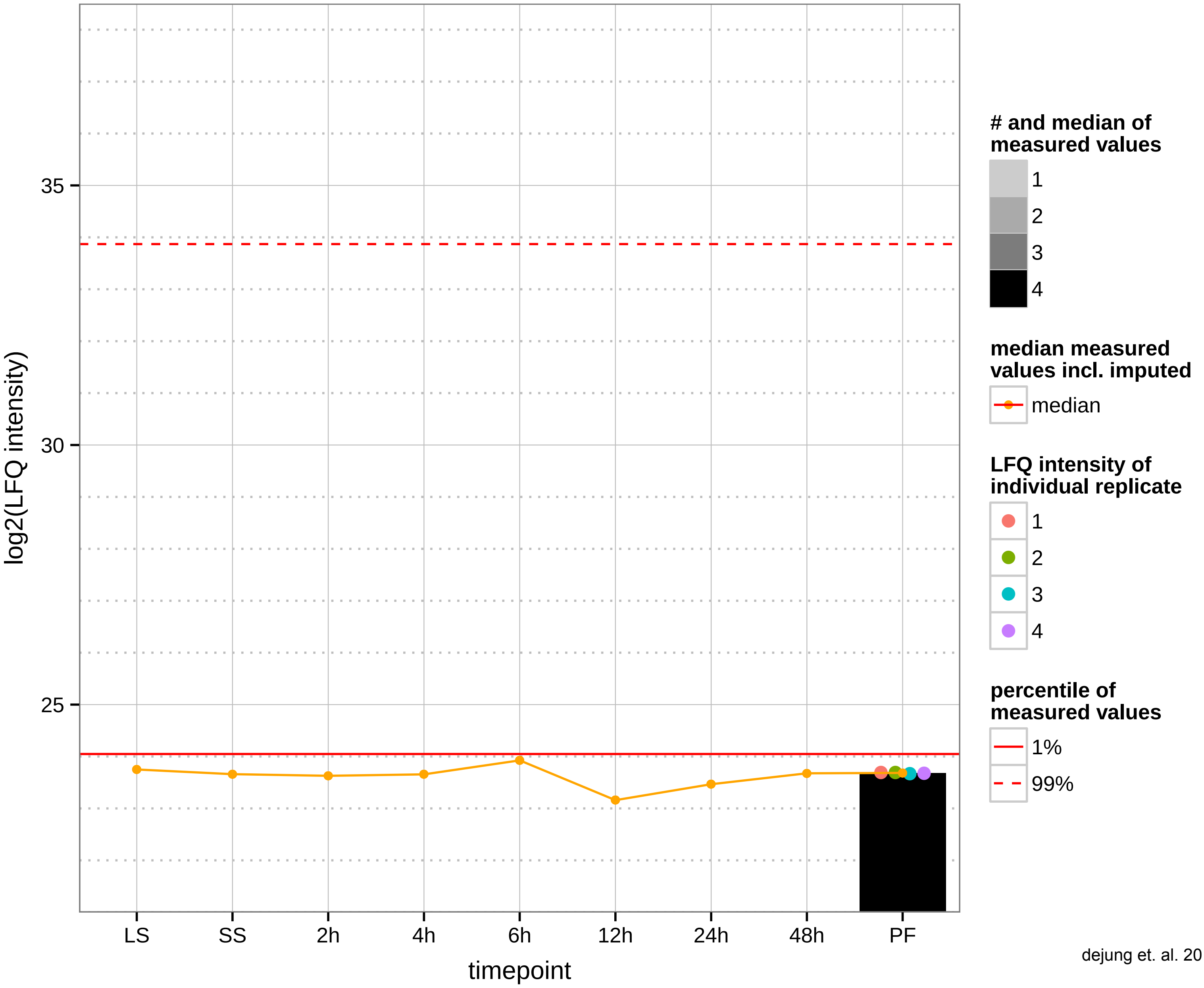
hypothetical protein, conserved
Tb927.11.7440
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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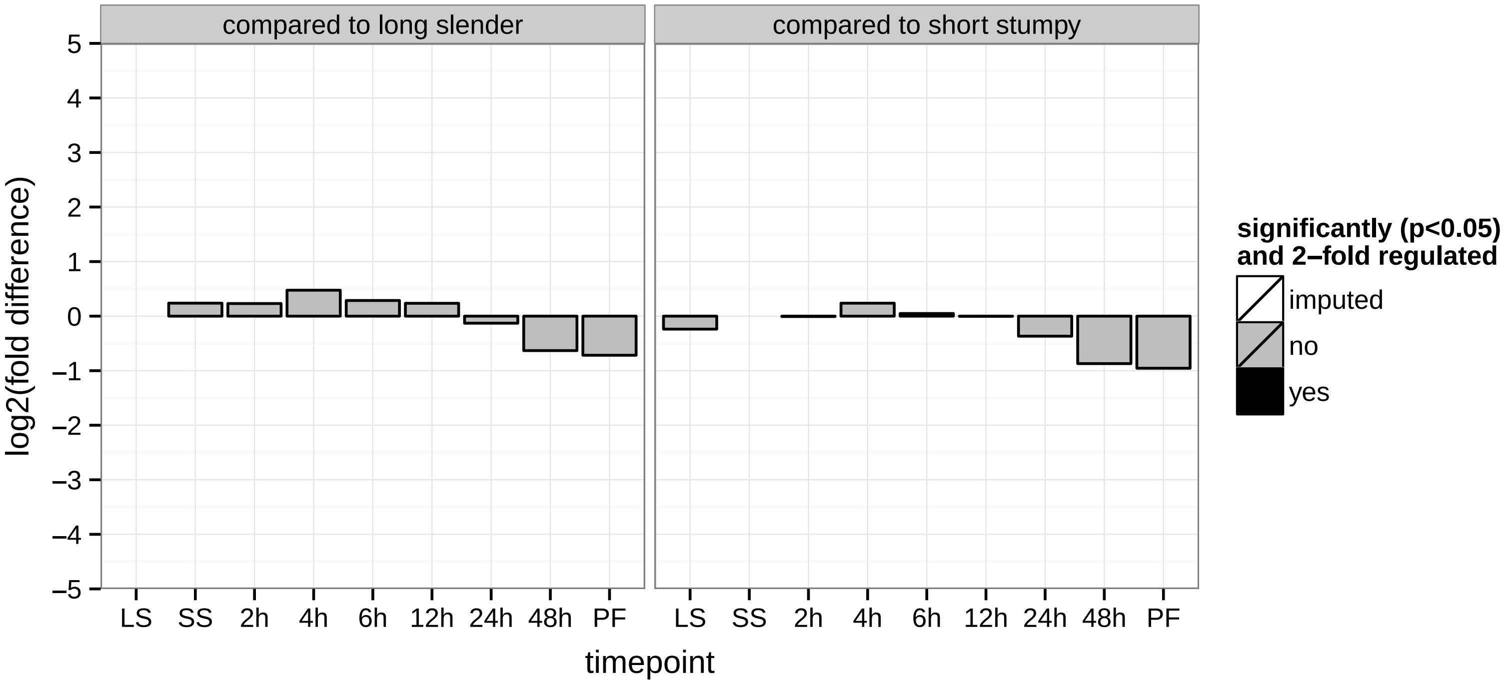
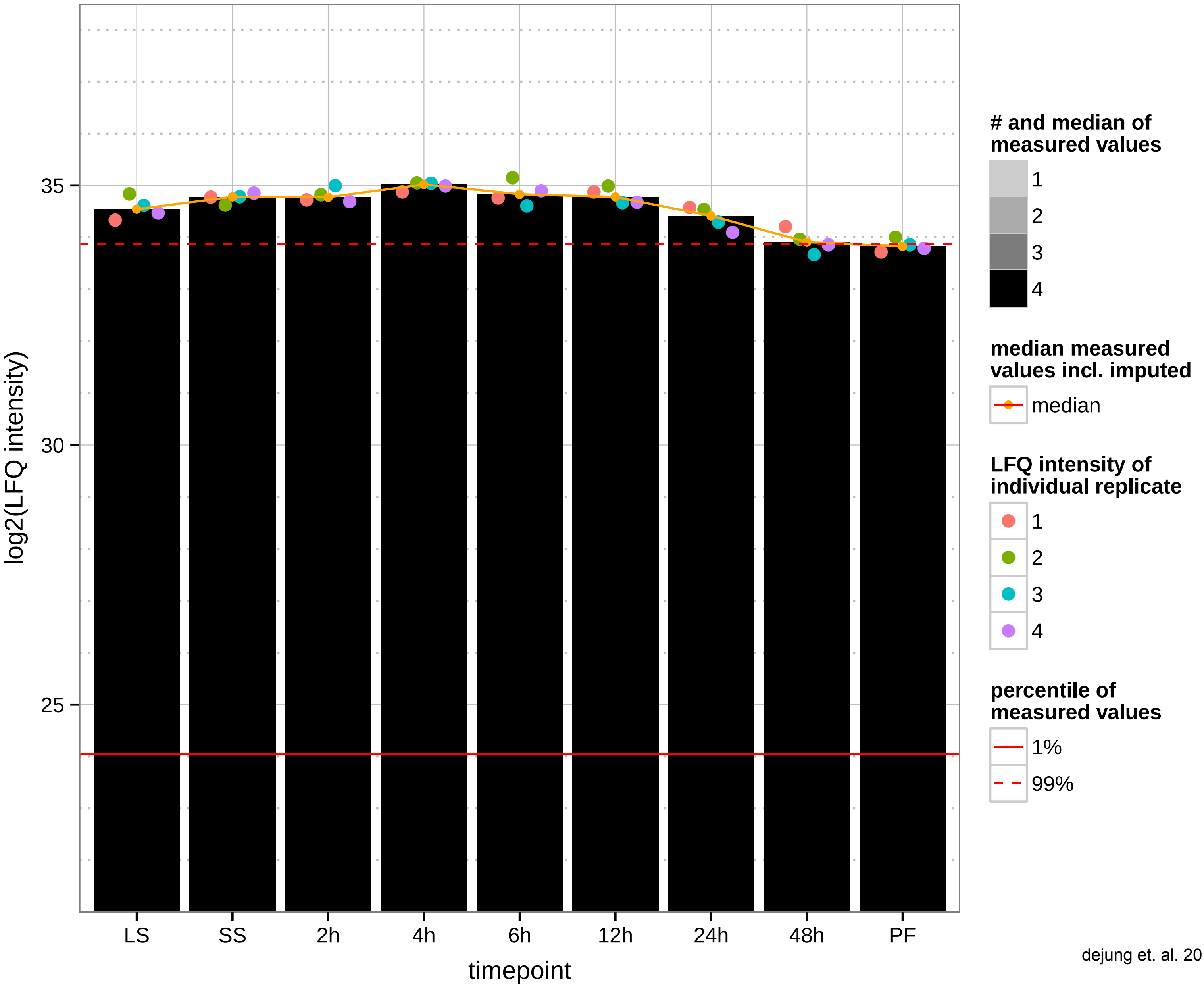
glucose–regulated protein 78, putative, luminal binding protein 1 (BiP)
Tb927.11.7510;Tb927.11.7460
AGOF: ATP binding
AGOC: endoplasmic reticulum
AGOP: SRP–dependent cotranslational protein targeting to membrane, protein folding
PGOF: null
PGOC: null
PGOP: null





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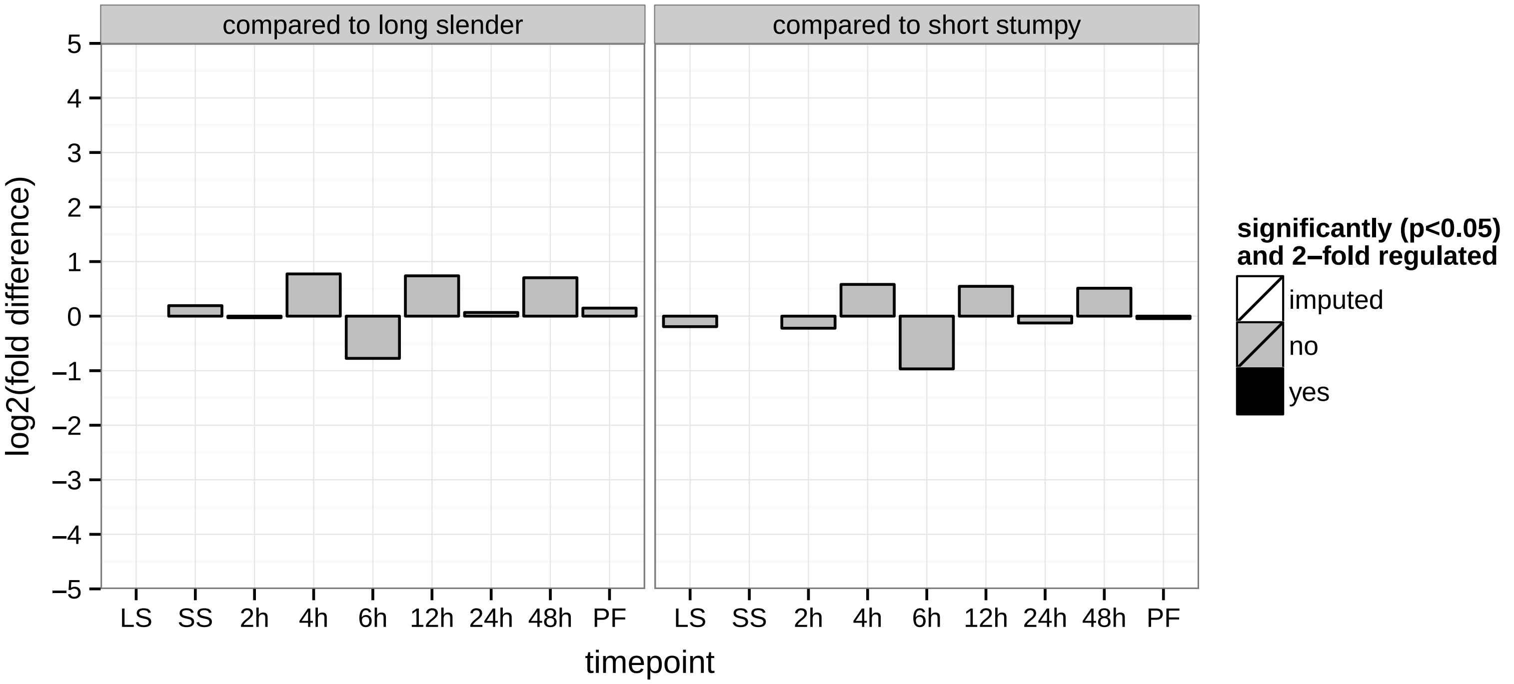
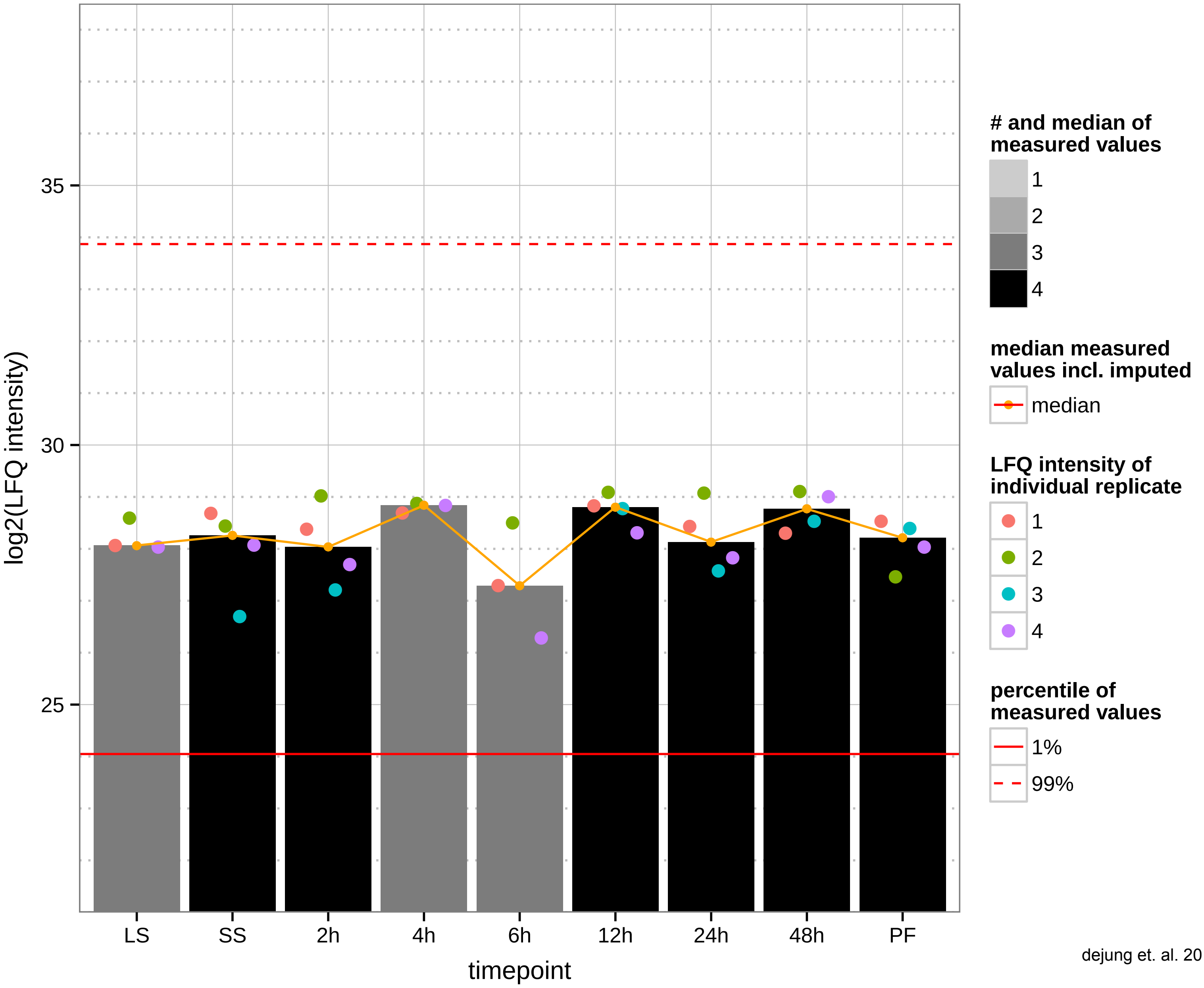
hypothetical protein, conserved
Tb927.11.7470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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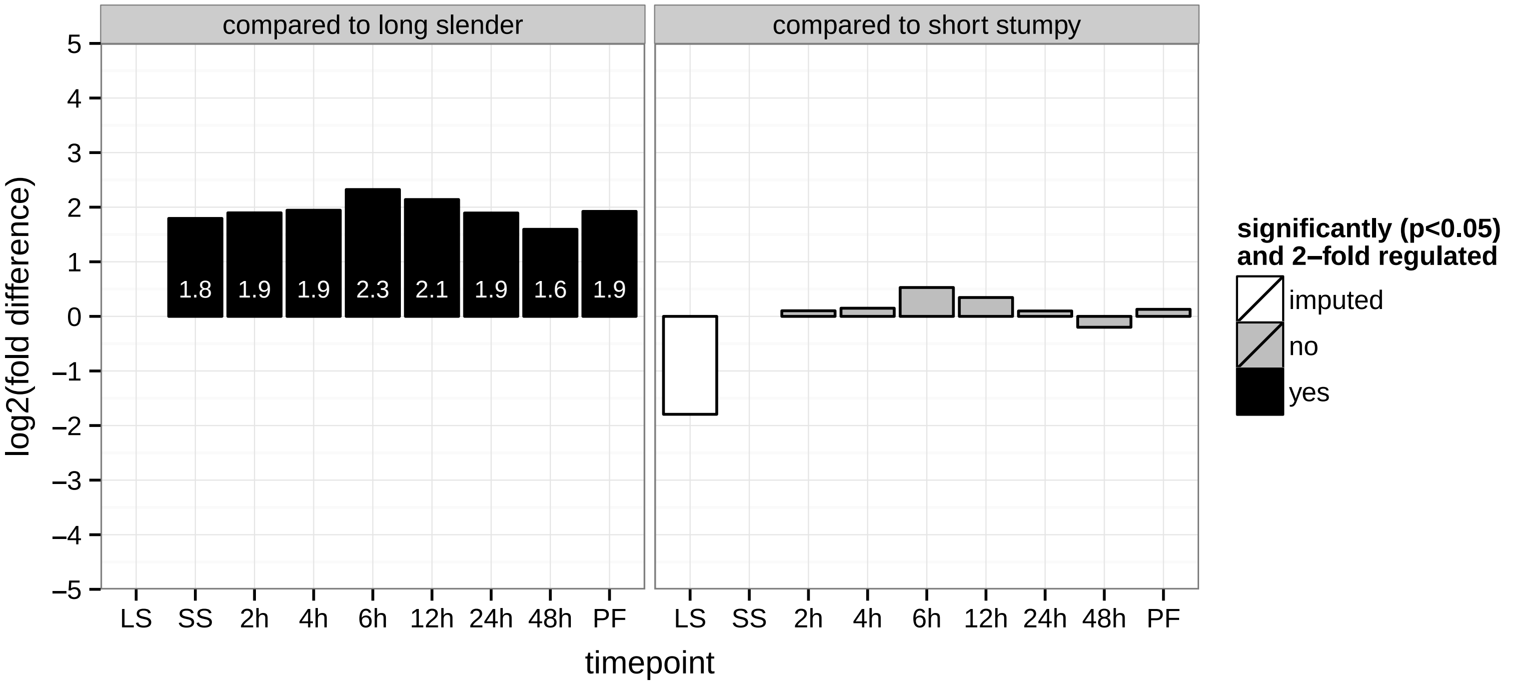
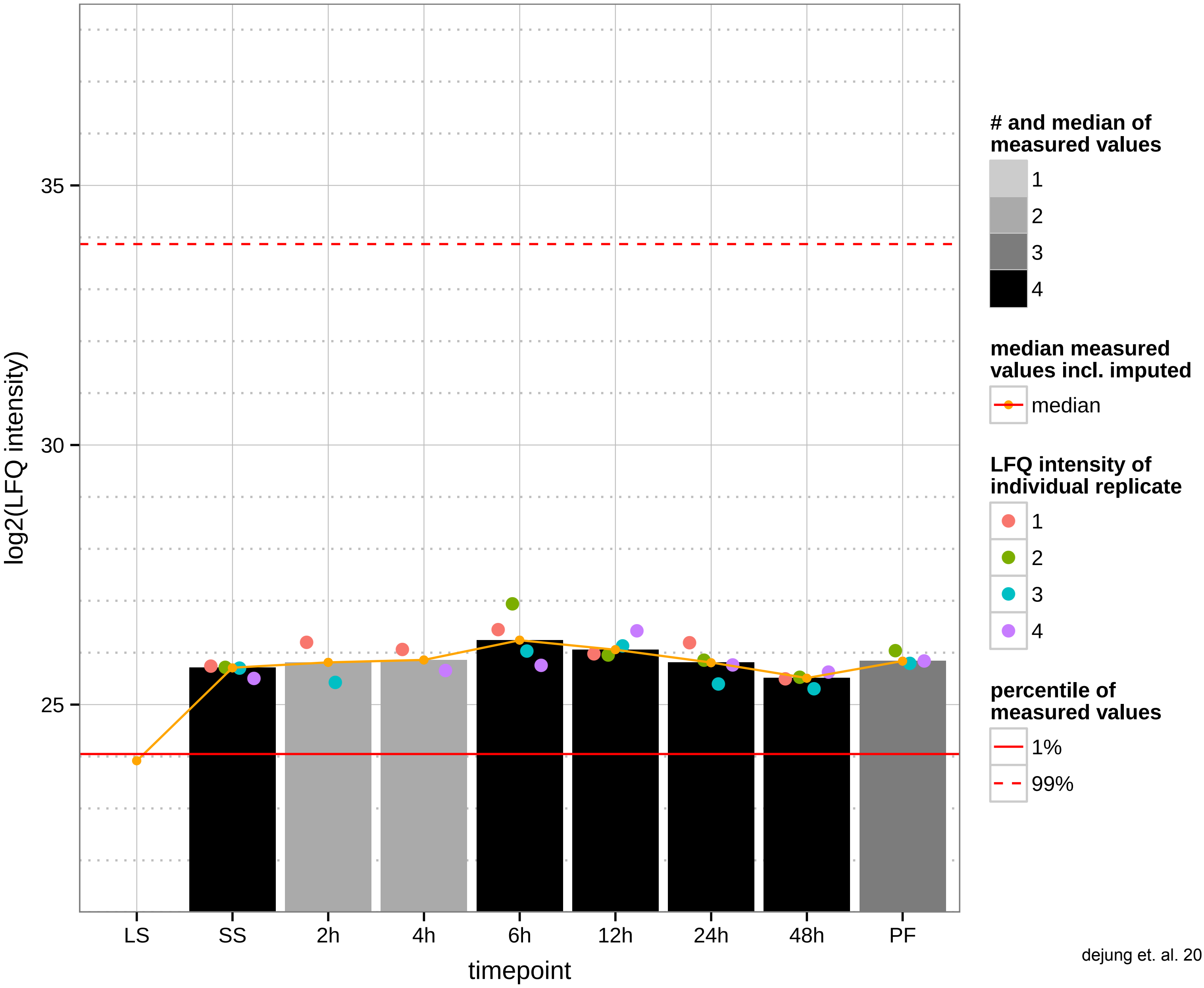
long−chain−fatty−acid−CoA ligase, putative
Tb927.11.7530
AGOF: catalytic activity
AGOC: null
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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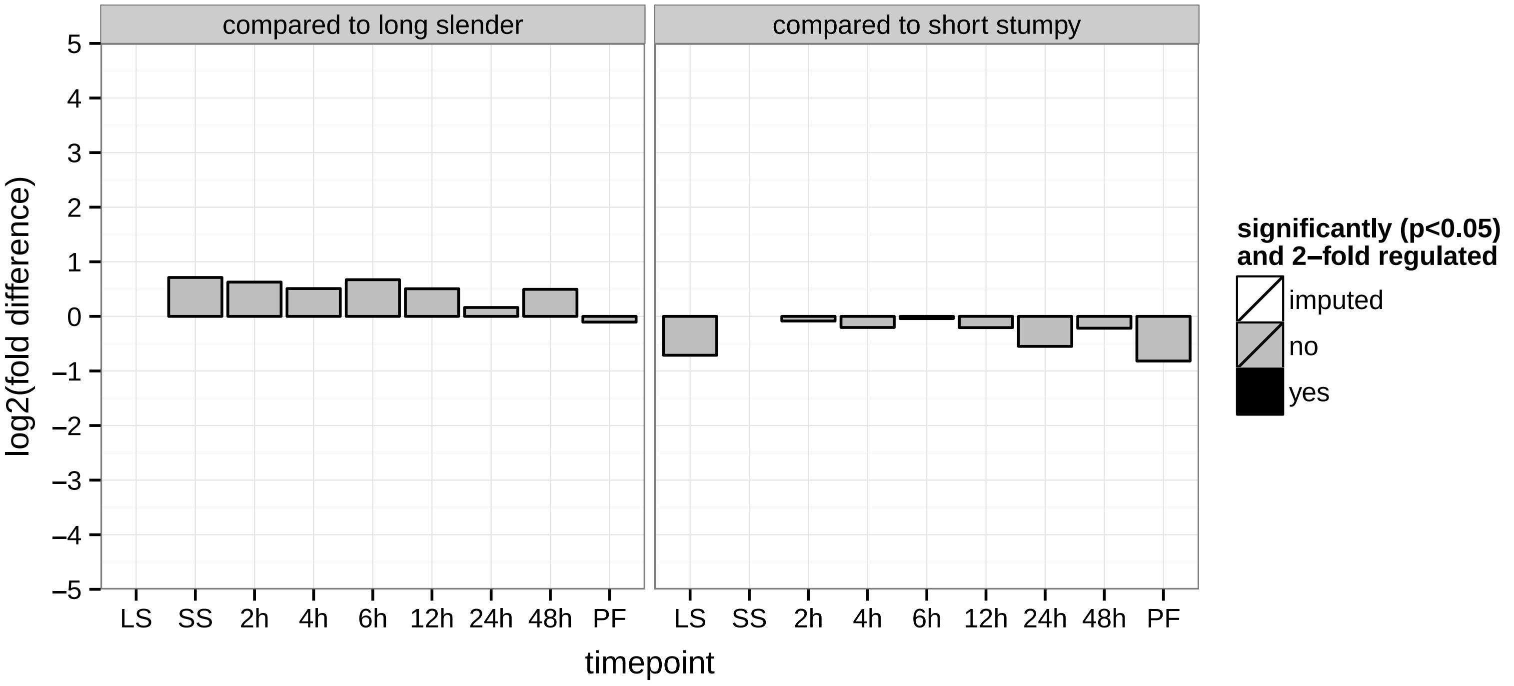
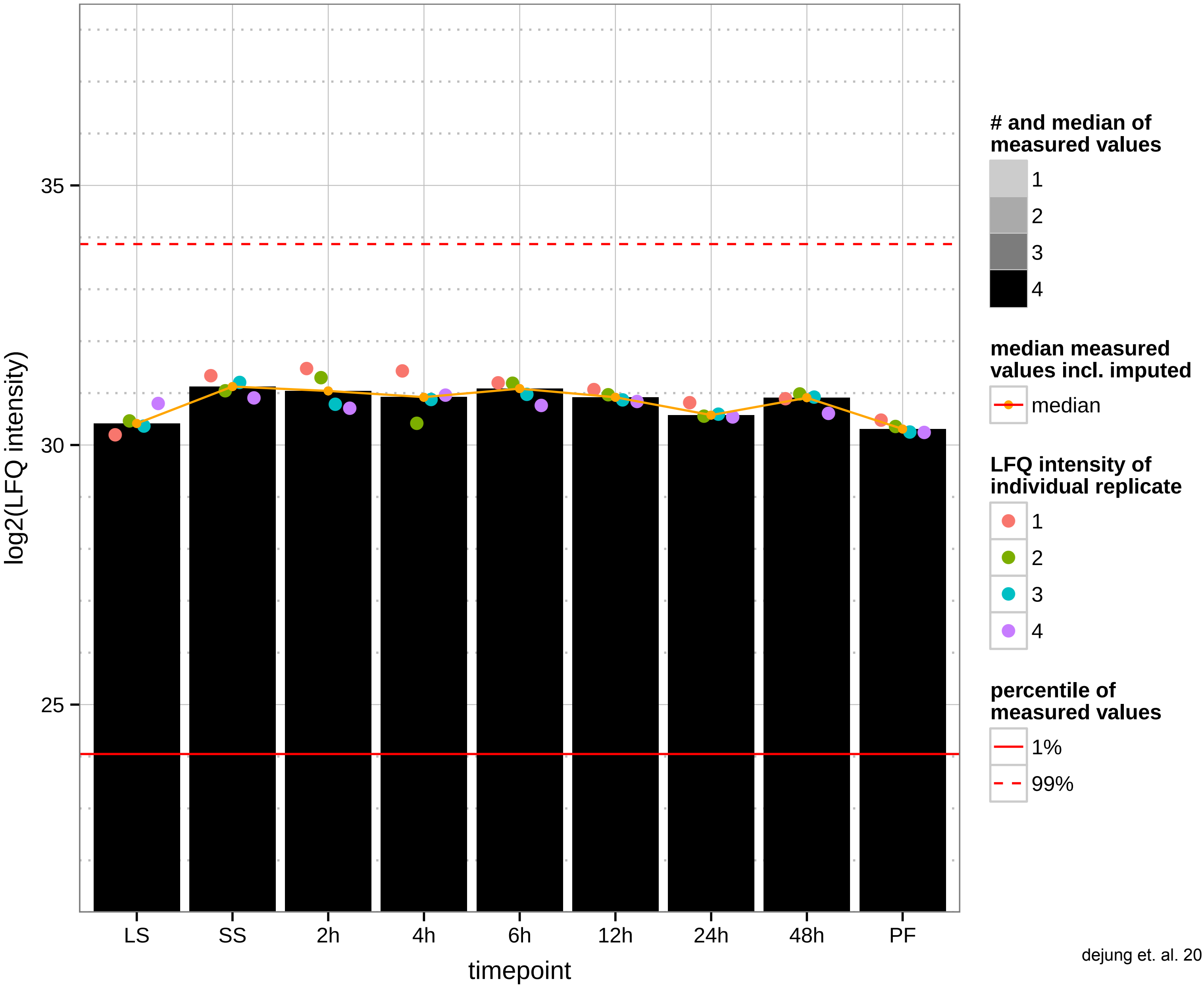
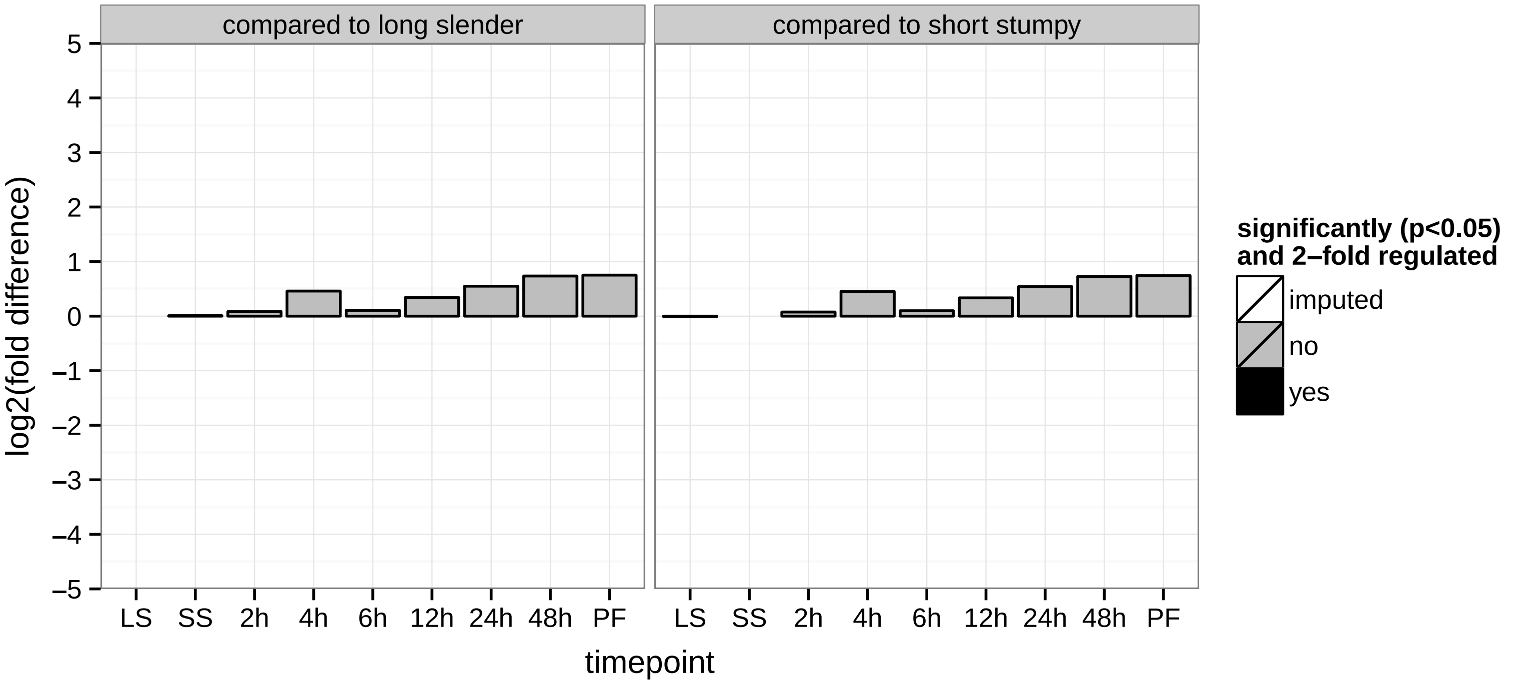
predicted WD40 repeat protein
Tb927.11.7560
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null

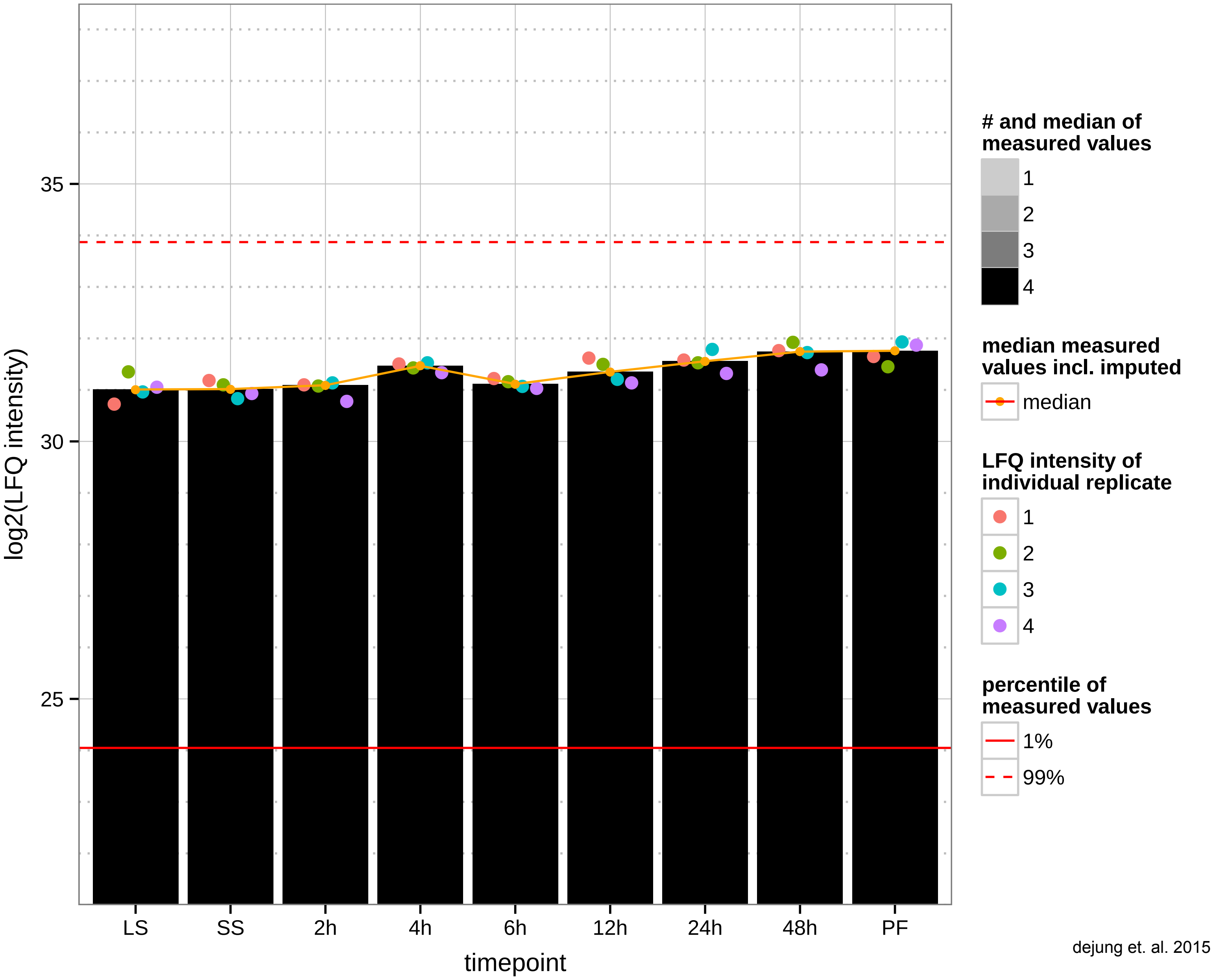




dejung et. al. 2015

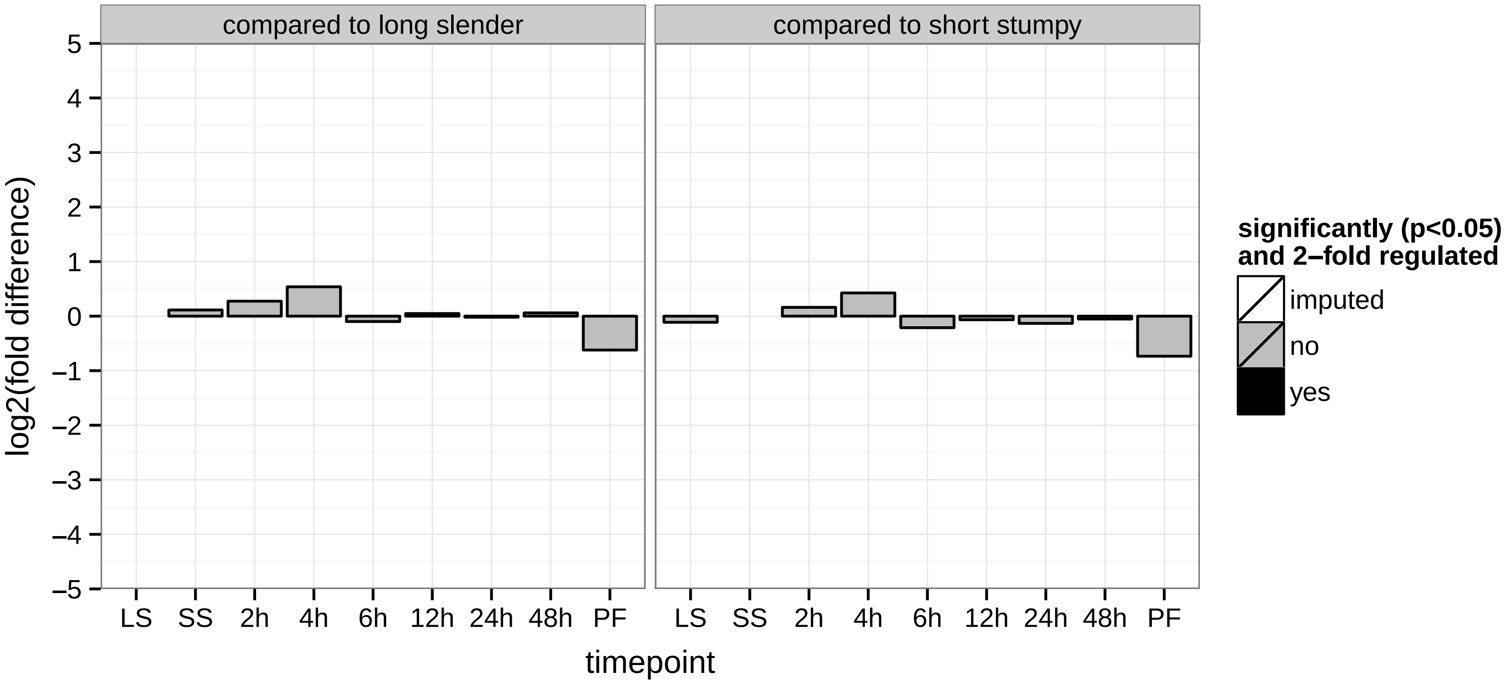
protein phosphatase 2C, putative
Tb927.11.760
AGOF: protein serine/threonine phosphatase activity
AGOC: protein serine/threonine phosphatase complex
AGOP: modulation of development of symbiont involved in interaction with host, protein dephosphorylation, quorum sensing i
PGOF: catalytic activity
PGOC: null
PGOP: null

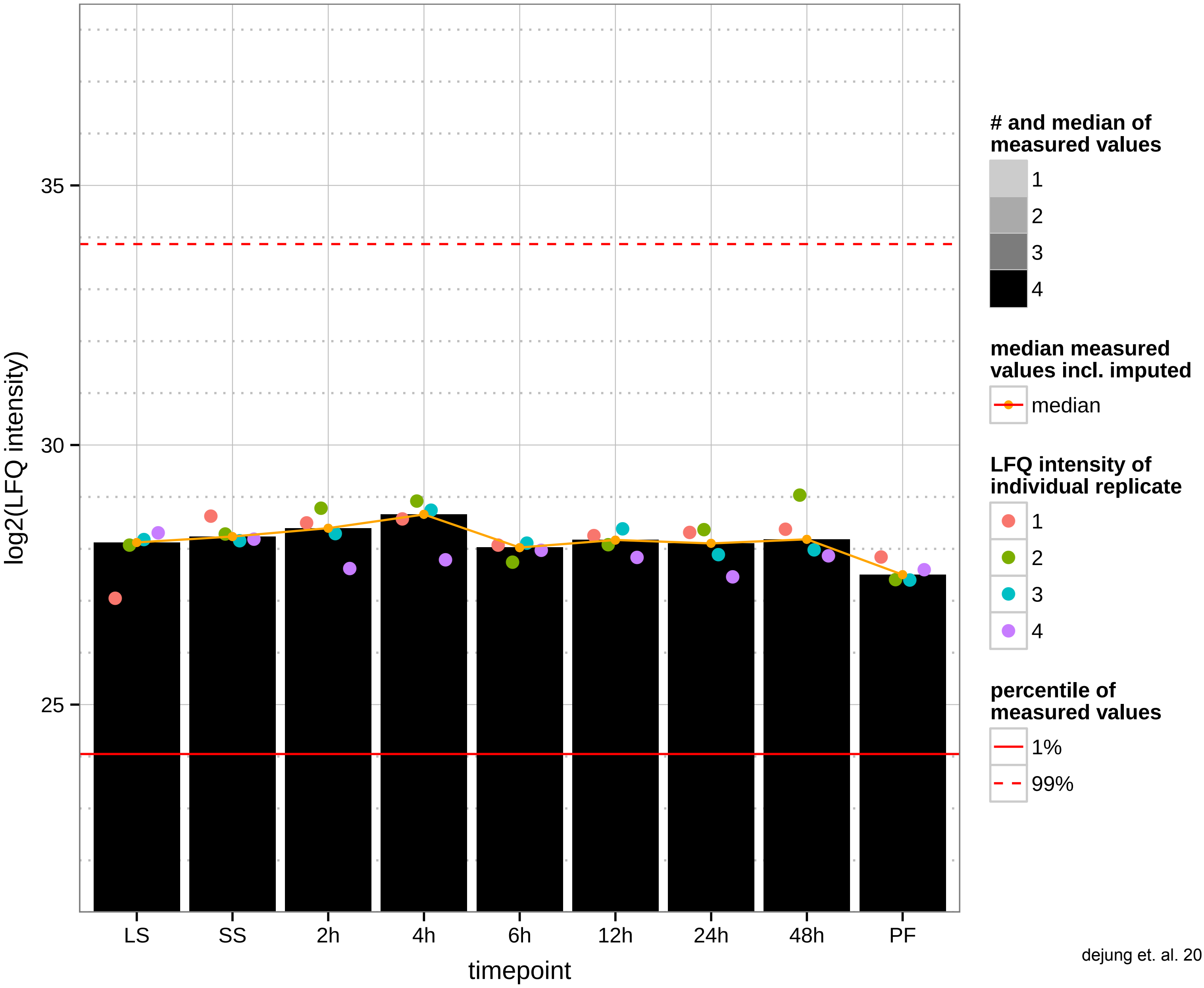




dejung et. al. 2015

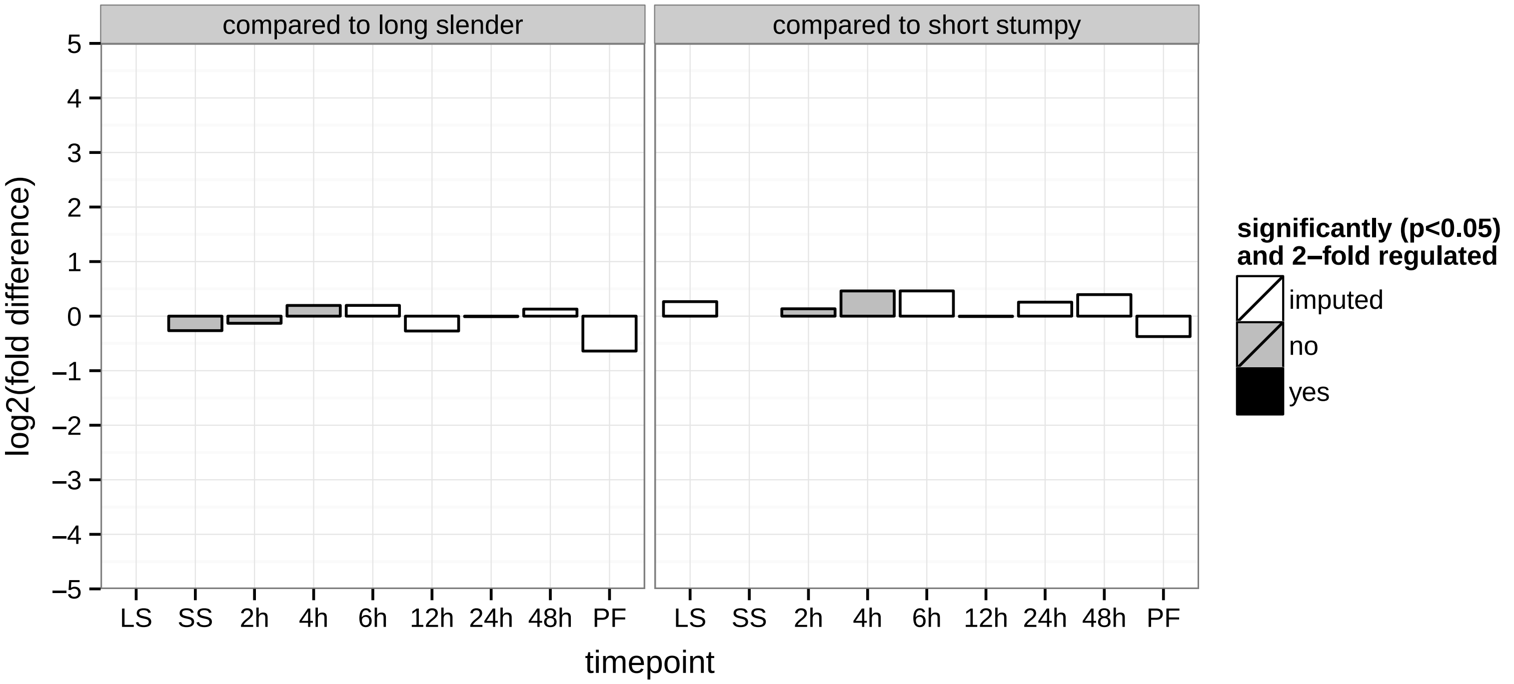
dynein light chain, putative, dynein Tctex2 family
Tb927.11.7740
AGOF: microtubule motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based process
PGOF: null
PGOC: null
PGOP: null

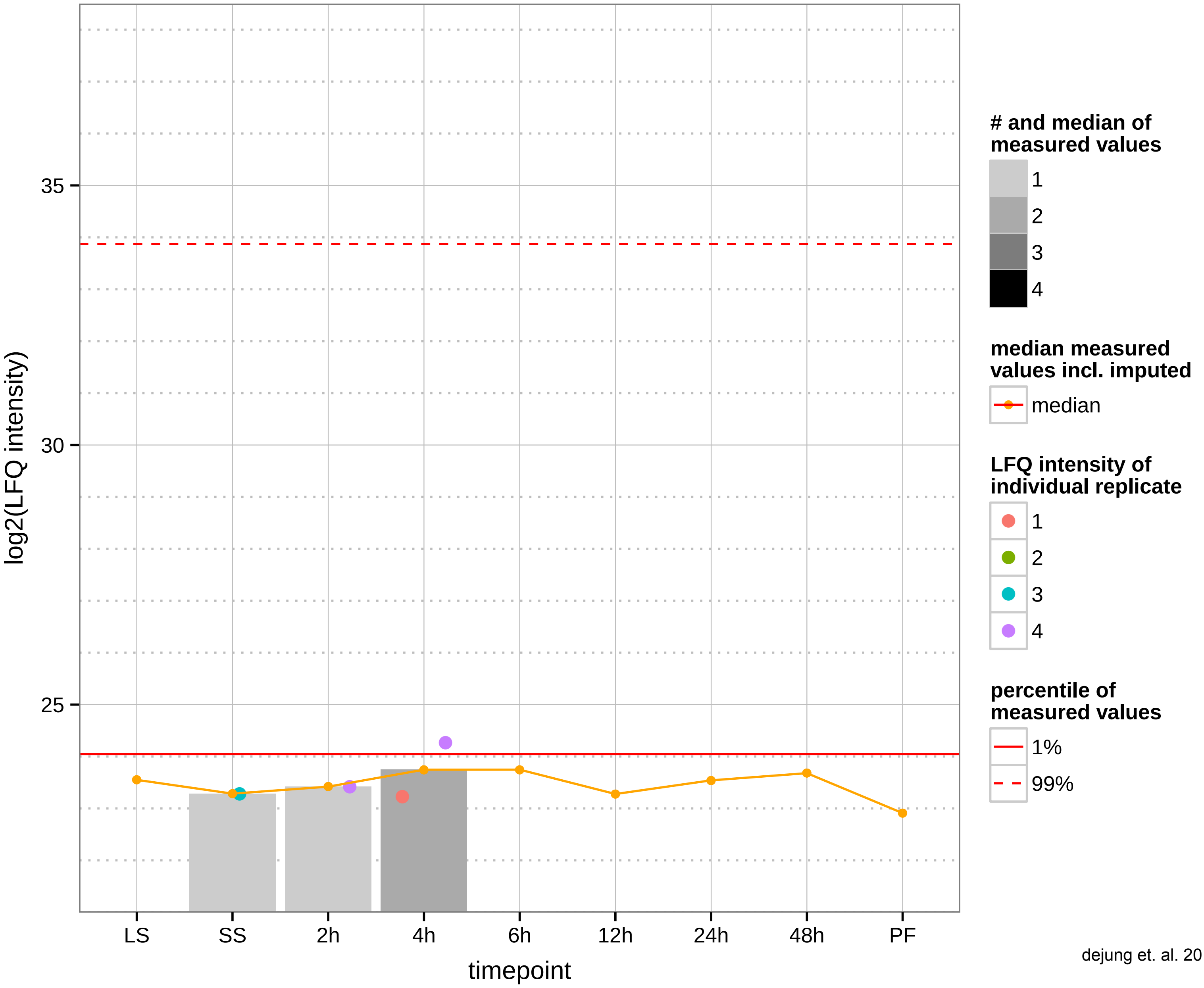




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.7800
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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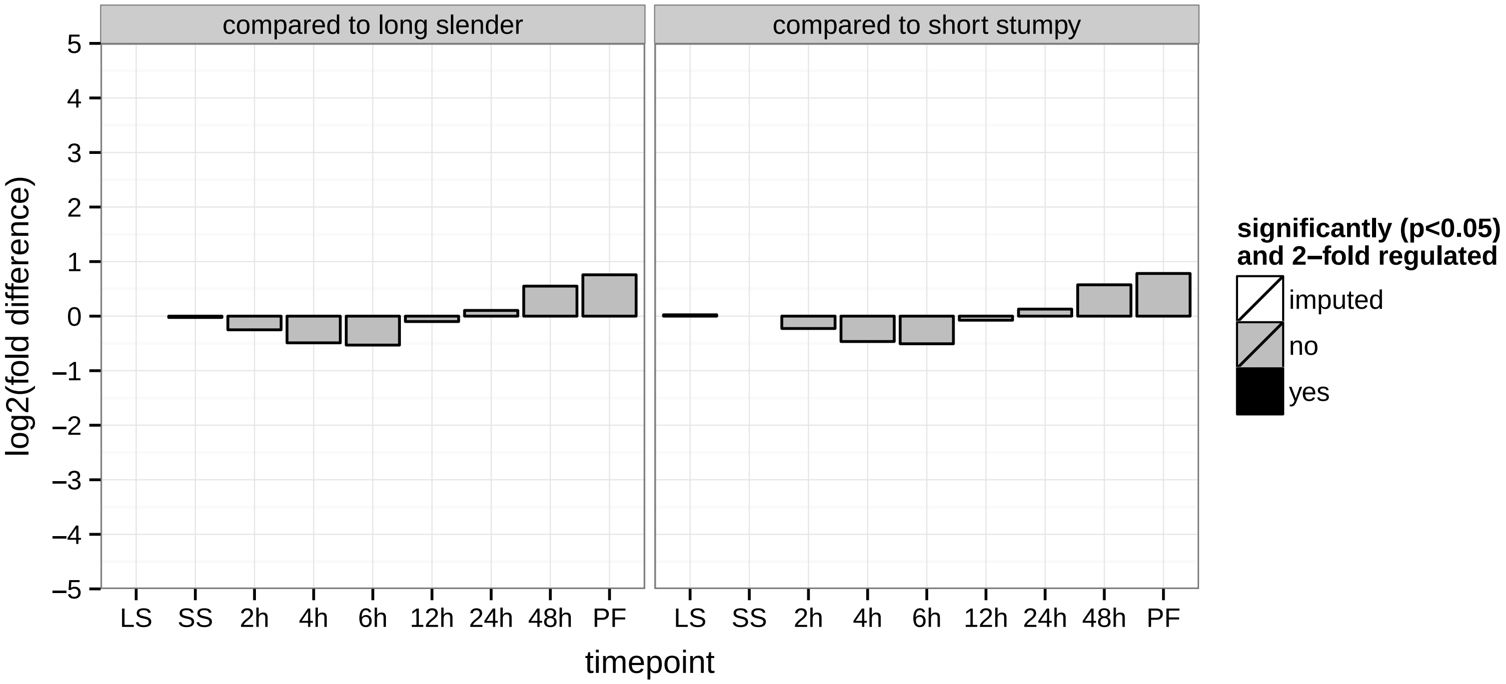
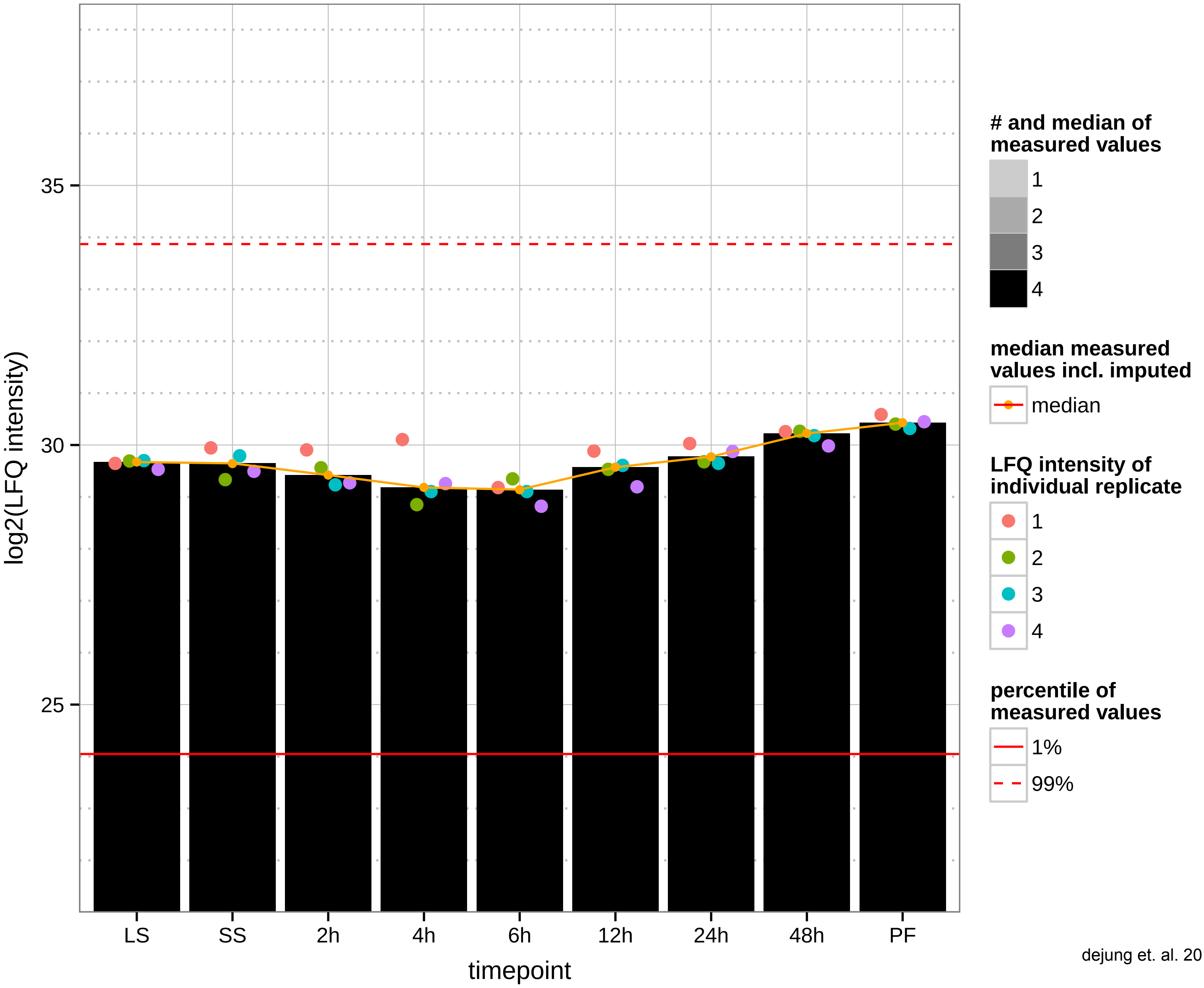
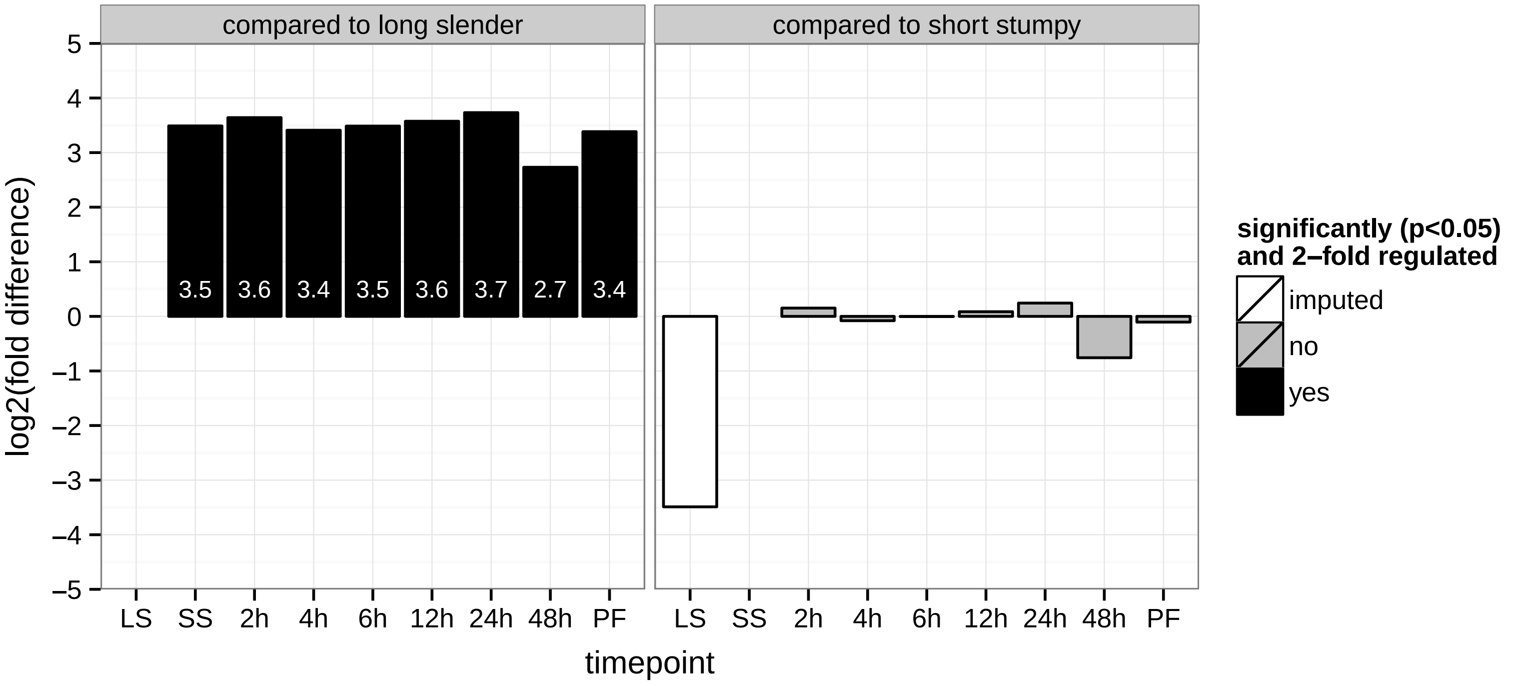
ribonucleoside–diphosphate reductase large chain (RNR1)
Tb927.11.7840
AGOF: ATP binding, ribonucleoside–diphosphate reductase activity, thioredoxin disulfide as acceptor
AGOC: ribonucleoside–diphosphate reductase complex
AGOP: DNA replication, oxidation–reduction process
PGOF: ATP binding, ribonucleoside–diphosphate reductase activity, thioredoxin disulfide as acceptor
PGOC: ribonucleoside–diphosphate reductase complex
PGOP: DNA replication, oxidation–reduction process

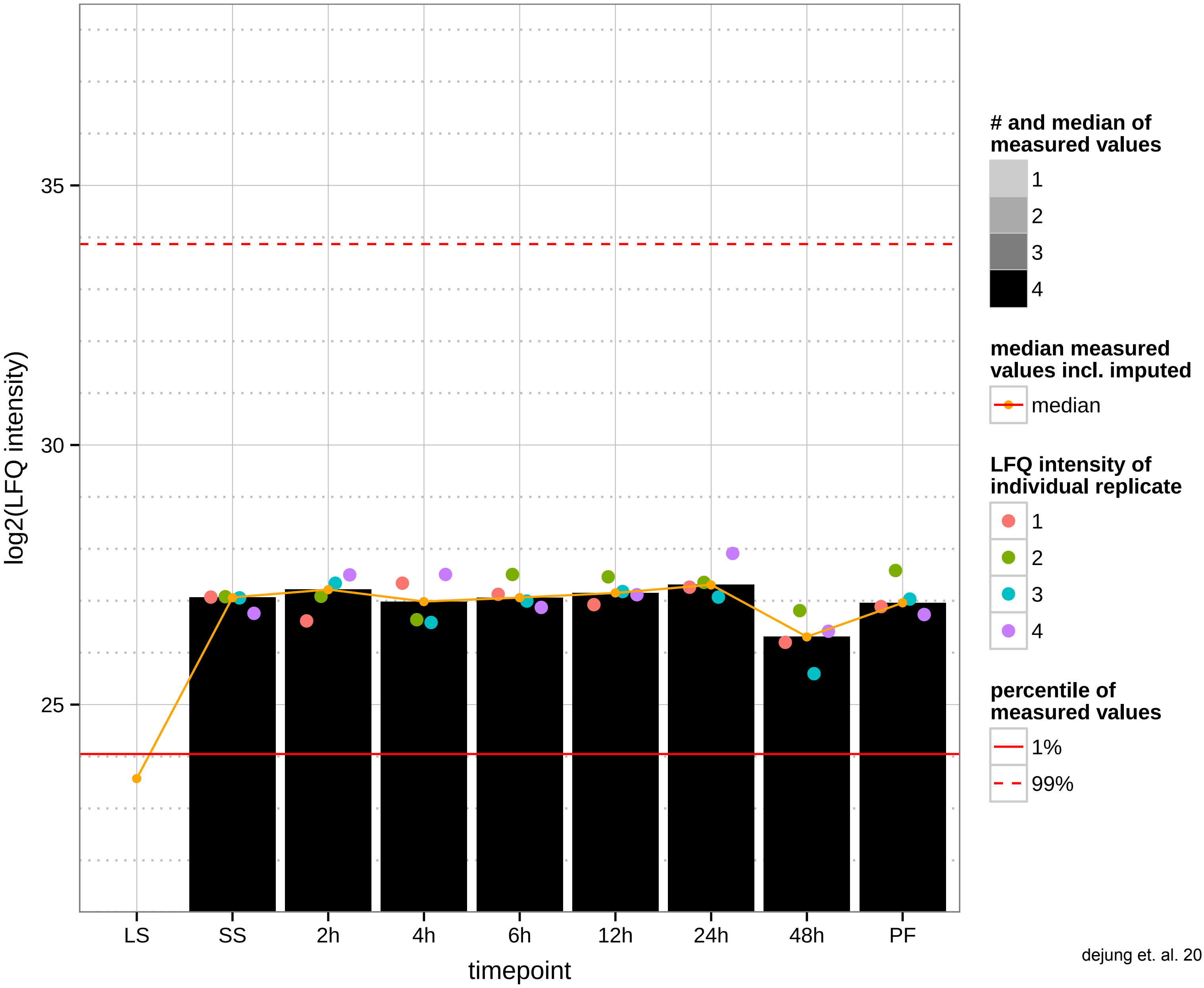




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.7850
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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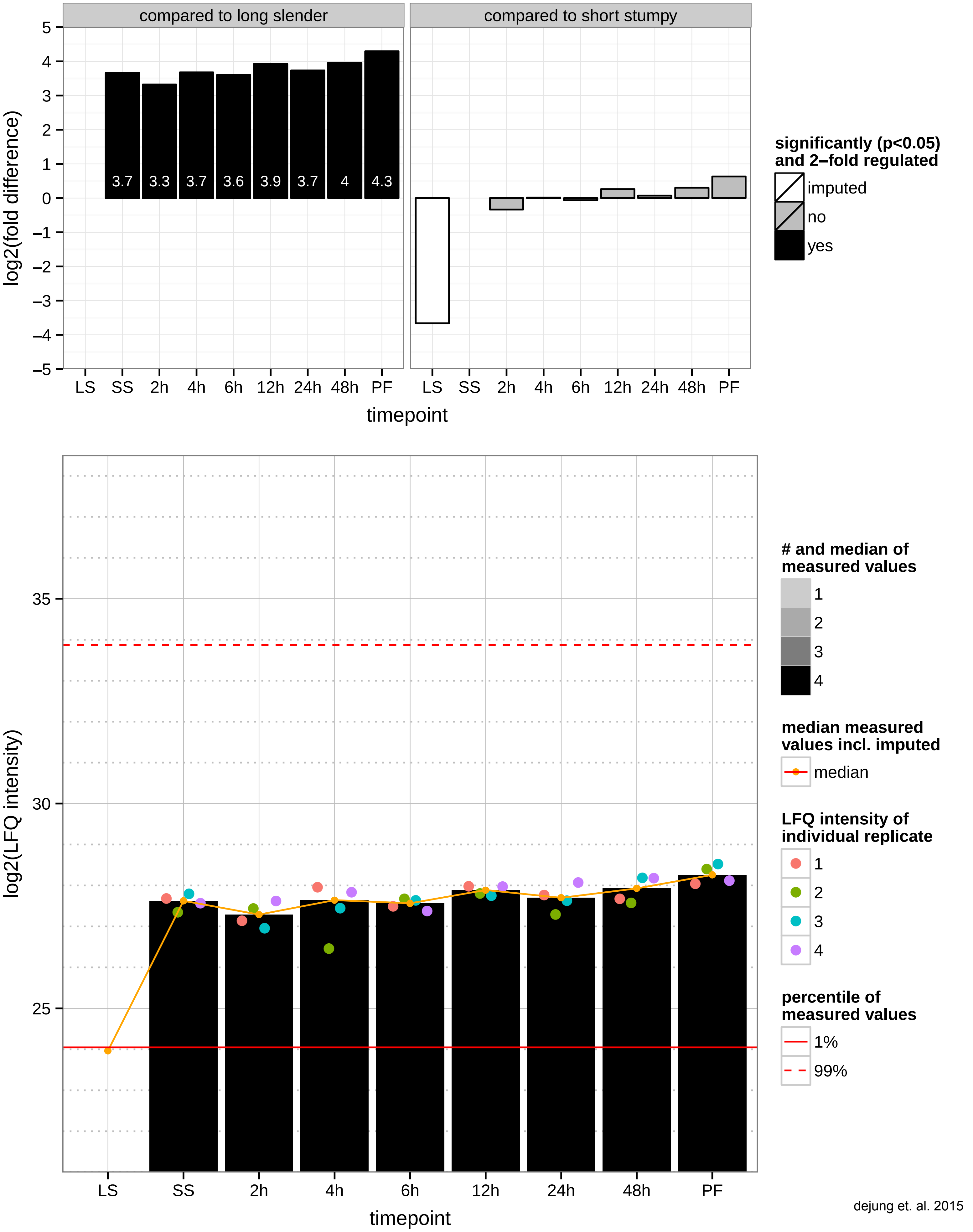
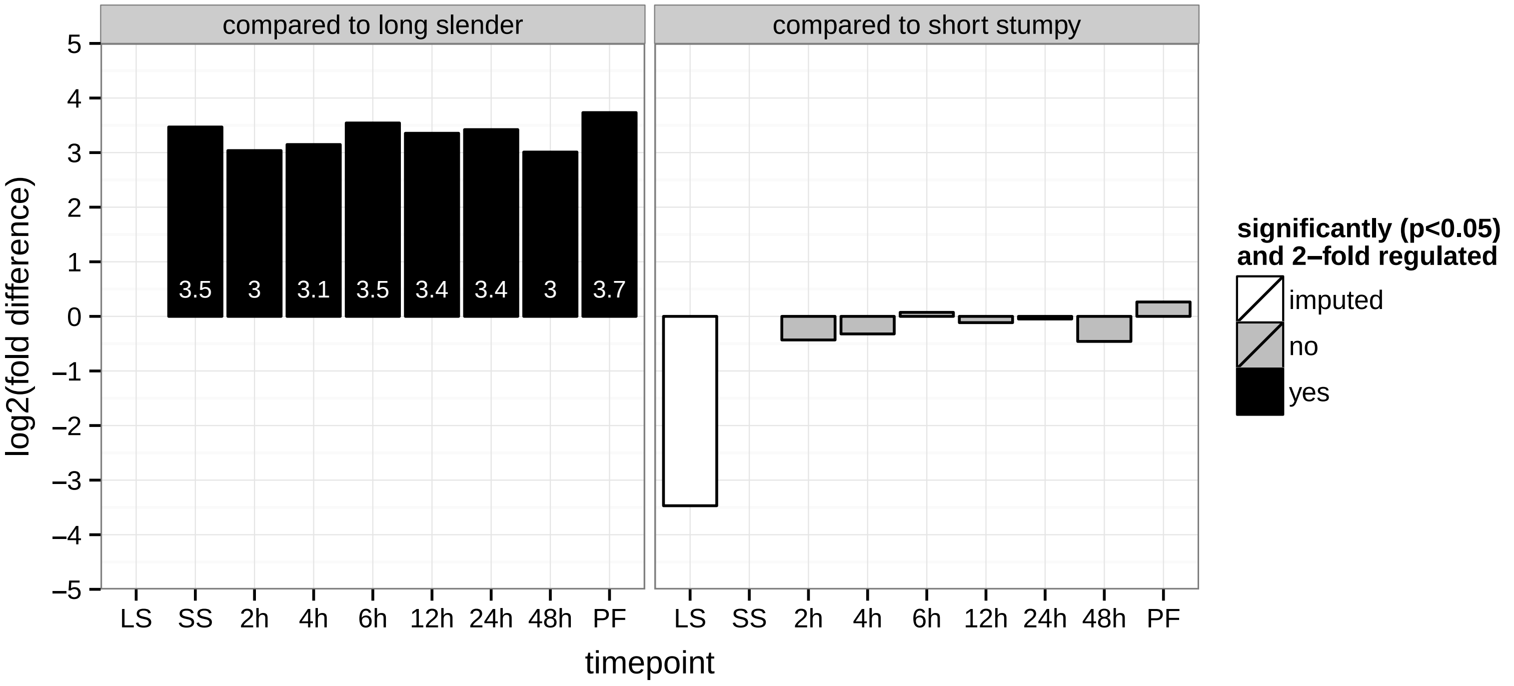
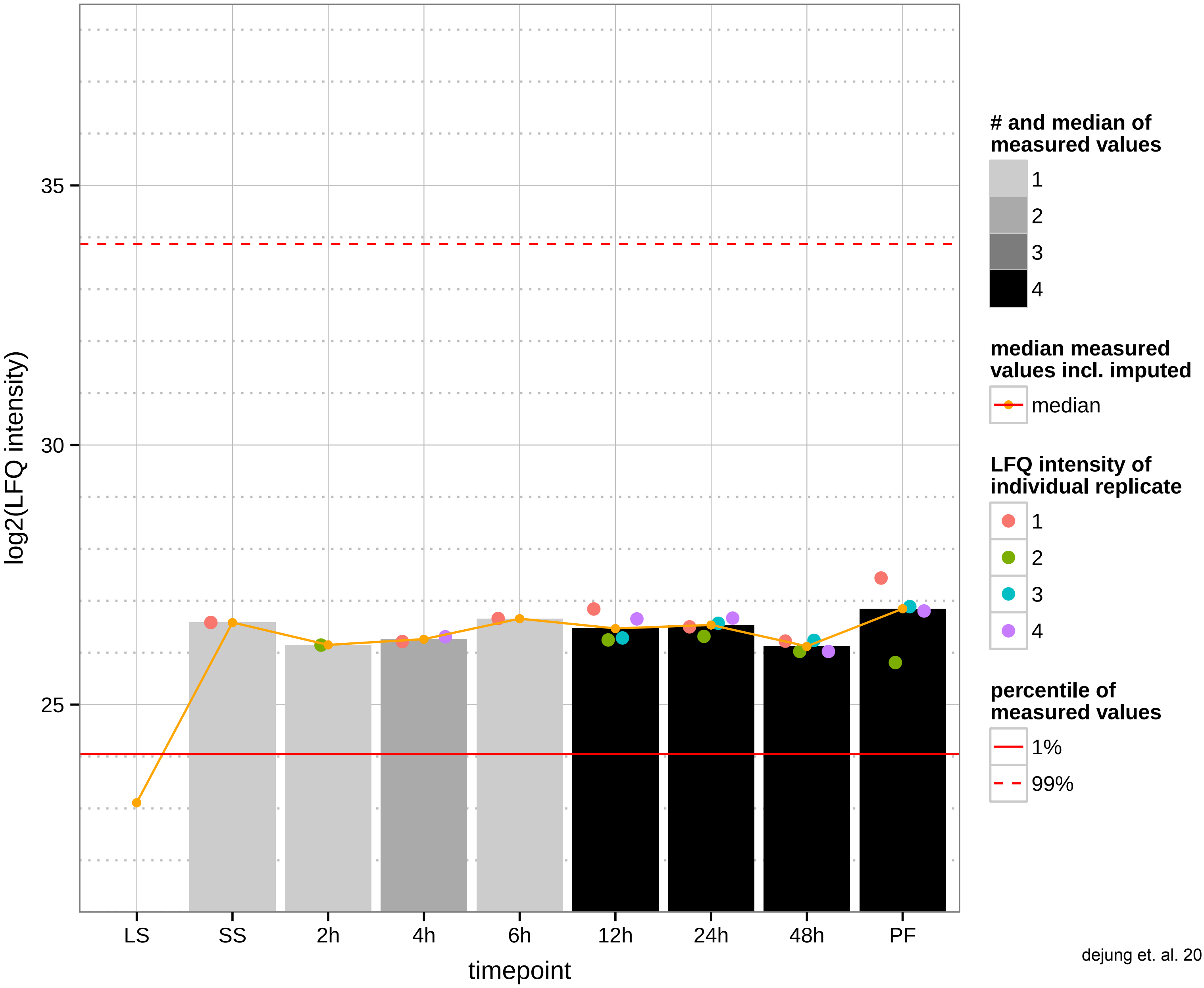
zinc finger CCCH domain containing protein 44 (ZC3H44)
Tb927.11.7890
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null



RNA polymerase B subunit RPB8, putative (RPB8)
Tb927.11.7930
AGOF: DNA–directed RNA polymerase activity
AGOC: null
AGOP: transcription, DNA–dependent
PGOF: null
PGOC: null
PGOP: transcription, DNA–dependent





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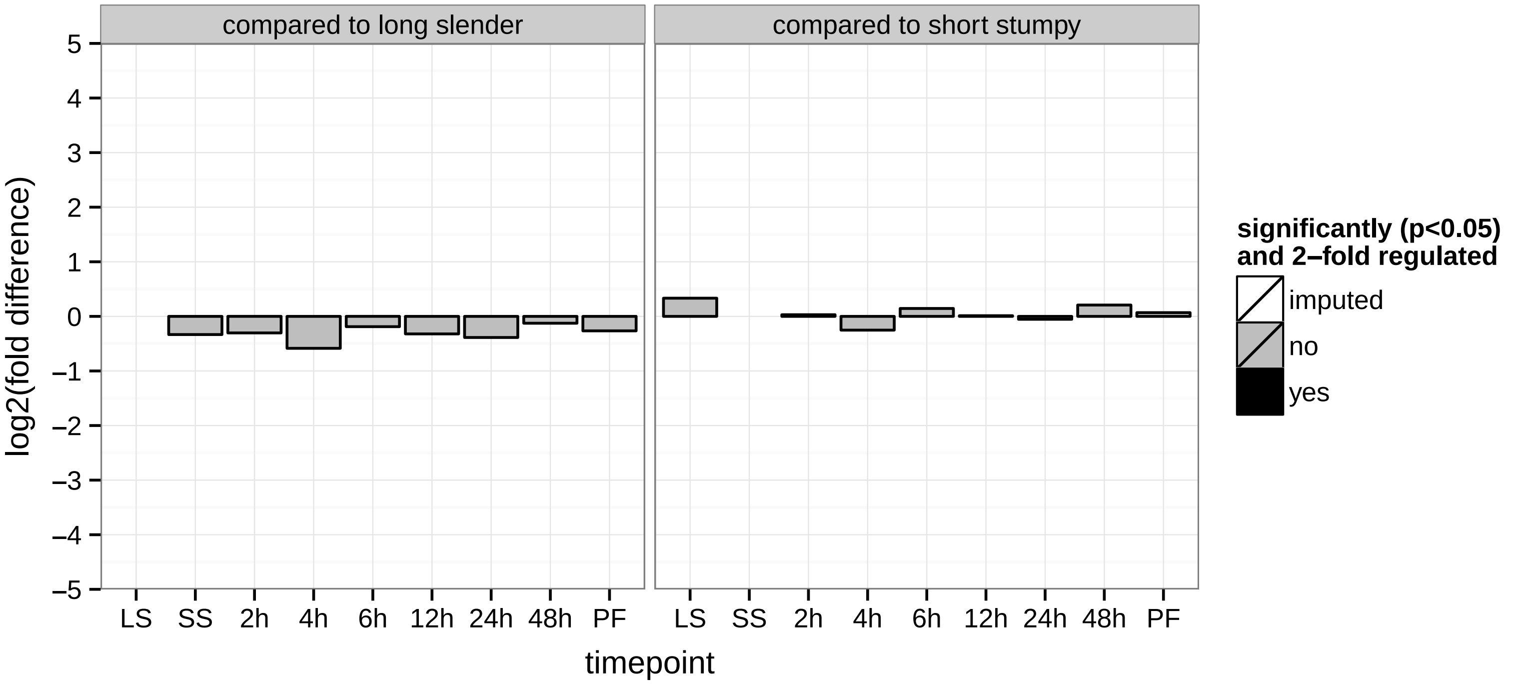
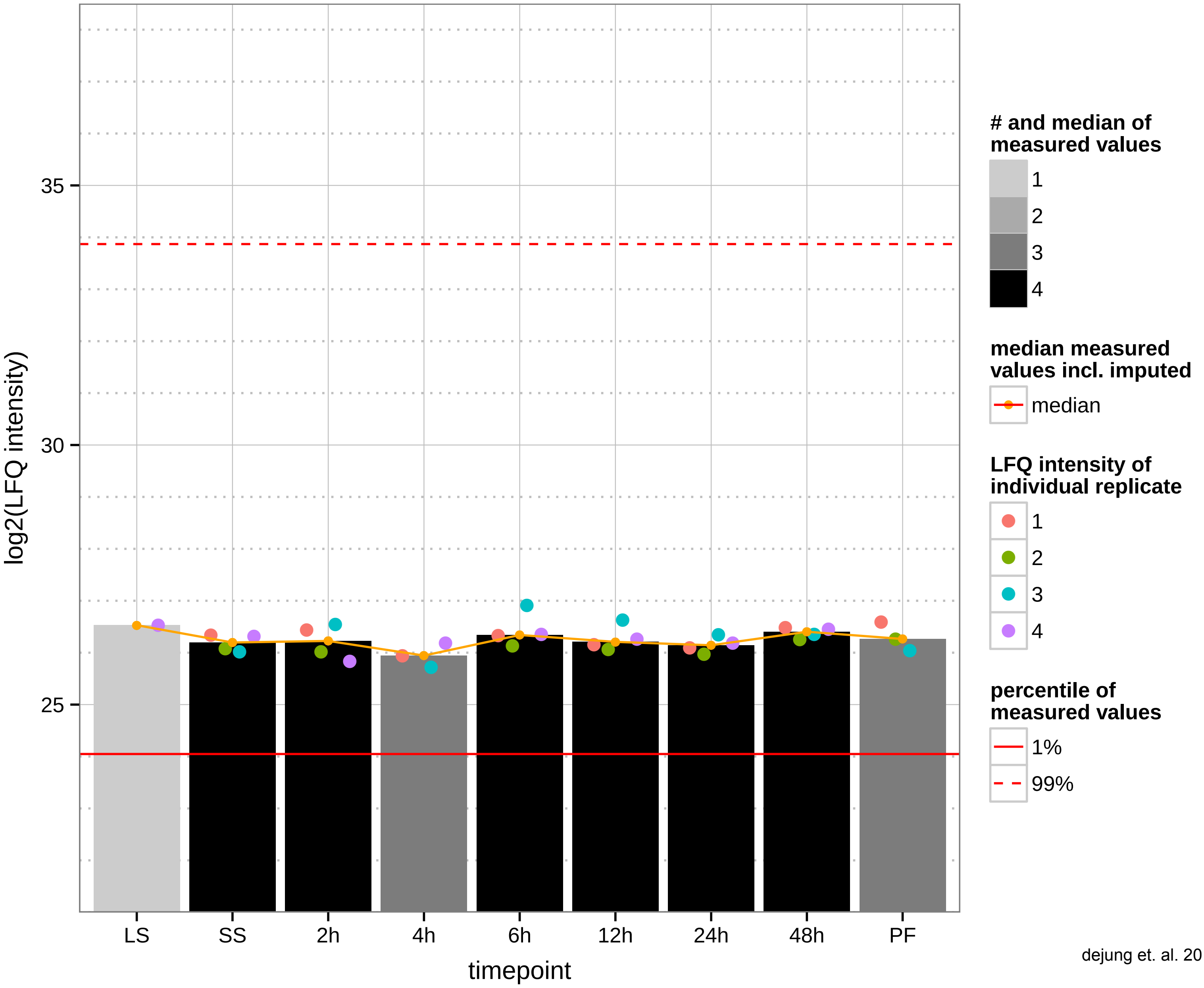
kinetoplast poly(A) polymerase 1, KPAP1
Tb927.11.7960
AGOF: polynucleotide adenylyltransferase activity
AGOC: mitochondrion
AGOP: mRNA polyadenylation
PGOF: null
PGOC: null
PGOP: null





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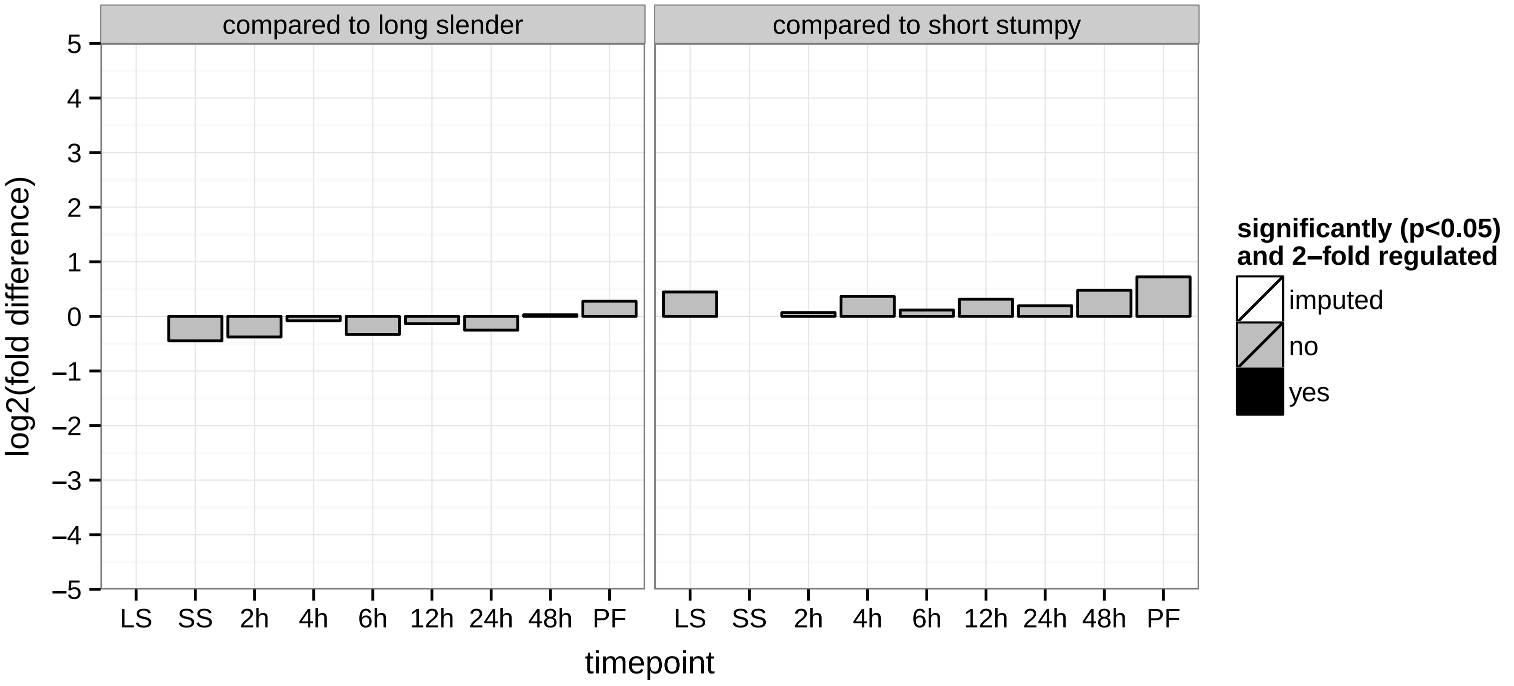
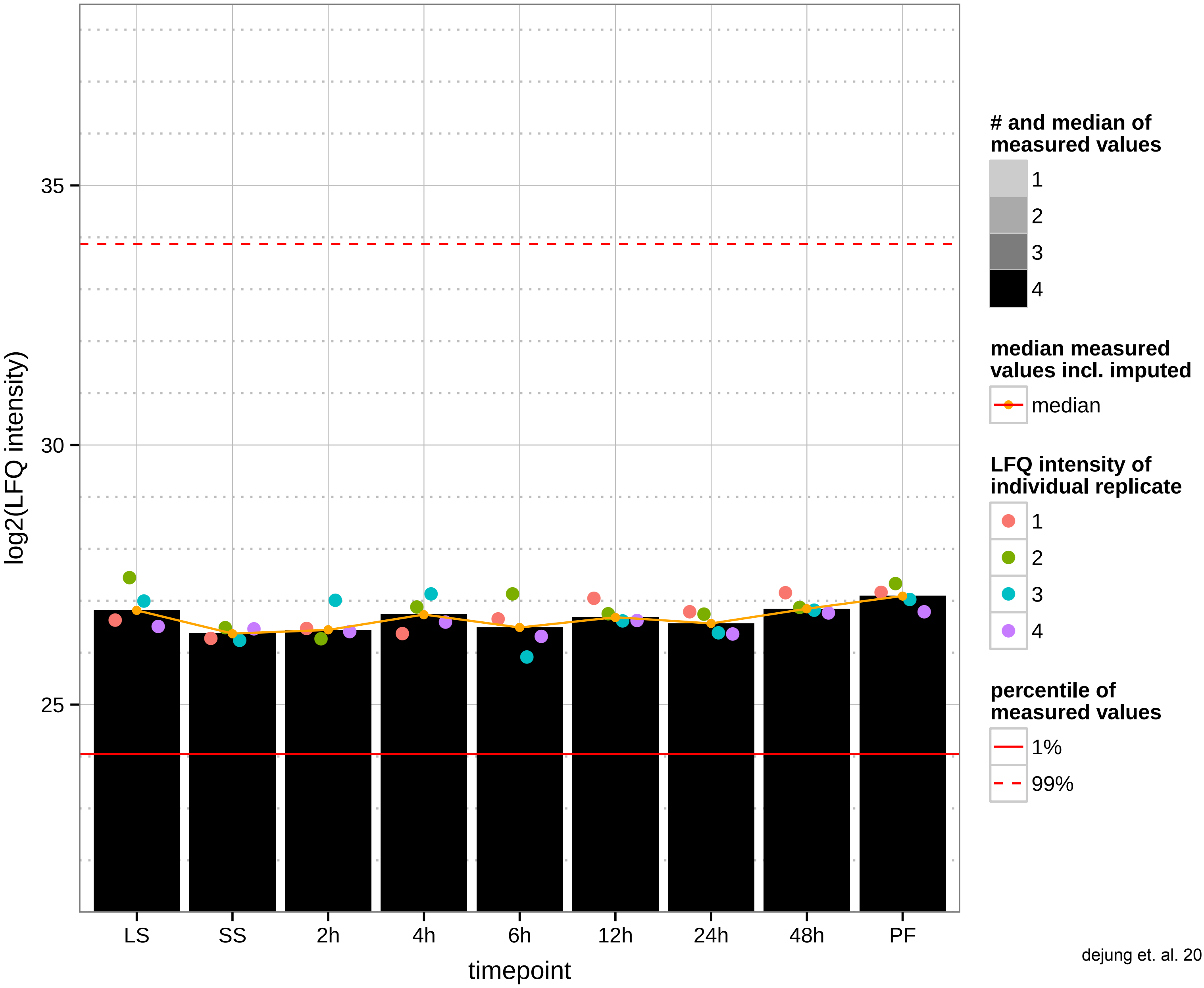
hypothetical protein, conserved
Tb927.11.8030
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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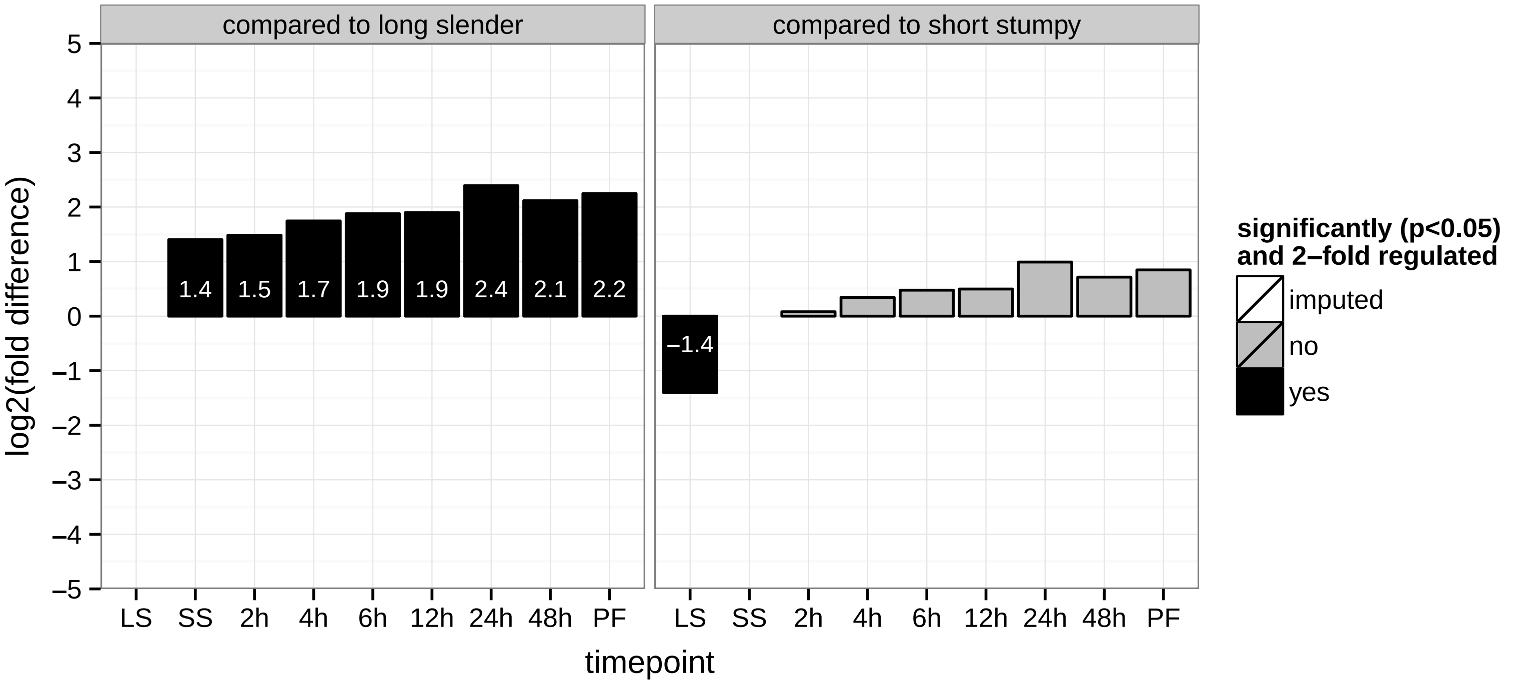
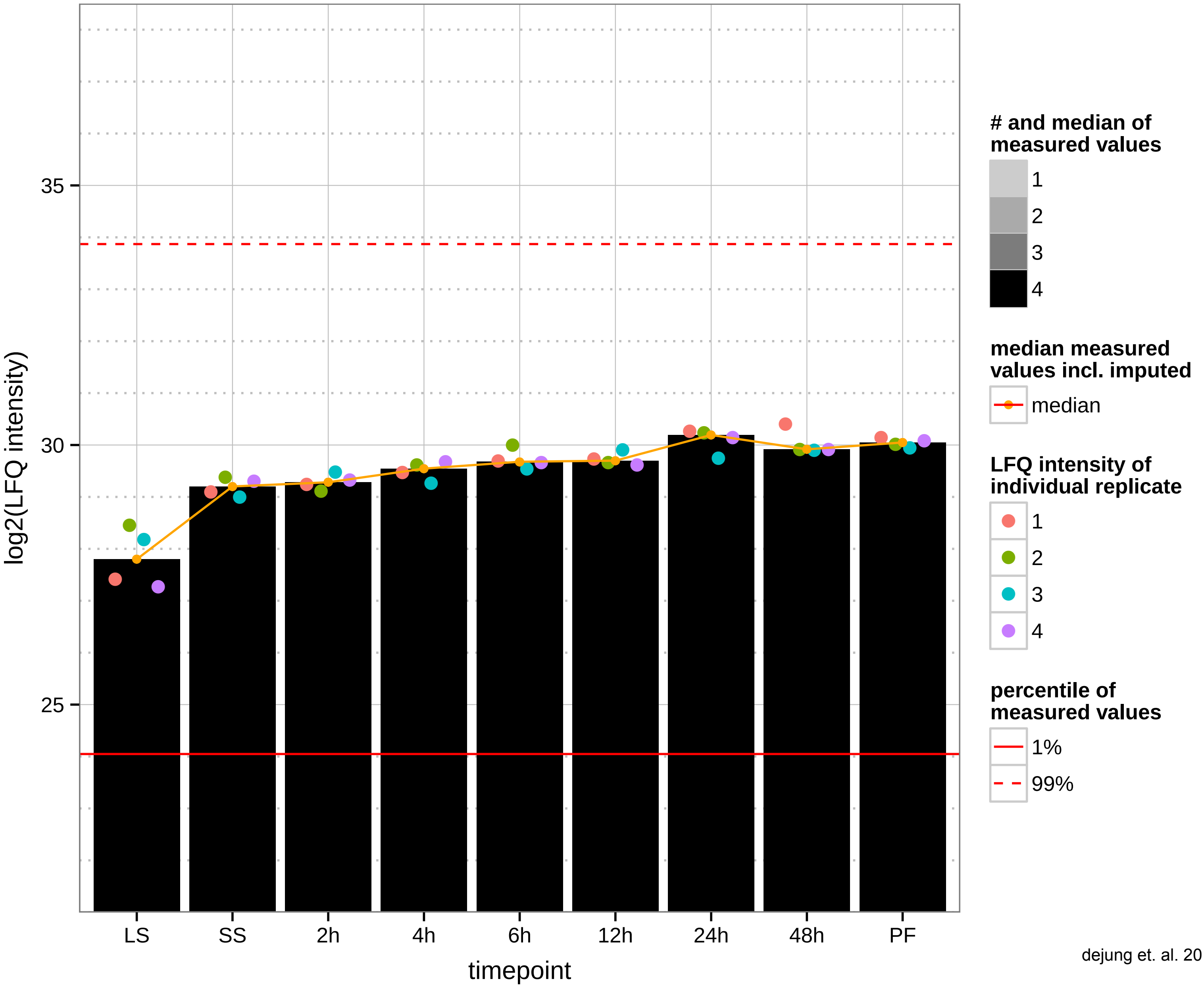
hypothetical protein, conserved
Tb927.11.8050
AGOF: null
AGOC: nucleus
AGOP: gene silencing
PGOF: null
PGOC: nucleus
PGOP: gene silencing





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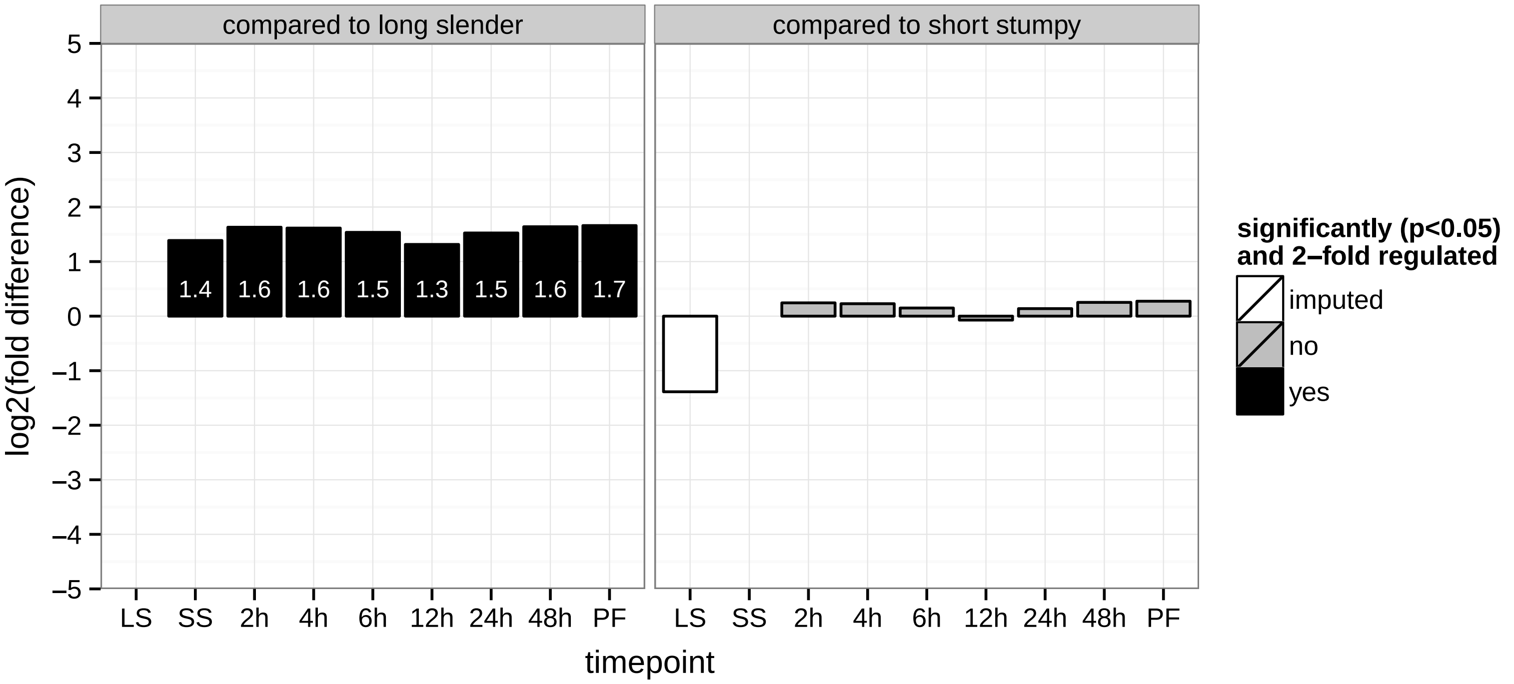
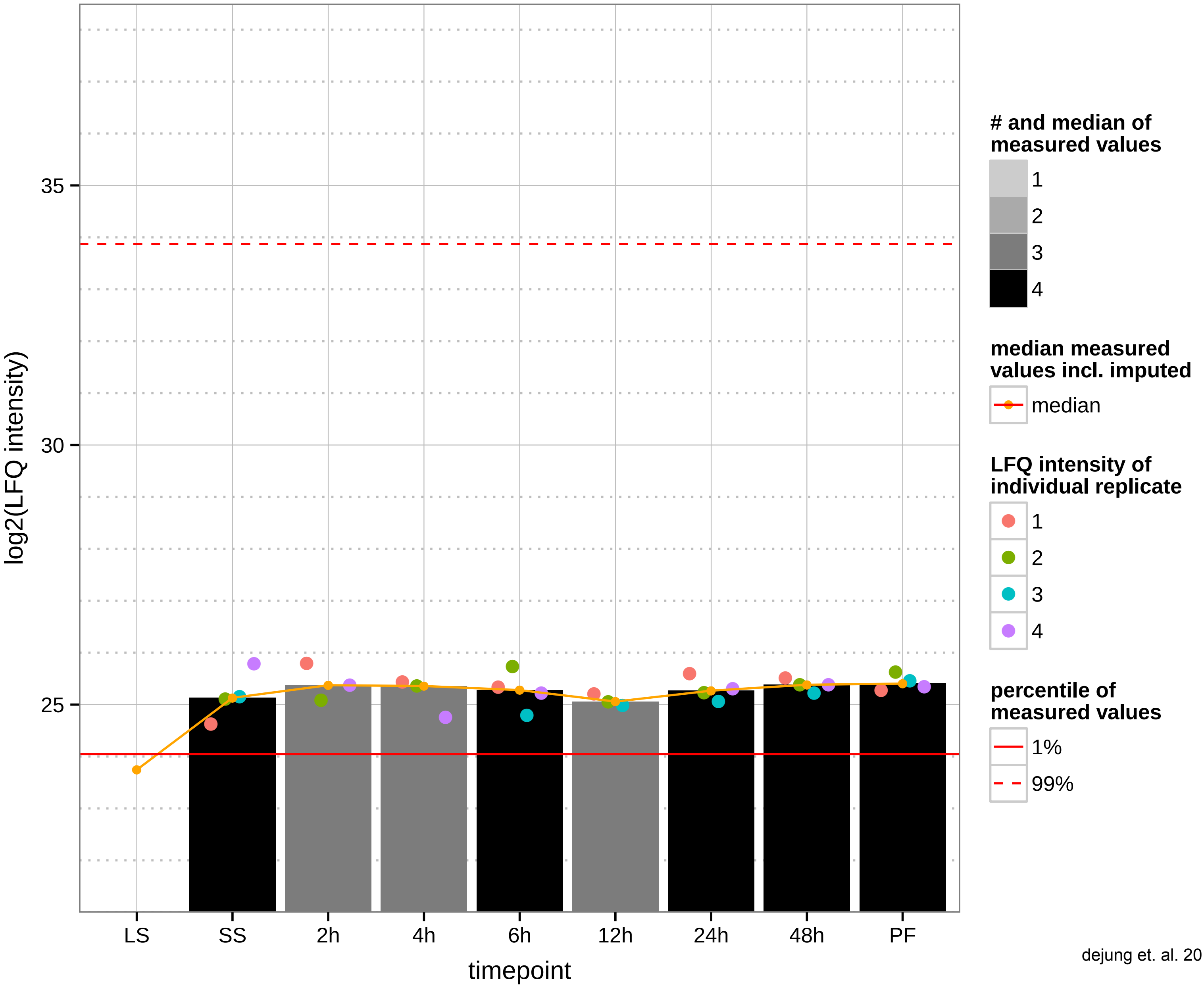
hypothetical protein, conserved
Tb927.11.8080
AGOF: voltage−gated potassium channel activity
AGOC: membrane, voltage−gated potassium channel complex
AGOP: potassium ion transport
PGOF: protein binding
PGOC: null
PGOP: protein homooligomerization





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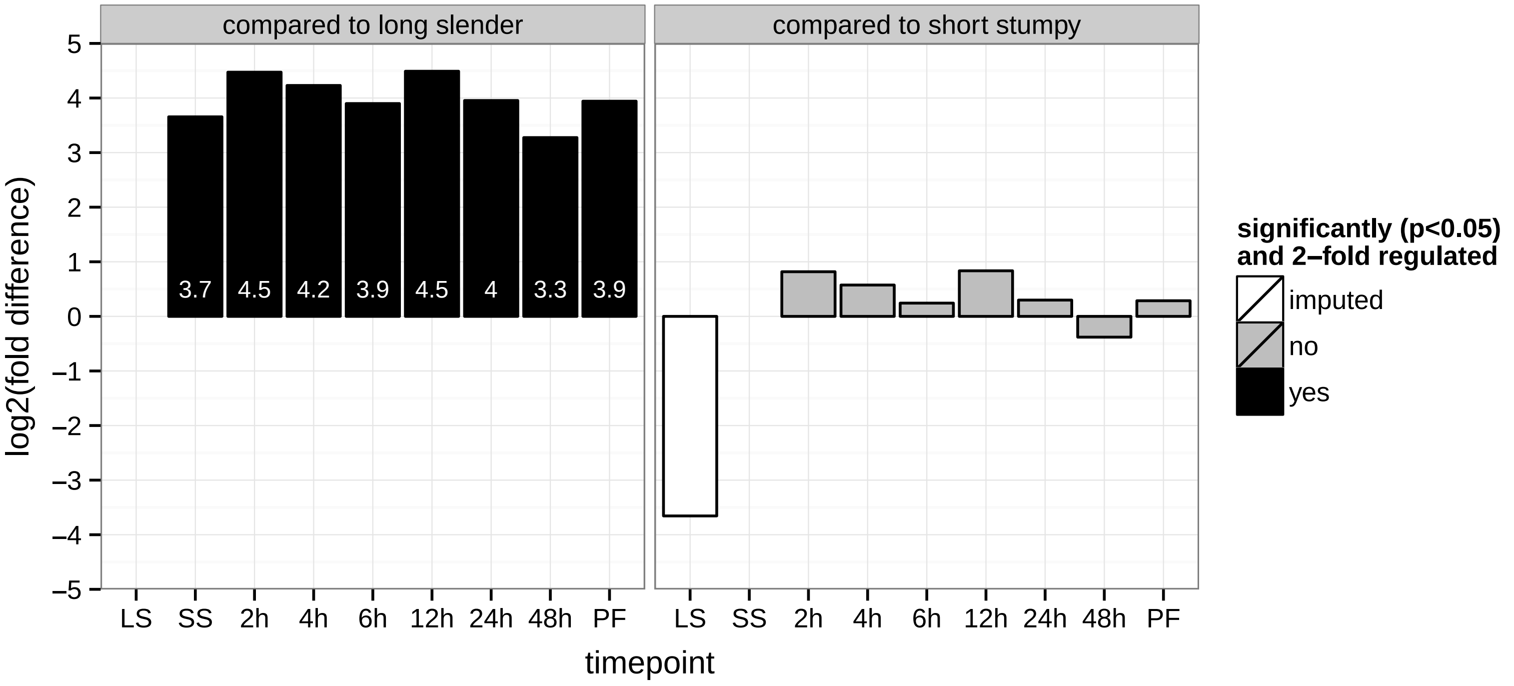
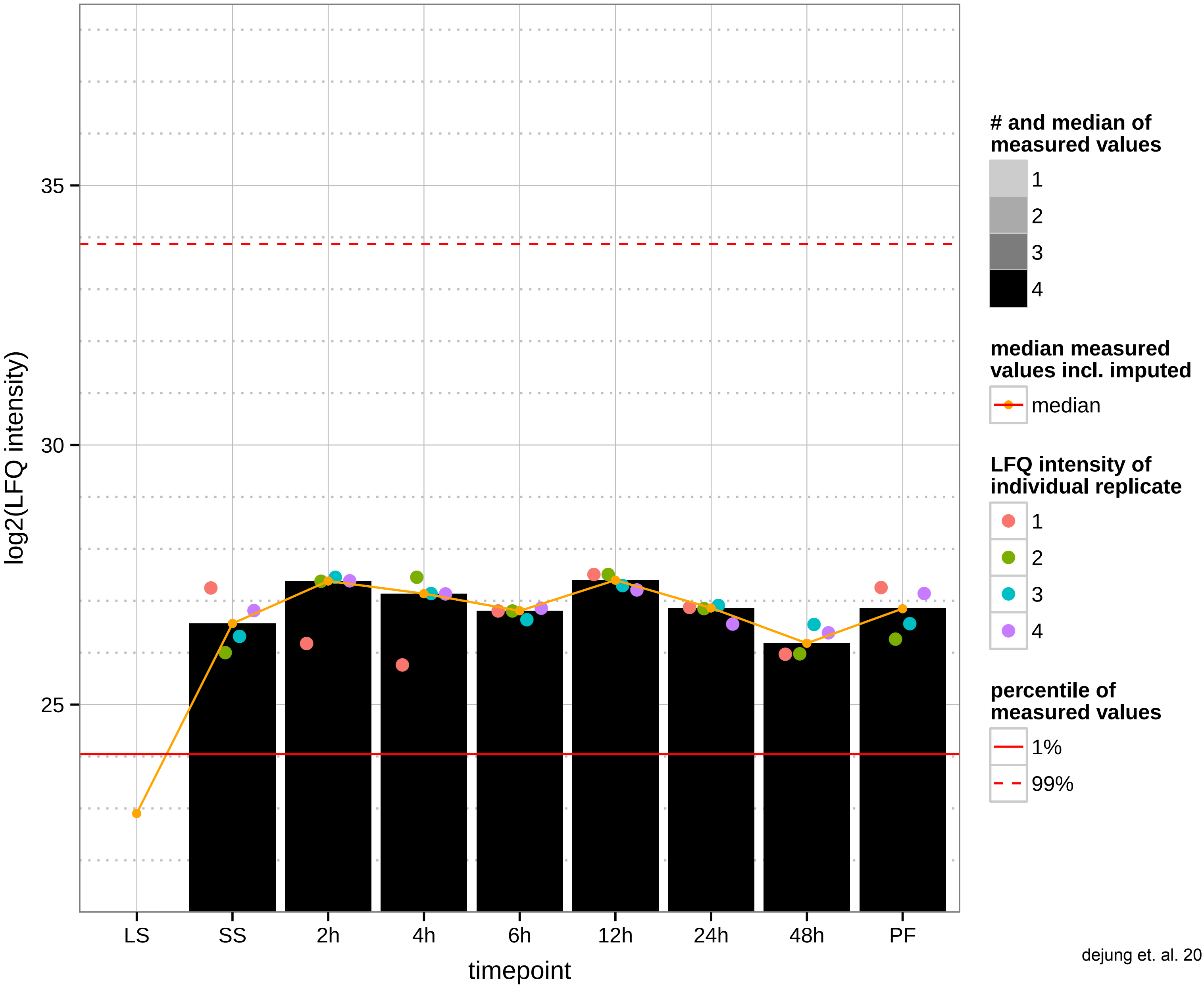
protein transport protein SEC13, putative
Tb927.11.8120
AGOF: null
AGOC: null
AGOP: intracellular protein transport
PGOF: protein binding
PGOC: null
PGOP: null





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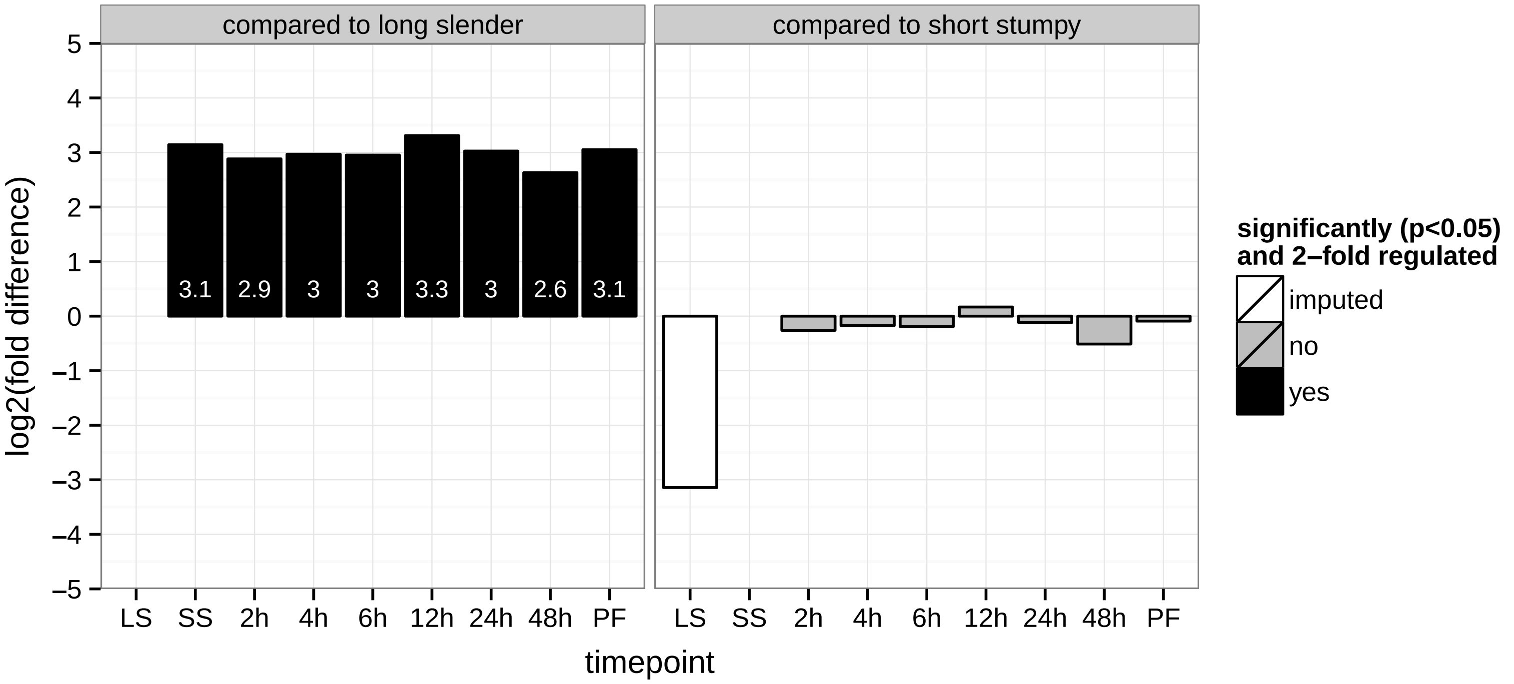
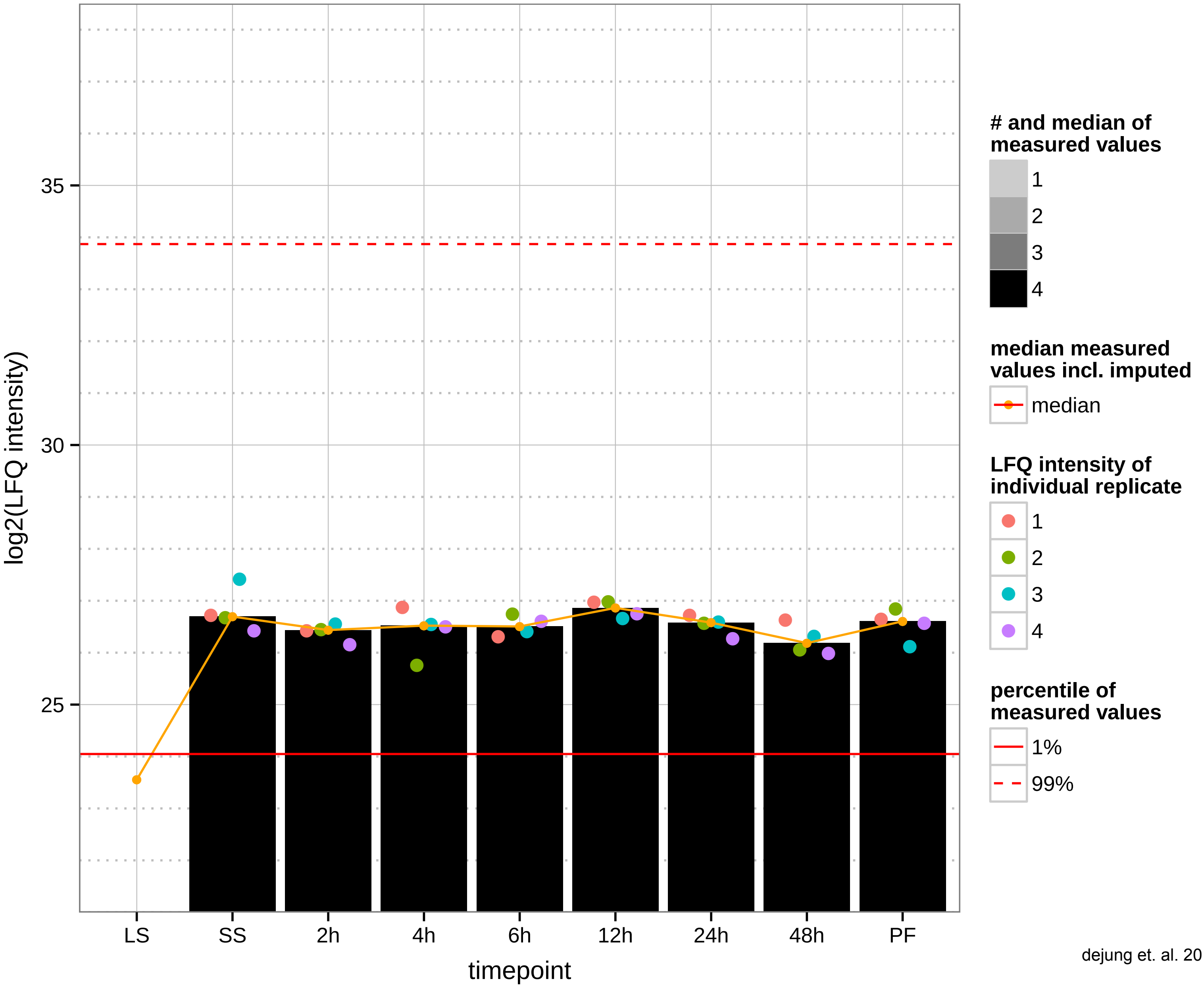
ER lumen retaining receptor protein, putative
Tb927.11.8140
AGOF: ER retention sequence binding
AGOC: integral to membrane
AGOP: protein retention in ER lumen
PGOF: ER retention sequence binding
PGOC: integral to membrane
PGOP: protein retention in ER lumen





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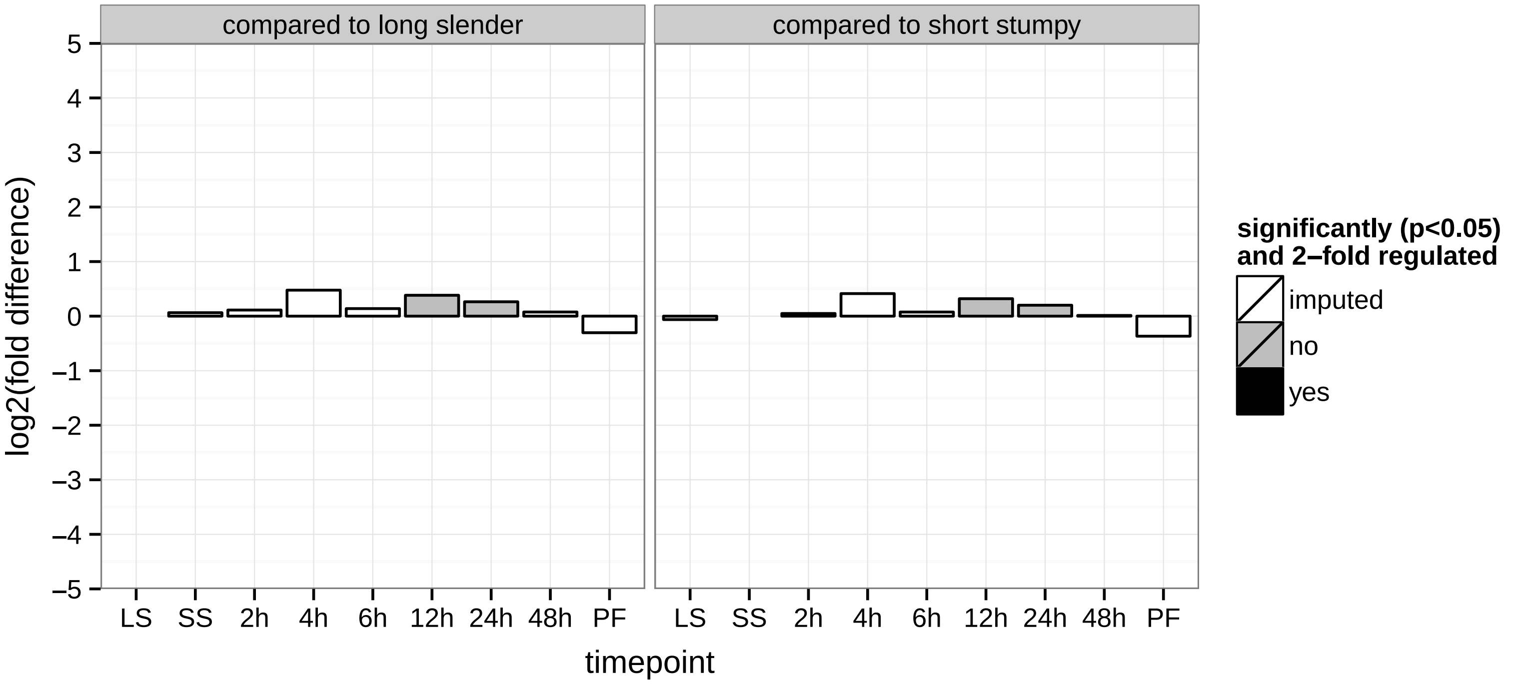
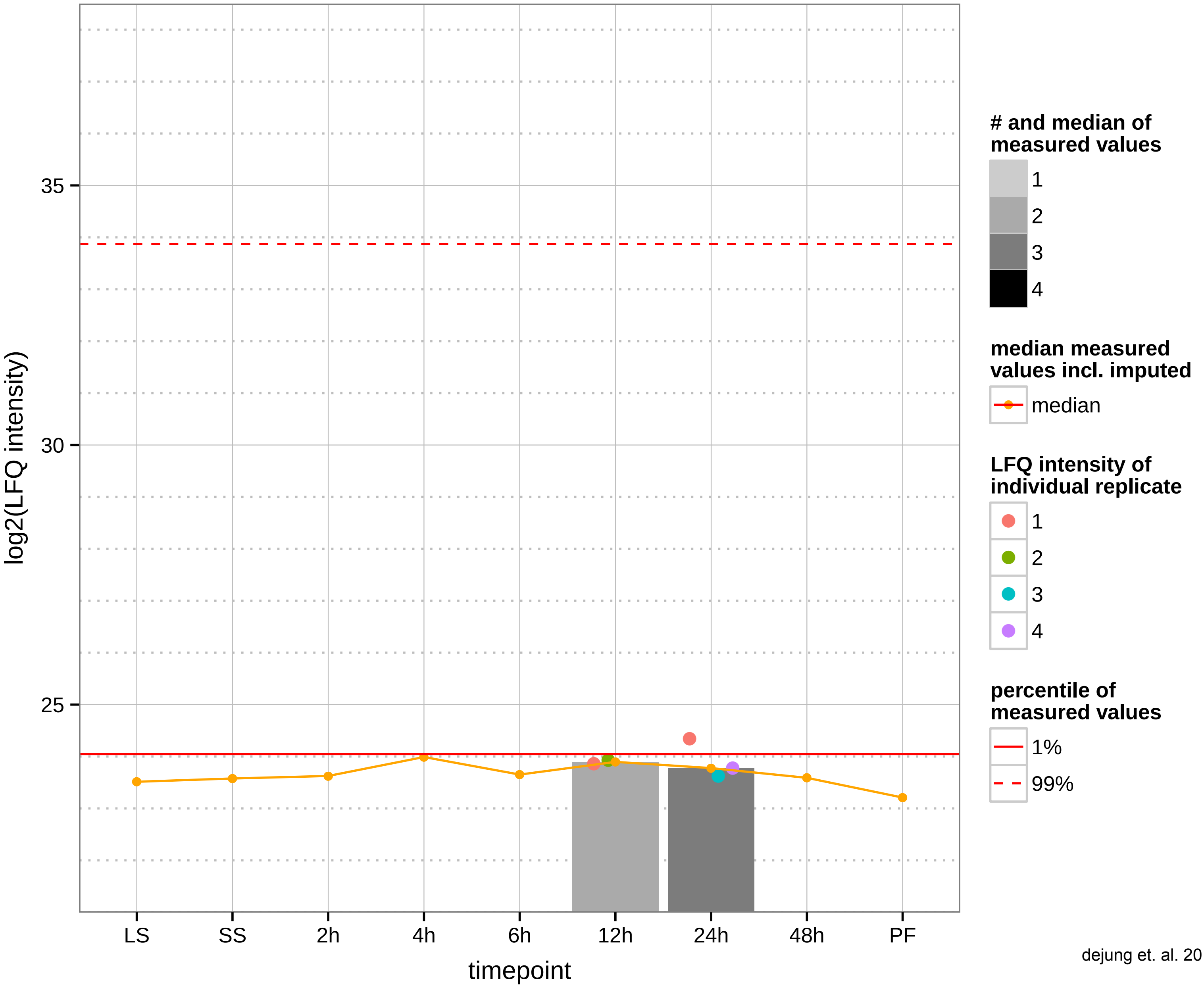
protein kinase, putative
Tb927.11.8150
AGOF: null, ATP binding, protein tyrosine kinase activity
AGOC: null
AGOP: null, protein phosphorylation
PGOF: binding, ATP binding, binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: null, protein phosphorylation





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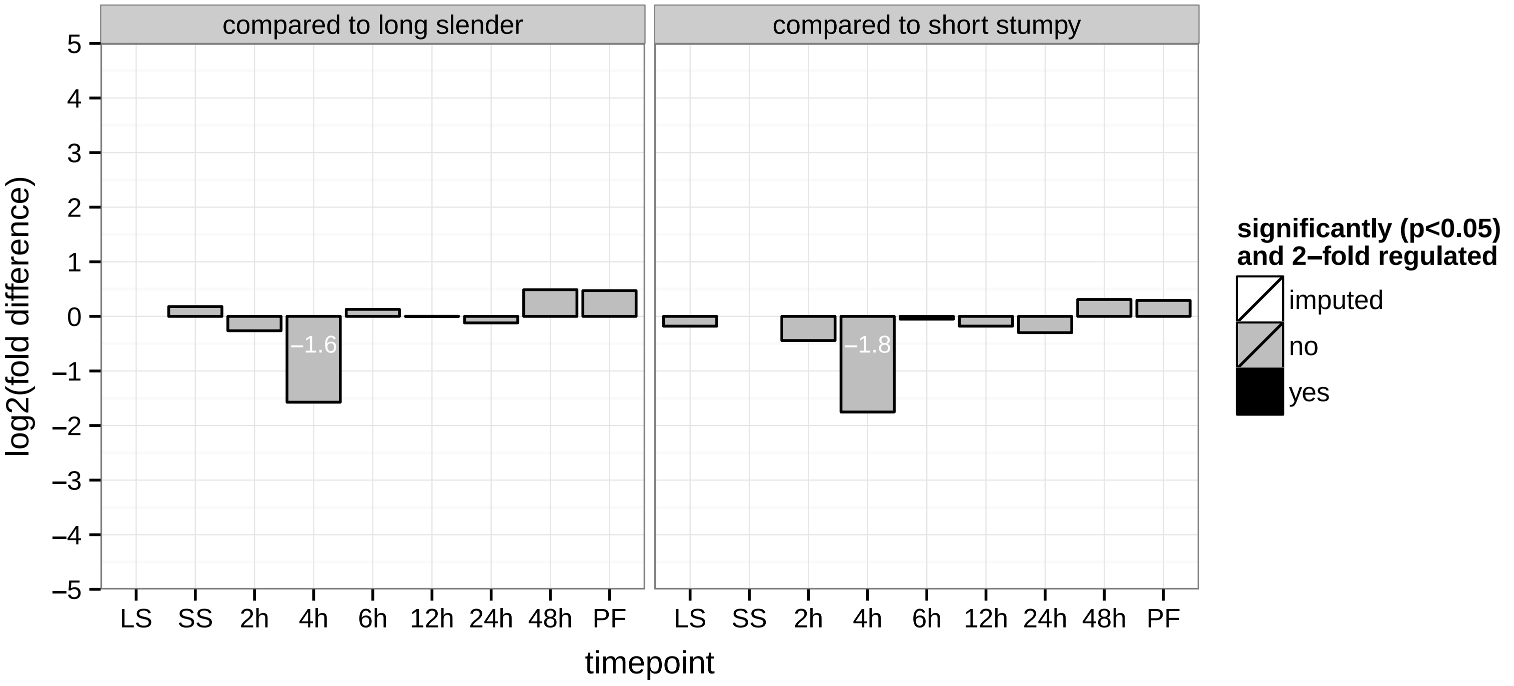
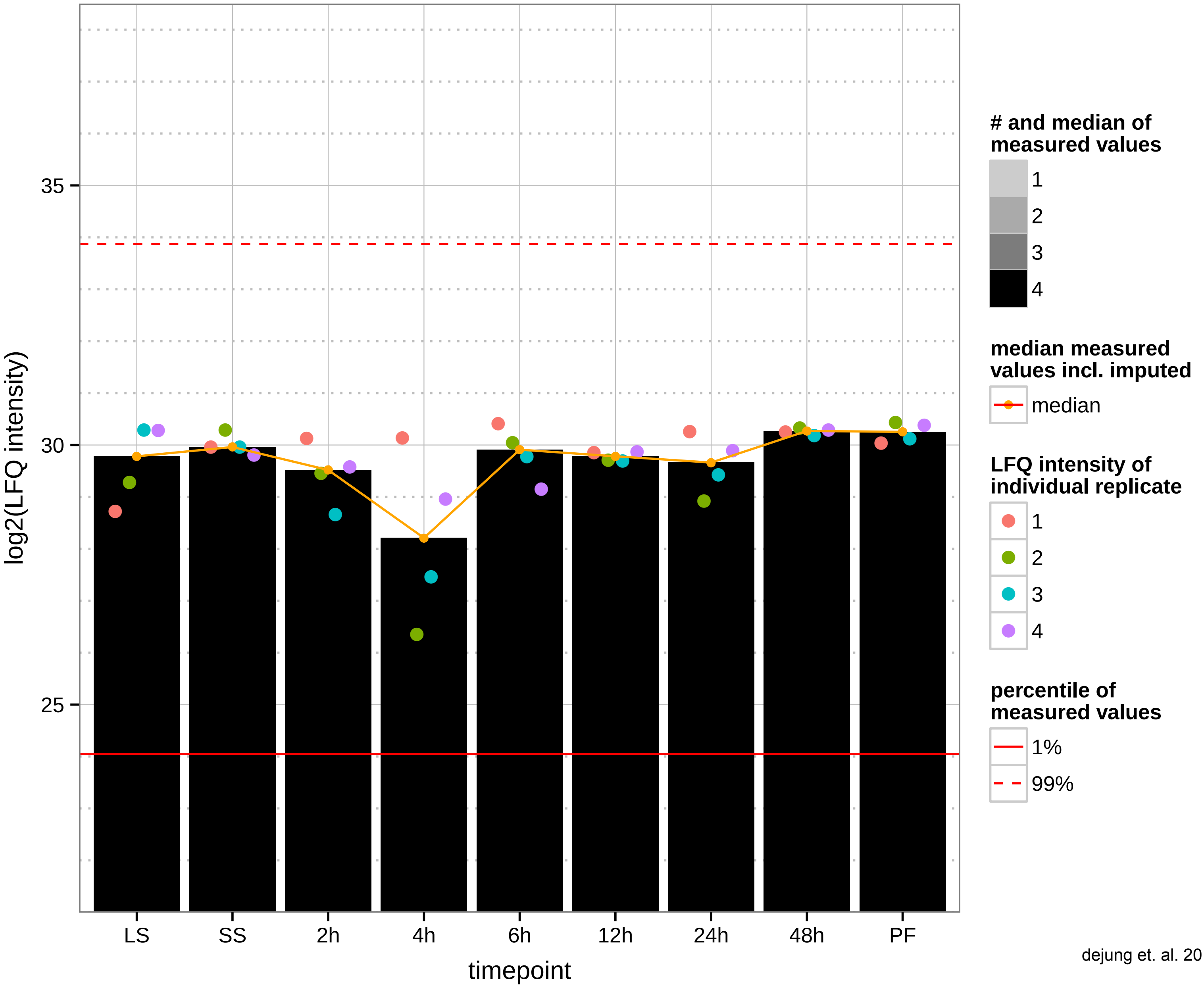
dynein heavy chain, putative
Tb927.11.8160
AGOF: ATP binding, ATPase activity, microtubule motor activity
AGOC: dynein complex
AGOP: microtubule–based movement
PGOF: microtubule motor activity
PGOC: dynein complex
PGOP: microtubule–based movement





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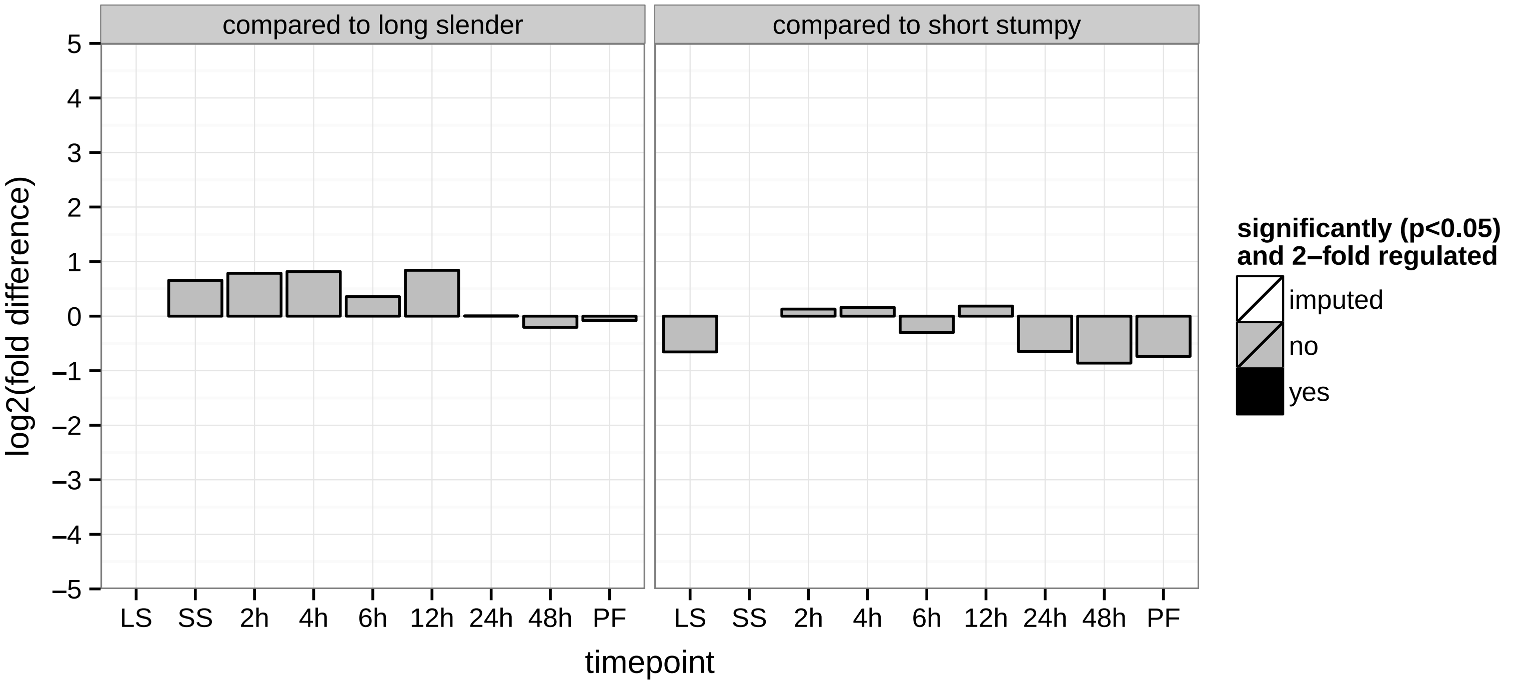
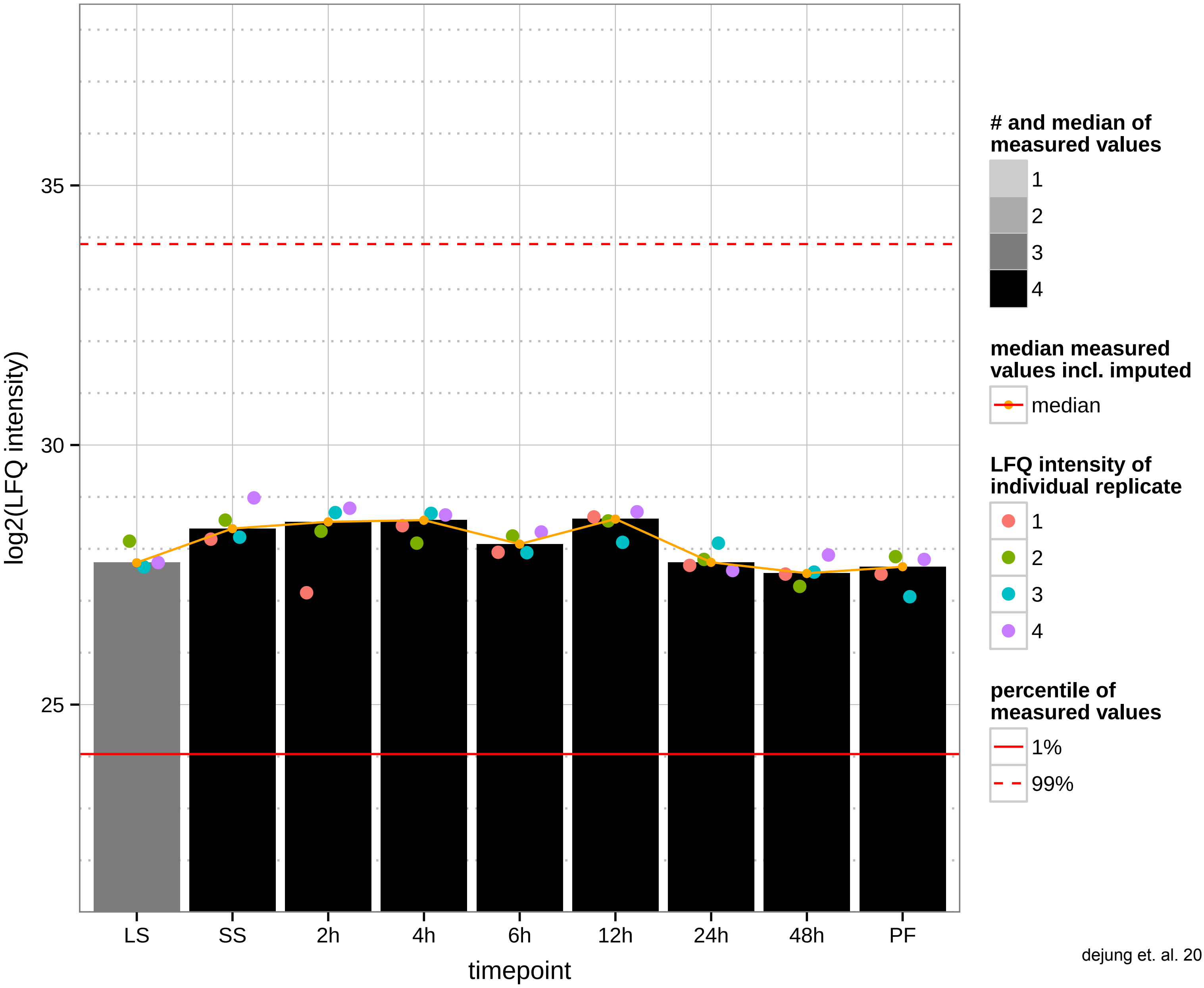
carbonic anhydrase–like protein
Tb927.11.8260
AGOF: carbonate dehydratase activity, zinc ion binding
AGOC: null
AGOP: one–carbon metabolic process
PGOF: null
PGOC: null
PGOP: null





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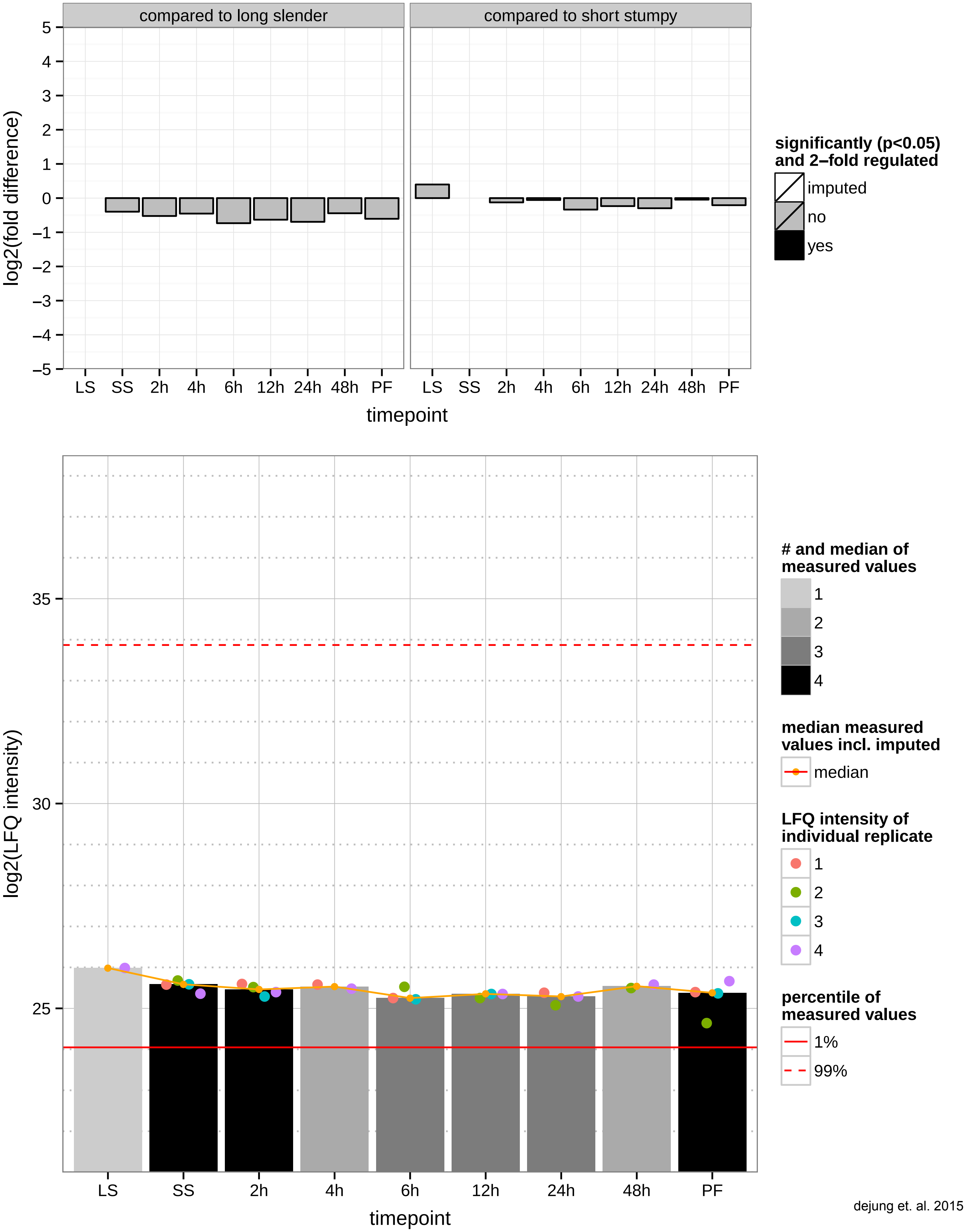
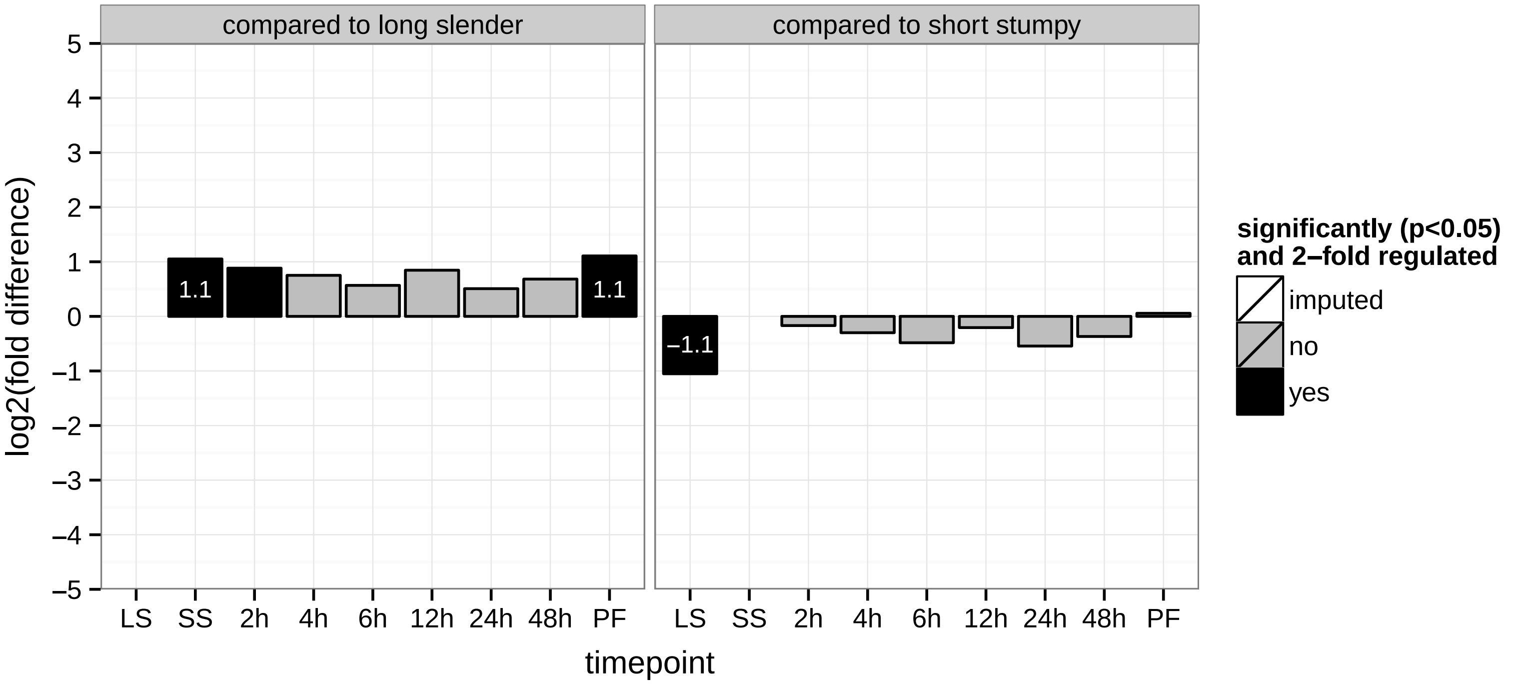
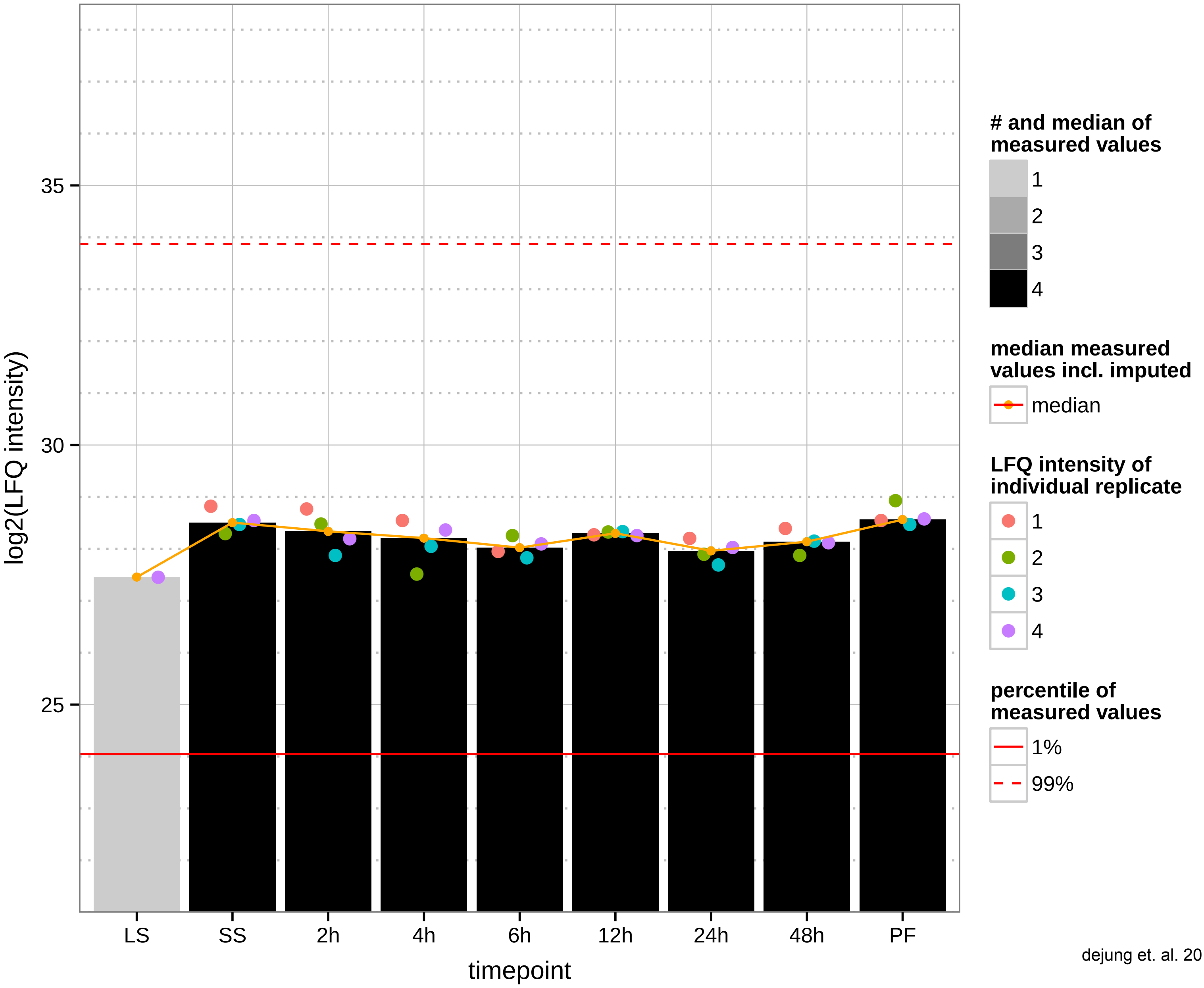
hypothetical protein, conserved
Tb927.11.8300
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



class I transcription factor A, subunit 4 (CITFA−4)
Tb927.11.8310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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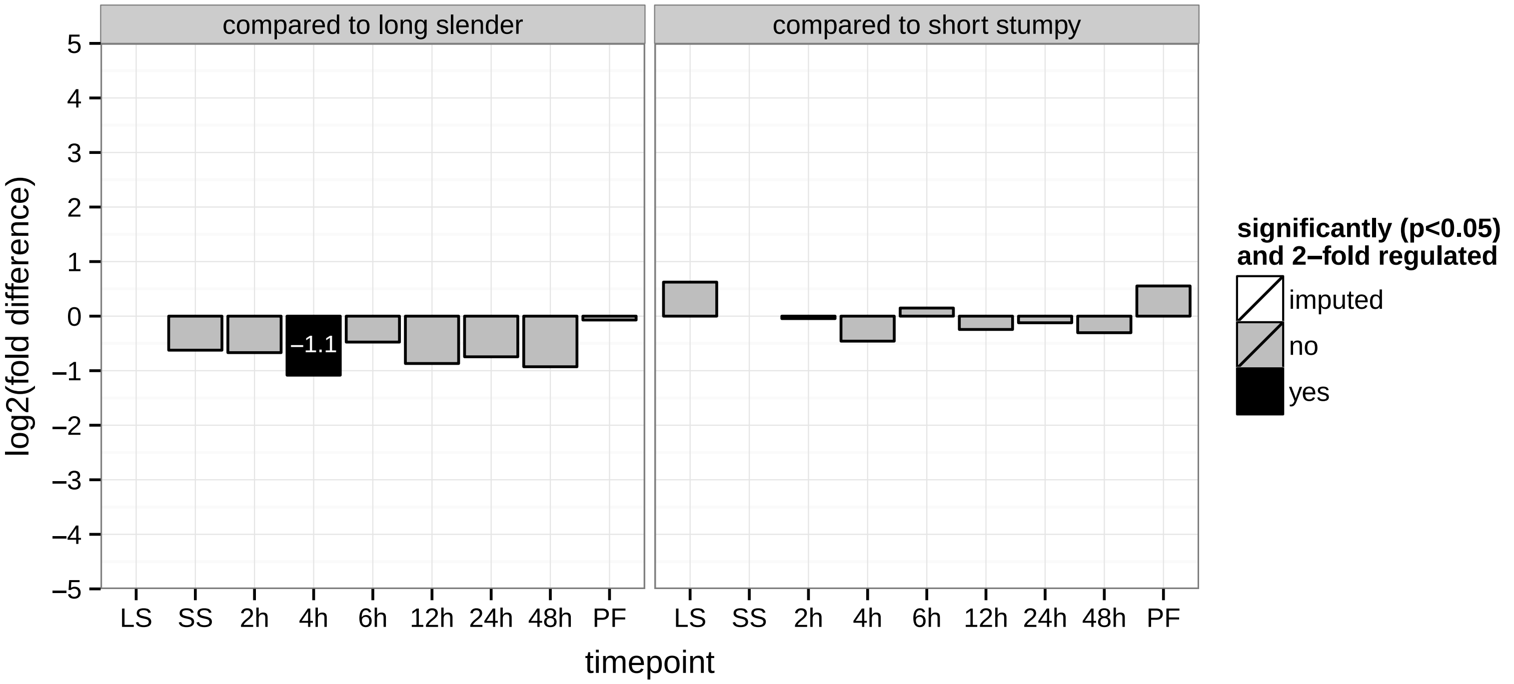
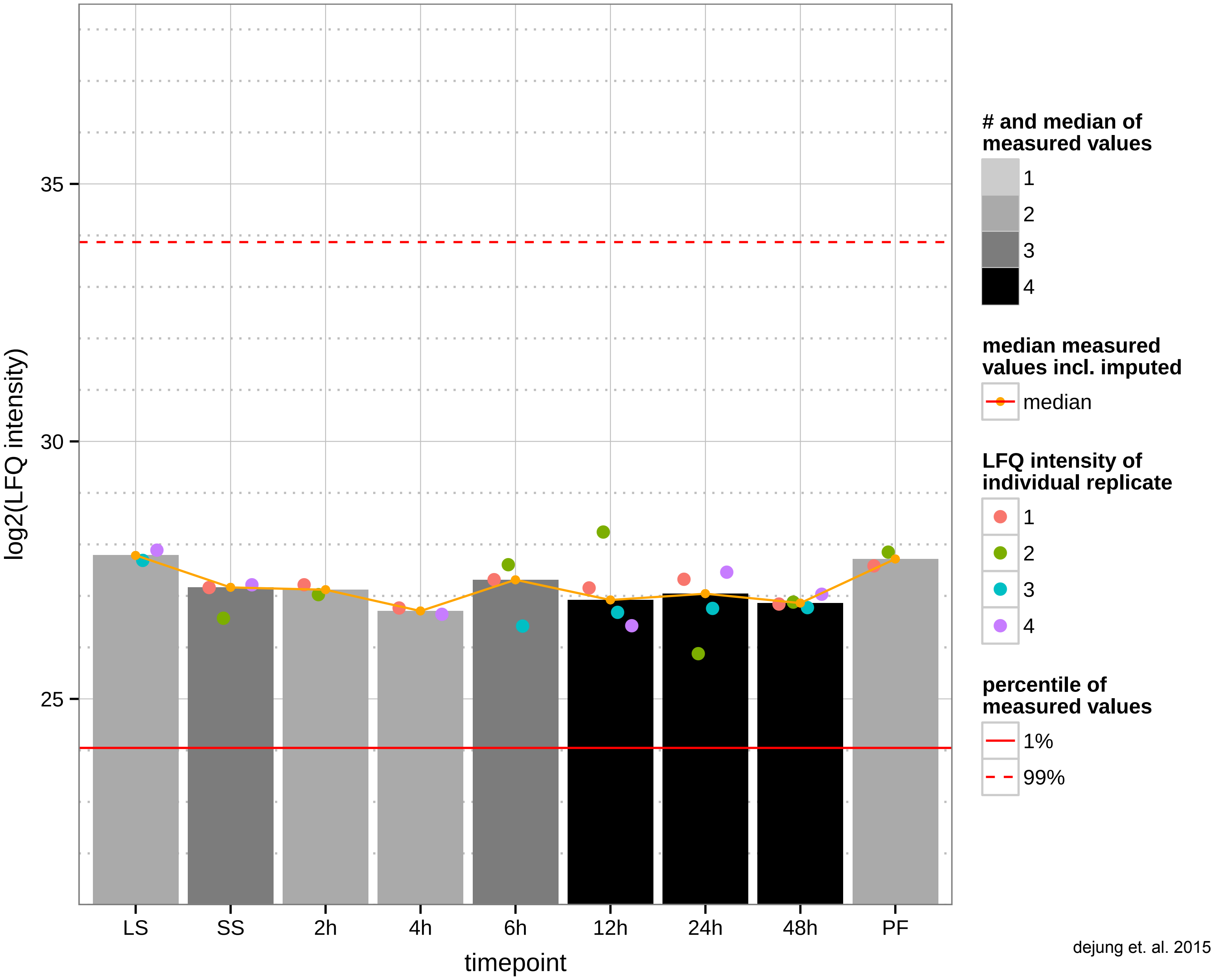
hypothetical protein, conserved
Tb927.11.8390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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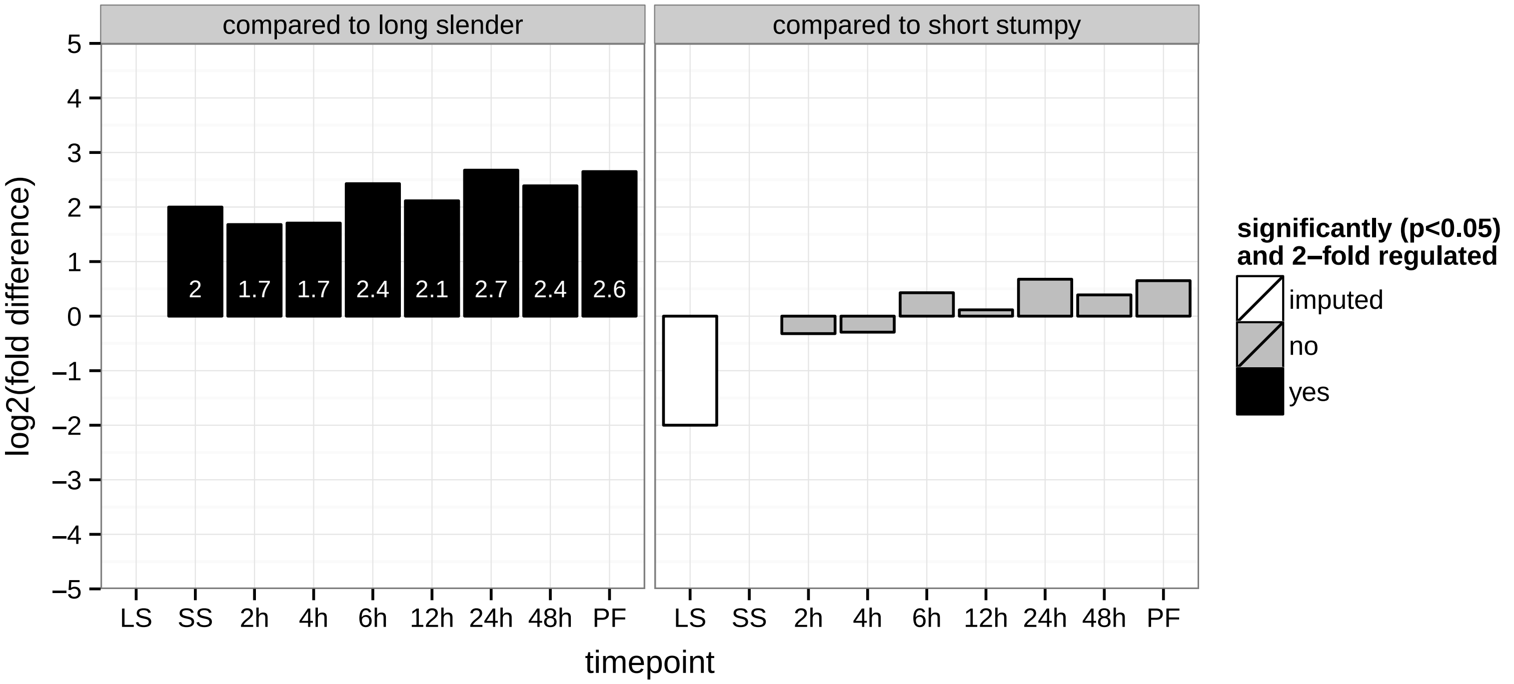
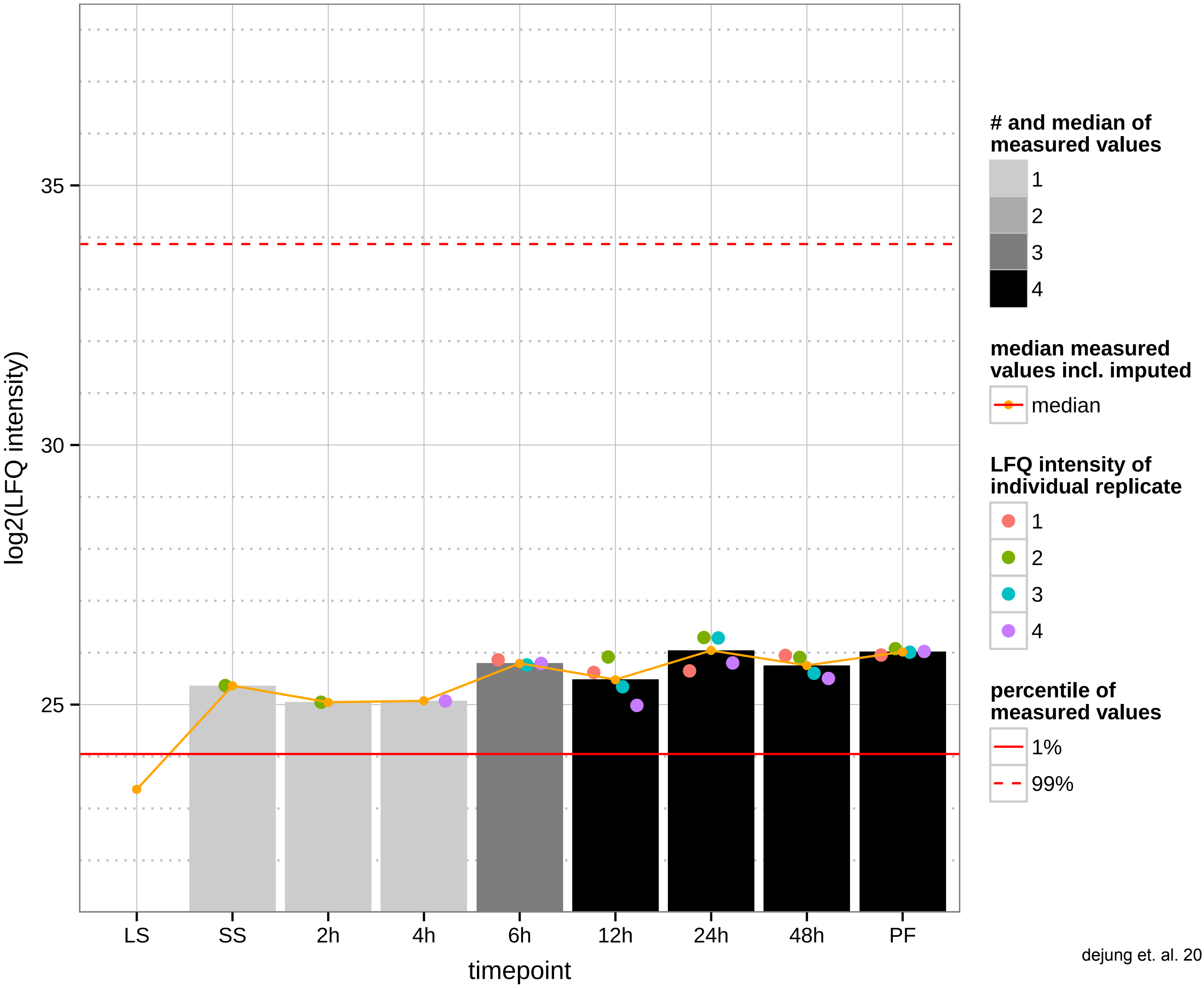
hypothetical protein, conserved
Tb927.11.8450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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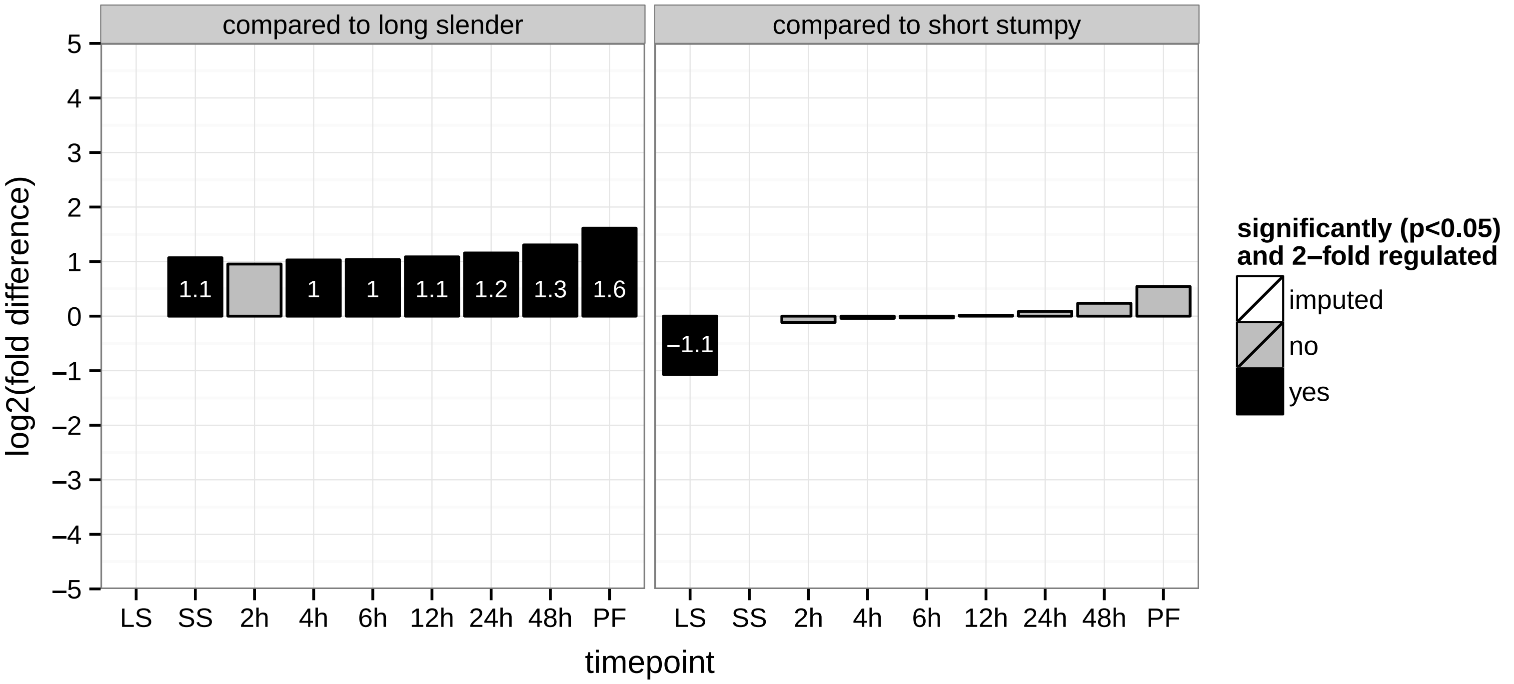
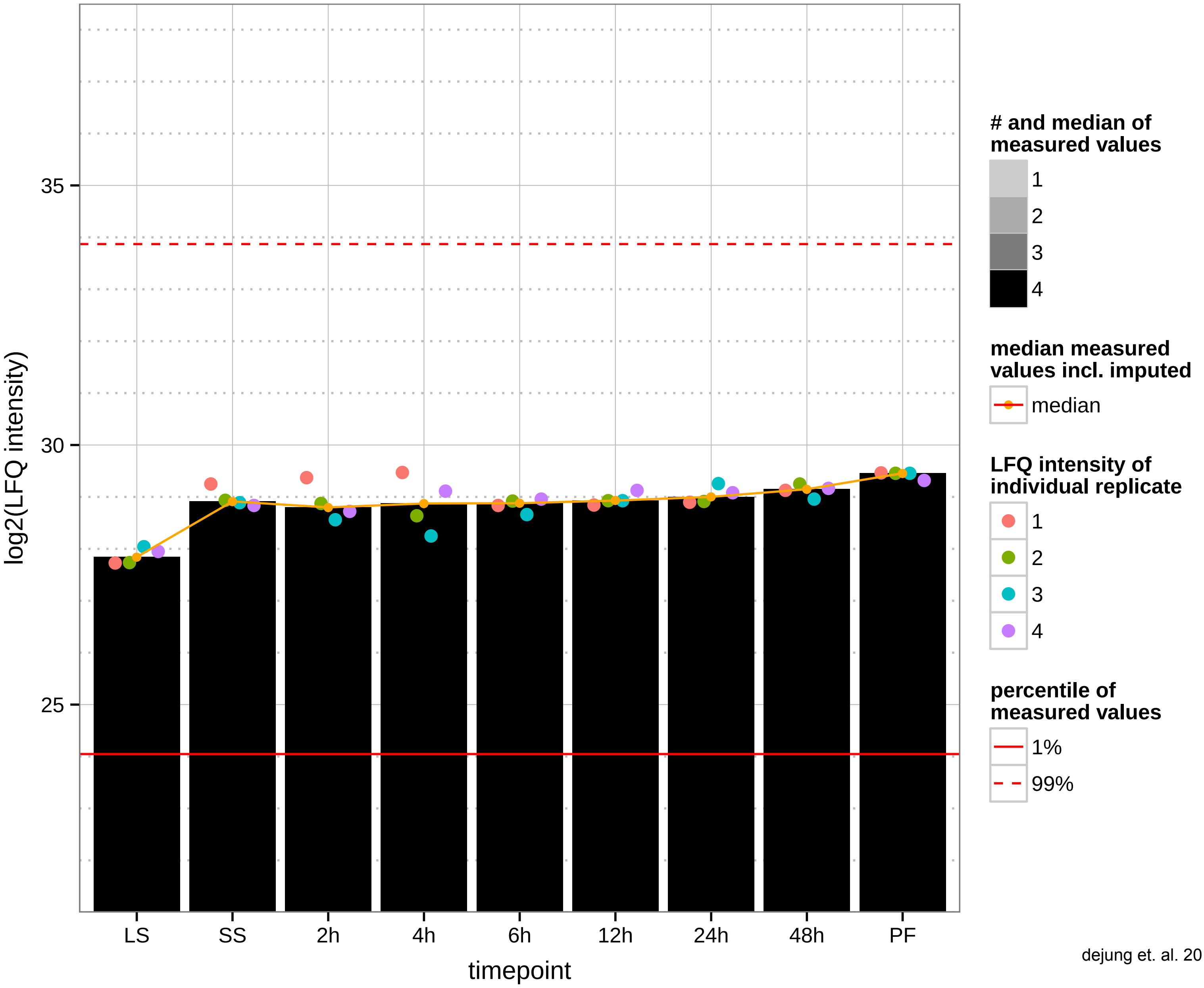
ATP−dependent RNA helicase FAL1, putative
Tb927.11.8770
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: nucleolus
AGOP: maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA)
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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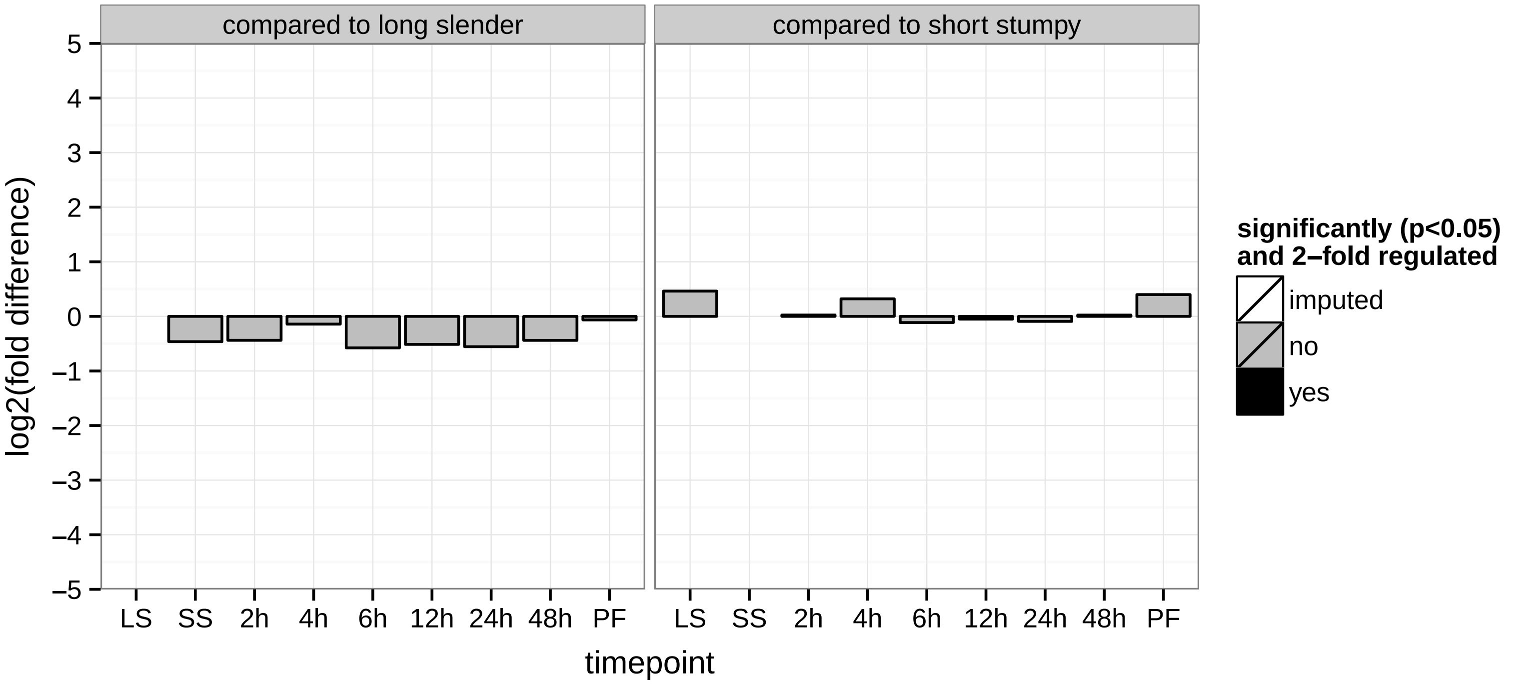
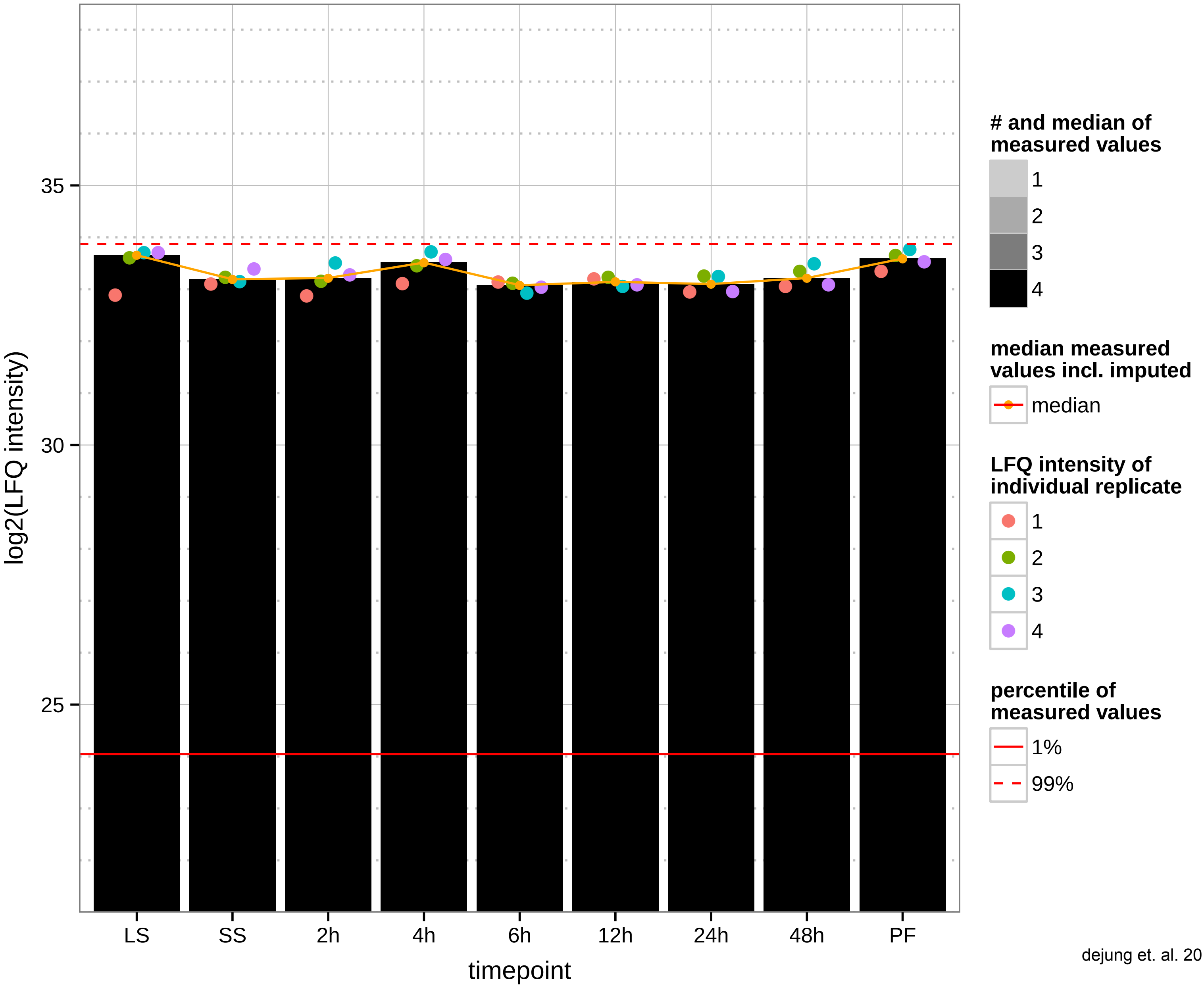
cyclophilin a, cyclophilin type peptidyl–prolyl cis–trans isomerase (CYPA)
Tb927.11.880
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: cilium, cytosol
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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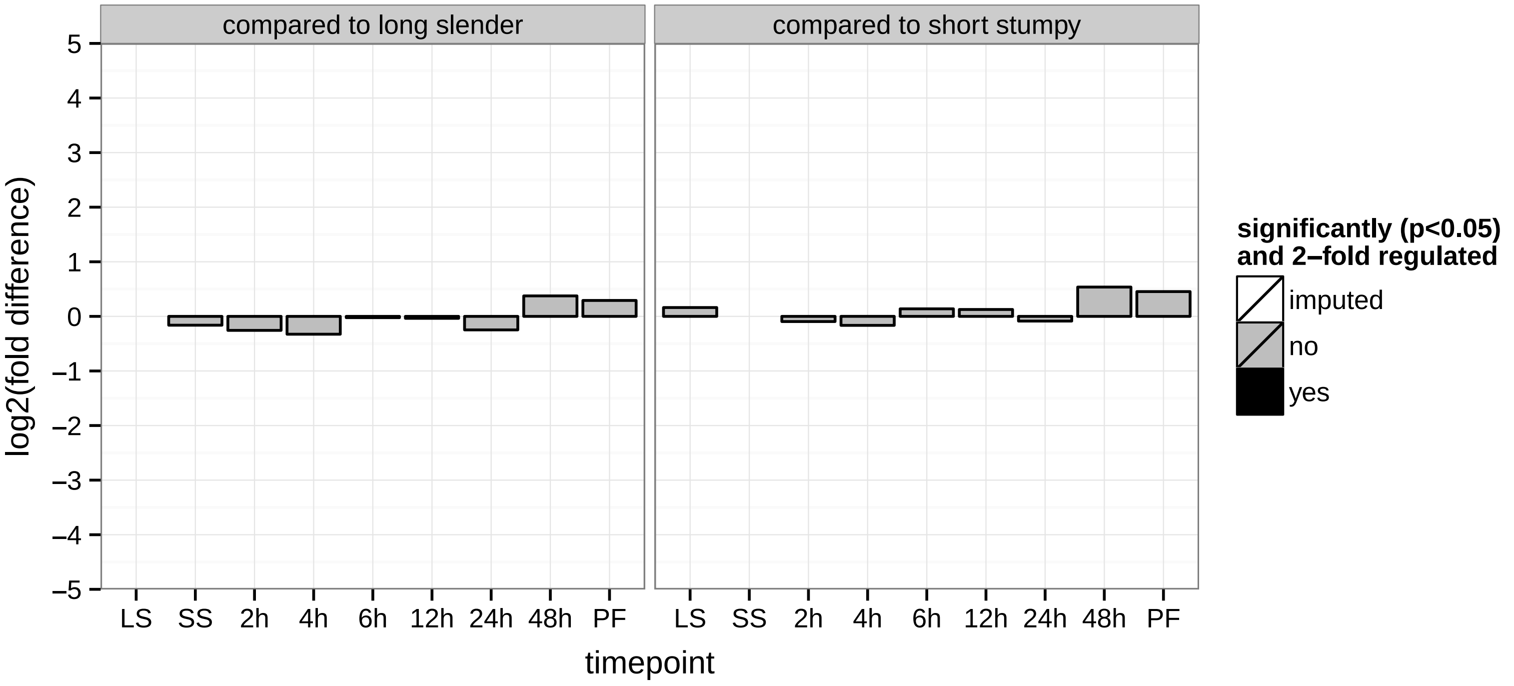
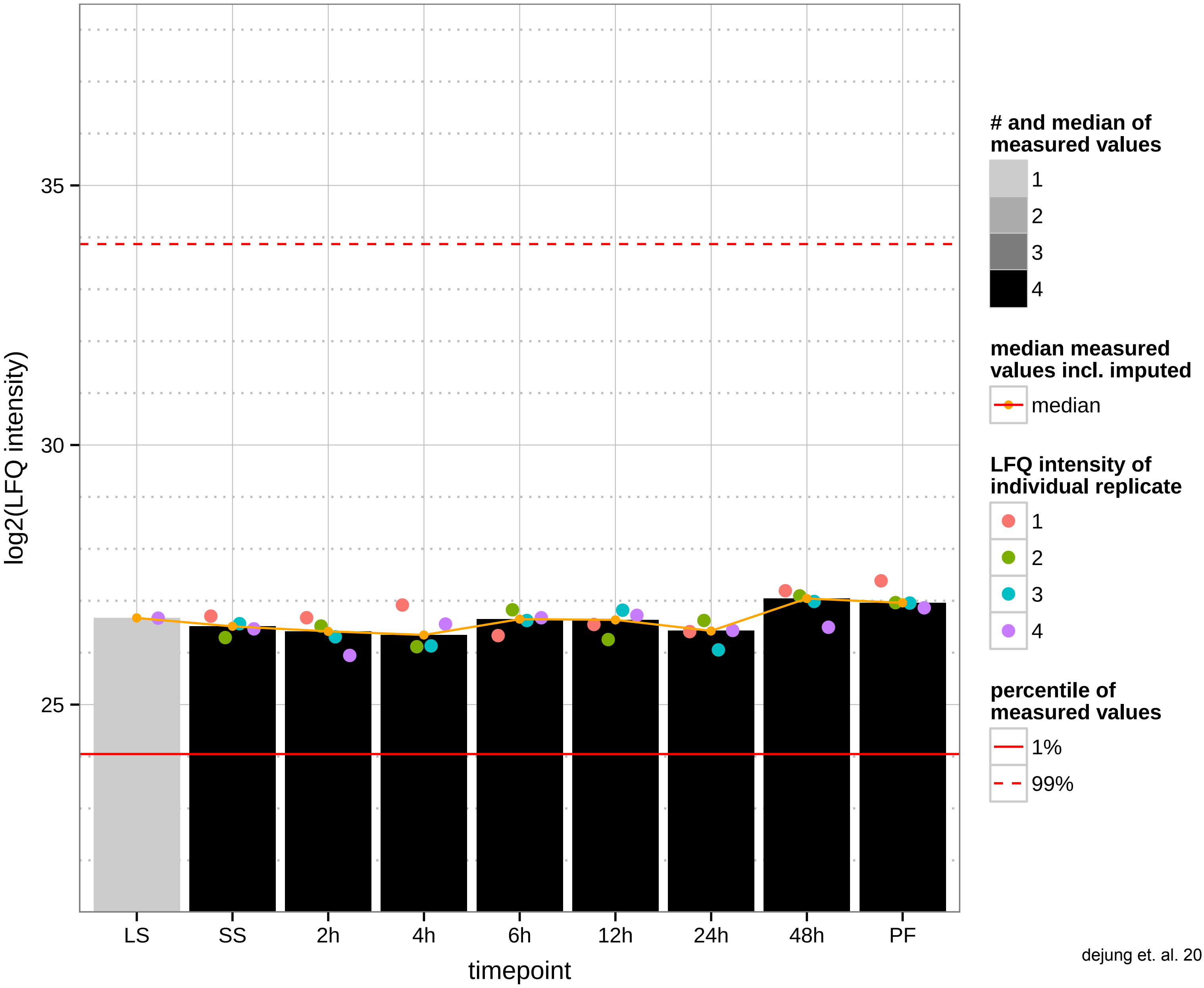
hypothetical protein, conserved
Tb927.11.8800
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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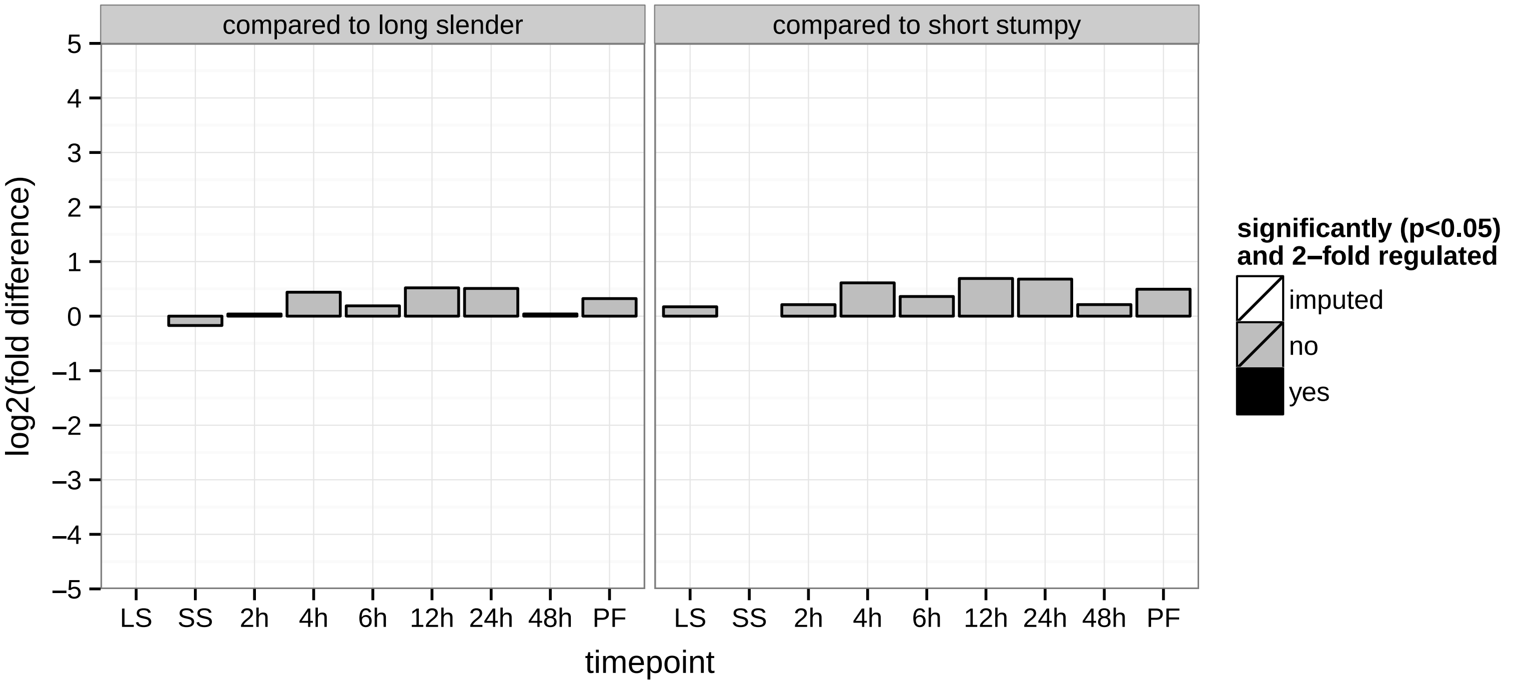
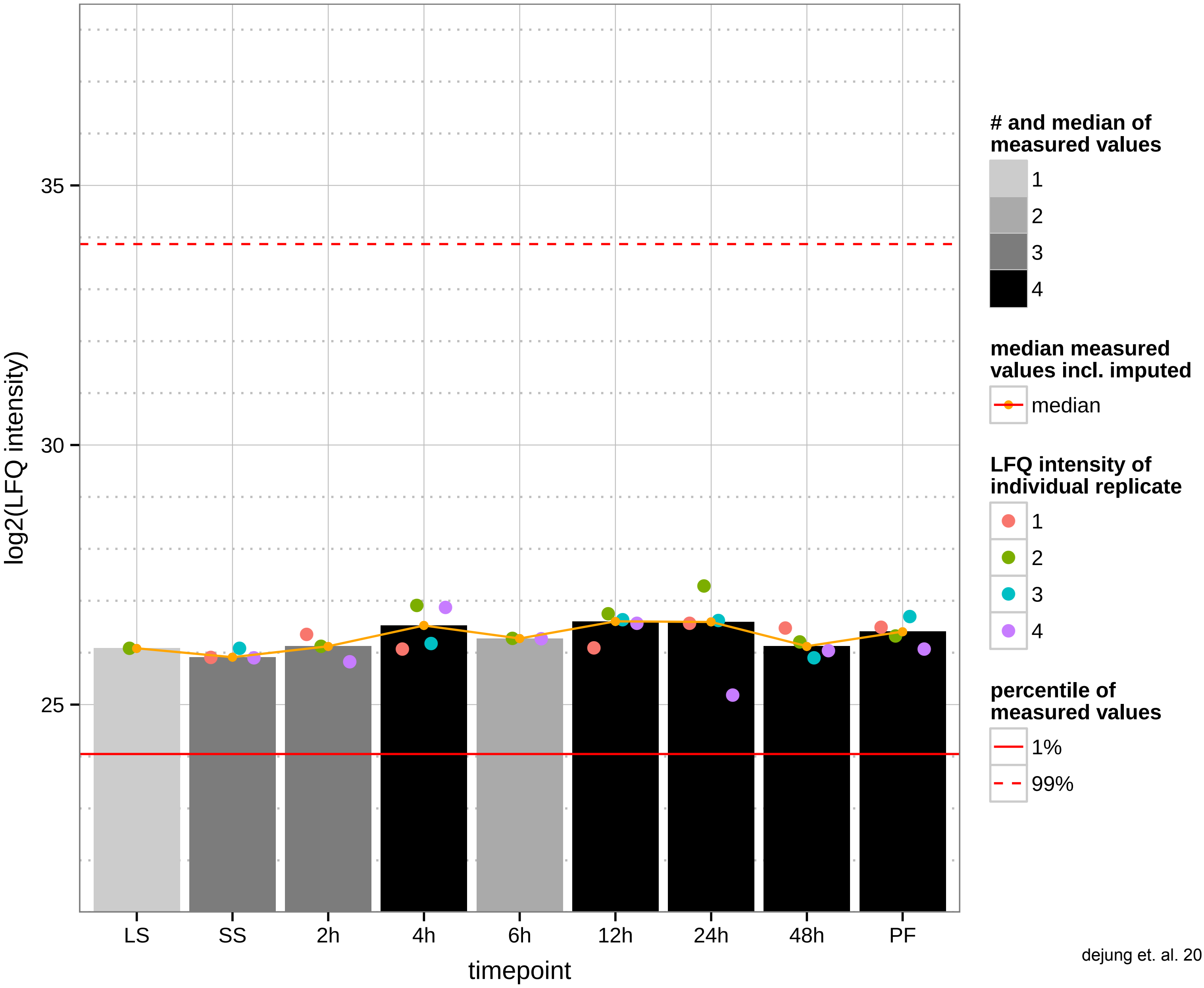
DNA–dependent RNA polymerases, putative (RPC19)
Tb927.11.8890
AGOF: DNA binding, DNA–directed RNA polymerase activity, protein dimerization activity
AGOC: nucleus
AGOP: transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA–dependent





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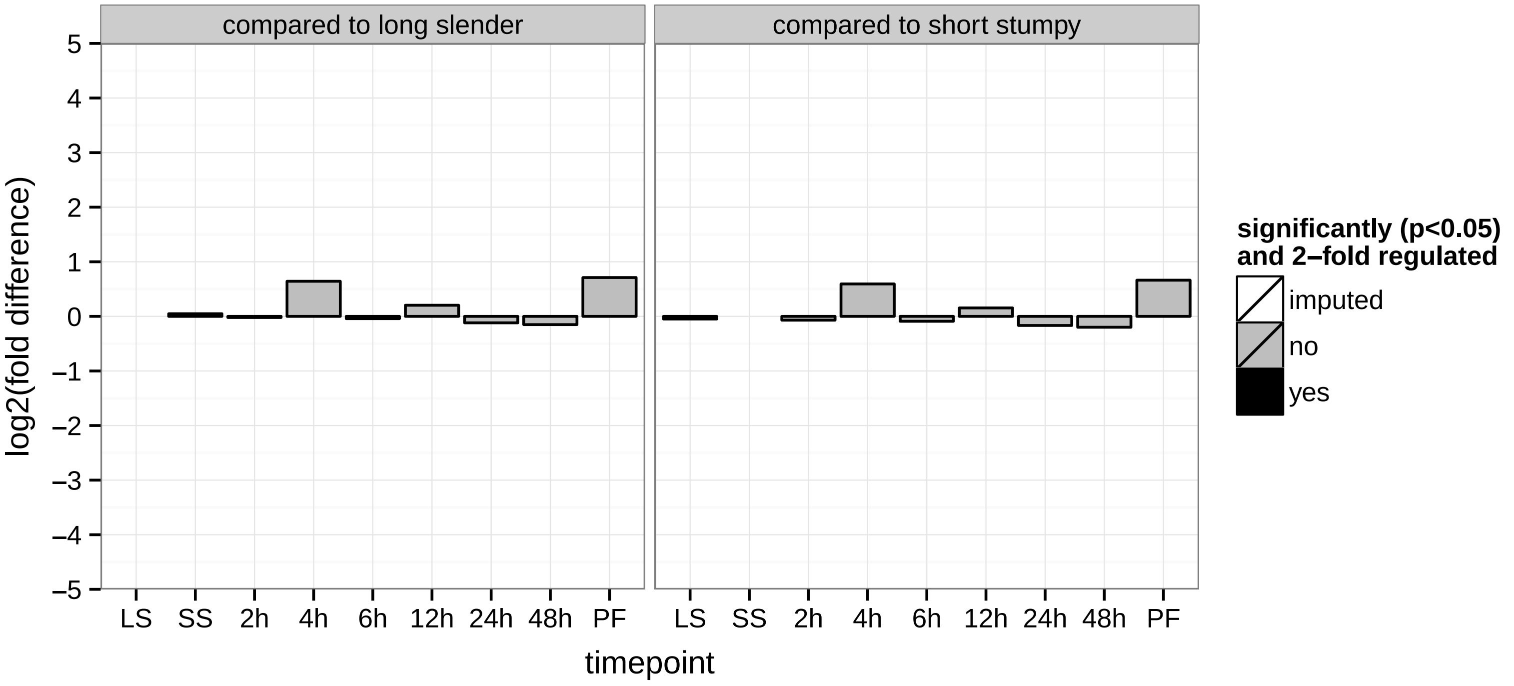
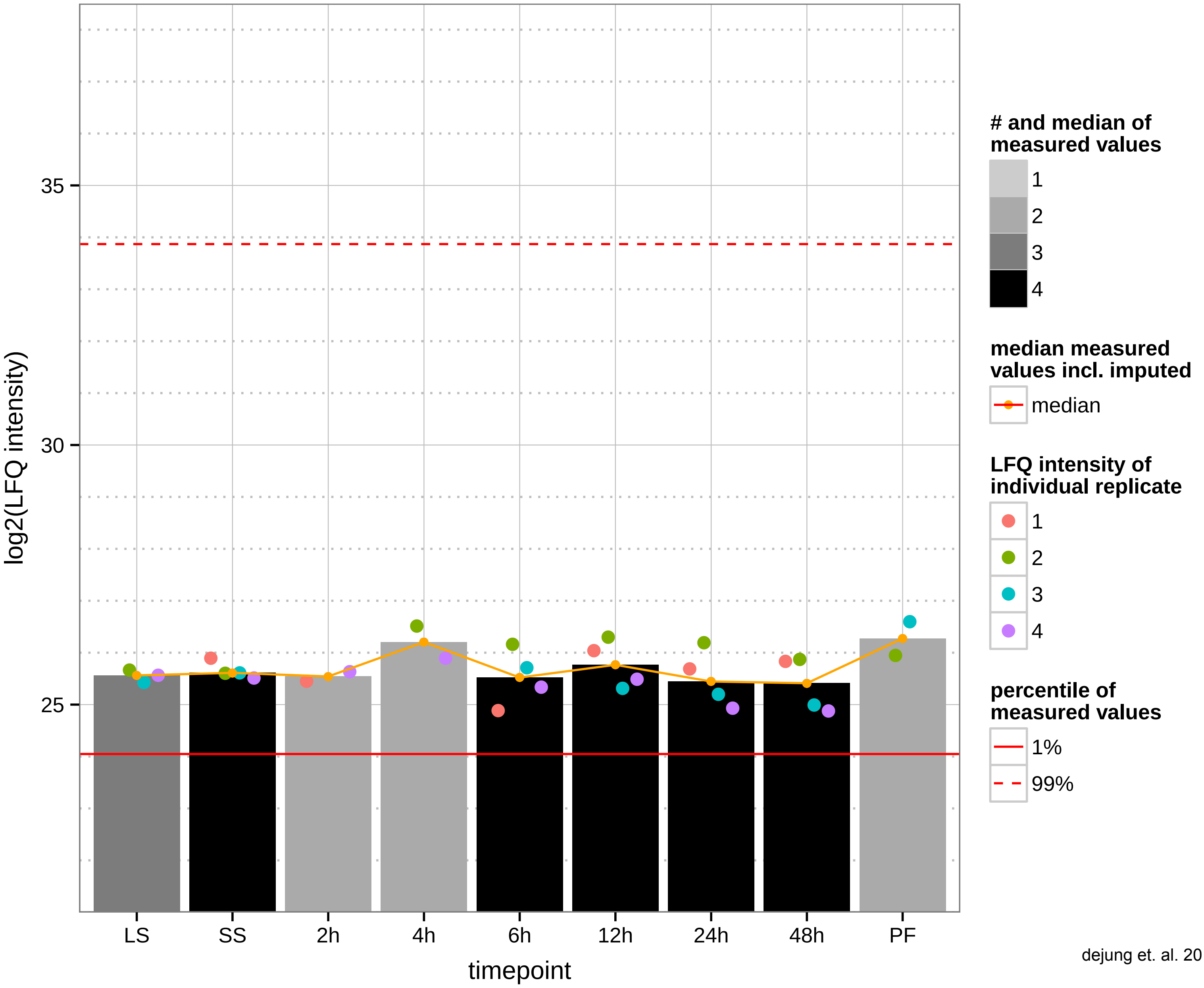
hypothetical protein, conserved
Tb927.11.8900
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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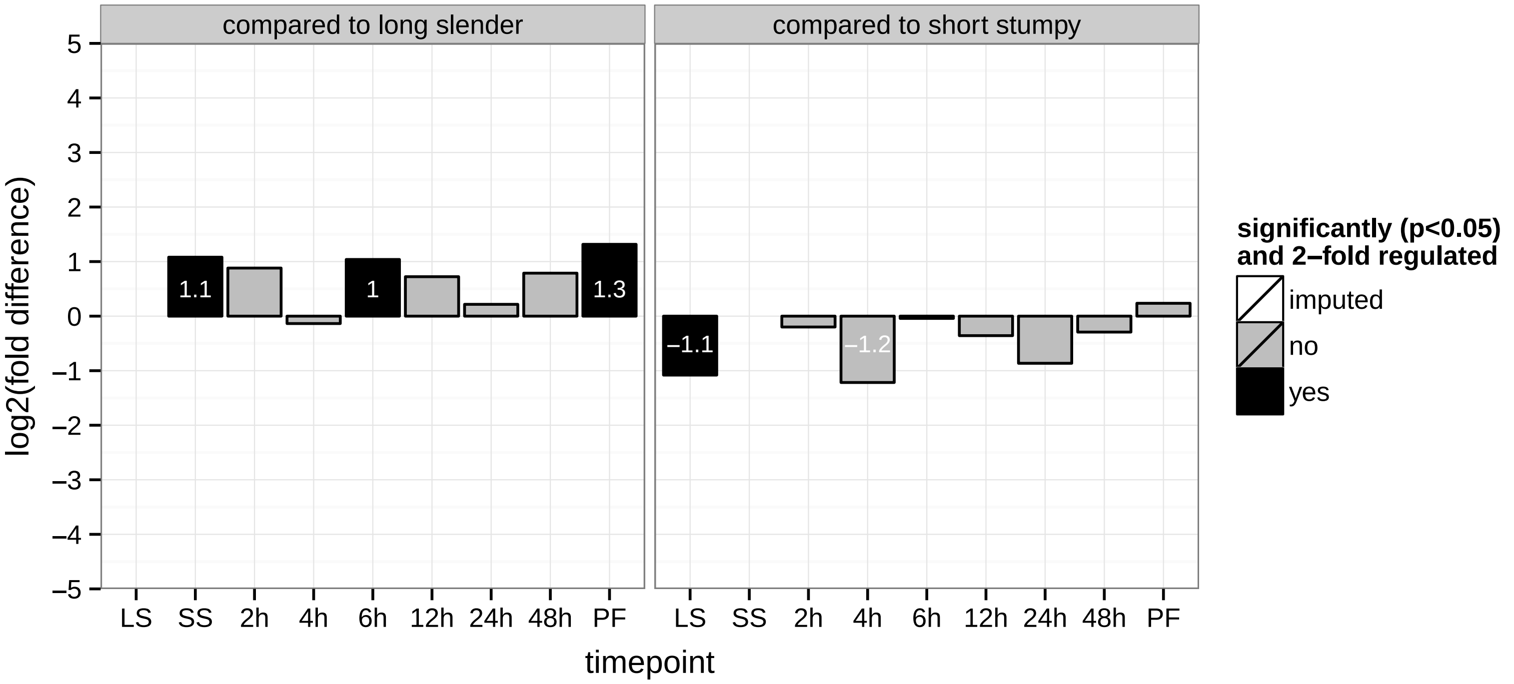
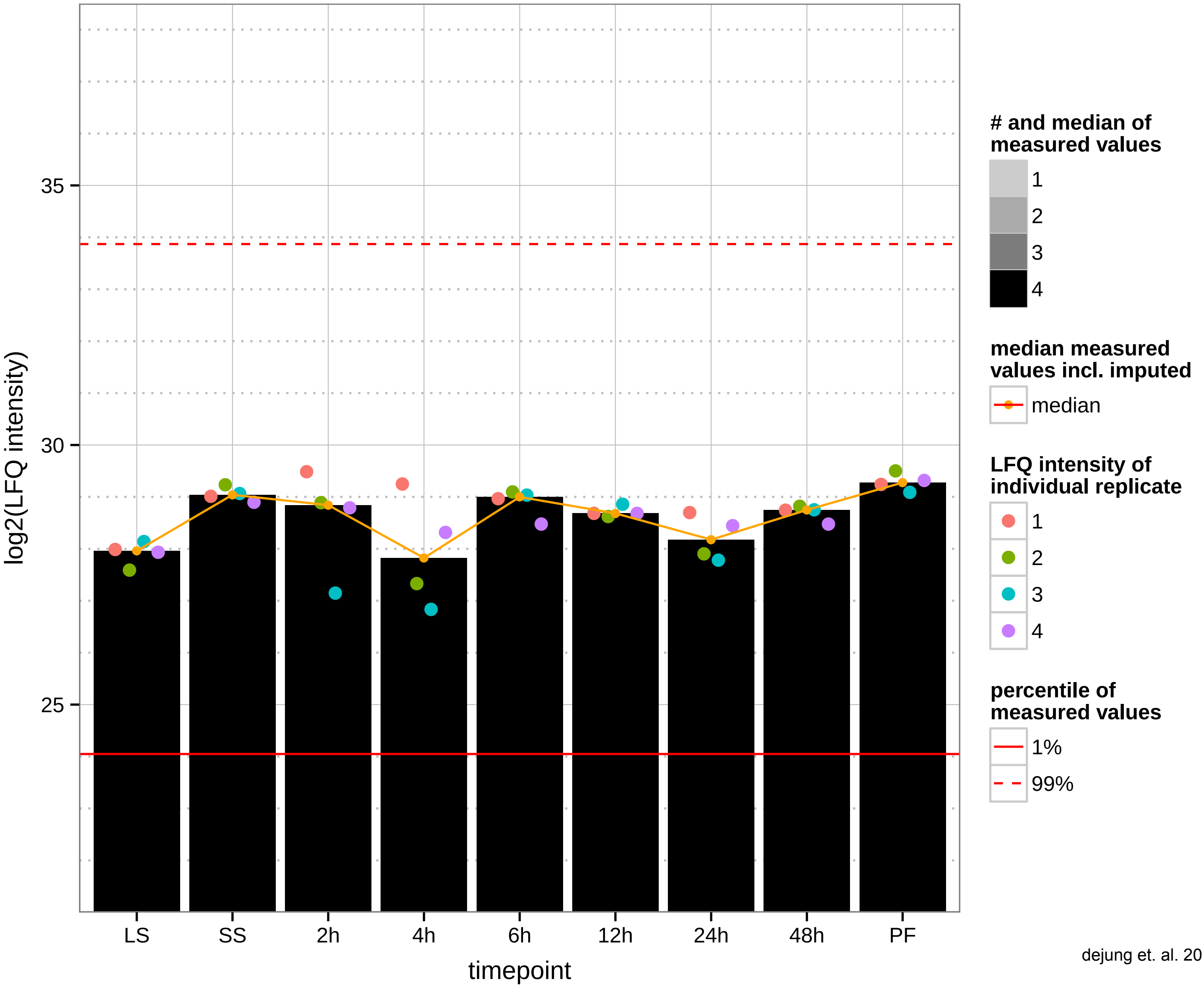
leucine rich repeat (TbLRRP1)
Tb927.11.8950
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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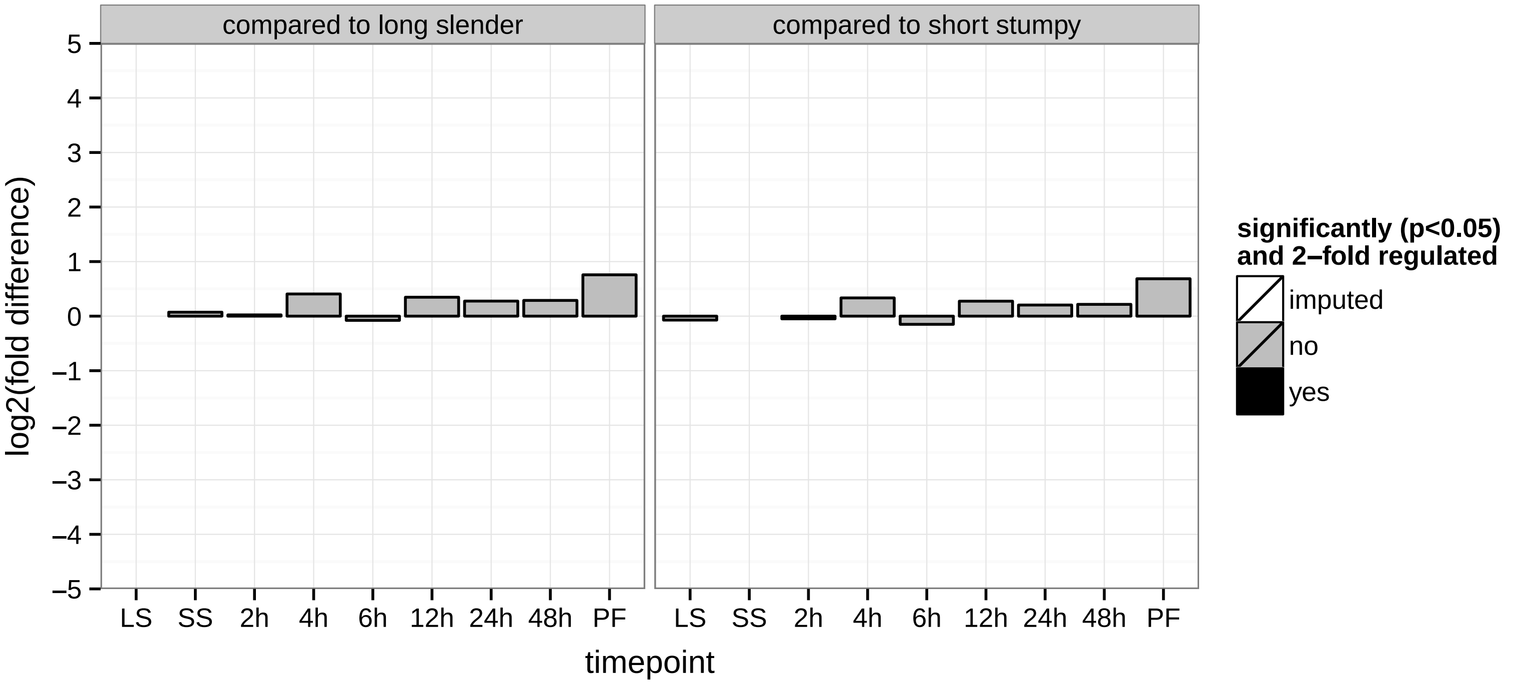
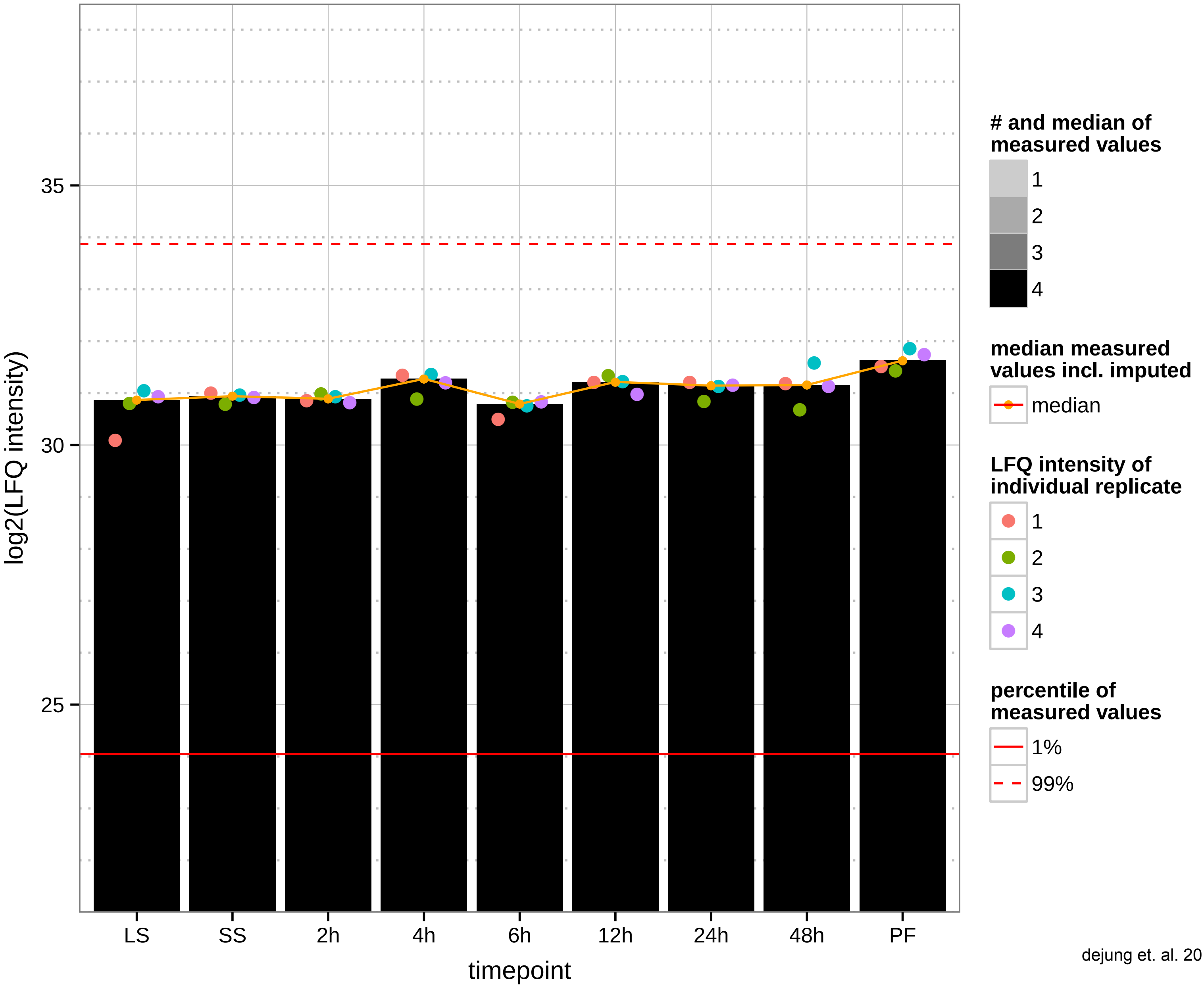
ribose 5−phosphate isomerase, putative
Tb927.11.8970
AGOF: ribose−5−phosphate isomerase activity
AGOC: null
AGOP: pentose−phosphate shunt, pentose−phosphate shunt, non−oxidative branch
PGOF: ribose−5−phosphate isomerase activity
PGOC: null
PGOP: carbohydrate metabolic process, pentose−phosphate shunt





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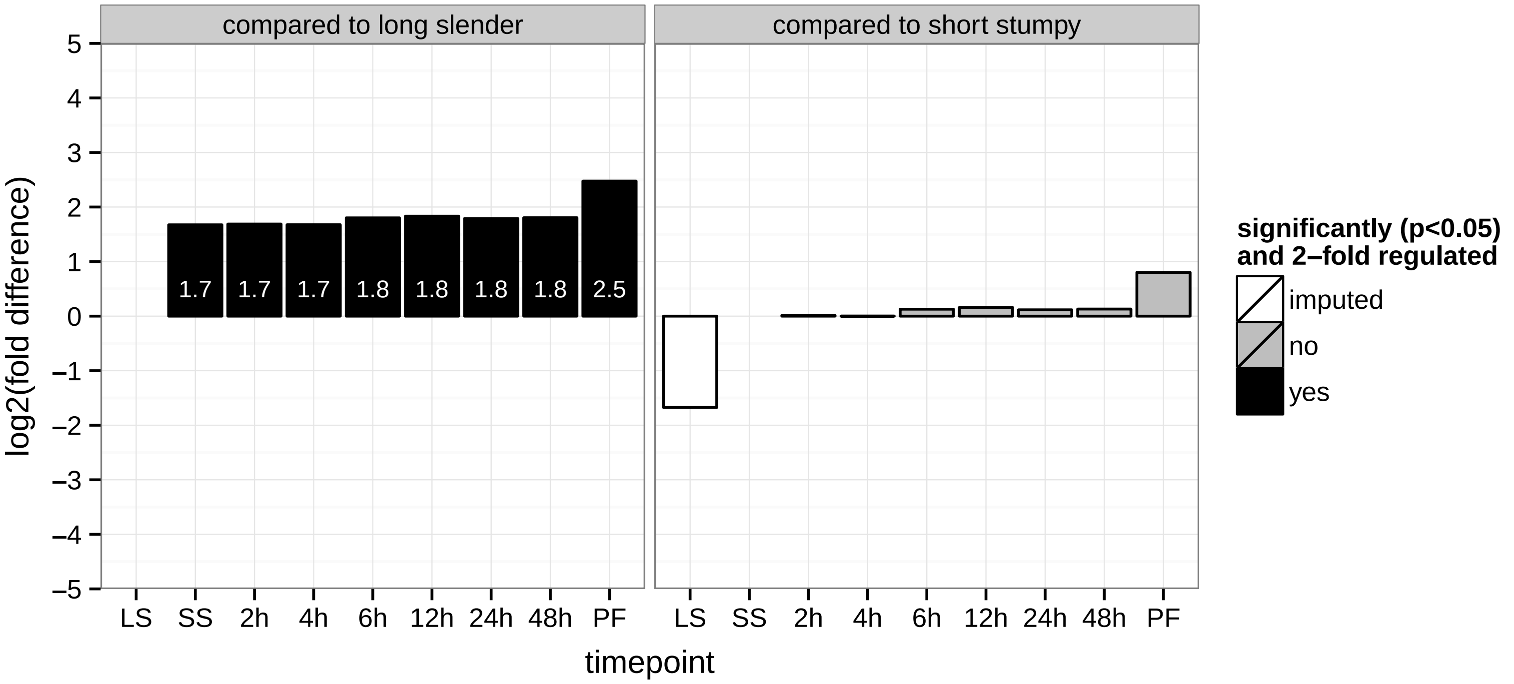
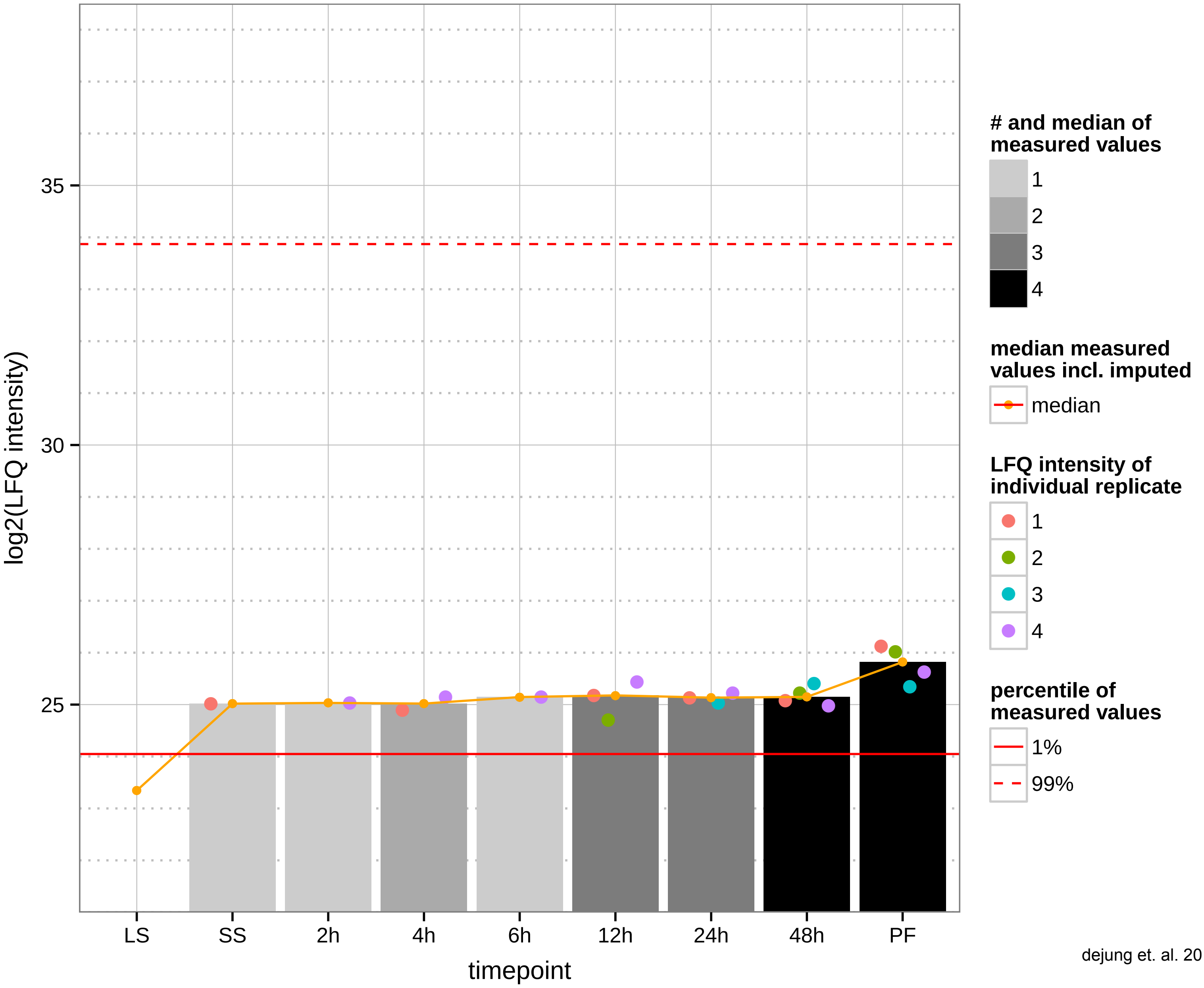
Elongation factor G 2, mitochondrial, putative (EF−G2)
Tb927.11.8980
AGOF: GTP binding, GTPase activity
AGOC: mitochondrion
AGOP: null
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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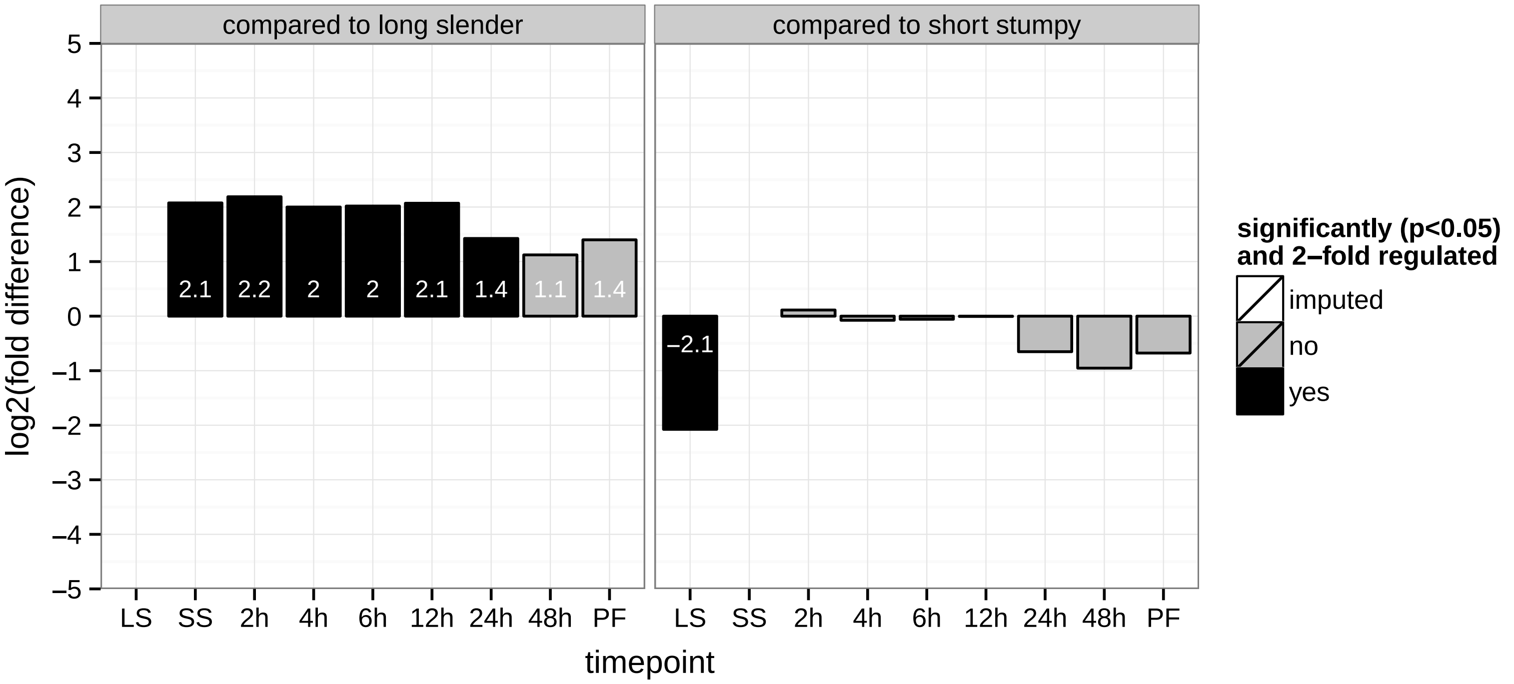
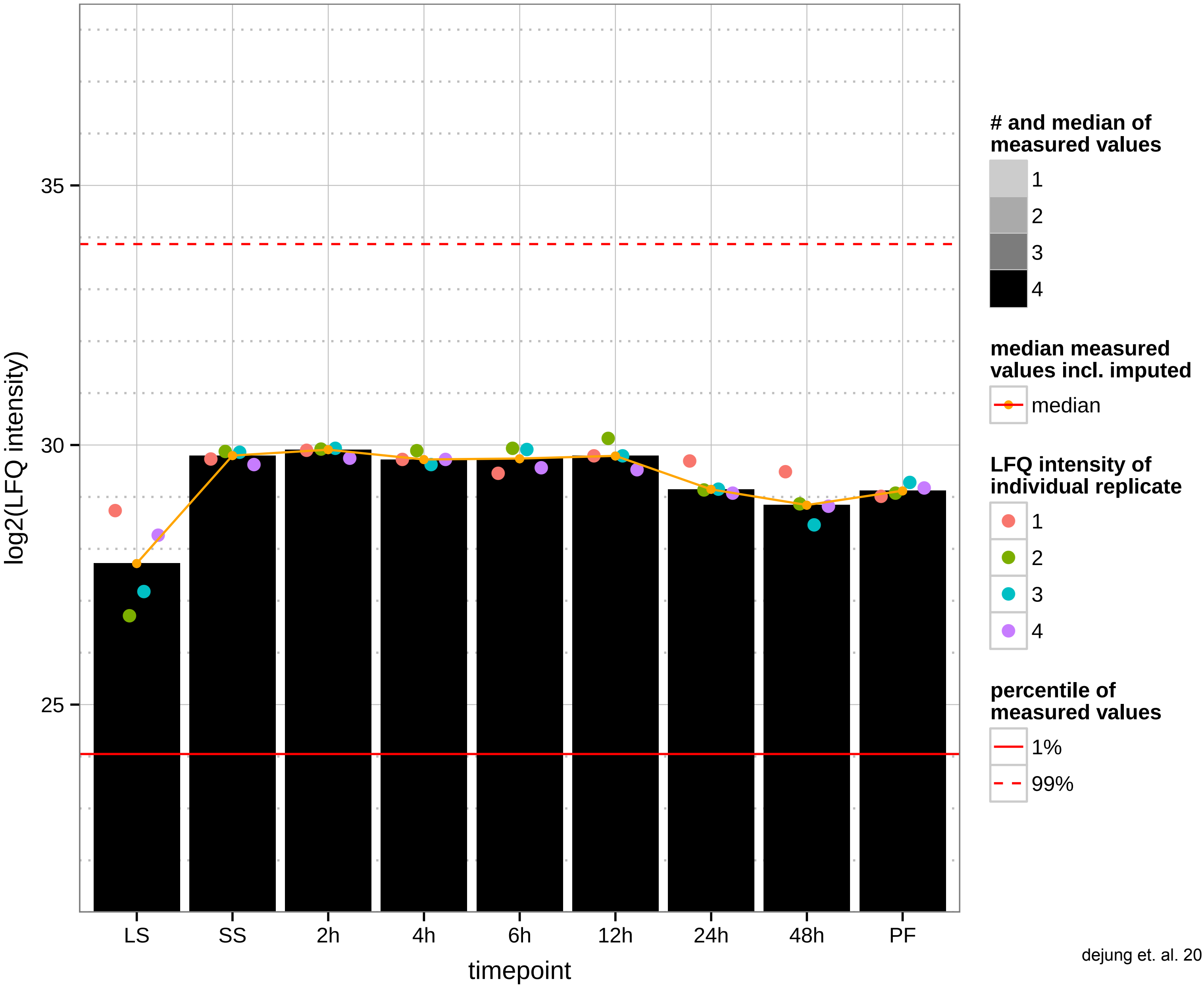
isocitrate dehydrogenase, putative (IDH)
Tb927.11.900
AGOF: NAD binding, isocitrate dehydrogenase (NADP+) activity, magnesium ion binding
AGOC: null
AGOP: isocitrate metabolic process, oxidation–reduction process
PGOF: isocitrate dehydrogenase (NADP+) activity, oxidoreductase activity, acting on the CH–OH group of donors, NAD or NA
PGOC: null
PGOP: isocitrate metabolic process, oxidation–reduction process





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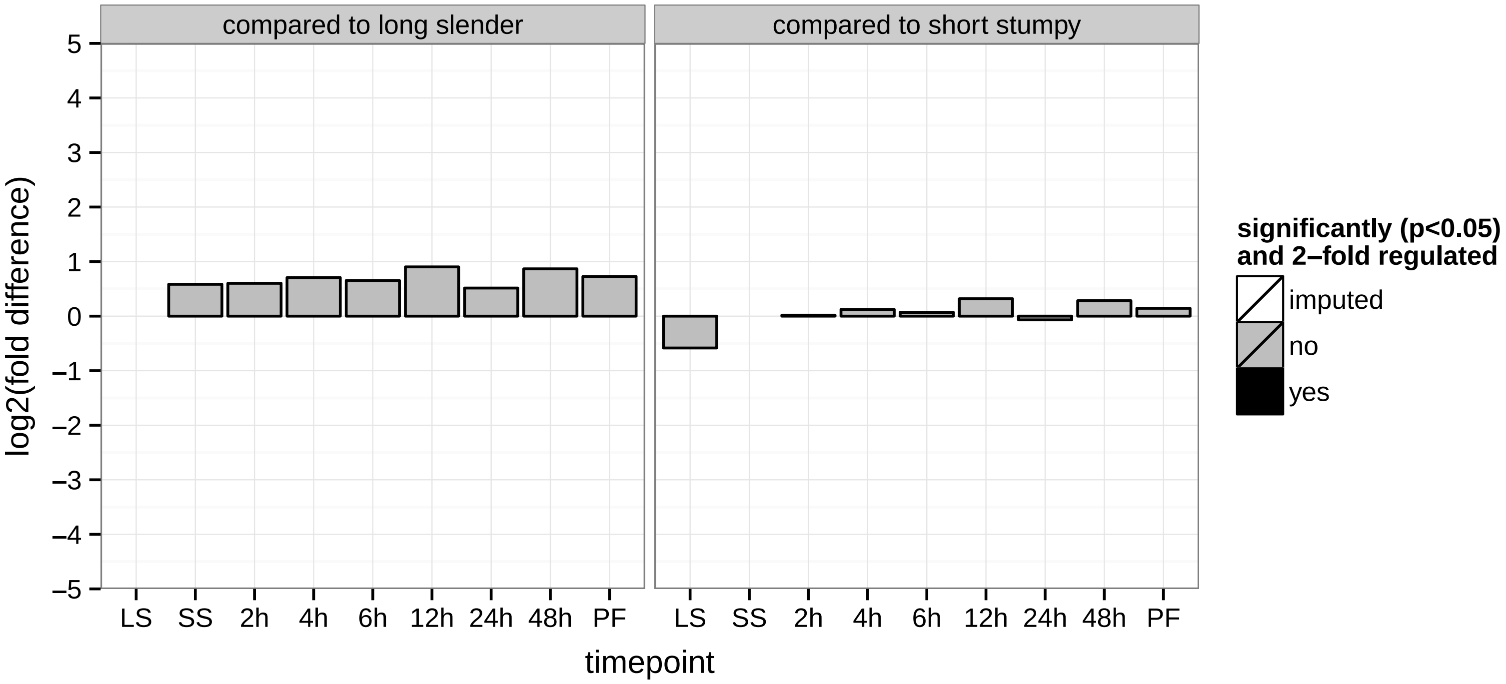
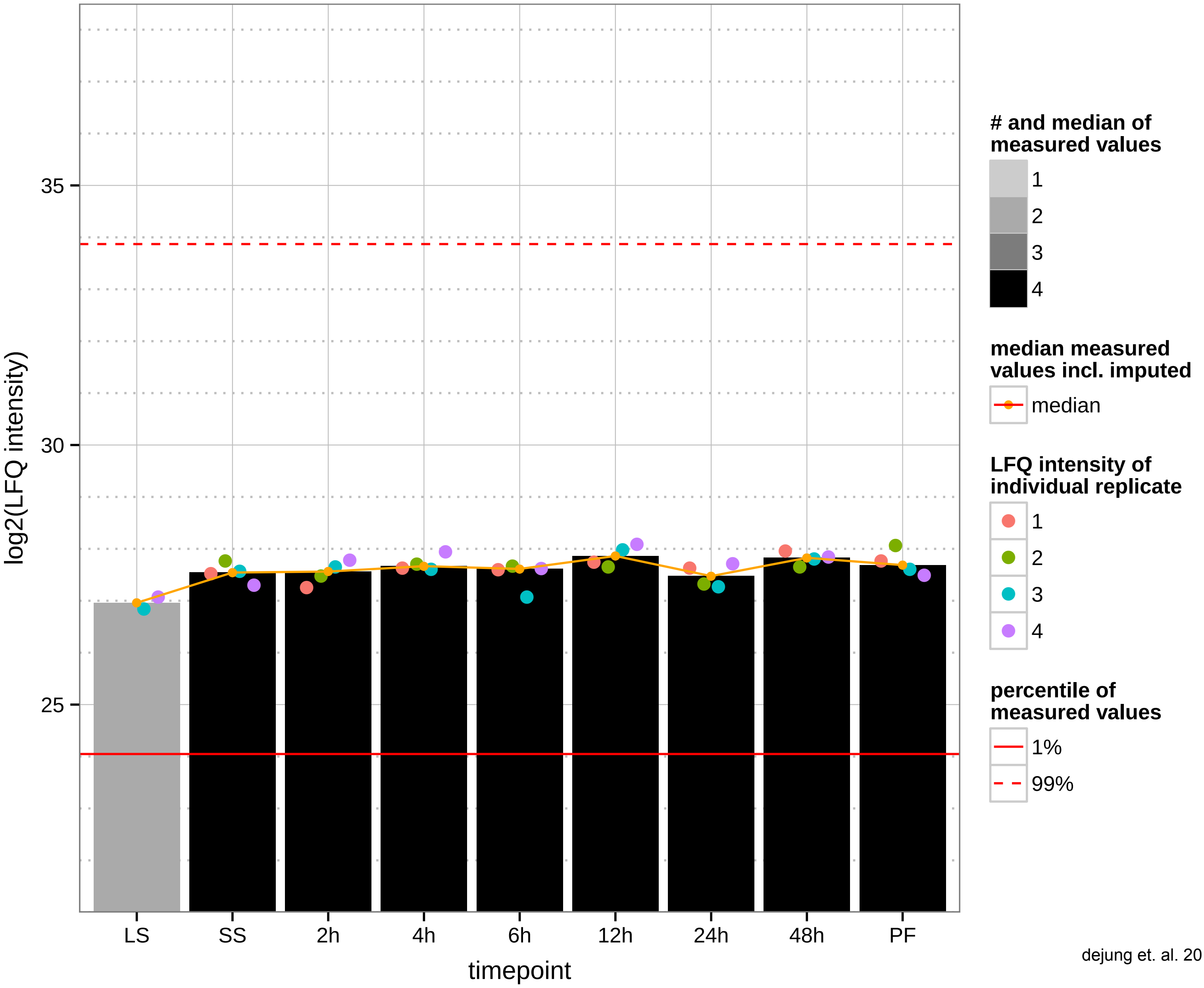
hypothetical protein, conserved
Tb927.11.9050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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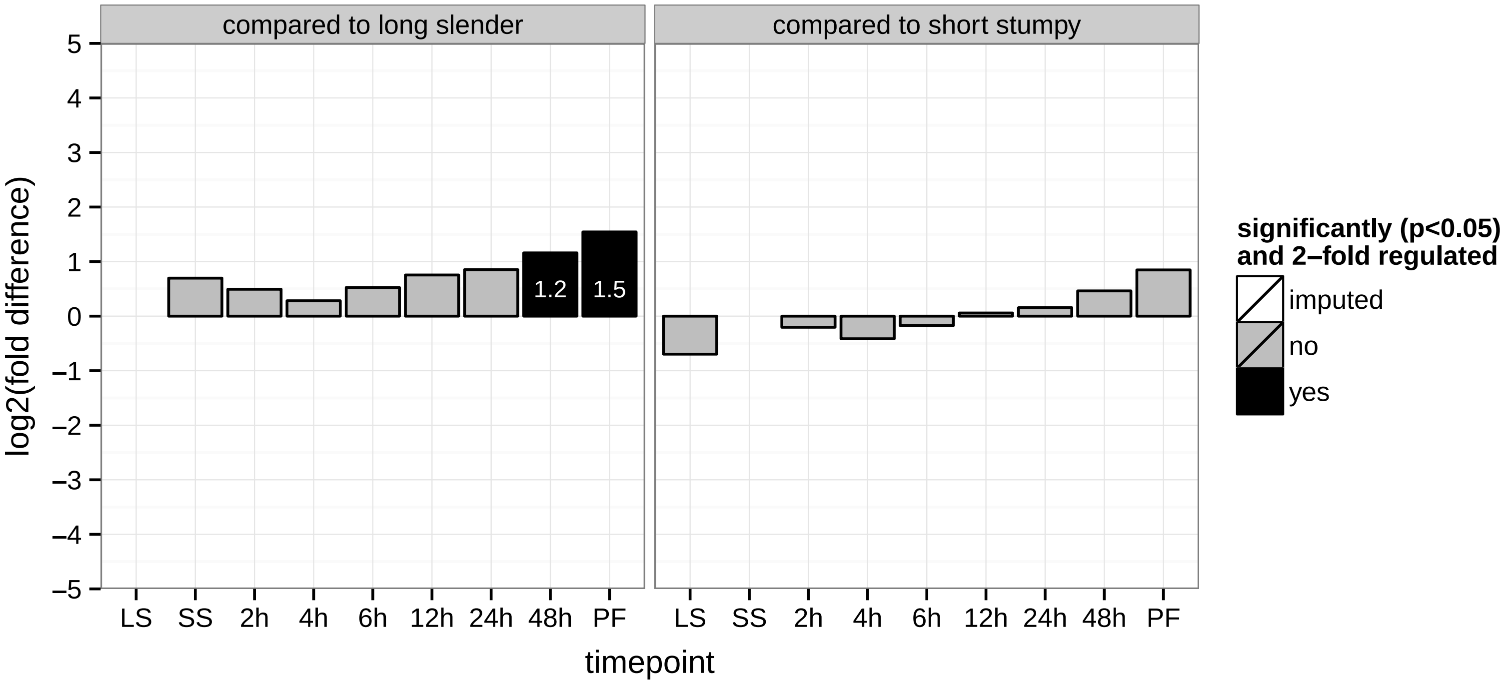
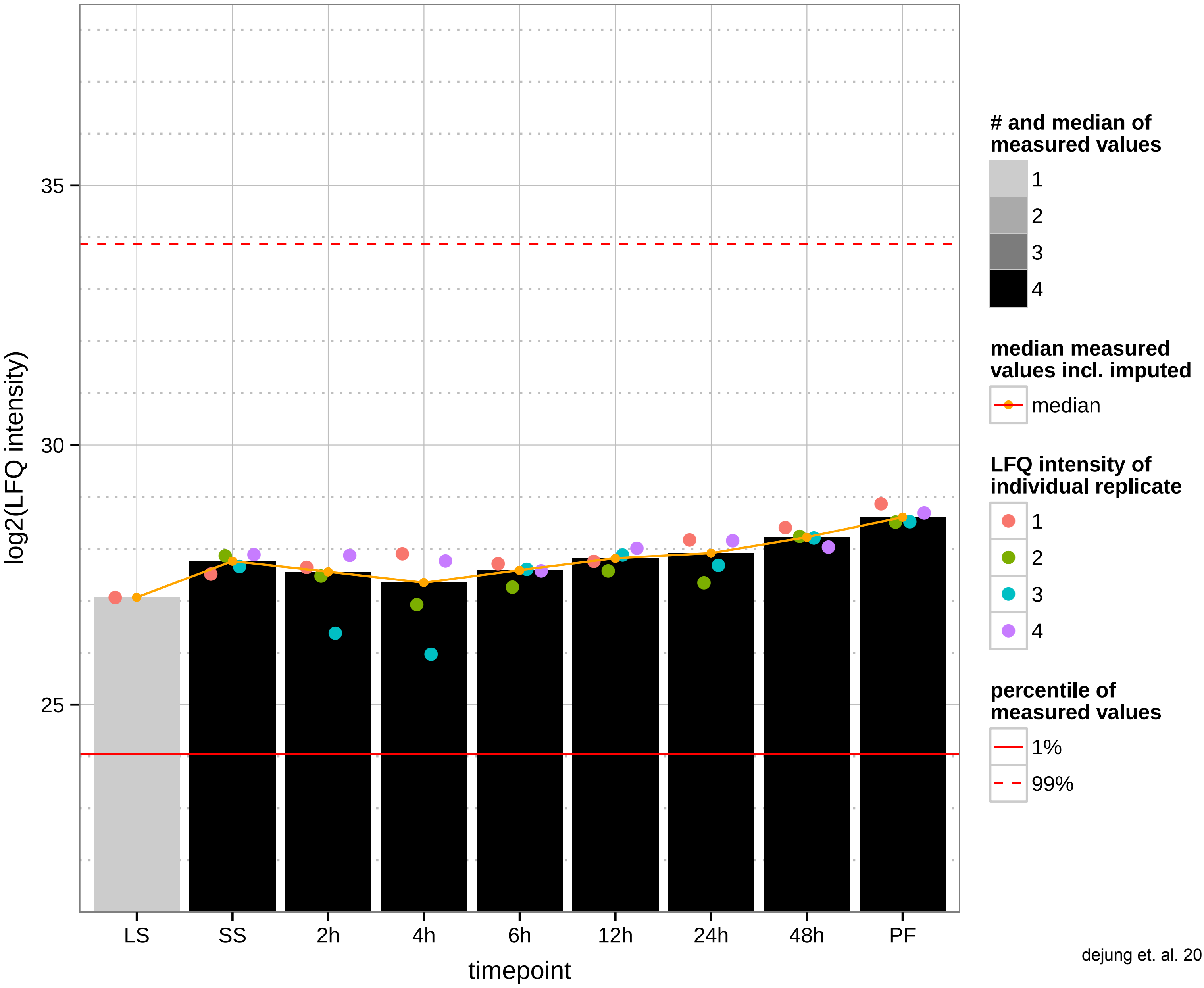
hypothetical protein, conserved
Tb927.11.9080
AGOF: nucleotide binding
AGOC: nucleus
AGOP: ribosome biogenesis
PGOF: null
PGOC: nucleus
PGOP: ribosome biogenesis





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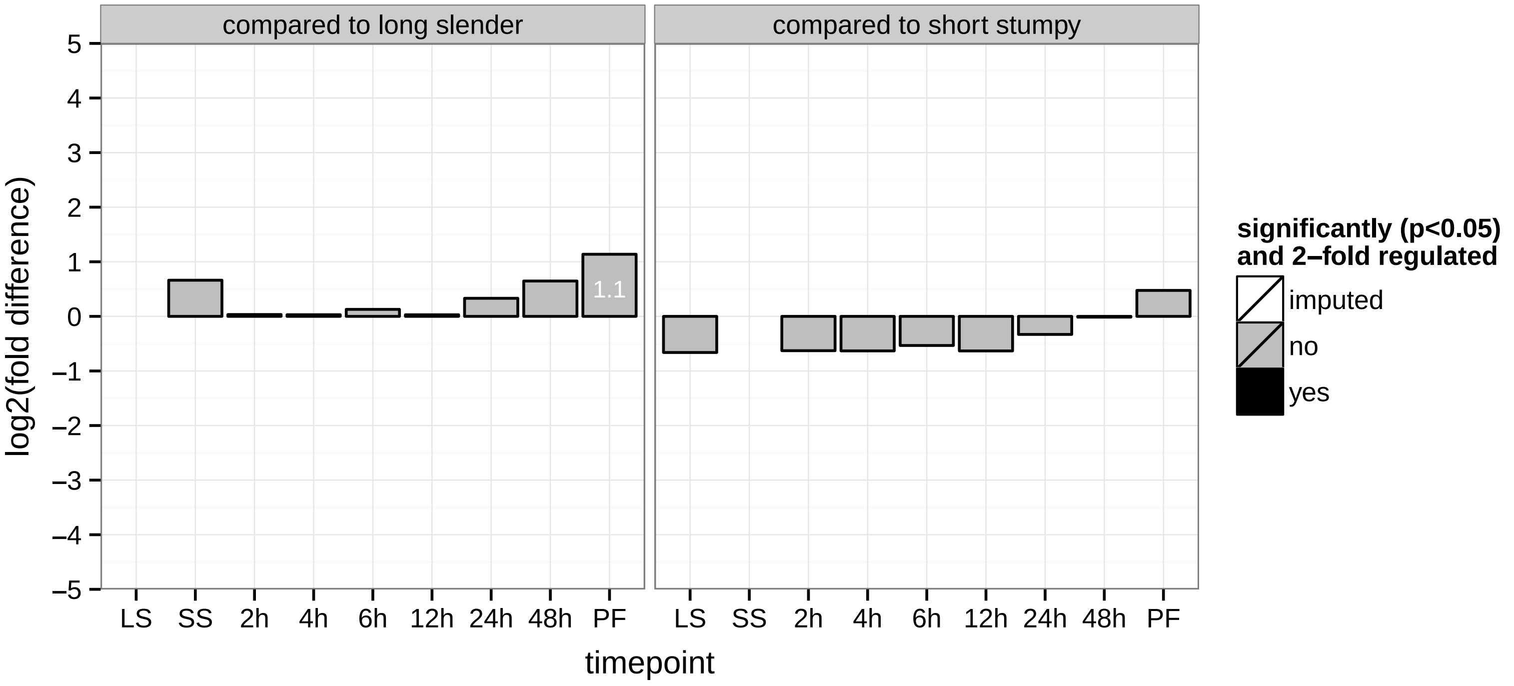
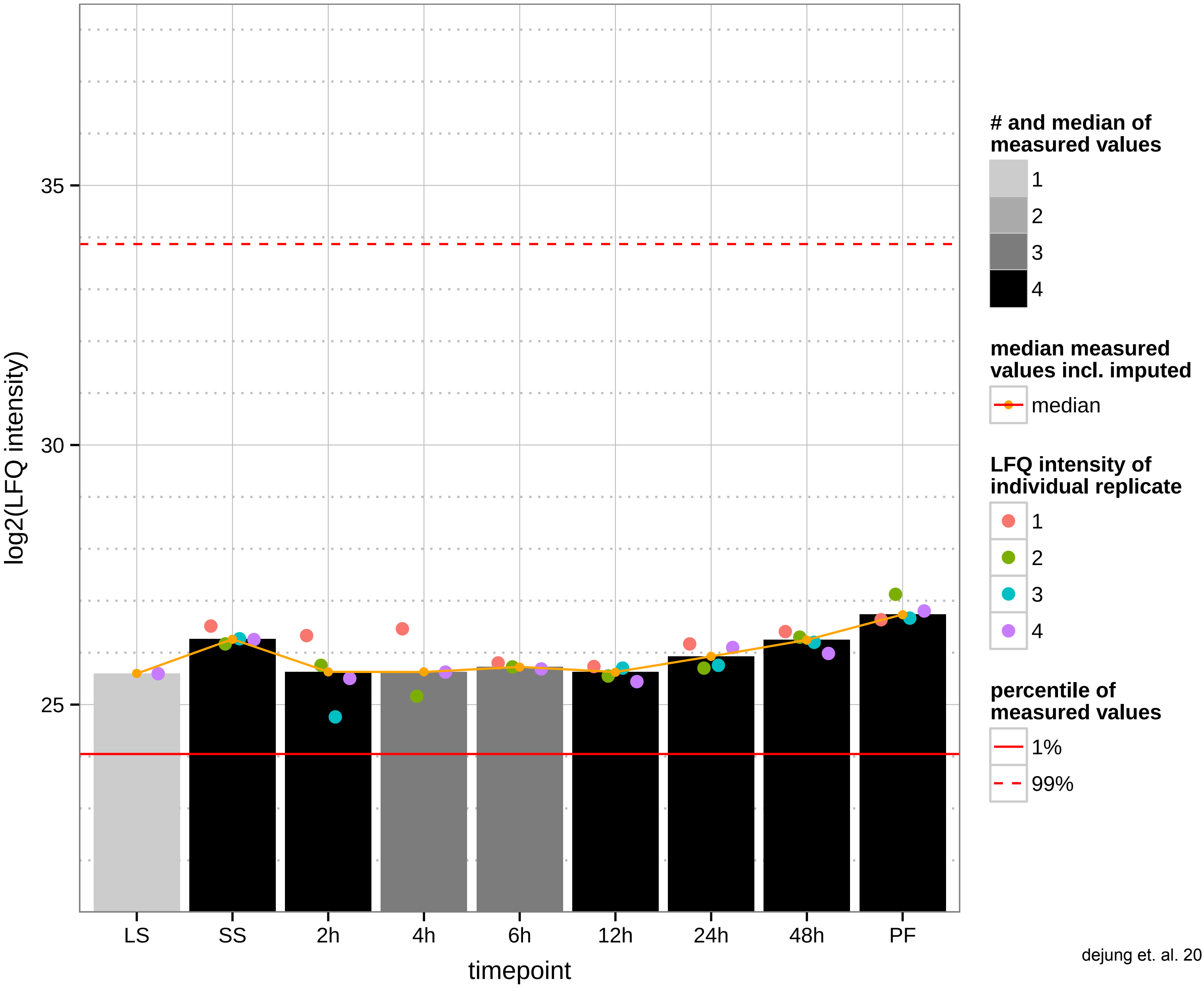
DNA topoisomerase III, putative
Tb927.11.9170
AGOF: DNA binding, DNA topoisomerase type I activity
AGOC: chromosome
AGOP: DNA modification, DNA topological change, DNA unwinding involved in replication
PGOF: DNA binding, DNA topoisomerase activity
PGOC: chromosome
PGOP: DNA topological change





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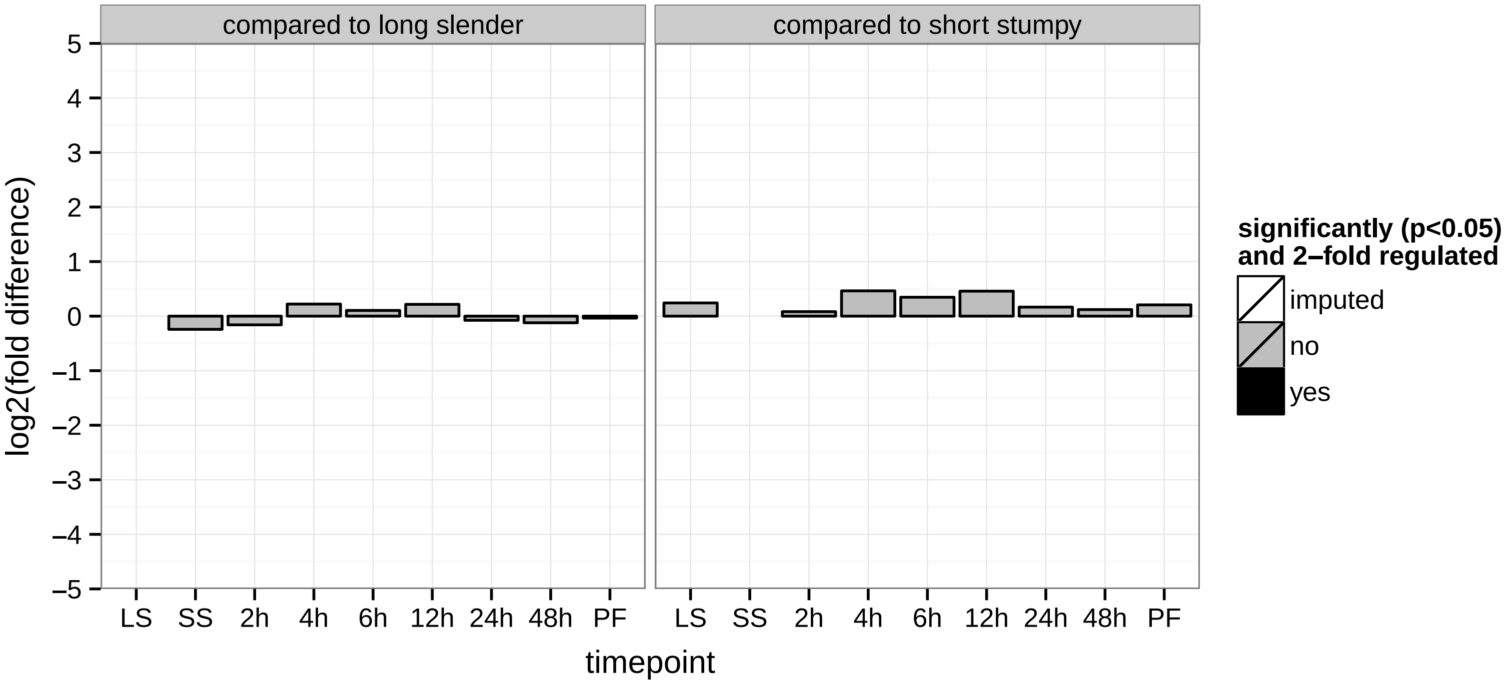
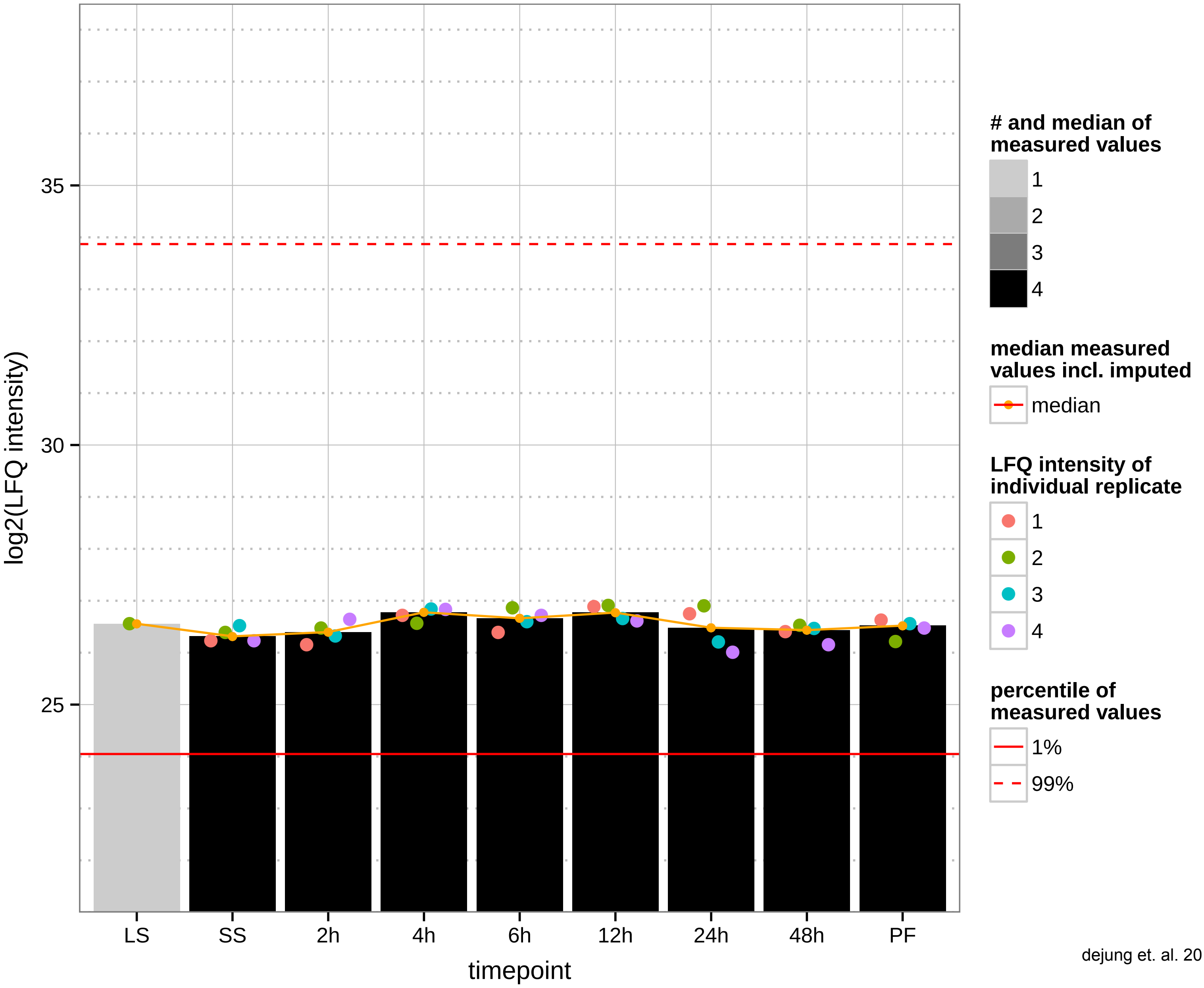
ADP–ribosylation factor GTPase activating protein, putative, putative (Cnt–b5)
Tb927.11.9180
AGOF: ARF GTPase activator activity, DNA binding, zinc ion binding
AGOC: nucleus
AGOP: ER to Golgi vesicle–mediated transport, regulation of ARF GTPase activity
PGOF: ARF GTPase activator activity, zinc ion binding
PGOC: null
PGOP: regulation of ARF GTPase activity





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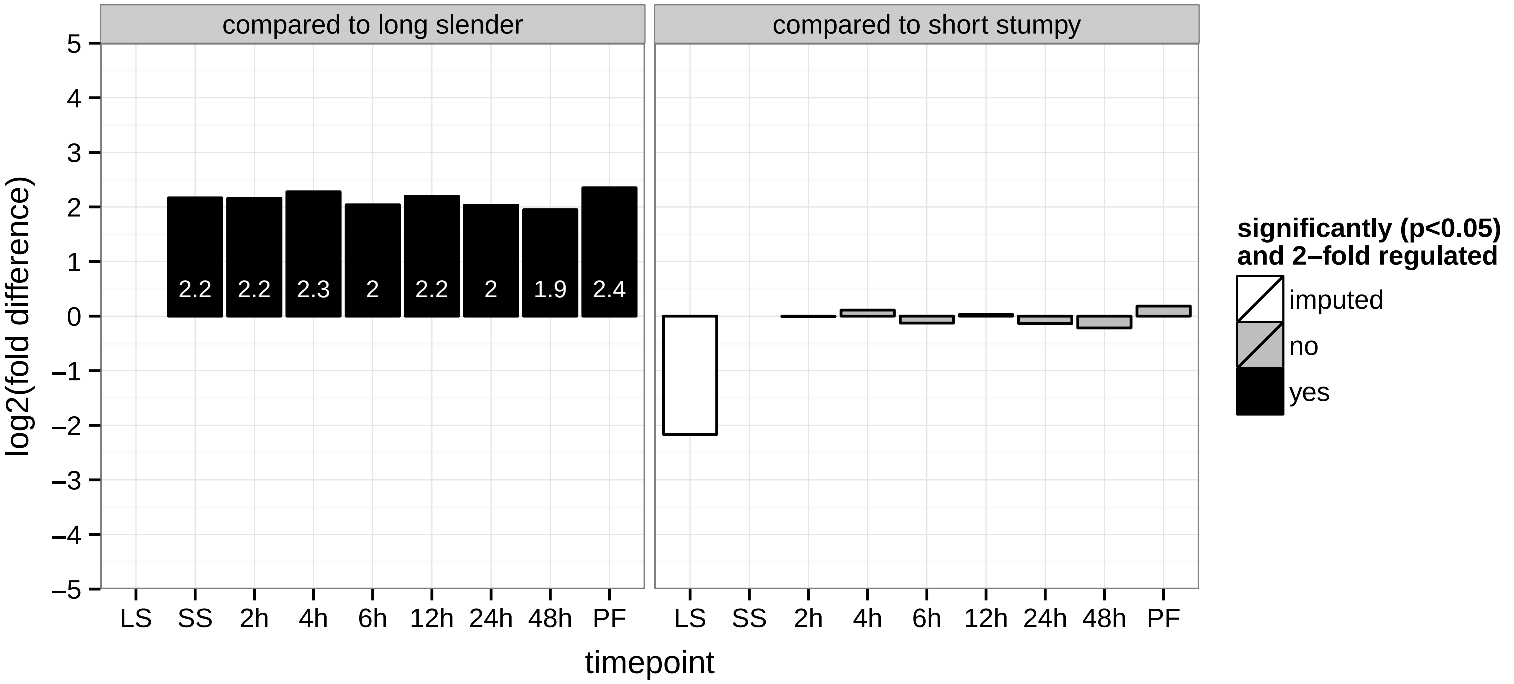
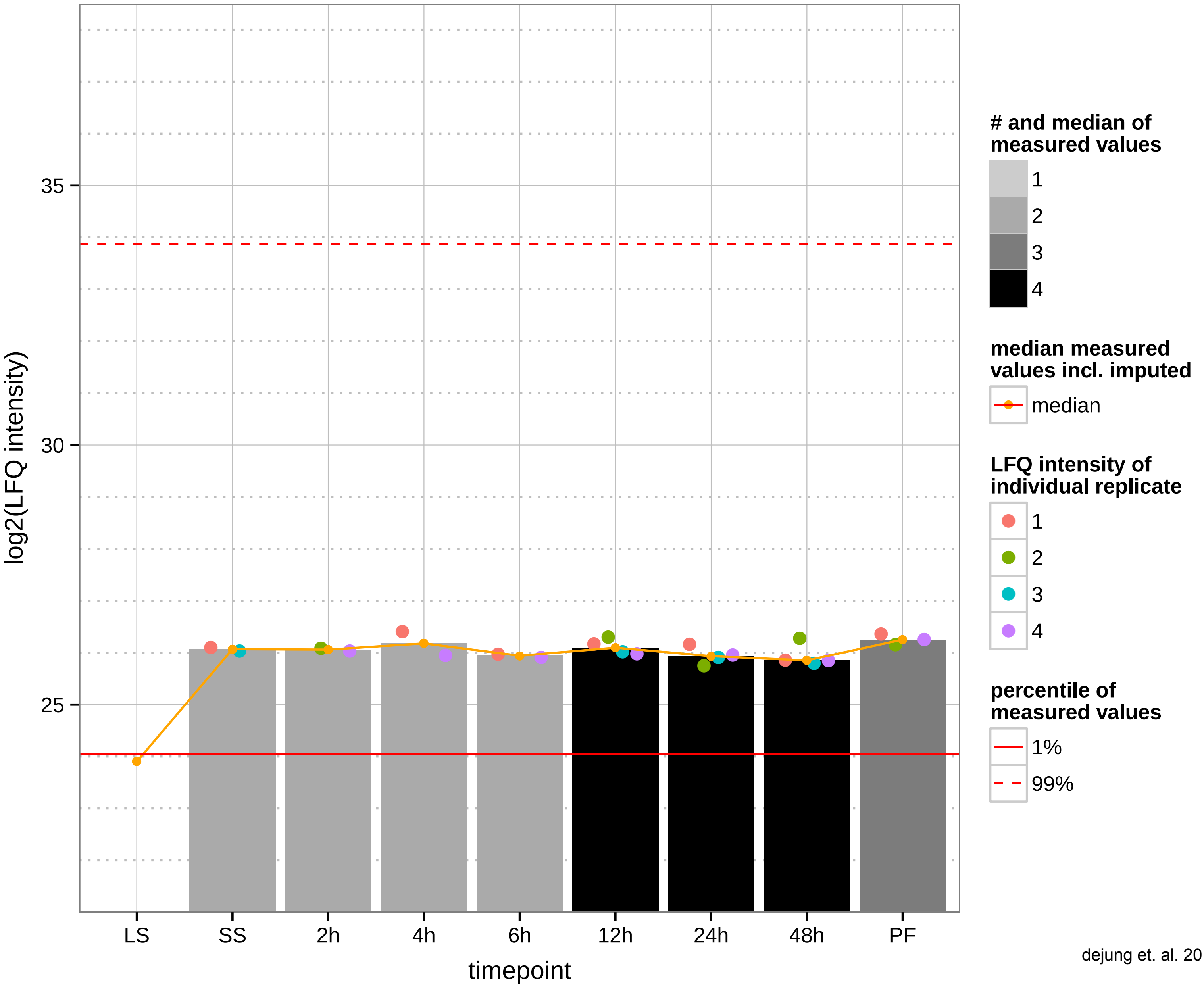
protein kinase, putative
Tb927.11.9190
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, binding, protein binding, protein kinase activity, transferase activity, transferring phosphorus–containing g
PGOC: null
PGOP: protein phosphorylation





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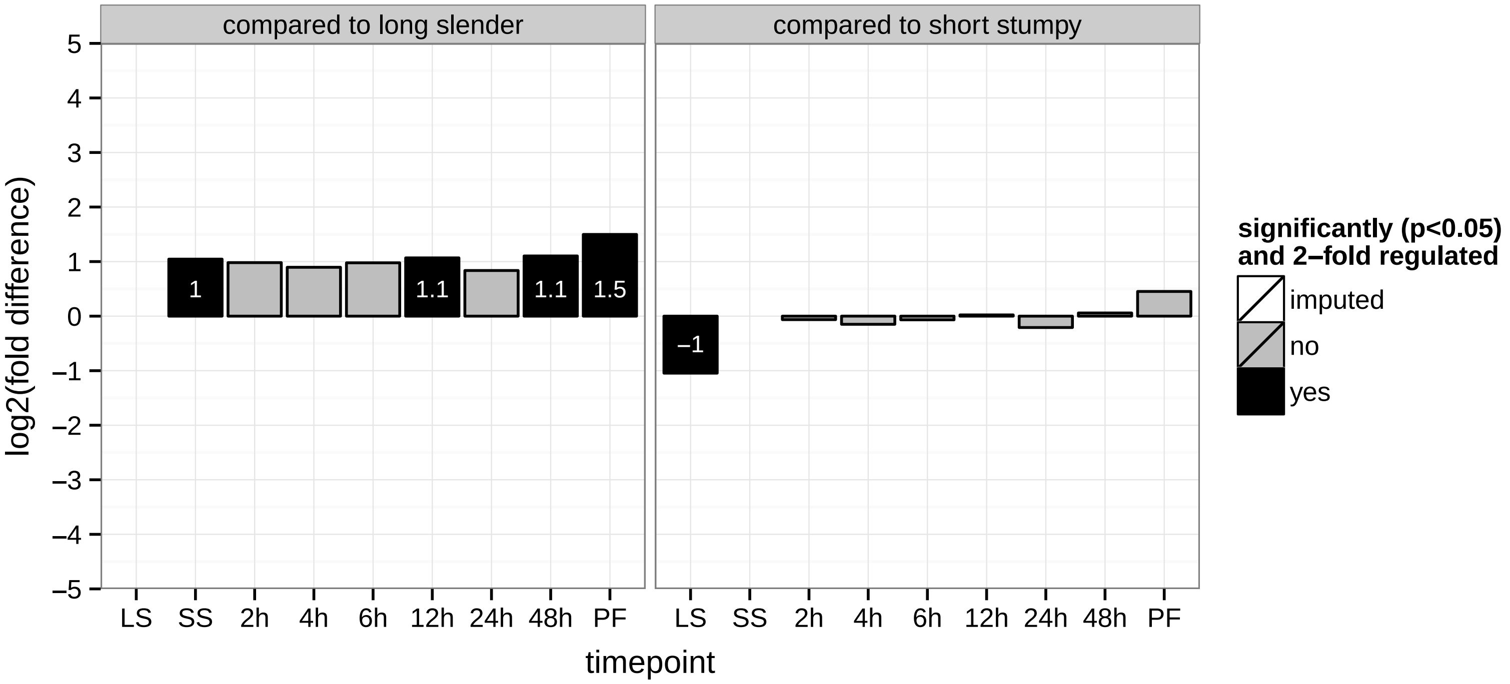
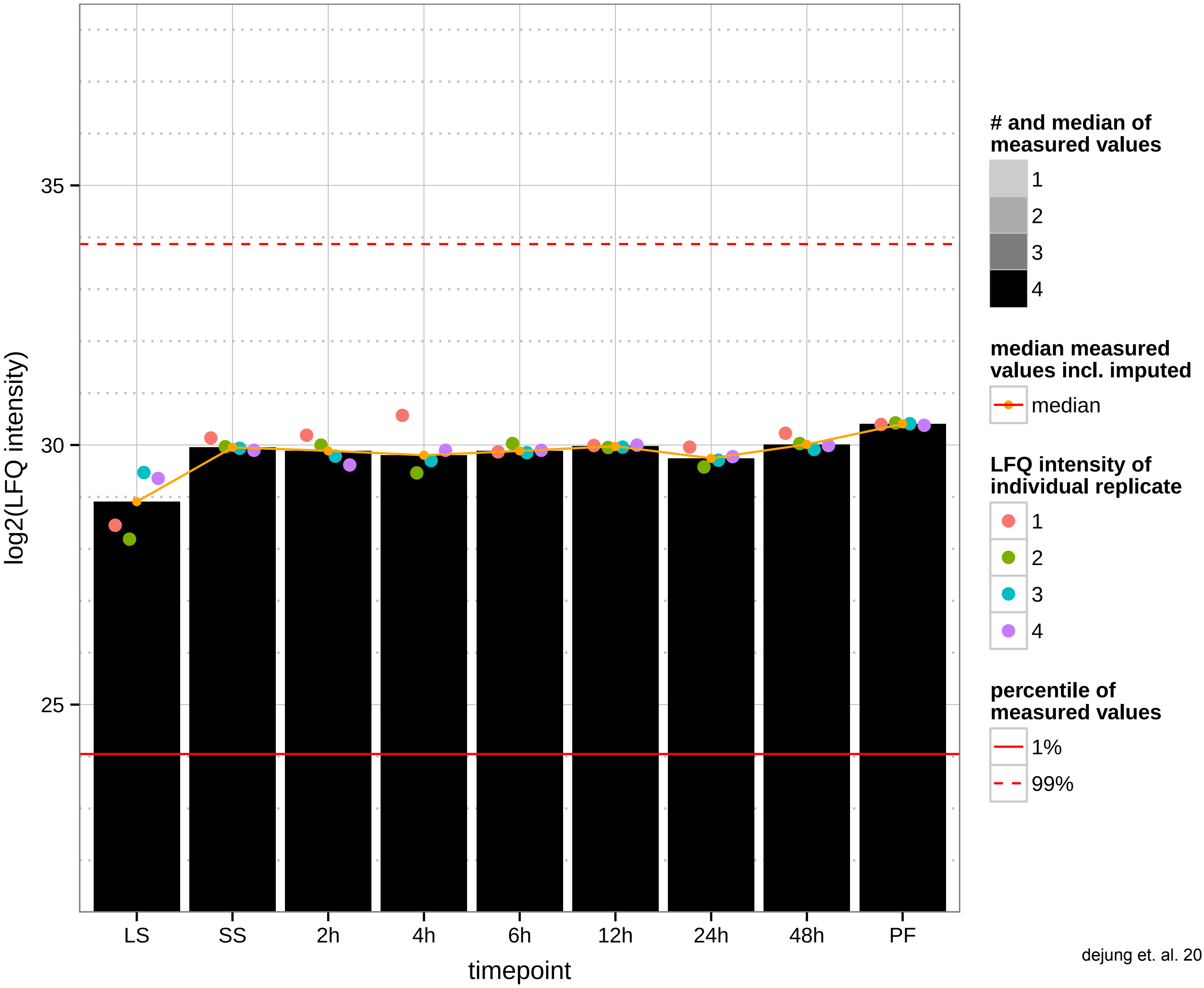
proteasome regulatory non–ATP–ase subunit 2 (RPN2)
Tb927.11.9220
AGOF: endopeptidase activity, enzyme regulator activity
AGOC: proteasome complex, proteasome regulatory particle
AGOP: proteasomal ubiquitin–dependent protein catabolic process, regulation of protein catabolic process
PGOF: binding, enzyme regulator activity
PGOC: proteasome complex
PGOP: regulation of protein catabolic process





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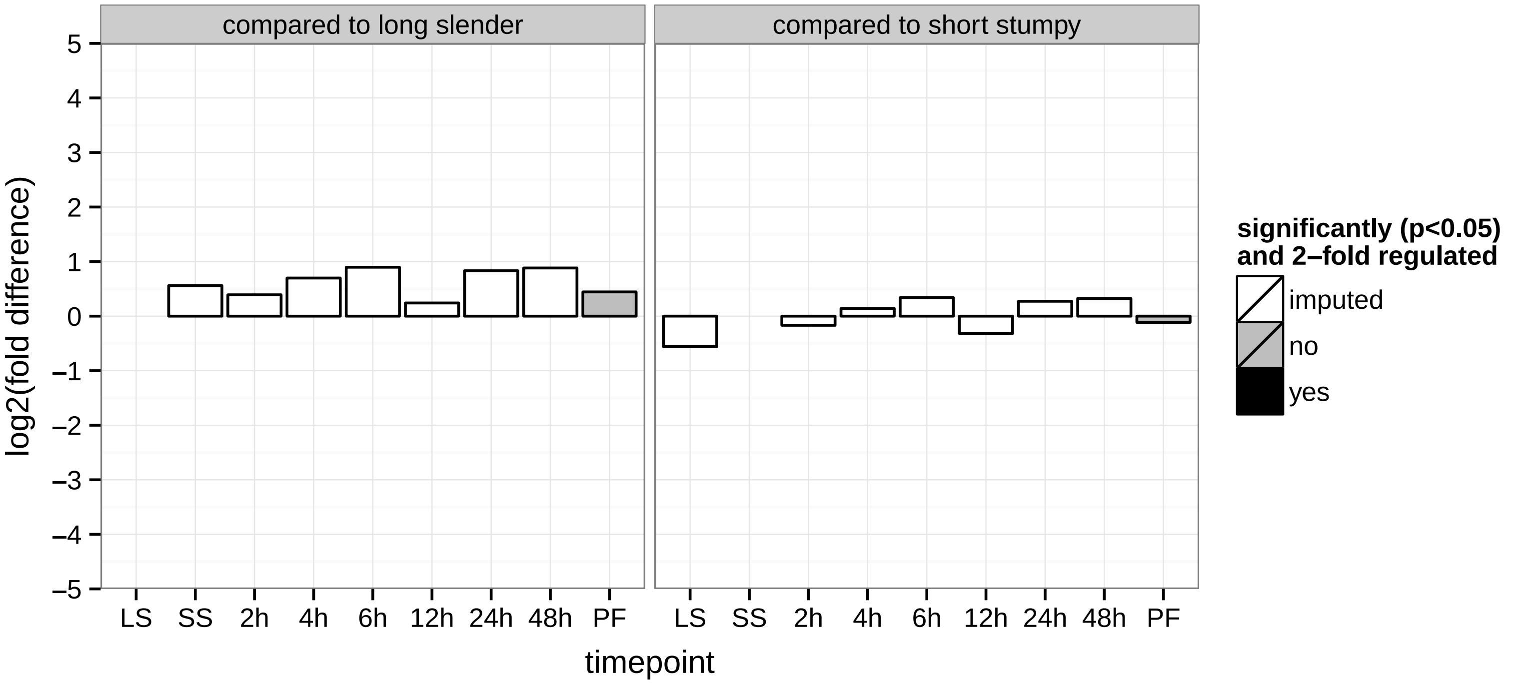
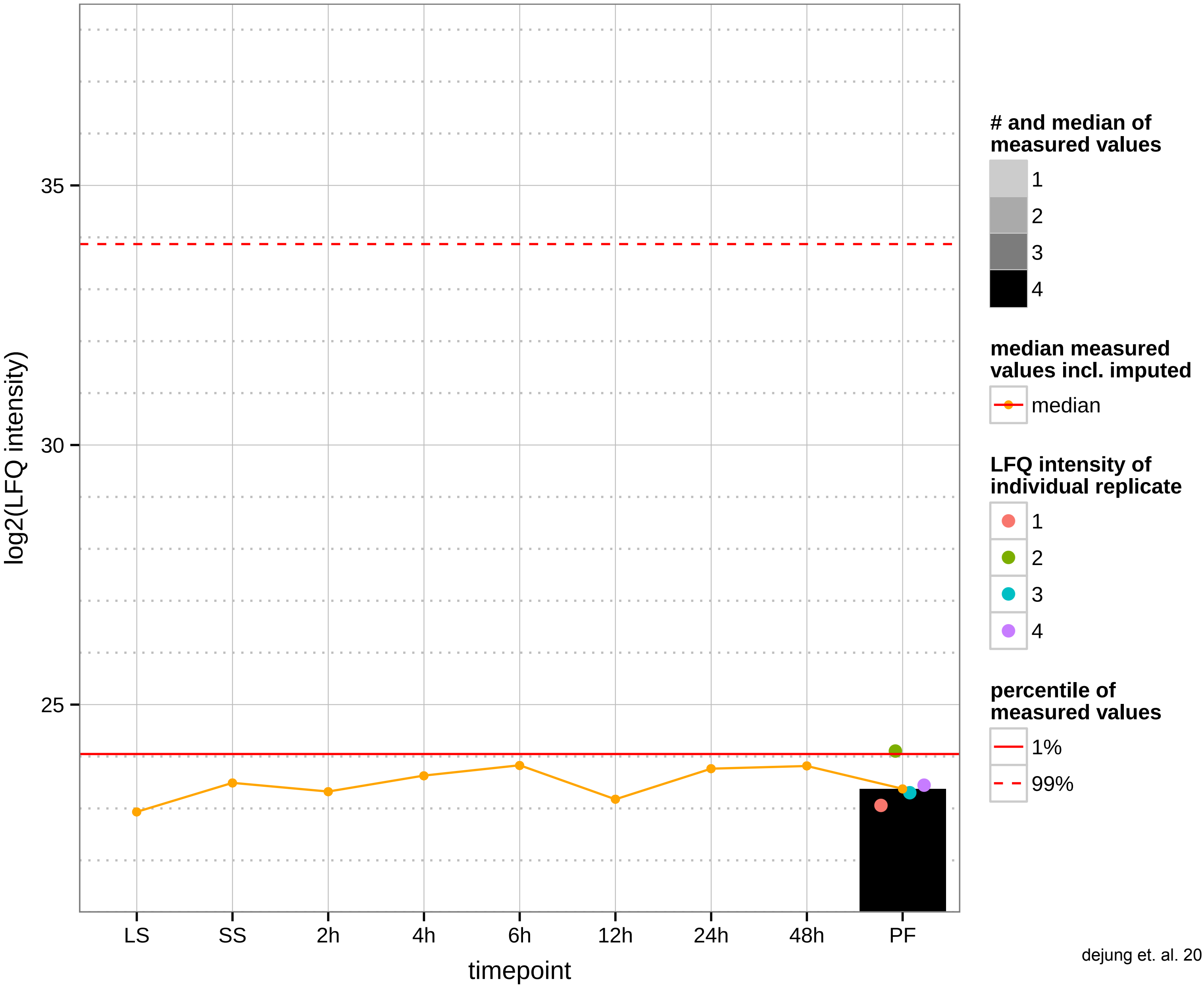
hypothetical protein, conserved
Tb927.11.9300
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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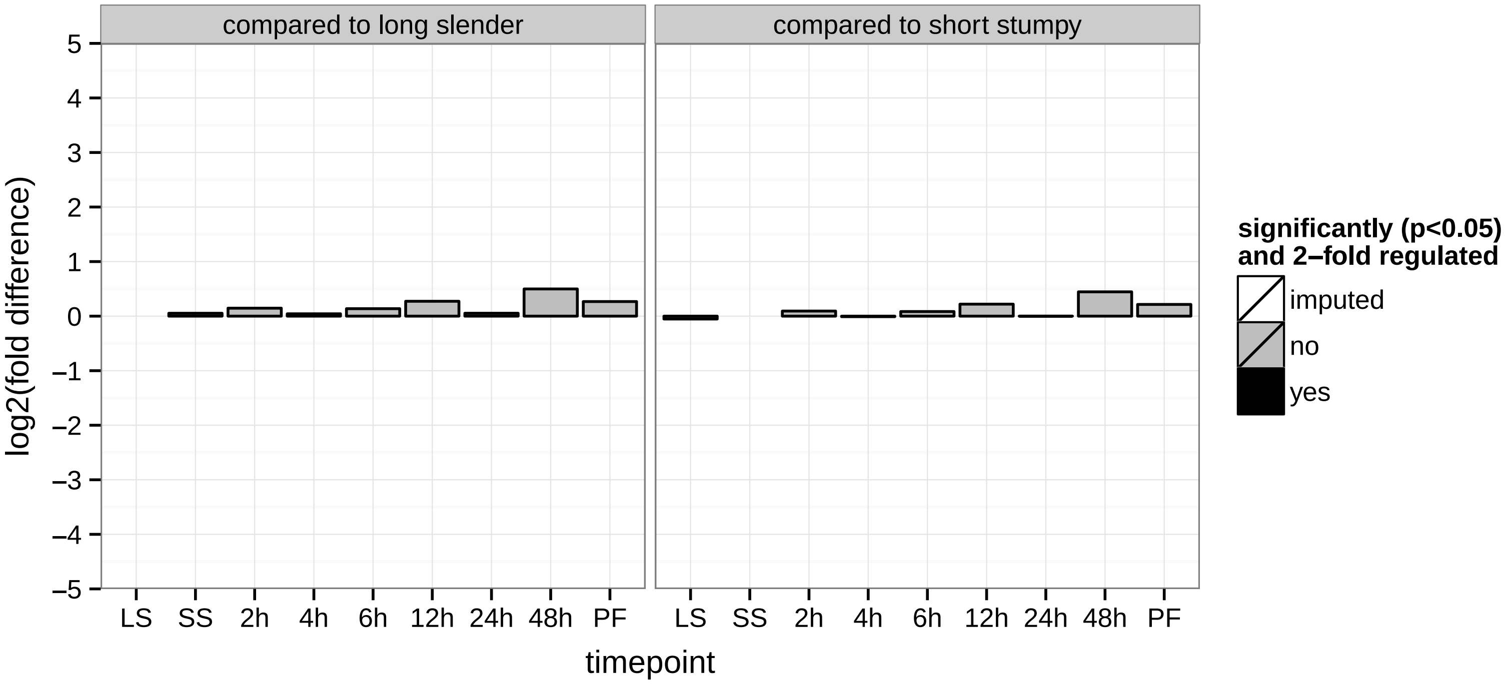
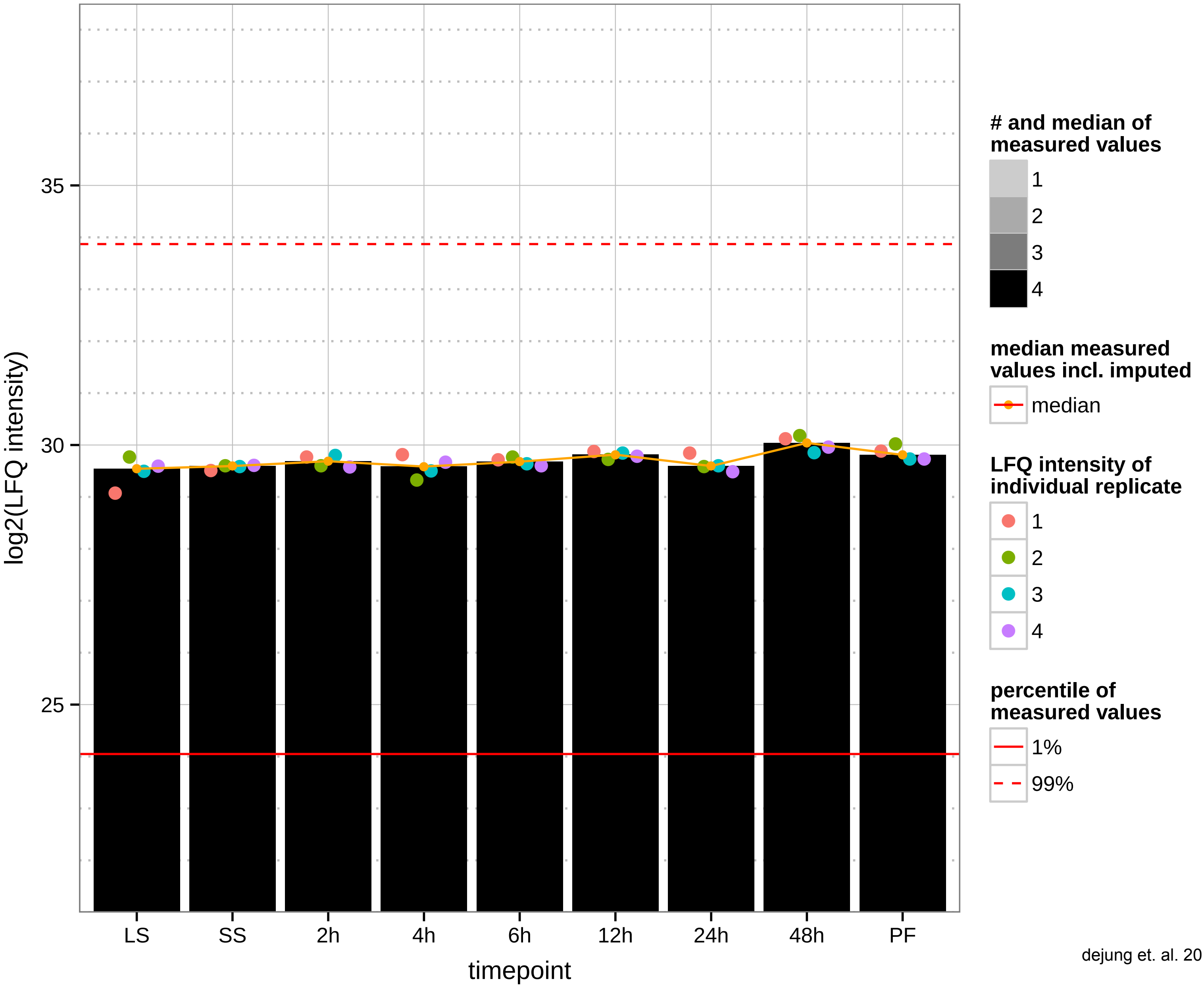
hypothetical protein, conserved
Tb927.11.9400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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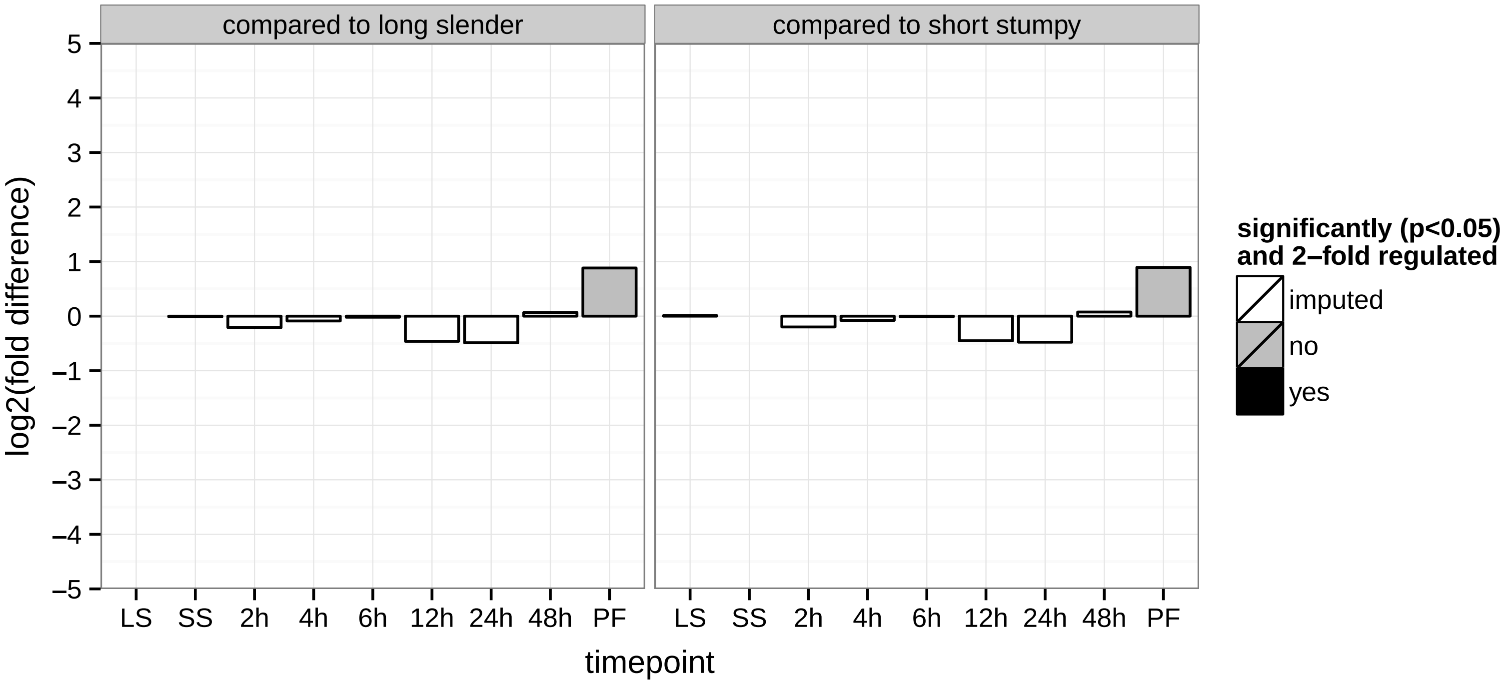
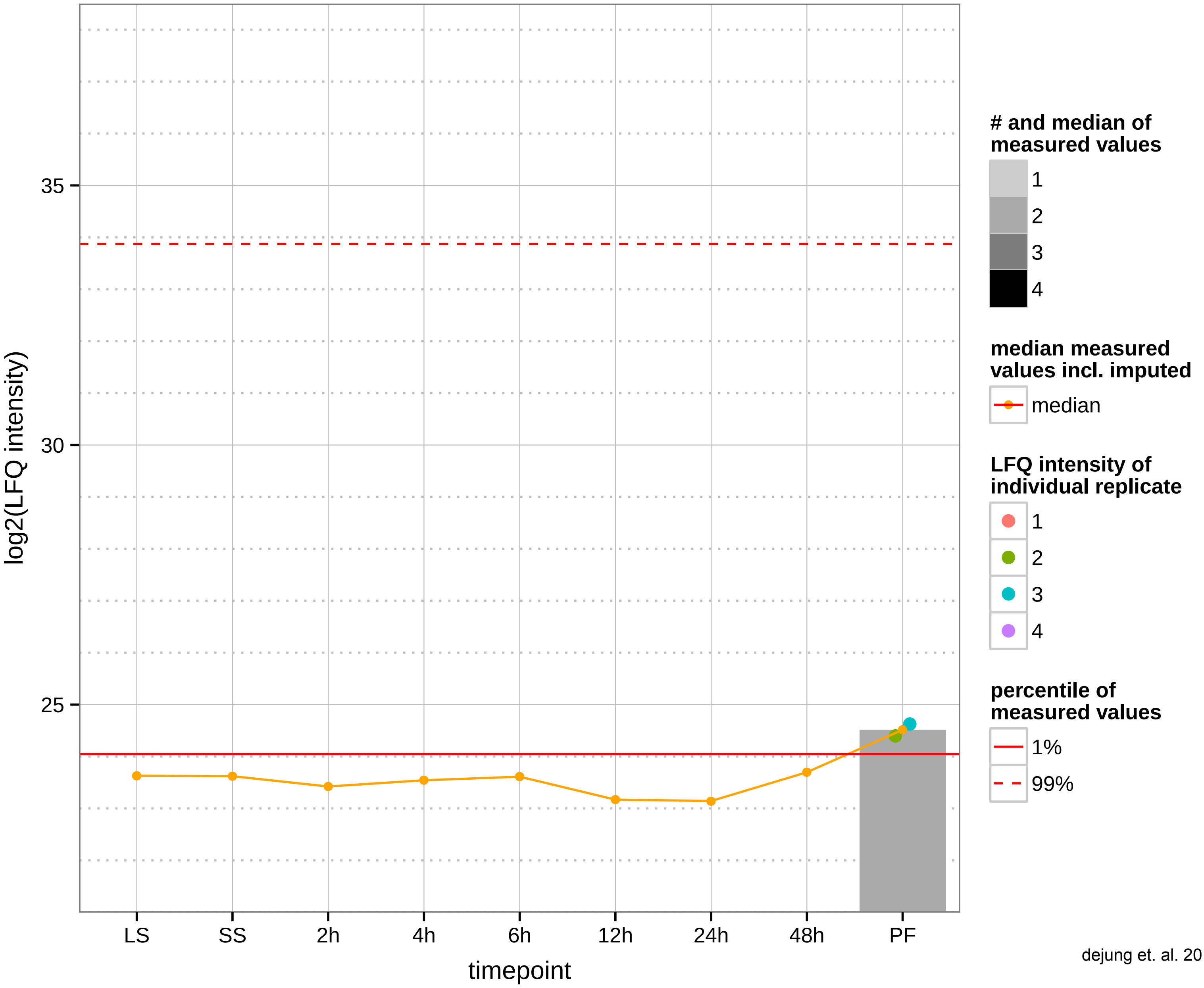
TFIIH basal transcription factor subunit (p62)
Tb927.11.9430
AGOF: sequence−specific DNA binding transcription factor activity
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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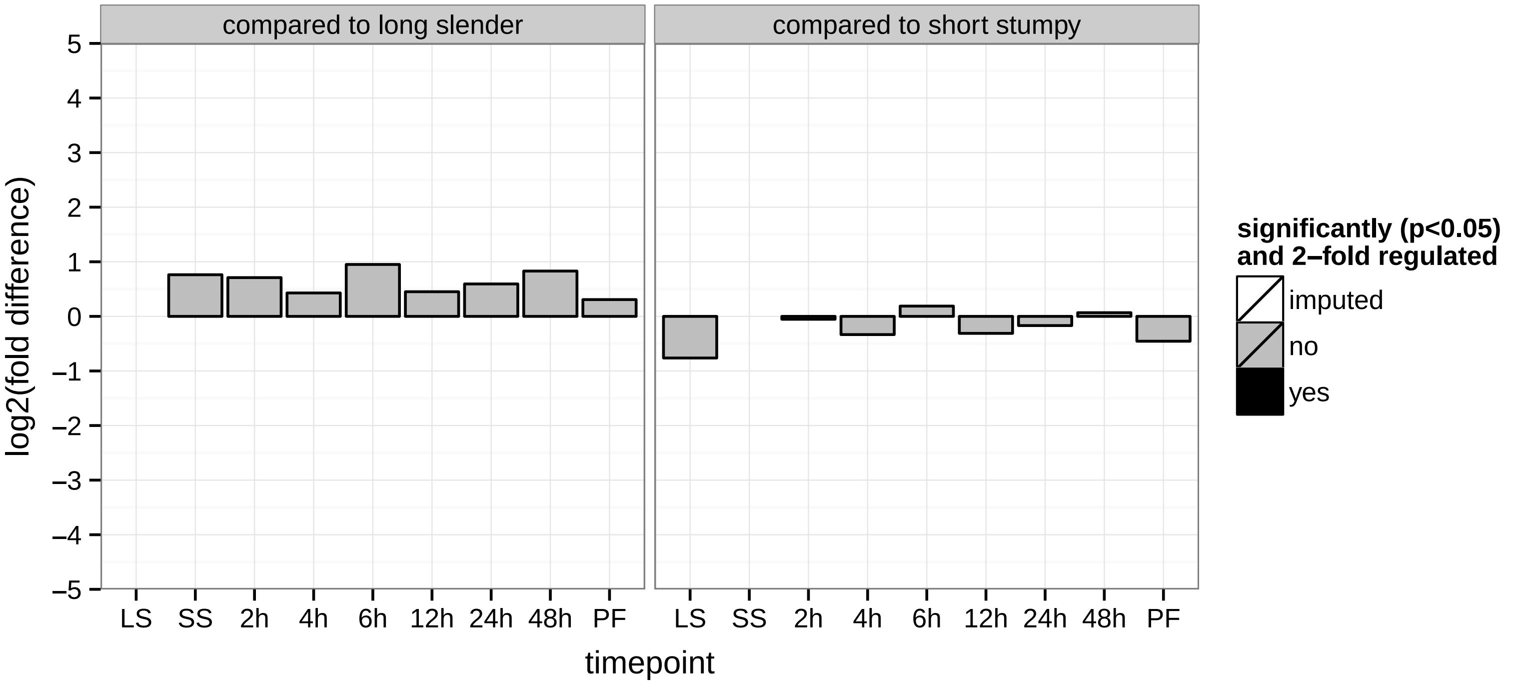
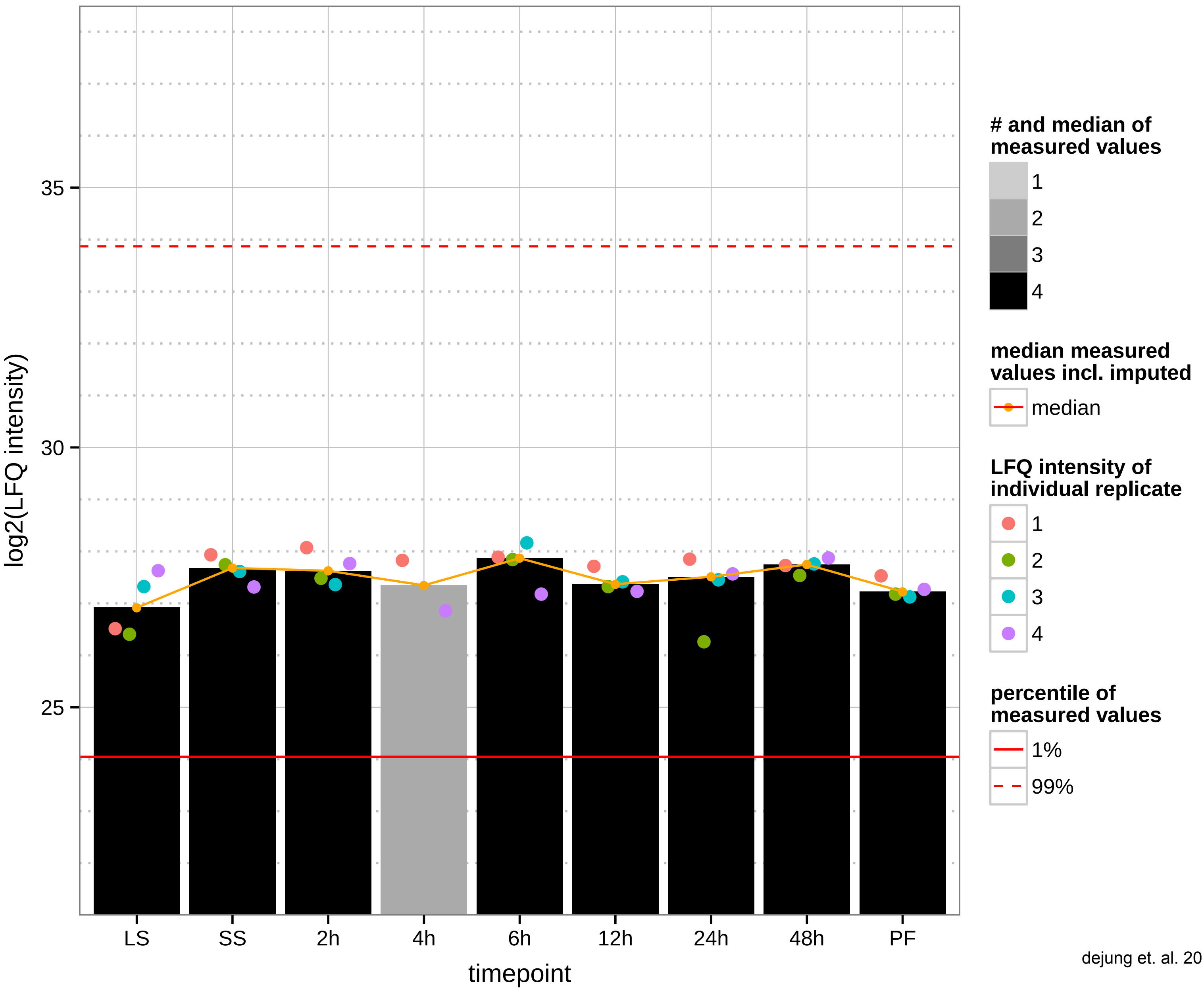
hypothetical protein, conserved
Tb927.11.9440
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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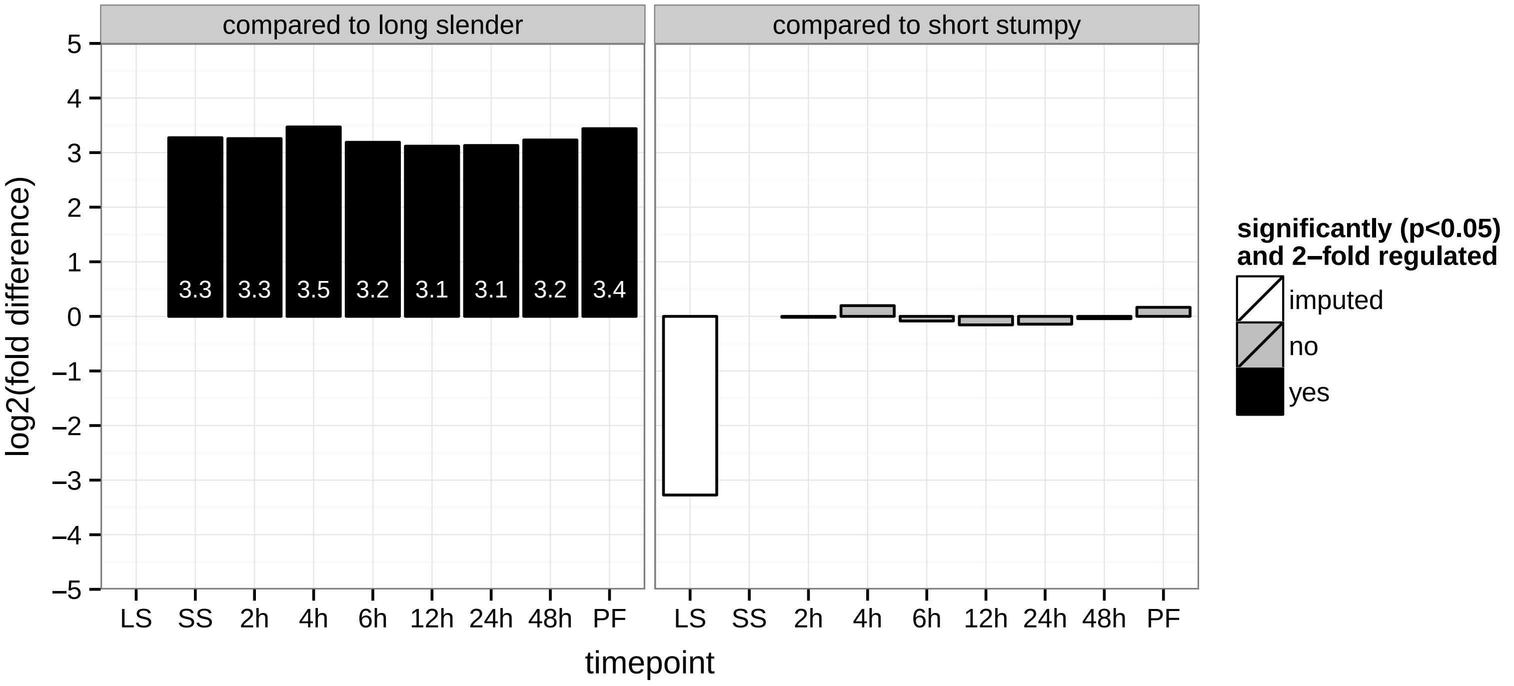
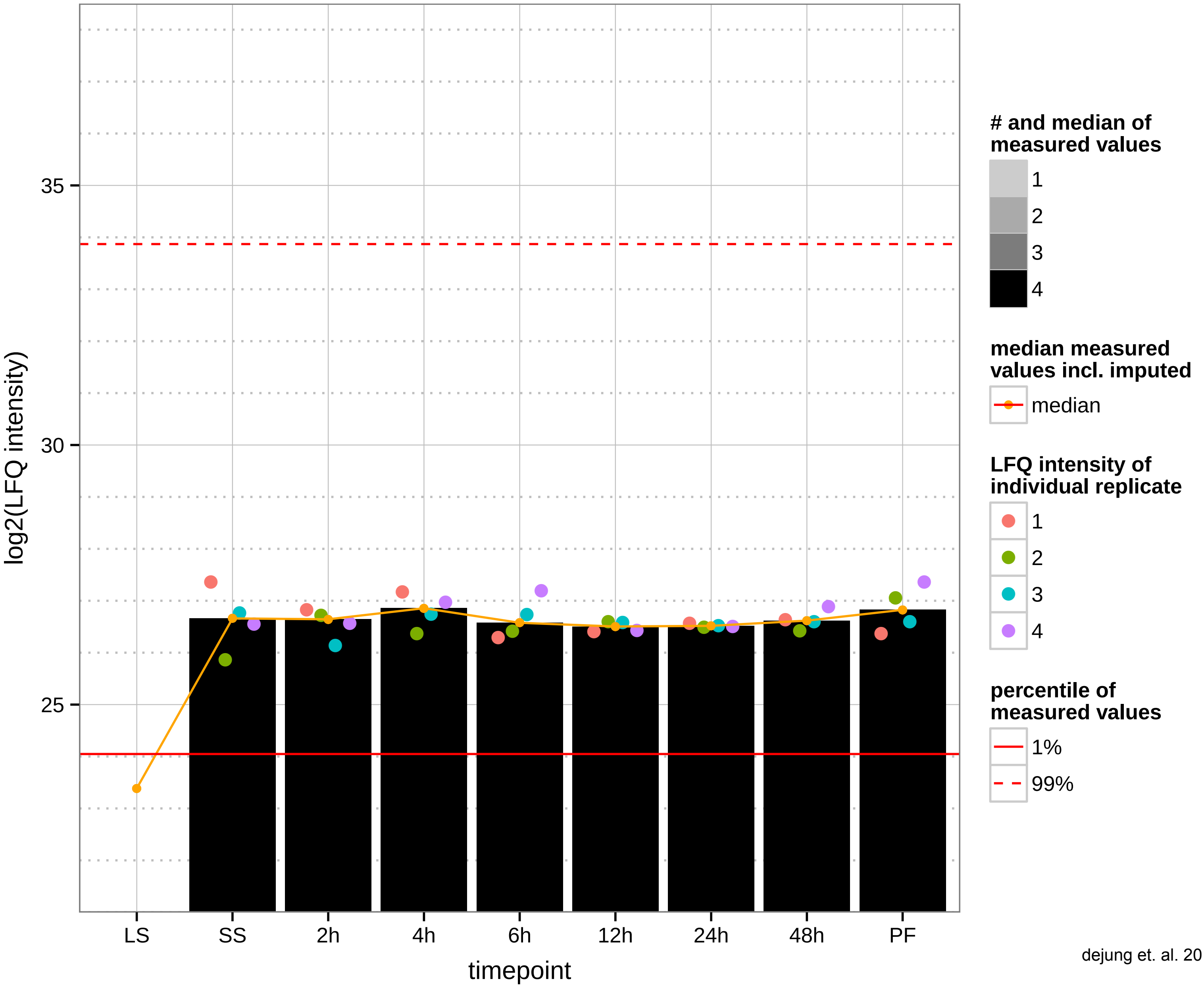
hypothetical protein, conserved
Tb927.11.9490
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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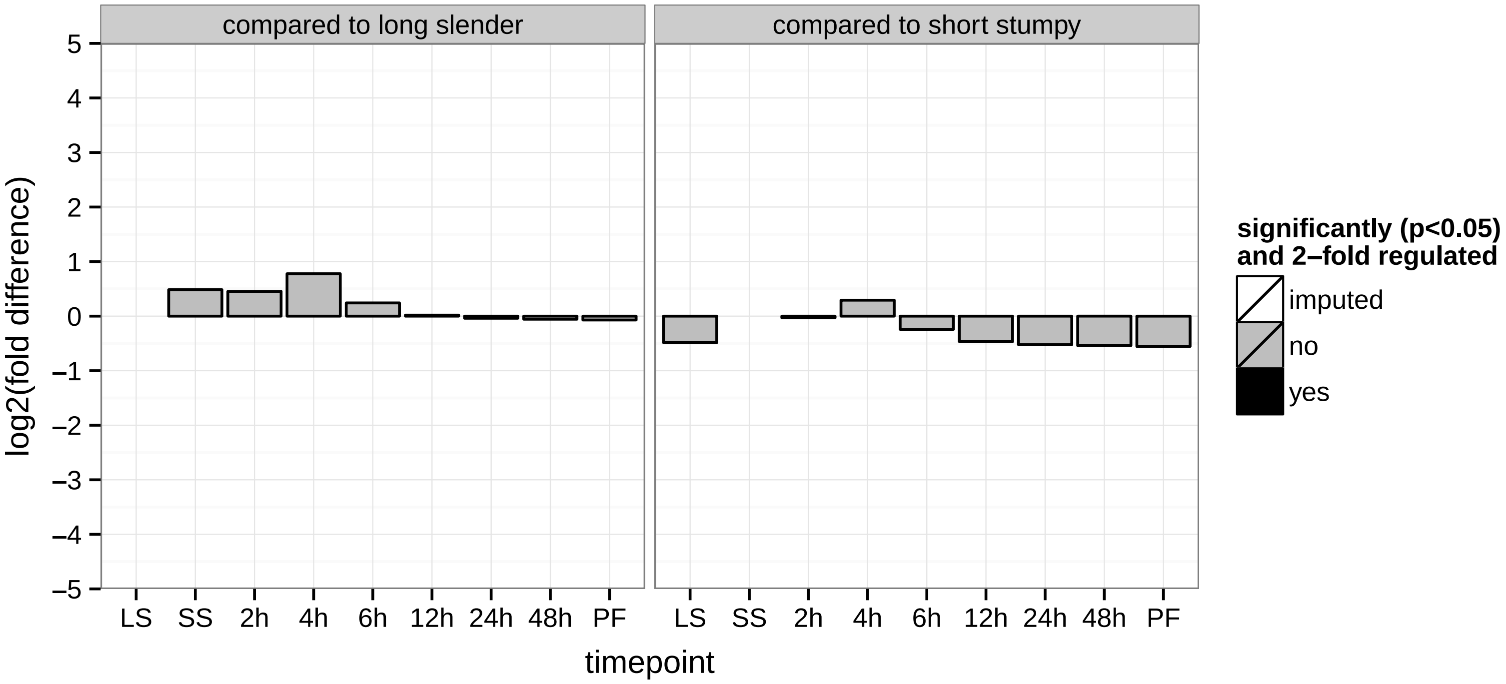
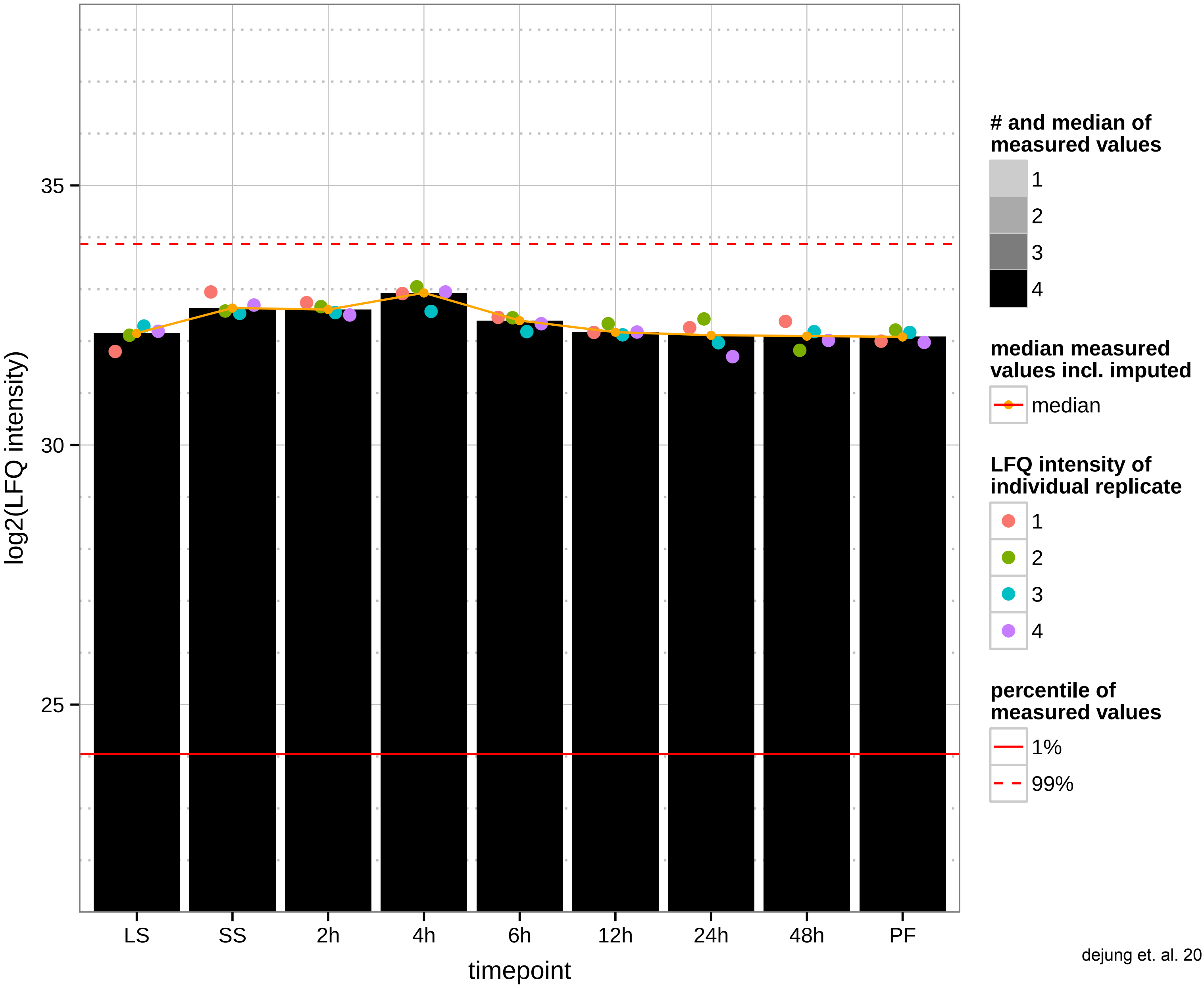
14–3–3–I protein
Tb927.11.9530
AGOF: DNA binding, protein binding, protein domain specific binding
AGOC: eukaryotic translation initiation factor 4F complex
AGOP: Ras protein signal transduction, endocytosis
PGOF: protein domain specific binding
PGOC: null
PGOP: null





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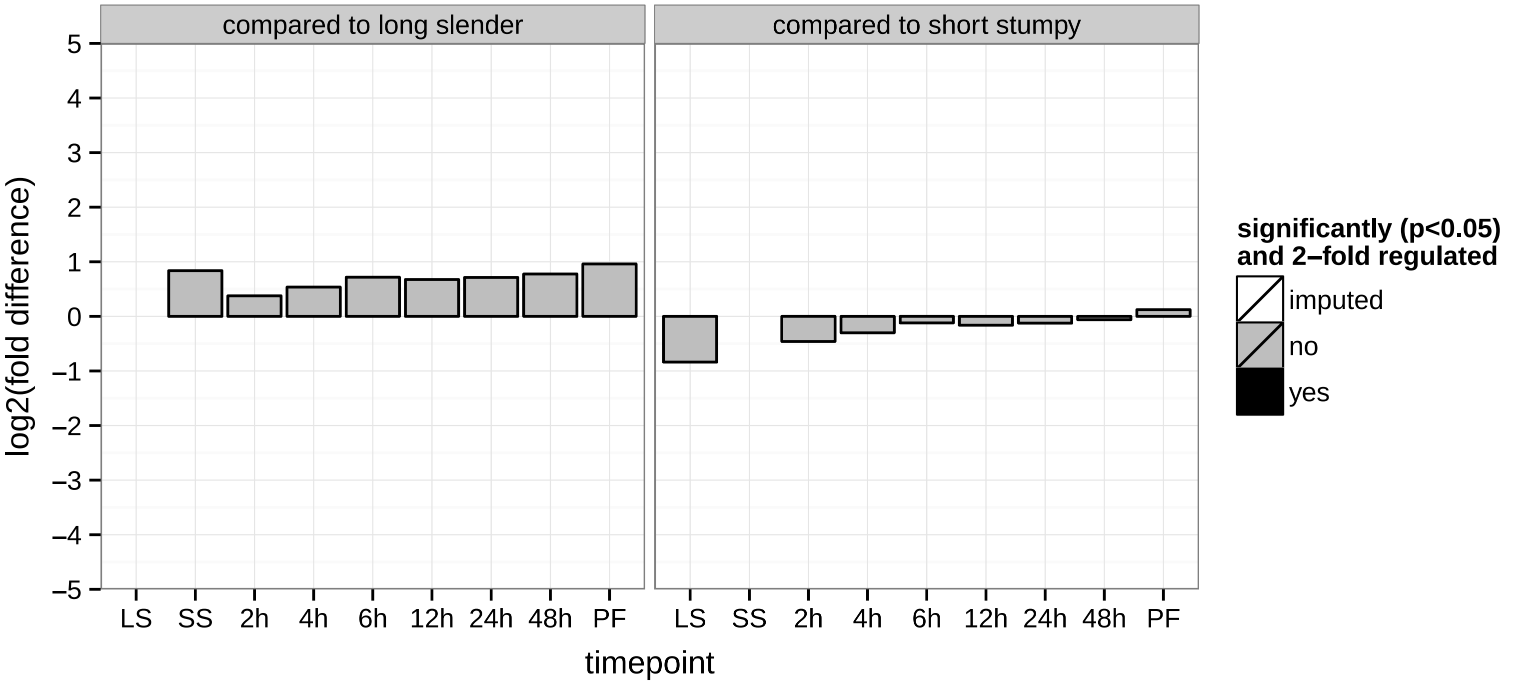
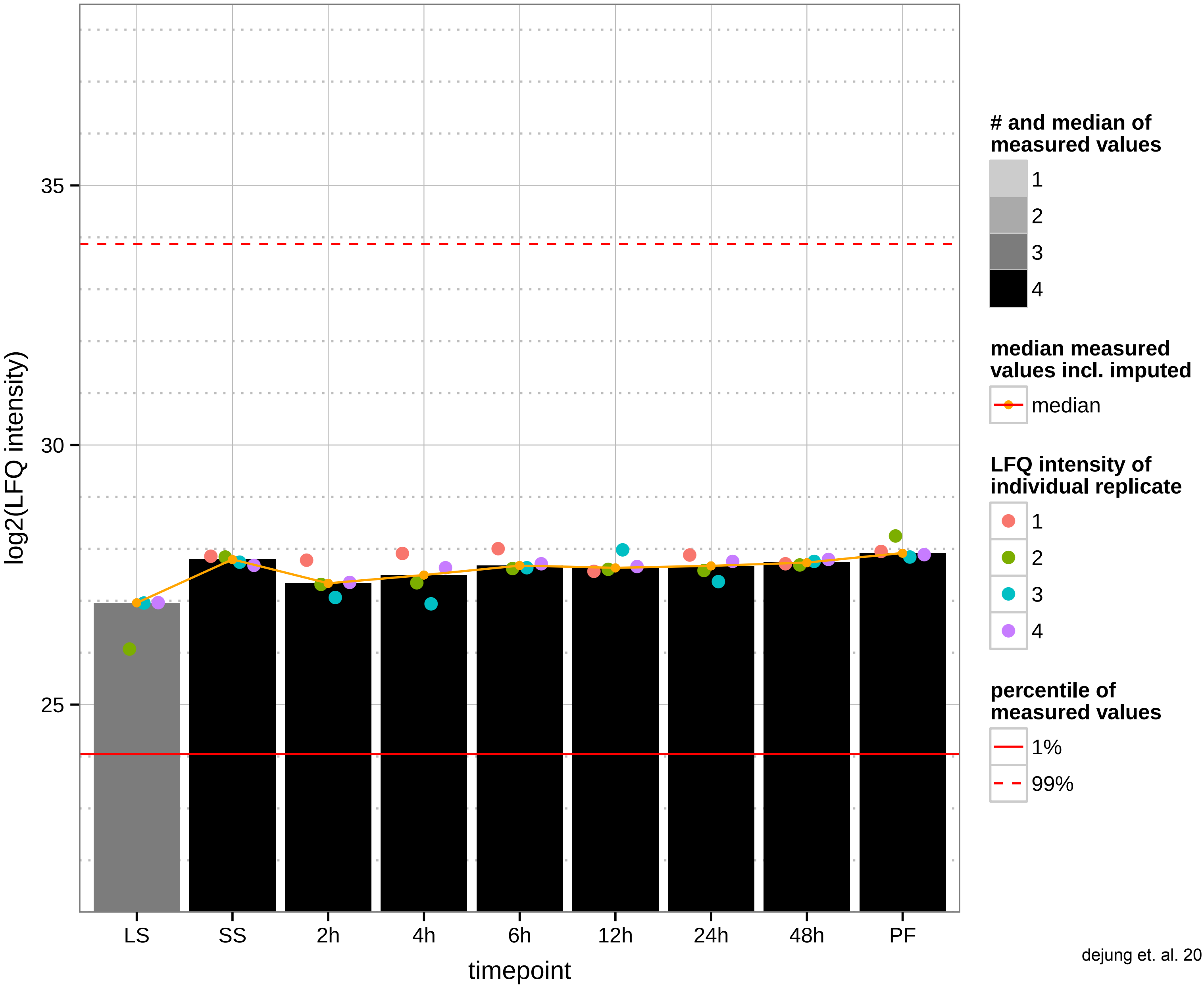
replication factor C, subunit 4, putative
Tb927.11.9550
AGOF: ATP binding, DNA binding, DNA clamp loader activity
AGOC: DNA replication factor C complex
AGOP: DNA replication
PGOF: DNA binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: DNA replication





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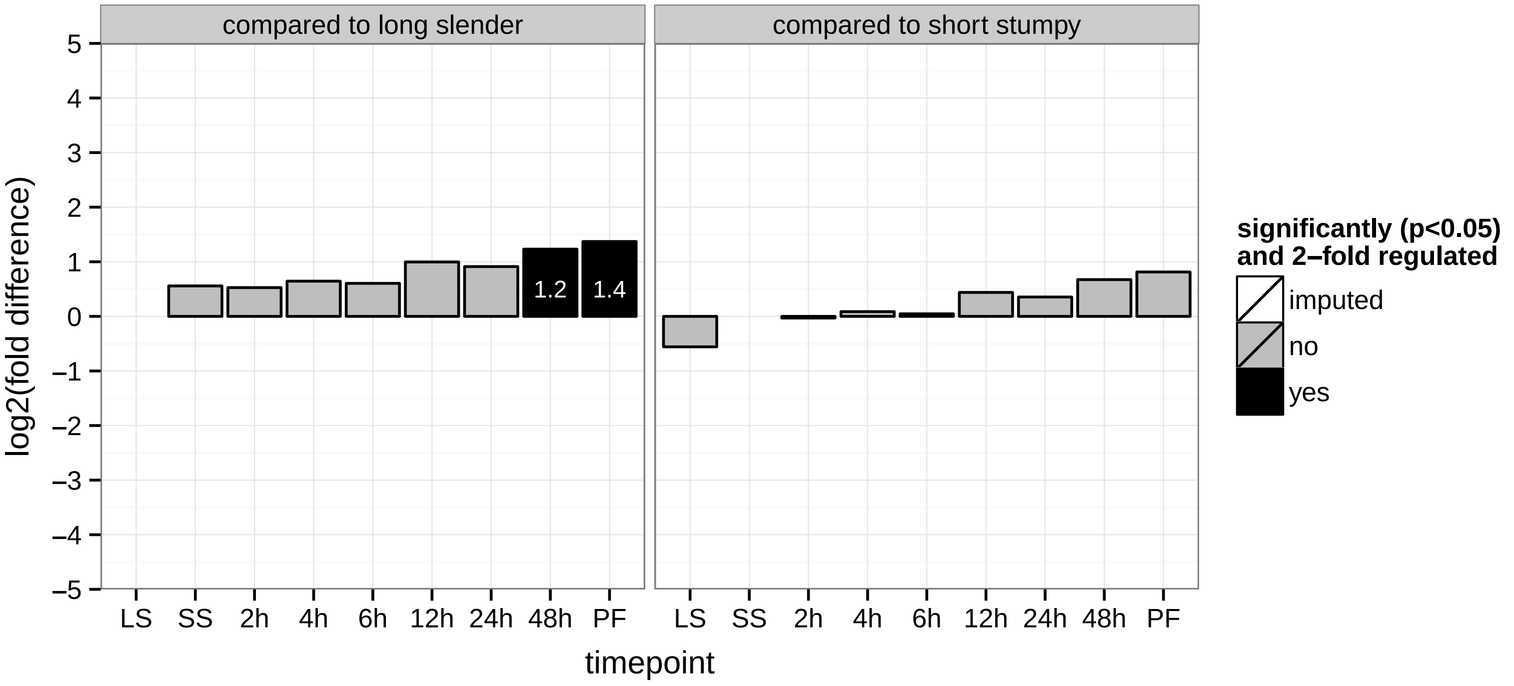
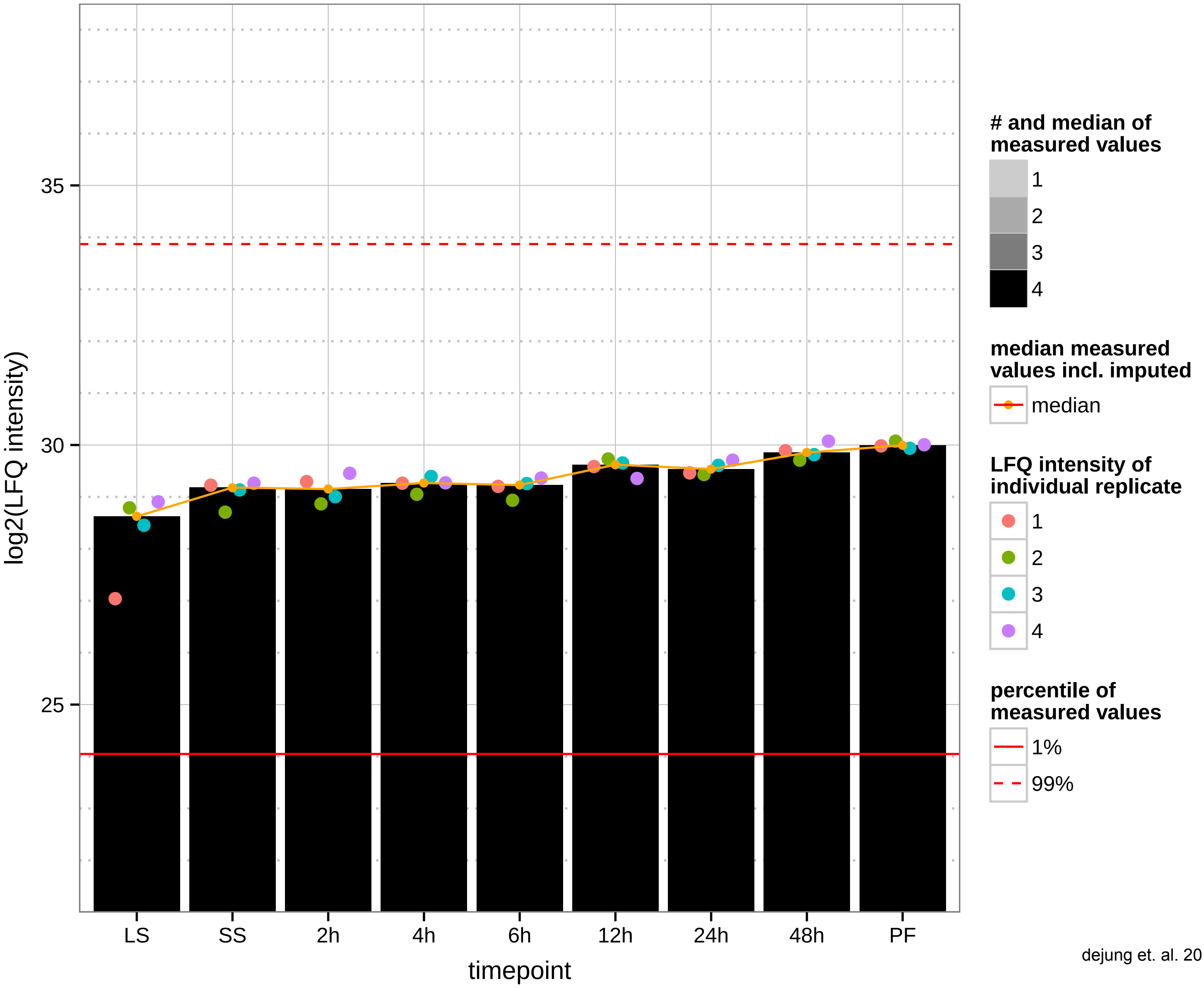
eukaryotic translation initiation factor 3 subunit 2, putative (eIF–3 beta)
Tb927.11.9610
AGOF: translation initiation factor activity
AGOC: eukaryotic translation initiation factor 3 complex
AGOP: regulation of translational initiation
PGOF: protein binding
PGOC: null
PGOP: null





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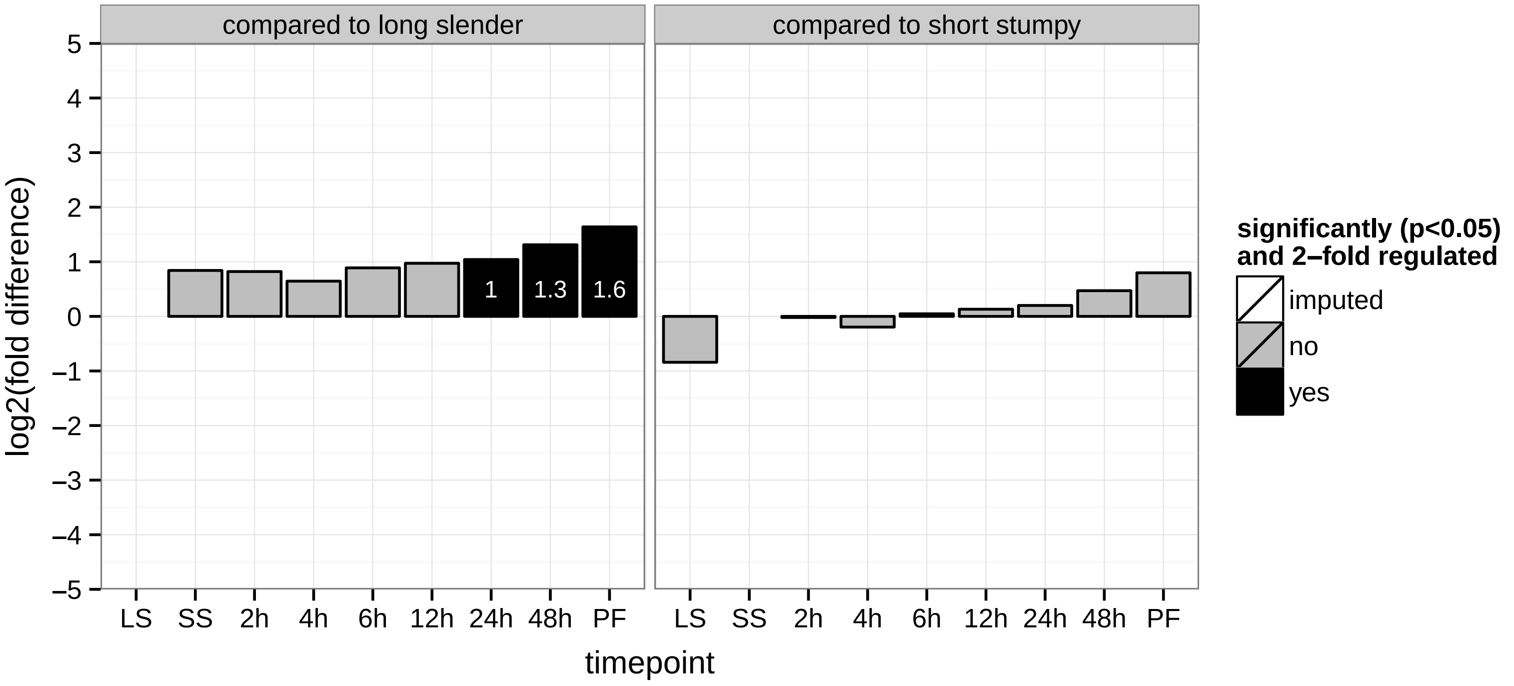
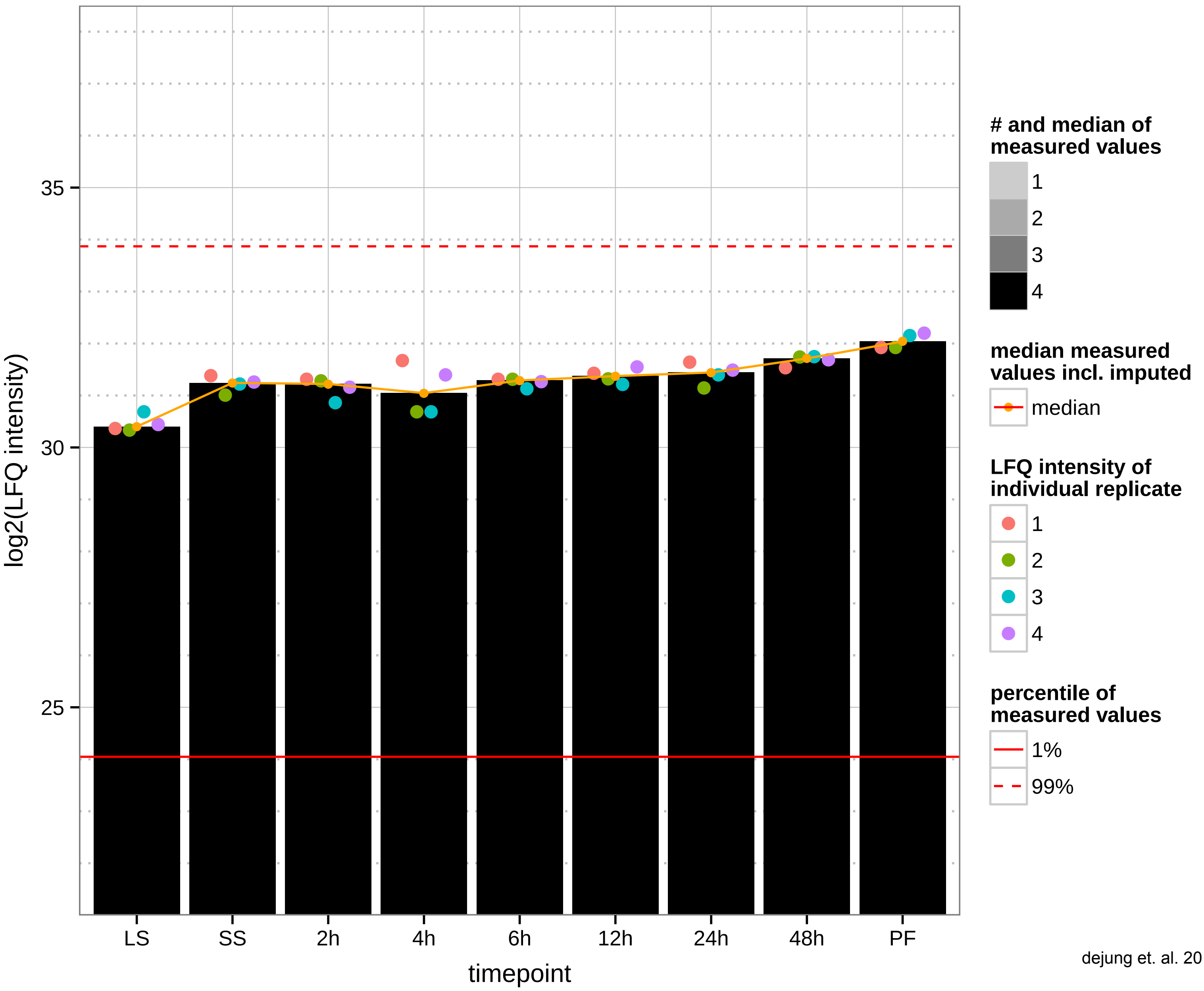
glycyl–tRNA synthetase, putative
Tb927.11.9640
AGOF: ATP binding, glycine–tRNA ligase activity
AGOC: cytoplasm, glycine–tRNA ligase complex
AGOP: glycyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, glycine–tRNA ligase activity, nucleotide binding
PGOC: cytoplasm
PGOP: glycyl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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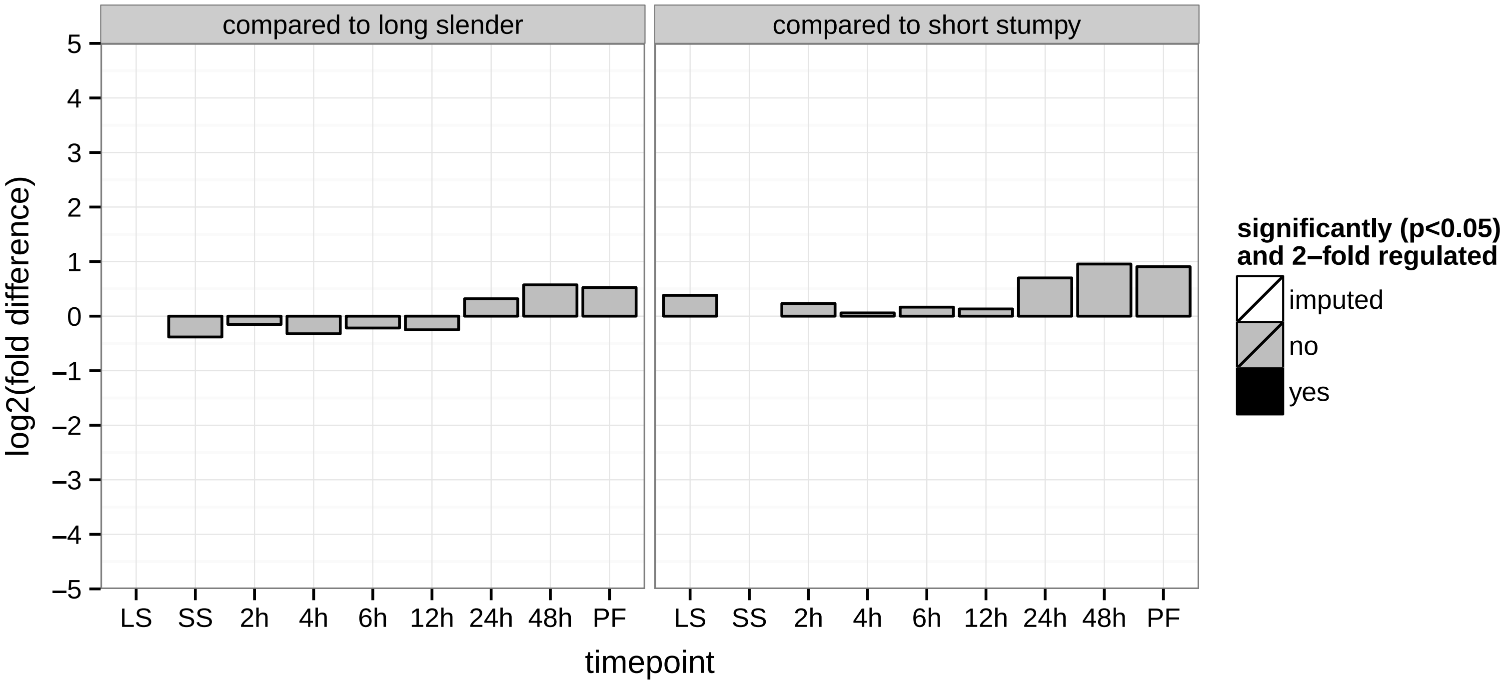
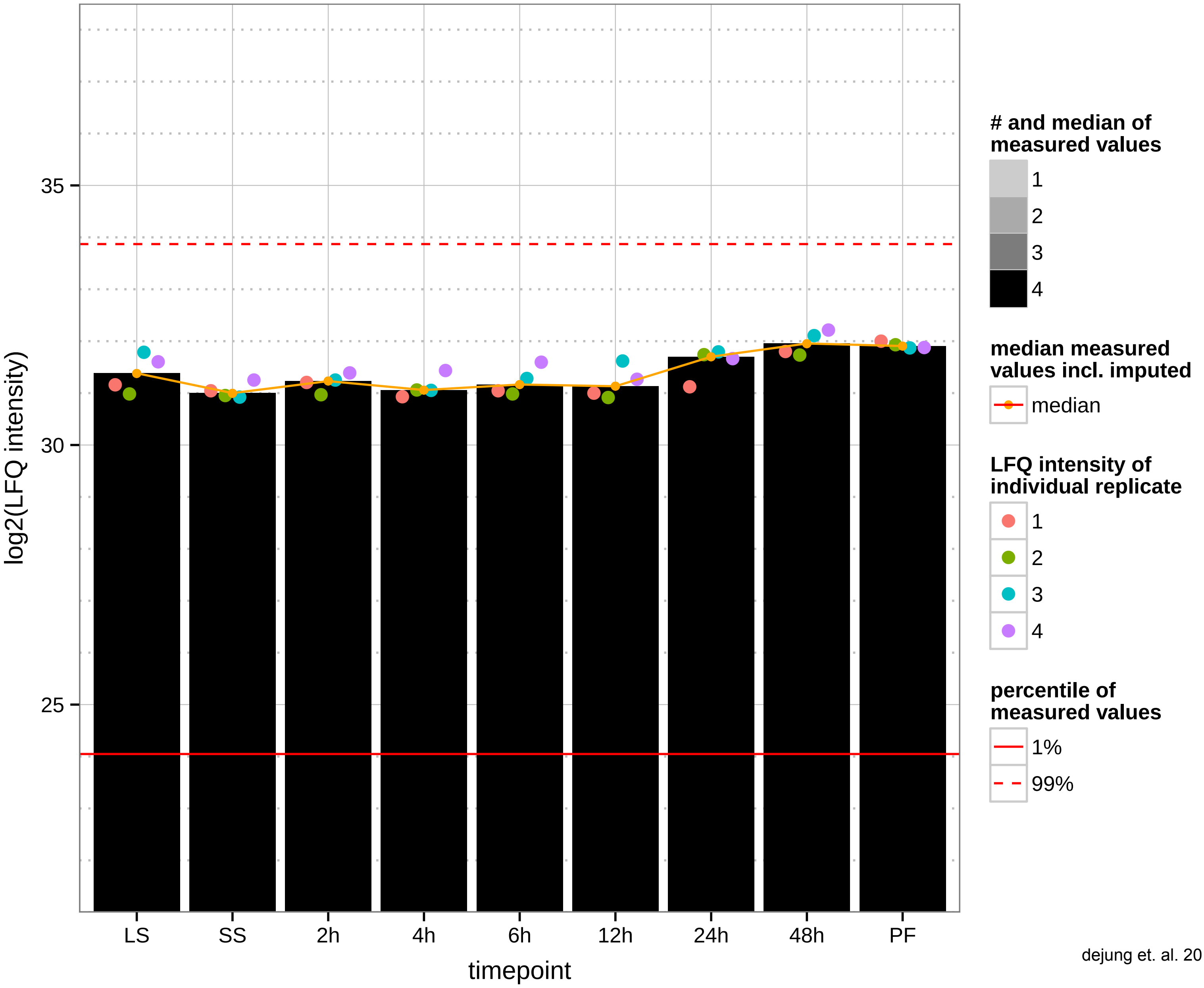
40S ribosomal protein S27, putative
Tb927.11.9720
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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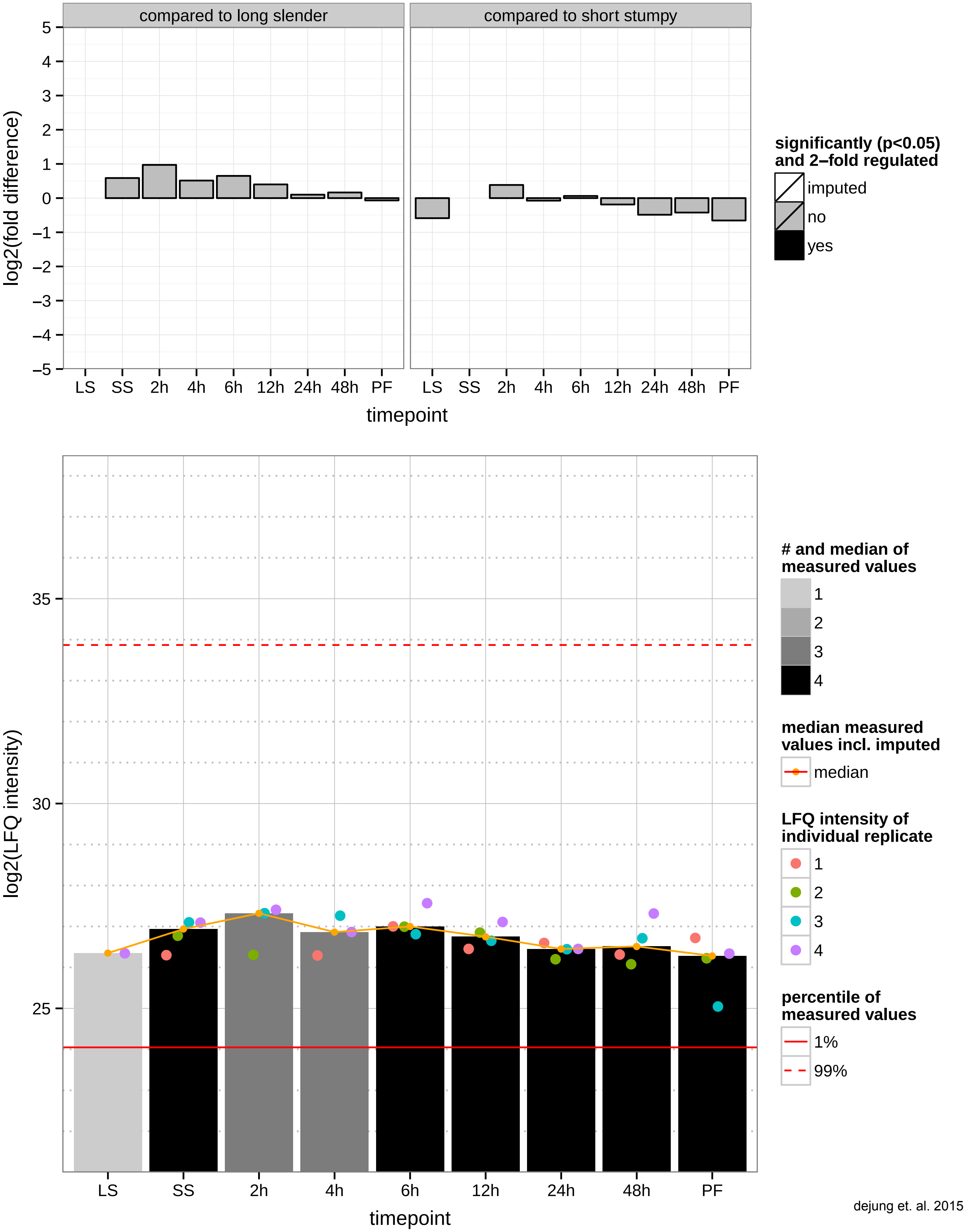
hypothetical protein, conserved
Tb927.11.9760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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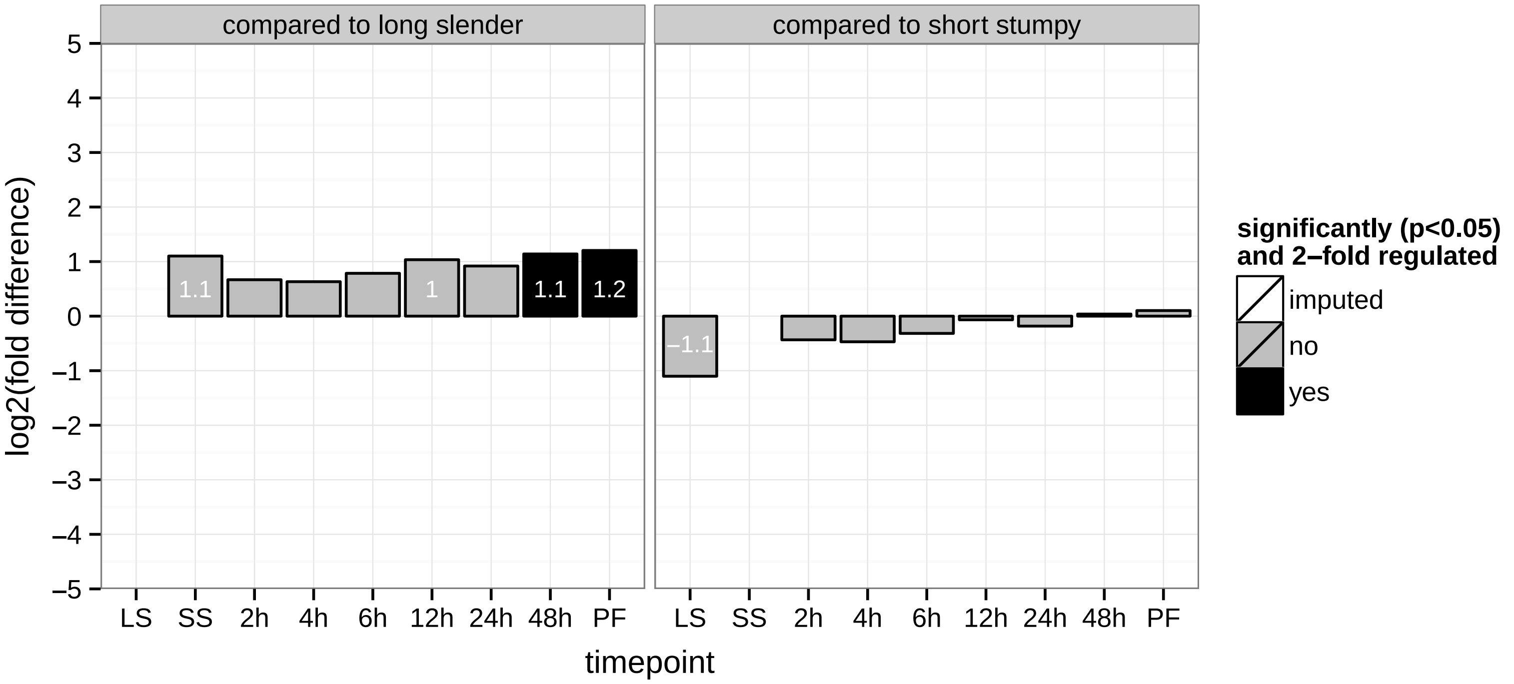
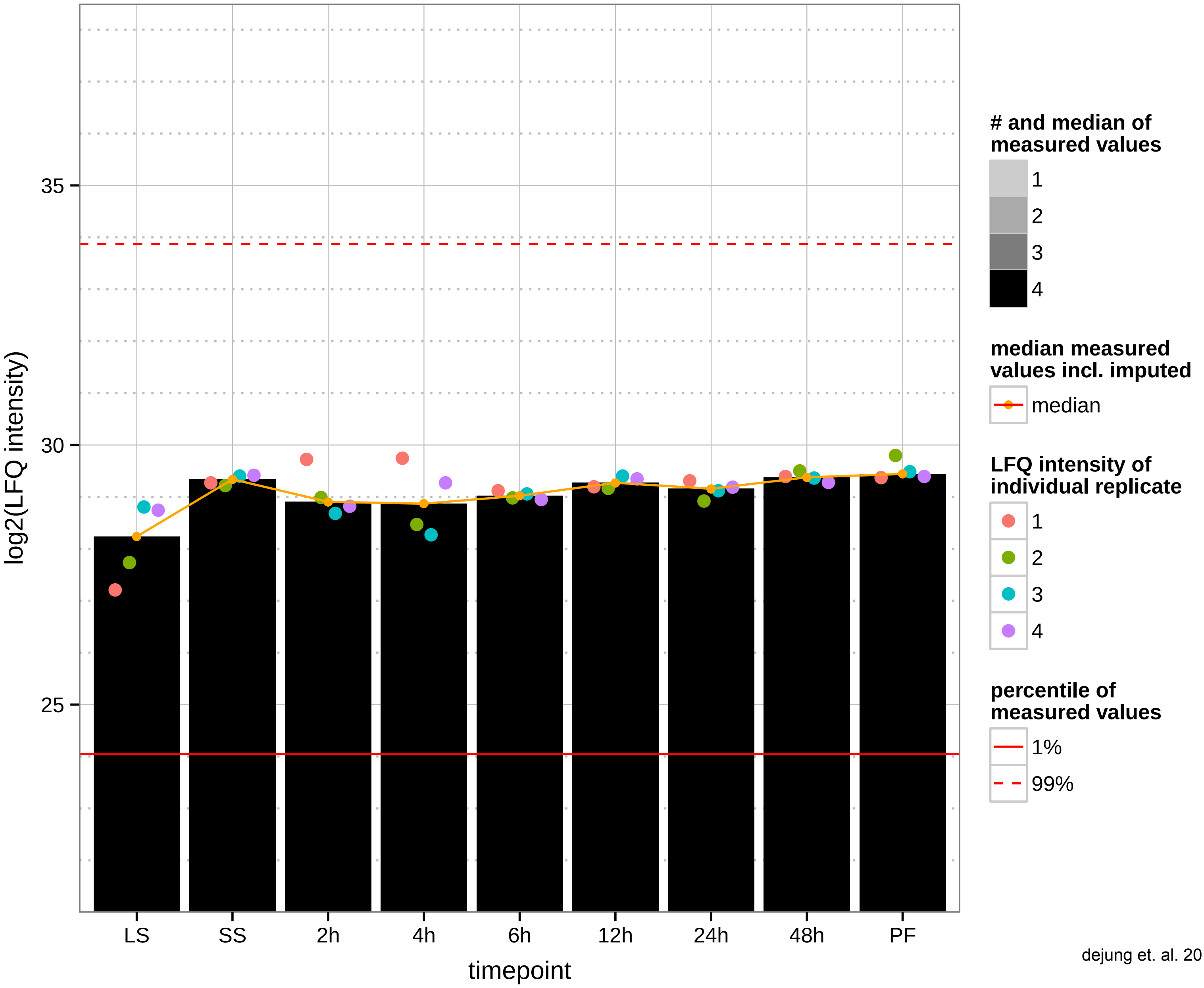
Nucleoporin, serine peptidase, Clan SP, family S59, putative (TbNup158)
Tb927.11.980
AGOF: null
AGOC: membrane, nuclear pore
AGOP: protein homooligomerization, transport
PGOF: null
PGOC: nuclear pore
PGOP: transport





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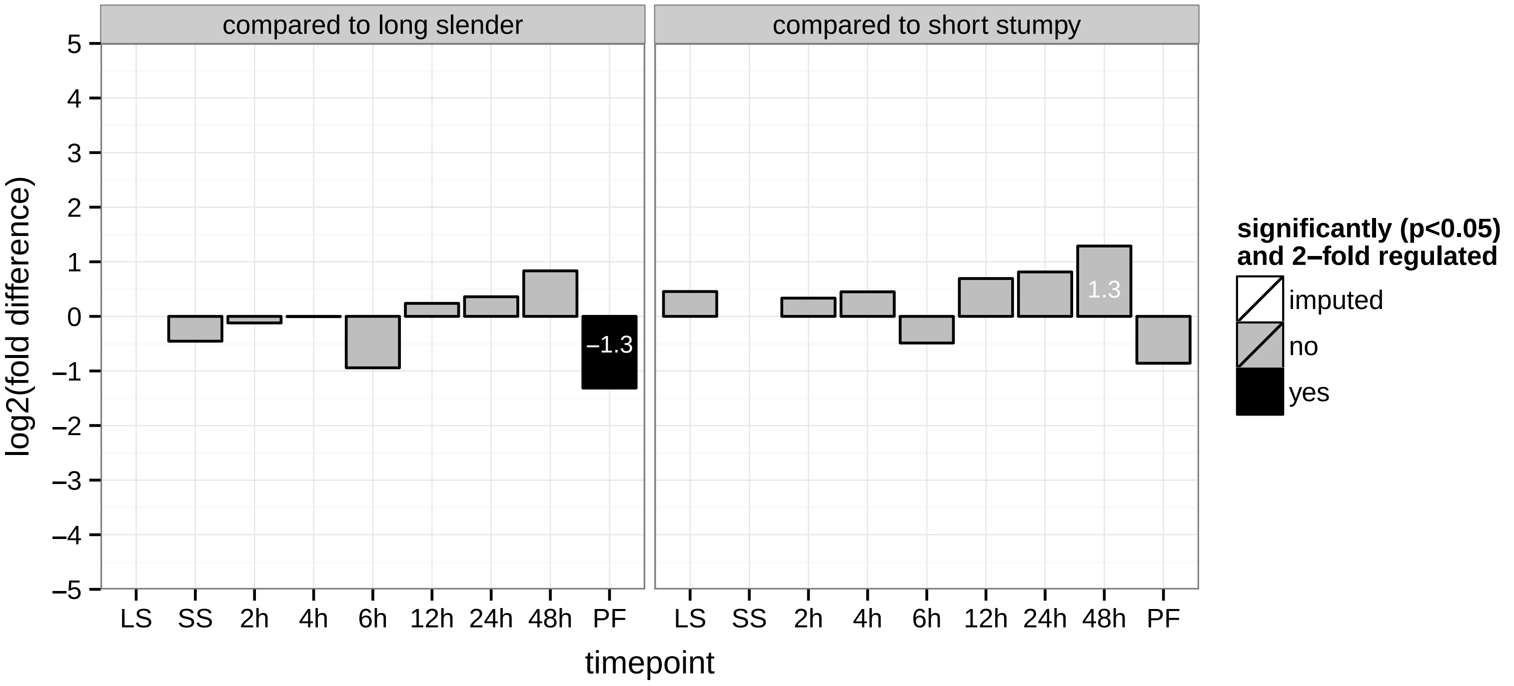
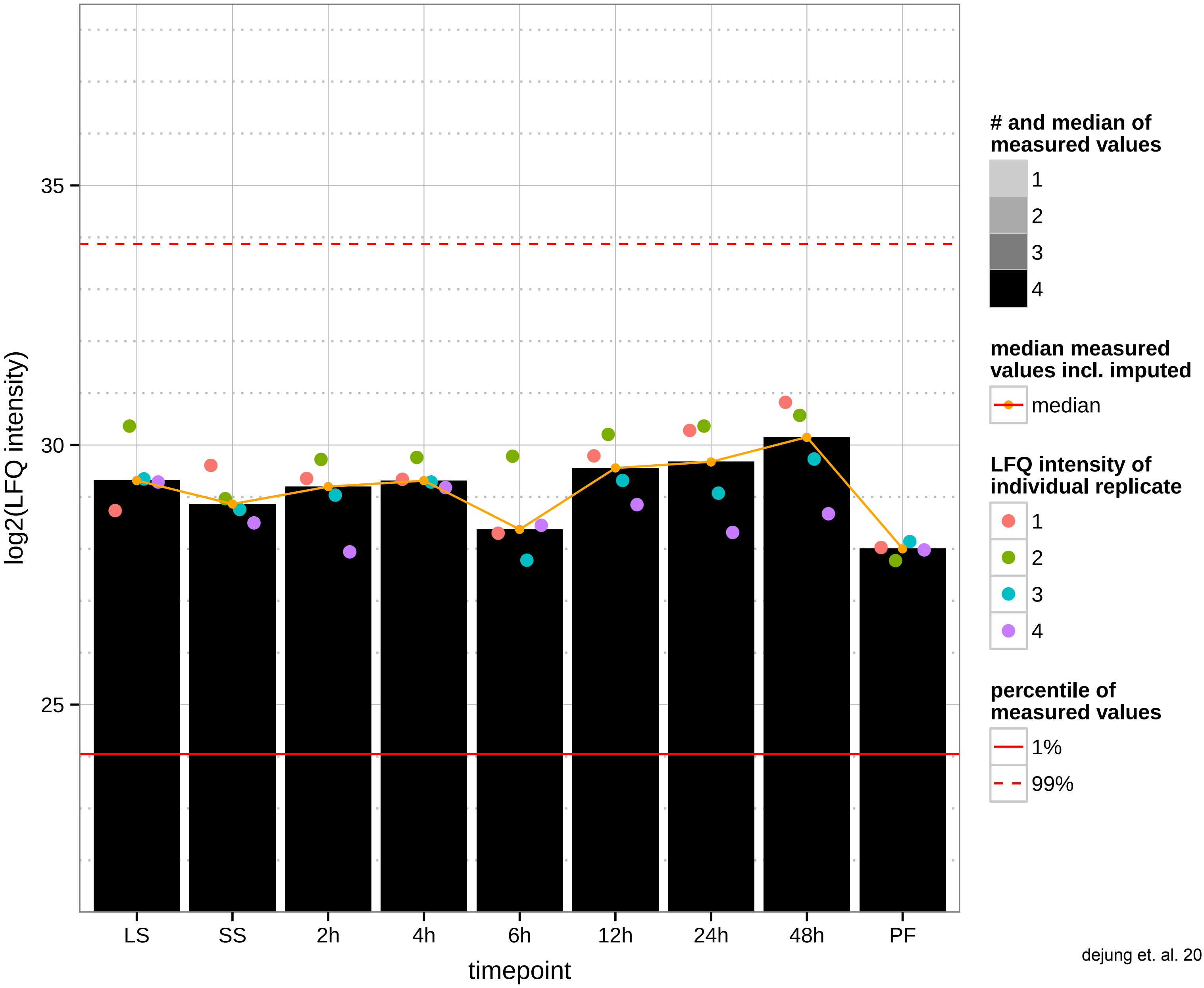
hypothetical protein, conserved
Tb927.11.9860
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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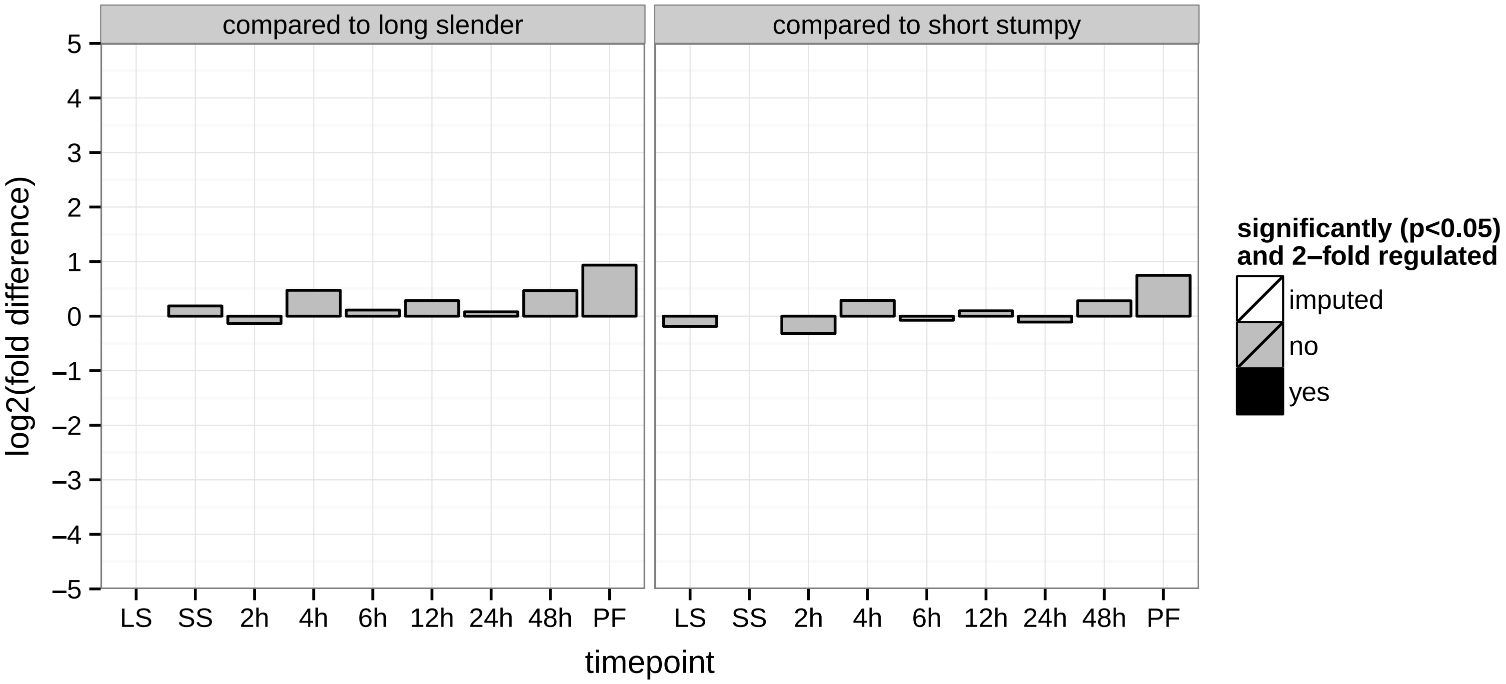
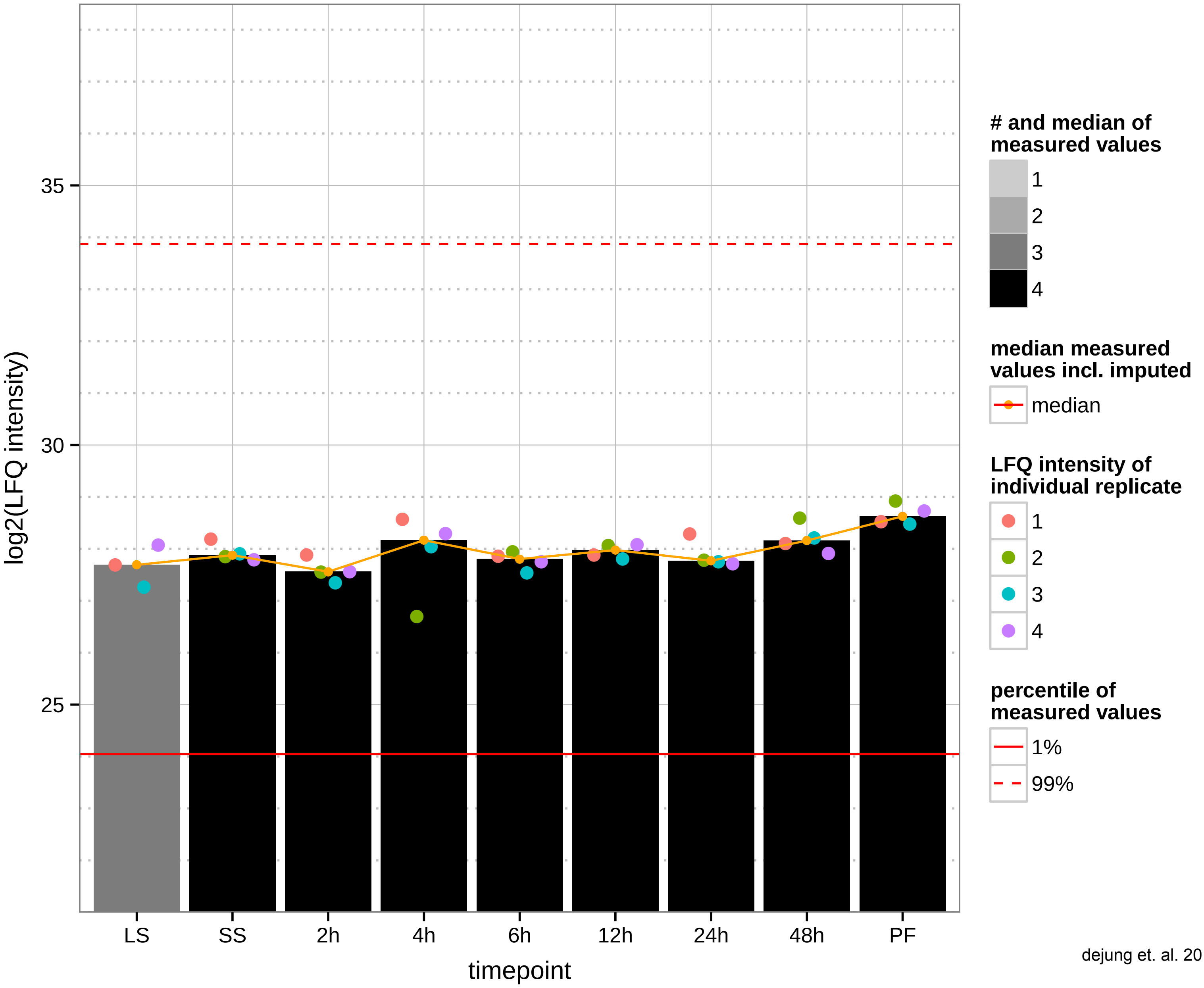
hypothetical protein, conserved
Tb927.11.9880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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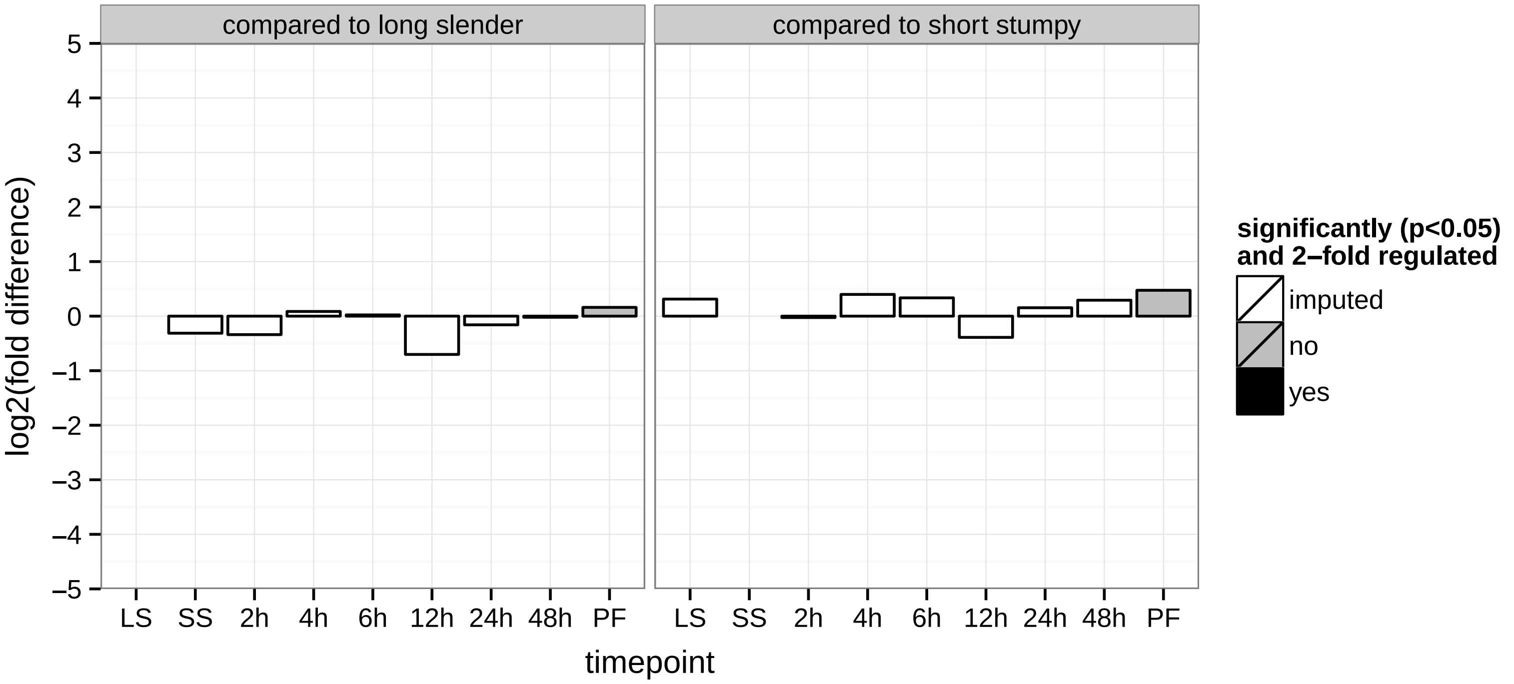
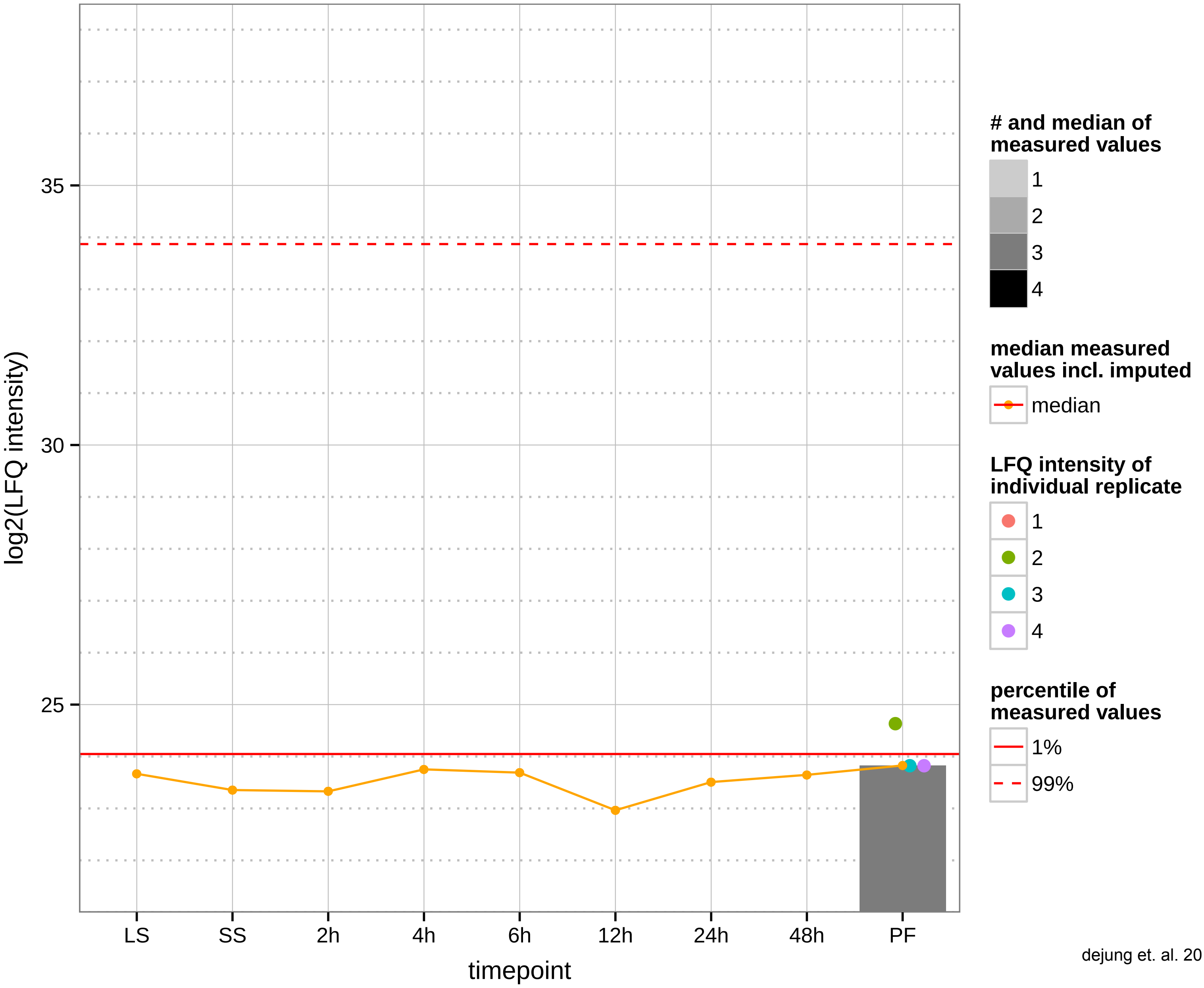
NADH–ubiquinone oxidoreductase complex I subunit, putative
Tb927.11.9930
AGOF: NADH dehydrogenase (ubiquinone) activity, oxidoreductase activity
AGOC: mitochondrial respiratory chain complex I, mitochondrion
AGOP: mitochondrial electron transport, NADH to ubiquinone
PGOF: null
PGOC: null
PGOP: null





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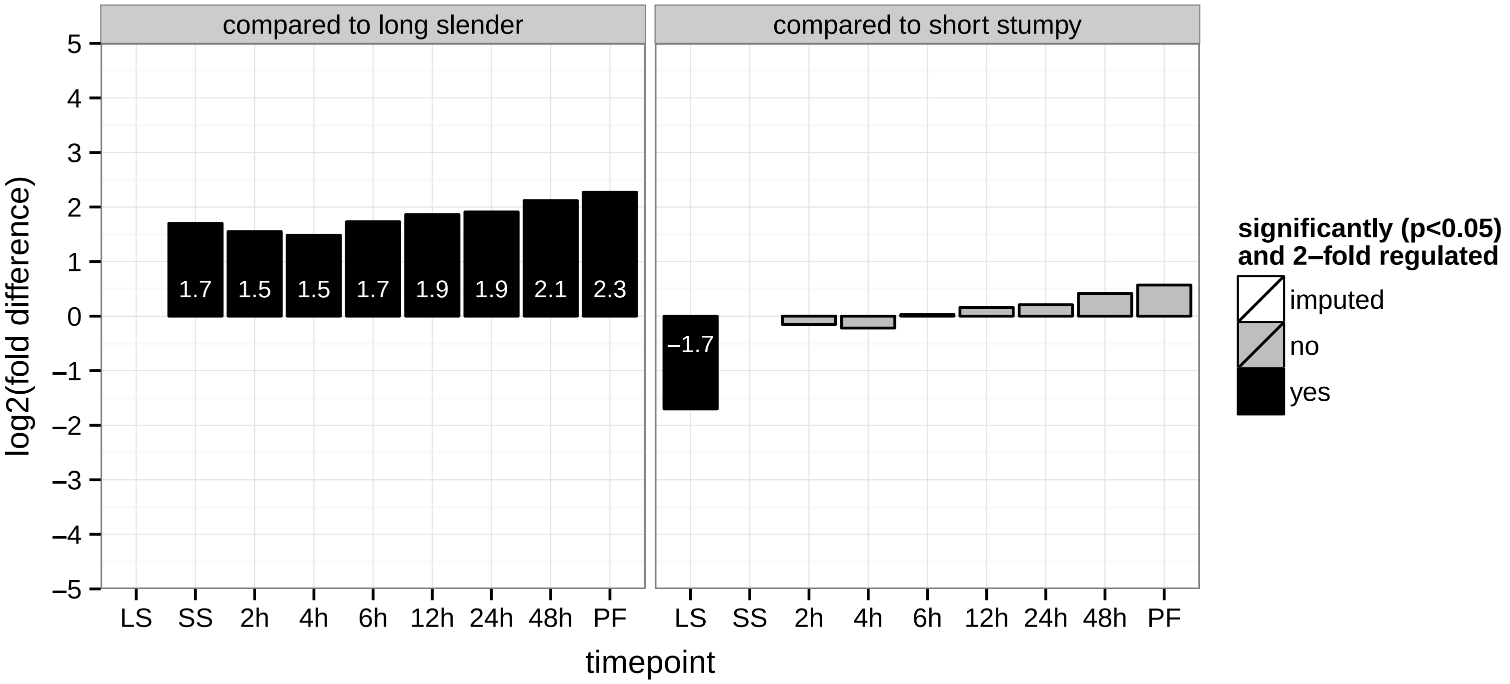
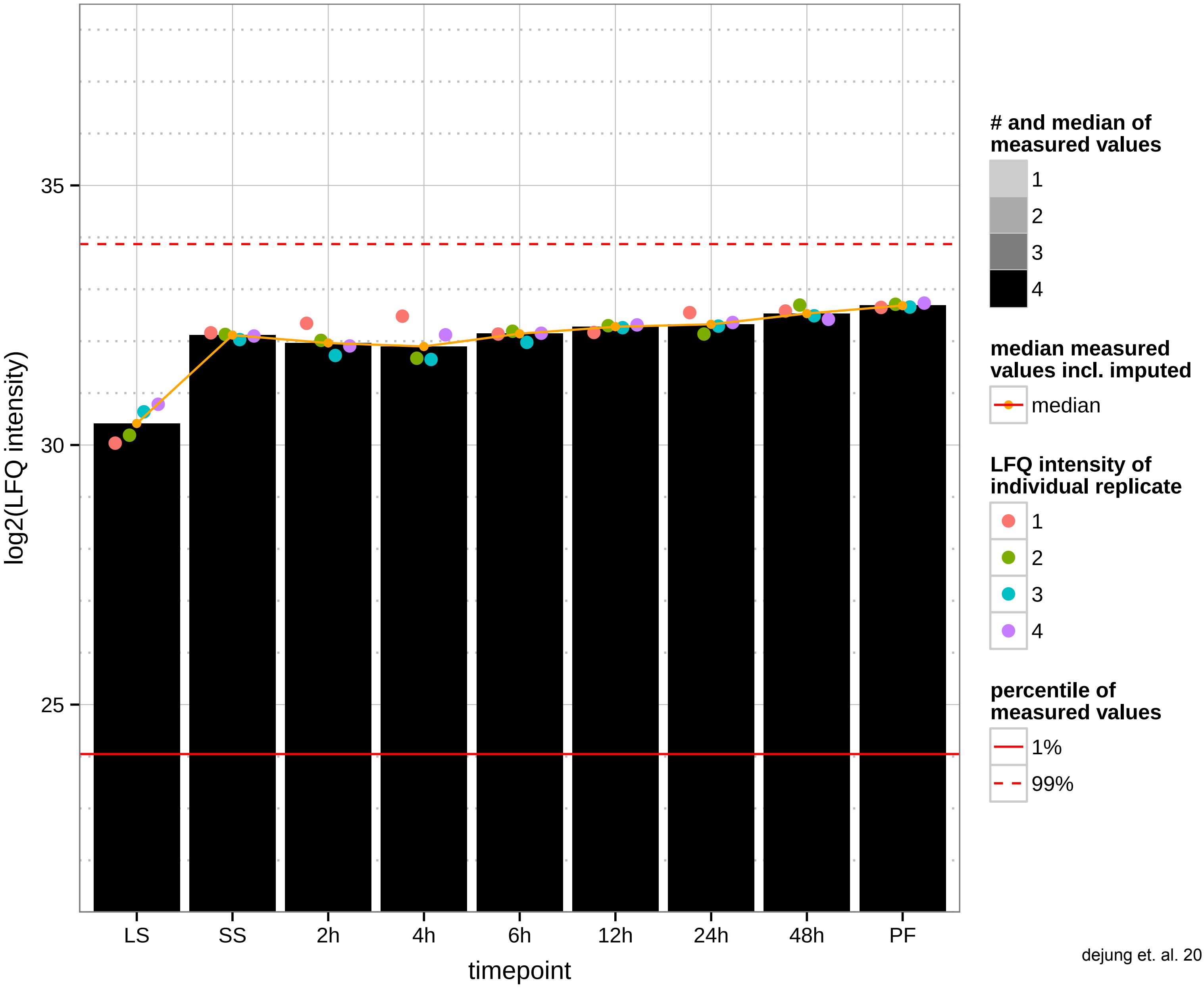
retrotransposon hot spot protein 1 (RHS1), putative, retrotransposon hot spot protein (RHS, pseudogene), interrupted
Tb927.2.100
AGOF: null
AGOC: nucleus, null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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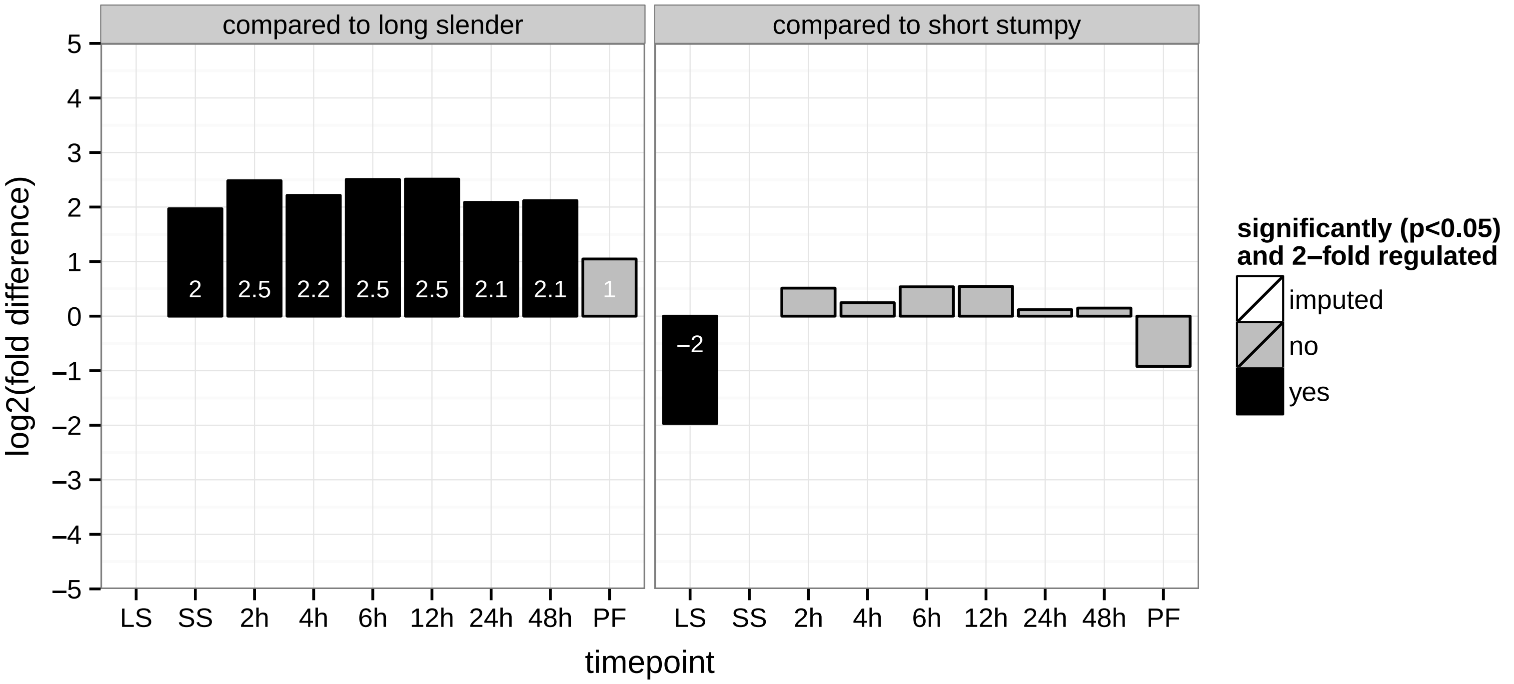
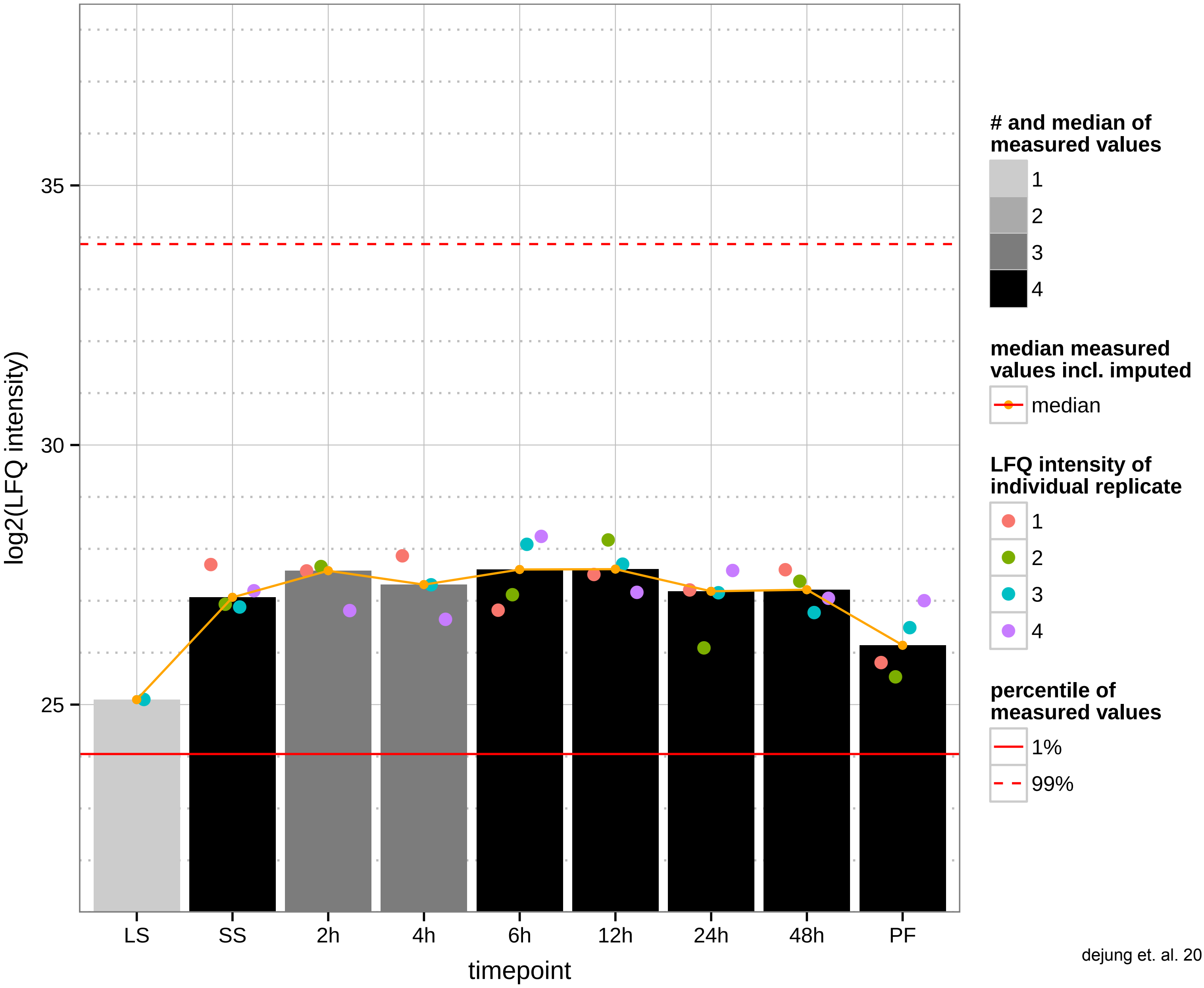
retrotransposon hot spot protein (RHS, pseudogene), putative, retrotransposon hot spot protein 4 (RHS4), point mutation
Tb927.2.1120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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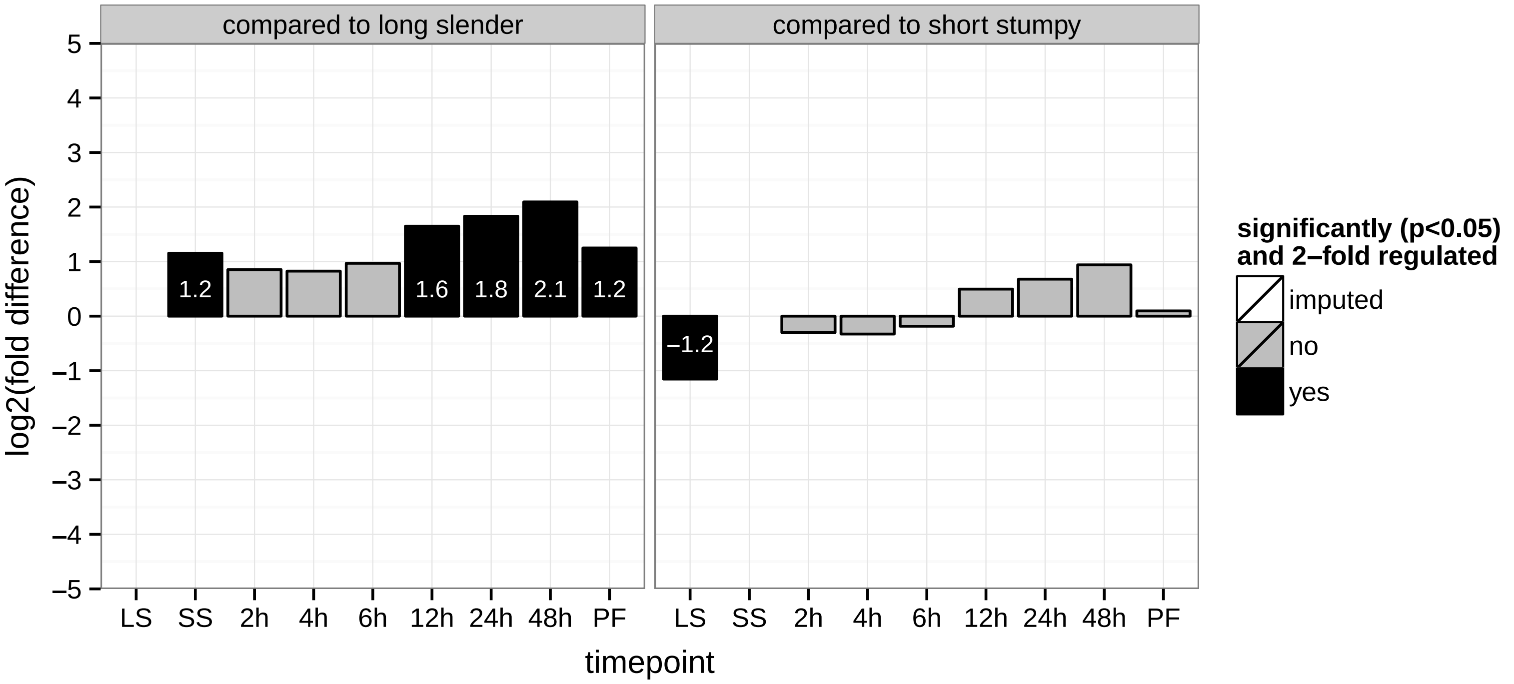
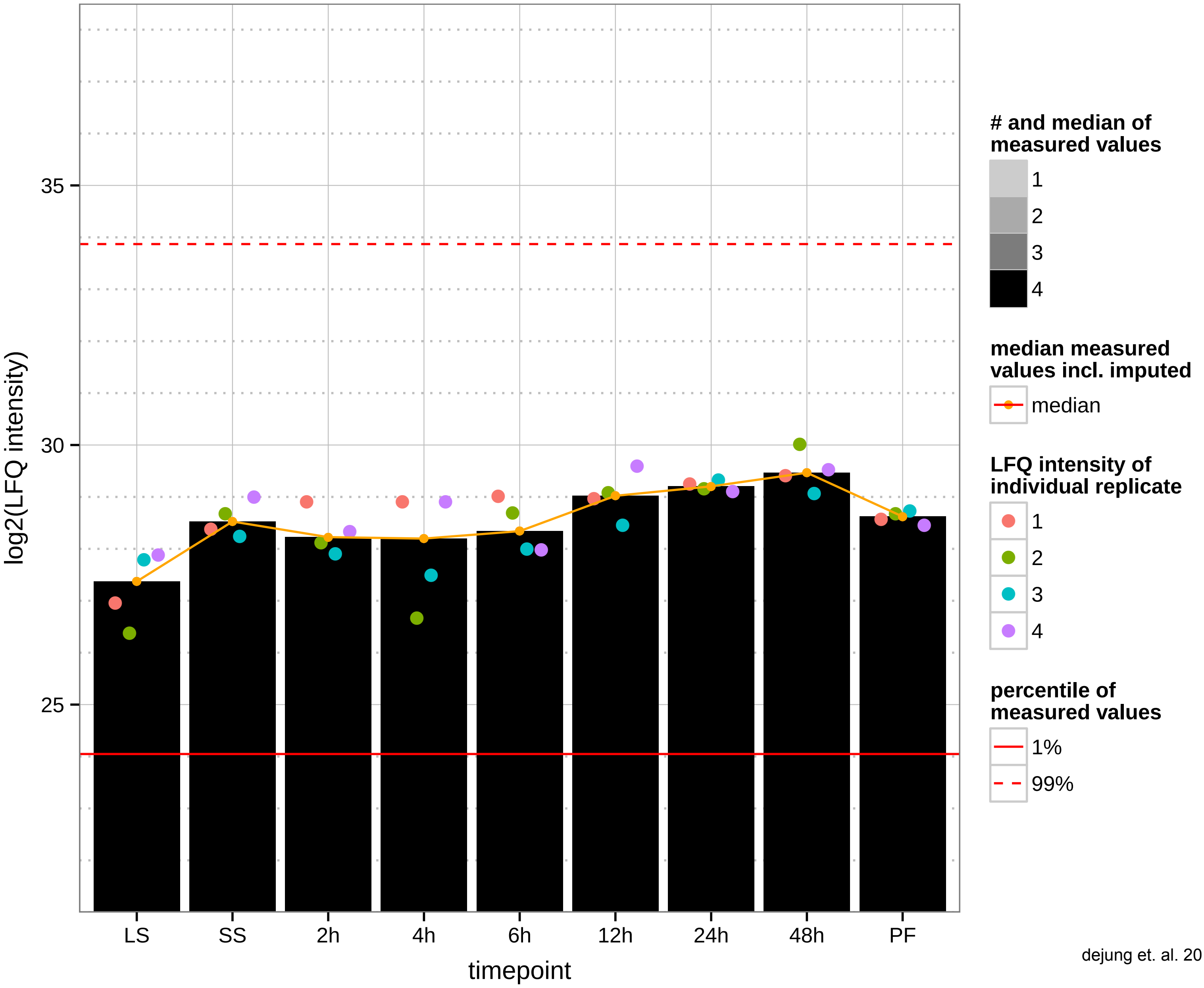
retrotransposon hot spot protein 3 (RHS3), putative
Tb927.2.1180
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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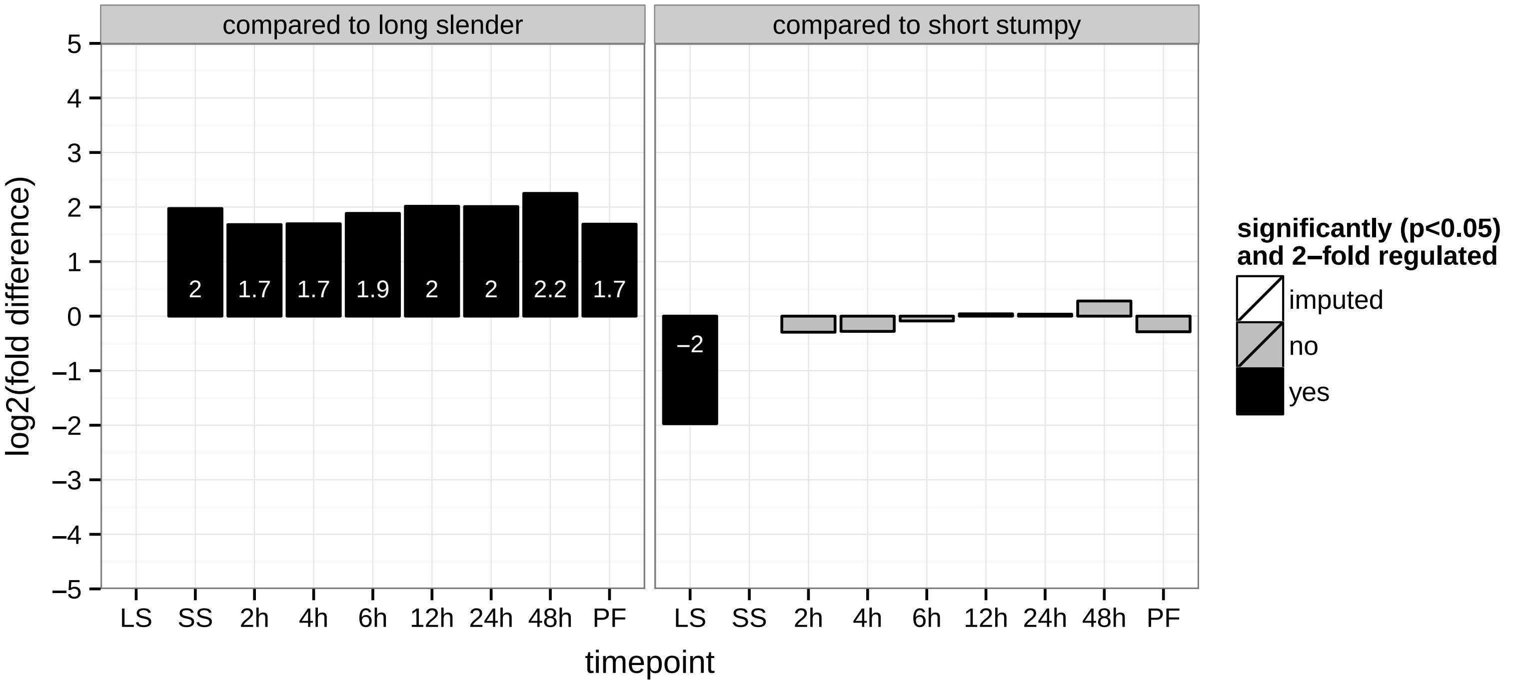
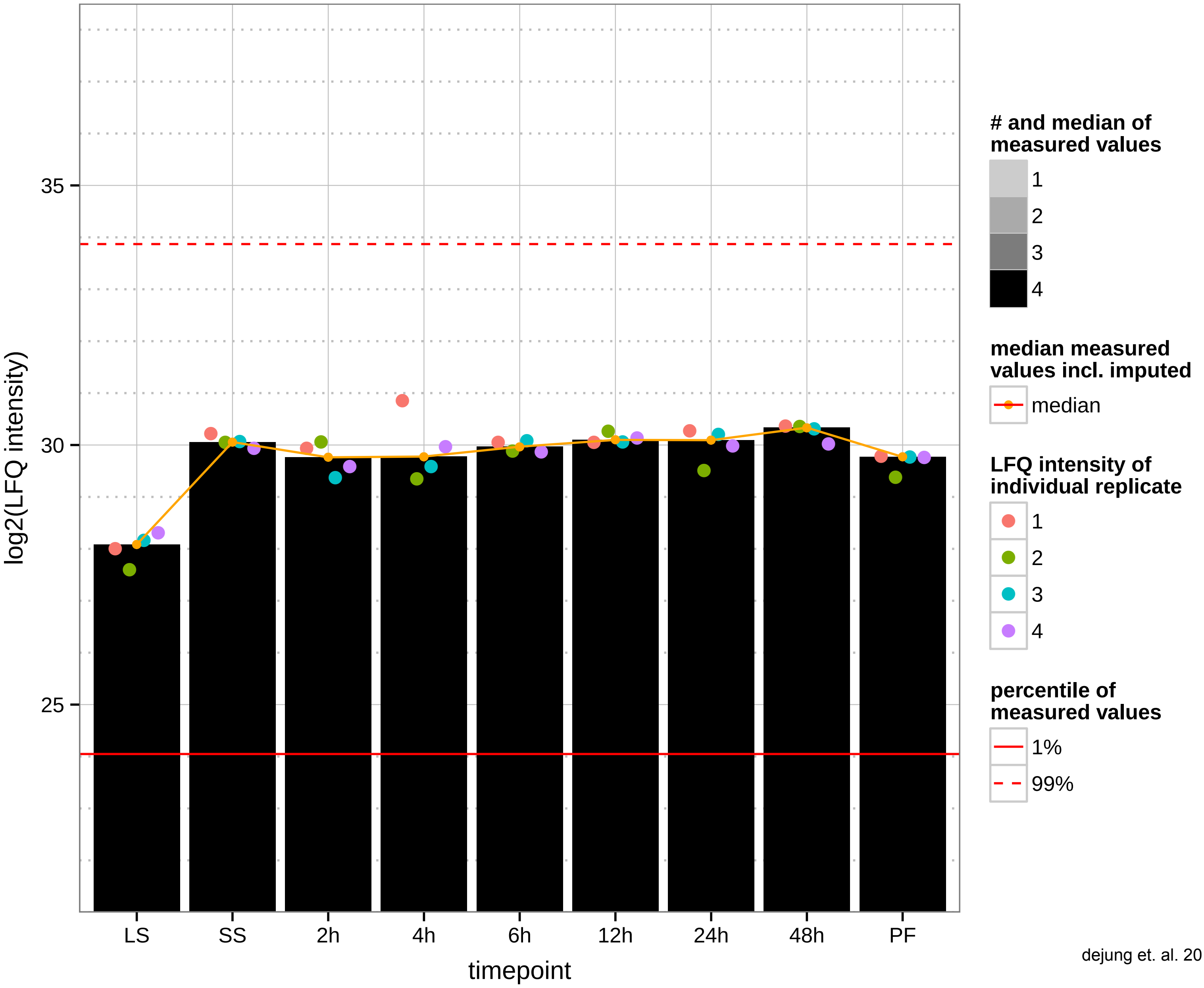
retrotransposon hot spot protein 4 (RHS4), putative
Tb927.2.1210
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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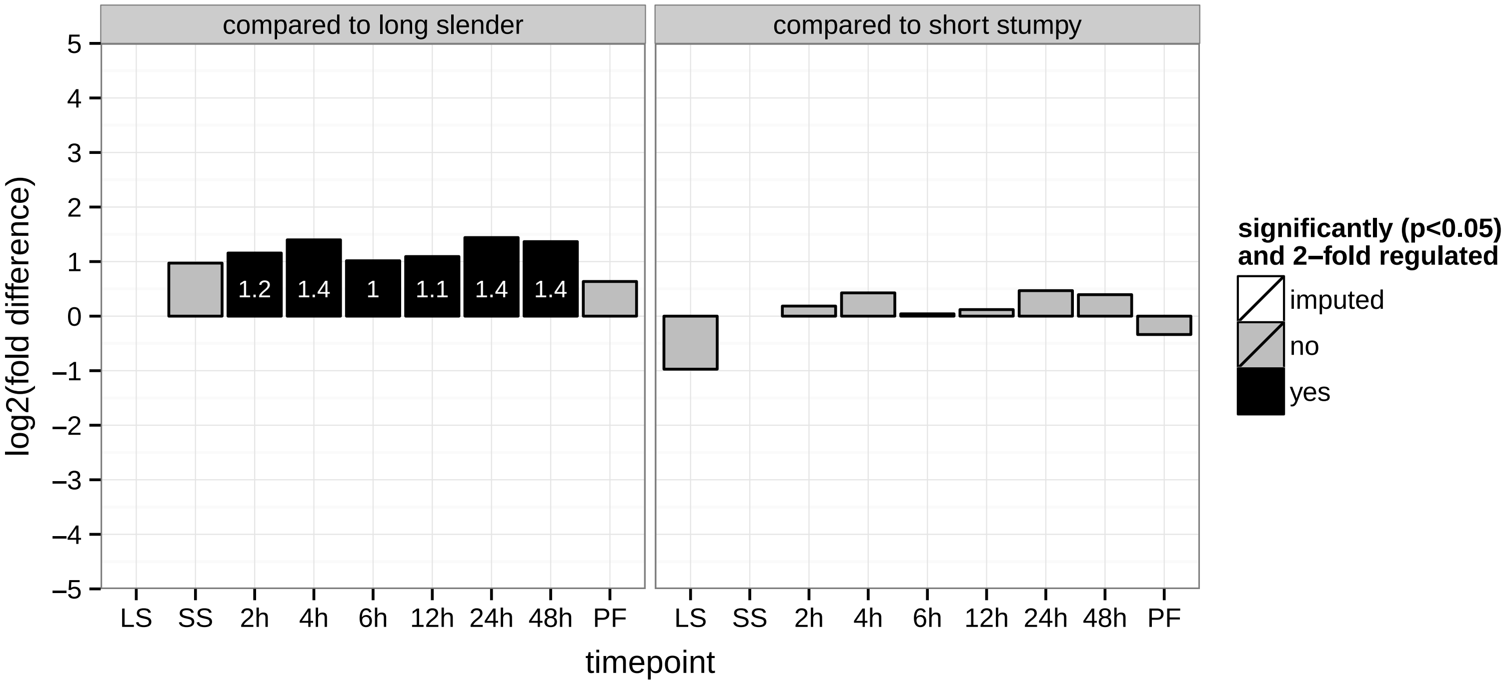
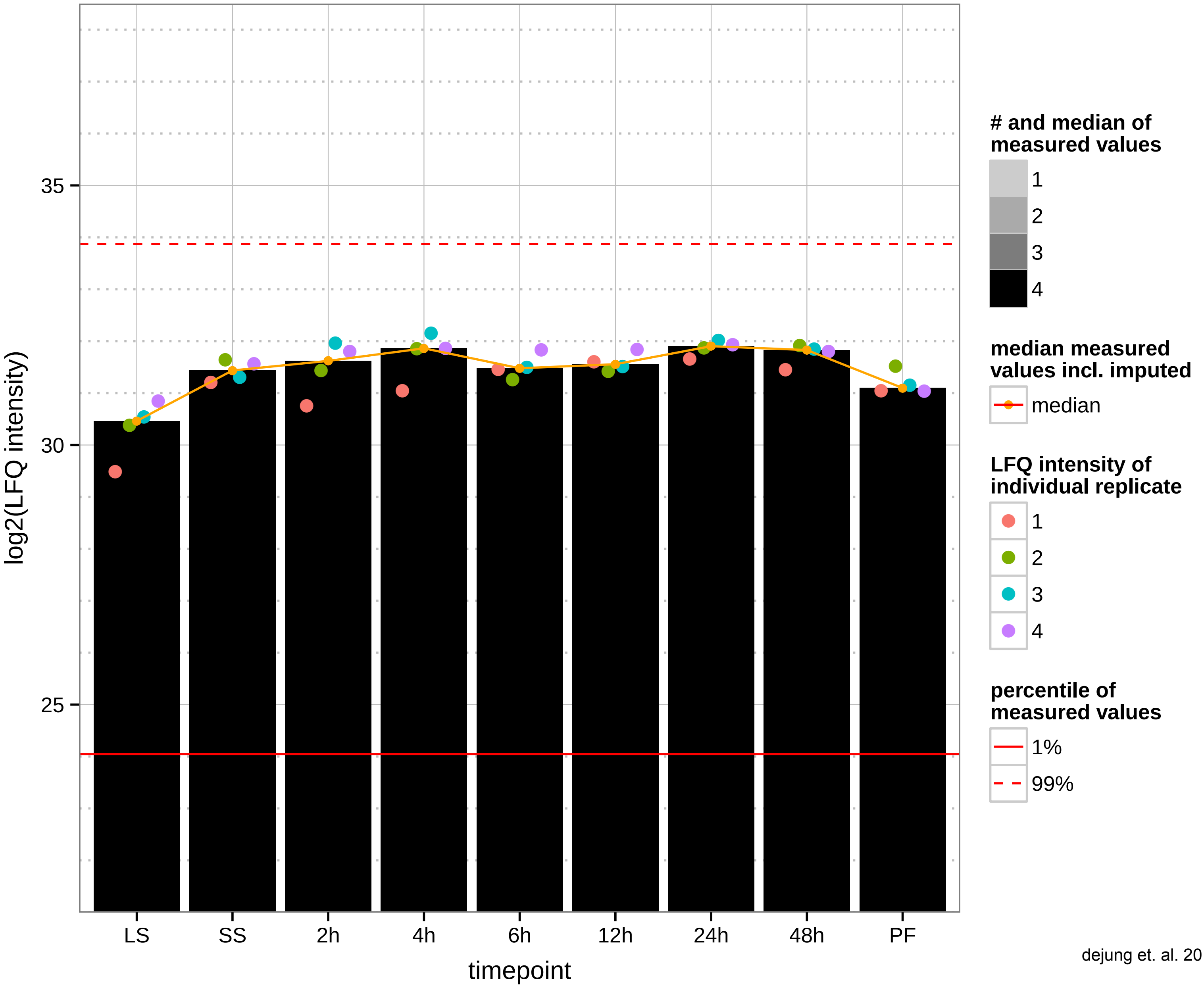
cyclophilin–type peptidyl–prolyl cis–trans isomerase, putative
Tb927.2.1680;Tb927.2.1560
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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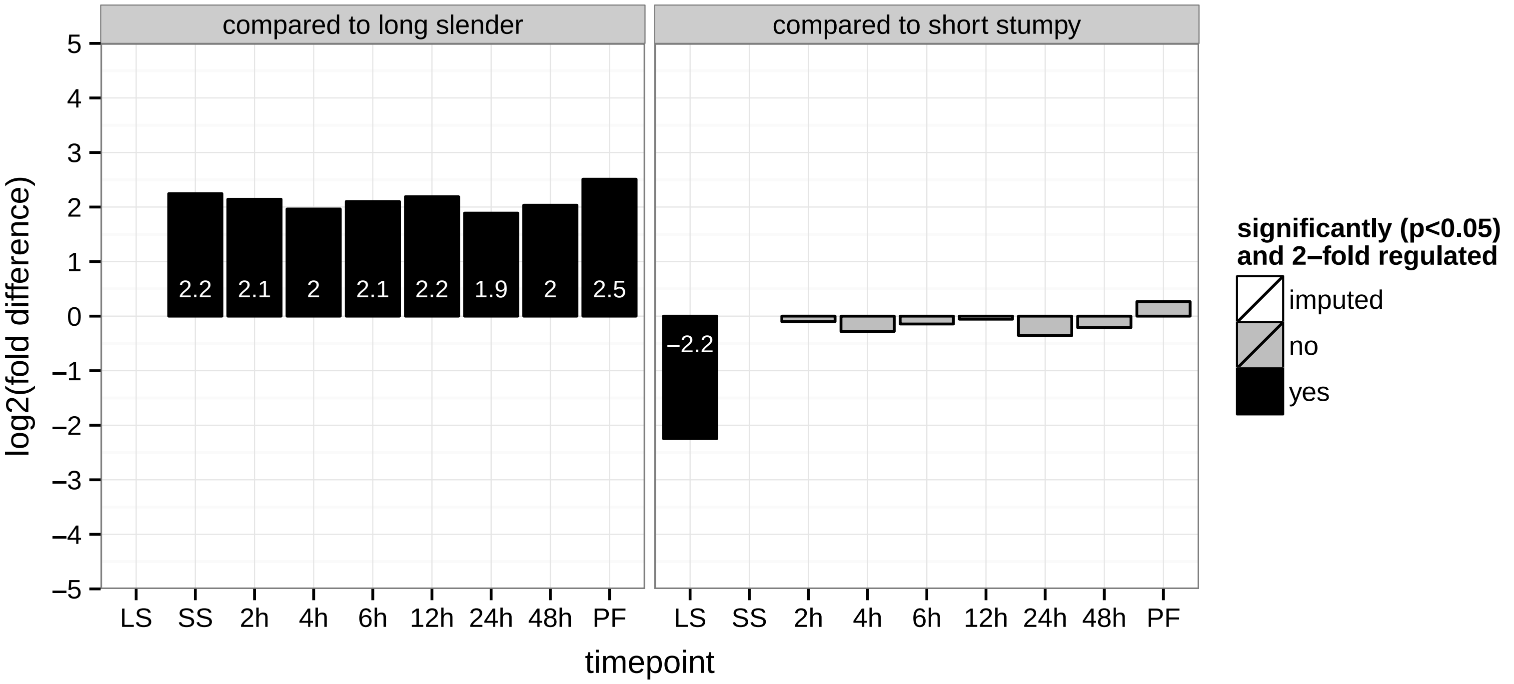
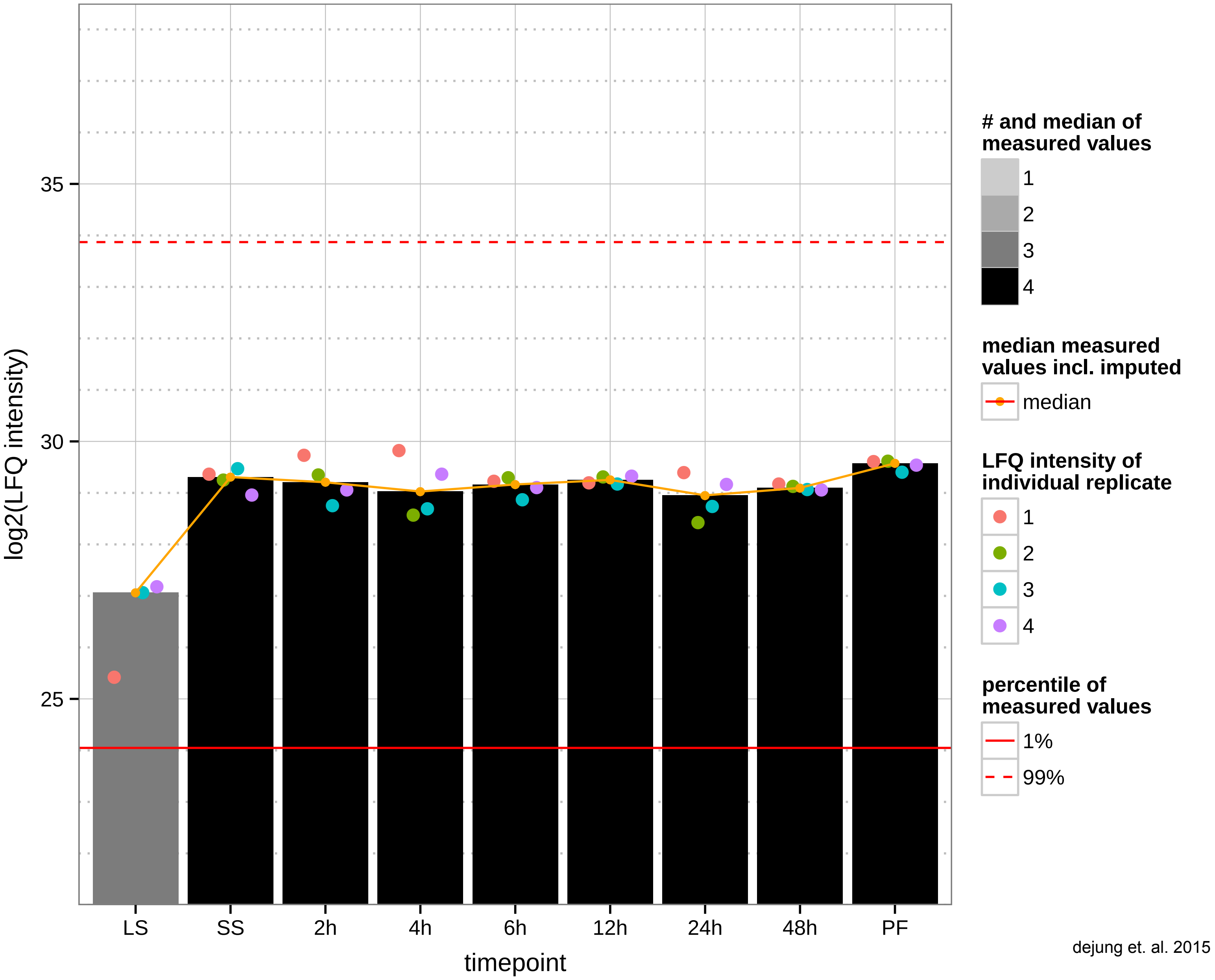
transcription silencer (ISWI)
Tb927.2.1810
AGOF: ATP binding, DNA binding, helicase activity, hydrolase activity, acting on acid anhydrides, in phosphorus–containing ar
AGOC: chromatin remodeling complex, nucleus
AGOP: ATP–dependent chromatin remodeling, modulation of development of symbiont involved in interaction with host, quoru
PGOF: ATP binding, DNA binding, helicase activity, hydrolase activity, acting on acid anhydrides, in phosphorus–containing ar
PGOC: chromatin remodeling complex, nucleus
PGOP: ATP–dependent chromatin remodeling, chromatin remodeling





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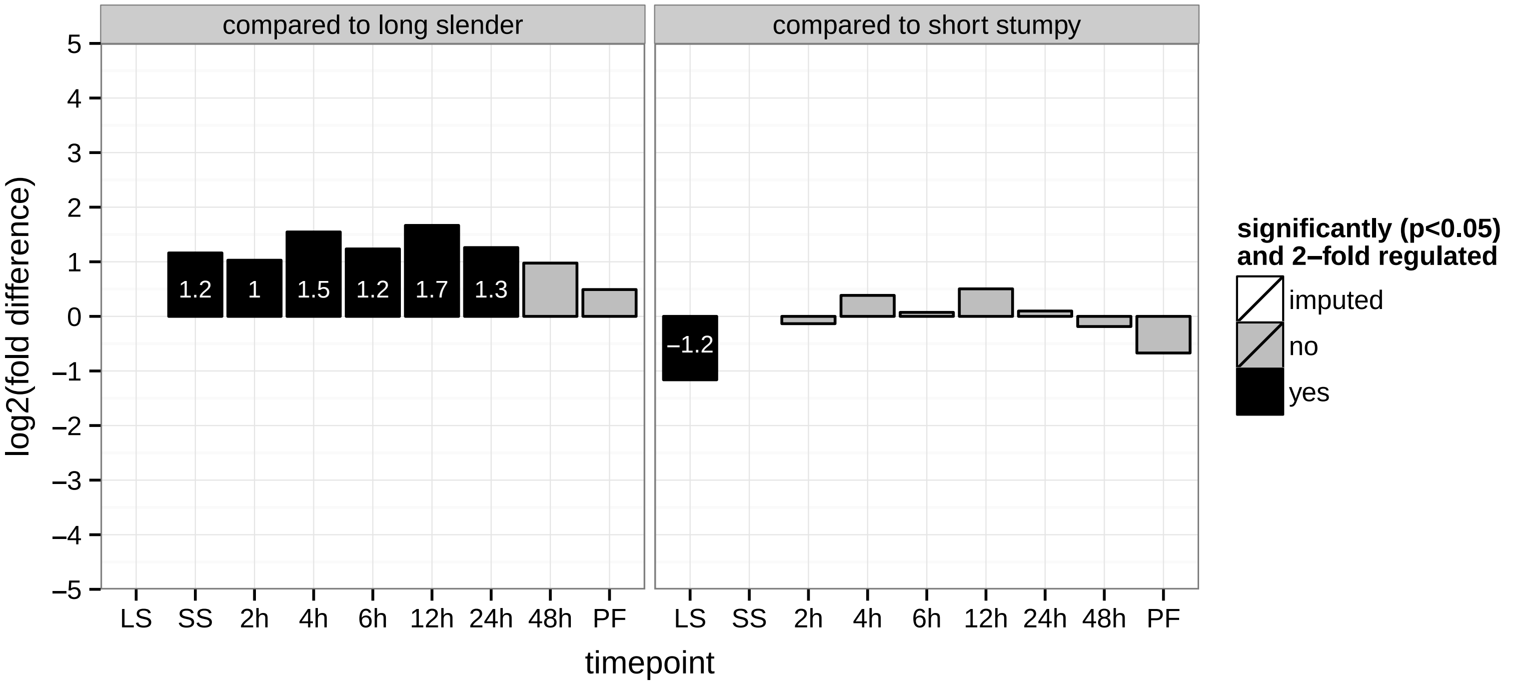
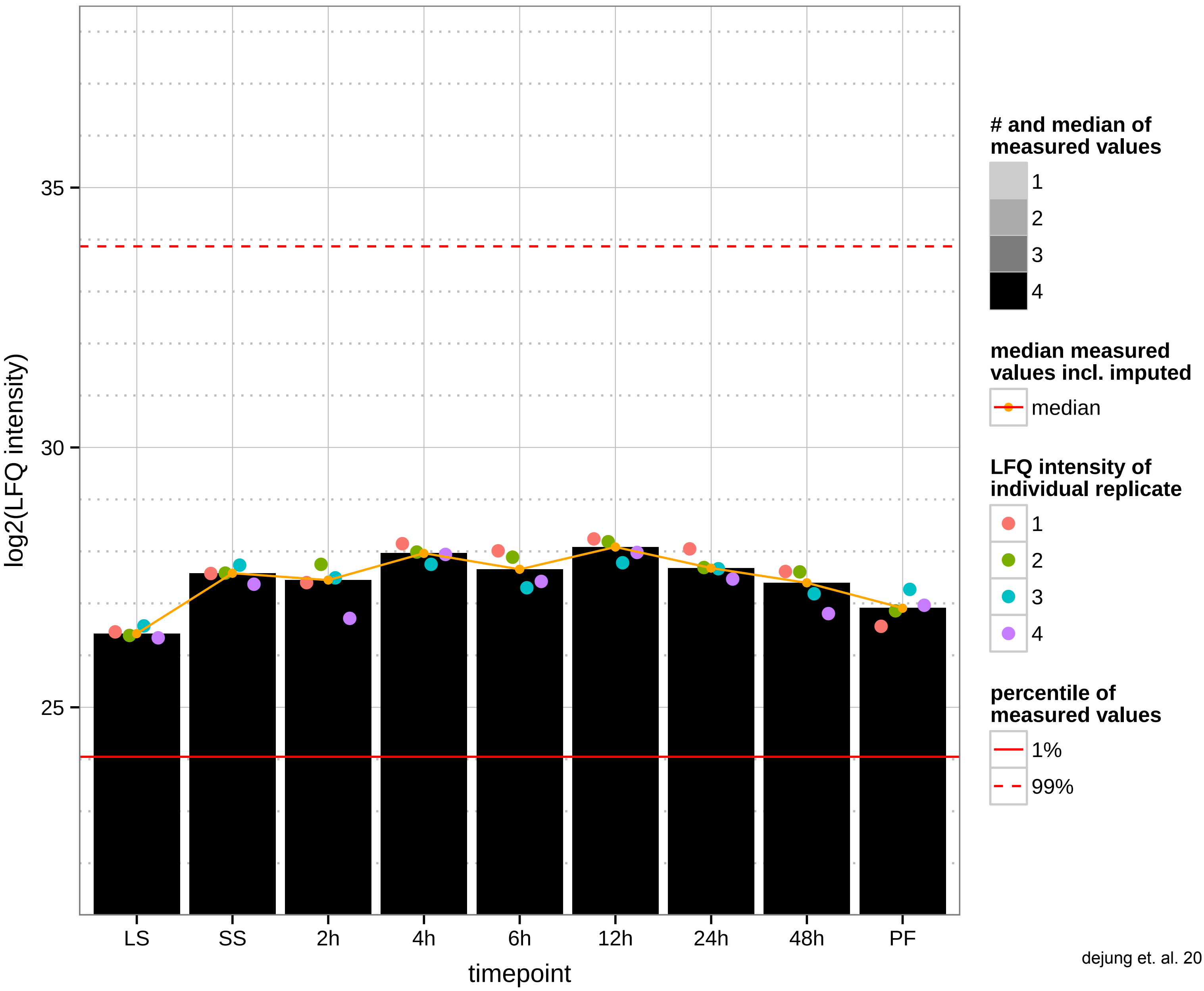
E2–like ubiquitin–conjugation enzyme (ATG3)
Tb927.2.1890
AGOF: null
AGOC: null
AGOP: autophagy, protein transport
PGOF: null
PGOC: null
PGOP: null





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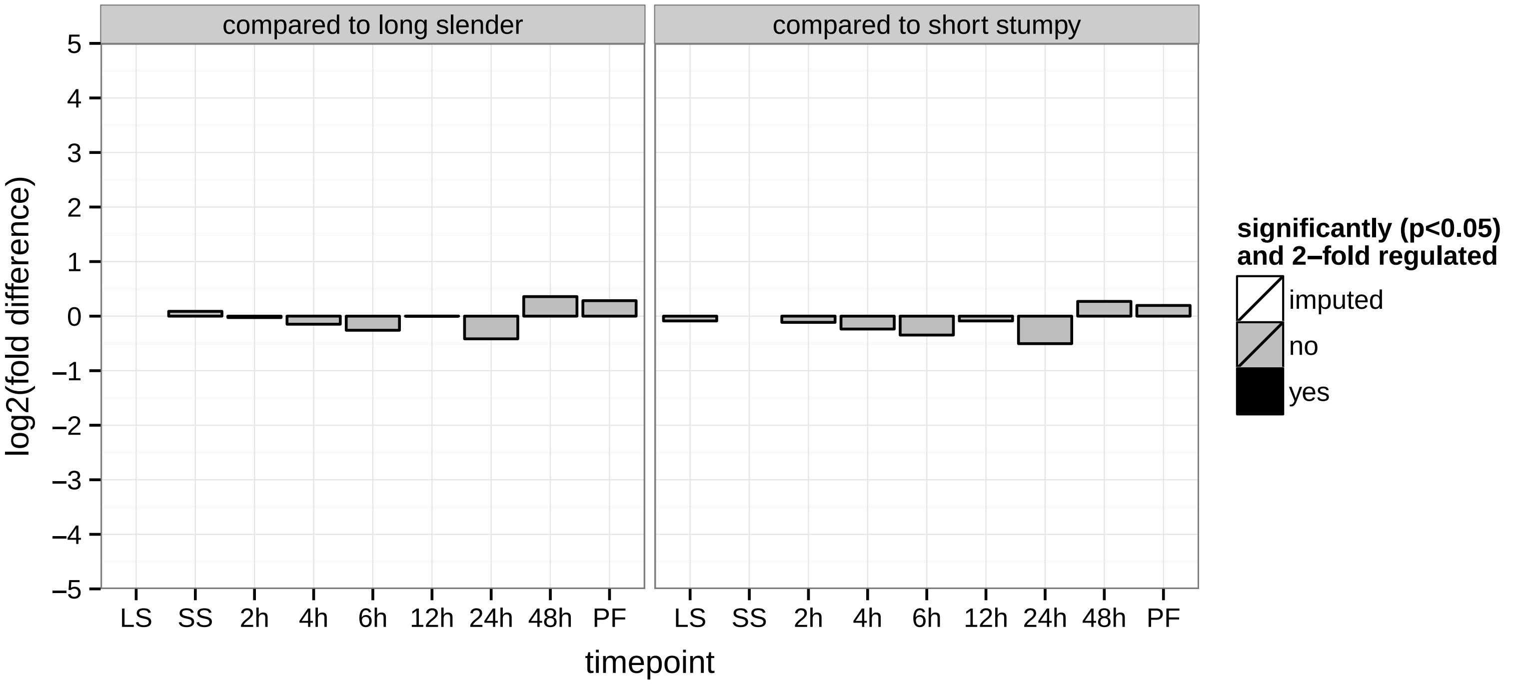
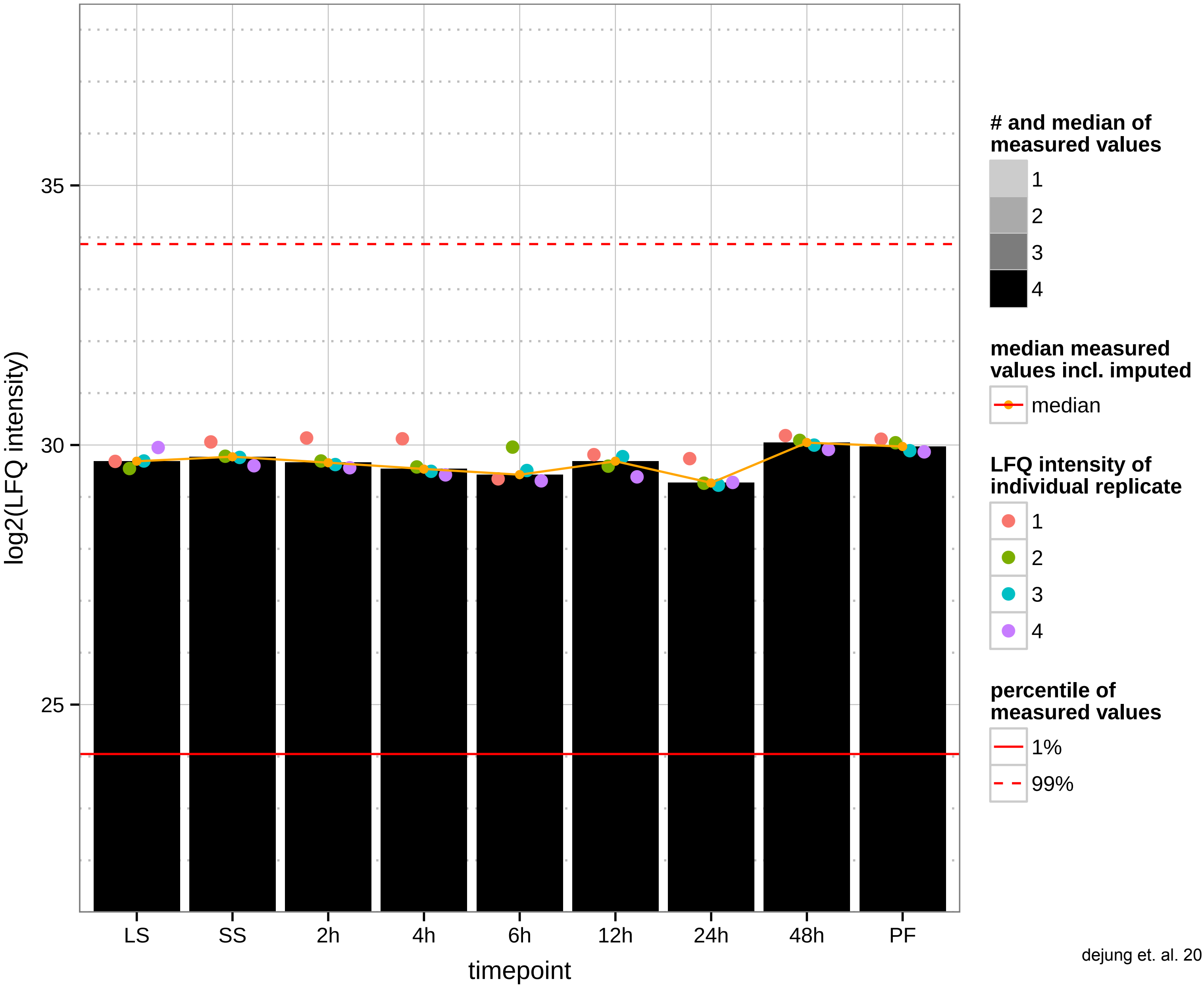
paraflagellar rod component, putative (PFC11)
Tb927.2.2160
AGOF: null
AGOC: Golgi apparatus, endoplasmic reticulum
AGOP: intracellular protein transport
PGOF: null
PGOC: null
PGOP: null





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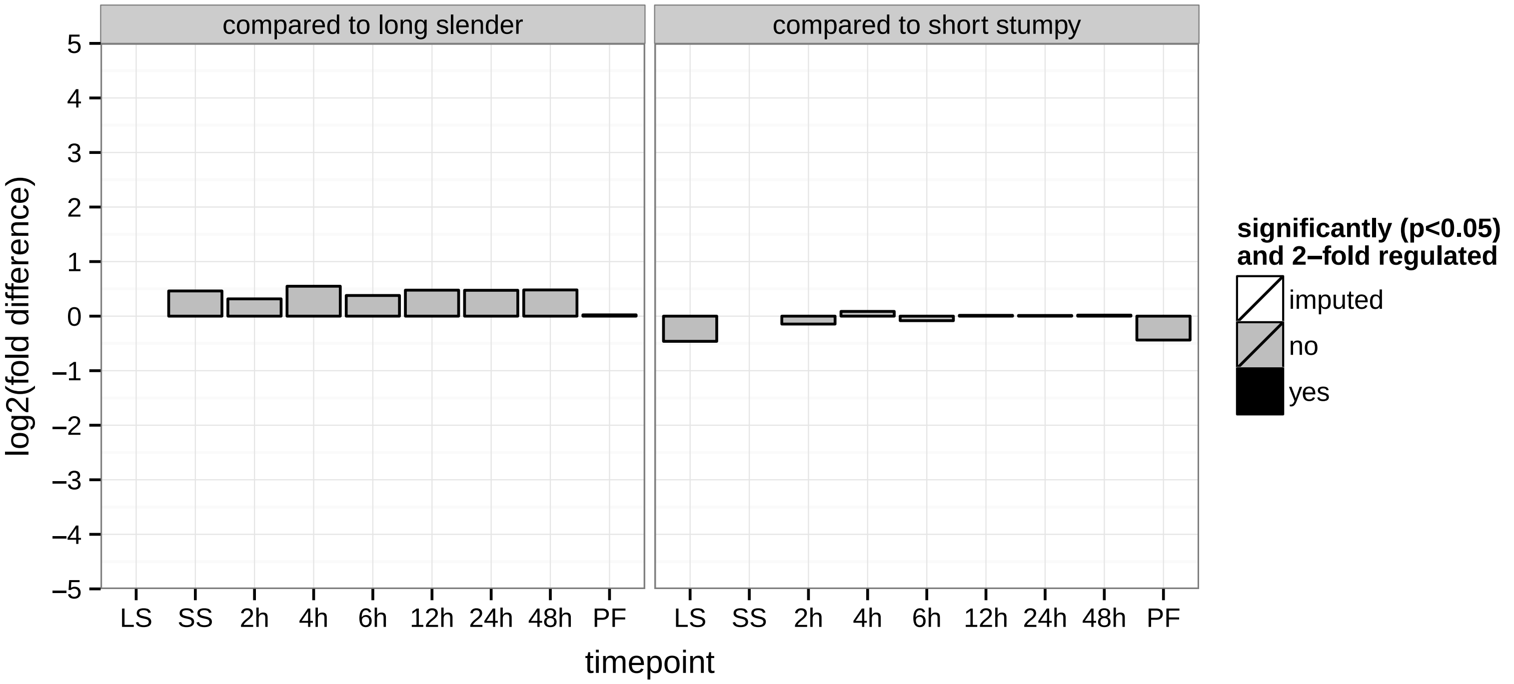
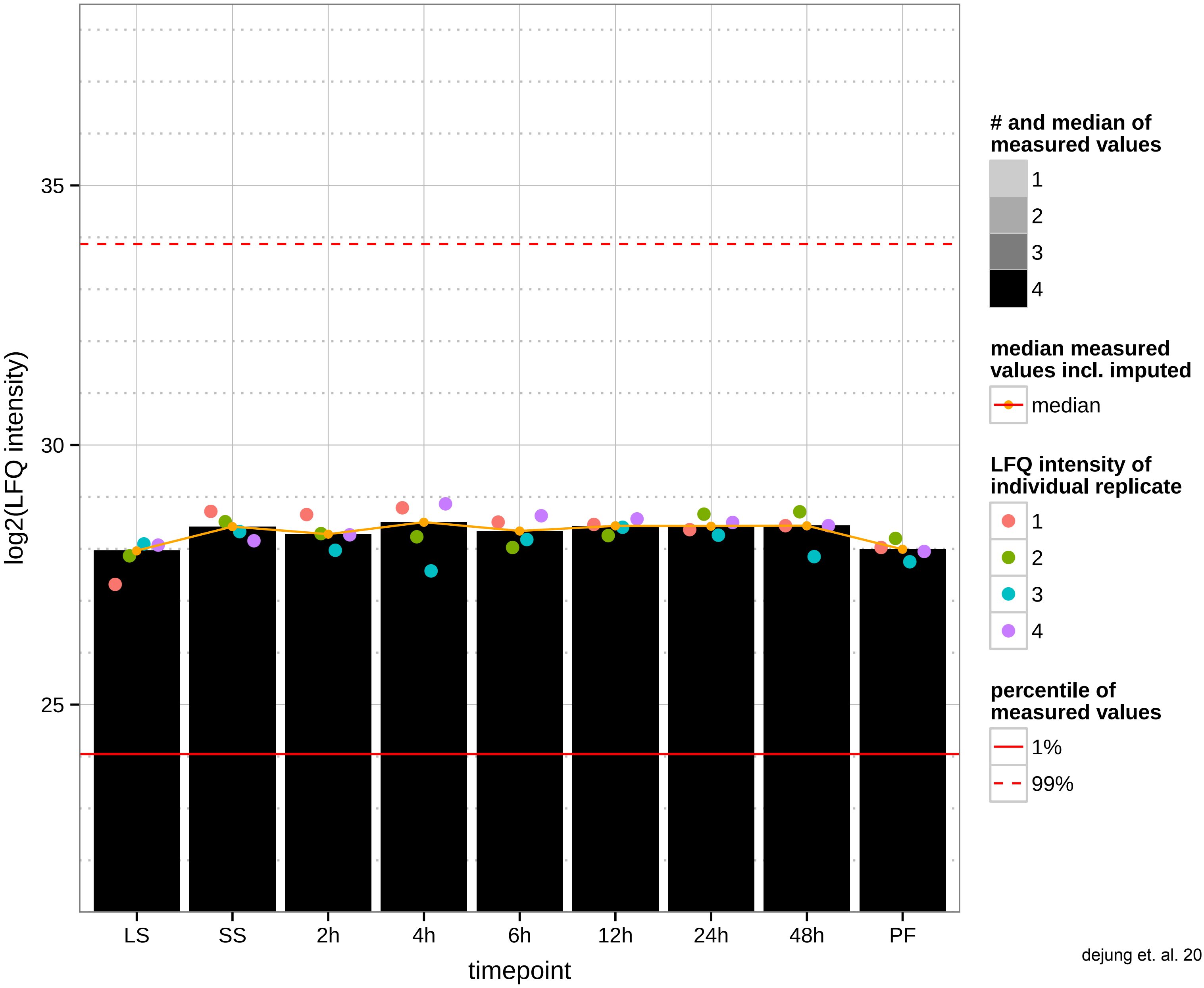
hypothetical protein, conserved
Tb927.2.2230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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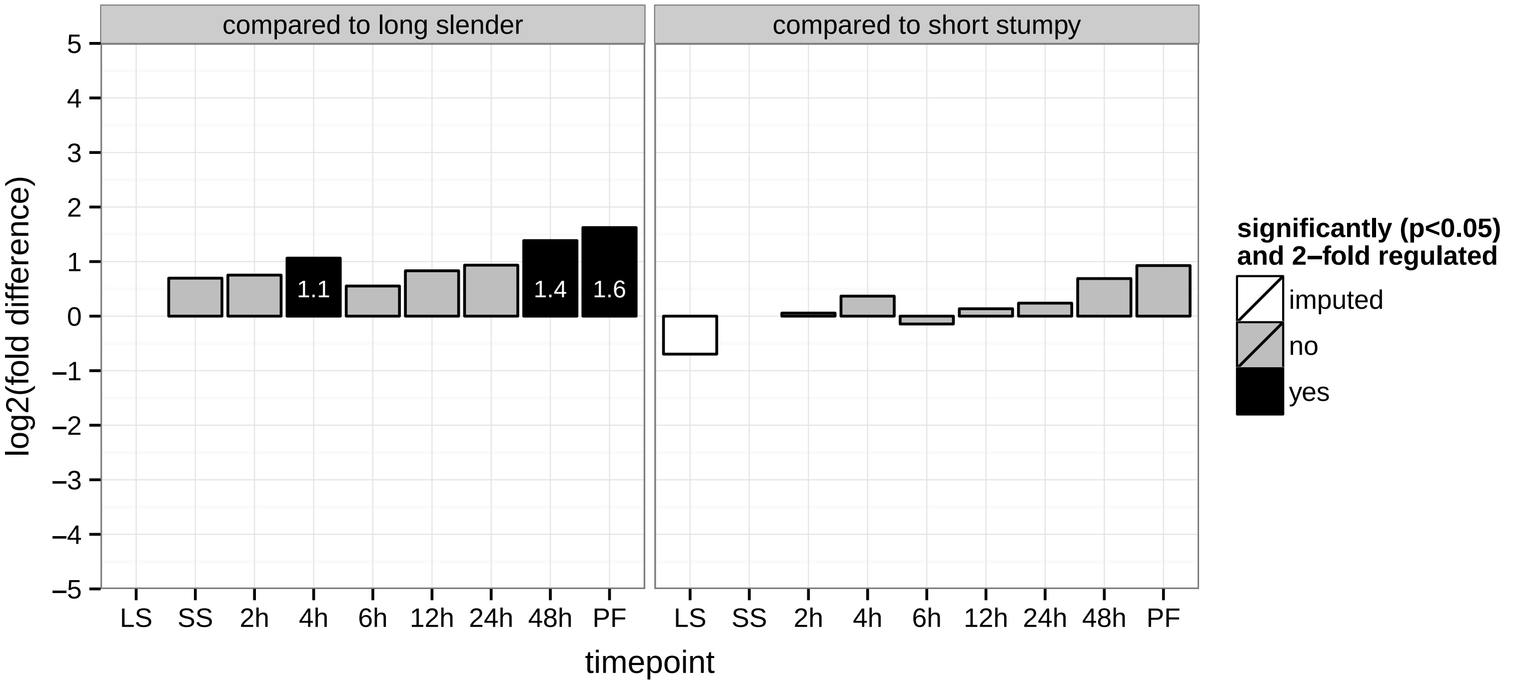
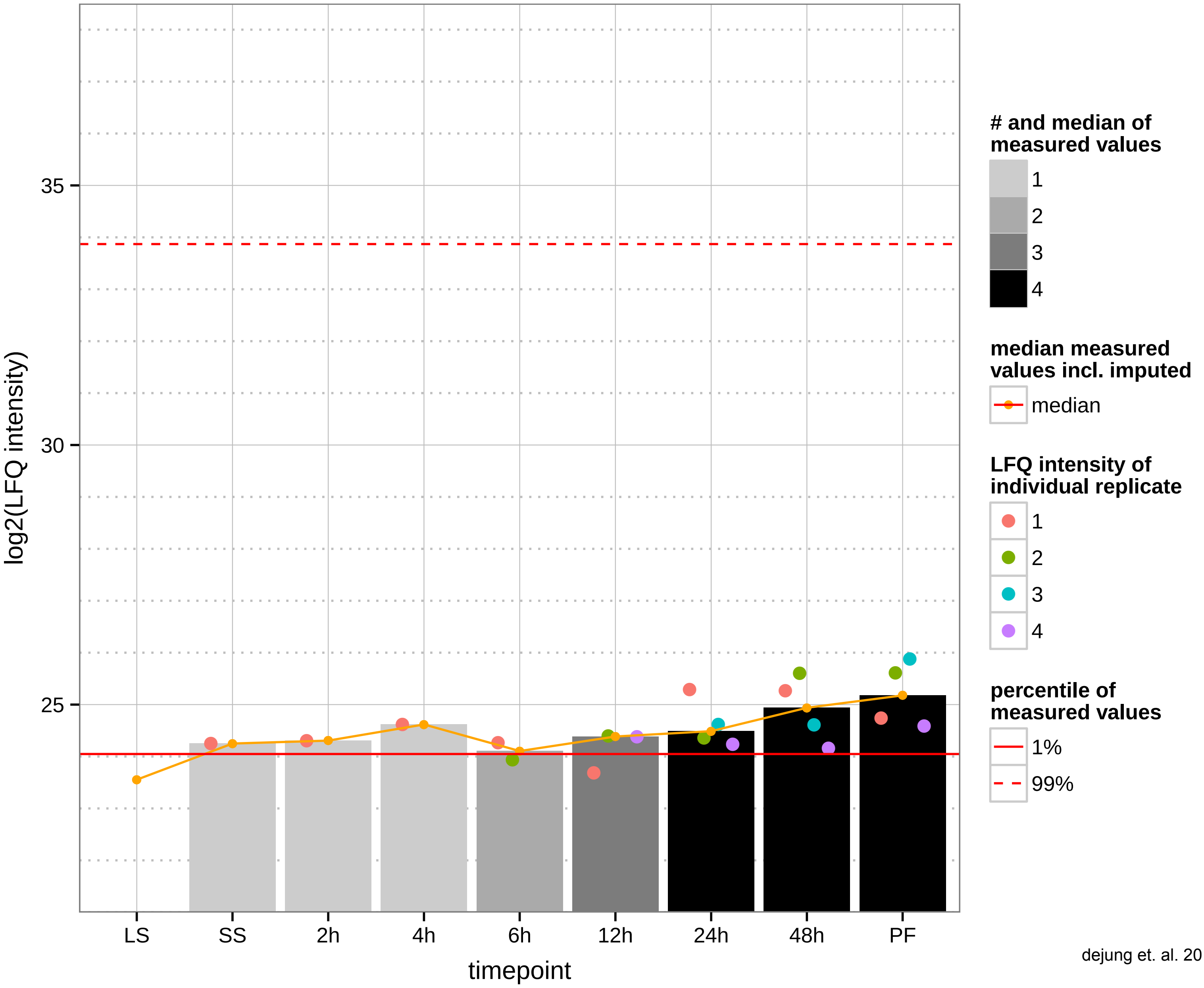
tRNA exportin, putative, exportin−T
Tb927.2.2240
AGOF: tRNA binding
AGOC: nucleus
AGOP: transport
PGOF: binding
PGOC: null
PGOP: null





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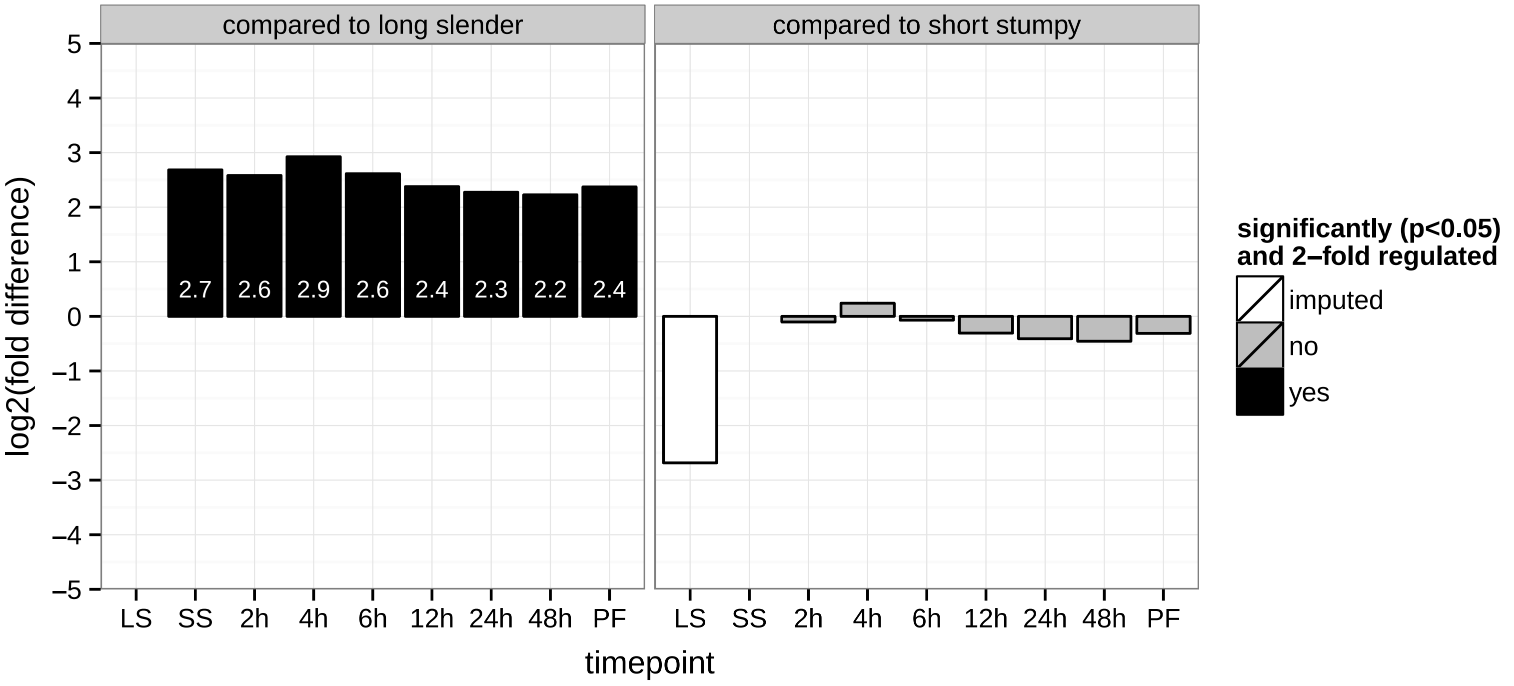
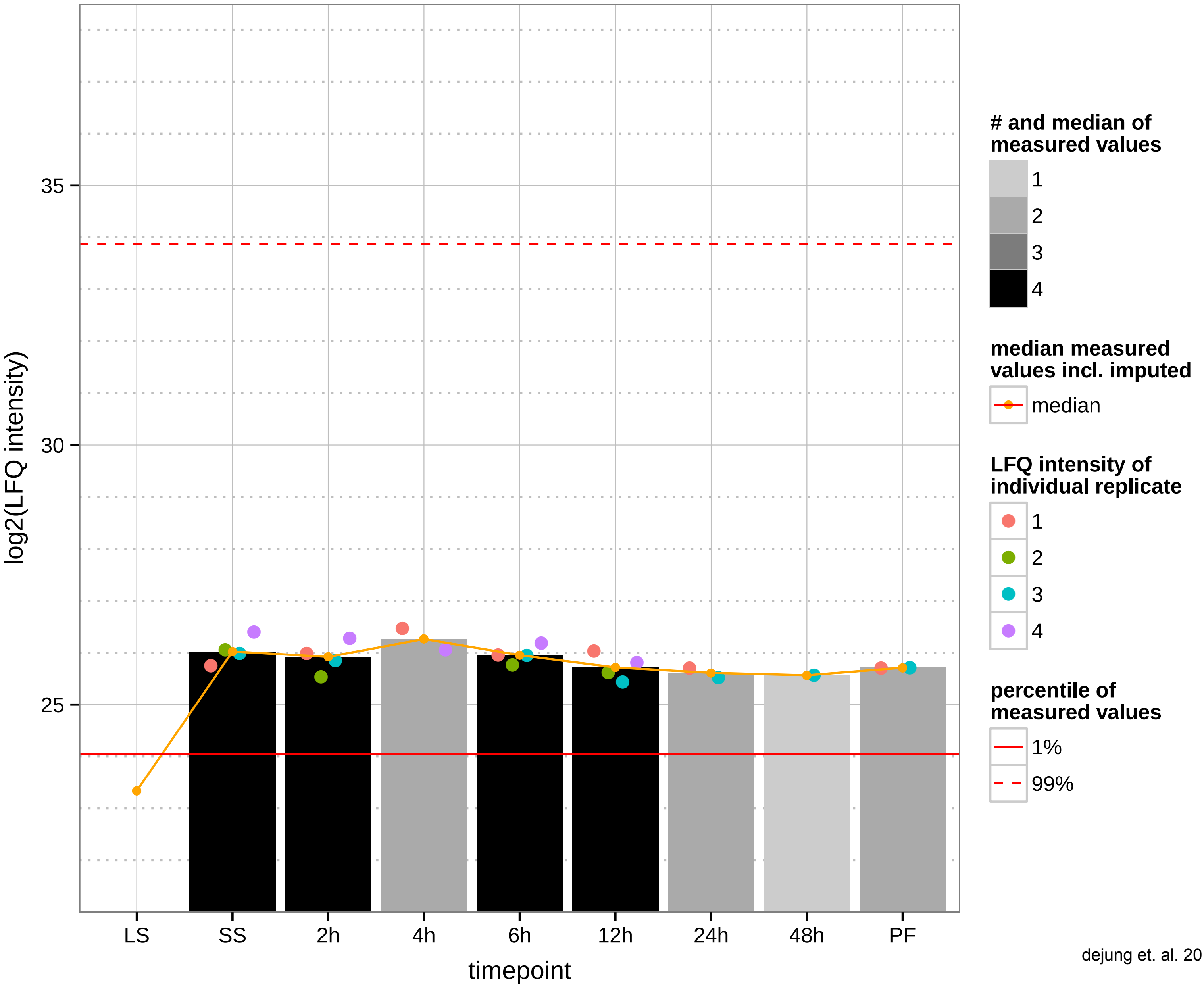
hypothetical protein, conserved
Tb927.2.2360
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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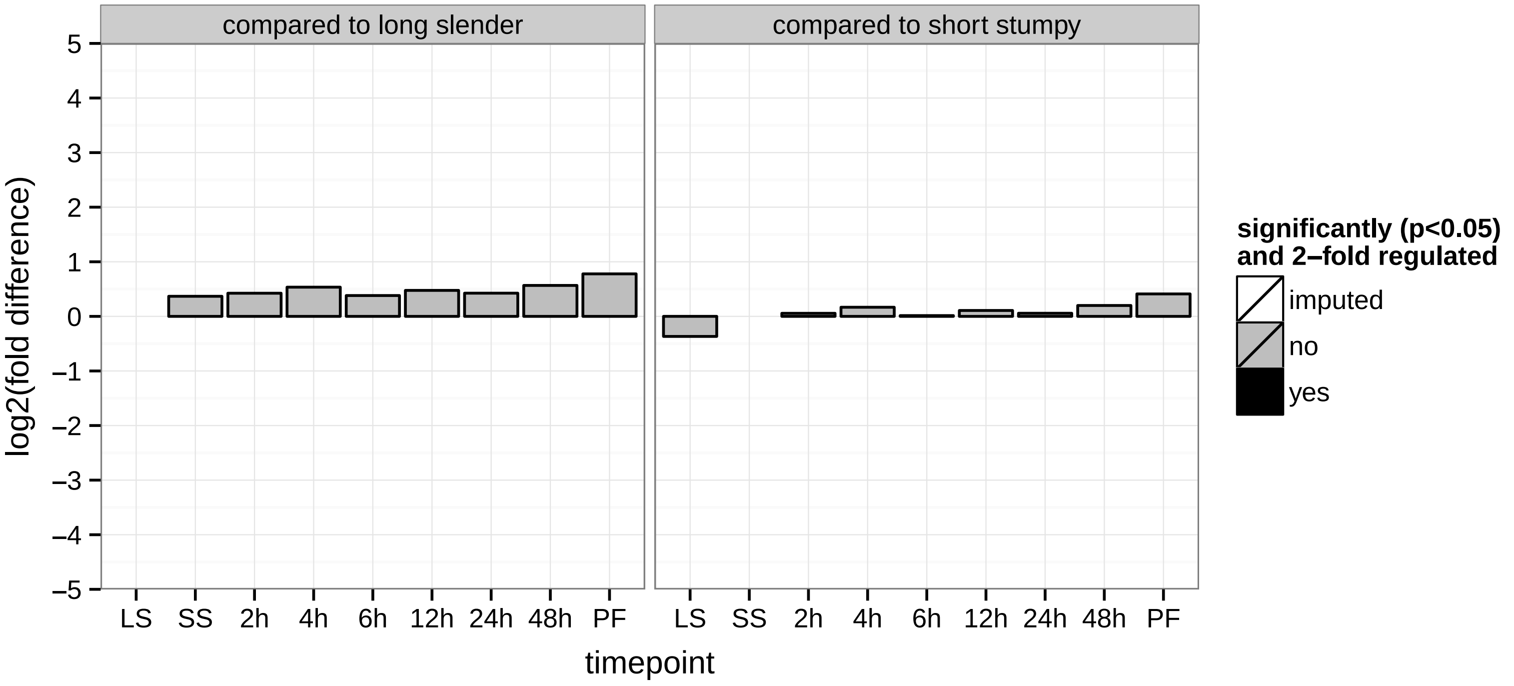
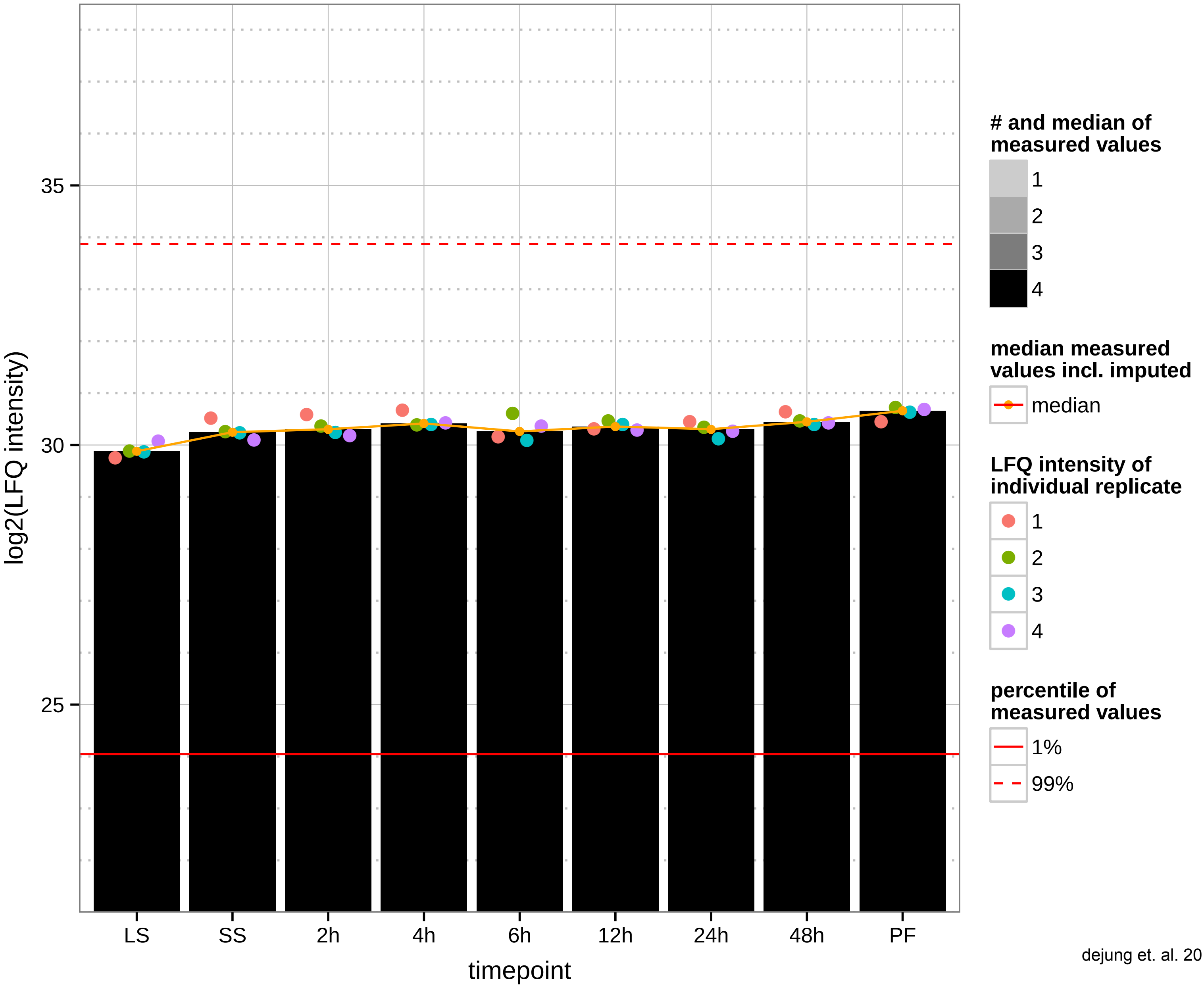
proteasome regulatory non–ATPase subunit 6 (RPN6)
Tb927.2.2440
AGOF: endopeptidase activity
AGOC: proteasome regulatory particle
AGOP: ubiquitin–dependent protein catabolic process
PGOF: protein binding
PGOC: null
PGOP: null





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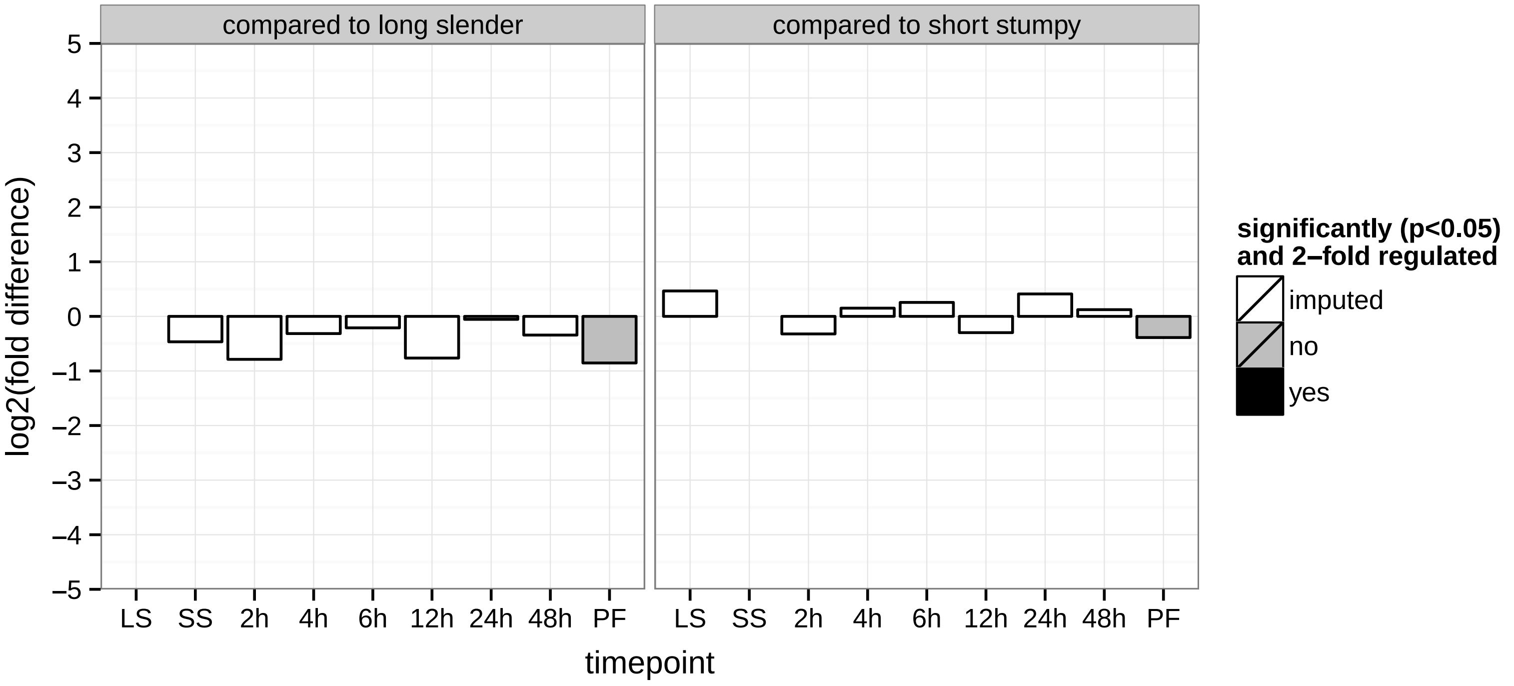
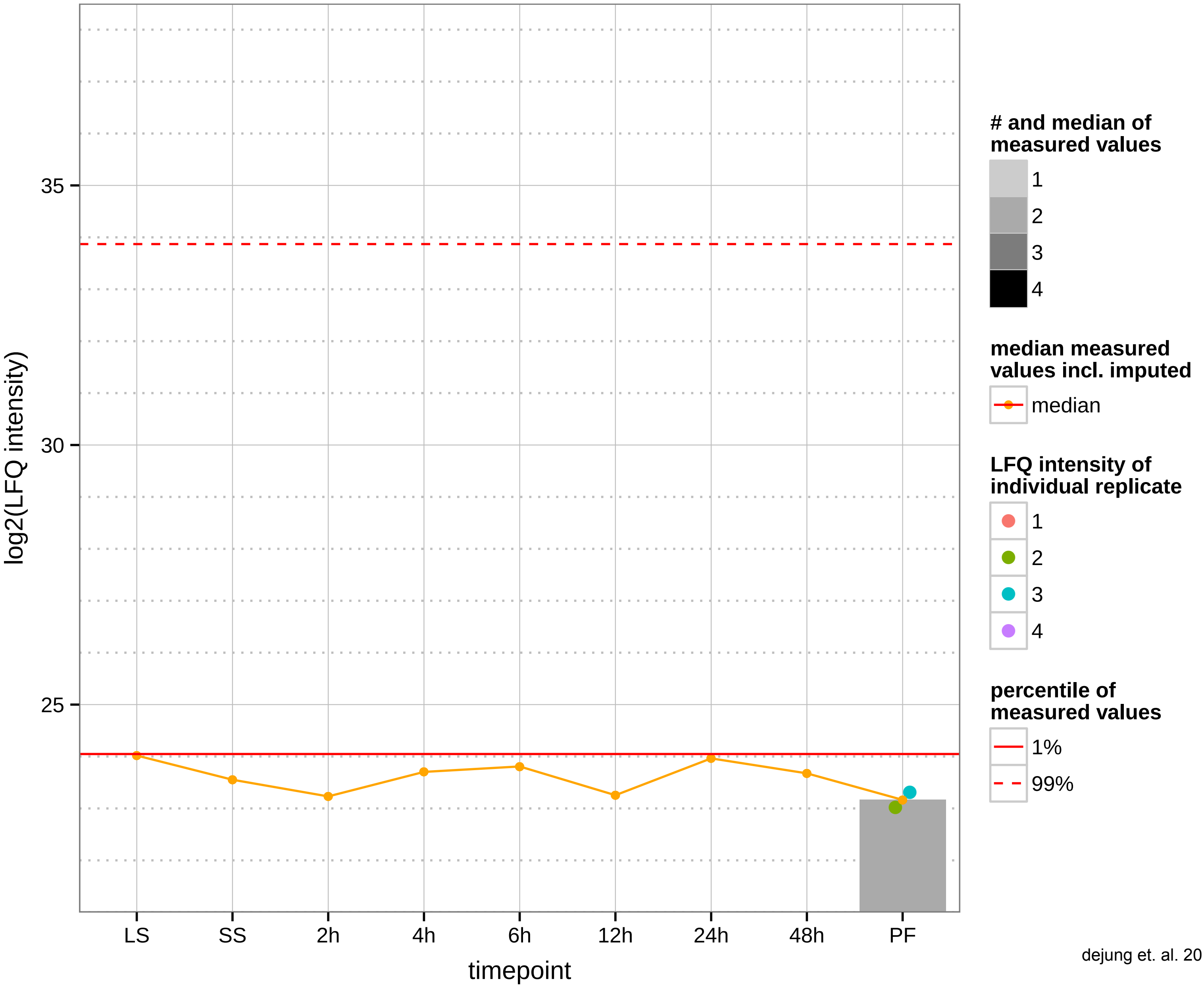
hypothetical protein, conserved
Tb927.2.2880
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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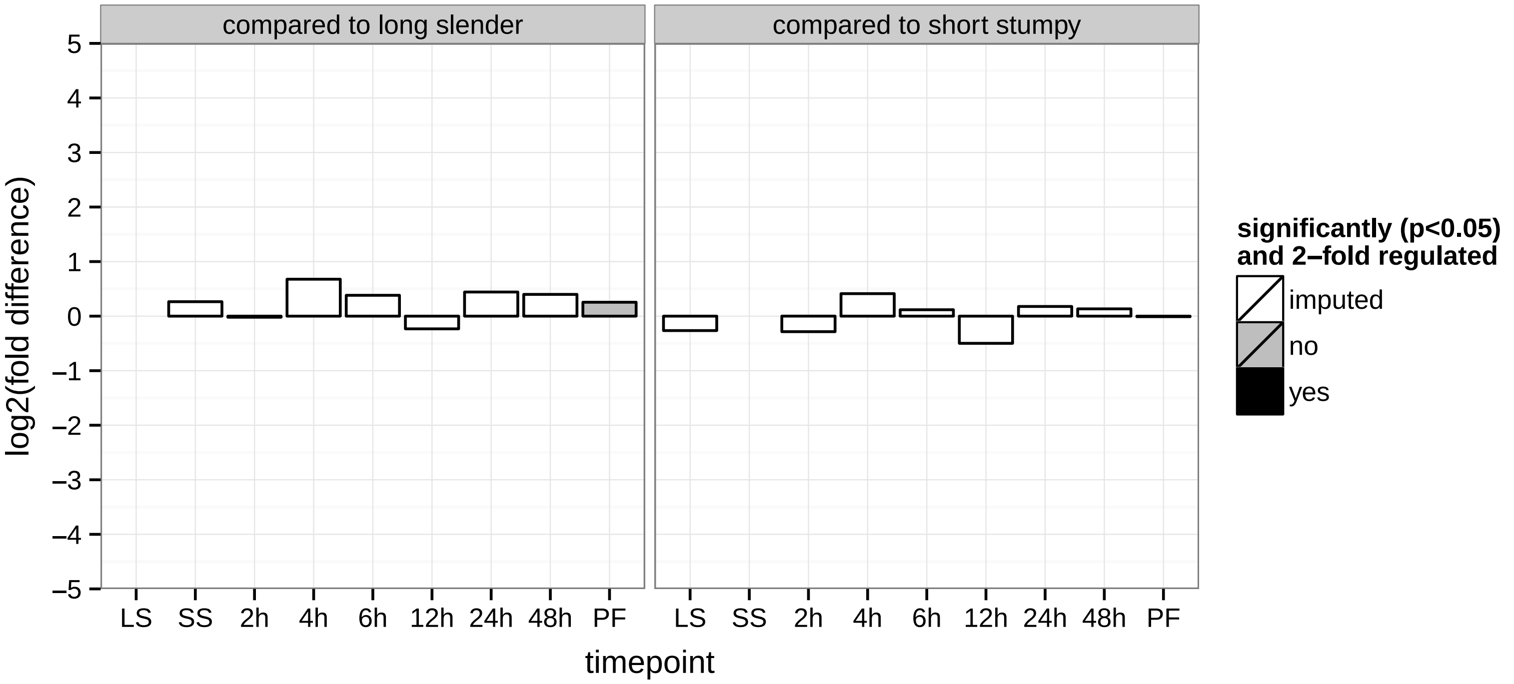
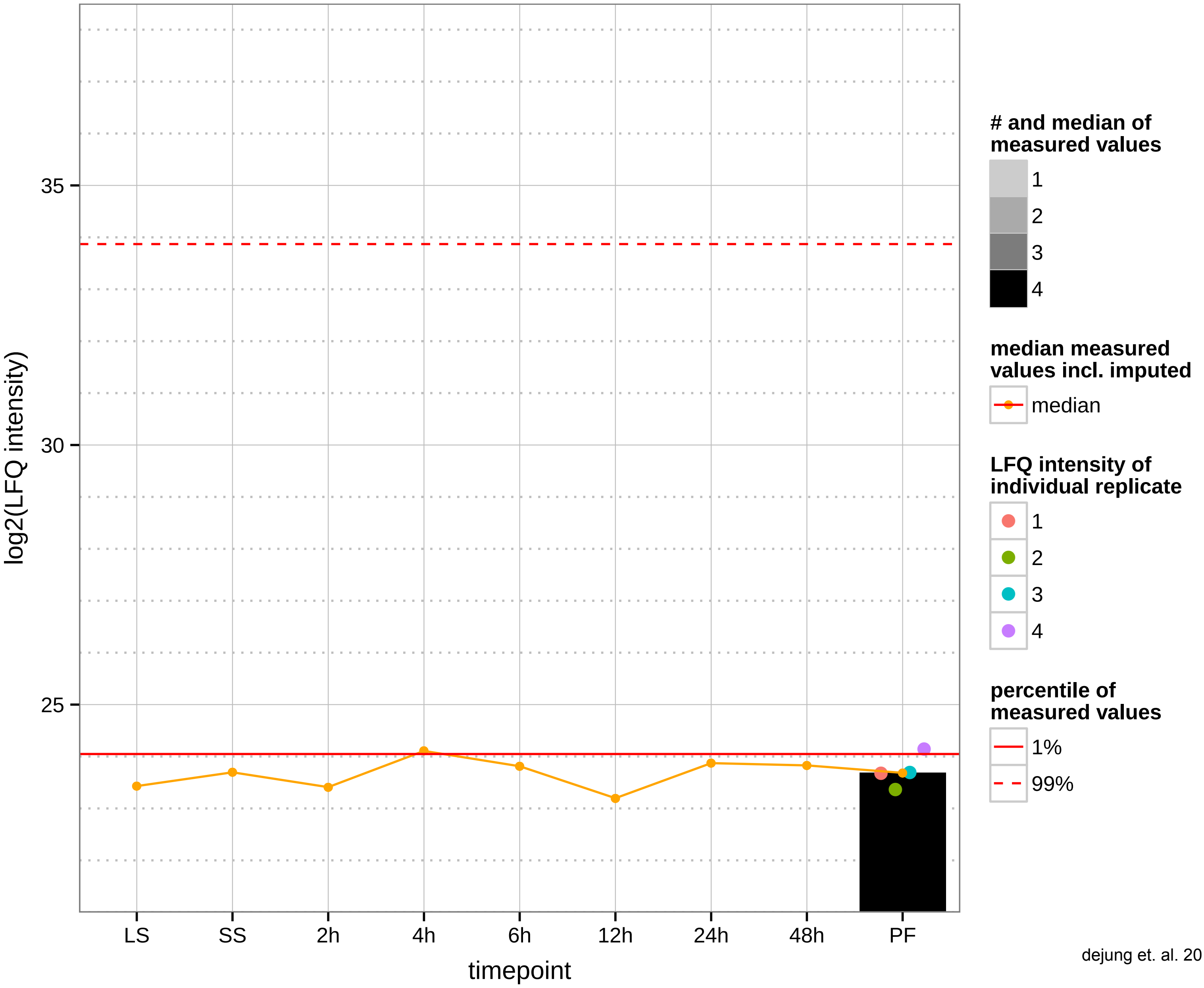
hypothetical protein, conserved
Tb927.2.2920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: transmembrane transport





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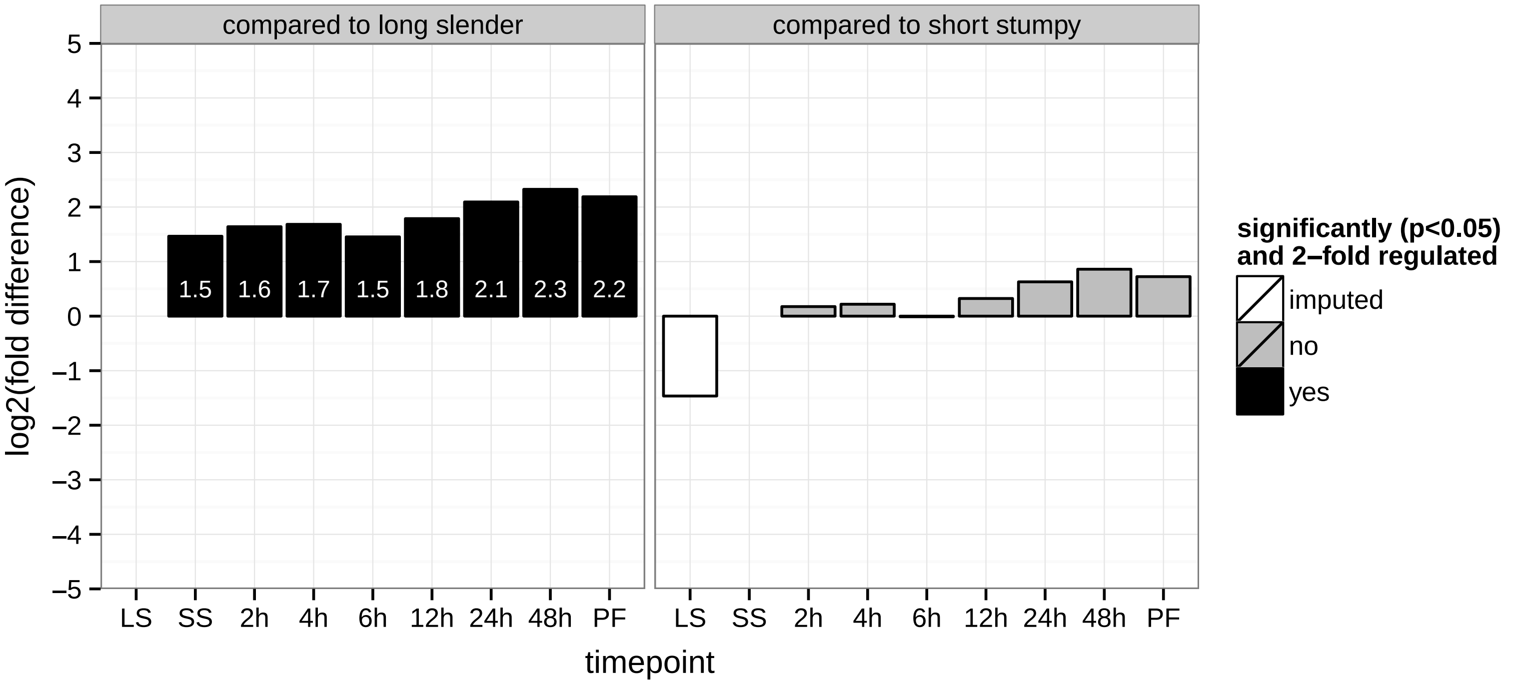
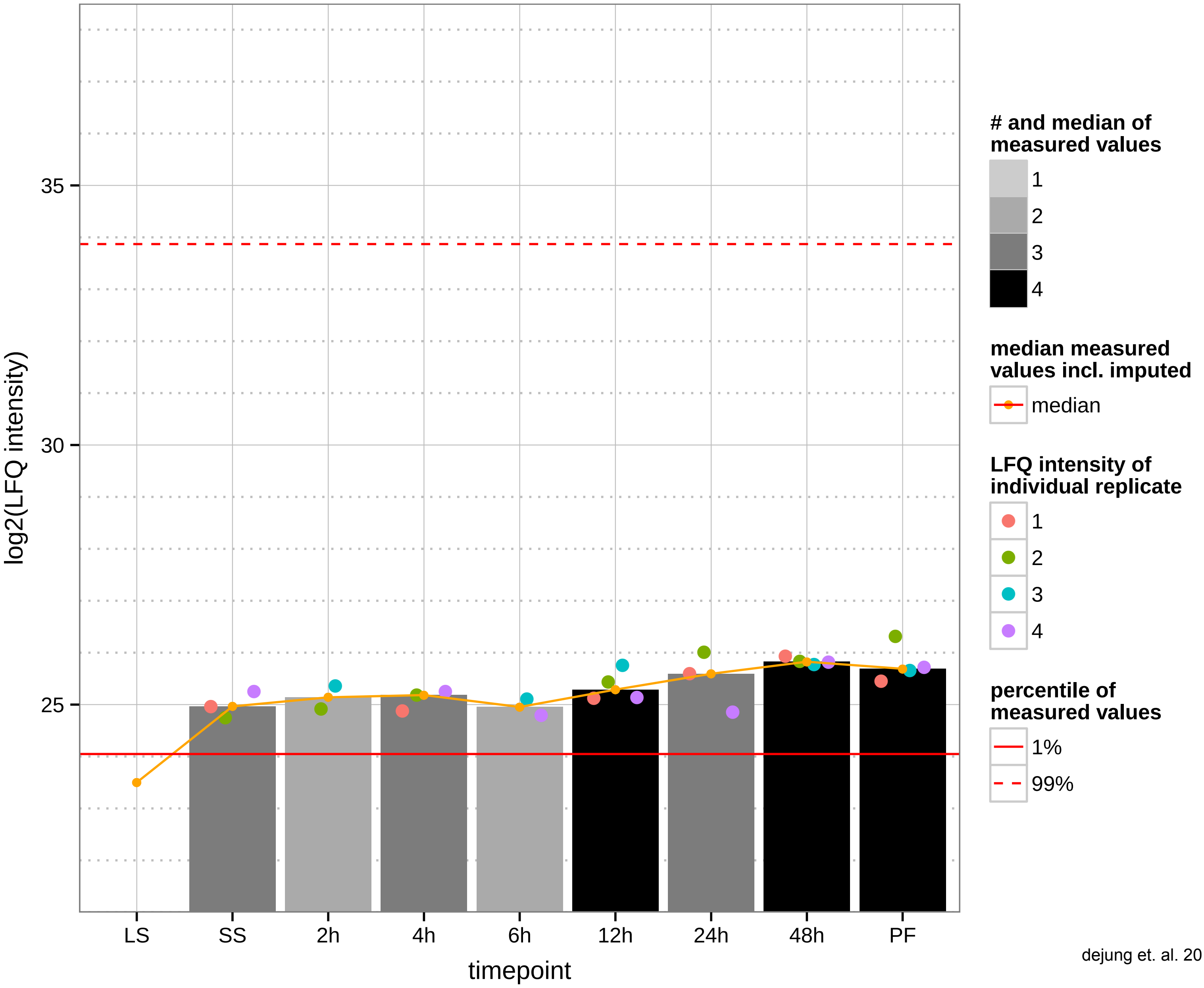
hypothetical protein, conserved
Tb927.2.2940
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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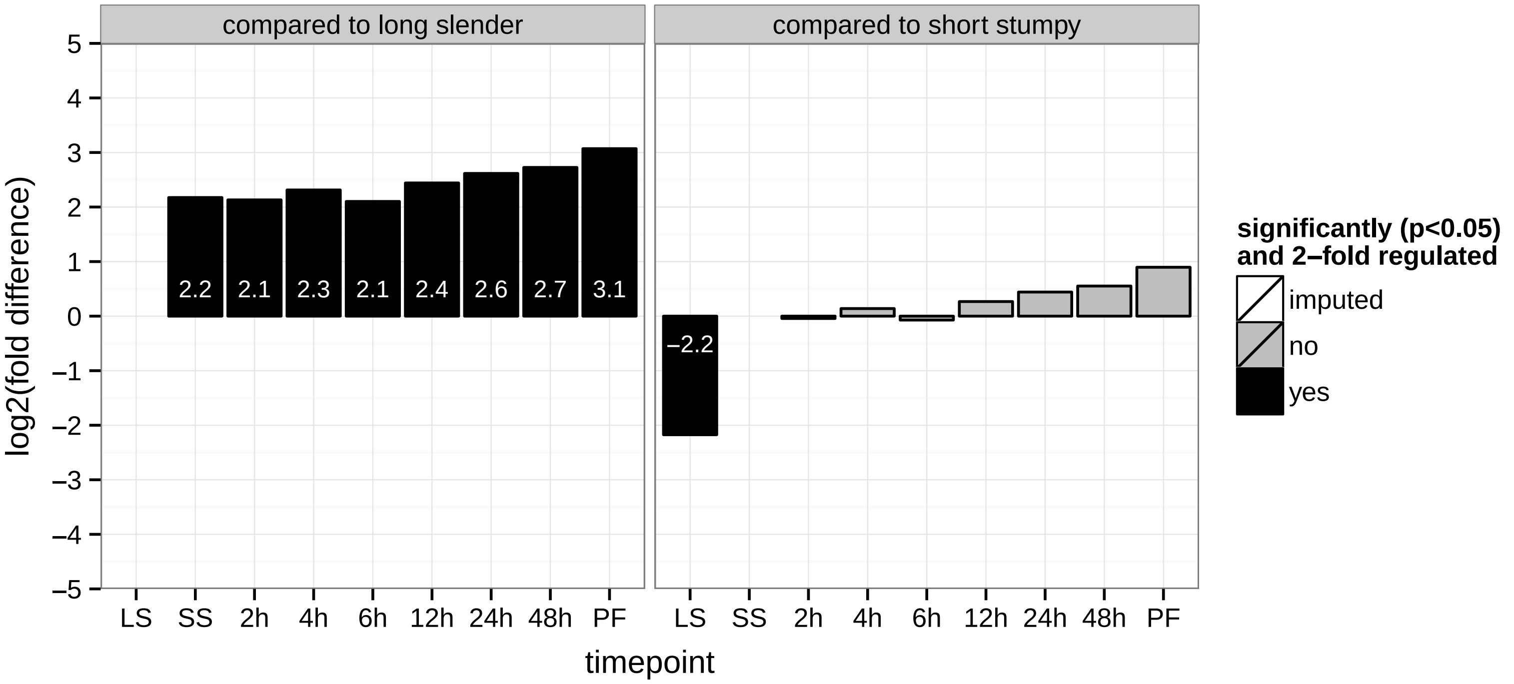
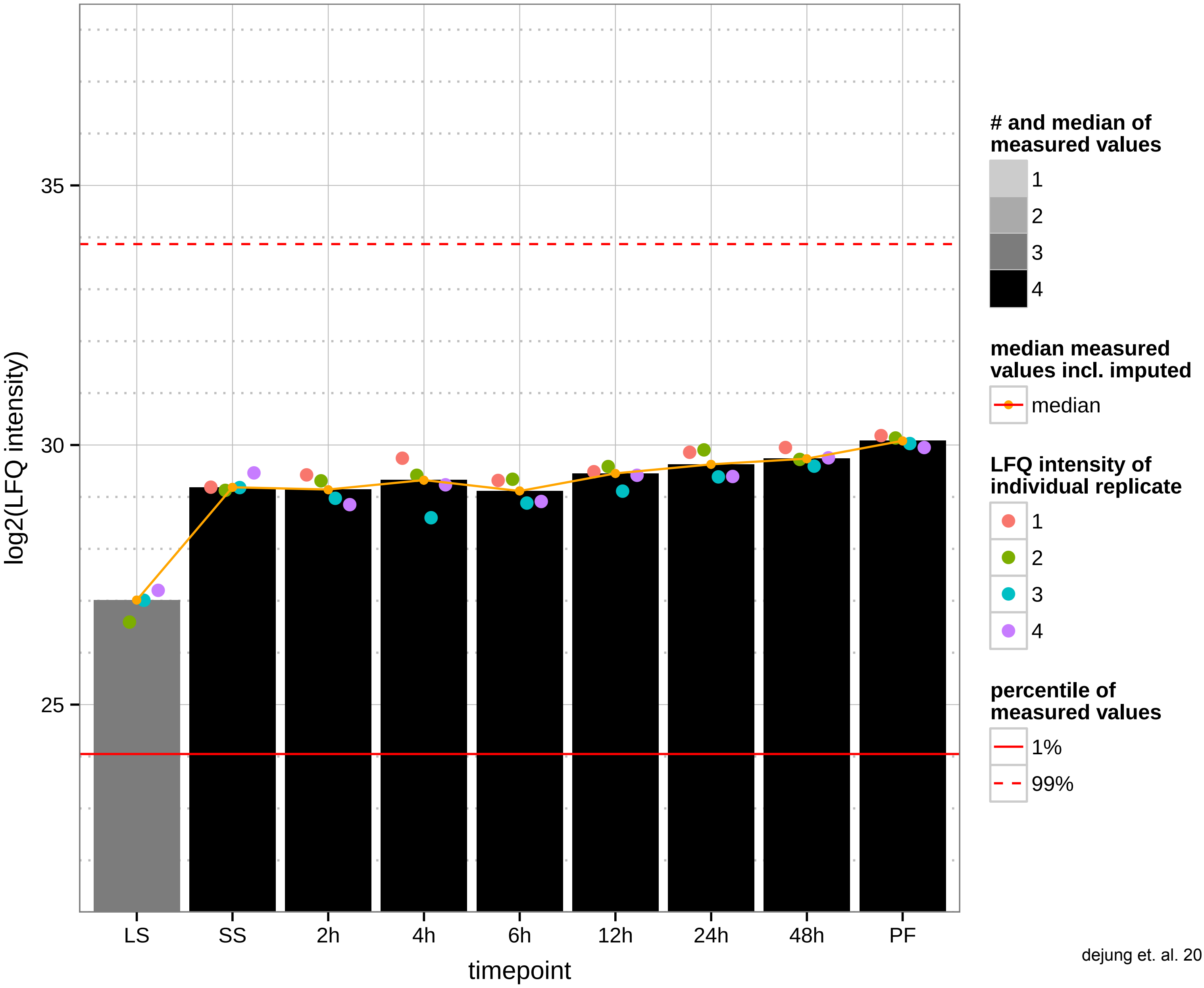
mitochondrial carrier protein (MCP13)
Tb927.2.2970
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrial part
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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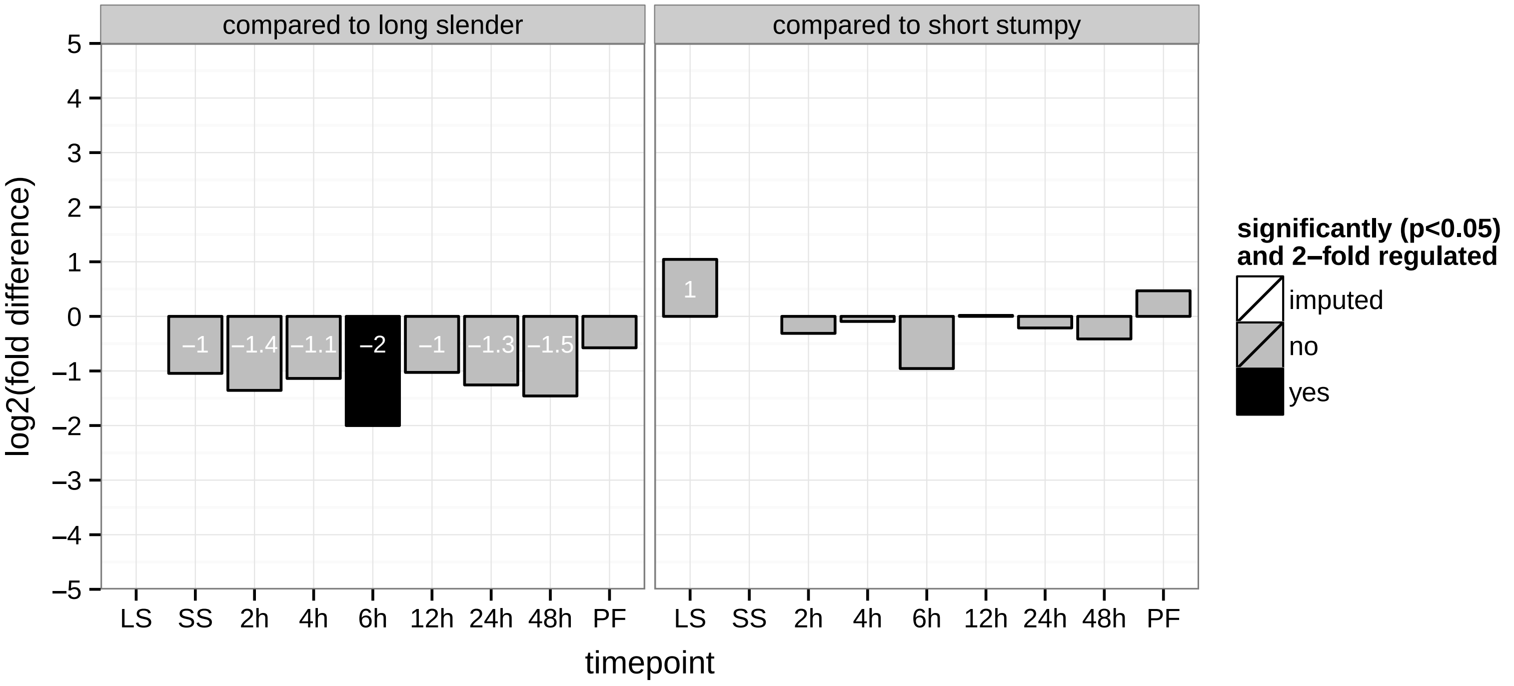
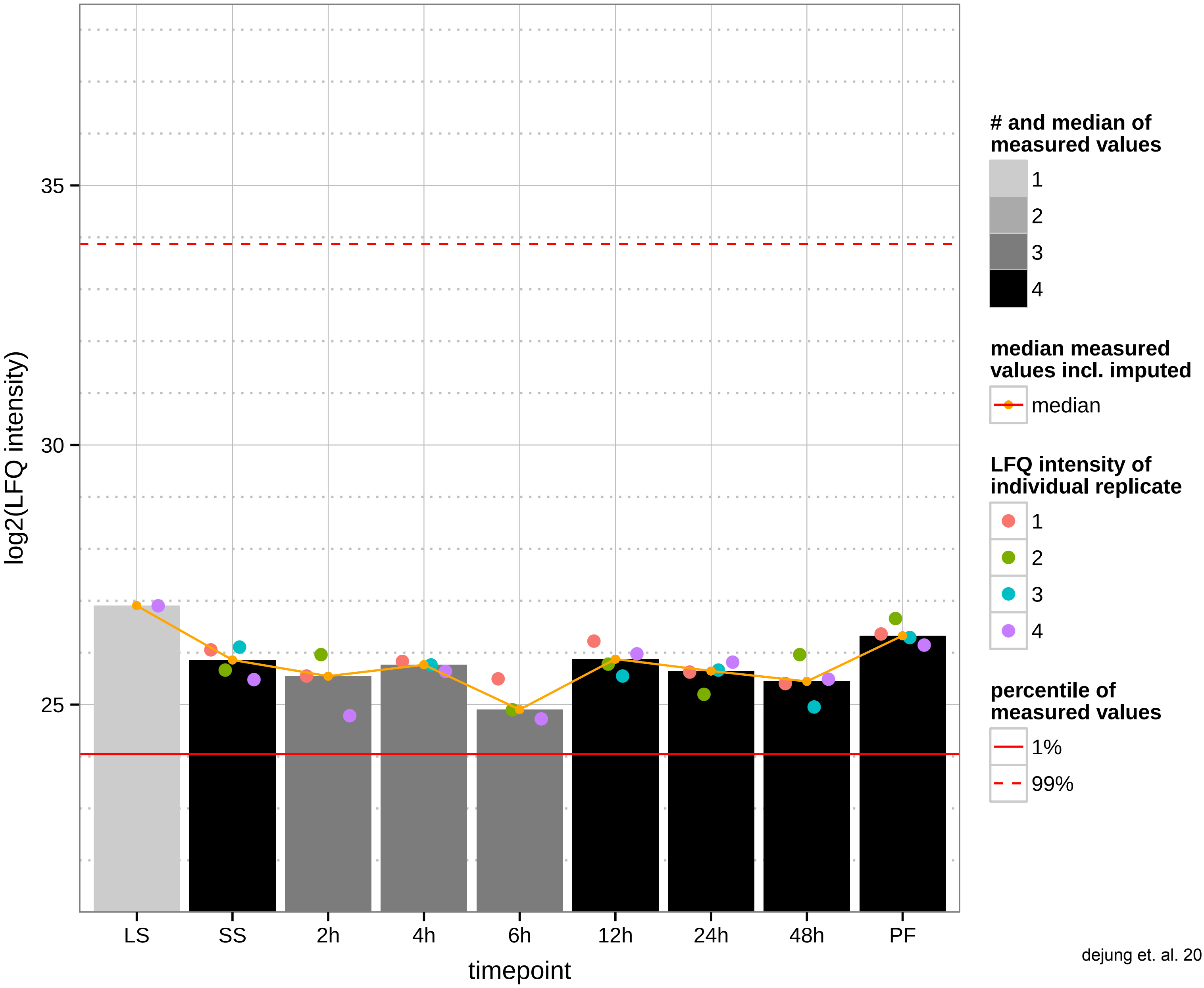
hypothetical protein, conserved
Tb927.2.2990
AGOF: DNA binding, DNA−directed RNA polymerase activity
AGOC: null
AGOP: transcription, DNA−dependent
PGOF: null
PGOC: null
PGOP: null





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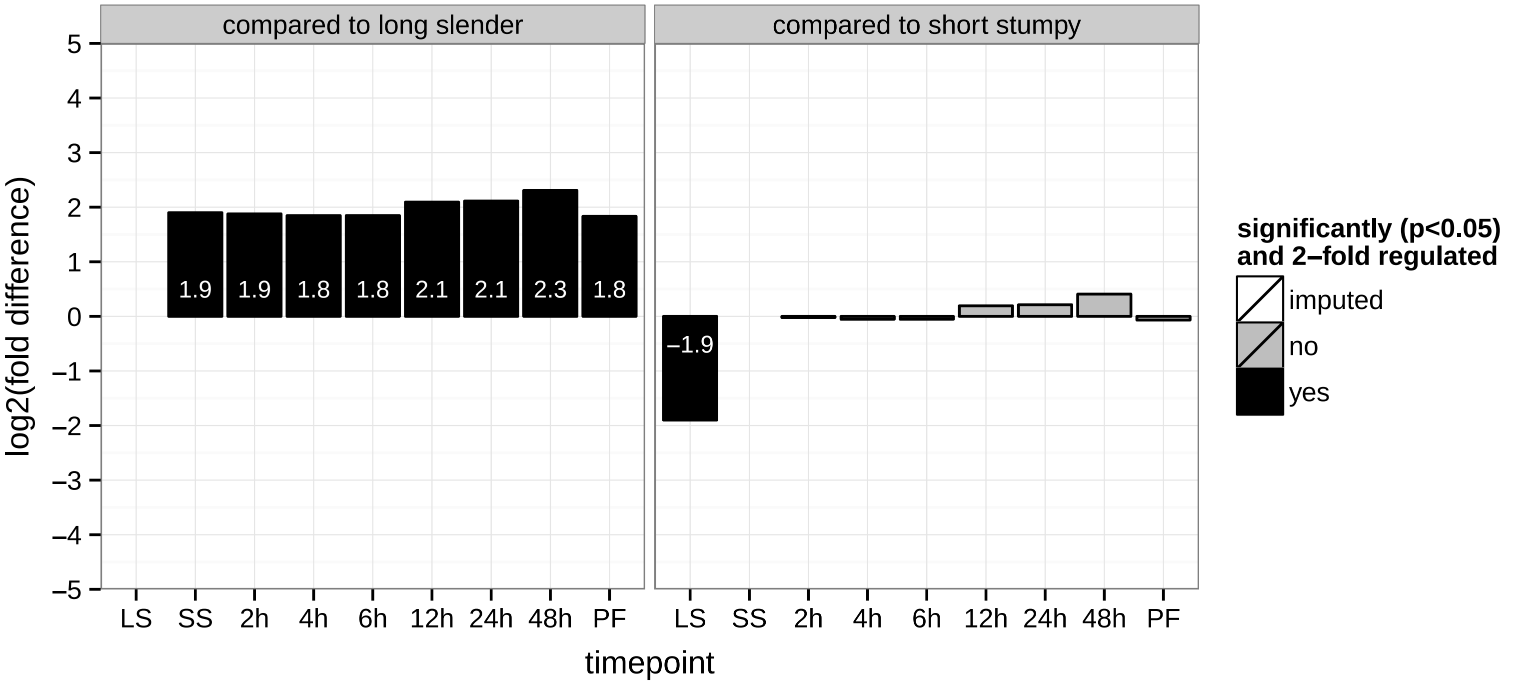
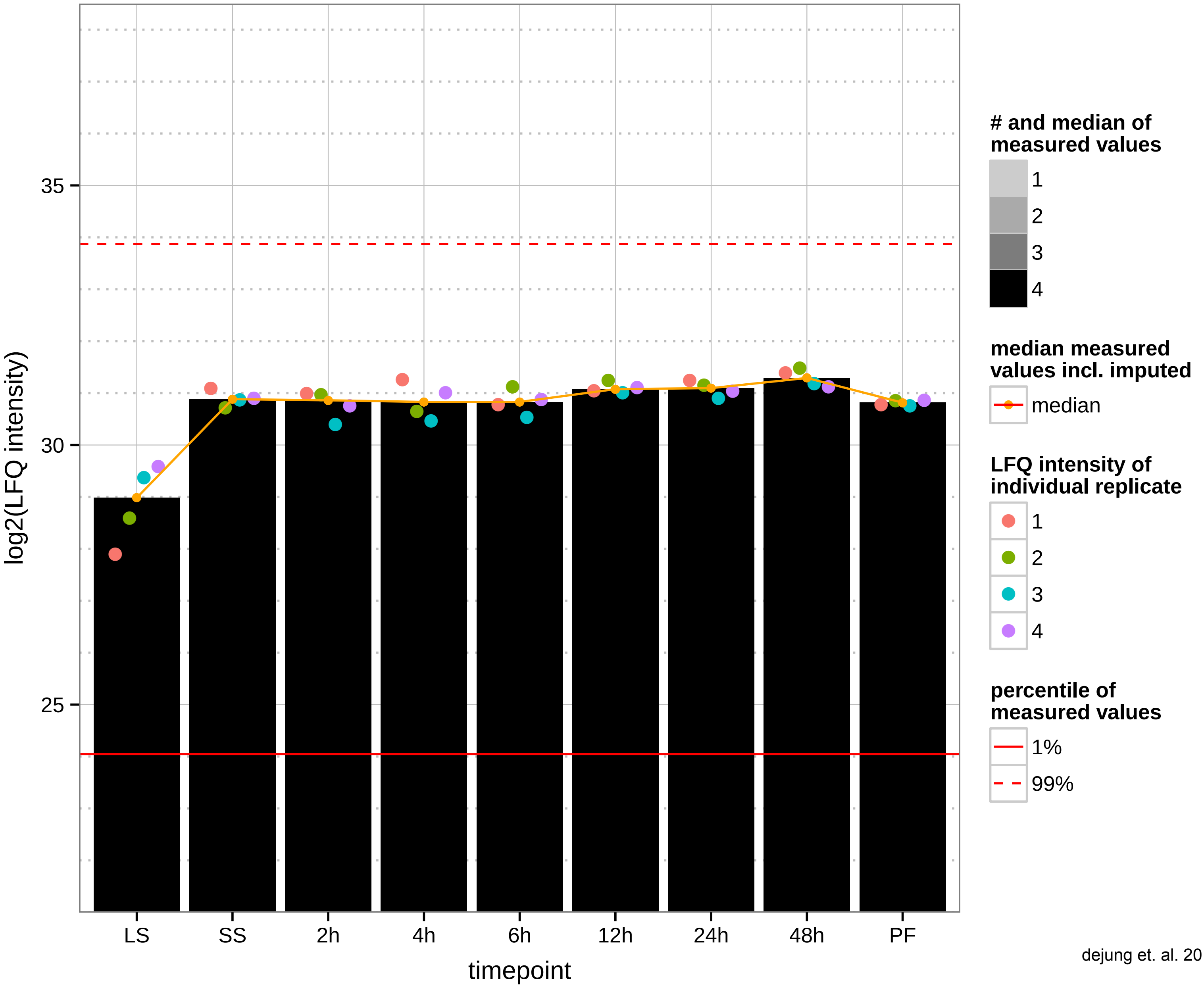
ATP–dependent Clp protease subunit, heat shock protein 78 (HSP78), putative
Tb927.2.3030
AGOF: ATP binding, nucleoside–triphosphatase activity, serine–type endopeptidase activity, unfolded protein binding
AGOC: mitochondrial endopeptidase Clp complex, mitochondrion
AGOP: protein folding, proteolysis
PGOF: ATP binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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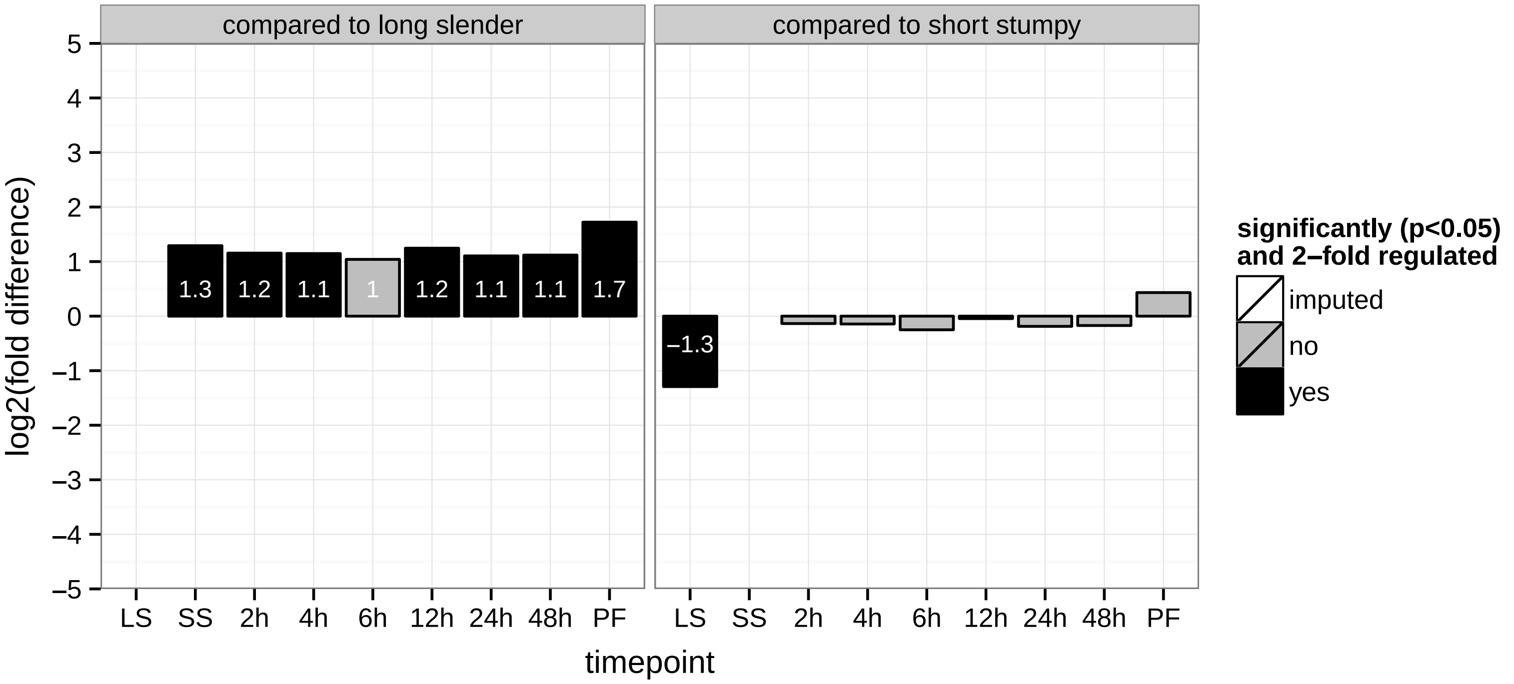
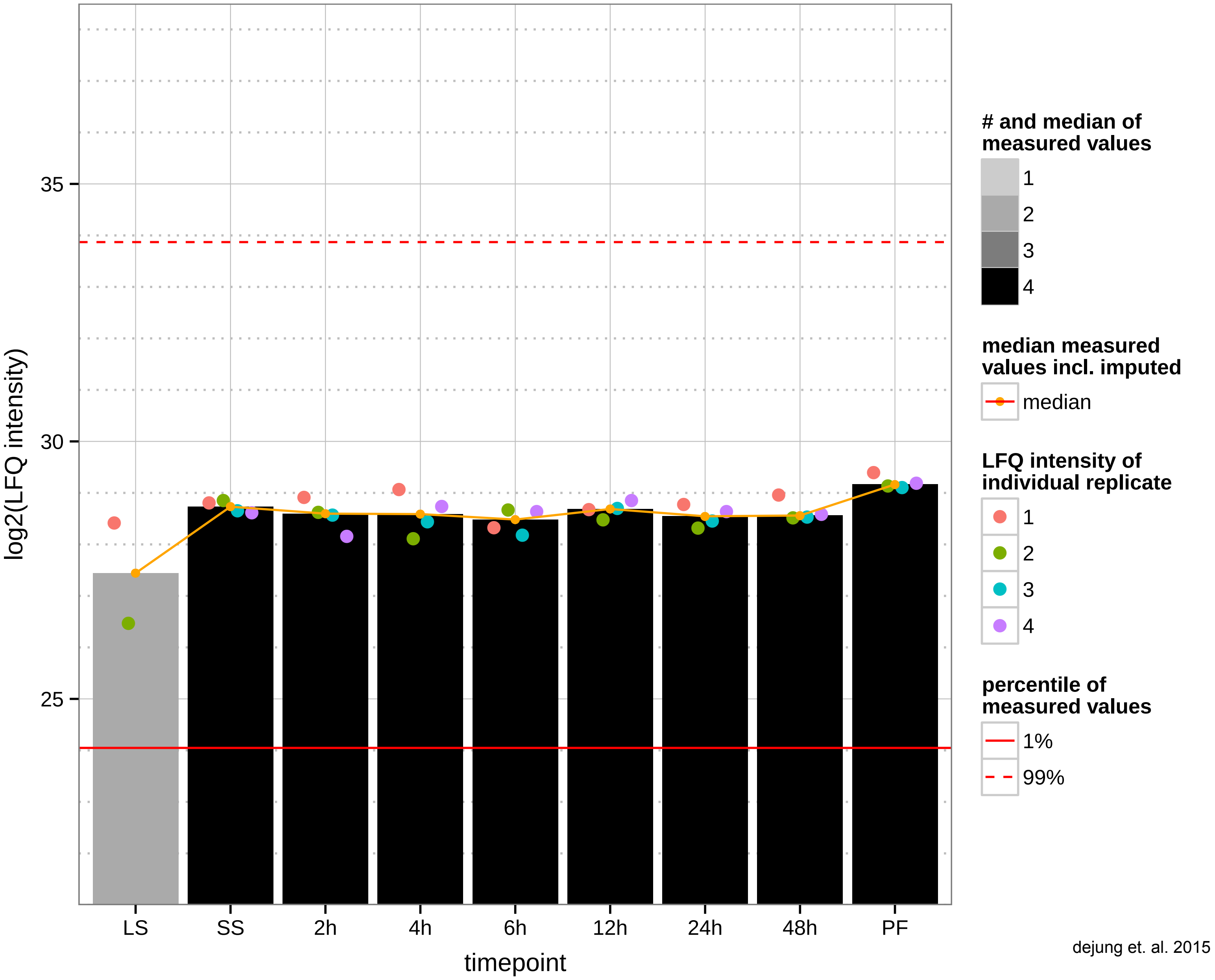
hypothetical protein, conserved, kinetoplast polyadenylation/uridylation factor 1, mitochondrial RNA binding protein 1 (KPAF1)
Tb927.2.3180;Tb11.v5.0782
AGOF: null, protein binding, ribosome binding
AGOC: null, mitochondrion
AGOP: null, mRNA 3'−end processing, mRNA polyadenylation, regulation of mRNA stability
PGOF: null
PGOC: null
PGOP: null





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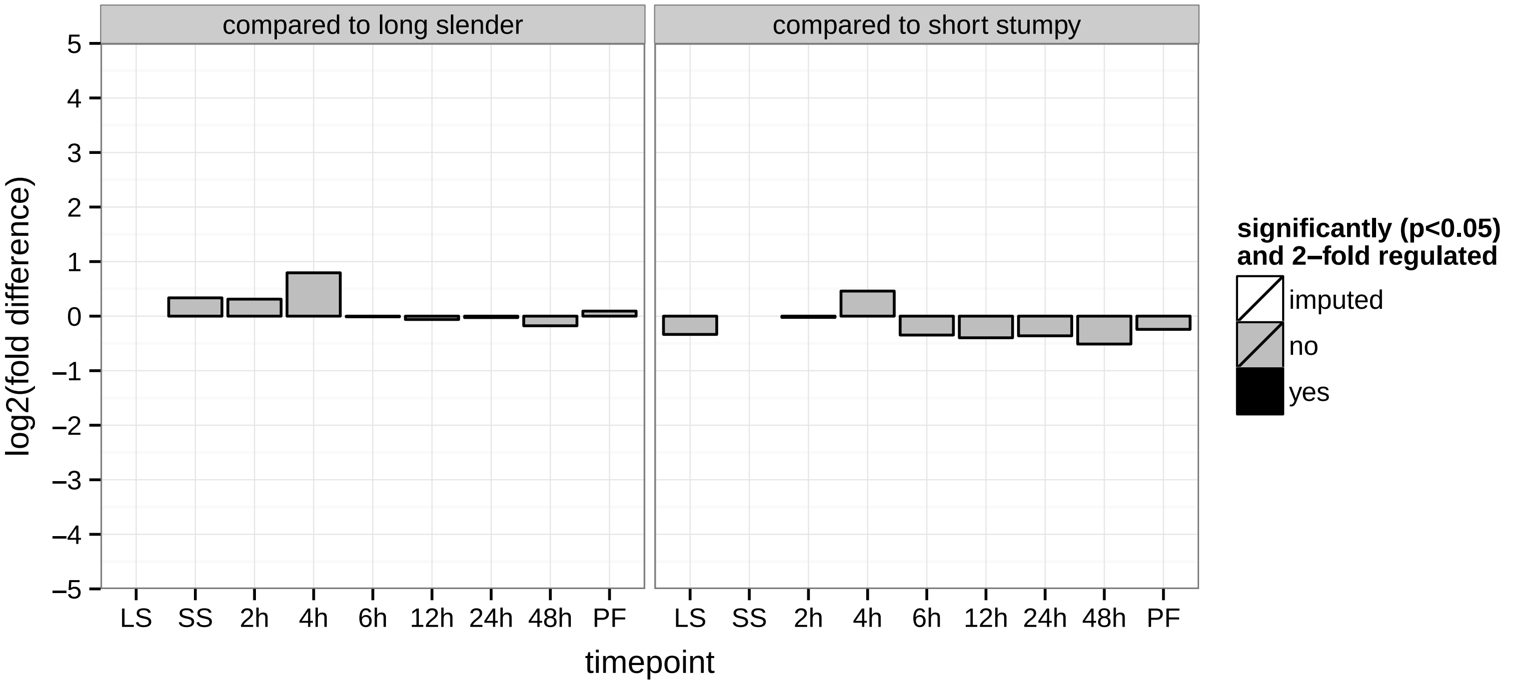
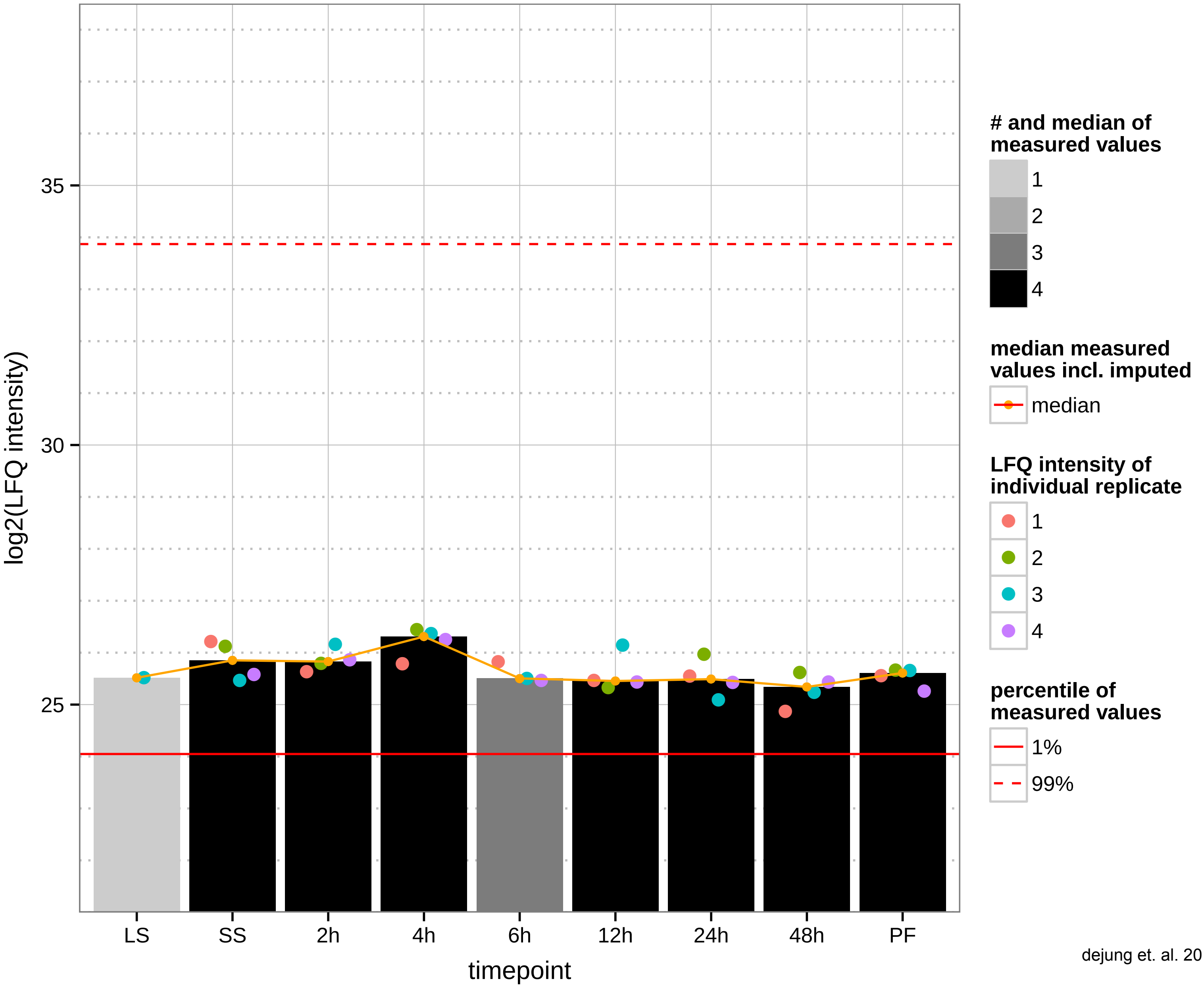
transcription elongation factor s–II, putative (TFIIS2–2)
Tb927.2.3480
AGOF: DNA binding
AGOC: nucleus
AGOP: transcription, DNA–dependent
PGOF: DNA binding
PGOC: nucleus
PGOP: transcription, DNA–dependent





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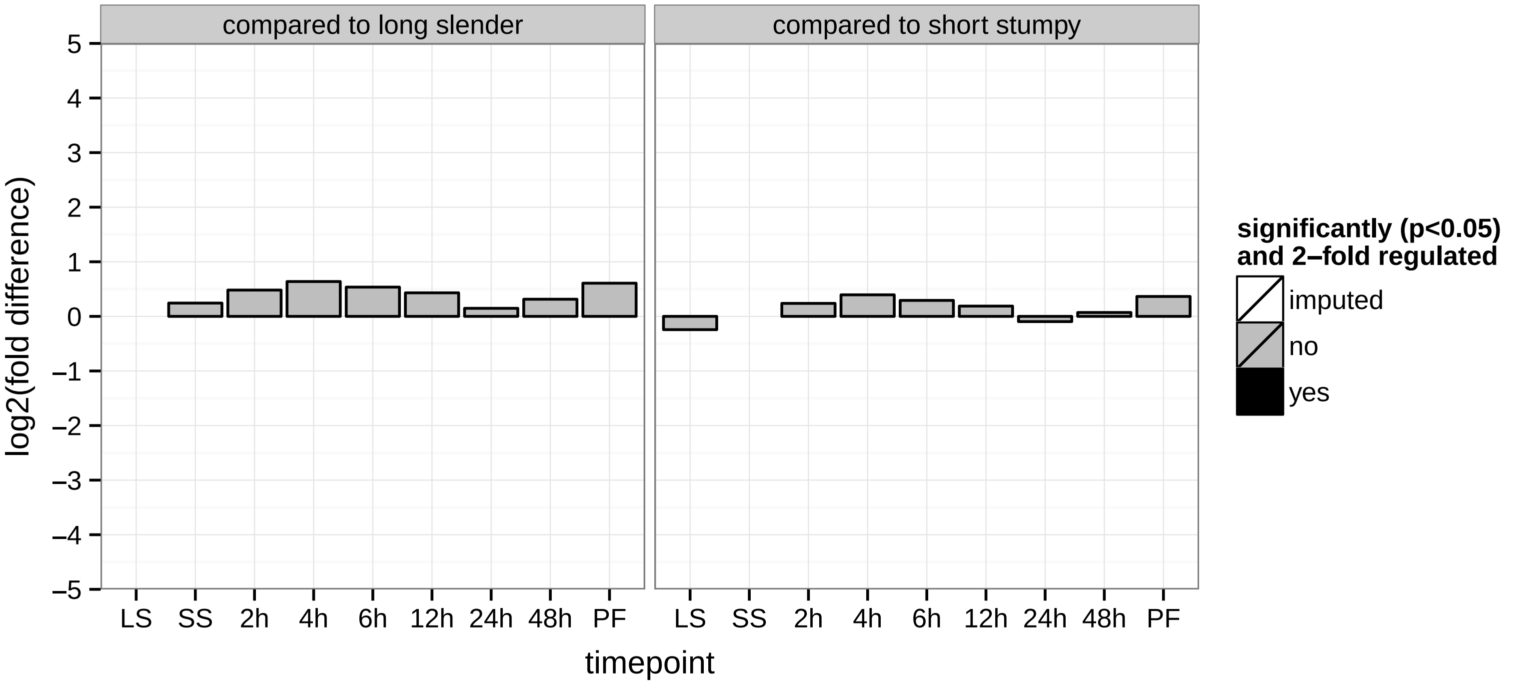
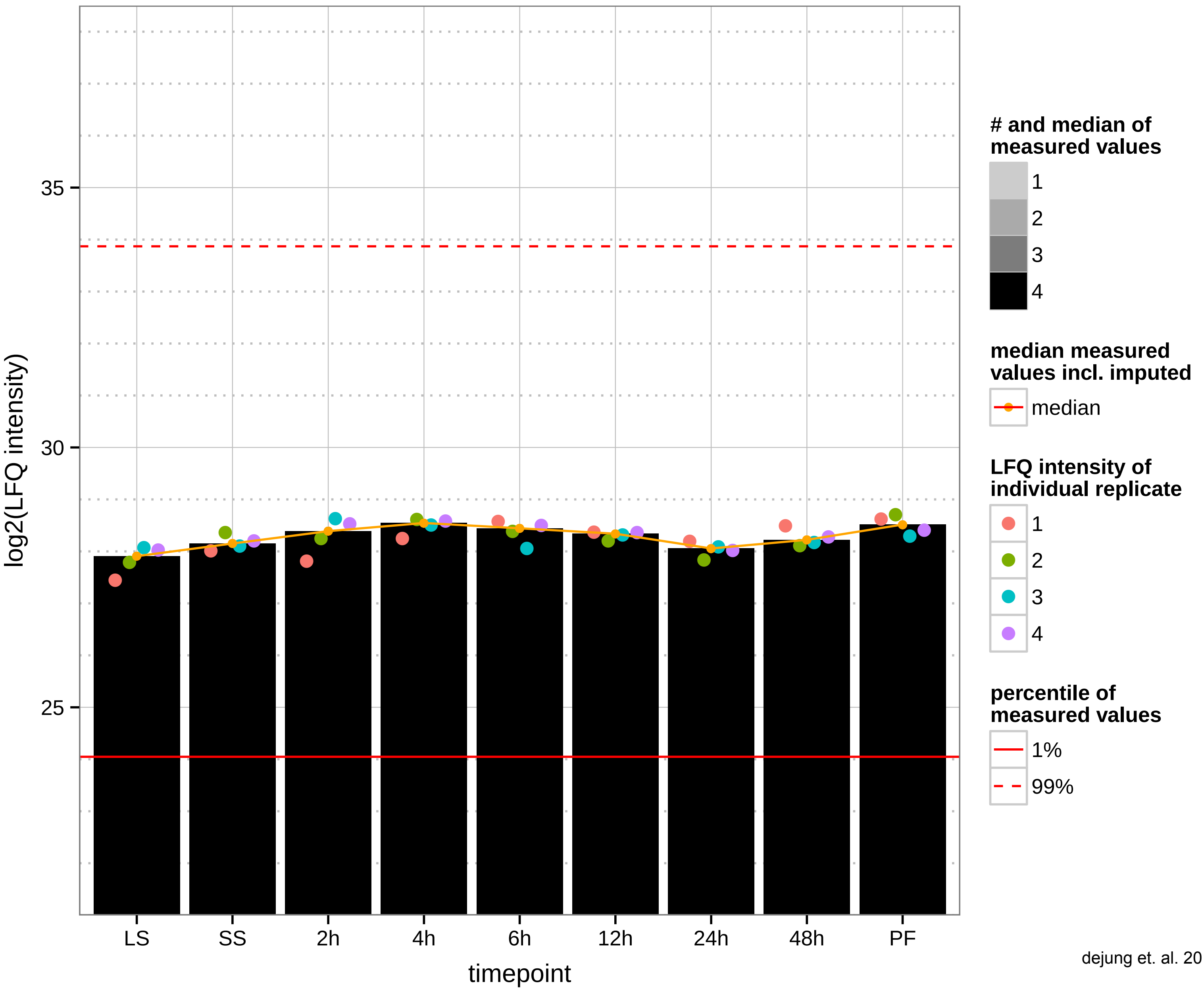
transcription elongation factor s–II, putative (TFIIS2–1)
Tb927.2.3580
AGOF: DNA binding, sequence–specific DNA binding transcription factor activity, zinc ion binding
AGOC: nucleus
AGOP: DNA–dependent transcription, elongation, regulation of transcription, DNA–dependent, transcription
PGOF: DNA binding, nucleic acid binding, zinc ion binding
PGOC: nucleus
PGOP: transcription, DNA–dependent





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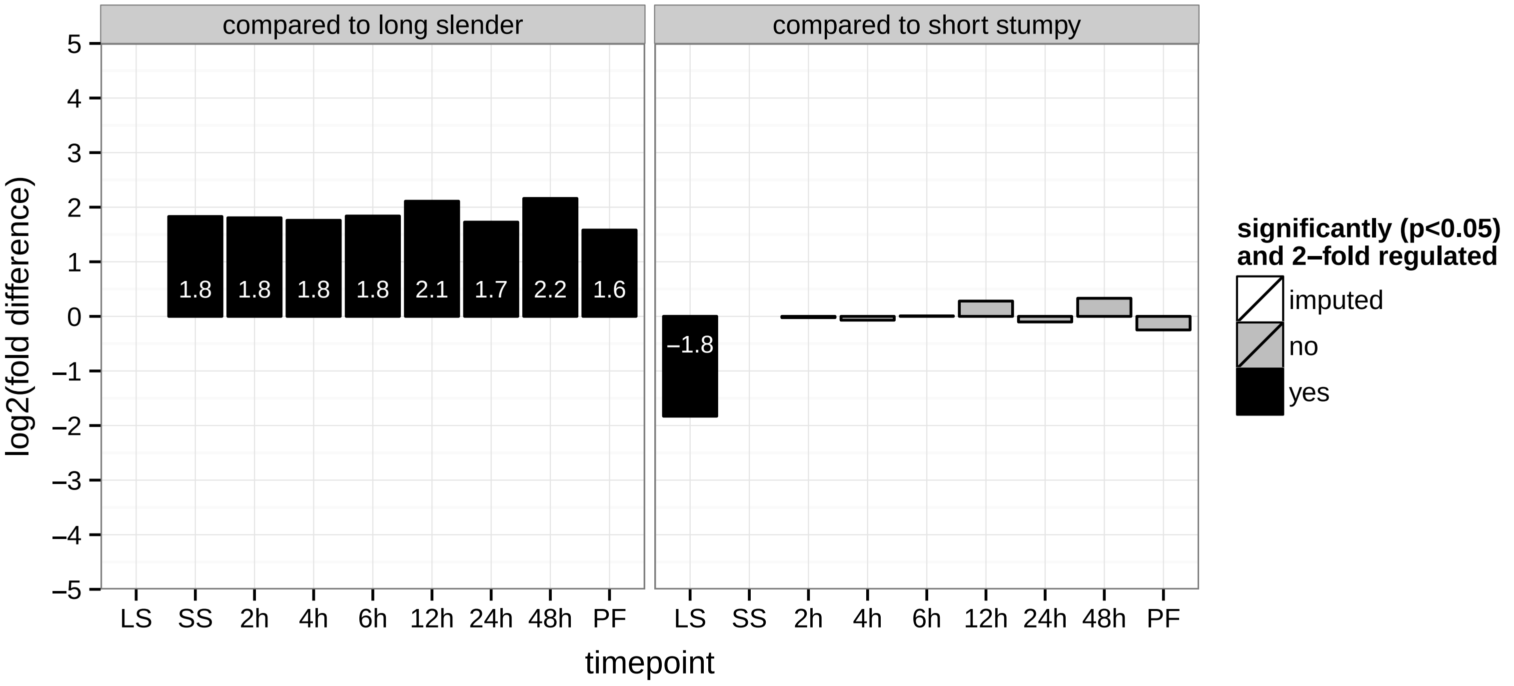
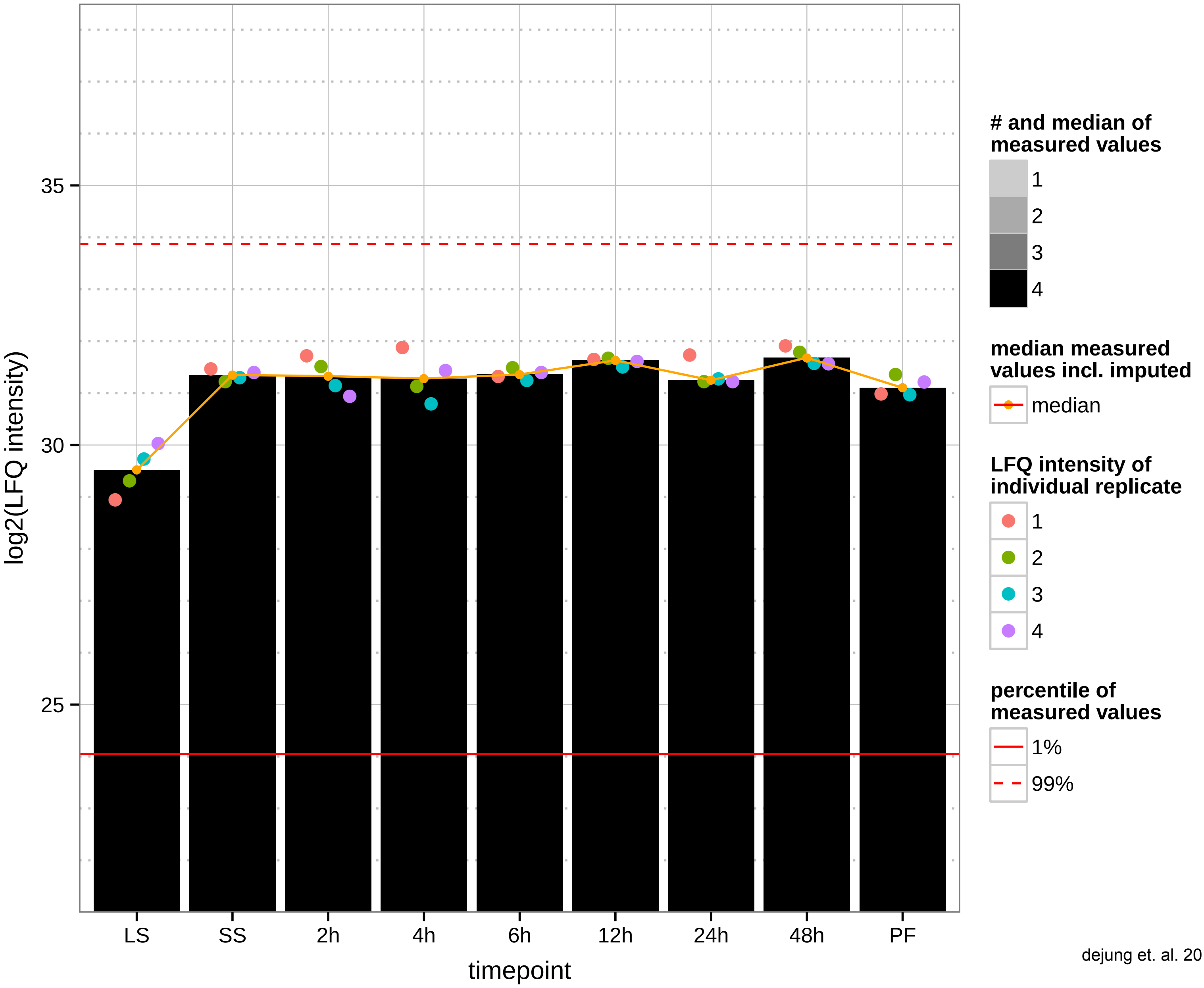
retrotransposon hot spot protein 1 (RHS1), putative
Tb927.2.370
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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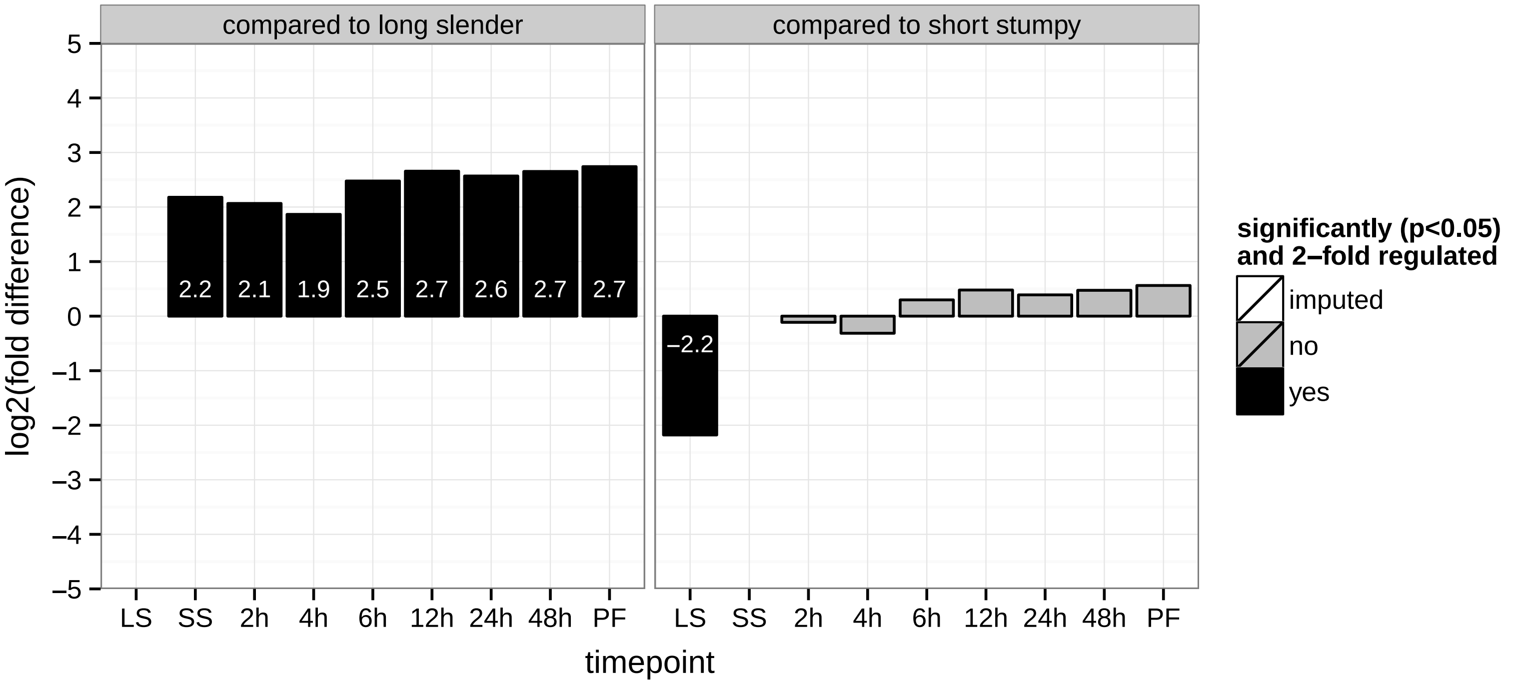
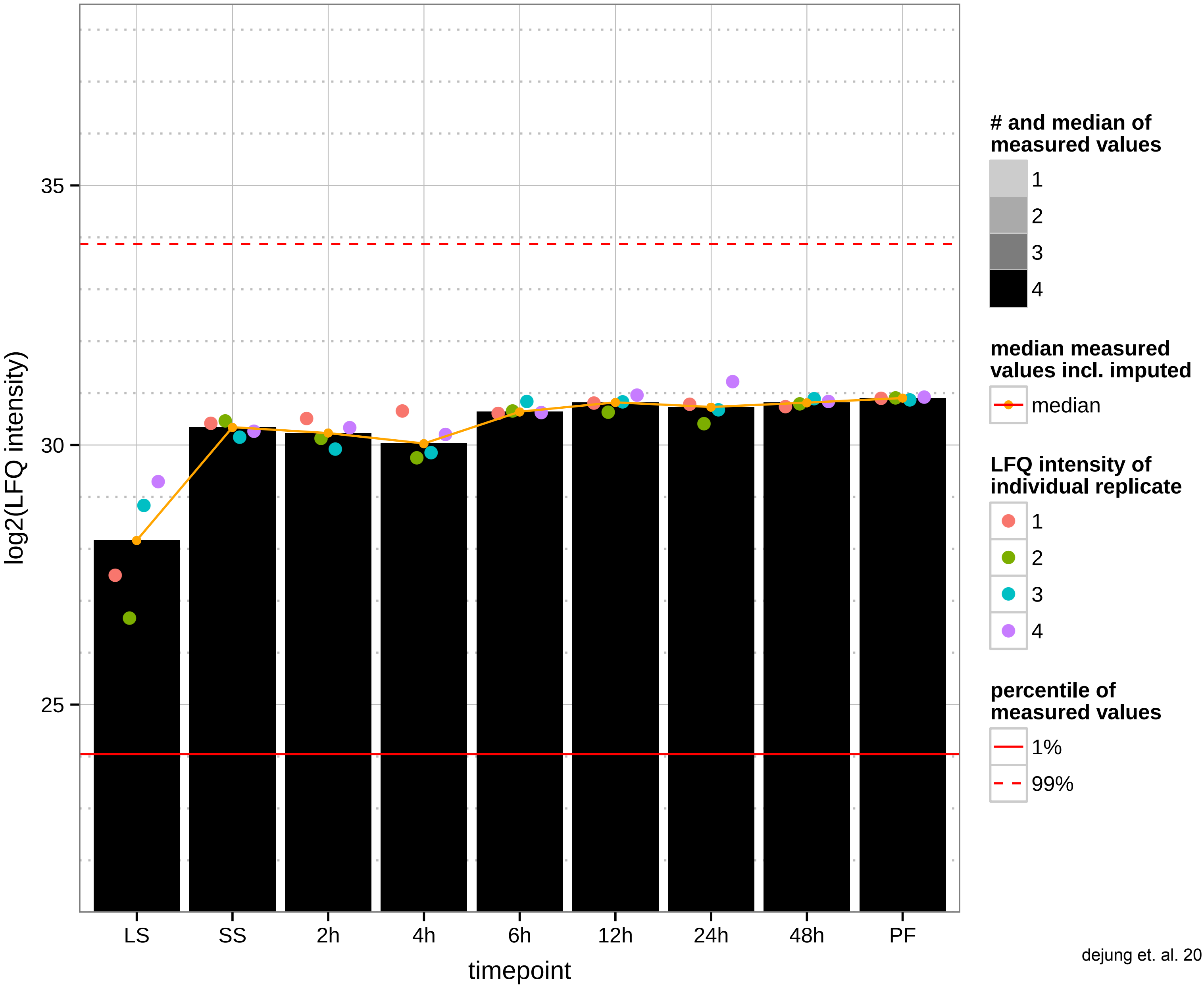
retrotransposon hot spot protein 2 (RHS2), putative
Tb927.2.380
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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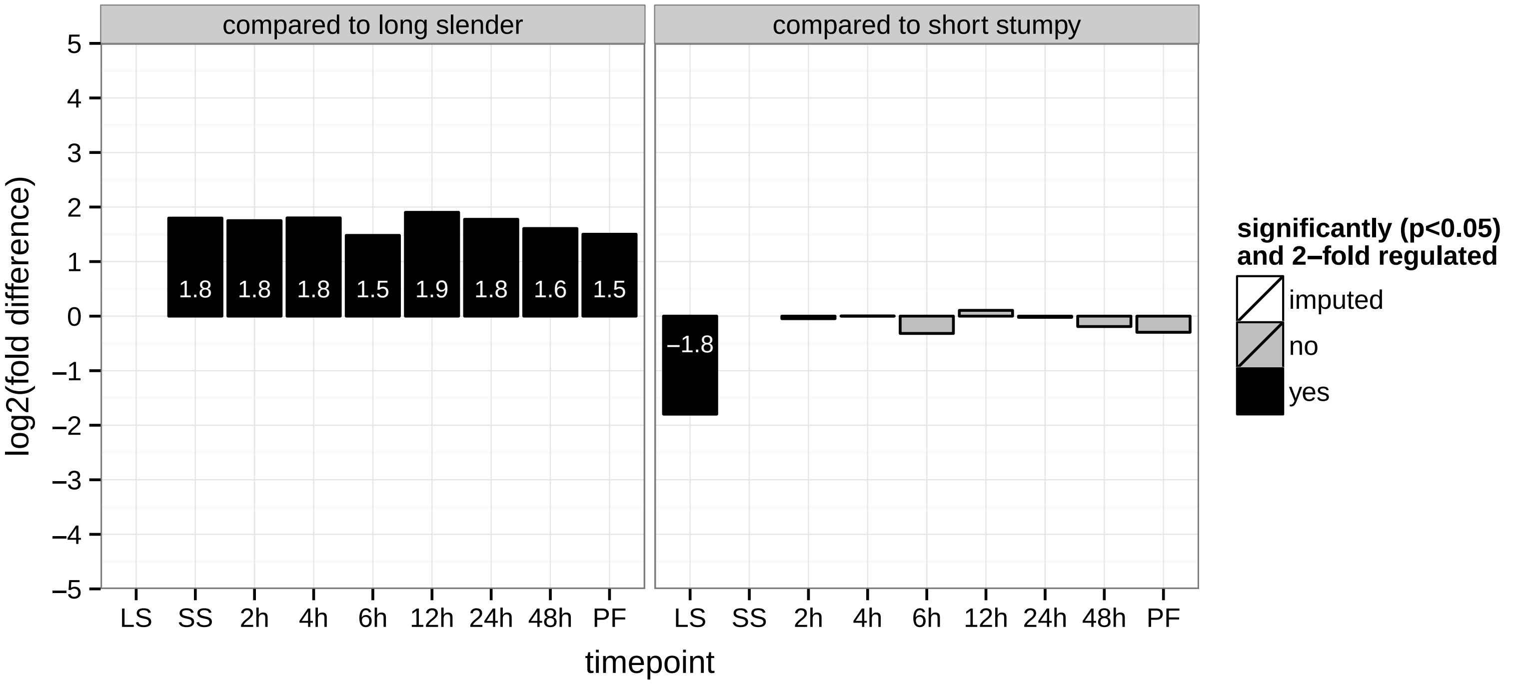
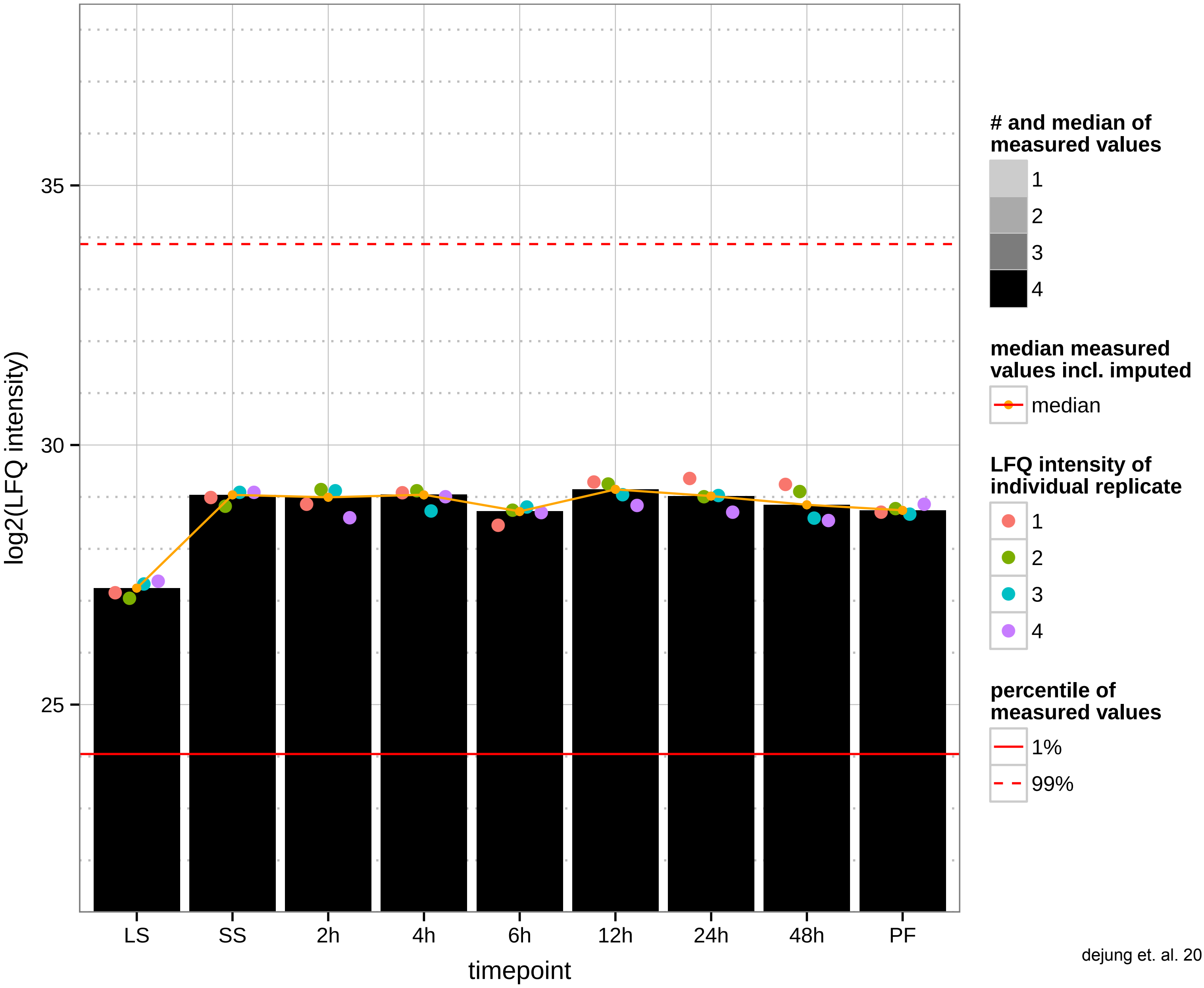
guide RNA associated protein, GAP1, MRB1−associated protein
Tb927.2.3800
AGOF: mRNA binding
AGOC: mitochondrion
AGOP: mitochondrial RNA processing
PGOF: null
PGOC: null
PGOP: null





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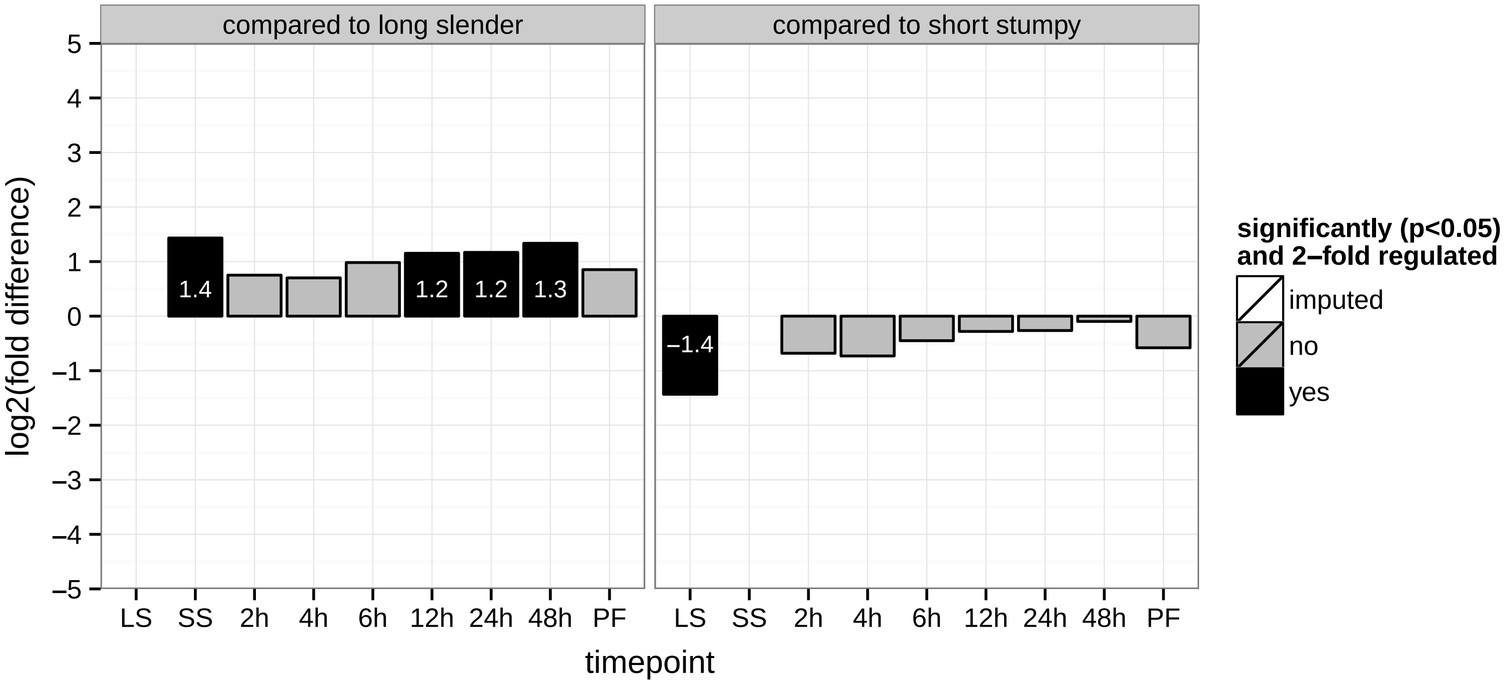
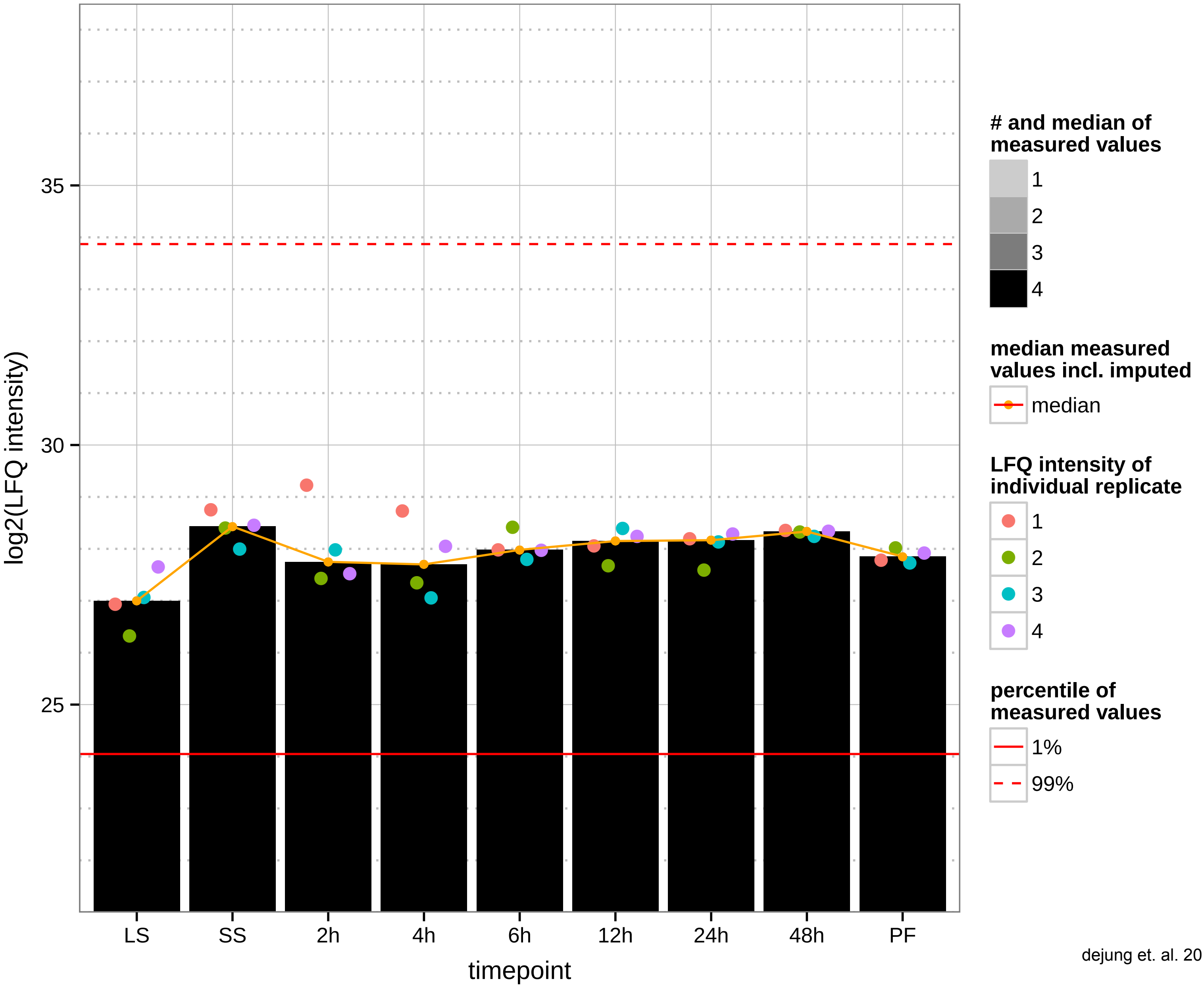
retrotransposon hot spot protein 2 (RHS2), putative
Tb927.2.400
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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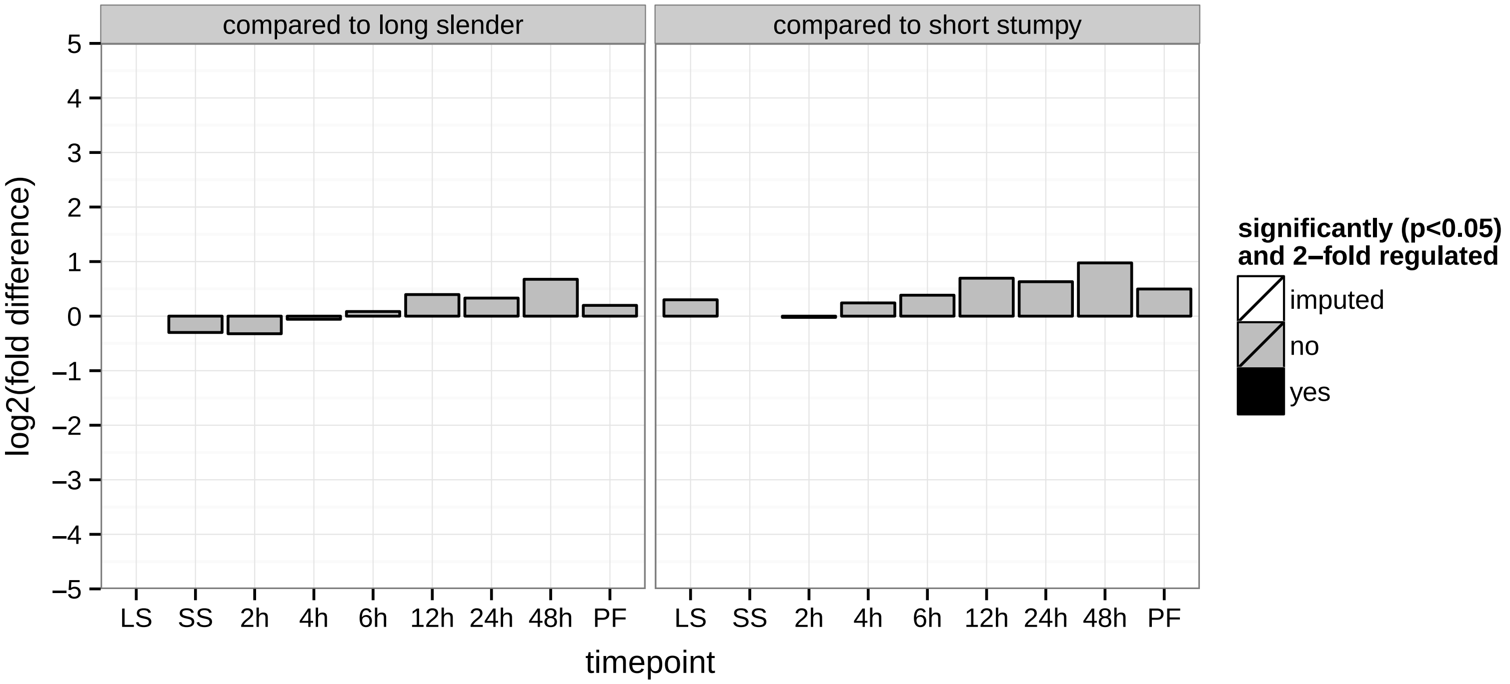
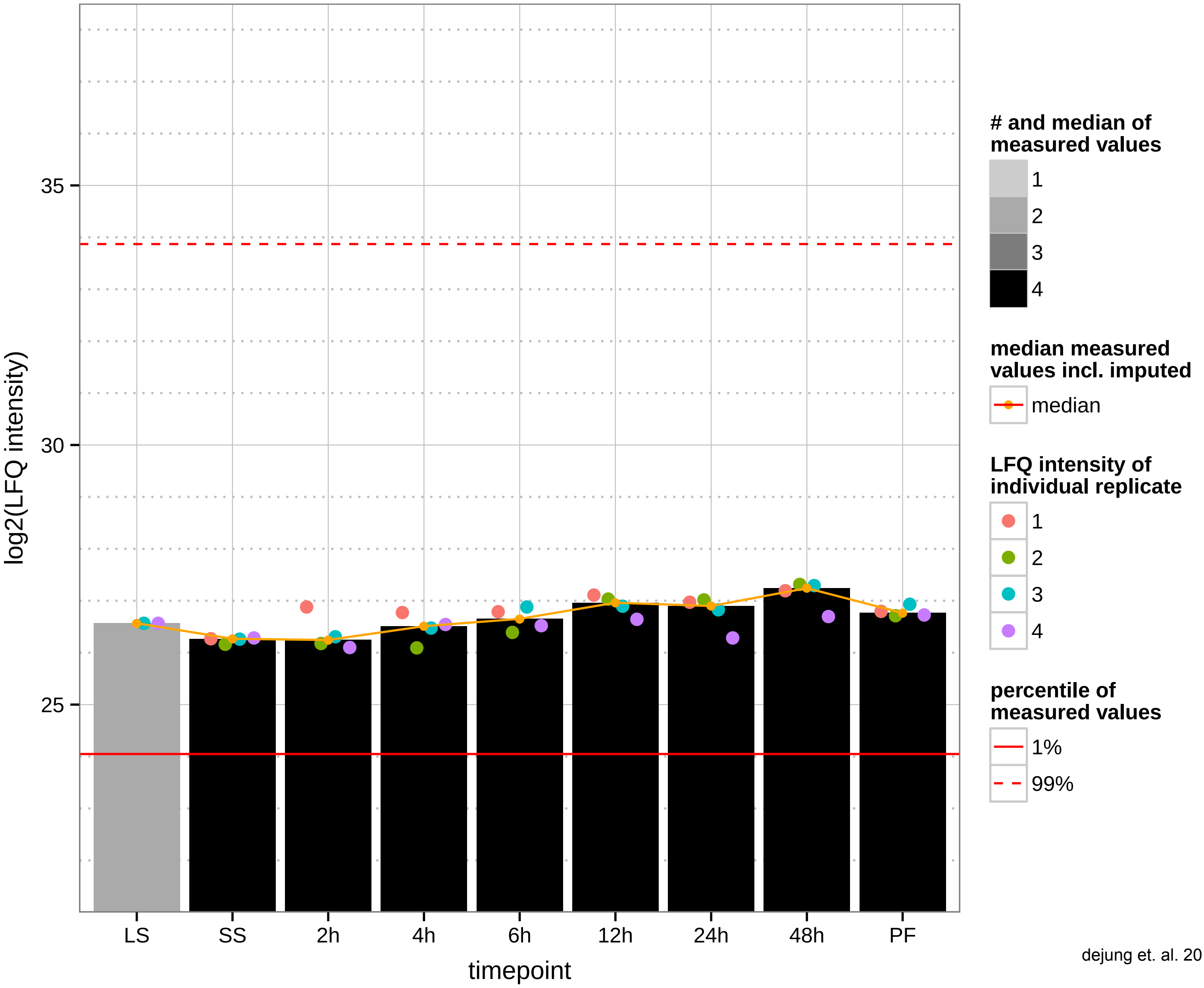
dynein intermediate chain IC 138, putative
Tb927.2.4060
AGOF: motor activity
AGOC: cytoskeleton, dynein complex
AGOP: microtubule−based movement
PGOF: protein binding
PGOC: null
PGOP: null





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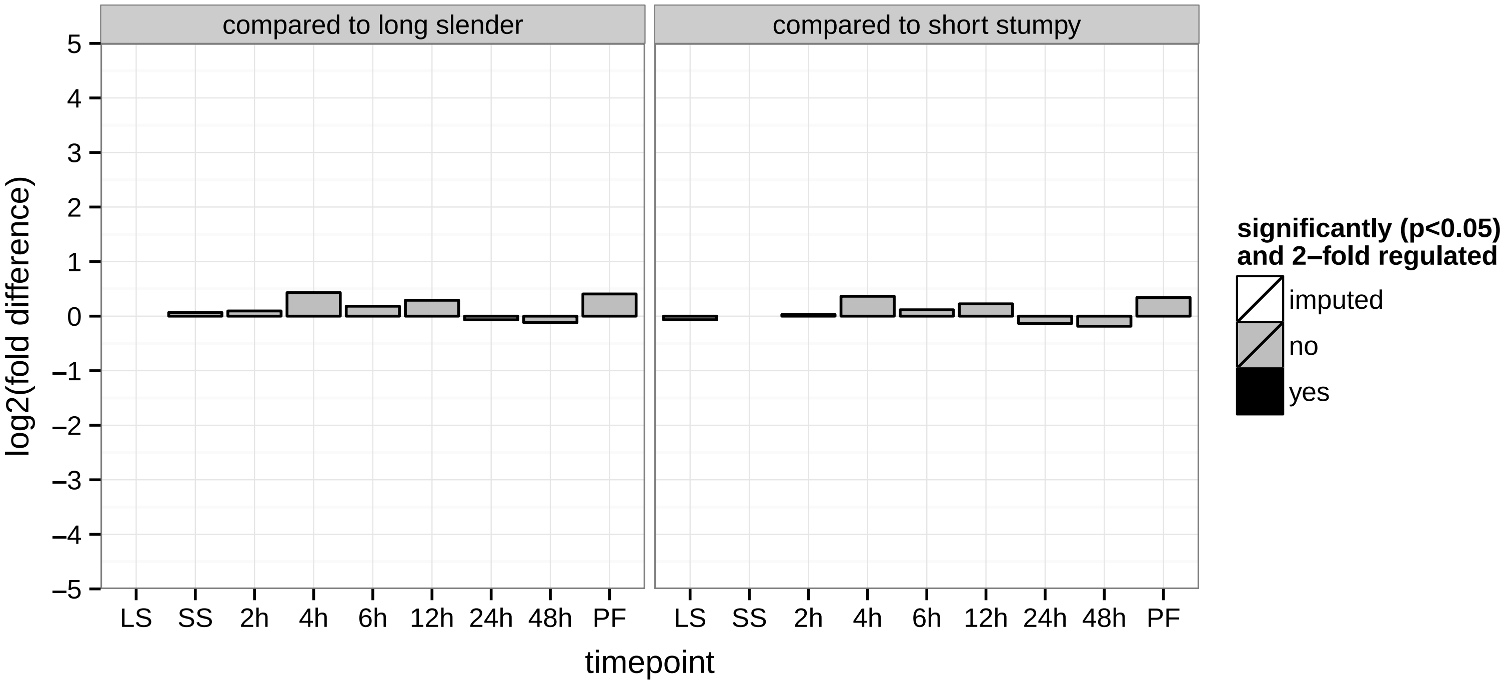
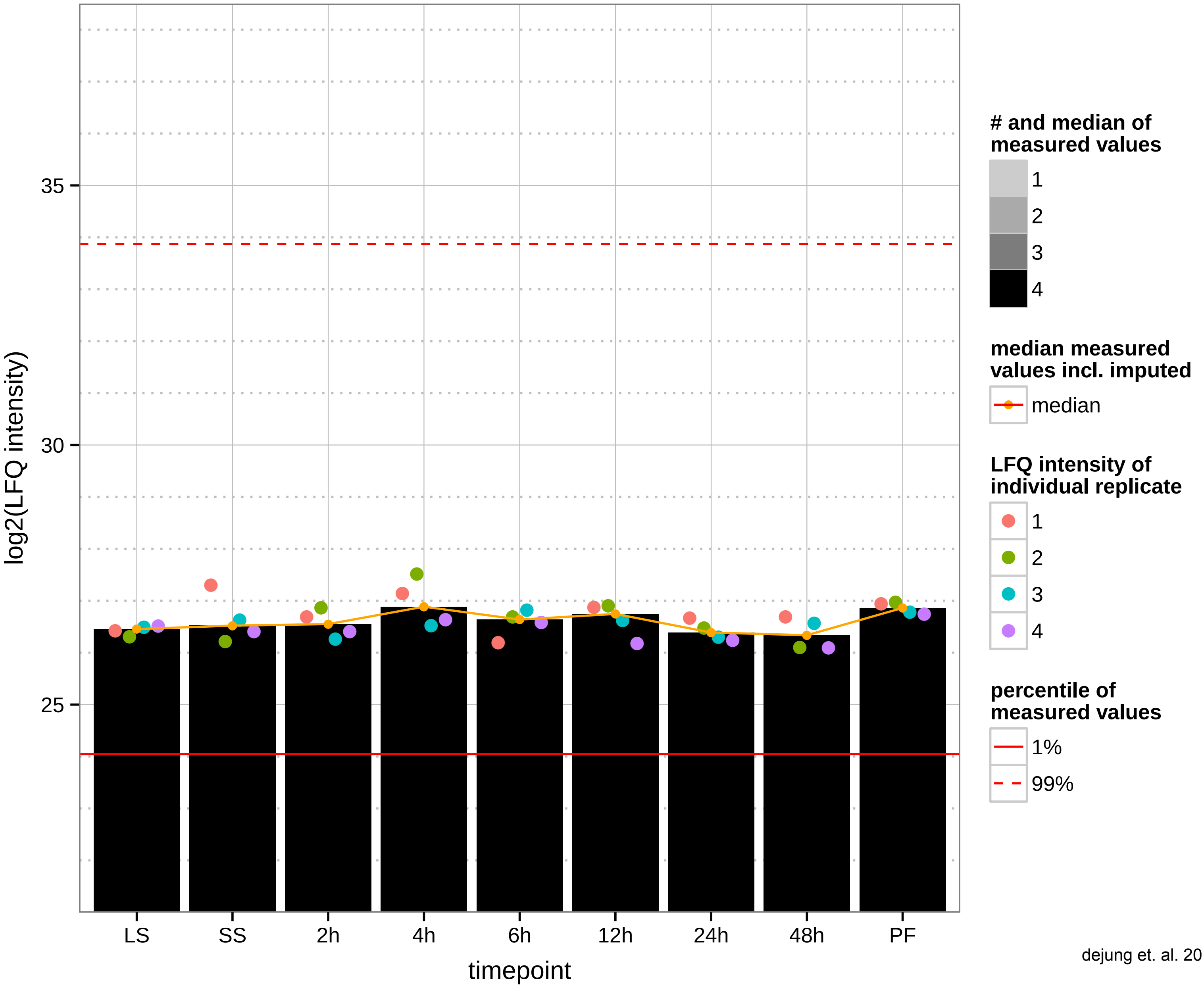
hypothetical protein, conserved
Tb927.2.4090
AGOF: null
AGOC: mitochondrial inner membrane
AGOP: null
PGOF: GTP binding
PGOC: null
PGOP: SRP−dependent cotranslational protein targeting to membrane





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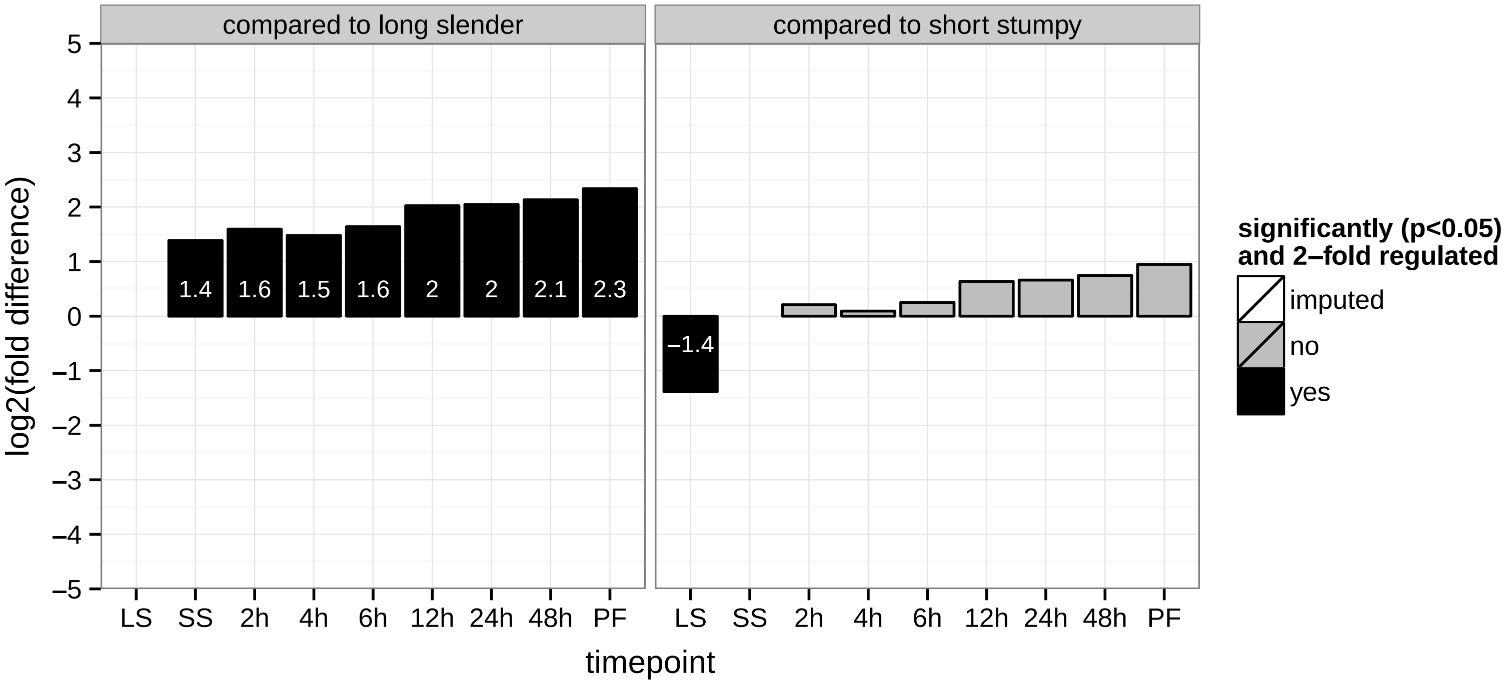
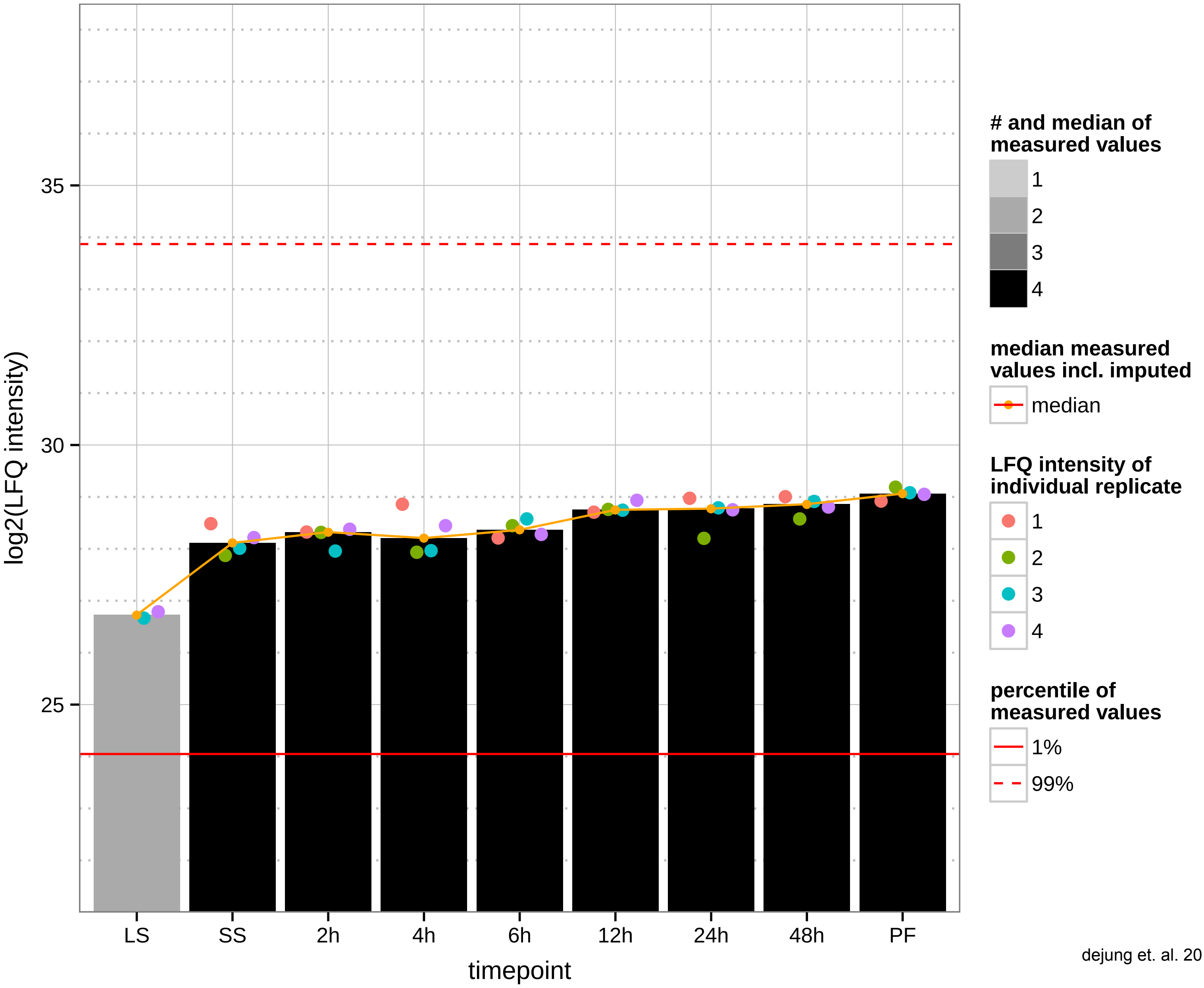
mitochondrial processing peptidase alpha subunit, putative, metallo–peptidase, Clan ME, Family M16
Tb927.2.4110
AGOF: catalytic activity, metalloendopeptidase activity, zinc ion binding
AGOC: mitochondrion
AGOP: proteolysis
PGOF: catalytic activity, metal ion binding, metalloendopeptidase activity, zinc ion binding
PGOC: null
PGOP: proteolysis





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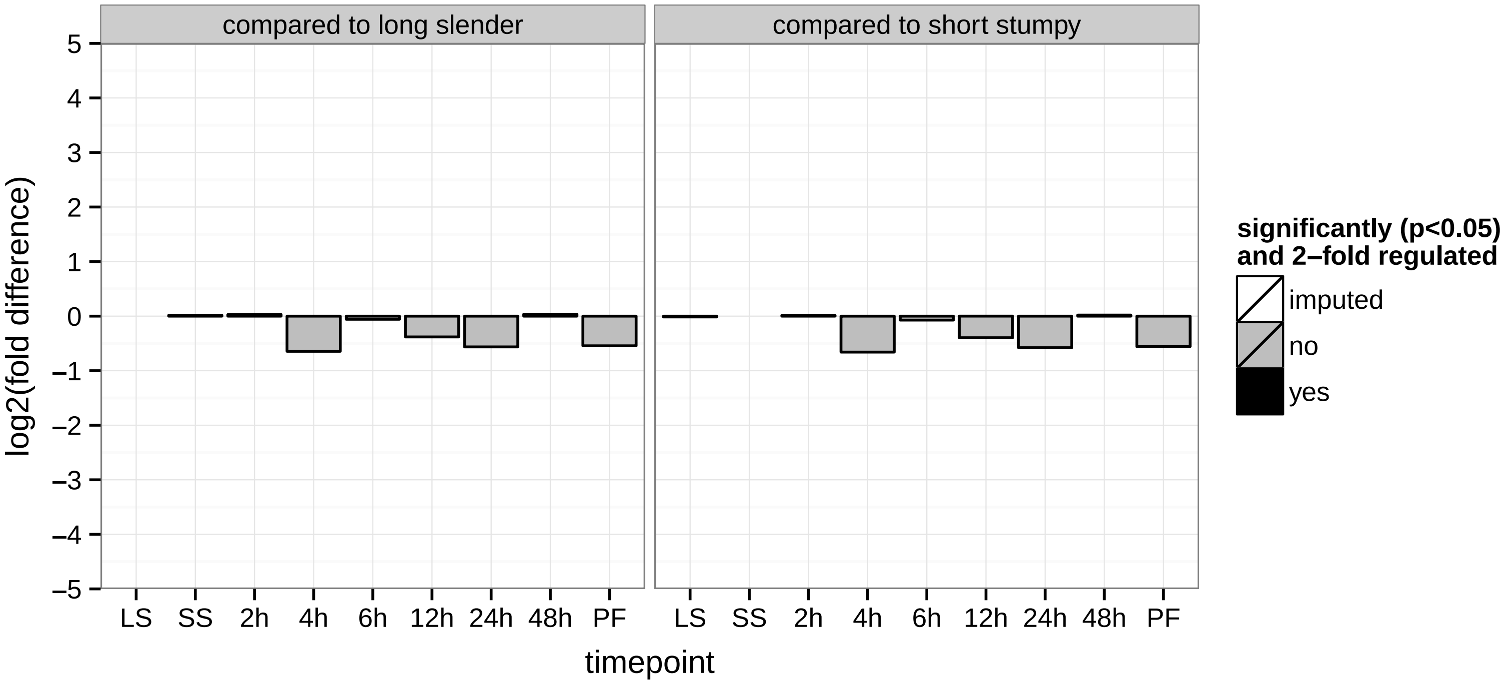
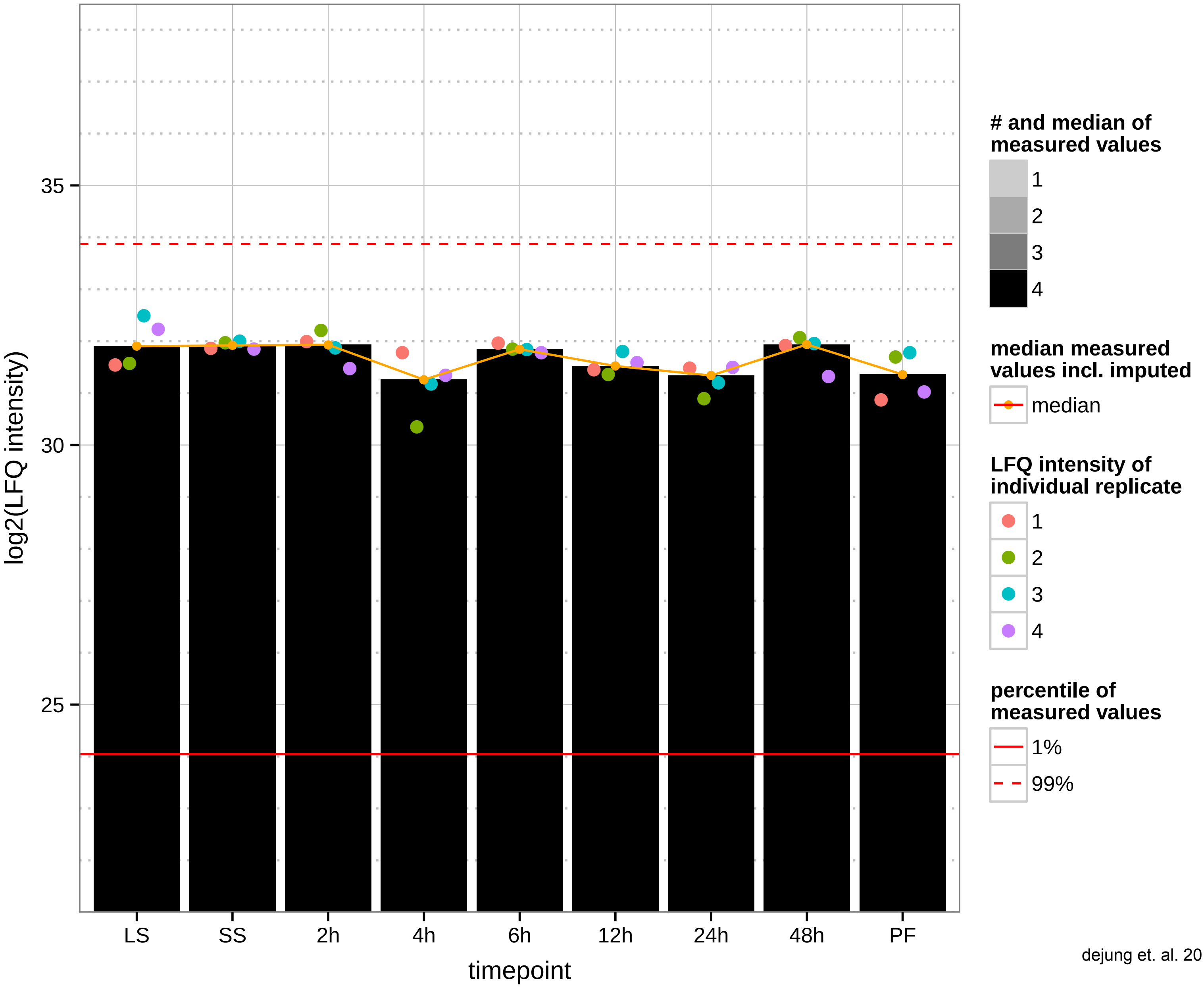
paraflagellar rod protein, putative, PFR5
Tb927.2.4330;Tb11.v5.0777
AGOF: null, calmodulin binding, structural molecule activity
AGOC: null, microtubule–based flagellum
AGOP: null, ciliary or flagellar motility
PGOF: calmodulin binding, protein binding
PGOC: microtubule–based flagellum
PGOP: null





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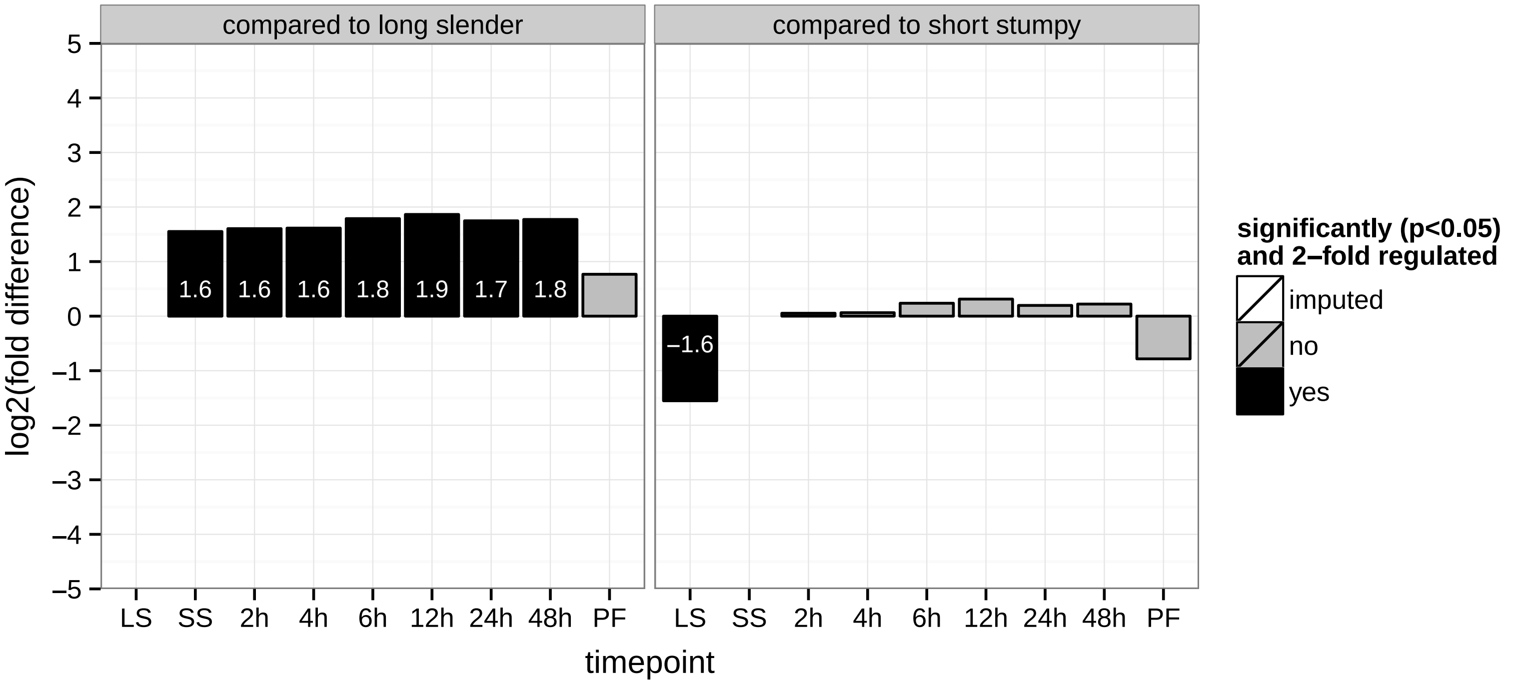
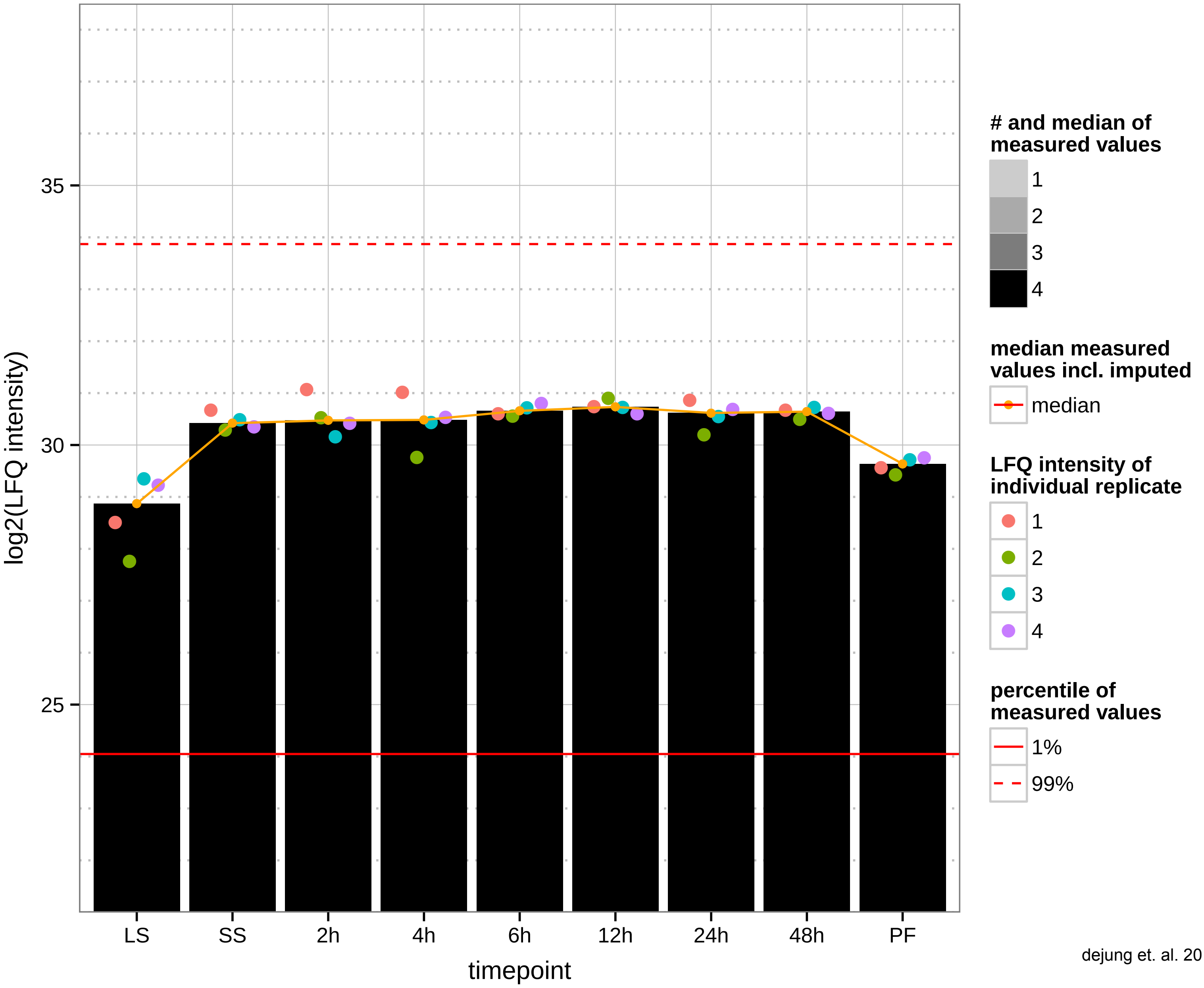
retrotransposon hot spot protein 4 (RHS4), putative
Tb927.2.450
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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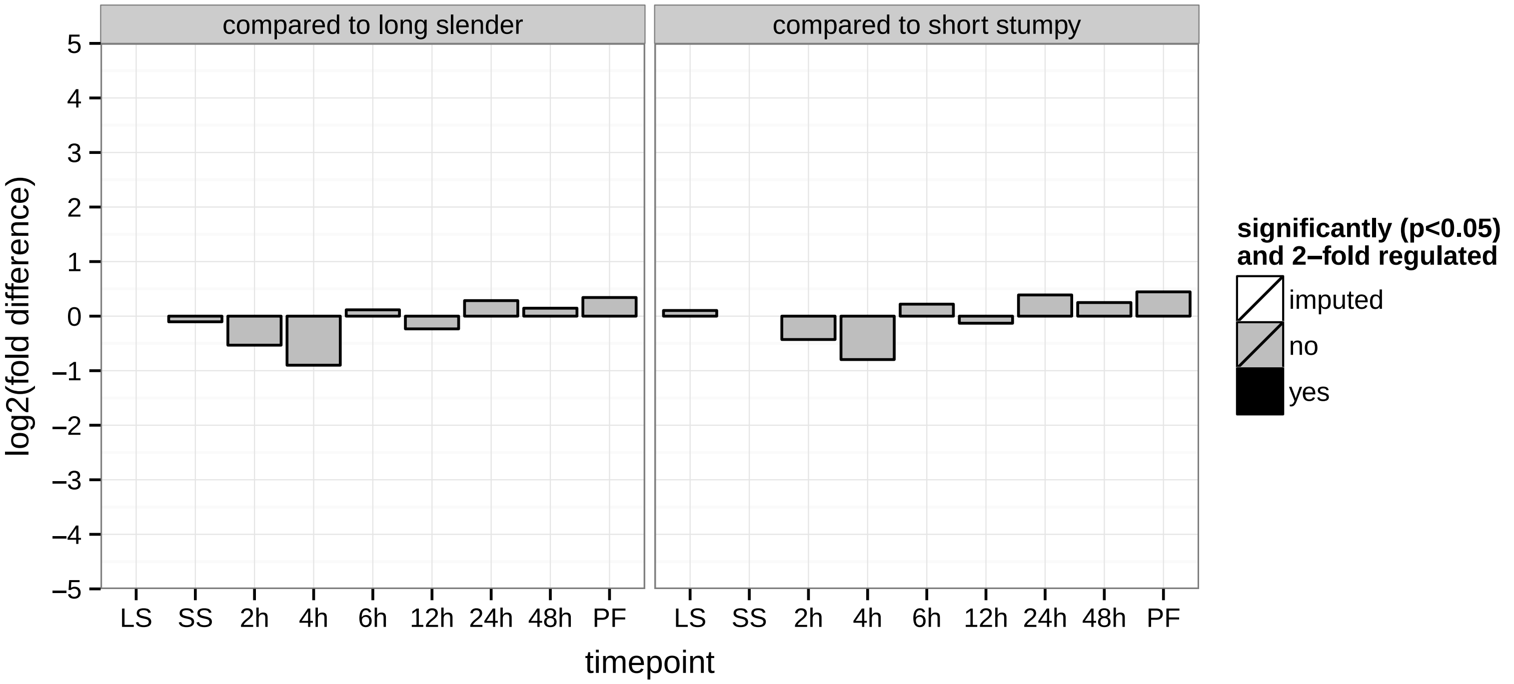
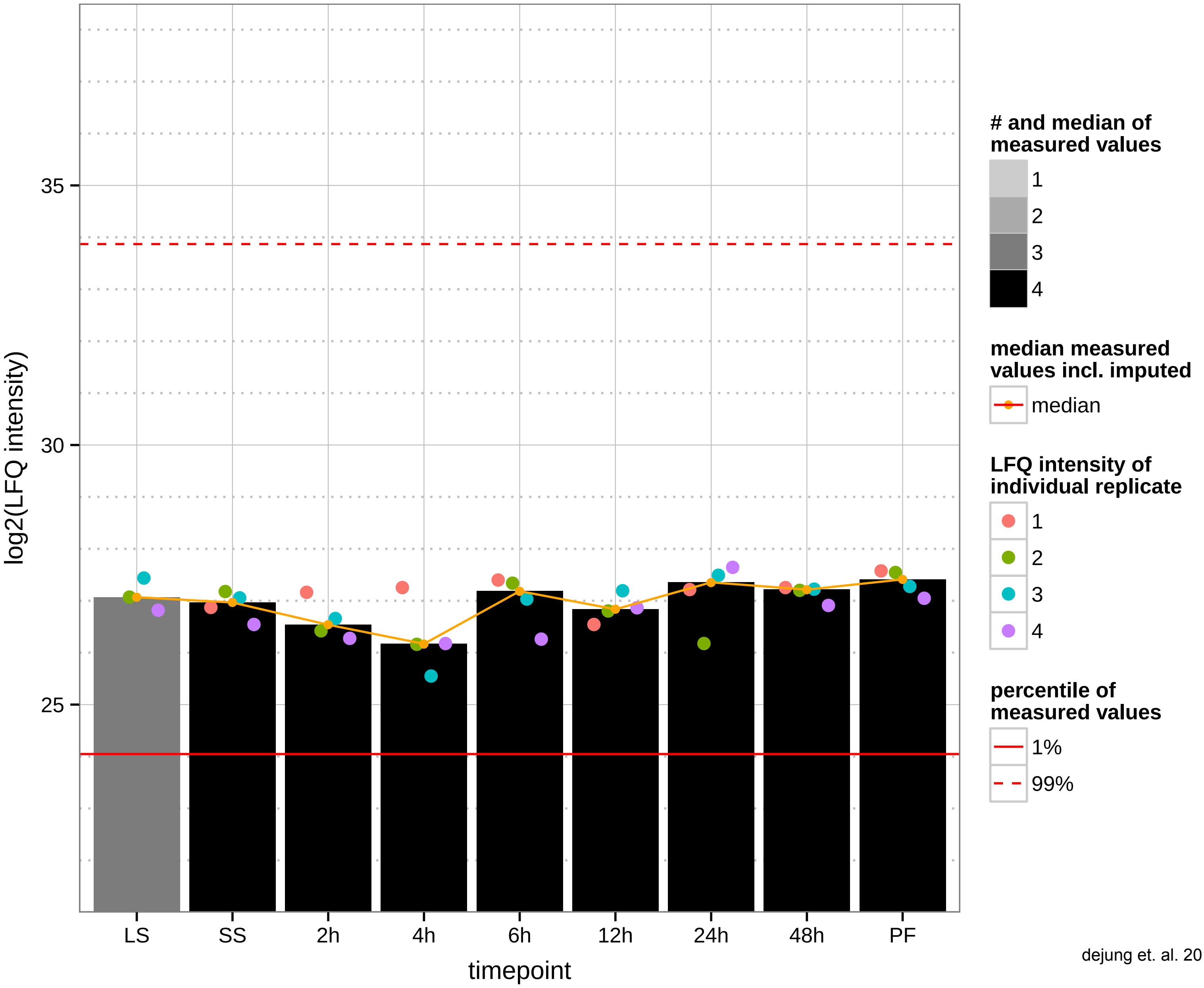
hypothetical protein, conserved
Tb927.2.4520
AGOF: catalytic activity
AGOC: null
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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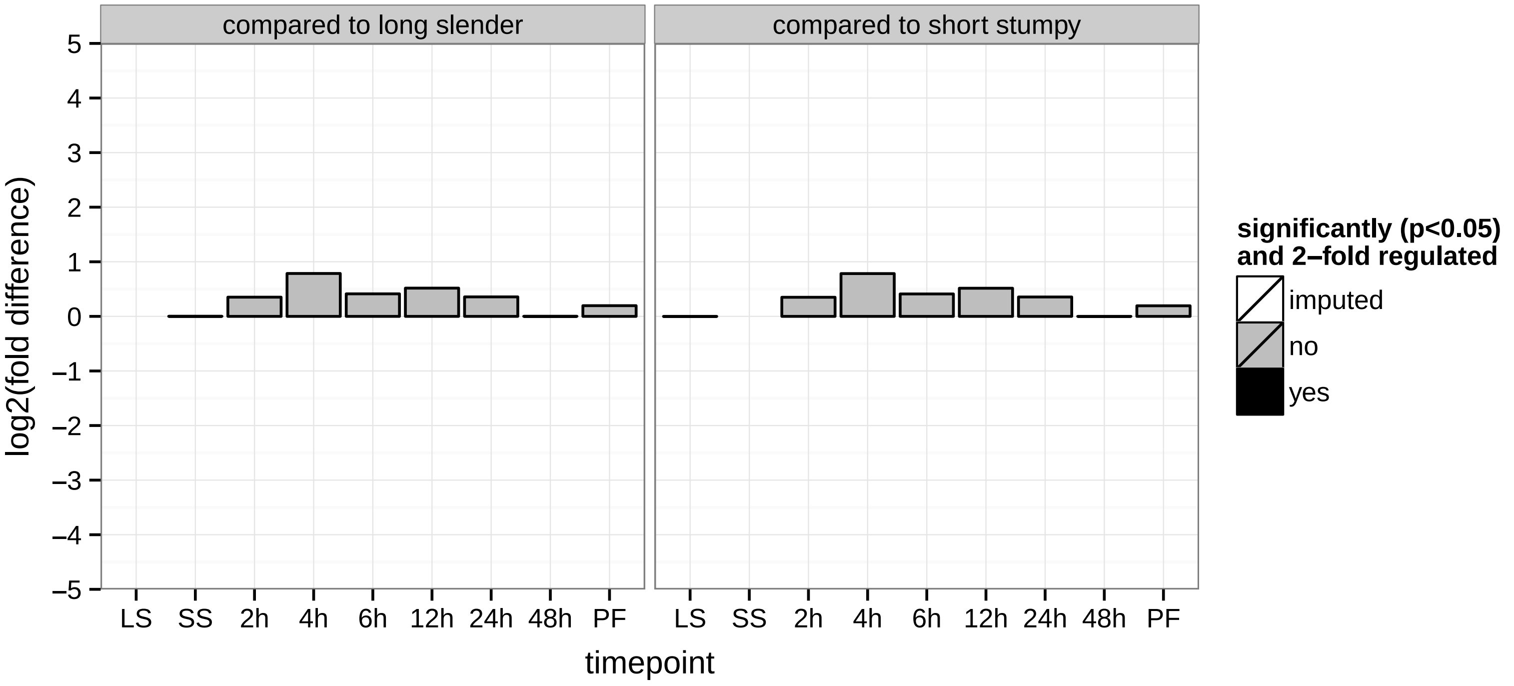
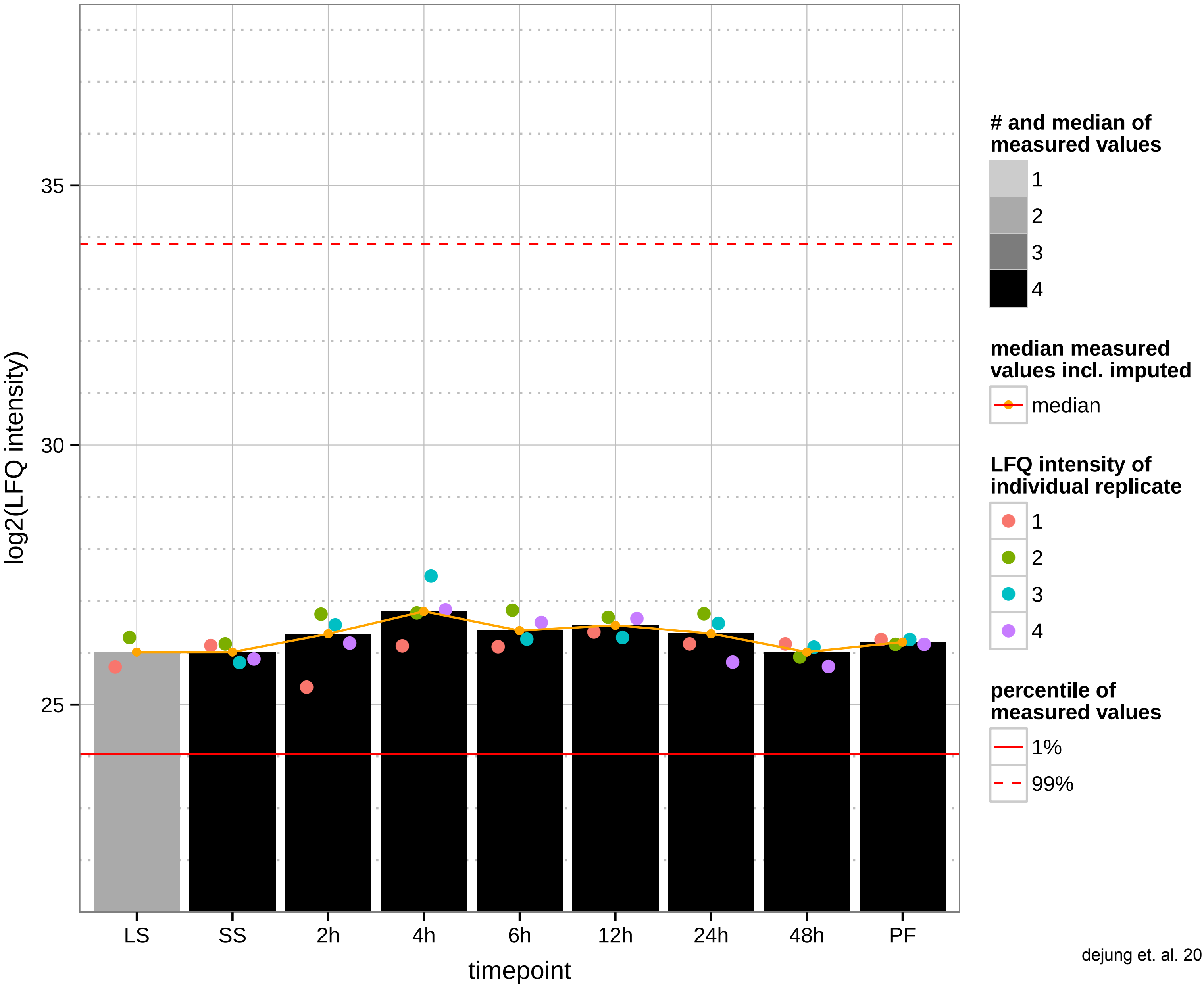
hypothetical protein, conserved
Tb927.2.4530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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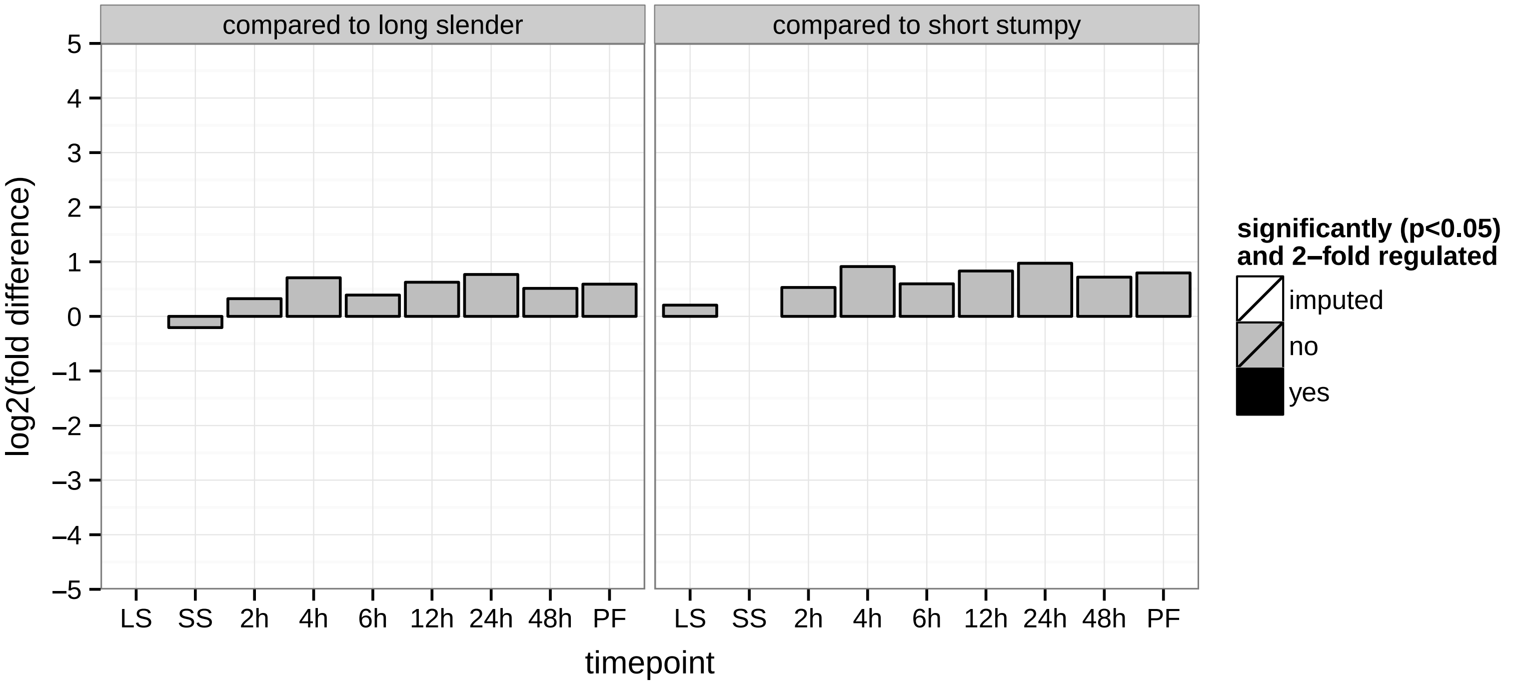
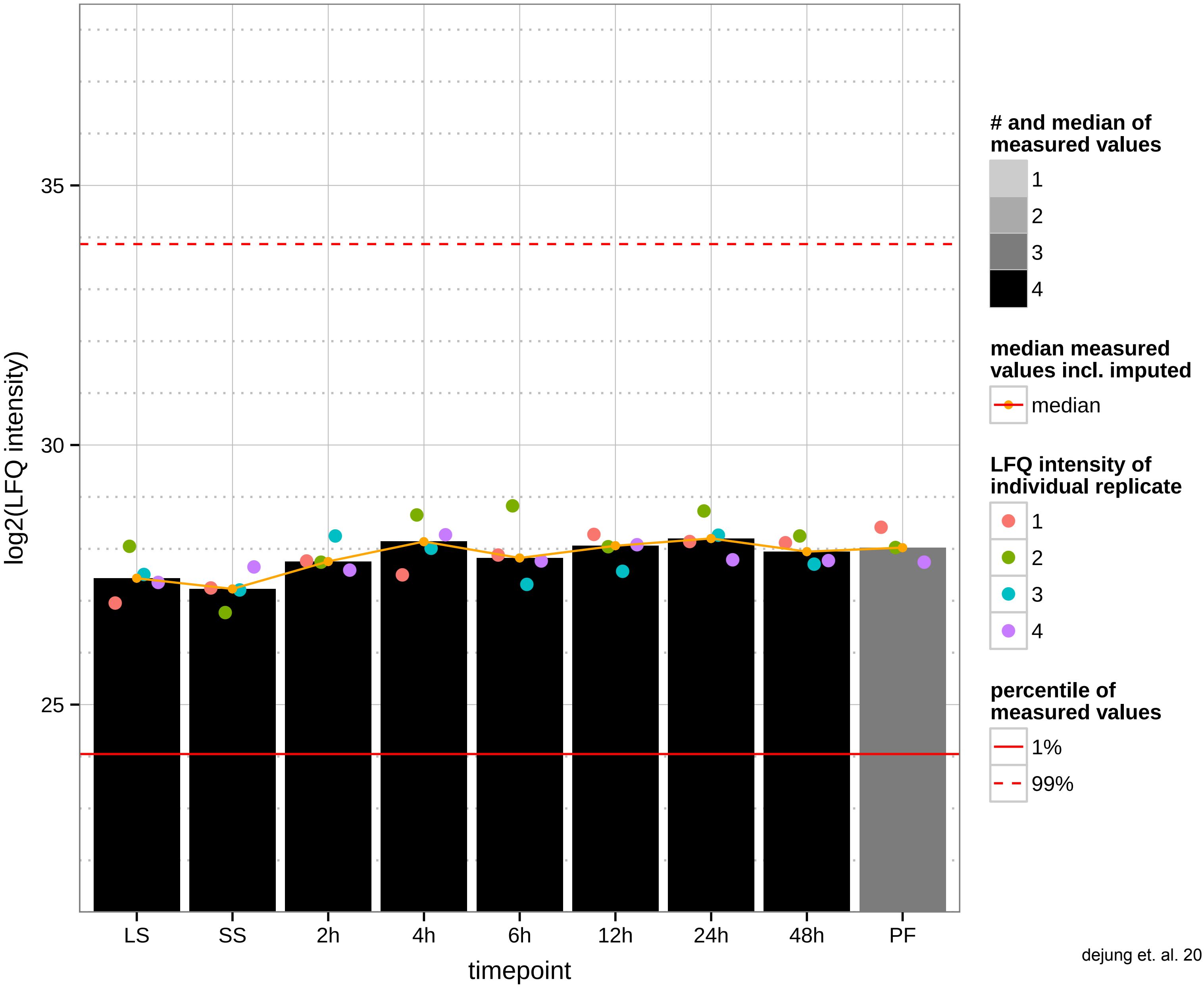
Small nuclear ribonucleoprotein–associated protein B (snRNP–B) (Sm protein B) (Sm–B) (SmB), putative (TbSmB)
Tb927.2.4540
AGOF: null
AGOC: nucleus, small nucleolar ribonucleoprotein complex
AGOP: RNA splicing, RNA splicing, via transesterification reactions
PGOF: null
PGOC: null
PGOP: null





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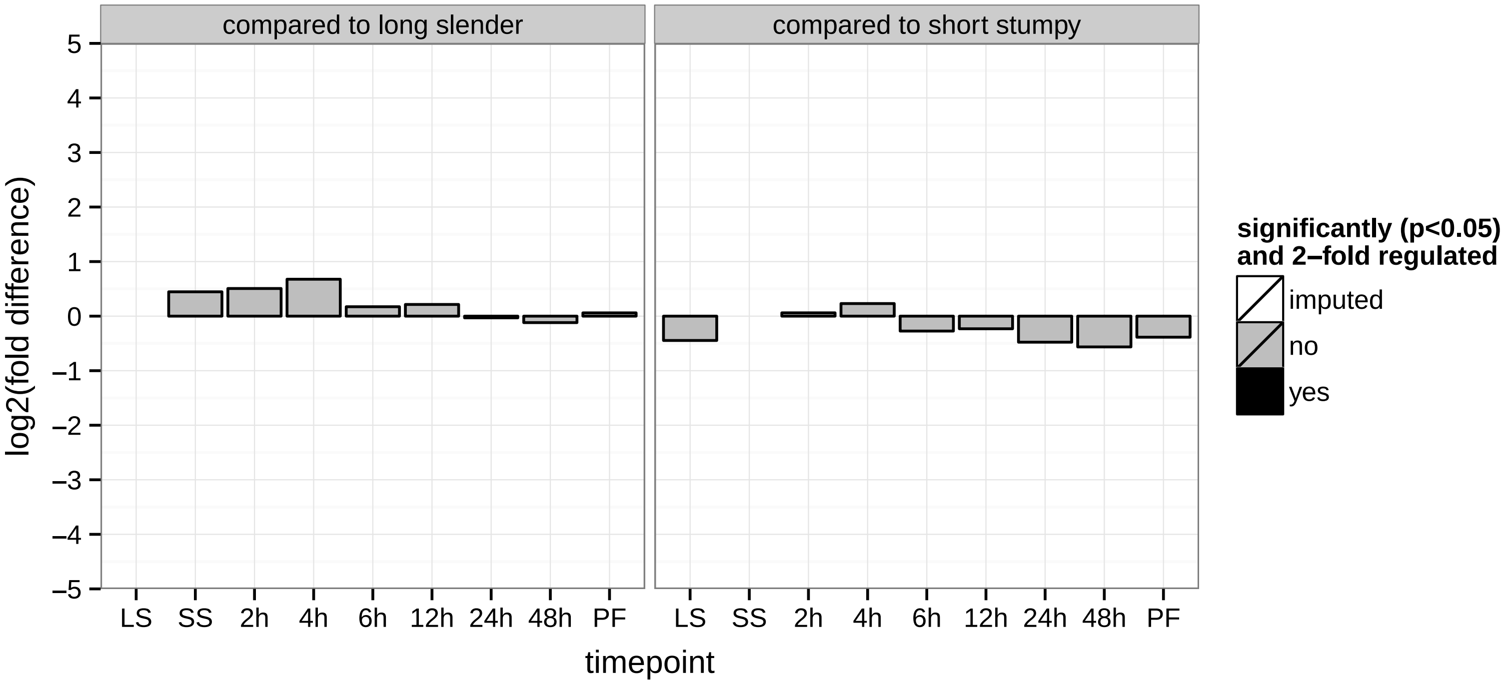
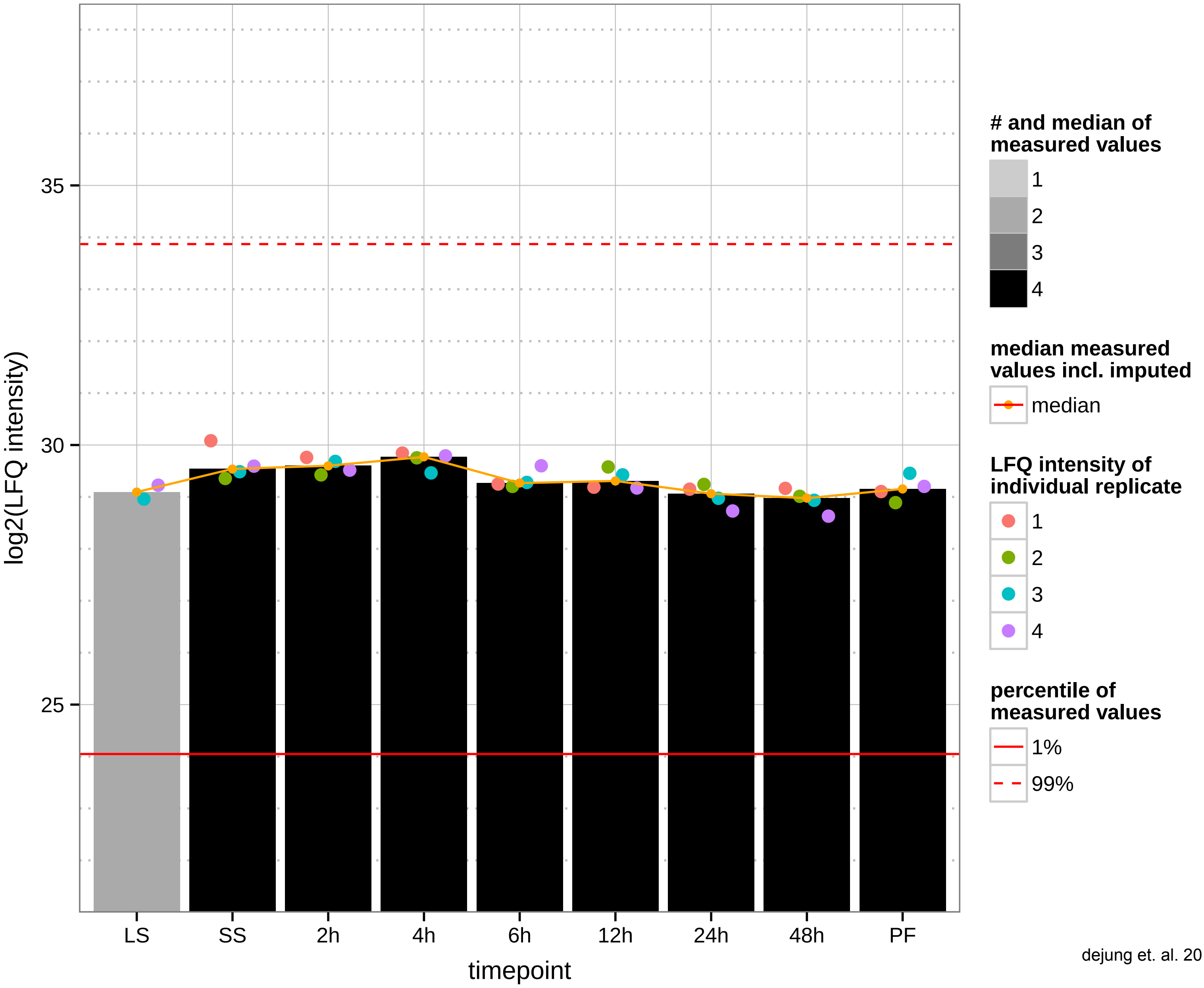
UNC119 (unc119)
Tb927.2.4580
AGOF: null
AGOC: cilium
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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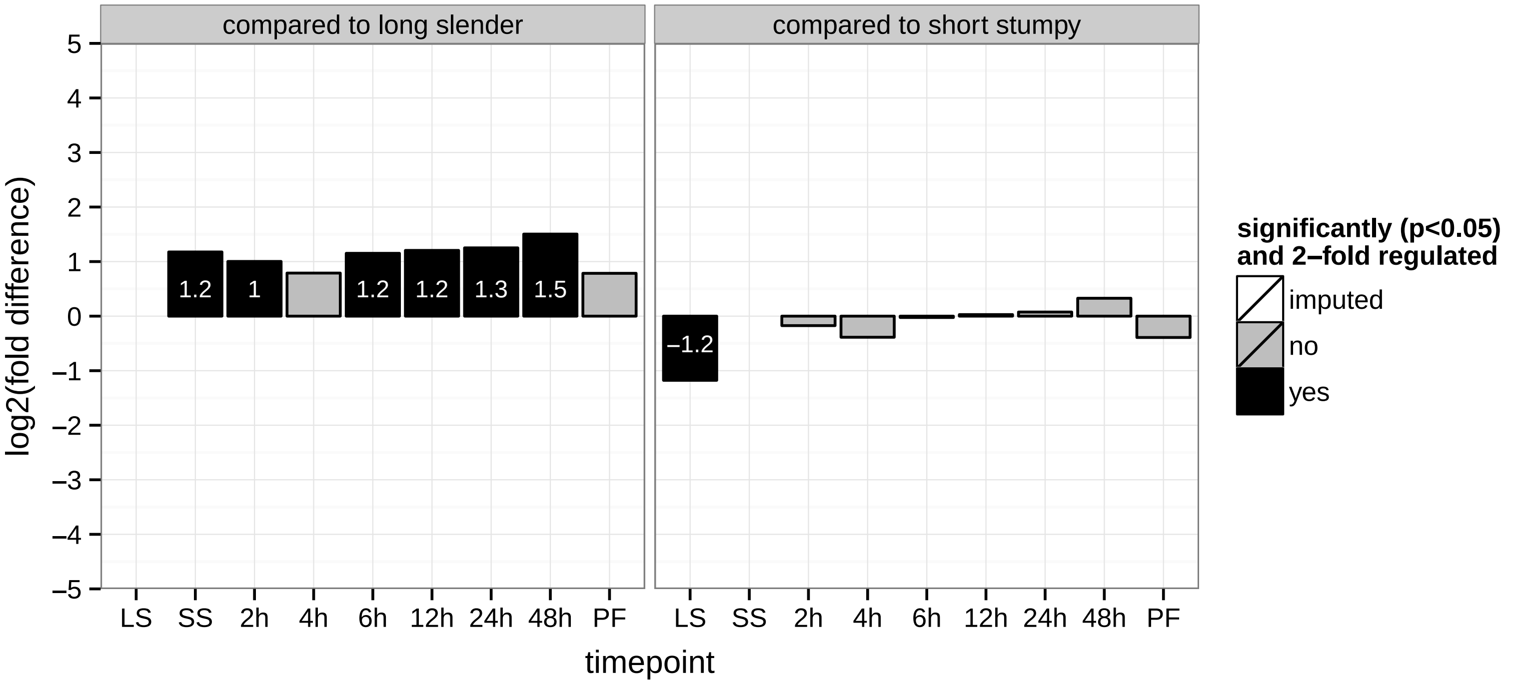
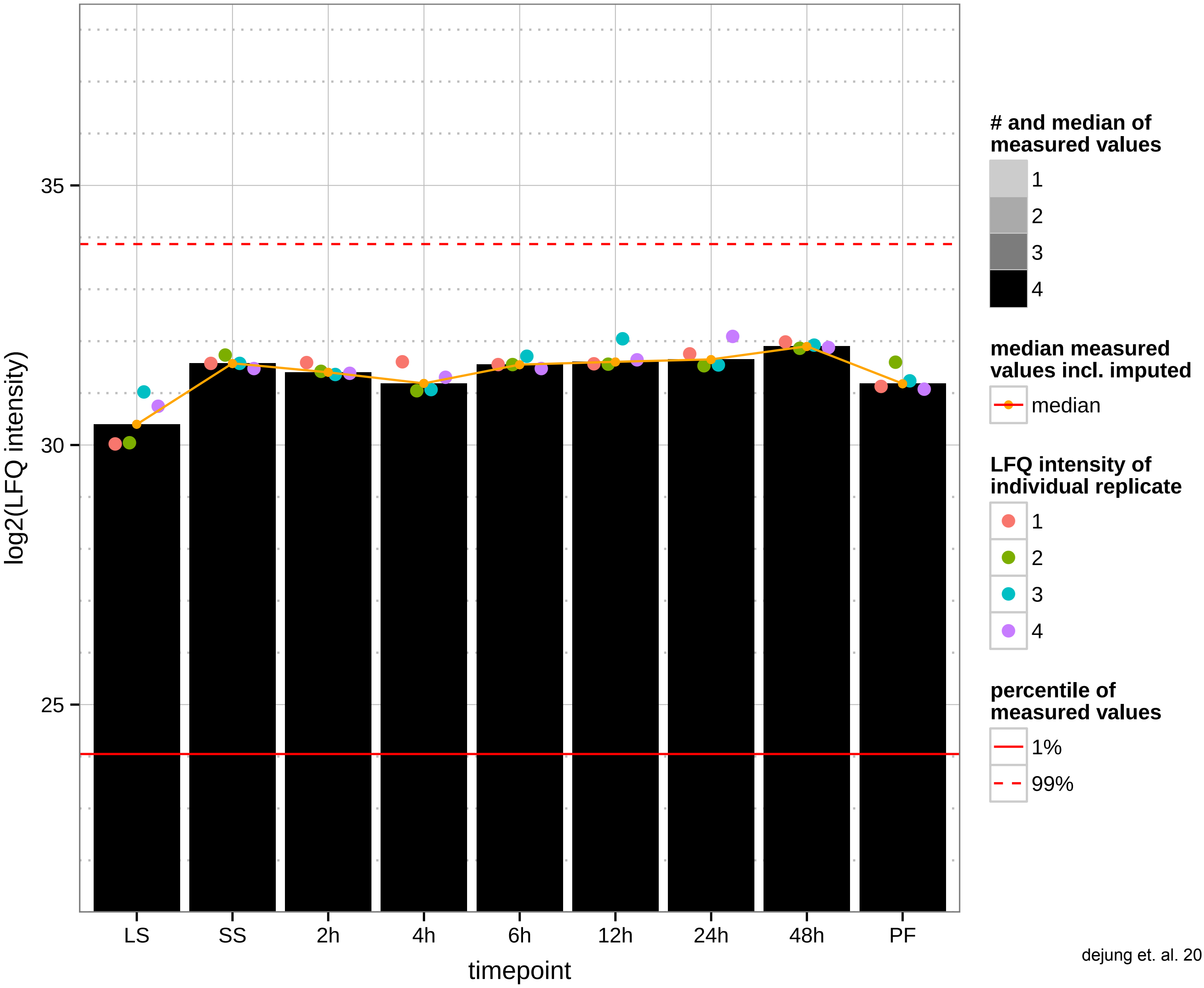
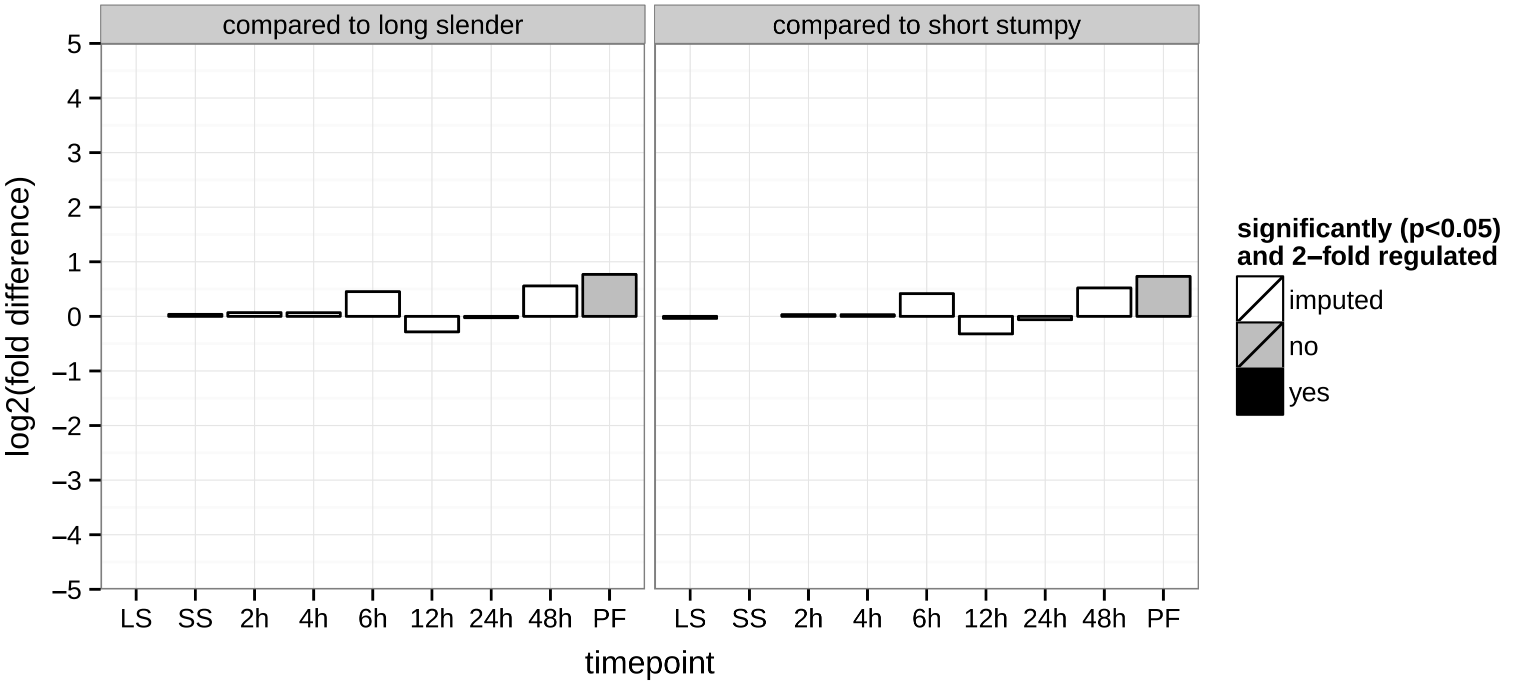
RNA–binding protein, putative (TRRM1)
Tb927.2.4710
AGOF: molecular_function, nucleic acid binding, zinc ion binding
AGOC: nuclear speck
AGOP: RNA processing
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null

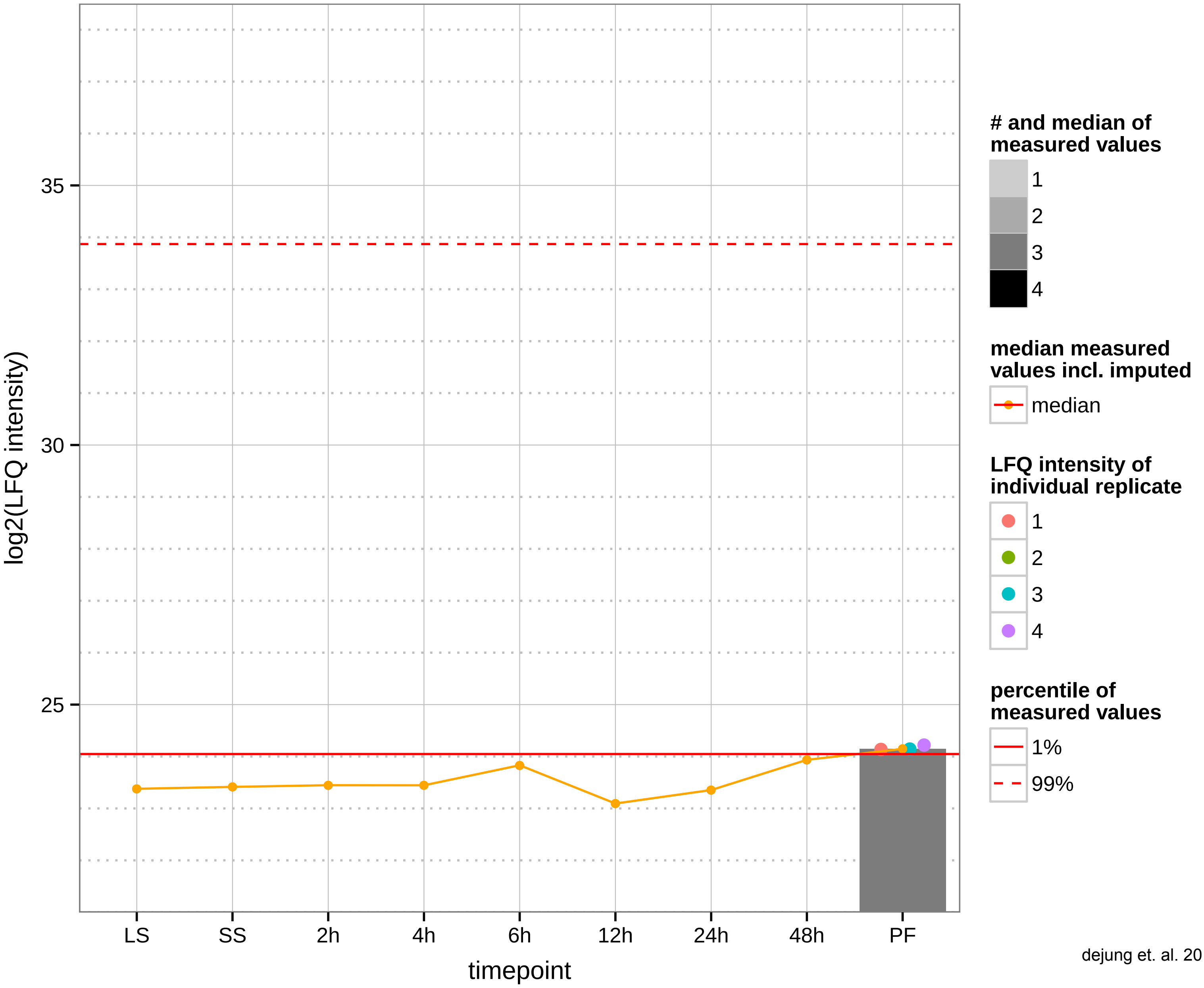




dejung et. al. 2015

hypothetical protein, conserved
Tb927.2.4800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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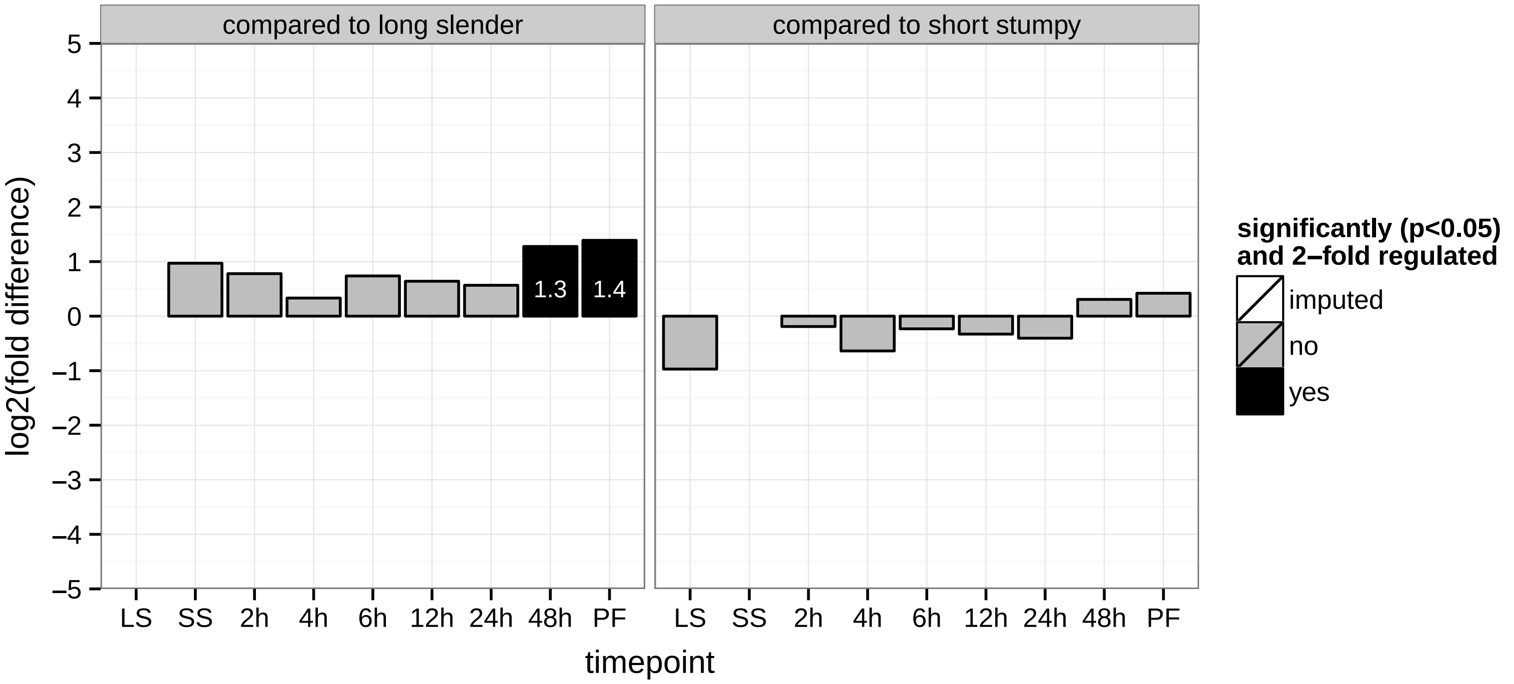
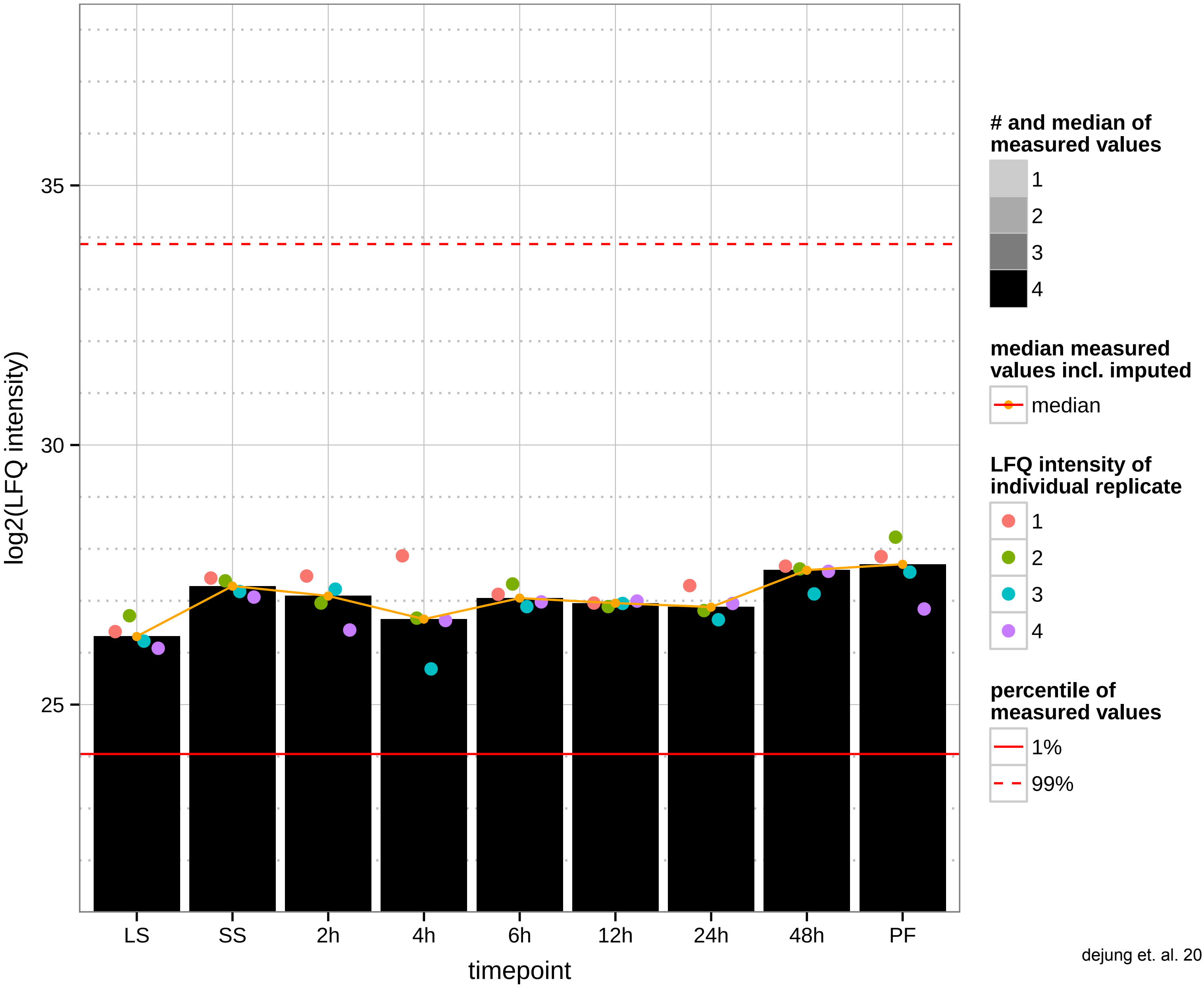
hypothetical protein, conserved
Tb927.2.4810
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null





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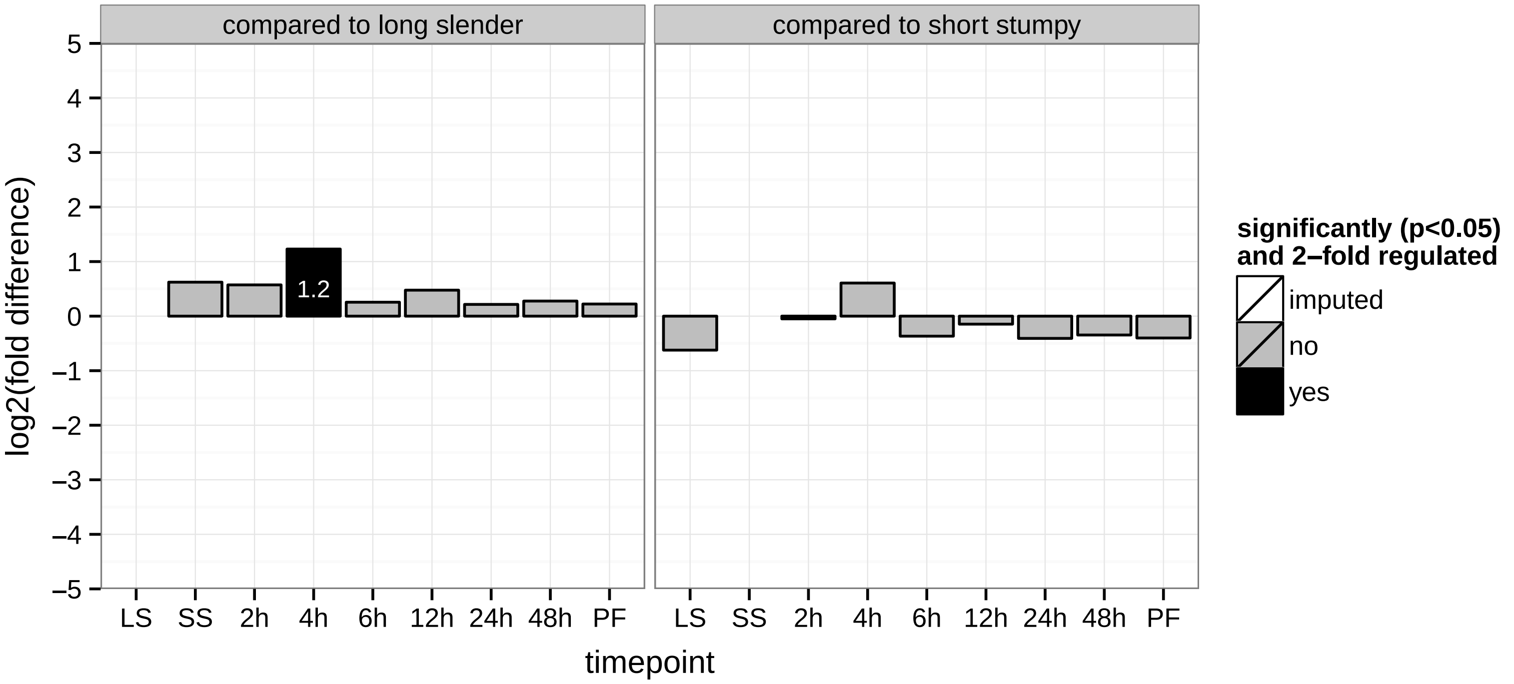
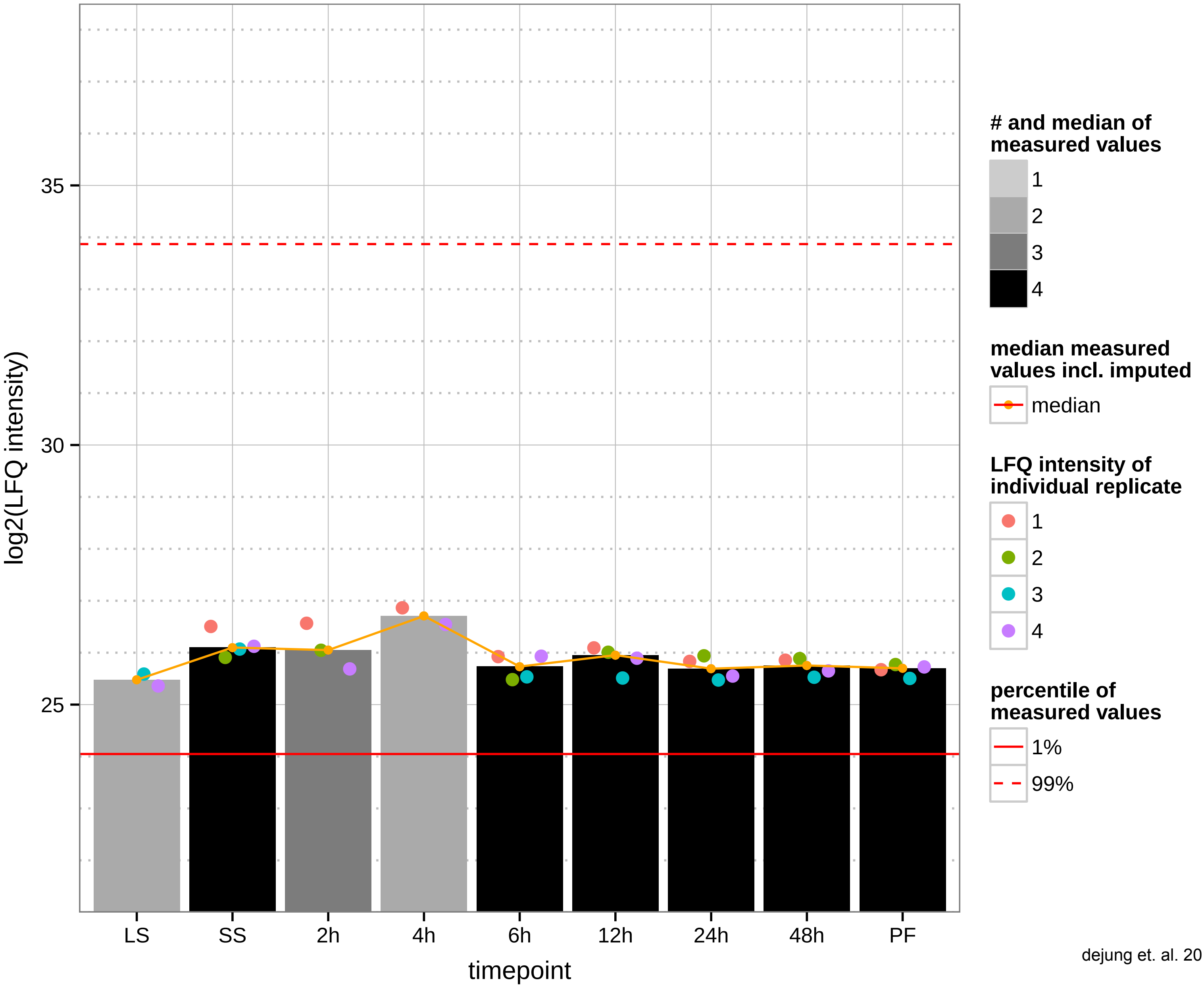
kinetoplastid–specific dual specificity phosphatase, putative
Tb927.2.4870
AGOF: protein tyrosine/serine/threonine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: phosphatase activity, protein tyrosine/serine/threonine phosphatase activity
PGOC: null
PGOP: dephosphorylation, protein dephosphorylation





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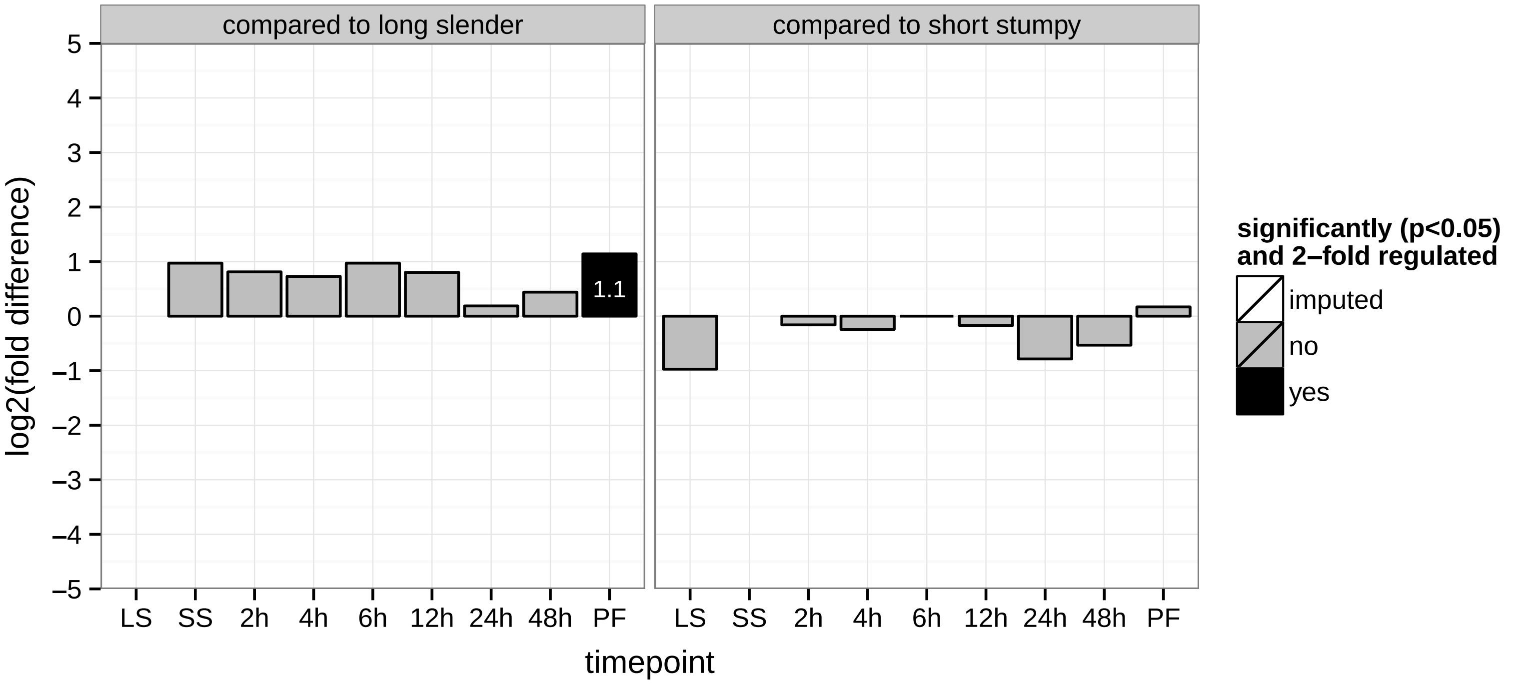
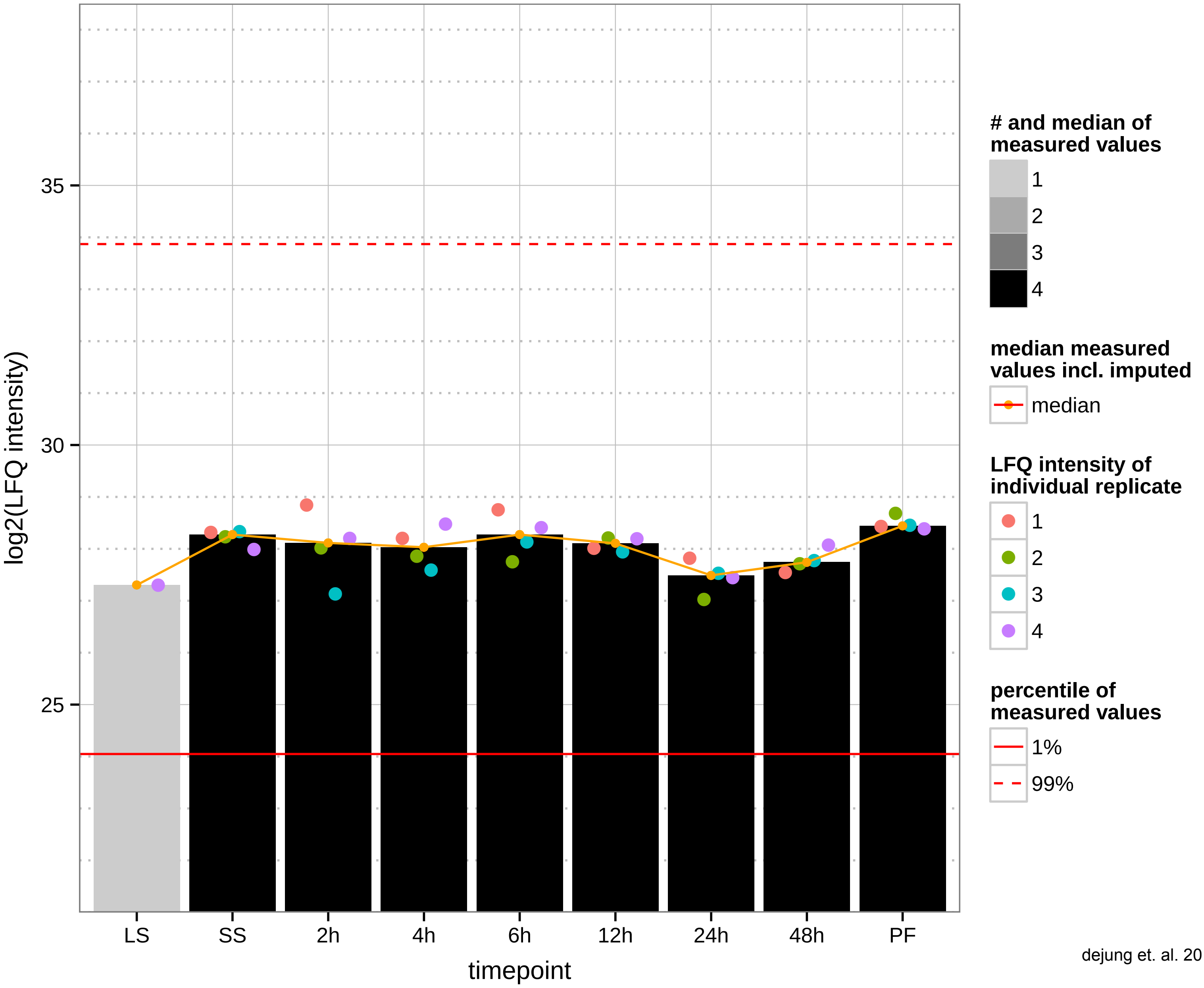
esterase, putative
Tb927.2.4930
AGOF: catalytic activity, hydrolase activity, acting on ester bonds
AGOC: null
AGOP: lipid metabolic process
PGOF: null
PGOC: null
PGOP: null





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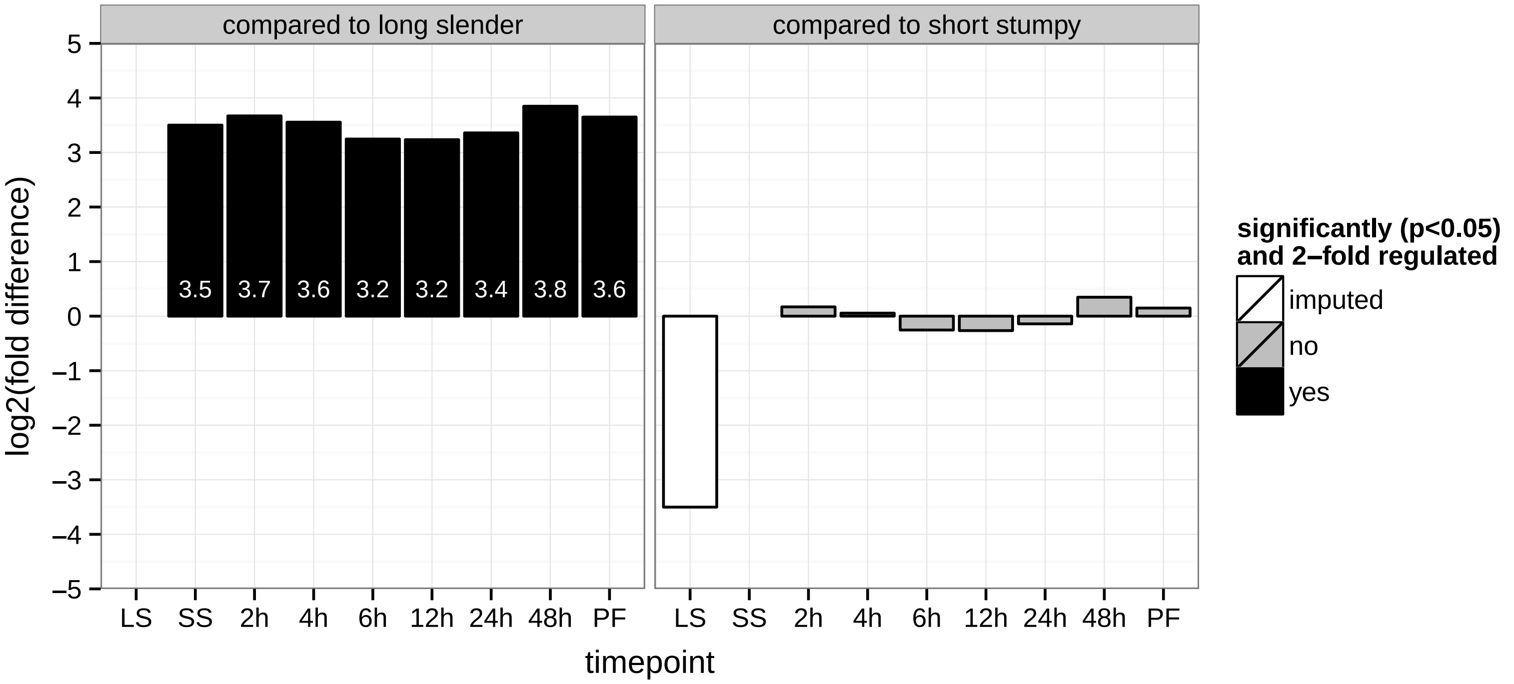
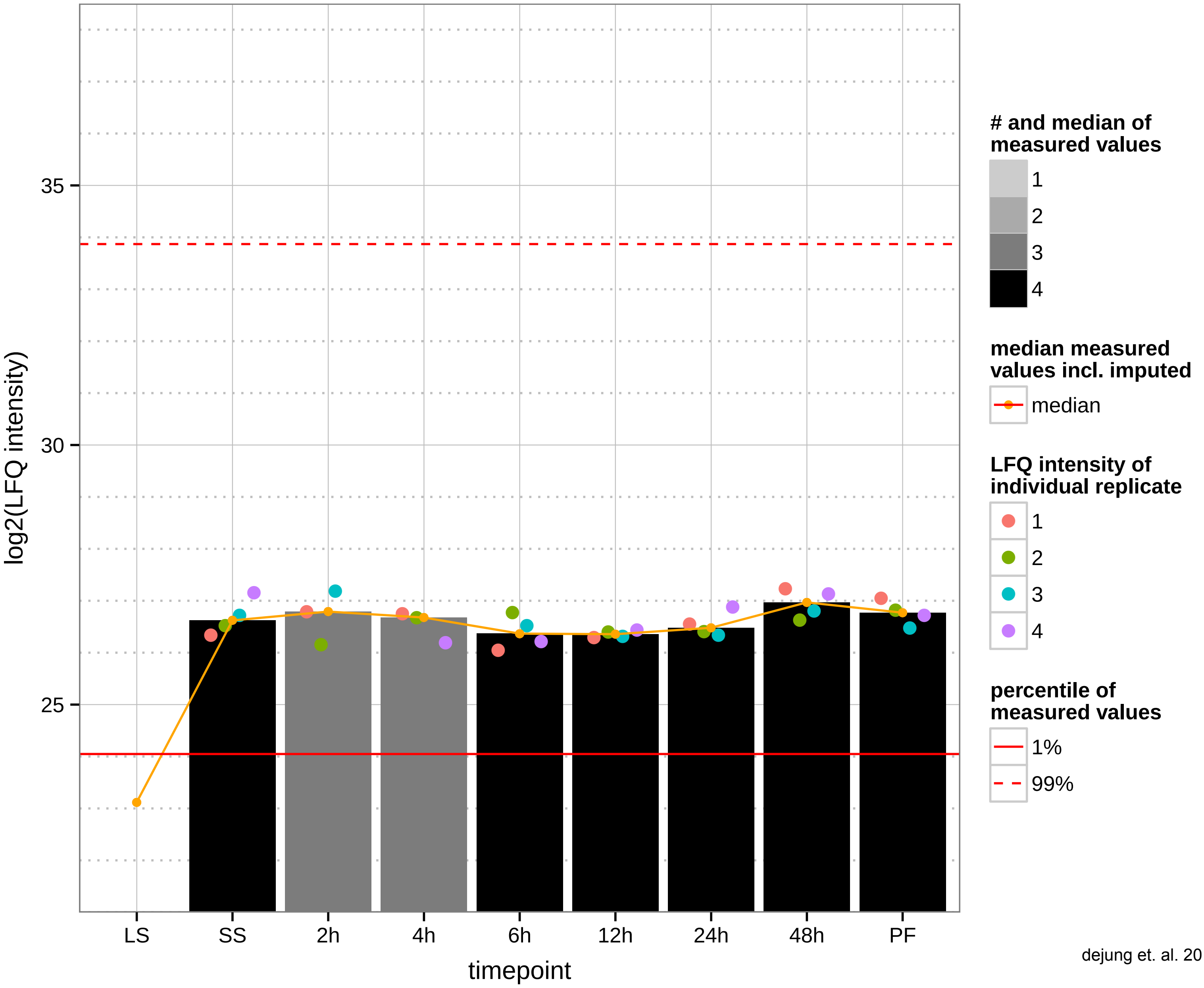
transcription initiation protein, putative
Tb927.2.5030
AGOF: structural constituent of ribosome
AGOC: ribosome
AGOP: regulation of transcription, DNA–dependent
PGOF: null
PGOC: null
PGOP: null





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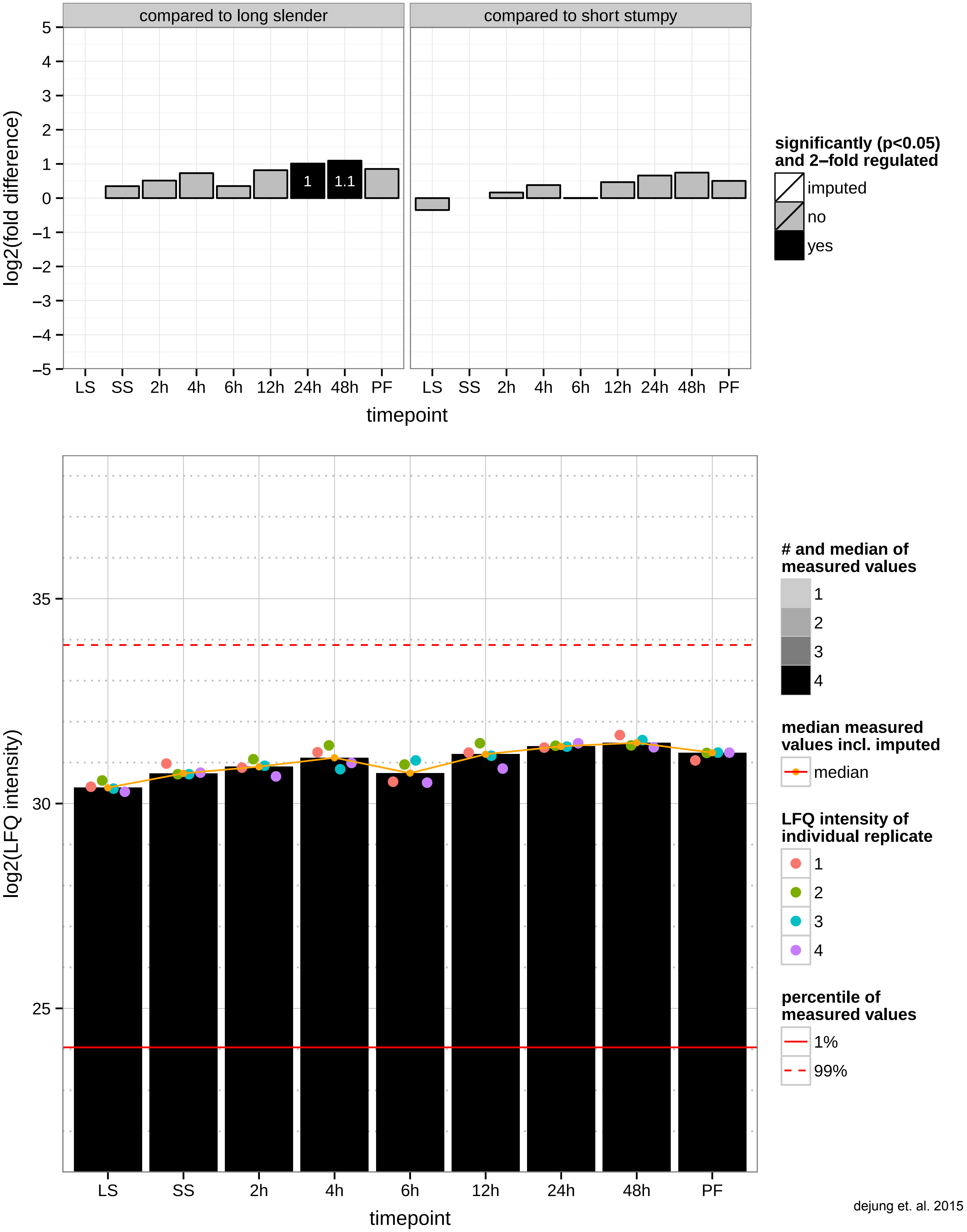
GTP binding protein, putative
Tb927.2.5060
AGOF: GTP binding
AGOC: intracellular
AGOP: null
PGOF: GTP binding
PGOC: null
PGOP: null



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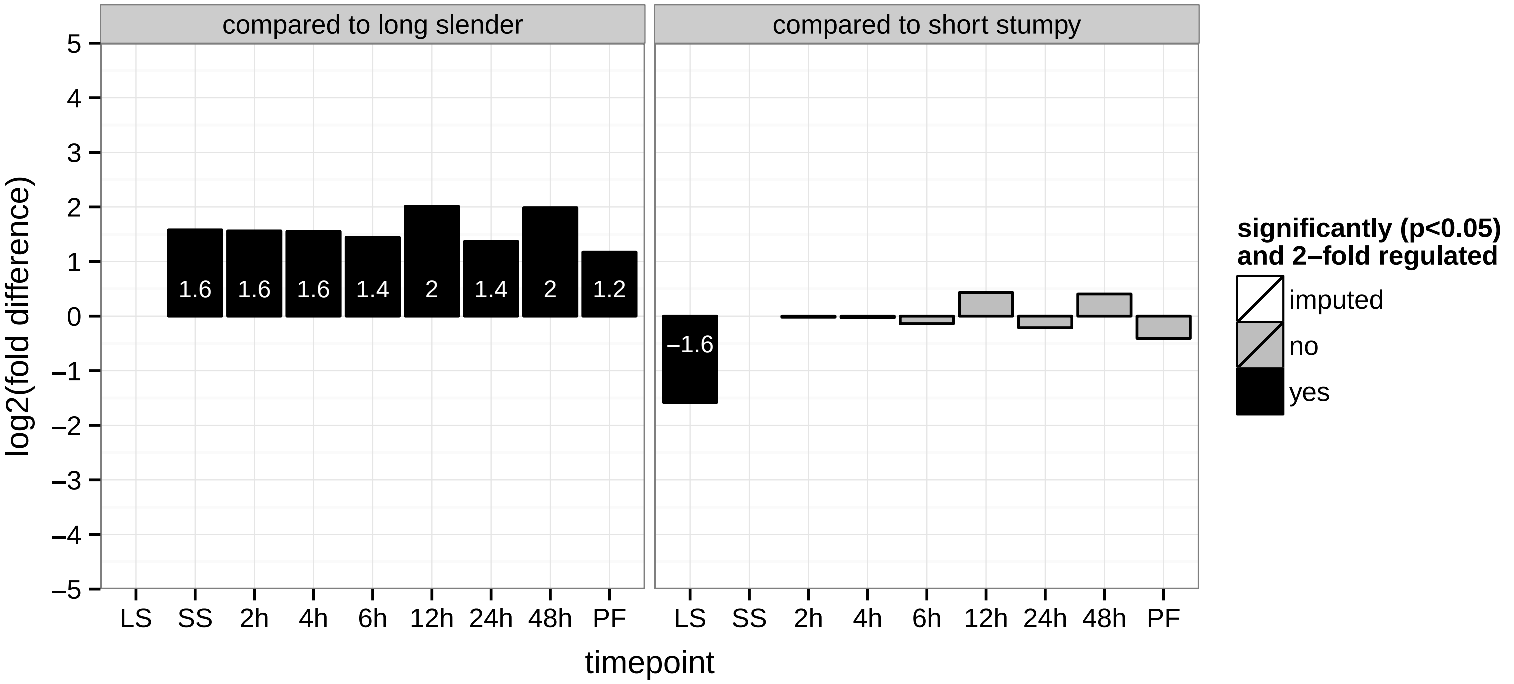
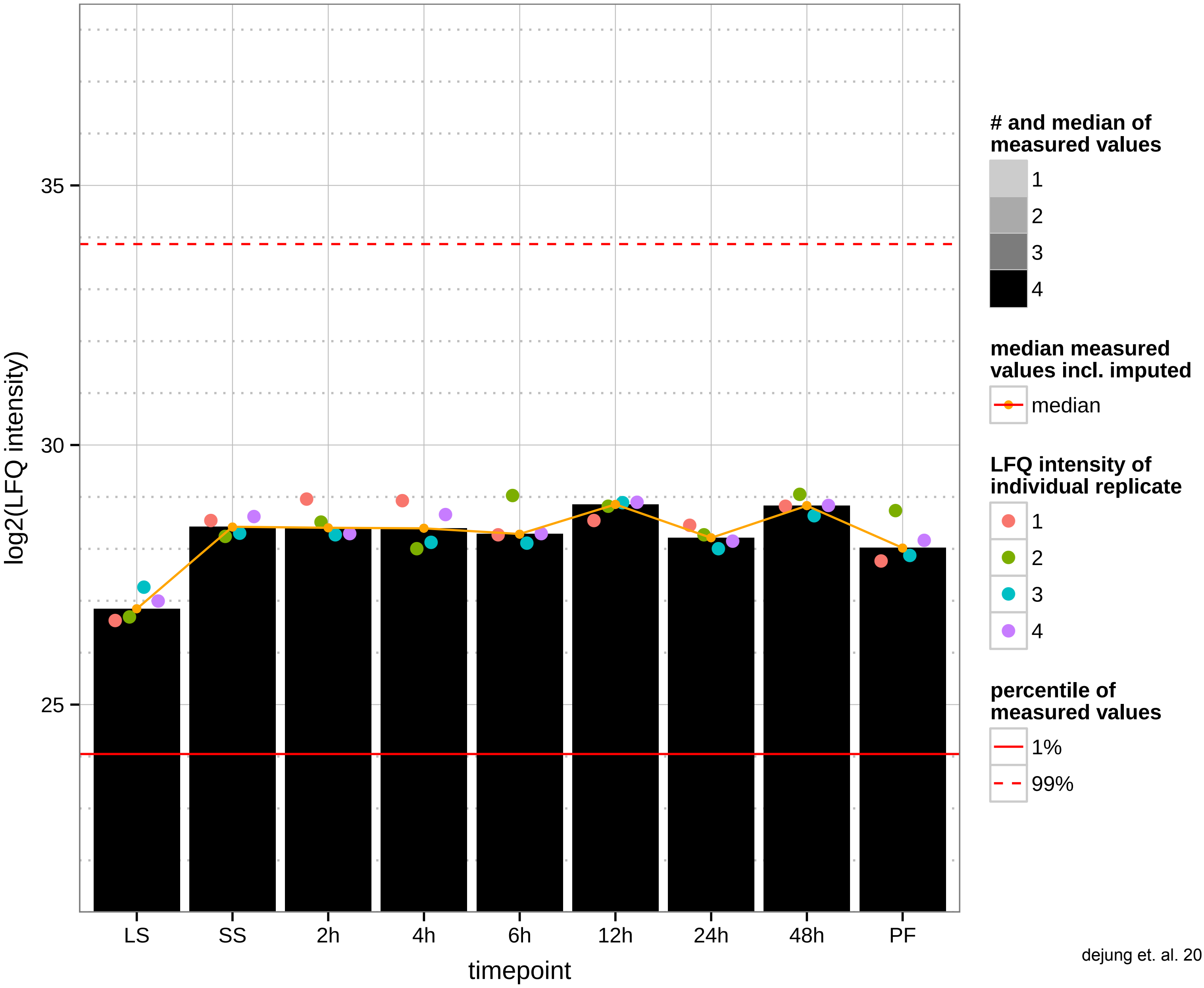
retrotransposon hot spot (RHS) protein, putative, retrotransposon hot spot protein 4 (RHS4)
Tb927.2.510
AGOF: null
AGOC: null, nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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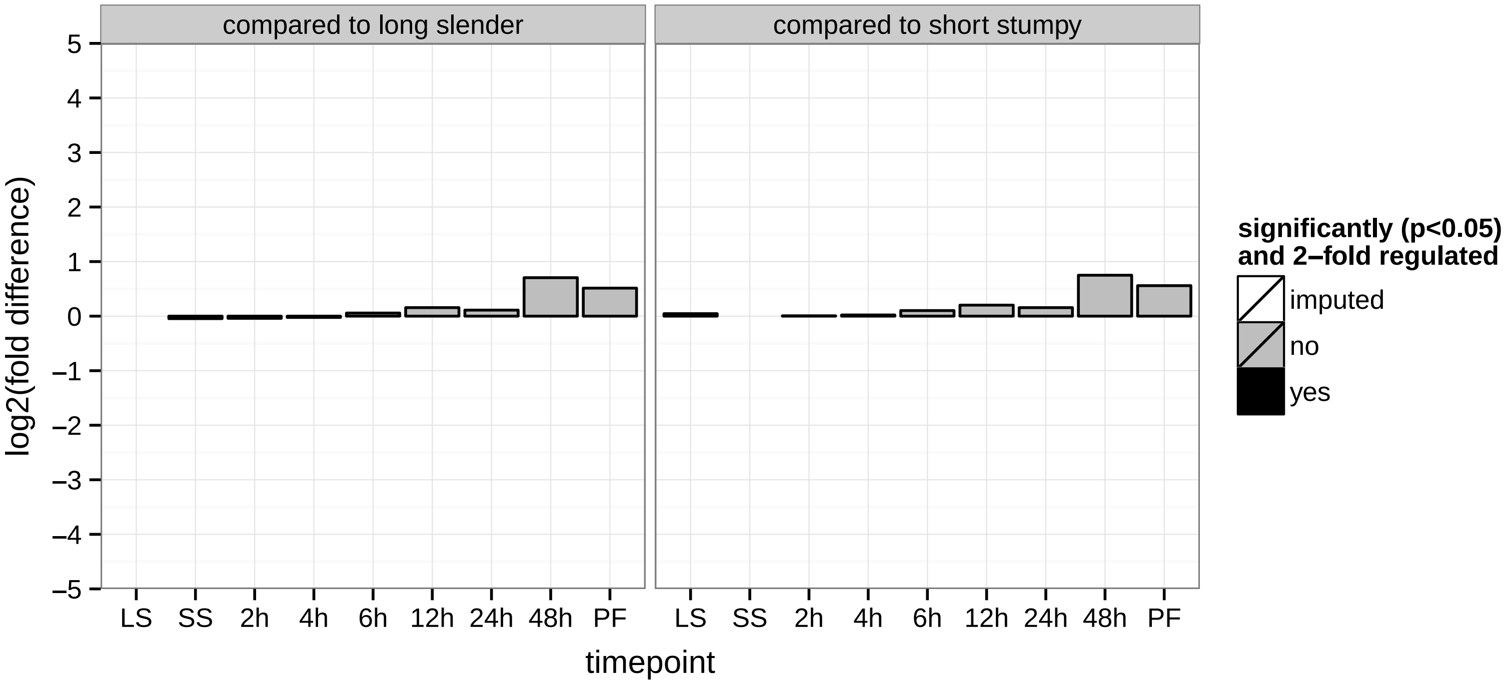
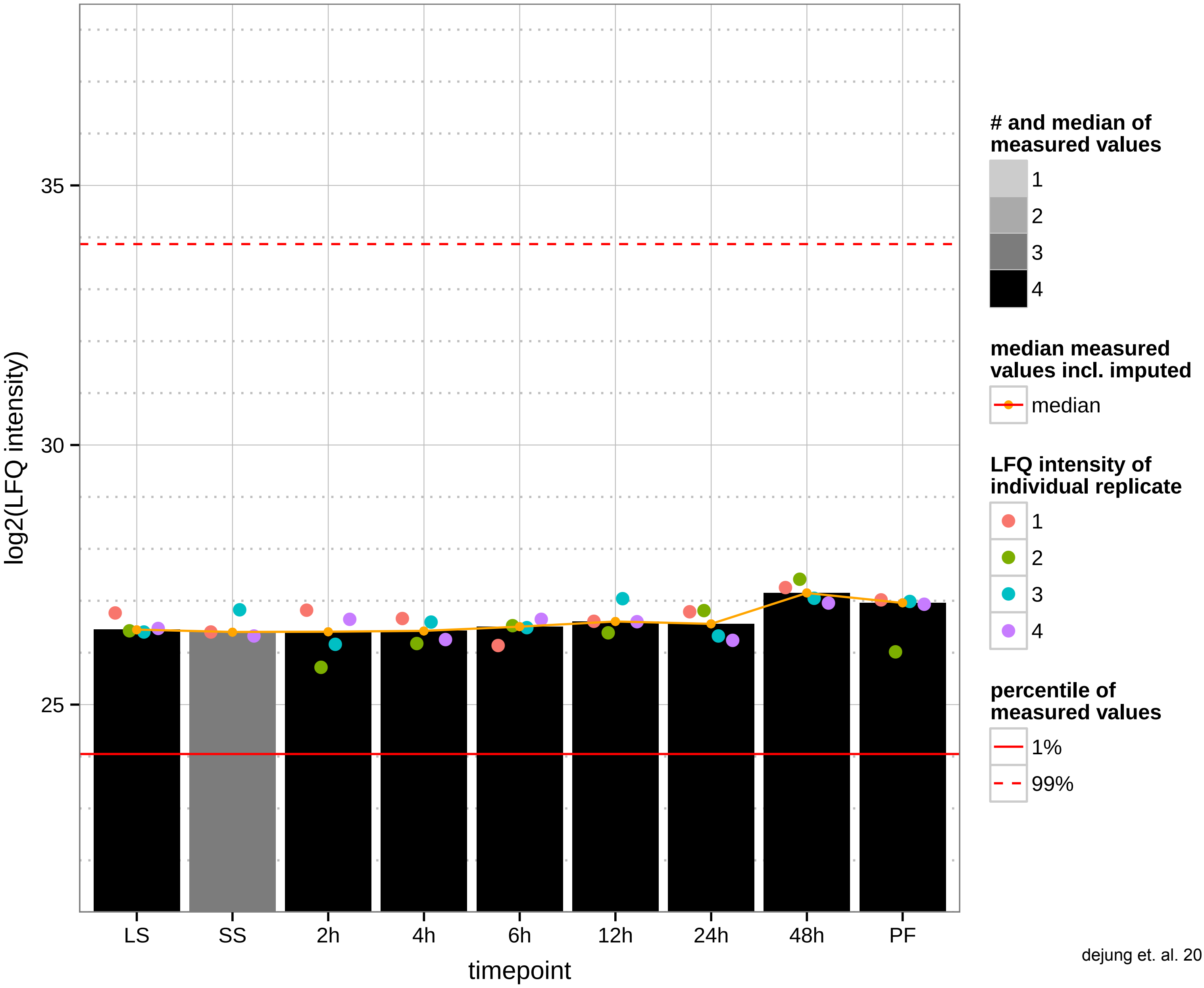
TPR–repeat protein, putative
Tb927.2.5150
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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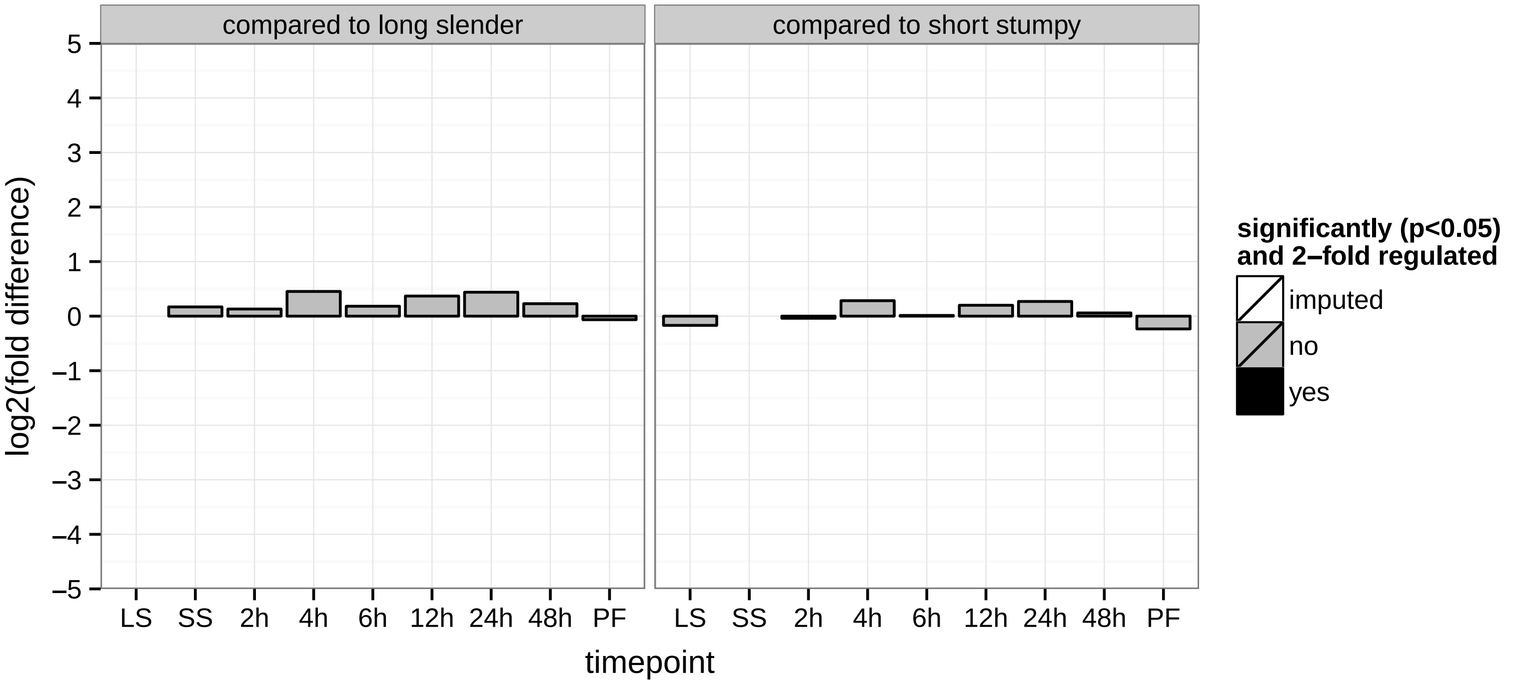
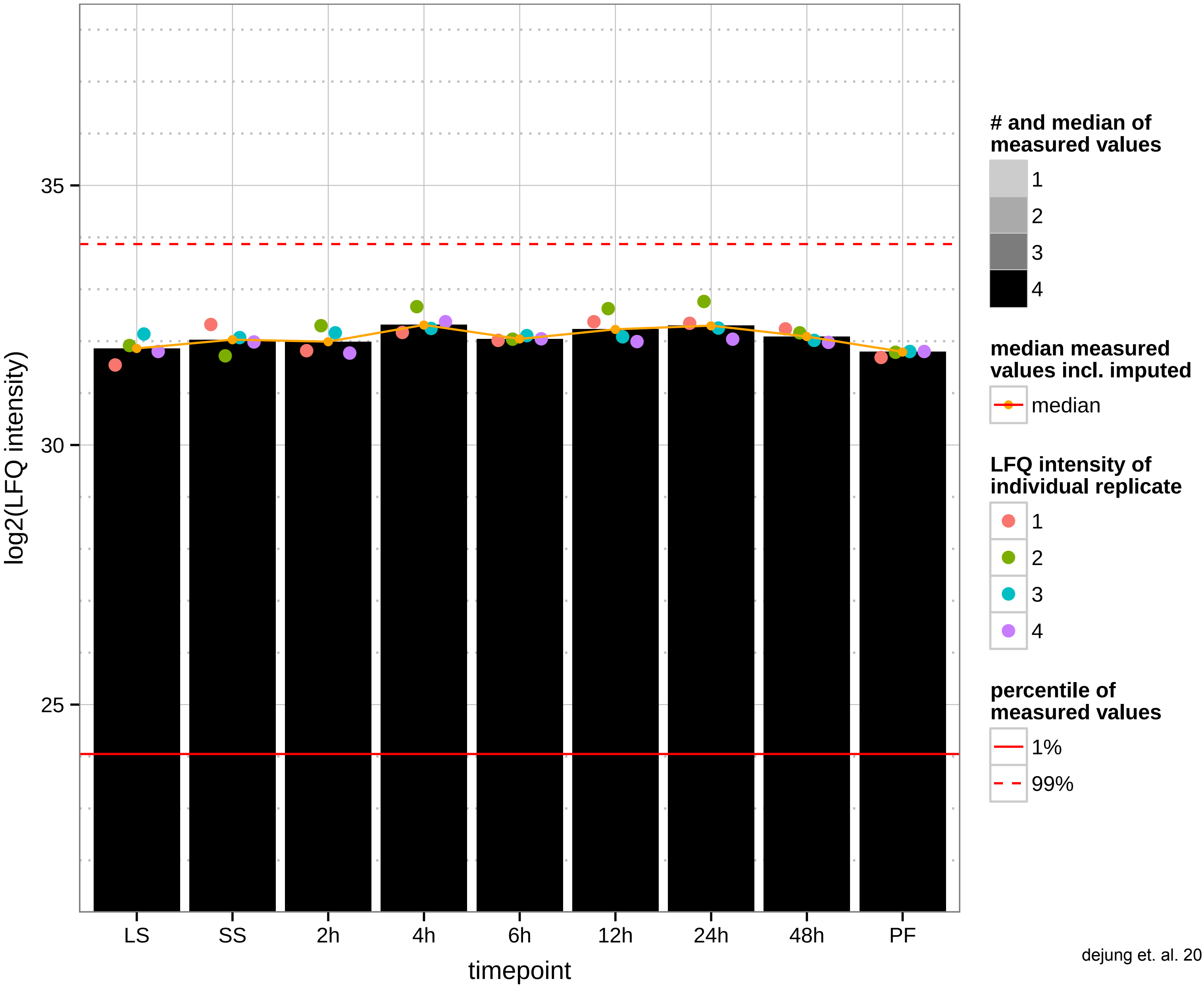
chaperone protein DNAj, putative
Tb927.2.5160
AGOF: chaperone binding, heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding, unfolded protein binding
PGOC: null
PGOP: protein folding





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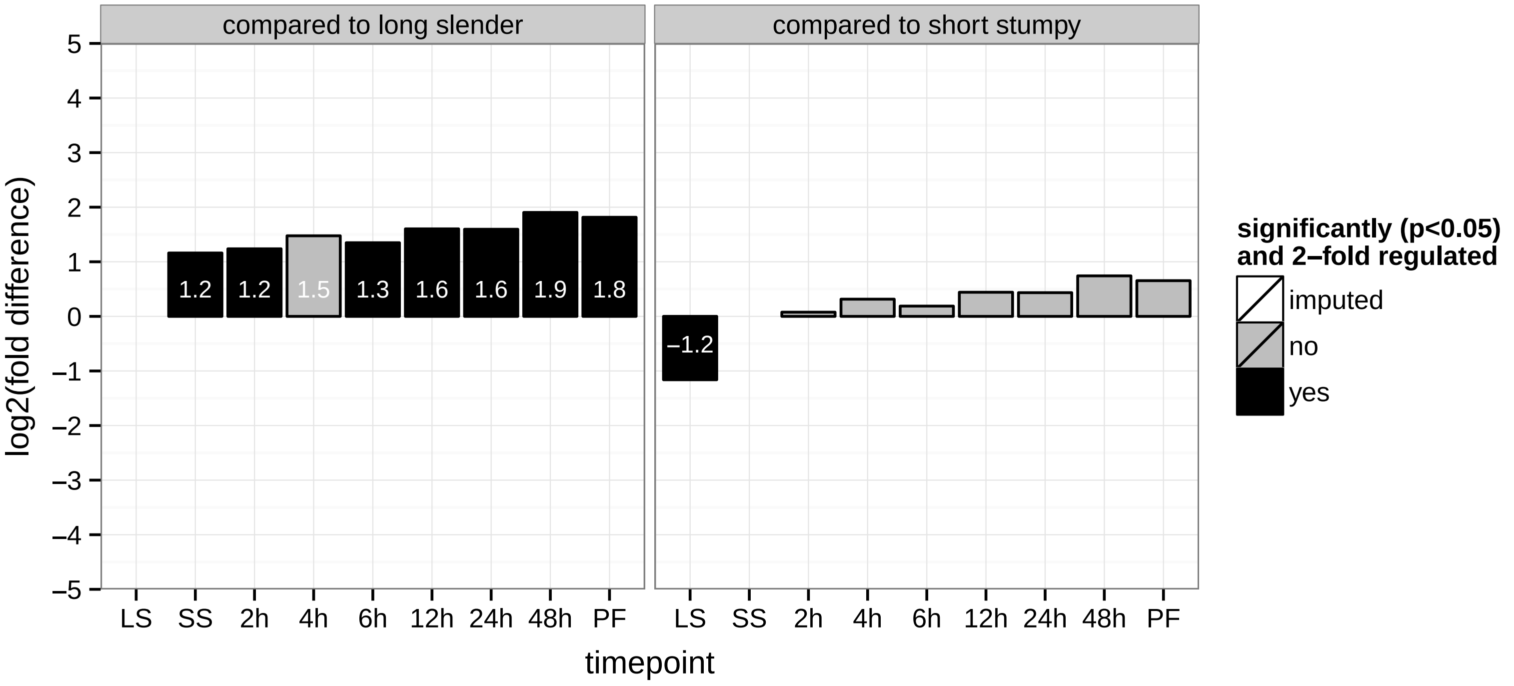
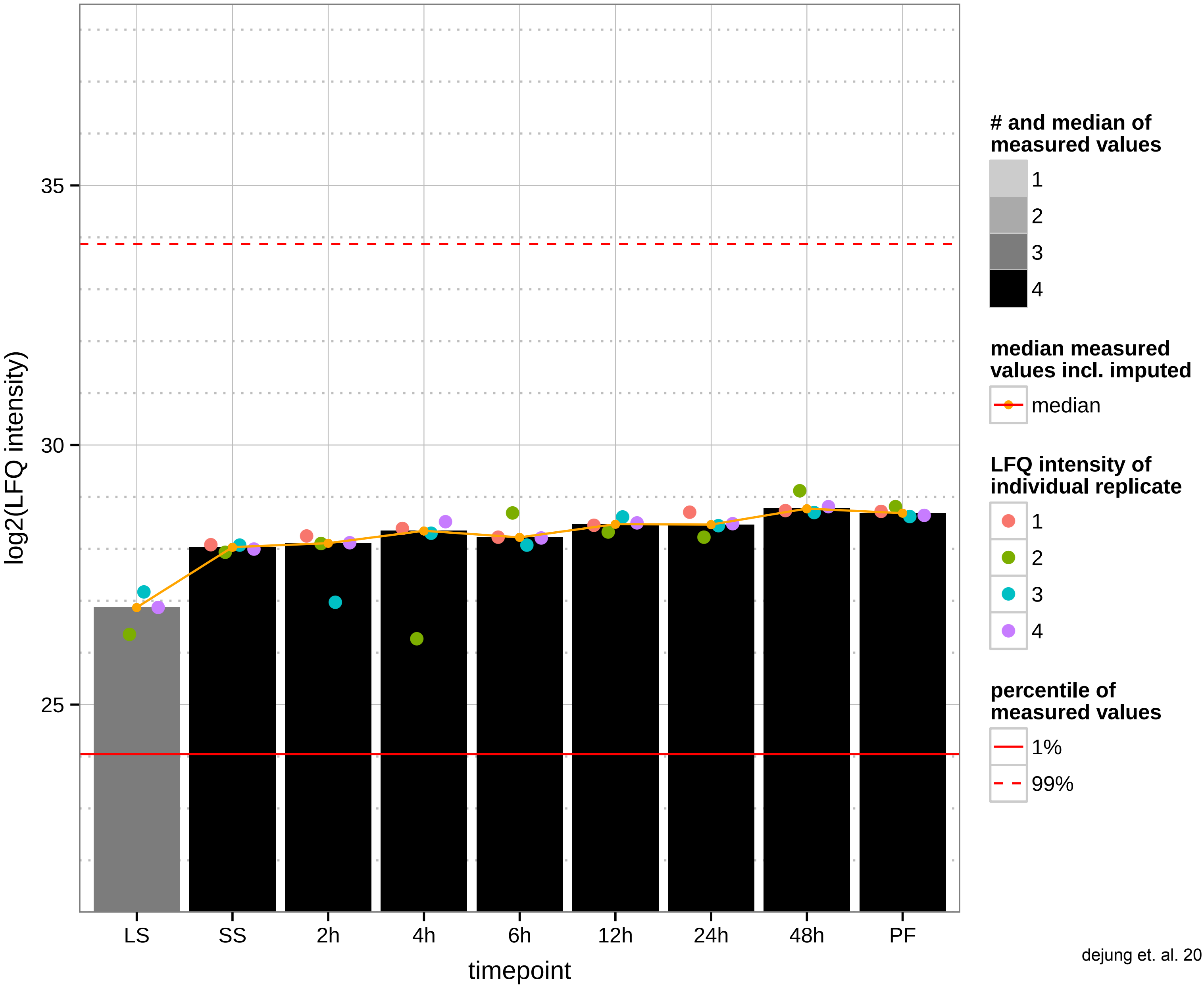
PRP19–like protein, putative (TbPRP19)
Tb927.2.5240
AGOF: ubiquitin–protein ligase activity
AGOC: ubiquitin ligase complex
AGOP: protein ubiquitination
PGOF: protein binding, ubiquitin–protein ligase activity
PGOC: ubiquitin ligase complex
PGOP: protein ubiquitination





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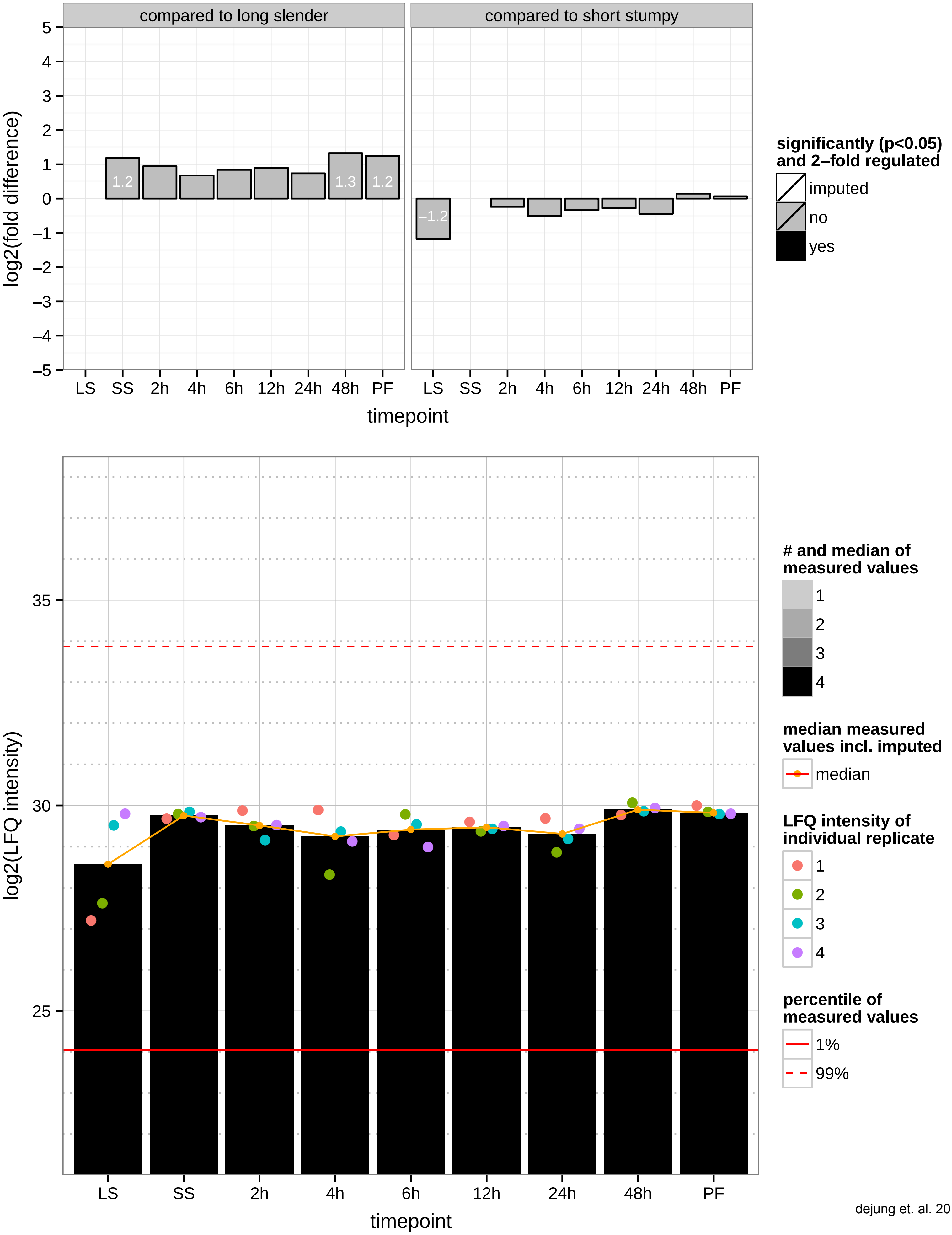
dynein heavy chain, putative
Tb927.2.5270
AGOF: ATP binding, ATPase activity
AGOC: cellular_component, dynein complex
AGOP: microtubule−based movement
PGOF: microtubule motor activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: dynein complex
PGOP: microtubule−based movement



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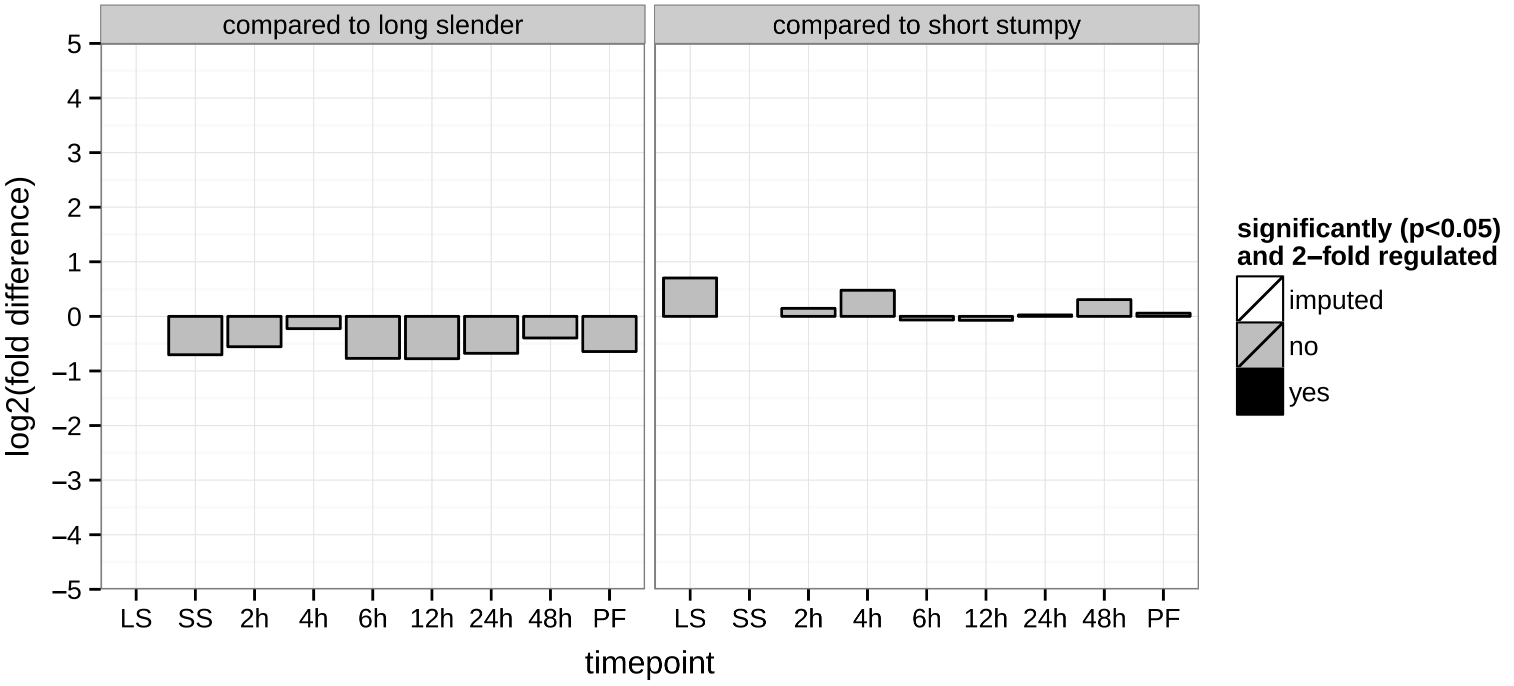
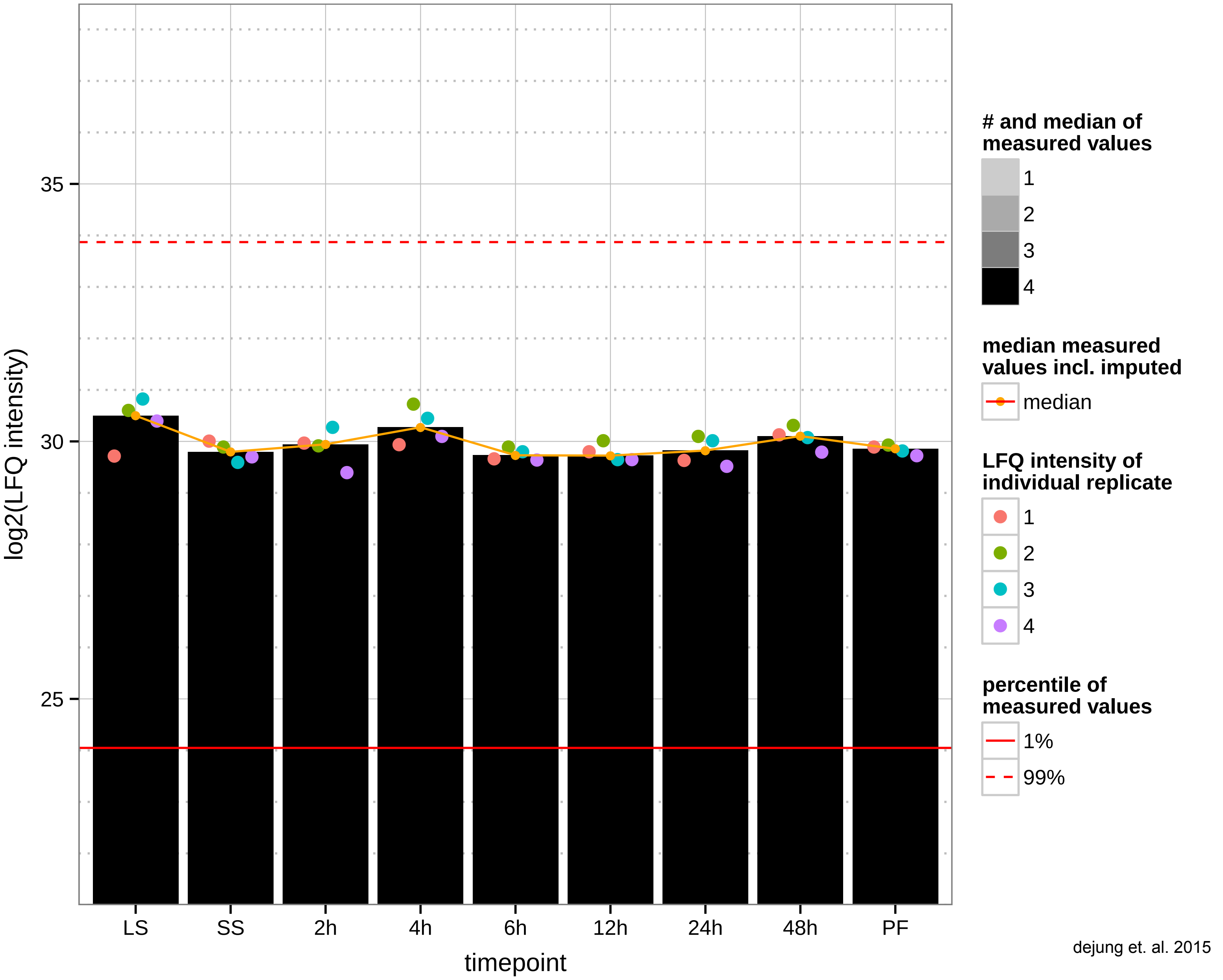
adenylate kinase, putative (ADKA)
Tb927.2.5660
AGOF: ATP binding, adenylate kinase activity
AGOC: cilium part
AGOP: nucleobase–containing compound metabolic process
PGOF: ATP binding, adenylate kinase activity, cAMP–dependent protein kinase regulator activity, nucleobase–containing com
PGOC: null
PGOP: nucleobase–containing compound metabolic process, signal transduction





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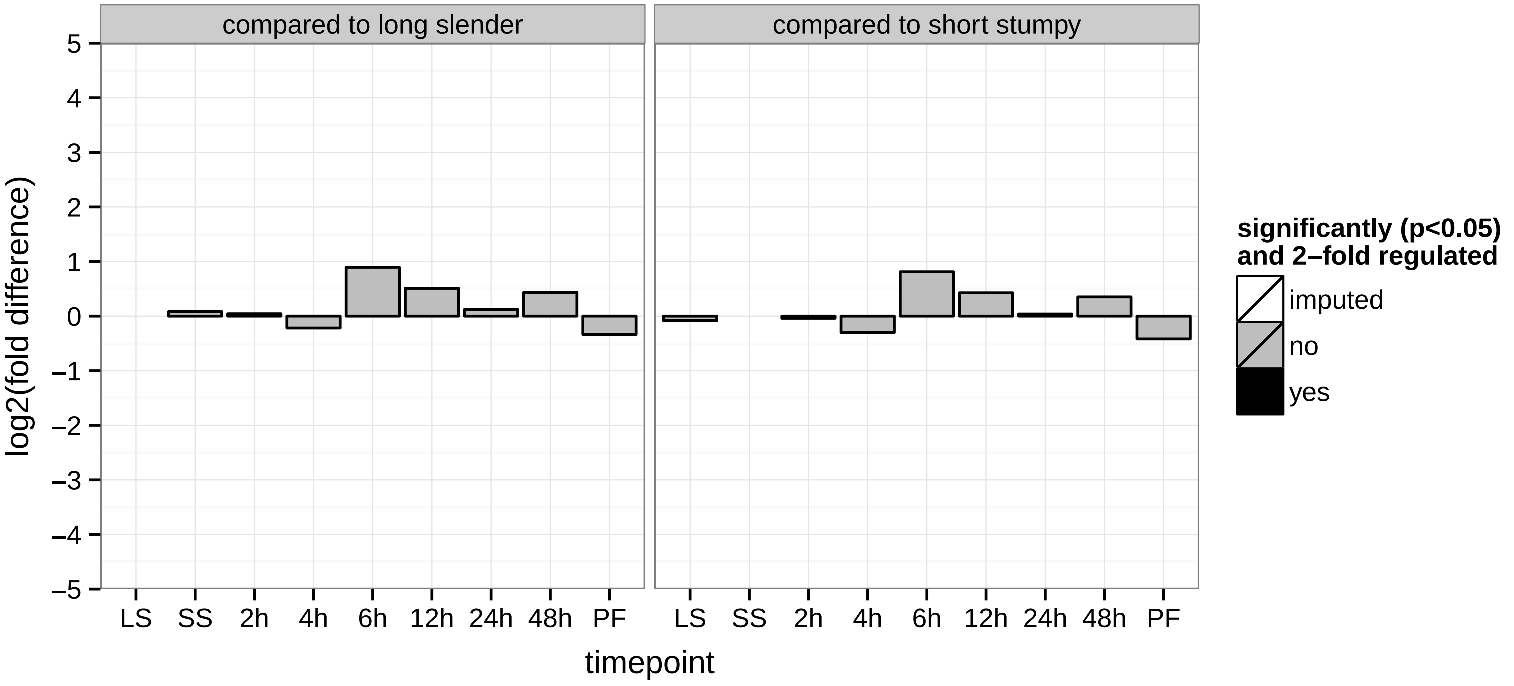
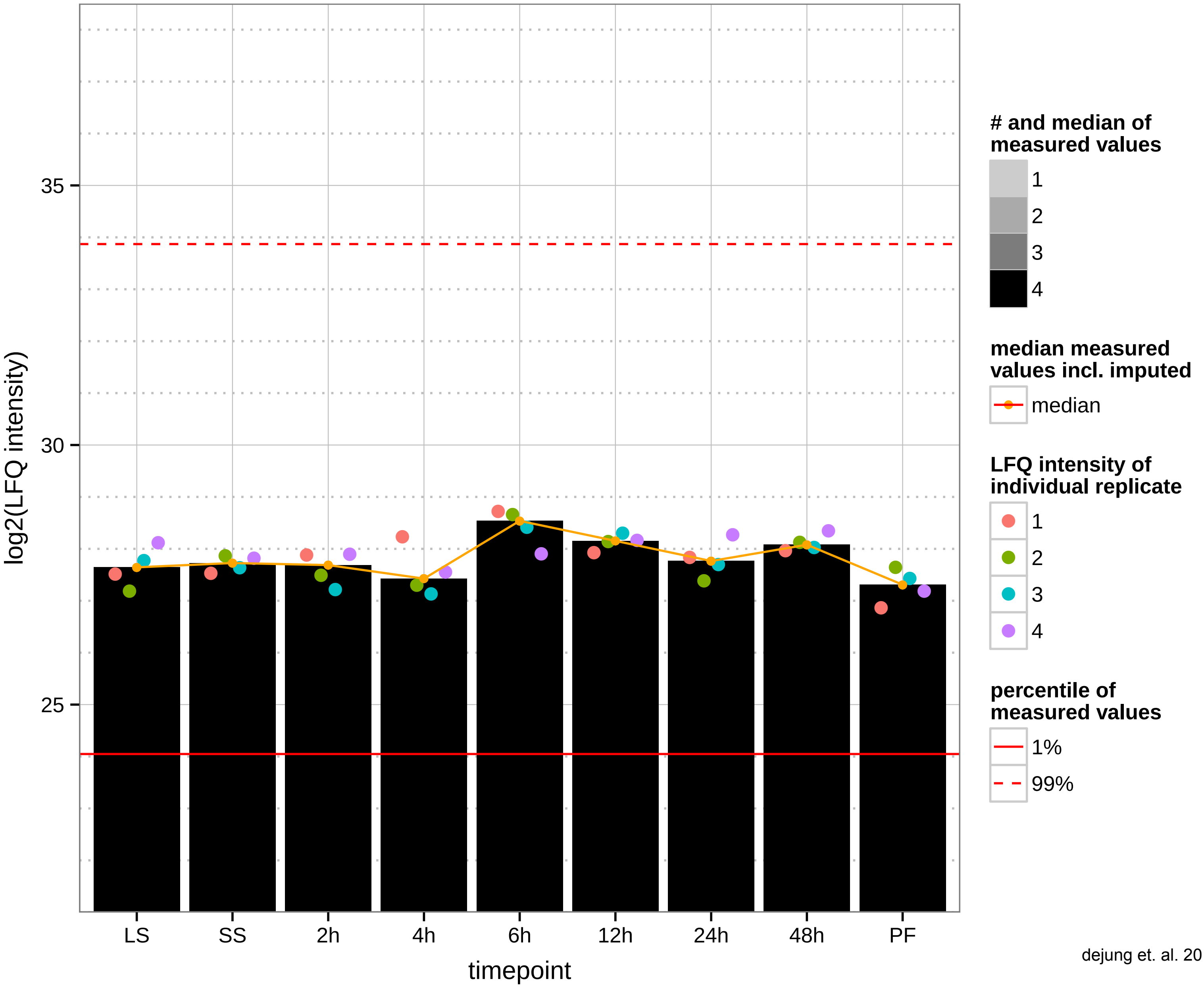
hypothetical protein, conserved
Tb927.2.5760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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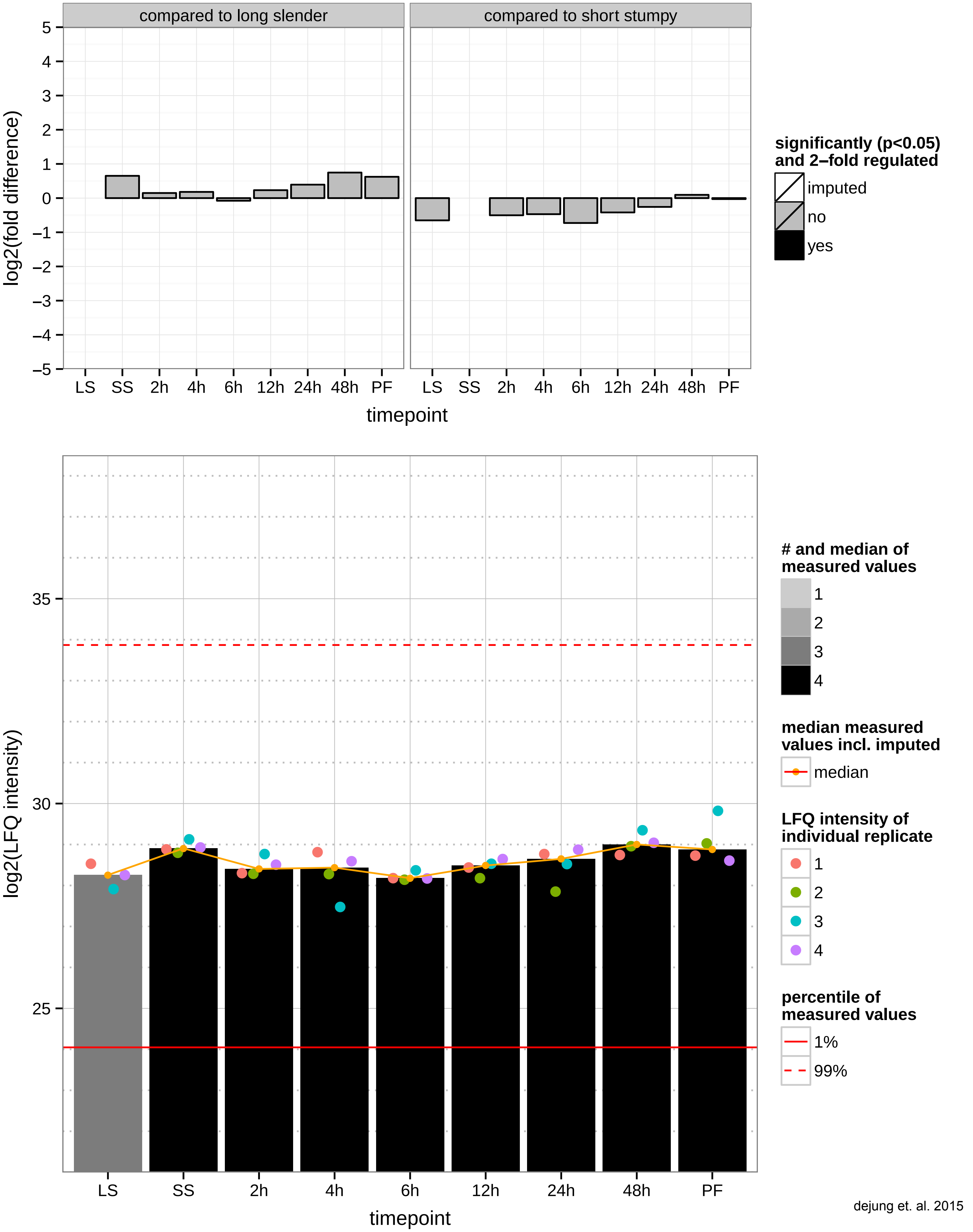
hypothetical protein, conserved
Tb927.2.5810
AGOF: null
AGOC: null
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null



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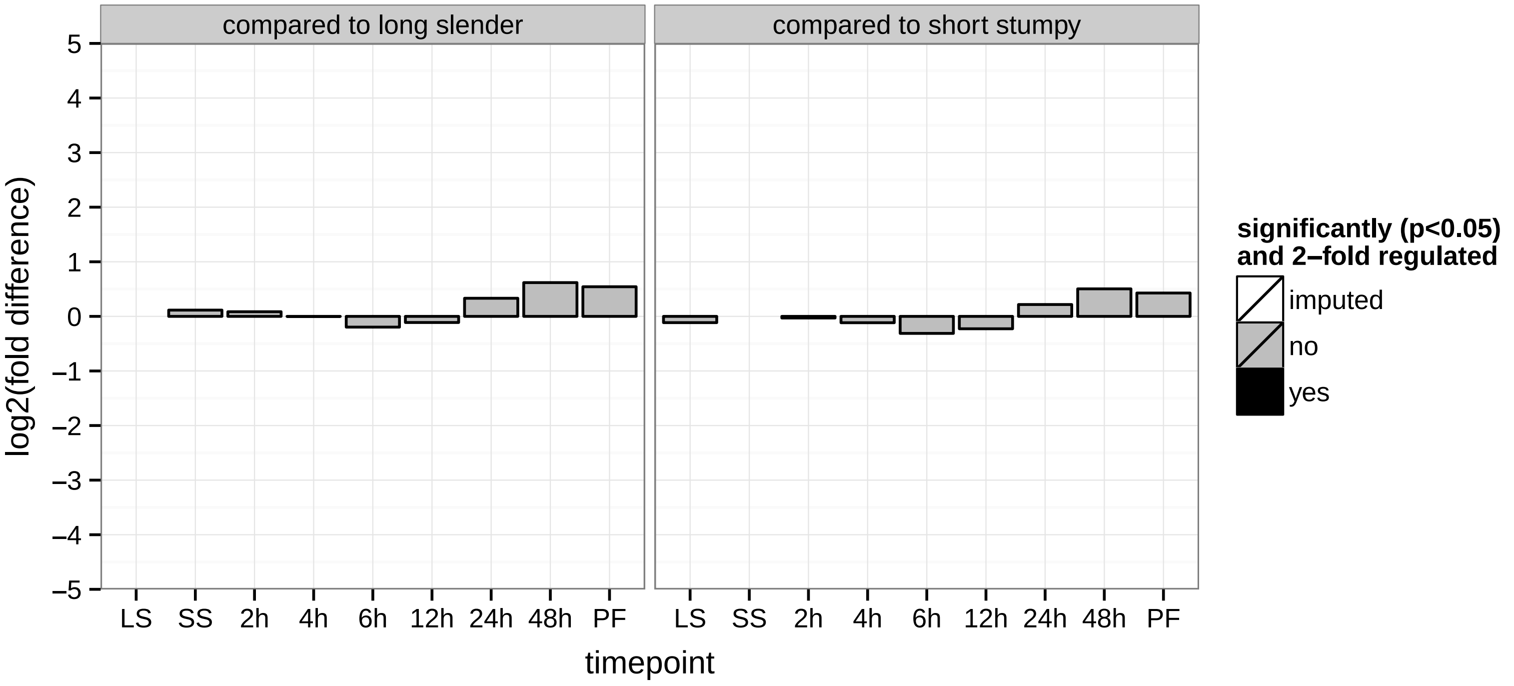
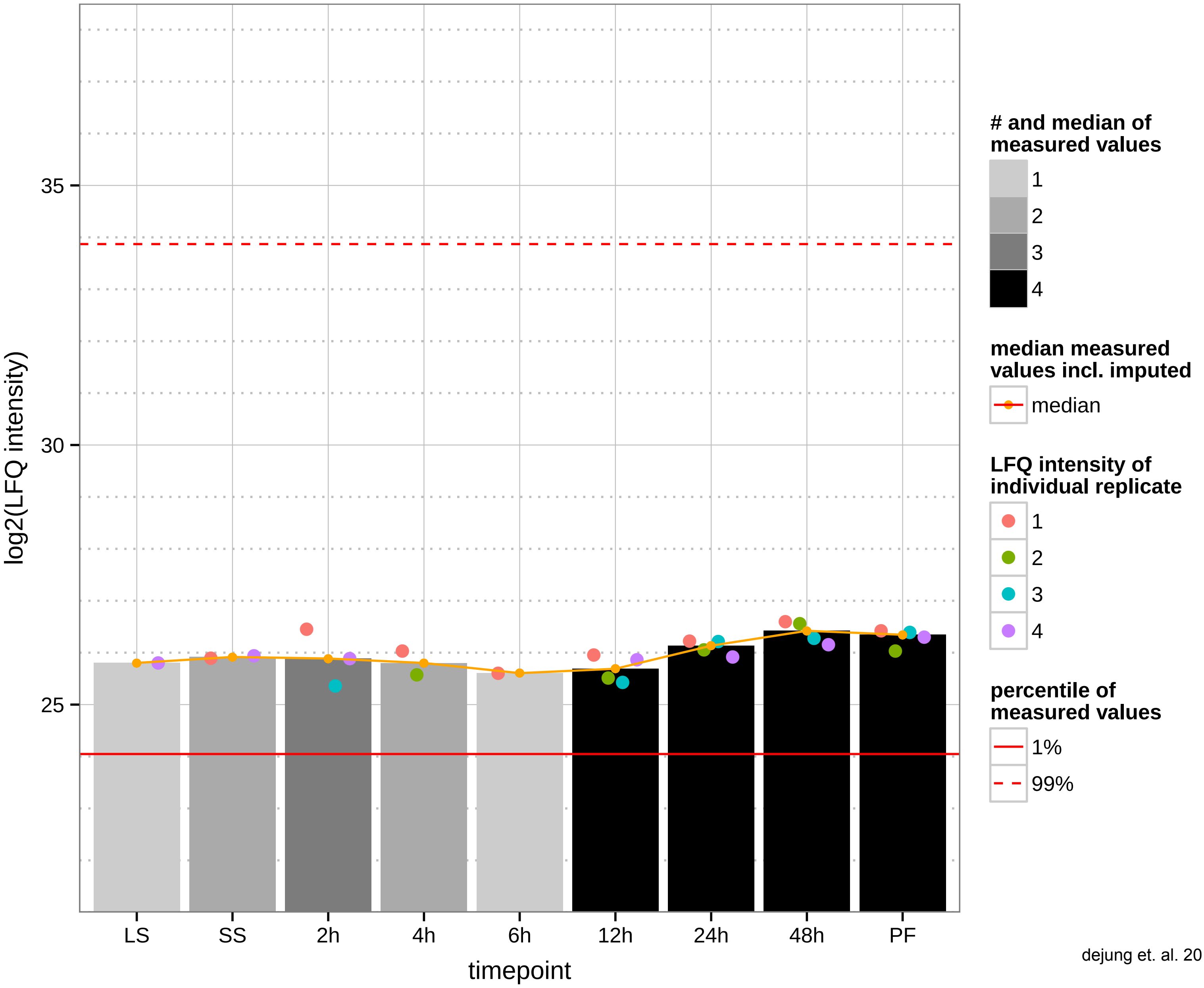
hypothetical protein, conserved
Tb927.2.5820
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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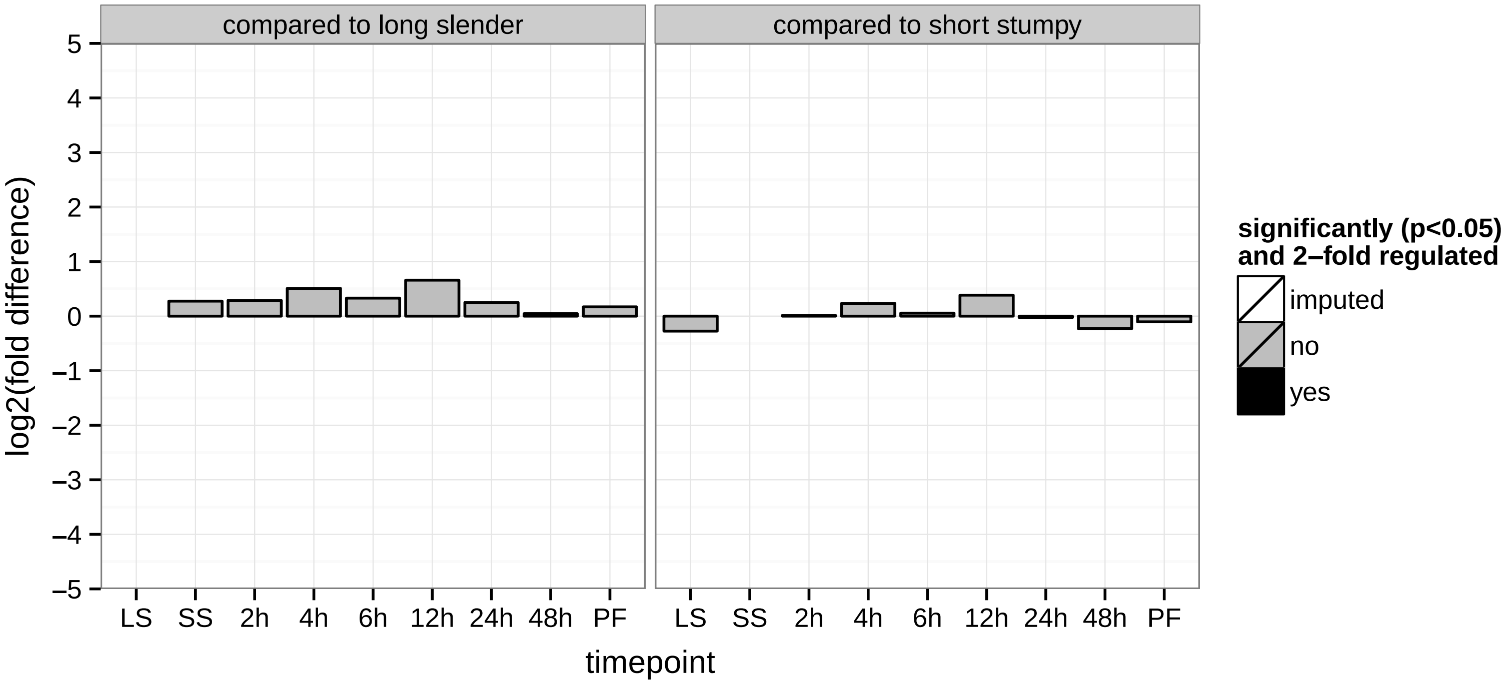
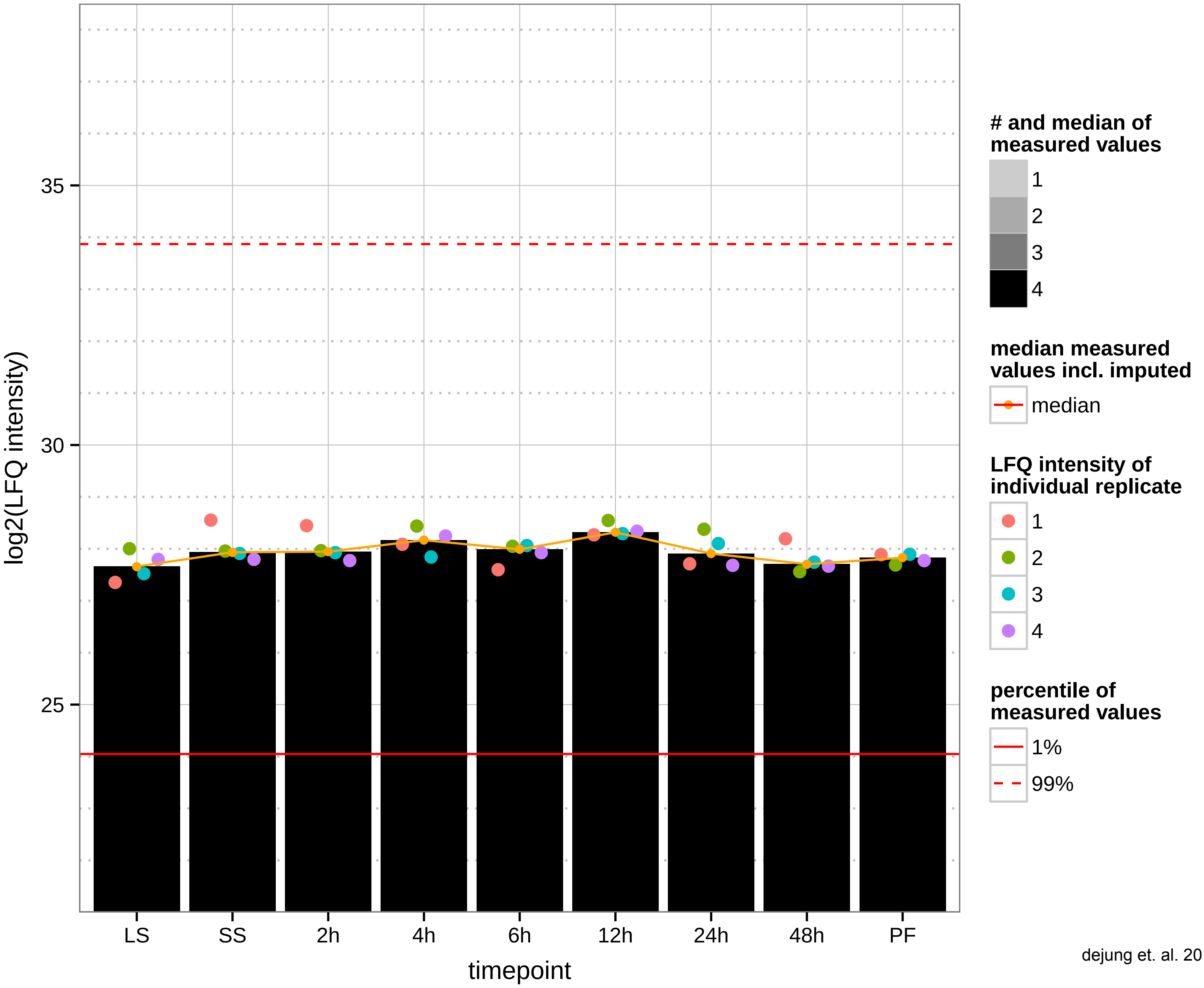
small nuclear ribonucleoprotein SmD2 (Sm–D2)
Tb927.2.5850
AGOF: snRNA binding
AGOC: nucleus, small nuclear ribonucleoprotein complex, small nucleolar ribonucleoprotein complex
AGOP: nuclear mRNA trans splicing, SL addition
PGOF: null
PGOC: null
PGOP: null





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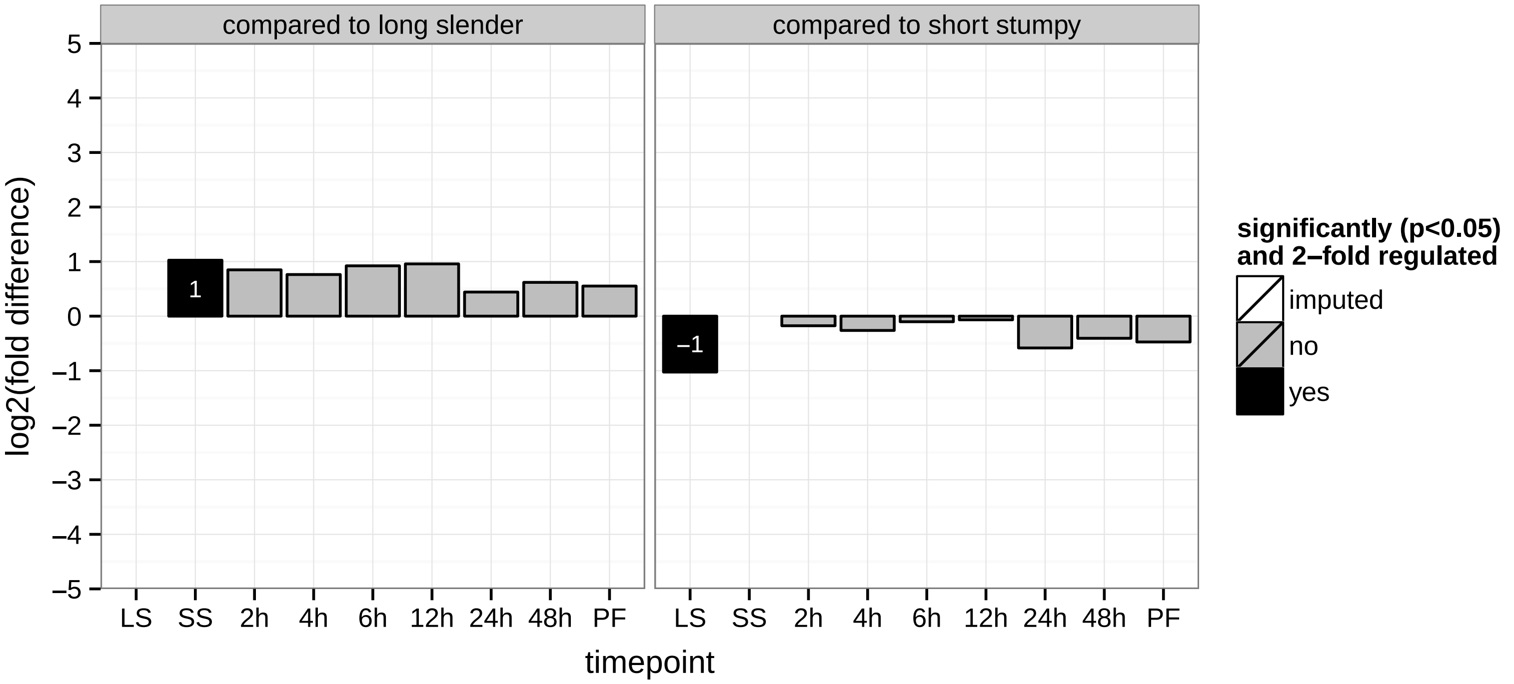
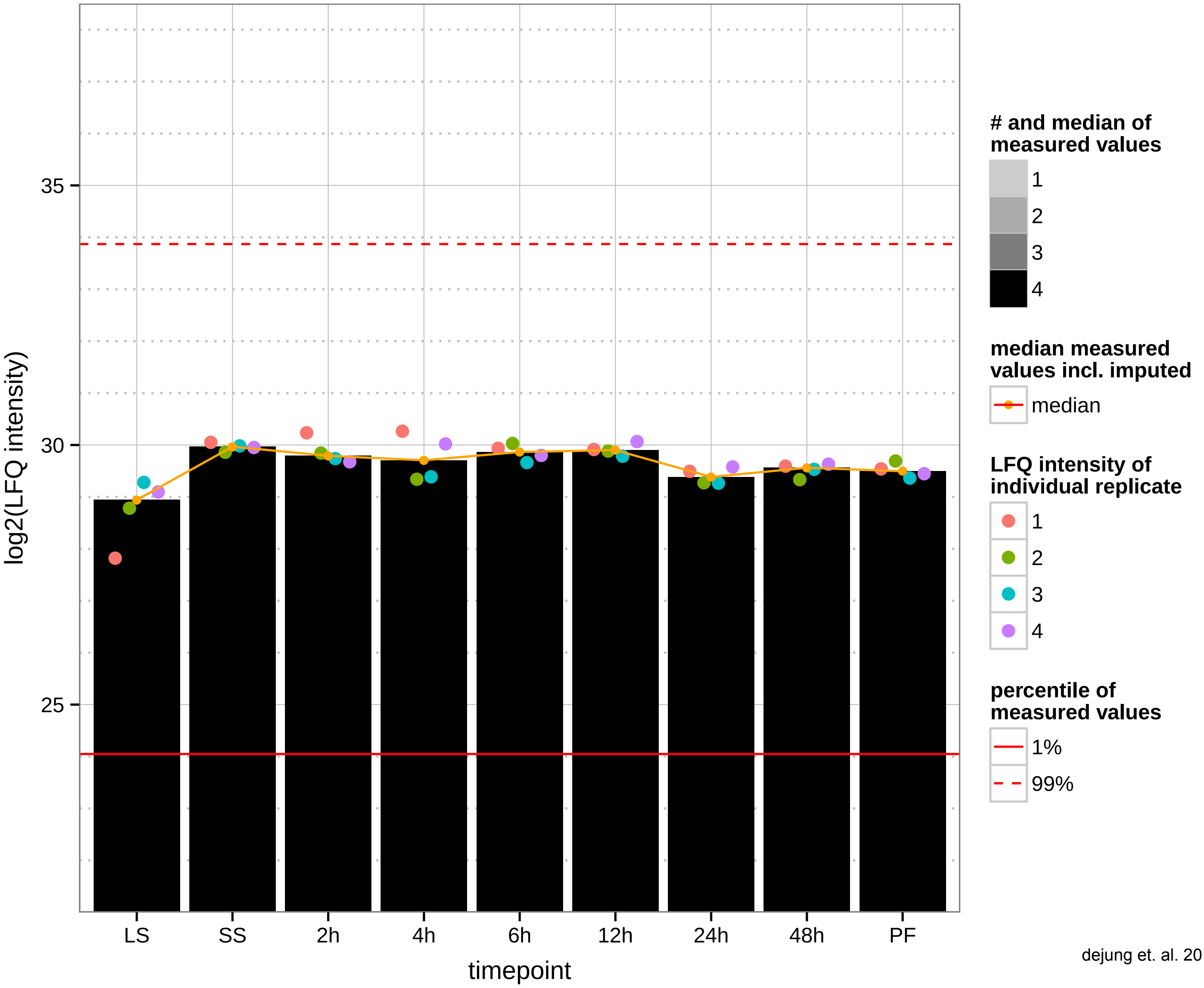
beta prime COP protein
Tb927.2.6050
AGOF: structural molecule activity
AGOC: COPI vesicle coat, Golgi apparatus
AGOP: intracellular protein transport, retrograde vesicle–mediated transport, Golgi to ER
PGOF: protein binding, structural molecule activity
PGOC: membrane coat
PGOP: intracellular protein transport, vesicle–mediated transport





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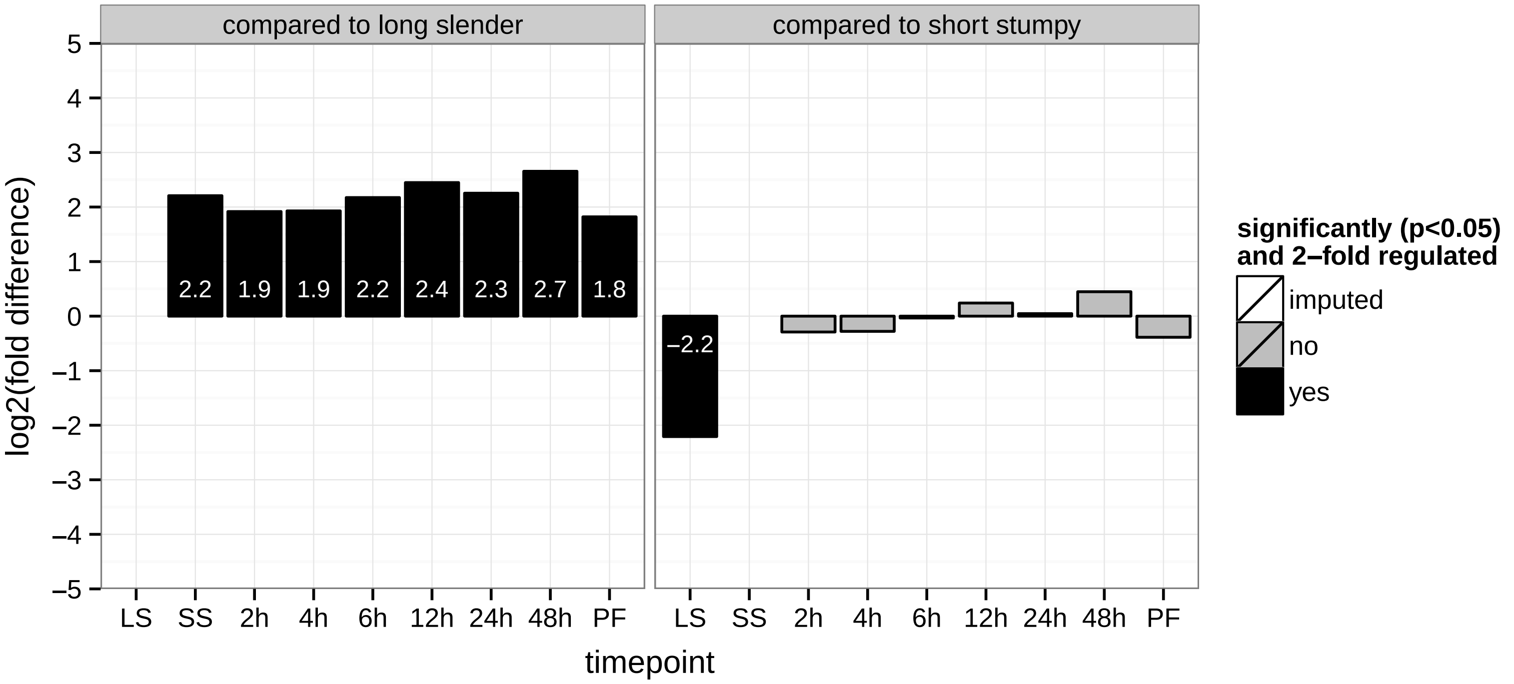
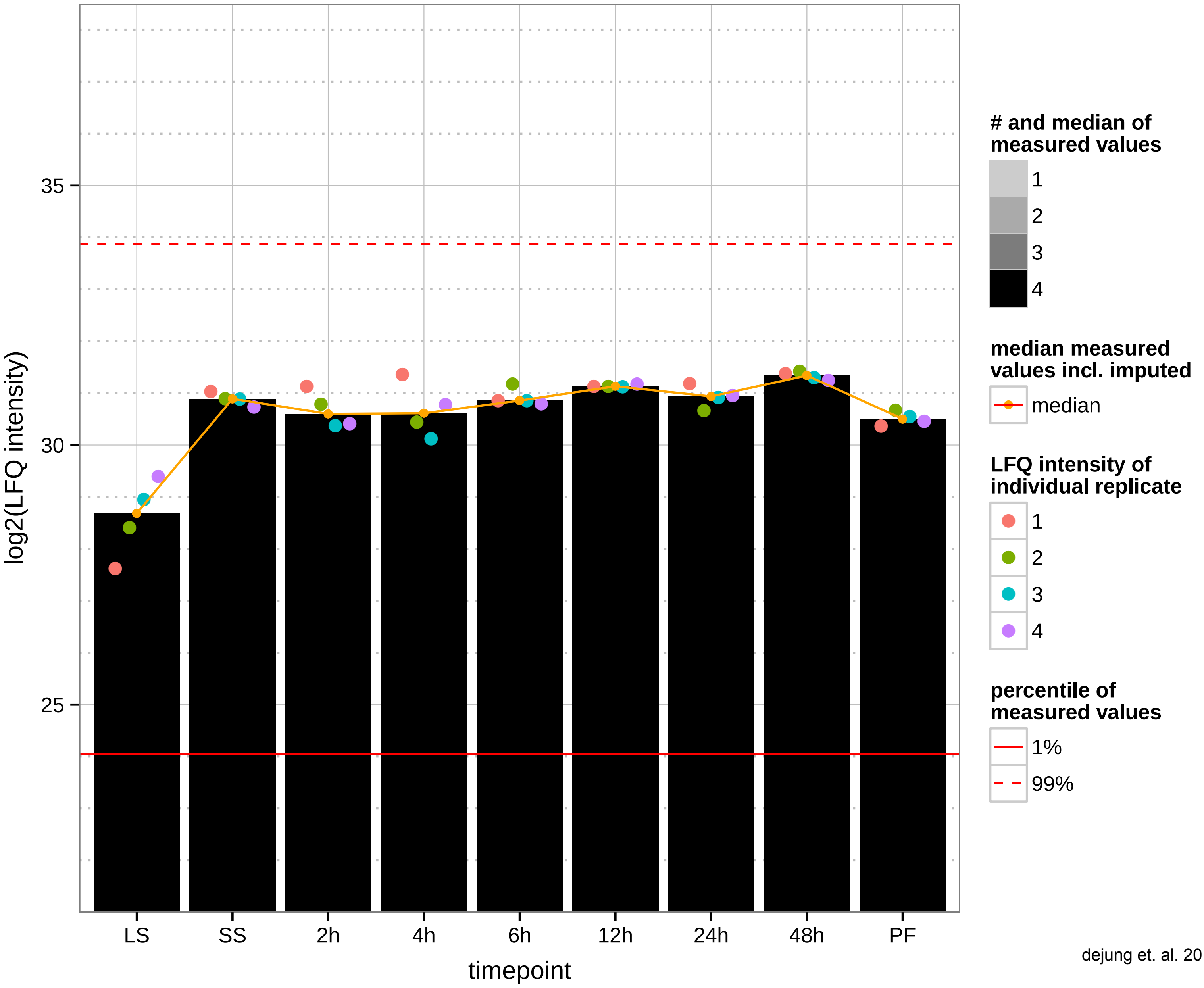
retrotransposon hot spot protein (RHS, pseudogene), putative, retrotransposon hot spot protein 1 (RHS1), interrupted
Tb927.2.820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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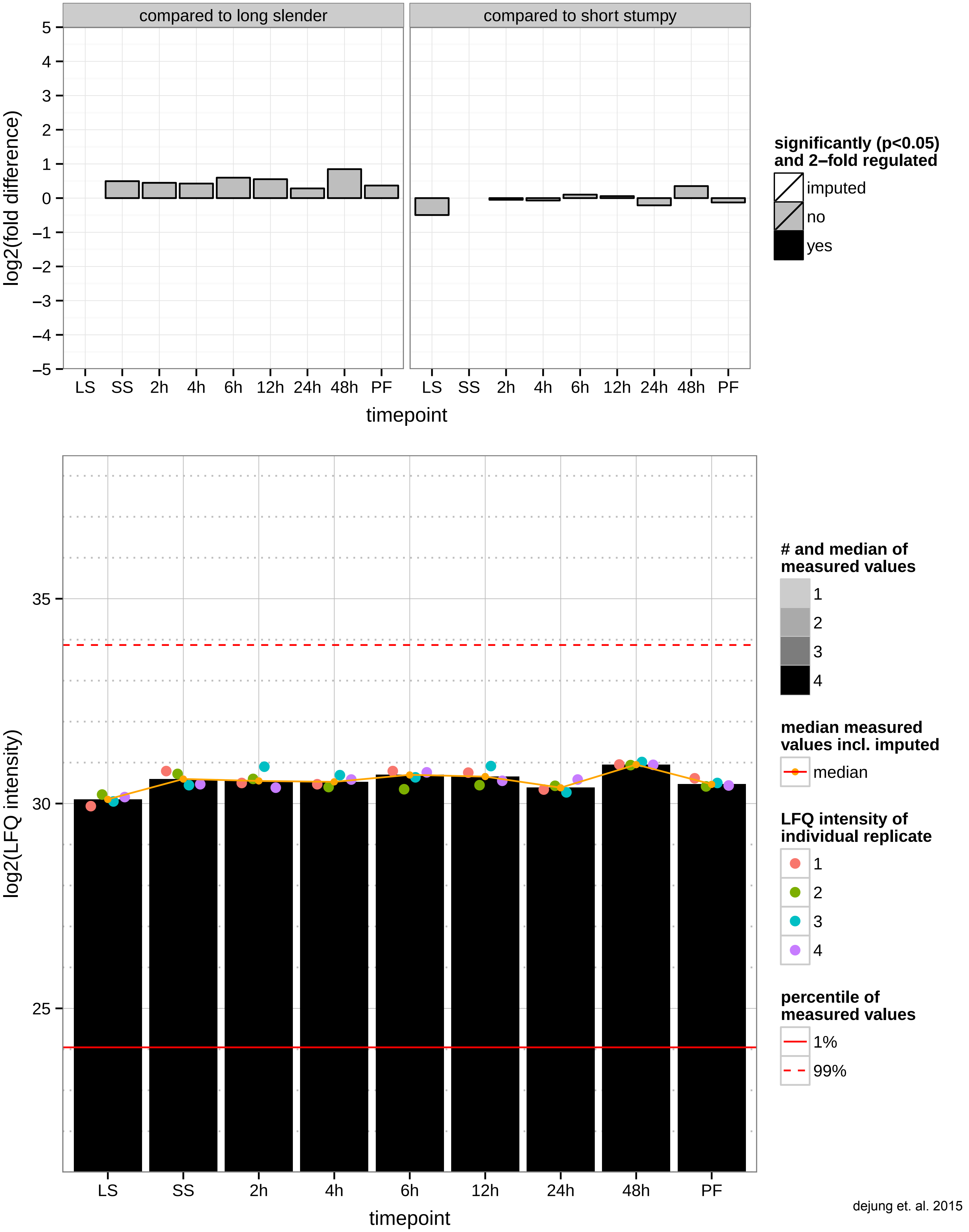
hypothetical protein, conserved
Tb927.3.1010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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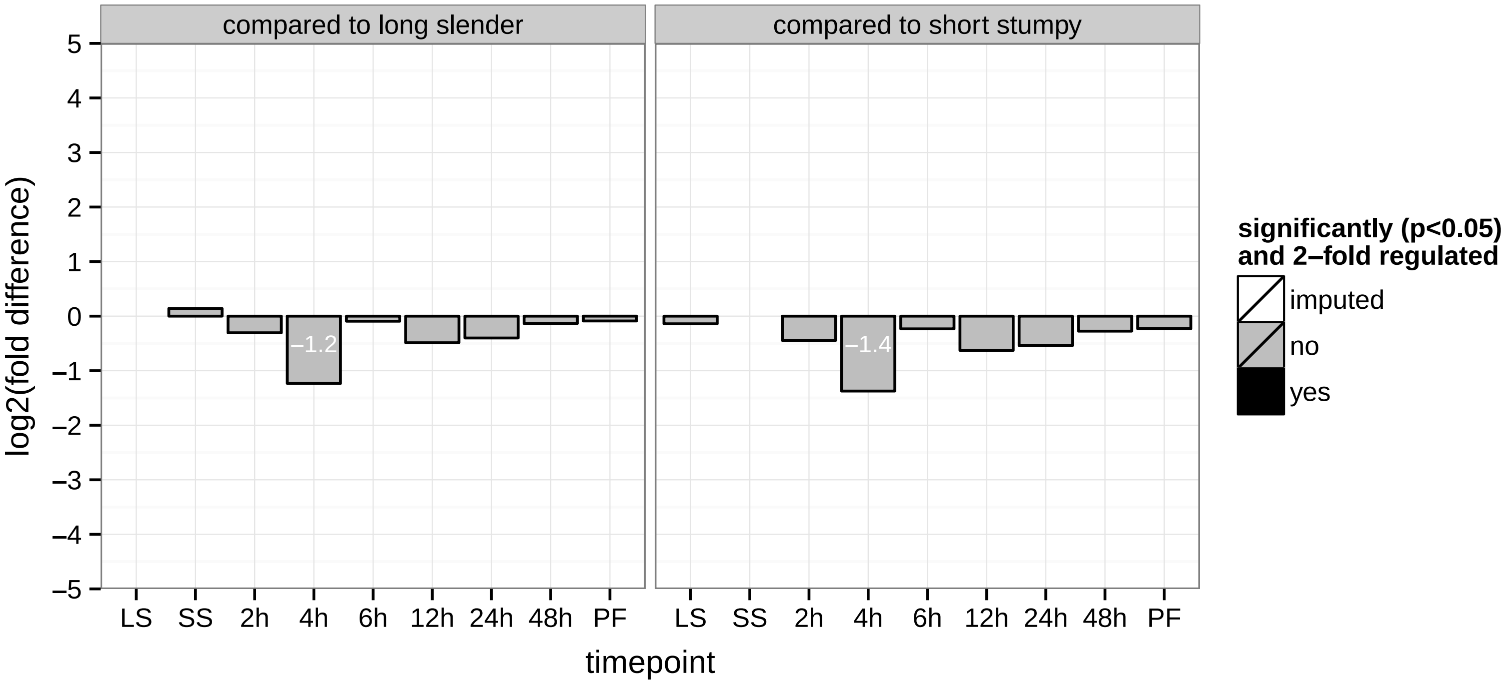
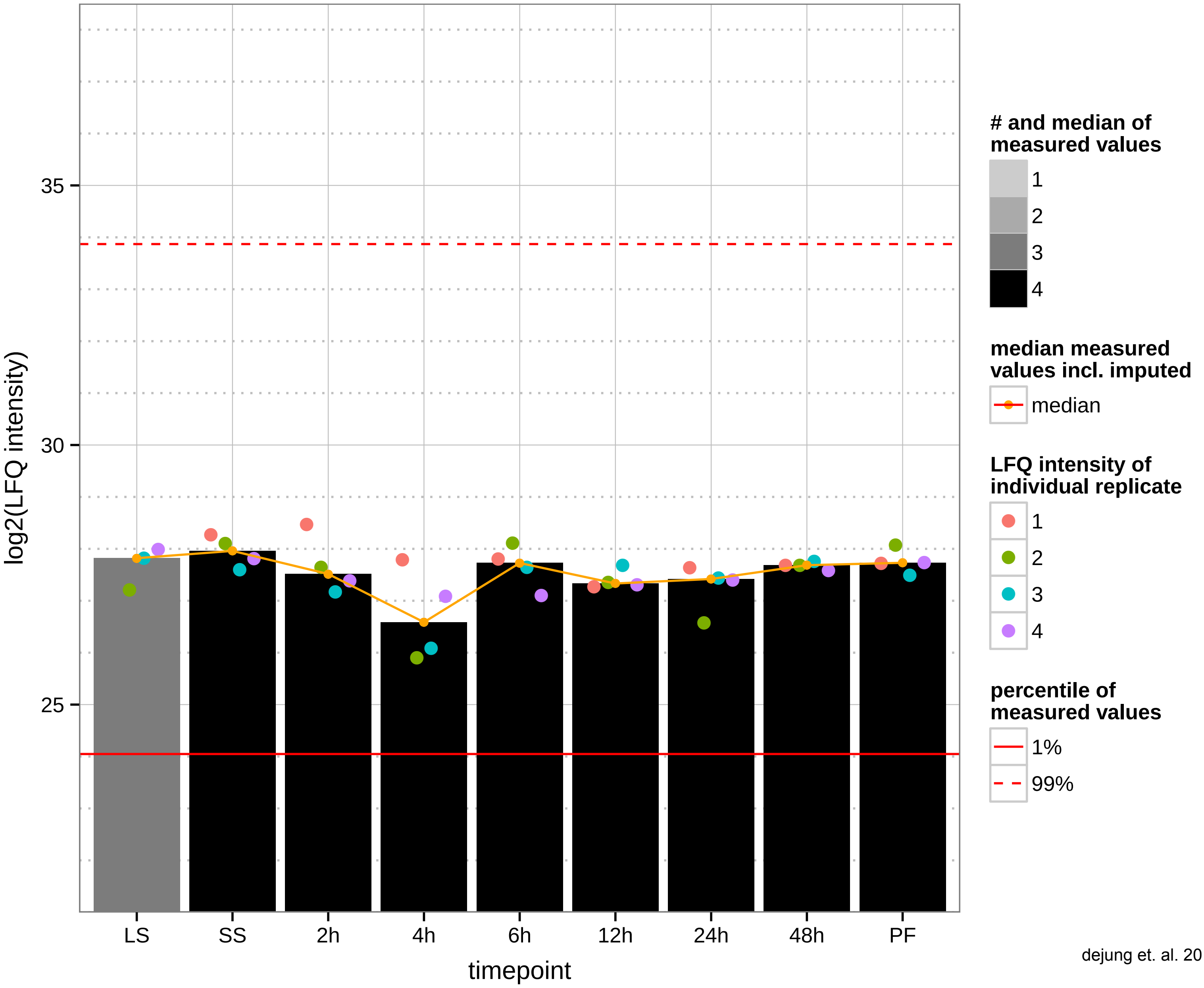
unspecified product
Tb927.3.1040
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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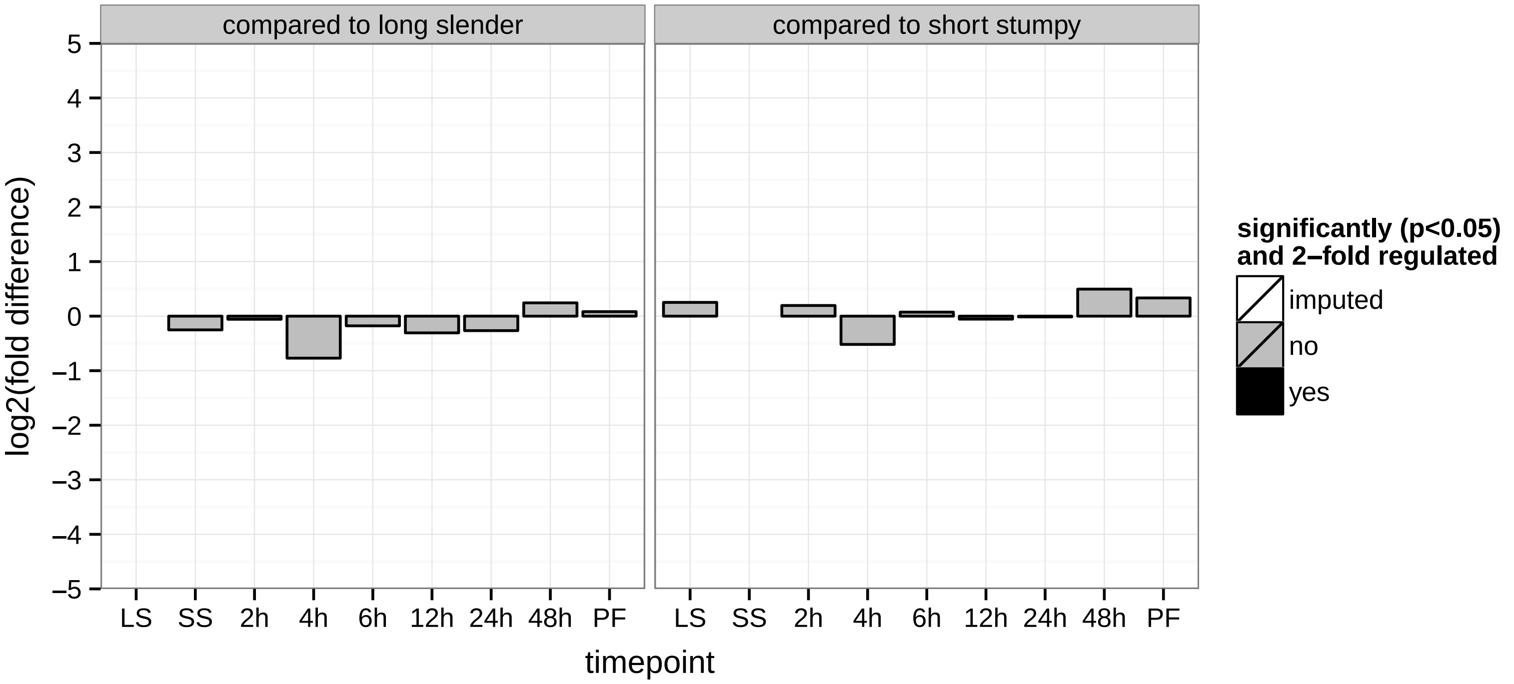
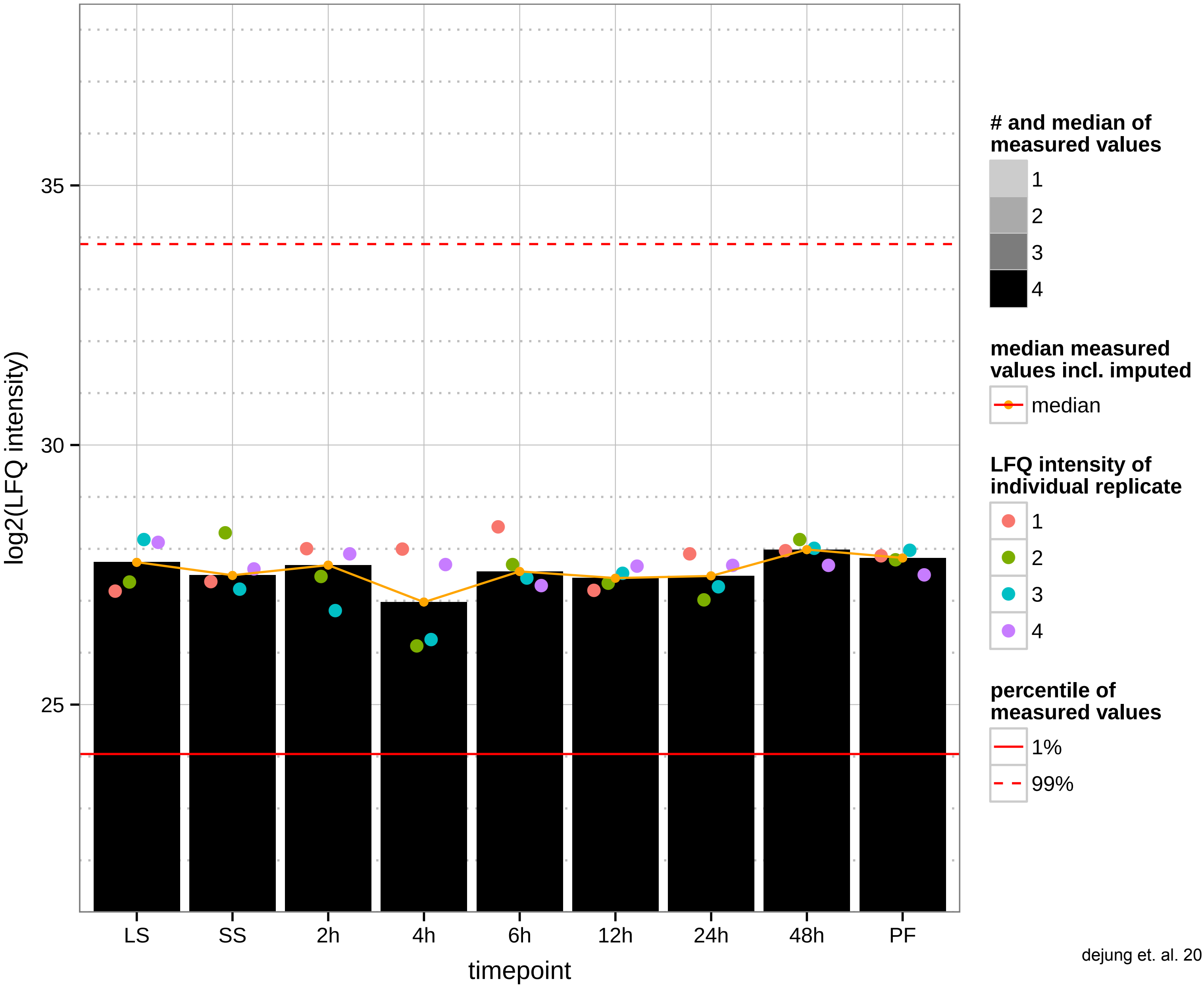
cAMP response protein, putative (CARP4)
Tb927.3.1060
AGOF: null
AGOC: null
AGOP: response to drug
PGOF: null
PGOC: null
PGOP: null





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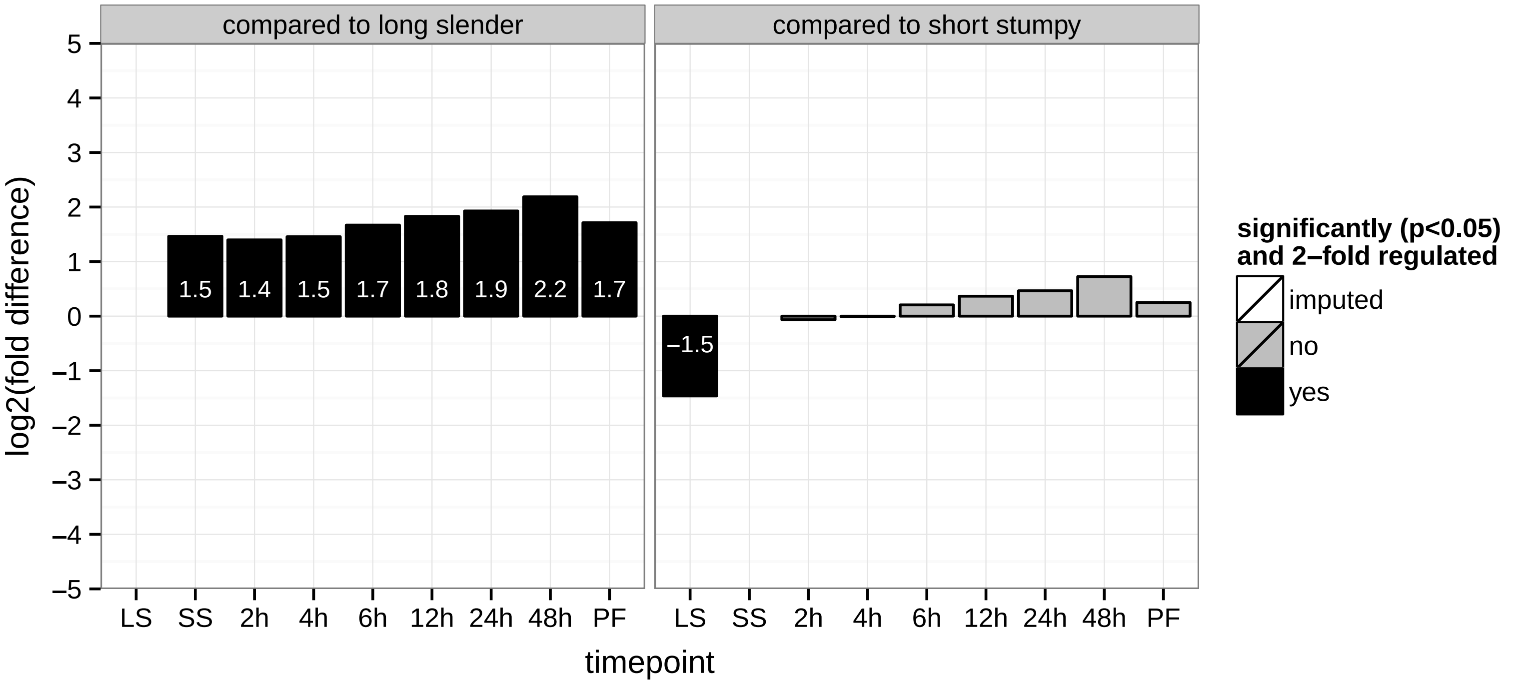
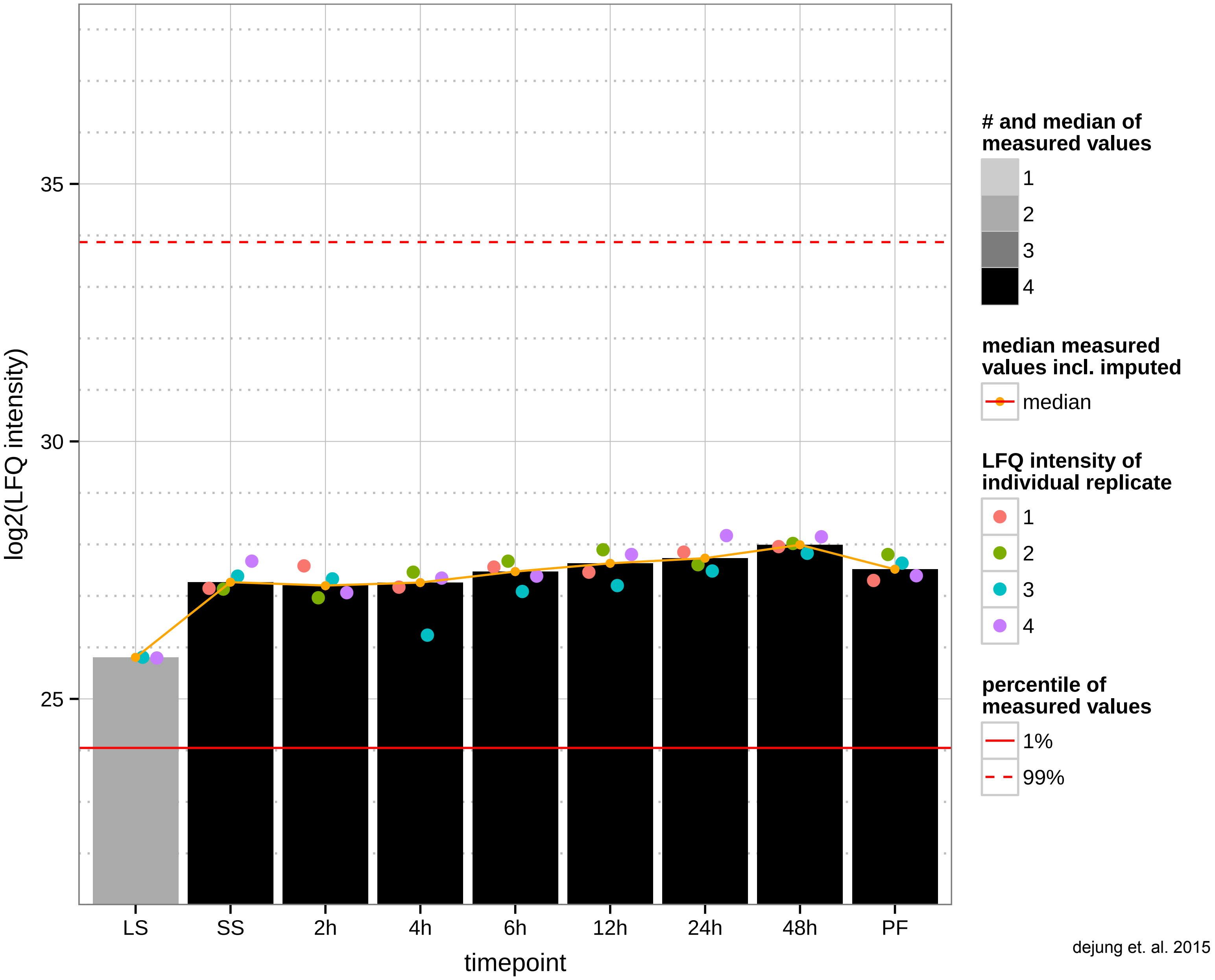
hypothetical protein, conserved
Tb927.3.1080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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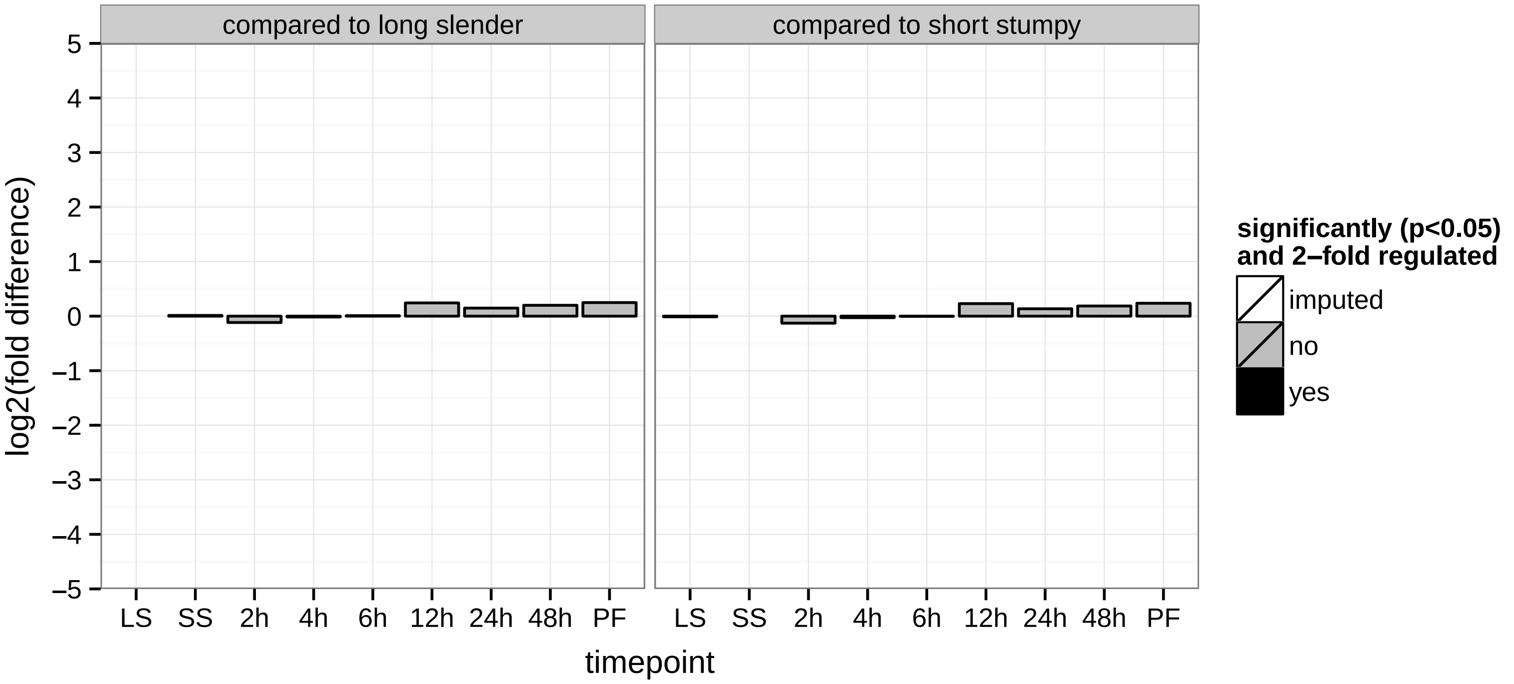
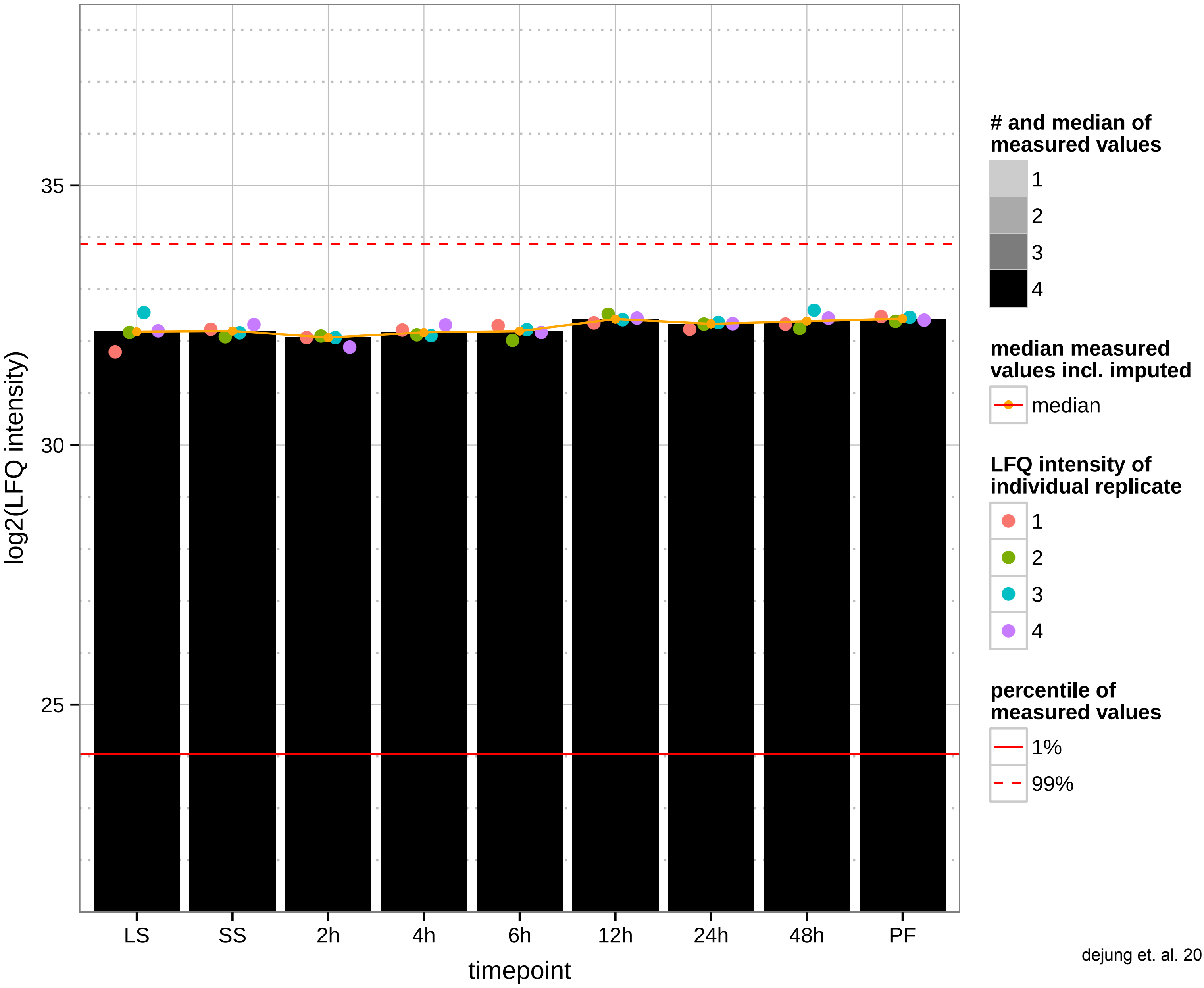
GTP−binding nuclear protein rtb2, putative (rtb2)
Tb927.3.1120
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti





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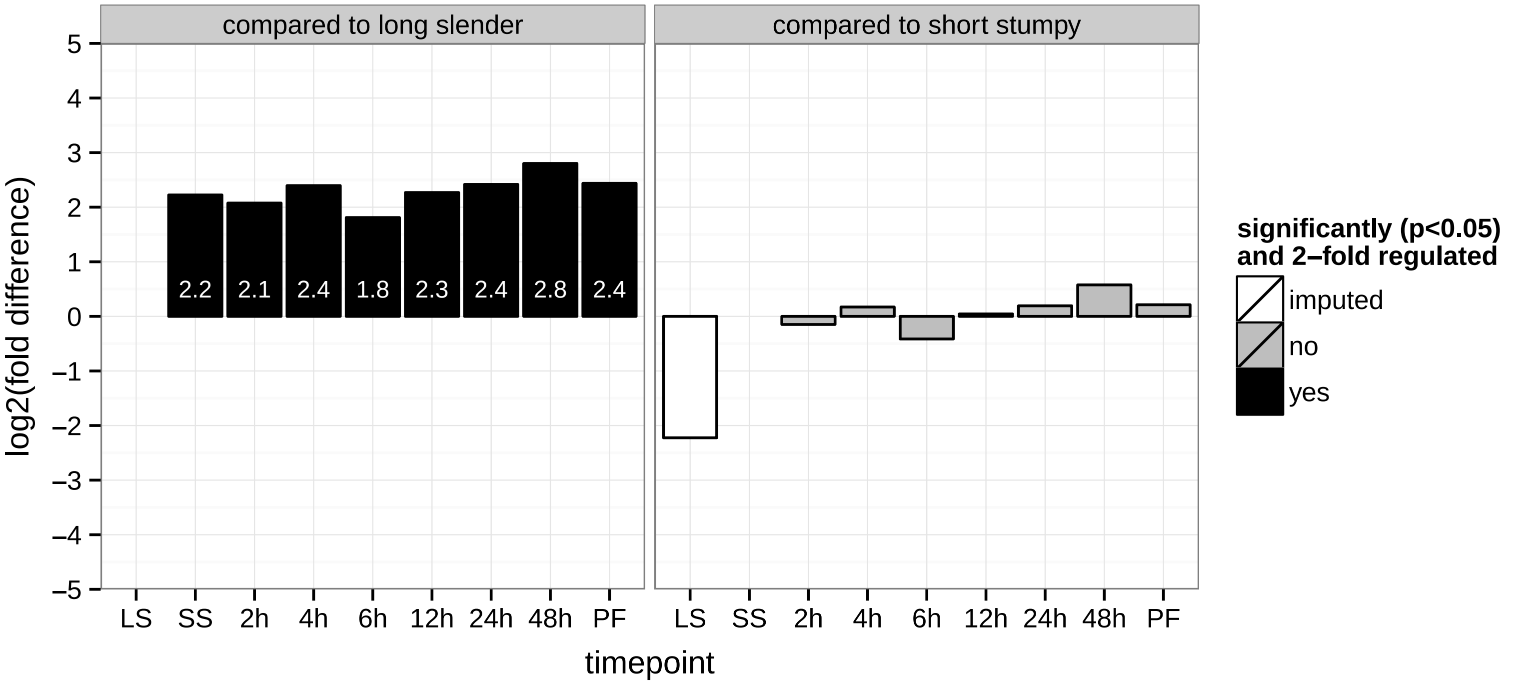
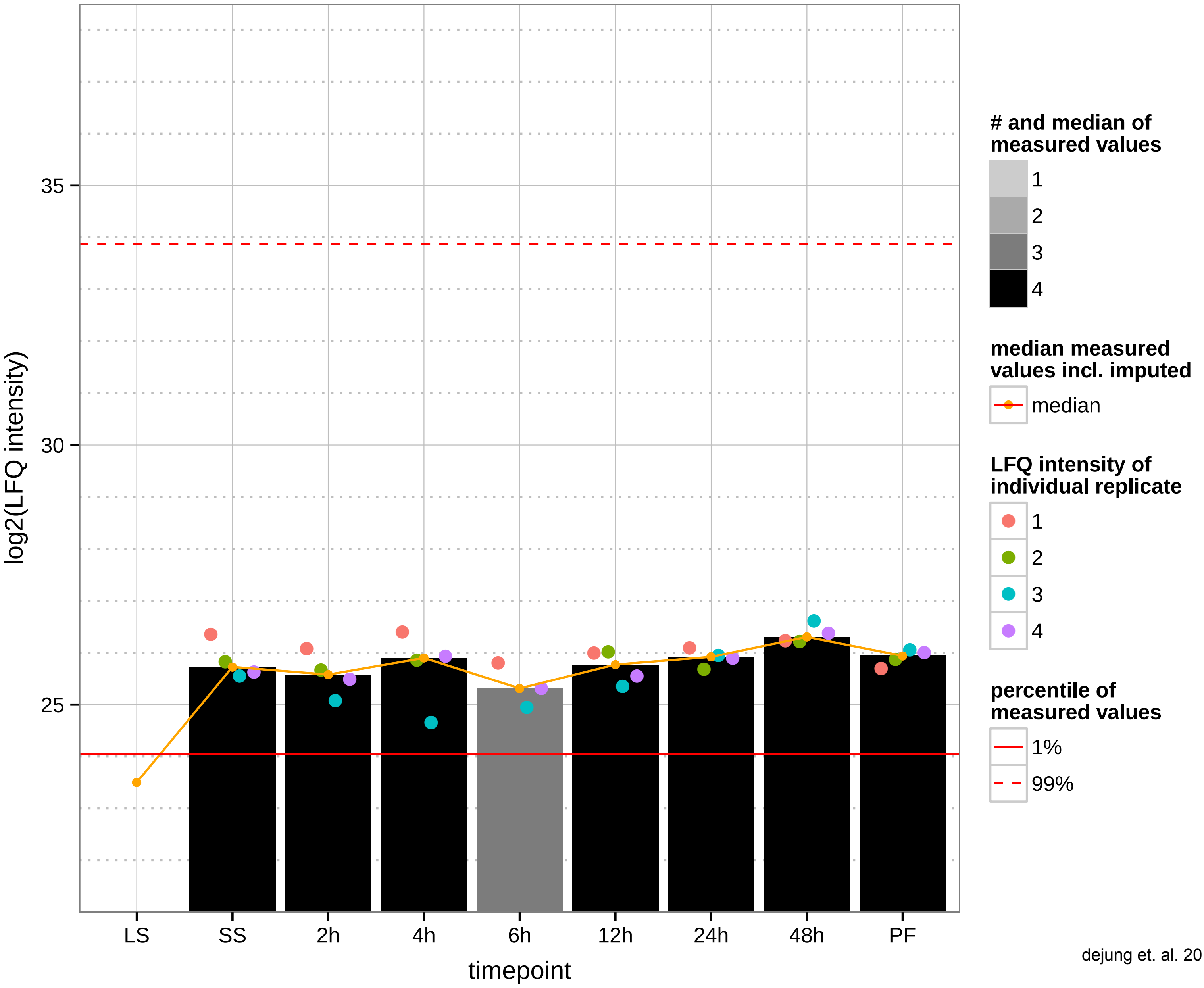
hypothetical protein, conserved
Tb927.3.1150
AGOF: nucleotide binding
AGOC: null
AGOP: null
PGOF: nucleotide binding
PGOC: null
PGOP: null





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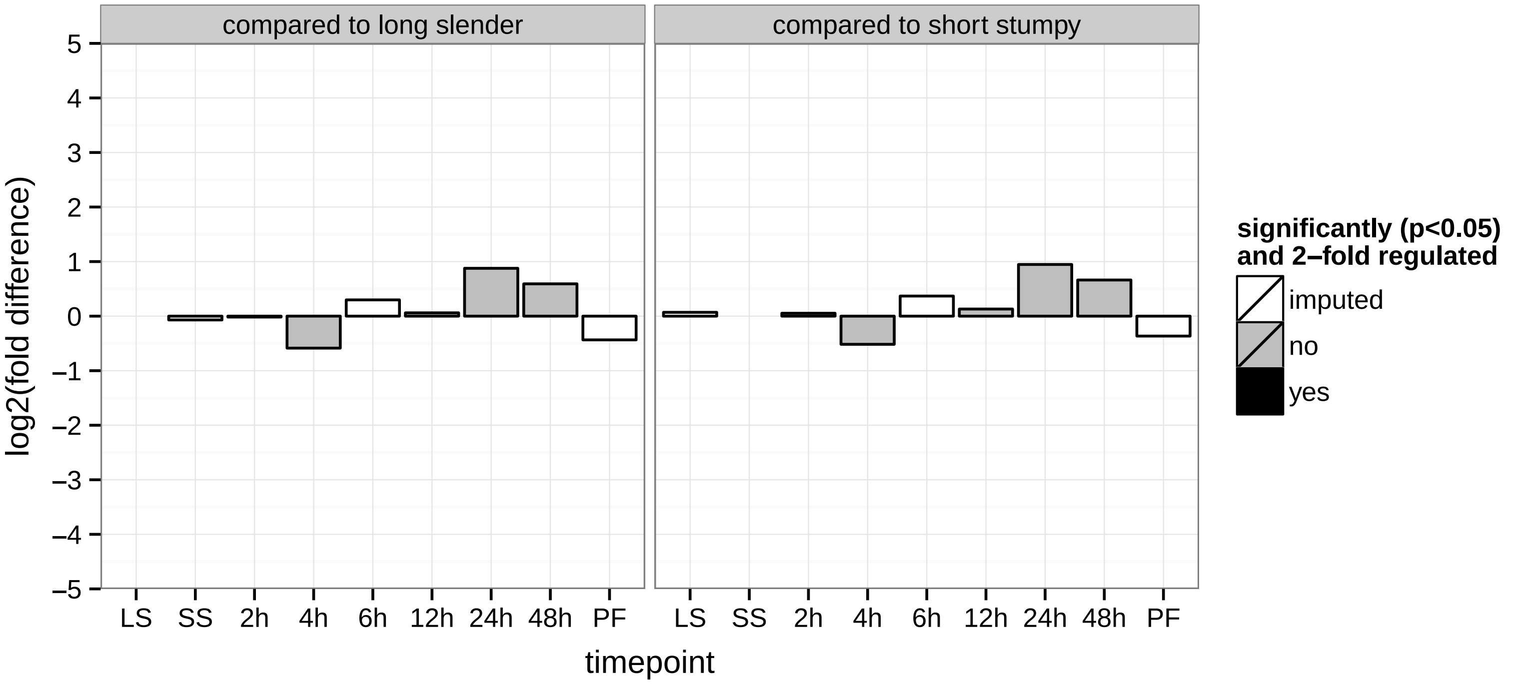
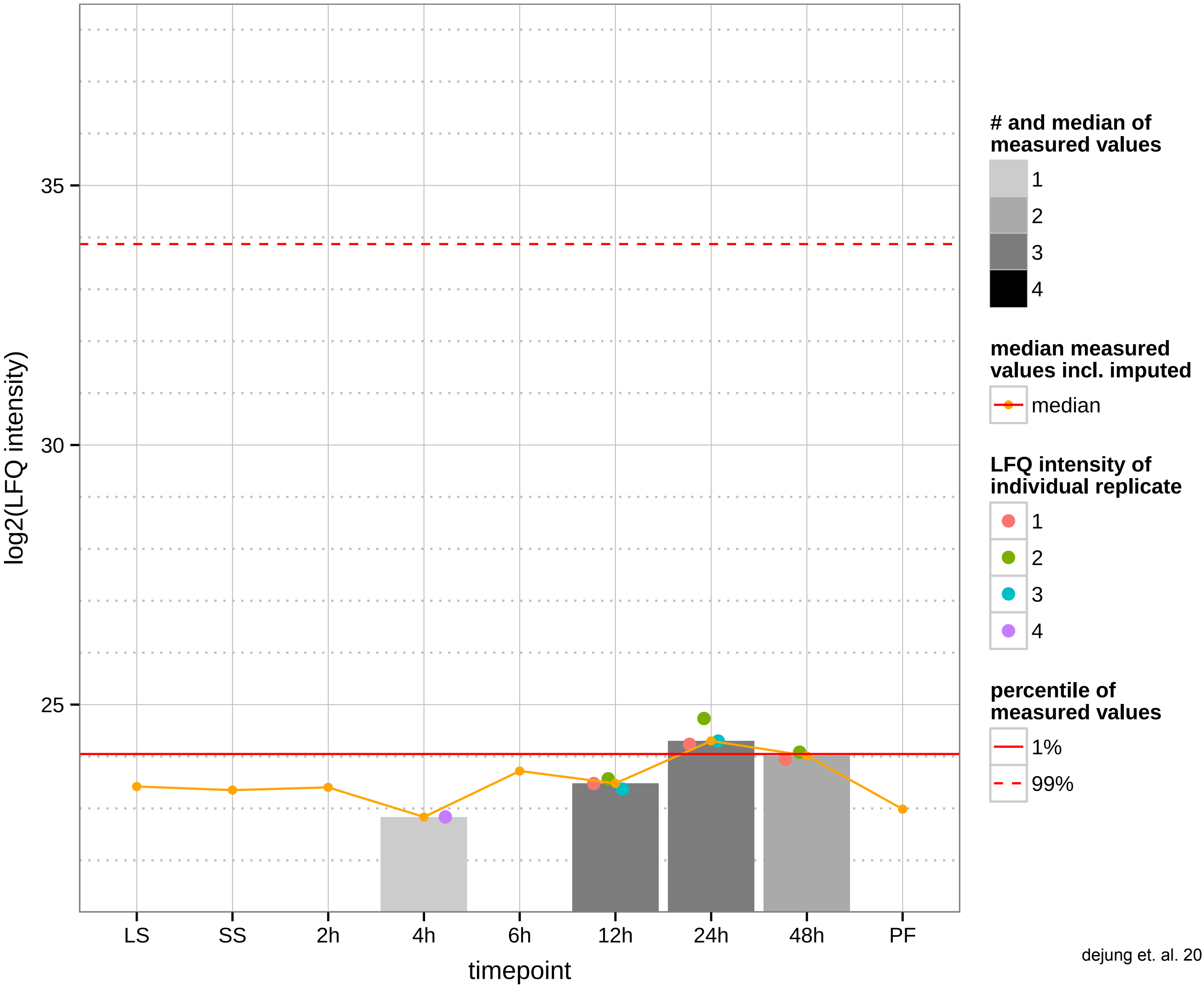
hypothetical protein, conserved
Tb927.3.1160
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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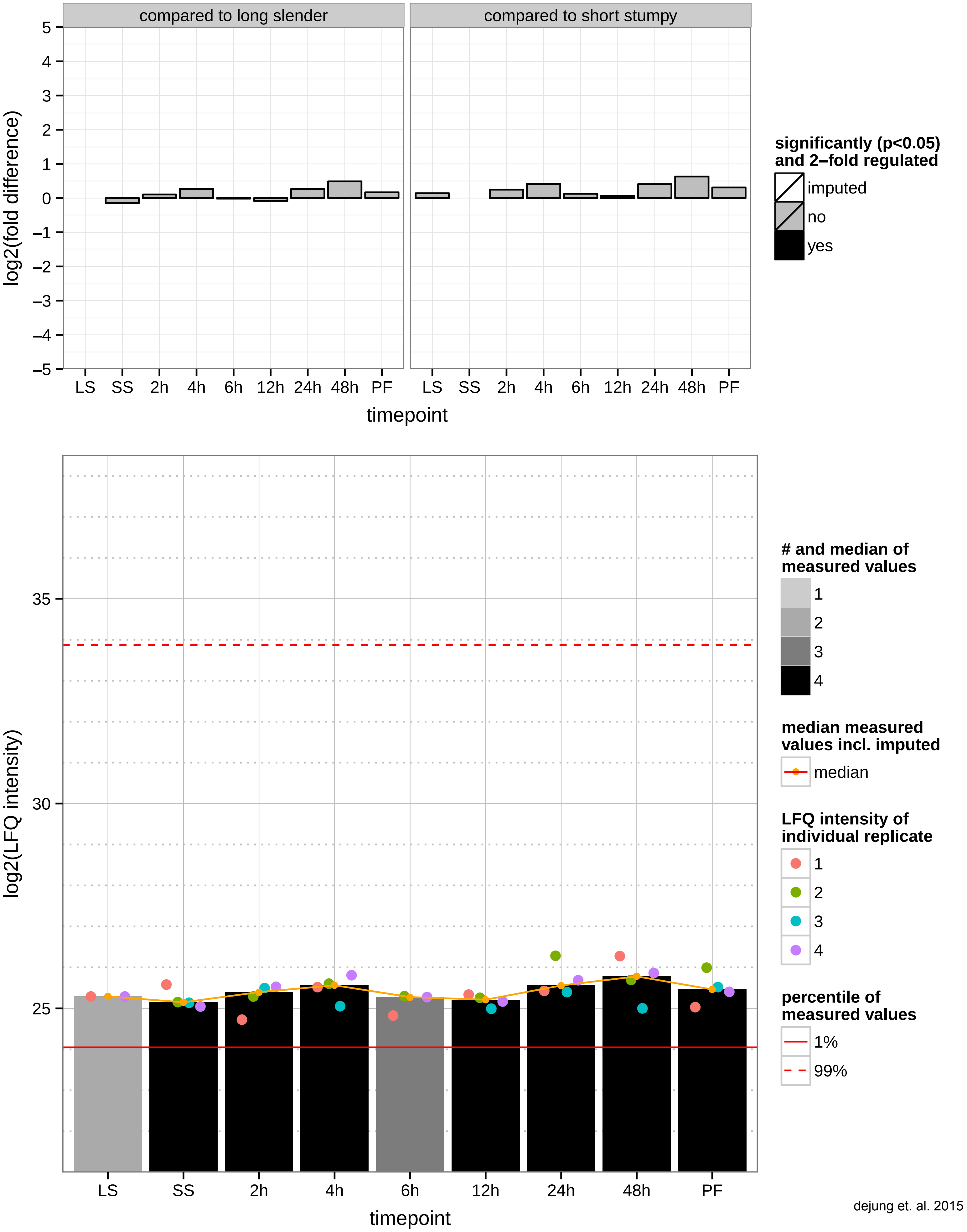
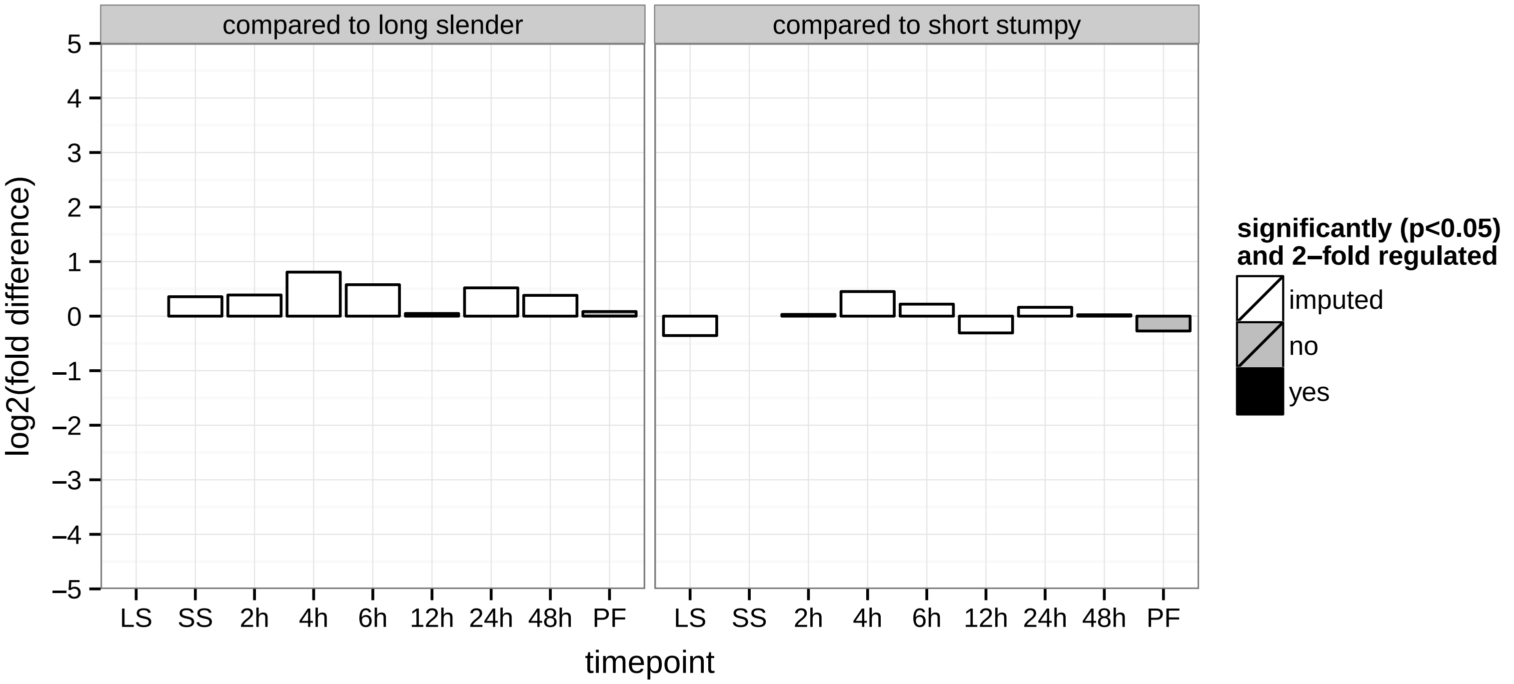
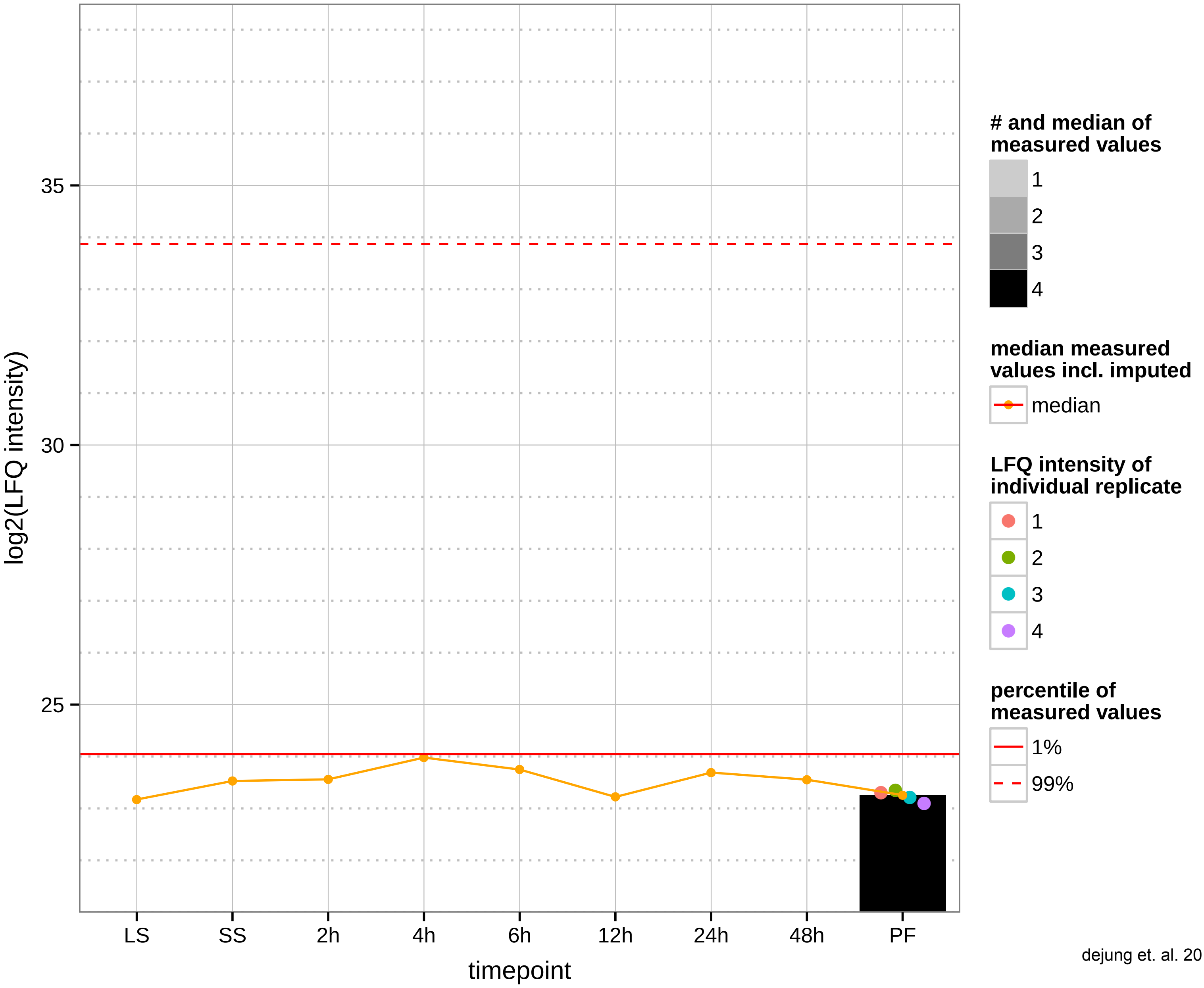
hypothetical protein, conserved
Tb927.3.1170
AGOF: null
AGOC: null
AGOP: regulation of signal transduction, response to biotic stimulus
PGOF: null
PGOC: null
PGOP: regulation of signal transduction



dejung et. al. 2015

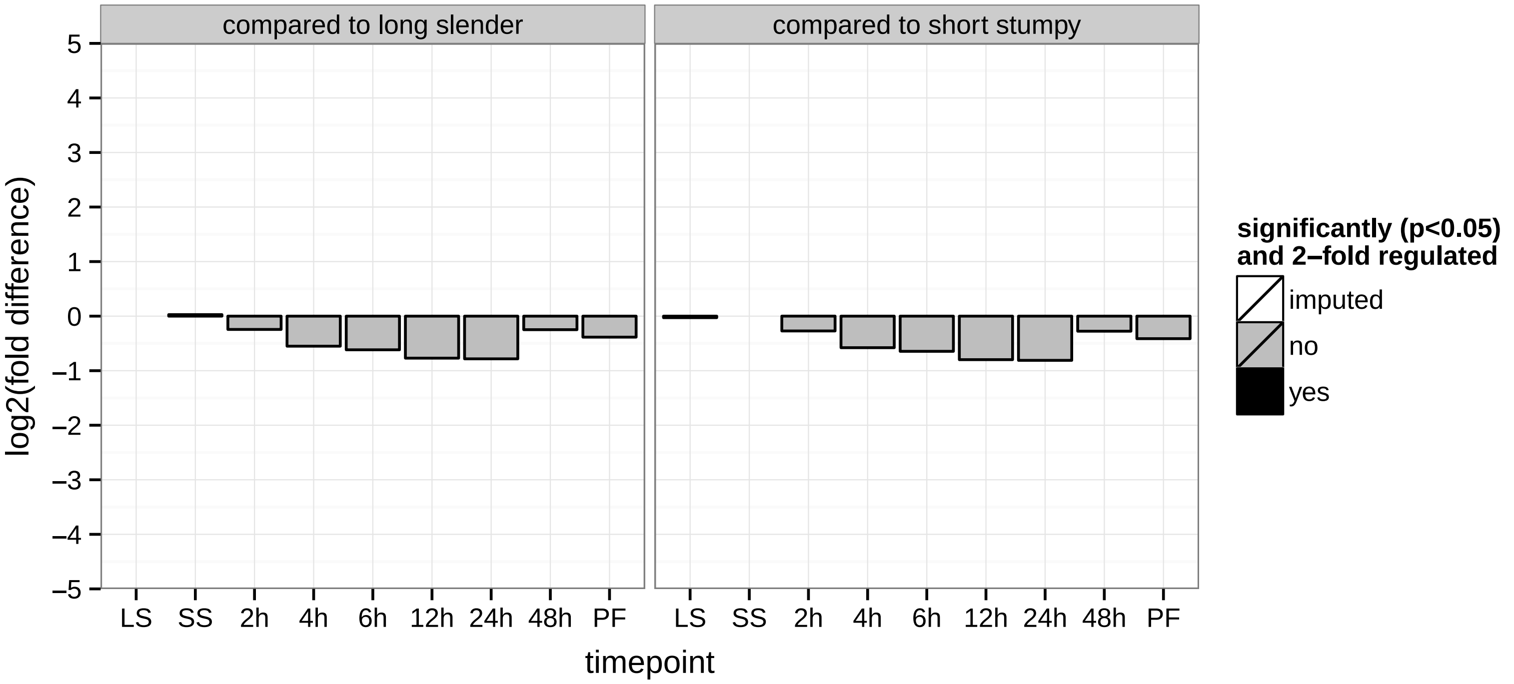
hypothetical protein, conserved
Tb927.3.1180
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

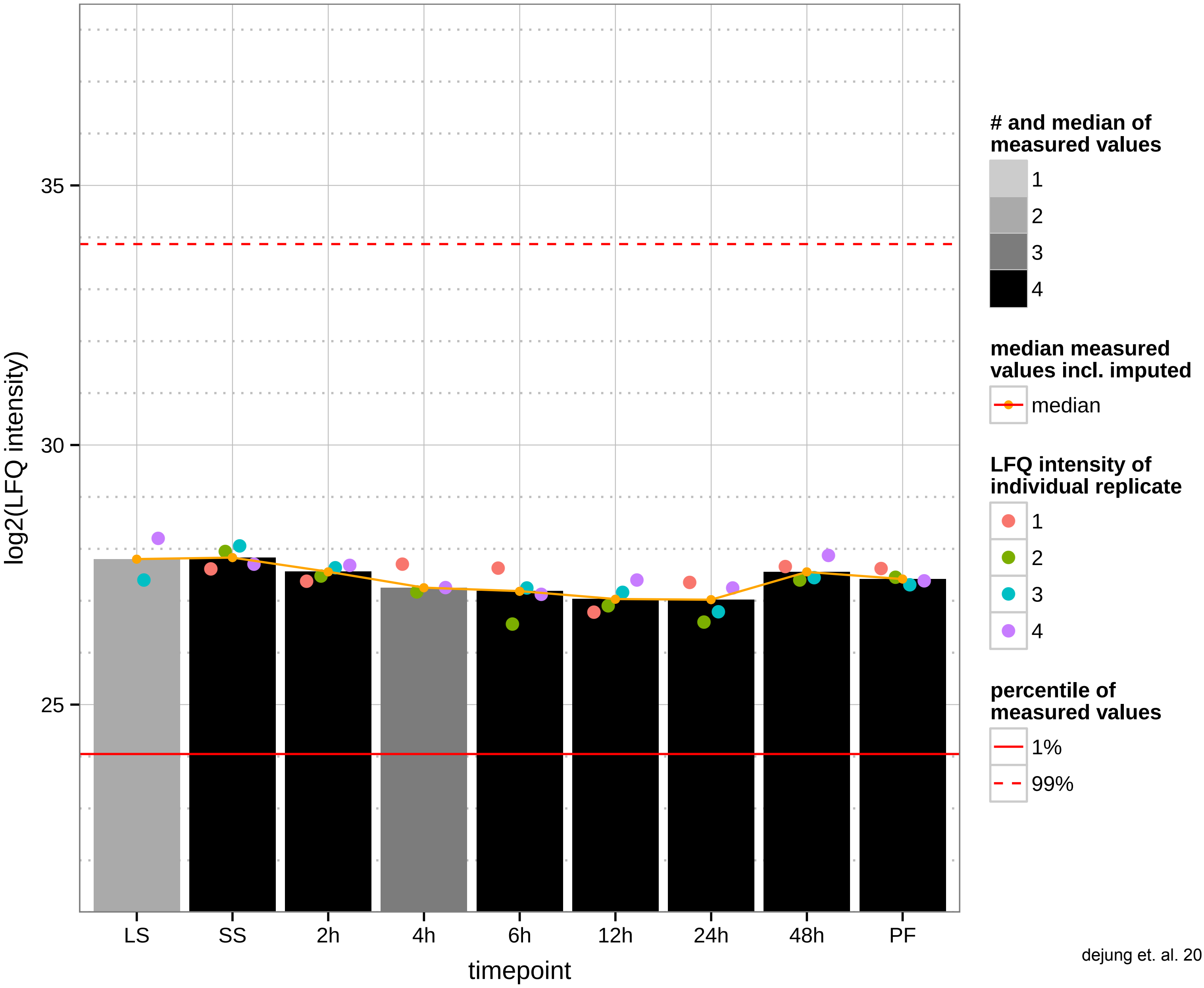




dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.1190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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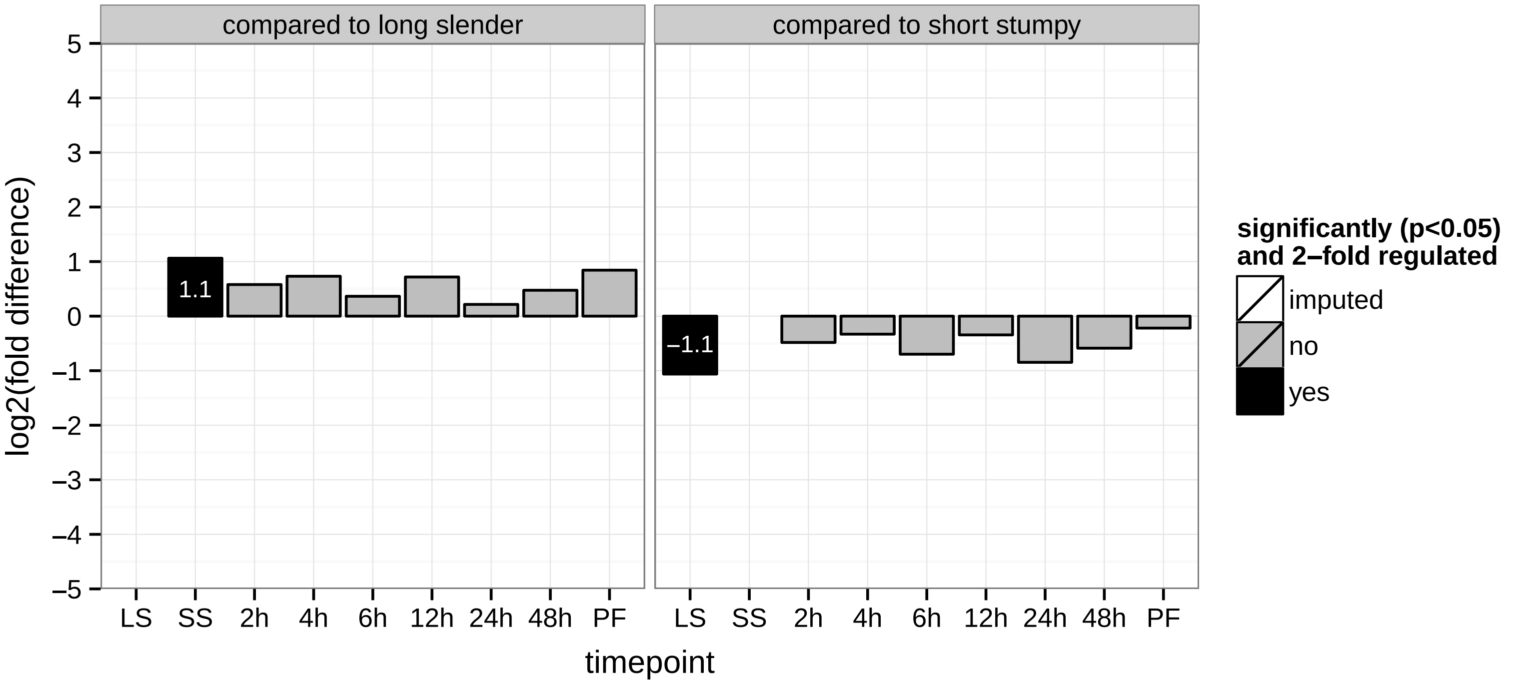
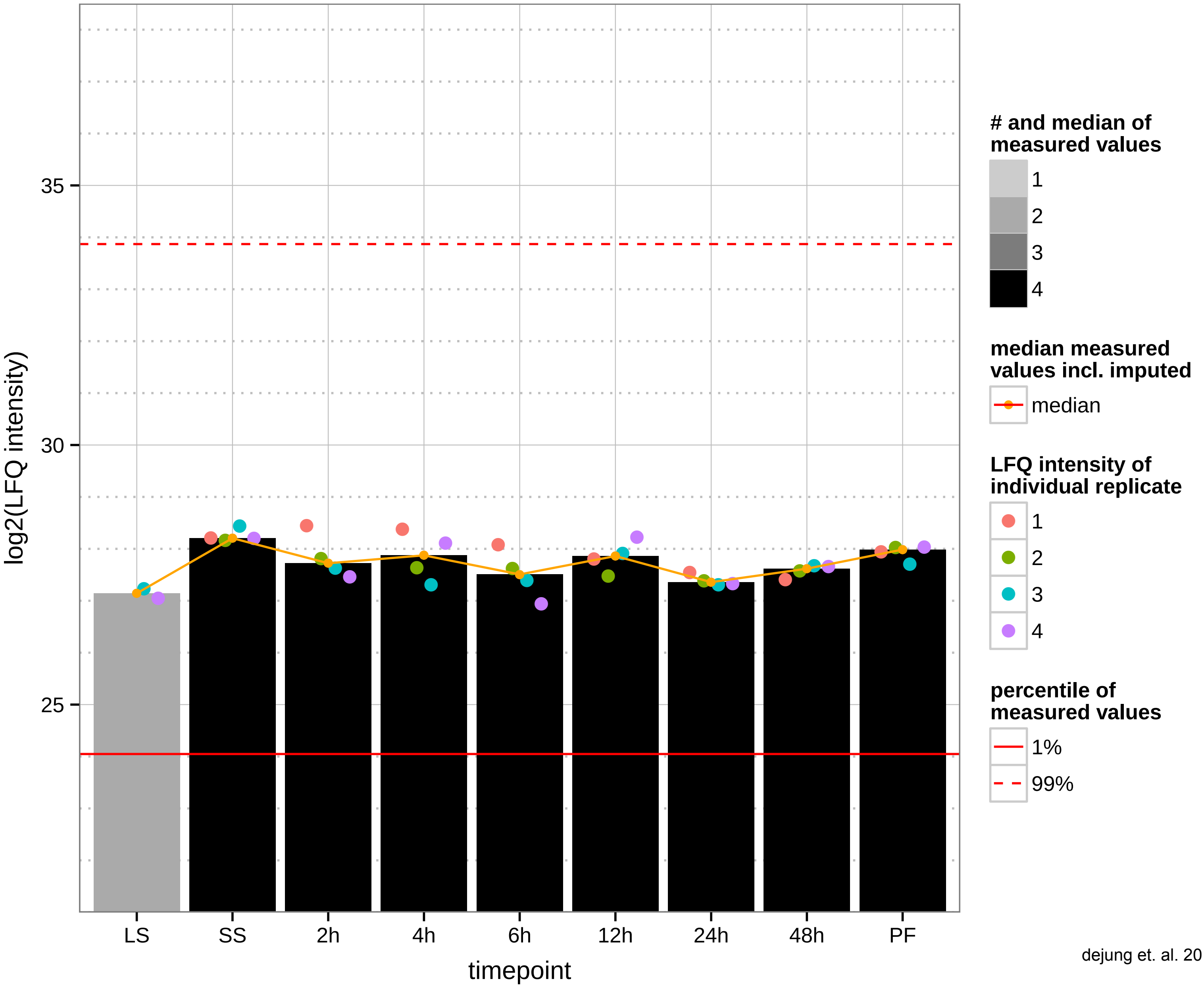
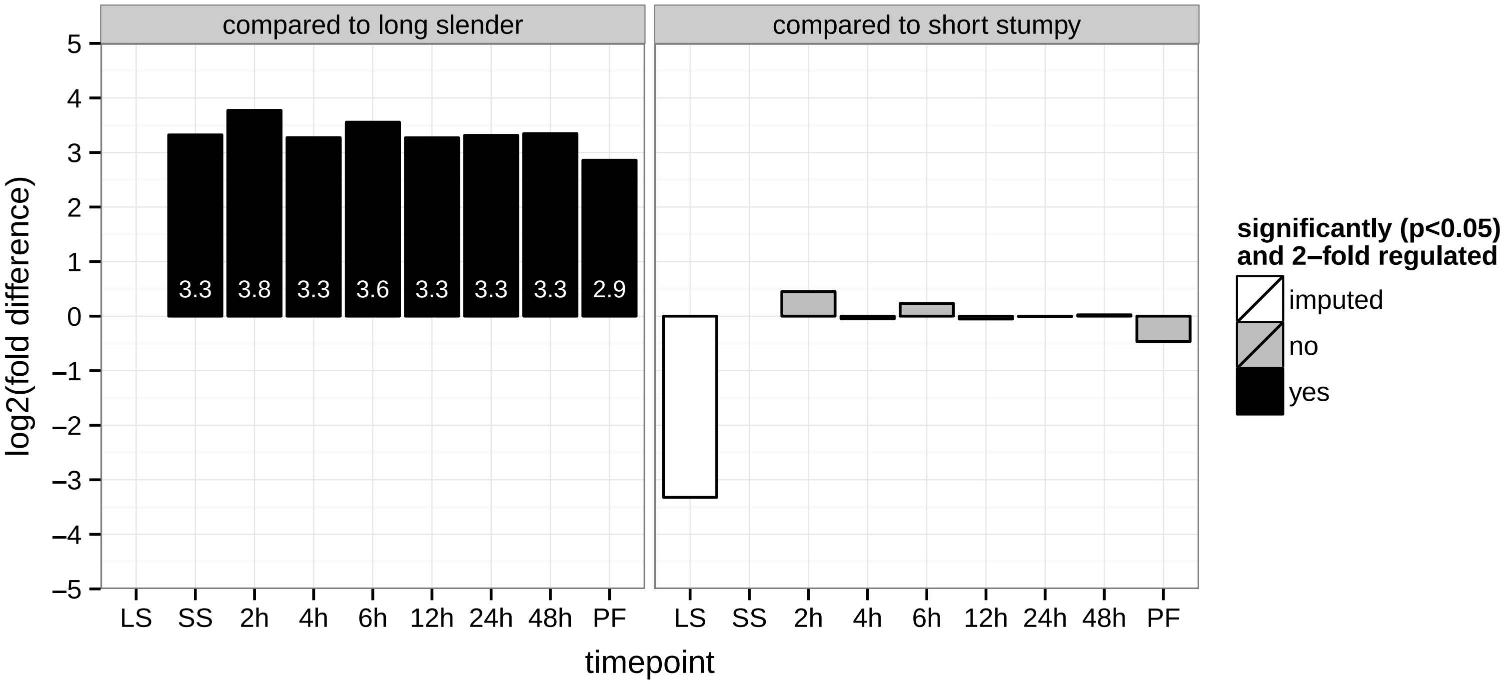
protein transport protein Sec24 (SEC24.1)
Tb927.3.1210
AGOF: protein binding, zinc ion binding
AGOC: COPII vesicle coat
AGOP: ER to Golgi vesicle–mediated transport, intracellular protein transport
PGOF: zinc ion binding
PGOC: COPII vesicle coat
PGOP: ER to Golgi vesicle–mediated transport, intracellular protein transport

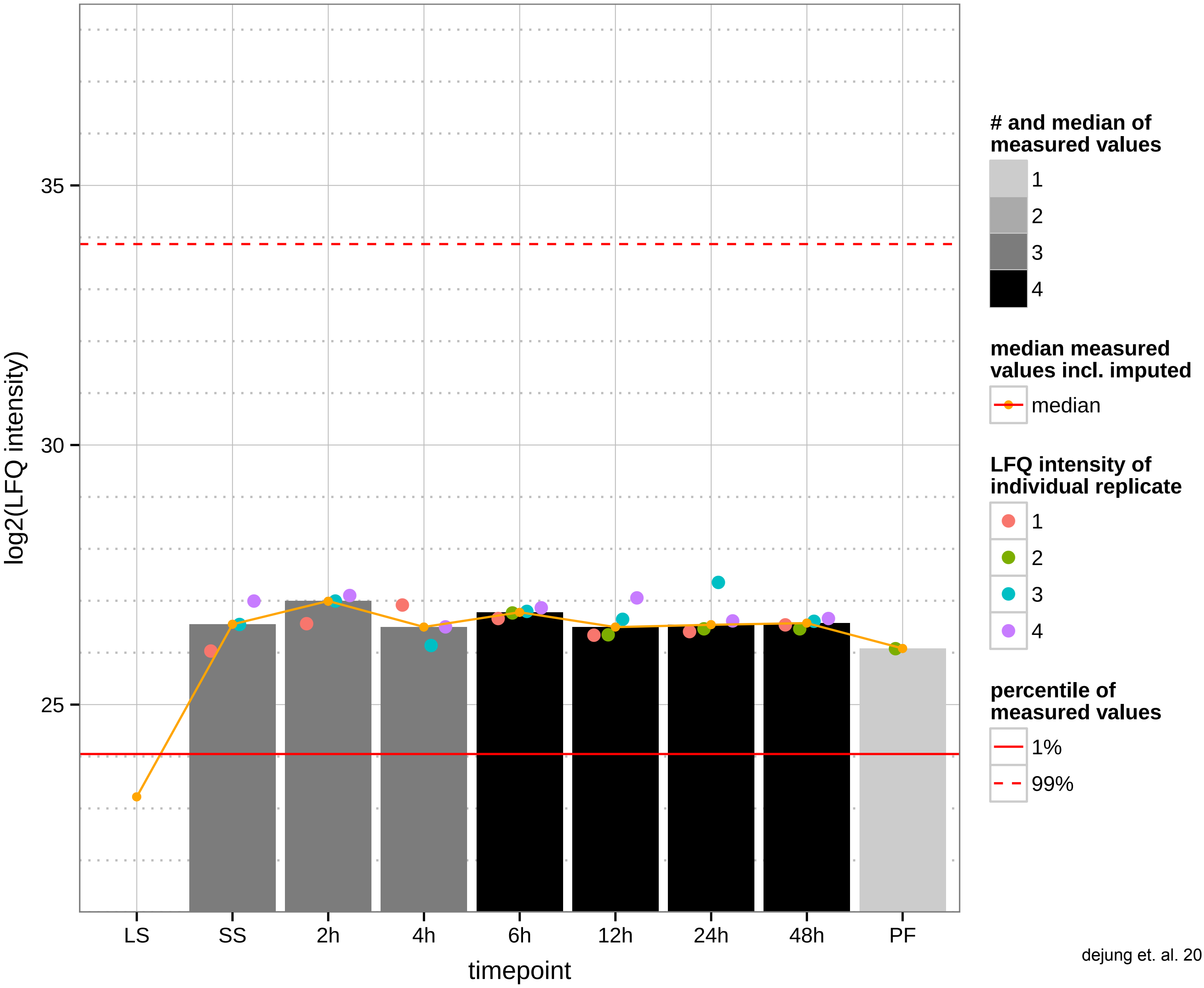




dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.1270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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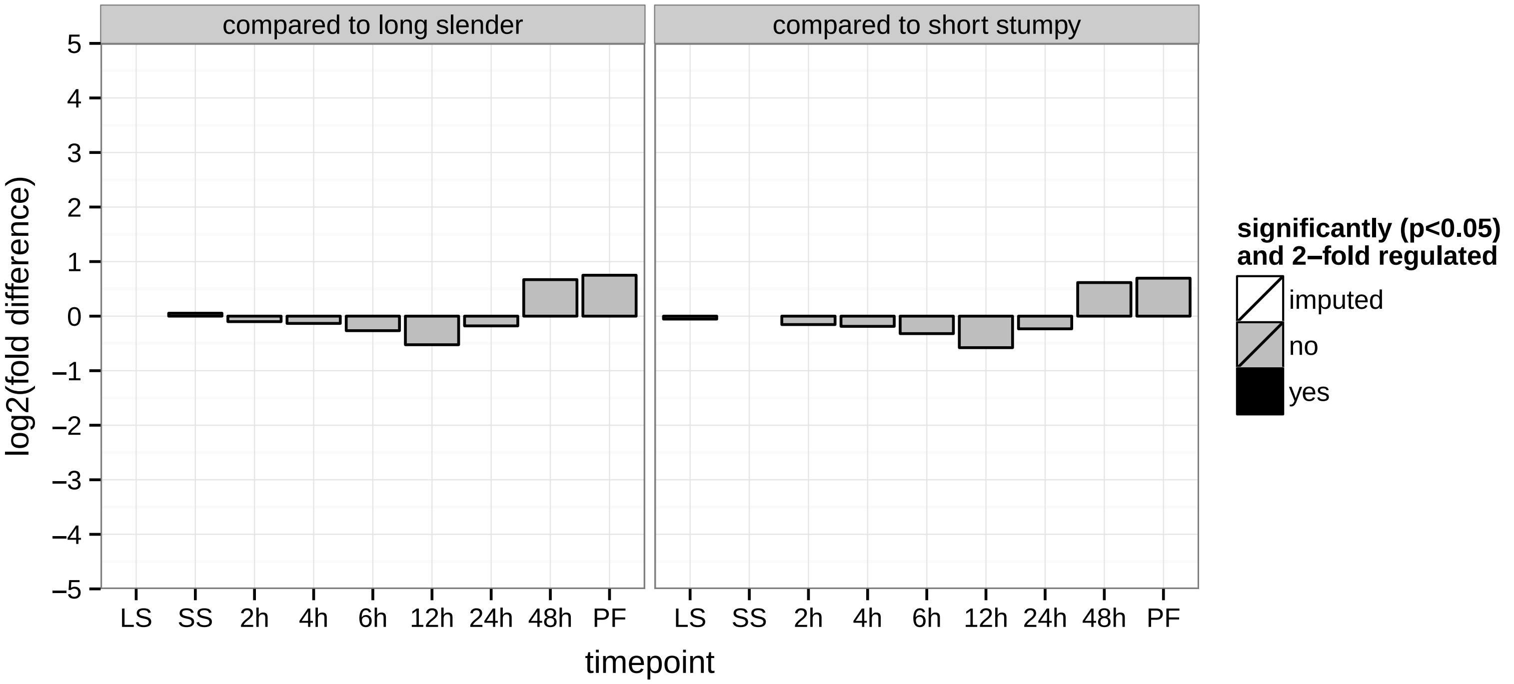
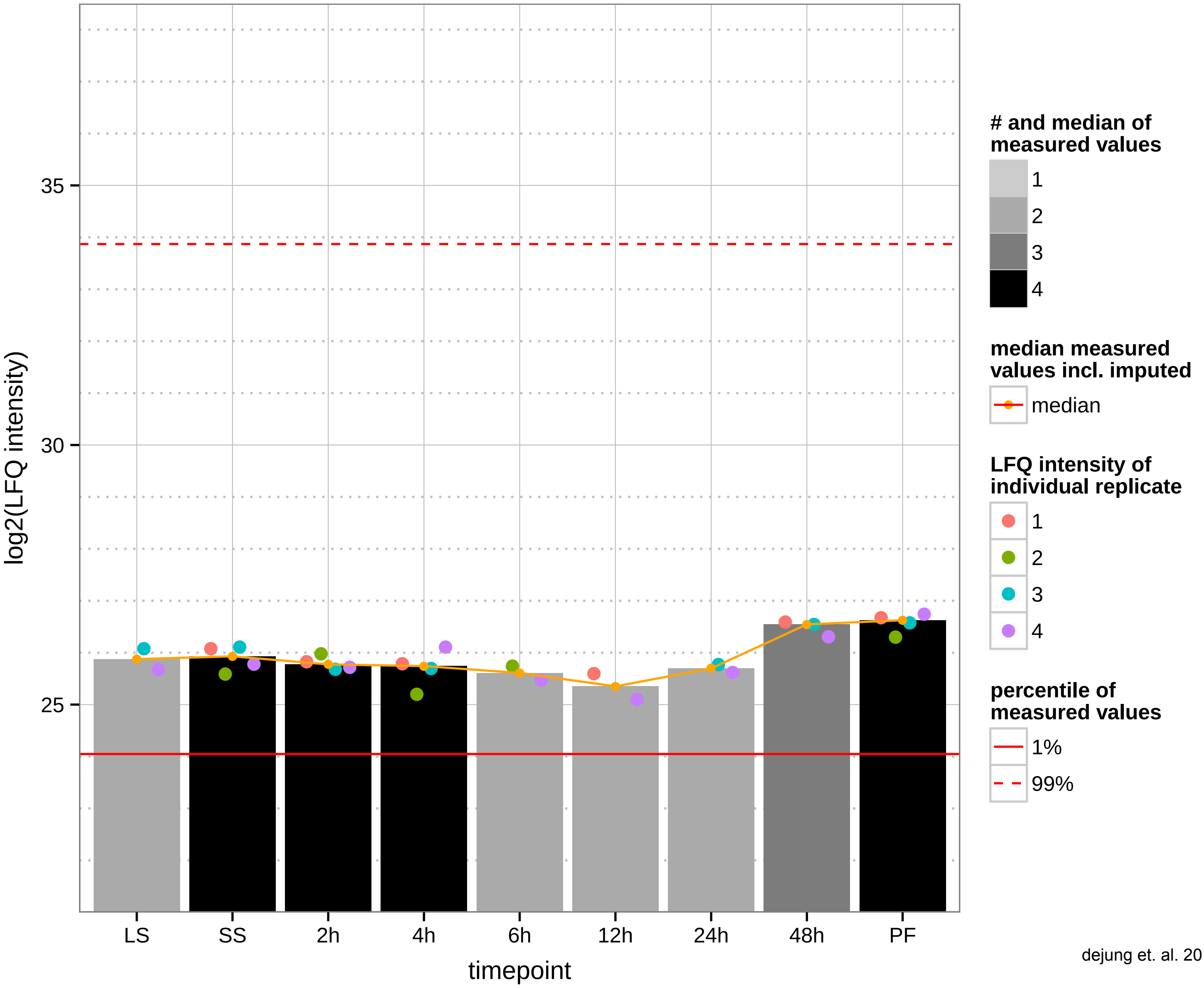
hypothetical protein, conserved
Tb927.3.1280
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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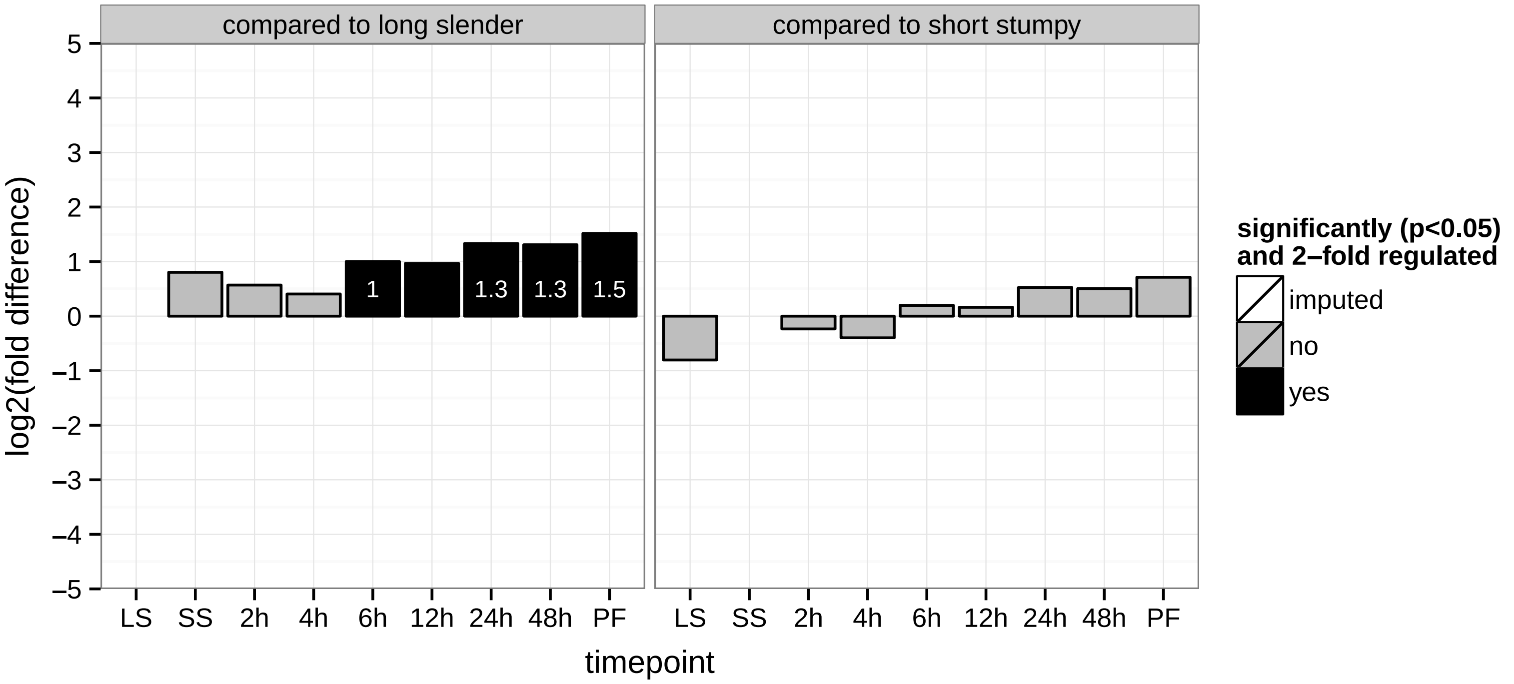
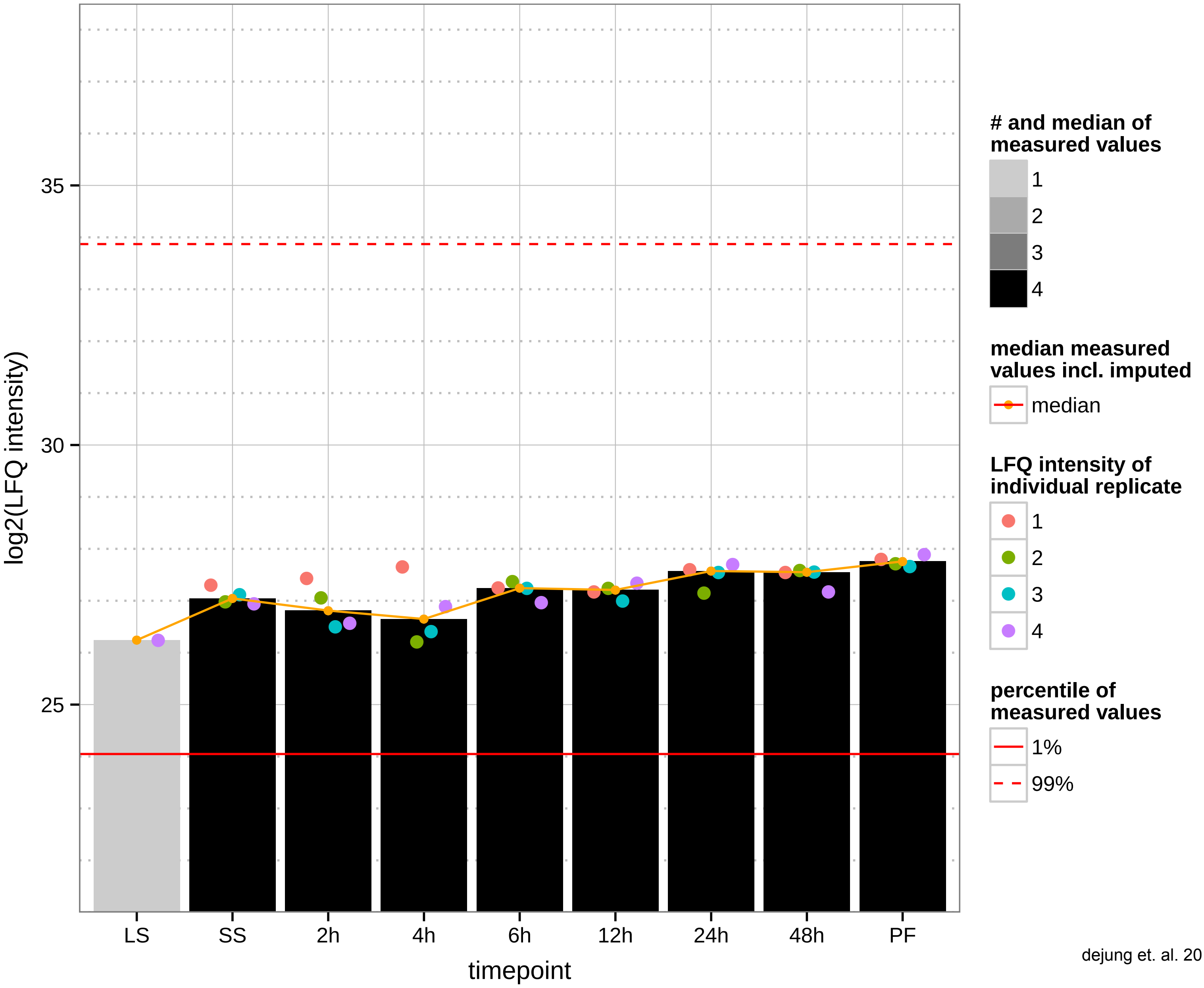
cullin 4B, putative
Tb927.3.1290
AGOF: ubiquitin protein ligase binding
AGOC: cullin–RING ubiquitin ligase complex
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ubiquitin protein ligase binding
PGOC: cullin–RING ubiquitin ligase complex
PGOP: ubiquitin–dependent protein catabolic process





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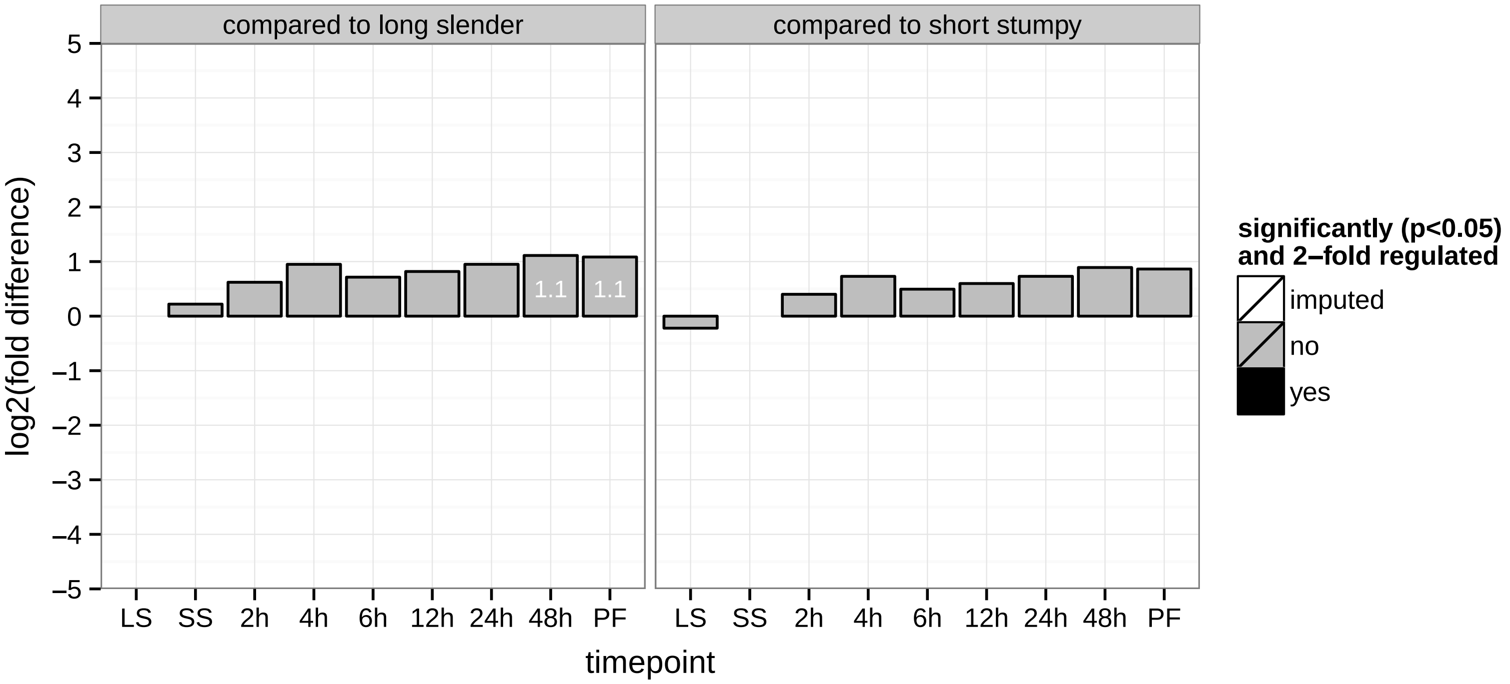
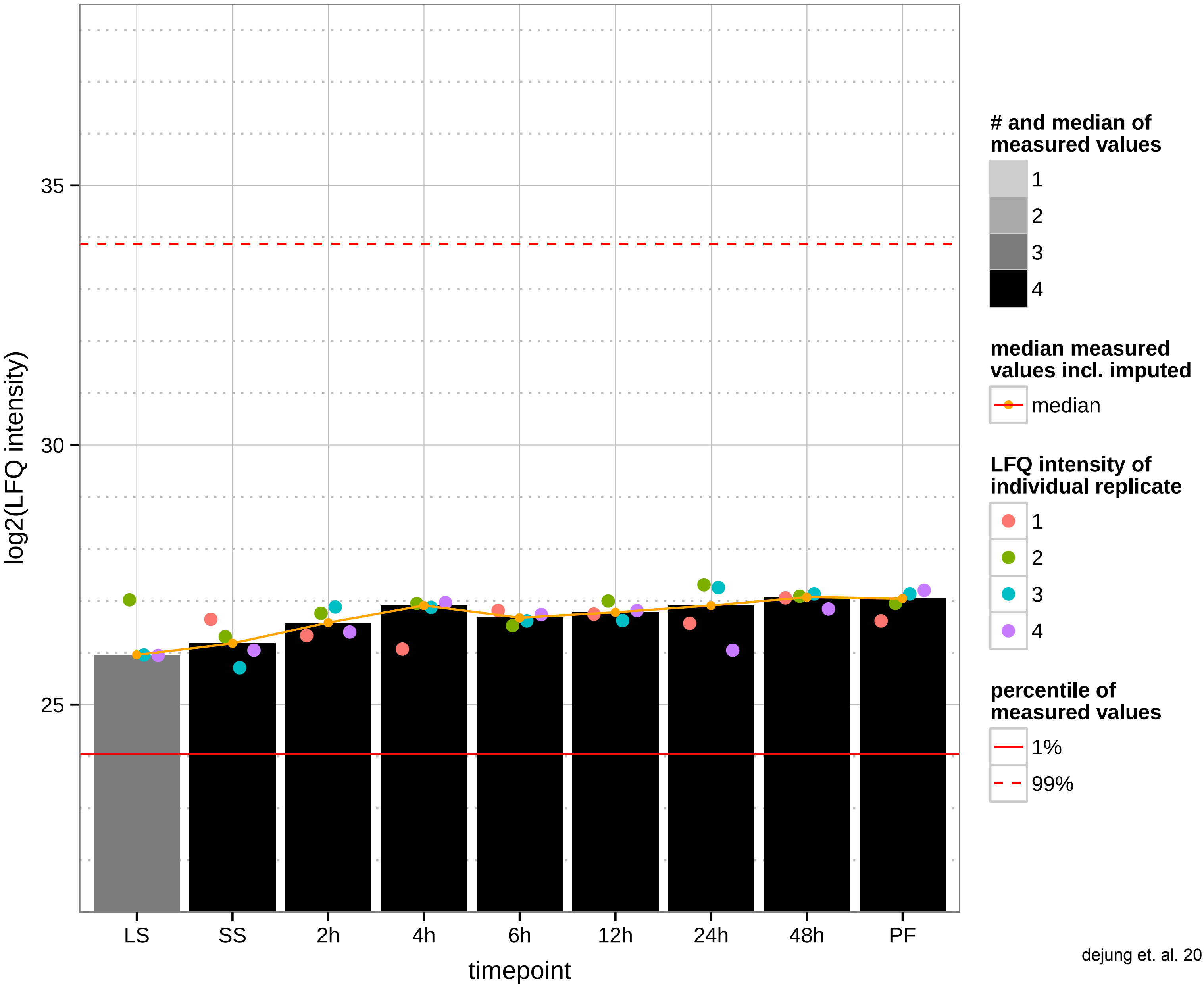
hypothetical protein, conserved
Tb927.3.1300
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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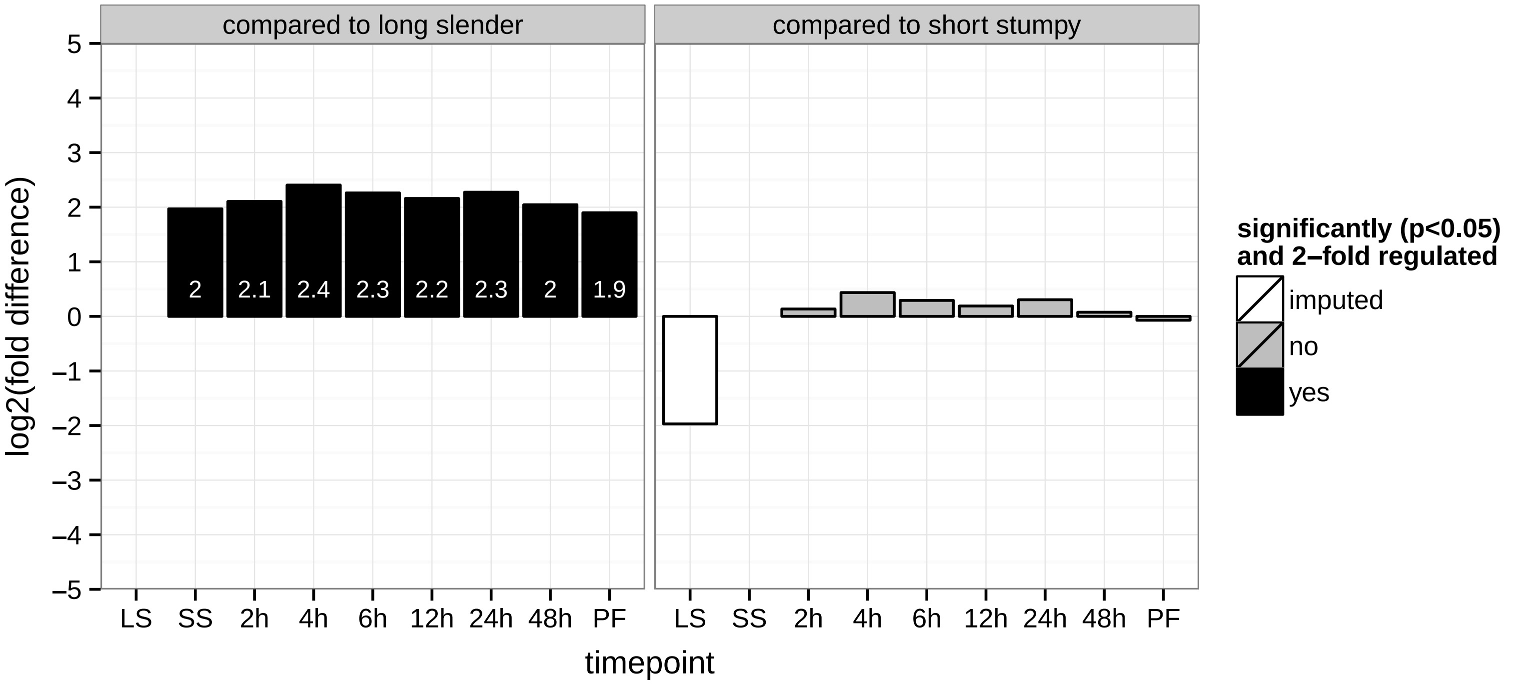
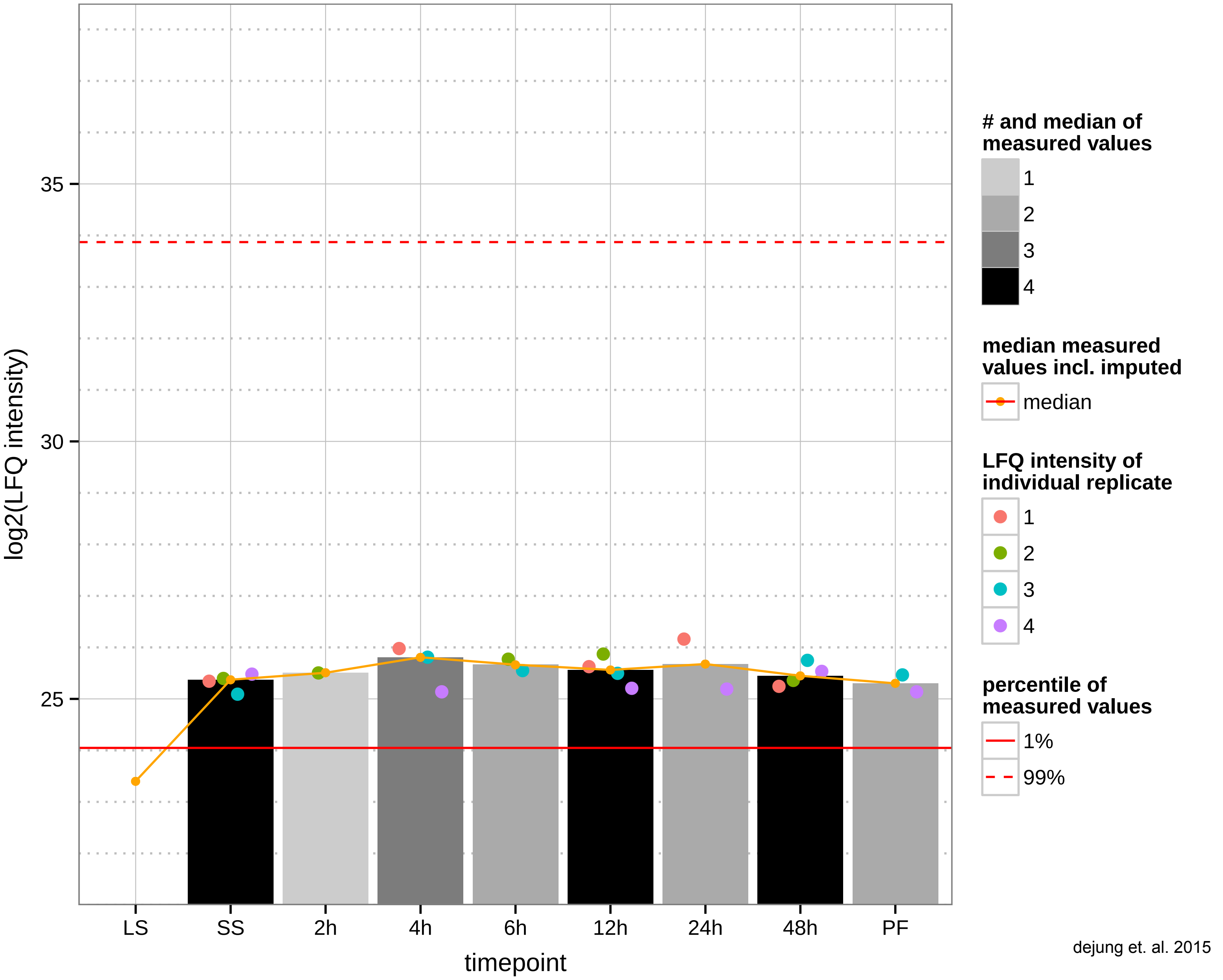
Nuclear cap–binding protein subunit 66, zinc finger CCCH domain containing protein 7 (CBP66)
Tb927.3.1340
AGOF: RNA binding
AGOC: nuclear cap binding complex
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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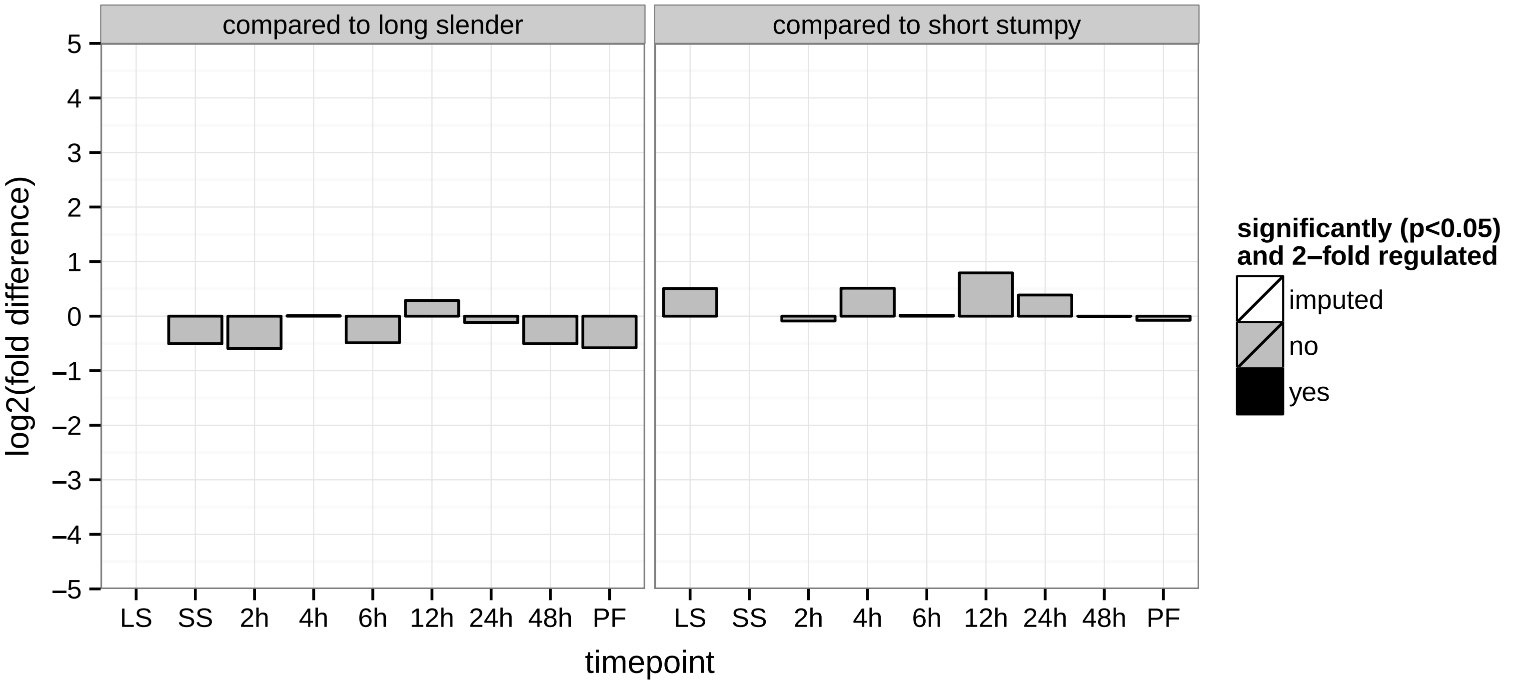
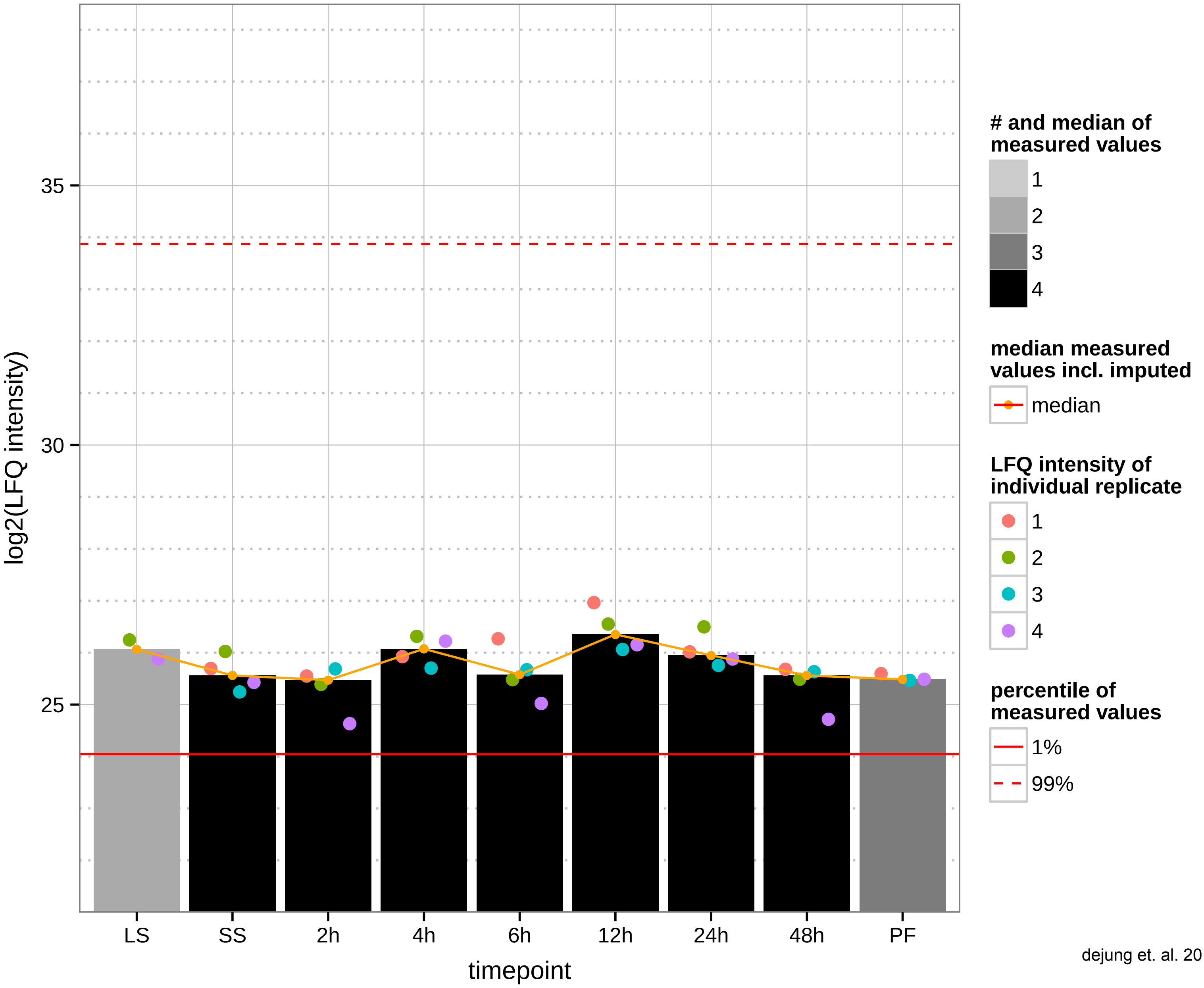
chaperone protein DNAj, putative
Tb927.3.1430
AGOF: chaperone binding, heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding, unfolded protein binding
PGOC: null
PGOP: protein folding





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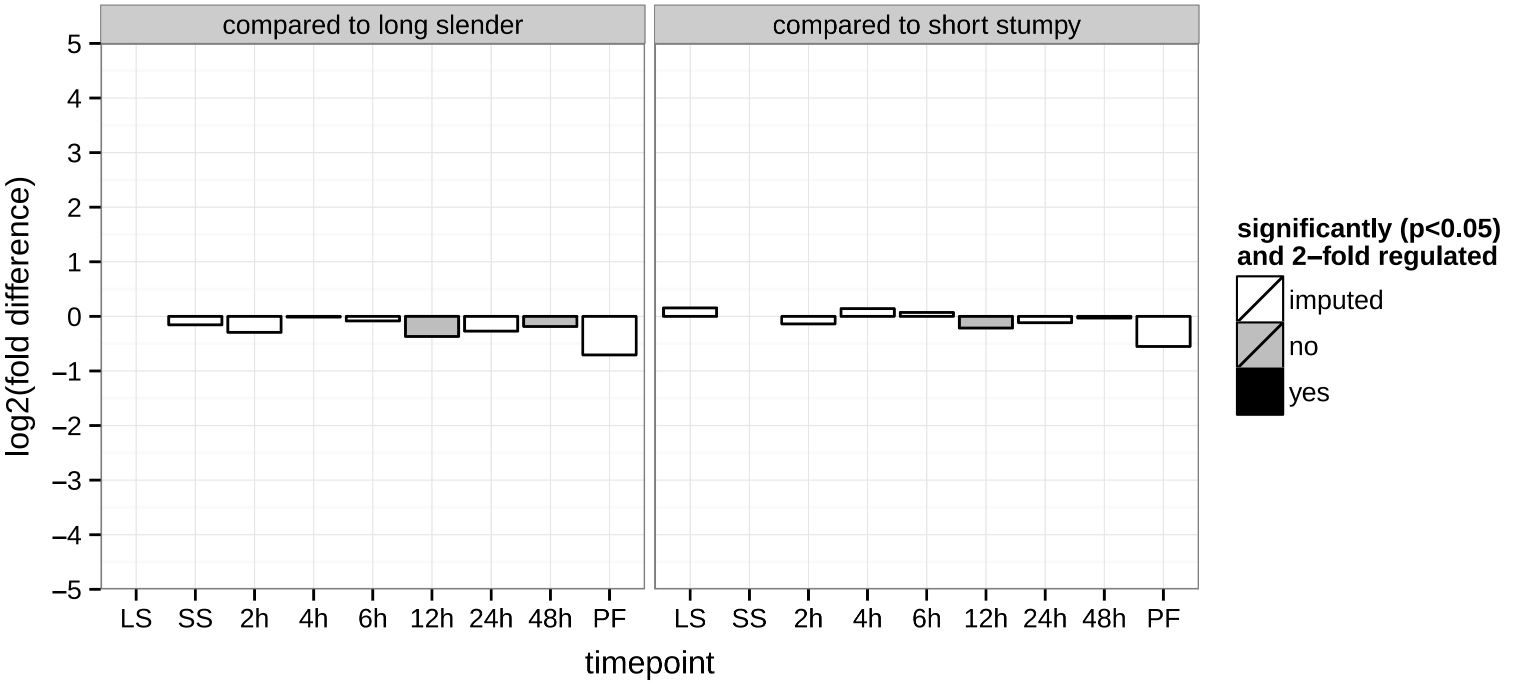
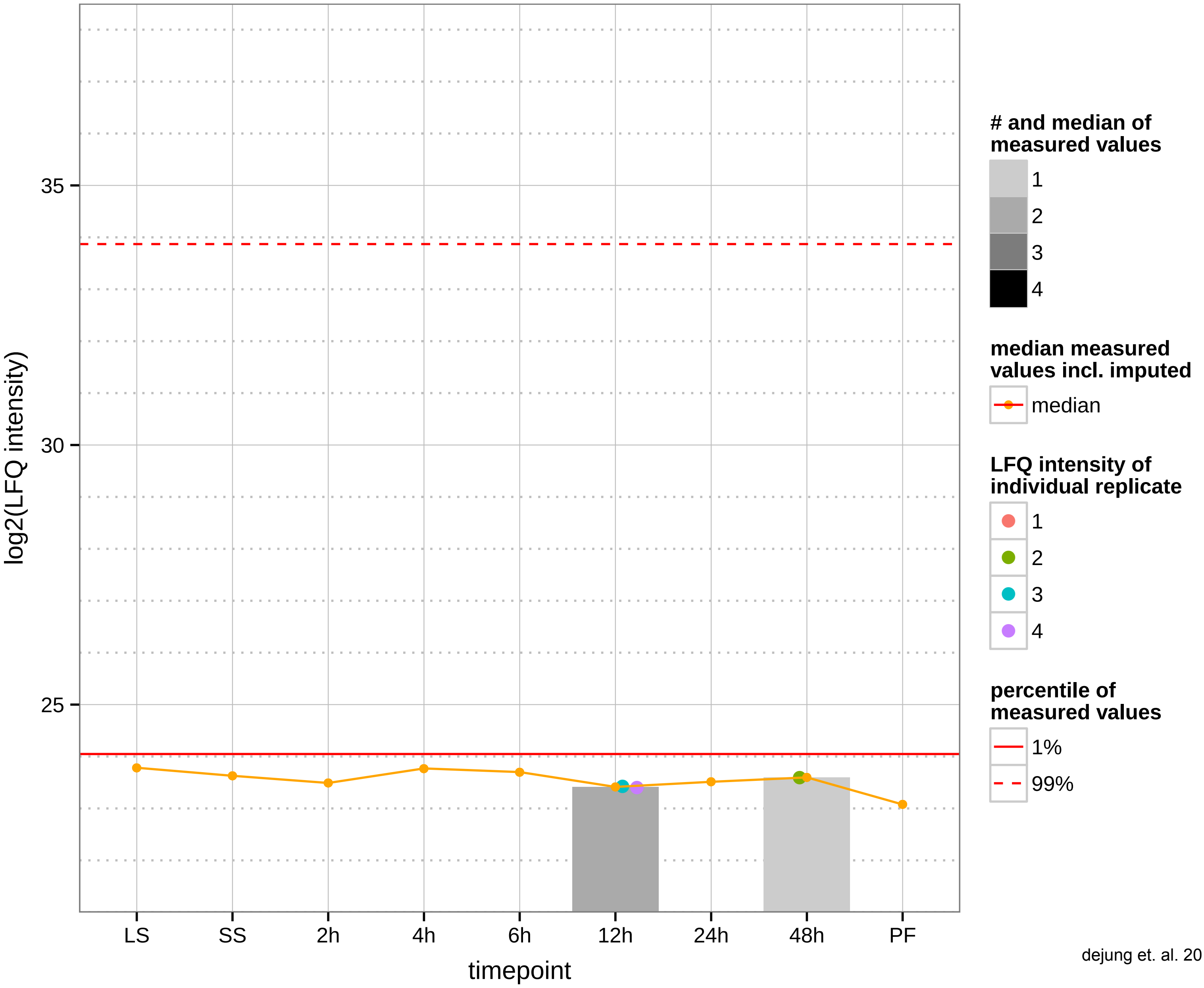
hypothetical protein, conserved
Tb927.3.1530;Tb927.3.1450
AGOF: metal ion transmembrane transporter activity, null
AGOC: membrane, null
AGOP: metal ion transport, null
PGOF: metal ion transmembrane transporter activity
PGOC: membrane
PGOP: metal ion transport, transmembrane transport





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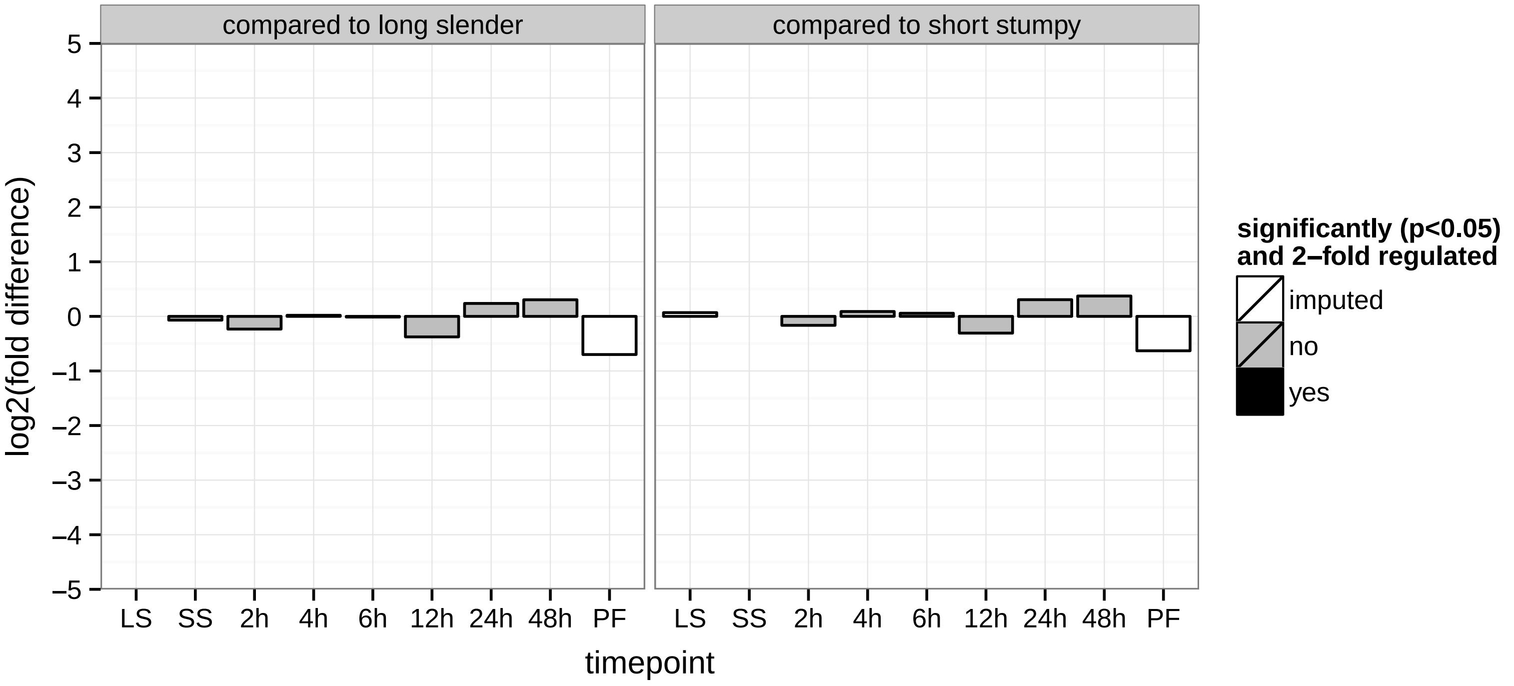
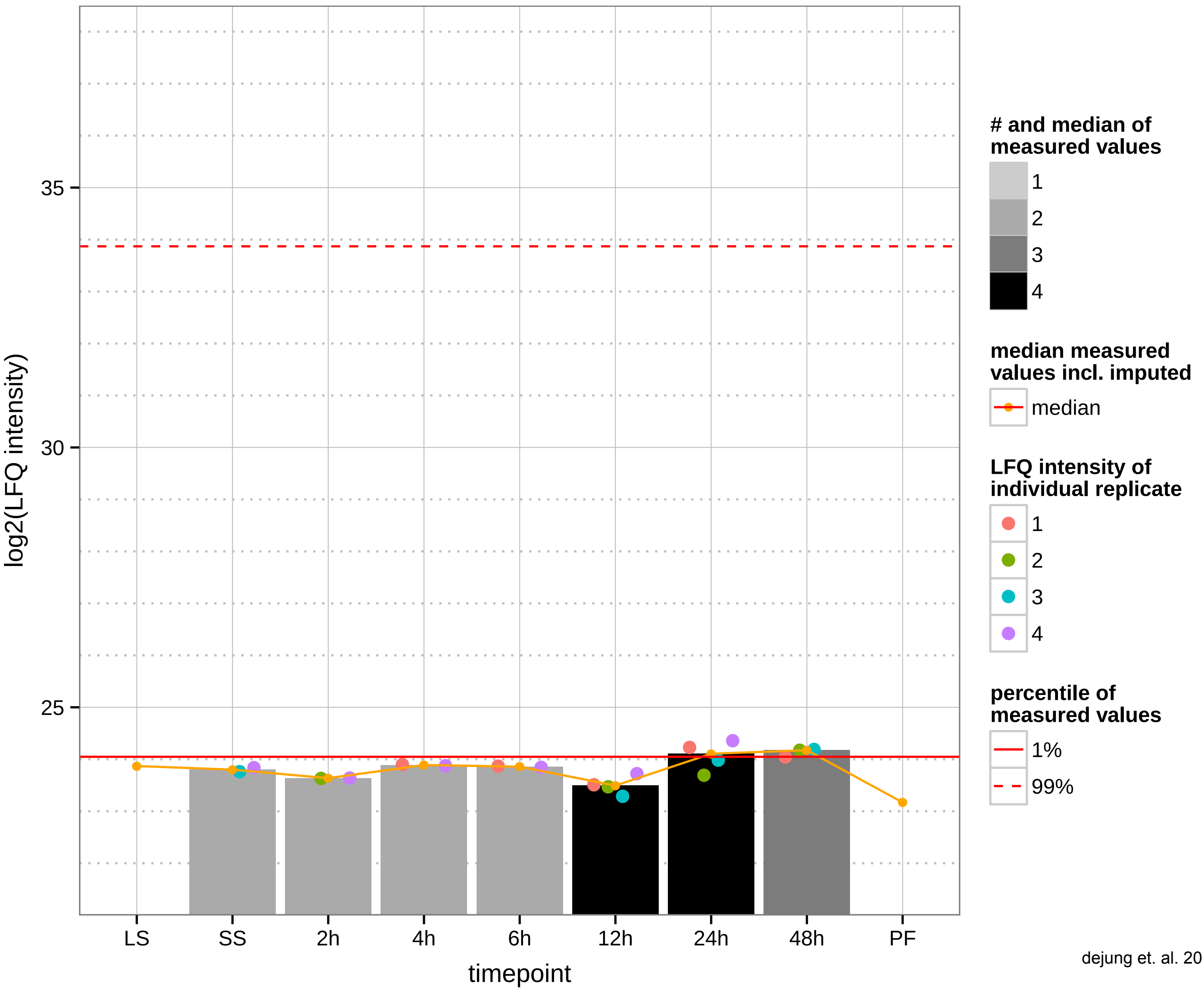
protein kinase, putative
Tb927.3.1570
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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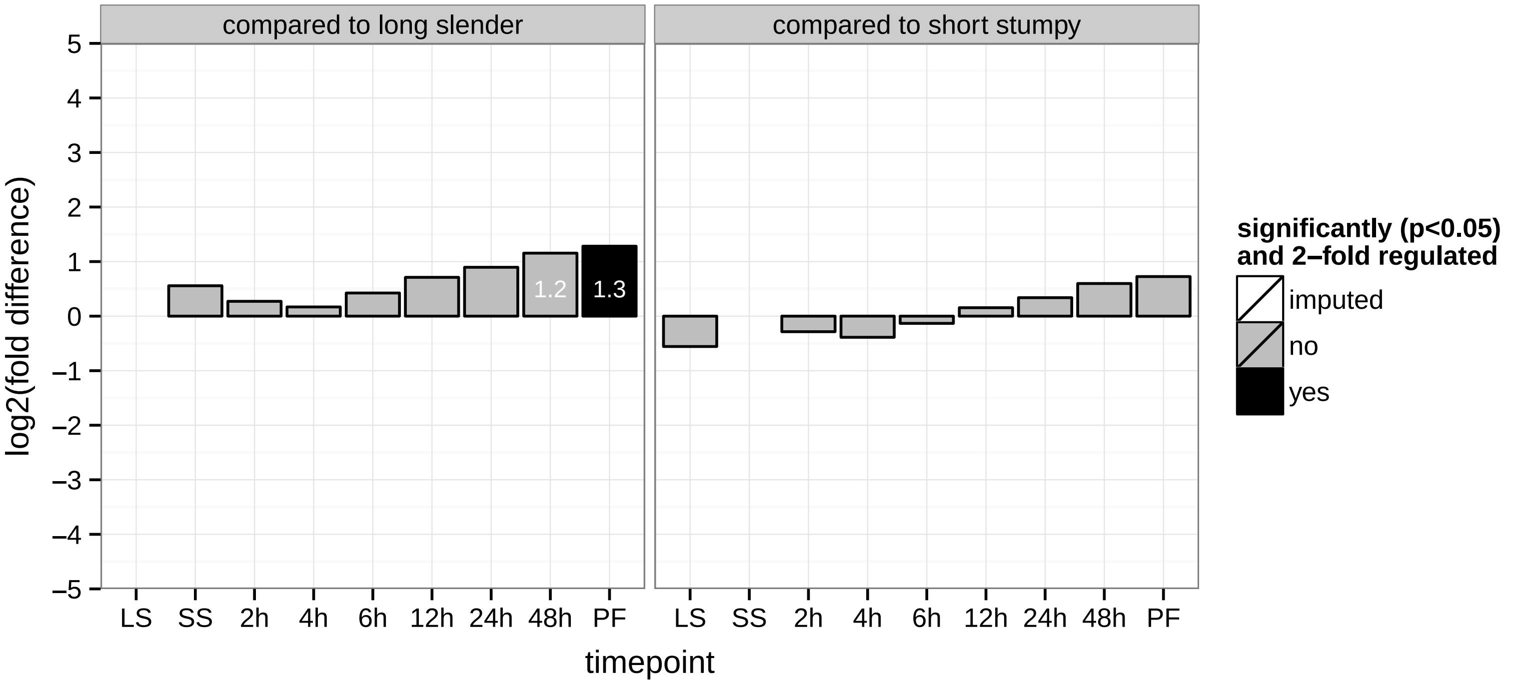
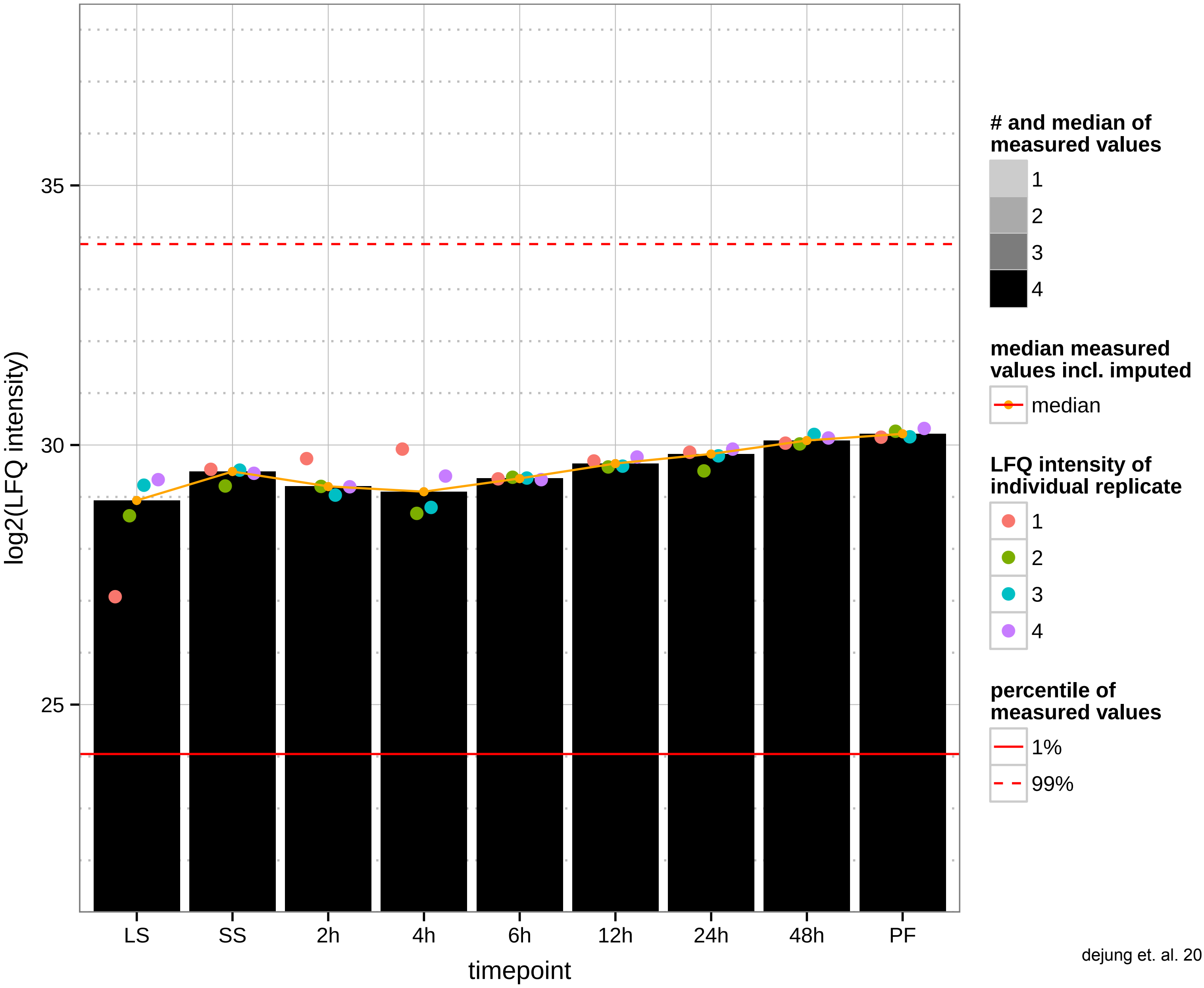
mitochondrial RNA binding complex 1 subunit (MRB1590)
Tb927.3.1590
AGOF: RNA binding
AGOC: mitochondrion
AGOP: cytidine to uridine editing, mRNA stabilization
PGOF: null
PGOC: null
PGOP: null





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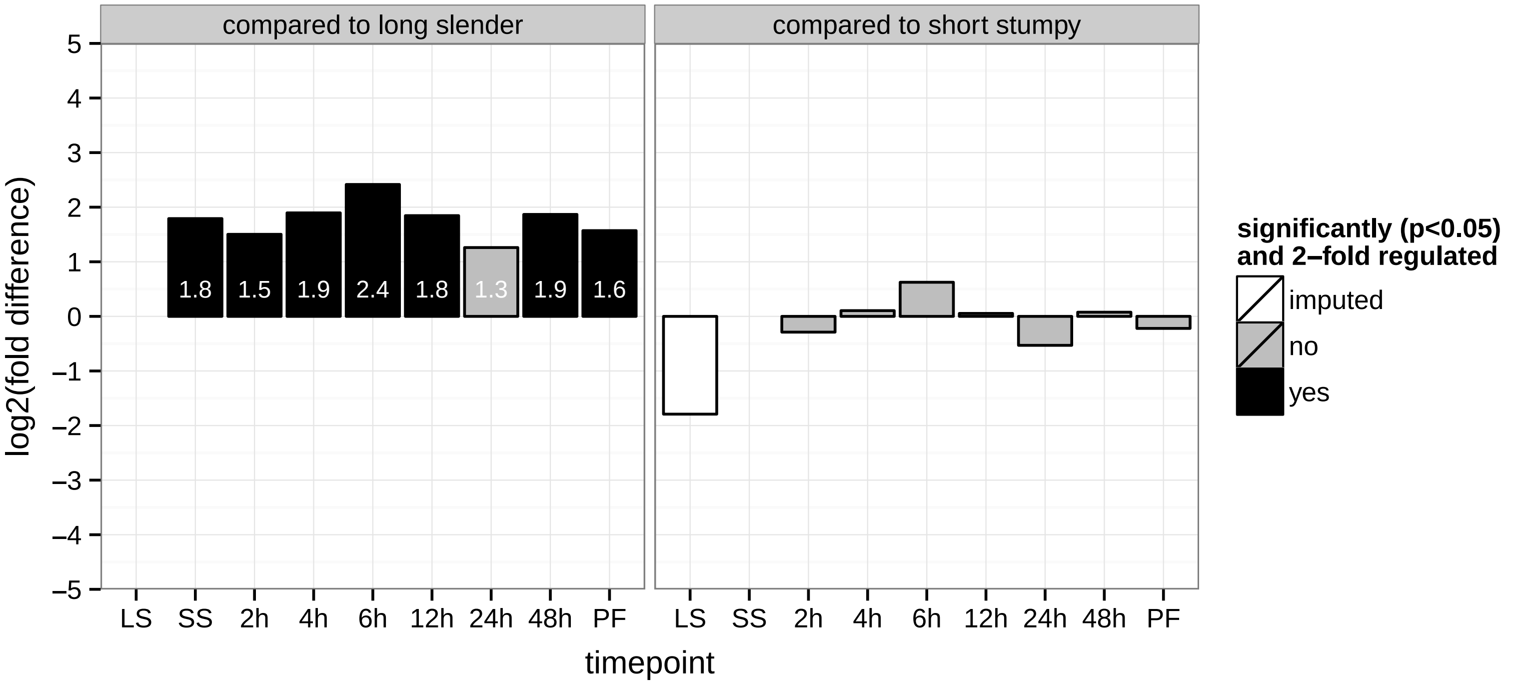
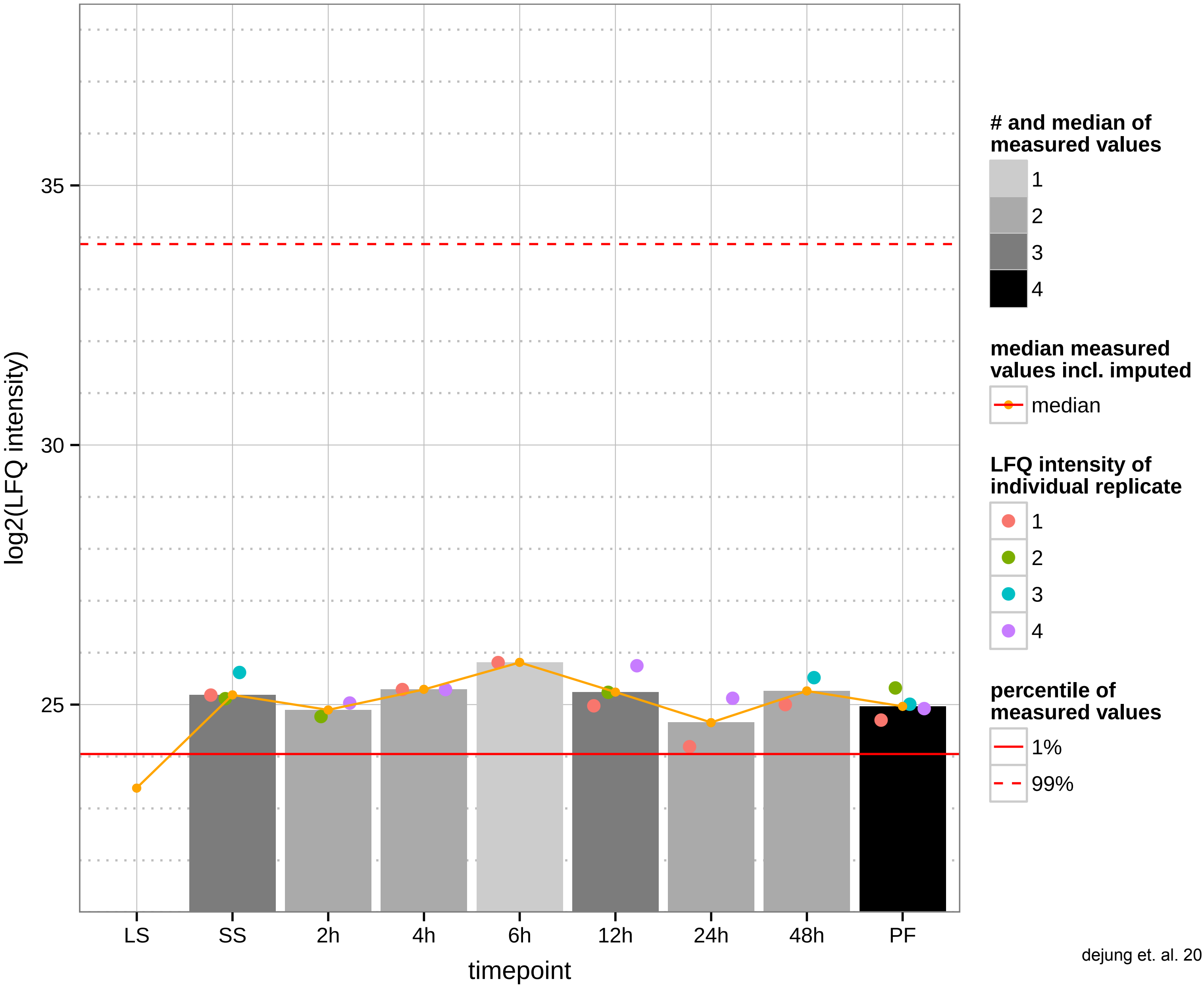
hypothetical protein, conserved
Tb927.3.1620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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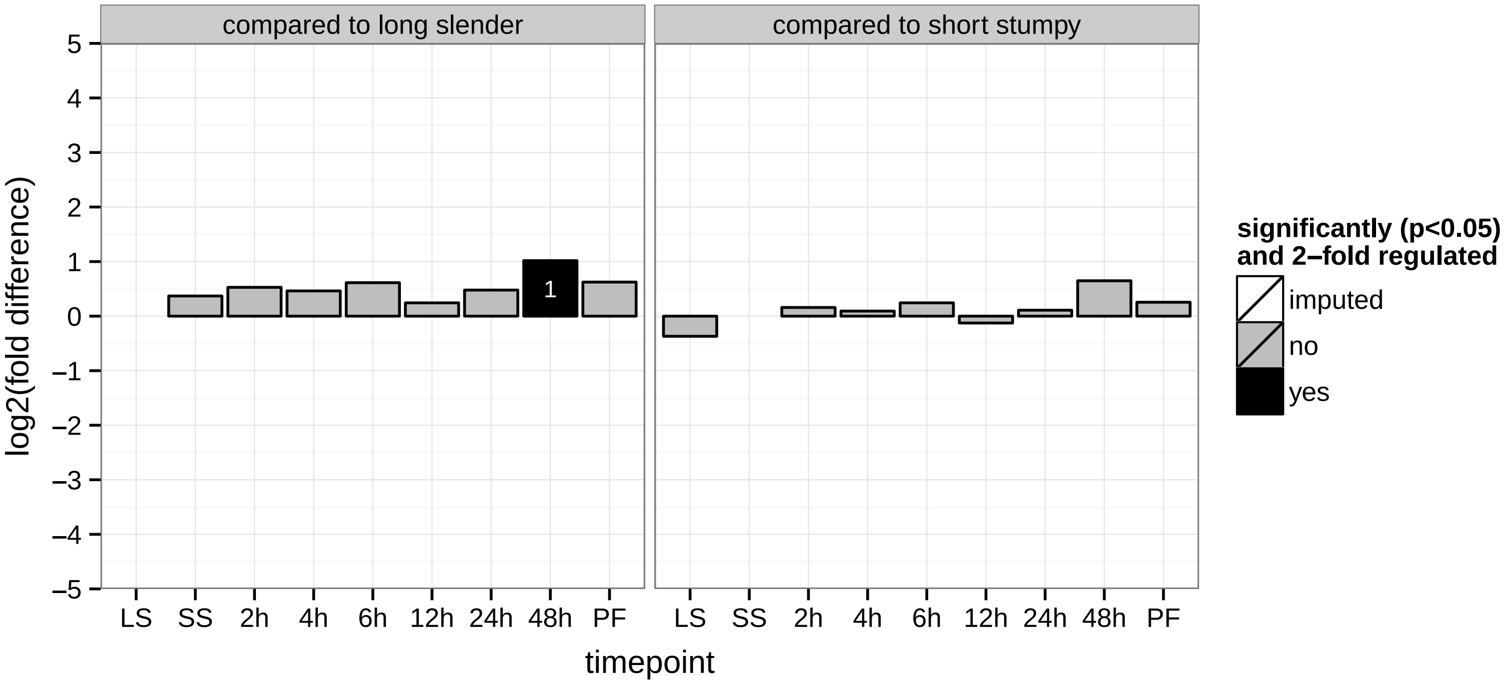
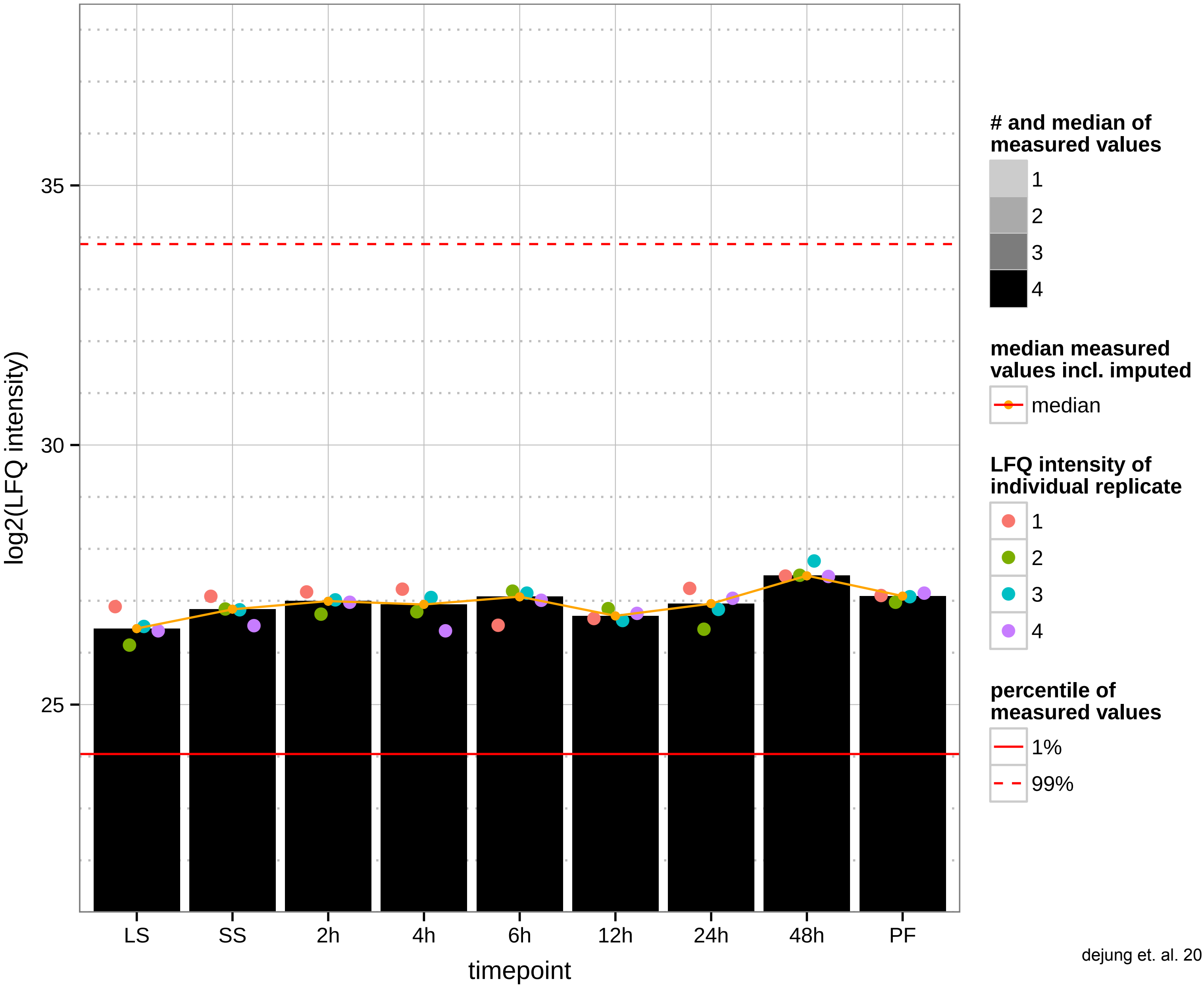
hypothetical protein, conserved
Tb927.3.1670
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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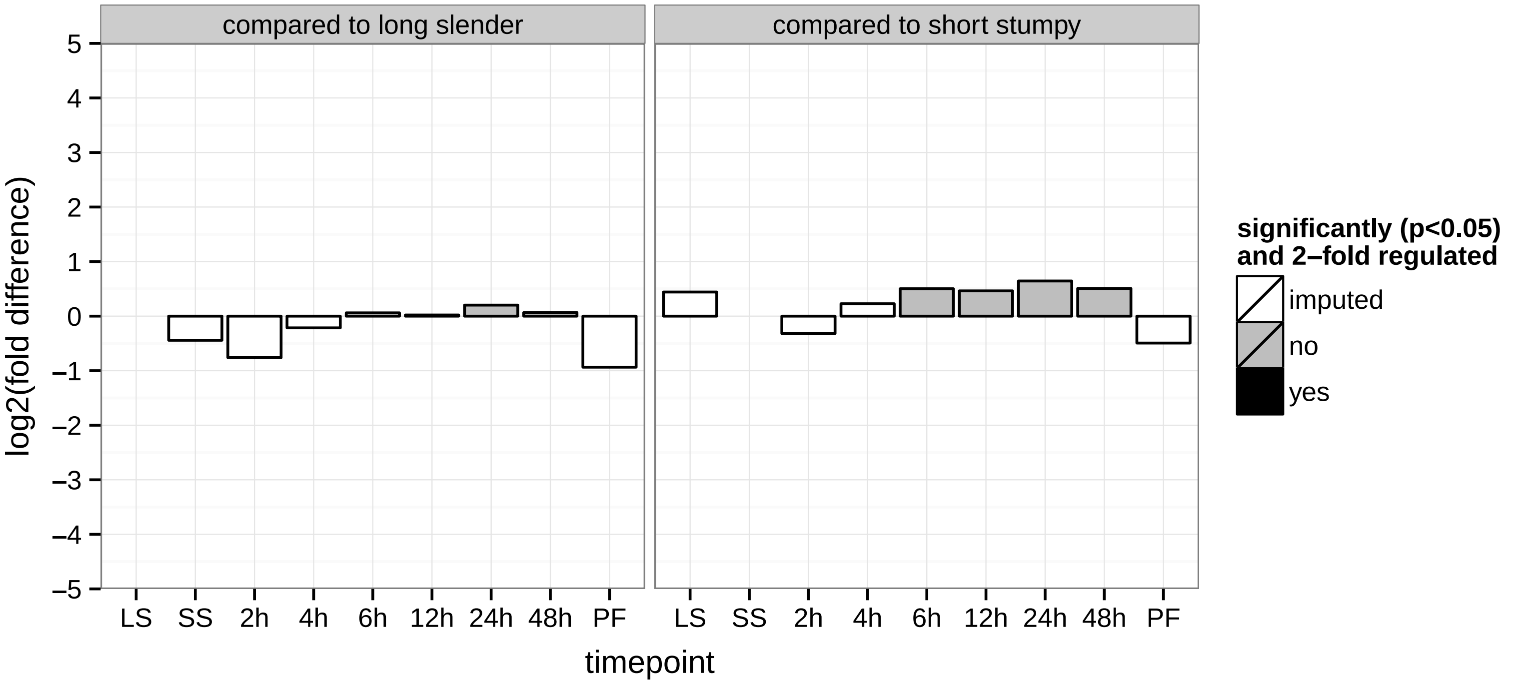
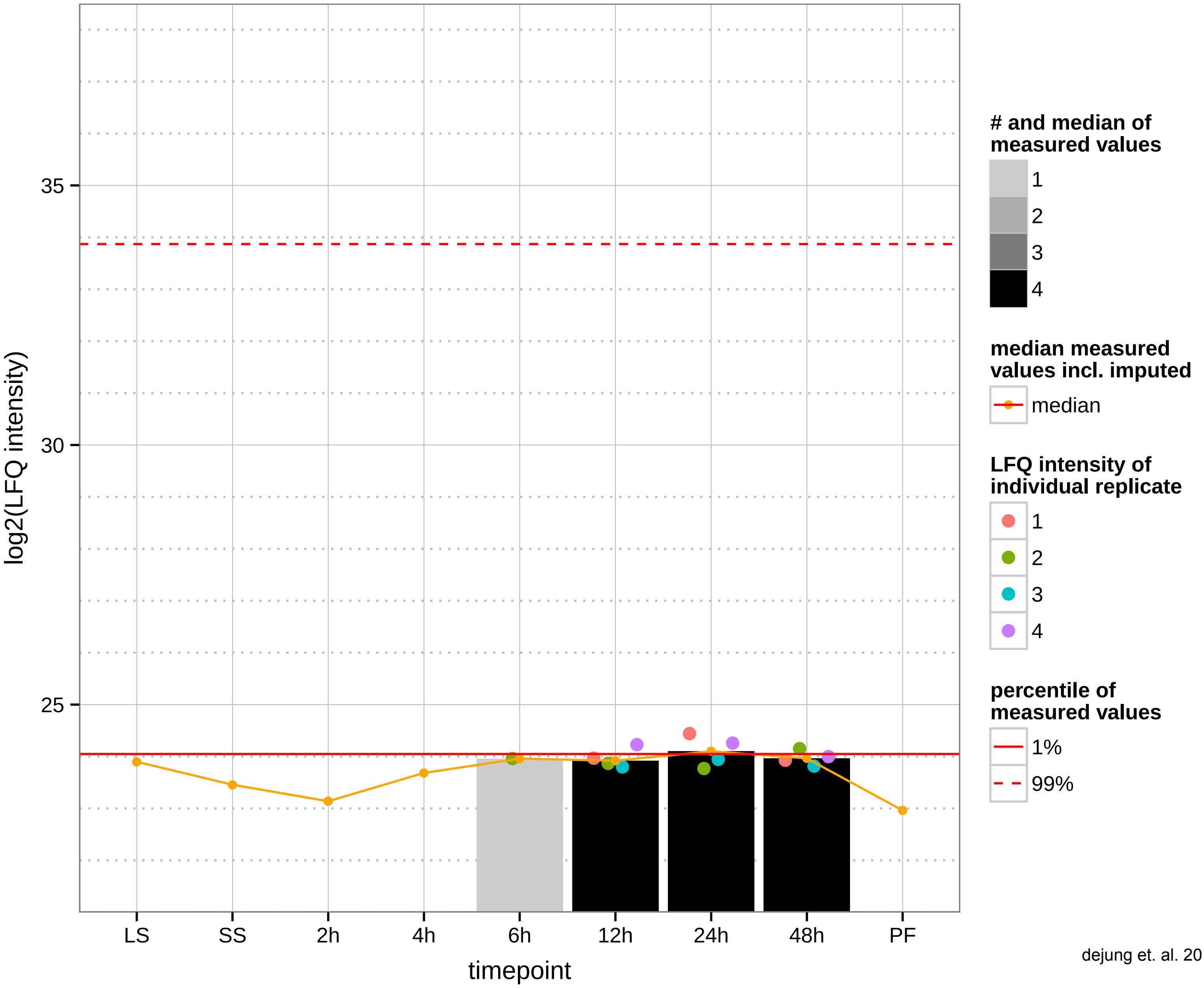
diacylglycerol acyltransferase, putative
Tb927.3.1700
AGOF: diacylglycerol O−acyltransferase activity
AGOC: integral to membrane
AGOP: membrane lipid biosynthetic process
PGOF: transferase activity, transferring acyl groups other than amino−acyl groups
PGOC: null
PGOP: null





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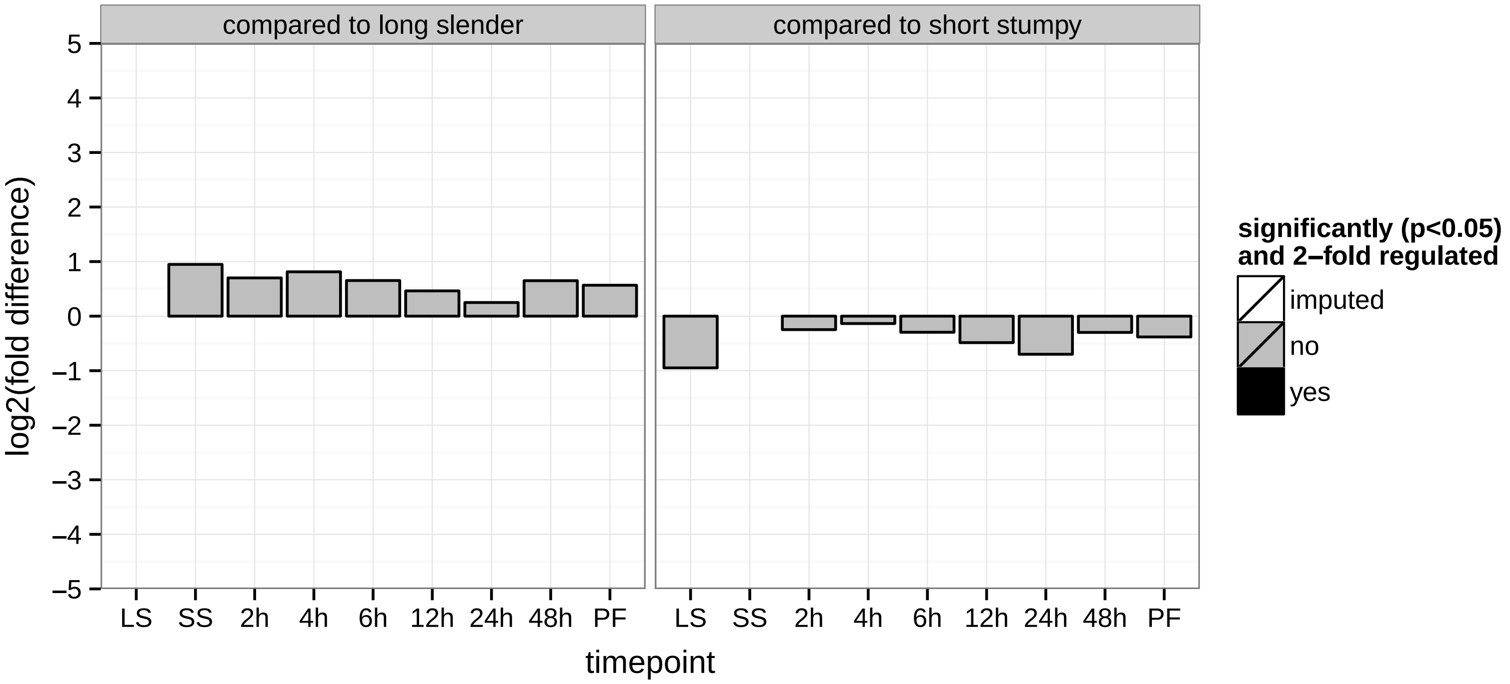
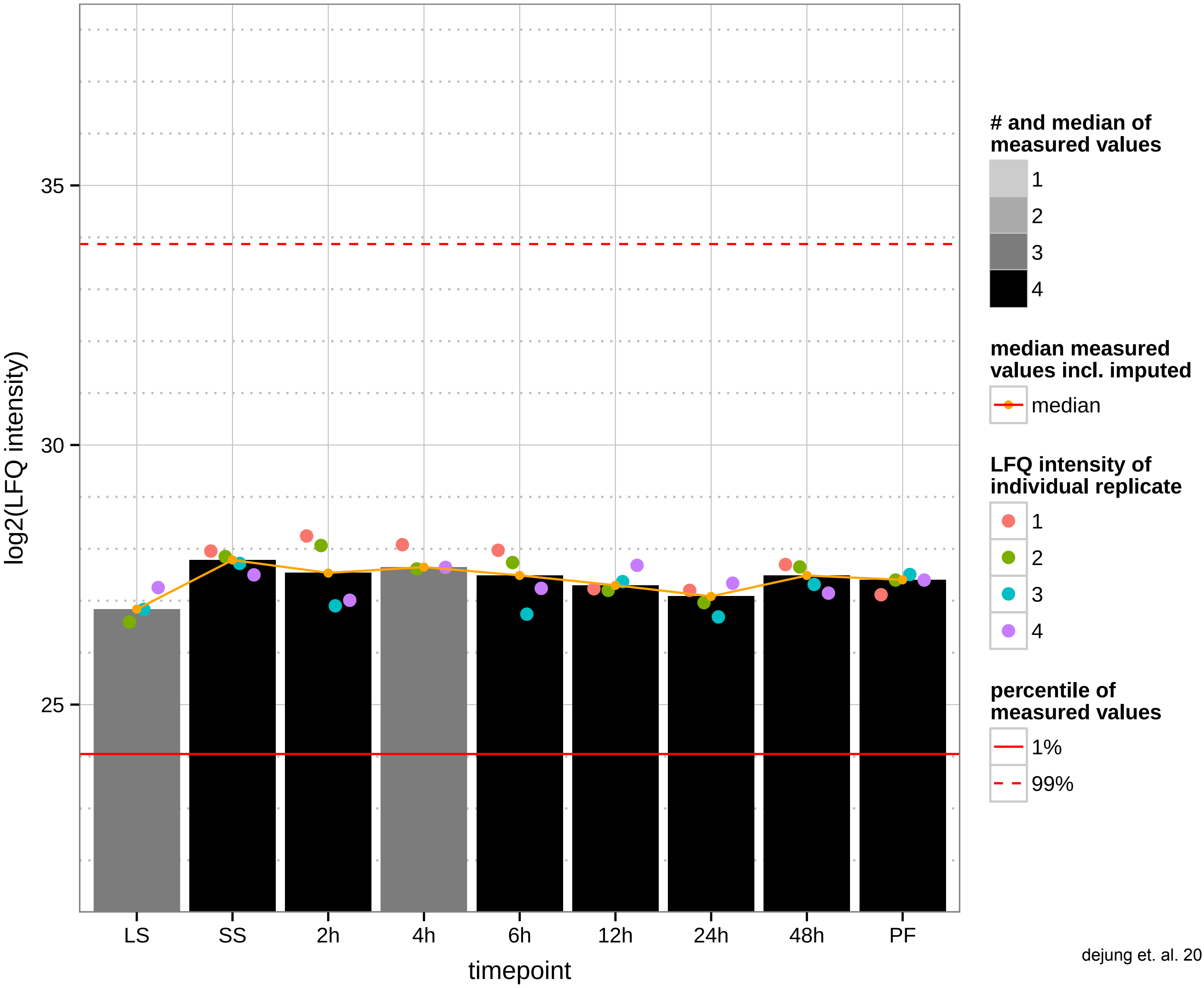
hypothetical protein, conserved
Tb927.3.1740
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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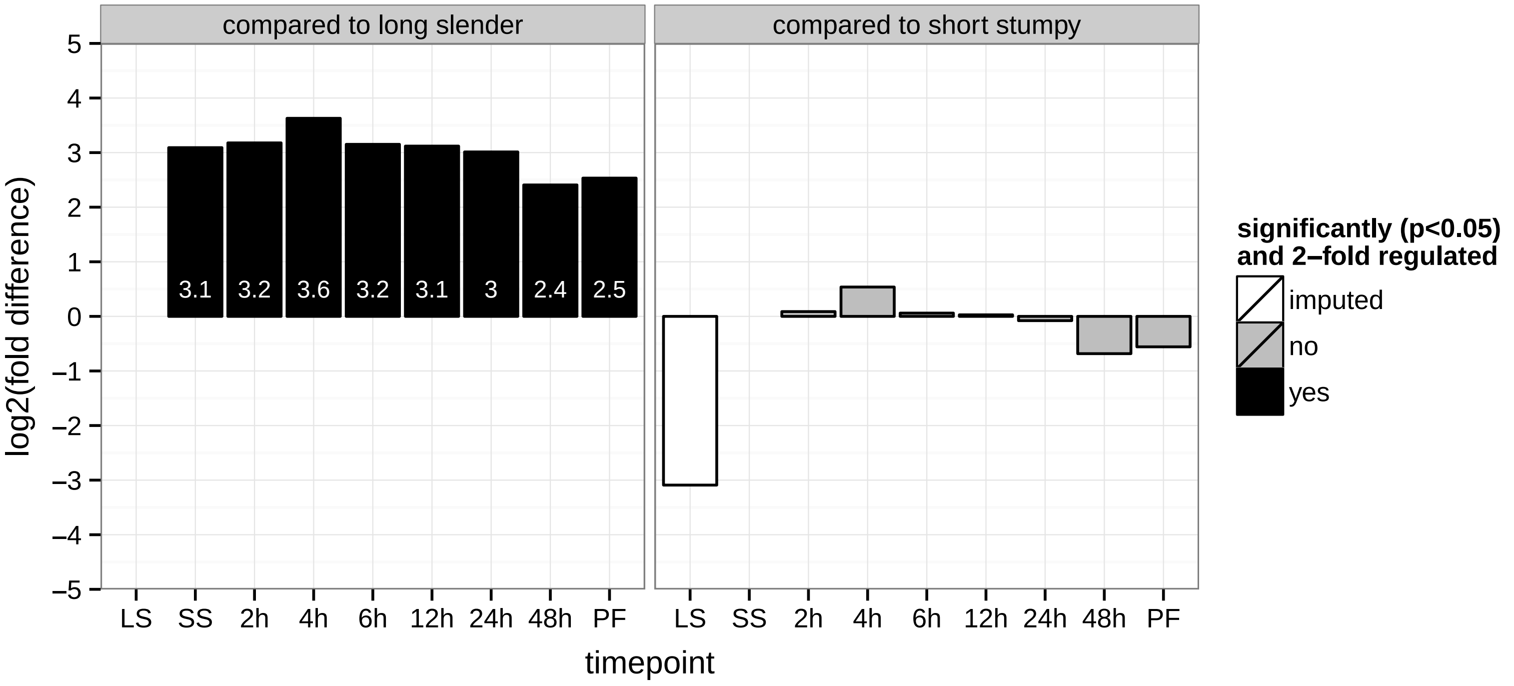
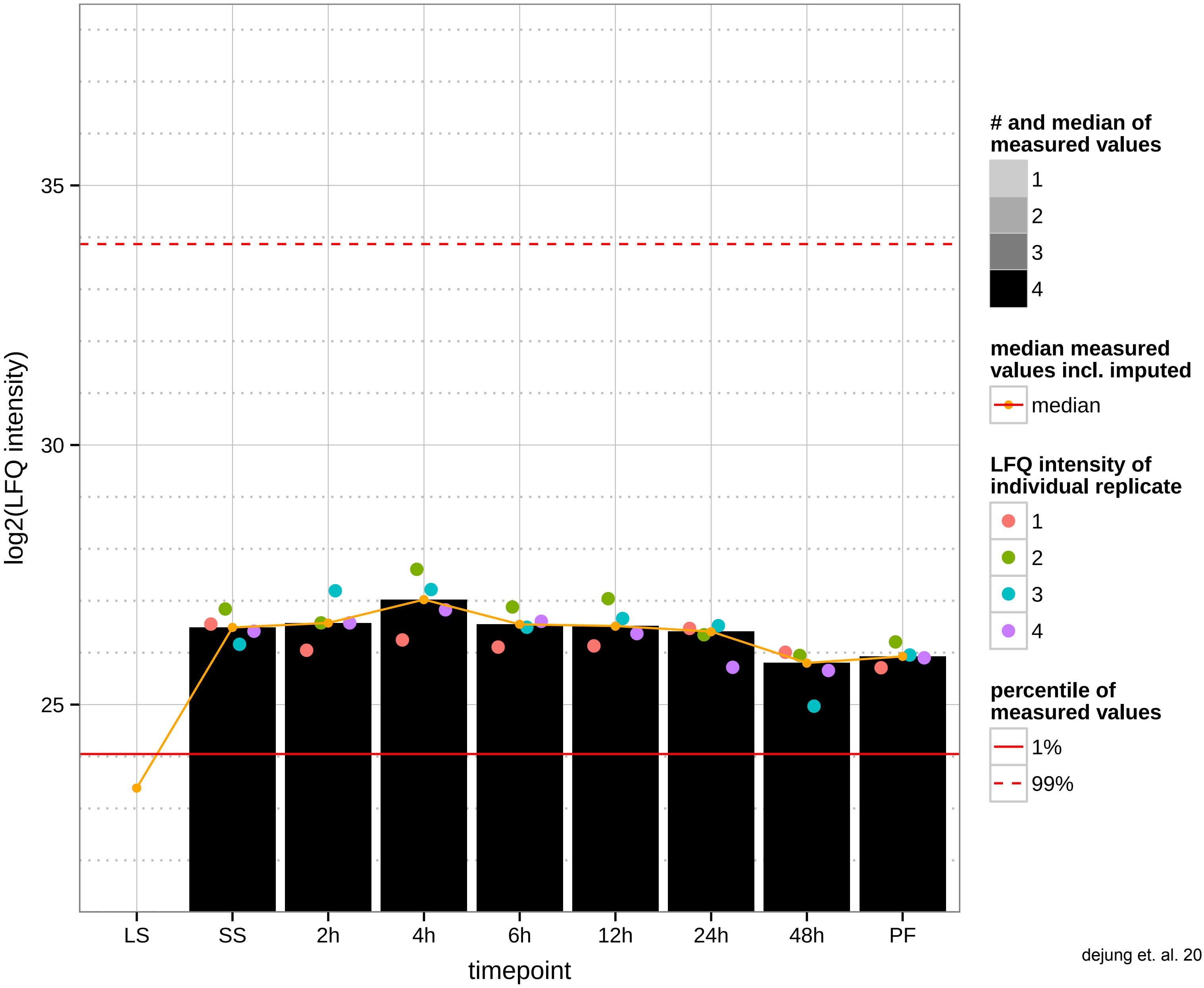
chaperone protein DNAj, putative
Tb927.3.1760
AGOF: heat shock protein binding, unfolded protein binding
AGOC: mitochondrion
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: protein folding





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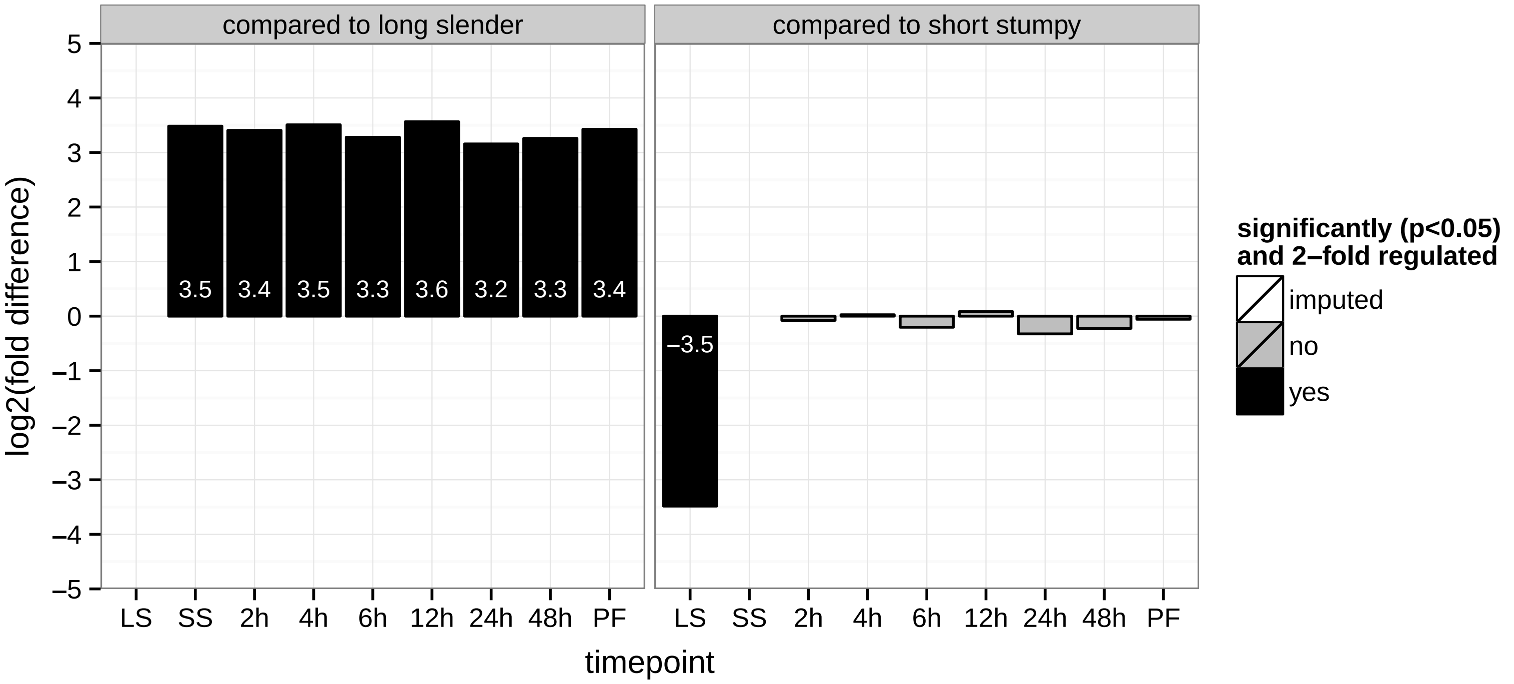
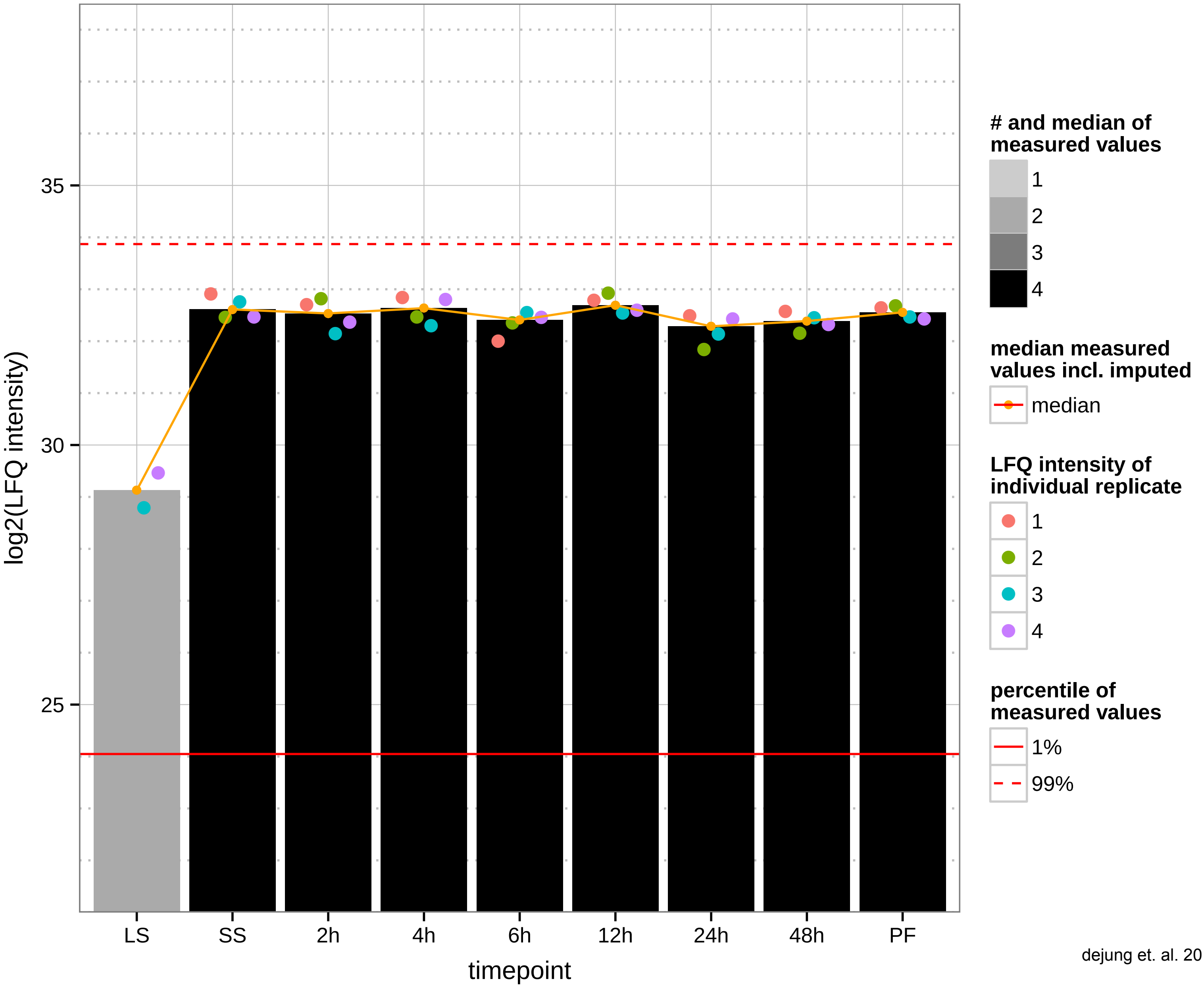
pyruvate dehydrogenase E1 beta subunit, putative
Tb927.3.1790
AGOF: catalytic activity
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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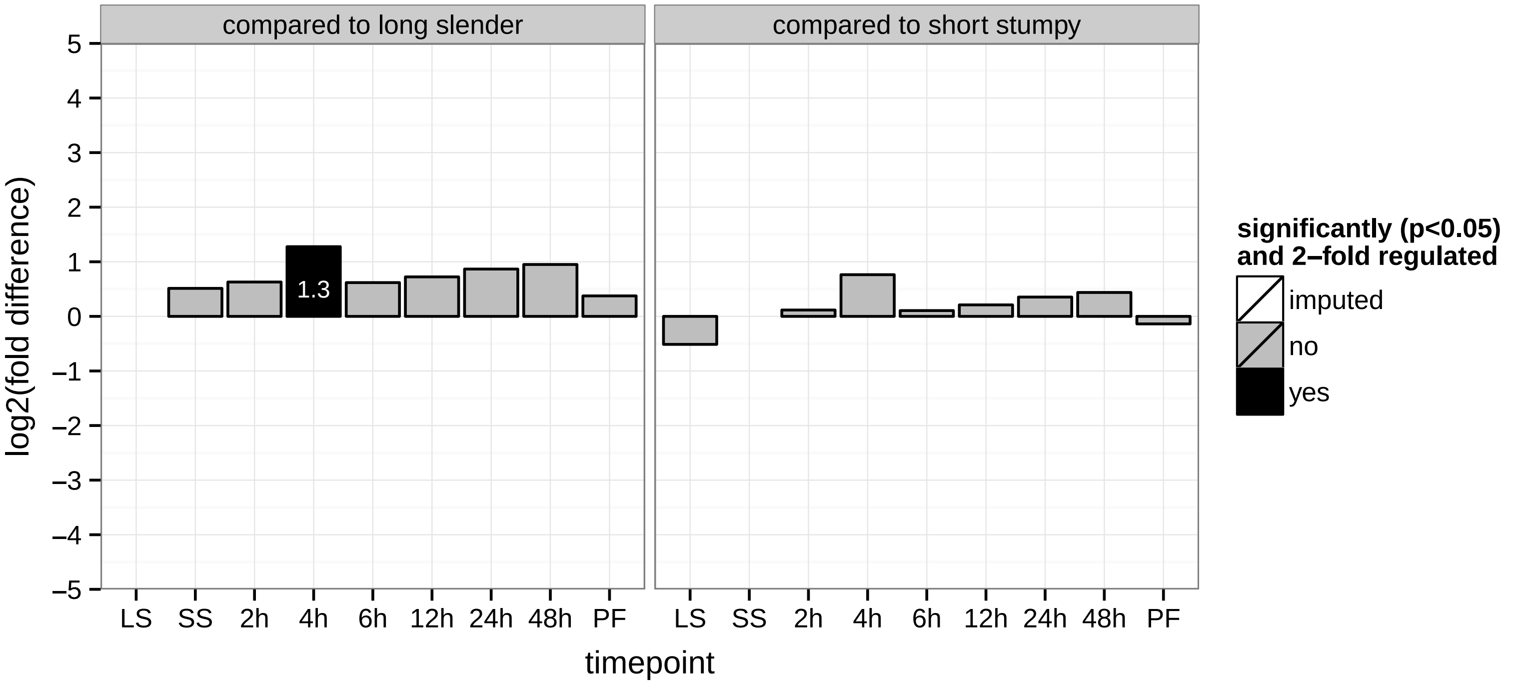
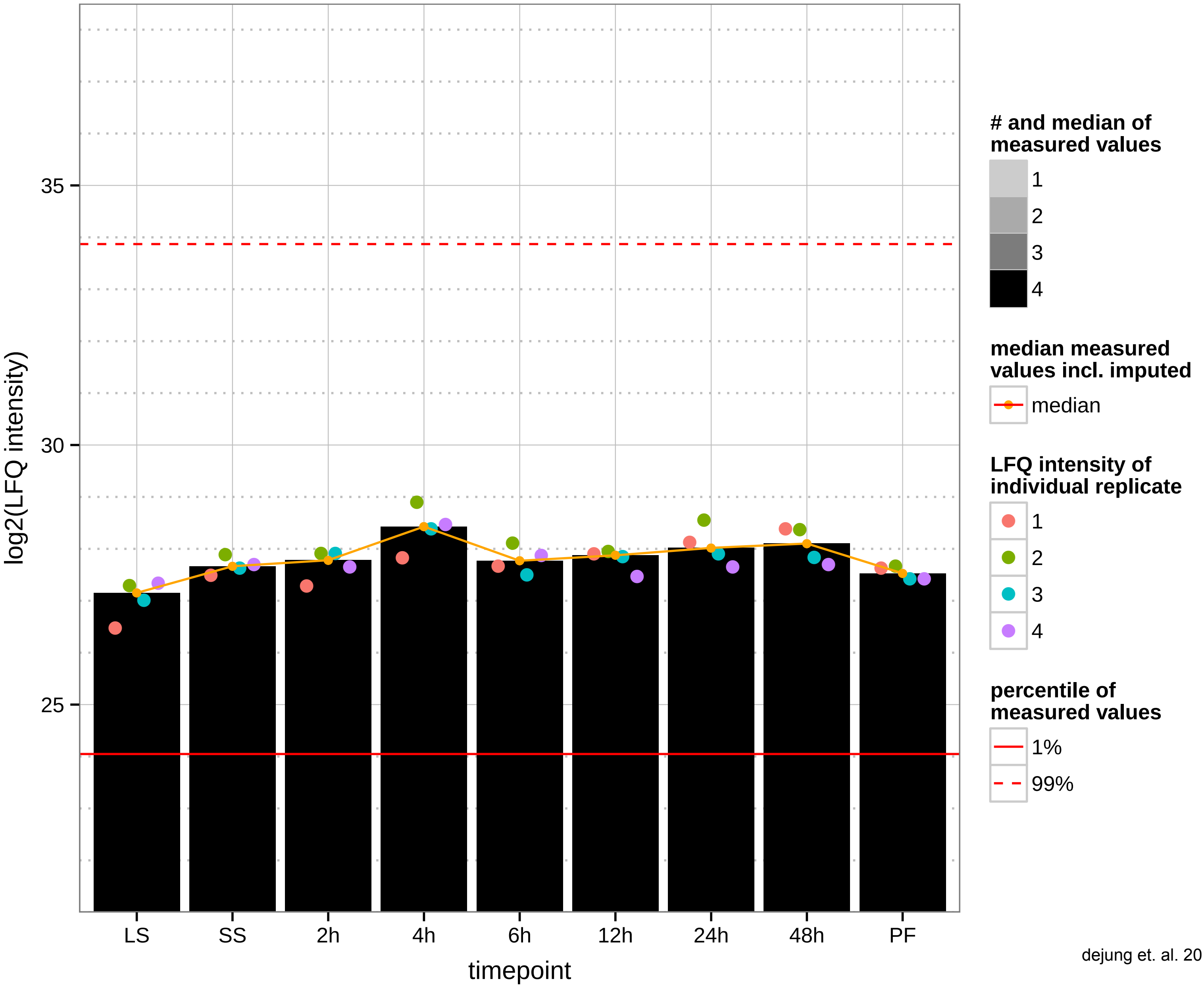
mitochondrial RNA binding complex 1 subunit (MRB1820)
Tb927.3.1820
AGOF: RNA binding
AGOC: mitochondrion
AGOP: cytidine to uridine editing, mRNA stabilization
PGOF: null
PGOC: null
PGOP: null





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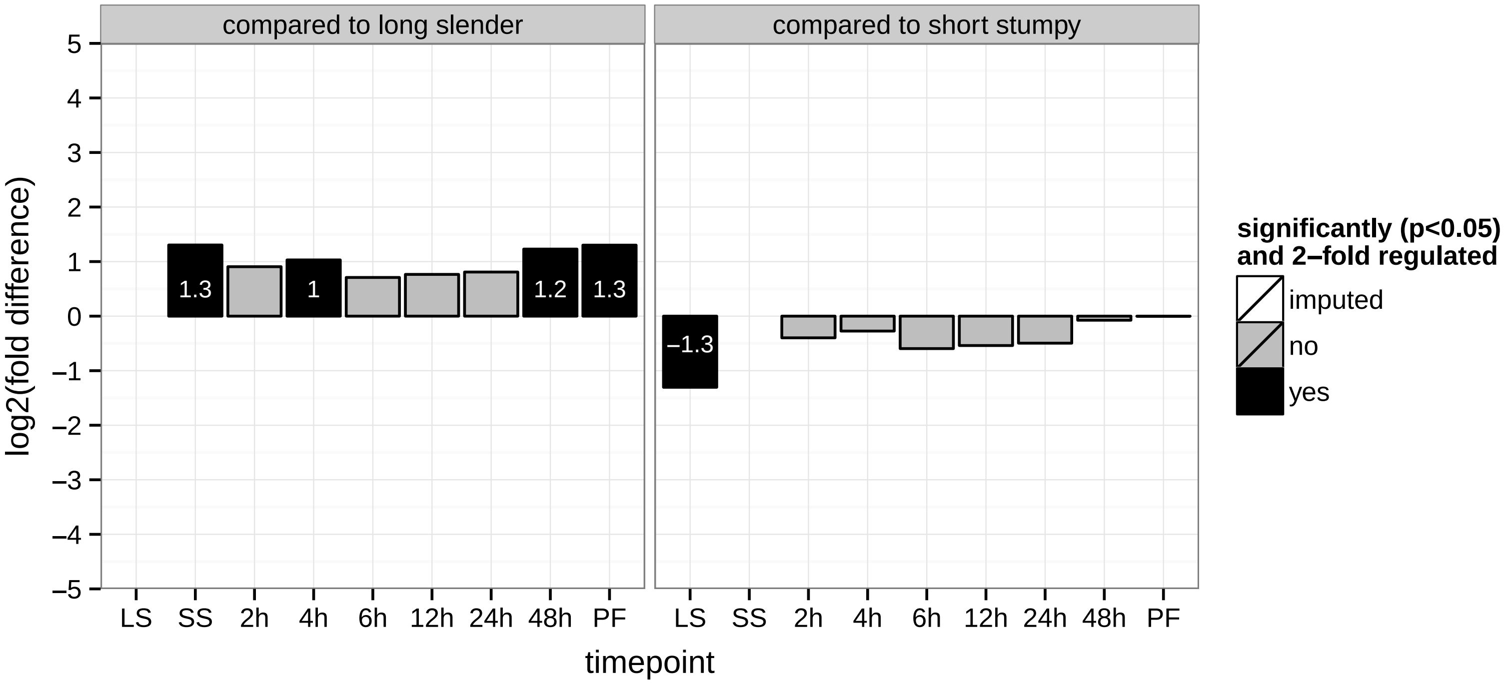
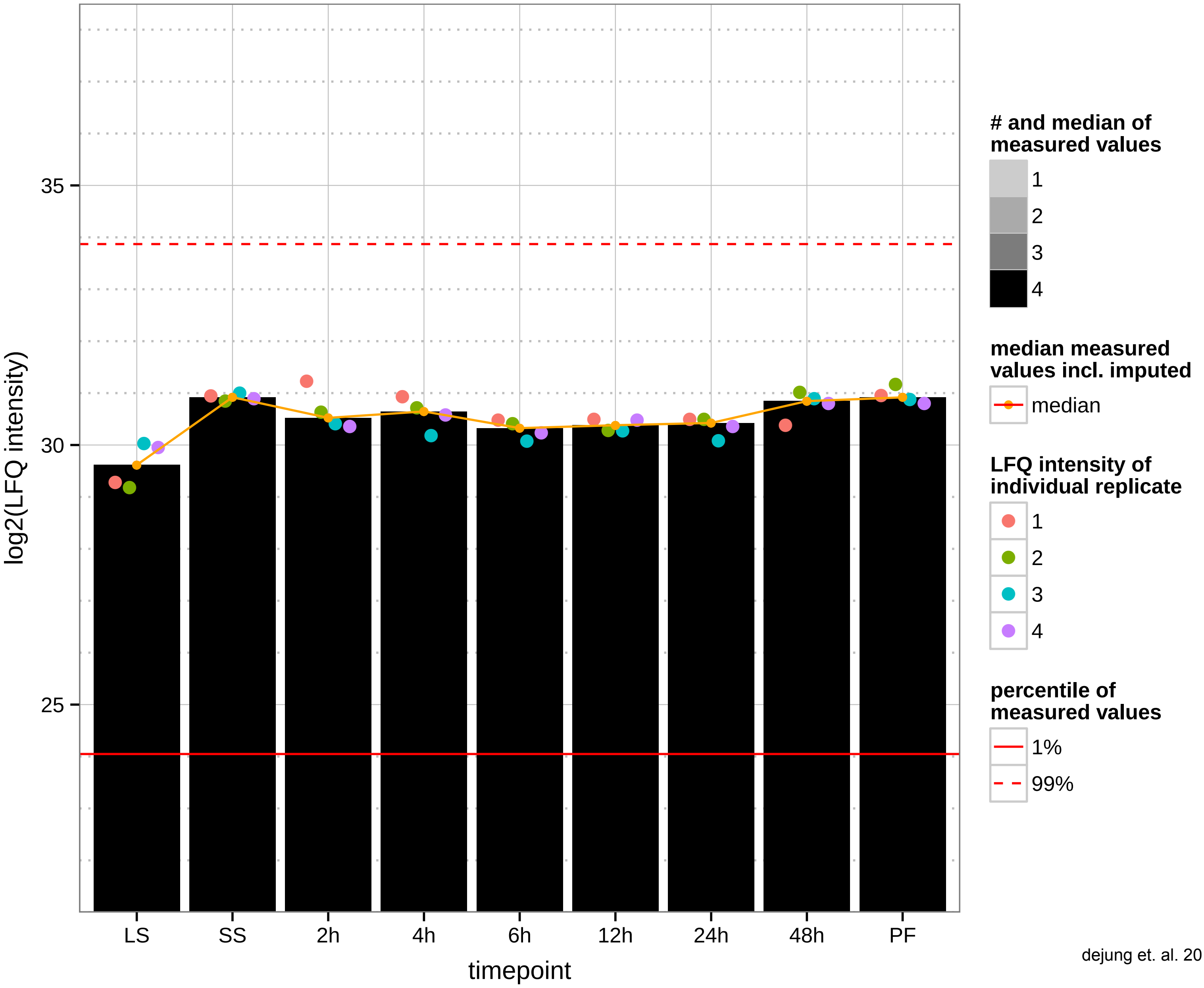
3–oxo–5–alpha–steroid 4–dehydrogenase, putative, polyprenol reductase
Tb927.3.1840
AGOF: oxidoreductase activity, acting on the CH–CH group of donors
AGOC: cytoplasm, integral to membrane, mitochondrial inner membrane
AGOP: dolichol biosynthetic process, glycosylation
PGOF: oxidoreductase activity, acting on the CH–CH group of donors
PGOC: cytoplasm, integral to membrane
PGOP: lipid metabolic process





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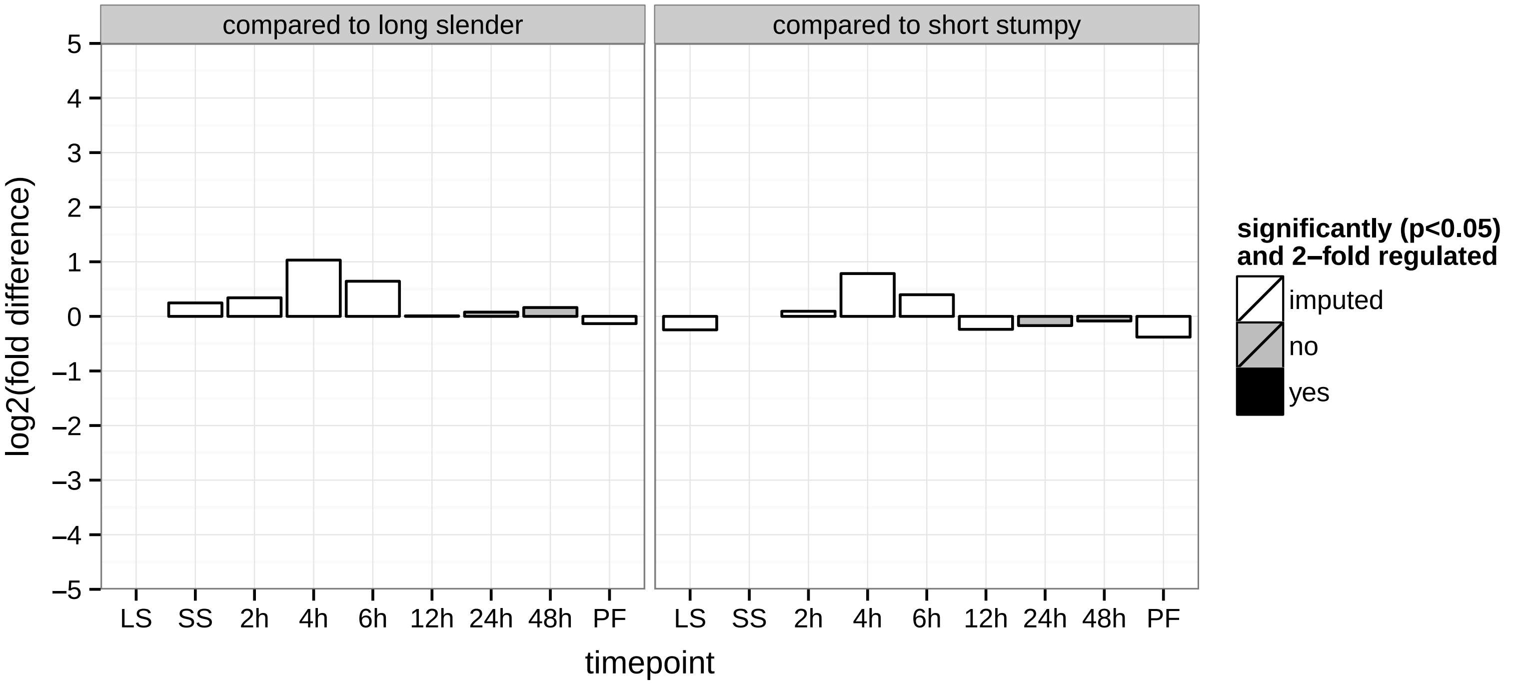
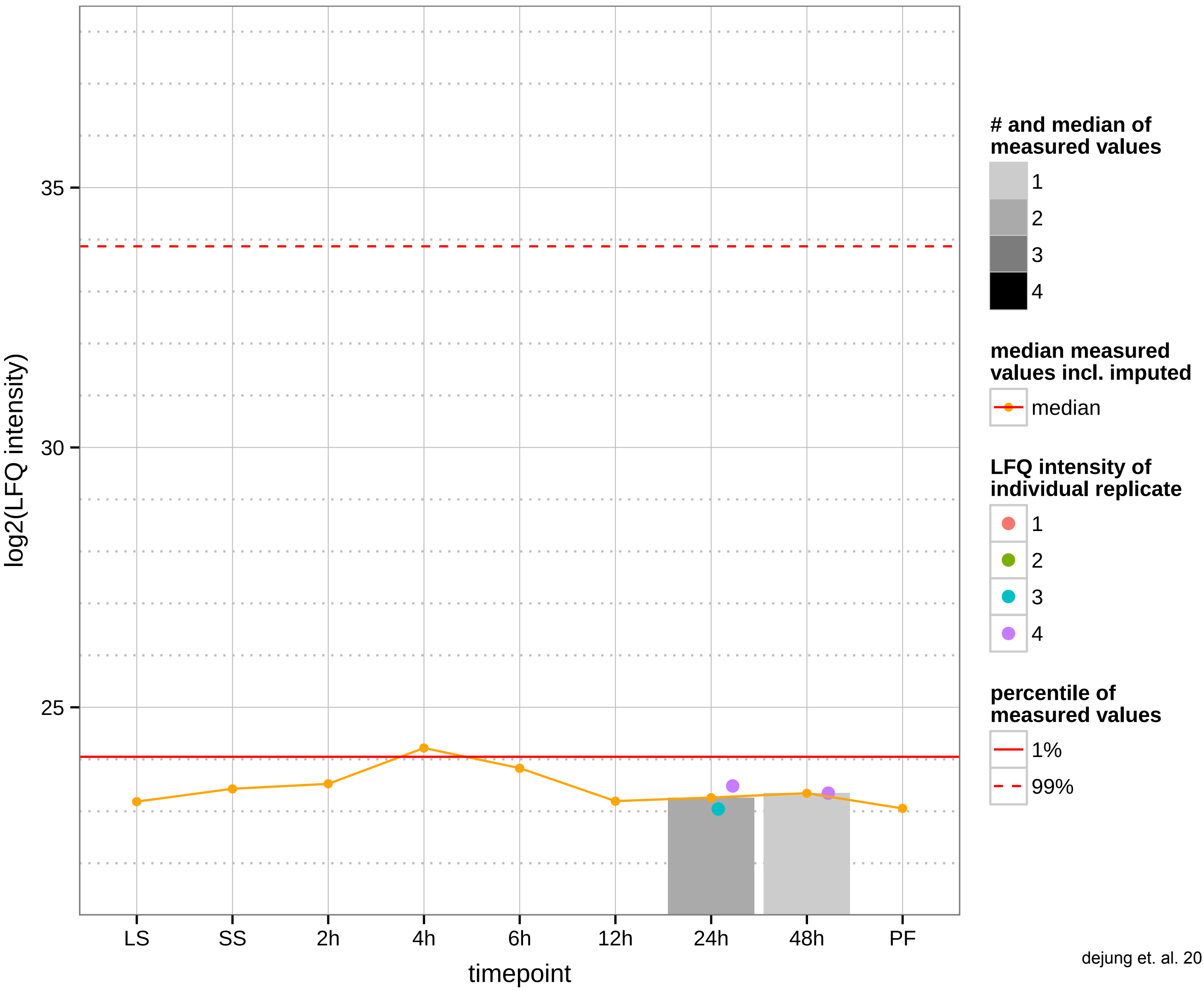
hypothetical protein, conserved
Tb927.3.1860
AGOF: ATP binding, catalytic activity
AGOC: null
AGOP: null
PGOF: ATP binding, metal ion binding, protein binding
PGOC: null
PGOP: null





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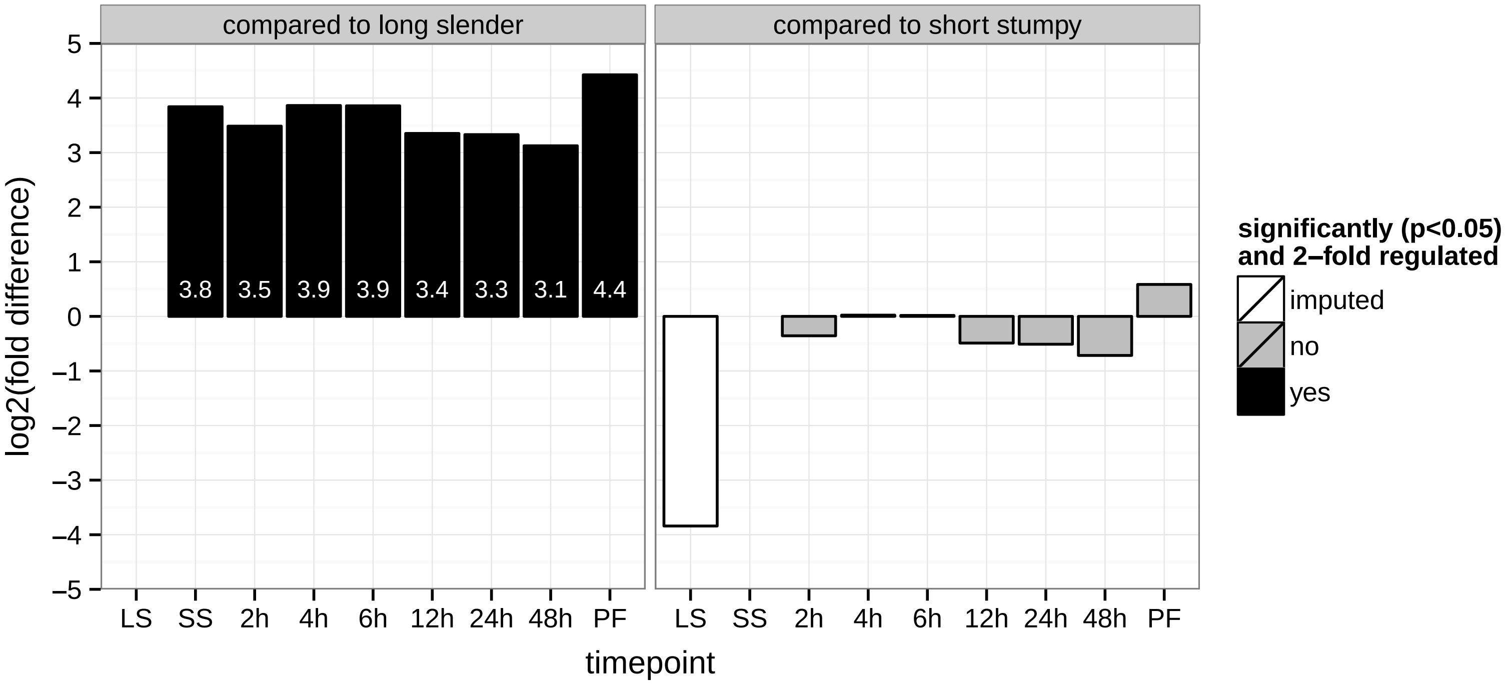
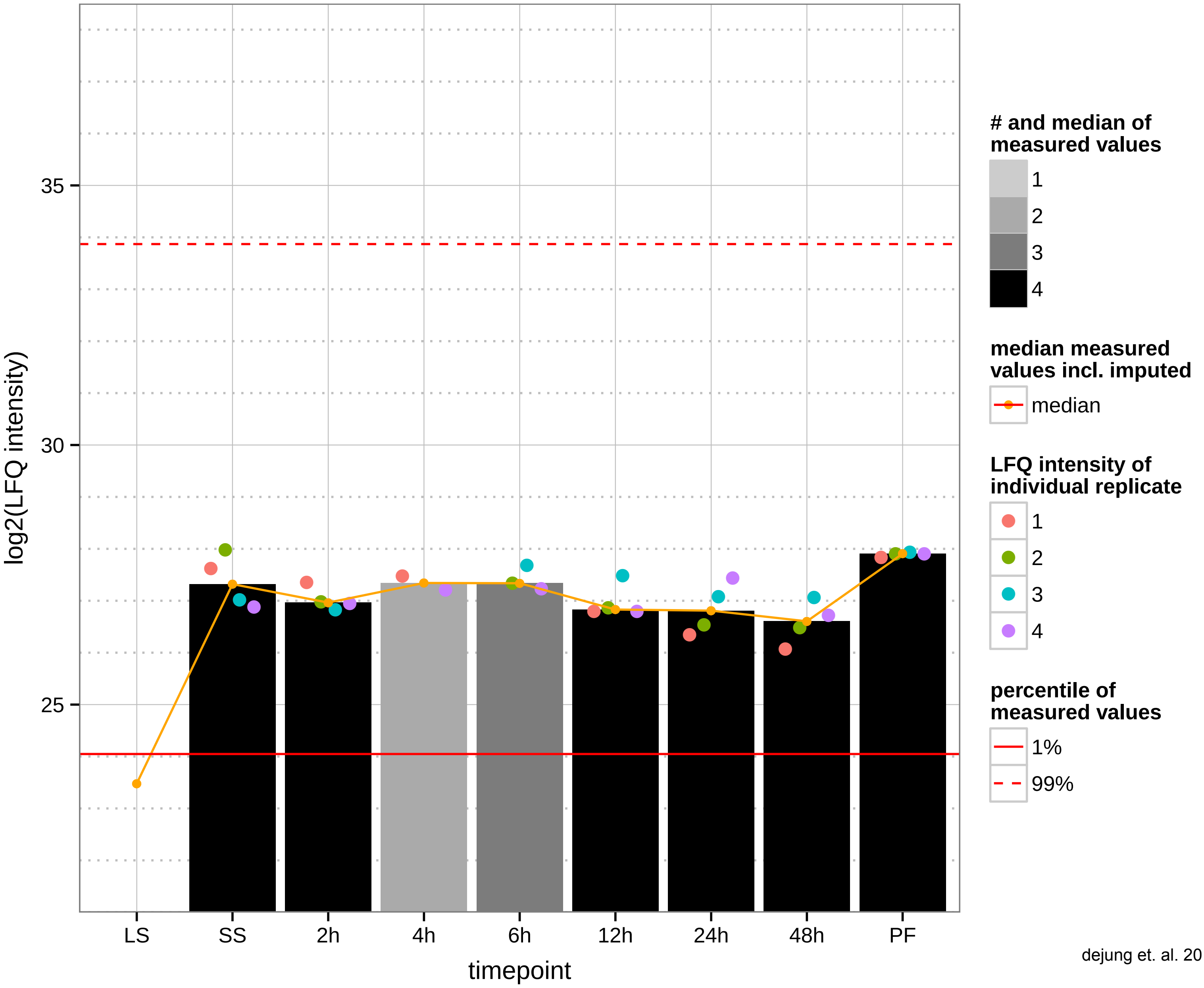
hypothetical protein, conserved
Tb927.3.1900
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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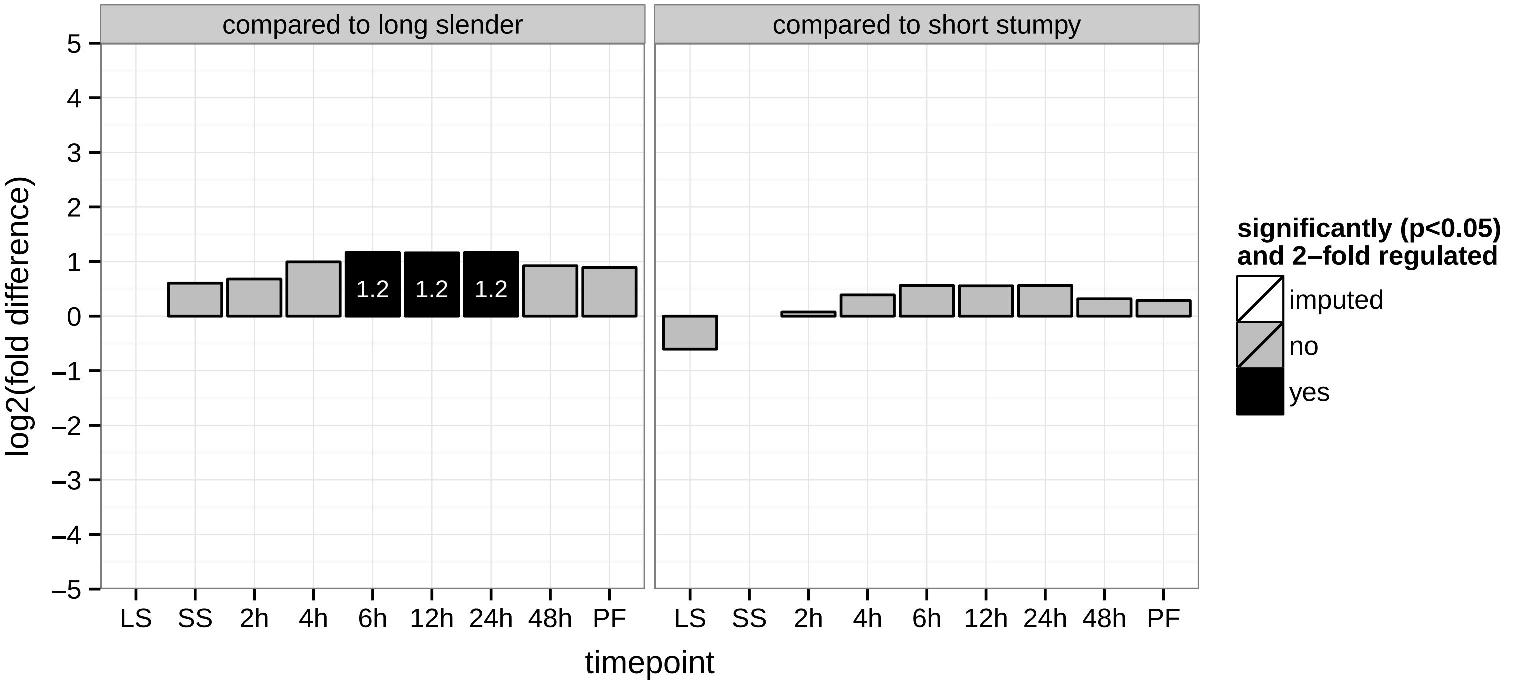
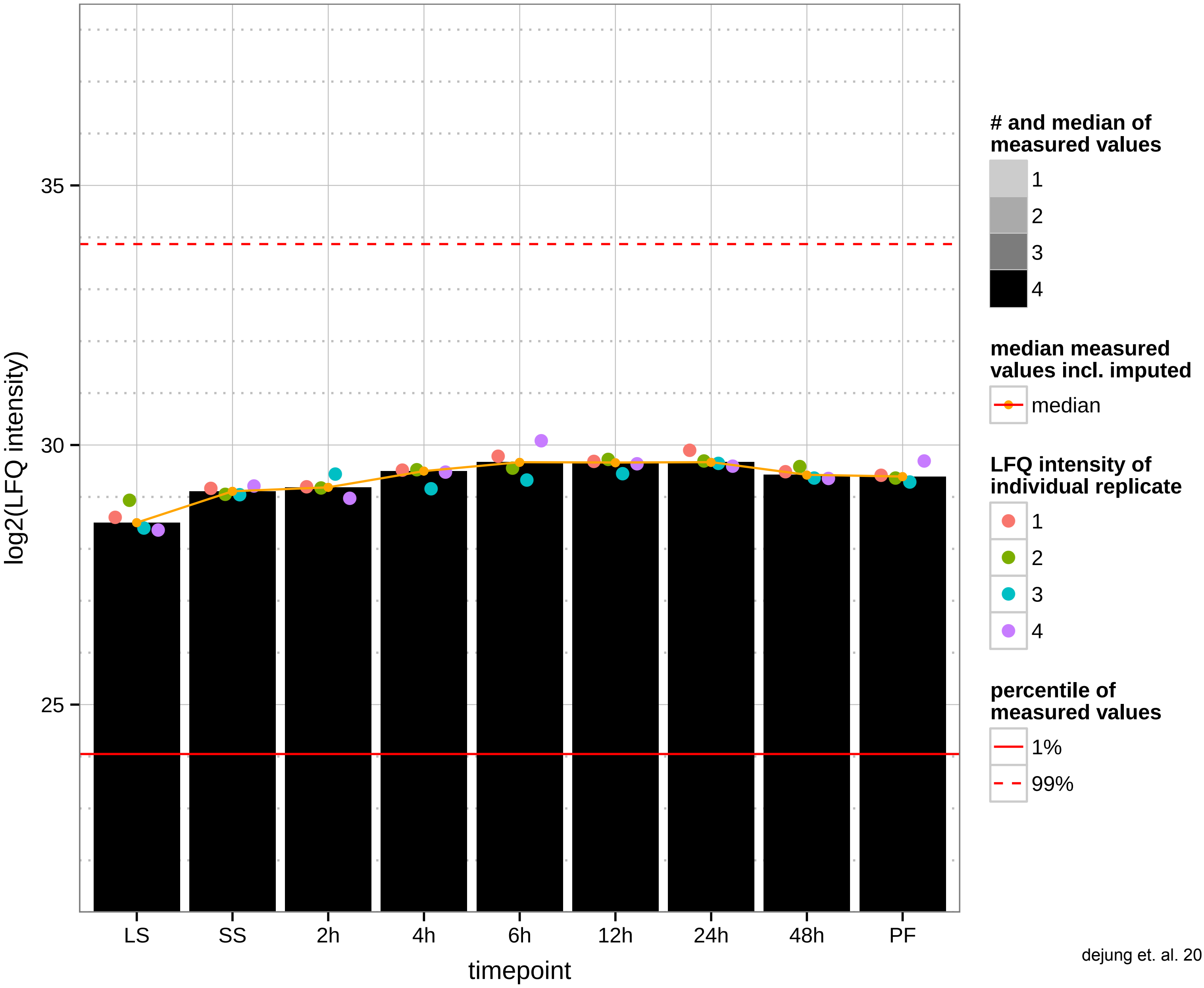
NOT5 protein (NOT5)
Tb927.3.1920
AGOF: null
AGOC: nucleus
AGOP: regulation of transcription, DNA–dependent
PGOF: null
PGOC: nucleus
PGOP: regulation of transcription, DNA–dependent





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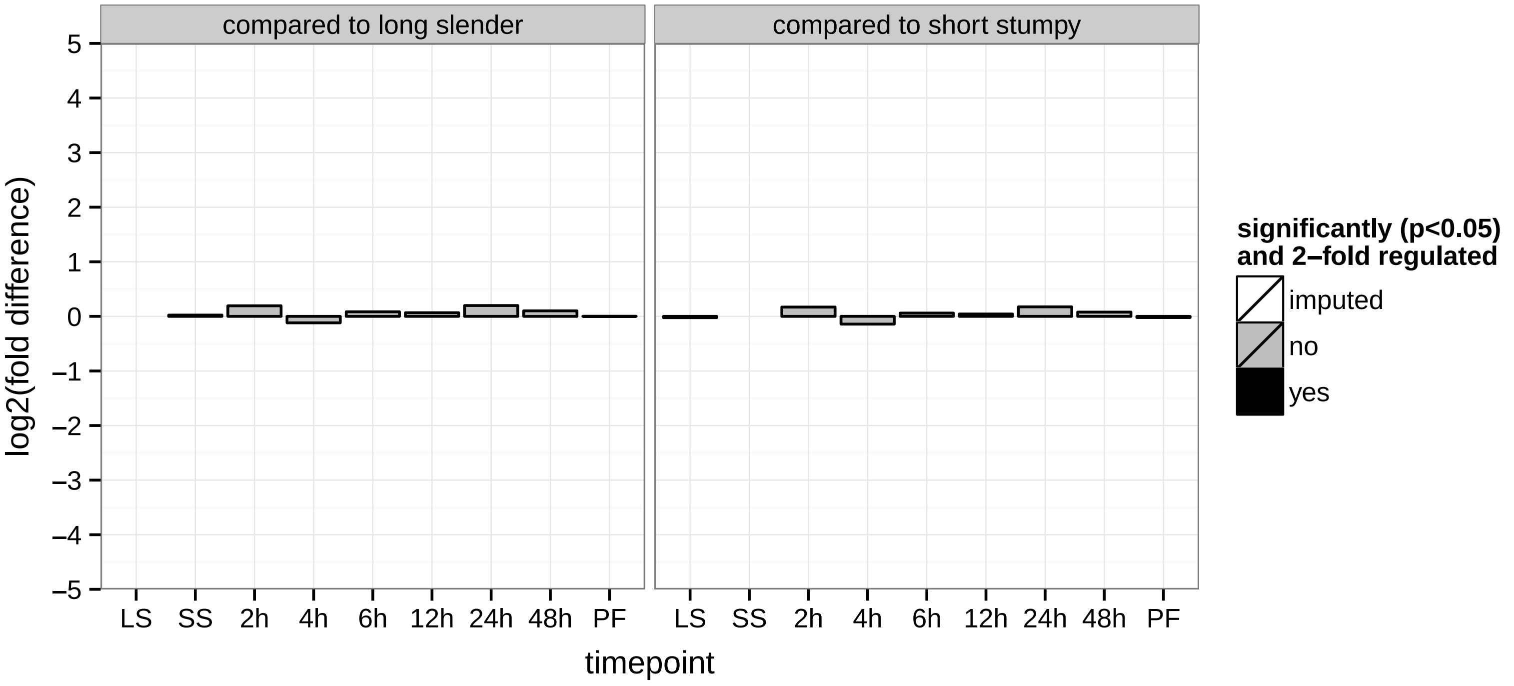
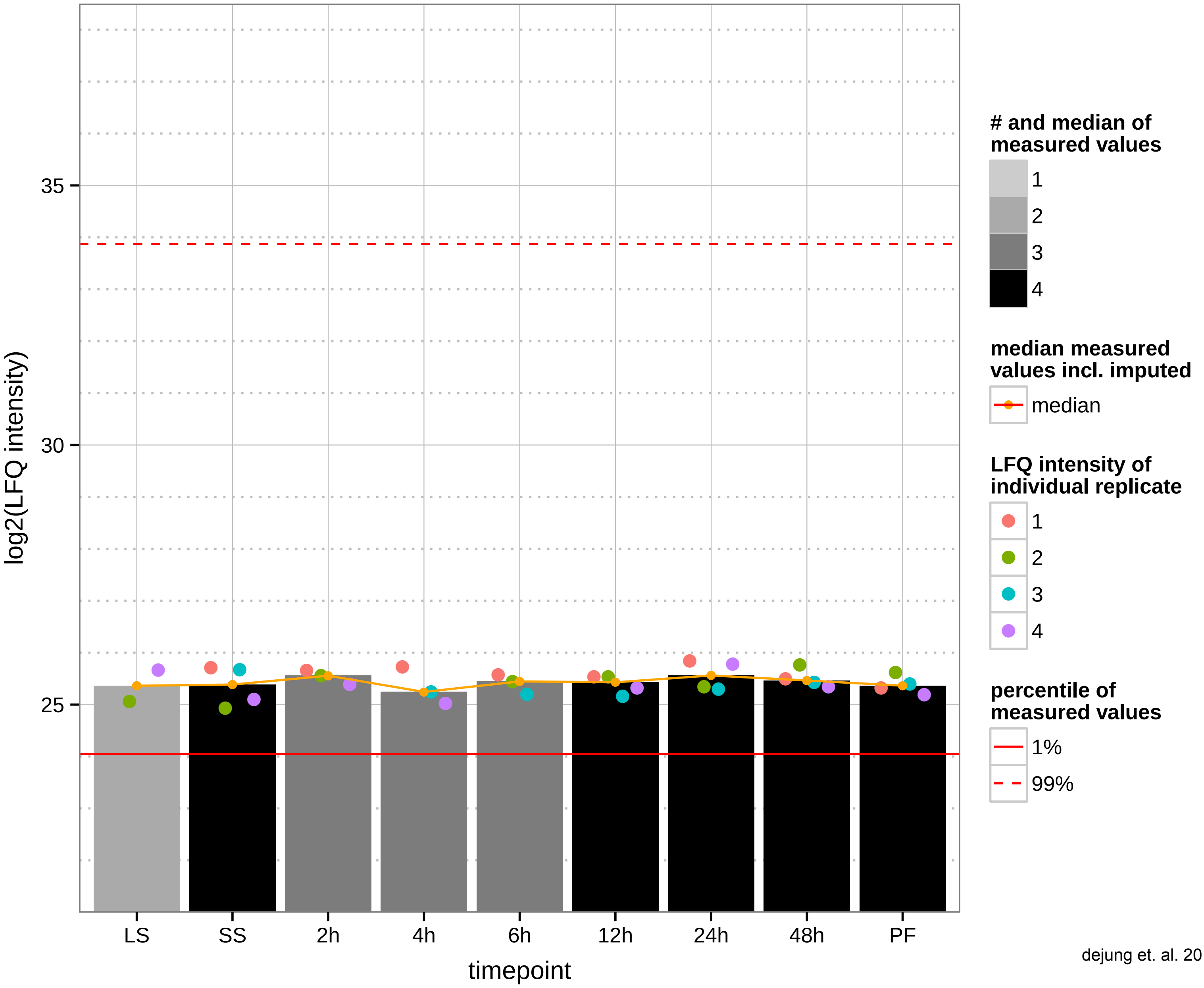
hypothetical protein, conserved
Tb927.3.1990
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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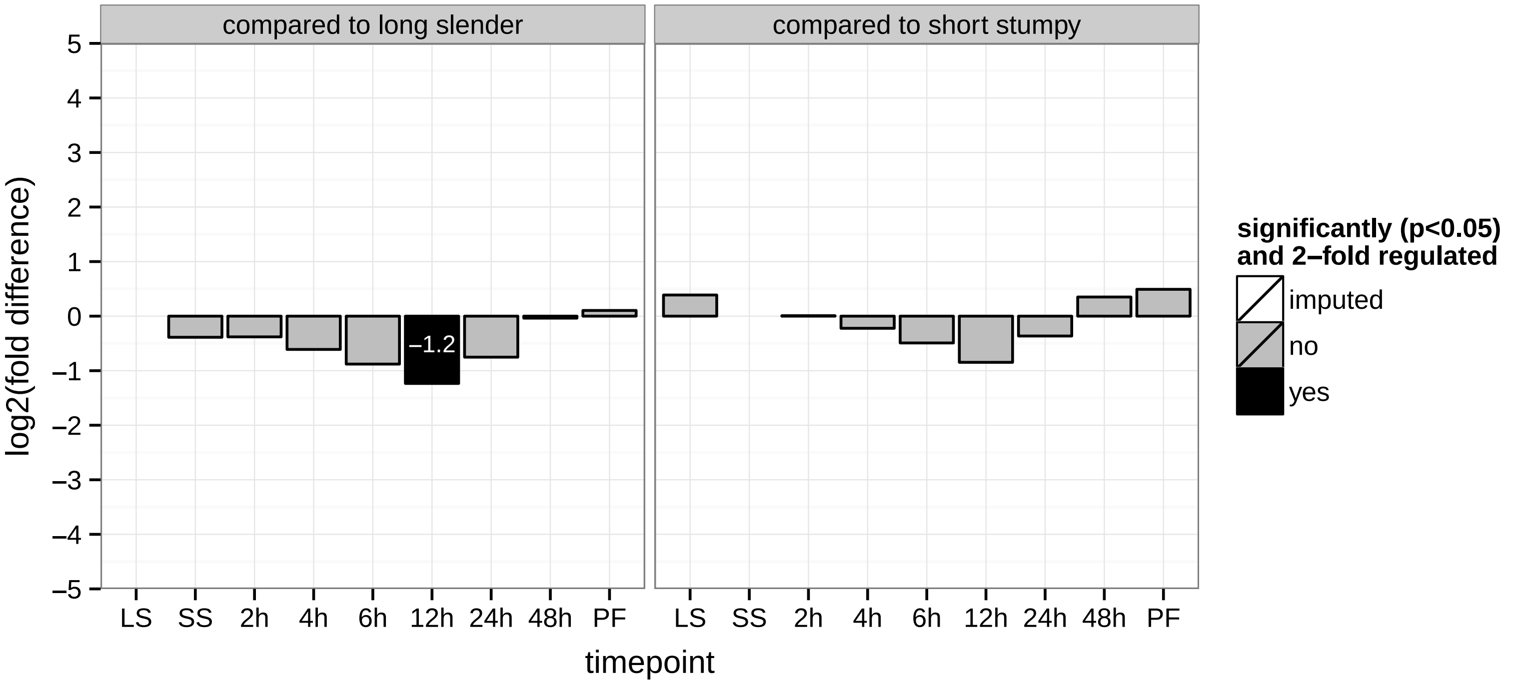
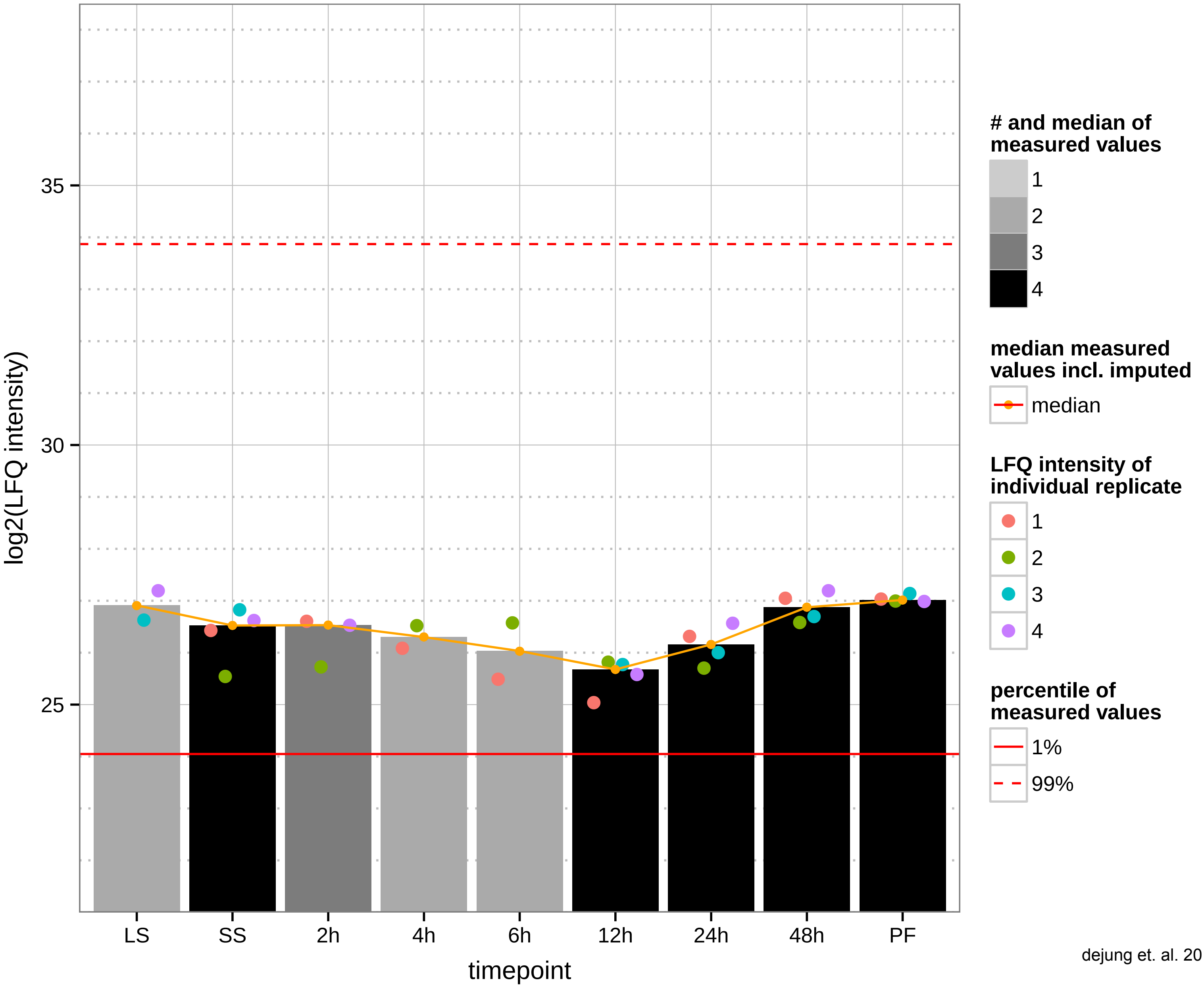
hypothetical protein, conserved
Tb927.3.2050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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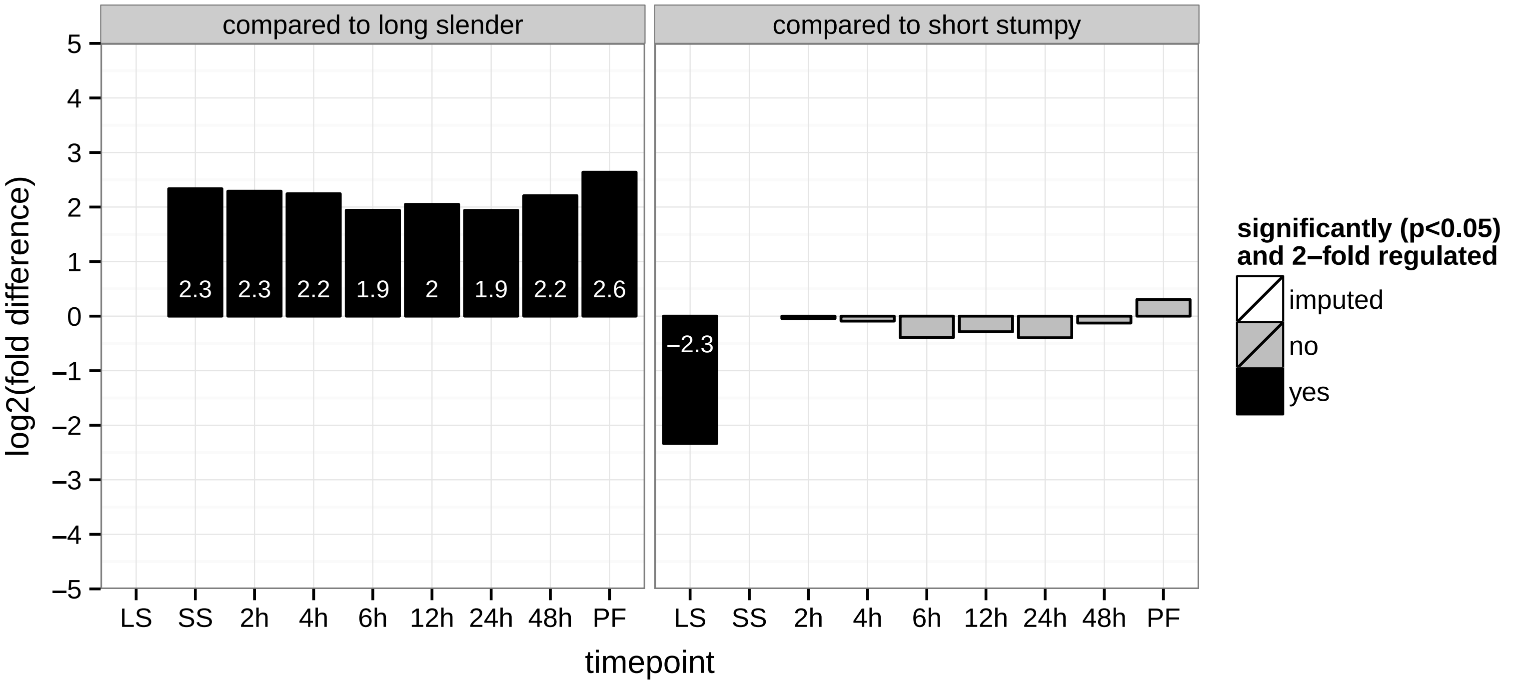
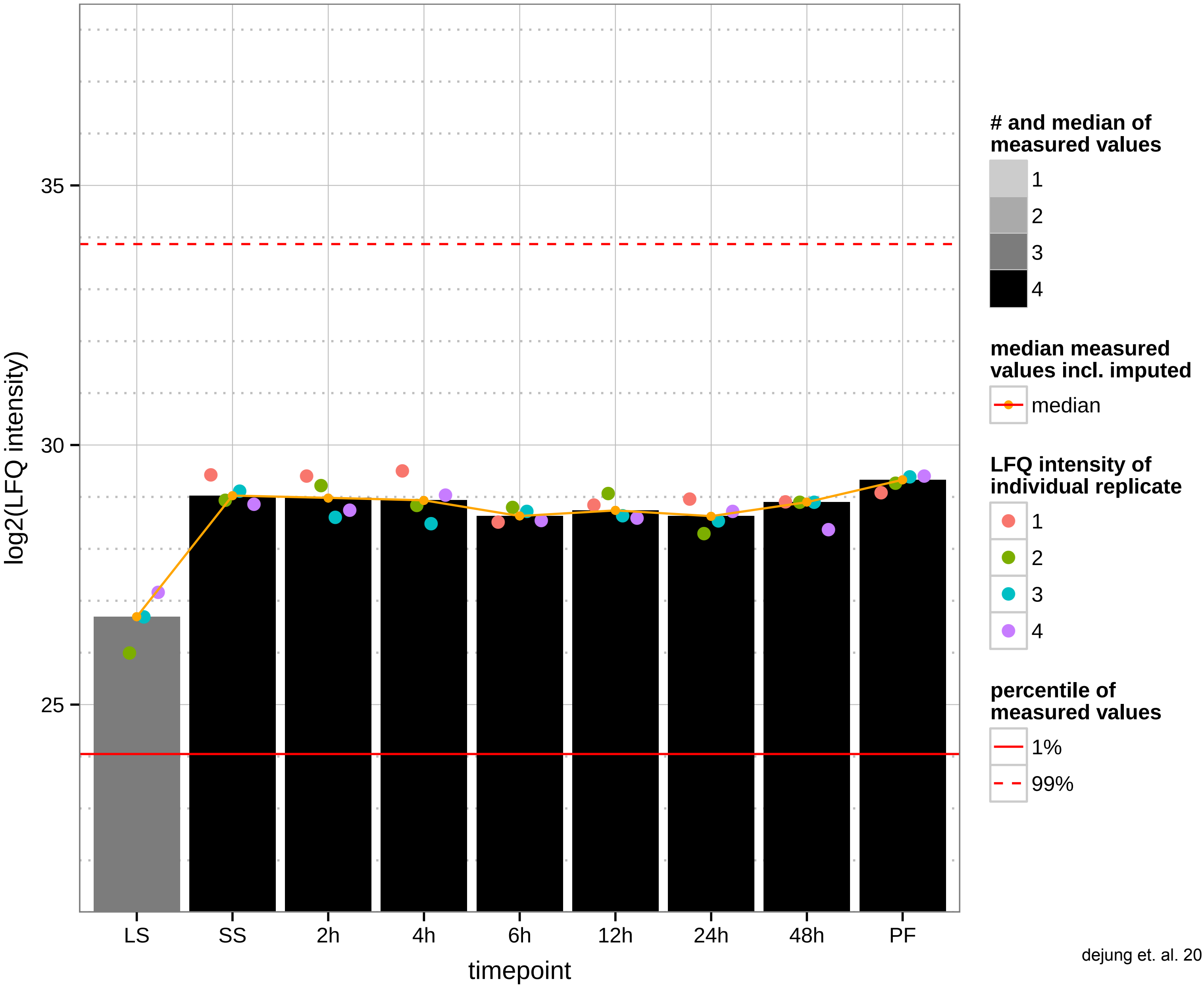
aminopeptidase P1, putative, metallo–peptidase, Clan MG, Family M24
Tb927.3.2090;Tb11.v5.0697
AGOF: null, hydrolase activity
AGOC: null
AGOP: null, cellular process
PGOF: hydrolase activity
PGOC: null
PGOP: cellular process





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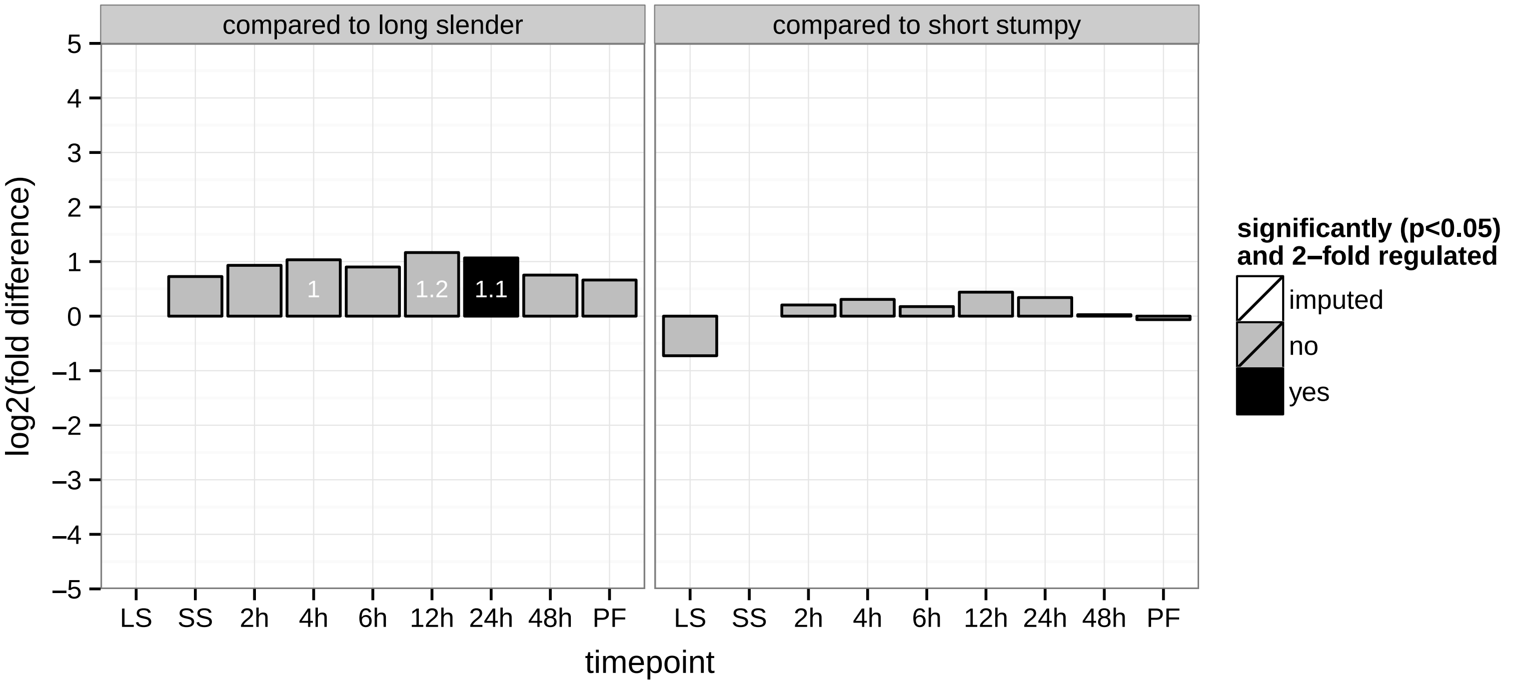
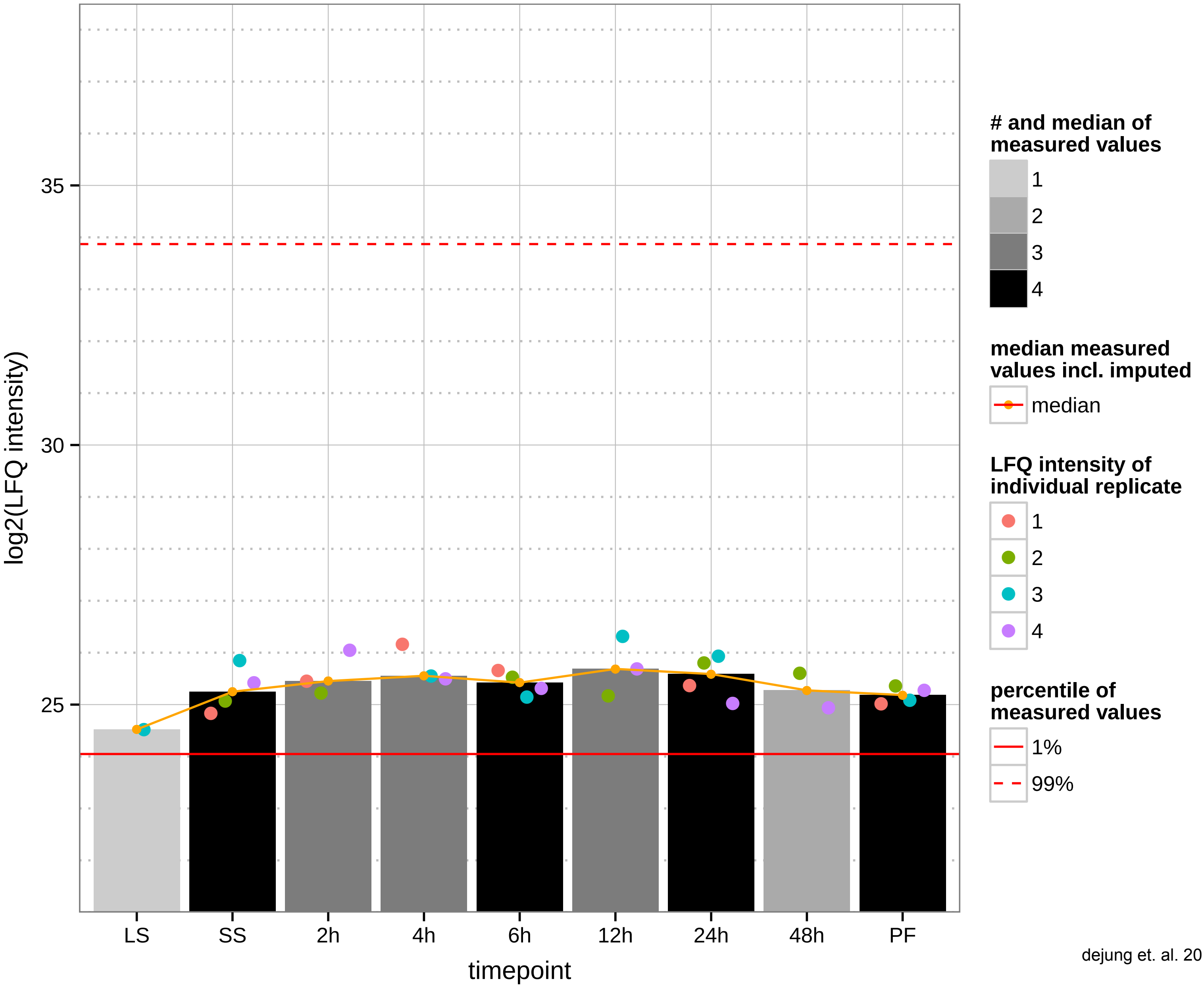
hypothetical protein, conserved, TFIIF−stimulated CTD phosphatase, putative
Tb927.3.2110
AGOF: null, phosphatase activity
AGOC: null, mitochondrion
AGOP: null
PGOF: protein binding, phosphatase activity, protein binding
PGOC: null
PGOP: null





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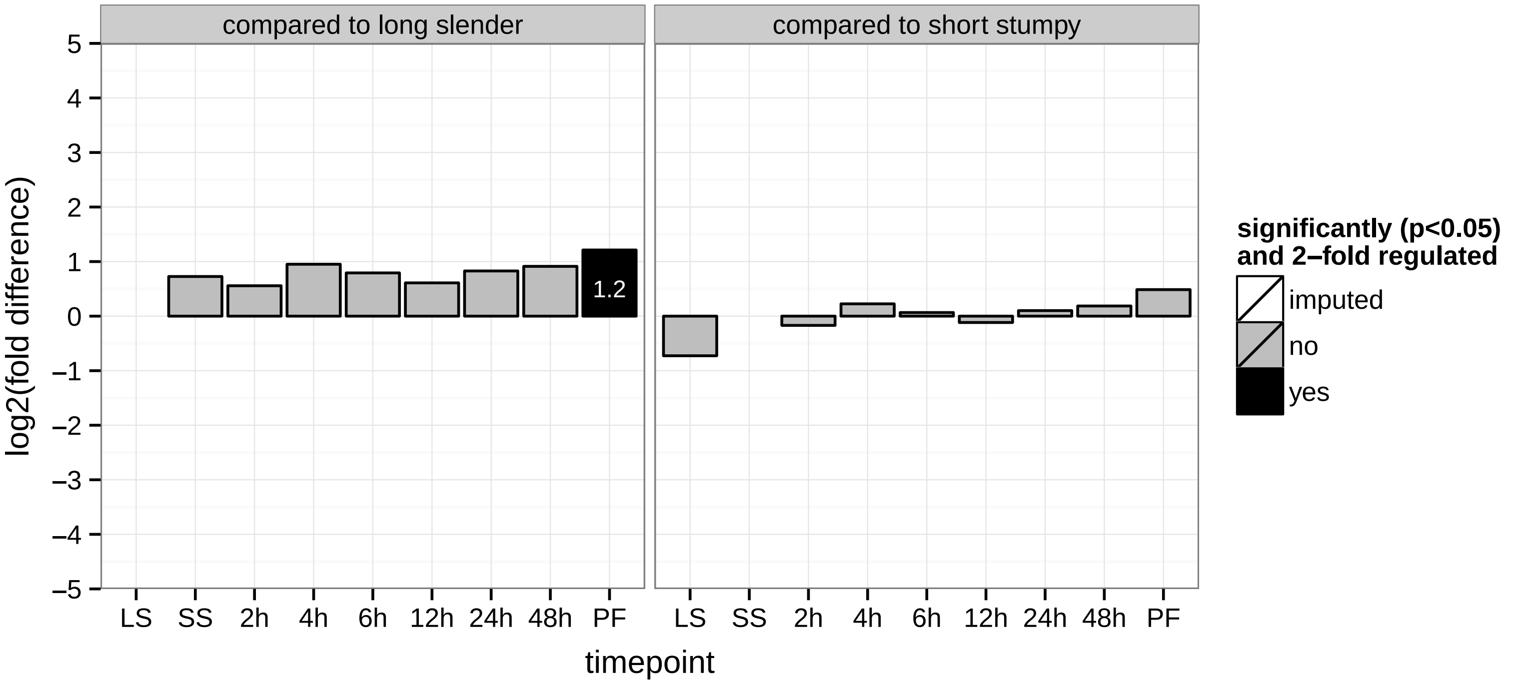
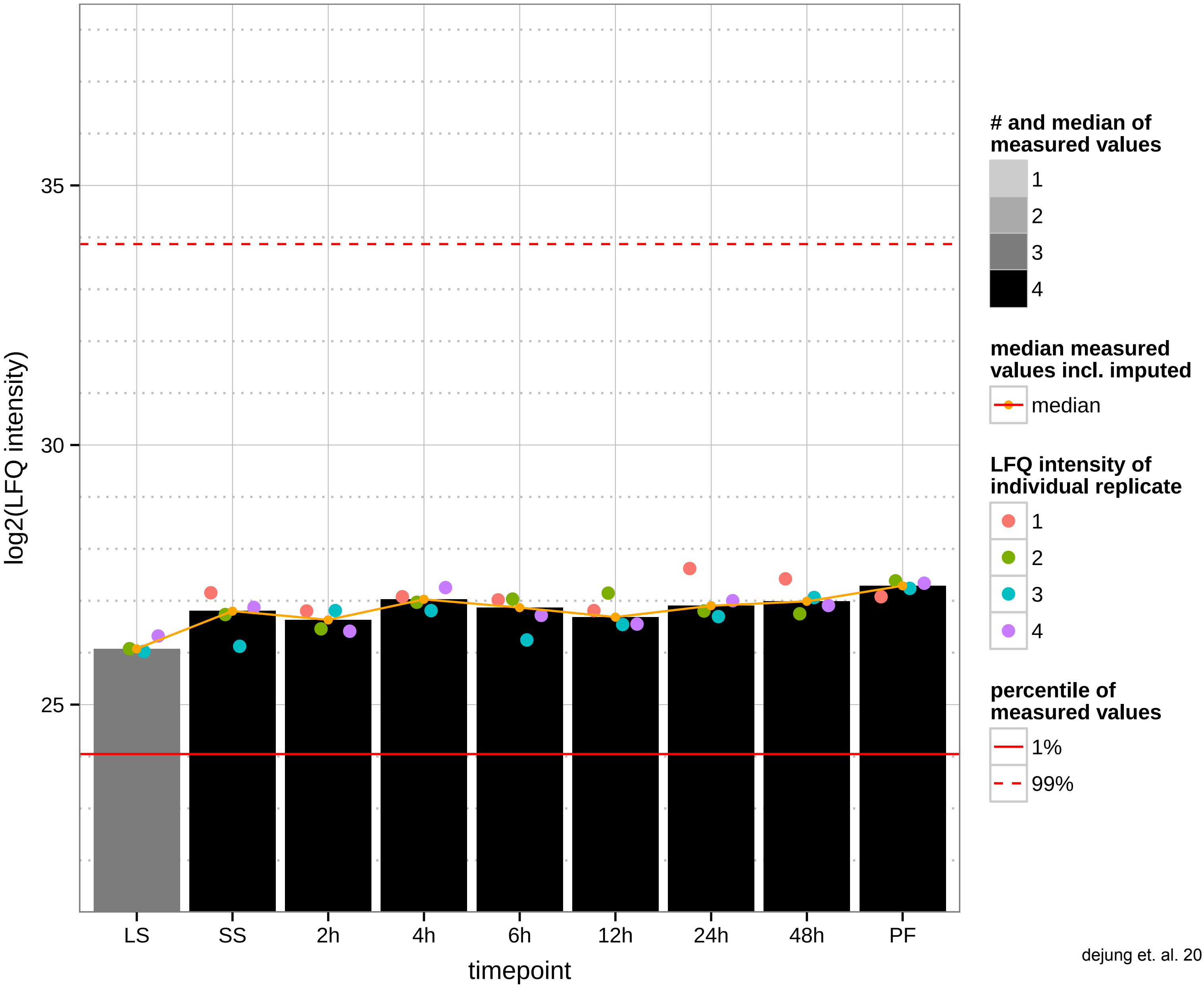
RNA triphosphatase (TbCET1)
Tb927.3.2190
AGOF: nucleoside−triphosphatase activity, polynucleotide 5'−phosphatase activity
AGOC: mRNA cap methyltransferase complex
AGOP: 7−methylguanosine mRNA capping
PGOF: polynucleotide 5'−phosphatase activity, transferase activity
PGOC: null
PGOP: null





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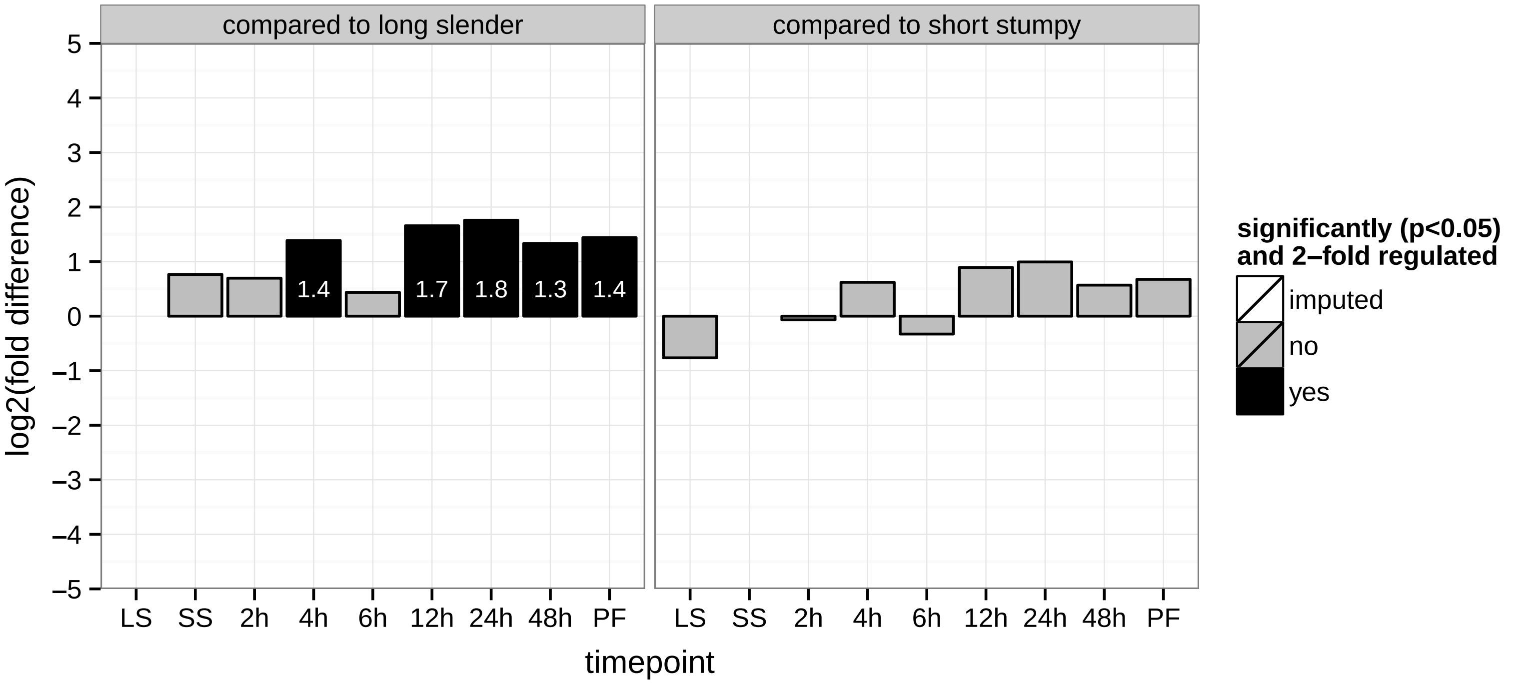
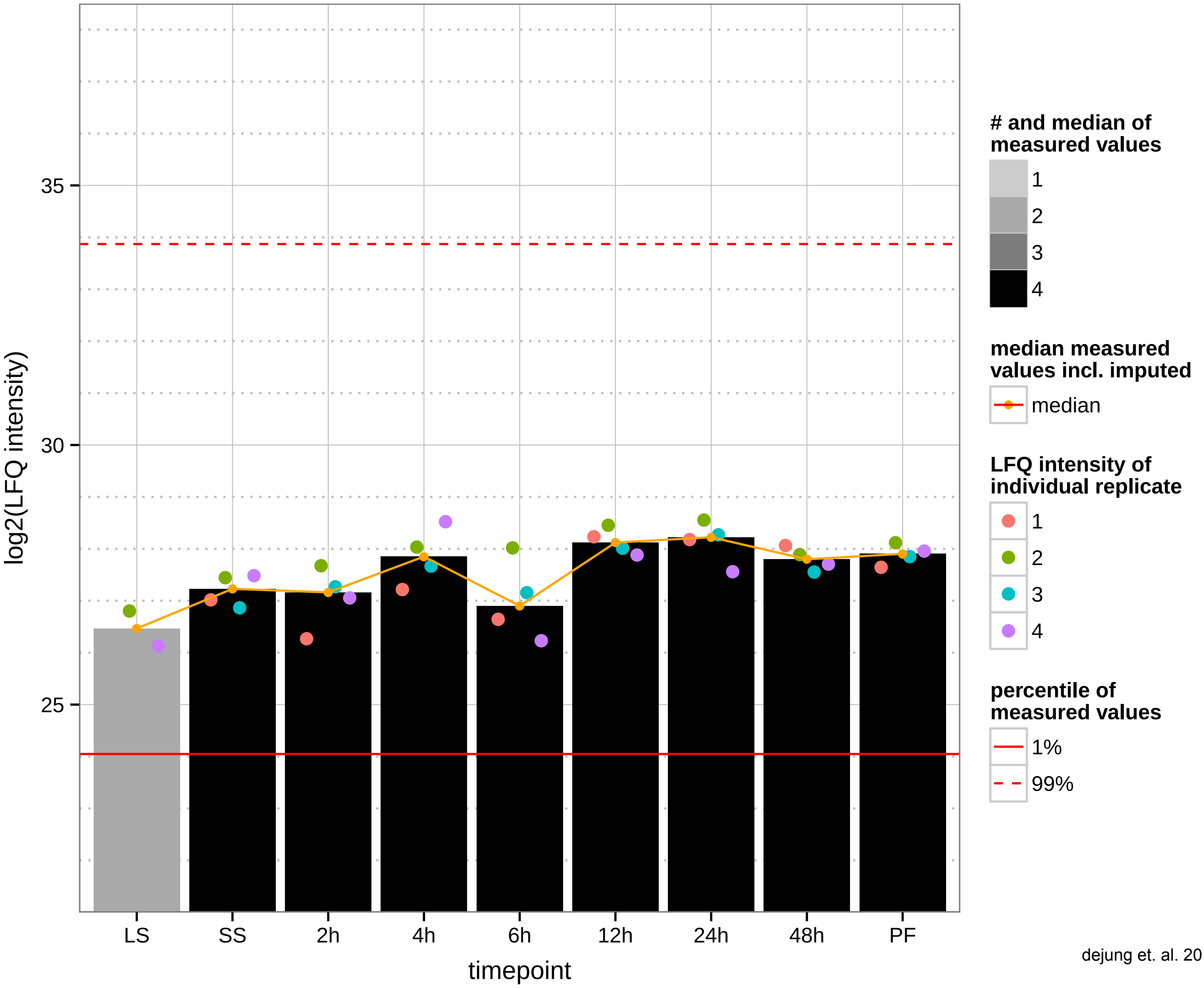
hypothetical protein, conserved
Tb927.3.2220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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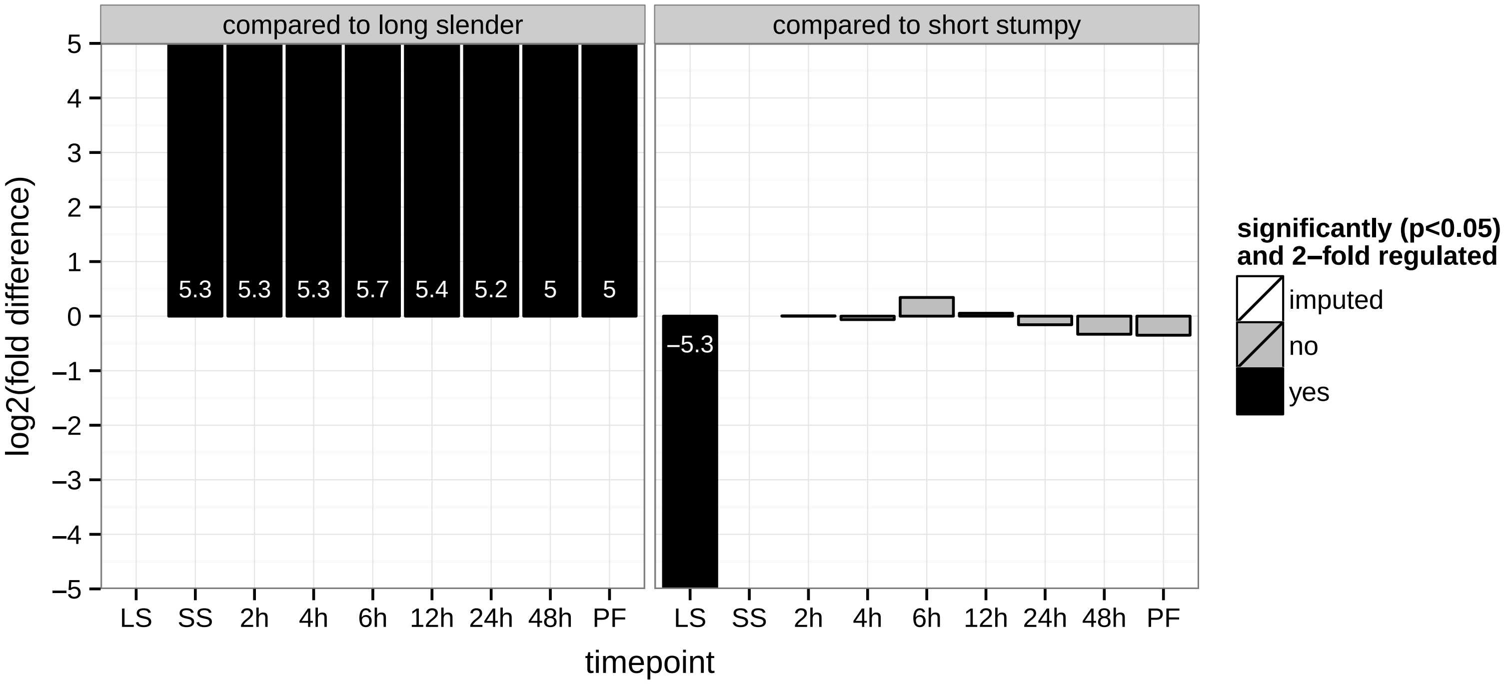
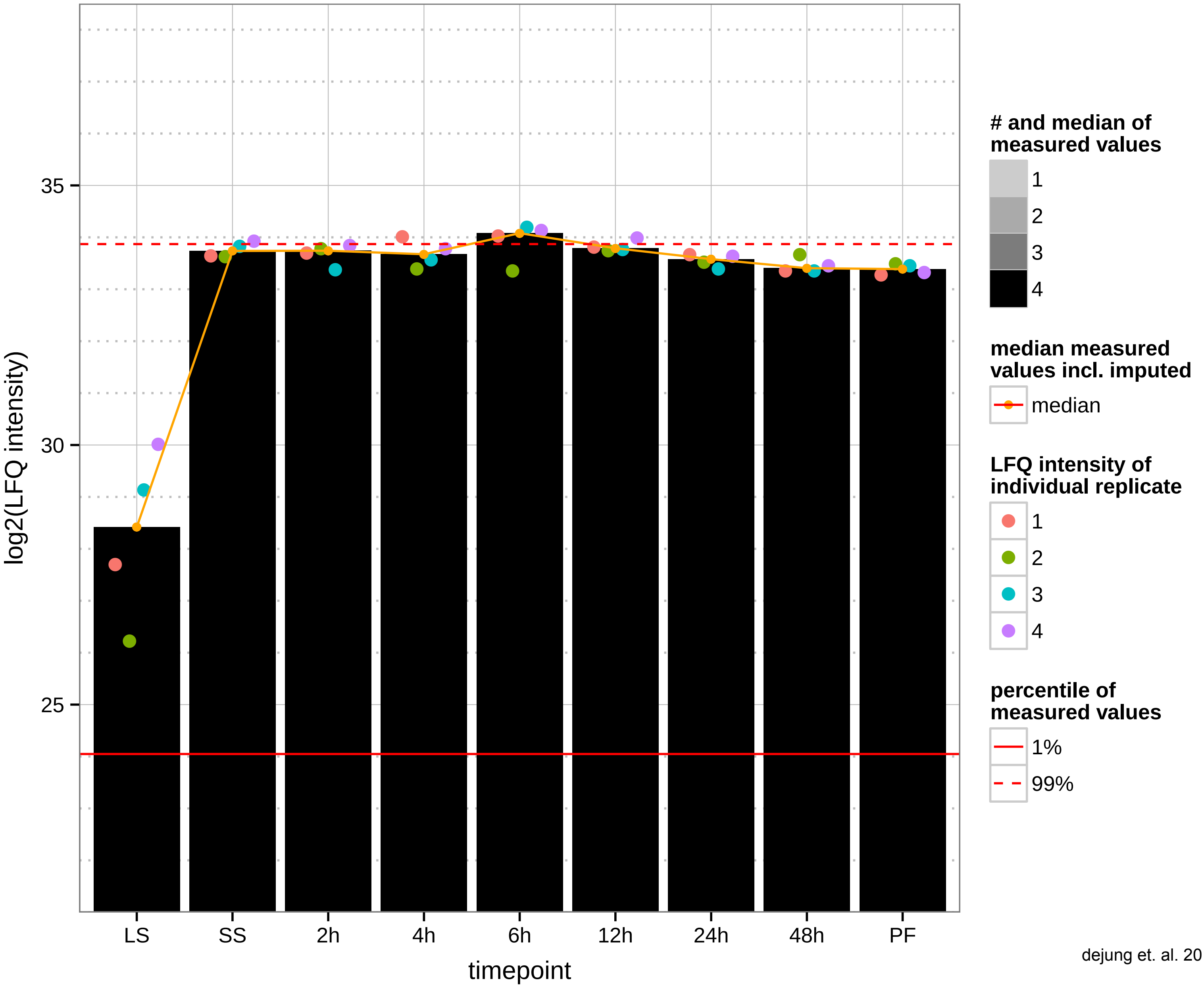
succinyl–CoA synthetase alpha subunit, putative
Tb927.3.2230
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity, cofactor binding
PGOC: null
PGOP: metabolic process





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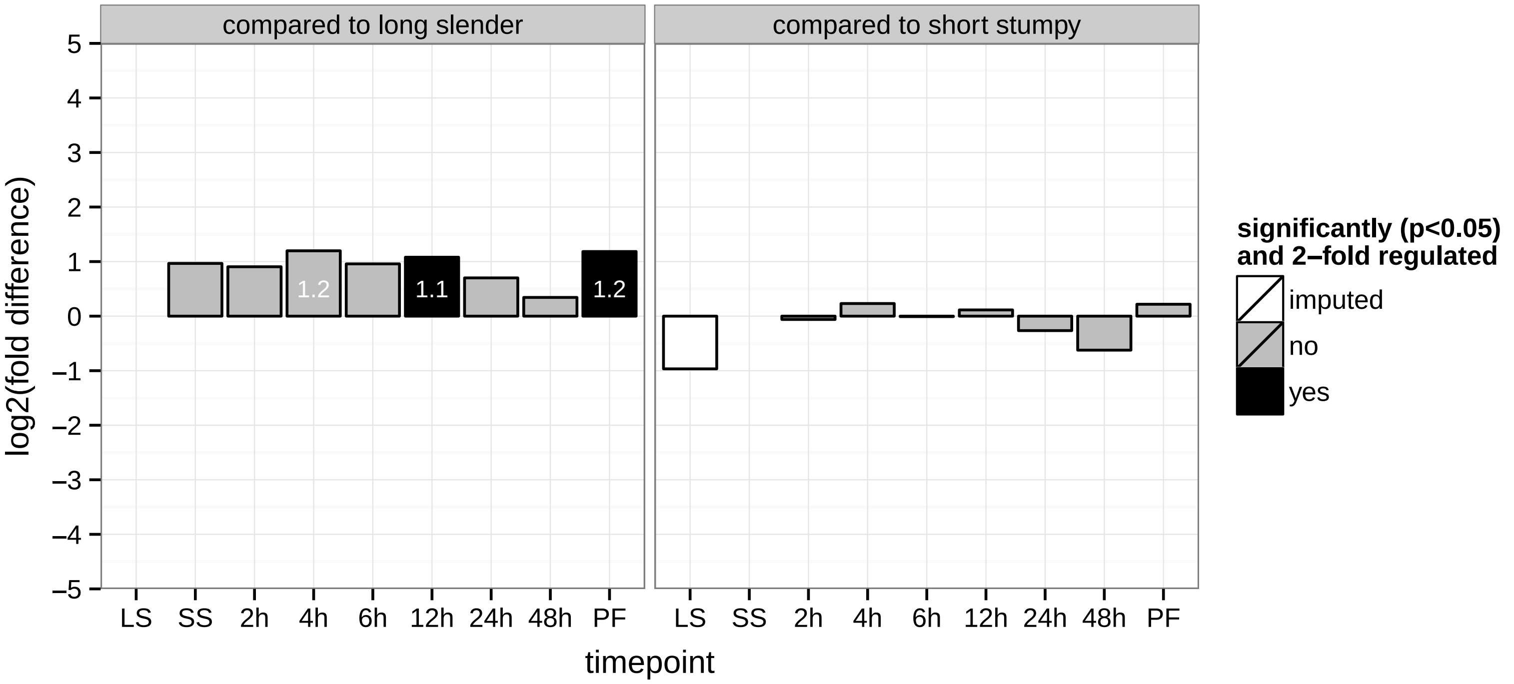
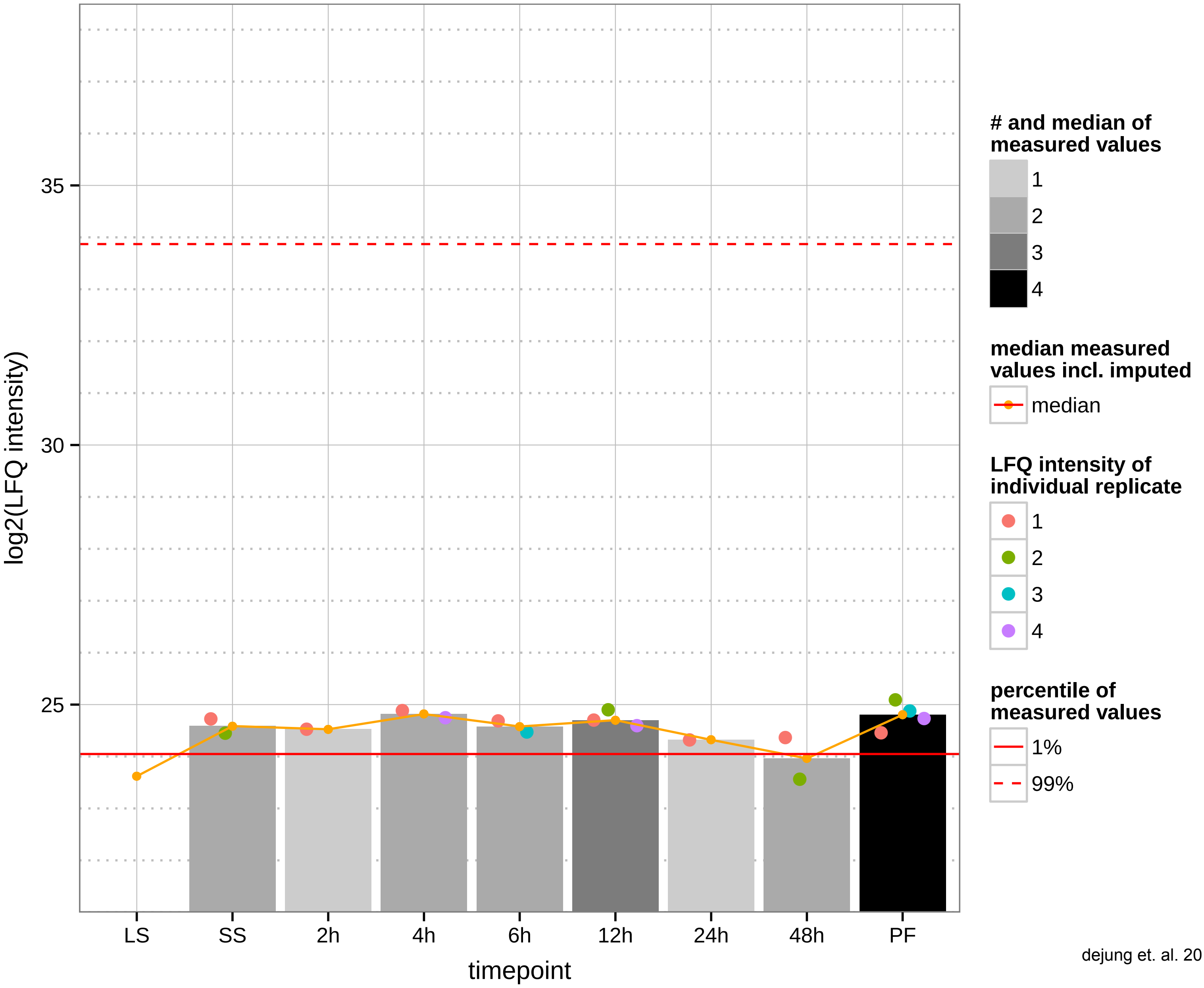
hypothetical protein, conserved
Tb927.3.2270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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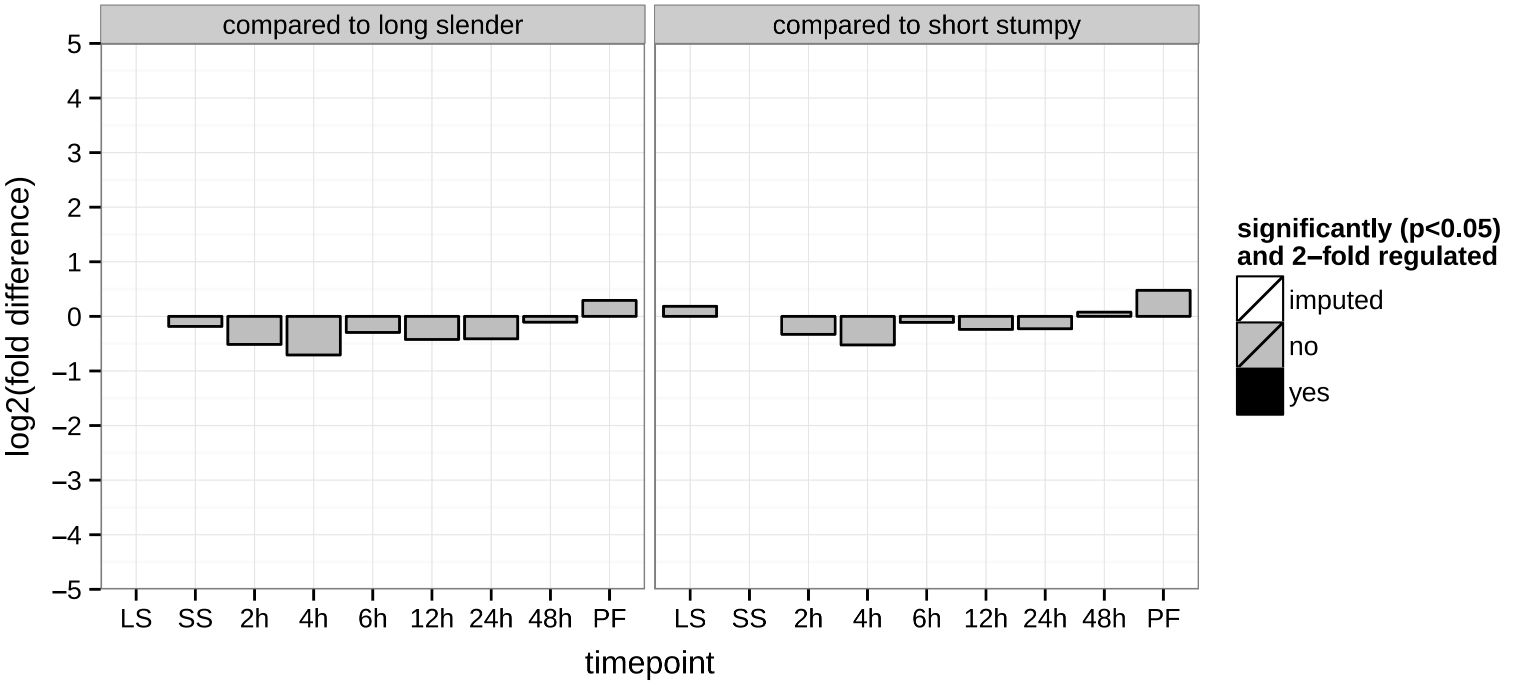
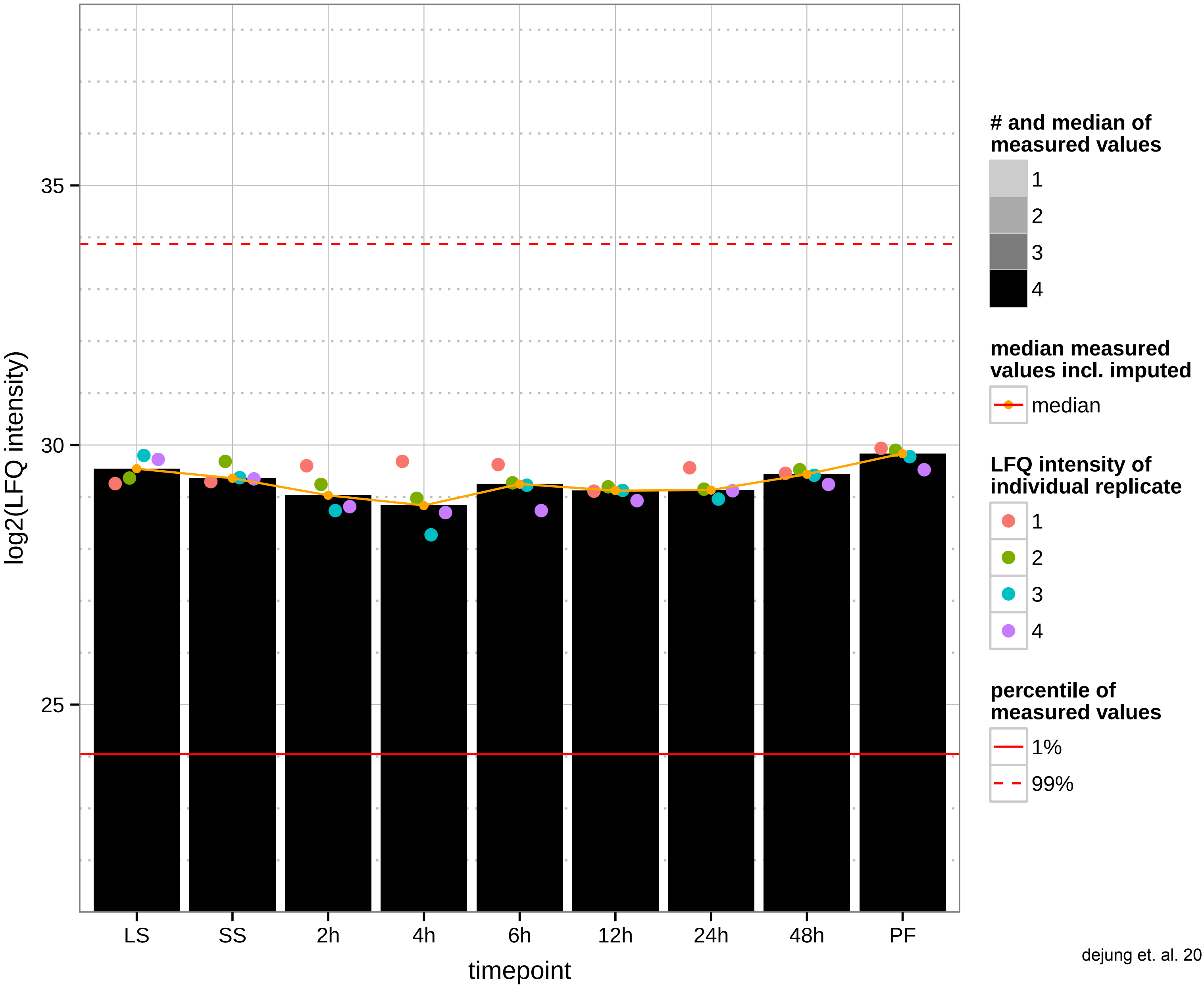
PACRGA, flagellar component
Tb927.3.2310
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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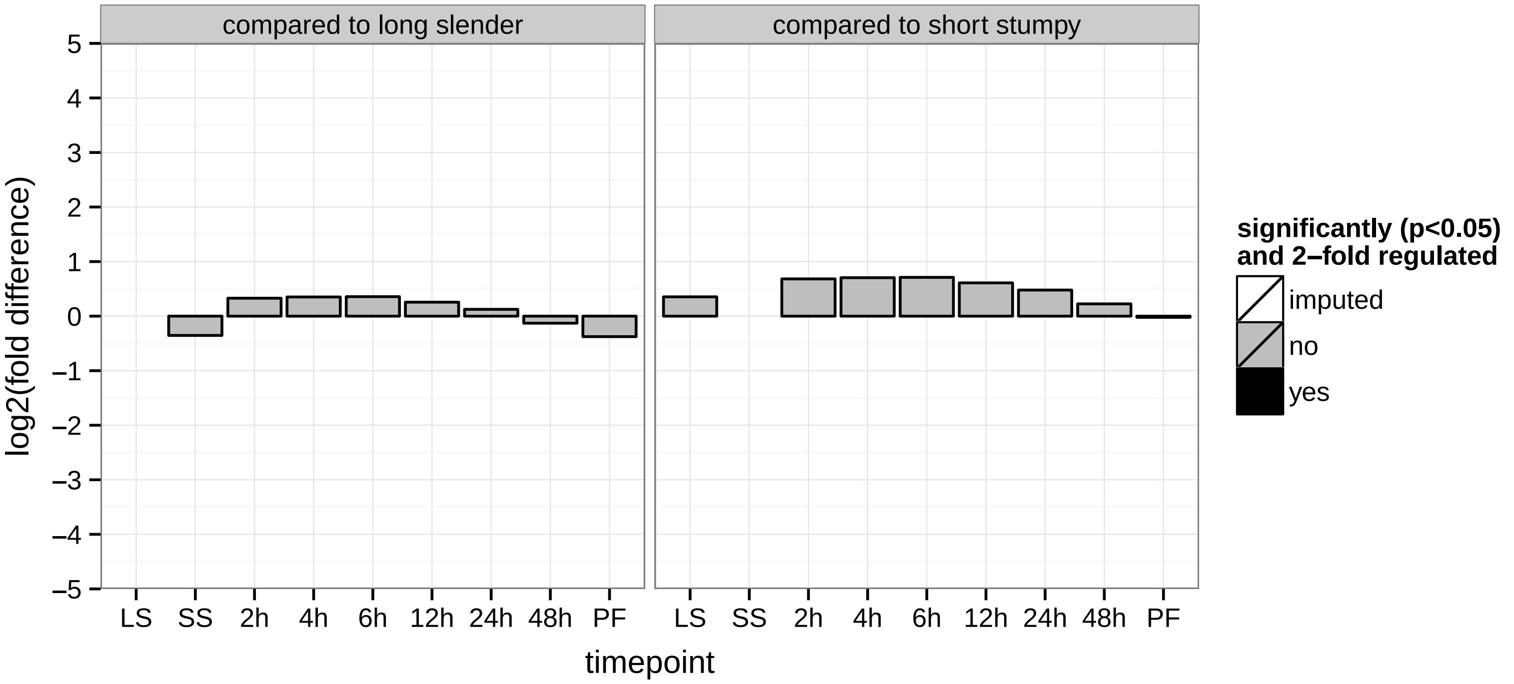
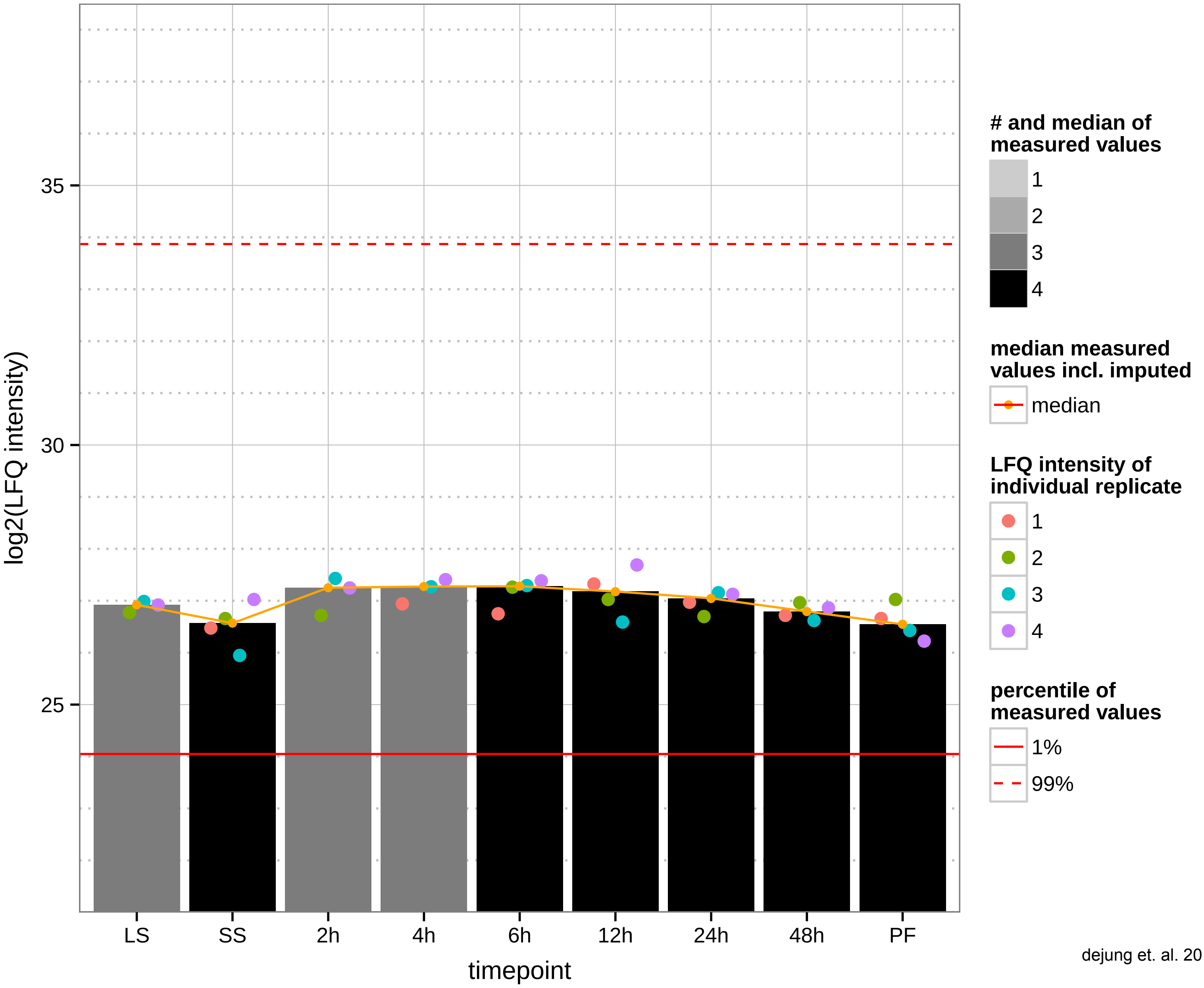
hypothetical protein, conserved
Tb927.3.2420
AGOF: null
AGOC: null
AGOP: null
PGOF: peptidase activity
PGOC: integral to membrane, signal peptidase complex
PGOP: signal peptide processing





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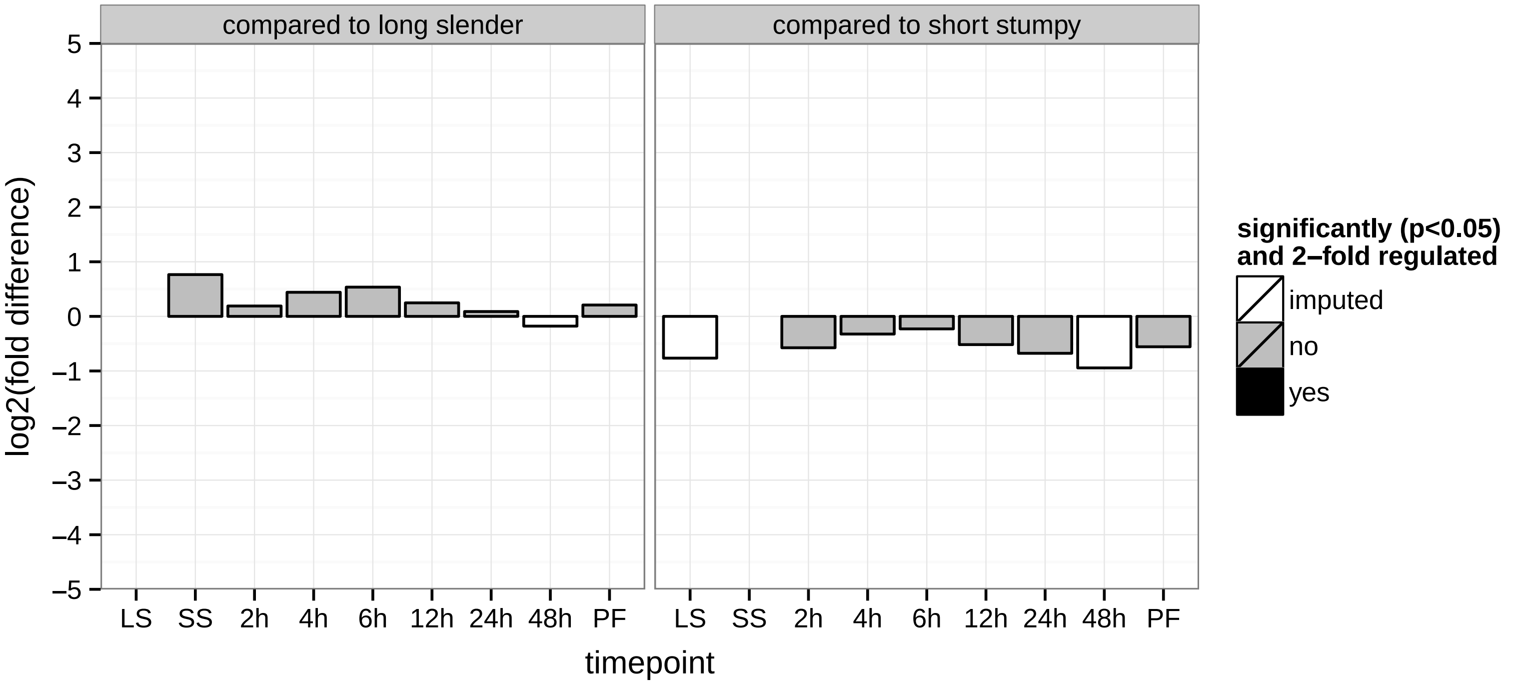
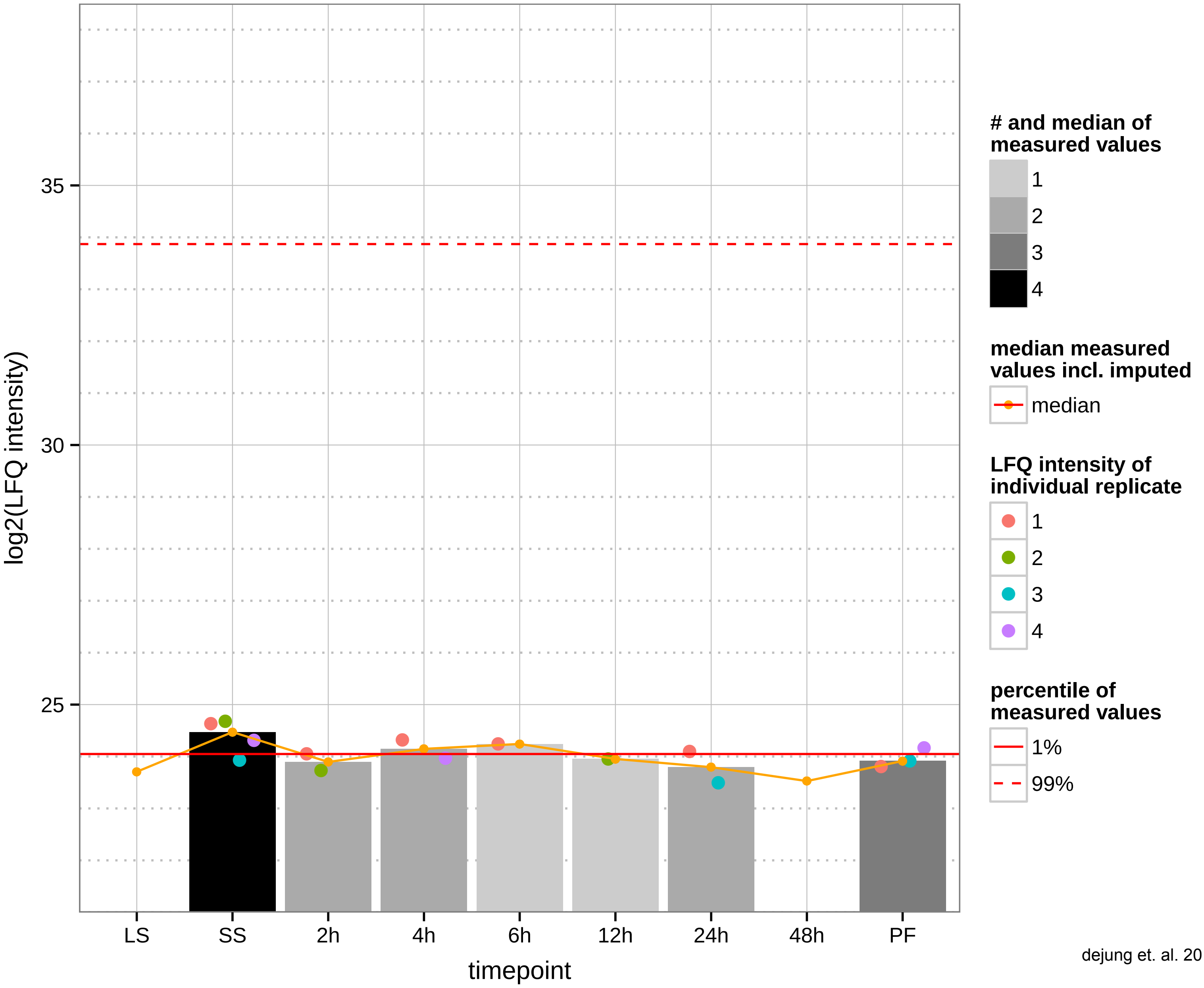
hypothetical protein, conserved
Tb927.3.2430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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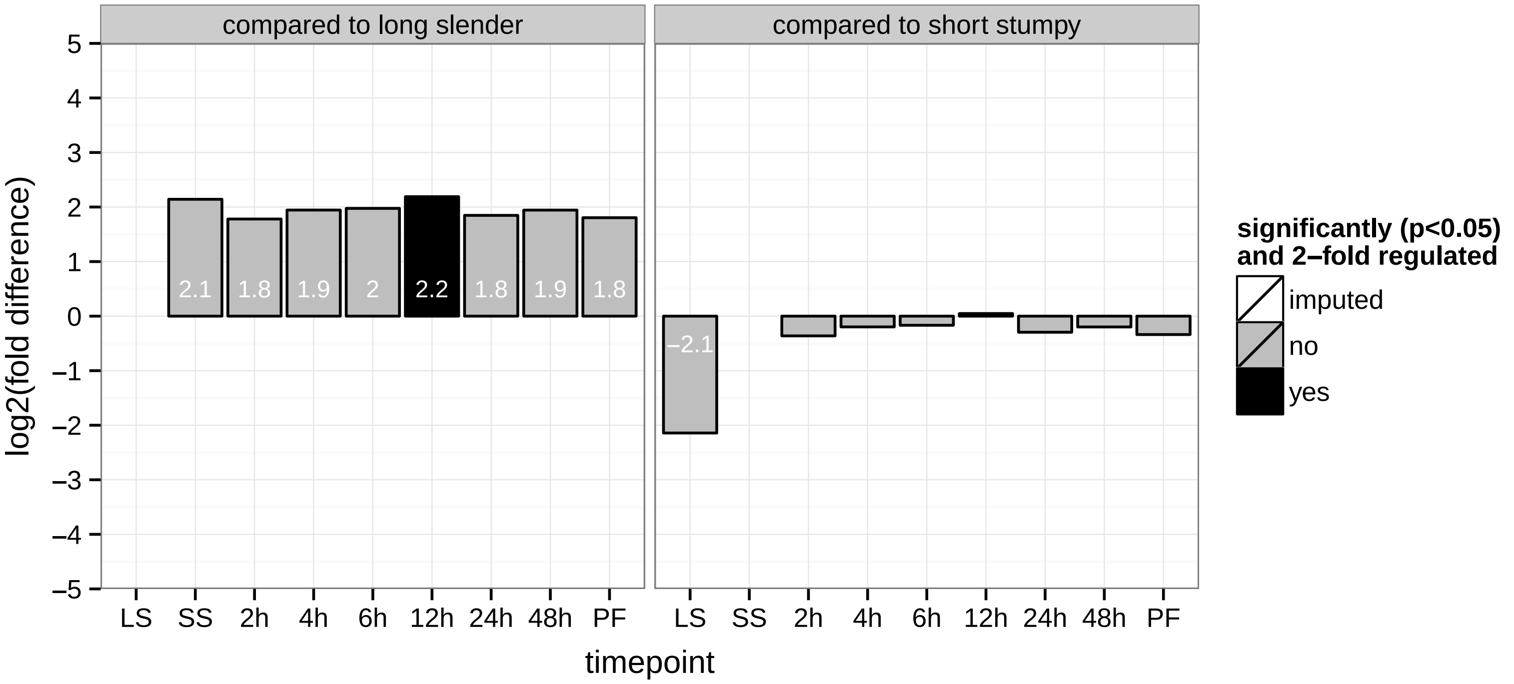
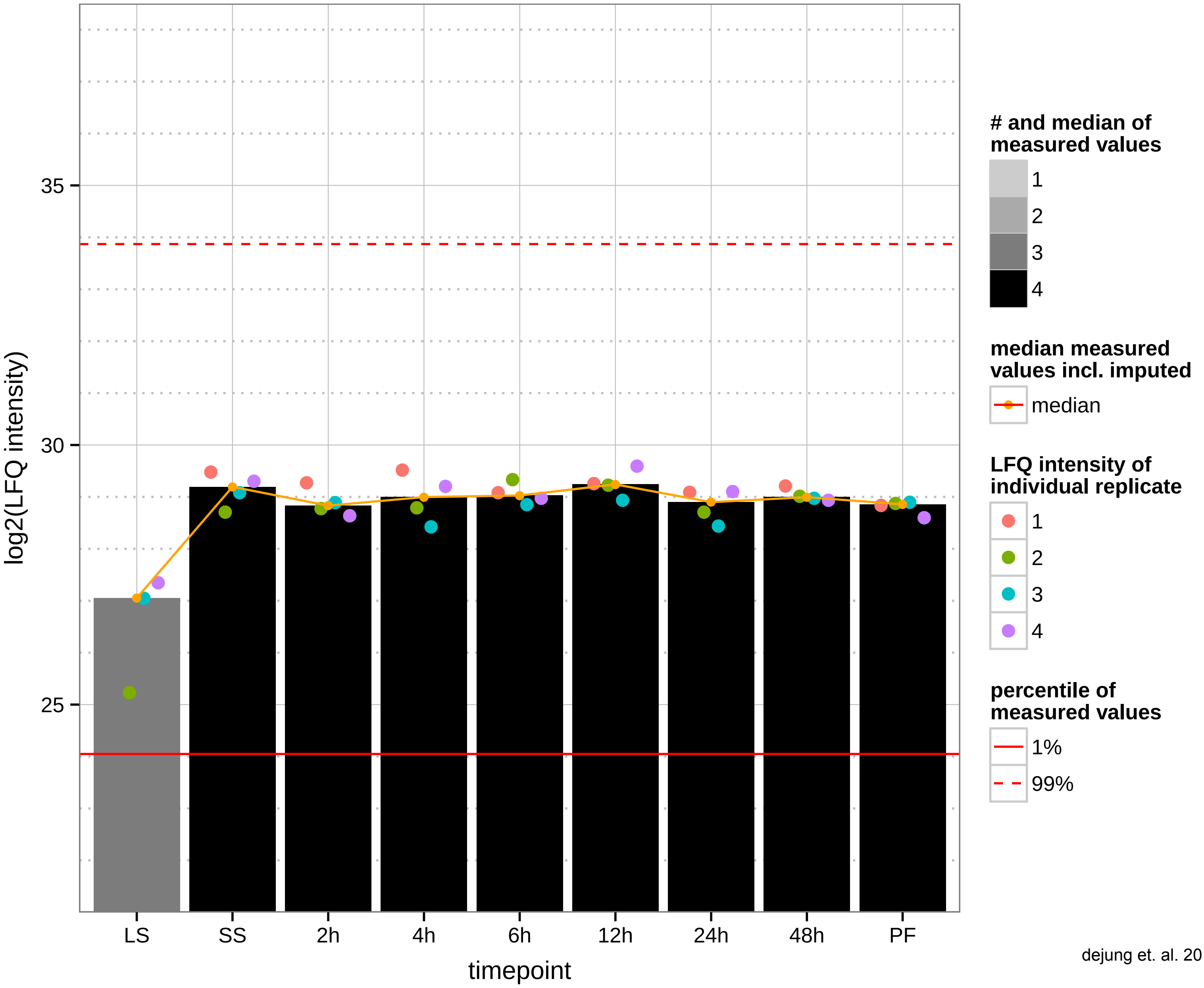
serine/threonine–protein kinase, putative, protein kinase
Tb927.3.2440
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: cytokinesis after mitosis, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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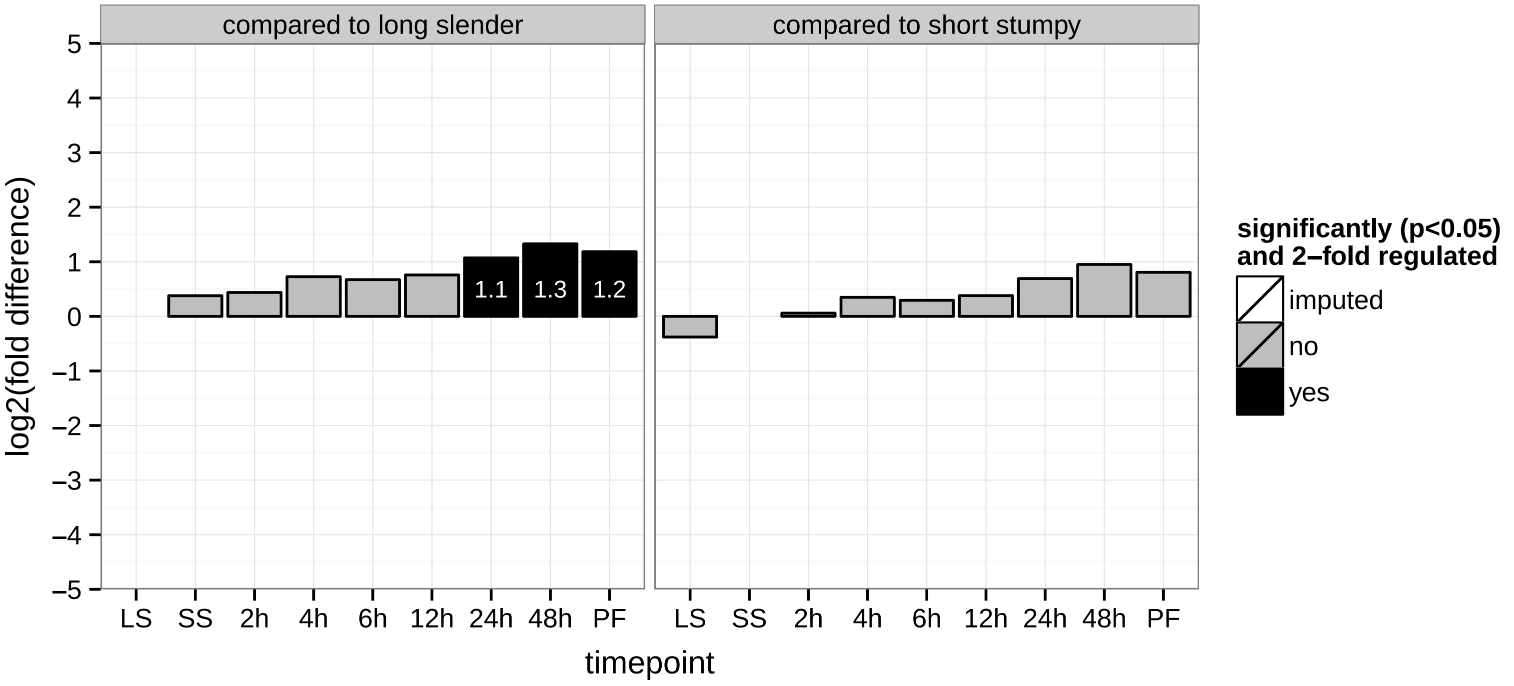
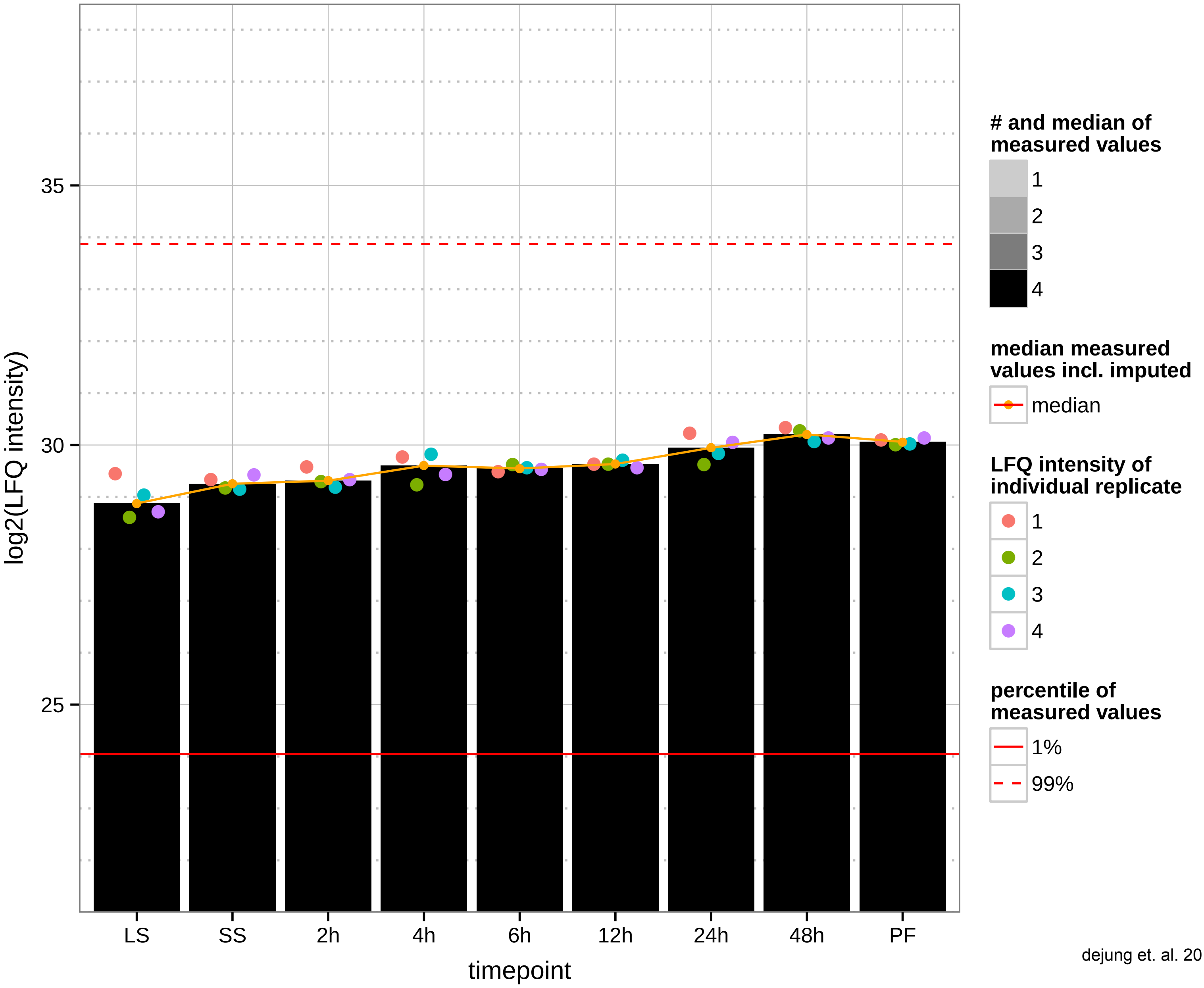
hypothetical protein, conserved
Tb927.3.2490
AGOF: null
AGOC: null
AGOP: null
PGOF: DNA binding
PGOC: null
PGOP: null





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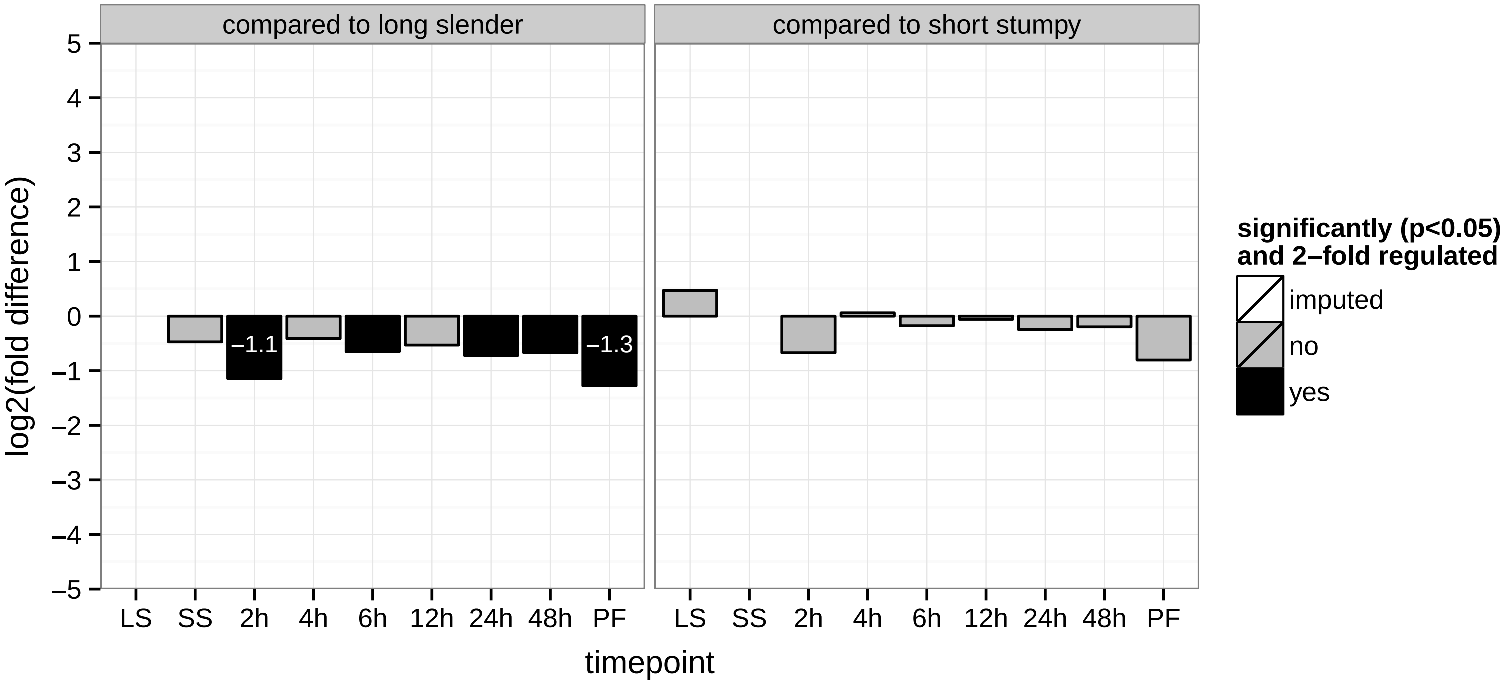
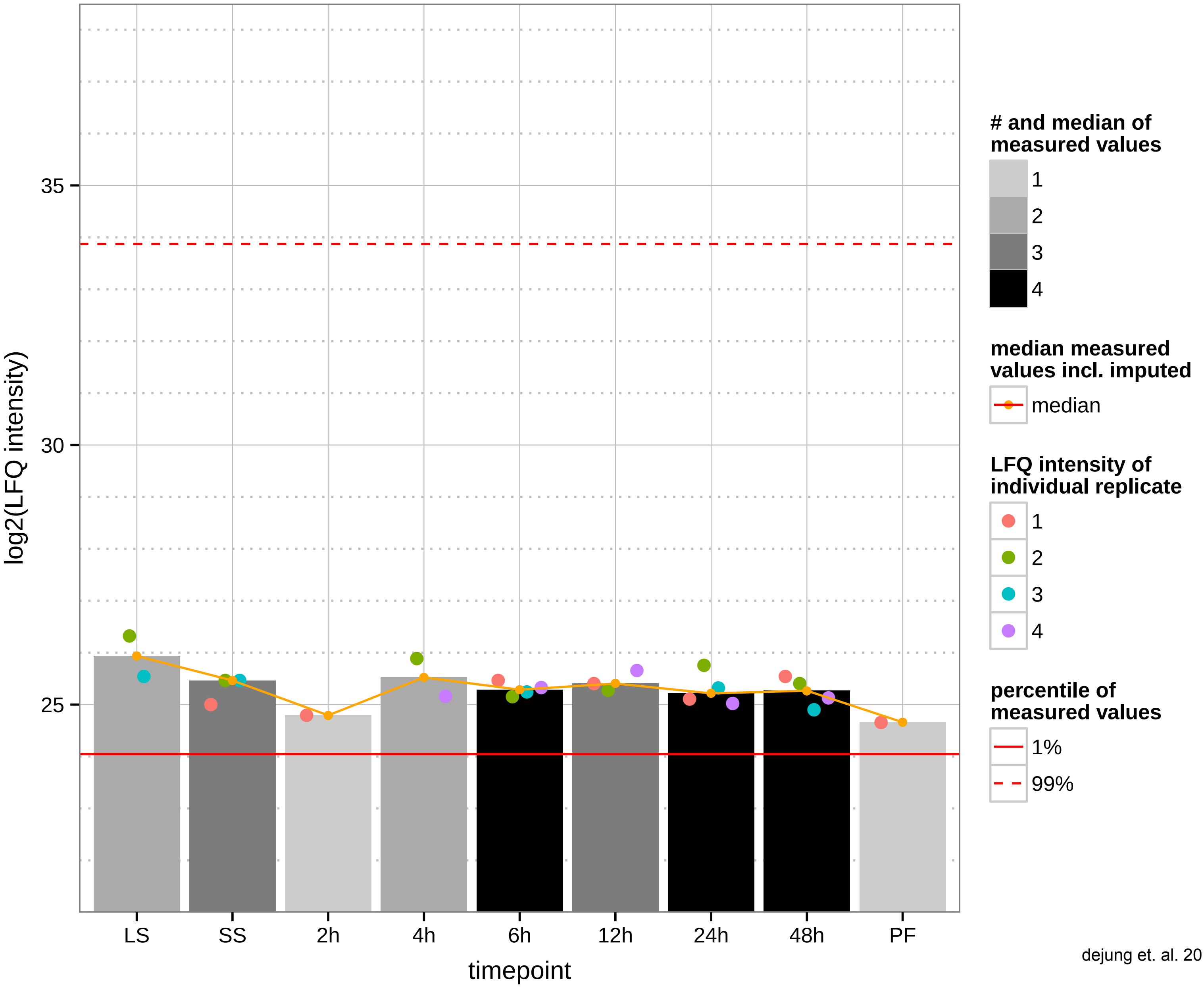
hypothetical protein, conserved
Tb927.3.2700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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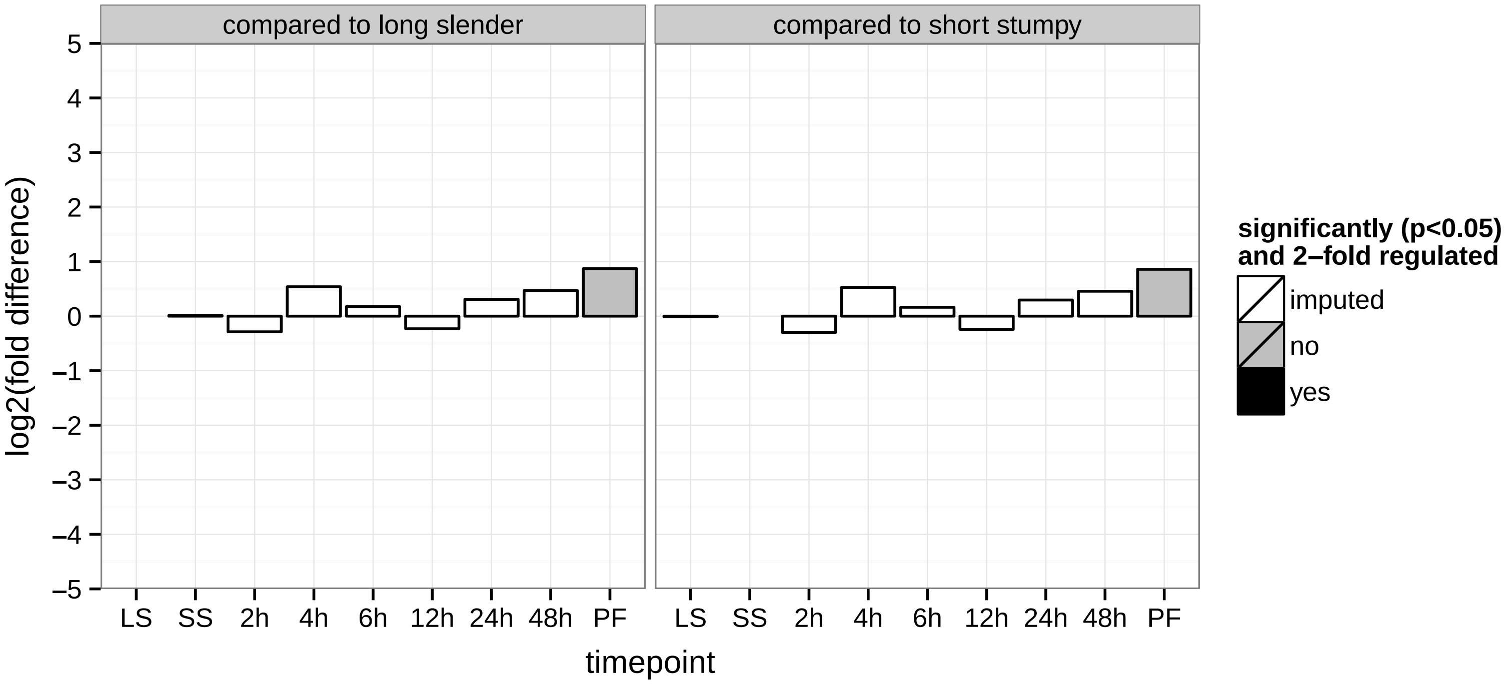
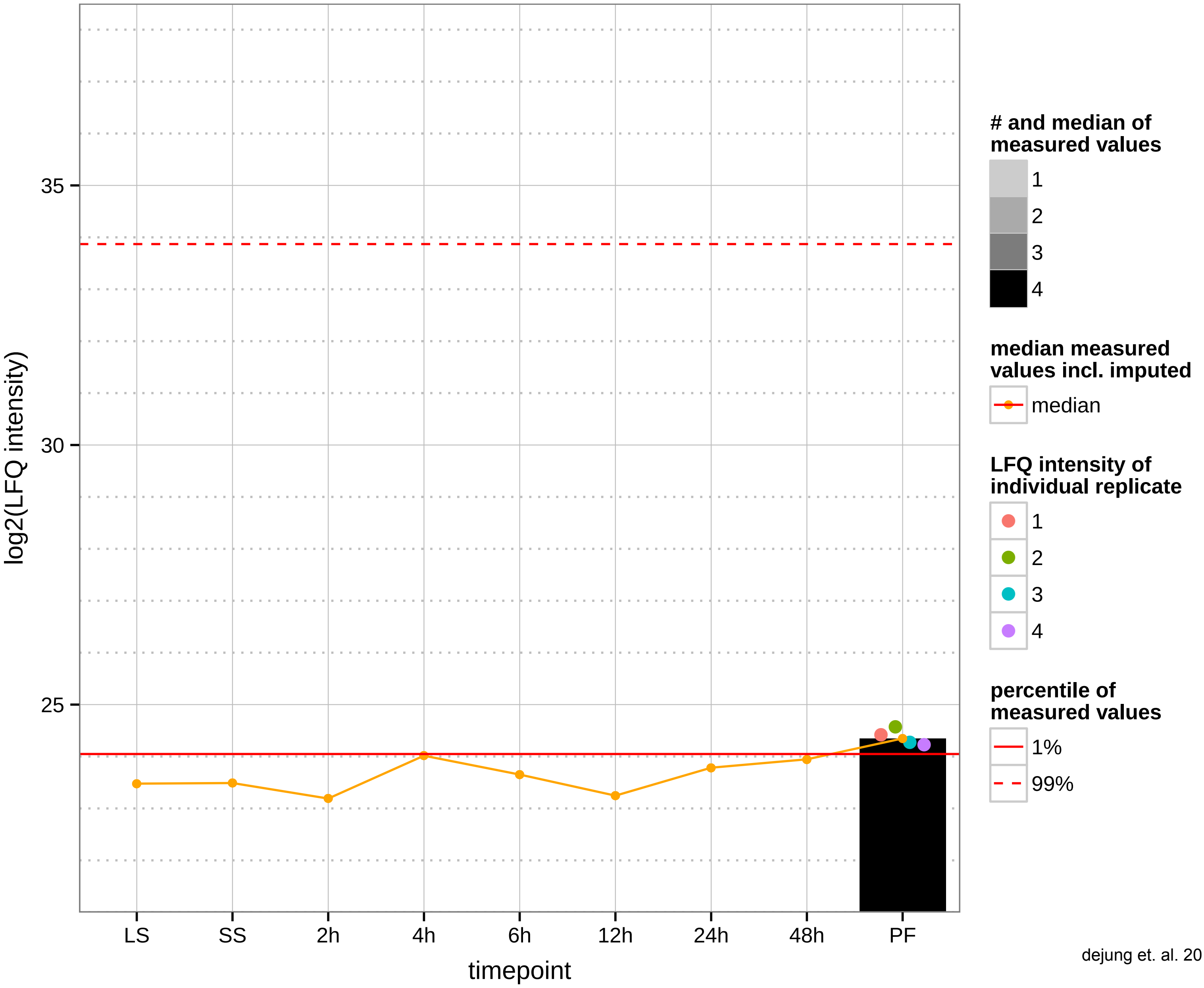
hypothetical protein, conserved
Tb927.3.2810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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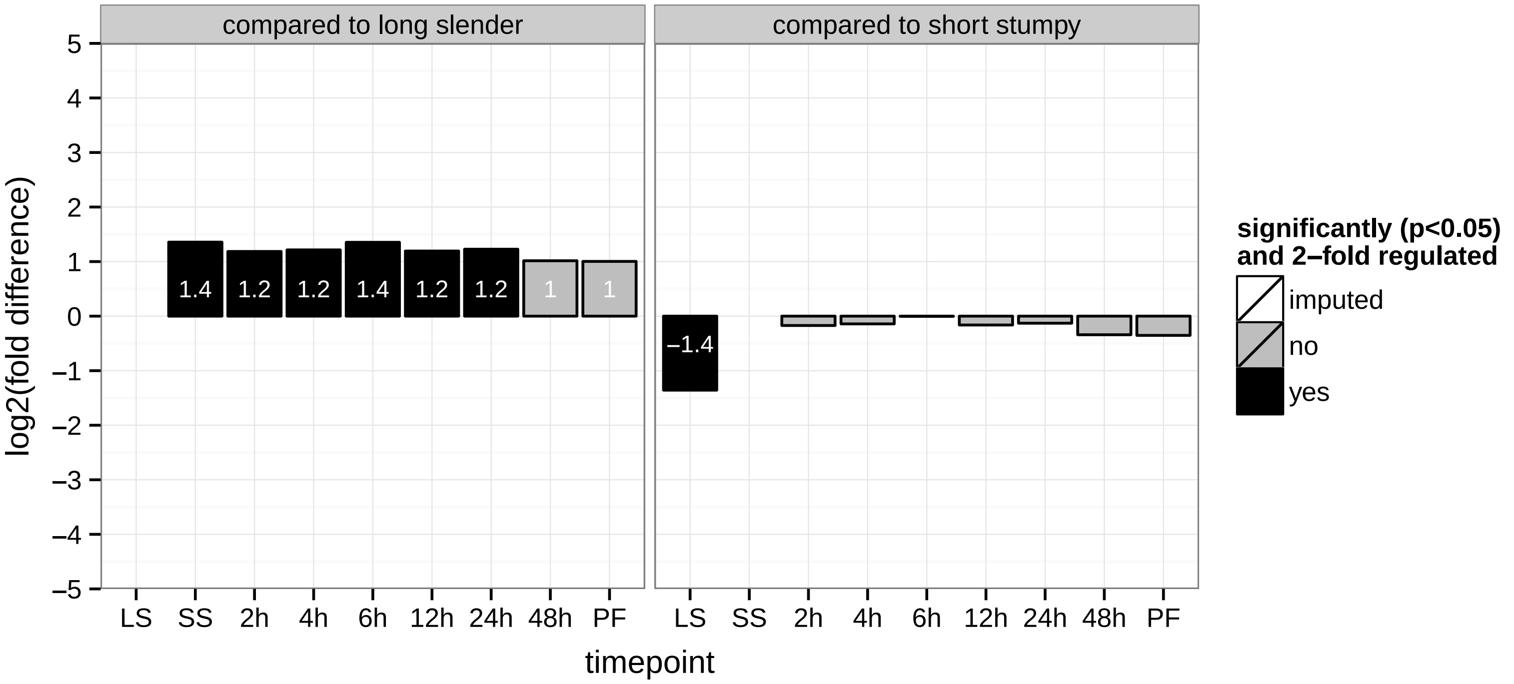
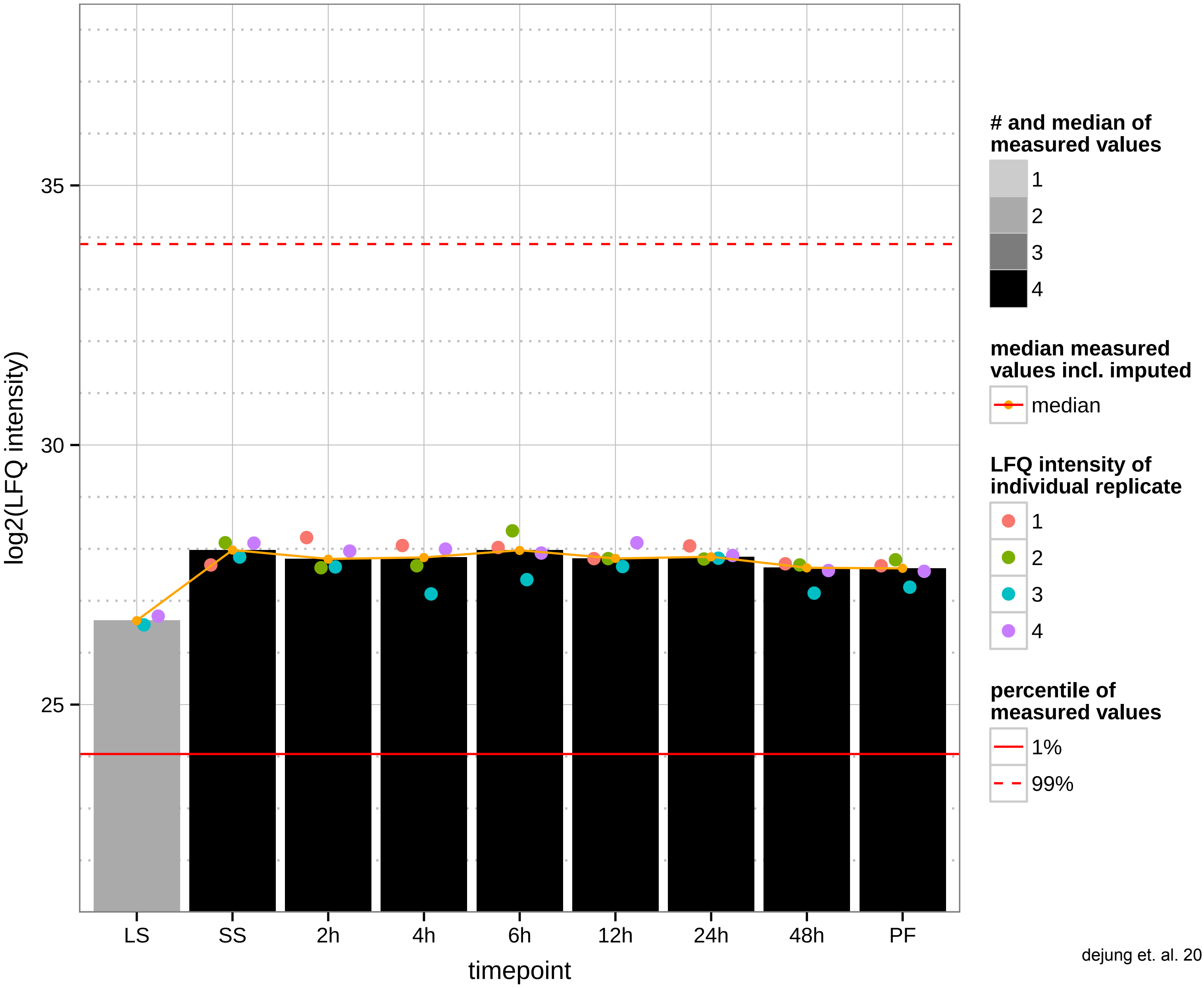
hypothetical protein, conserved
Tb927.3.2830
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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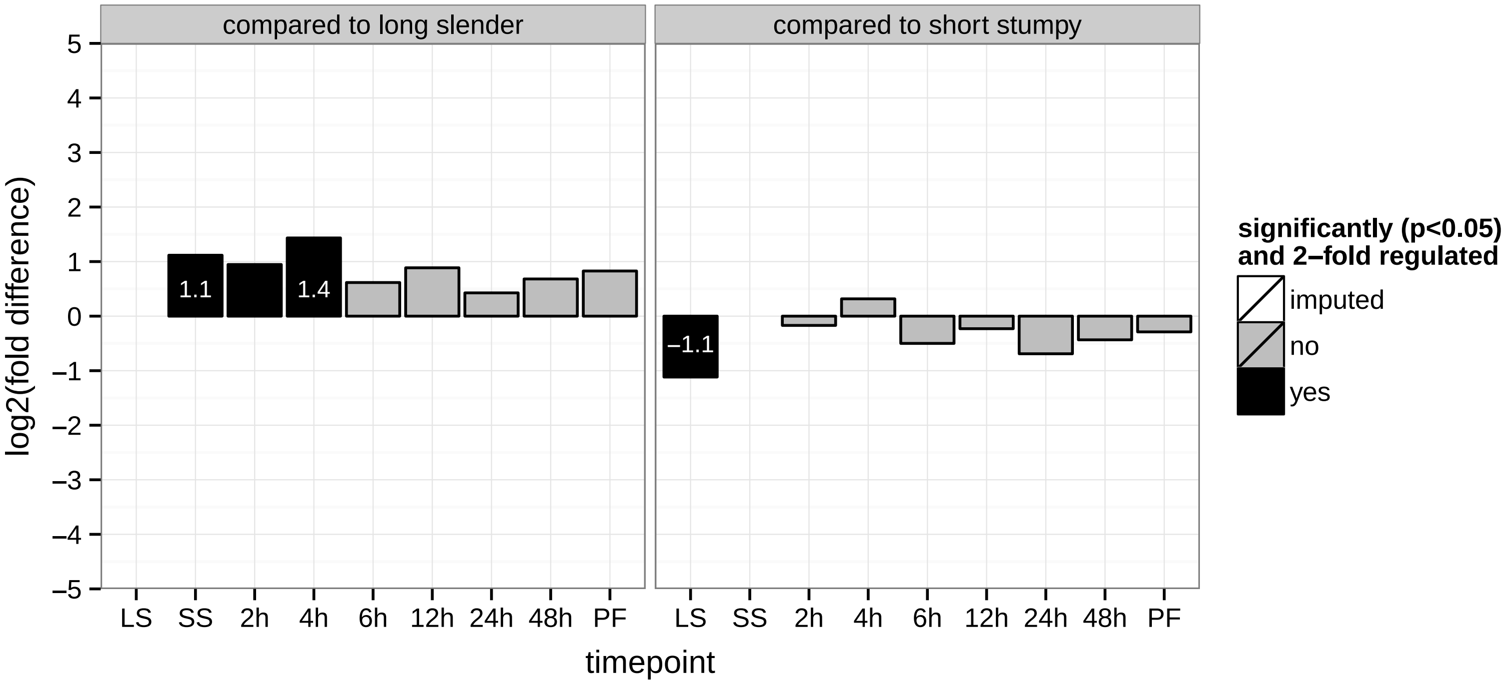
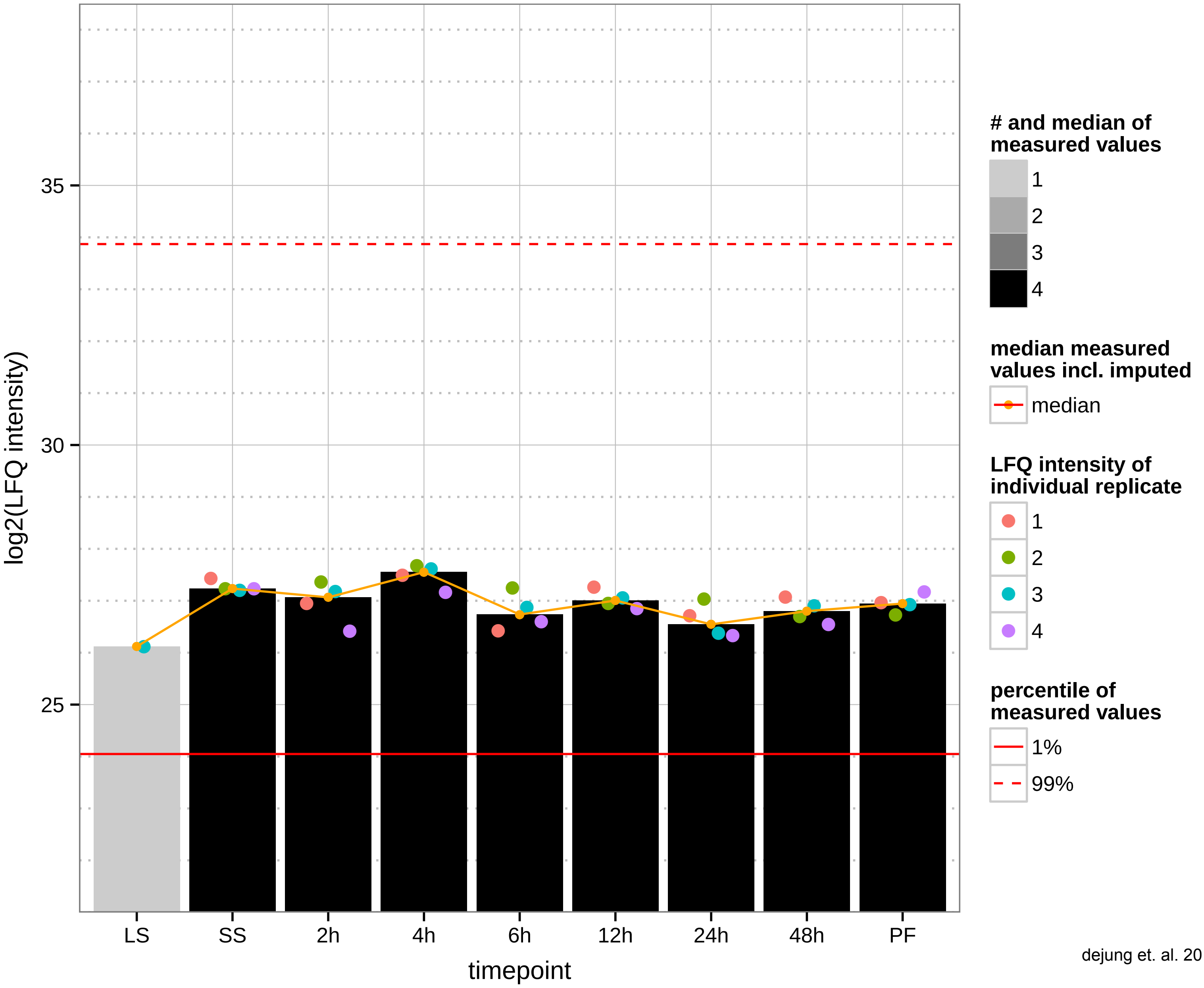
inorganic pyrophosphatase, putative
Tb927.3.2840
AGOF: inorganic diphosphatase activity, magnesium ion binding
AGOC: cytoplasm
AGOP: phosphate–containing compound metabolic process
PGOF: inorganic diphosphatase activity, magnesium ion binding
PGOC: cytoplasm
PGOP: phosphate–containing compound metabolic process





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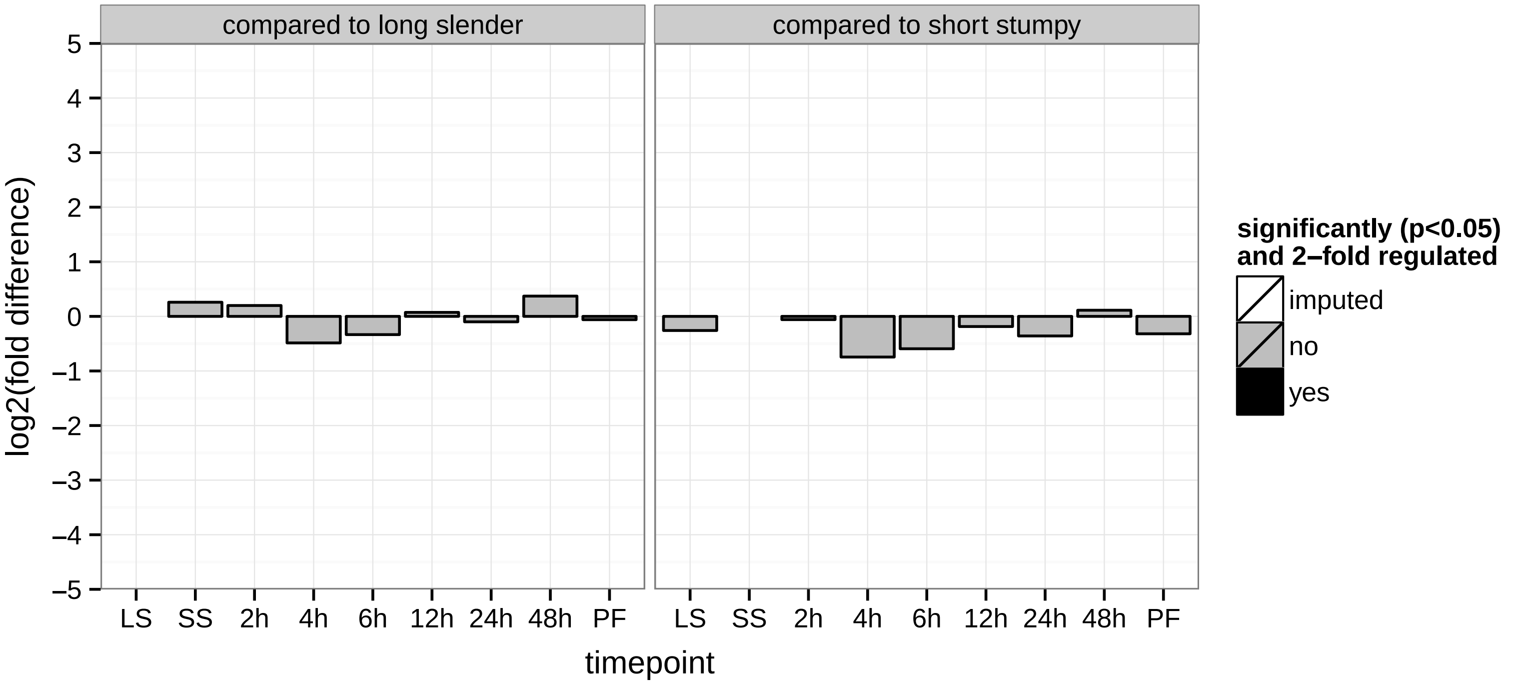
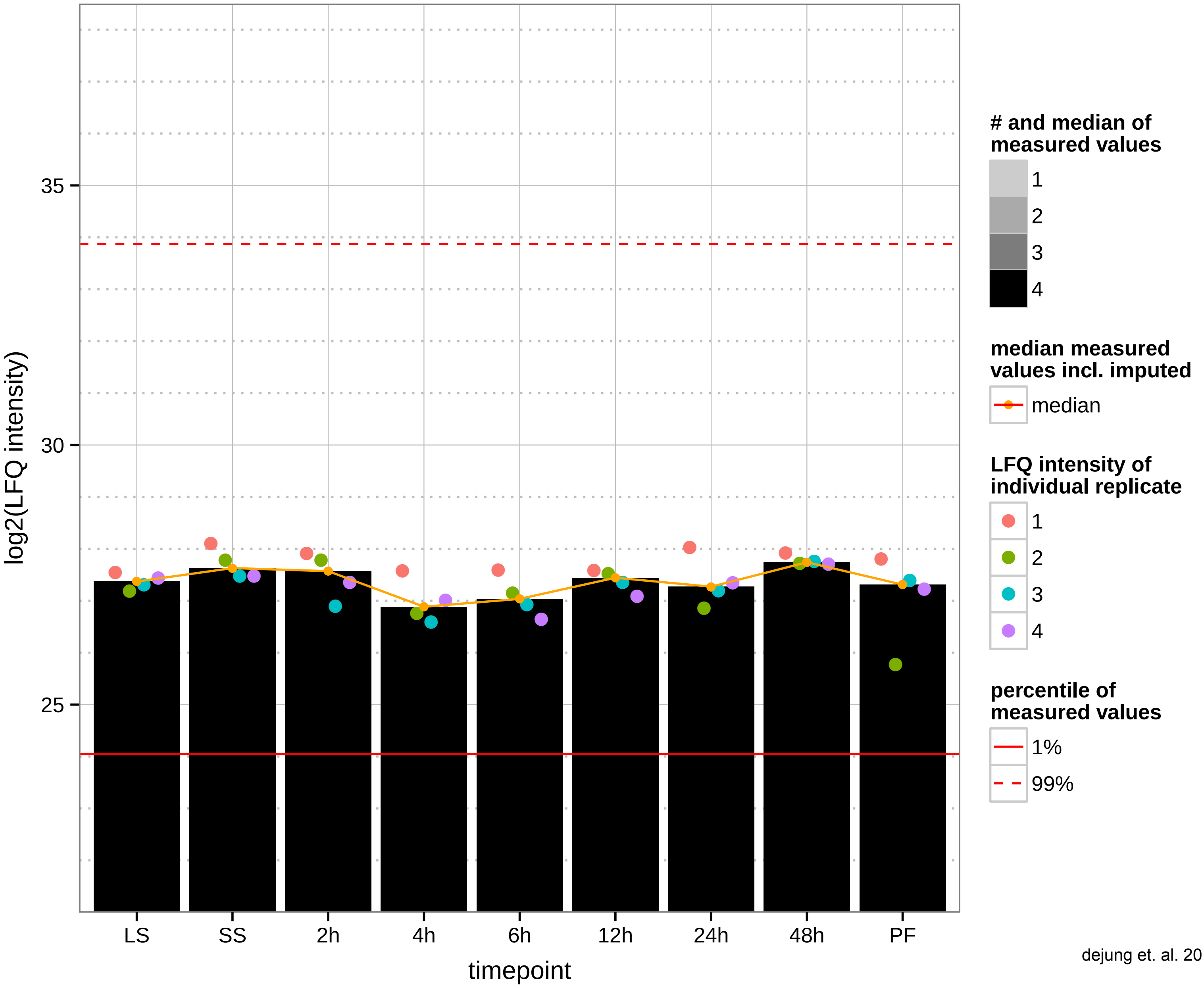
radial spoke protein RSP10, putative
Tb927.3.2890
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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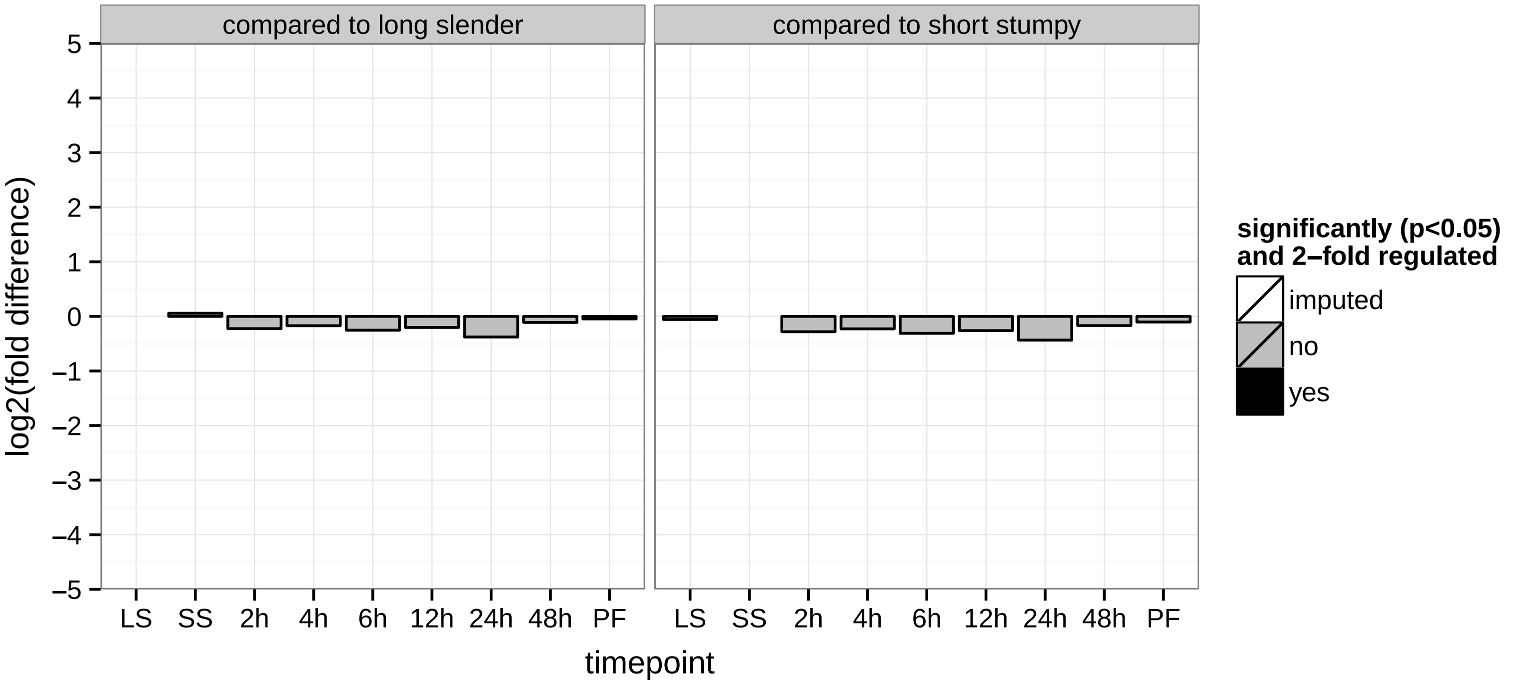
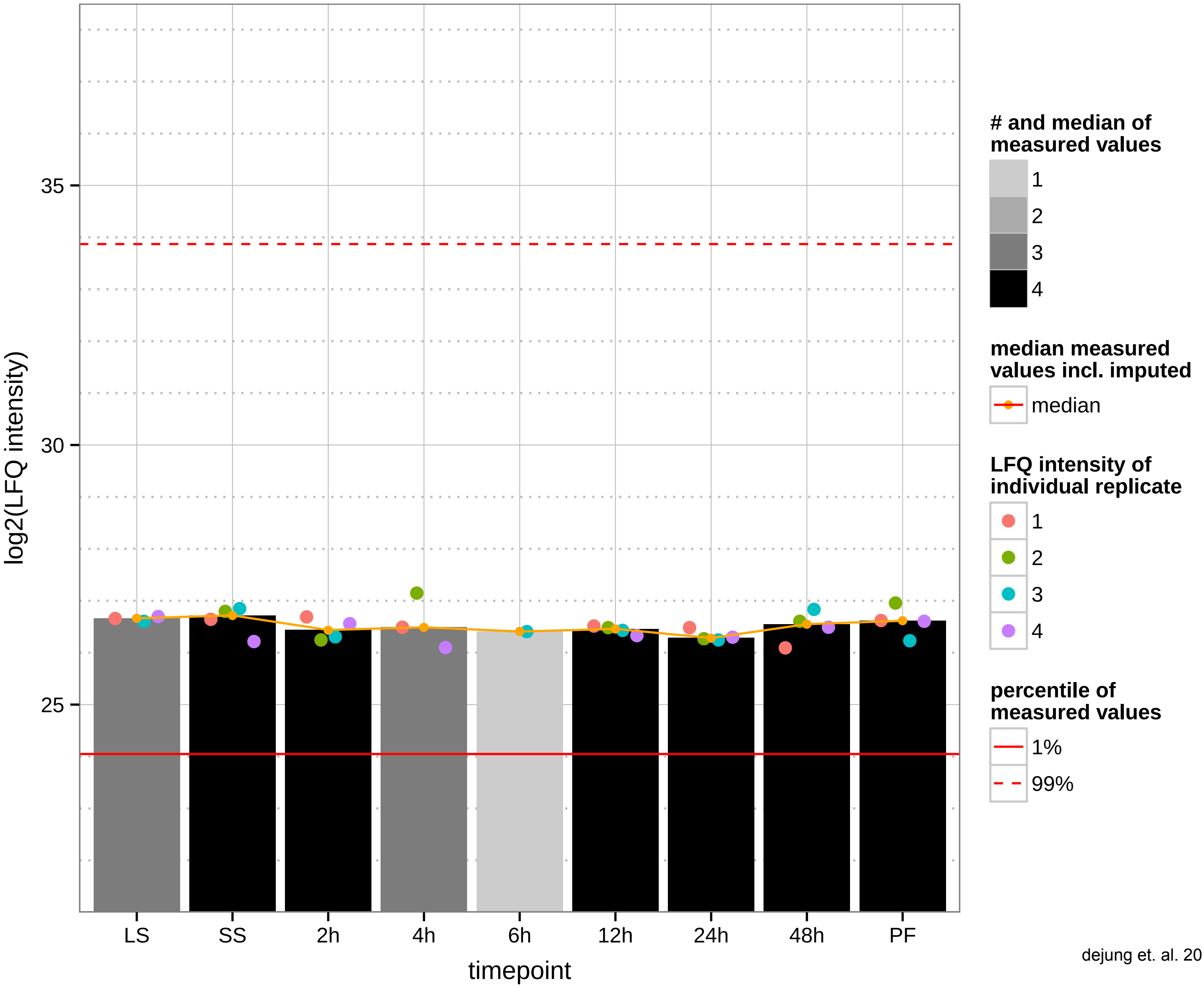
ribonuclease inhibitor– like protein, leucine–rich repeat protein (LRRP), putative
Tb927.3.2950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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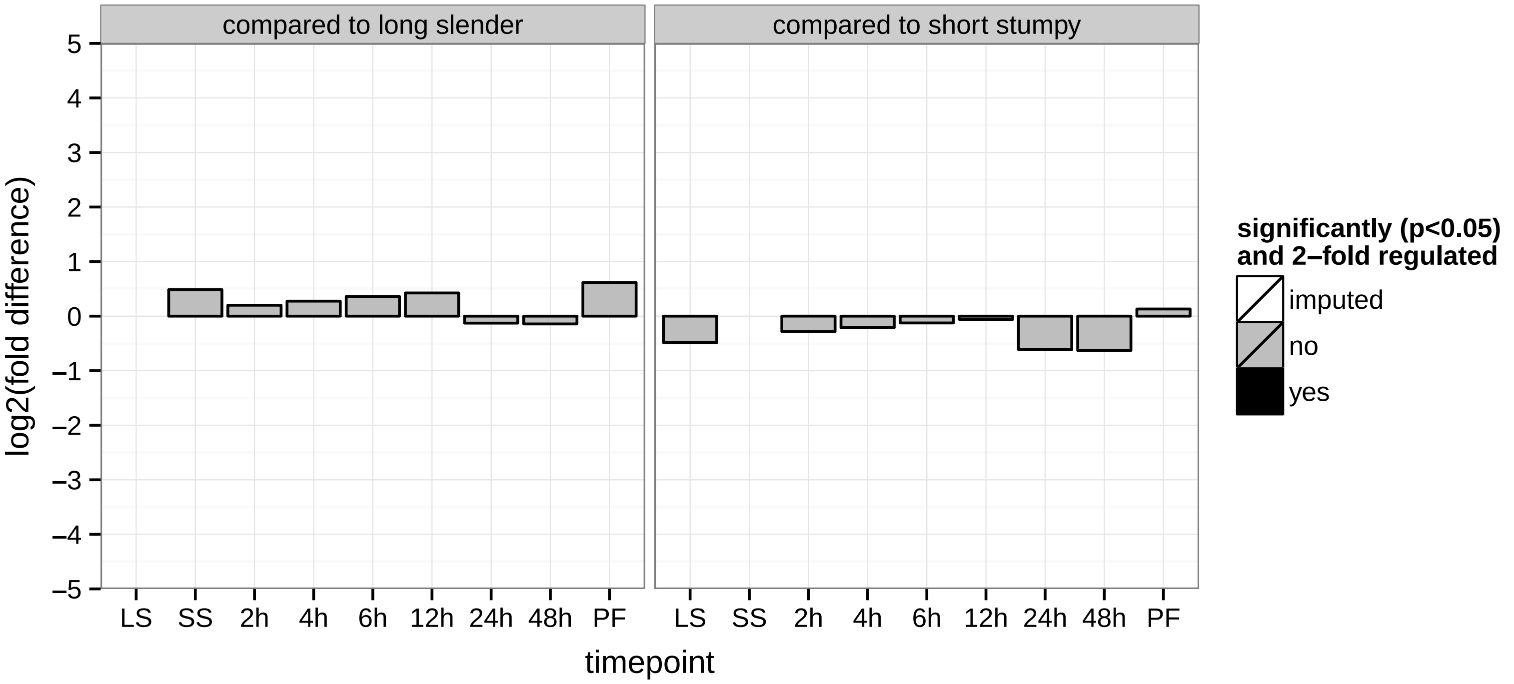
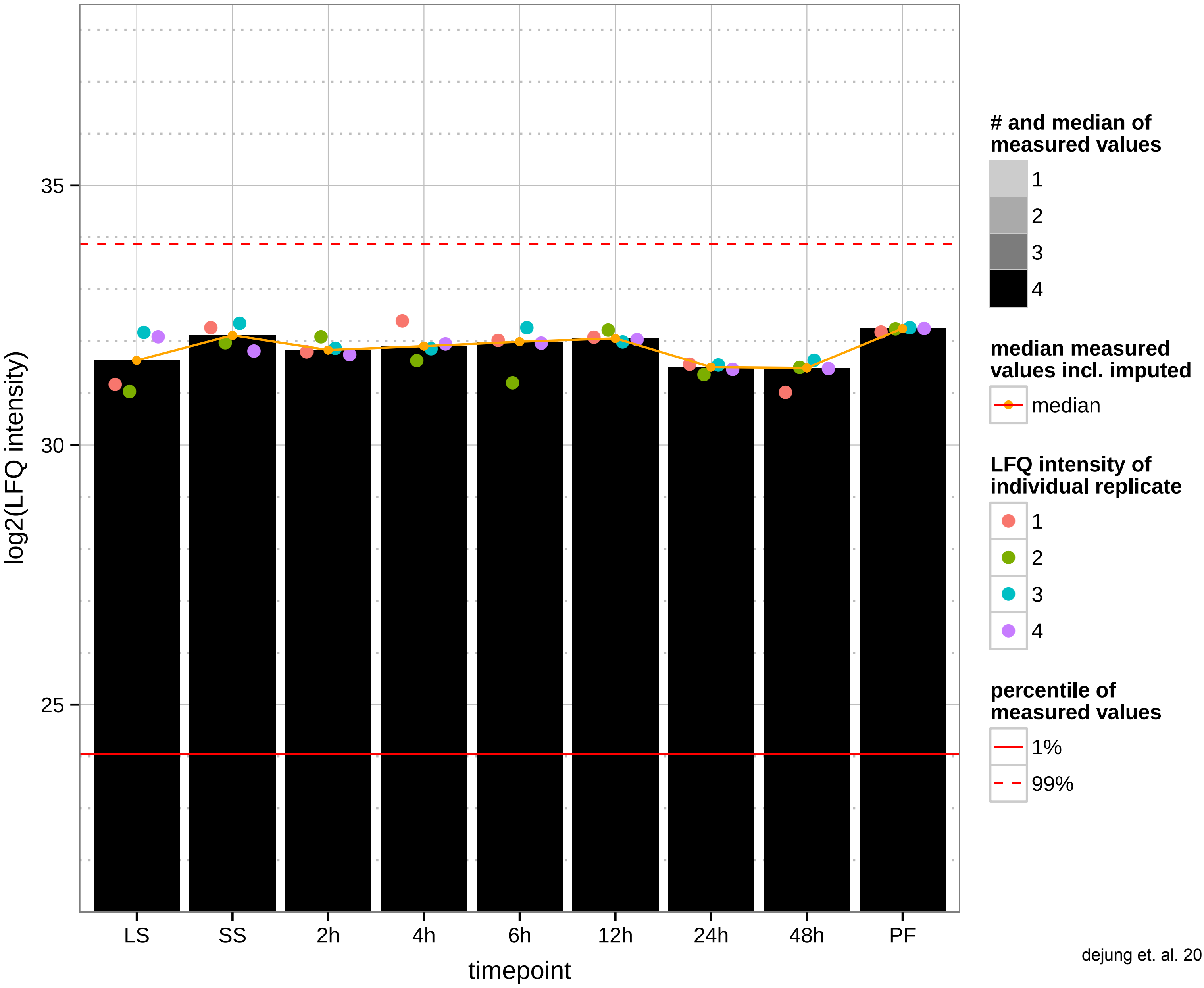
inosine–adenosine–guanosine–nucleosidehydrolase, IAG–nucleoside hydrolase (IAGNH)
Tb927.3.2960
AGOF: hydrolase activity, acting on carbon–nitrogen (but not peptide) bonds
AGOC: cytosol
AGOP: purine ribonucleoside salvage
PGOF: null
PGOC: null
PGOP: null





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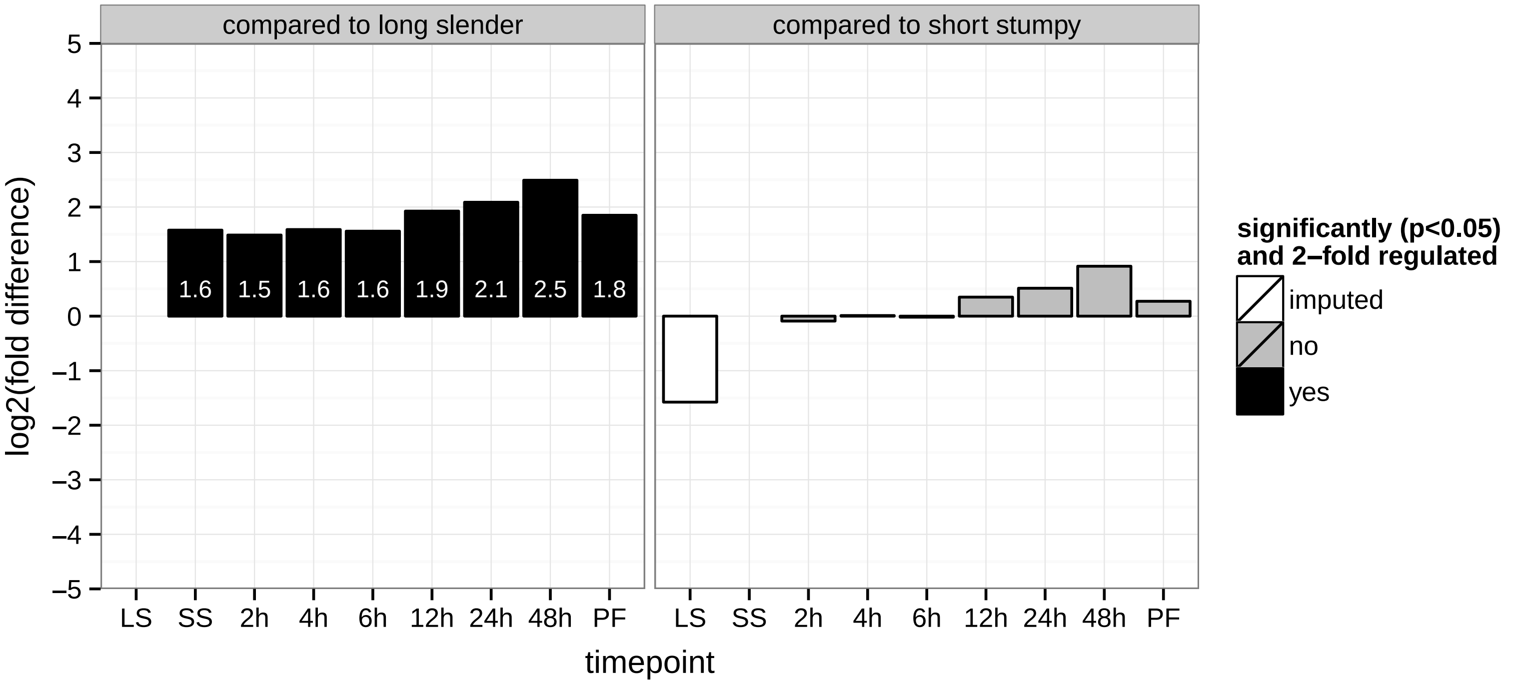
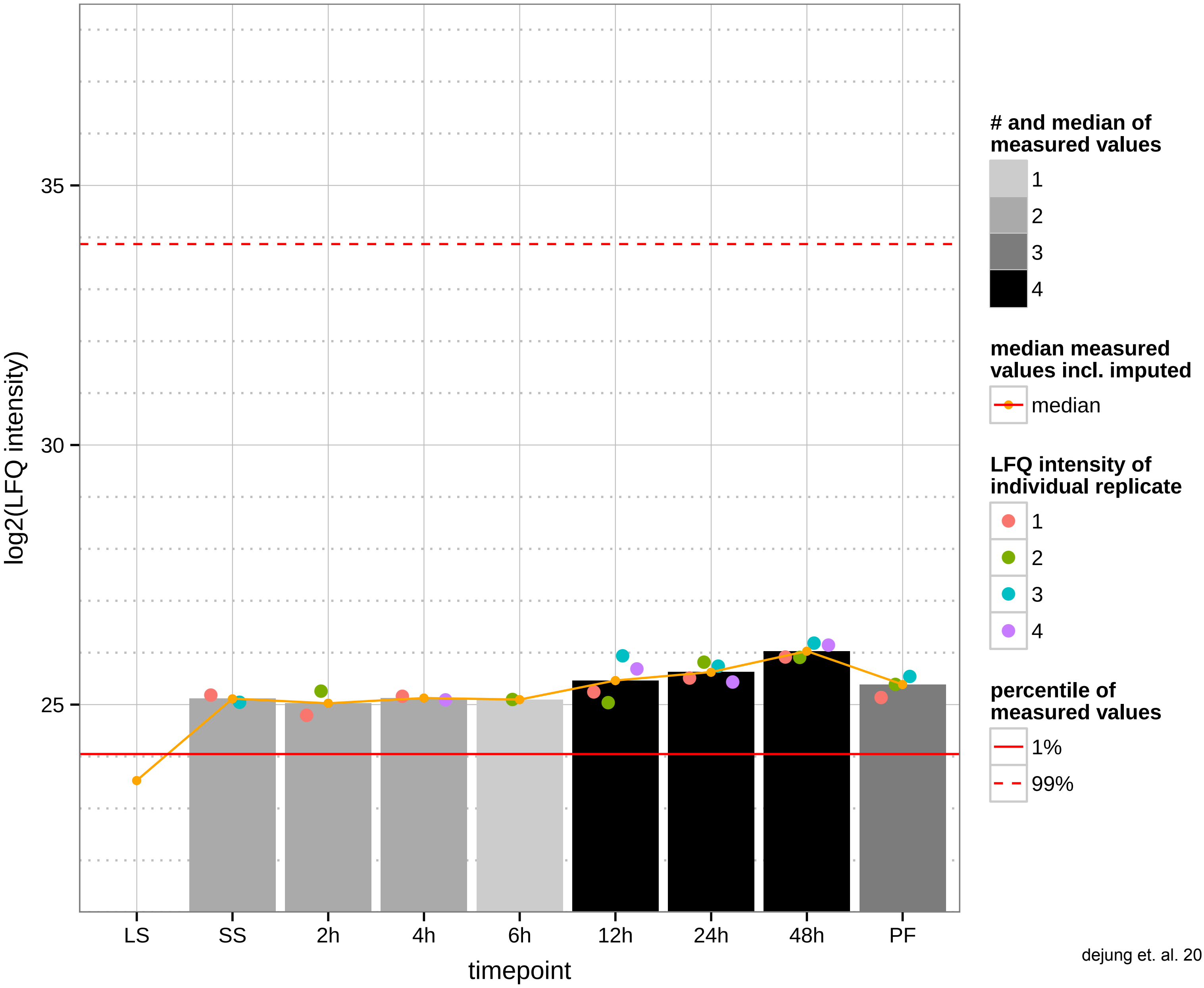
mitochondrial carrier protein (MCP17)
Tb927.3.2980
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrial membrane, mitochondrial part
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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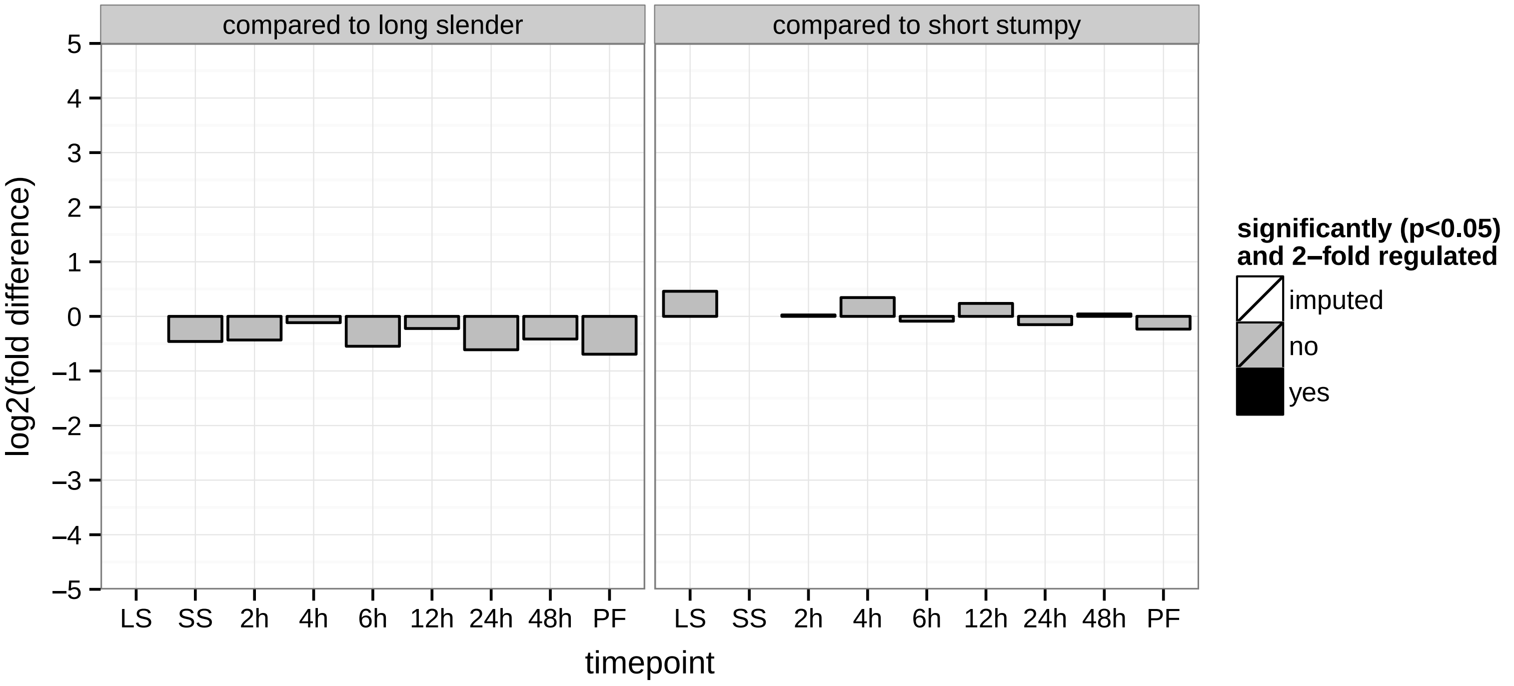
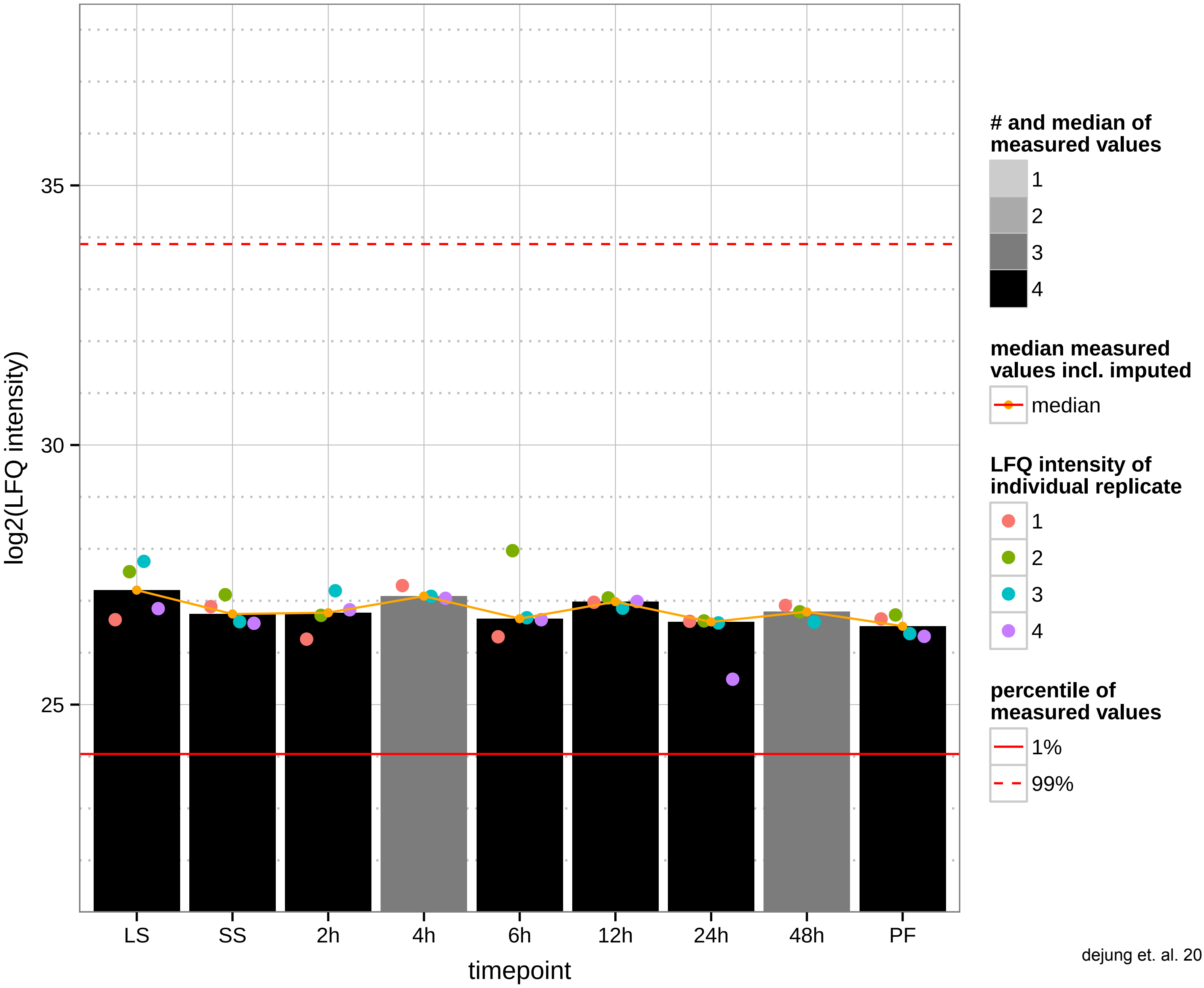
hypothetical protein, conserved
Tb927.3.3040
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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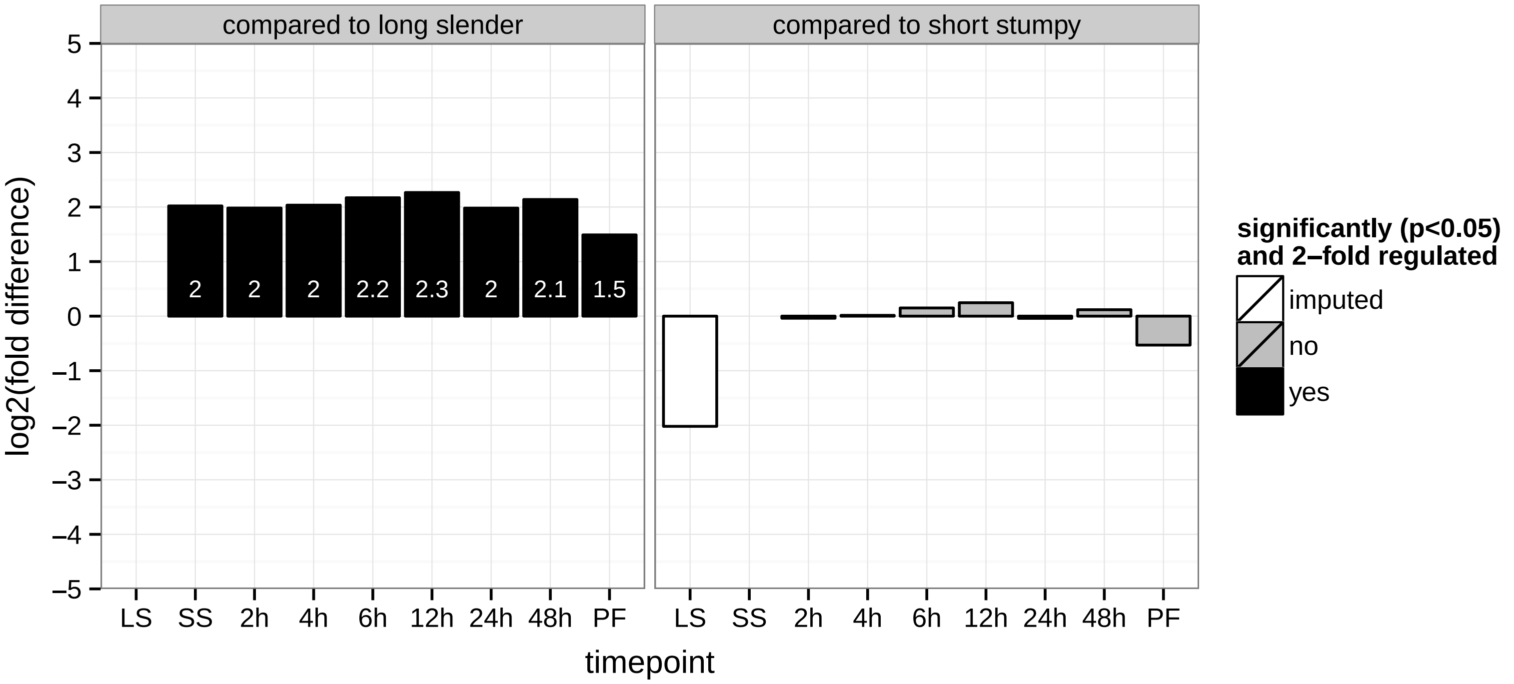
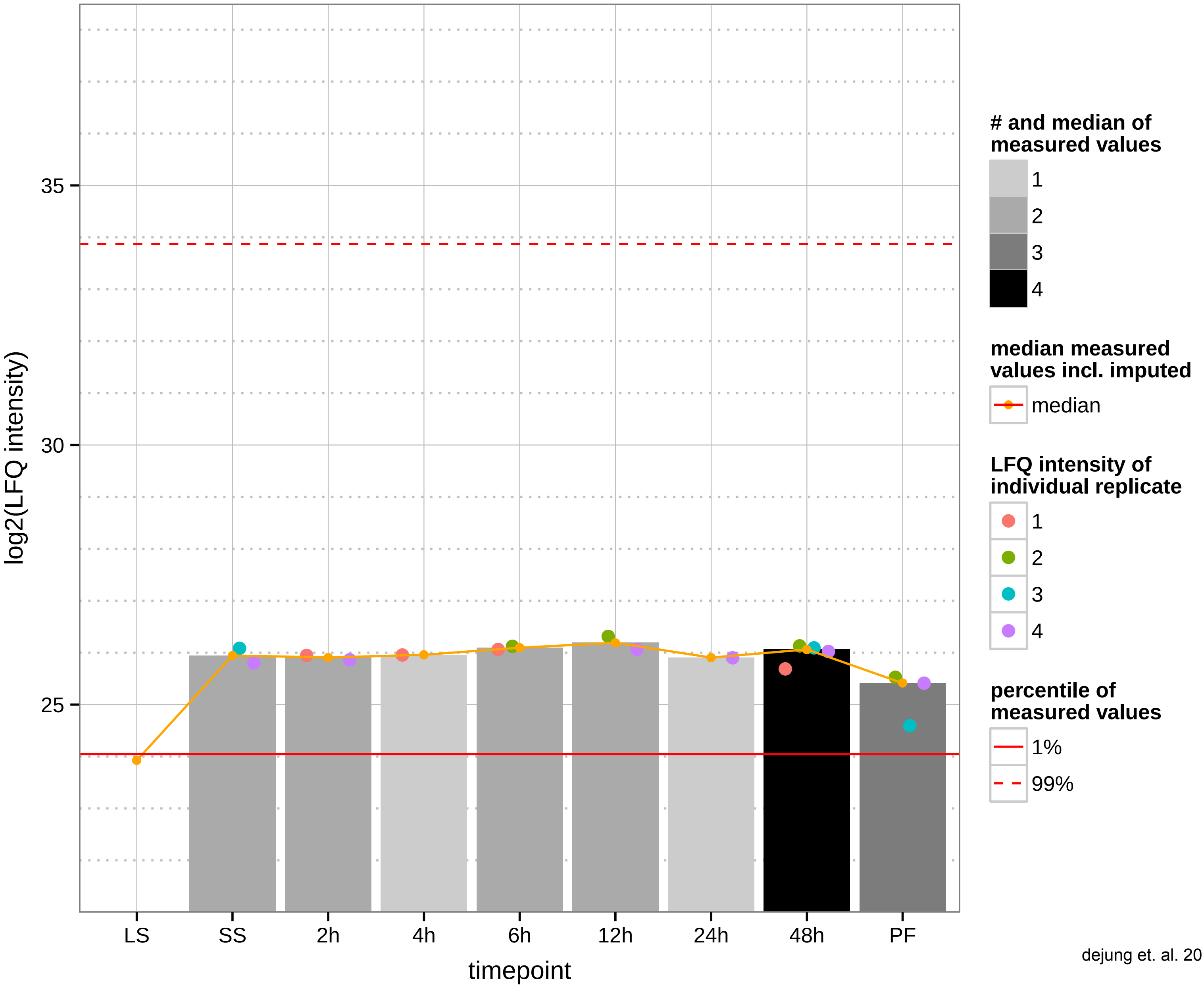
hypothetical protein, conserved
Tb927.3.3120
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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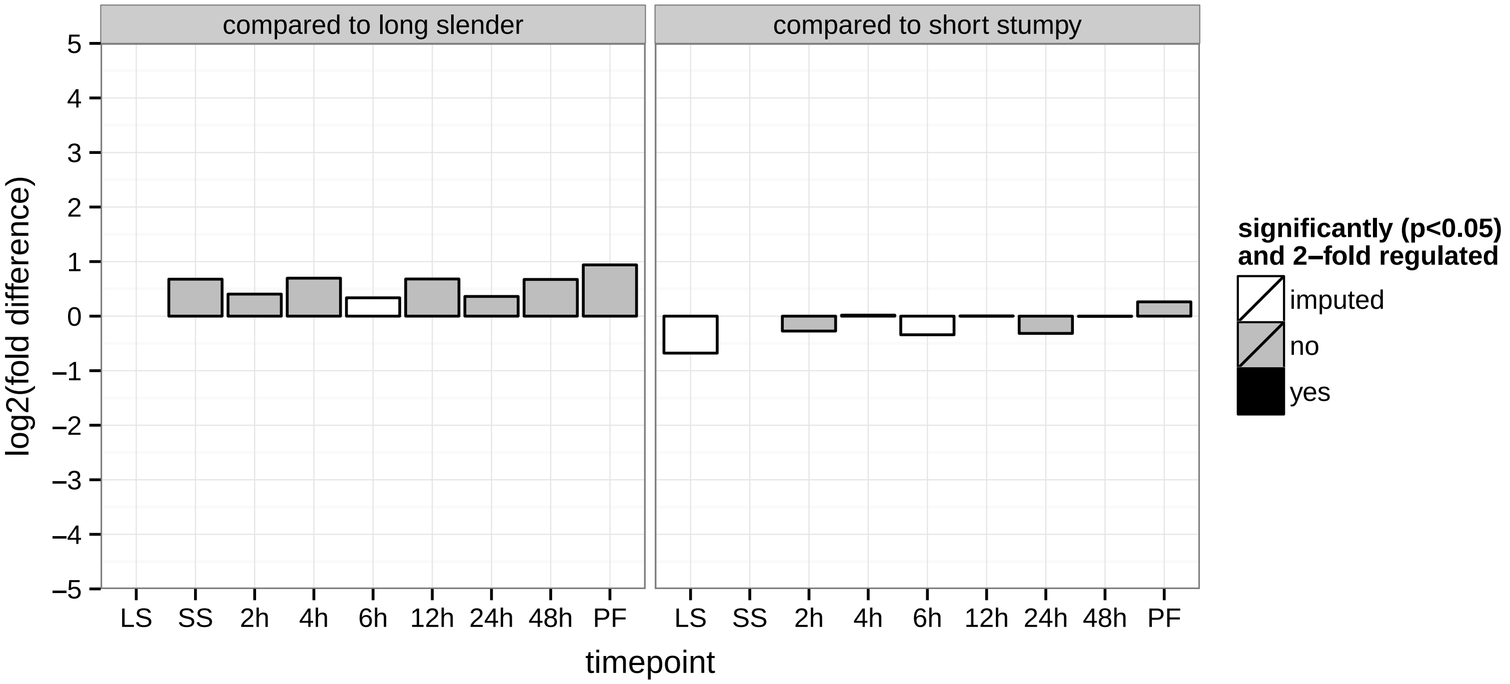
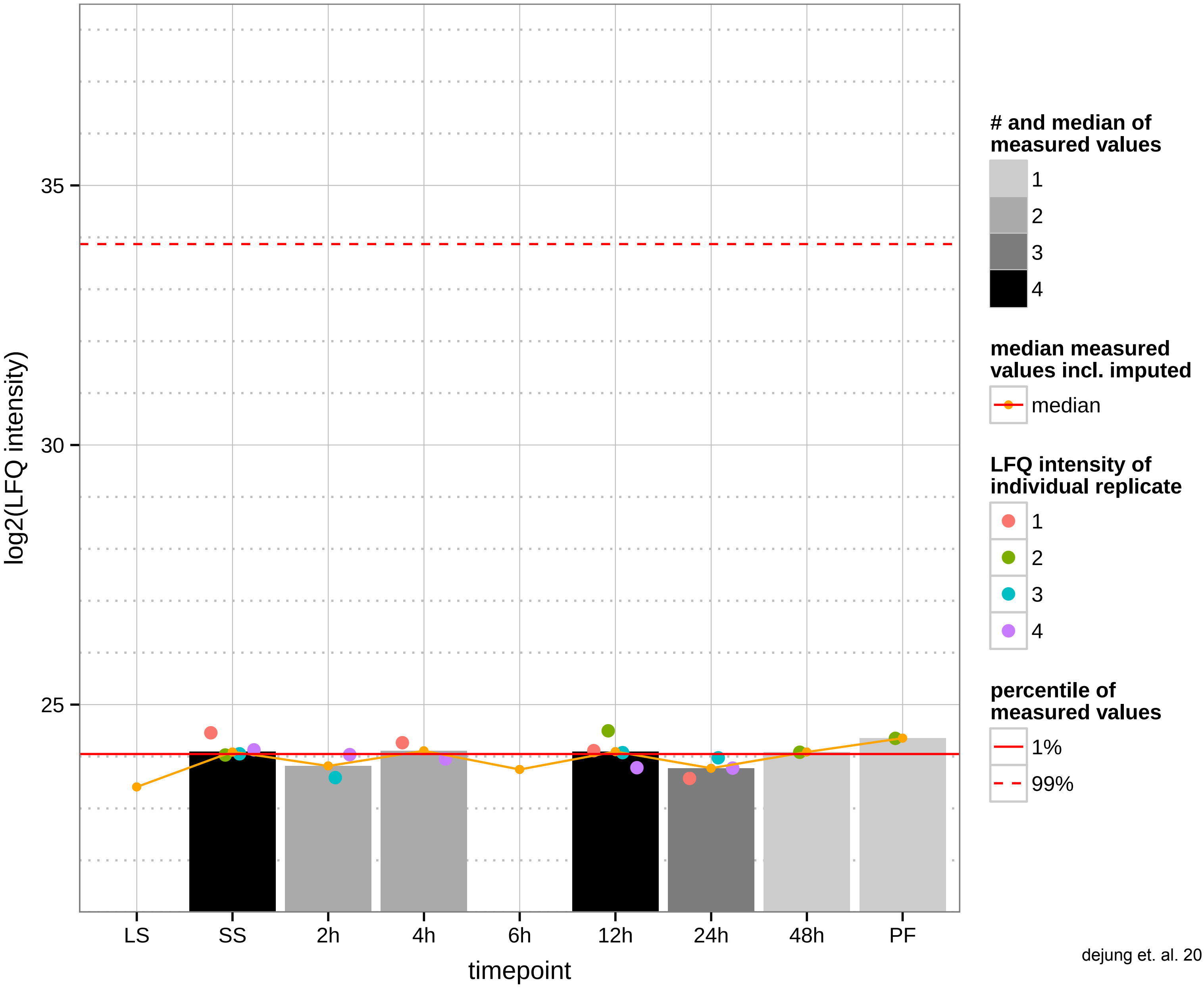
poly(A) polymerase, polynucleotide adenylyltransferase (PAP)
Tb927.3.3160
AGOF: RNA binding, nucleic acid binding, nucleotidyltransferase activity, polynucleotide adenylyltransferase activity
AGOC: null
AGOP: RNA 3'–end processing, transcription, DNA–dependent
PGOF: RNA binding, nucleotidyltransferase activity, polynucleotide adenylyltransferase activity
PGOC: nucleus
PGOP: RNA 3'–end processing, RNA polyadenylation, transcription, DNA–dependent





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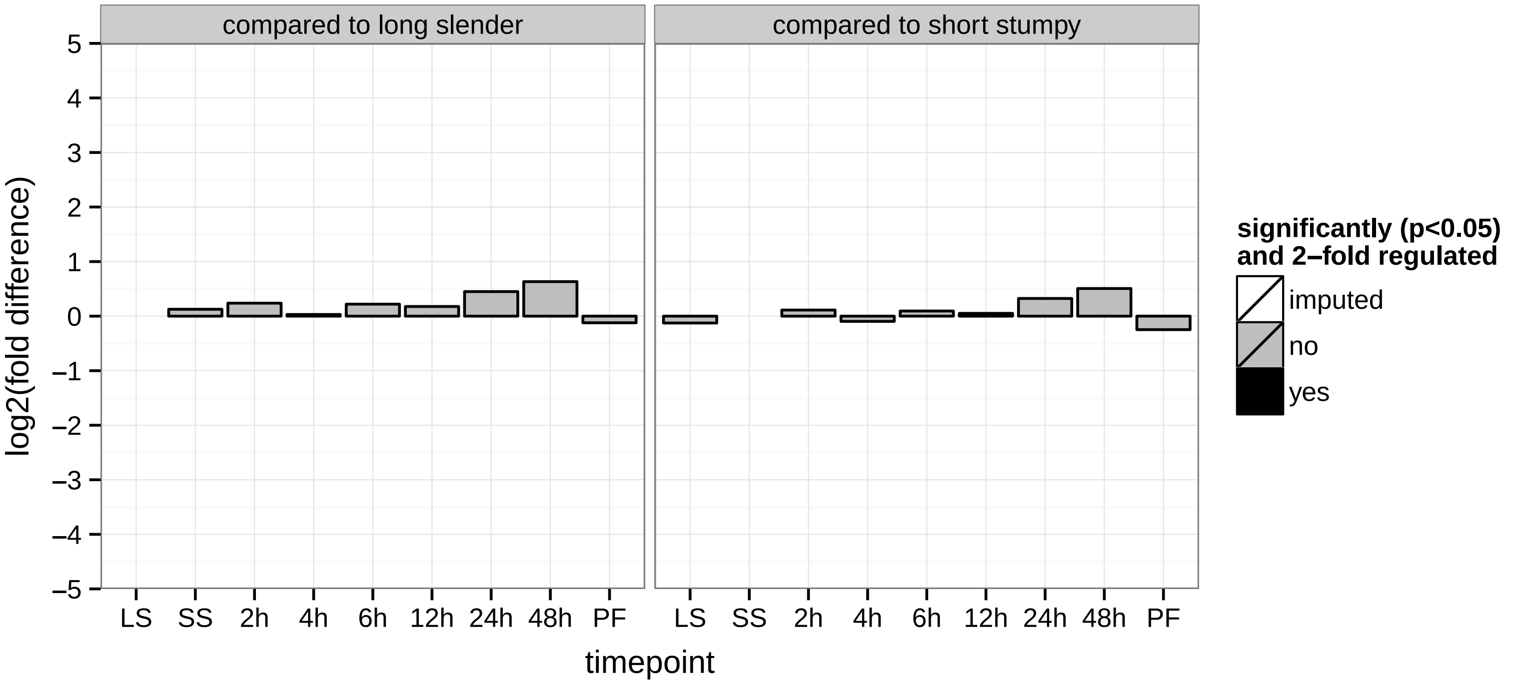
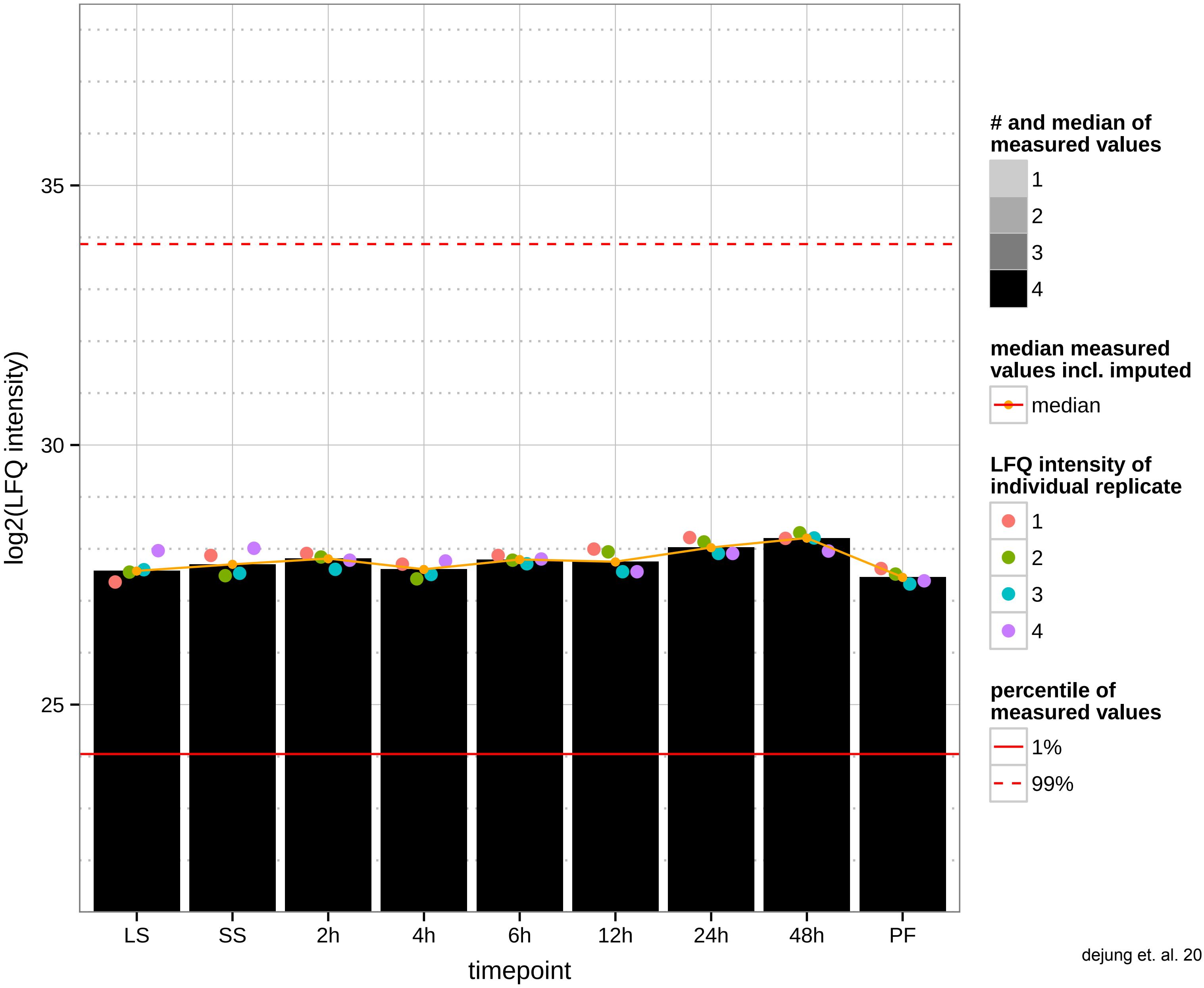
hypothetical protein, conserved, Nucleoporin (TbNup98)
Tb927.3.3180;Tb11.v5.0584
AGOF: null
AGOC: null, nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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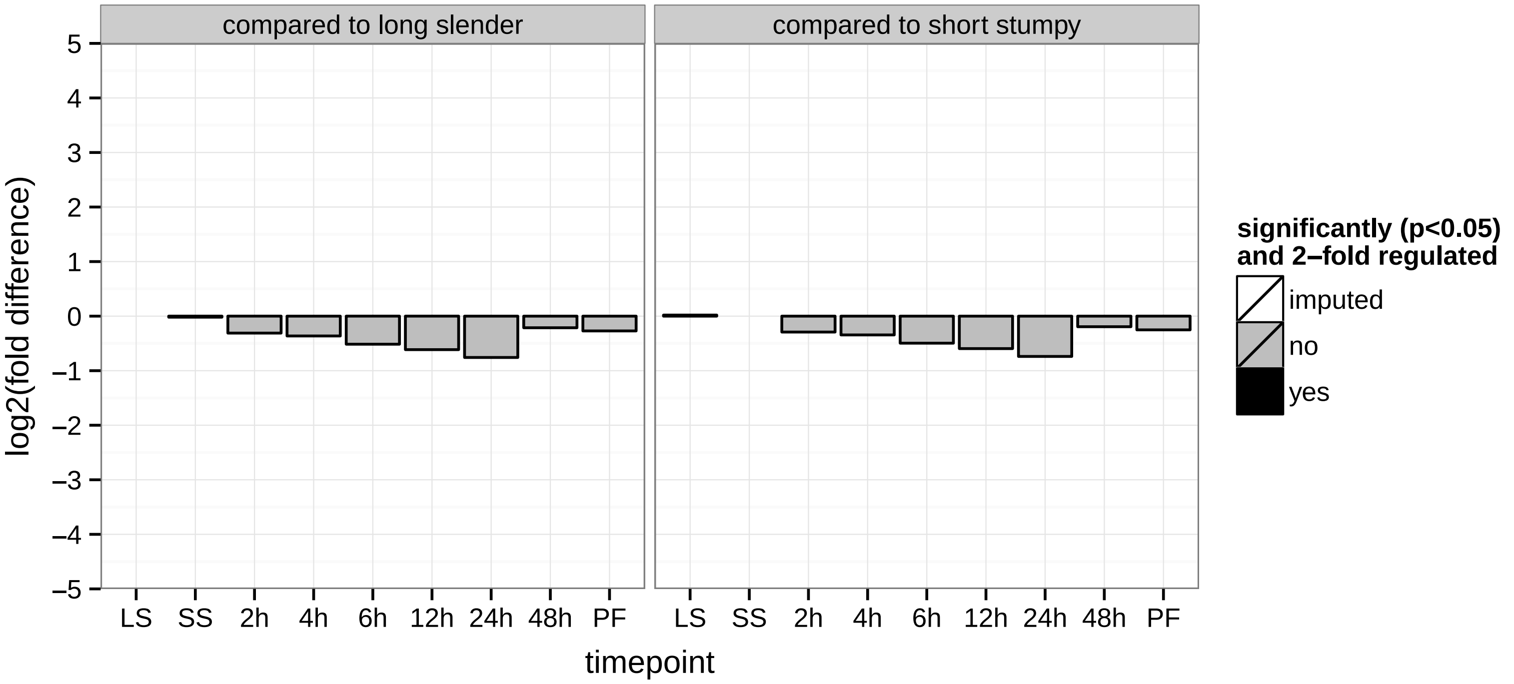
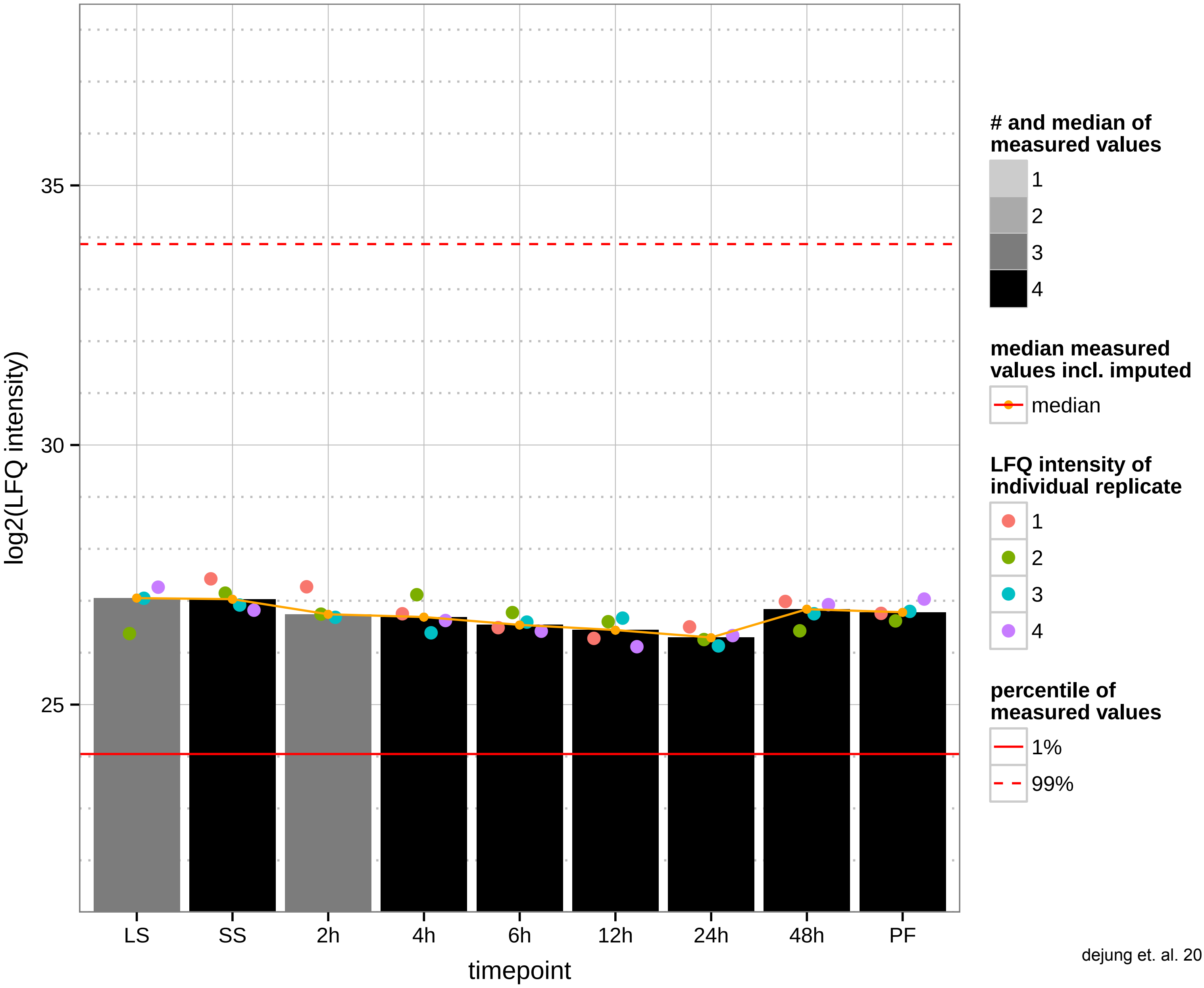
hypothetical protein, conserved
Tb927.3.3200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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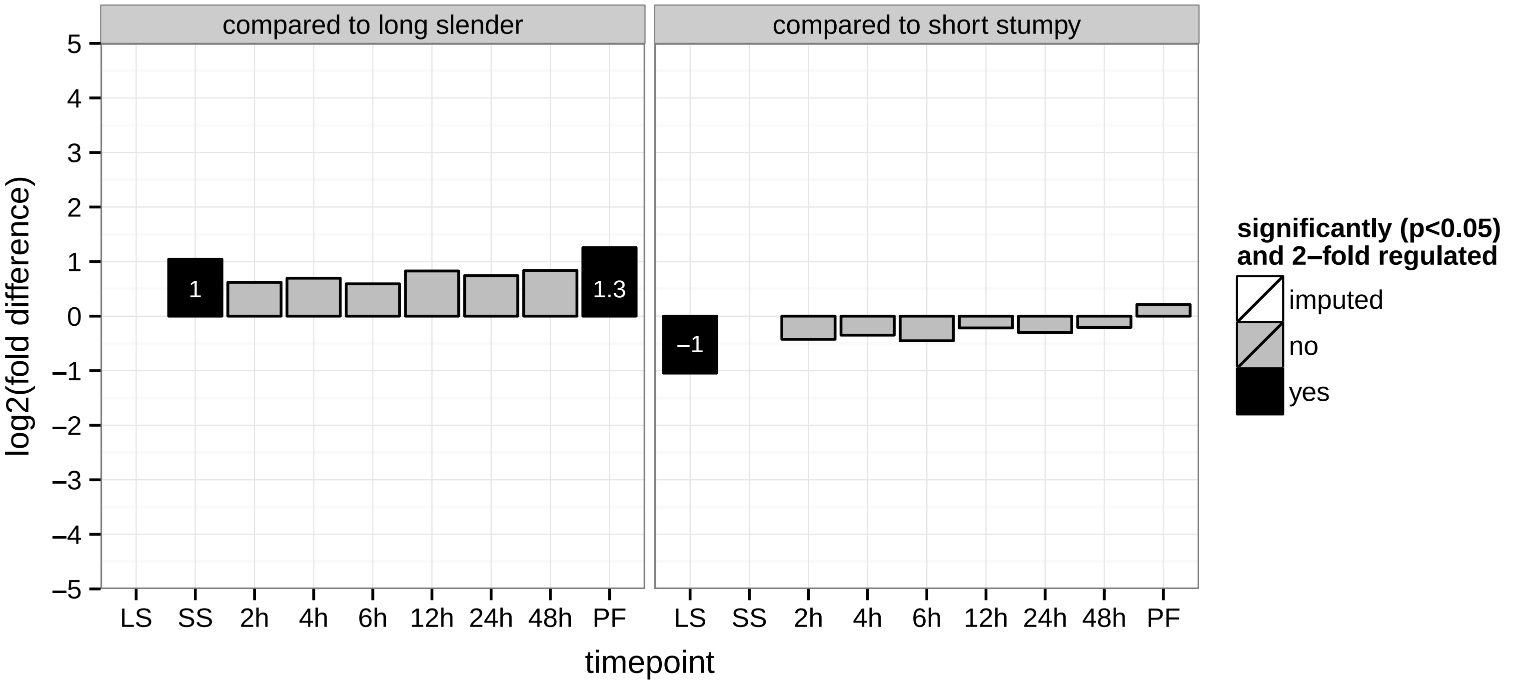
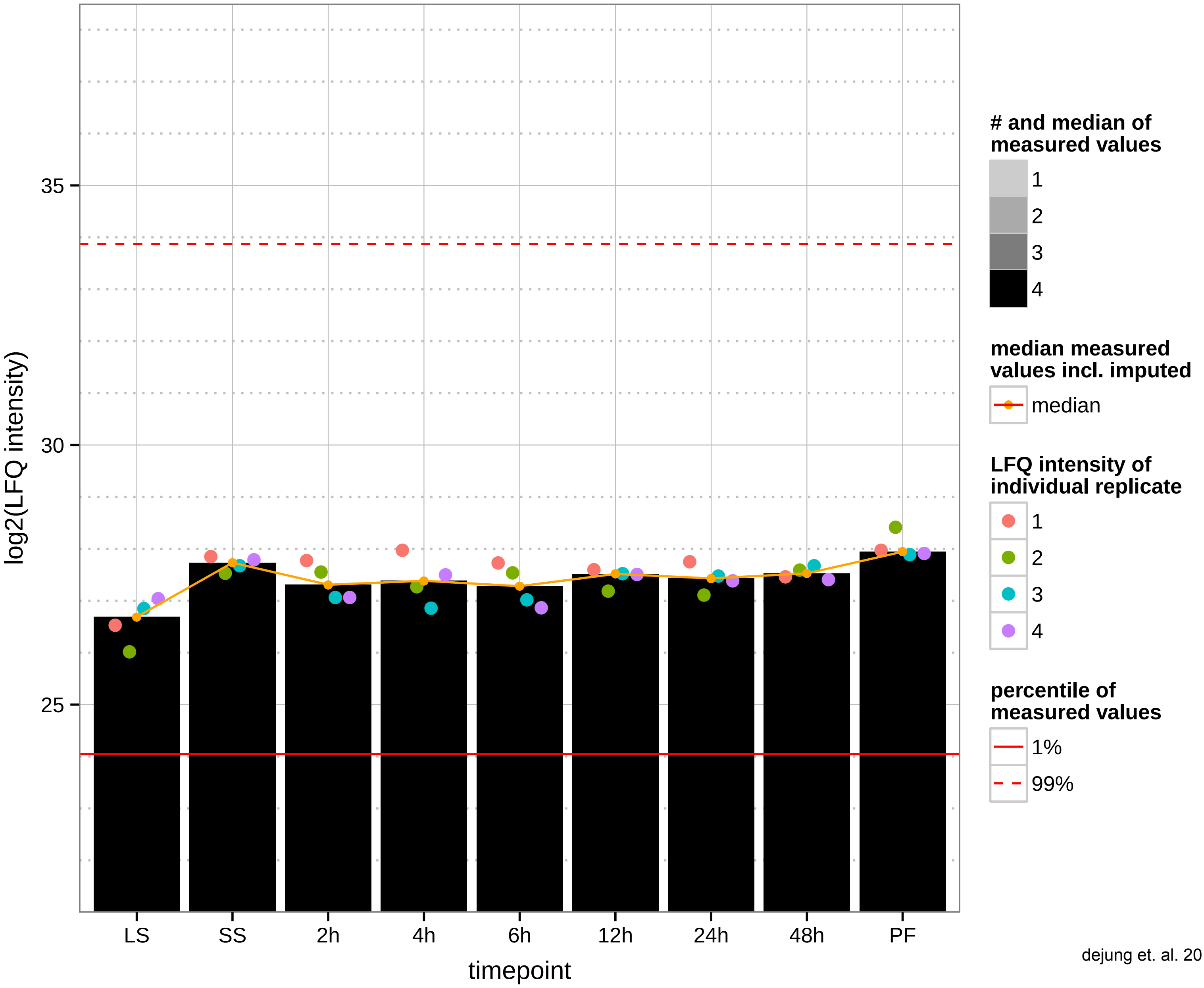
RNA polymerase–associated protein CTR9, putative
Tb927.3.3220
AGOF: null
AGOC: cytoplasm, nucleus
AGOP: transcription elongation from RNA polymerase II promoter
PGOF: protein binding
PGOC: null
PGOP: null





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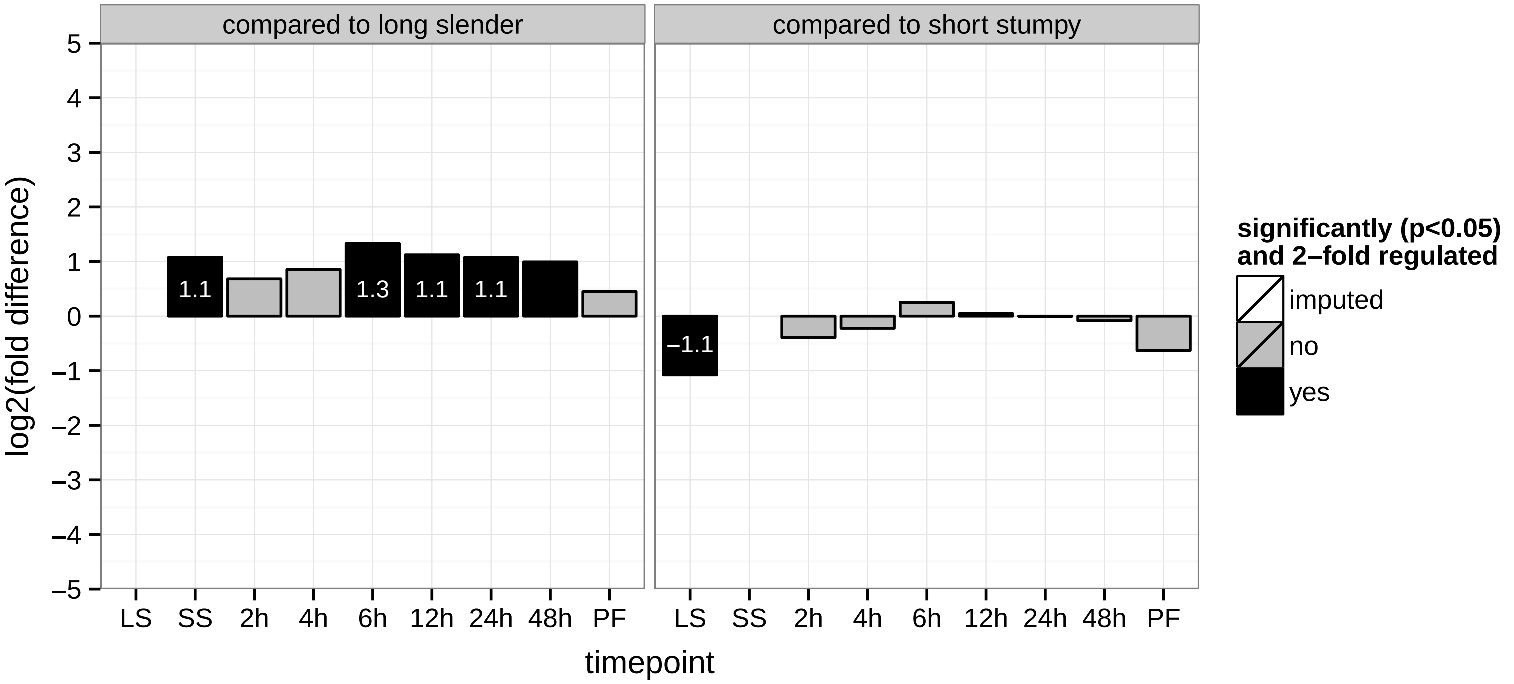
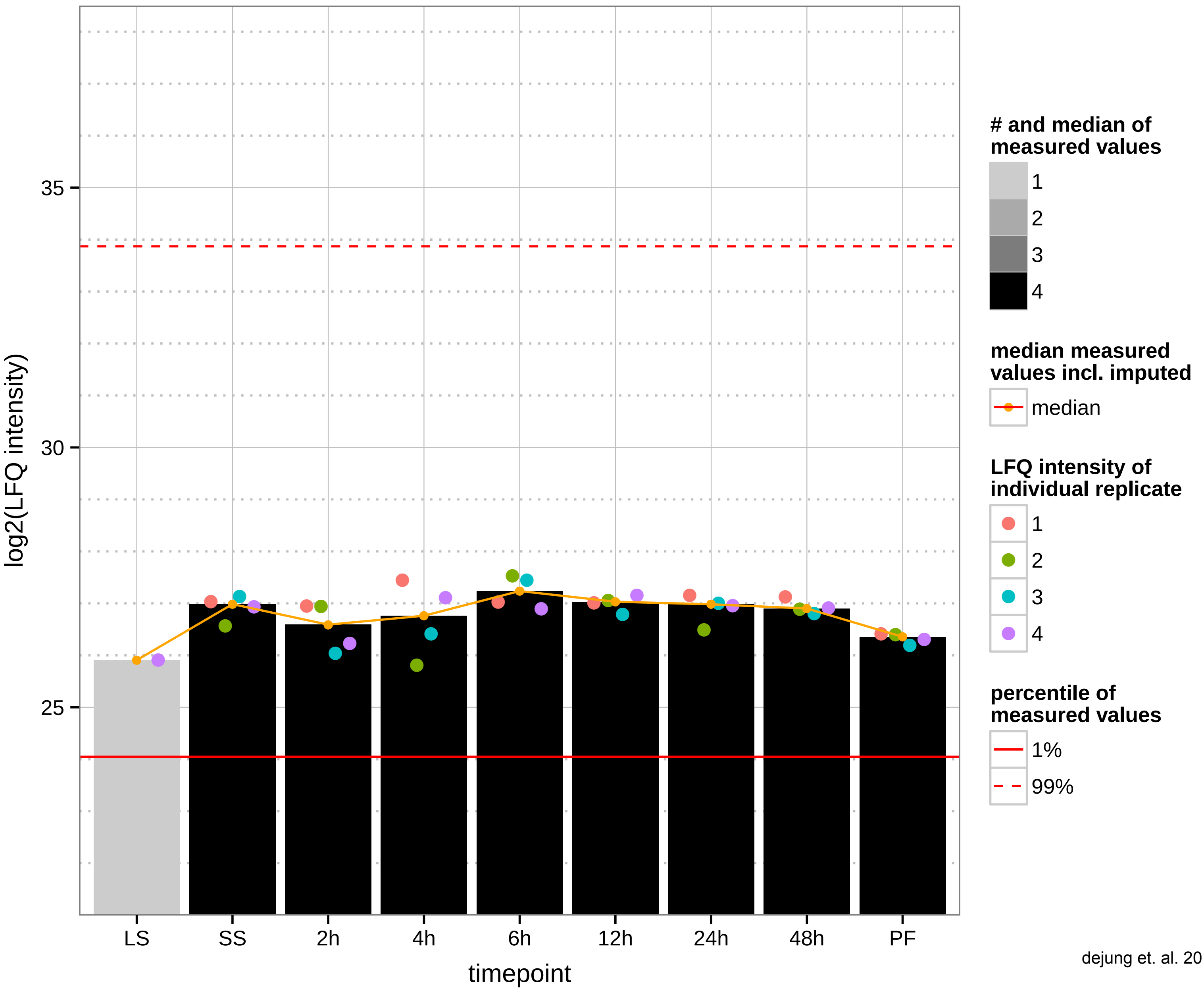
hypothetical protein, conserved
Tb927.3.3230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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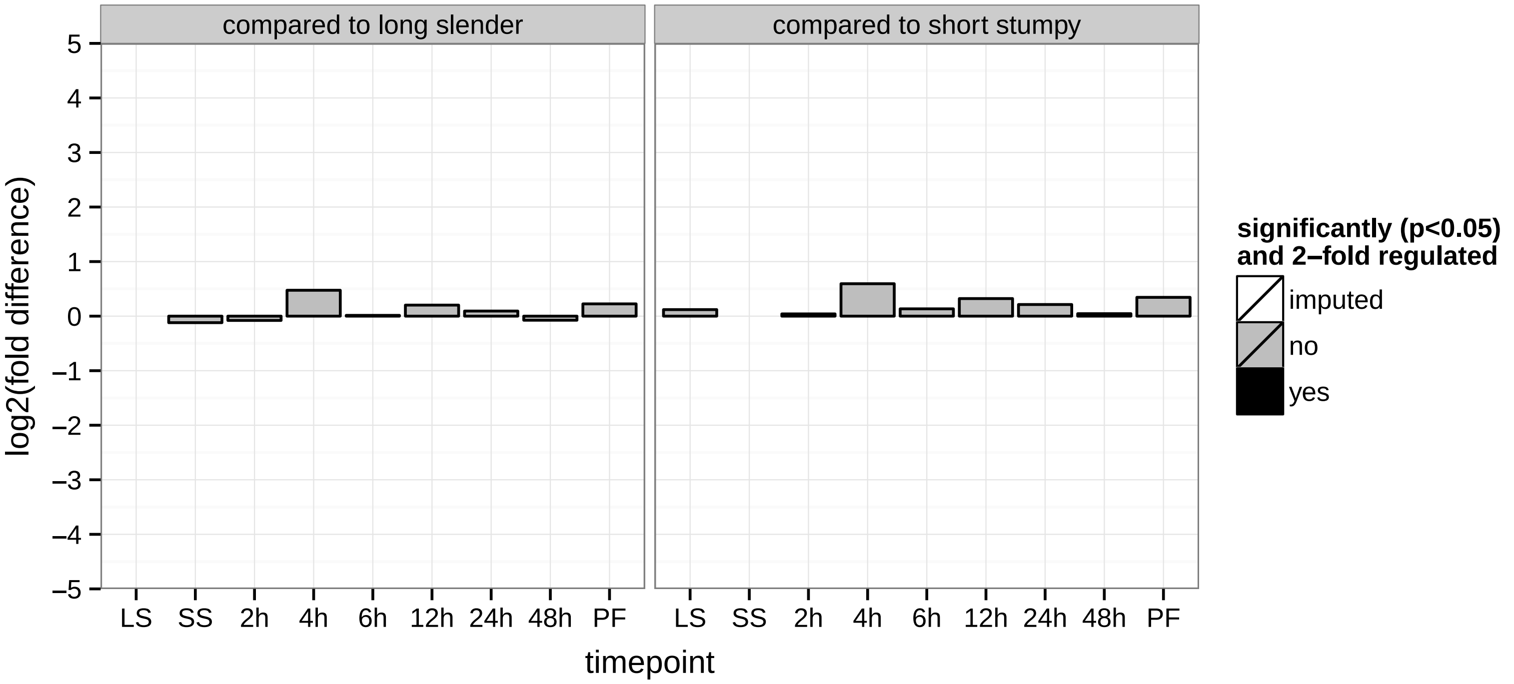
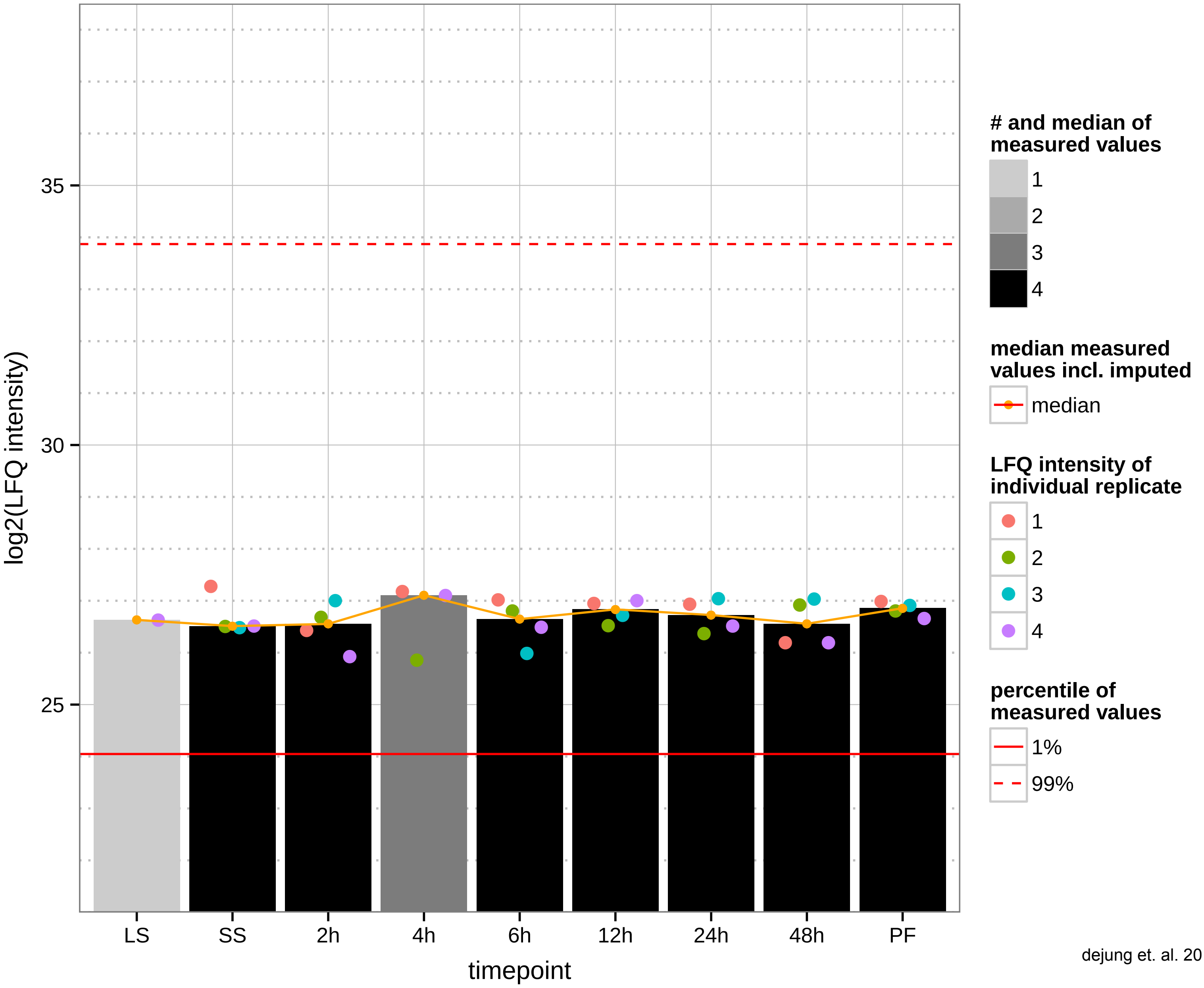
vacuolar protein sorting–associated protein 4, putative (VPS4)
Tb927.3.3280
AGOF: ATP binding
AGOC: null
AGOP: null
PGOF: ATP binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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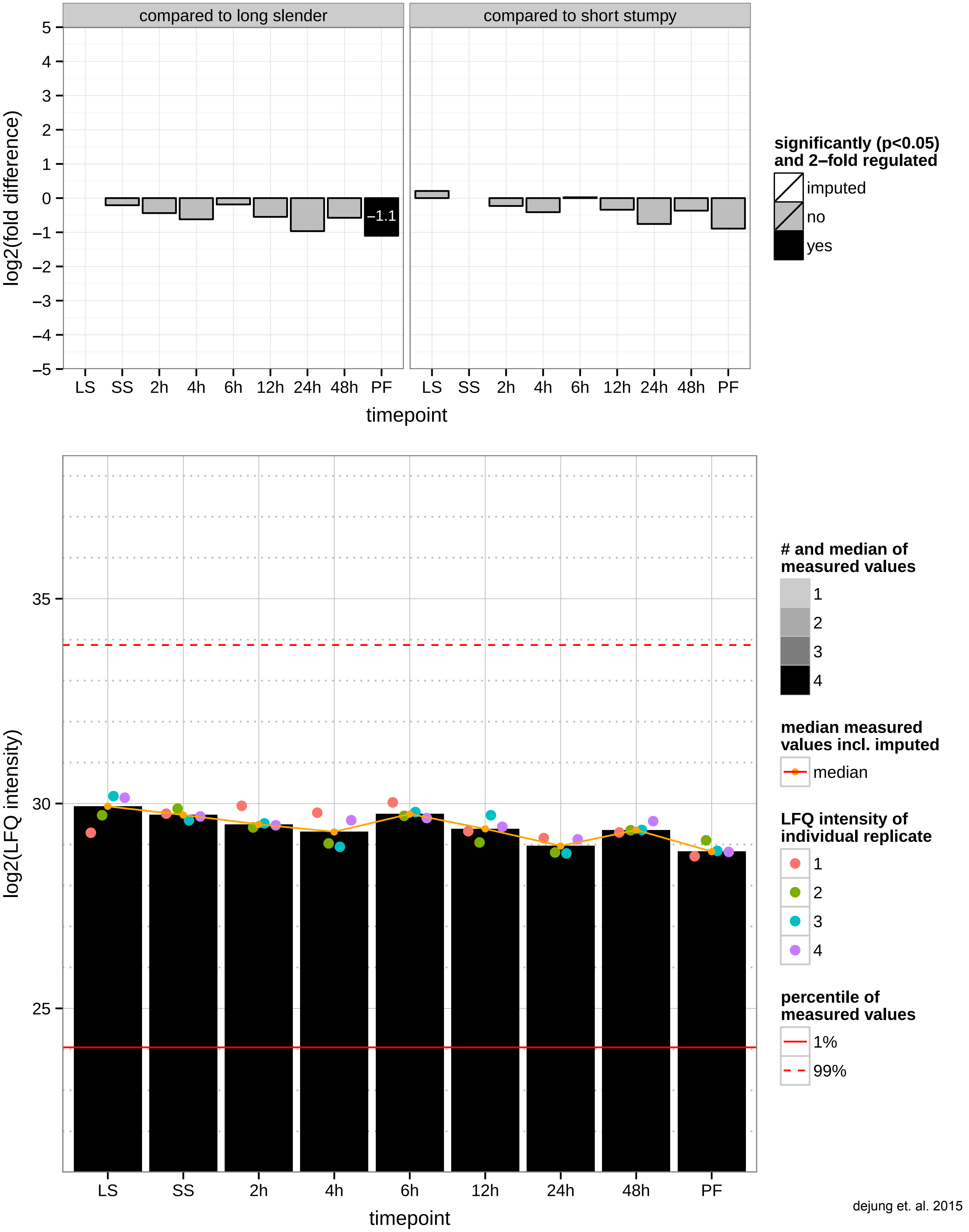
hypothetical protein, conserved
Tb927.3.3300
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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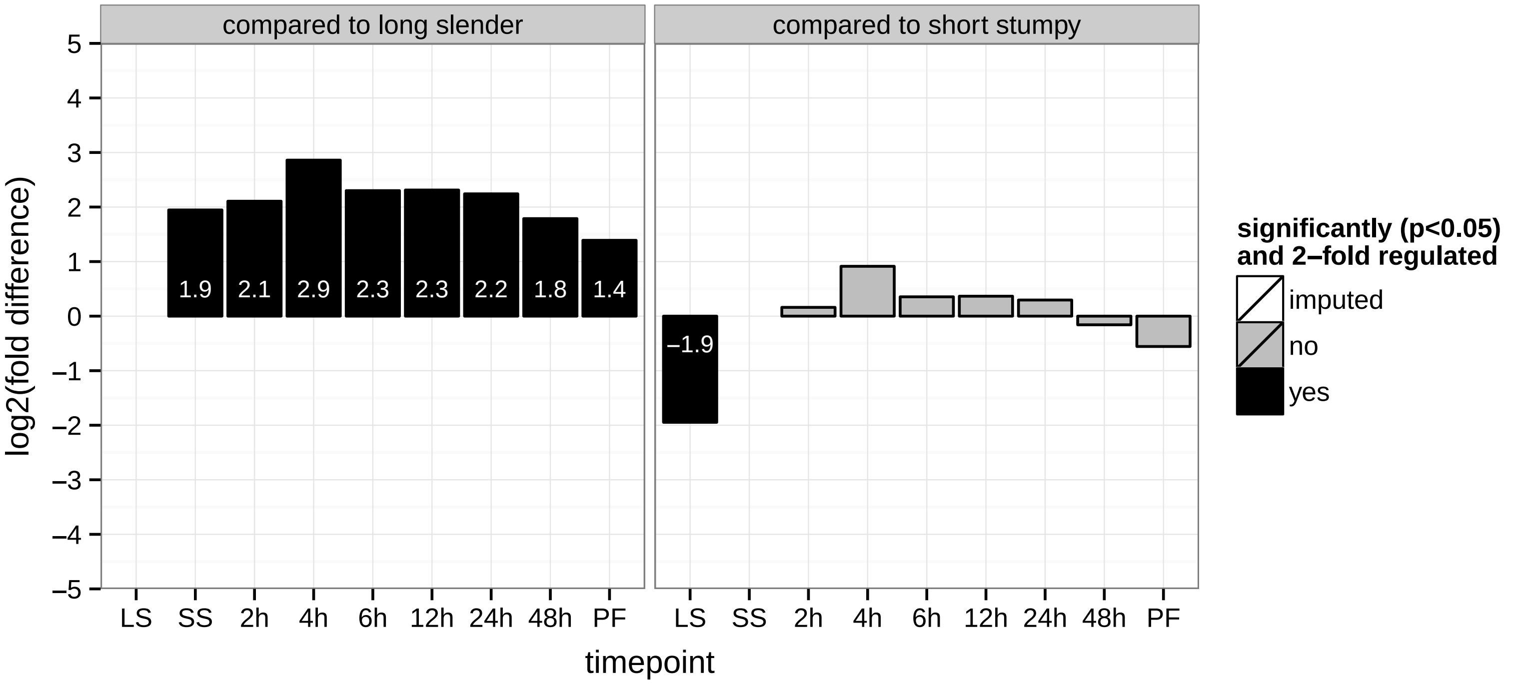
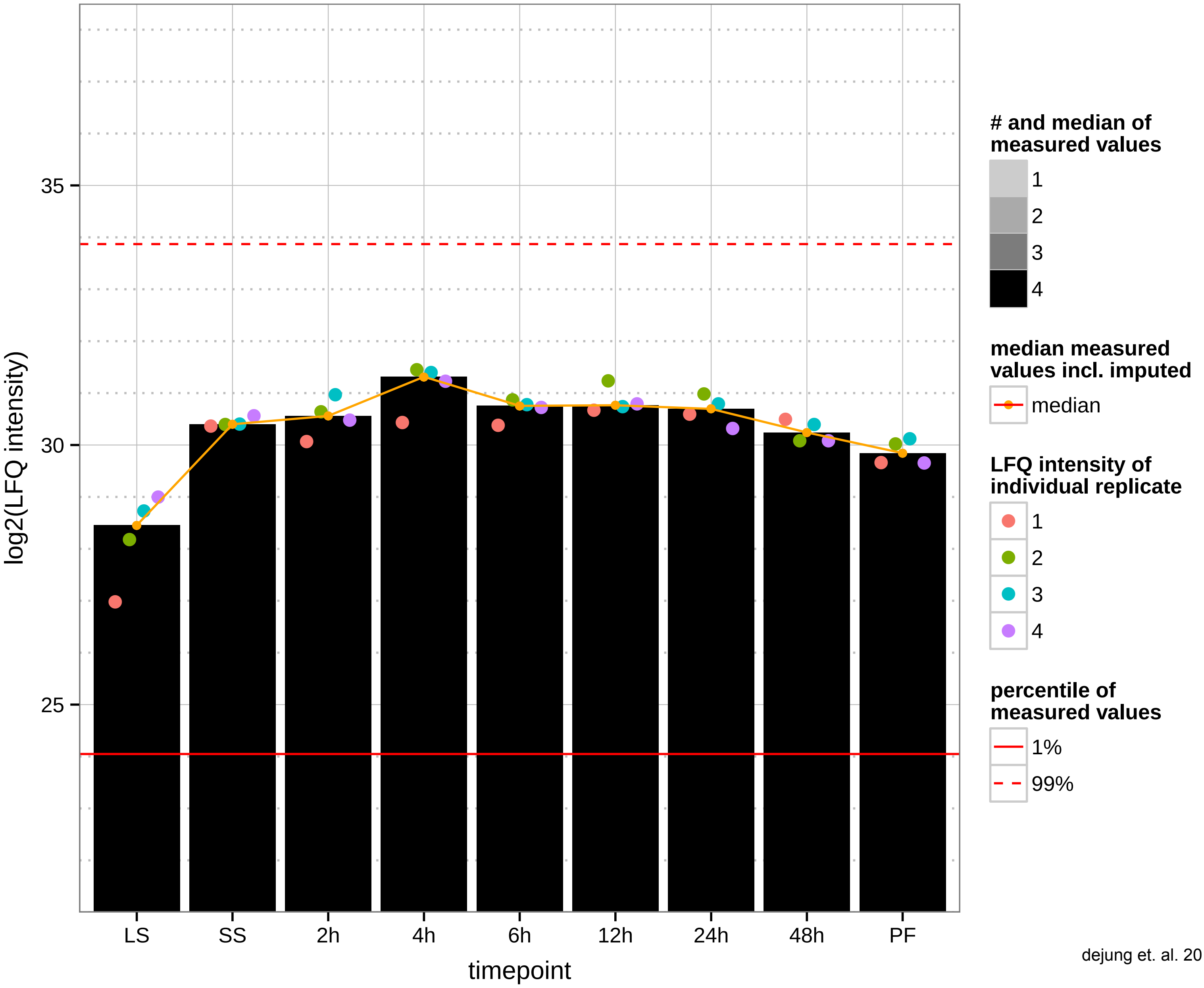
heat shock protein 20, putative
Tb927.3.3330
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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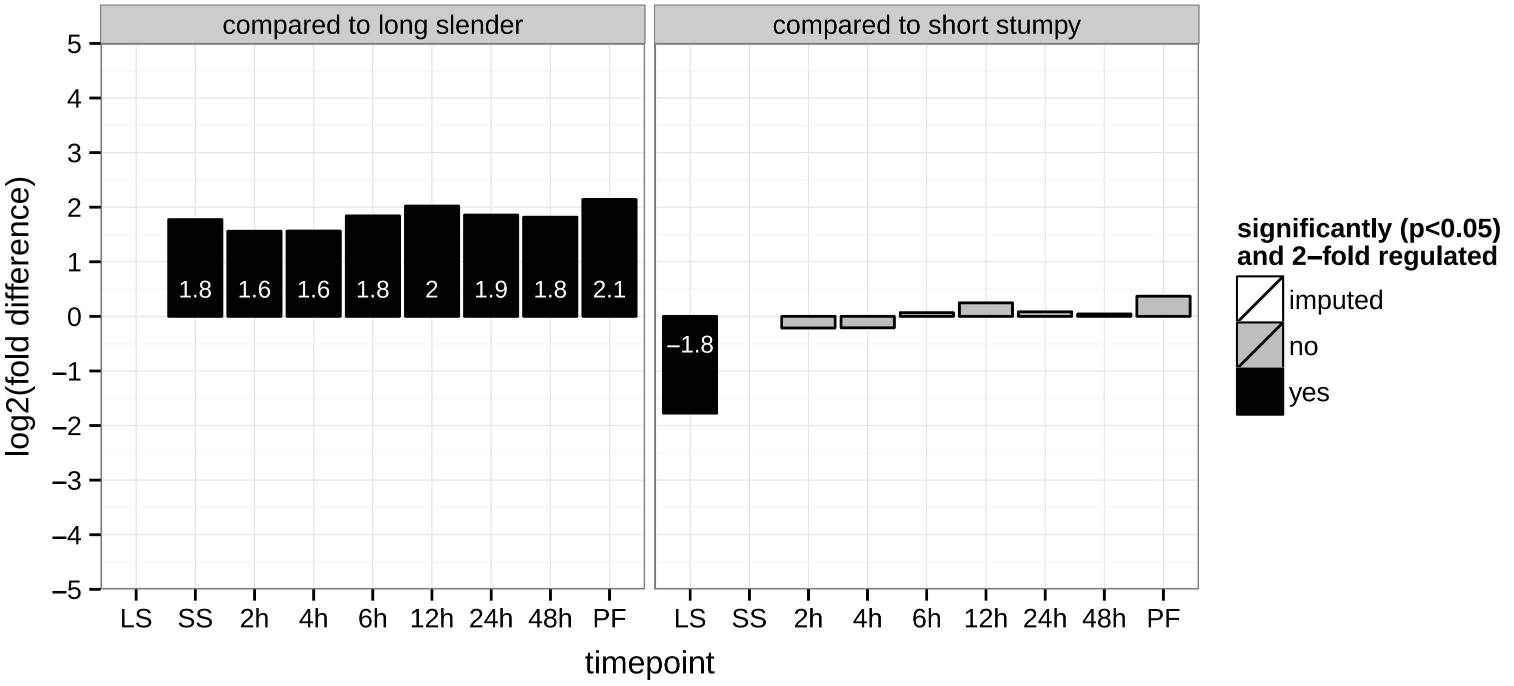
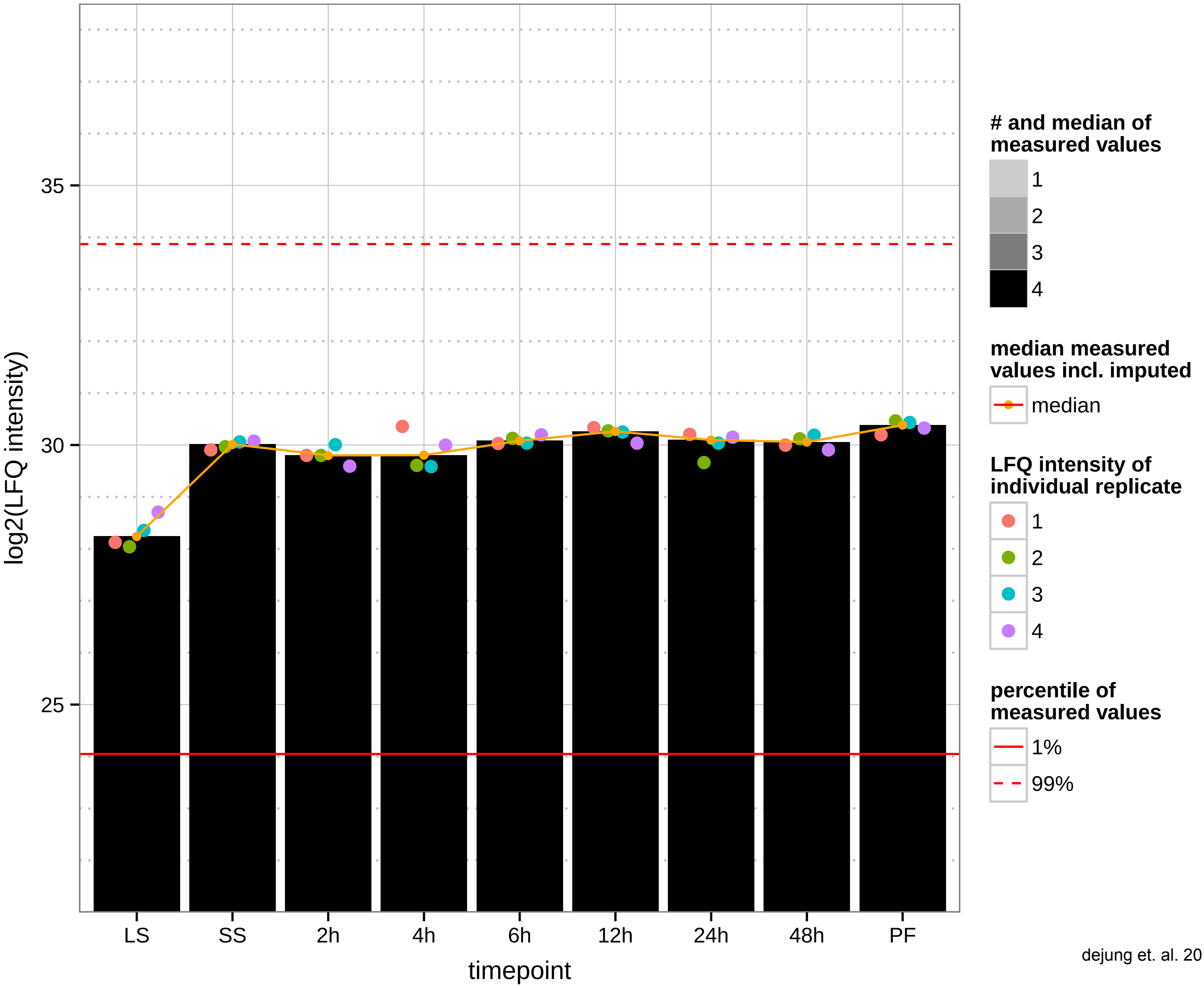
aspartyl aminopeptidase, putative, metallo−peptidase, Clan MH, Family M20
Tb927.3.3410;Tb11.v5.0768
AGOF: null, aminopeptidase activity, zinc ion binding
AGOC: null, vacuole
AGOP: null, proteolysis
PGOF: aminopeptidase activity, zinc ion binding
PGOC: null
PGOP: proteolysis





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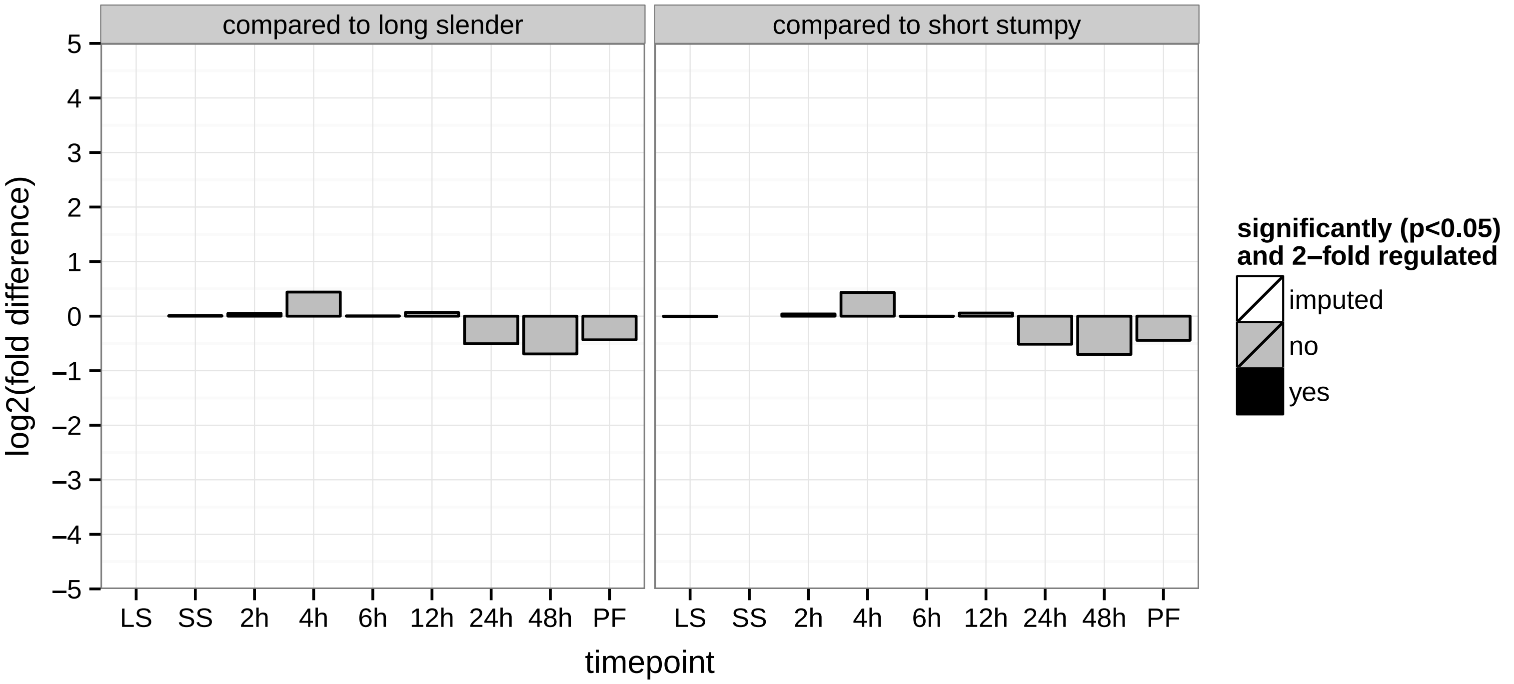
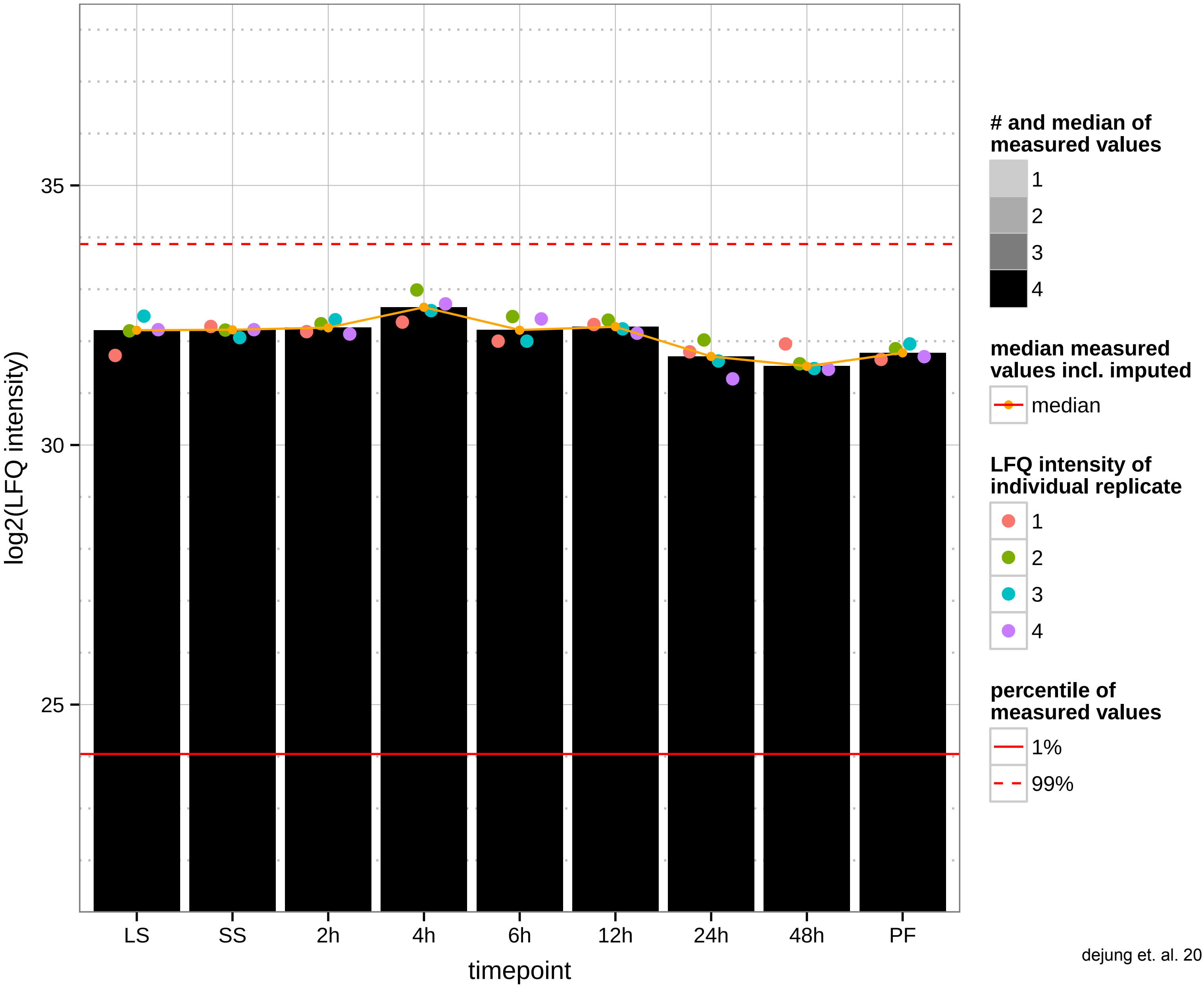
ADP–ribosylation factor–like protein 3, putative (arl3)
Tb927.3.3450
AGOF: GTP binding
AGOC: cilium membrane, flagellar pocket membrane, intracellular, plasma membrane
AGOP: cell proliferation, cilium morphogenesis, dissemination or transmission of symbiont from host by vector, intracellular pr
PGOF: GTP binding
PGOC: intracellular
PGOP: intracellular protein transport, protein transport, small GTPase mediated signal transduction





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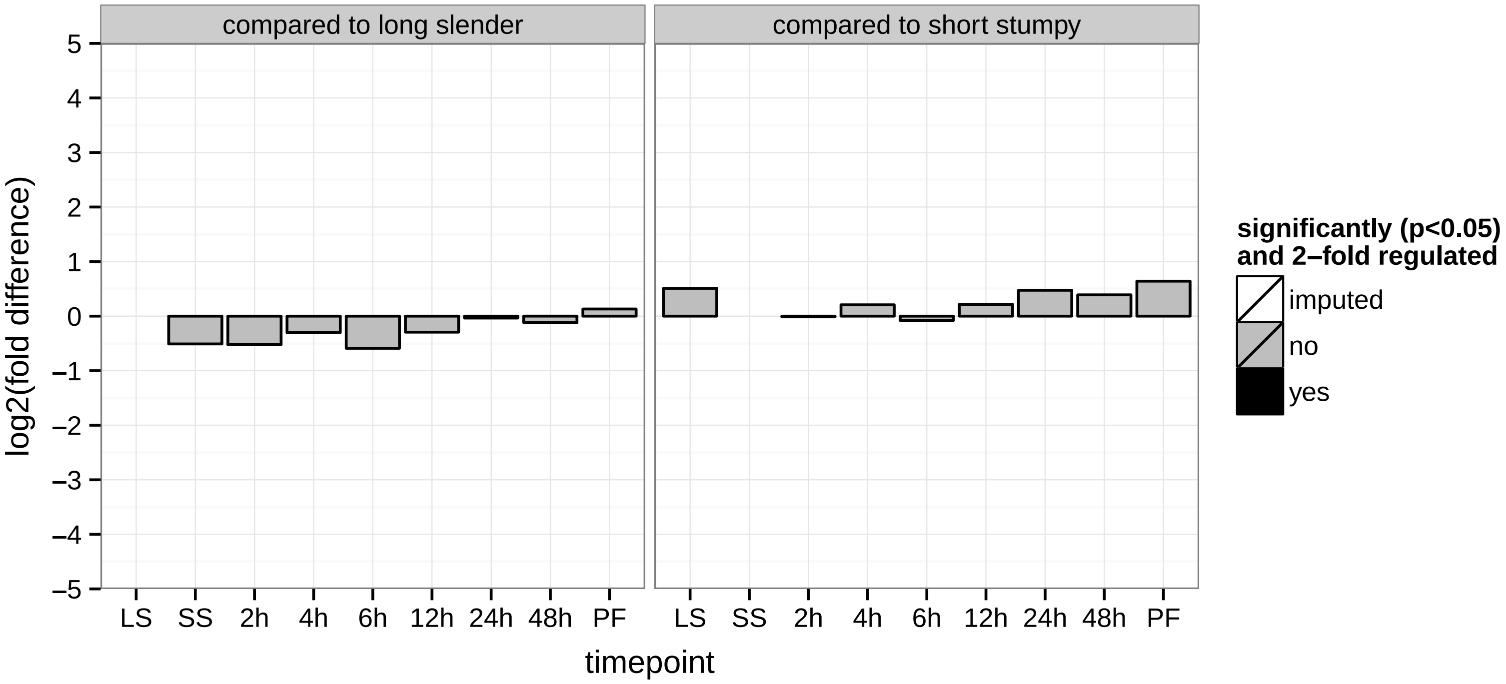
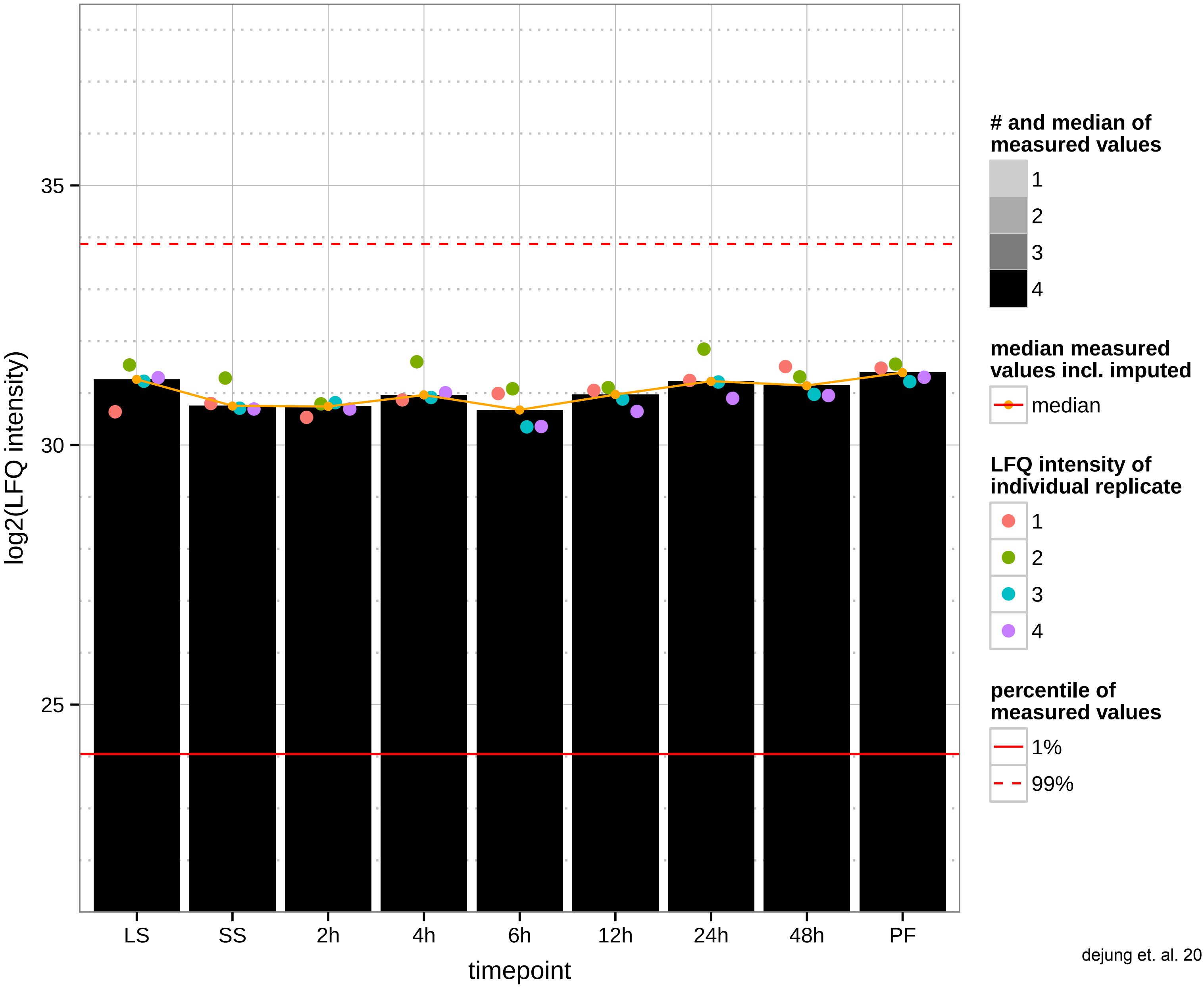
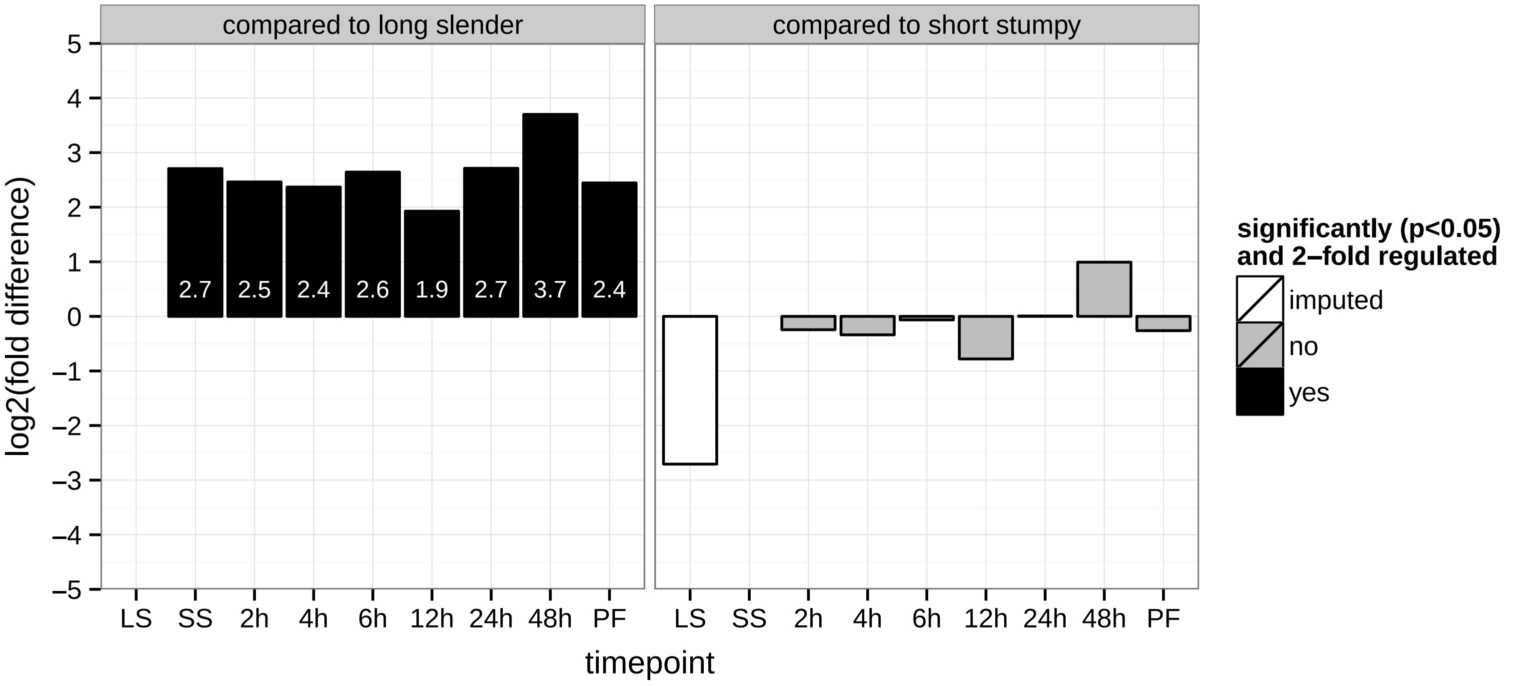
high mobility group protein, putative (TDP1)
Tb927.3.3490
AGOF: DNA binding
AGOC: nucleus
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

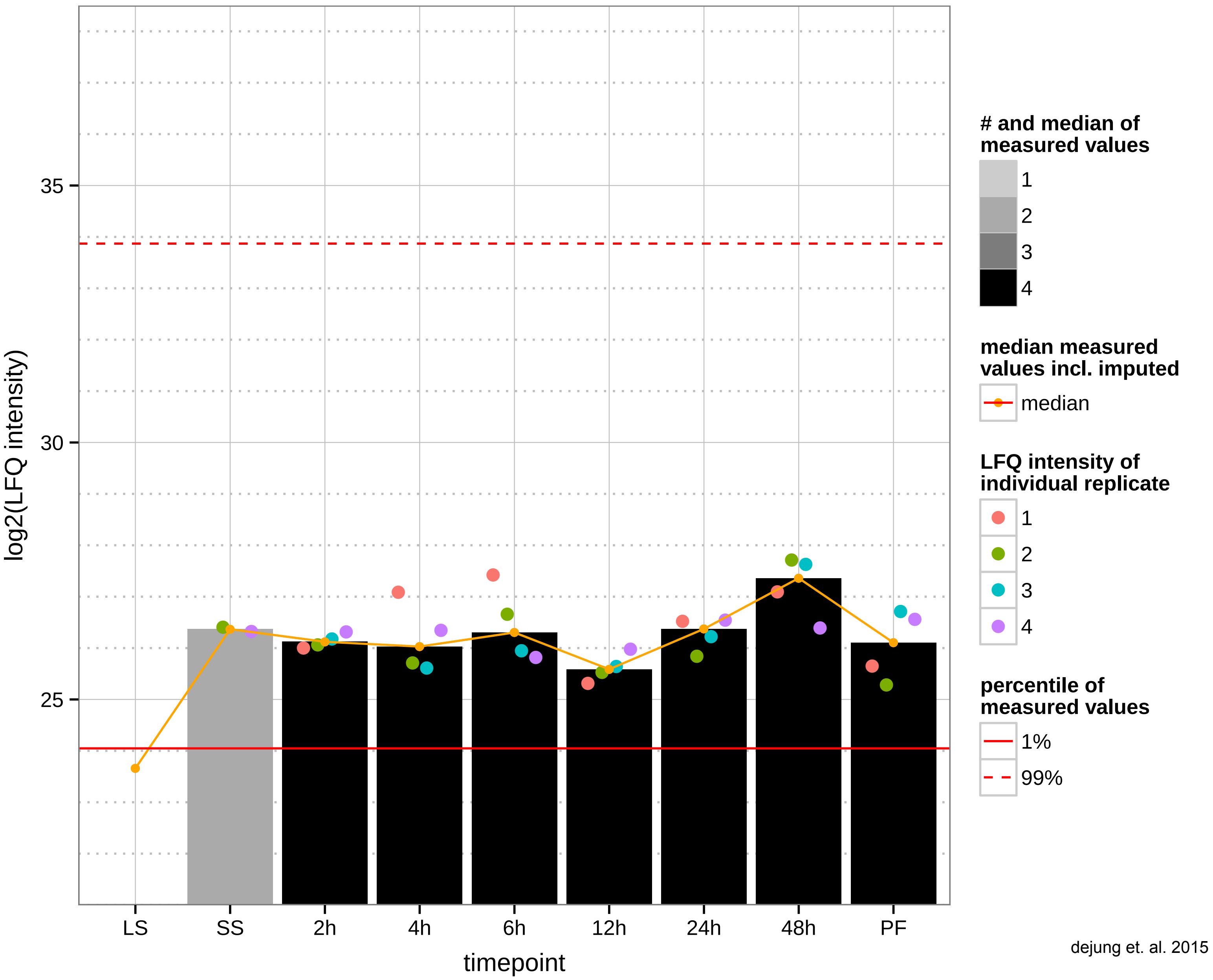




dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.3520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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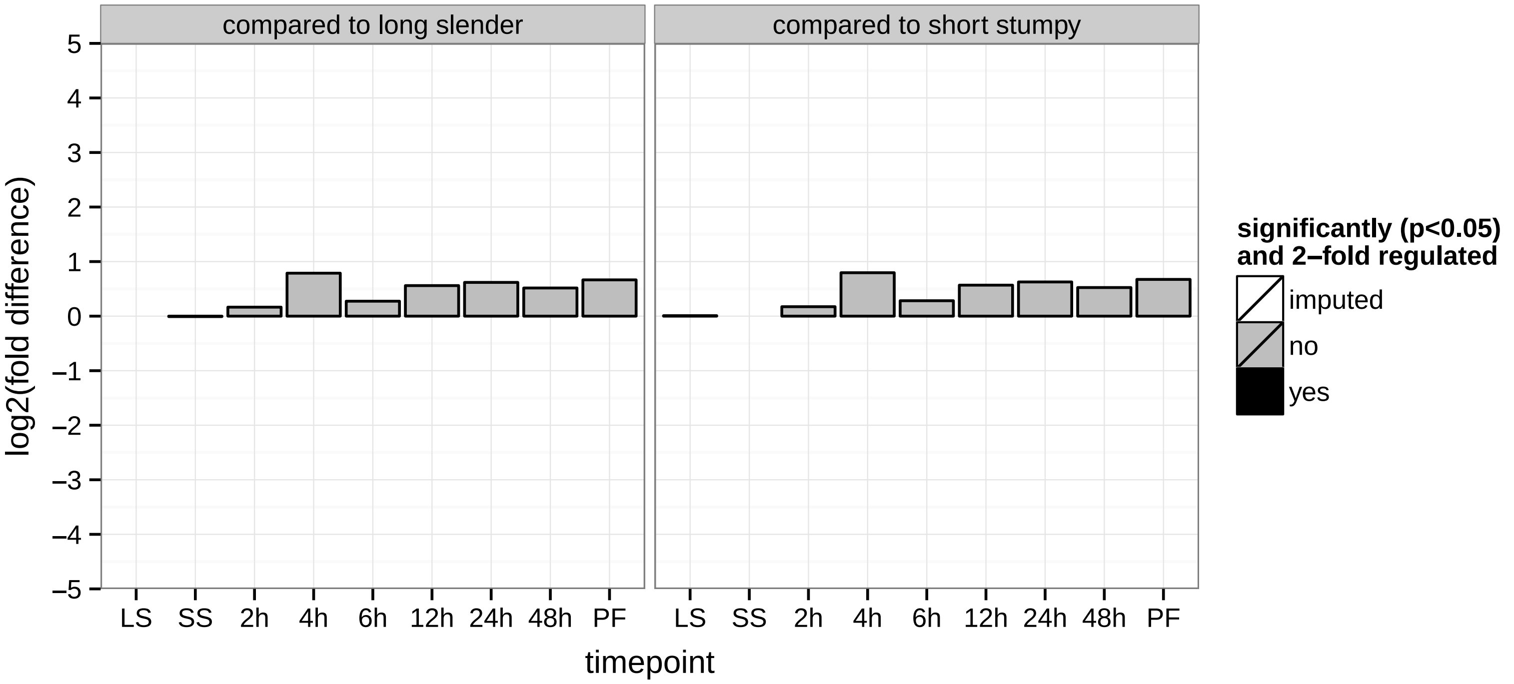
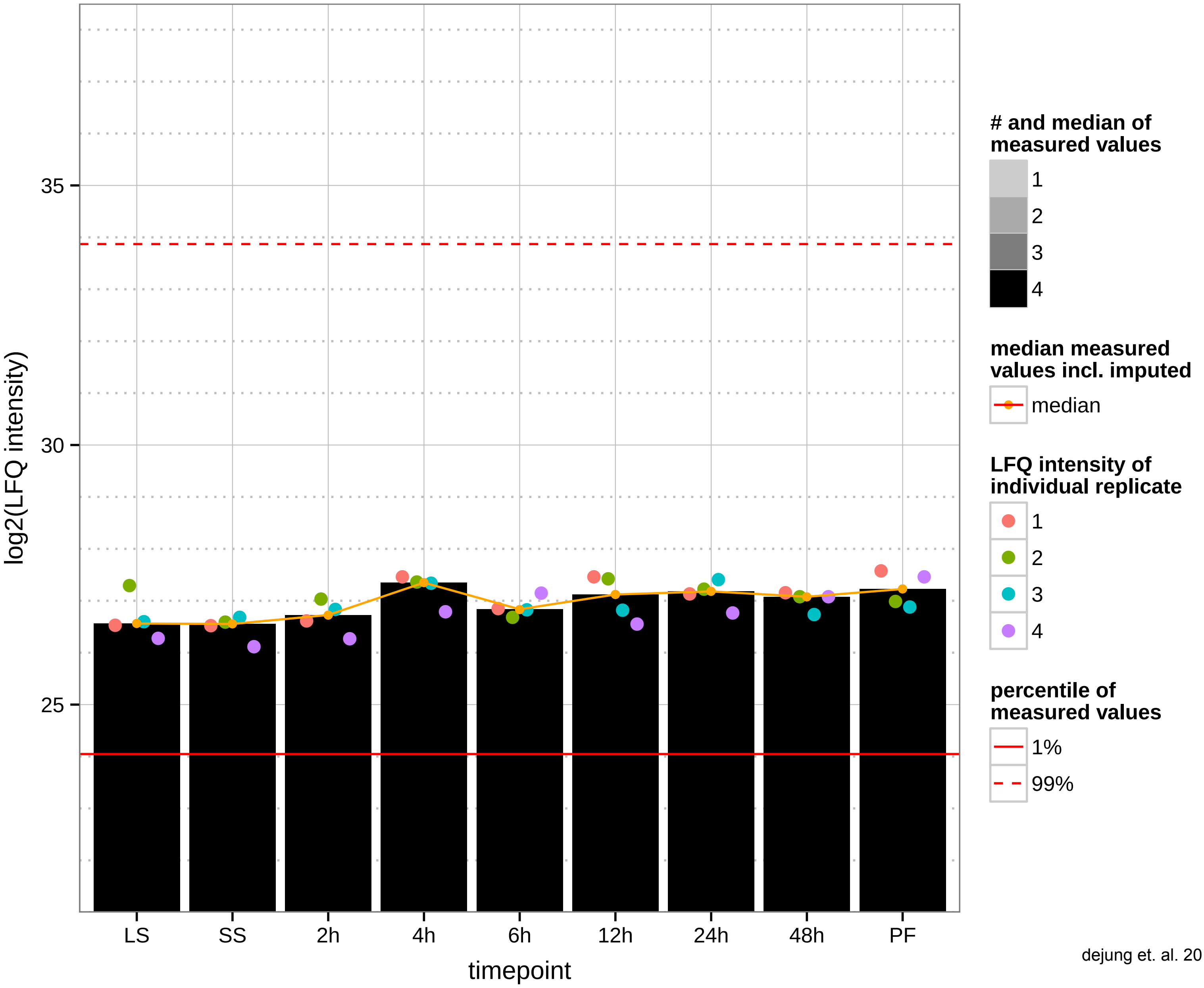
Nucleoporin (TbNup53b)
Tb927.3.3540
AGOF: null
AGOC: nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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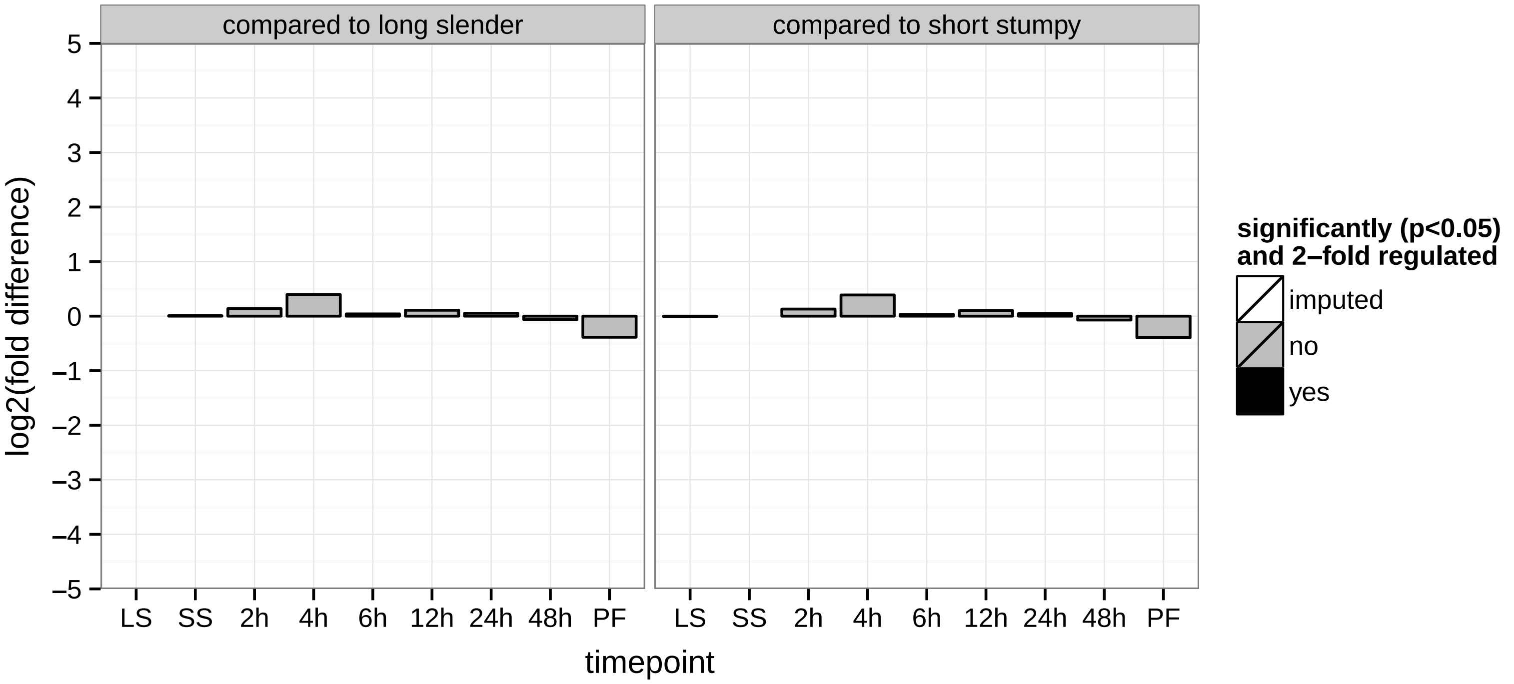
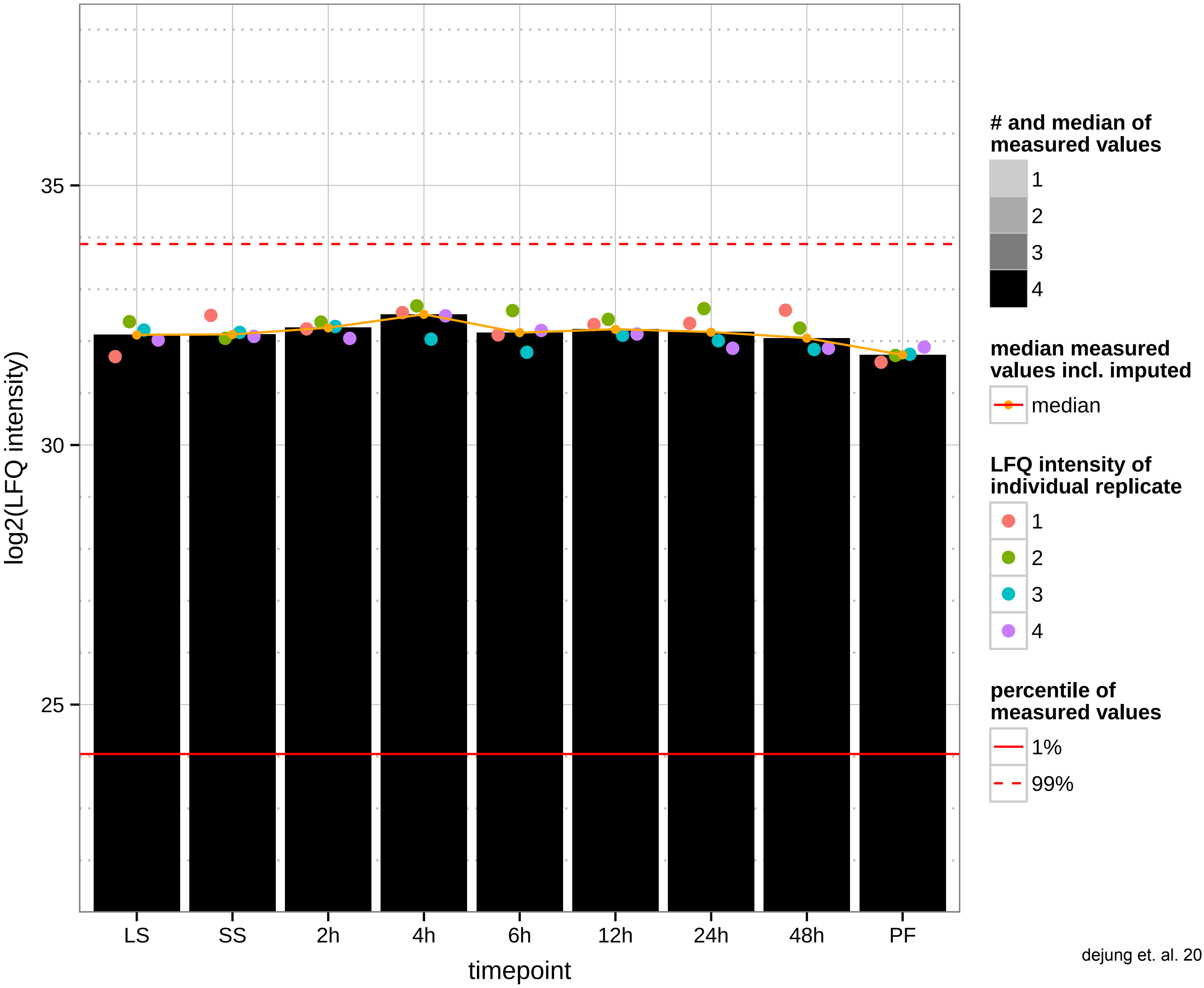
heat shock protein 90, putative, lipophosphoglycan biosynthetic protein, glucose regulated protein 94, putative (LPG3)
Tb927.3.3580
AGOF: ATP binding, unfolded protein binding
AGOC: null
AGOP: protein folding, response to stress
PGOF: ATP binding, unfolded protein binding
PGOC: null
PGOP: protein folding, response to stress





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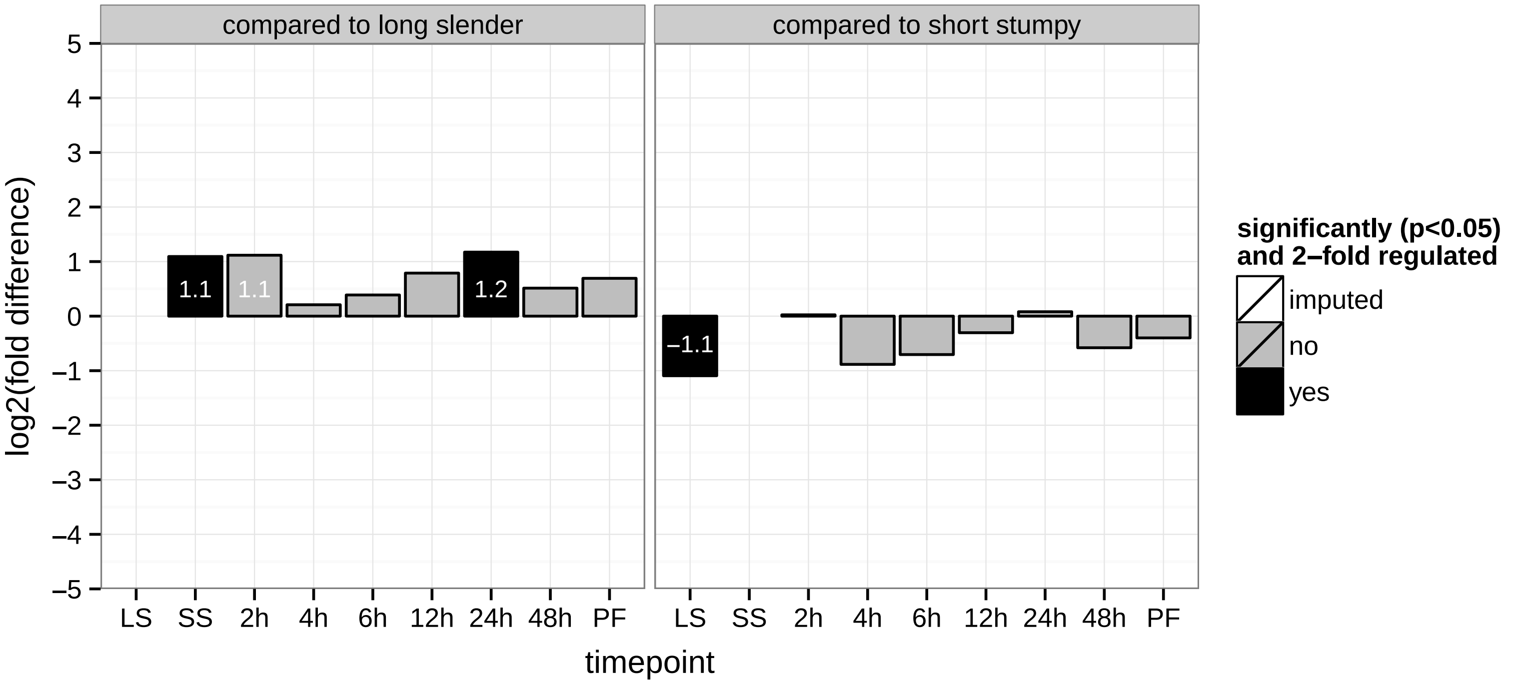
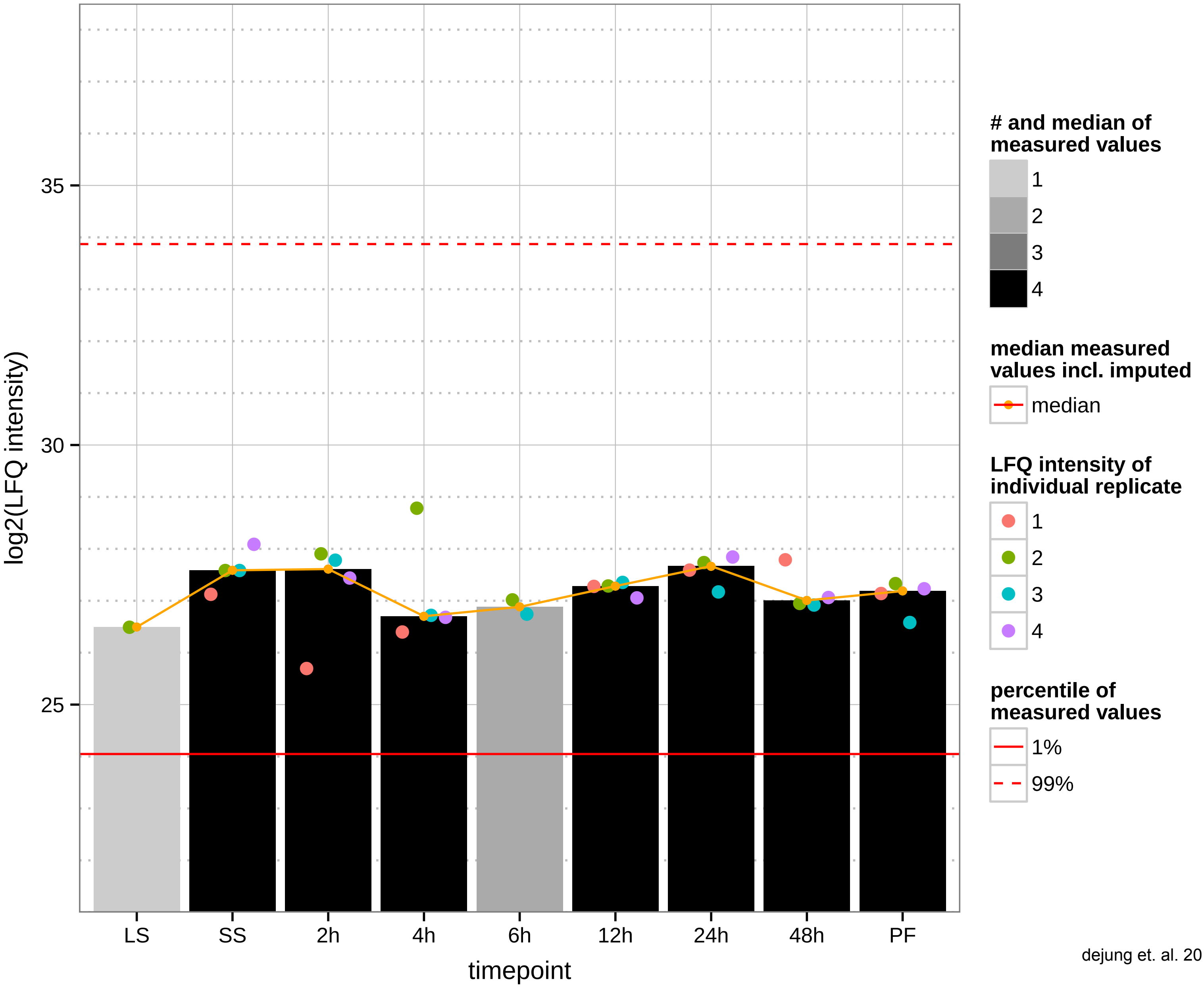
U3 small nucleolar ribonucleoprotein protein MPP10, putative
Tb927.3.3590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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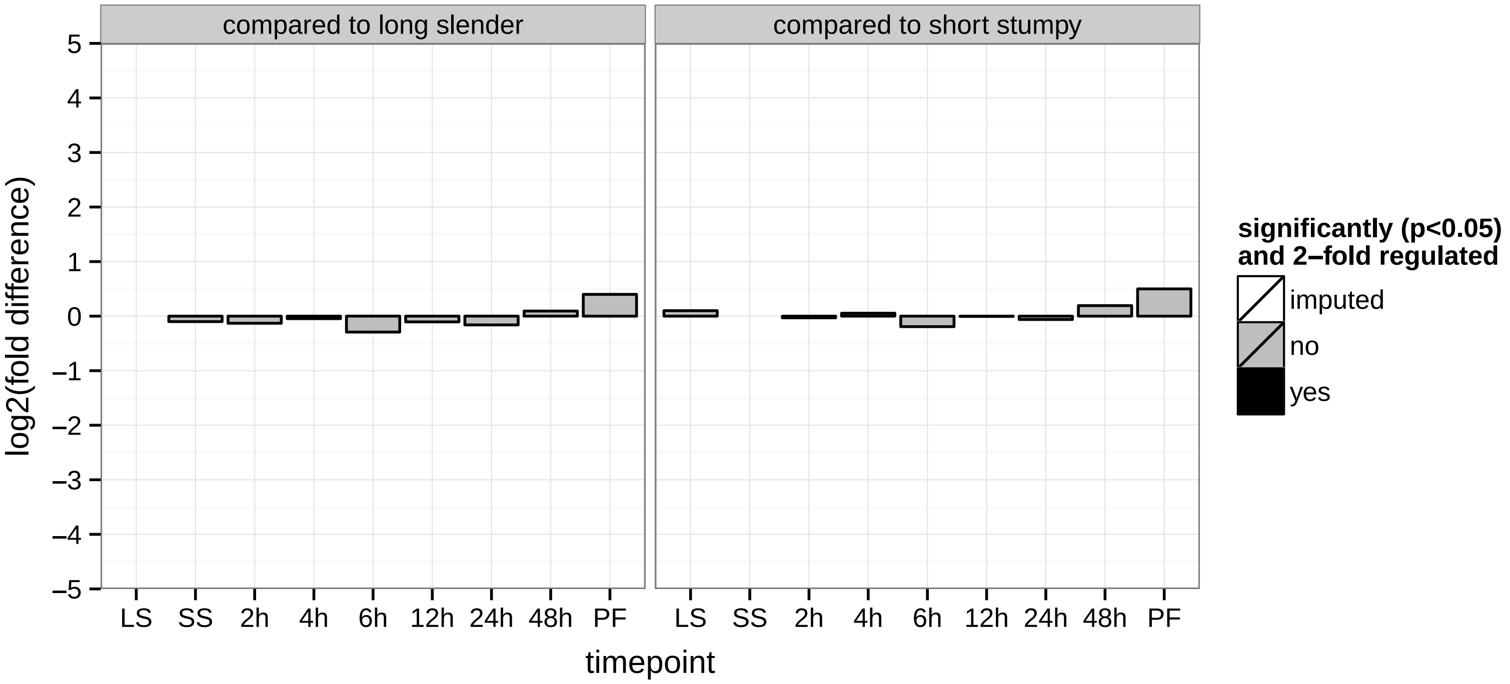
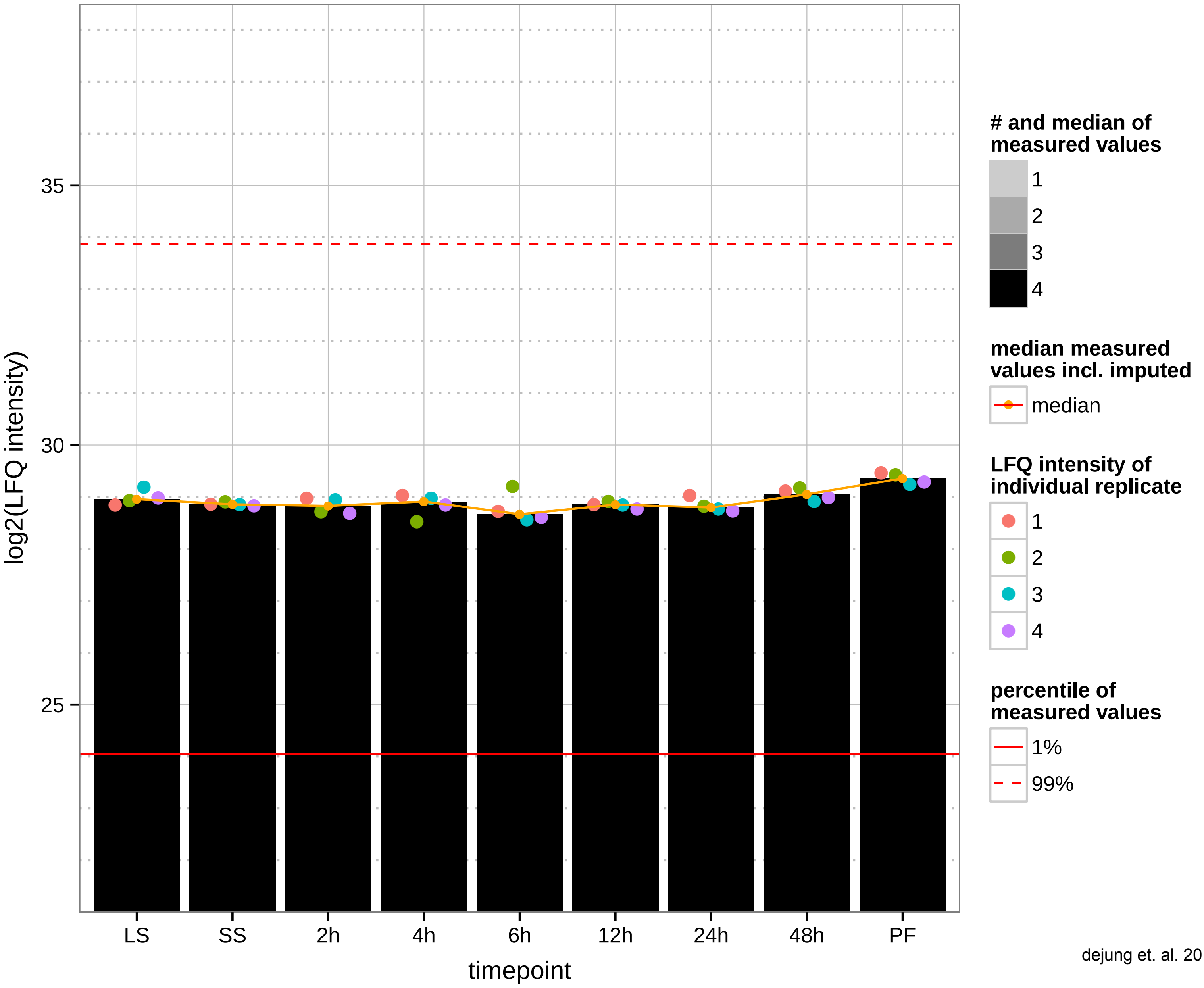
flagellar radial spoke protein–like, putative
Tb927.3.3690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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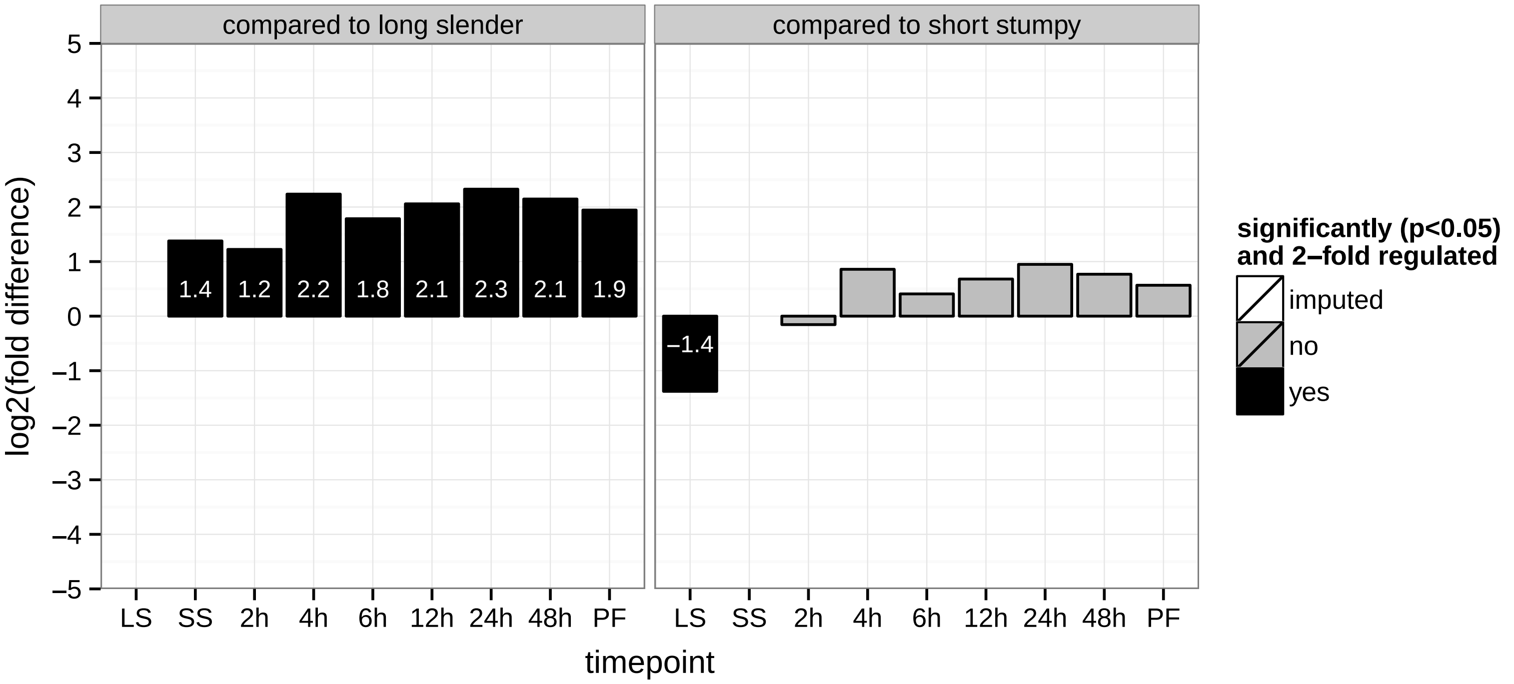
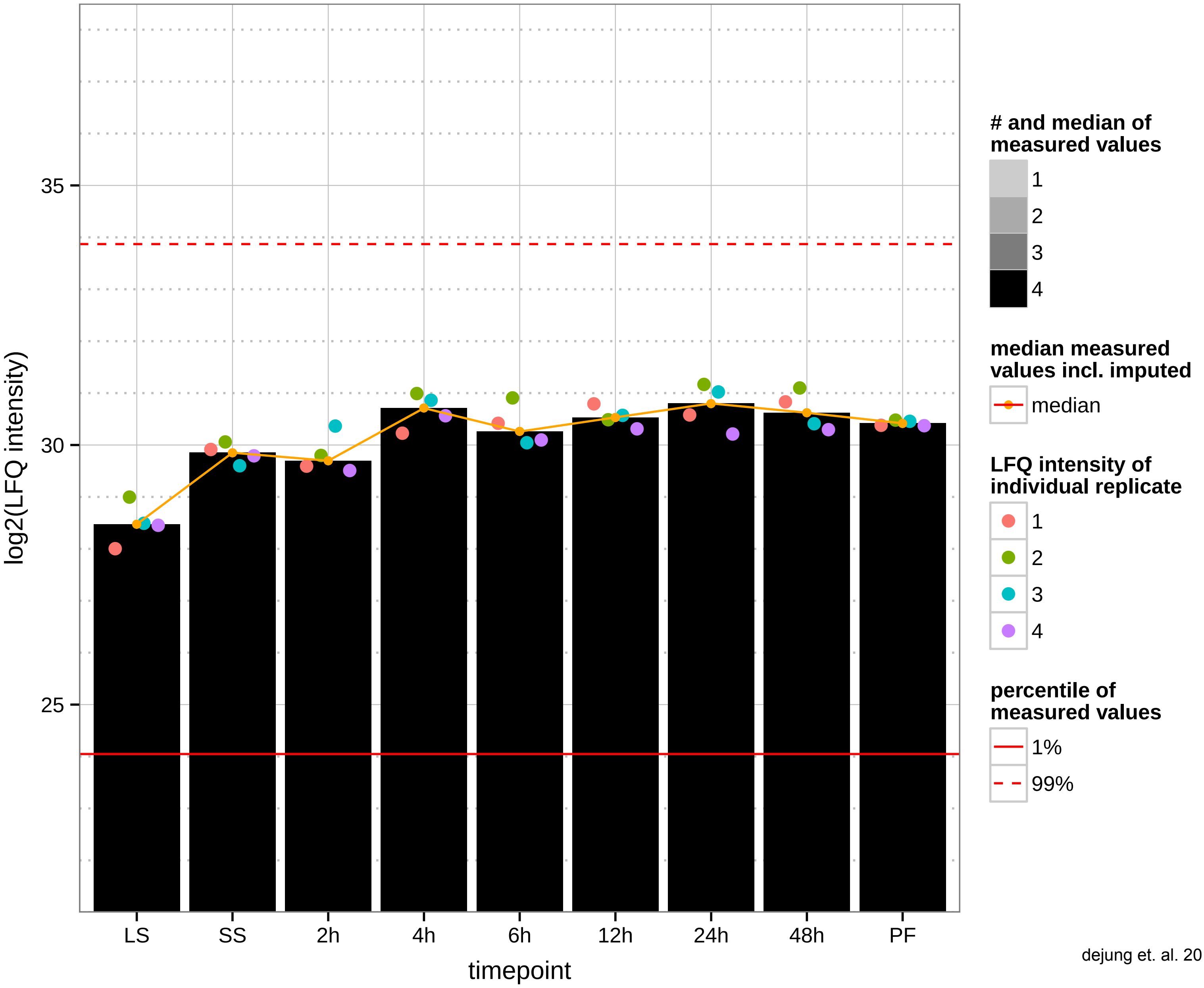
paraflagellar rod component, putative (PFC7)
Tb927.3.3750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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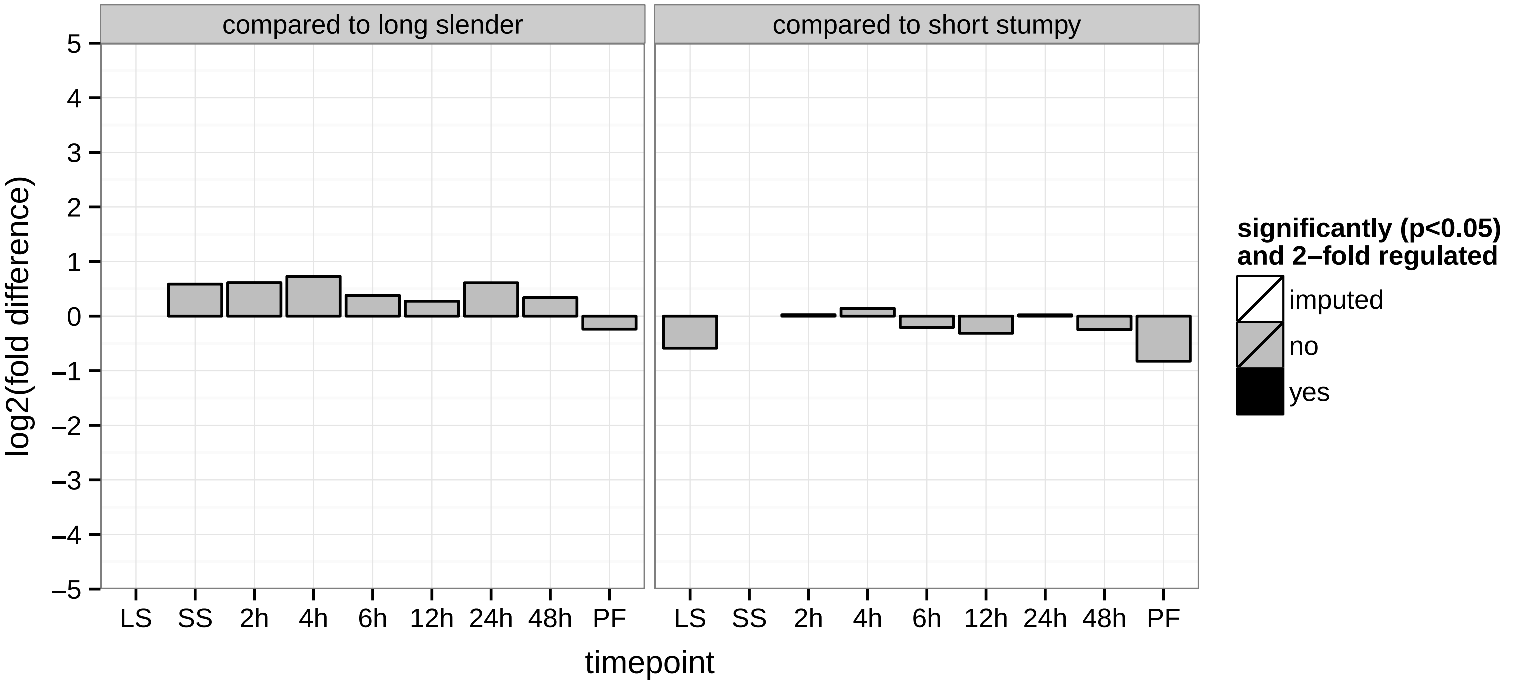
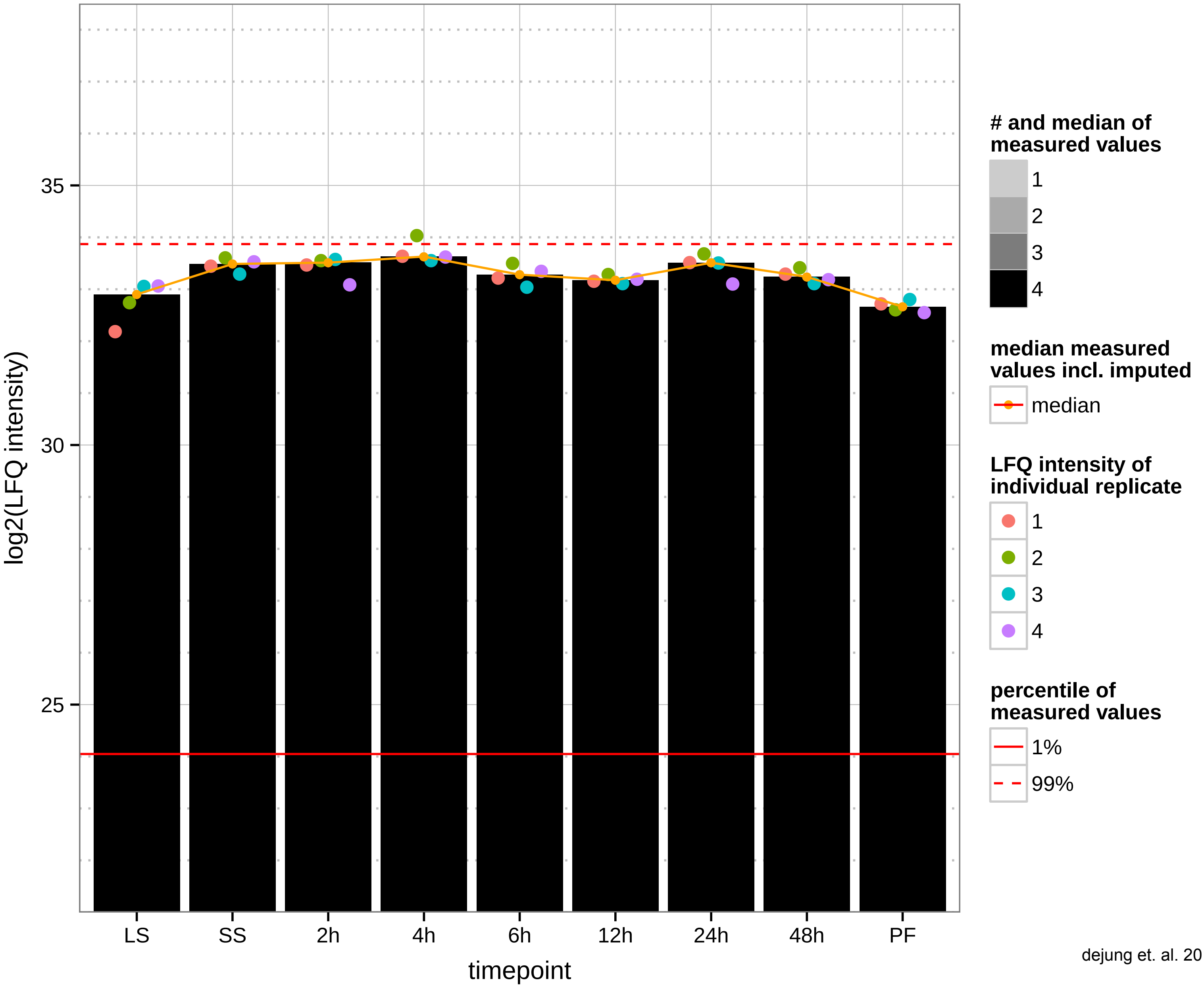
tryparedoxin 1b, putative (TXN1b), tryparedoxin 1a, putative (TXN1a)
Tb927.3.3780;Tb927.3.3760
AGOF: null
AGOC: null
AGOP: hydrogen peroxide catabolic process
PGOF: null
PGOC: null
PGOP: null





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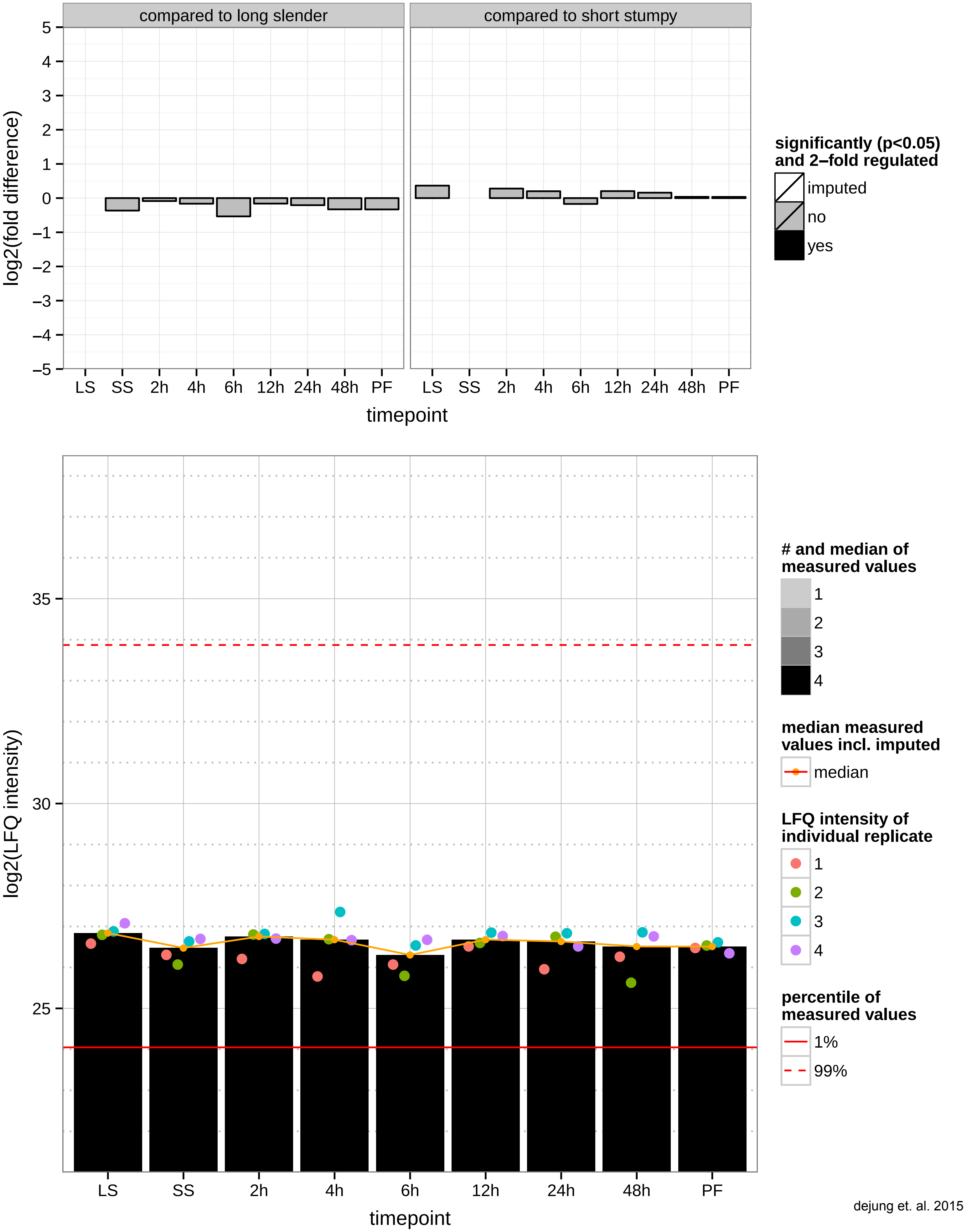
hypothetical protein, conserved
Tb927.3.3820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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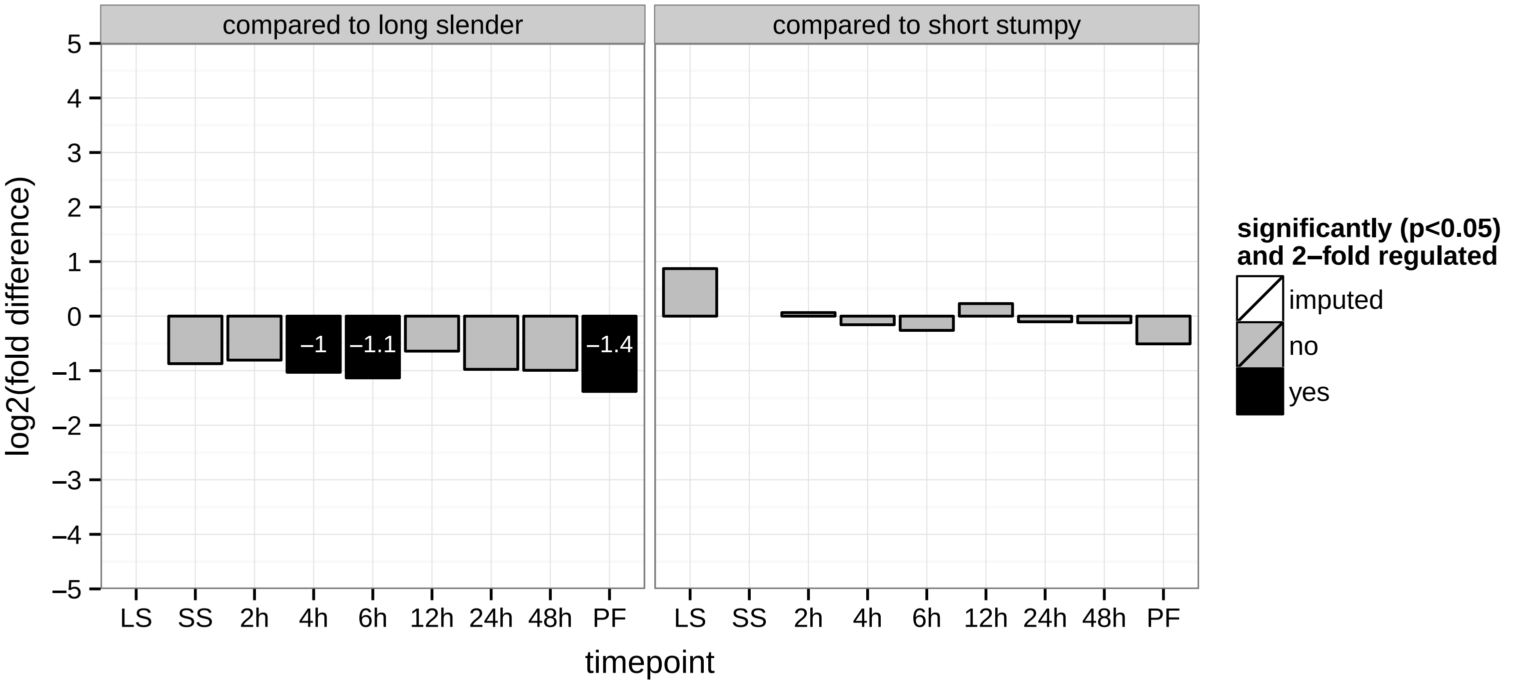
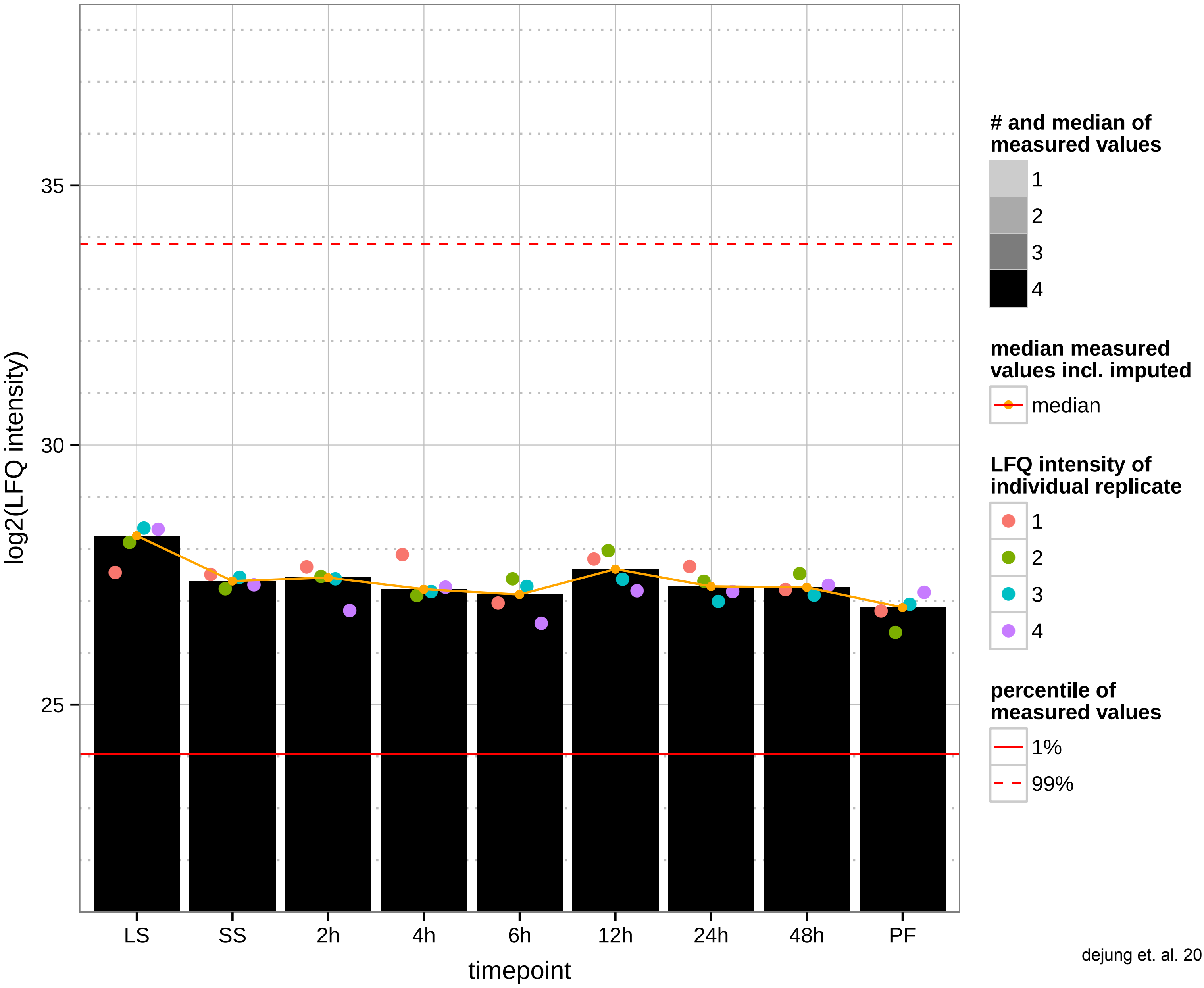
hypothetical protein, conserved
Tb927.3.3830
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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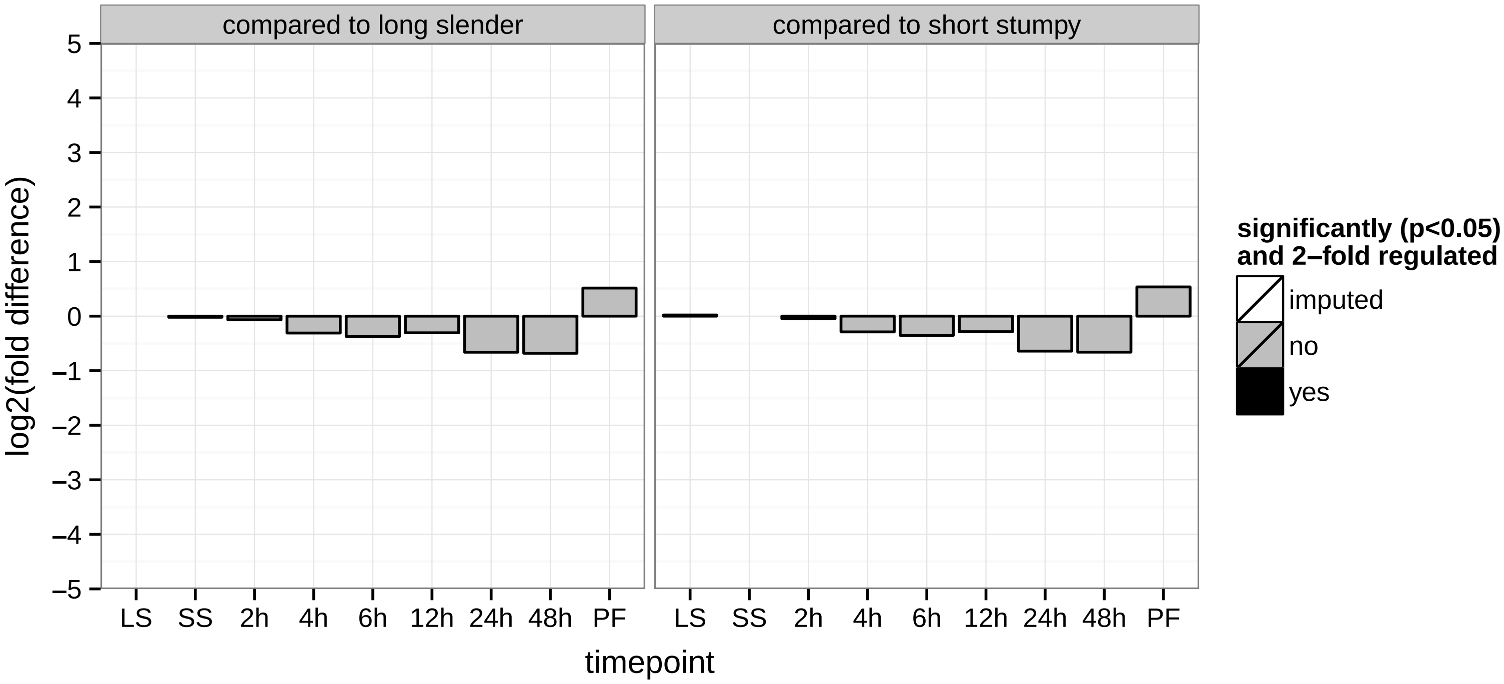
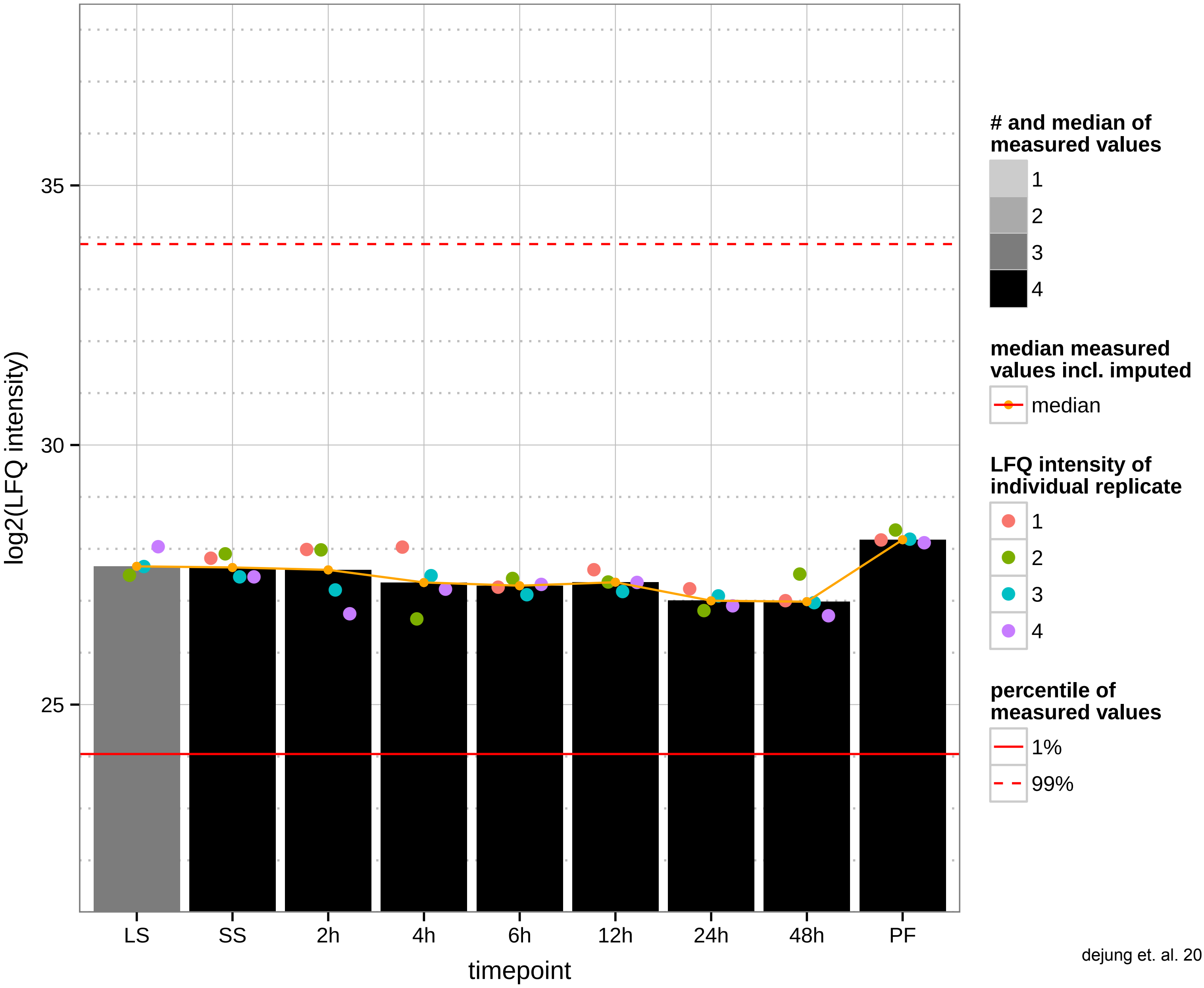
COPII coat assembly protein sec16 (sec16)
Tb927.3.3850
AGOF: null
AGOC: endoplasmic reticulum exit site
AGOP: ER to Golgi vesicle–mediated transport, Golgi organization, endoplasmic reticulum organization, protein localization to
PGOF: null
PGOC: null
PGOP: null





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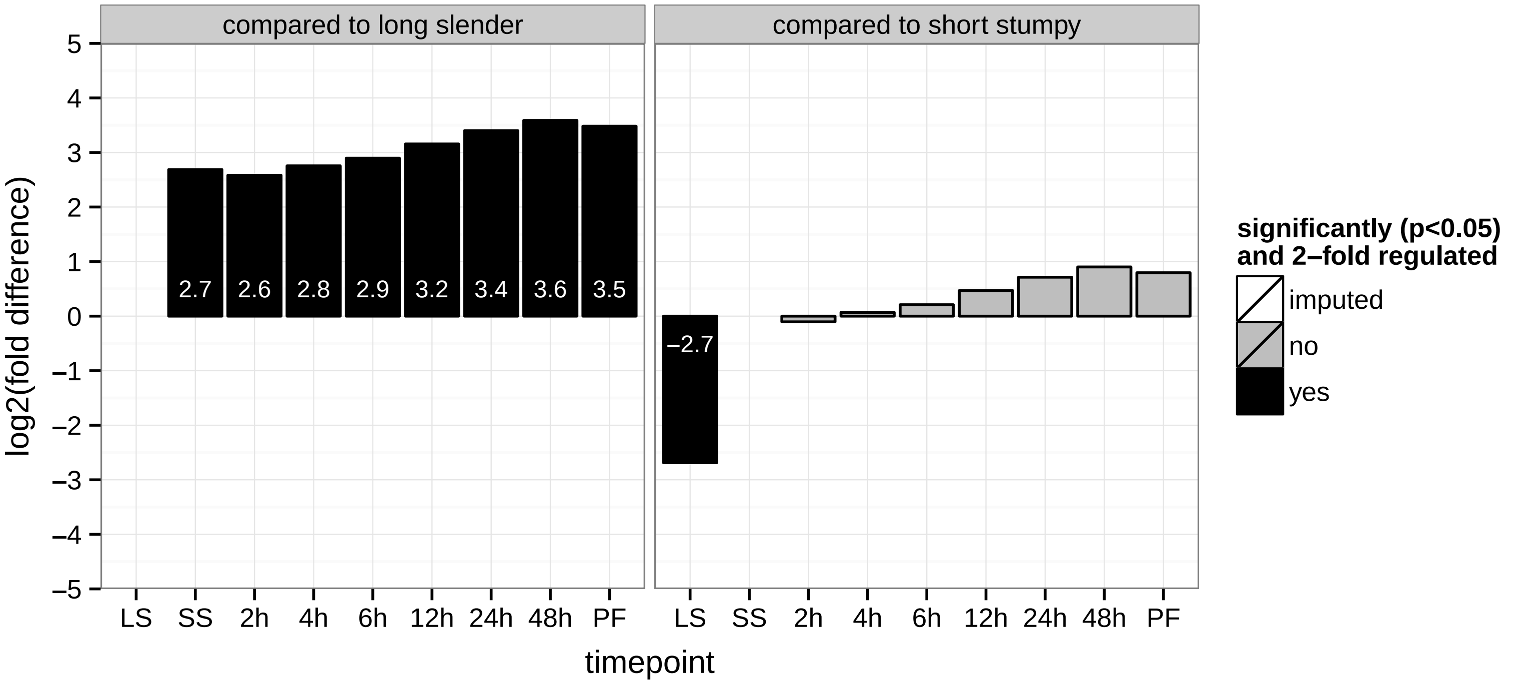
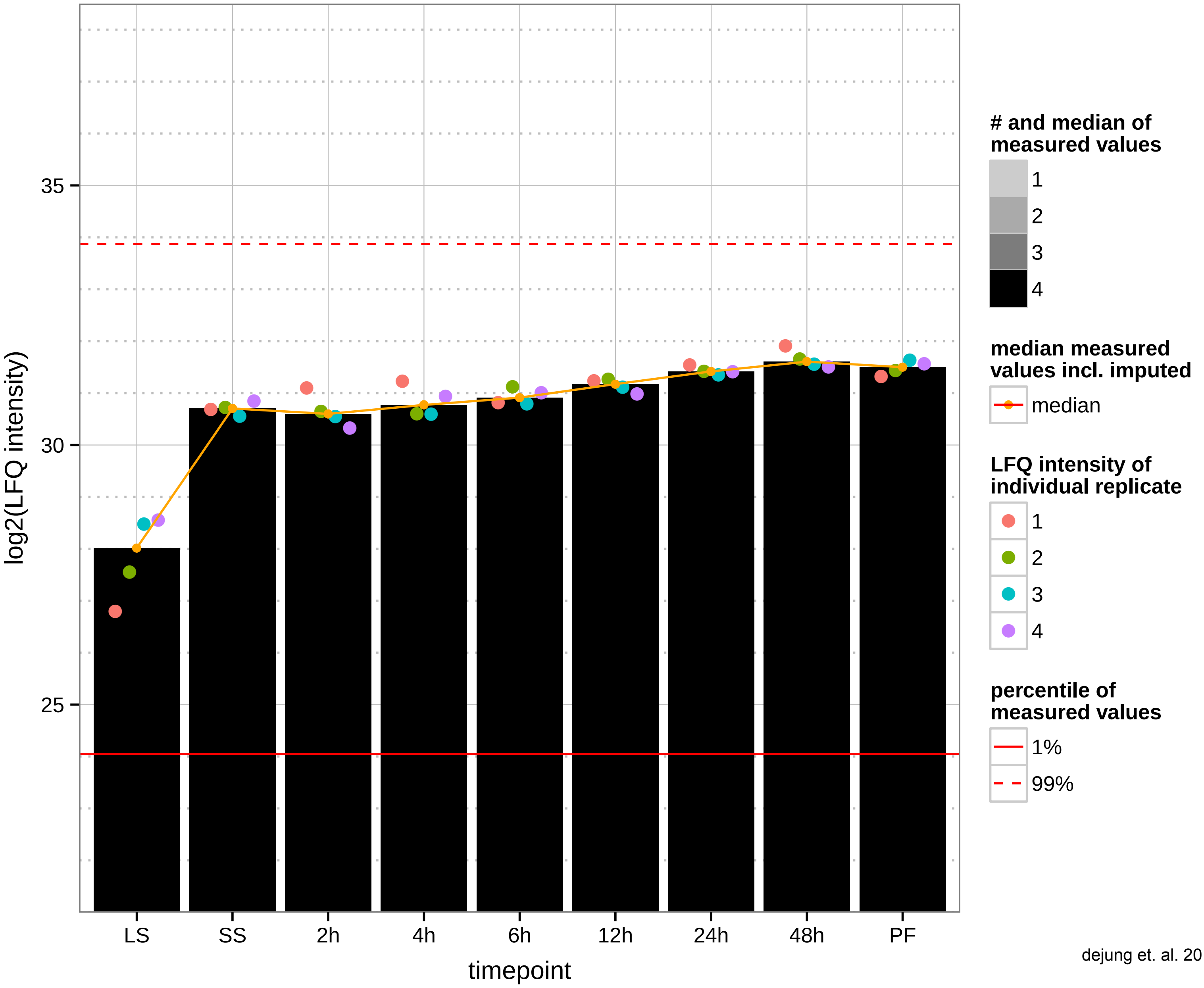
carnitine O−palmitoyltransferase II, putative (CPT II)
Tb927.3.3900
AGOF: transferase activity, transferring acyl groups
AGOC: null
AGOP: null
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: null





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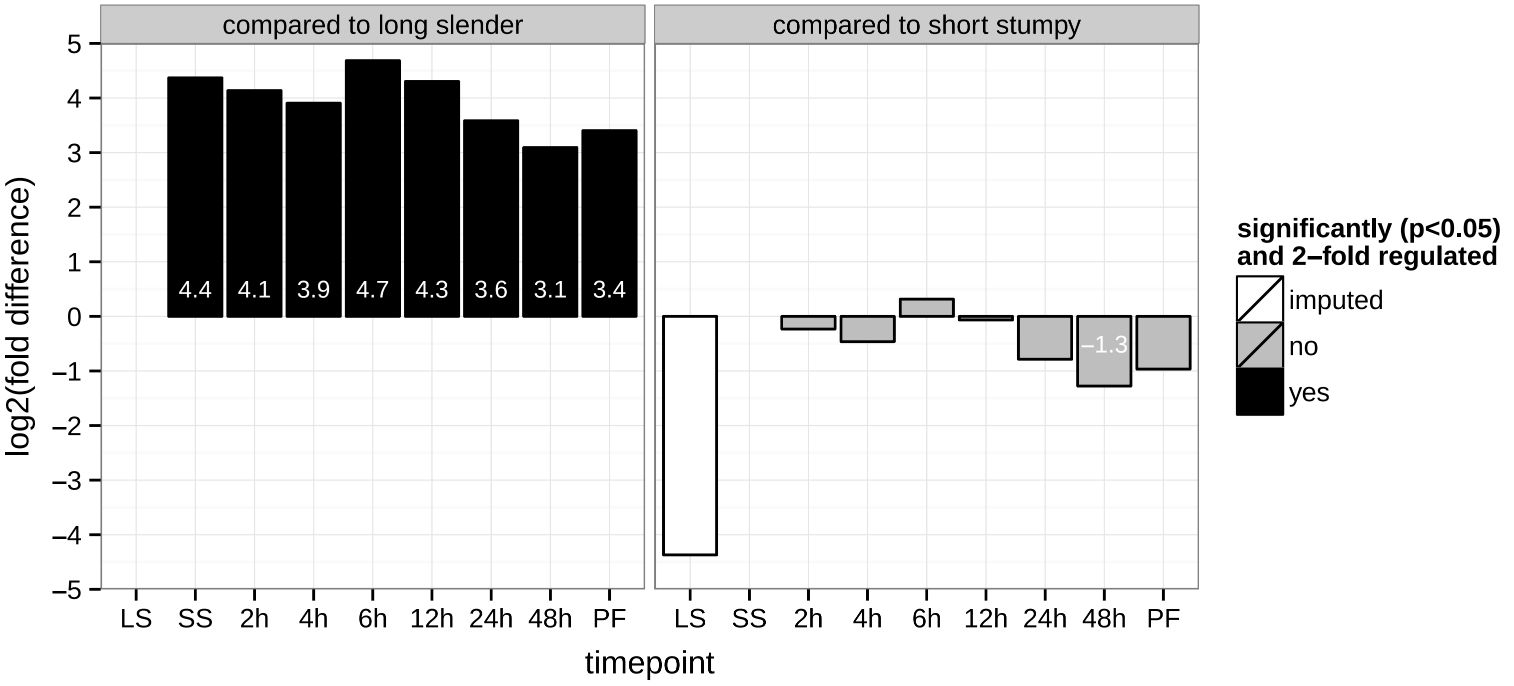
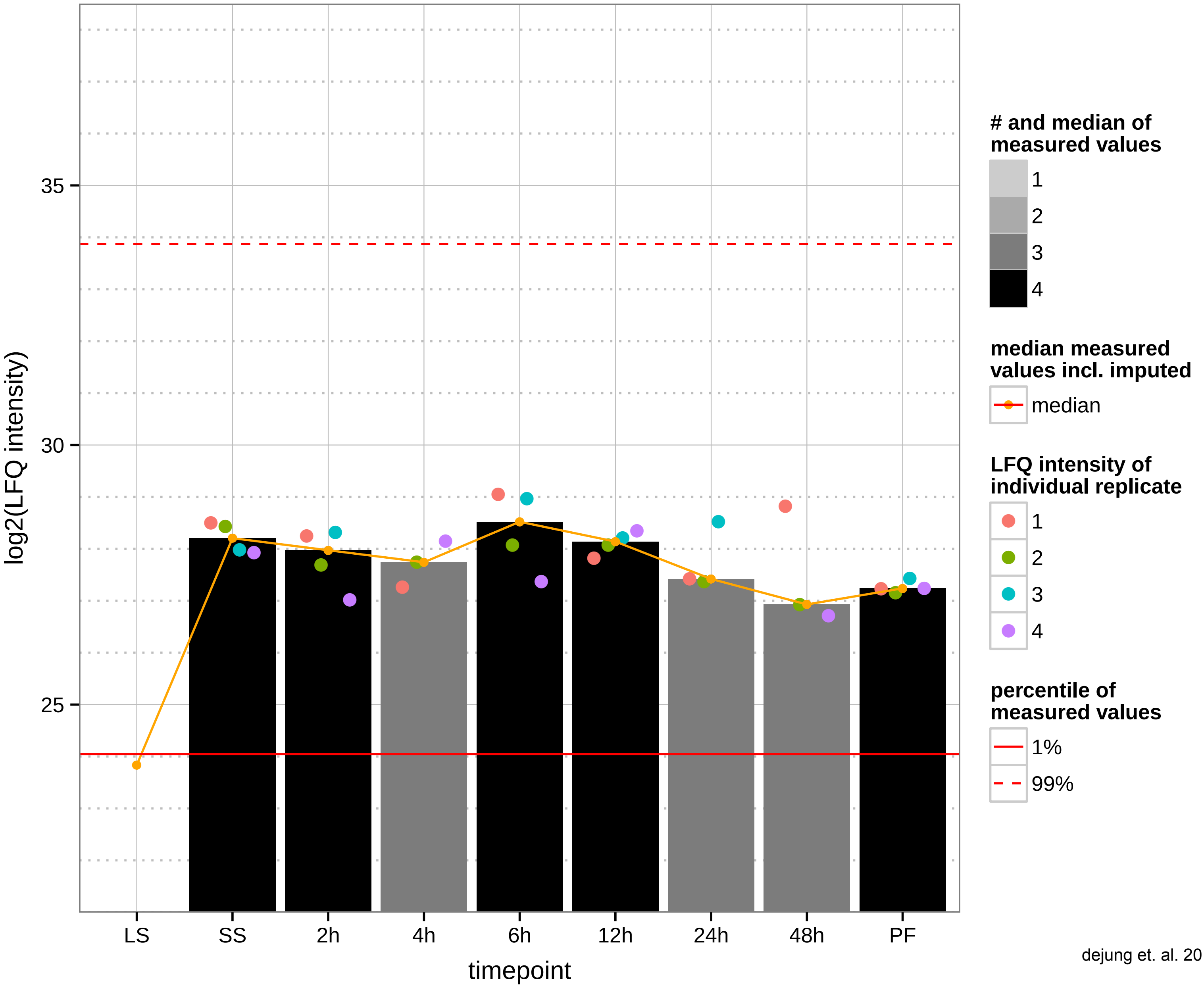
clathrin coat assembly protein ap19, putative
Tb927.3.4000
AGOF: protein transporter activity
AGOC: clathrin adaptor complex, clathrin coat of trans−Golgi network vesicle
AGOP: intracellular protein transport, vesicle−mediated transport
PGOF: protein transporter activity
PGOC: null
PGOP: protein transport, transport





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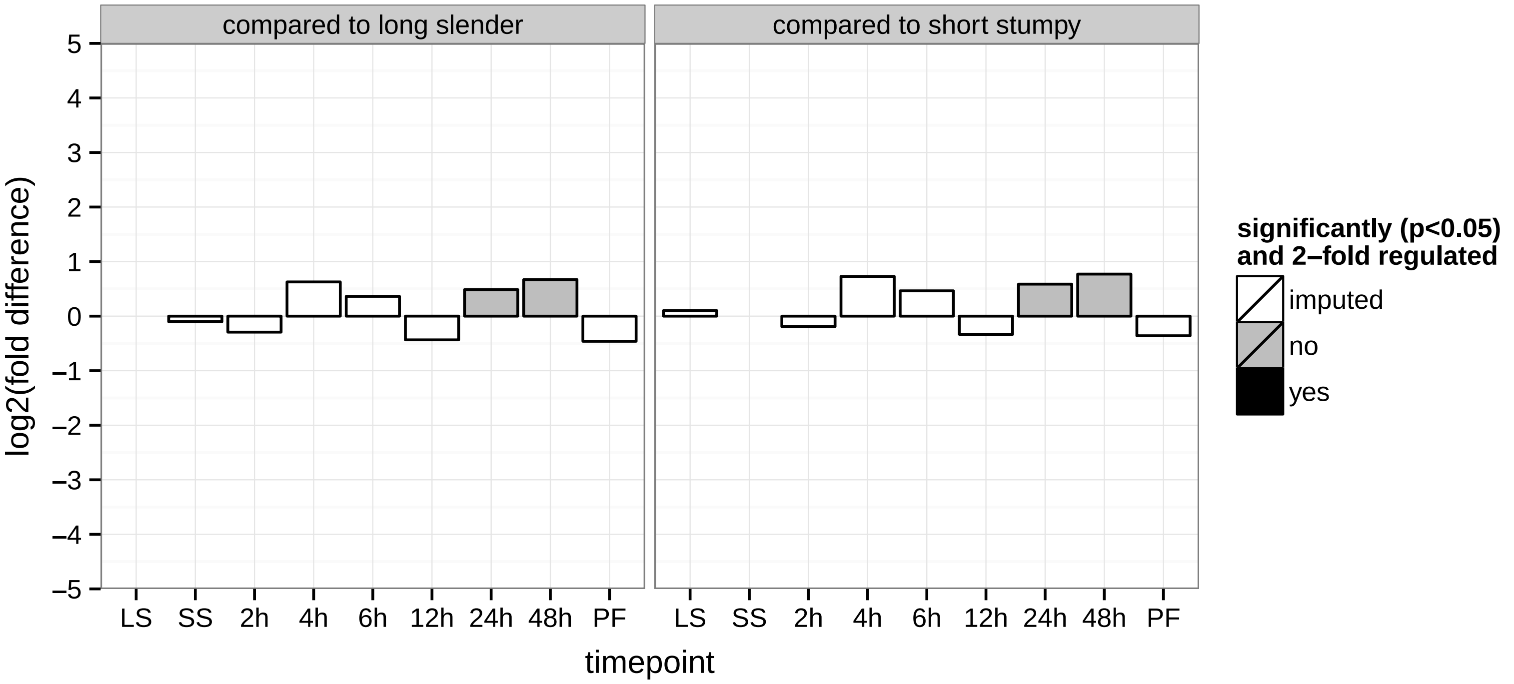
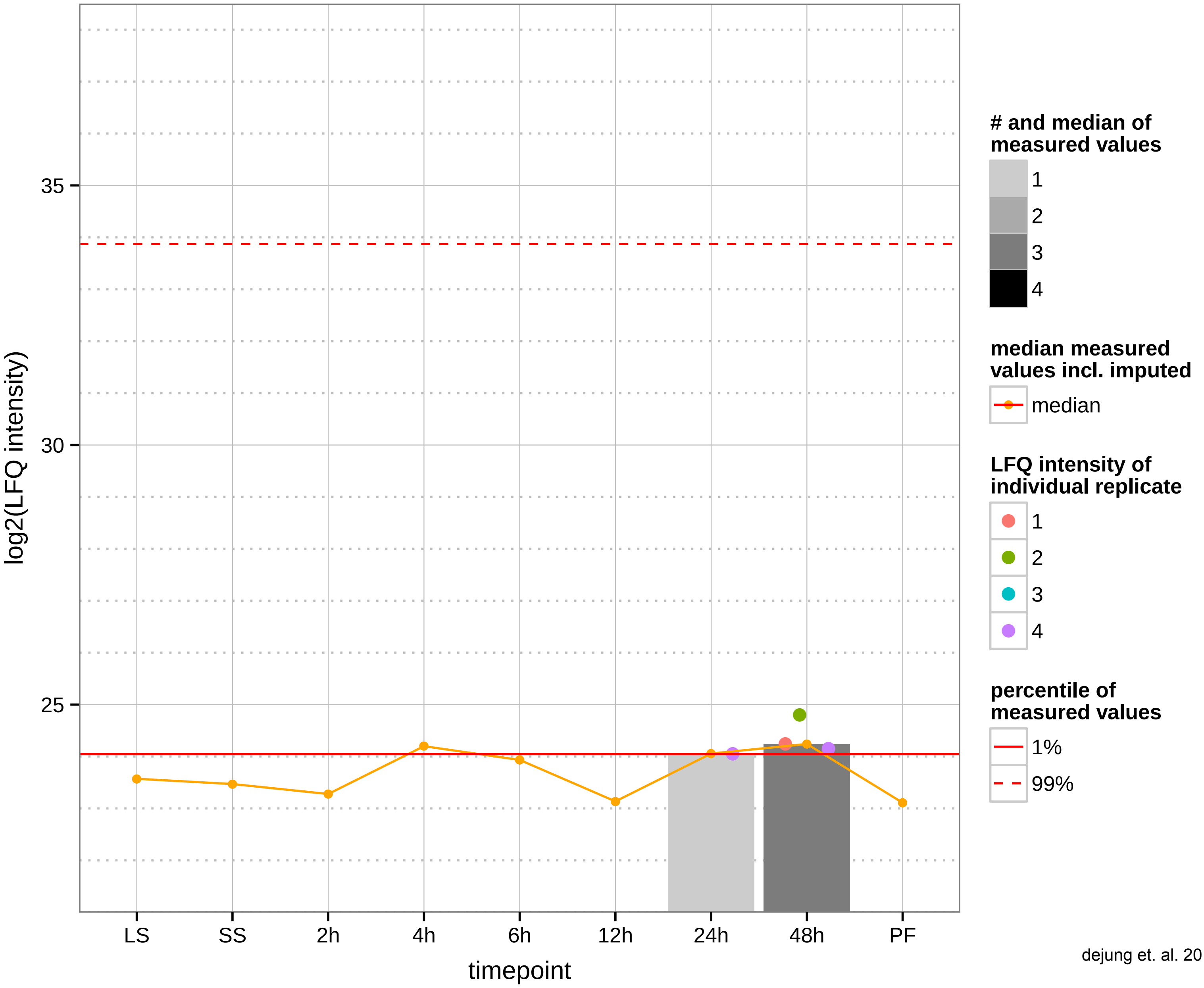
phosphatidylinositol 4−kinase alpha, putative
Tb927.3.4020
AGOF: 1−phosphatidylinositol 4−kinase activity, phosphotransferase activity, alcohol group as acceptor
AGOC: cytosol
AGOP: phosphatidylinositol phosphorylation, phosphatidylinositol−mediated signaling
PGOF: binding, phosphotransferase activity, alcohol group as acceptor, transferase activity, transferring phosphorus−containin
PGOC: null
PGOP: null





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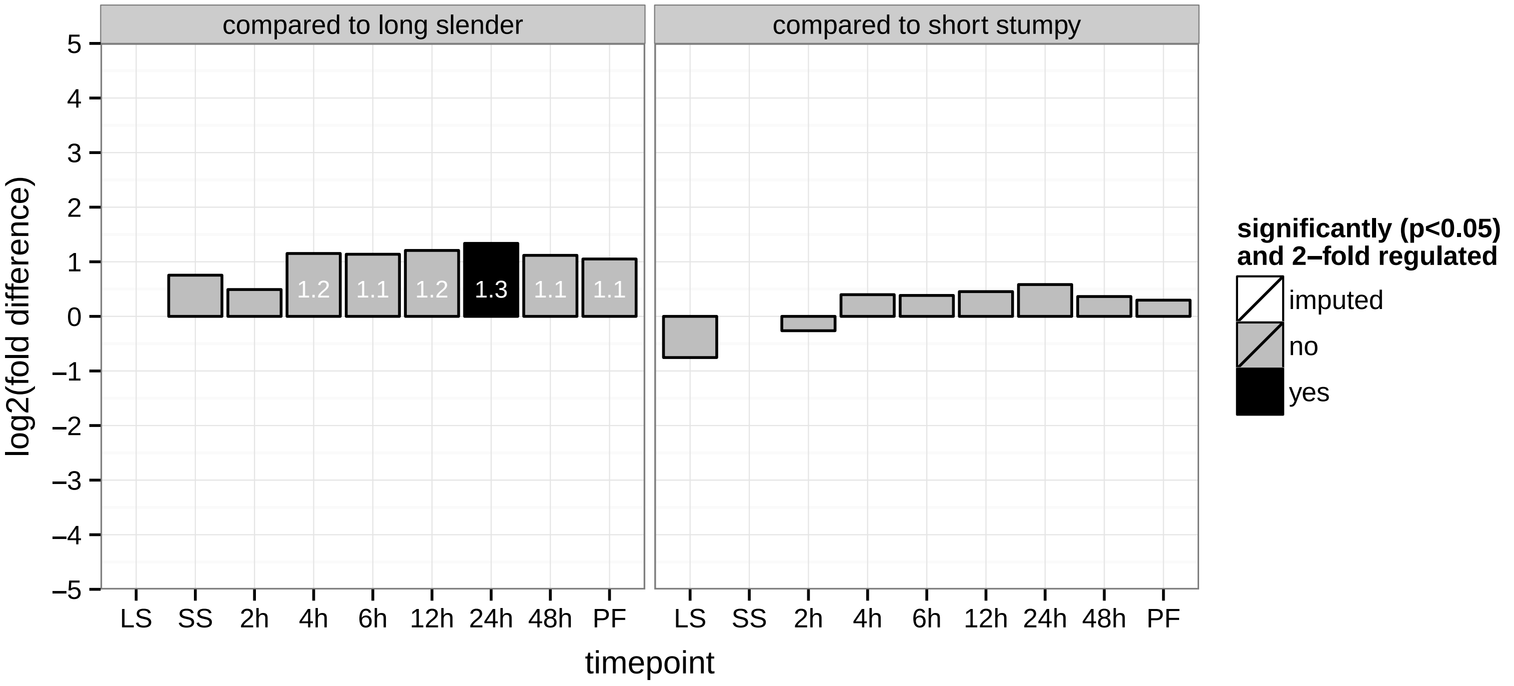
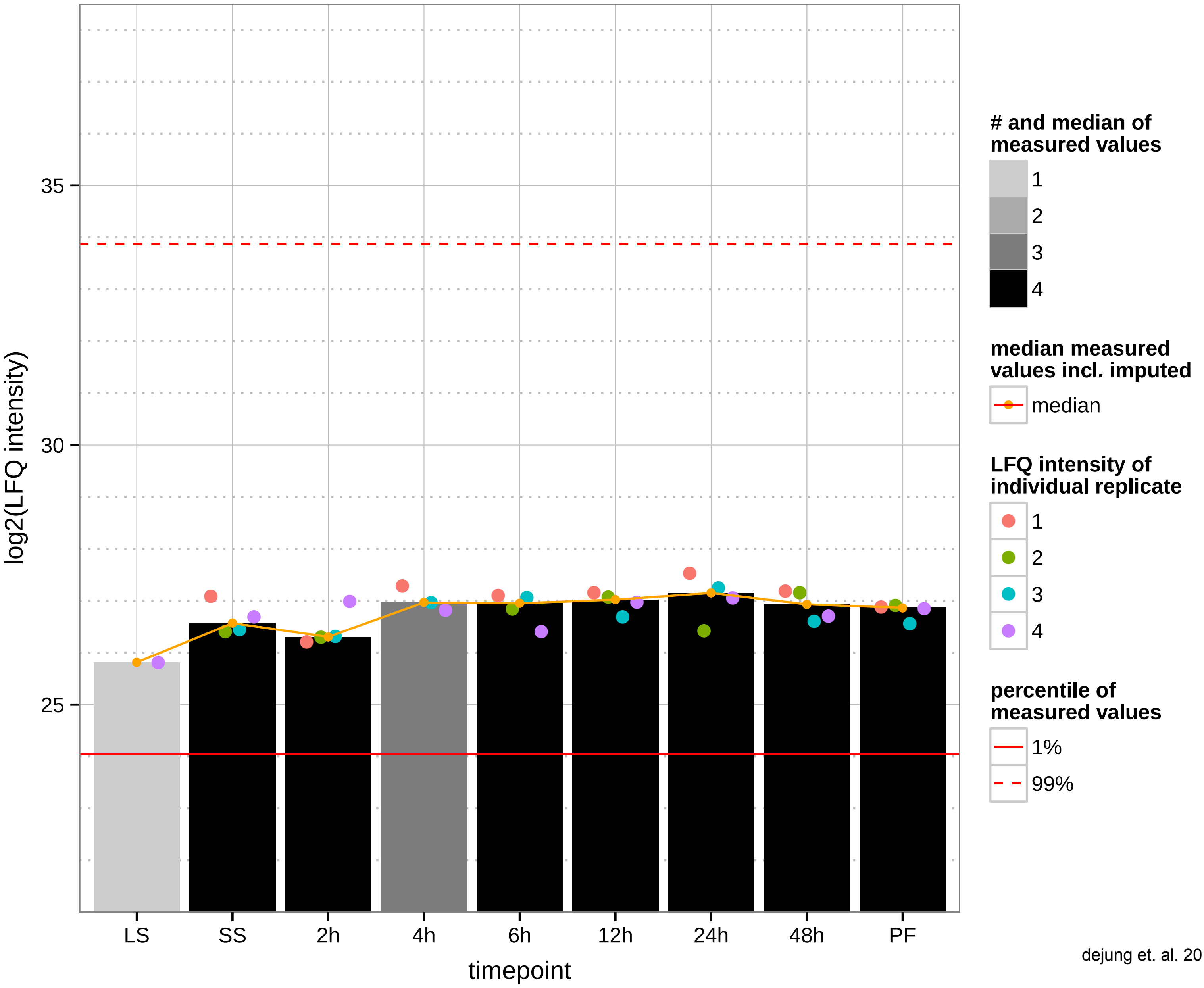
hypothetical protein, conserved
Tb927.3.4030
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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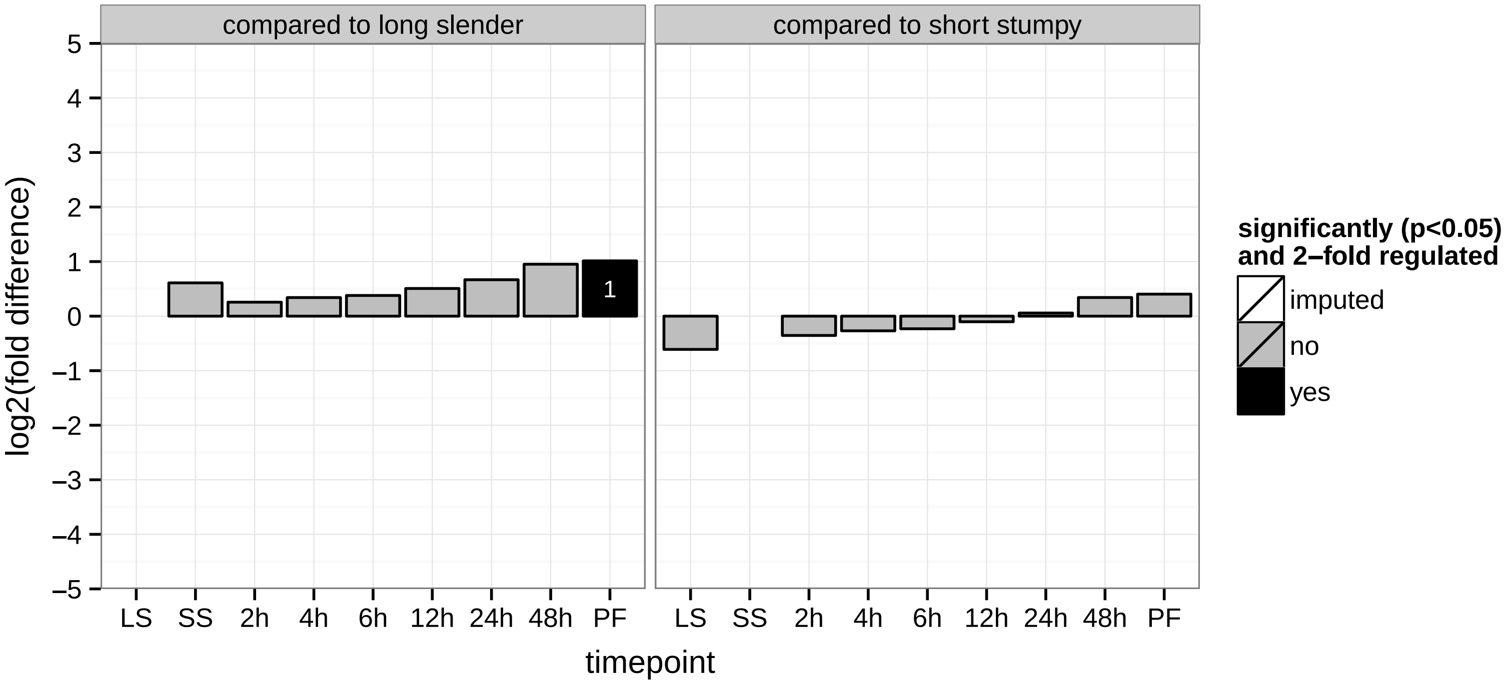
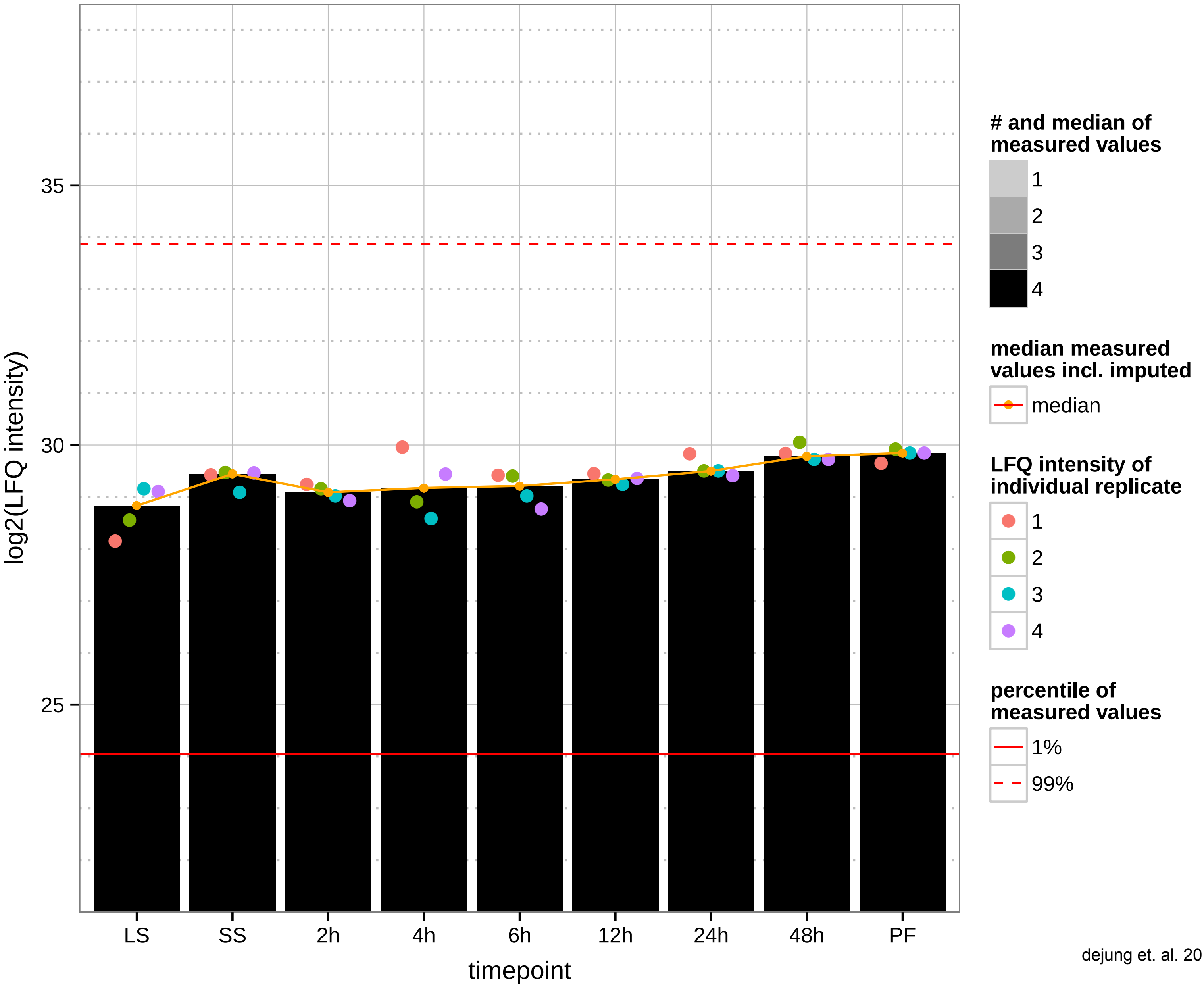
hypothetical protein, conserved
Tb927.3.4040
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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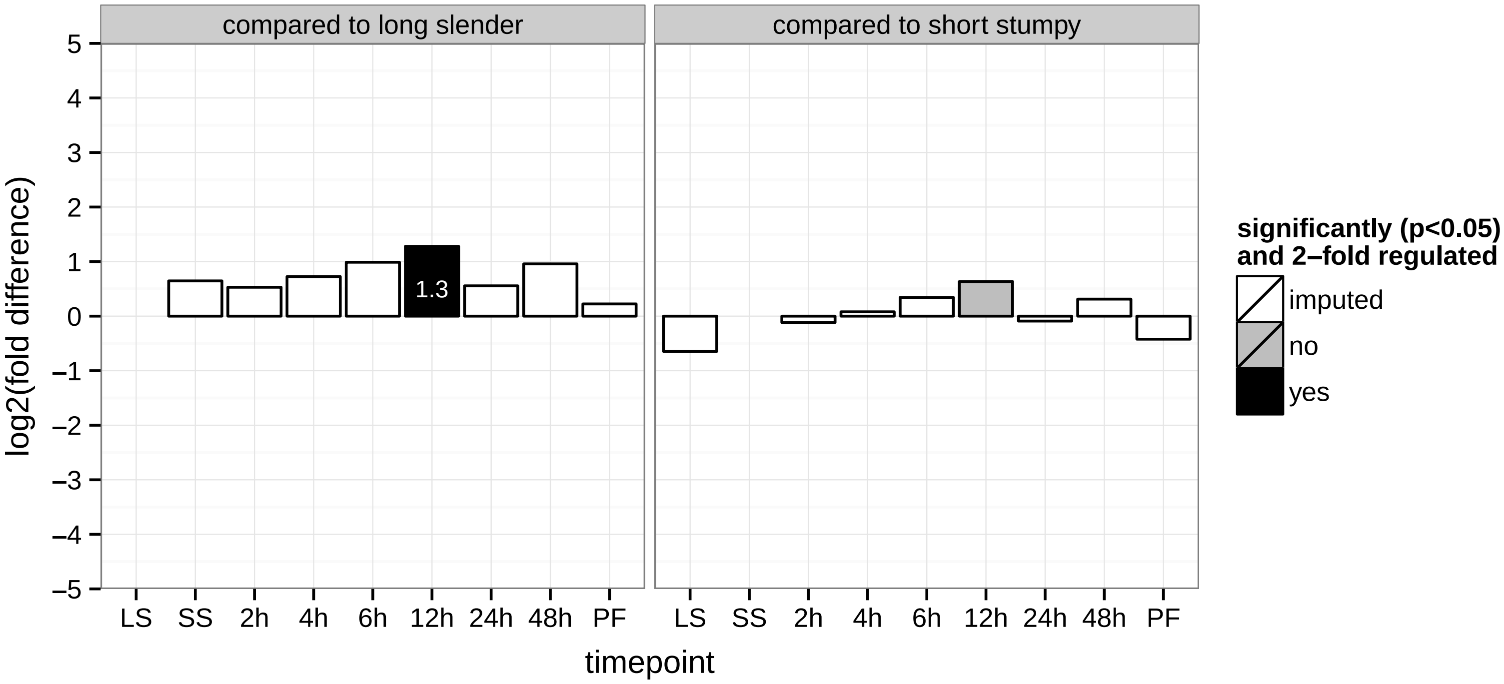
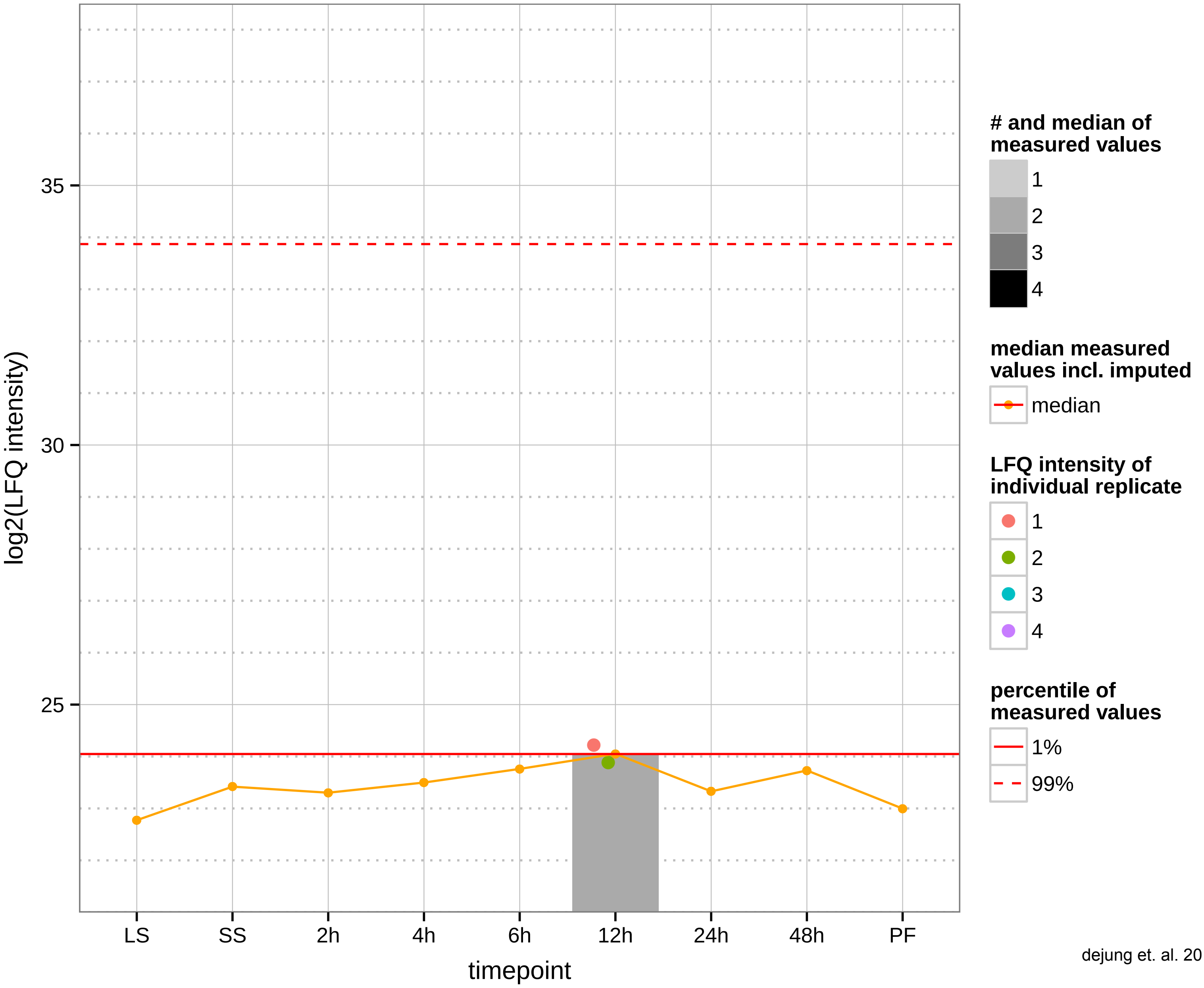
hypothetical protein, conserved
Tb927.3.4120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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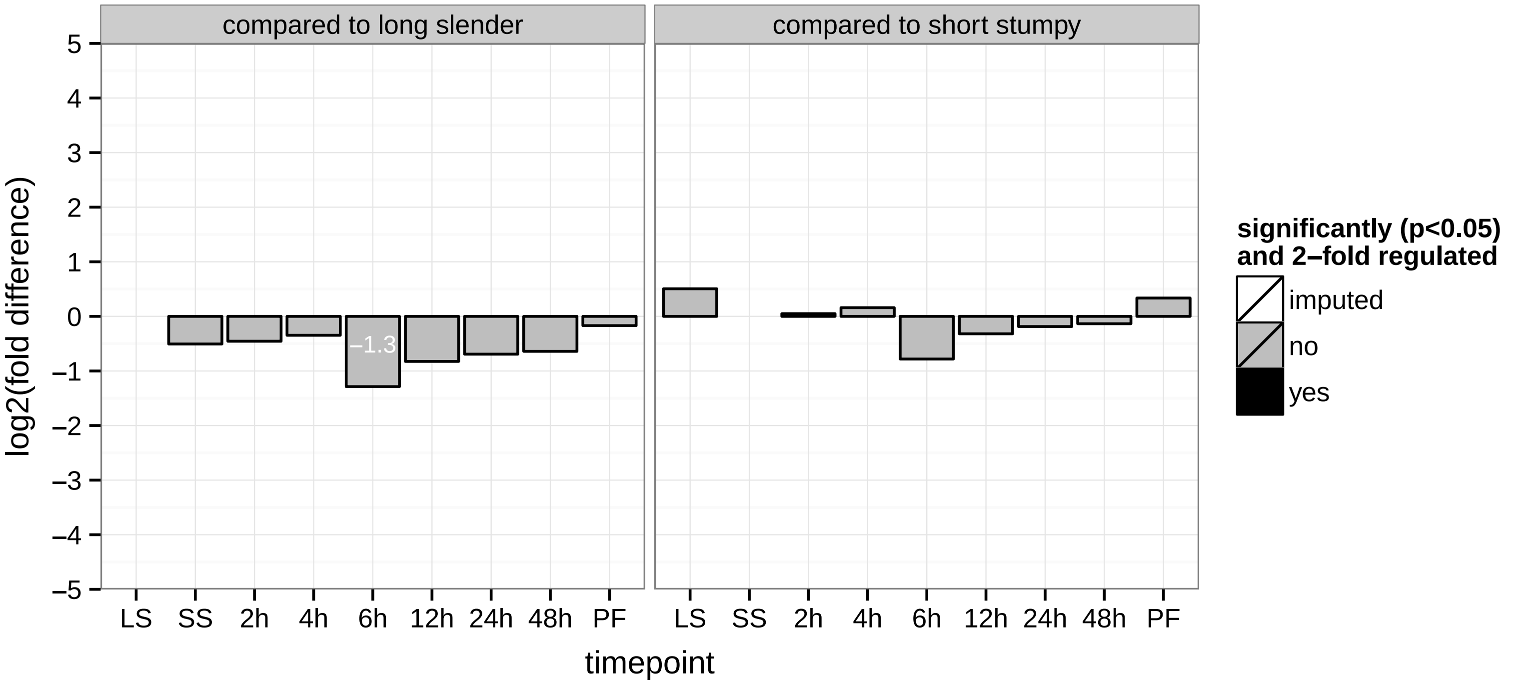
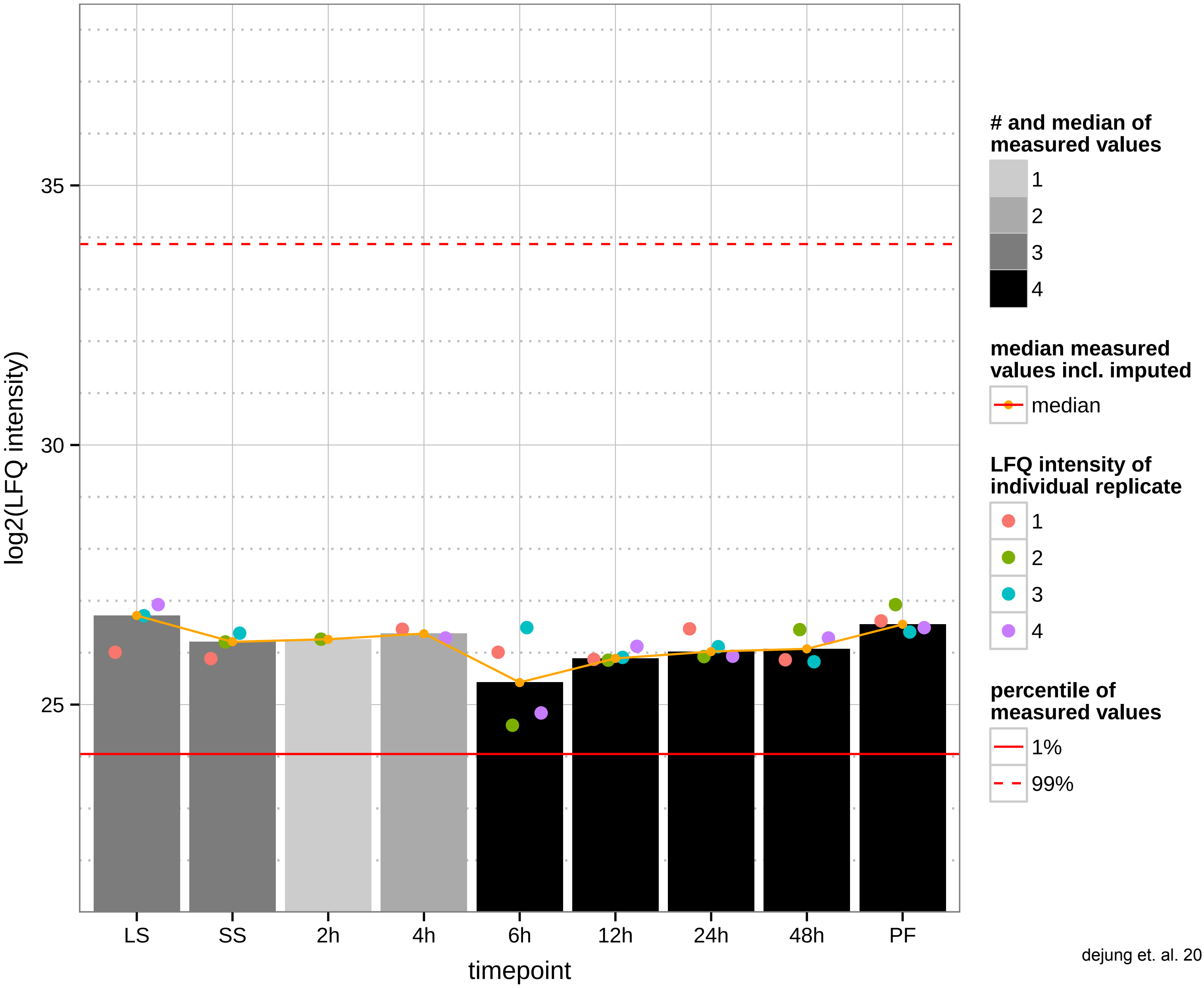
hypothetical protein, conserved
Tb927.3.4140
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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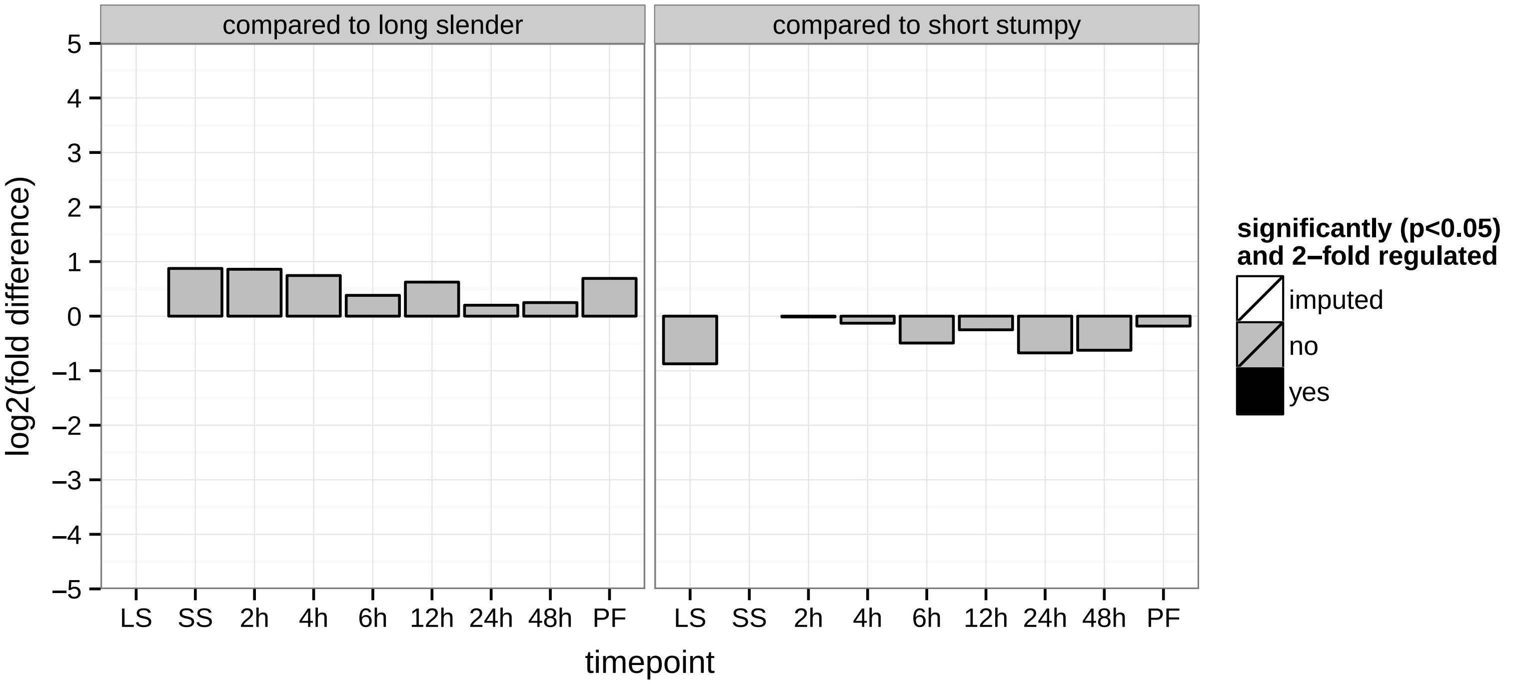
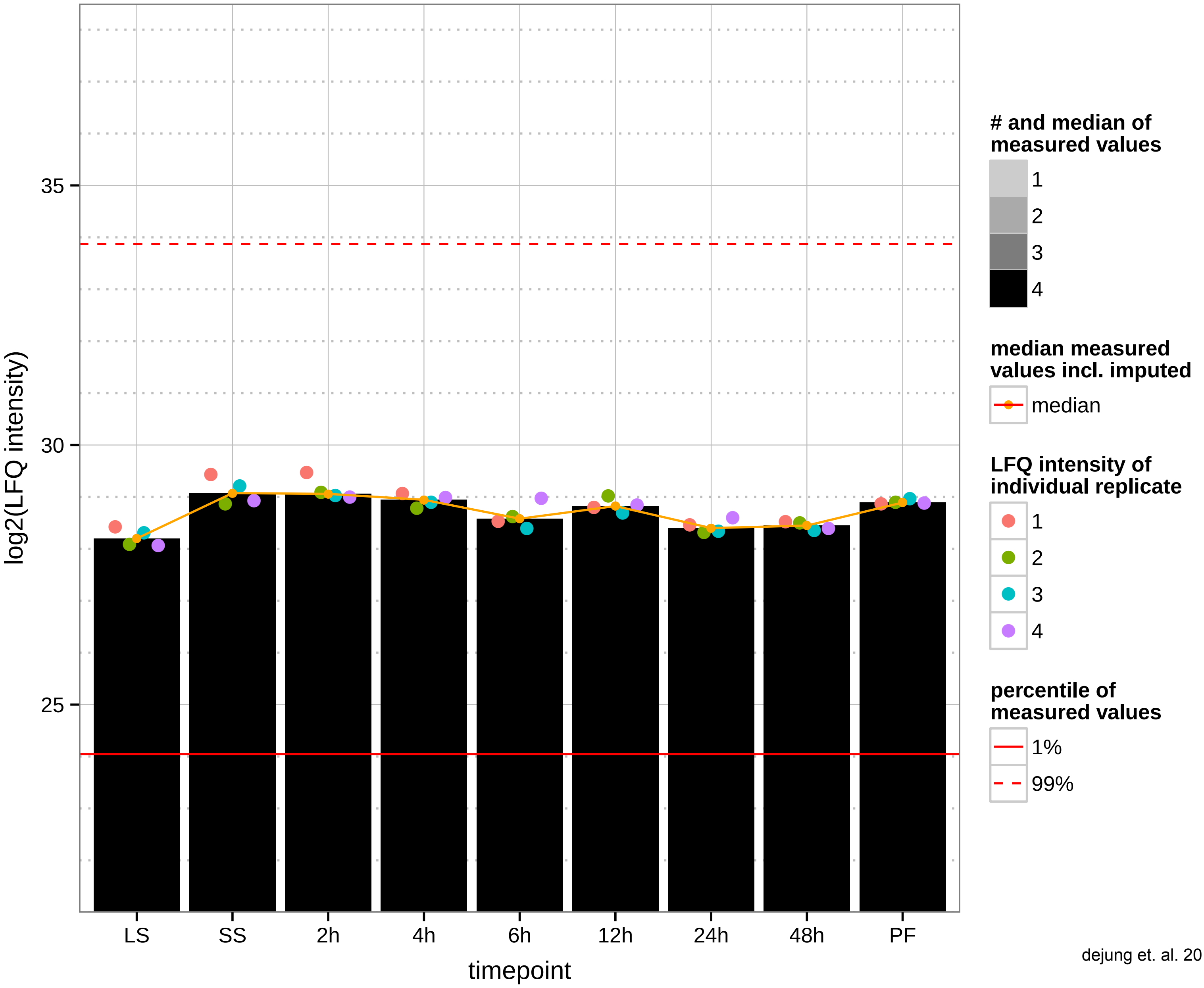
endosomal integral membrane protein, putative
Tb927.3.4190
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: integral to membrane
PGOP: null





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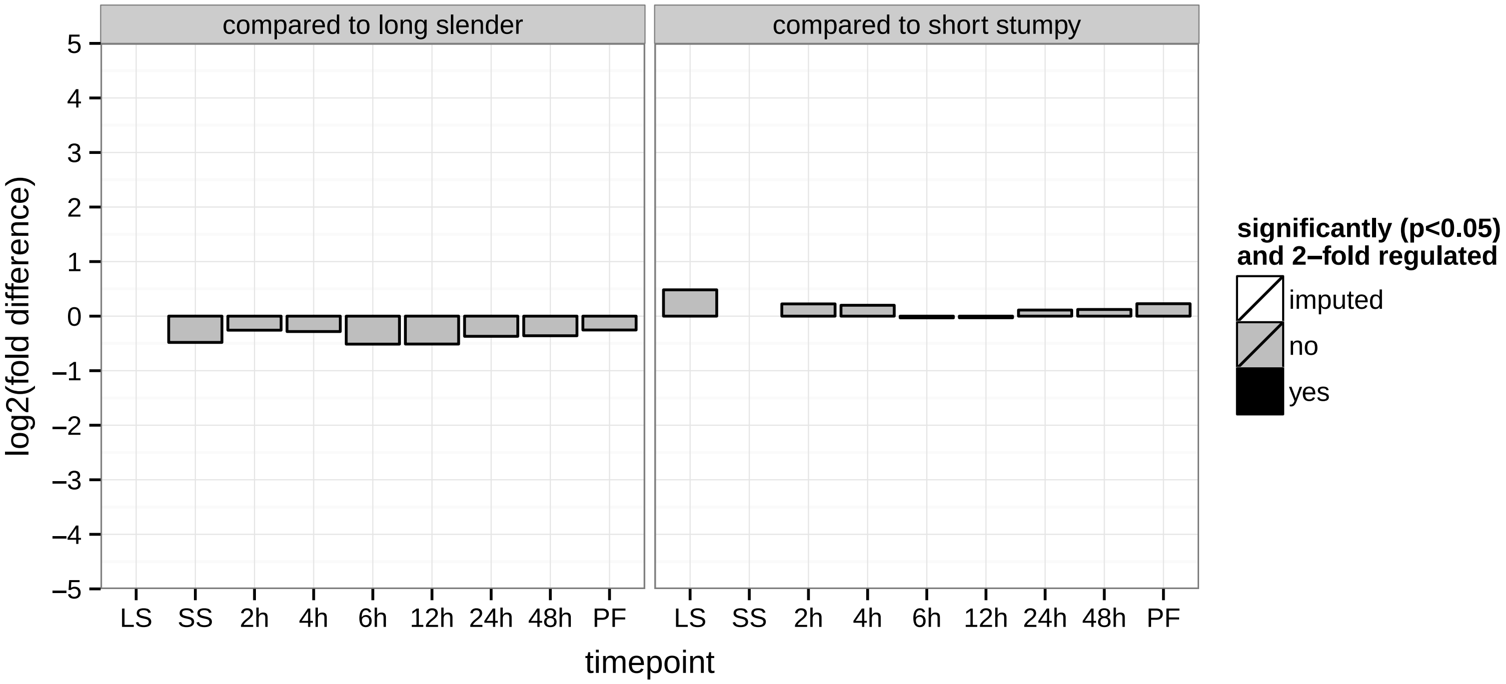
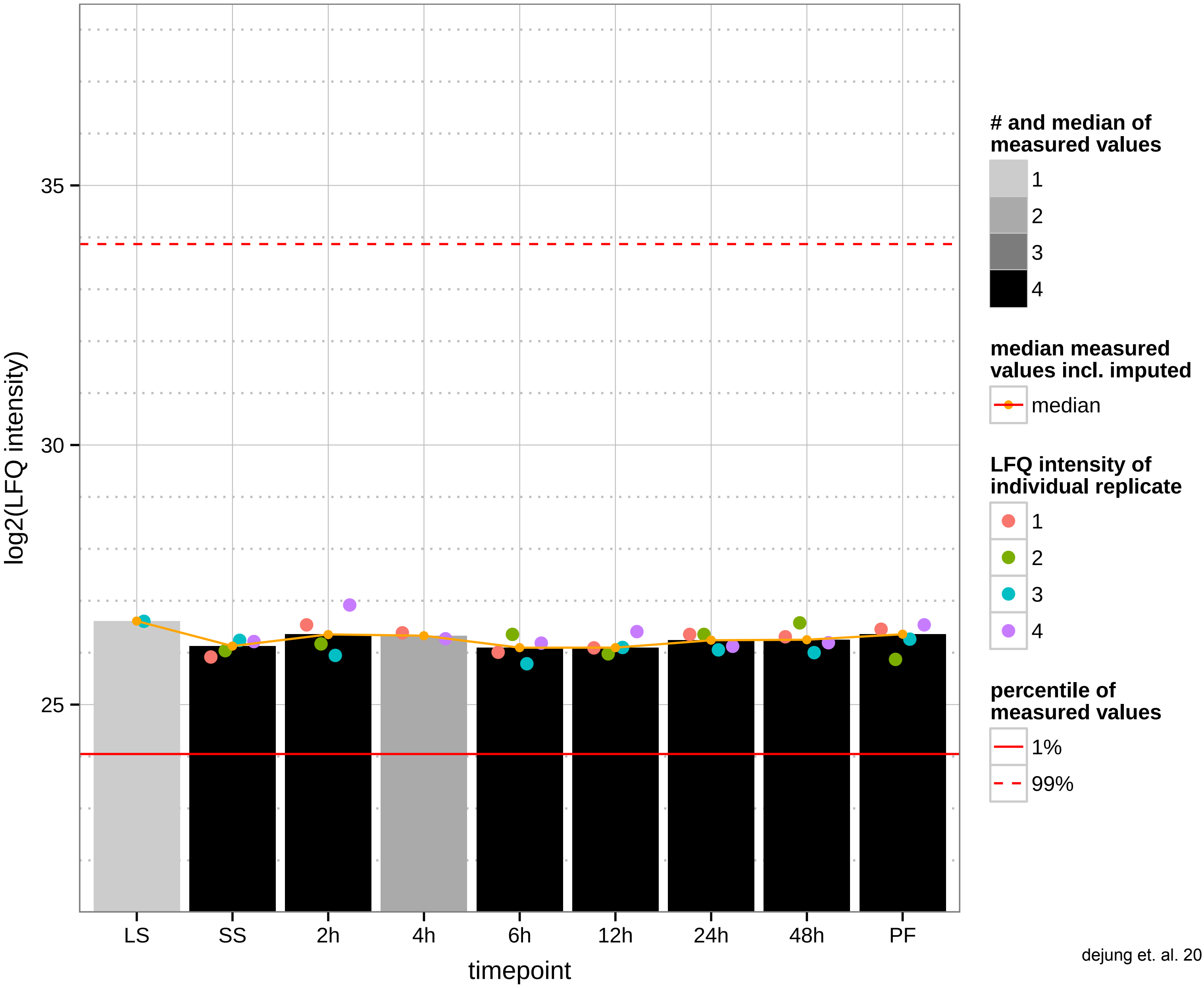
Tob55, putative
Tb927.3.4380
AGOF: null
AGOC: mitochondrial outer membrane
AGOP: cellular protein complex assembly, protein complex assembly
PGOF: null
PGOC: outer membrane
PGOP: null





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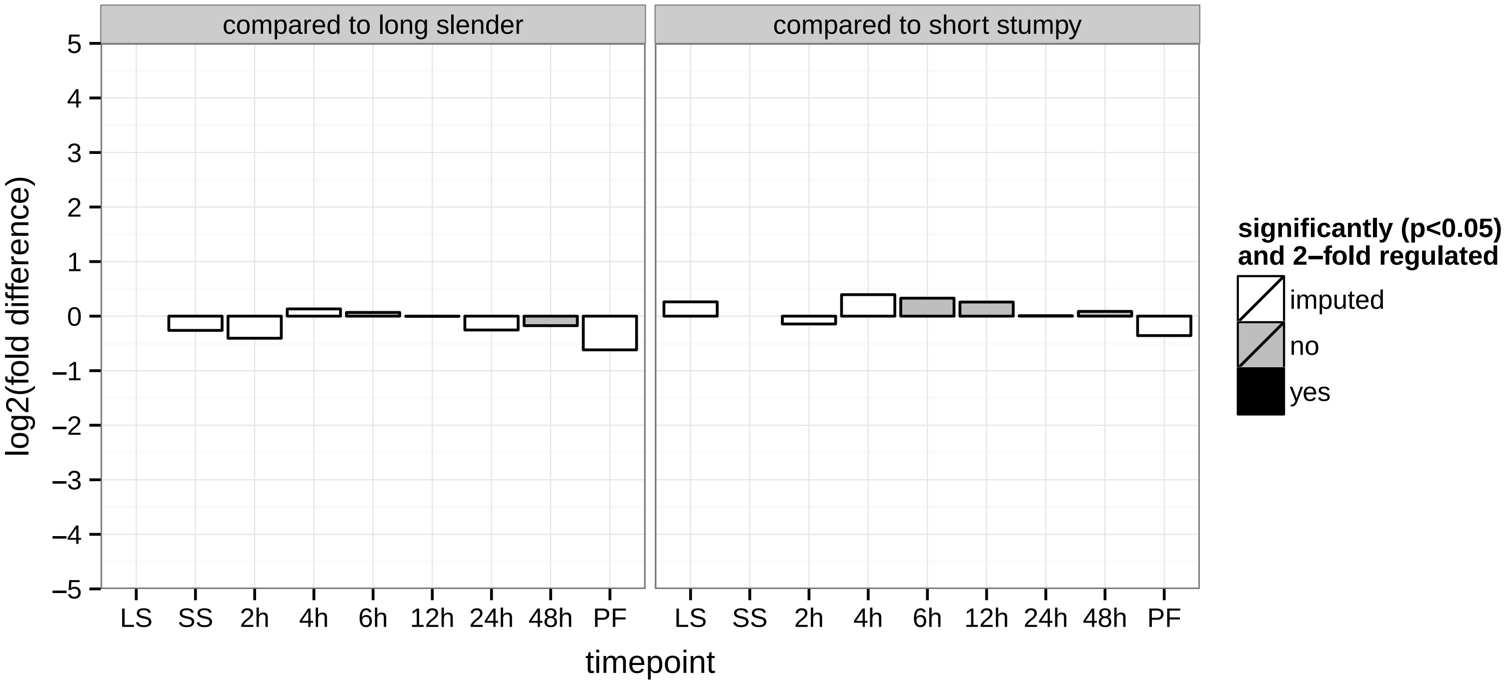
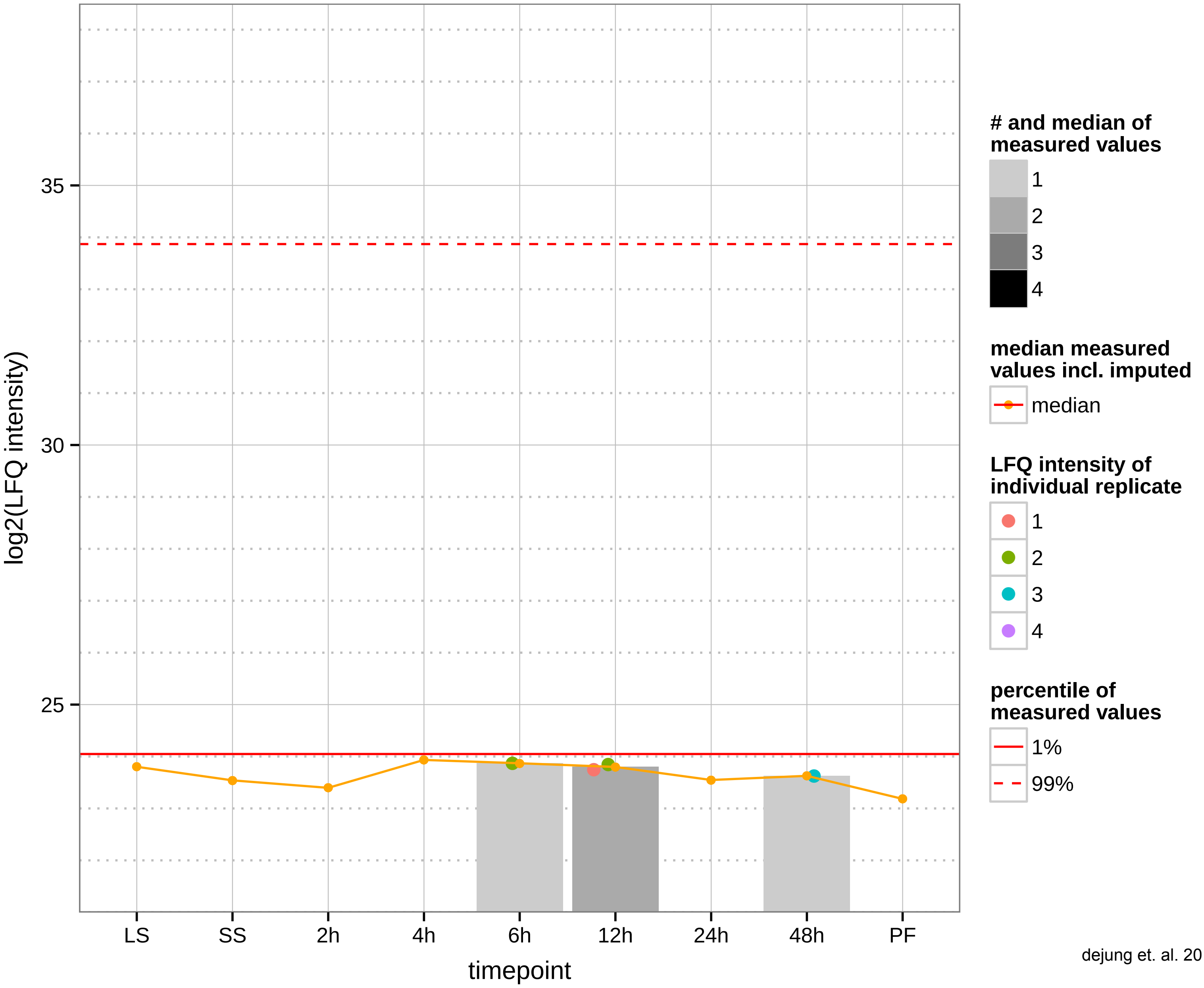
hypothetical protein, conserved
Tb927.3.4550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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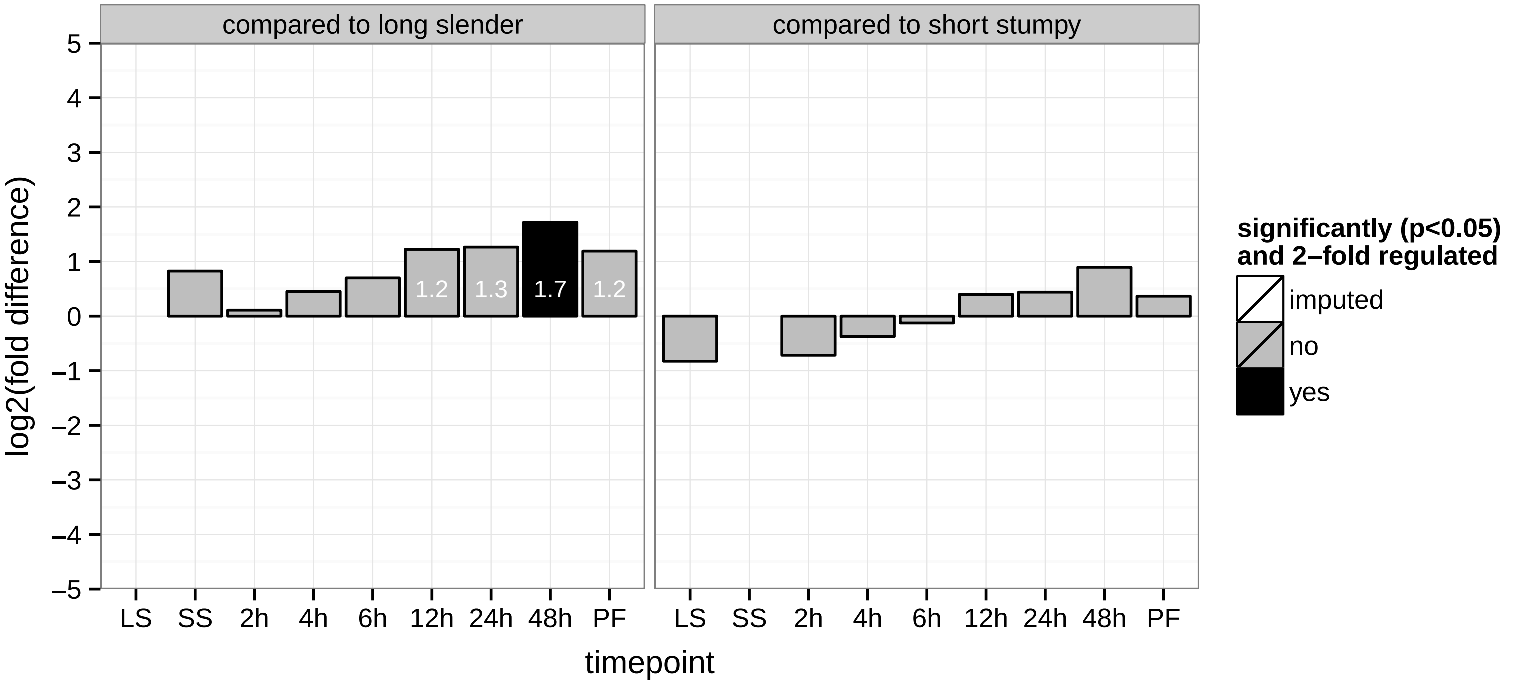
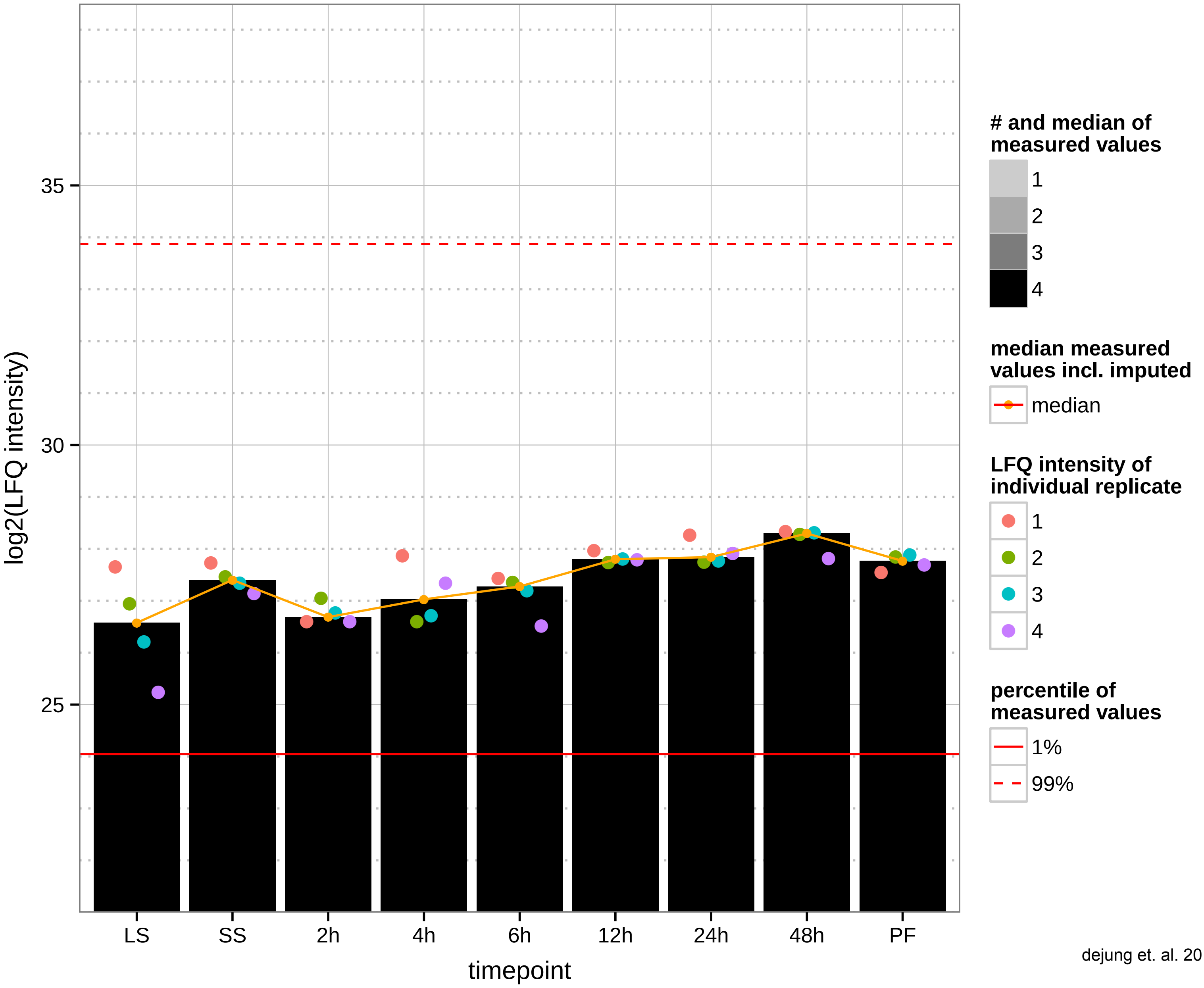
hypothetical protein, conserved
Tb927.3.4600
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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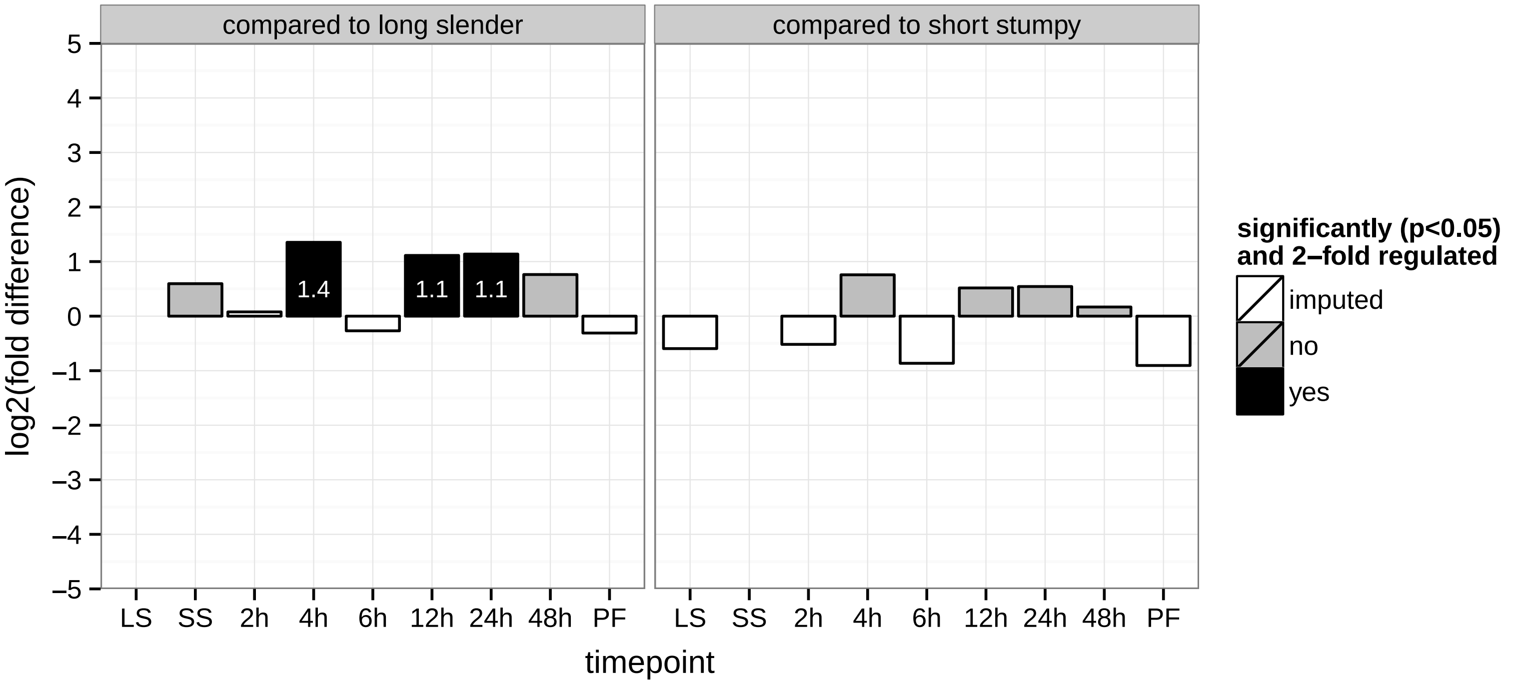
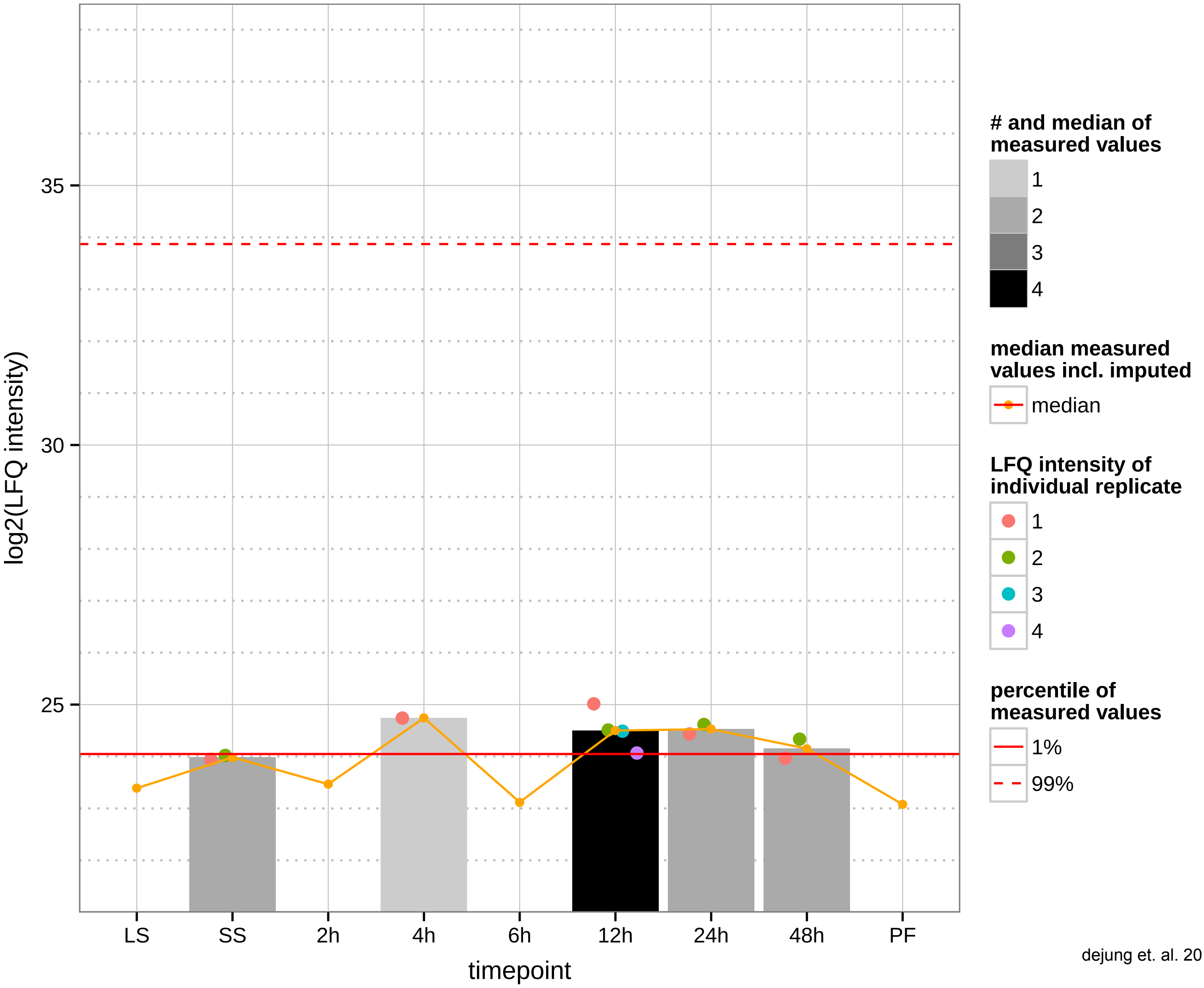
hypothetical protein, conserved
Tb927.3.4640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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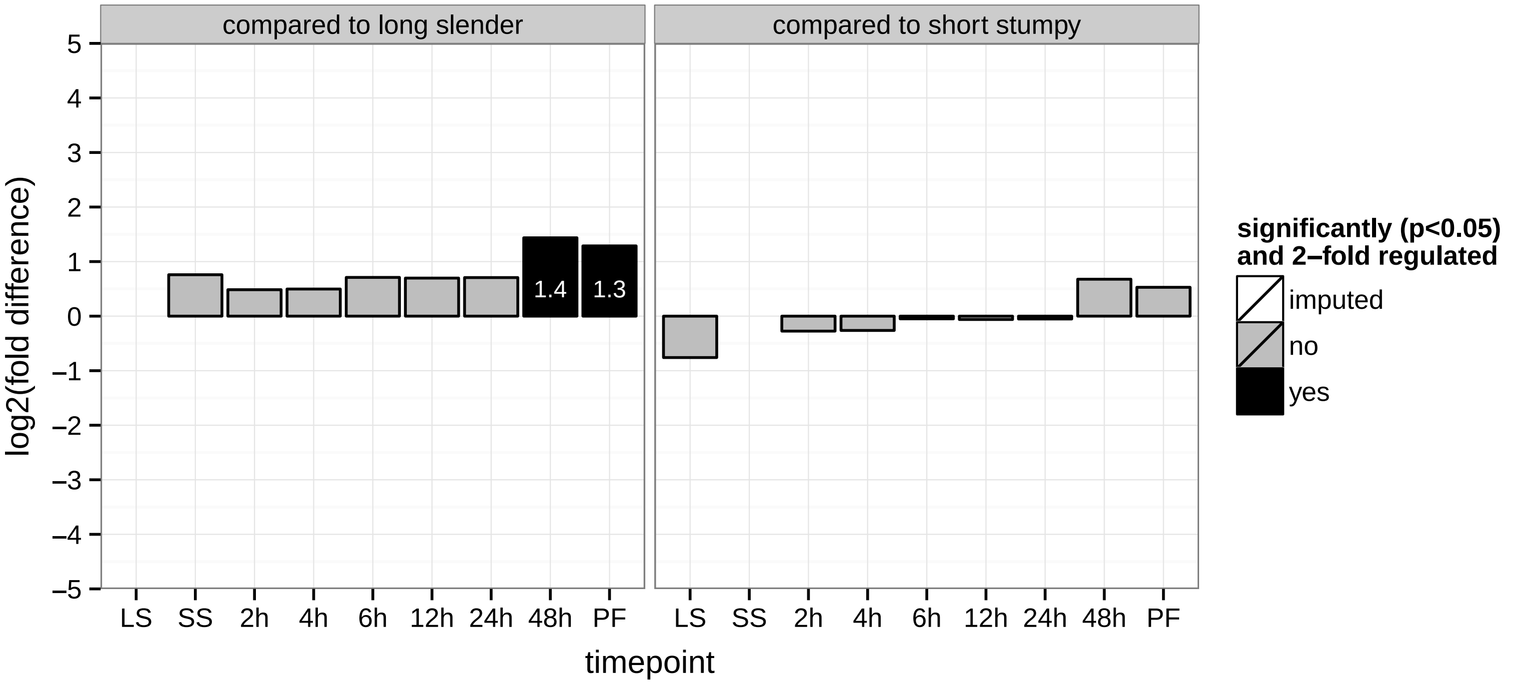
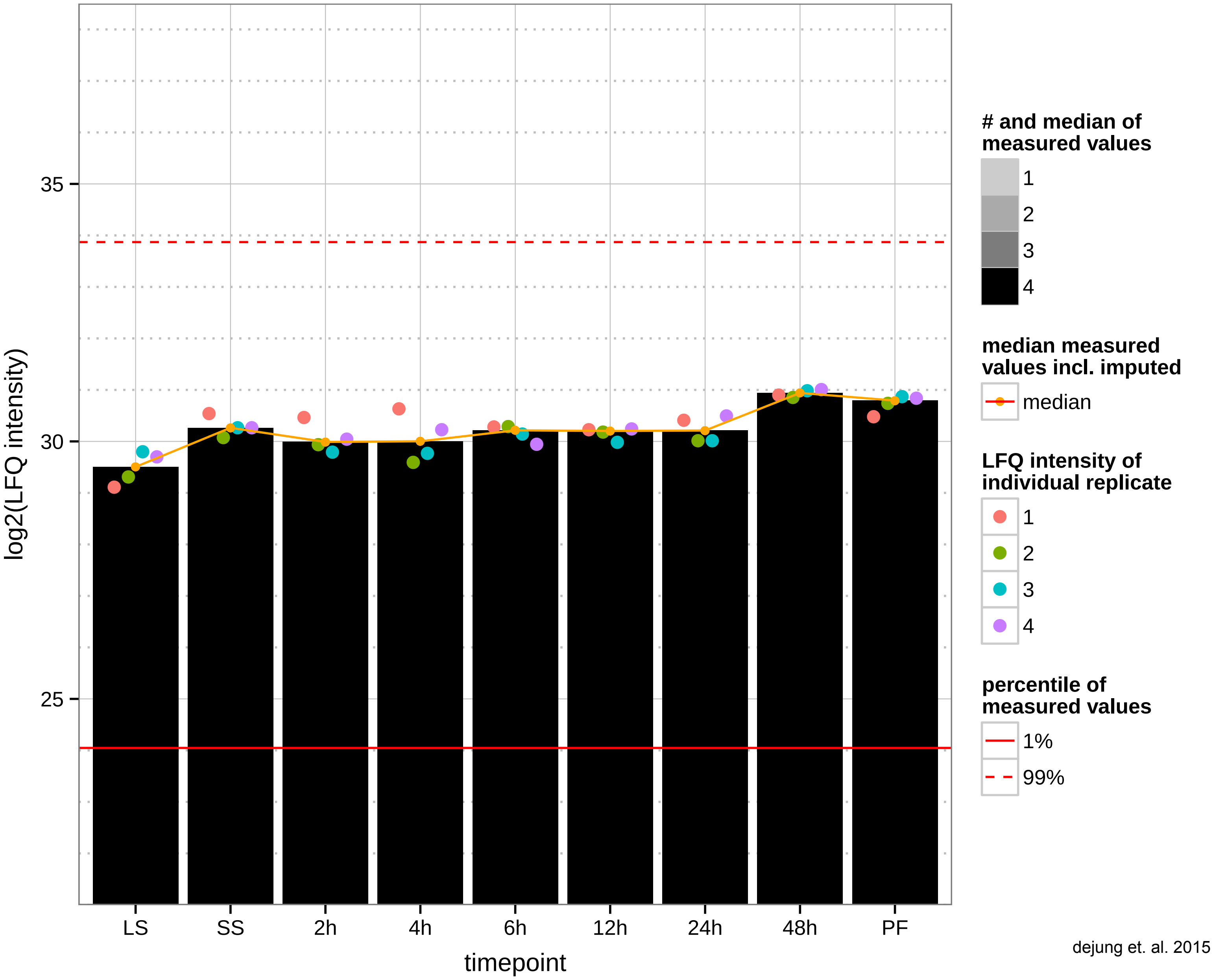
aminopeptidase, putative, metallo–peptidase, Clan MA(E) Family M1
Tb927.3.4790;Tb927.3.4750
AGOF: metallopeptidase activity, zinc ion binding
AGOC: null
AGOP: proteolysis
PGOF: metallopeptidase activity, zinc ion binding
PGOC: null
PGOP: null





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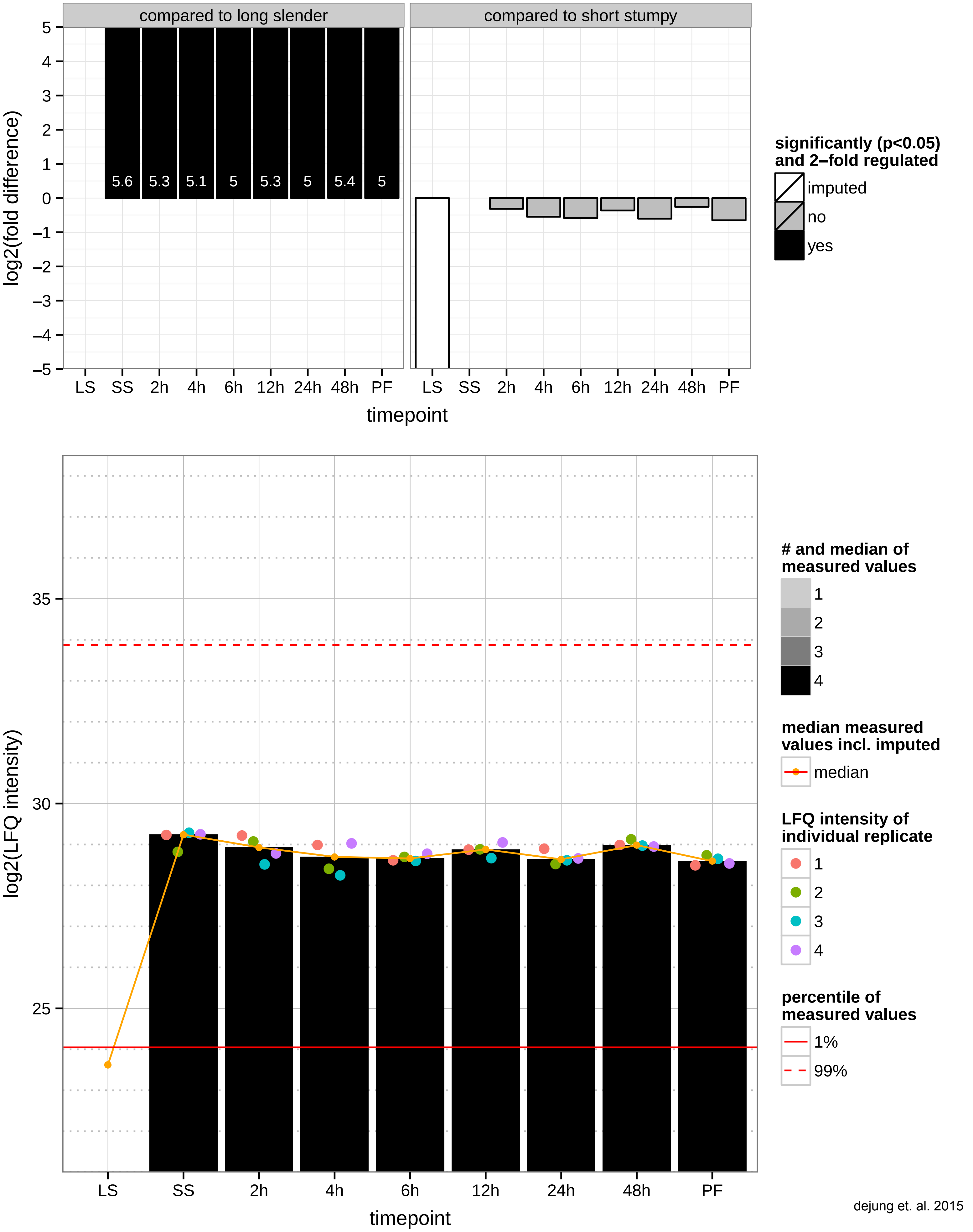
dynamin, putative, vacuolar sortin protein 1
Tb927.3.4760
AGOF: GTP binding, GTPase activity
AGOC: null
AGOP: null
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null



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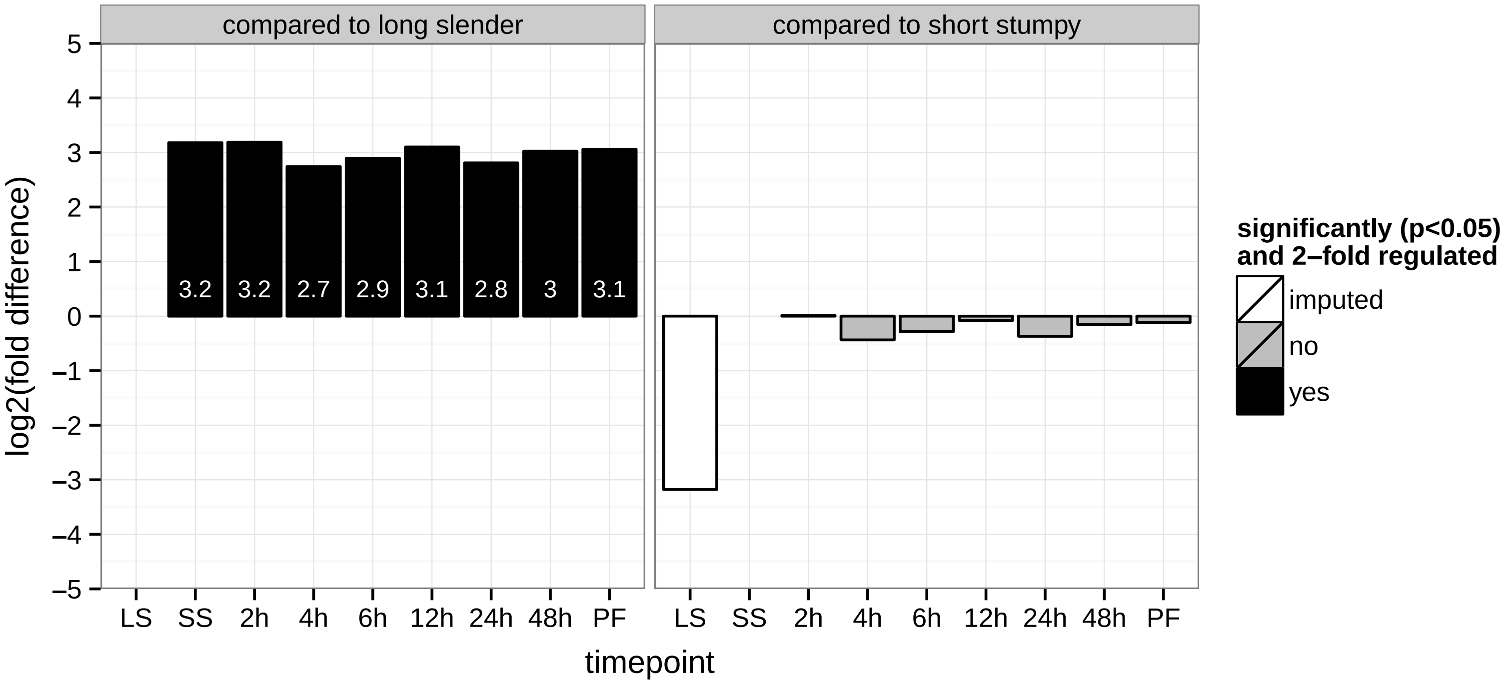
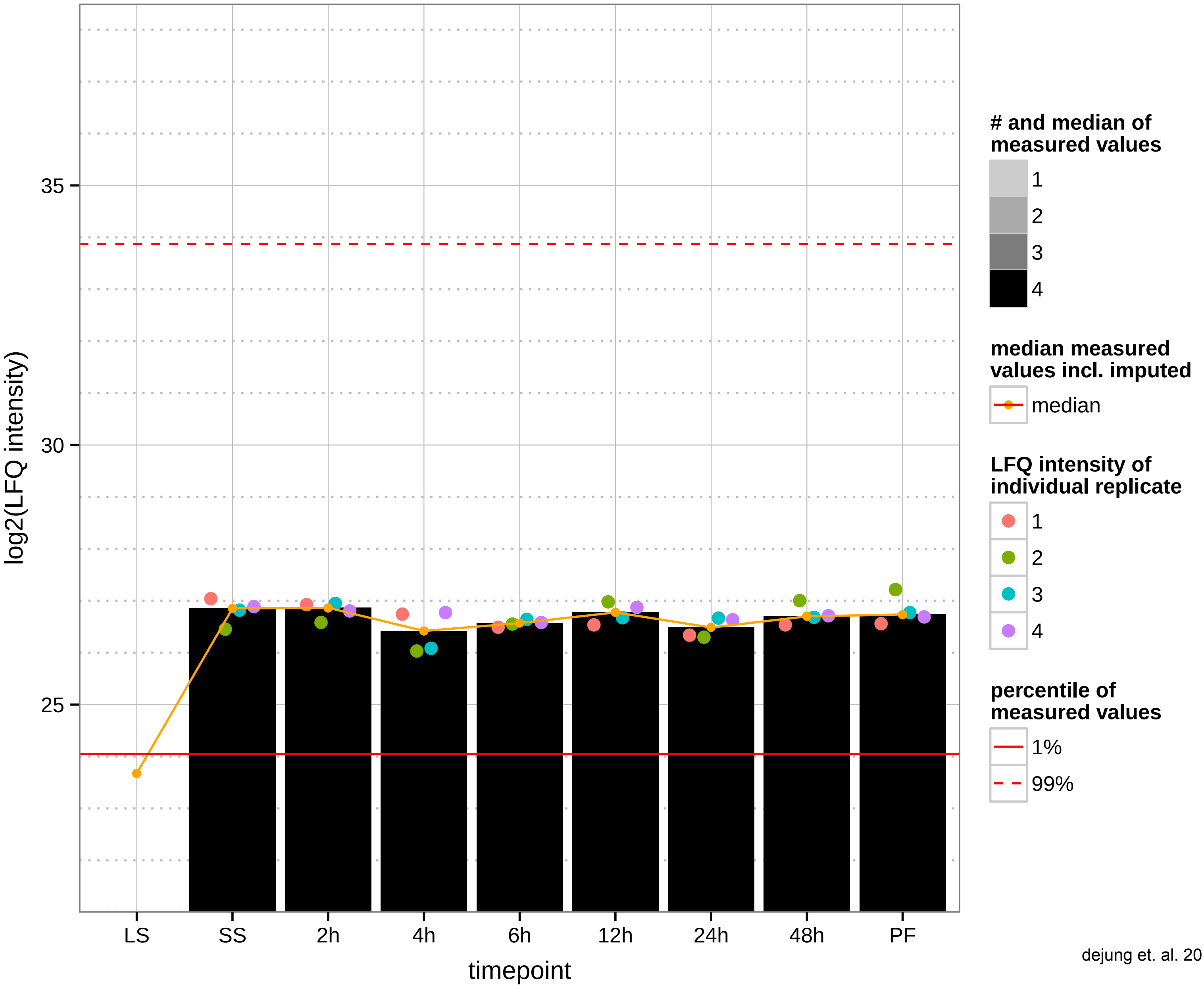
acyltransferase, putative
Tb927.3.4820
AGOF: transferase activity, transferring acyl groups
AGOC: null
AGOP: metabolic process
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: metabolic process





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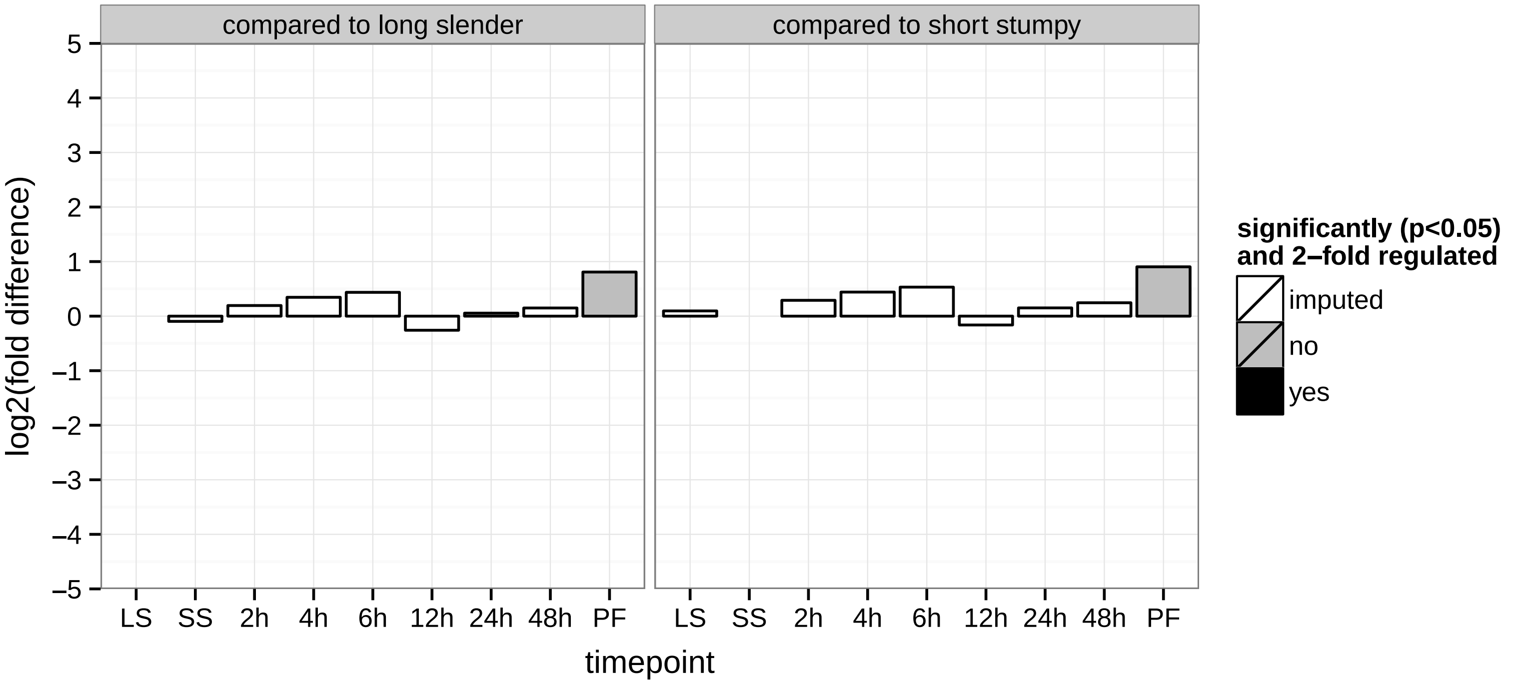
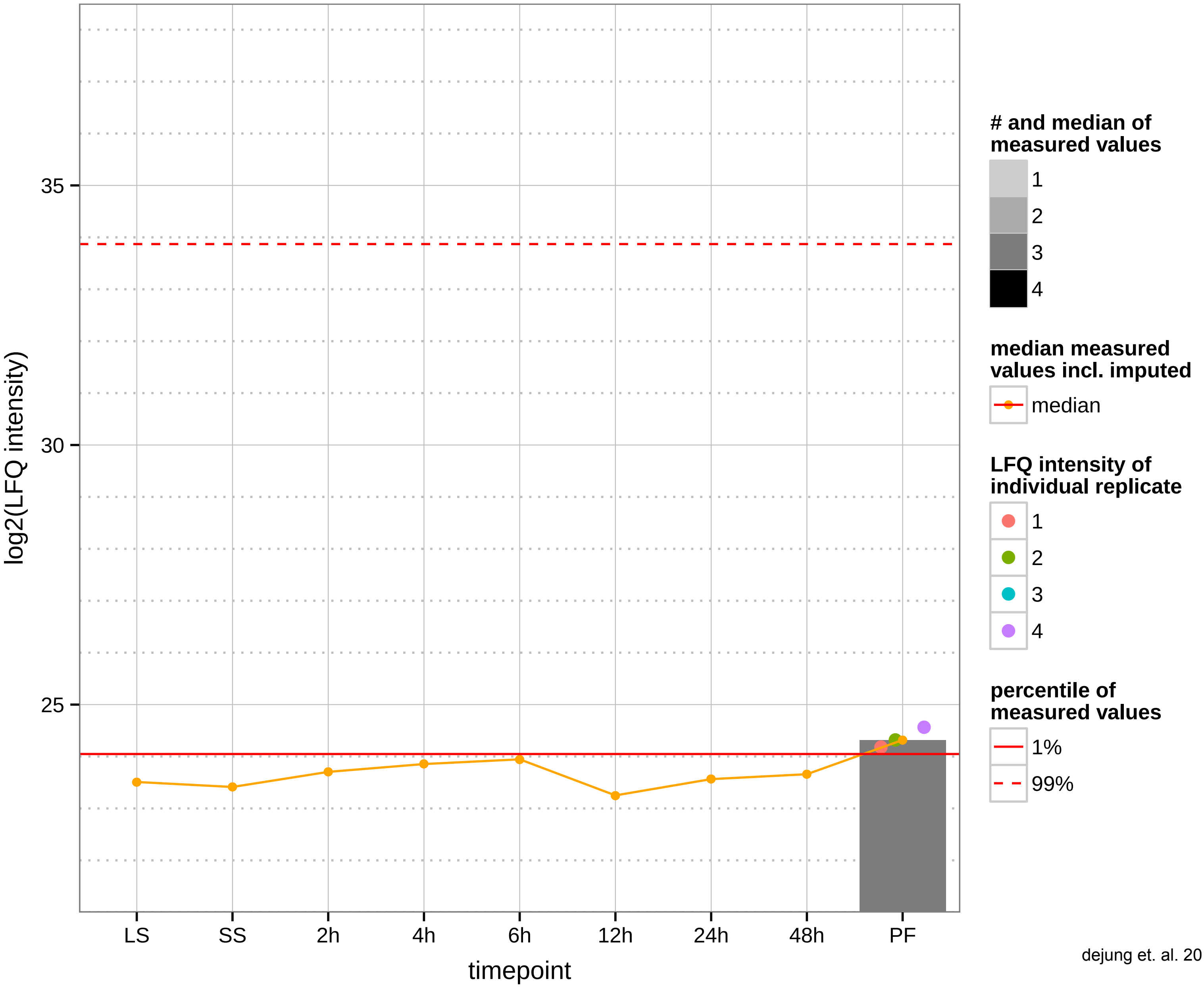
mitogen–activated protein kinase kinase, putative (MKK1)
Tb927.3.4860
AGOF: ATP binding, mitogen–activated protein kinase binding, protein kinase activity, protein serine/threonine kinase activity,
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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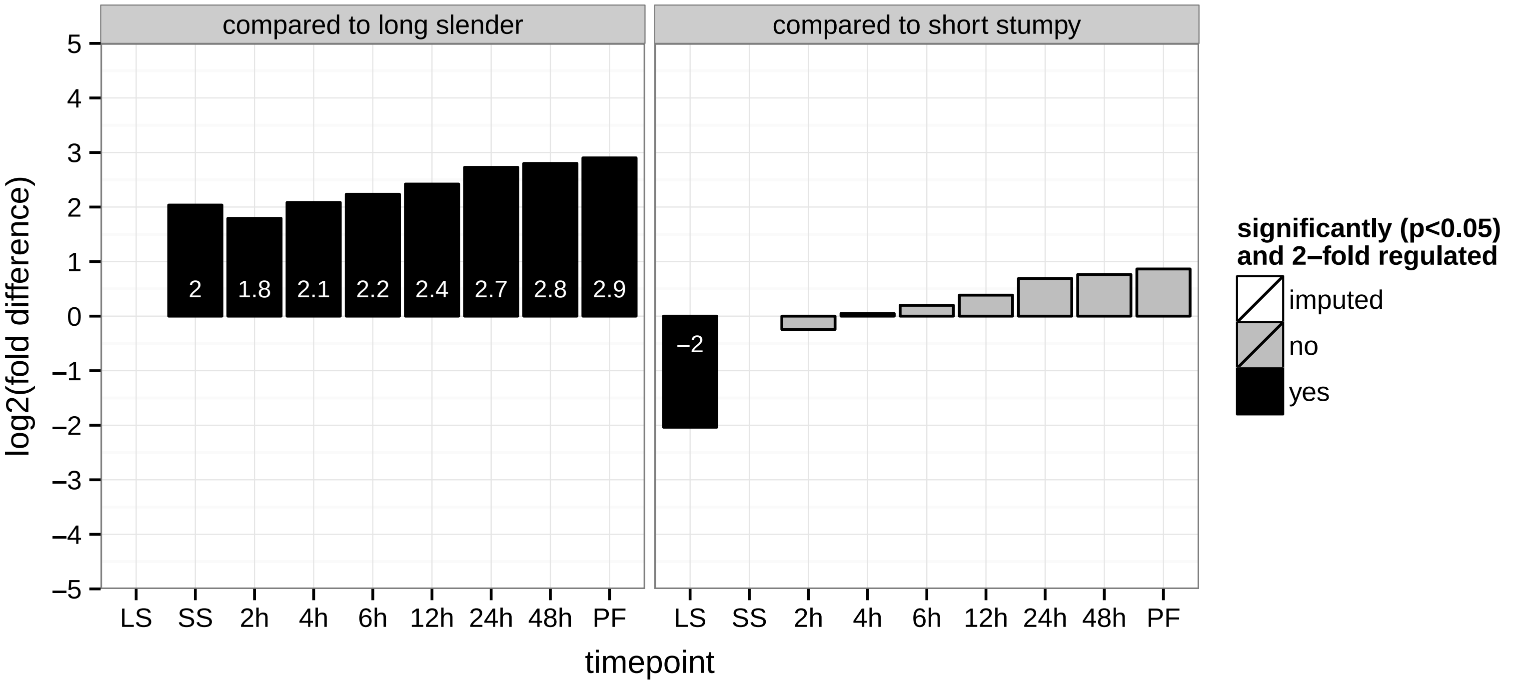
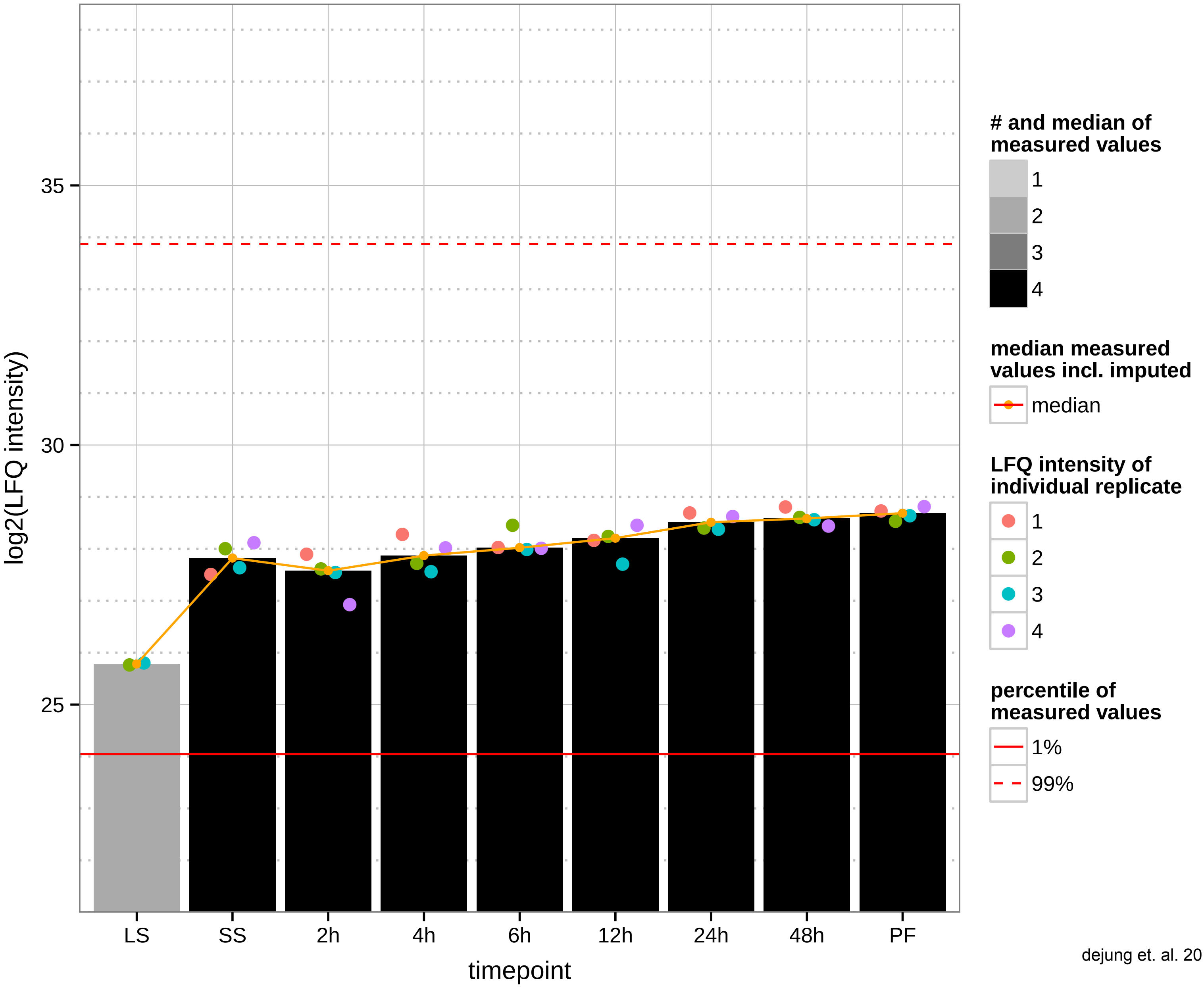
LETM1 and EF−hand domain−containing protein 1, putative
Tb927.3.4920
AGOF: calcium ion binding, calcium:sodium antiporter activity
AGOC: integral to membrane, mitochondrial inner membrane
AGOP: mitochondrial calcium ion transport
PGOF: null
PGOC: null
PGOP: null





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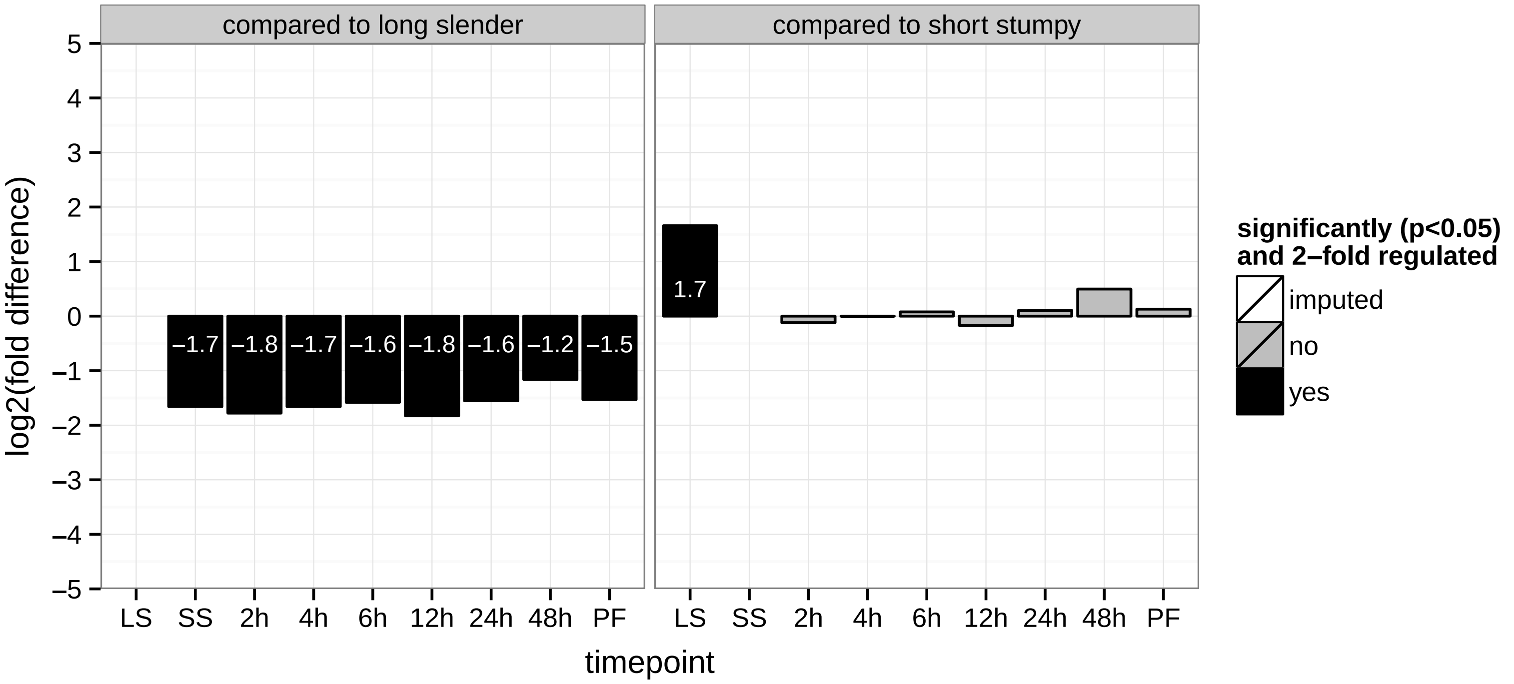
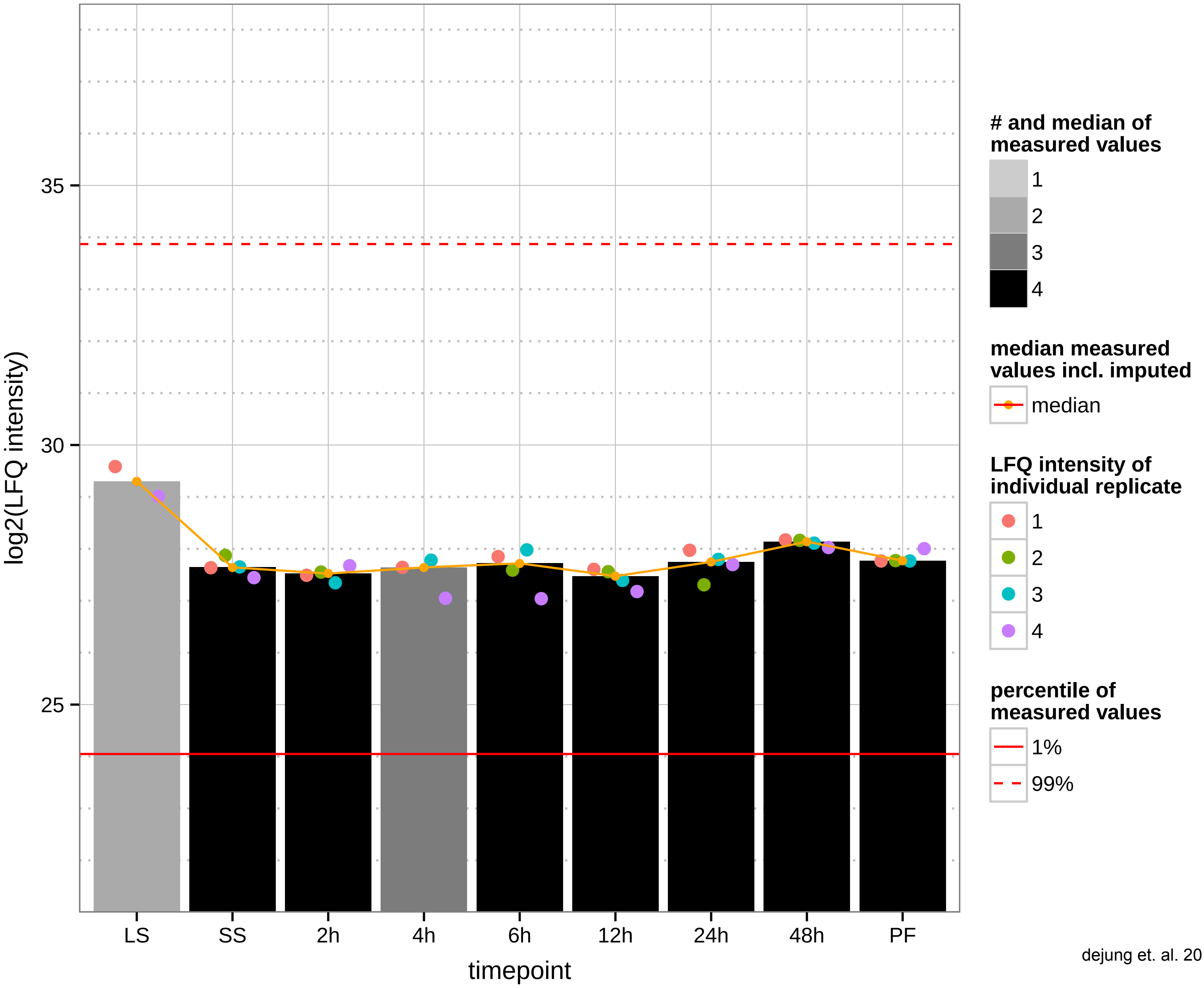
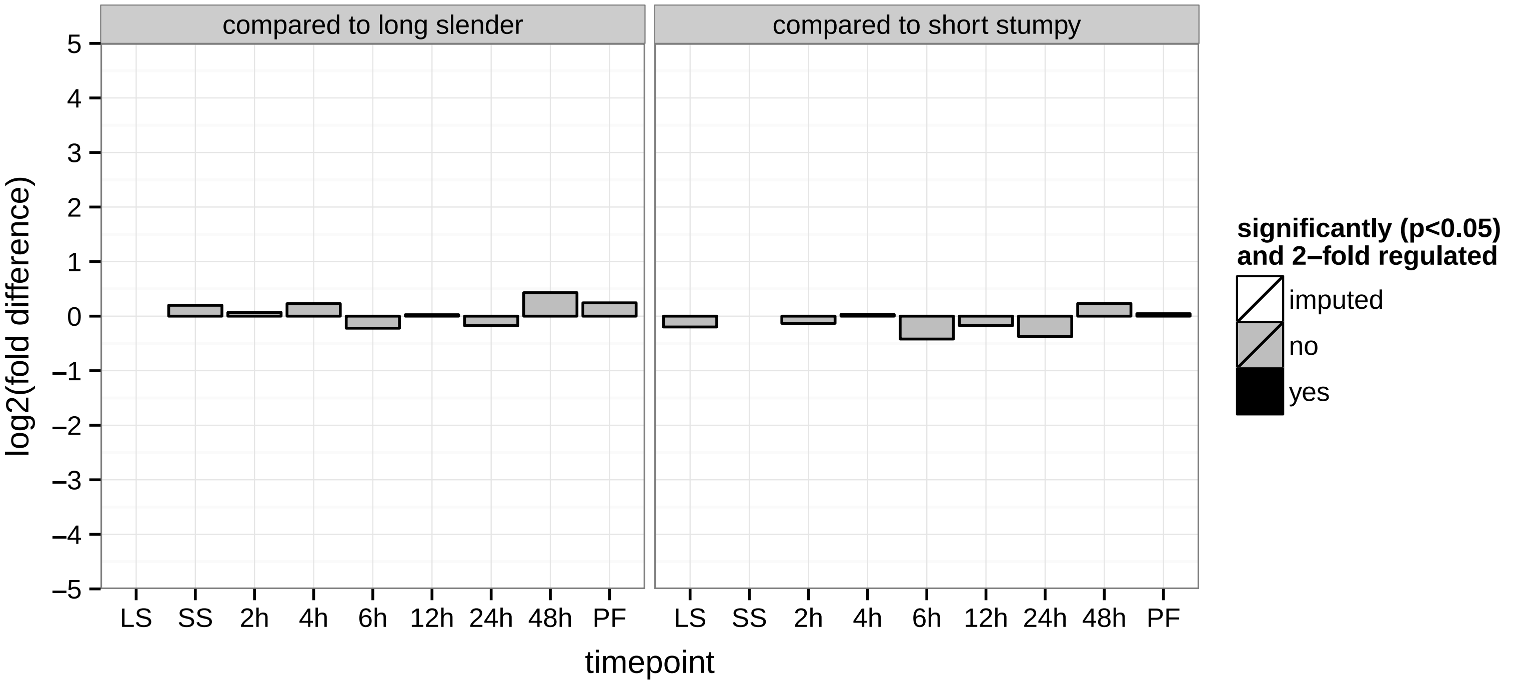
5–histidylcysteine sulfoxide synthase, putative
Tb927.3.4940
AGOF: ferrous iron binding
AGOC: null
AGOP: peptidyl–cysteine oxidation, response to iron(II) ion
PGOF: null
PGOC: null
PGOP: null

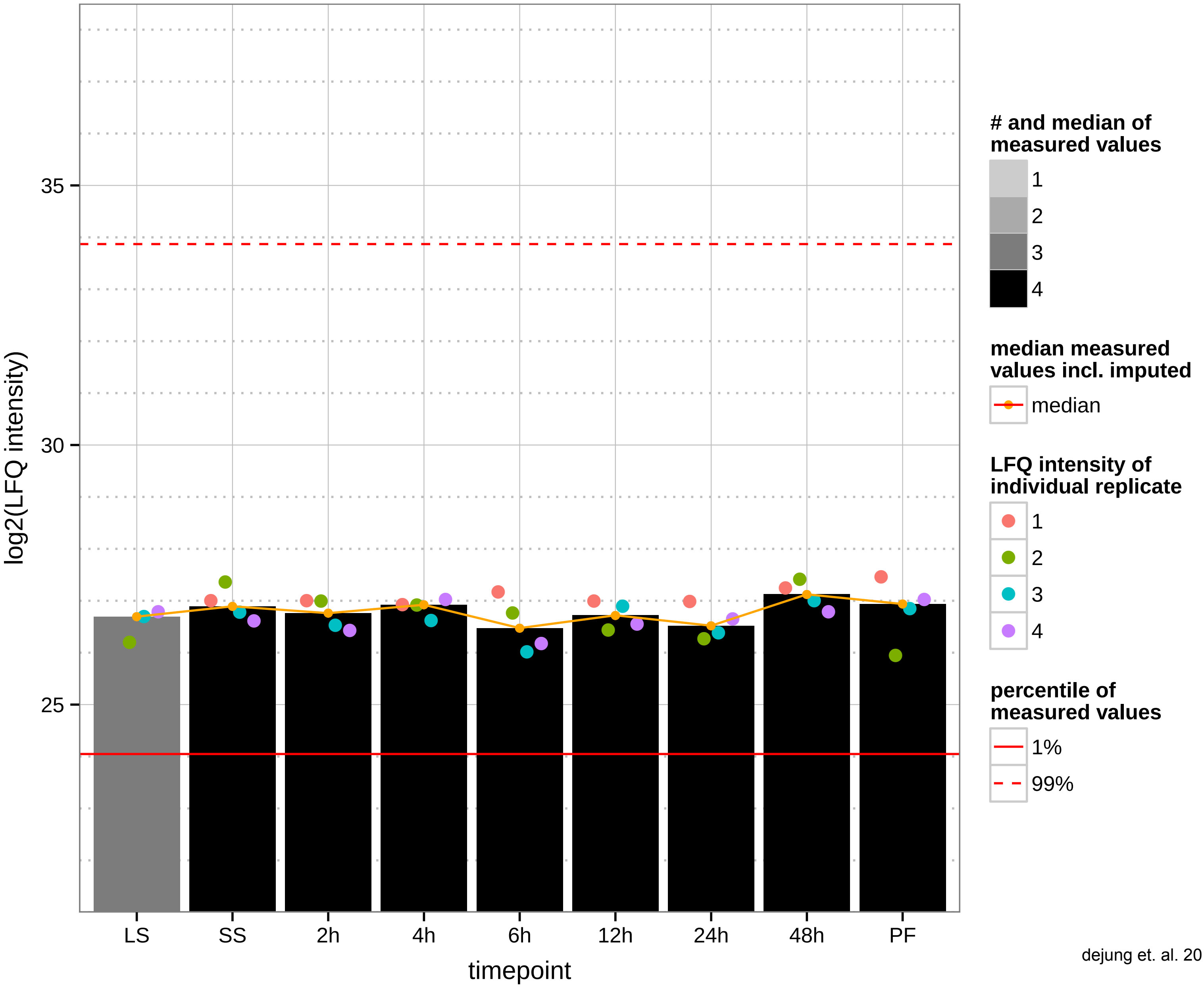




dejung et. al. 2015

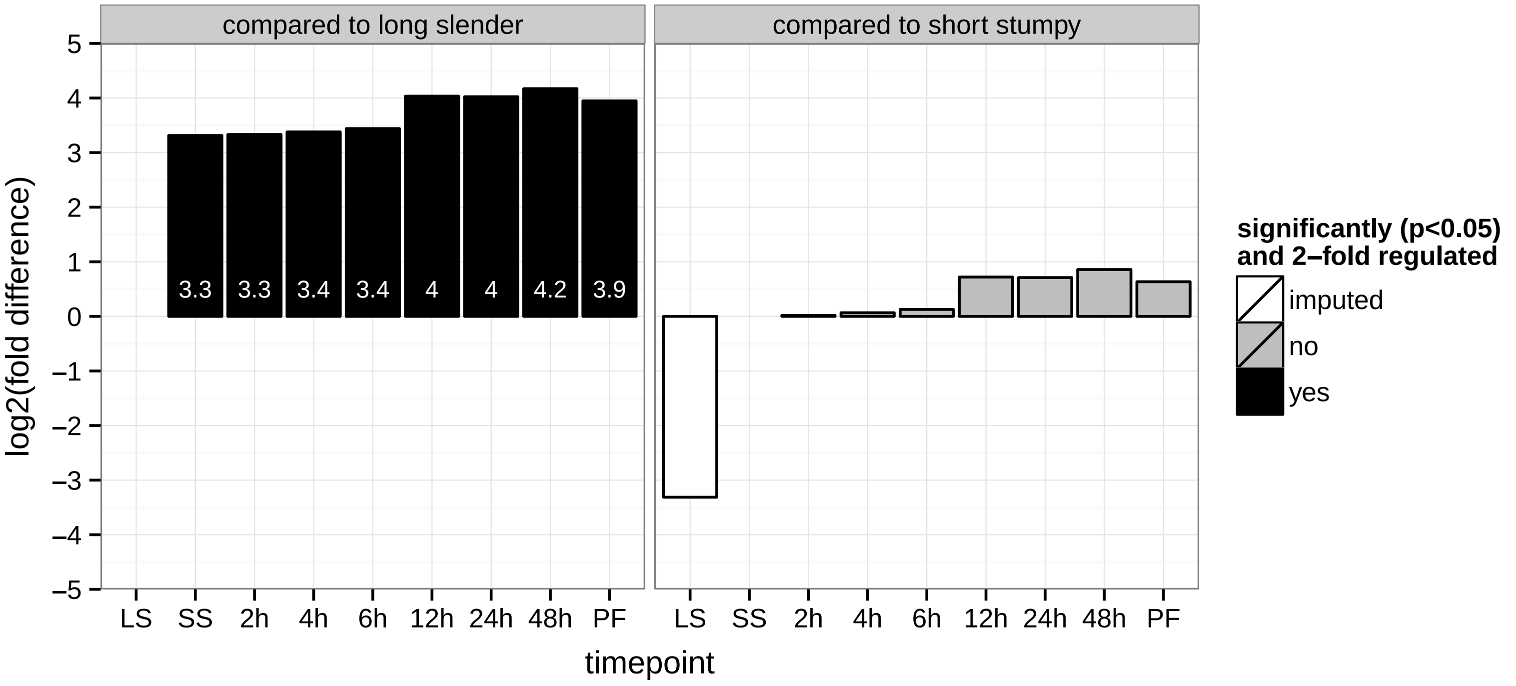
hypothetical protein, conserved
Tb927.3.4970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

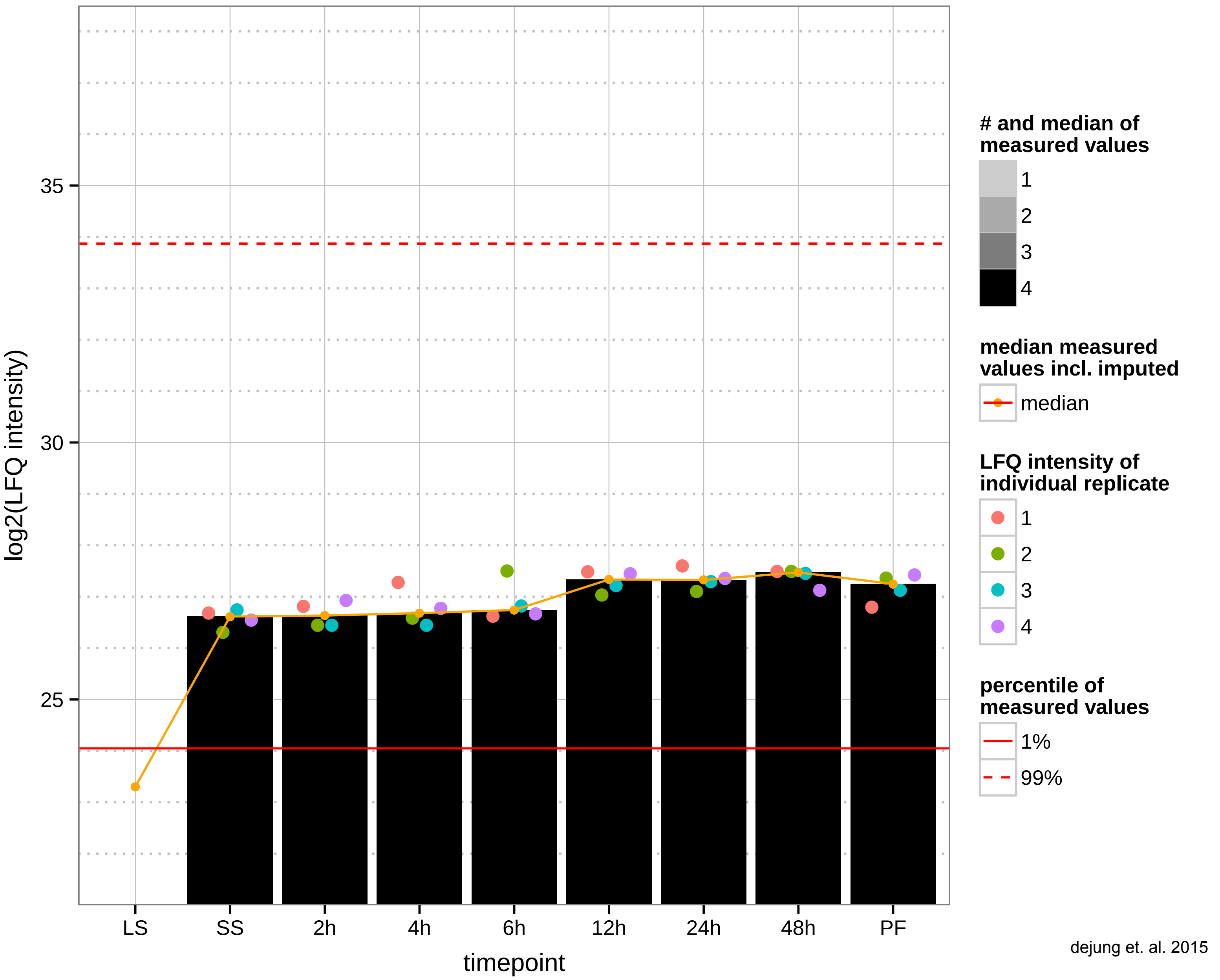




dejung et. al. 2015

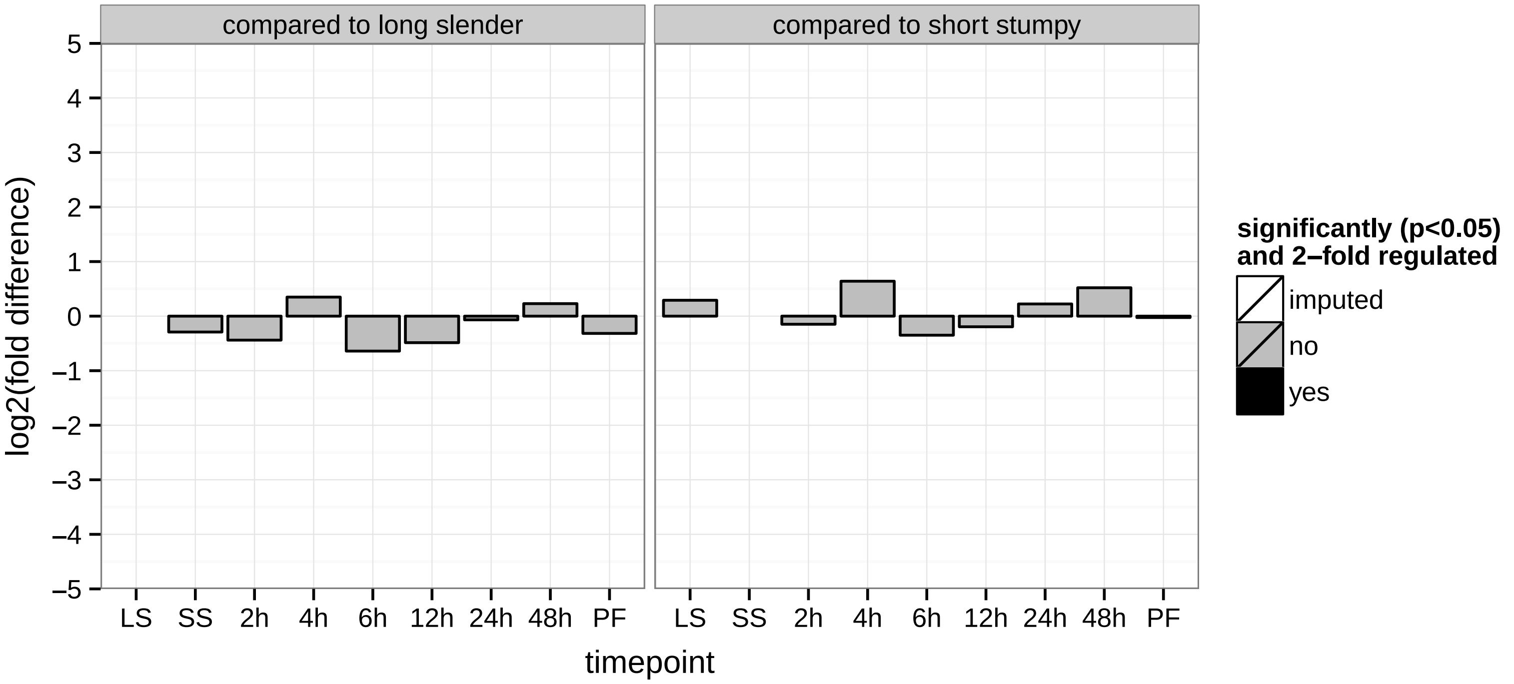
oxidoreductase, putative
Tb927.3.4990
AGOF: oxidoreductase activity, zinc ion binding
AGOC: null
AGOP: metabolic process, oxidation–reduction process
PGOF: oxidoreductase activity, transferase activity, transferring acyl groups other than amino–acyl groups, zinc ion binding
PGOC: null
PGOP: oxidation–reduction process

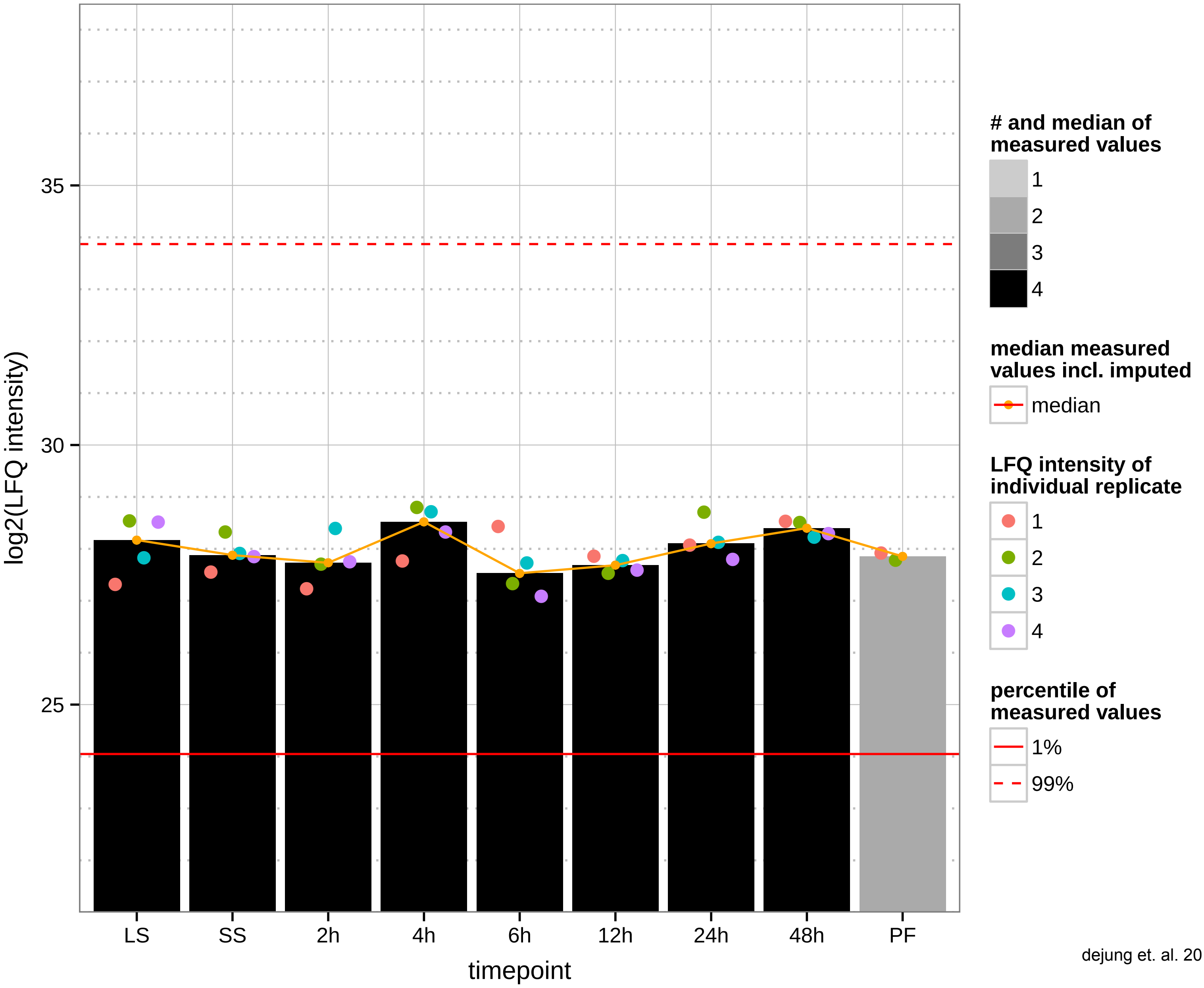




dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.5010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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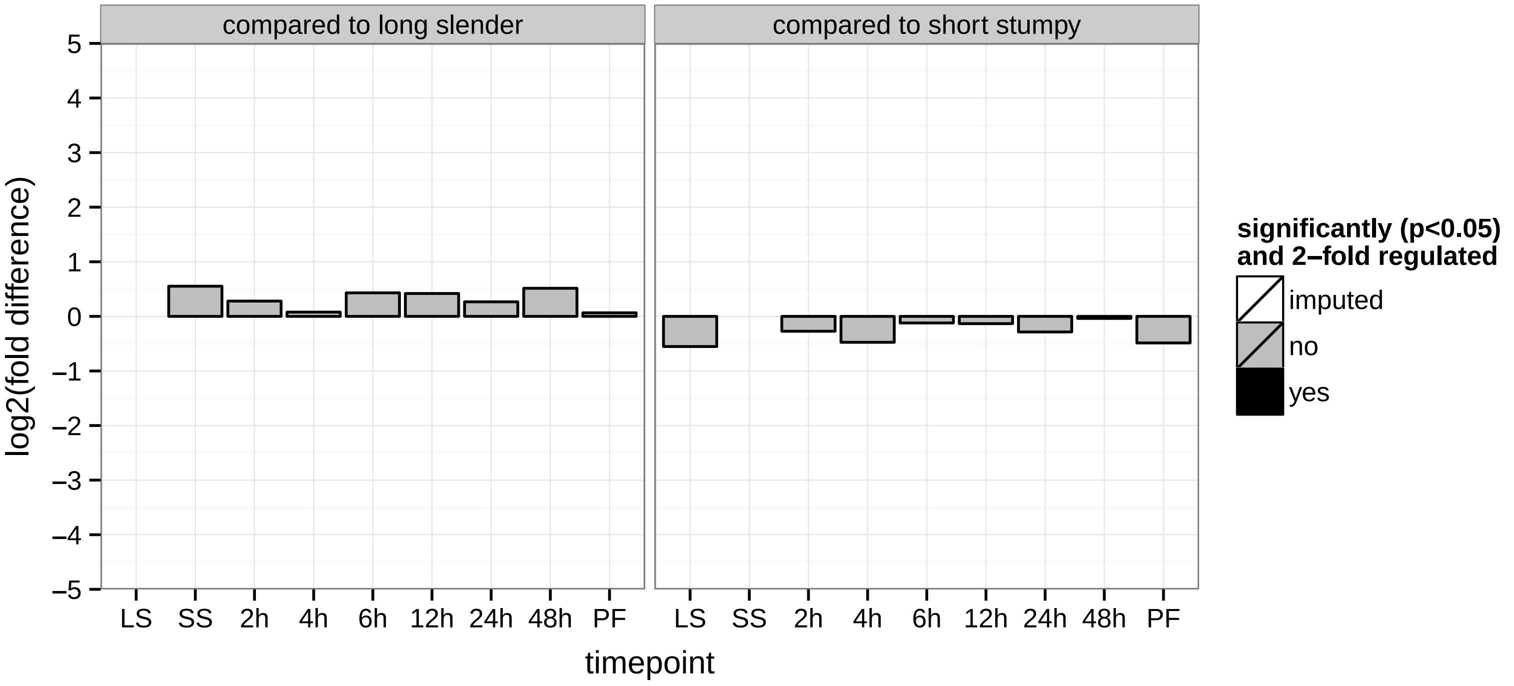
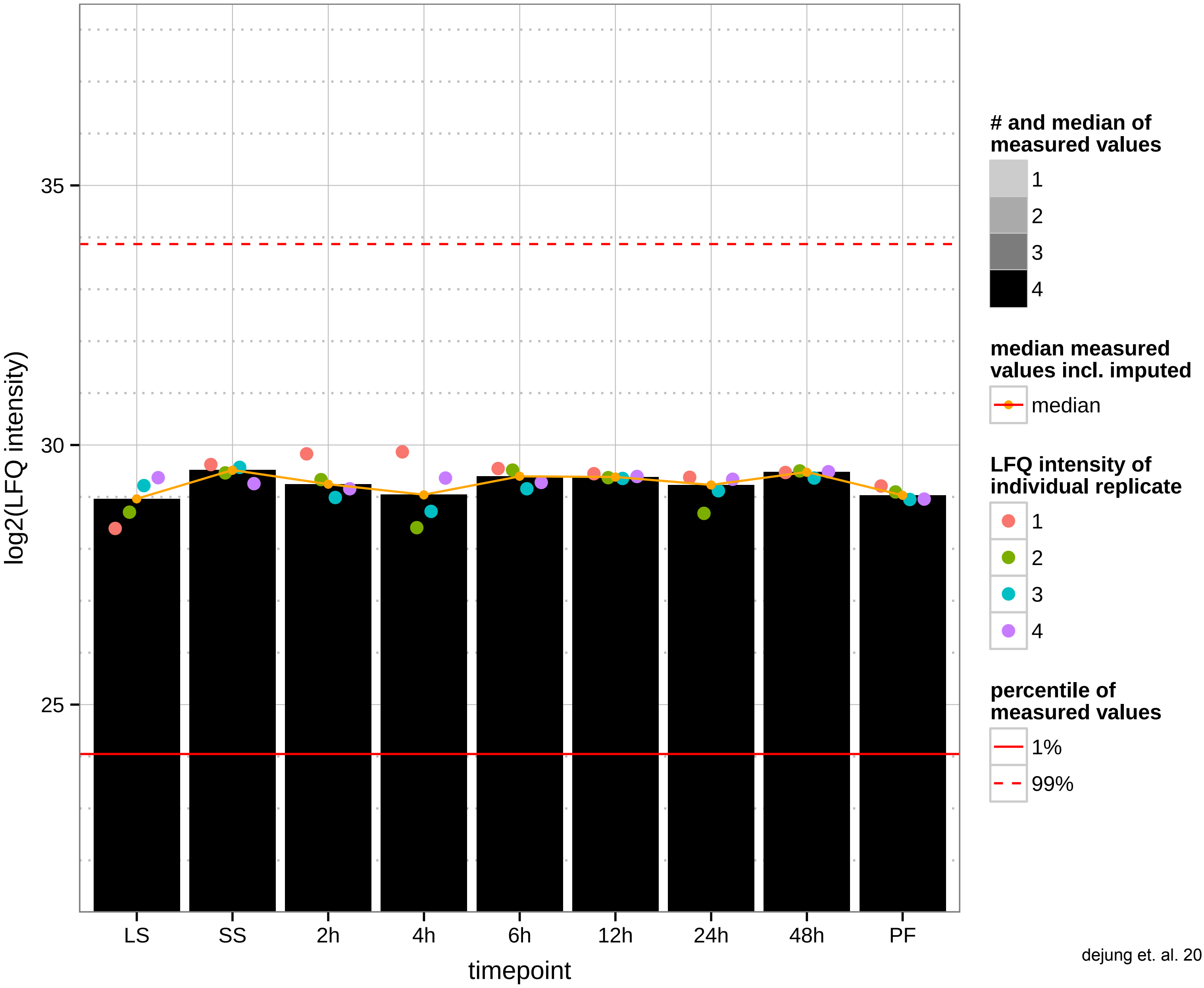
hypothetical protein, conserved
Tb927.3.5020
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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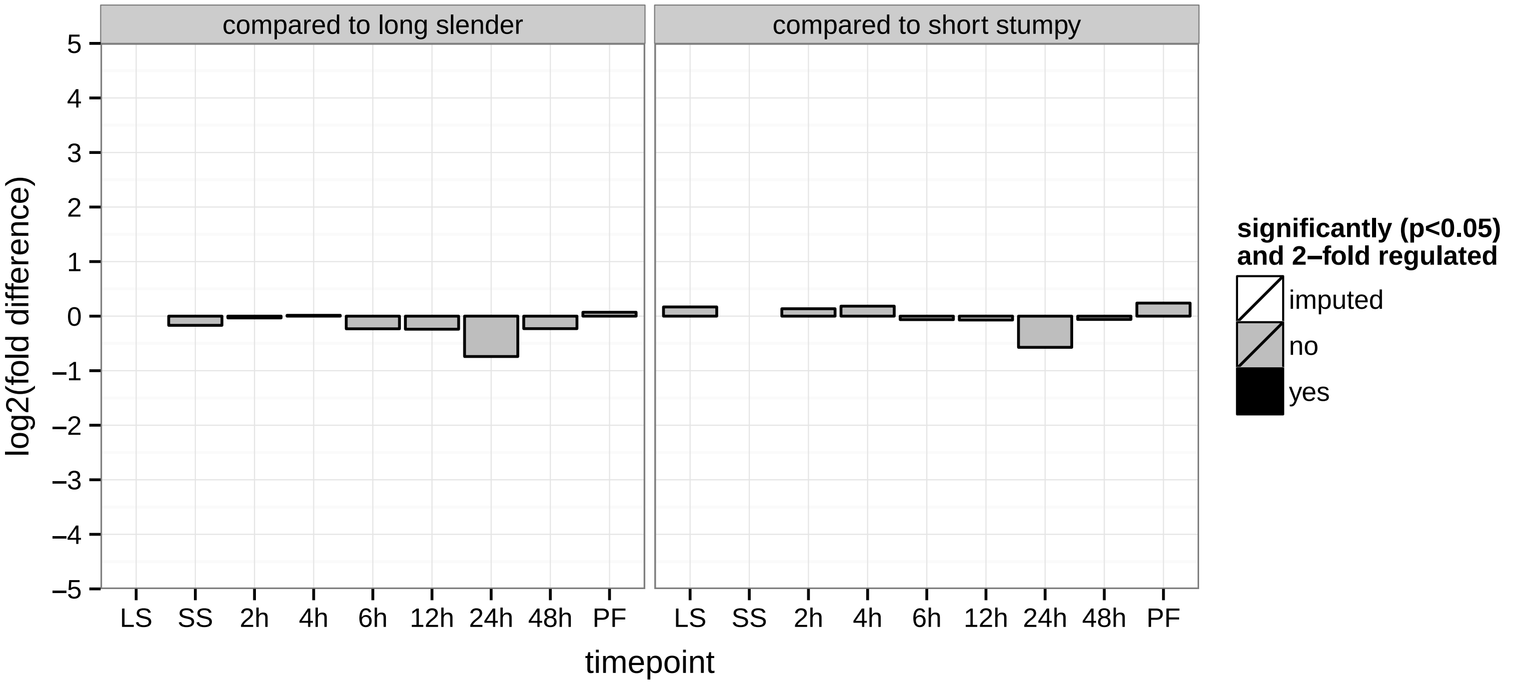
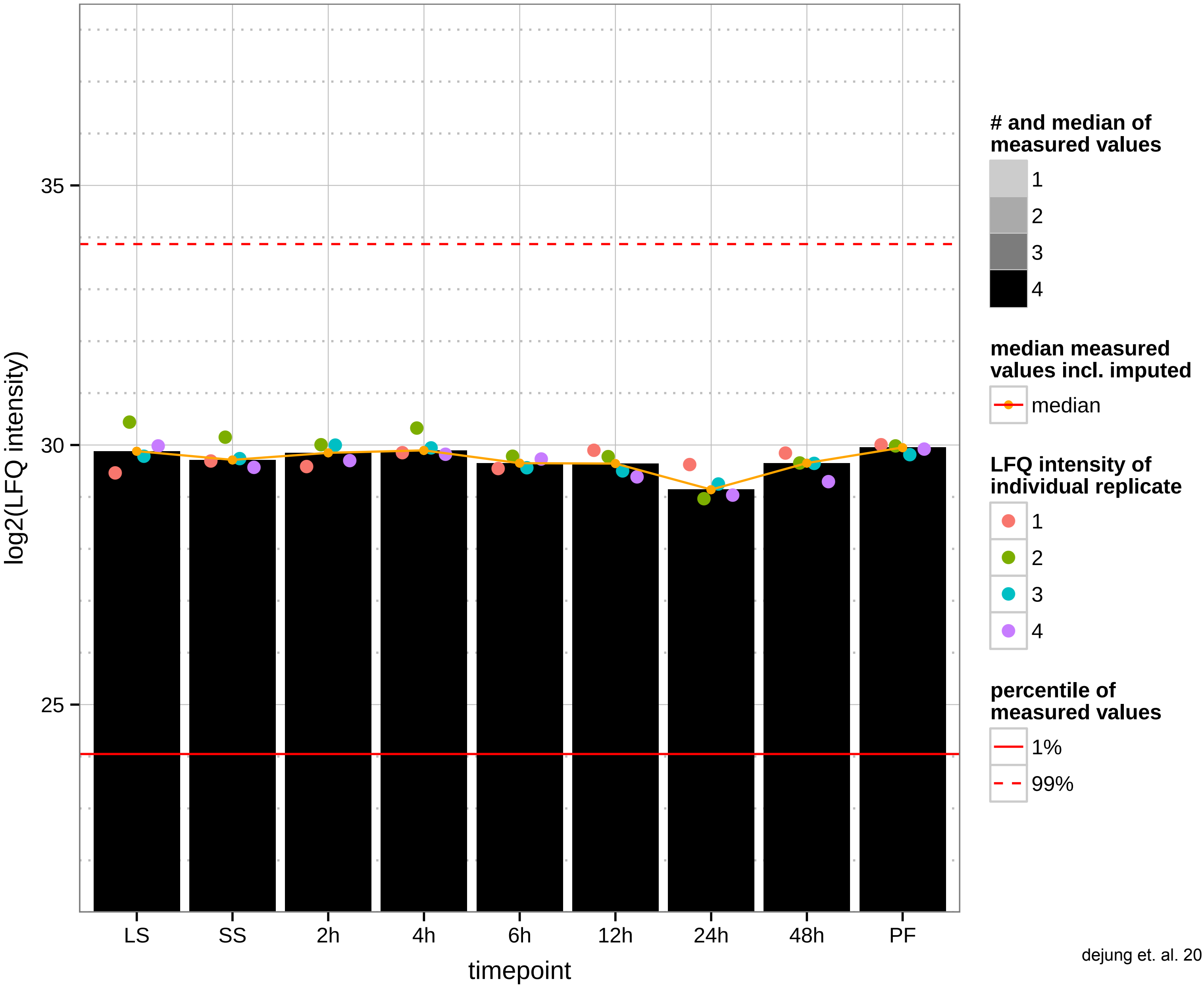
hypothetical protein, conserved
Tb927.3.5060
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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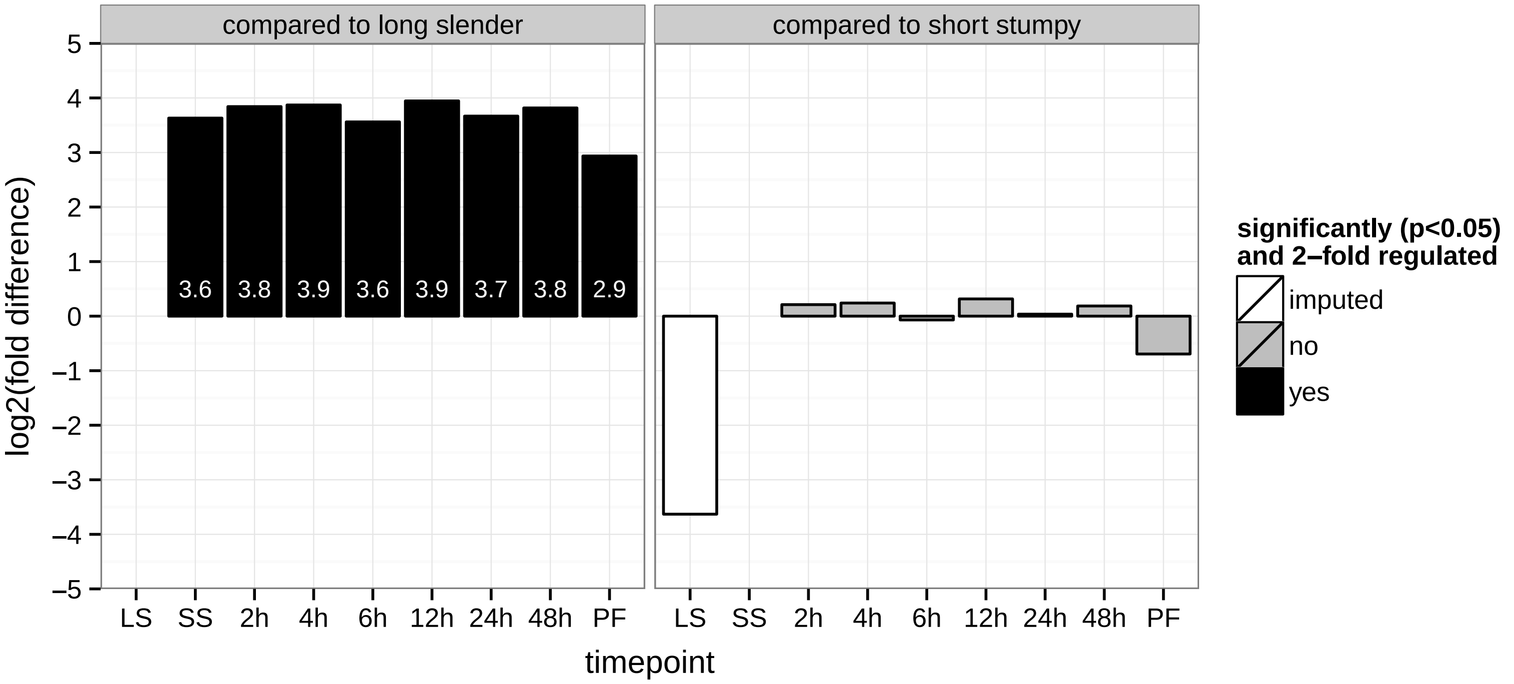
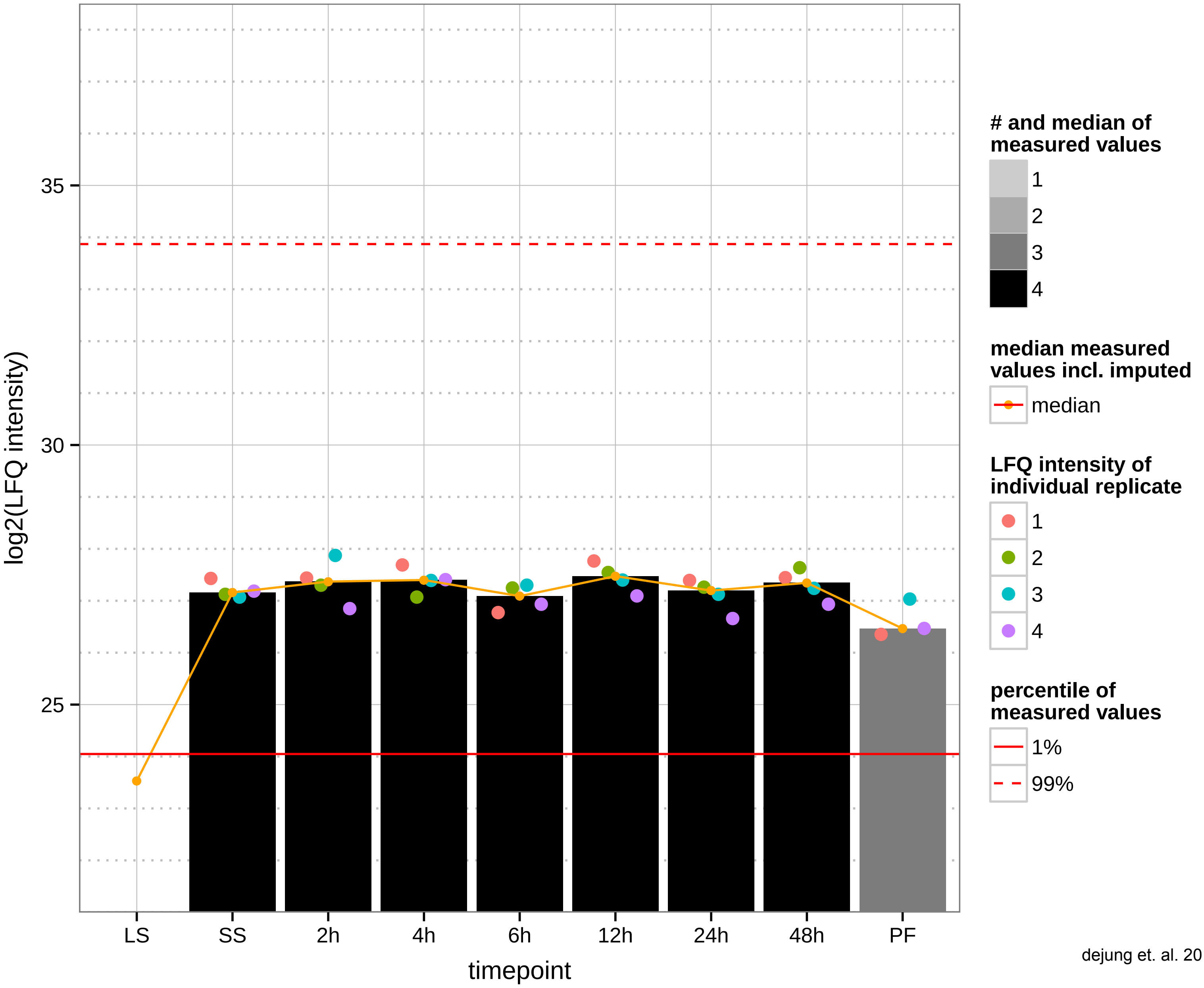
hypothetical protein, conserved
Tb927.3.5070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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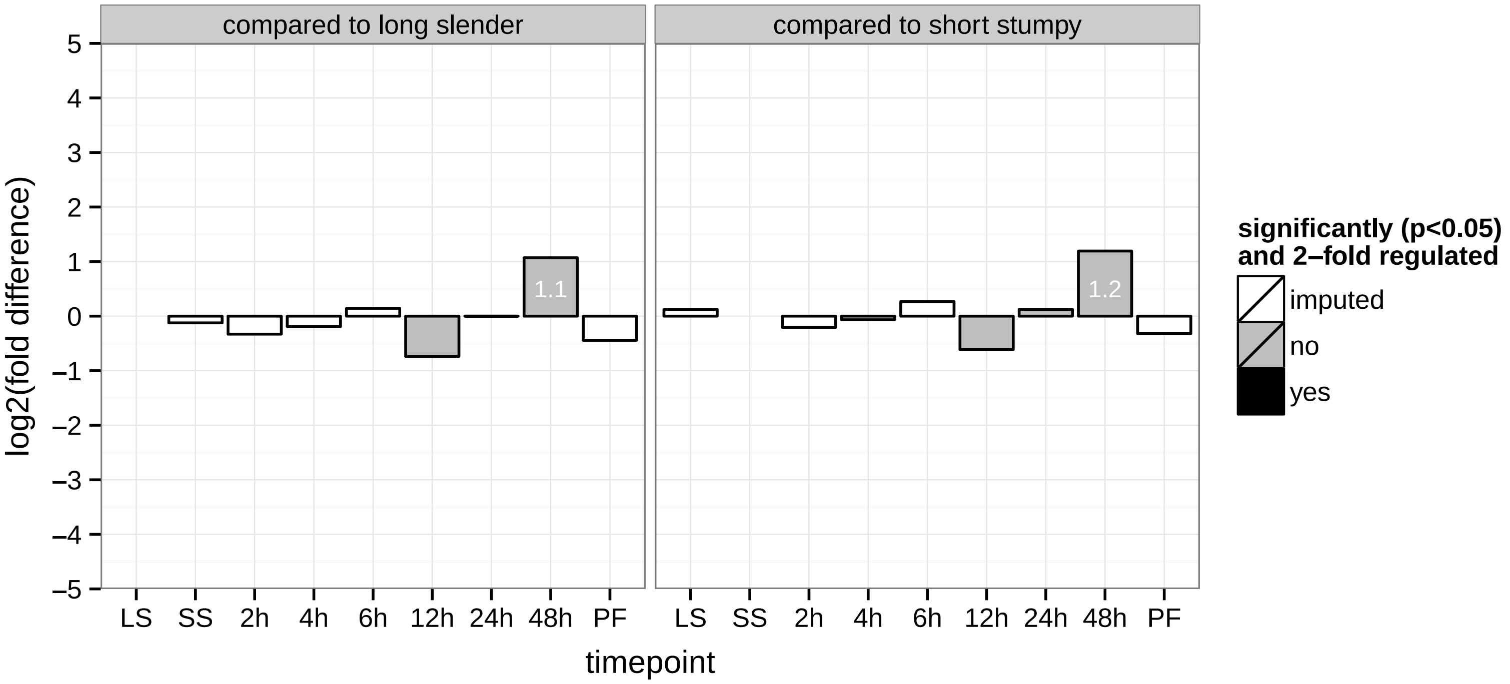
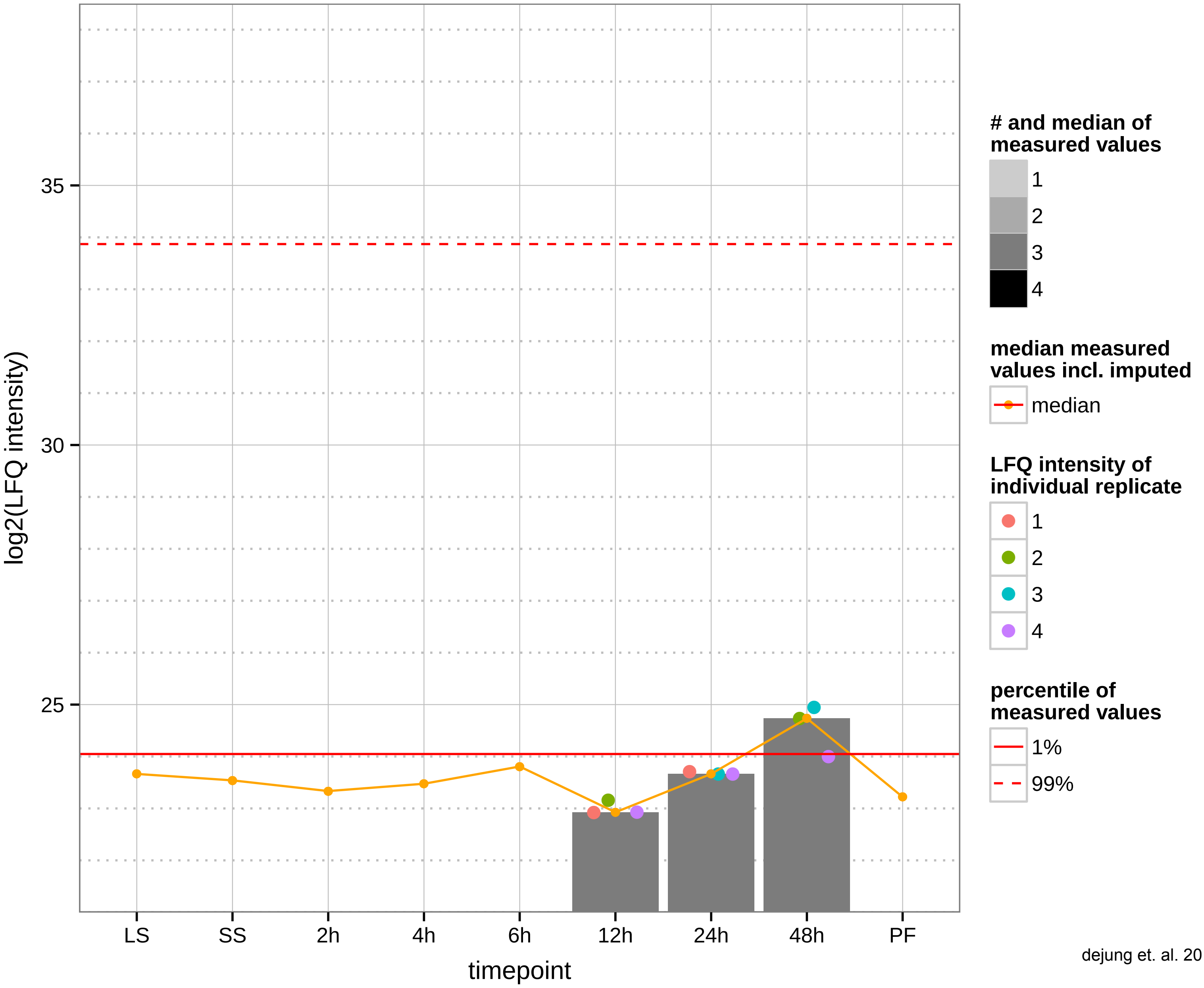
exonuclease, putative
Tb927.3.5150
AGOF: exonuclease activity, nucleic acid binding
AGOC: intracellular
AGOP: null
PGOF: exonuclease activity, nucleic acid binding
PGOC: intracellular
PGOP: null





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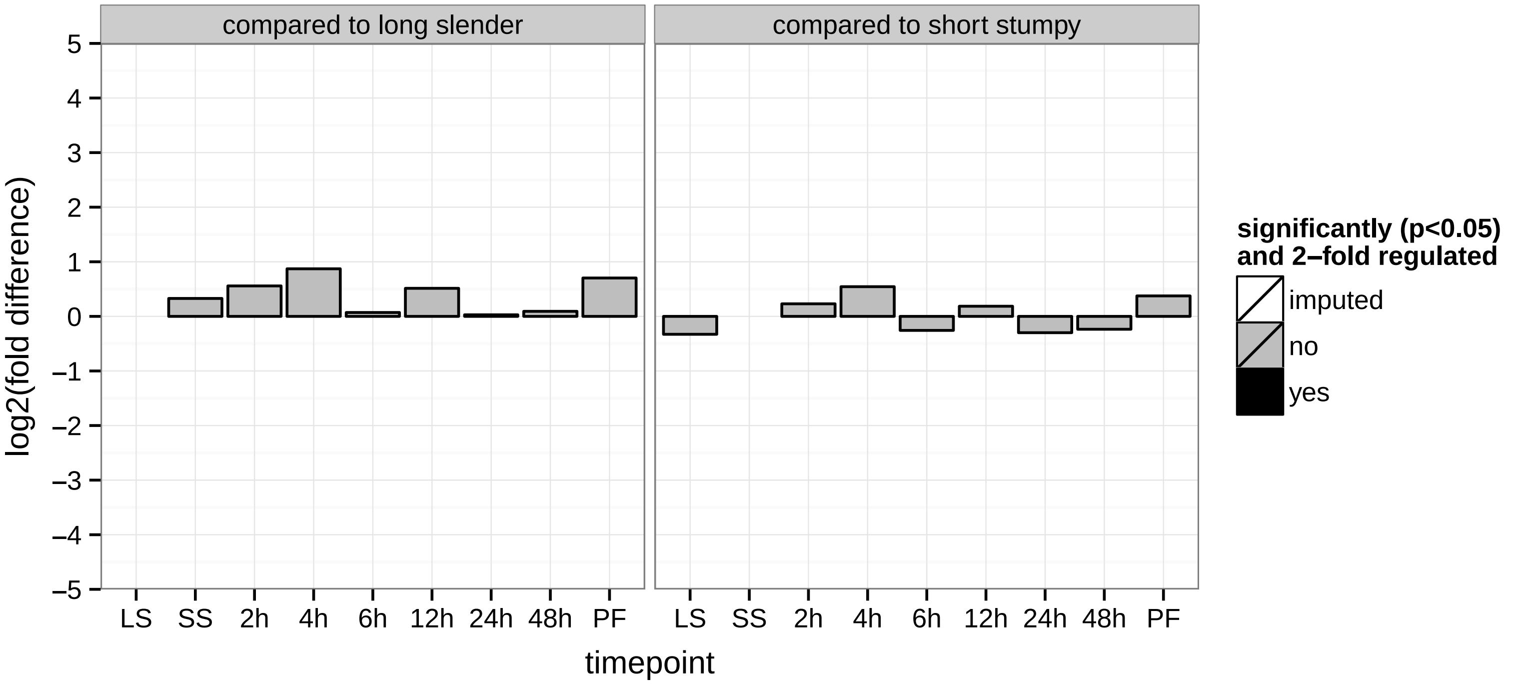
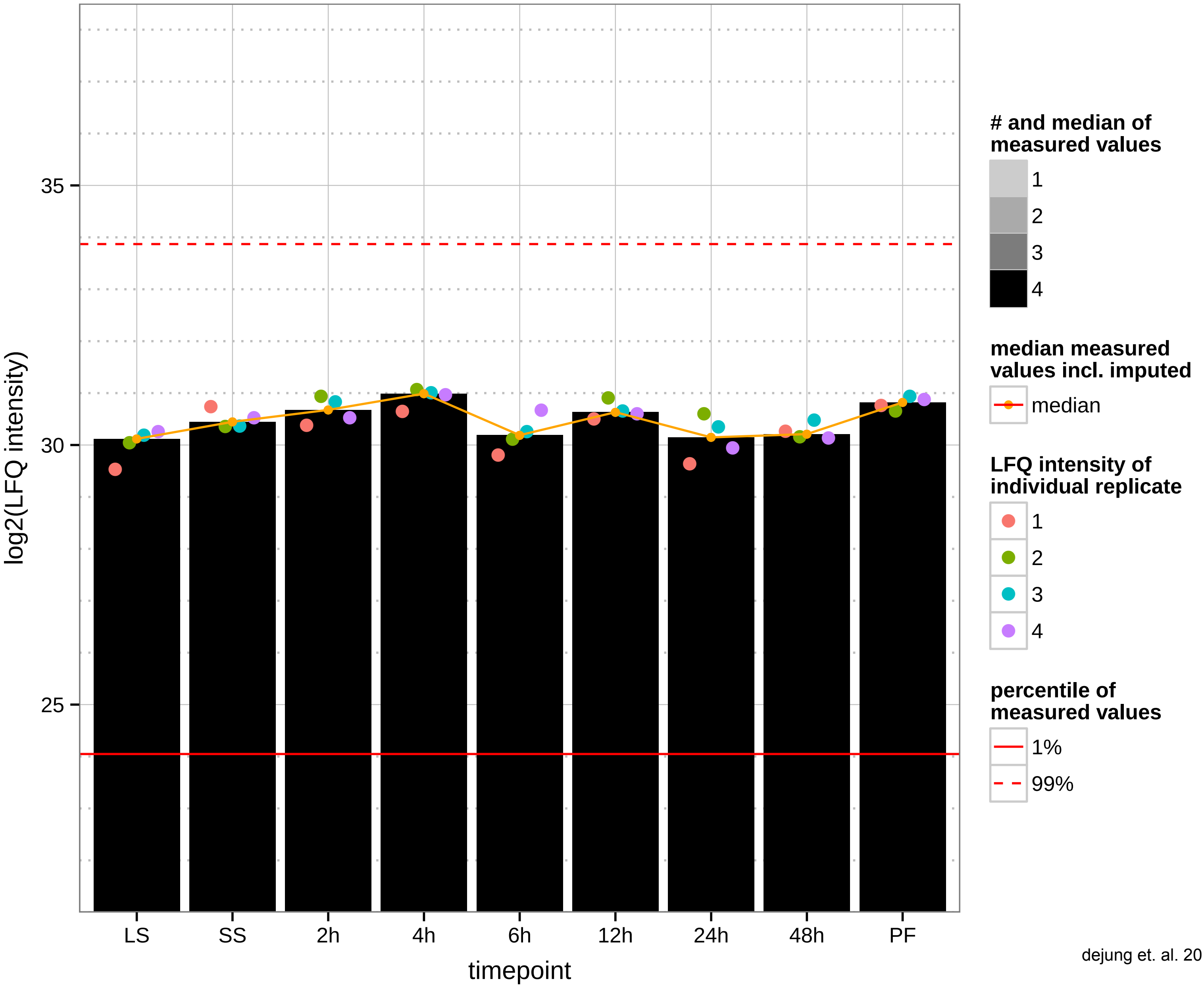
cofilin/actin depolymerizing factor, putative, cofilin–like protein
Tb927.3.5180
AGOF: actin binding
AGOC: intracellular
AGOP: actin filament depolymerization, cell division, intracellular transport, microtubule basal body duplication
PGOF: actin binding
PGOC: intracellular
PGOP: null





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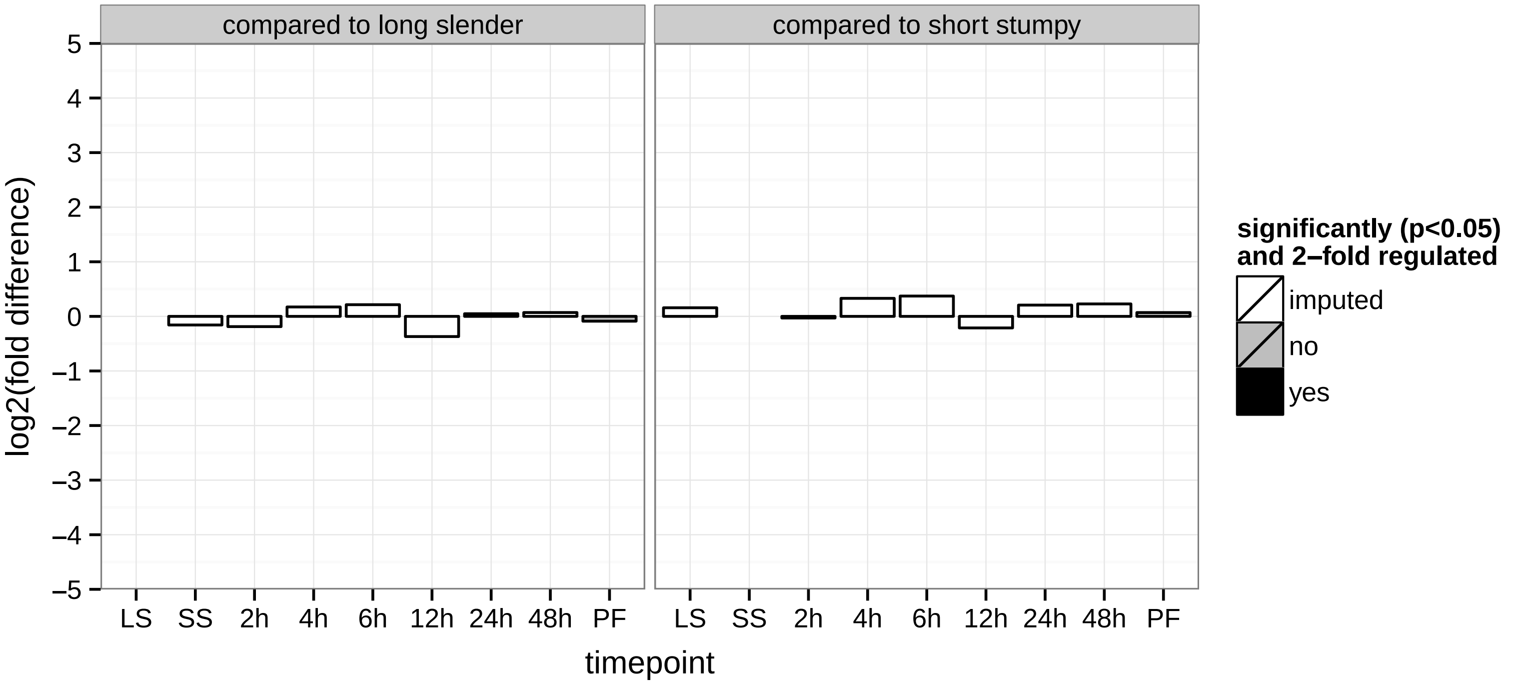
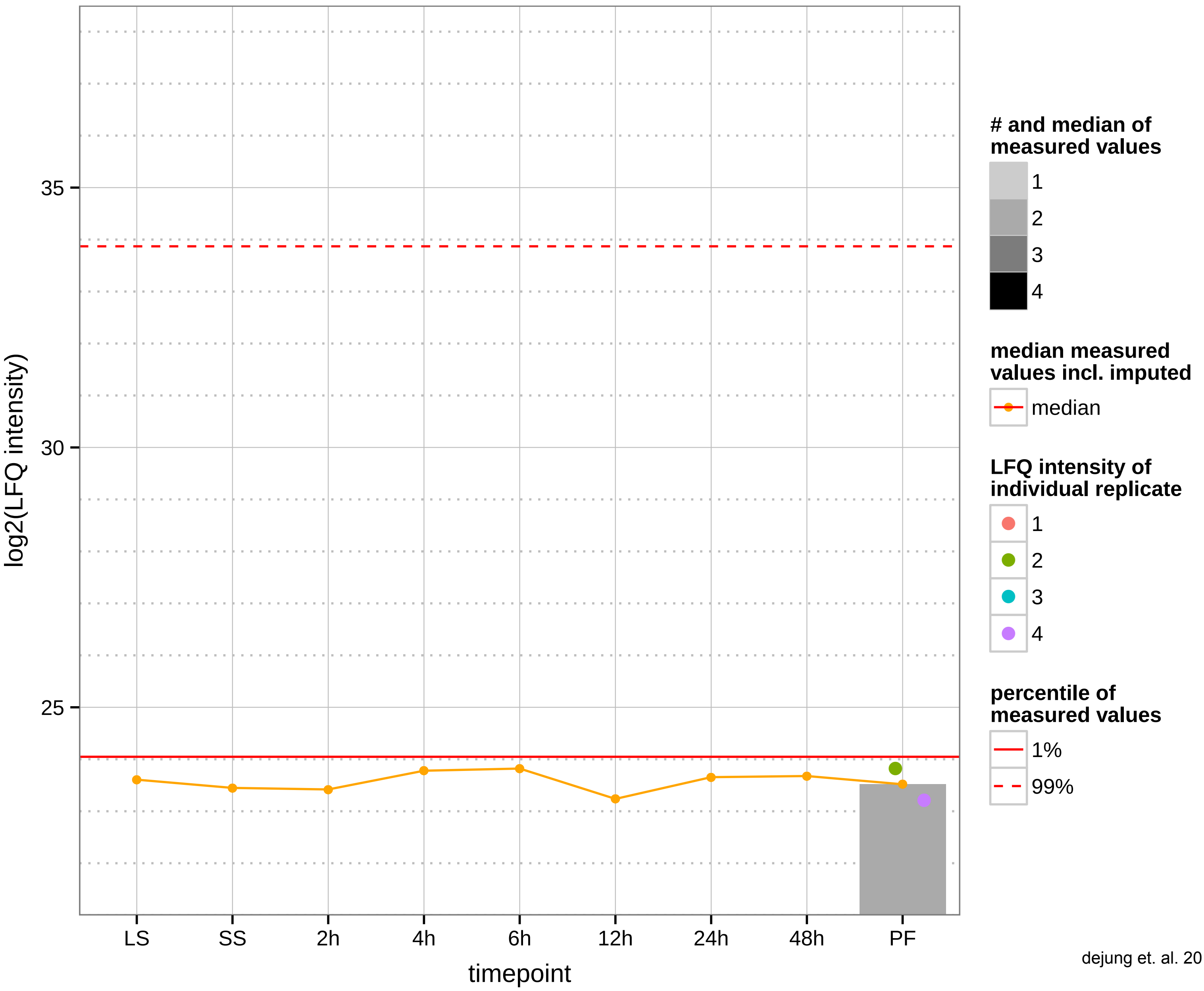
DNA repair protein, putative
Tb927.3.5230
AGOF: ATP binding, DNA binding, DNA–dependent ATPase activity
AGOC: null
AGOP: DNA metabolic process
PGOF: ATP binding, DNA binding, DNA–dependent ATPase activity
PGOC: null
PGOP: DNA metabolic process





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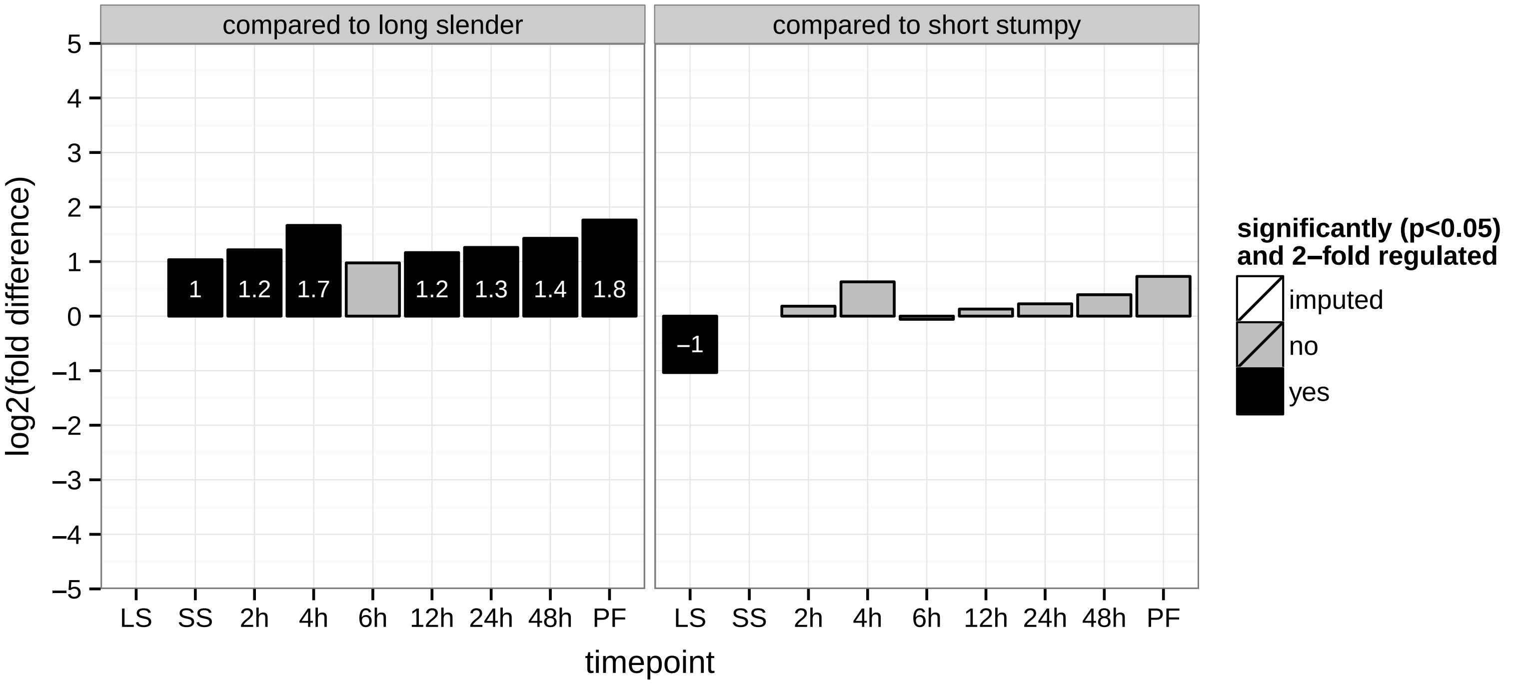
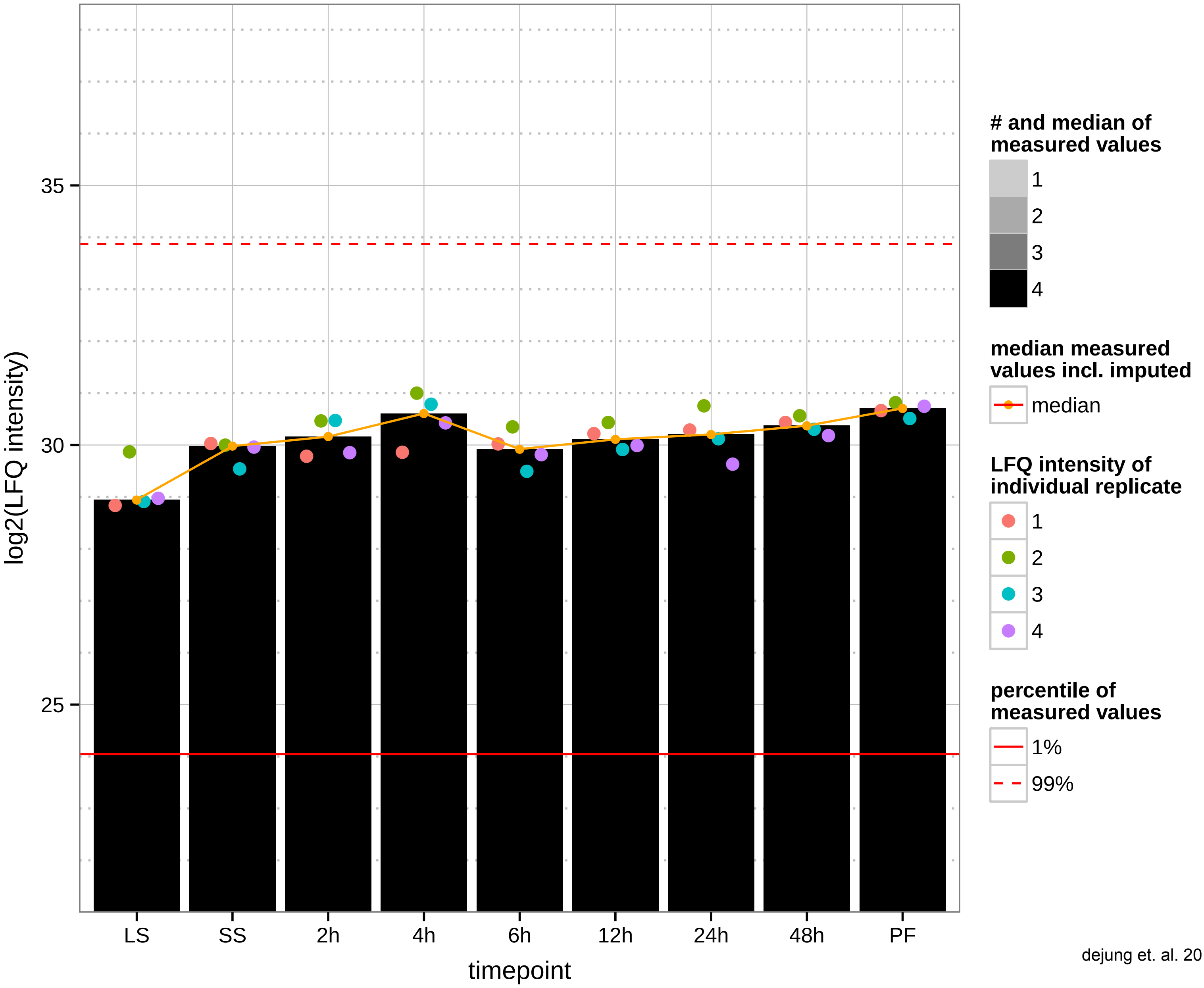
Hsc70–interacting protein (Hip), putative
Tb927.3.5340
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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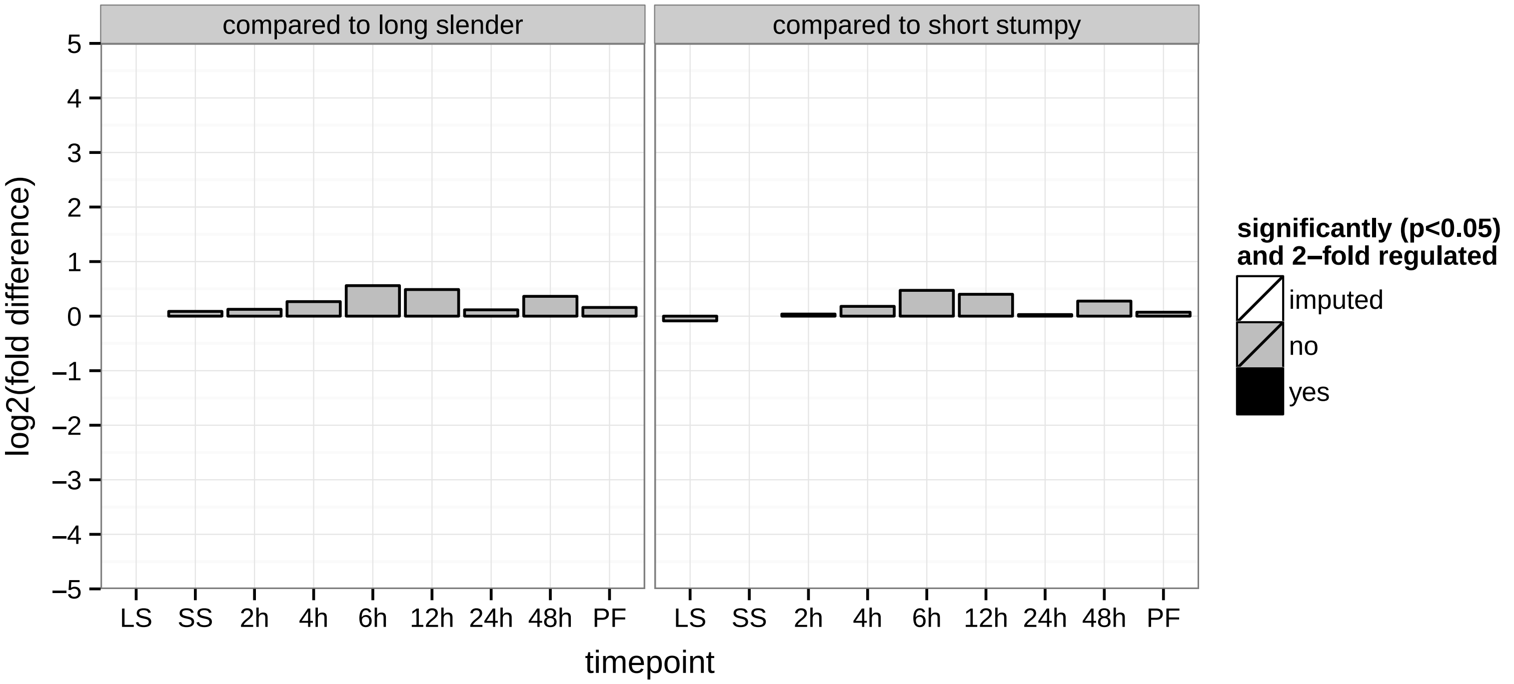
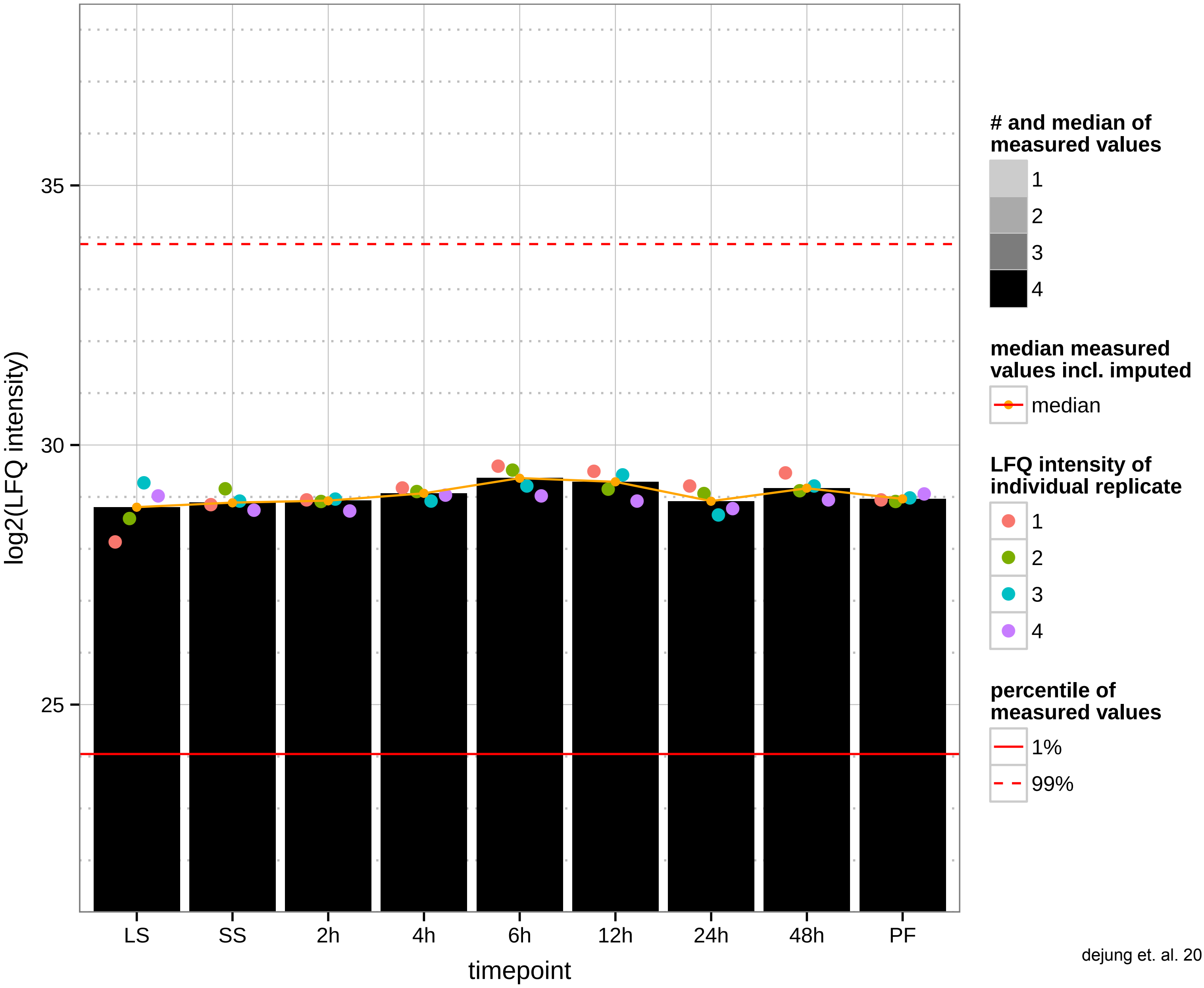
hypothetical protein, conserved
Tb927.3.5370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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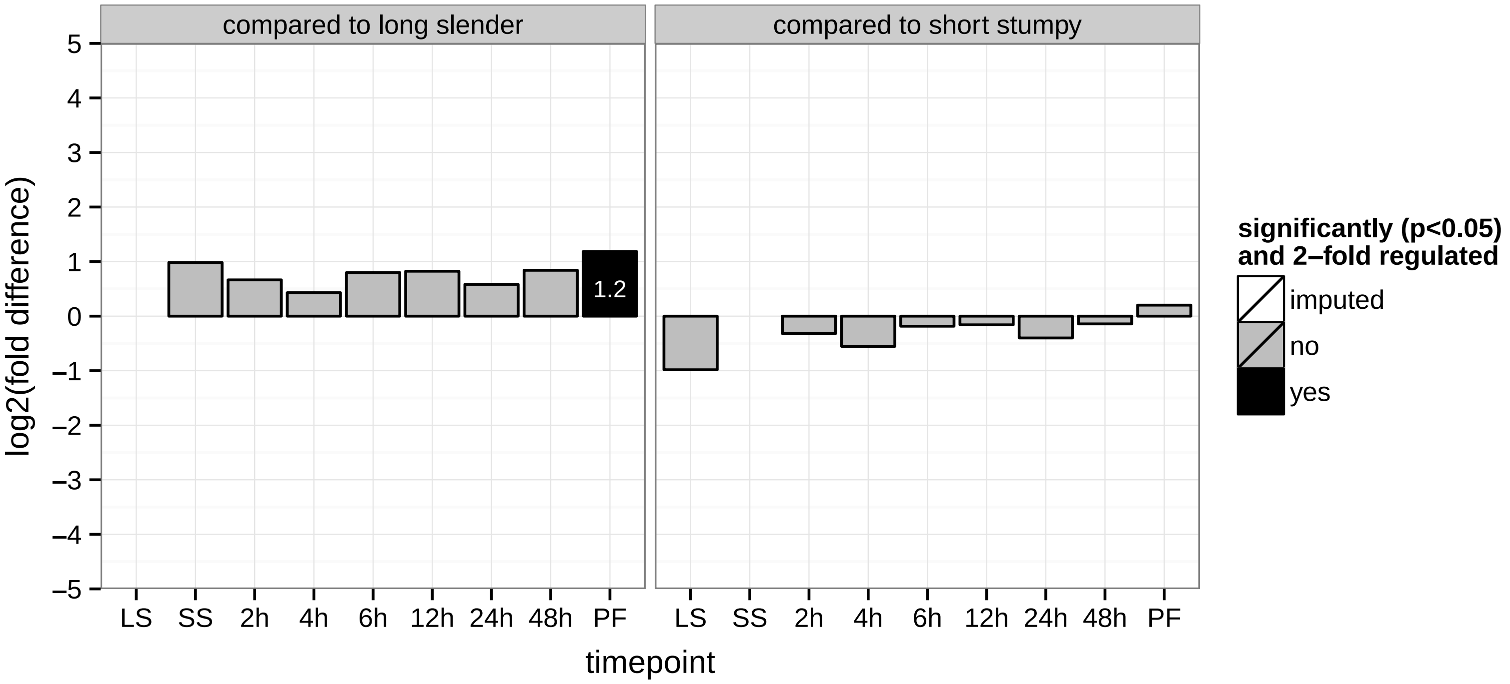
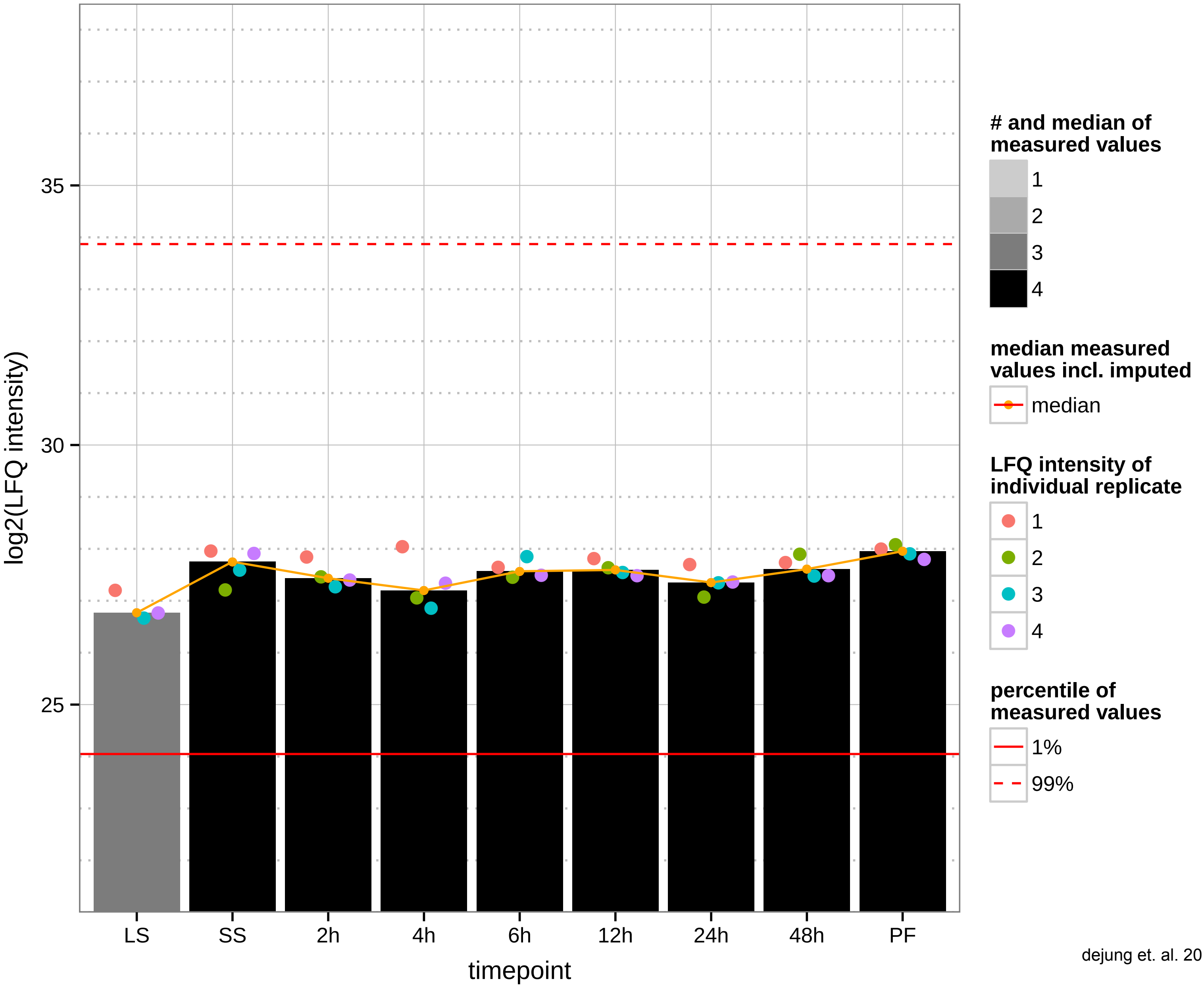
protein transport protein Sec24 (SEC24.2)
Tb927.3.5420
AGOF: protein binding, zinc ion binding
AGOC: COPII vesicle coat
AGOP: ER to Golgi vesicle–mediated transport, intracellular protein transport
PGOF: zinc ion binding
PGOC: COPII vesicle coat
PGOP: ER to Golgi vesicle–mediated transport, intracellular protein transport





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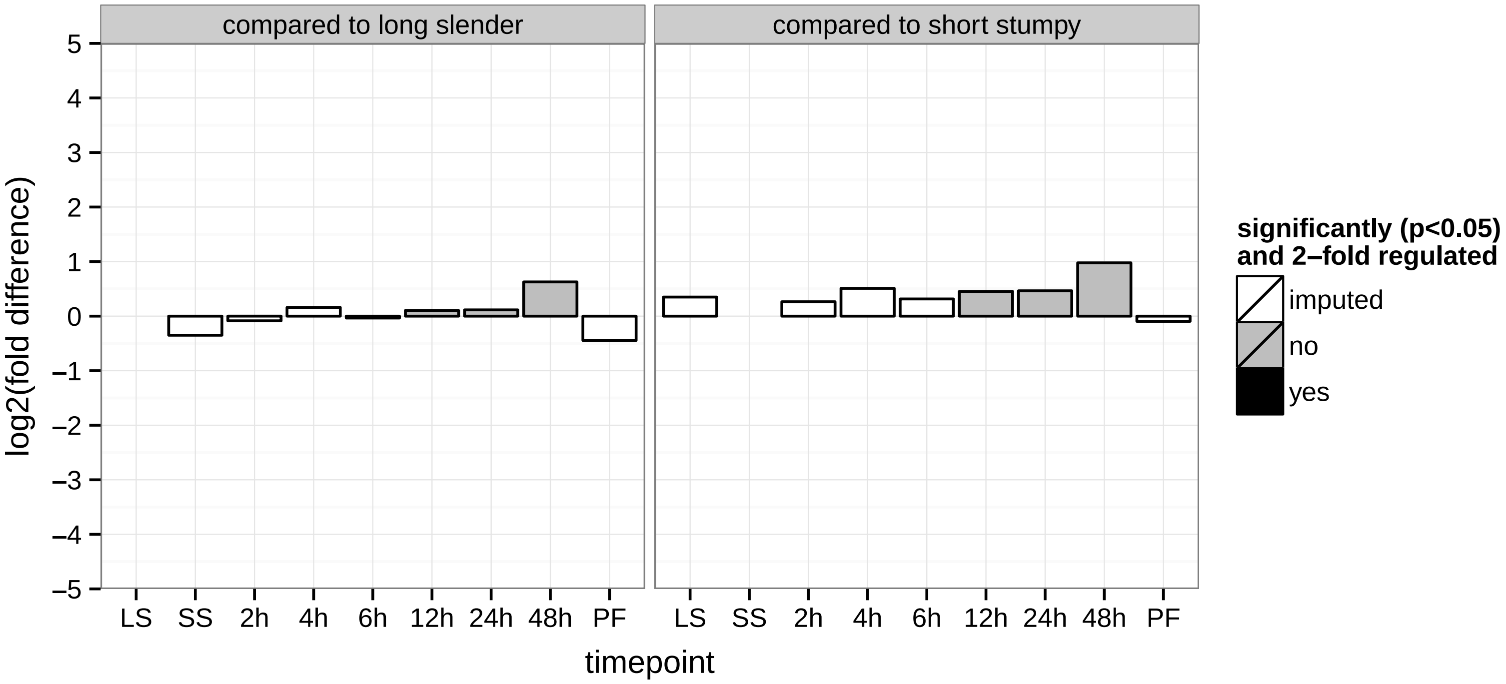
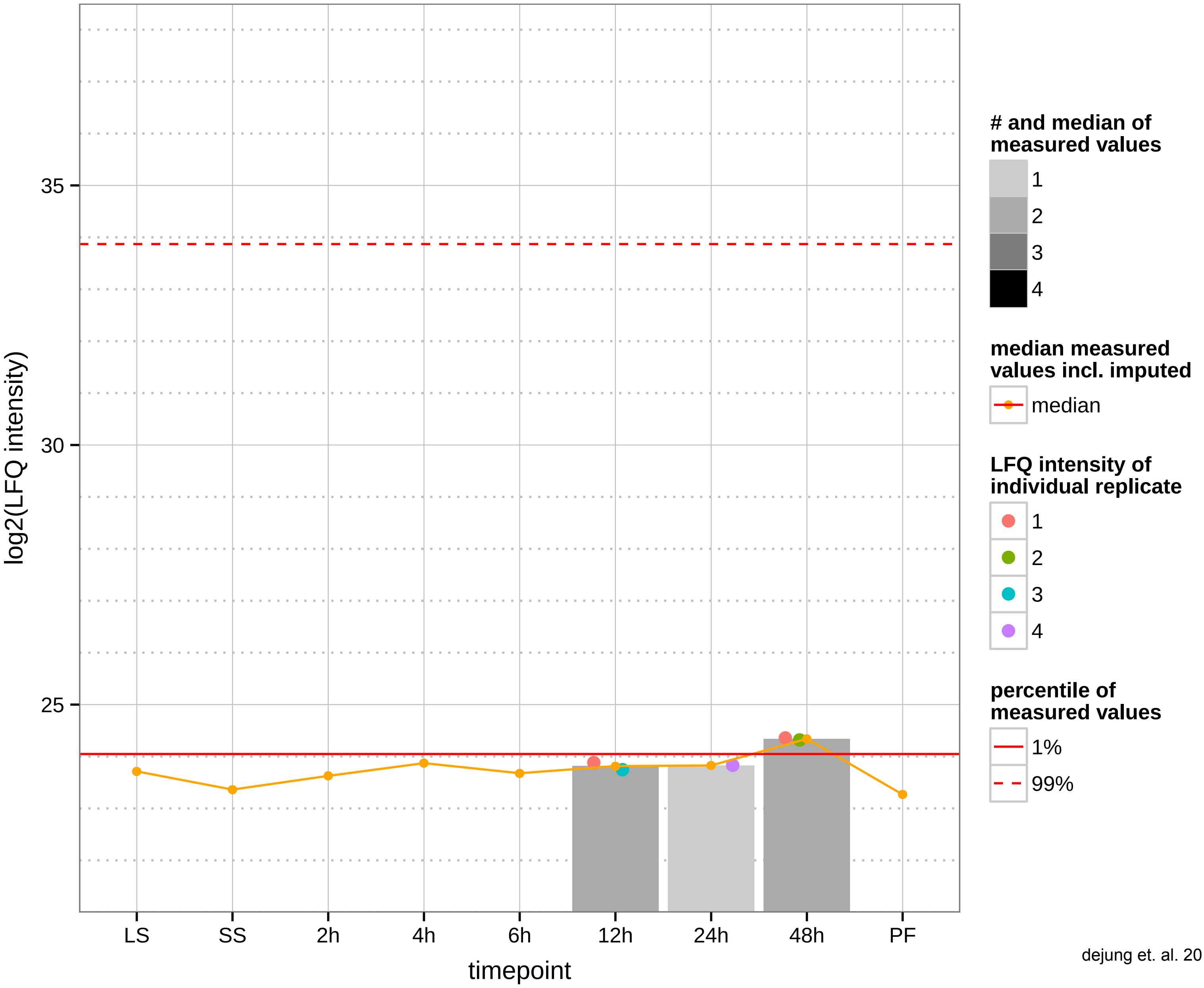
SNF2 DNA repair protein, putative
Tb927.3.5440
AGOF: ATP binding, DNA binding, helicase activity
AGOC: null
AGOP: null
PGOF: ATP binding, DNA binding, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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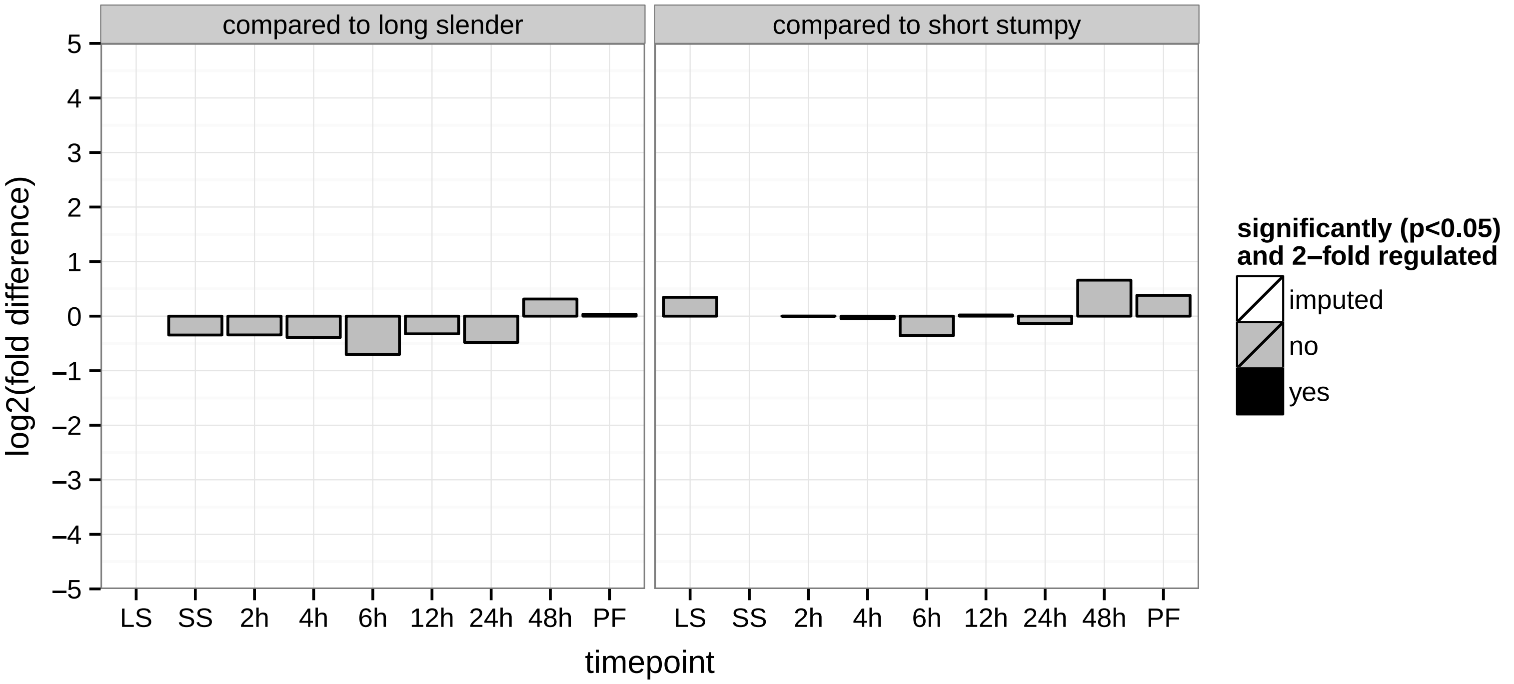
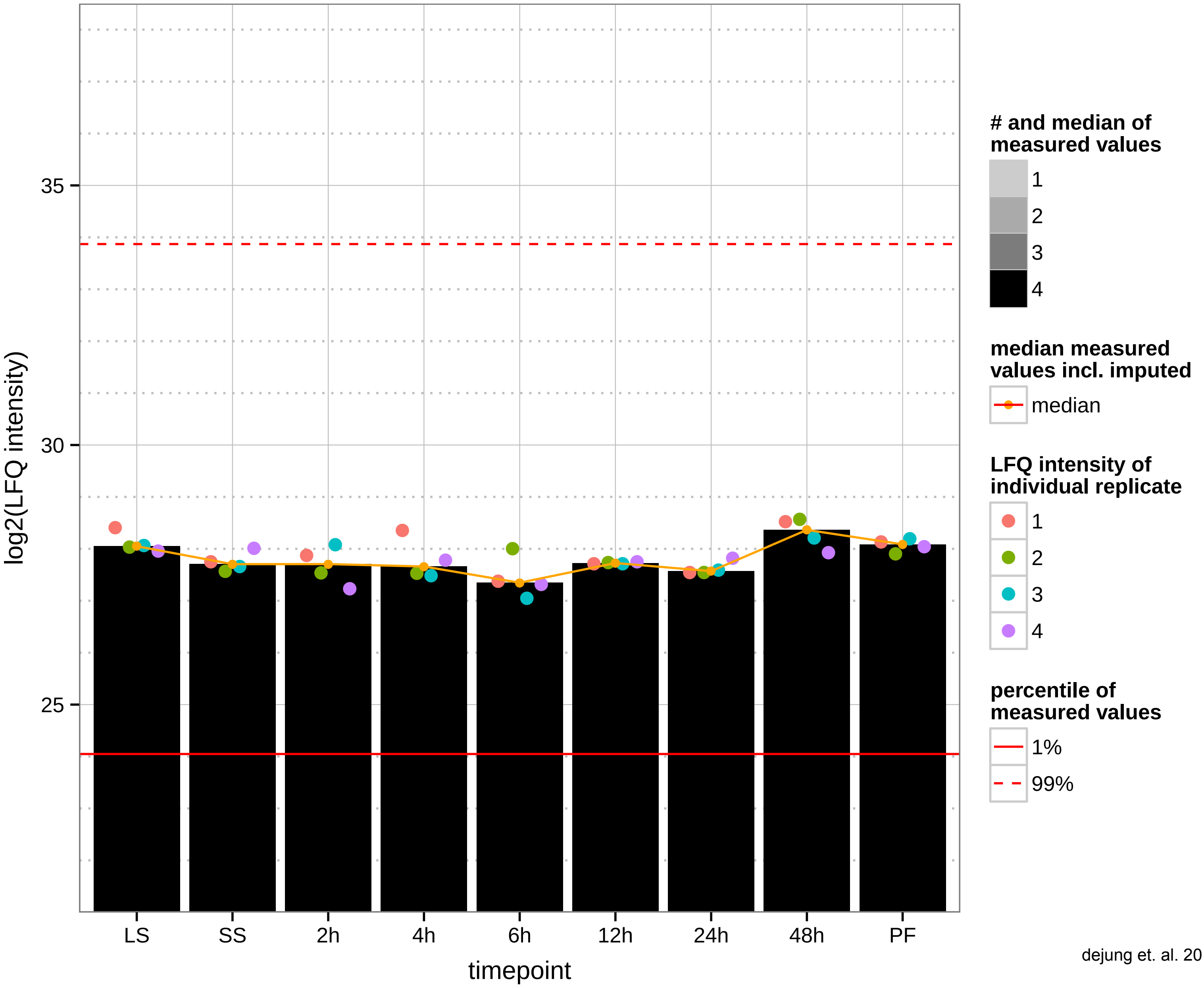
DNA–directed RNA polymerase II subunit 3, putative, RNA polymerase subunit, putative (RPB3)
Tb927.3.5500
AGOF: DNA binding, DNA–directed RNA polymerase activity, protein dimerization activity
AGOC: null
AGOP: transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity, protein dimerization activity
PGOC: null
PGOP: transcription, DNA–dependent





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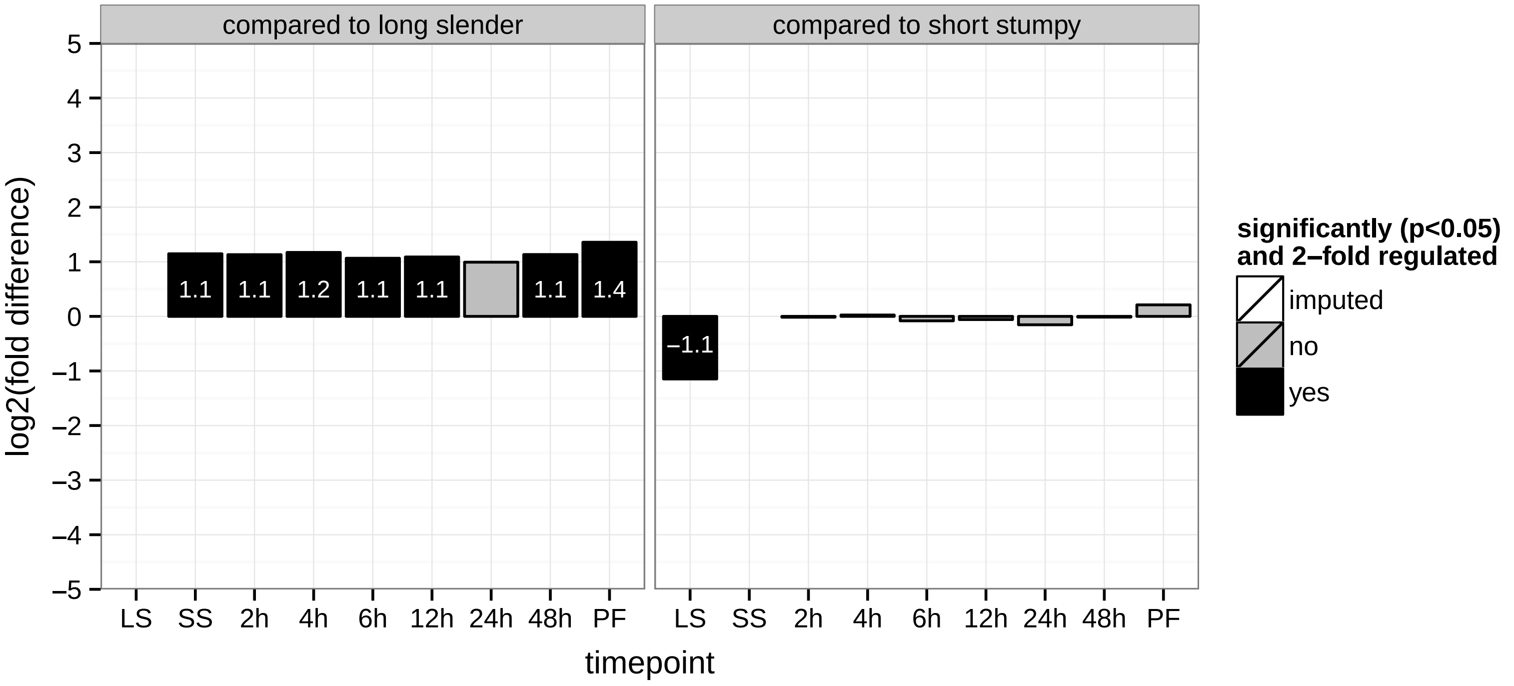
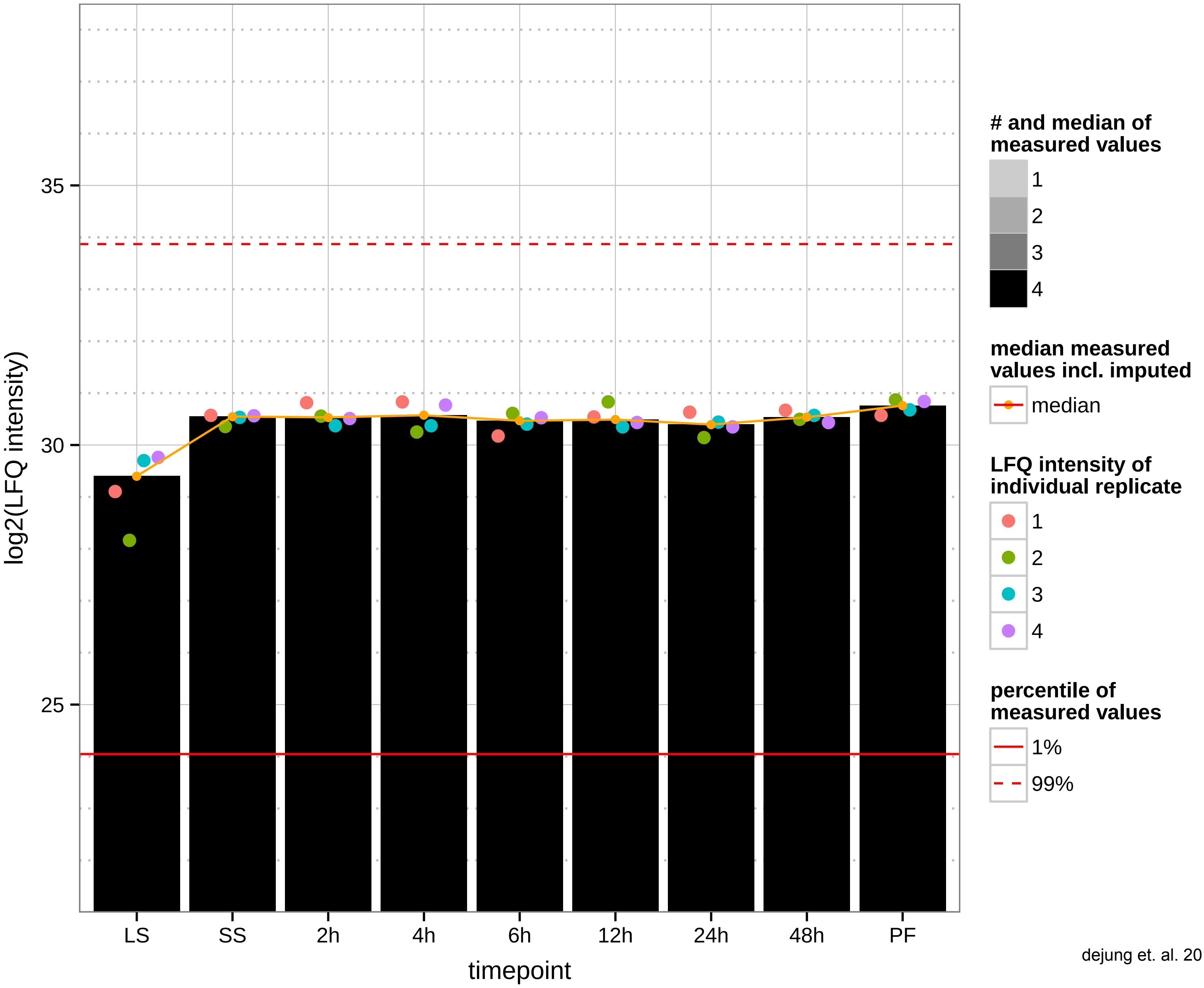
NA, 26S proteasome regulatory non–ATPase subunit (RPN1)
Tb927.3.5520
AGOF: NA, enzyme regulator activity
AGOC: NA, proteasome complex
AGOP: NA, regulation of protein catabolic process
PGOF: NA, binding, enzyme regulator activity
PGOC: NA, proteasome complex
PGOP: NA, regulation of protein catabolic process





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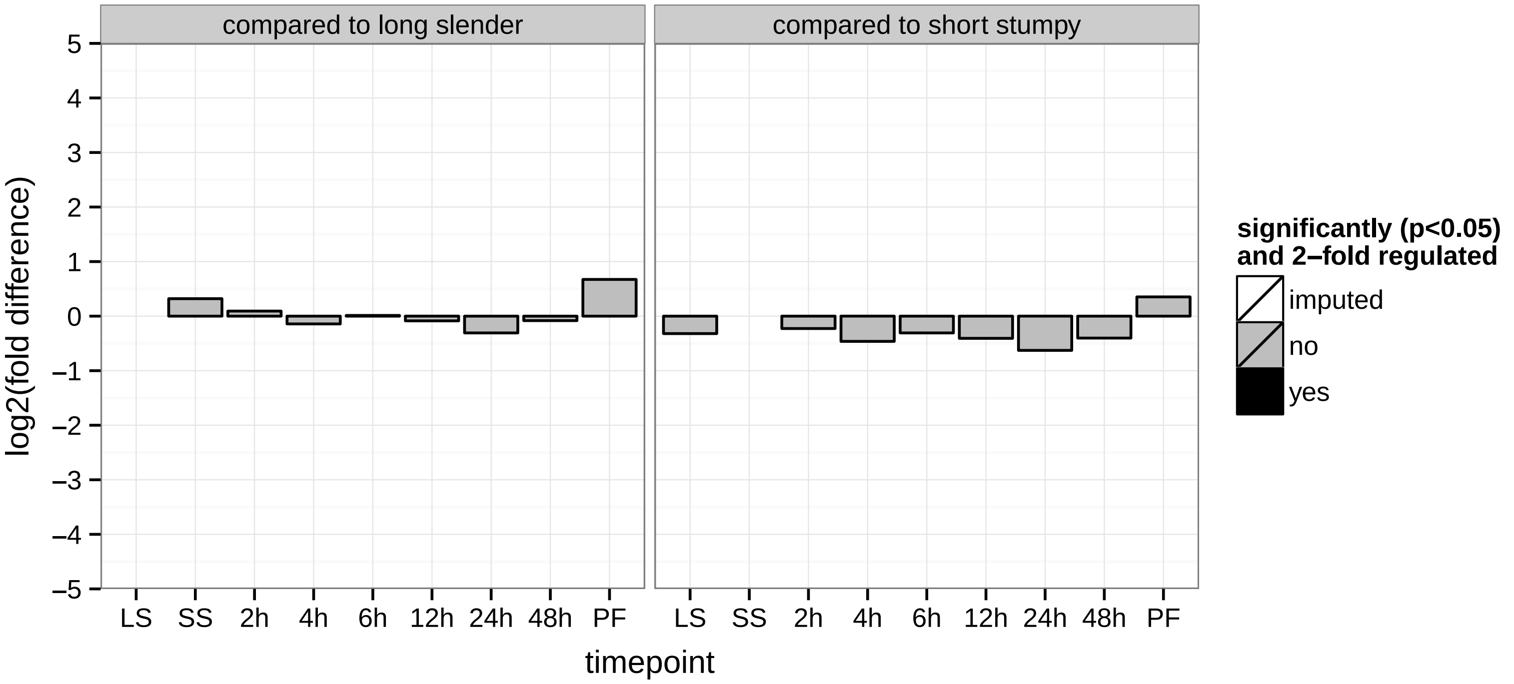
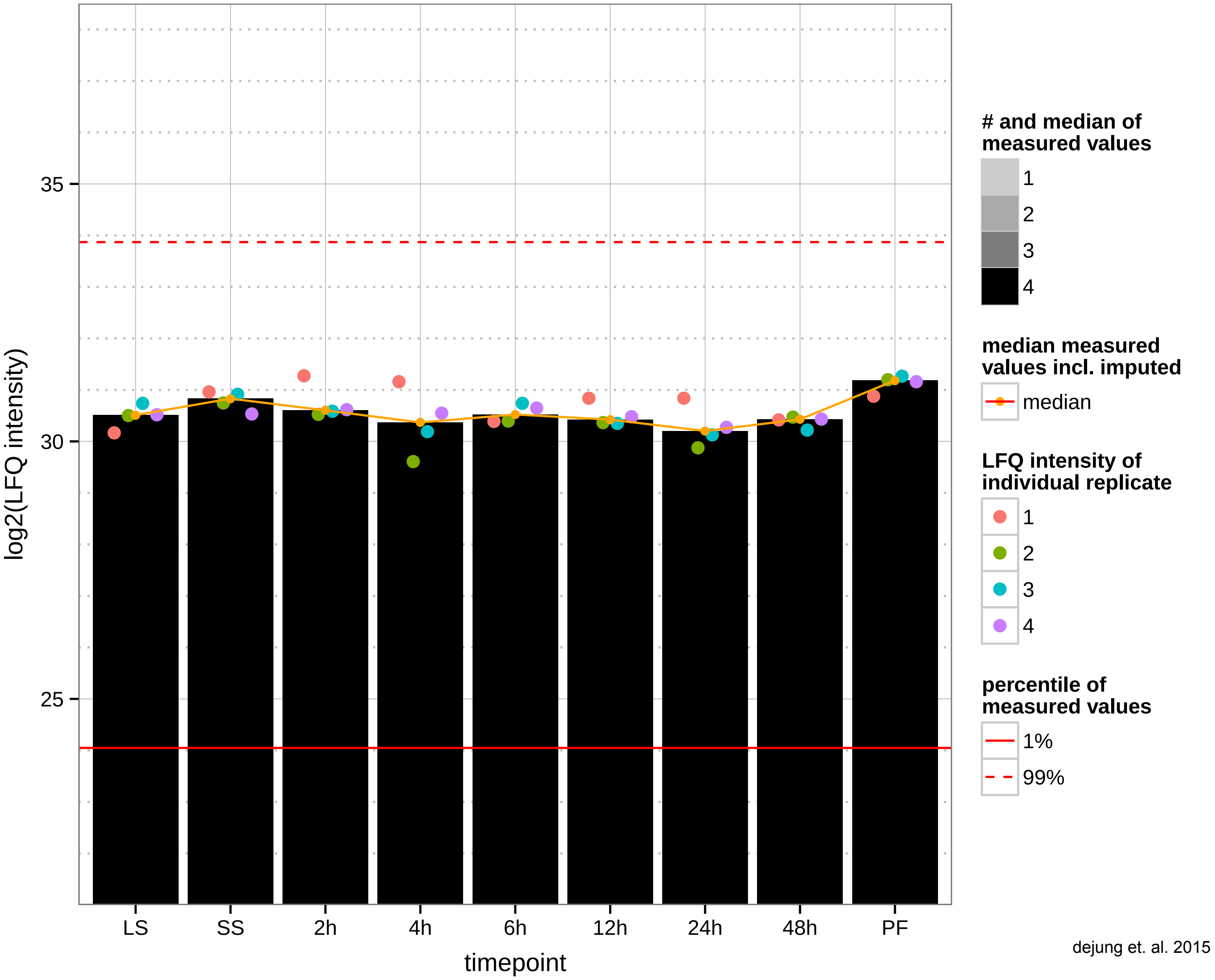
Tb–292 membrane associated protein (Tb–292)
Tb927.3.5530
AGOF: null
AGOC: endocytic vesicle, flagellar pocket membrane, nuclear outer membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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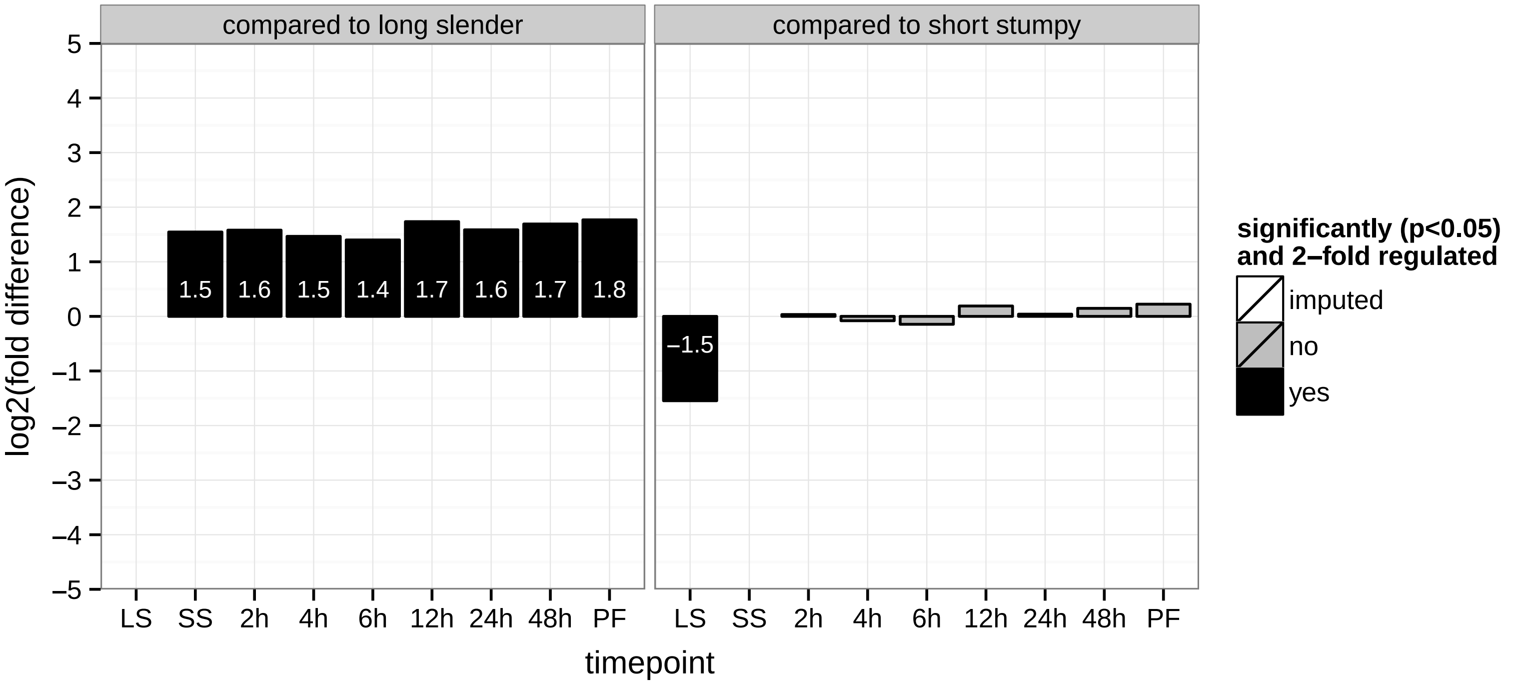
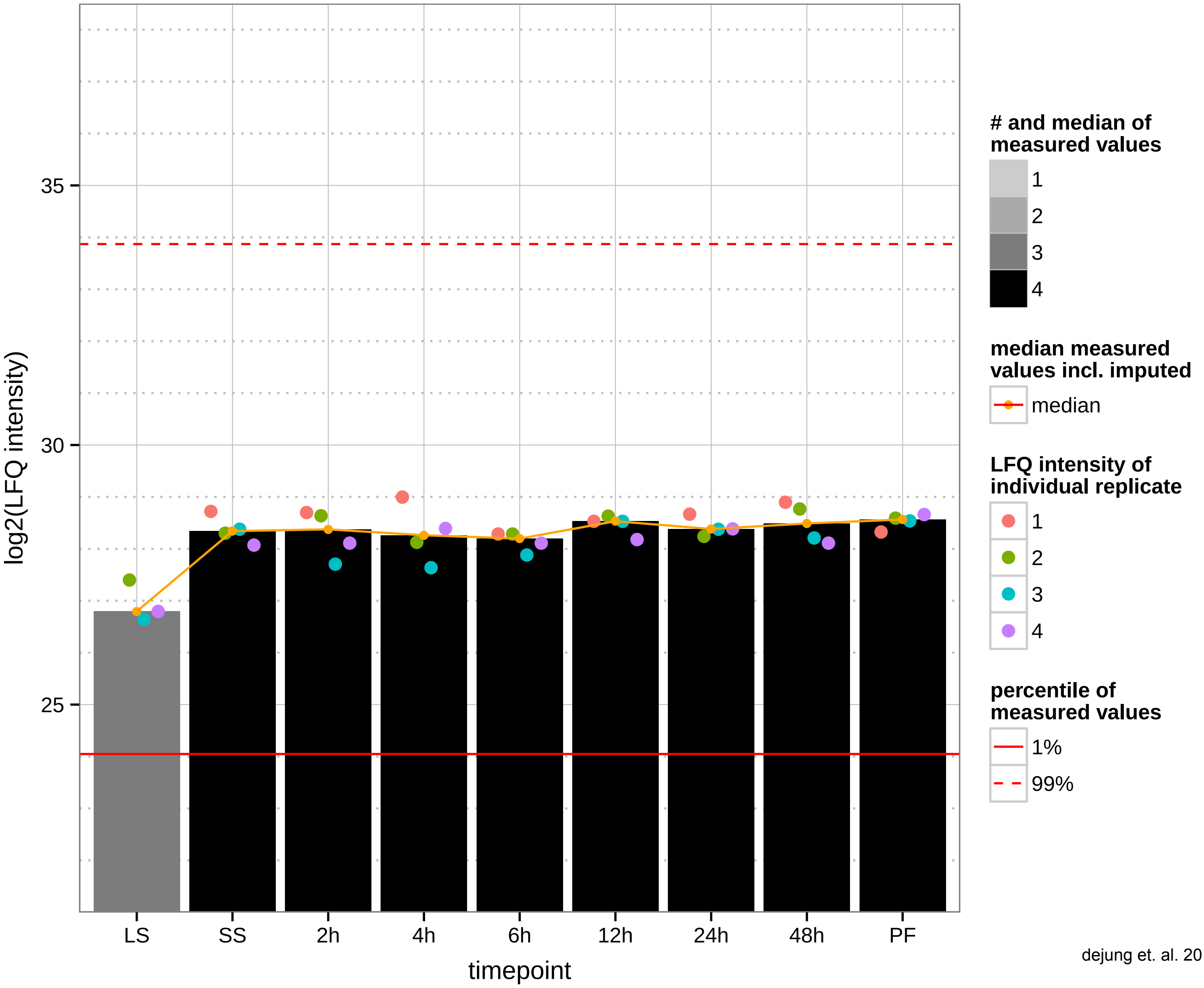
tryptophanyl–tRNA synthetase
Tb927.3.5580
AGOF: ATP binding, tryptophan–tRNA ligase activity
AGOC: cytoplasm, cytosol
AGOP: translation, tryptophanyl–tRNA aminoacylation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, nucleotide binding, tryptophan–tRNA ligase activity
PGOC: cytoplasm
PGOP: tRNA aminoacylation for protein translation, tryptophanyl–tRNA aminoacylation





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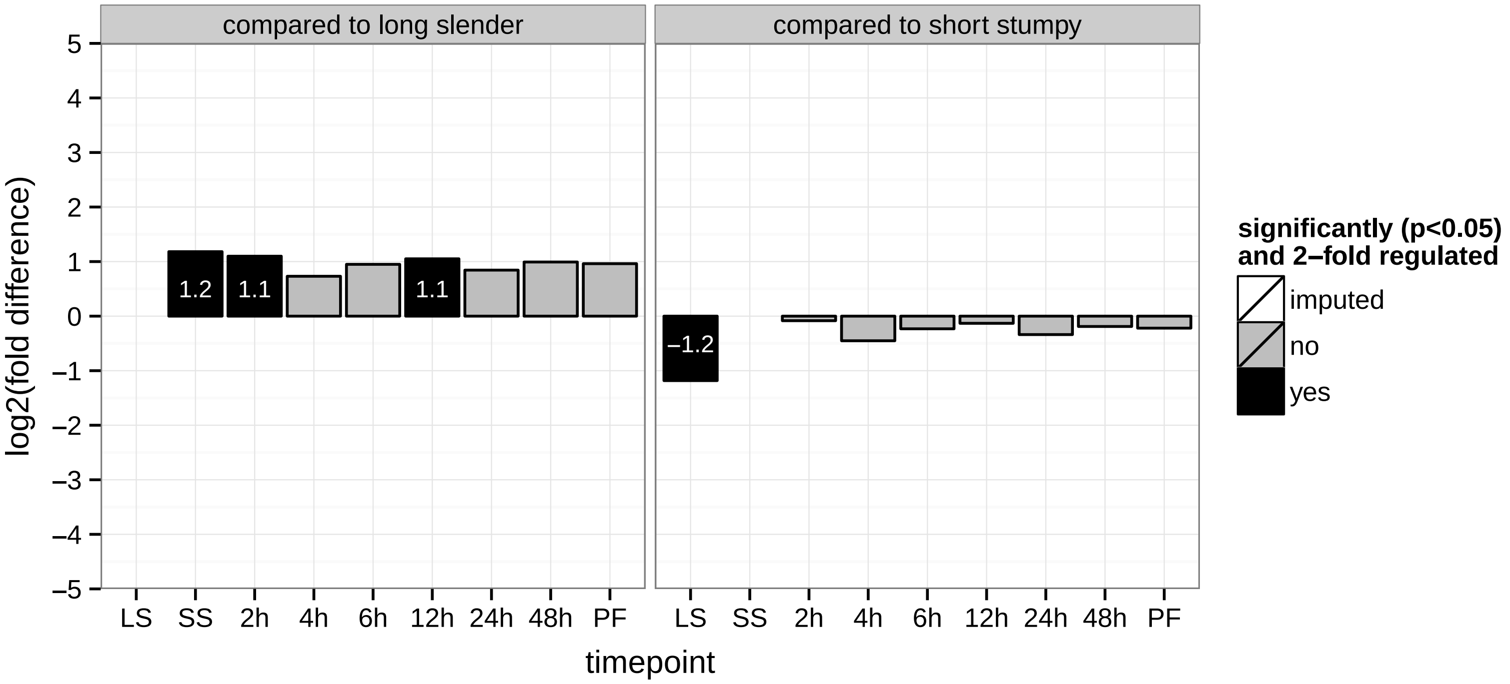
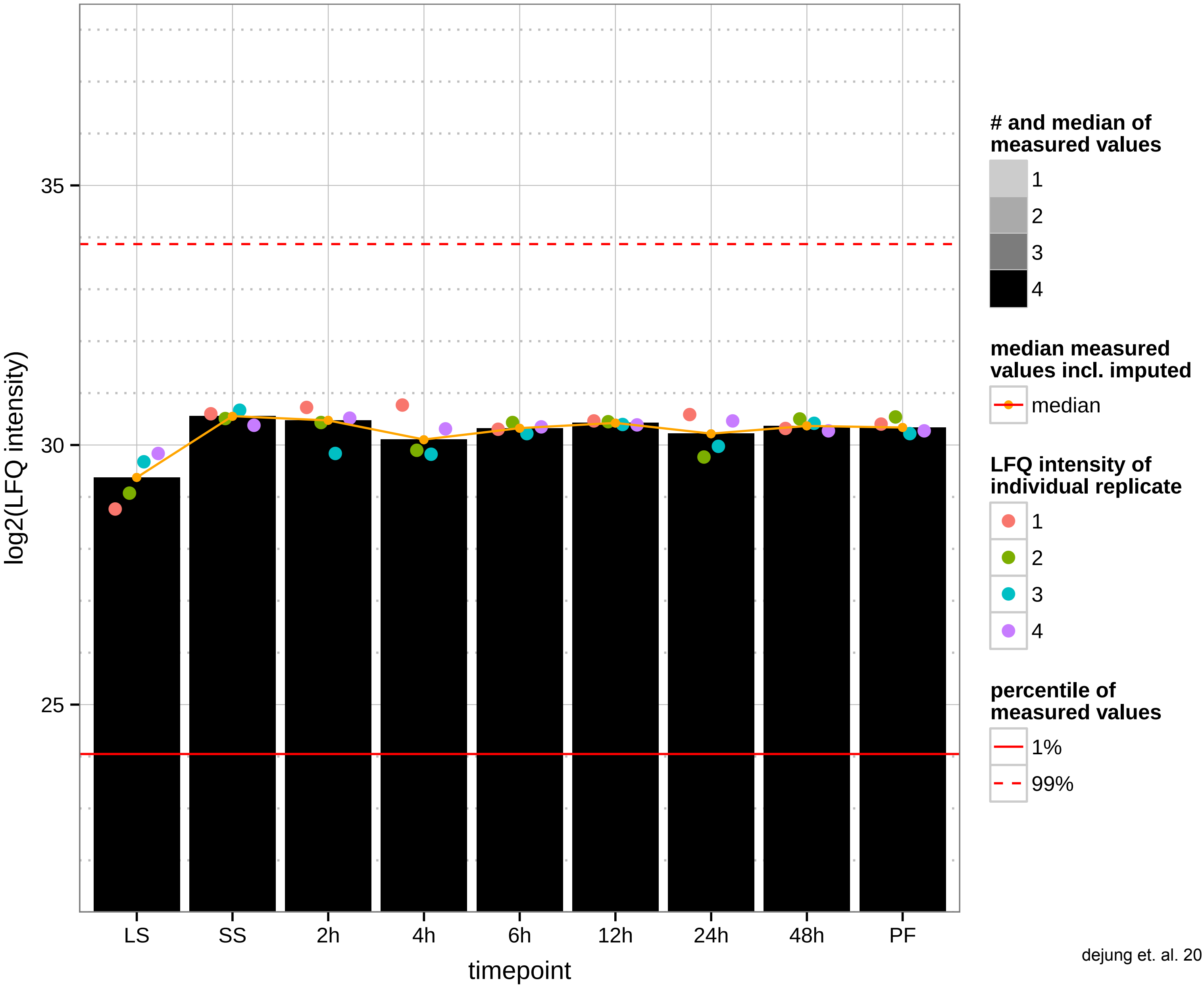
hypothetical protein, conserved
Tb927.3.5620
AGOF: null
AGOC: null
AGOP: cellular process
PGOF: null
PGOC: null
PGOP: cellular process





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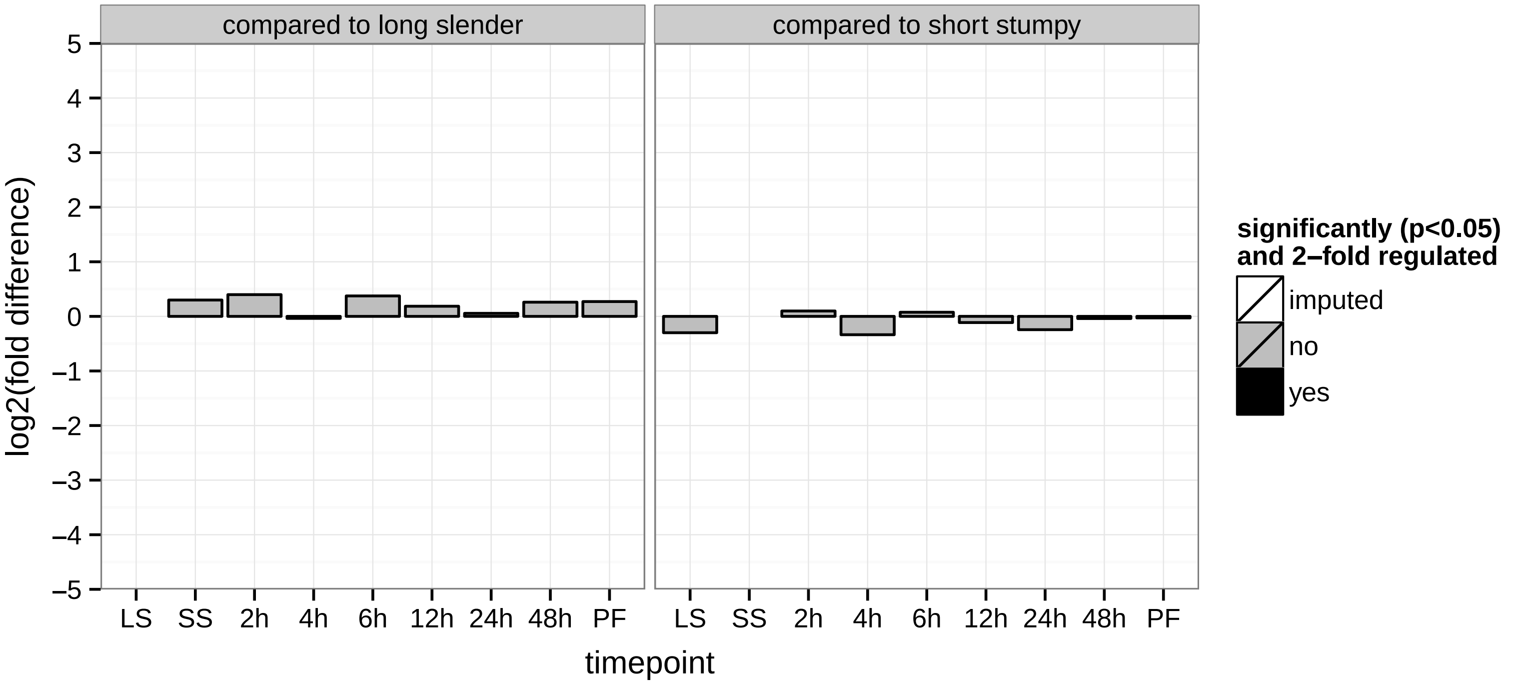
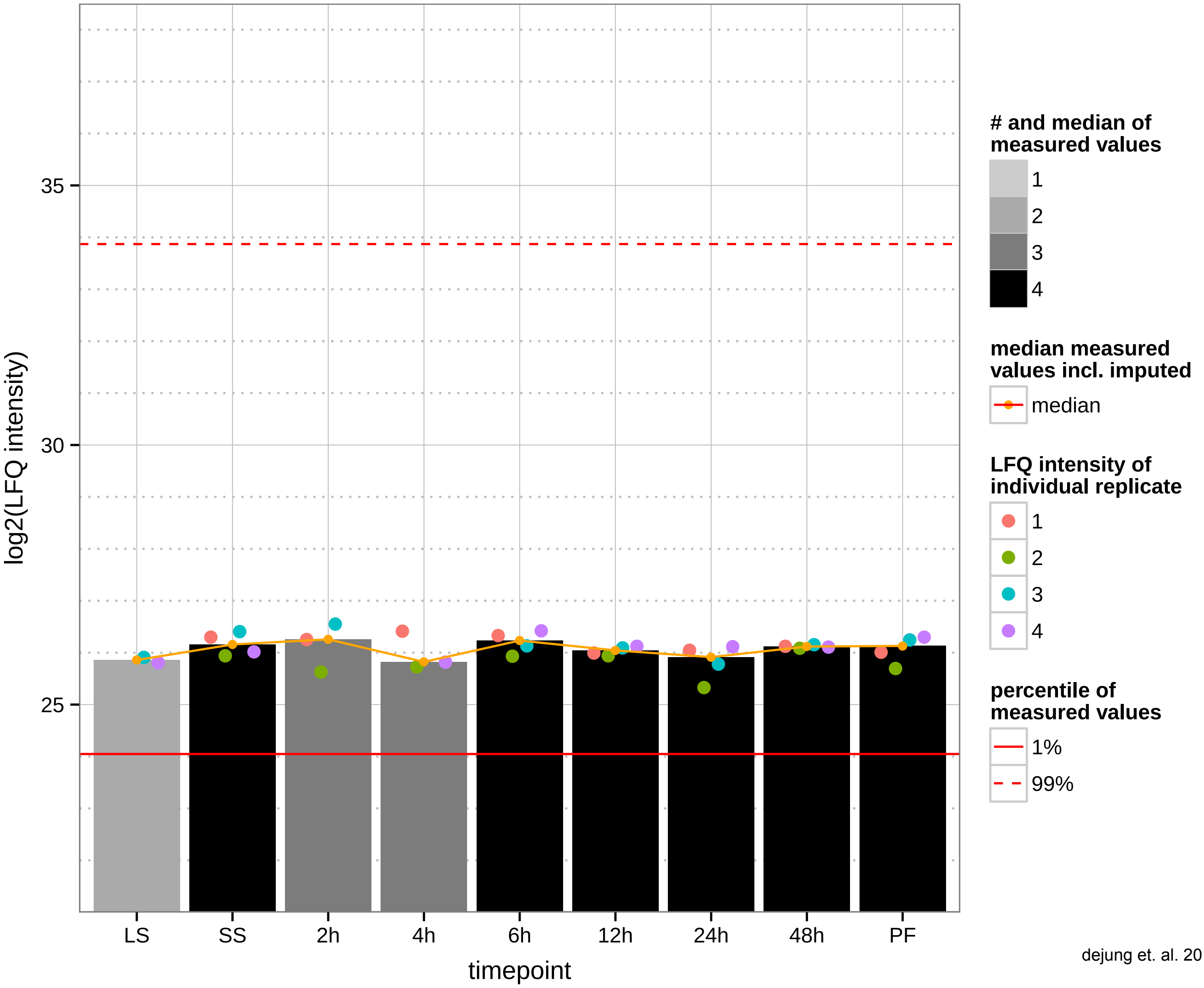
hypothetical protein, conserved
Tb927.3.760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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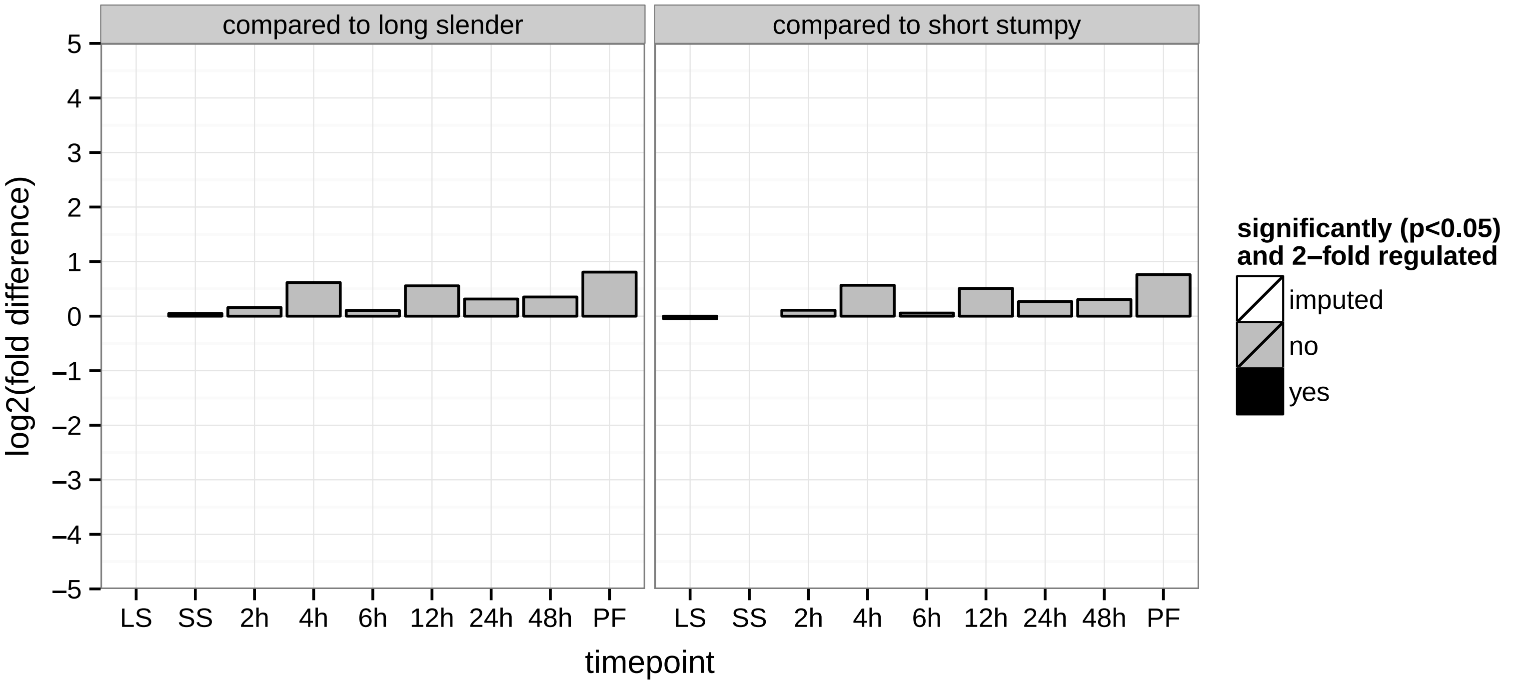
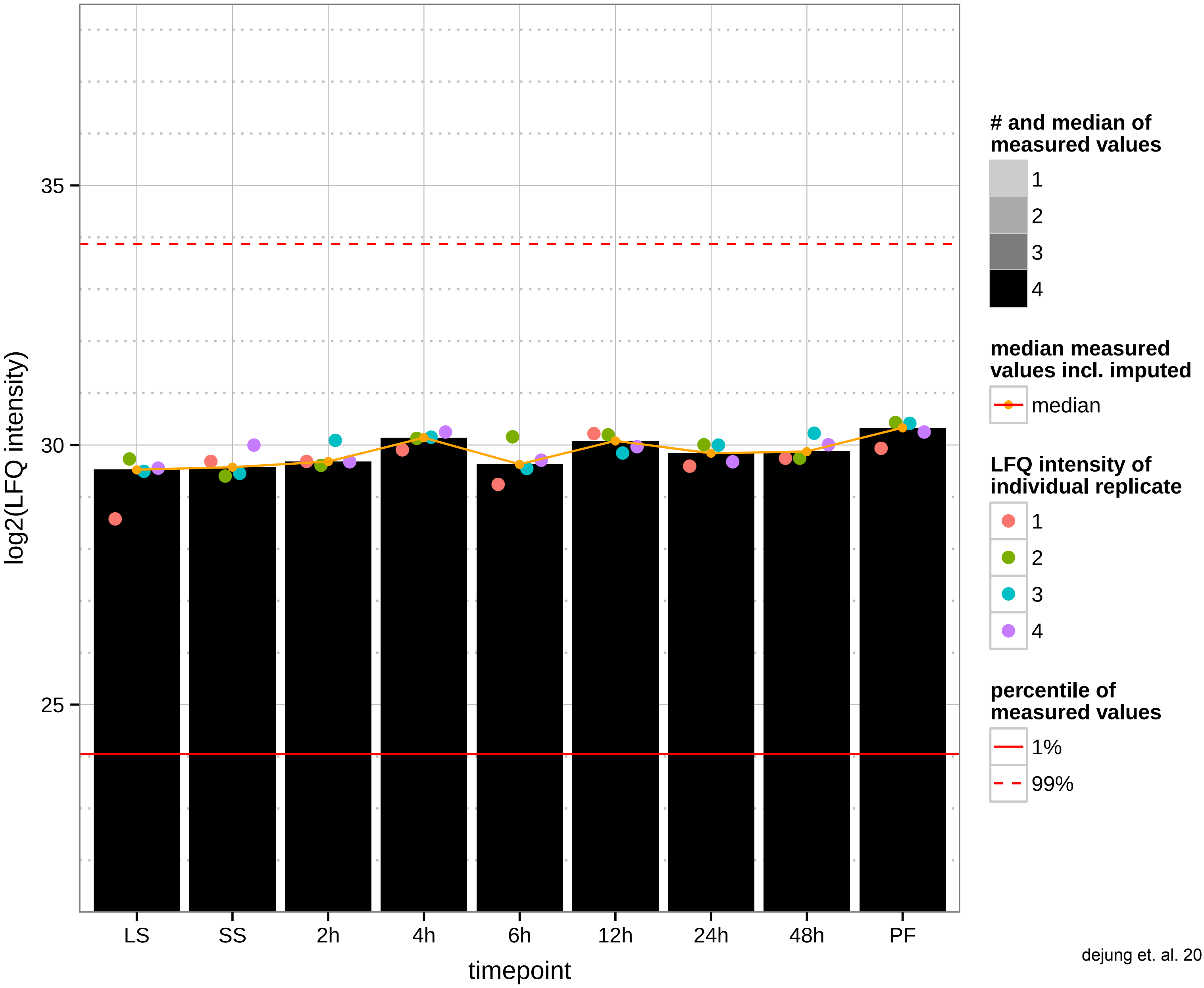
proteasome alpha 7 subunit (TbPSA7)
Tb927.3.780
AGOF: endopeptidase activity, threonine–type endopeptidase activity
AGOC: proteasome core complex, proteasome core complex, alpha–subunit complex
AGOP: protein metabolic process, ubiquitin–dependent protein catabolic process
PGOF: endopeptidase activity, threonine–type endopeptidase activity
PGOC: proteasome core complex, proteasome core complex, alpha–subunit complex
PGOP: proteolysis involved in cellular protein catabolic process, ubiquitin–dependent protein catabolic process





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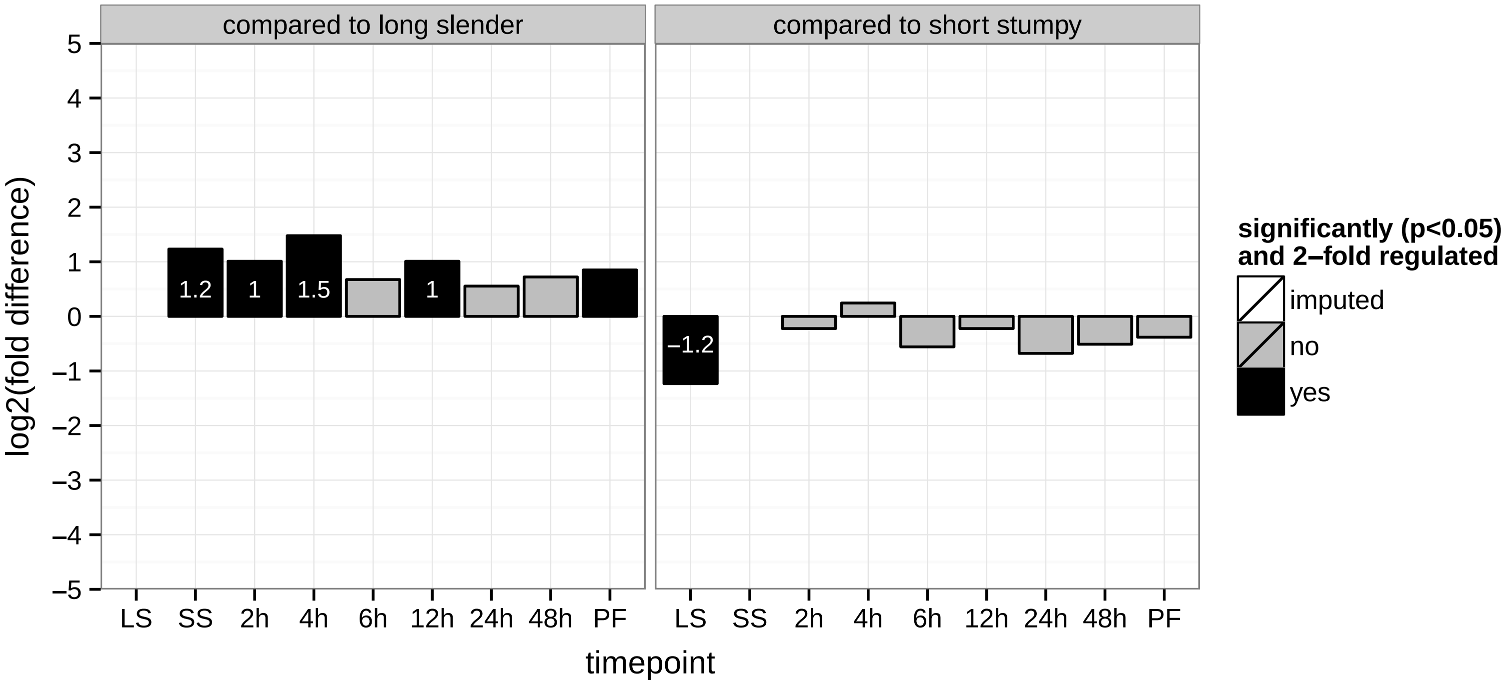
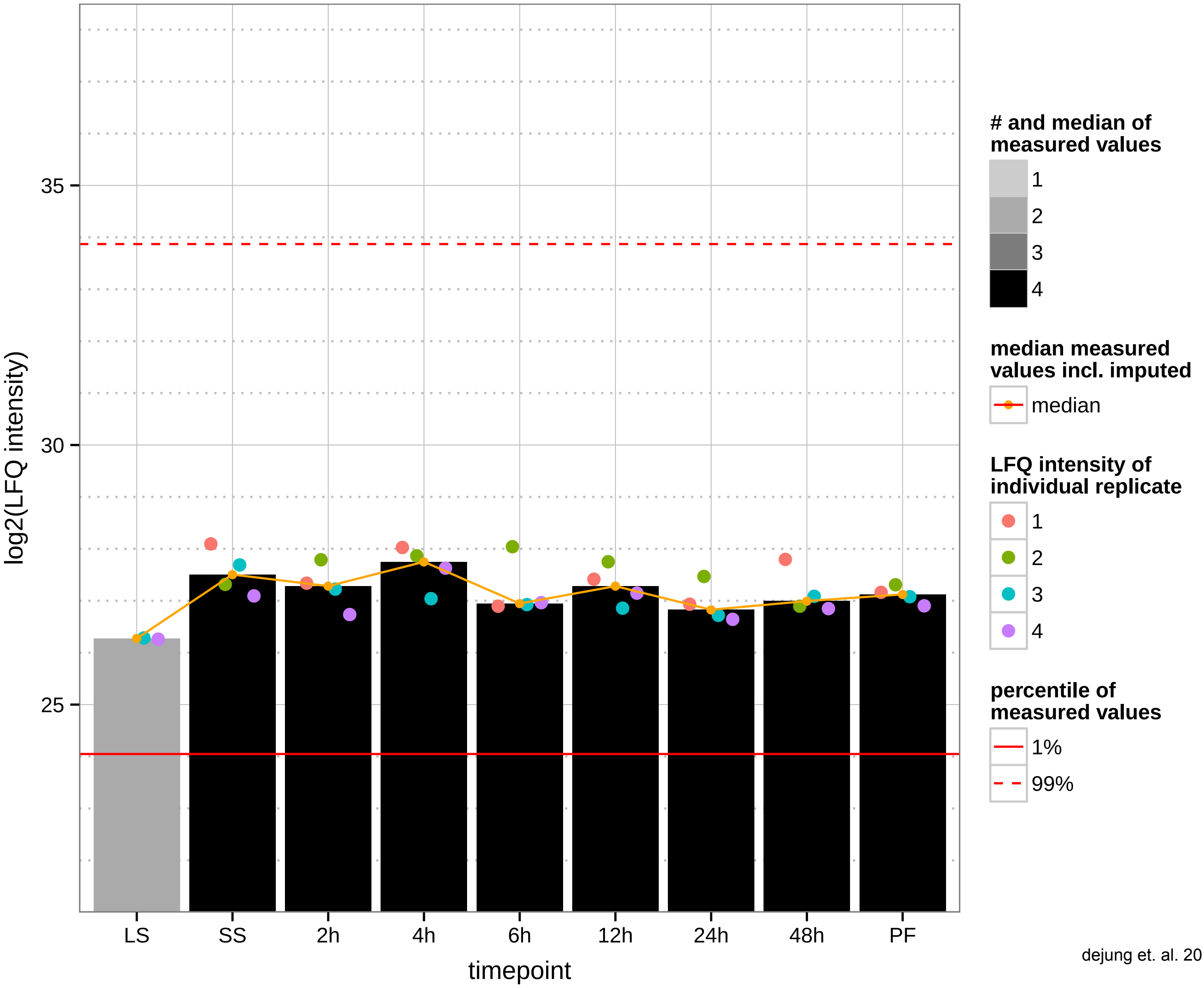
hypothetical protein, conserved
Tb927.3.800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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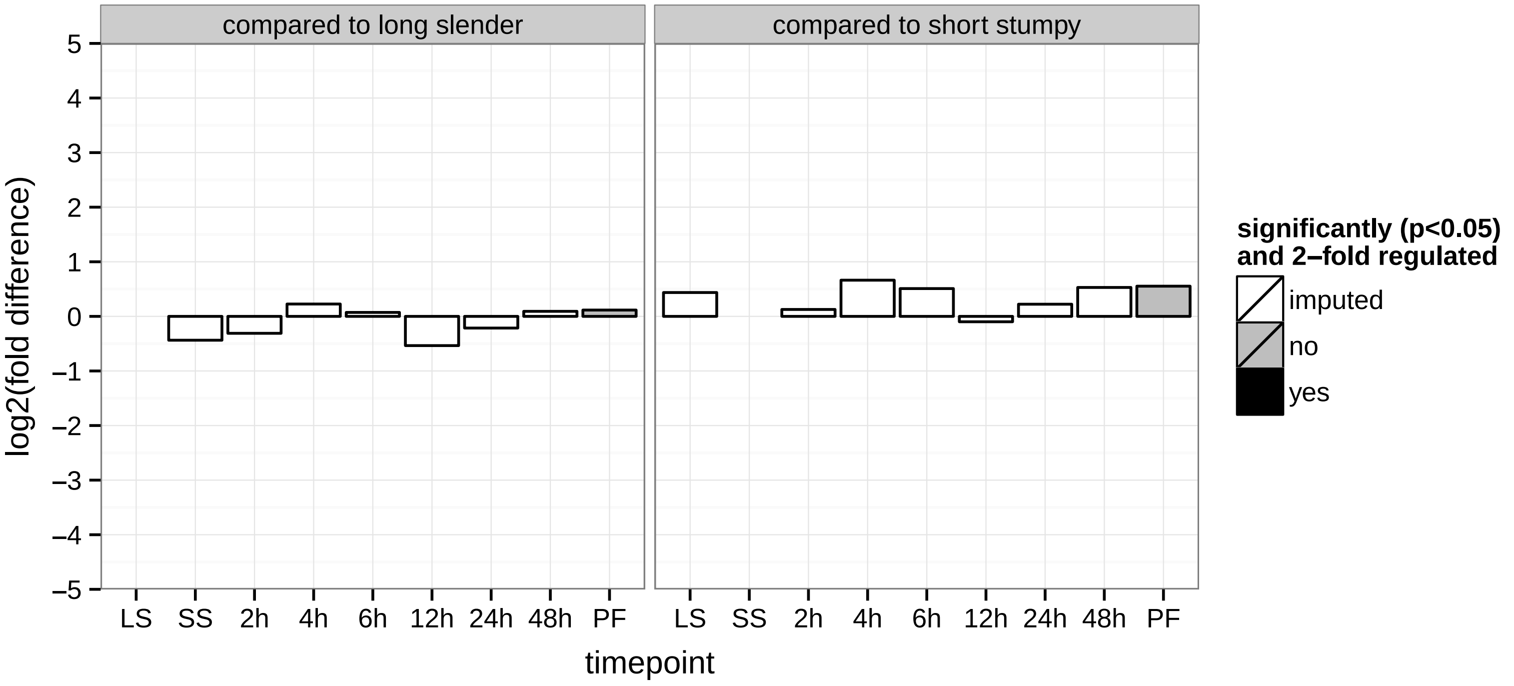
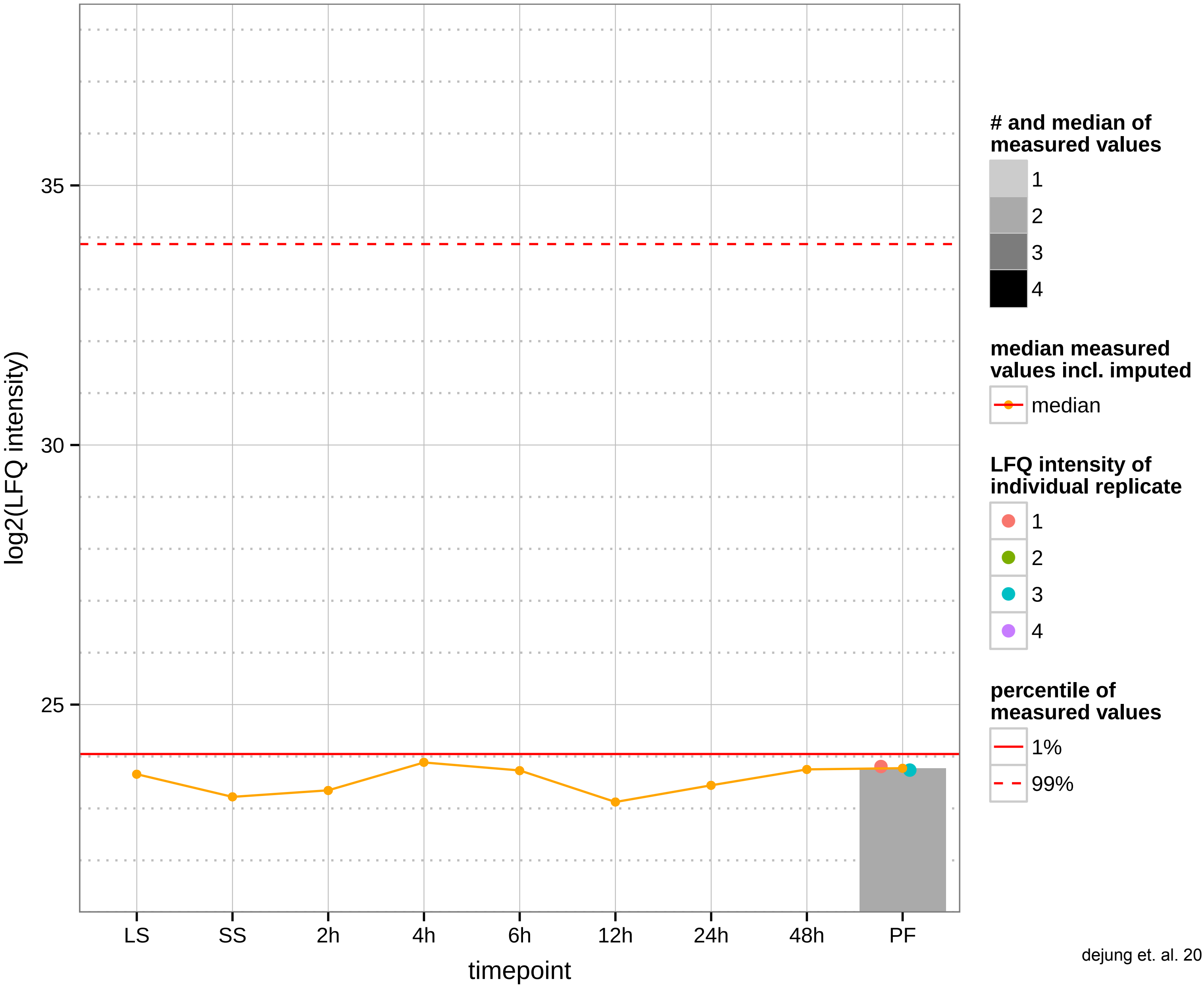
hypothetical protein, conserved
Tb927.3.900
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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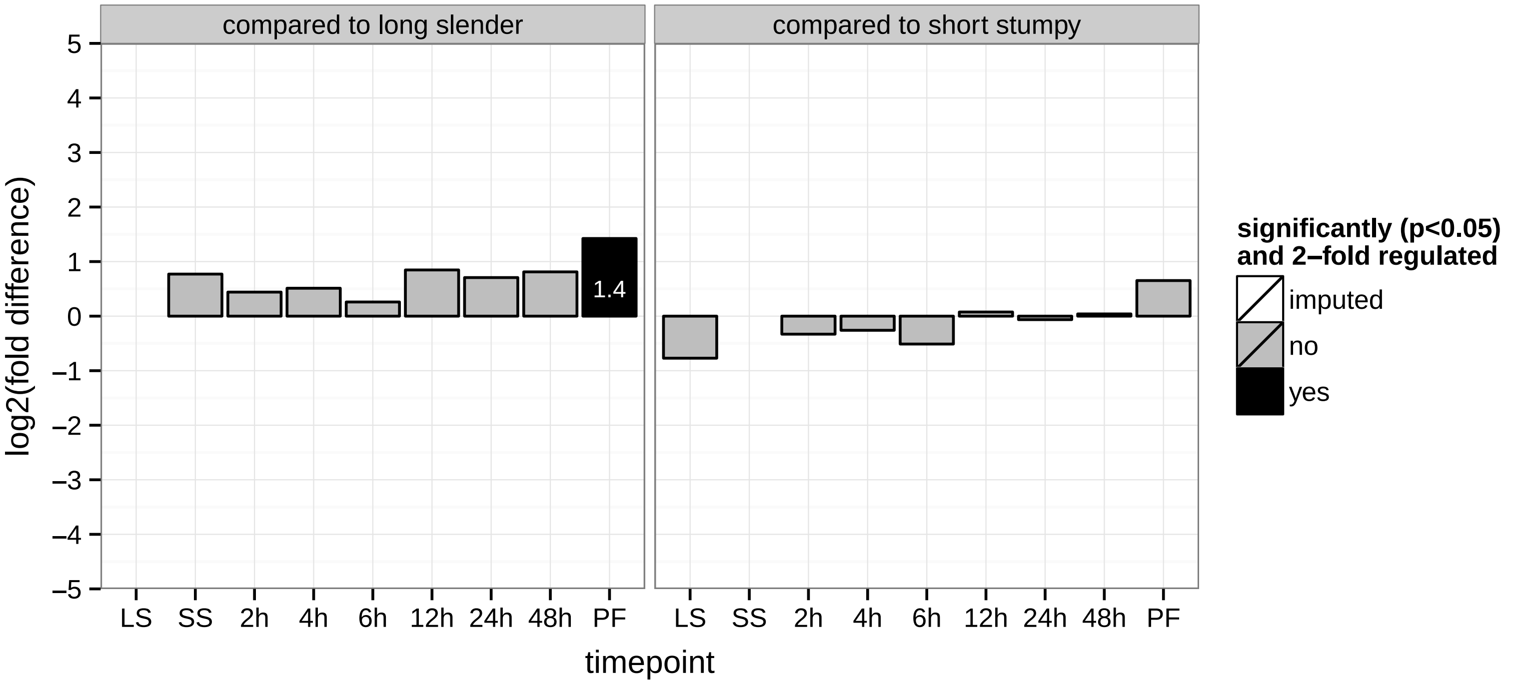
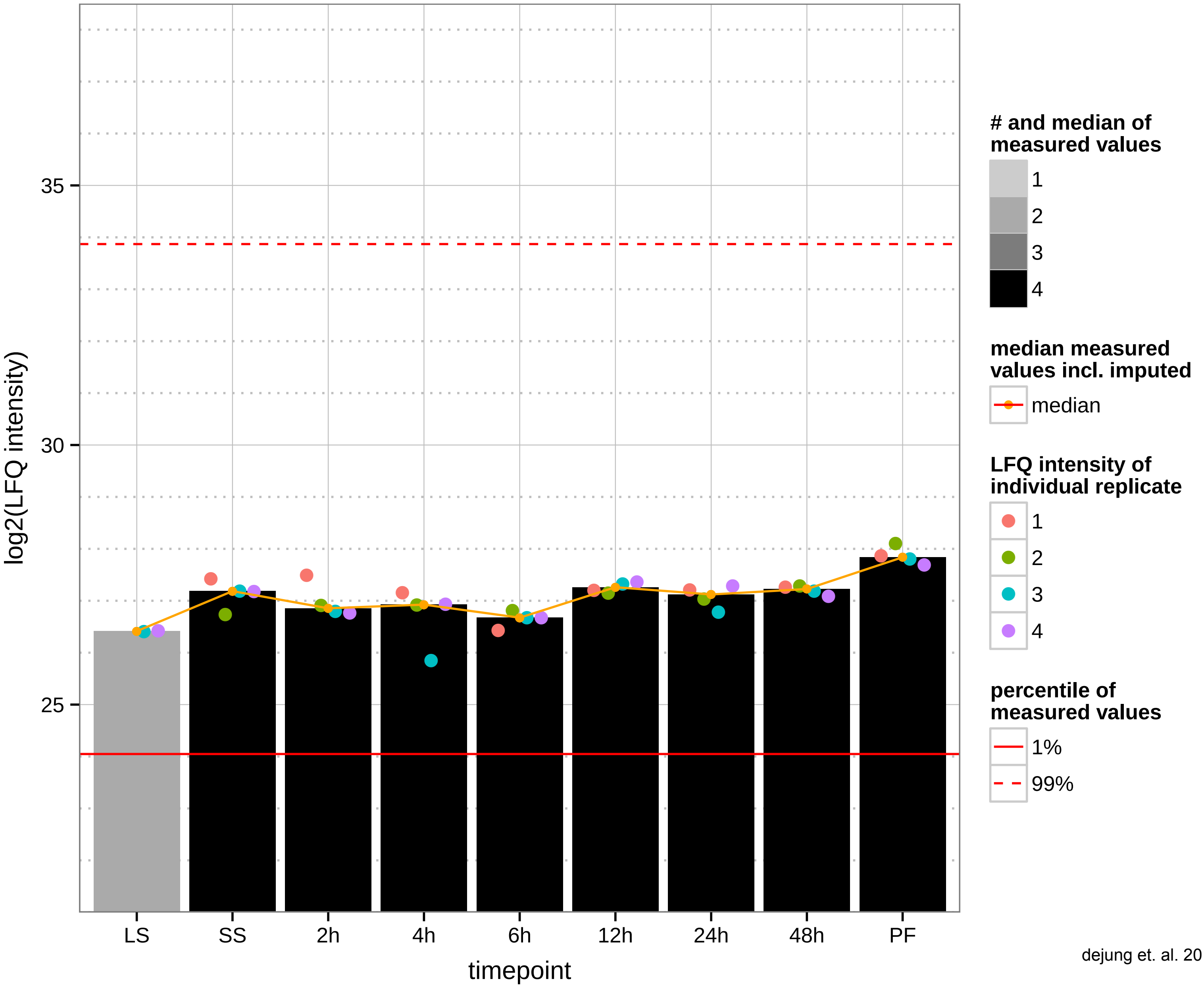
gamma–tubulin, tubulin gamma chain
Tb927.3.910
AGOF: GTP binding, GTPase activity, microtubule binding
AGOC: cilium basal body, microtubule organizing center, protein complex, spindle pole
AGOP: cell growth, microtubule nucleation, protein polymerization
PGOF: GTP binding, GTPase activity
PGOC: protein complex
PGOP: GTP catabolic process, protein polymerization





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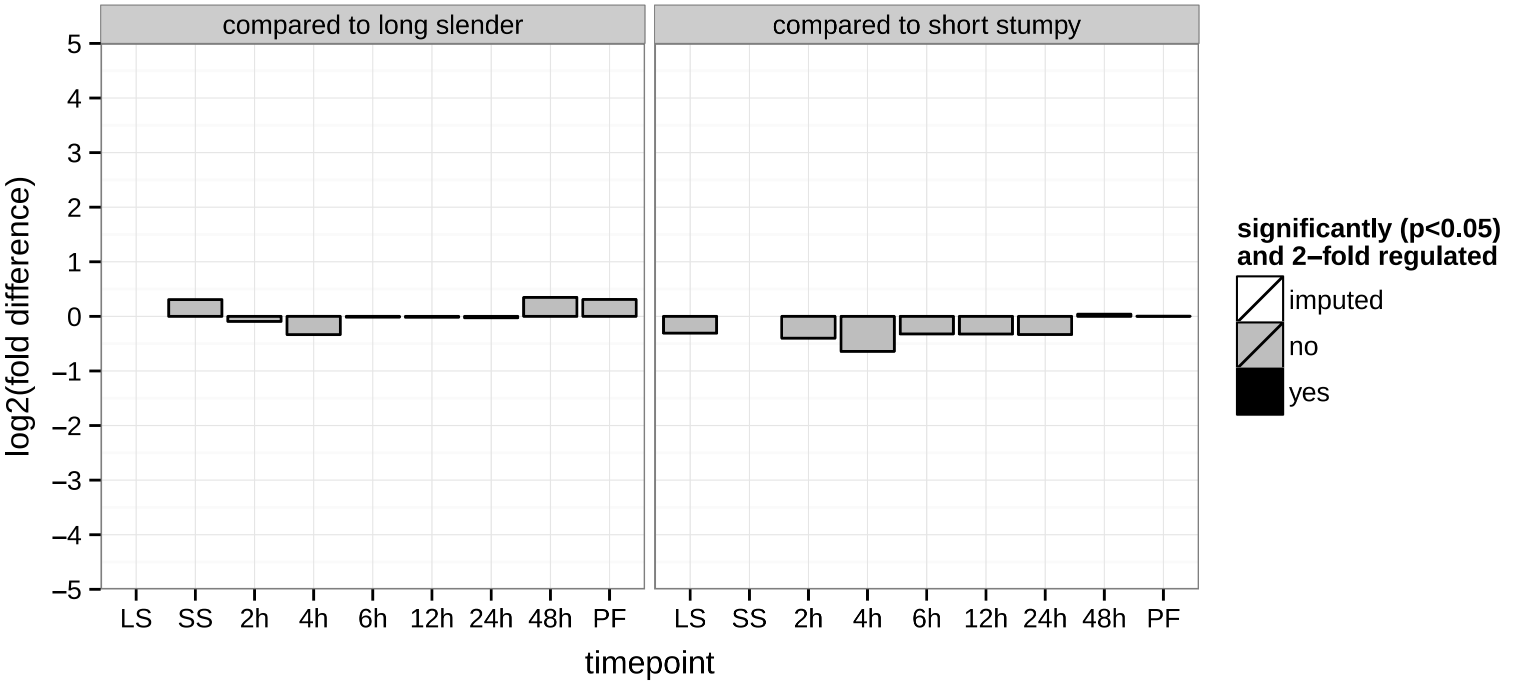
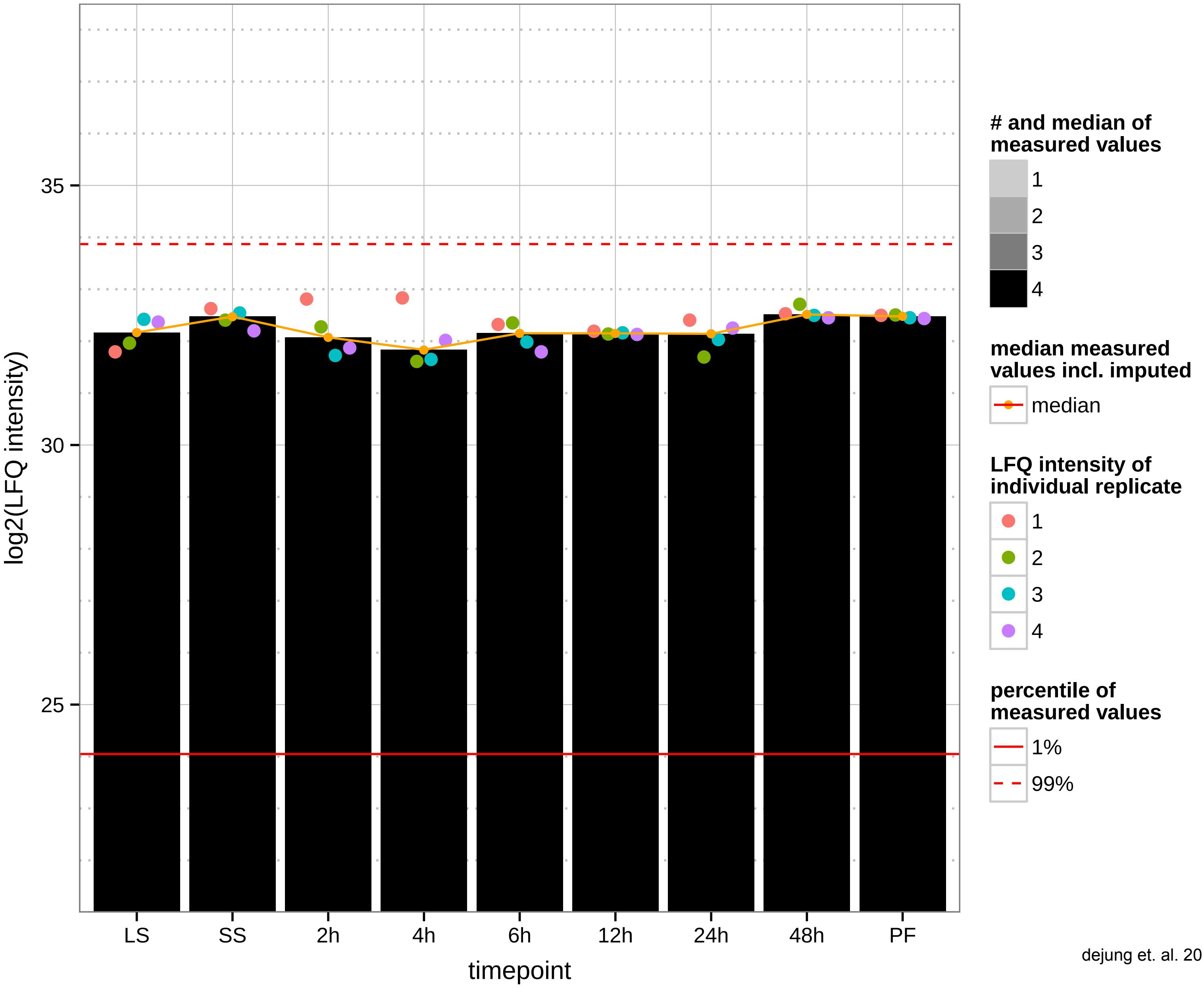
dynein heavy chain, putative
Tb927.3.930
AGOF: ATP binding, ATPase activity, microtubule motor activity
AGOC: dynein complex
AGOP: microtubule–based movement
PGOF: microtubule motor activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: dynein complex
PGOP: microtubule–based movement





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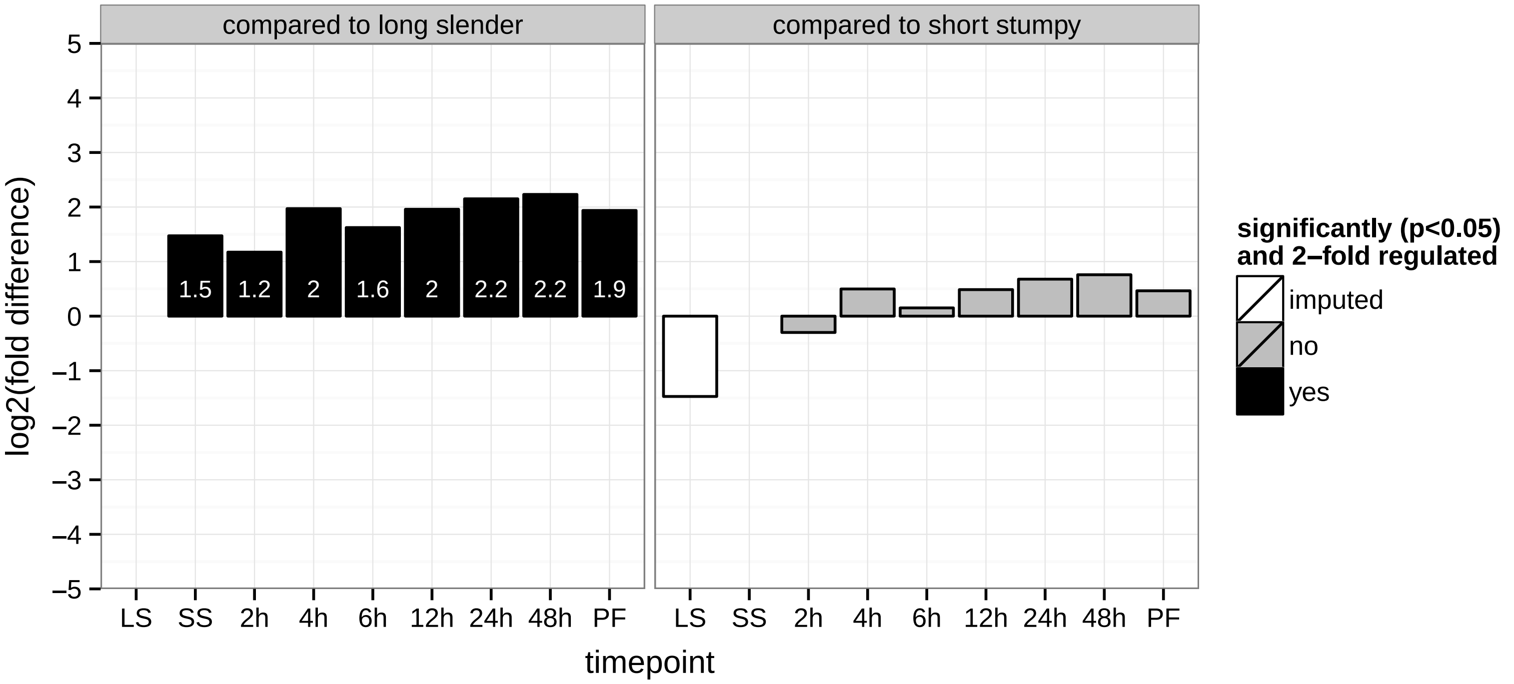
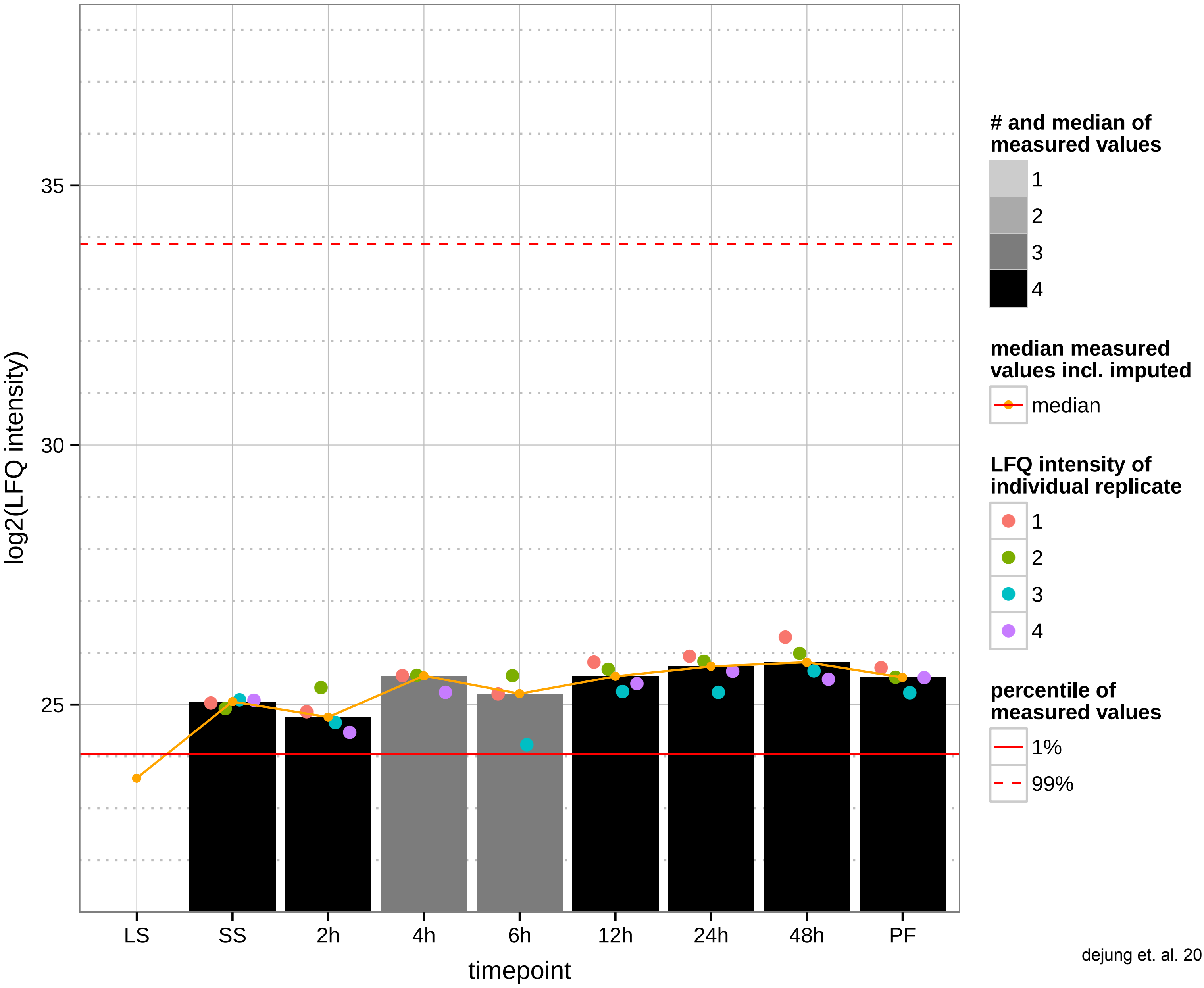
hypothetical protein, conserved
Tb927.3.970
AGOF: phosphogluconate dehydrogenase (decarboxylating) activity
AGOC: mitochondrion
AGOP: pentose−phosphate shunt
PGOF: phosphogluconate dehydrogenase (decarboxylating) activity
PGOC: null
PGOP: oxidation−reduction process, pentose−phosphate shunt





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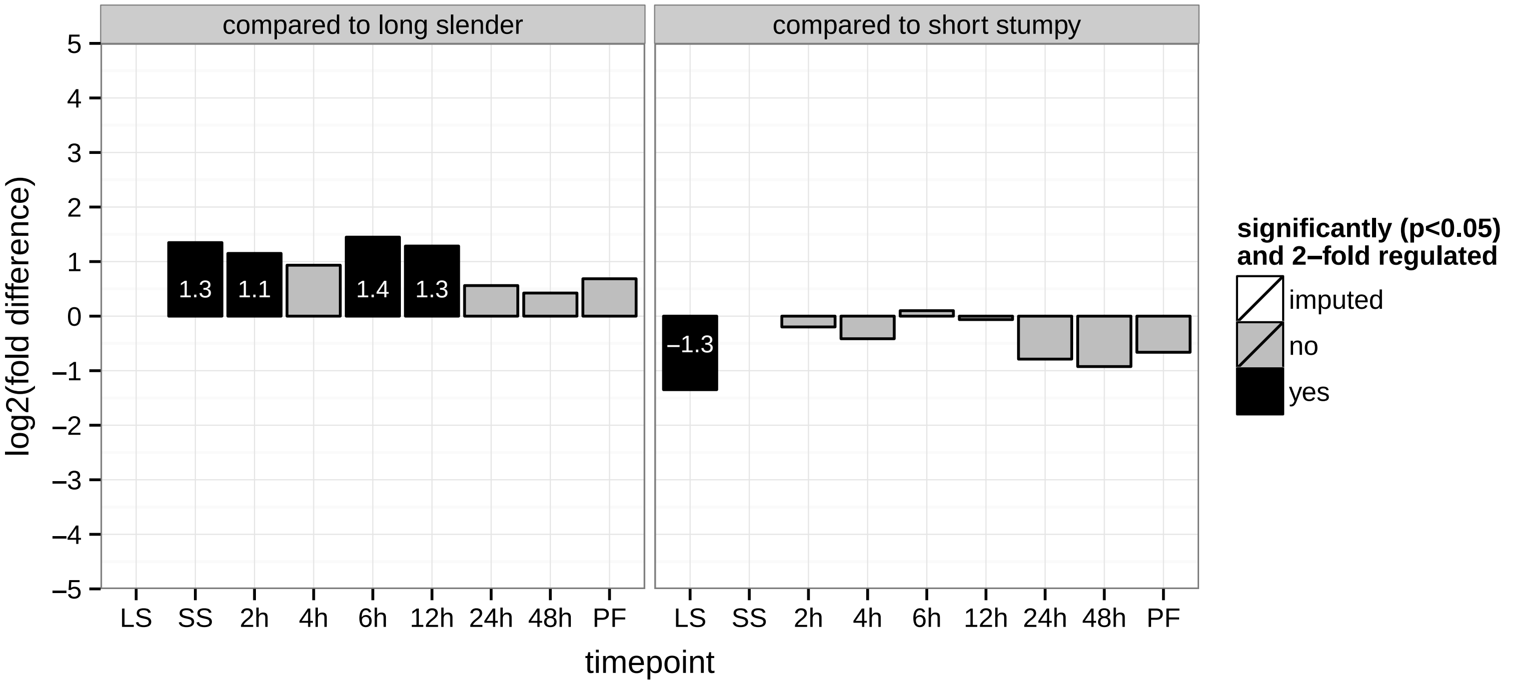
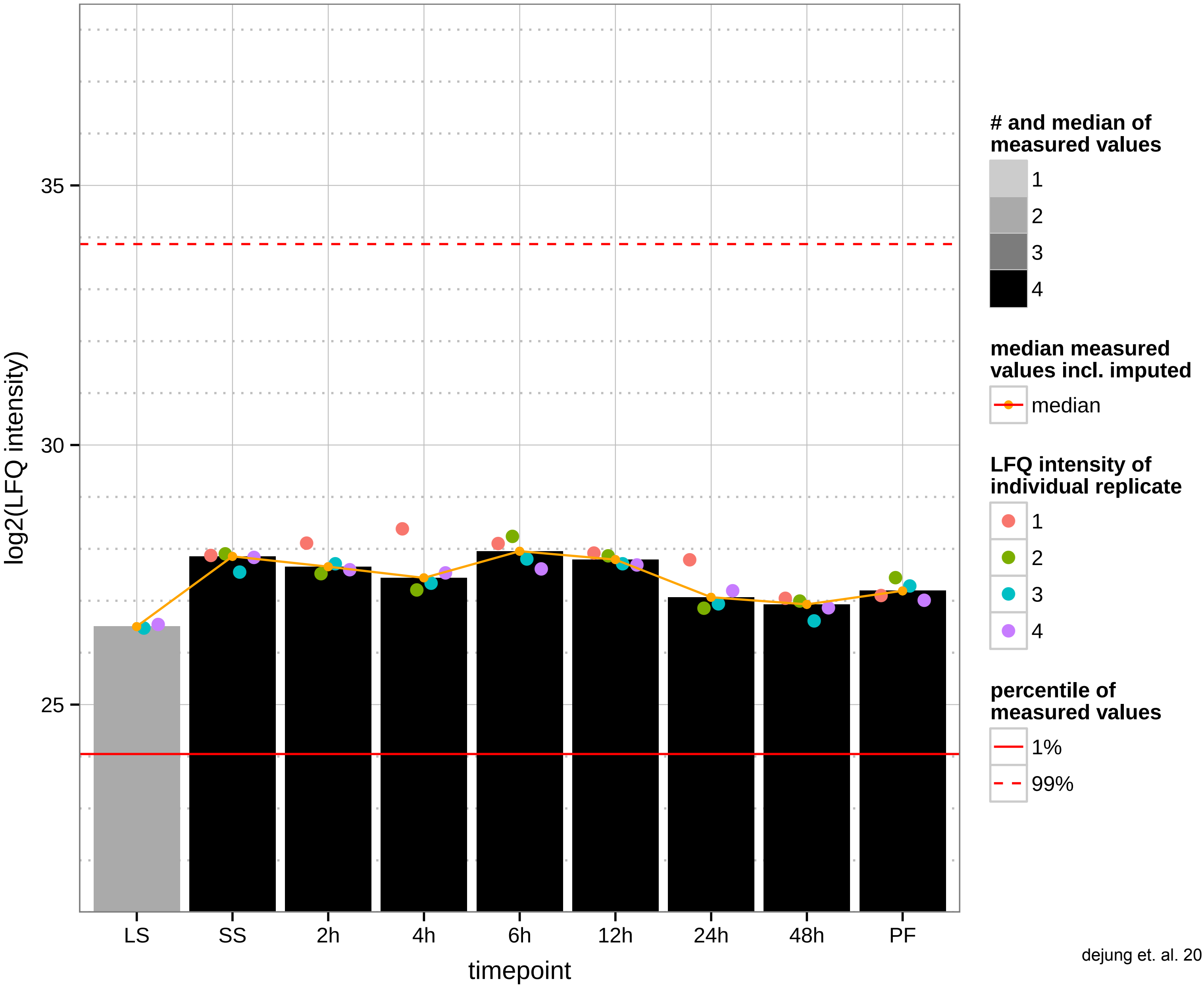
hypothetical protein, conserved
Tb927.3.980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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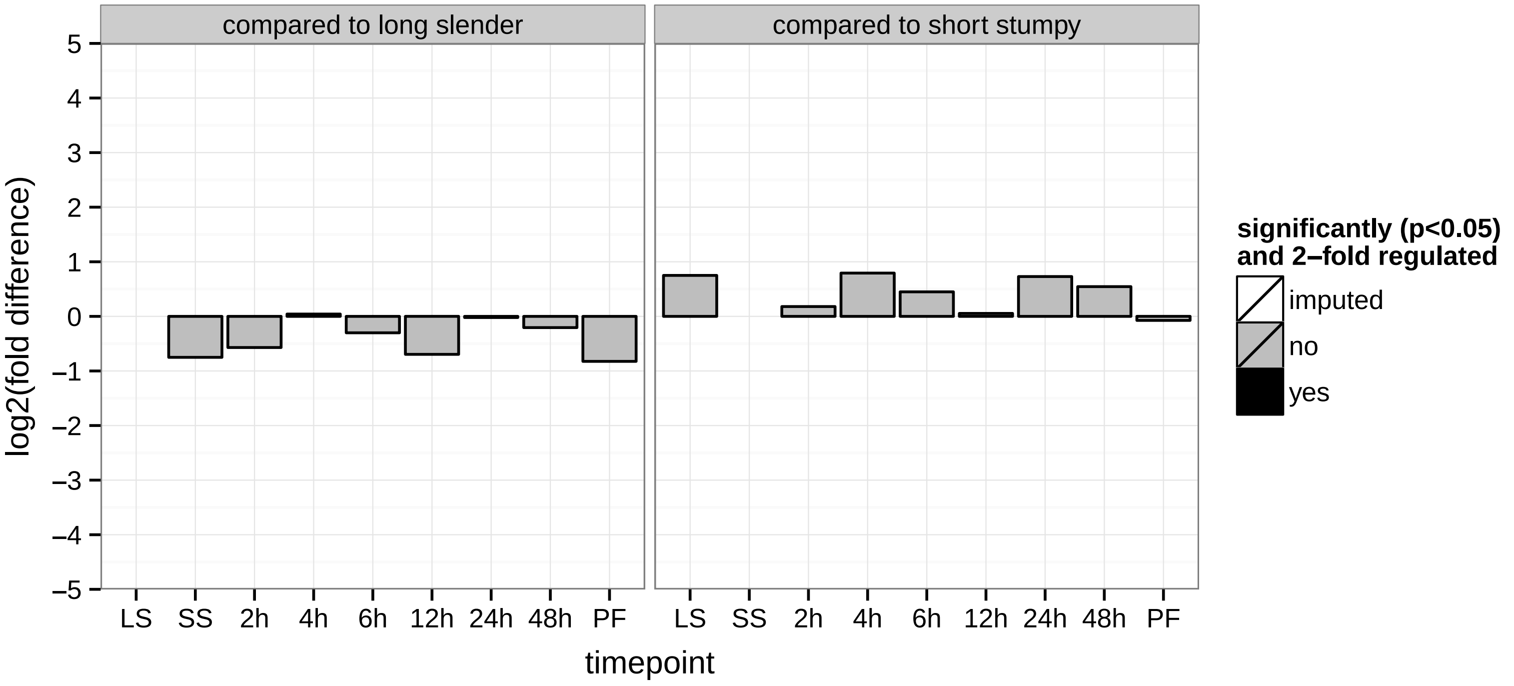
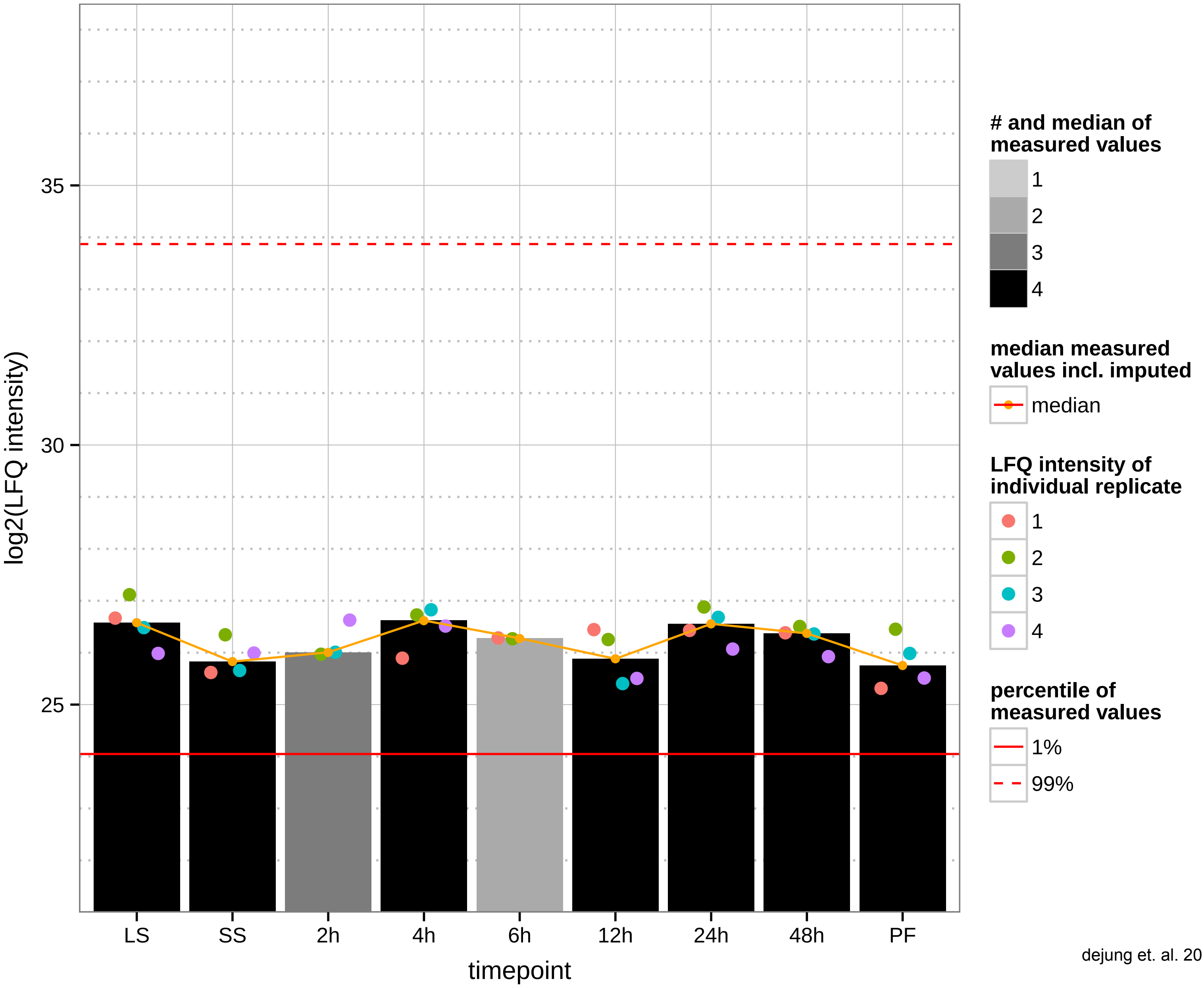
hypothetical protein, conserved
Tb927.4.1040
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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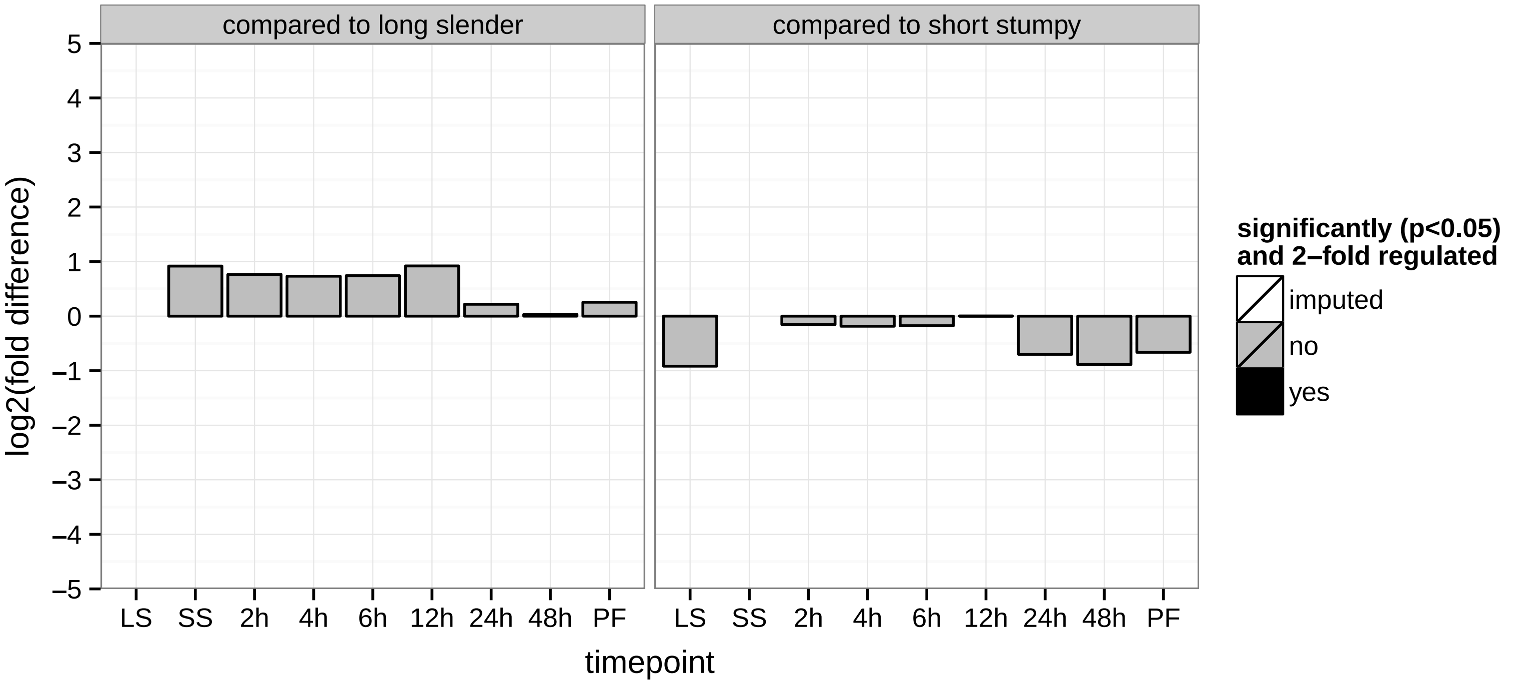
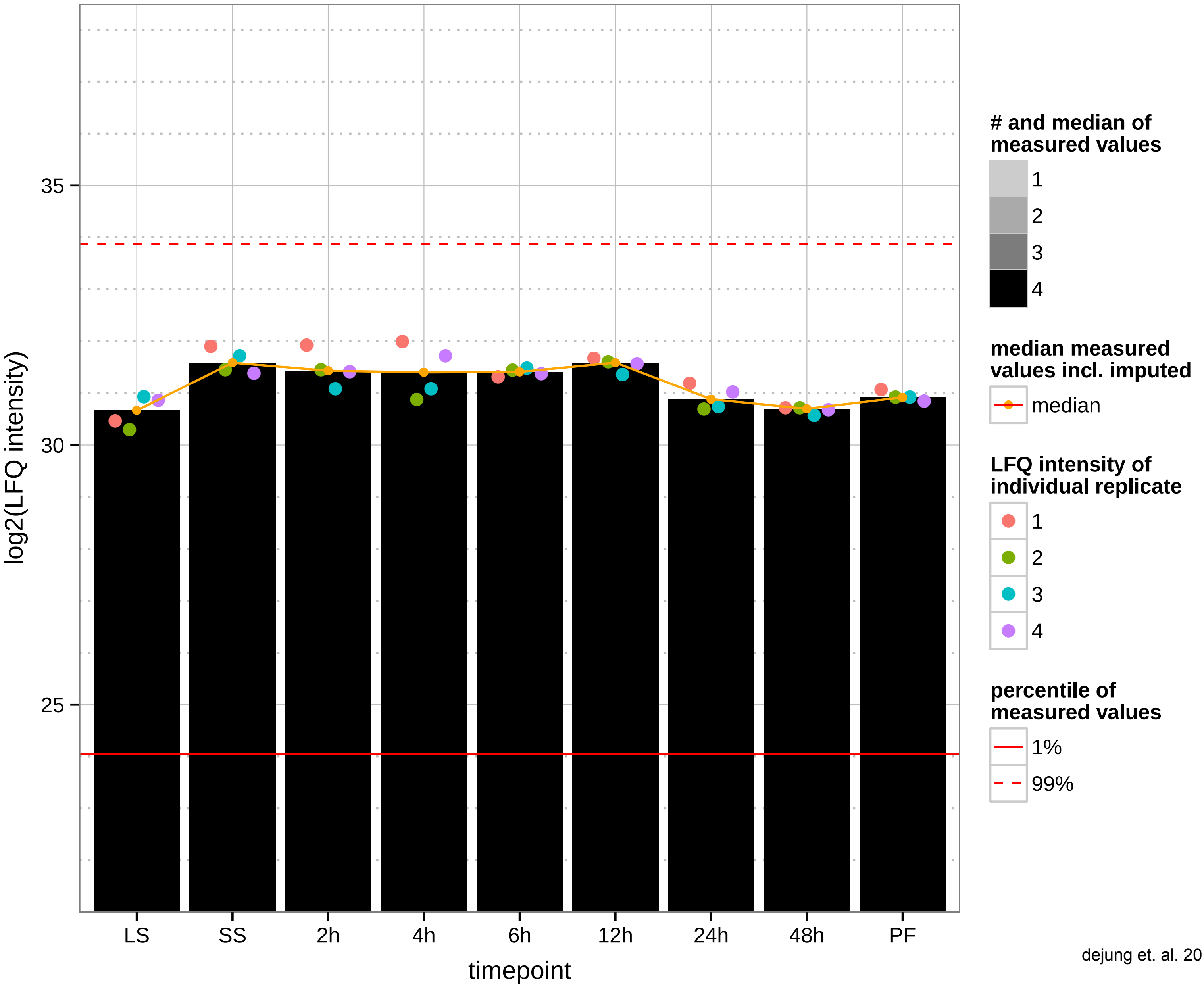
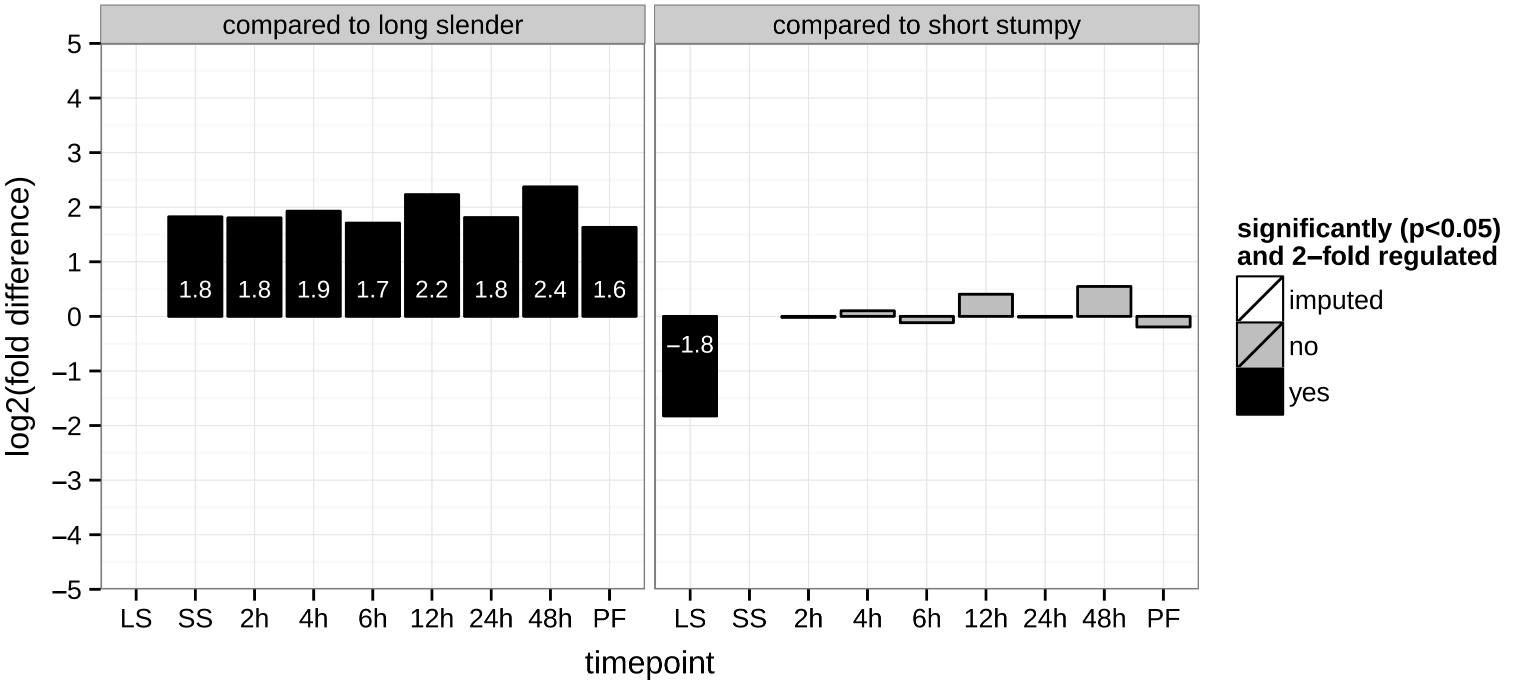
V−type ATPase, A subunit, putative
Tb927.4.1080
AGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, proton−transporting ATPase activity
AGOC: proton−transporting V−type ATPase, V1 domain, proton−transporting two−sector ATPase complex
AGOP: ATP synthesis coupled proton transport
PGOF: ATP binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrolase activity, acting on acid
PGOC: proton−transporting V−type ATPase, V1 domain, proton−transporting two−sector ATPase complex, catalytic domain
PGOP: ATP hydrolysis coupled proton transport, ATP metabolic process, proton transport

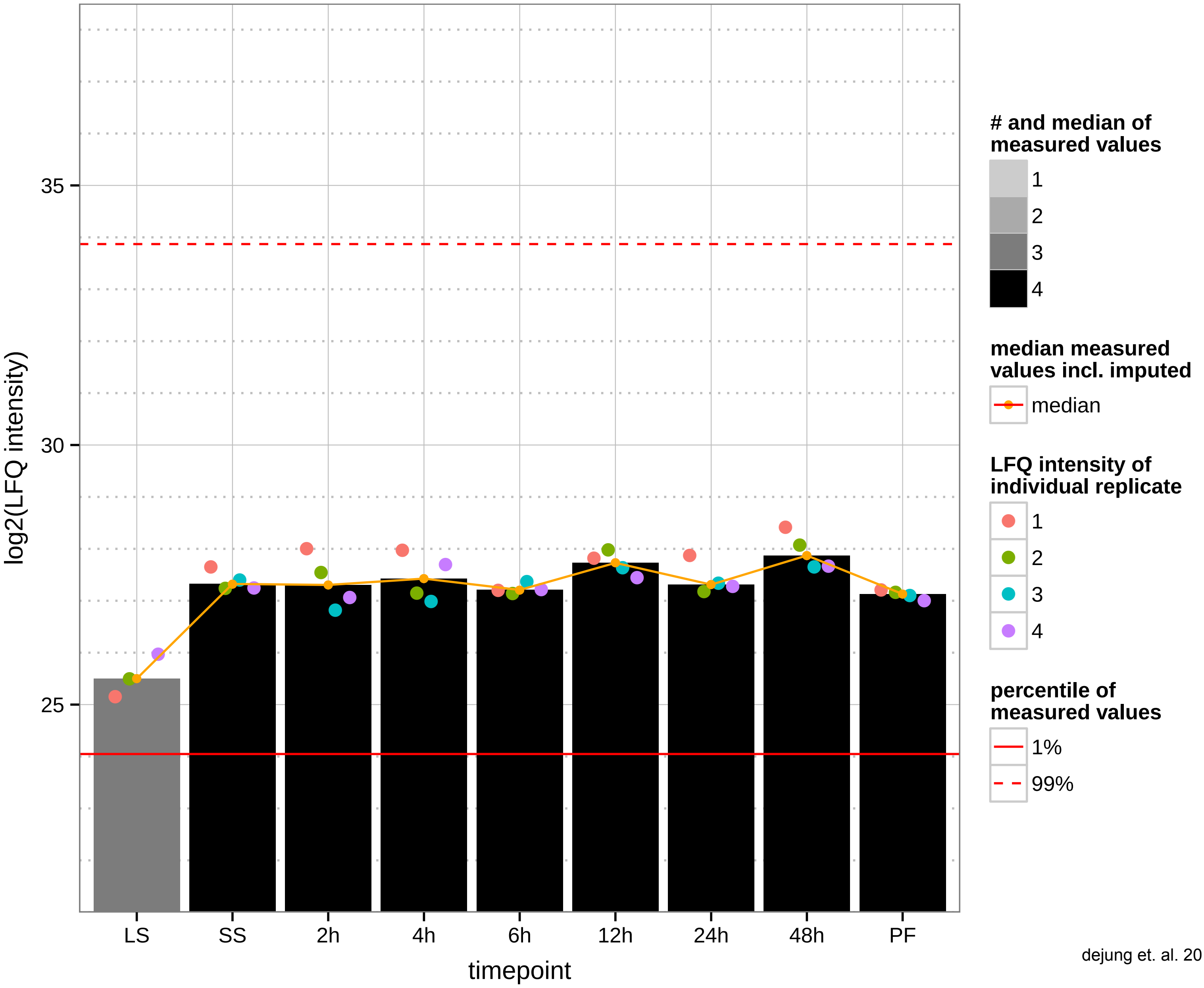




dejung et. al. 2015

retrotransposon hot spot protein (RHS, pseudogene), putative, retrotransposon hot spot protein 1 (RHS1), interrupted
Tb927.4.110
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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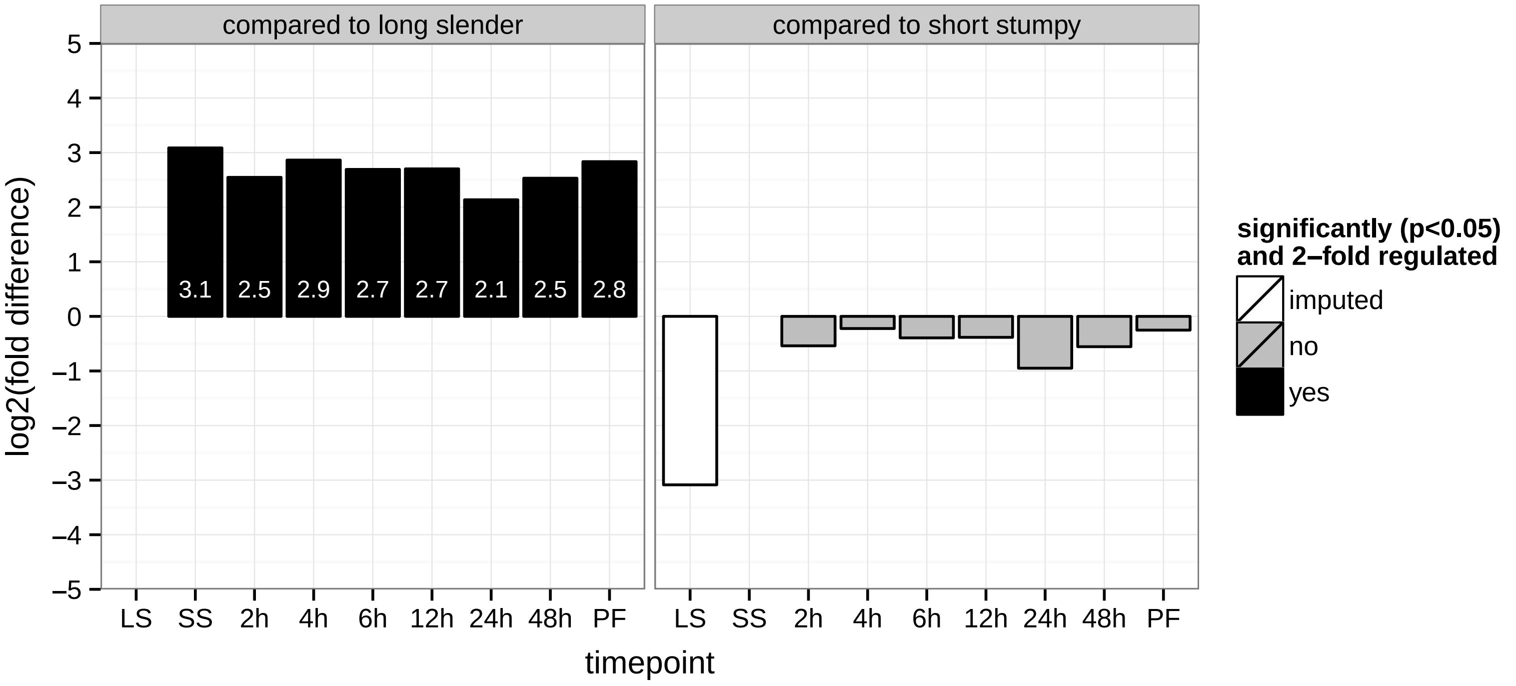
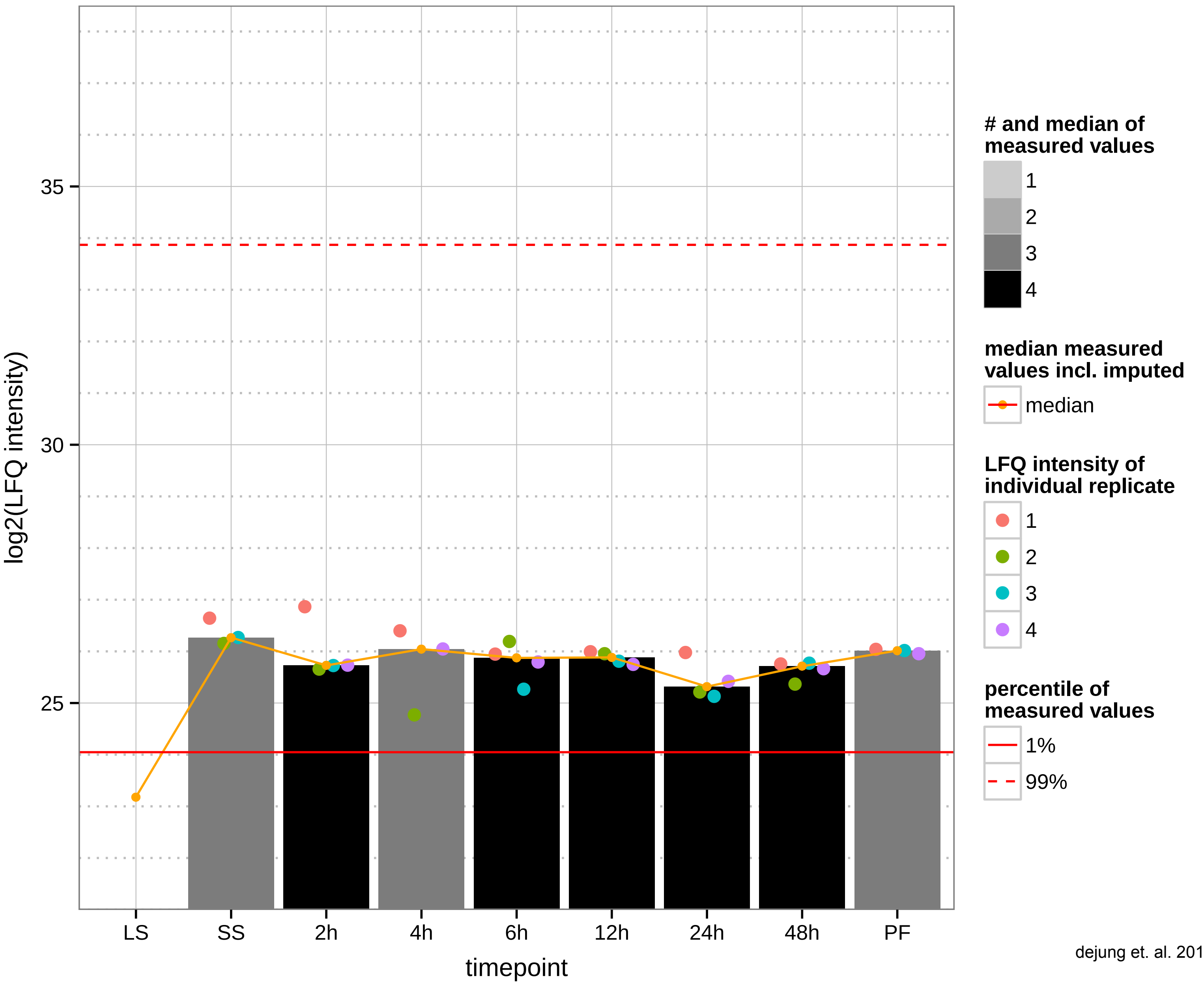
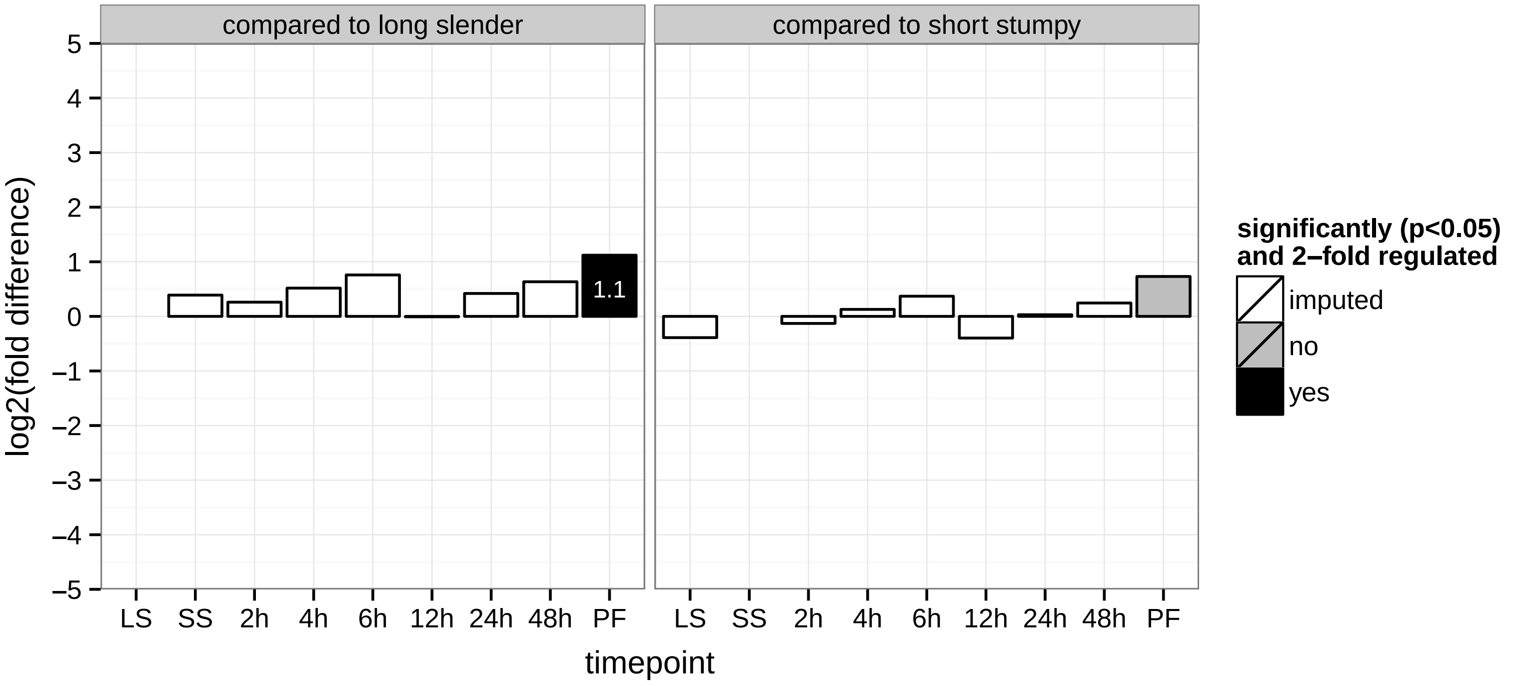
phosphatidylinositol 4−kinase, putative
Tb927.4.1140
AGOF: 1−phosphatidylinositol 4−kinase activity, phosphotransferase activity, alcohol group as acceptor
AGOC: cytosol
AGOP: phosphatidylinositol phosphorylation, phosphatidylinositol−mediated signaling
PGOF: phosphotransferase activity, alcohol group as acceptor, transferase activity, transferring phosphorus−containing group
PGOC: null
PGOP: null

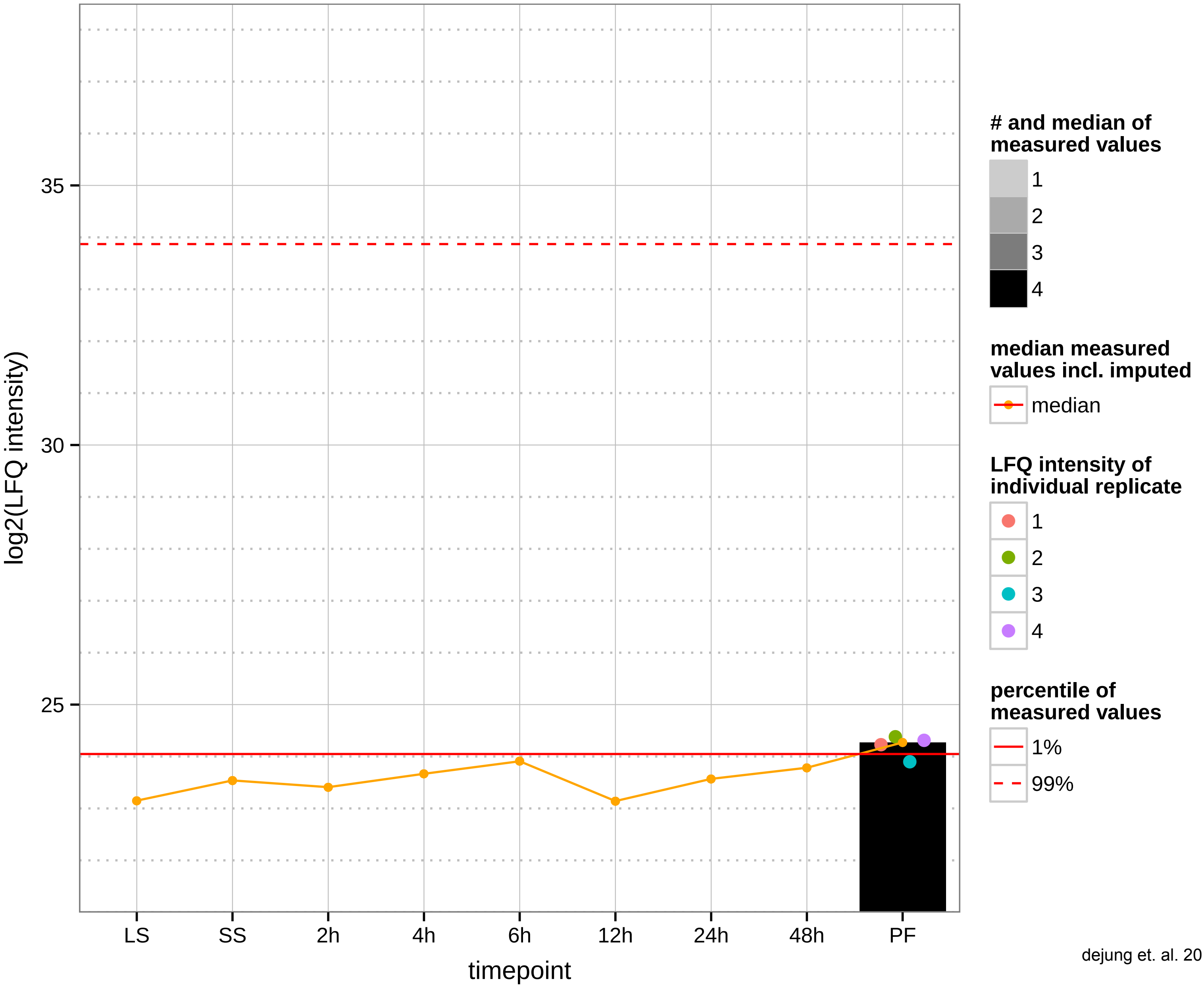




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.1150
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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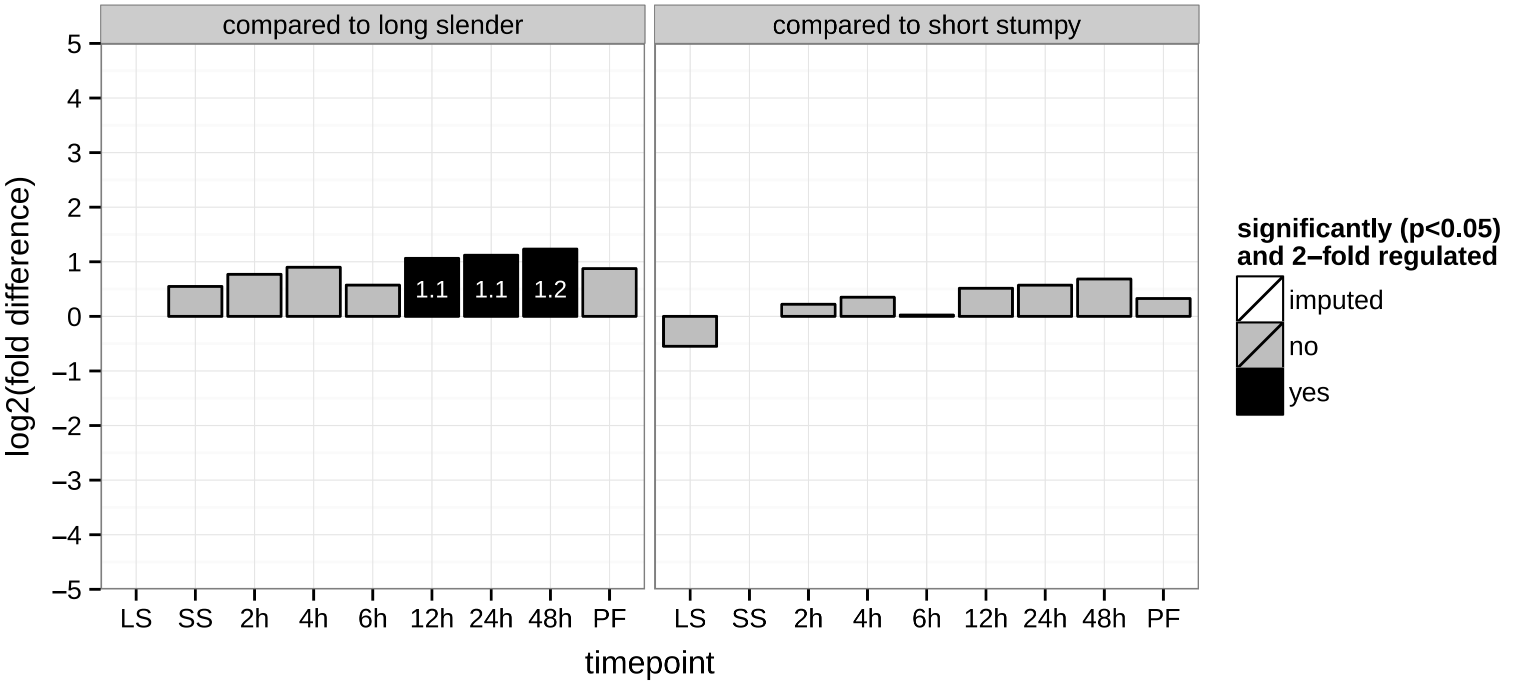
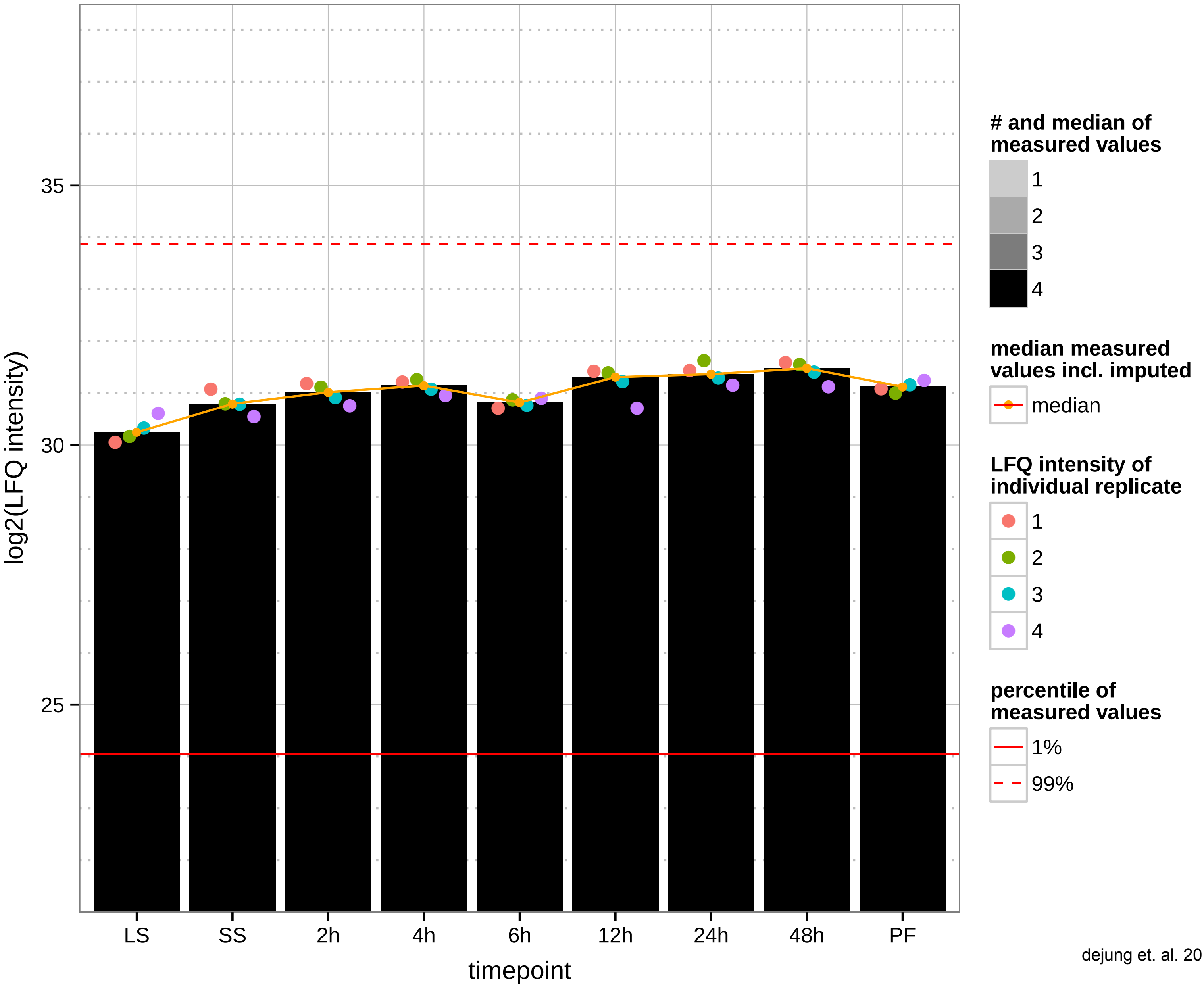
ruvB–like DNA helicase, putative
Tb927.4.1270
AGOF: ATP binding, DNA helicase activity, nucleoside–triphosphatase activity
AGOC: nucleus
AGOP: null
PGOF: ATP binding, DNA helicase activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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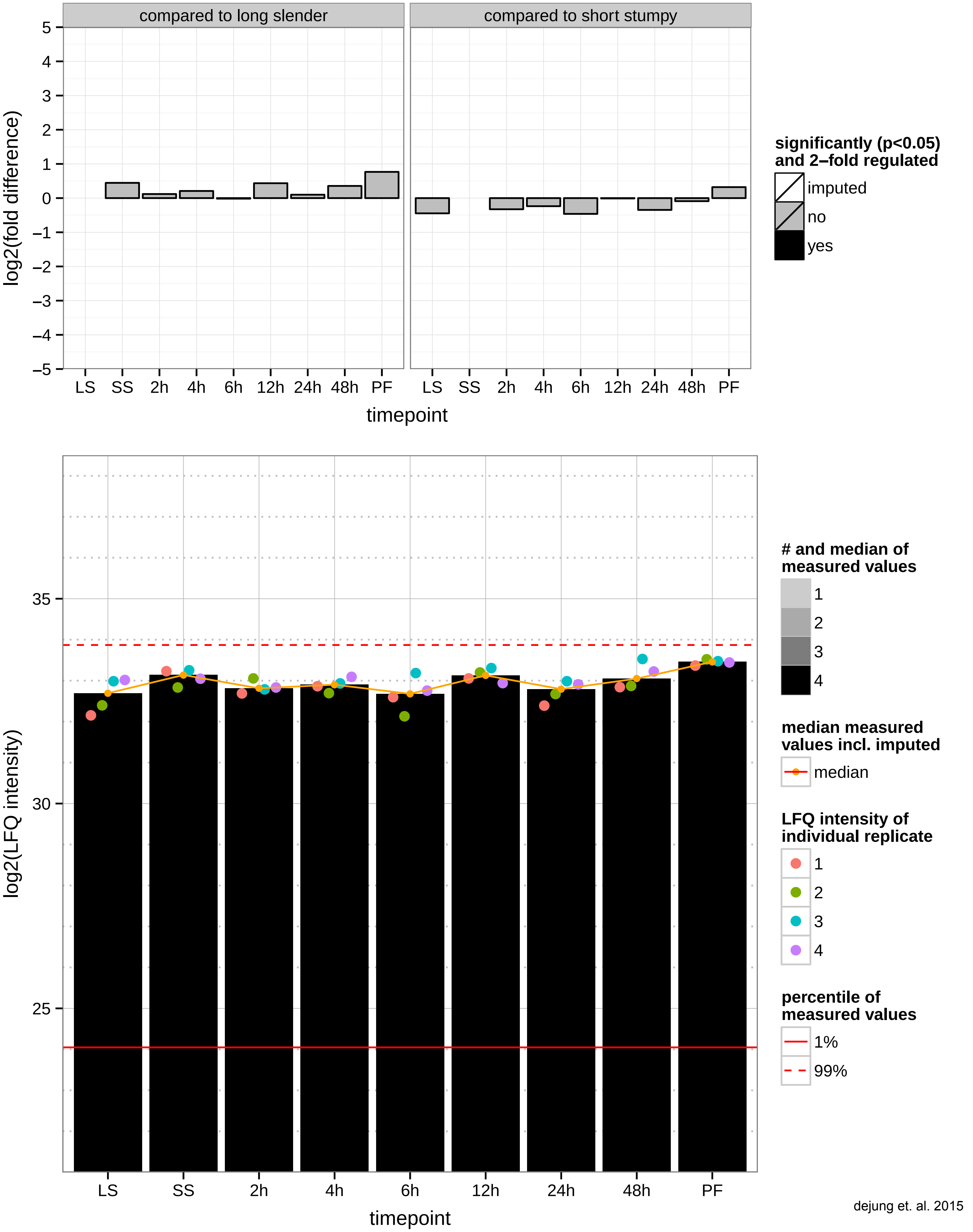
amidinotransferase, putative
Tb927.4.1300
AGOF: null
AGOC: null
AGOP: null
PGOF: hydrolase activity, acting on carbon–nitrogen (but not peptide) bonds, in linear amidines
PGOC: cytoplasm
PGOP: null



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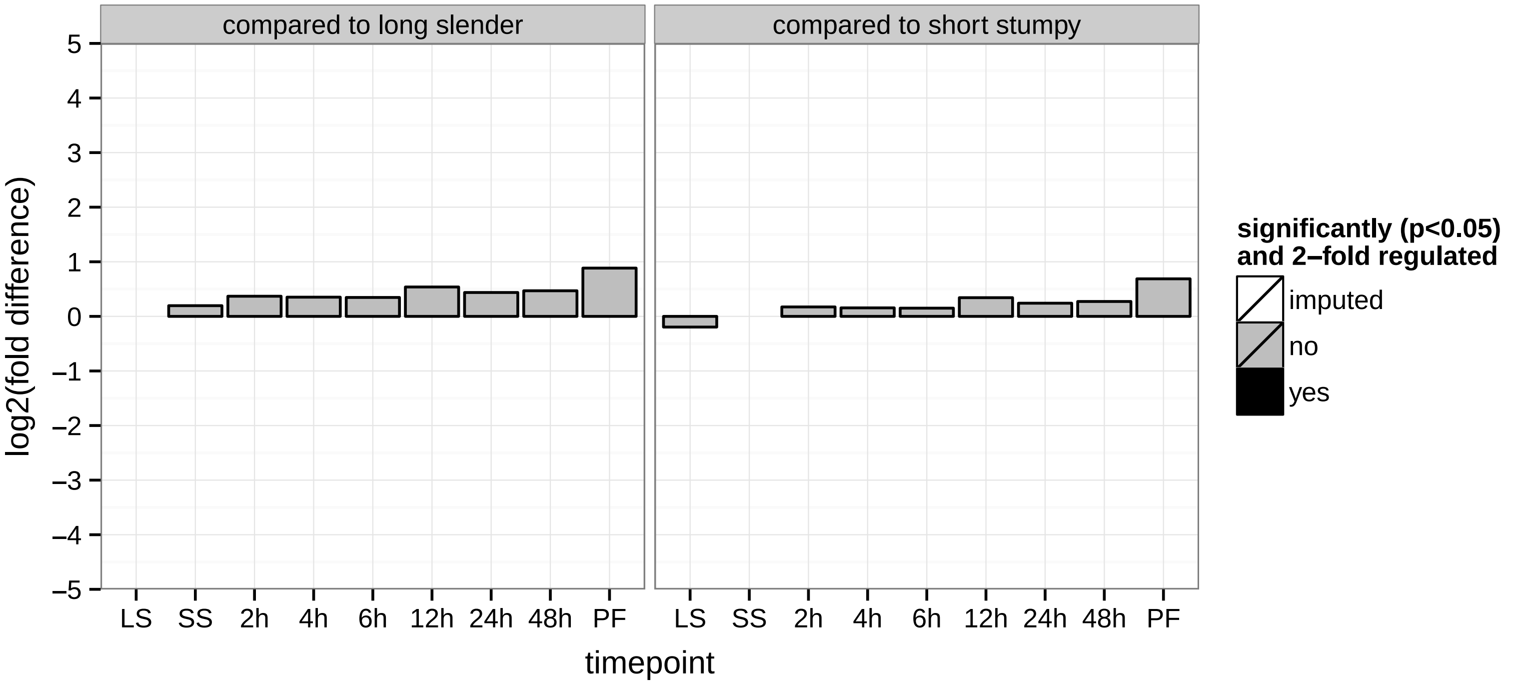
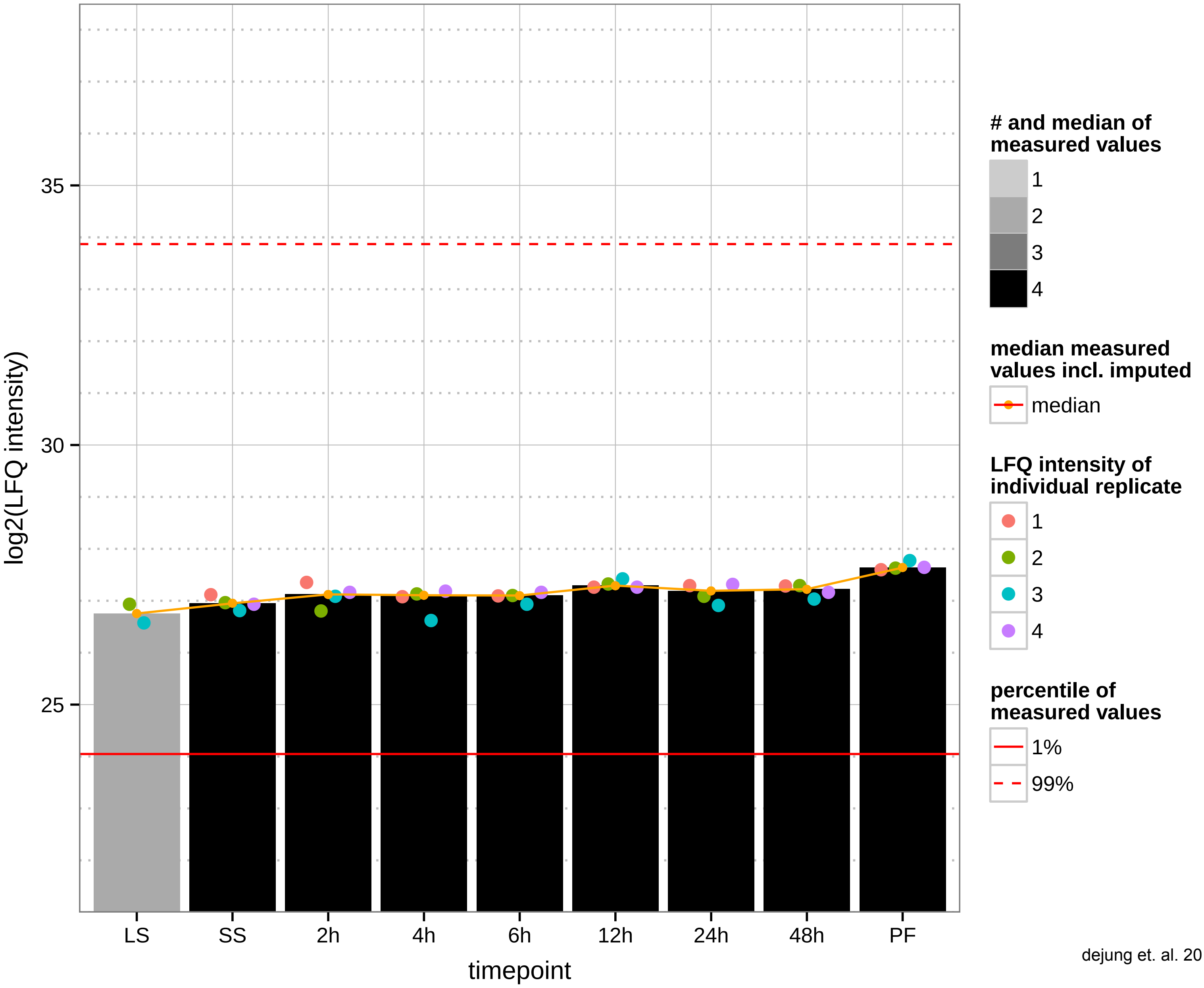
cleavage and polyadenylation specificity factor subunit, putative (CPSF3)
Tb927.4.1340
AGOF: hydrolase activity
AGOC: null
AGOP: null
PGOF: hydrolase activity
PGOC: null
PGOP: null





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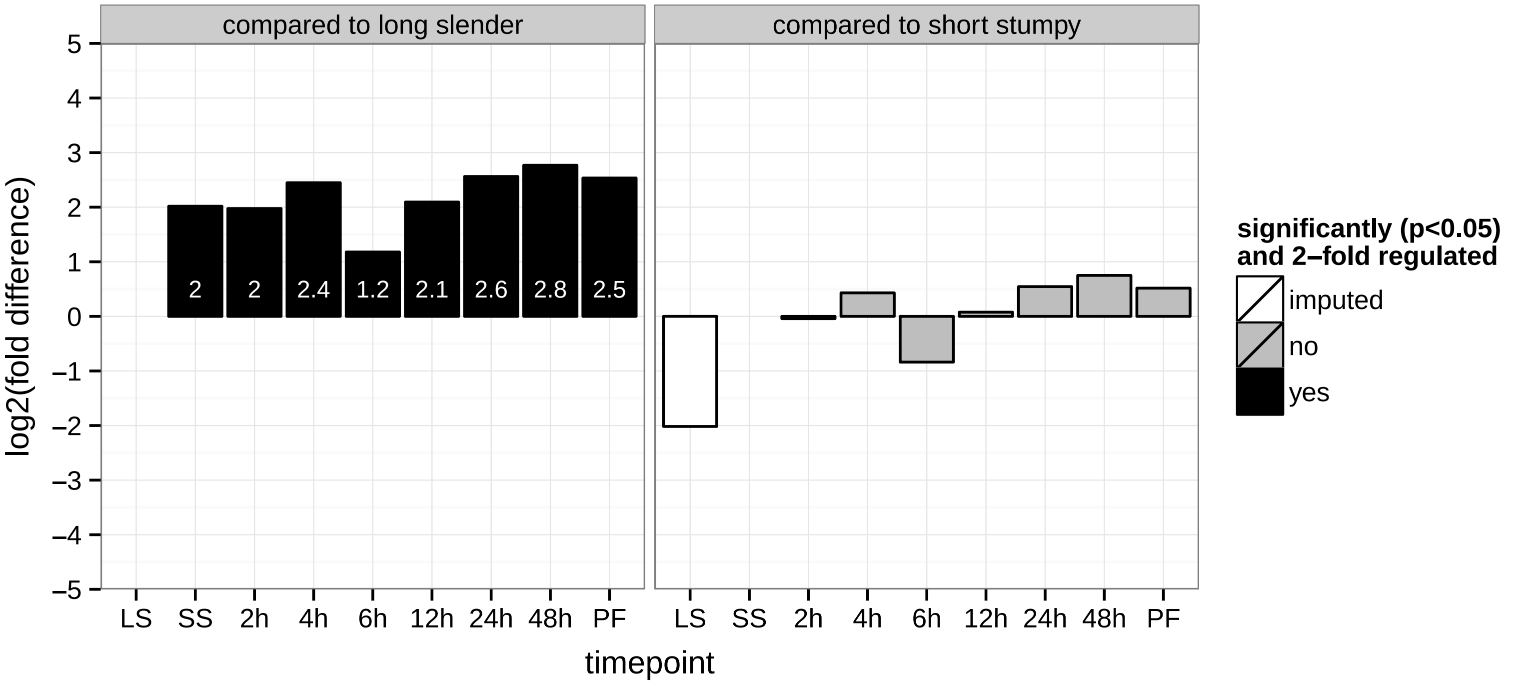
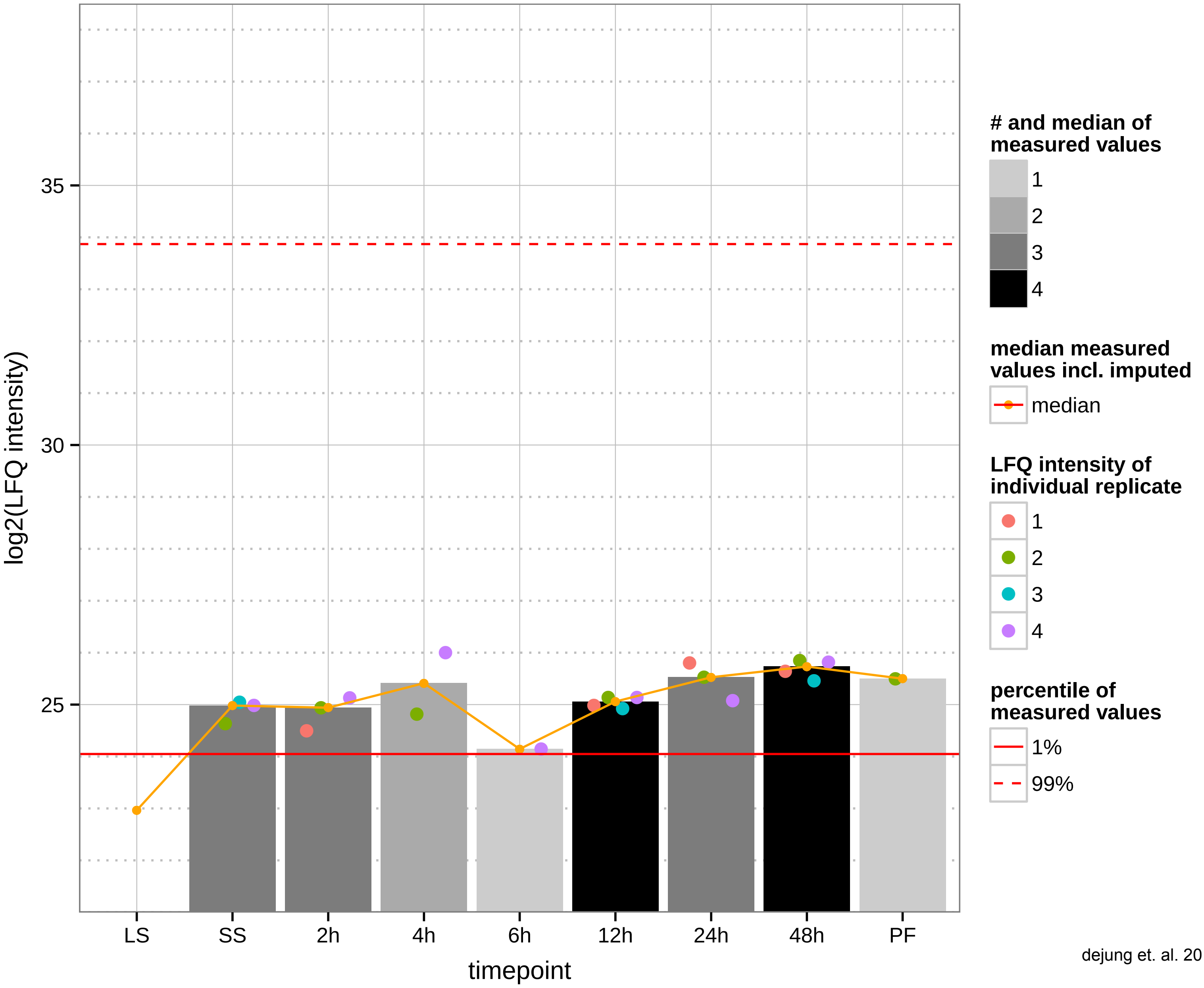
hypothetical protein, conserved
Tb927.4.1420
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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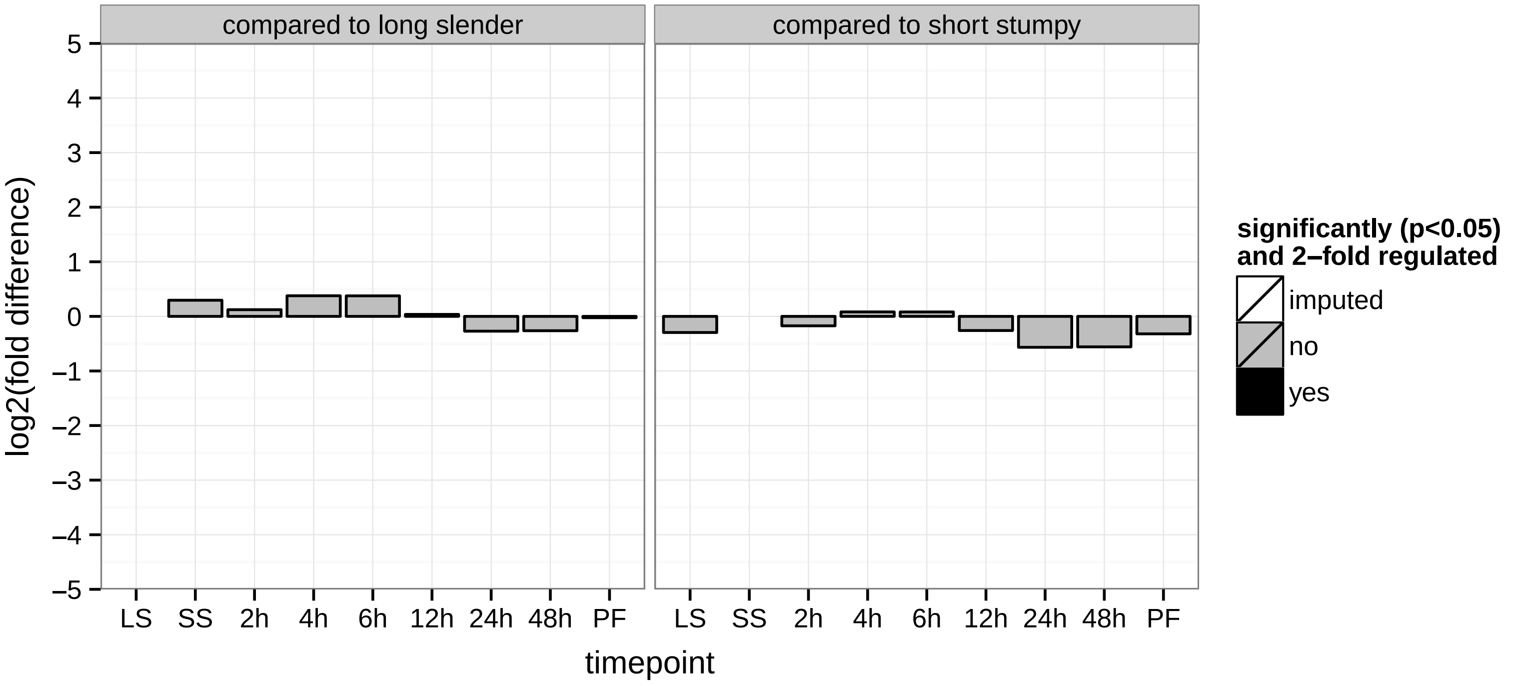
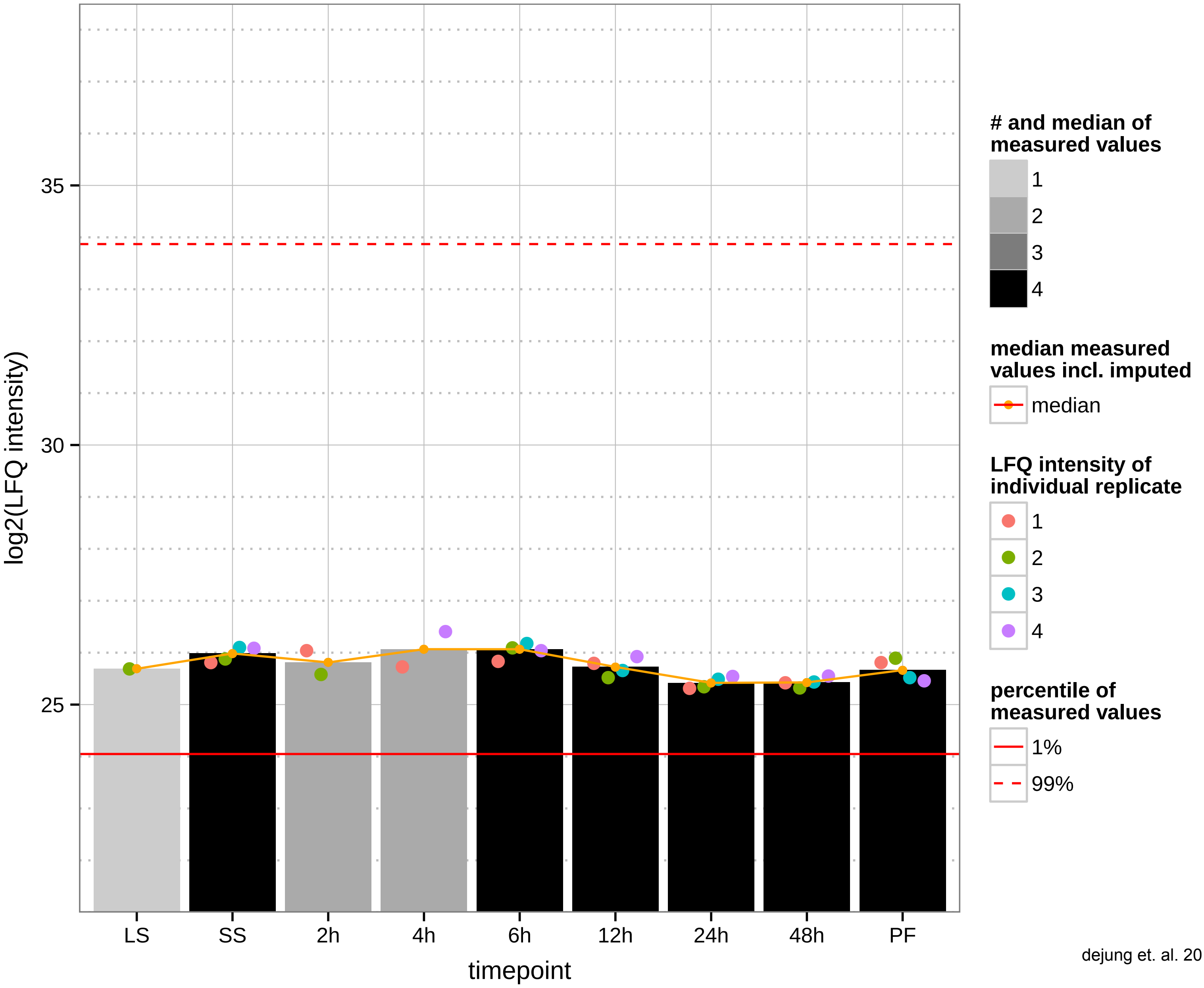
phospholipid–translocating ATPase, putative
Tb927.4.1510
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, magnesium
AGOC: integral to membrane, membrane
AGOP: ATP biosynthetic process, phospholipid transport
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, hydrolase ac
PGOC: integral to membrane, membrane
PGOP: cation transport, phospholipid transport





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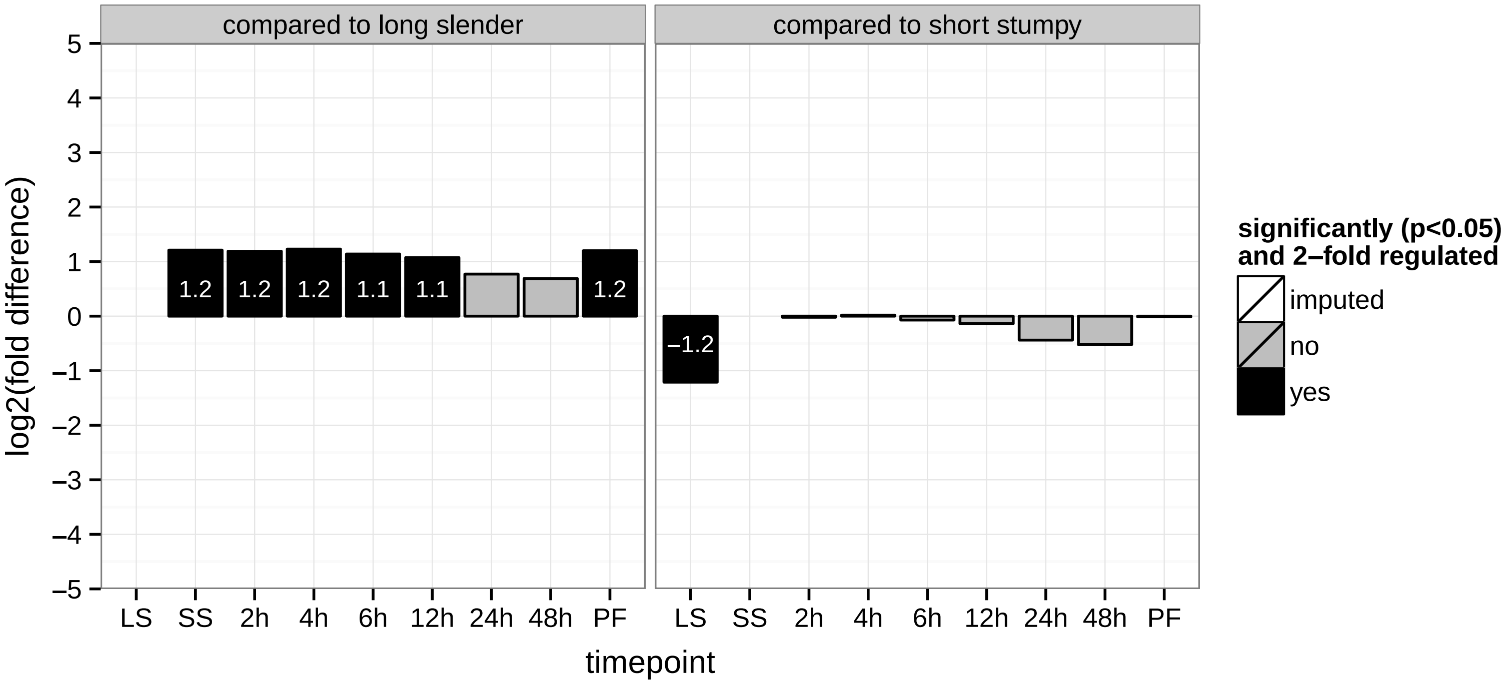
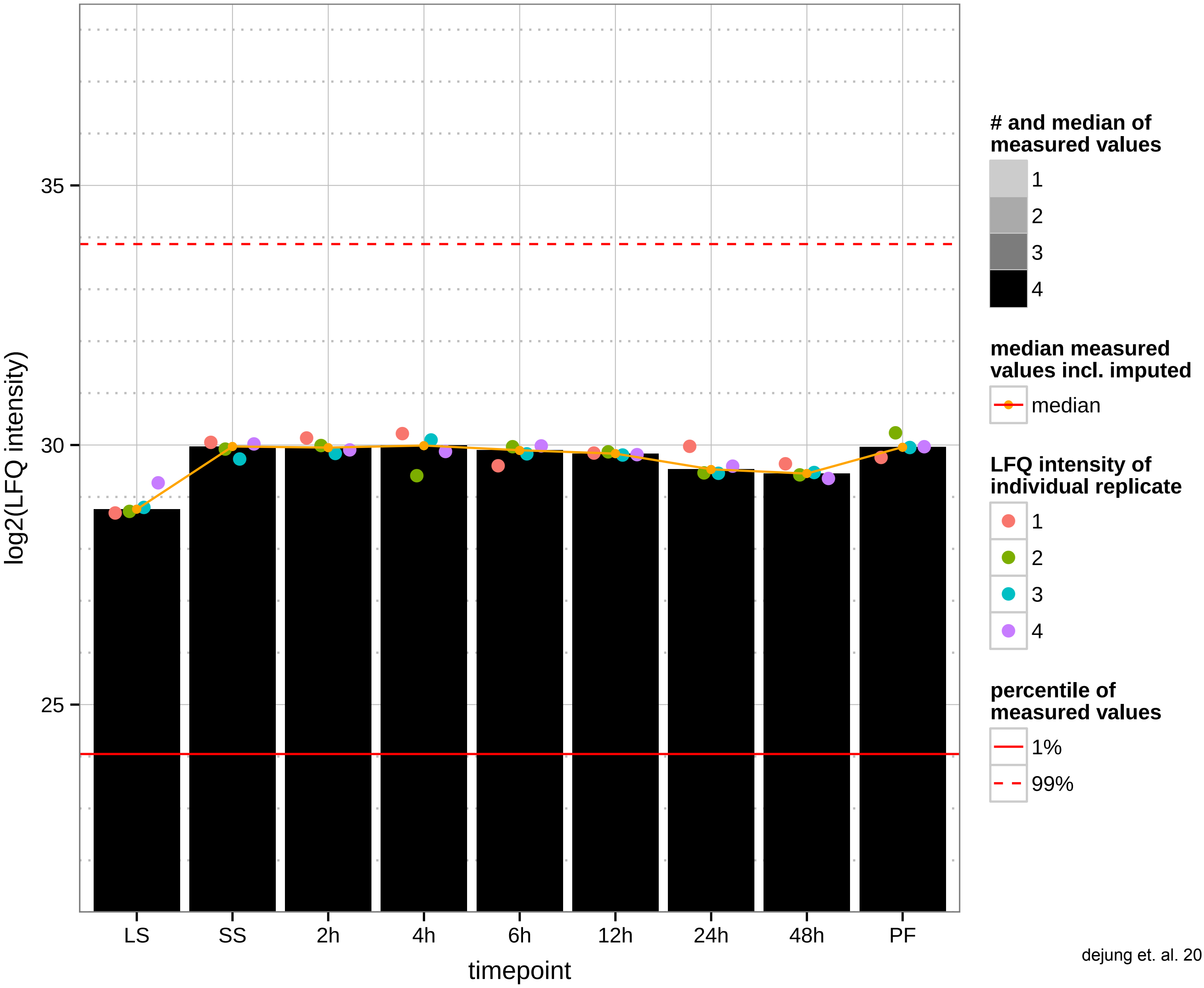
hypothetical protein, conserved
Tb927.4.1540
AGOF: catalytic activity, coenzyme binding
AGOC: mitochondrion
AGOP: cellular metabolic process
PGOF: catalytic activity, coenzyme binding
PGOC: null
PGOP: cellular metabolic process





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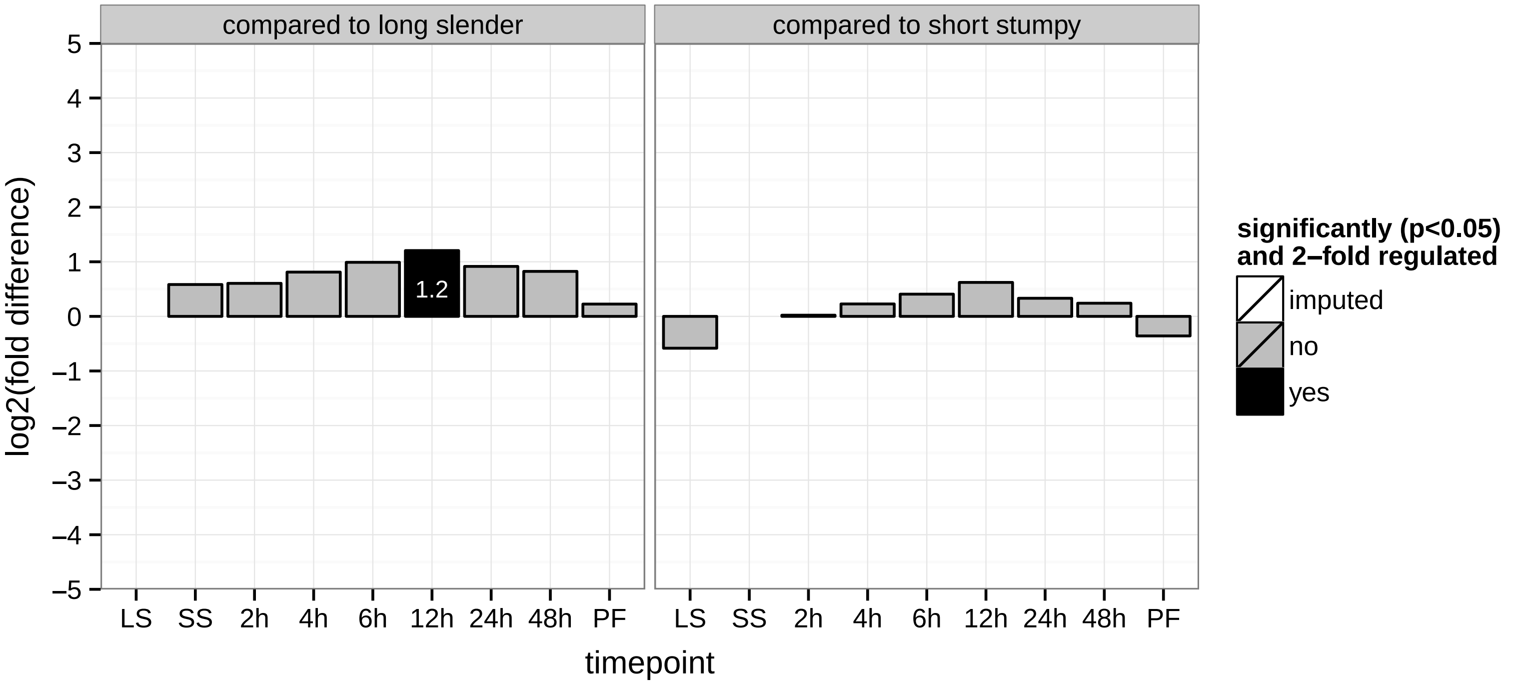
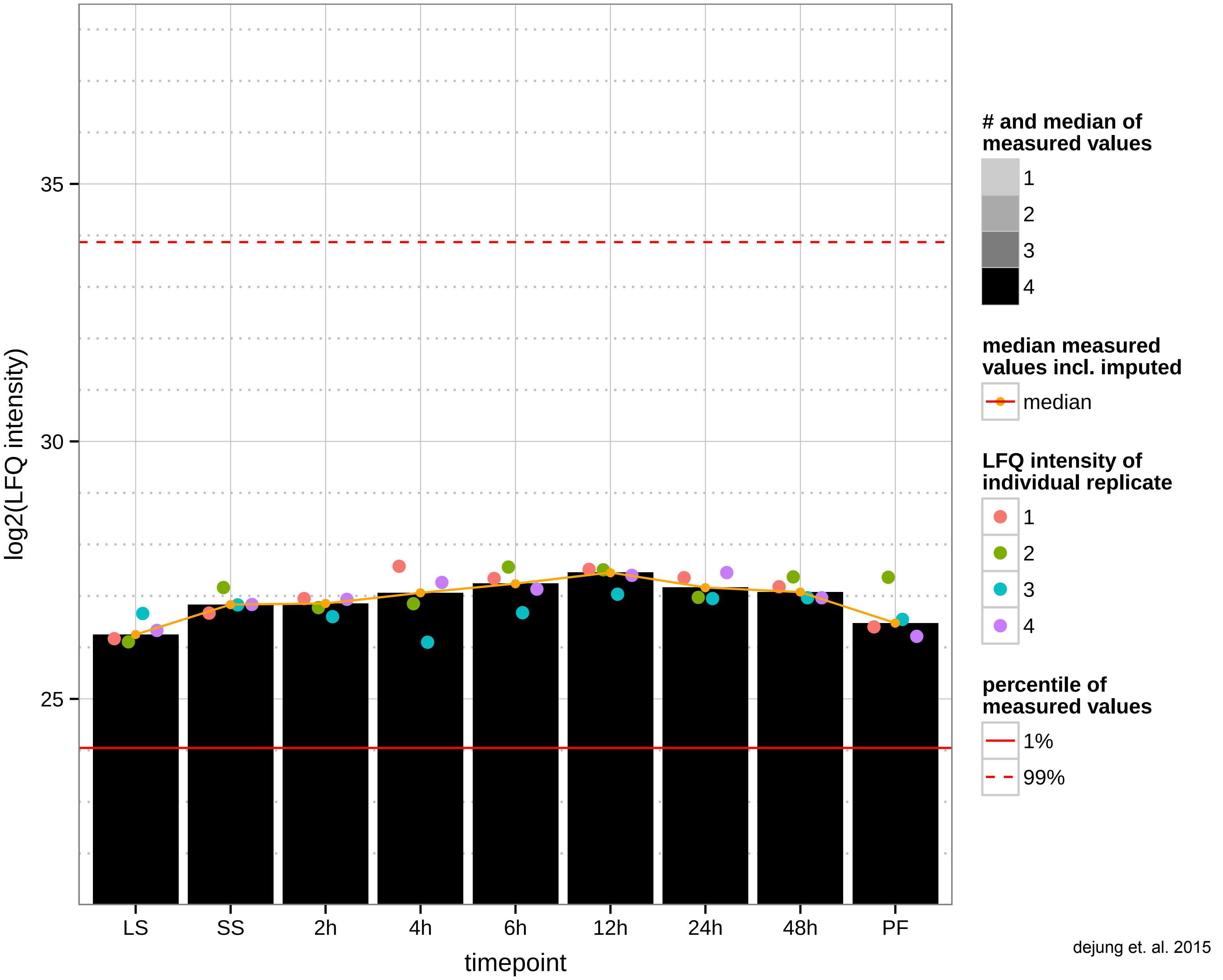
hypothetical protein, conserved
Tb927.4.1600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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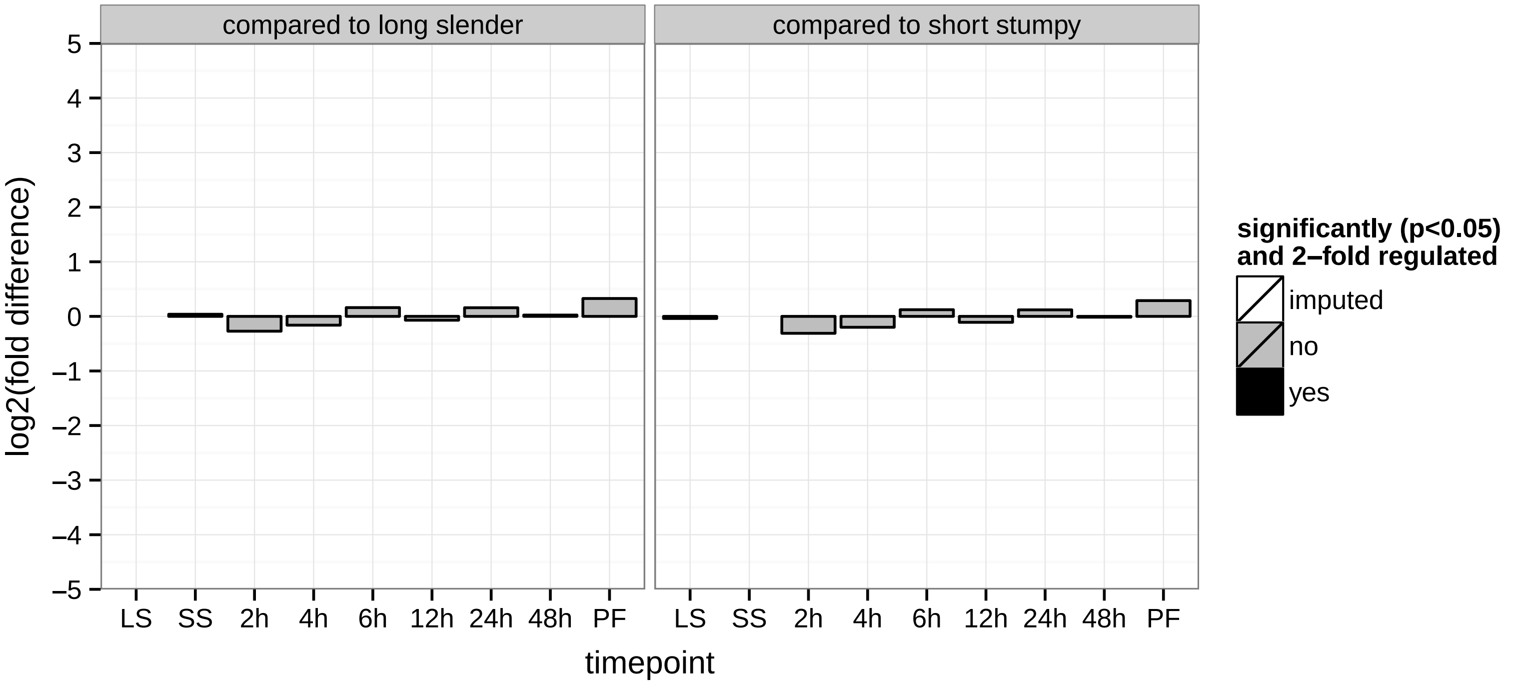
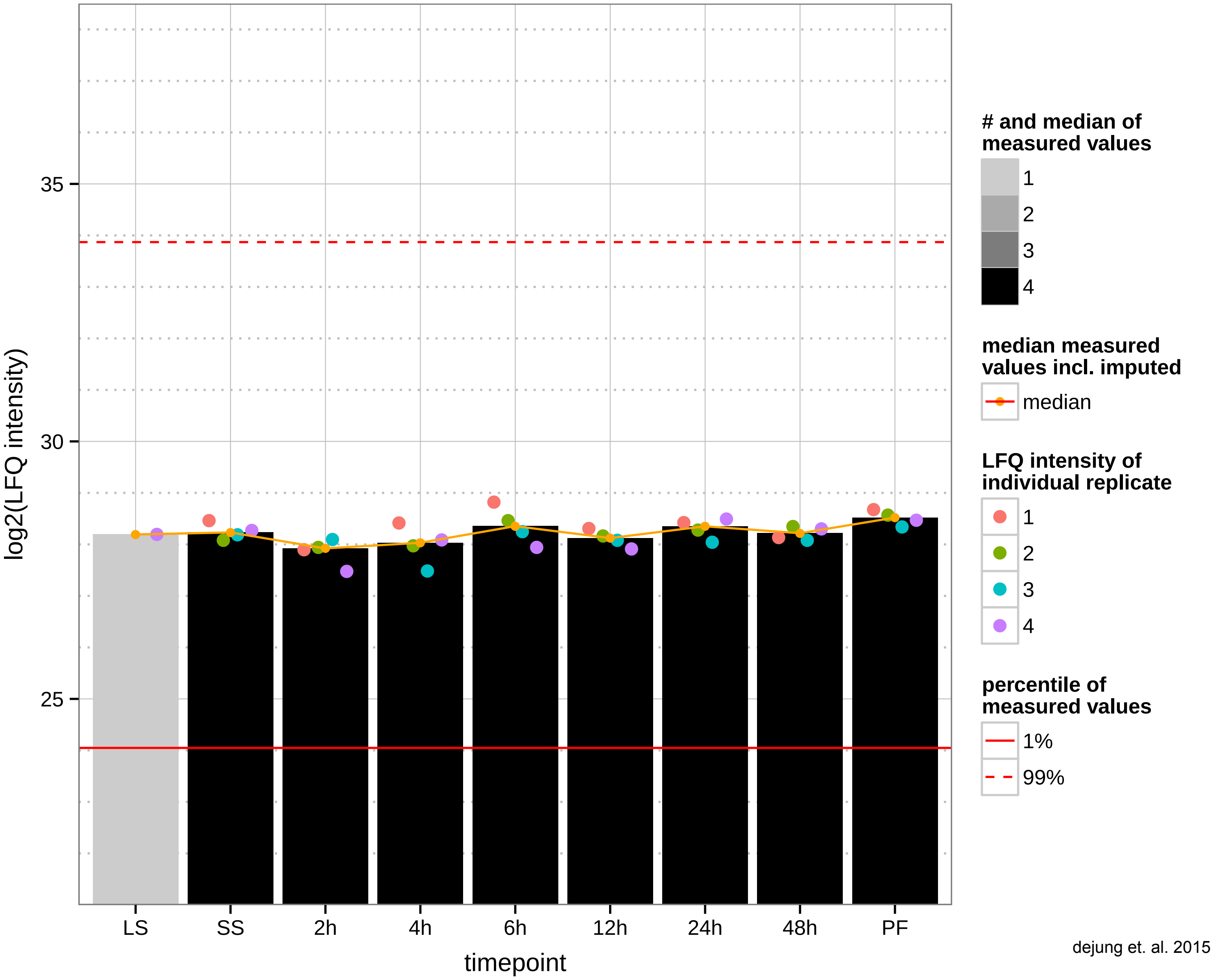
ribosomal RNA processing protein 6 (RRP6)
Tb927.4.1630
AGOF: 3'–5' exonuclease activity, nucleic acid binding
AGOC: cytoplasm, cytoplasmic exosome (RNase complex), intracellular, nuclear exosome (RNase complex), nucleus
AGOP: RNA processing, cell growth, rRNA processing
PGOF: 3'–5' exonuclease activity, catalytic activity, nucleic acid binding, nucleotide binding
PGOC: intracellular, nuclear exosome (RNase complex)
PGOP: RNA processing, cellular metabolic process, nucleobase–containing compound metabolic process





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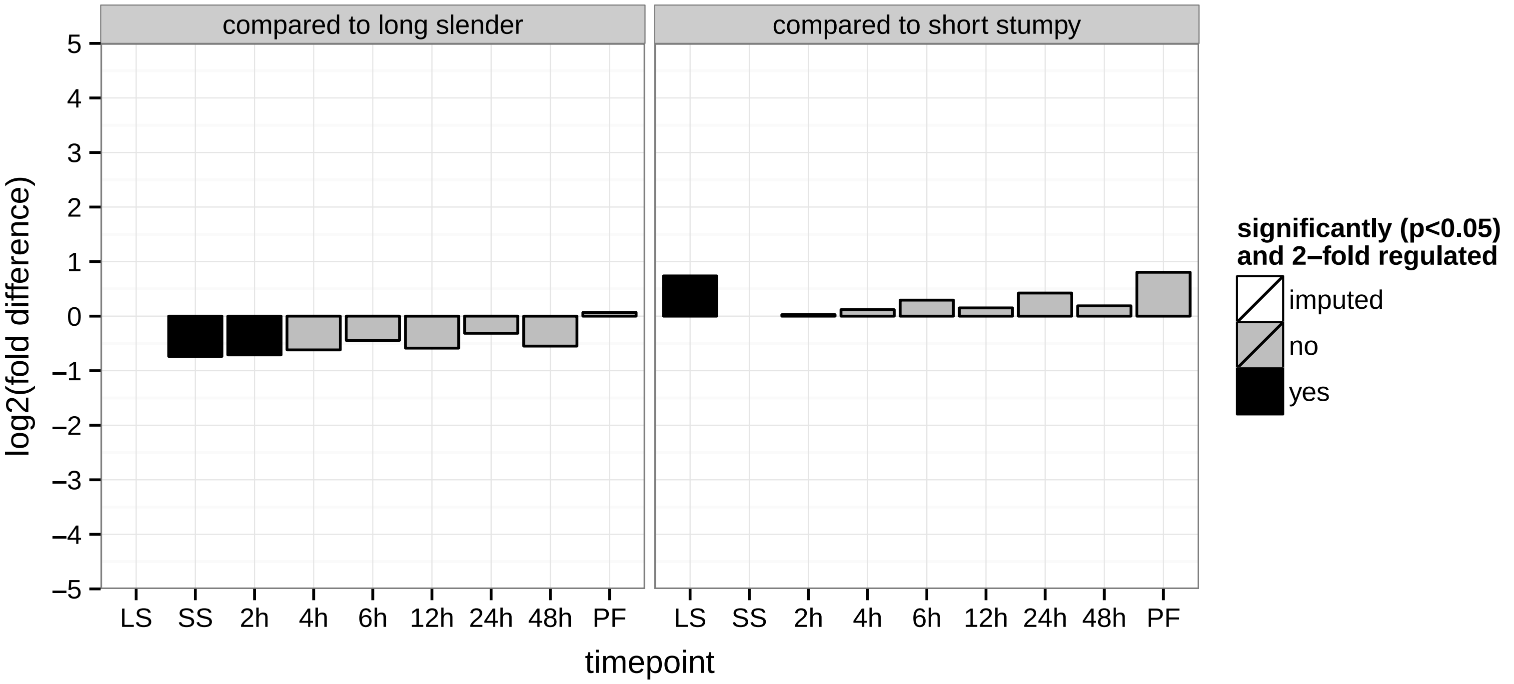
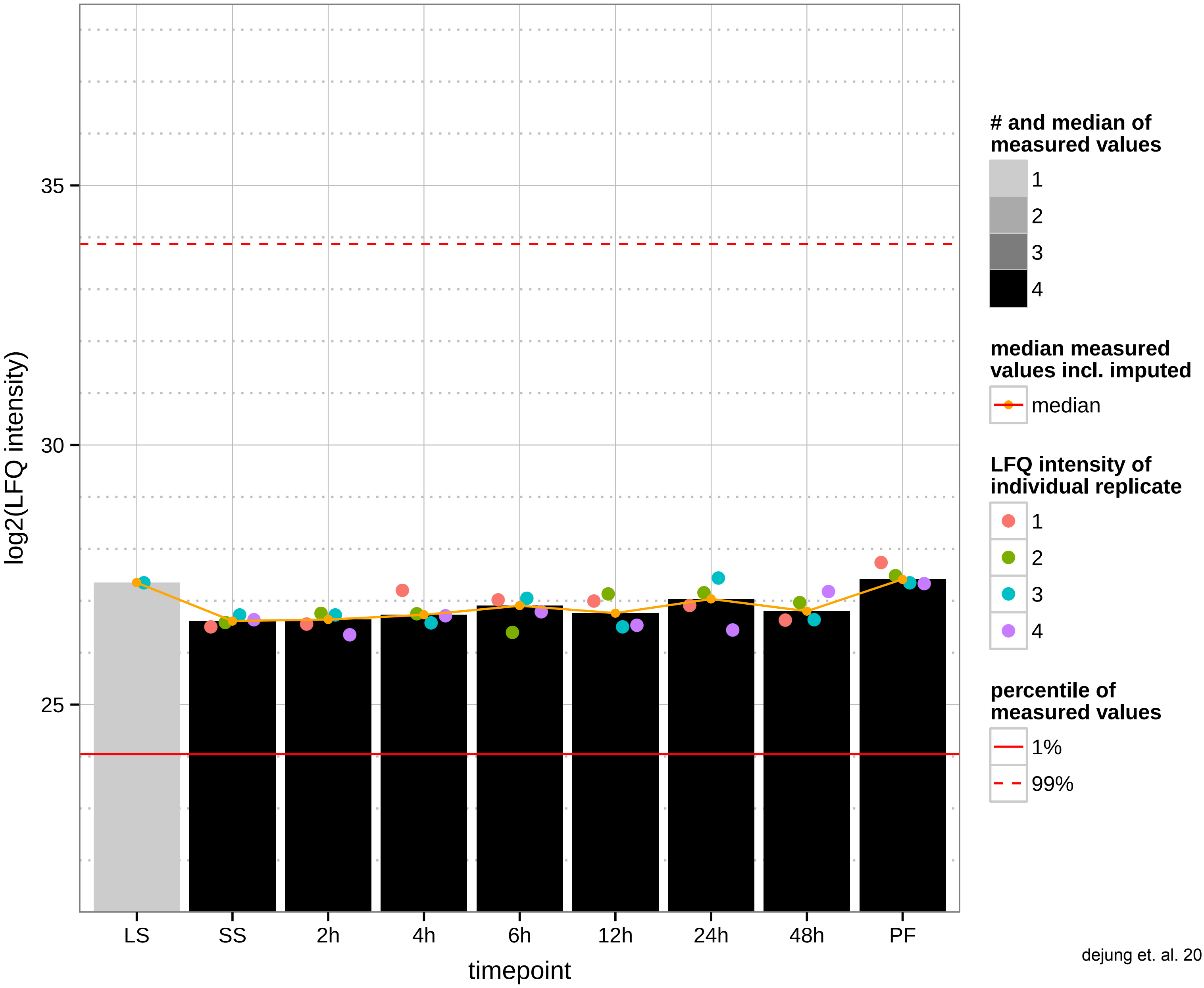
mitochondrial carrier protein, putative (MCP6)
Tb927.4.1660
AGOF: null
AGOC: glycosome, mitochondrial inner membrane, mitochondrial membrane, mitochondrion
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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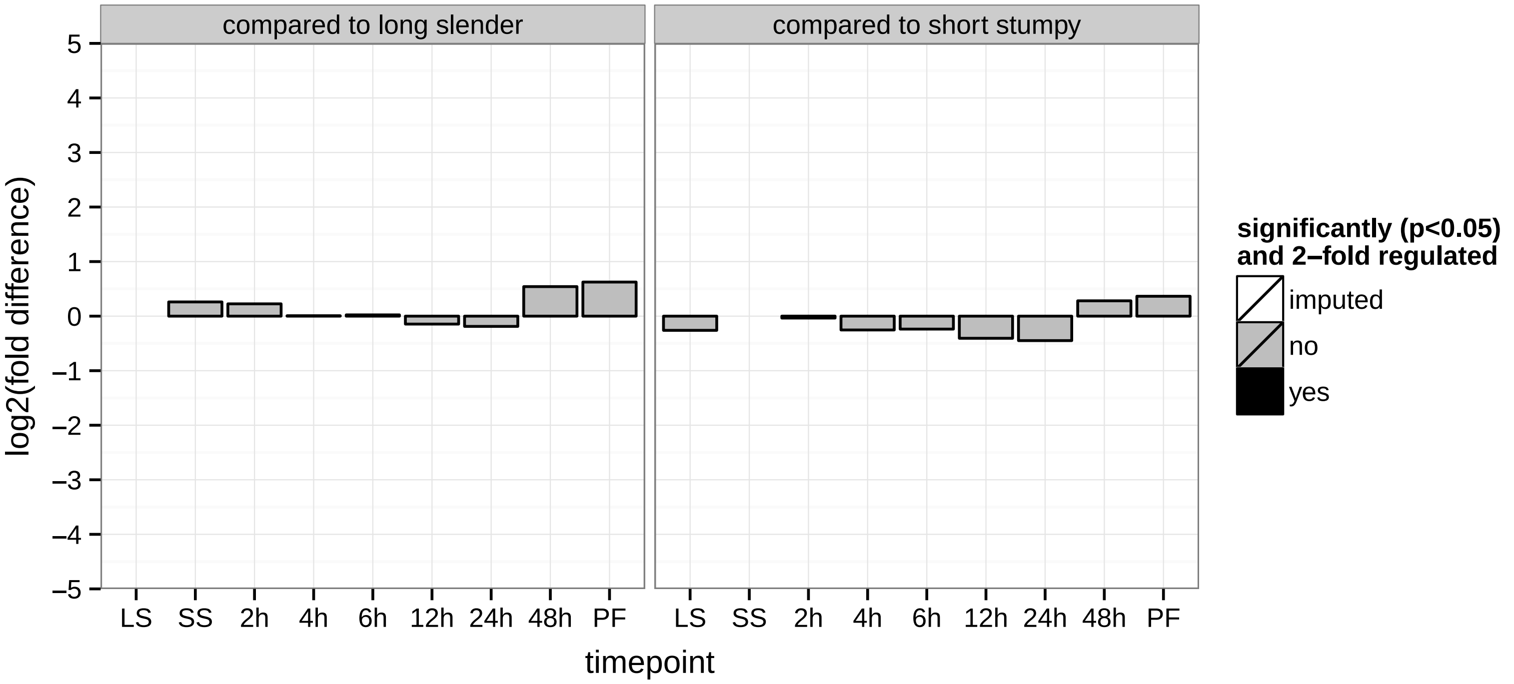
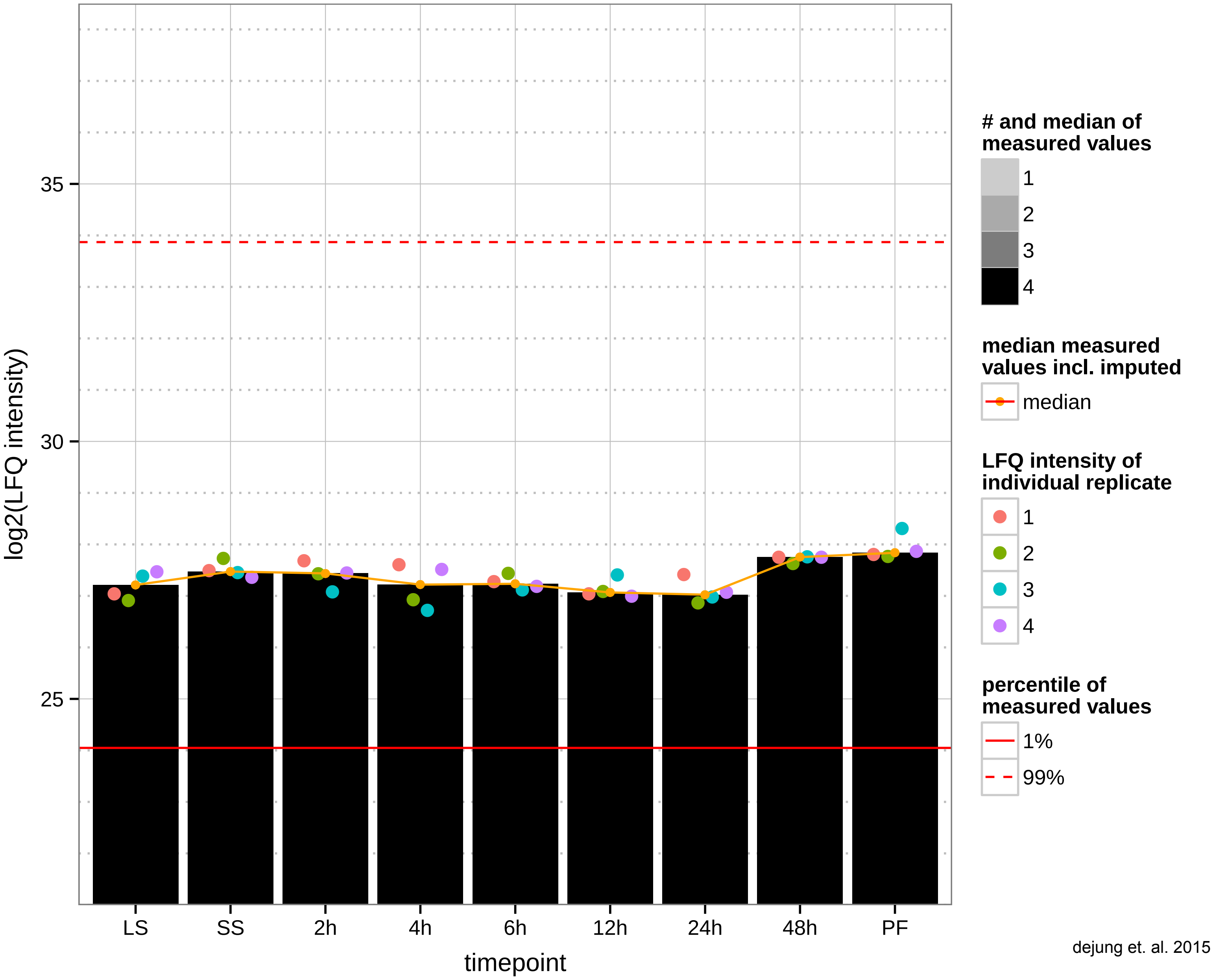
ZFP family member, putative (ZC3H10)
Tb927.4.1680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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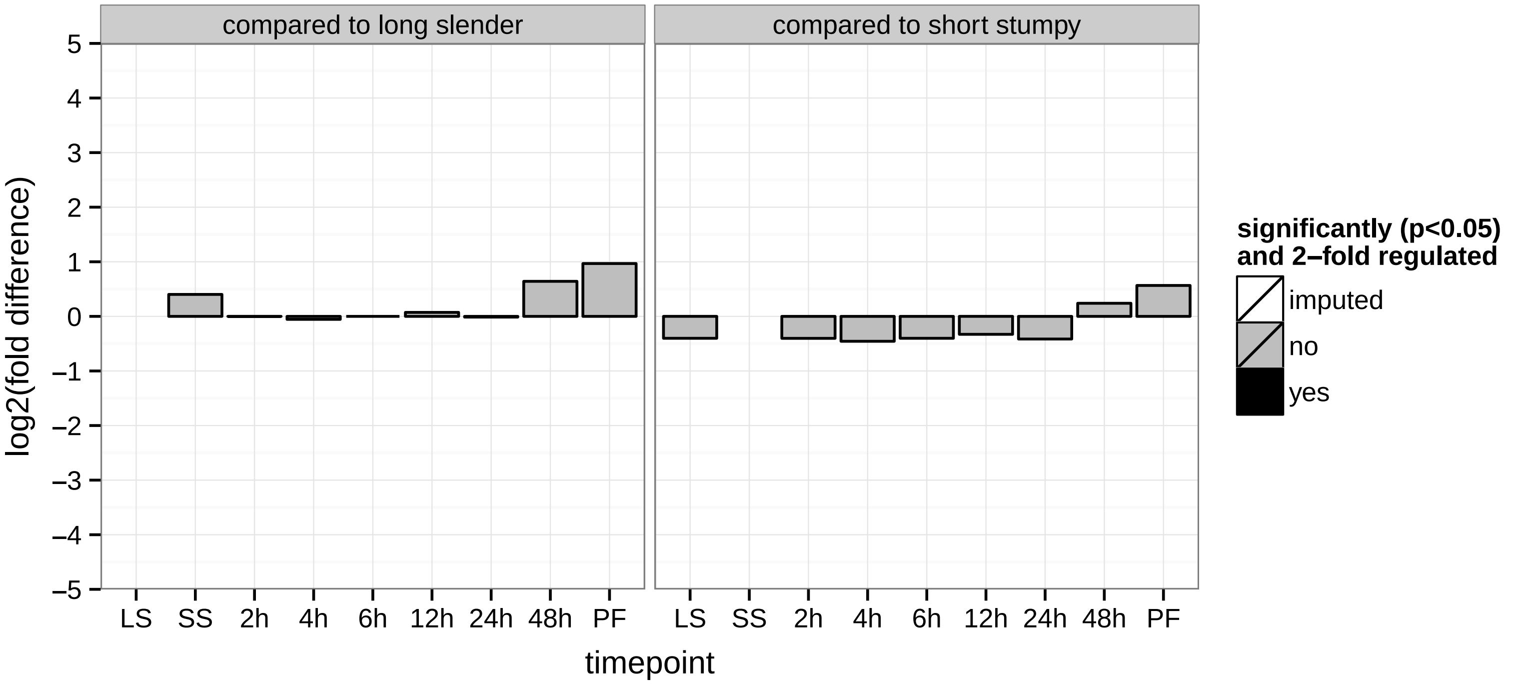
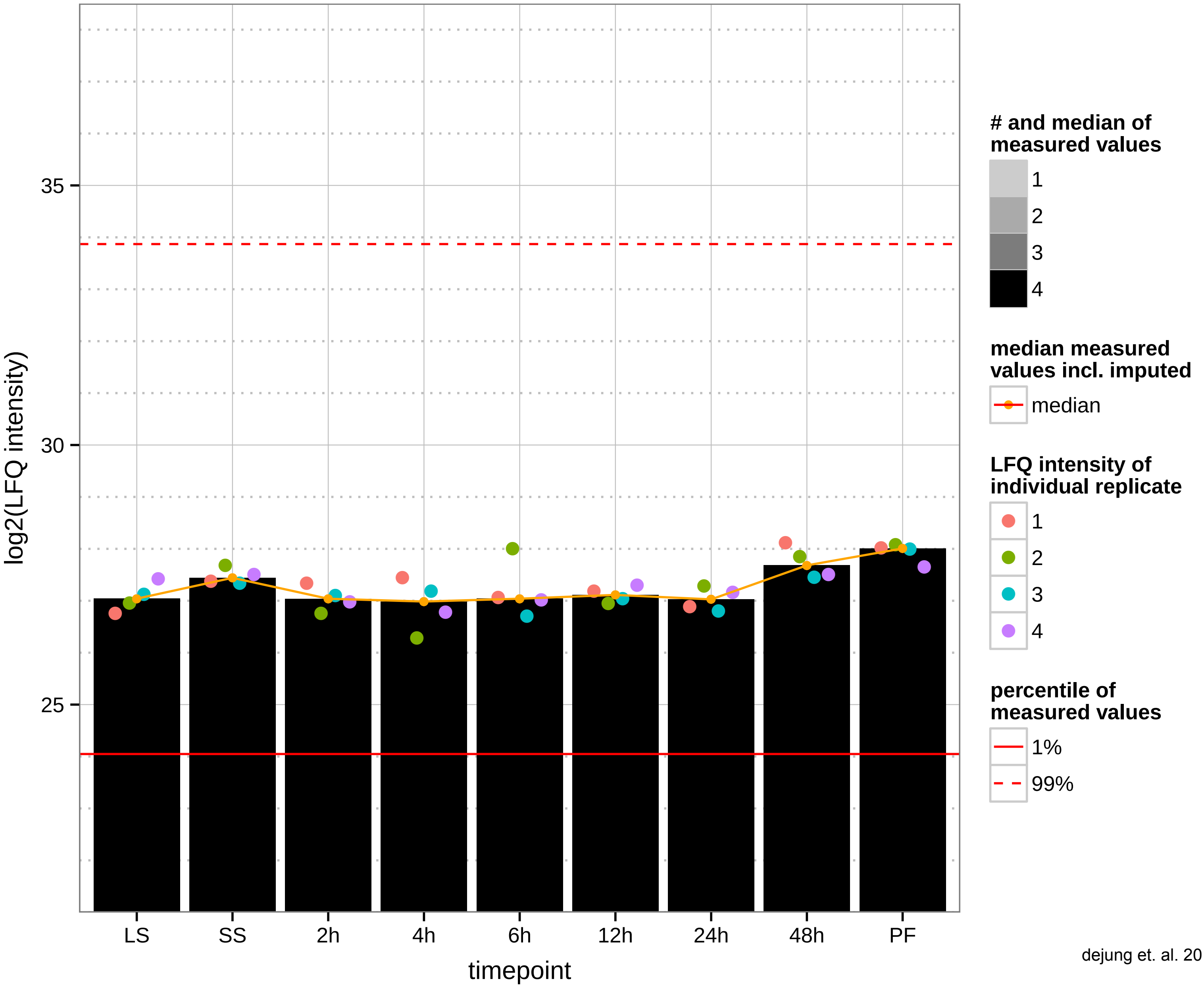
nucleoside diphosphate kinase, putative
Tb927.4.1720
AGOF: ATP binding, nucleoside diphosphate kinase activity
AGOC: null
AGOP: CTP biosynthetic process, GTP biosynthetic process, UTP biosynthetic process, ciliary or flagellar motility
PGOF: ATP binding, nucleoside diphosphate kinase activity
PGOC: null
PGOP: CTP biosynthetic process, GTP biosynthetic process, UTP biosynthetic process, nucleoside diphosphate phosphoryla





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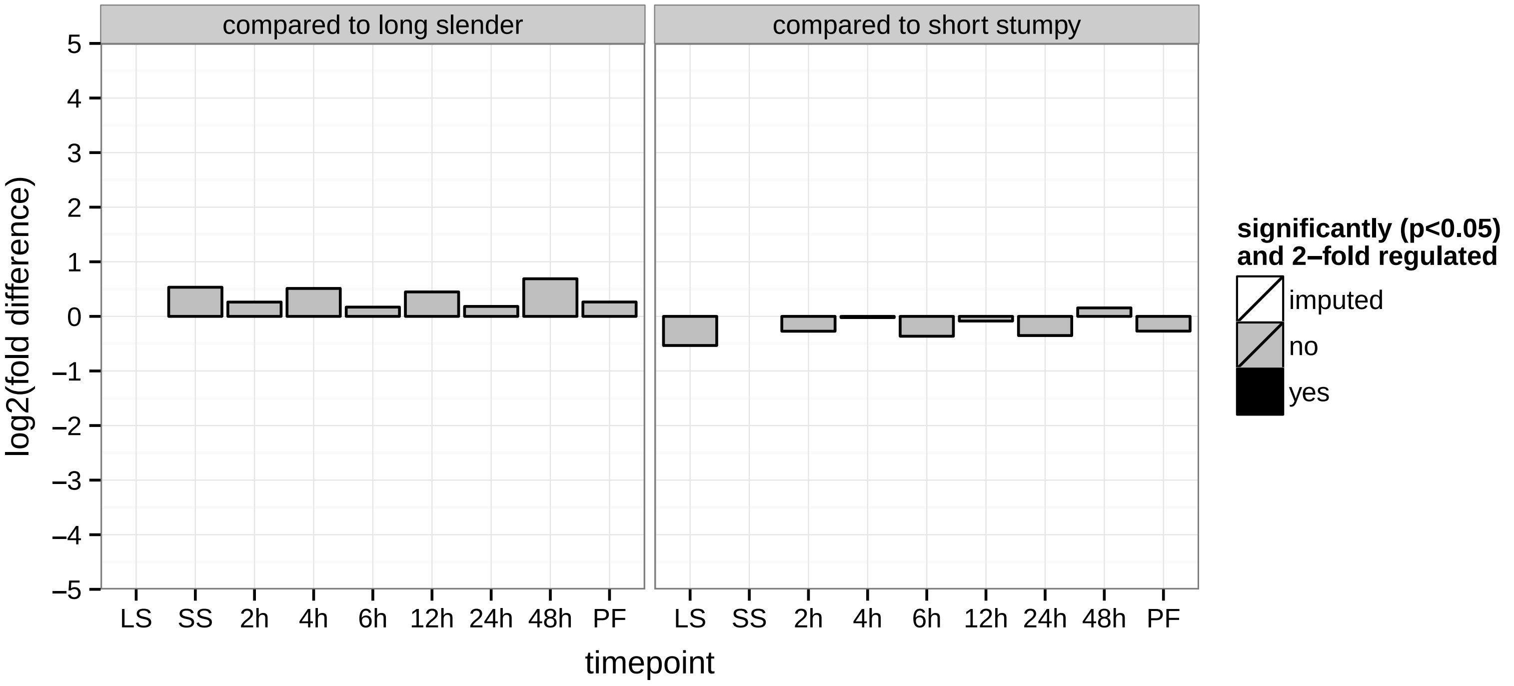
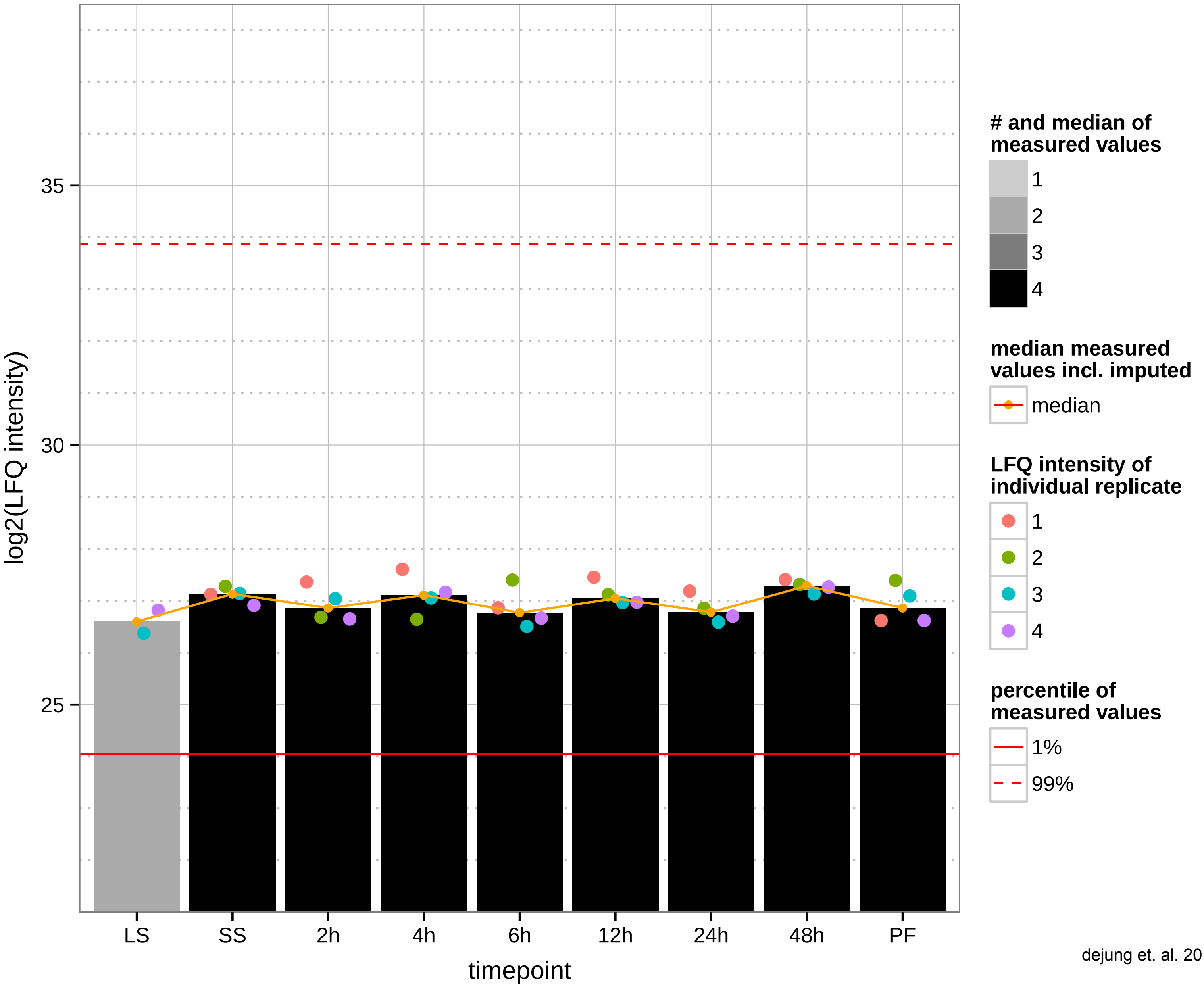
hypothetical protein, conserved
Tb927.4.1740
AGOF: calcium ion binding
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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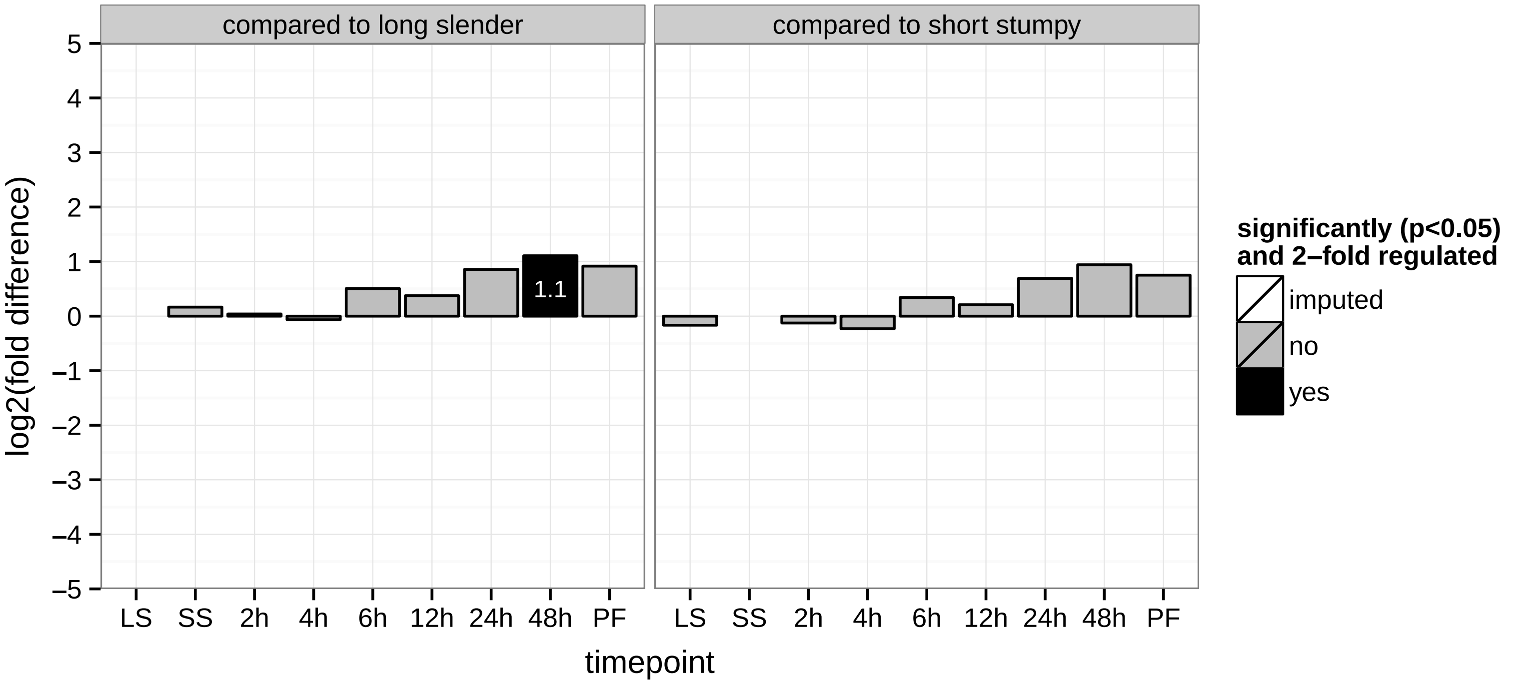
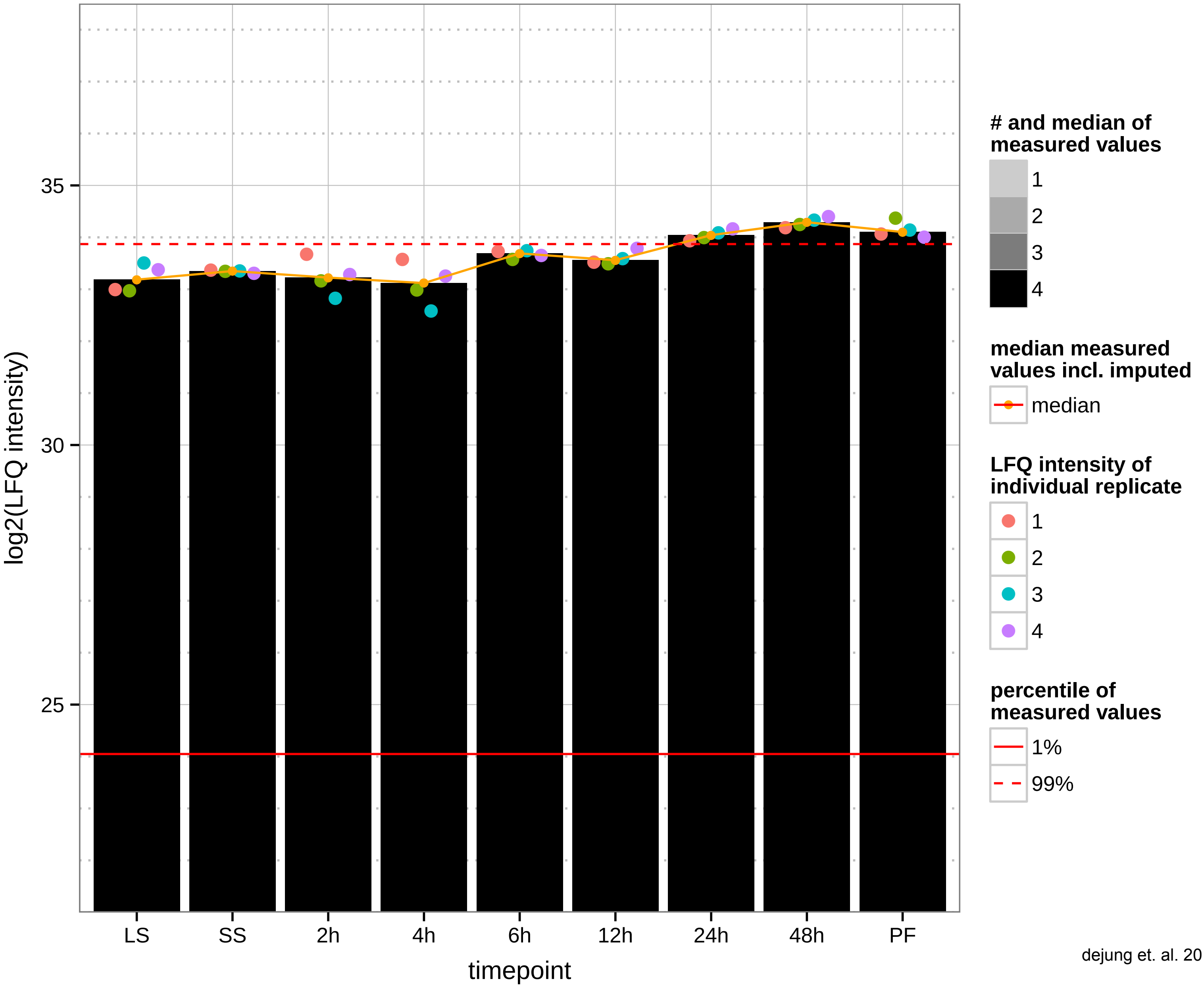
ribosomal protein L3, putative, mitochondrial
Tb927.4.1800;Tb927.4.1790
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome, null
PGOC: intracellular, ribosome, null
PGOP: translation, null





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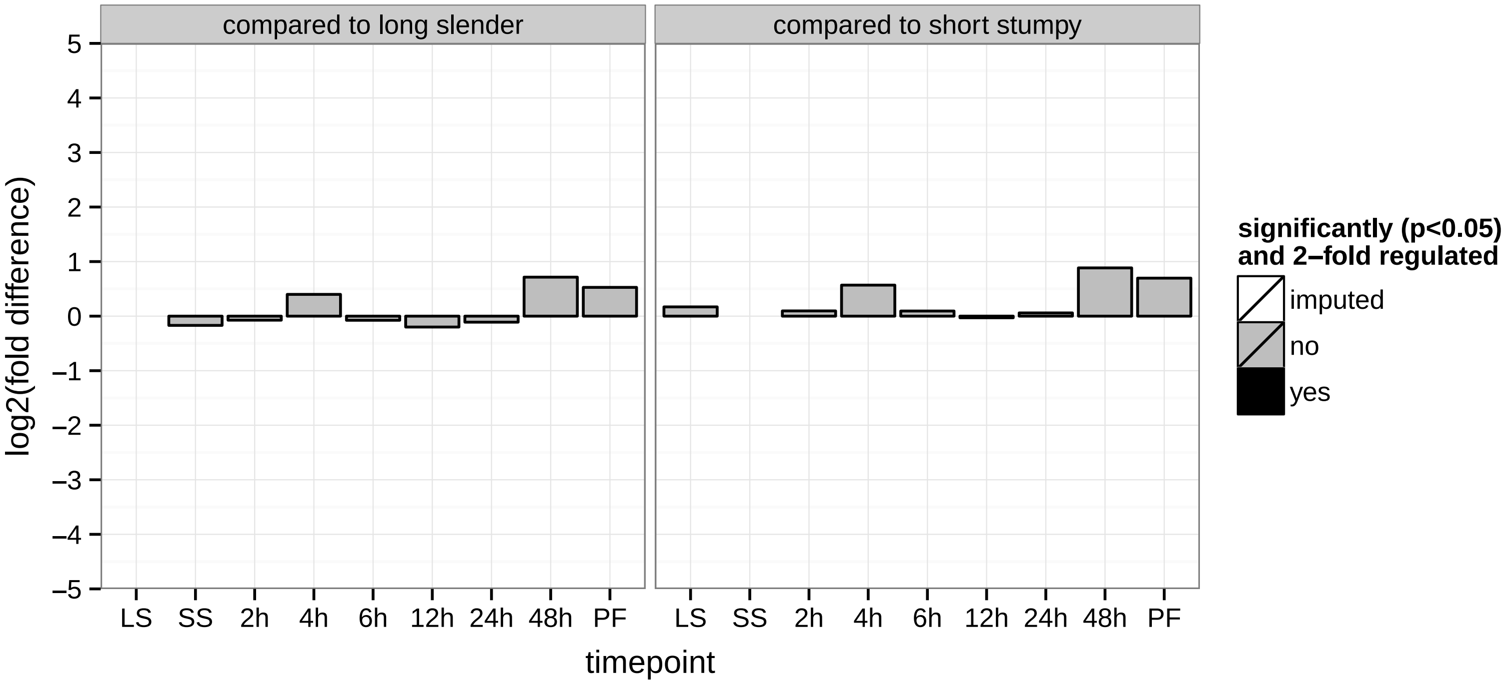
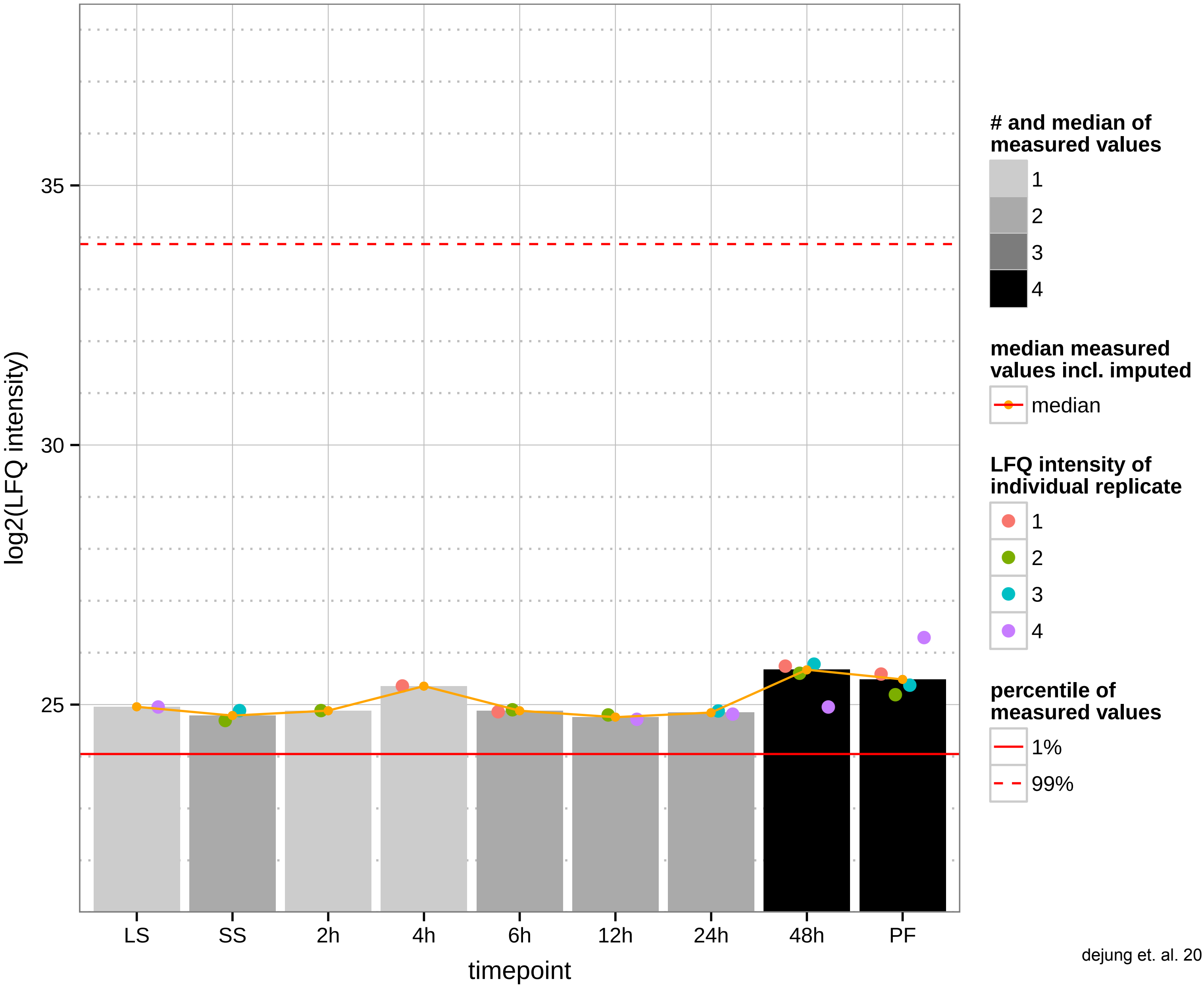
zinc carboxypeptidase, putative, metallo−peptidase, Clan MC, Family M14
Tb927.4.1840
AGOF: ADP binding, ATP binding, metallocarboxypeptidase activity, zinc ion binding
AGOC: cytosol
AGOP: proteolysis
PGOF: metallocarboxypeptidase activity, zinc ion binding
PGOC: null
PGOP: proteolysis





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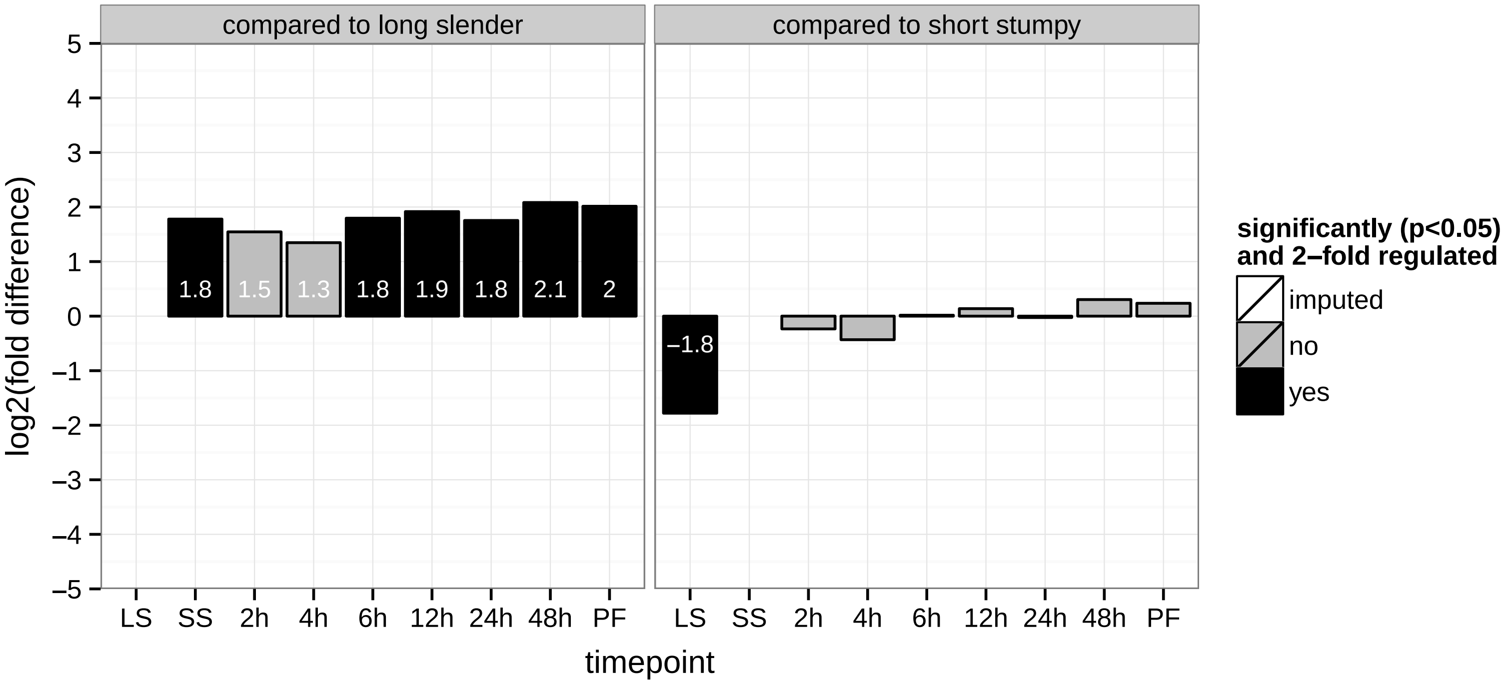
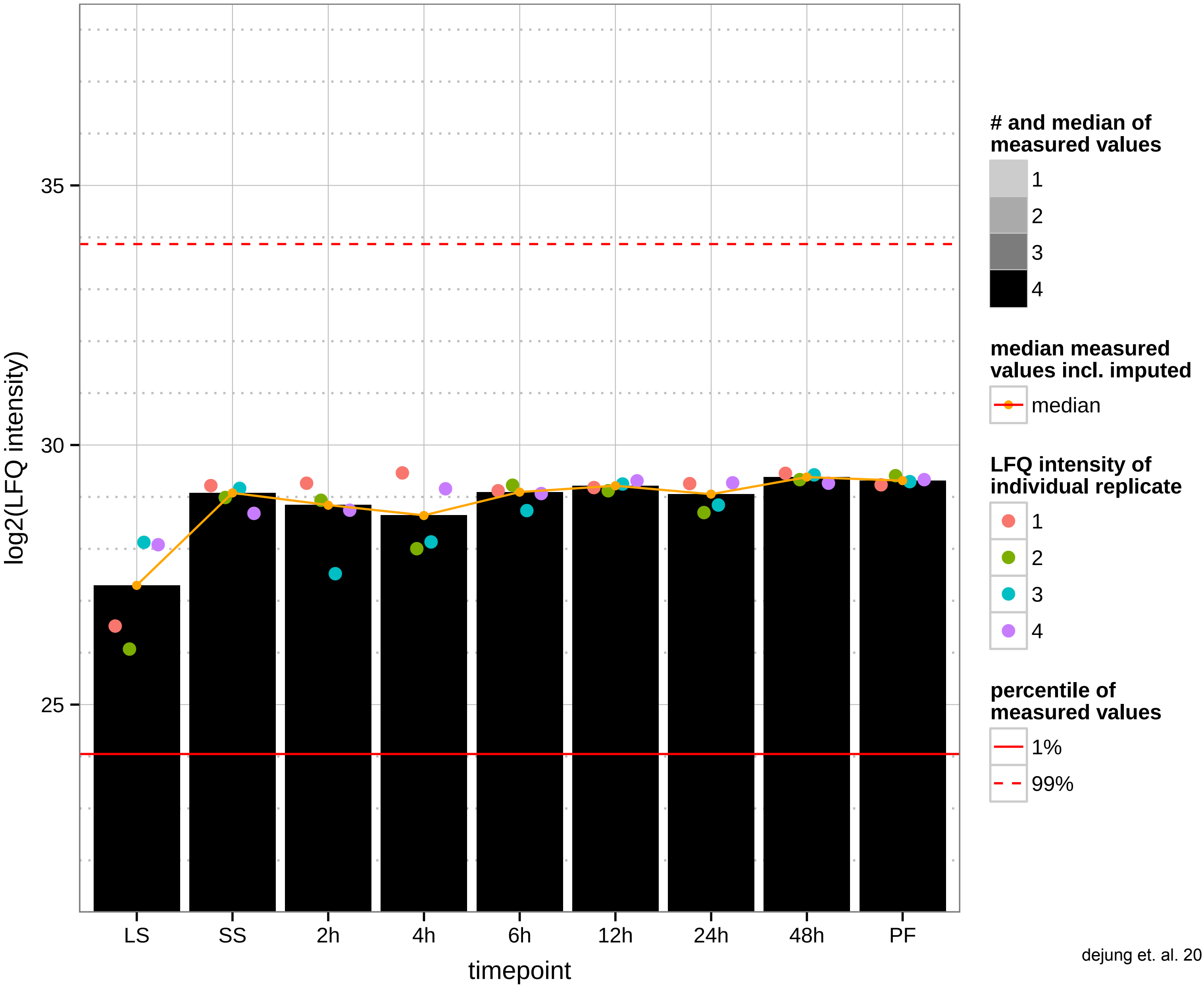
hypothetical protein, conserved
Tb927.4.1850
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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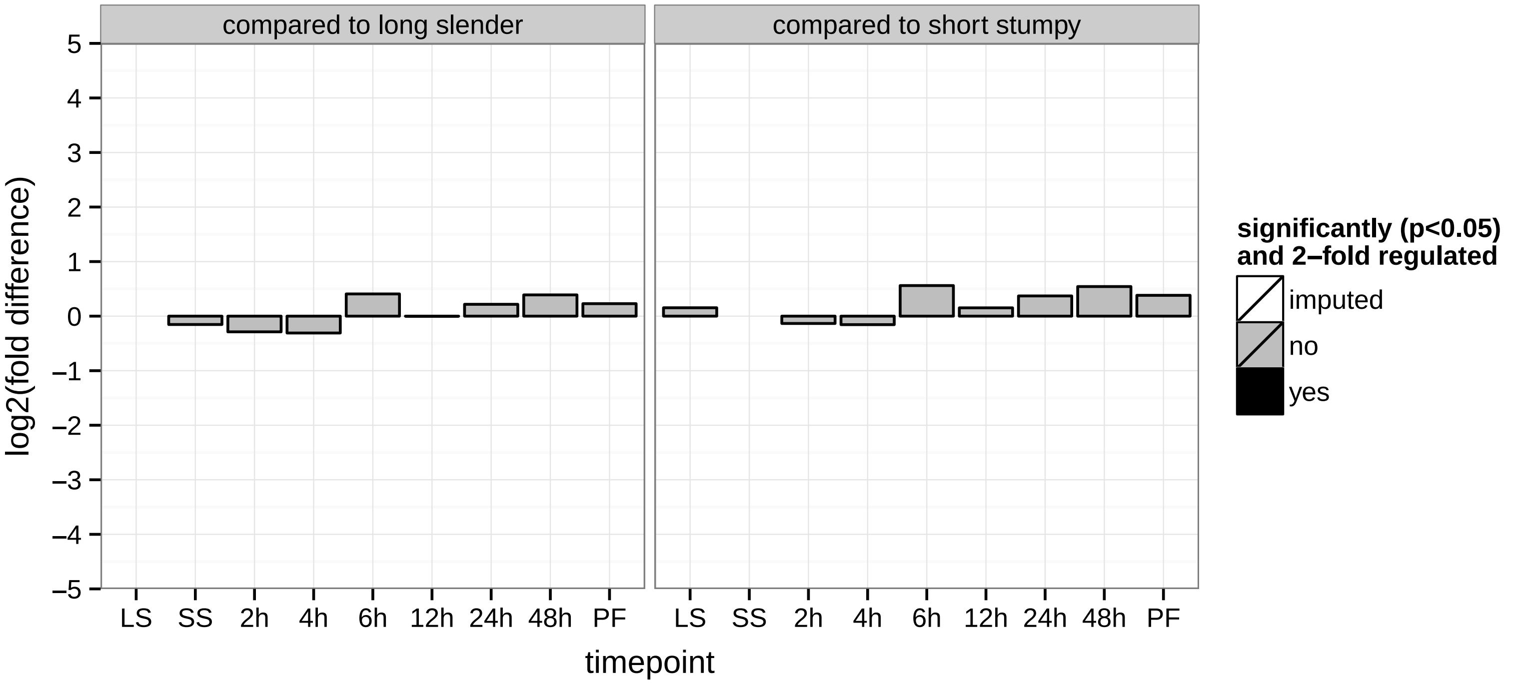
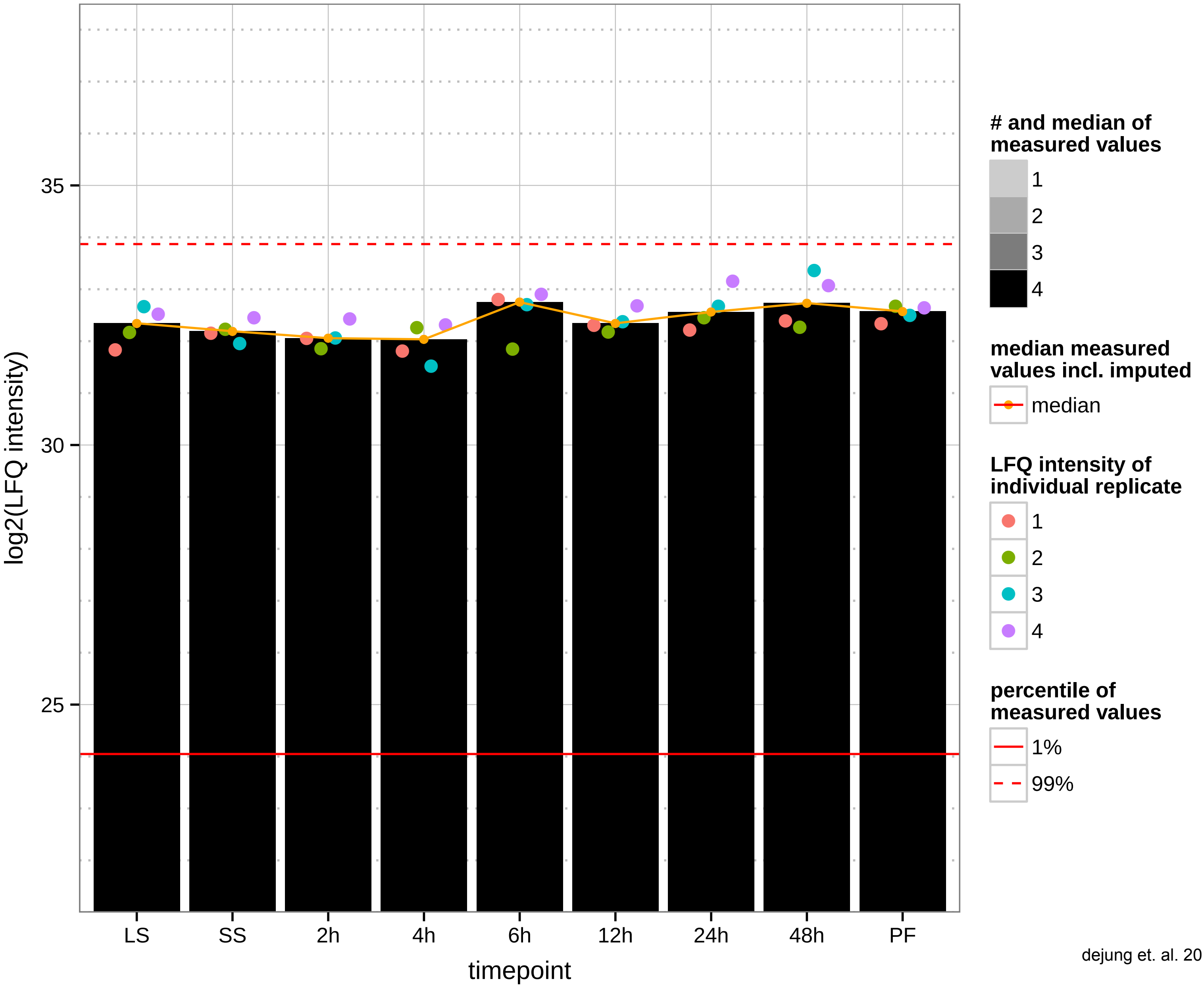
ribosomal protein S19, putative
Tb927.4.1860
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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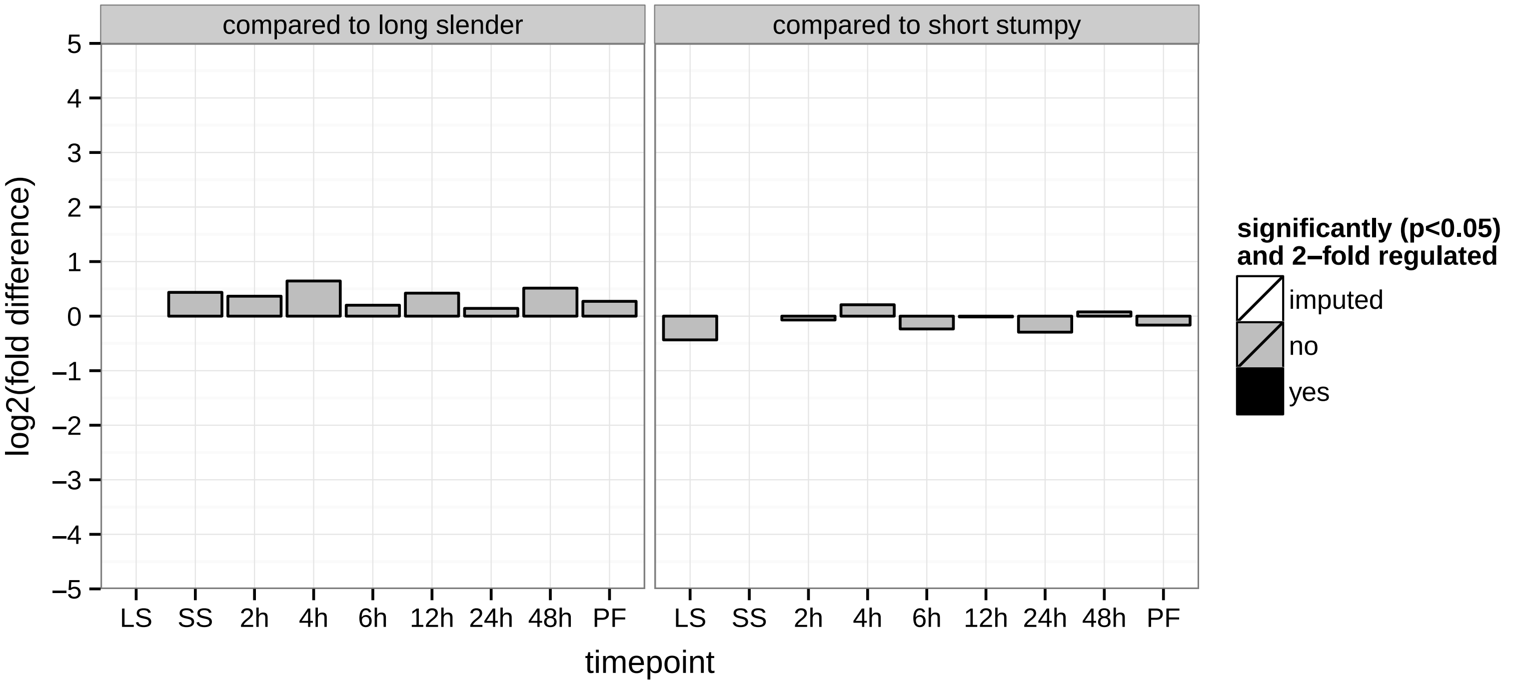
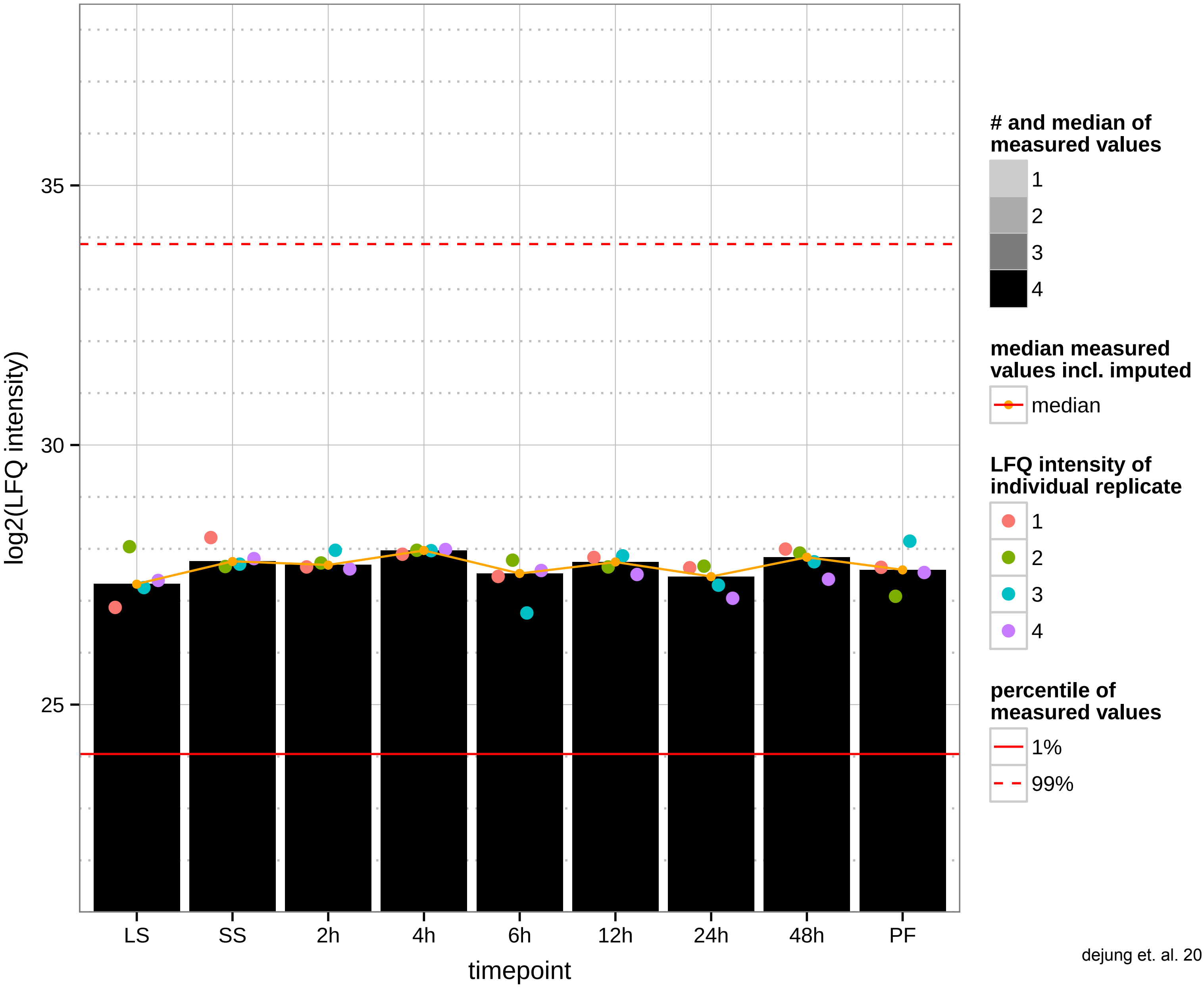
hypothetical protein, conserved
Tb927.4.1890
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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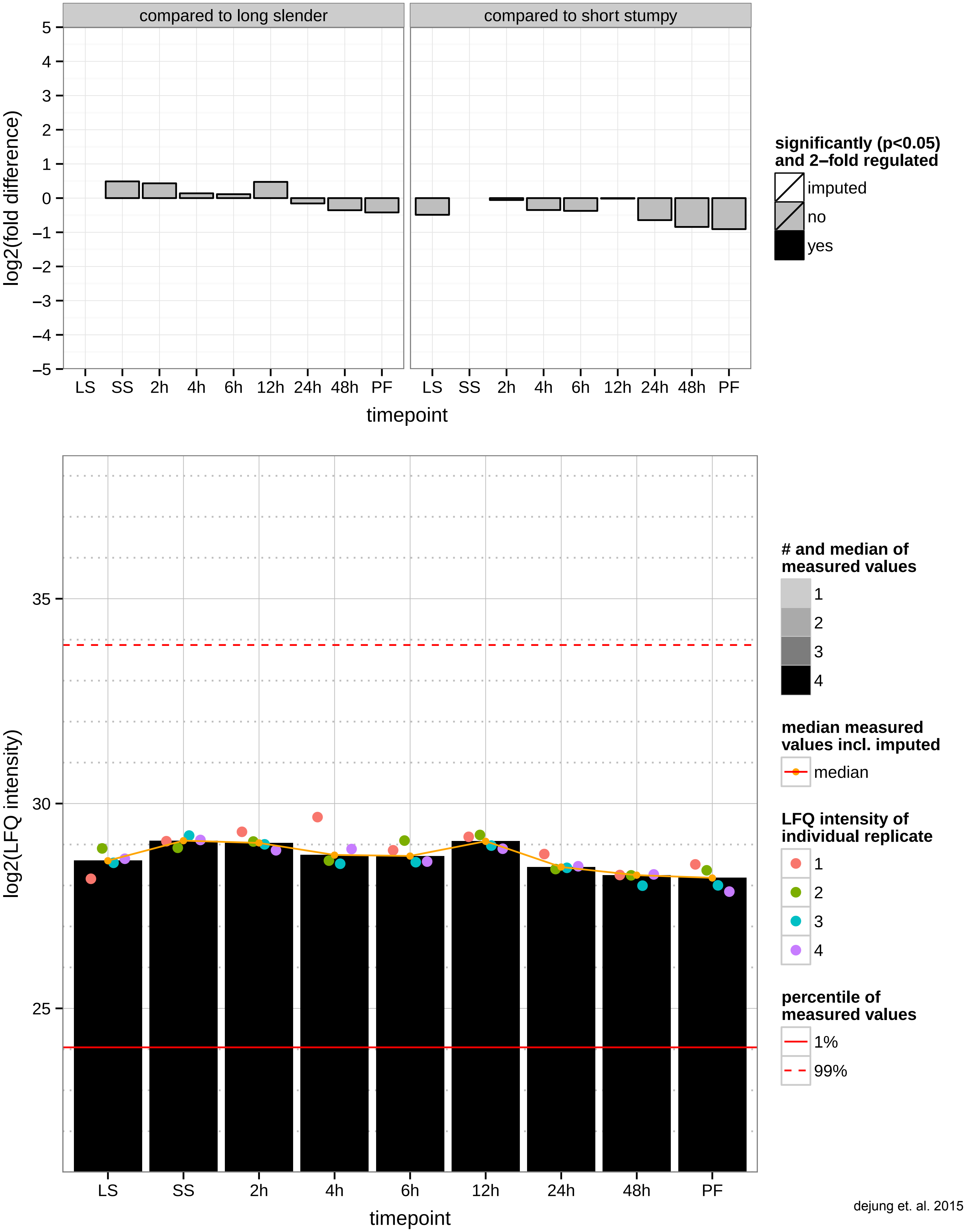
GPI transamidase, putative, glycosylphosphatidylinositol (GPI) anchor, putative (TbGPI16)
Tb927.4.1920
AGOF: GPI–anchor transamidase activity
AGOC: GPI–anchor transamidase complex
AGOP: attachment of GPI anchor to protein
PGOF: null
PGOC: null
PGOP: null



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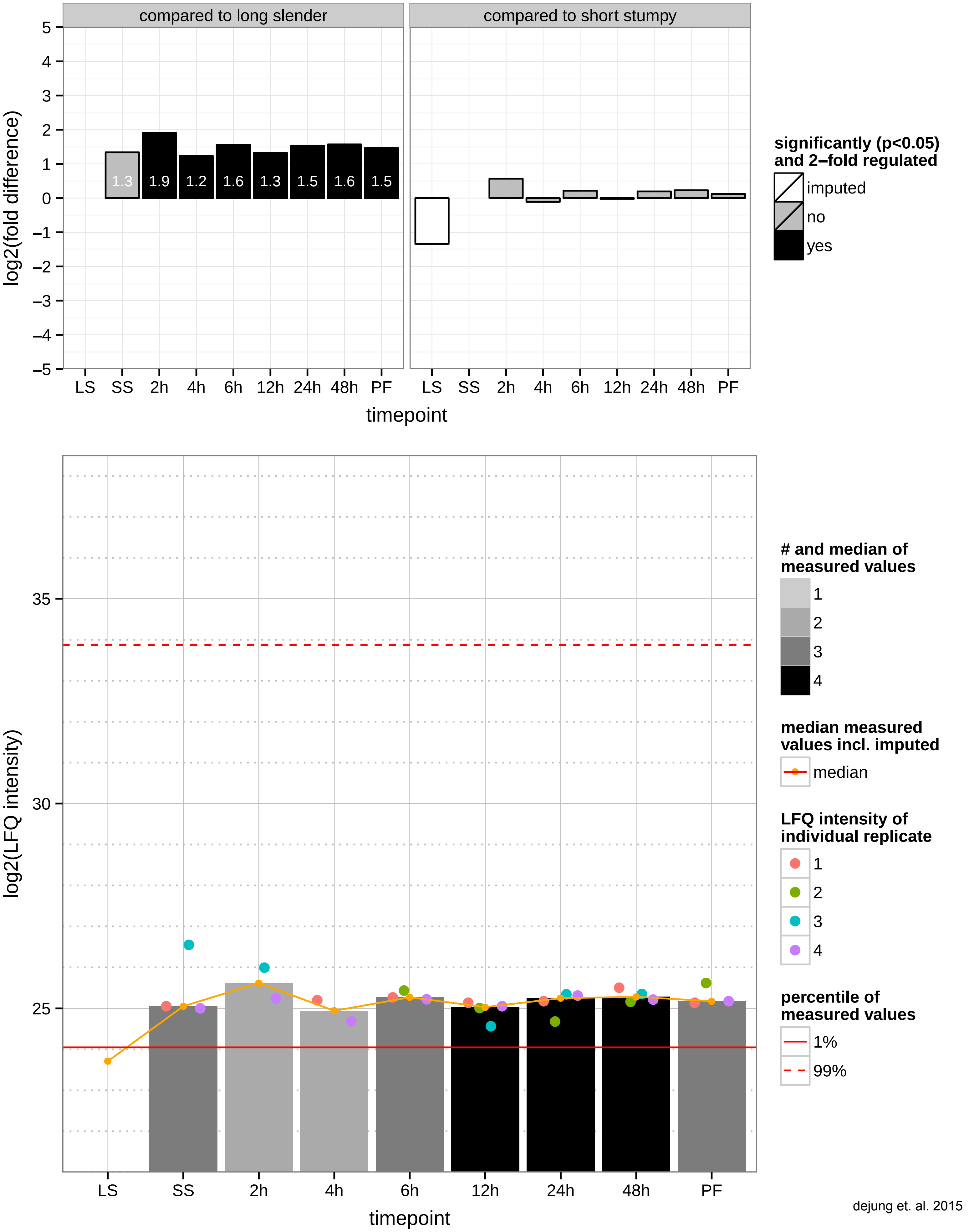
hypothetical protein, conserved
Tb927.4.1940
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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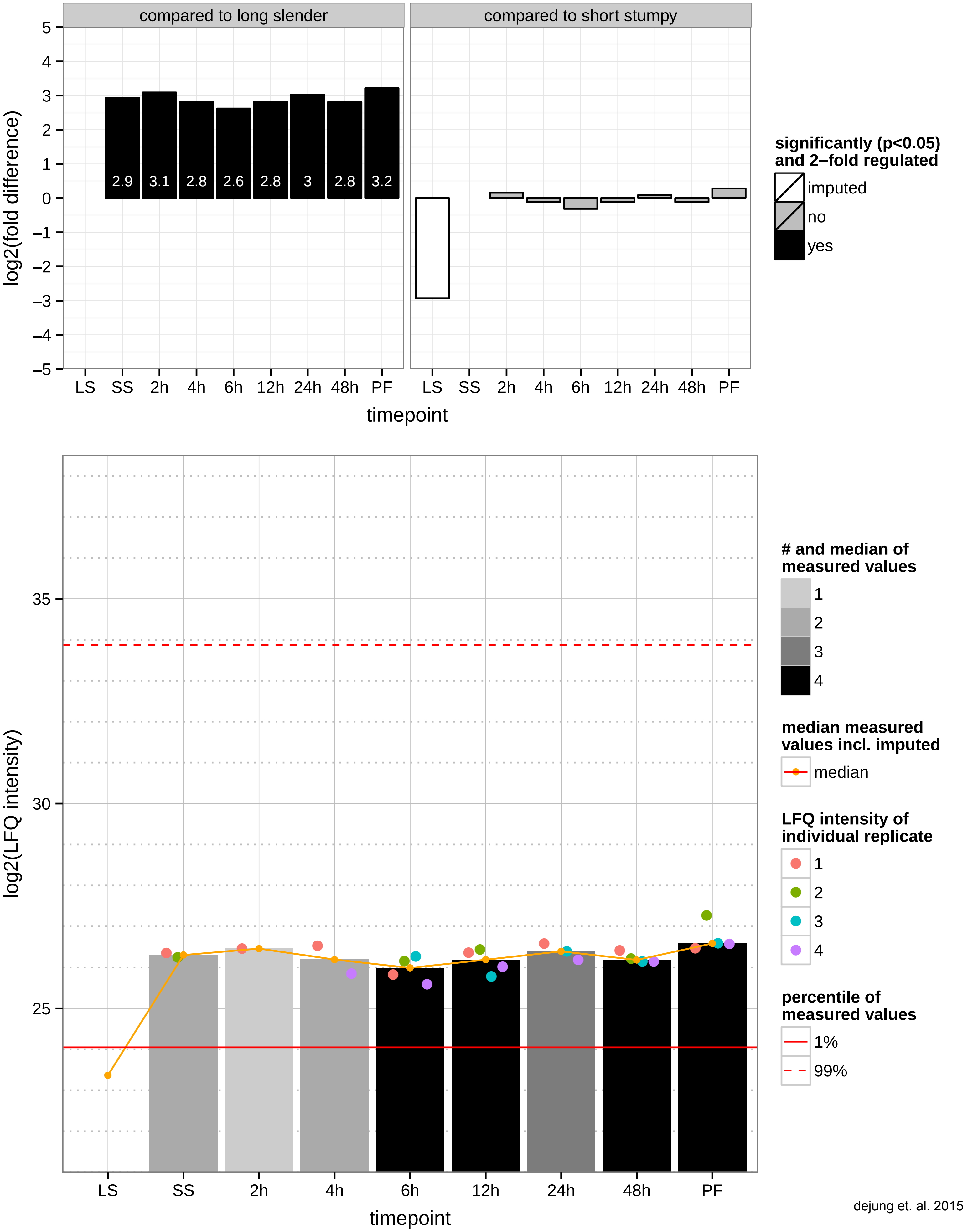
NADPH−−cytochrome p450 reductase, putative (CPR)
Tb927.4.1950
AGOF: FMN binding, electron carrier activity, iron ion binding, oxidoreductase activity
AGOC: null
AGOP: null
PGOF: FMN binding, oxidoreductase activity
PGOC: null
PGOP: oxidation−reduction process



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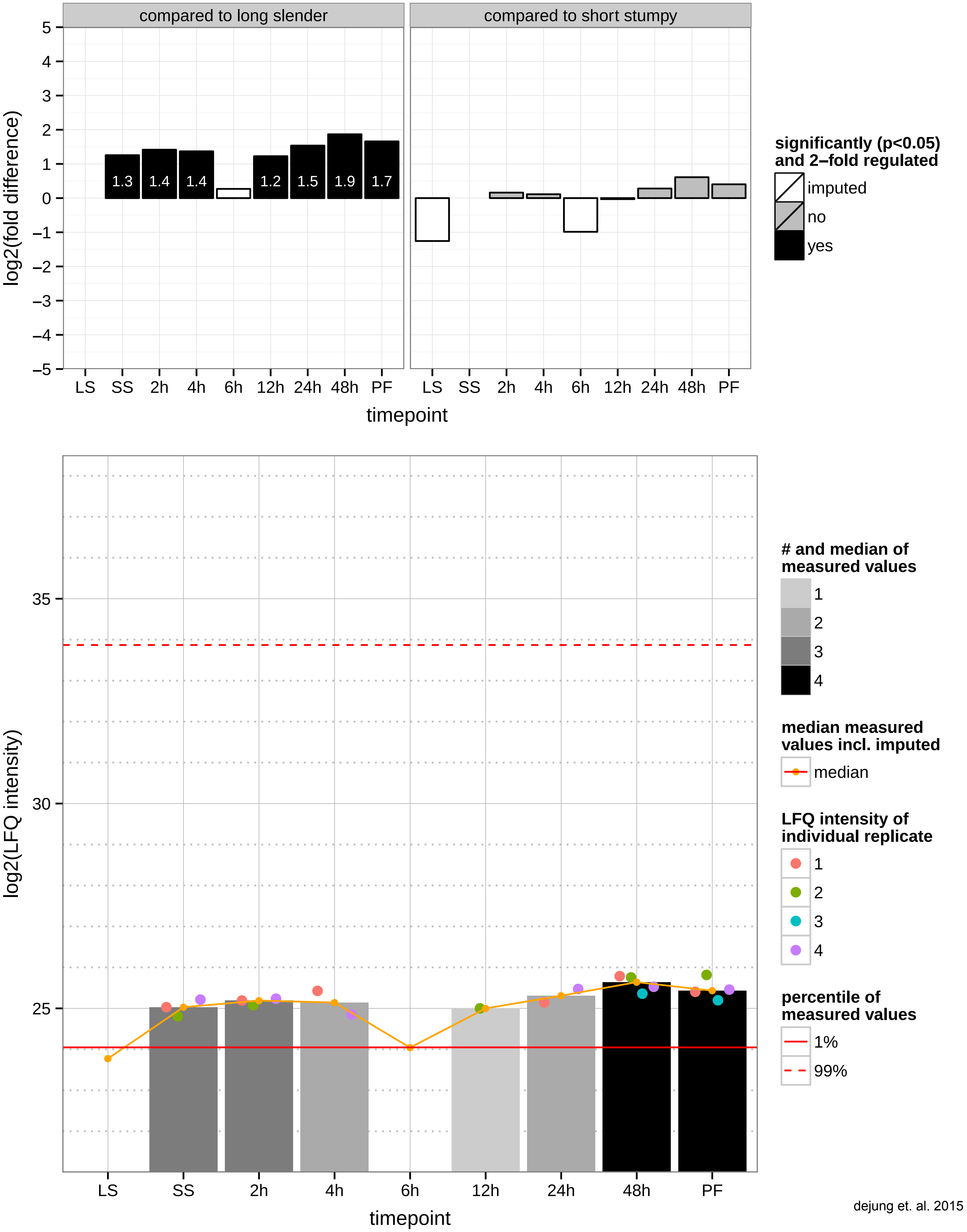
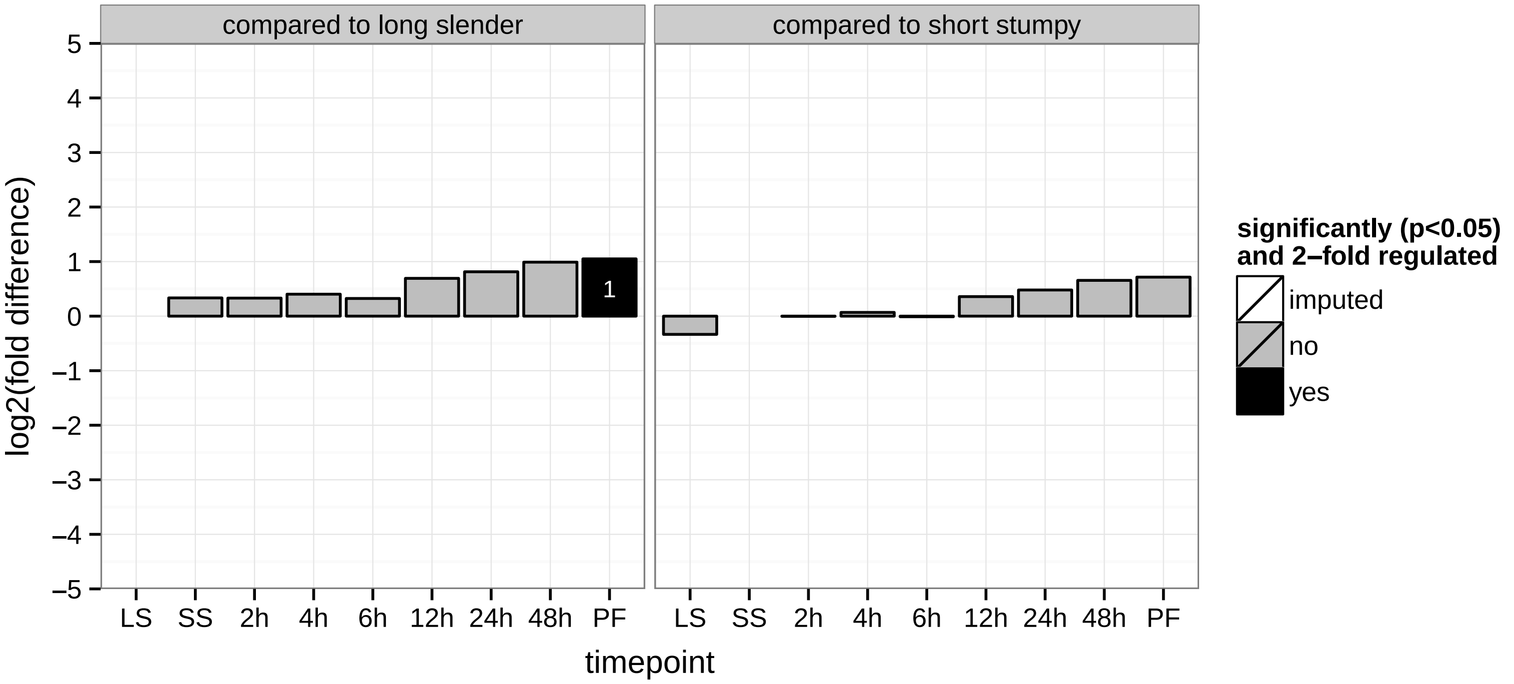
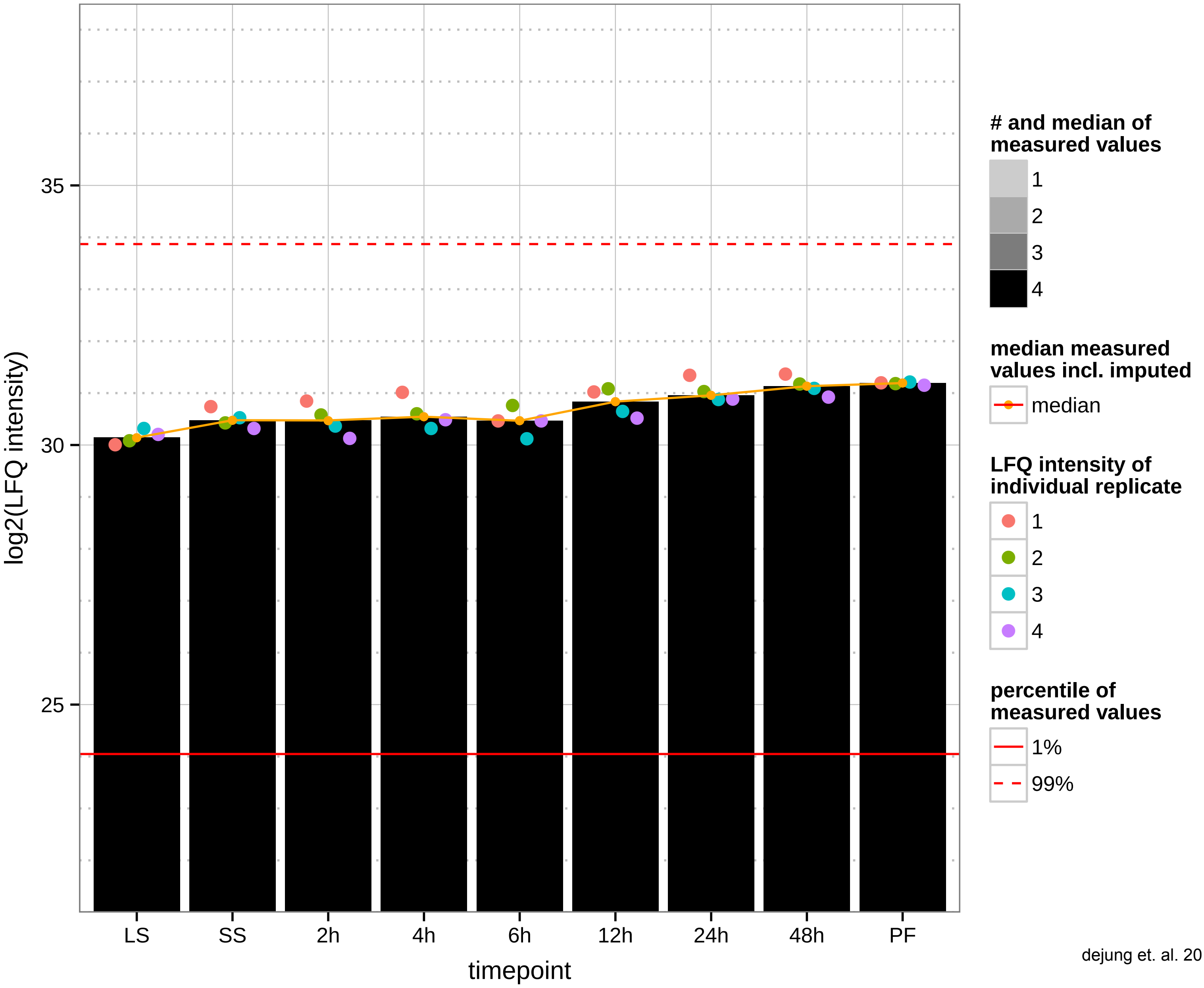
hypothetical protein, conserved
Tb927.4.1970
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



dejung et. al. 2015

ruvB–like DNA helicase, putative, ATP–dependent DNA helicase
Tb927.4.2000
AGOF: ATP binding, DNA helicase activity, nucleoside–triphosphatase activity
AGOC: nucleus
AGOP: null
PGOF: ATP binding, DNA helicase activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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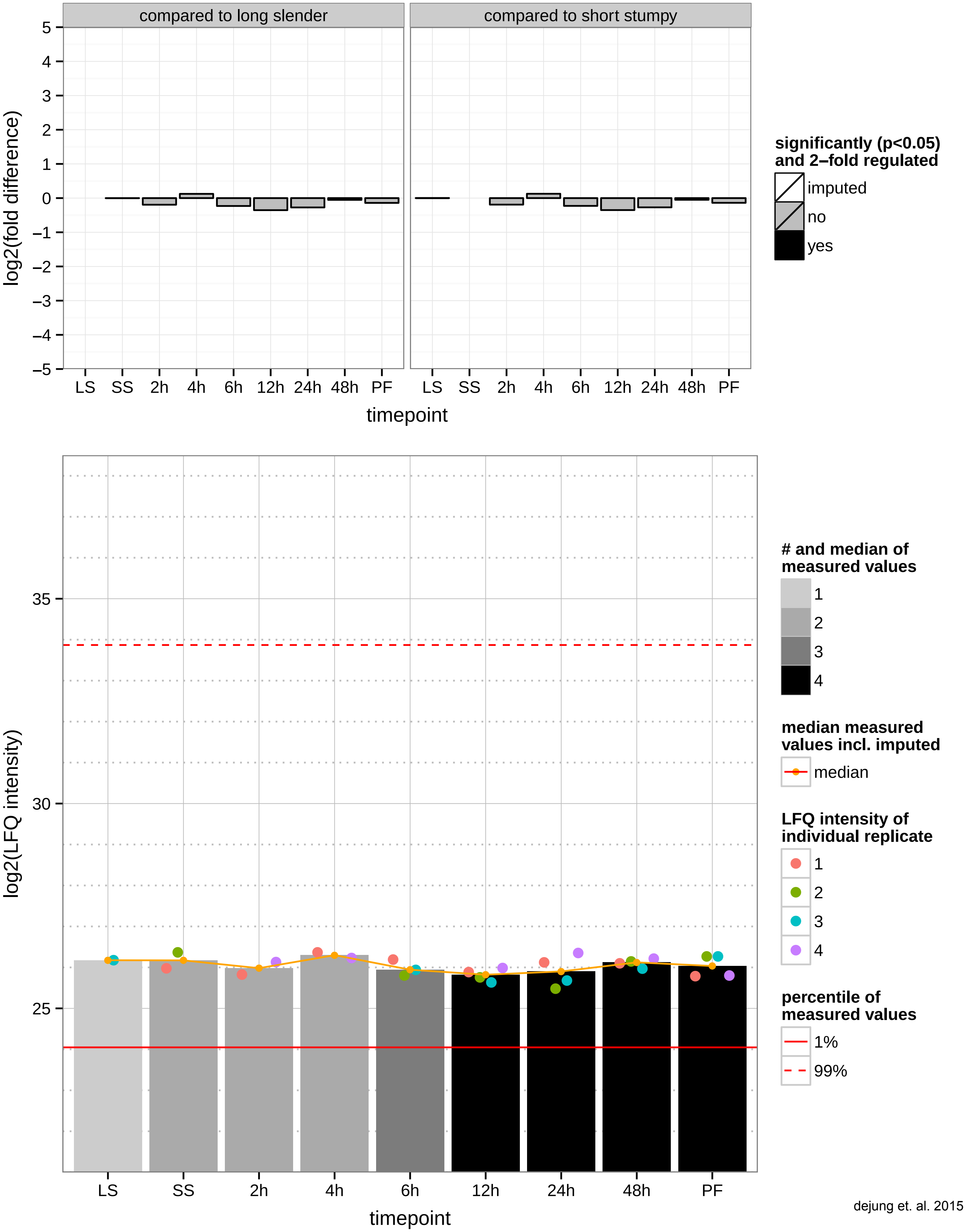
mu–adaptin 3, putative, adaptor complex AP–3 medium subunit
Tb927.4.2020
AGOF: clathrin binding
AGOC: clathrin adaptor complex
AGOP: intracellular protein transport, vesicle–mediated transport
PGOF: protein binding
PGOC: clathrin adaptor complex
PGOP: intracellular protein transport, transport, vesicle–mediated transport



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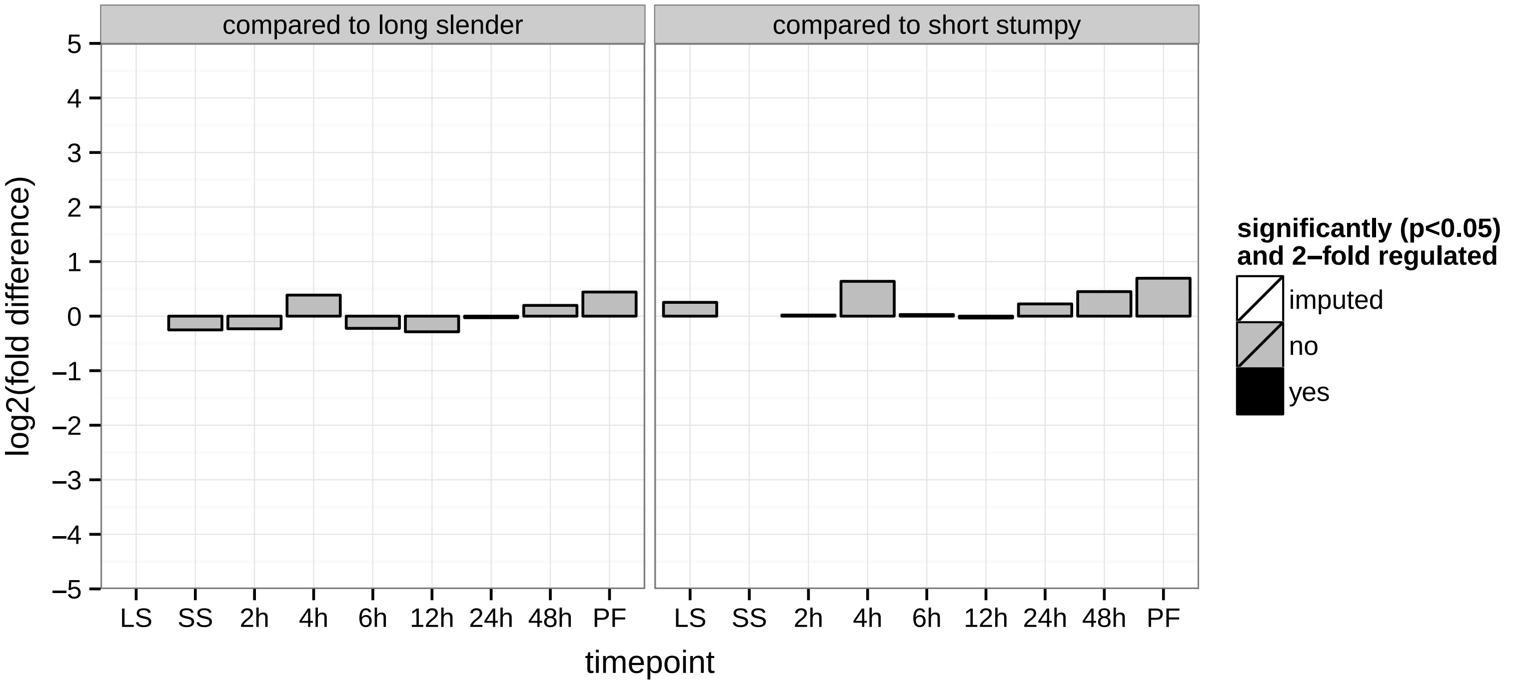
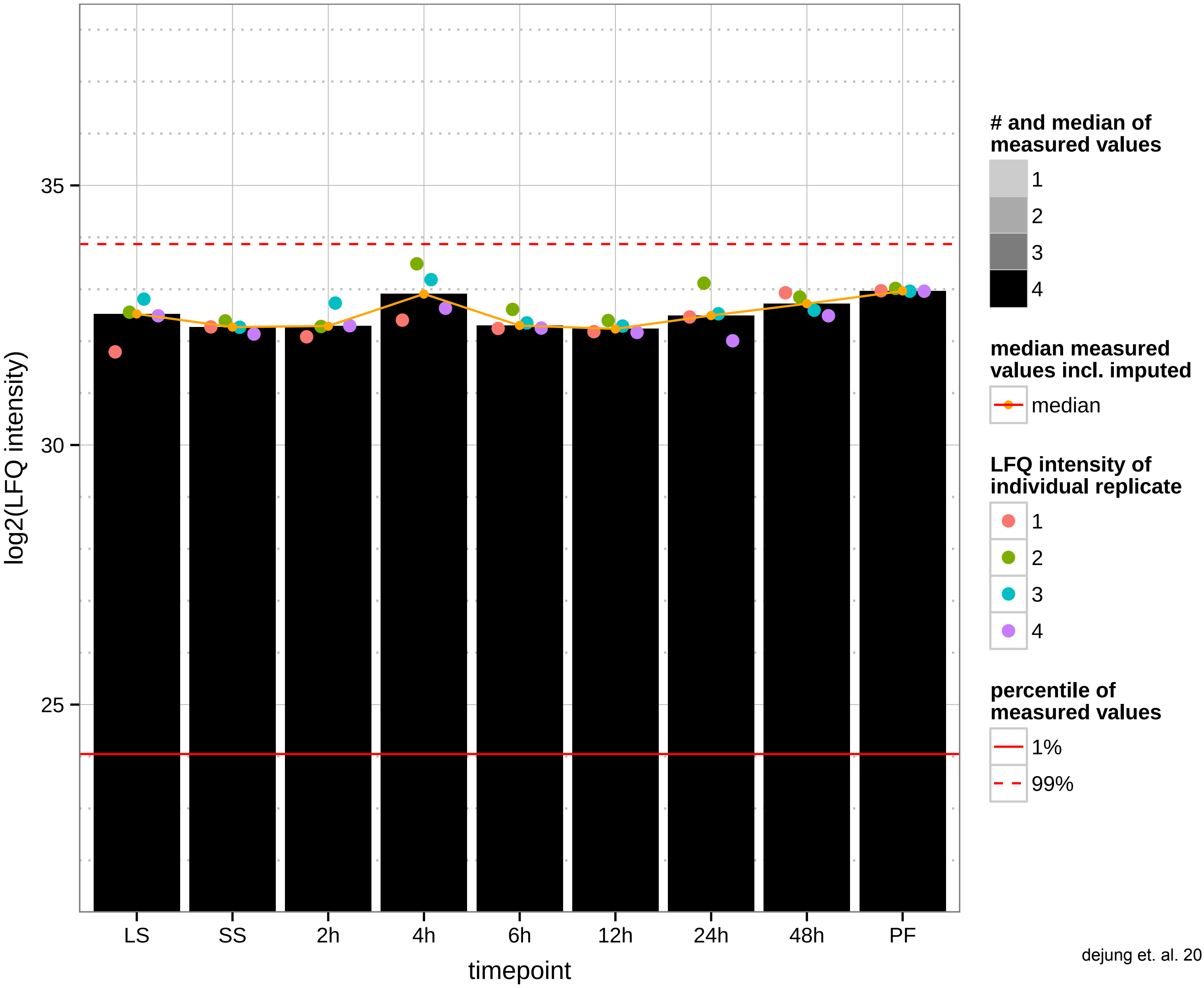
ALBA–Domain Protein (ALBA3)
Tb927.4.2040
AGOF: nucleic acid binding
AGOC: cytoplasm, cytoplasmic stress granule
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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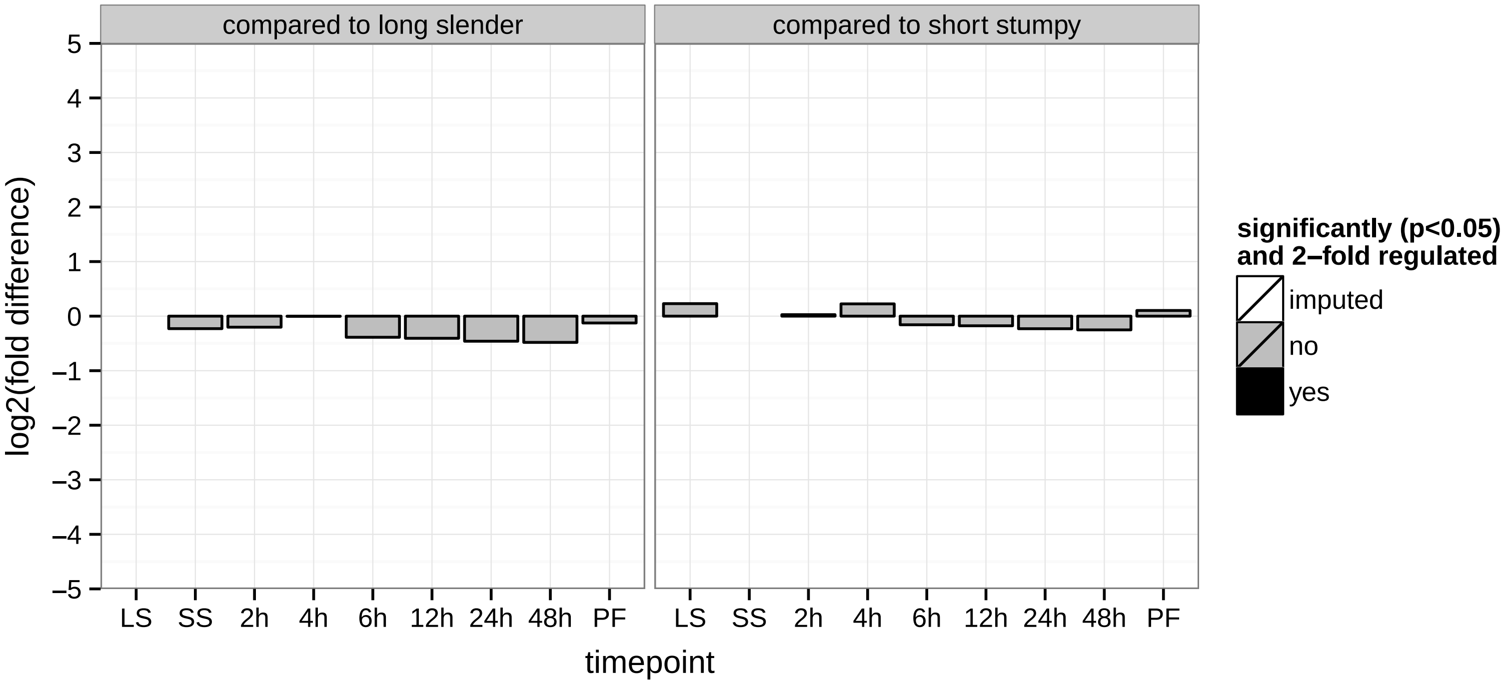
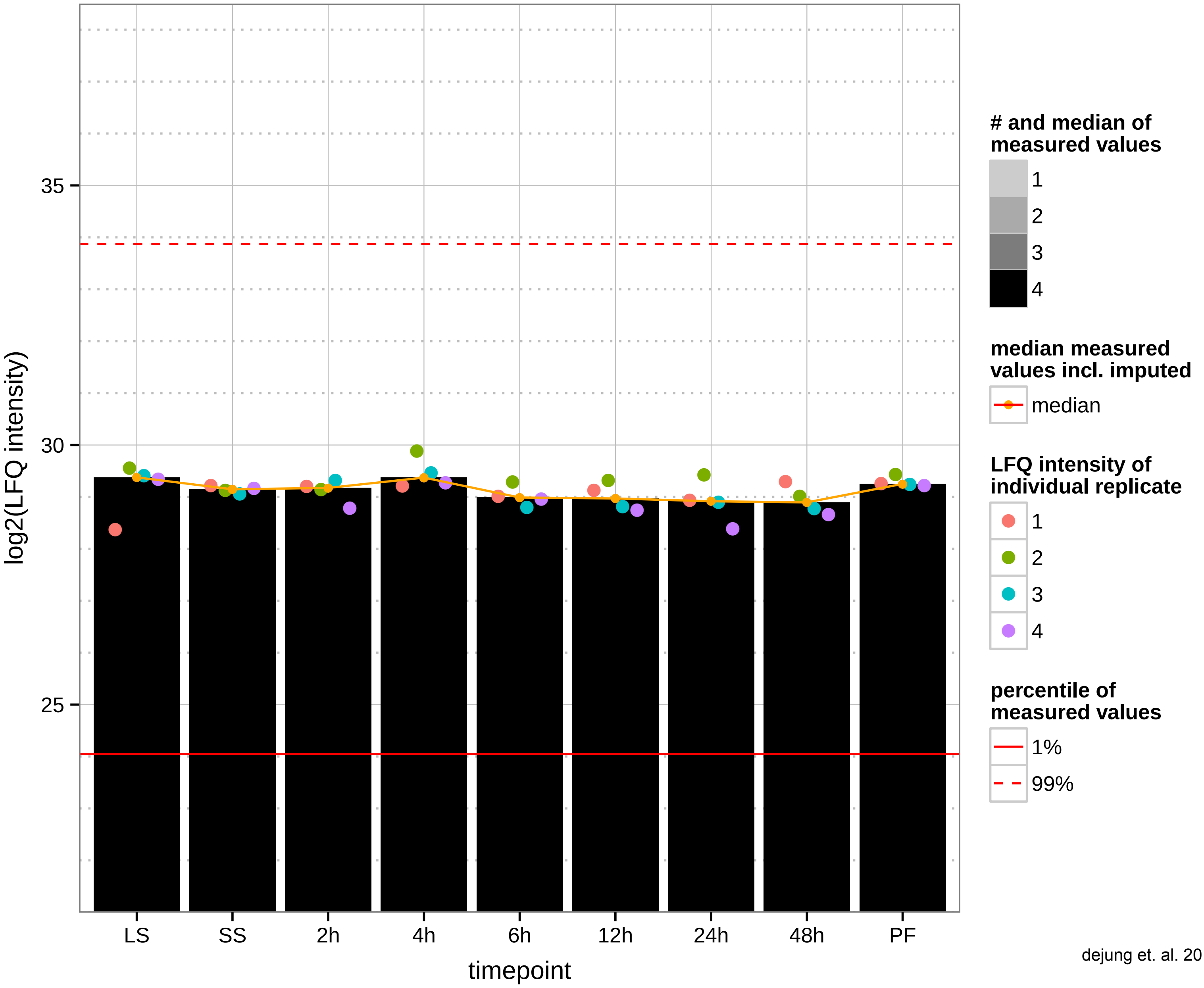
hypothetical protein, conserved
Tb927.4.2060
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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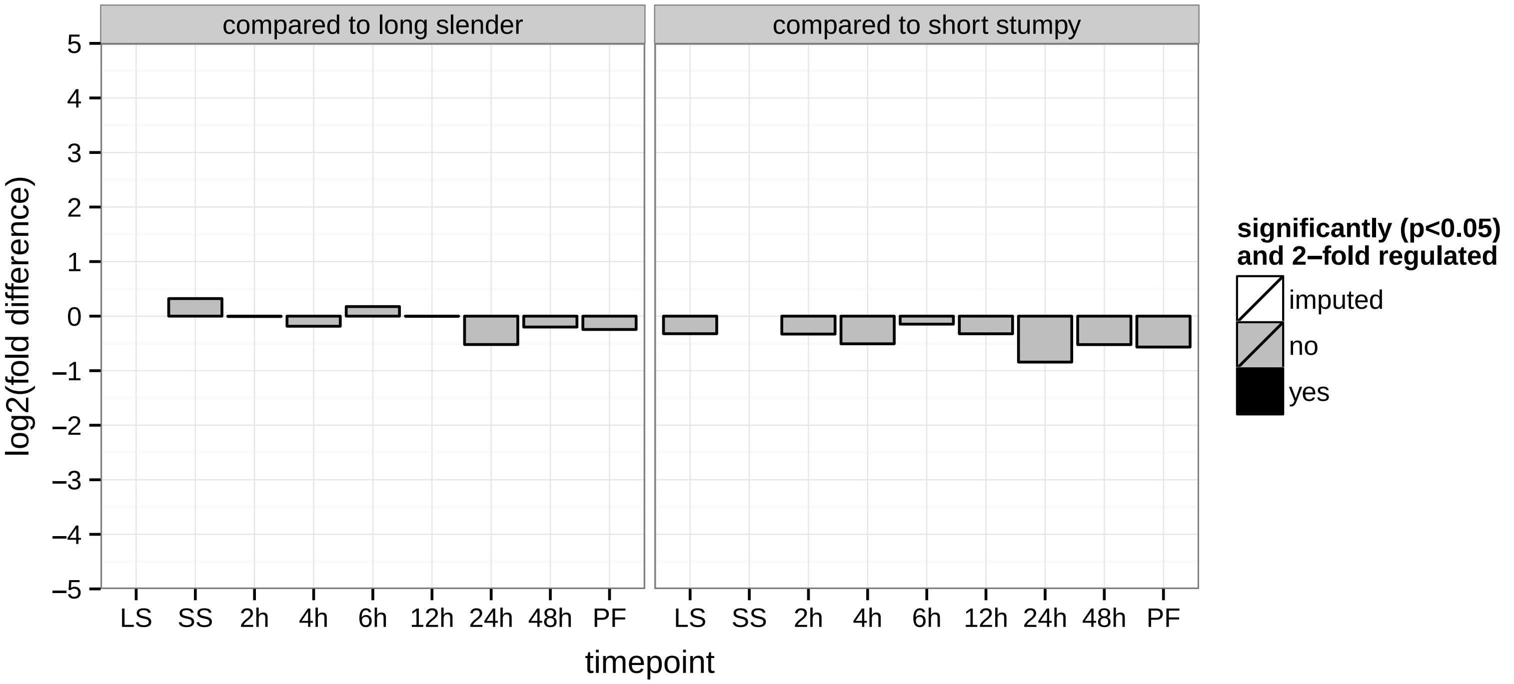
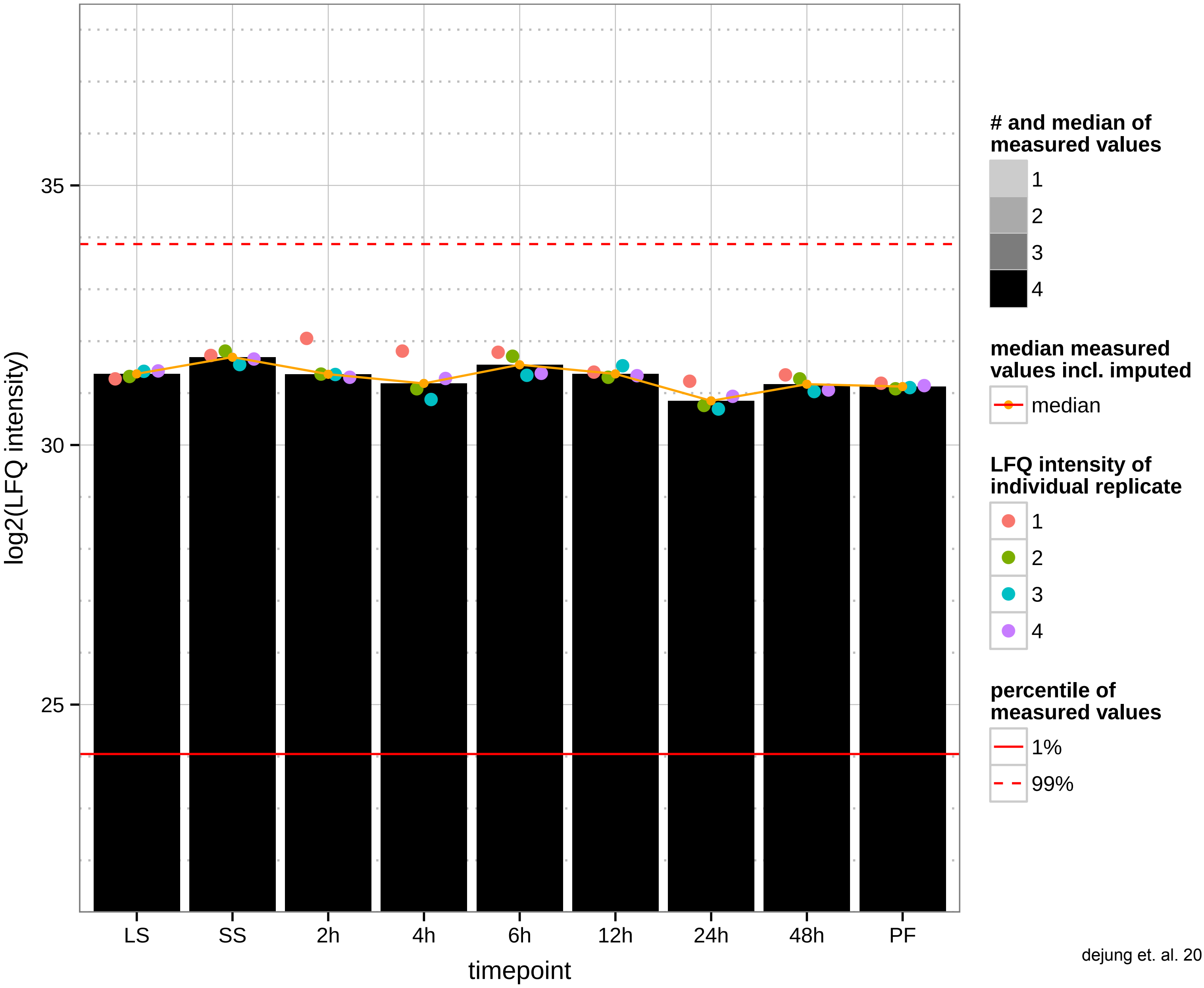
C2 domain containing protein (CC2D)
Tb927.4.2080
AGOF: null
AGOC: bacterial–type flagellum basal body, cell body
AGOP: cilium assembly
PGOF: protein binding
PGOC: null
PGOP: null





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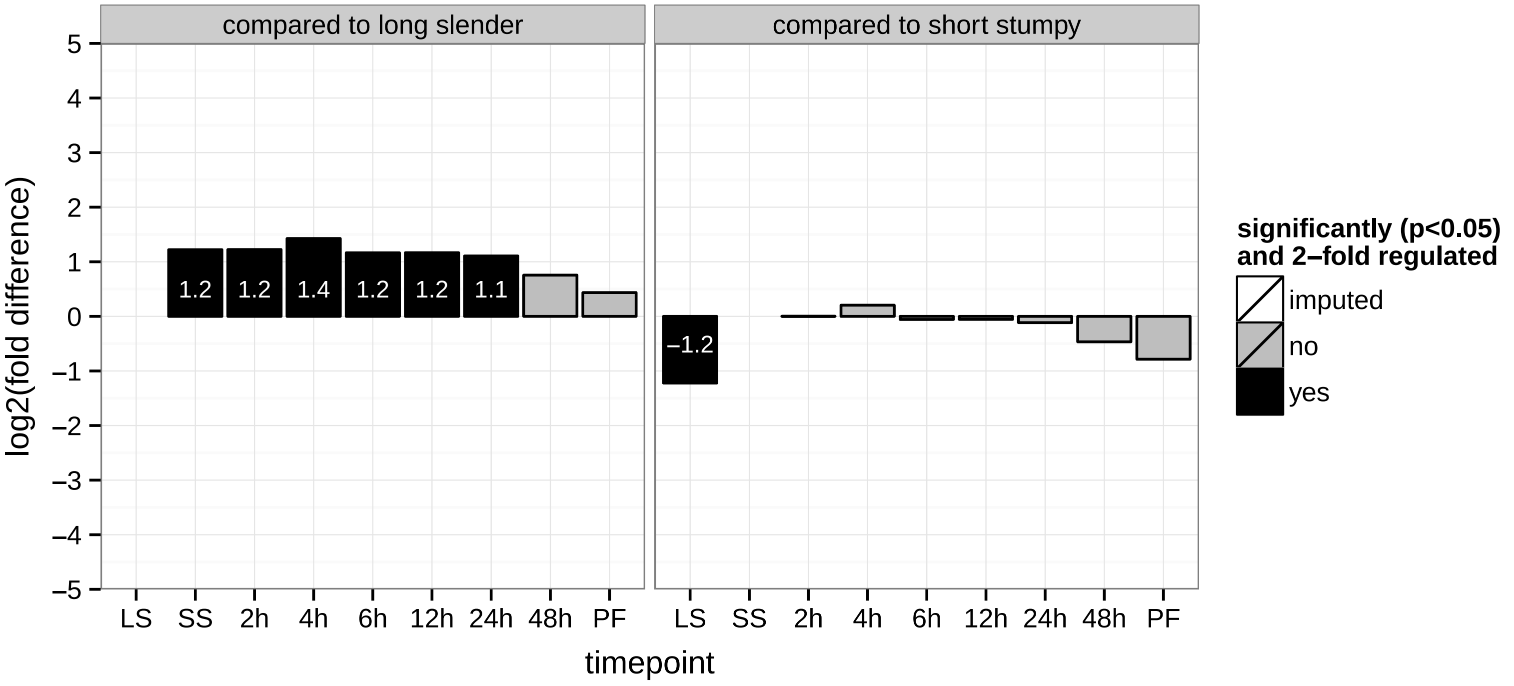
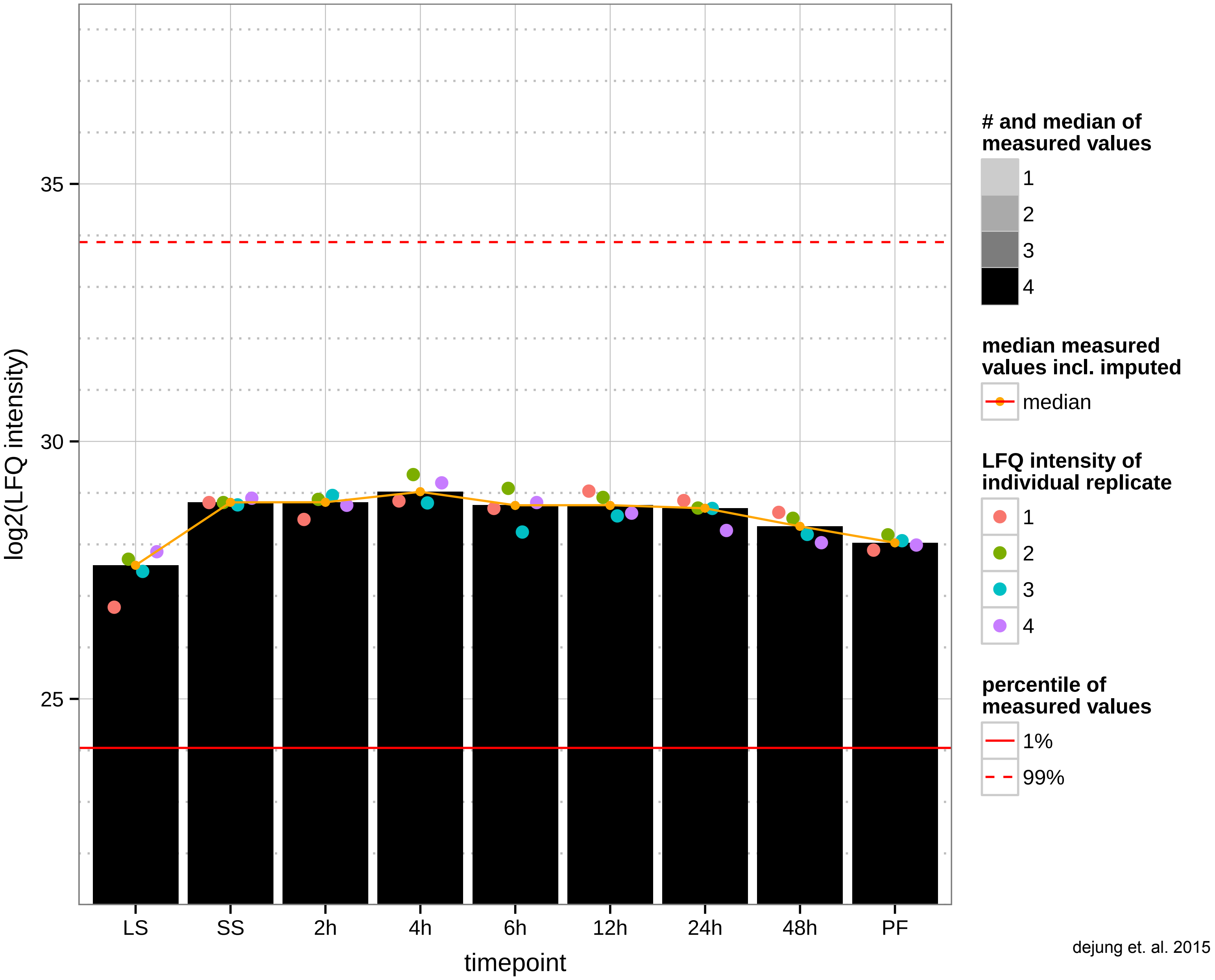
protein phosphatase 2C, putative
Tb927.4.2110
AGOF: phosphatase activity
AGOC: null
AGOP: dephosphorylation
PGOF: catalytic activity
PGOC: null
PGOP: null





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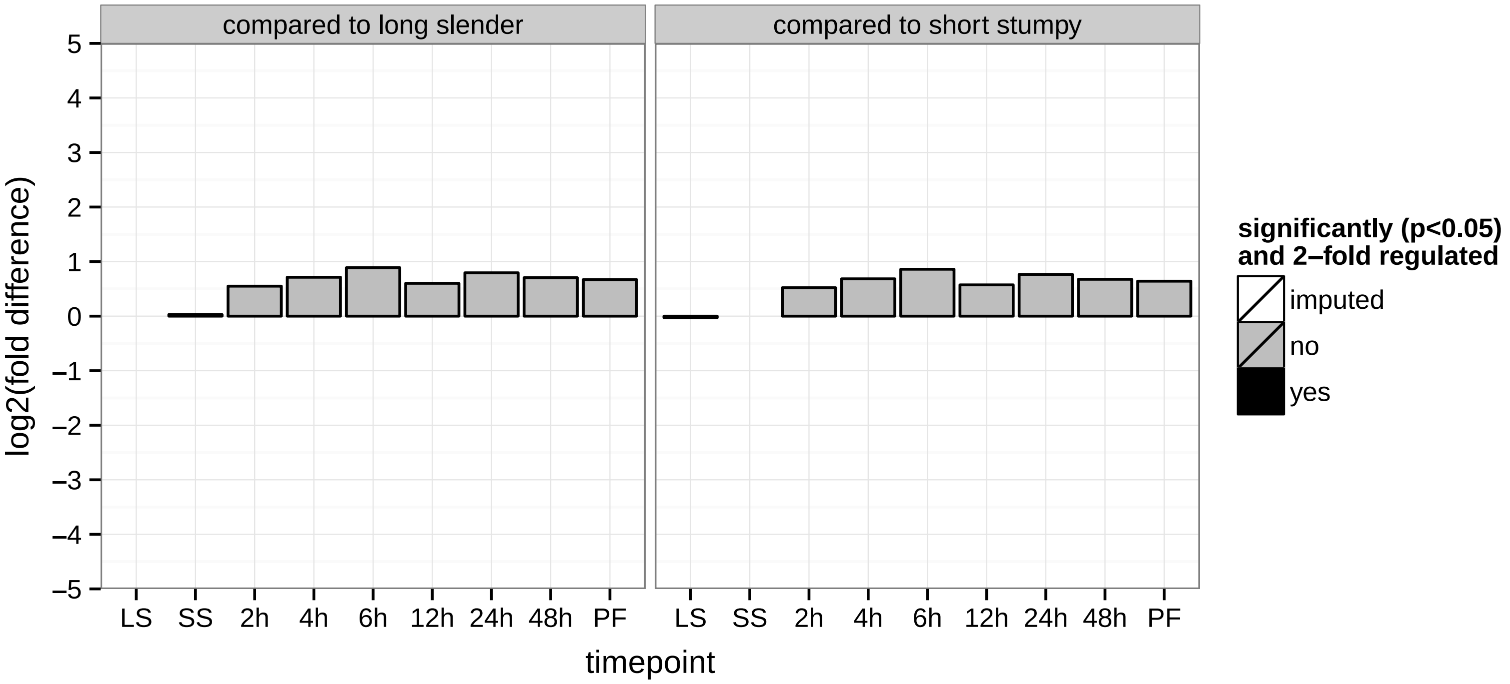
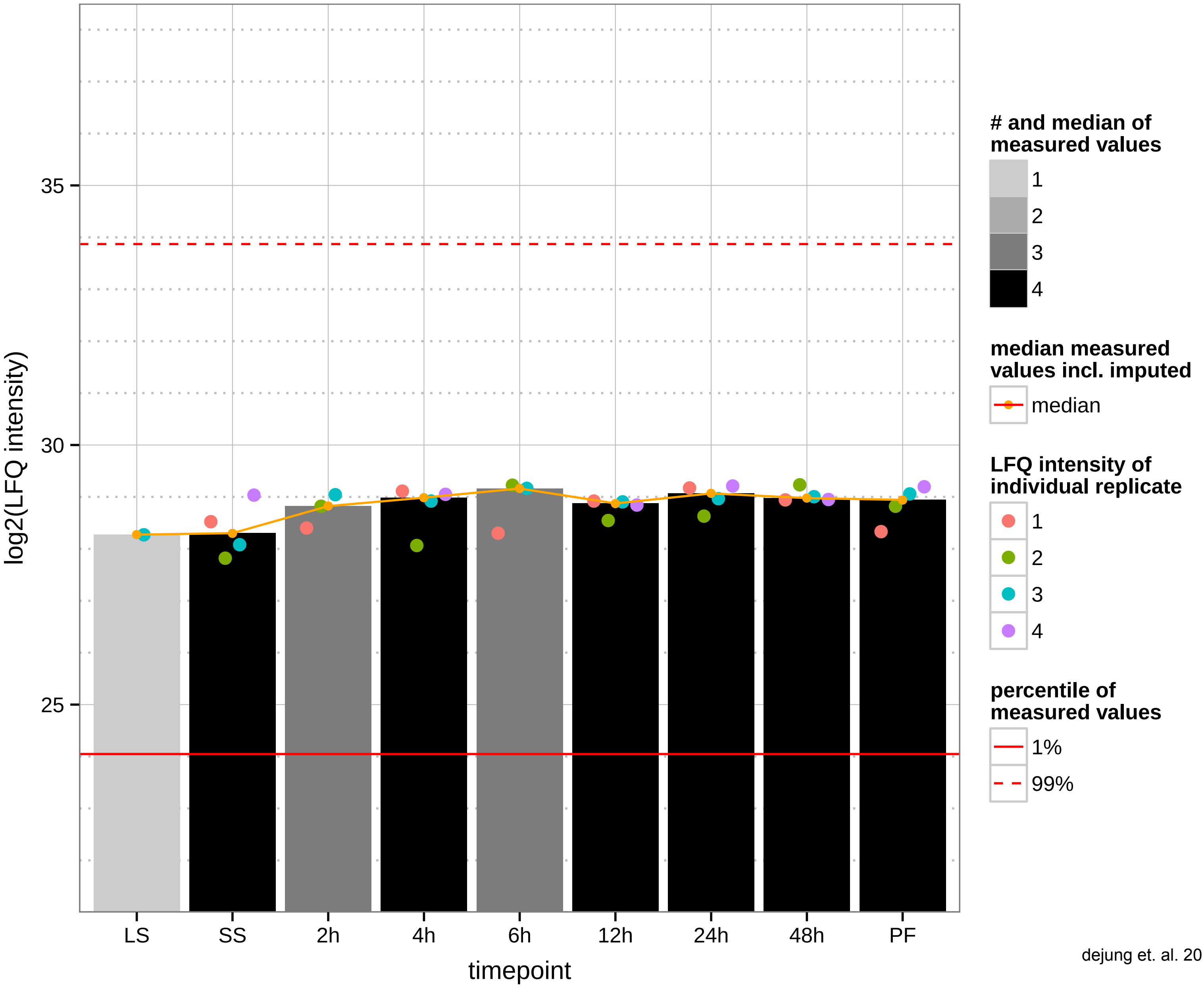
hypothetical protein, conserved
Tb927.4.2200
AGOF: null, ARF guanyl–nucleotide exchange factor activity
AGOC: null, intracellular
AGOP: null, regulation of ARF protein signal transduction
PGOF: null, ARF guanyl–nucleotide exchange factor activity
PGOC: null, intracellular
PGOP: null, regulation of ARF protein signal transduction





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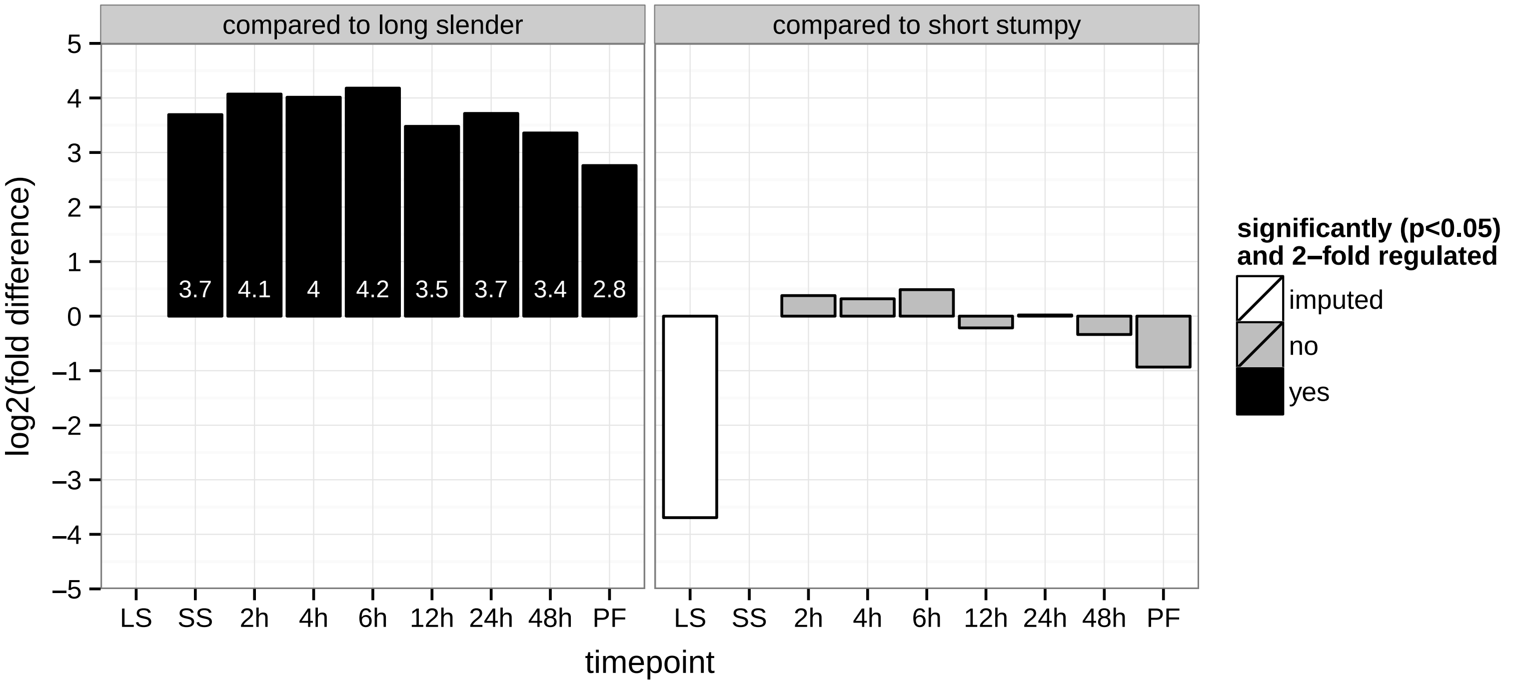
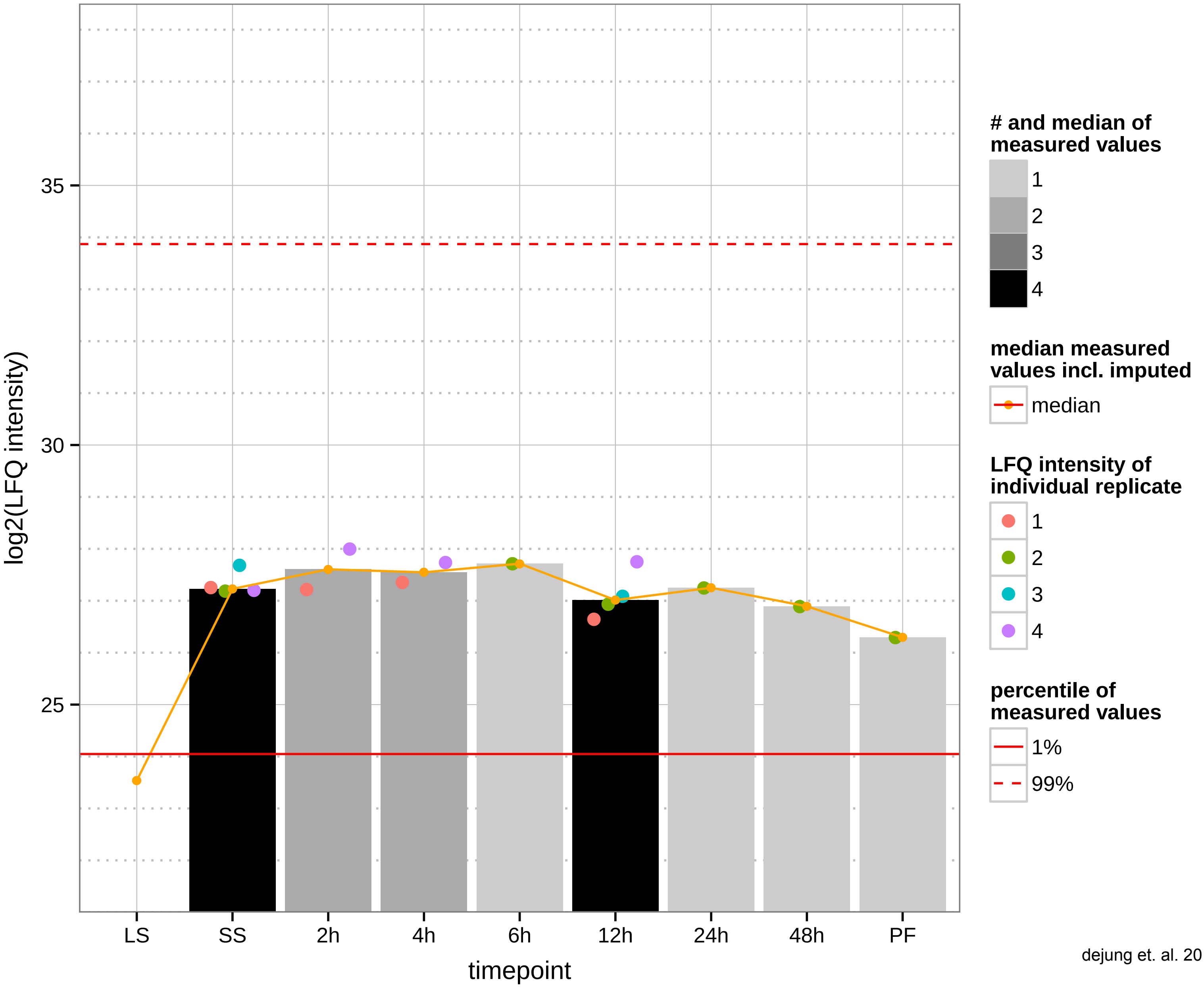
hypothetical protein, conserved
Tb927.4.2210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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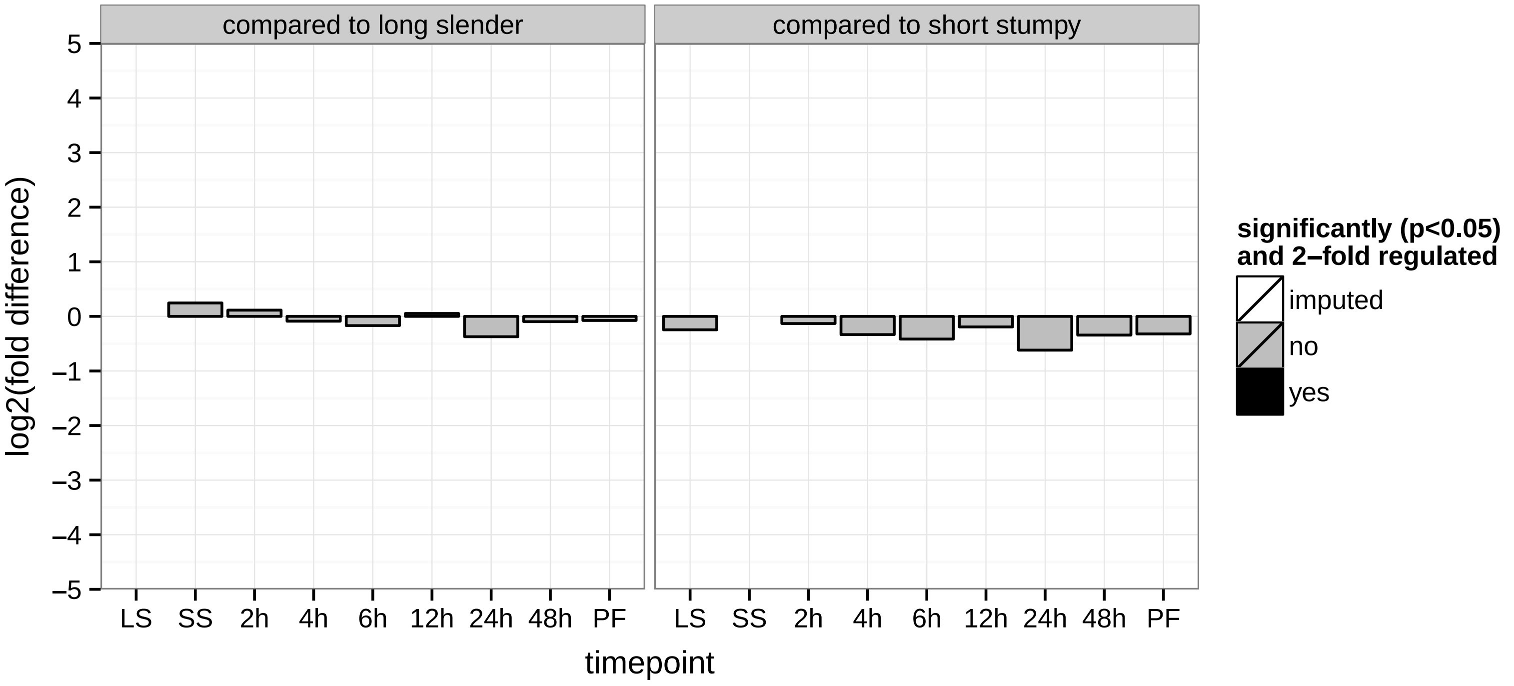
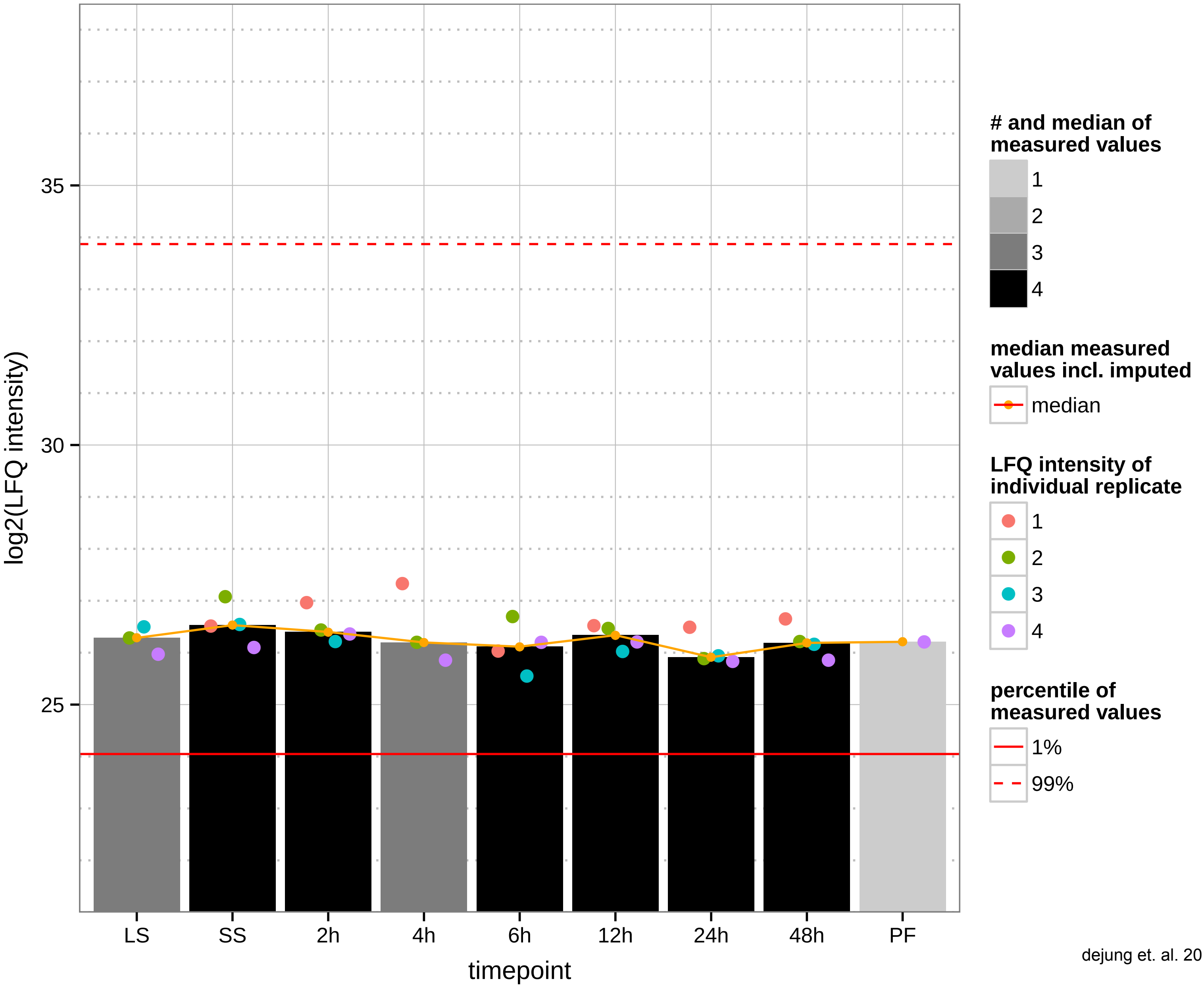
dolichyl−P−Man:GDP−Man1GlcNAc2−PP−dolichyl alpha−1, 3−mannosyltransferase, putative
Tb927.4.2230
AGOF: GDP−Man:Man1GlcNAc2−PP−Dol alpha−1, 3−mannosyltransferase activity
AGOC: null
AGOP: biosynthetic process, dolichol−linked oligosaccharide biosynthetic process
PGOF: null
PGOC: null
PGOP: biosynthetic process





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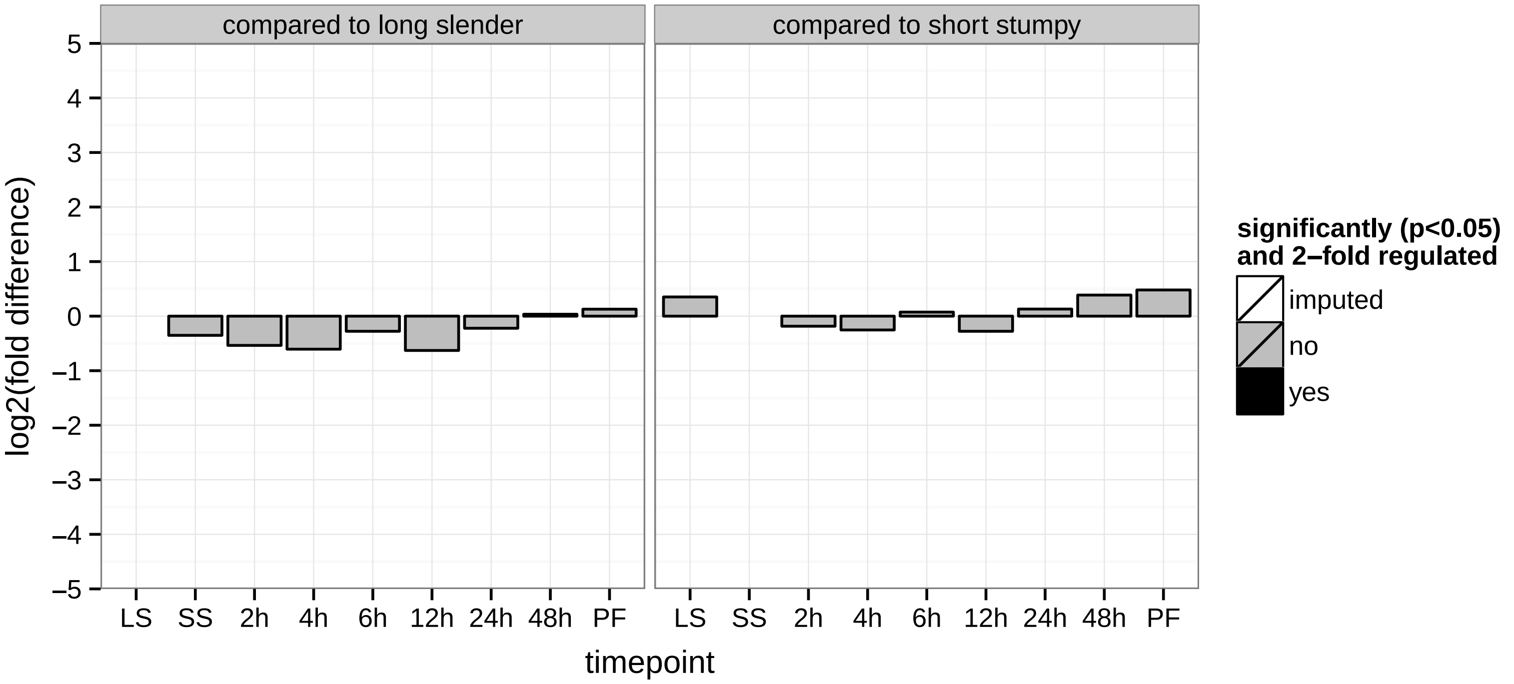
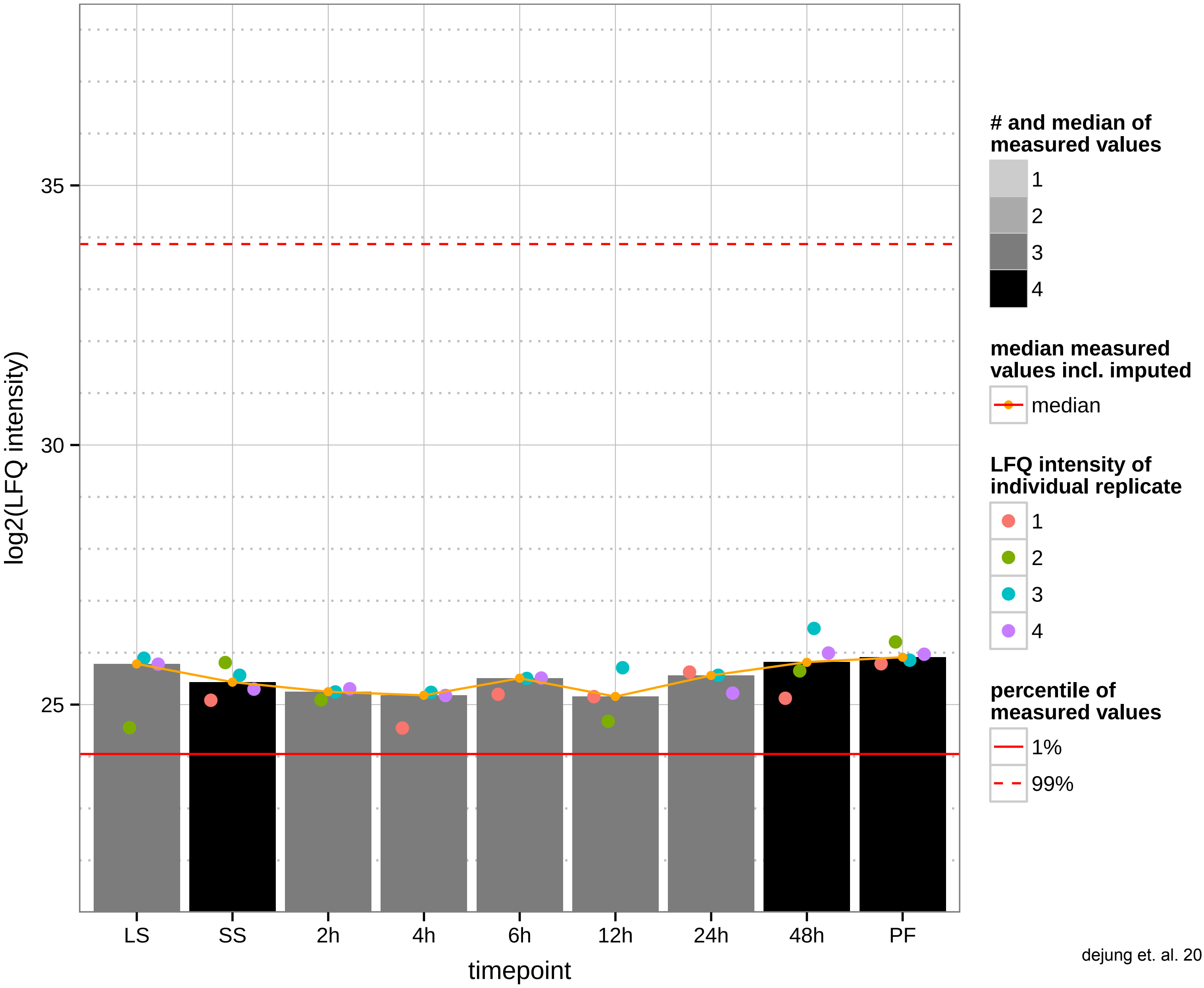
hypothetical protein, conserved
Tb927.4.2300
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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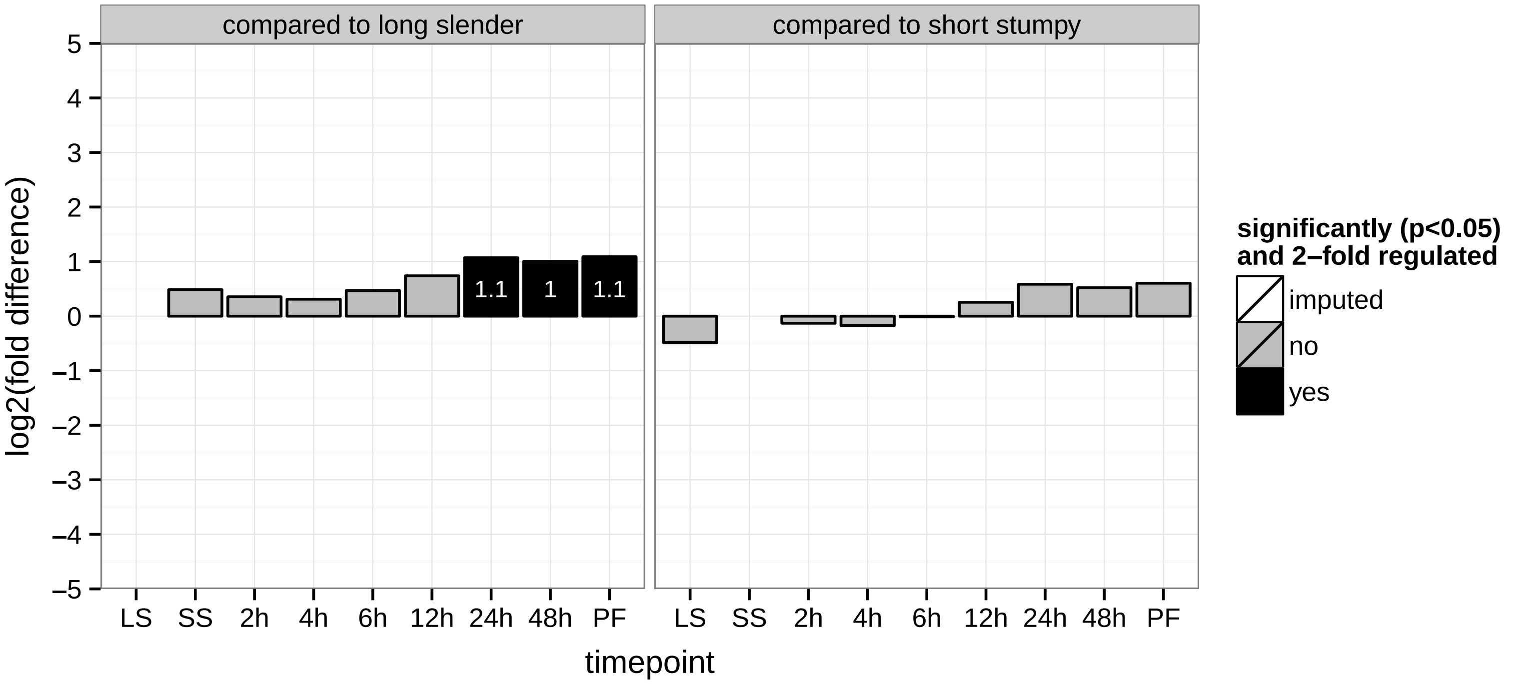
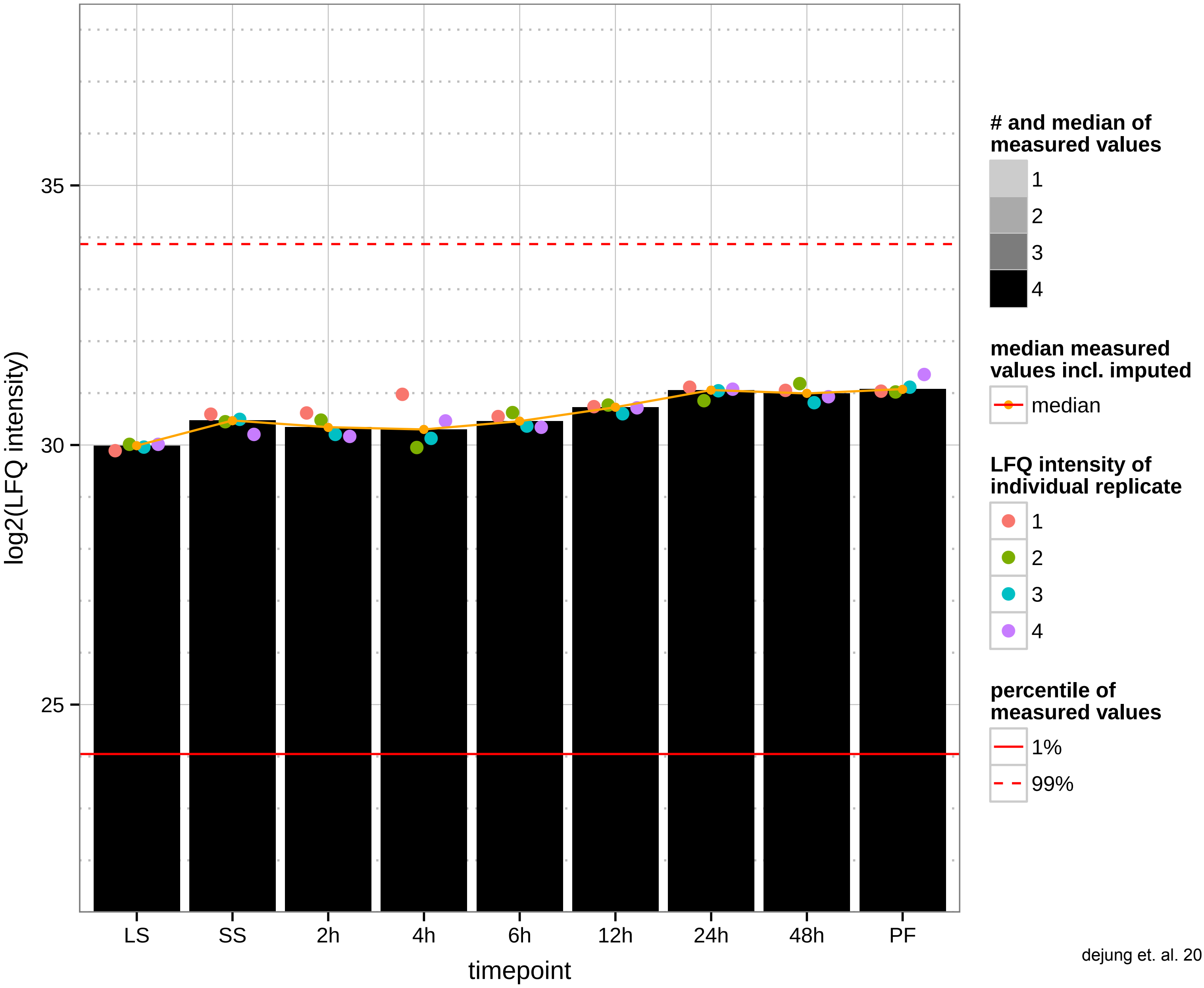
asparaginyl–tRNA synthetase, putative
Tb927.4.2310
AGOF: ATP binding, asparagine–tRNA ligase activity, aspartate–tRNA ligase activity, nucleic acid binding
AGOC: cytoplasm, mitochondrion
AGOP: asparaginyl–tRNA aminoacylation, aspartyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, asparagine–tRNA ligase activity, nucleic acid binding, nucleotide binding
PGOC: cytoplasm
PGOP: asparaginyl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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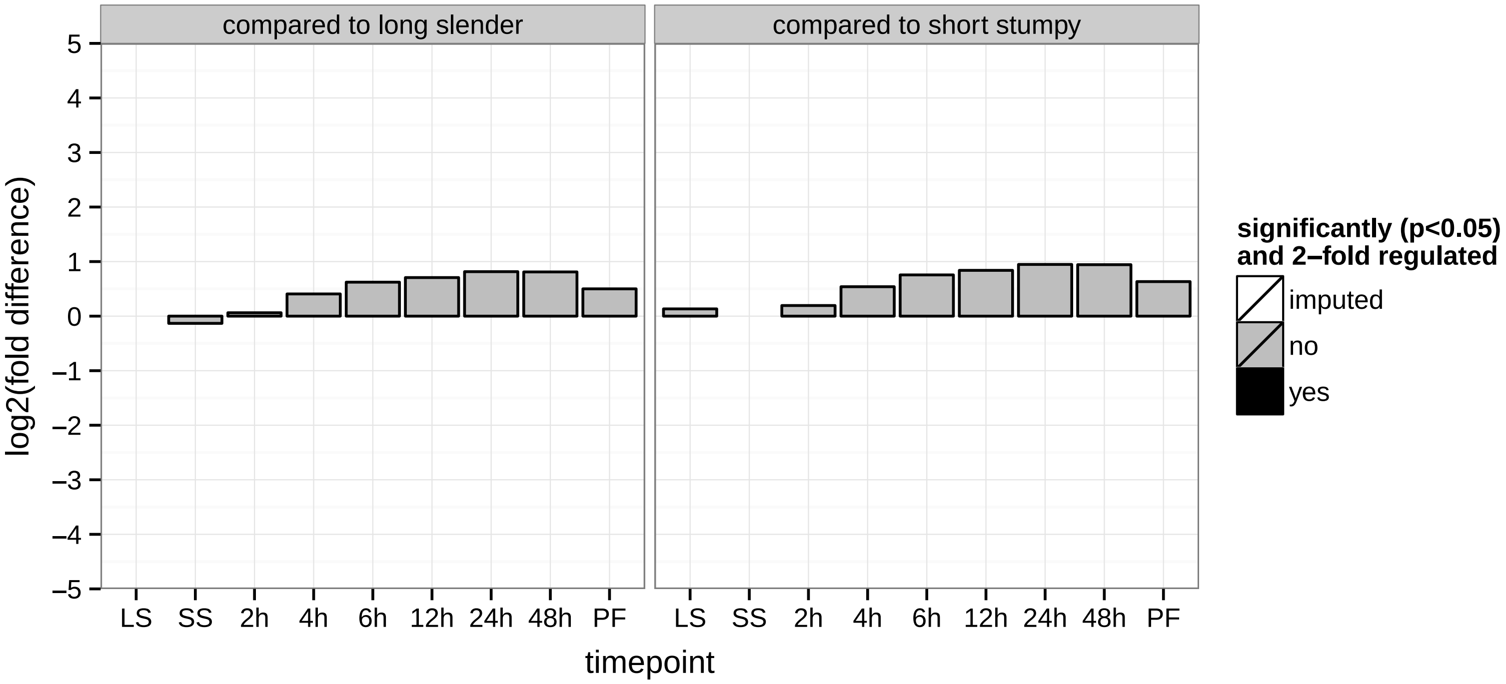
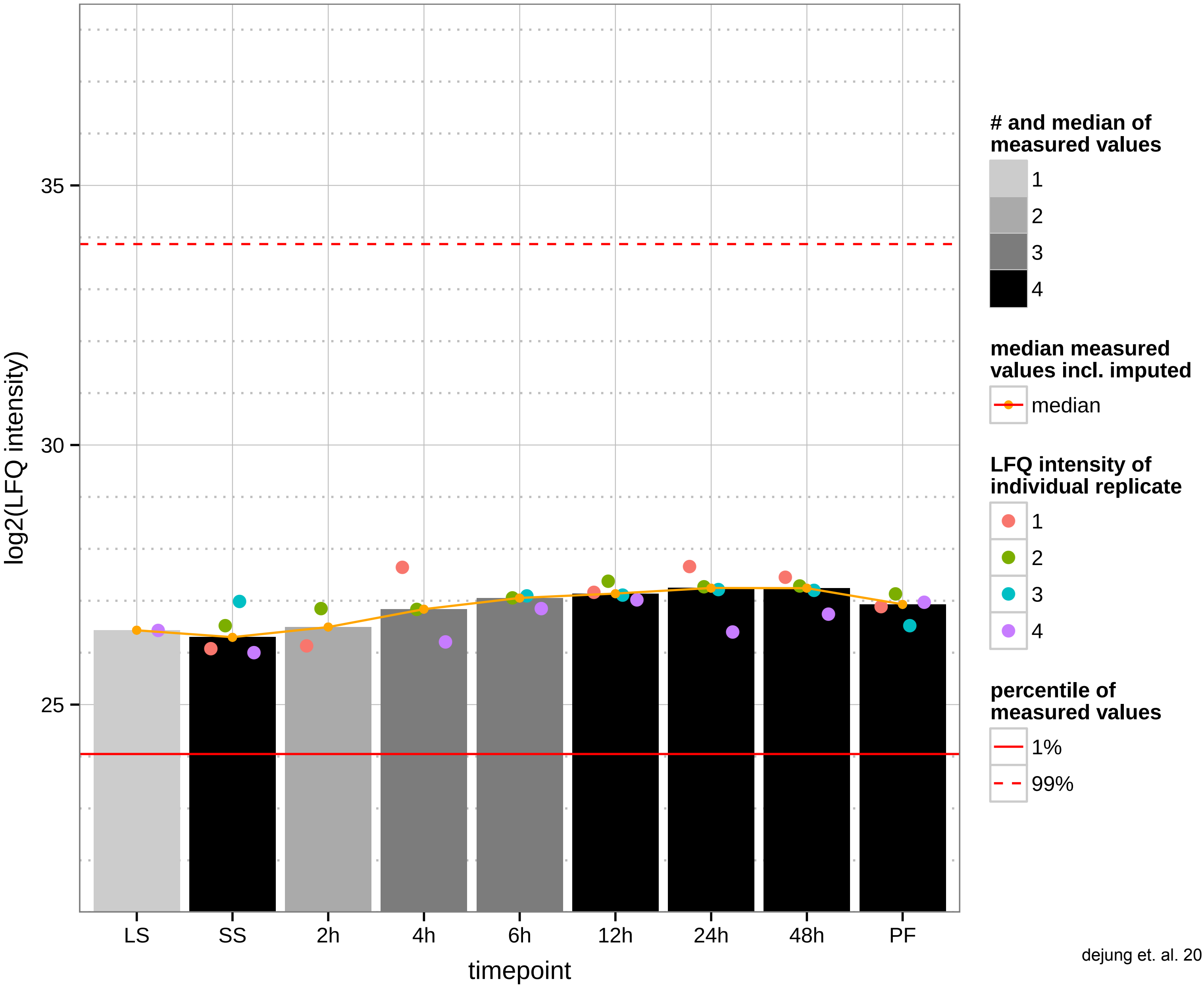
hypothetical protein, conserved
Tb927.4.2340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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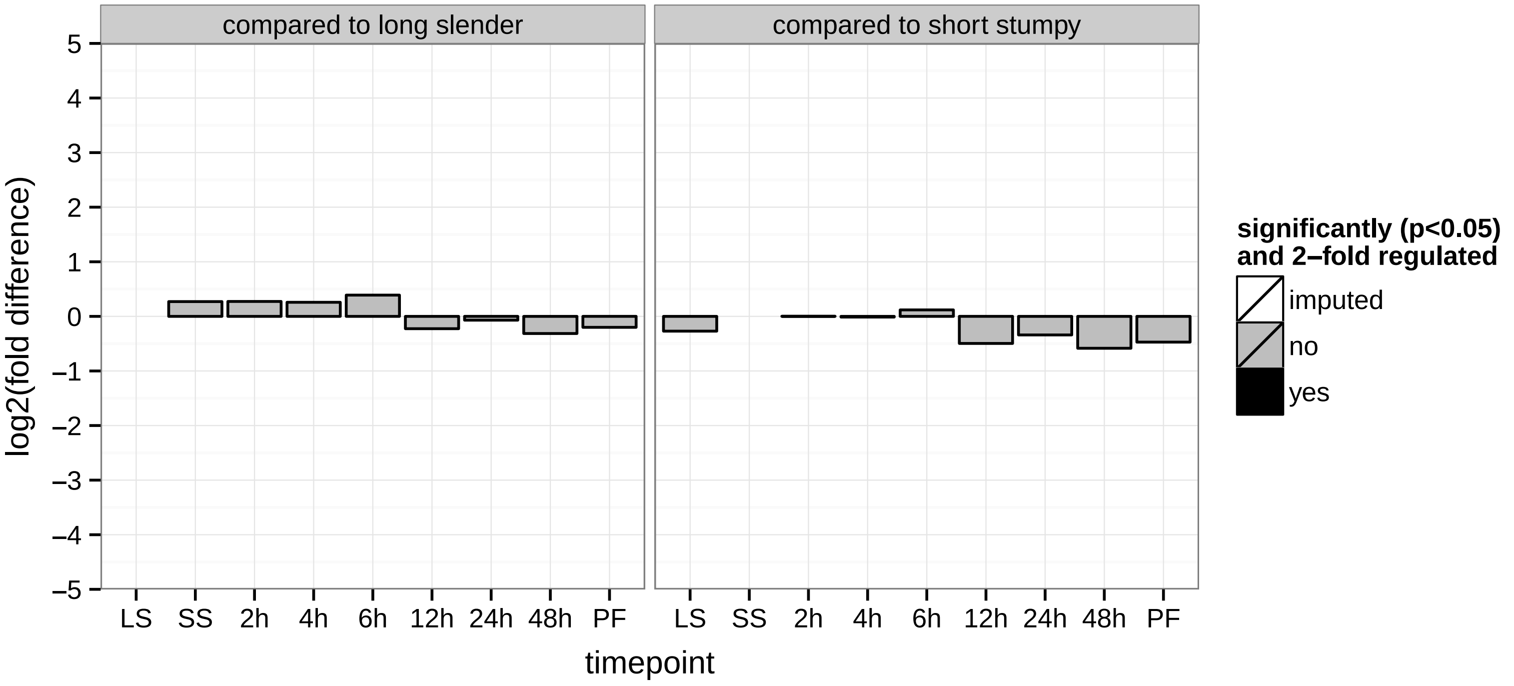
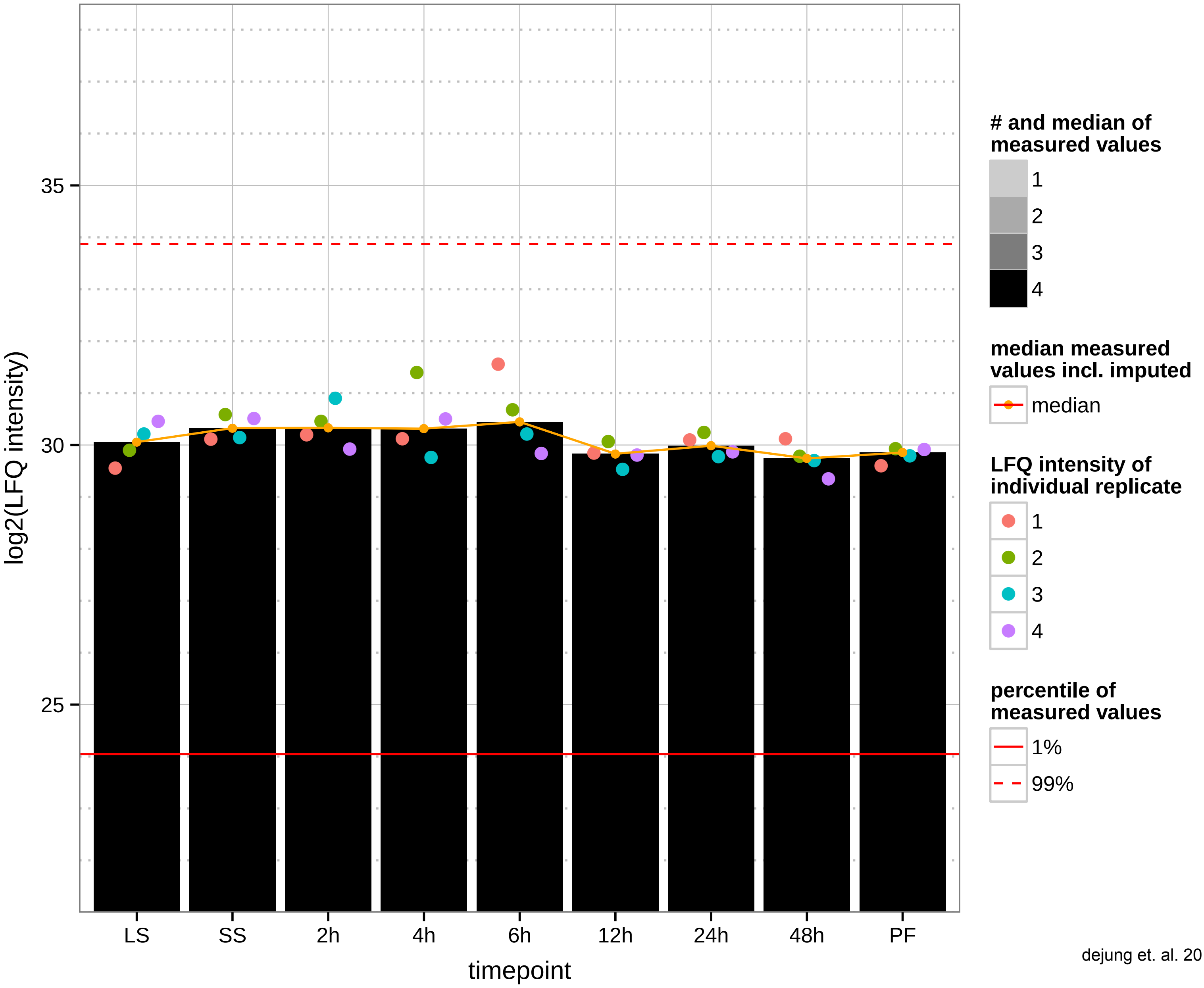
hypothetical protein, conserved
Tb927.4.2530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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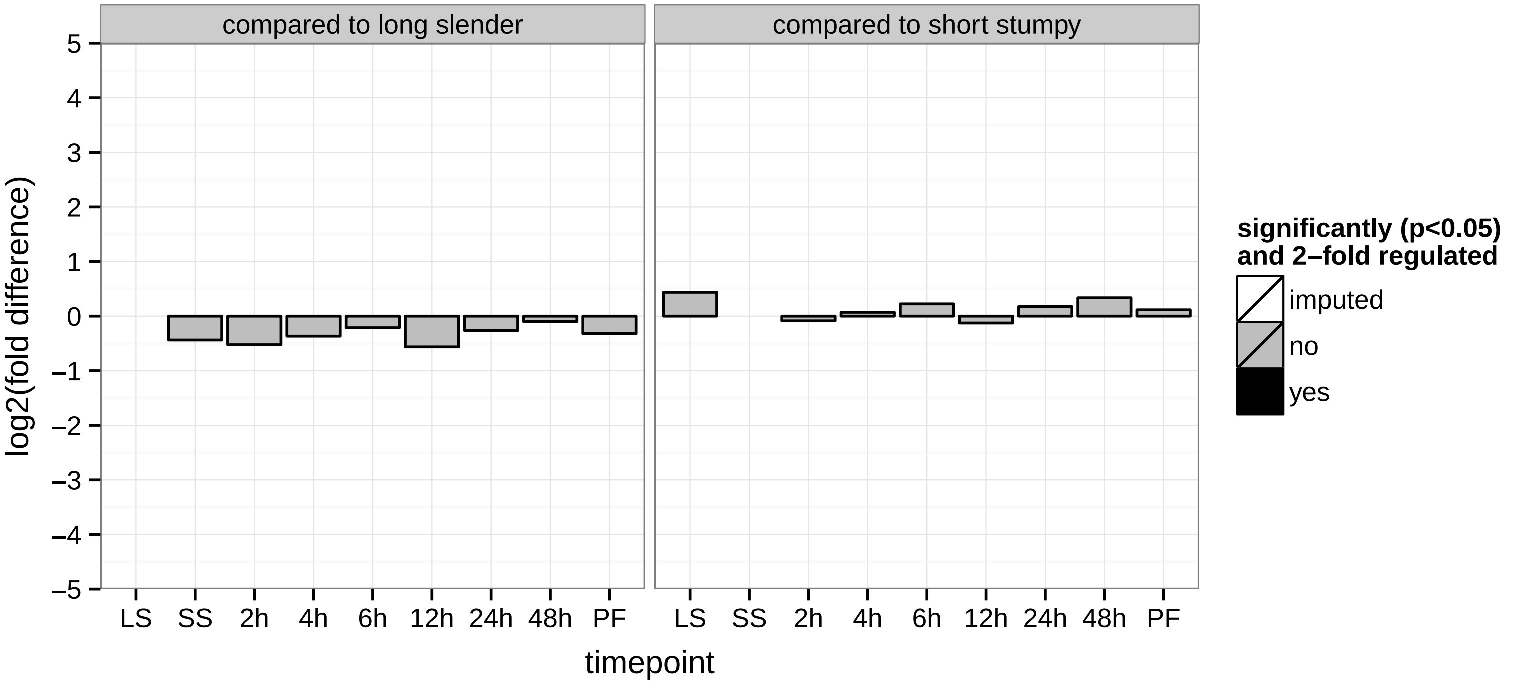
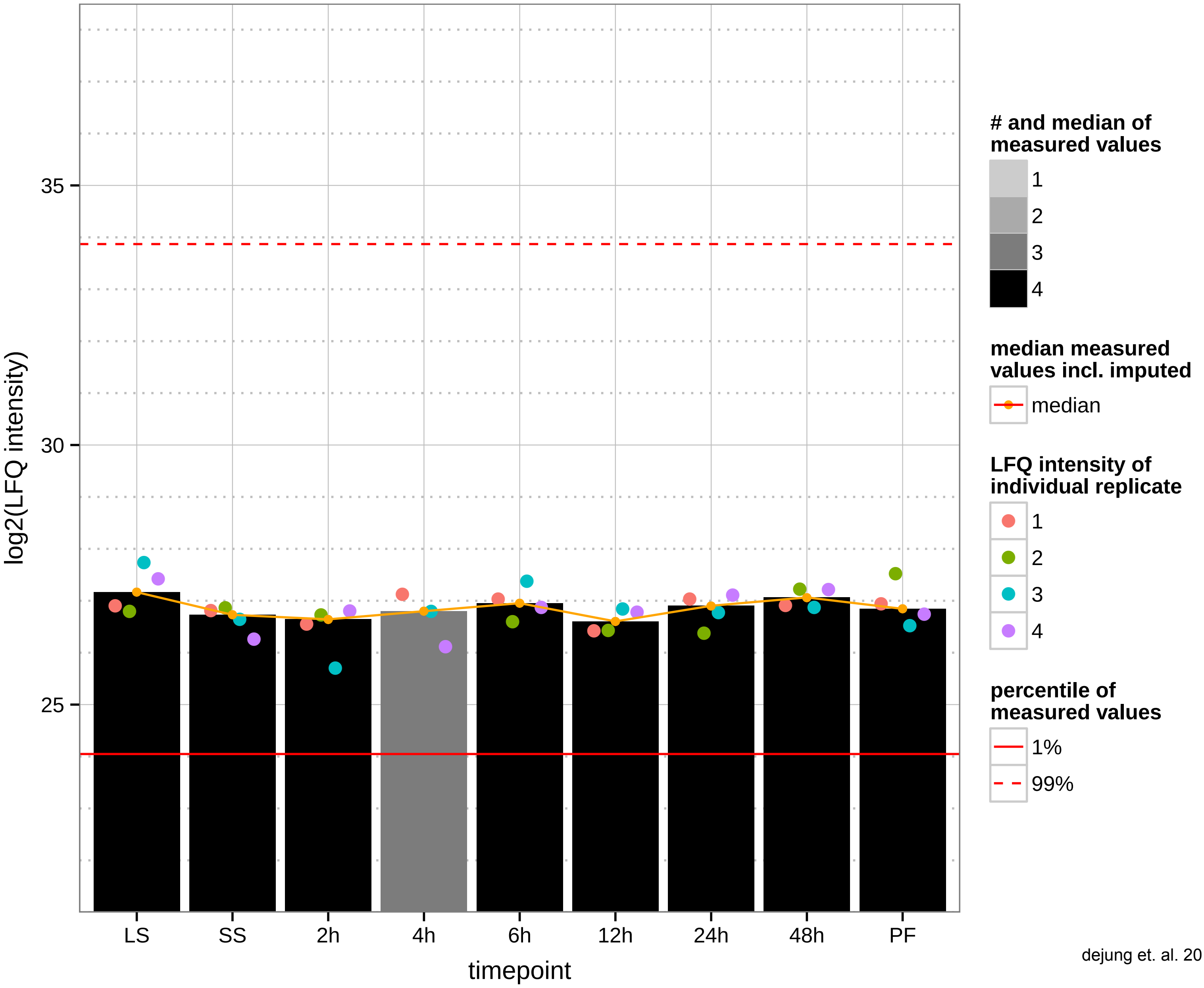
hypothetical protein, conserved
Tb927.4.2600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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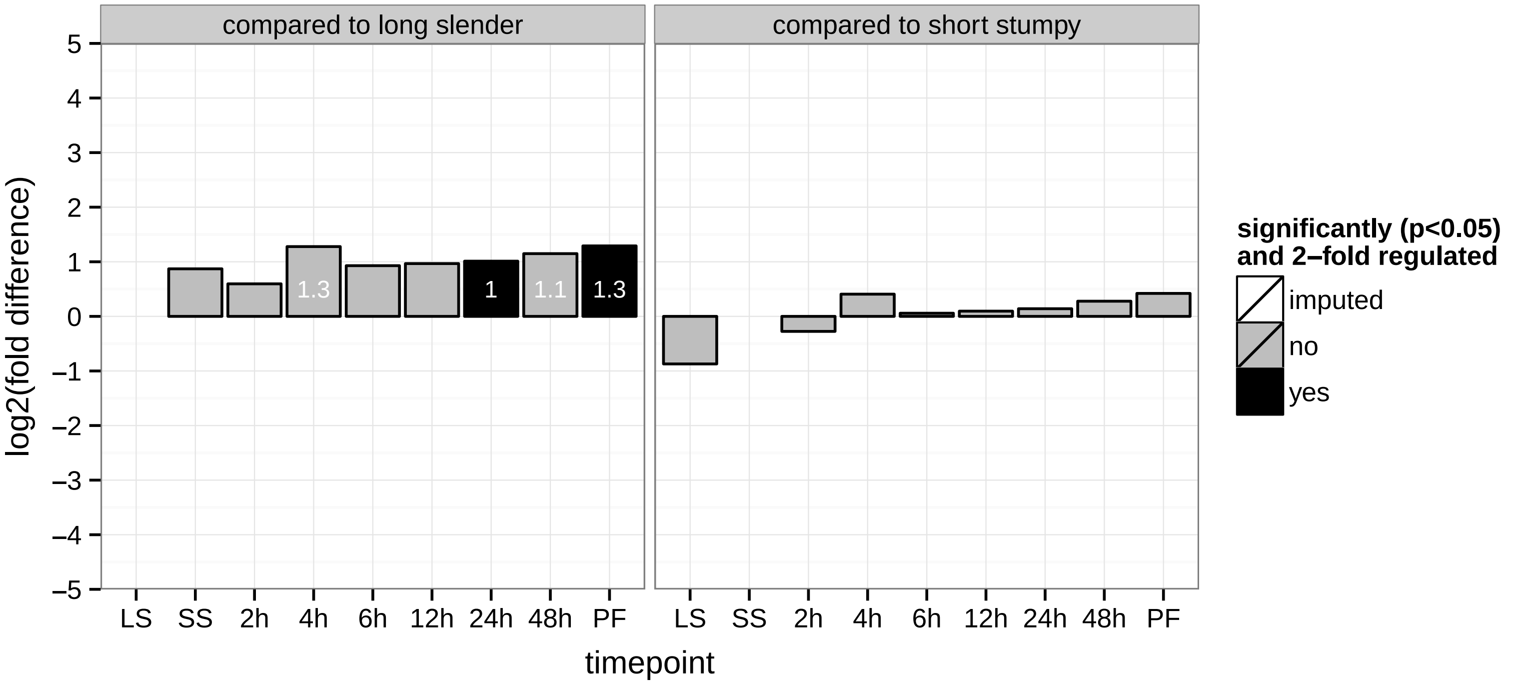
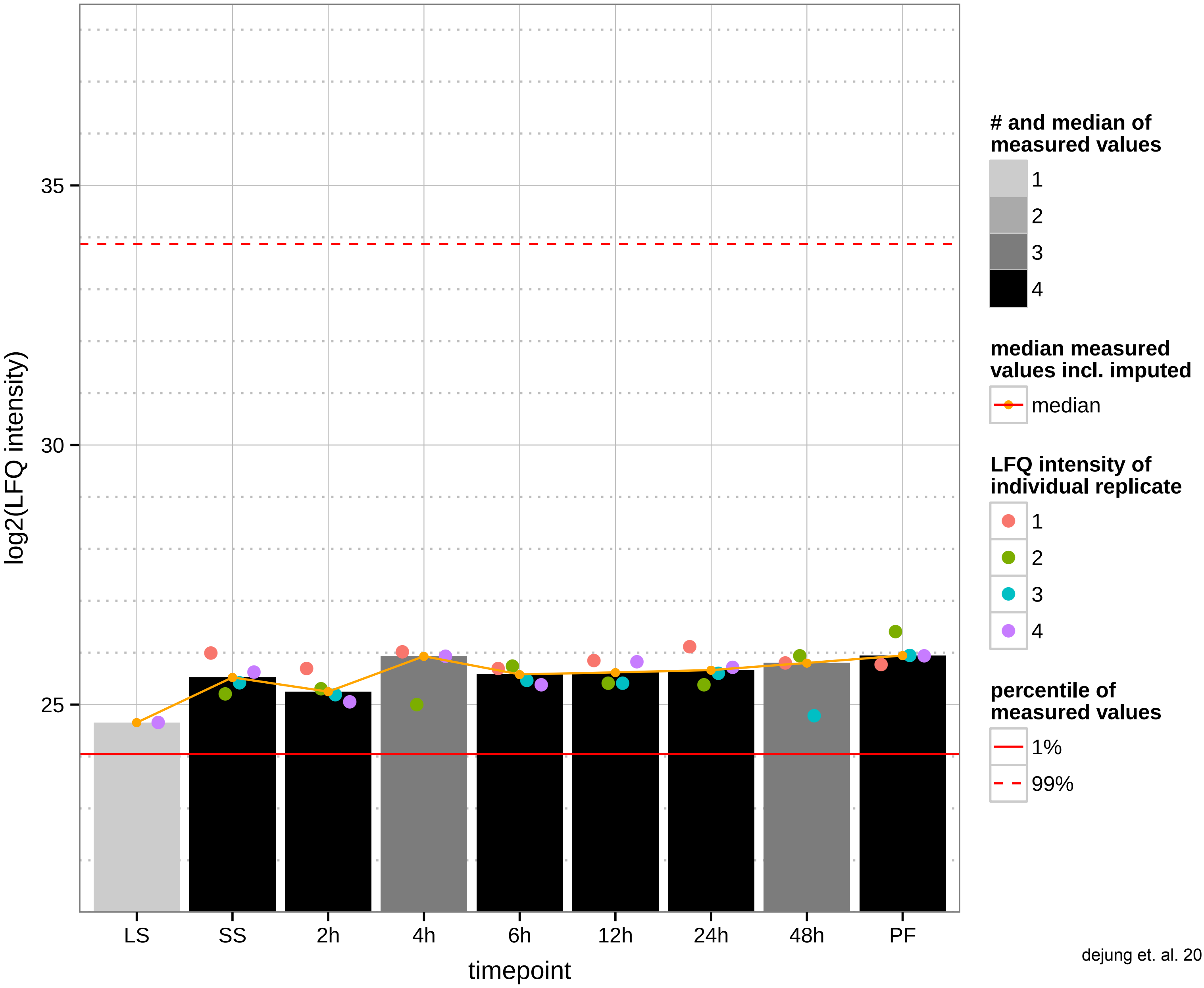
hypothetical protein, conserved
Tb927.4.2650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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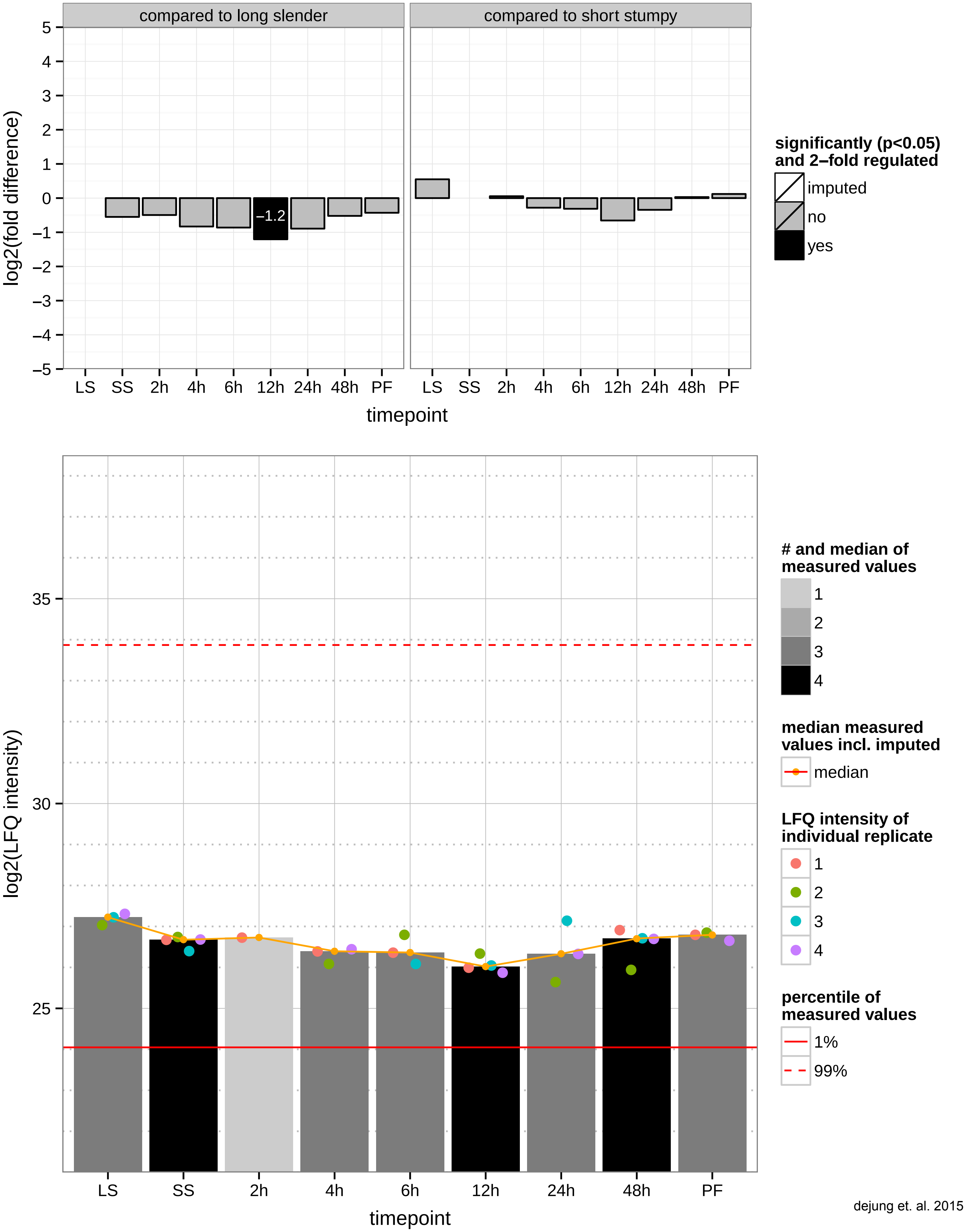
hypothetical protein, conserved
Tb927.4.2840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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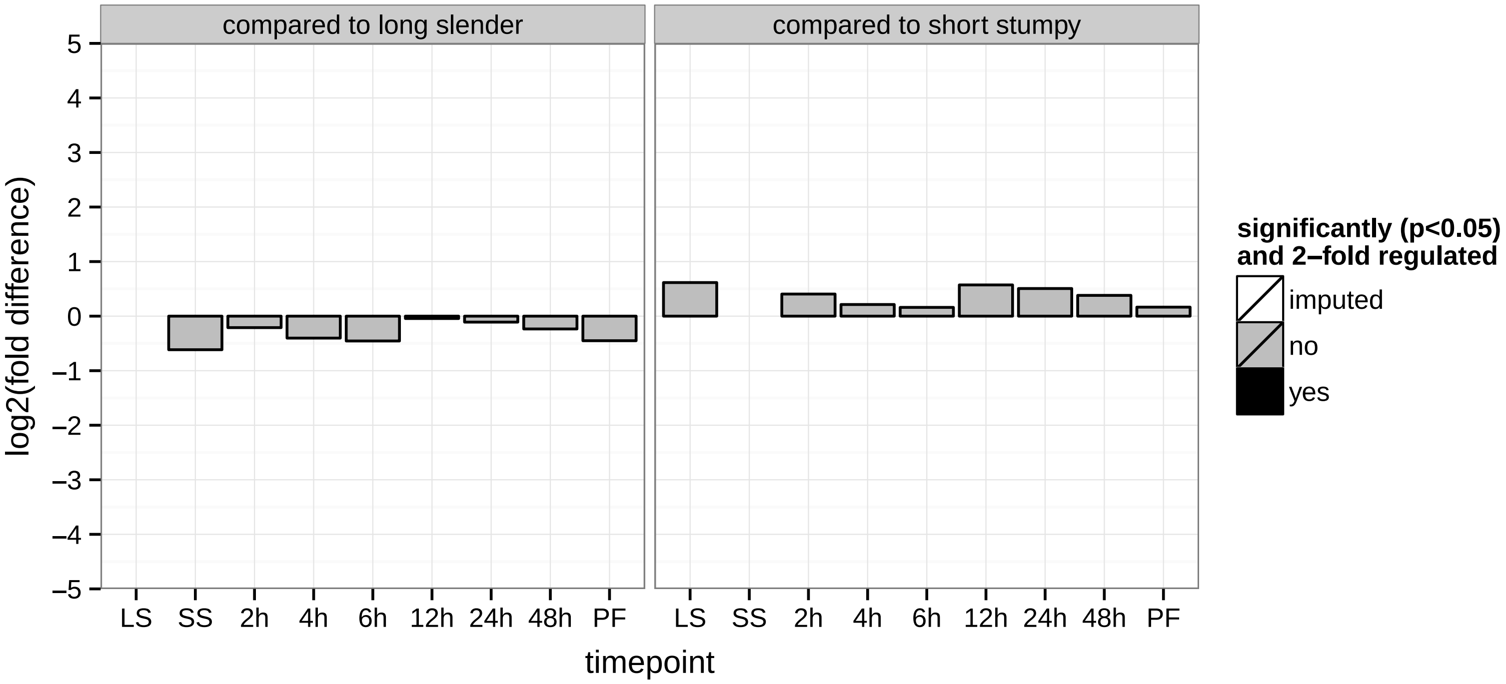
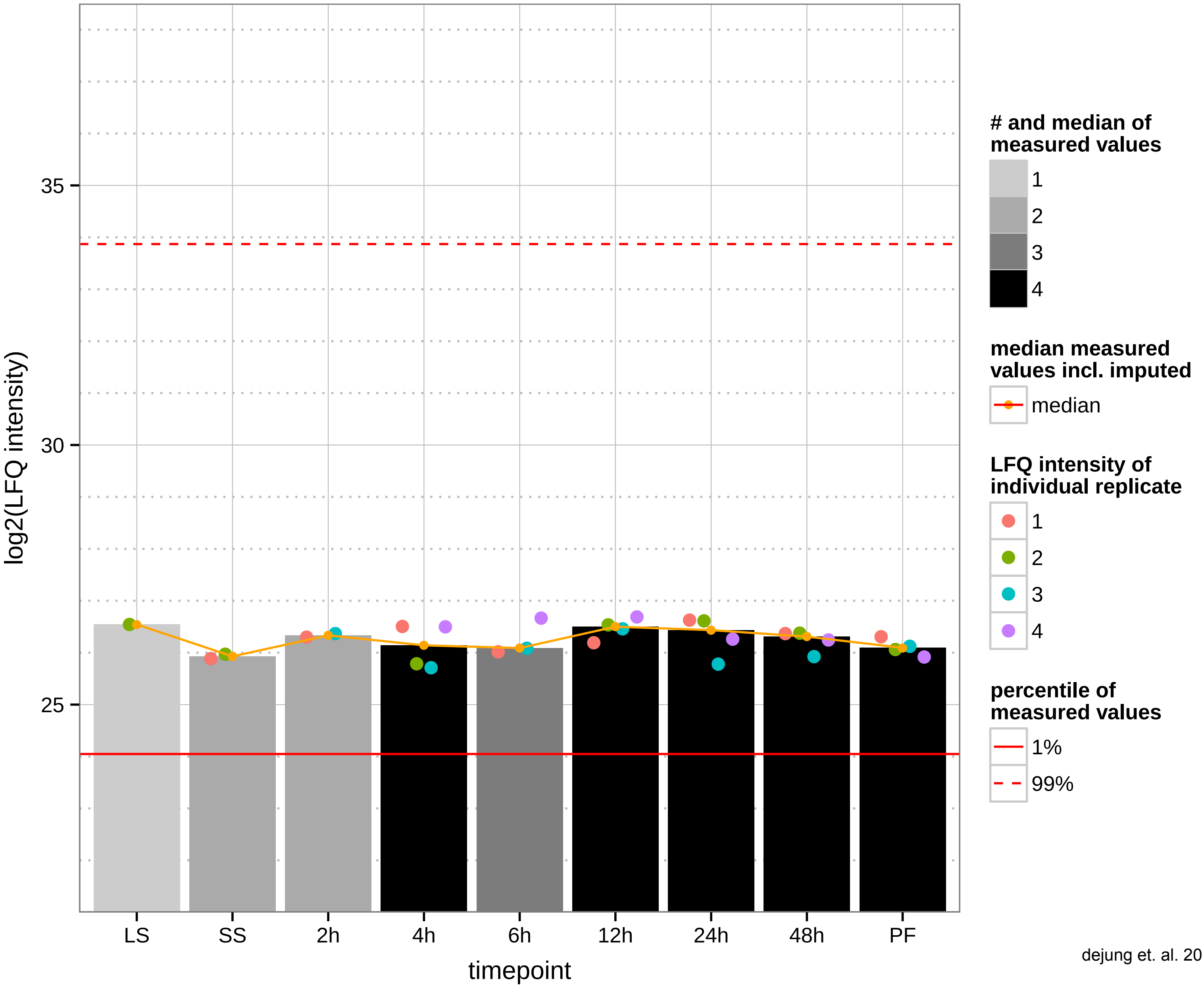
hypothetical protein, conserved
Tb927.4.2850
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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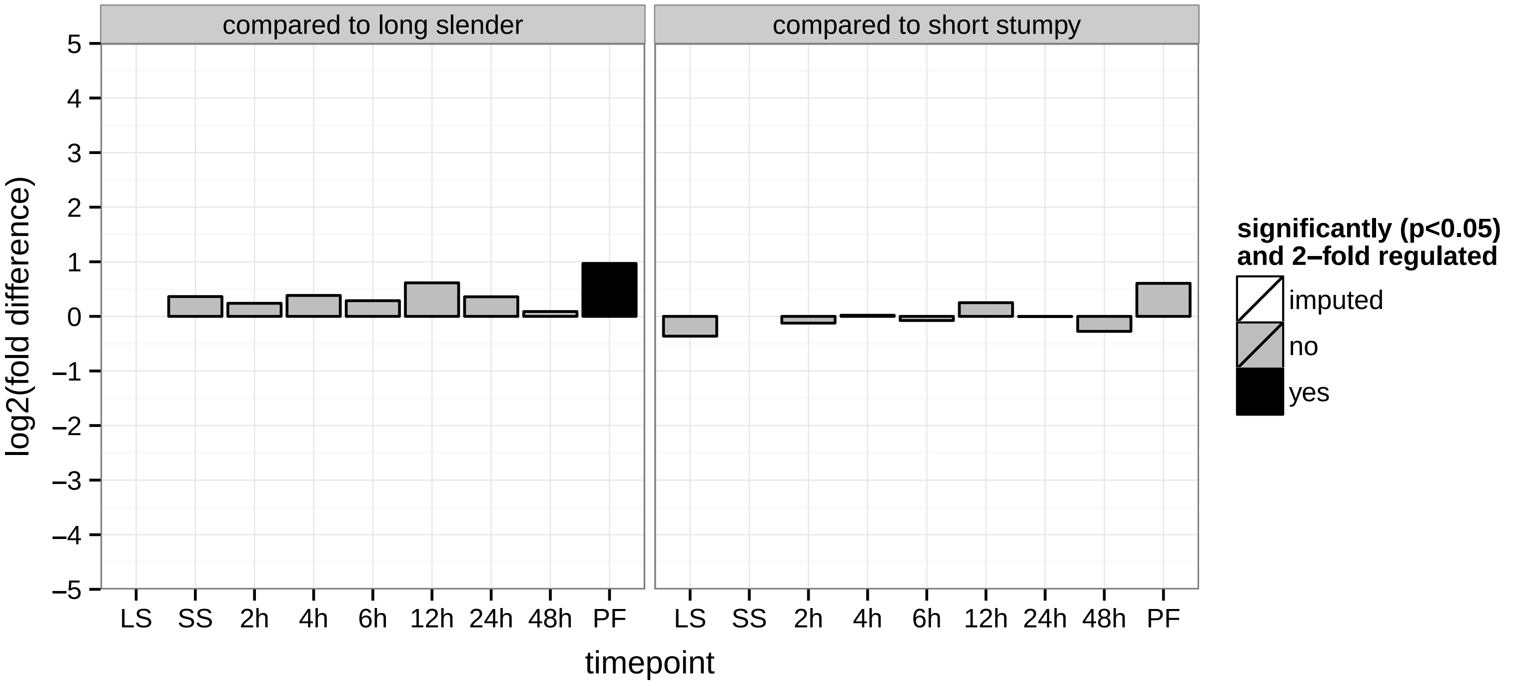
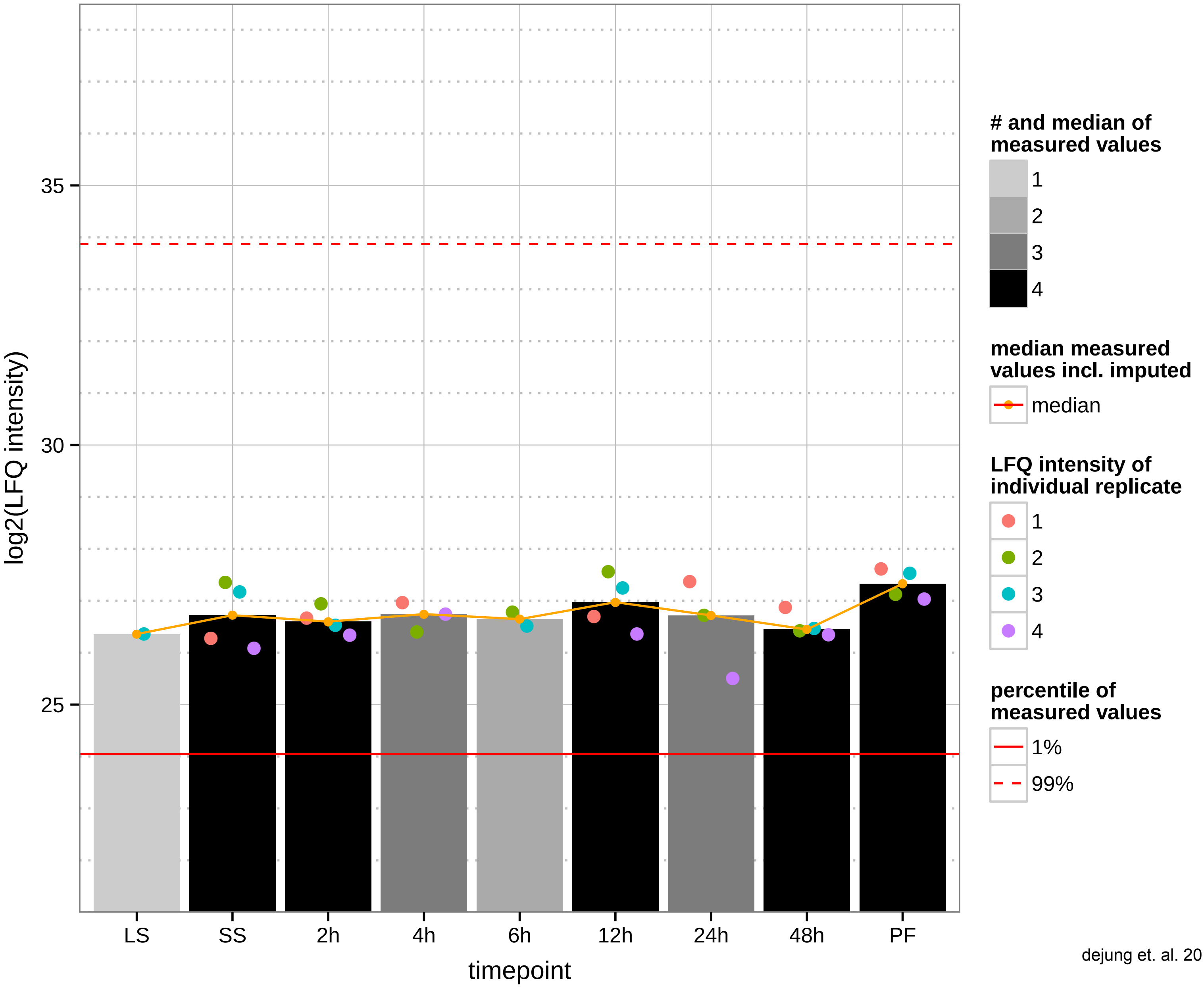
hypothetical protein, conserved
Tb927.4.2890
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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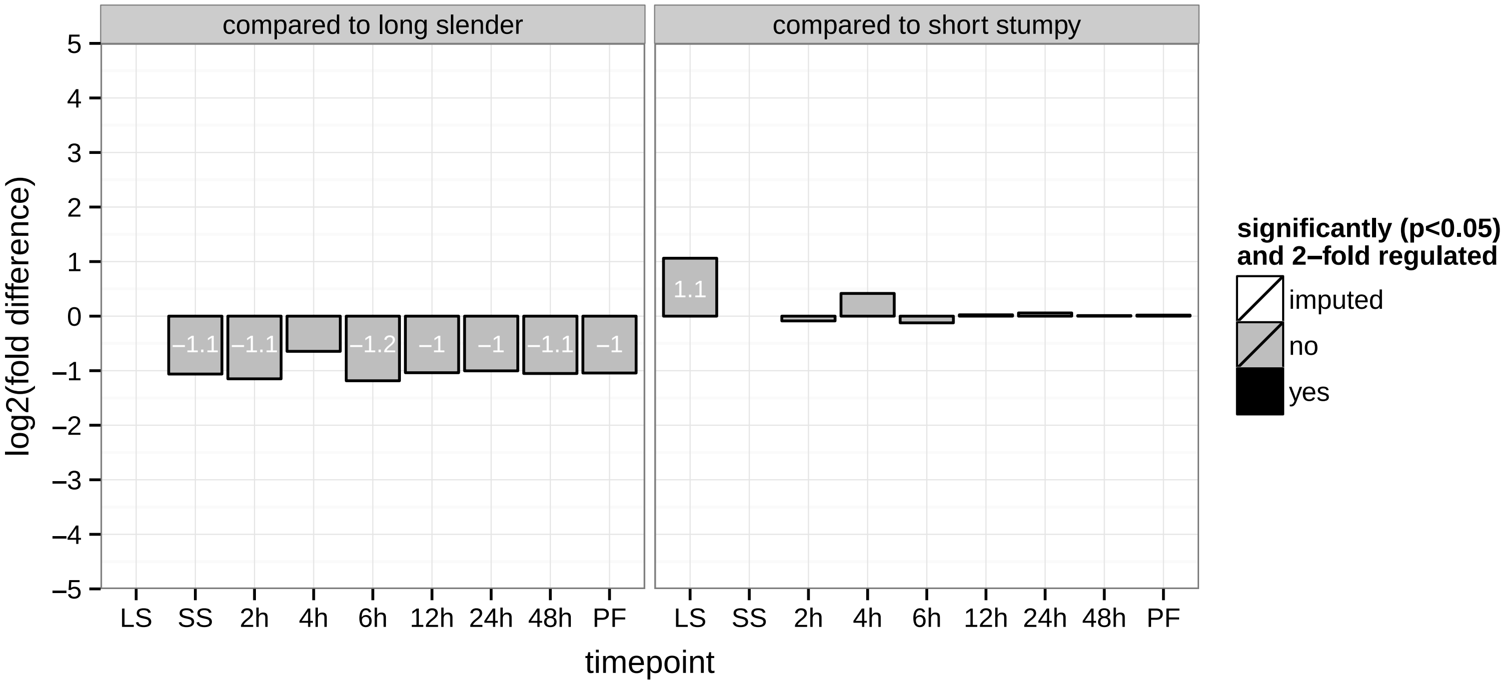
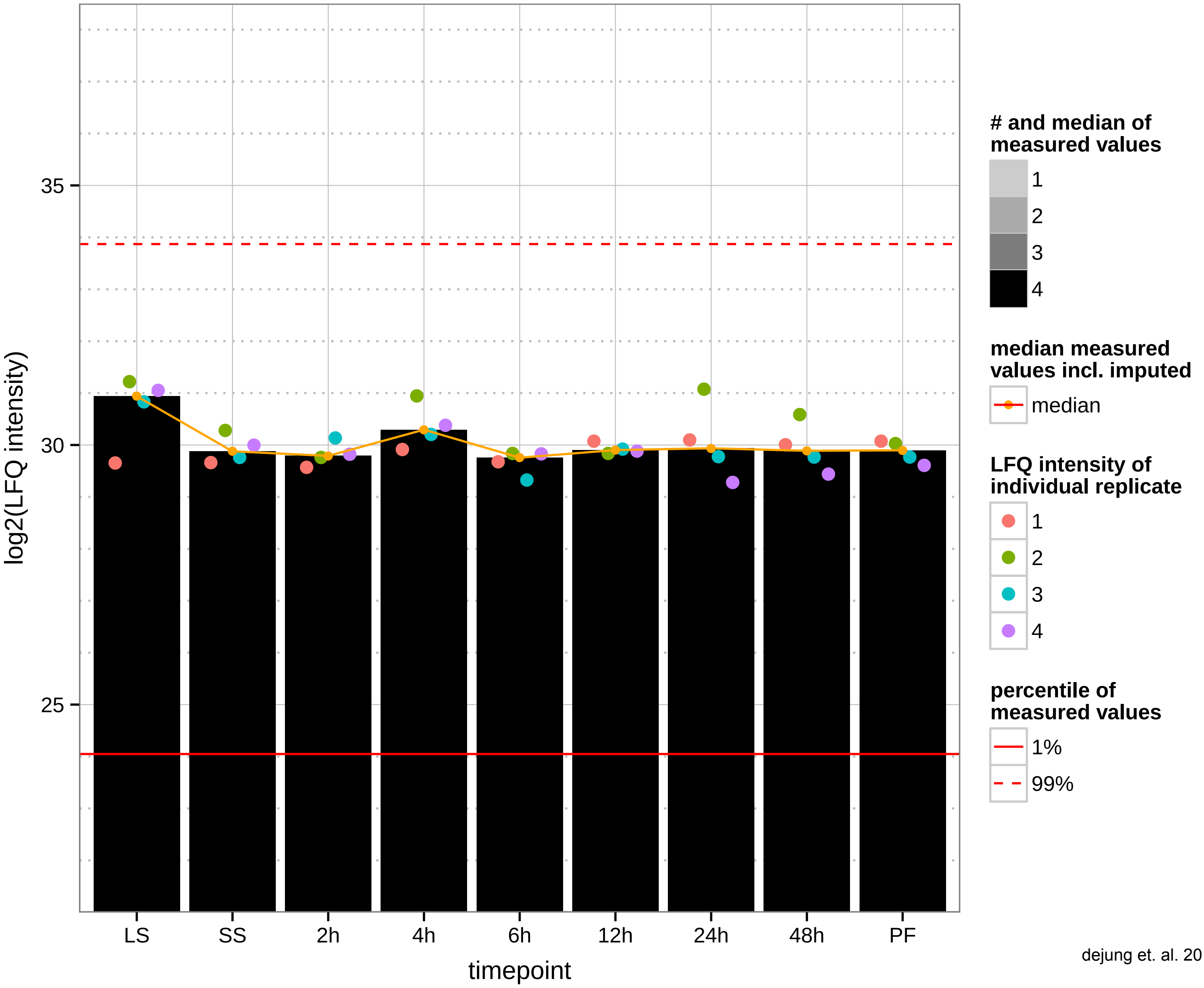
hypothetical protein, conserved
Tb927.4.3060
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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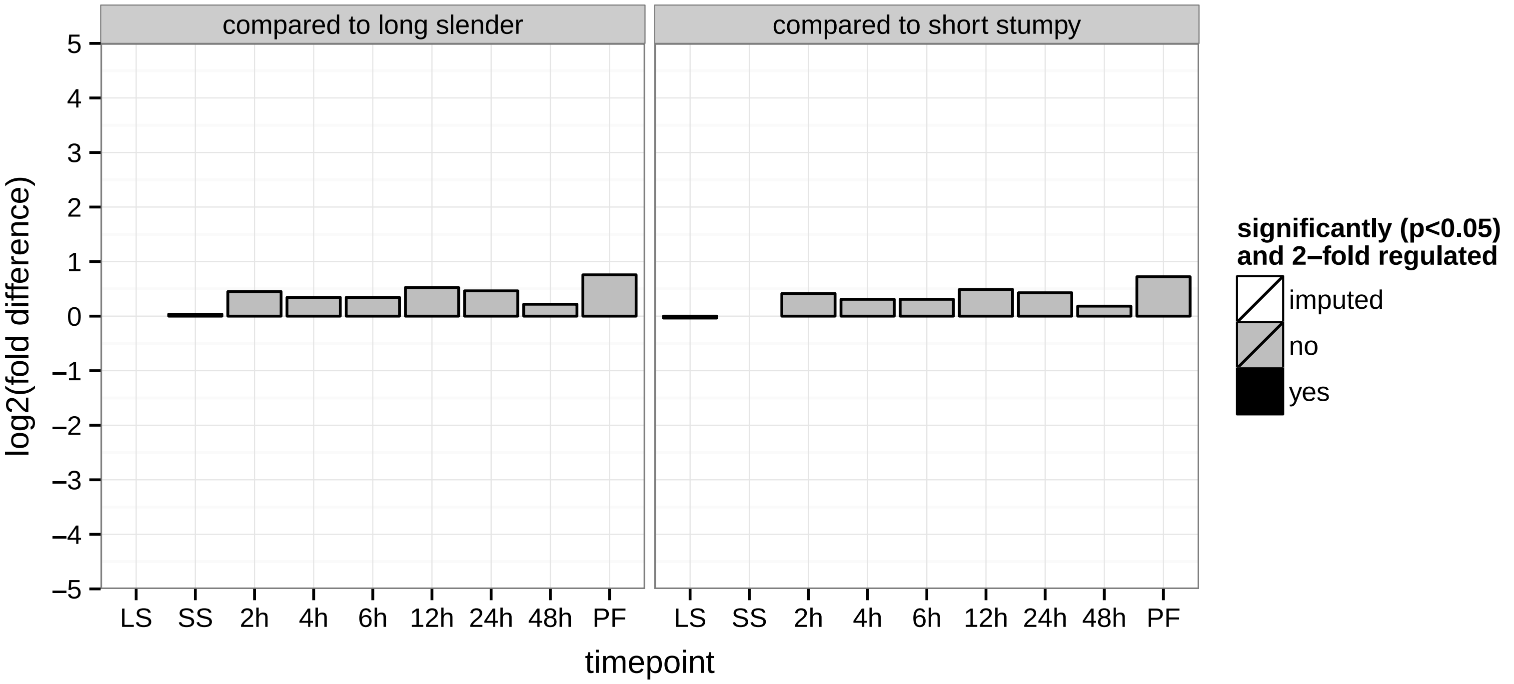
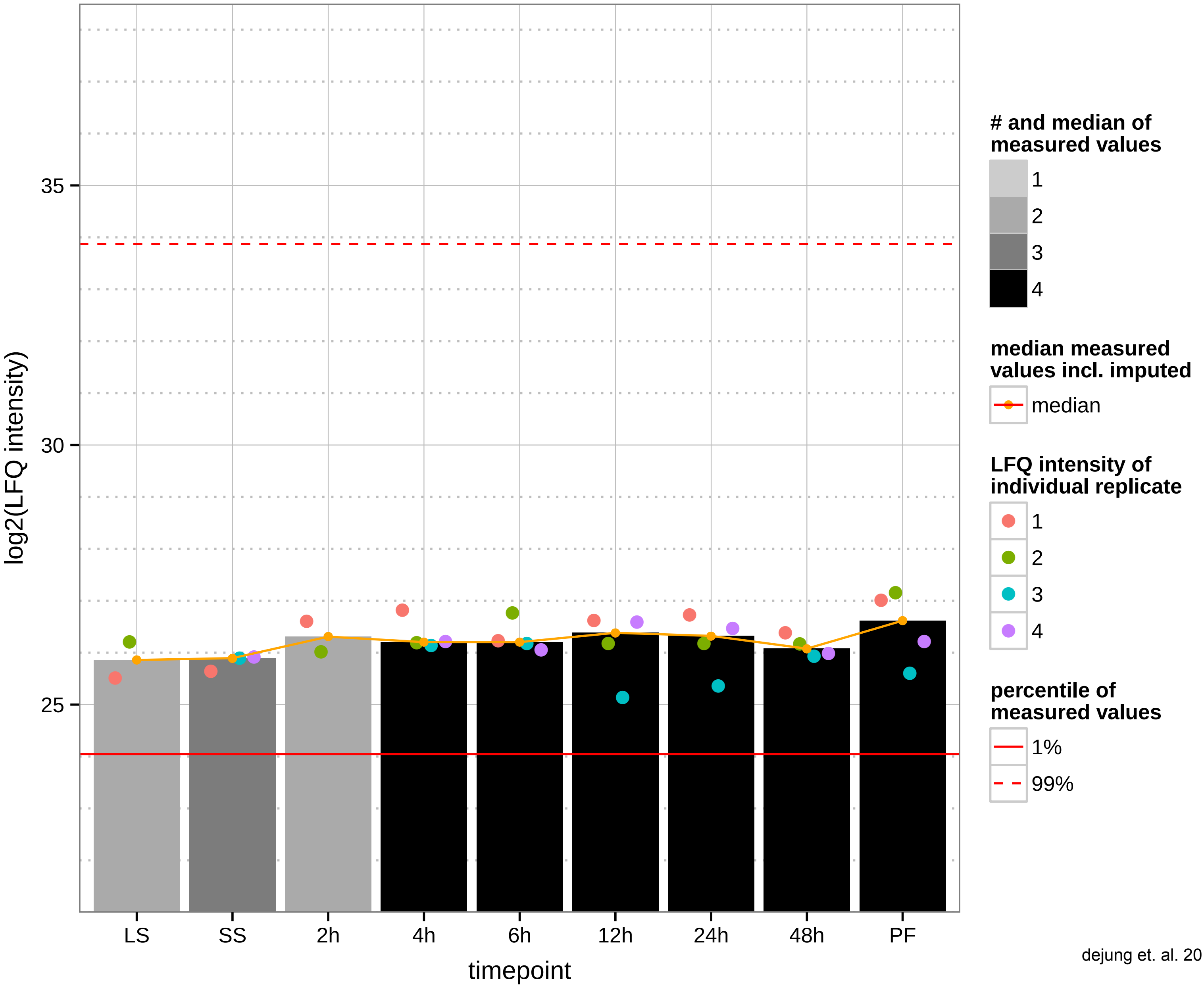
hypothetical protein, conserved
Tb927.4.3150
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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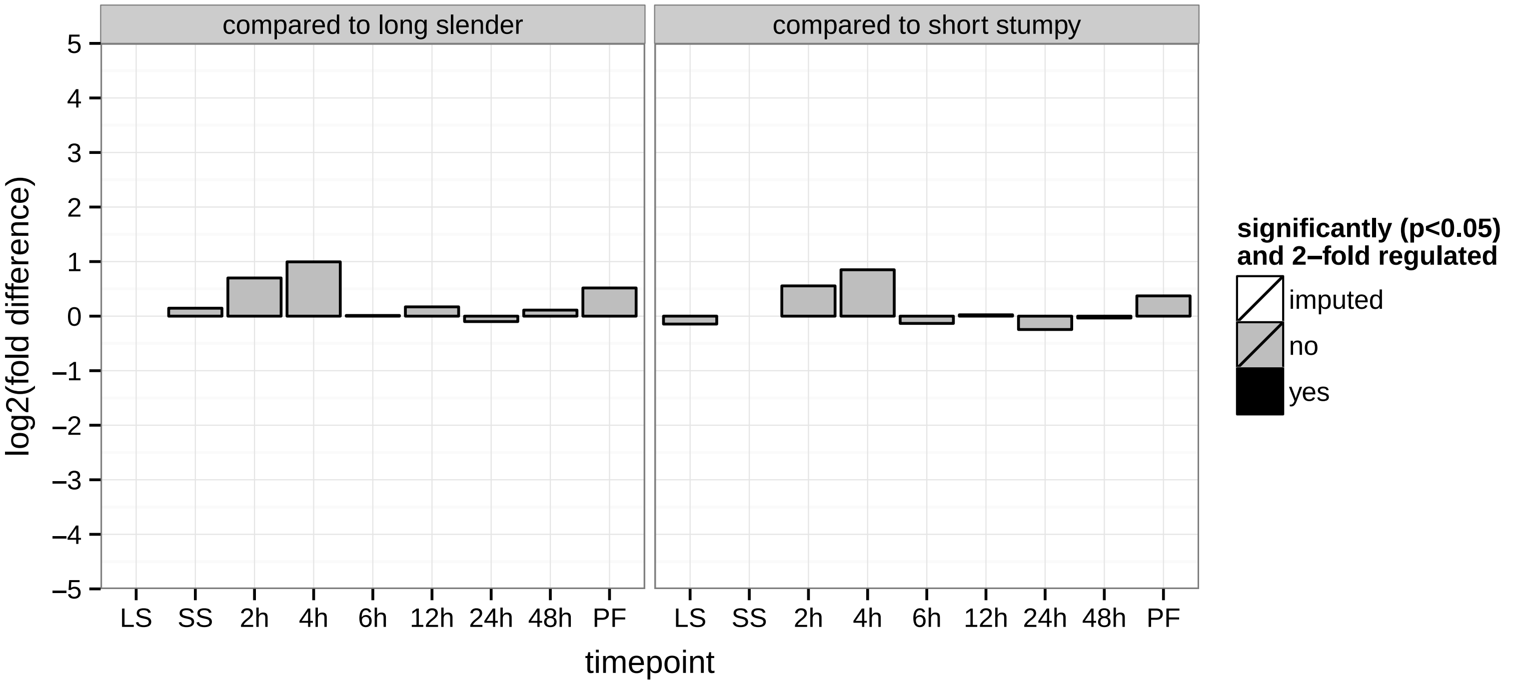
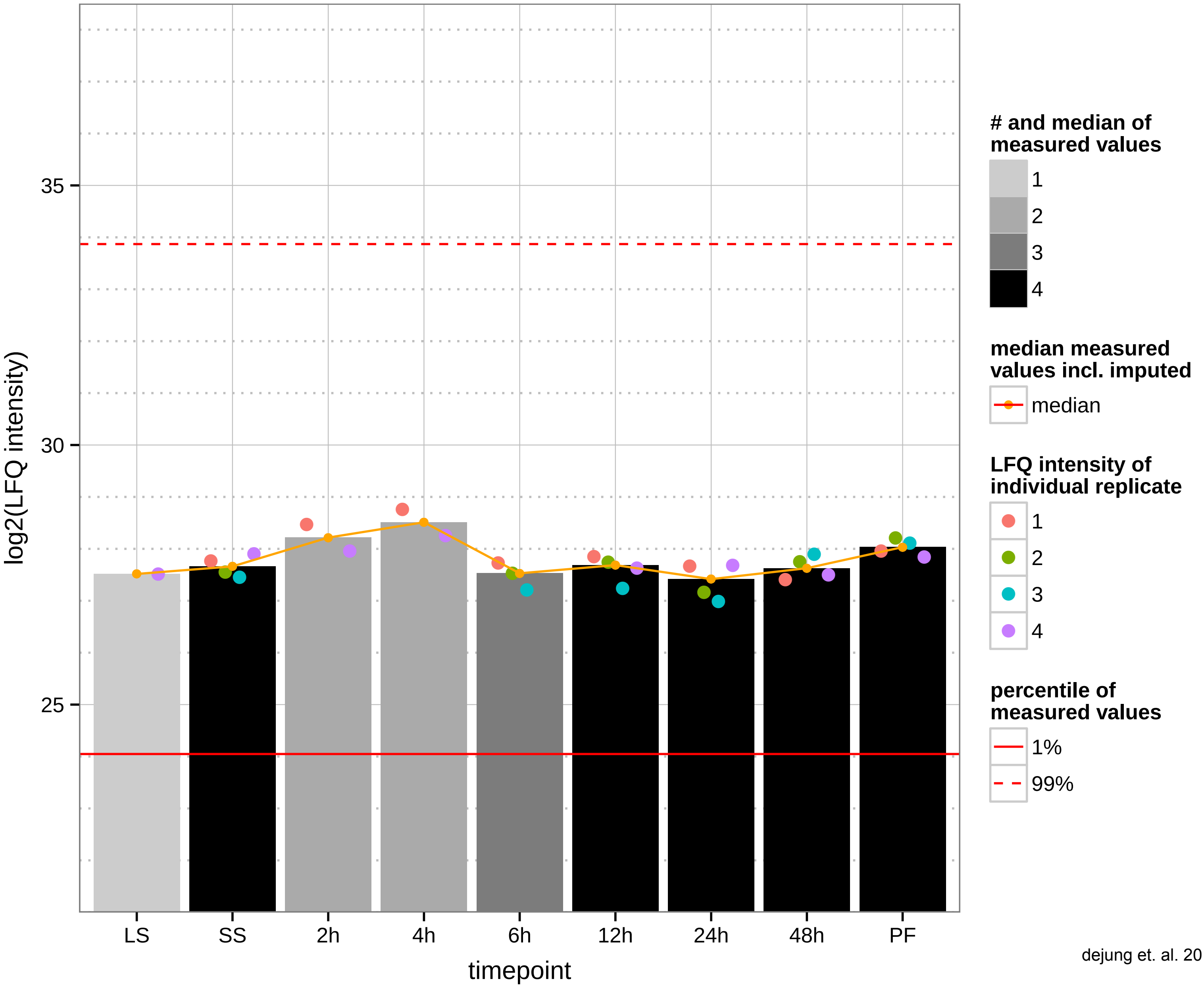
dihydroxyacetone phosphate acyltransferase, putative (DAT)
Tb927.4.3160
AGOF: null
AGOC: glycosome
AGOP: ether lipid biosynthetic process
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: metabolic process





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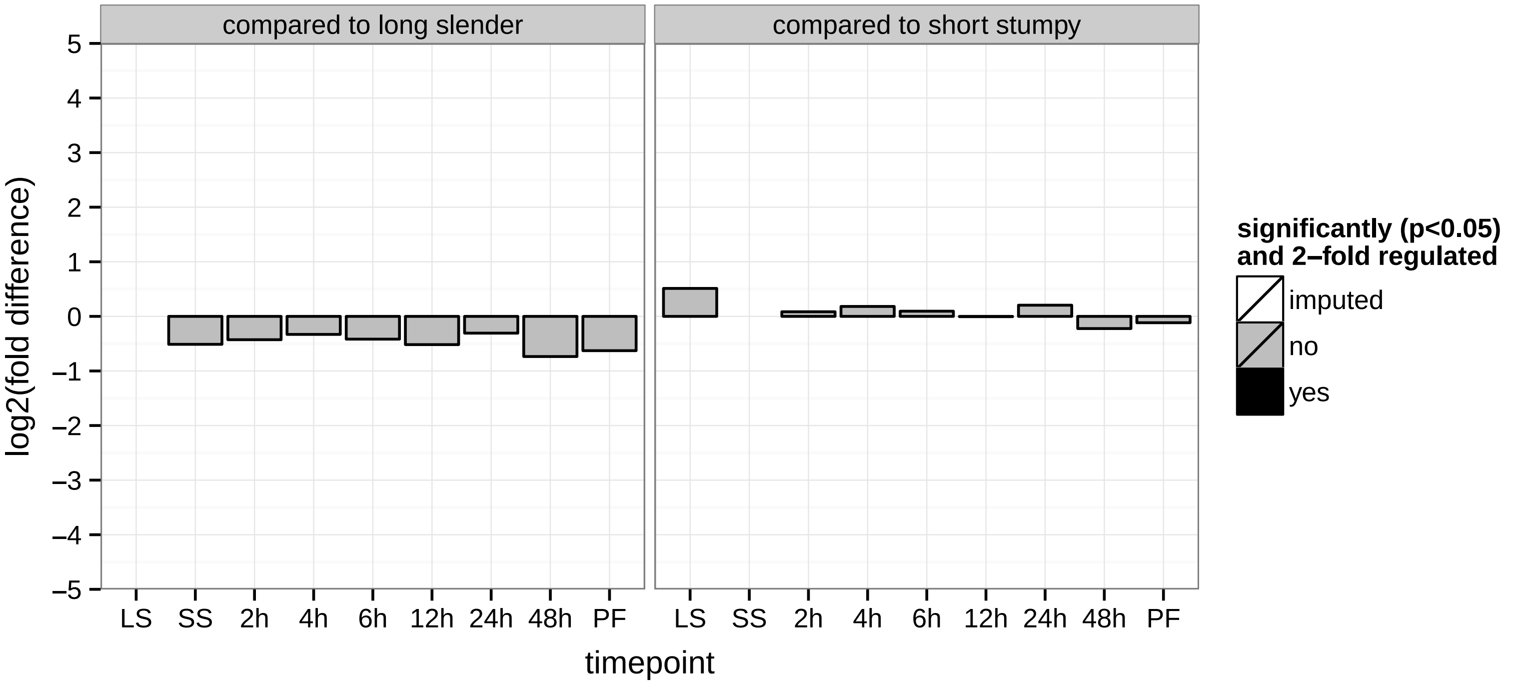
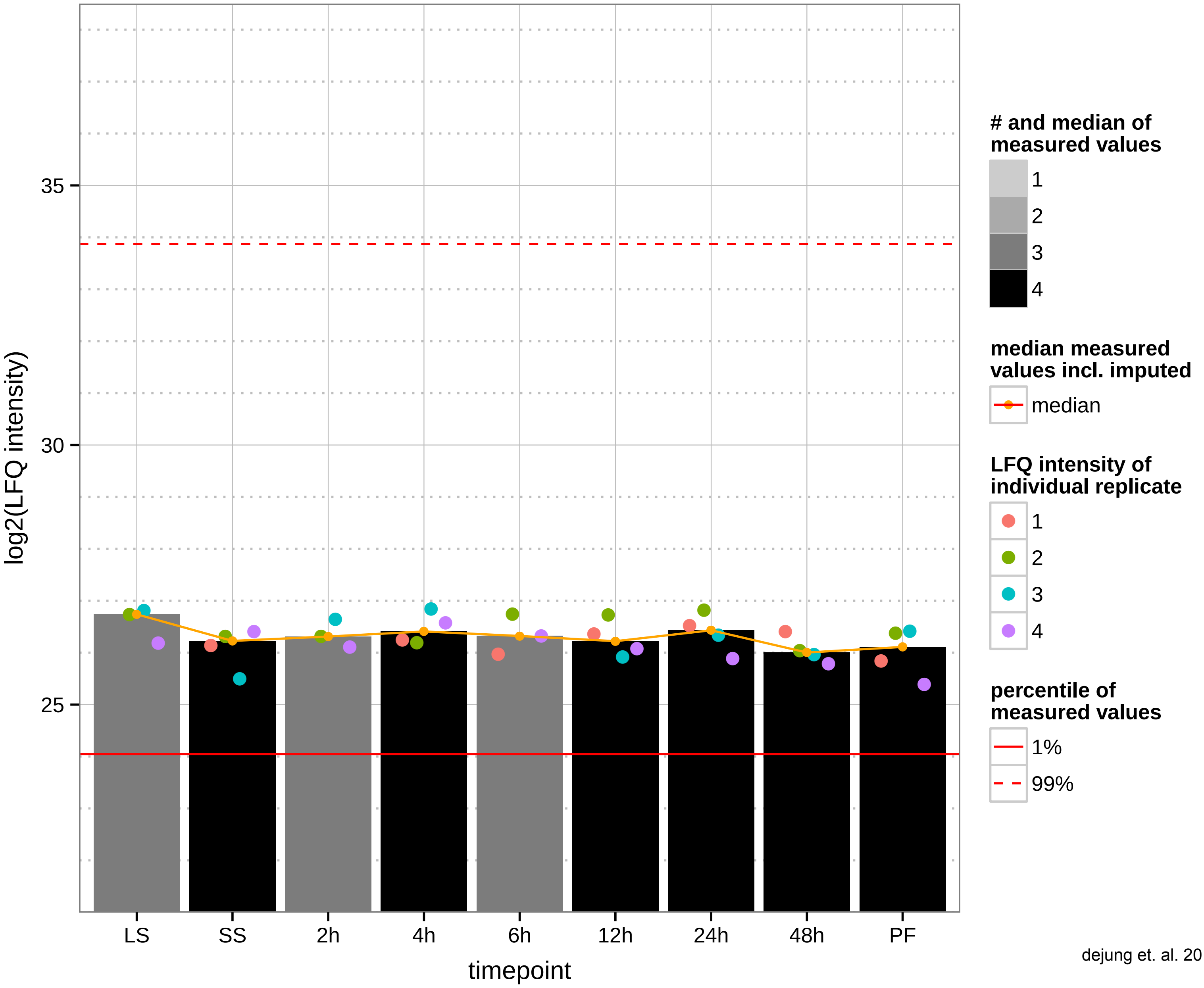
hypothetical protein, conserved
Tb927.4.3180
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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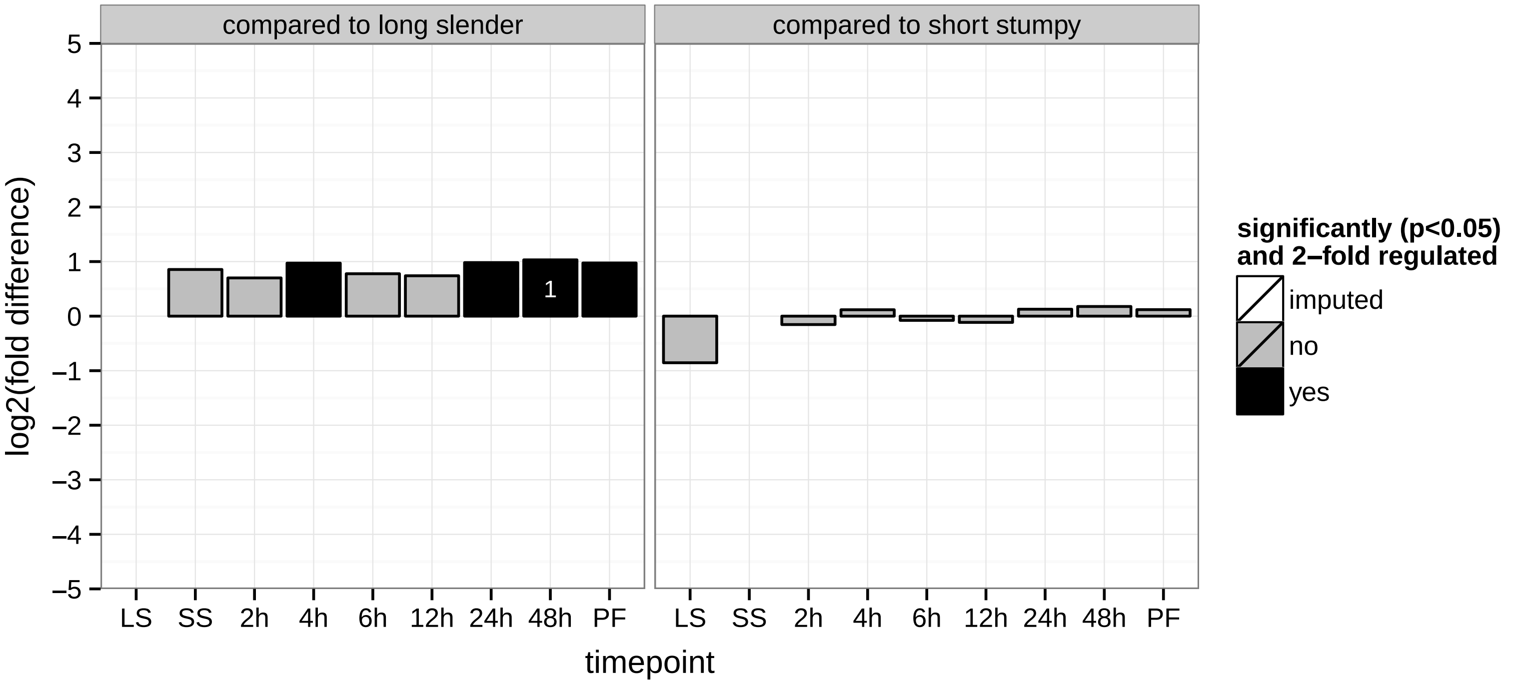
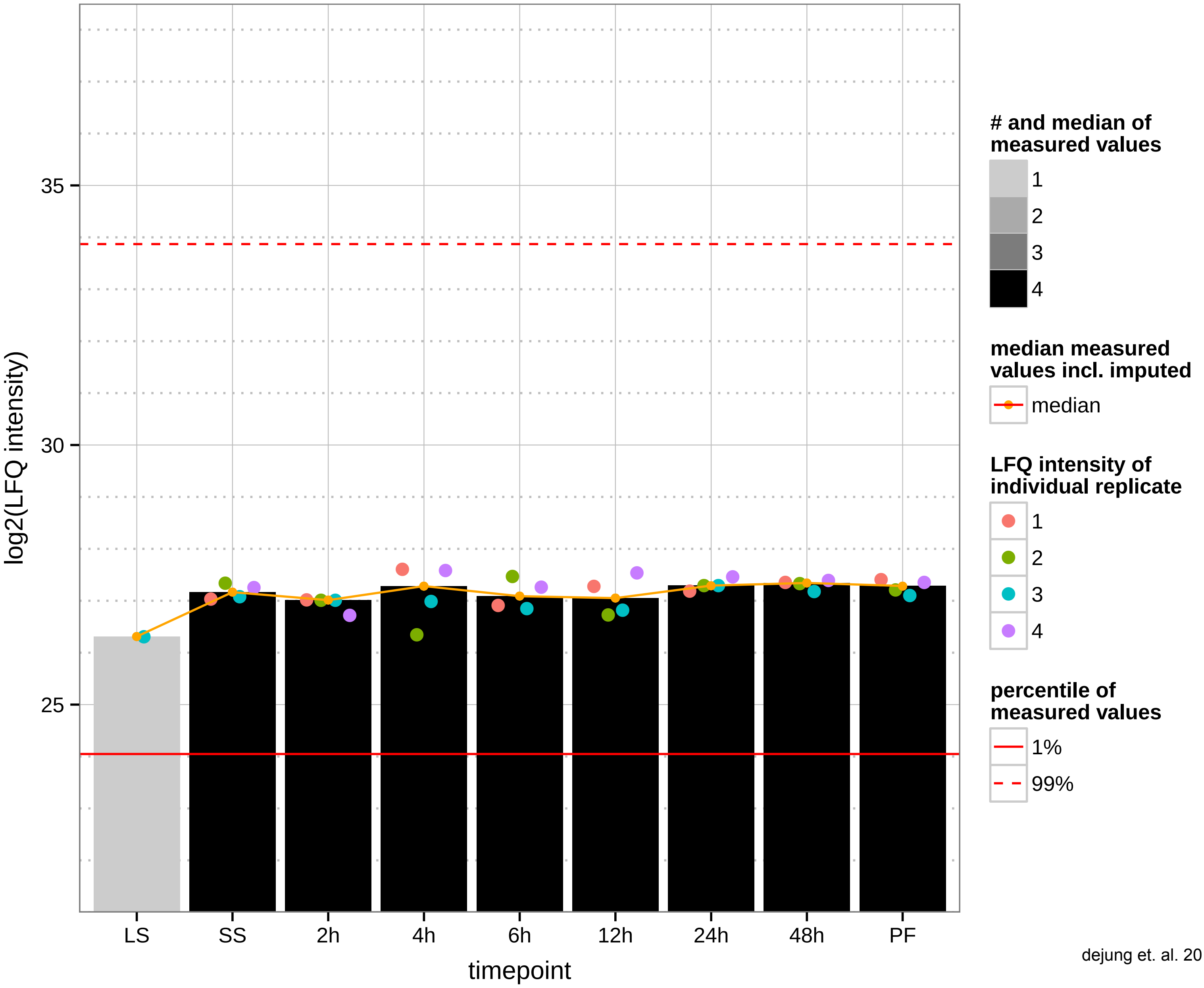
hypothetical protein, conserved
Tb927.4.330
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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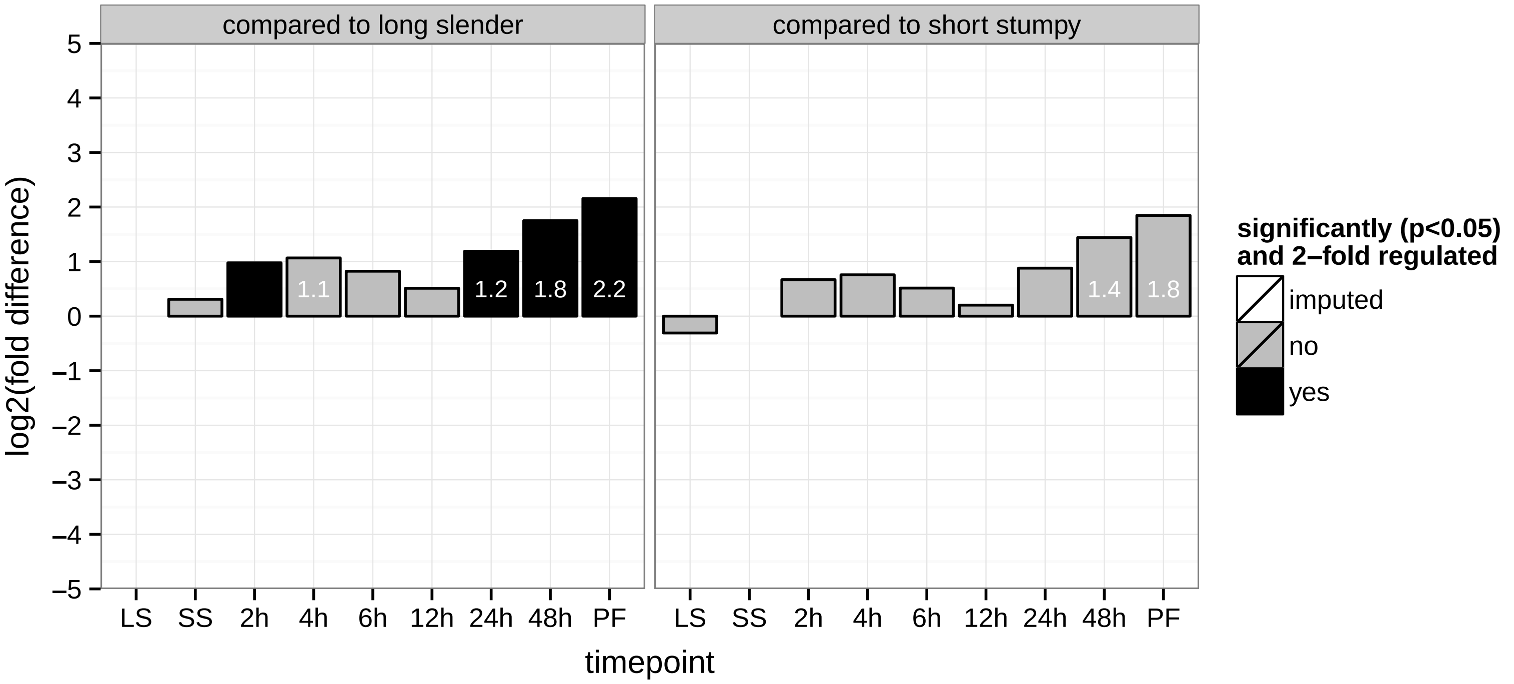
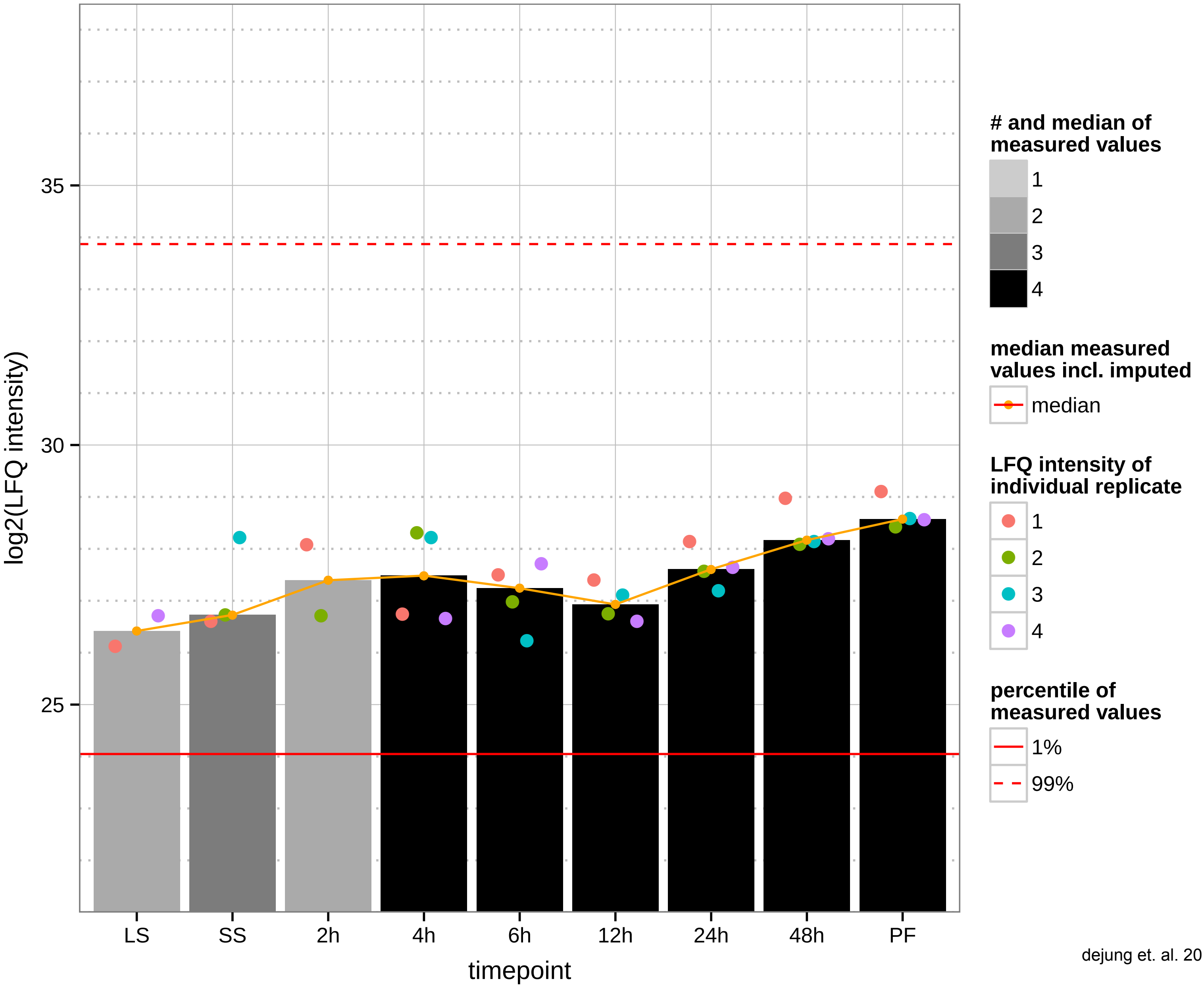
mitochondrial ATP−dependent zinc metallopeptidase, putative, metallo−peptidase, Clan MA(E) Family M41
Tb927.4.3300
AGOF: ATP binding, metalloendopeptidase activity, nucleoside−triphosphatase activity
AGOC: mitochondrial membrane, mitochondrion
AGOP: protein catabolic process, proteolysis
PGOF: ATP binding, metalloendopeptidase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: membrane
PGOP: protein catabolic process, proteolysis





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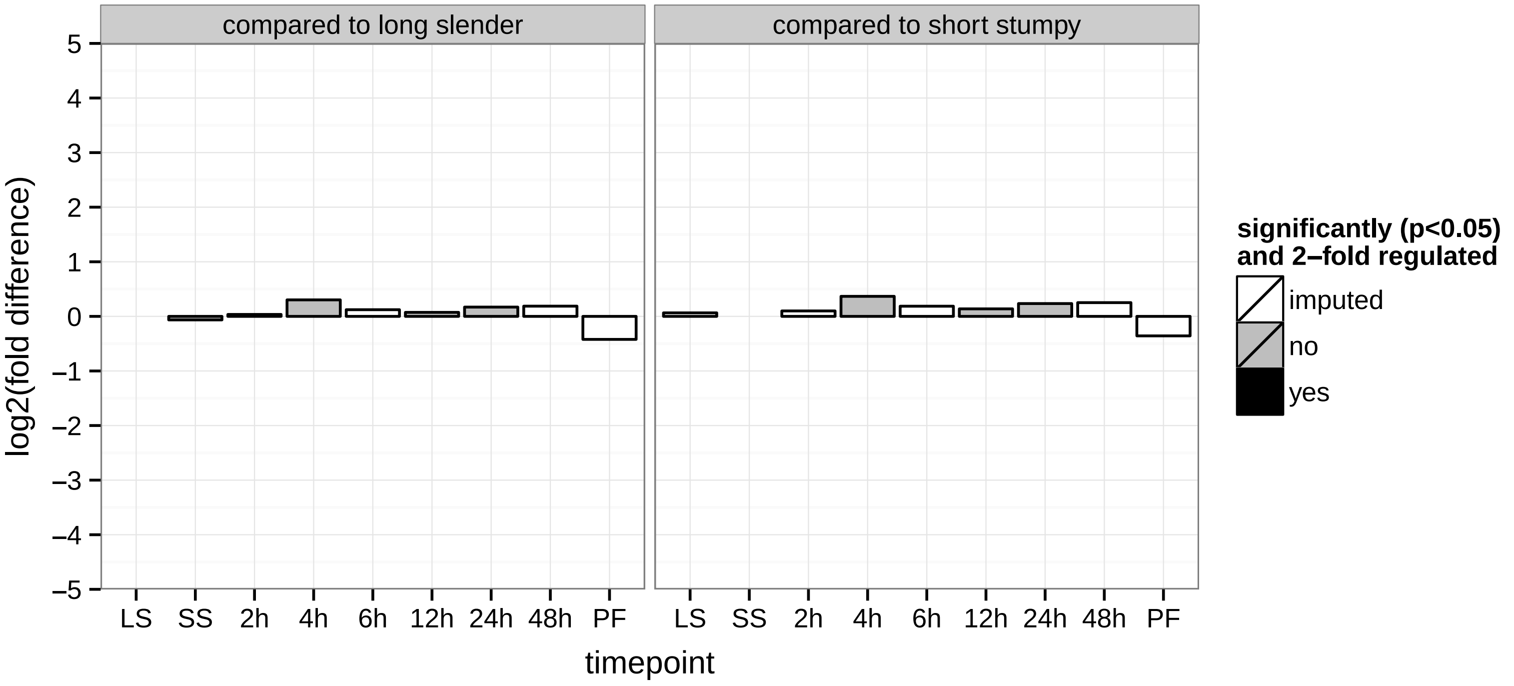
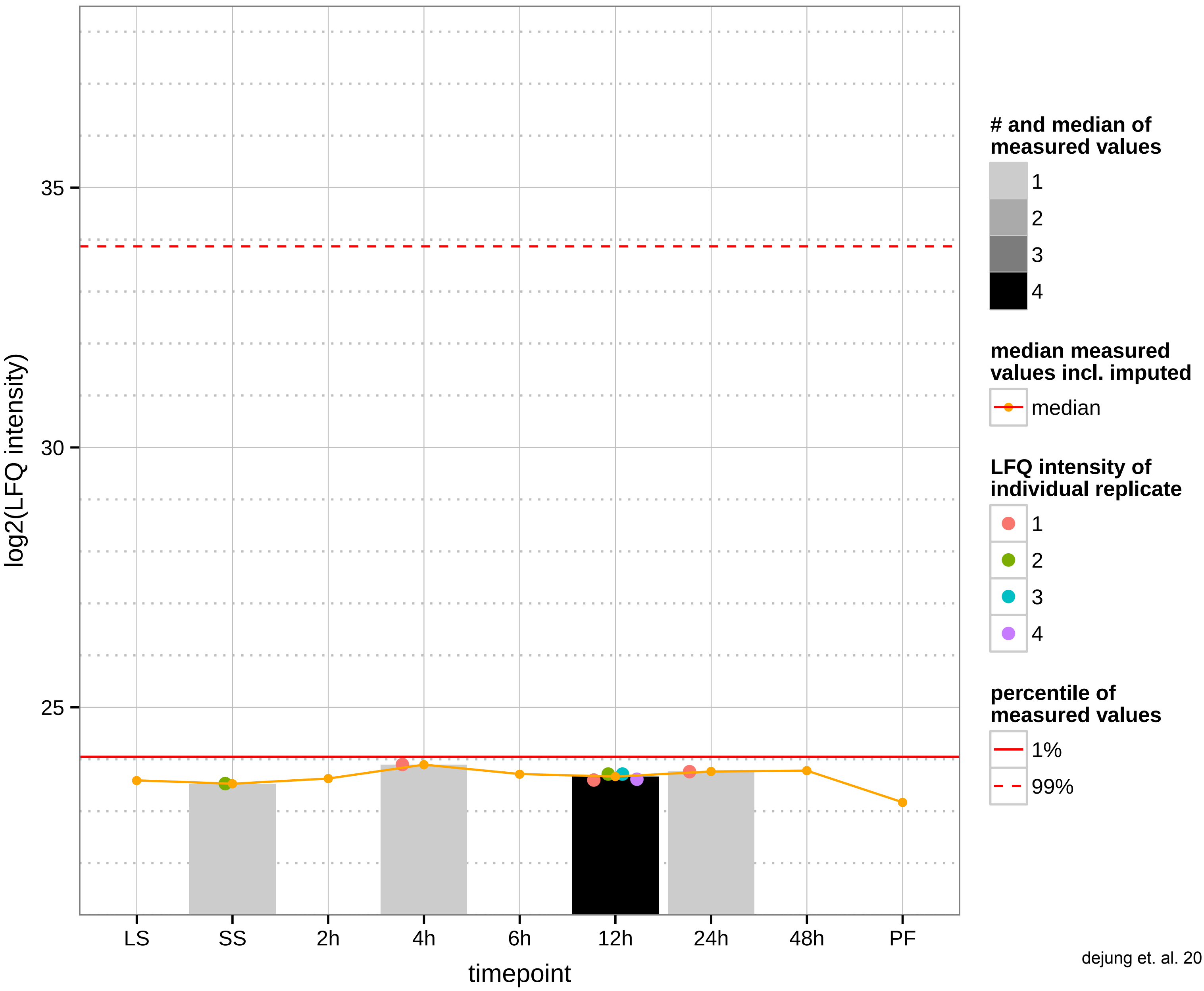
selenoprotein, putative
Tb927.4.3410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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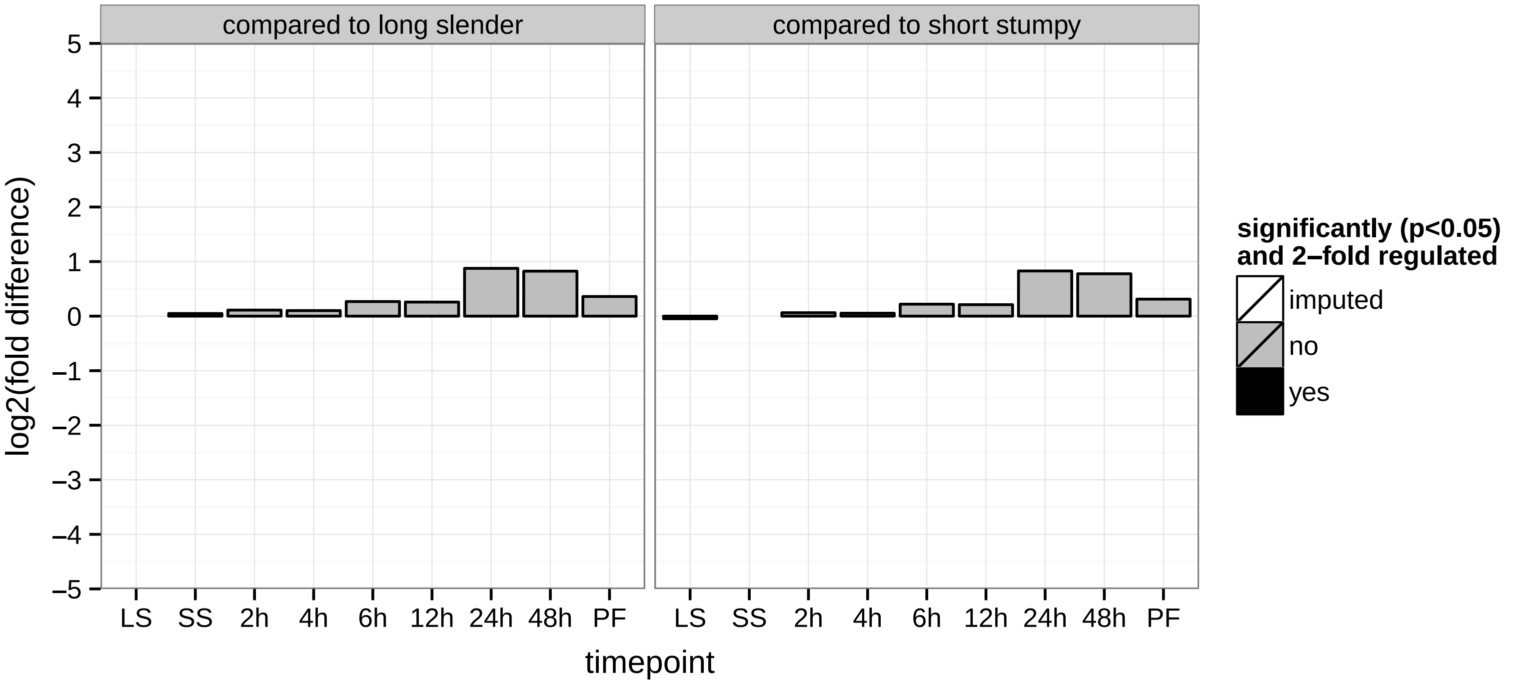
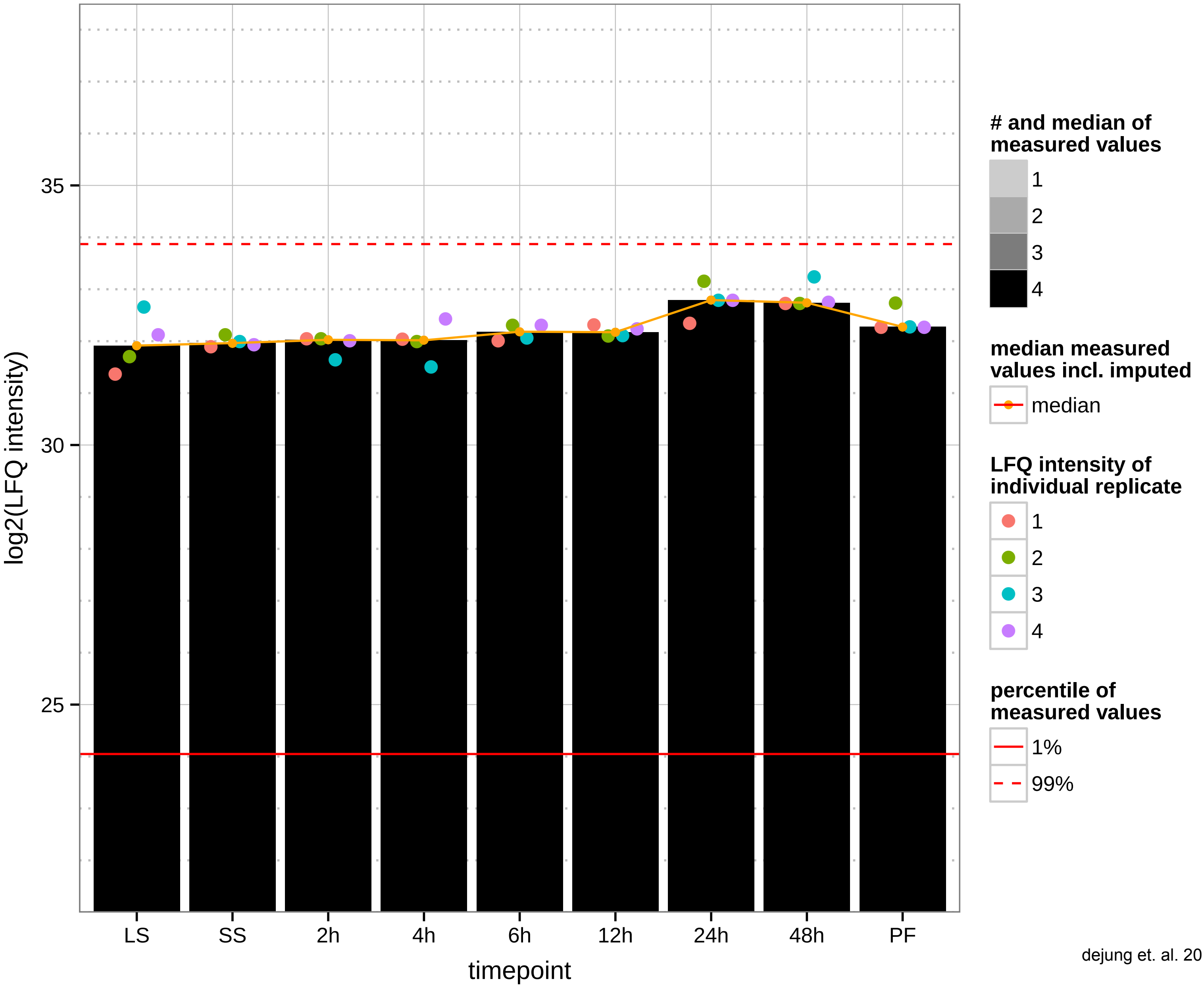
60S ribosomal protein L13a, putative
Tb927.5.1610;Tb927.4.3550
AGOF: structural constituent of ribosome
AGOC: intracellular, large ribosomal subunit, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: large ribosomal subunit, ribosome
PGOP: translation





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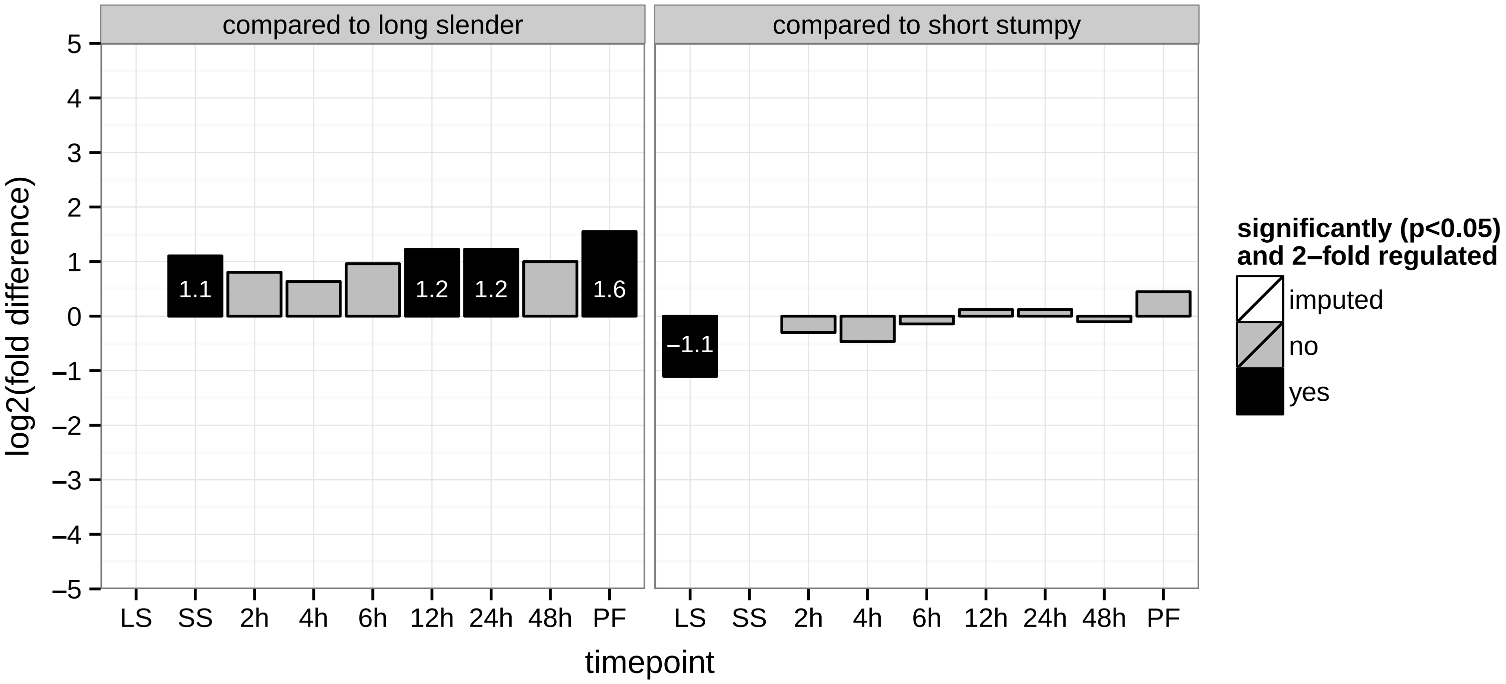
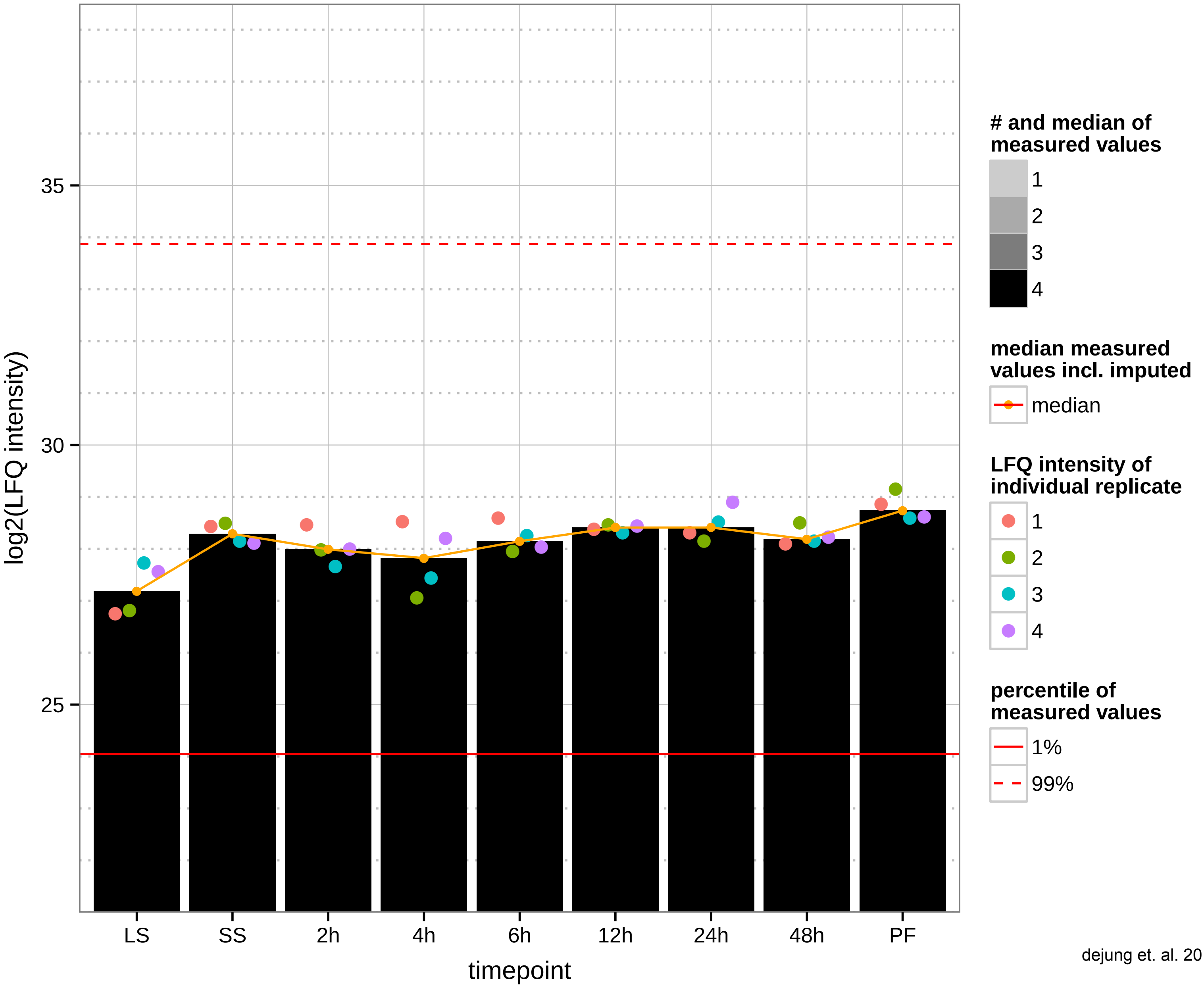
protein phoshatase 1, putative, protein phosphatase 1
Tb927.4.3560;Tb927.4.3610
AGOF: hydrolase activity, protein serine/threonine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: hydrolase activity
PGOC: null
PGOP: null





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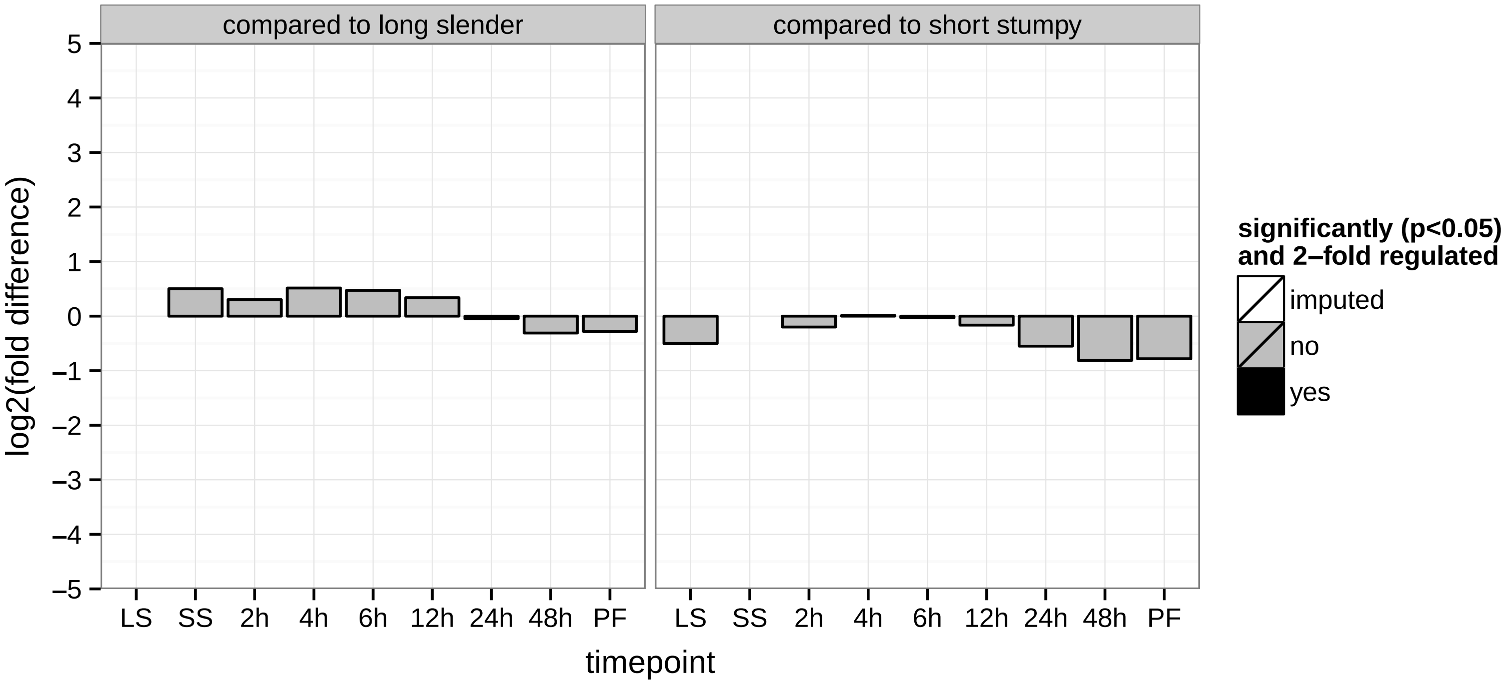
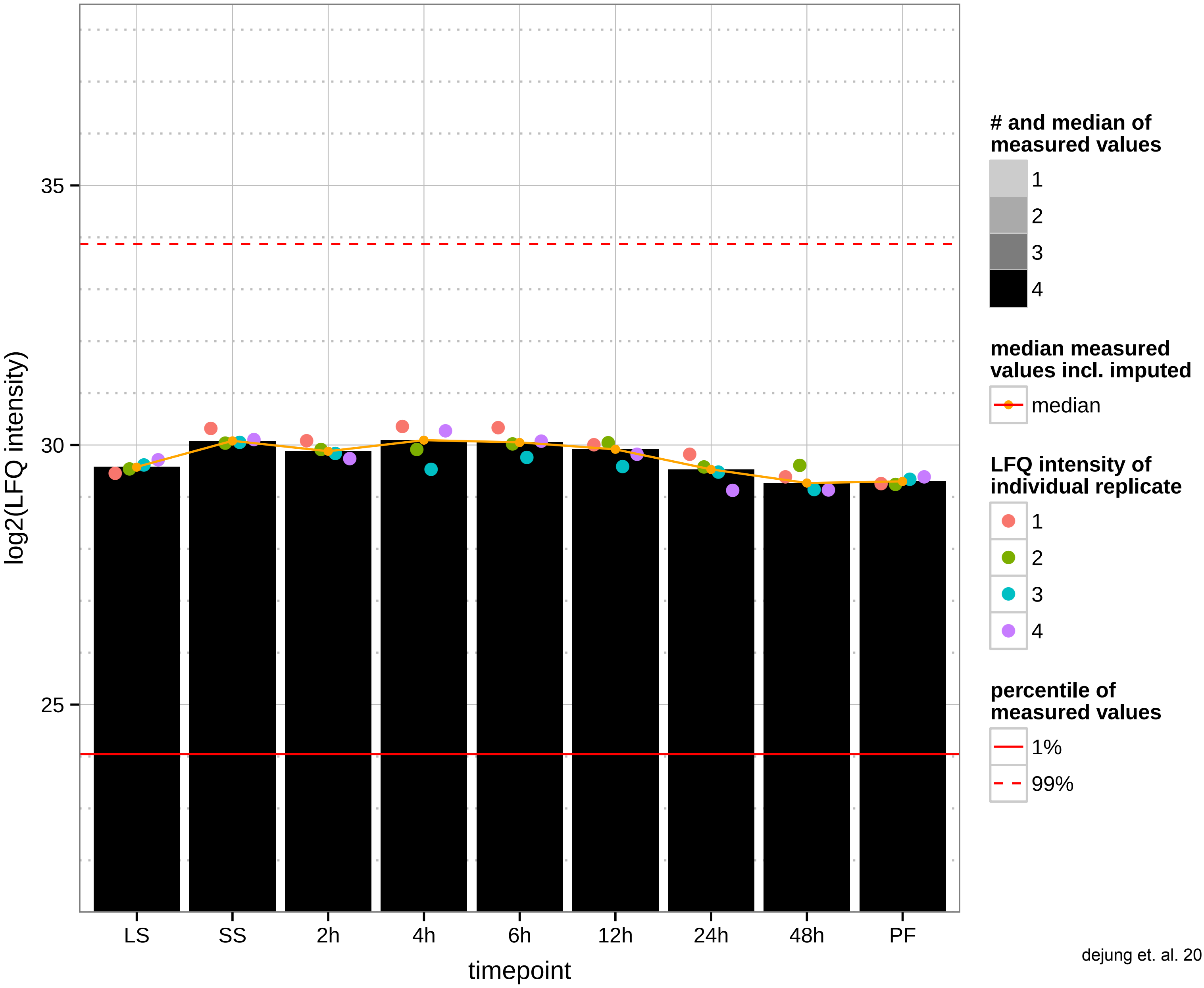
1, 2–Dihydroxy–3–keto–5–methylthiopentene dioxygenase, putative
Tb927.4.360
AGOF: dioxygenase activity, metal ion binding
AGOC: cytosol
AGOP: L–methionine salvage from methylthioadenosine
PGOF: acireductone dioxygenase [iron(II)–requiring] activity
PGOC: null
PGOP: oxidation–reduction process





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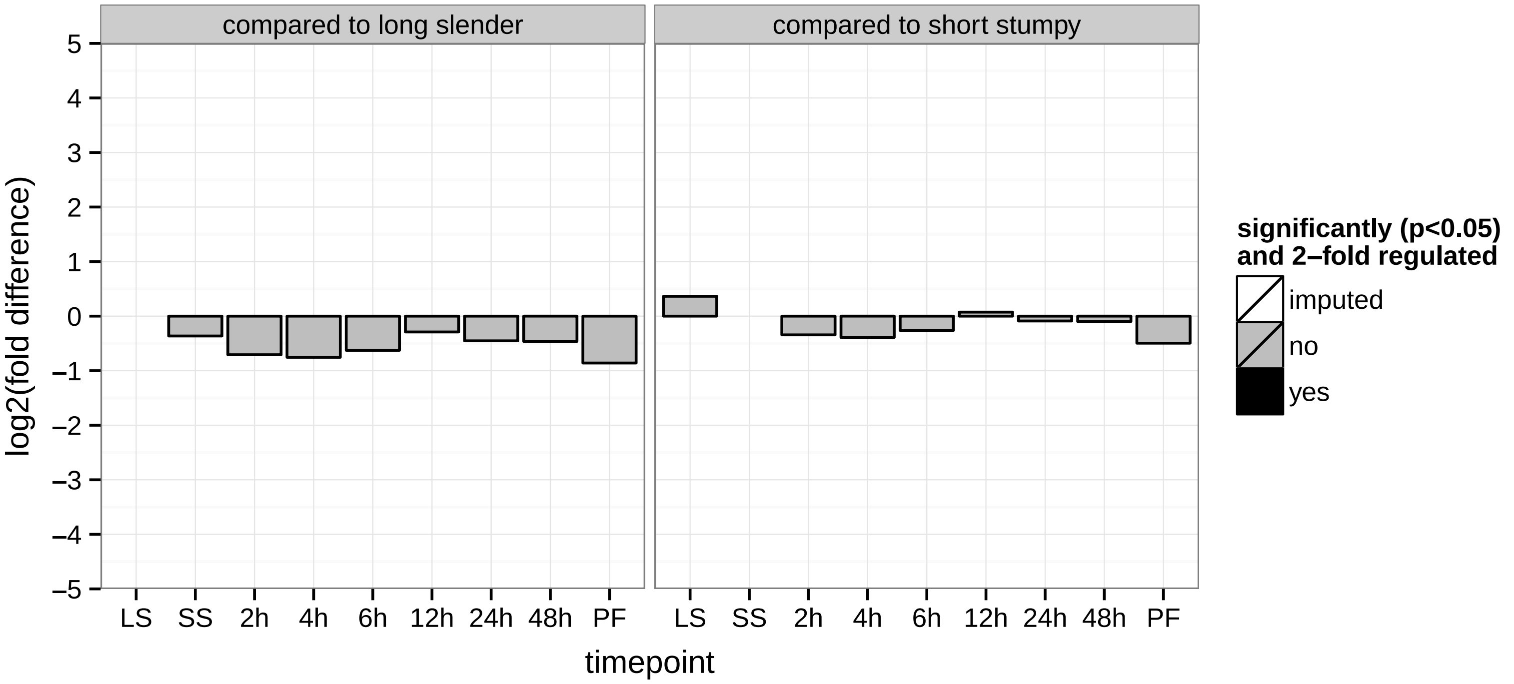
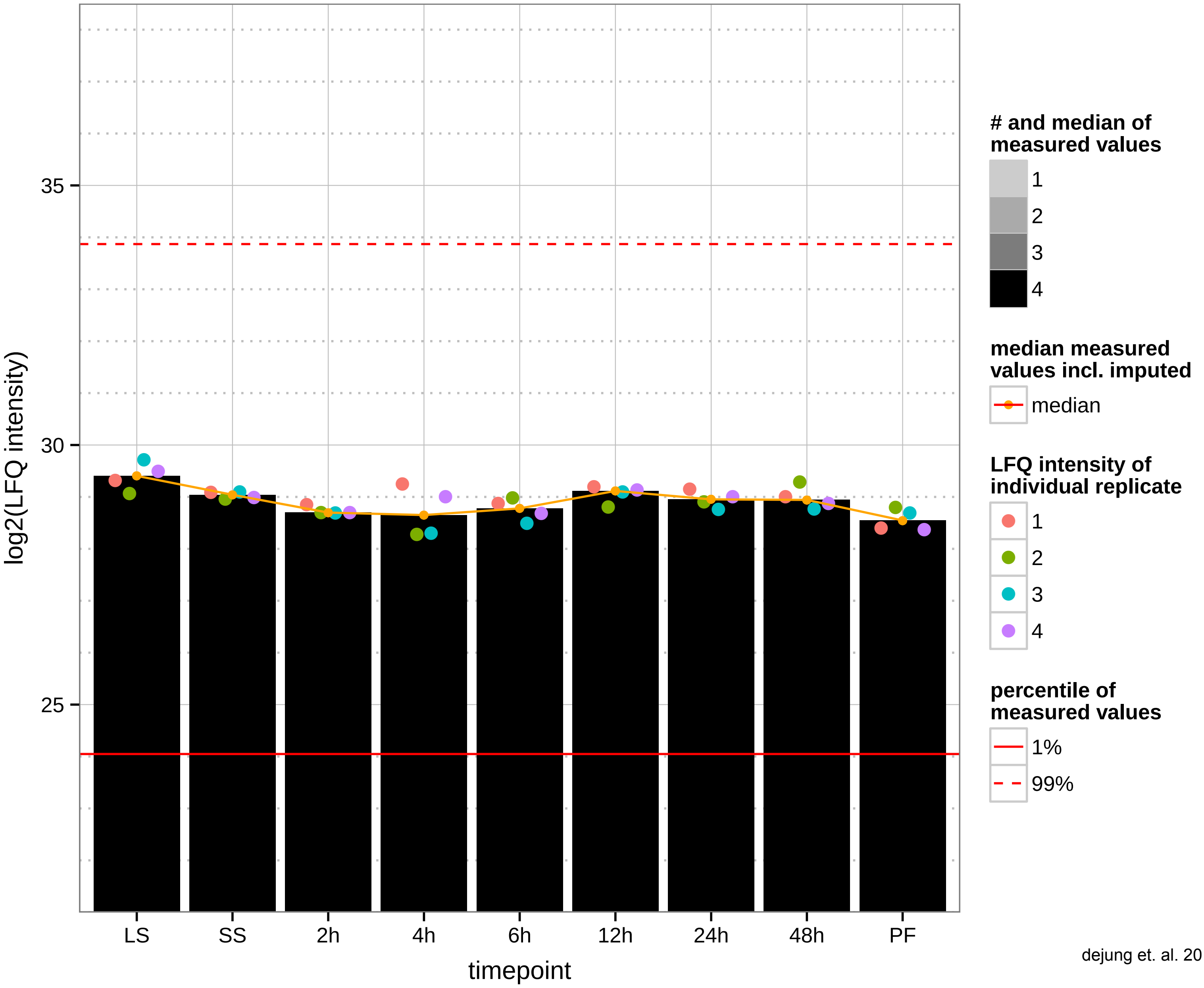
serine threonine–protein phosphatase PP1, putative (PP1–6)
Tb927.4.3620
AGOF: hydrolase activity, protein serine/threonine phosphatase activity
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, protein dephosphorylation, quorum sensing i
PGOF: hydrolase activity
PGOC: null
PGOP: null





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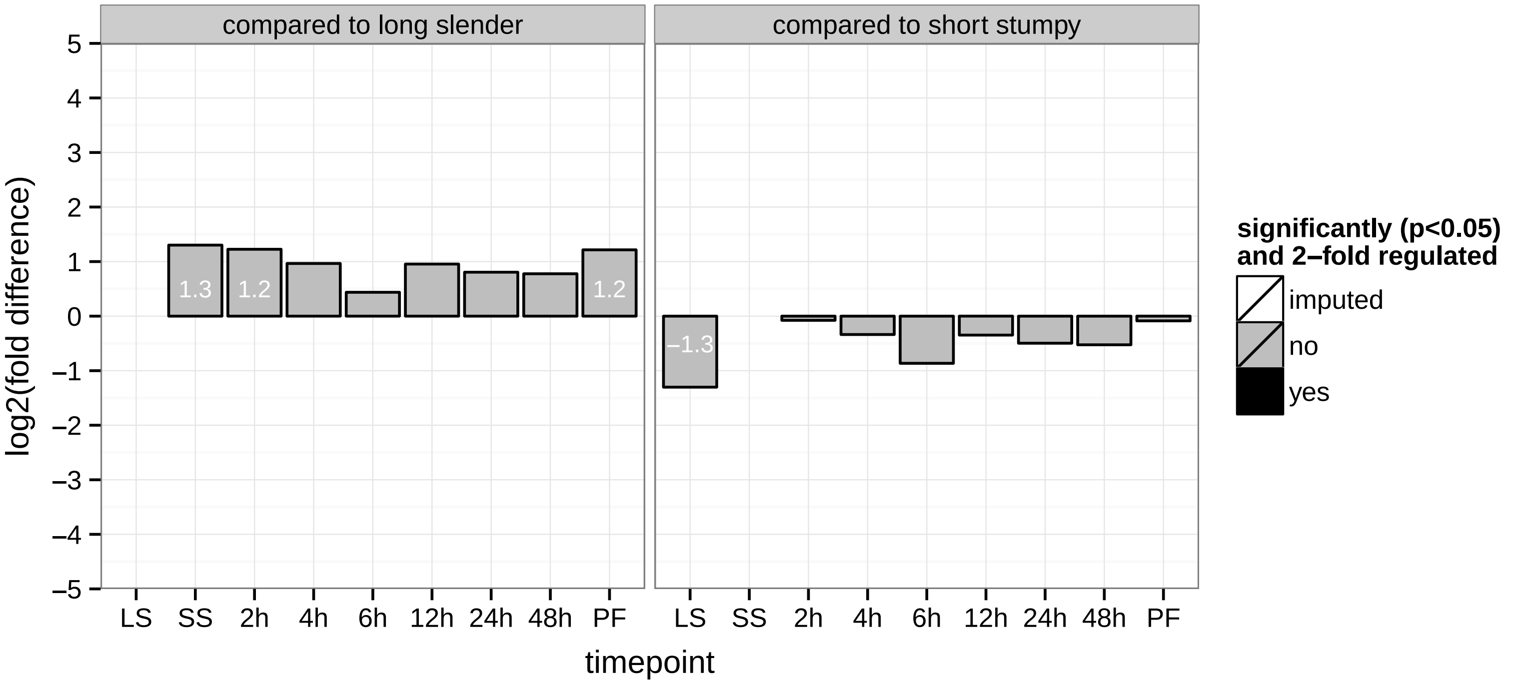
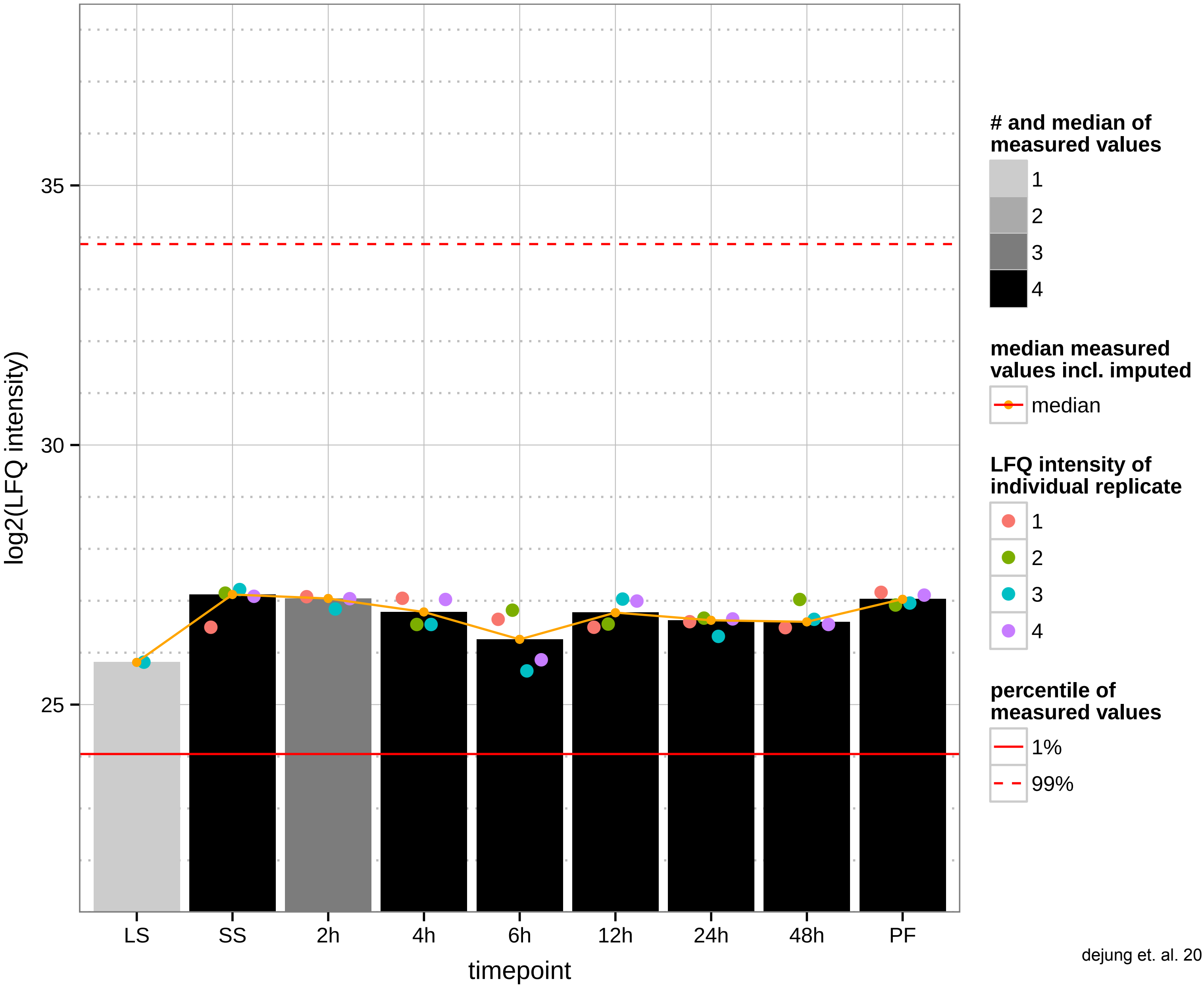
hypothetical protein, conserved
Tb927.4.3660
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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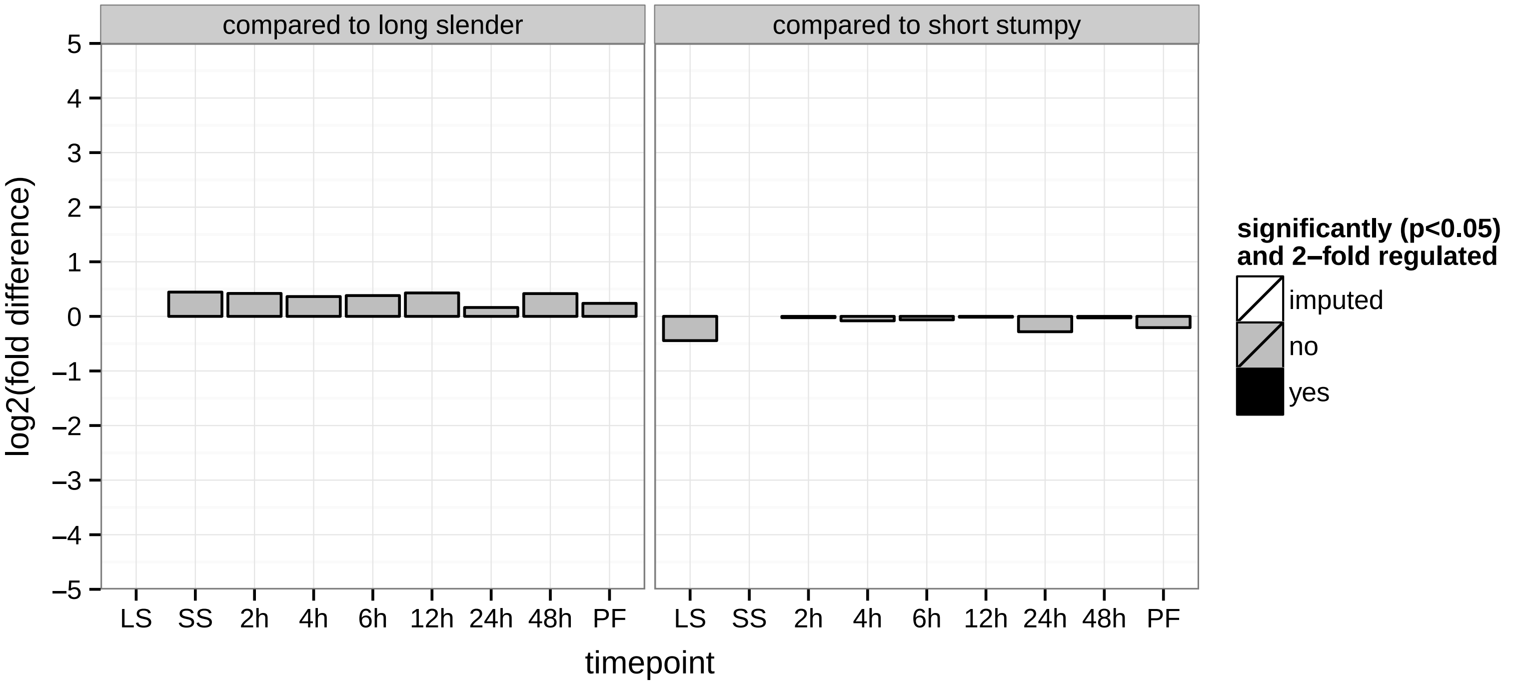
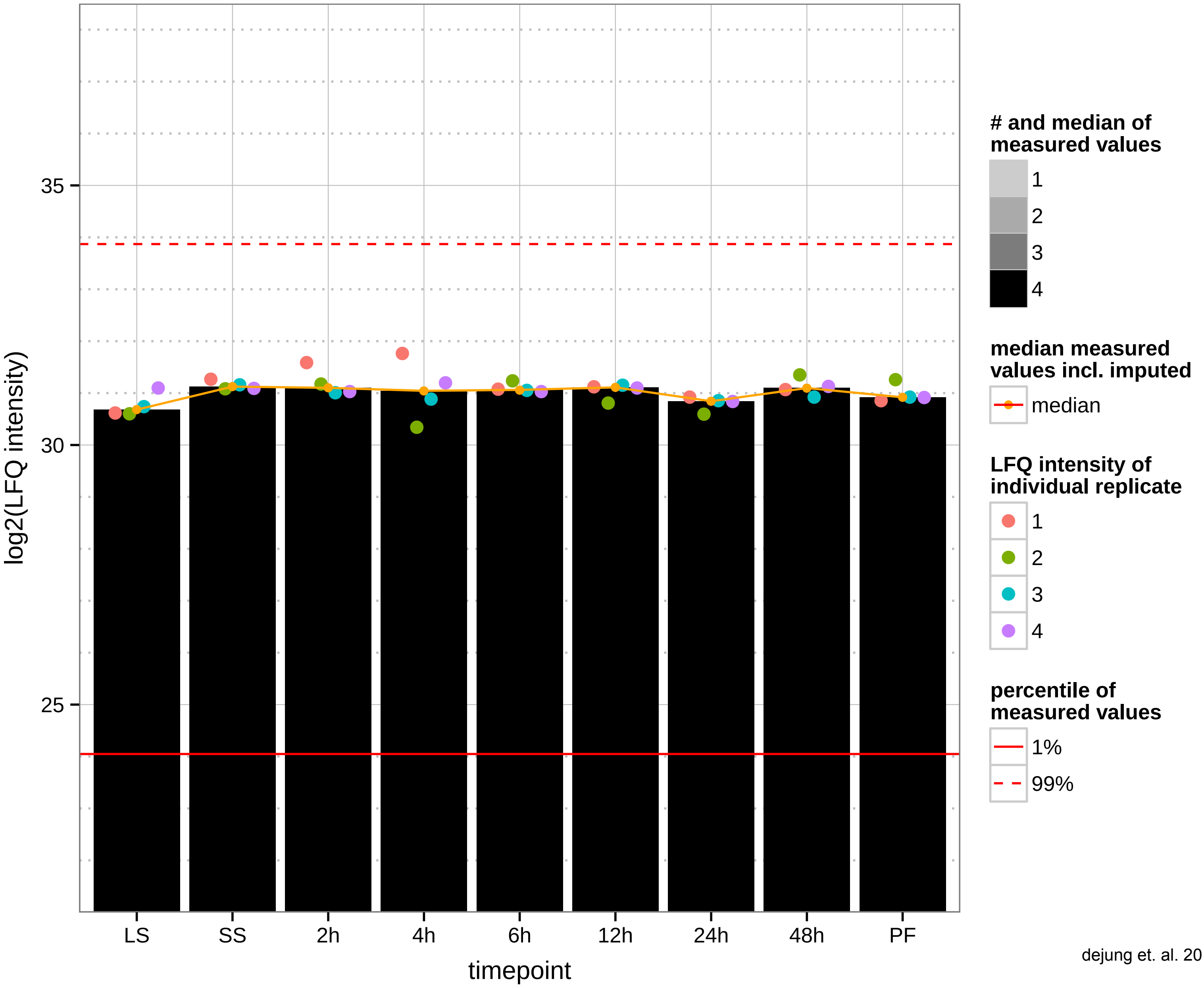
flagellar attachment zone protein (FAZ1)
Tb927.4.3740
AGOF: null
AGOC: cilium part, cytoskeletal part
AGOP: cilium assembly, cytokinesis
PGOF: null
PGOC: null
PGOP: null





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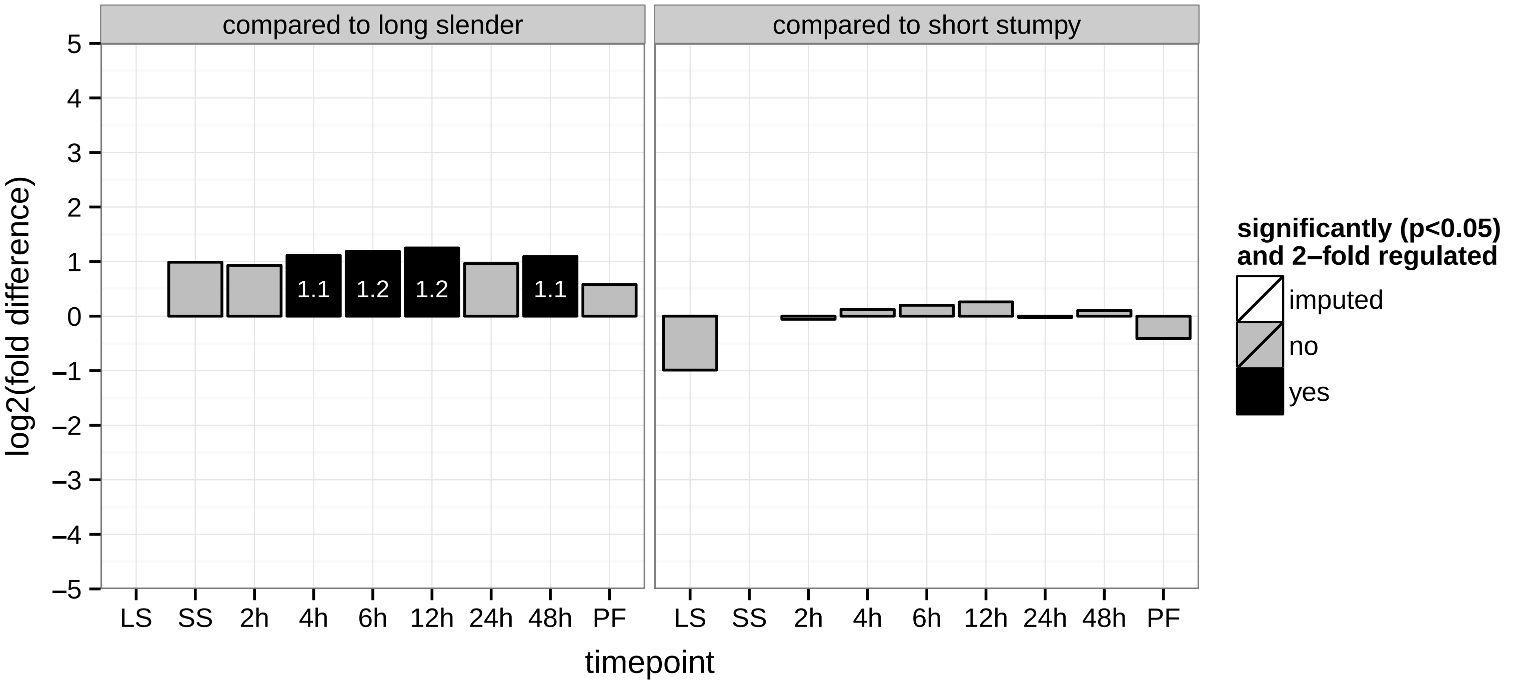
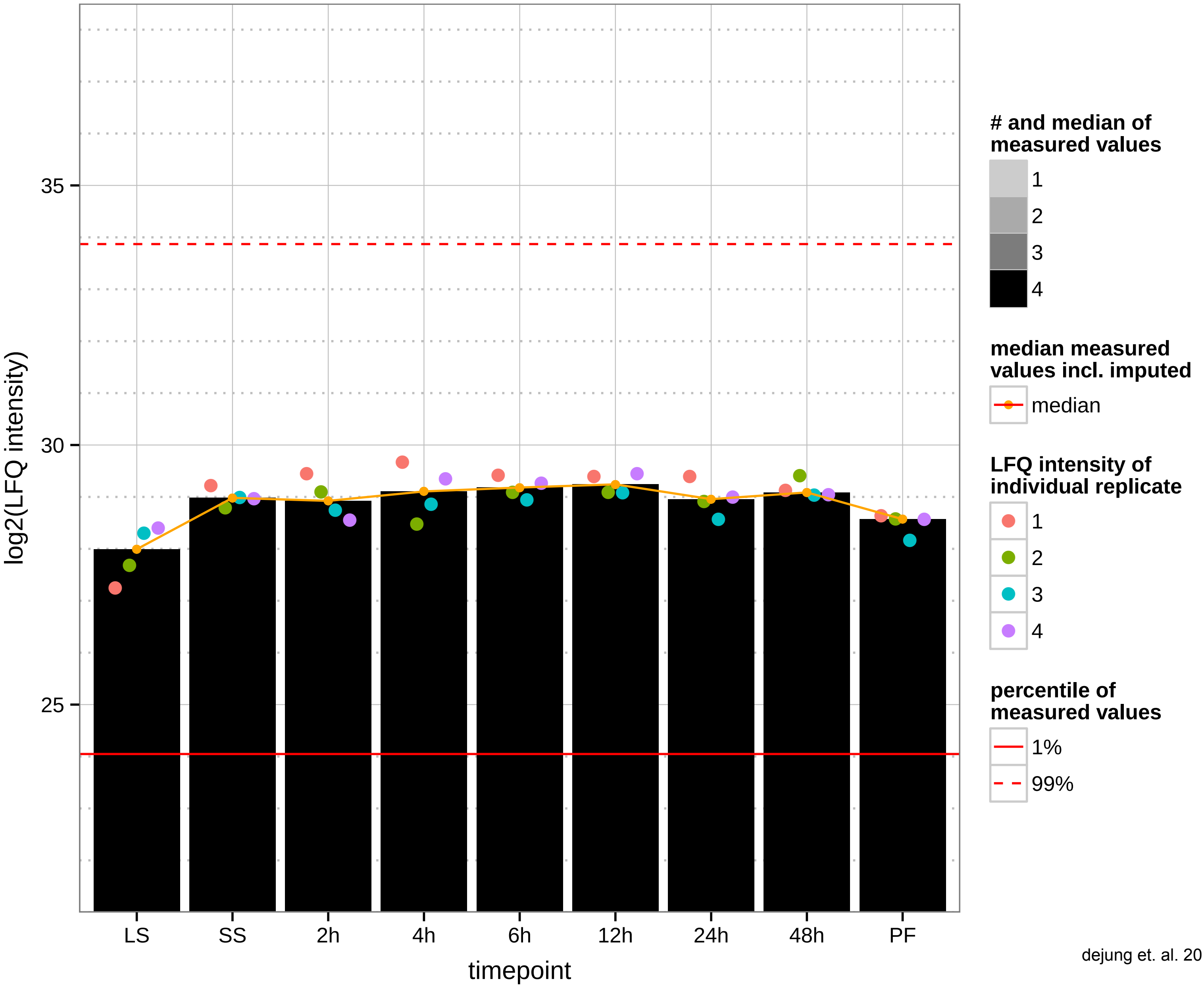
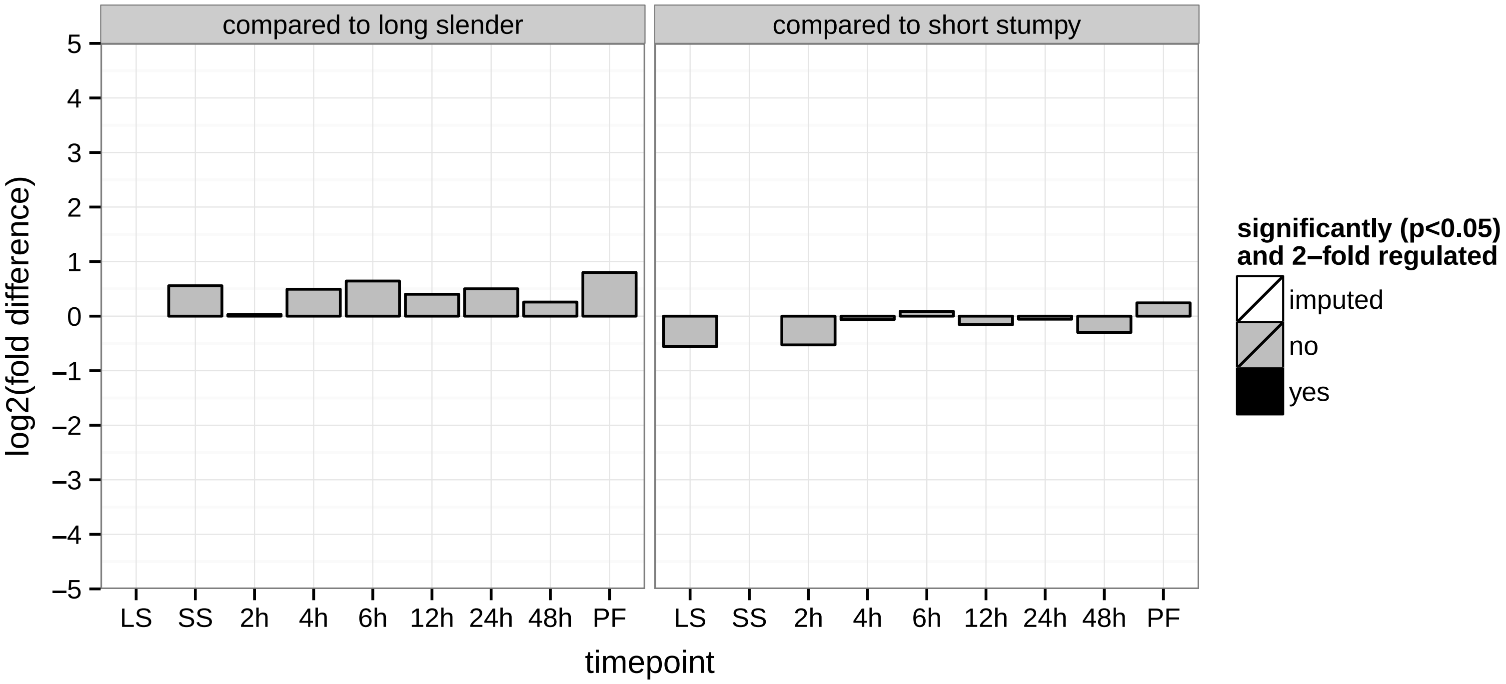
ubiquitin carboxyl–terminal hydrolase, putative, cysteine peptidase, Clan CA, family C19
Tb927.4.3790
AGOF: ubiquitin thiolesterase activity
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: protein binding, ubiquitin thiolesterase activity
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process

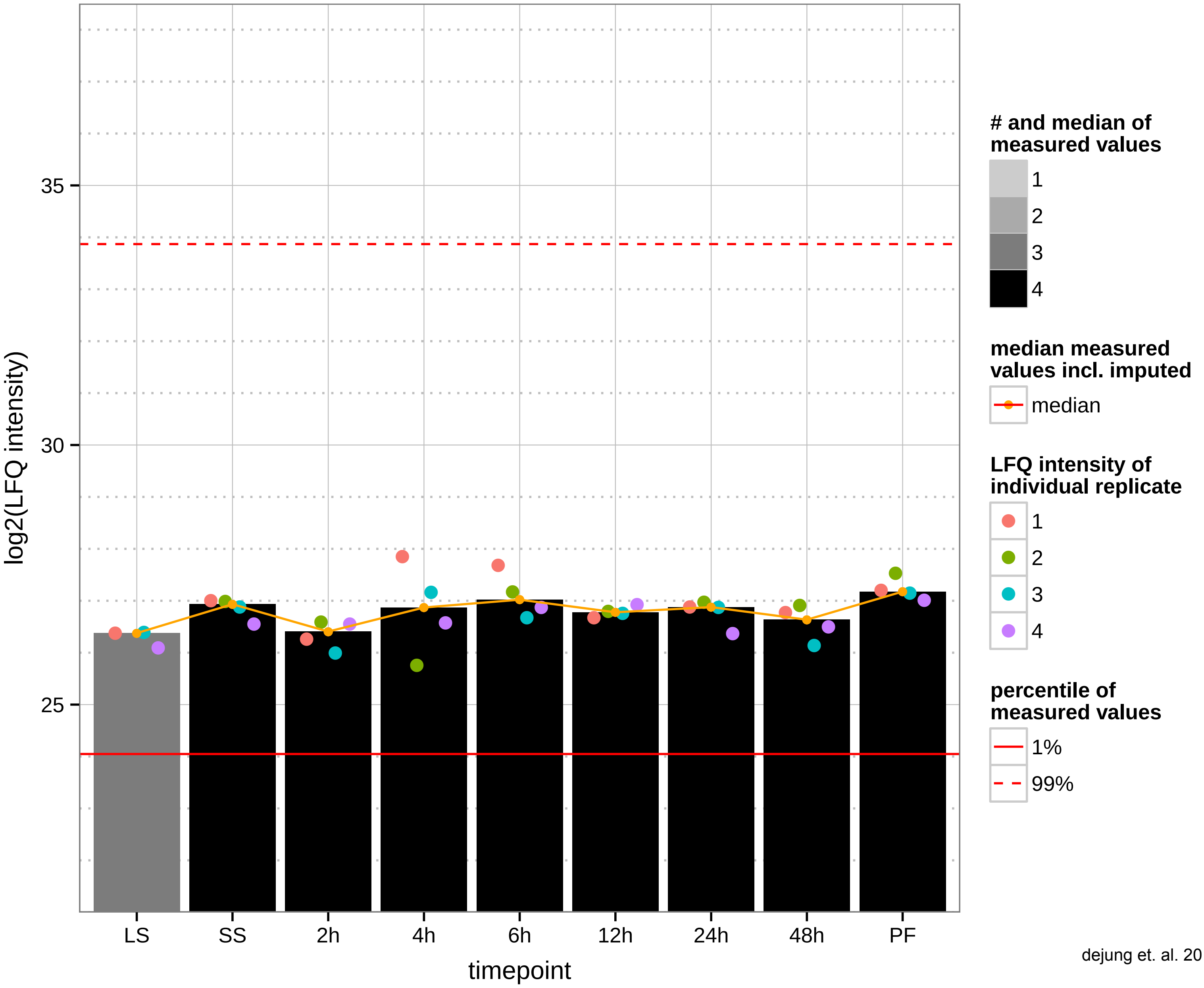




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.380
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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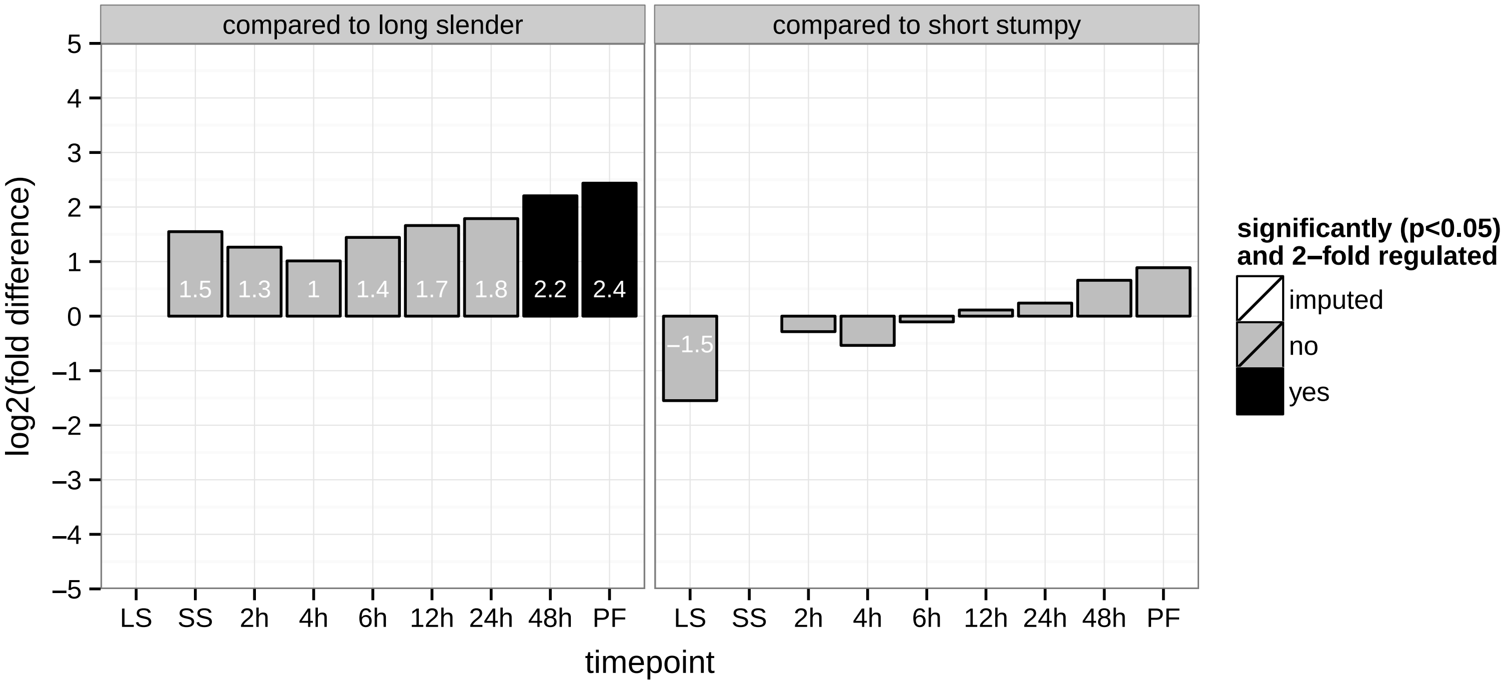
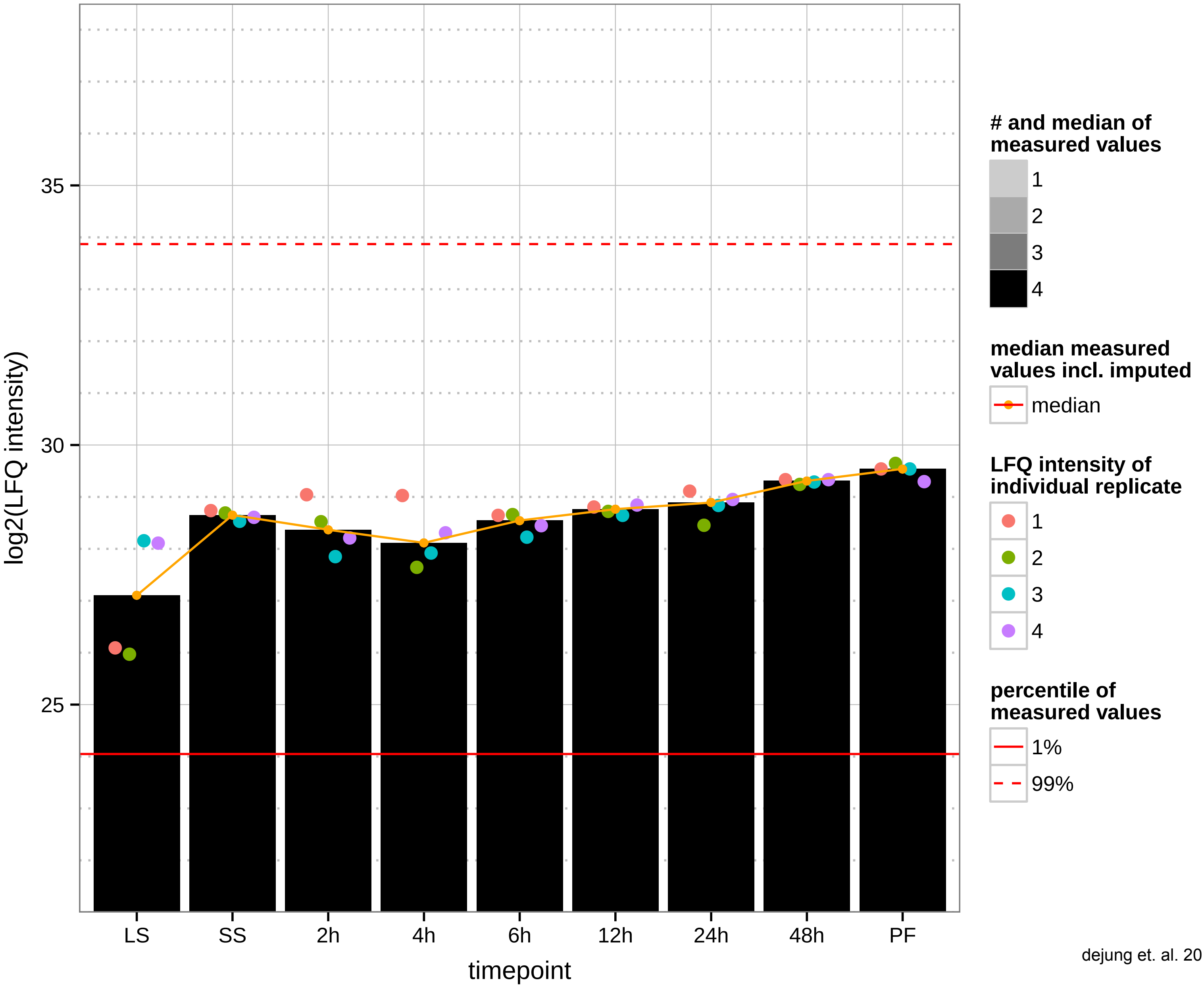
DNA–directed RNA polymerase II subunit 2, putative, RNA polymerase subunit, putative (RPB2)
Tb927.4.3810
AGOF: DNA binding, DNA–directed RNA polymerase activity, ribonucleoside binding
AGOC: null
AGOP: transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA–dependent





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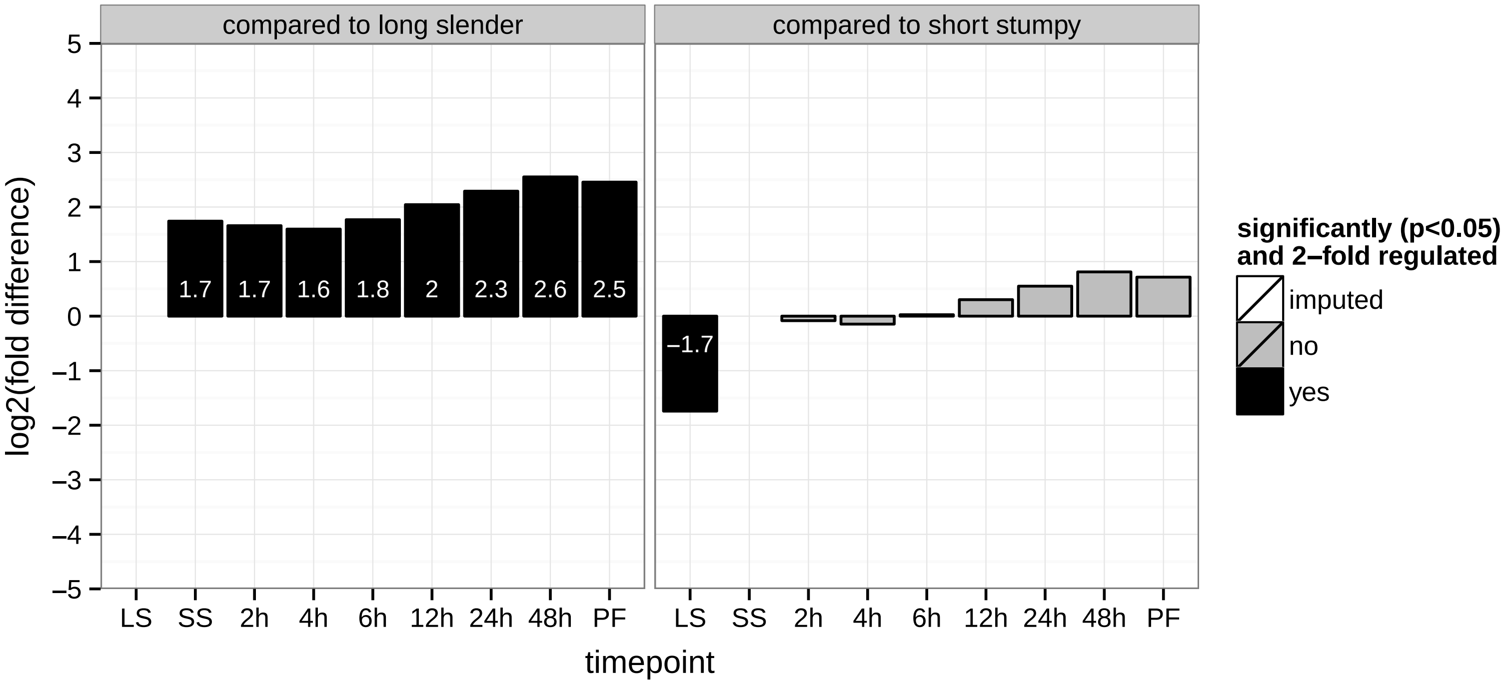
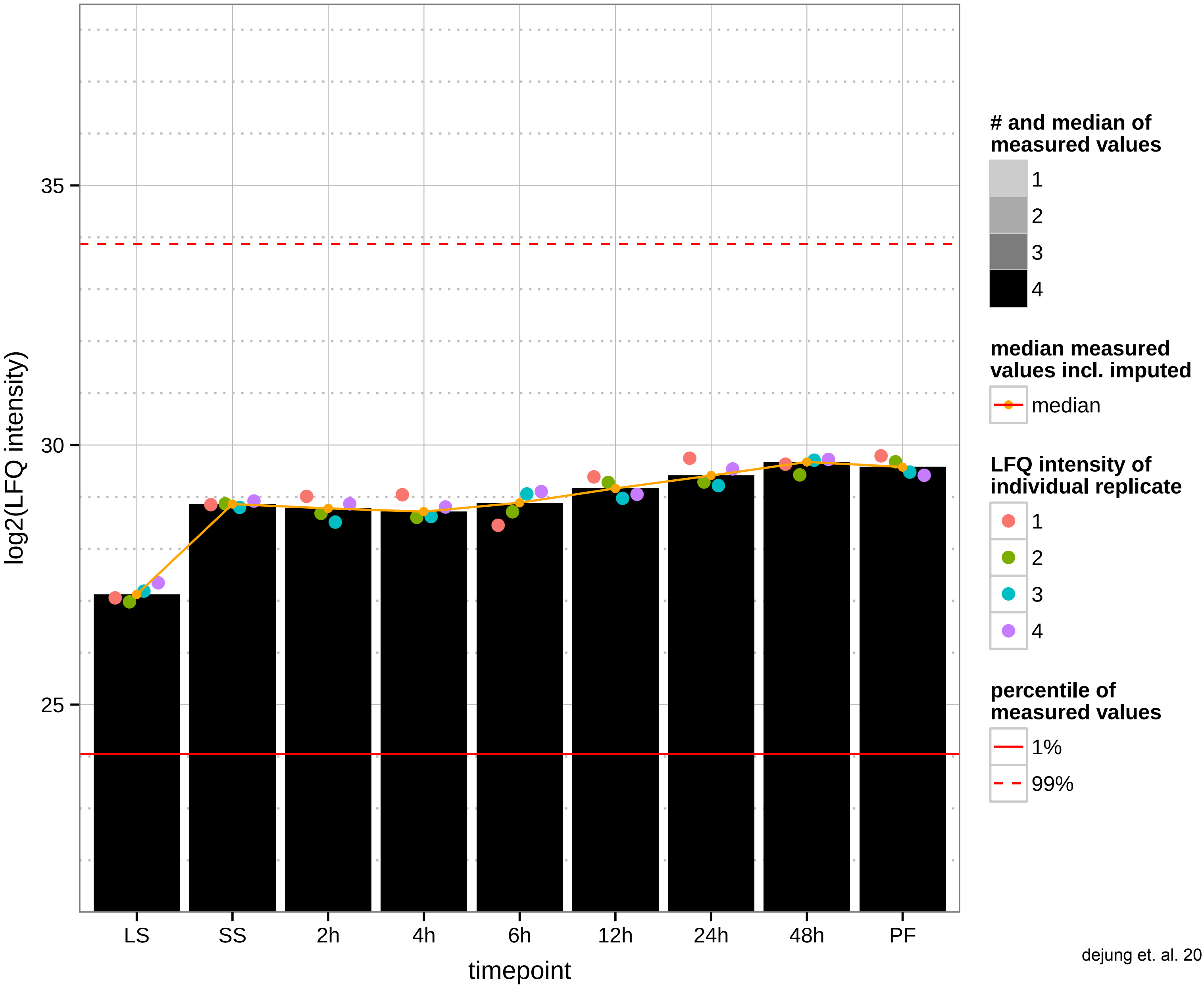
nucleolar protein, putative
Tb927.4.3840
AGOF: RNA binding, S–adenosylmethionine–dependent methyltransferase activity
AGOC: null
AGOP: rRNA processing
PGOF: RNA binding, S–adenosylmethionine–dependent methyltransferase activity
PGOC: null
PGOP: rRNA processing





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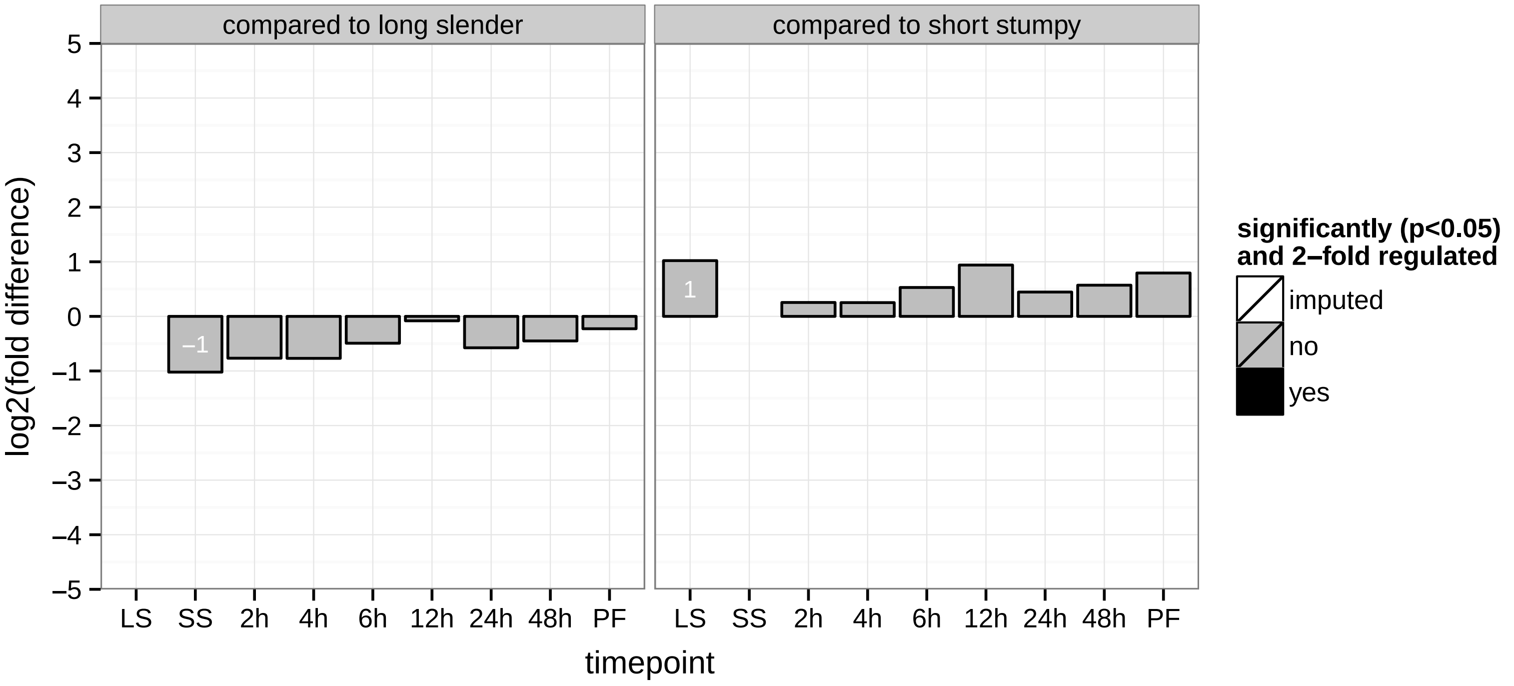
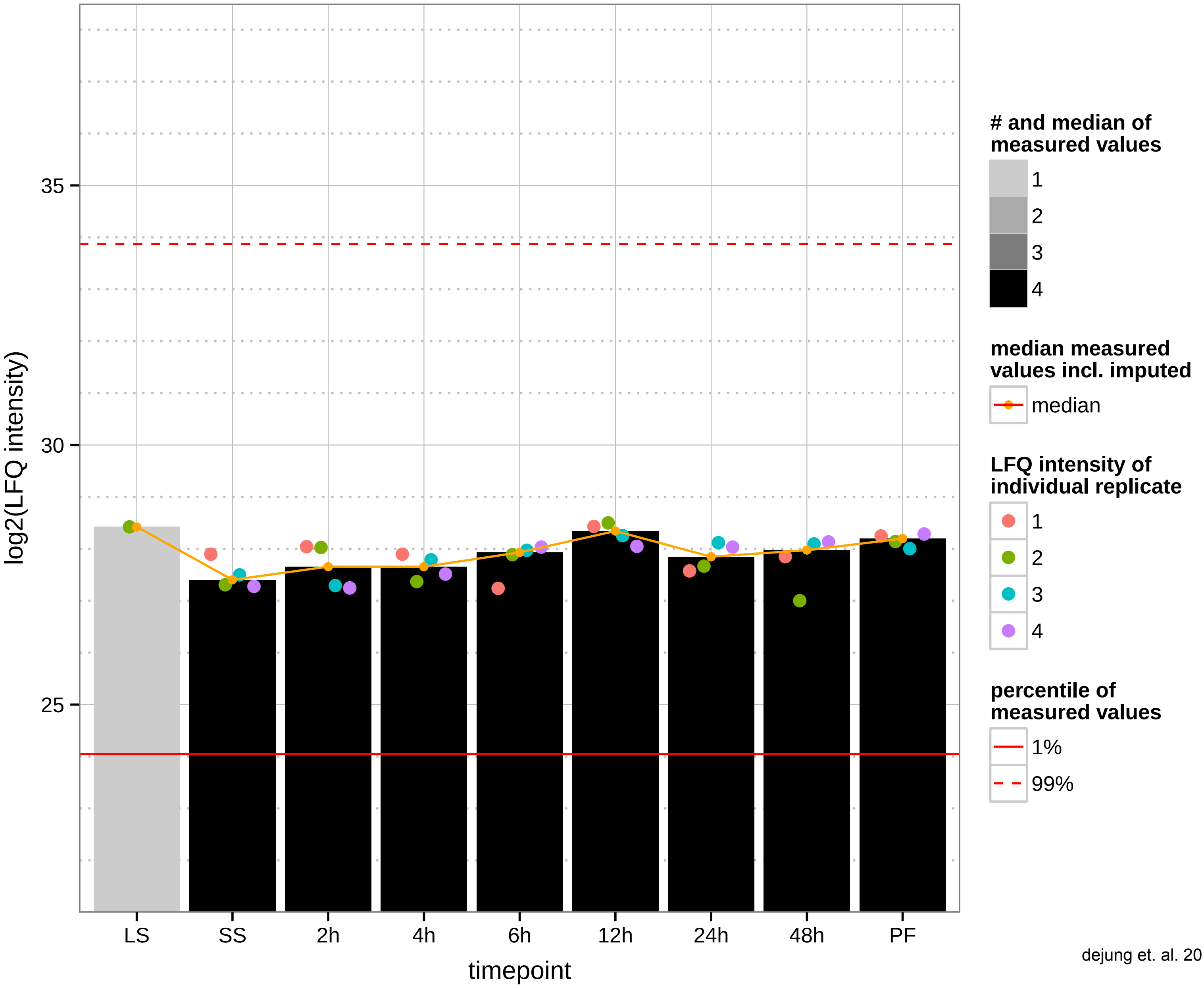
hypothetical protein, conserved
Tb927.4.3850
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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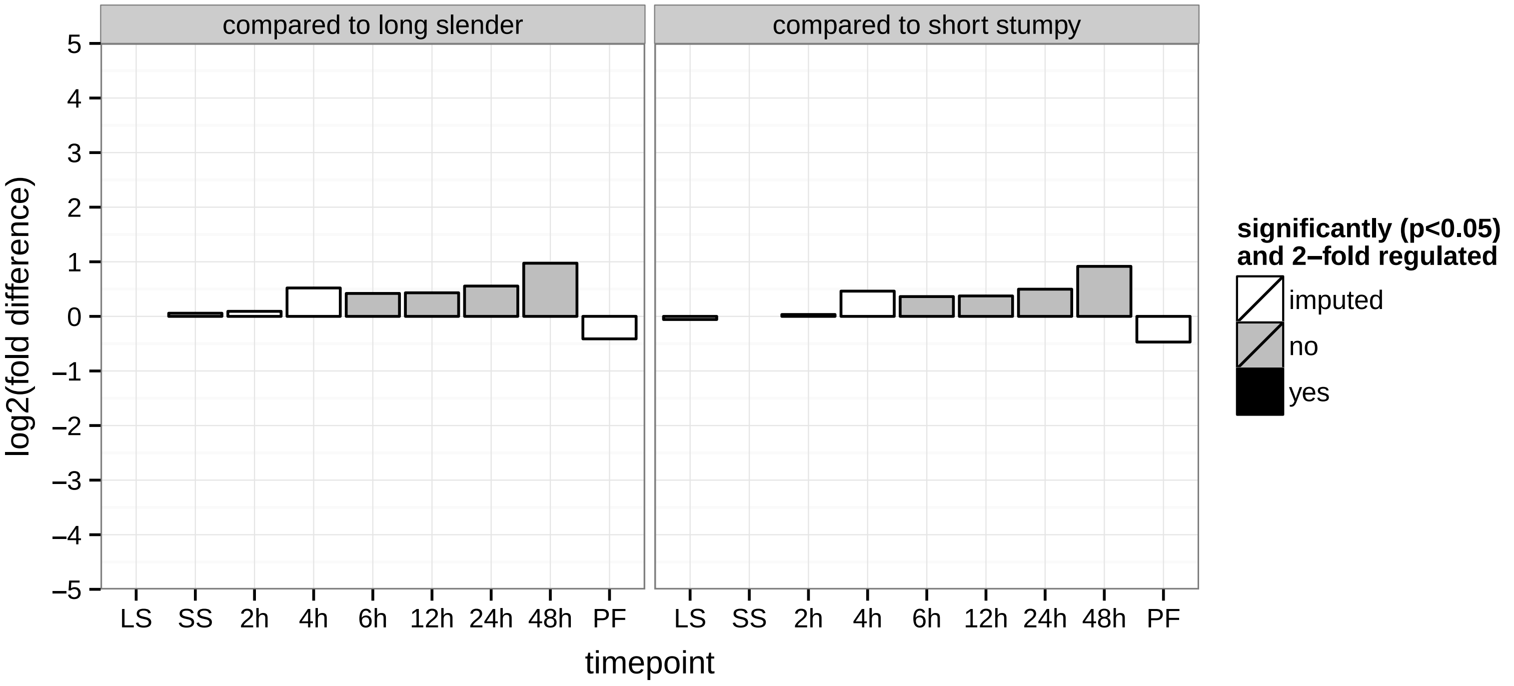
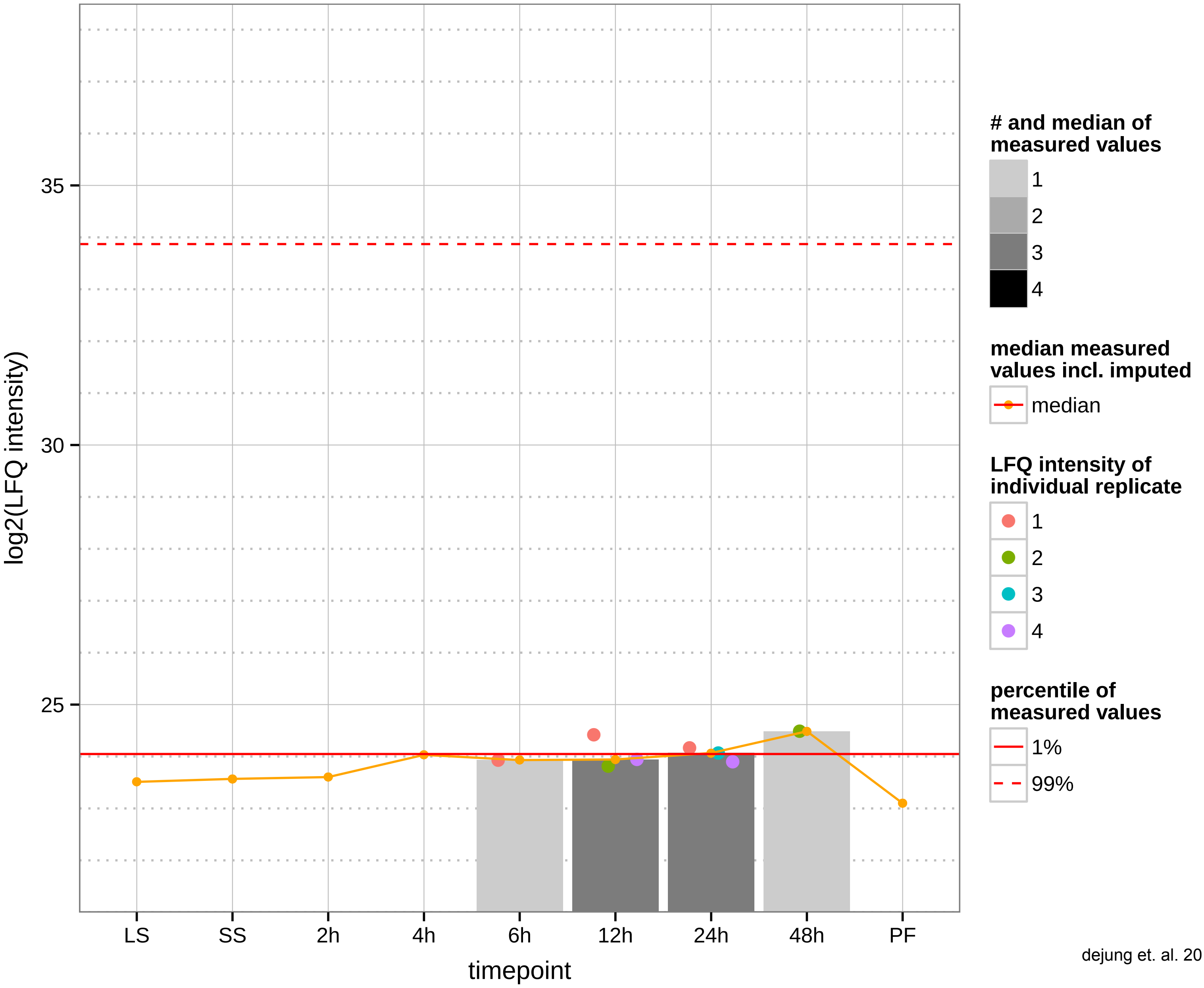
hypothetical protein, conserved
Tb927.4.4090
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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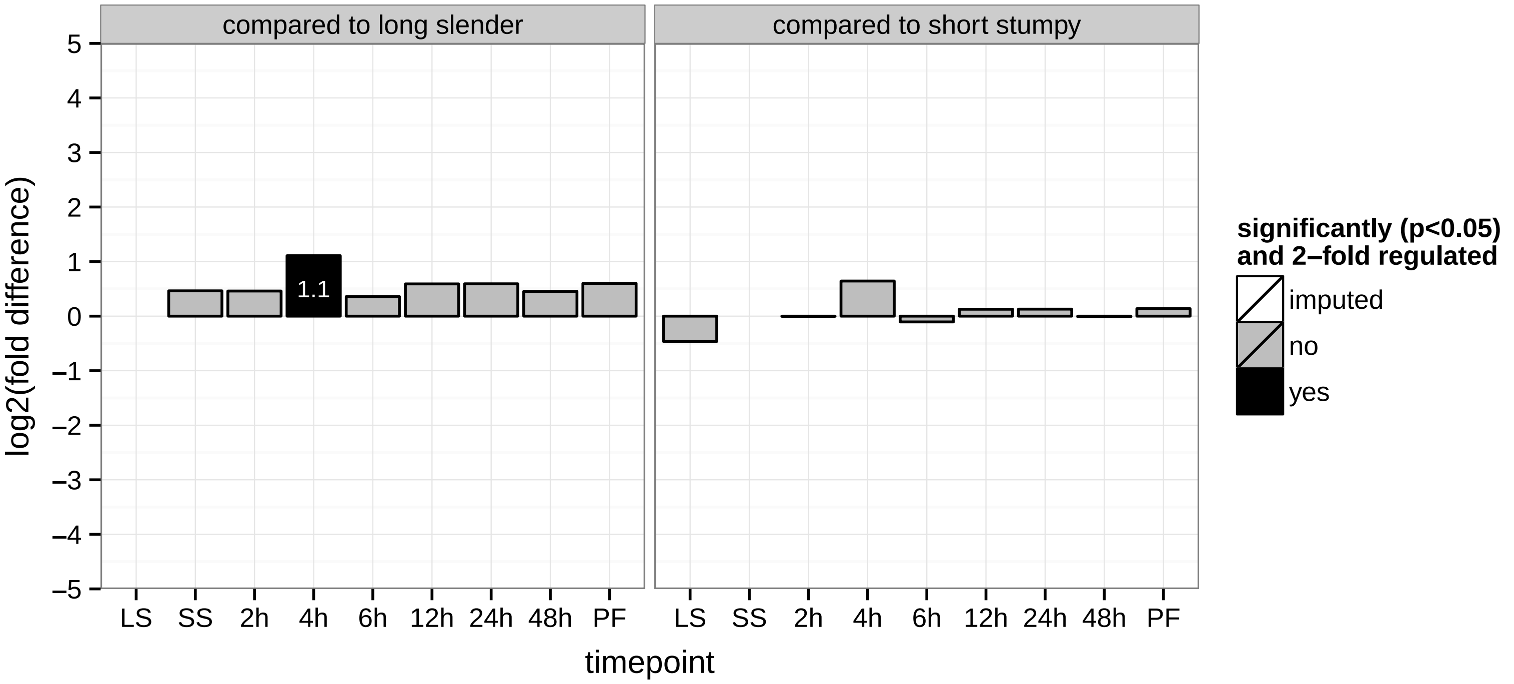
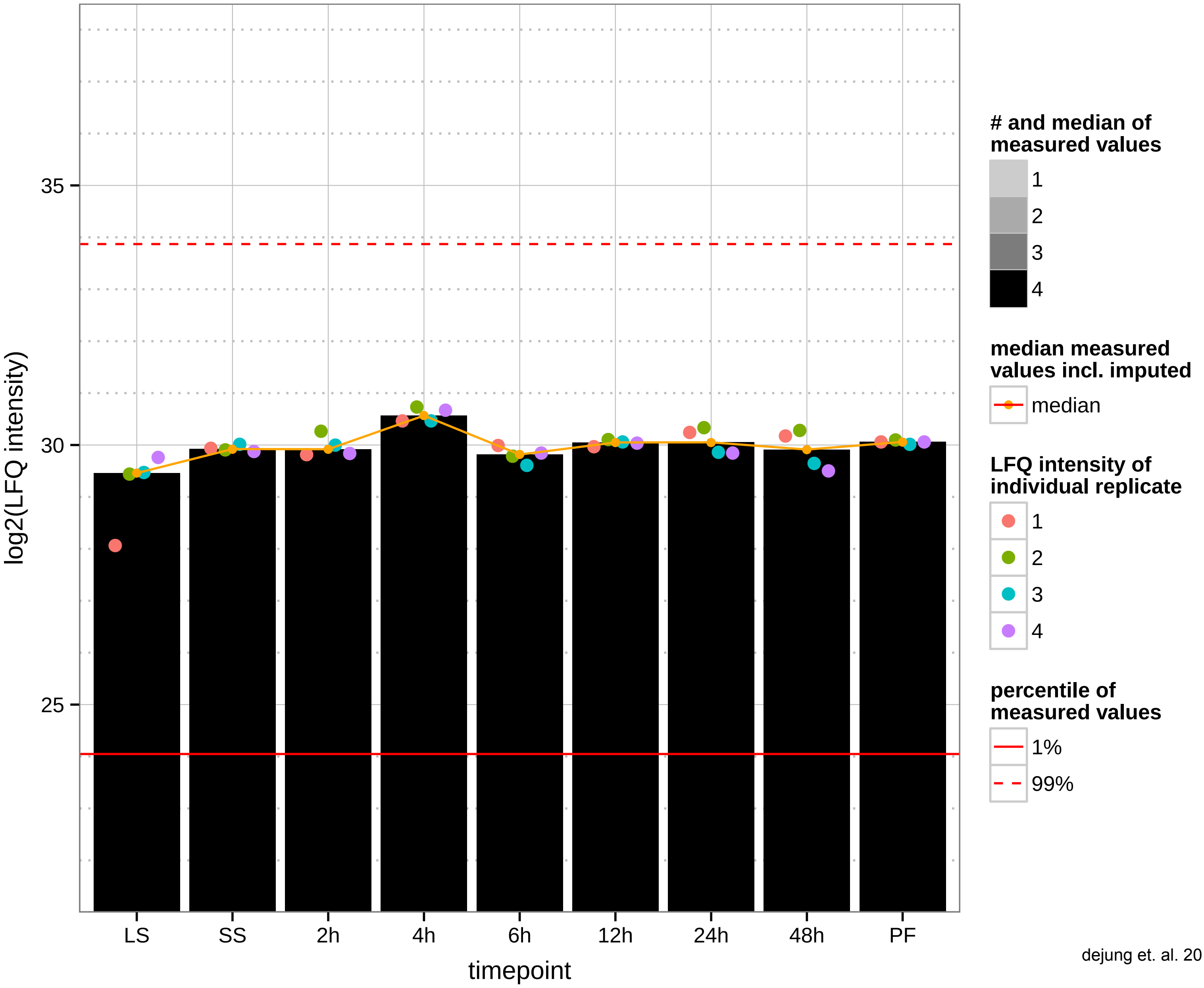
CAF 40 (CAF40)
Tb927.4.410
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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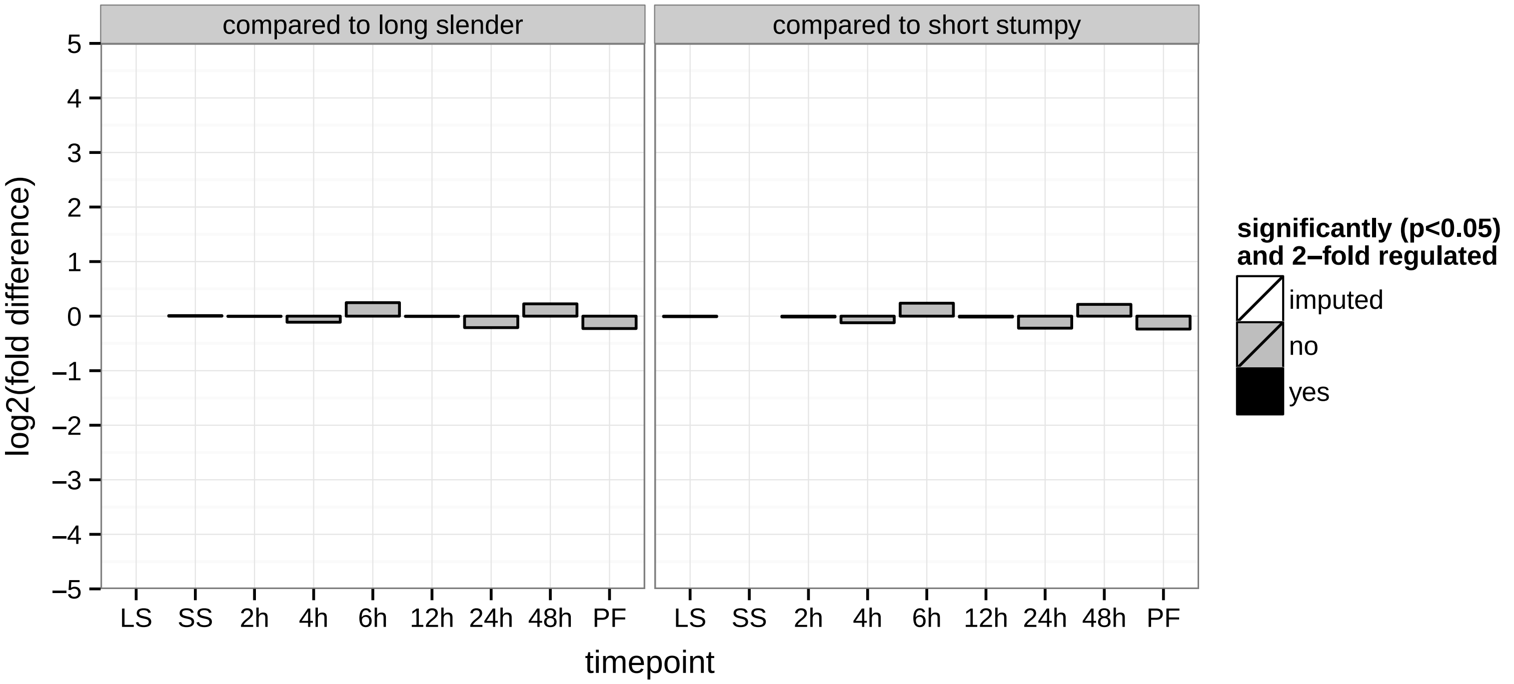
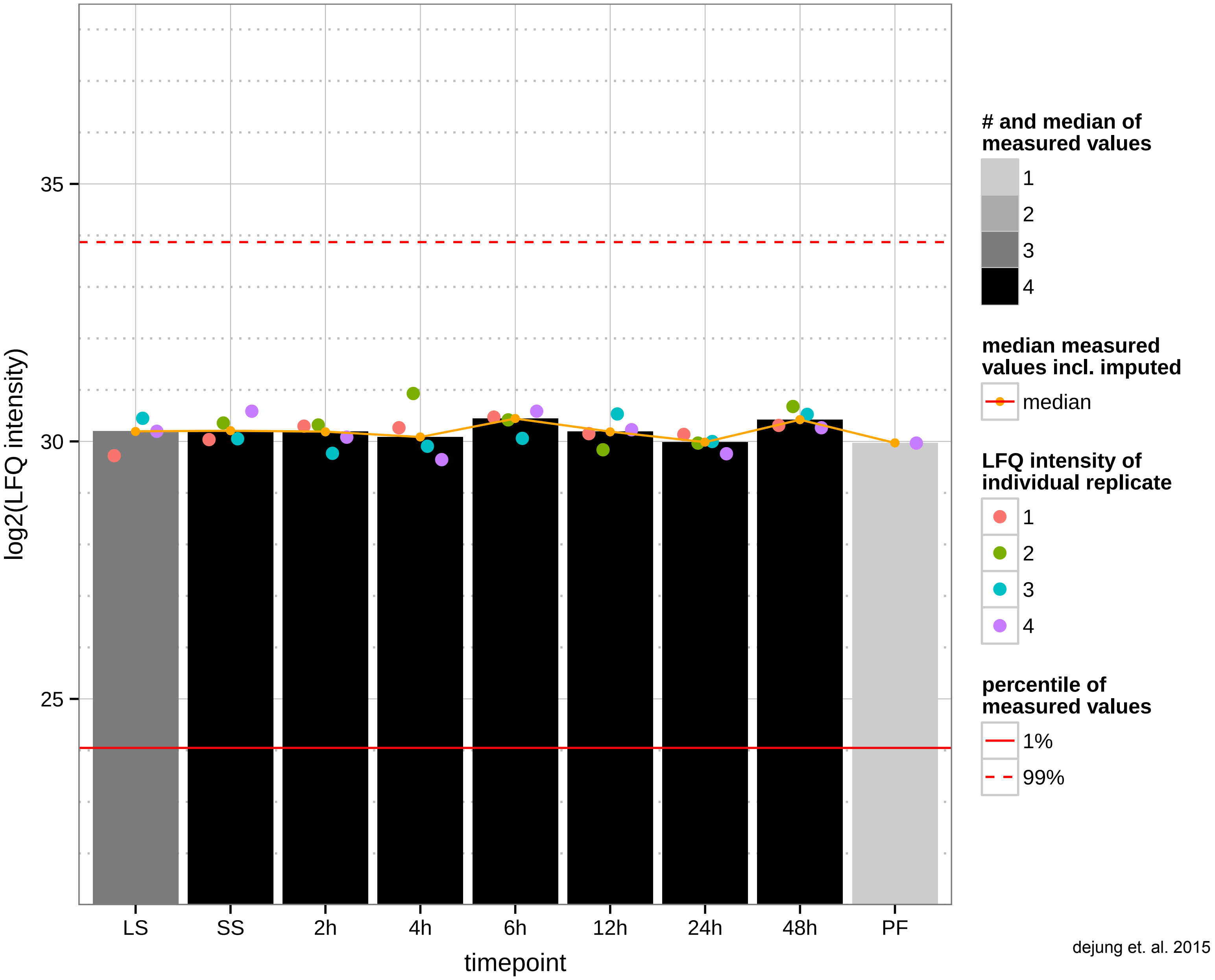
hypothetical protein, conserved
Tb927.4.4130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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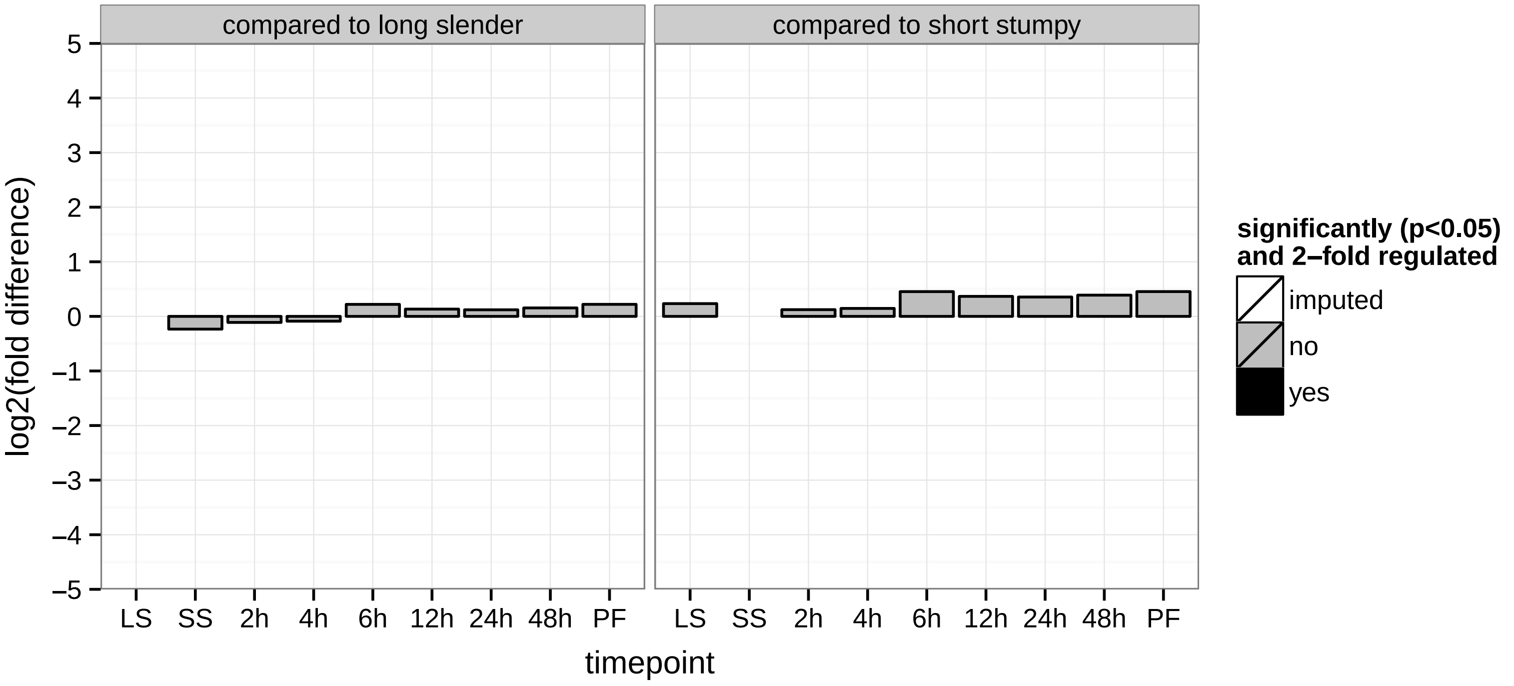
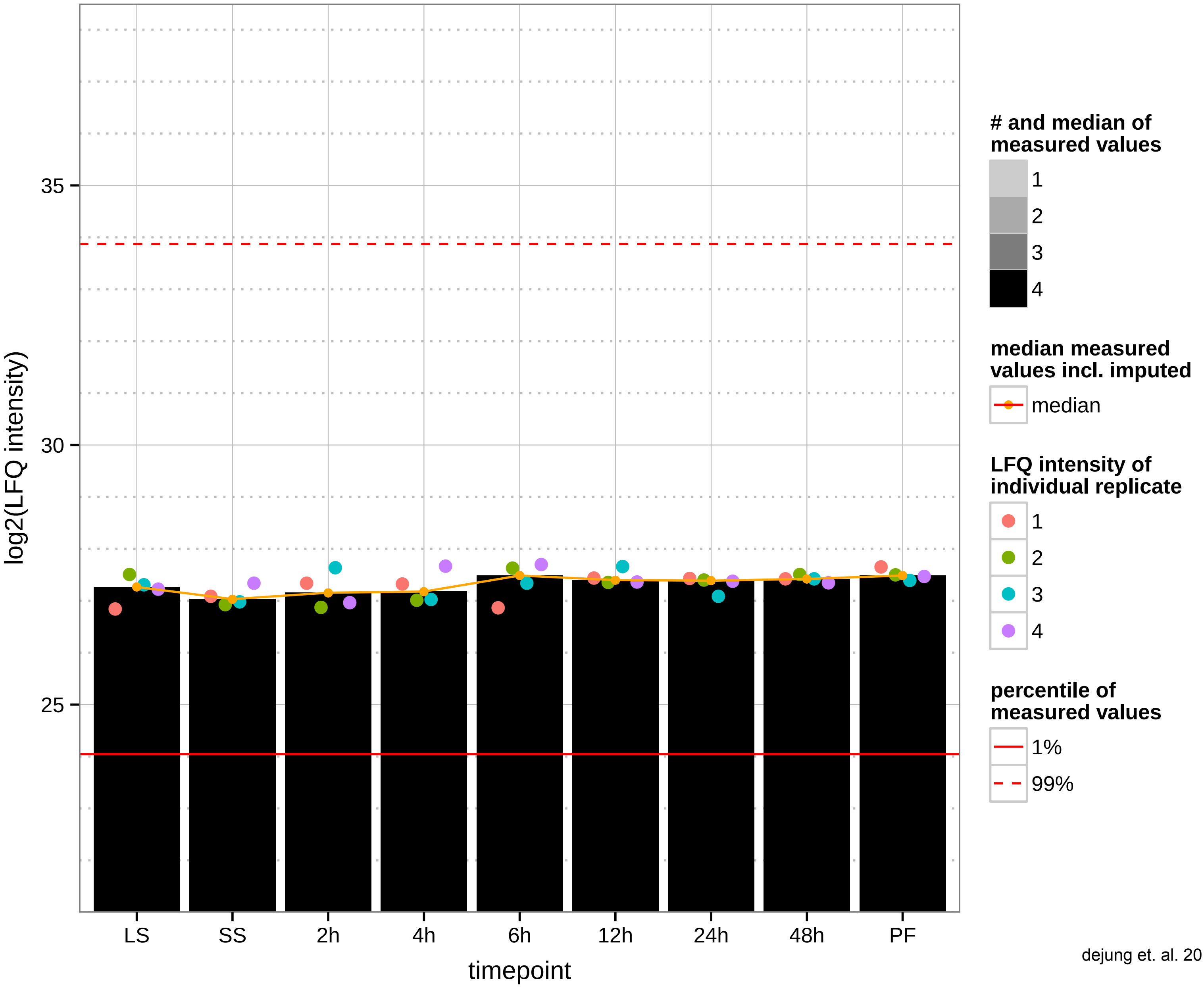
Nucleoporin (TbNup64)
Tb927.4.4310
AGOF: null
AGOC: nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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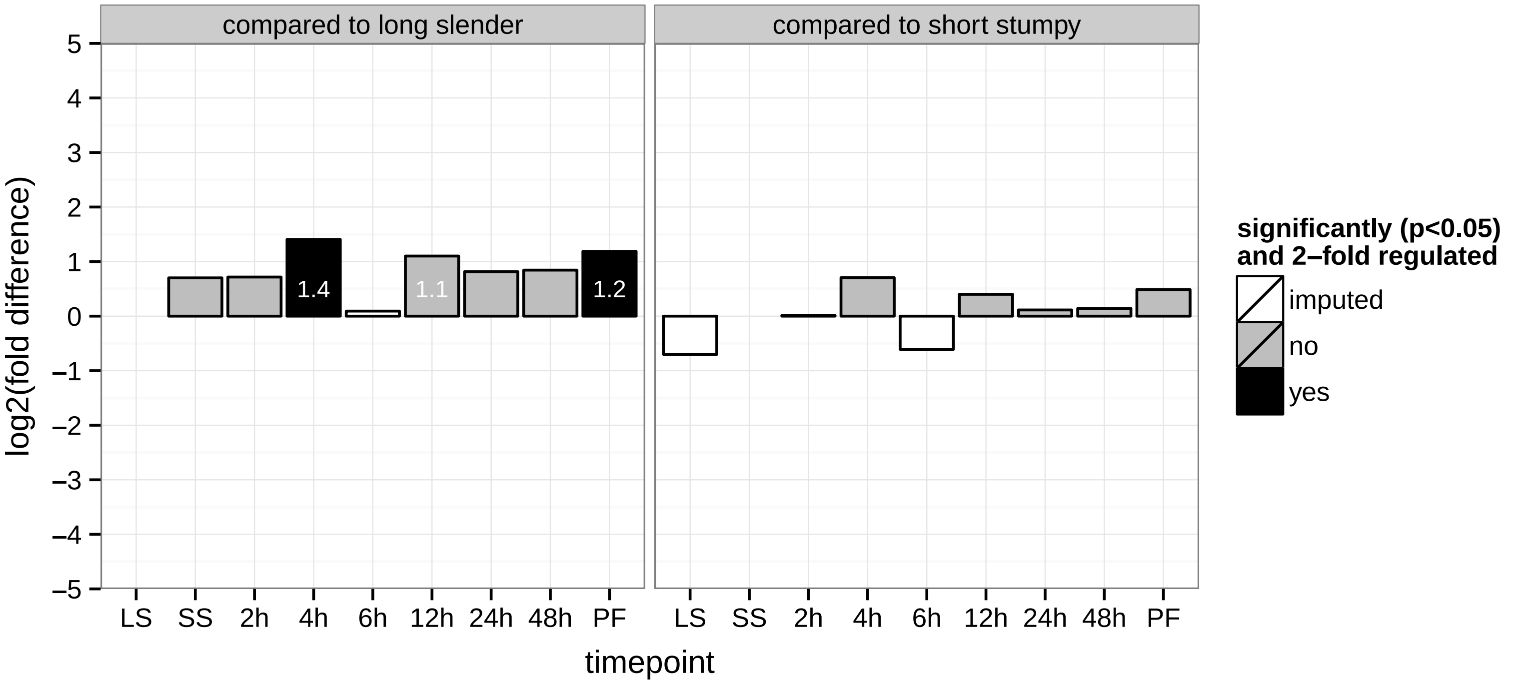
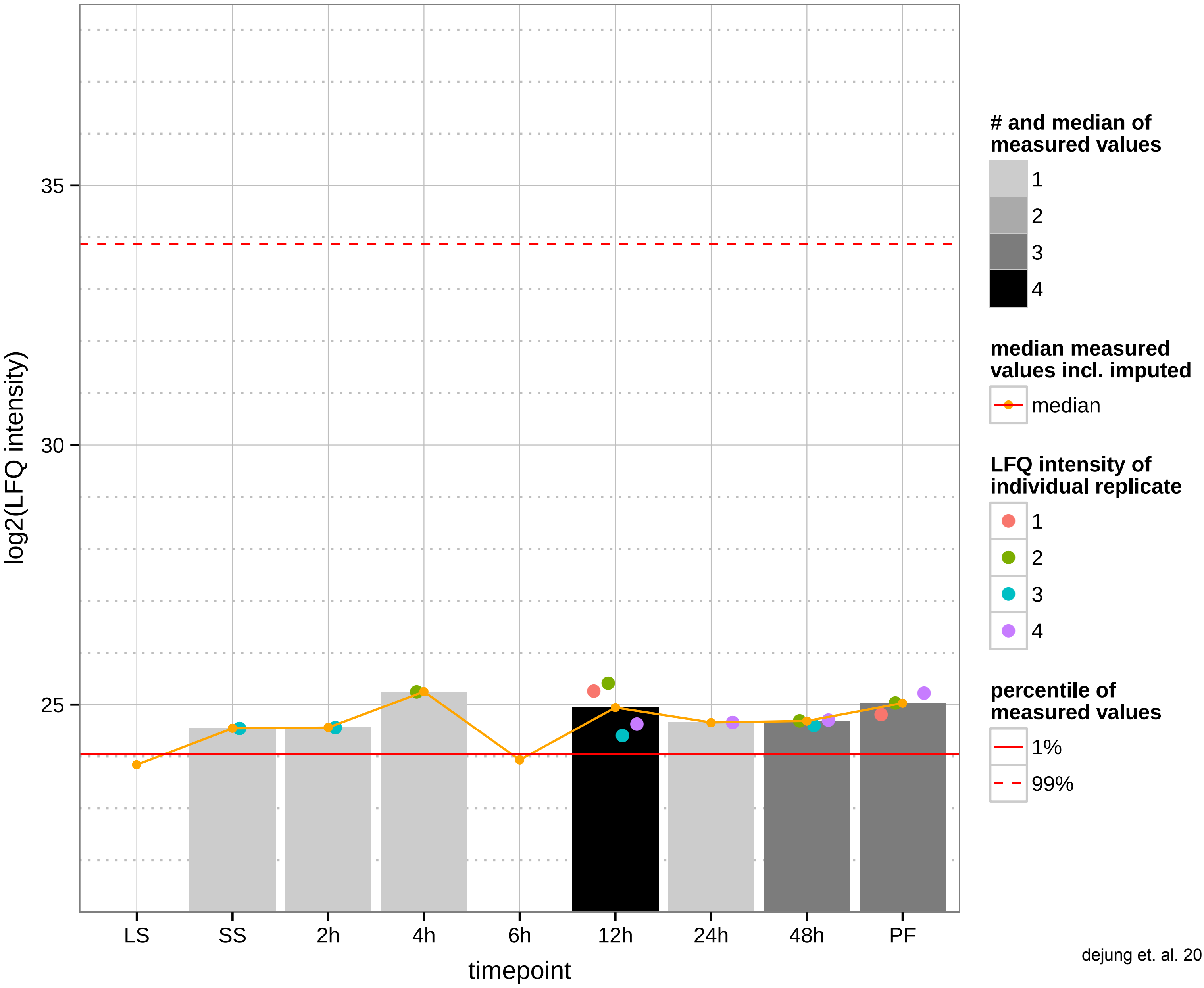
divalent cation tolerance protein, putative
Tb927.4.4320
AGOF: null
AGOC: null
AGOP: response to metal ion
PGOF: null
PGOC: null
PGOP: response to metal ion





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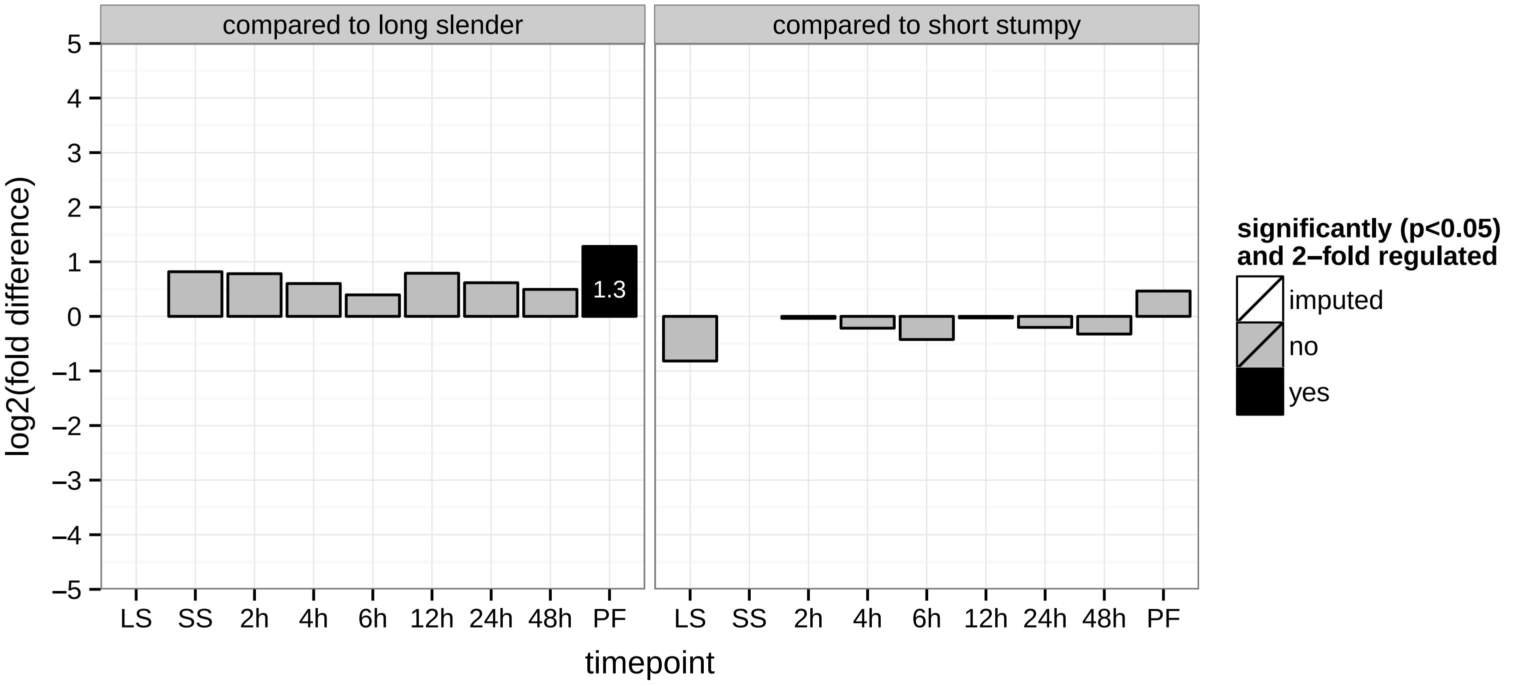
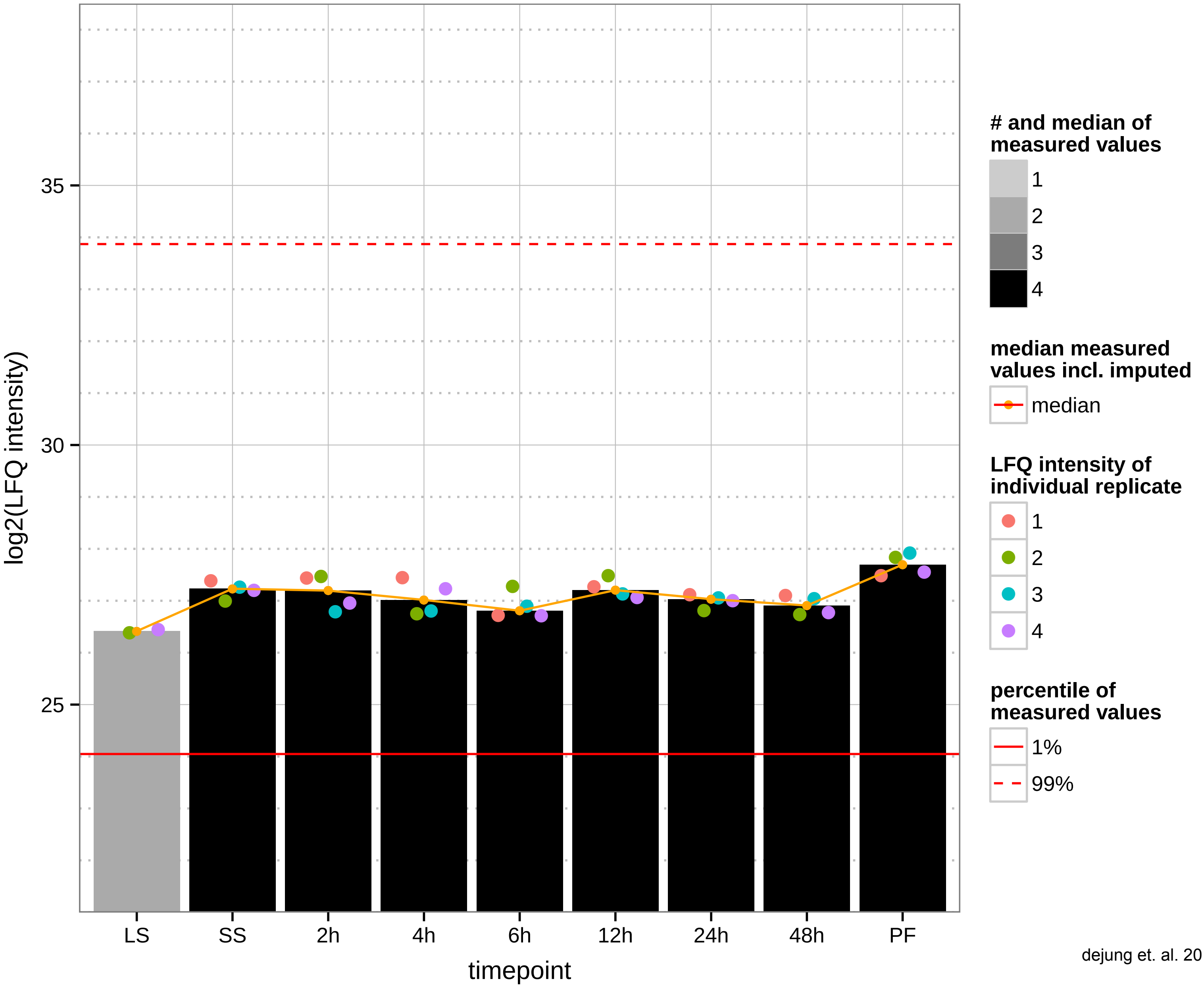
monoglyceride lipase, putative
Tb927.4.4360
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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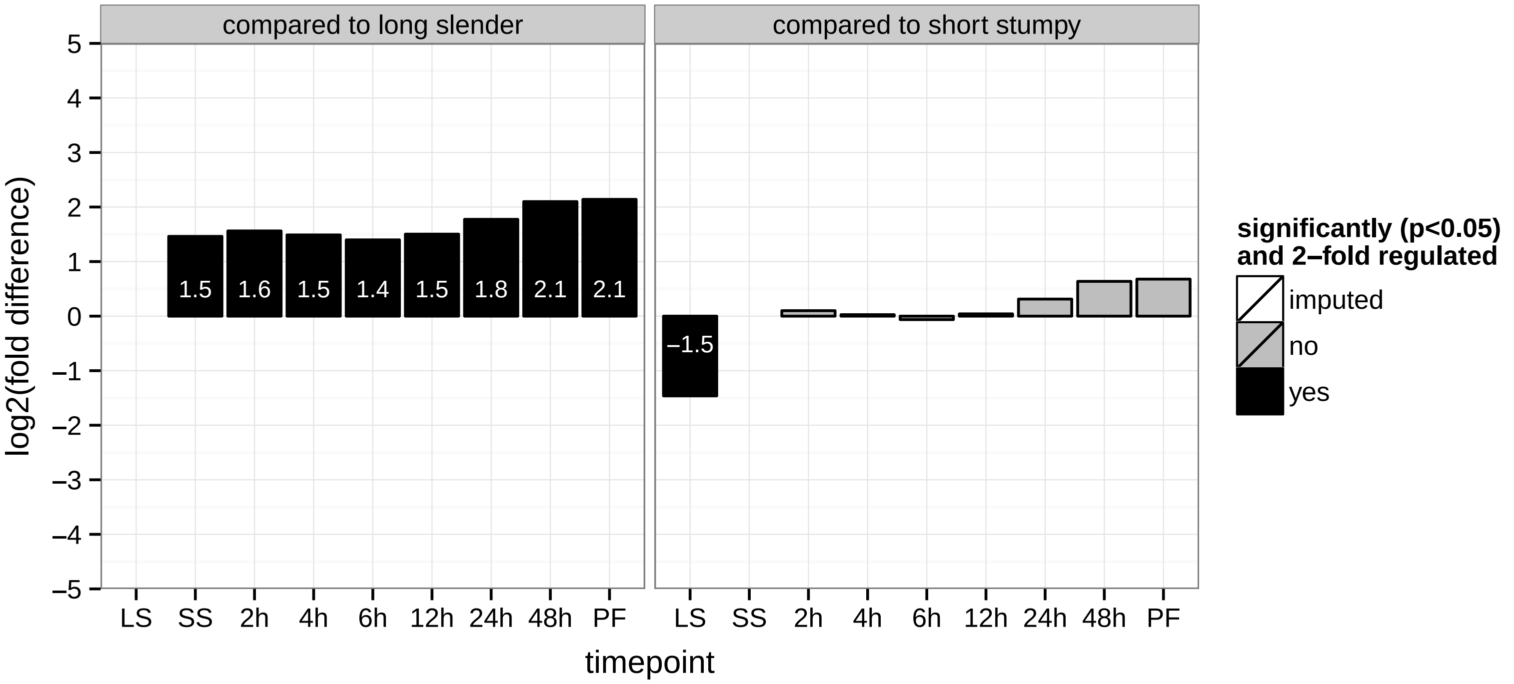
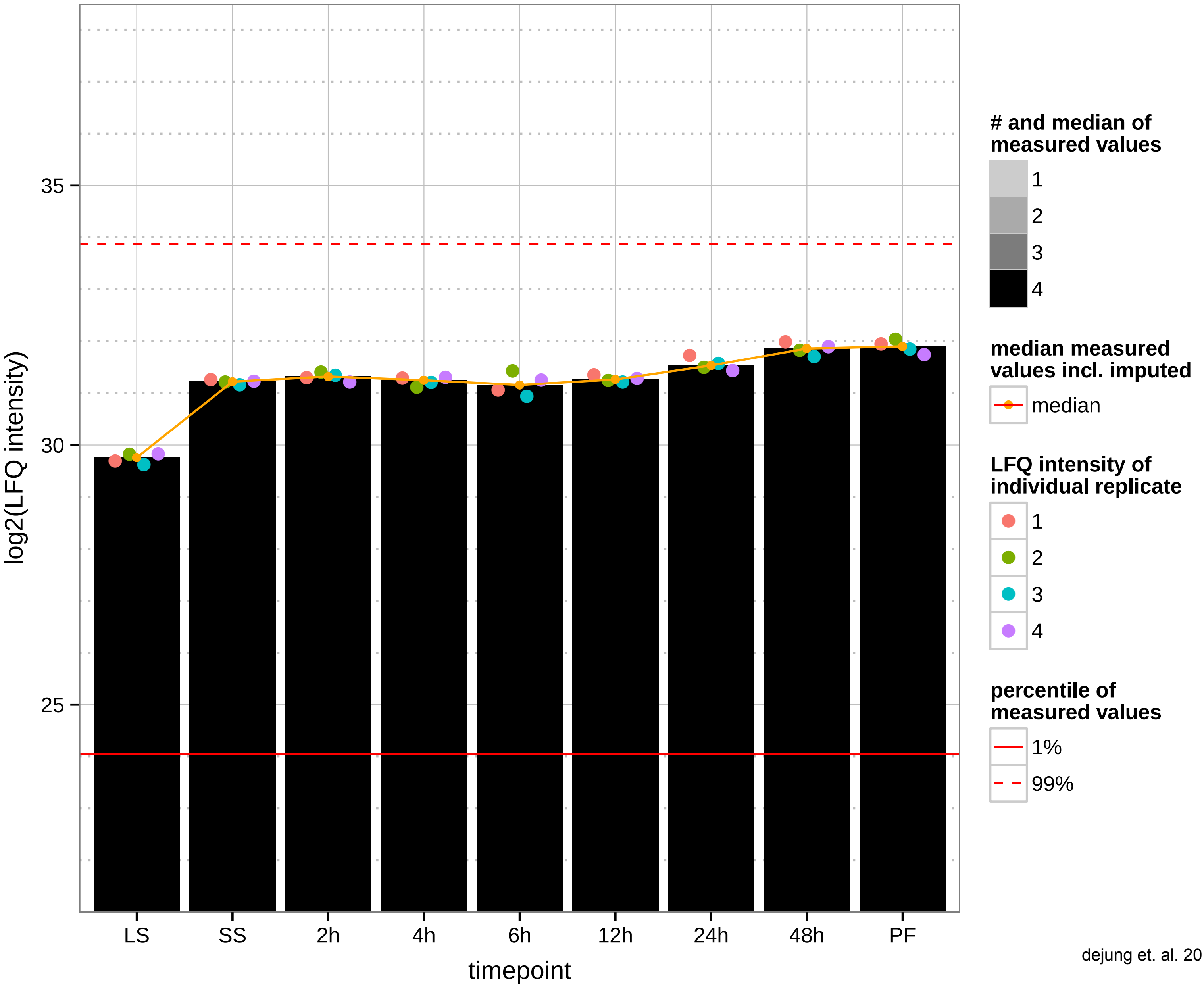
vacuolar–type proton translocating pyrophosphatase 1, putative (PPase1), vacuolar–type proton translocating pyrophosphatas
Tb927.8.7980;Tb927.4.4380
AGOF: hydrogen–translocating pyrophosphatase activity, inorganic diphosphatase activity
AGOC: Golgi membrane, acidocalcisome, contractile vacuole, integral to membrane
AGOP: proton transport
PGOF: hydrogen–translocating pyrophosphatase activity, inorganic diphosphatase activity
PGOC: membrane
PGOP: proton transport





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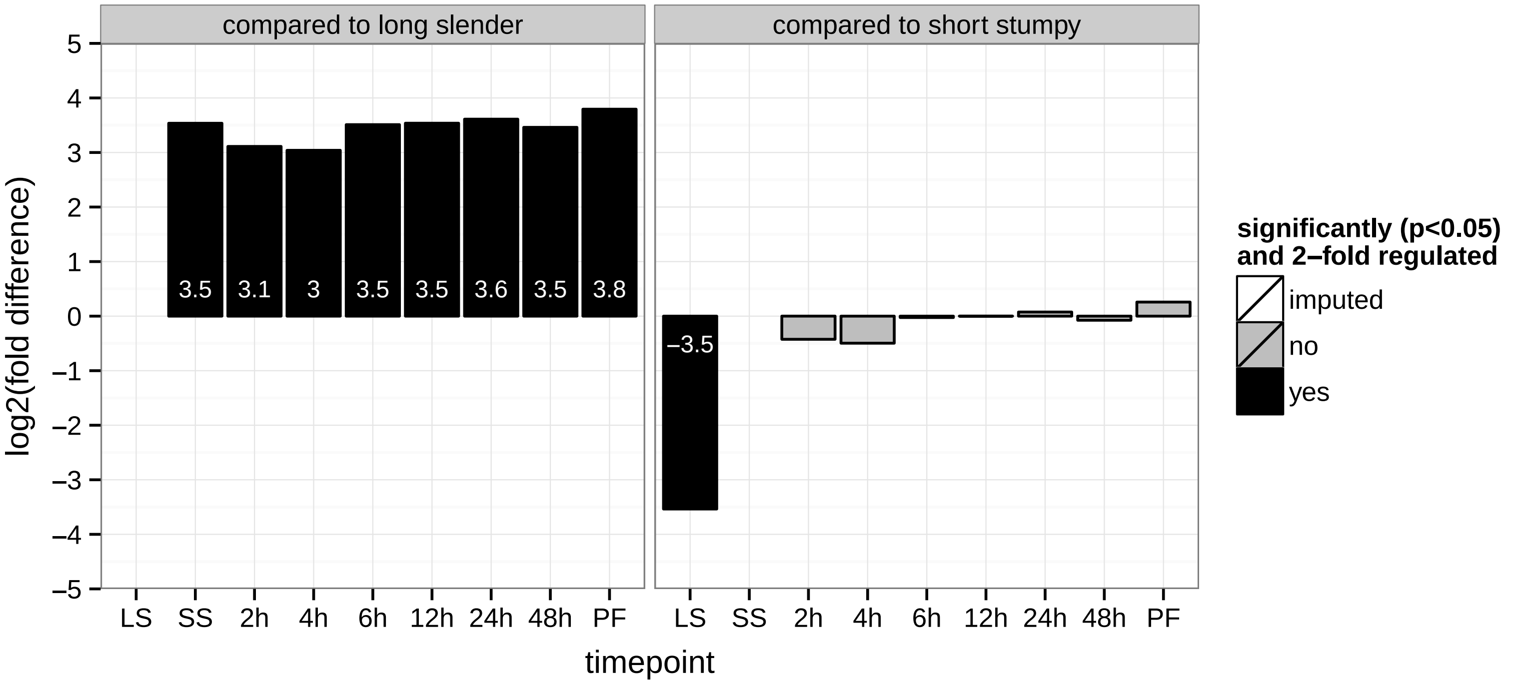
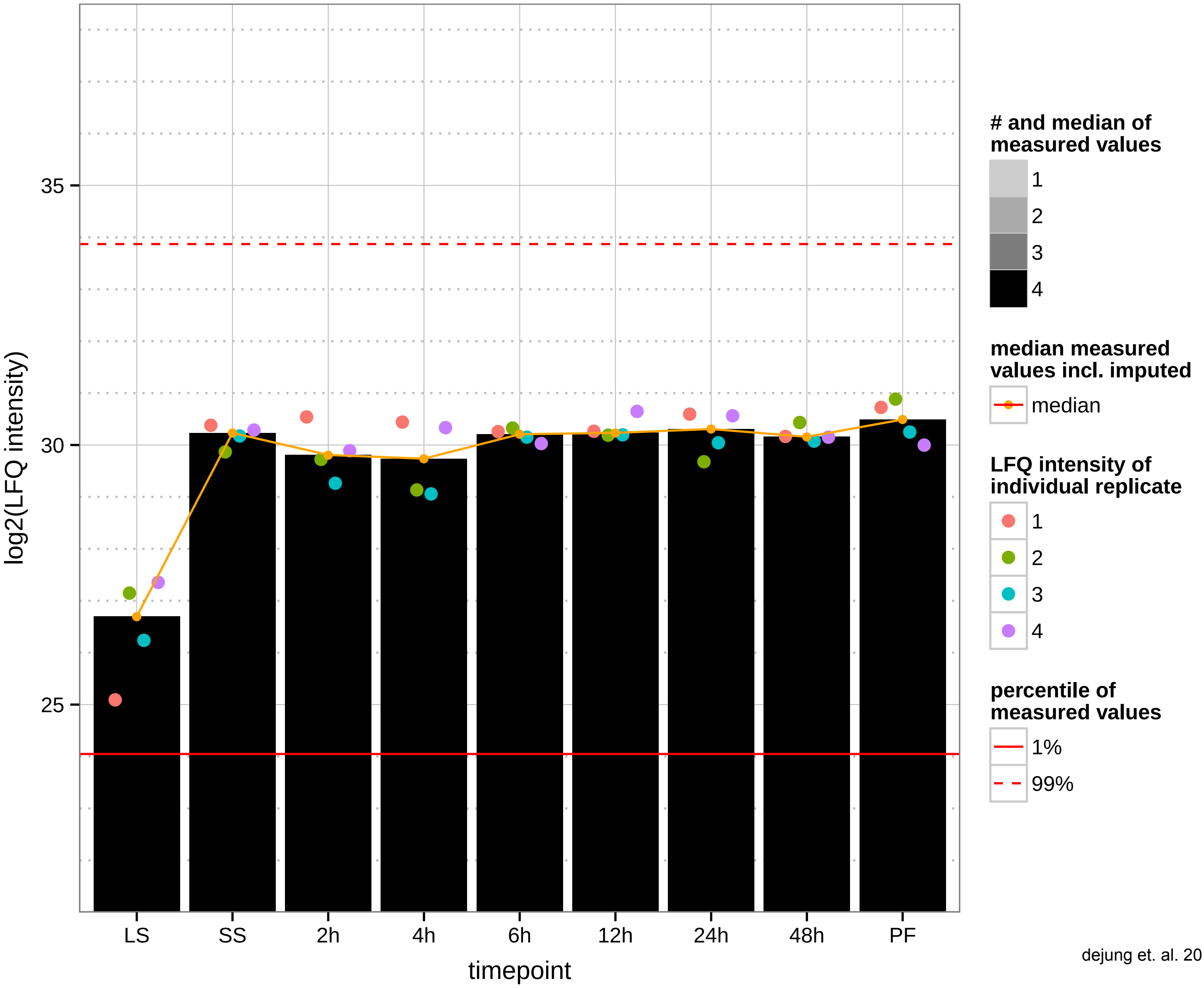
multidrug resistance protein E, p–glycoprotein (MRPE)
Tb927.4.4490
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances
AGOC: ATP–binding cassette (ABC) transporter complex, integral to membrane
AGOP: response to drug, transport
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances, nucleoside–triphosphatase activity
PGOC: integral to membrane
PGOP: transmembrane transport, transport





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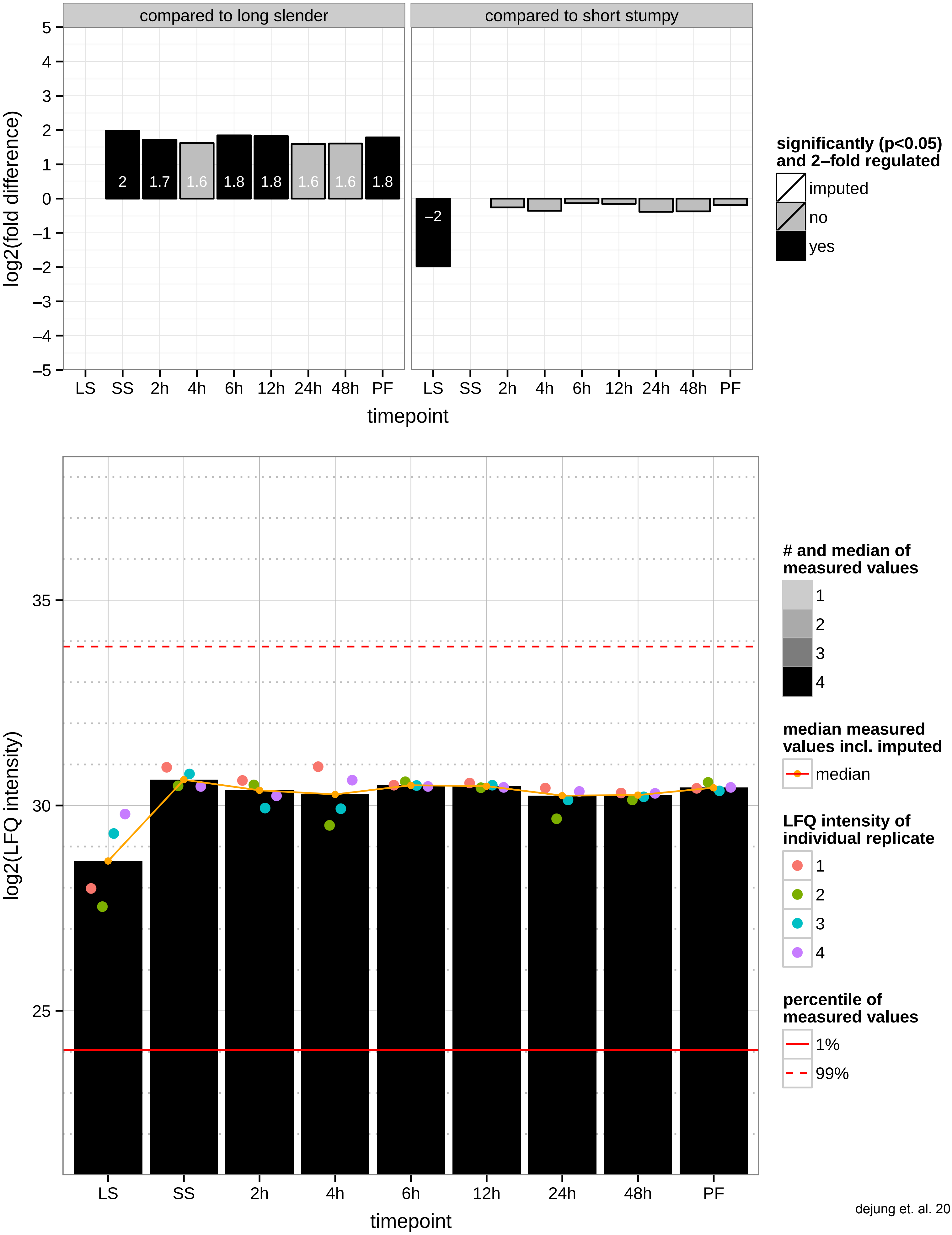
coatomer alpha subunit, putative (TbCoatomerAlpha)
Tb927.4.450
AGOF: structural molecule activity, transporter activity
AGOC: COPI vesicle coat
AGOP: ER to Golgi vesicle−mediated transport, intracellular protein transport
PGOF: protein binding, structural molecule activity
PGOC: COPI vesicle coat, membrane coat
PGOP: intracellular protein transport, vesicle−mediated transport



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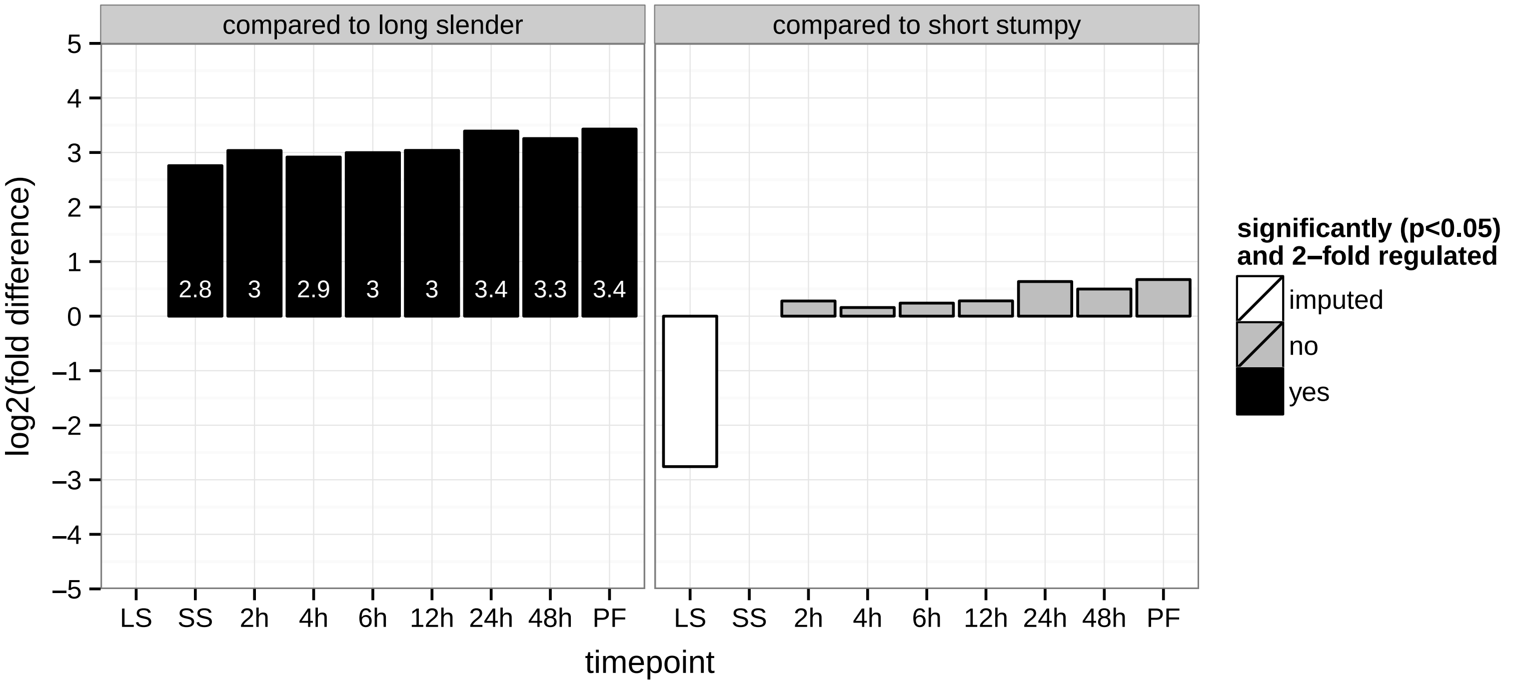
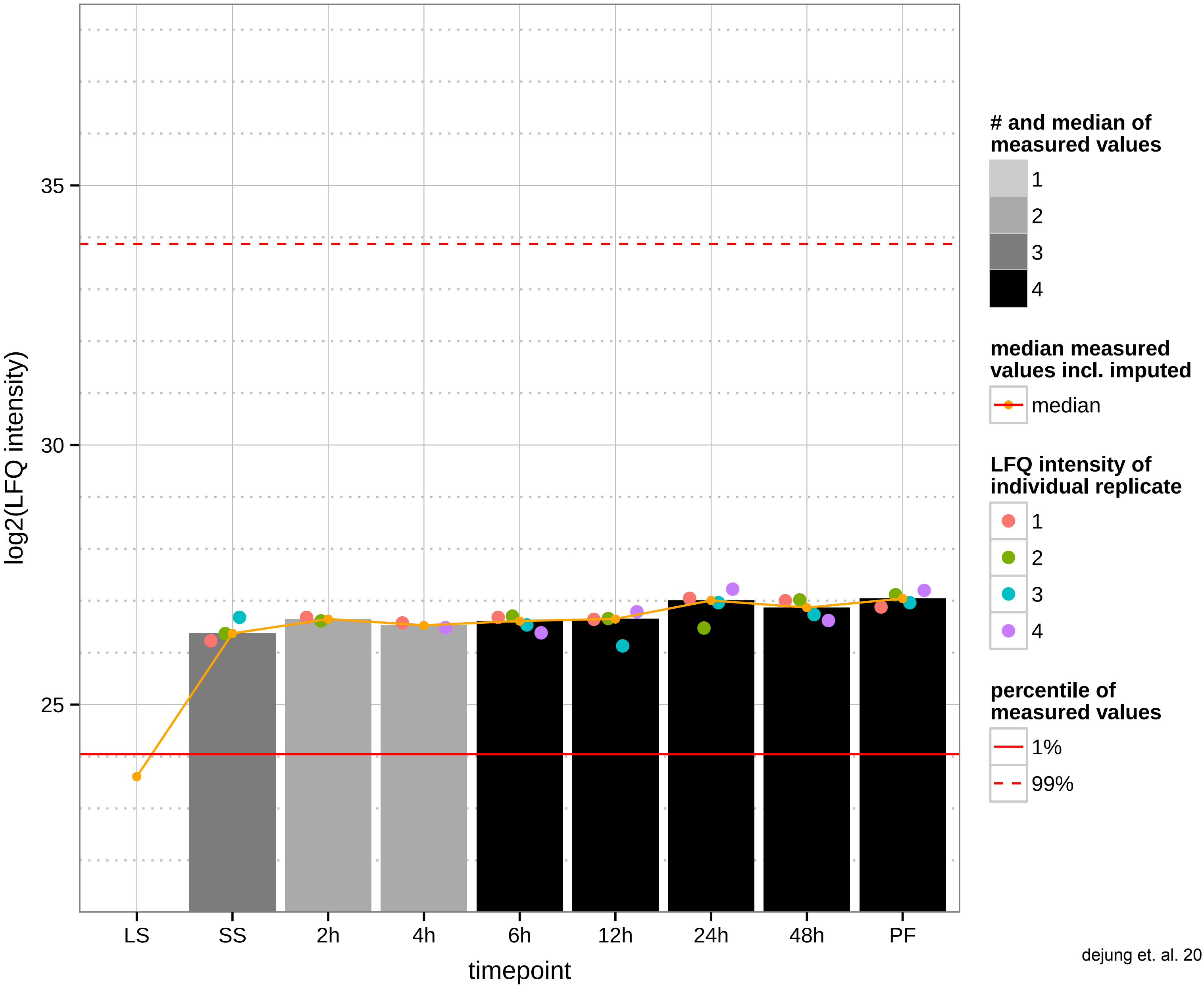
hypothetical protein, conserved
Tb927.4.4550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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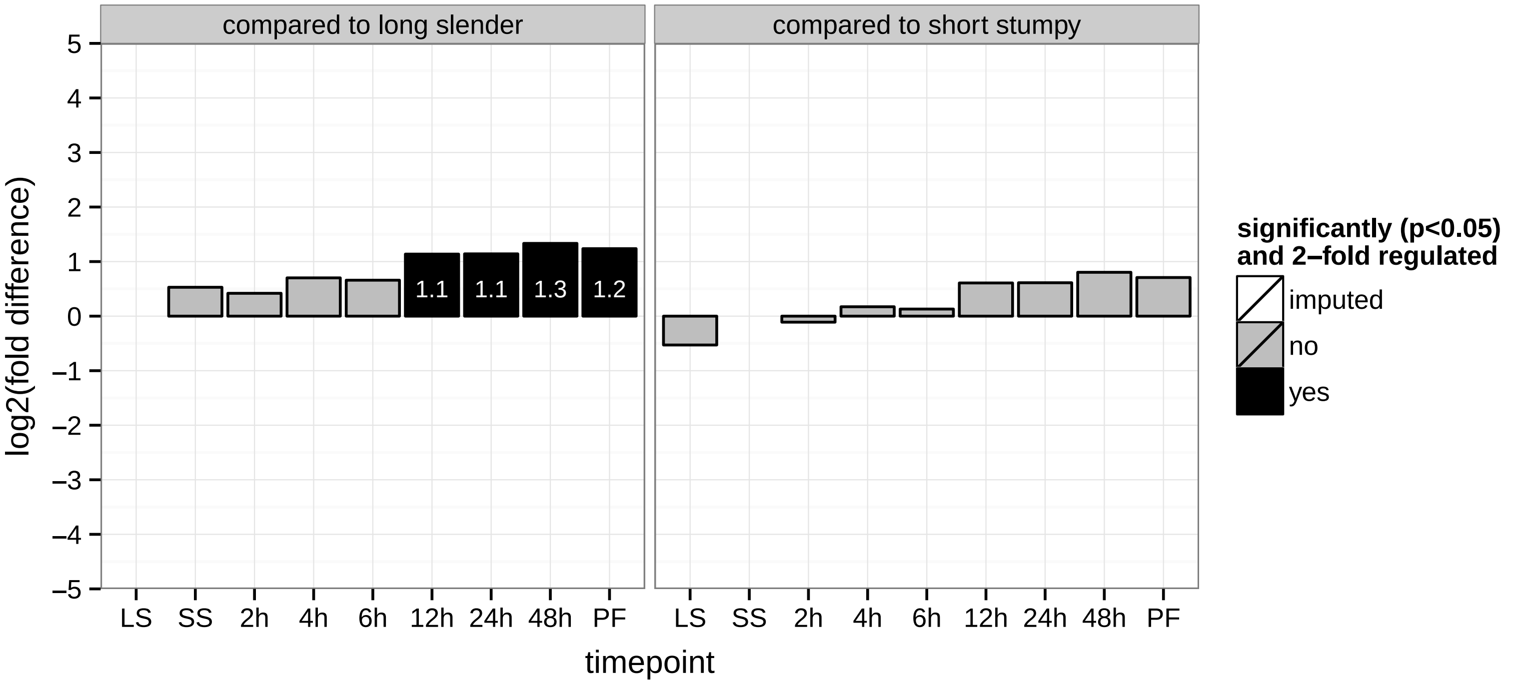
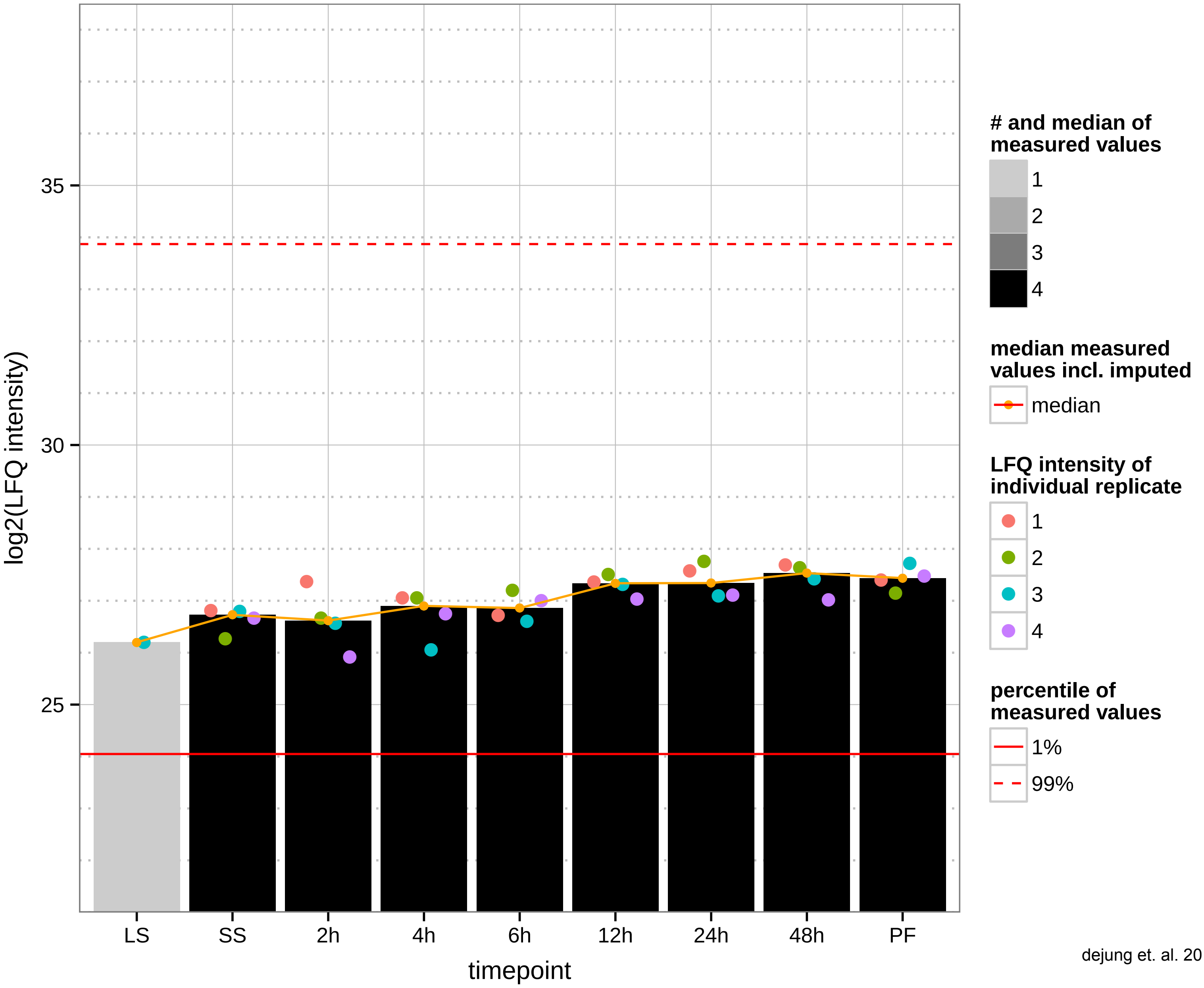
diphthine synthase, putative
Tb927.4.4650
AGOF: diphthine synthase activity
AGOC: null
AGOP: peptidyl–diphthamide biosynthetic process from peptidyl–histidine
PGOF: diphthine synthase activity, methyltransferase activity
PGOC: null
PGOP: metabolic process, peptidyl–diphthamide biosynthetic process from peptidyl–histidine





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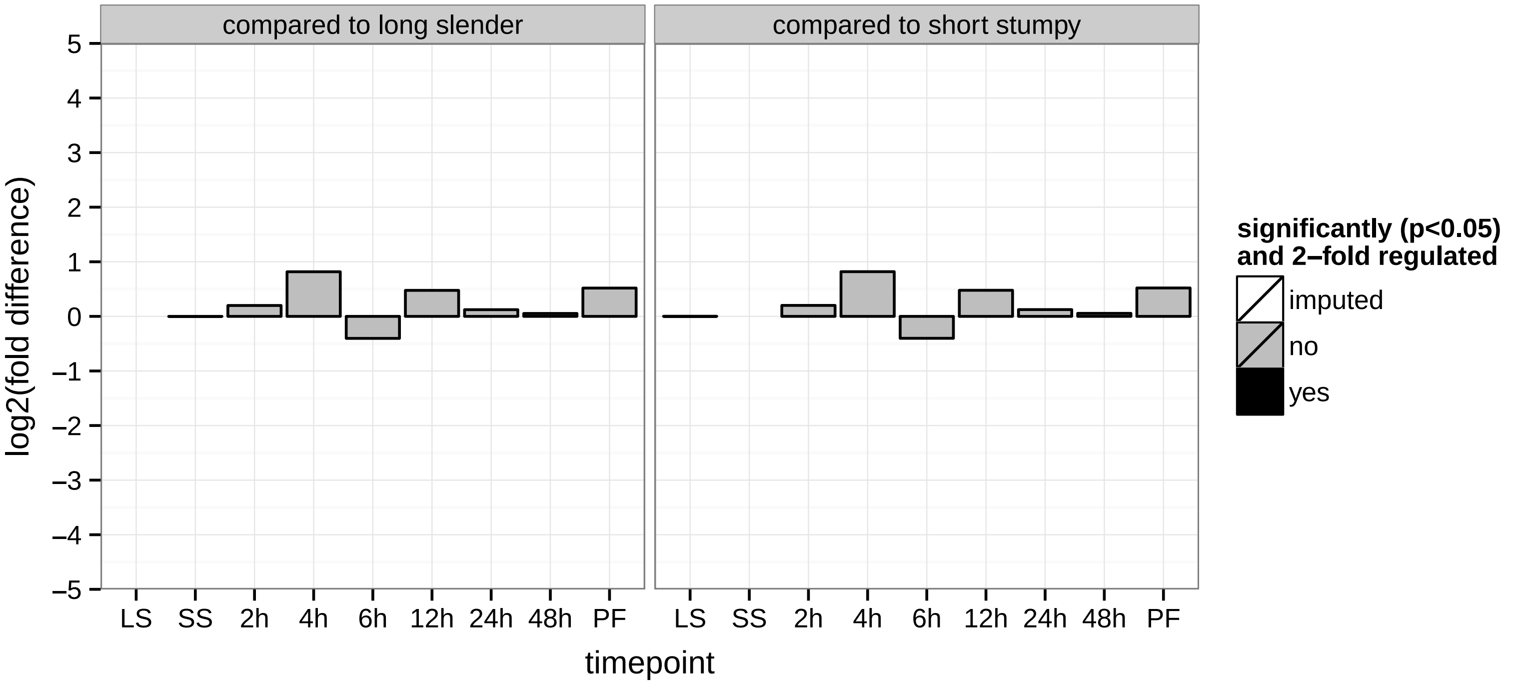
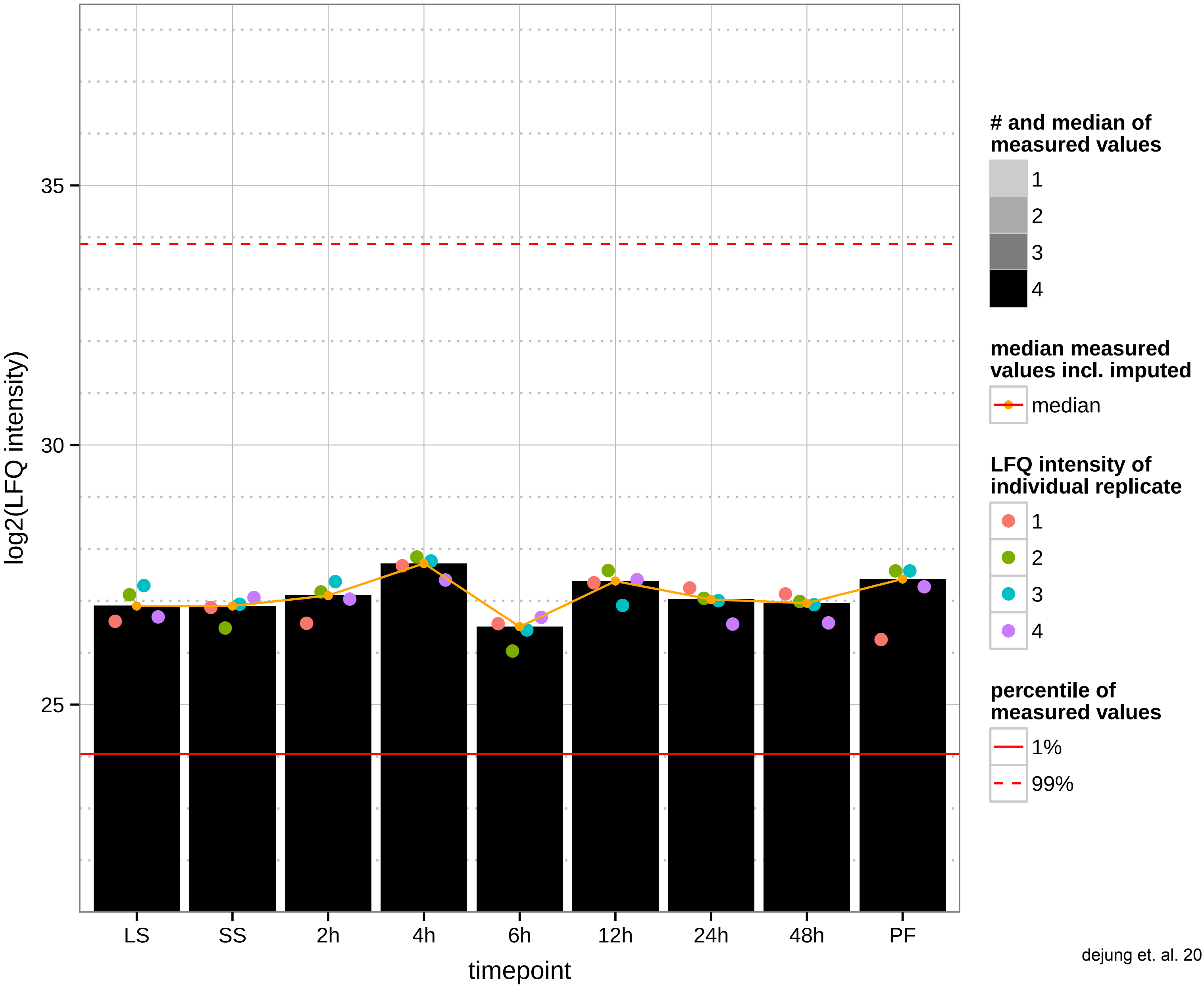
hypothetical protein, conserved
Tb927.4.4660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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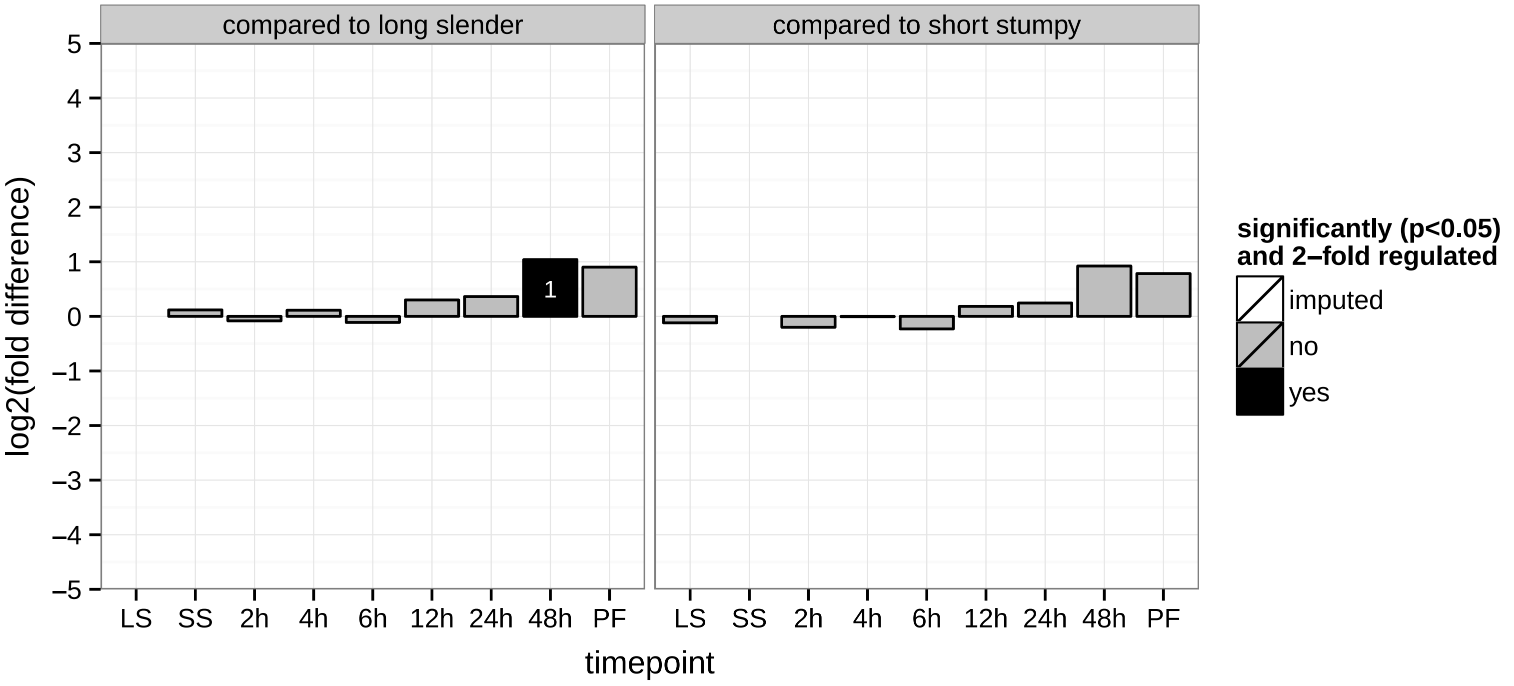
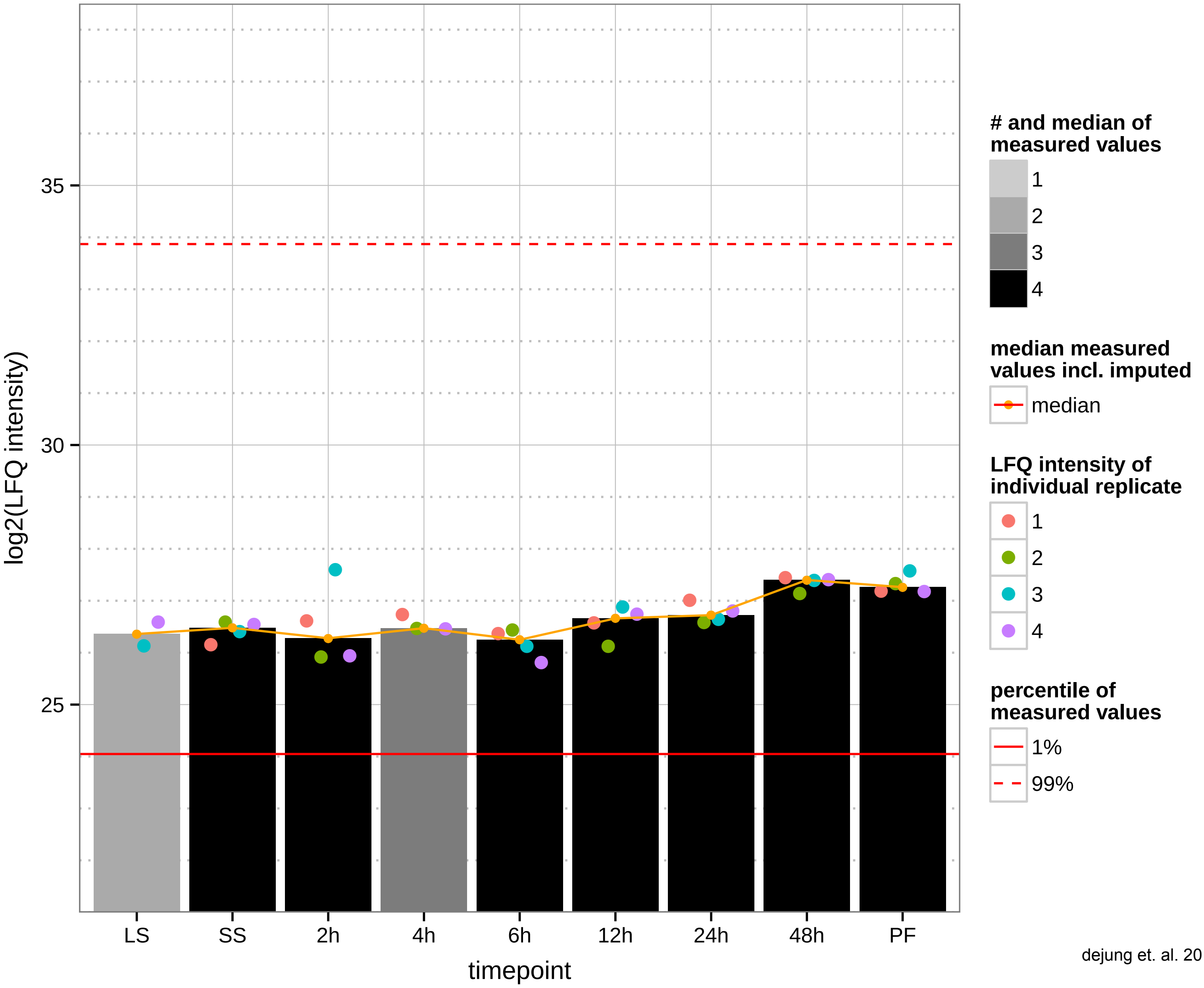
hypothetical protein, conserved
Tb927.4.4670
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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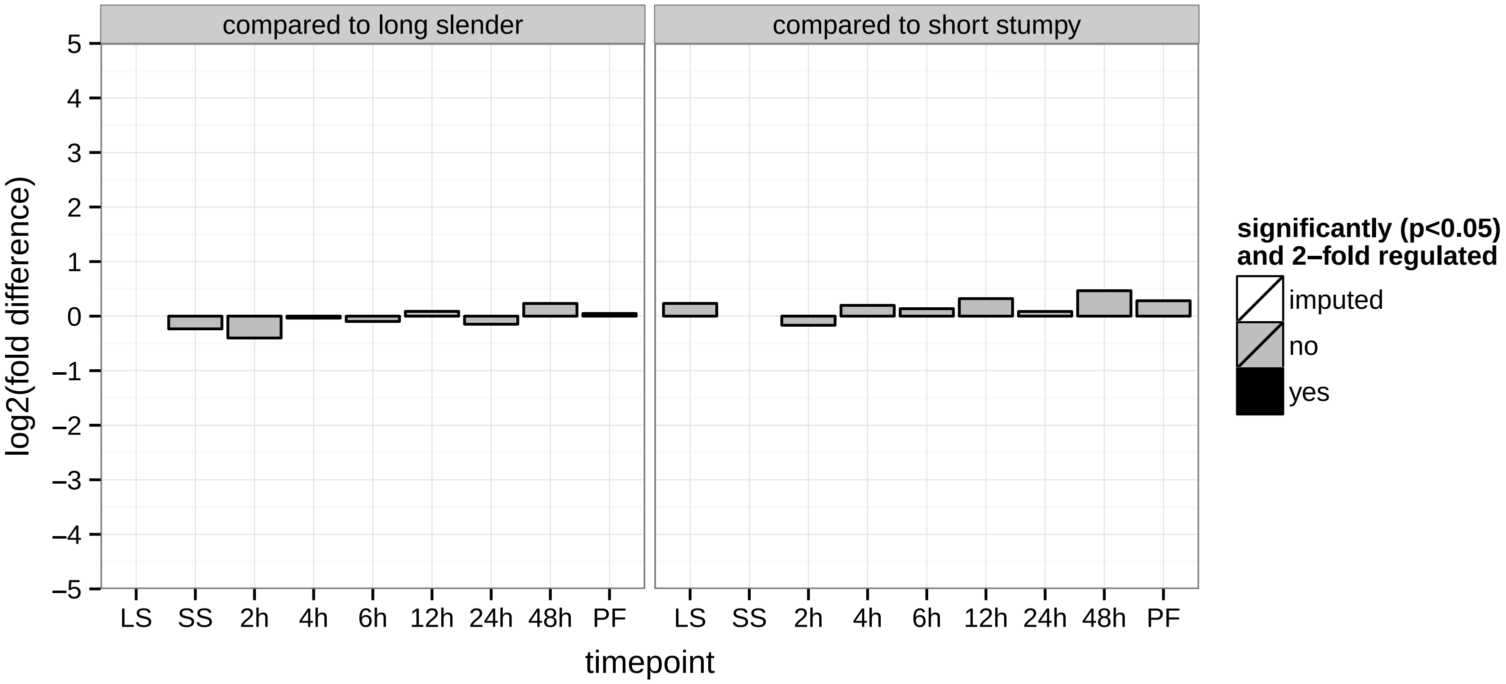
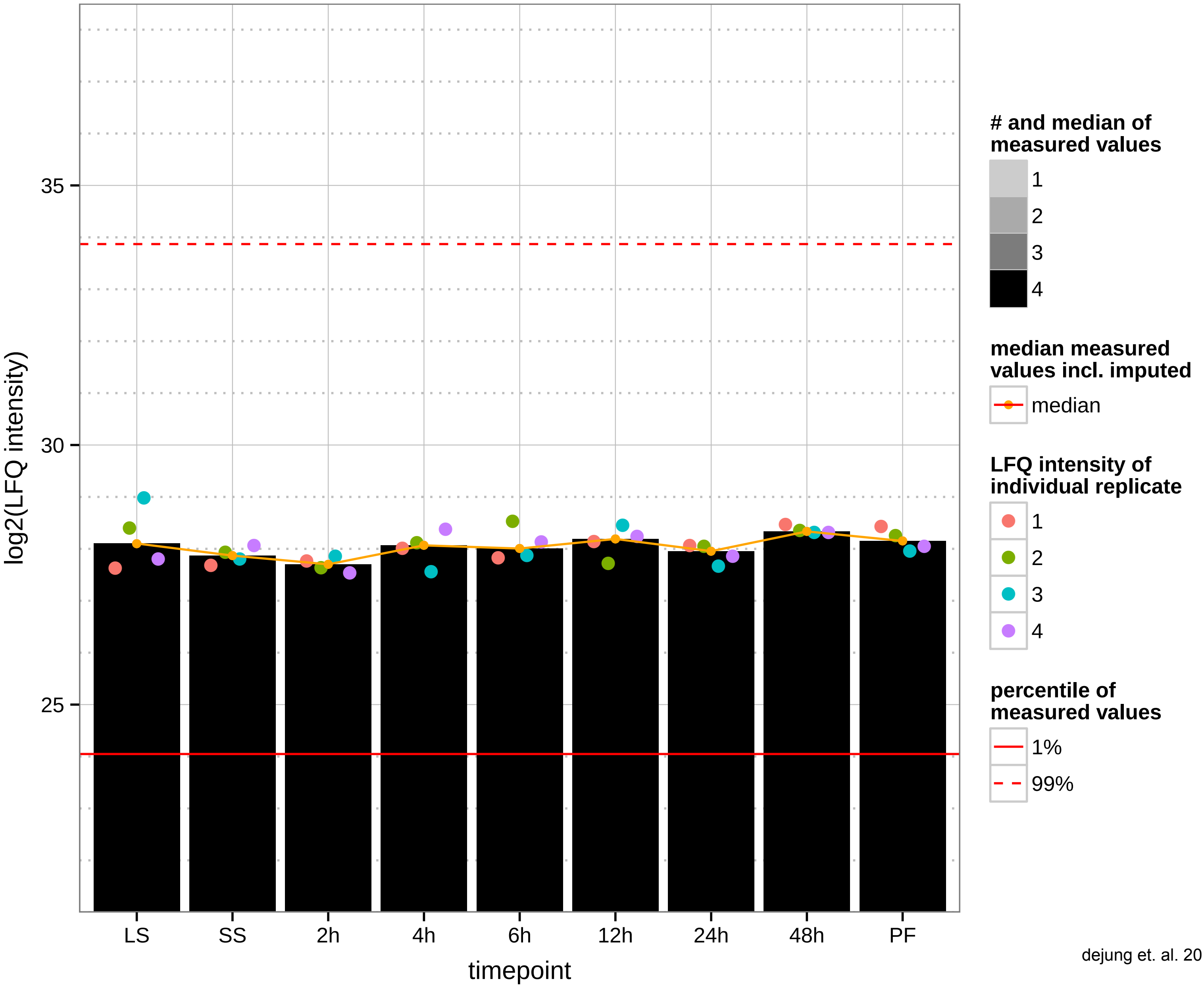
hypothetical protein, conserved
Tb927.4.4690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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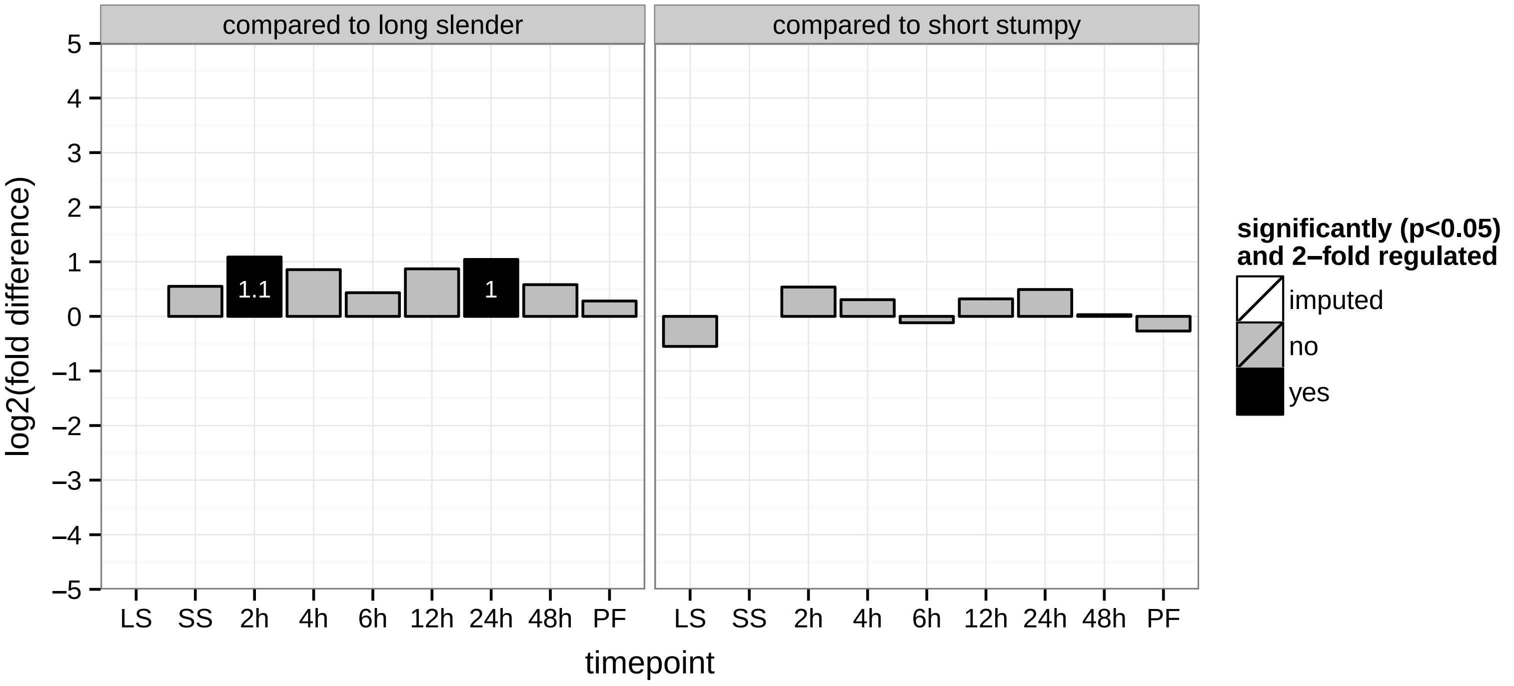
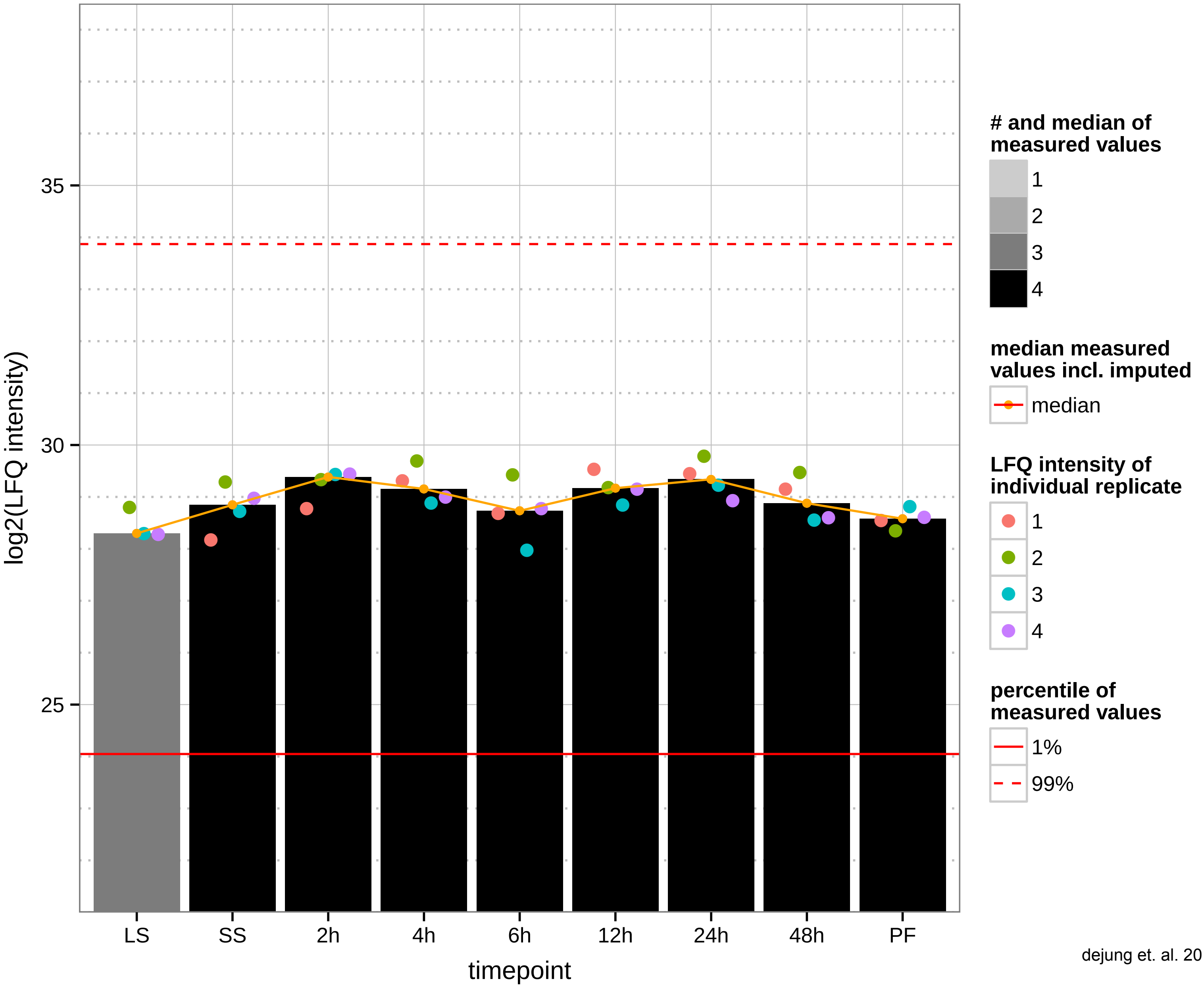
snoRNP protein GAR1, putative
Tb927.4.470
AGOF: rRNA binding
AGOC: small nucleolar ribonucleoprotein complex
AGOP: rRNA processing
PGOF: pseudouridine synthase activity, snoRNA binding
PGOC: box H/ACA snoRNP complex
PGOP: ribosome biogenesis, snRNA pseudouridine synthesis





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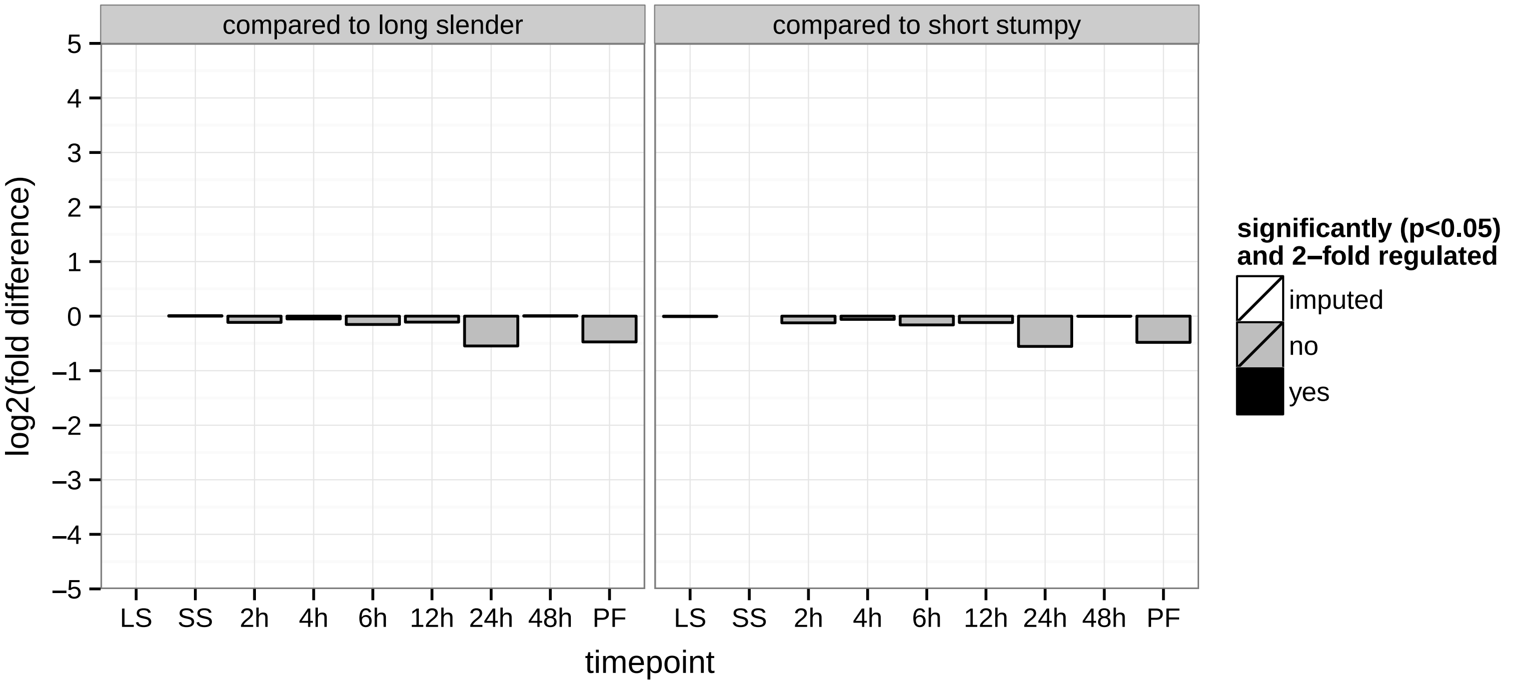
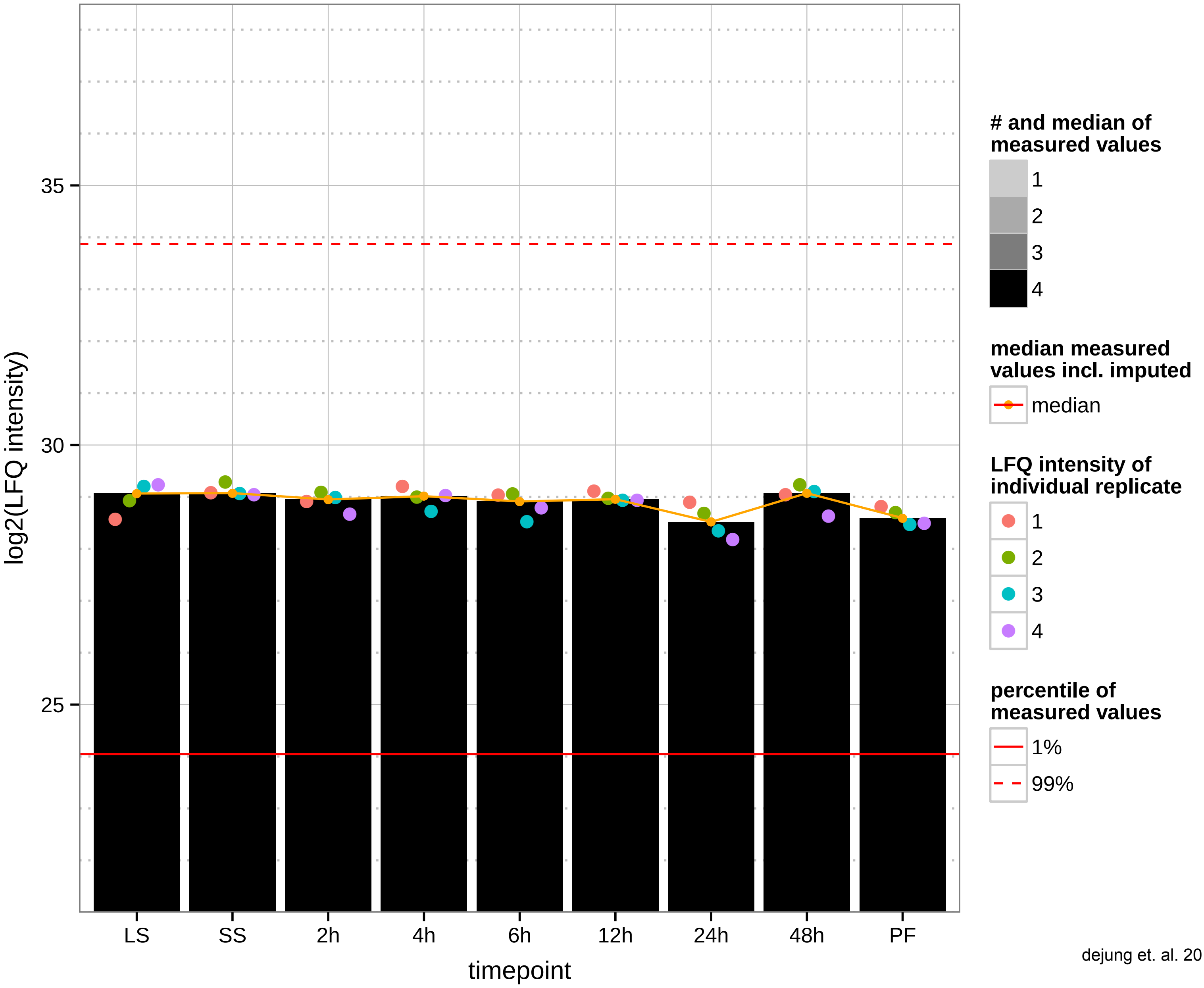
hypothetical protein, conserved
Tb927.4.4700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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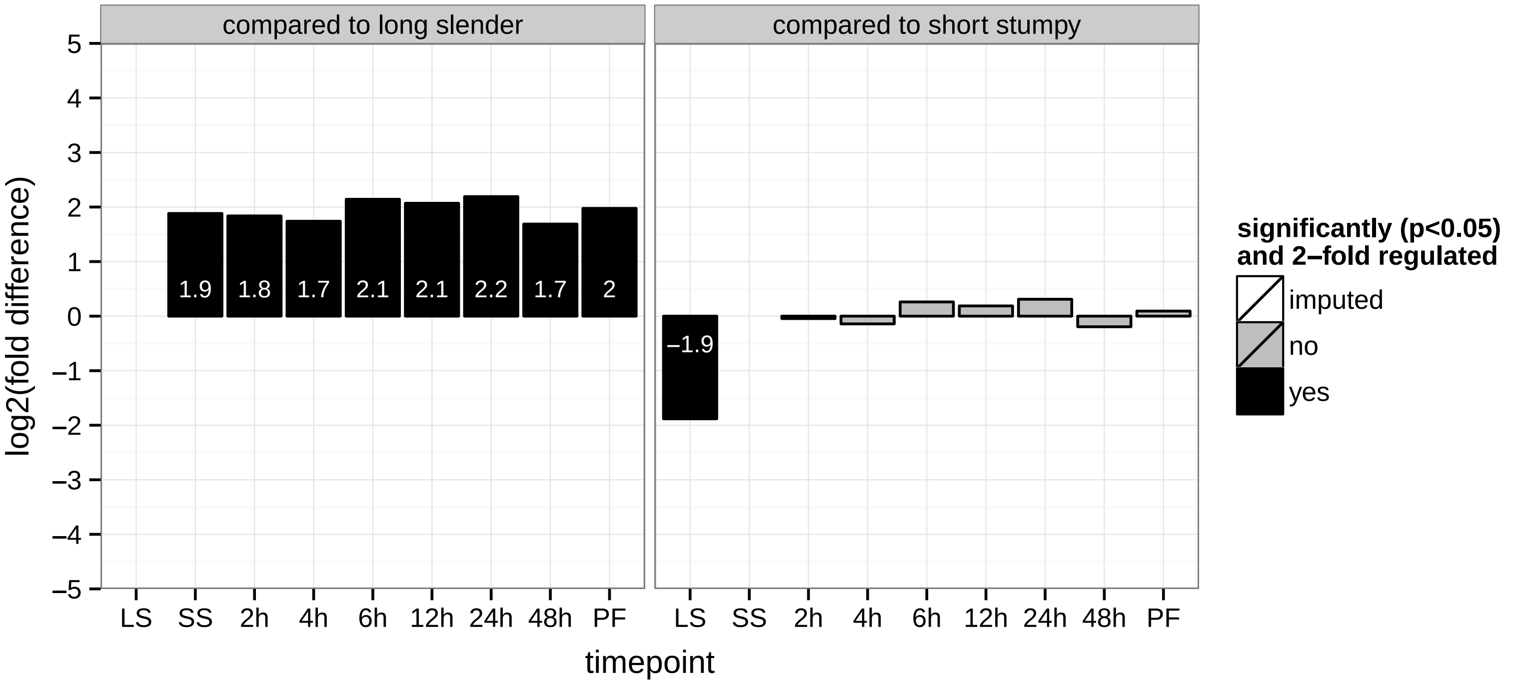
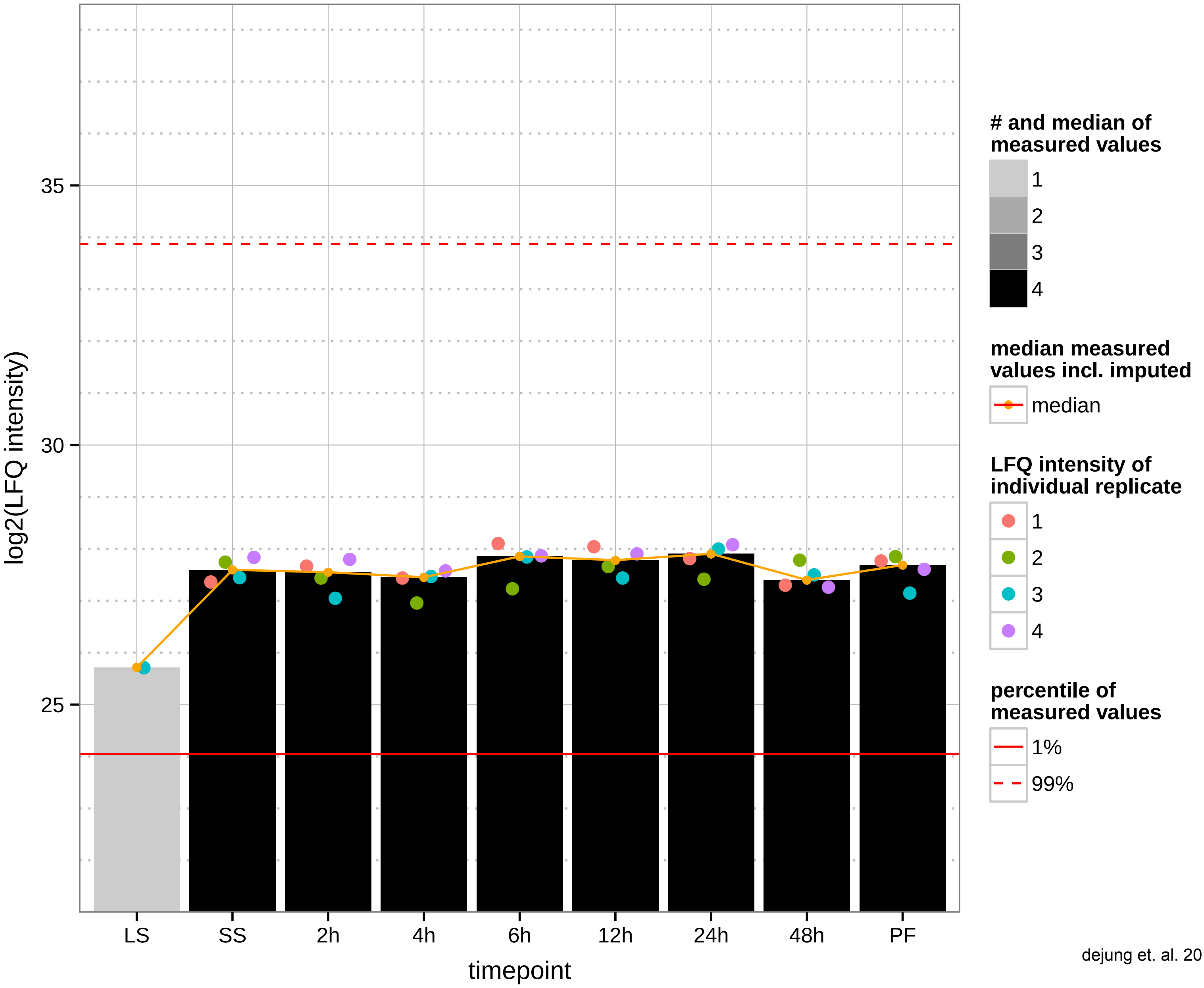
hypothetical protein, conserved
Tb927.4.4950;Tb927.8.7470
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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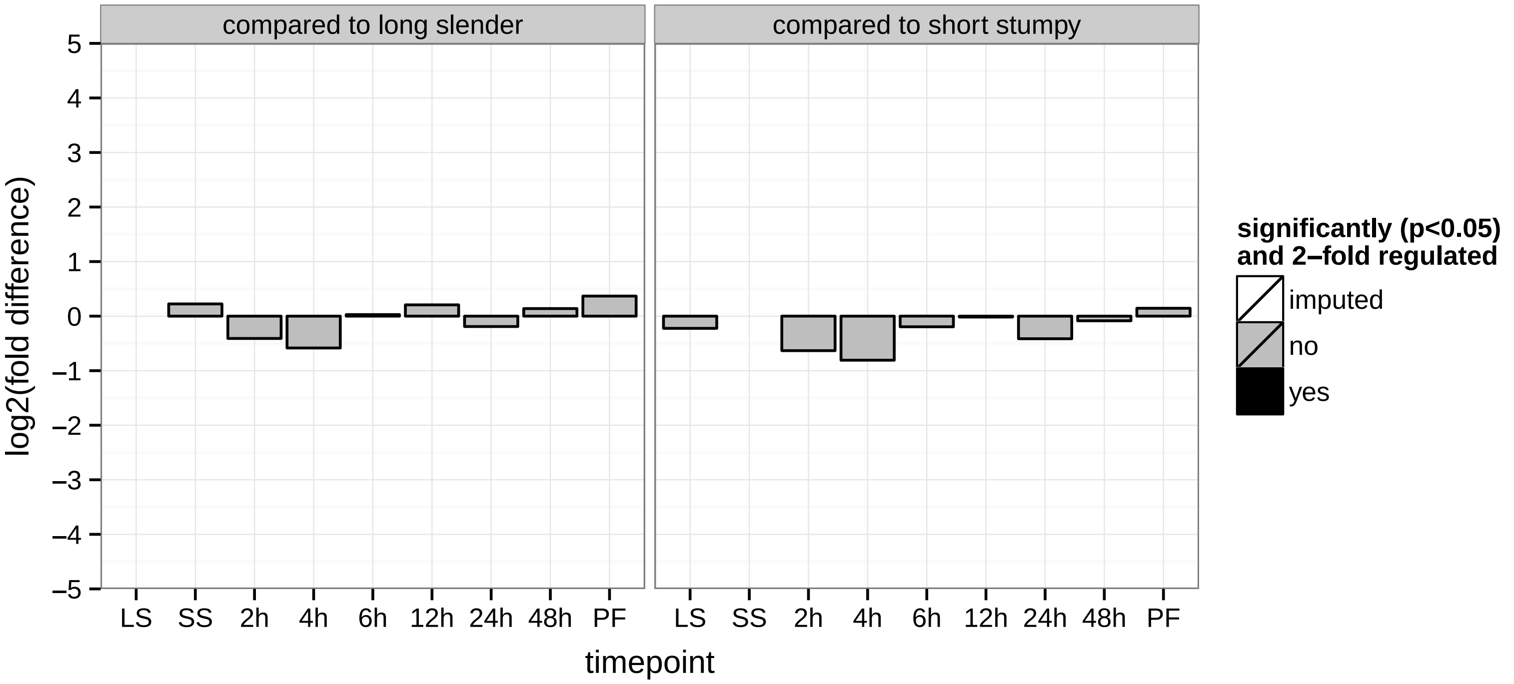
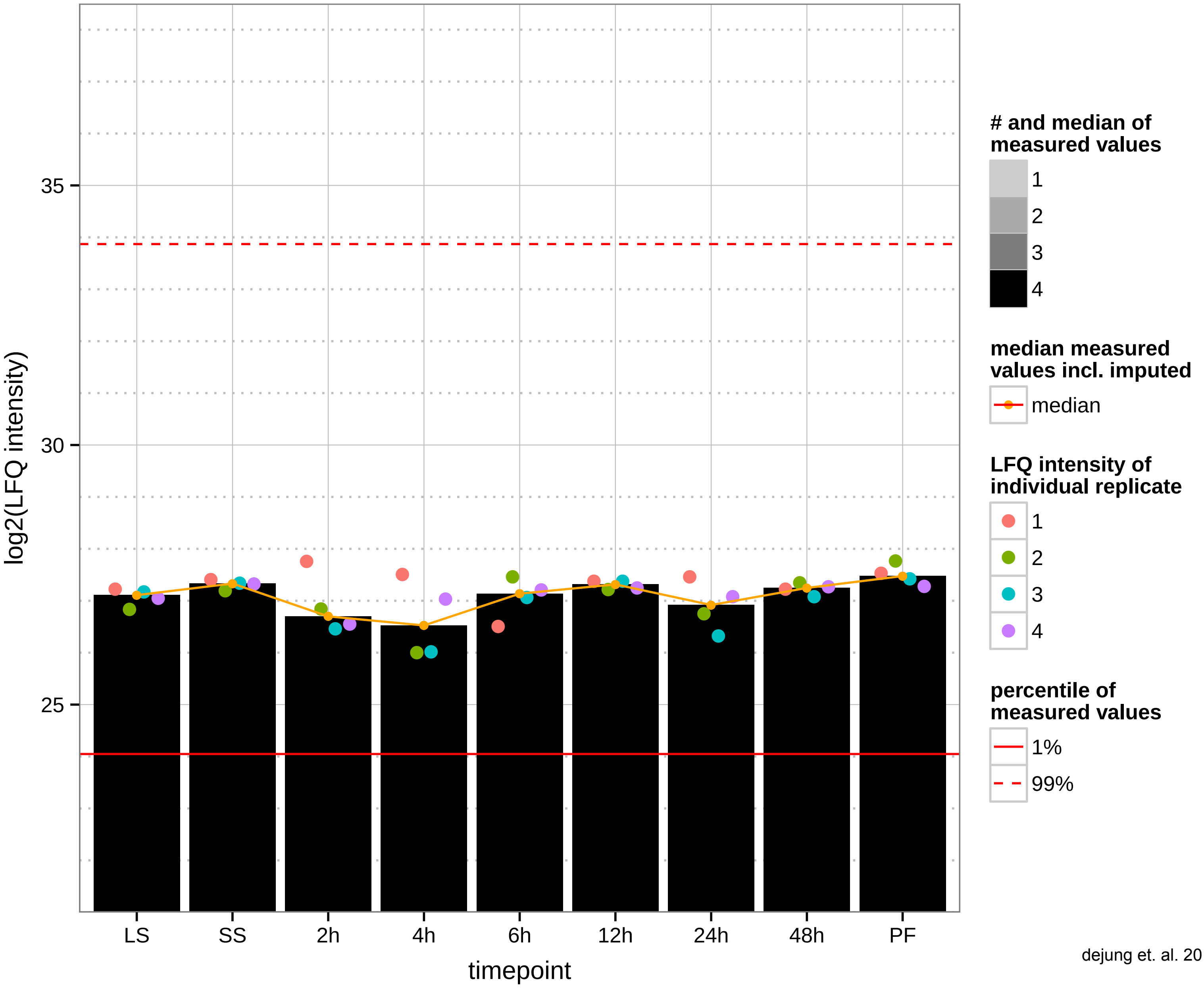
hypothetical protein, conserved
Tb927.4.5000;Tb927.8.7420
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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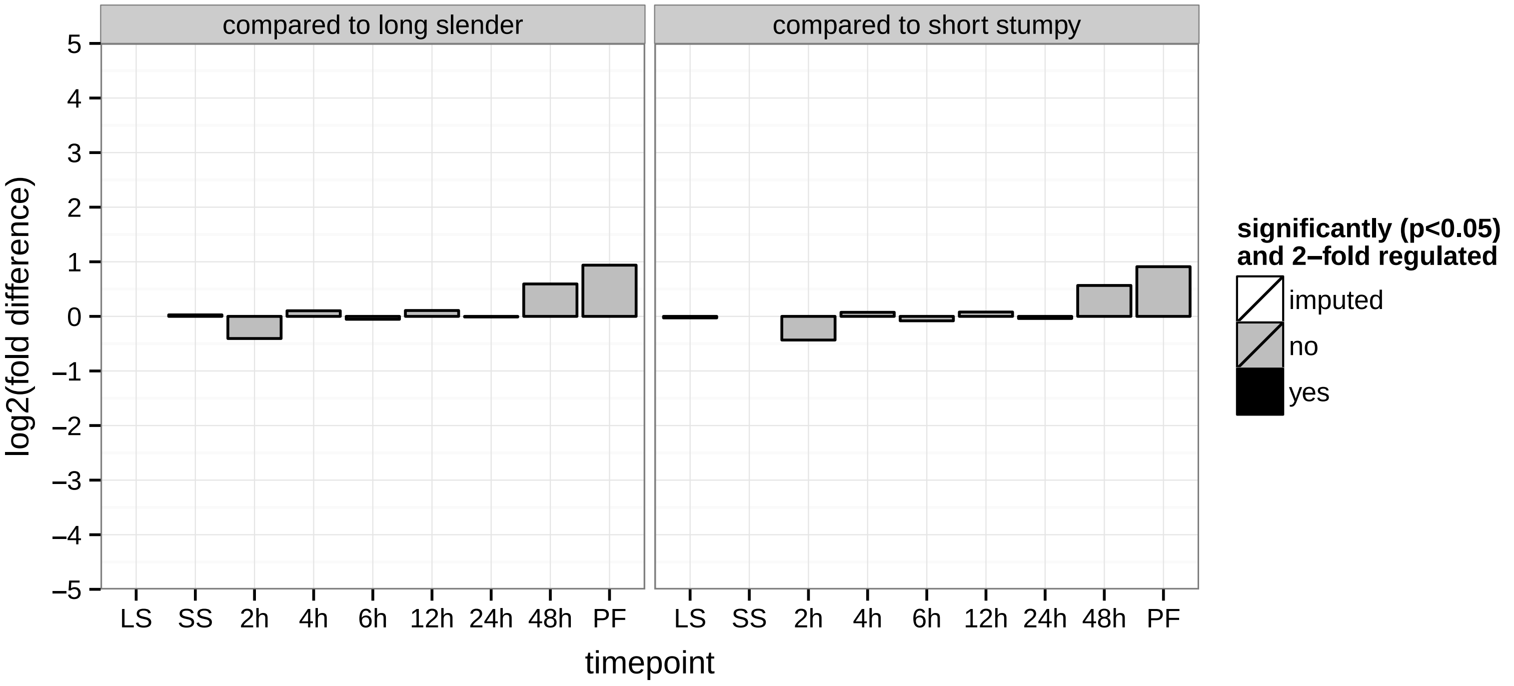
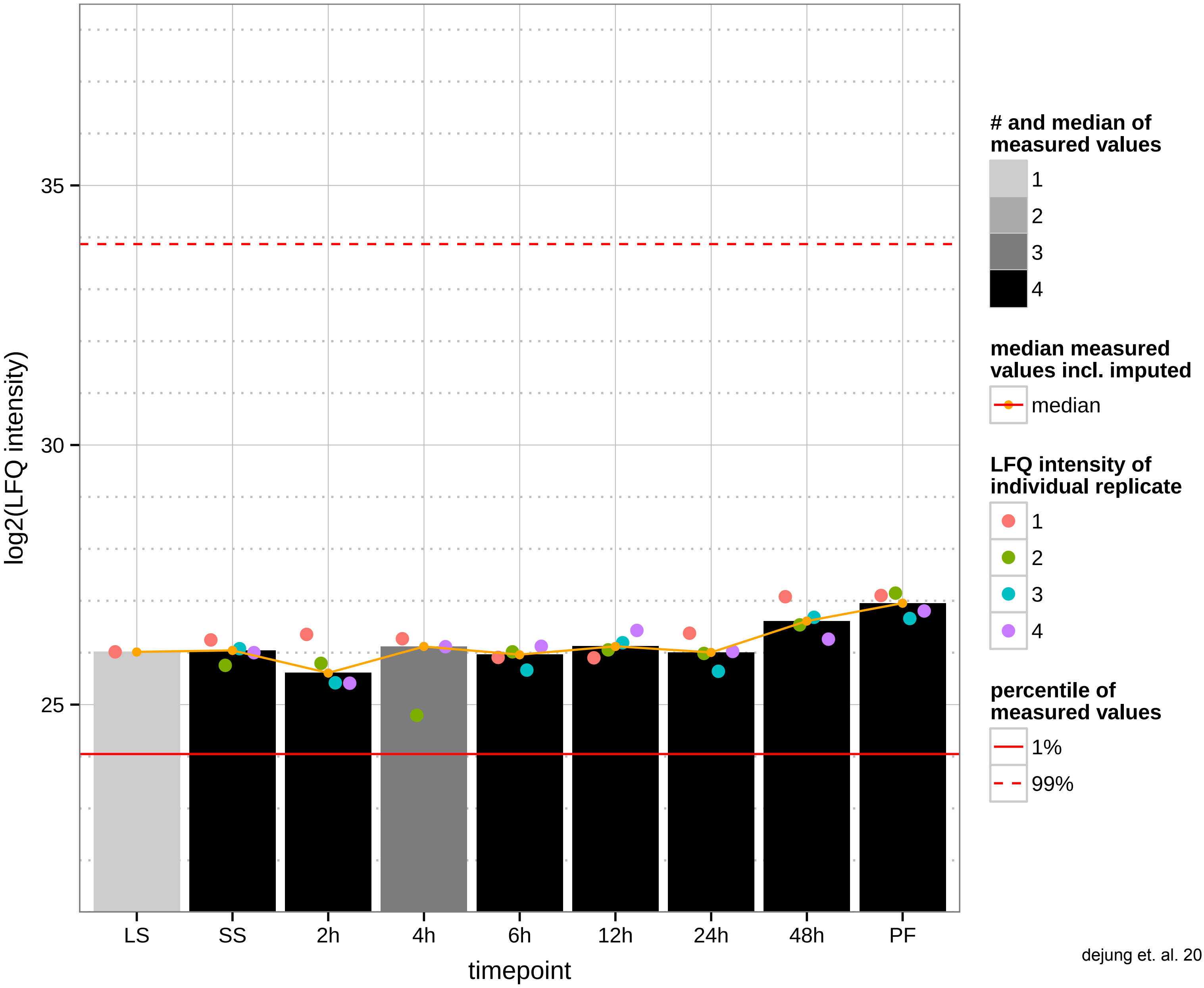
dihydrolipoamide dehydrogenase, putative
Tb927.4.5040
AGOF: dihydrolipoyl dehydrogenase activity, flavin adenine dinucleotide binding
AGOC: cytoplasm
AGOP: cell redox homeostasis
PGOF: flavin adenine dinucleotide binding, oxidoreductase activity
PGOC: cytoplasm
PGOP: cell redox homeostasis, oxidation–reduction process





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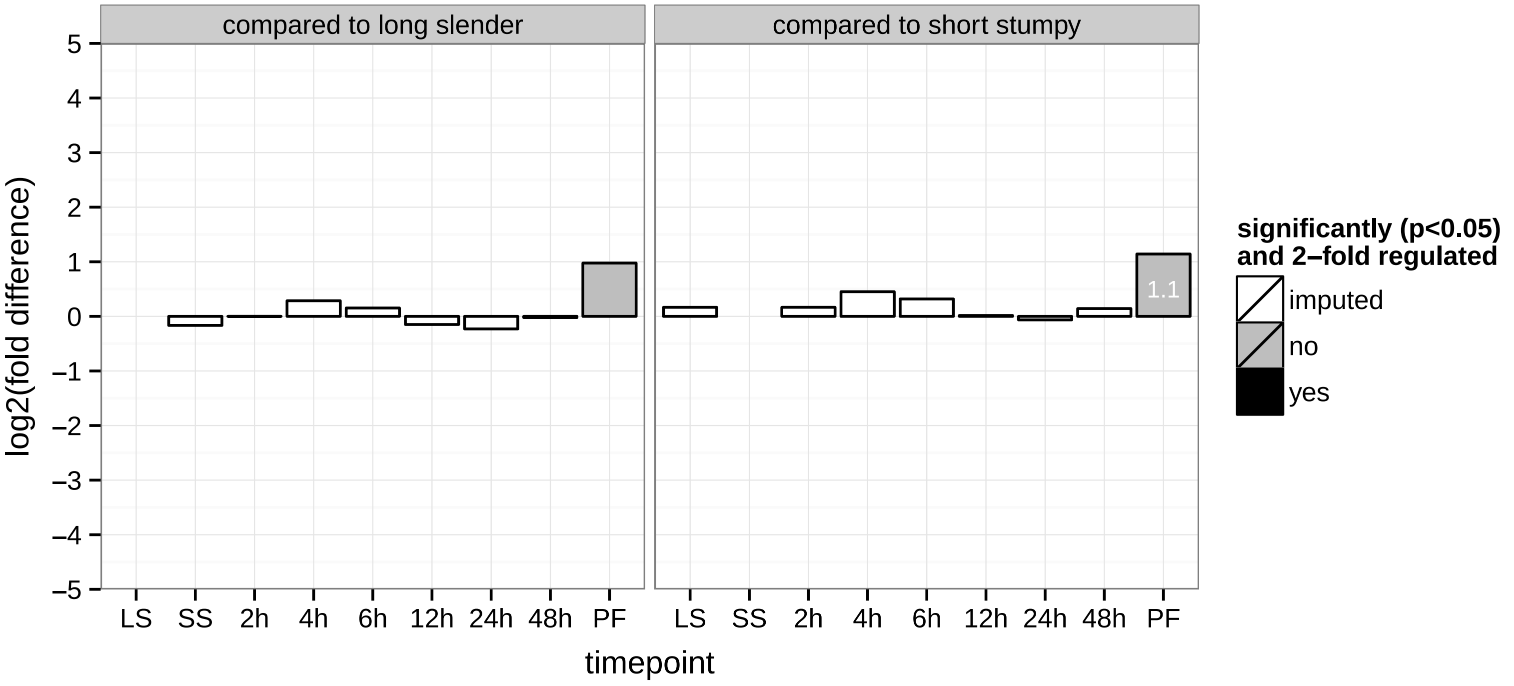
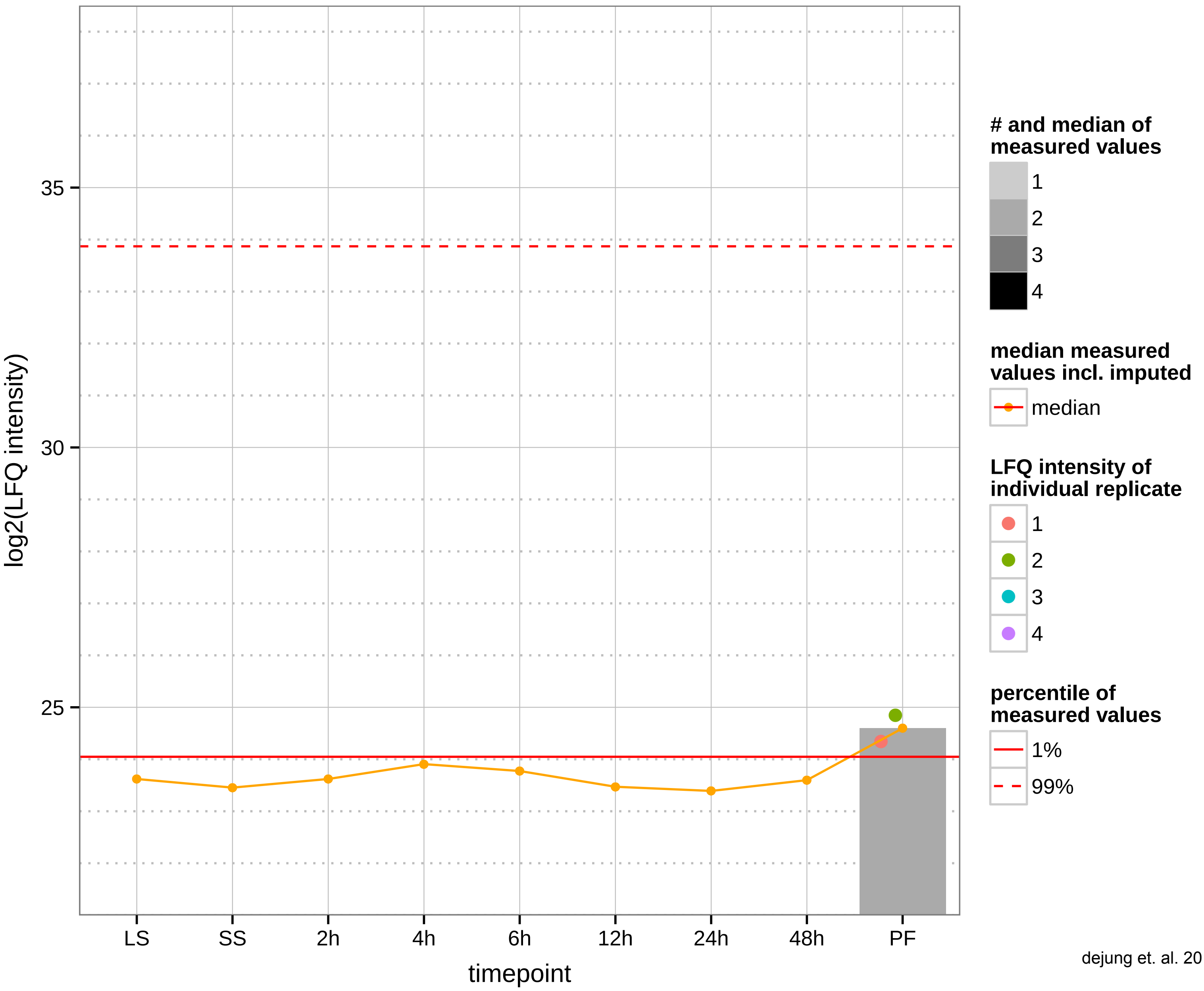
hypothetical protein, conserved
Tb927.4.5130
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: RNA binding
PGOC: null
PGOP: null





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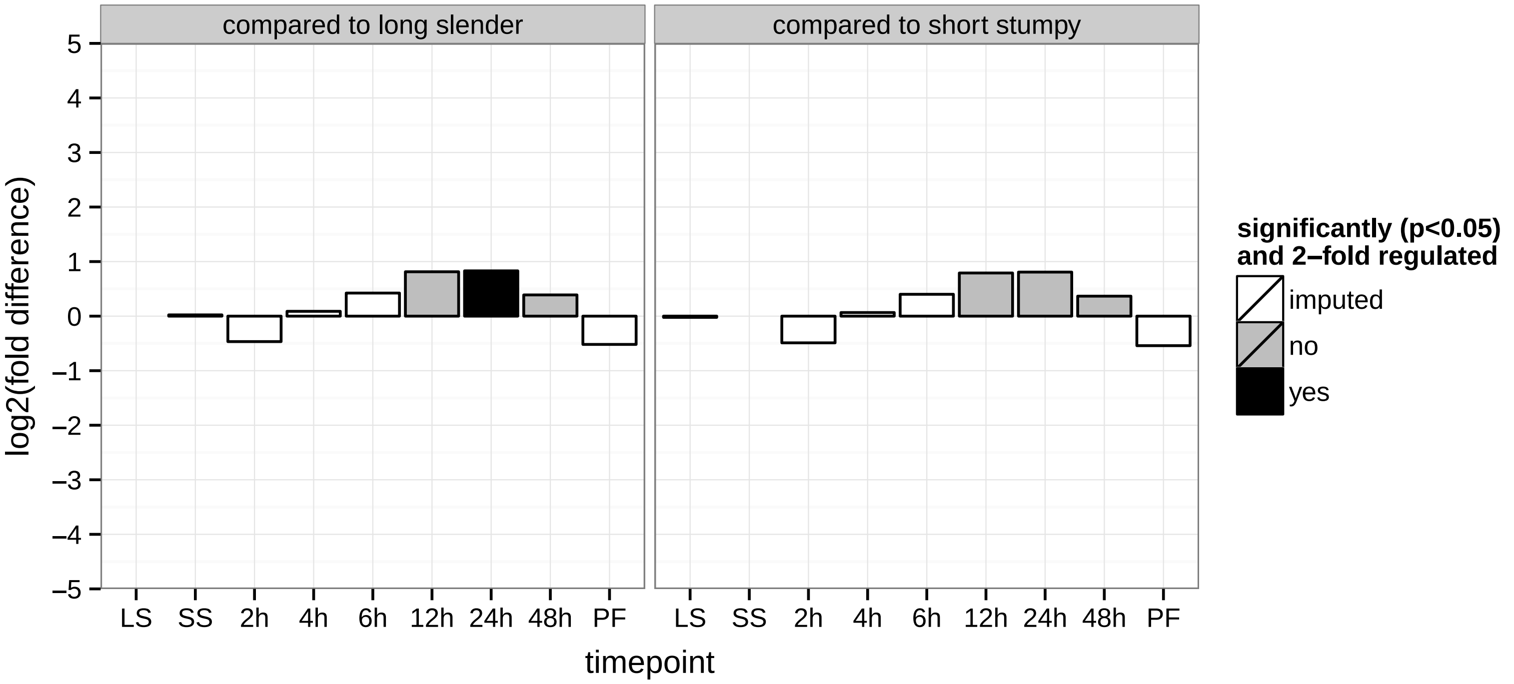
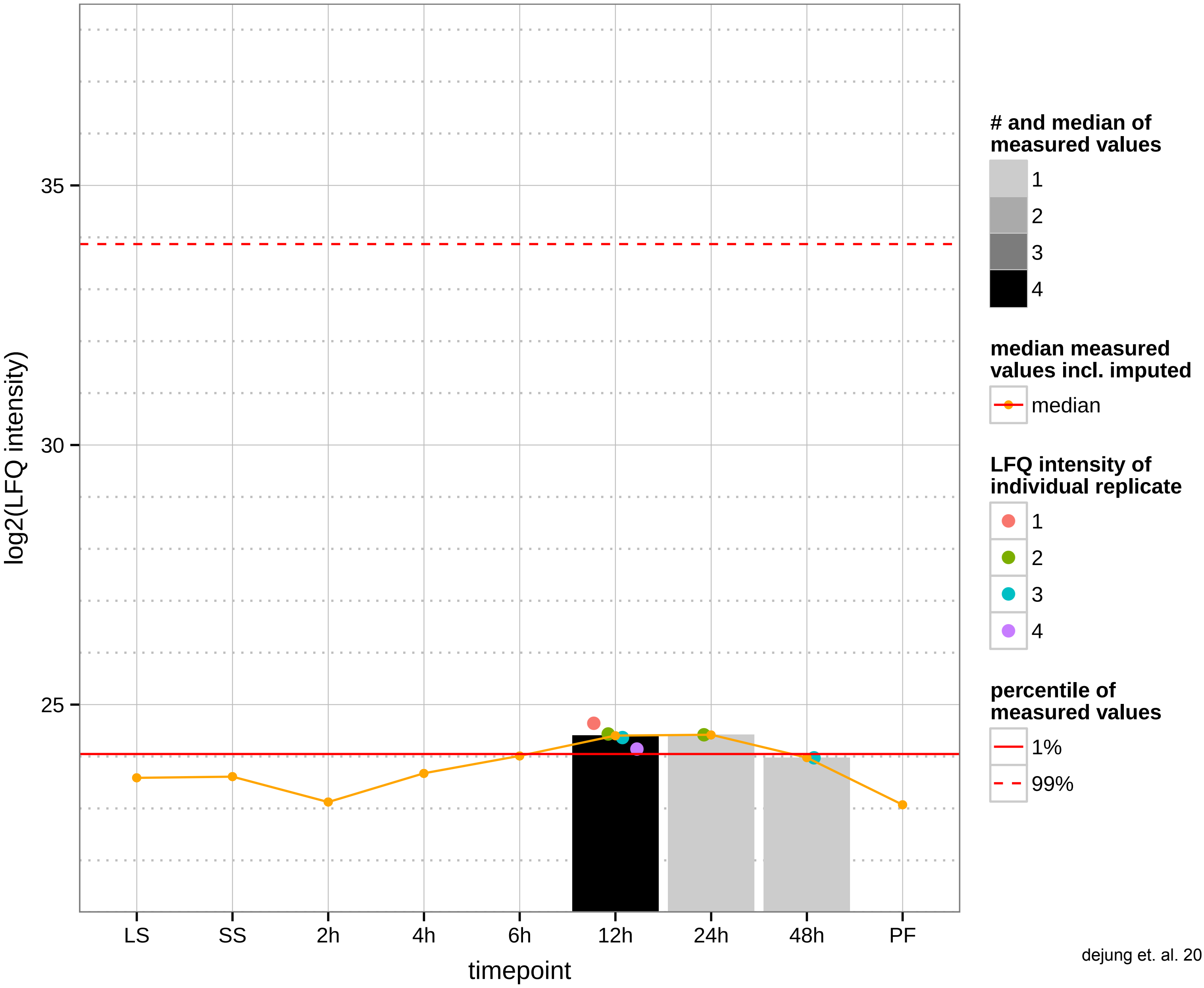
hypothetical protein, conserved
Tb927.4.520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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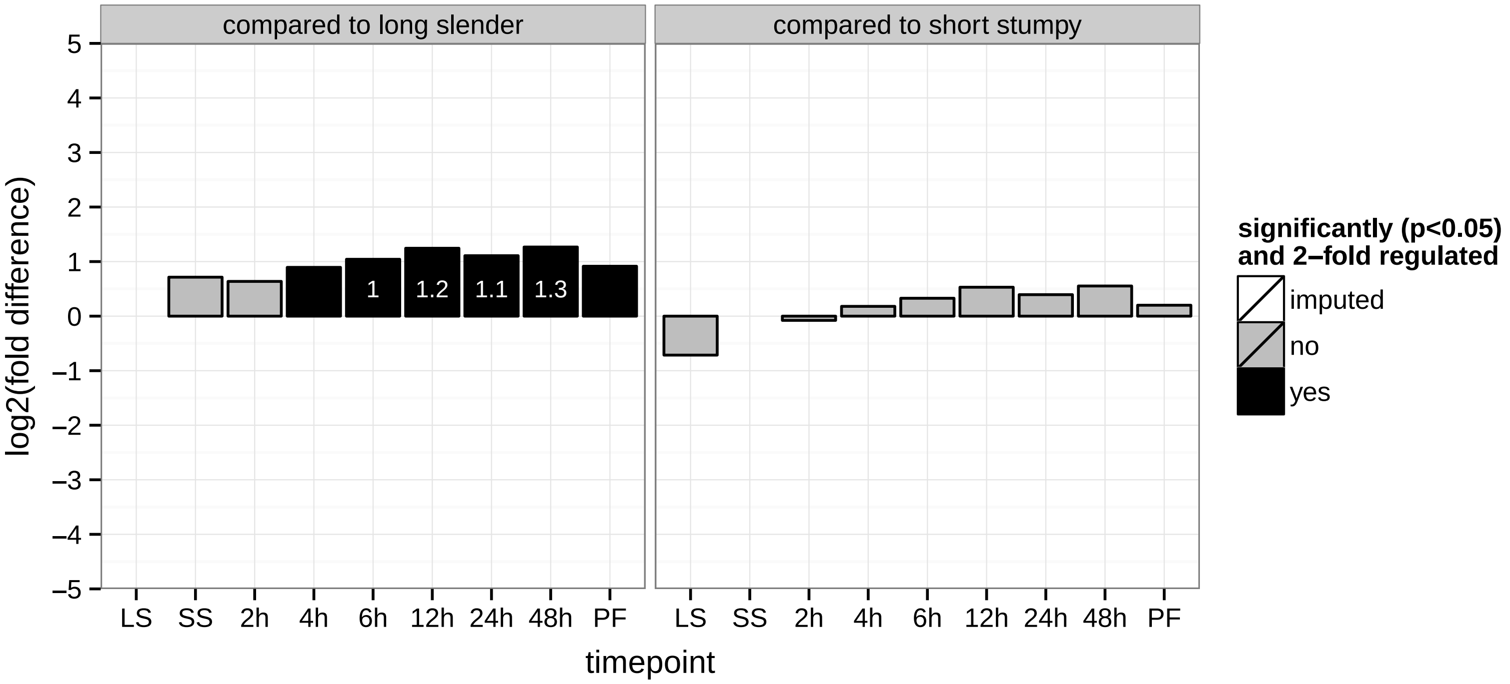
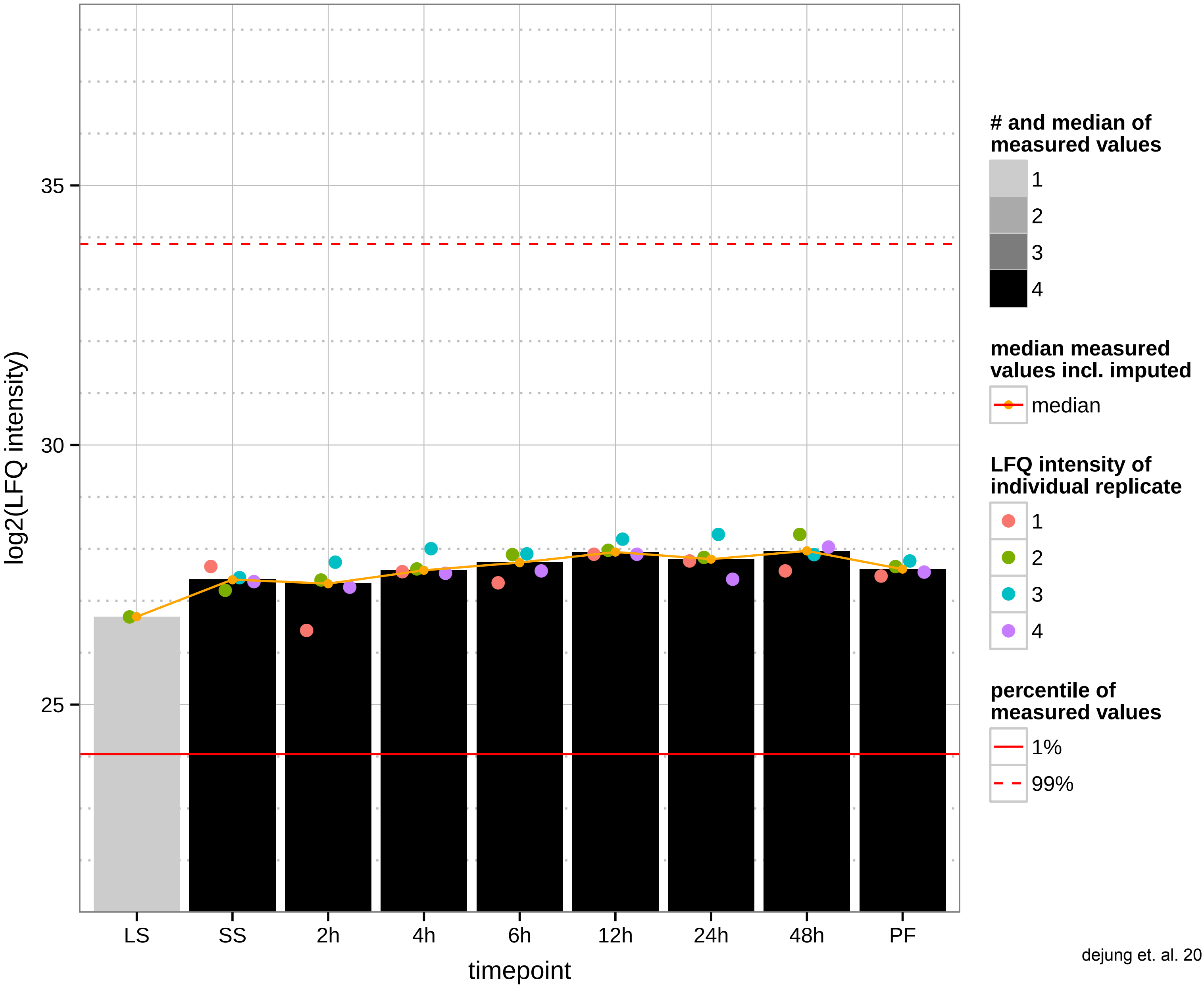
nucleoporin (NUP54/57), putative (TbNup62)
Tb927.4.5200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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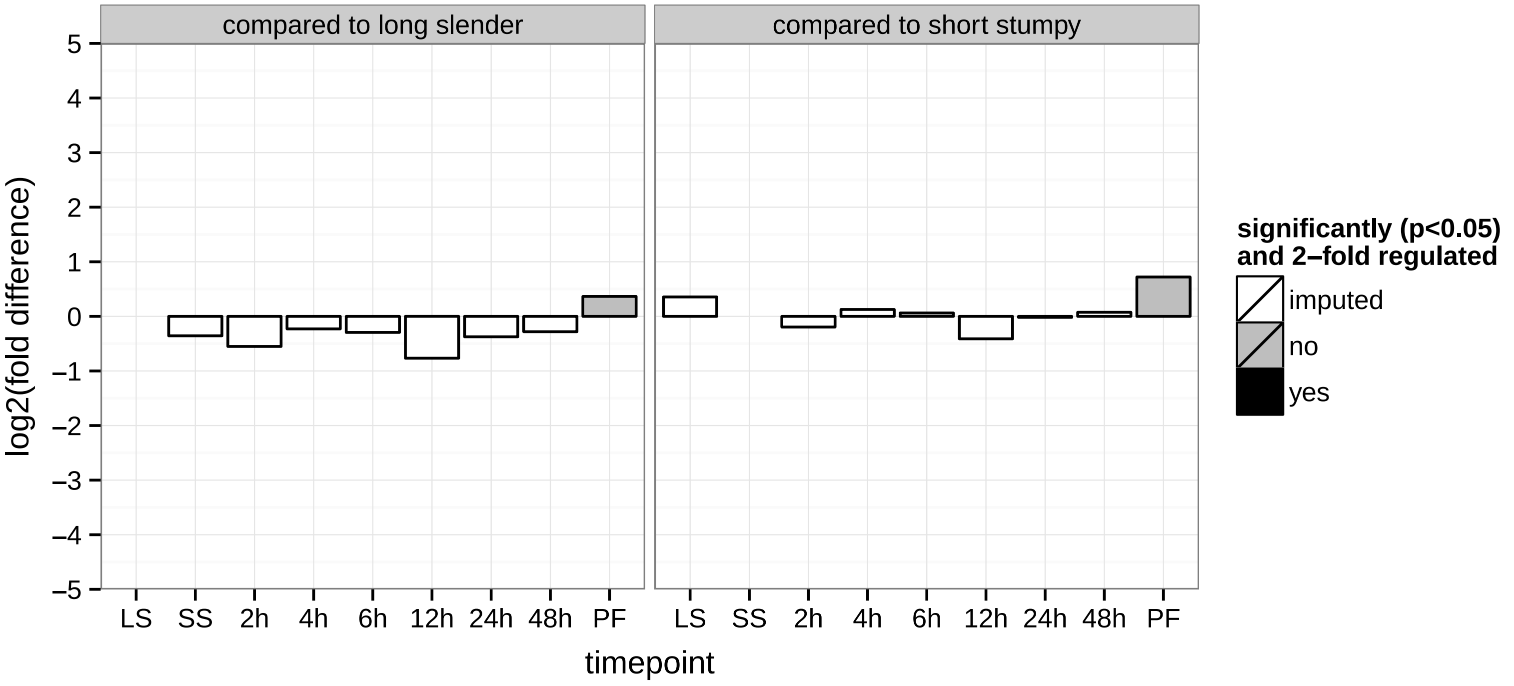
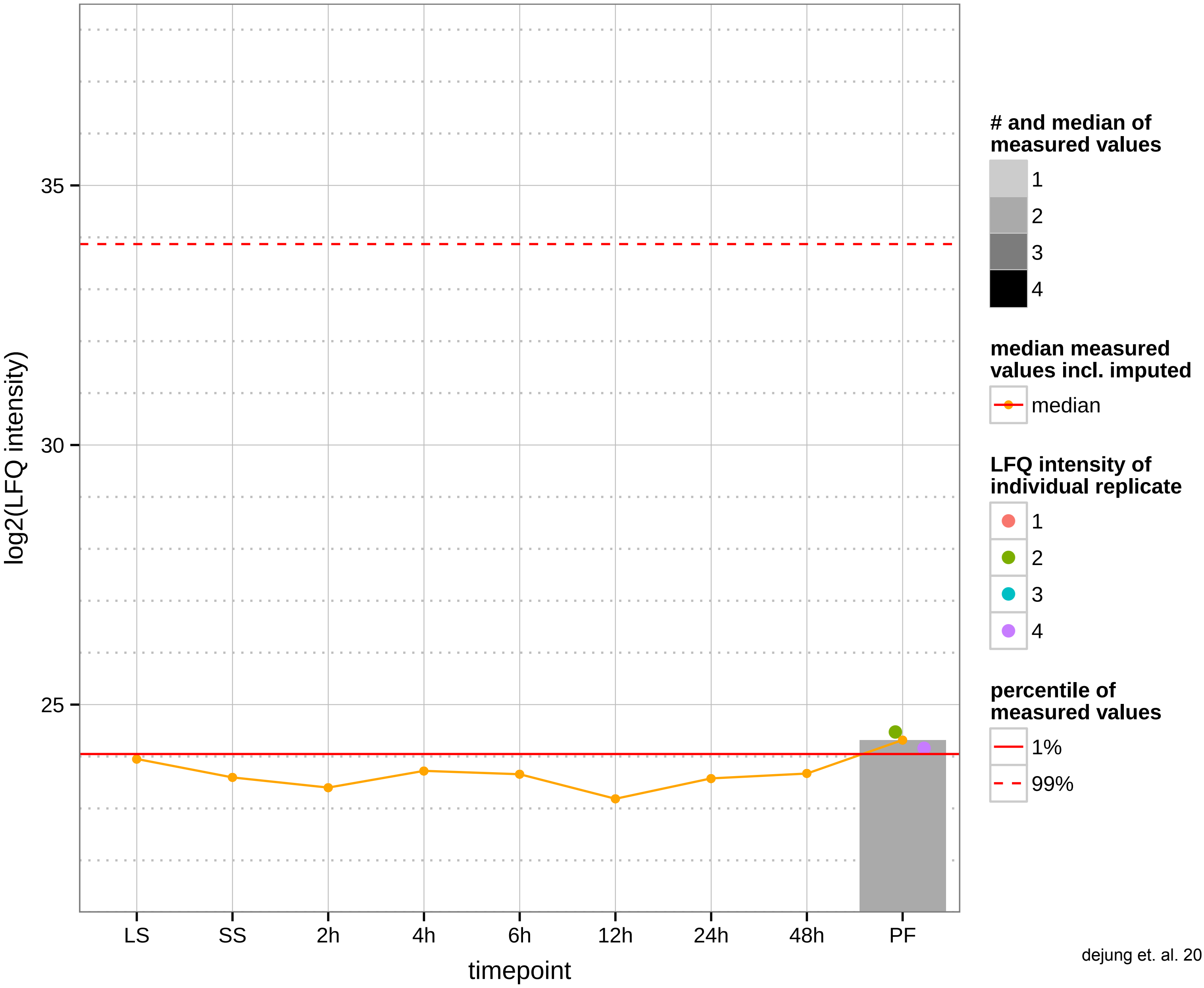
hypothetical protein
Tb927.4.5220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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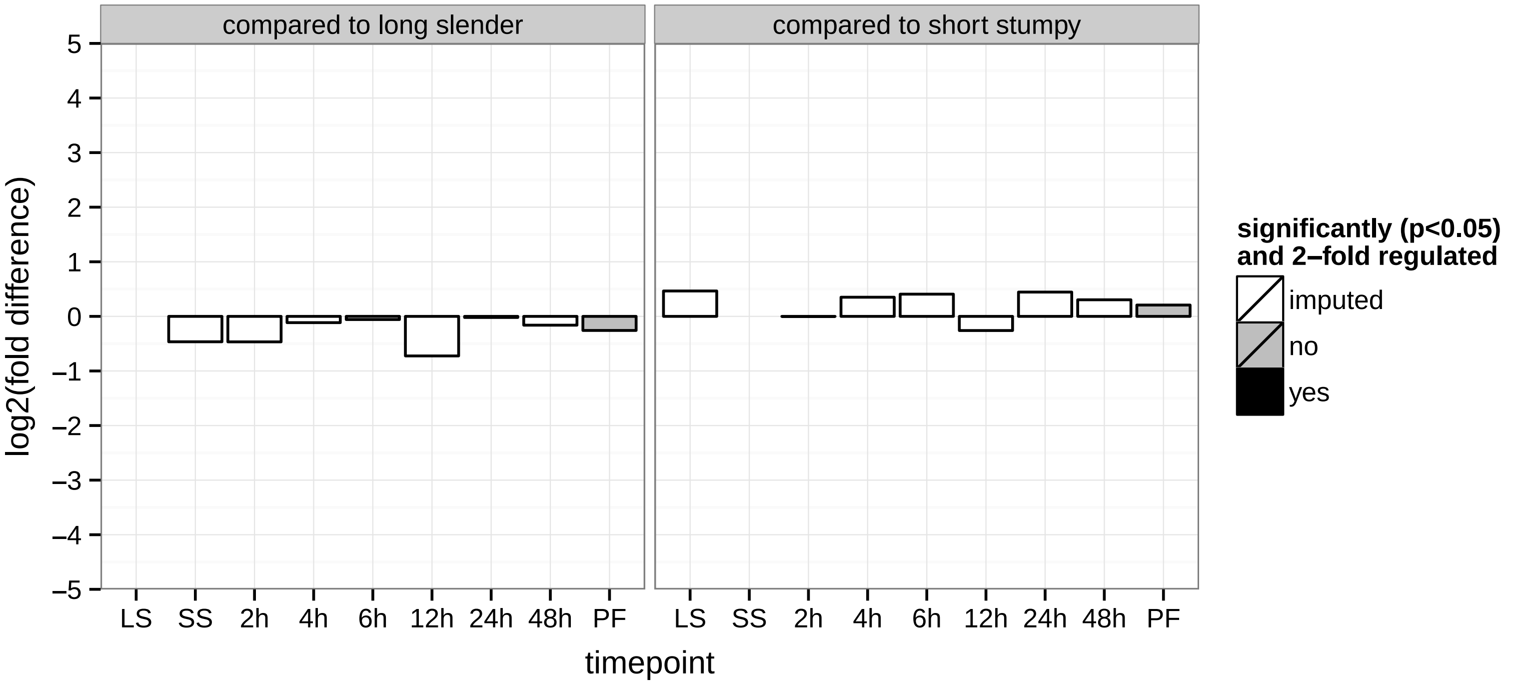
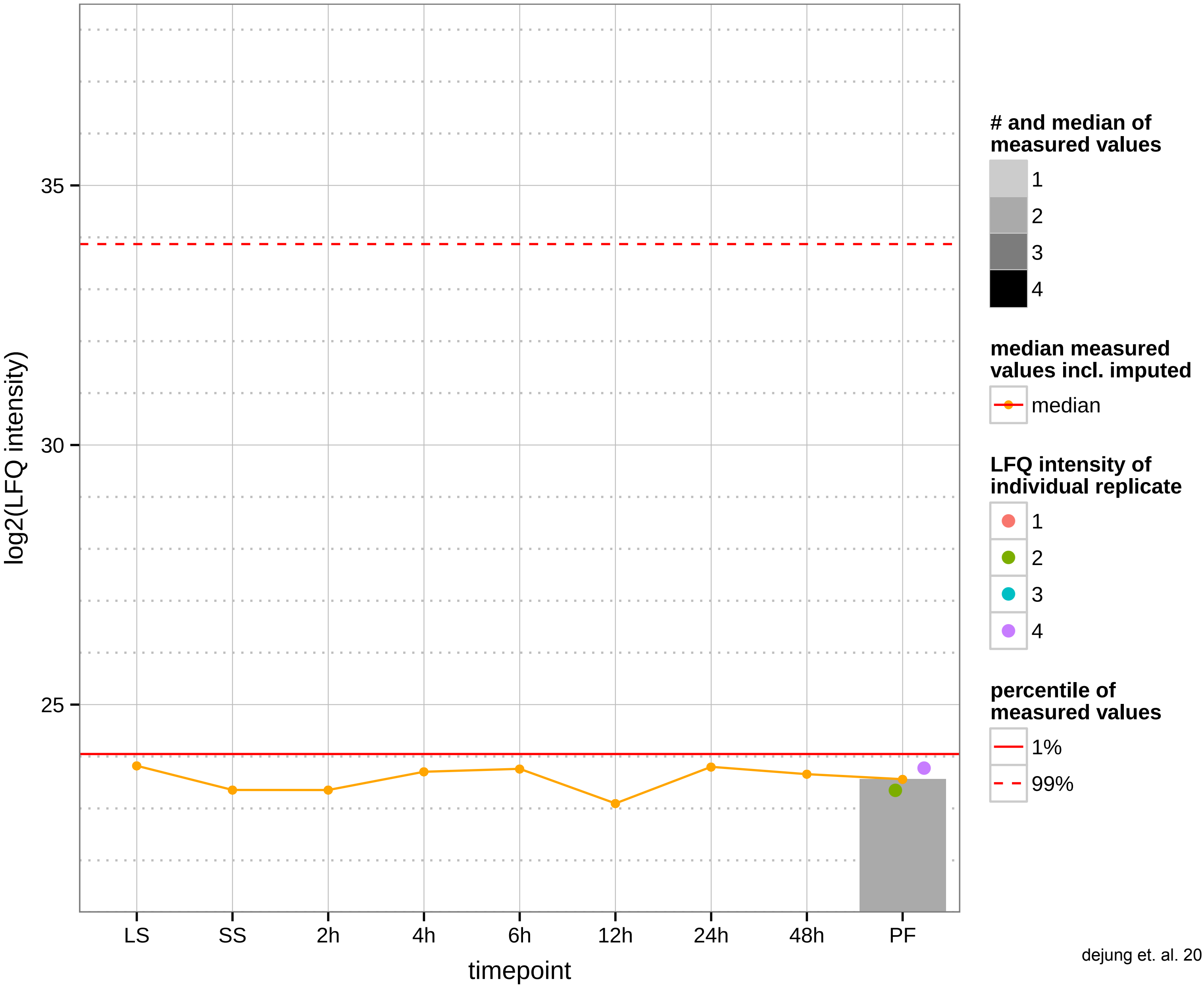
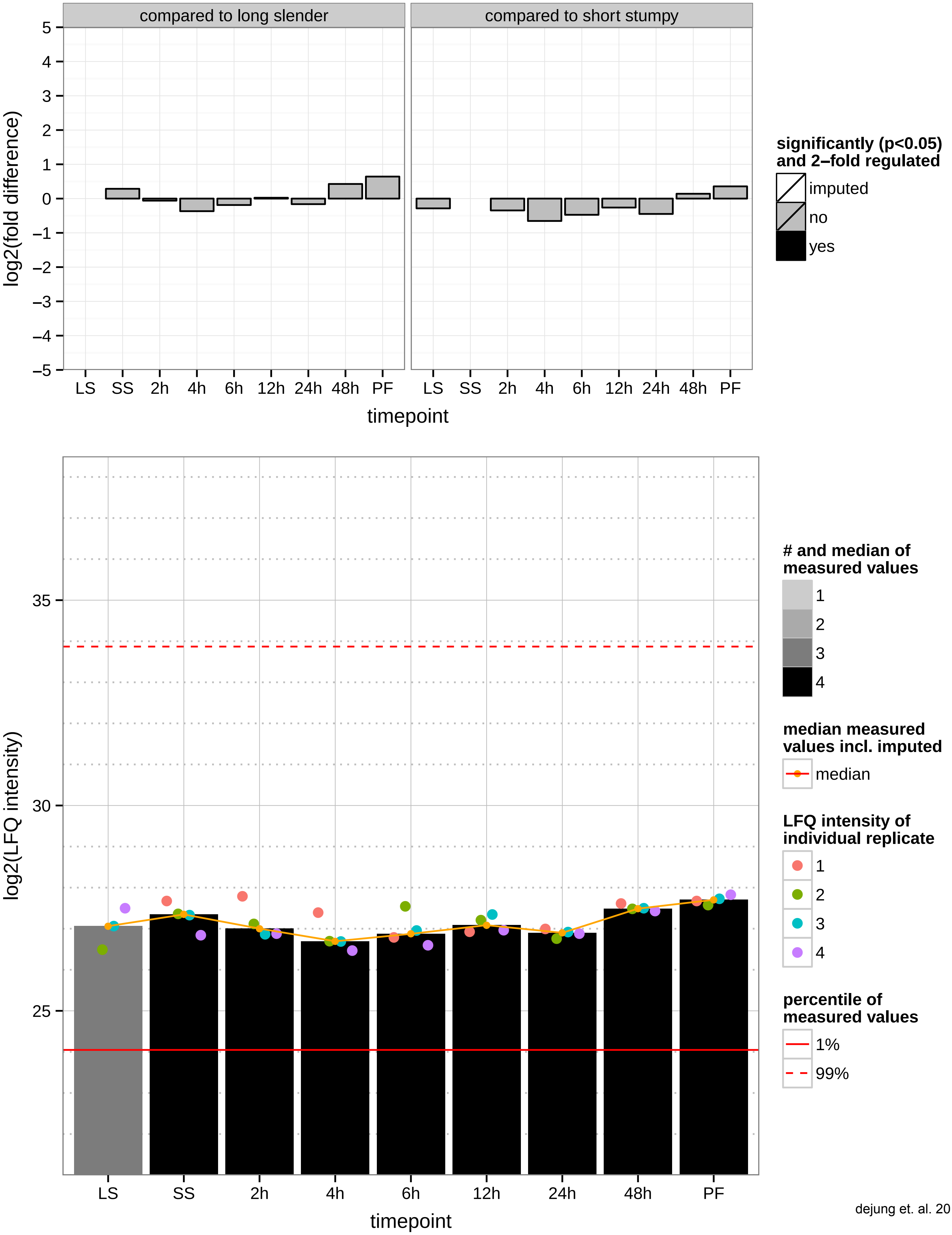
hypothetical protein, conserved
Tb927.4.5320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





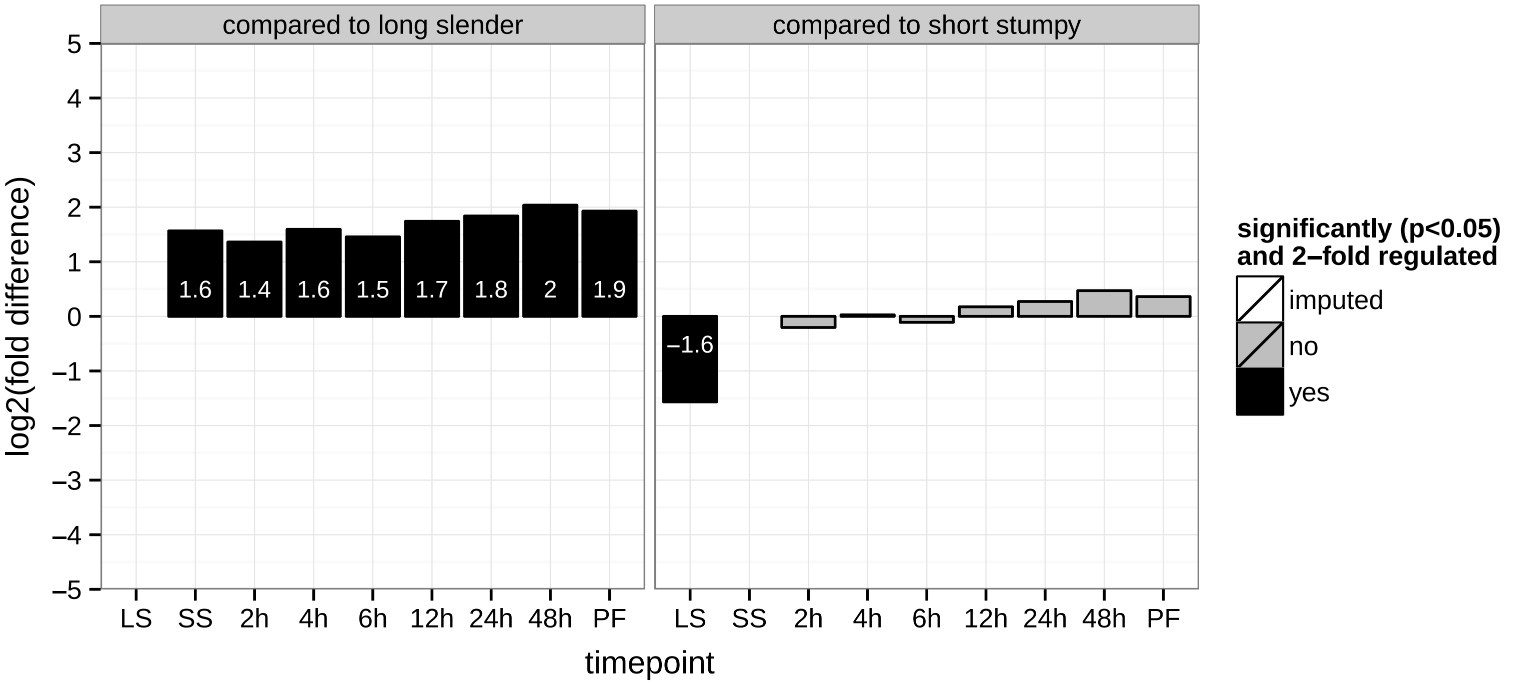
dejung et. al. 2015

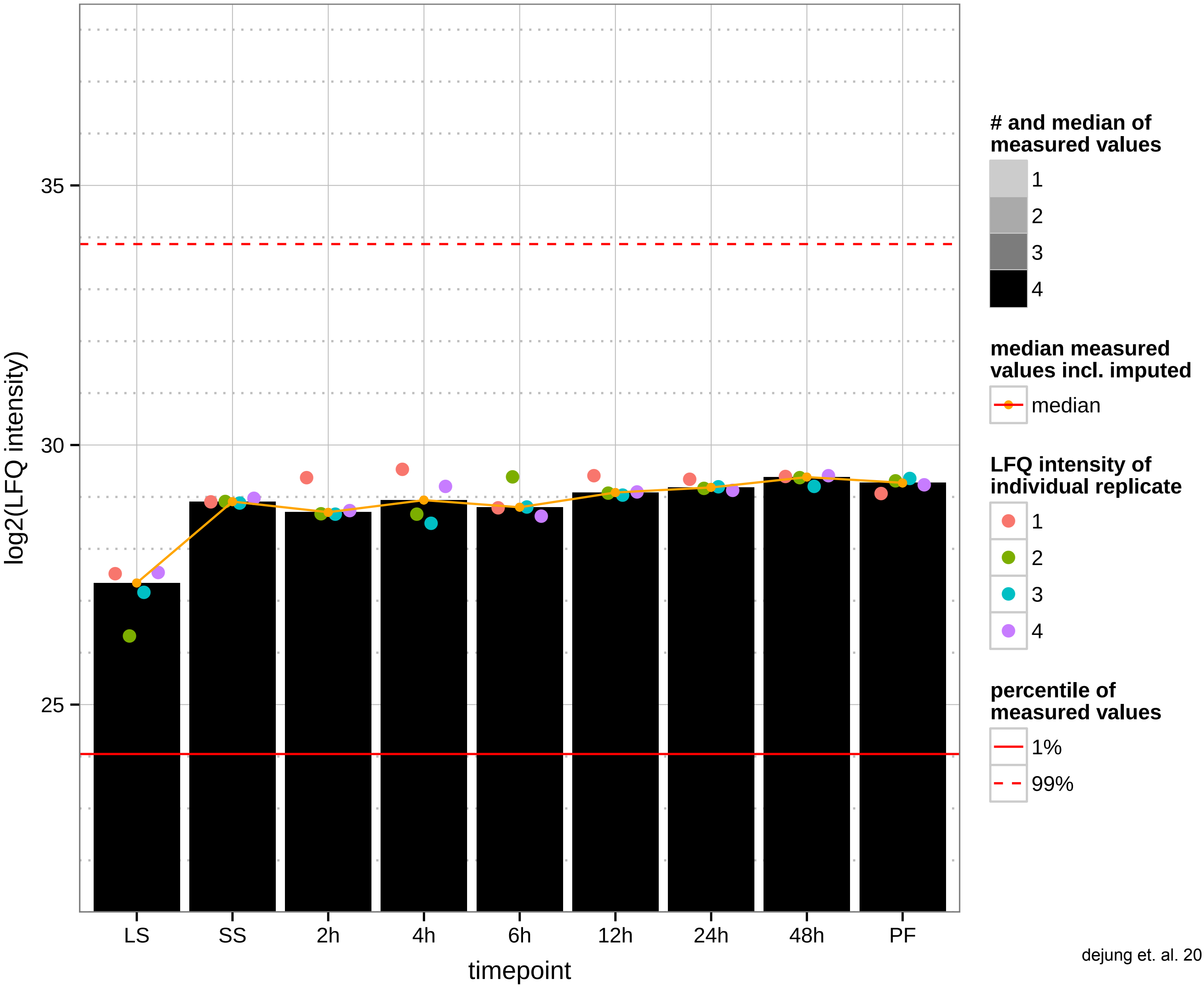
hypothetical protein, conserved
Tb927.4.5380;Tb927.8.6940
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.600
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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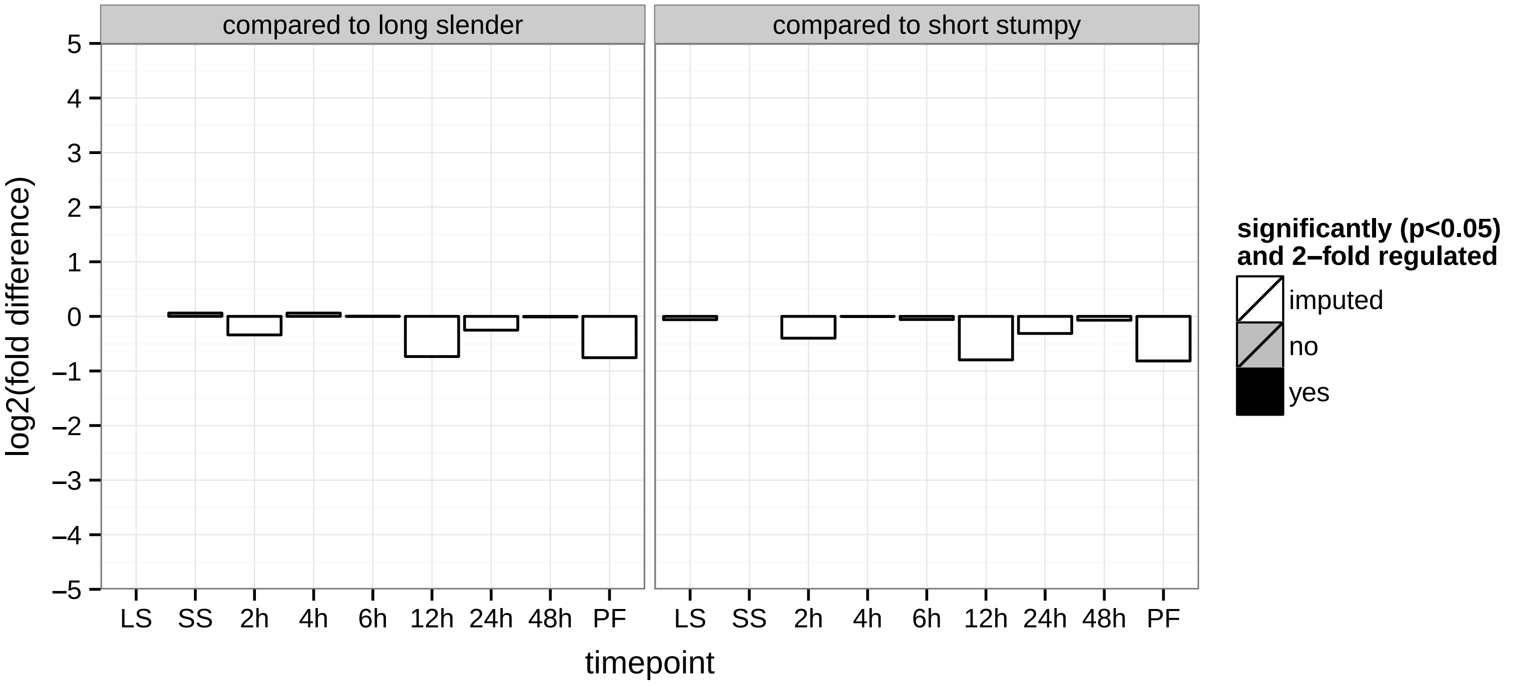
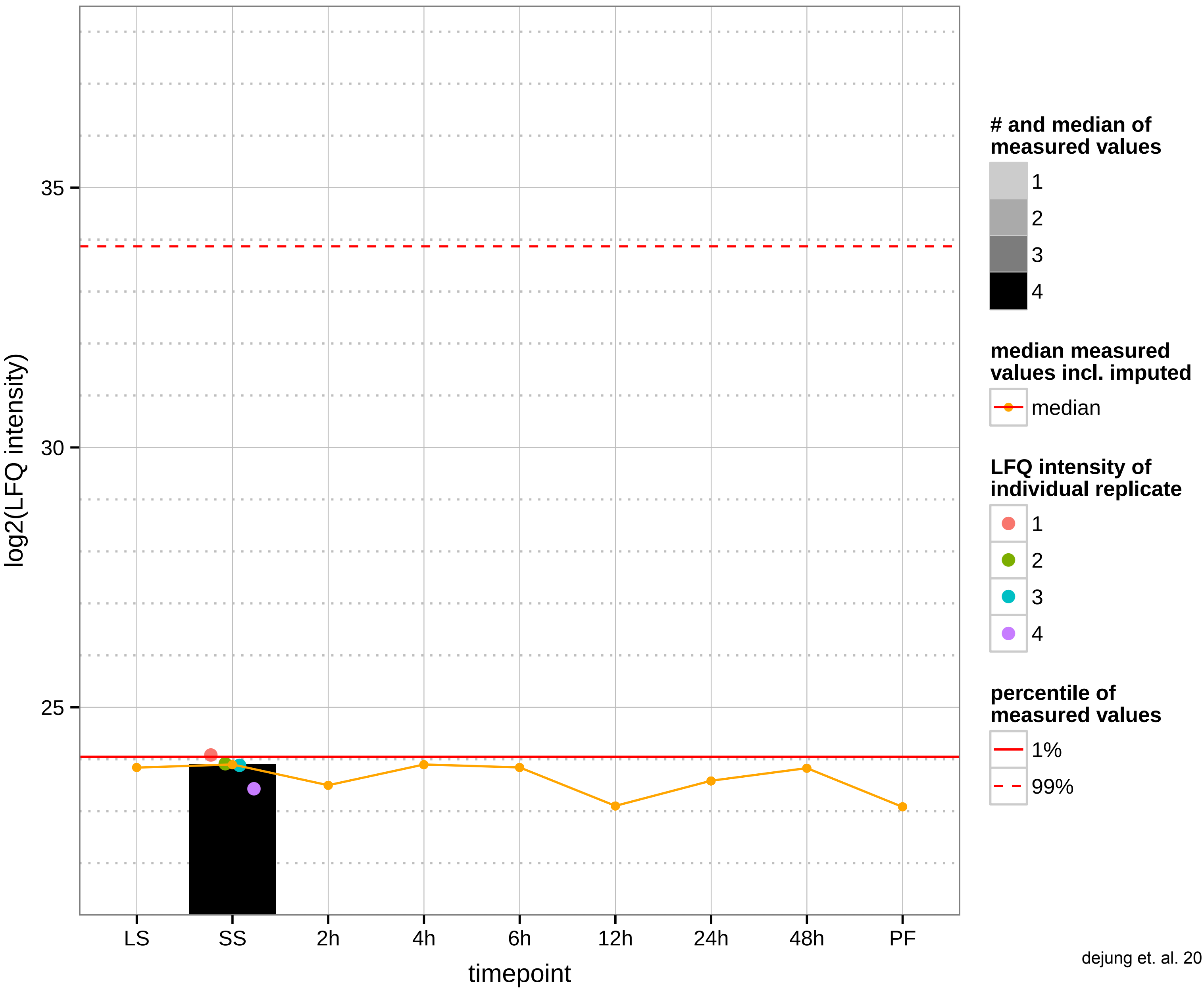
hypothetical protein, conserved
Tb927.4.620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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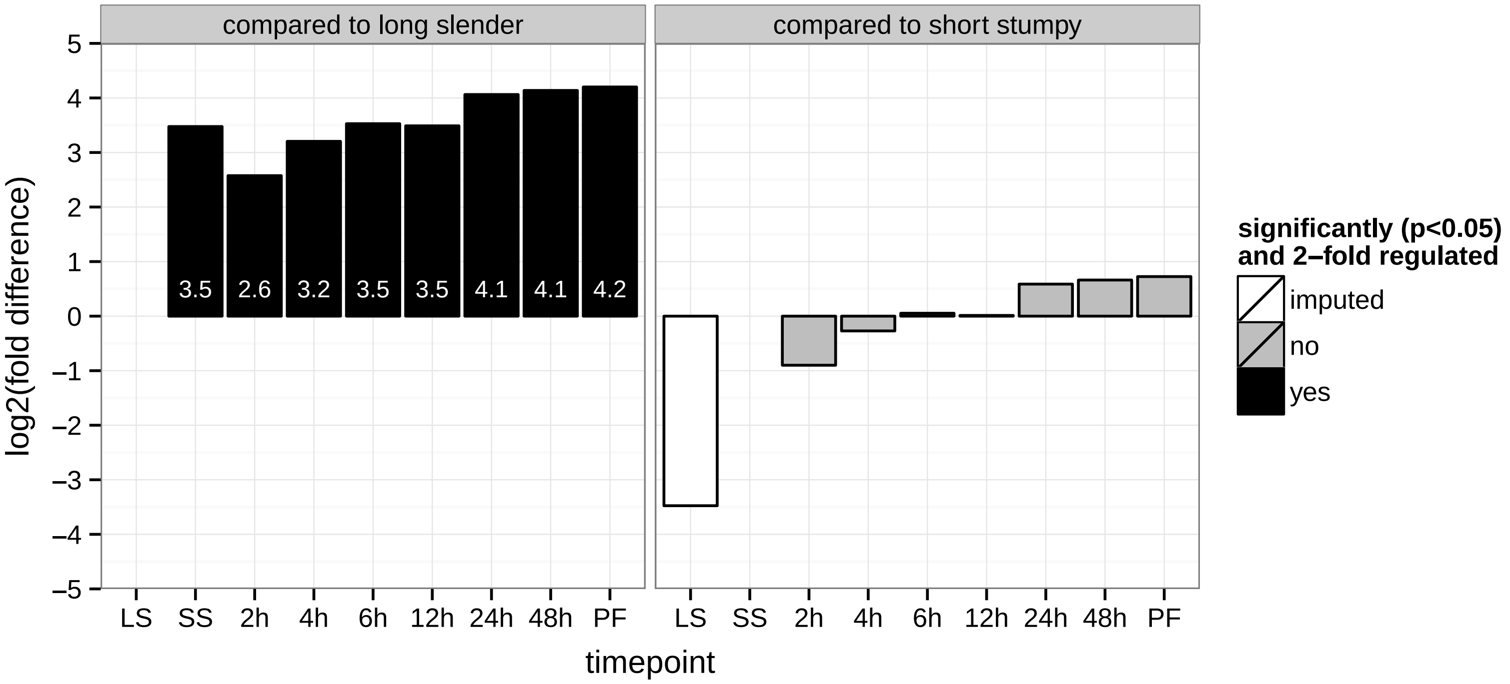
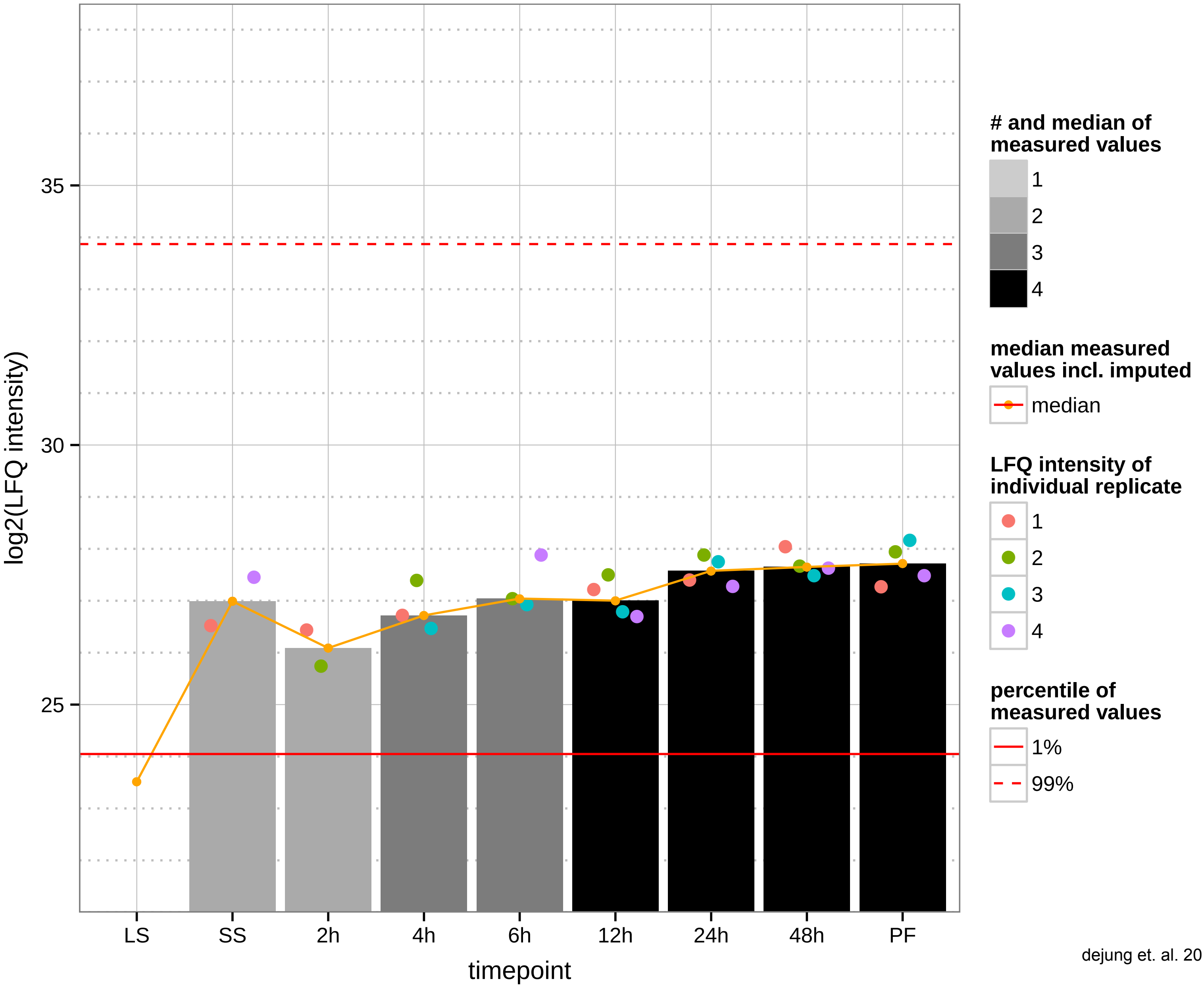
hypothetical protein, conserved
Tb927.4.630
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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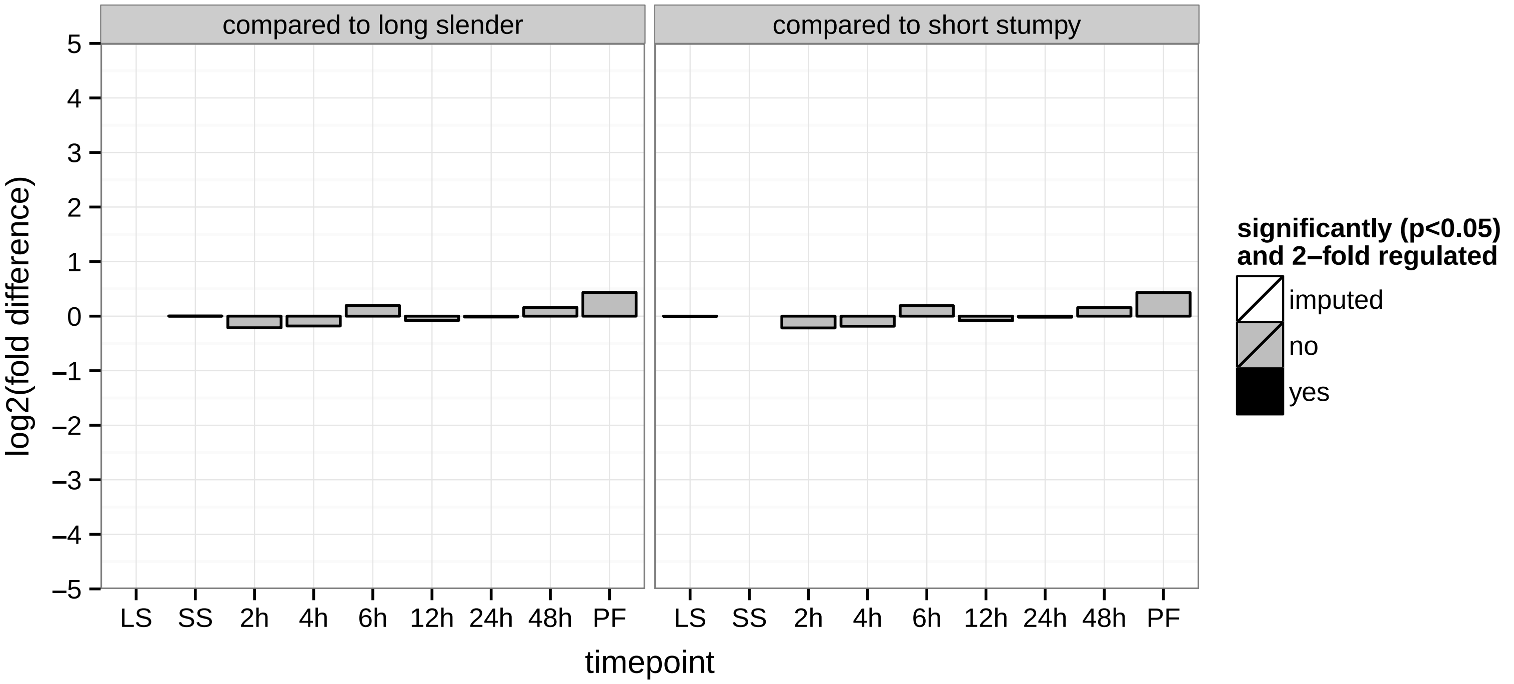
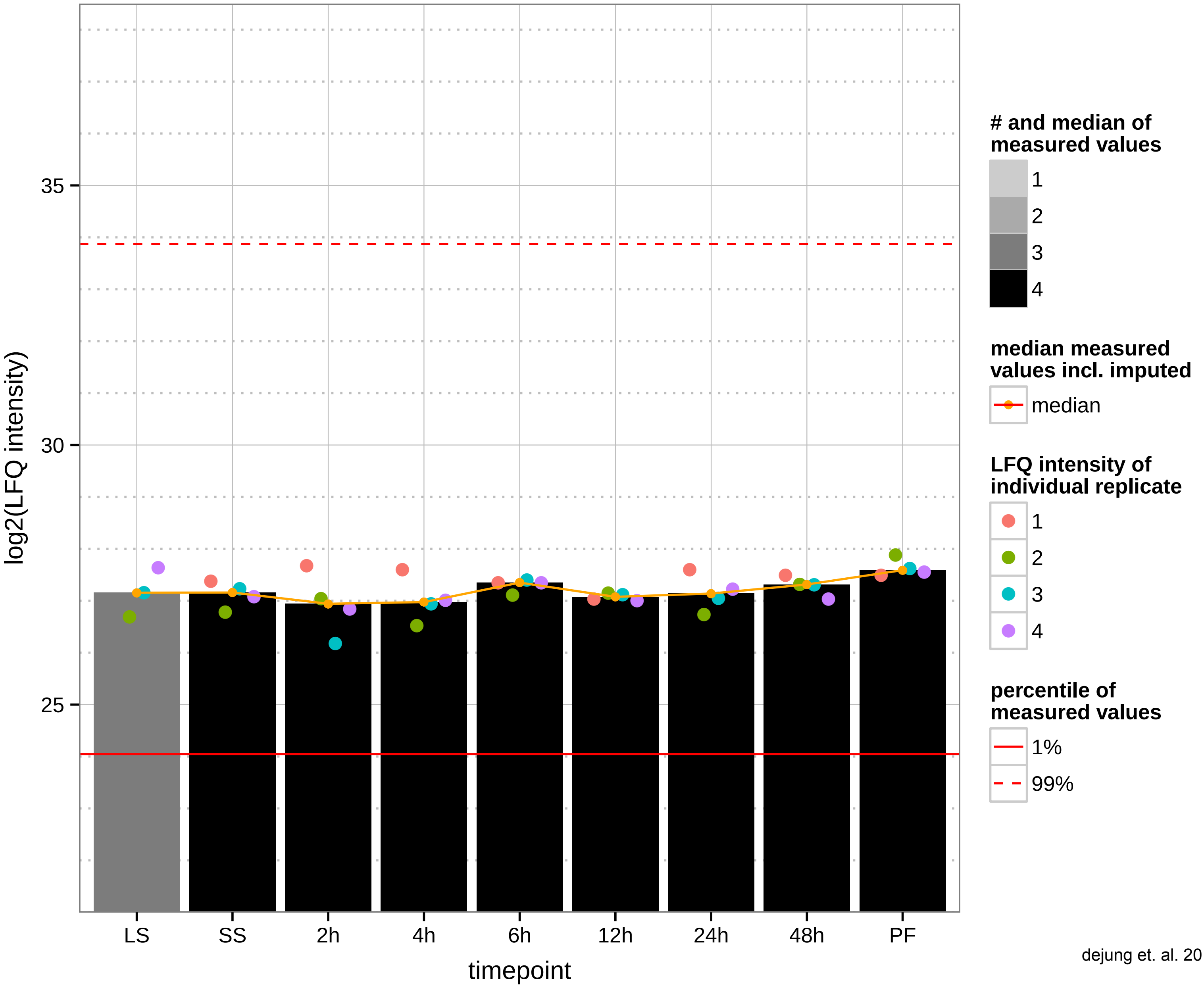
hypothetical protein, conserved
Tb927.4.660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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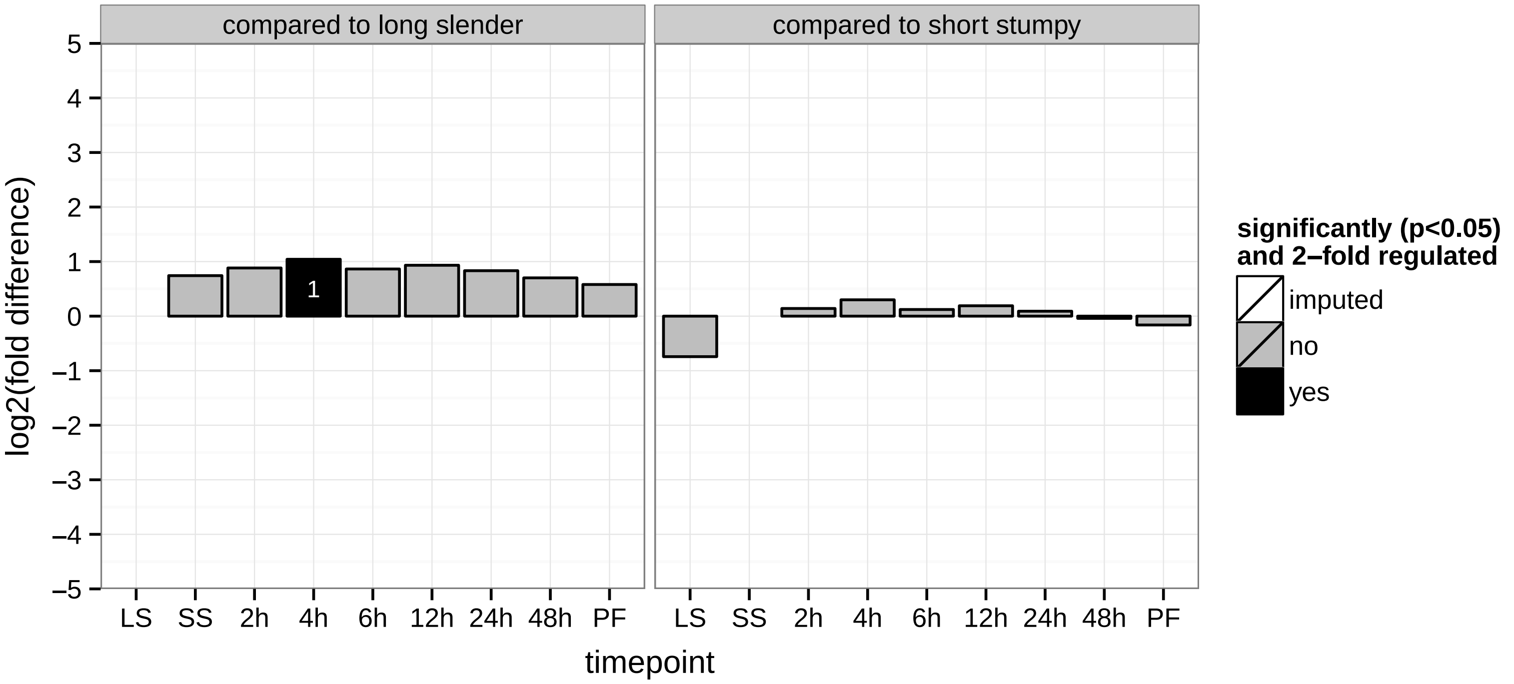
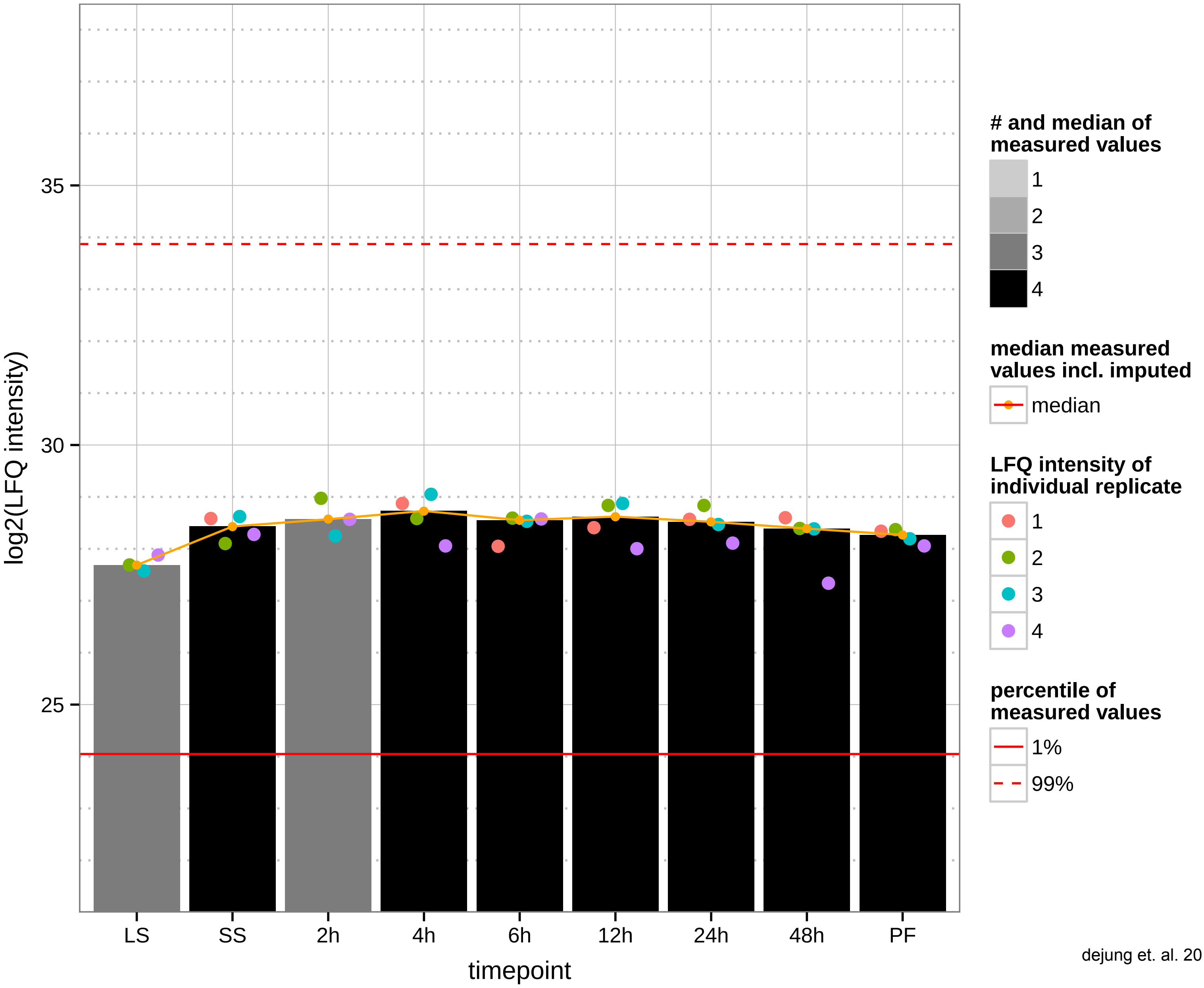
50S ribosomal protein L7Ae, putative
Tb927.4.750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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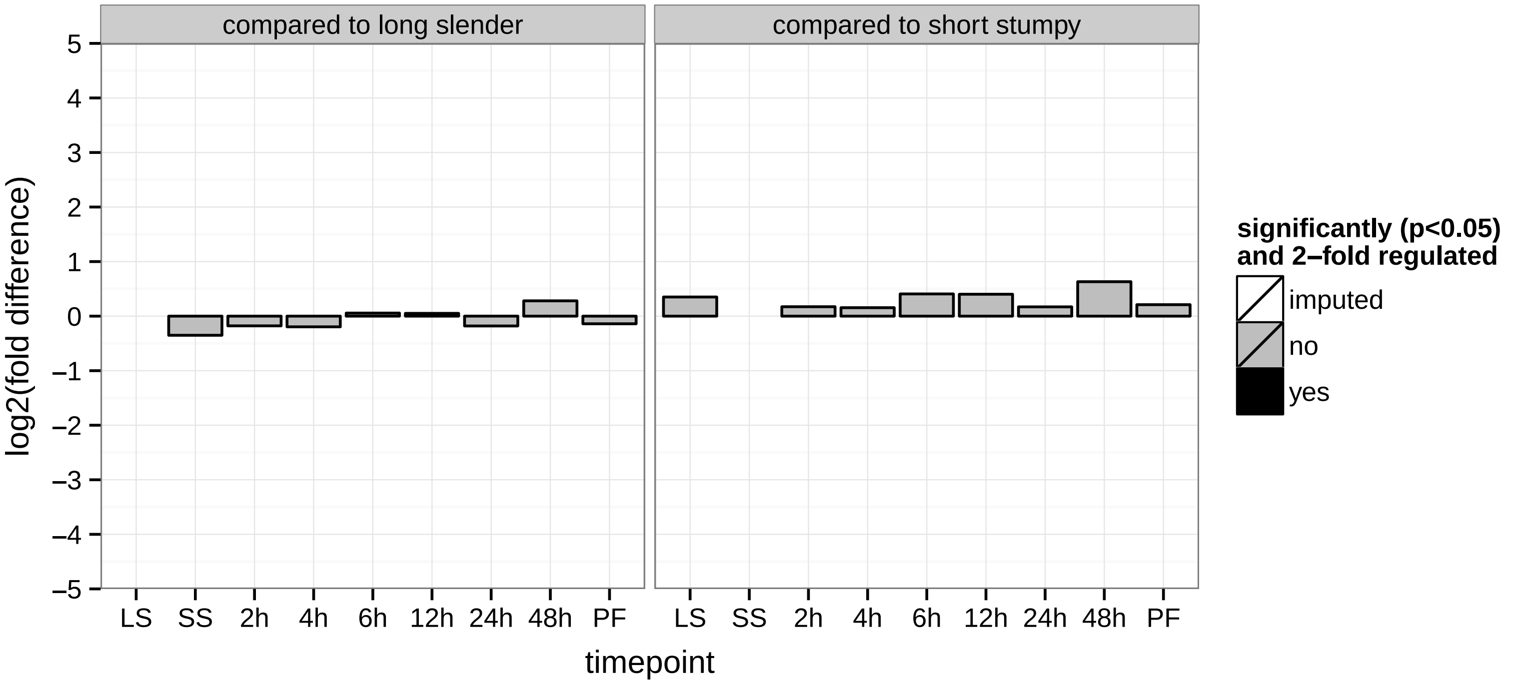
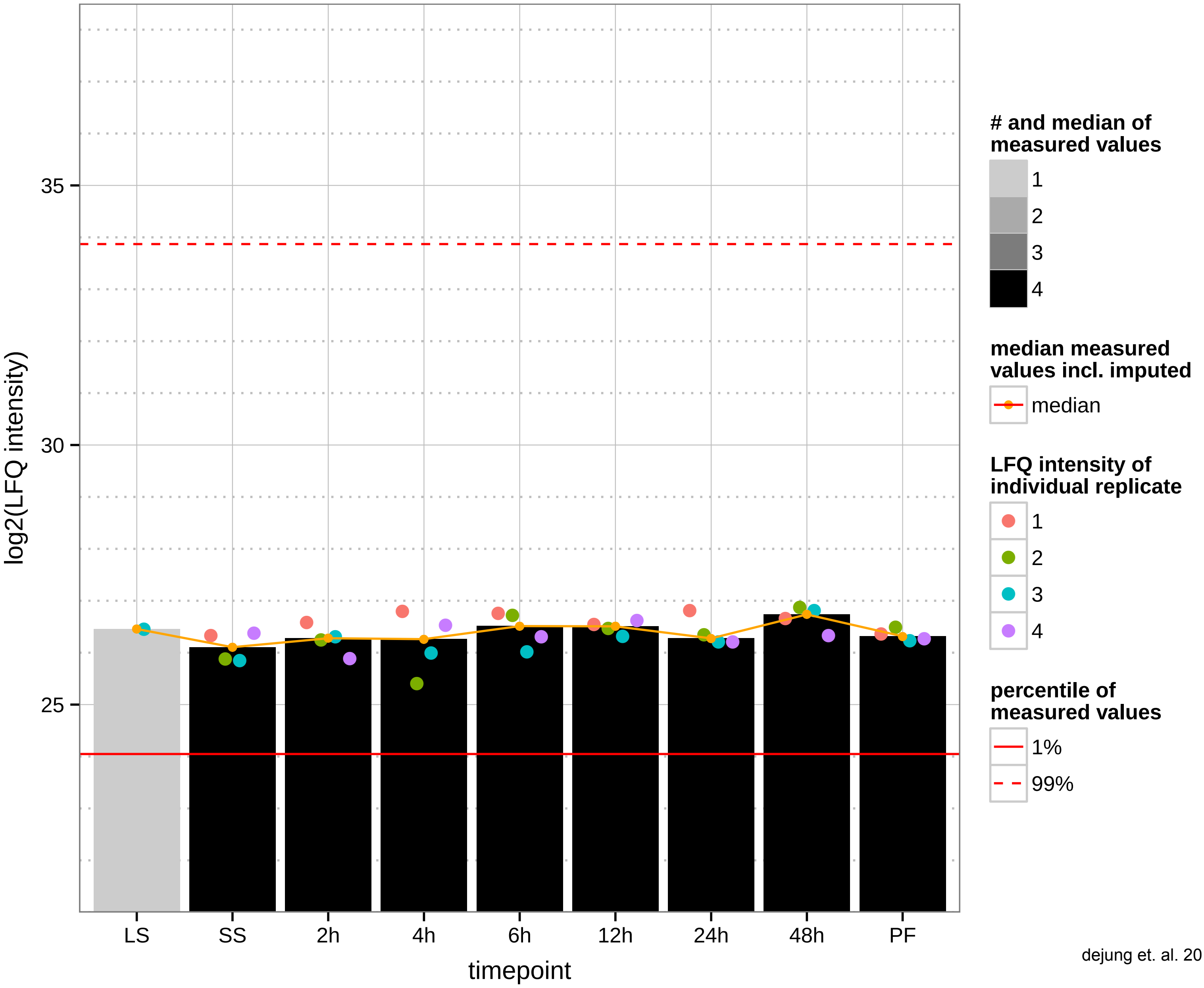
hypothetical protein, conserved
Tb927.4.840
AGOF: ATP binding, two–component sensor activity
AGOC: null
AGOP: peptidyl–histidine phosphorylation, signal transduction
PGOF: ATP binding, protein histidine kinase activity, two–component sensor activity
PGOC: null
PGOP: peptidyl–histidine phosphorylation, signal transduction





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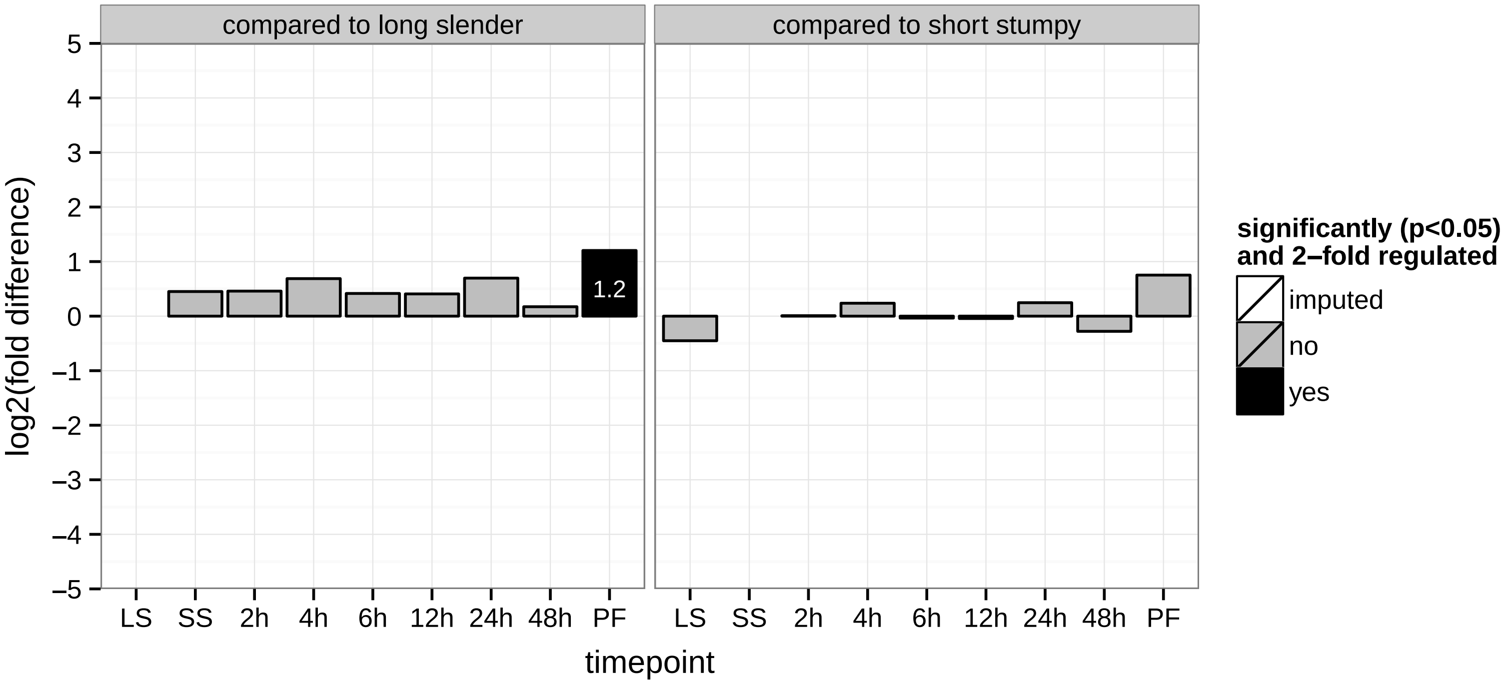
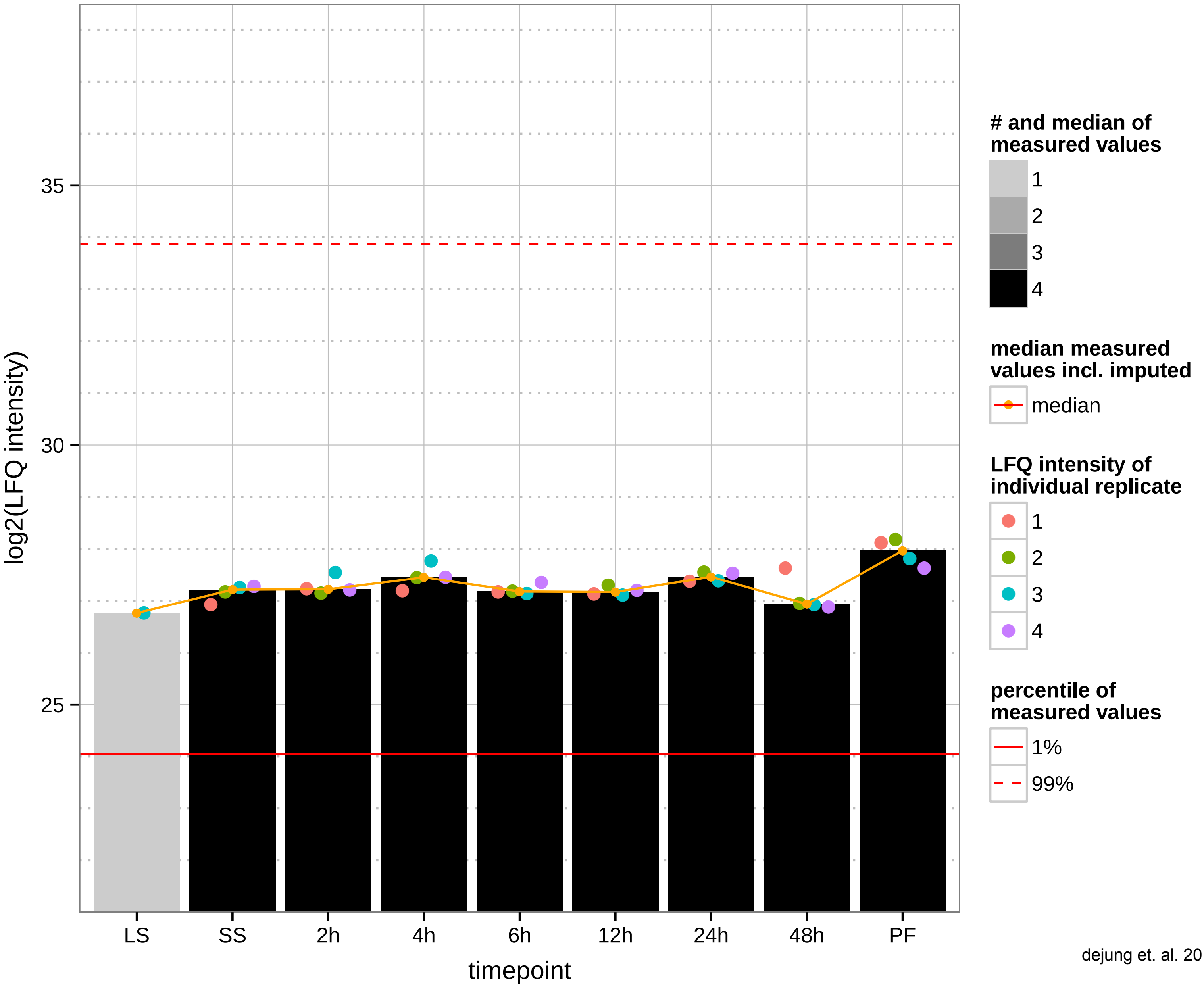
hypothetical protein, conserved
Tb927.4.860
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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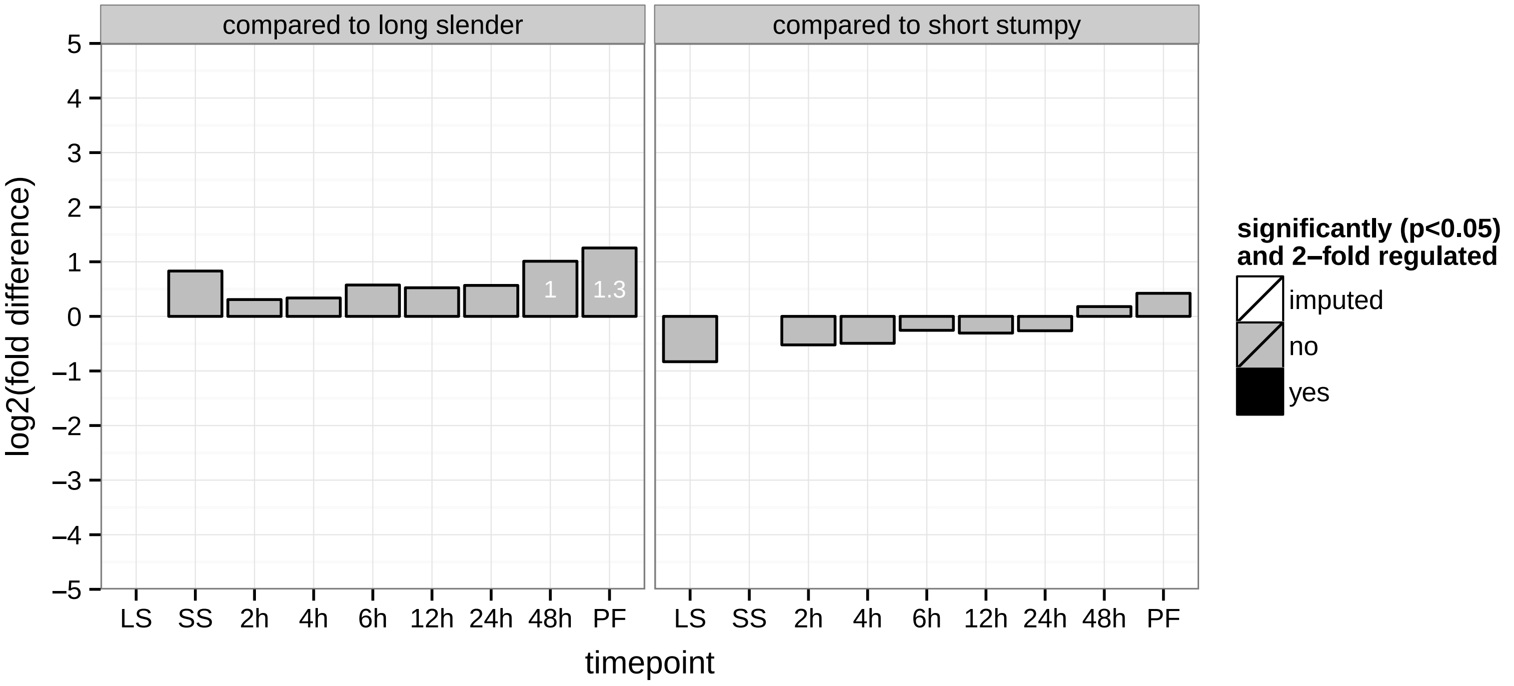
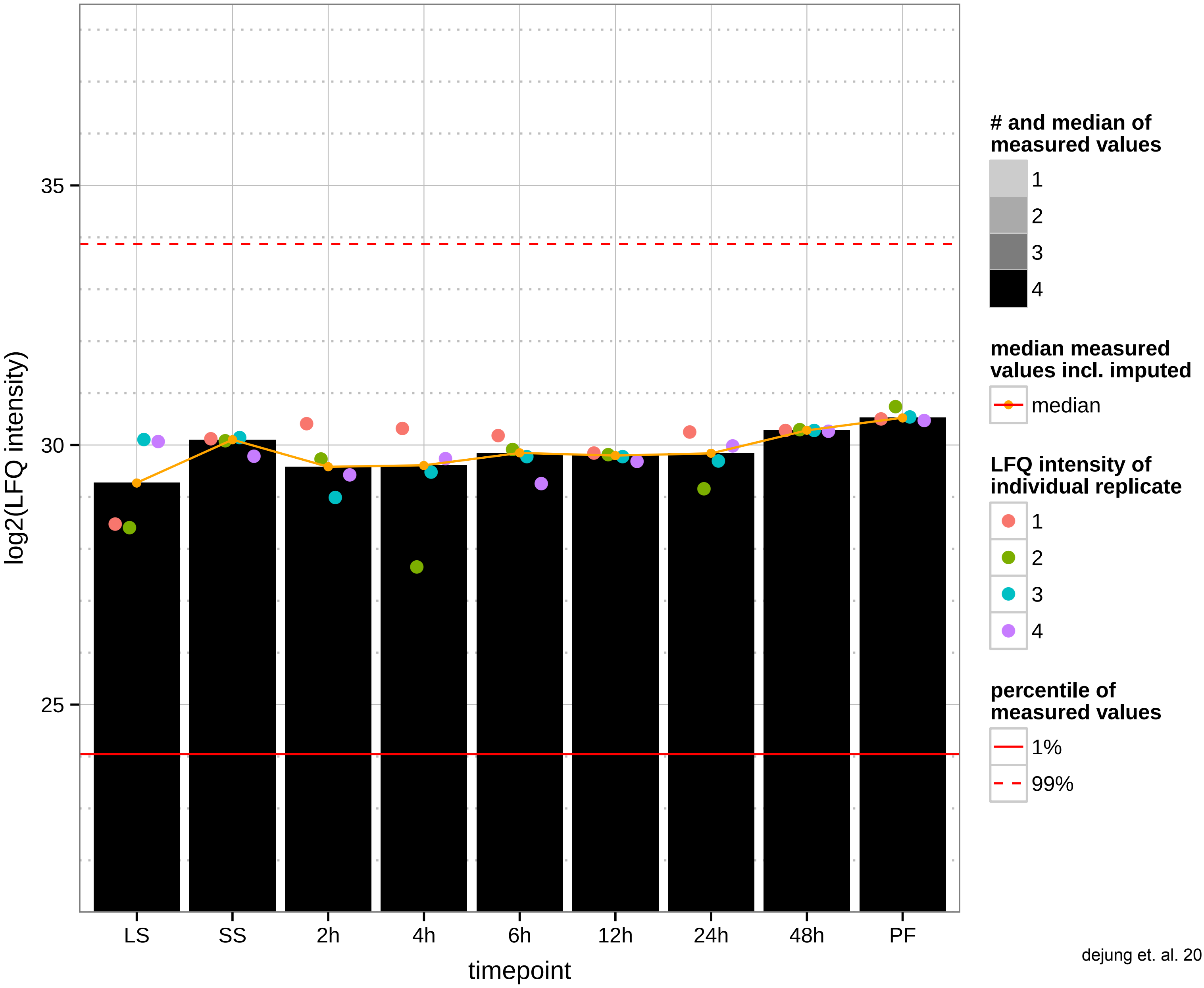
dynein heavy chain, putative
Tb927.4.870
AGOF: ATP binding, ATPase activity, microtubule motor activity
AGOC: axonemal dynein complex
AGOP: microtubule–based movement
PGOF: ATP binding, ATPase activity, microtubule motor activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: dynein complex
PGOP: microtubule–based movement





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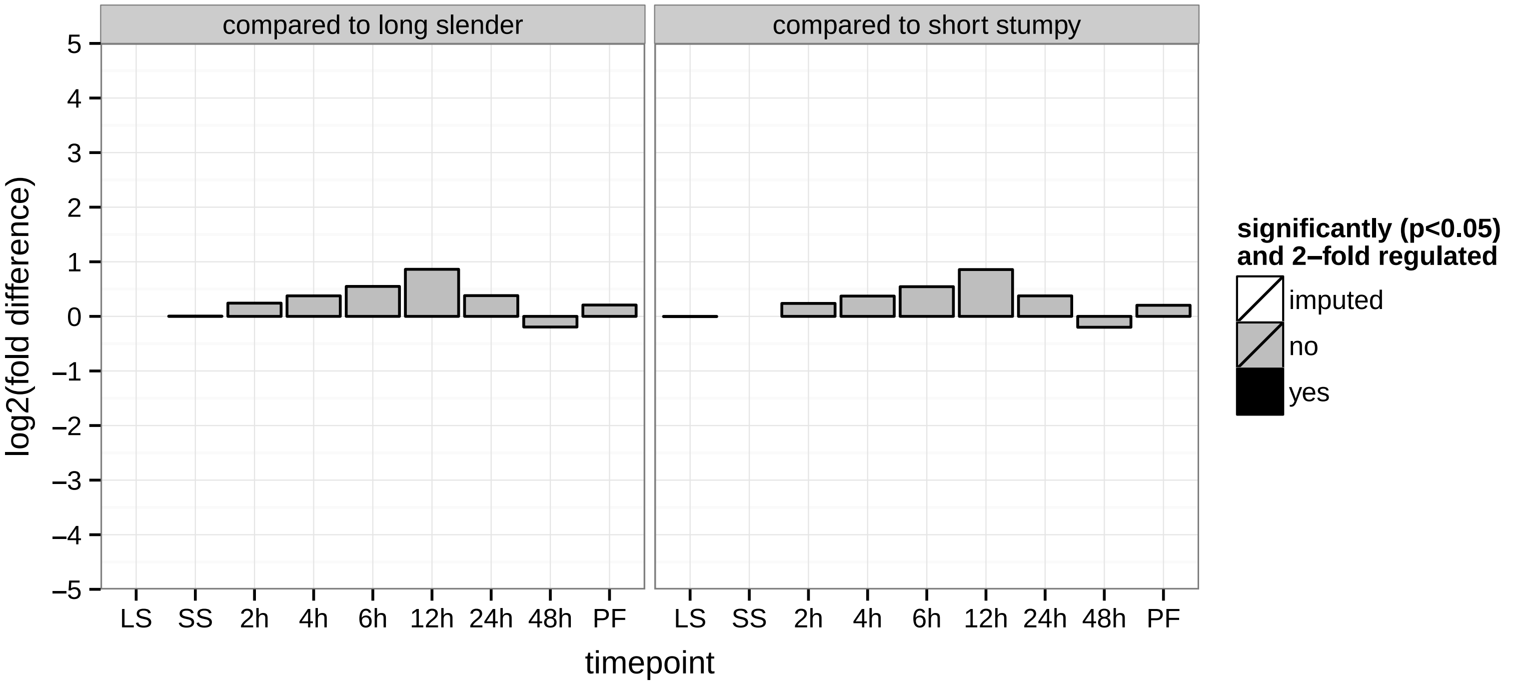
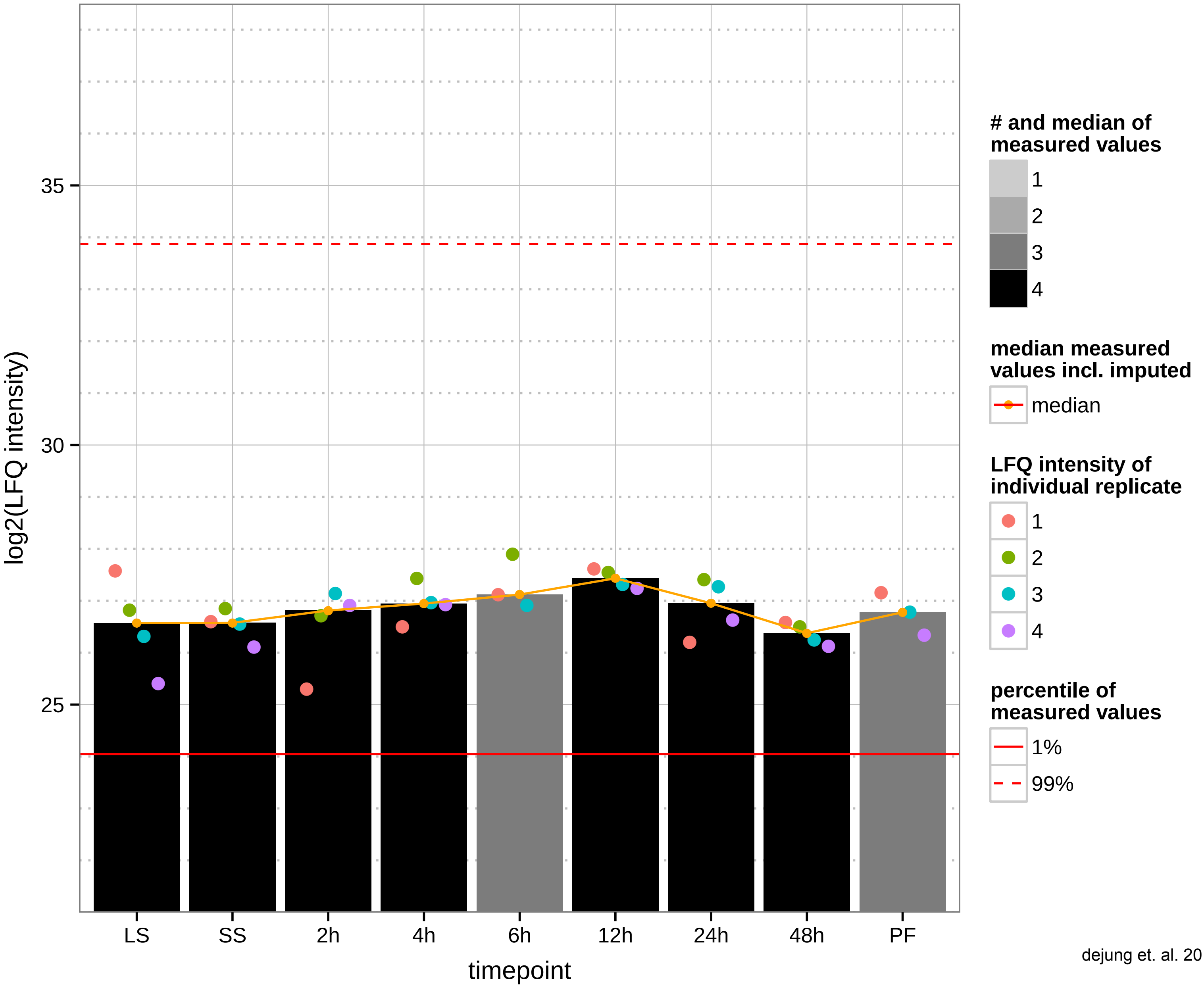
small nuclear ribonucleoprotein SmD3, putative (SmD3)
Tb927.4.890
AGOF: null
AGOC: nucleus, small nuclear ribonucleoprotein complex
AGOP: RNA splicing, RNA splicing, via transesterification reactions, mRNA processing
PGOF: null
PGOC: null
PGOP: null





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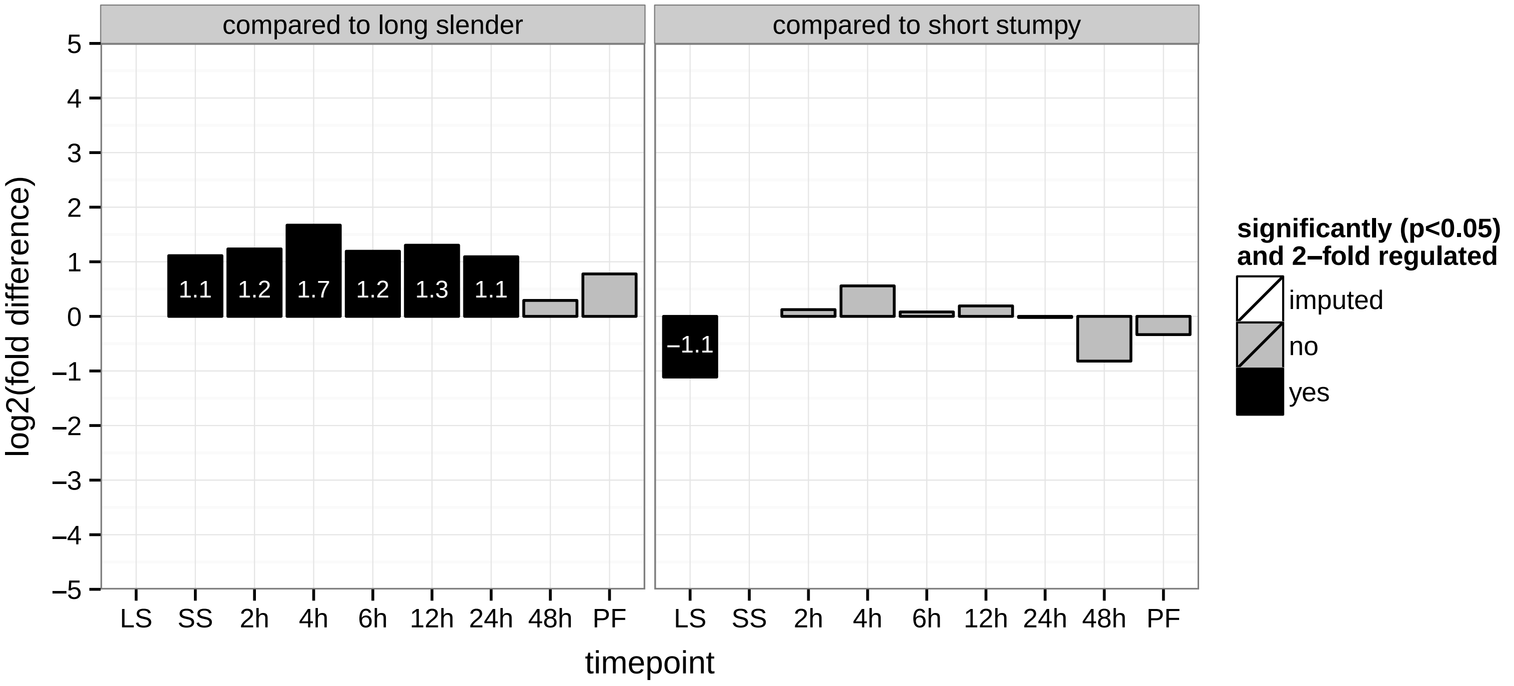
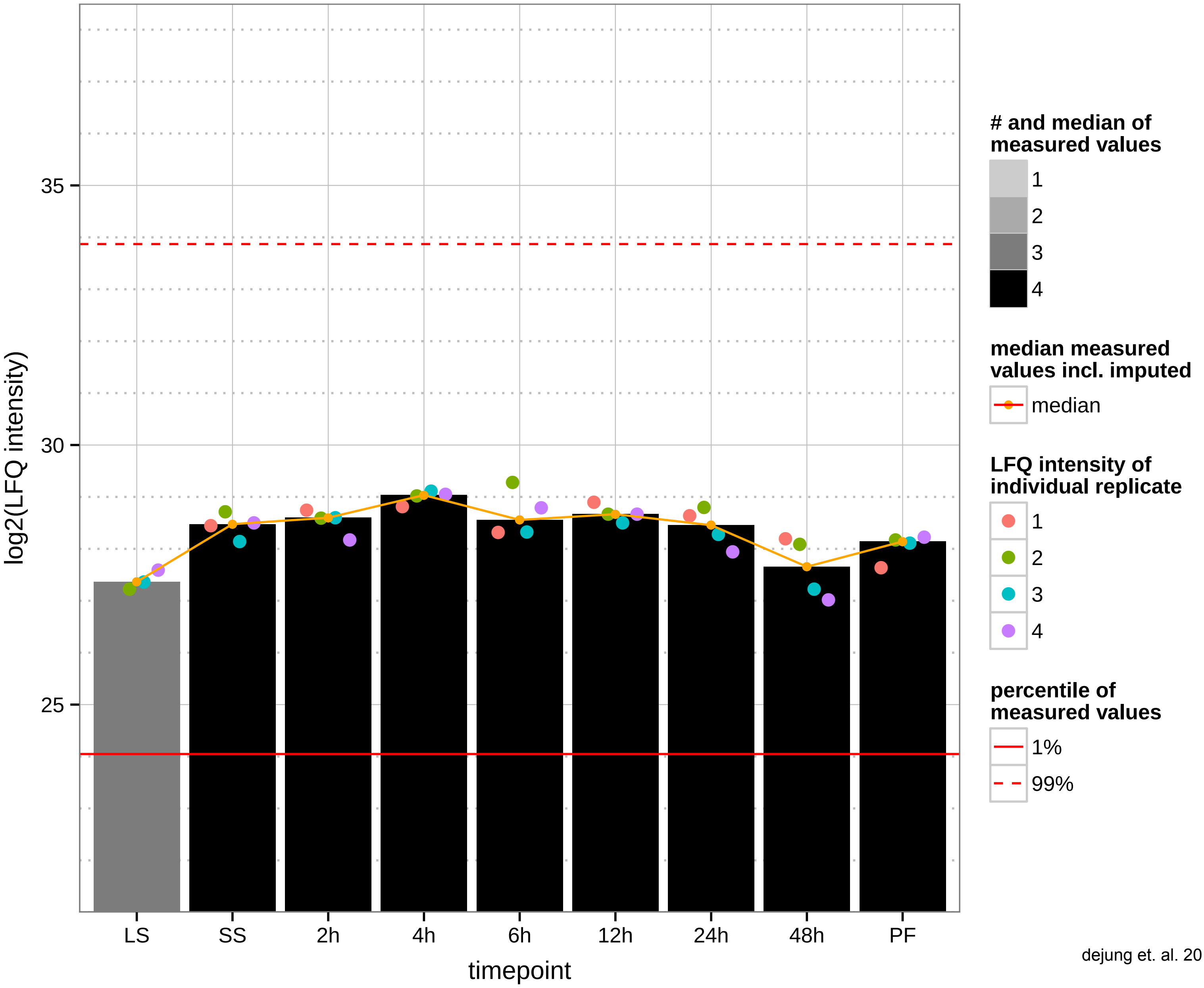
hypothetical protein, conserved
Tb927.4.920
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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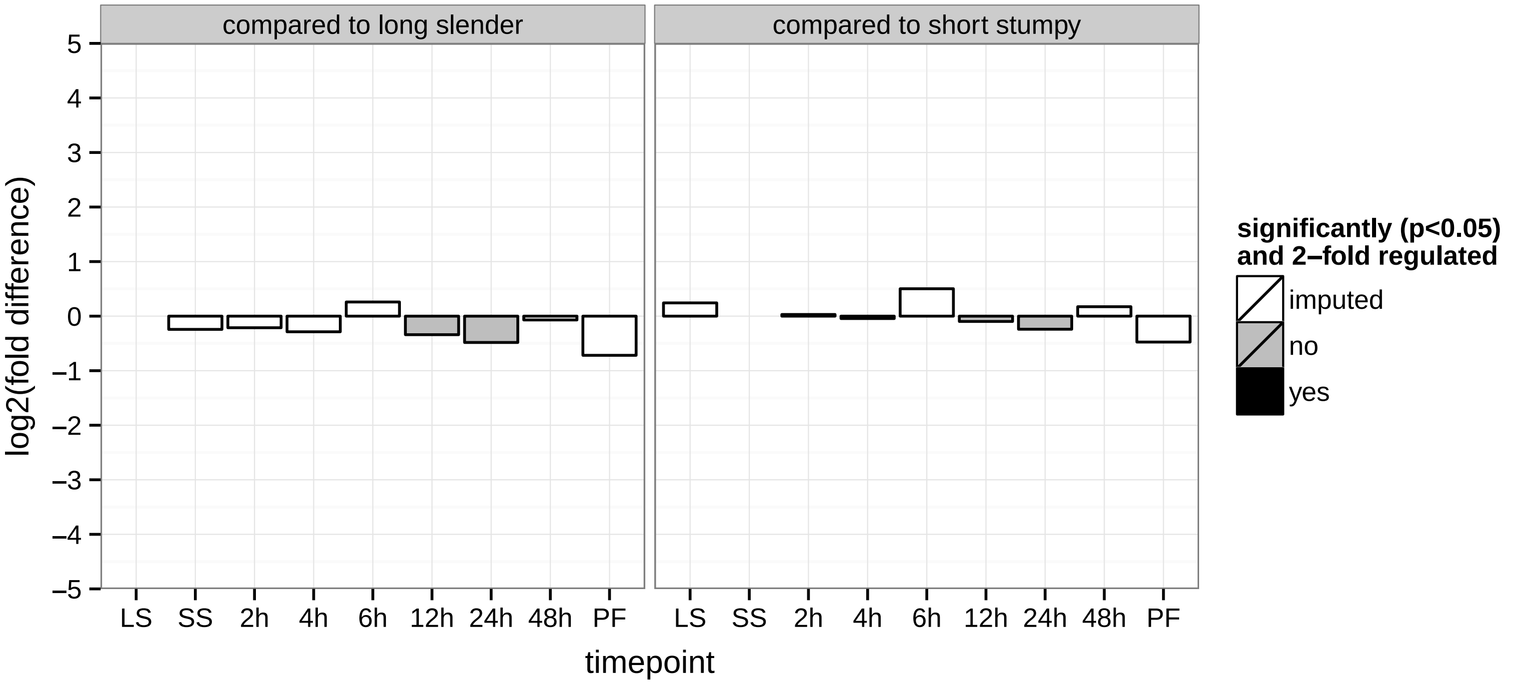
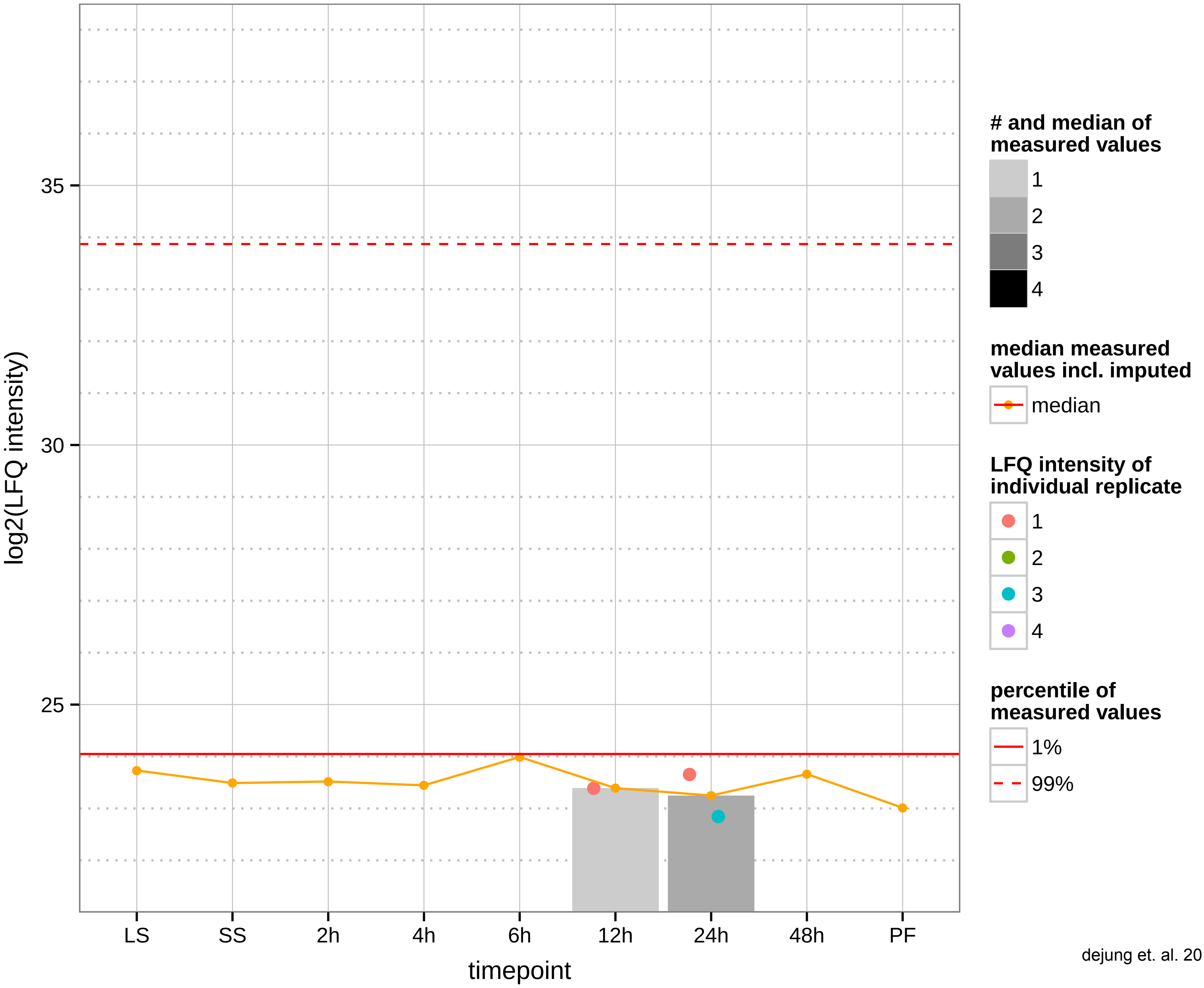
hypothetical protein, conserved
Tb927.4.970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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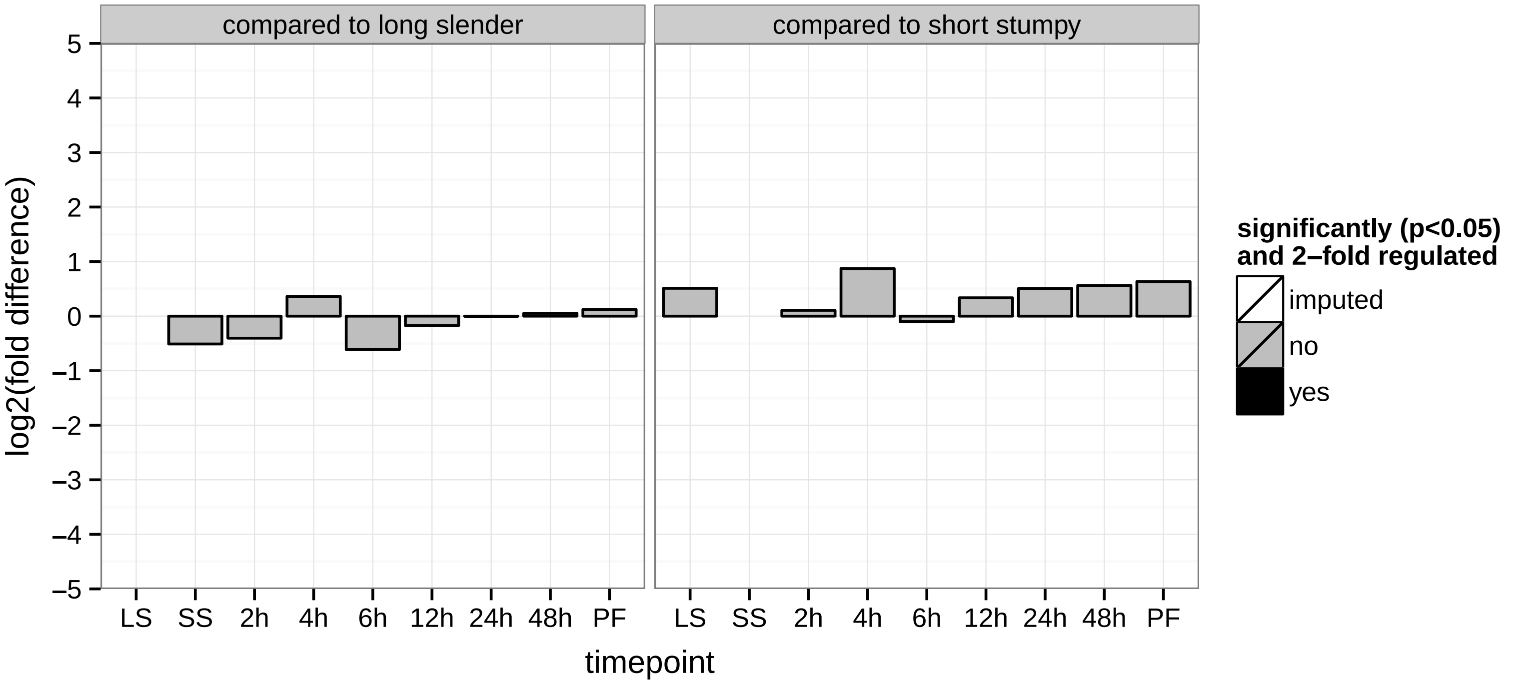
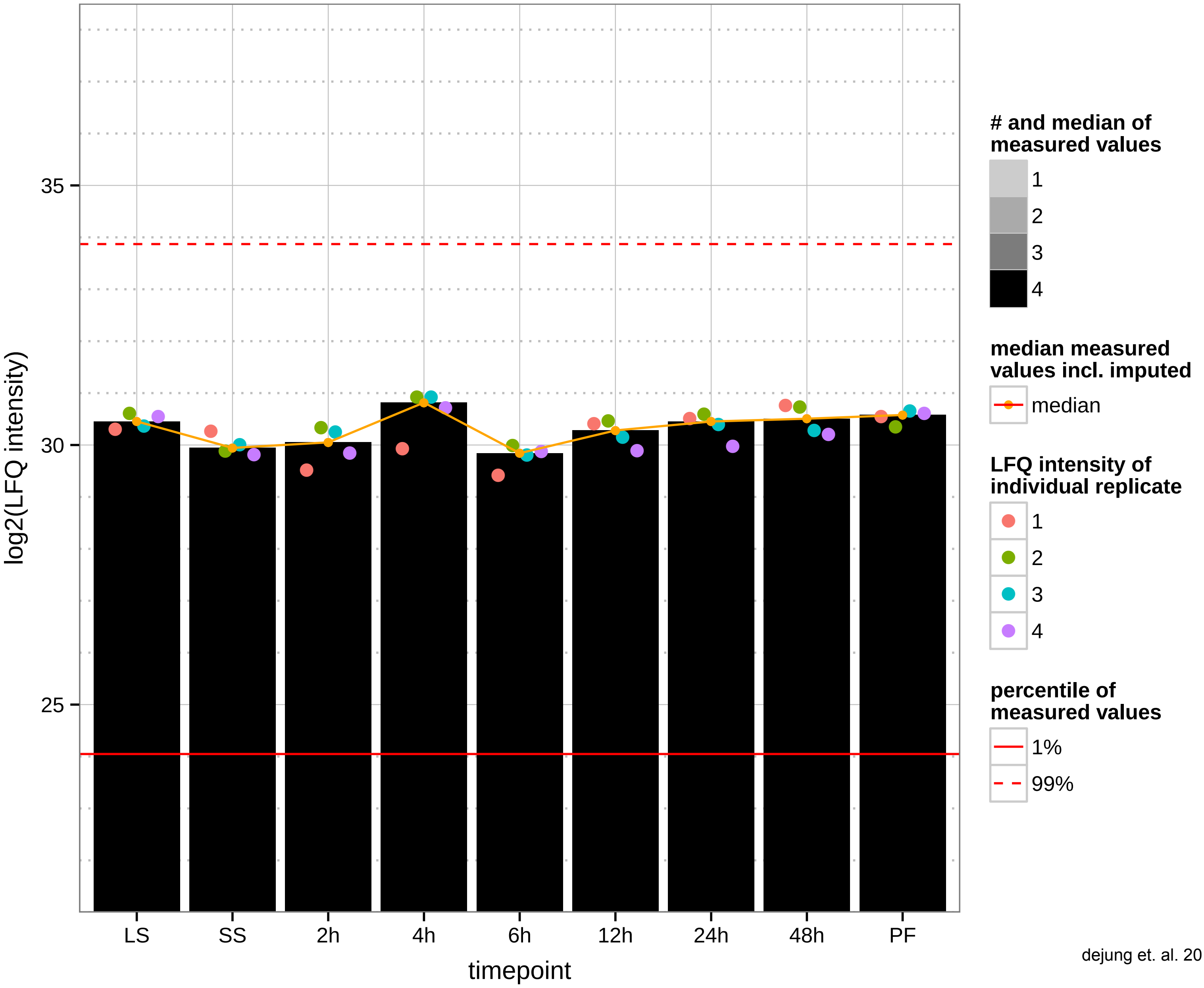
ubiquitin–conjugating enzyme E2, putative, ubiquitin carrier protein, ubiquitin–protein ligase
Tb927.5.1000
AGOF: ubiquitin–protein ligase activity
AGOC: null
AGOP: cellular protein modification process, post–translational protein modification, regulation of protein metabolic process
PGOF: acid–amino acid ligase activity
PGOC: null
PGOP: null





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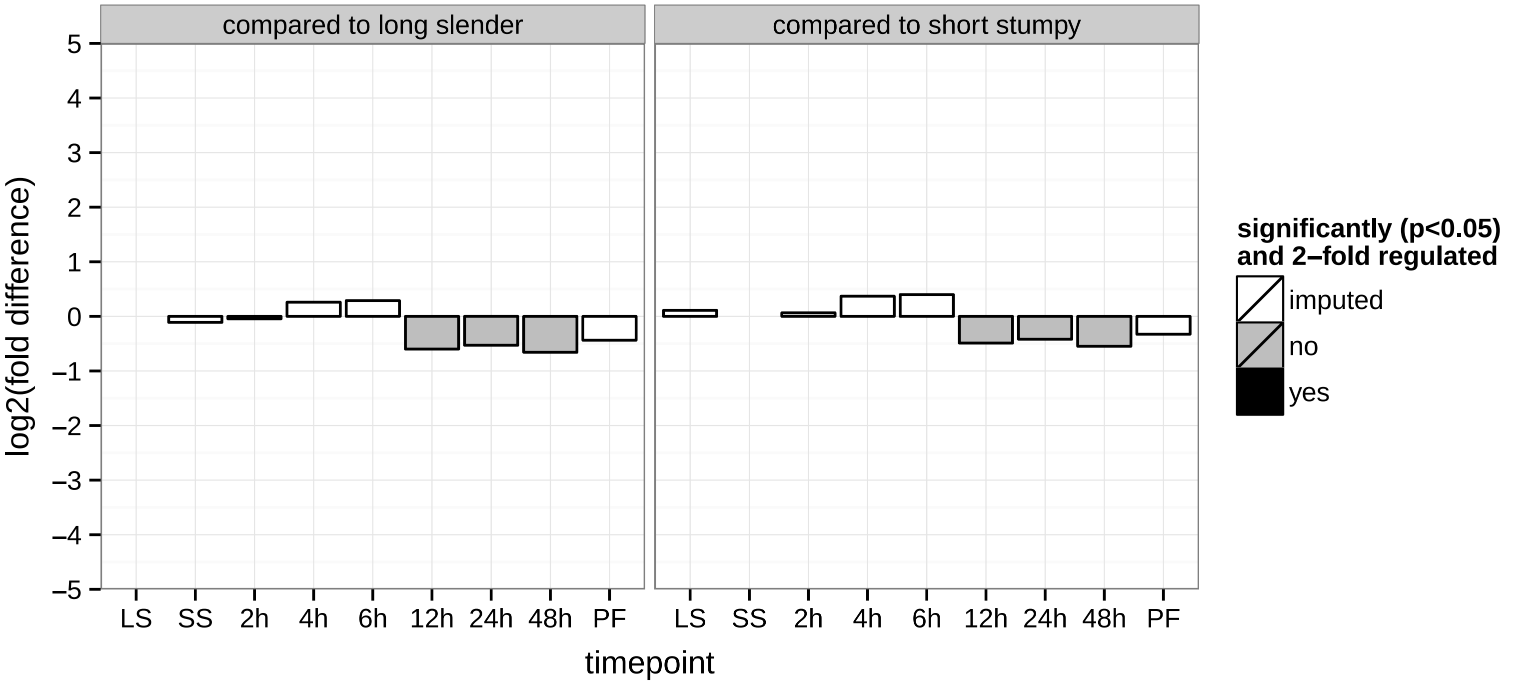
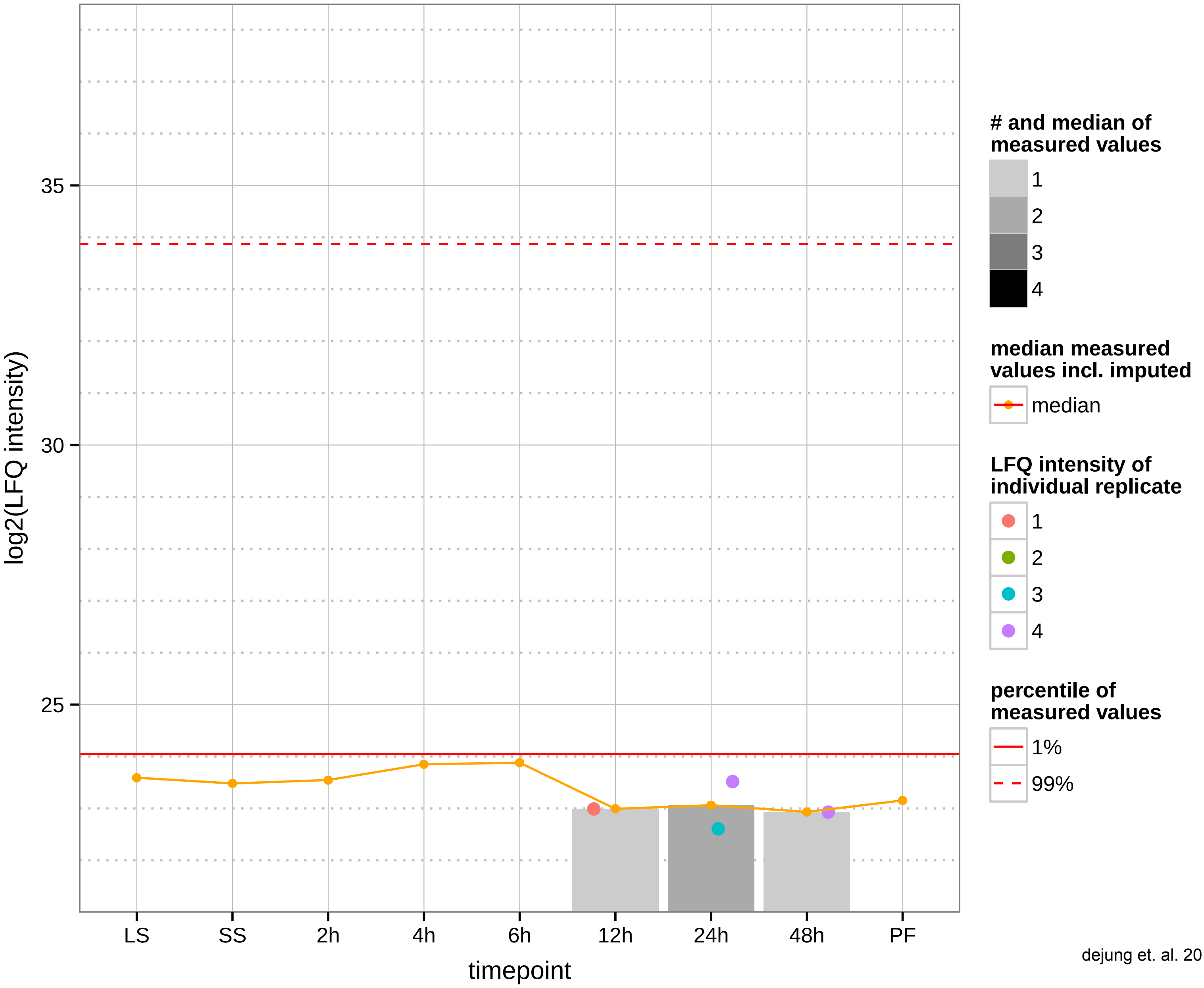
hypothetical protein, conserved
Tb927.5.1010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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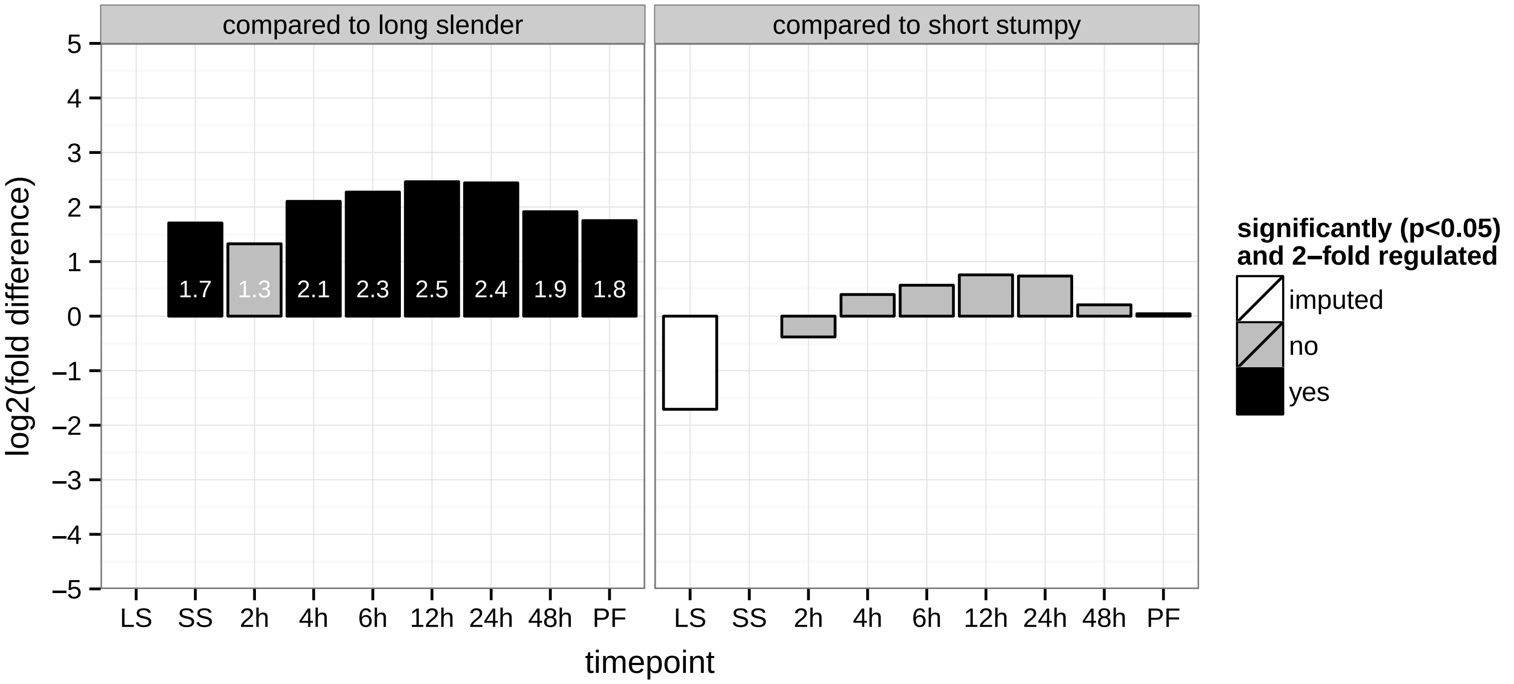
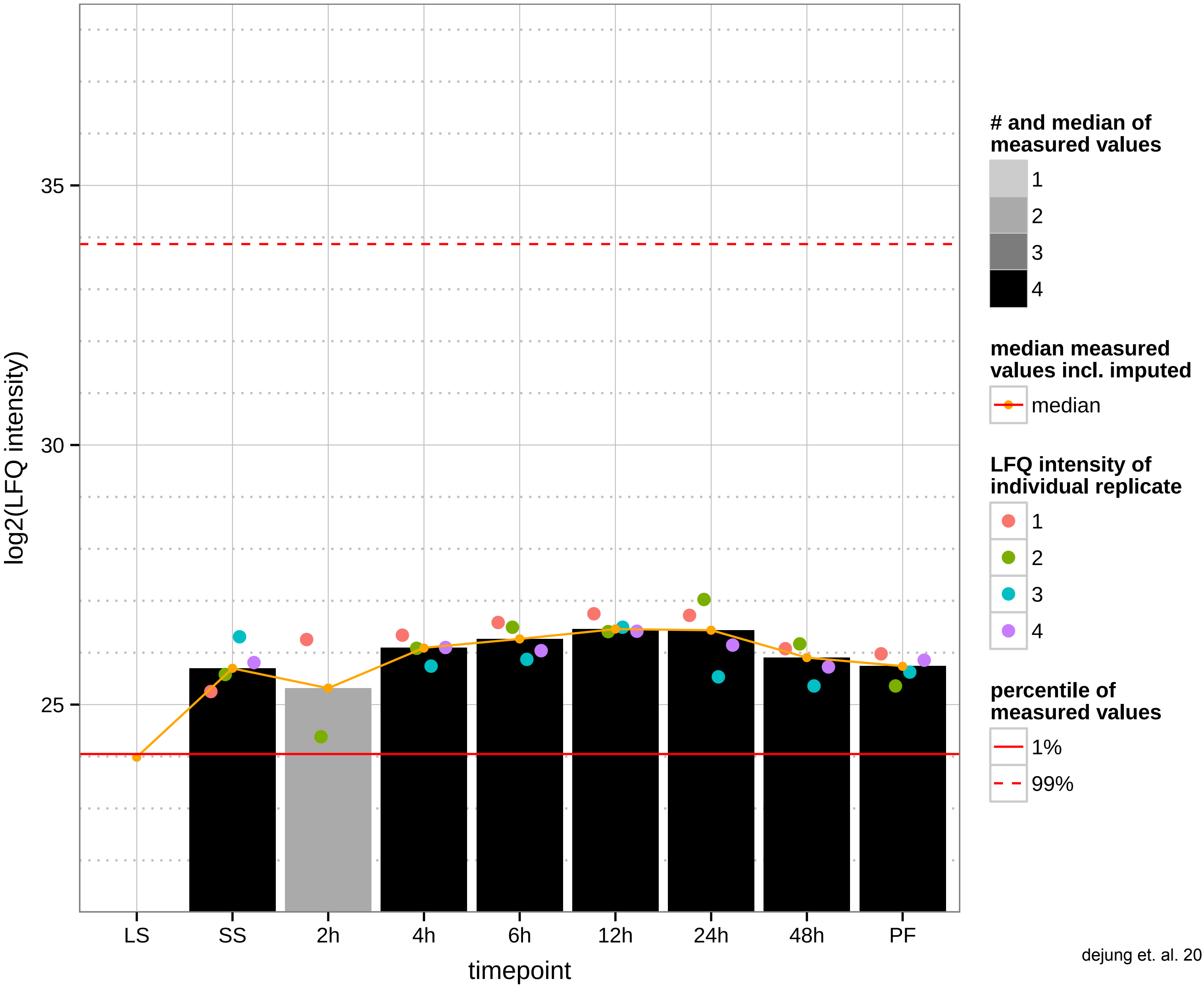
RNA–binding protein, putative (RBP22)
Tb927.5.1080
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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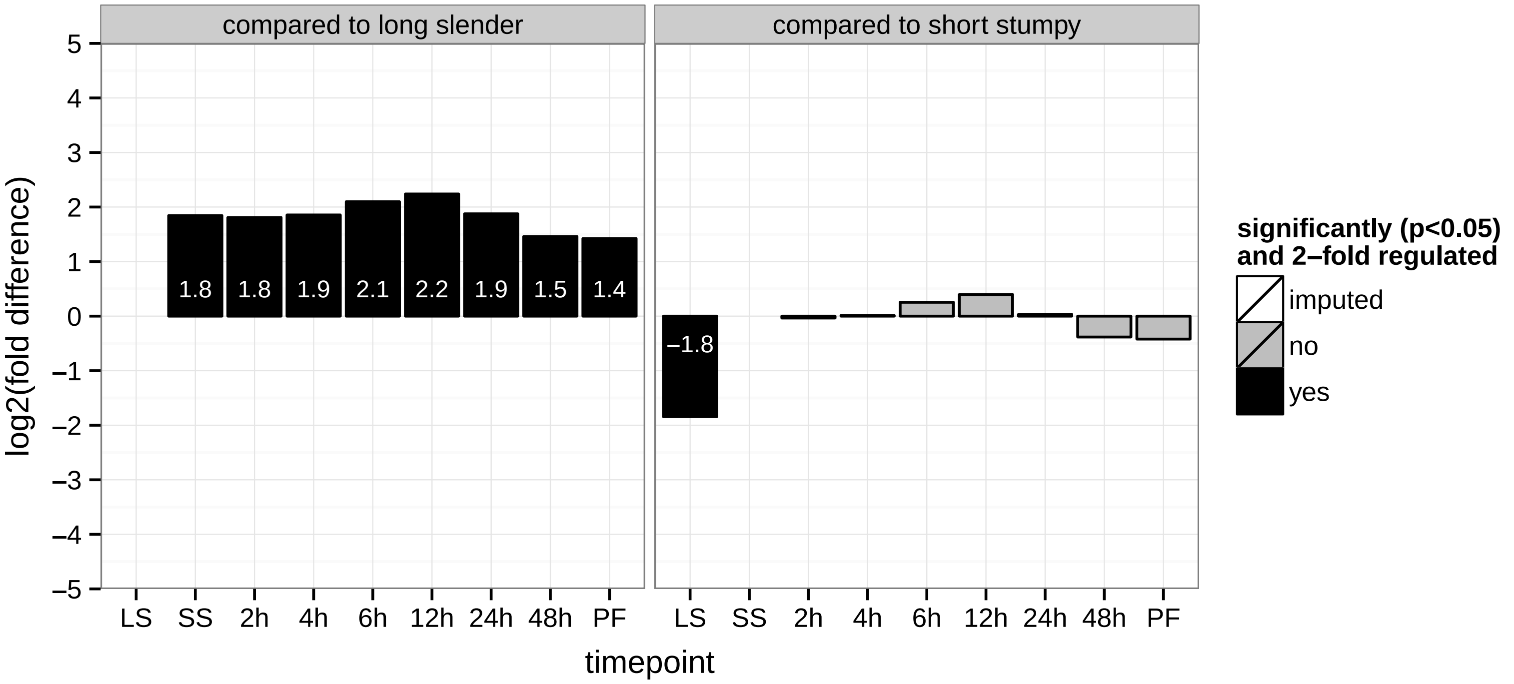
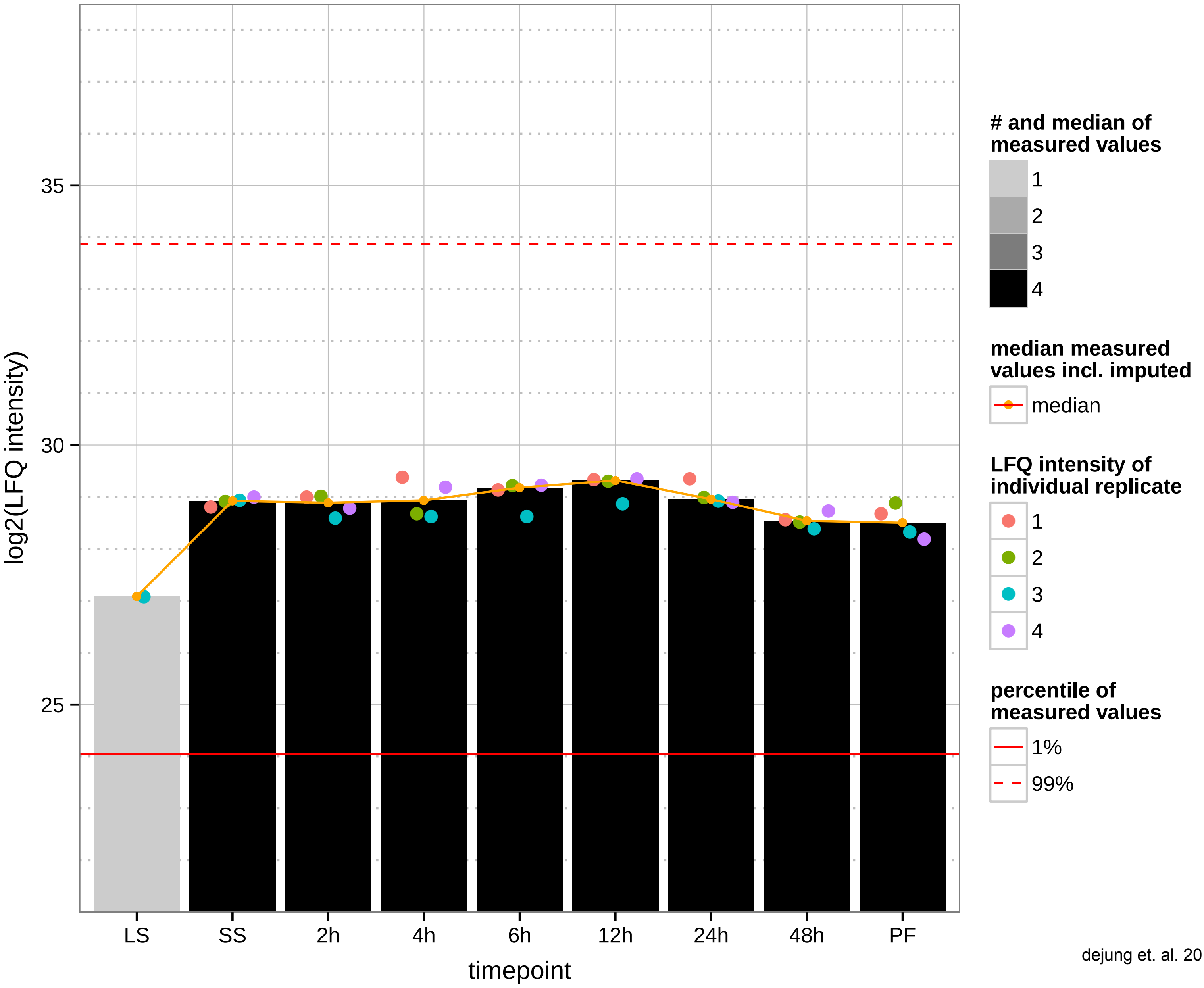
hypothetical protein, conserved
Tb927.5.1130
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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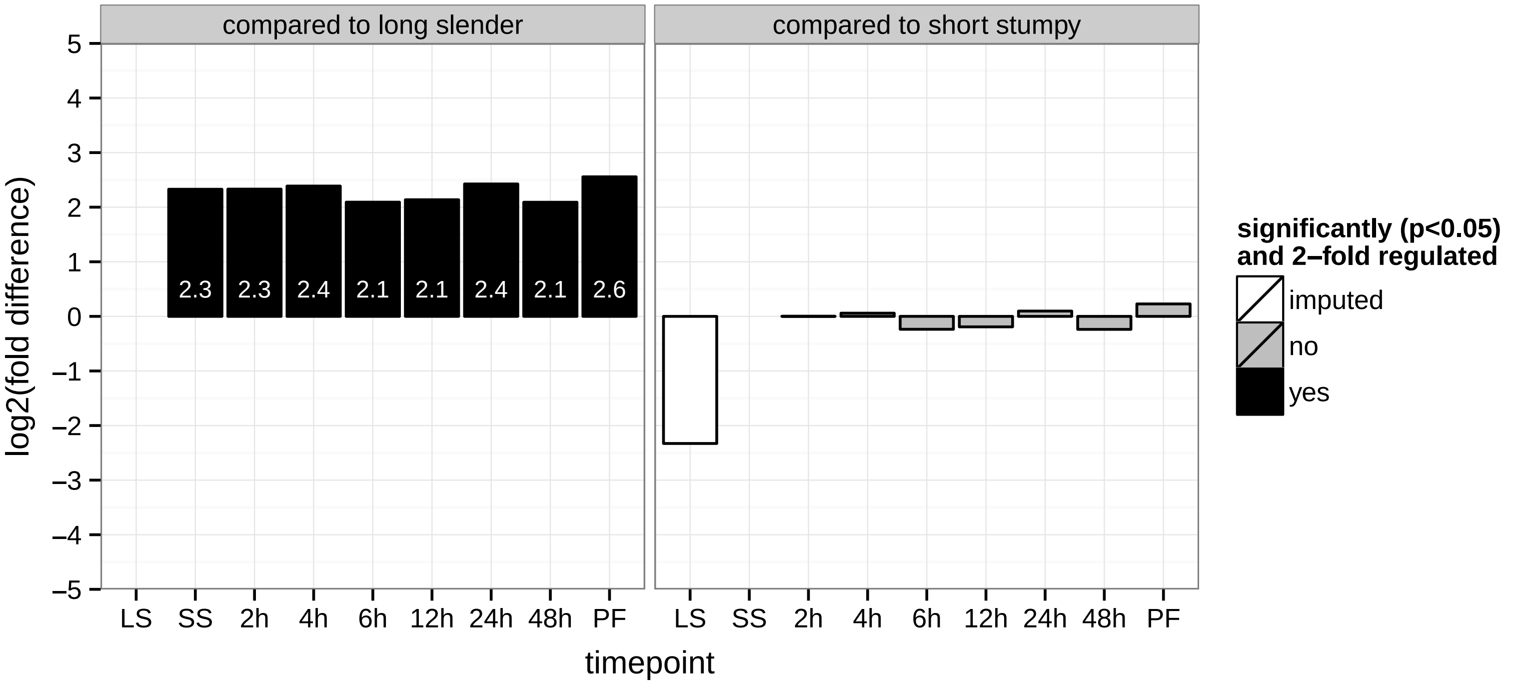
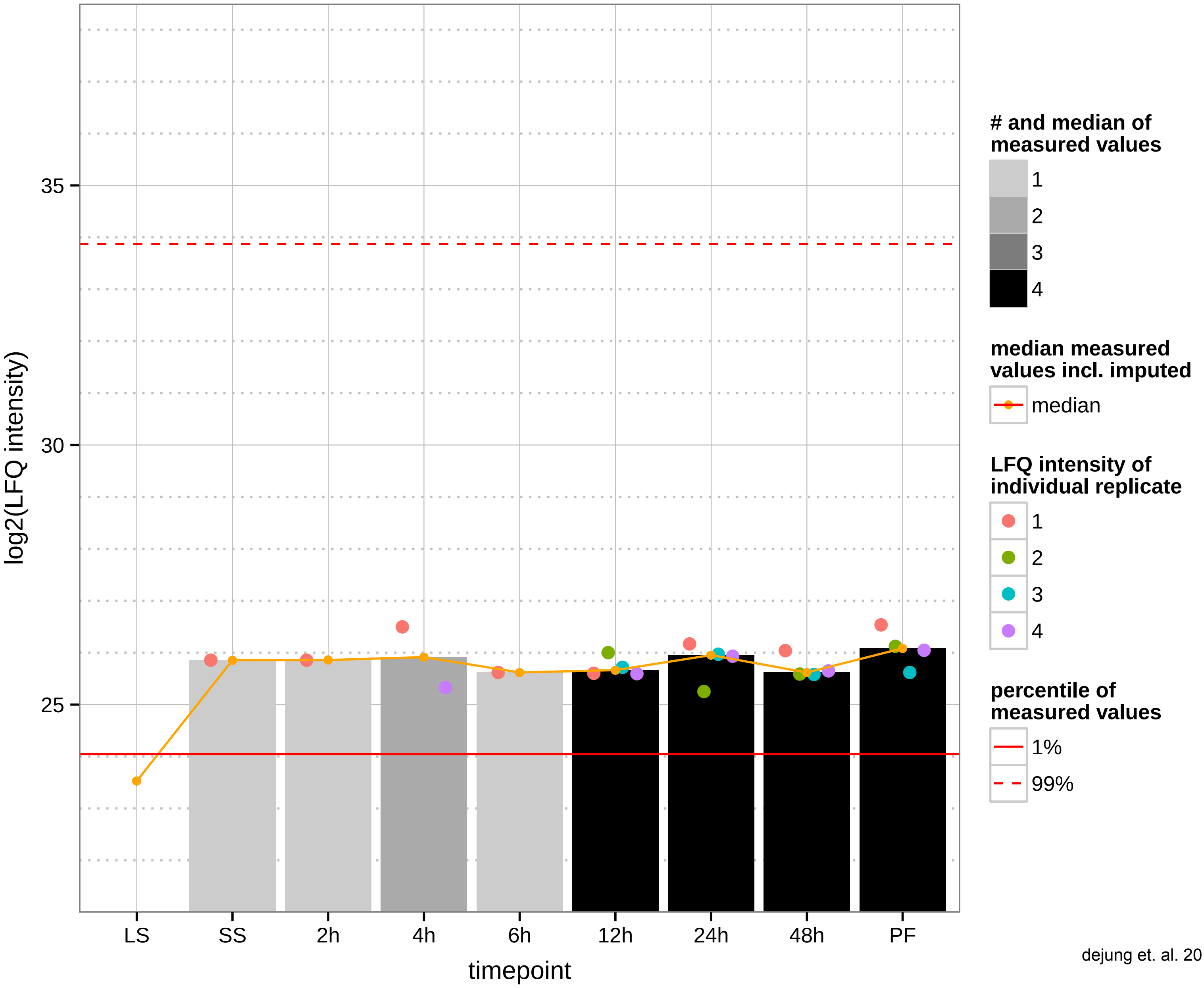
exosome component CSL4, Csl4p homologue (CSL4)
Tb927.5.1200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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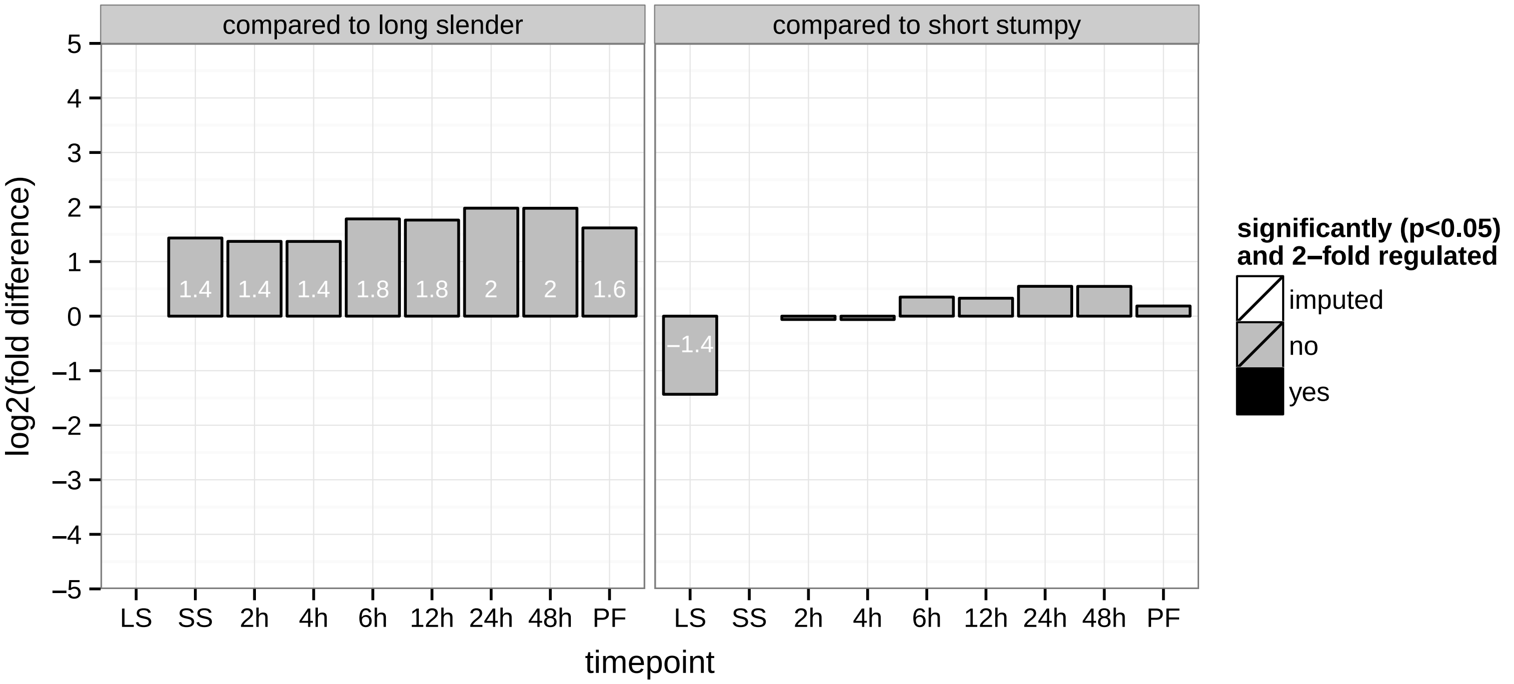
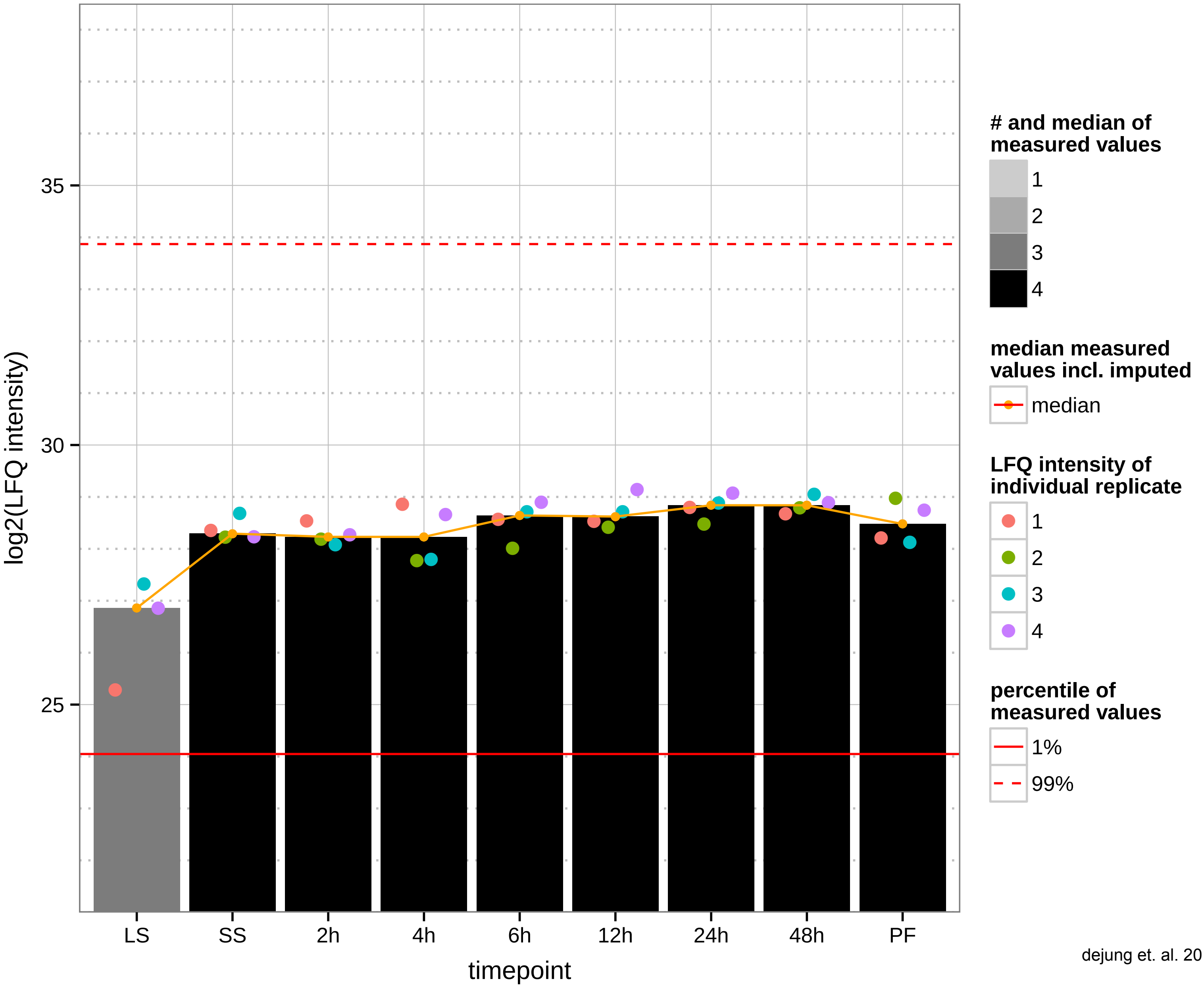
hypothetical protein, conserved
Tb927.5.1250
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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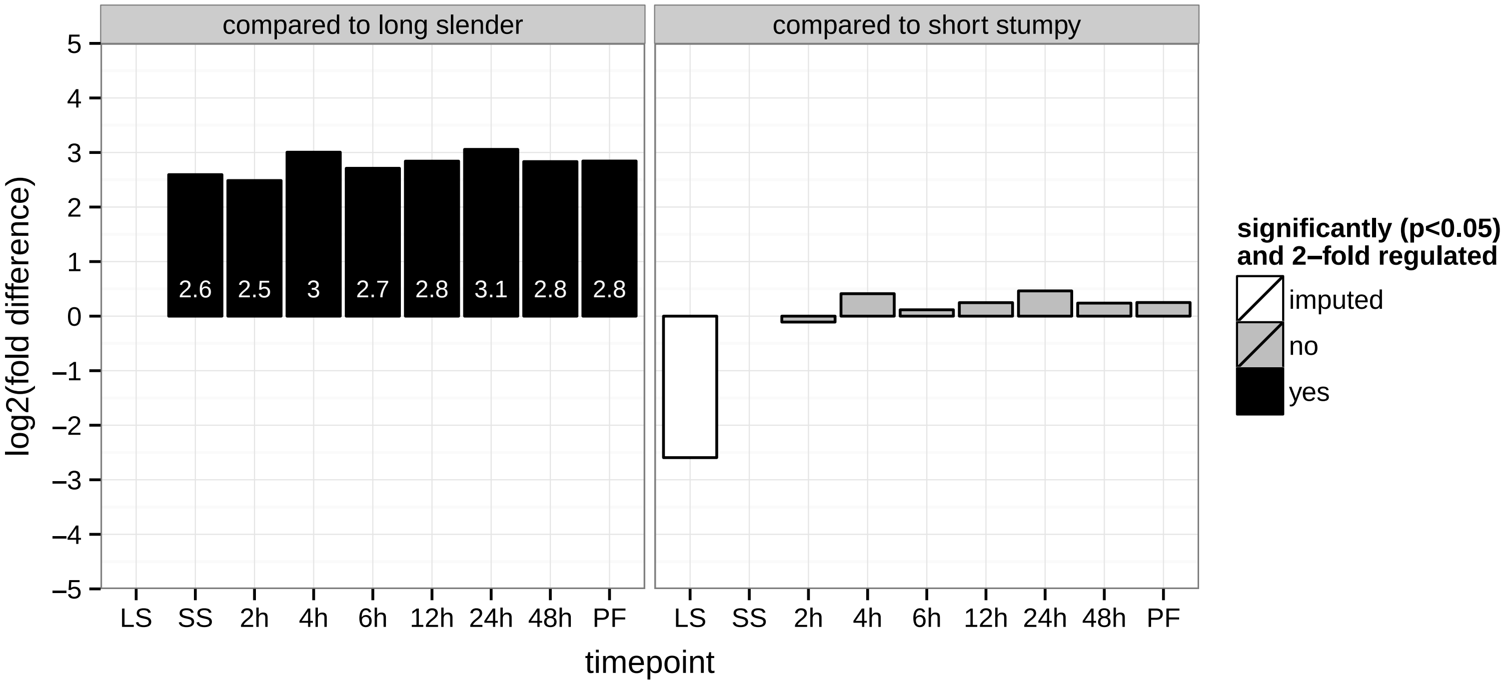
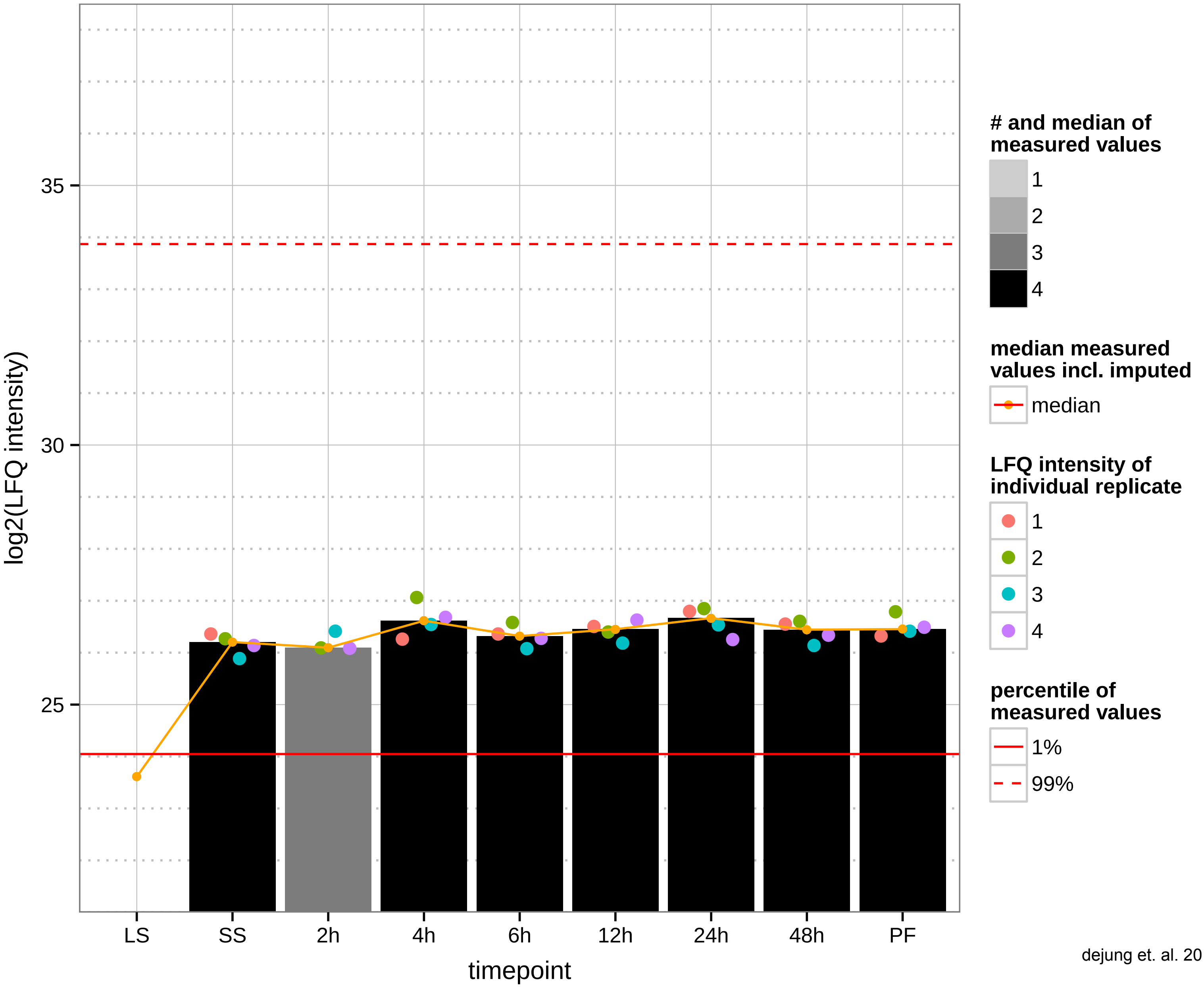
hypothetical protein, conserved
Tb927.5.1270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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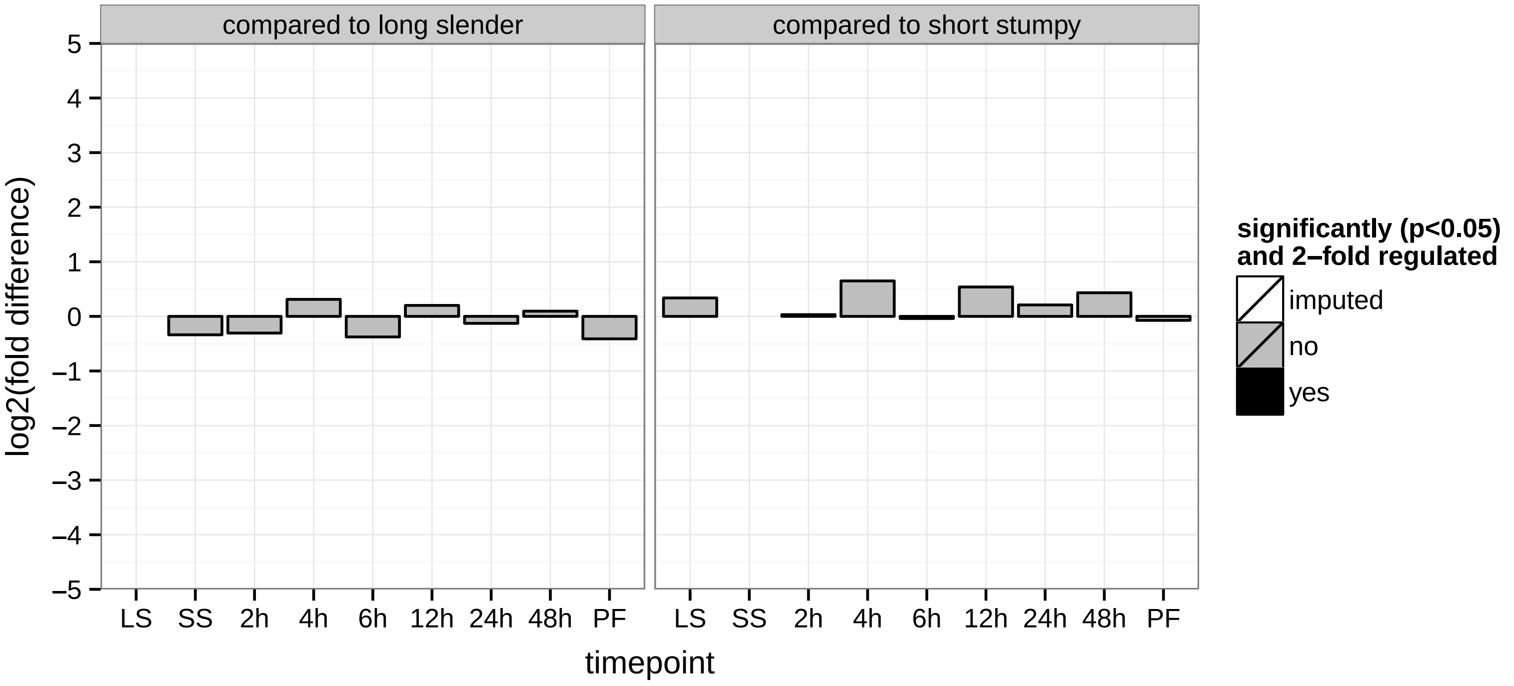
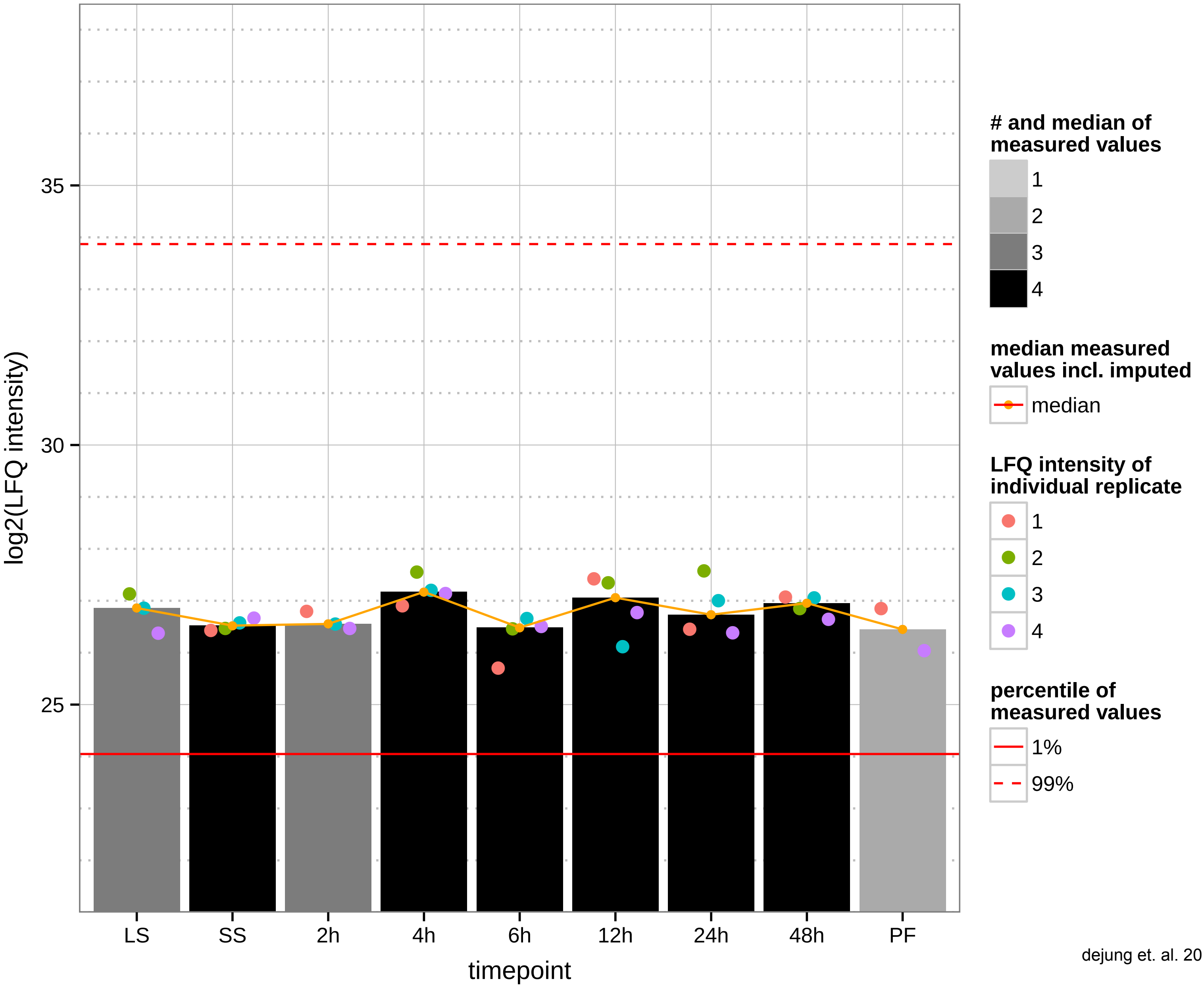
nucleoside 2–deoxyribosyltransferase (NDRT)
Tb927.5.1360
AGOF: null
AGOC: null
AGOP: null
PGOF: deoxyribonucleoside 5'–monophosphate N–glycosidase activity, nucleoside deoxyribosyltransferase activity
PGOC: null
PGOP: deoxyribonucleoside monophosphate catabolic process





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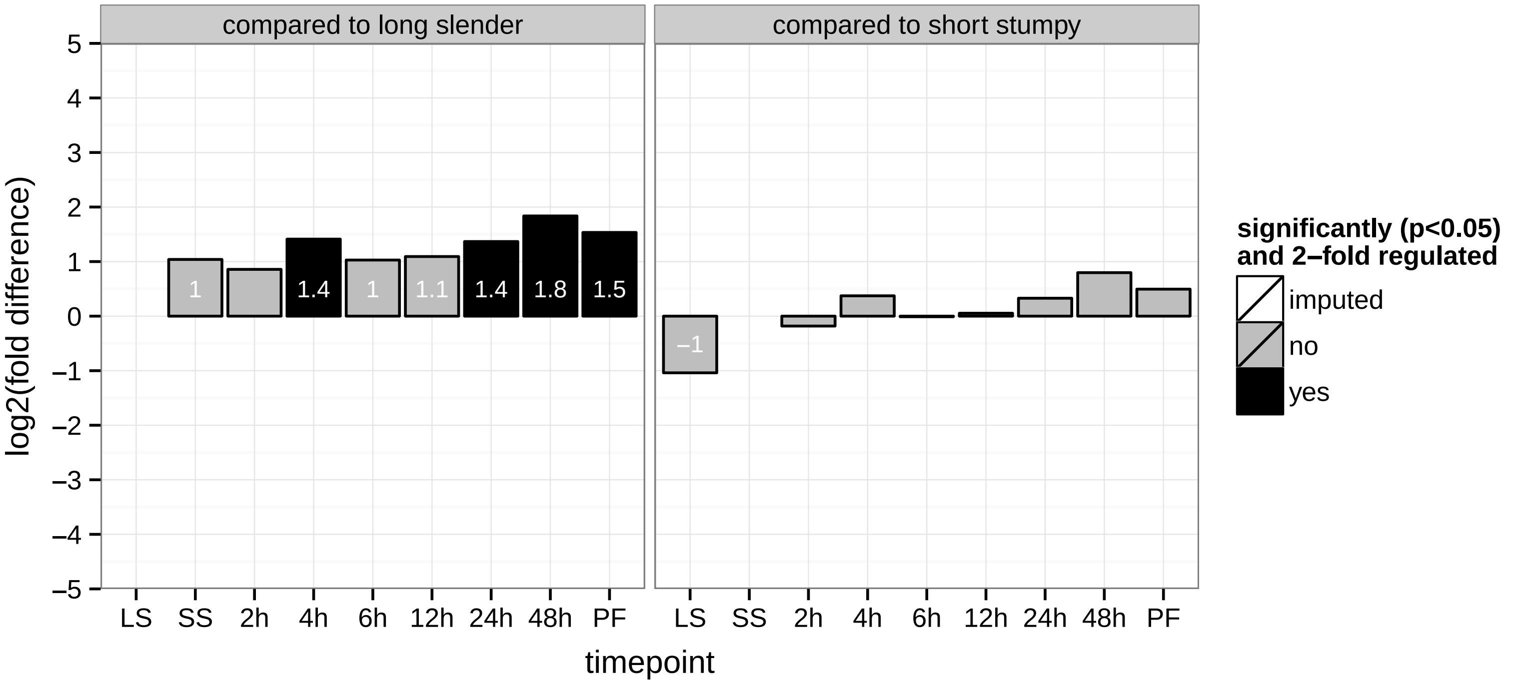
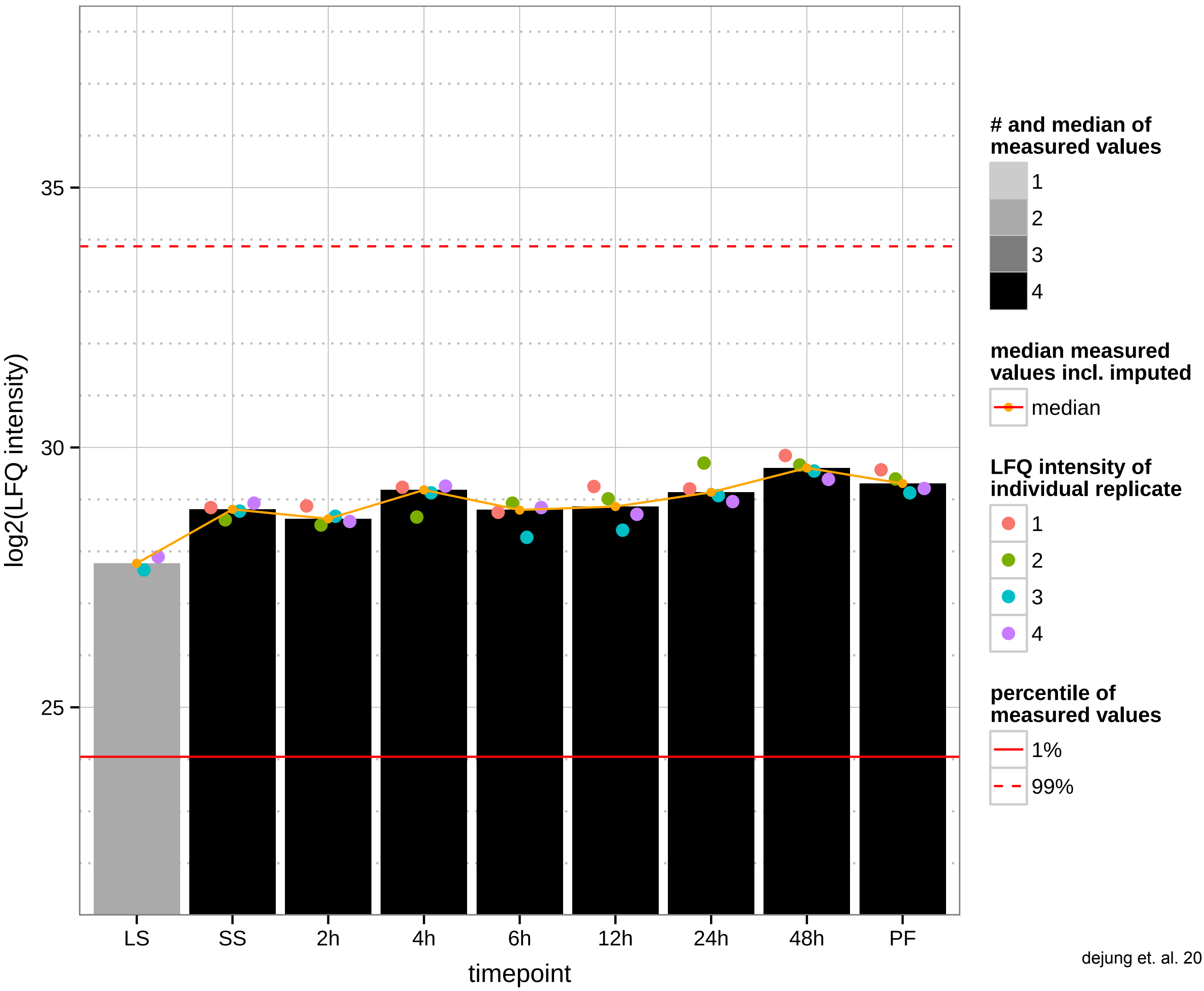
NADH–cytochrome b5 reductase, putative (B5R)
Tb927.5.1470
AGOF: electron carrier activity, oxidoreductase activity
AGOC: null
AGOP: null
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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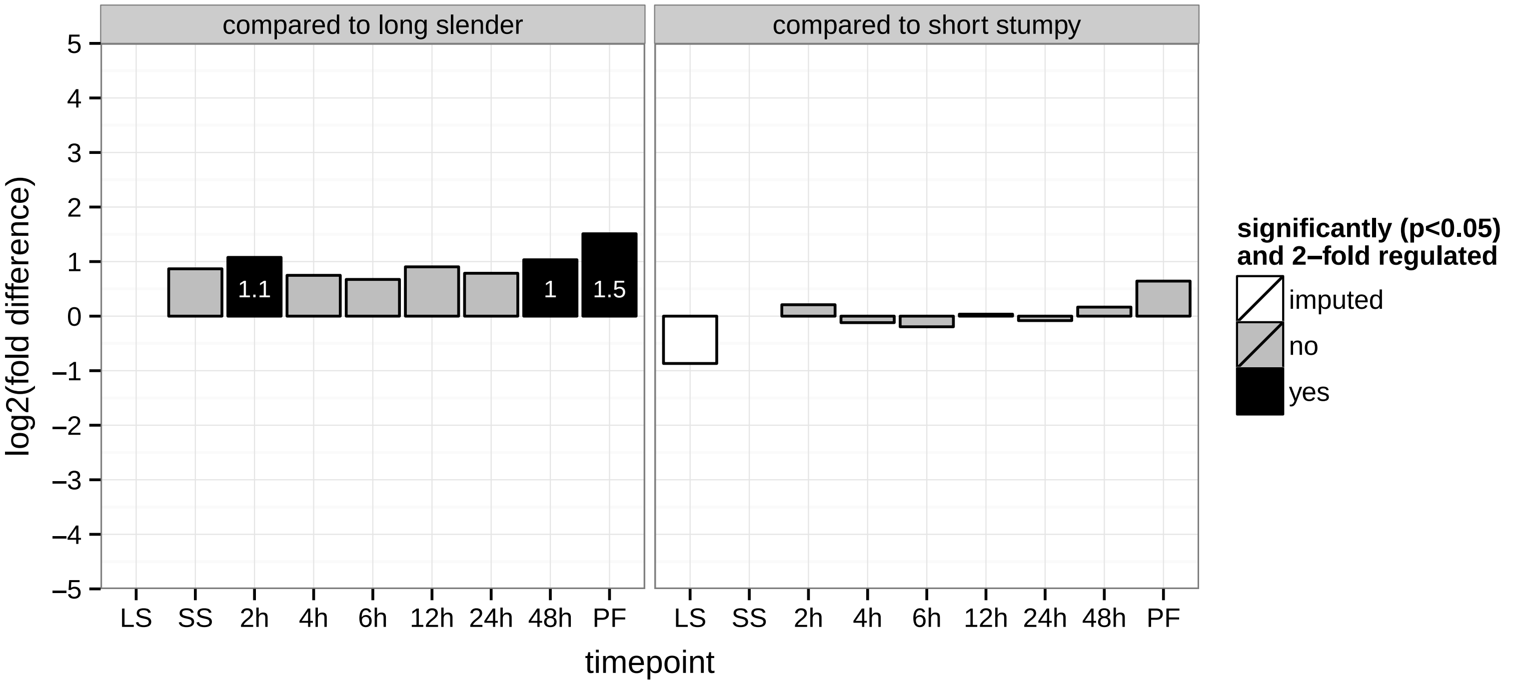
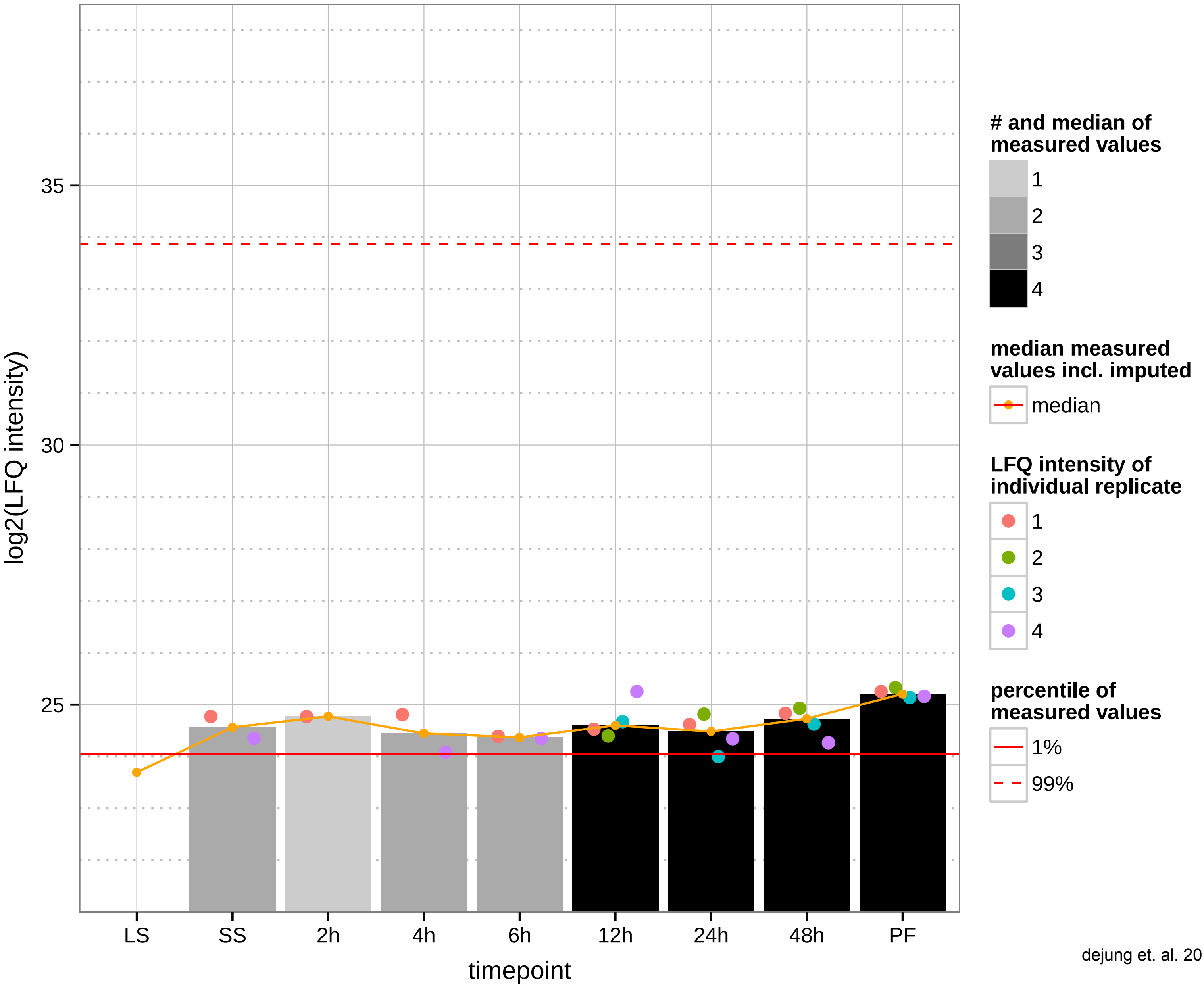
hypothetical protein, conserved
Tb927.5.1530
AGOF: N, N−dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding
AGOC: mitochondrion
AGOP: null
PGOF: N, N−dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding
PGOC: null
PGOP: oxidation−reduction process





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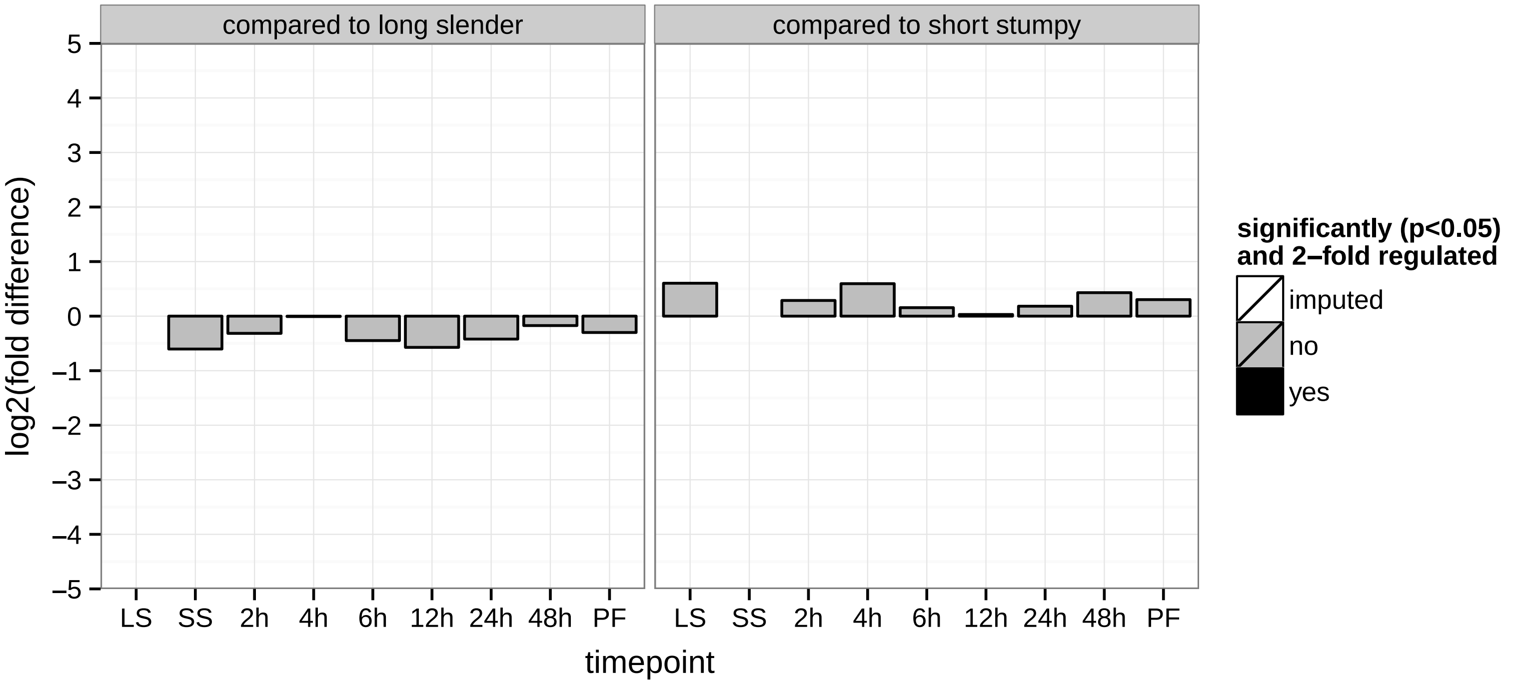
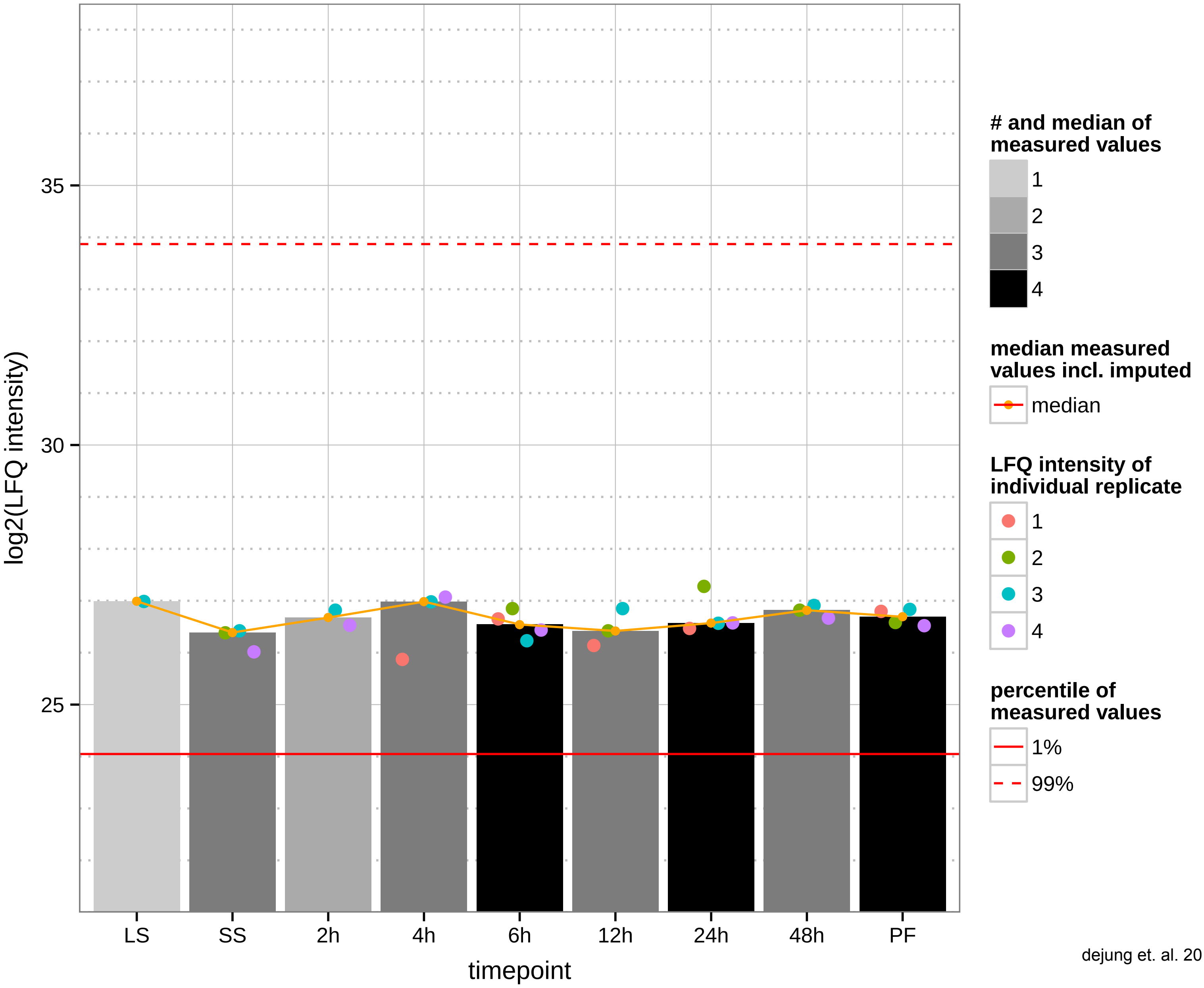
hypothetical protein, conserved
Tb927.5.1630
AGOF: heme binding
AGOC: null
AGOP: null
PGOF: heme binding
PGOC: null
PGOP: null





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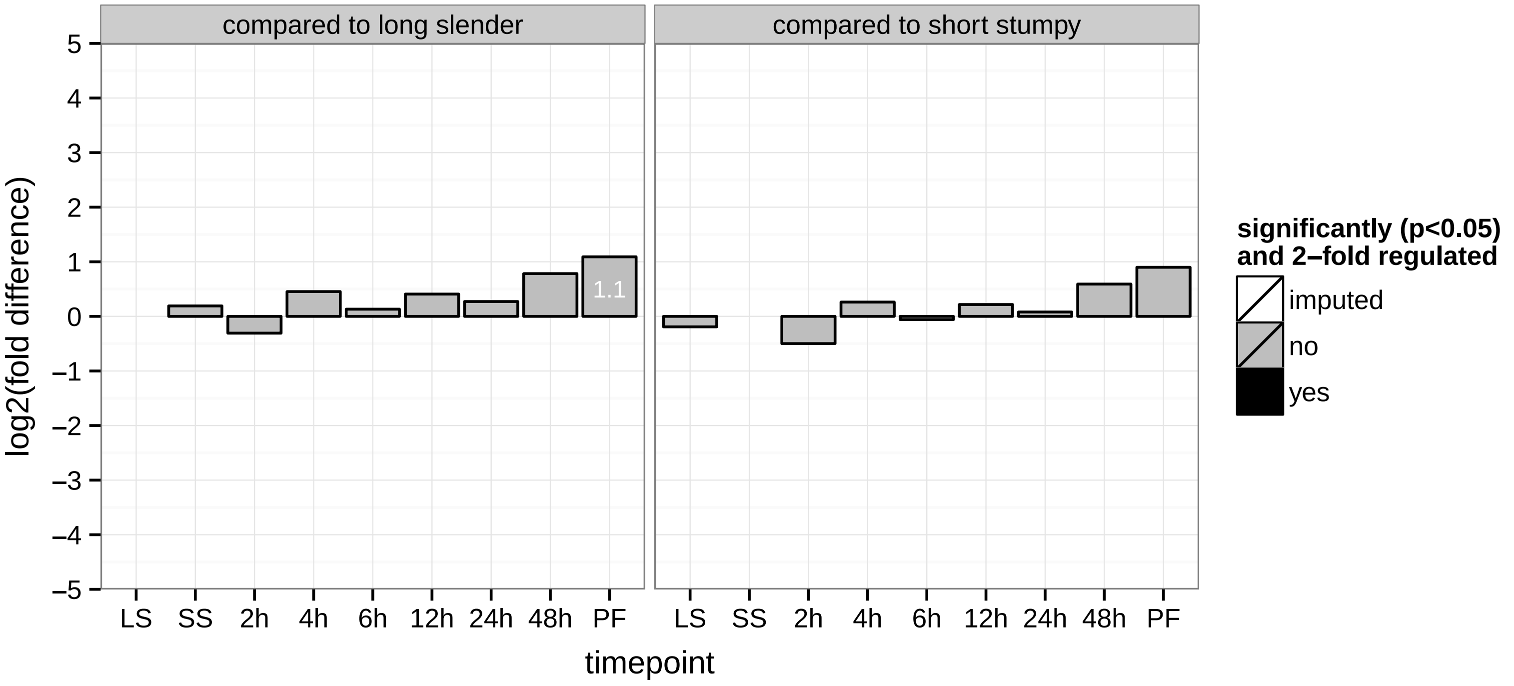
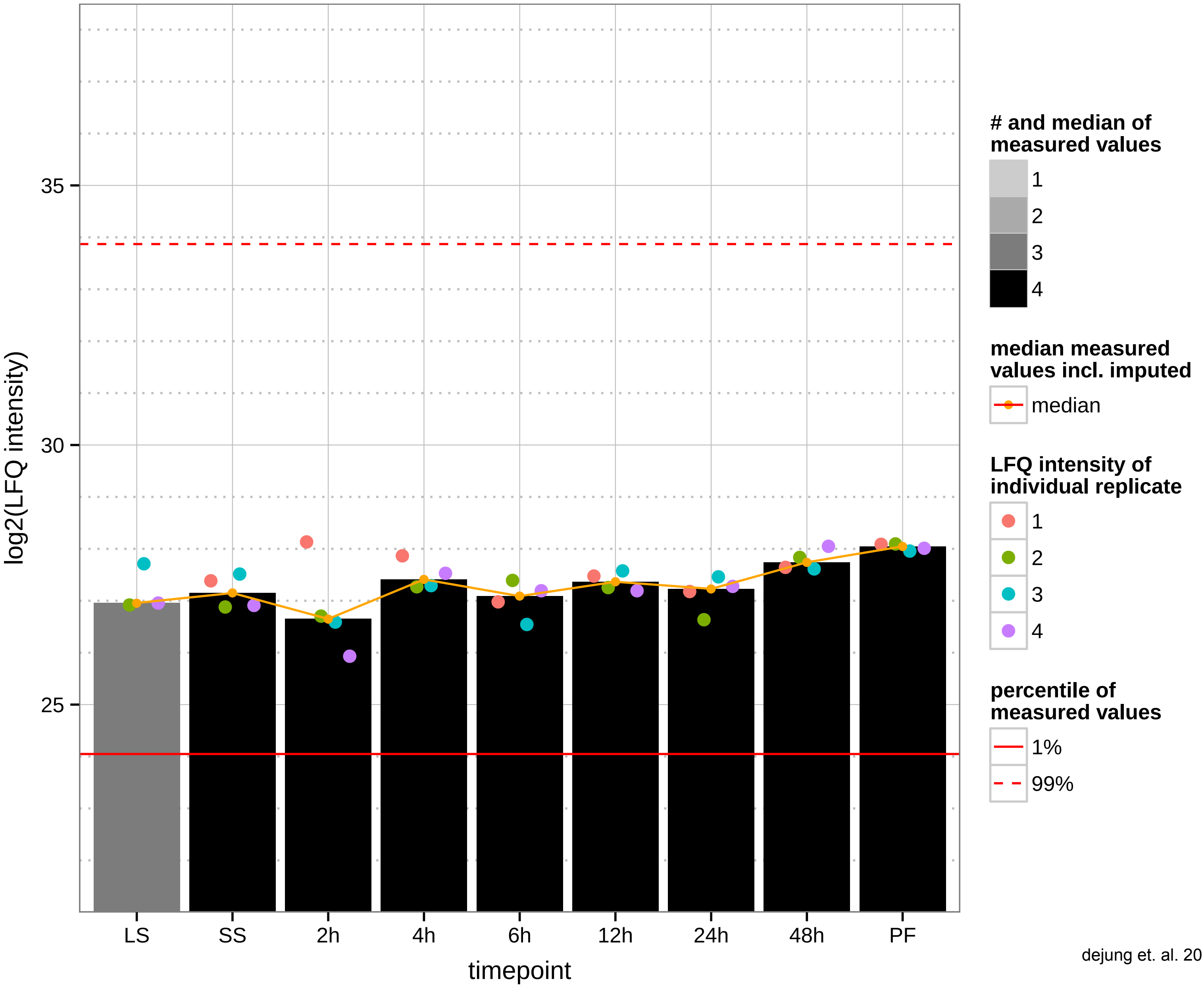
hypothetical protein, conserved
Tb927.5.1680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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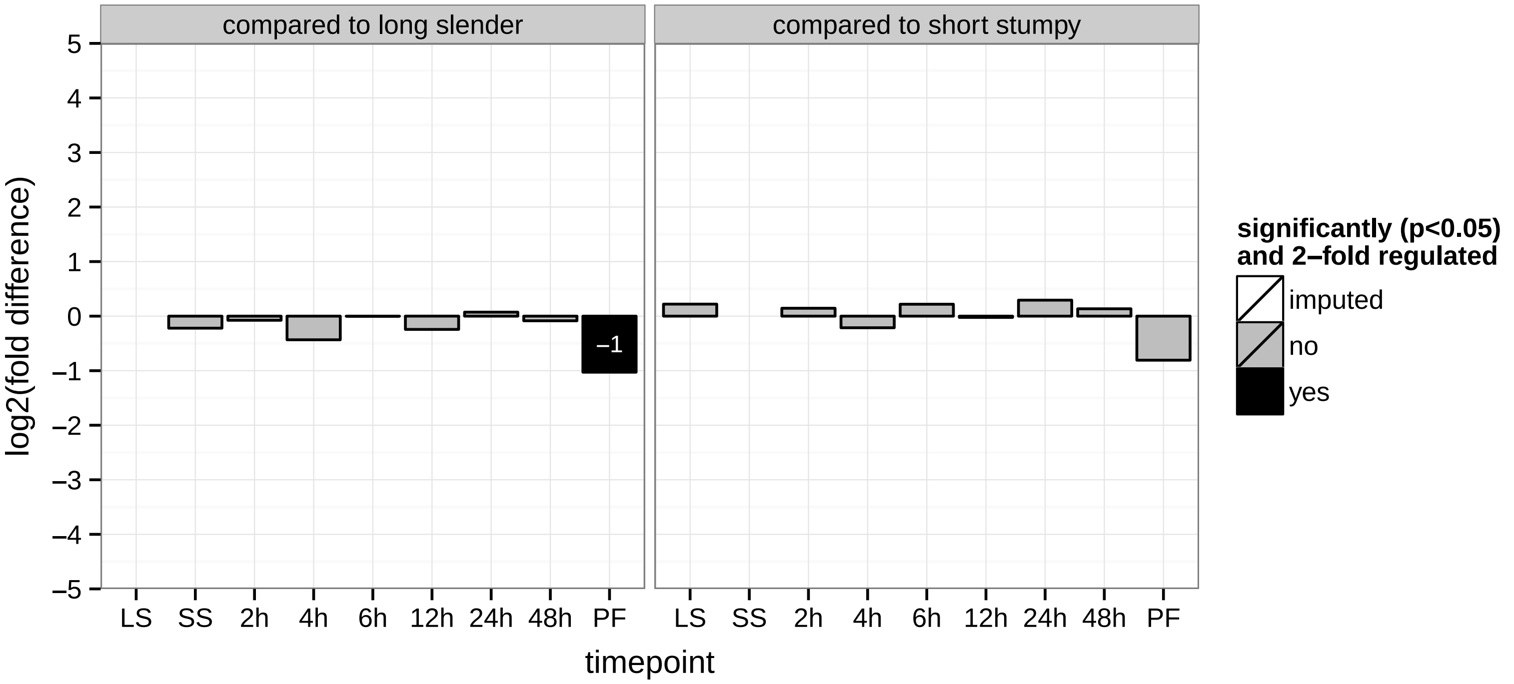
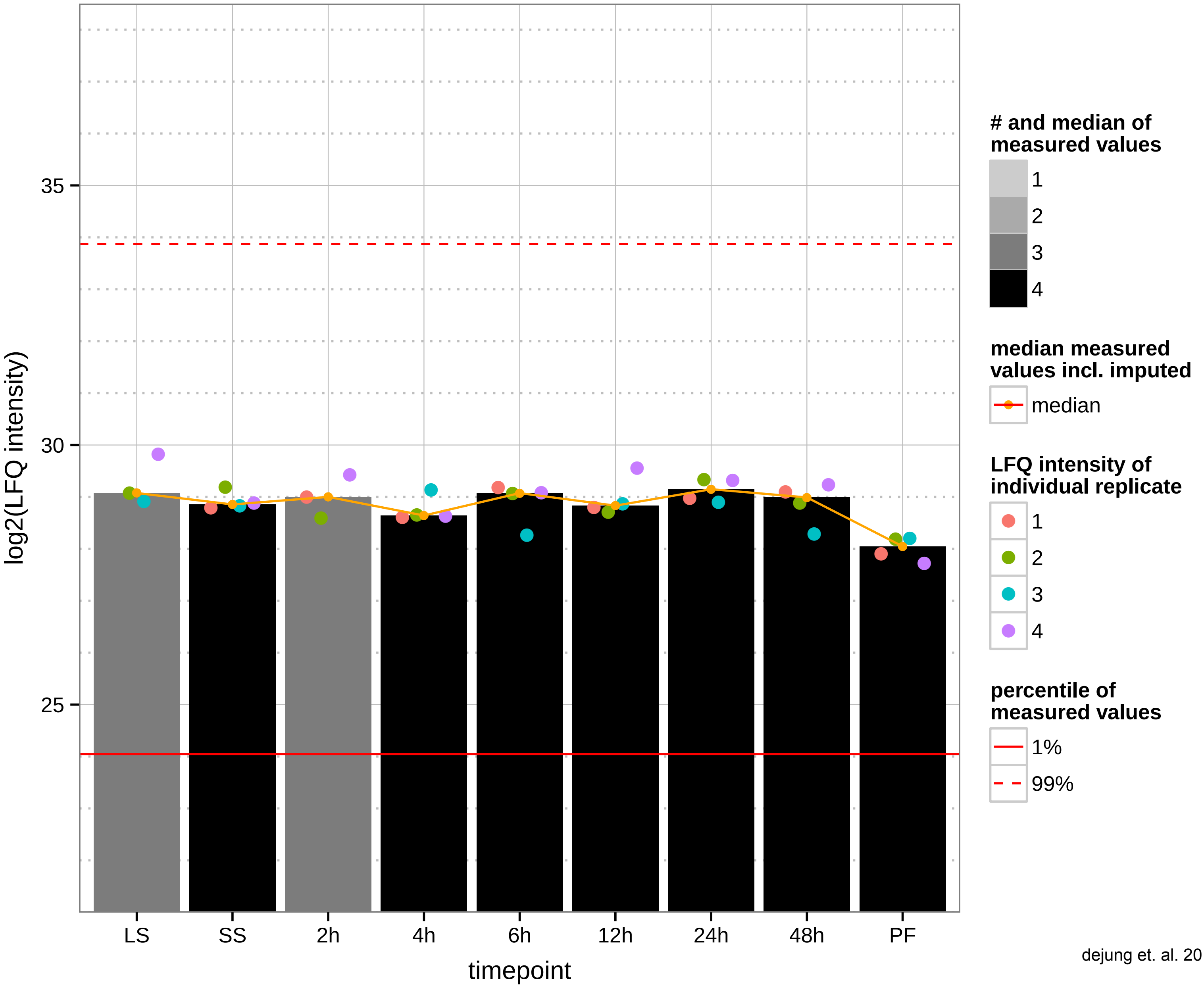
hypothetical protein, conserved
Tb927.5.1690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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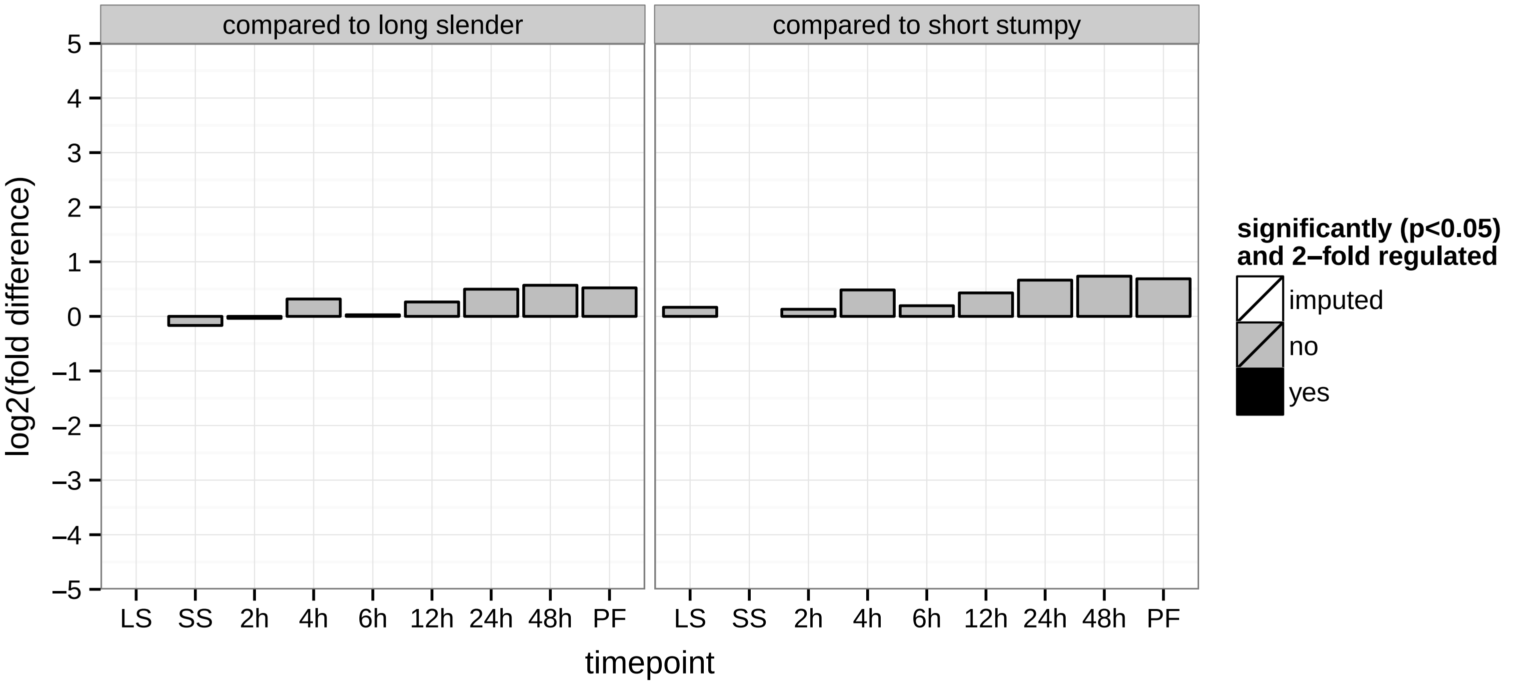
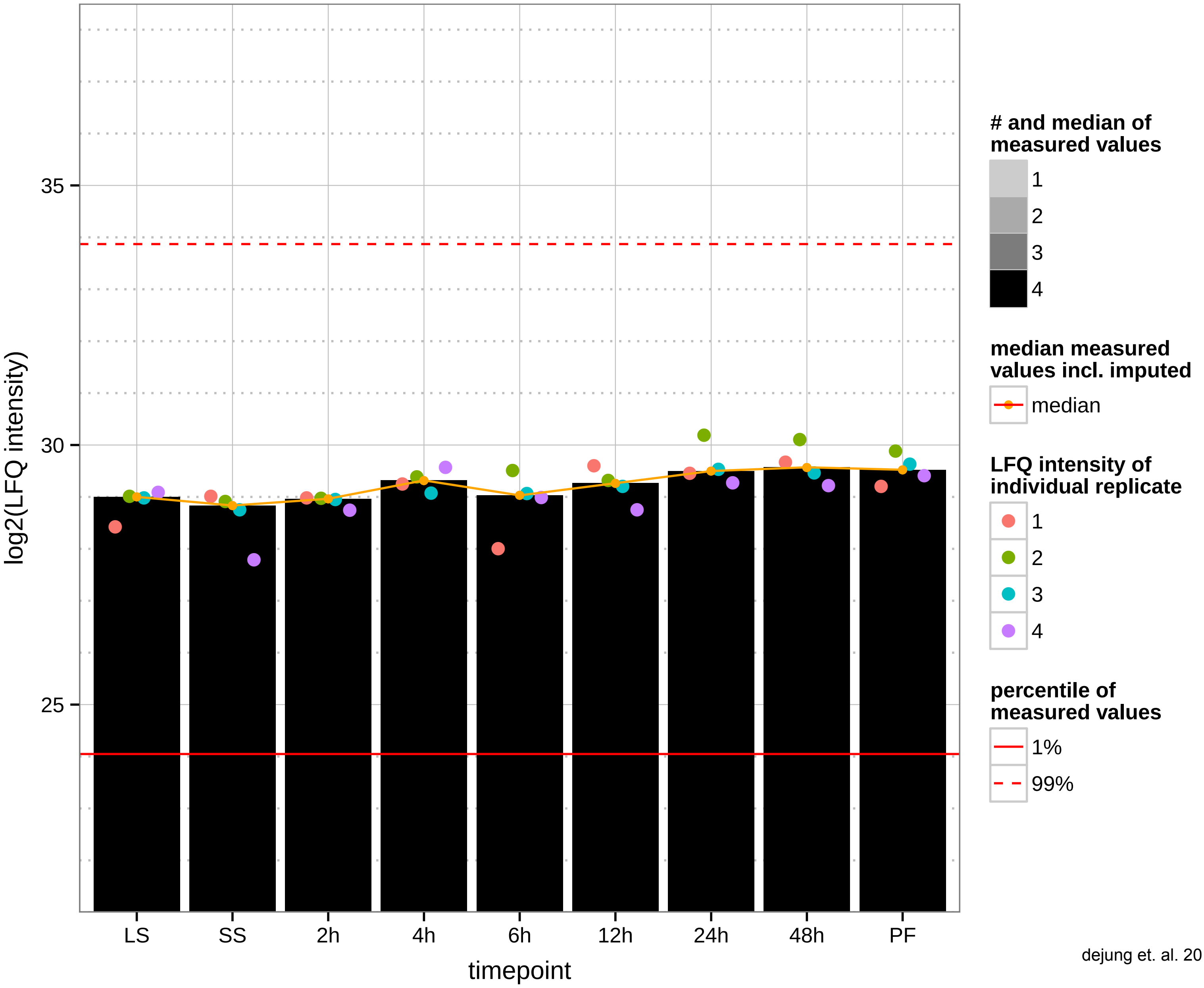
replication Factor A 28 kDa subunit, putative
Tb927.5.1700
AGOF: nucleic acid binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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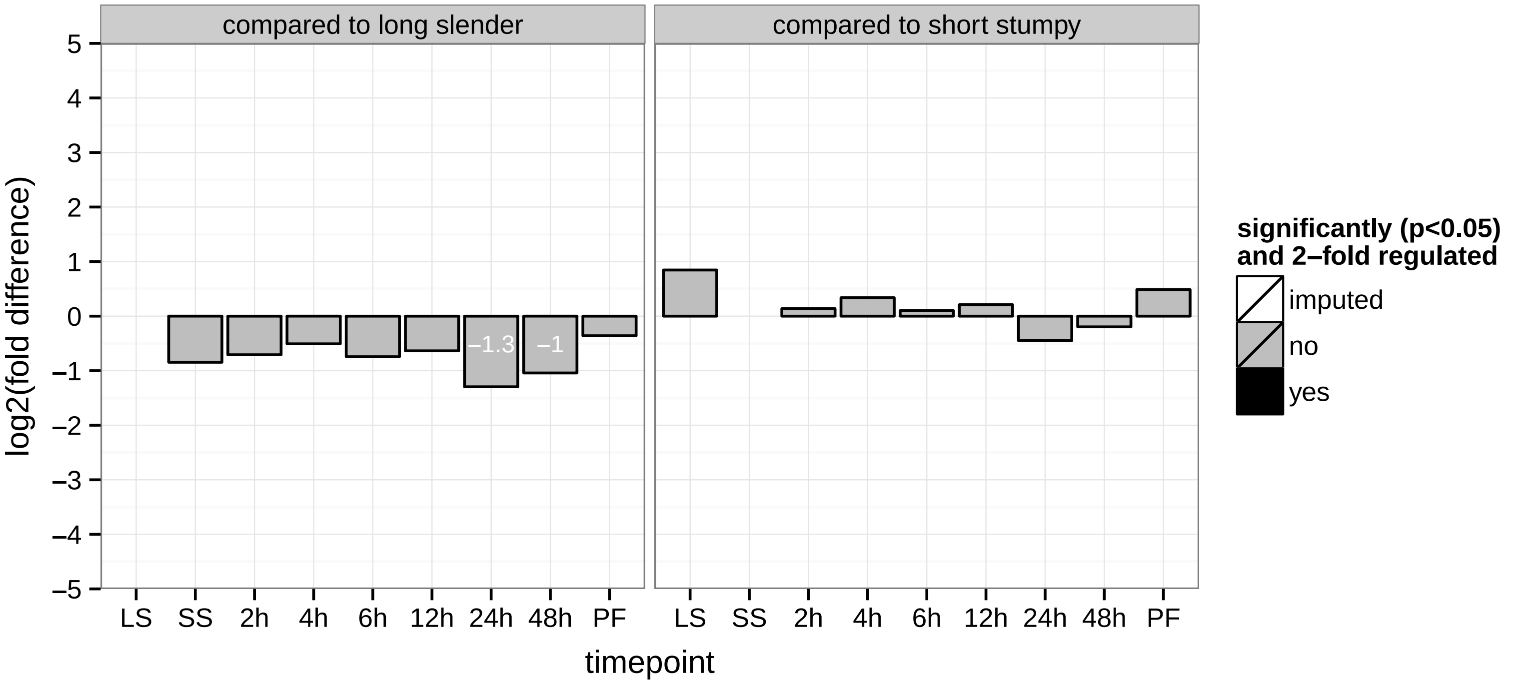
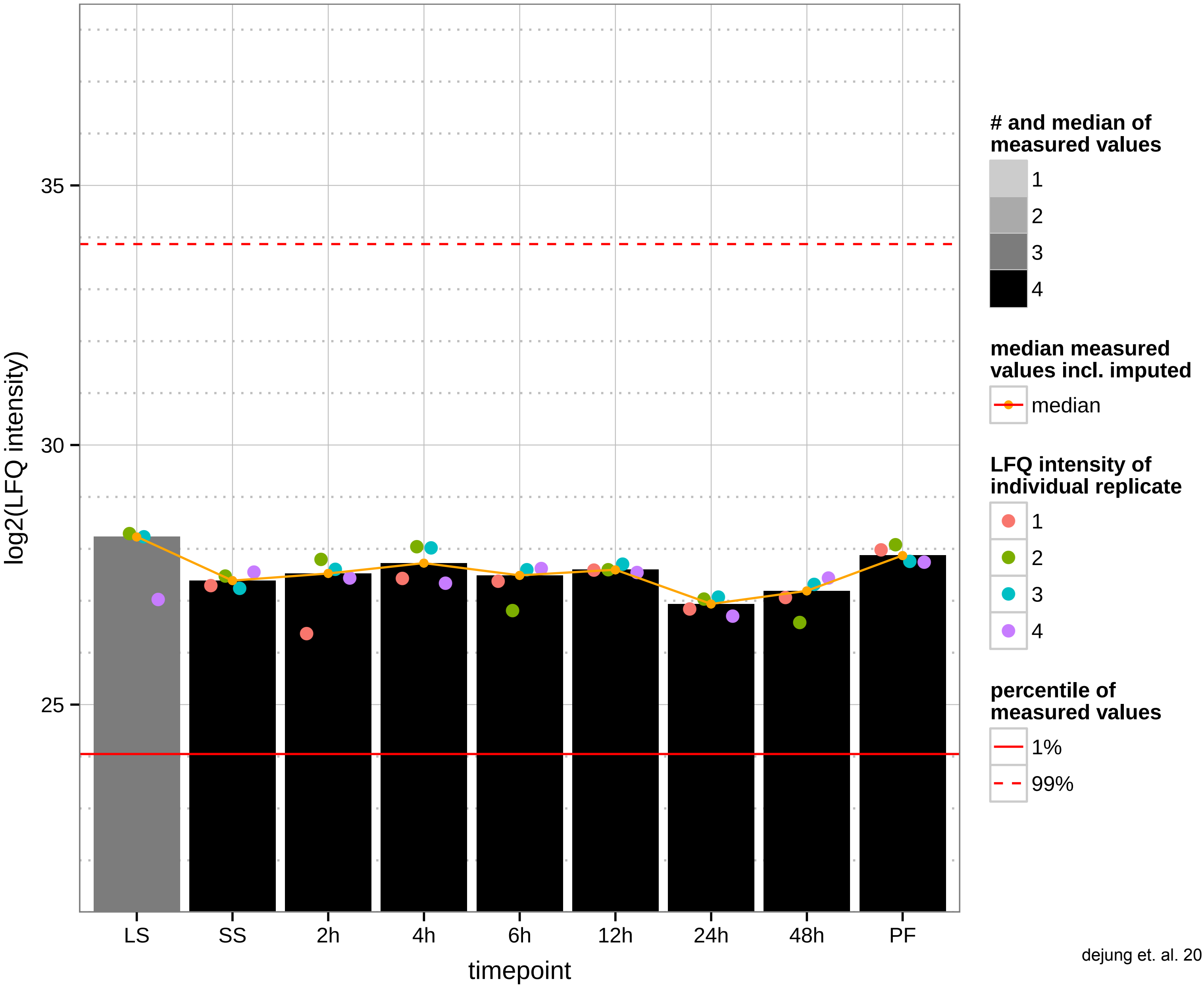
ecotin family (I11), putative, inhibitor of serine peptidase (ISP), putative (ISP)
Tb927.5.1730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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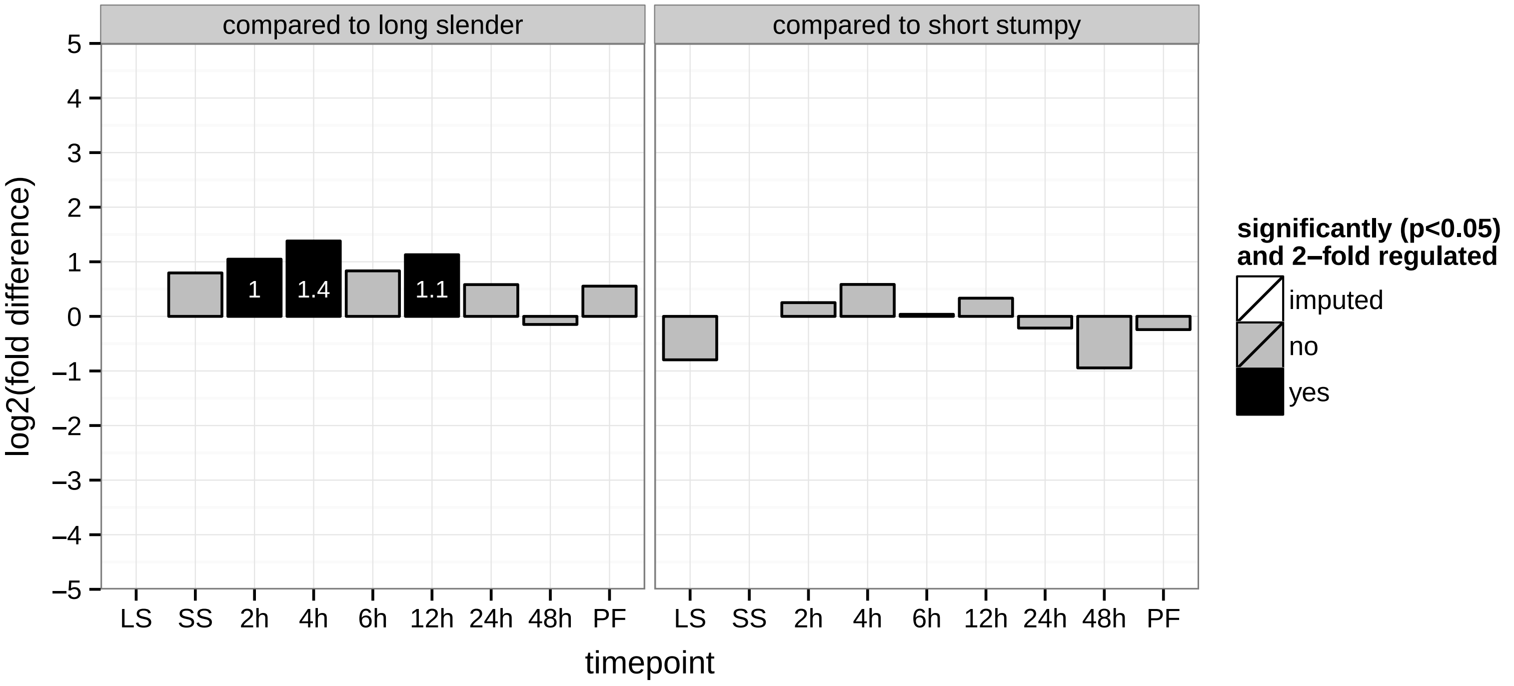
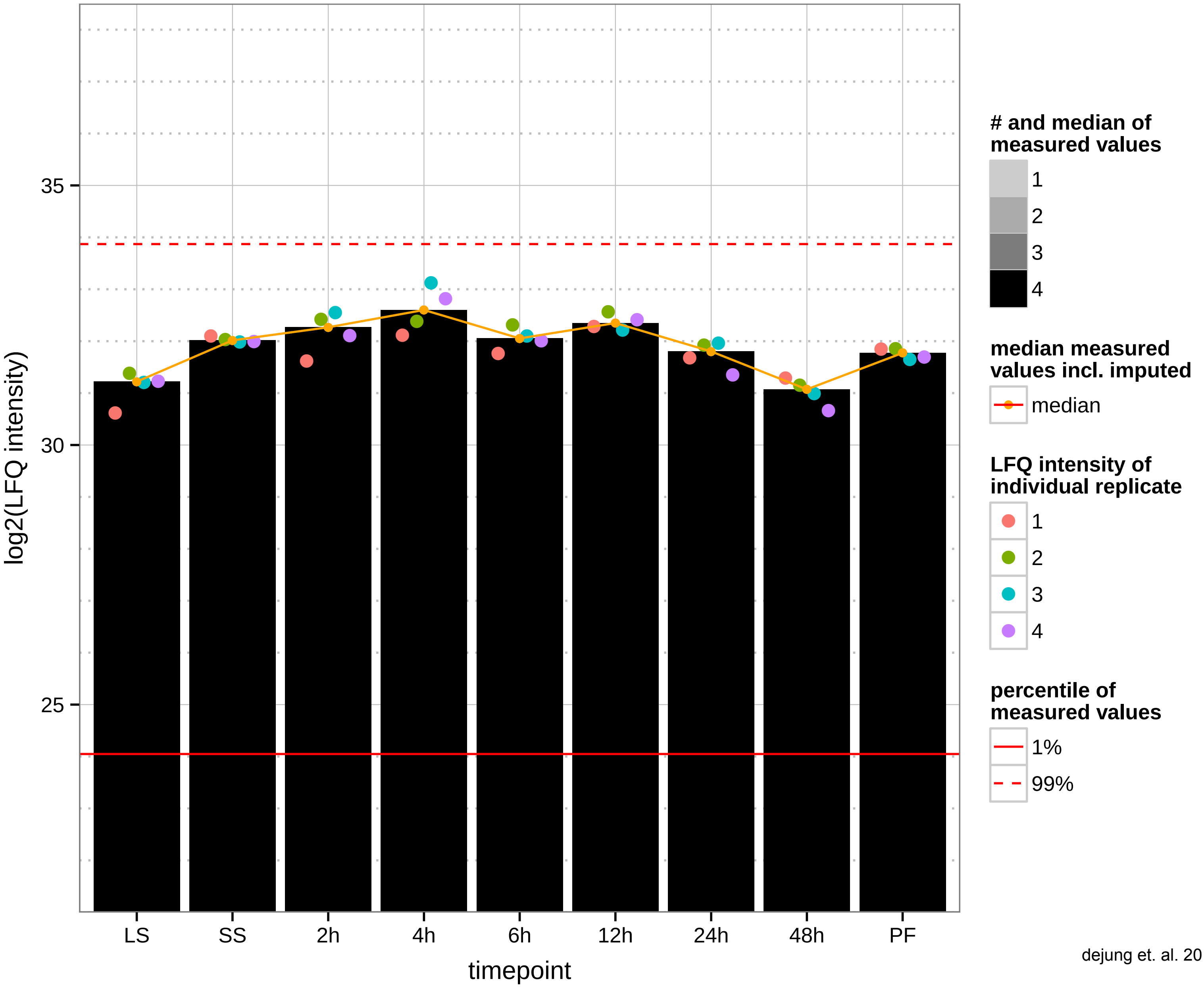
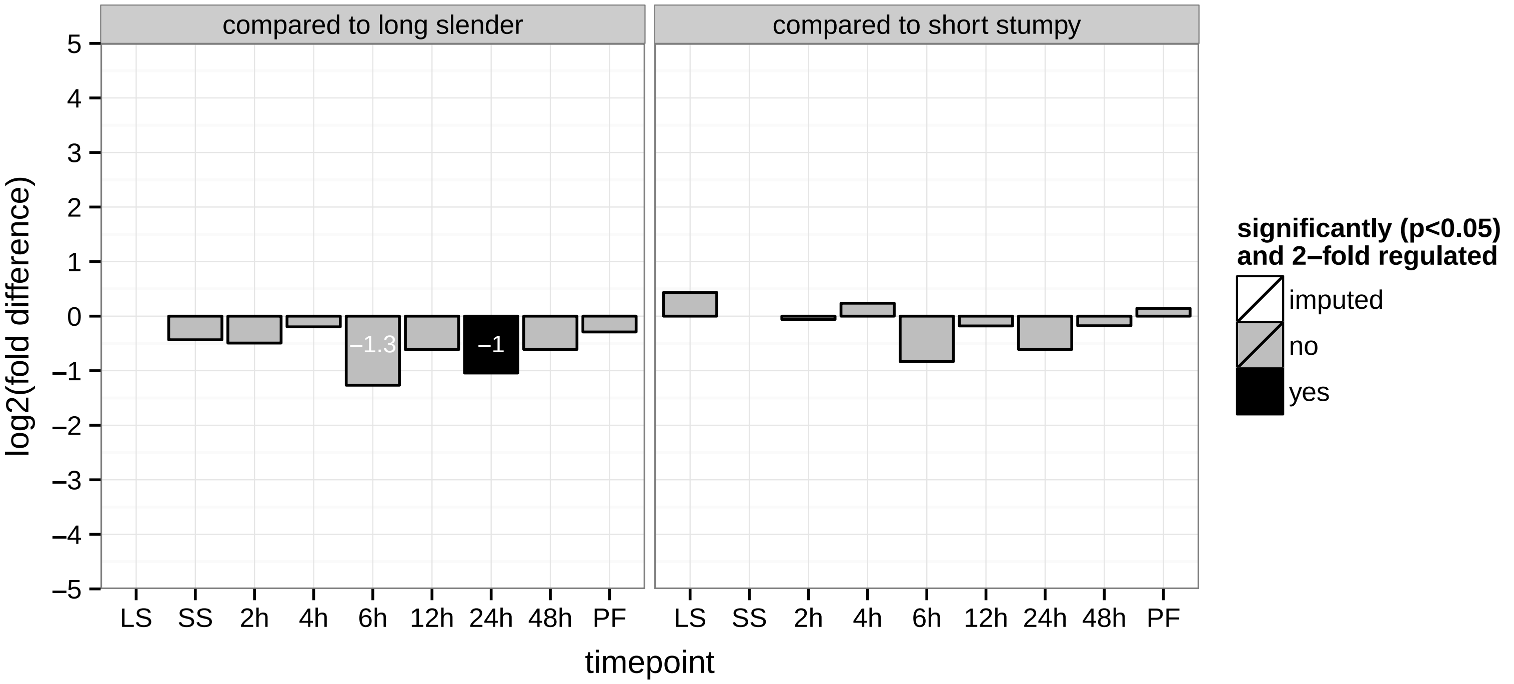
lysosomal/endosomal membrane protein p67 (p67), lysosomal/endosomal membrane protein p67, lysosomal membrane glyco
Tb927.5.1810;Tb927.5.1830
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

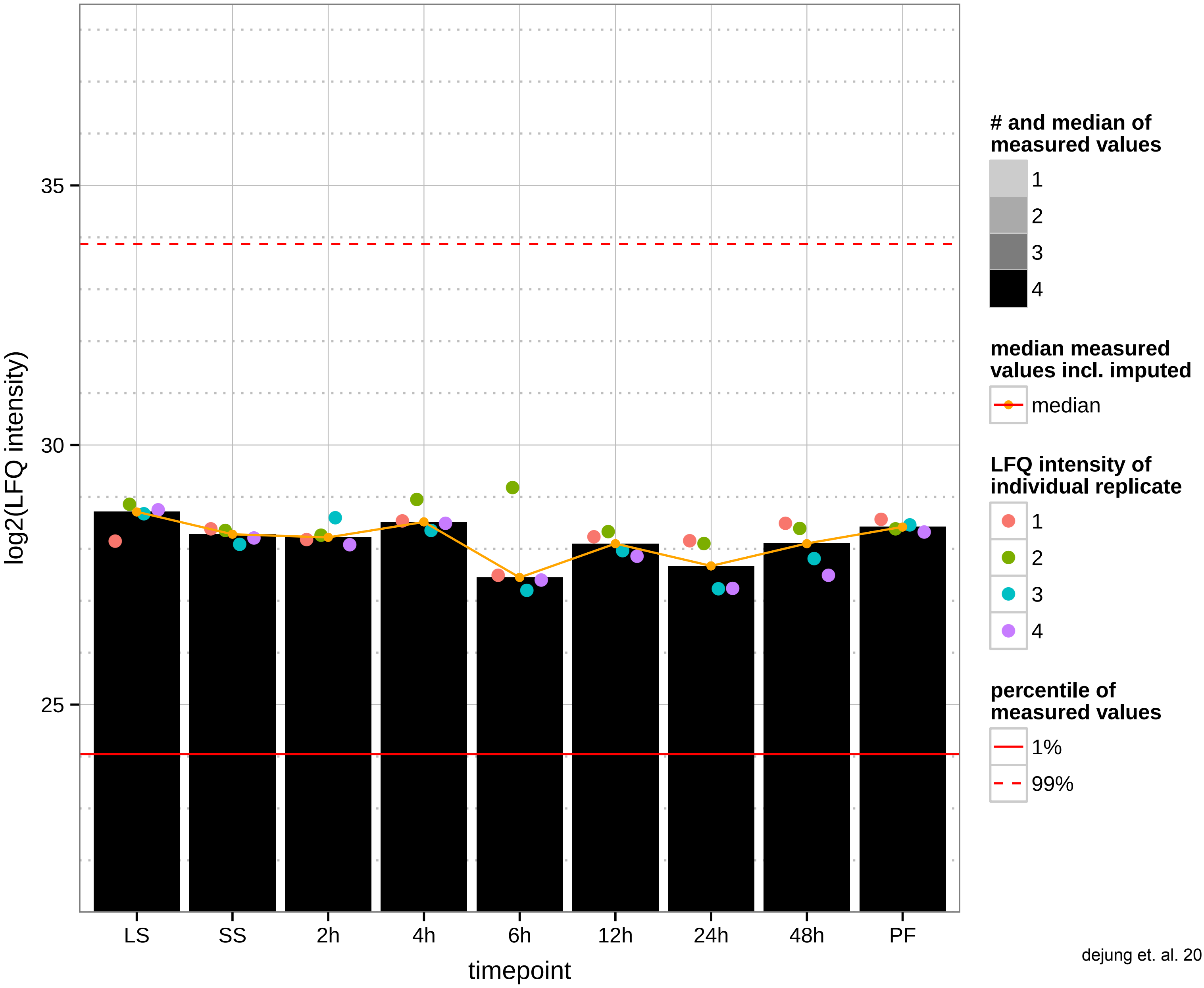




dejung et. al. 2015

ecotin family (I11), putative, inhibitor of serine peptidase (ISP), putative (ISP2)
Tb927.5.1880
AGOF: null
AGOC: null
AGOP: active evasion of host immune response via regulation of host complement system, modulation by symbiont of host ph
PGOF: null
PGOC: null
PGOP: null





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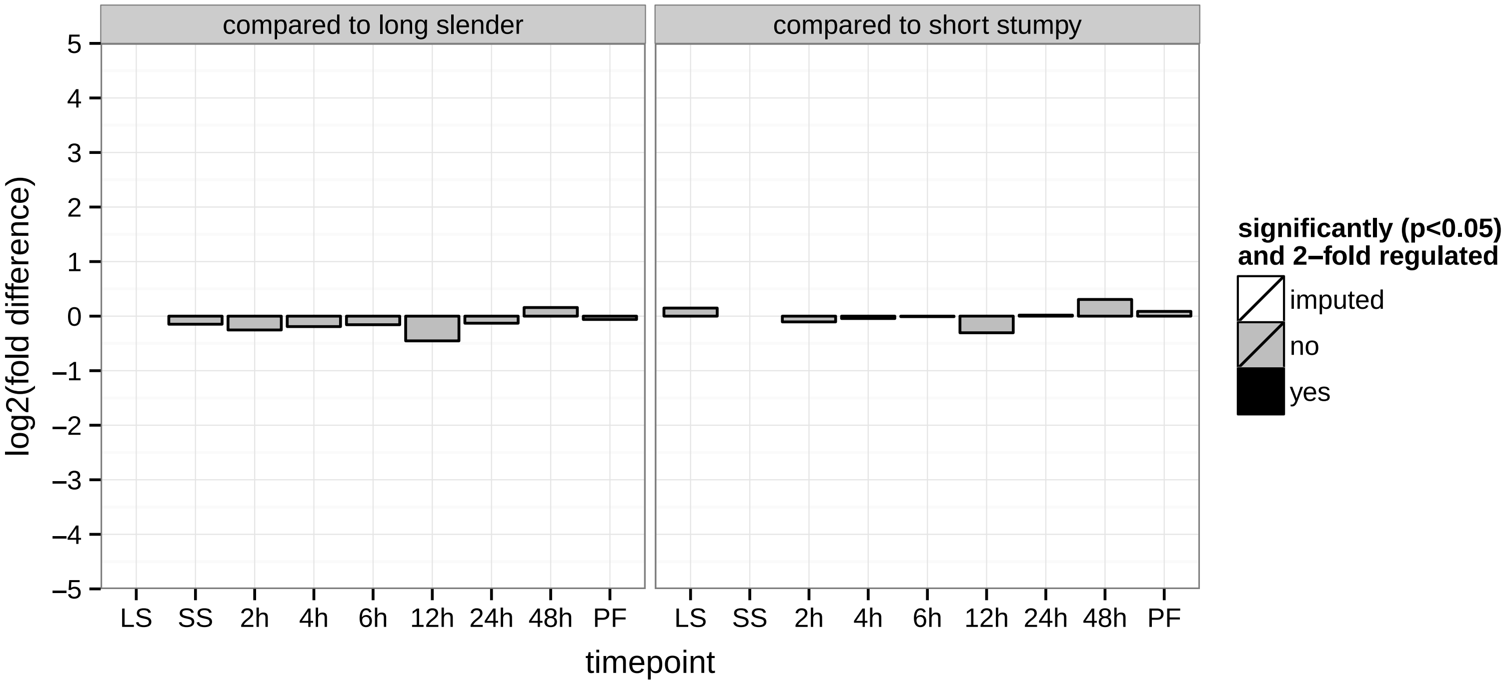
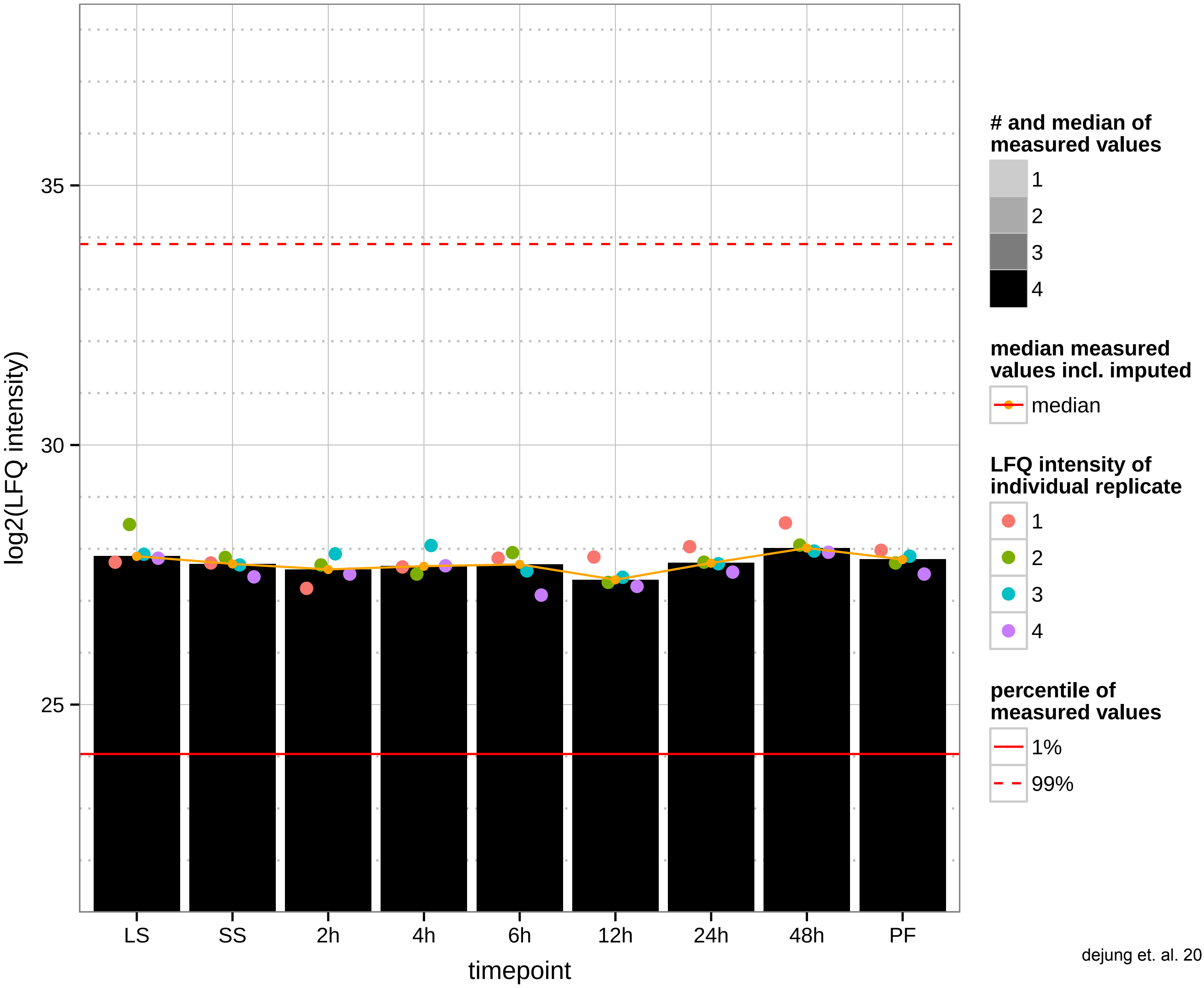
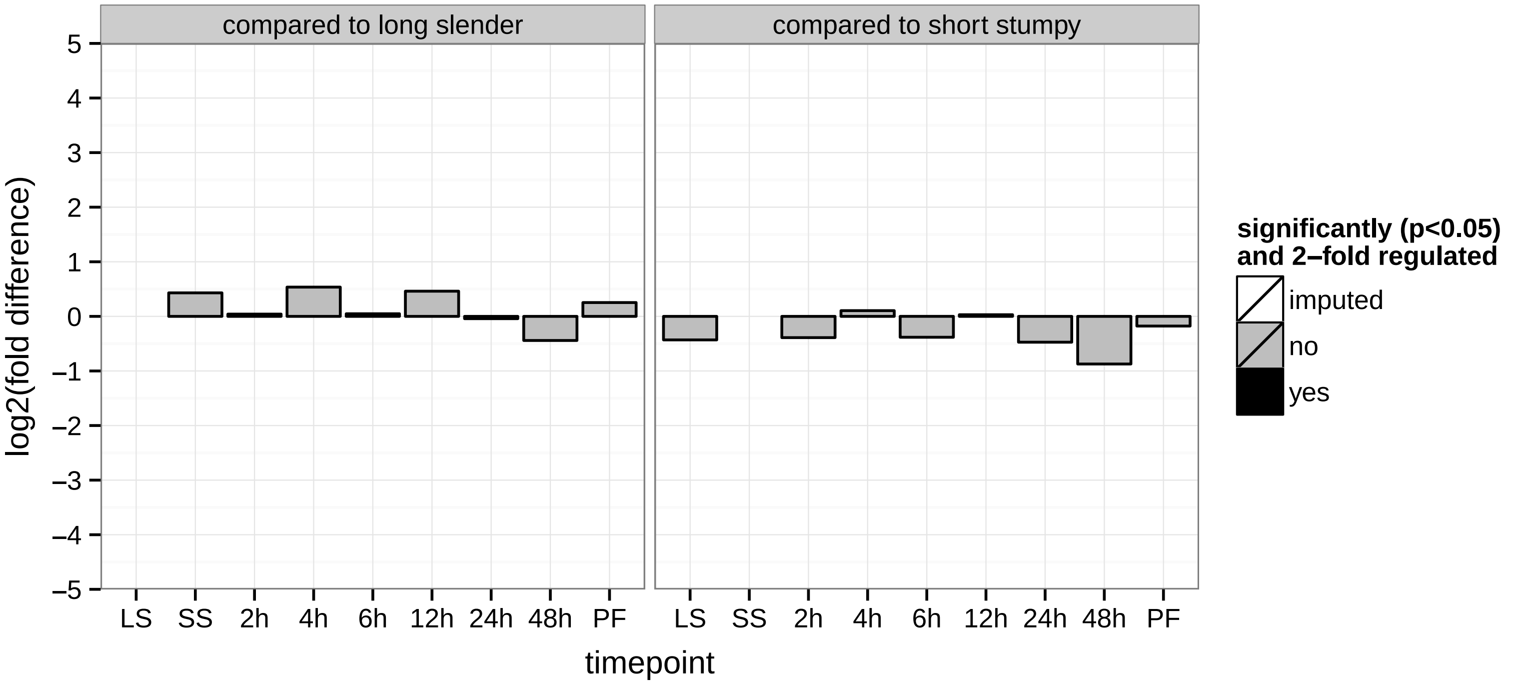
hypothetical protein, conserved
Tb927.5.1900
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

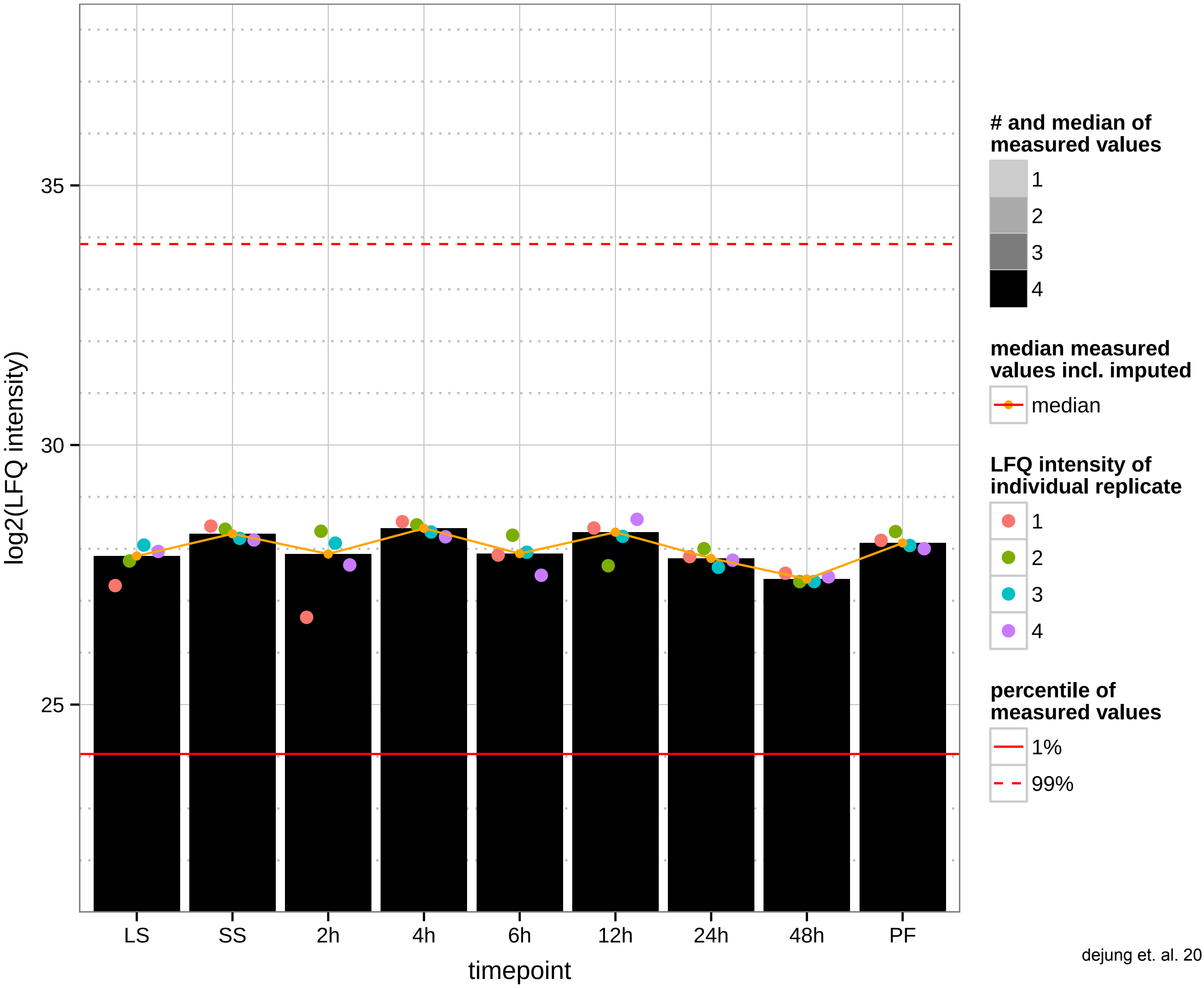




dejung et. al. 2015

hypothetical protein, conserved
Tb927.5.1930
AGOF: peptidase activity
AGOC: integral to membrane, signal peptidase complex
AGOP: signal peptide processing
PGOF: peptidase activity
PGOC: integral to membrane, signal peptidase complex
PGOP: signal peptide processing





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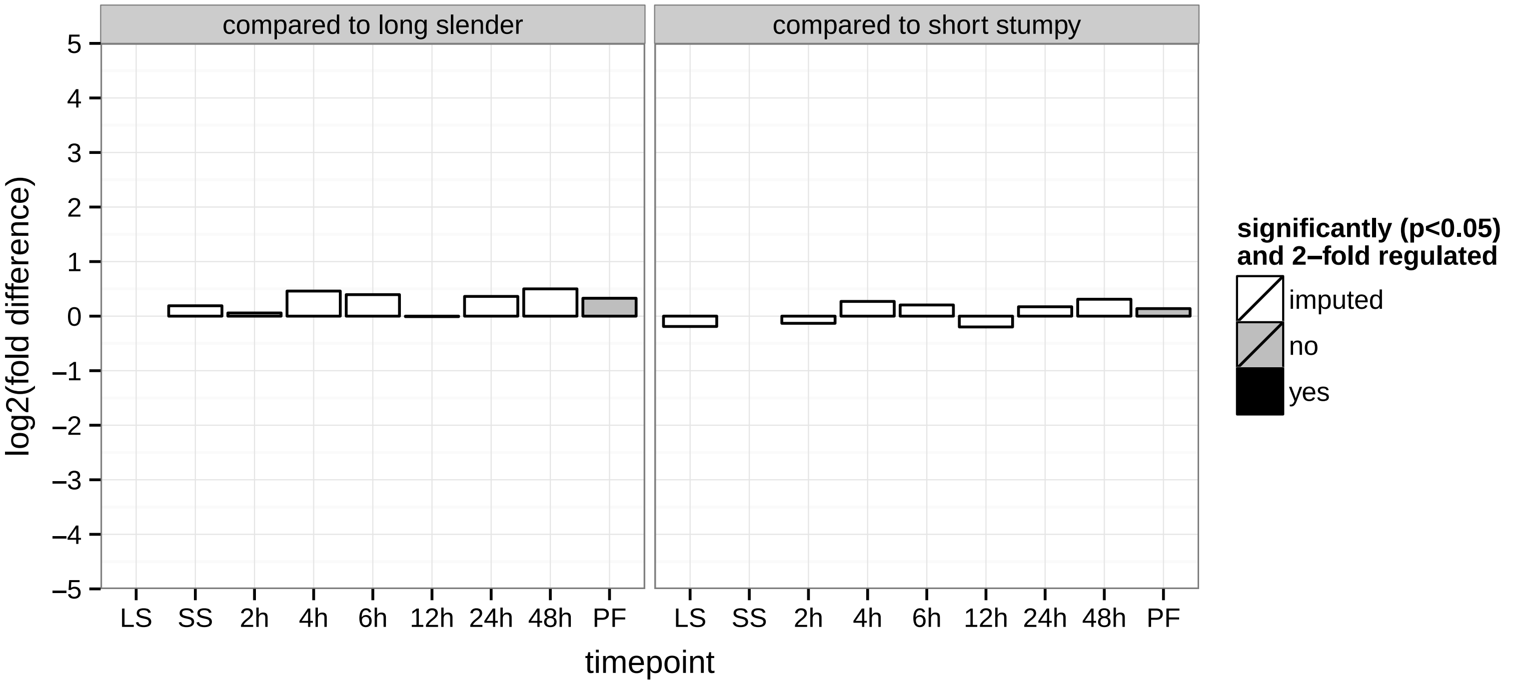
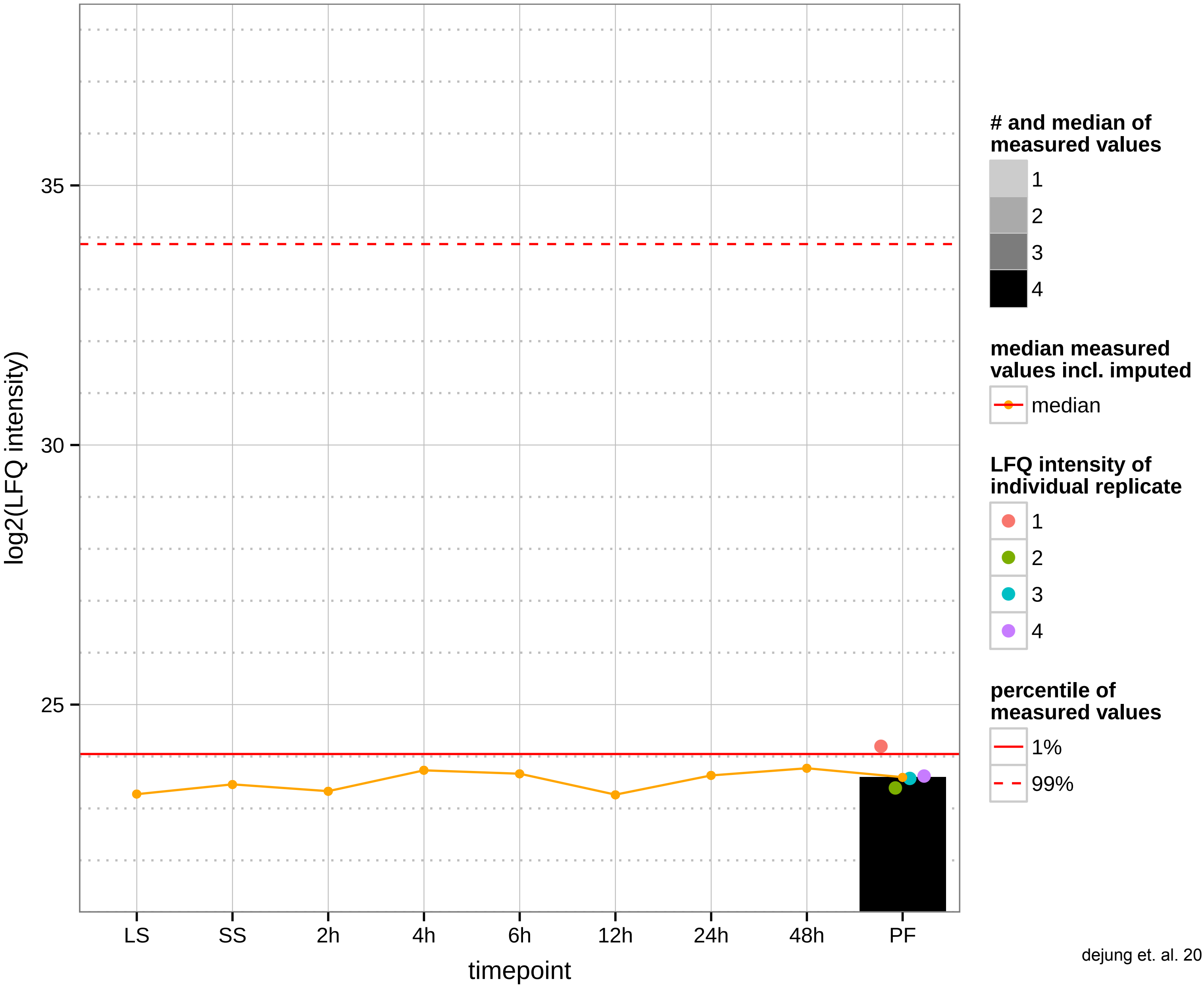
hypothetical protein, conserved
Tb927.5.2050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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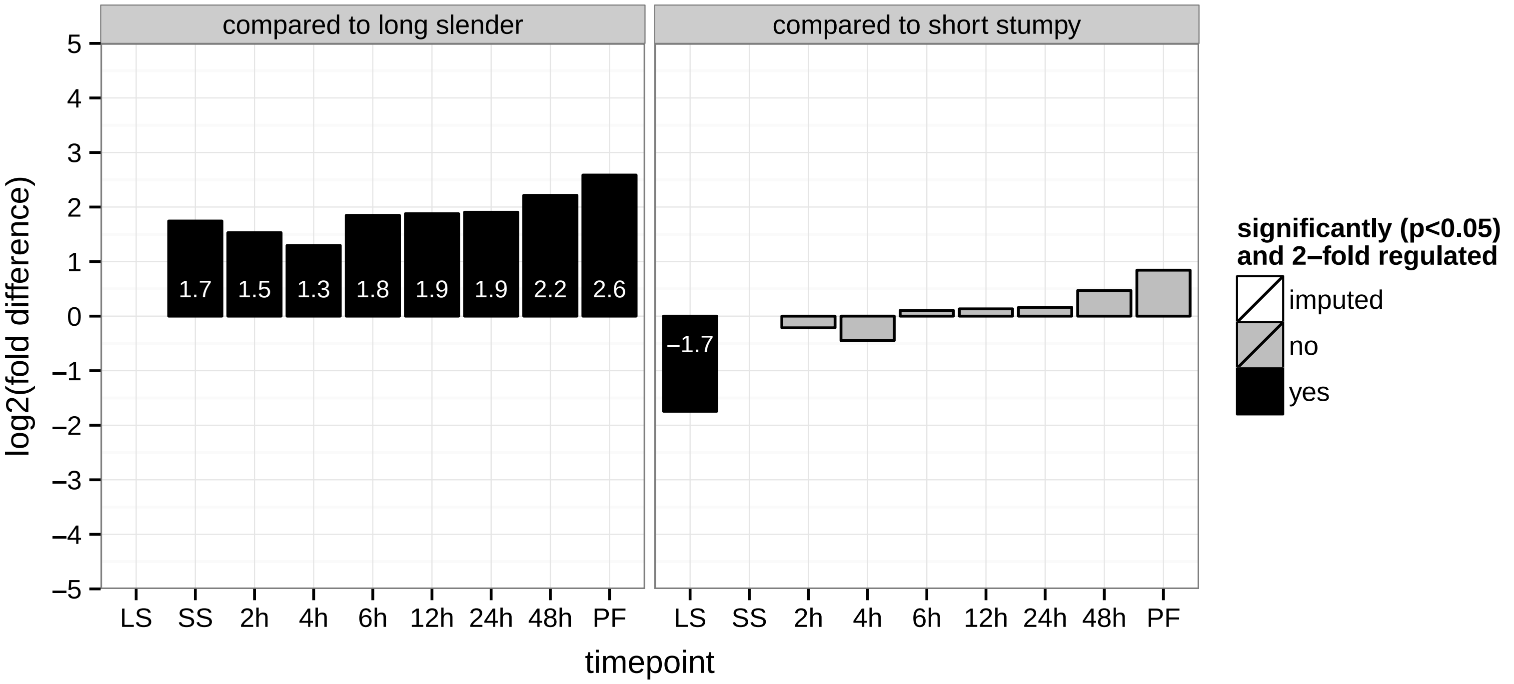
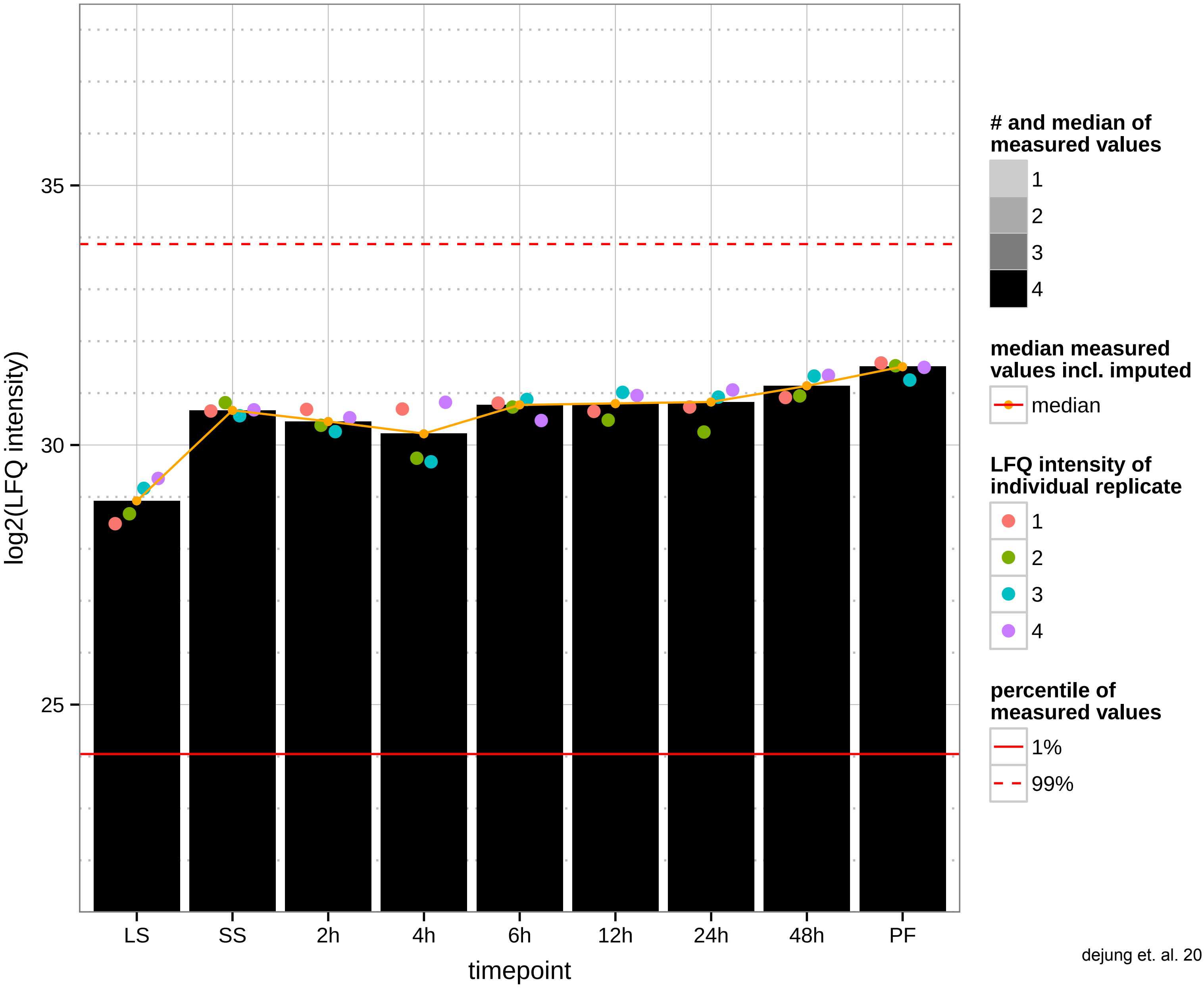
guanosine monophosphate reductase, putative
Tb927.5.2080
AGOF: IMP dehydrogenase activity, guanosine deaminase activity
AGOC: null
AGOP: null
PGOF: IMP dehydrogenase activity, catalytic activity, protein binding
PGOC: null
PGOP: oxidation–reduction process





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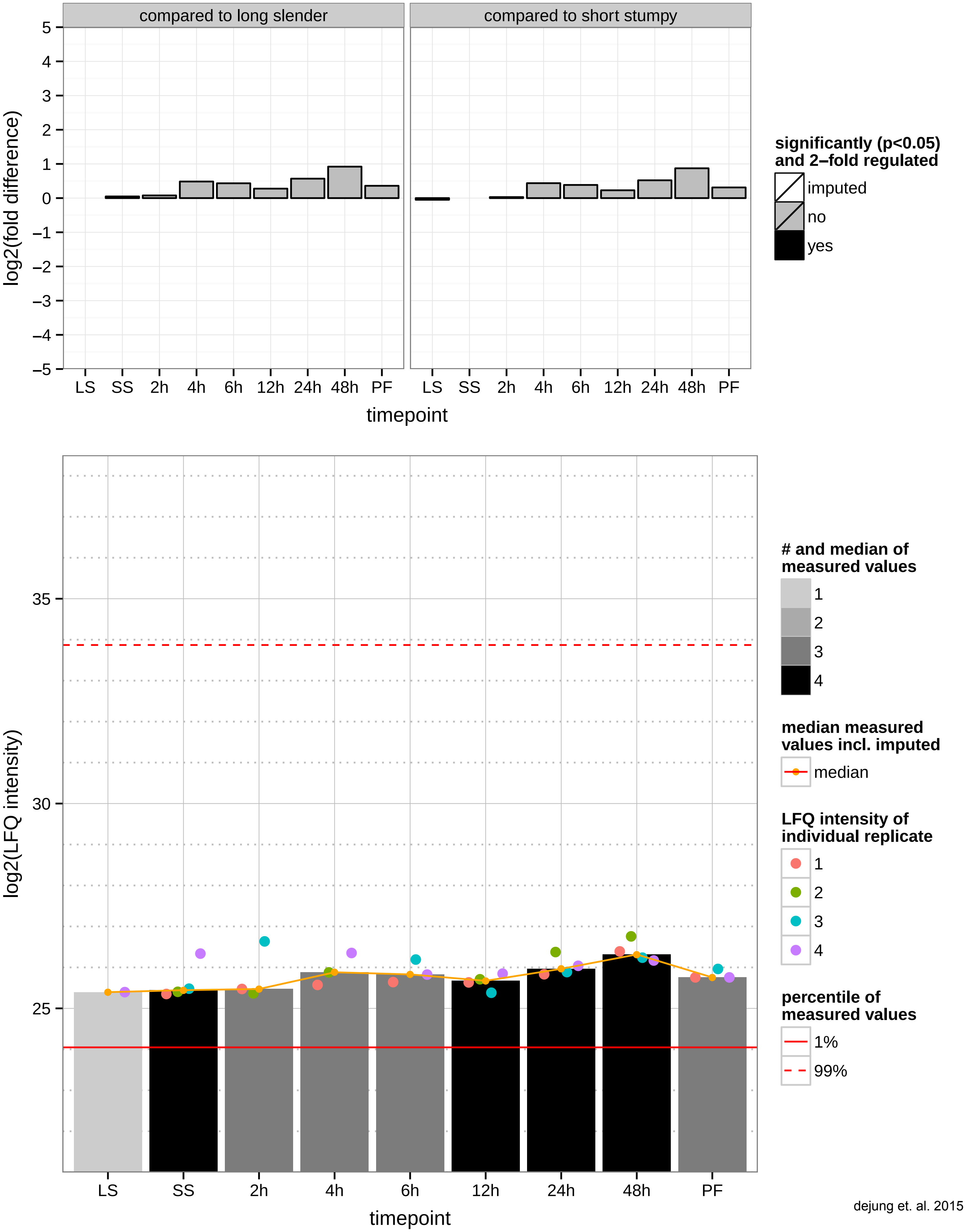
RNA–binding protein, putative (RBP30)
Tb927.5.2100
AGOF: RNA binding
AGOC: mitochondrion
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null



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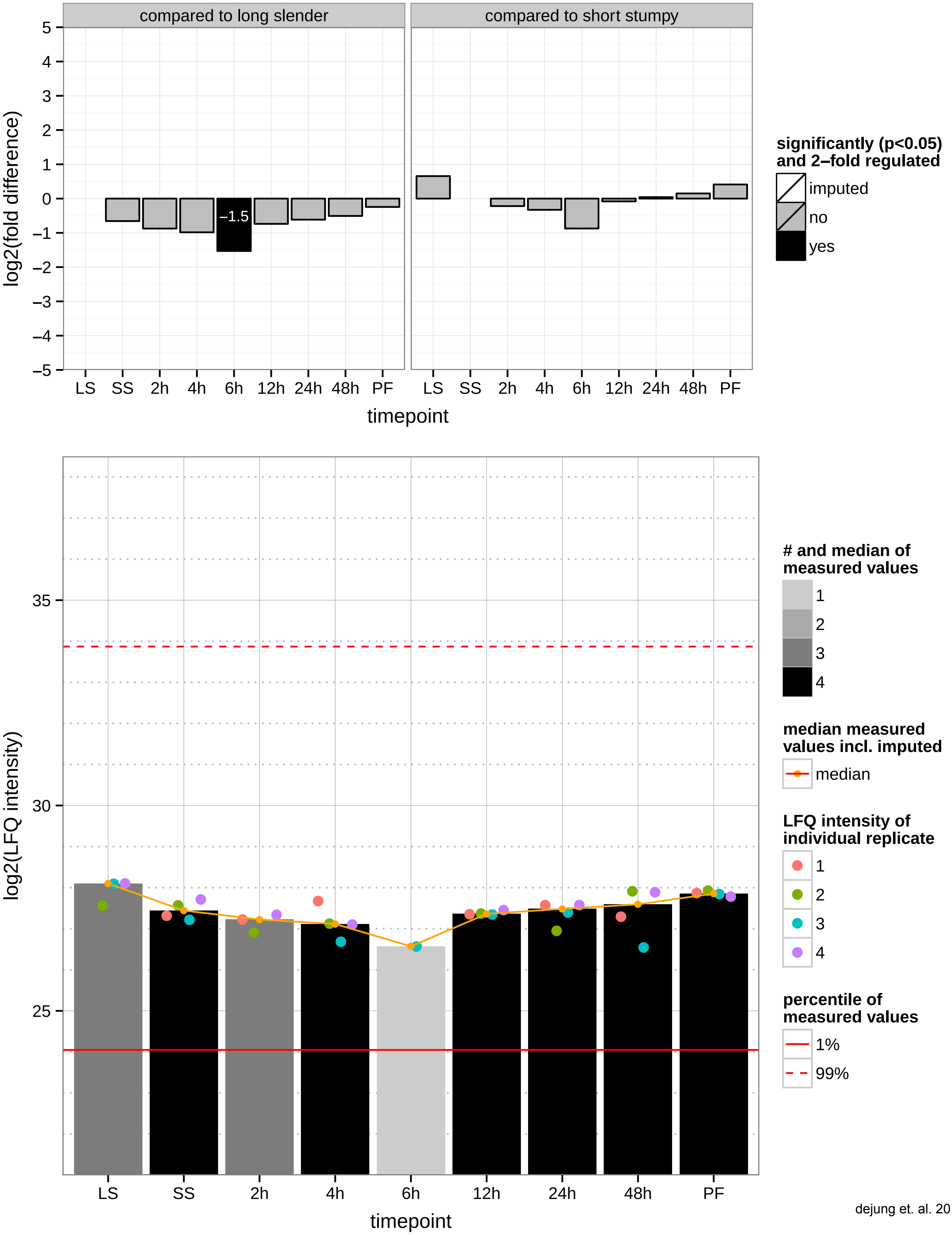
hypothetical protein, conserved
Tb927.5.2270
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null



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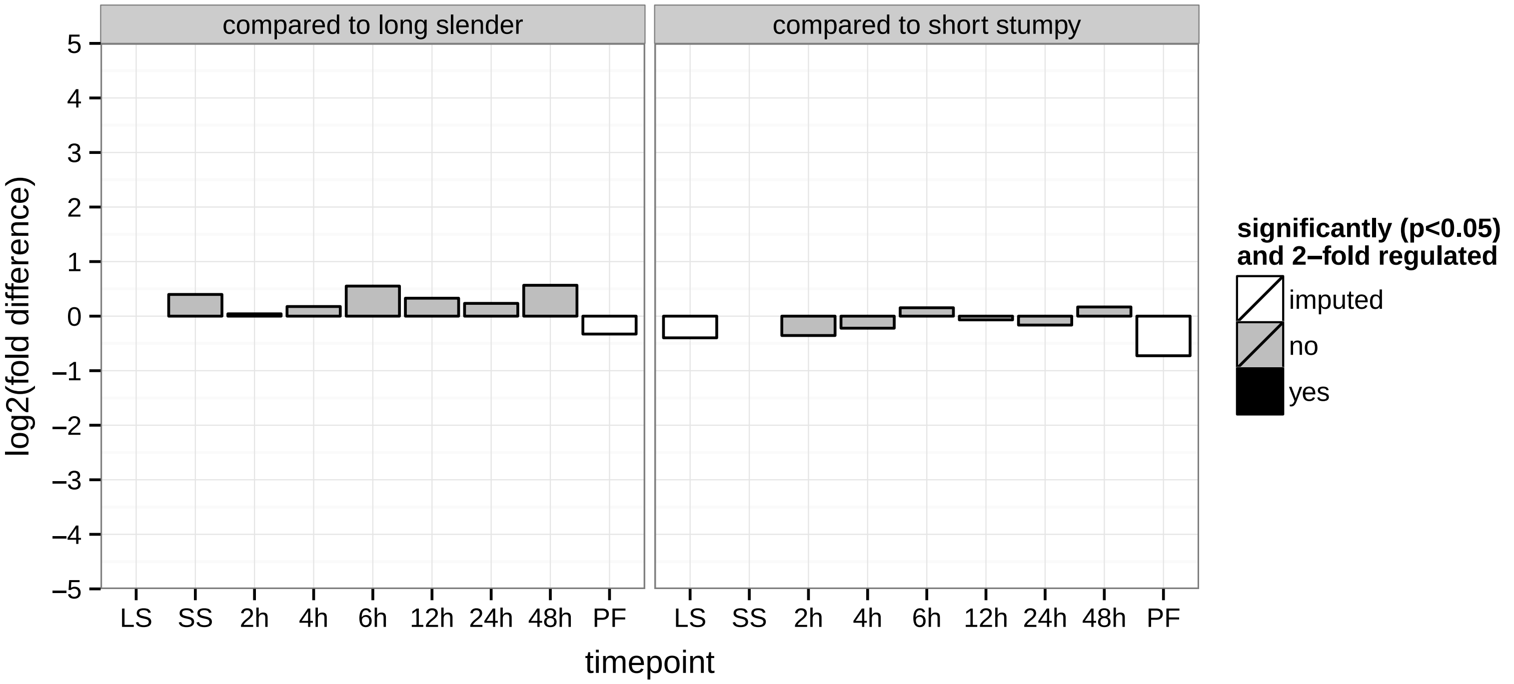
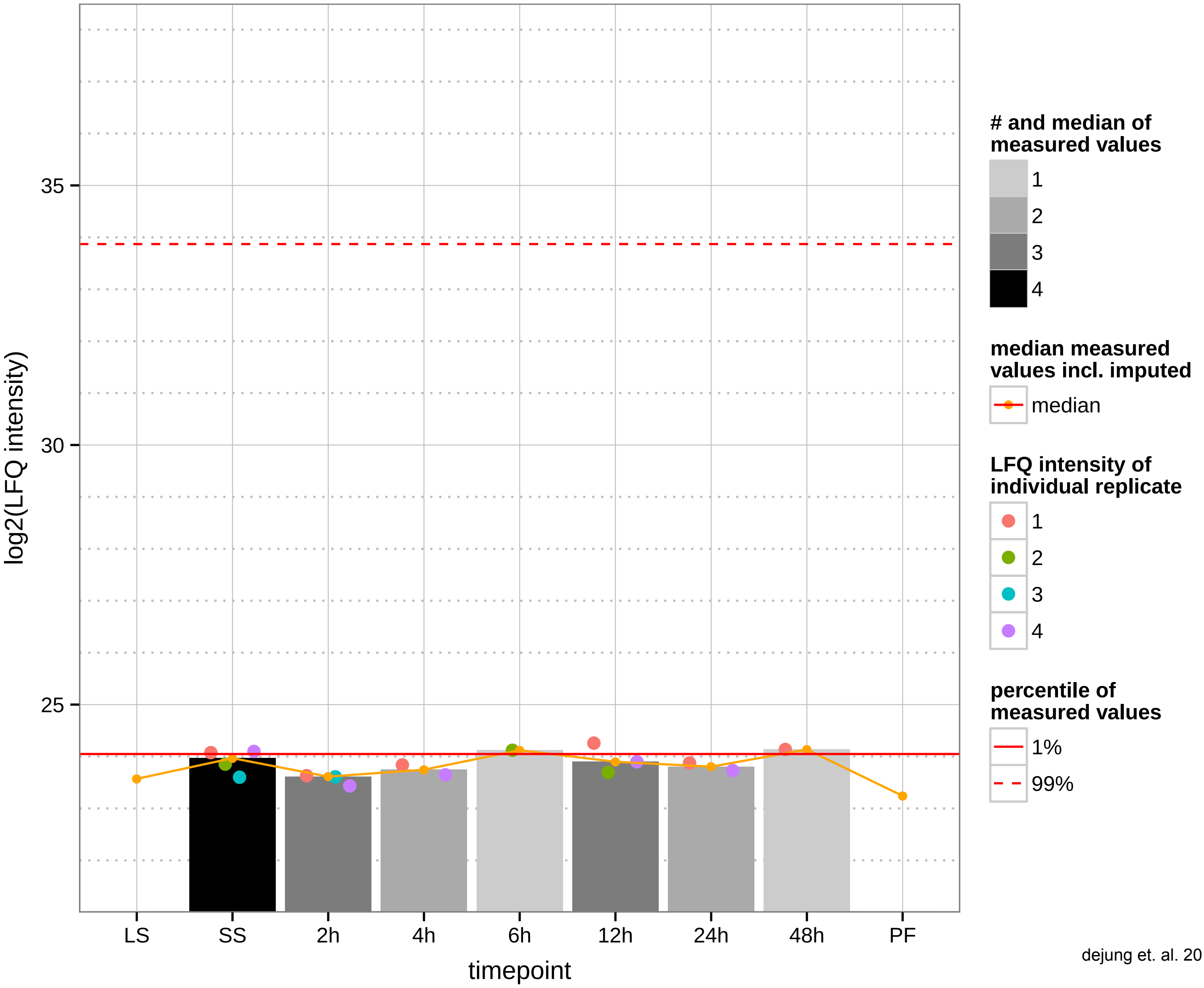
hypothetical protein, conserved
Tb927.5.2310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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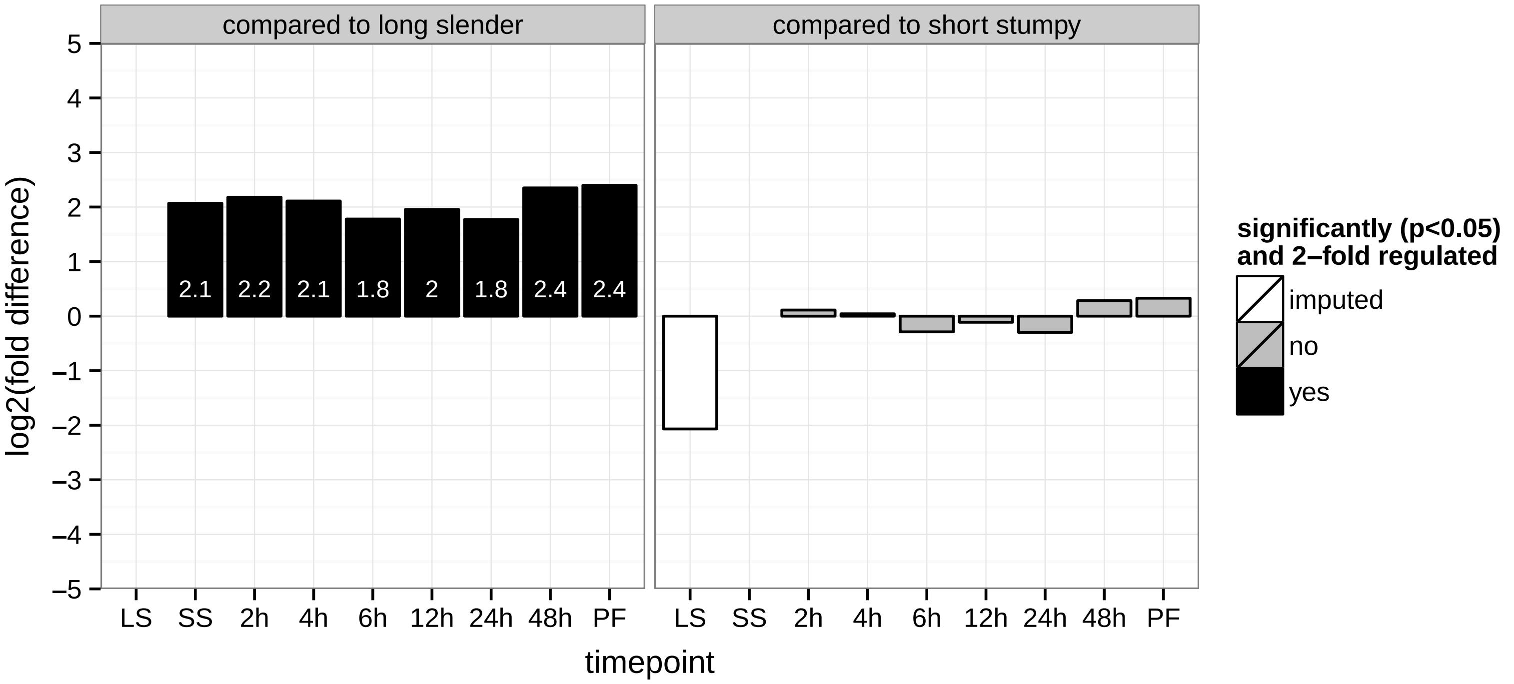
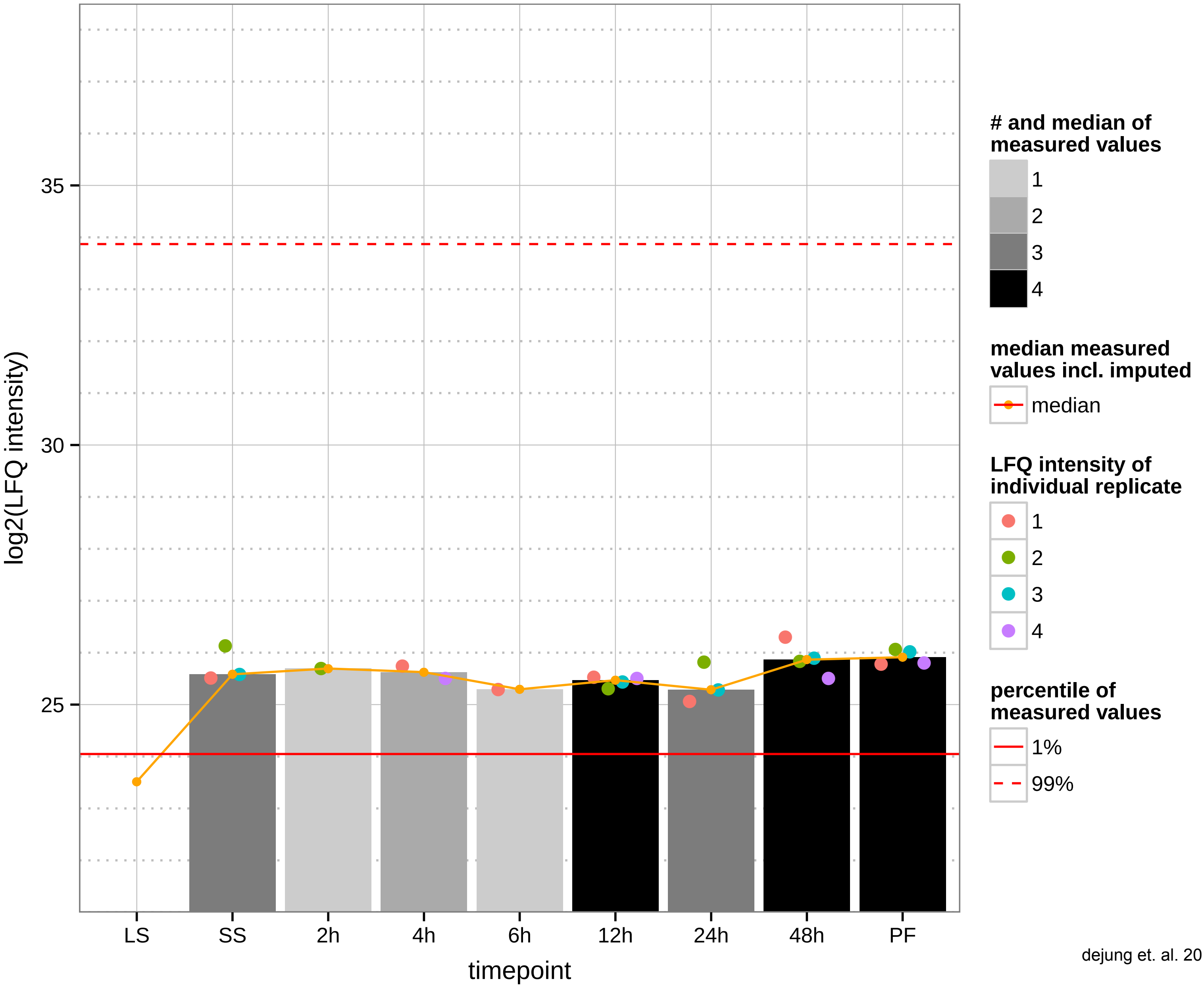
hydrolase, alpha/beta fold family, putative
Tb927.5.2380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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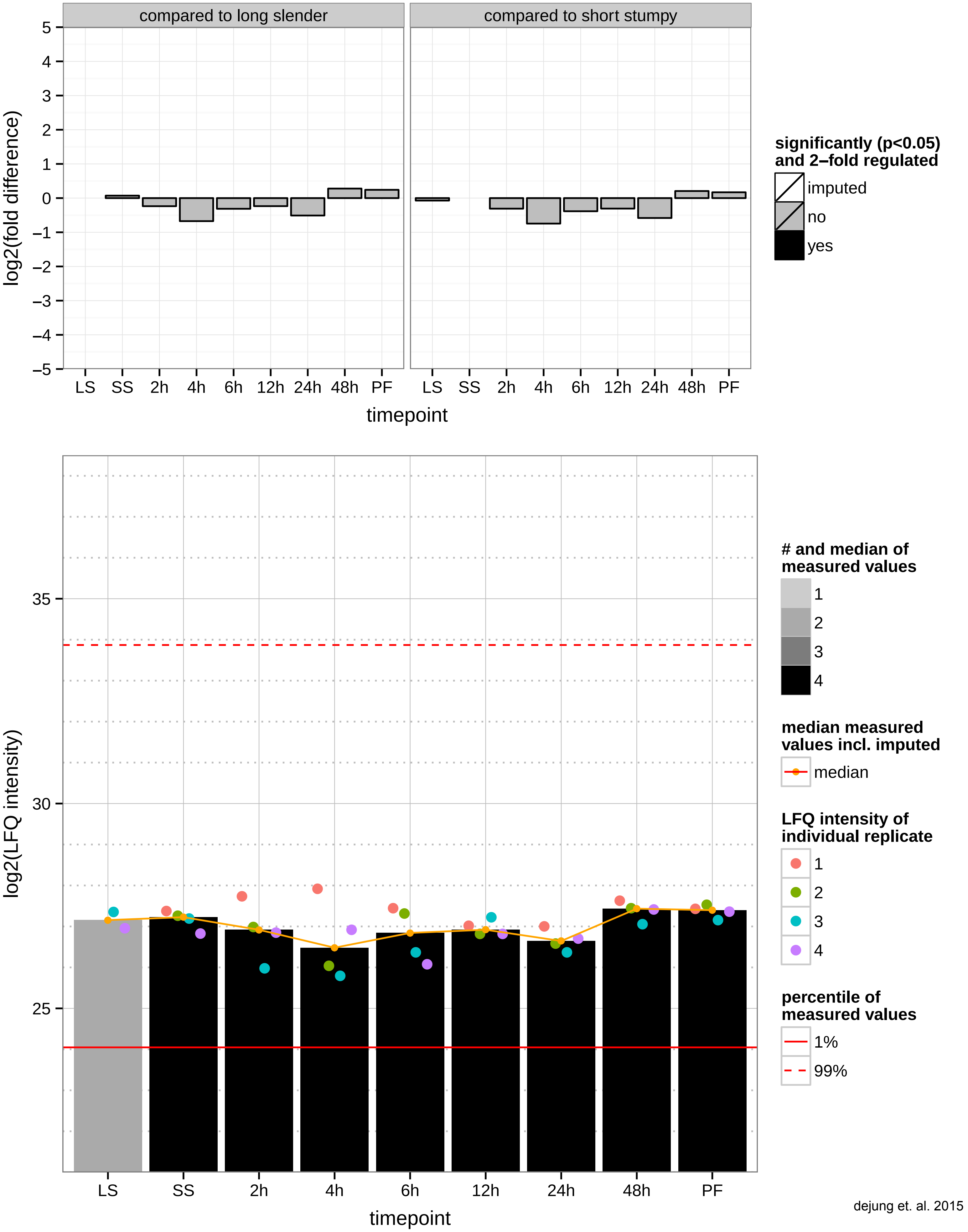
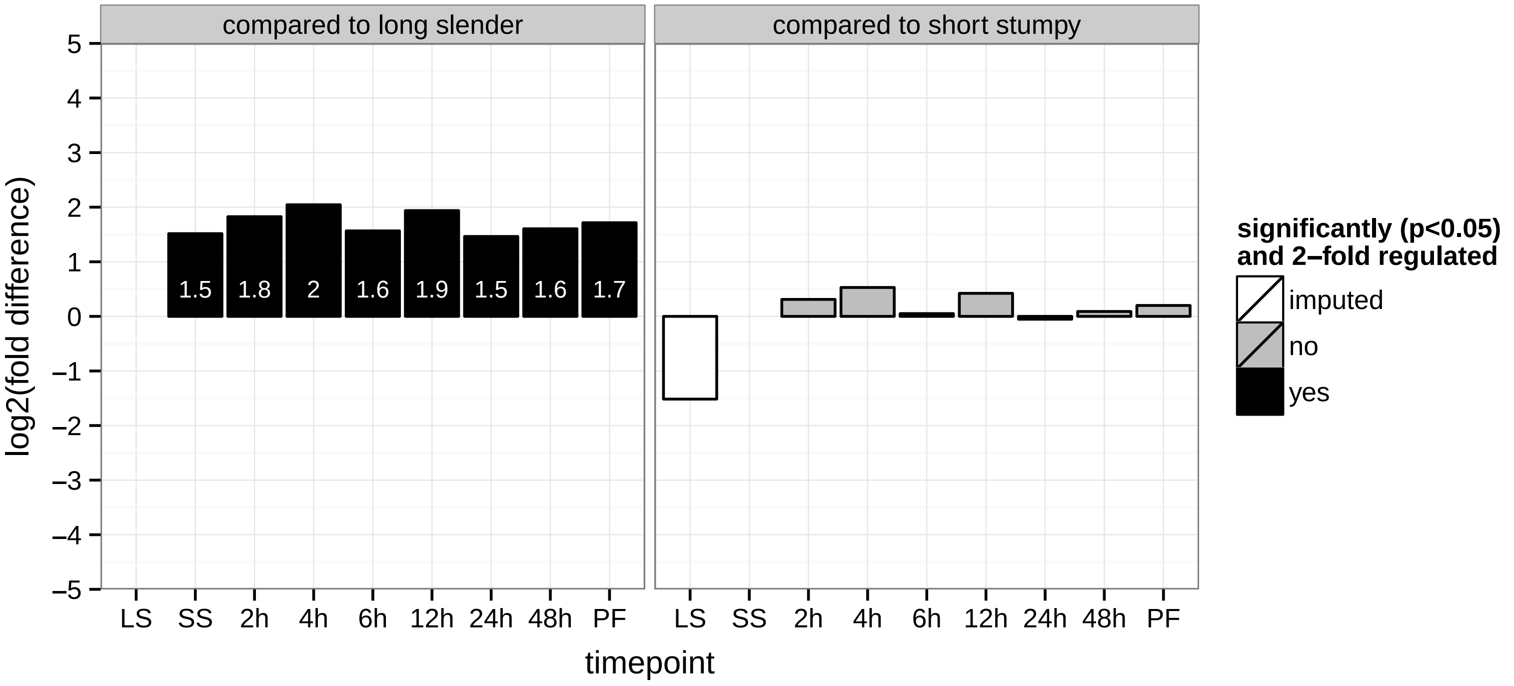
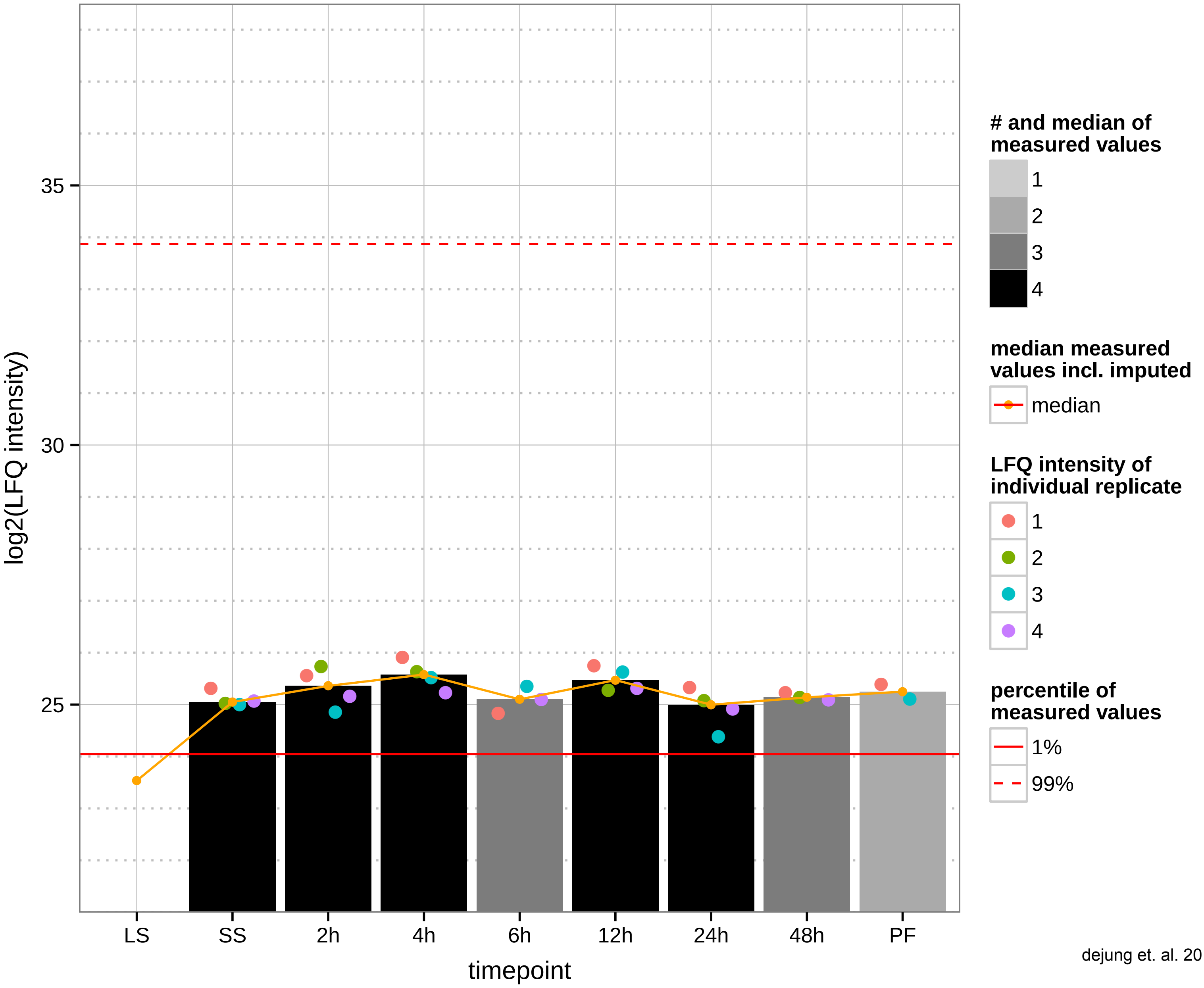
kinesin, putative
Tb927.5.2410
AGOF: ATP binding, calcium–dependent cysteine–type endopeptidase activity, microtubule motor activity
AGOC: intracellular
AGOP: microtubule–based movement, proteolysis
PGOF: ATP binding, binding, microtubule motor activity, protein binding
PGOC: null
PGOP: microtubule–based movement



hypothetical protein, conserved
Tb927.5.2500
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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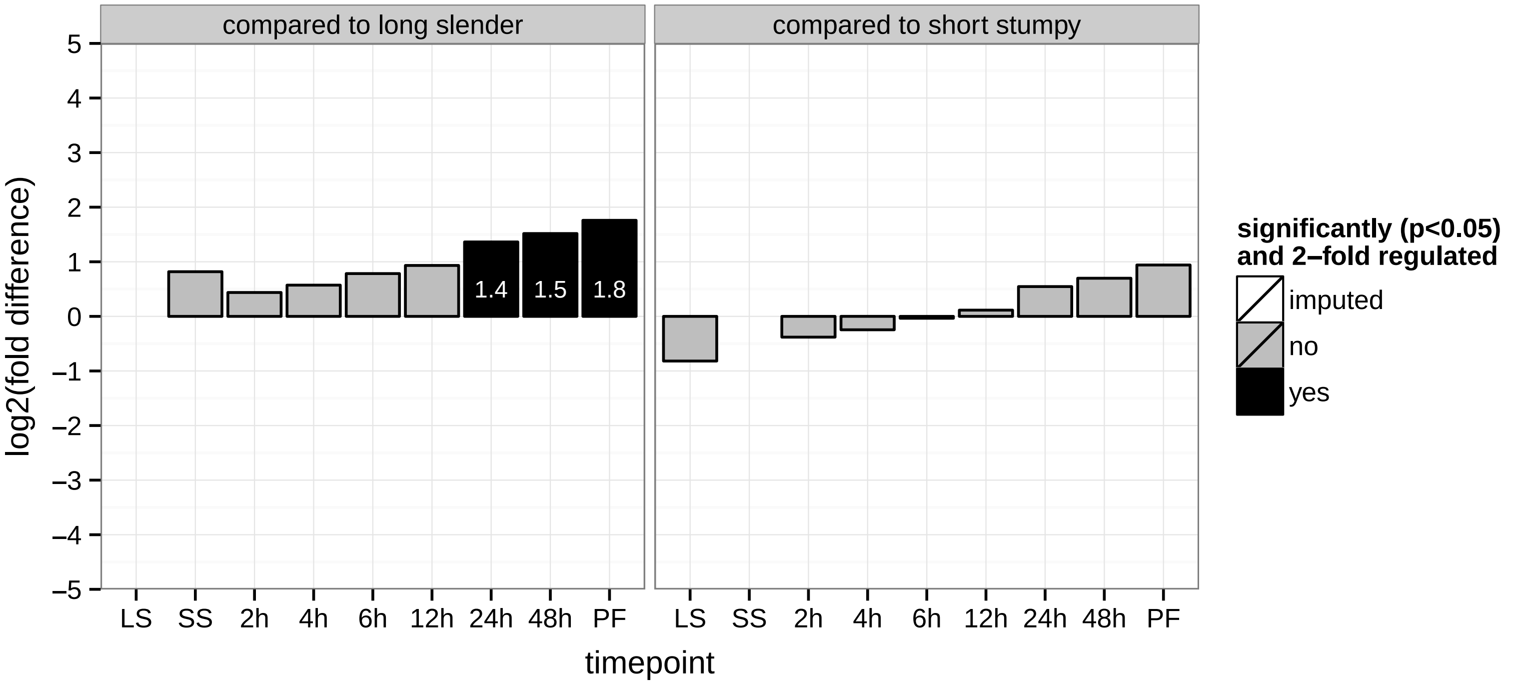
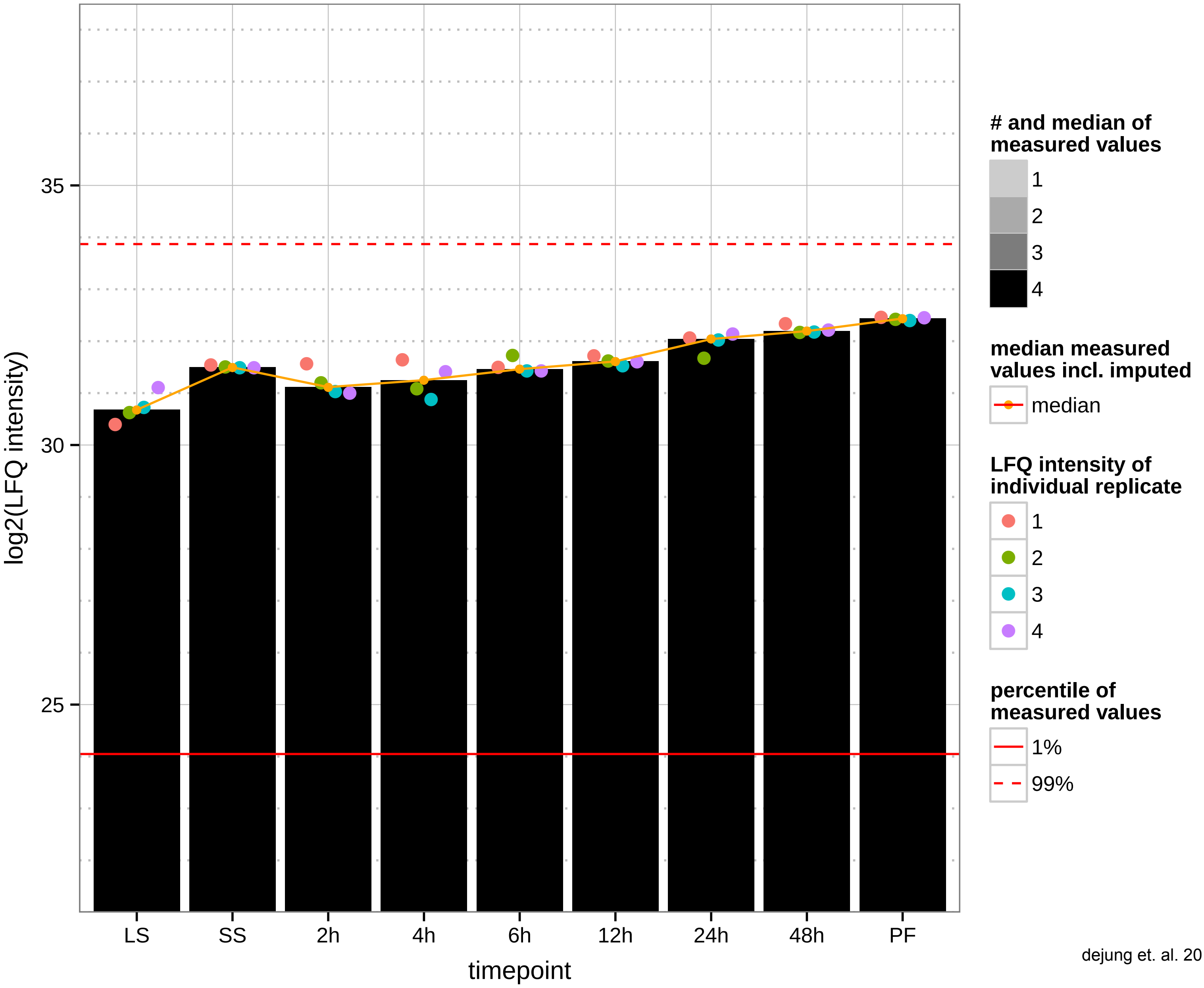
translation initiation factor, putative (EIF3B)
Tb927.5.2570
AGOF: RNA binding, translation initiation factor activity
AGOC: null
AGOP: translational initiation
PGOF: null
PGOC: null
PGOP: null





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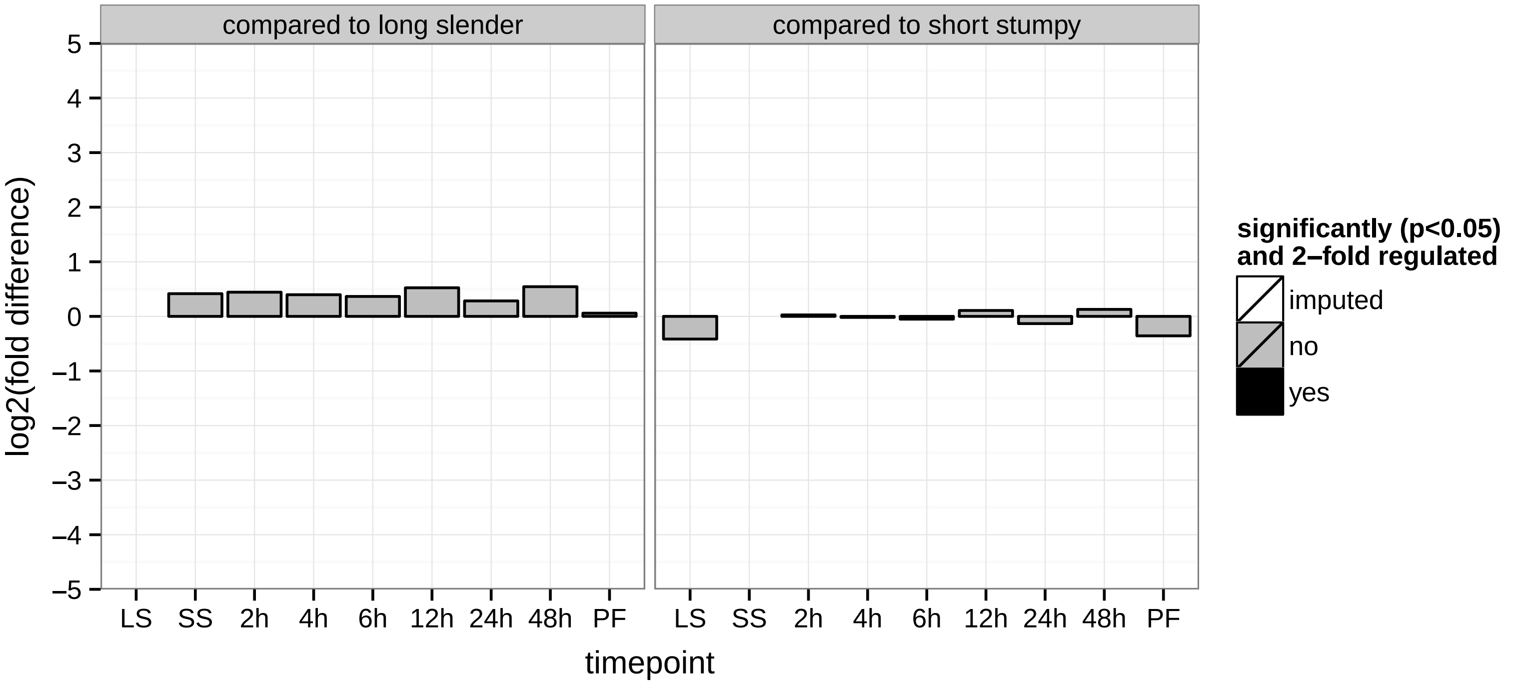
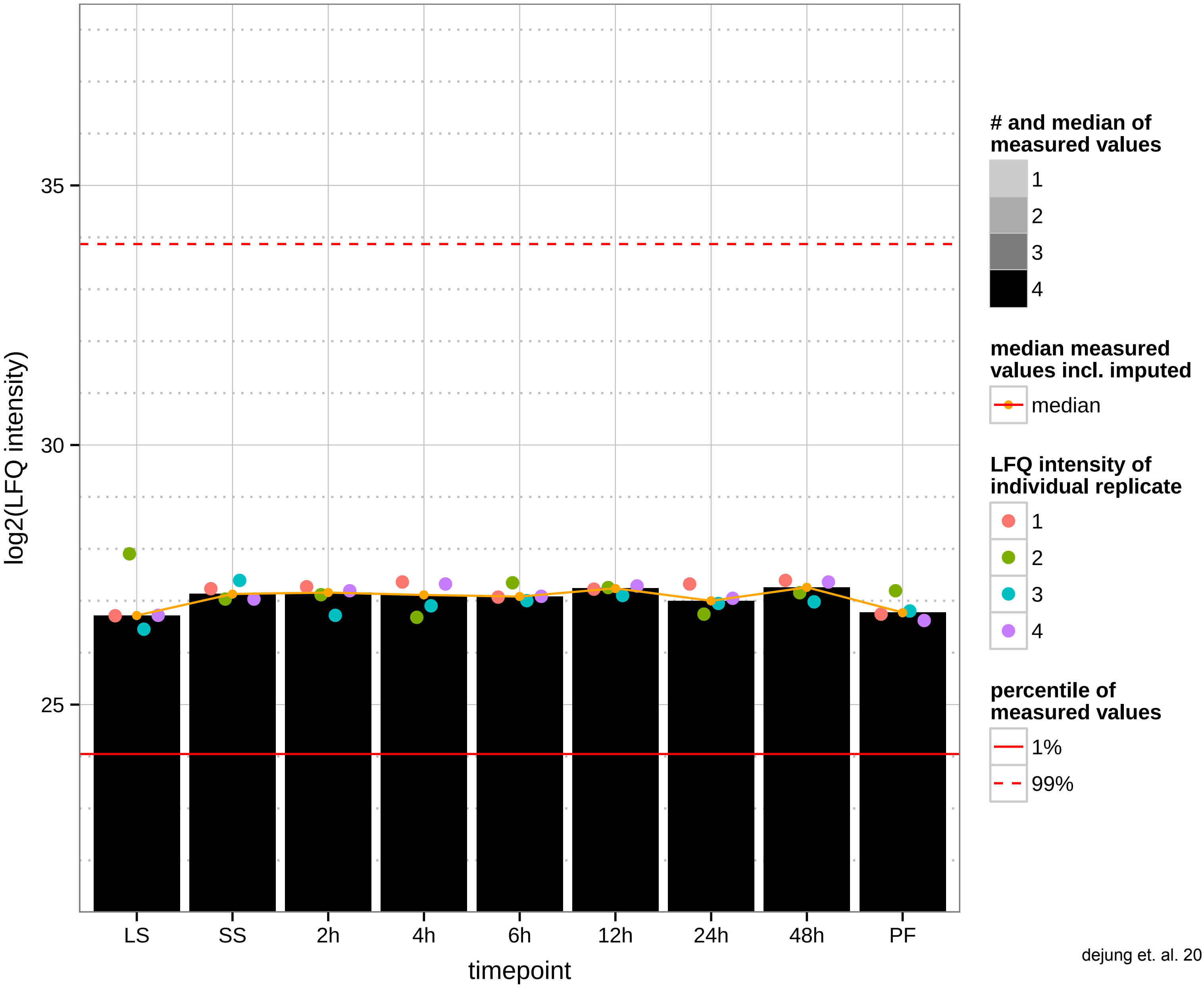
hypothetical protein, conserved
Tb927.5.2590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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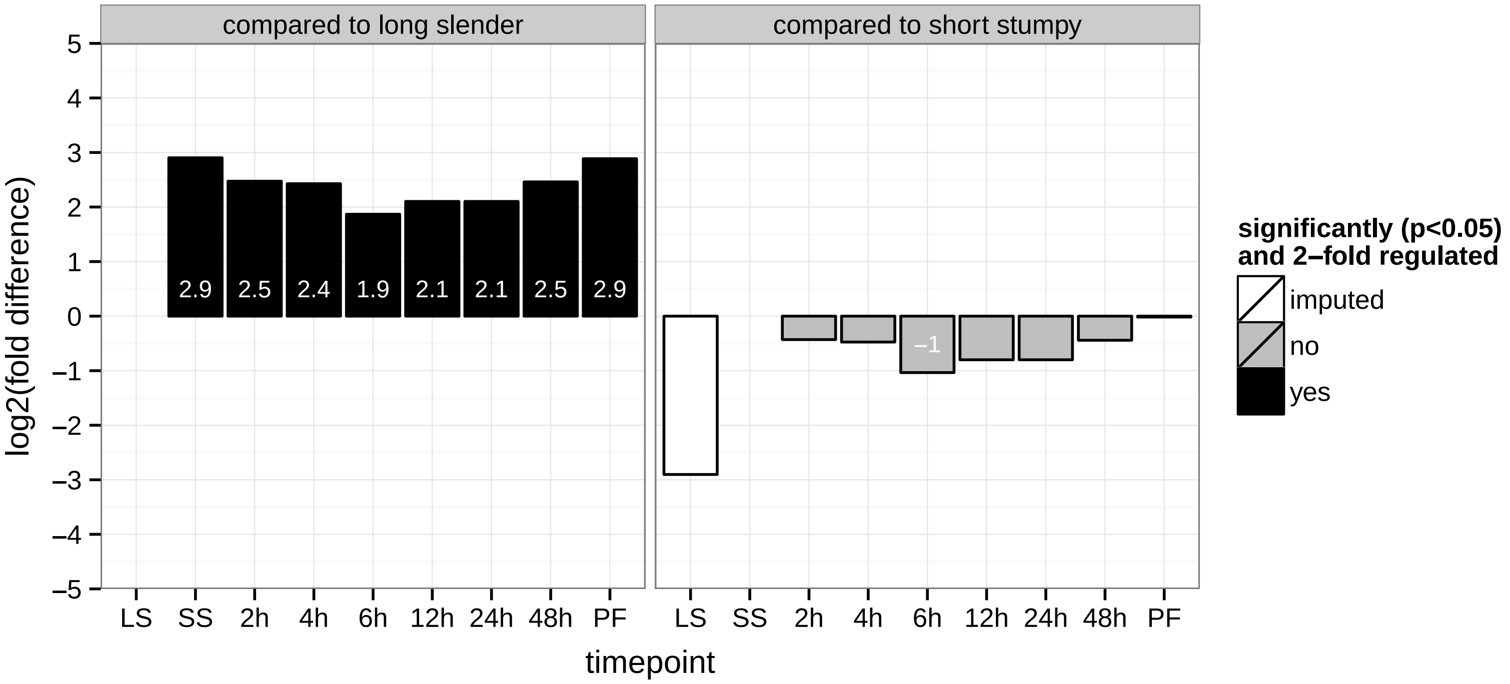
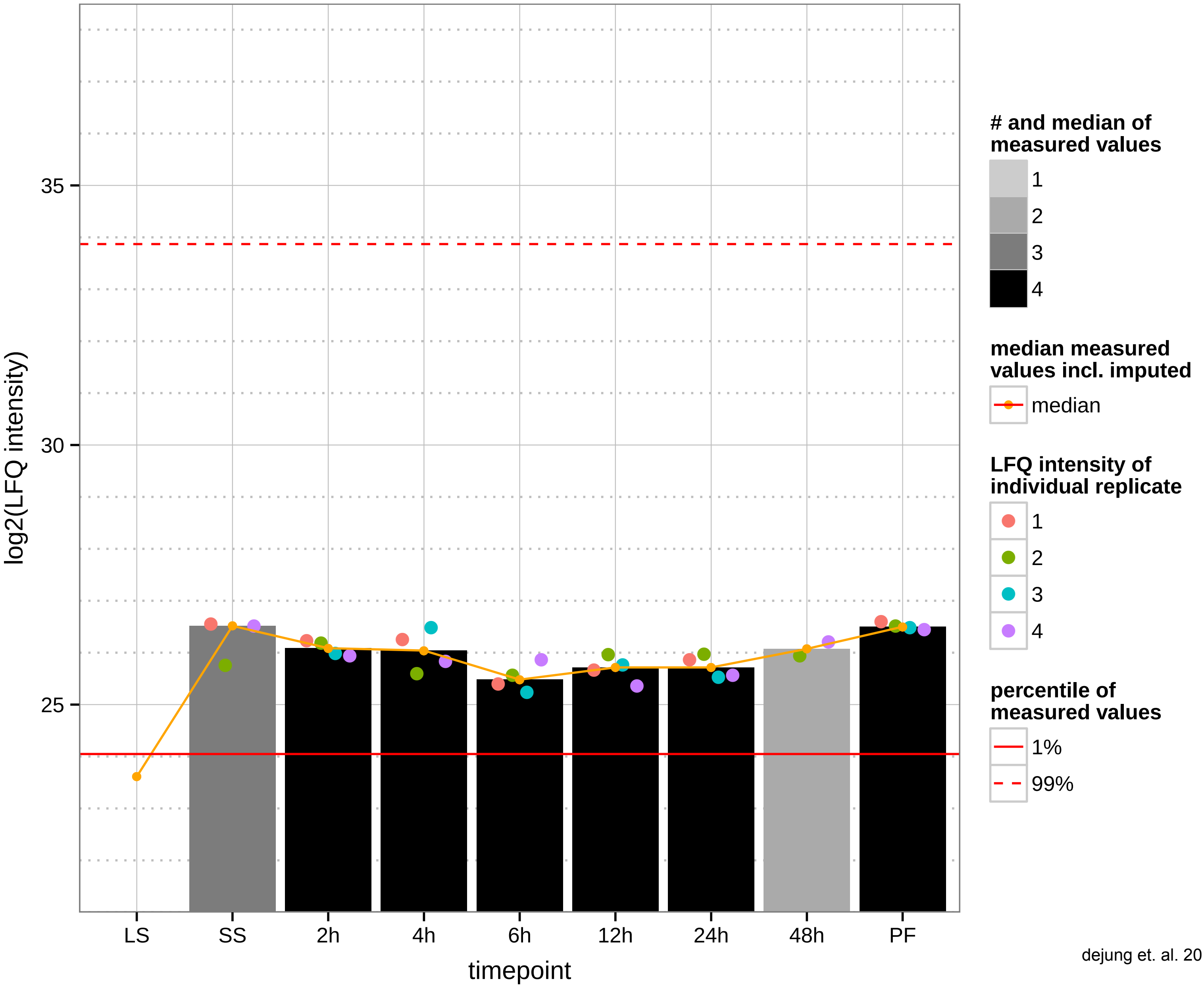
hypothetical protein, conserved
Tb927.5.2640
AGOF: nucleotidyltransferase activity
AGOC: null
AGOP: NAD biosynthetic process
PGOF: nucleotidyltransferase activity
PGOC: null
PGOP: biosynthetic process





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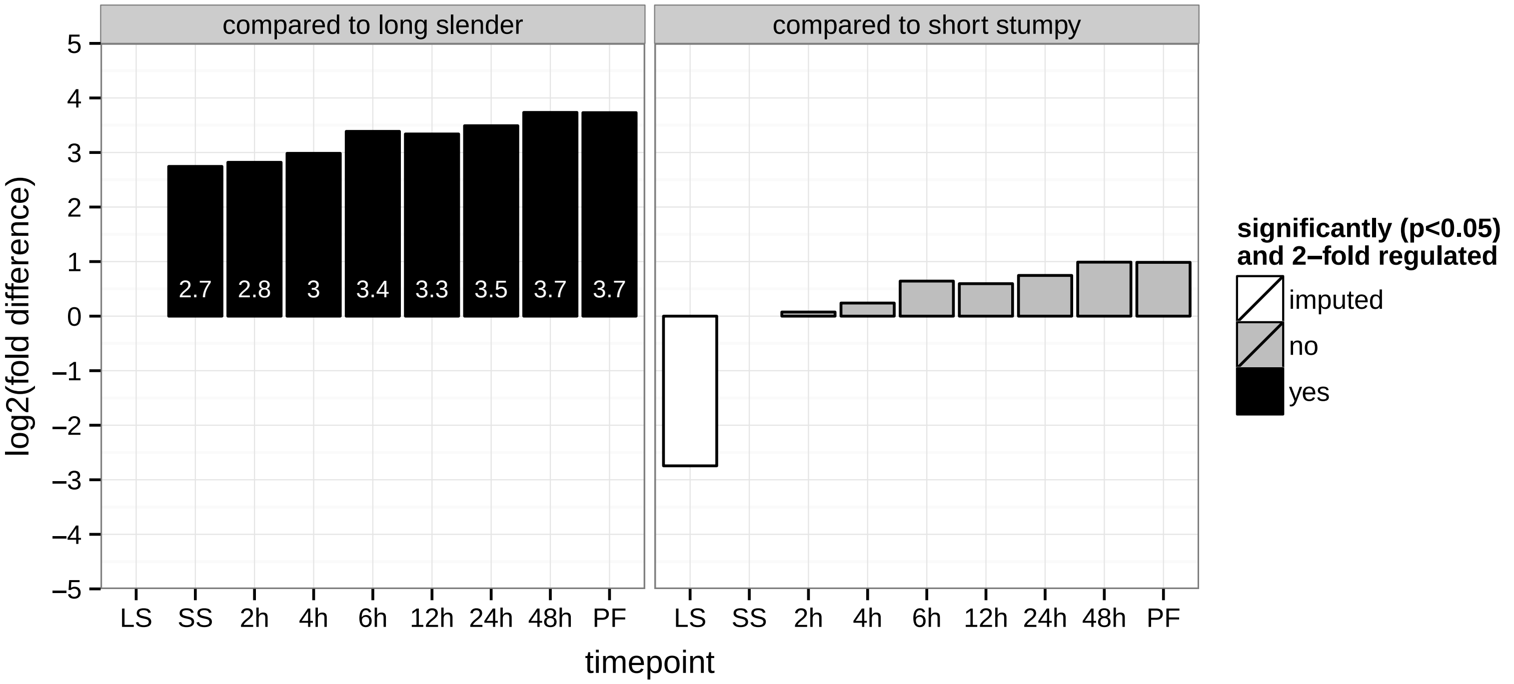
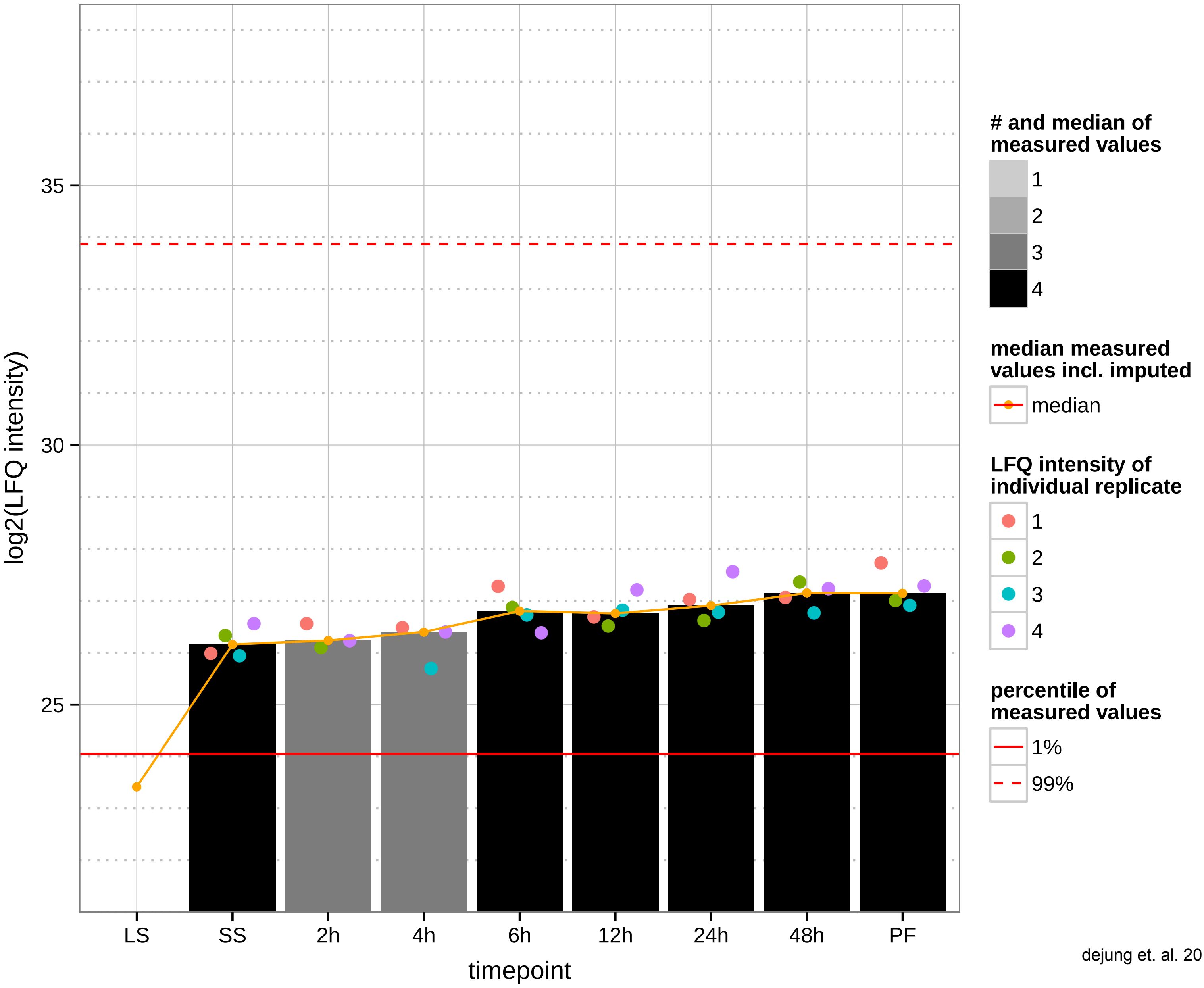
hypothetical protein, conserved
Tb927.5.2660
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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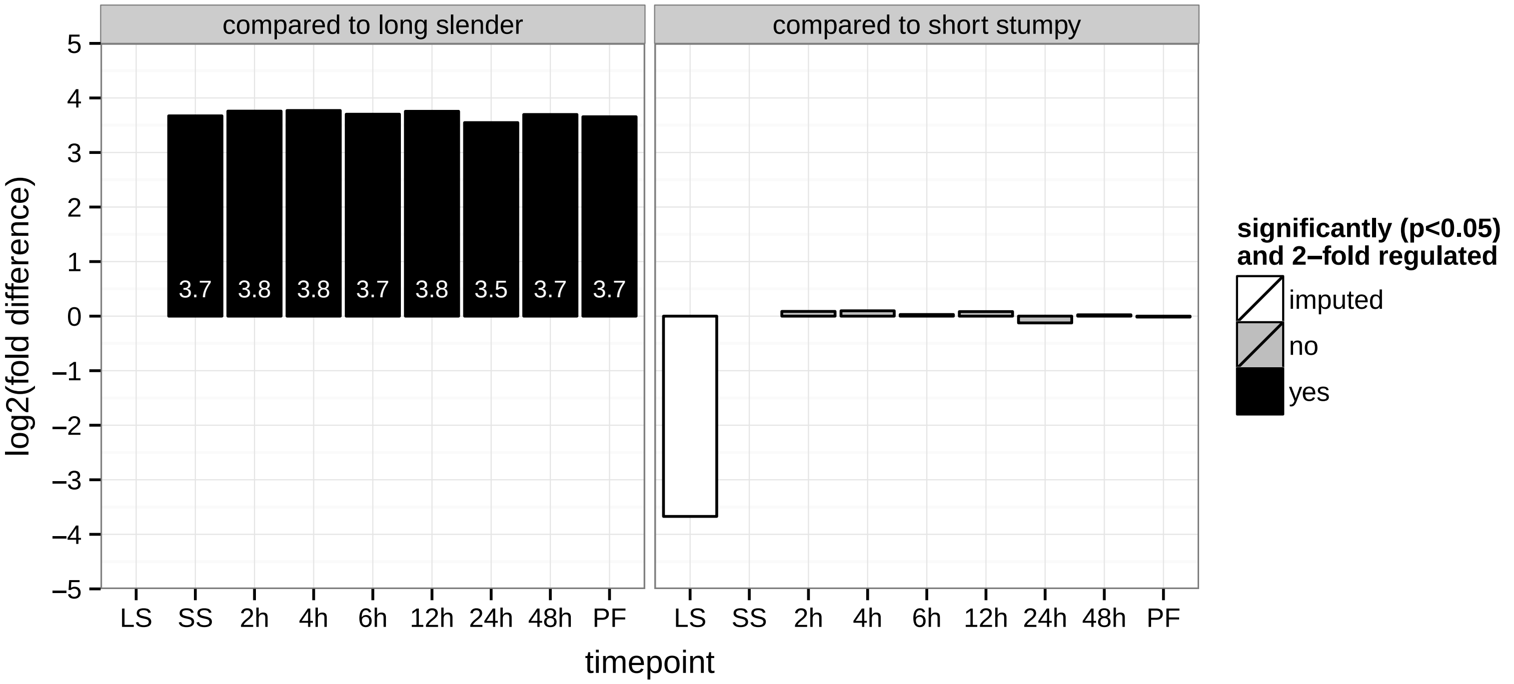
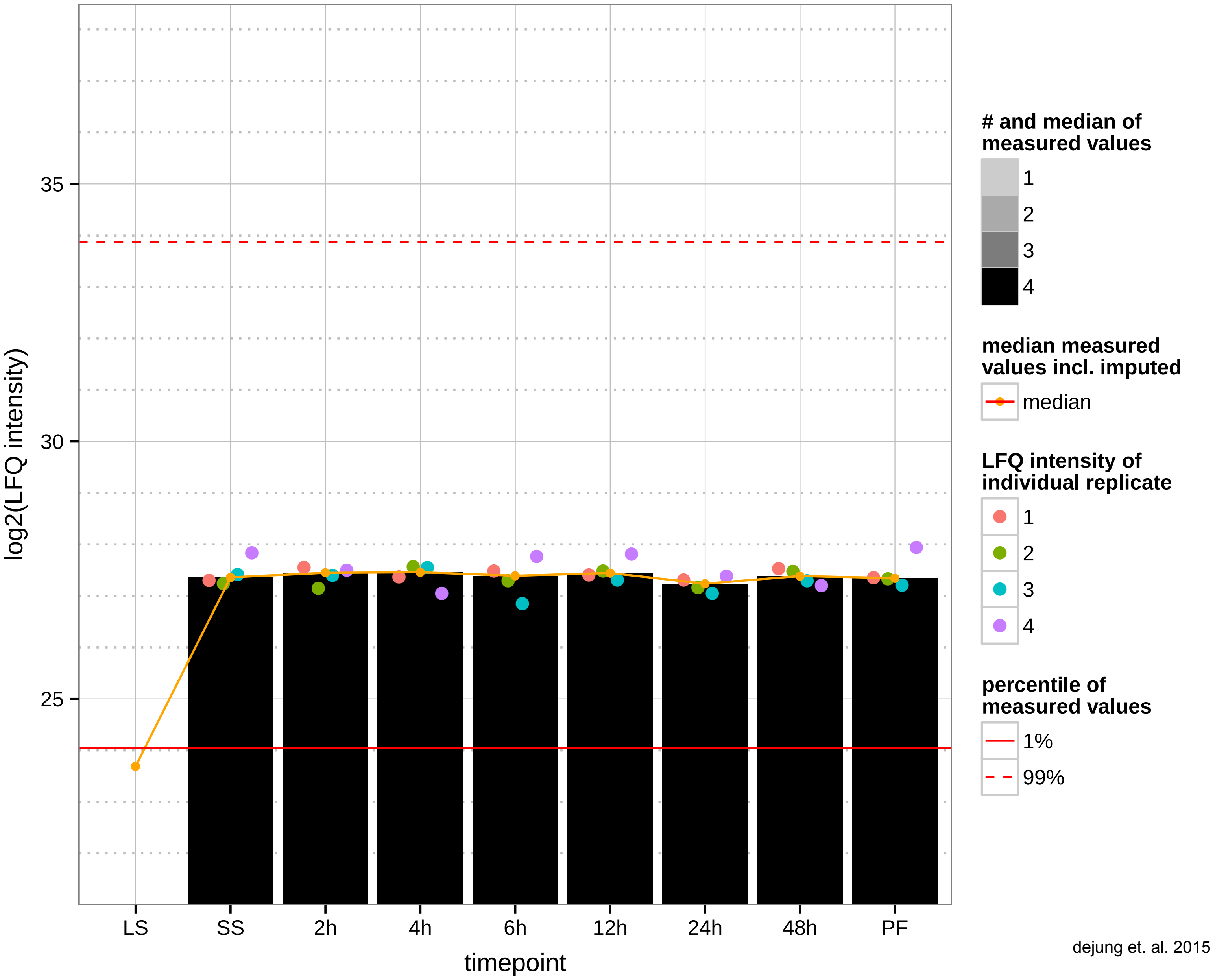
otubain, putative, otubain cysteine peptidase, Clan CA, family C65
Tb927.5.2700
AGOF: null
AGOC: null
AGOP: null
PGOF: omega peptidase activity
PGOC: null
PGOP: protein metabolic process





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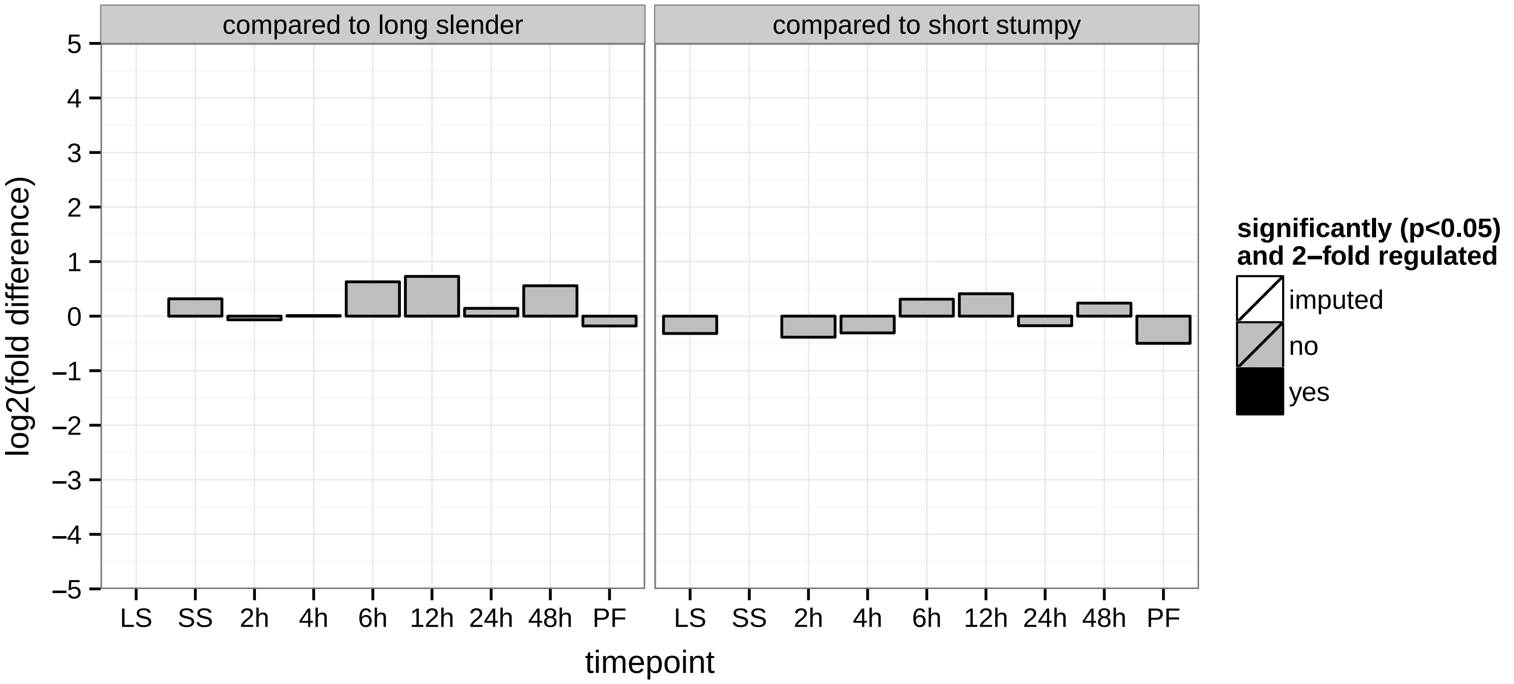
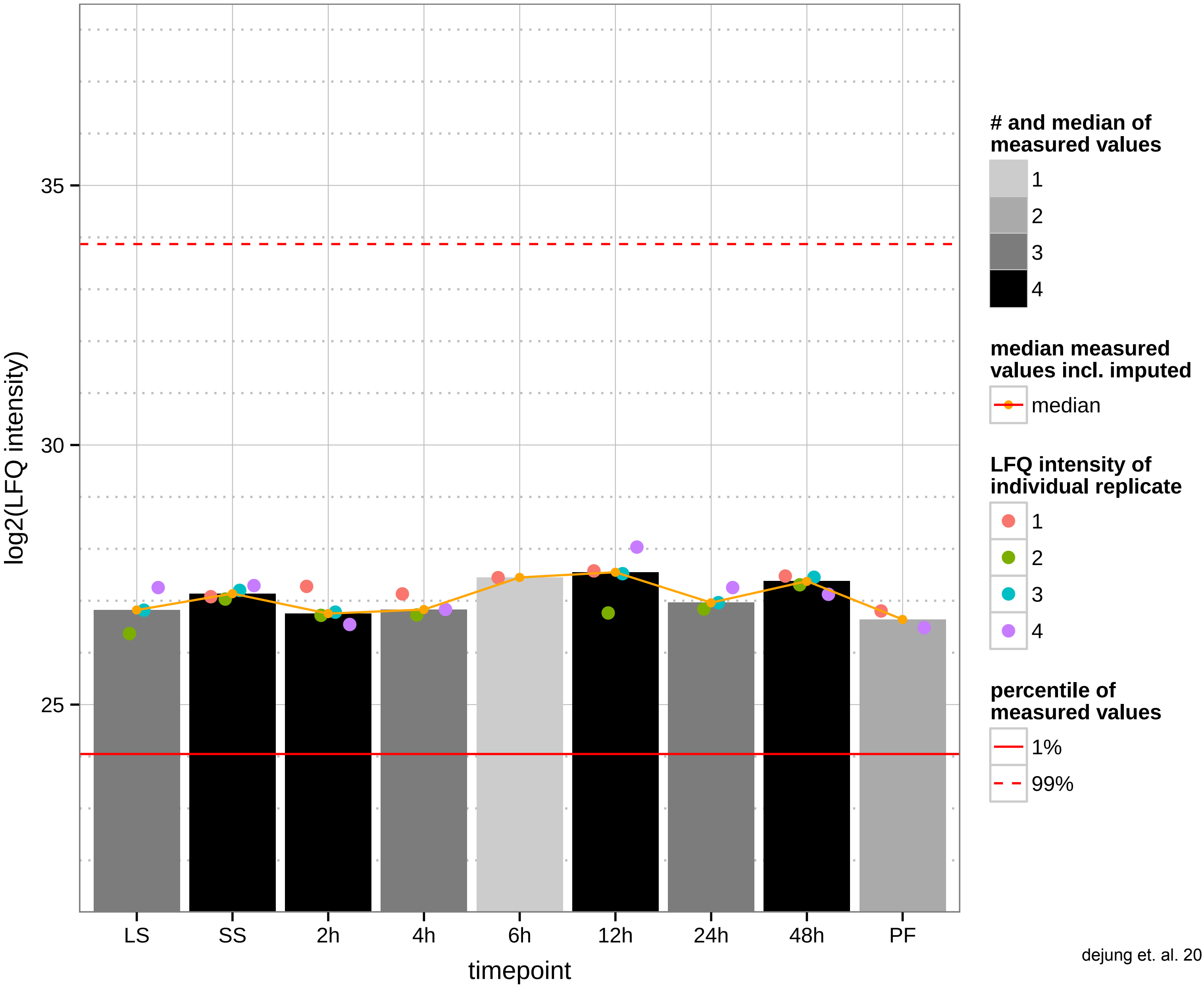
hypothetical protein, conserved
Tb927.5.2770
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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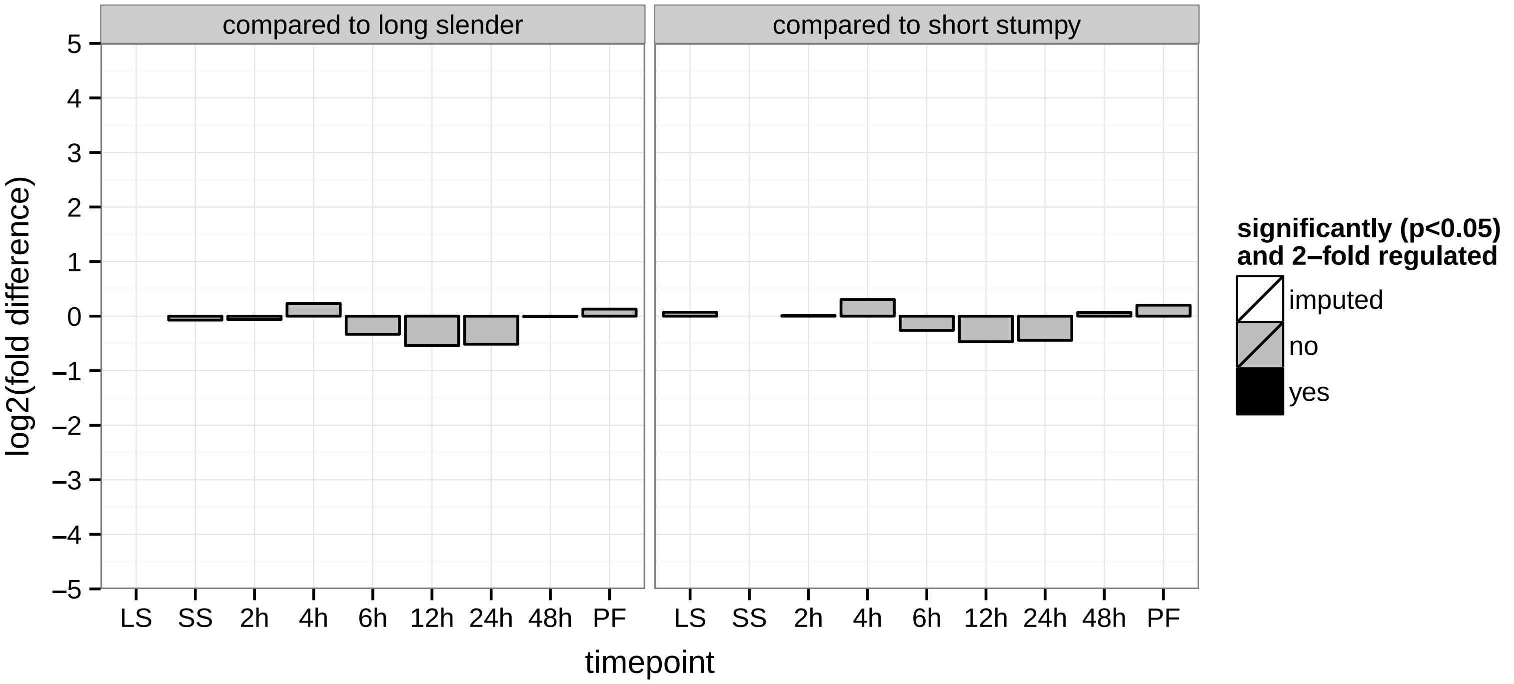
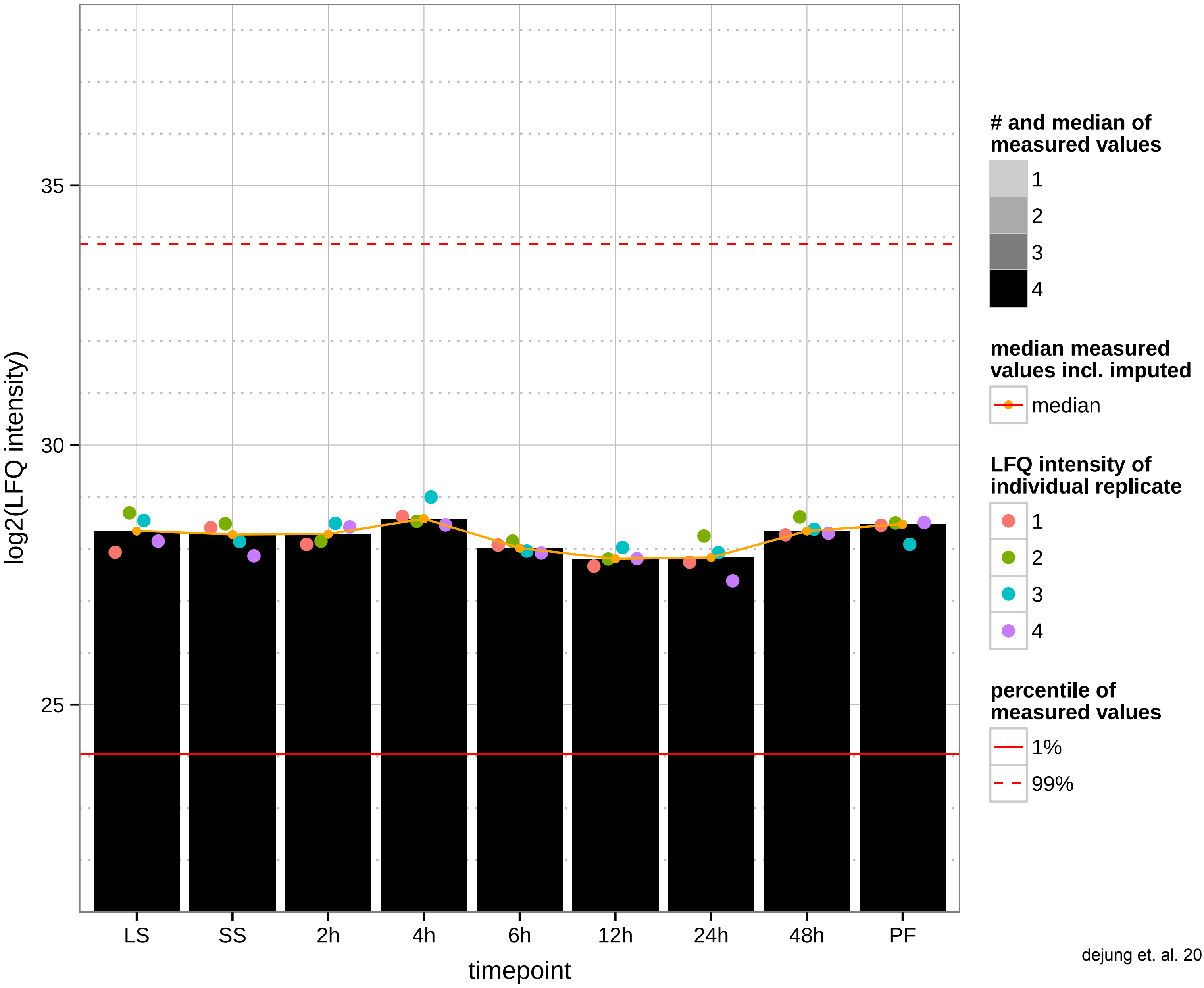
radial spoke protein RSP2, putative
Tb927.5.2850
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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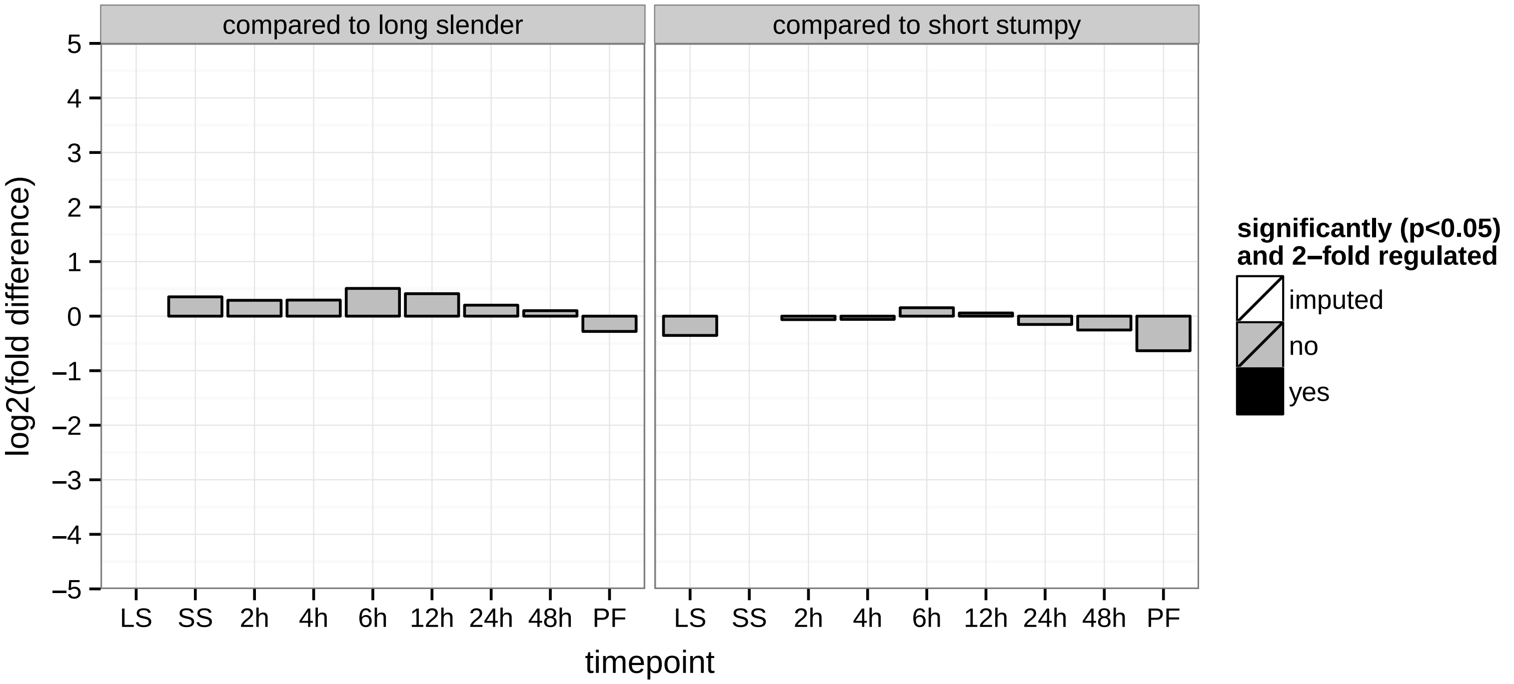
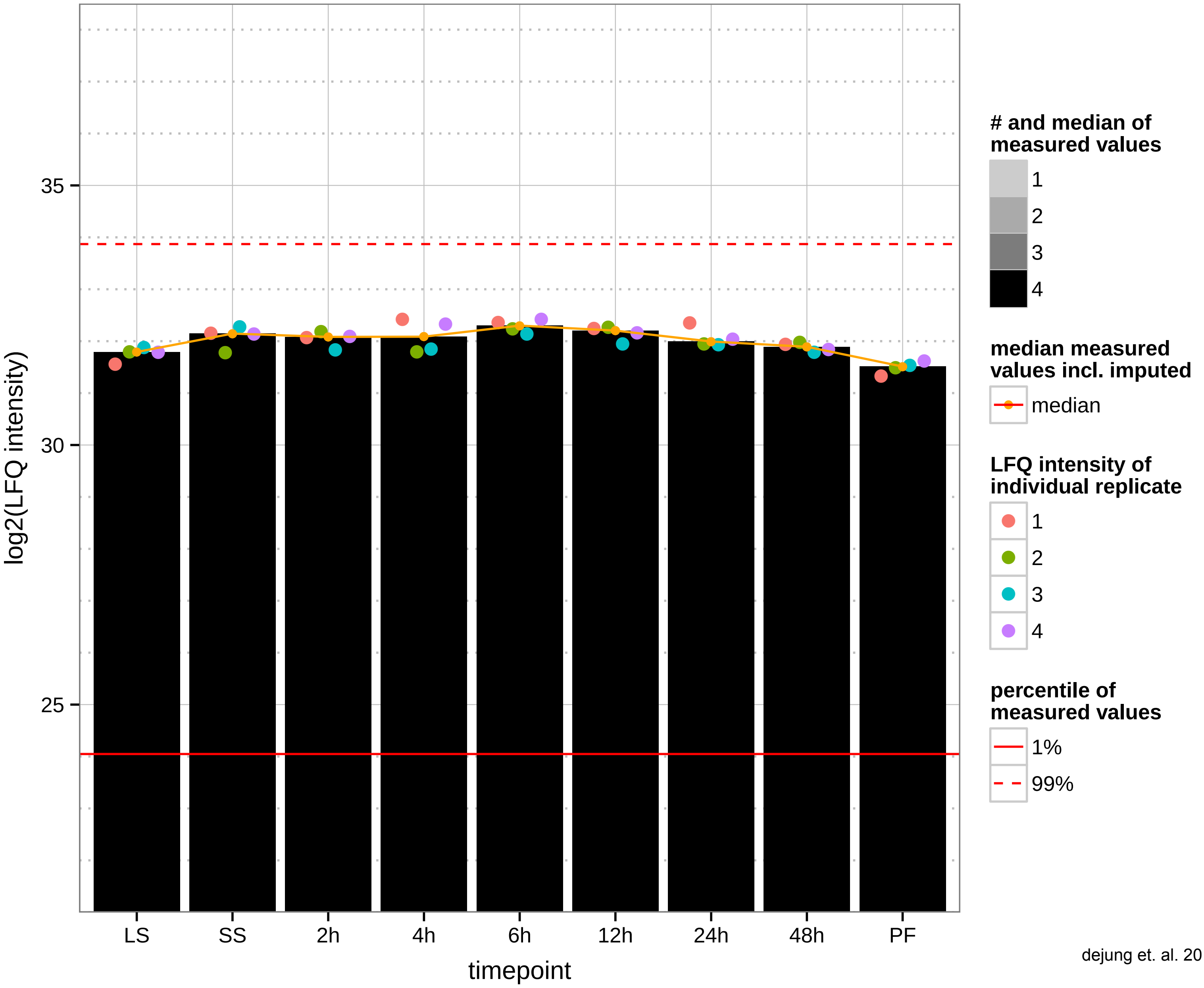
stress–induced protein sti1, putative
Tb927.5.2940
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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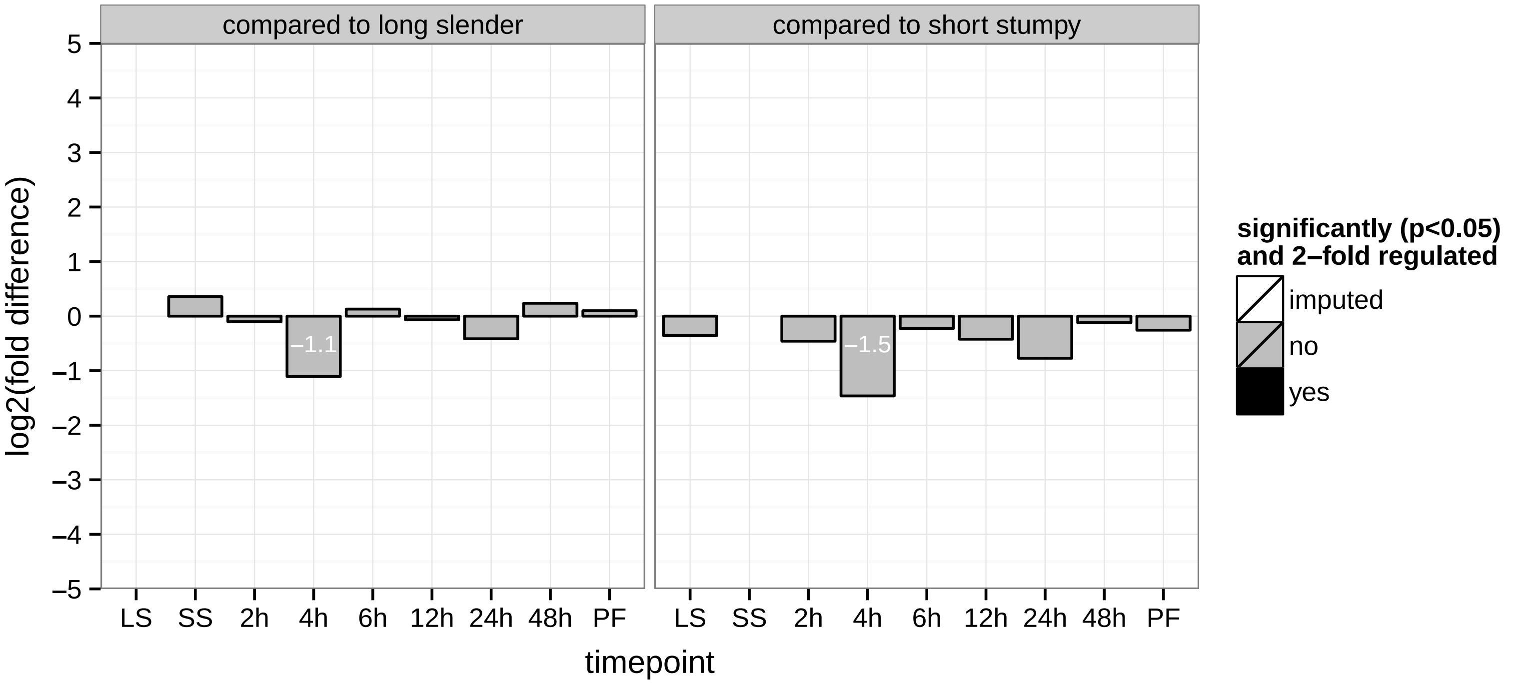
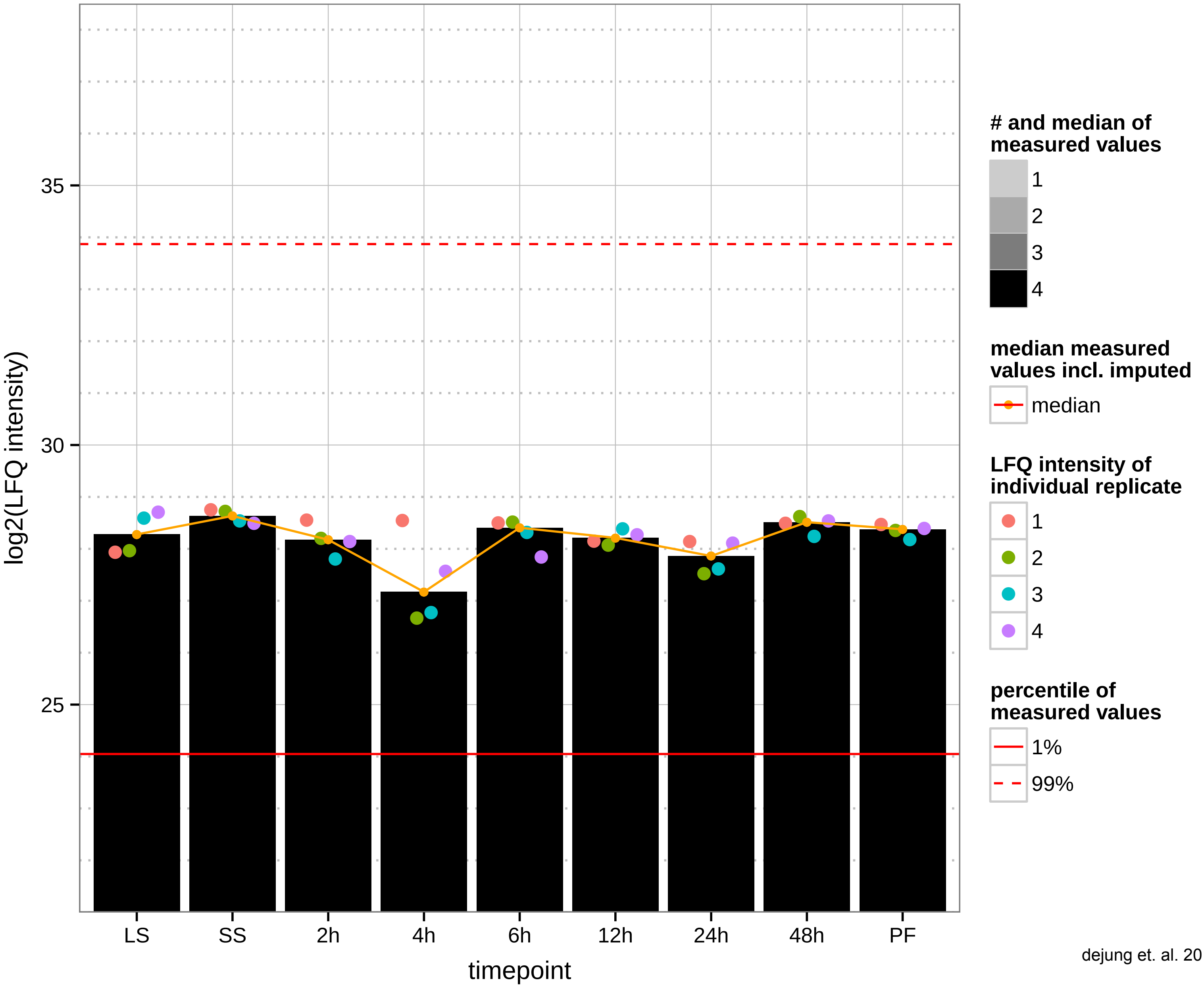
hypothetical protein, conserved
Tb927.5.2950
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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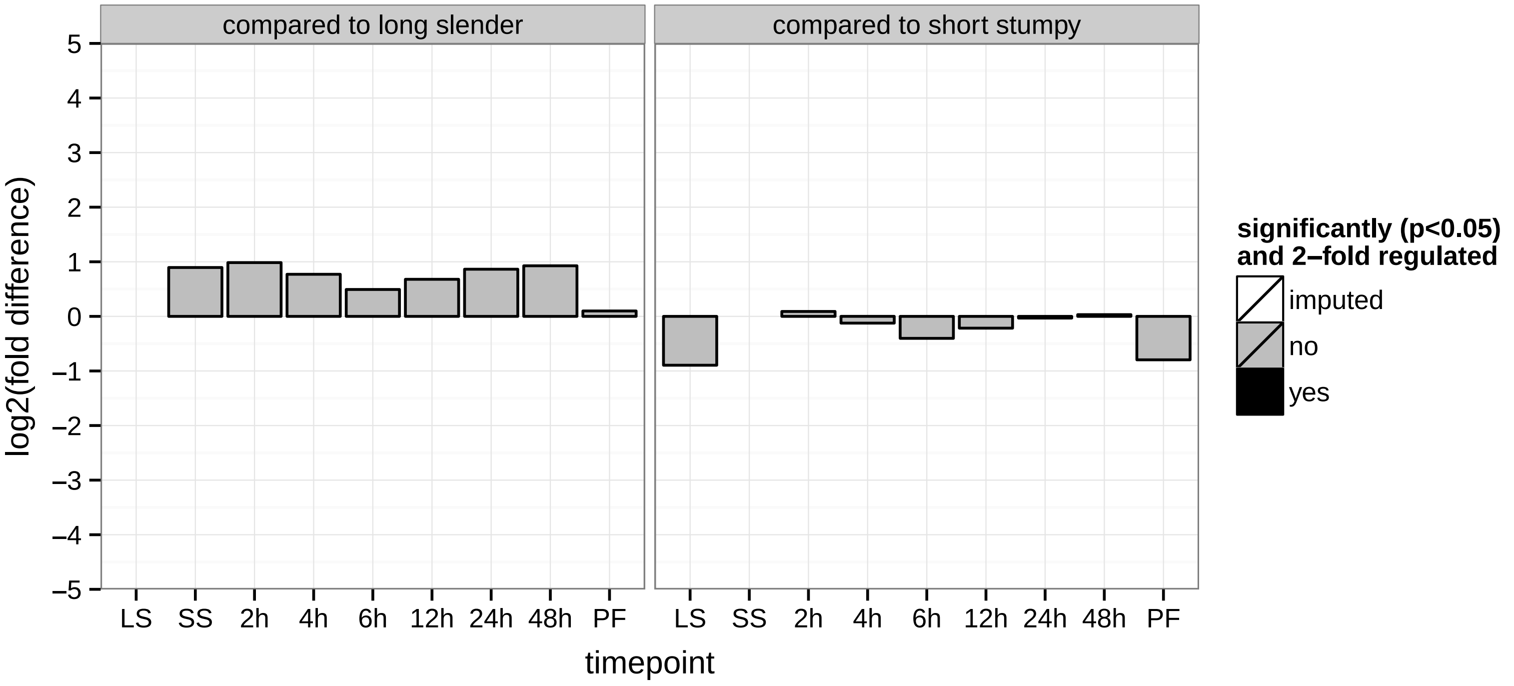
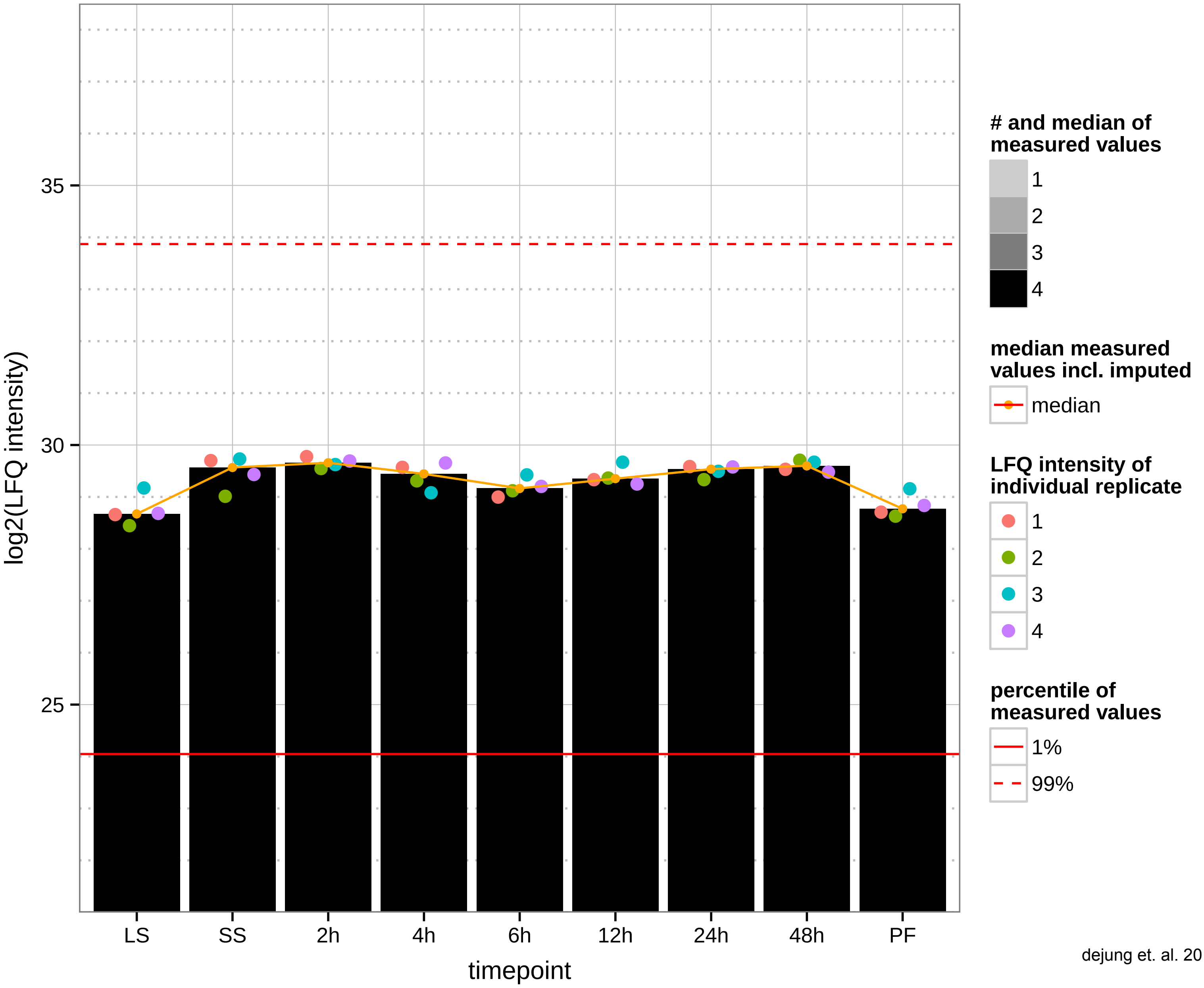
phosphoribosylpyrophosphate synthetase, putative (PRS)
Tb927.5.2960
AGOF: magnesium ion binding, ribose phosphate diphosphokinase activity
AGOC: null
AGOP: nucleoside metabolic process, nucleotide biosynthetic process
PGOF: magnesium ion binding, ribose phosphate diphosphokinase activity
PGOC: null
PGOP: nucleotide biosynthetic process





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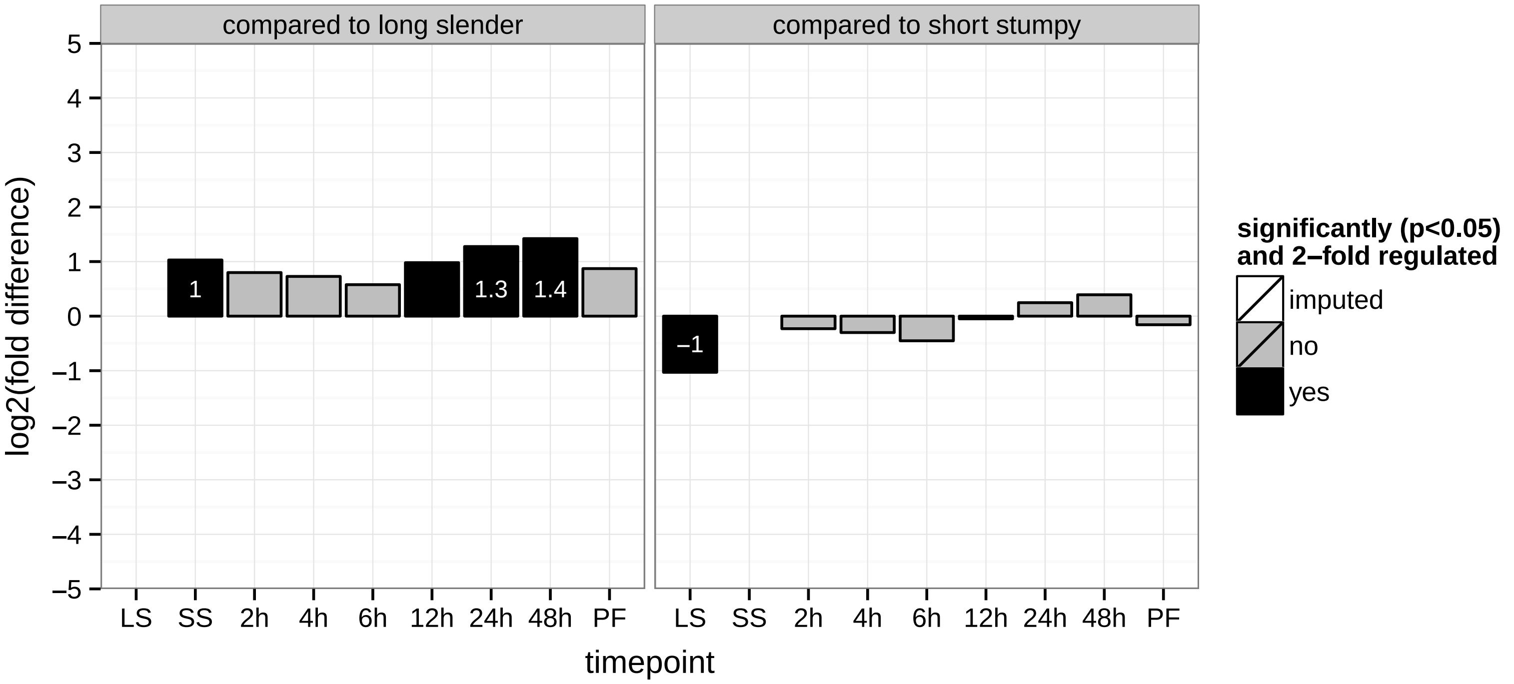
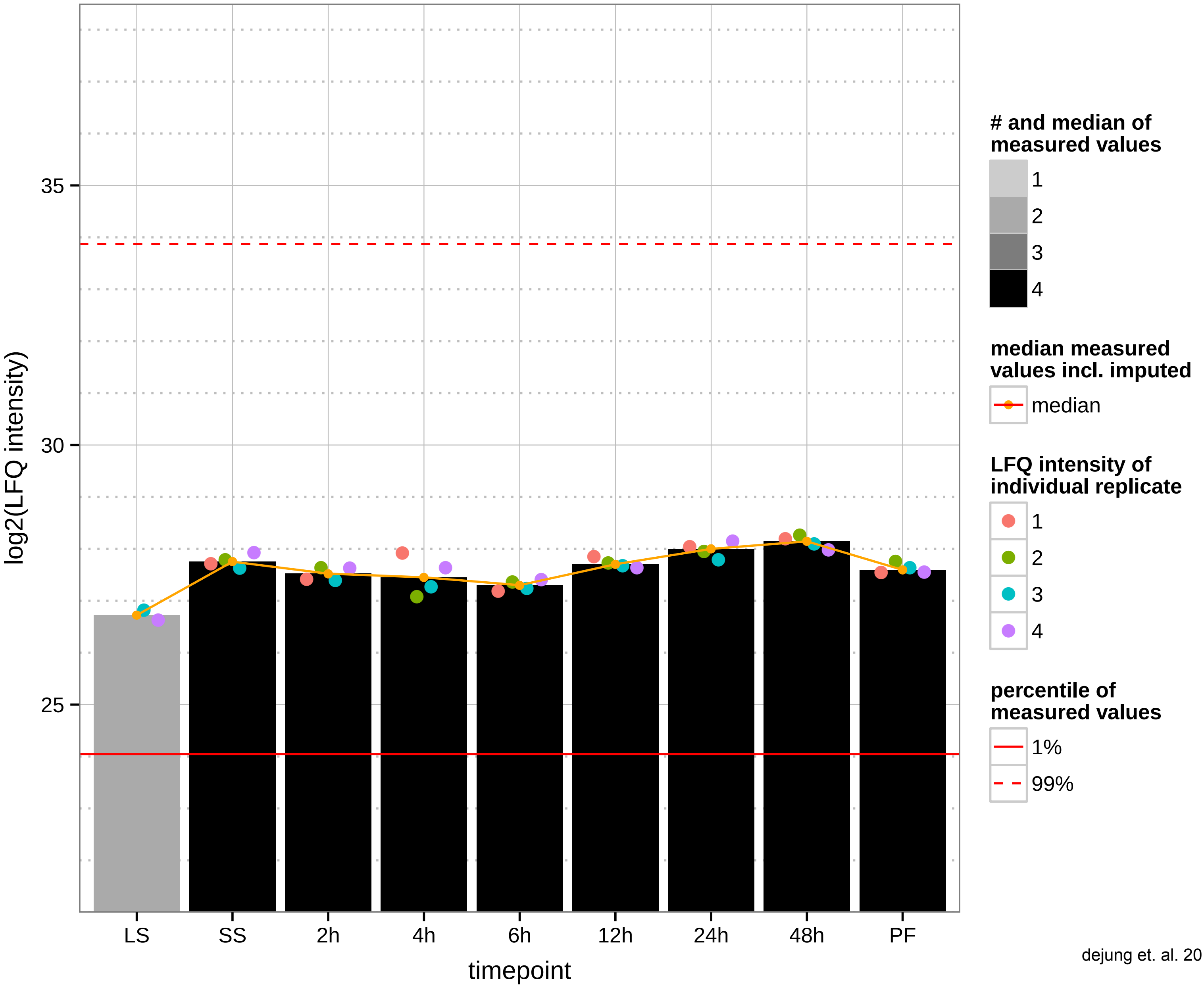
hypothetical protein, conserved, MRB1−associated protein, putative, guide RNA binding protein, putative (mrb3010)
Tb927.5.3010;Tb11.v5.0691
AGOF: null, mRNA binding
AGOC: null, mitochondrion
AGOP: null, RNA processing
PGOF: null
PGOC: null
PGOP: null





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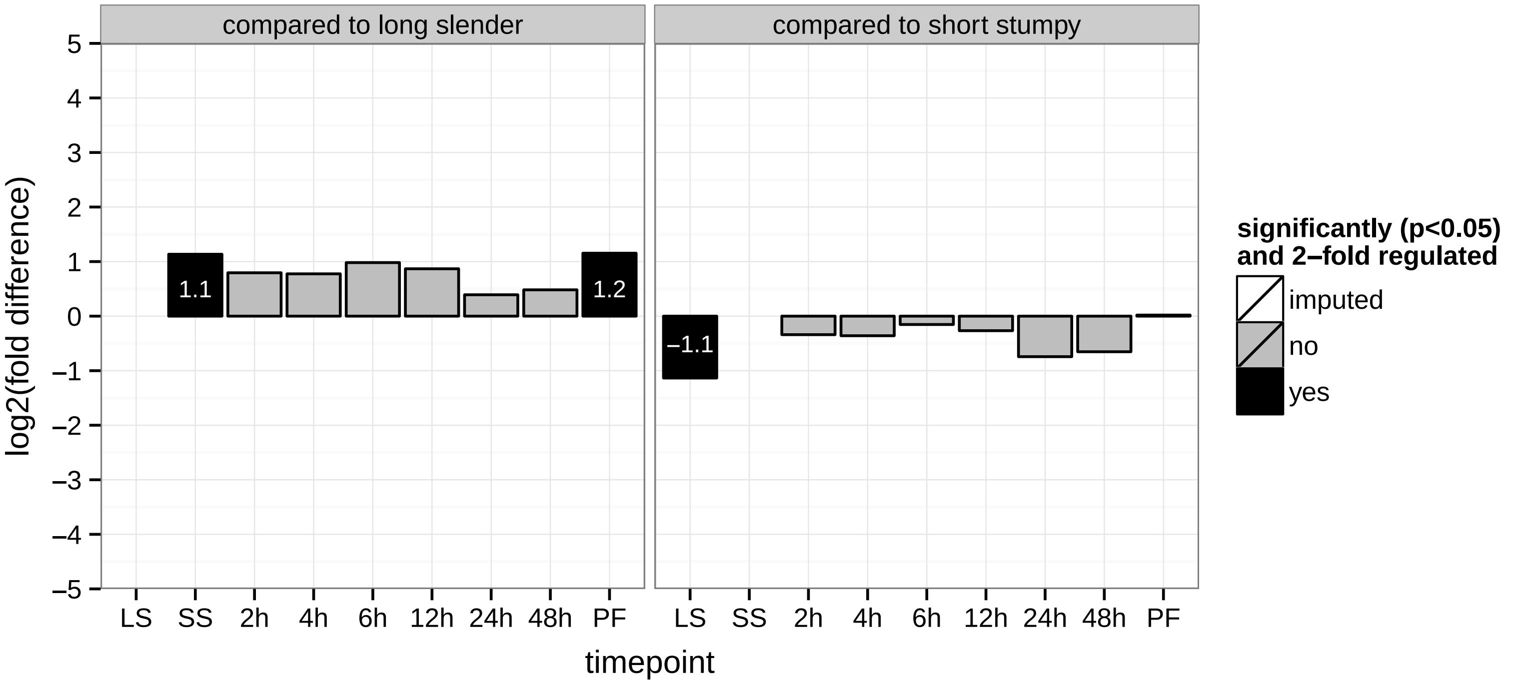
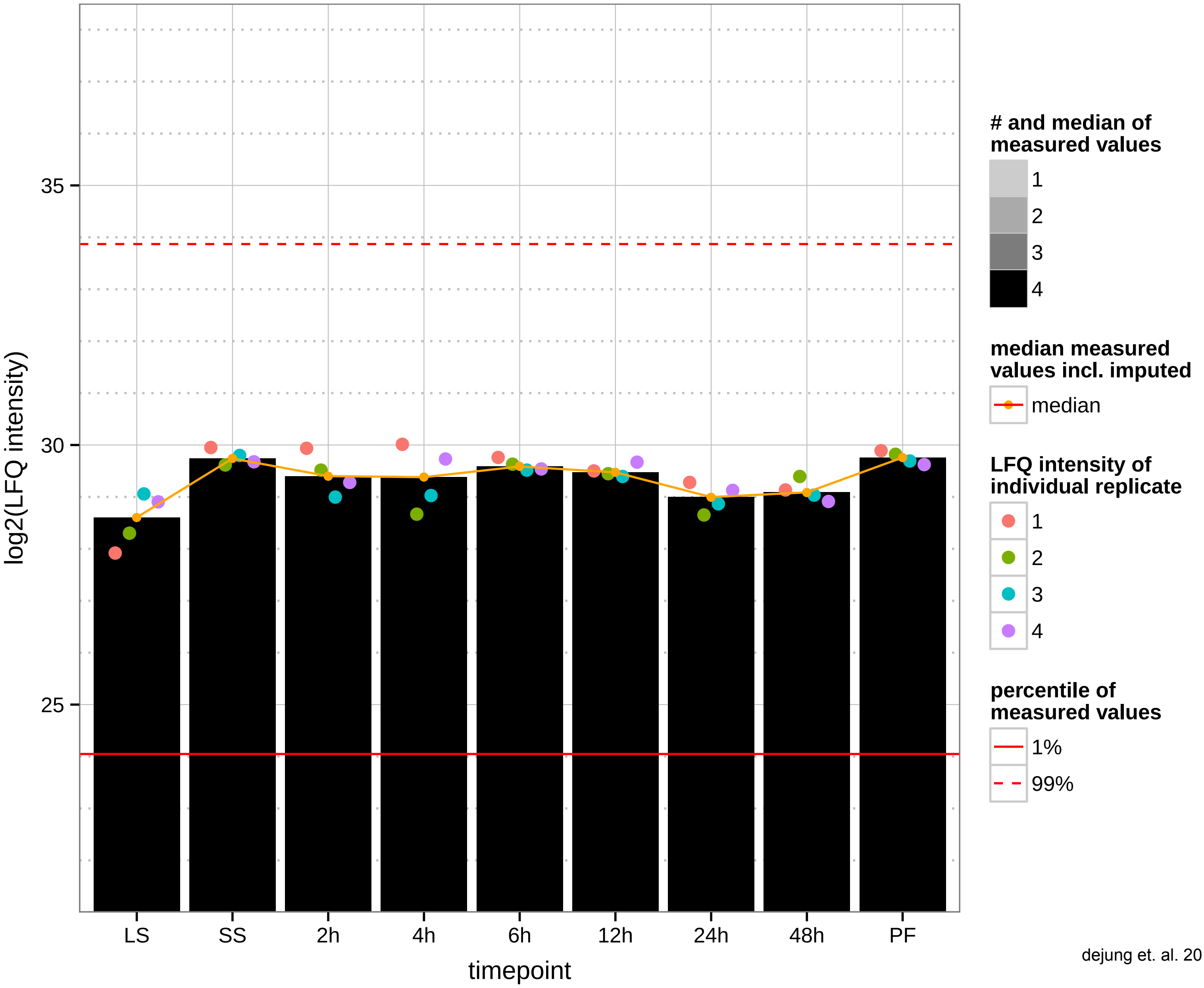
intraflagellar transport protein IFT122, putative (IFT122B)
Tb927.5.3030
AGOF: null
AGOC: bacterial–type flagellum basal body
AGOP: intraflagellar transport
PGOF: protein binding
PGOC: null
PGOP: null





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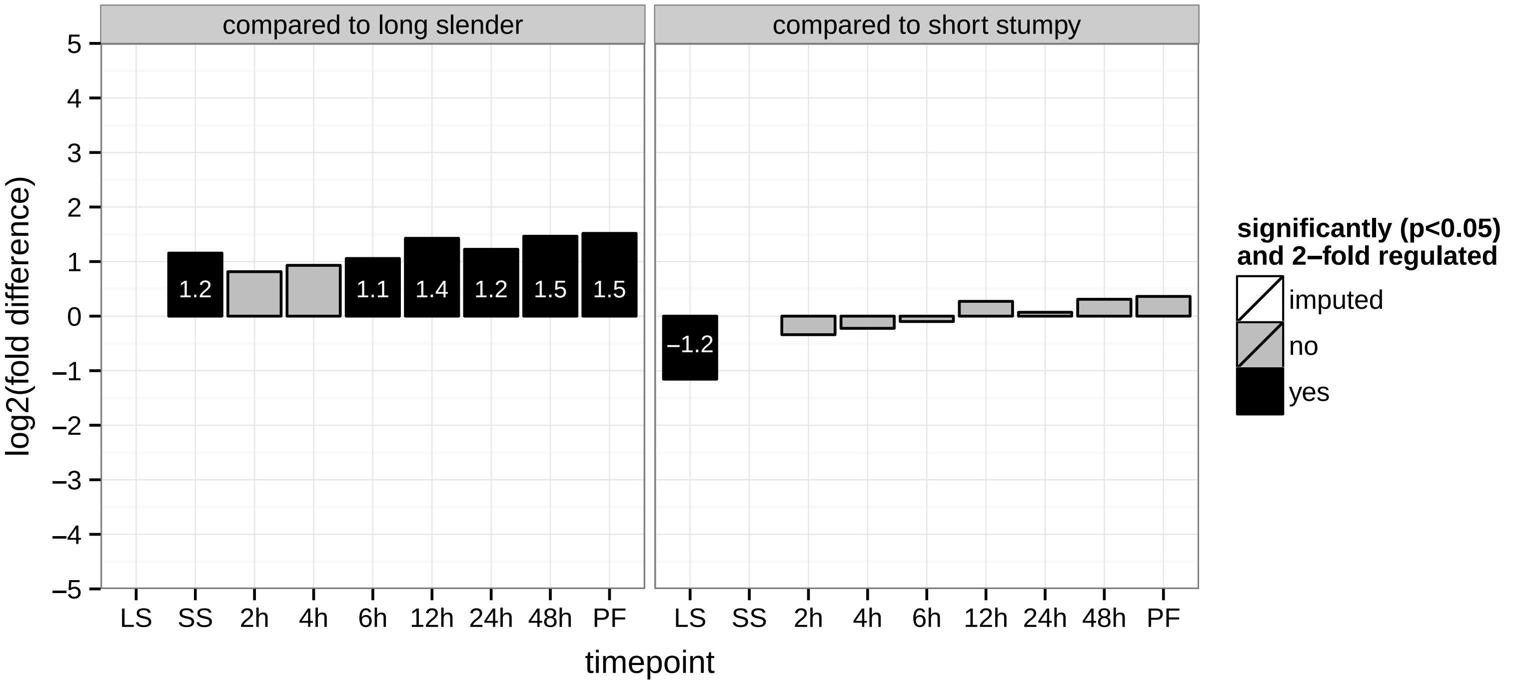
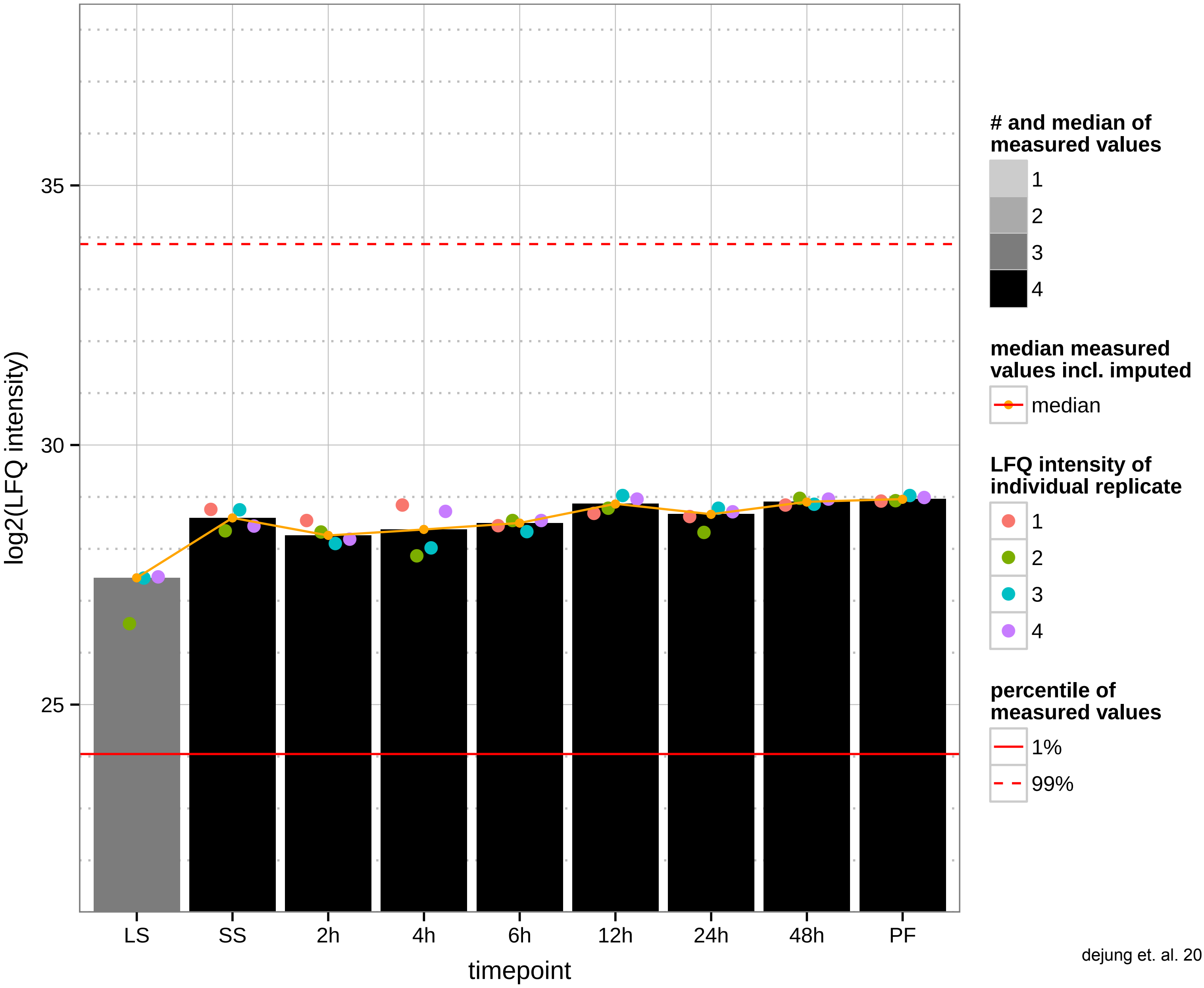
ribose–phosphate pyrophosphokinase, putative (PRPS5)
Tb927.5.3170
AGOF: magnesium ion binding, ribose phosphate diphosphokinase activity
AGOC: null
AGOP: nucleotide biosynthetic process
PGOF: null
PGOC: null
PGOP: null





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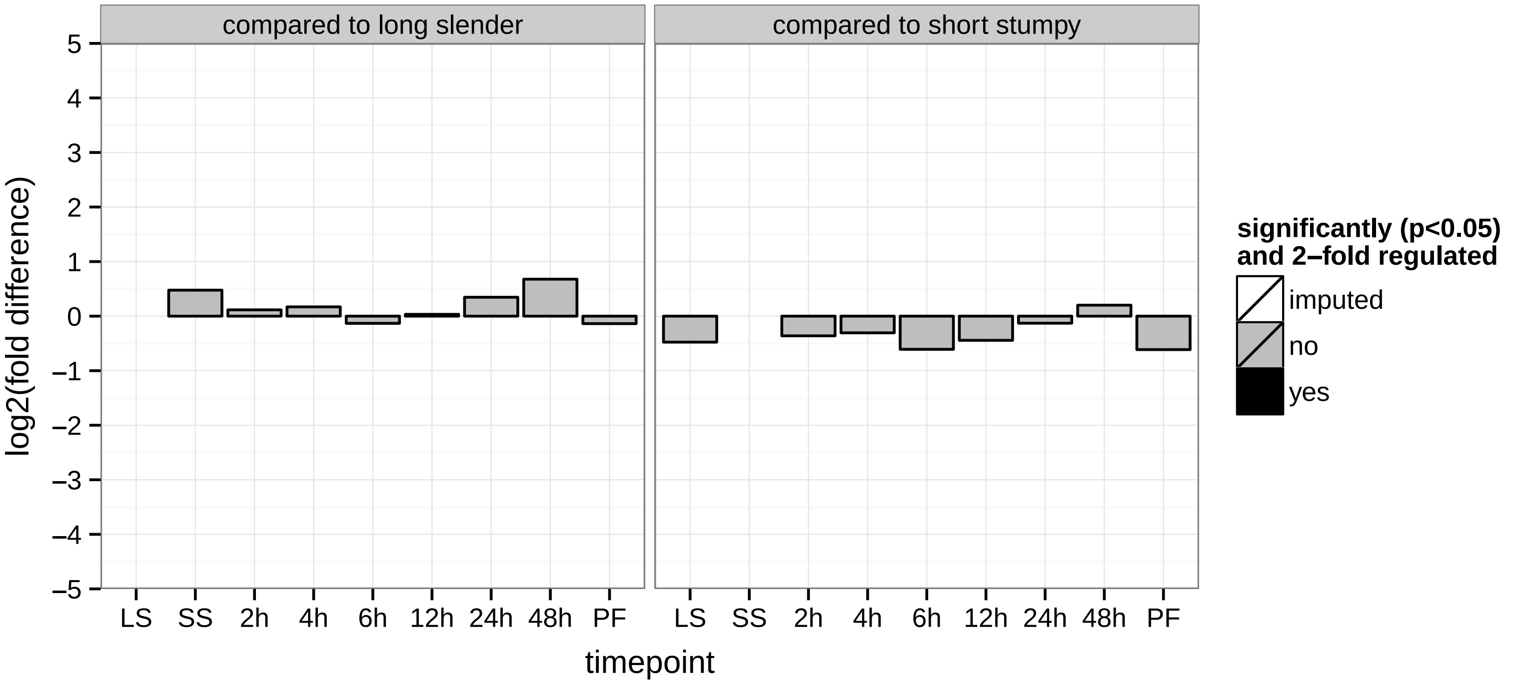
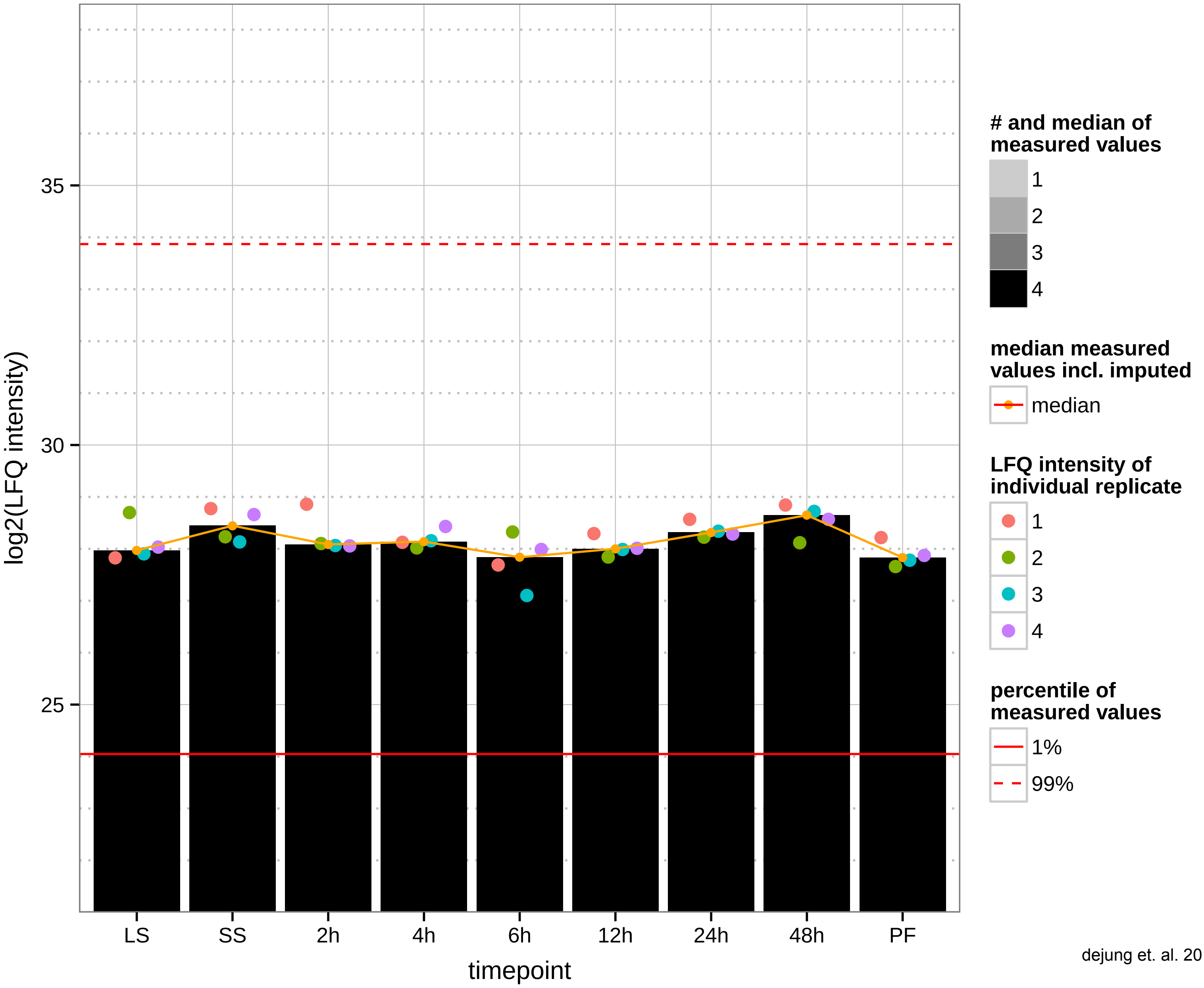
small ubiquitin–related modifier (SUMO)
Tb927.5.3210
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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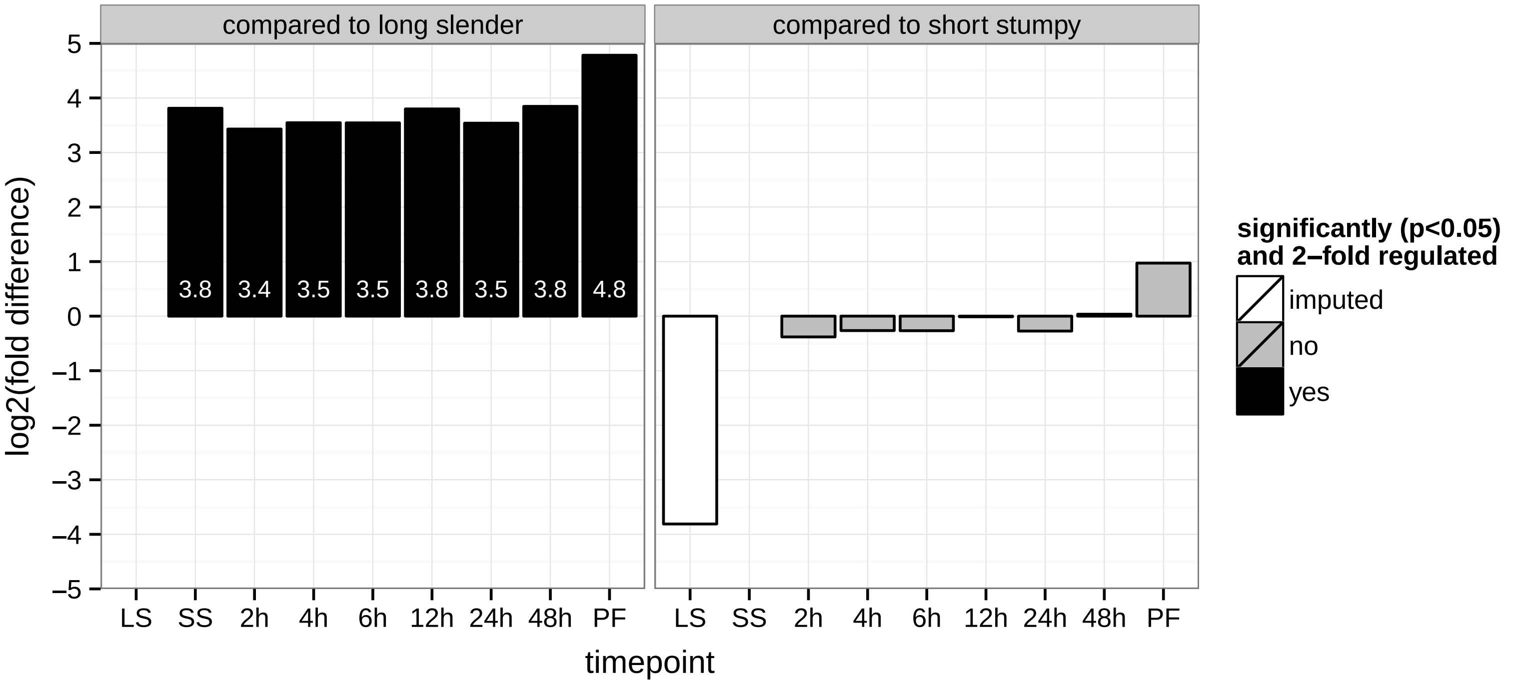
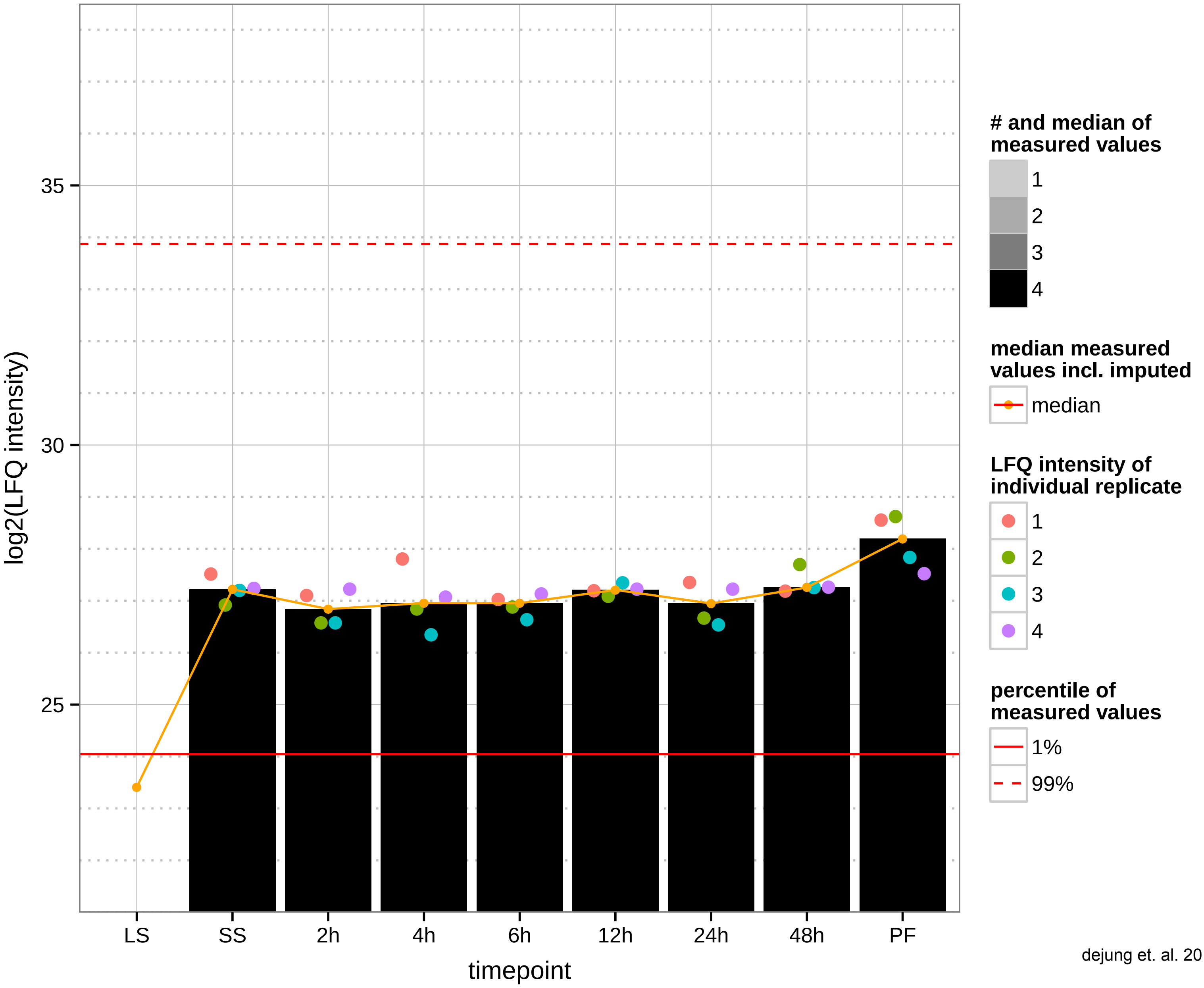
hypothetical protein, conserved
Tb927.5.3250
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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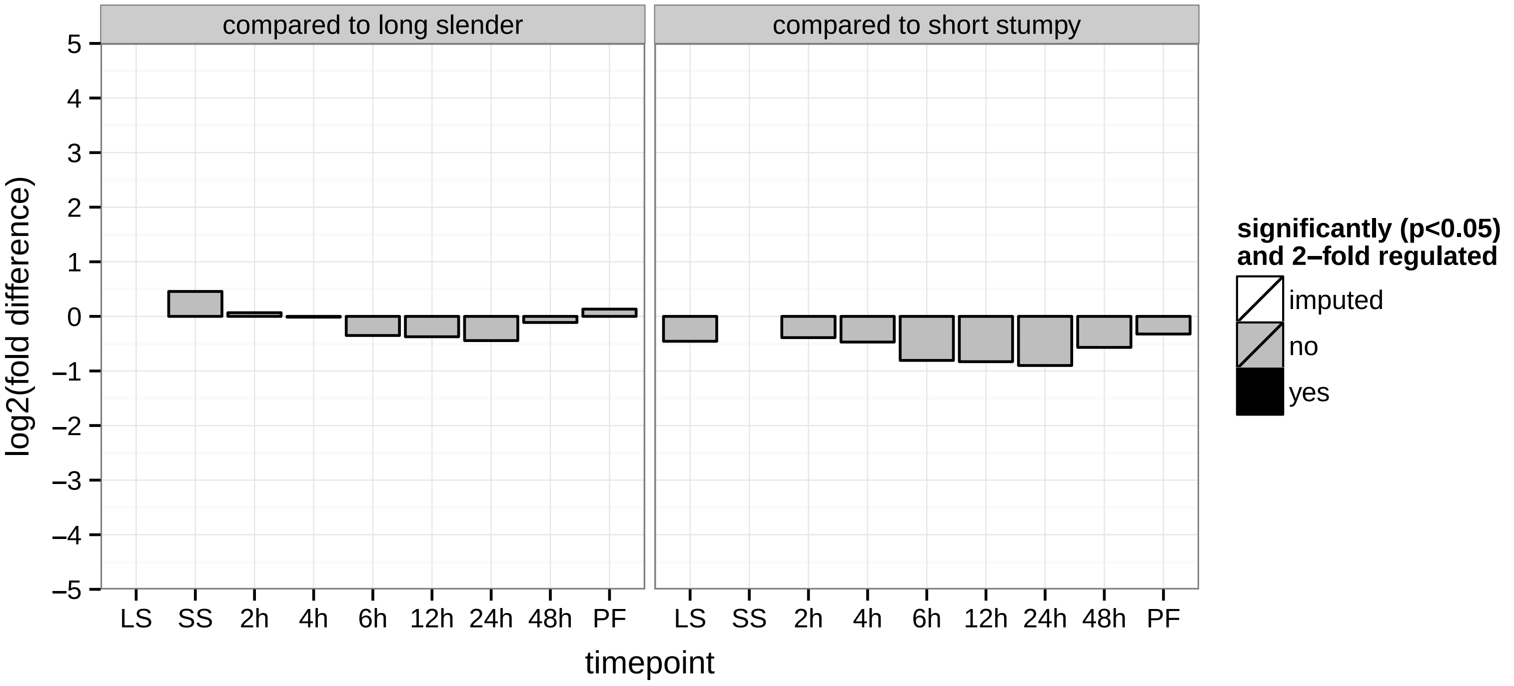
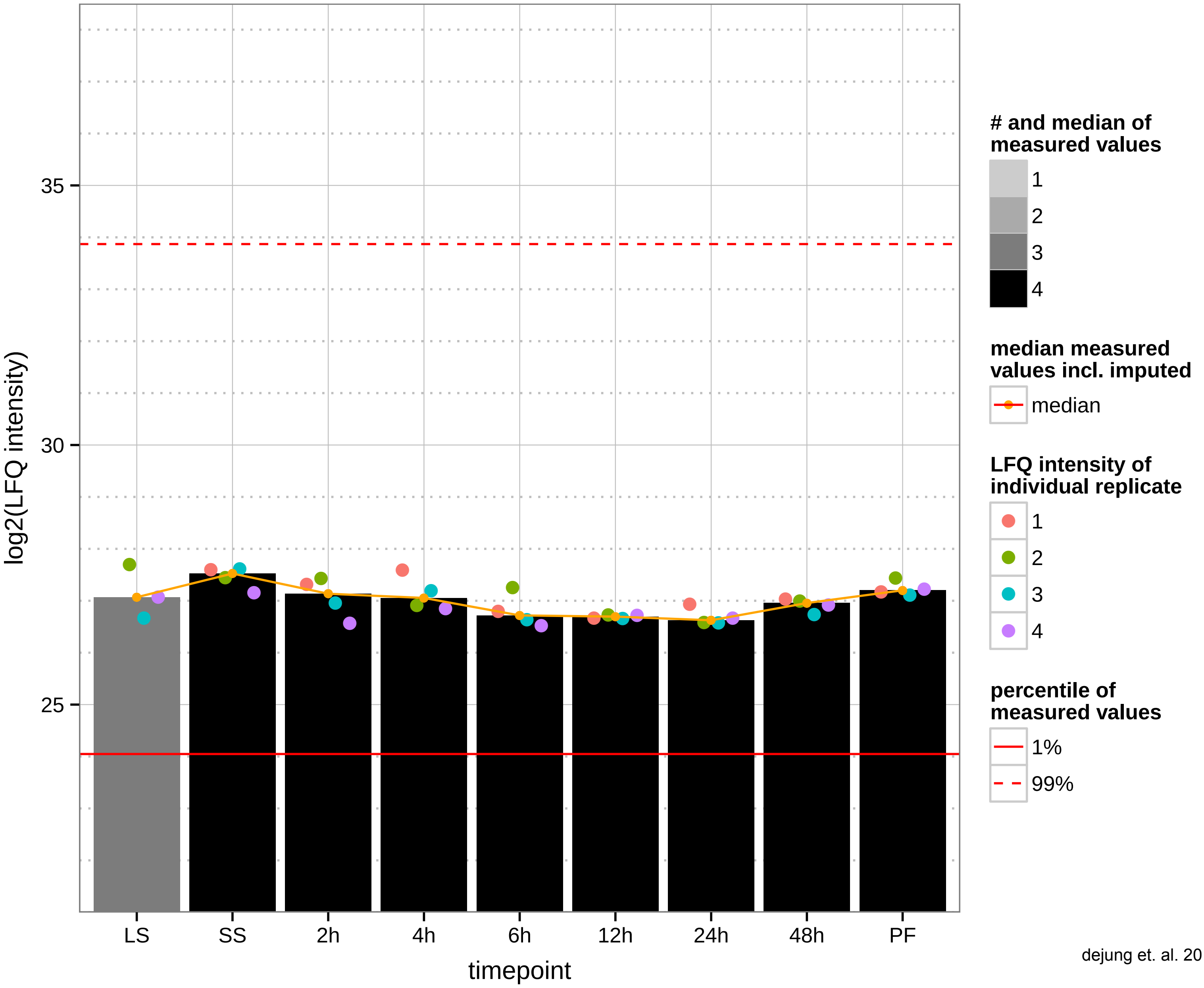
hypothetical protein, conserved
Tb927.5.3260
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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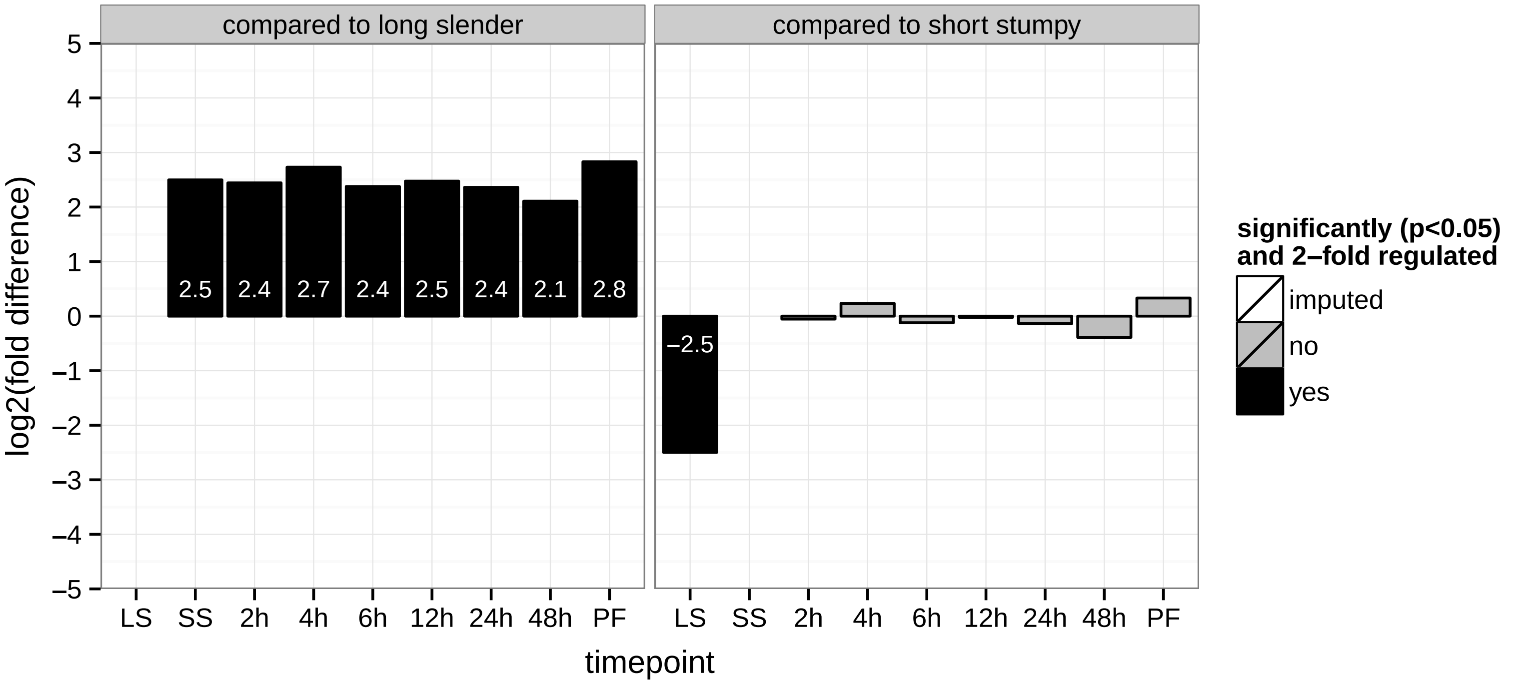
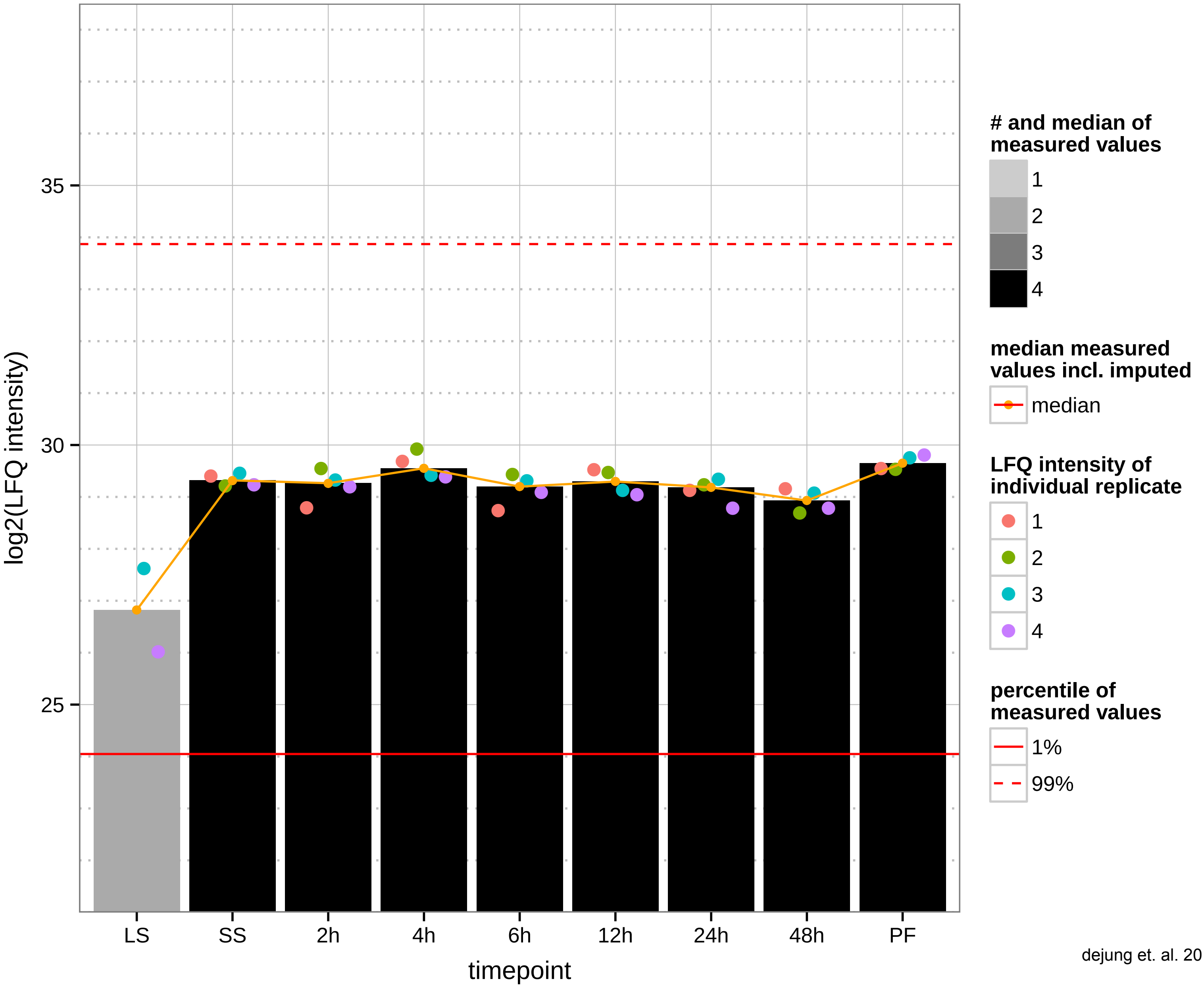
iron superoxide dismutase, putative
Tb927.5.3350
AGOF: metal ion binding, superoxide dismutase activity
AGOC: mitochondrion
AGOP: oxidation–reduction process, superoxide metabolic process
PGOF: metal ion binding, superoxide dismutase activity
PGOC: null
PGOP: oxidation–reduction process, superoxide metabolic process





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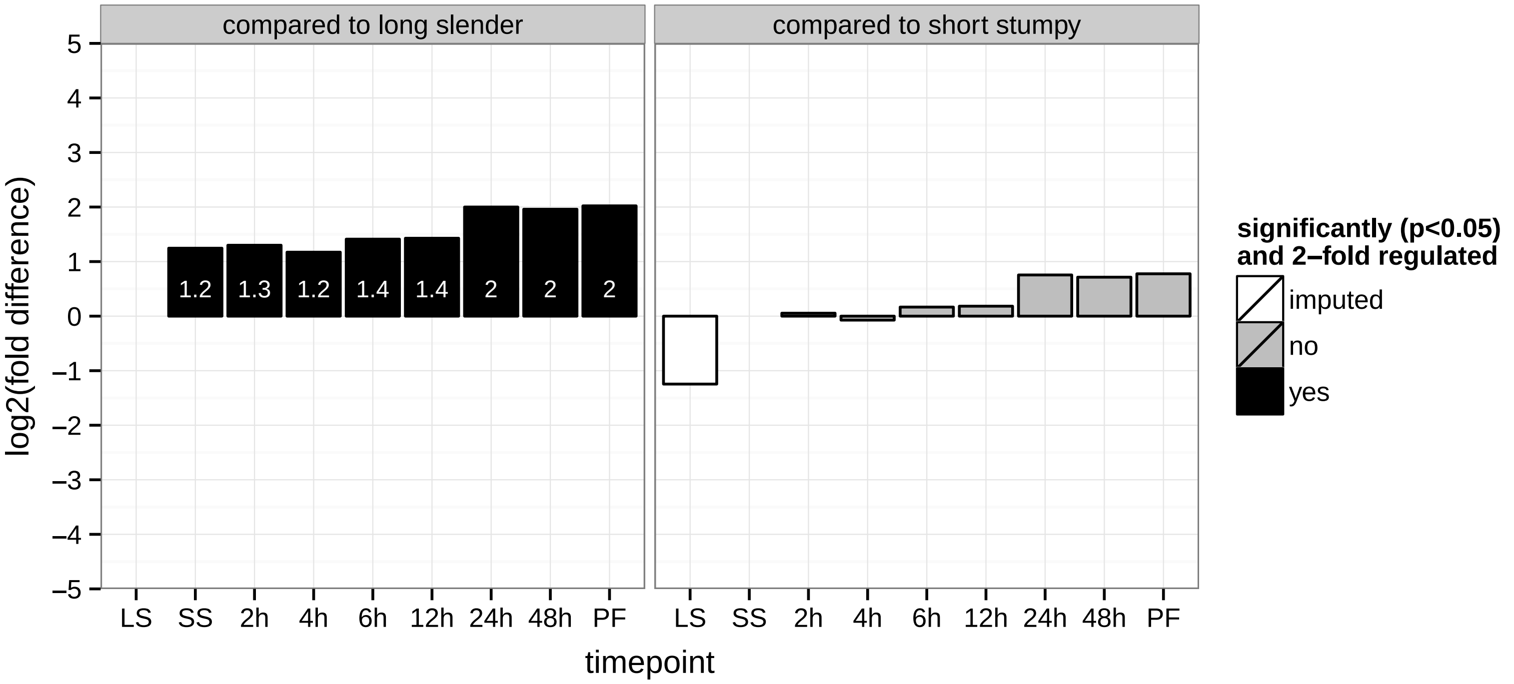
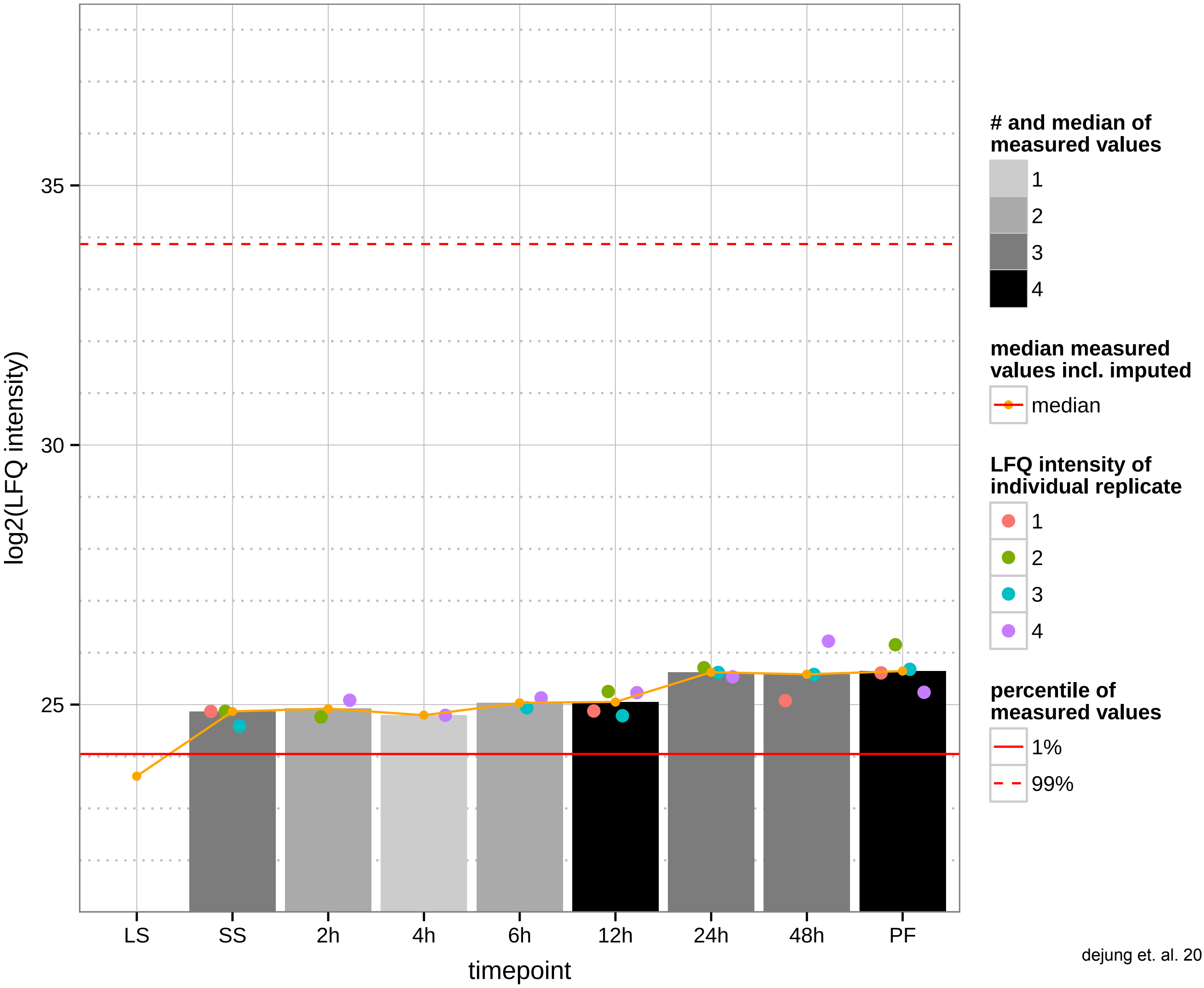
50S ribosomal protein L2, putative
Tb927.5.3360
AGOF: structural constituent of ribosome
AGOC: intracellular, mitochondrion, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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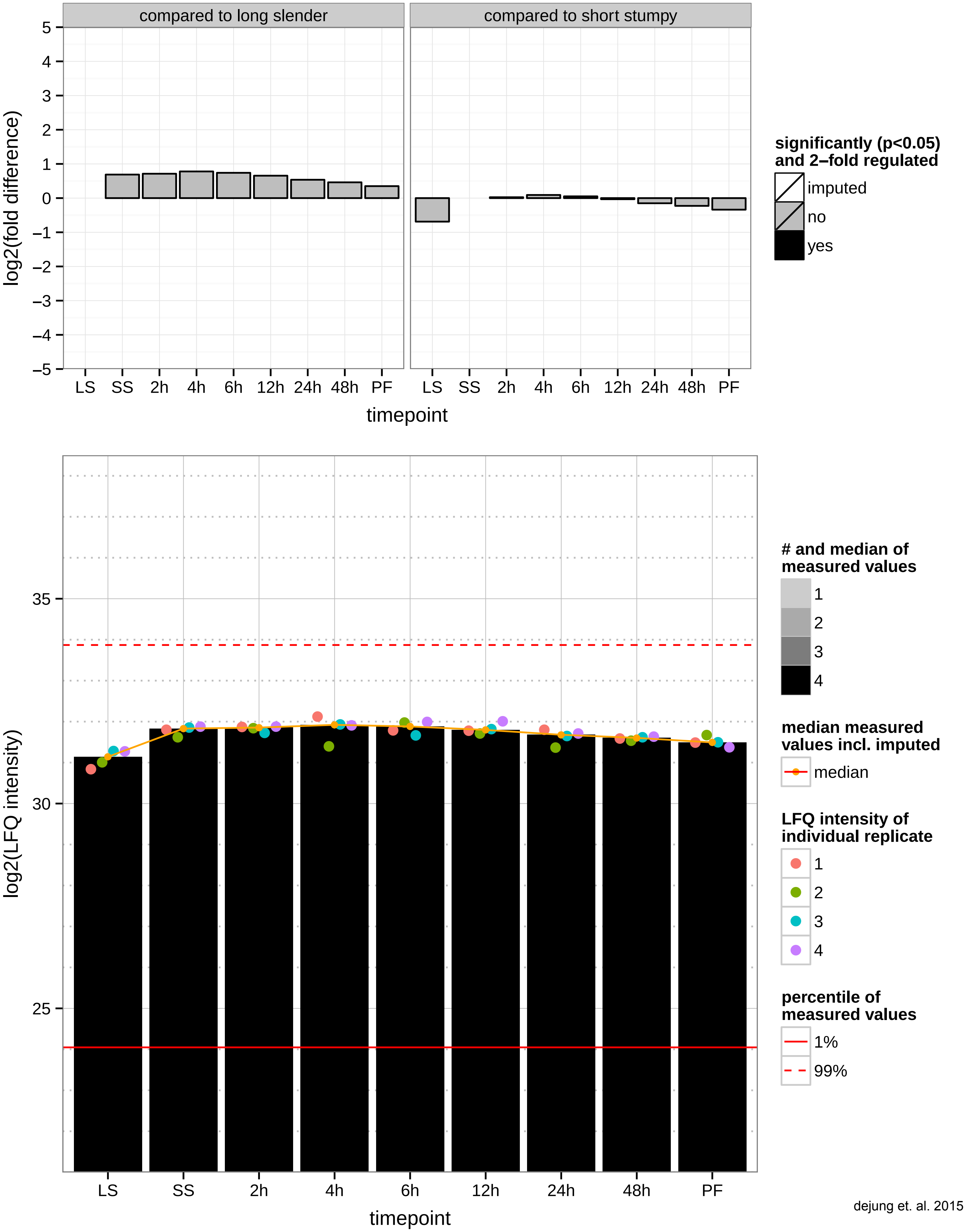
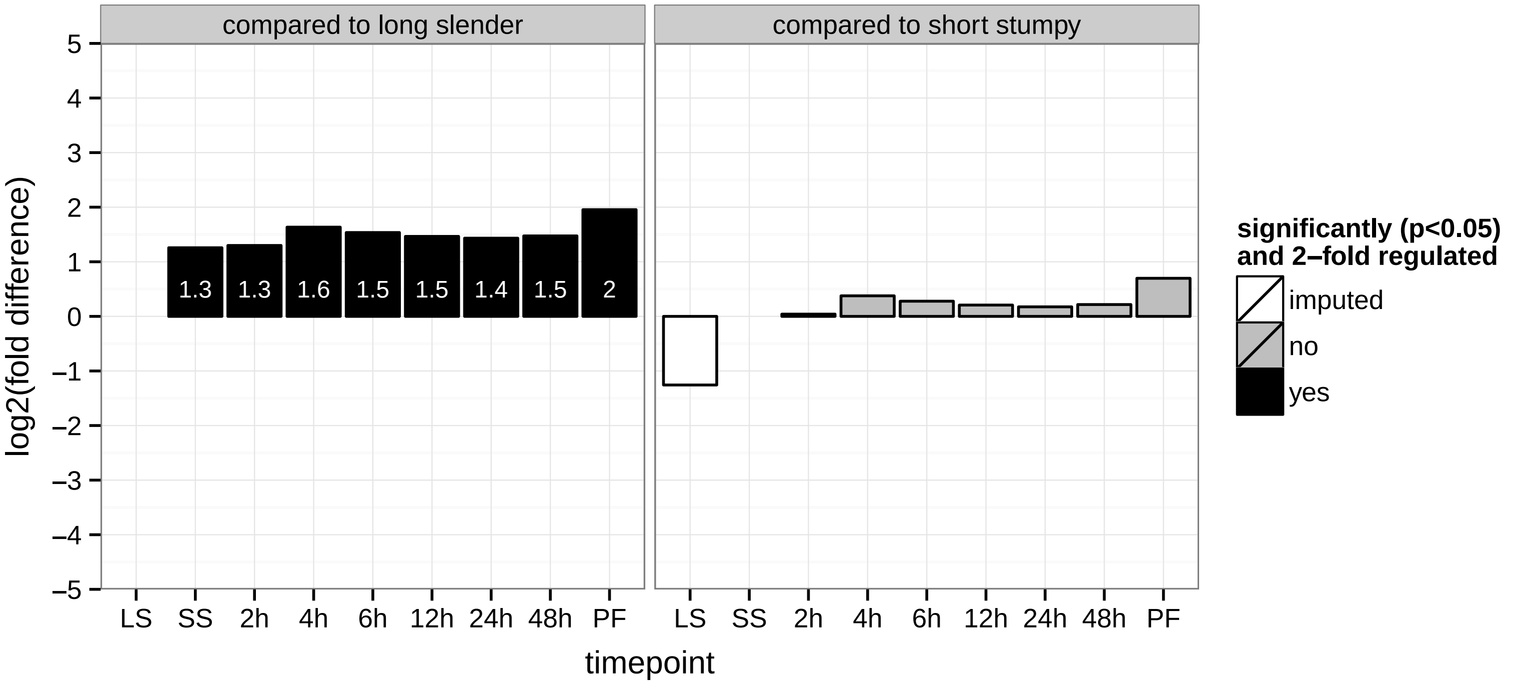
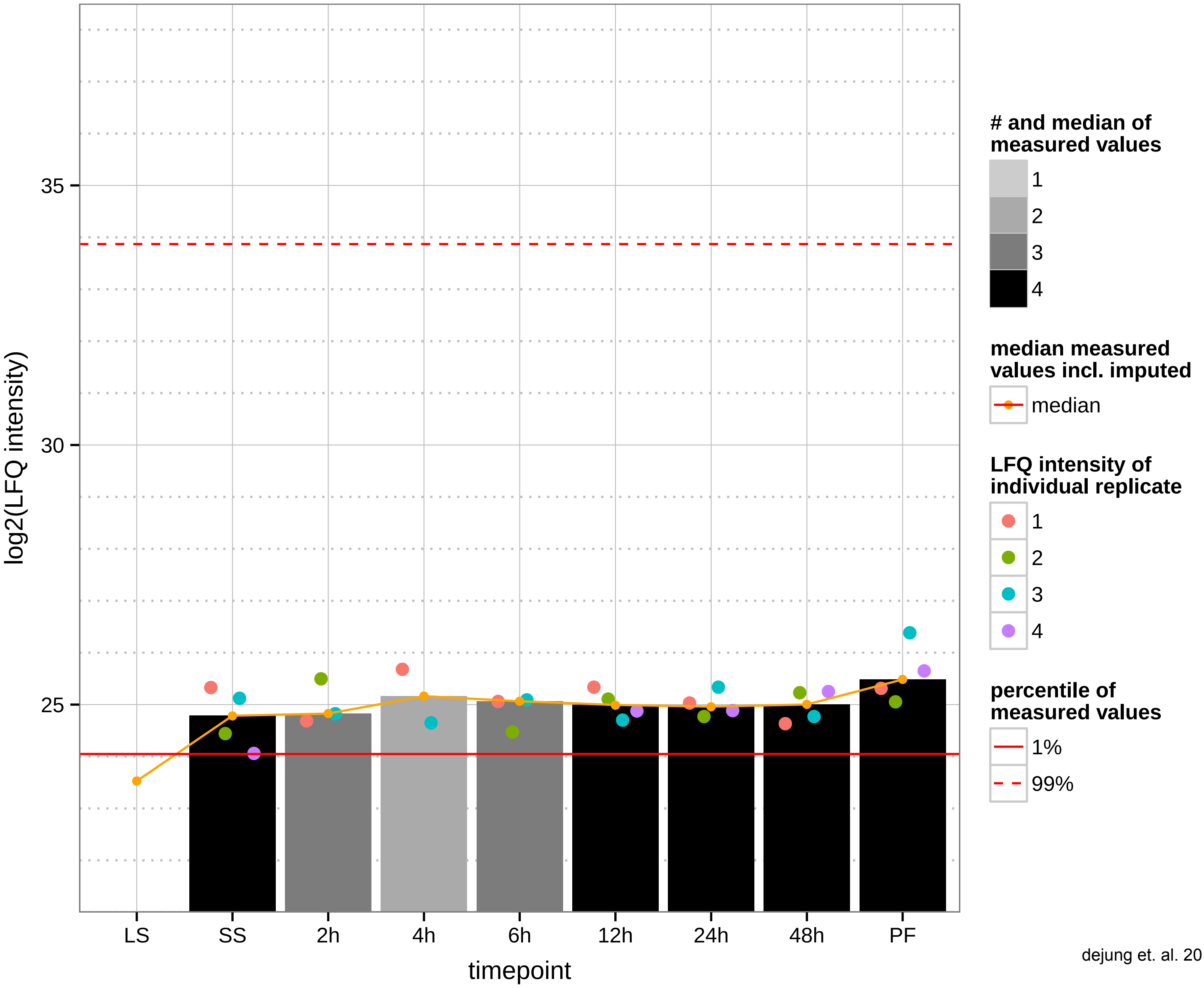
calcium−translocating P−type ATPase, calcium pump
Tb927.5.3400
AGOF: ATP binding, calcium−transporting ATPase activity
AGOC: integral to membrane, mitochondrial inner membrane
AGOP: ATP biosynthetic process, calcium ion transport, metabolic process
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, calcium−tran
PGOC: integral to membrane, membrane
PGOP: ATP biosynthetic process, calcium ion transport, cation transport, metabolic process



dejung et. al. 2015

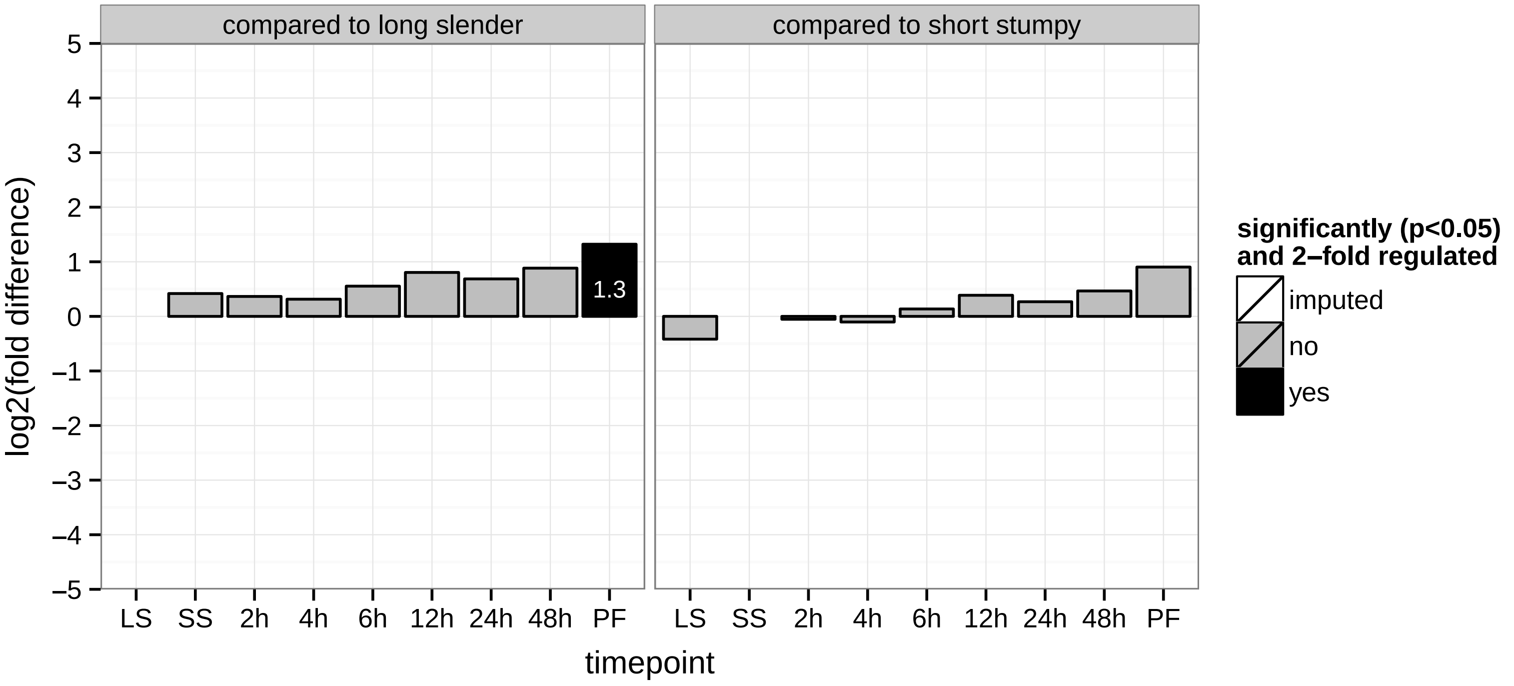
ubiquitin–activating enzyme E1, putative
Tb927.5.3430
AGOF: ATP binding, small protein activating enzyme activity
AGOC: null
AGOP: cellular protein modification process
PGOF: ATP binding, catalytic activity, small protein activating enzyme activity
PGOC: null
PGOP: cellular protein modification process

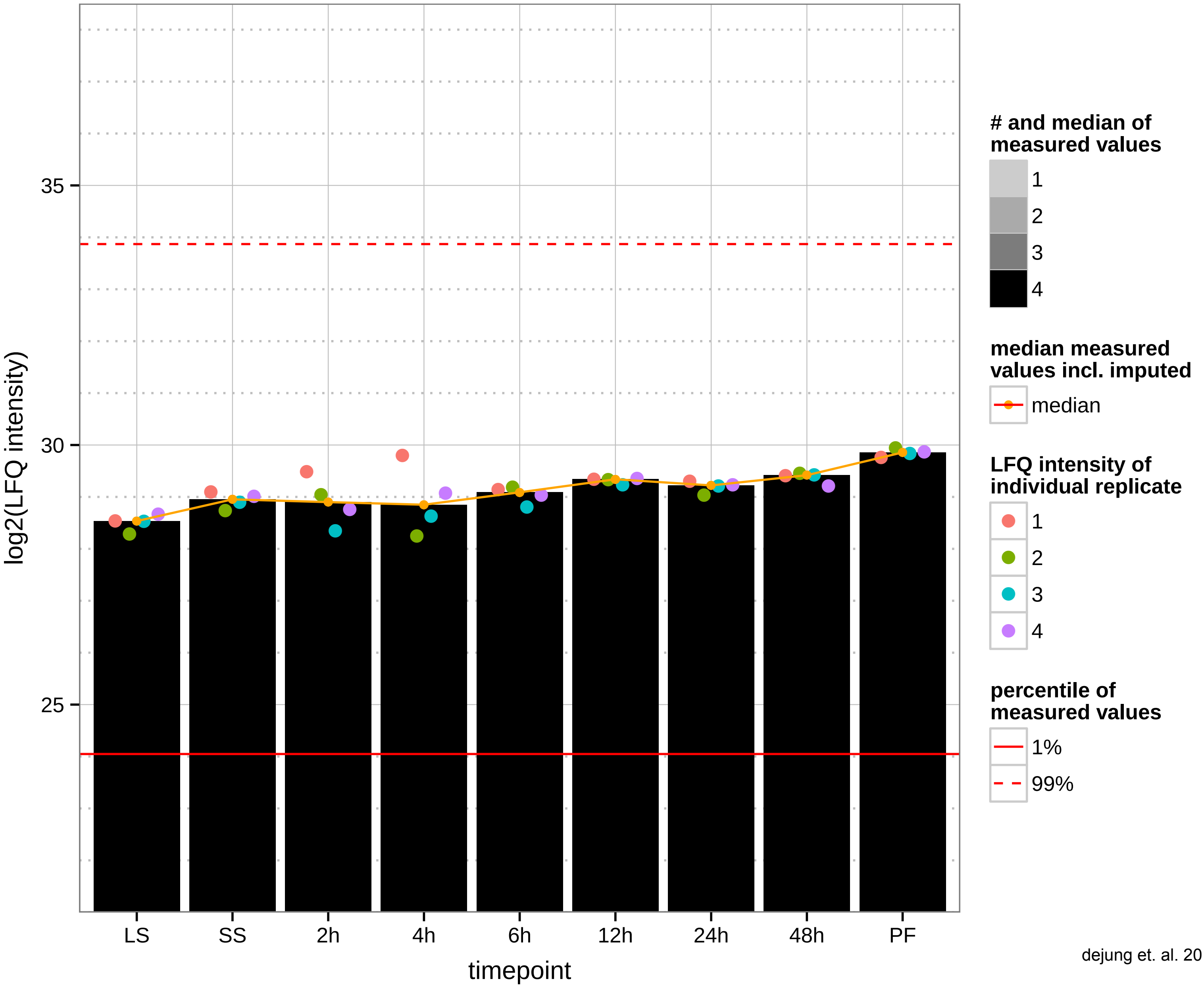




dejung et. al. 2015

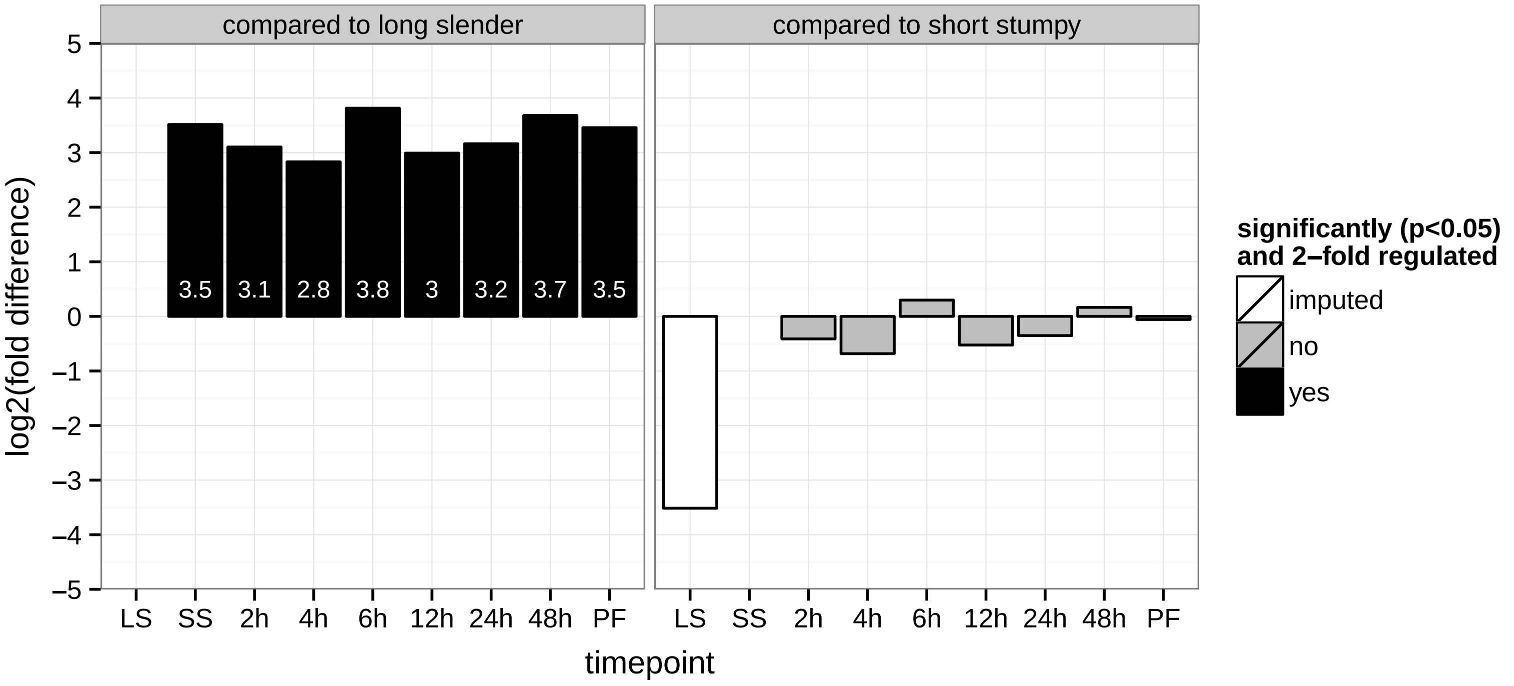
hypothetical protein, conserved
Tb927.5.3450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

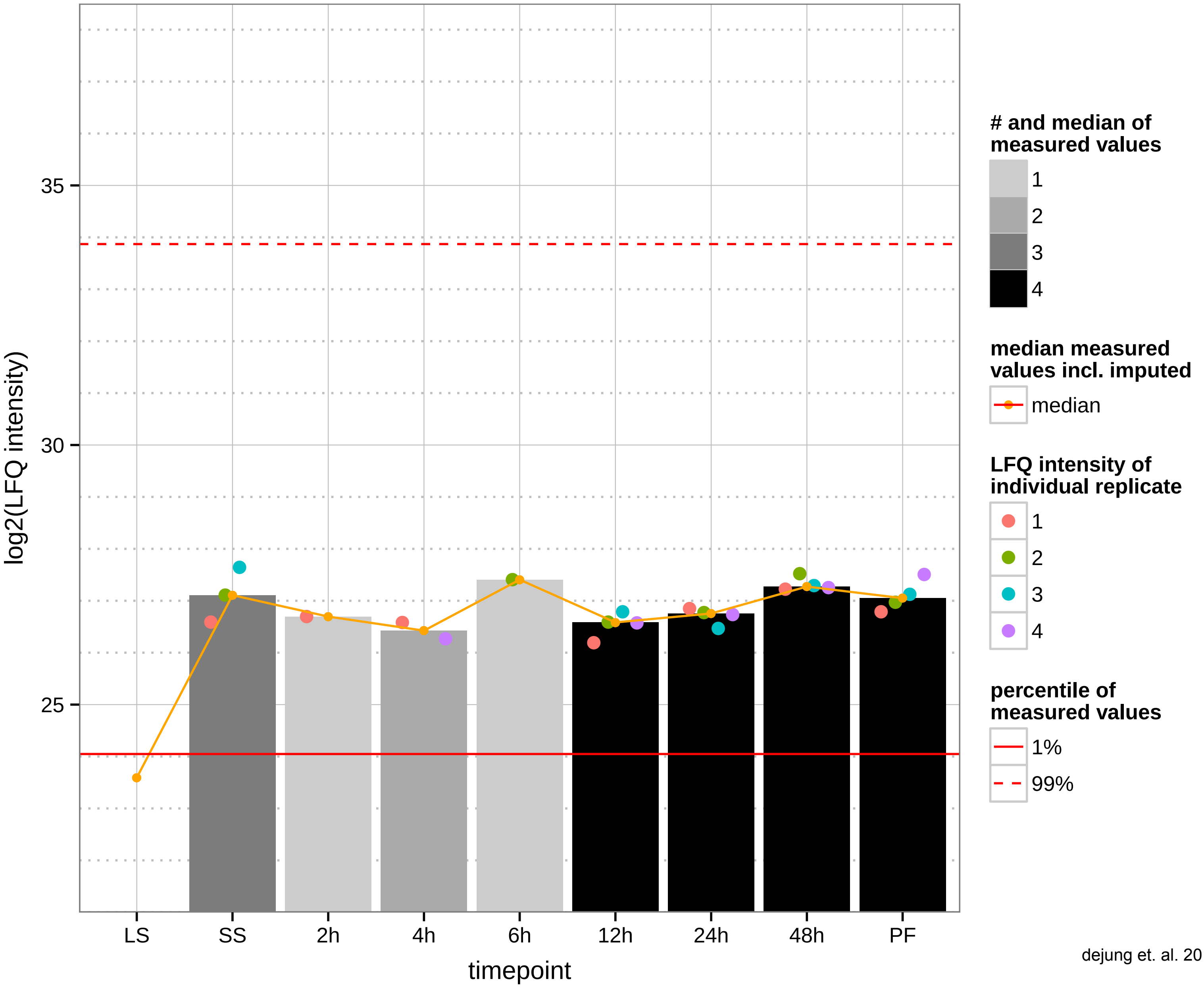




dejung et. al. 2015

structural maintenance of chromosome 3, putative (SMC3)
Tb927.5.3510
AGOF: ATP binding
AGOC: chromosome
AGOP: chromosome organization
PGOF: ATP binding, protein binding
PGOC: chromosome
PGOP: chromosome organization





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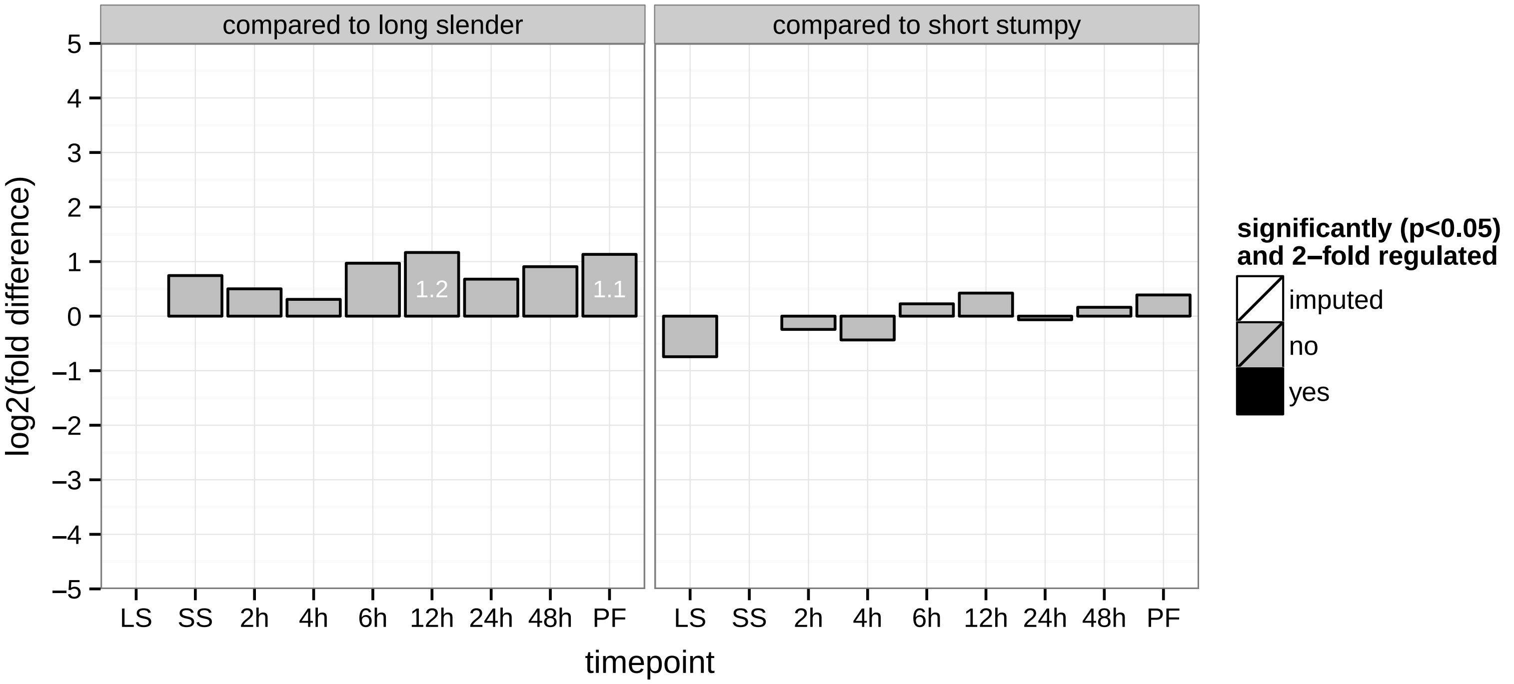
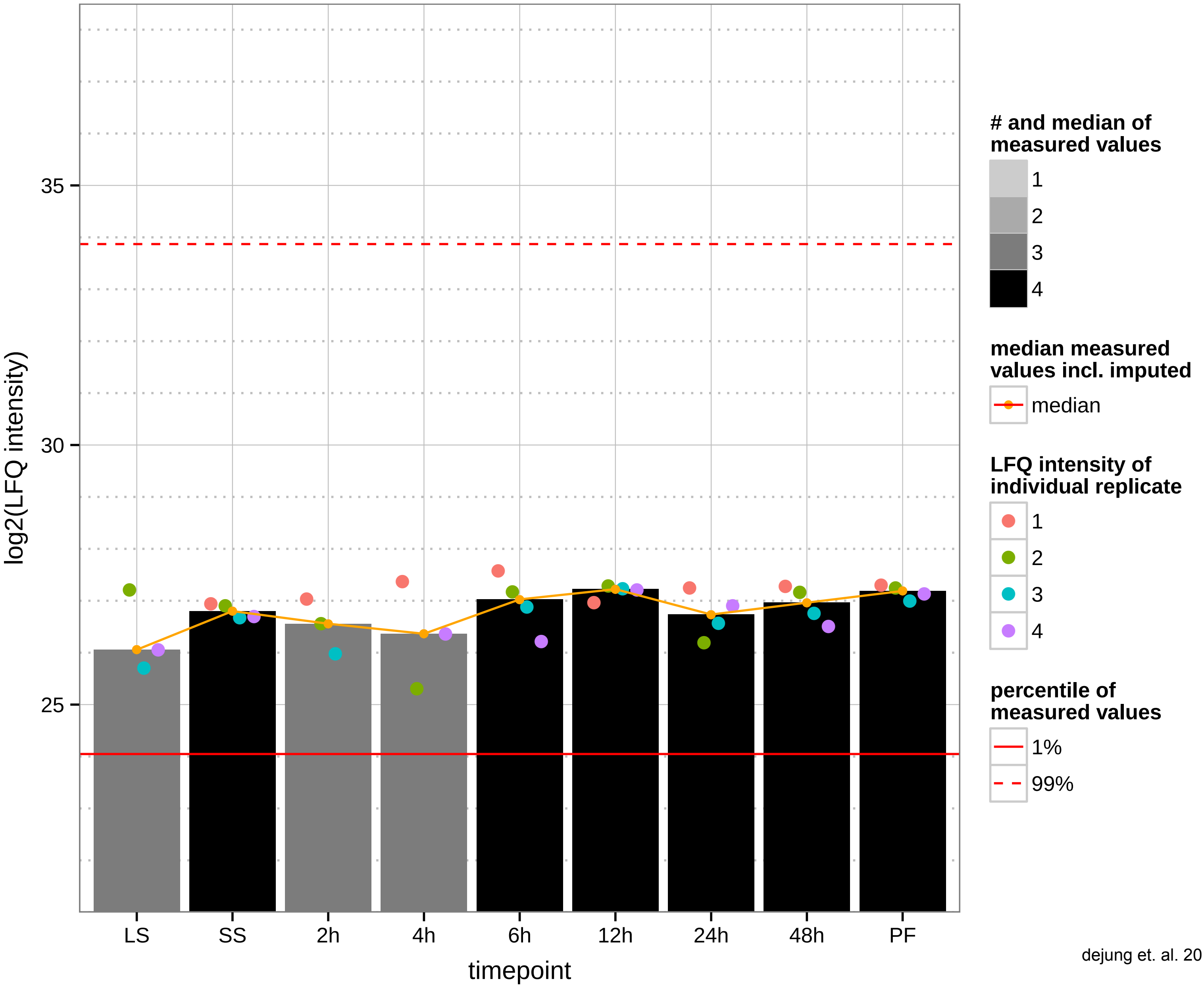
adaptor complex protein (AP) 3 delta subunit 1, putative
Tb927.5.3610
AGOF: protein transporter activity
AGOC: Golgi apparatus, membrane coat
AGOP: intracellular protein transport, vesicle–mediated transport
PGOF: binding, protein transporter activity
PGOC: Golgi apparatus, membrane coat
PGOP: intracellular protein transport, protein transport, vesicle–mediated transport





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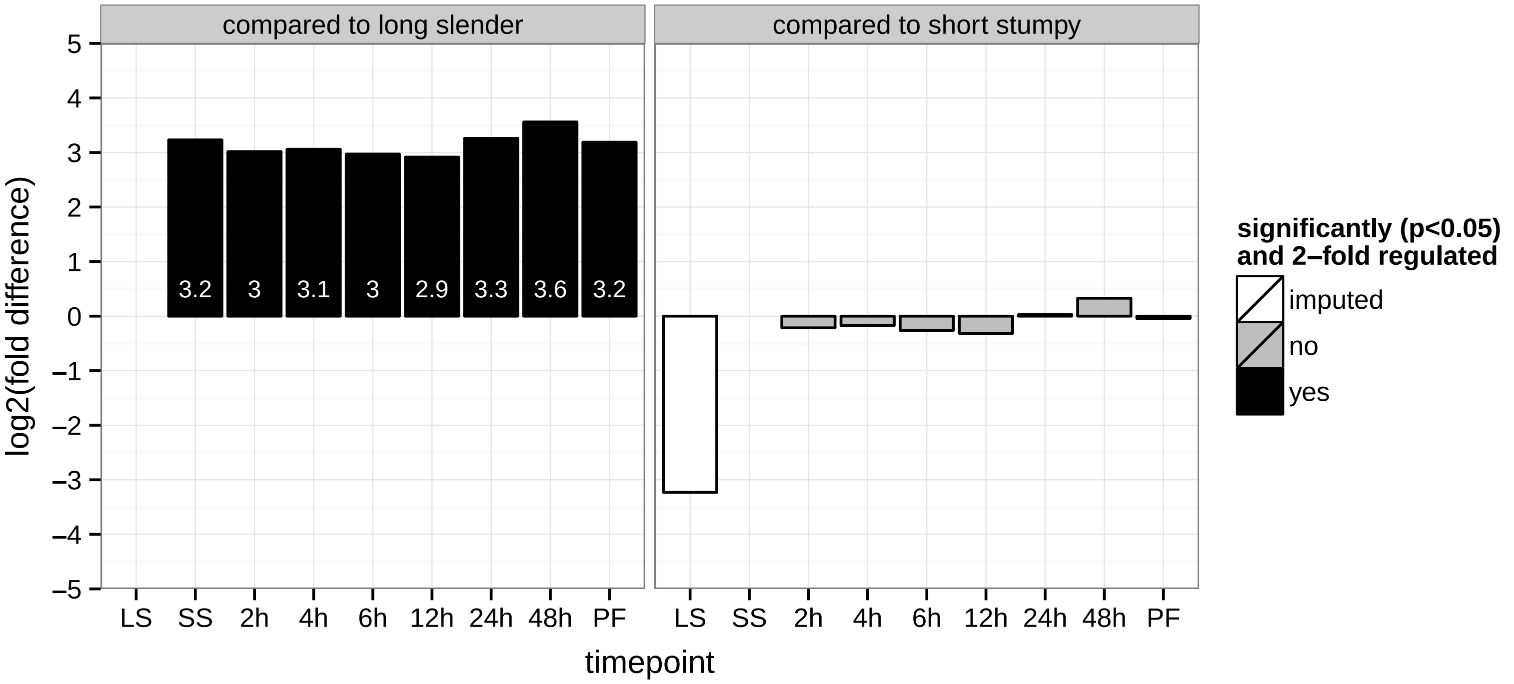
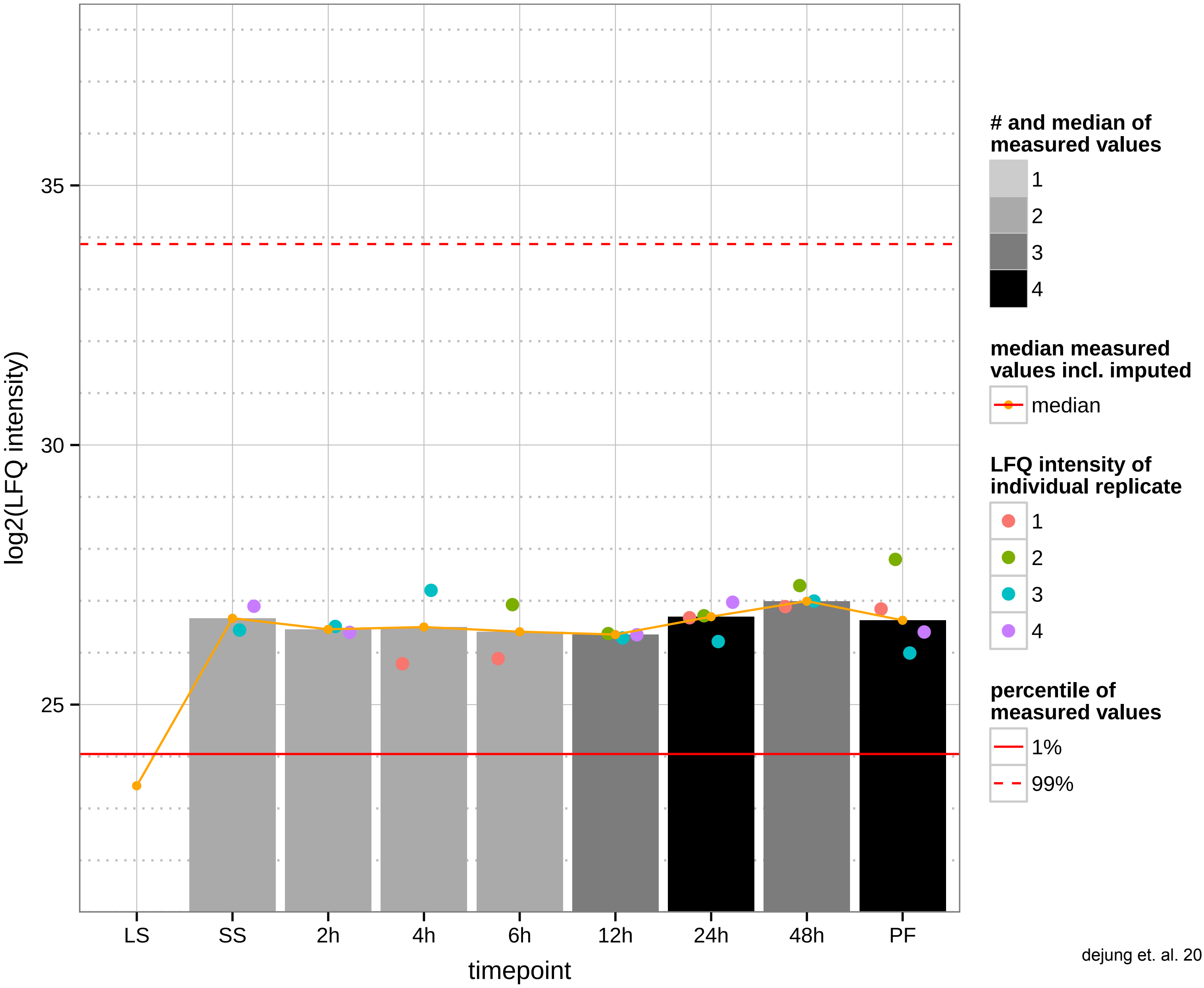
hypothetical protein, conserved
Tb927.5.3640
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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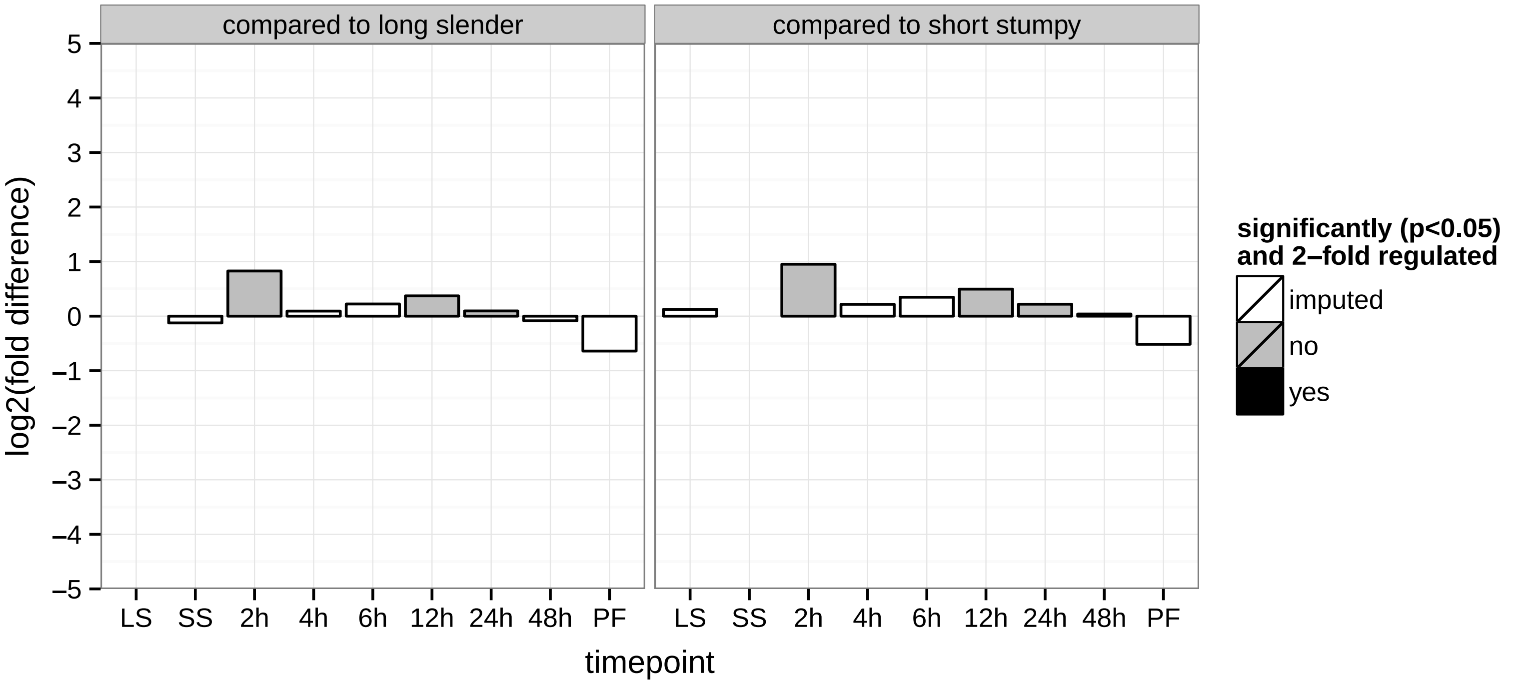
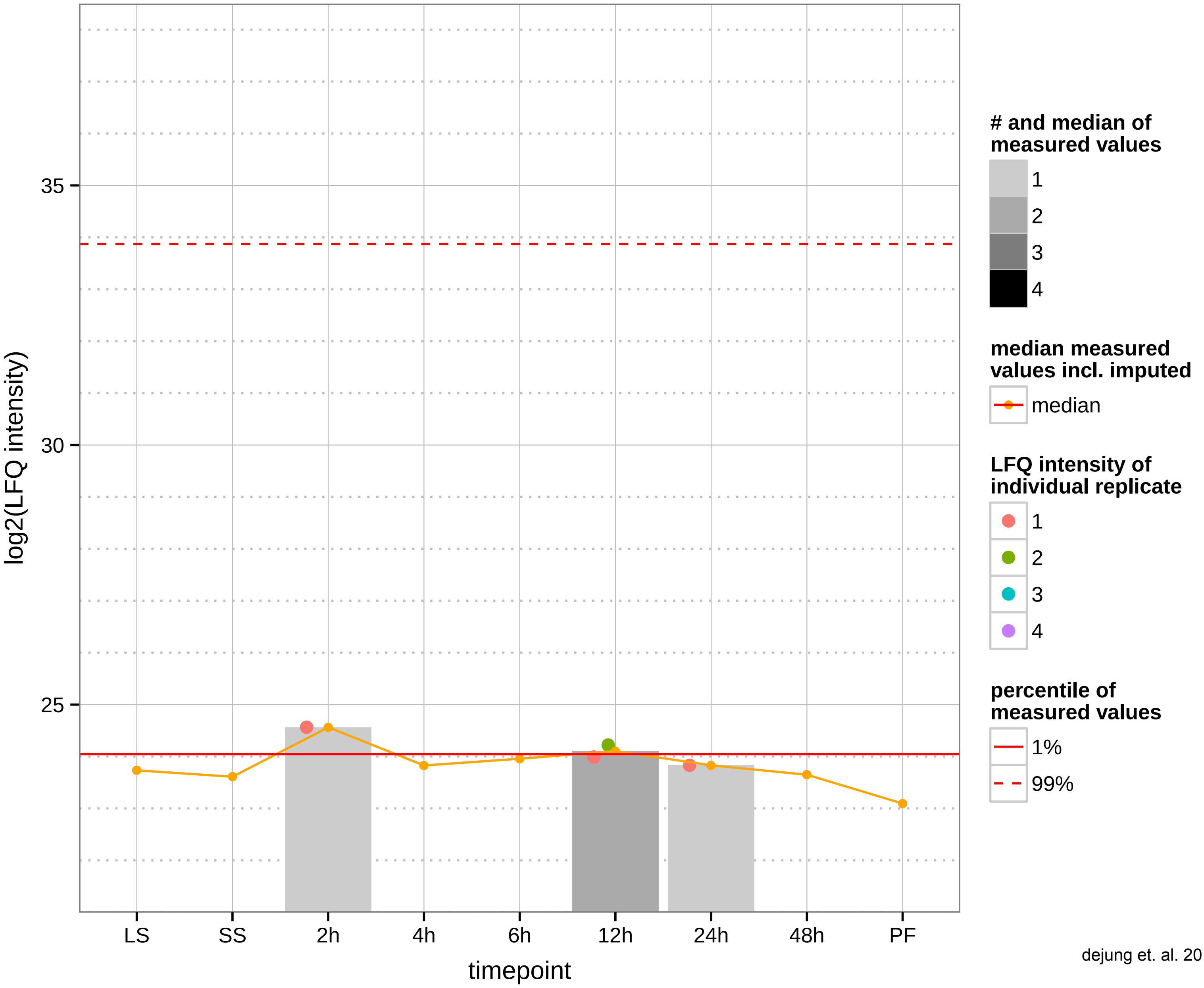
hypothetical protein, conserved
Tb927.5.3650
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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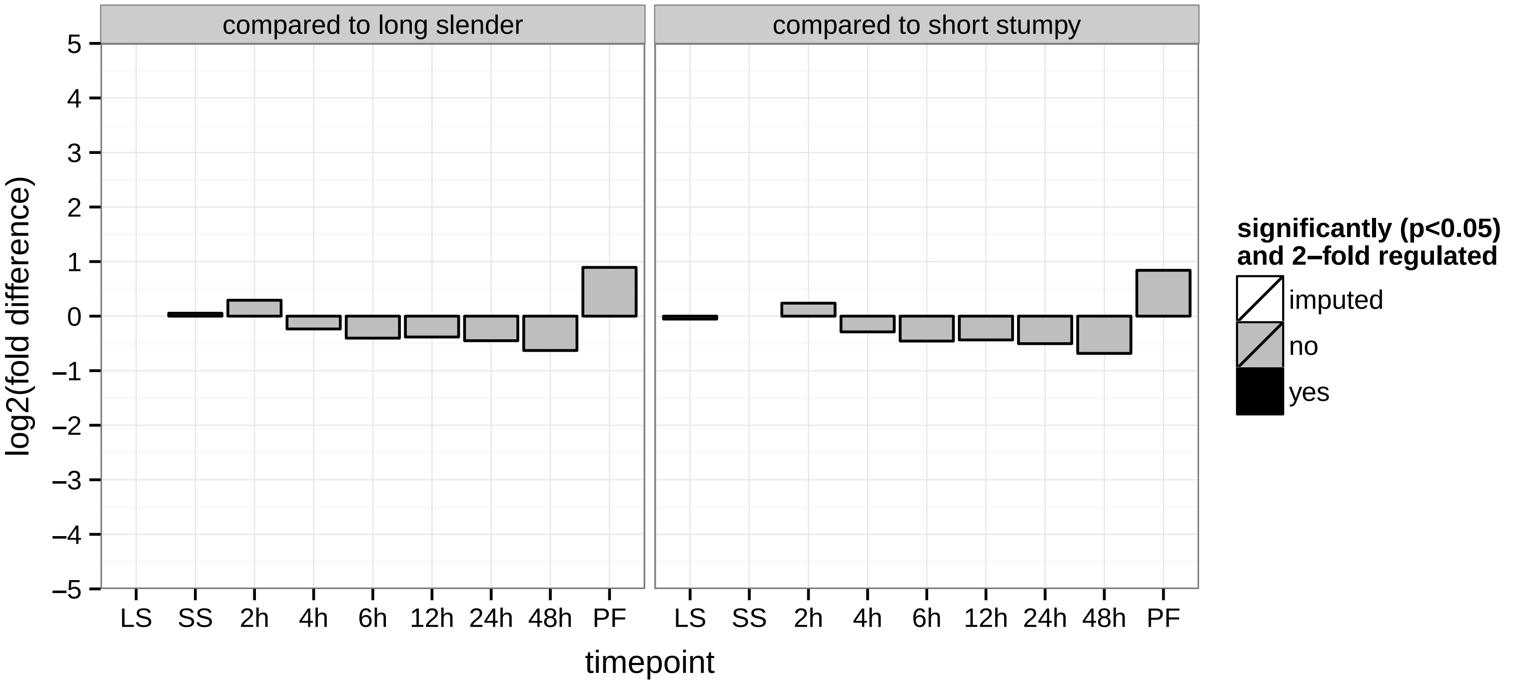
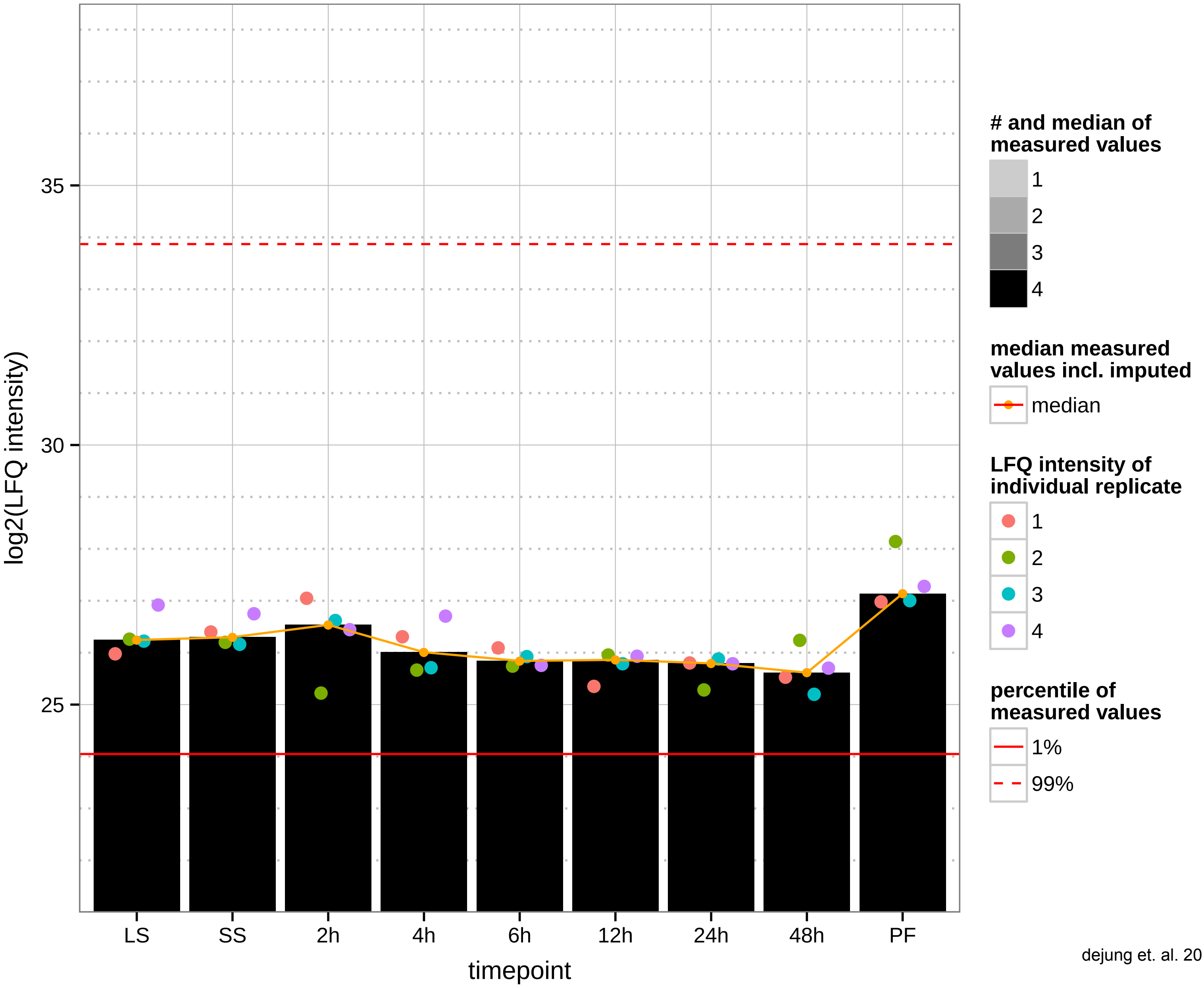
essential neutral sphingomyelinase (TbnSMase)
Tb927.5.3710
AGOF: sphingomyelin phosphodiesterase activity
AGOC: endoplasmic reticulum
AGOP: ceramide biosynthetic process, sphingomyelin catabolic process
PGOF: null
PGOC: null
PGOP: null





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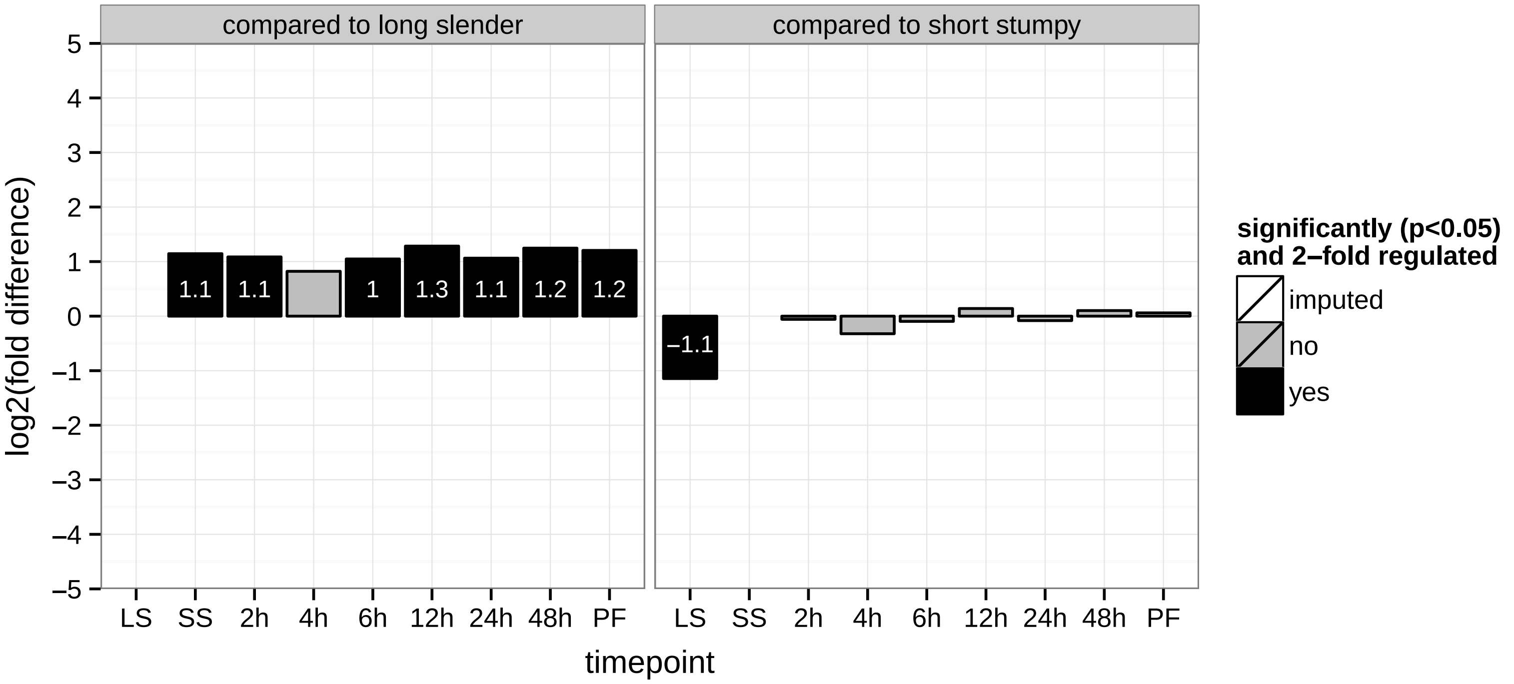
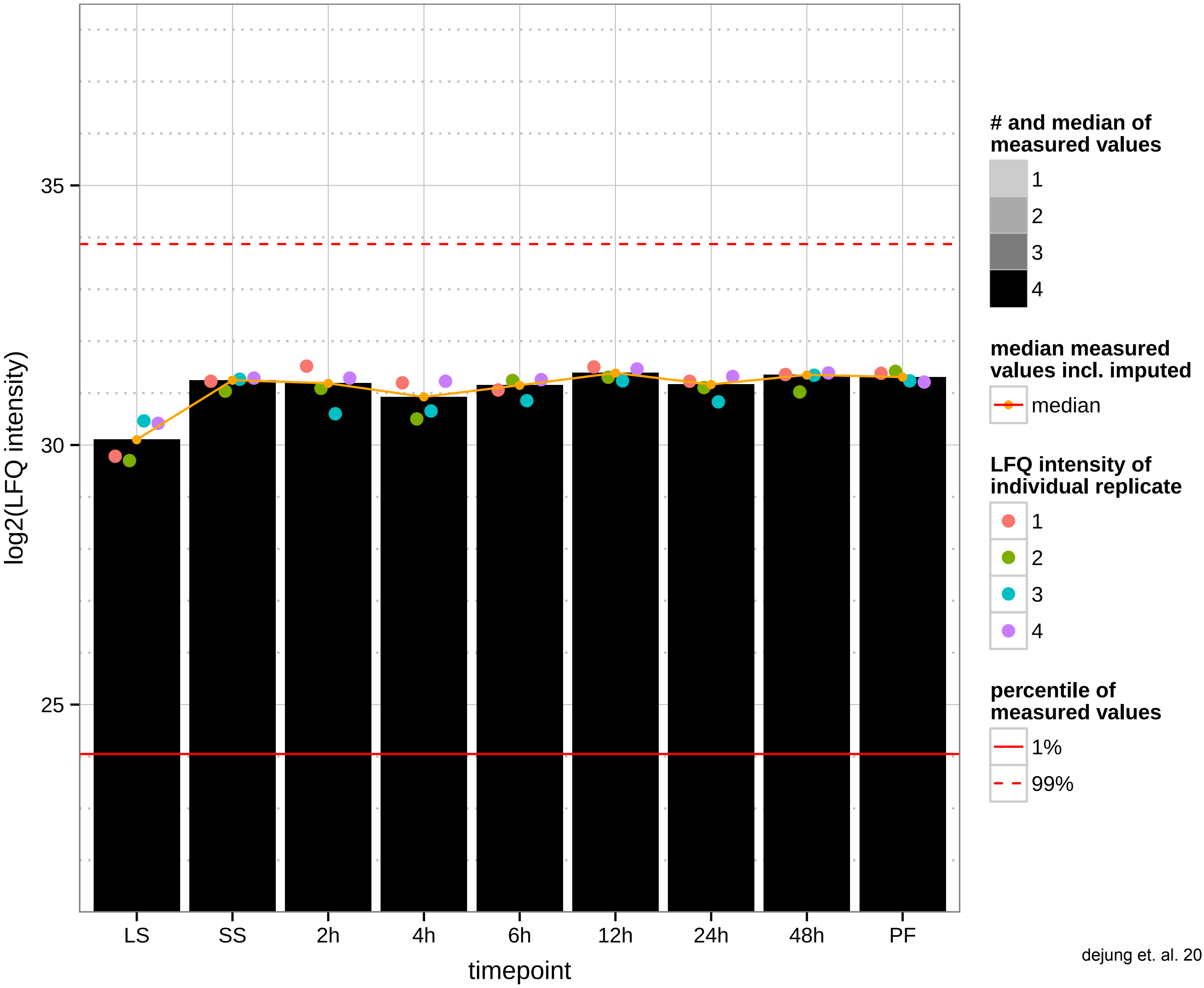
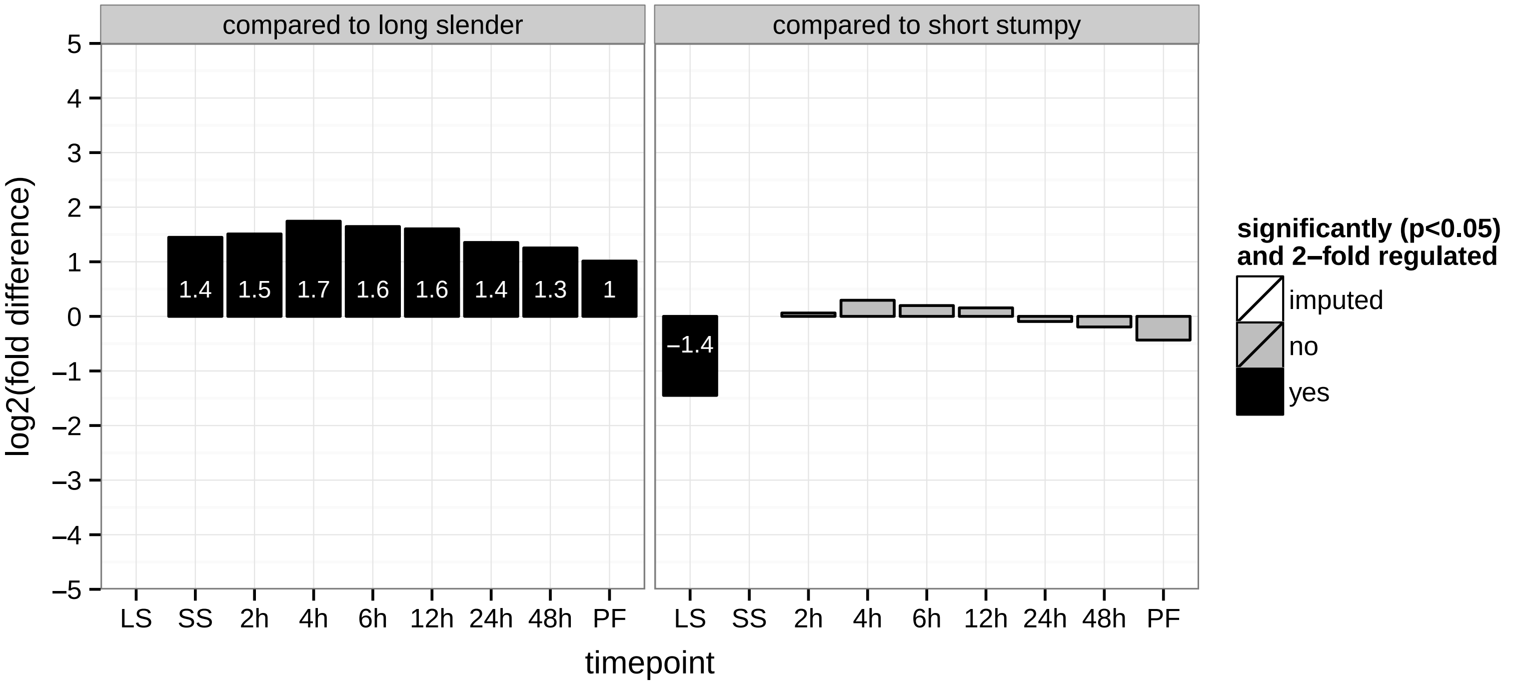
orotidine−5−phosphate decarboxylase/orotate phosphoribosyltransferase, putative, OMPDCase−OPRTase
Tb927.5.3810
AGOF: orotate phosphoribosyltransferase activity, orotidine−5'−phosphate decarboxylase activity
AGOC: glycosome
AGOP: 'de novo' pyrimidine nucleobase biosynthetic process, nucleoside metabolic process, pyrimidine ribonucleotide biosynt
PGOF: catalytic activity, orotate phosphoribosyltransferase activity, orotidine−5'−phosphate decarboxylase activity
PGOC: null
PGOP: 'de novo' pyrimidine nucleobase biosynthetic process, metabolic process, nucleoside metabolic process, pyrimidine nu

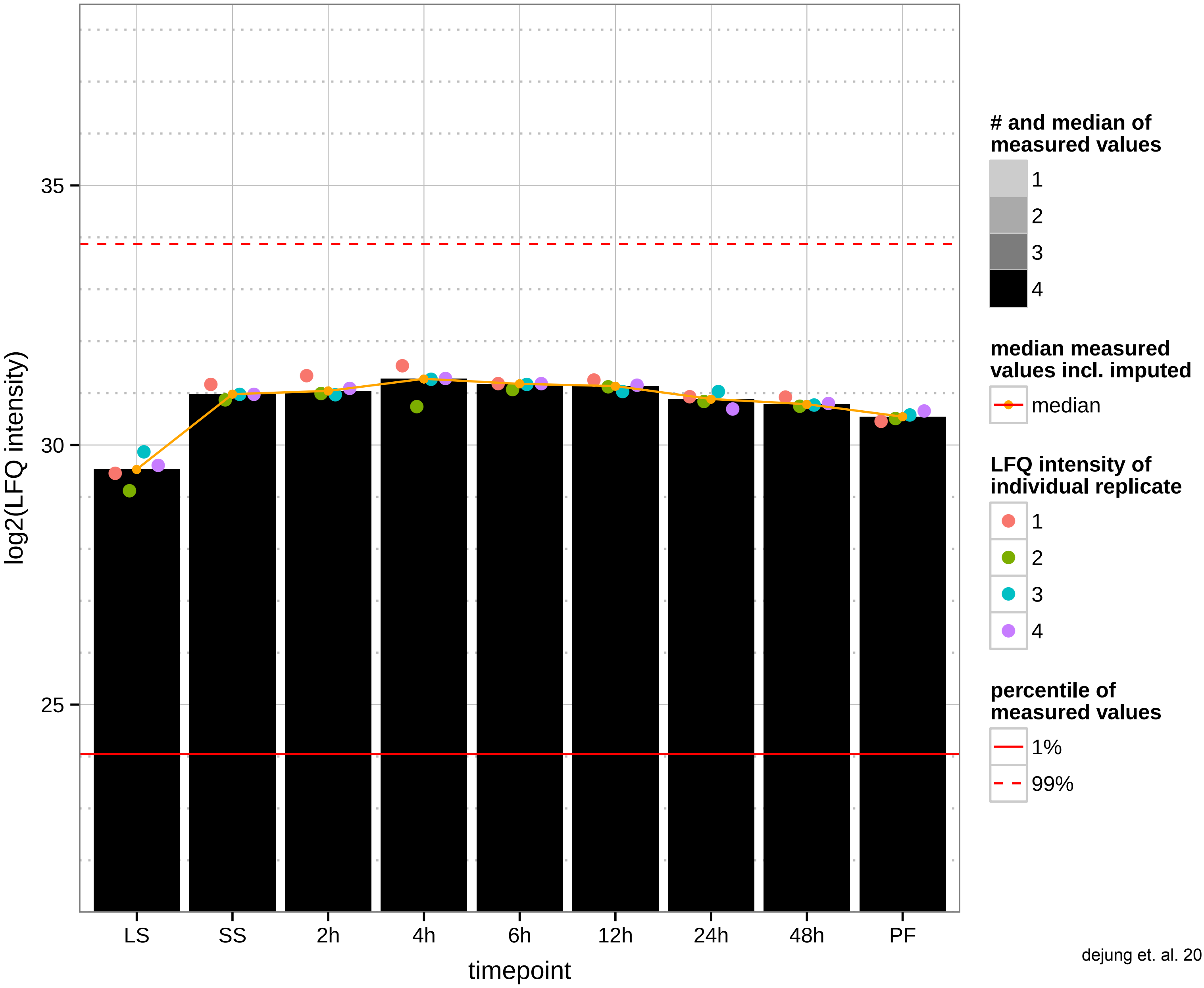




dejung et. al. 2015

aspartate carbamoyltransferase, putative
Tb927.5.3820
AGOF: amino acid binding, aspartate carbamoyltransferase activity
AGOC: null
AGOP: 'de novo' pyrimidine nucleobase biosynthetic process, cellular amino acid metabolic process
PGOF: amino acid binding, aspartate carbamoyltransferase activity, carboxyl– or carbamoyltransferase activity
PGOC: null
PGOP: 'de novo' pyrimidine nucleobase biosynthetic process, cellular amino acid metabolic process





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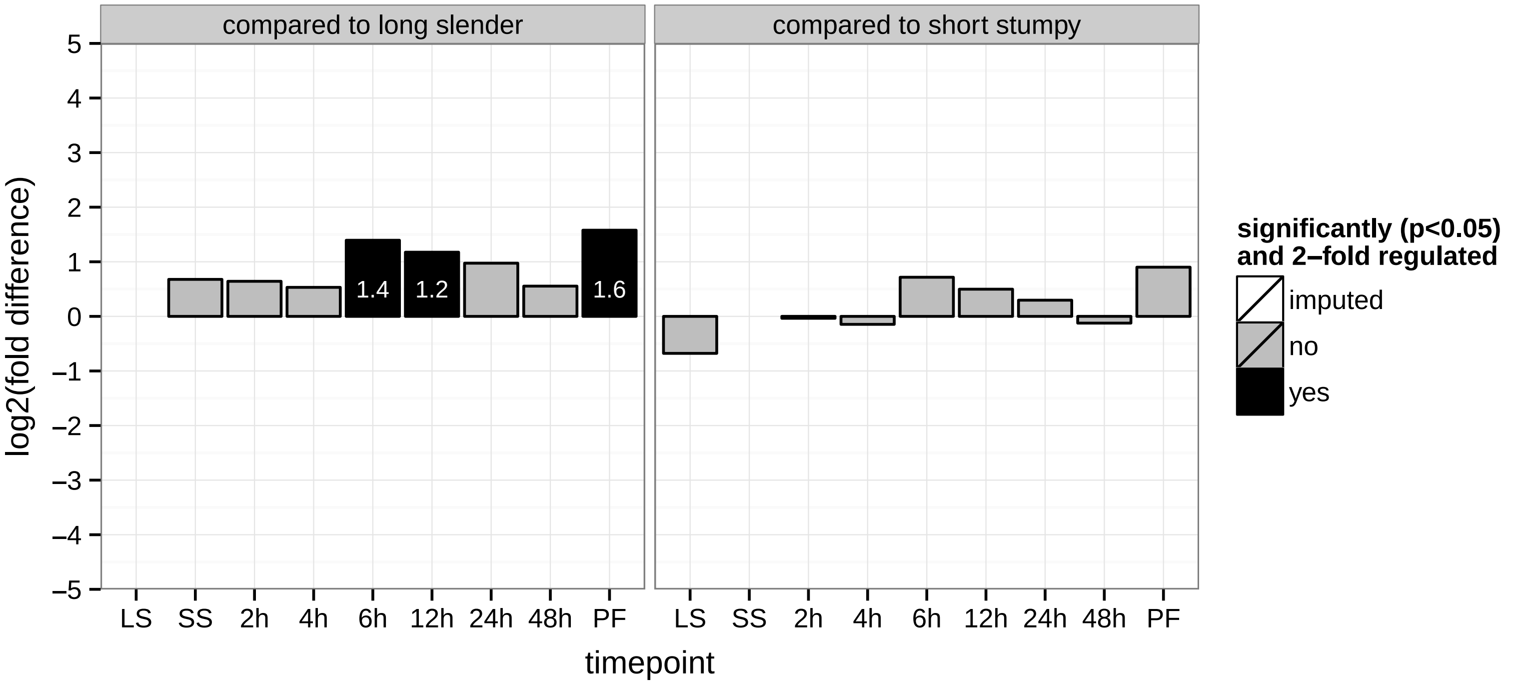
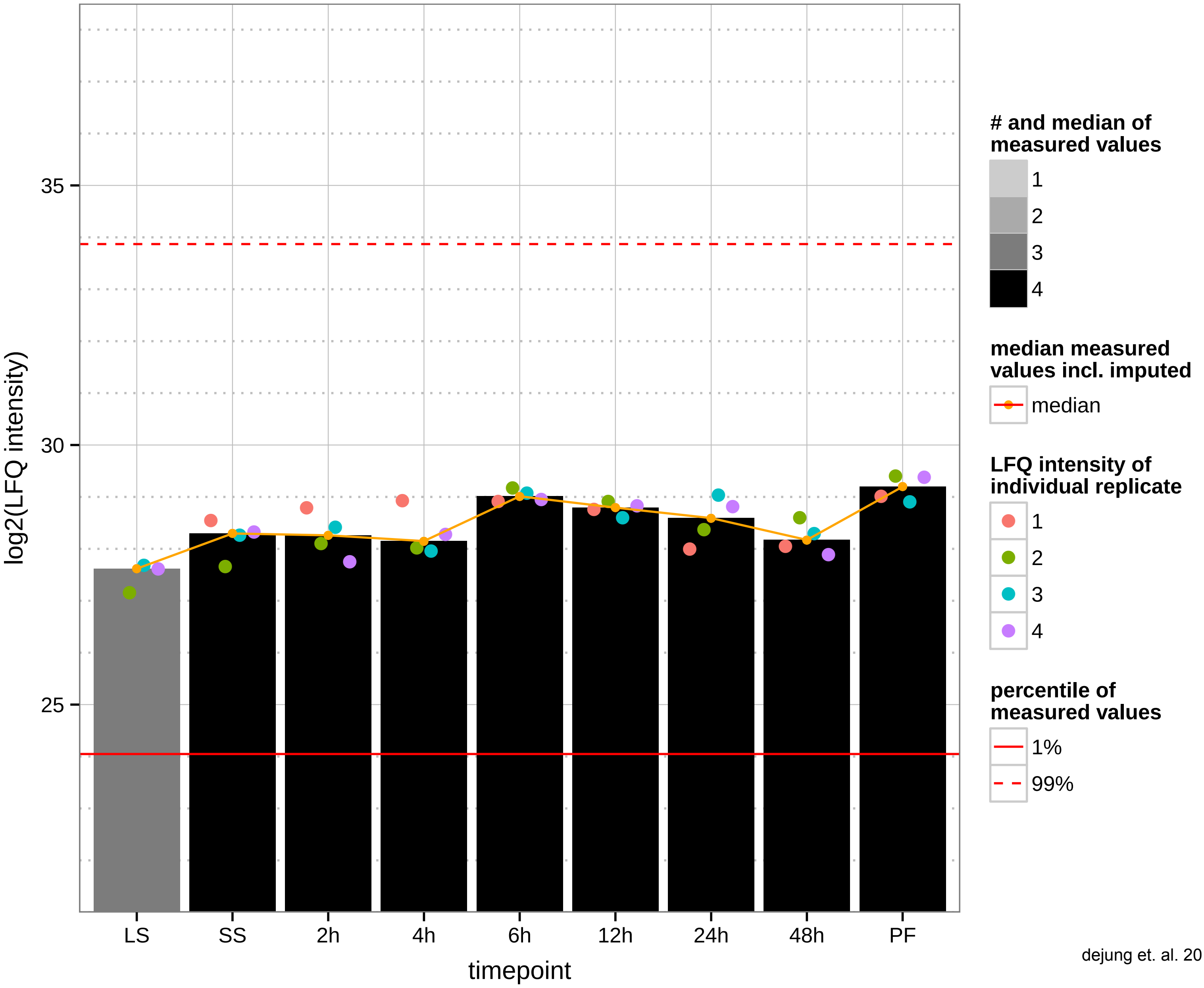
dihydroorotate oxidase
Tb927.5.3830
AGOF: FMN binding, dihydroorotate dehydrogenase activity, dihydroorotate oxidase activity
AGOC: cytoplasm, glycosome
AGOP: 'de novo' pyrimidine nucleobase biosynthetic process, UMP biosynthetic process, fumarate metabolic process
PGOF: dihydroorotate dehydrogenase activity, dihydroorotate oxidase activity
PGOC: cytoplasm
PGOP: UMP biosynthetic process, oxidation–reduction process





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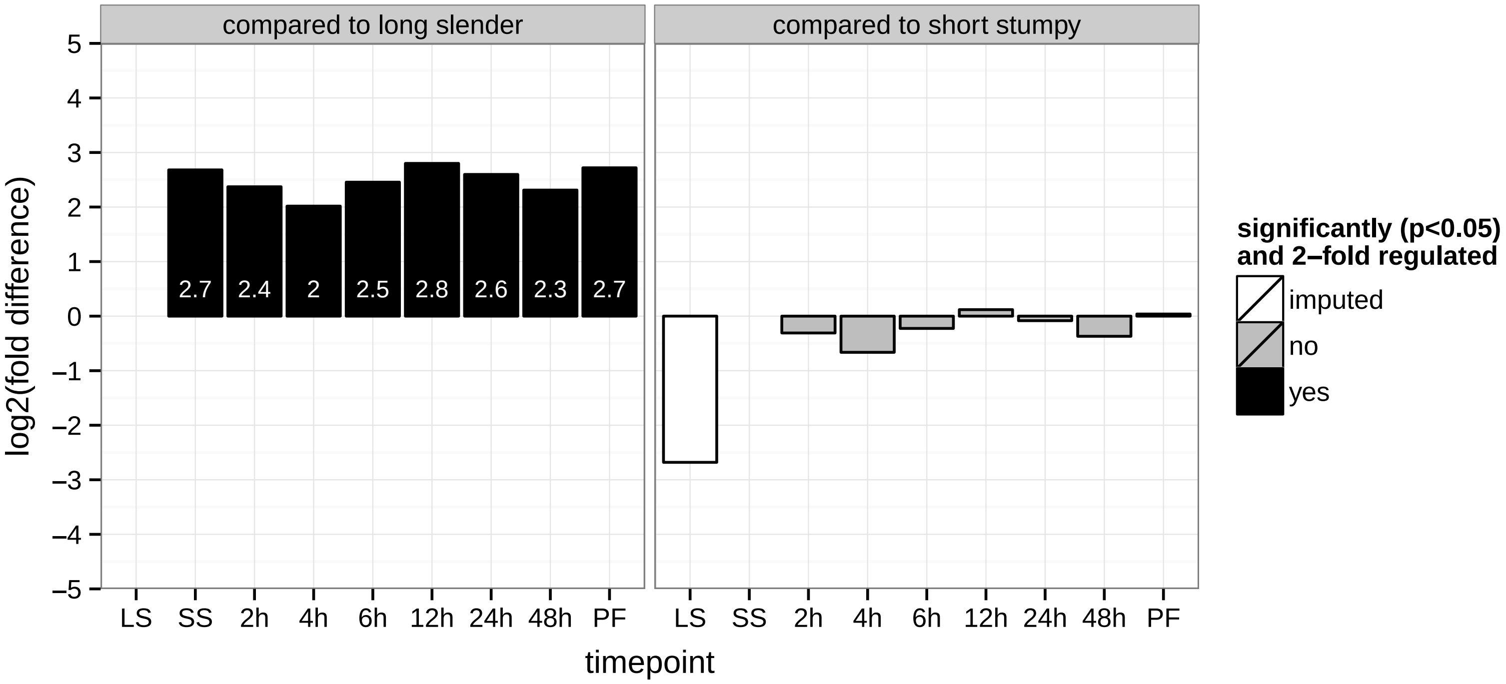
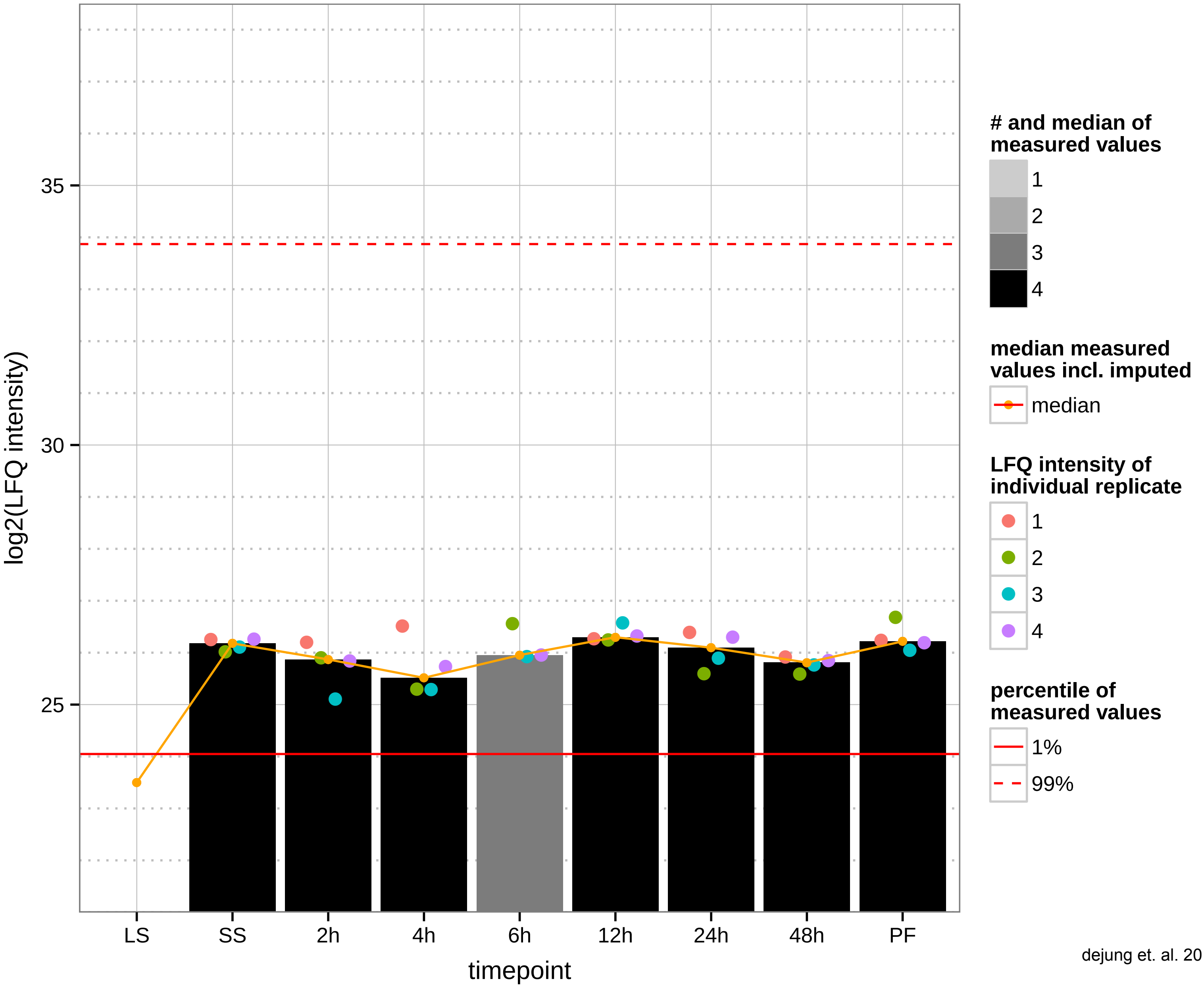
hypothetical protein, conserved
Tb927.5.3850
AGOF: null
AGOC: null
AGOP: null
PGOF: exonuclease activity, nucleic acid binding
PGOC: intracellular
PGOP: null





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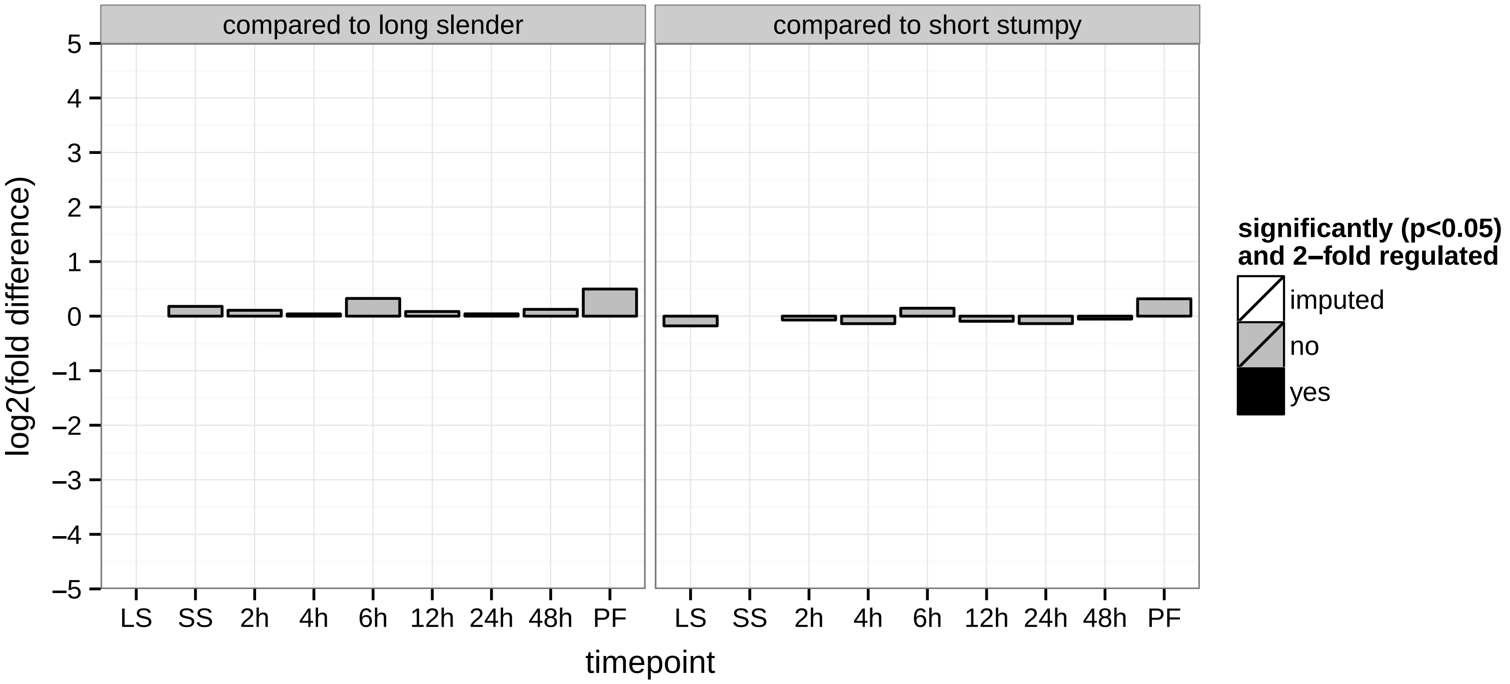
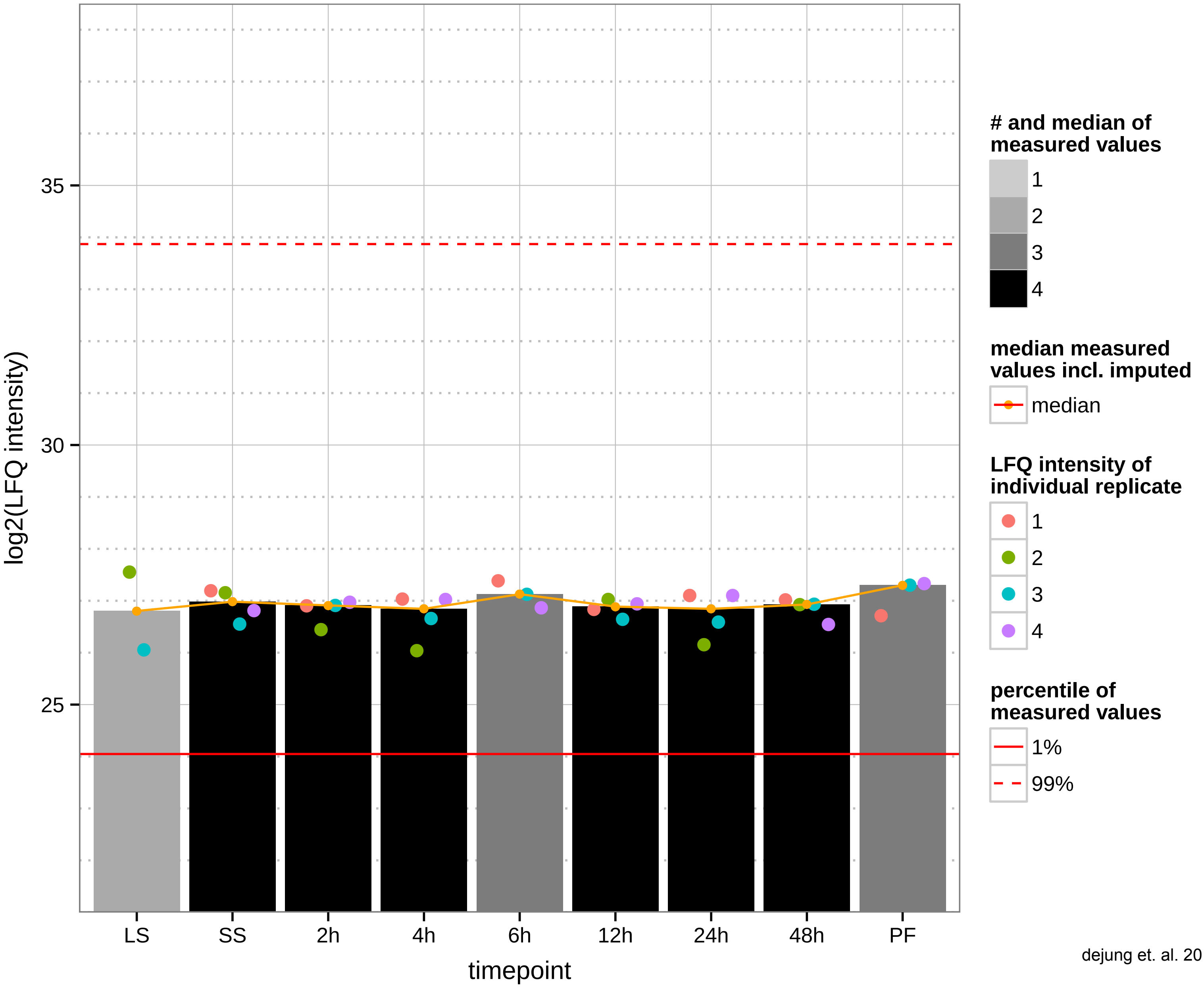
hypothetical protein, conserved
Tb927.5.3900
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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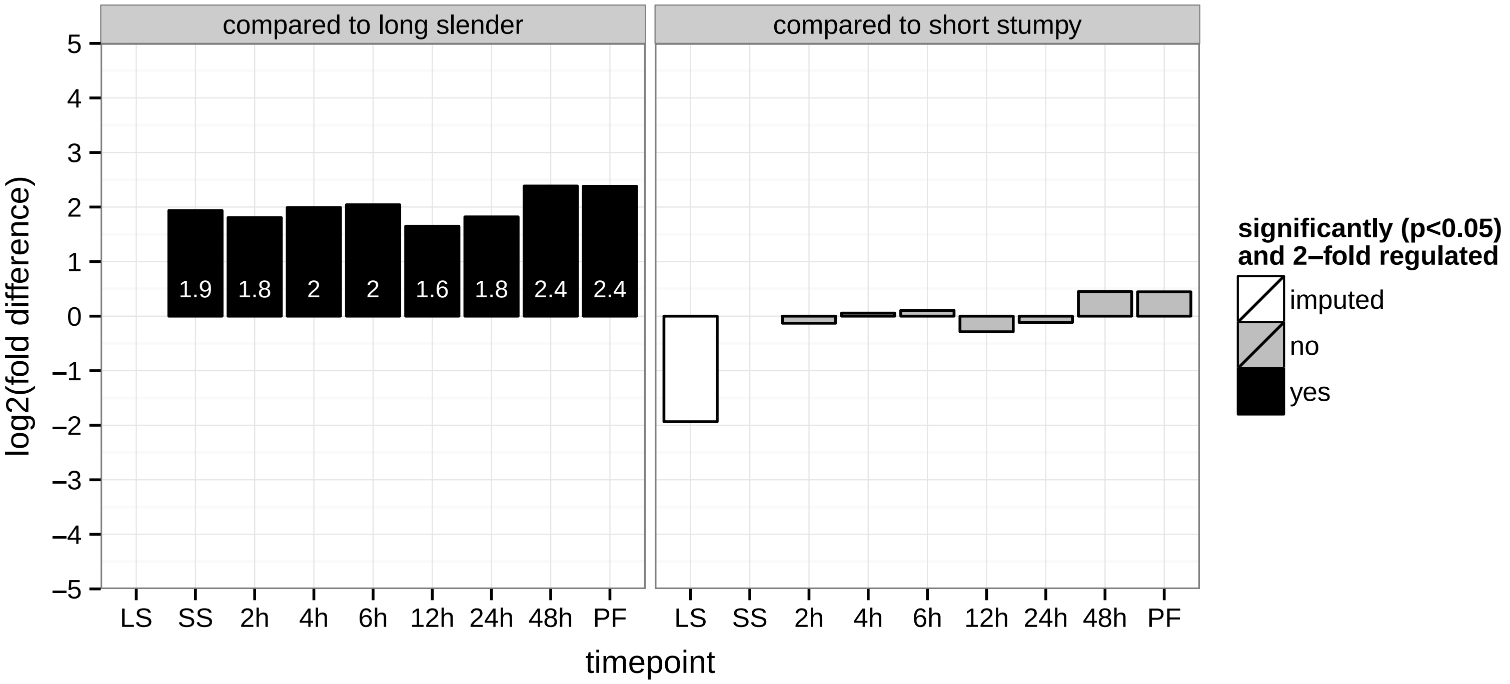
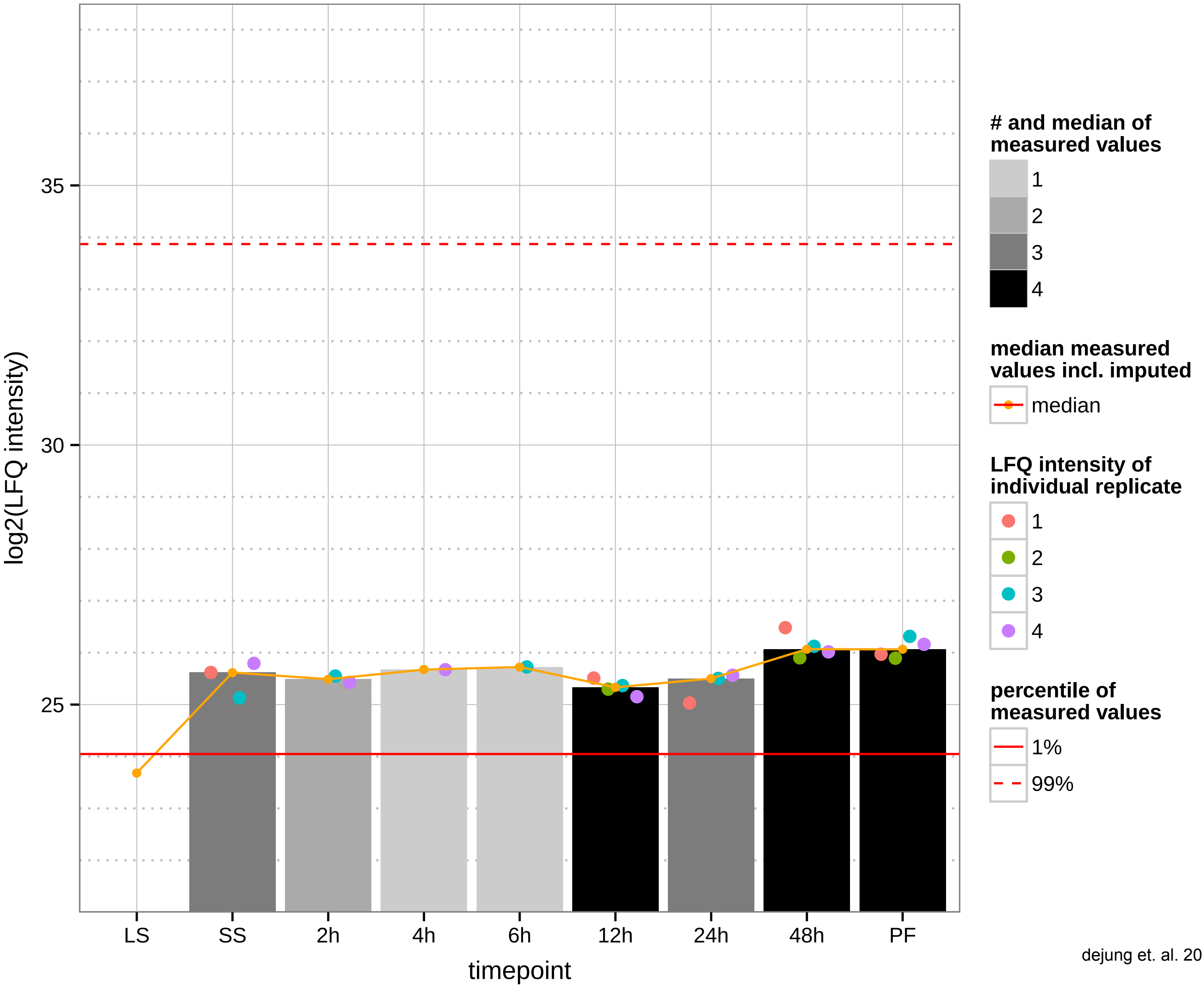
peroxisome assembly protein, putative
Tb927.5.3920
AGOF: ATP binding, ATPase activity
AGOC: null
AGOP: peroxisome organization
PGOF: ATP binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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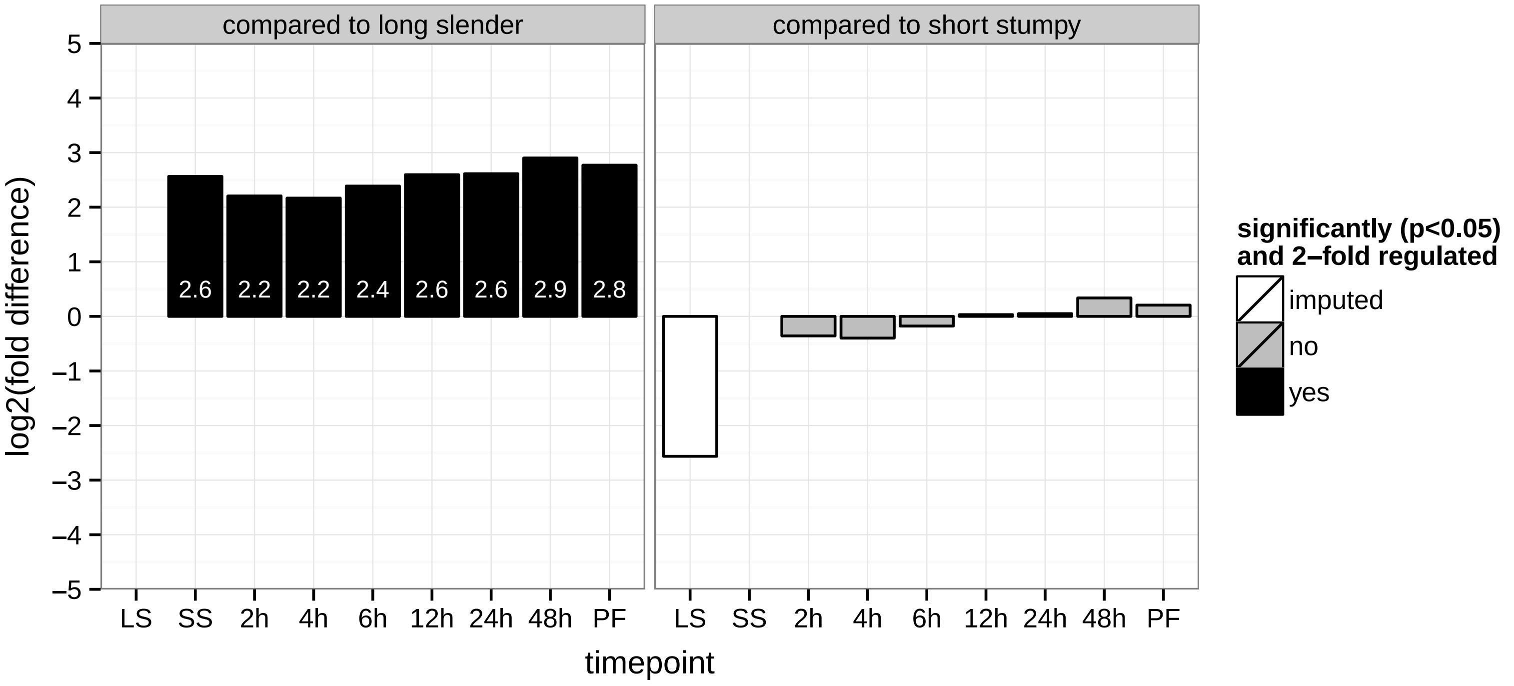
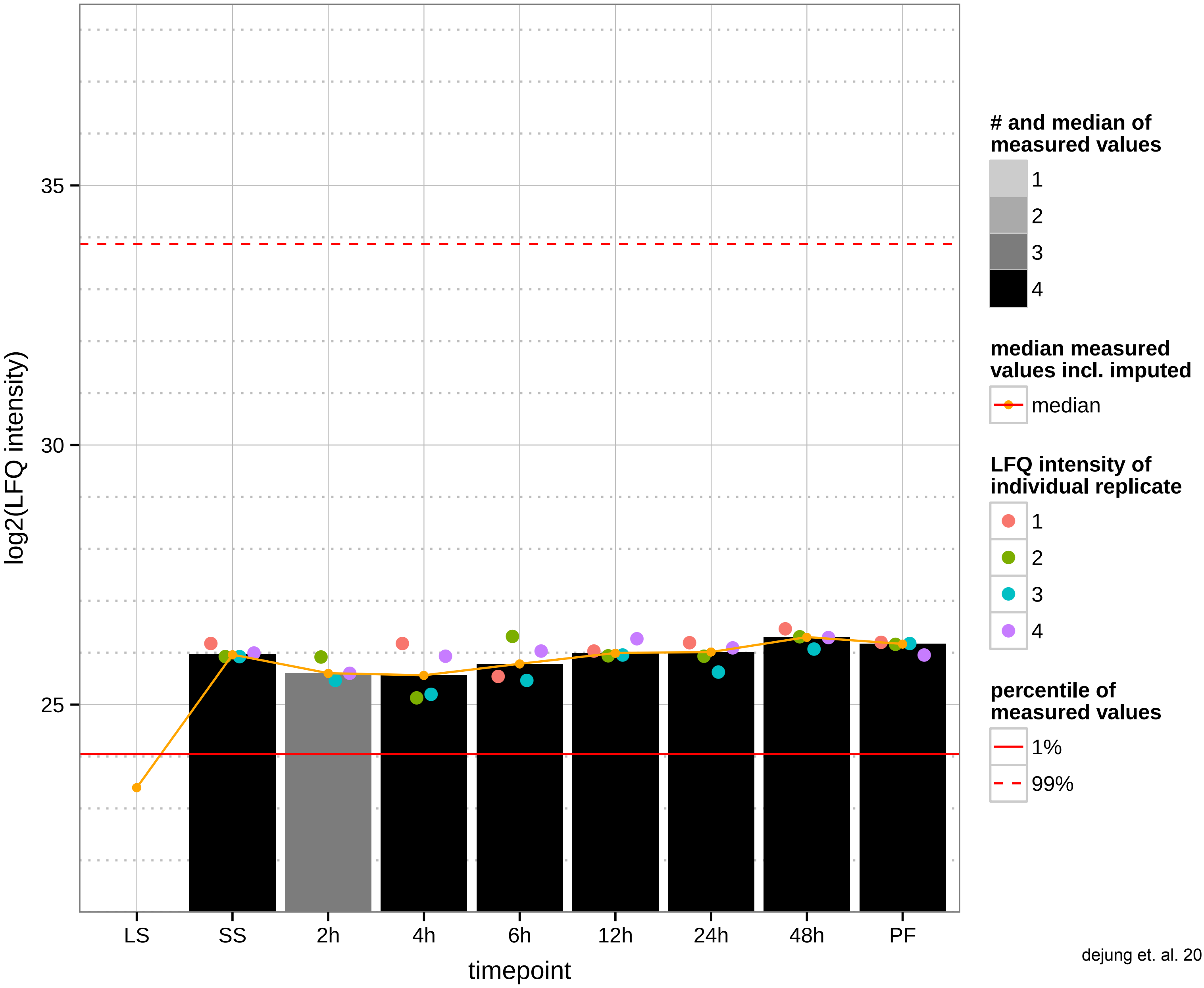
helicase, putative
Tb927.5.3940
AGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: null
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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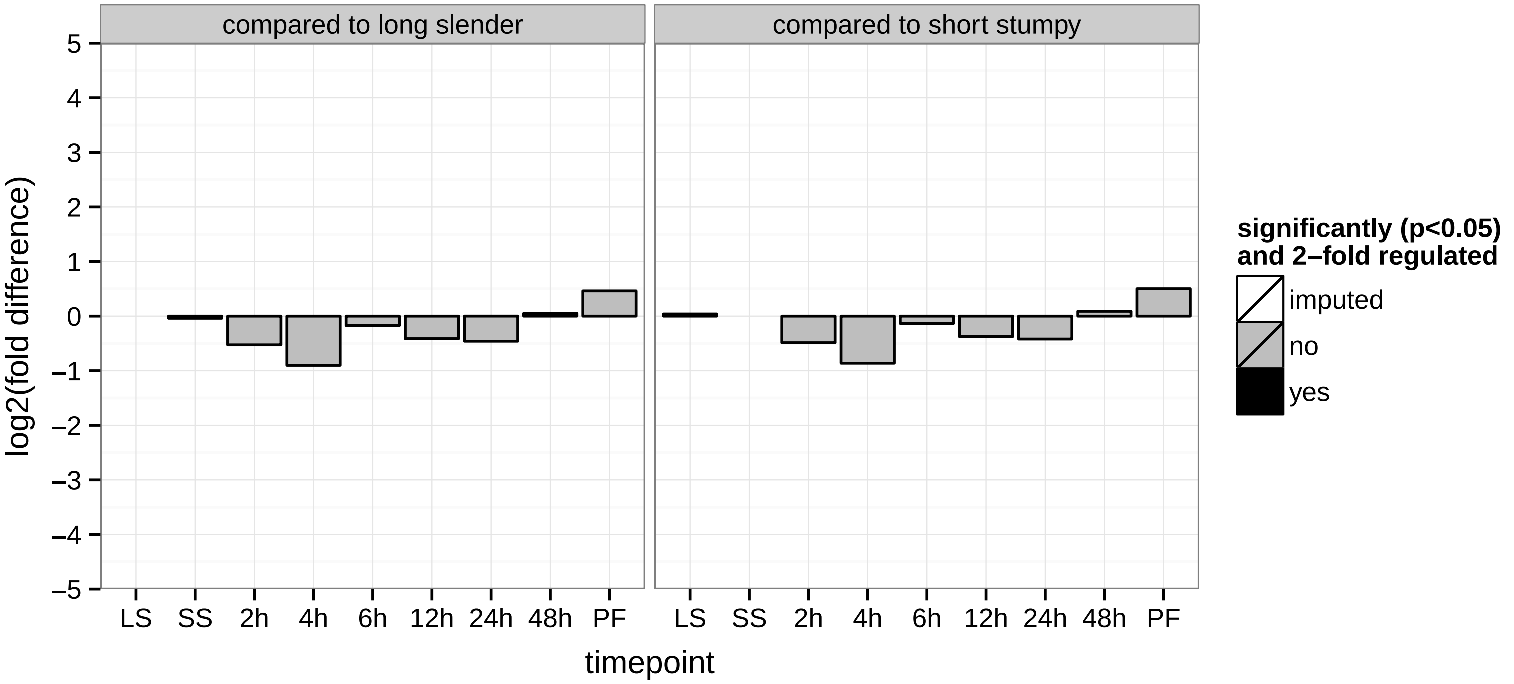
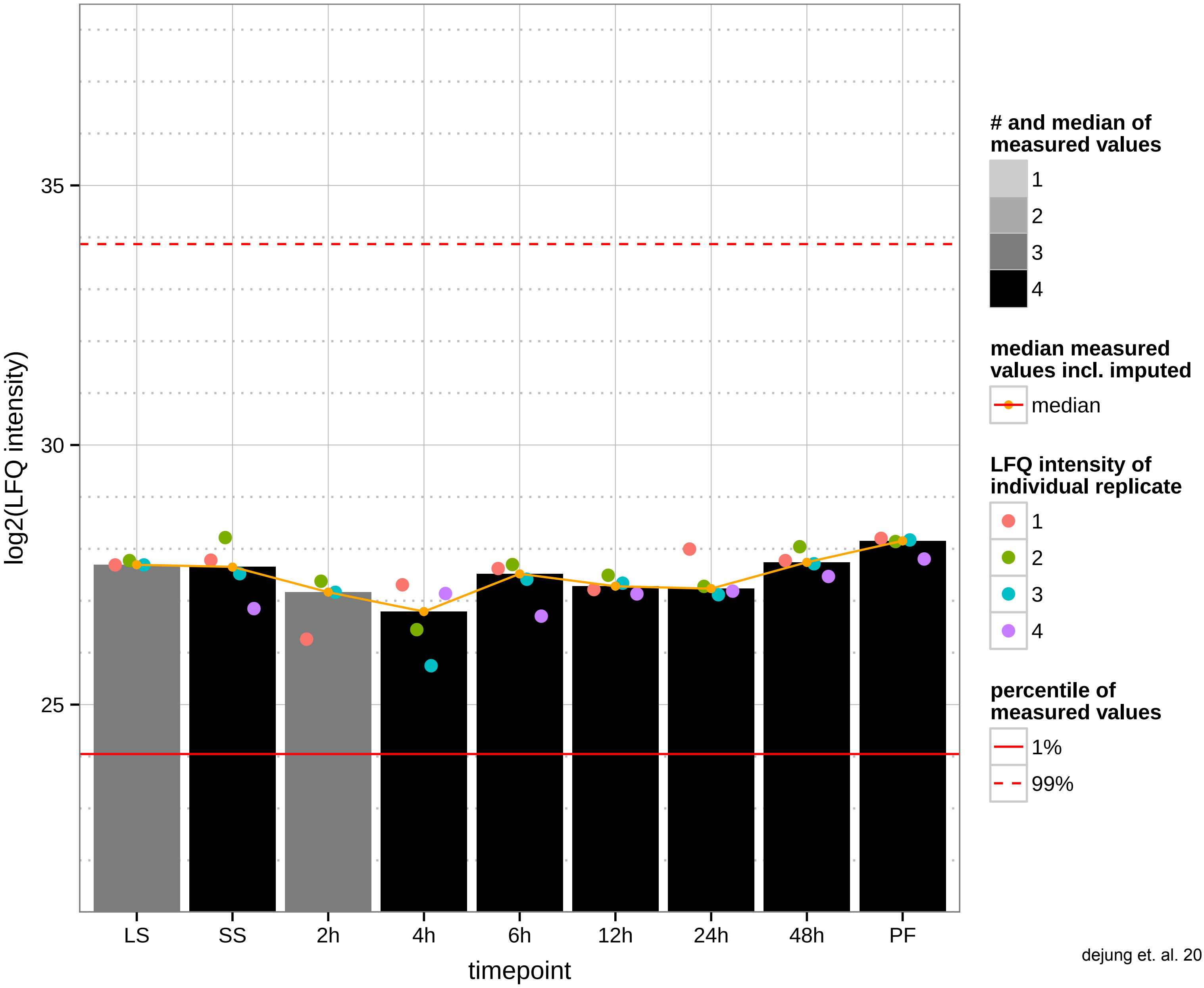
adenylate kinase, putative (ADKE)
Tb927.5.3970
AGOF: ATP binding, adenylate kinase activity
AGOC: axoneme
AGOP: nucleobase–containing compound metabolic process, nucleobase–containing small molecule interconversion
PGOF: ATP binding, cAMP–dependent protein kinase regulator activity, nucleobase–containing compound kinase activity
PGOC: null
PGOP: nucleobase–containing compound metabolic process, signal transduction





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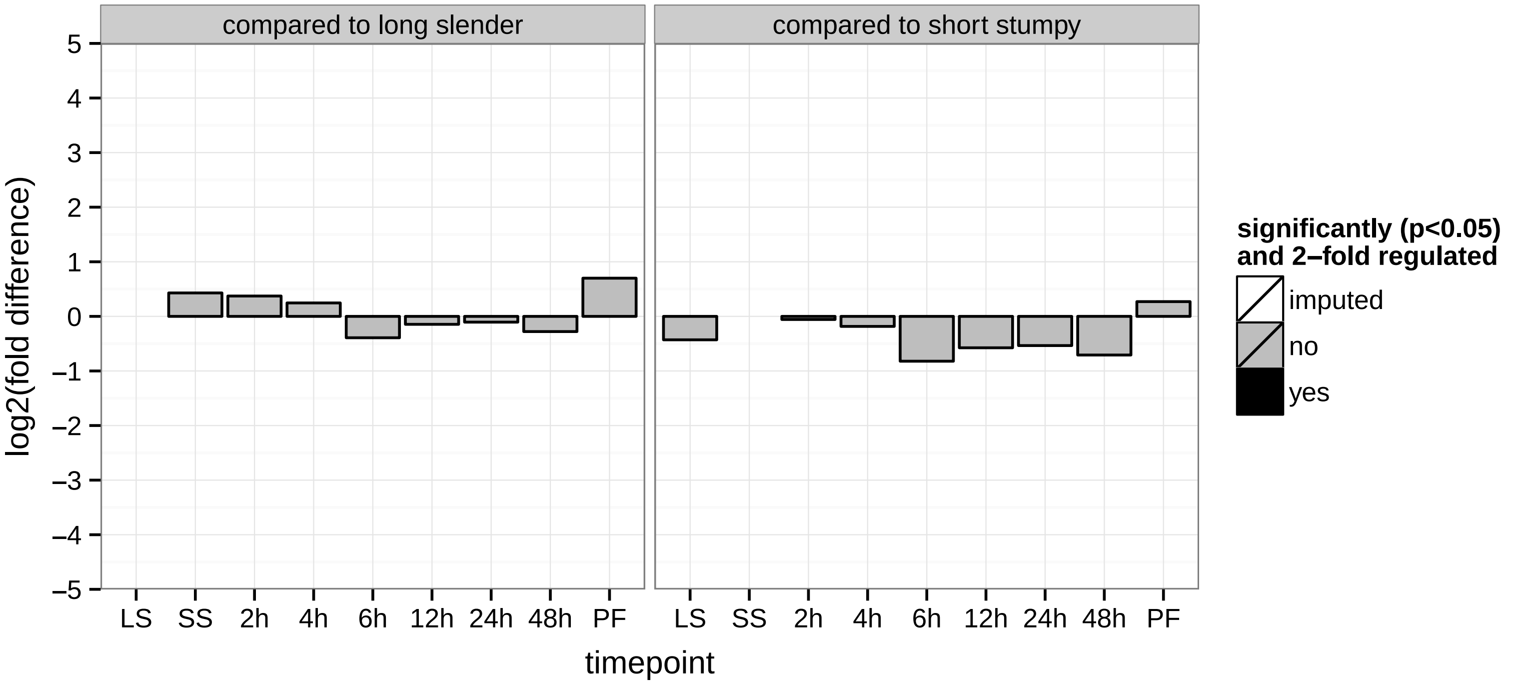
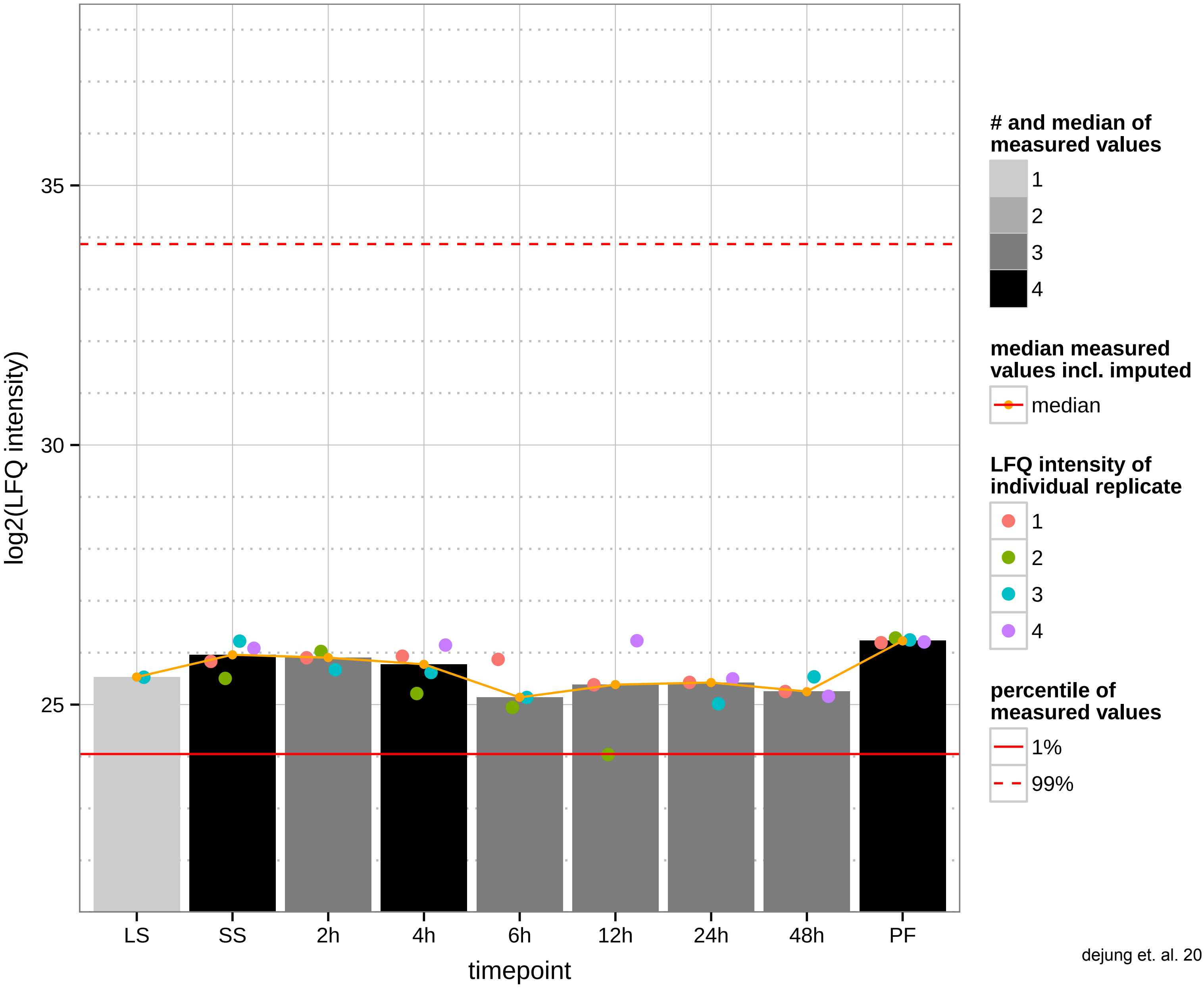
hypothetical protein, conserved
Tb927.5.4100
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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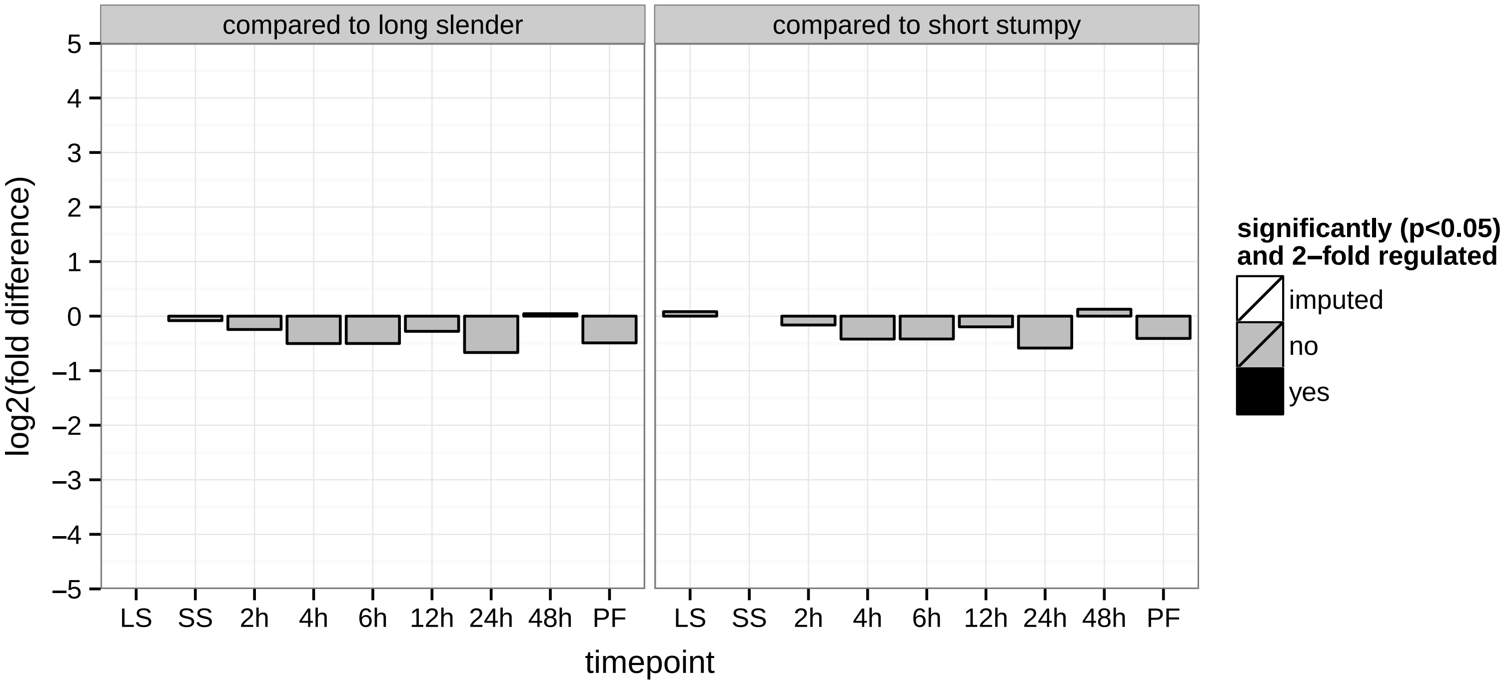
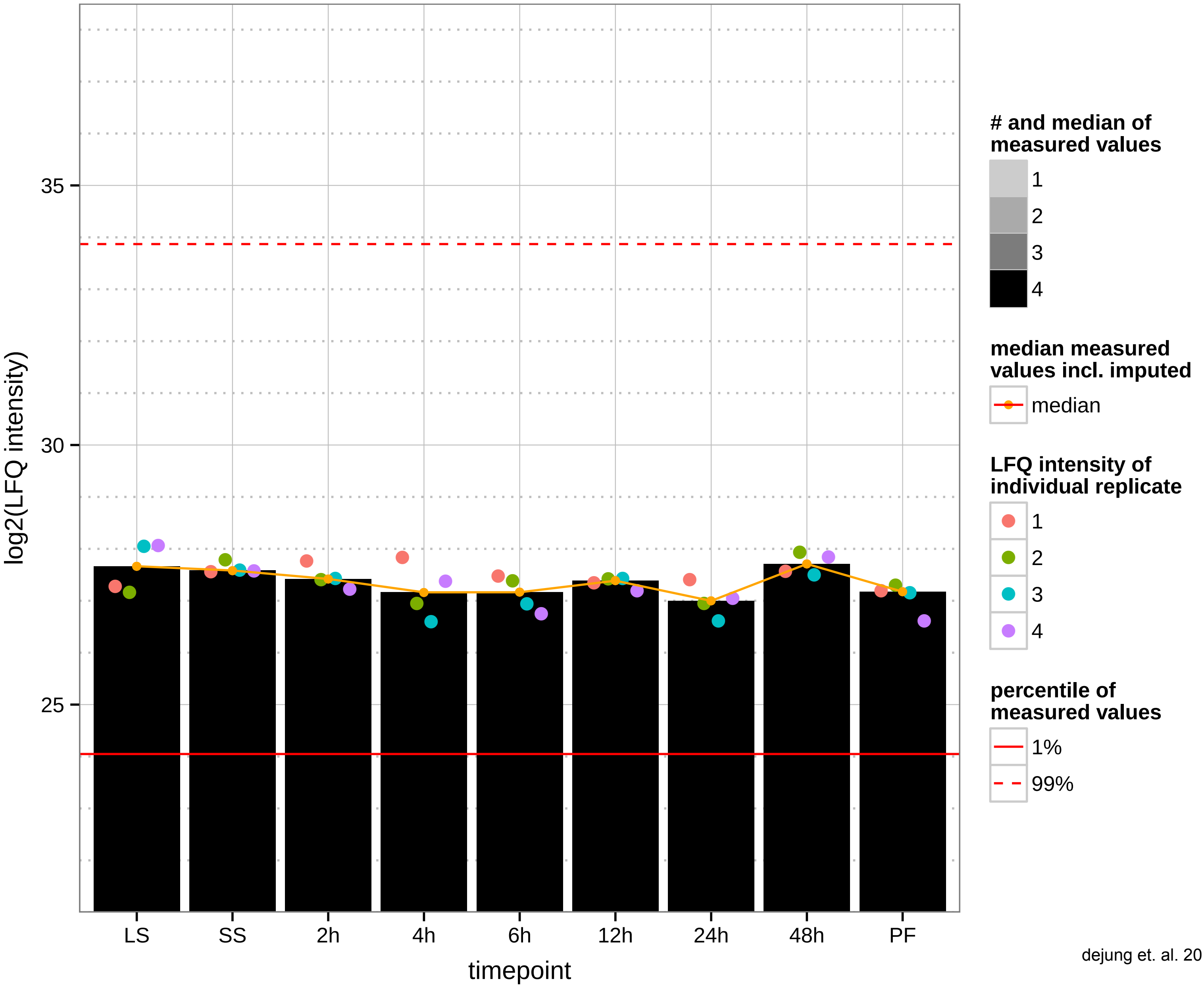
hypothetical protein, conserved
Tb927.5.4150
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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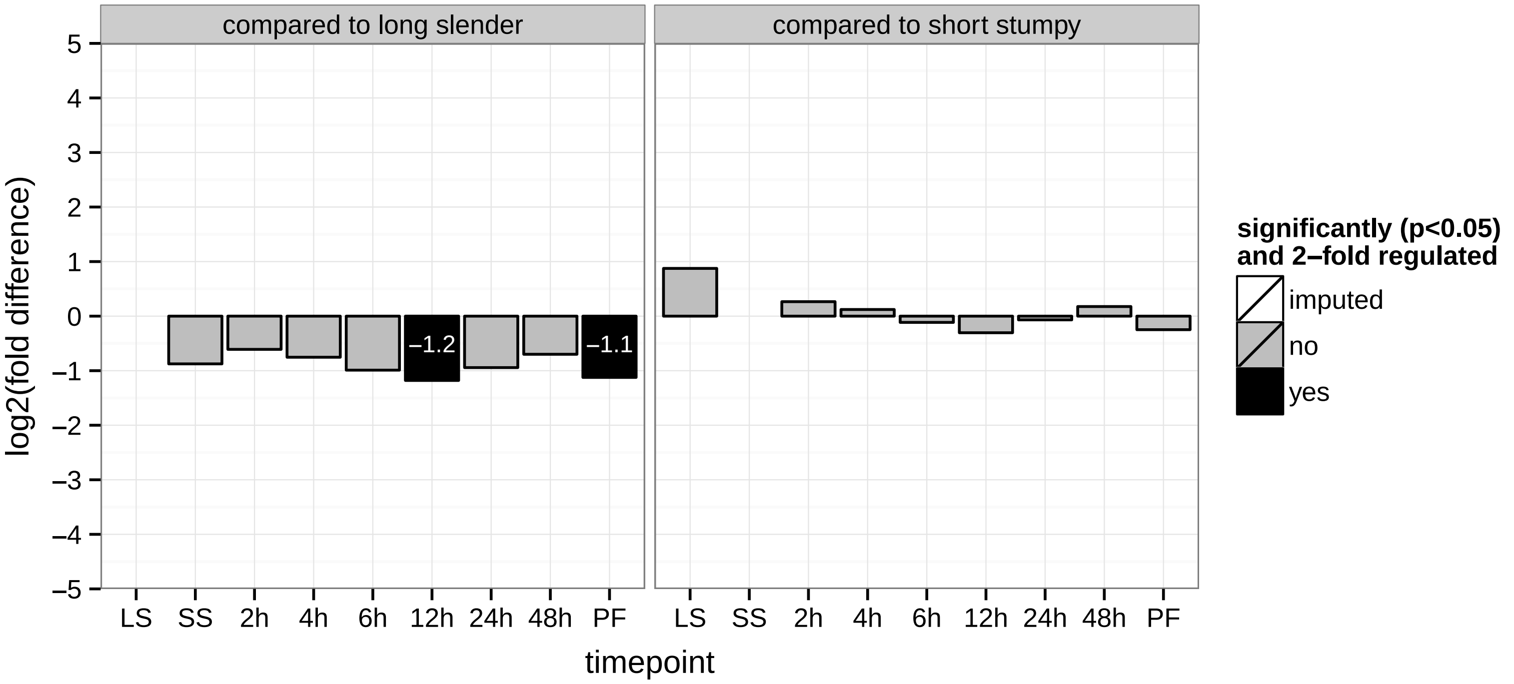
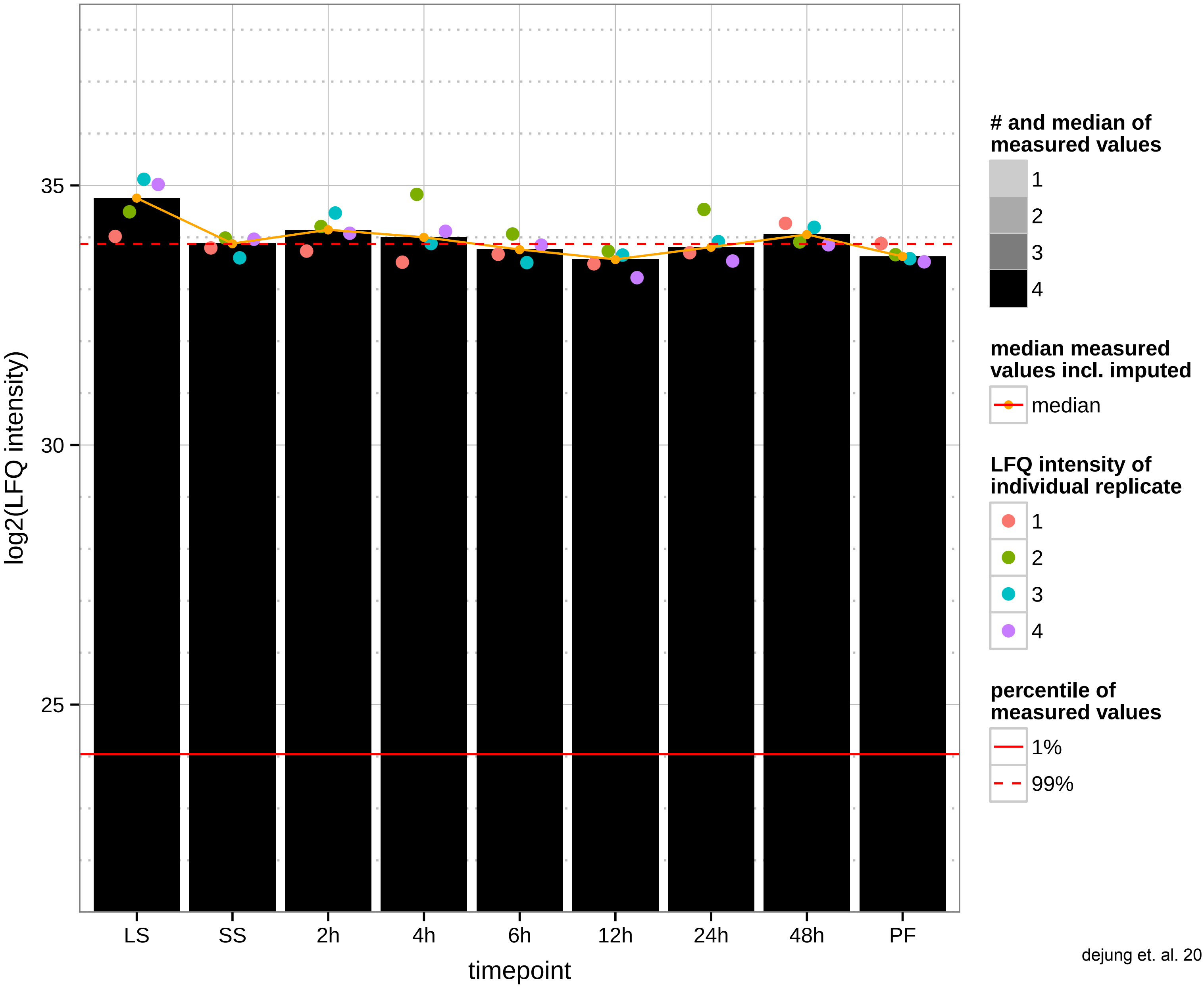
histone H4, putative
Tb927.5.4260;Tb927.5.4250;Tb927.5.4240;Tb927.5.4230;Tb927.5.4220;Tb927.5.4210;Tb927.5.4200;Tb927.5.4190;Tb927.5
AGOF: DNA binding
AGOC: nucleosome, nucleus
AGOP: nucleosome assembly
PGOF: null, DNA binding
PGOC: null, nucleosome, nucleus
PGOP: null, nucleosome assembly





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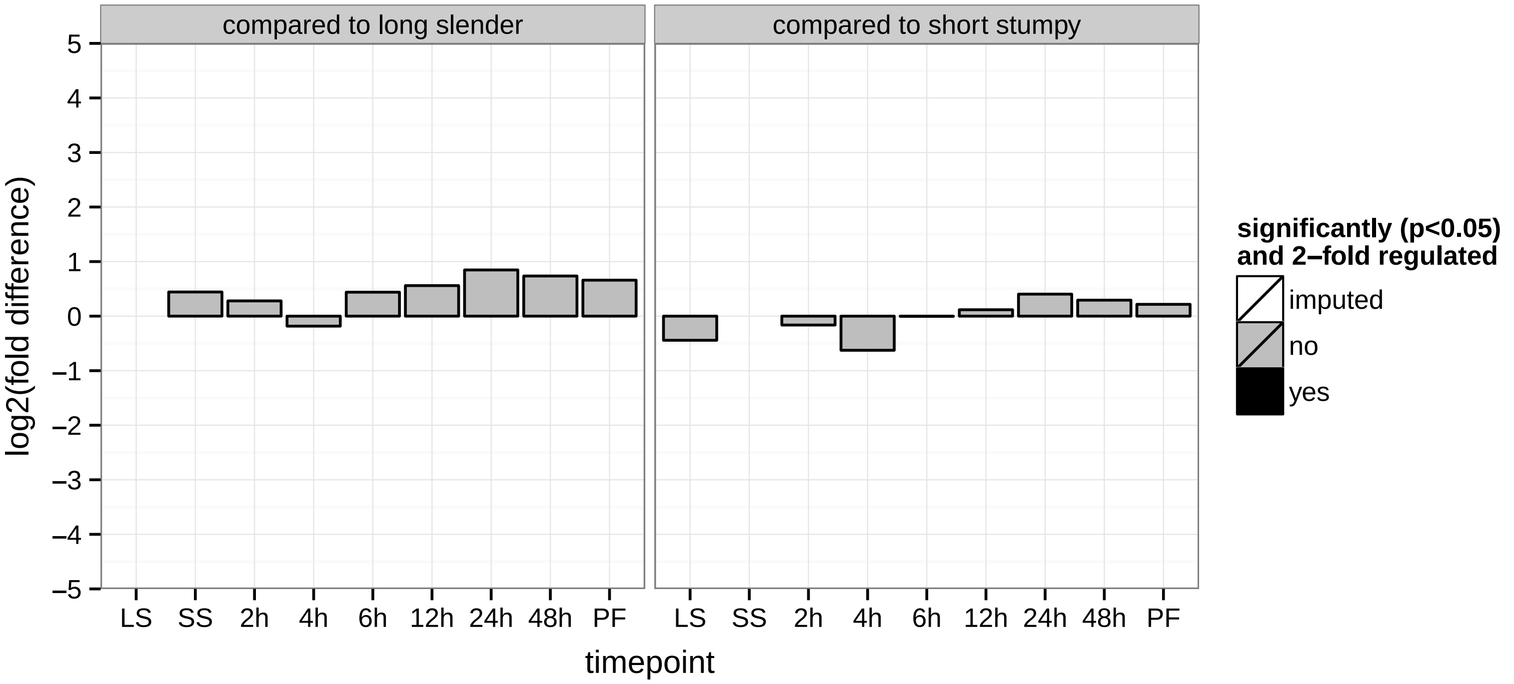
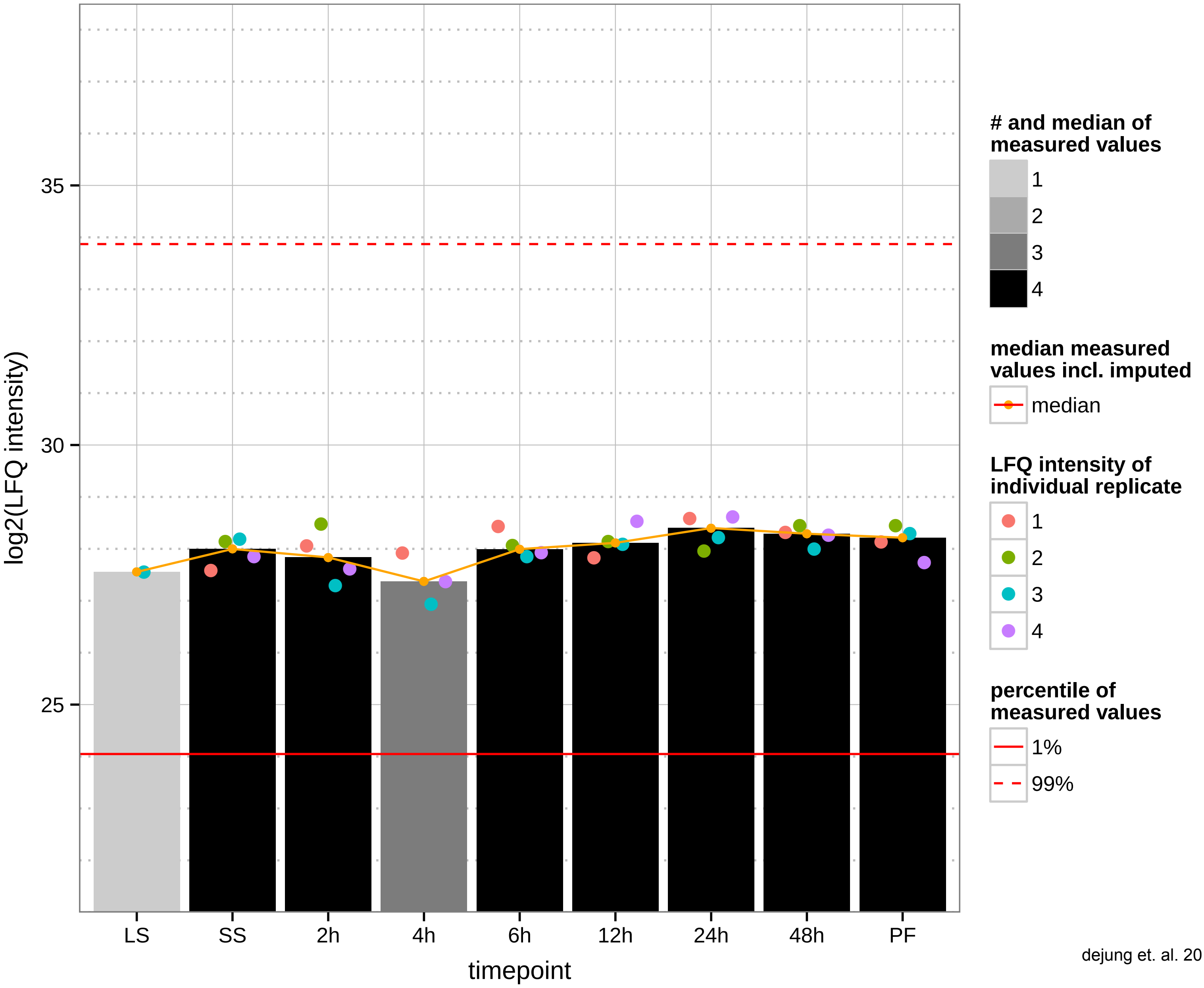
ATP−dependent DEAD/H RNA helicase, putative
Tb927.5.4270
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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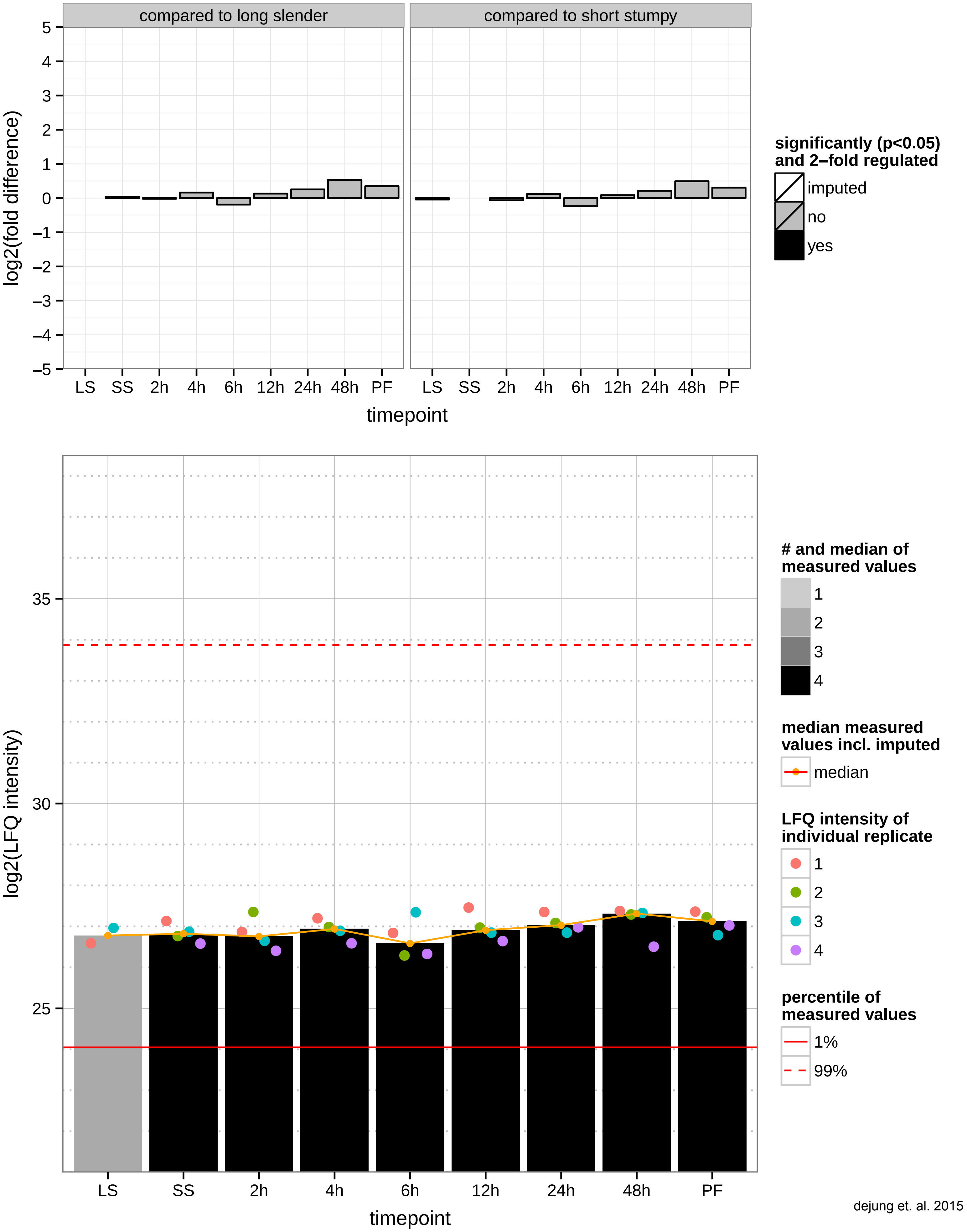
NUDIX hydrolase, putative
Tb927.5.4350
AGOF: hydrolase activity
AGOC: null
AGOP: null
PGOF: hydrolase activity
PGOC: null
PGOP: null



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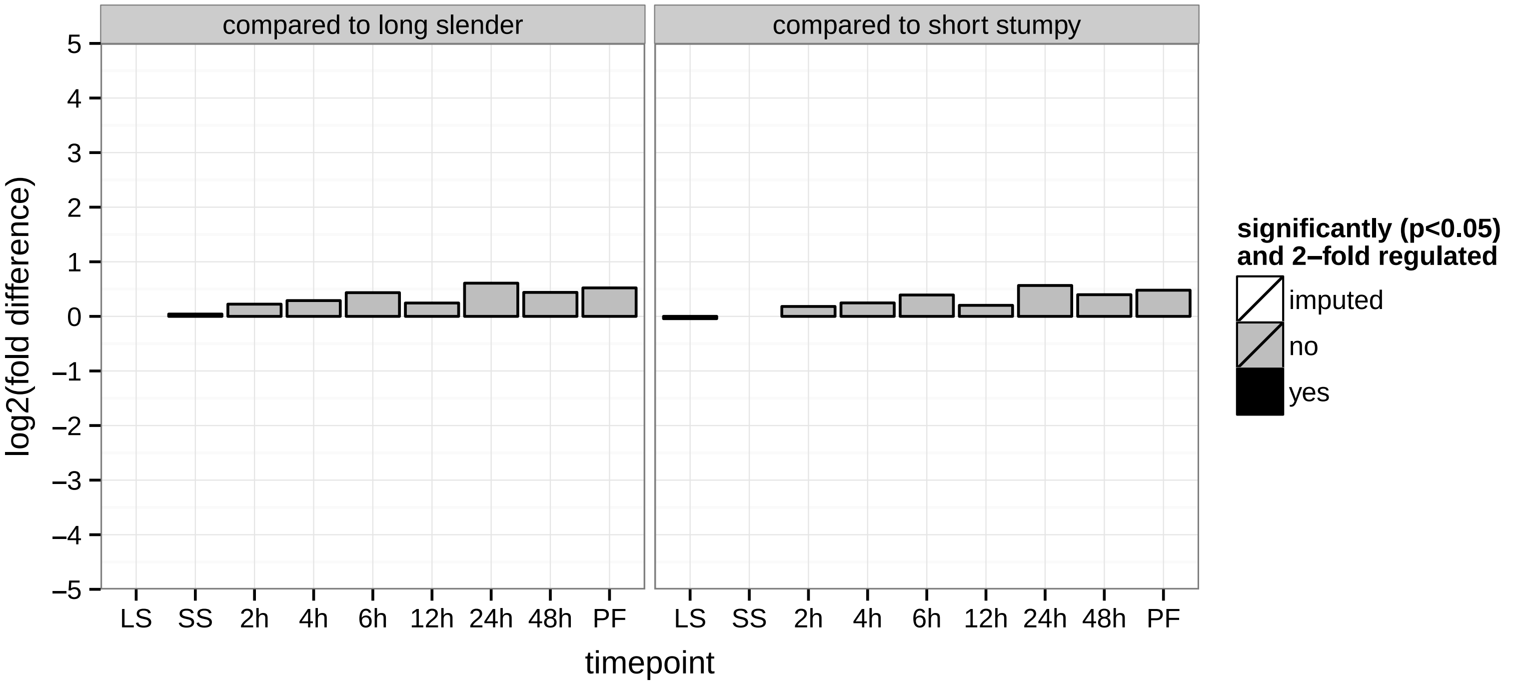
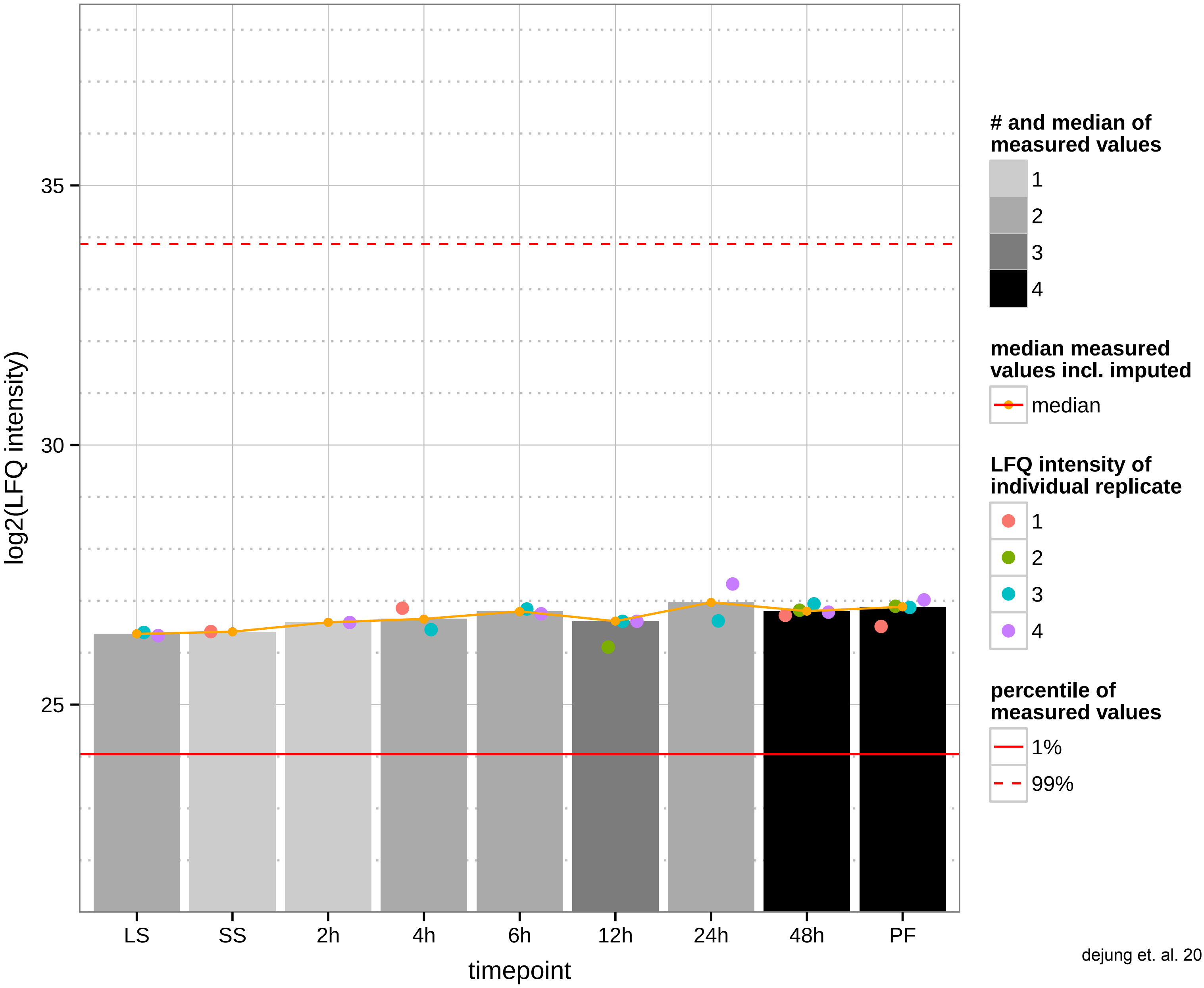
Variant Surface Glycoprotein, putative
Tb927.5.5370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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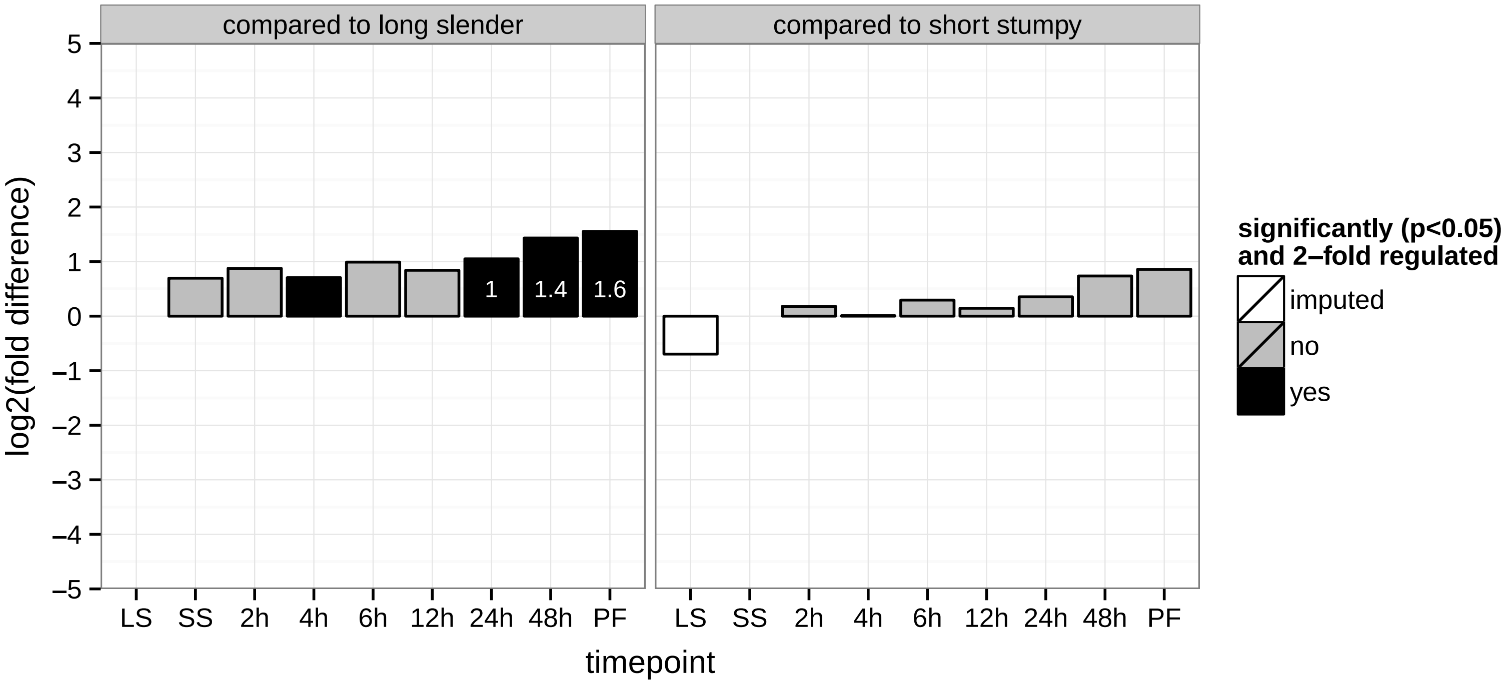
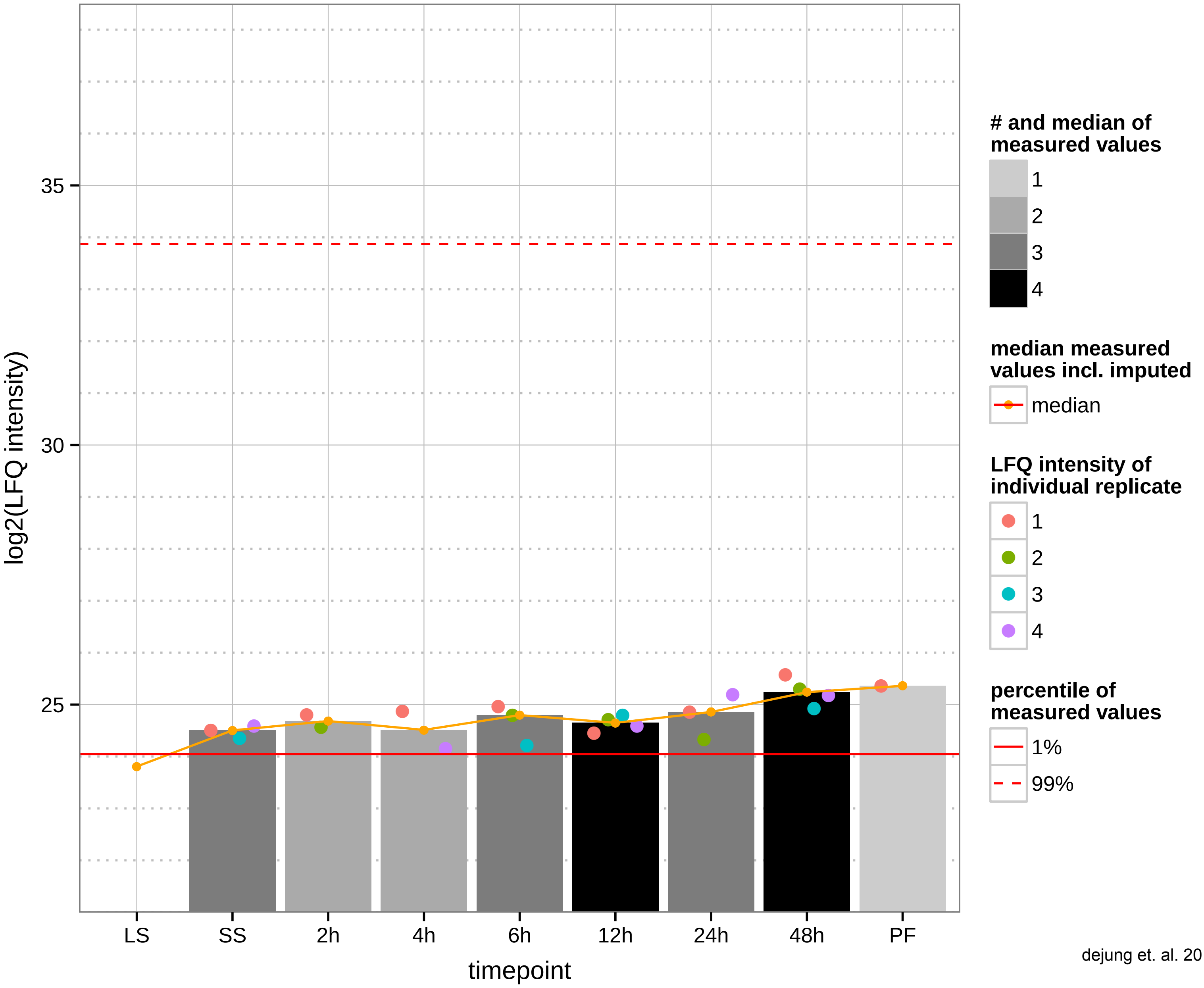
hypothetical protein, conserved
Tb927.5.570
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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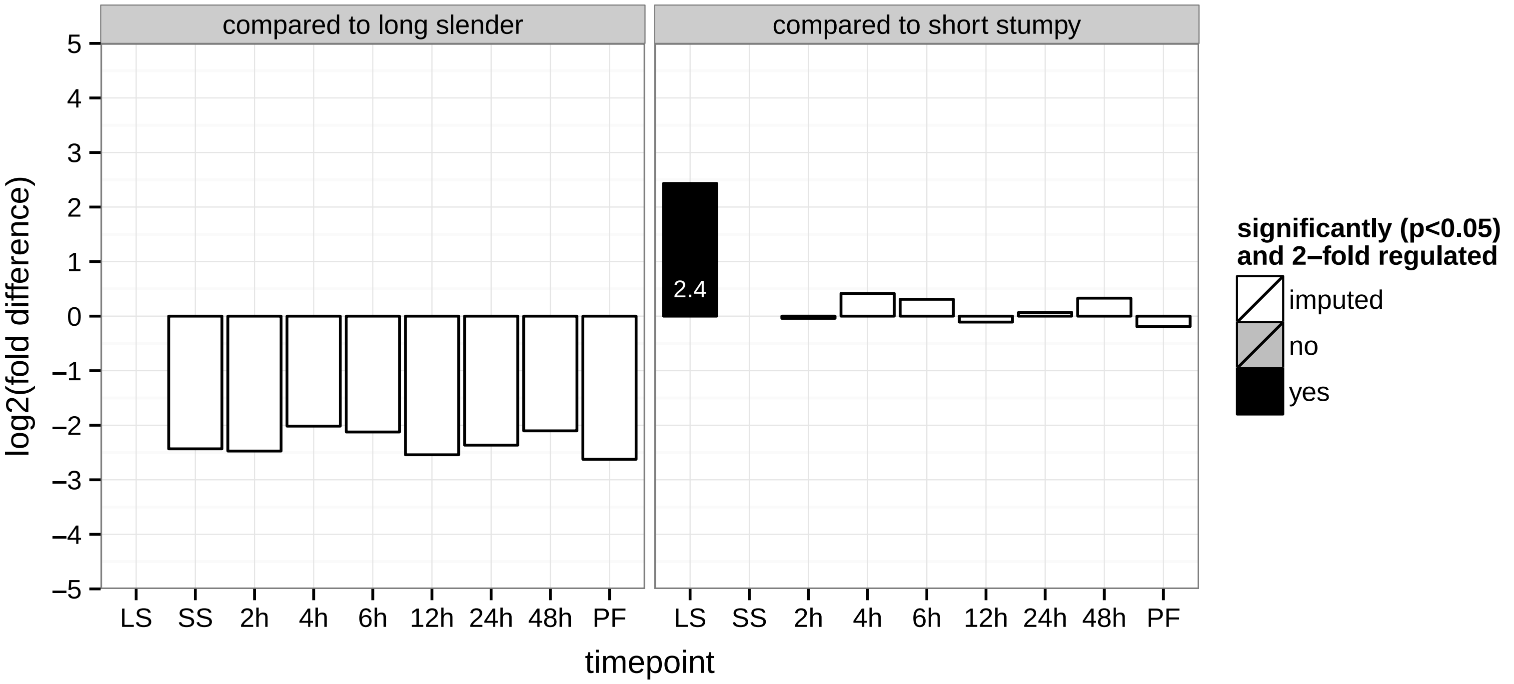
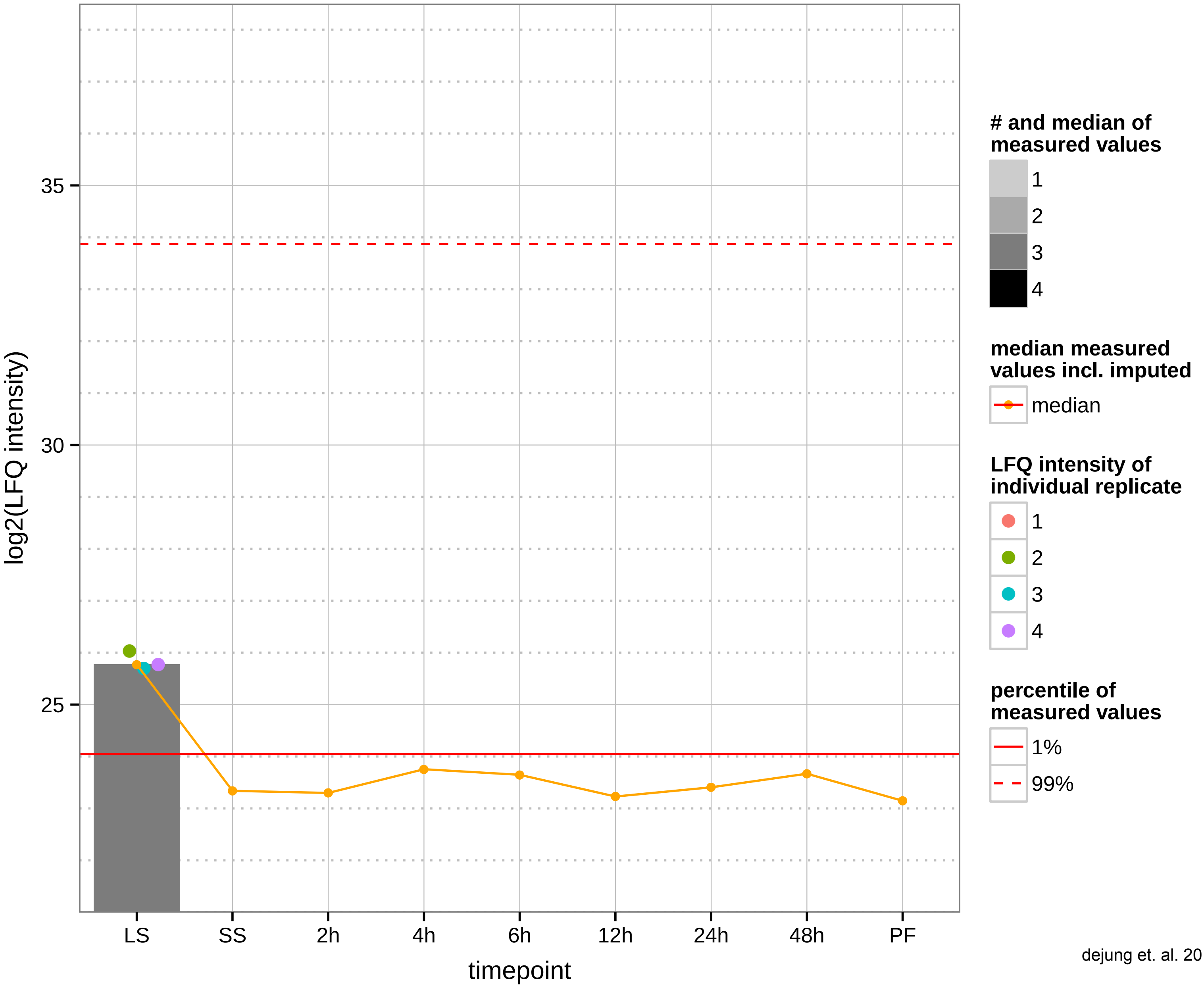
acidic phosphatase, putative
Tb927.5.610
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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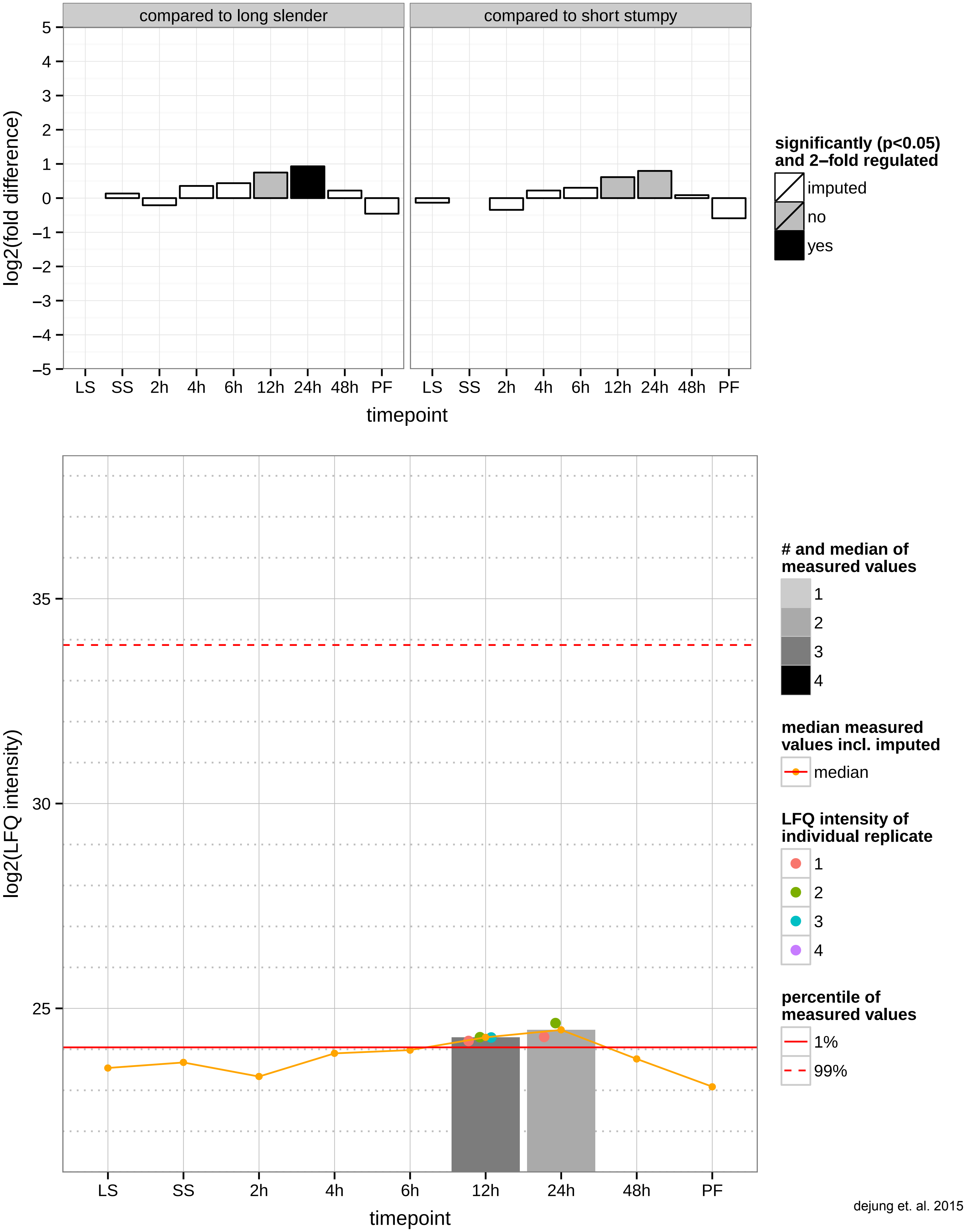
hypothetical protein, conserved
Tb927.5.740
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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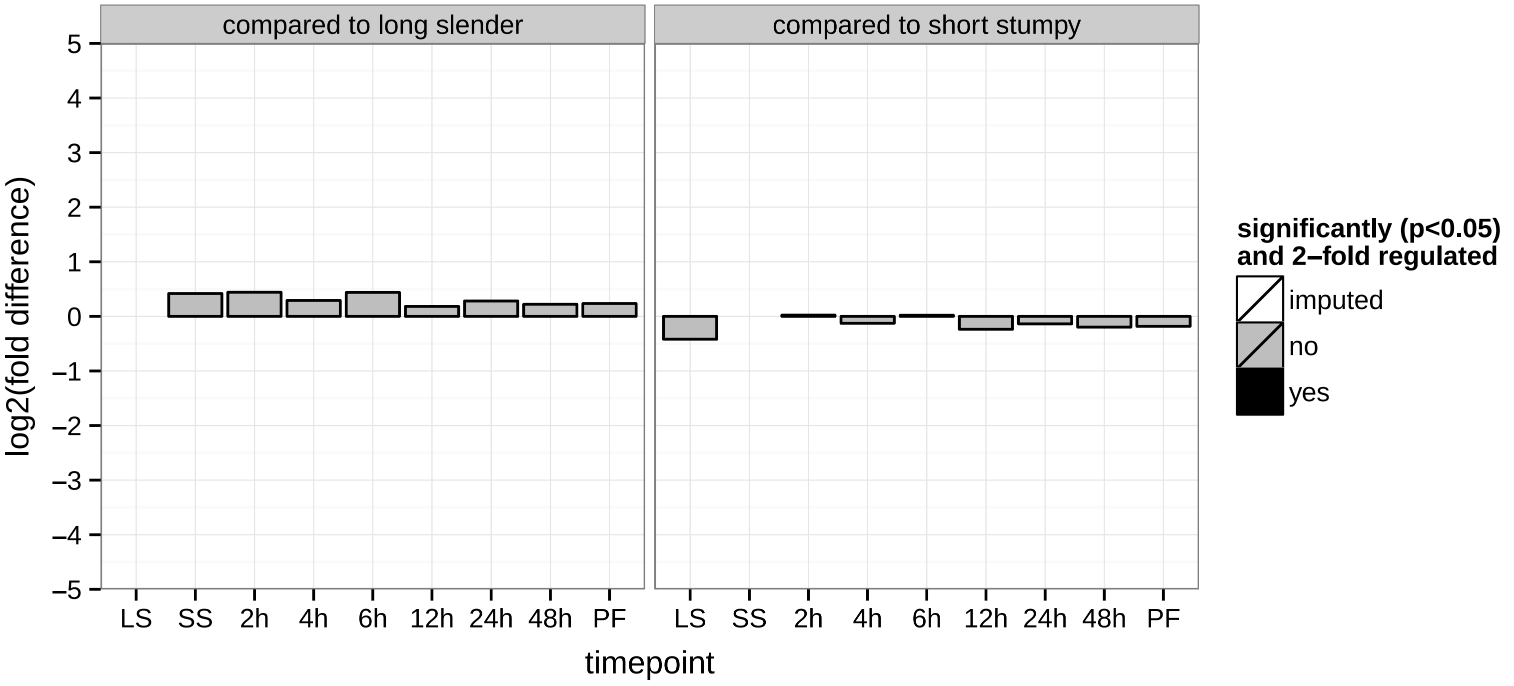
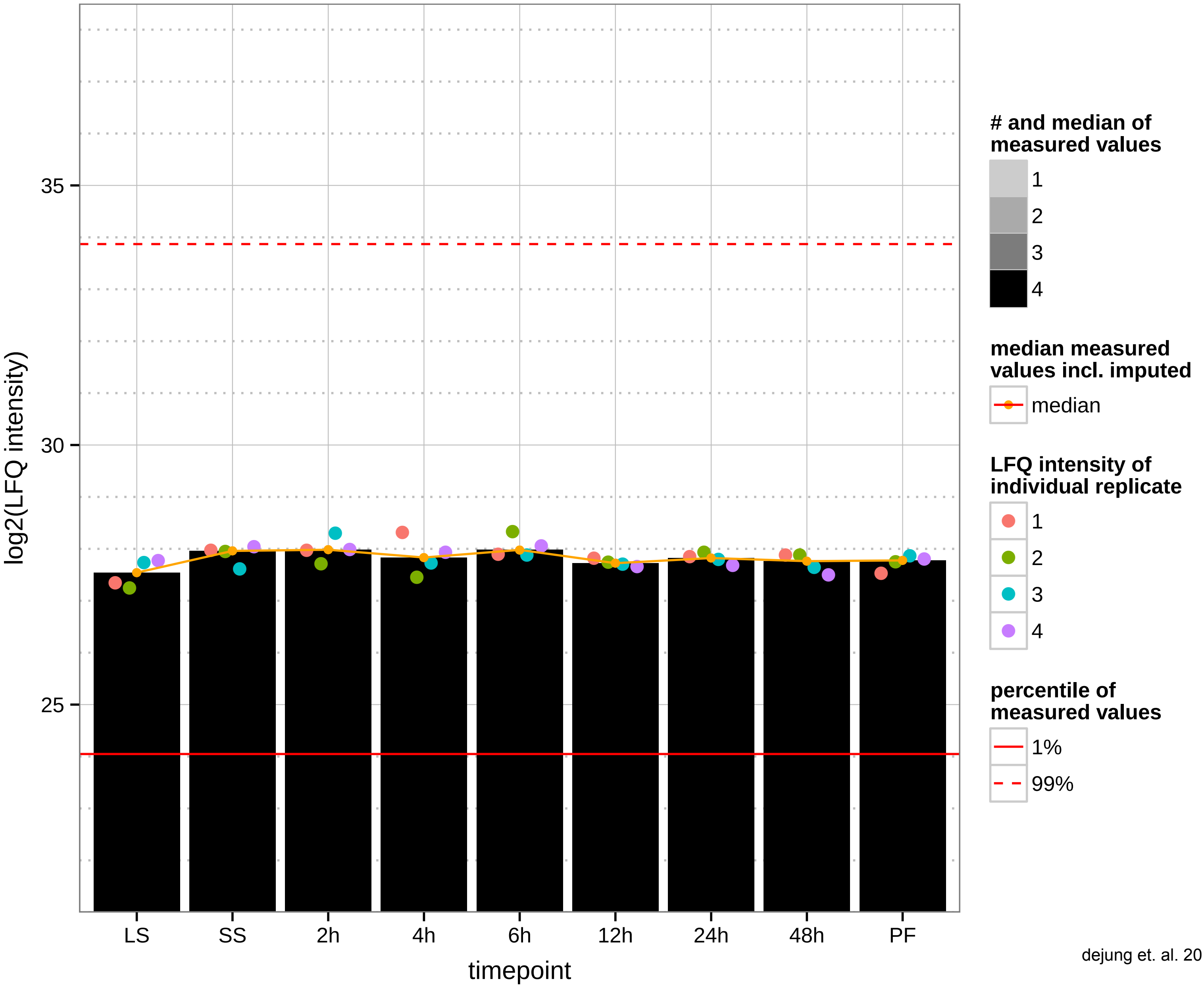
hypothetical protein, conserved
Tb927.5.780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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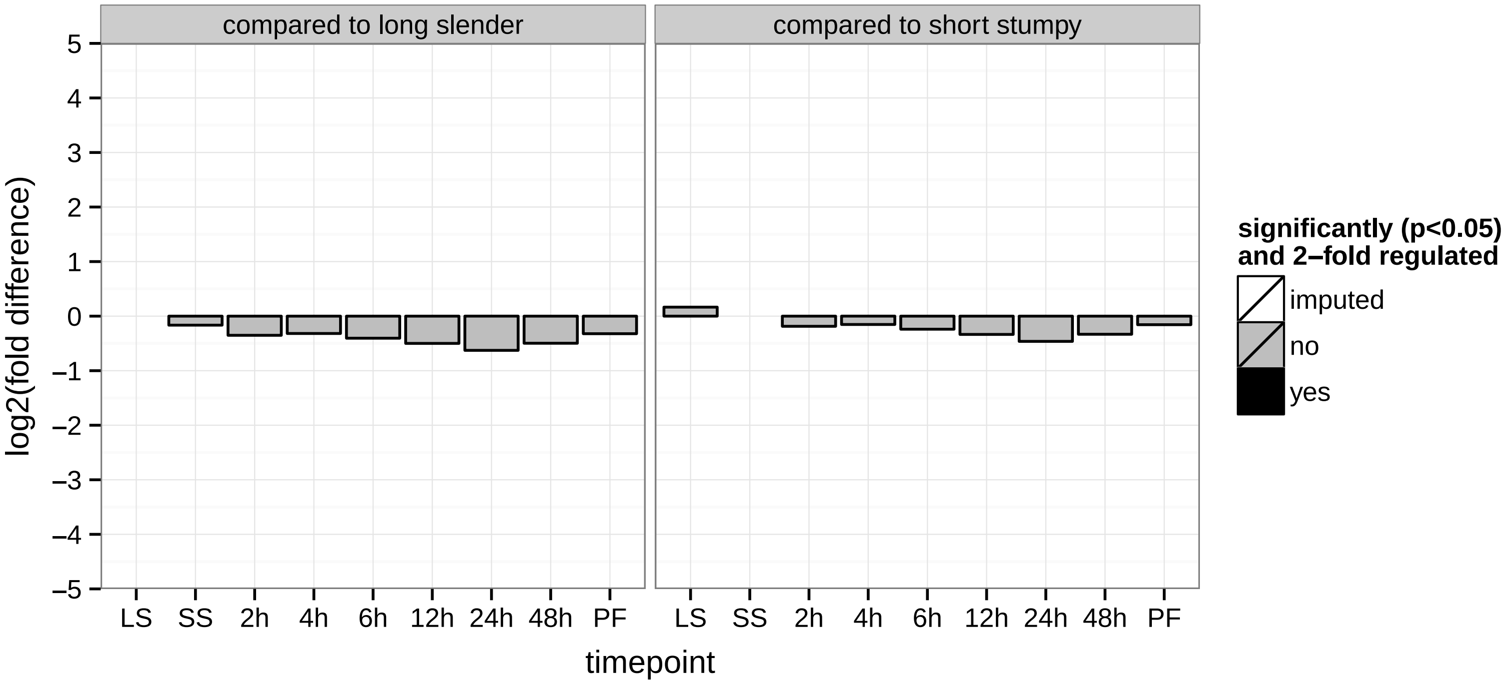
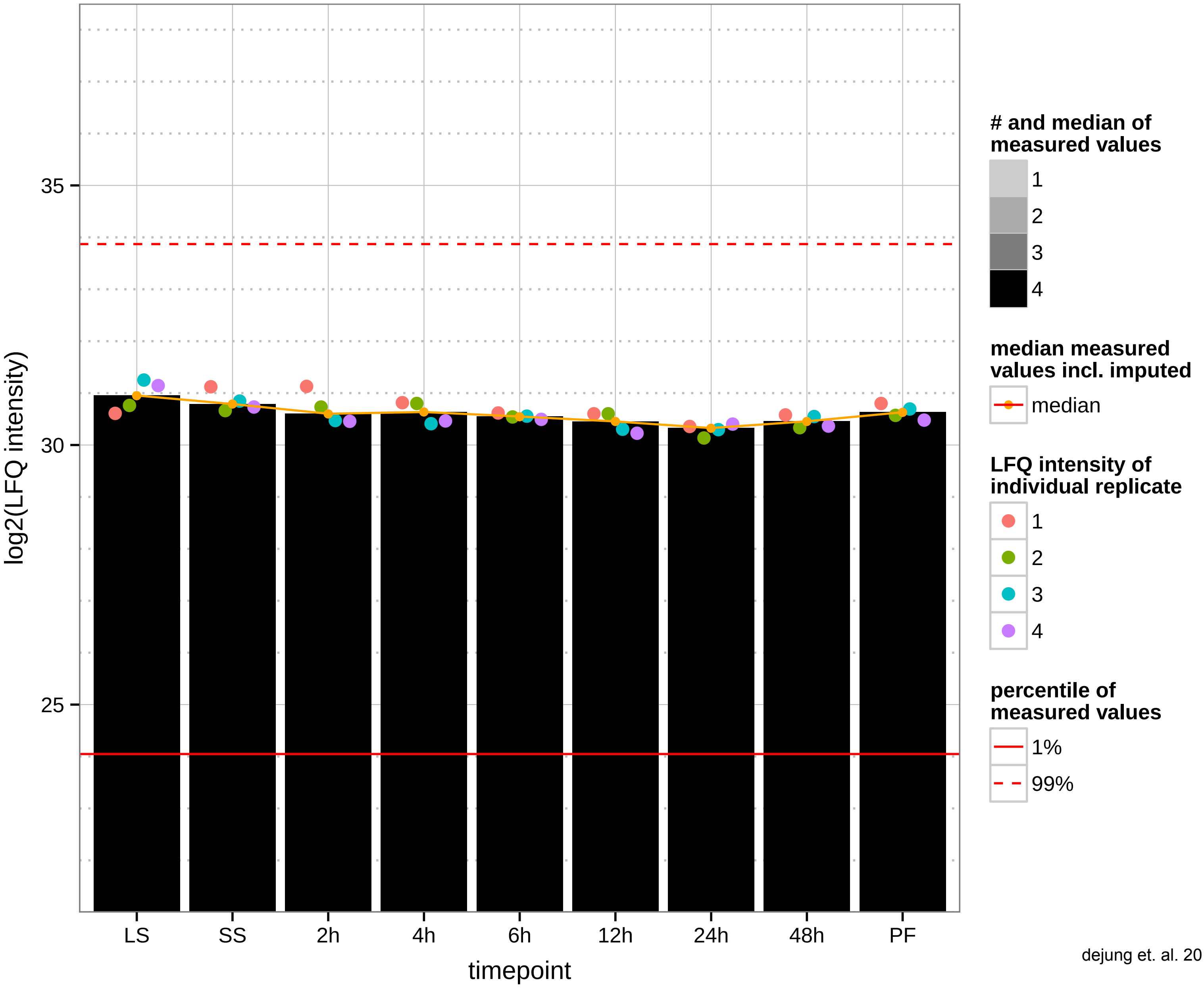
casein kinase I isoform 1 (CK1.1), casein kinase I, isoform 2 (CK1.2)
Tb927.5.800
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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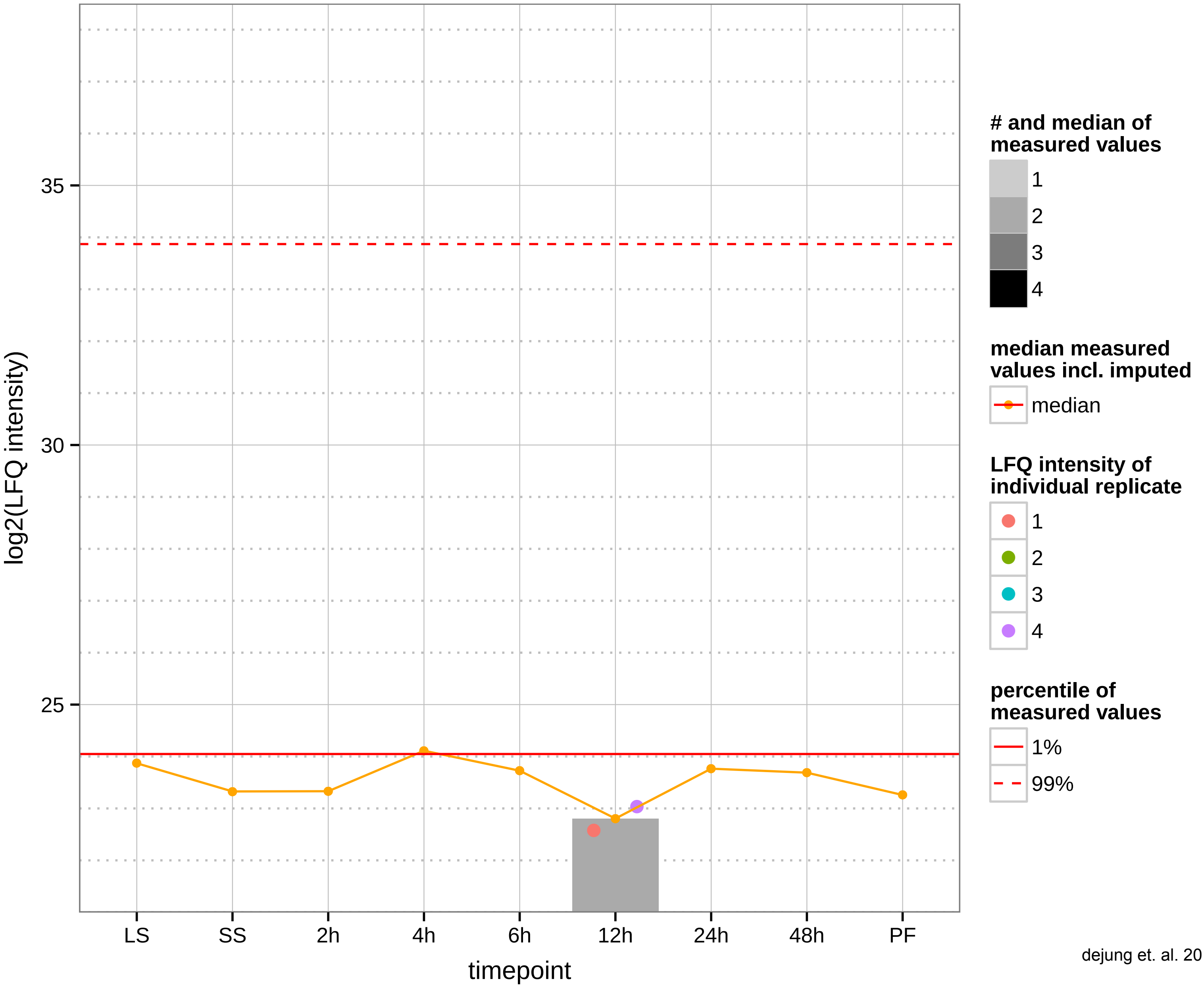
hypothetical protein, conserved
Tb927.5.830
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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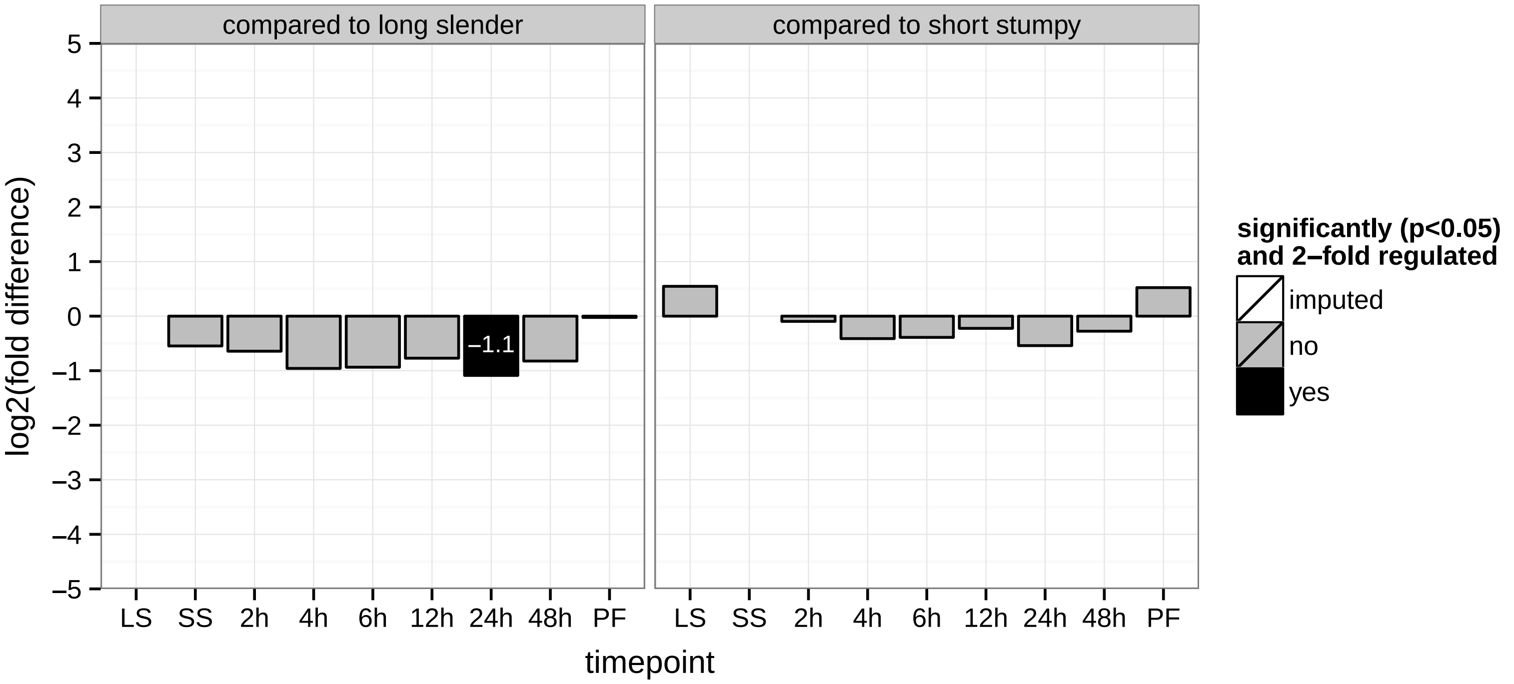
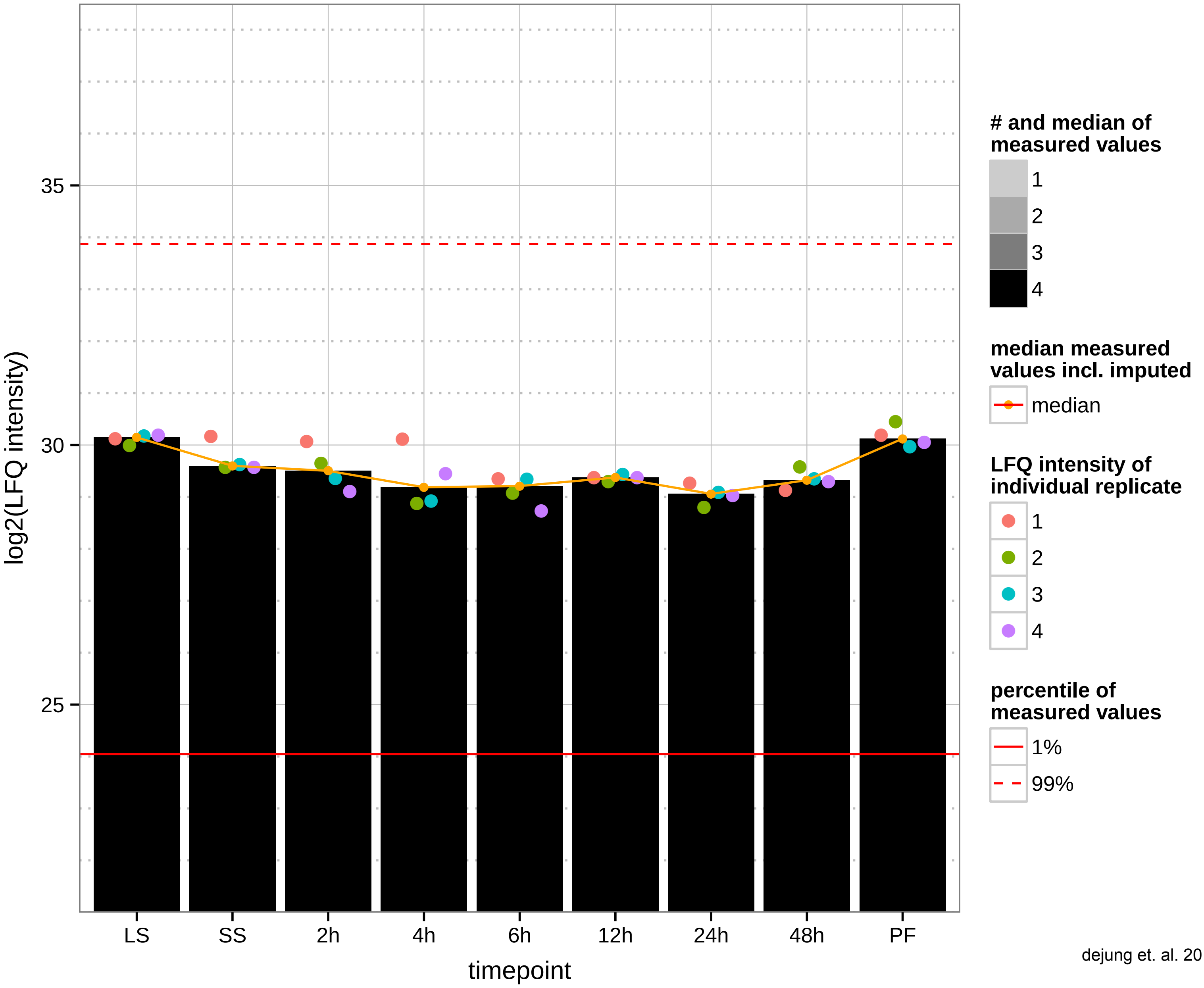
oligosaccharyl transferase subunit, putative
Tb927.5.900;Tb11.v5.0559
AGOF: null, oligosaccharyl transferase activity
AGOC: null, membrane
AGOP: null, protein glycosylation
PGOF: oligosaccharyl transferase activity
PGOC: membrane
PGOP: protein glycosylation





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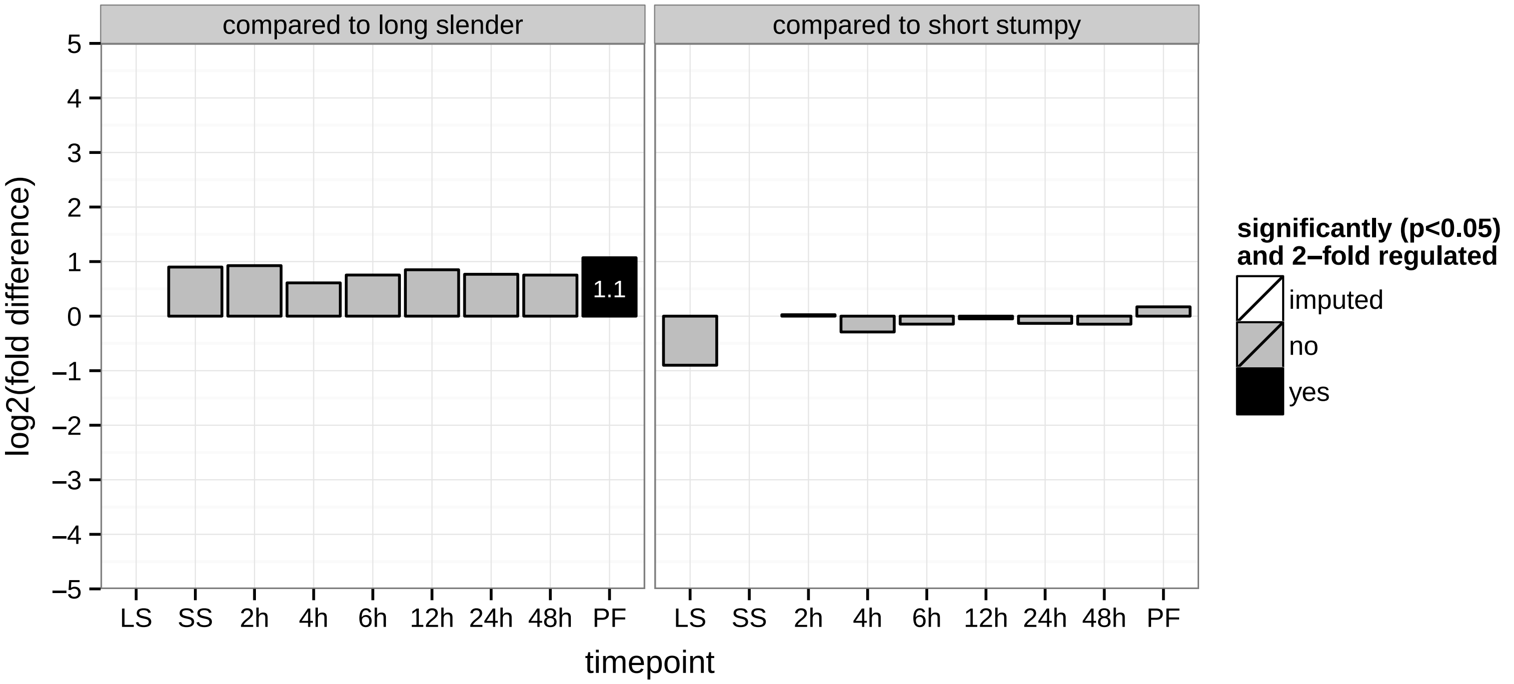
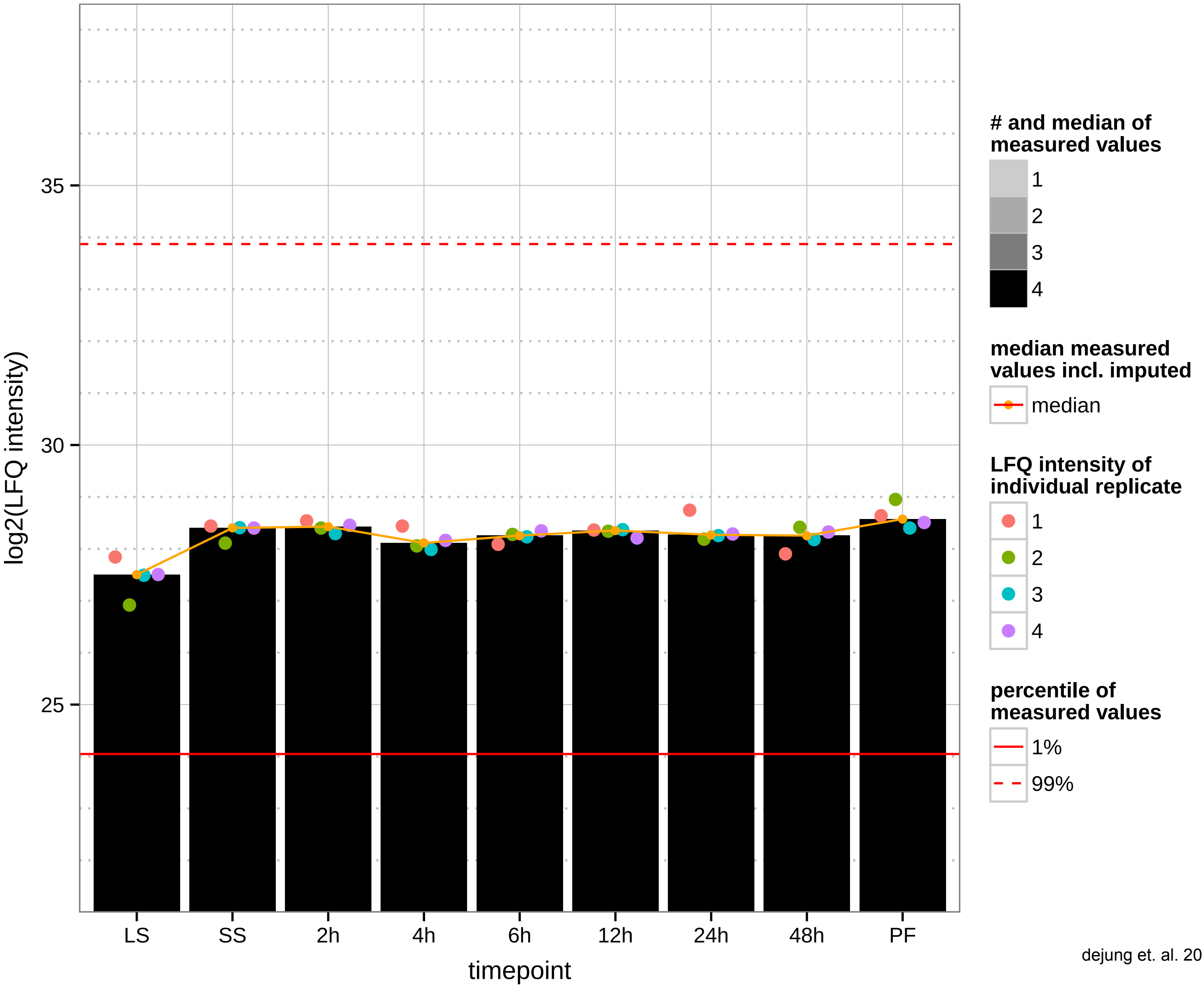
hypothetical protein, conserved
Tb927.5.960
AGOF: ATP binding, nucleoside−triphosphatase activity
AGOC: null
AGOP: null
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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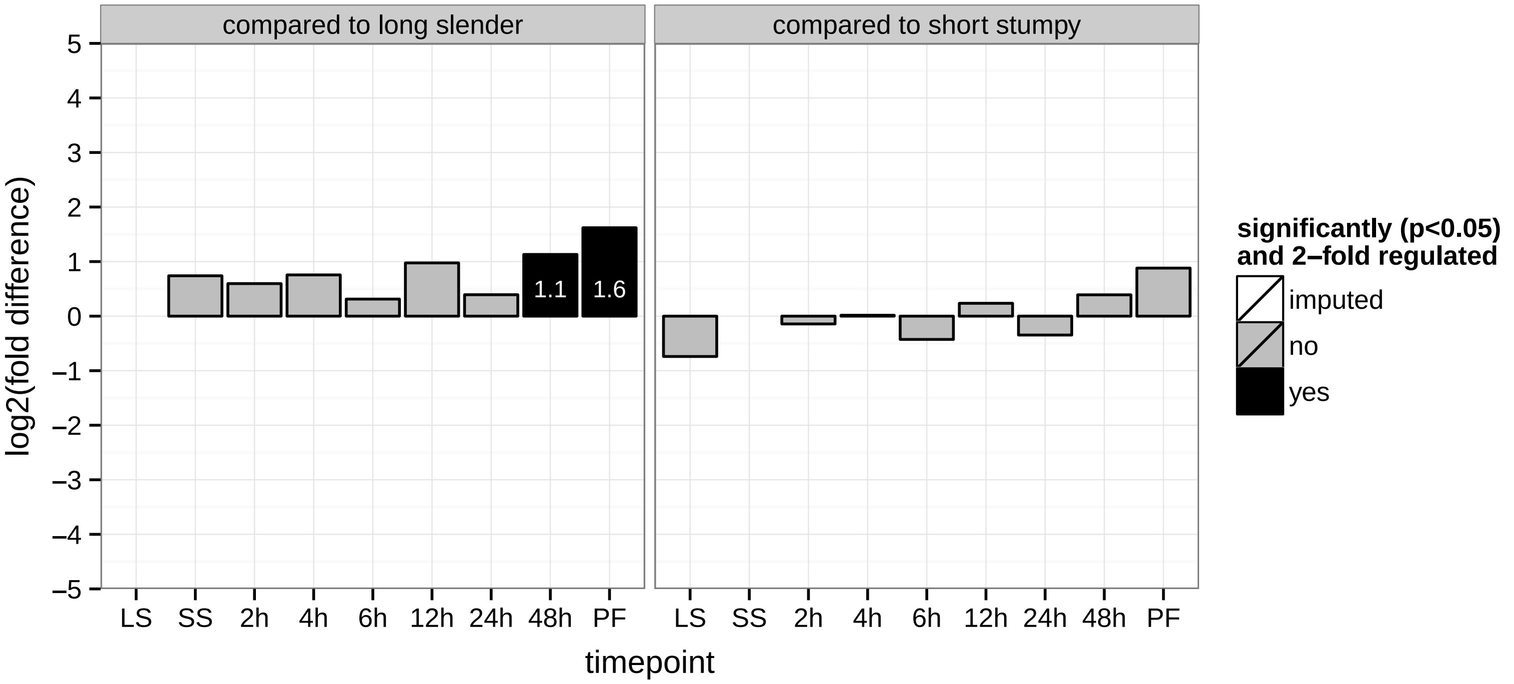
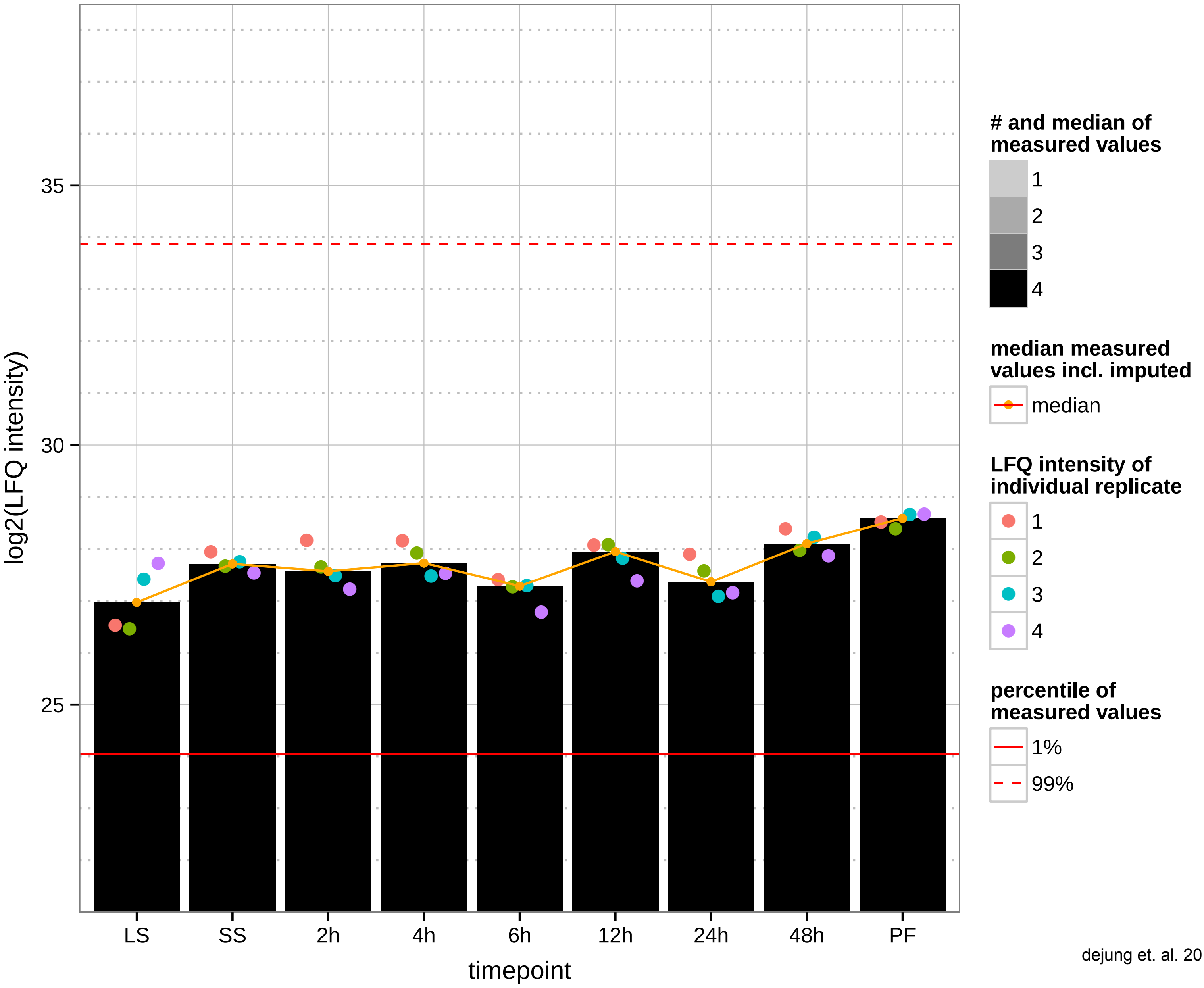
glyoxalase II, hydroxyacylglutathione hydrolase, putative (glxII)
Tb927.6.1080
AGOF: hydrolase activity
AGOC: null
AGOP: null
PGOF: hydrolase activity
PGOC: null
PGOP: null





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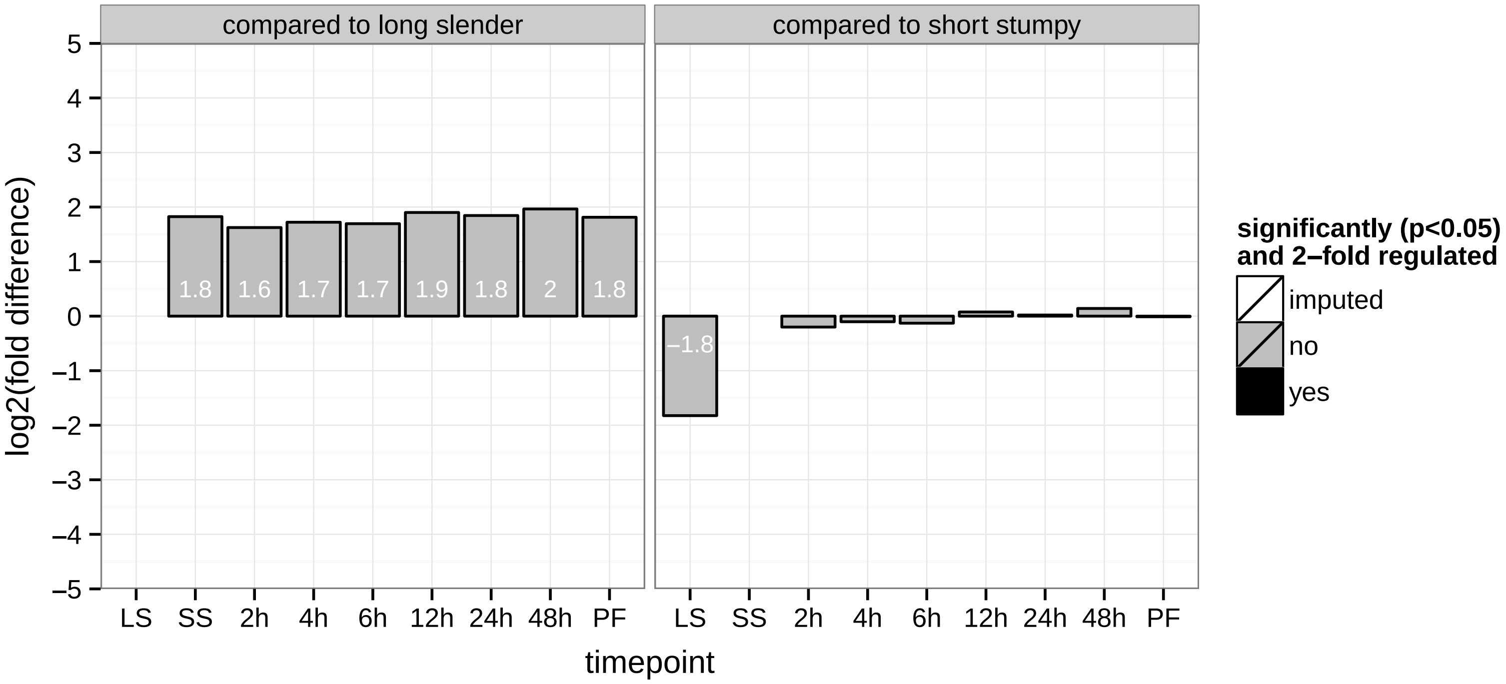
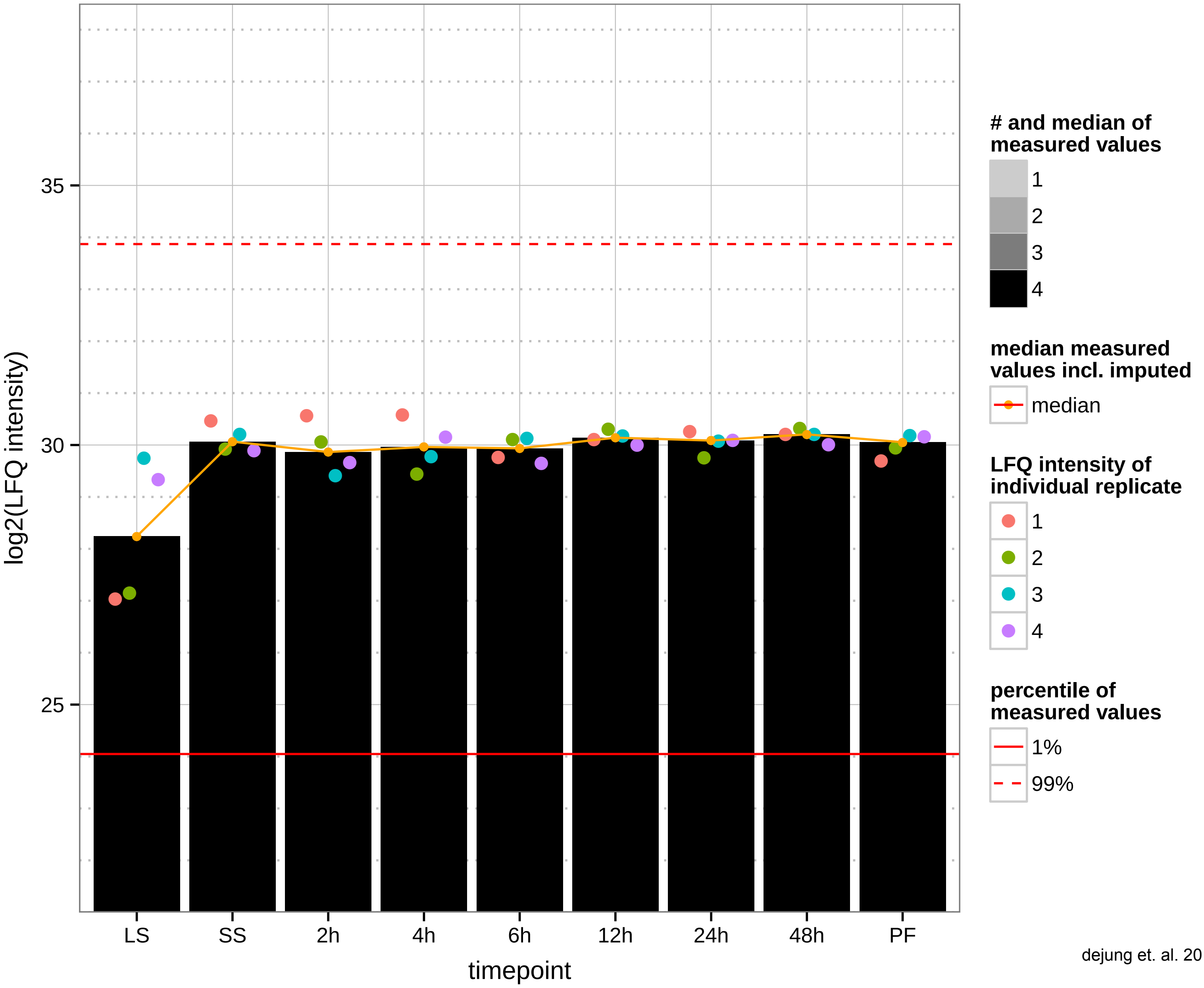
proteasome regulatory ATPase subunit 3 (RPT3)
Tb927.6.1090
AGOF: ATP binding, ATPase activity
AGOC: cytoplasm, nucleus, proteasome regulatory particle
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ATP binding, hydrolase activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: cytoplasm
PGOP: protein catabolic process





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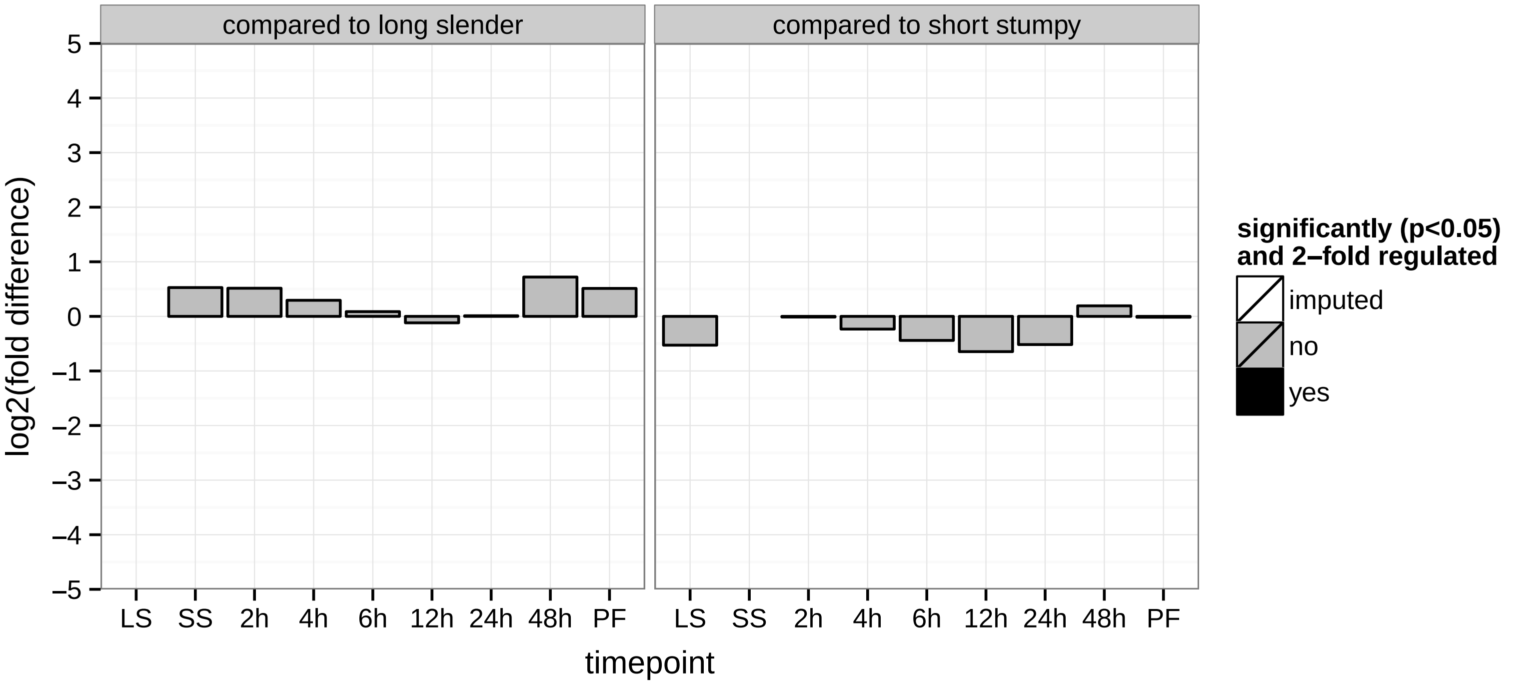
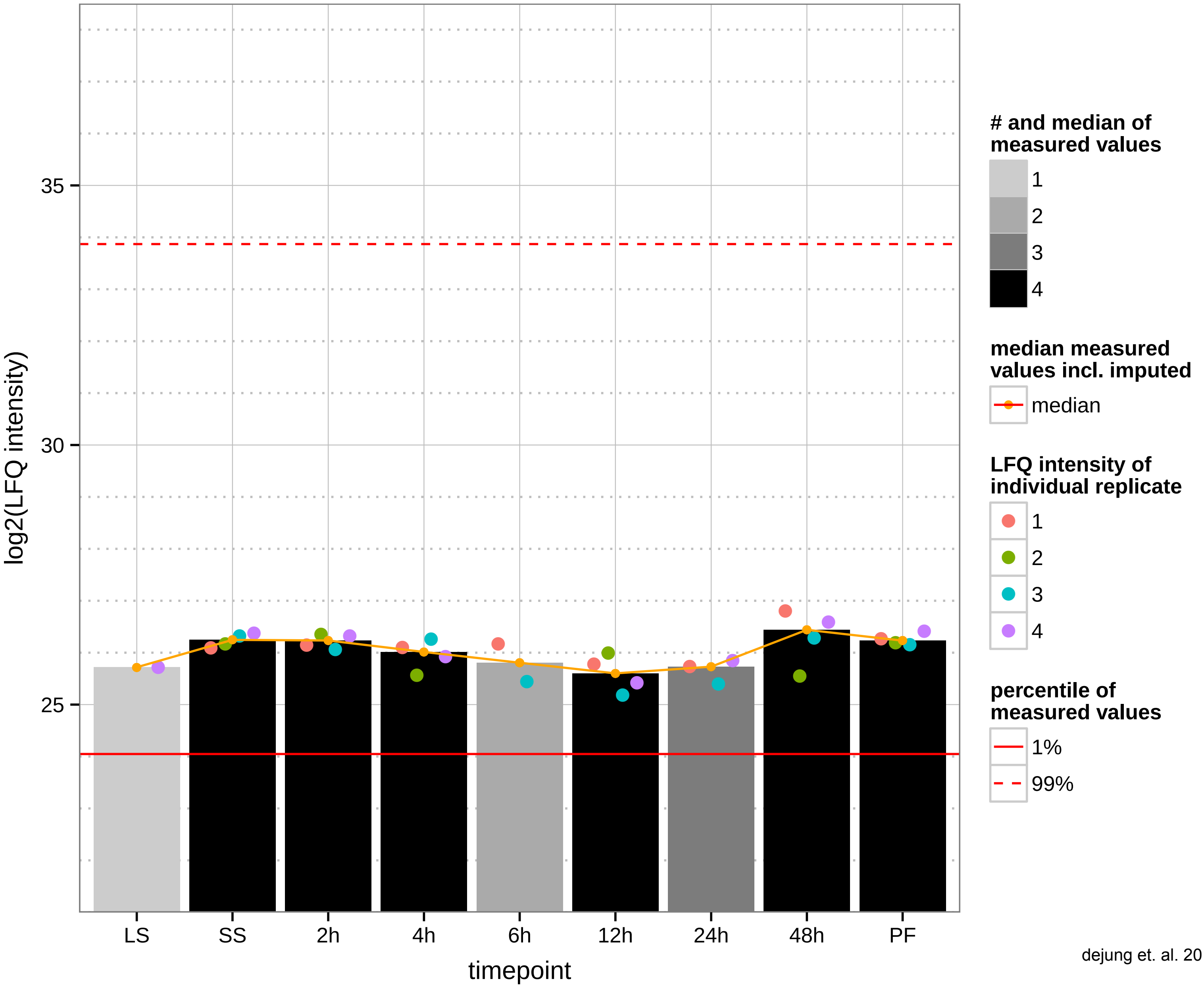
dolichyl−P−Man:GDP−Man5GlcNAc2−PP−dolichyl alpha−1, 2−mannosyltransferase, putative, Asparagine−linked glycosylatio
Tb927.6.1140
AGOF: alpha−1, 2−mannosyltransferase activity
AGOC: intrinsic to endoplasmic reticulum membrane
AGOP: GPI anchor biosynthetic process, dolichol−linked oligosaccharide biosynthetic process
PGOF: transferase activity, transferring glycosyl groups
PGOC: intrinsic to endoplasmic reticulum membrane
PGOP: GPI anchor biosynthetic process





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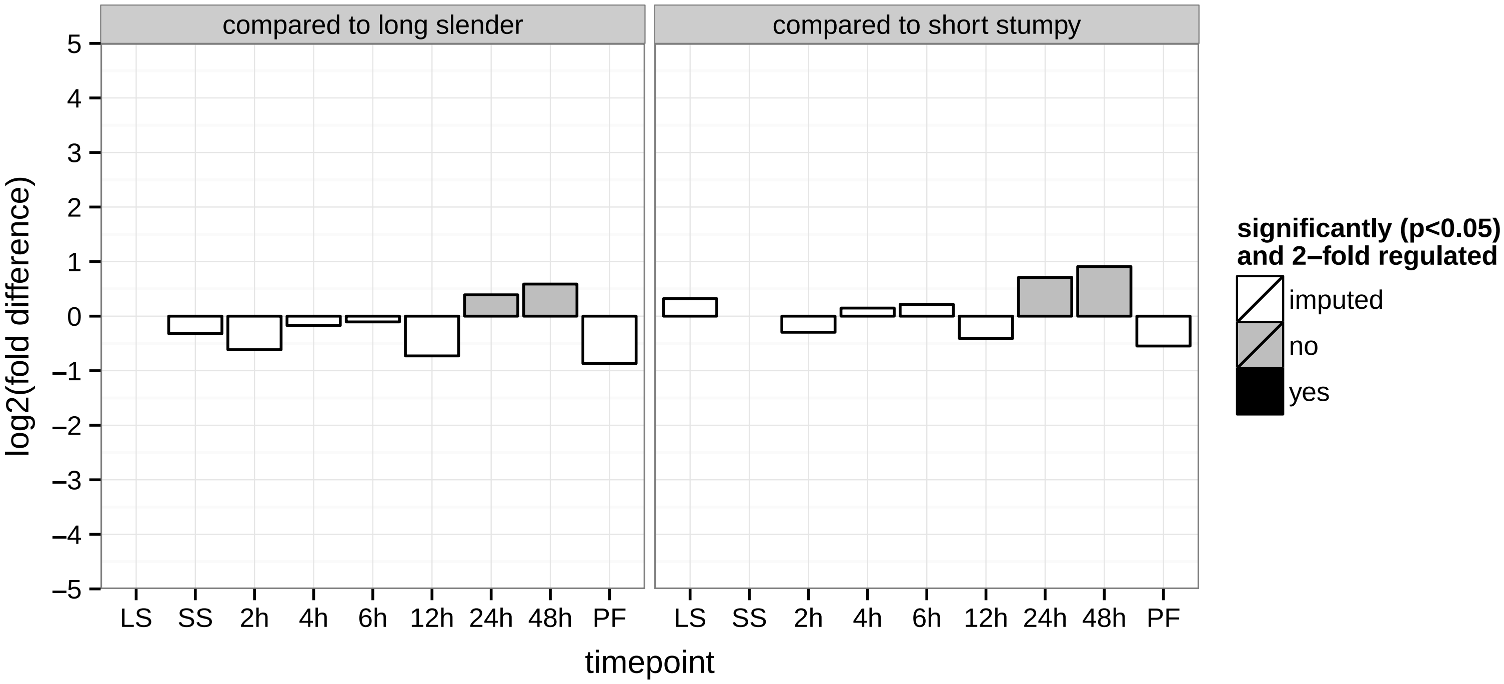
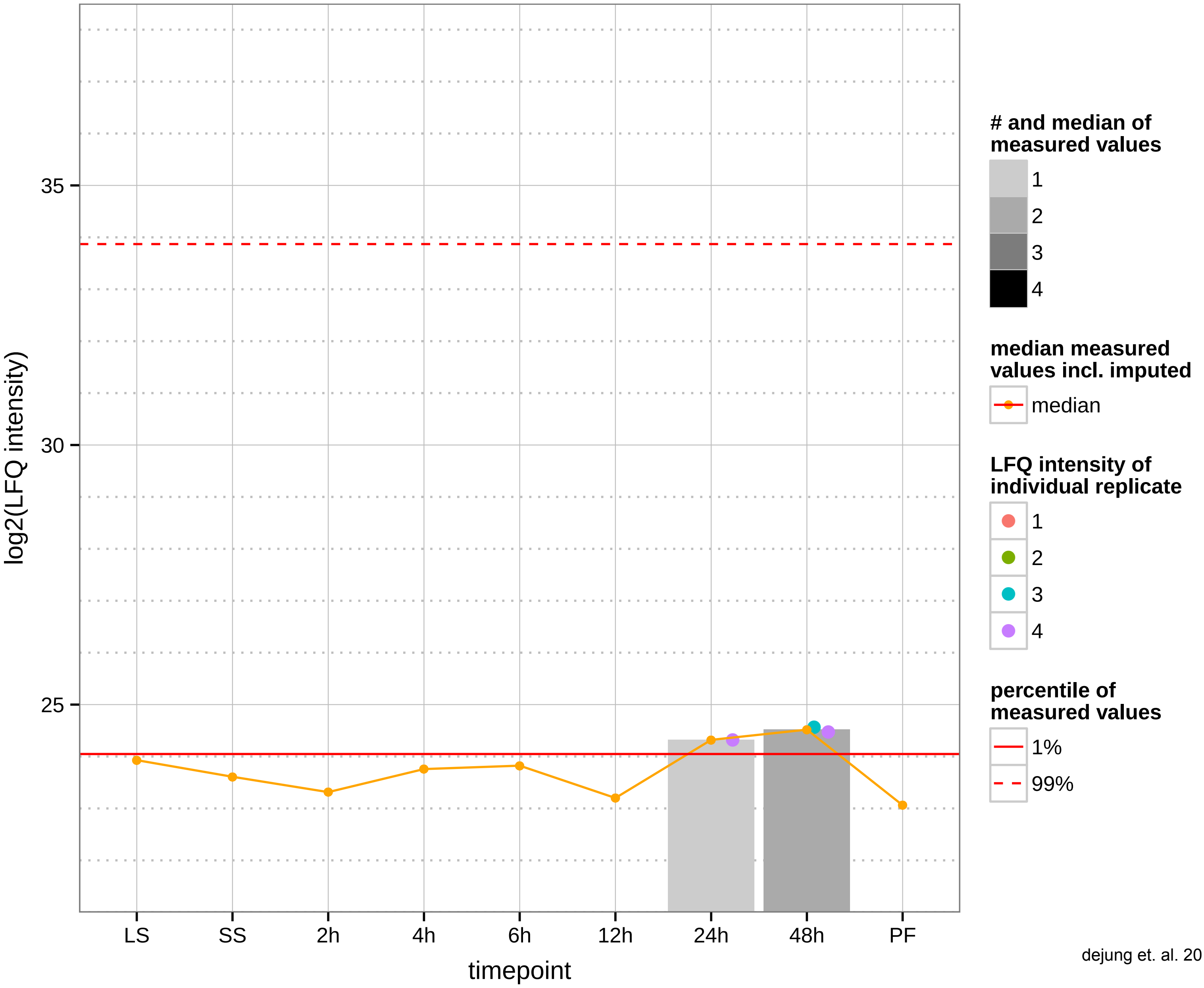
hypothetical protein, conserved
Tb927.6.1190
AGOF: DNA binding
AGOC: nucleus
AGOP: DNA–dependent transcription, initiation, histone modification
PGOF: DNA binding
PGOC: nucleus
PGOP: DNA–dependent transcription, initiation, histone modification





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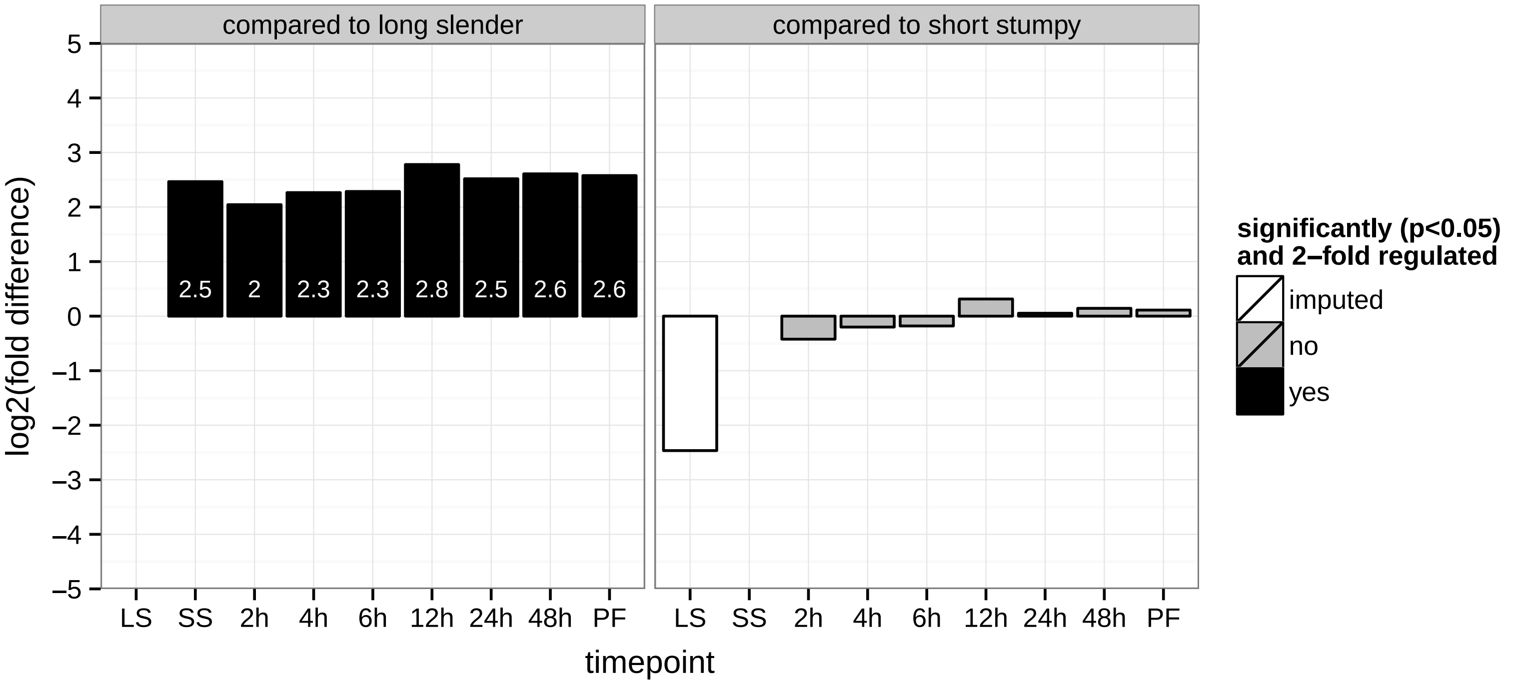
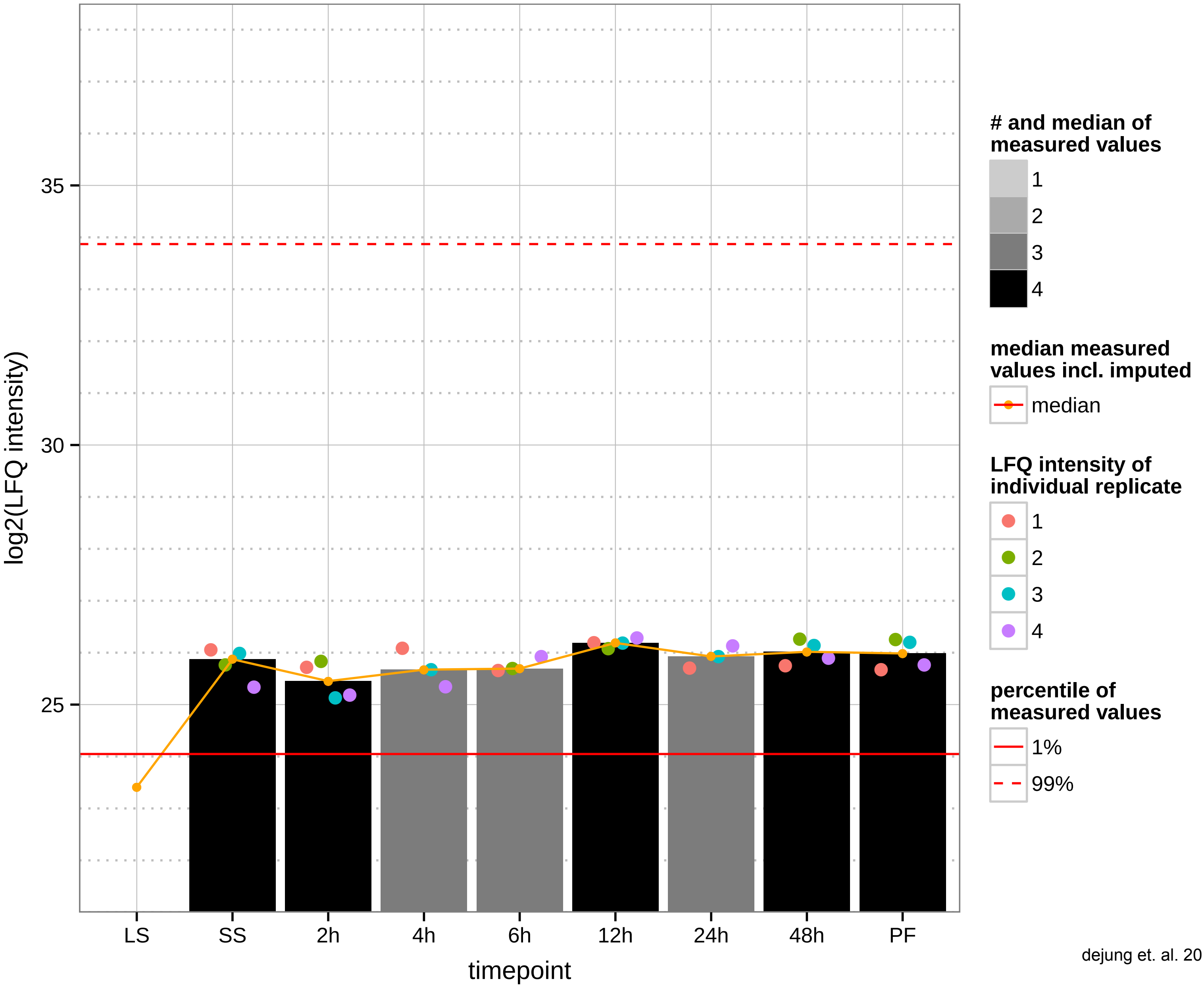
translation initiation factor EIF−2b alpha subunit, putative, eIF−2B GDP−GTP exchange factor
Tb927.6.1280
AGOF: null
AGOC: null
AGOP: cellular metabolic process
PGOF: null
PGOC: null
PGOP: cellular metabolic process





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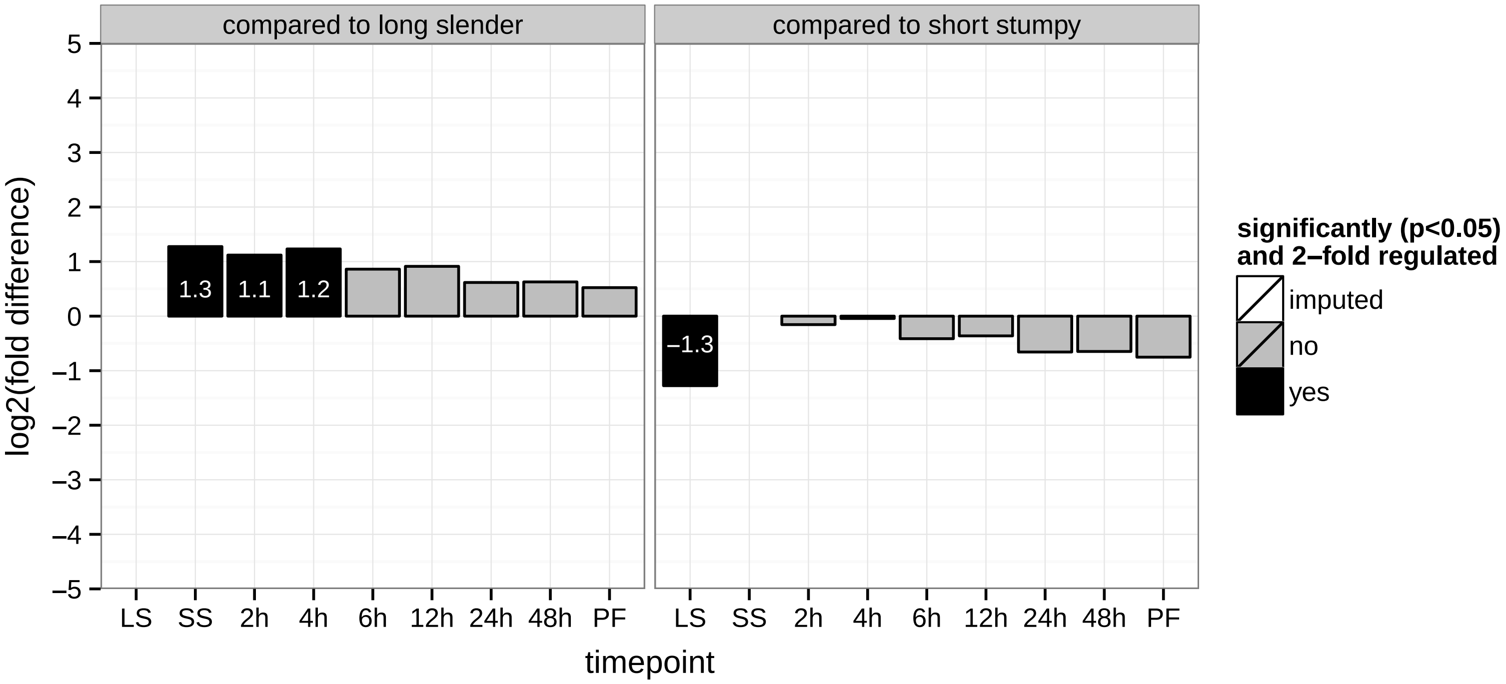
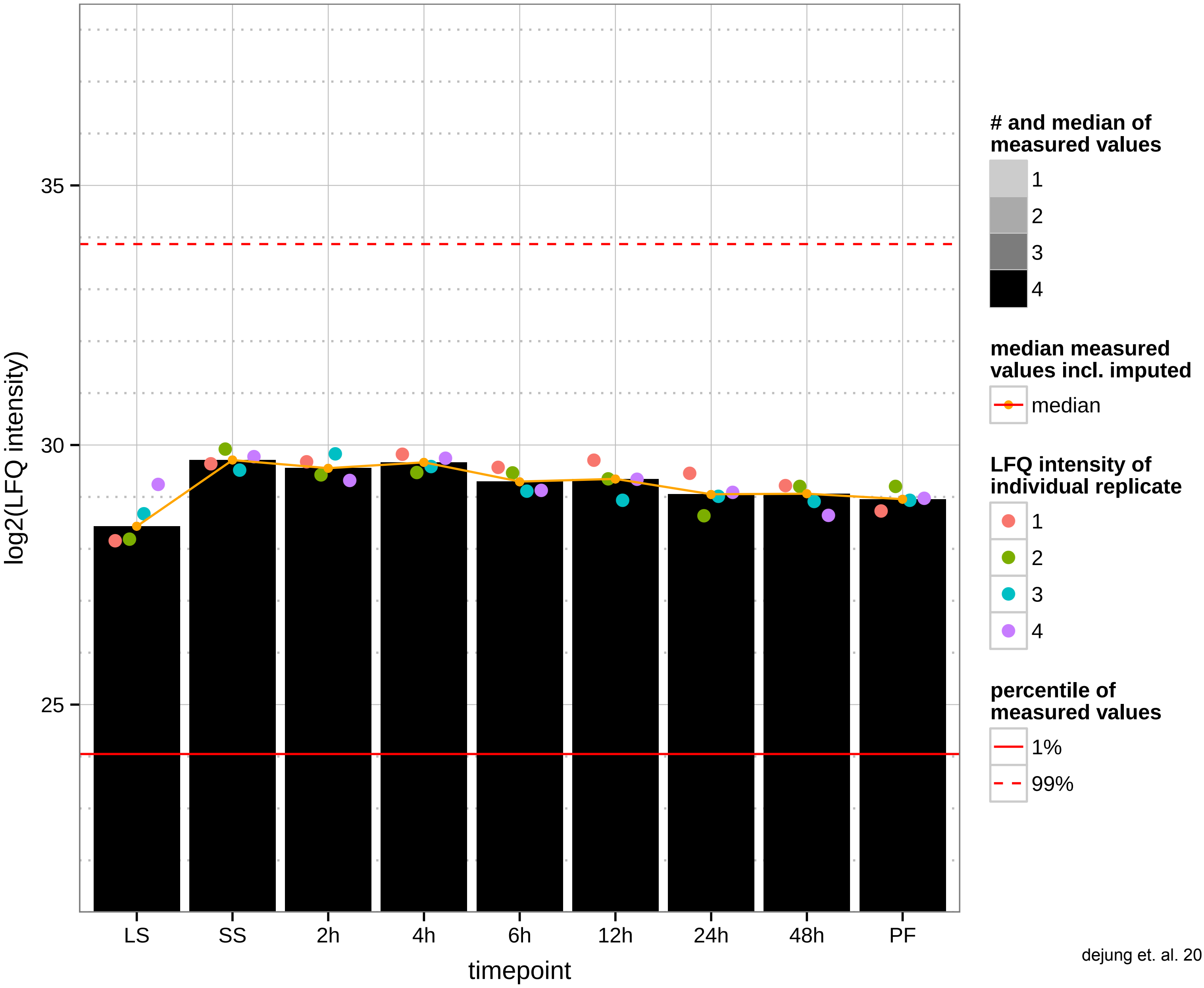
2–hydroxy–3–oxopropionate reductase, putative
Tb927.6.1570
AGOF: phosphogluconate dehydrogenase (decarboxylating) activity
AGOC: null
AGOP: pentose–phosphate shunt
PGOF: oxidoreductase activity, phosphogluconate dehydrogenase (decarboxylating) activity
PGOC: null
PGOP: oxidation–reduction process, pentose–phosphate shunt





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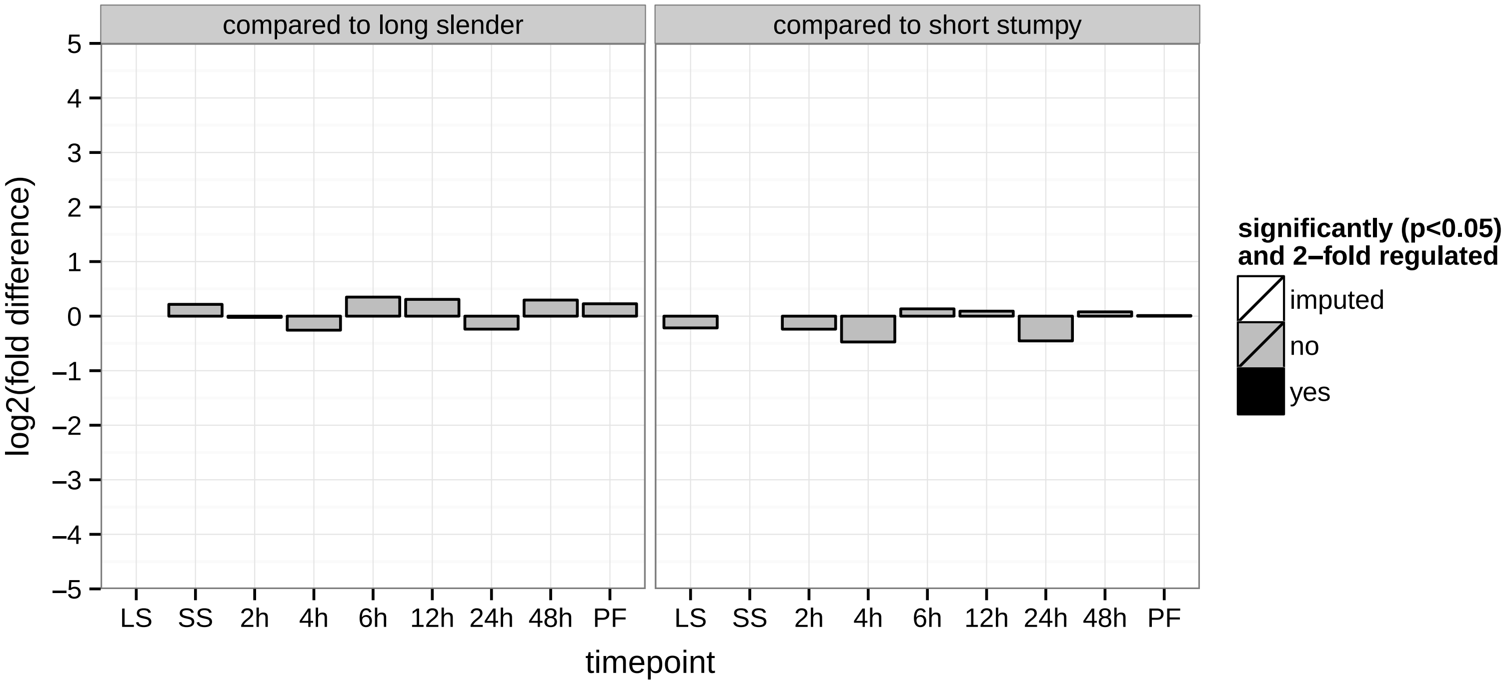
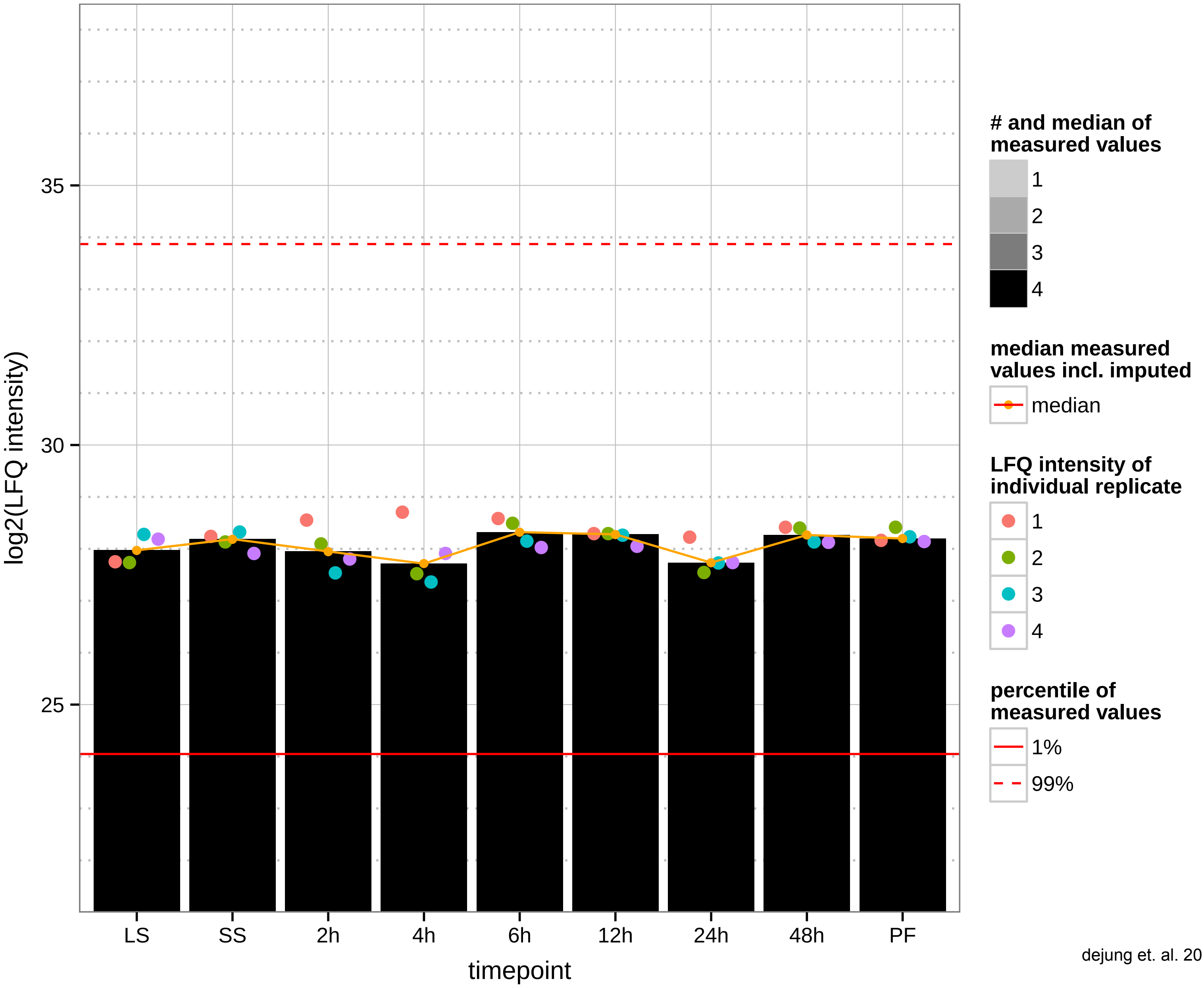
hypothetical protein, conserved
Tb927.6.1660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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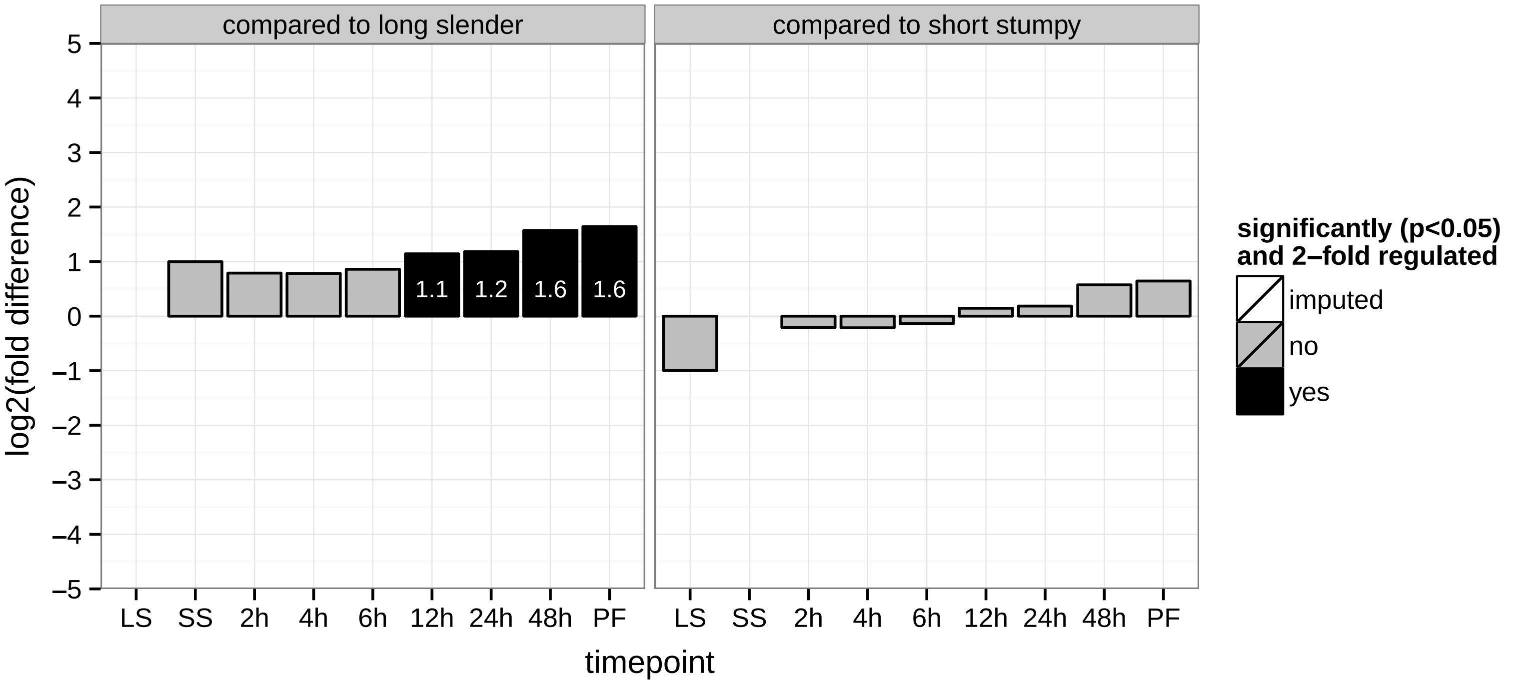
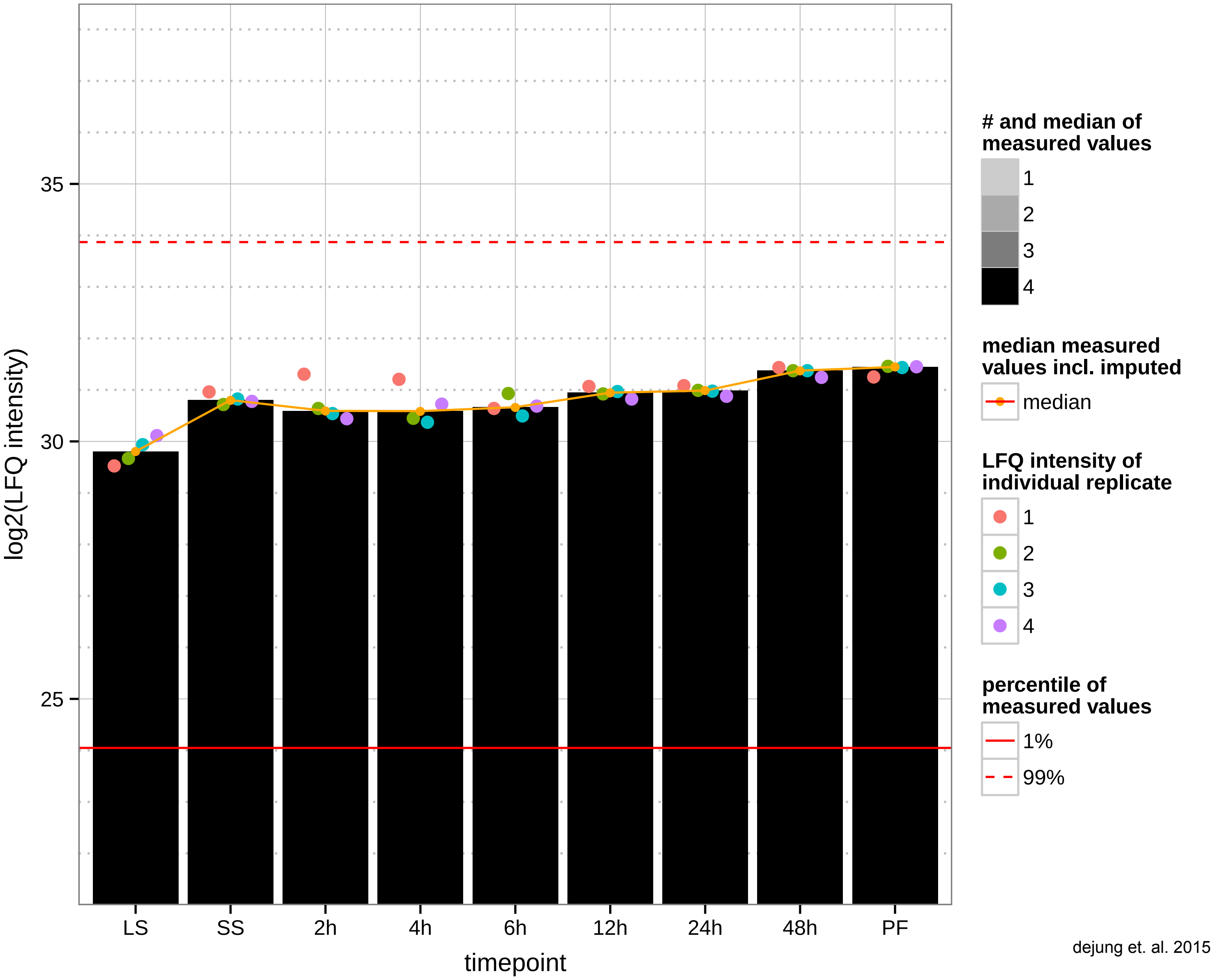
aspartyl–tRNA synthetase, putative
Tb927.6.1880
AGOF: ATP binding, aspartate–tRNA ligase activity, nucleic acid binding
AGOC: cytoplasm
AGOP: aspartyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, aspartate–tRNA ligase activity, nucleic acid binding, nucleotide binding
PGOC: cytoplasm
PGOP: aspartyl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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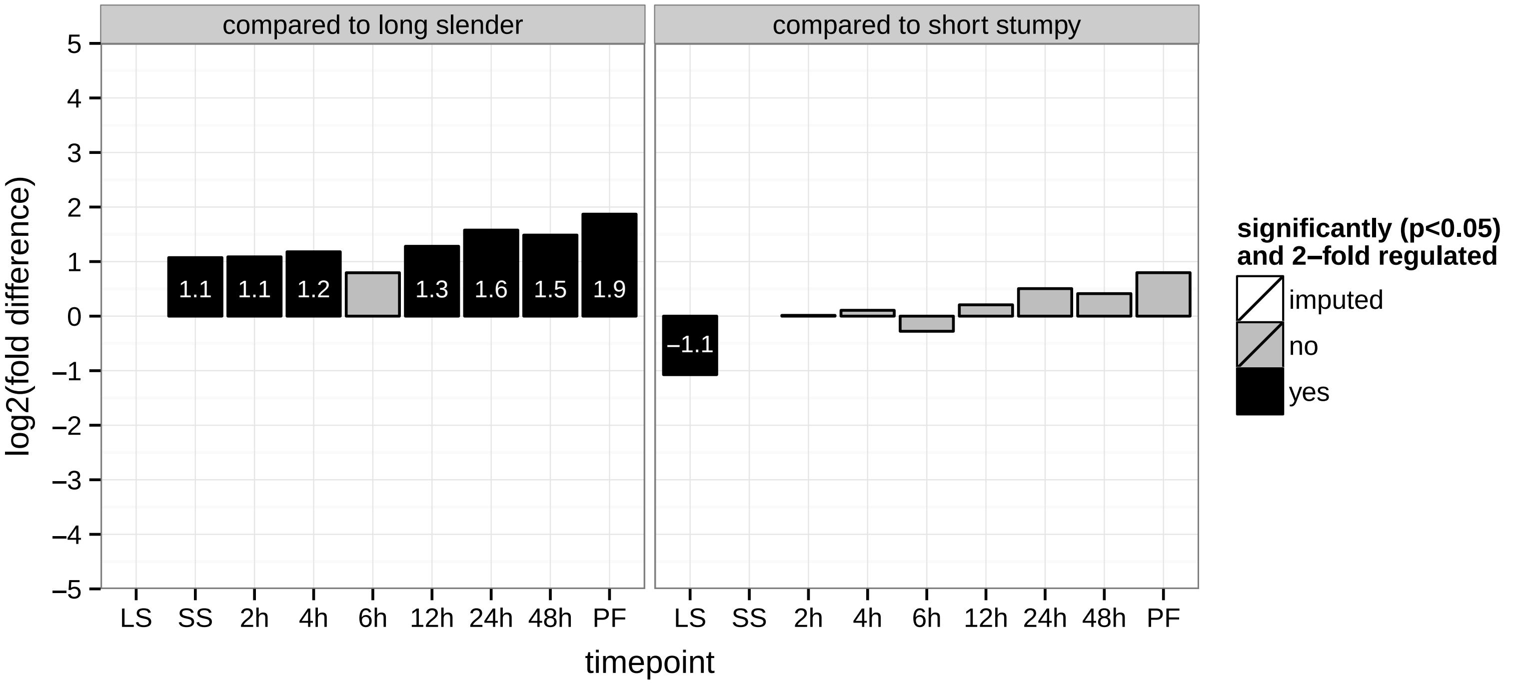
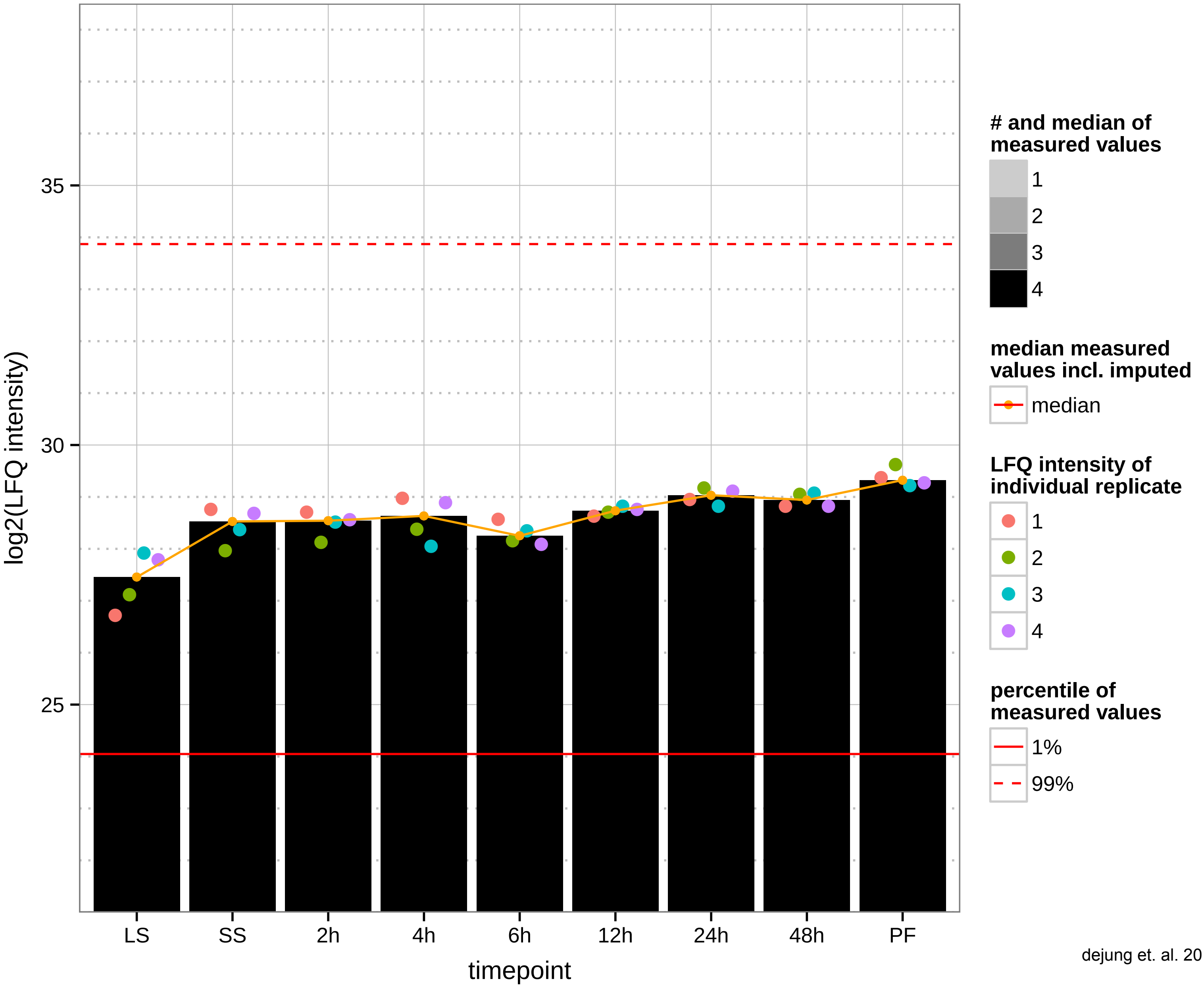
Essential nuclear protein 1, putative (enp1)
Tb927.6.1900
AGOF: snoRNA binding
AGOC: nucleolus
AGOP: maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA), rRNA processing
PGOF: null
PGOC: null
PGOP: null





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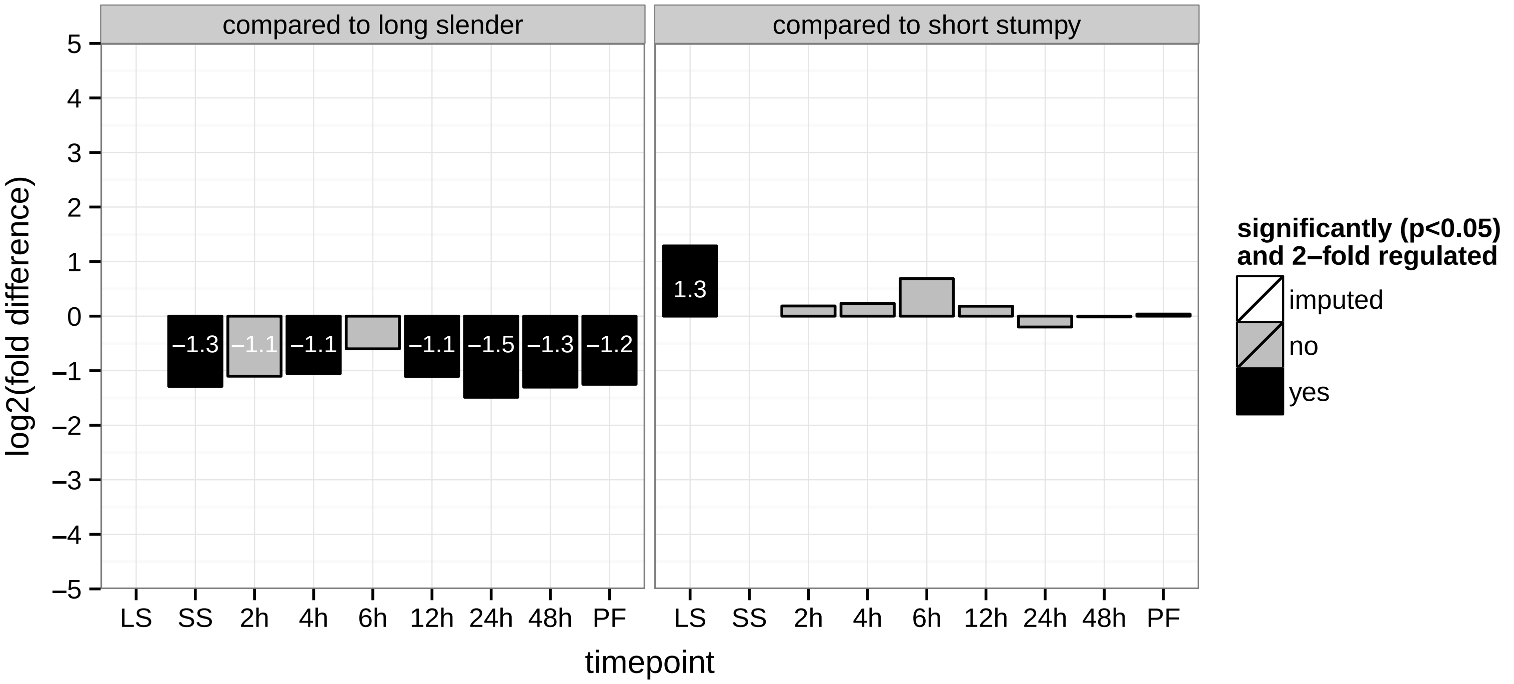
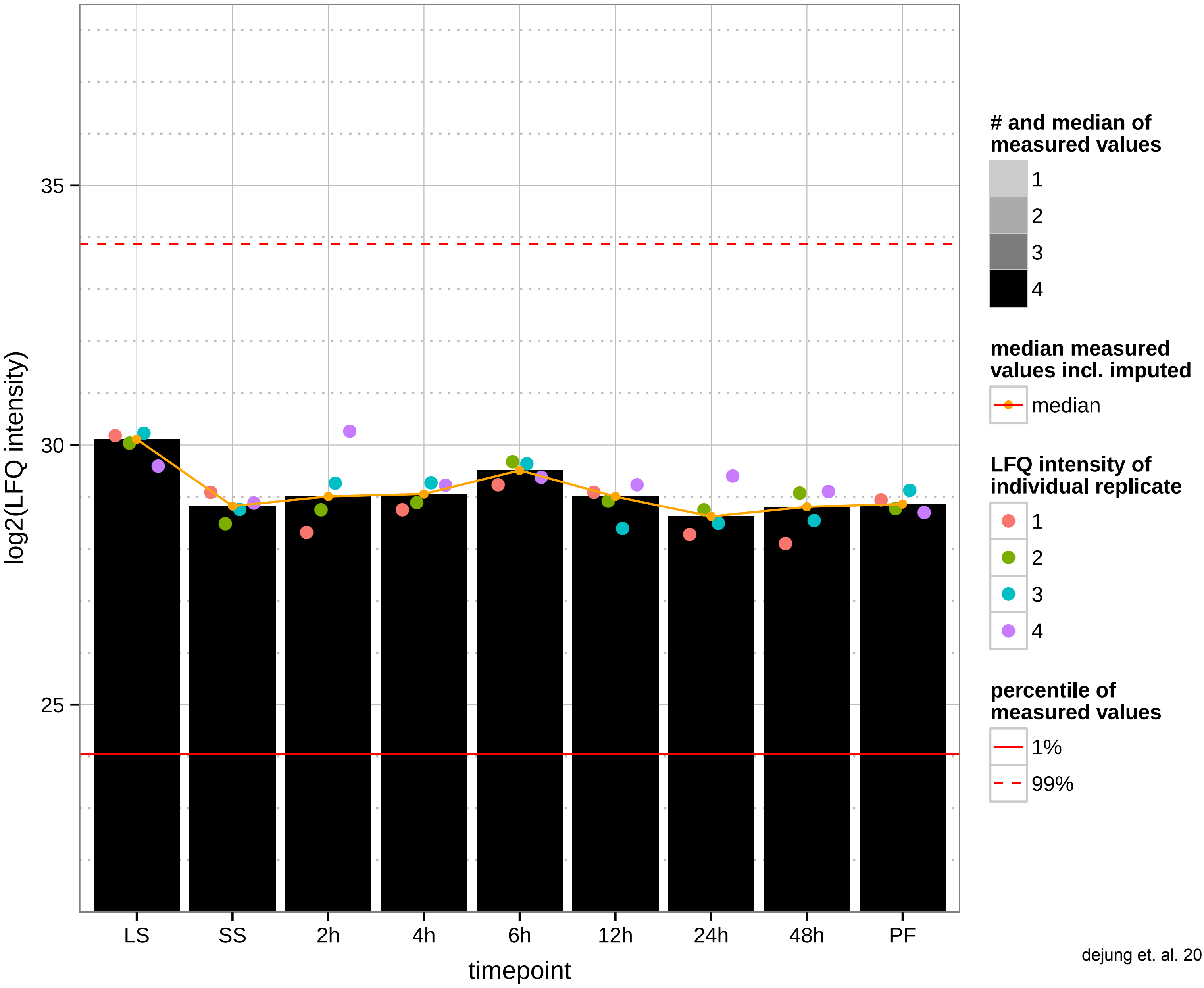
hypothetical protein, conserved
Tb927.6.1920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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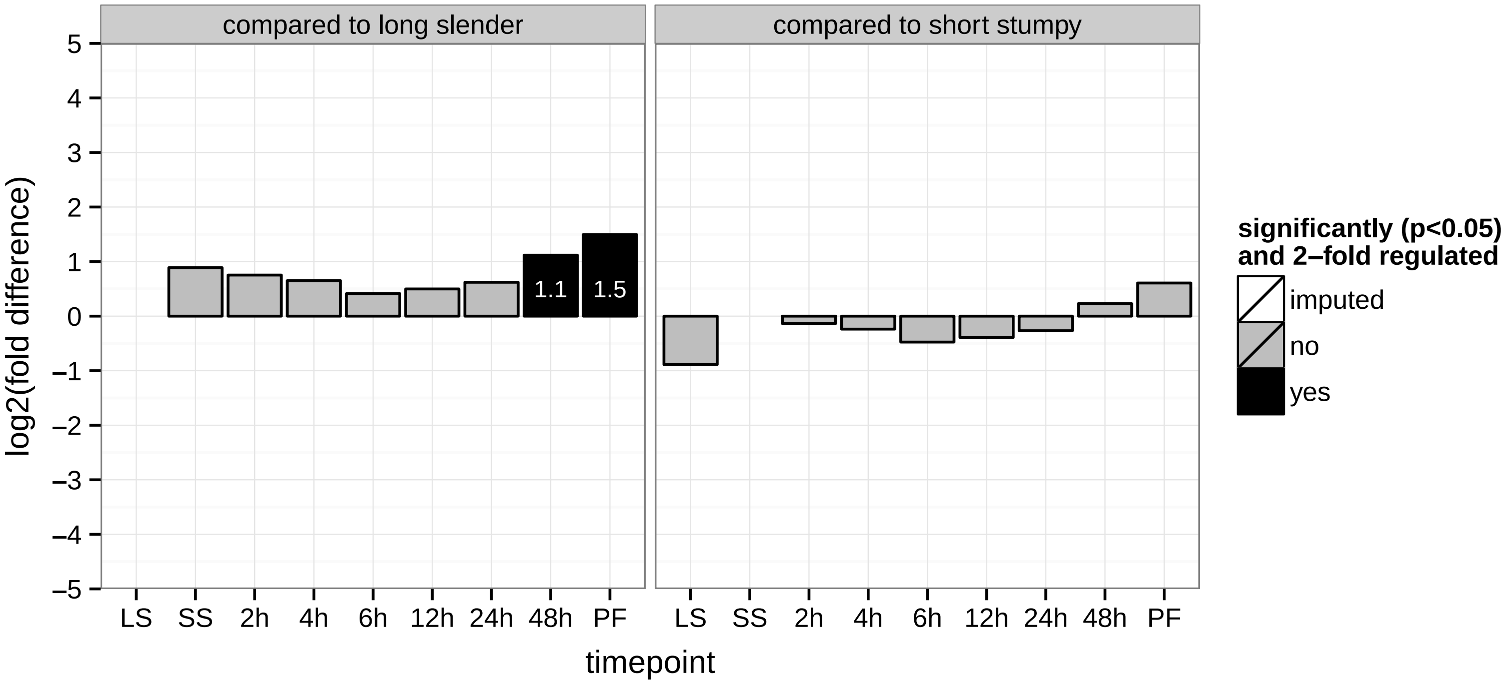
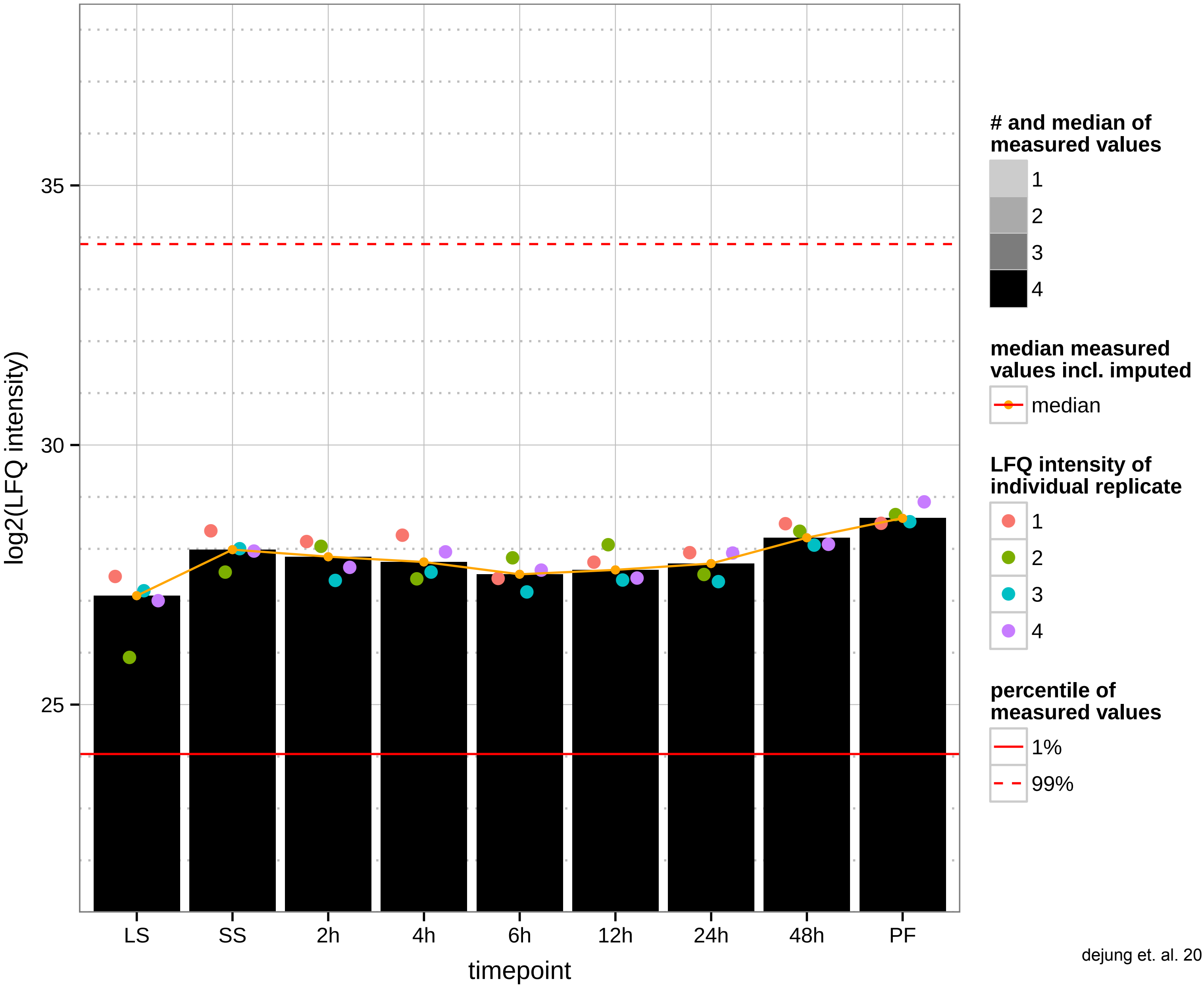
hypothetical protein, conserved
Tb927.6.1950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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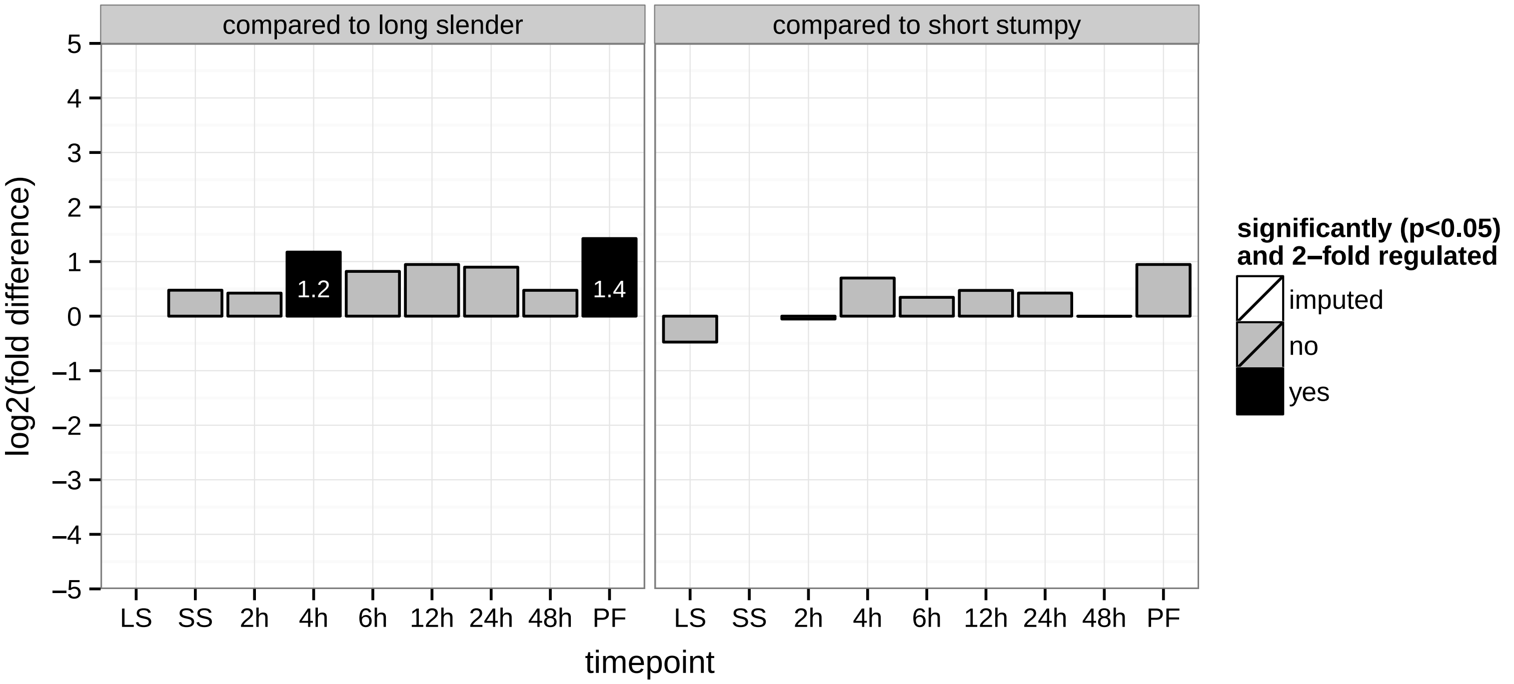
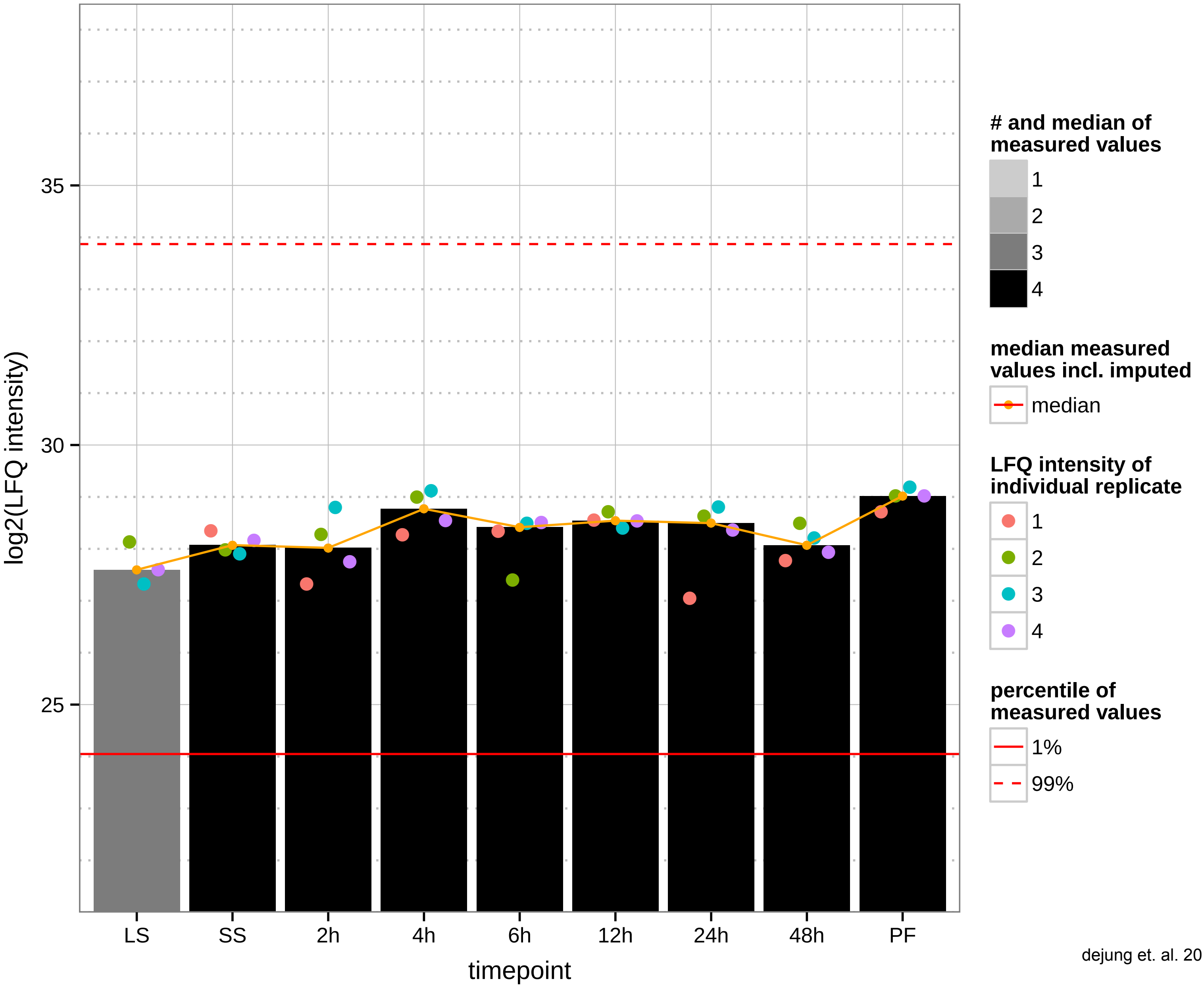
NA, hypothetical protein, conserved
Tb927.6.1990
AGOF: NA, null
AGOC: NA, null
AGOP: NA, null
PGOF: NA, null
PGOC: NA, null
PGOP: NA, null





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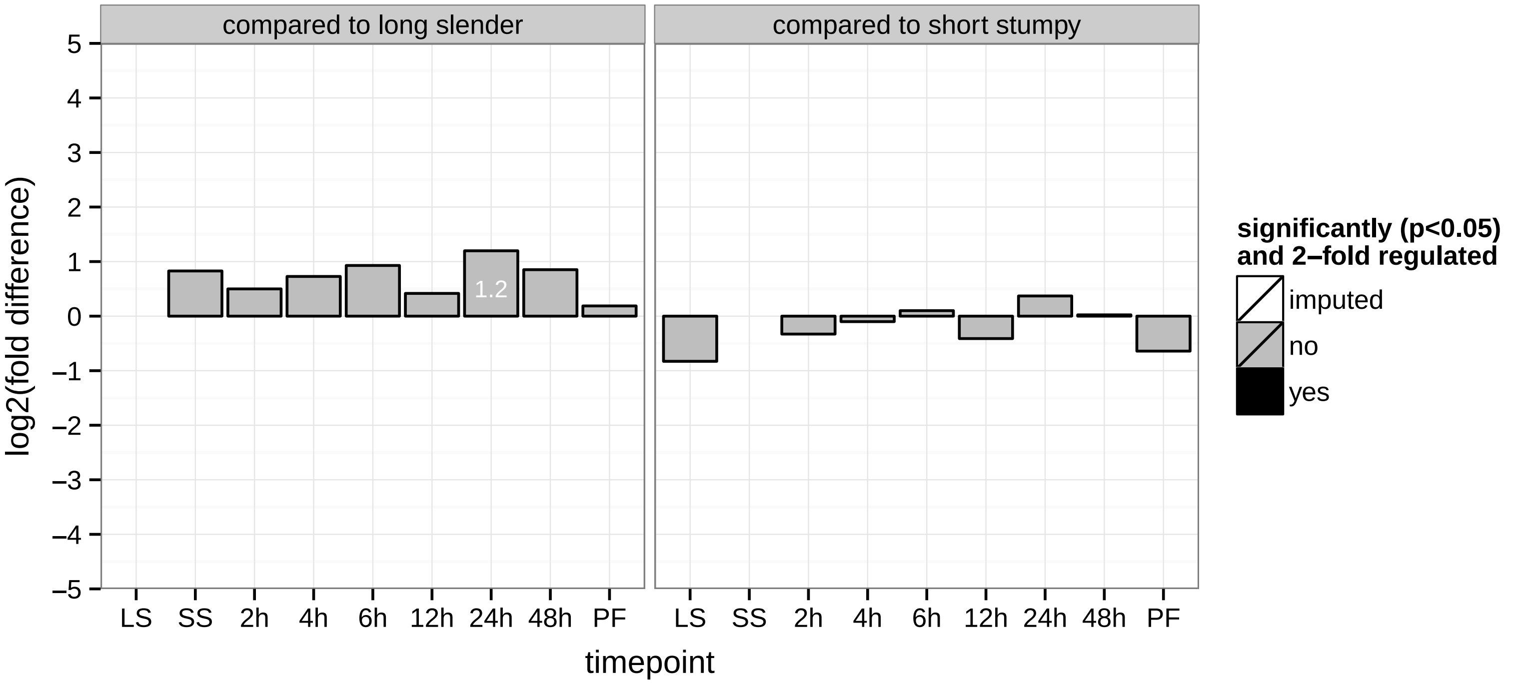
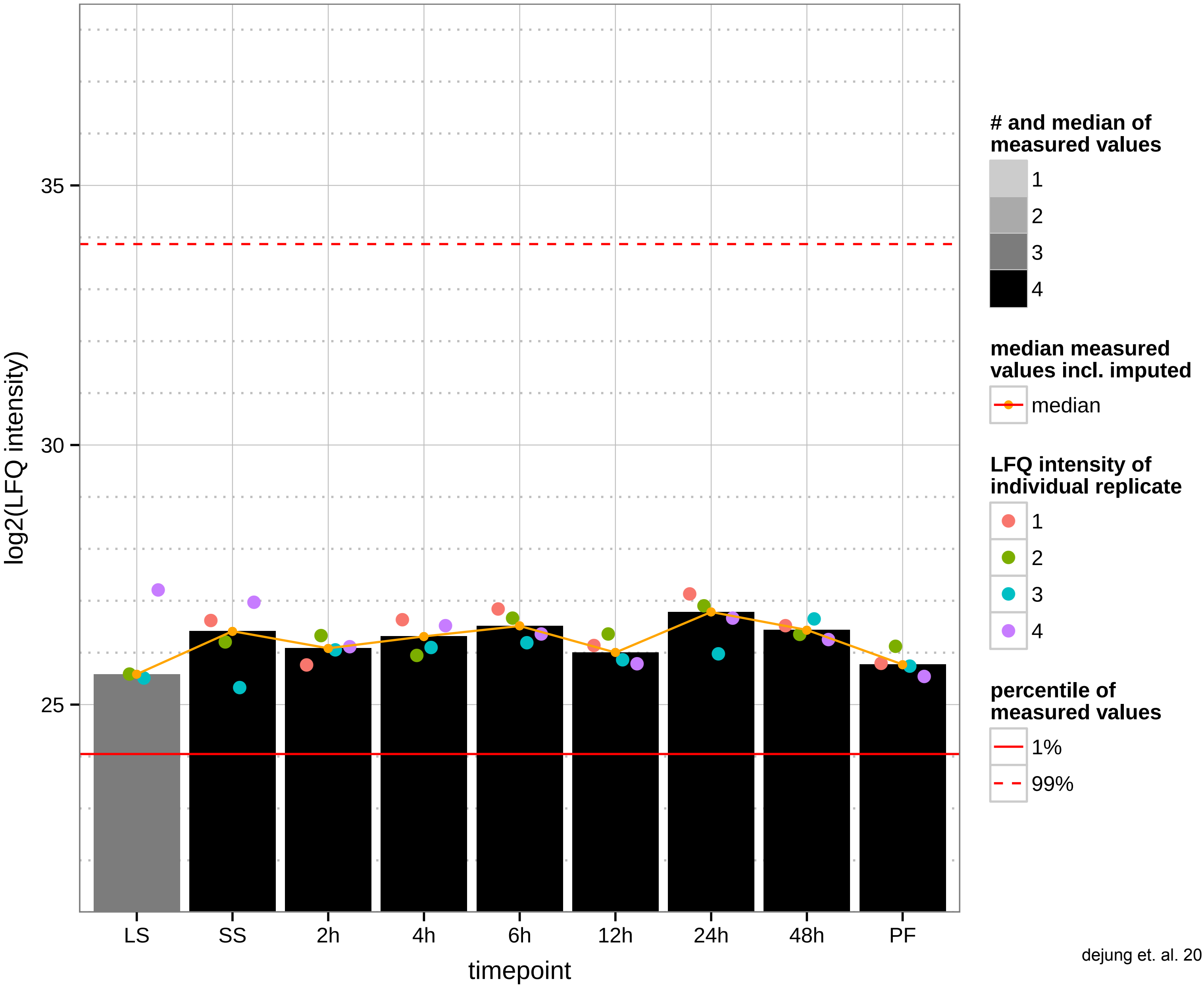
spliceosome–associated protein, putative
Tb927.6.2000
AGOF: null
AGOC: nucleus
AGOP: mRNA processing
PGOF: null
PGOC: nucleus
PGOP: null





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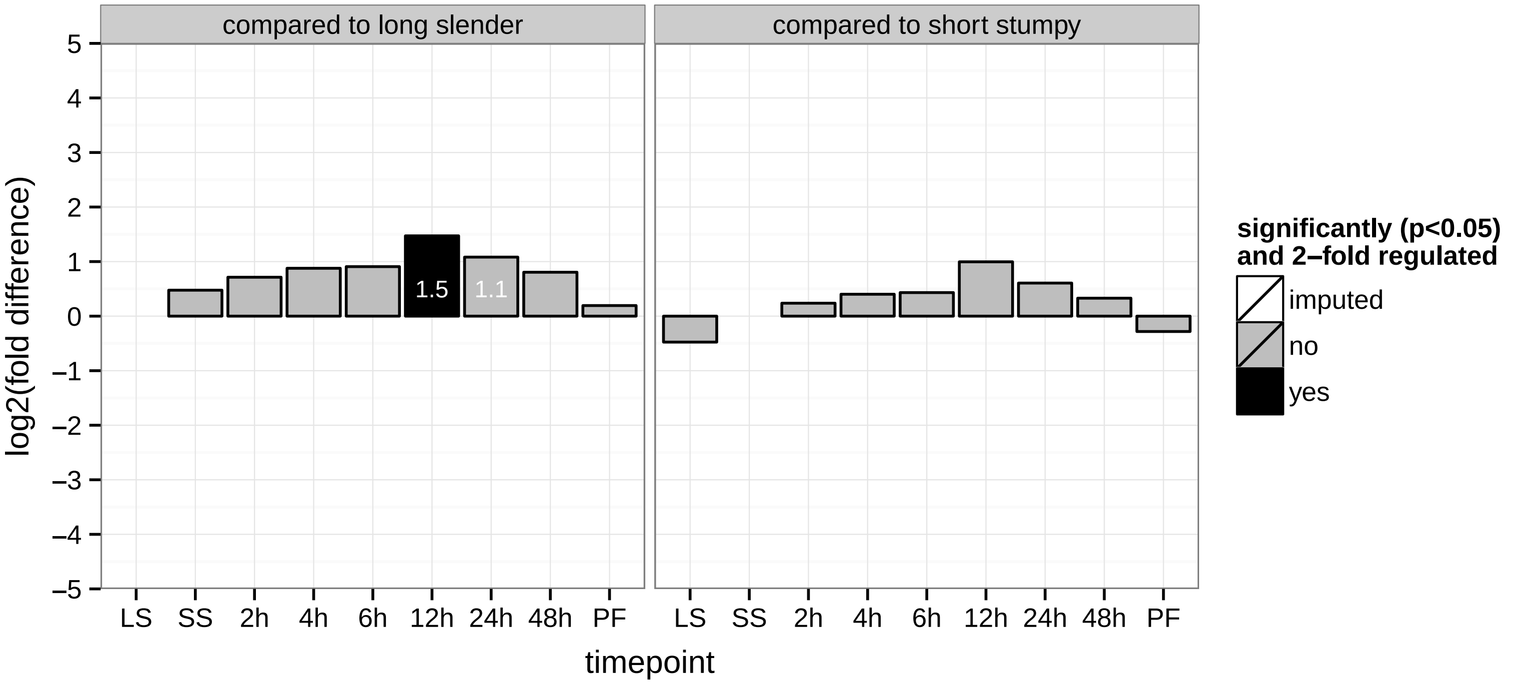
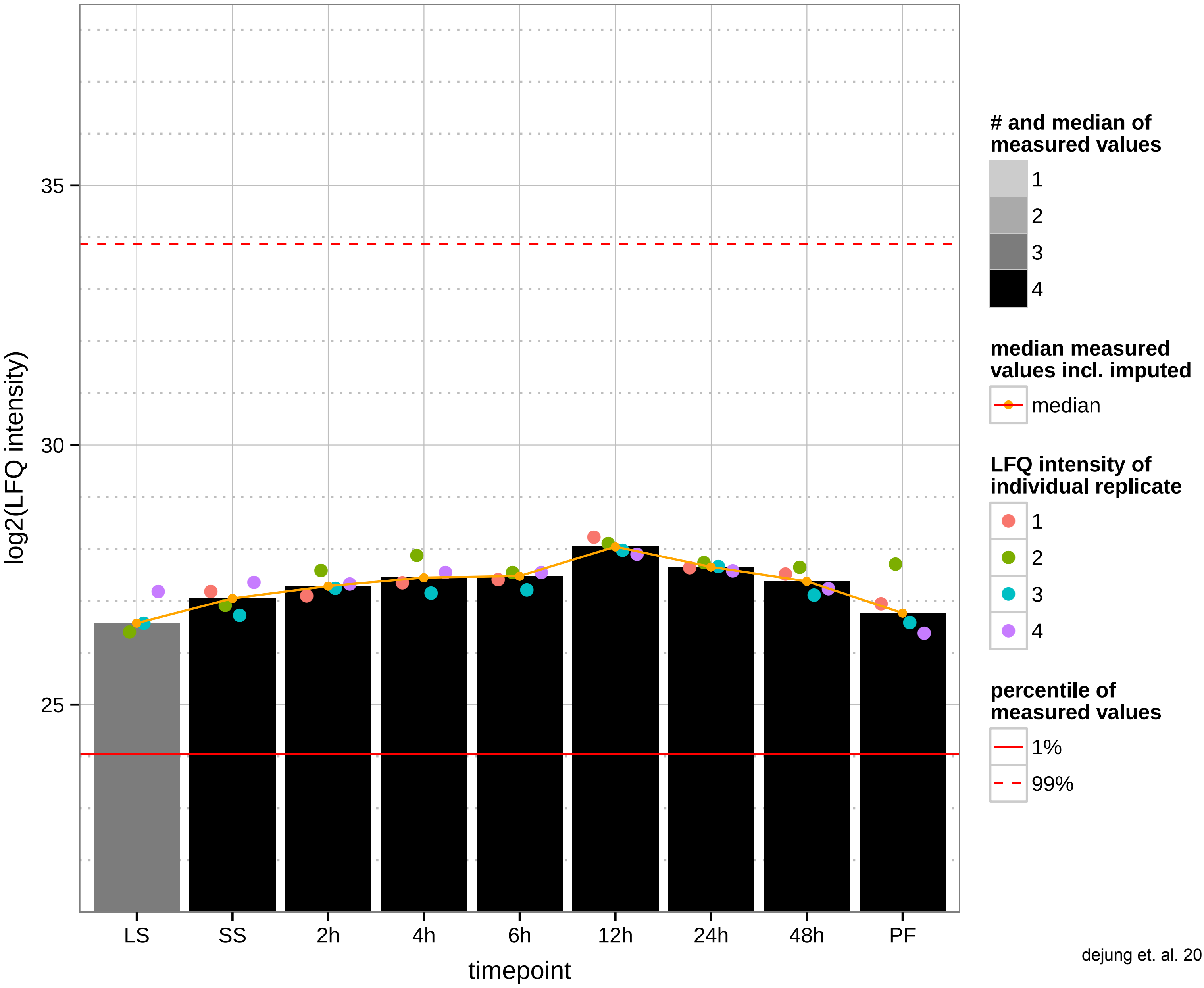
ribosome biogenesis regulatory protein (RRS1), putative
Tb927.6.2050
AGOF: null
AGOC: nucleus
AGOP: ribosome biogenesis
PGOF: null
PGOC: nucleus
PGOP: ribosome biogenesis





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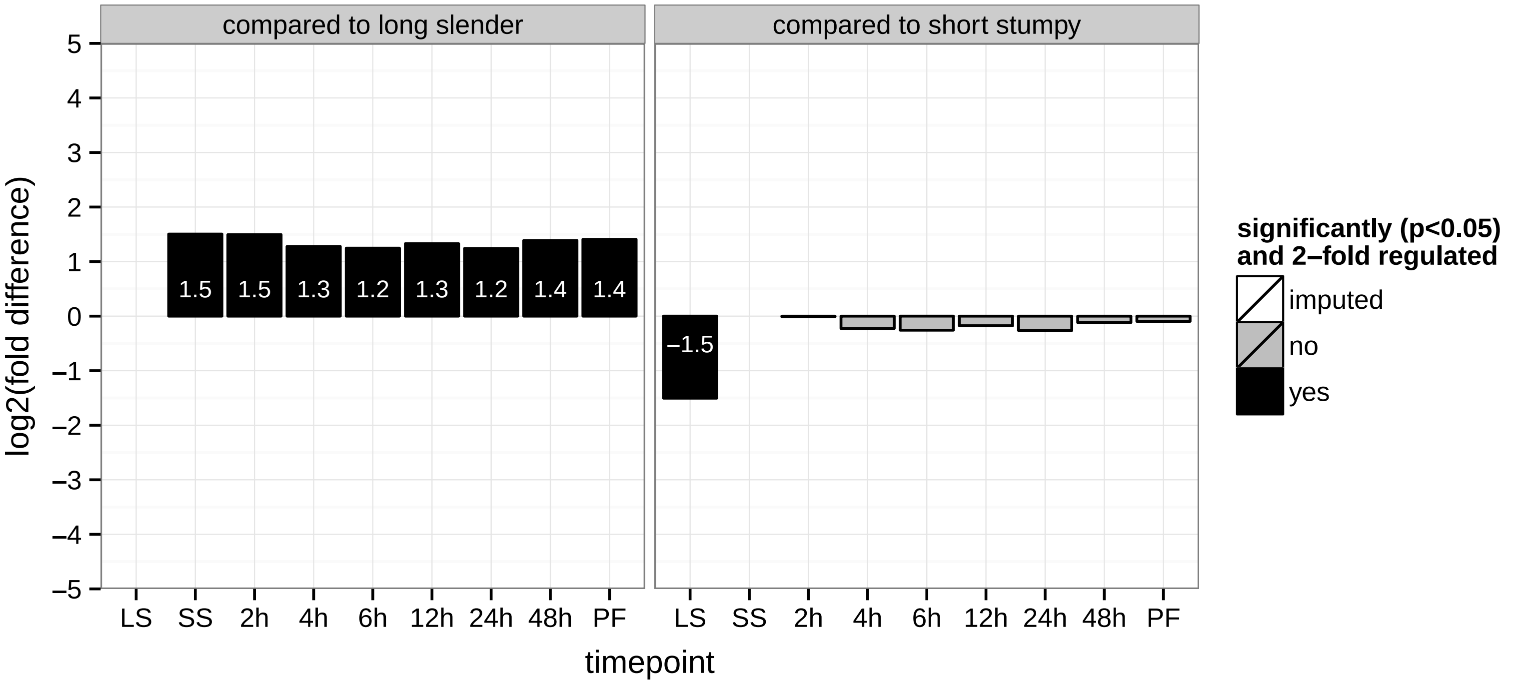
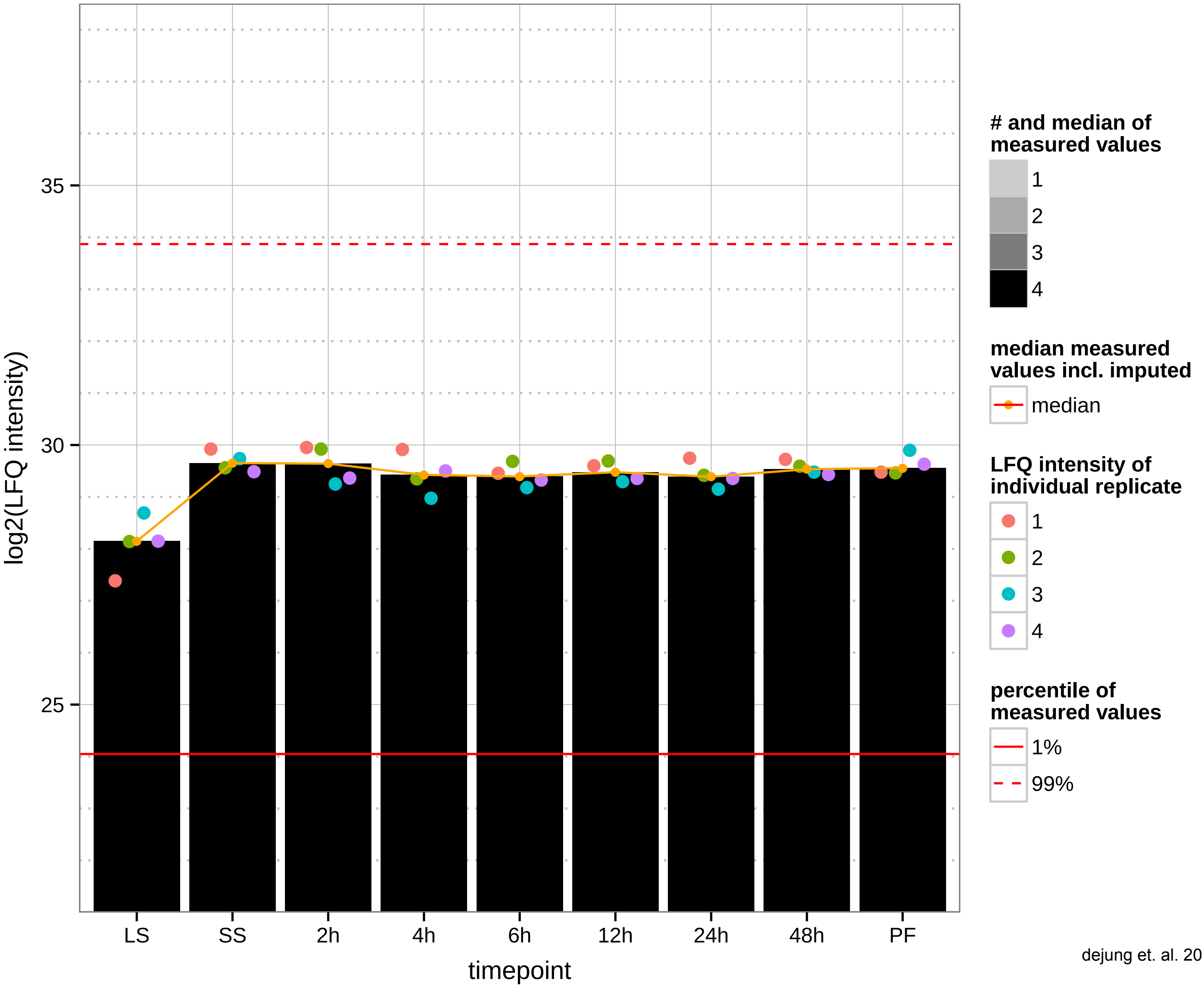
histidyl–tRNA synthetase
Tb927.6.2060
AGOF: null
AGOC: cytoplasm
AGOP: translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, histidine–tRNA ligase activity, nucleotide binding
PGOC: cytoplasm
PGOP: histidyl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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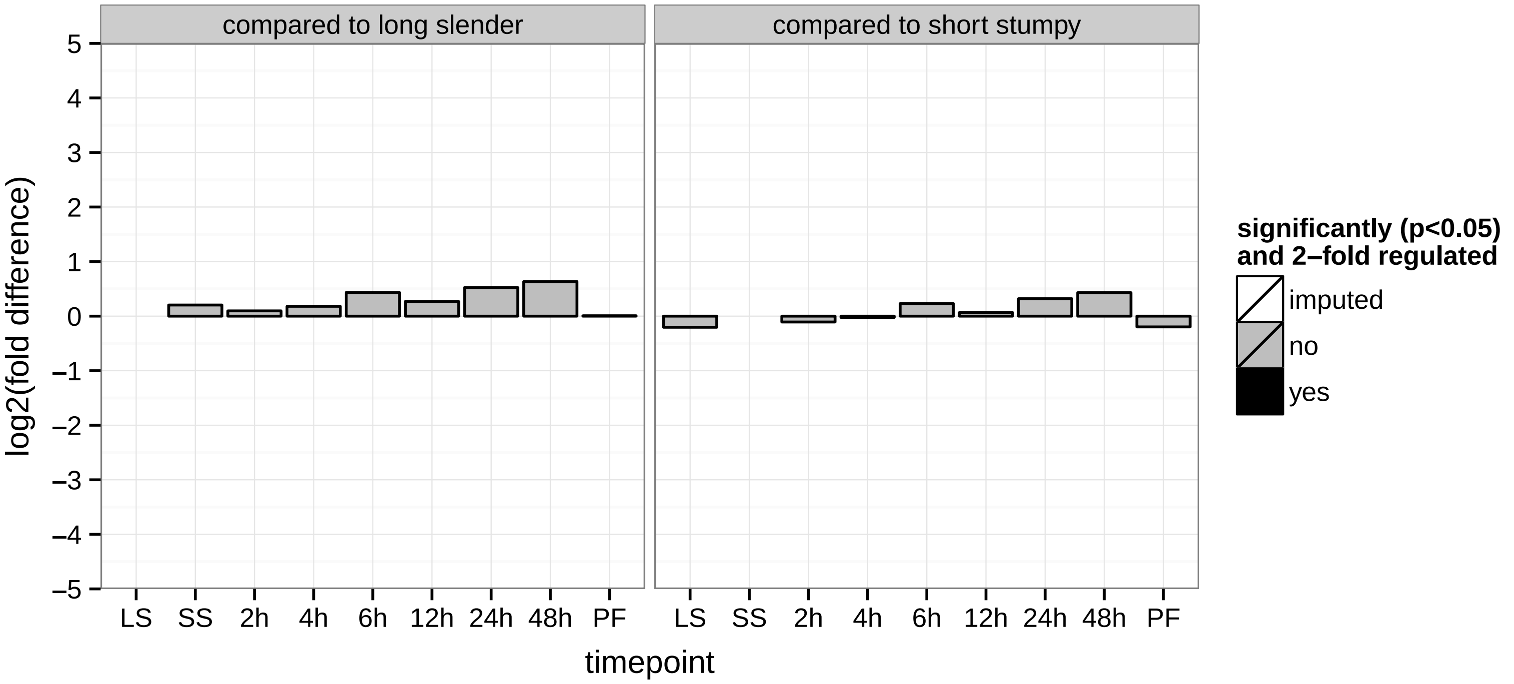
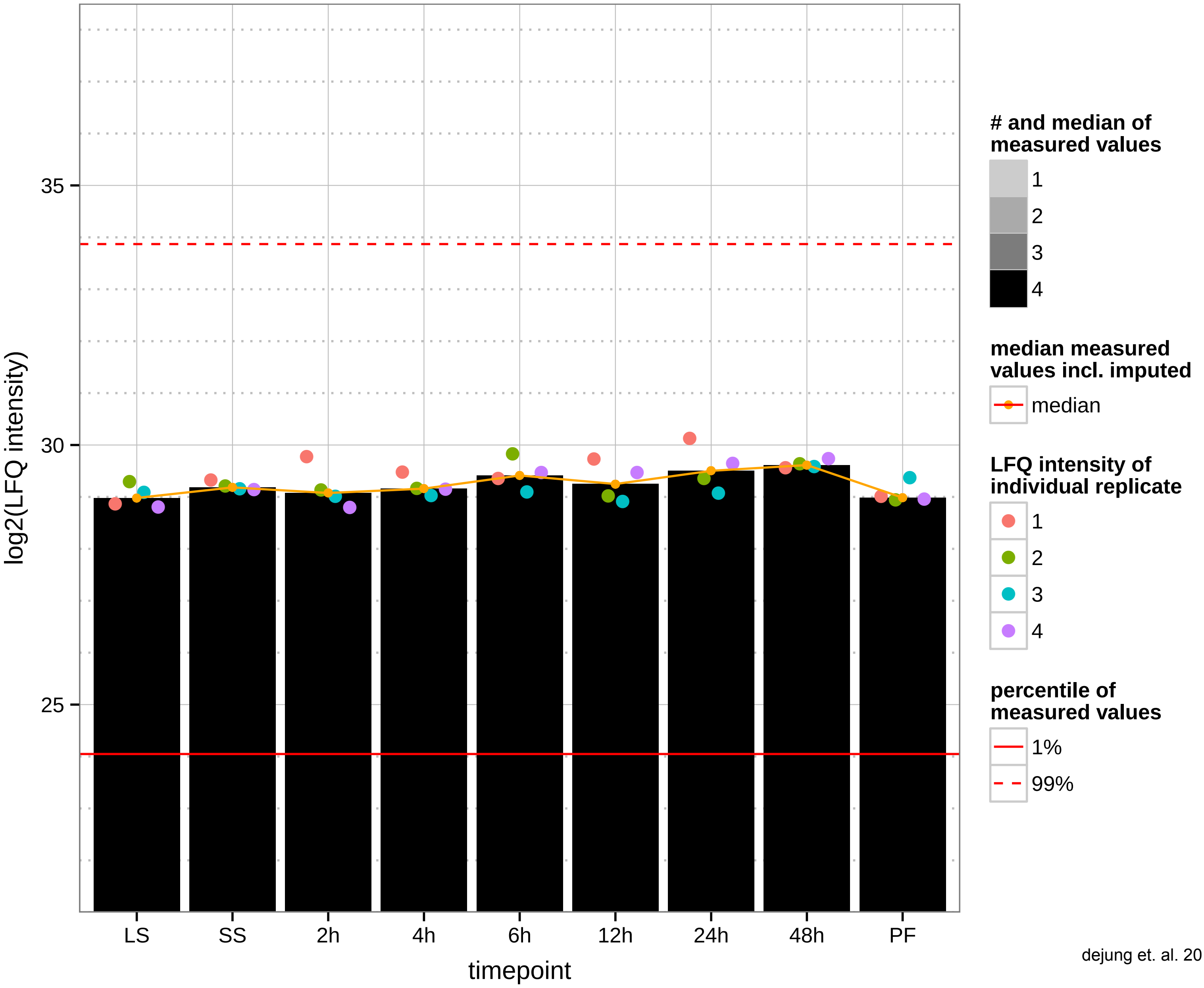
hypothetical protein, conserved
Tb927.6.2090
AGOF: phospholipase C activity
AGOC: null
AGOP: intracellular signal transduction, lipid metabolic process
PGOF: phospholipase C activity, phosphoric diester hydrolase activity
PGOC: null
PGOP: intracellular signal transduction, lipid metabolic process





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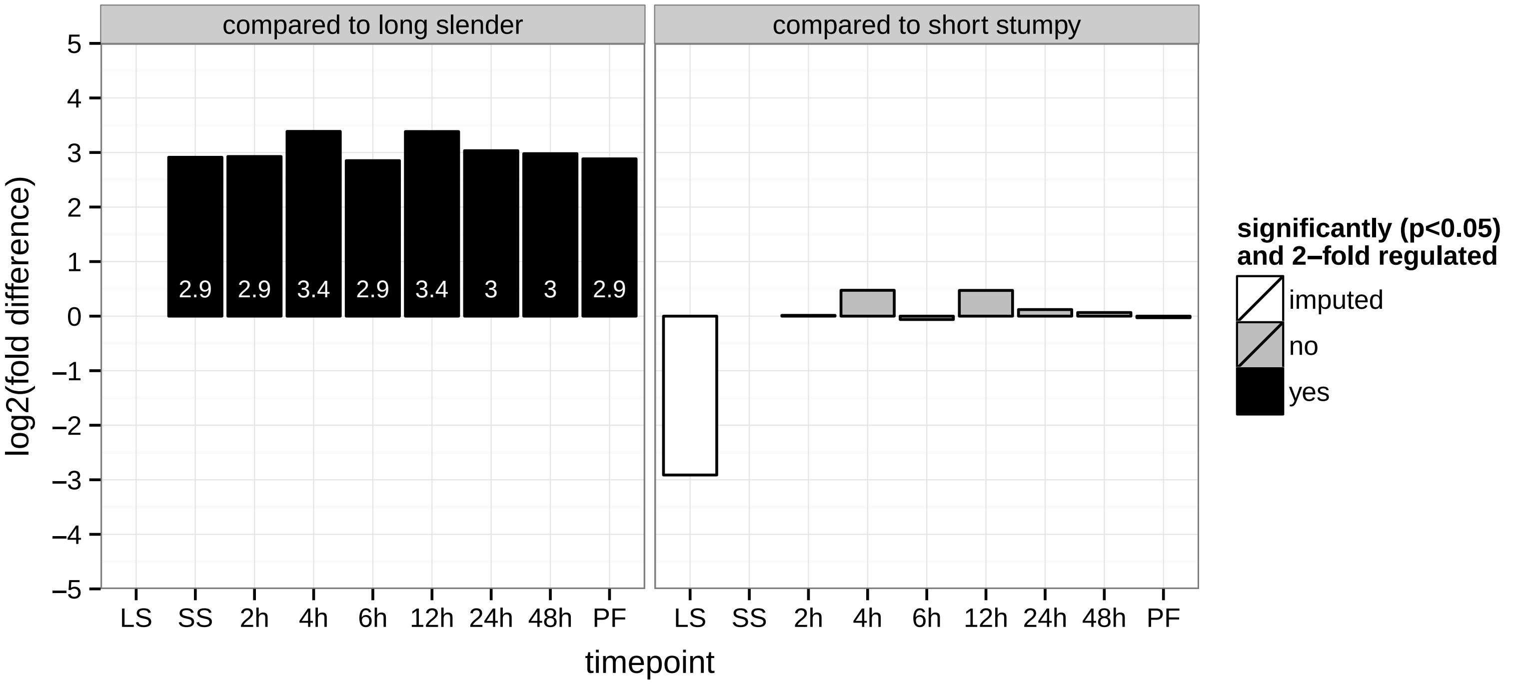
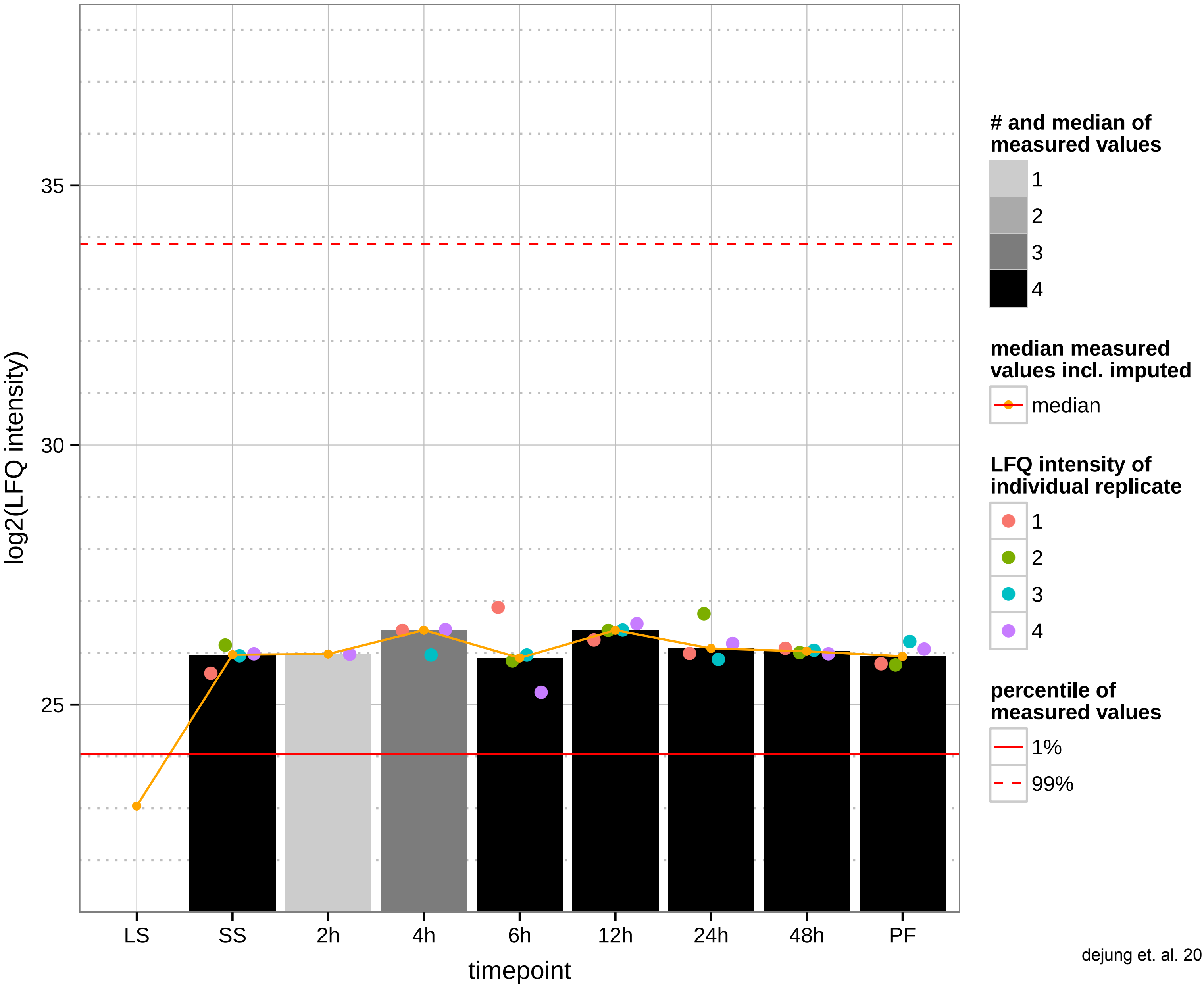
nuclear movement protein, putative, NUDC–like protein
Tb927.6.2130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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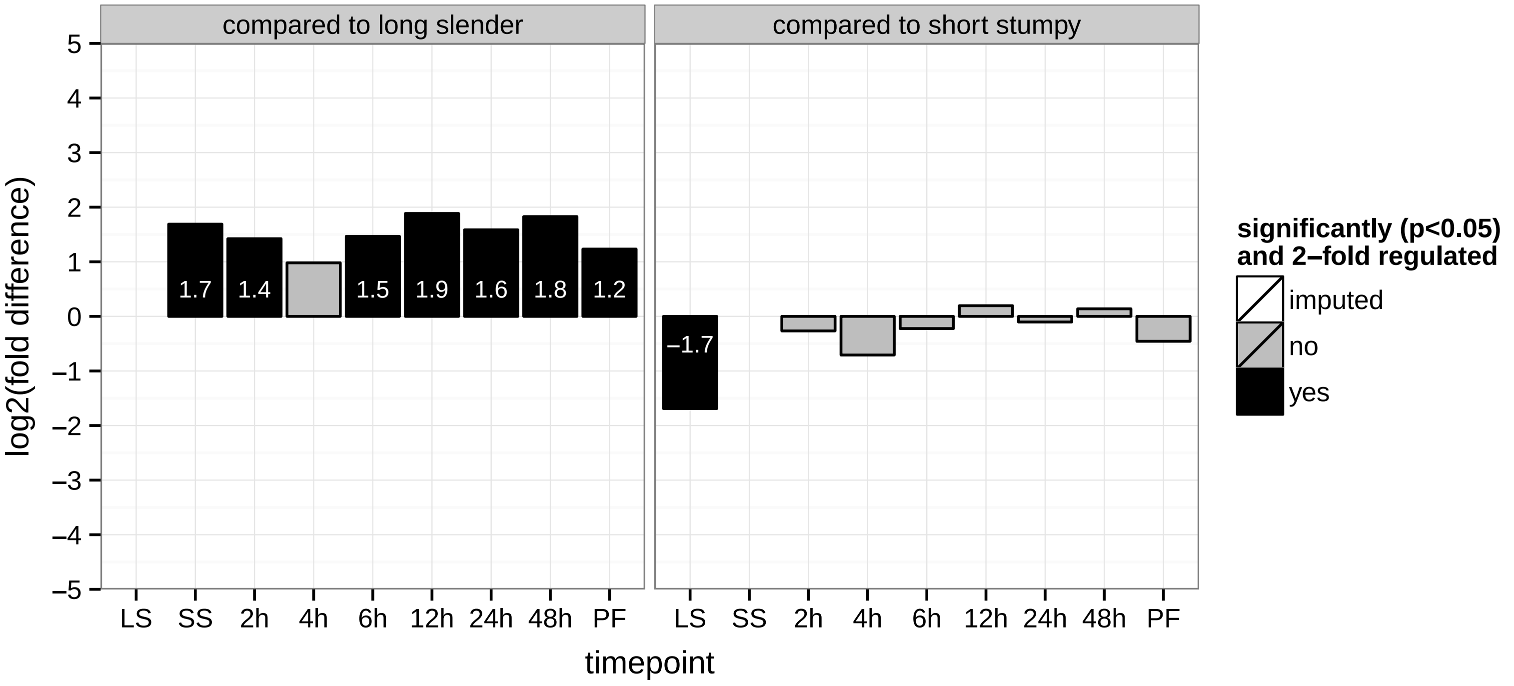
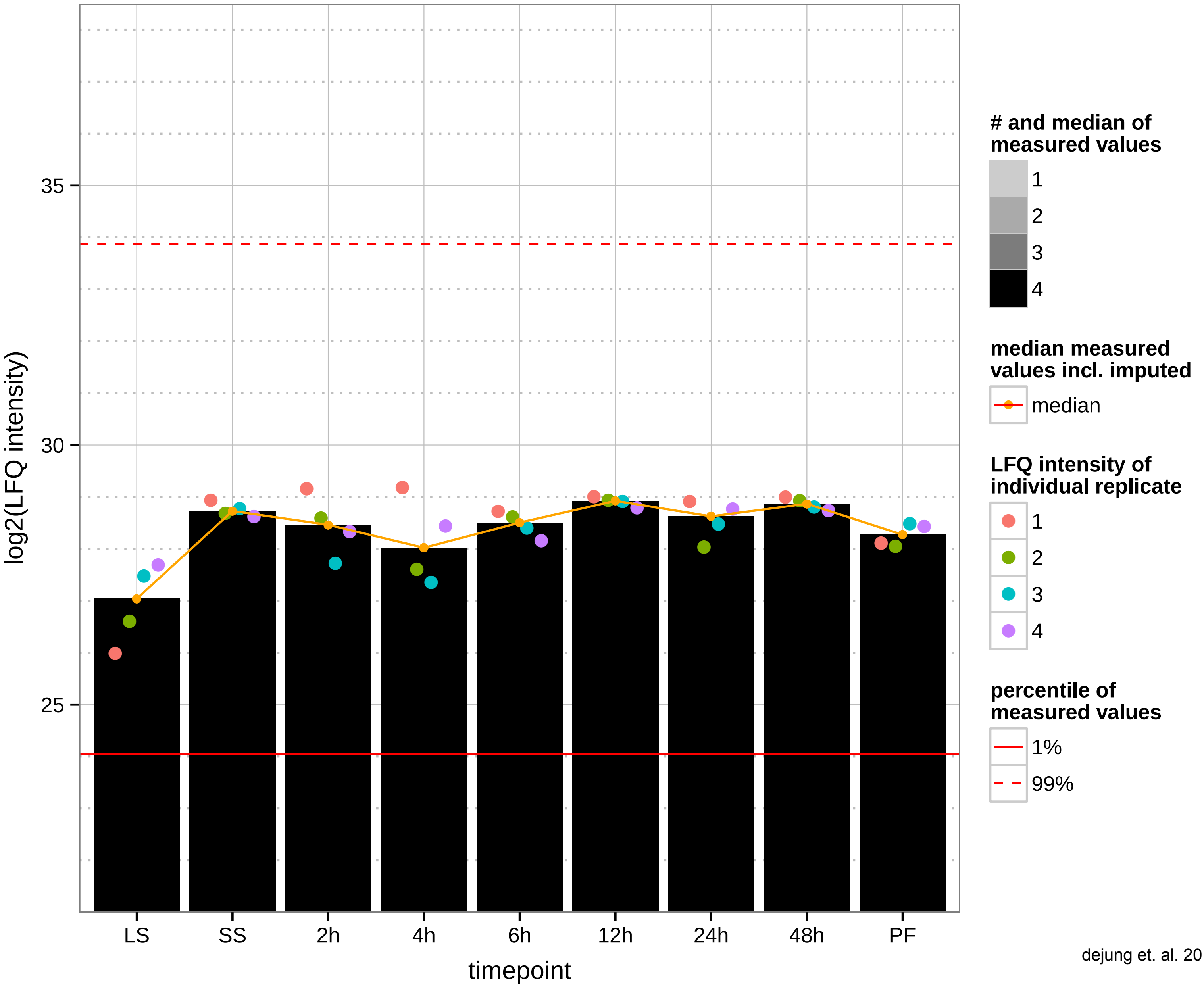
hypothetical protein, conserved
Tb927.6.2210
AGOF: null
AGOC: null
AGOP: null
PGOF: binding, protein binding
PGOC: null
PGOP: null





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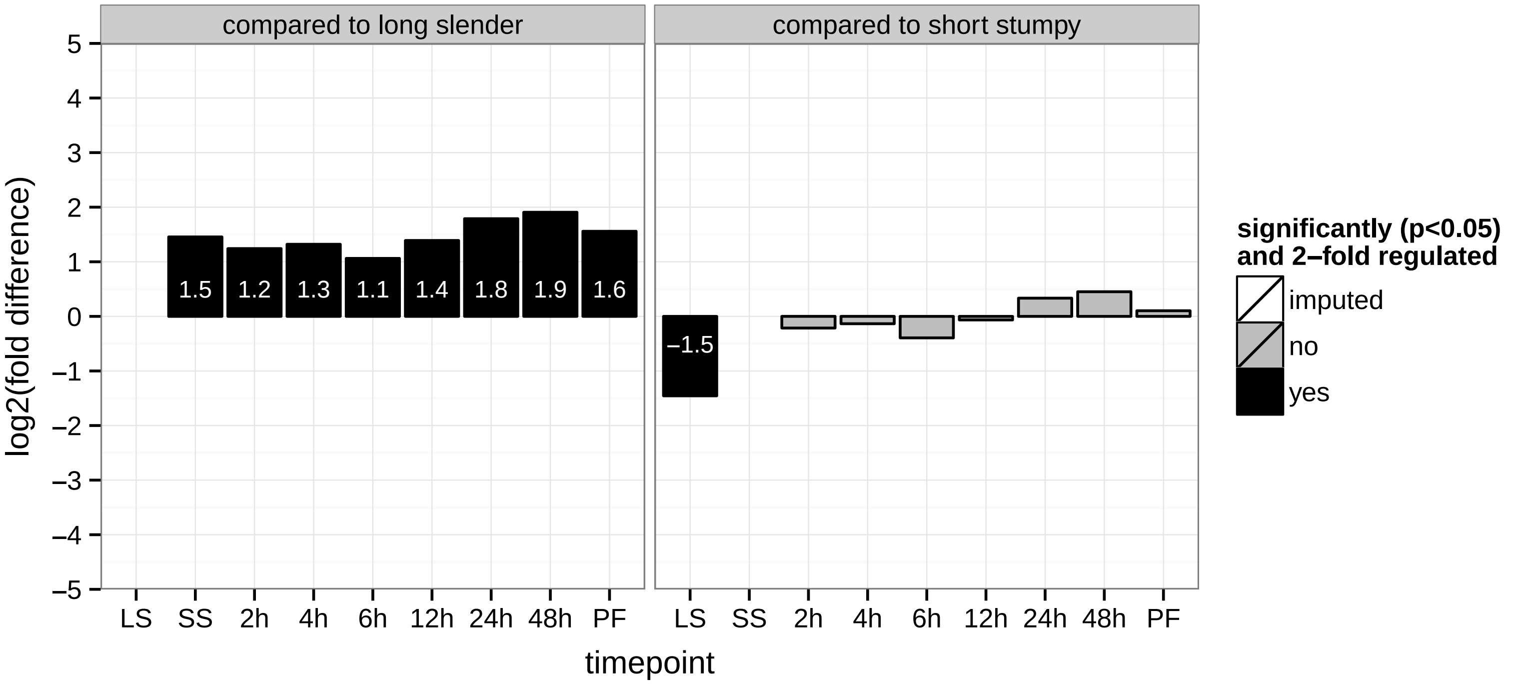
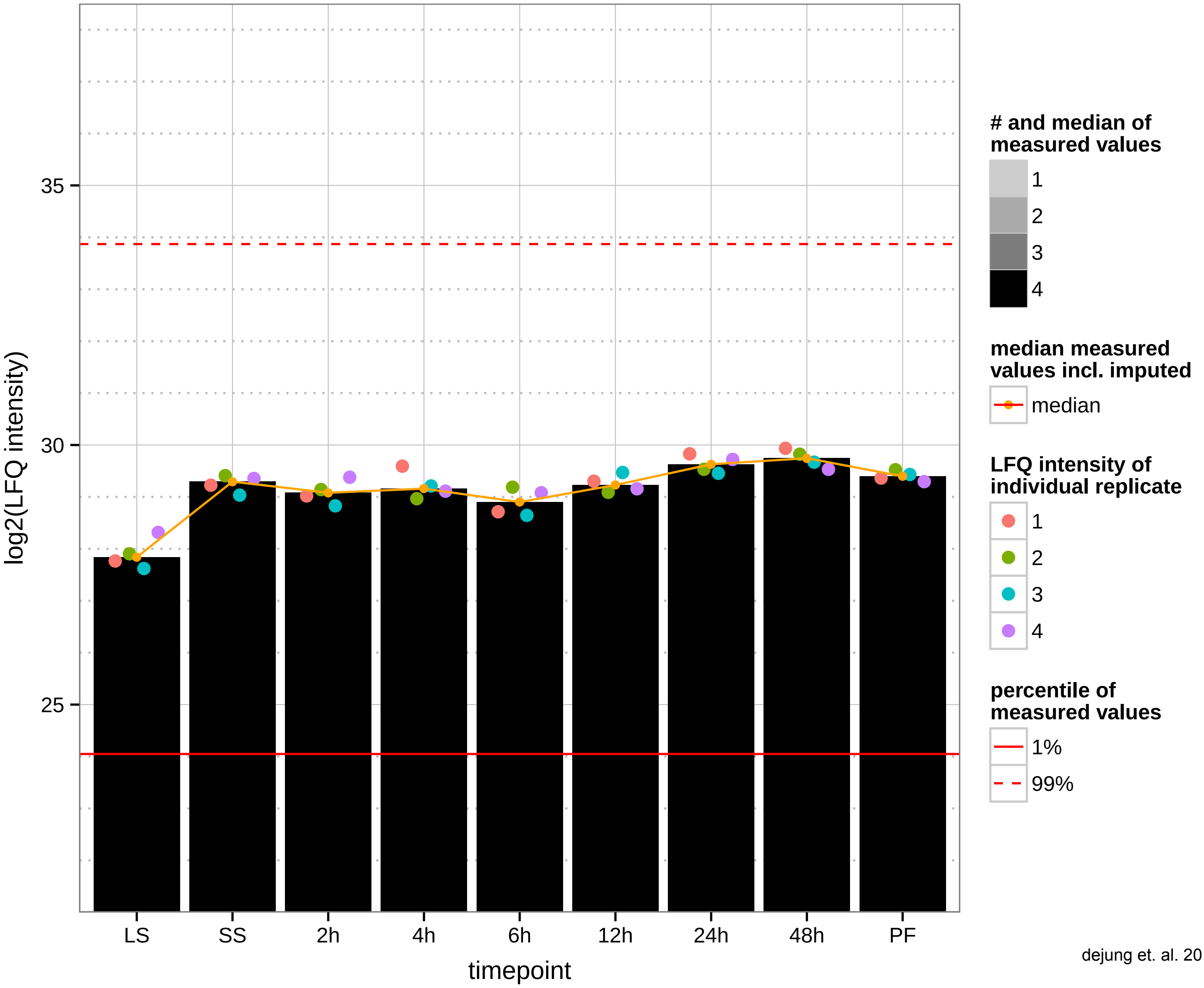
RGG protein
Tb927.6.2230
AGOF: RNA binding
AGOC: mitochondrion
AGOP: RNA biosynthetic process
PGOF: null
PGOC: null
PGOP: null





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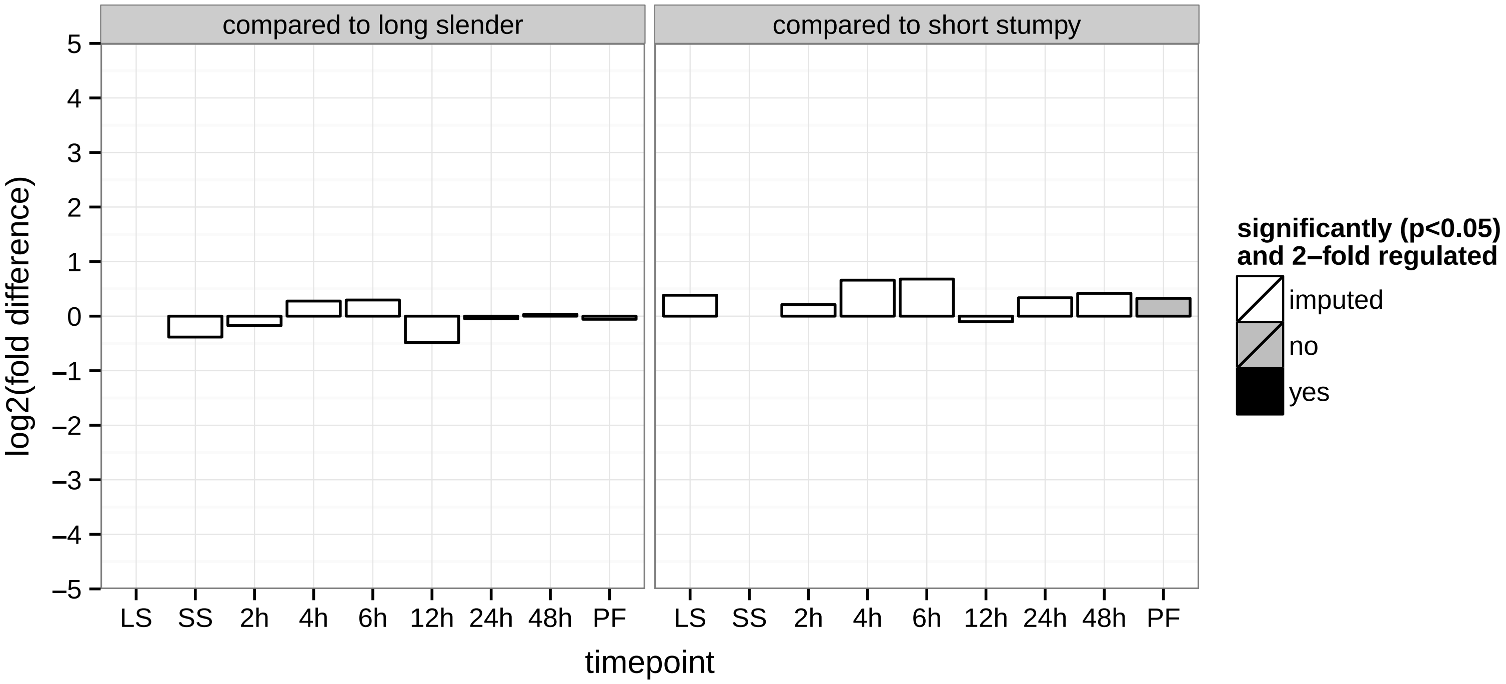
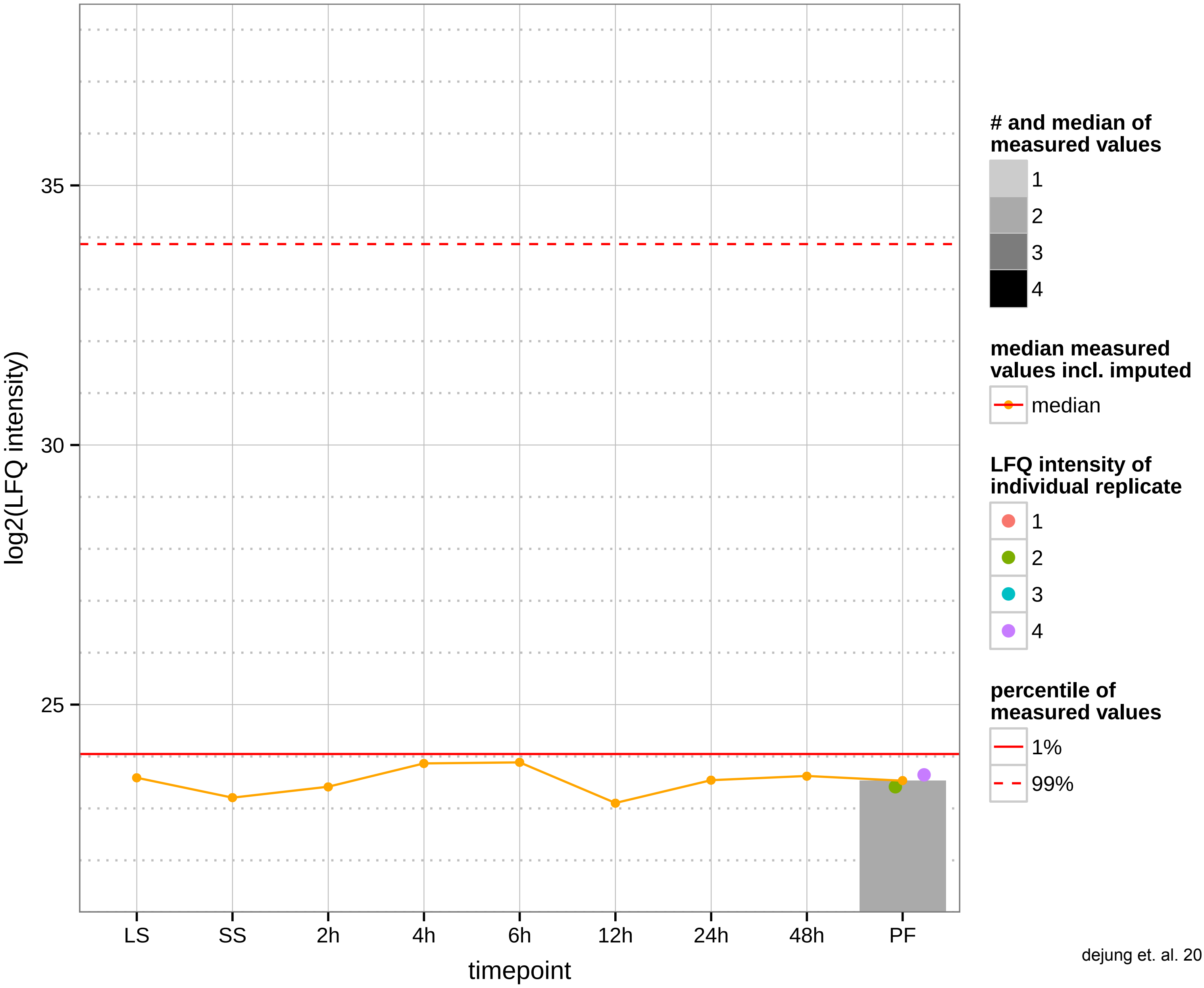
hypothetical protein, conserved
Tb927.6.2350;Tb927.6.2290
AGOF: null
AGOC: mitochondrion, null
AGOP: null
PGOF: GTP binding, null
PGOC: null
PGOP: null





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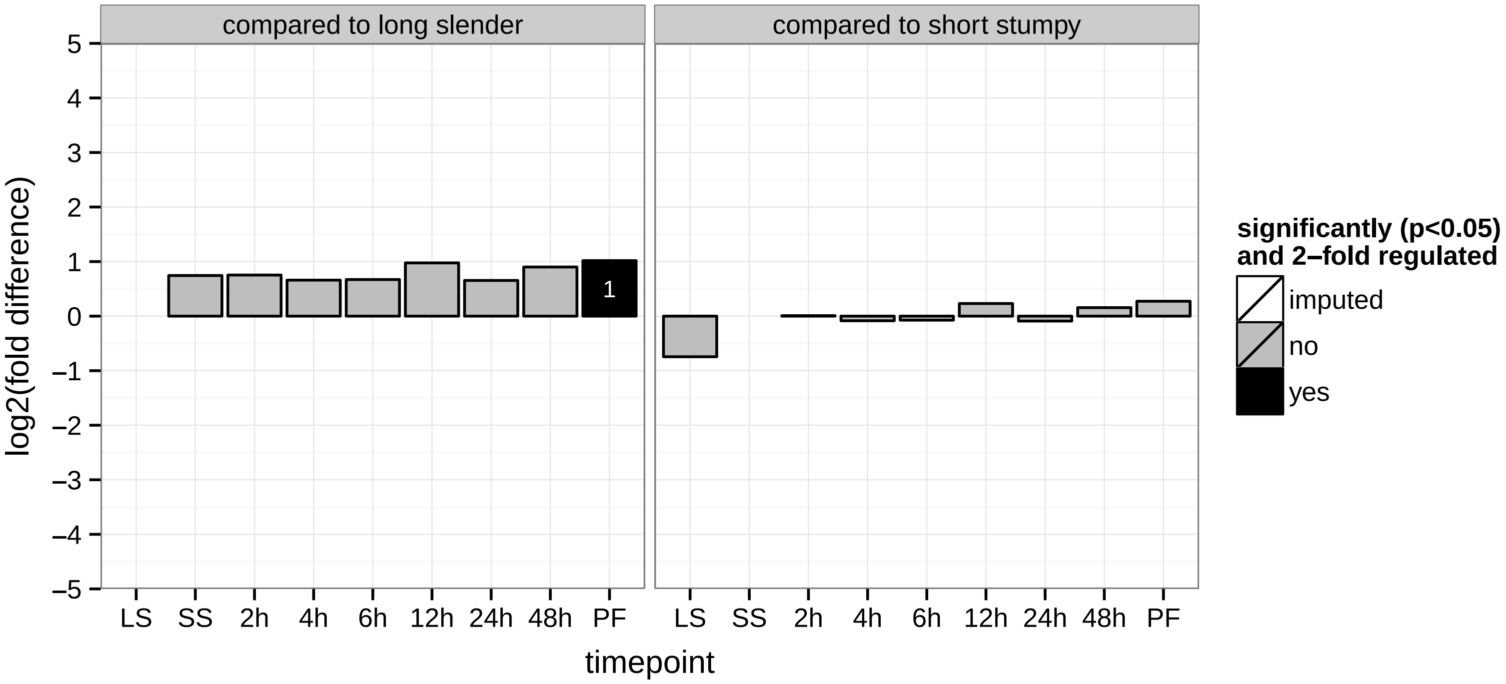
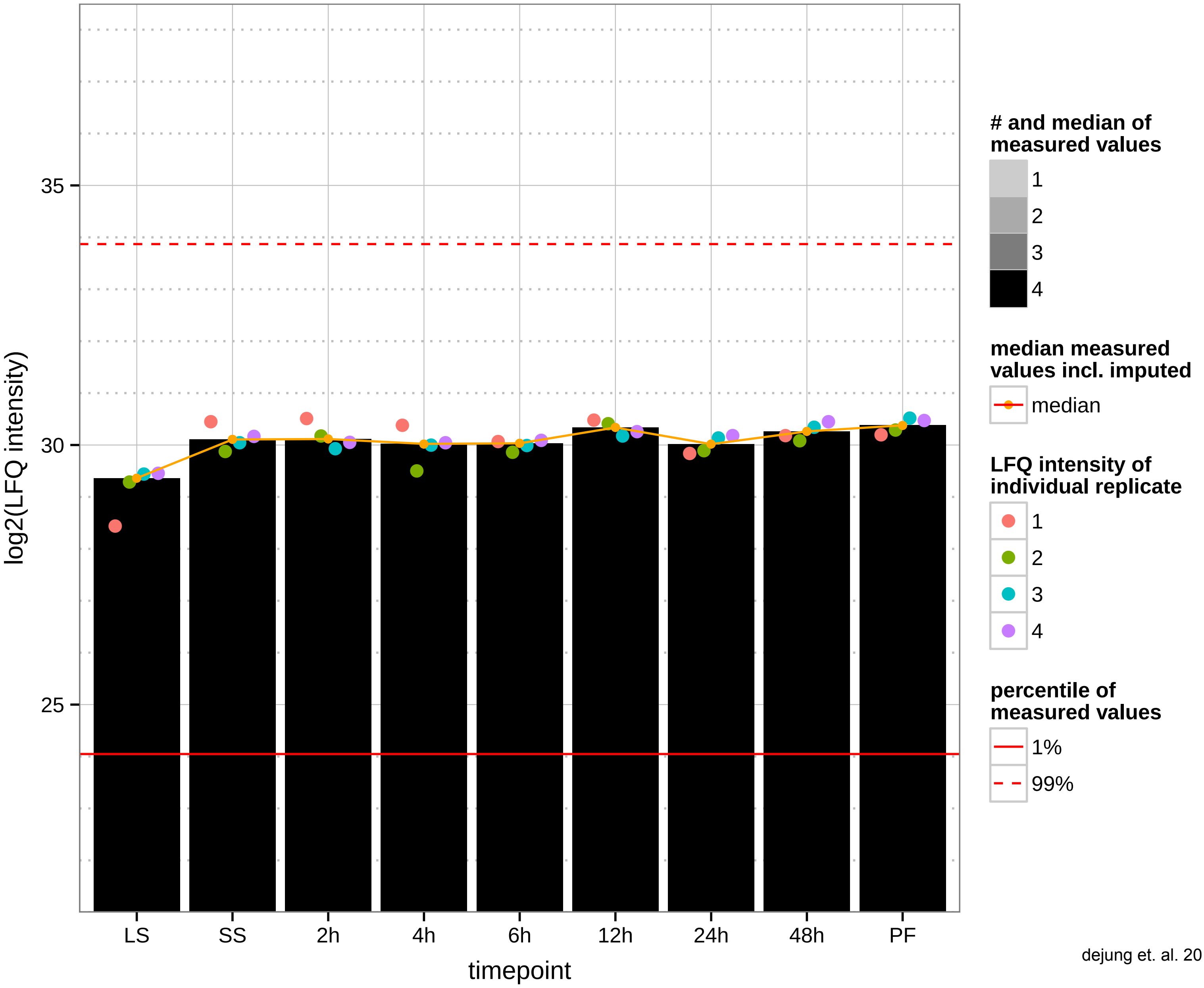
adenosine kinase, putative
Tb927.6.2360;Tb927.6.2300
AGOF: adenosine kinase activity
AGOC: null
AGOP: purine ribonucleoside salvage, purine ribonucleotide biosynthetic process
PGOF: null
PGOC: null
PGOP: null





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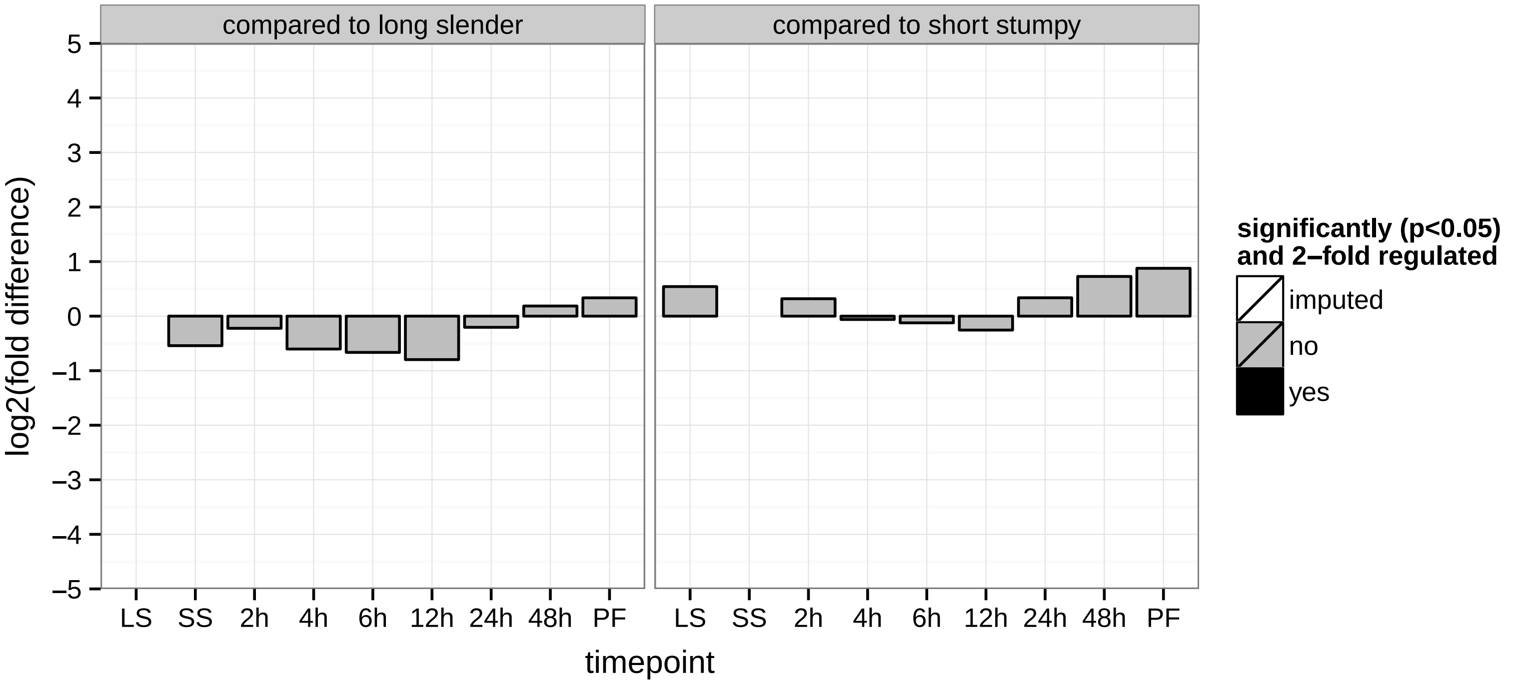
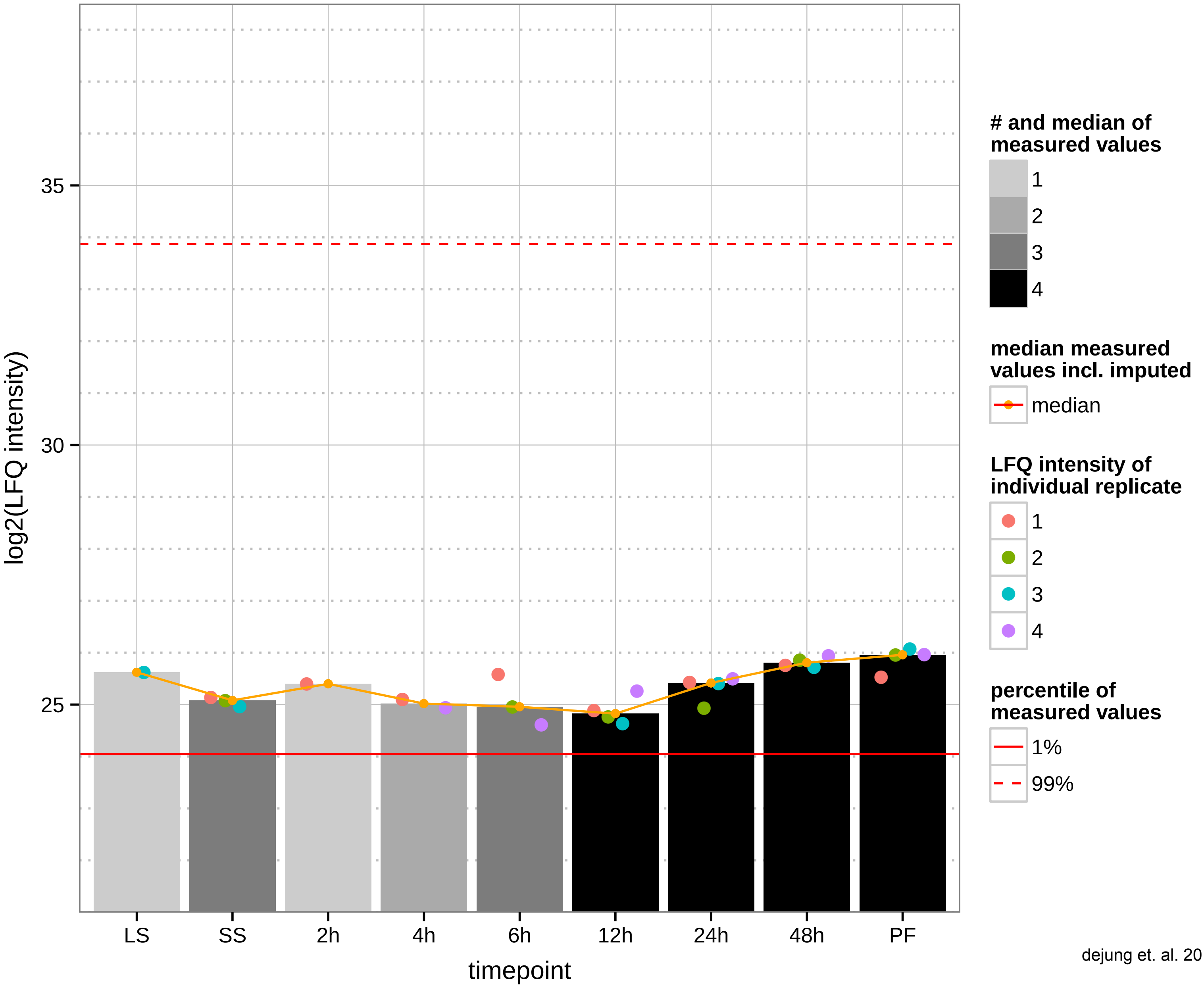
ubiquitin–protein ligase, putative
Tb927.6.2370
AGOF: acid–amino acid ligase activity
AGOC: intracellular
AGOP: cellular protein modification process
PGOF: acid–amino acid ligase activity, protein binding
PGOC: intracellular
PGOP: cellular protein modification process





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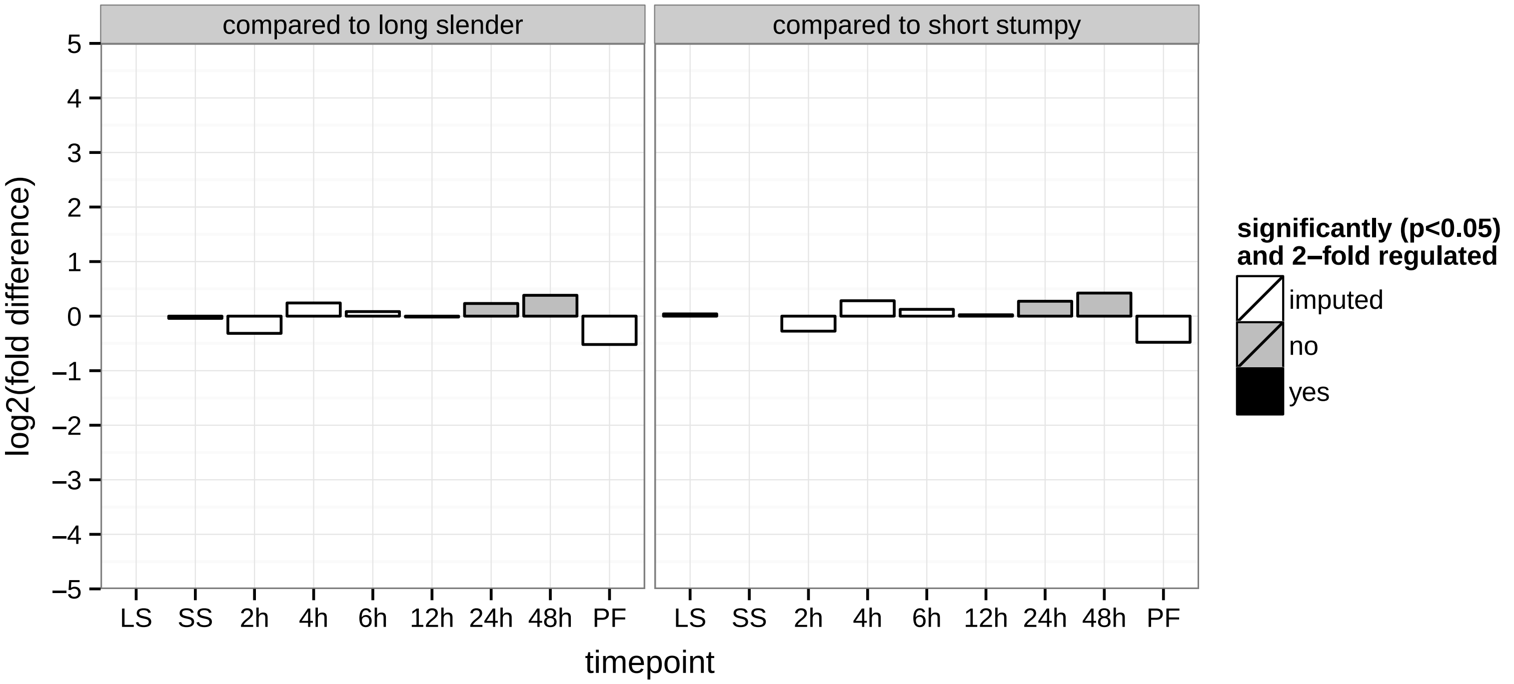
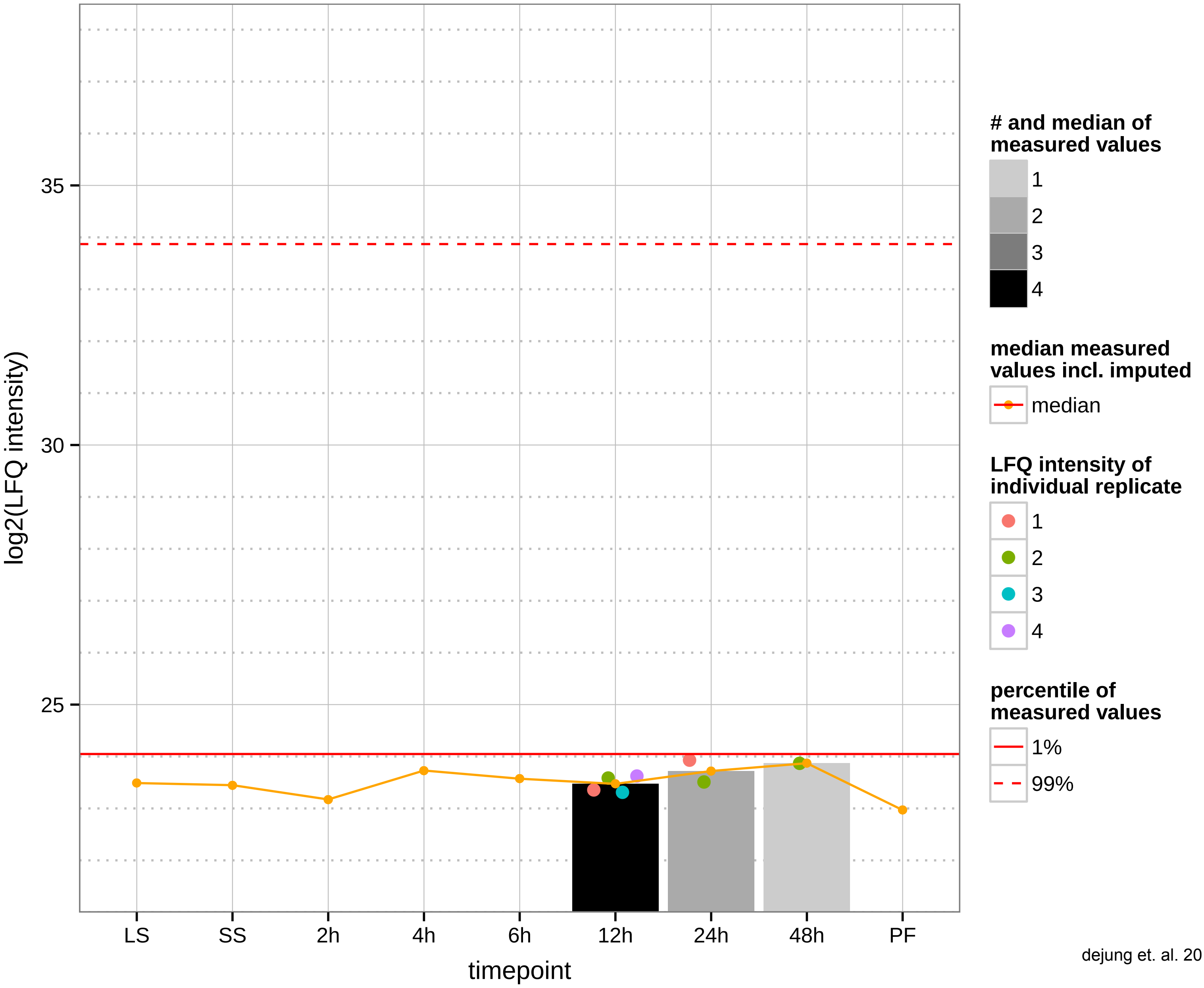
hypothetical protein, conserved
Tb927.6.2400
AGOF: null
AGOC: microtubule organizing center, spindle pole
AGOP: microtubule cytoskeleton organization
PGOF: null
PGOC: microtubule organizing center, spindle pole
PGOP: microtubule cytoskeleton organization





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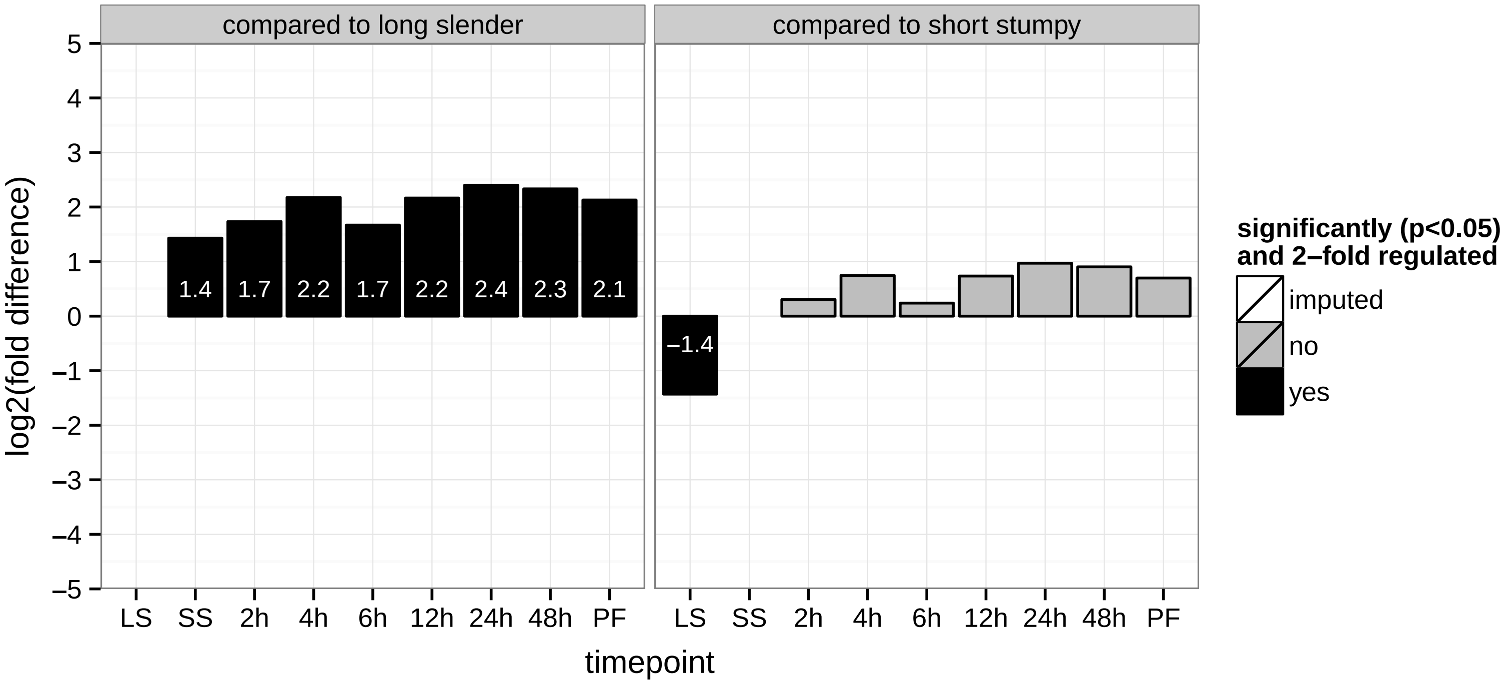
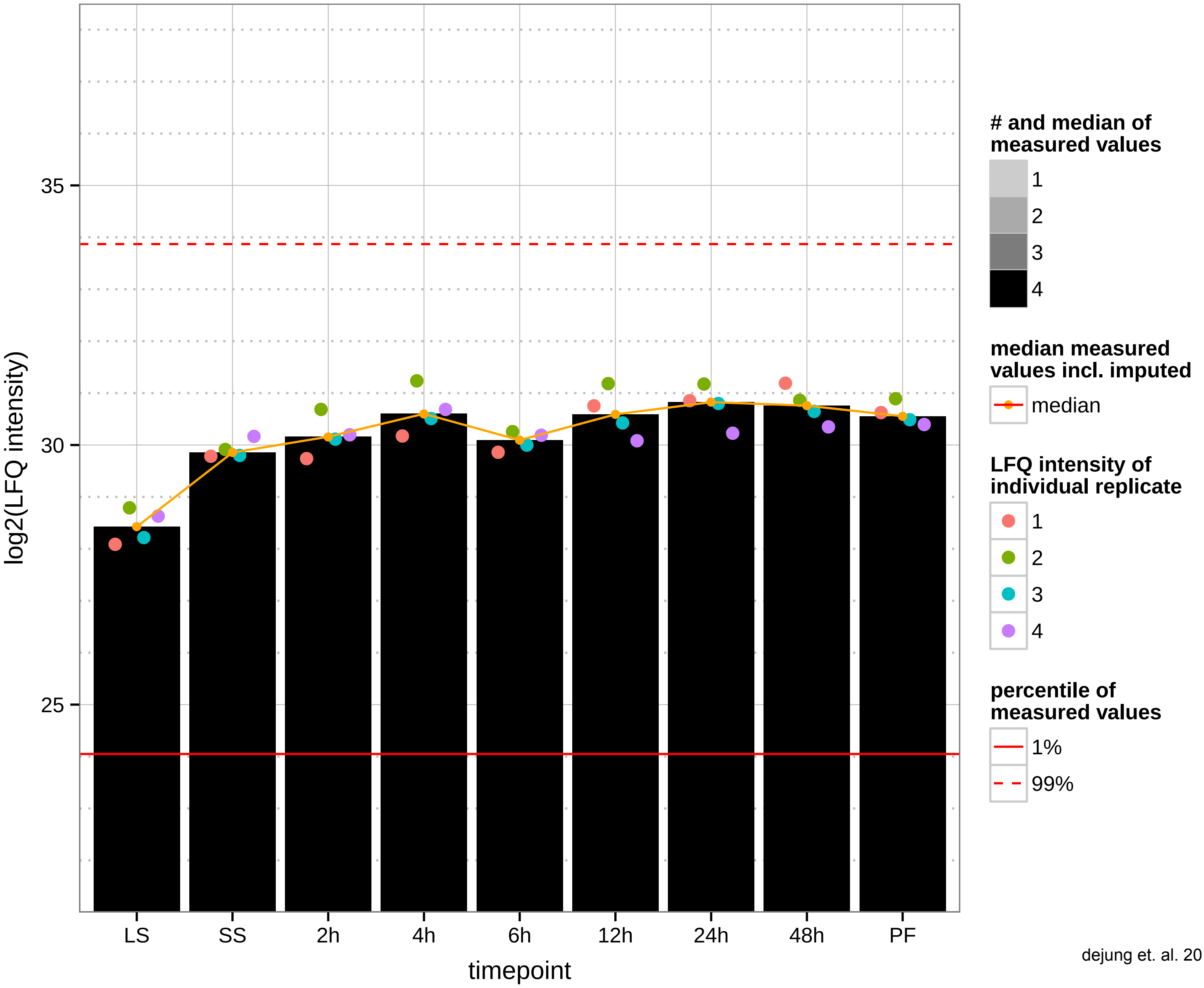
p22 protein precursor
Tb927.6.2420
AGOF: protein binding
AGOC: mitochondrial matrix, mitochondrion
AGOP: RNA modification
PGOF: null
PGOC: mitochondrial matrix
PGOP: null





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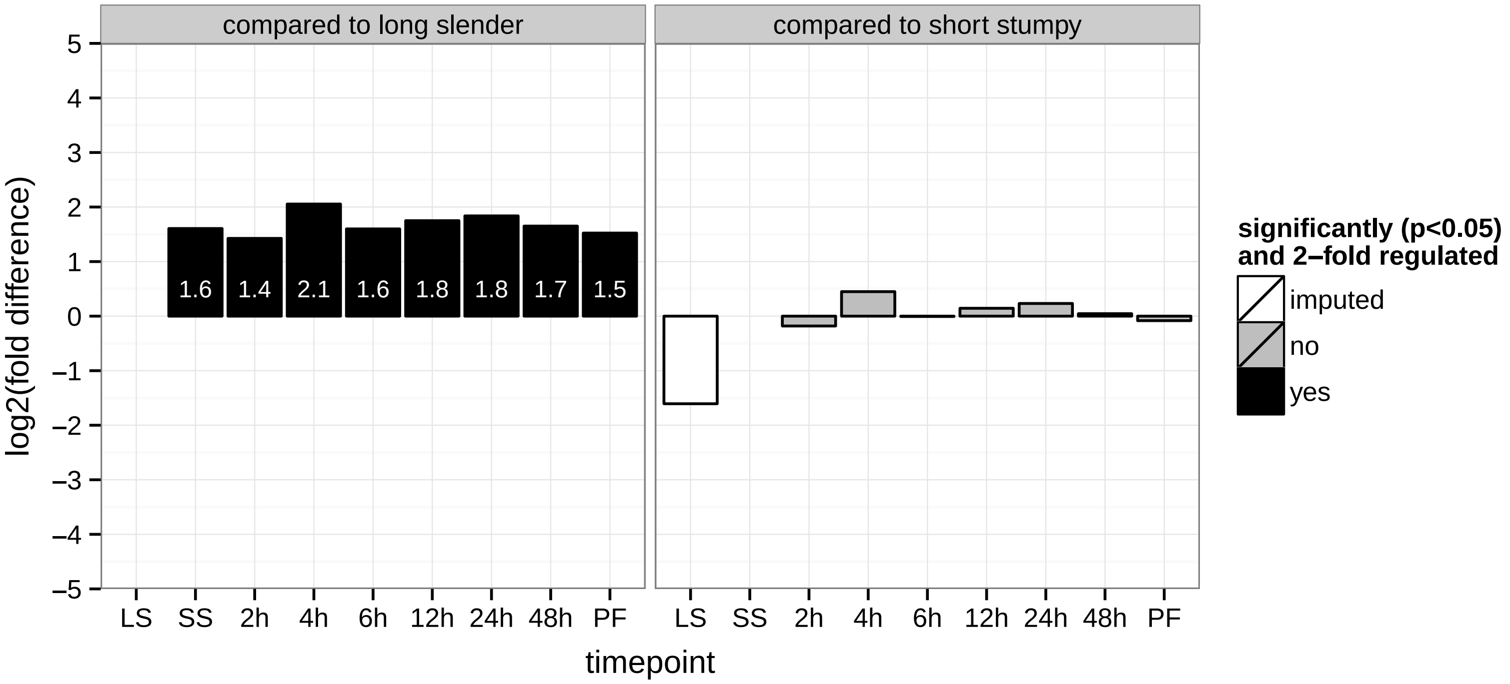
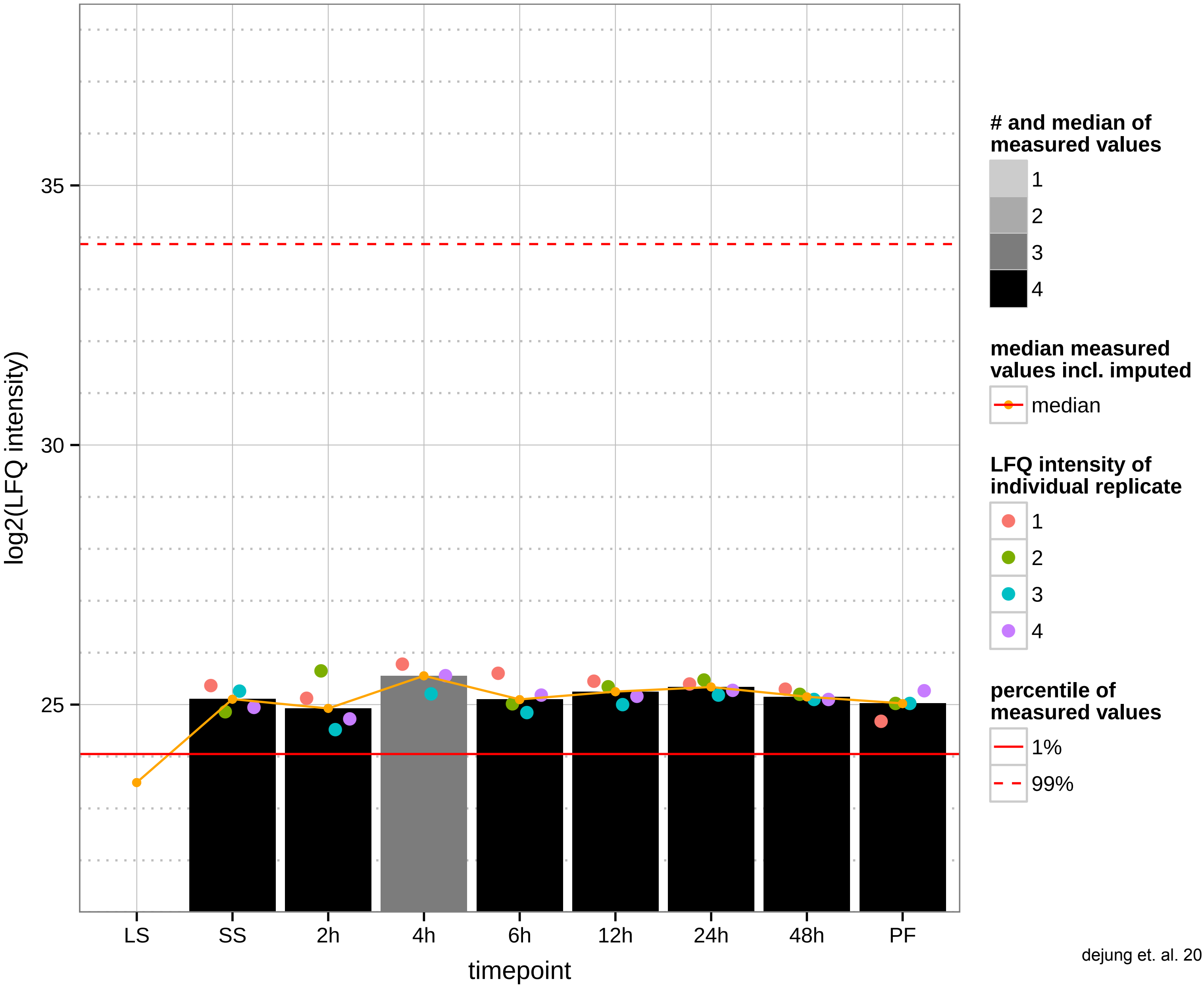
hypothetical protein, conserved
Tb927.6.2440
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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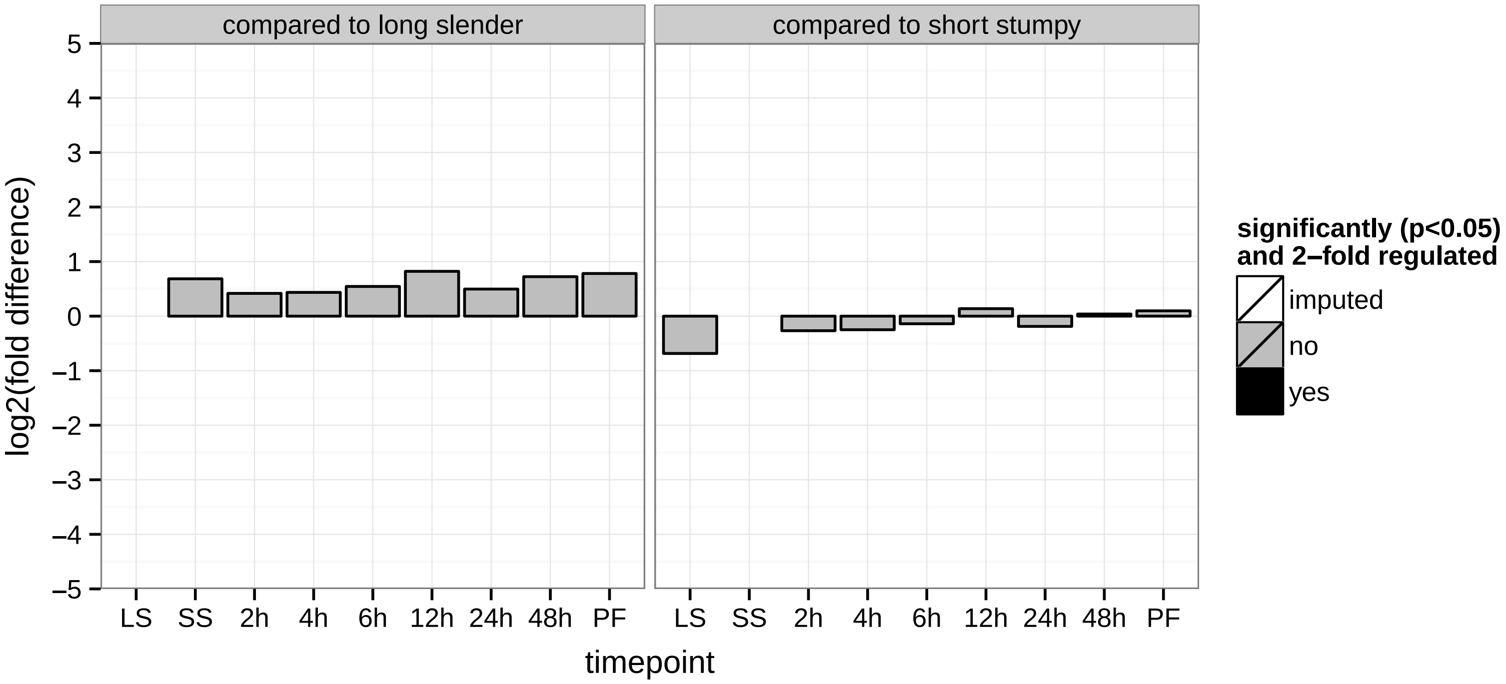
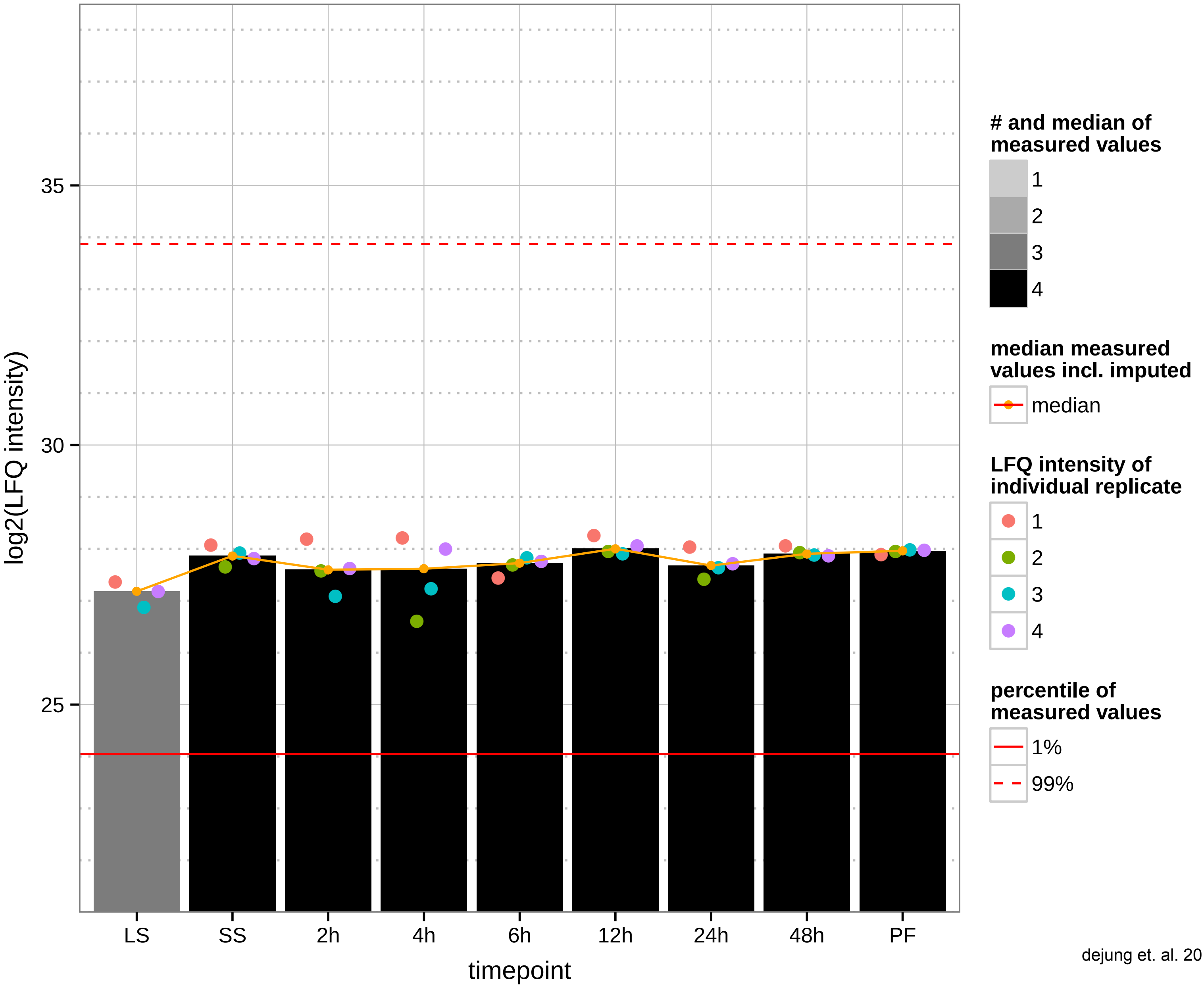
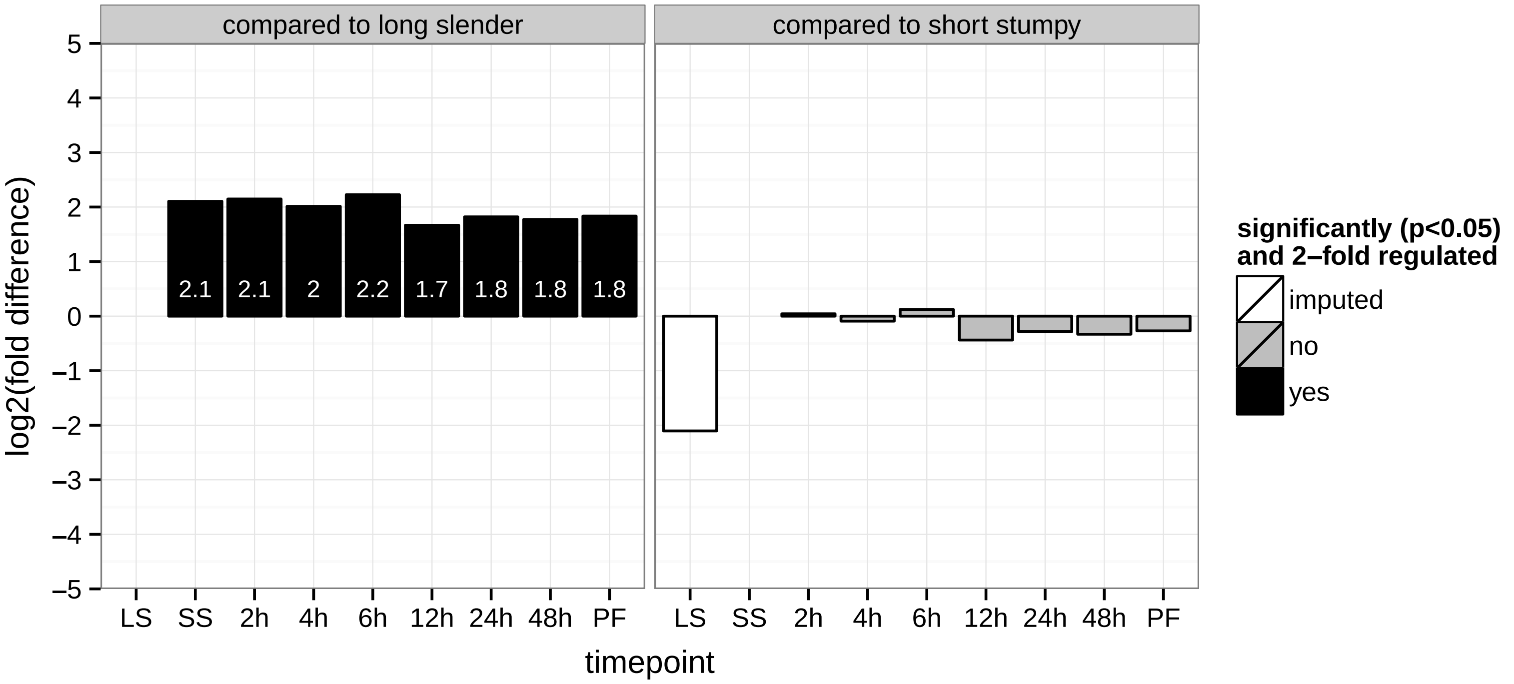
ubiquitin fusion degradation protein 2, putative, ubiquitin conjugation factor E4 B
Tb927.6.2460
AGOF: ubiquitin–ubiquitin ligase activity
AGOC: ubiquitin ligase complex
AGOP: cell redox homeostasis, protein ubiquitination, ubiquitin–dependent protein catabolic process
PGOF: ubiquitin–ubiquitin ligase activity
PGOC: ubiquitin ligase complex
PGOP: cell redox homeostasis, protein ubiquitination, ubiquitin–dependent protein catabolic process

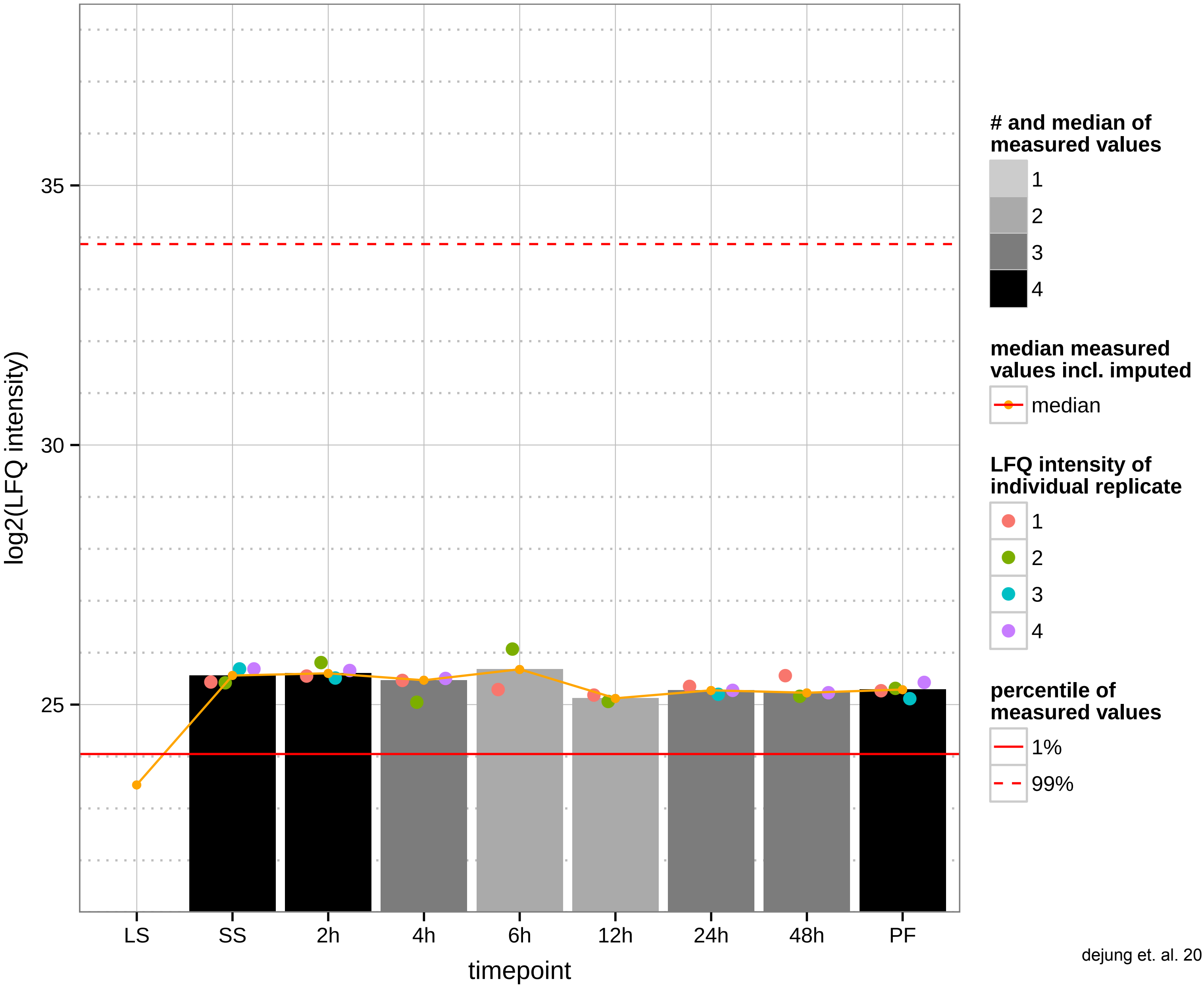




dejung et. al. 2015

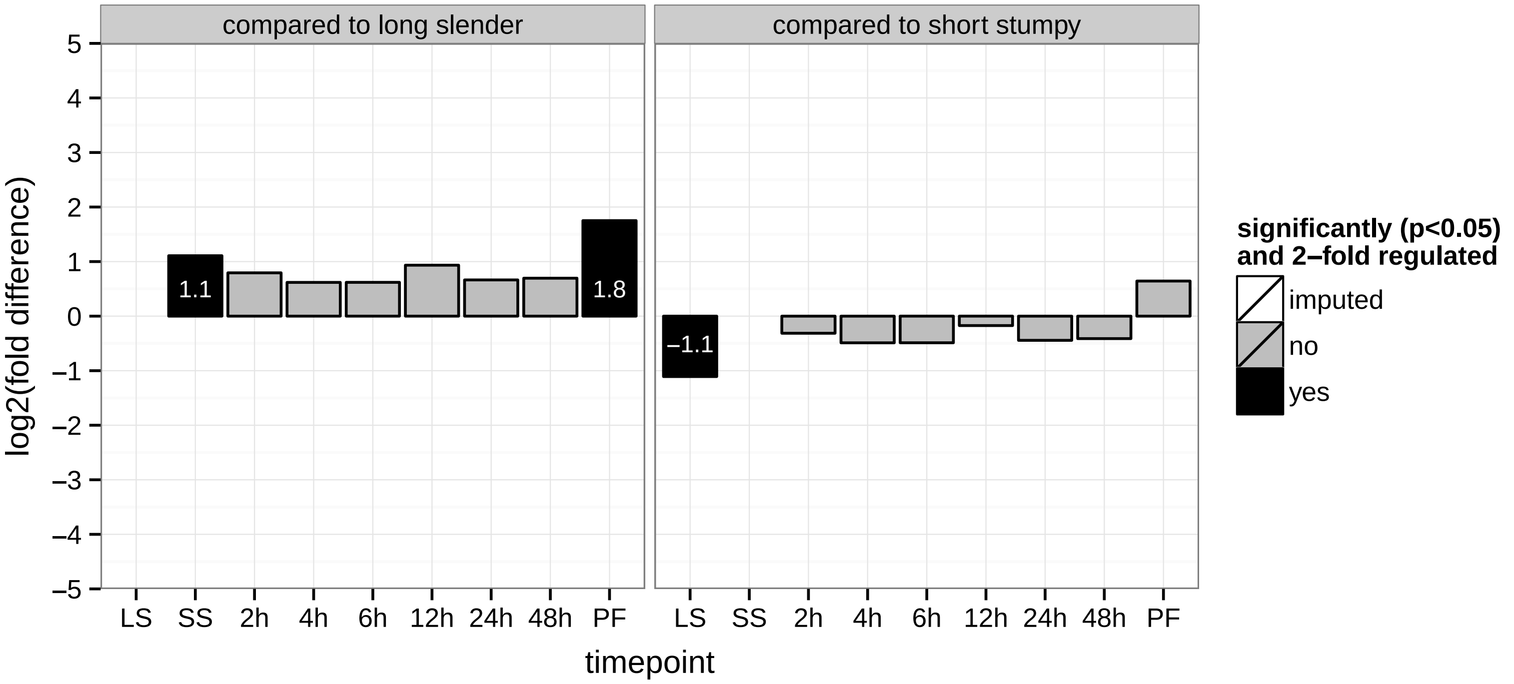
hypothetical protein, conserved
Tb927.6.2520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

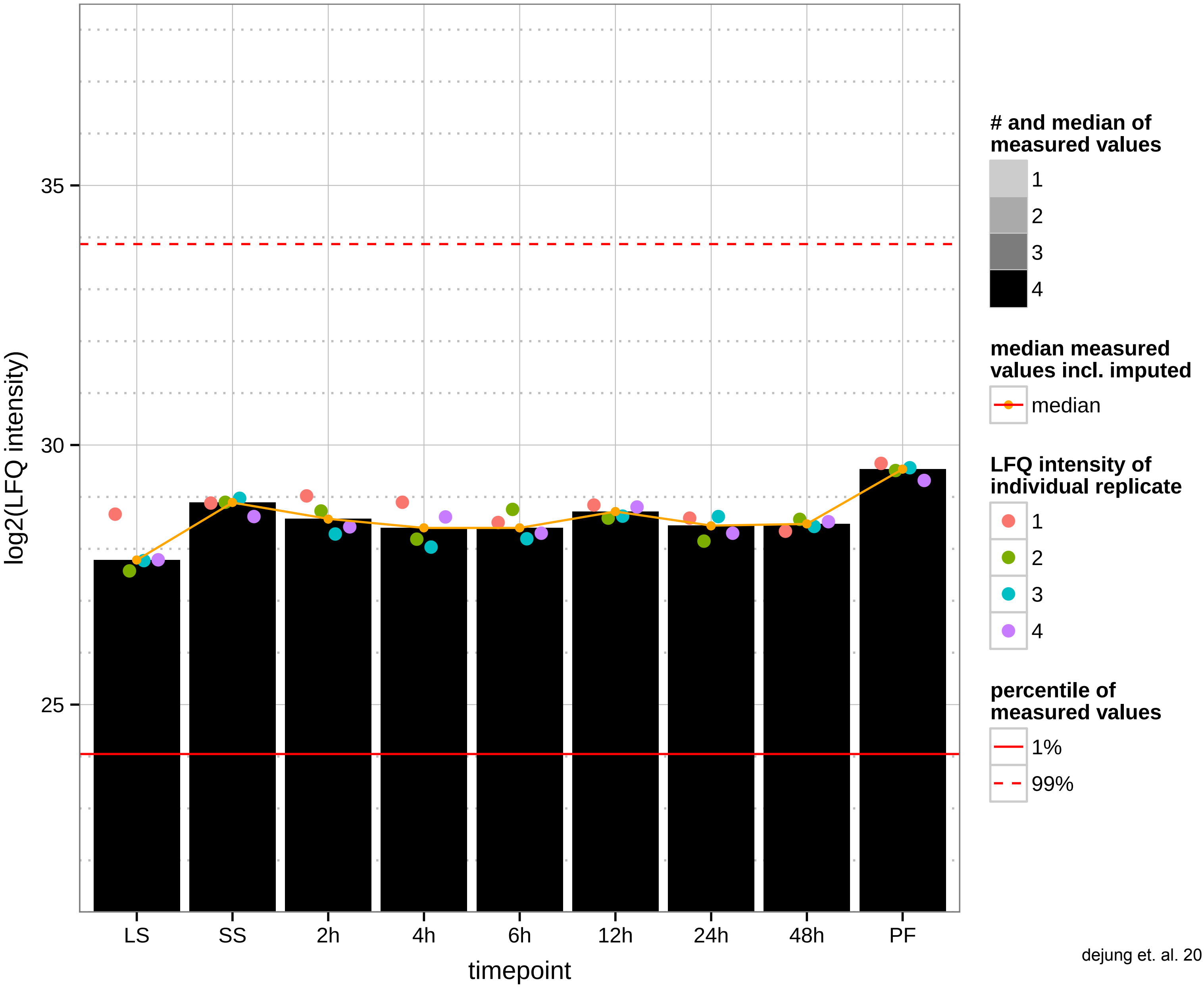




dejung et. al. 2015

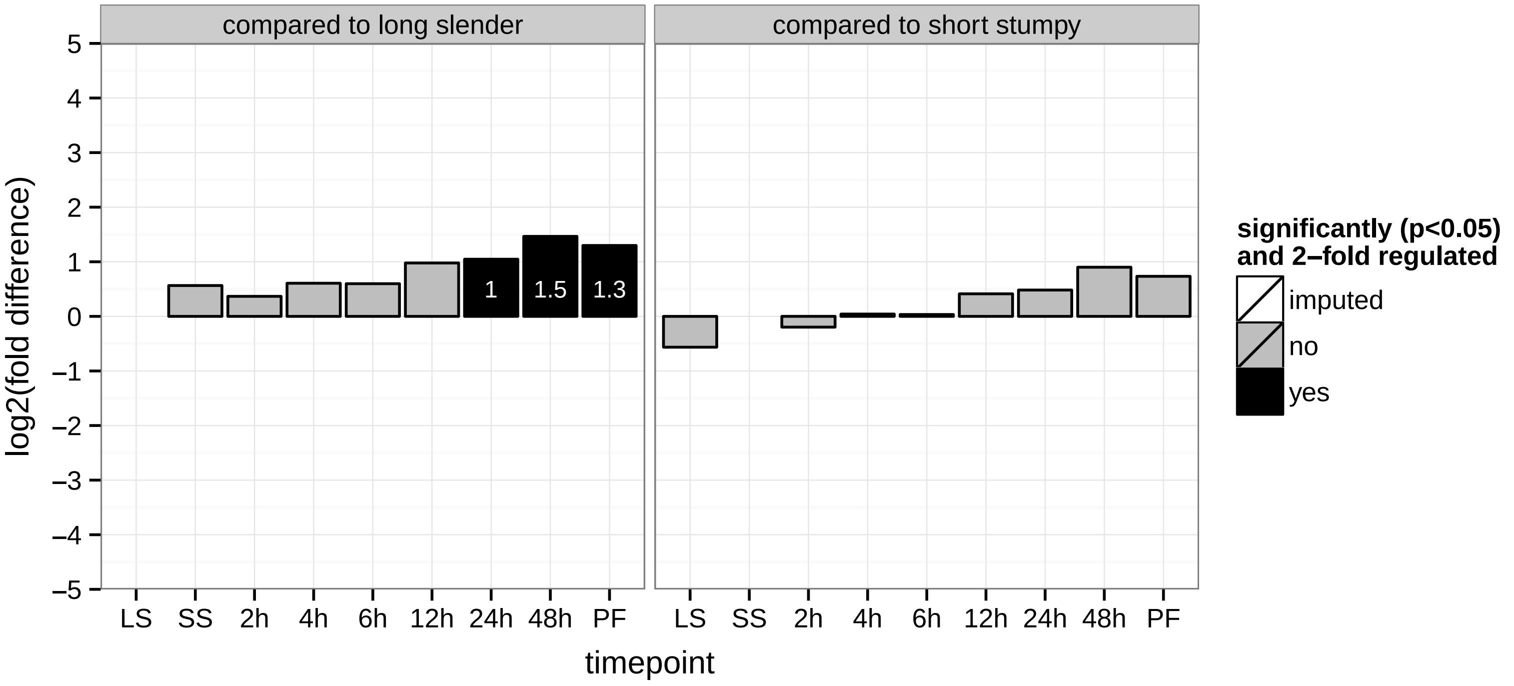
RNA–binding protein, putative (TRRM2)
Tb927.6.2550
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null

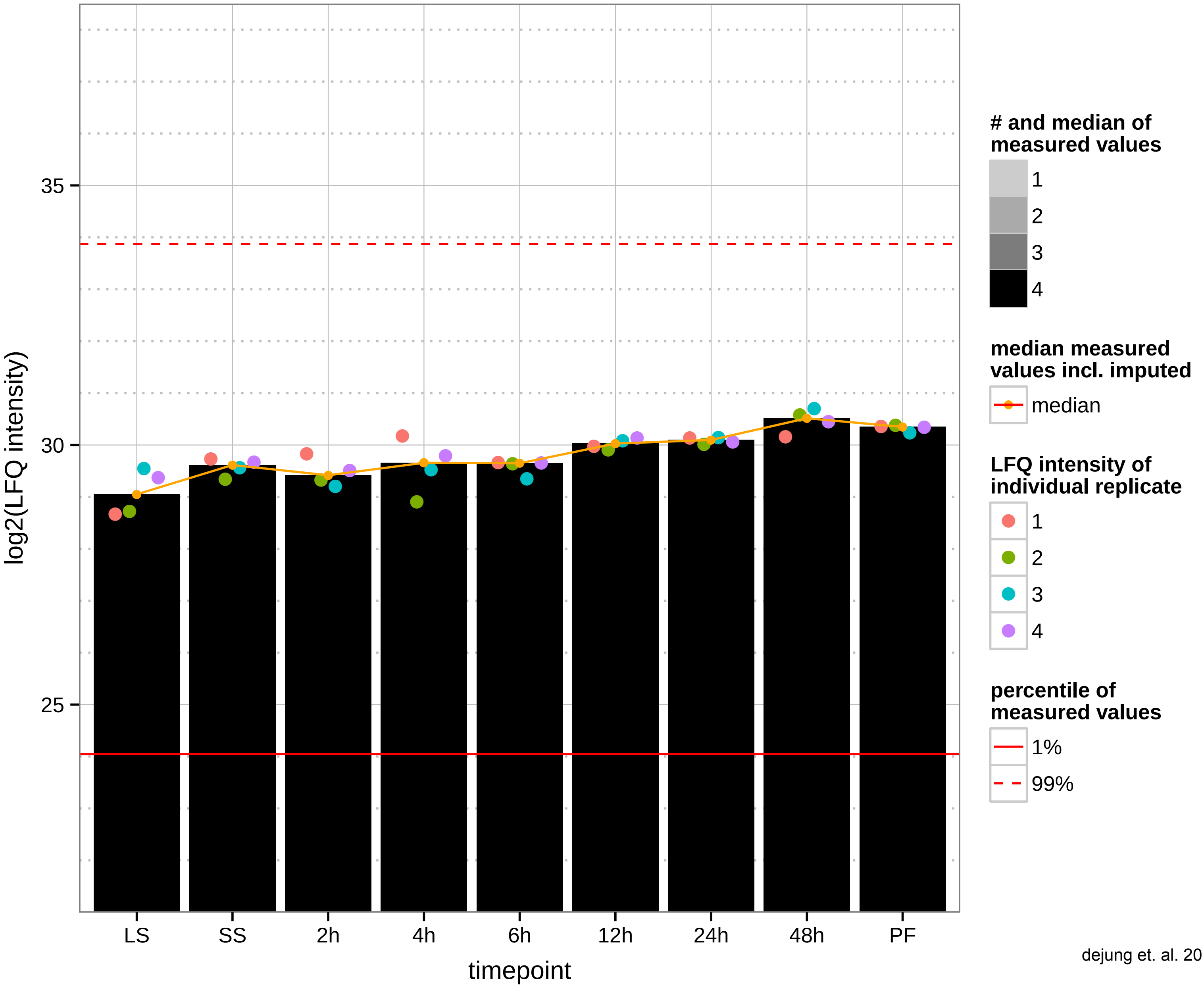




dejung et. al. 2015

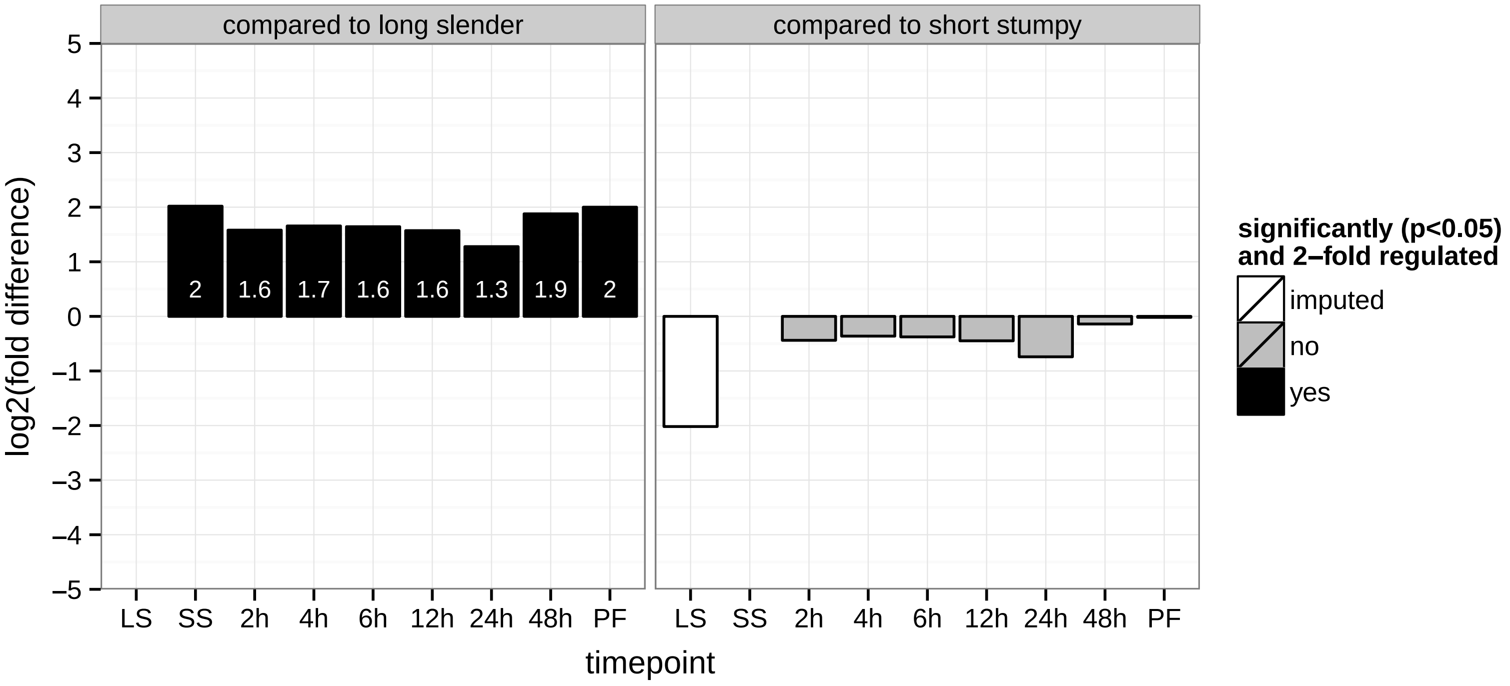
importin alpha subunit, putative (TbKap60)
Tb927.6.2640
AGOF: null
AGOC: null
AGOP: null
PGOF: binding, protein binding, protein transporter activity
PGOC: cytoplasm, nucleus
PGOP: protein import into nucleus

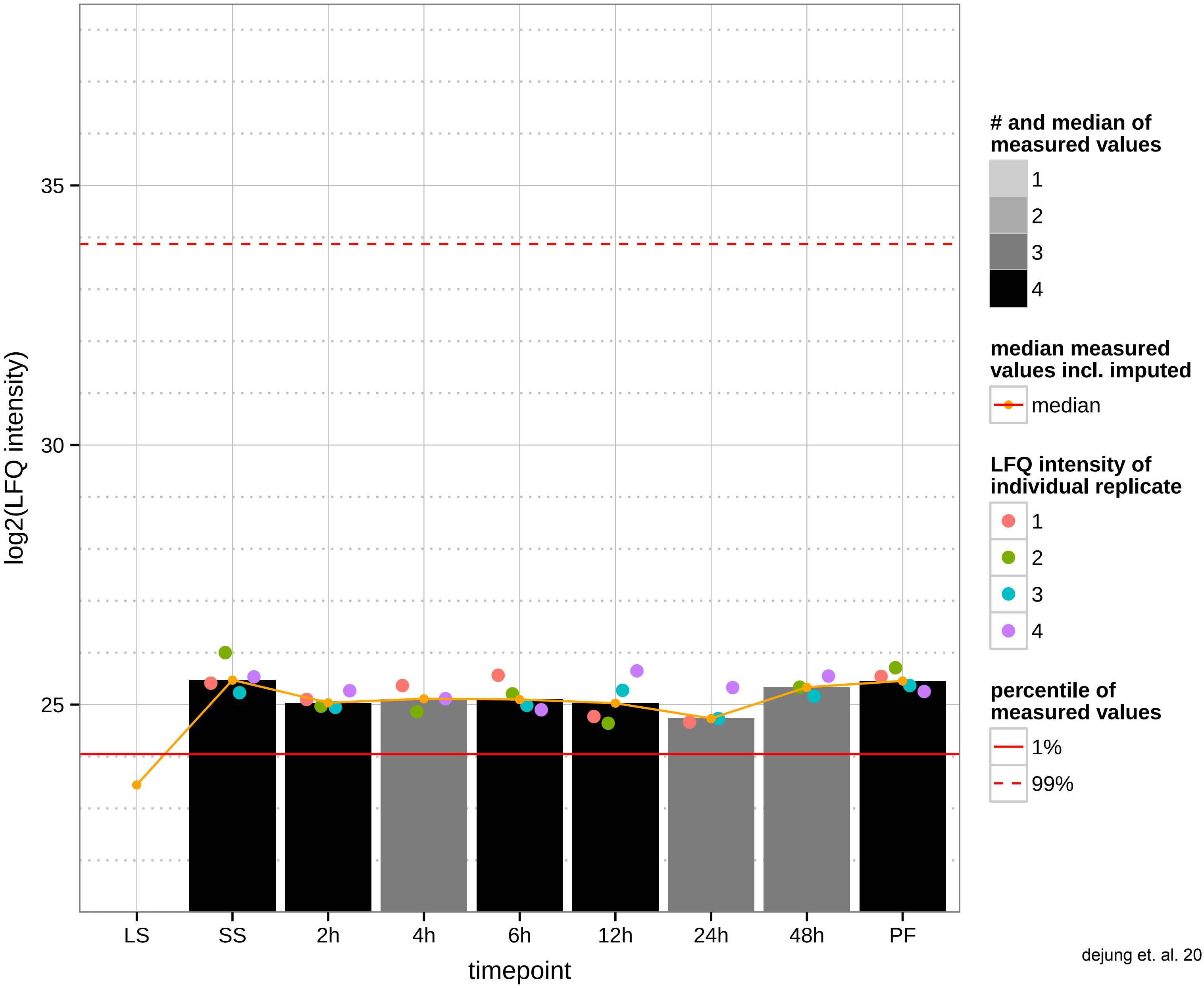




dejung et. al. 2015

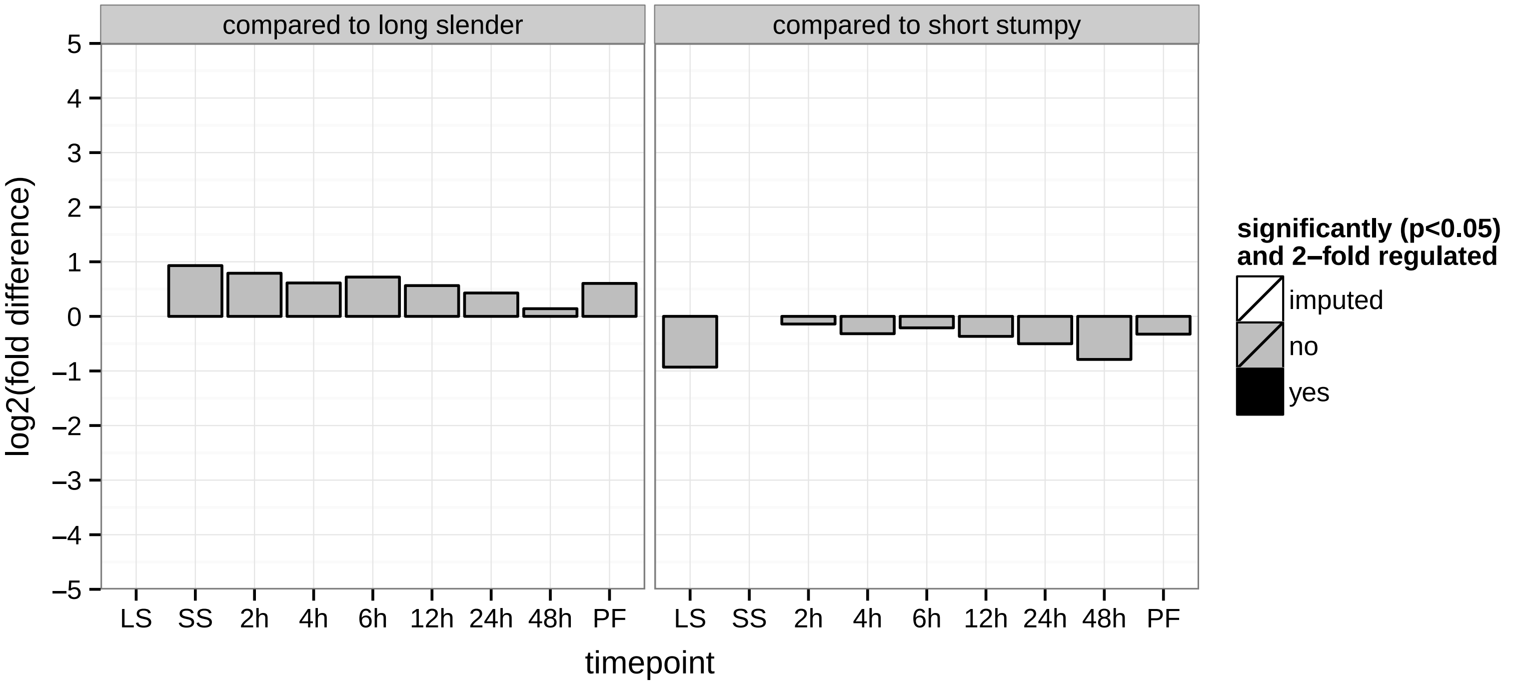
hypothetical protein, conserved
Tb927.6.2650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

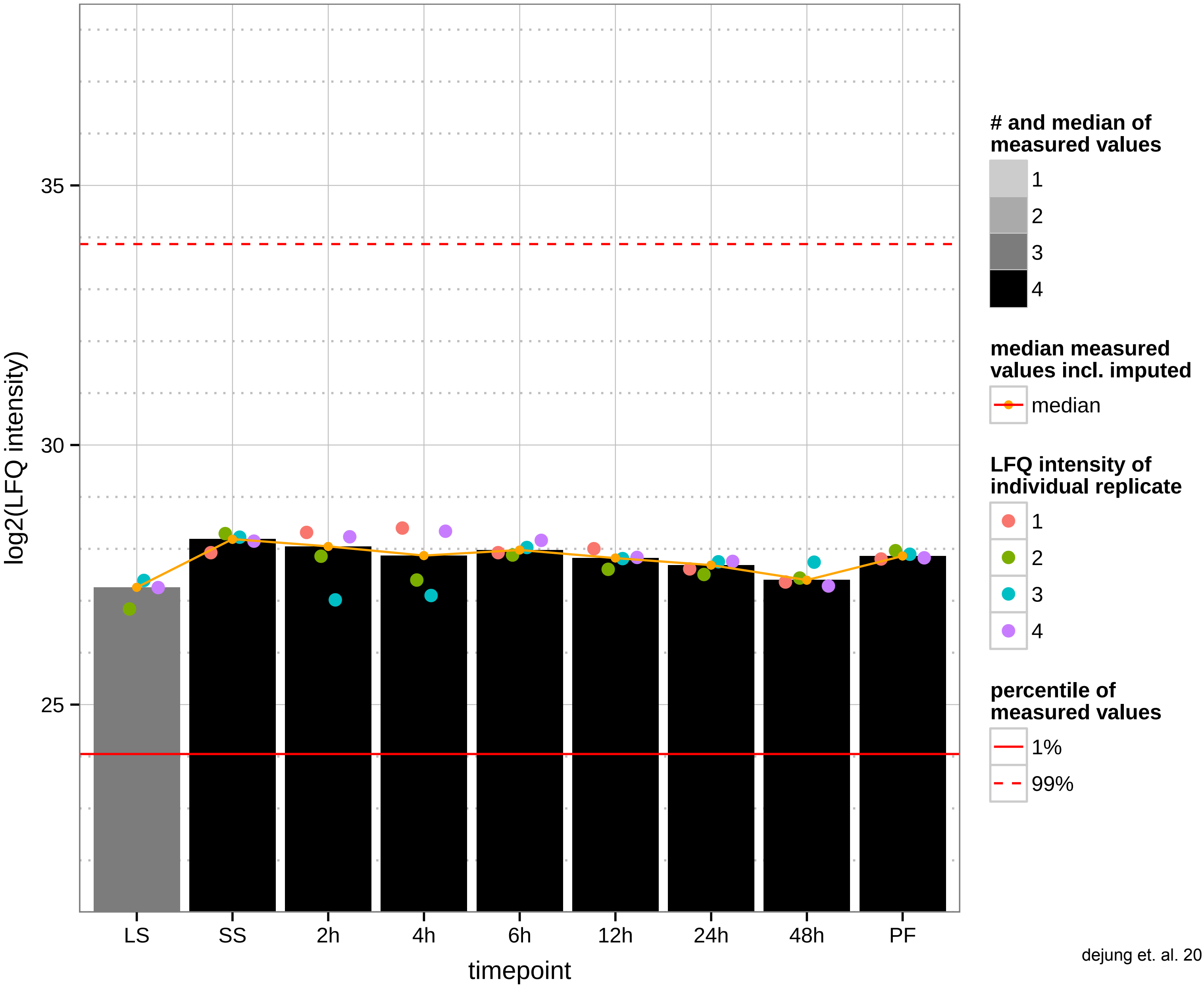




dejung et. al. 2015

ubiquitin carboxyl–terminal hydrolase, putative, cysteine peptidase, Clan CA, family C19
Tb927.6.2690
AGOF: ubiquitin thiolesterase activity
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ubiquitin thiolesterase activity
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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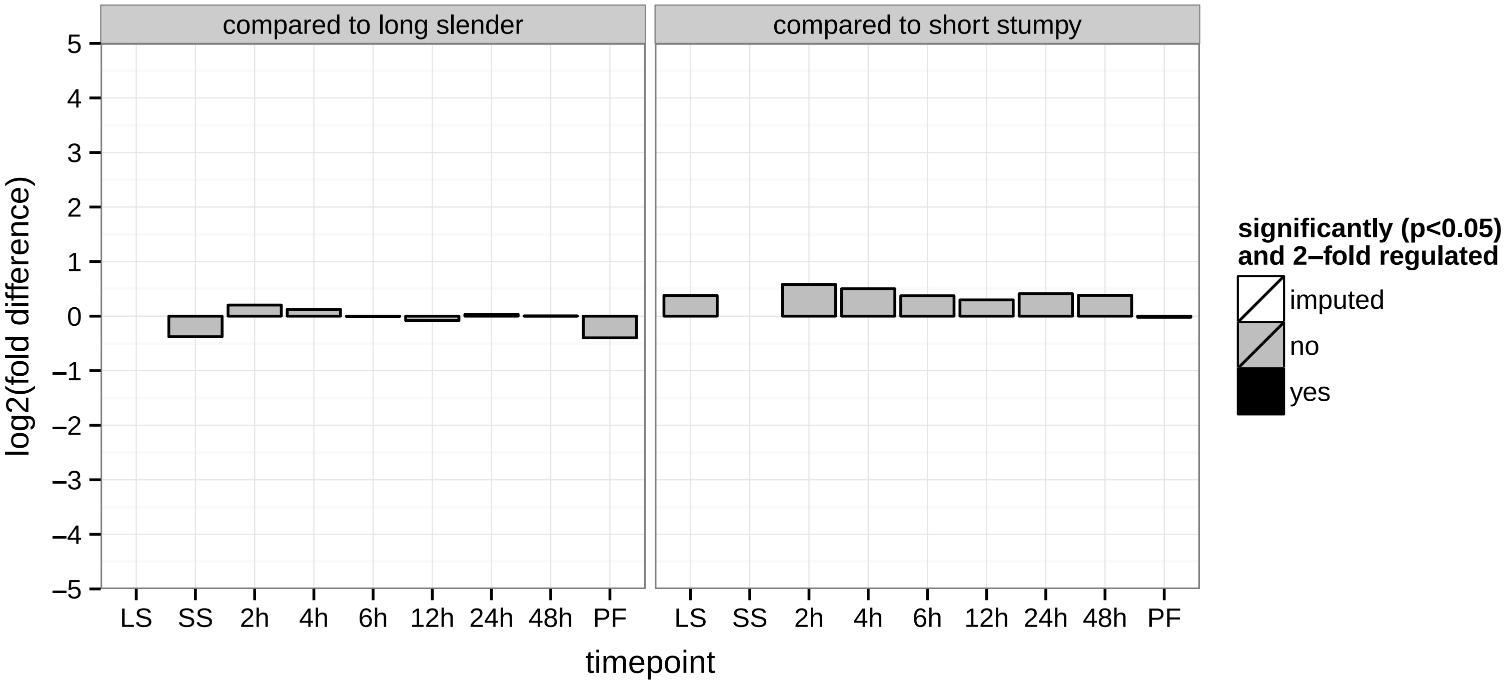
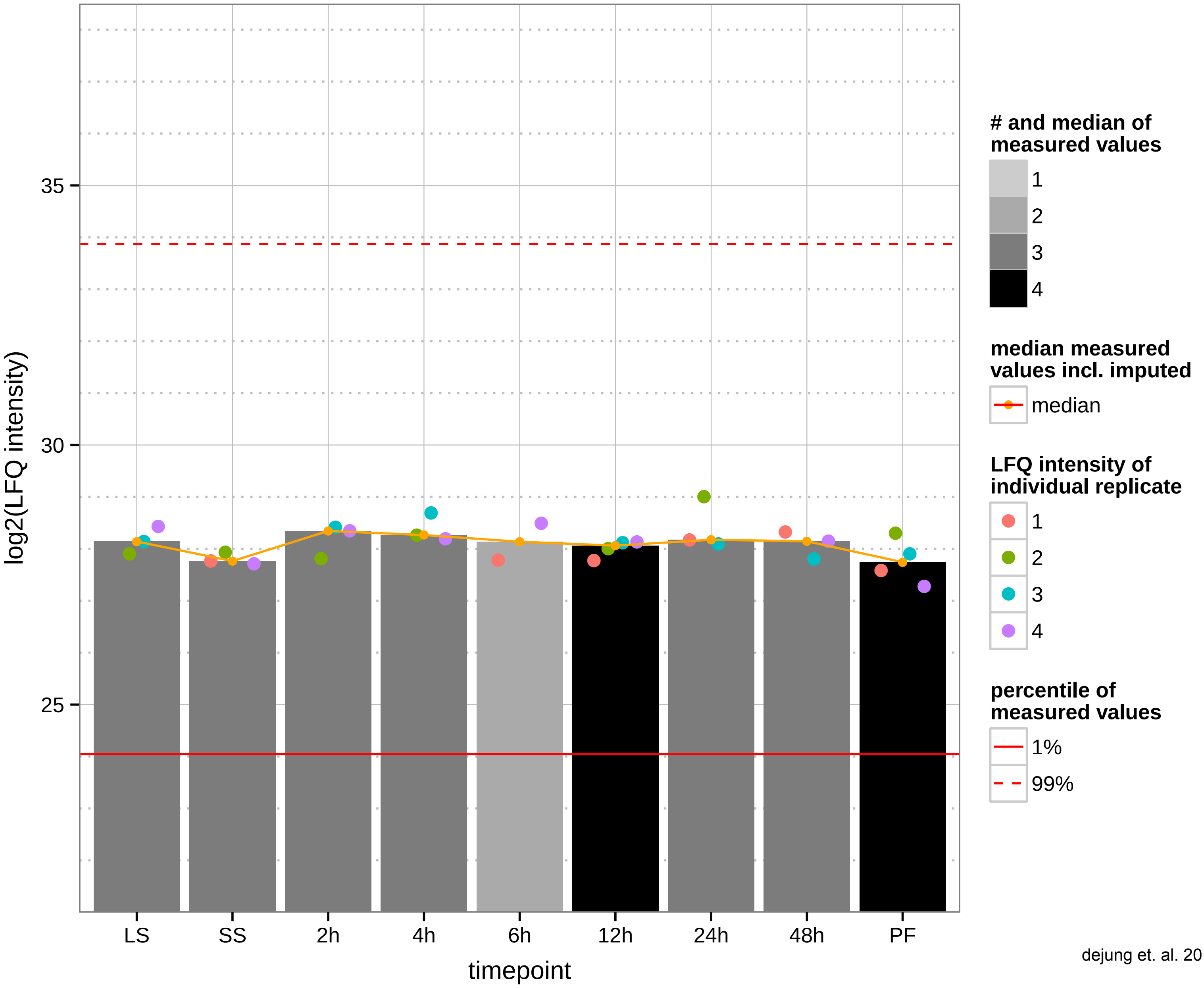
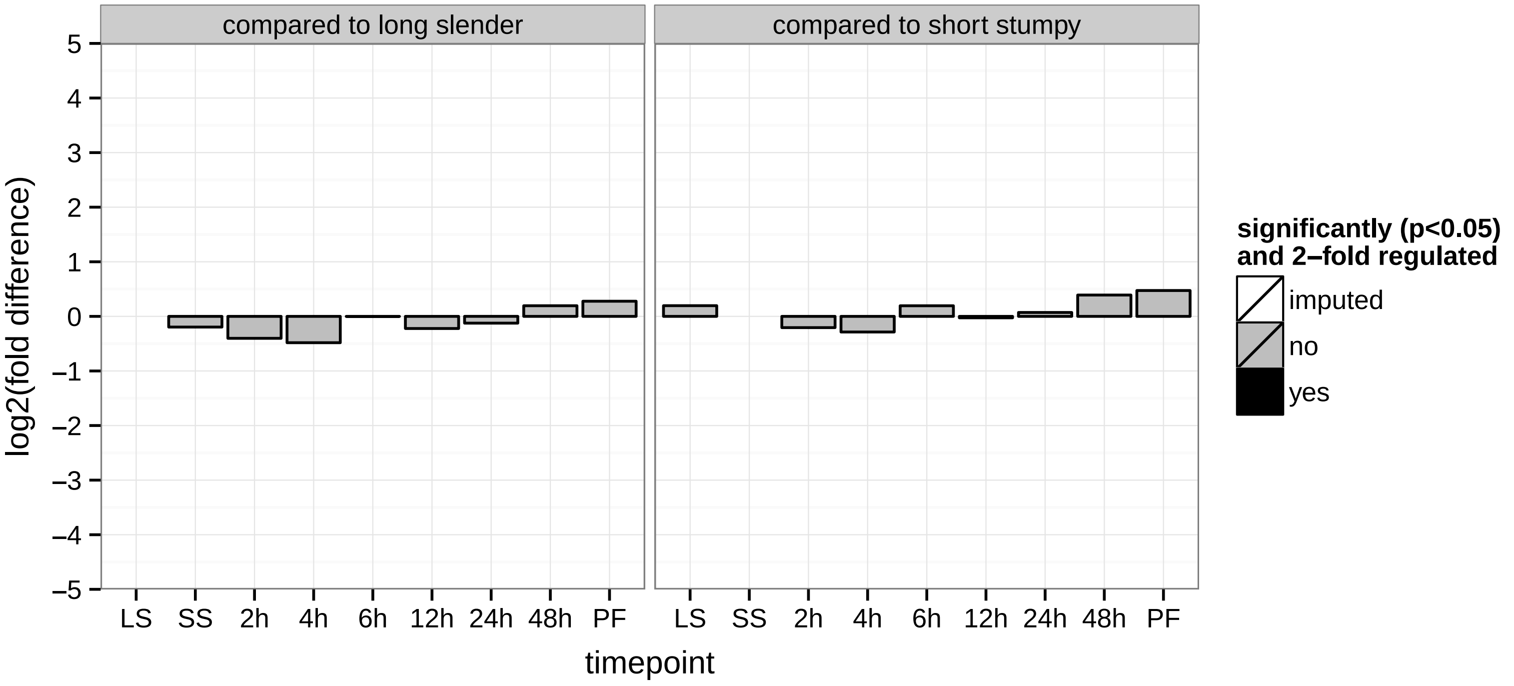
small nuclear ribonucleoprotein Sm–E (Sm–E)
Tb927.6.2700
AGOF: null
AGOC: nucleus, small nucleolar ribonucleoprotein complex
AGOP: RNA splicing, RNA splicing, via transesterification reactions, nuclear mRNA trans splicing, SL addition
PGOF: null
PGOC: null
PGOP: null

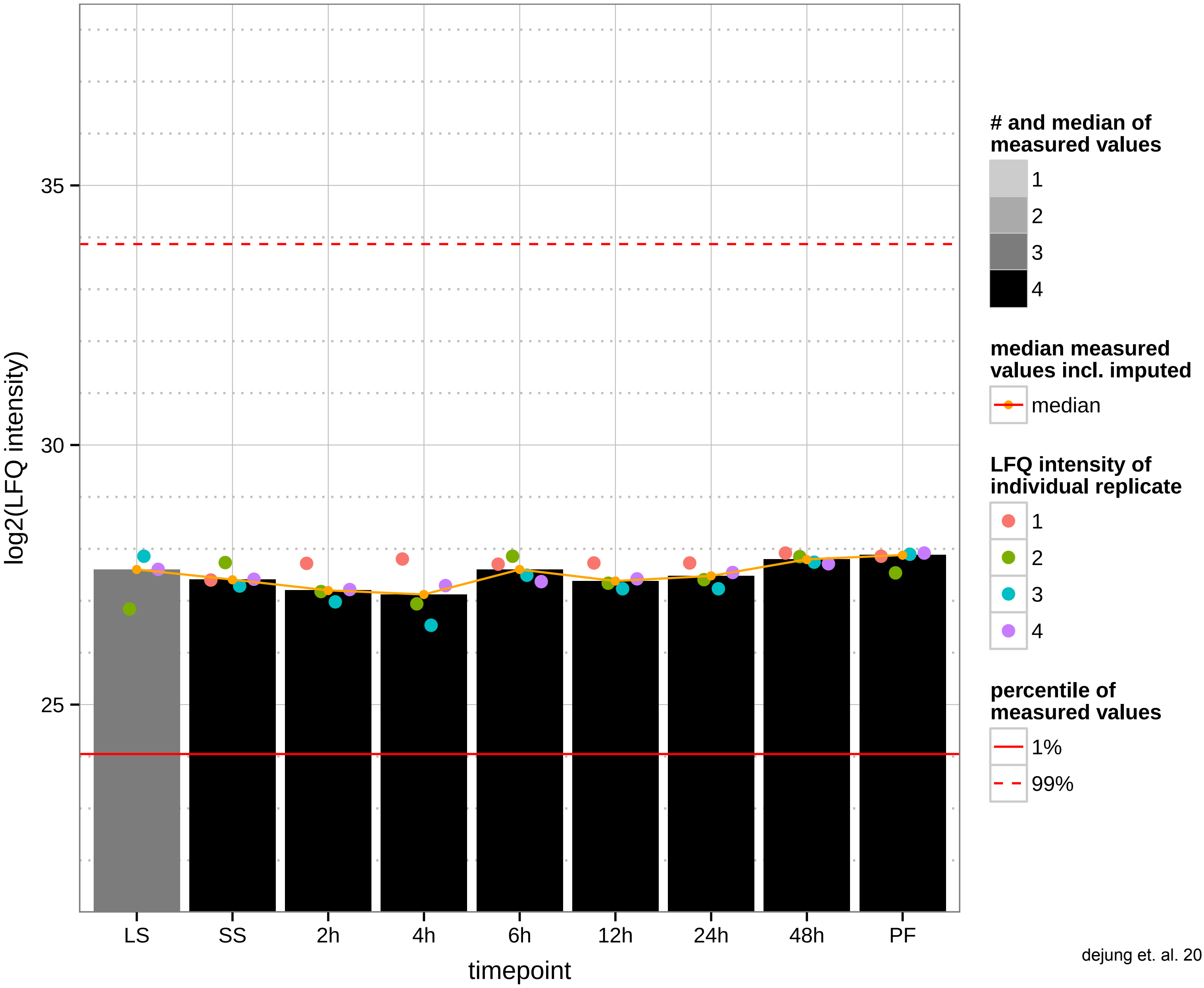




dejung et. al. 2015

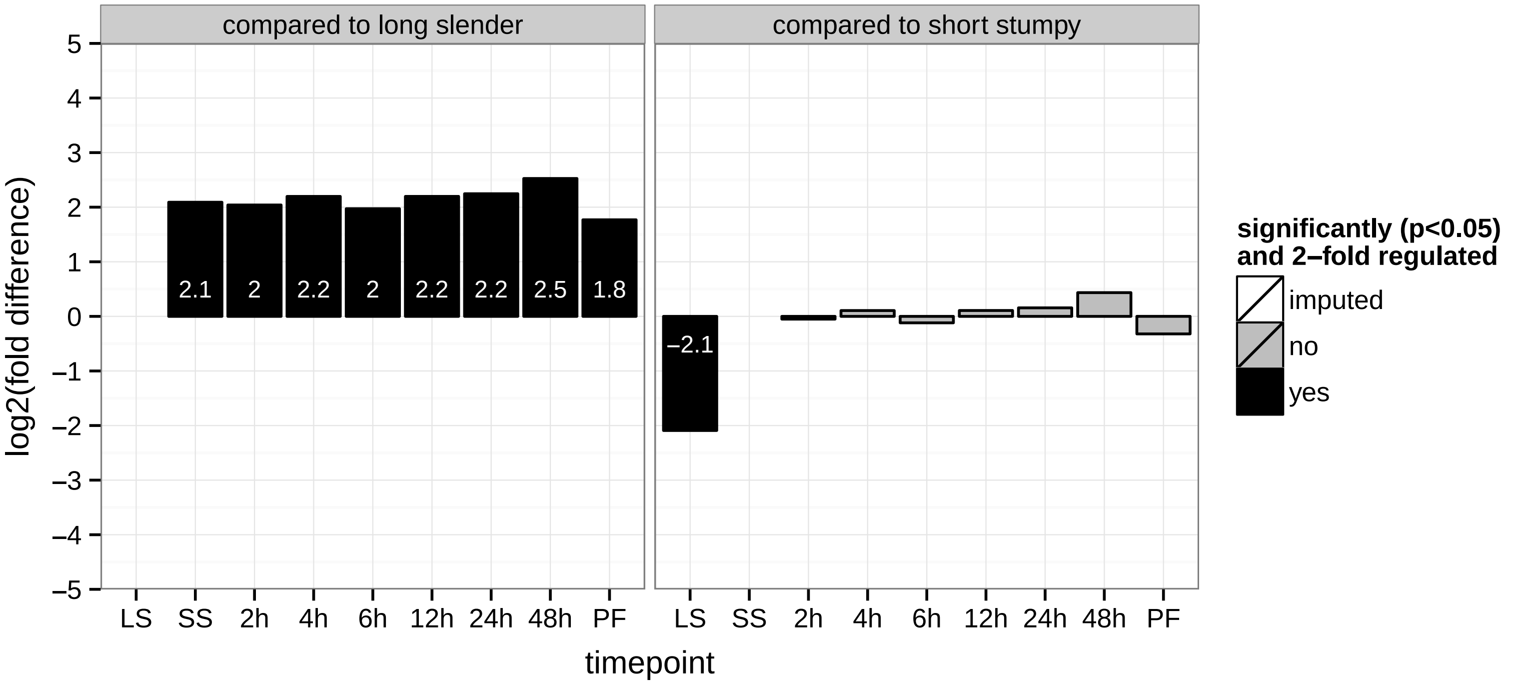
calcium–binding protein, putative
Tb927.6.2720
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

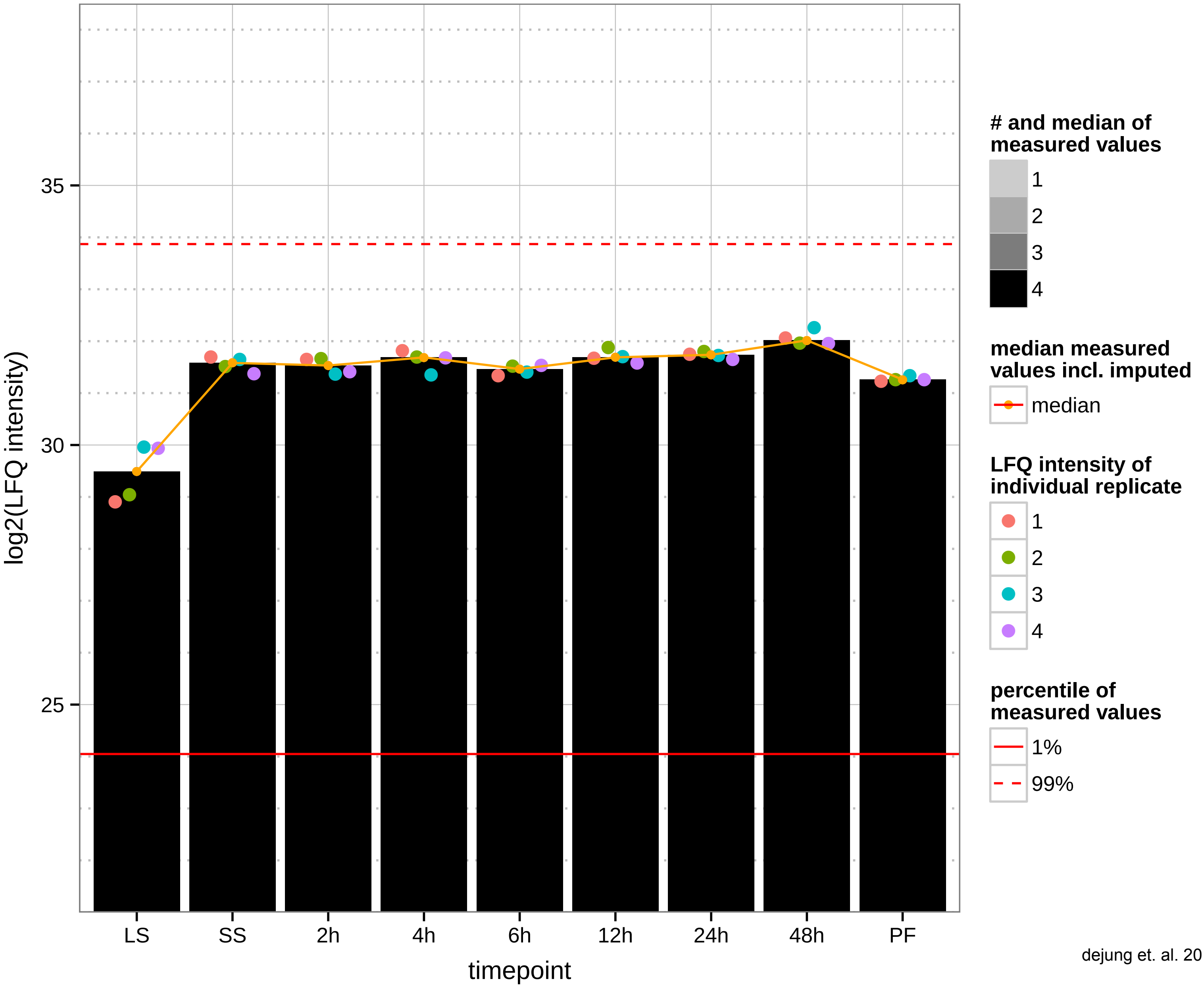




dejung et. al. 2015

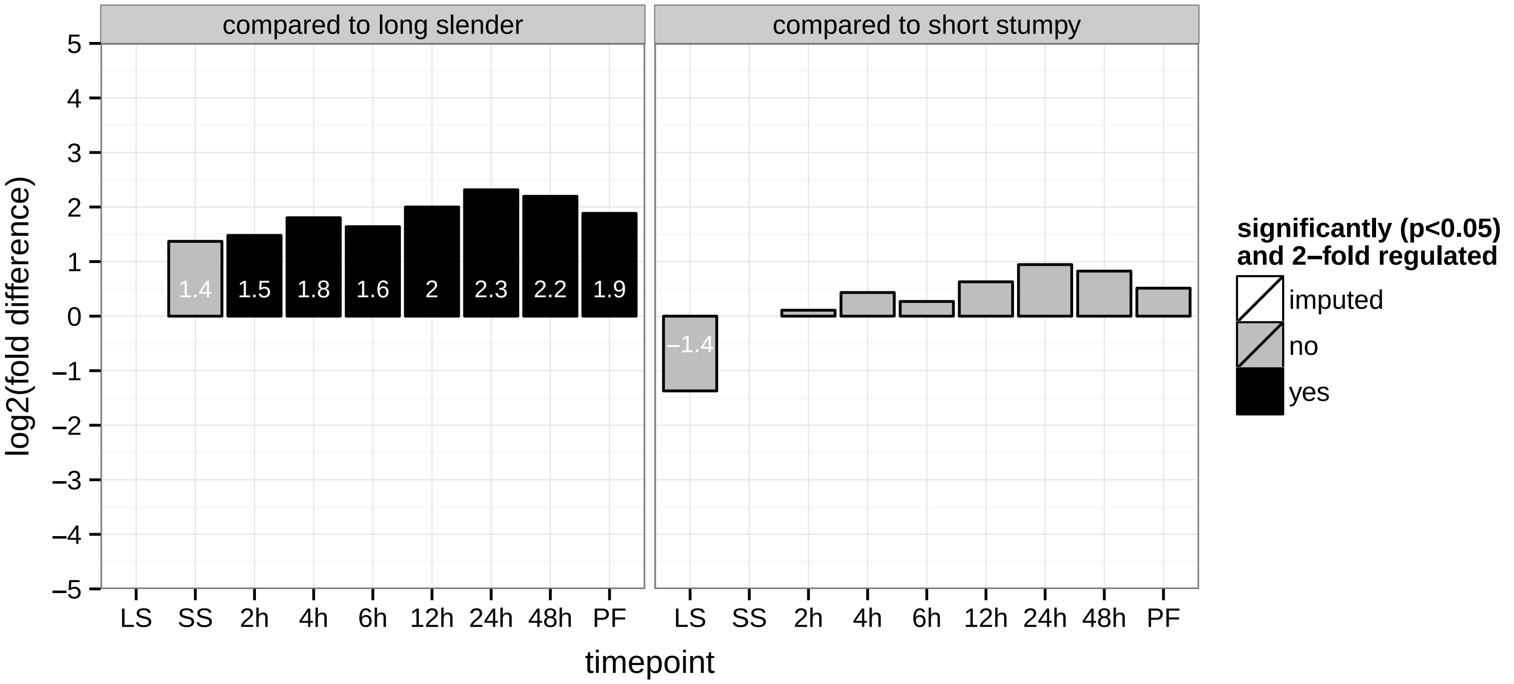
pyridoxal kinase (pdxK)
Tb927.6.2740
AGOF: pyridoxal kinase activity
AGOC: null
AGOP: pyridoxine biosynthetic process
PGOF: pyridoxal kinase activity
PGOC: null
PGOP: pyridoxal 5'−phosphate salvage

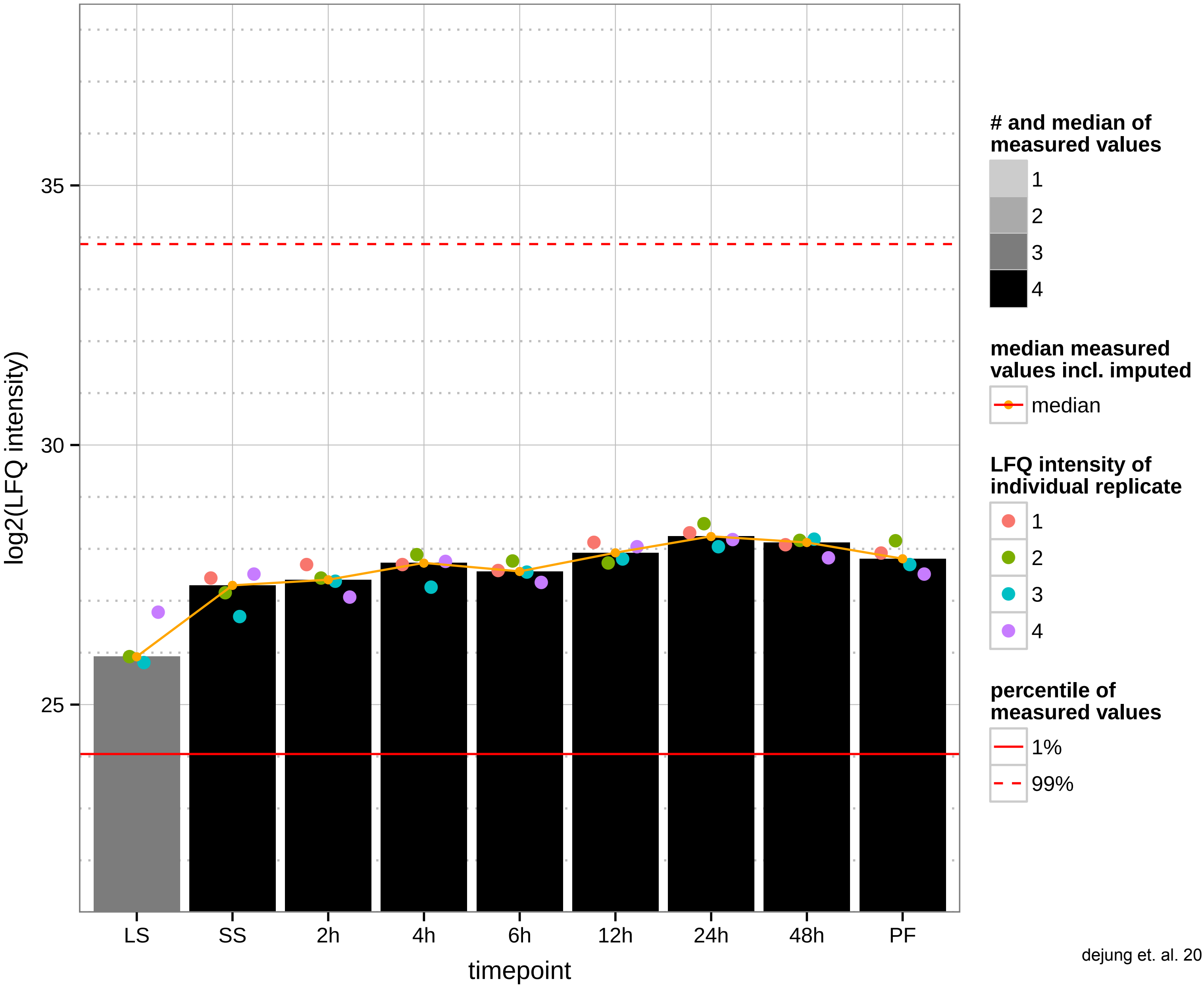




dejung et. al. 2015

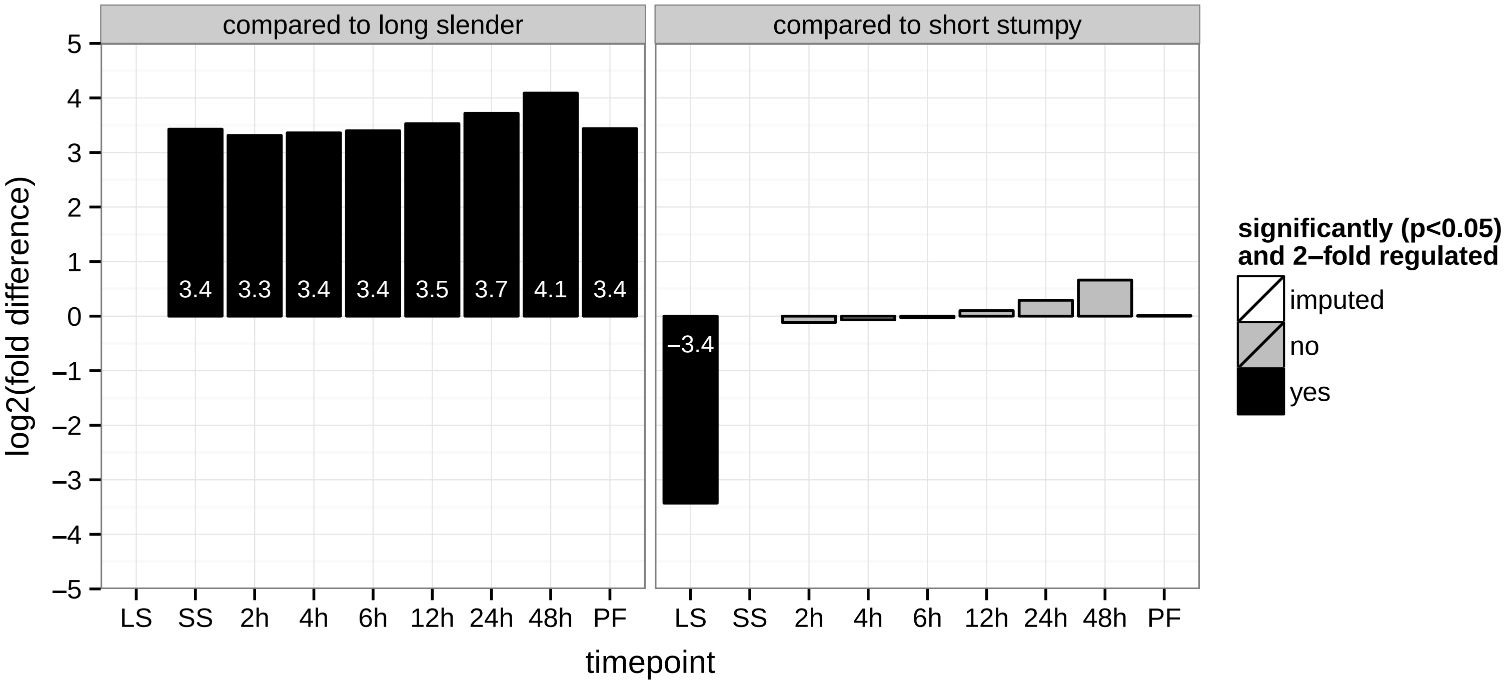
U3 small nuclear ribonucleoprotein (snRNP), putative
Tb927.6.2780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

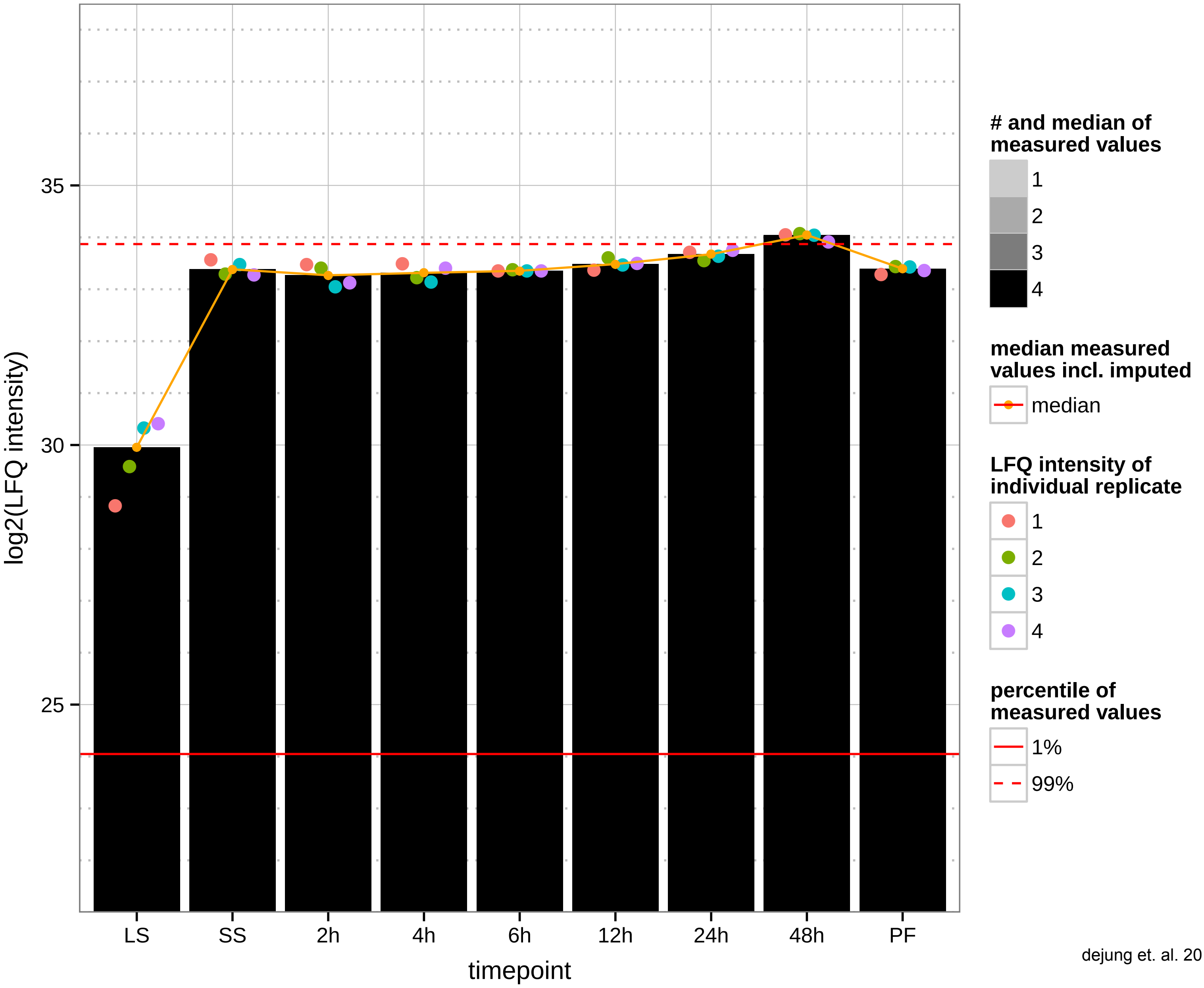




dejung et. al. 2015

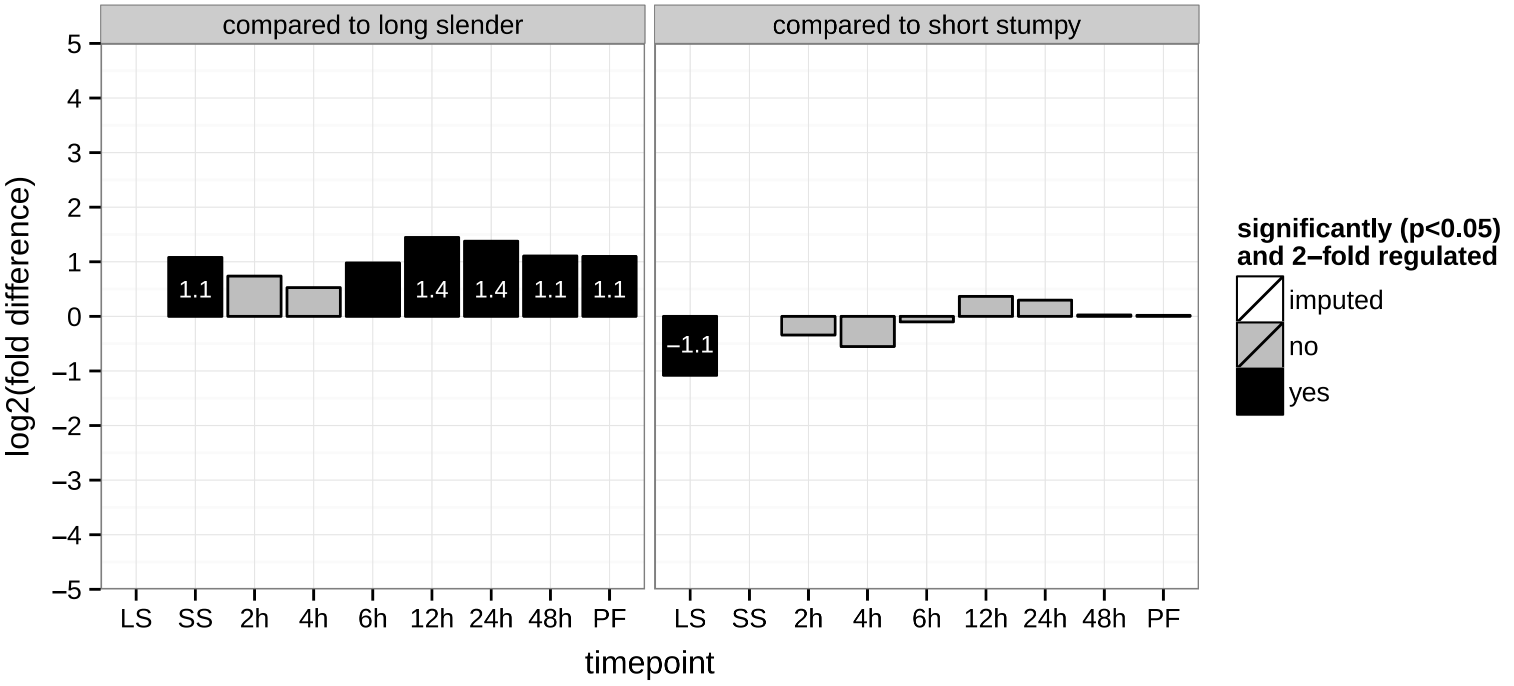
NA, L–threonine 3–dehydrogenase, putative
Tb927.6.2790
AGOF: NA, catalytic activity, coenzyme binding
AGOC: NA, mitochondrion
AGOP: NA, cellular metabolic process
PGOF: NA, catalytic activity, coenzyme binding
PGOC: NA, null
PGOP: NA, cellular metabolic process

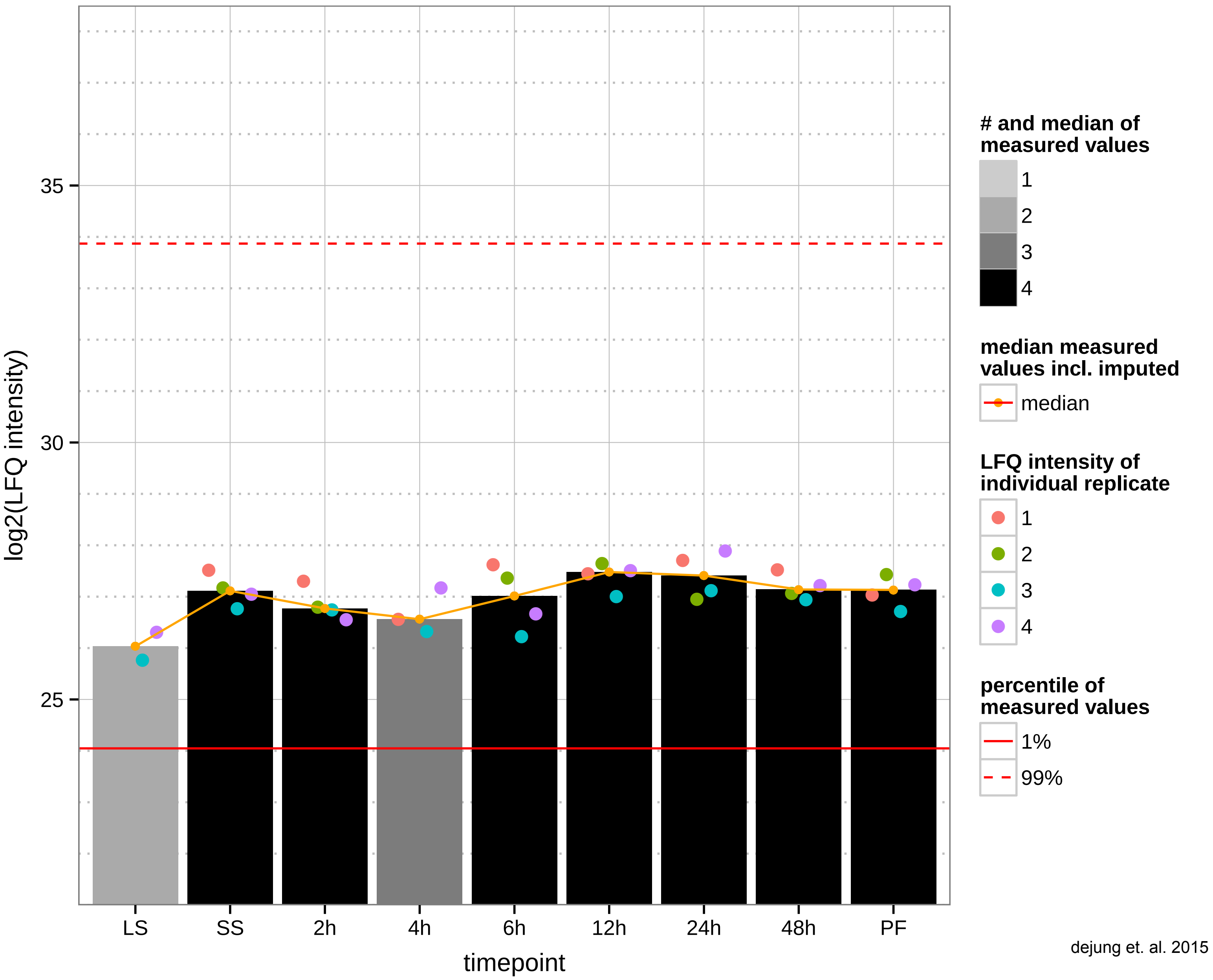




dejung et. al. 2015

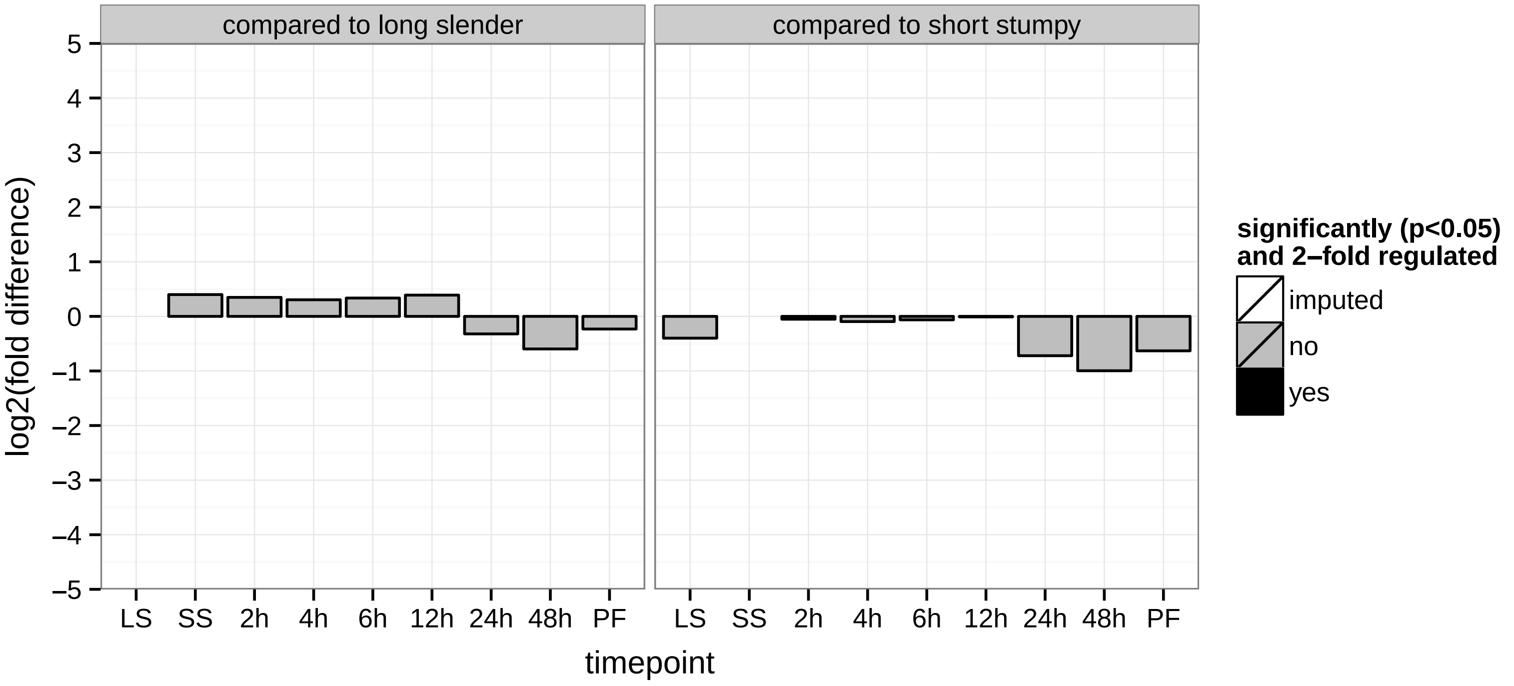
hypothetical protein, conserved
Tb927.6.2840
AGOF: ATP binding, protein serine/threonine kinase activity
AGOC: null
AGOP: growth, protein phosphorylation
PGOF: ATP binding, catalytic activity, protein serine/threonine kinase activity, transferase activity, transferring phosphorus–cor
PGOC: null
PGOP: protein phosphorylation

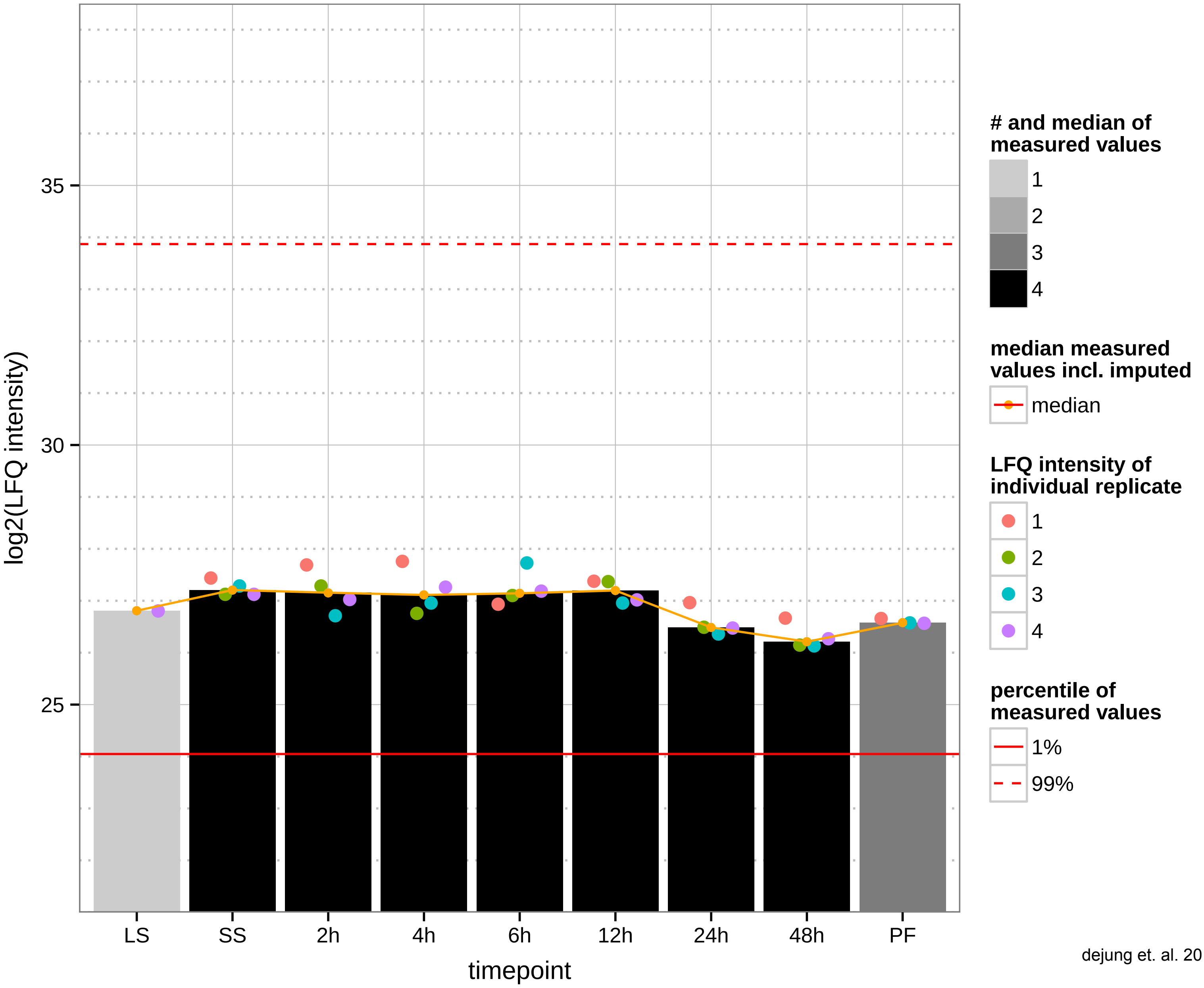




dejung et. al. 2015

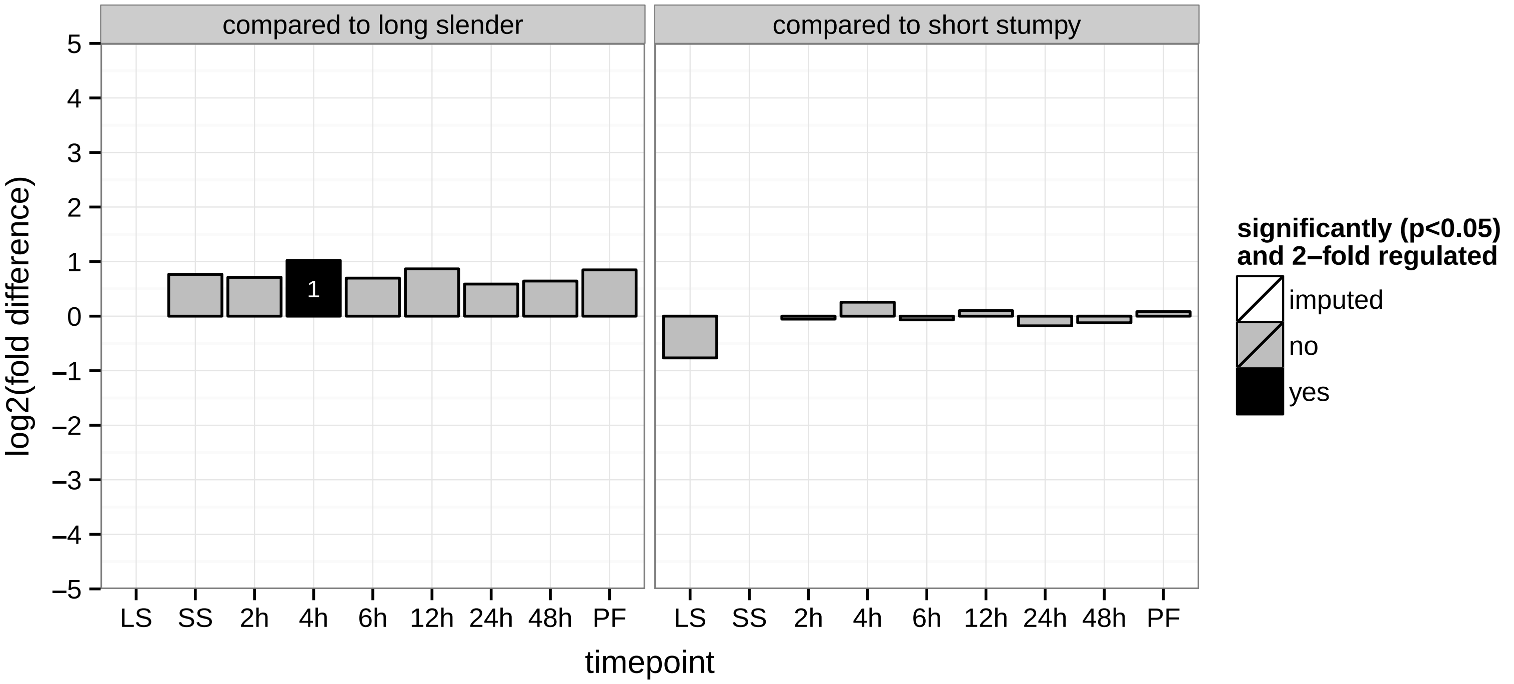
hypothetical protein, conserved
Tb927.6.2860
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

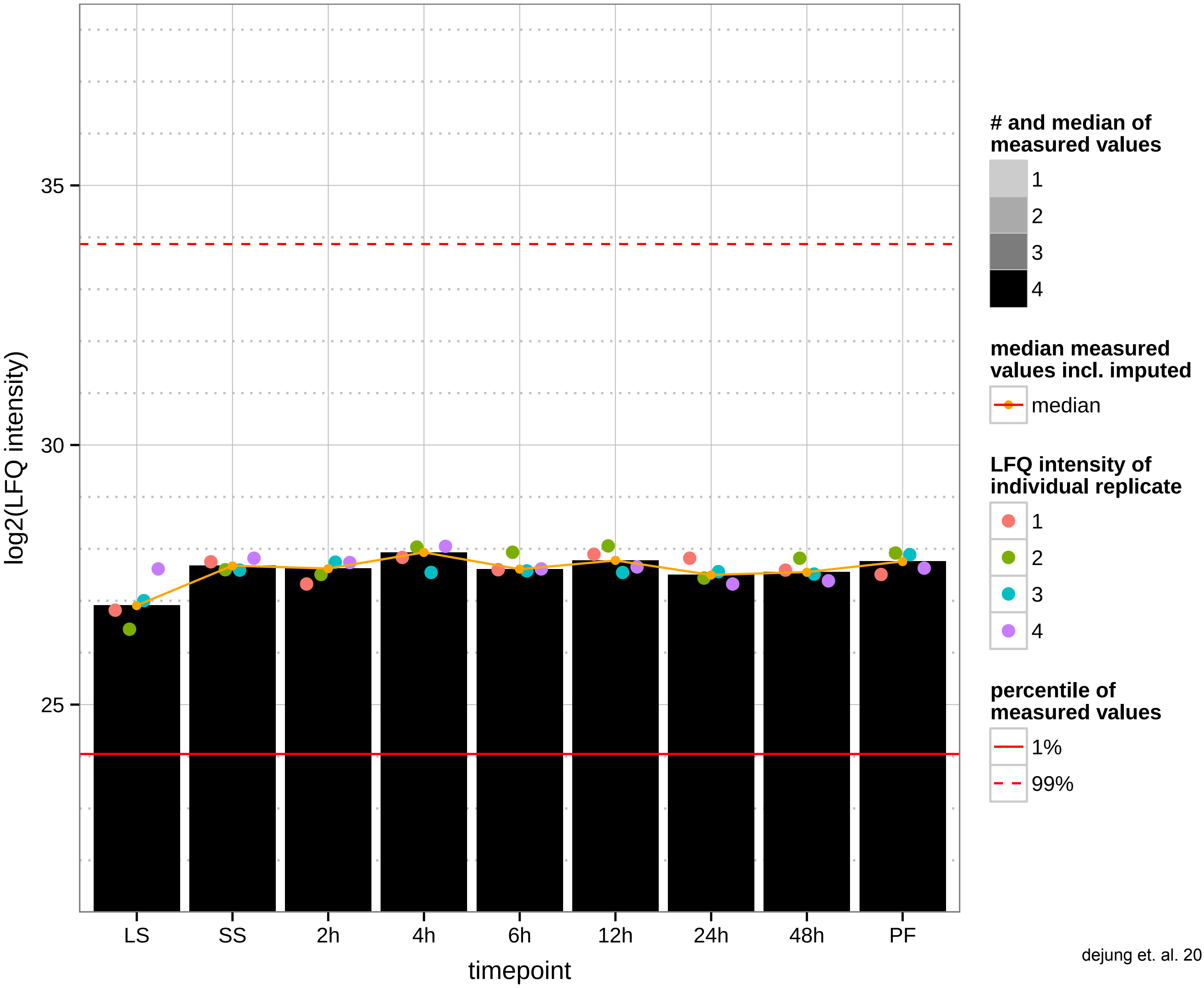




dejung et. al. 2015

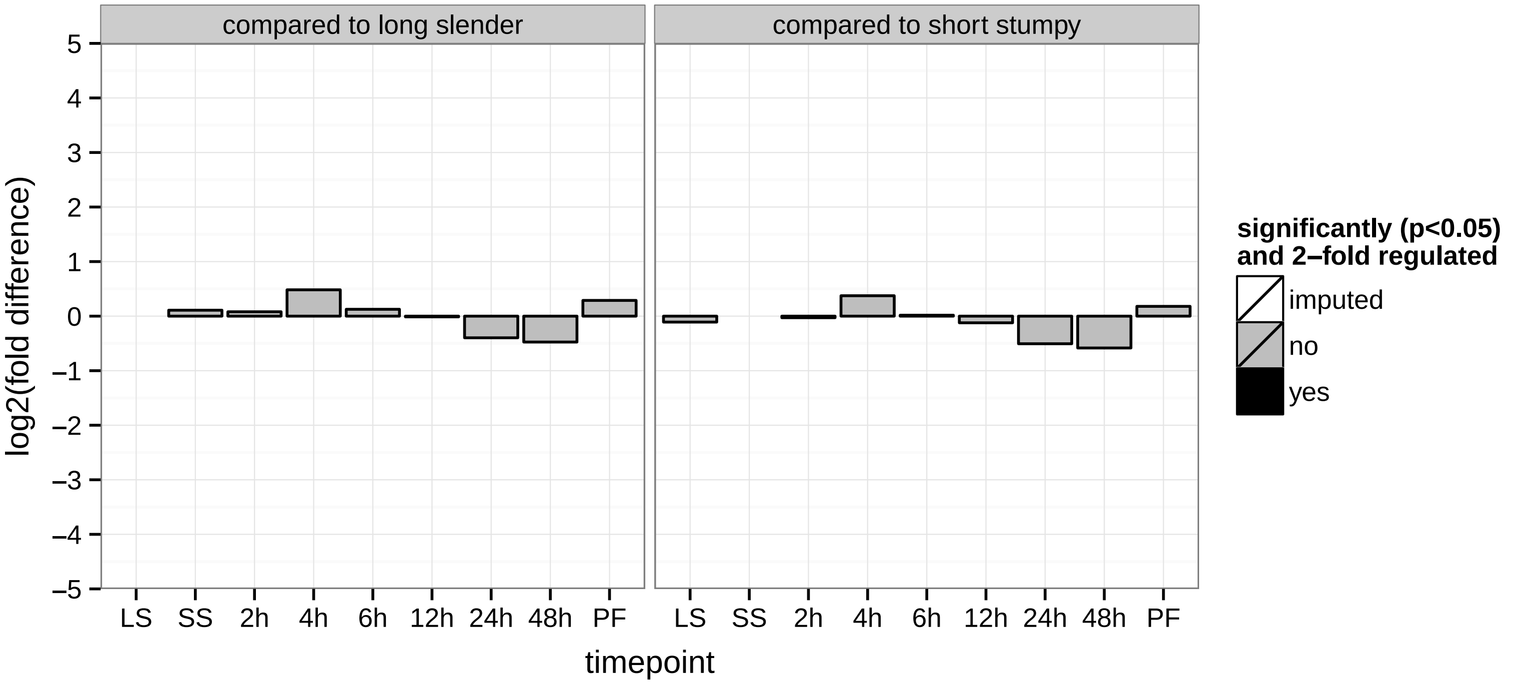
phosphopantothenoylcysteine decarboxylase, putative (PPCDC)
Tb927.6.2940
AGOF: phosphopantothenoylcysteine decarboxylase activity
AGOC: null
AGOP: coenzyme A biosynthetic process
PGOF: catalytic activity
PGOC: null
PGOP: null

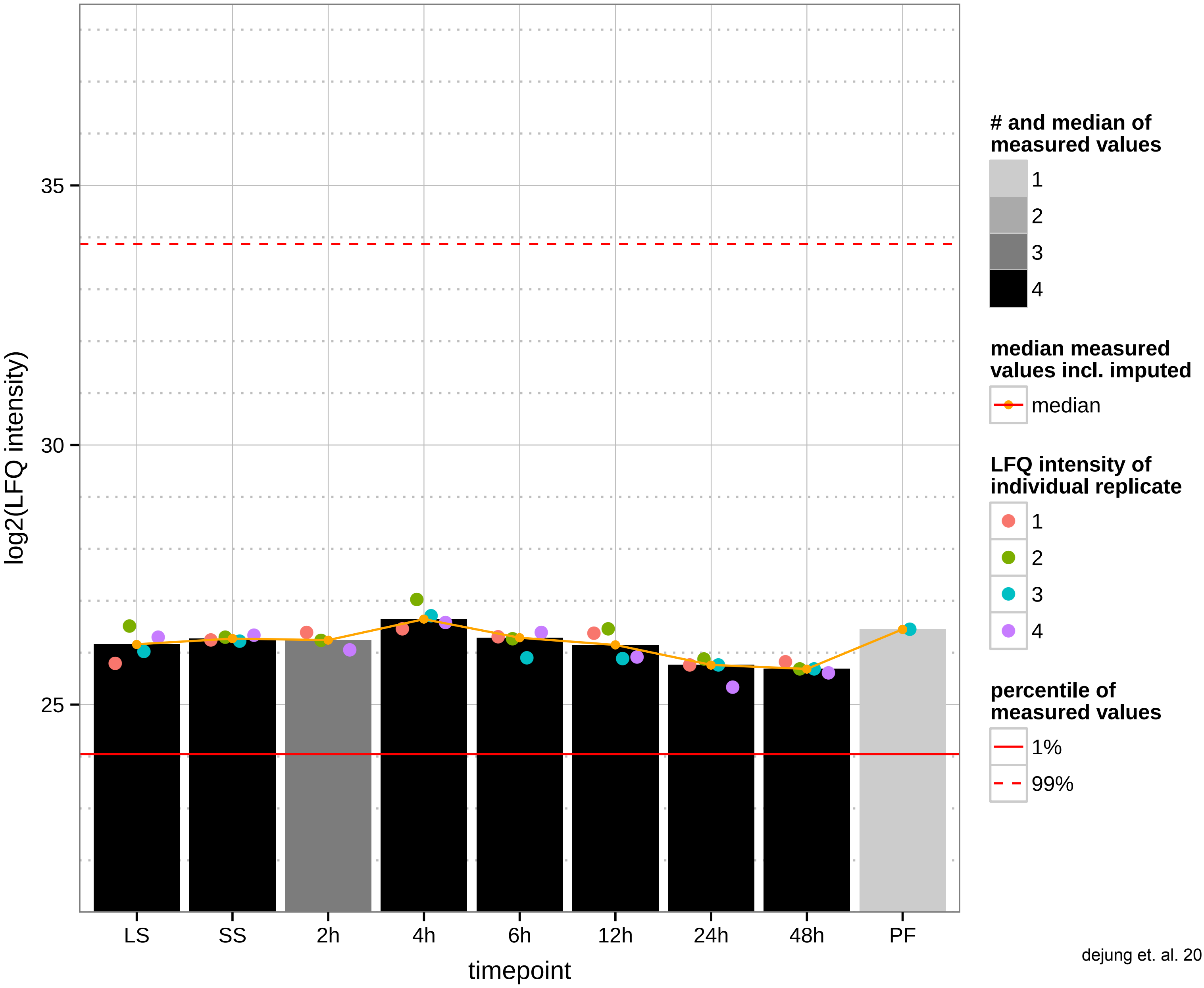




dejung et. al. 2015

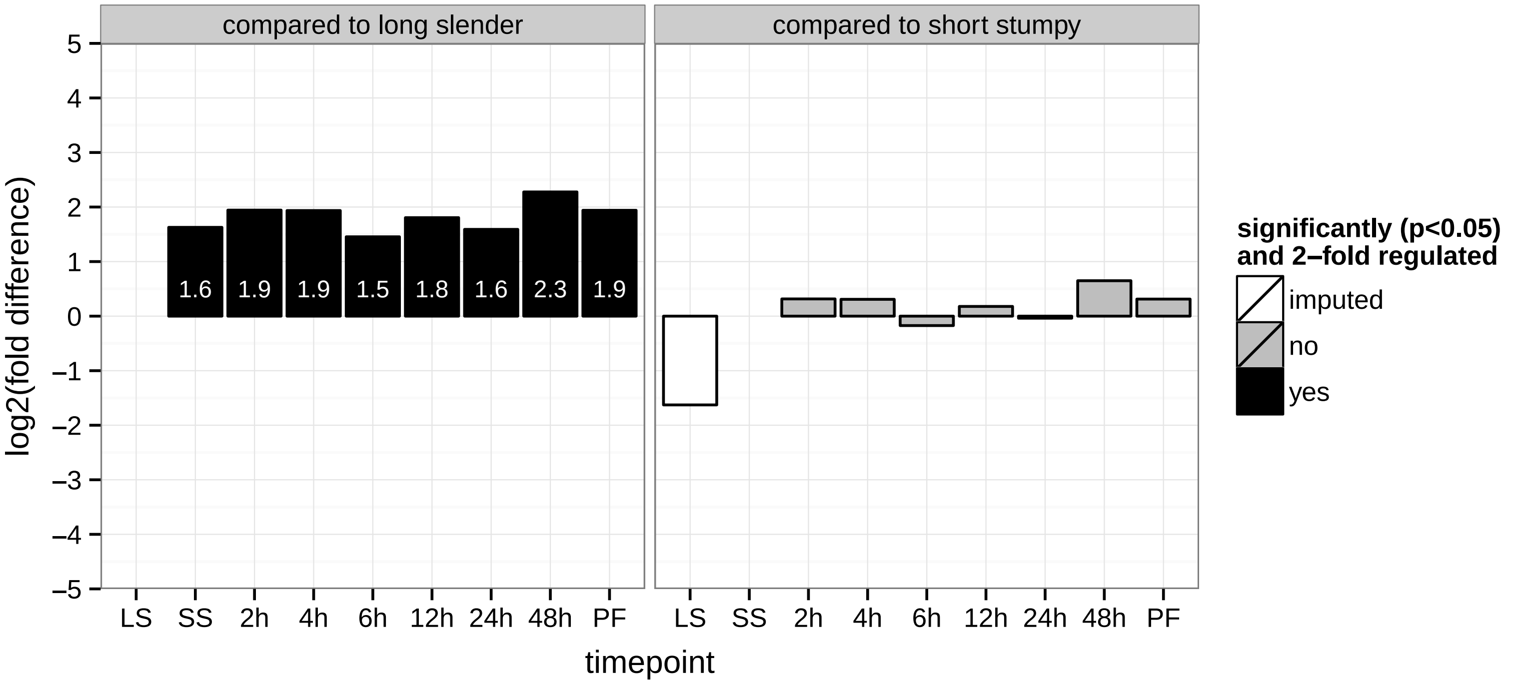
hypothetical protein, conserved
Tb927.6.3020
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

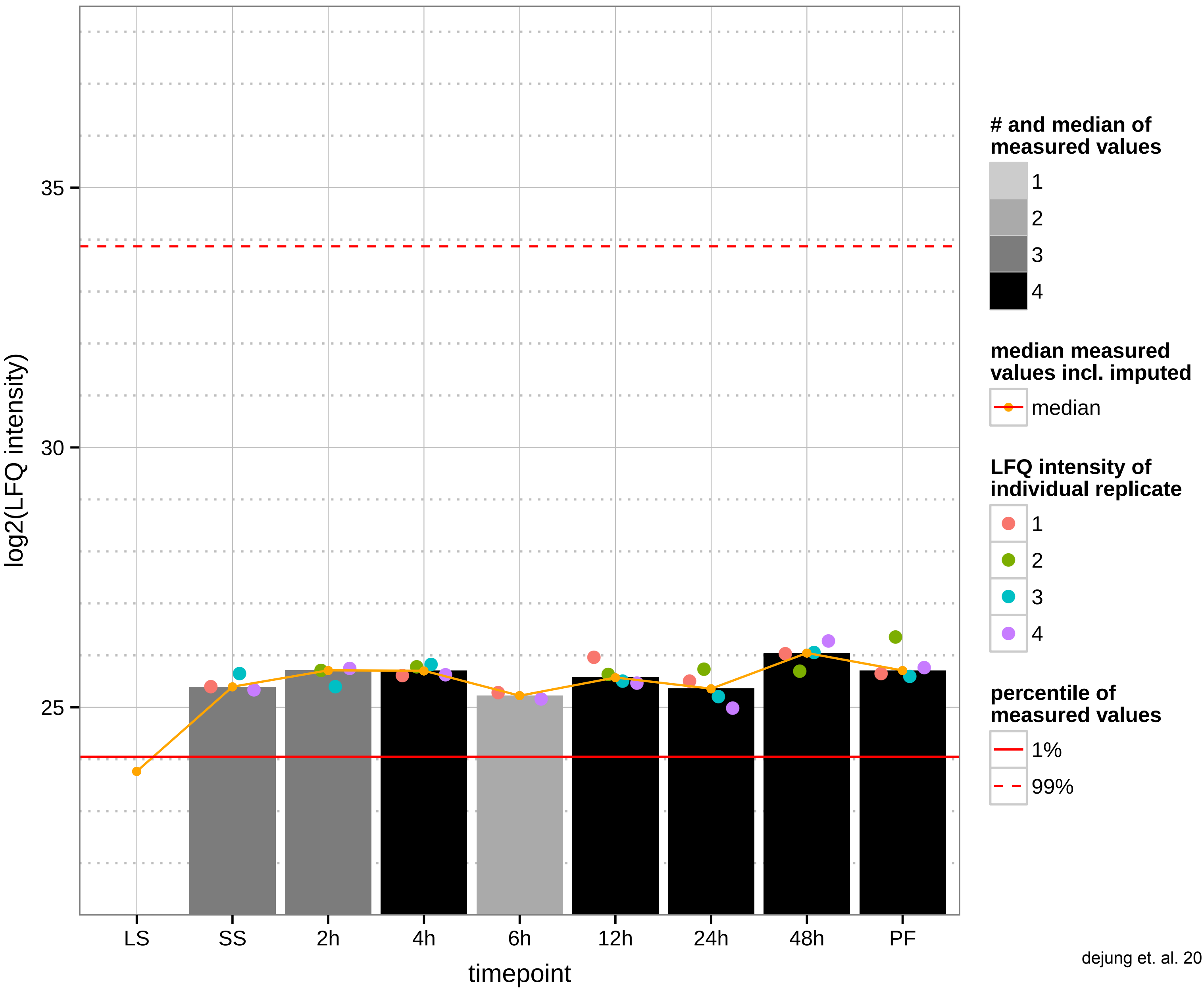




dejung et. al. 2015

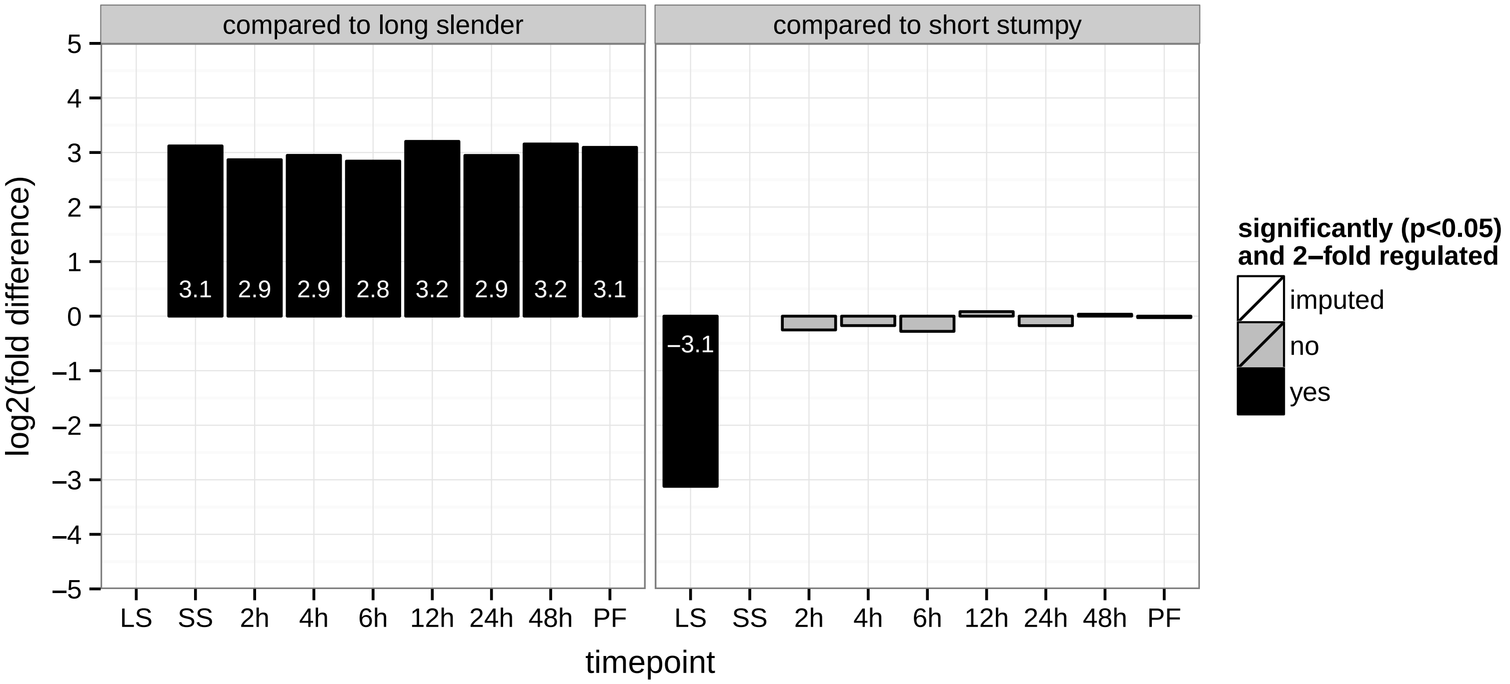
small GTP–binding protein Rab28, putative, Ras– related protein Rab–26 (Rab26)
Tb927.6.3040
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti

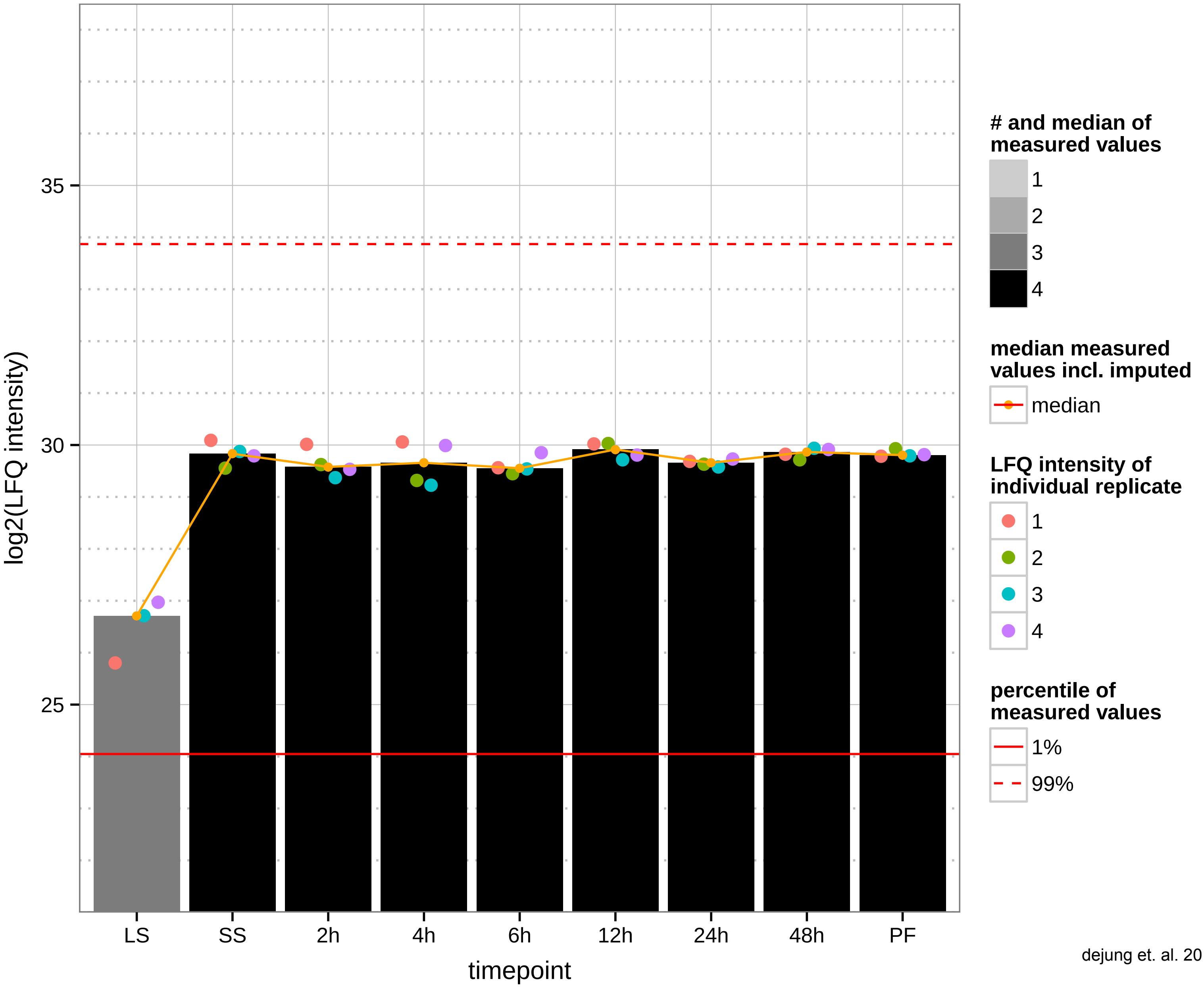




dejung et. al. 2015

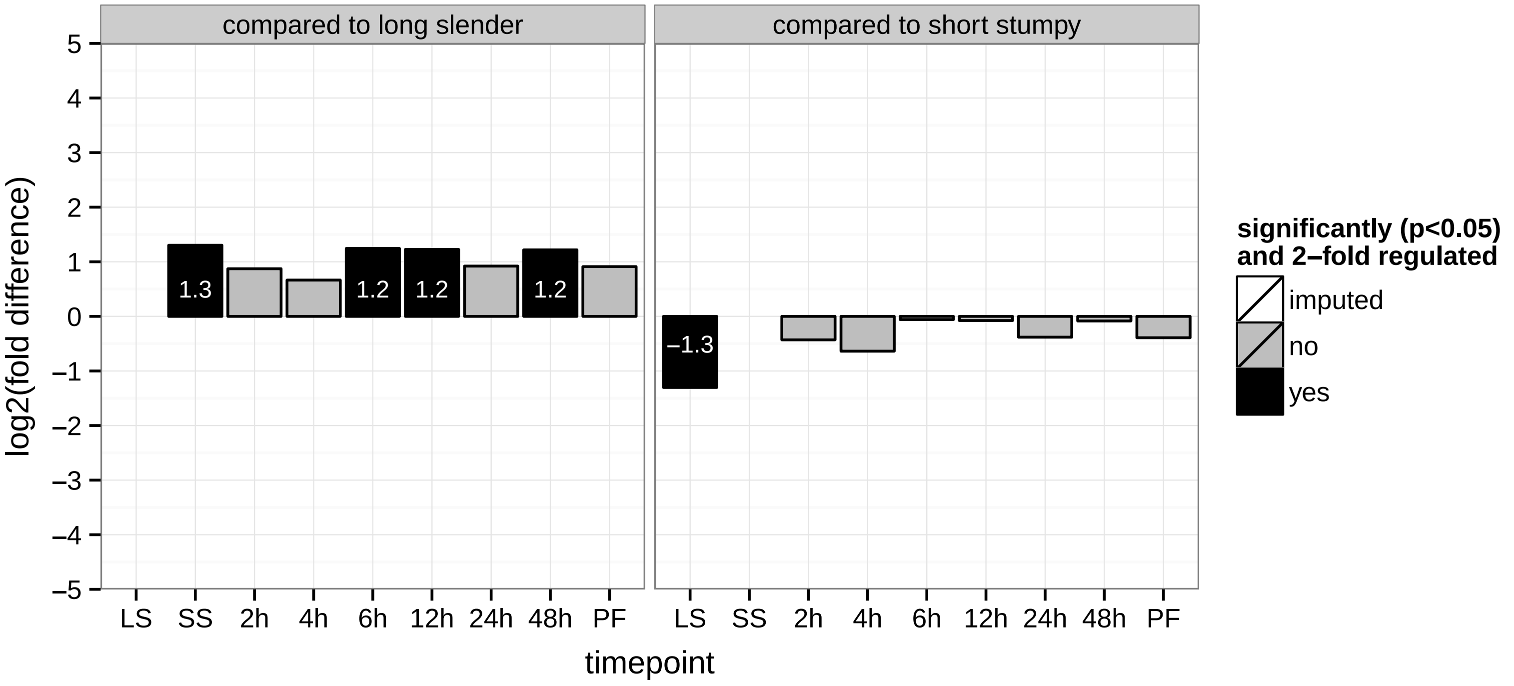
aldehyde dehydrogenase family, putative
Tb927.6.3050
AGOF: aldehyde dehydrogenase [NAD(P)+] activity
AGOC: null
AGOP: cellular aldehyde metabolic process, oxidation–reduction process
PGOF: aldehyde dehydrogenase [NAD(P)+] activity, oxidoreductase activity
PGOC: null
PGOP: cellular aldehyde metabolic process, metabolic process, oxidation–reduction process

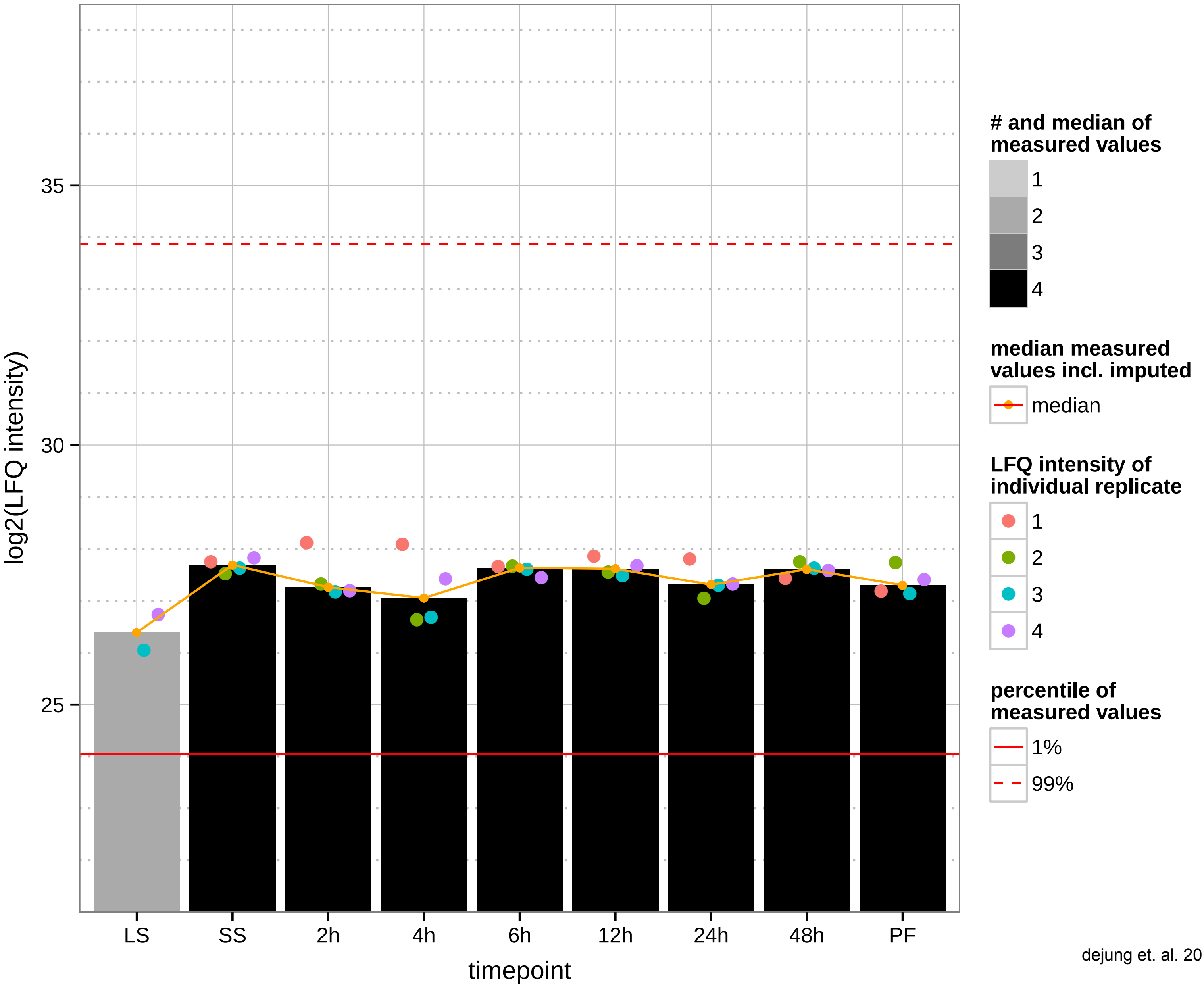




dejung et. al. 2015

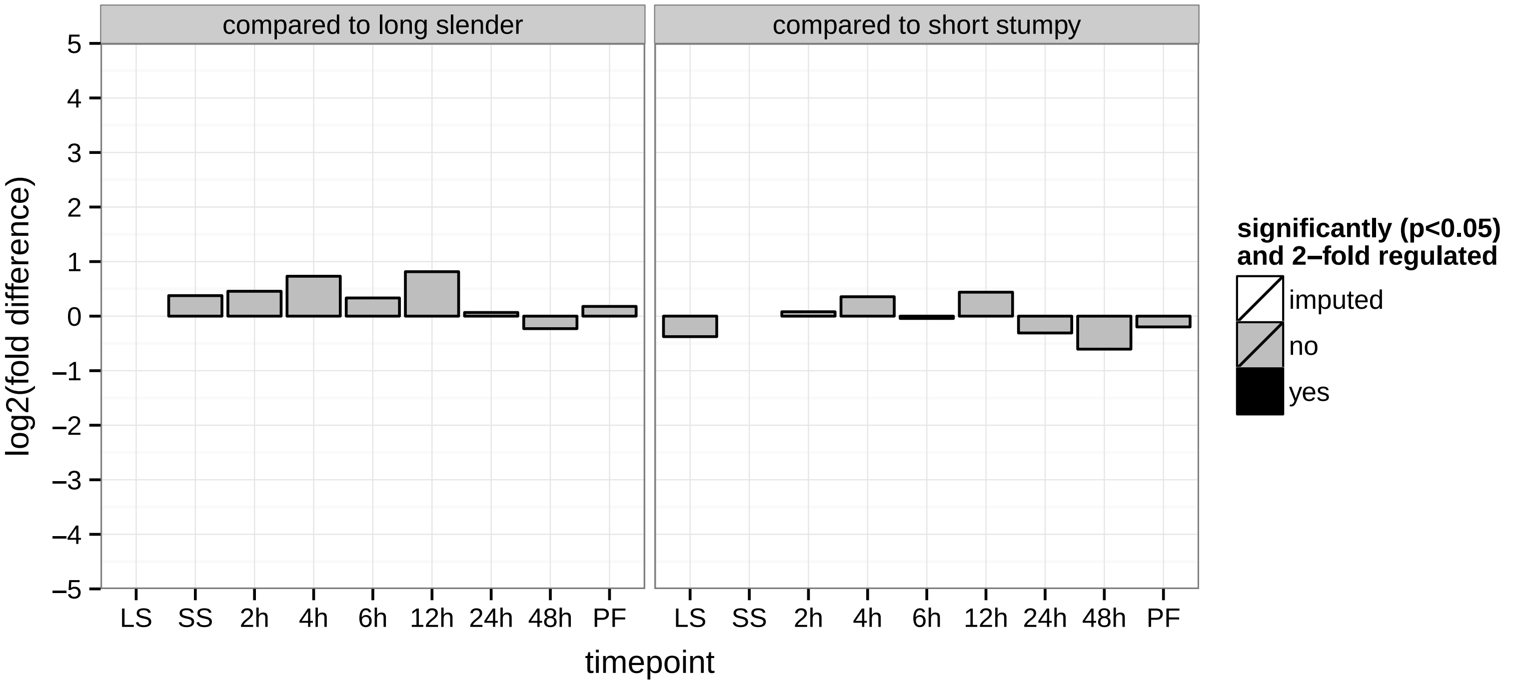
cytoskeleton–associated protein, putative
Tb927.6.3090
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

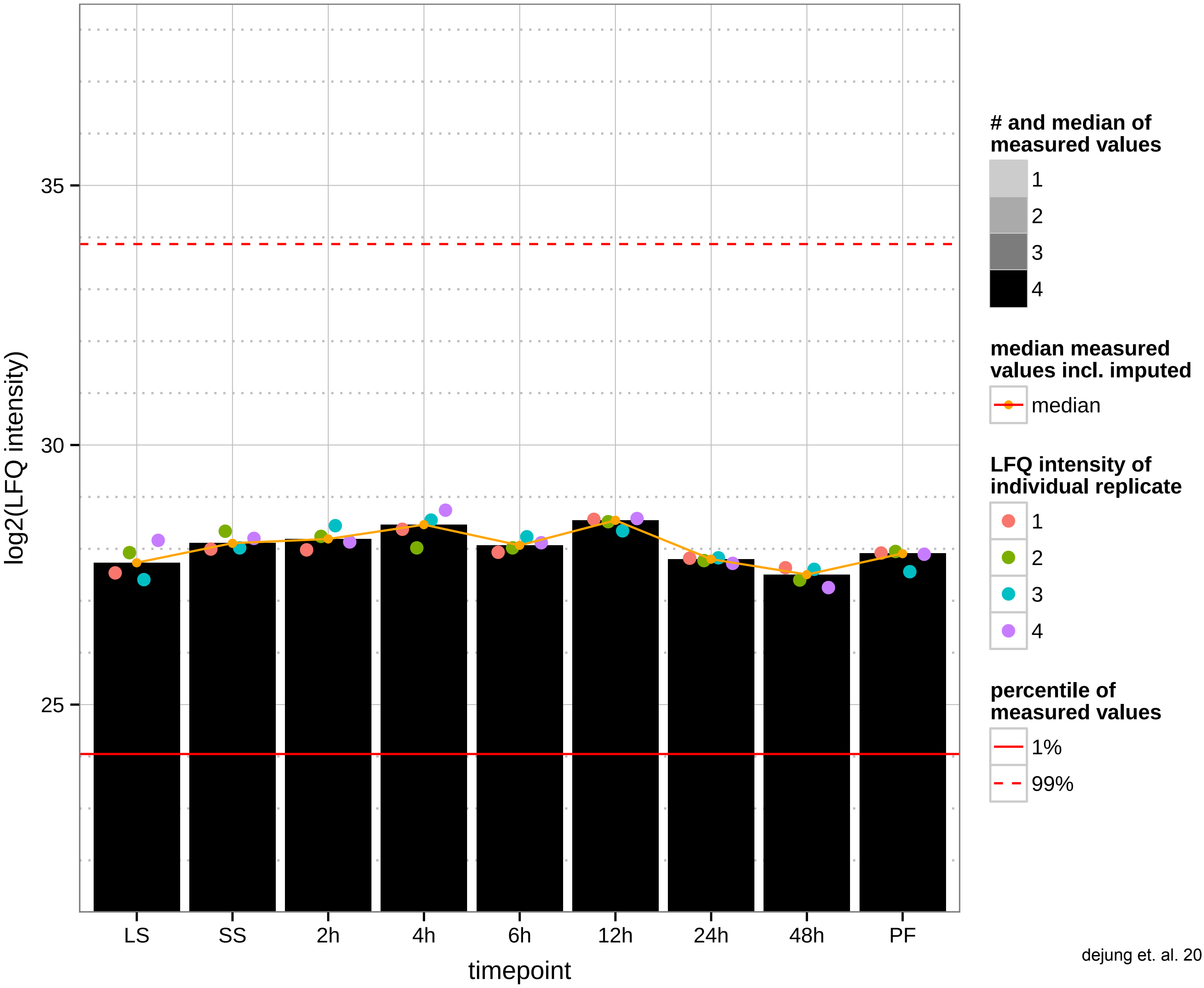




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.3100
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: intraflagellar transport





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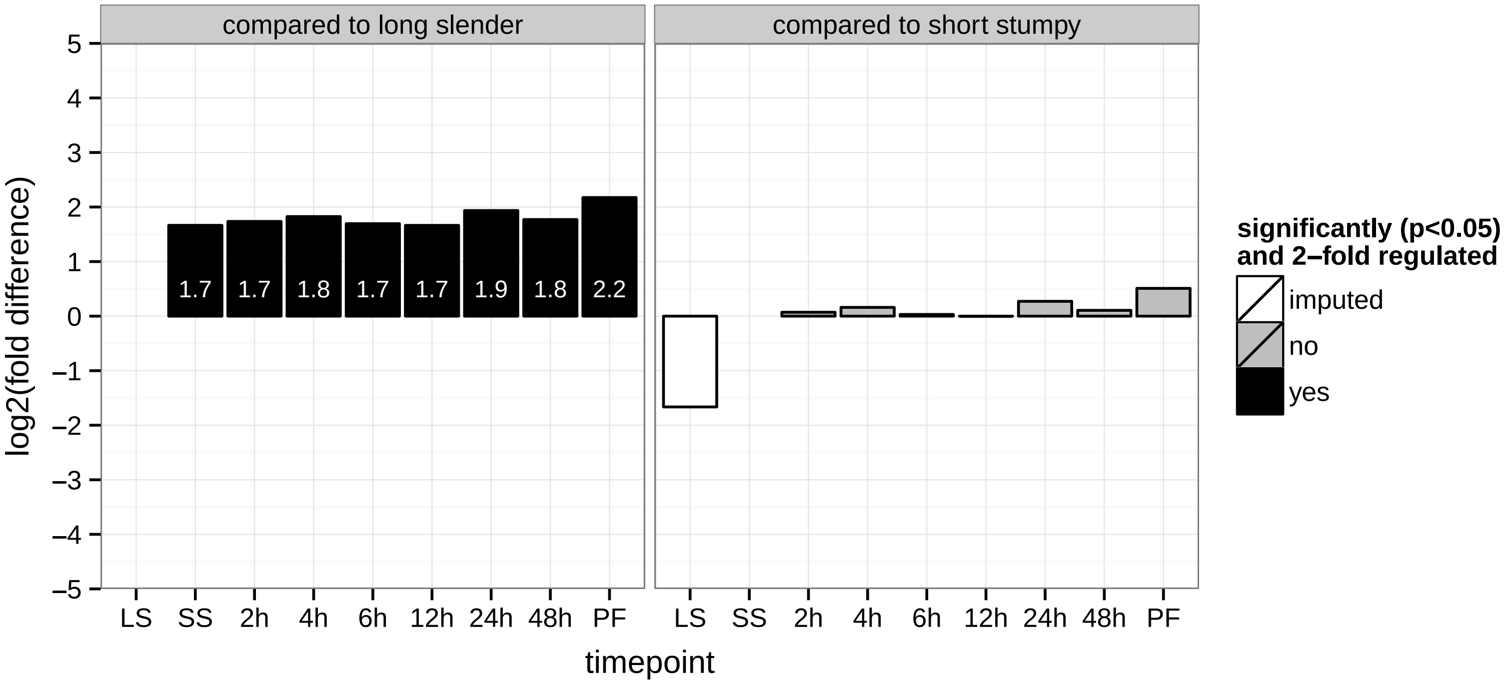
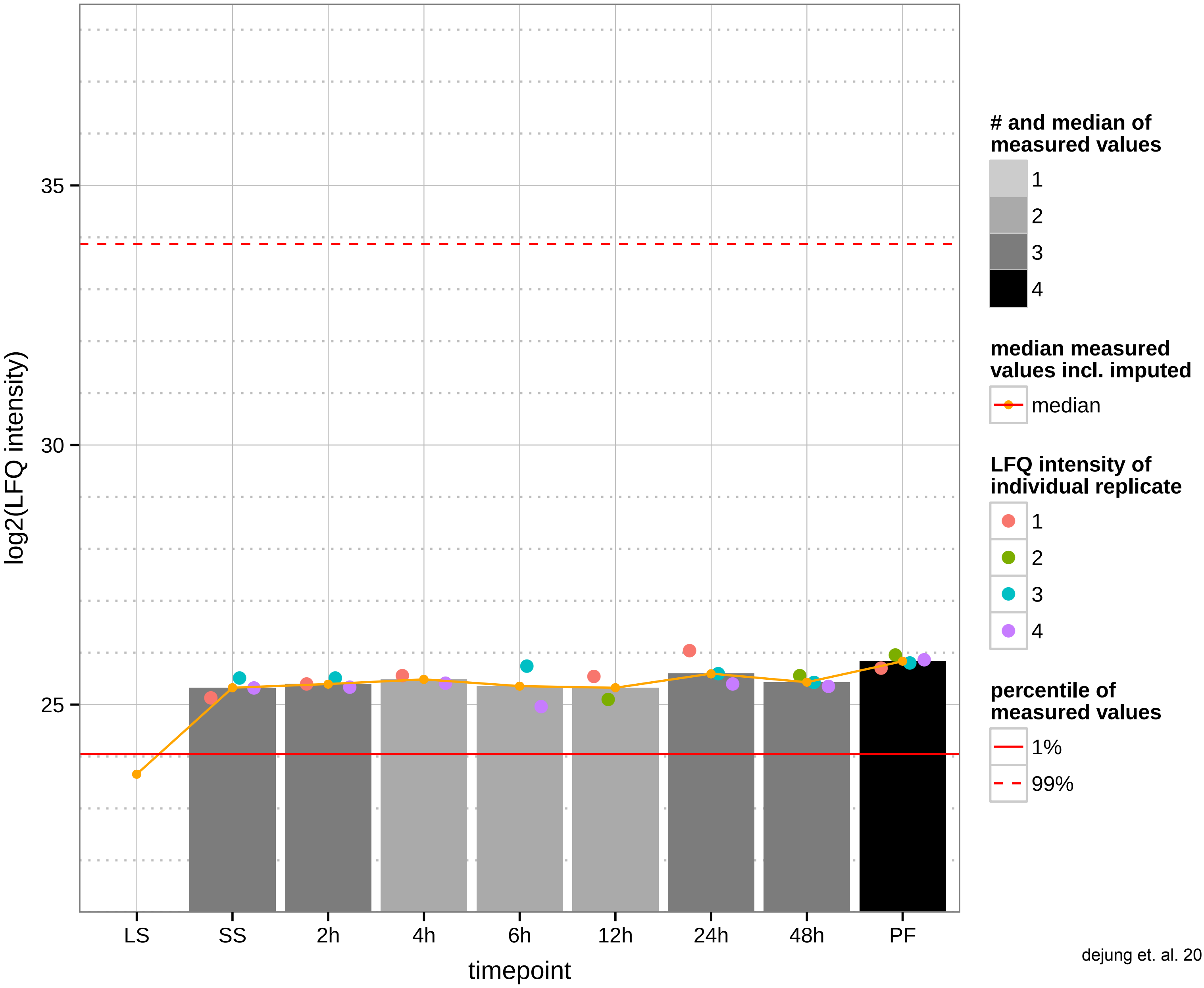
queuine tRNA–ribosyltransferase, putative
Tb927.6.3130
AGOF: queuine tRNA–ribosyltransferase activity
AGOC: null
AGOP: queuosine biosynthetic process
PGOF: queuine tRNA–ribosyltransferase activity
PGOC: null
PGOP: queuosine biosynthetic process, tRNA modification





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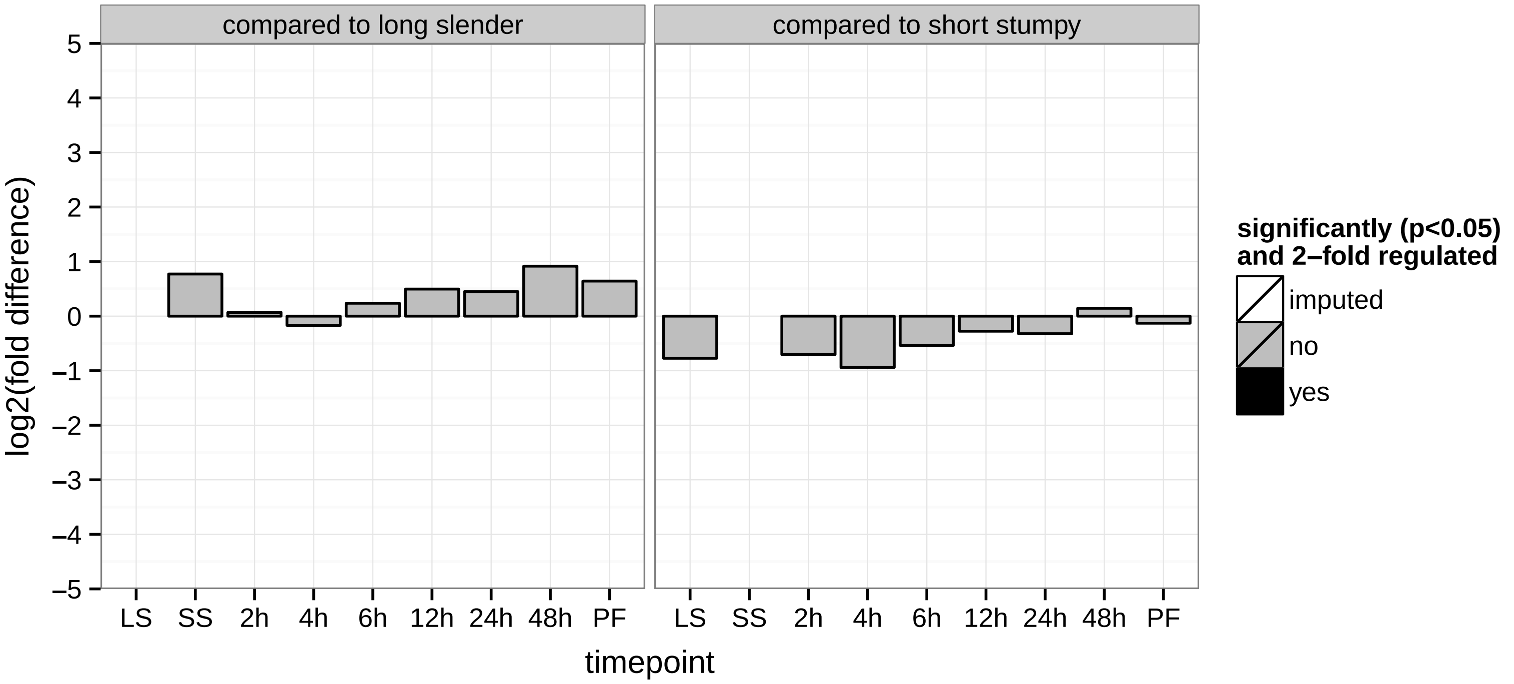
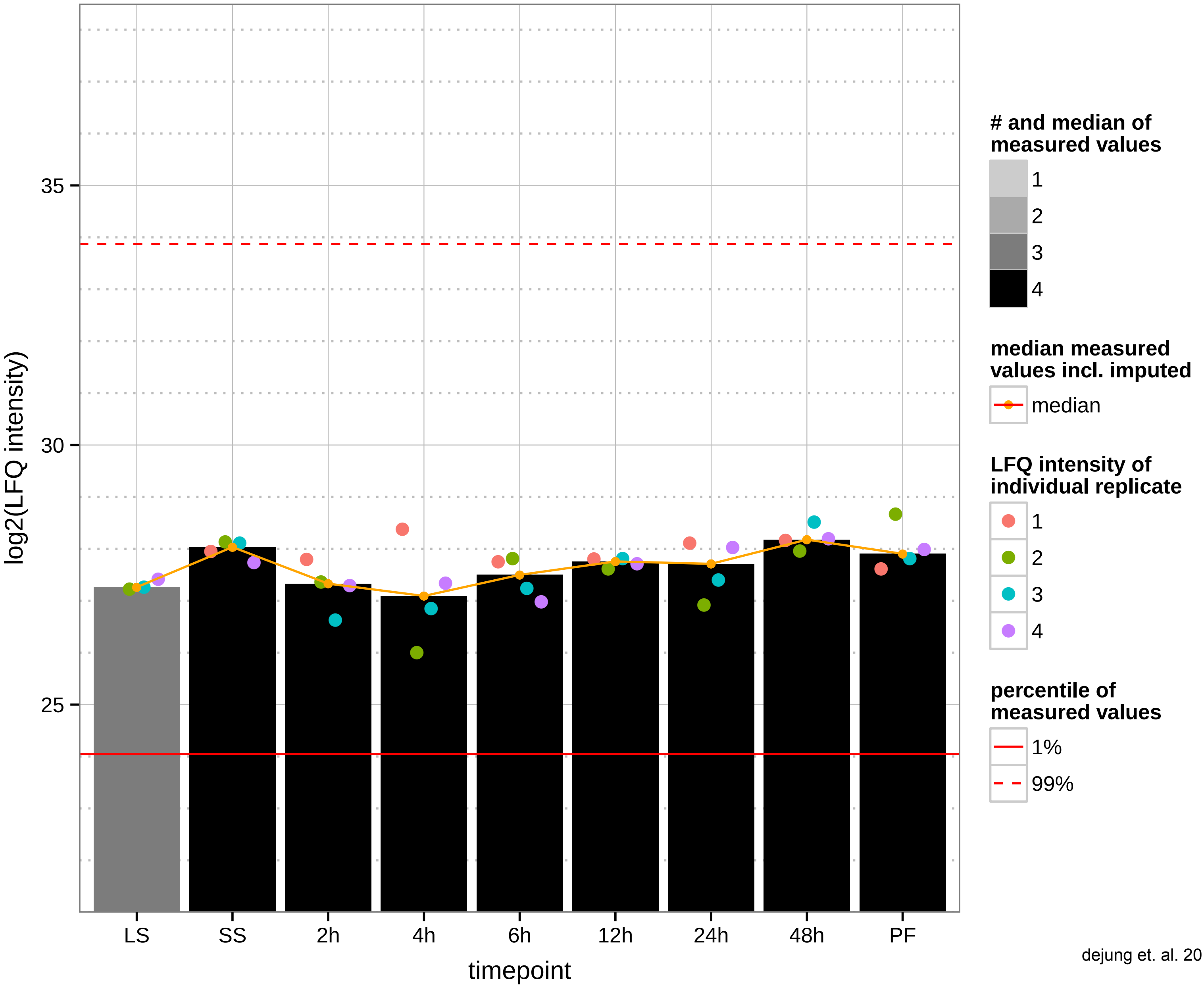
Hydin, flagellar component
Tb927.6.3150
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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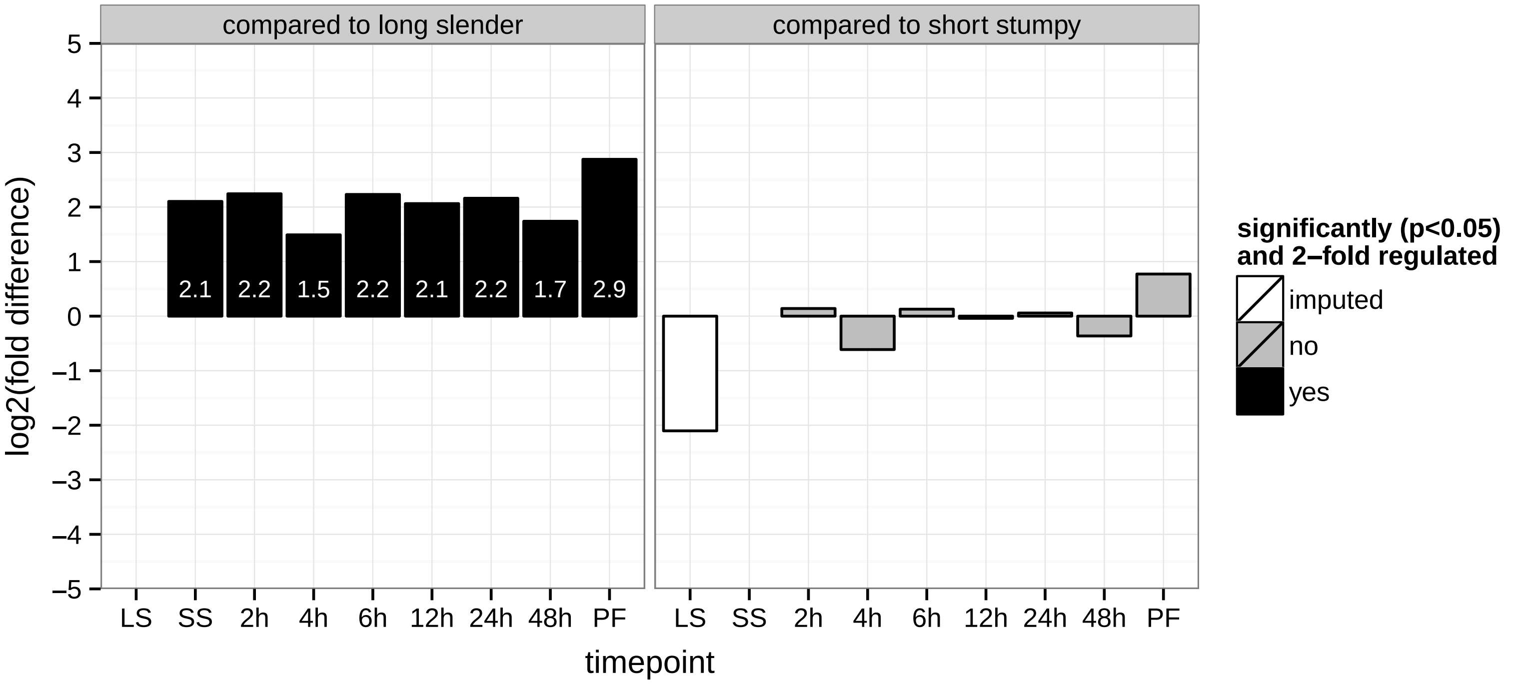
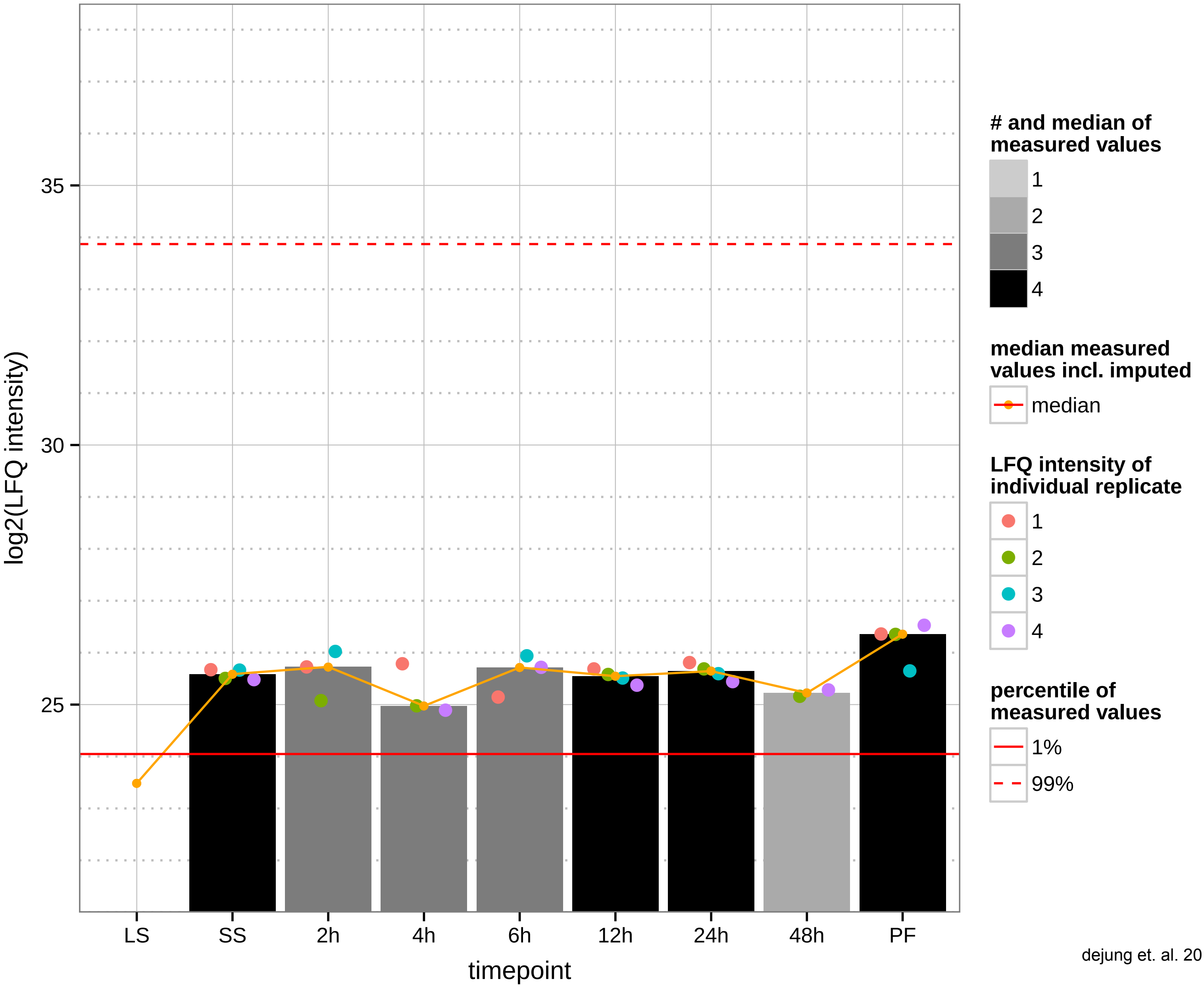
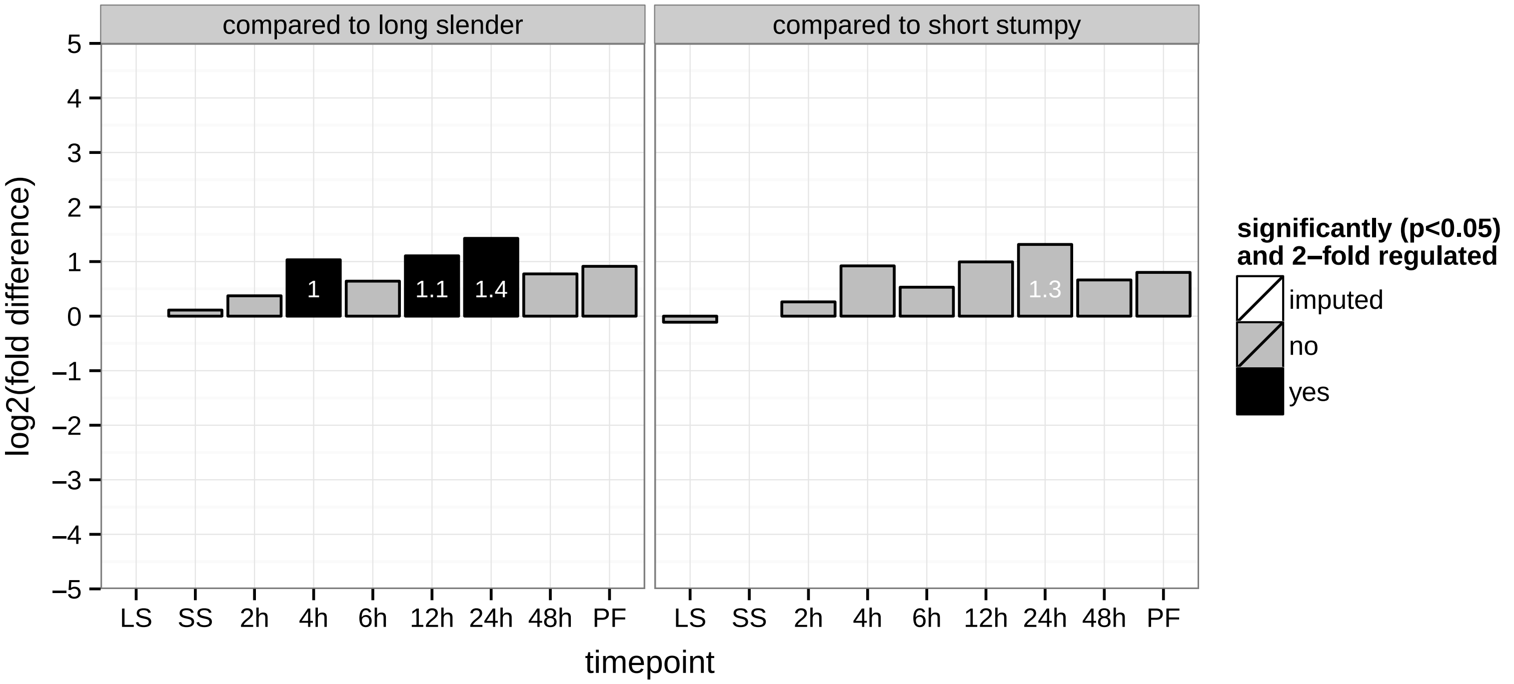
splicing factor 3a, putative
Tb927.6.3160
AGOF: nucleic acid binding, zinc ion binding
AGOC: nucleus
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: nucleus
PGOP: null

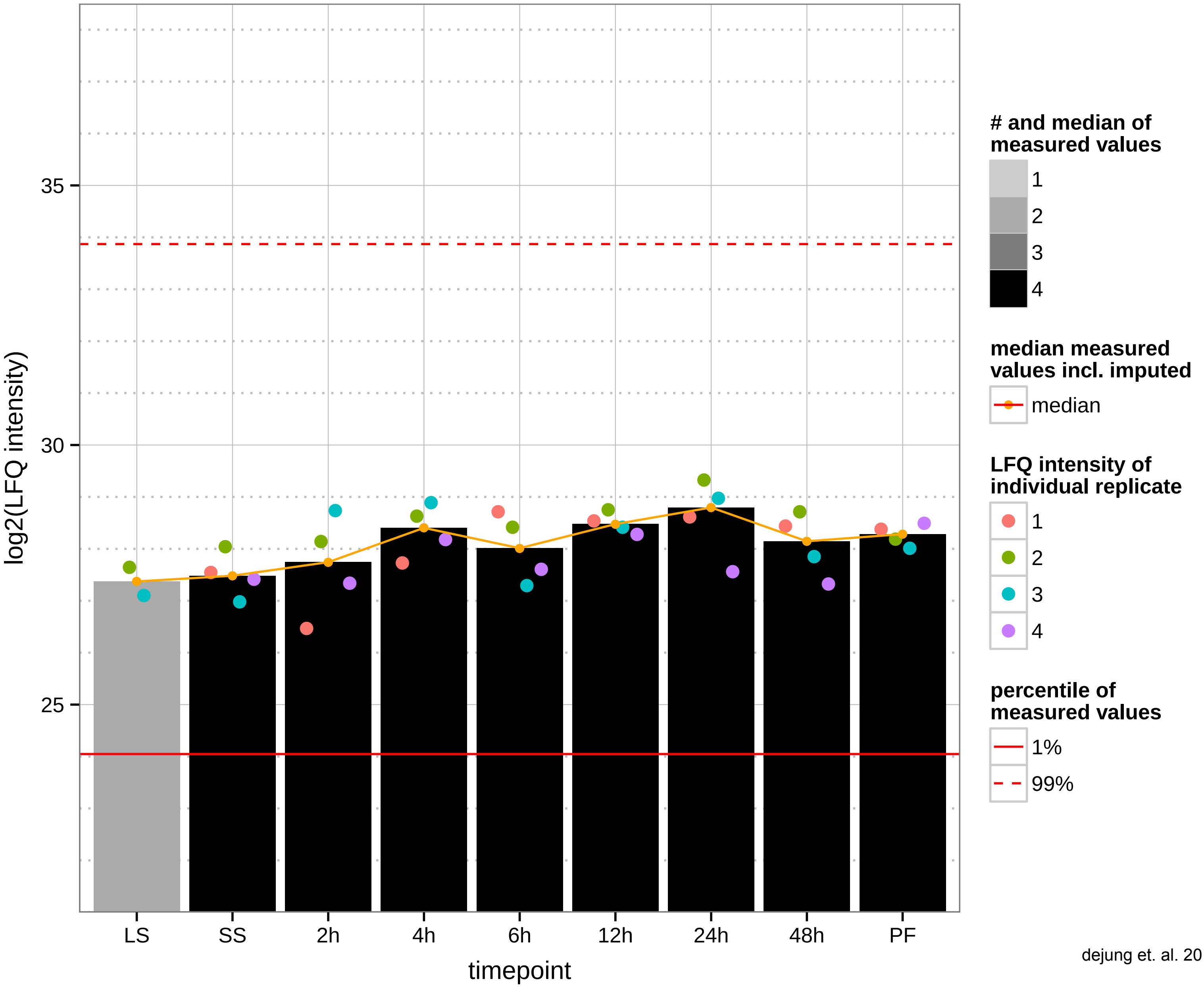




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.3210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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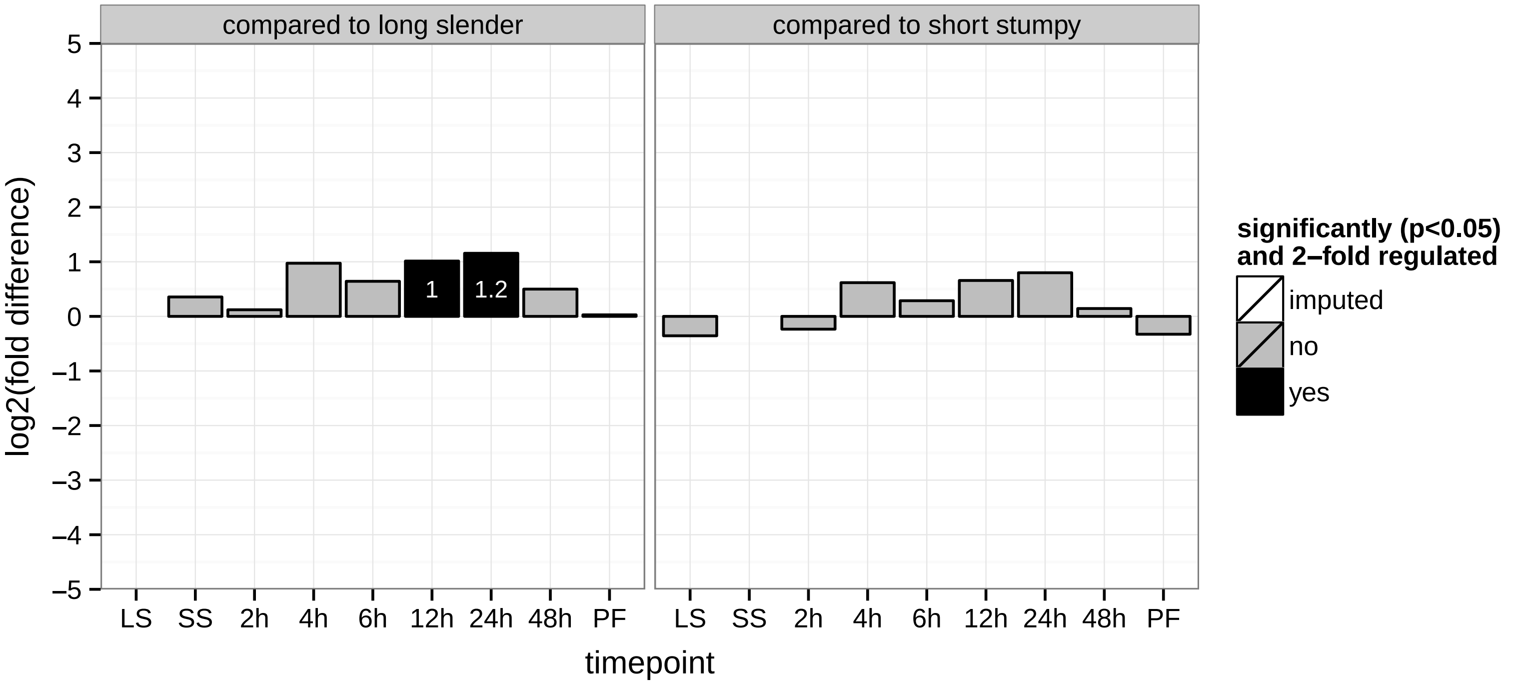
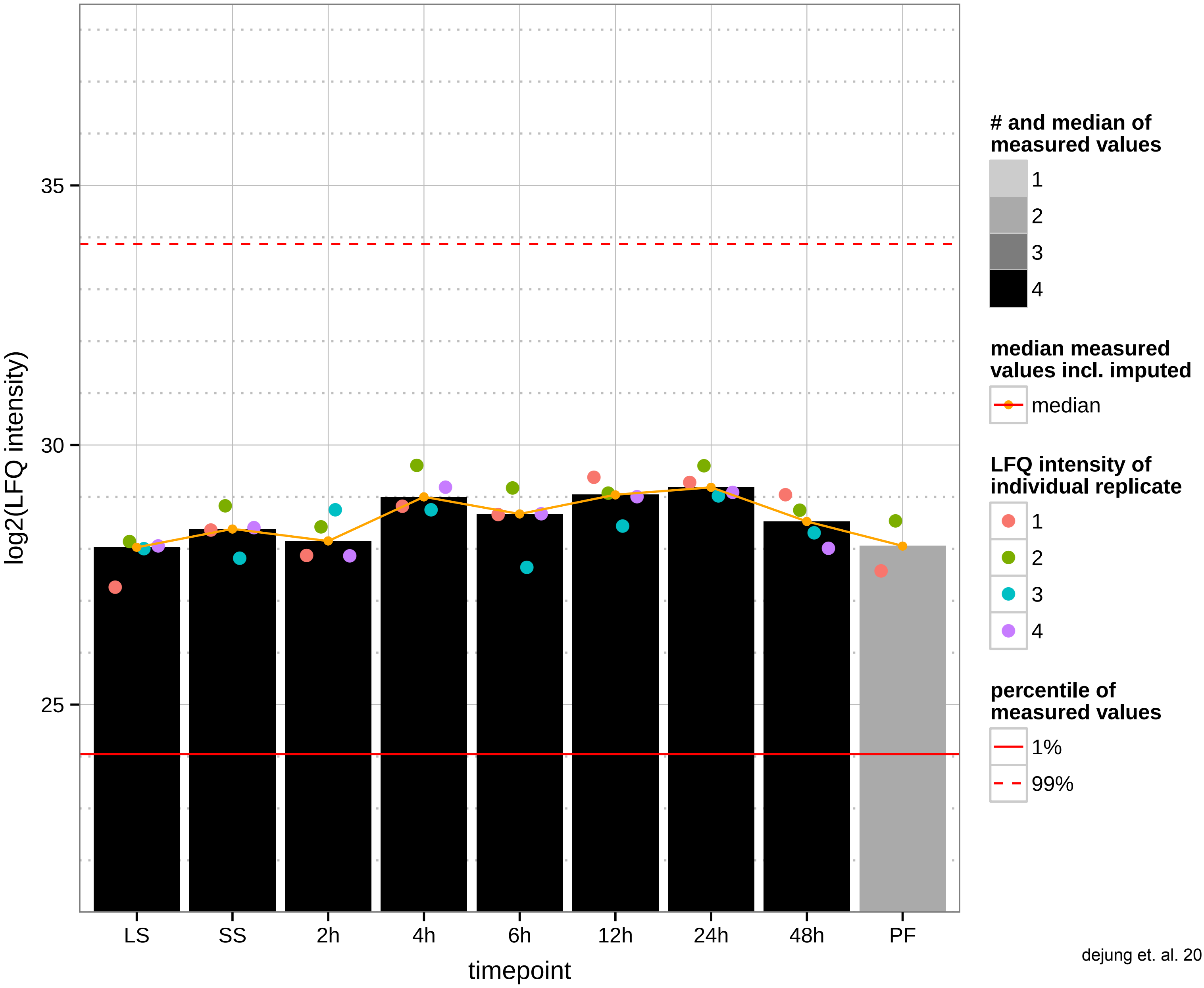
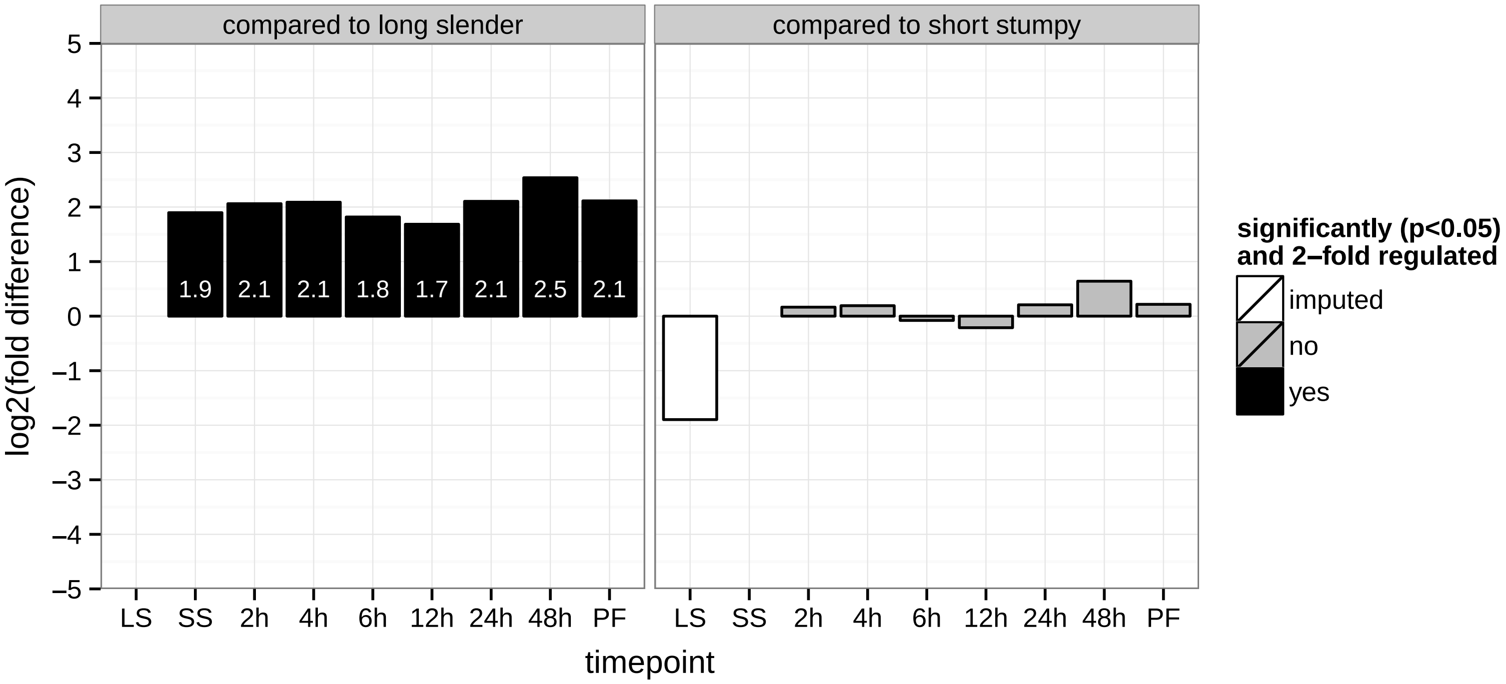
intraflagellar transport protein 20, putative (IFT20)
Tb927.6.3290
AGOF: null
AGOC: bacterial–type flagellum basal body
AGOP: null
PGOF: null
PGOC: null
PGOP: null

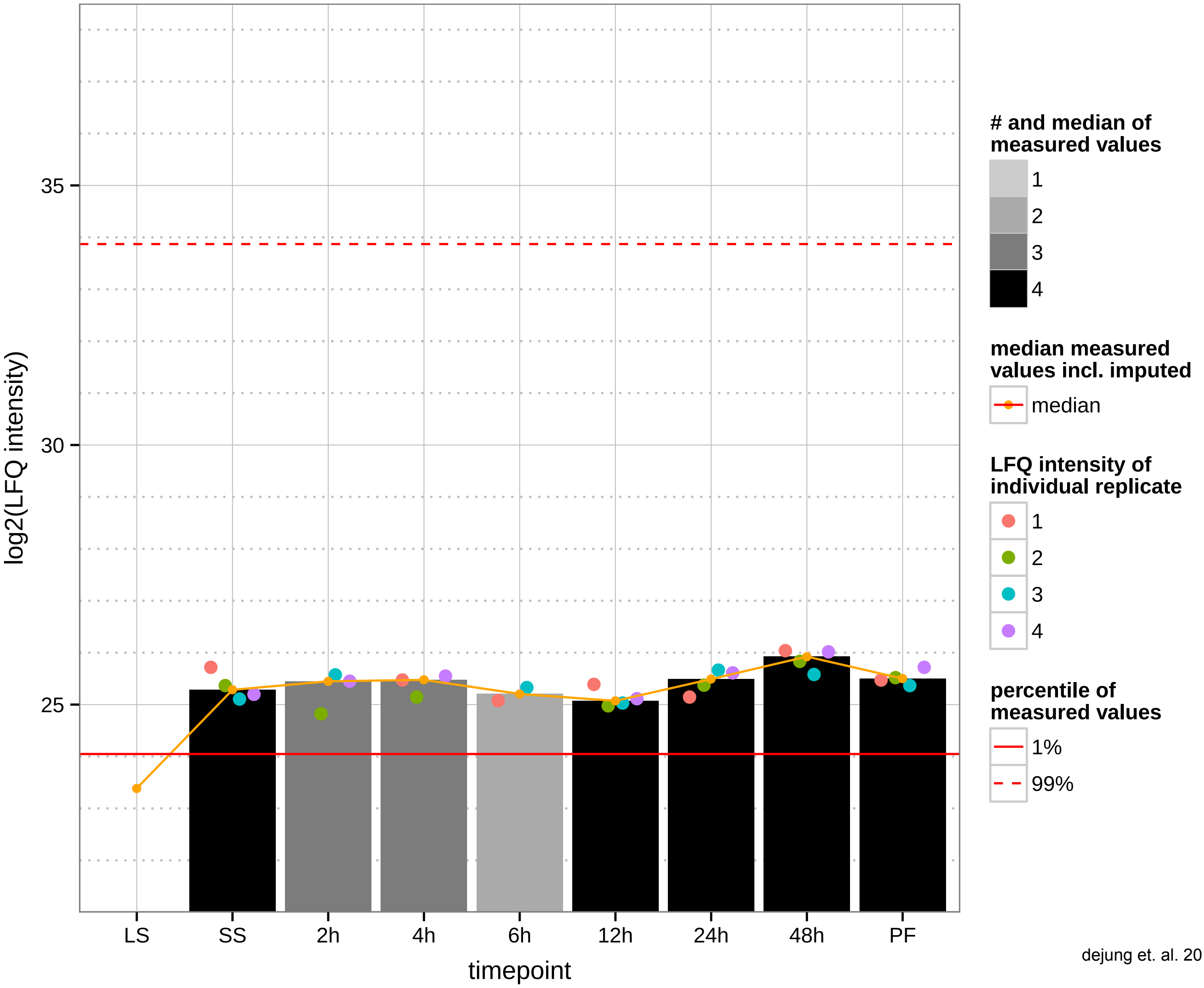




dejung et. al. 2015

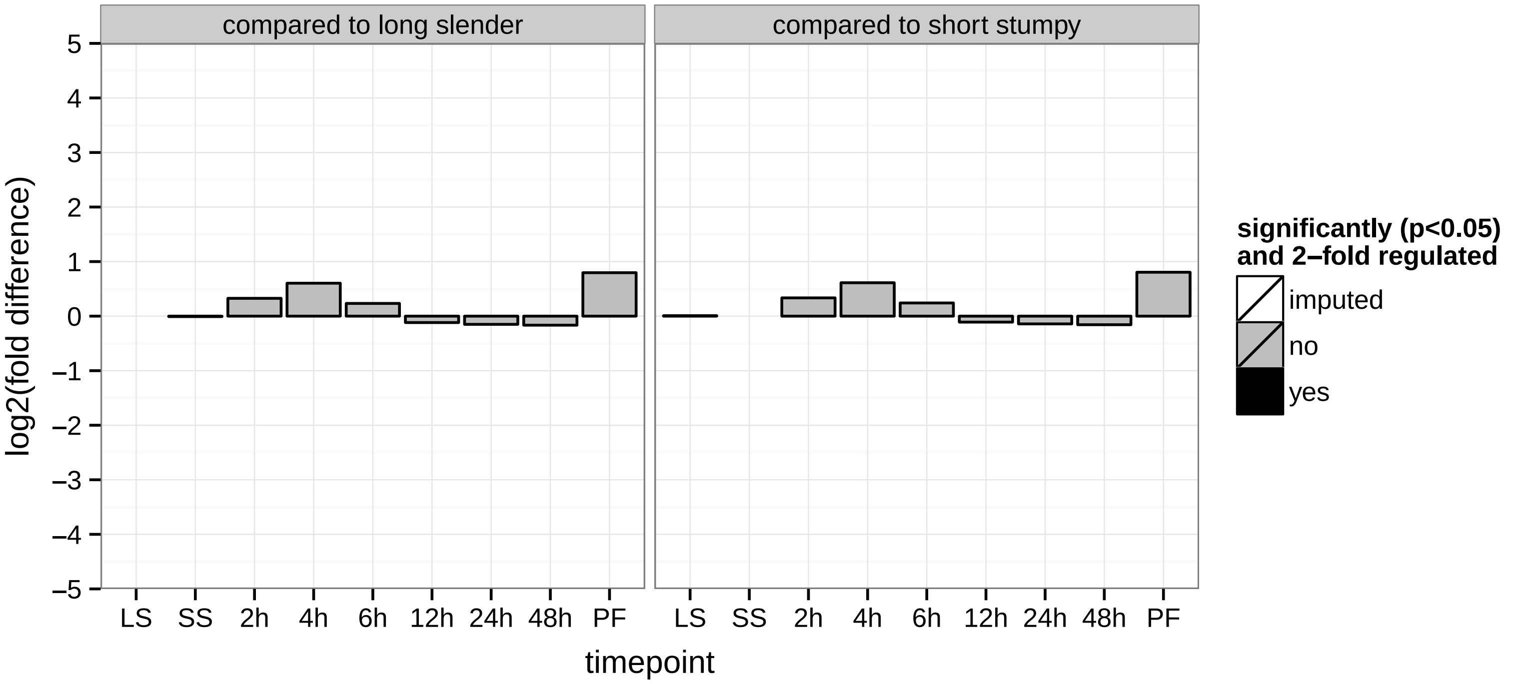
calpain–like cysteine peptidase, putative, cysteine peptidase, Clan CA, family C2
Tb927.6.3310
AGOF: calcium–dependent cysteine–type endopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: calcium–dependent cysteine–type endopeptidase activity
PGOC: intracellular
PGOP: proteolysis

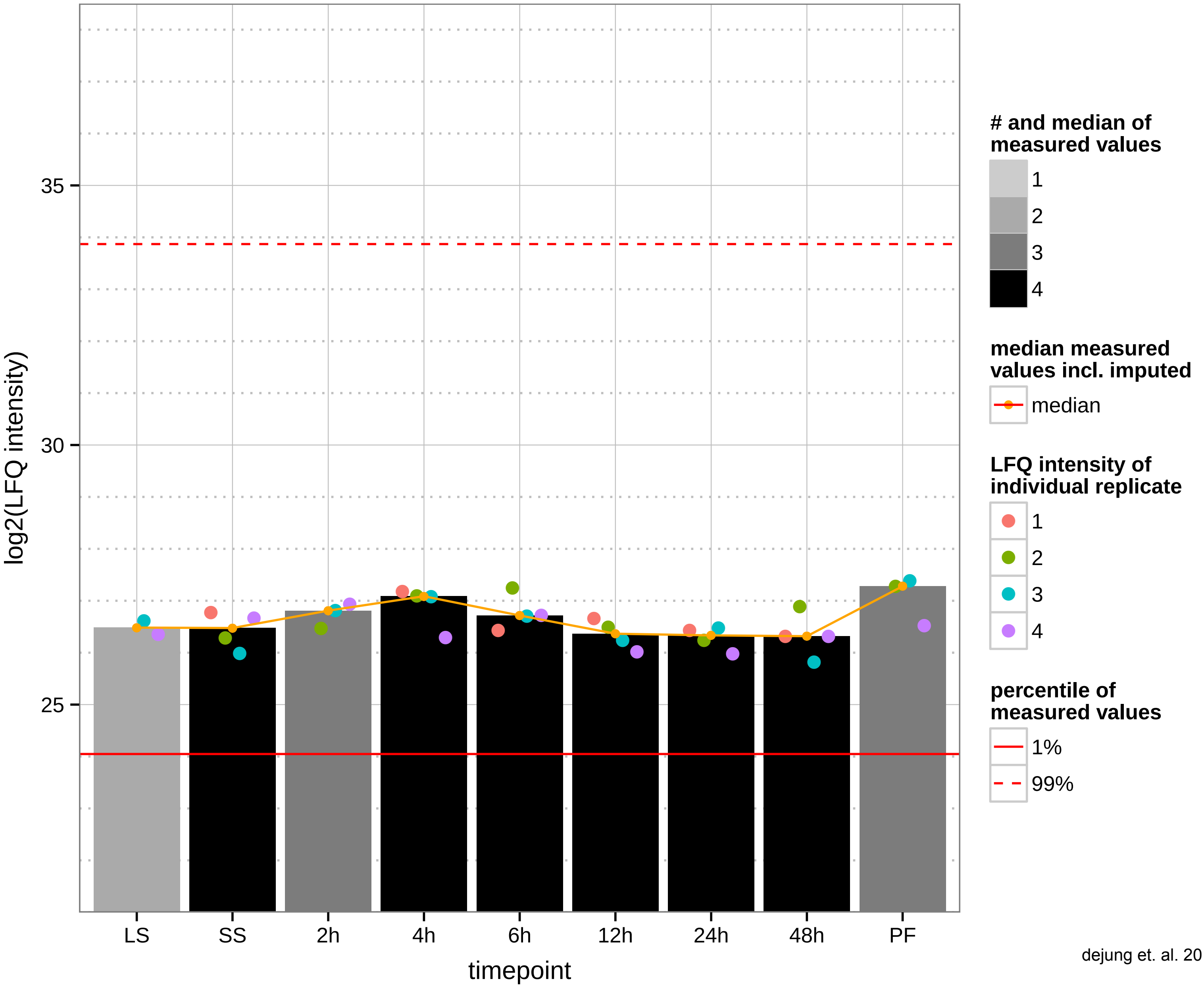




dejung et. al. 2015

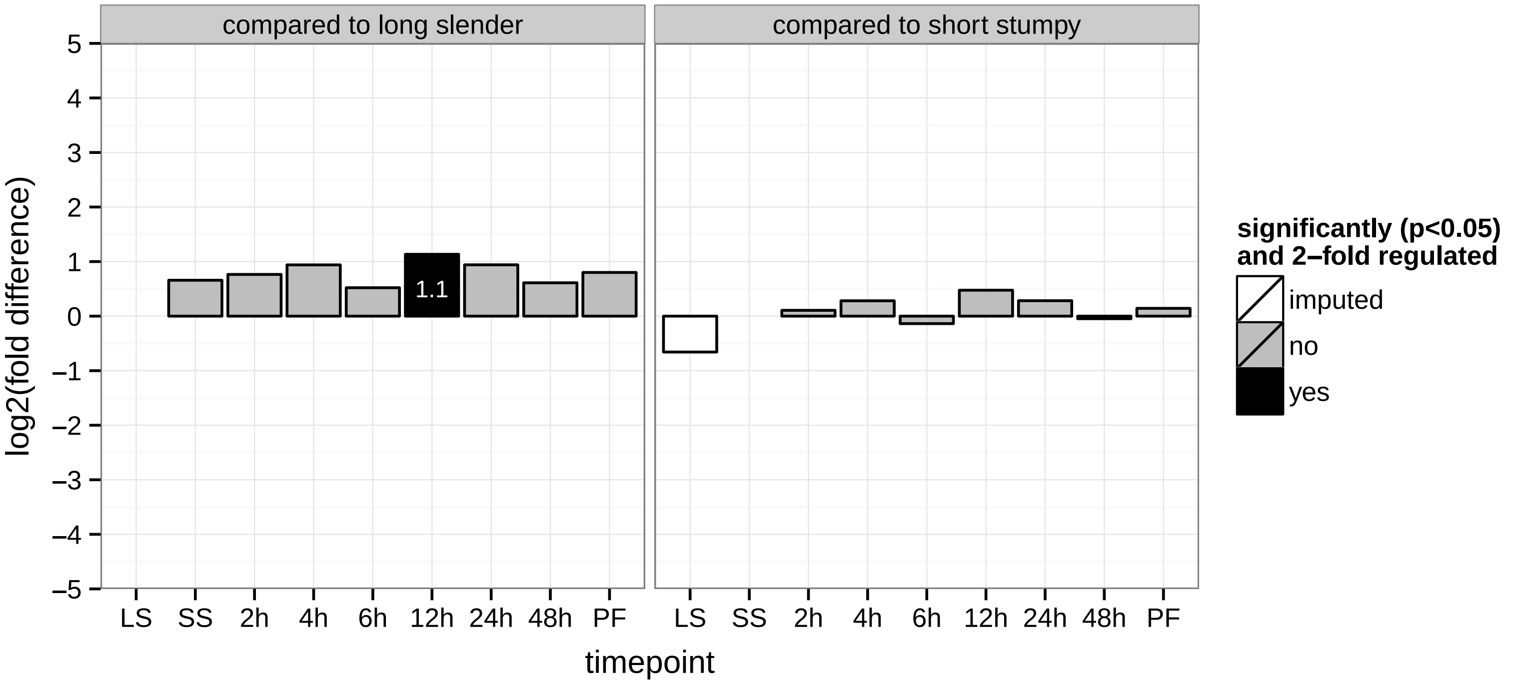
hypothetical protein, conserved
Tb927.6.3340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

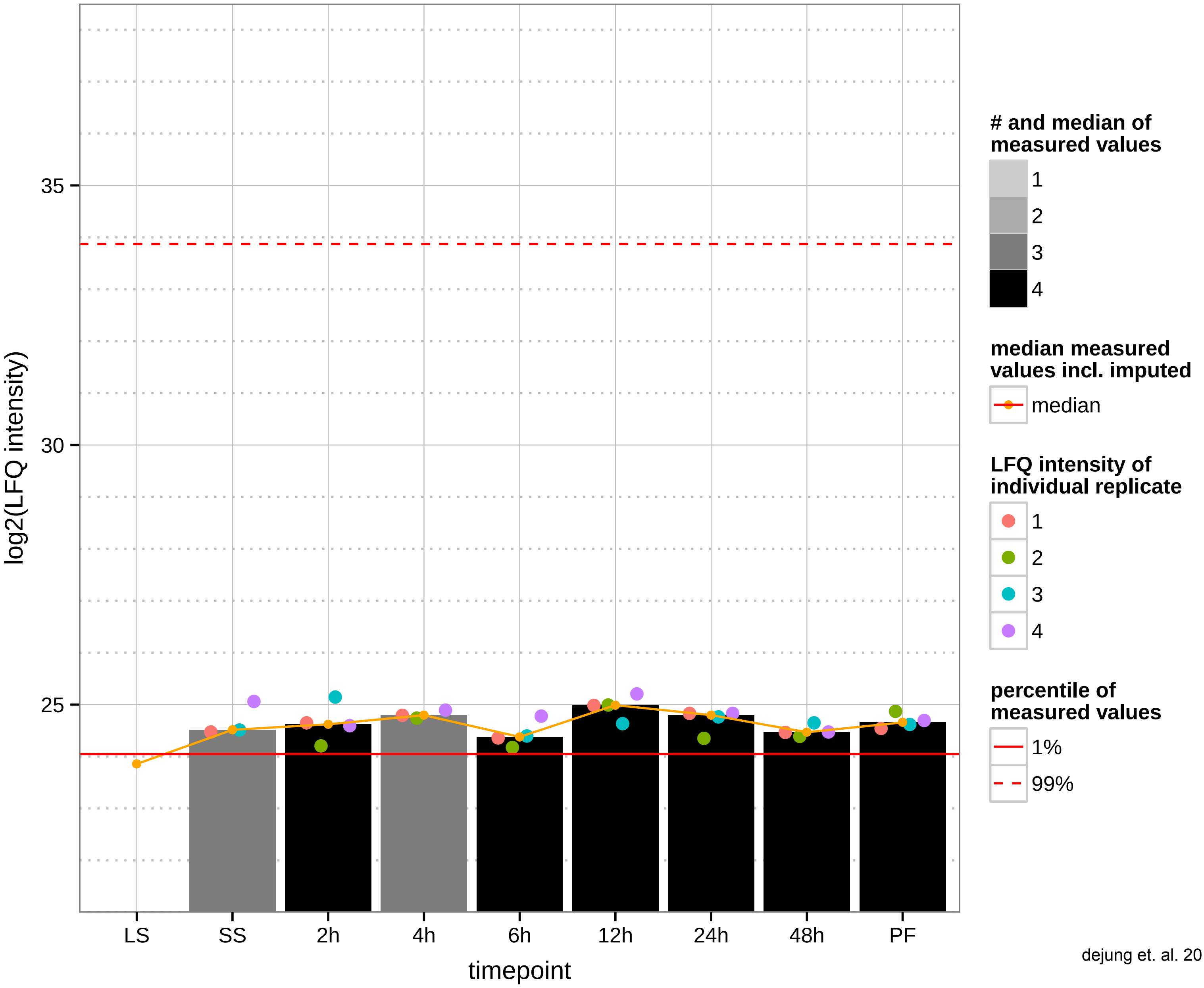




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.3520;Tb11.v5.0634
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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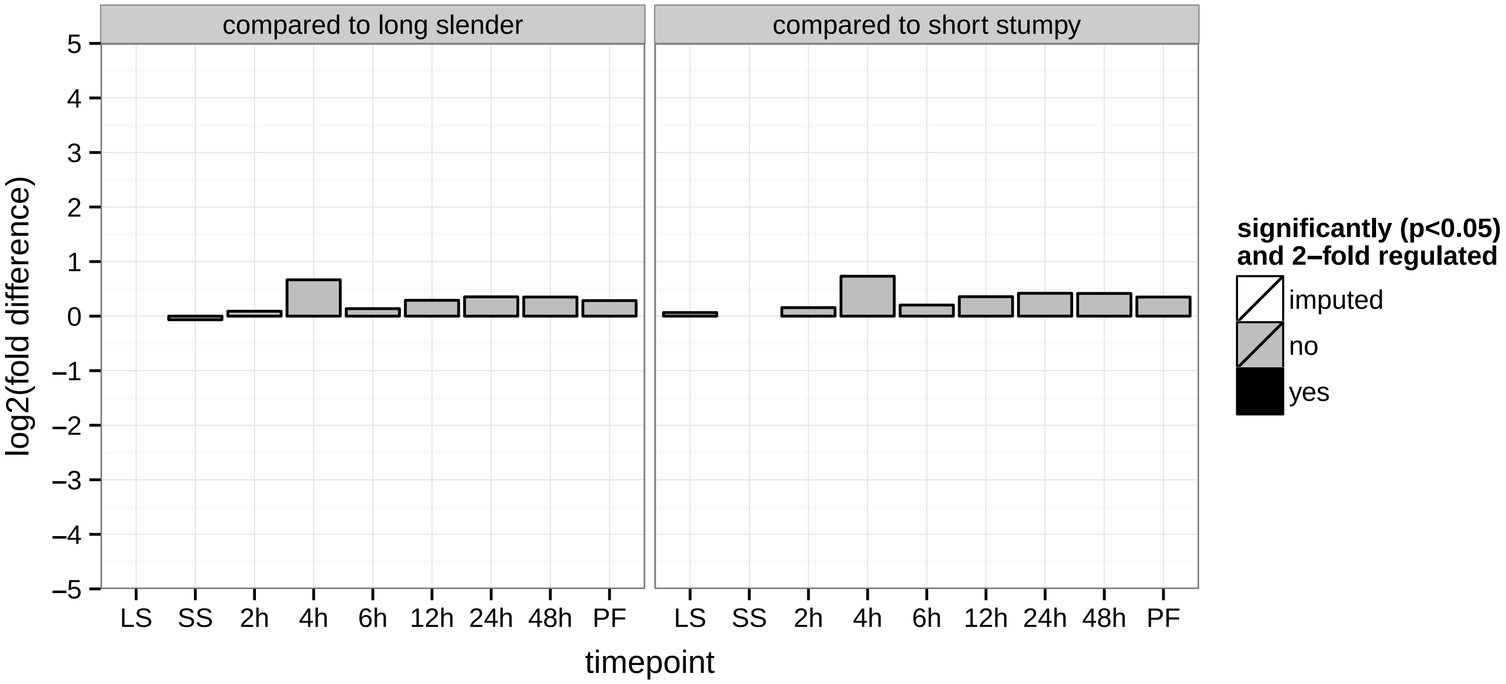
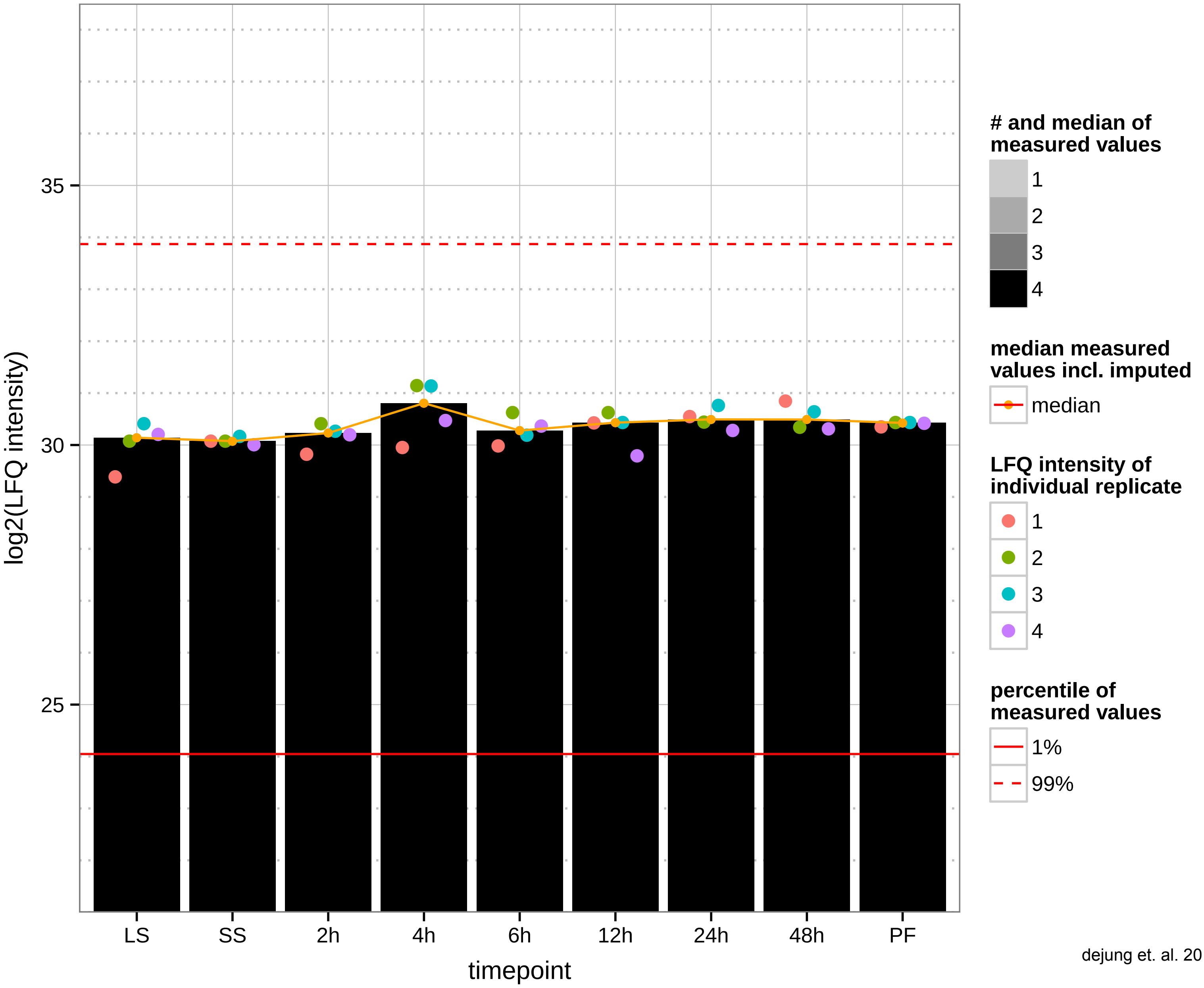
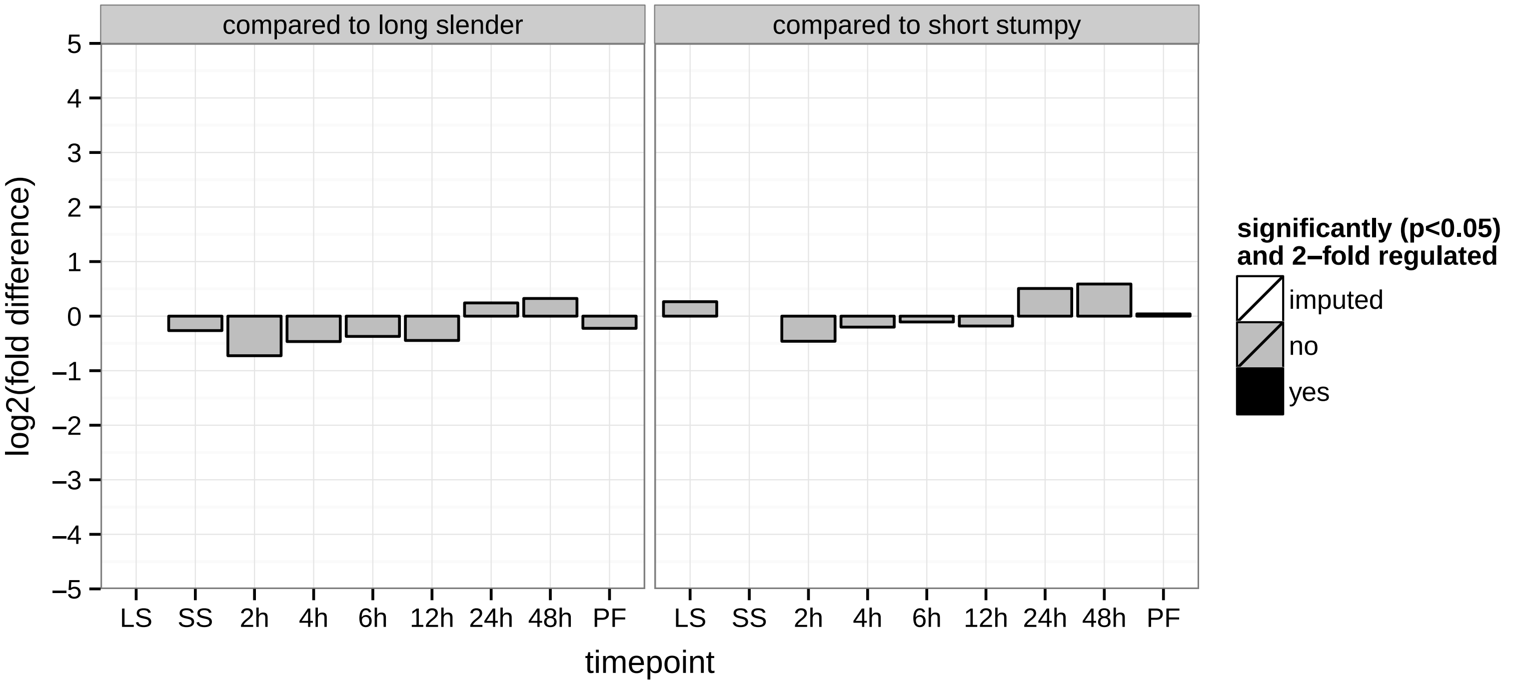
ADP–ribosylation factor, putative
Tb927.6.3650
AGOF: GTP binding
AGOC: intracellular
AGOP: intracellular protein transport, small GTPase mediated signal transduction
PGOF: GTP binding
PGOC: intracellular
PGOP: intracellular protein transport, small GTPase mediated signal transduction

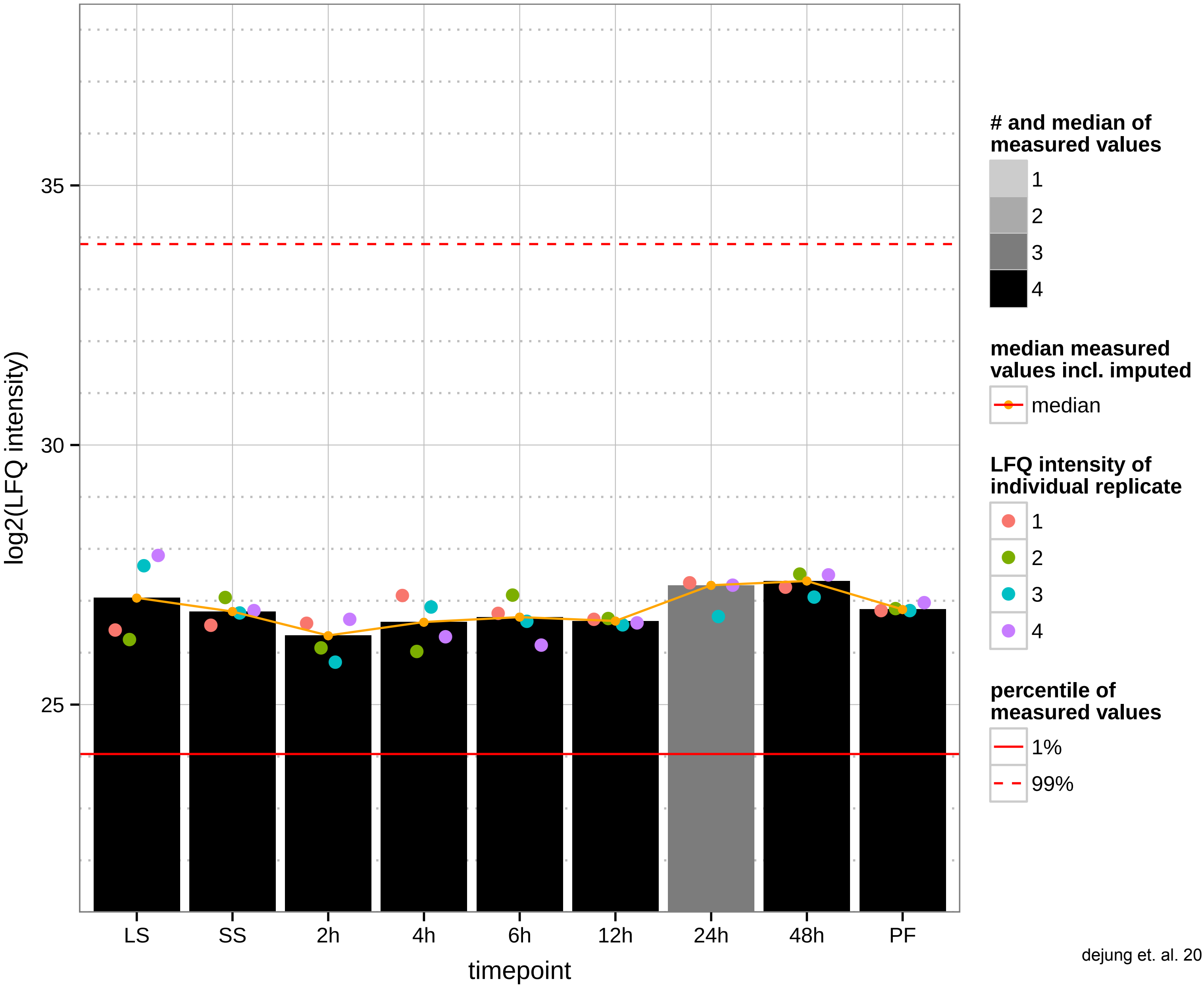




dejung et. al. 2015

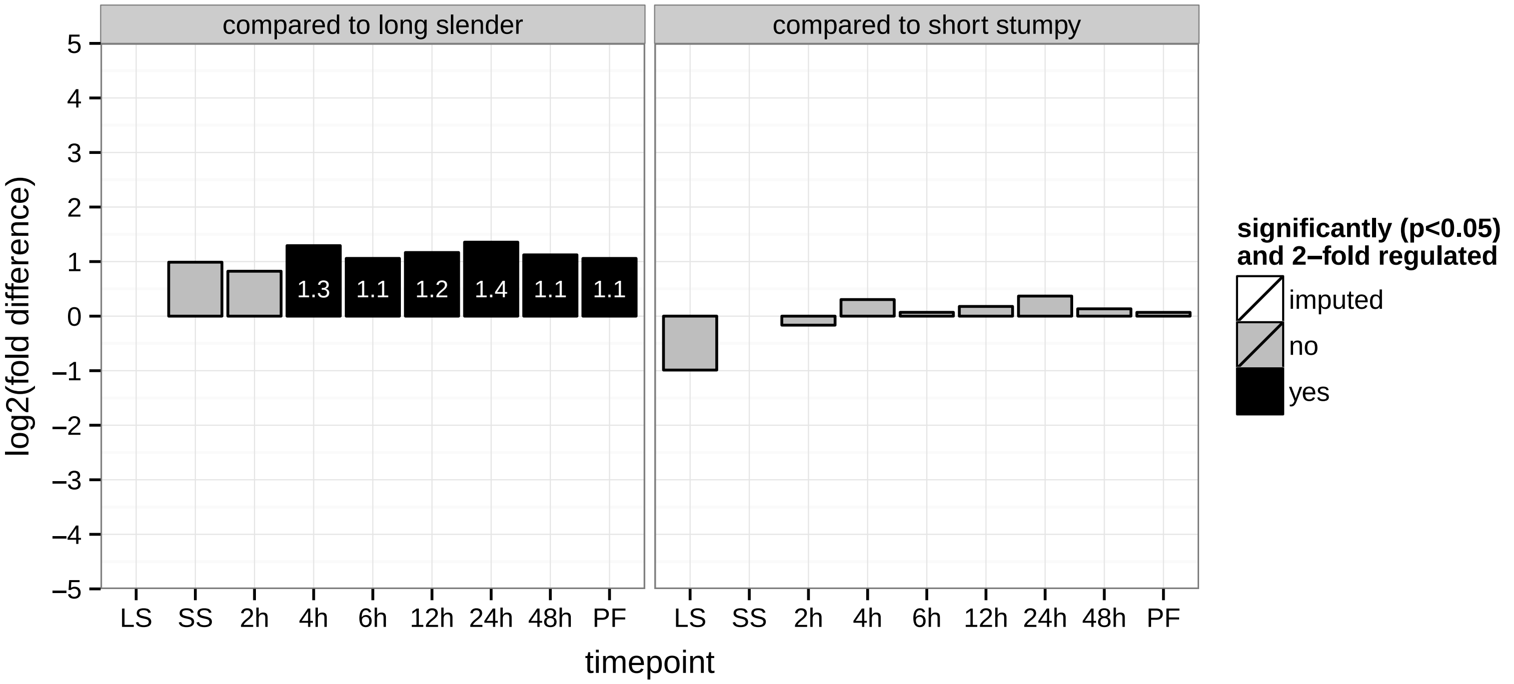
paraflagellar rod component, putative (PFC8)
Tb927.6.3670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

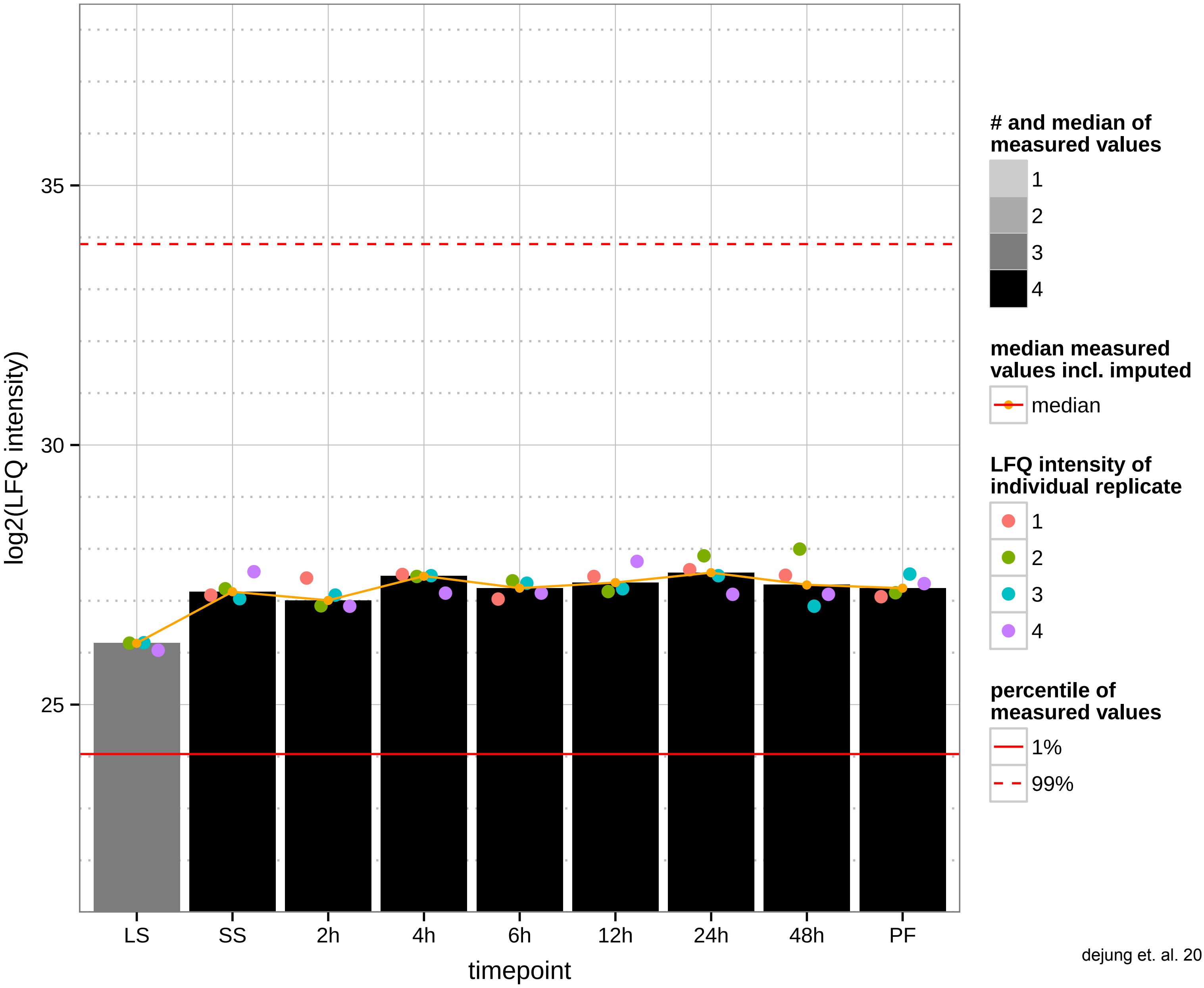




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.3680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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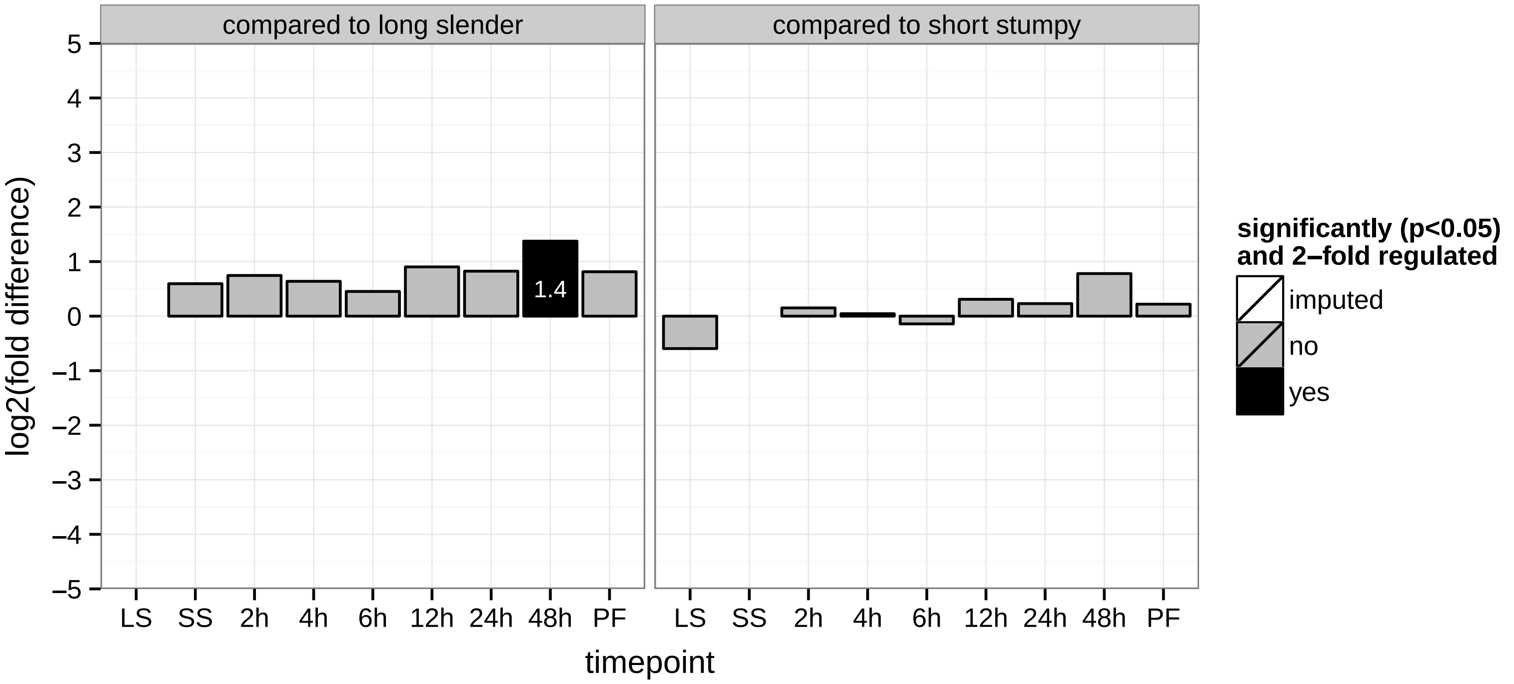
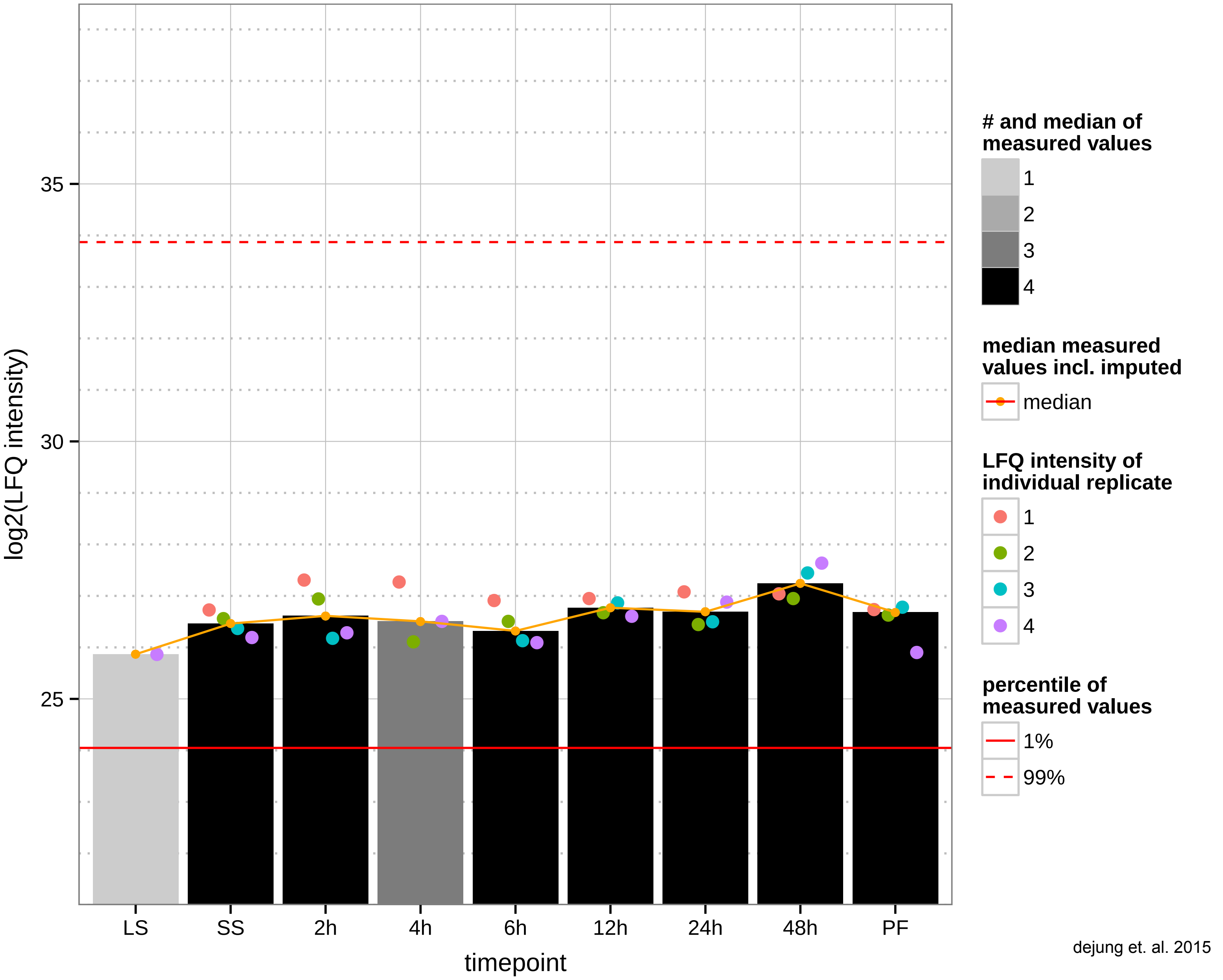
pre–mRNA cleavage complex II Clp1–like, conserved
Tb927.6.3690
AGOF: ATP–dependent polyribonucleotide 5'–hydroxyl–kinase activity
AGOC: tRNA–intron endonuclease complex
AGOP: tRNA splicing, via endonucleolytic cleavage and ligation, targeting of mRNA for destruction involved in RNA interferen
PGOF: null
PGOC: null
PGOP: null





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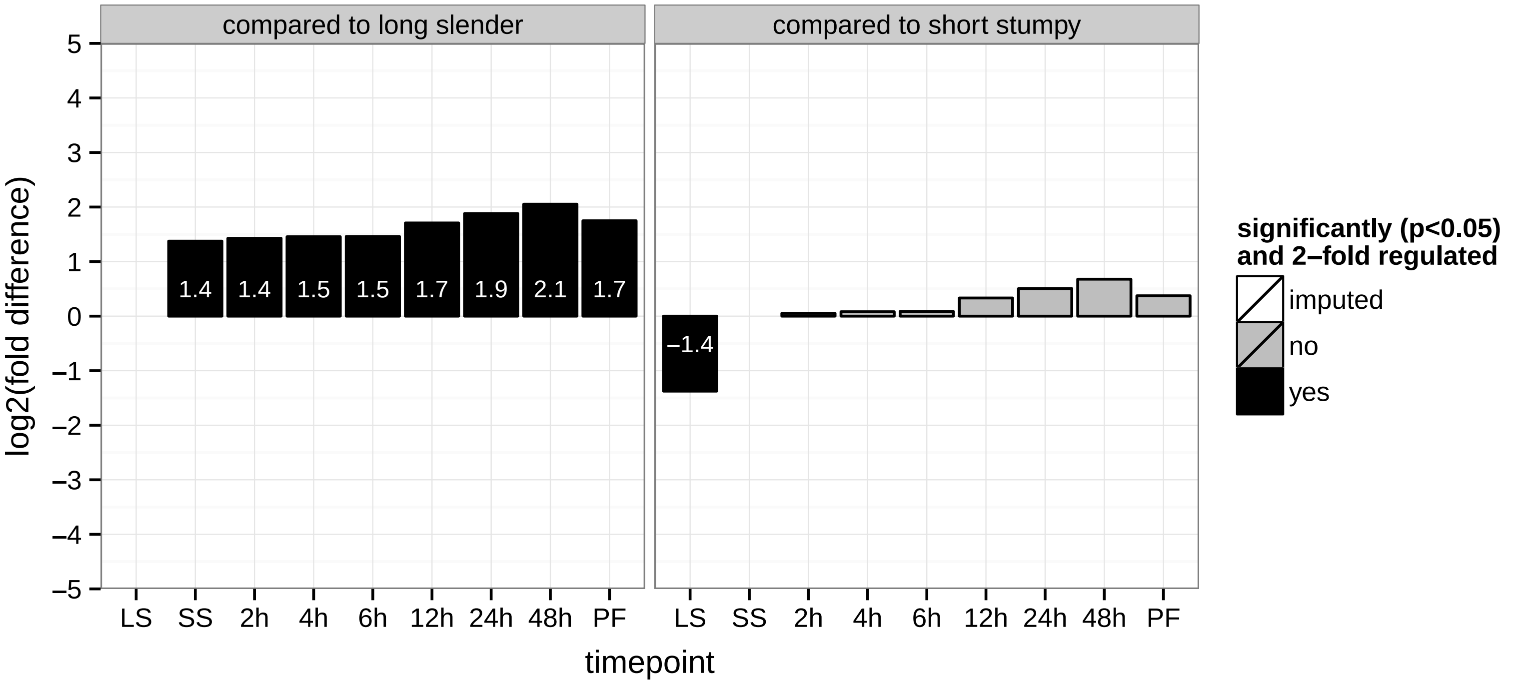
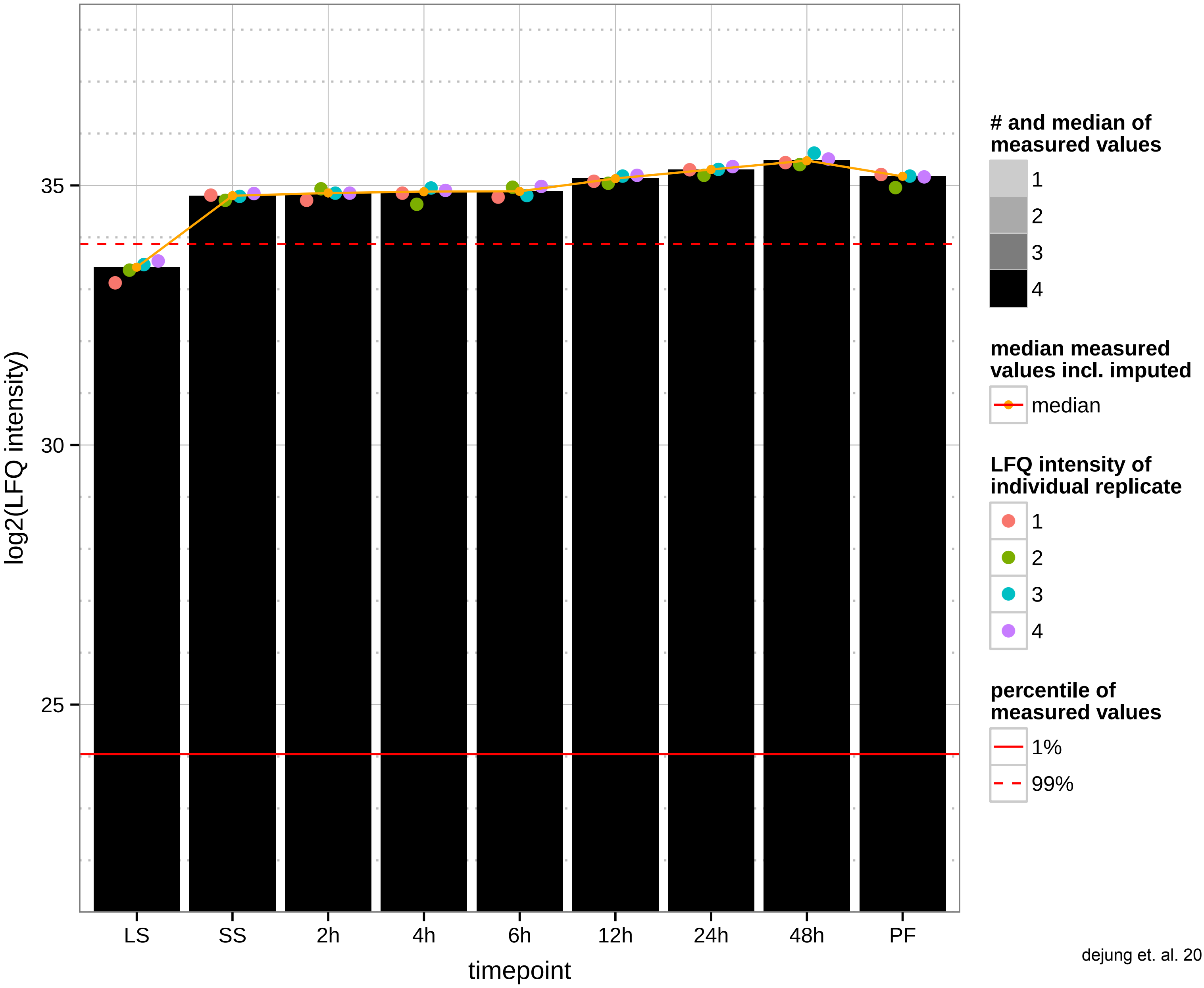
heat shock 70 kDa protein, mitochondrial precursor, putative
Tb927.6.3800;Tb927.6.3750;Tb927.6.3740
AGOF: ATP binding, unfolded protein binding
AGOC: mitochondrion, null
AGOP: protein folding
PGOF: ATP binding, unfolded protein binding
PGOC: null
PGOP: protein folding





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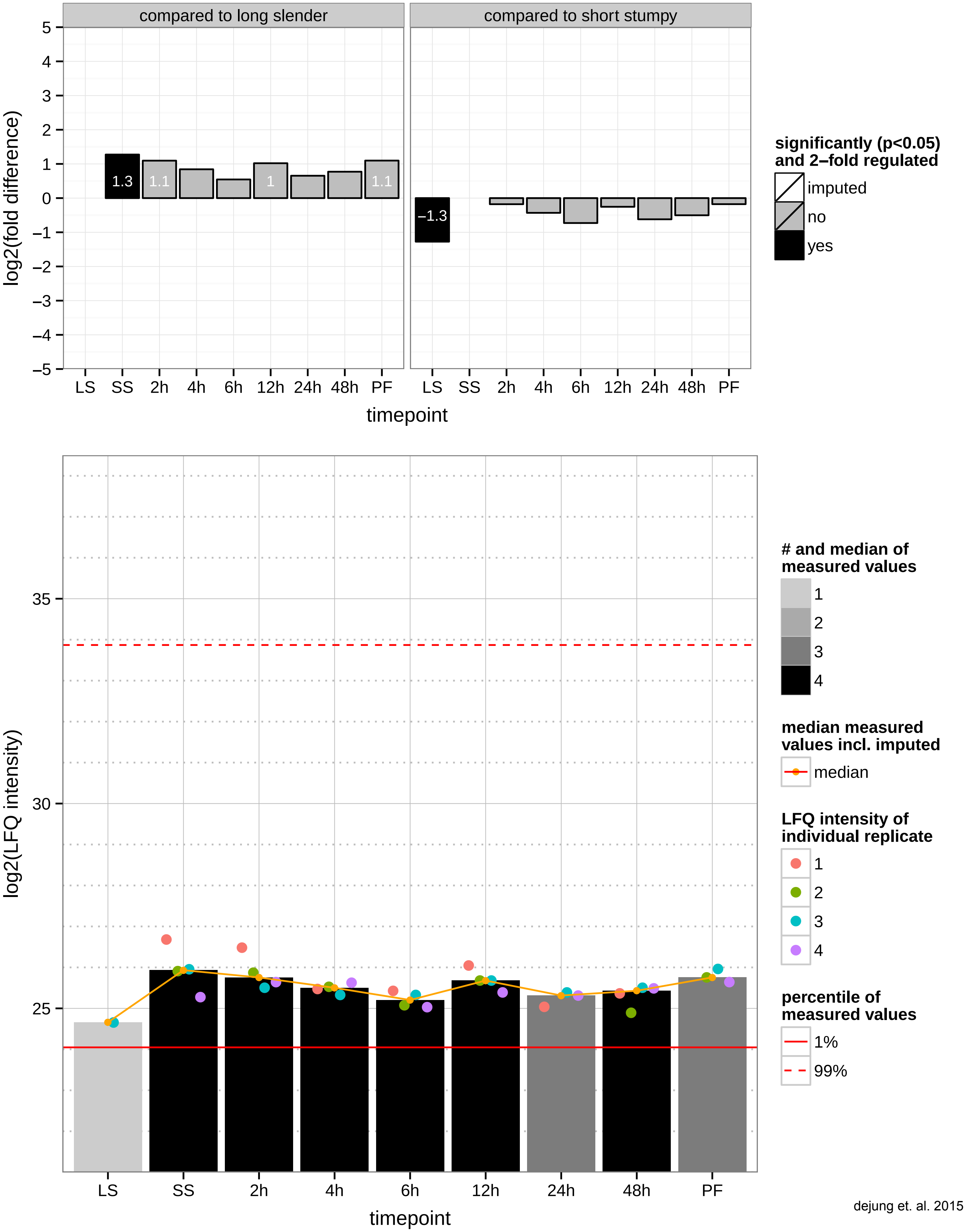
hypothetical protein, conserved
Tb927.6.3810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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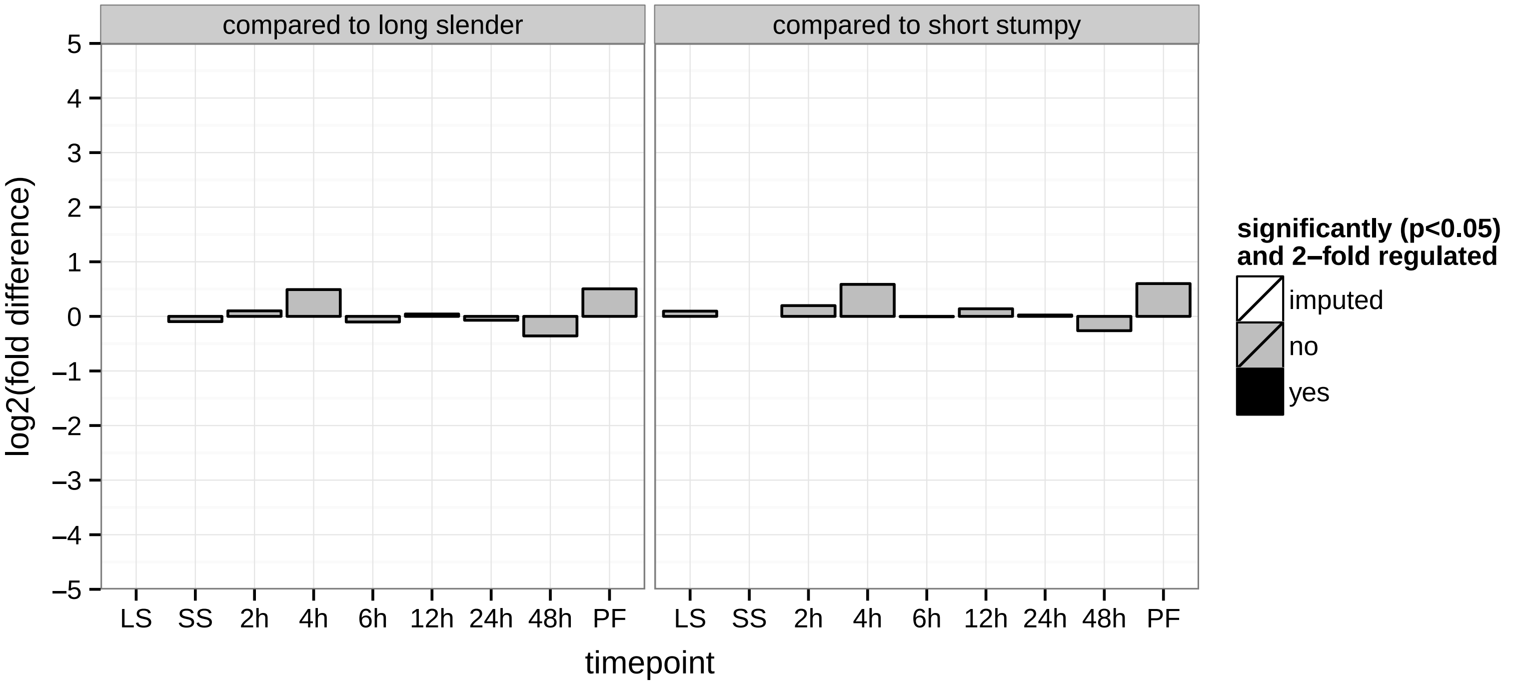
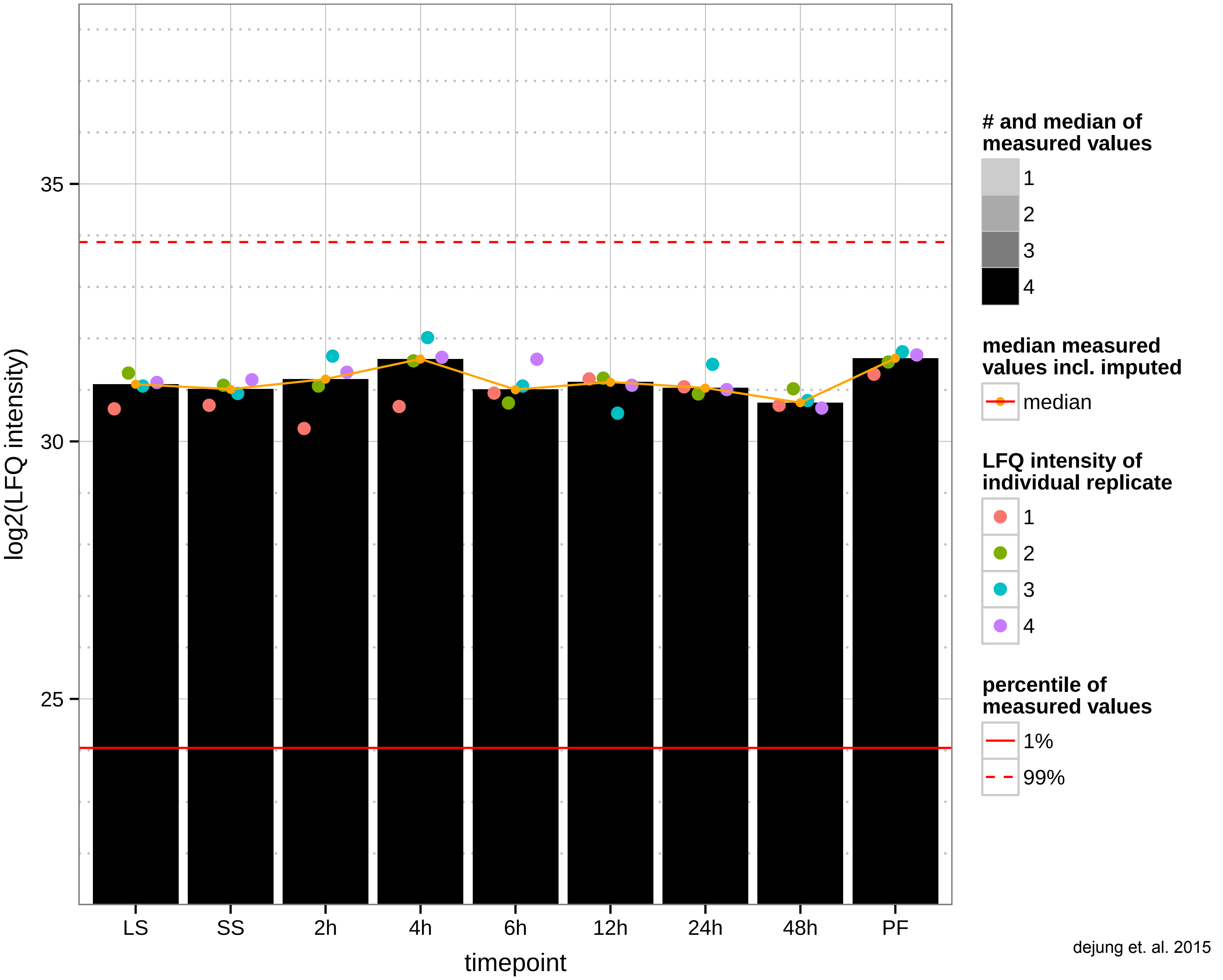
reticulon domain protein
Tb927.6.3840
AGOF: null
AGOC: endoplasmic reticulum
AGOP: null
PGOF: null
PGOC: endoplasmic reticulum
PGOP: null





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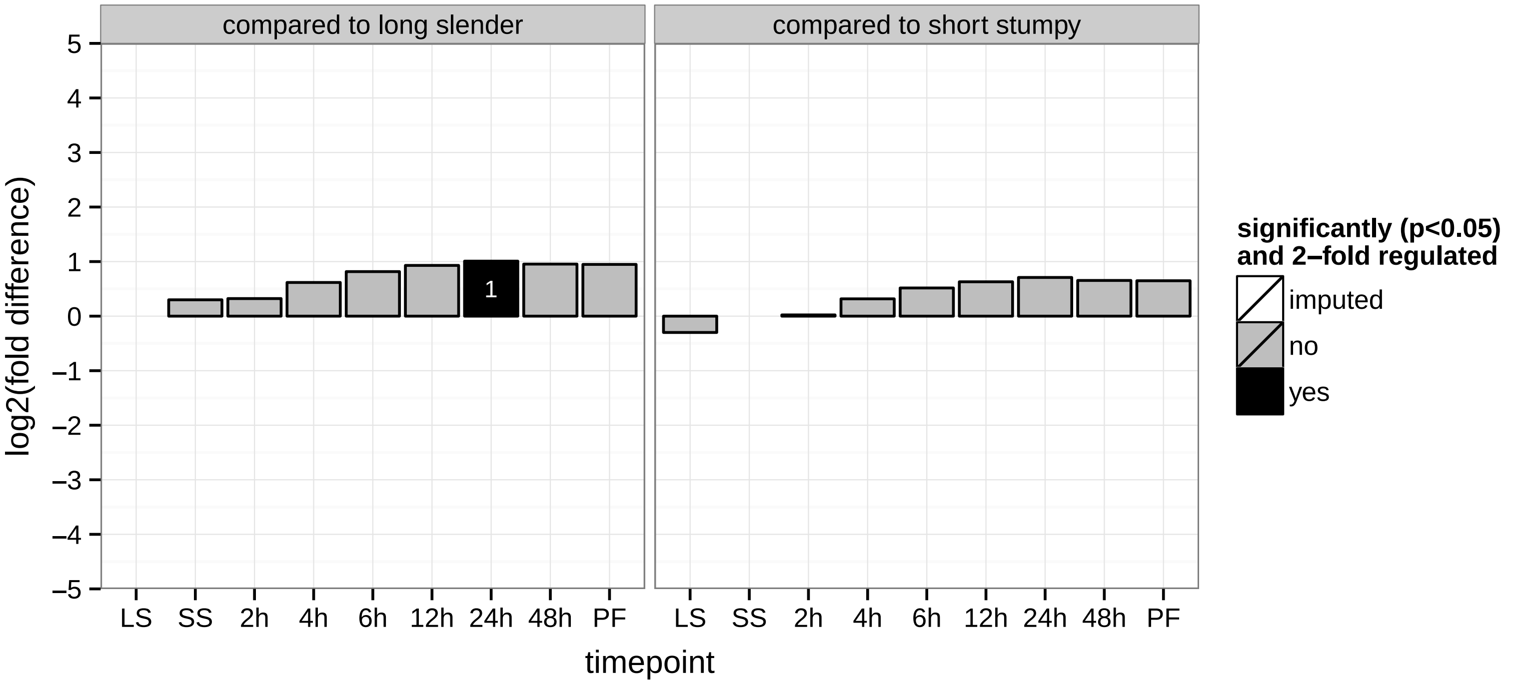
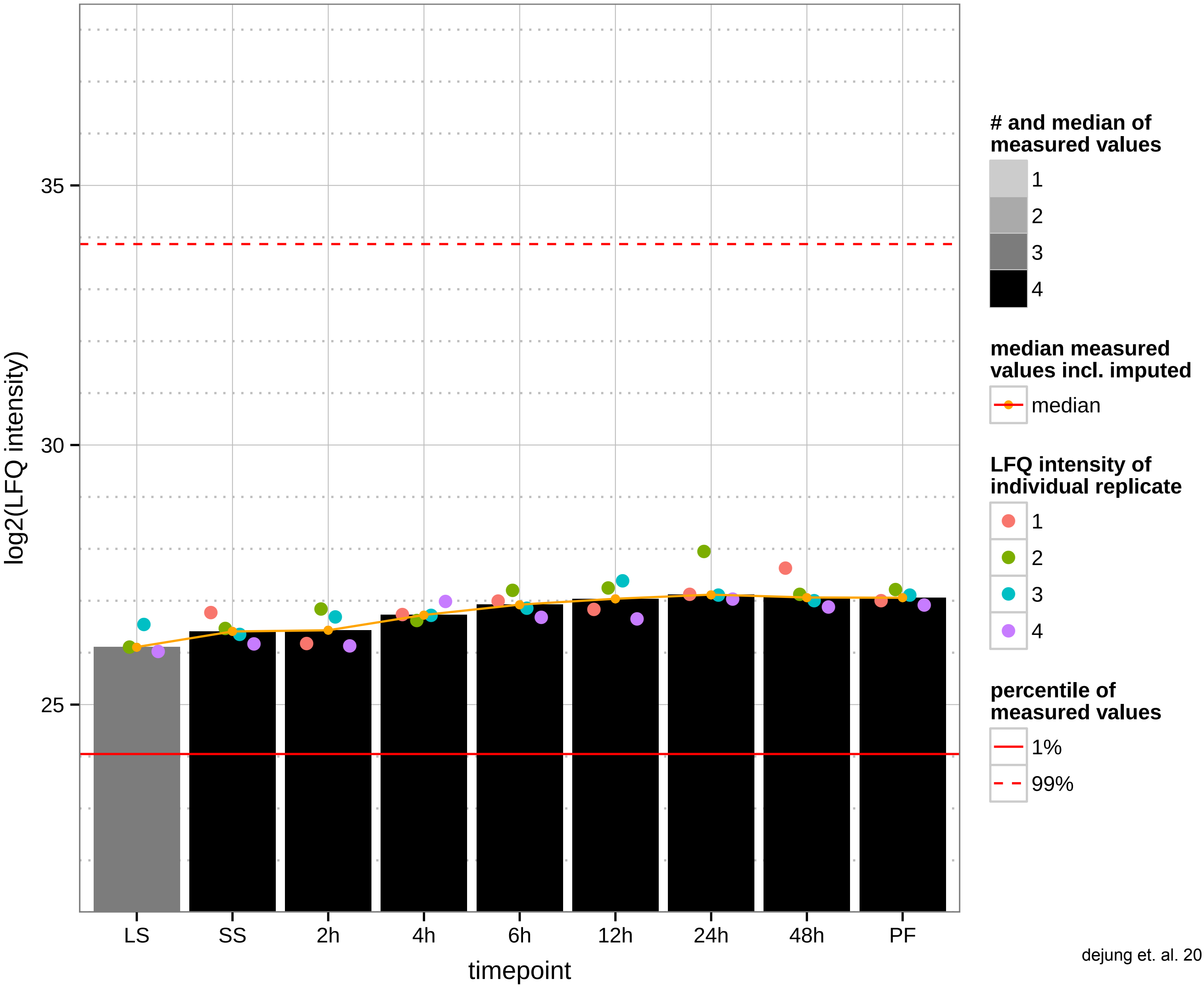
RNA–binding protein, putative (SGN1)
Tb927.6.3870
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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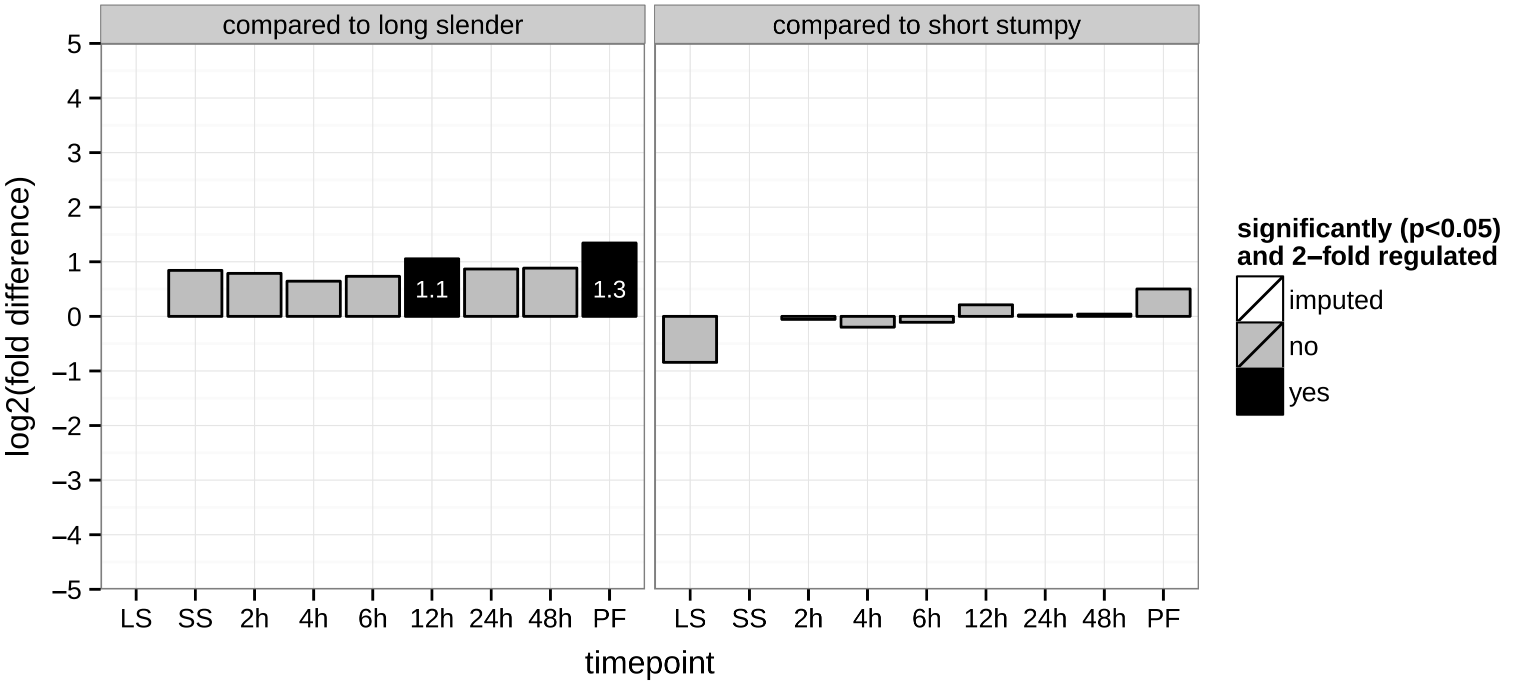
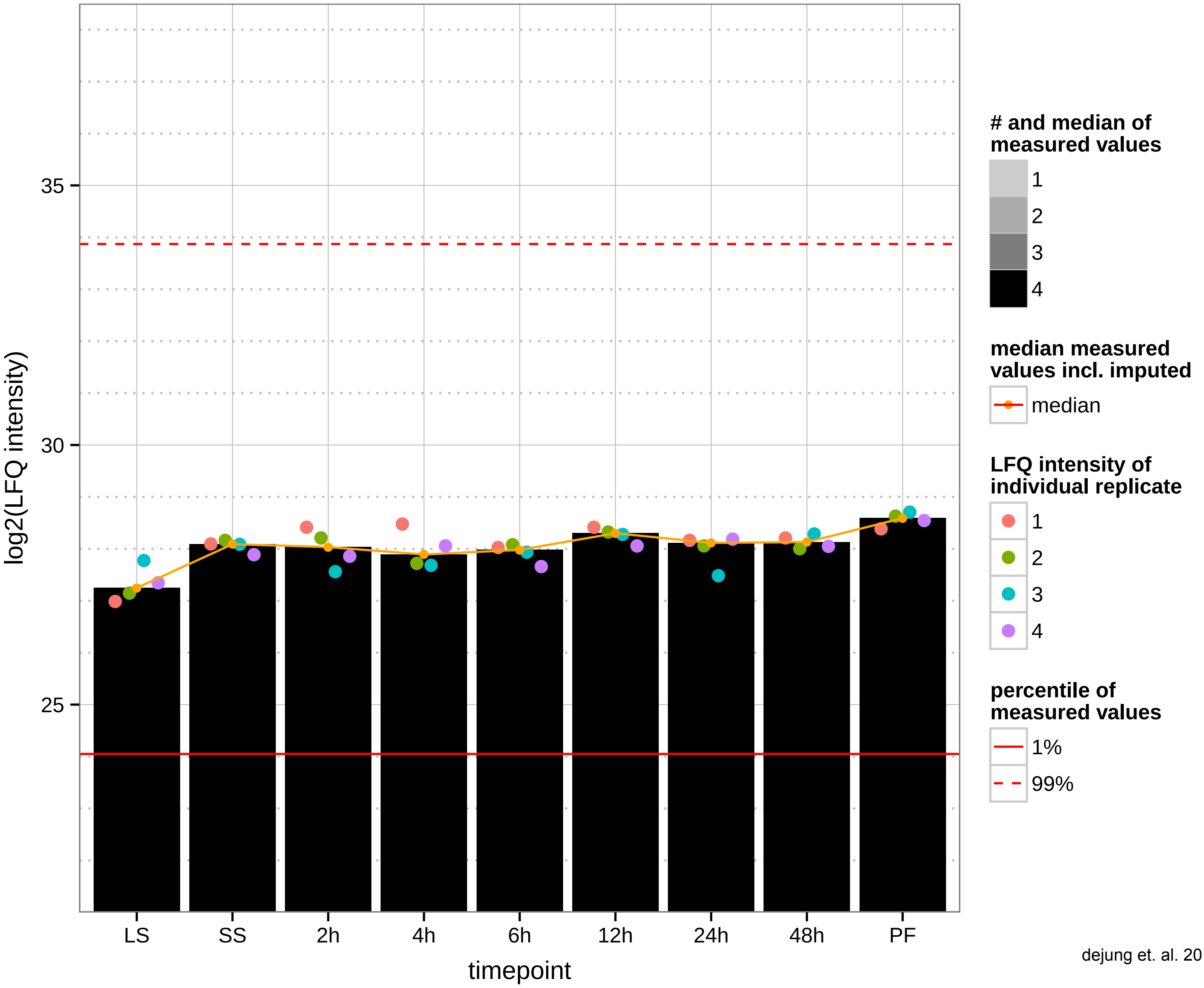
replication factor C, subunit 2, putative
Tb927.6.3890
AGOF: ATP binding, DNA binding, DNA clamp loader activity
AGOC: DNA replication factor C complex
AGOP: DNA replication
PGOF: ATP binding, DNA binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: DNA replication





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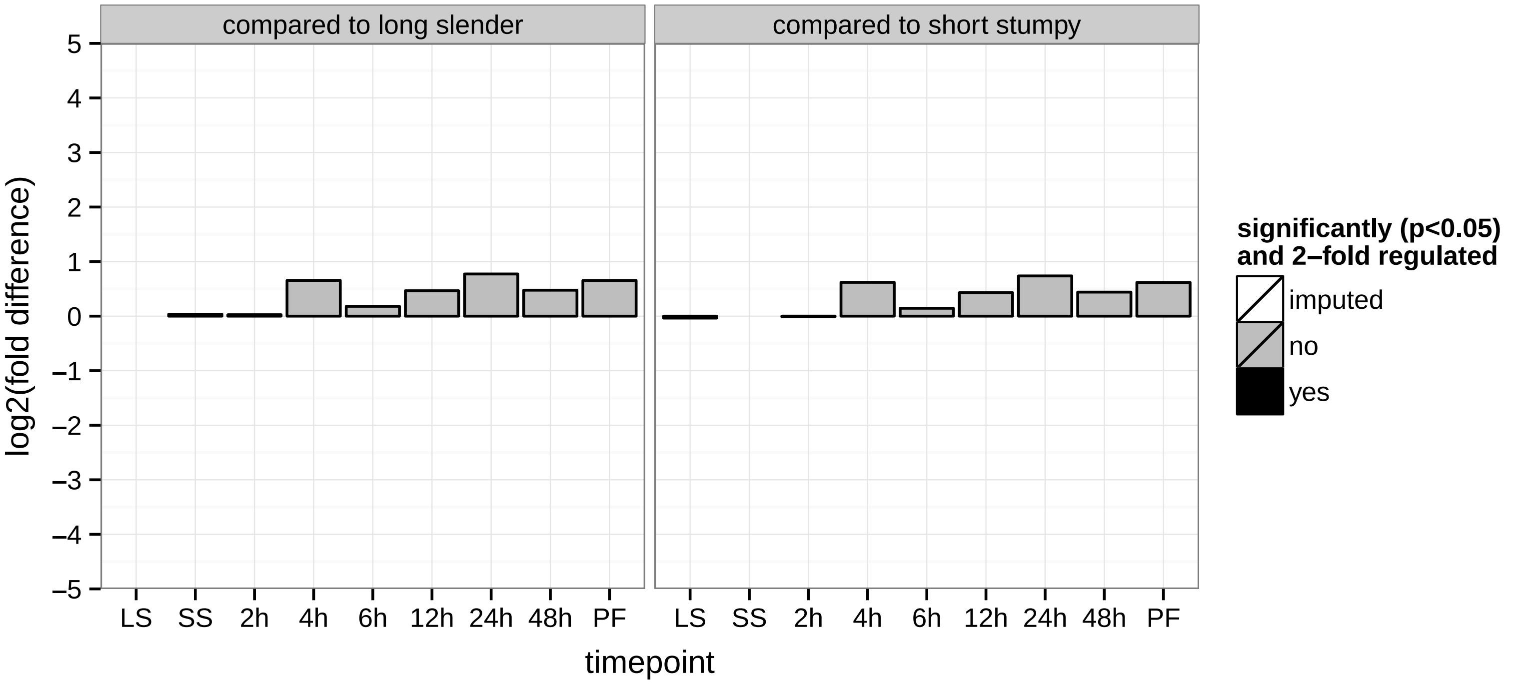
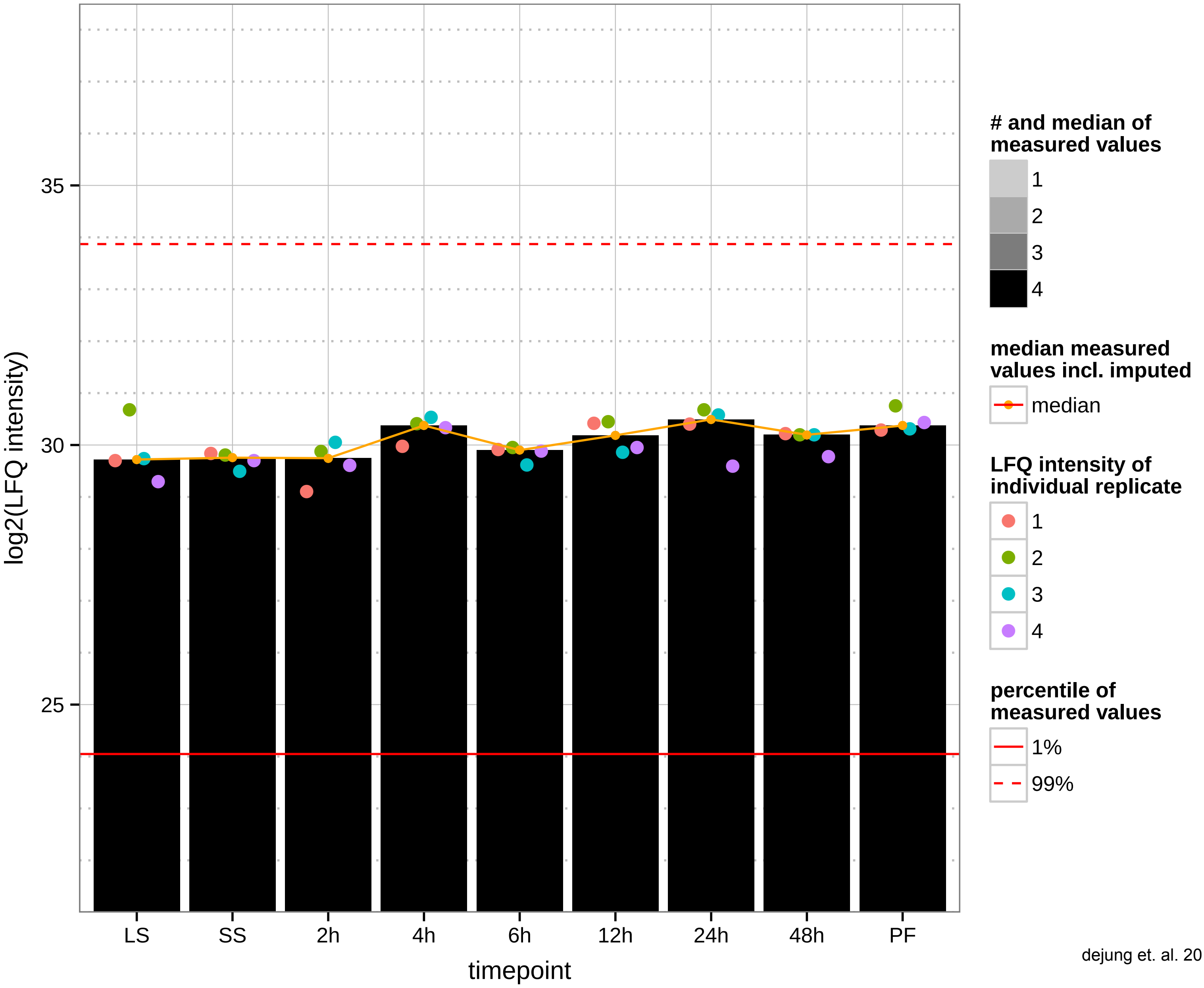
small glutamine−rich tetratricopeptide repeat protein, putative, putative (SGT)
Tb927.6.4000
AGOF: chaperone binding
AGOC: cytosol
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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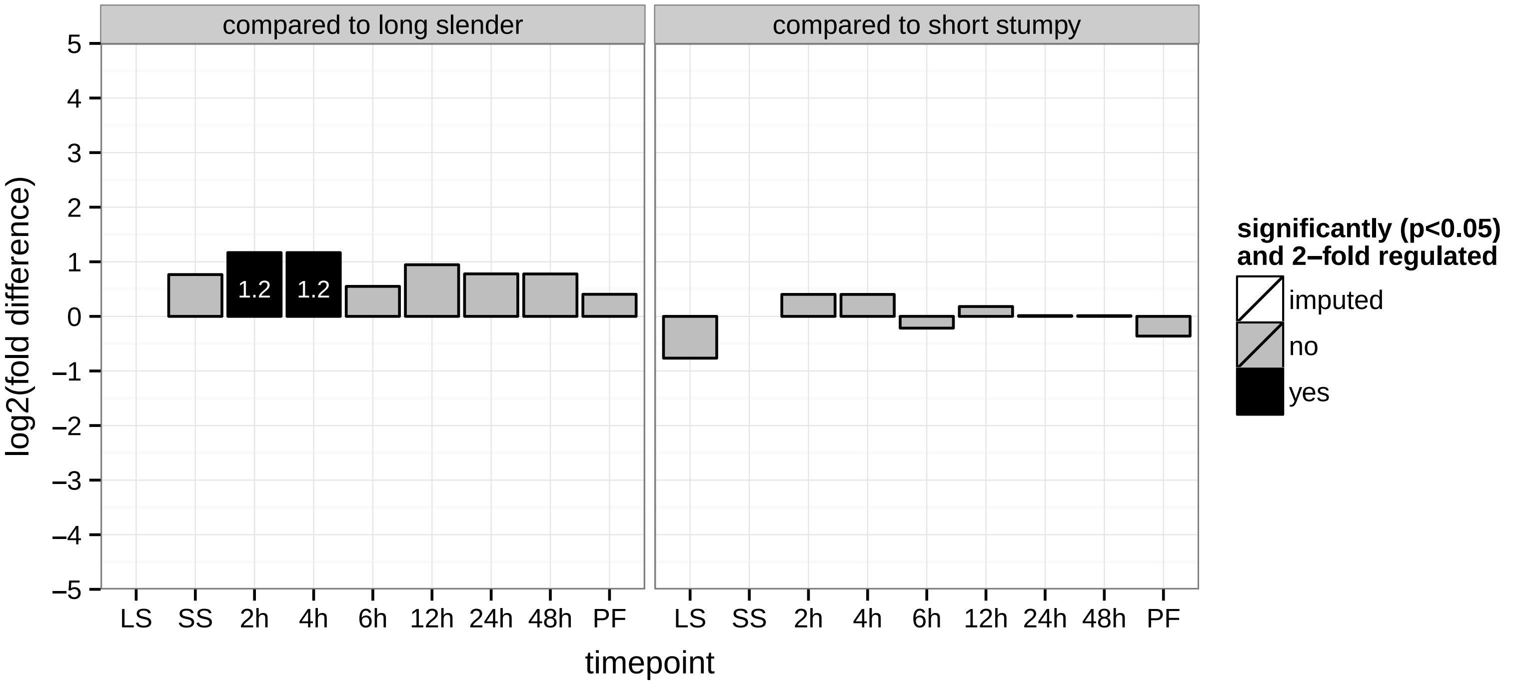
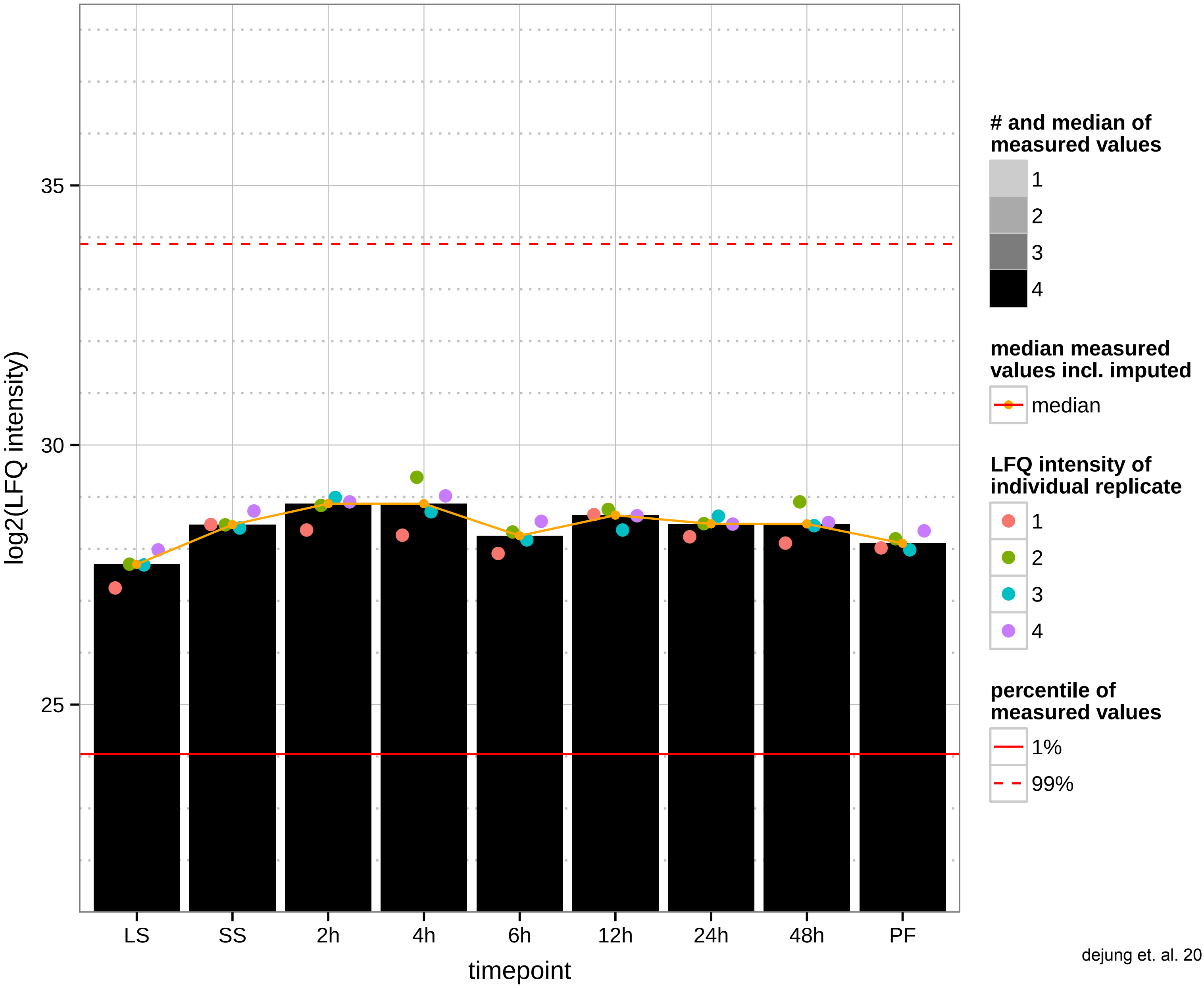
hypothetical protein, conserved
Tb927.6.4020
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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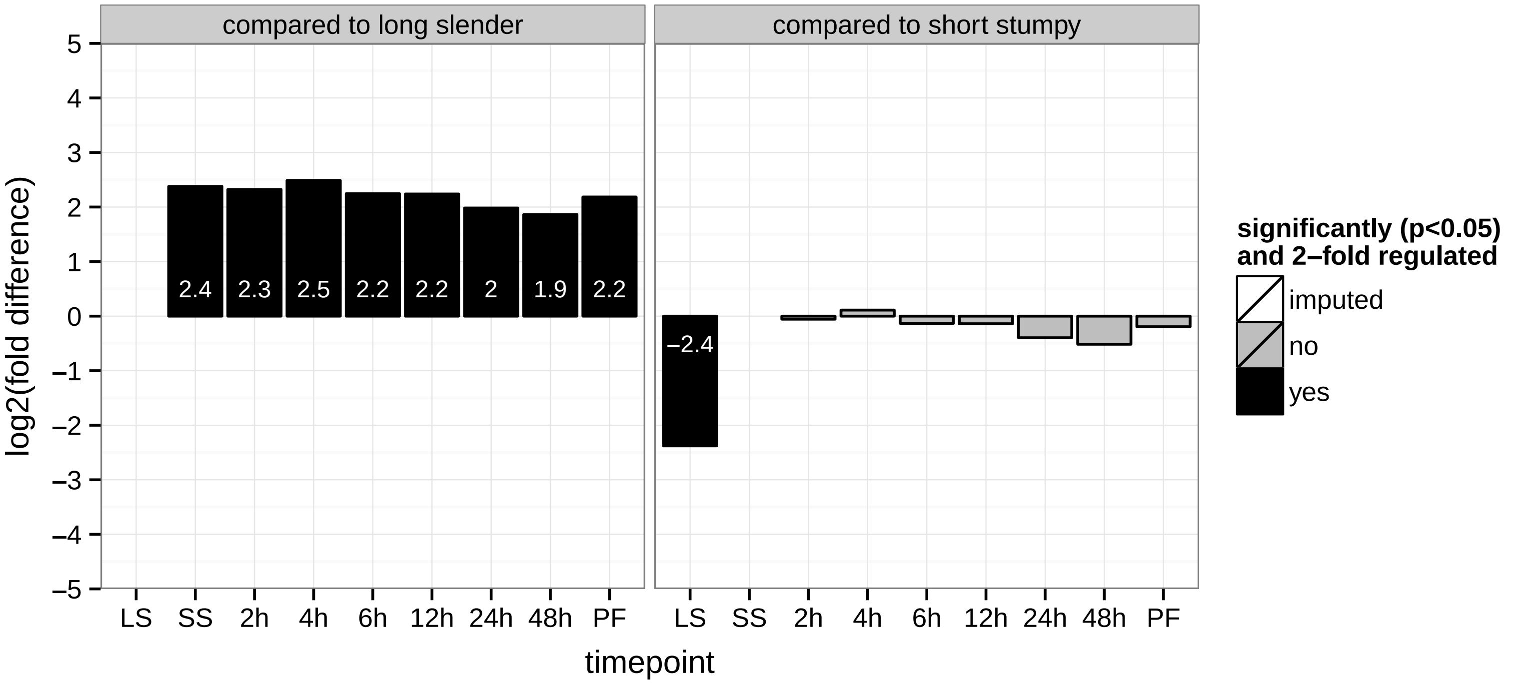
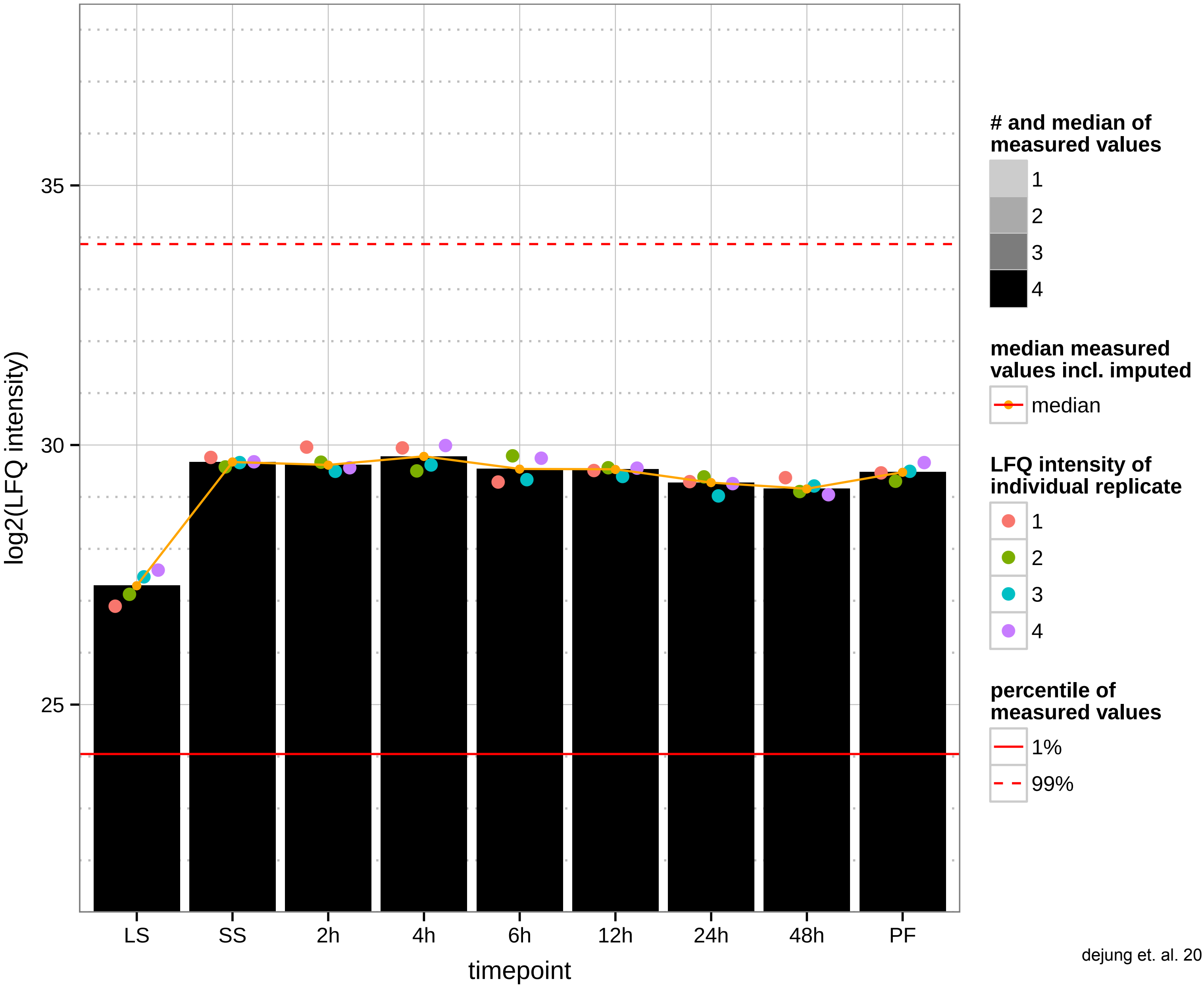
chaperonin HSP60, mitochondrial precursor, putative (HSP60)
Tb927.6.4090
AGOF: ATP binding
AGOC: null
AGOP: cellular protein metabolic process
PGOF: ATP binding
PGOC: null
PGOP: cellular protein metabolic process





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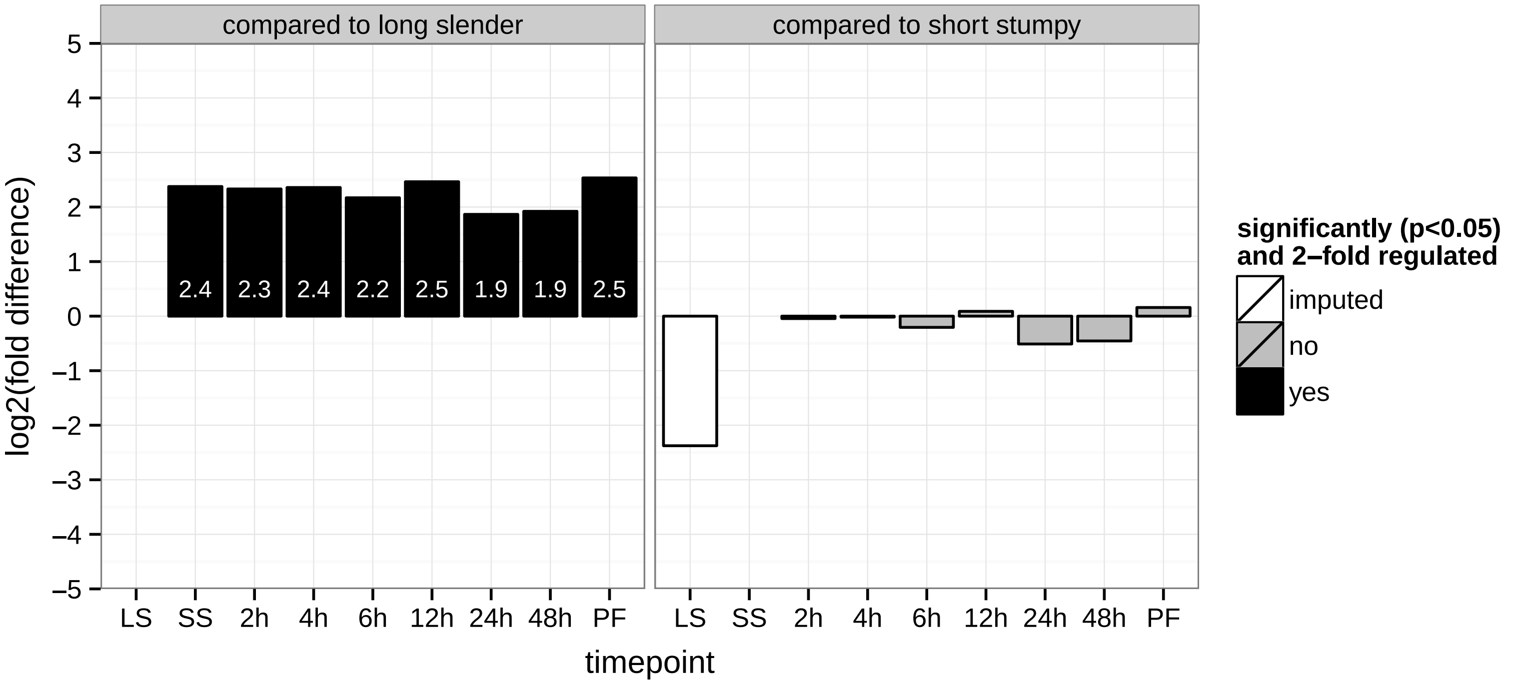
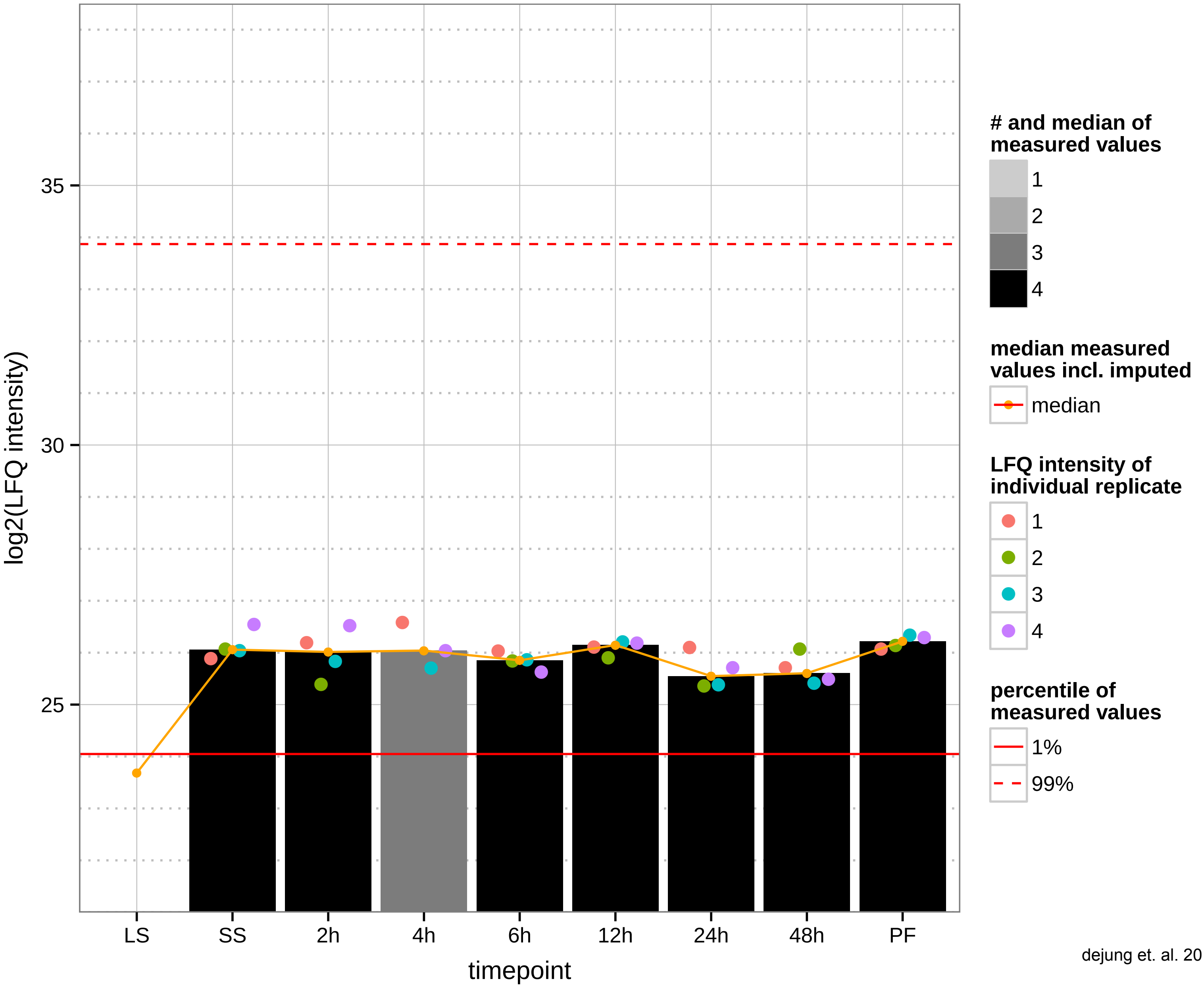
GTPase activating protein, putative
Tb927.6.4120
AGOF: Rab GTPase activator activity
AGOC: intracellular
AGOP: regulation of Rab GTPase activity
PGOF: Rab GTPase activator activity
PGOC: intracellular
PGOP: regulation of Rab GTPase activity





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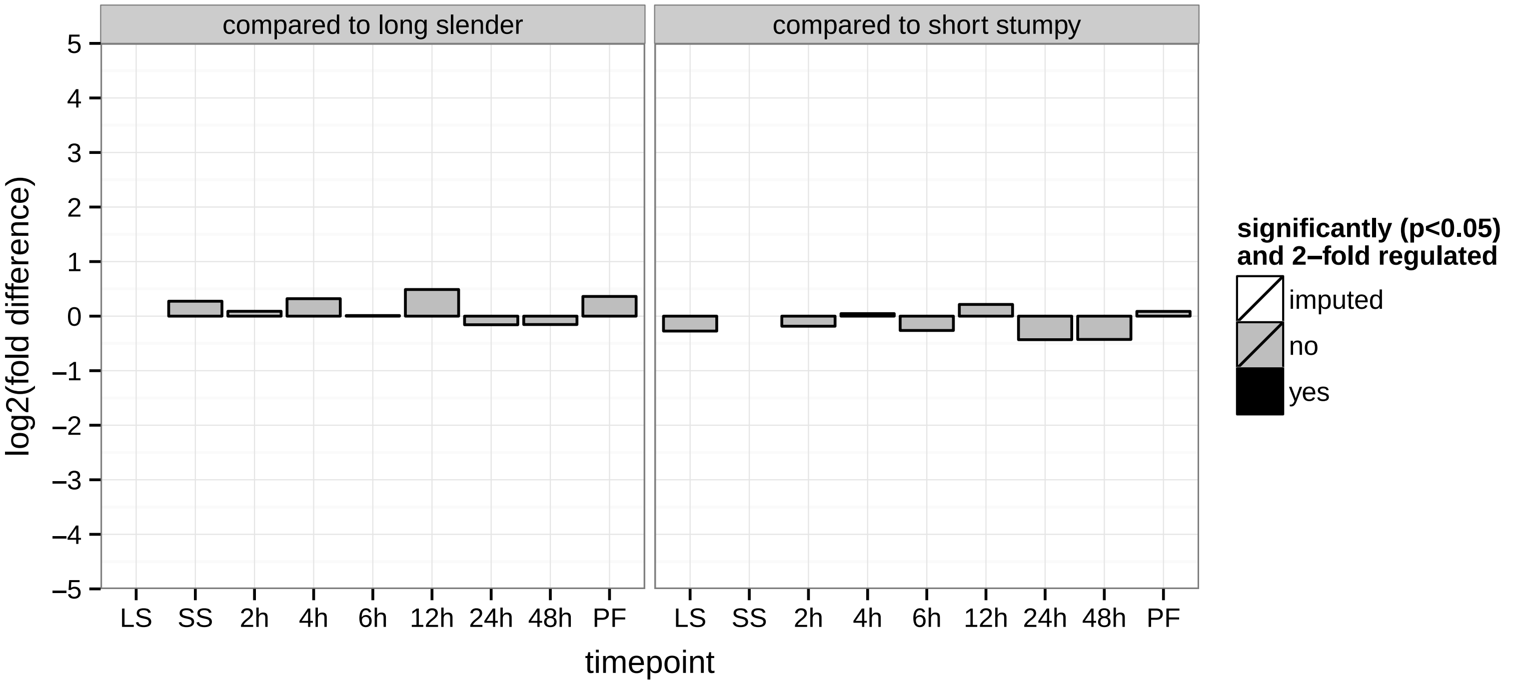
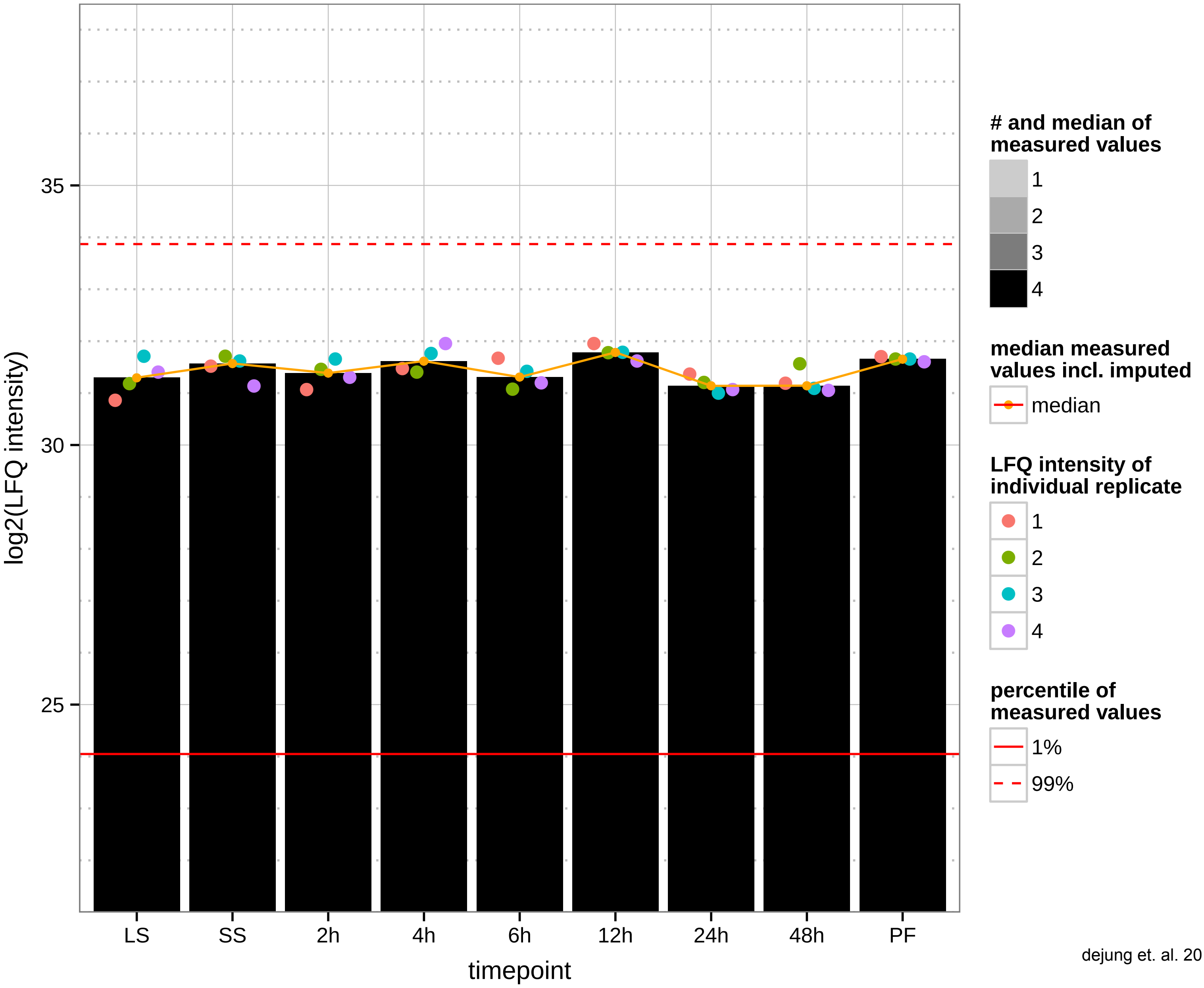
paraflagellar rod component, putative (PFC4)
Tb927.6.4140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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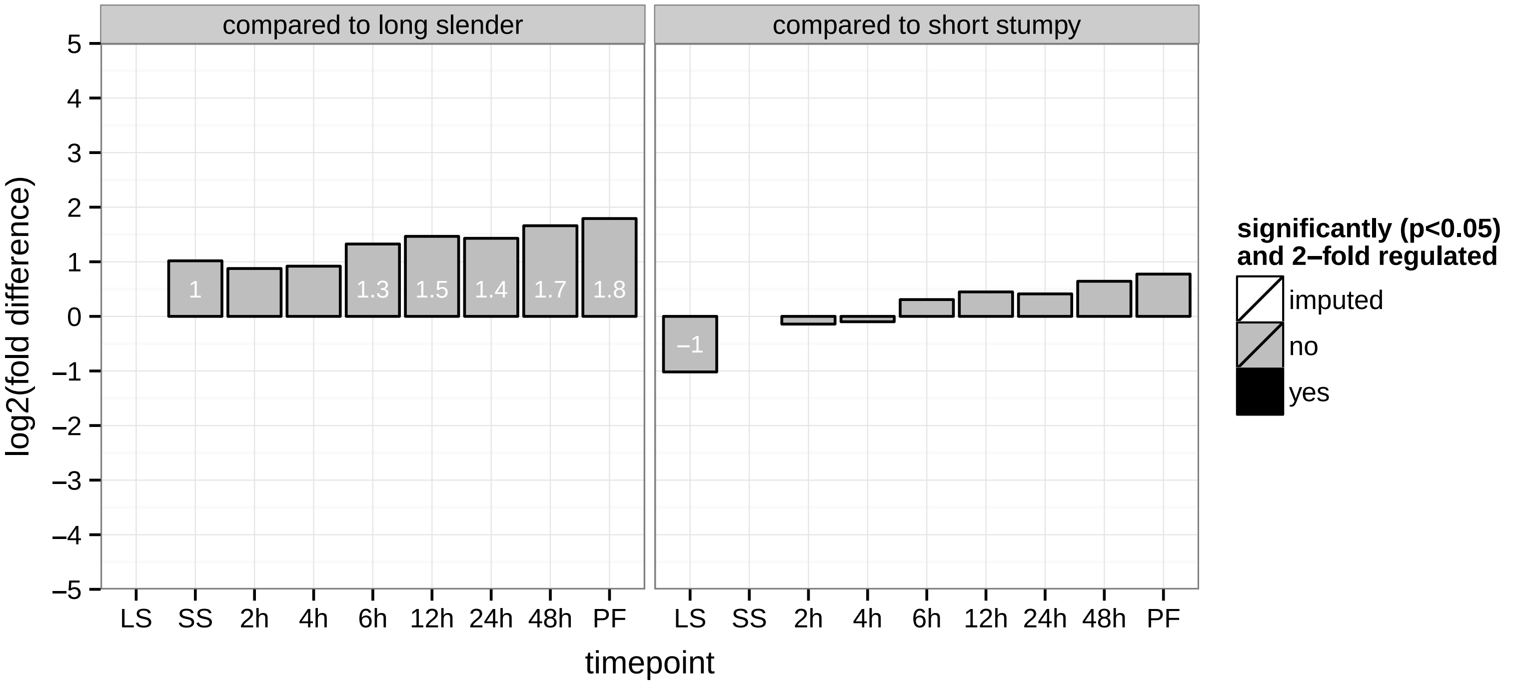
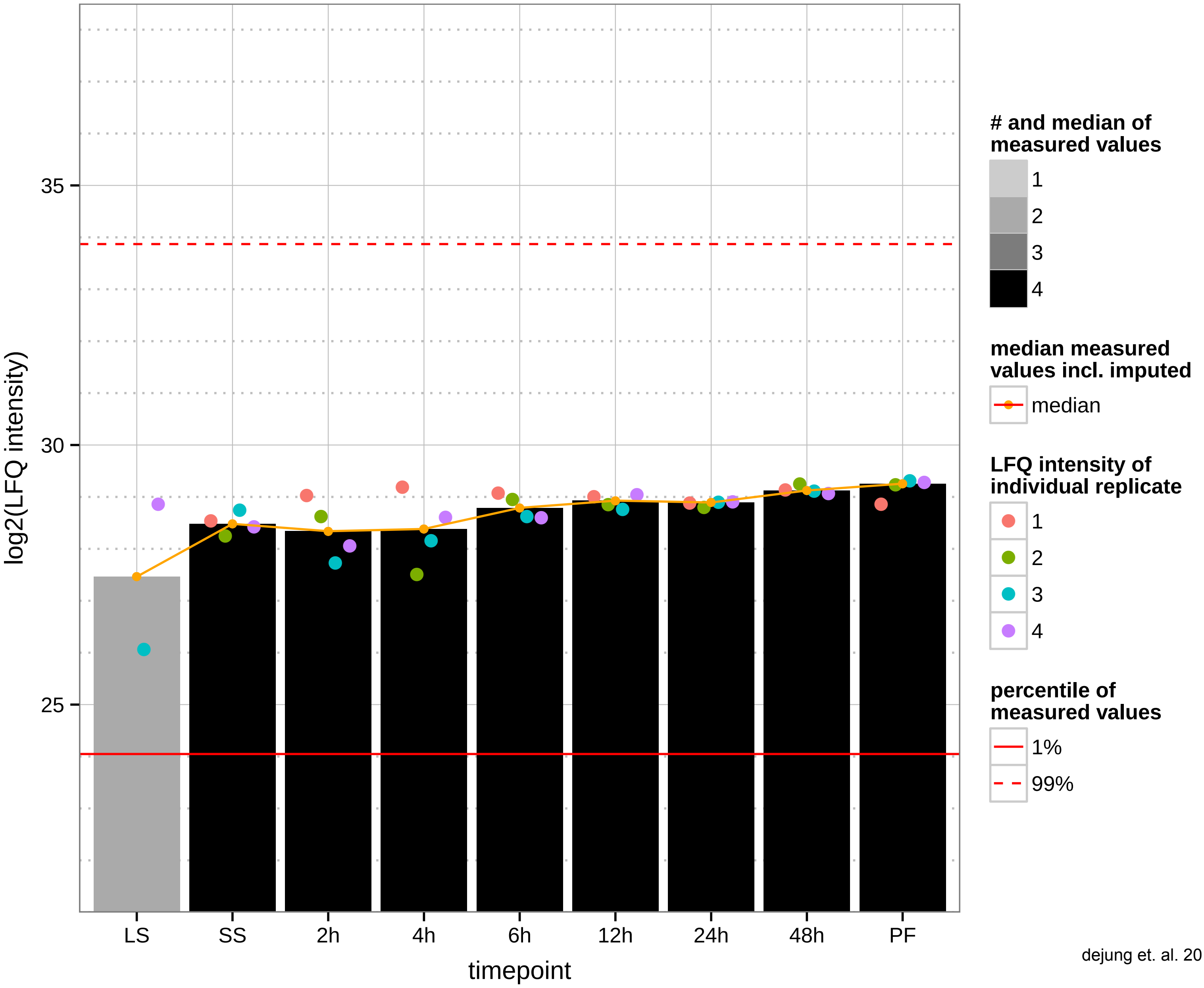
aldehyde dehydrogenase, putative (ALDH)
Tb927.6.4210
AGOF: oxidoreductase activity
AGOC: mitochondrial inner membrane
AGOP: metabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process, oxidation–reduction process





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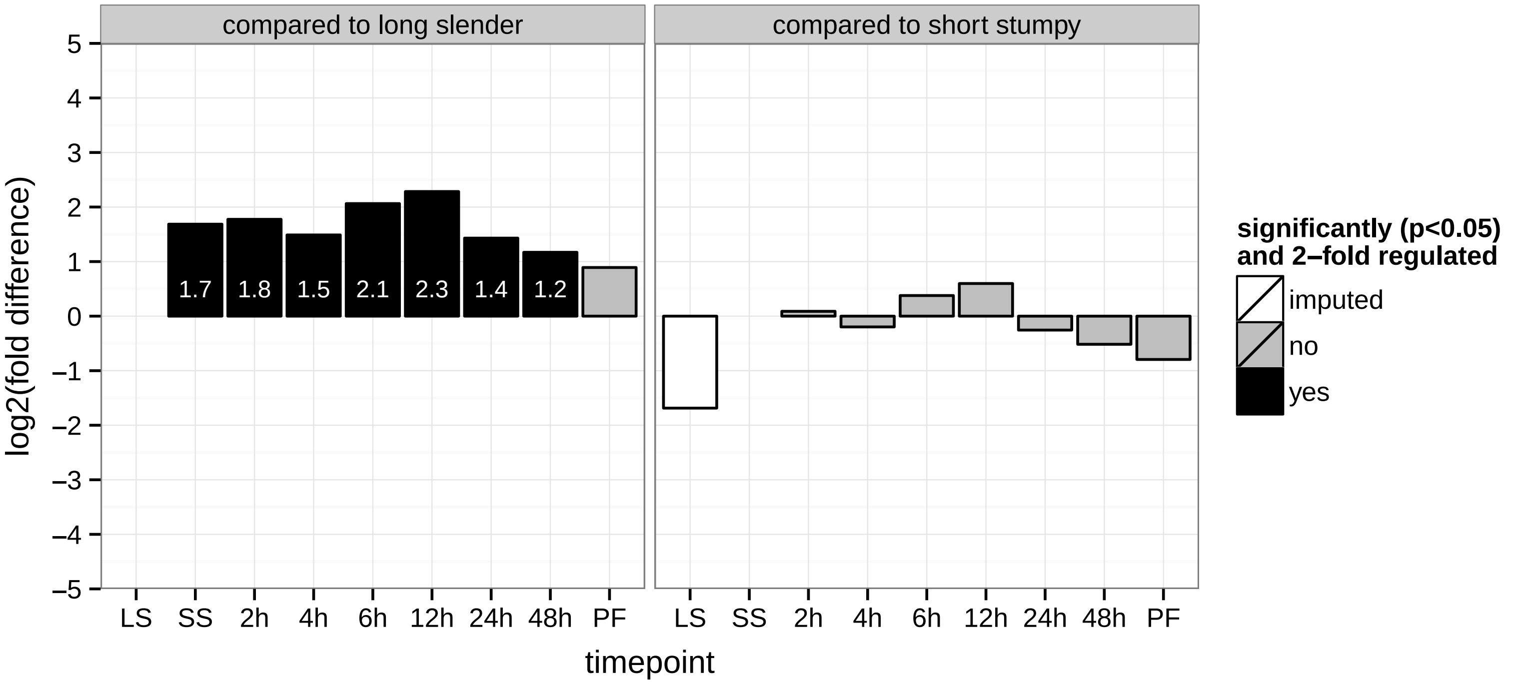
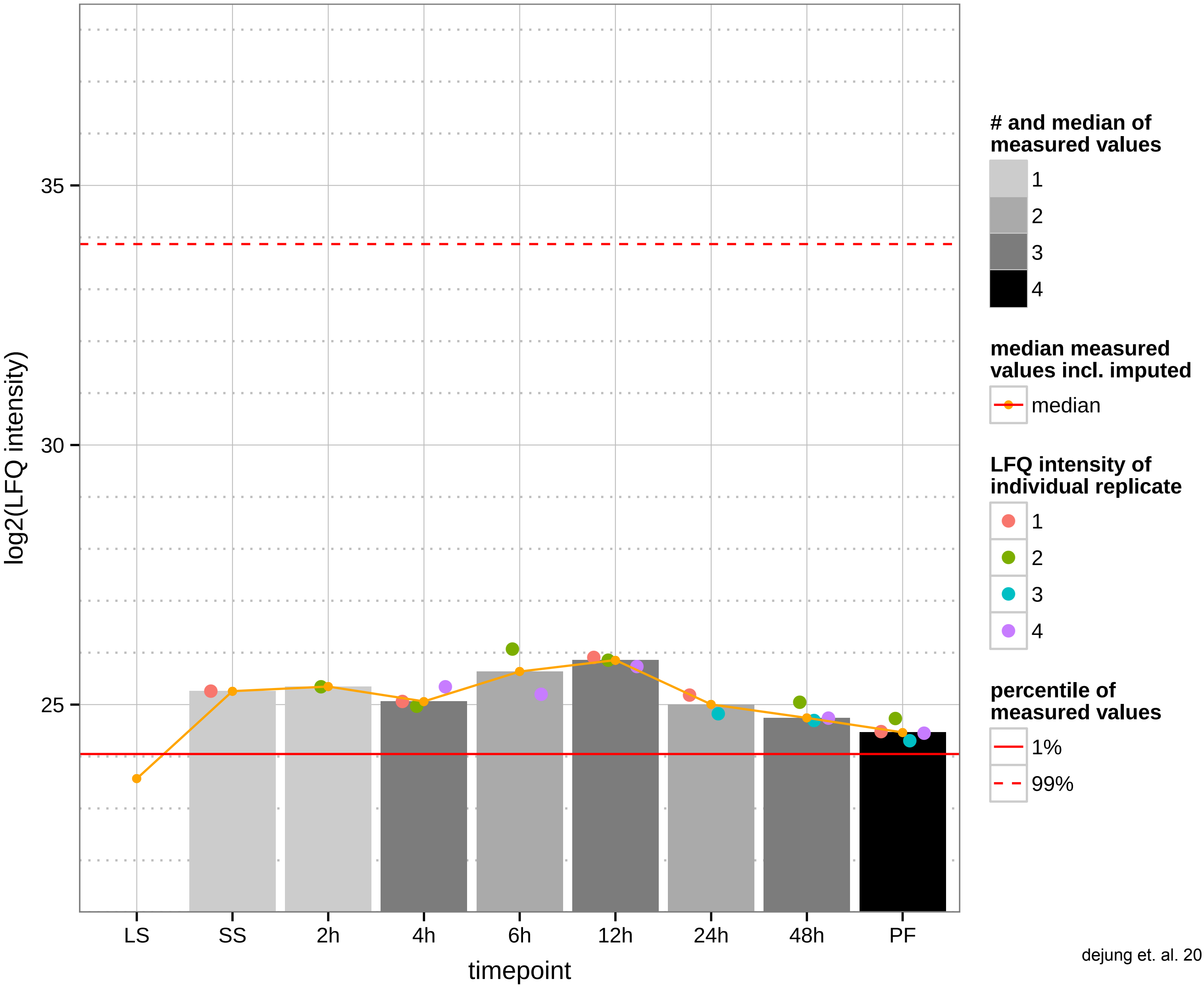
hypothetical protein, conserved
Tb927.6.4260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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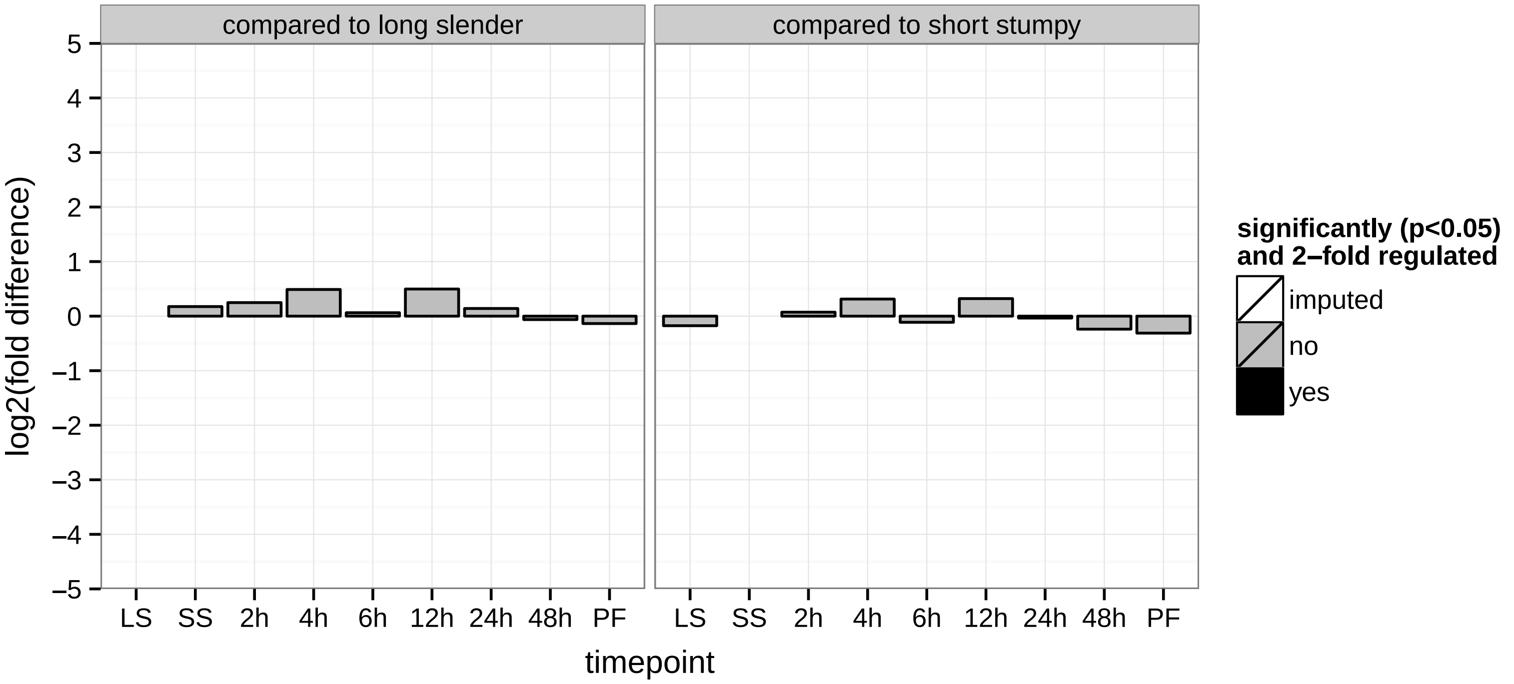
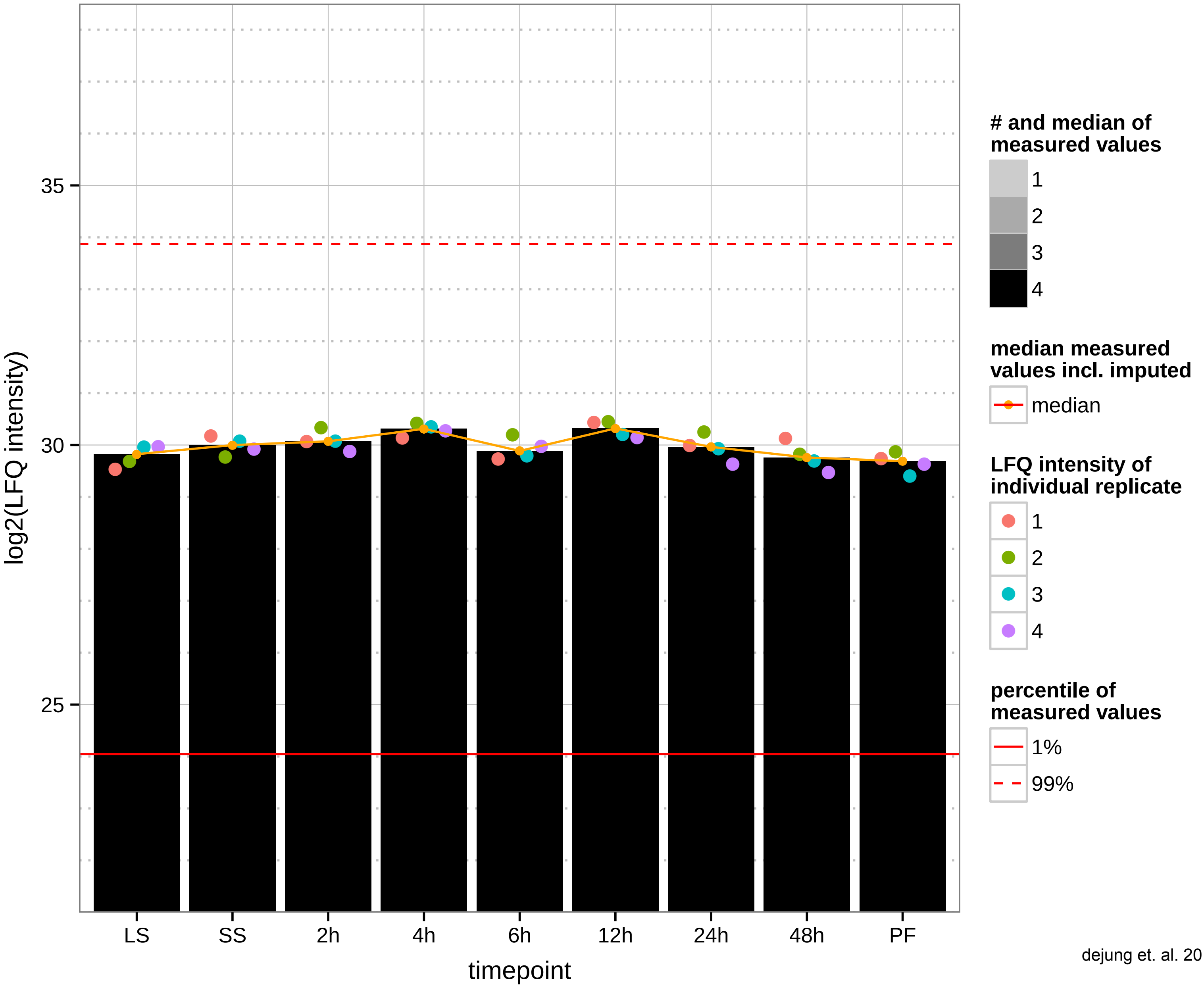
hypothetical protein, conserved
Tb927.6.4320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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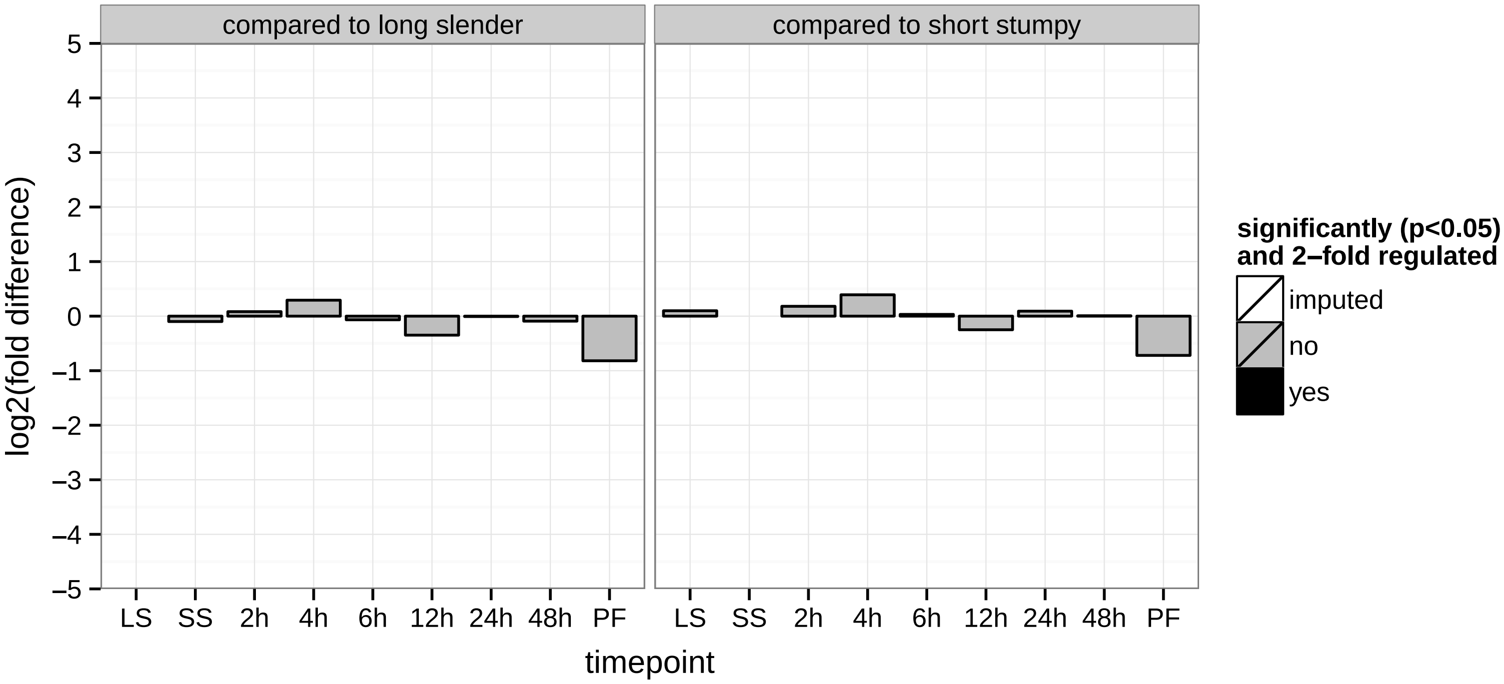
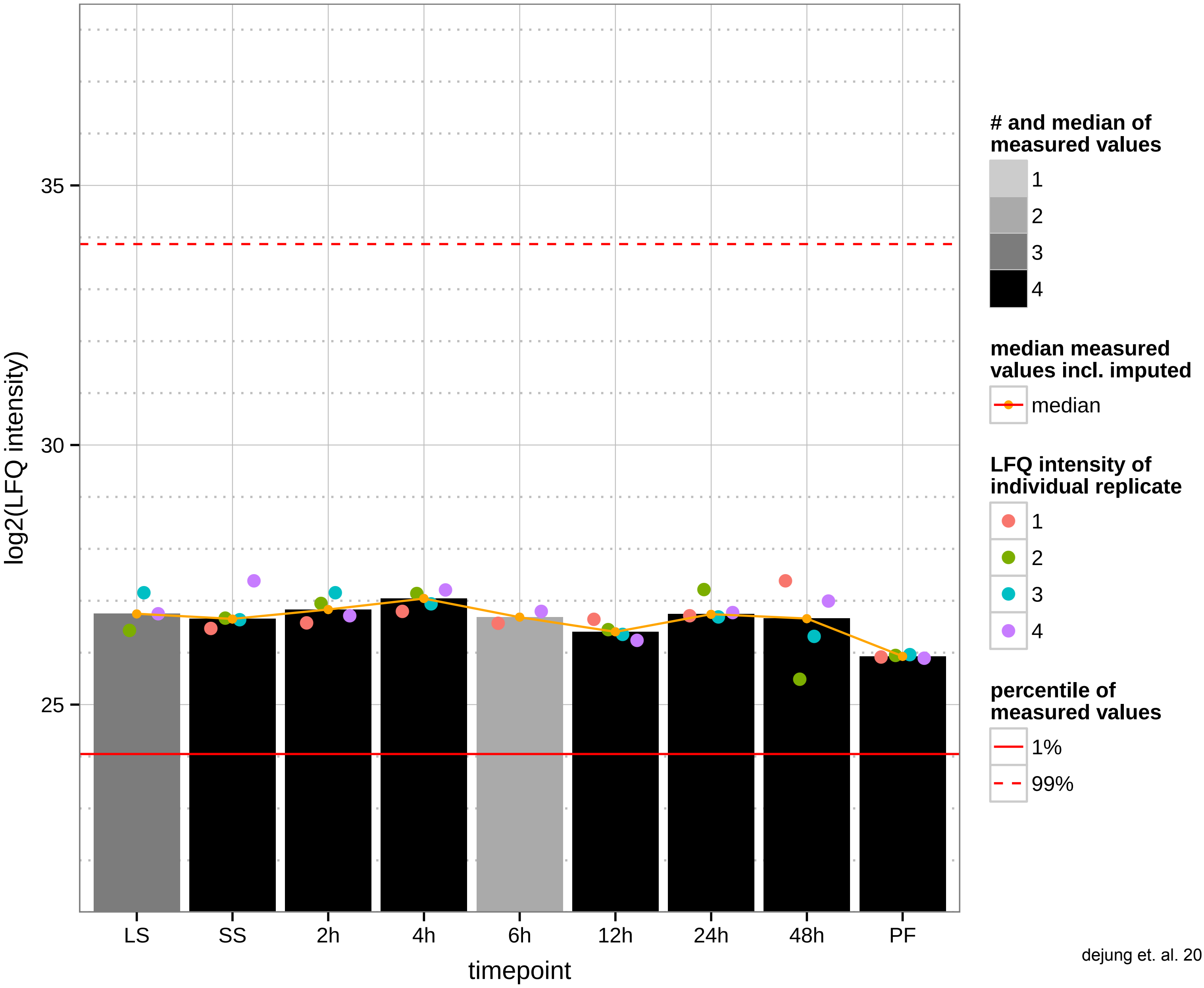
U6 snRNA–associated Sm–like protein LSm5p (TbLSm5)
Tb927.6.4340
AGOF: U6 snRNA 3'–end binding
AGOC: nucleus
AGOP: nuclear mRNA splicing, via spliceosome
PGOF: null
PGOC: null
PGOP: null





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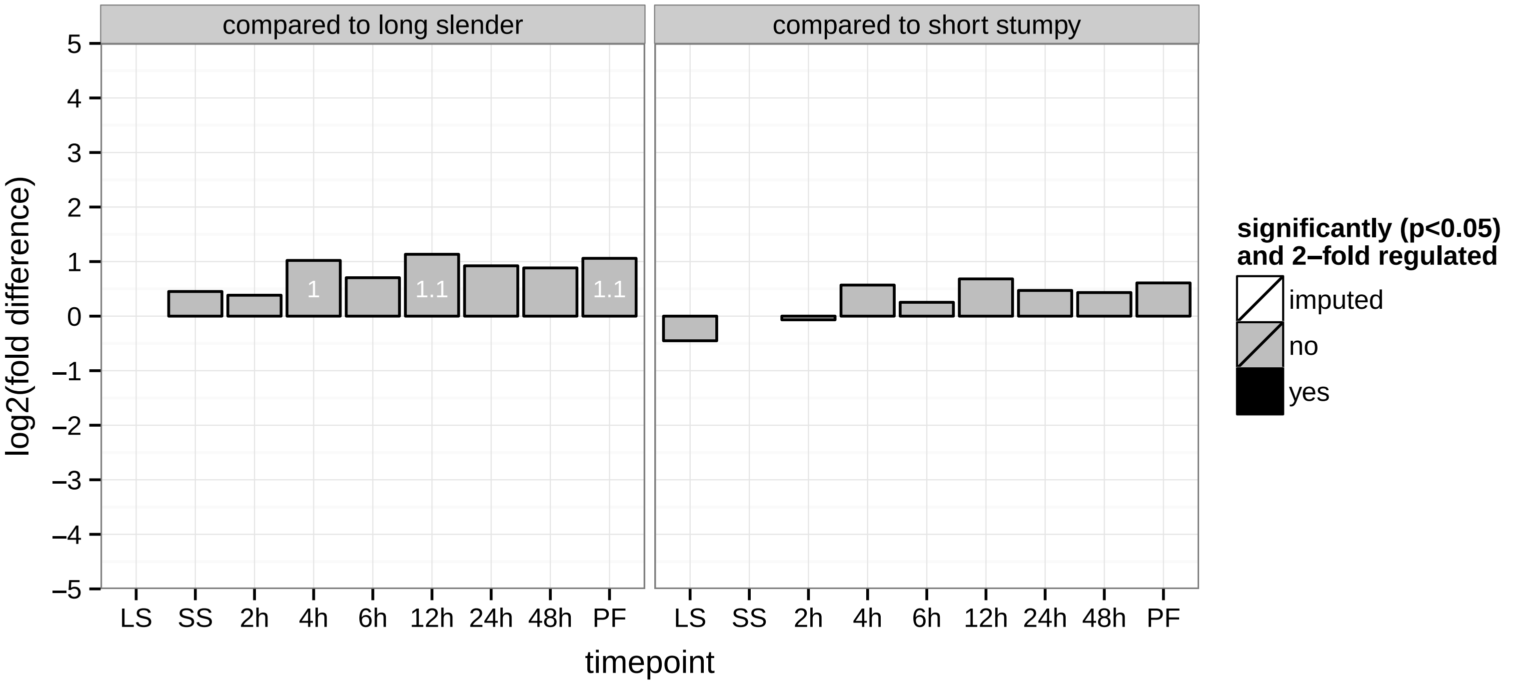
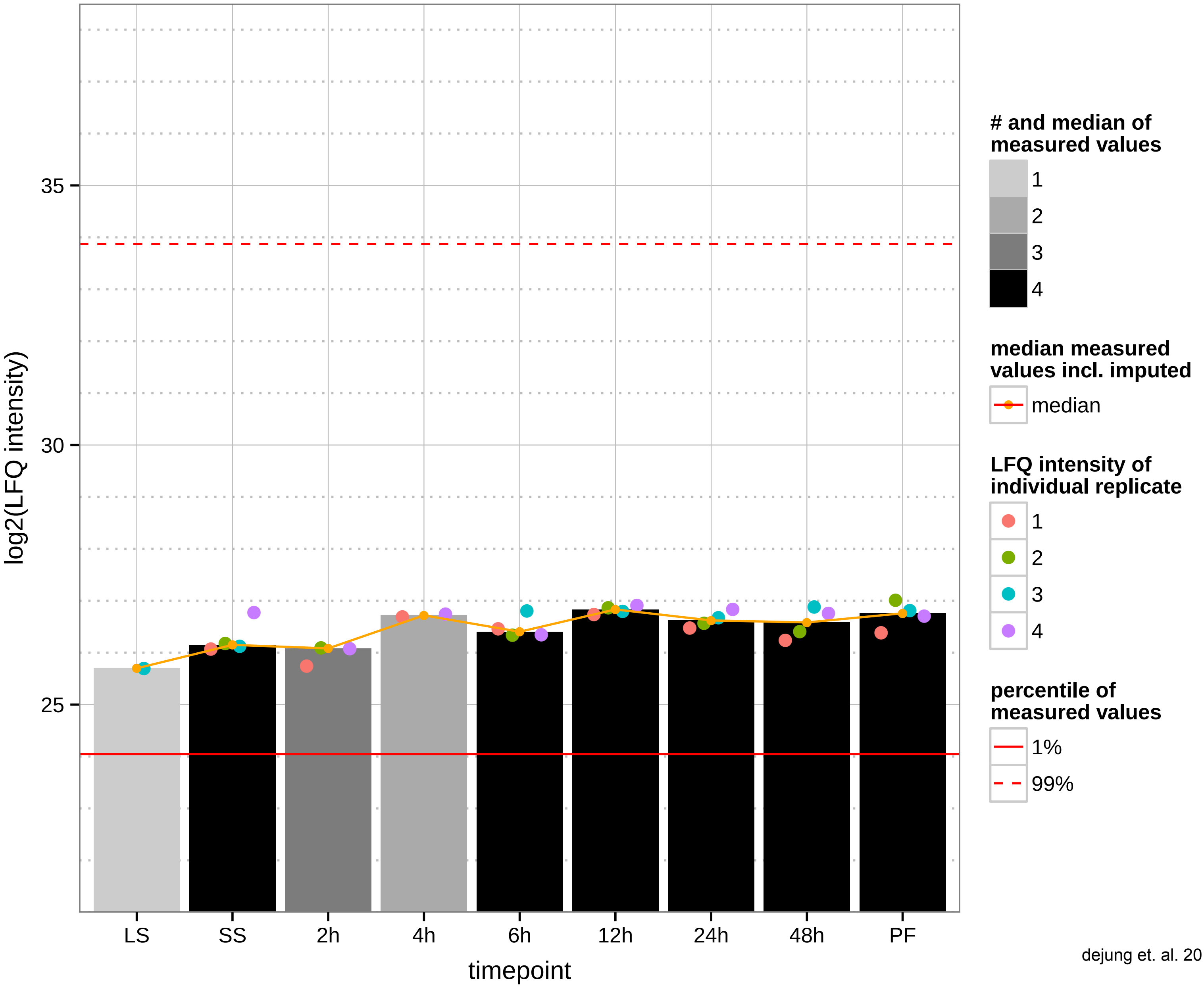
ribosomal RNA assembly protein, putative
Tb927.6.4350
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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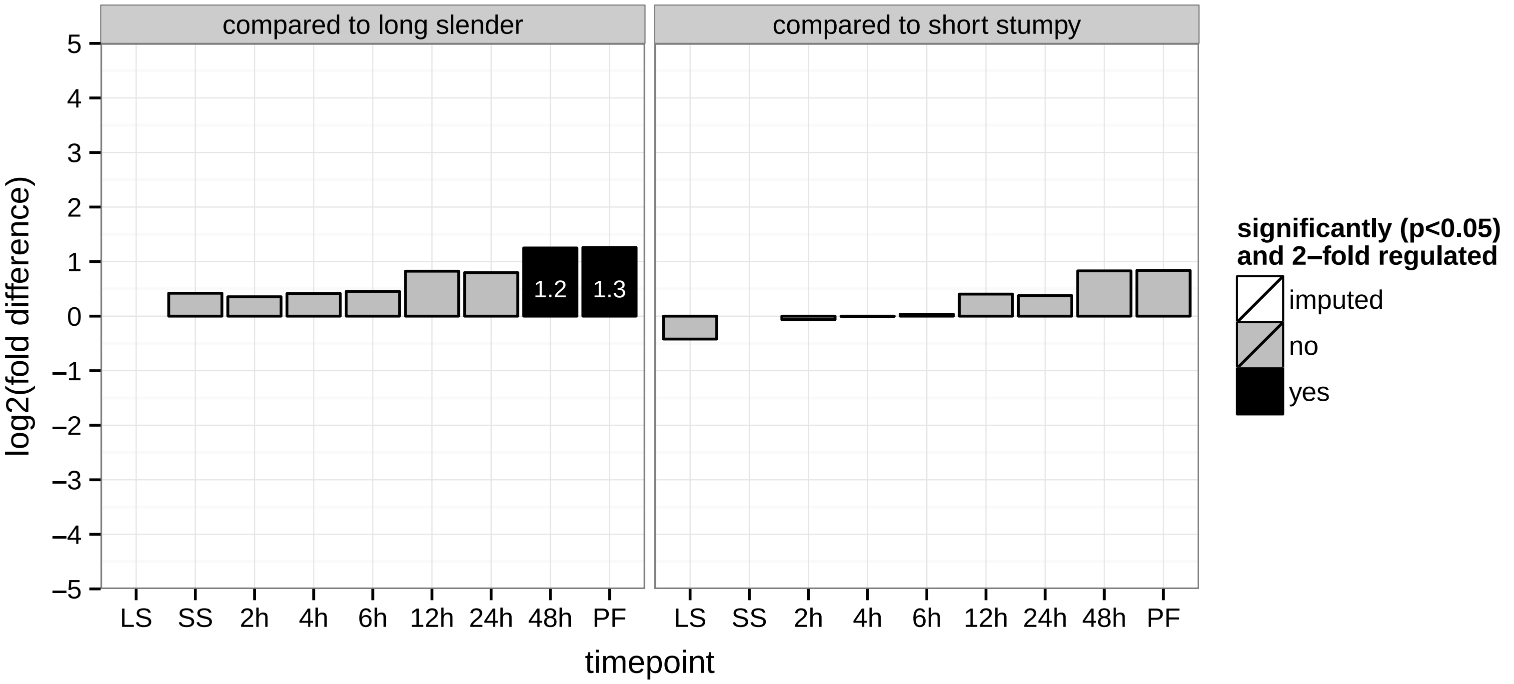
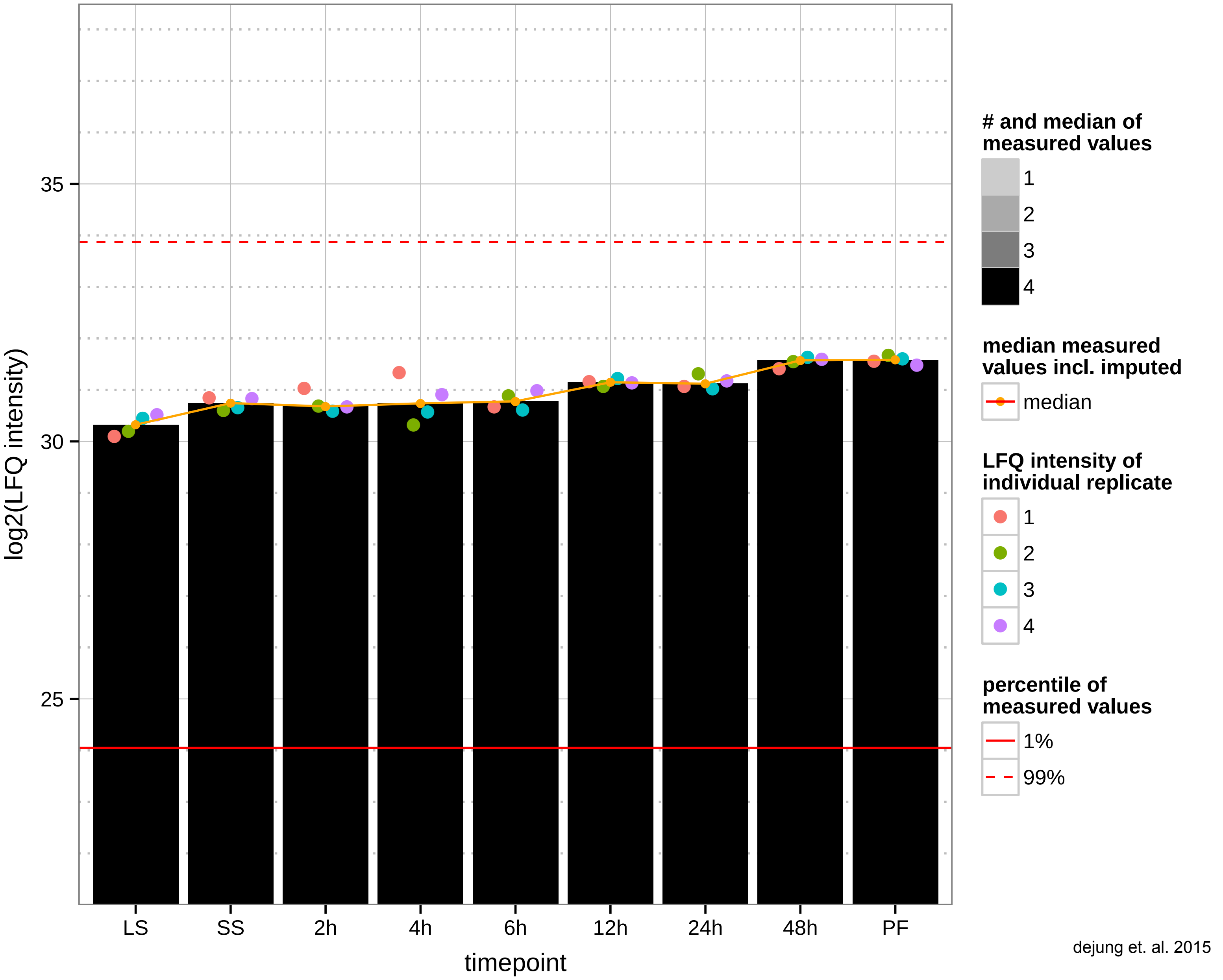
eukaryotic translation initiation factor 3 subunit 7–like protein
Tb927.6.4370
AGOF: translation initiation factor activity
AGOC: null
AGOP: translational initiation
PGOF: translation initiation factor activity
PGOC: null
PGOP: translational initiation





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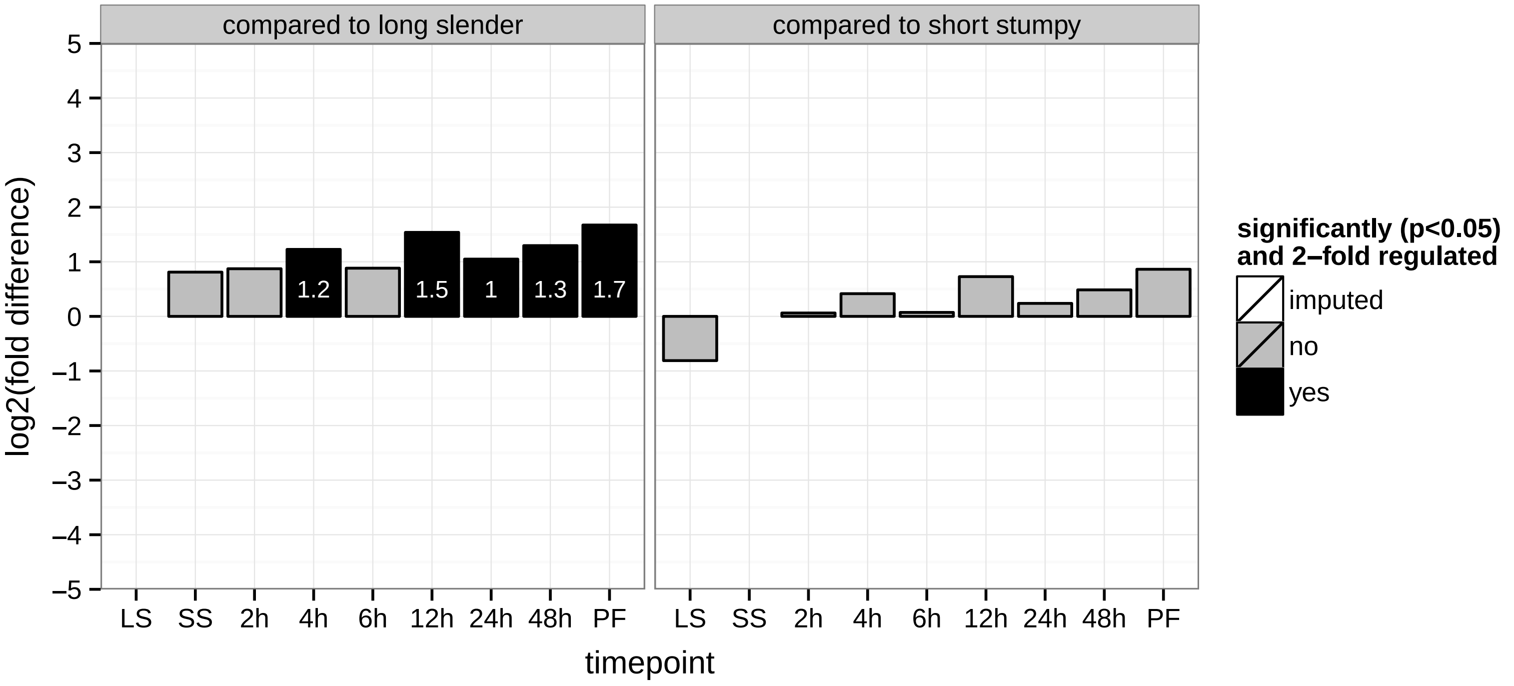
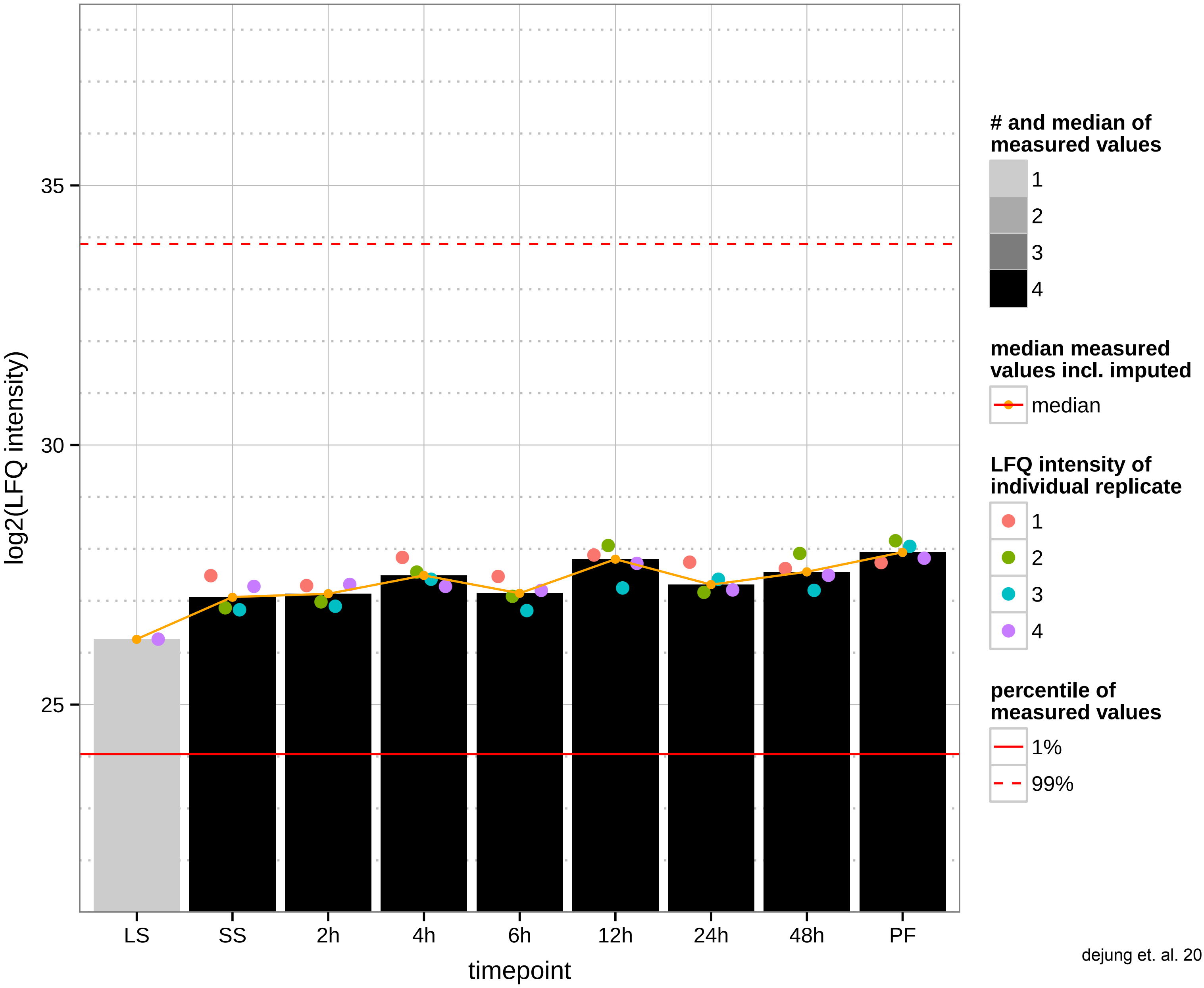
S–adenosylmethionine decarboxylase proenzyme, putative, S–adenosylmethionine decarboxylase (AdoMetDC)
Tb927.6.4460;Tb927.6.4410;Tb11.v5.0903
AGOF: null, adenosylmethionine decarboxylase activity
AGOC: null
AGOP: null, spermidine biosynthetic process, spermine biosynthetic process
PGOF: adenosylmethionine decarboxylase activity
PGOC: null
PGOP: spermidine biosynthetic process, spermine biosynthetic process





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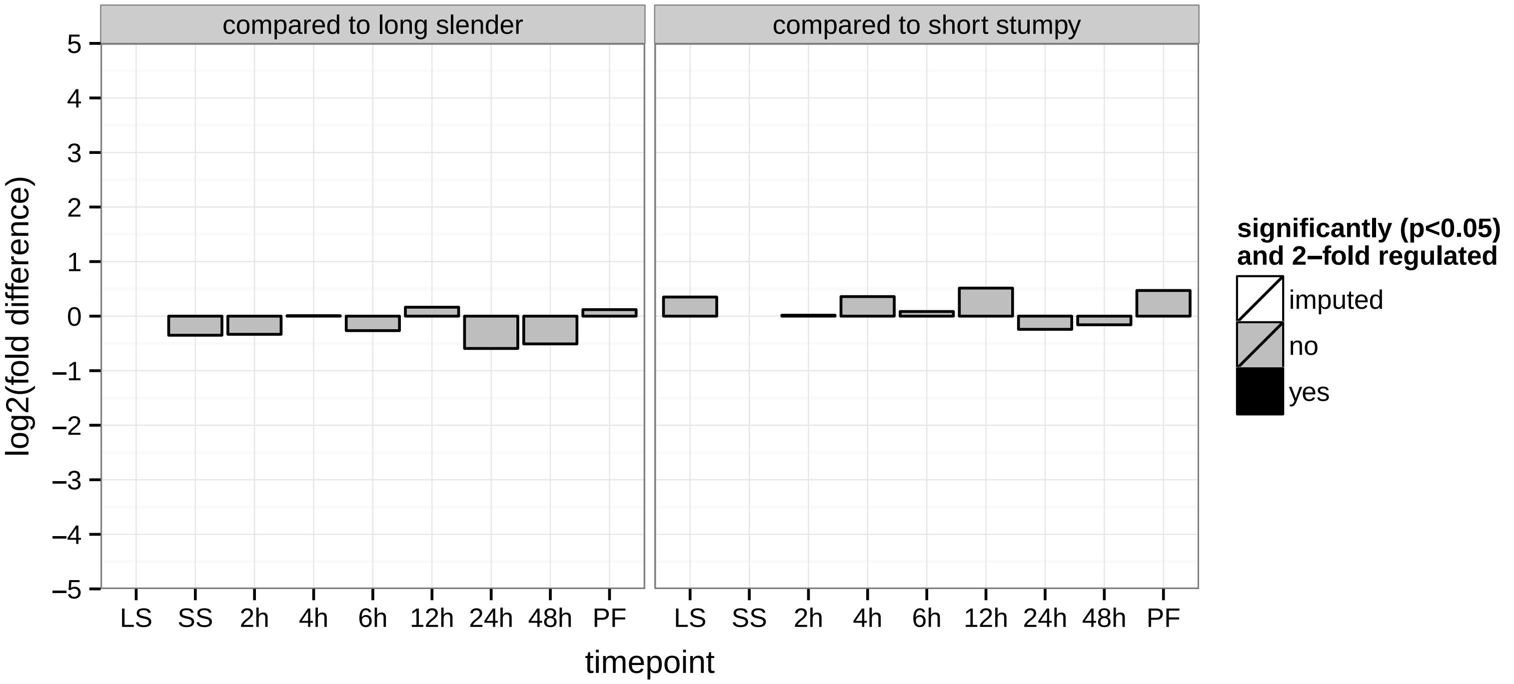
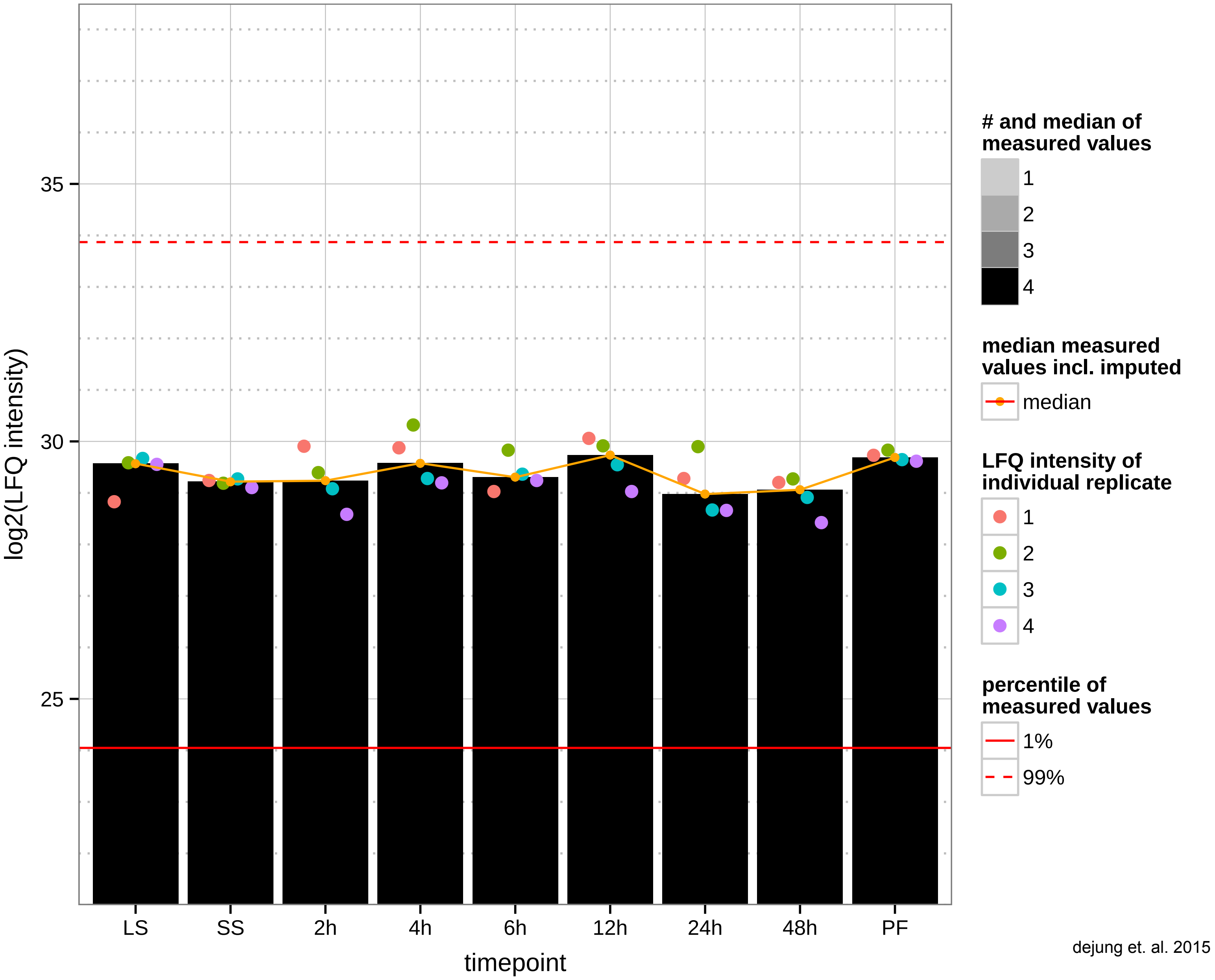
hypothetical protein, conserved
Tb927.6.4500
AGOF: null
AGOC: extrachromosomal circular DNA
AGOP: null
PGOF: null
PGOC: endoplasmic reticulum, extrachromosomal circular DNA, integral to membrane
PGOP: null





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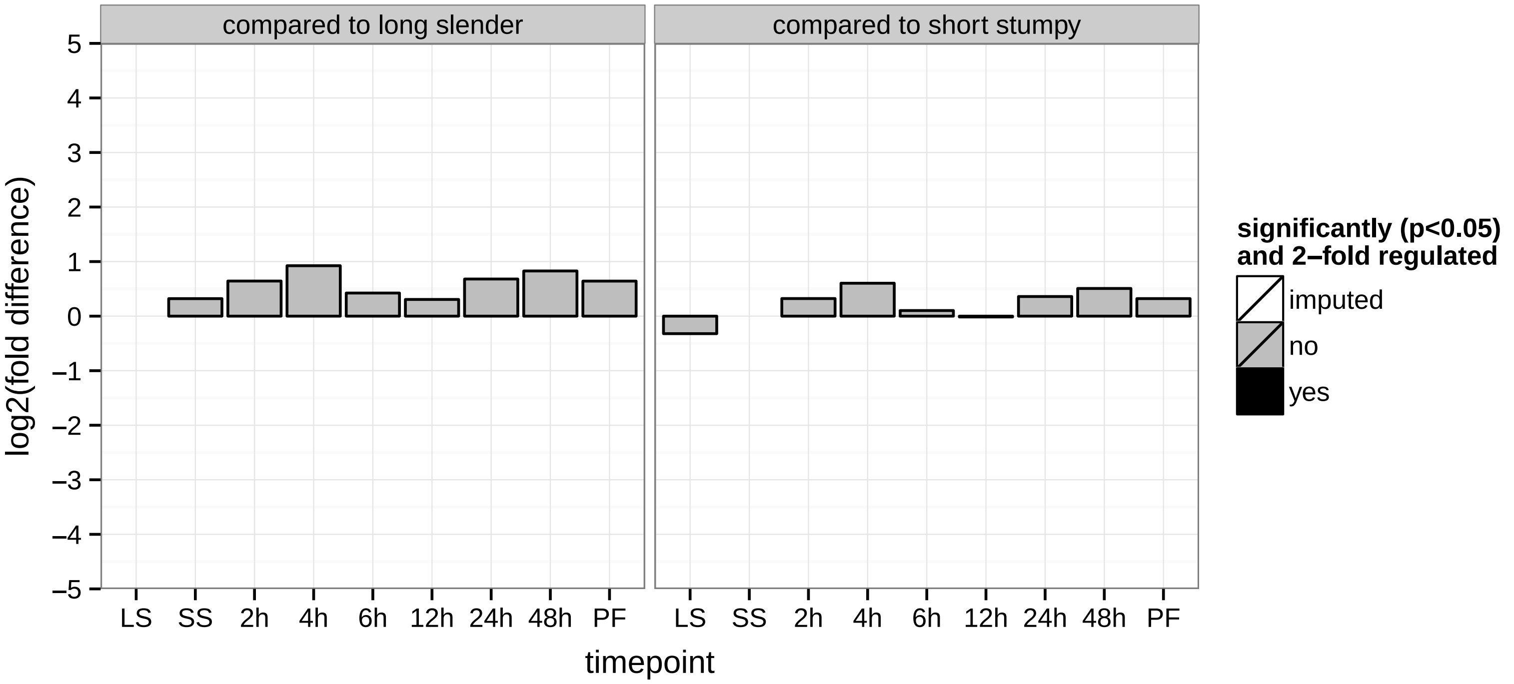
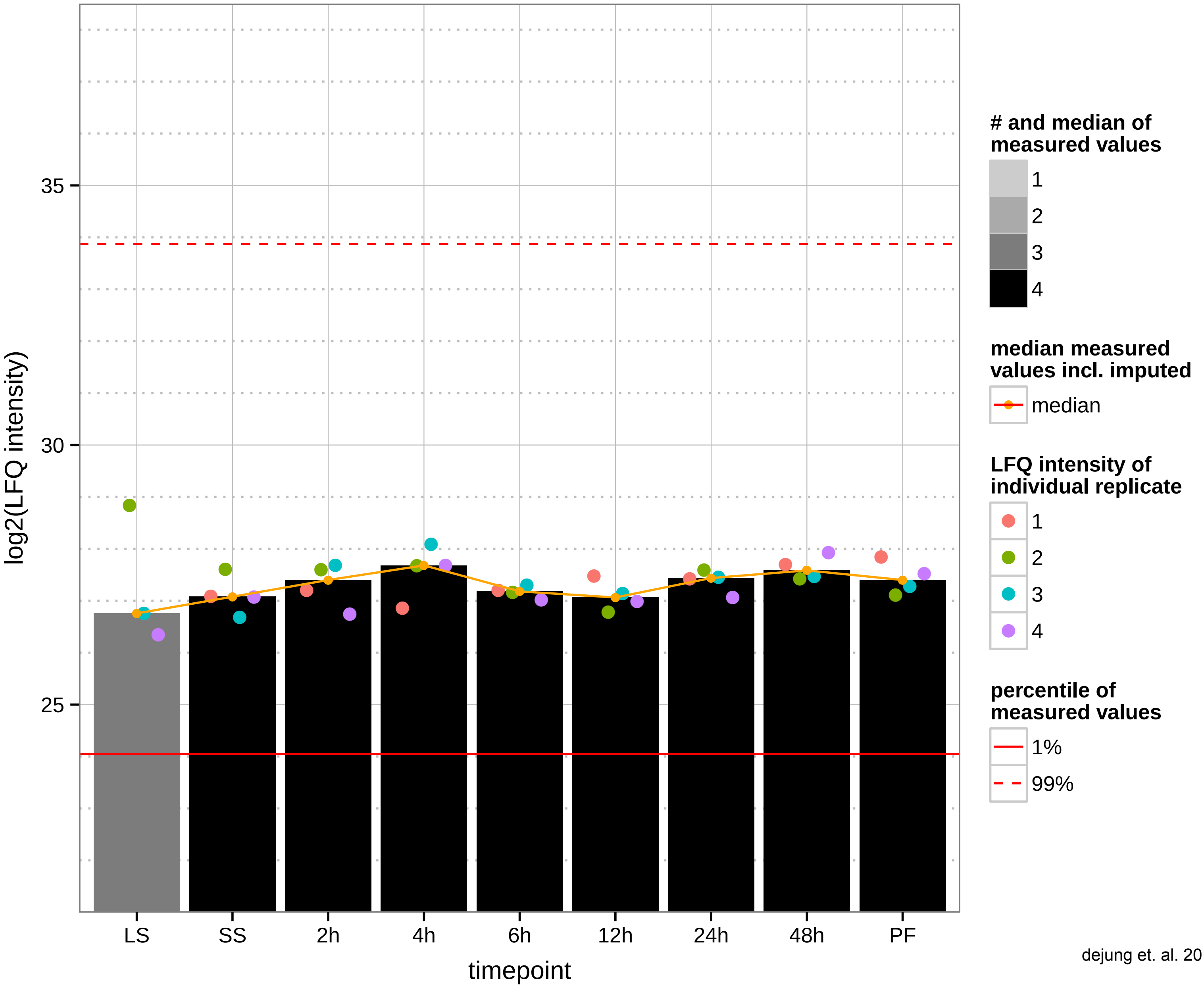
hypothetical protein, conserved
Tb927.6.4520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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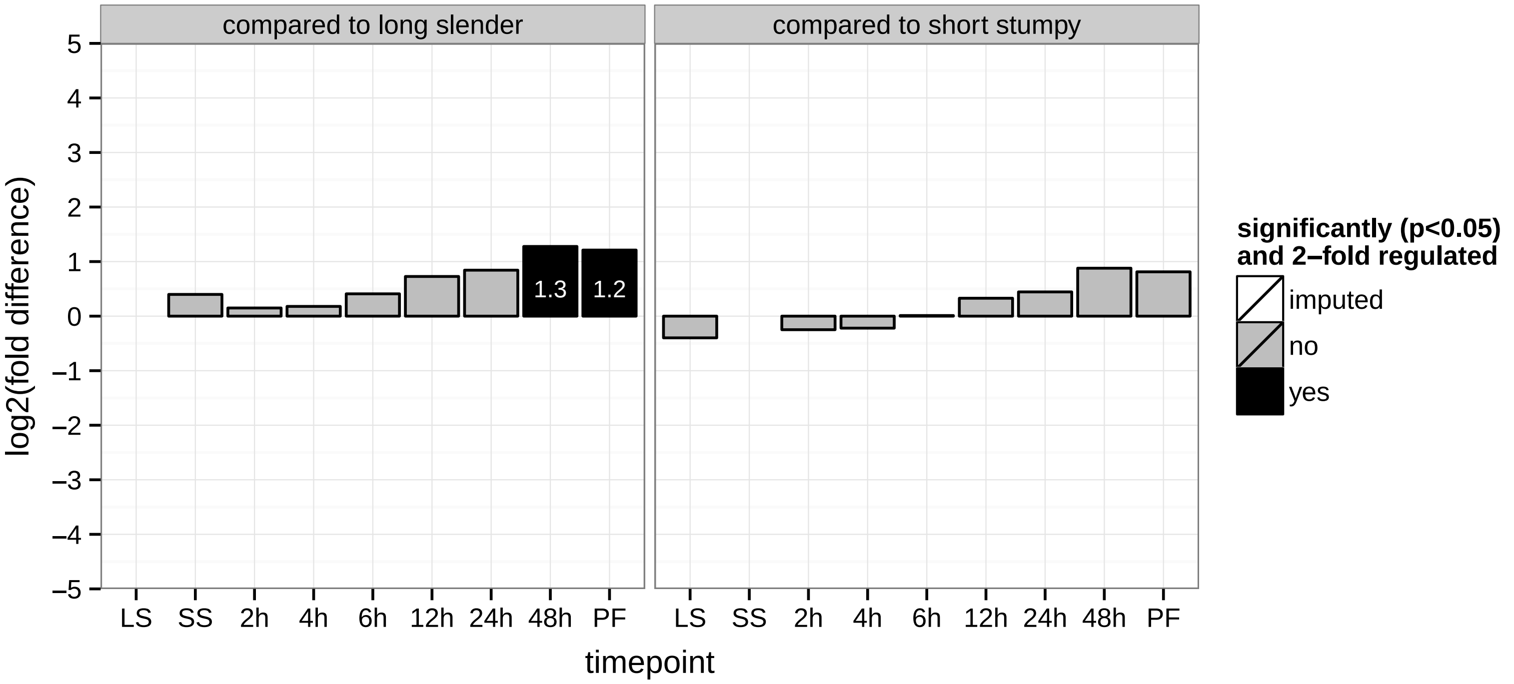
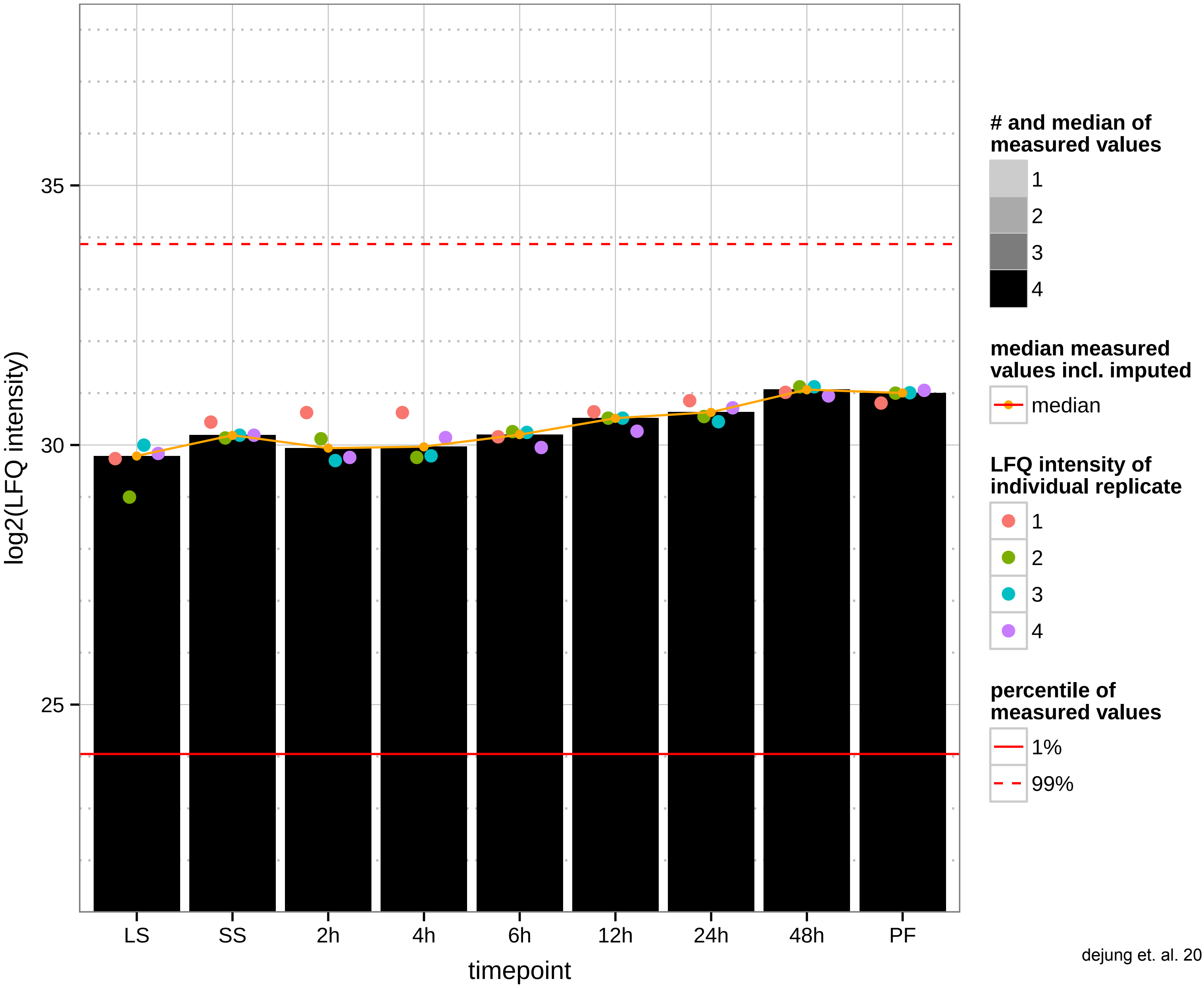
glutamyl–tRNA synthetase, putative
Tb927.6.4590;Tb11.v5.0810
AGOF: null, ATP binding, glutamate–tRNA ligase activity
AGOC: null, cytoplasm
AGOP: null, glutamyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, ligase activity, forming aminoacyl–tRNA and related compounds, nucleot
PGOC: cytoplasm
PGOP: tRNA aminoacylation, tRNA aminoacylation for protein translation, translation, glutamyl–tRNA aminoacylation, tRNA a





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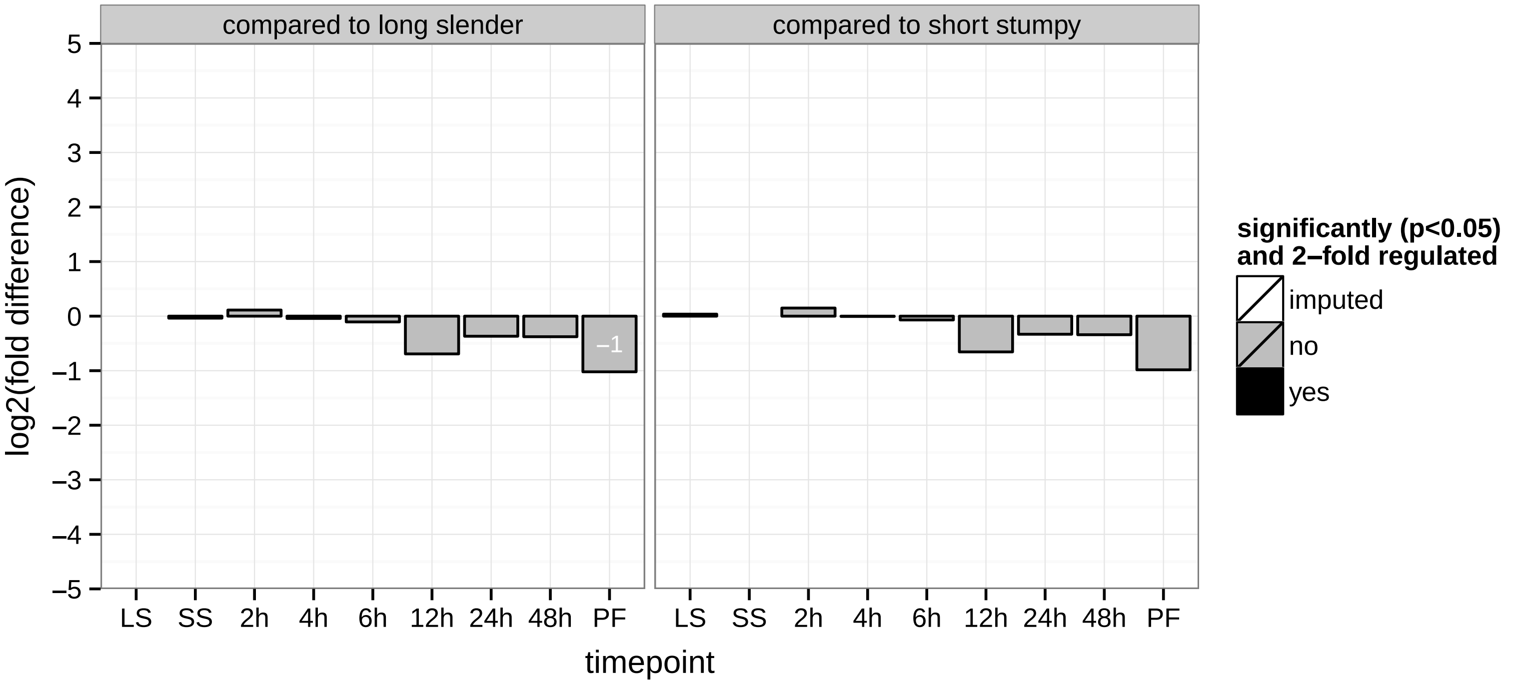
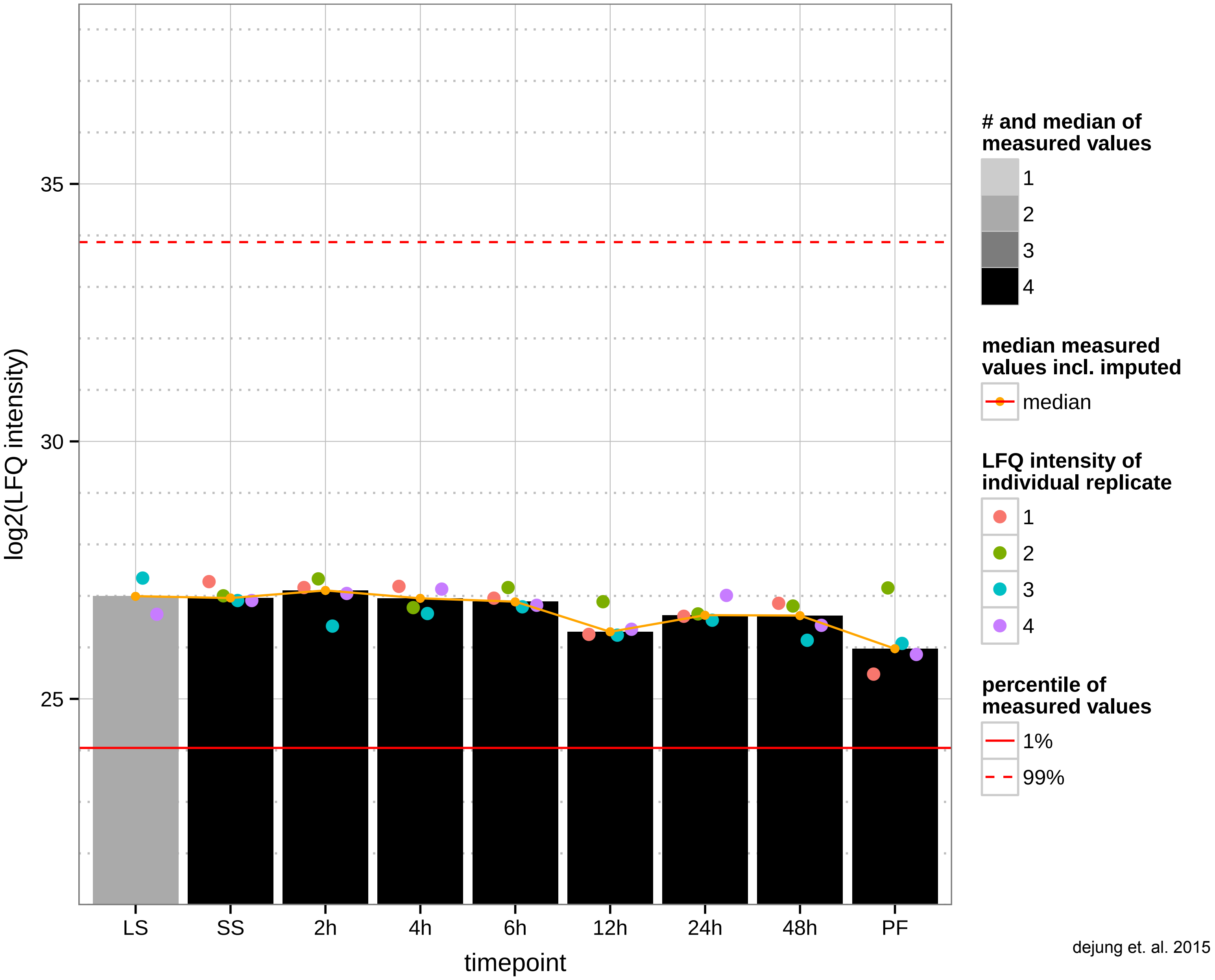
hypothetical protein, conserved
Tb927.6.4610
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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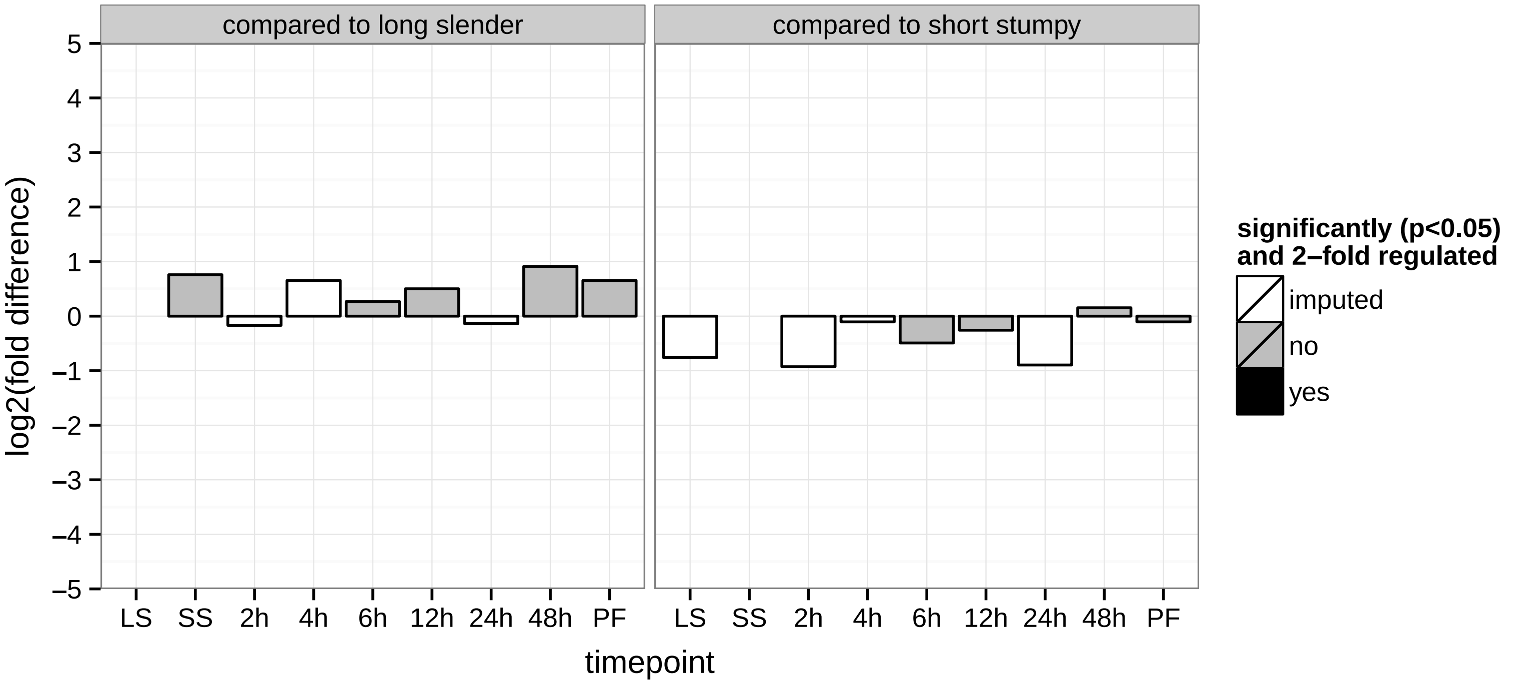
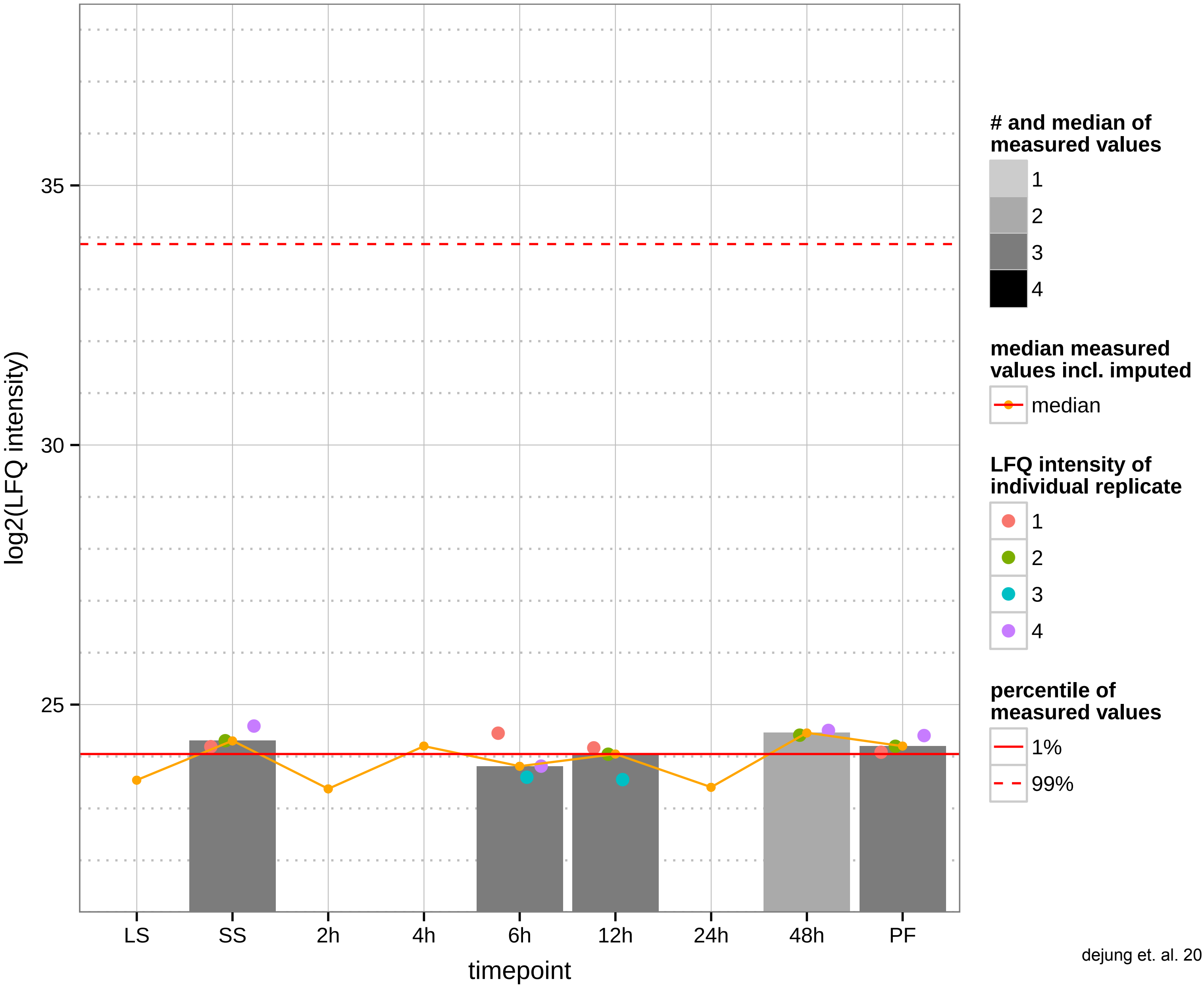
hypothetical protein, conserved
Tb927.6.4640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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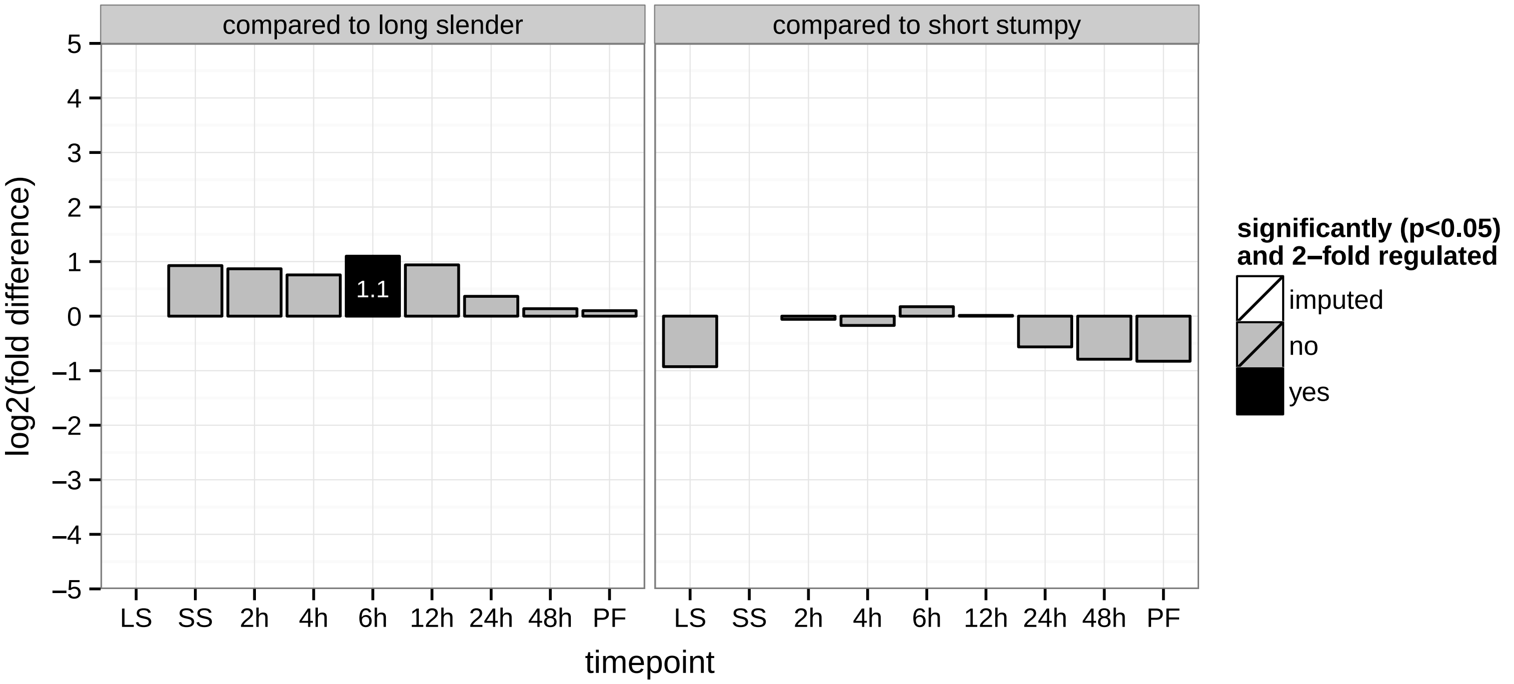
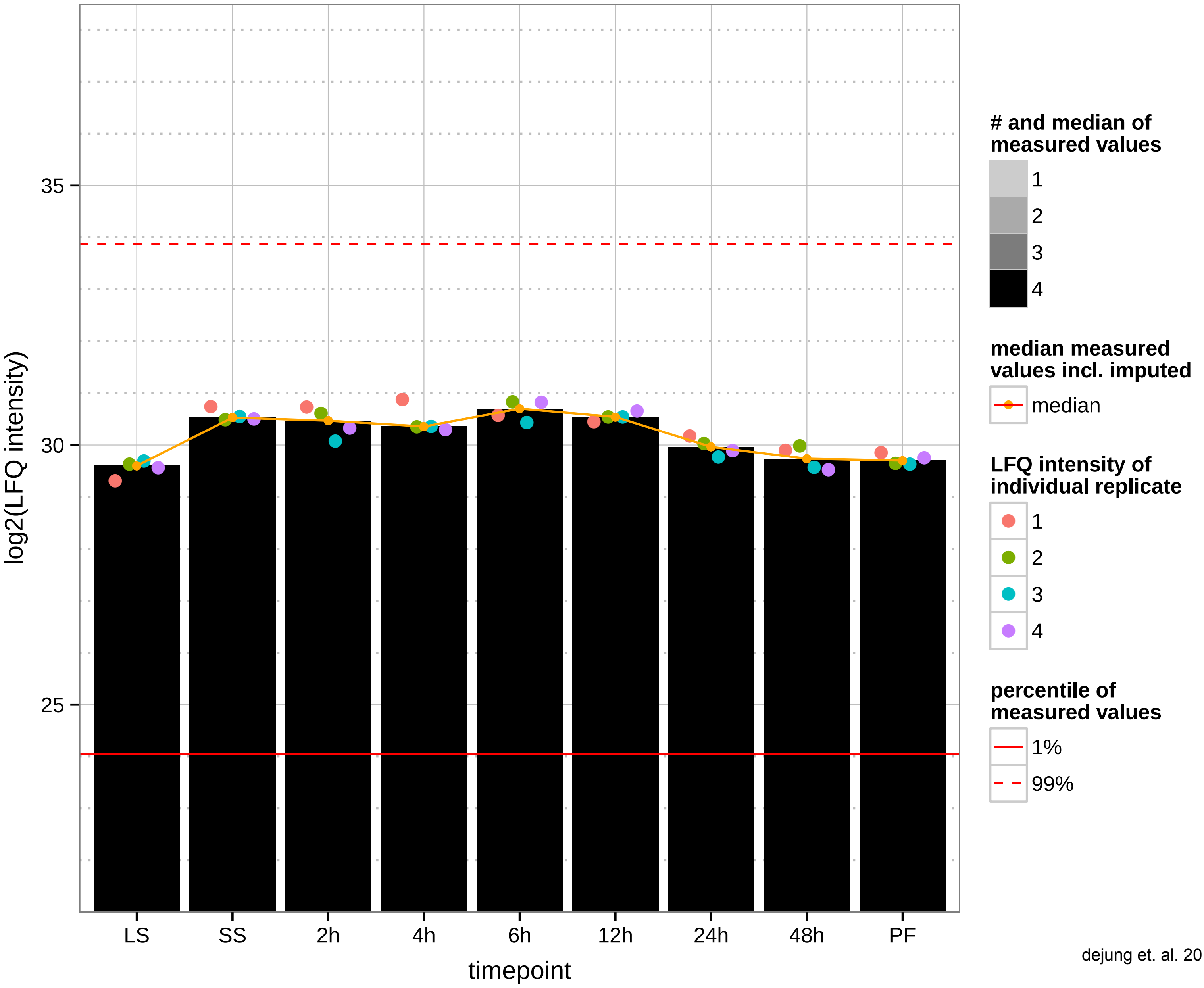
MORN repeat–containing protein, CMRP, flagellar component (TbMORN1)
Tb927.6.4670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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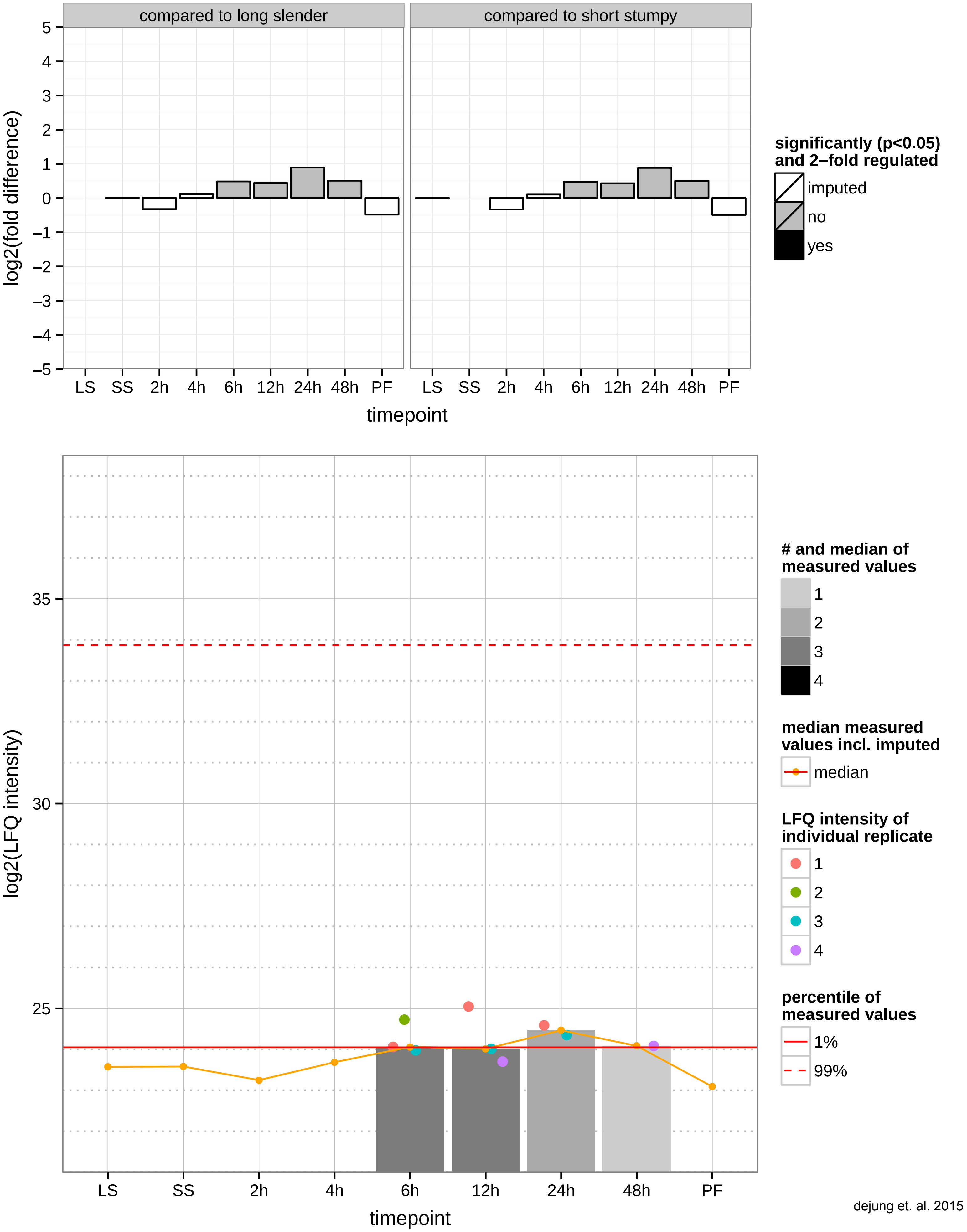
hypothetical protein, conserved
Tb927.6.4680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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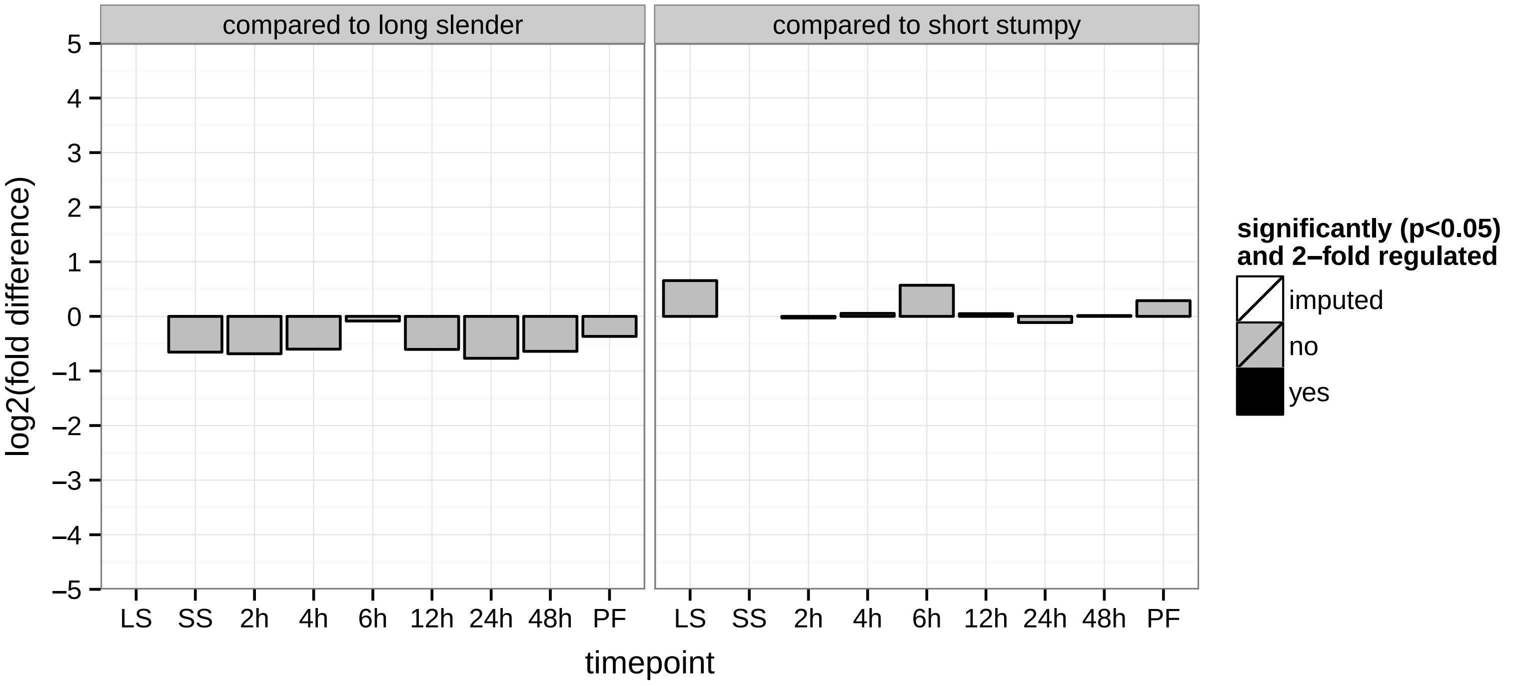
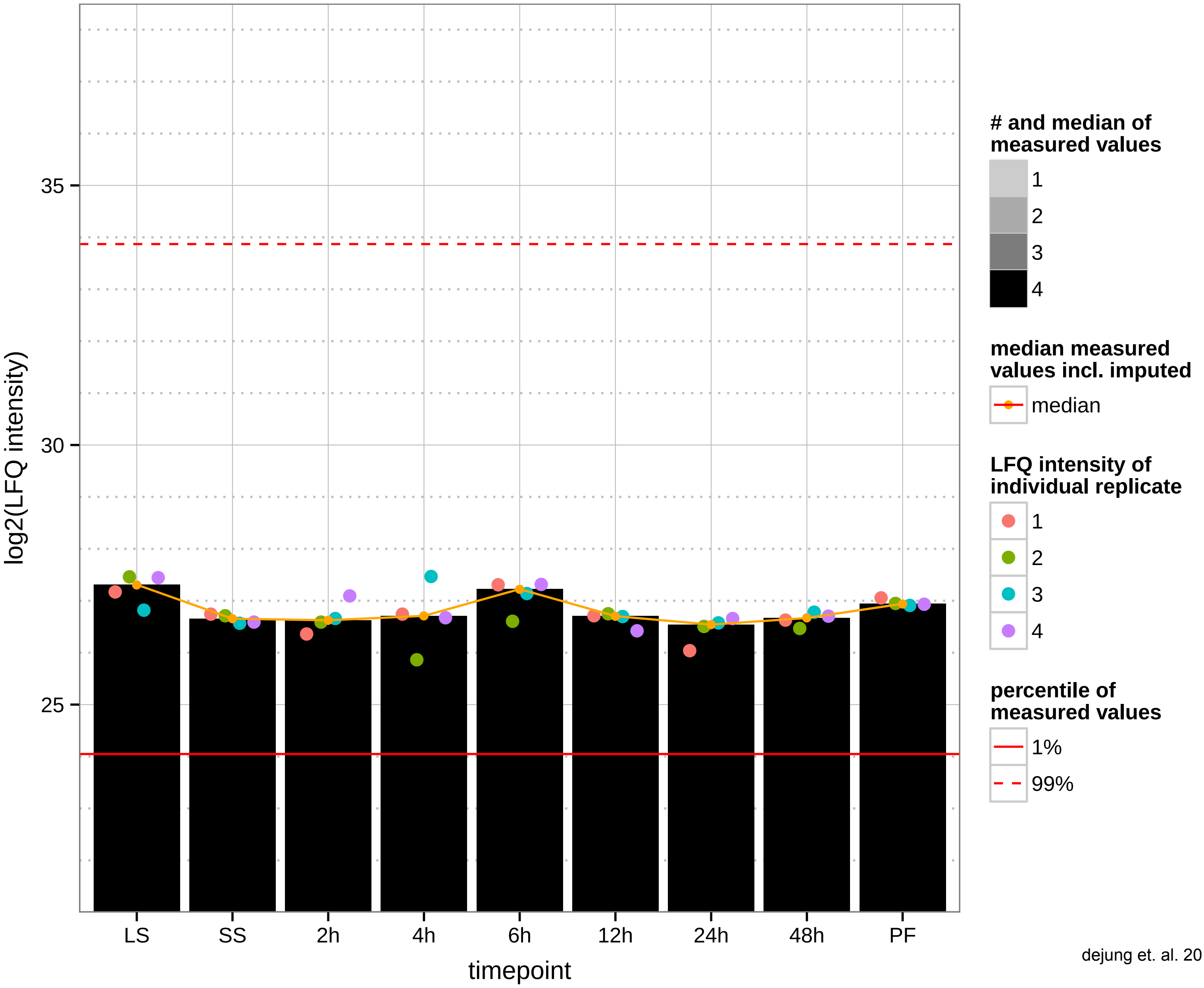
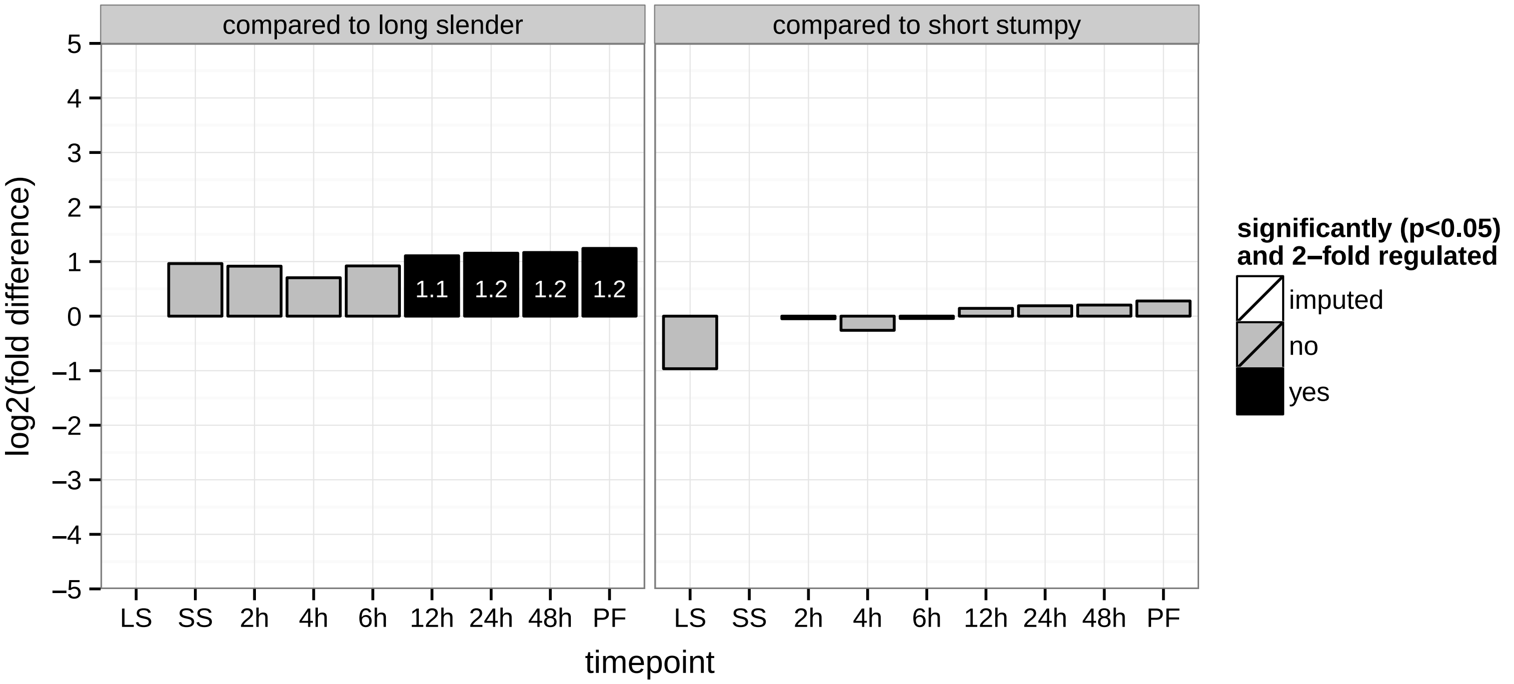
calmodulin, putative
Tb927.6.4710
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null

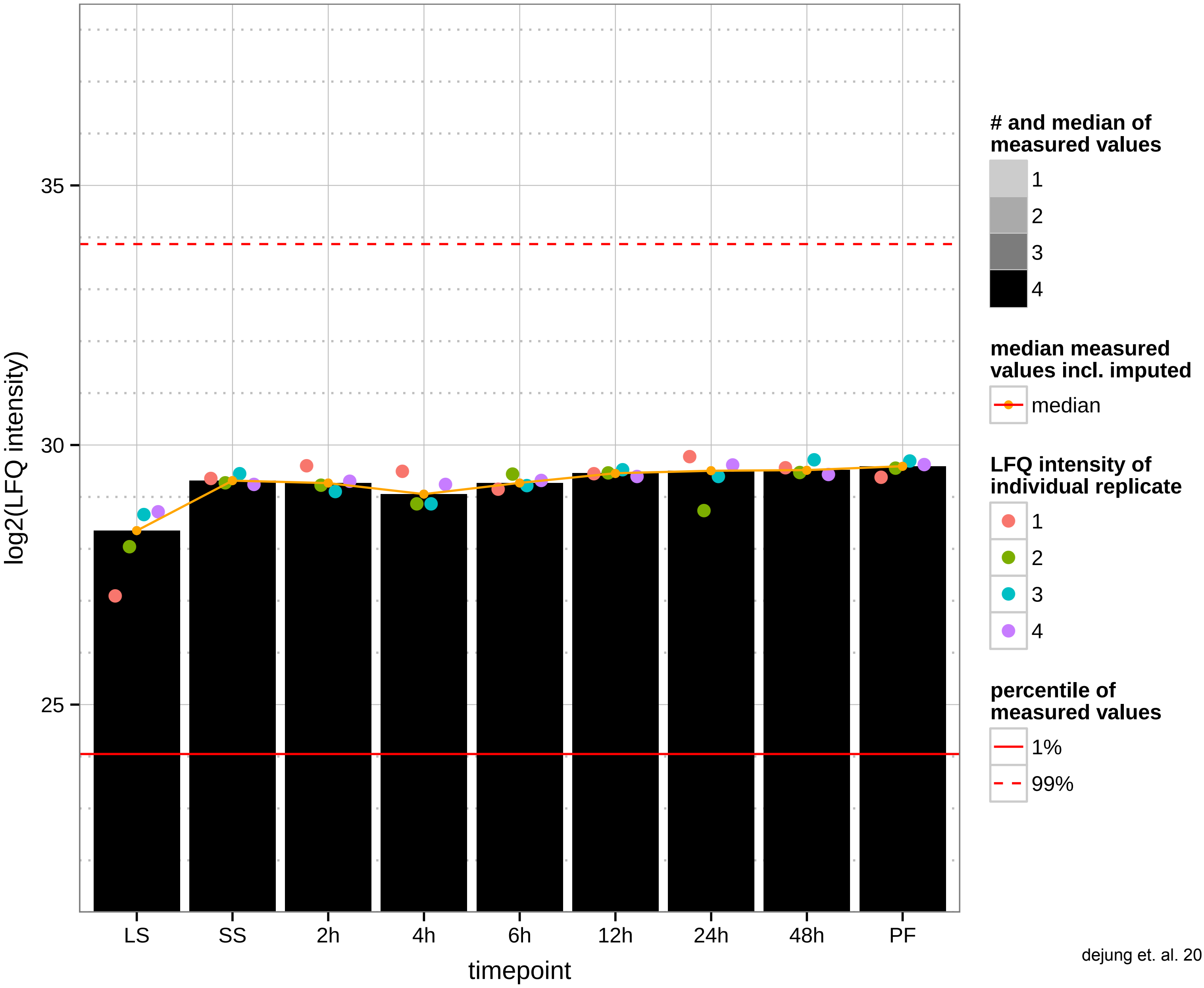




dejung et. al. 2015

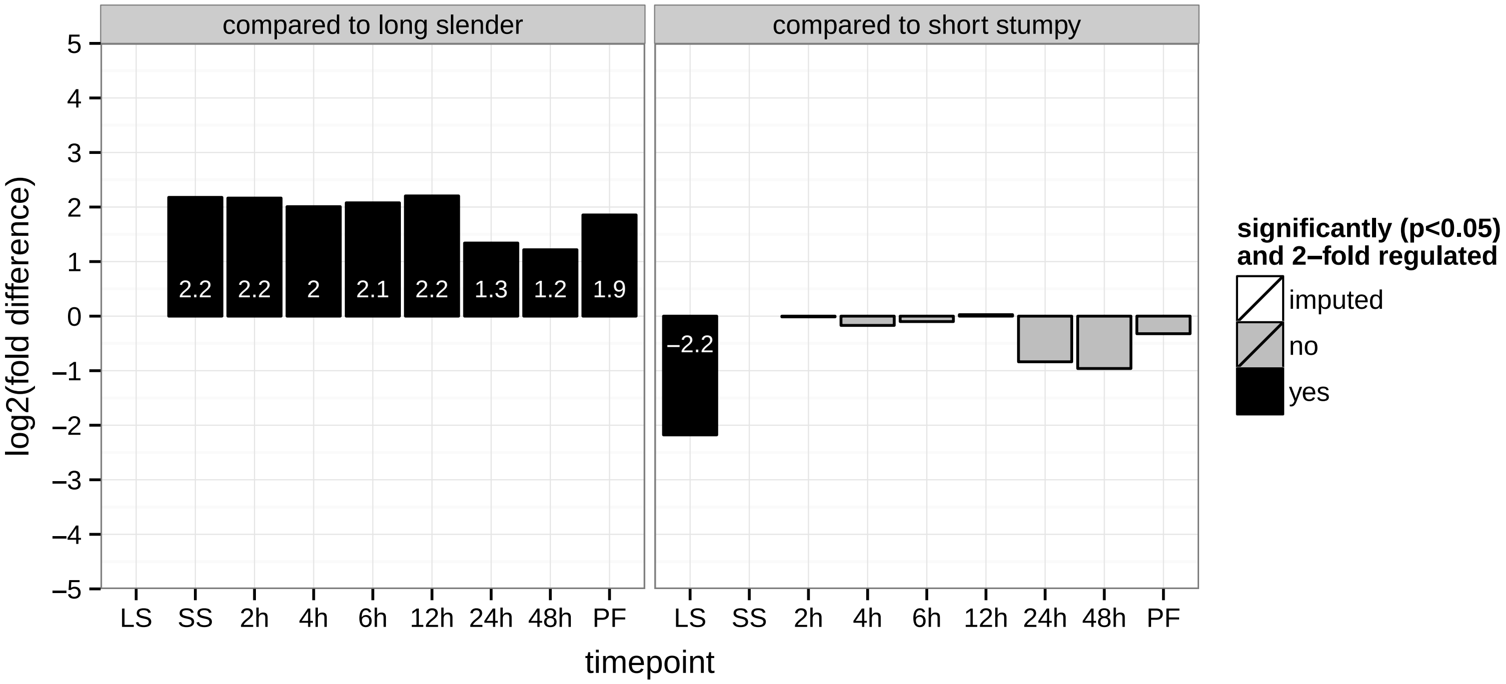
importin–alpha re–exporter protein, putative, cellular apoptosis susceptibility protein
Tb927.6.4740
AGOF: importin–alpha export receptor activity, protein transporter activity
AGOC: cytoplasm, nuclear pore, nucleus
AGOP: cell proliferation, intracellular protein transport, protein import into nucleus, docking
PGOF: binding, protein binding, protein transporter activity
PGOC: null
PGOP: intracellular protein transport

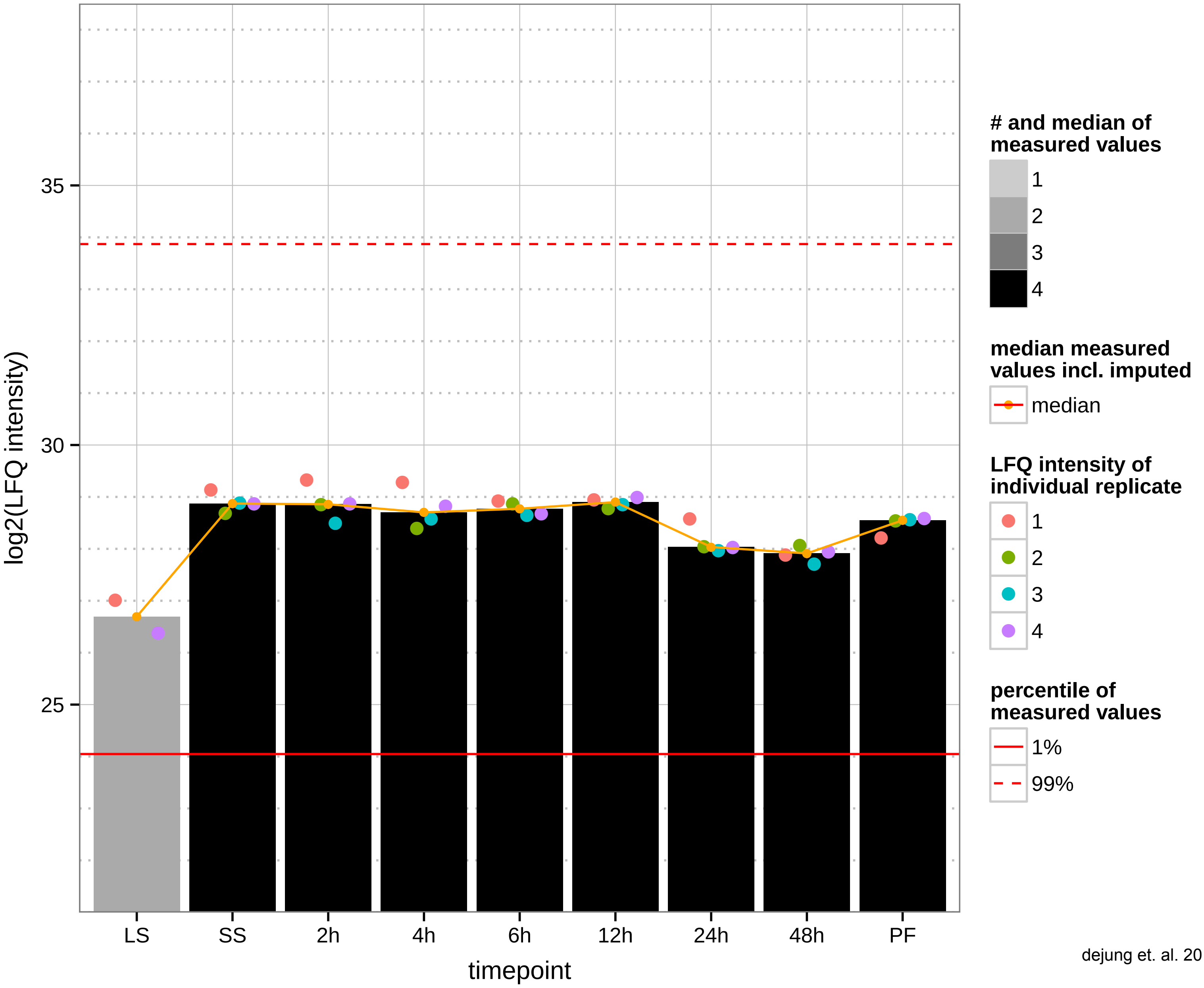




dejung et. al. 2015

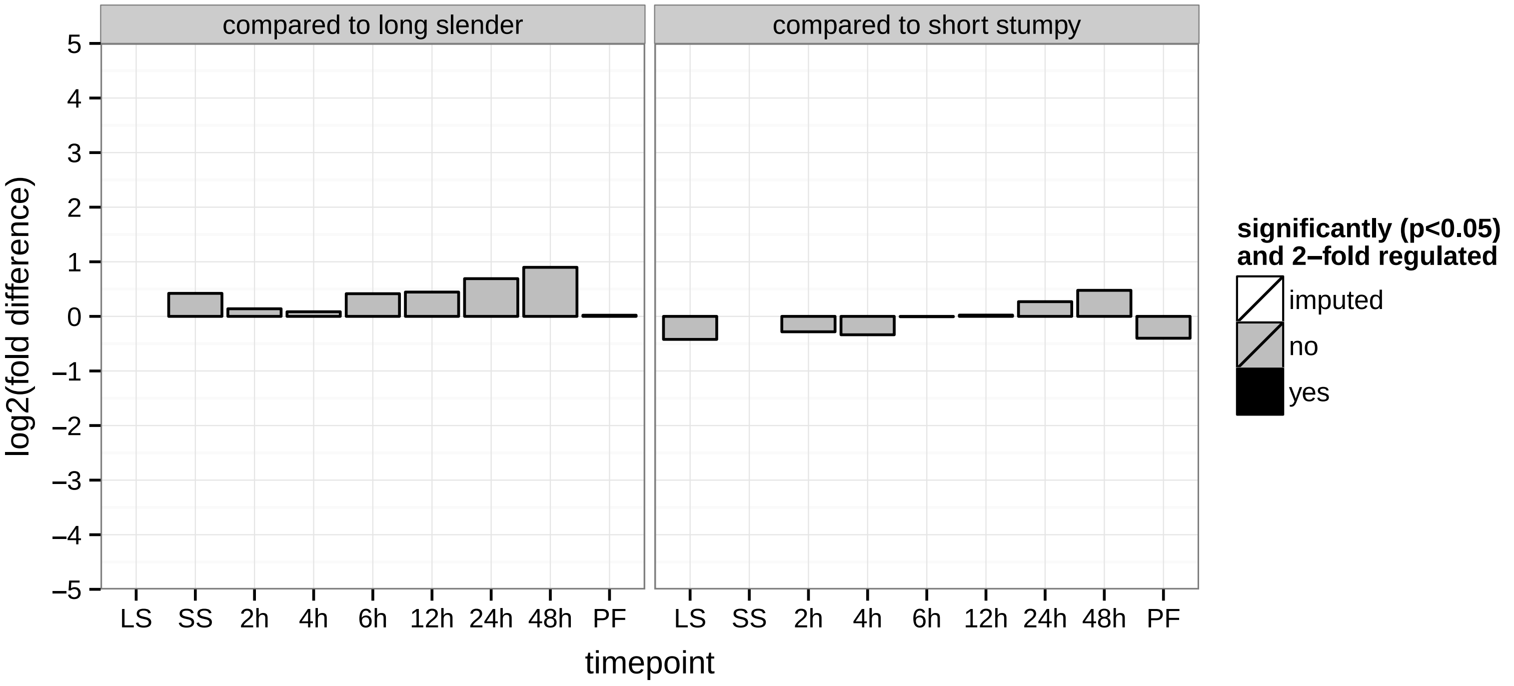
hypothetical protein, conserved
Tb927.6.4760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

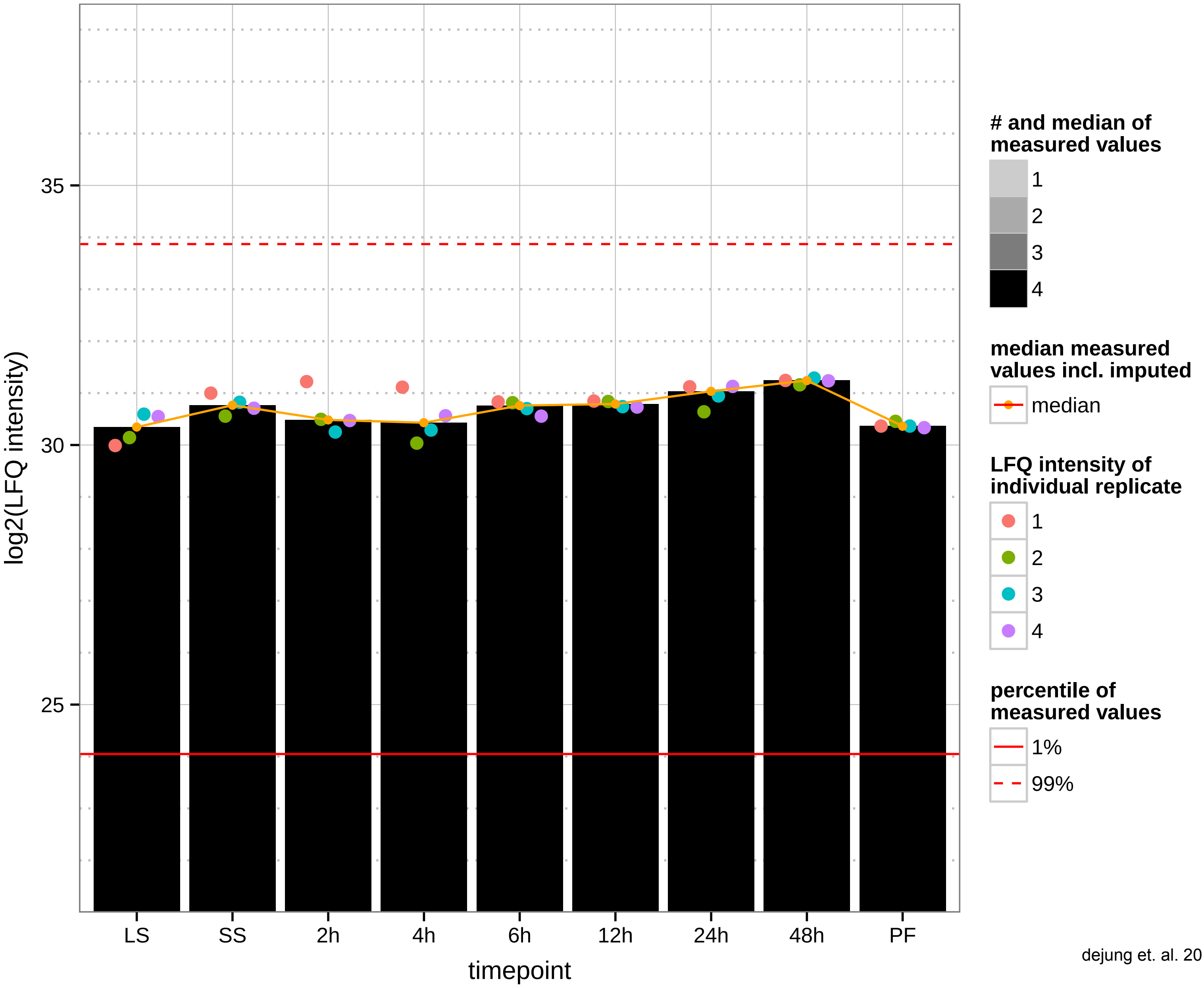




dejung et. al. 2015

protein mkt1, putative (MKT1)
Tb927.6.4770
AGOF: null
AGOC: polysome
AGOP: response to DNA damage stimulus
PGOF: null
PGOC: null
PGOP: null





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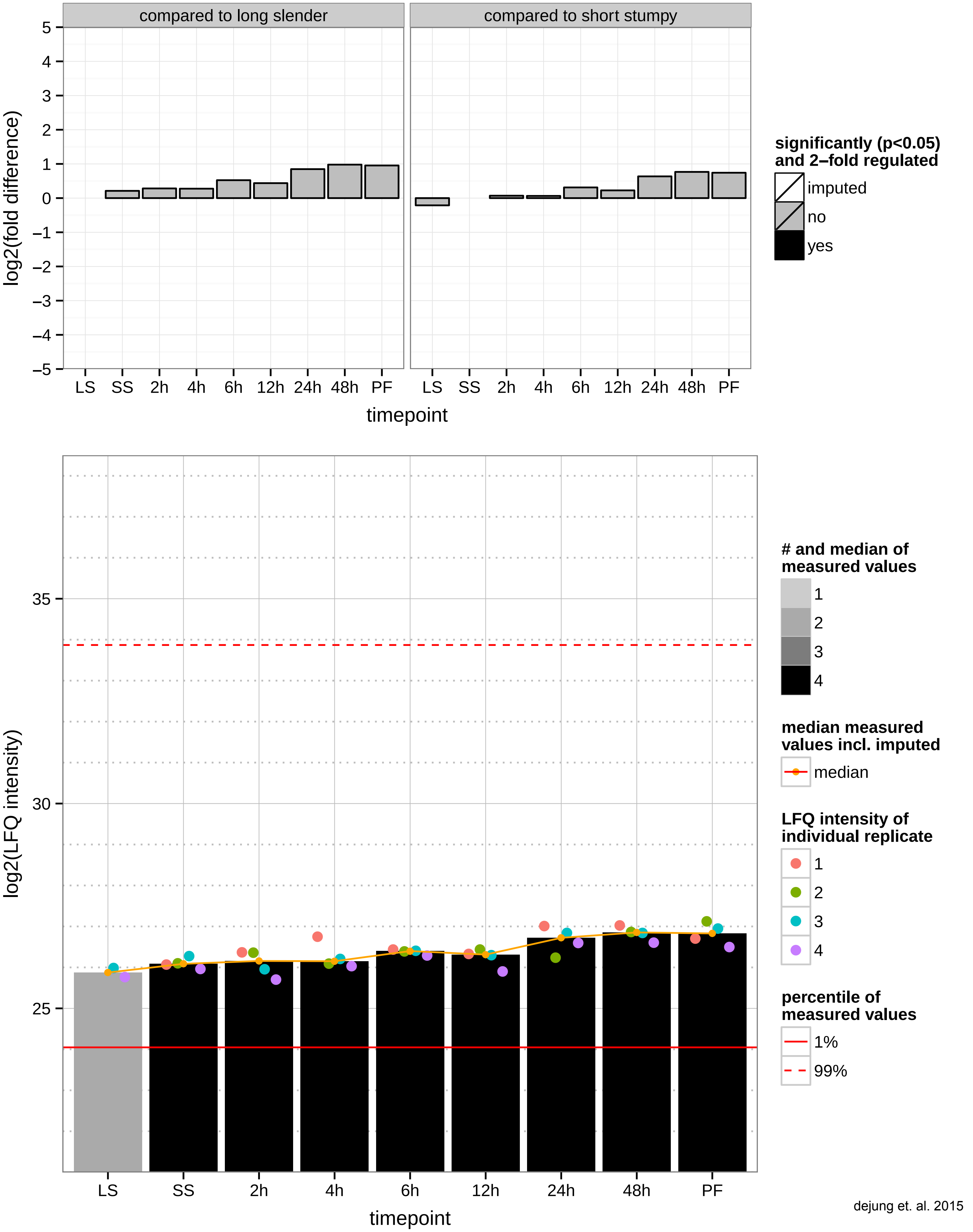
DNA ligase I, putative
Tb927.6.4780
AGOF: ATP binding, DNA binding, DNA ligase (ATP) activity
AGOC: null
AGOP: DNA recombination, DNA repair, DNA replication
PGOF: ATP binding, DNA binding, DNA ligase (ATP) activity
PGOC: null
PGOP: DNA recombination, DNA repair, DNA replication



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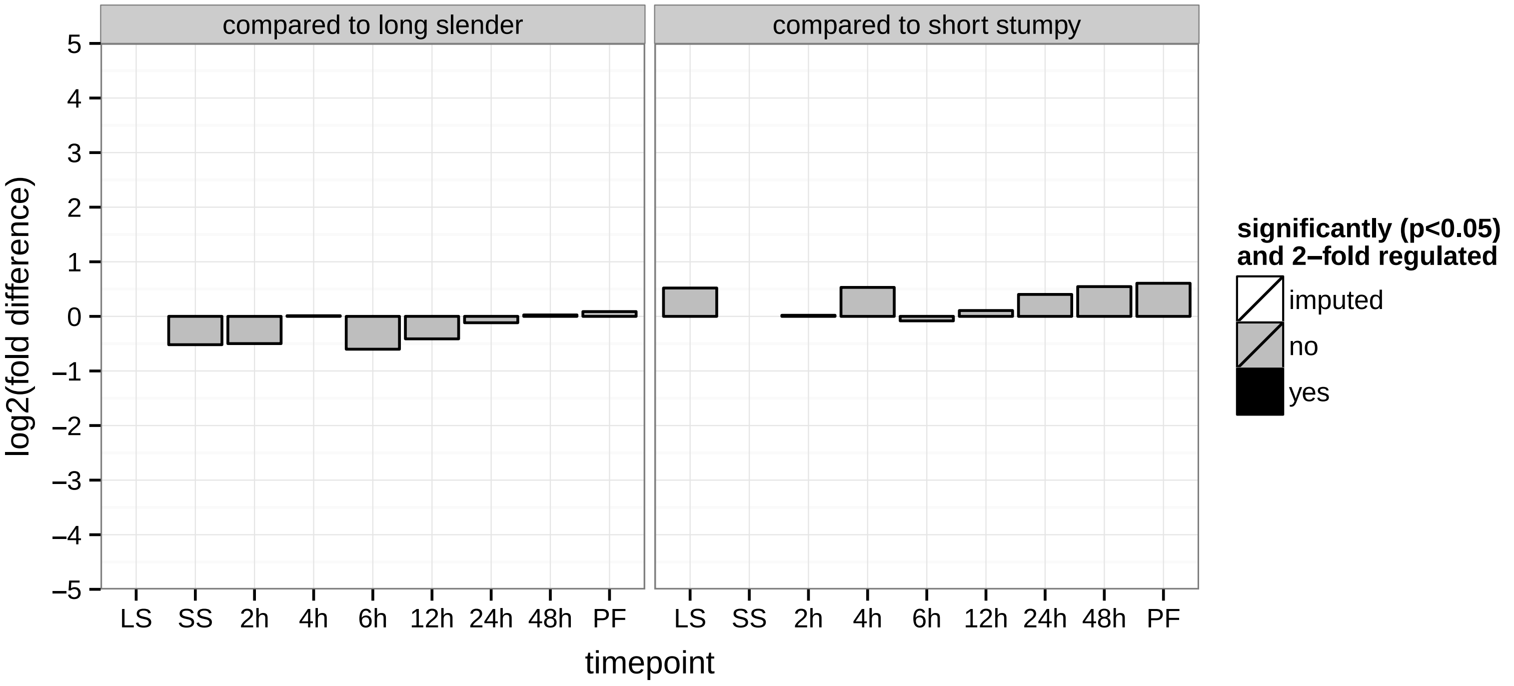
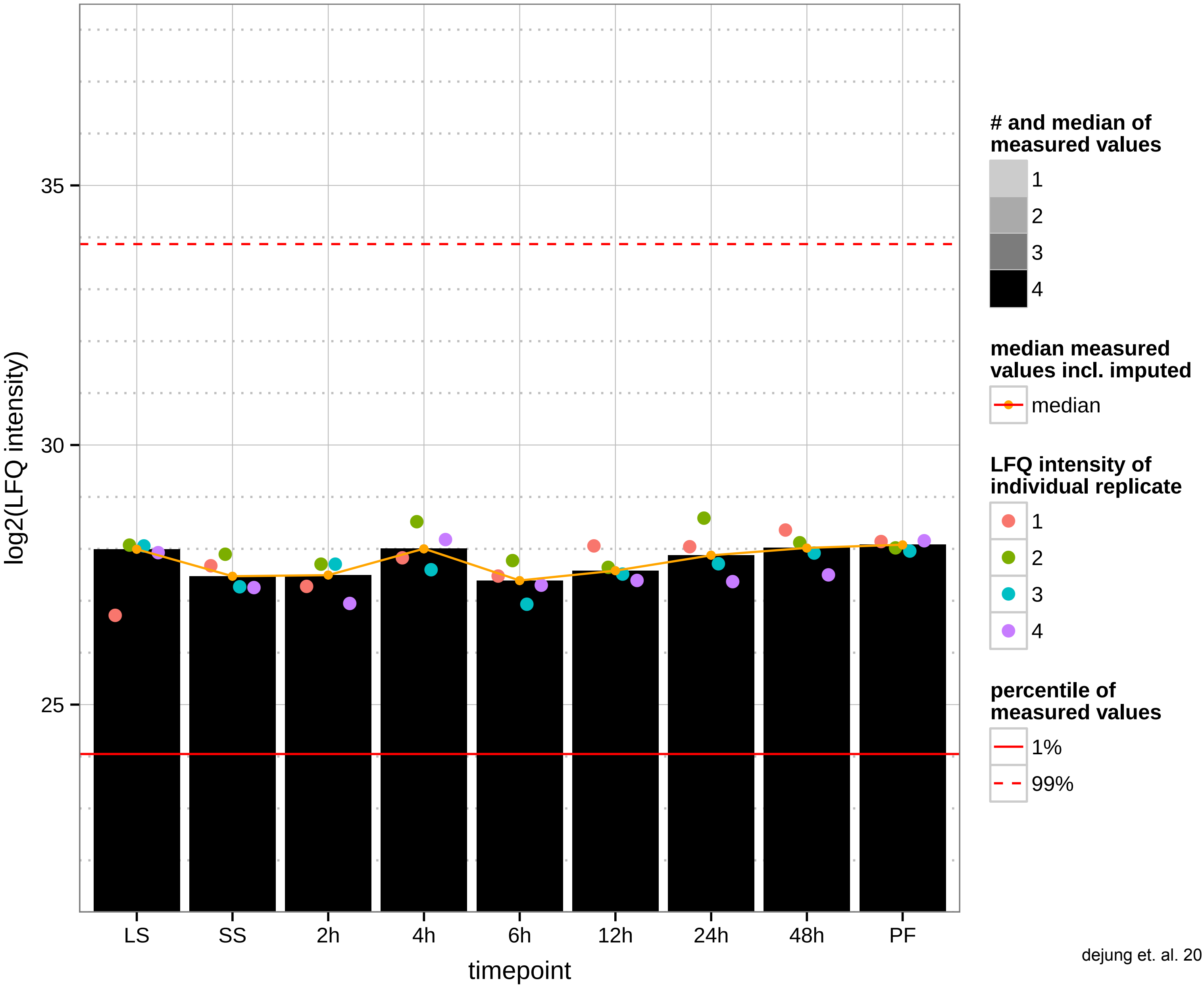
mago nashi–like protein, putative
Tb927.6.4950
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: nucleus
PGOP: null





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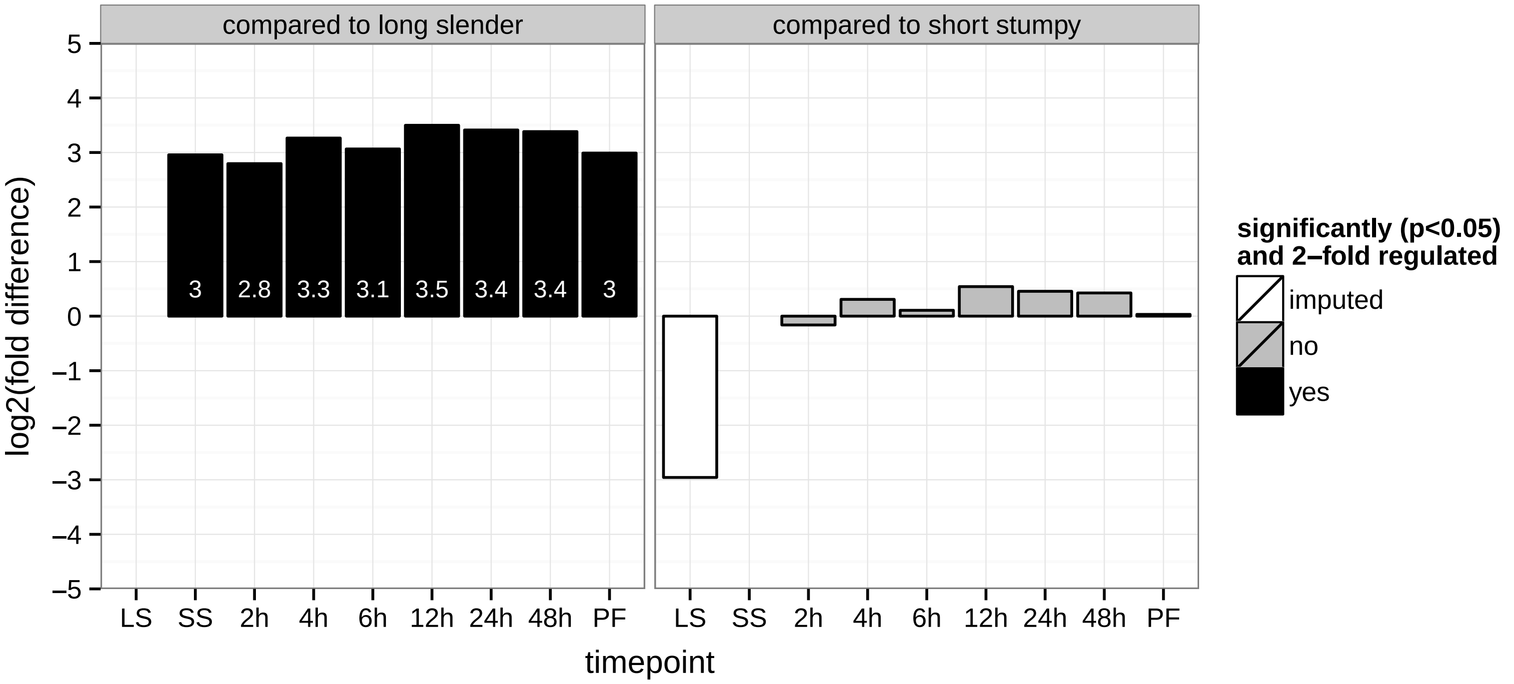
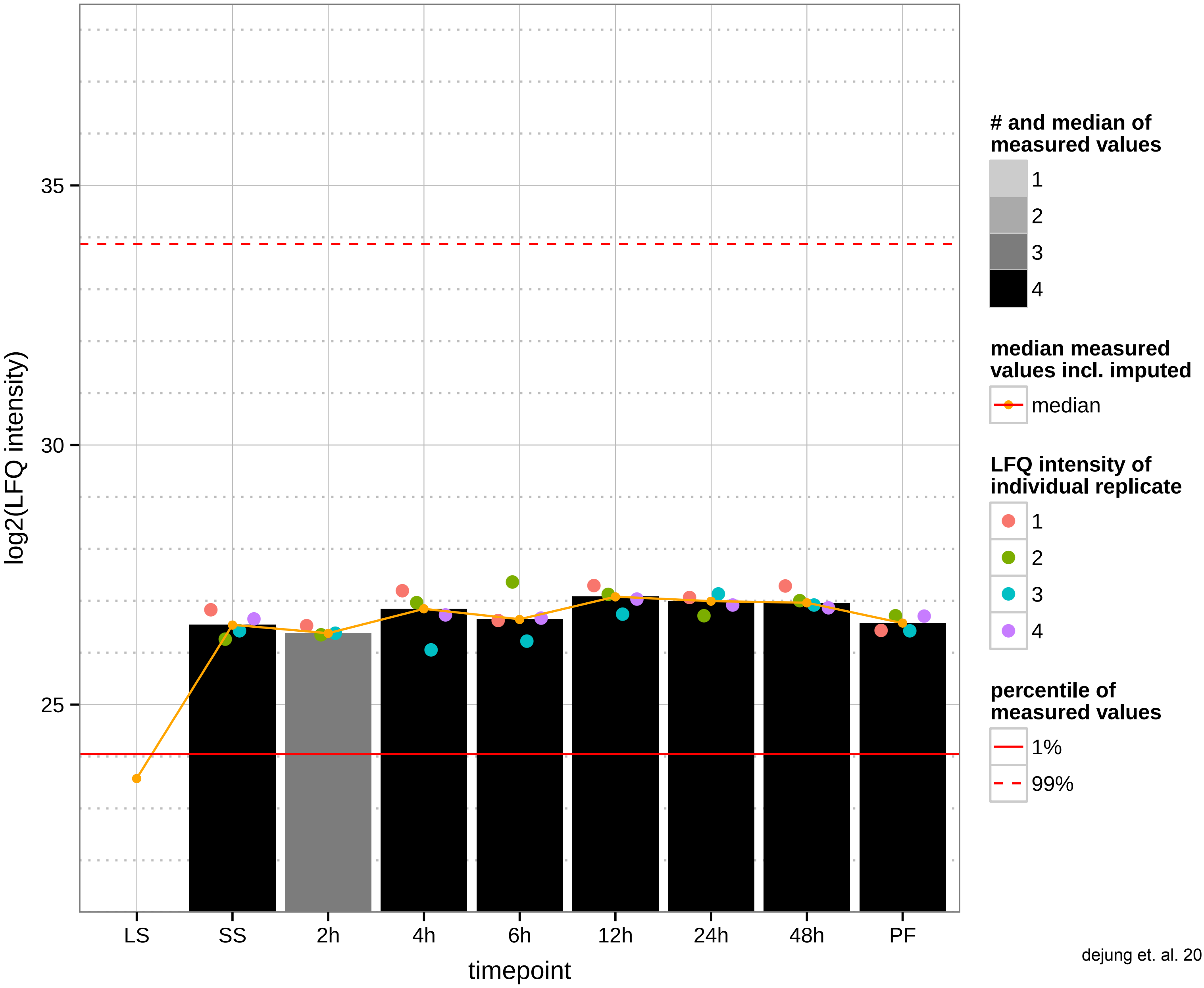
hypothetical protein, conserved
Tb927.6.5000
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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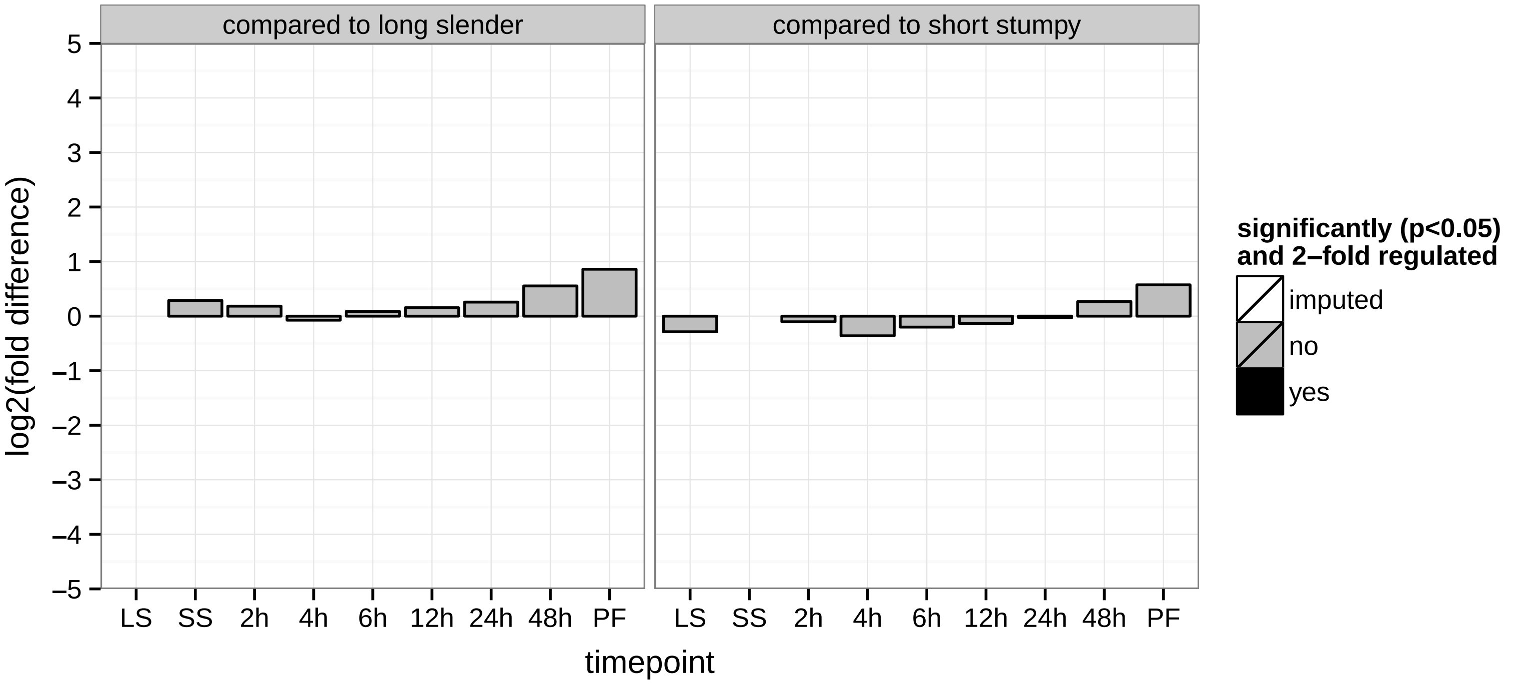
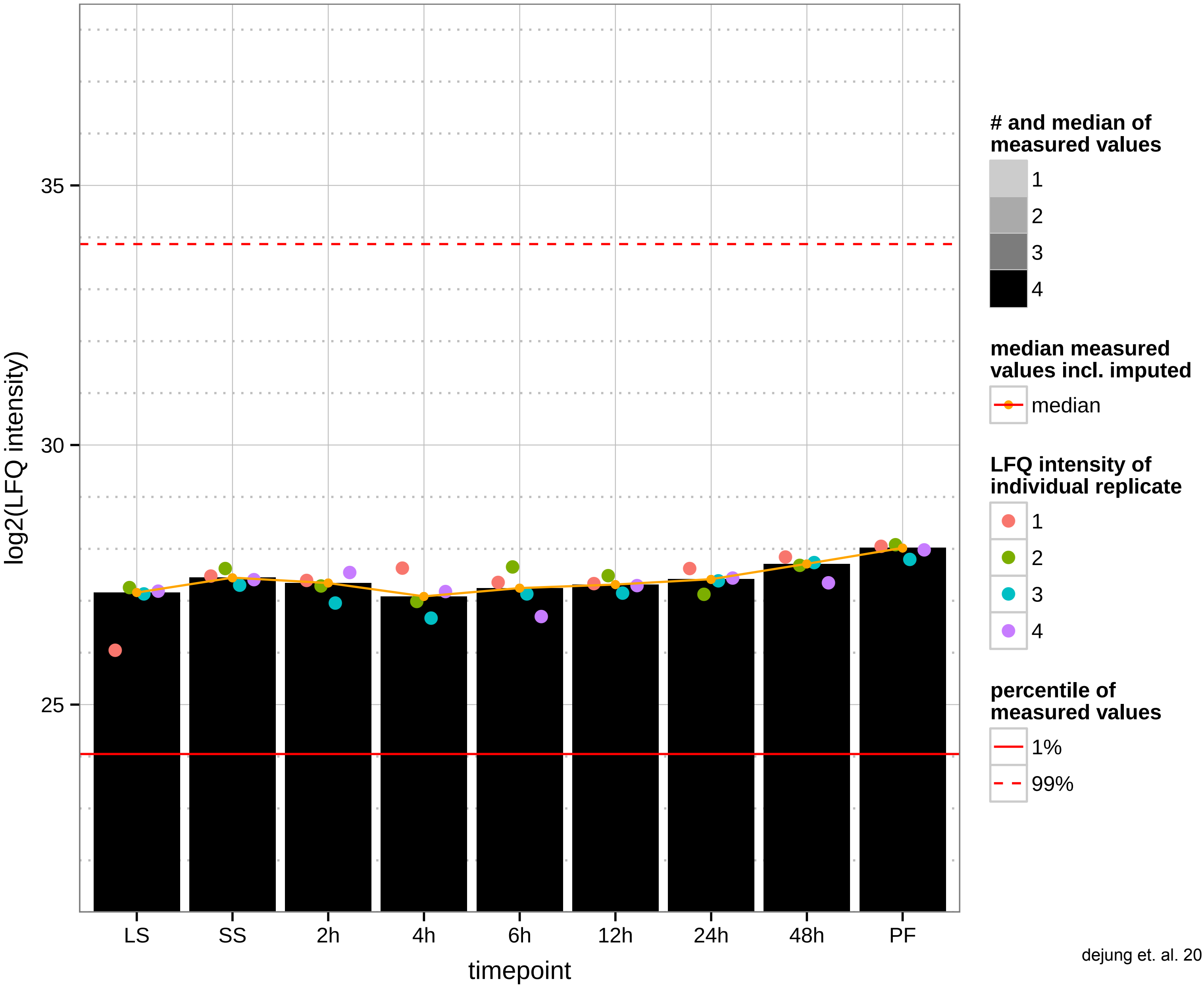
leucine–rich repeat protein (LRRP), putative
Tb927.6.5030
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null





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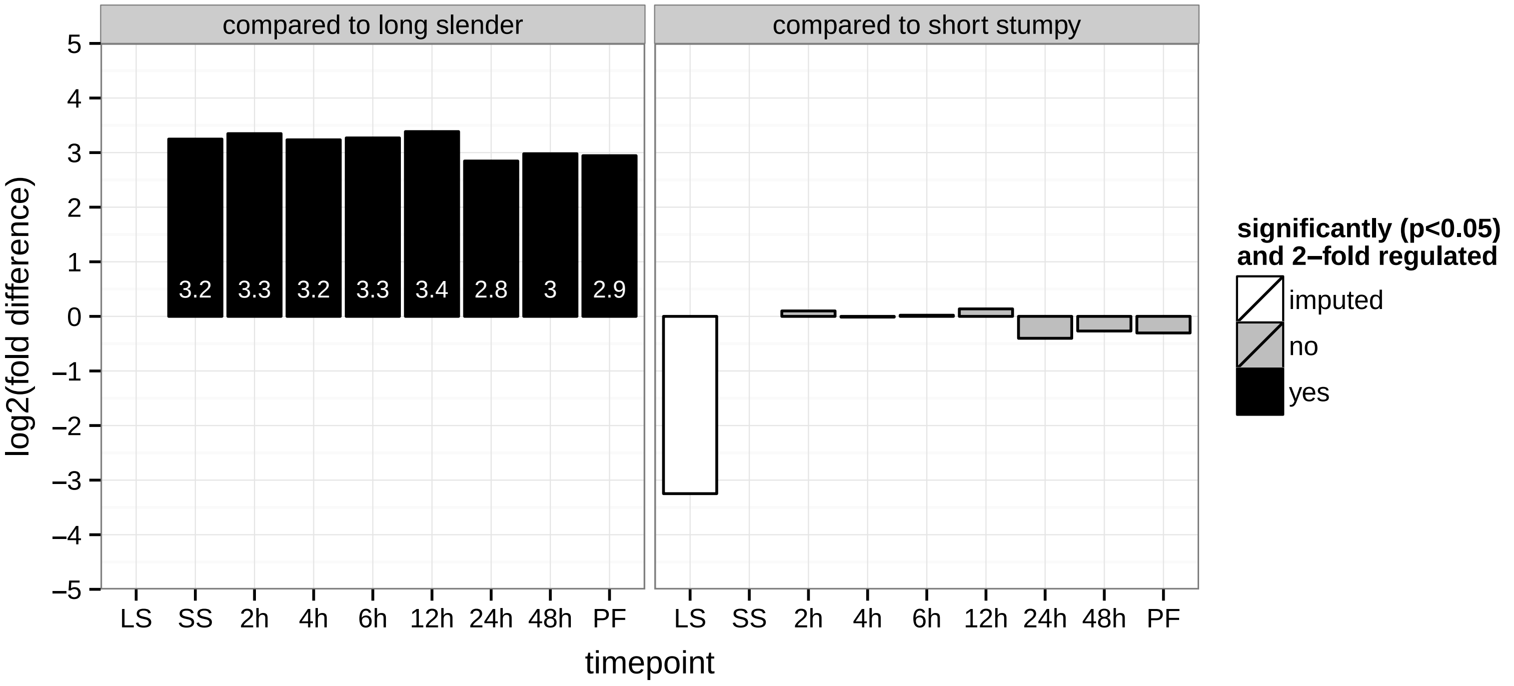
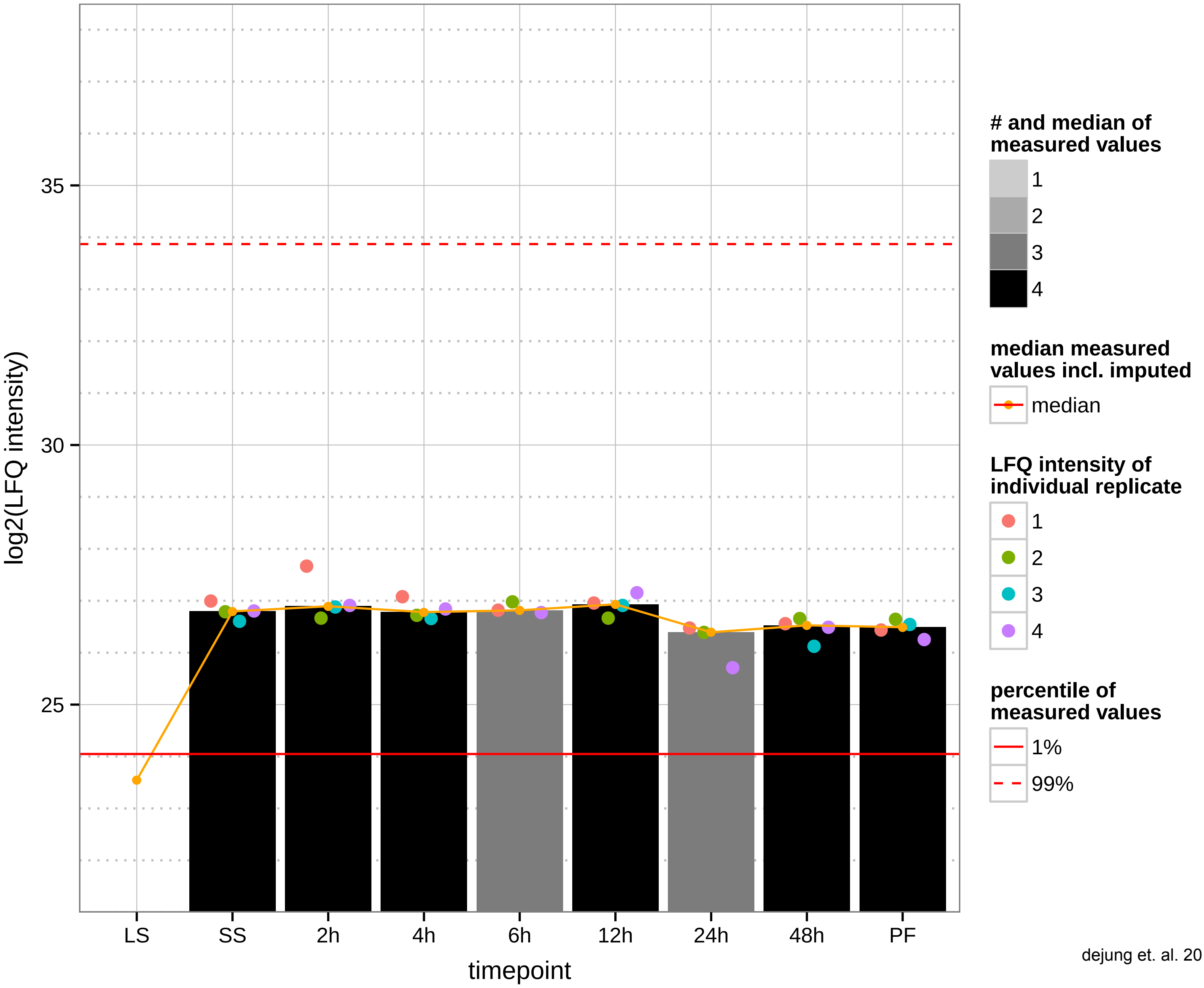
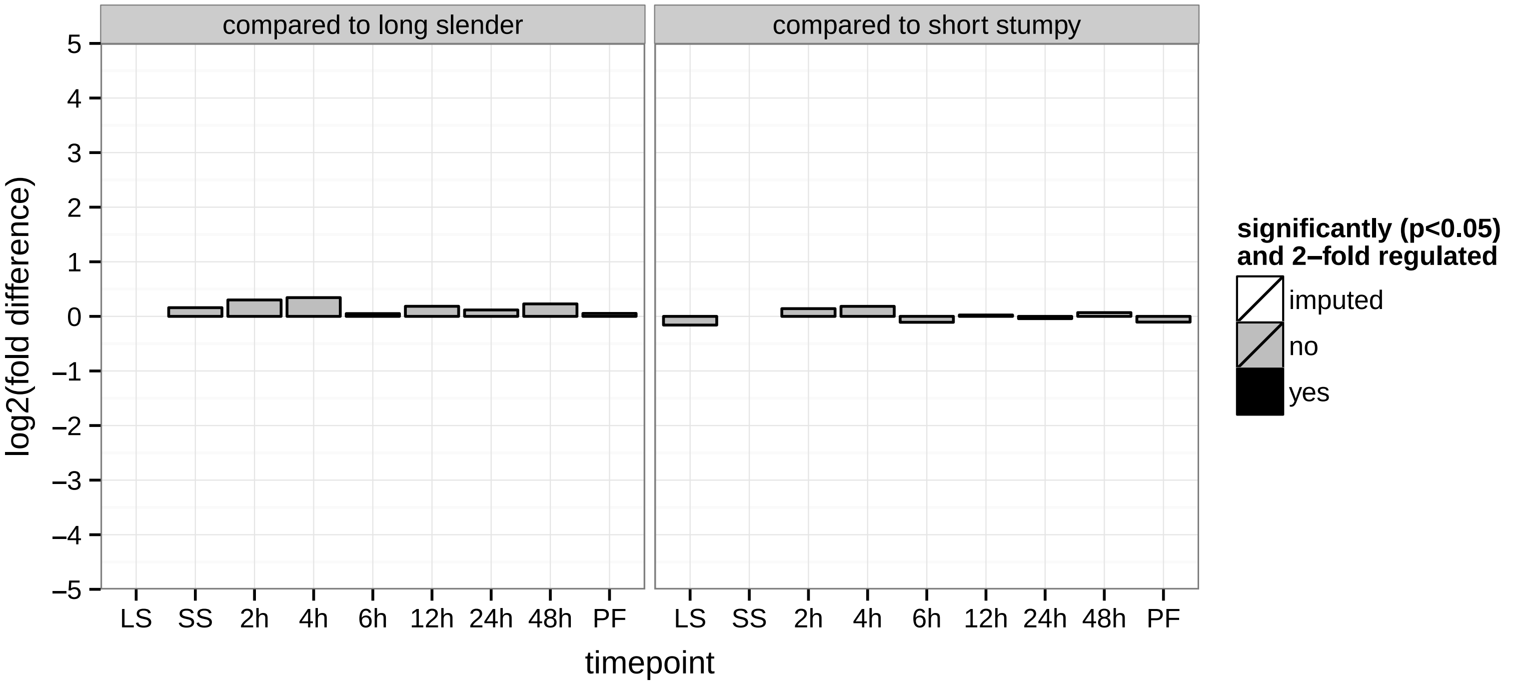
V–type ATPase, C subunit, putative
Tb927.6.5050
AGOF: hydrogen ion transmembrane transporter activity
AGOC: proton–transporting V–type ATPase, V0 domain
AGOP: ATP synthesis coupled proton transport
PGOF: hydrogen ion transmembrane transporter activity
PGOC: proton–transporting two–sector ATPase complex, proton–transporting domain
PGOP: ATP hydrolysis coupled proton transport

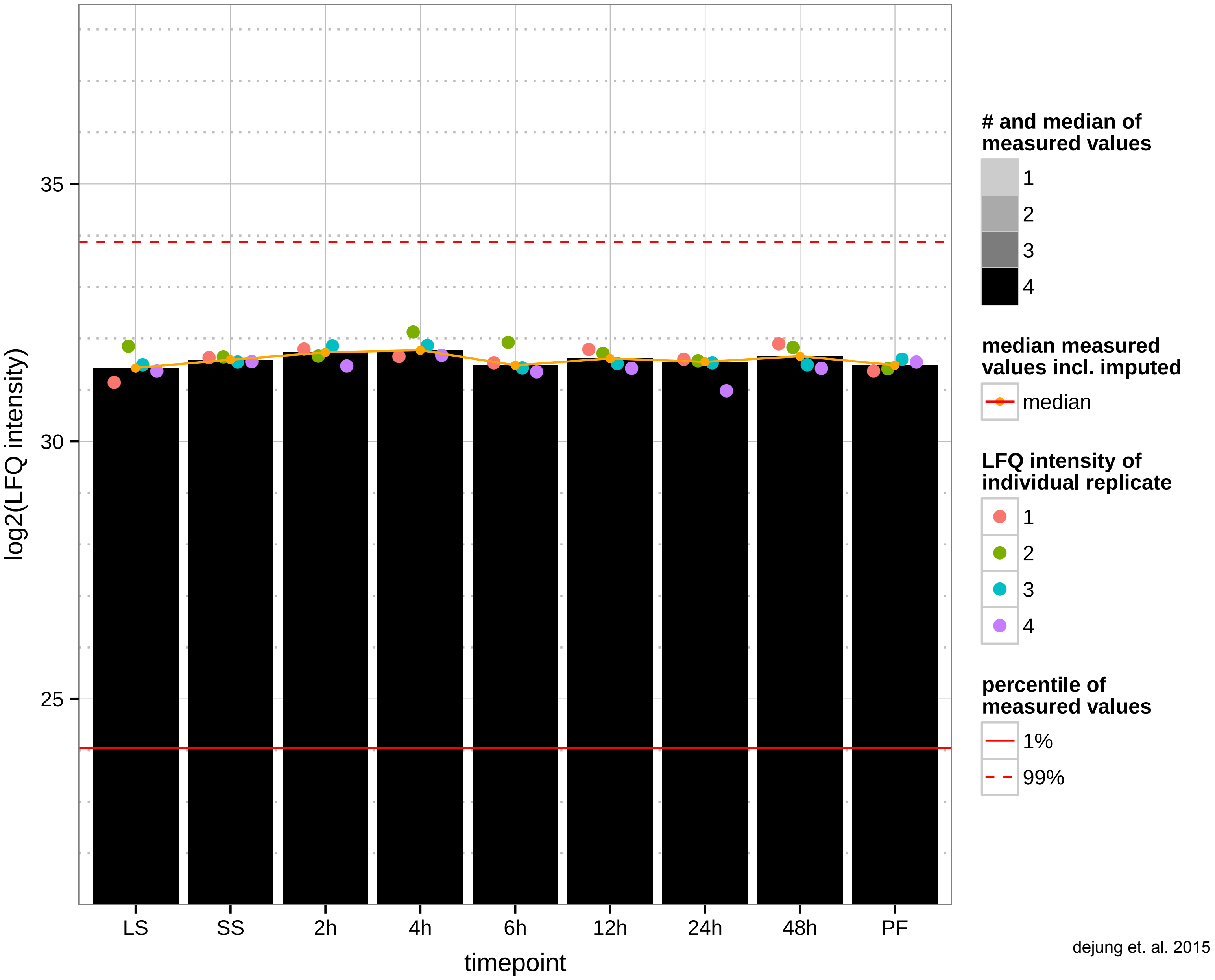




dejung et. al. 2015

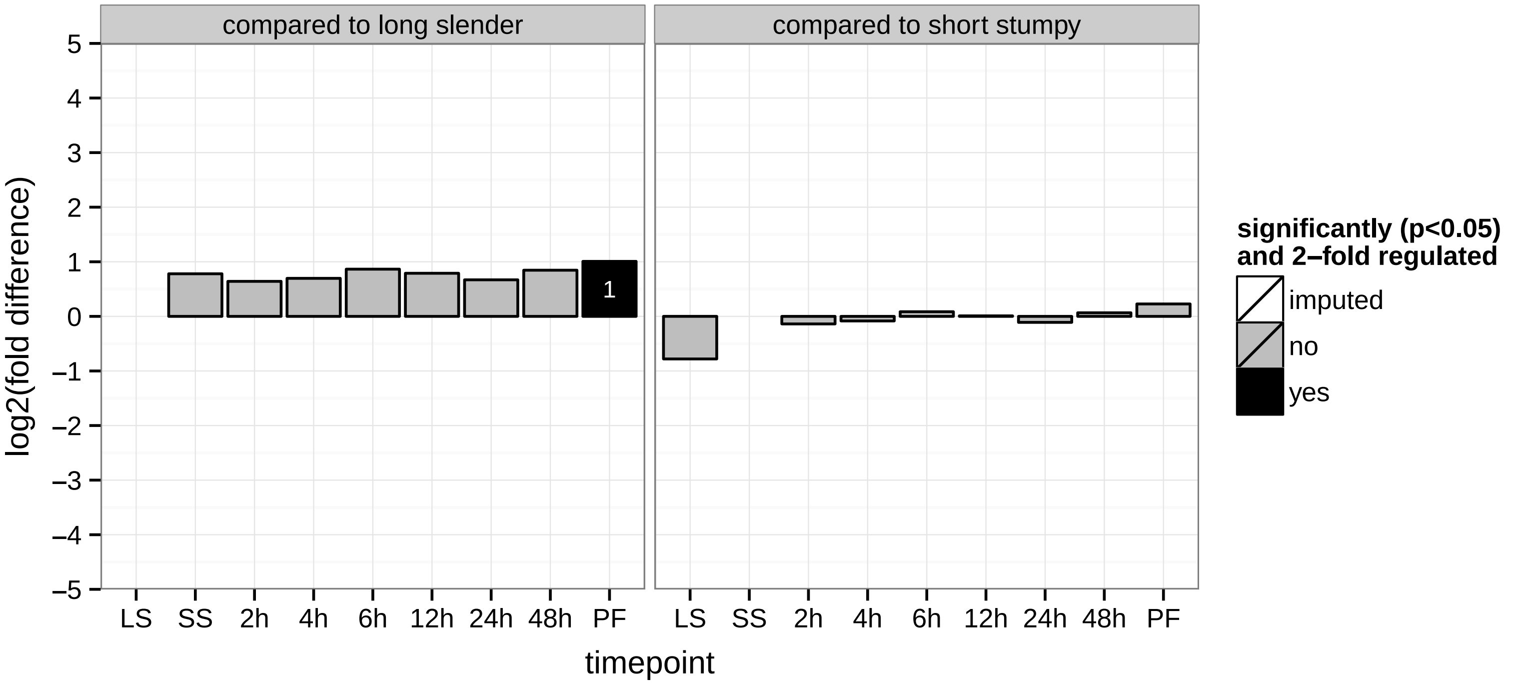
NA, hypothetical protein, conserved
Tb927.6.5070
AGOF: NA, null
AGOC: NA, null
AGOP: NA, null
PGOF: NA, null
PGOC: NA, null
PGOP: NA, null

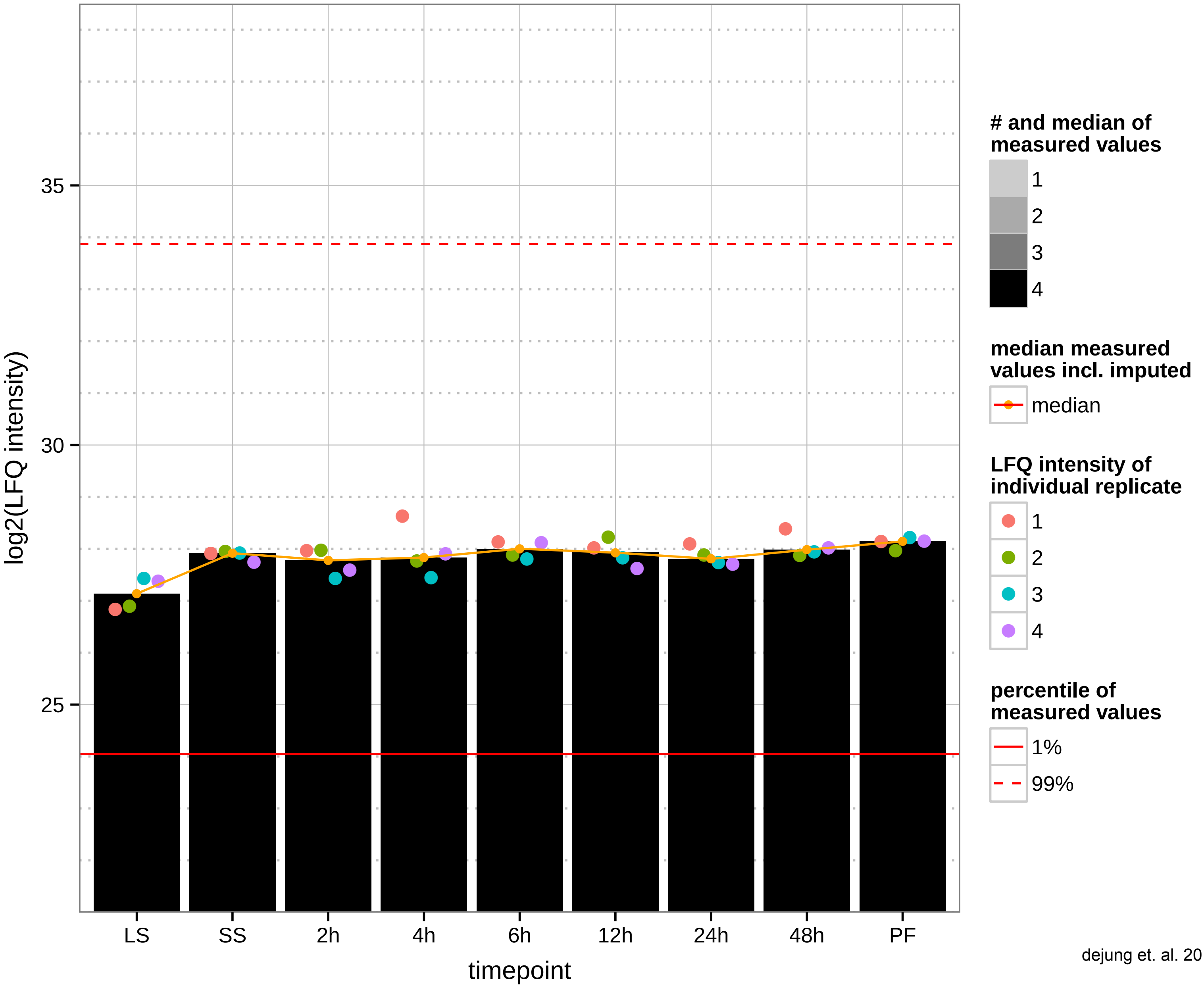




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.5080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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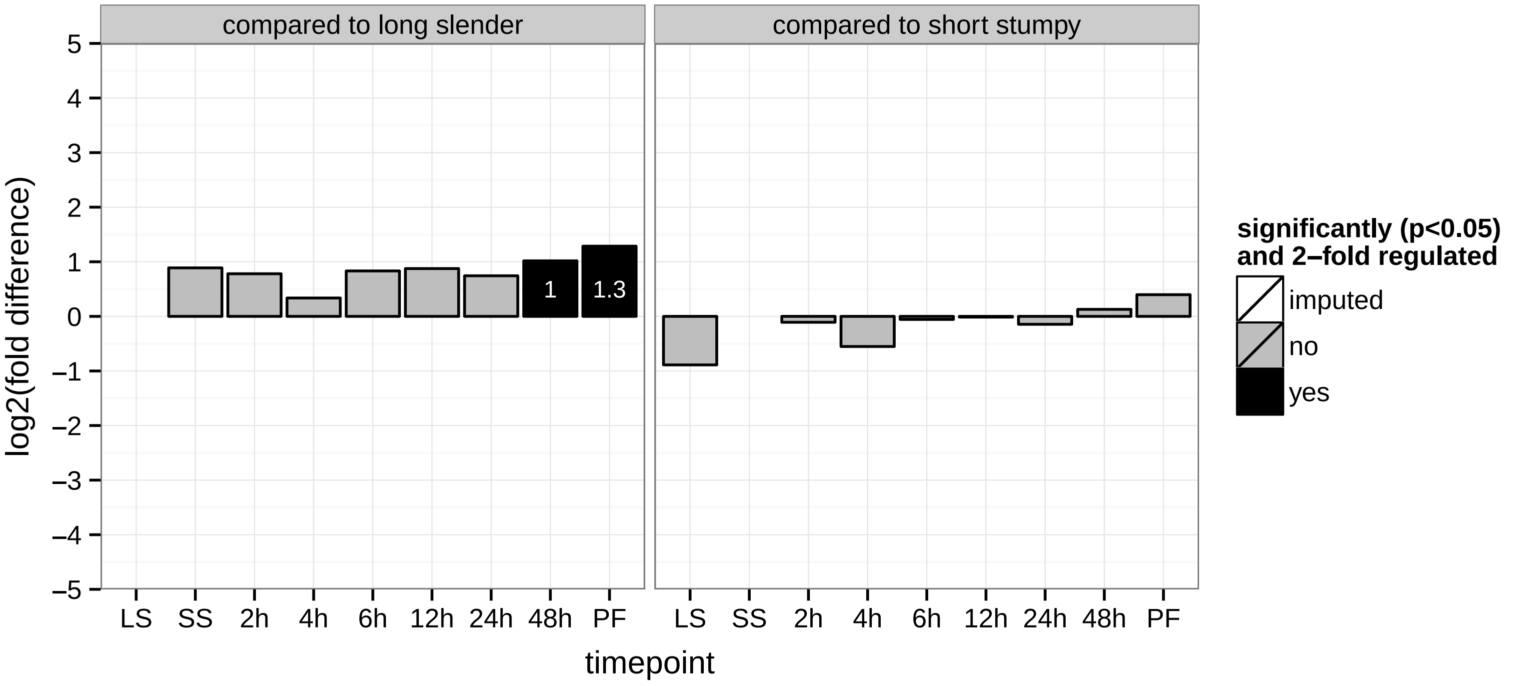
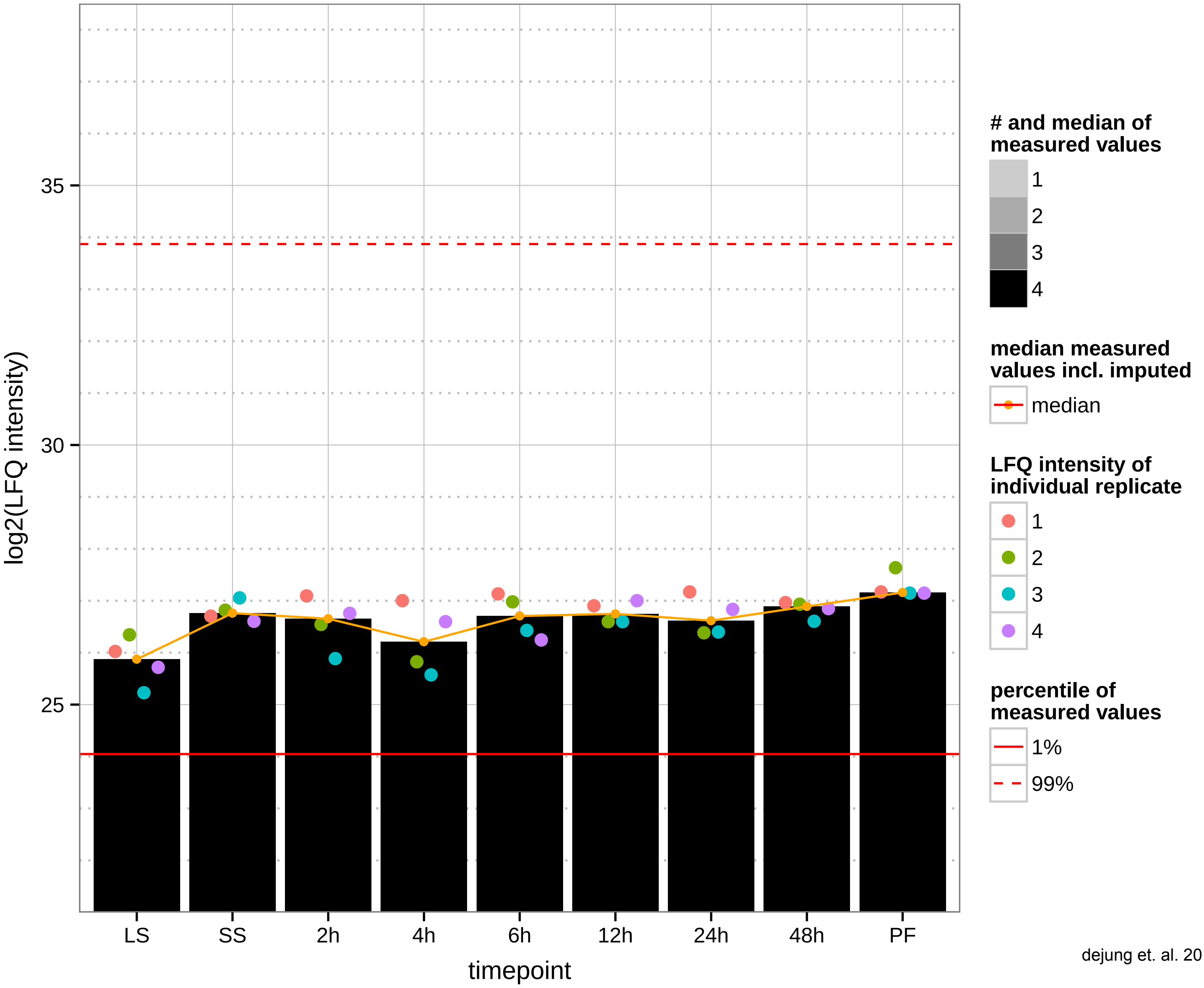
damage–specific DNA binding protein, putative
Tb927.6.5110
AGOF: nucleic acid binding
AGOC: nucleus
AGOP: null
PGOF: nucleic acid binding
PGOC: nucleus
PGOP: null





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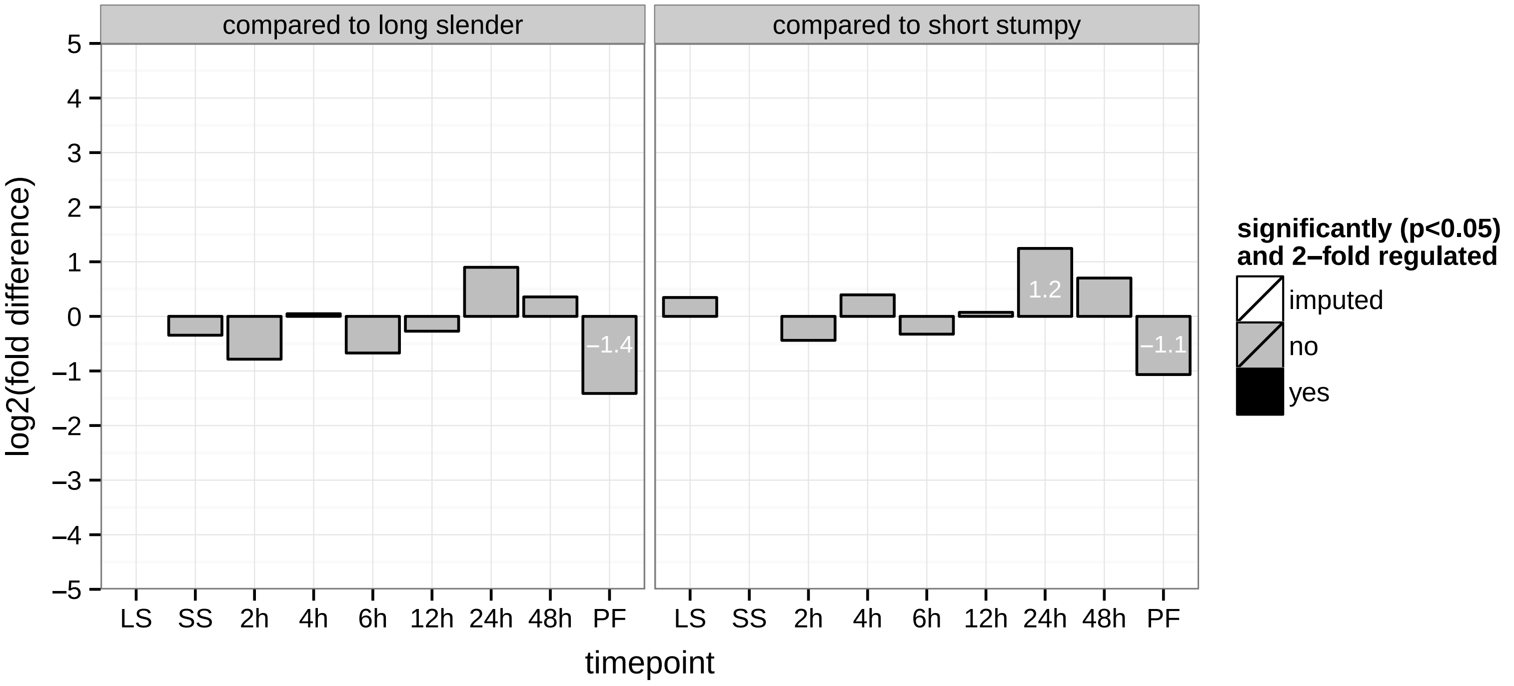
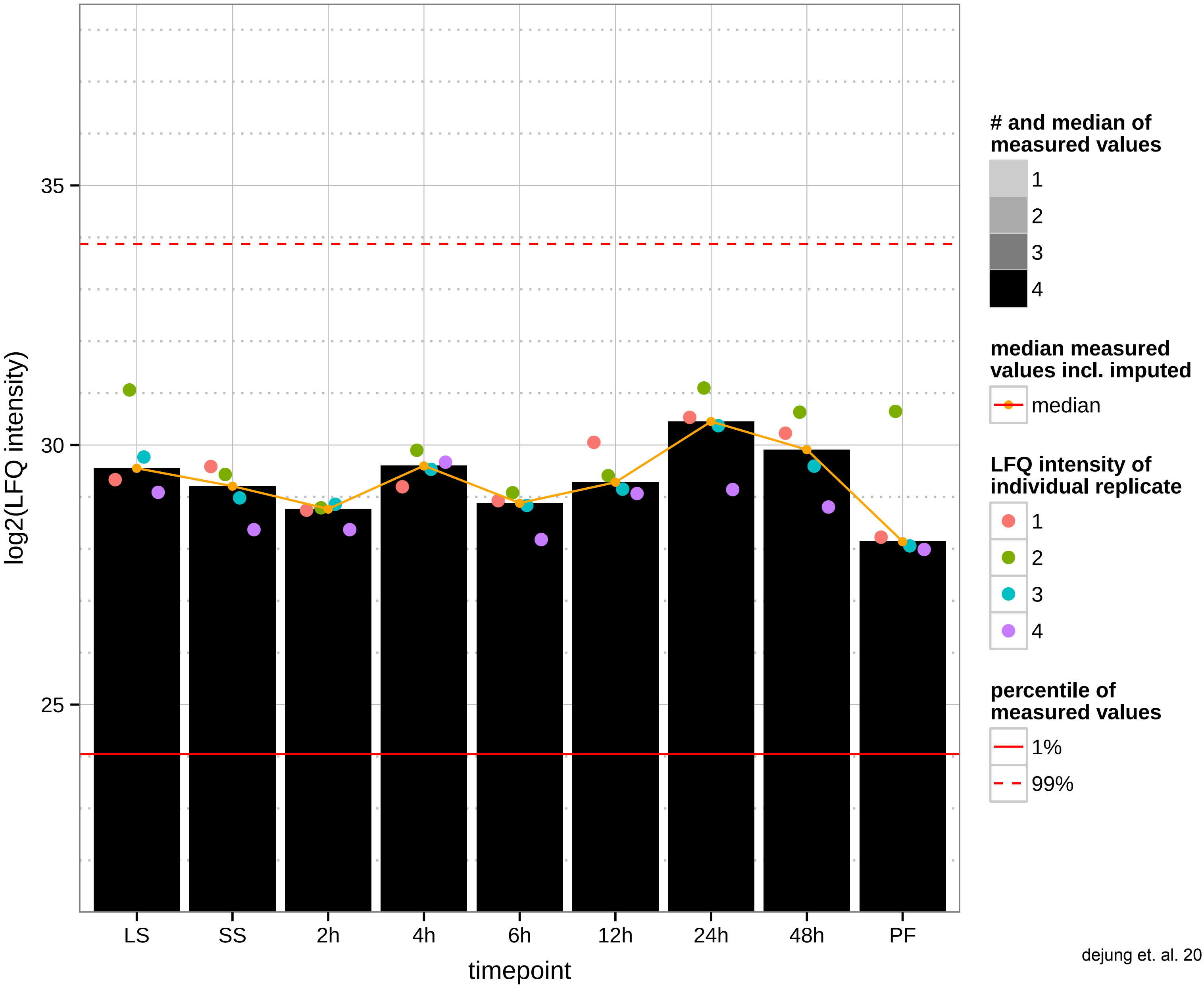
60S acidic ribosomal protein P2, putative
Tb927.6.5130;Tb927.6.5120
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation, translational elongation
PGOF: structural constituent of ribosome, null
PGOC: intracellular, ribosome, null
PGOP: translational elongation, null





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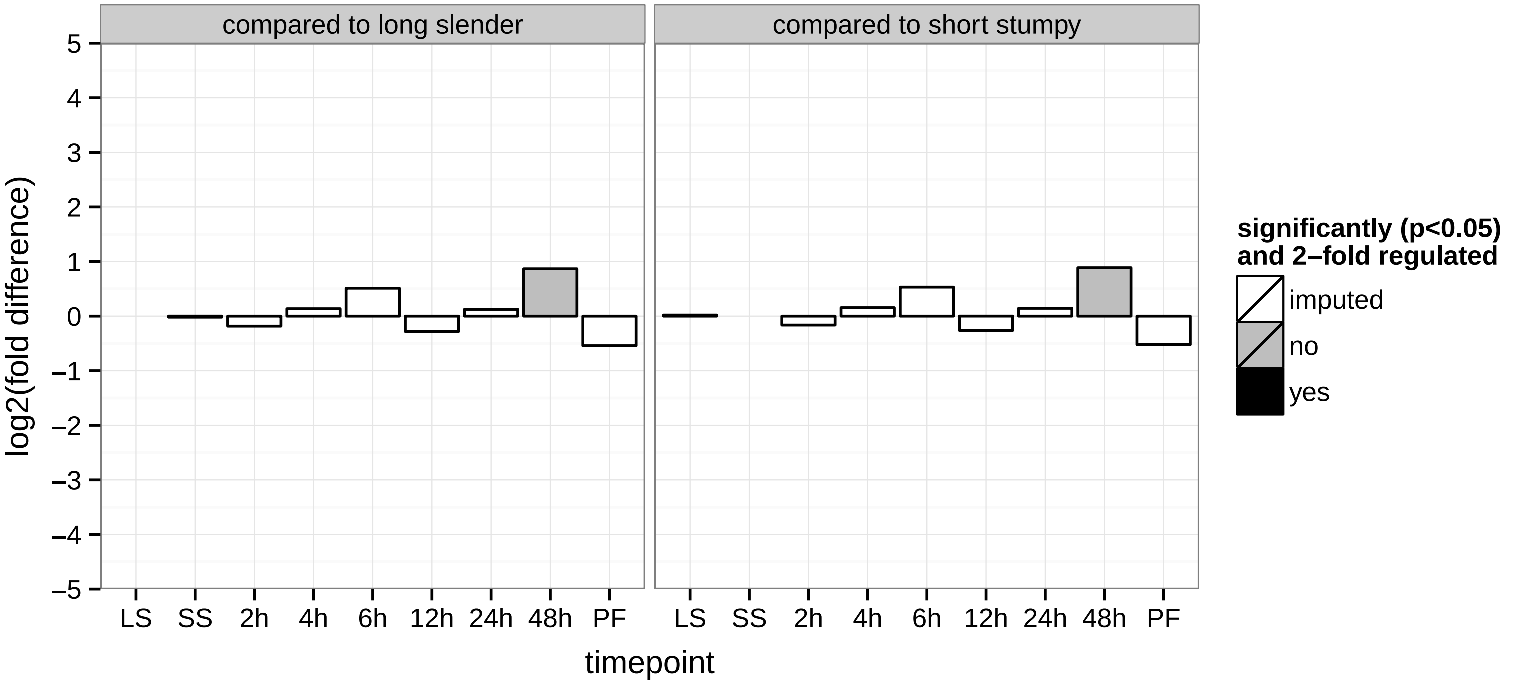
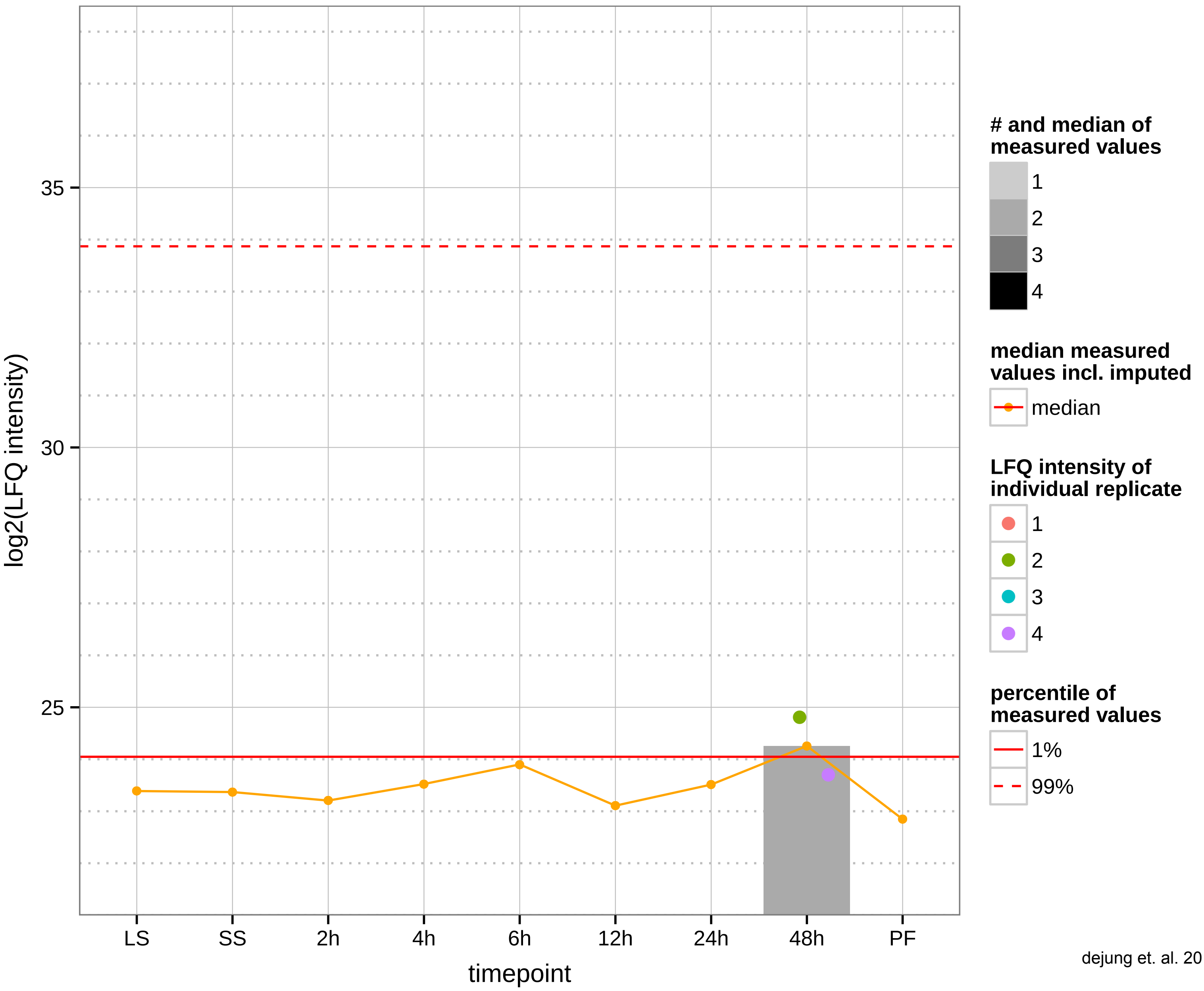
ribosomal P protein AGP2beta−1, putative
Tb927.6.5140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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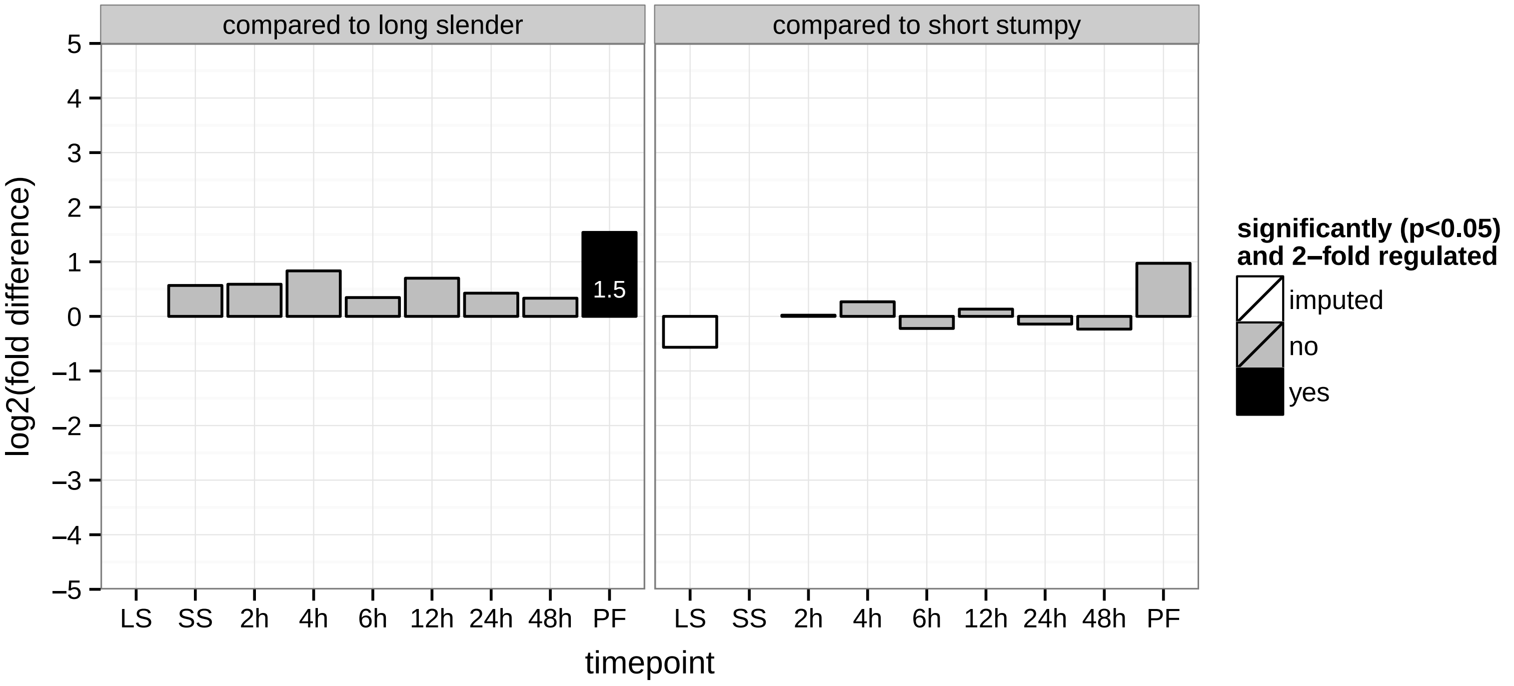
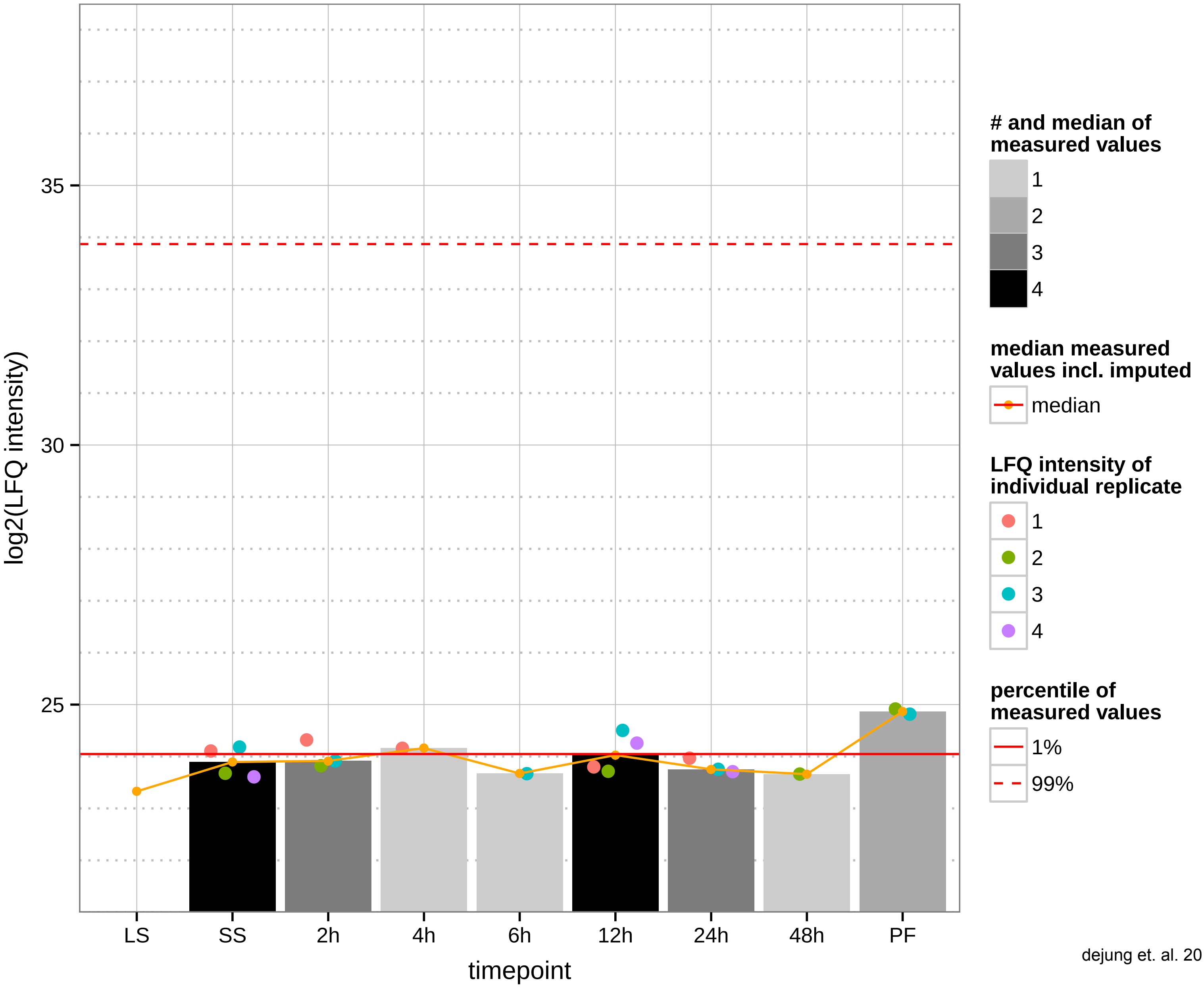
hypothetical protein, conserved
Tb927.6.610
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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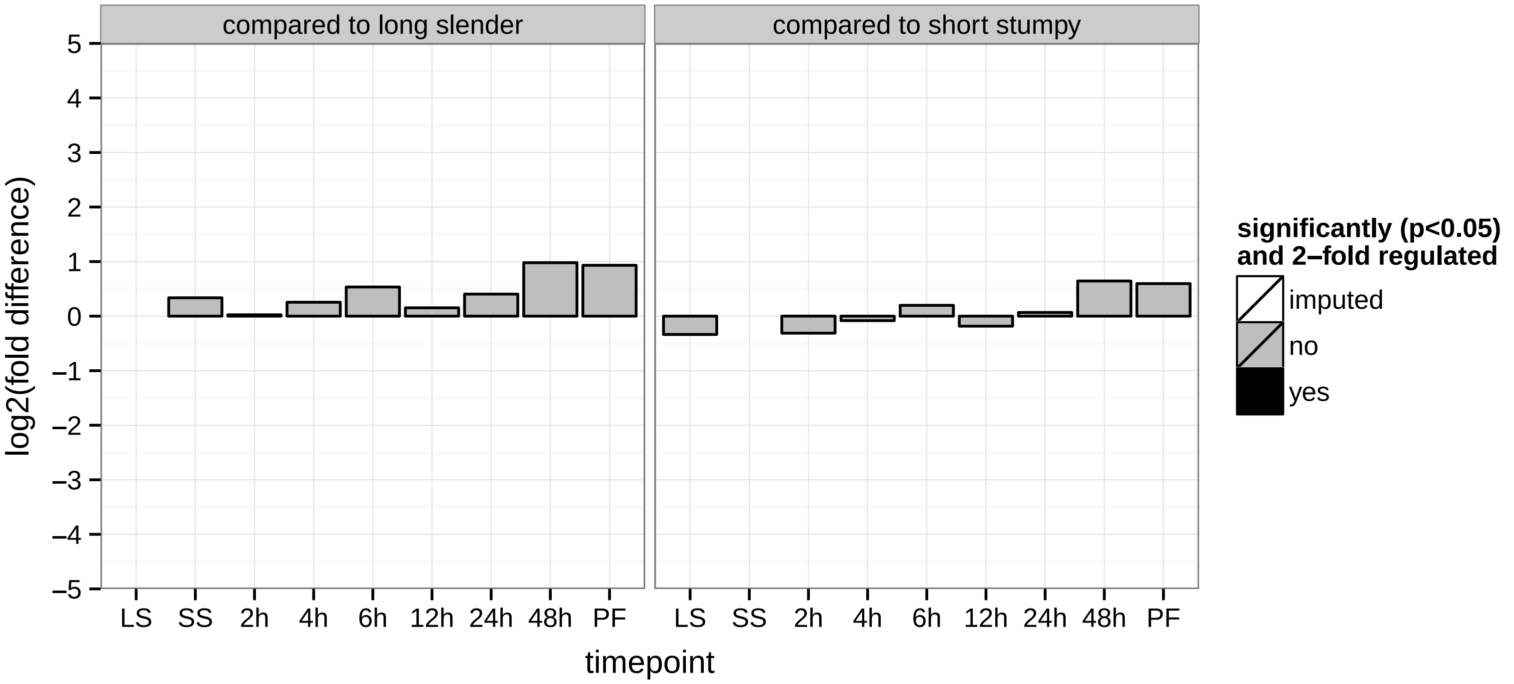
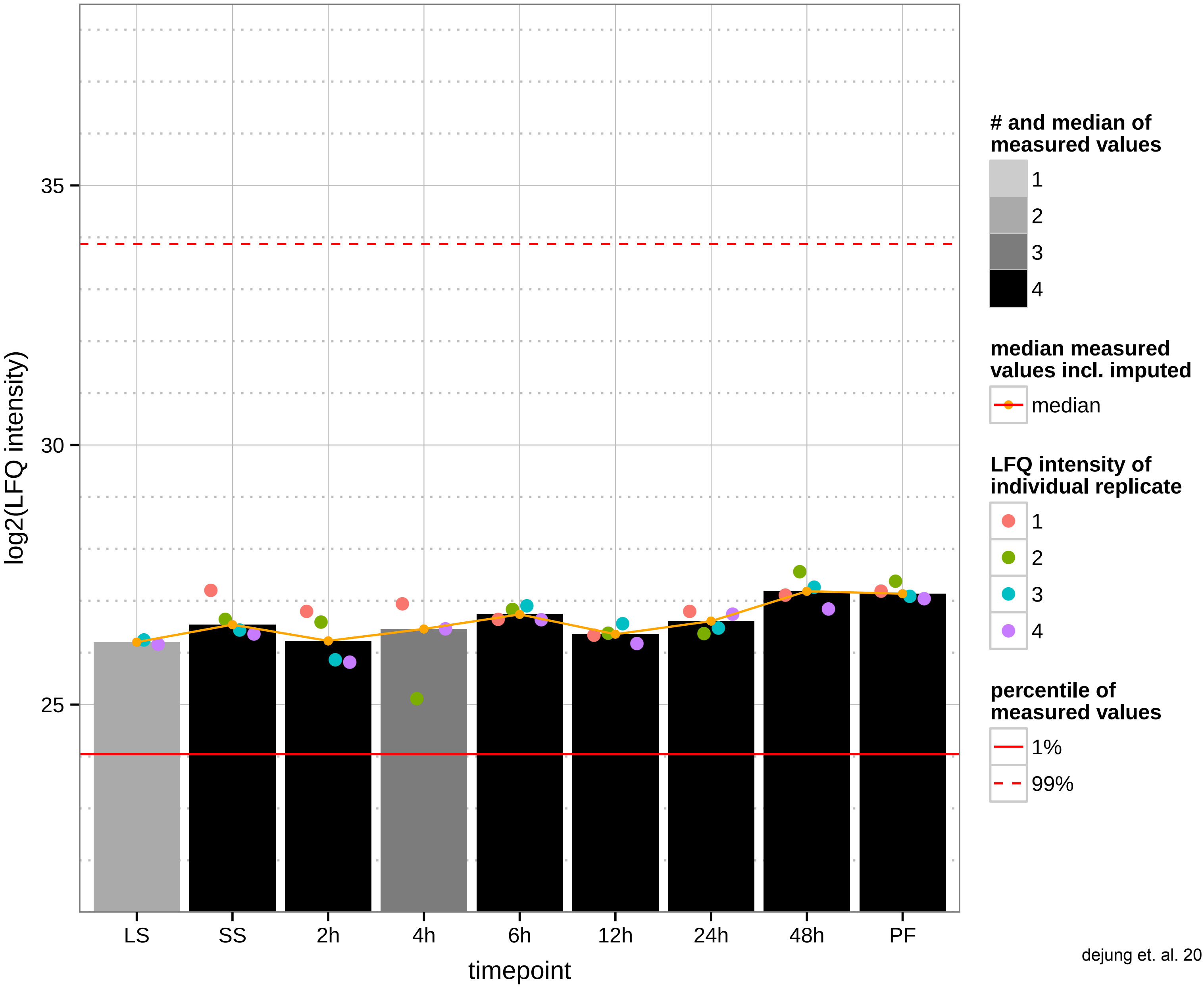
hypothetical protein, conserved
Tb927.6.620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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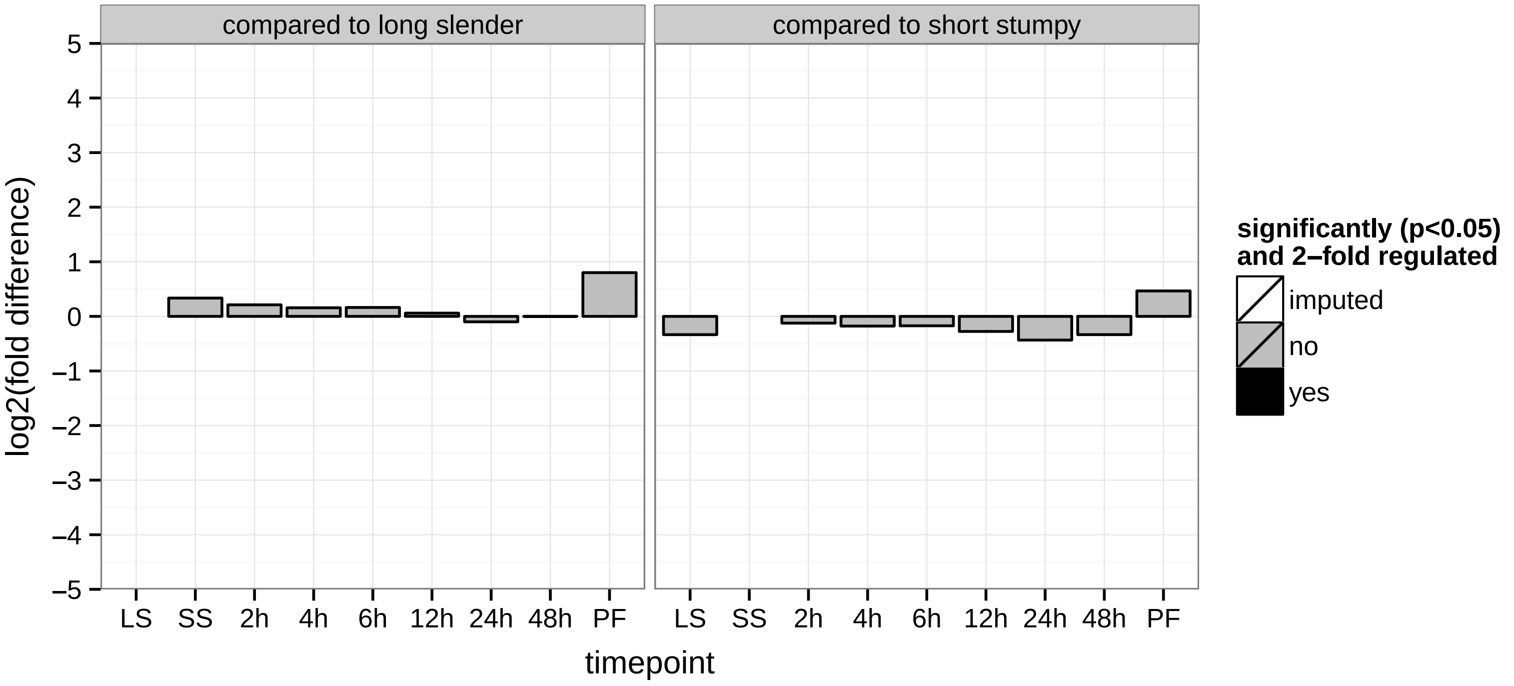
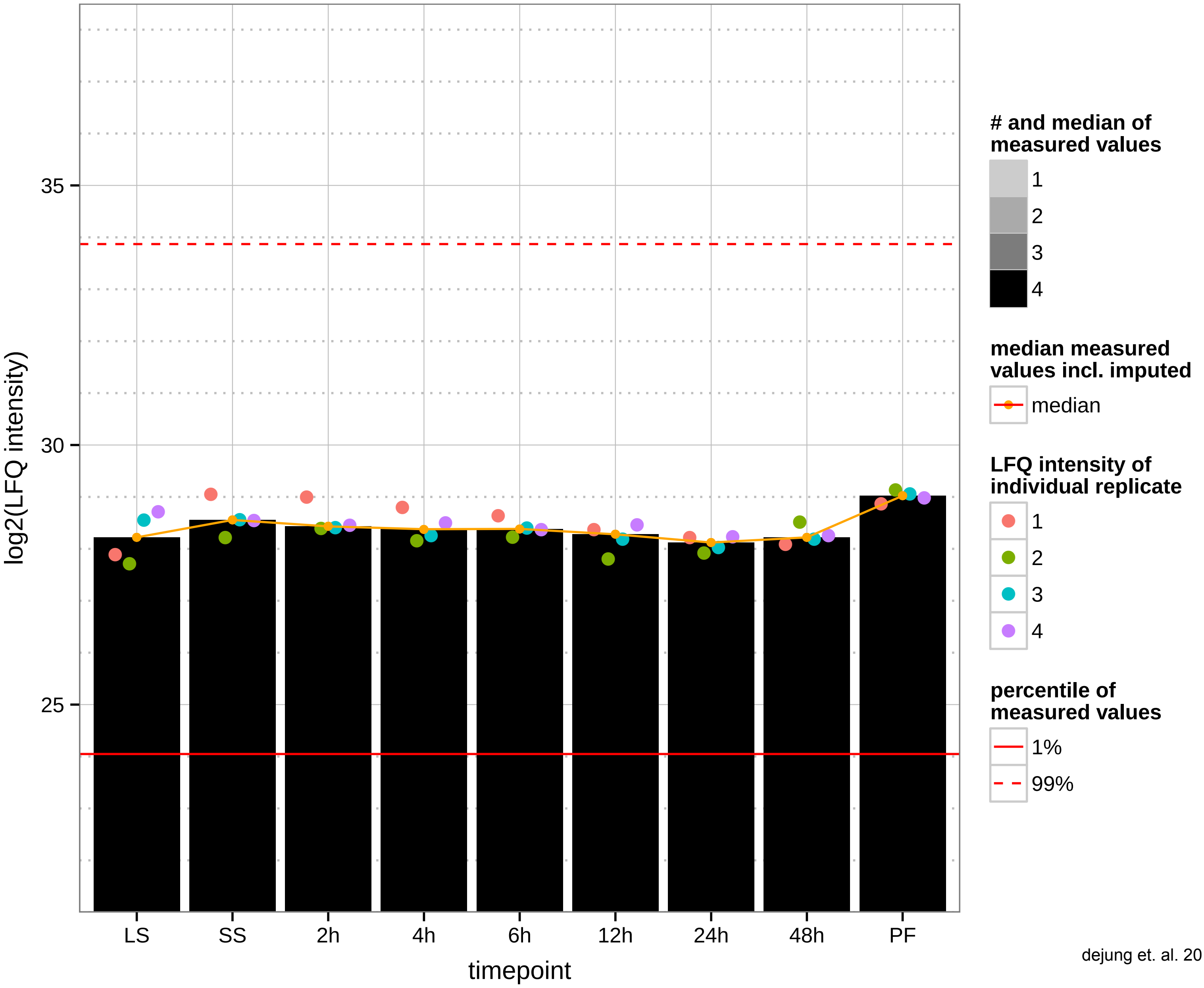
kinetoplastid–specific phospho–protein phosphatase, putative
Tb927.6.640
AGOF: protein serine/threonine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: hydrolase activity
PGOC: null
PGOP: null





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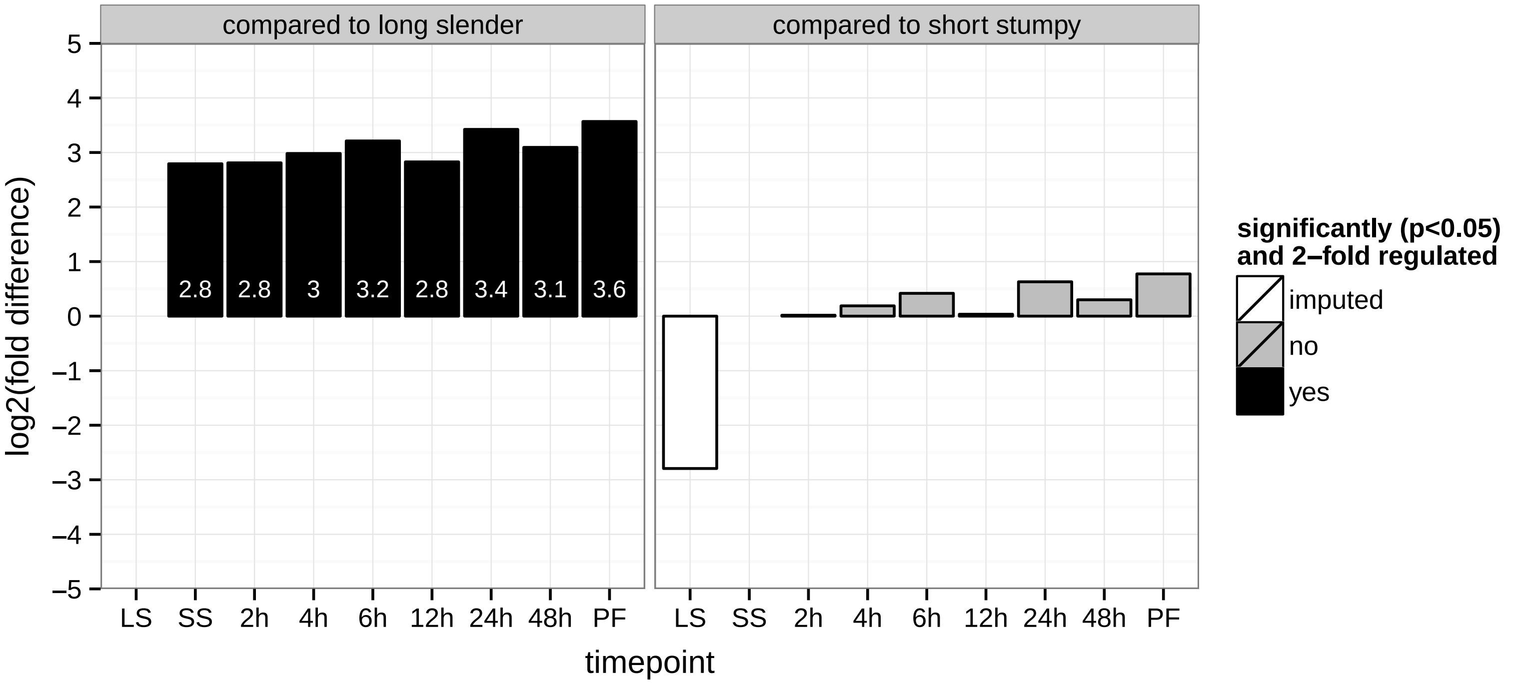
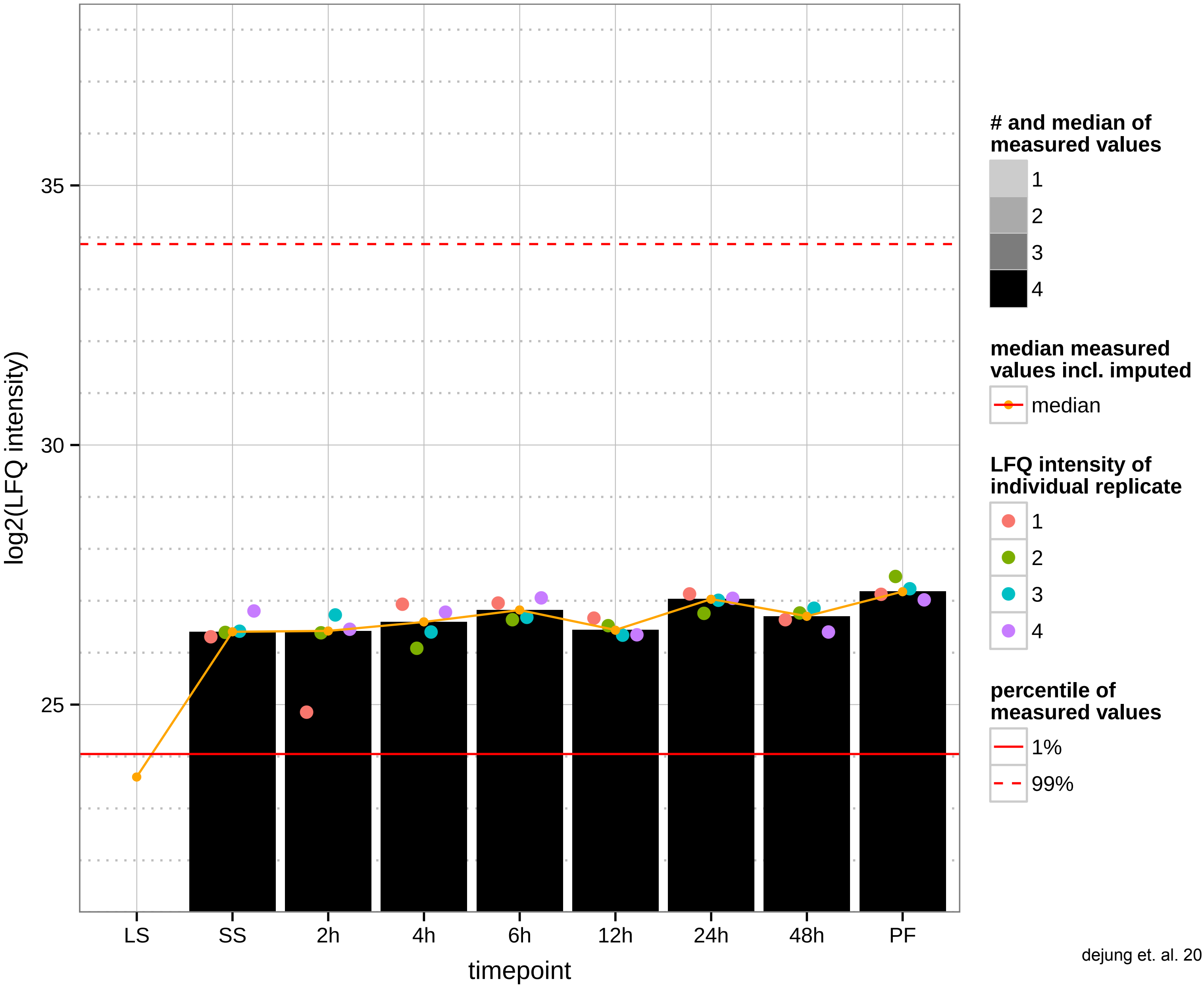
ribosomal RNA processing protein 45, exosome complex exonuclease (RRP45)
Tb927.6.670
AGOF: 3'−5'−exoribonuclease activity, RNA binding
AGOC: null
AGOP: RNA processing
PGOF: null
PGOC: null
PGOP: null





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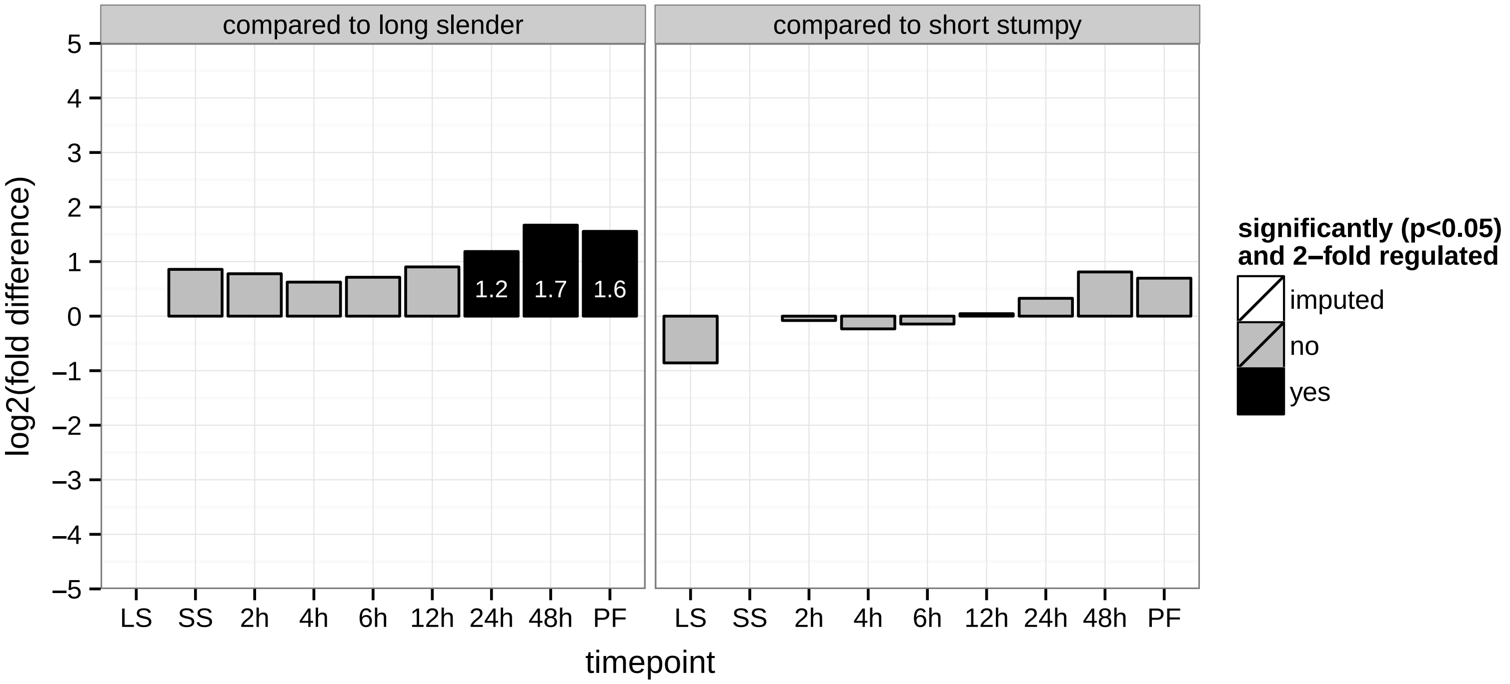
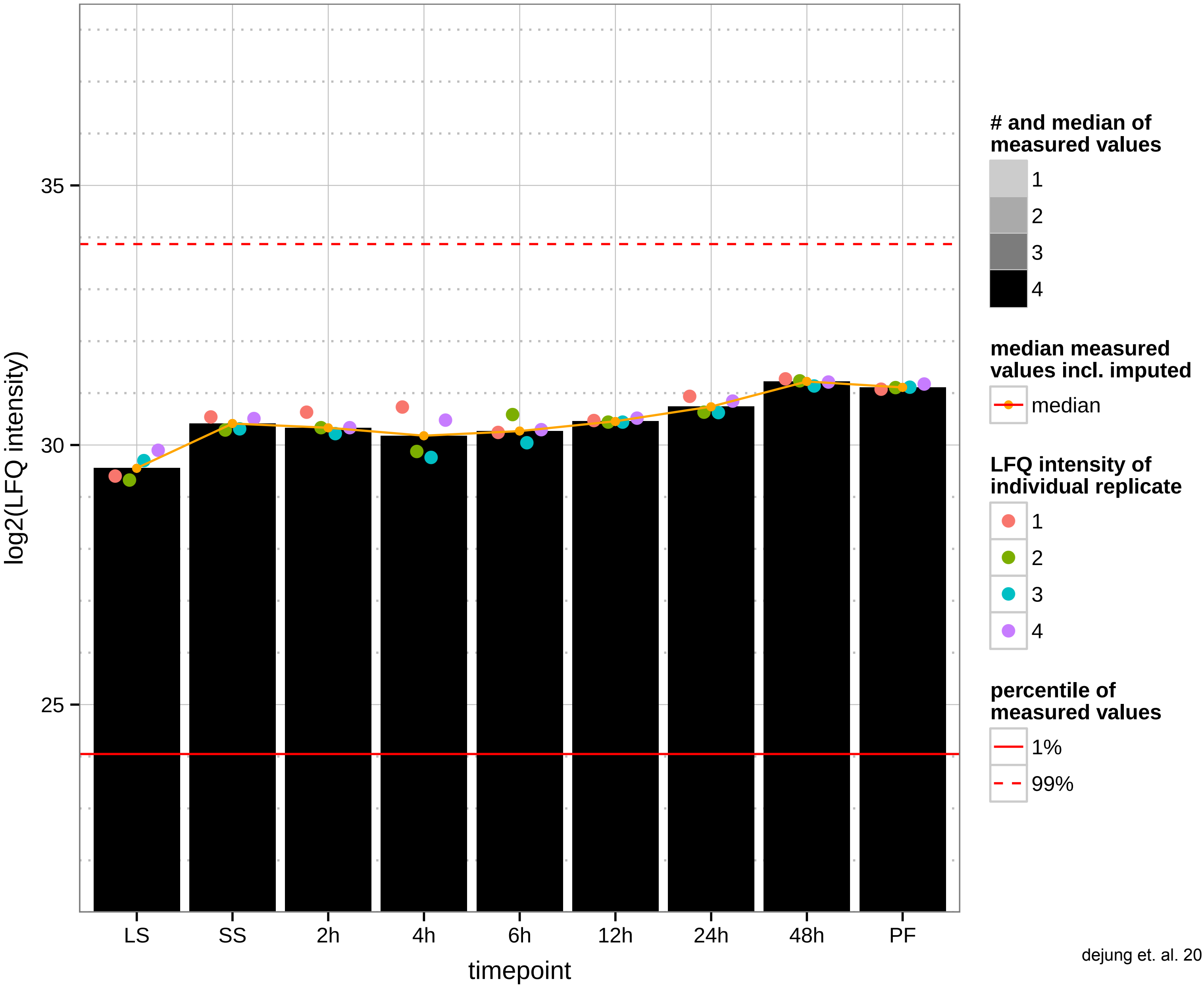
alanyl–tRNA synthetase, putative
Tb927.6.700
AGOF: ATP binding, alanine–tRNA ligase activity, nucleic acid binding
AGOC: cytoplasm
AGOP: alanyl–tRNA aminoacylation, translation
PGOF: ATP binding, alanine–tRNA ligase activity, ligase activity, forming aminoacyl–tRNA and related compounds, nucleic ac
PGOC: cytoplasm
PGOP: alanyl–tRNA aminoacylation, tRNA aminoacylation





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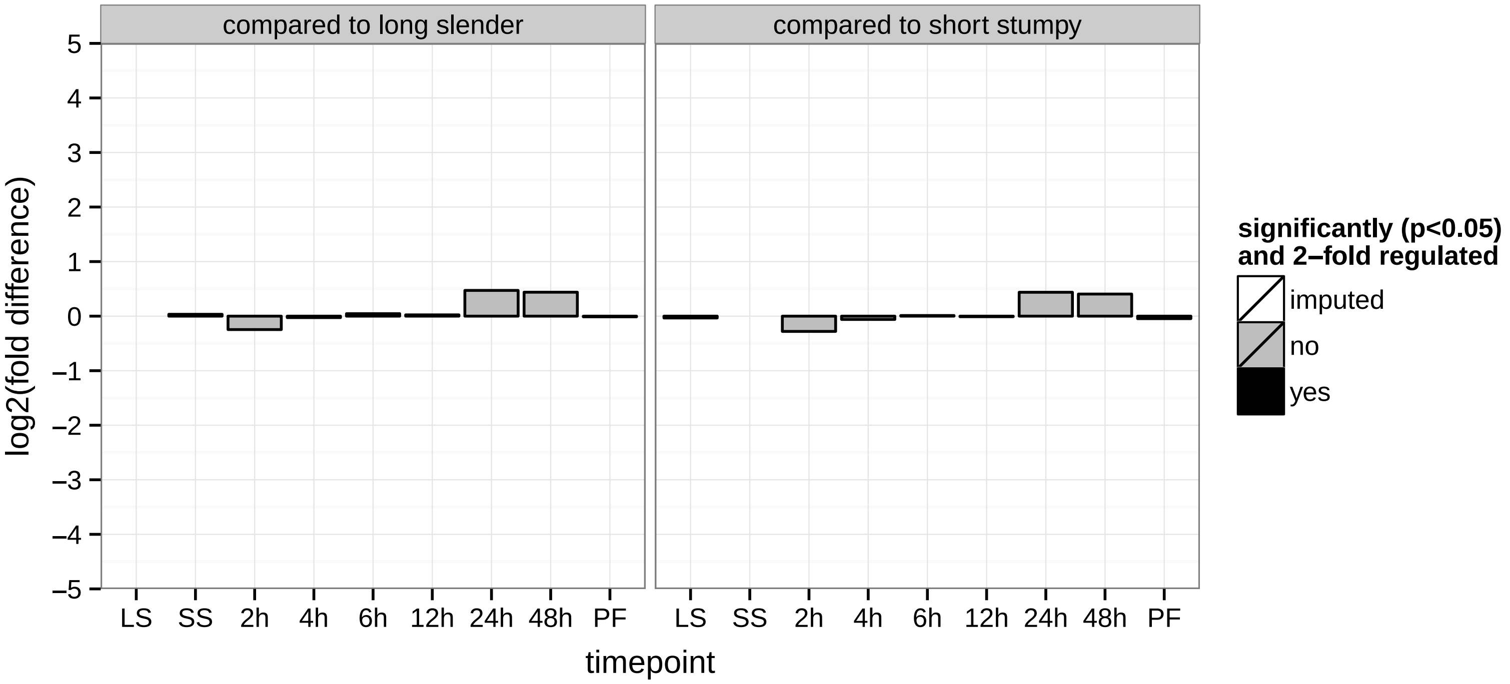
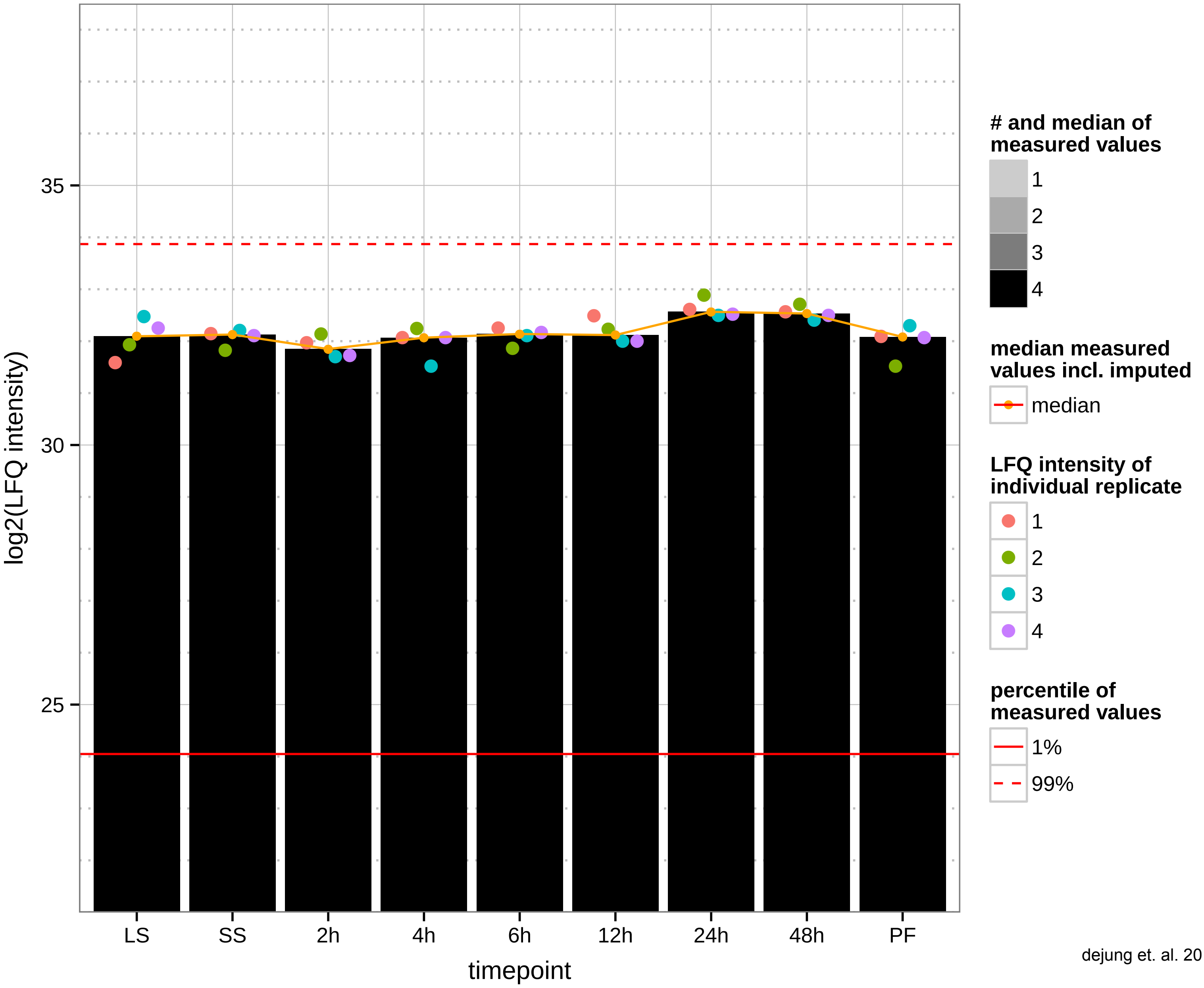
60S ribosomal protein L14, putative, 40S ribosomal protein L14
Tb927.6.720;Tb927.11.11230
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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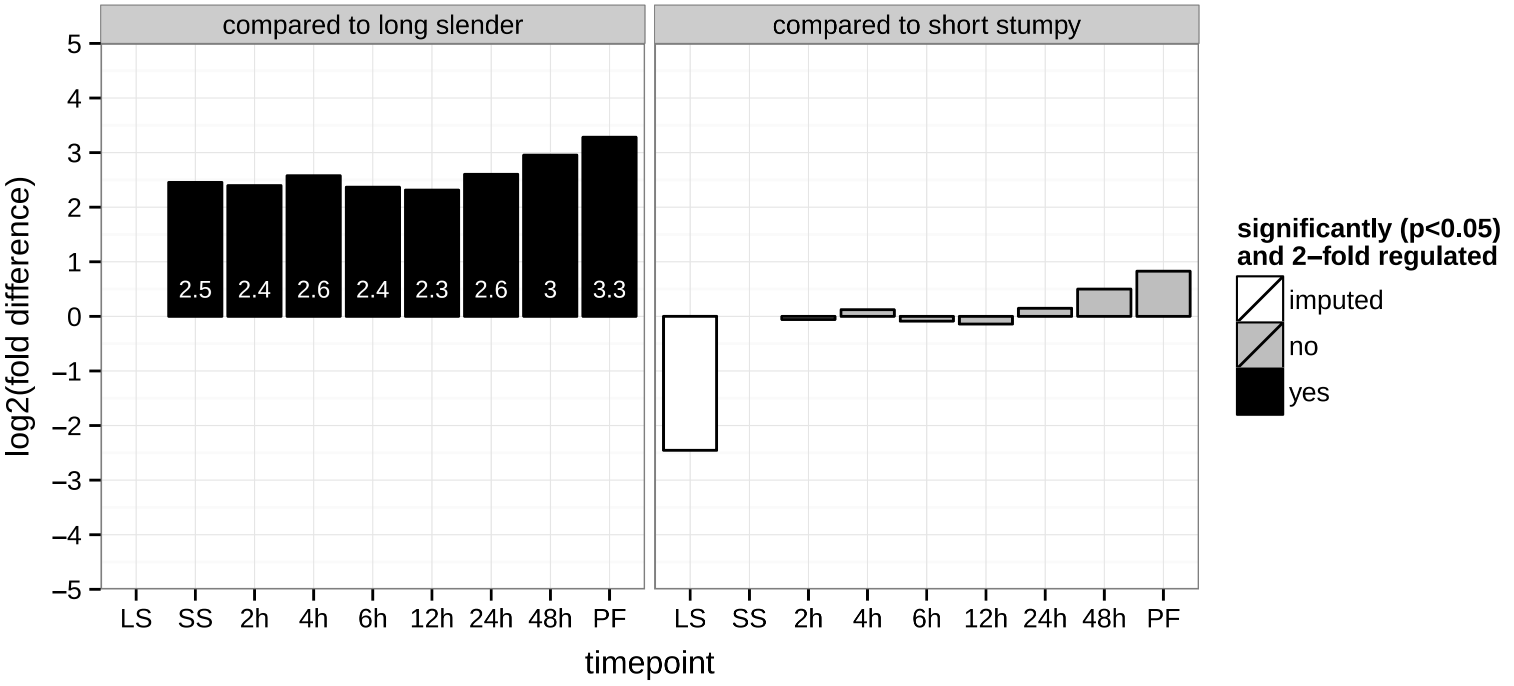
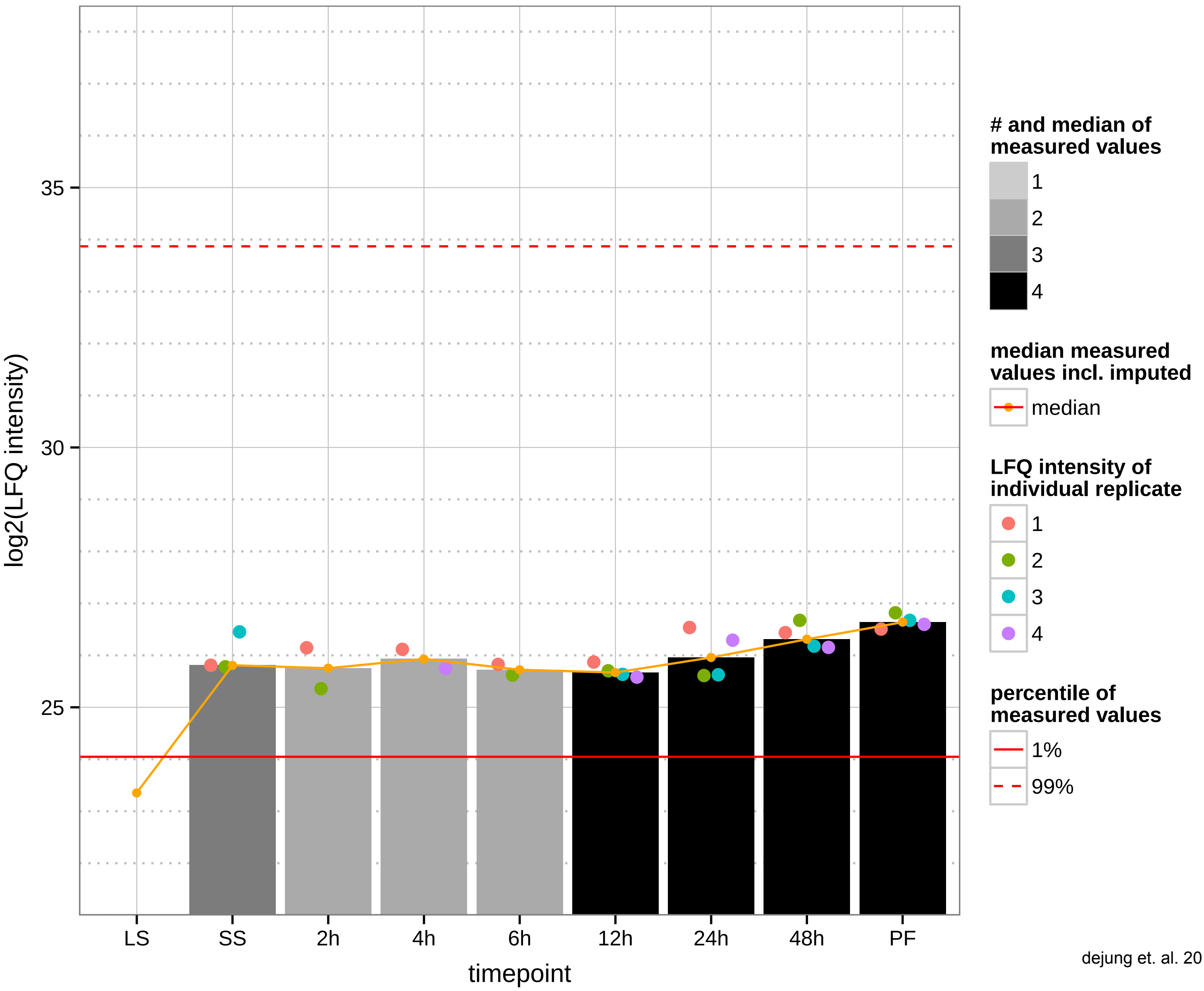
ATP−dependent DEAH−box RNA helicase, putative
Tb927.6.740
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: null
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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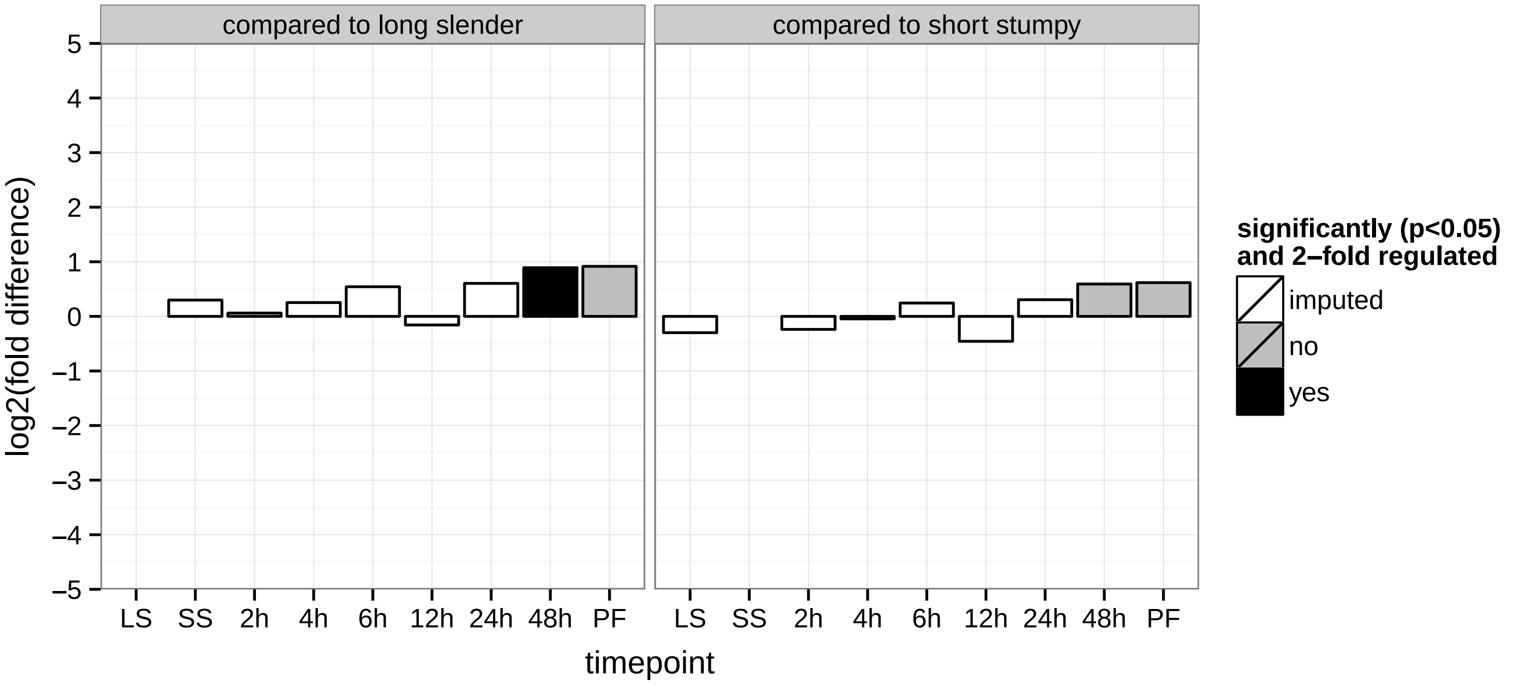
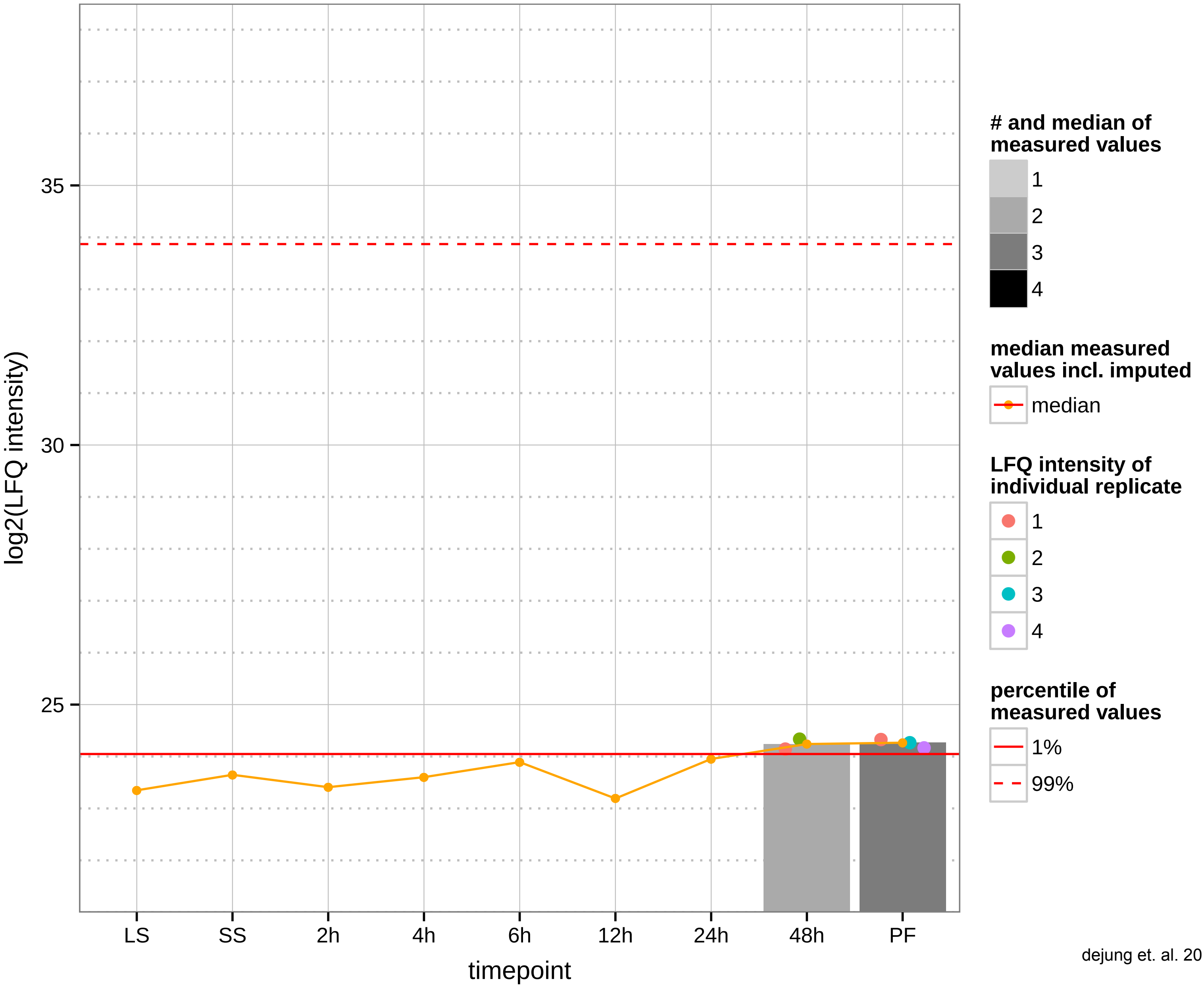
kinetoplastid−specific phospho−protein phosphatase, putative
Tb927.6.750
AGOF: protein serine/threonine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: hydrolase activity
PGOC: null
PGOP: null





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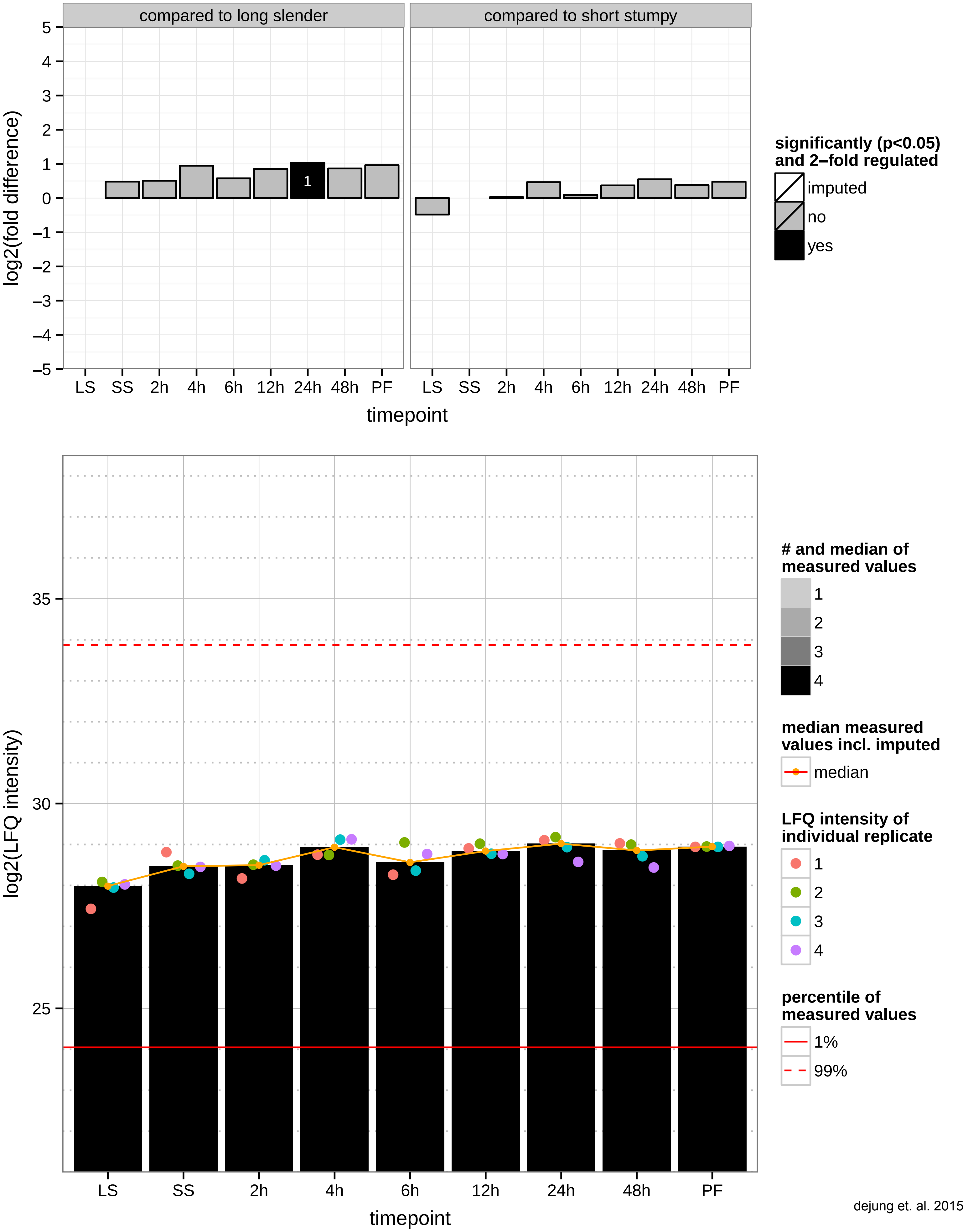
hypothetical protein, conserved, ccr4–not transcription complex subunit 2 (NOT2)
Tb927.6.850;Tb11.v5.0689
AGOF: null, RNA polymerase II transcription cofactor activity
AGOC: null, nucleus
AGOP: null, negative regulation of transcription from RNA polymerase II promoter
PGOF: null
PGOC: nucleus
PGOP: regulation of transcription, DNA–dependent



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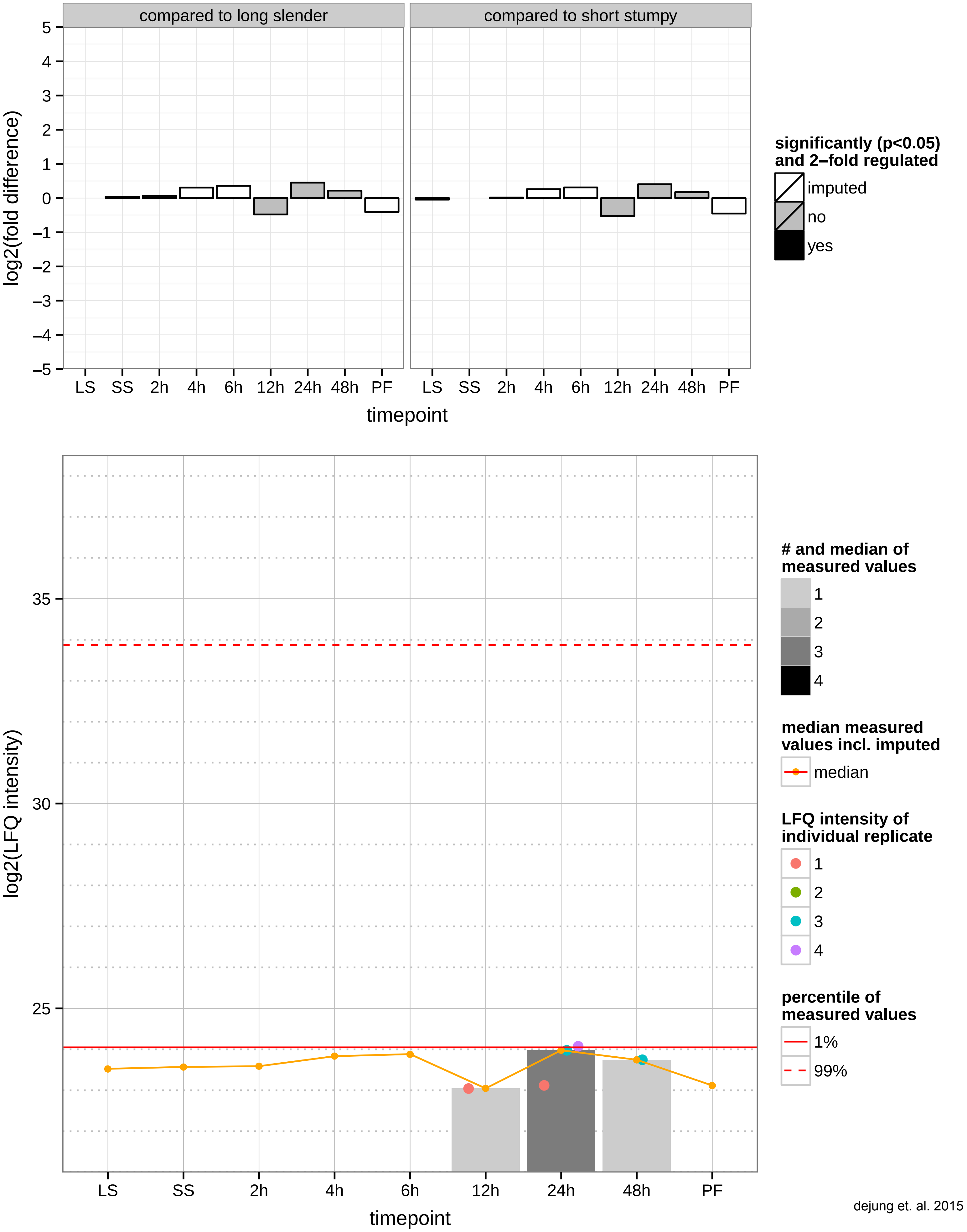
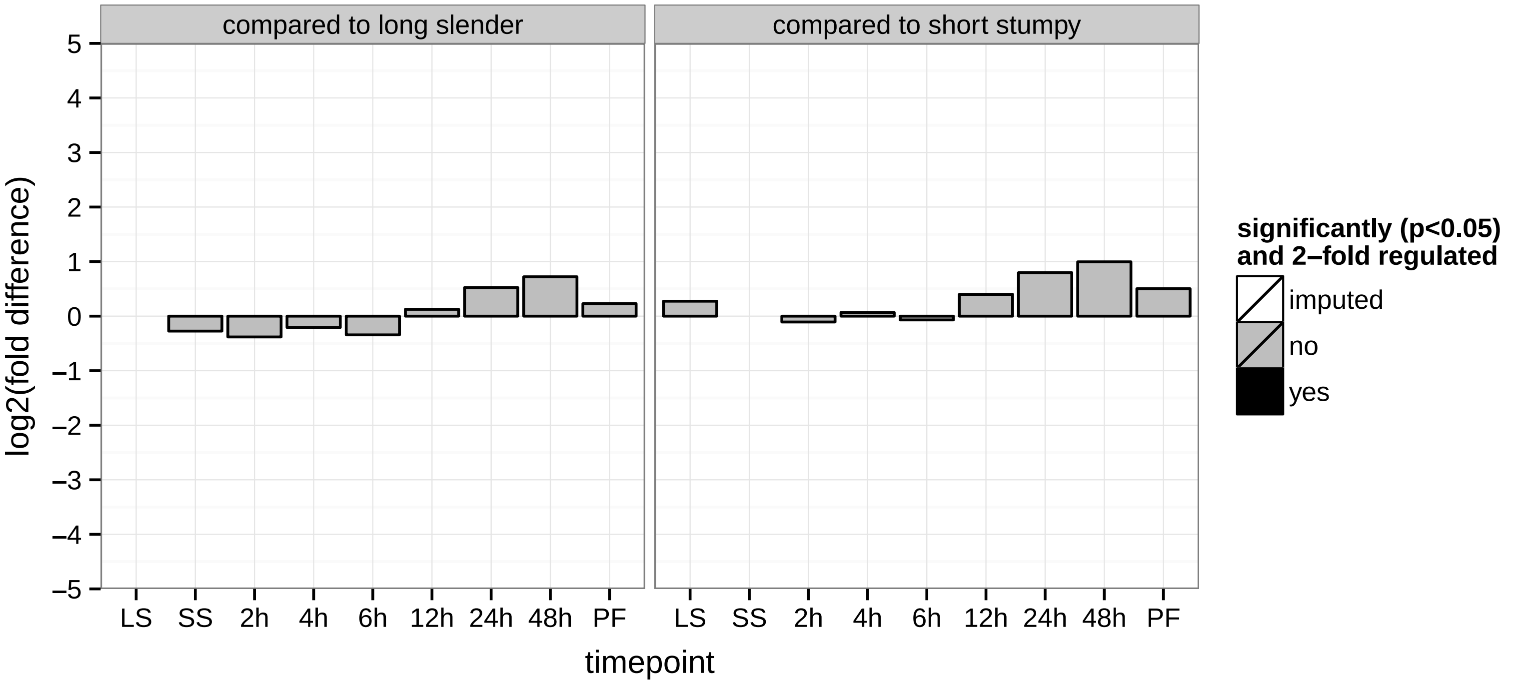
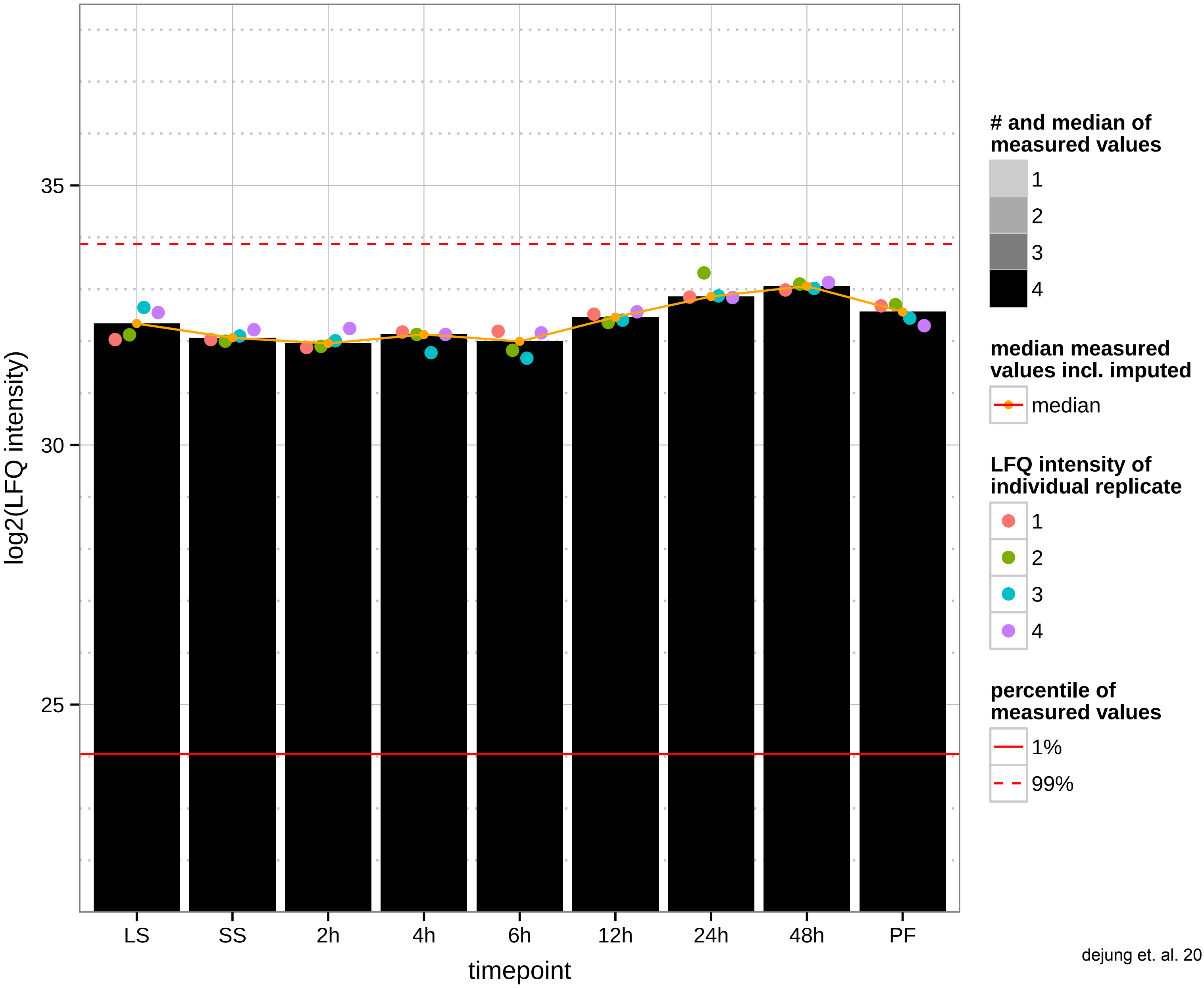
hypothetical protein, conserved
Tb927.7.1010
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



40S ribosomal protein S16, putative
Tb927.7.1050;Tb927.7.1040
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome, null
PGOC: intracellular, ribosome, null
PGOP: translation, null





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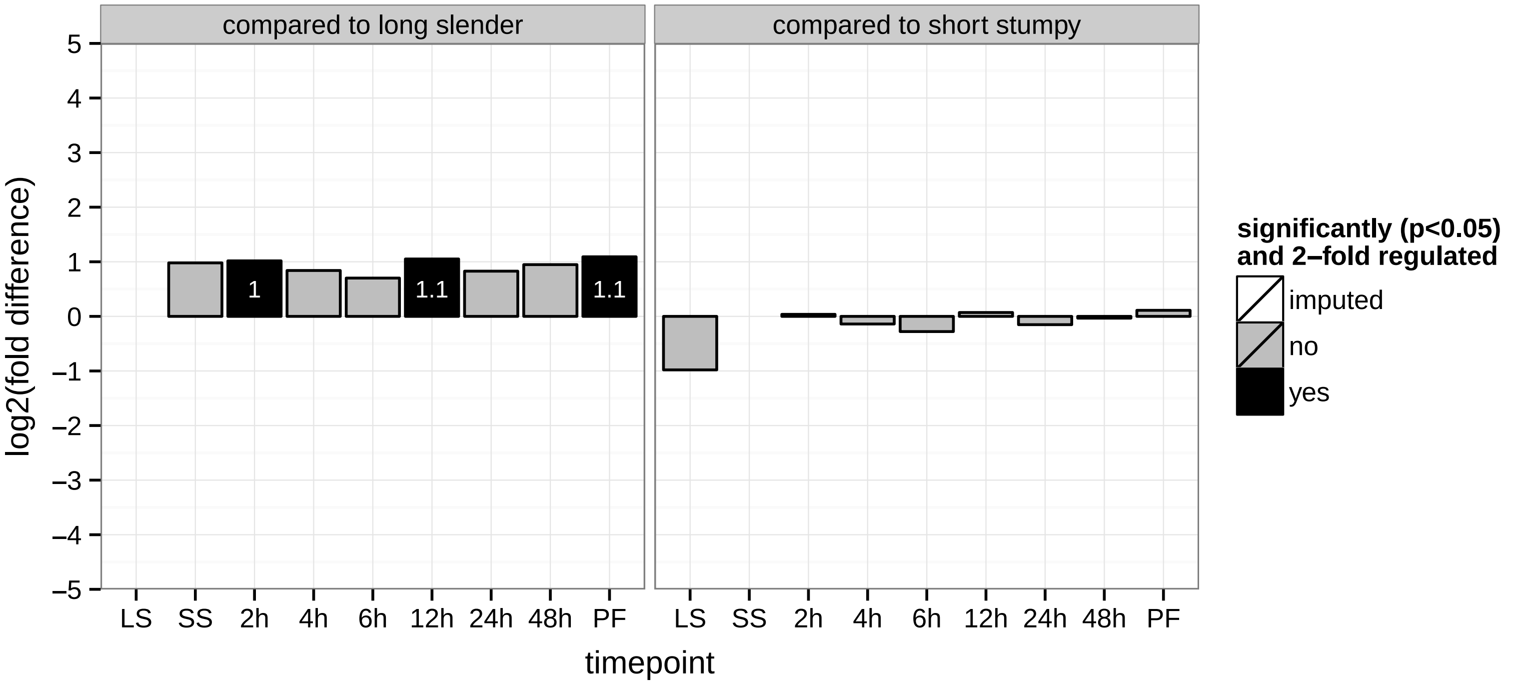
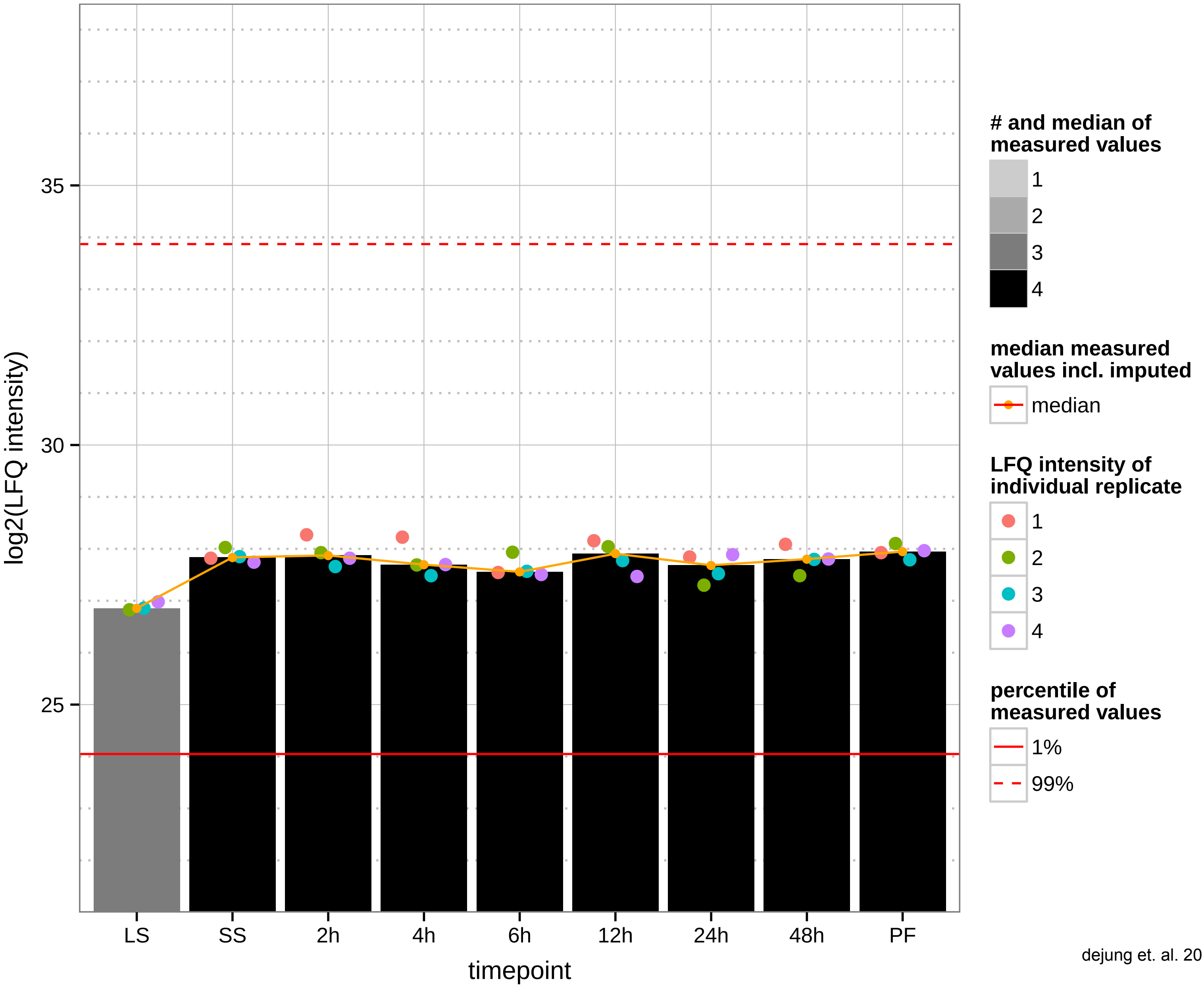
hypothetical protein, conserved
Tb927.7.1060
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: nucleus
PGOP: null





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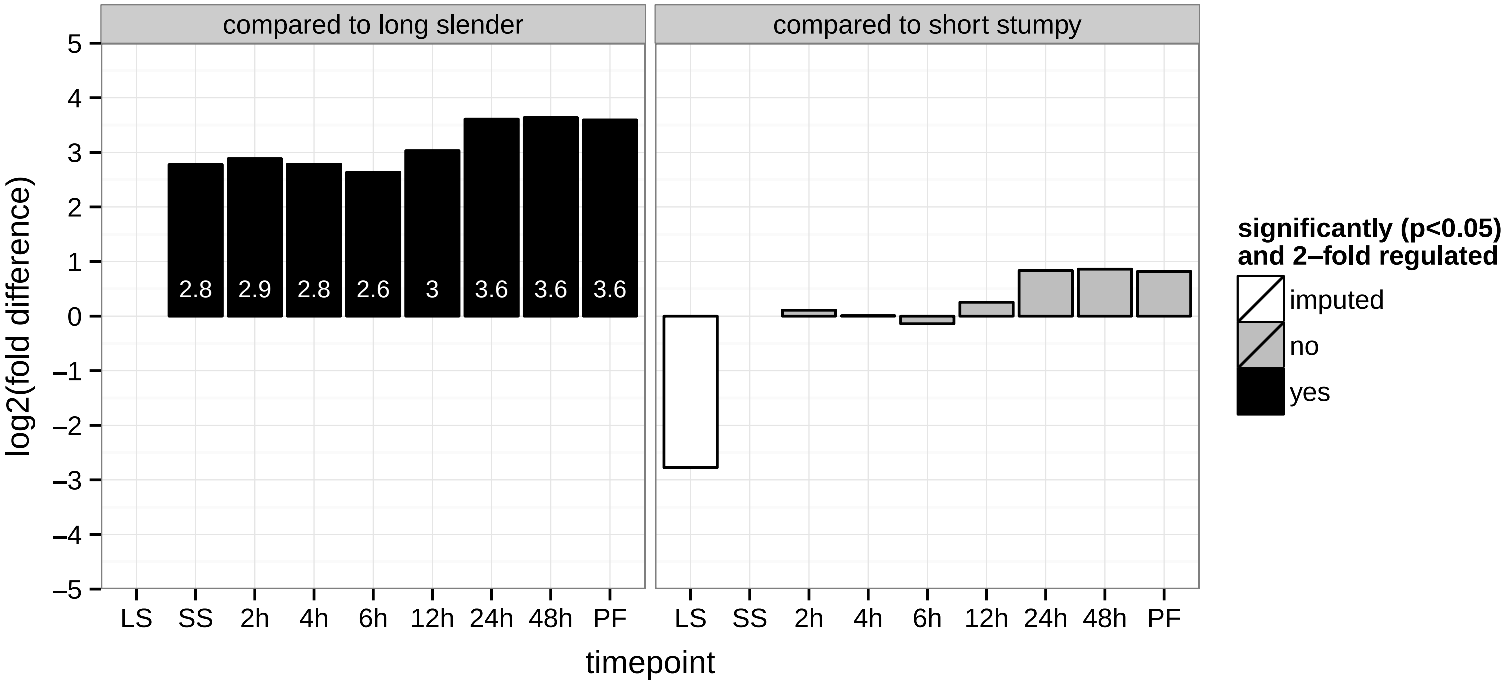
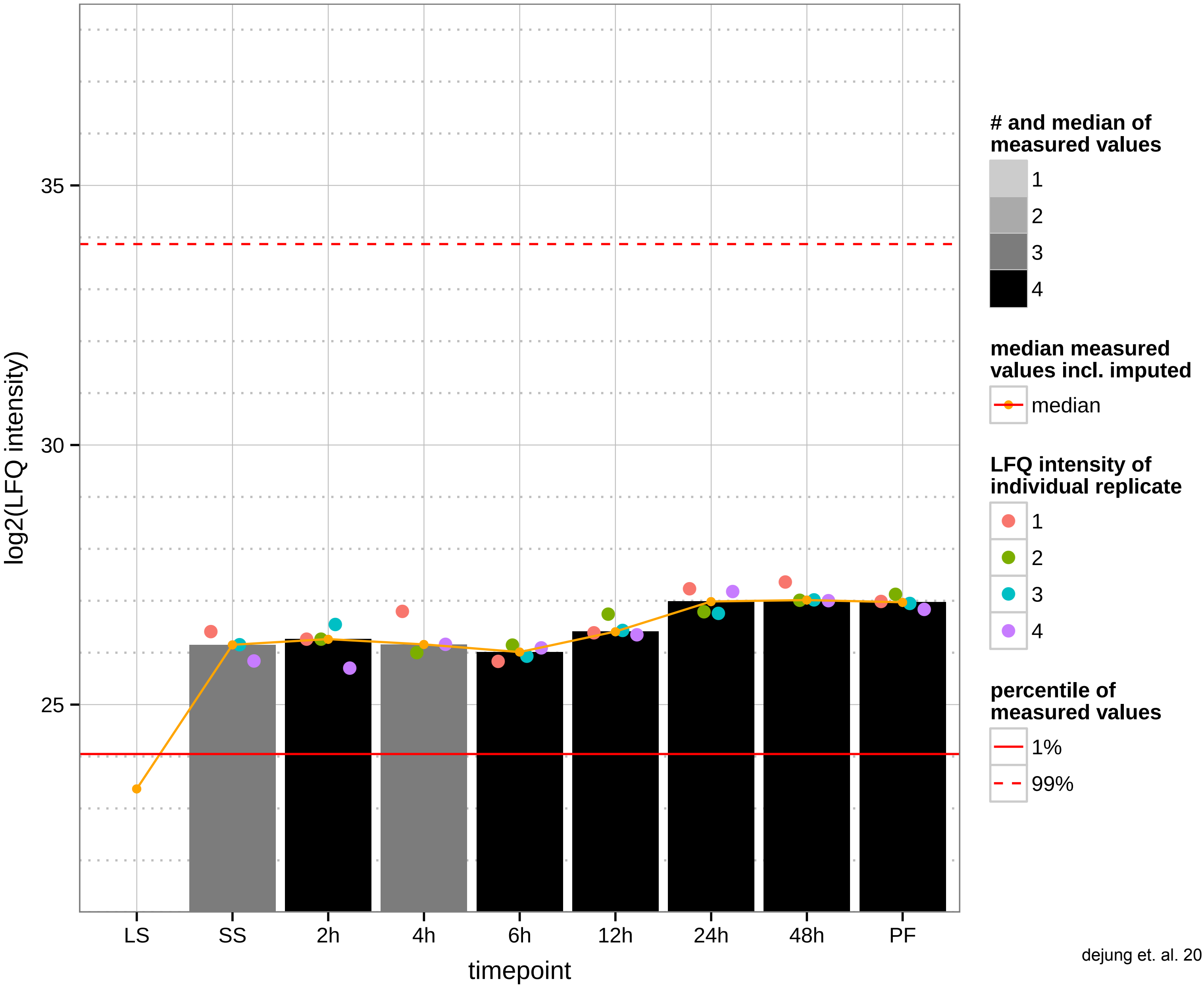
hypothetical protein, conserved
Tb927.7.1080
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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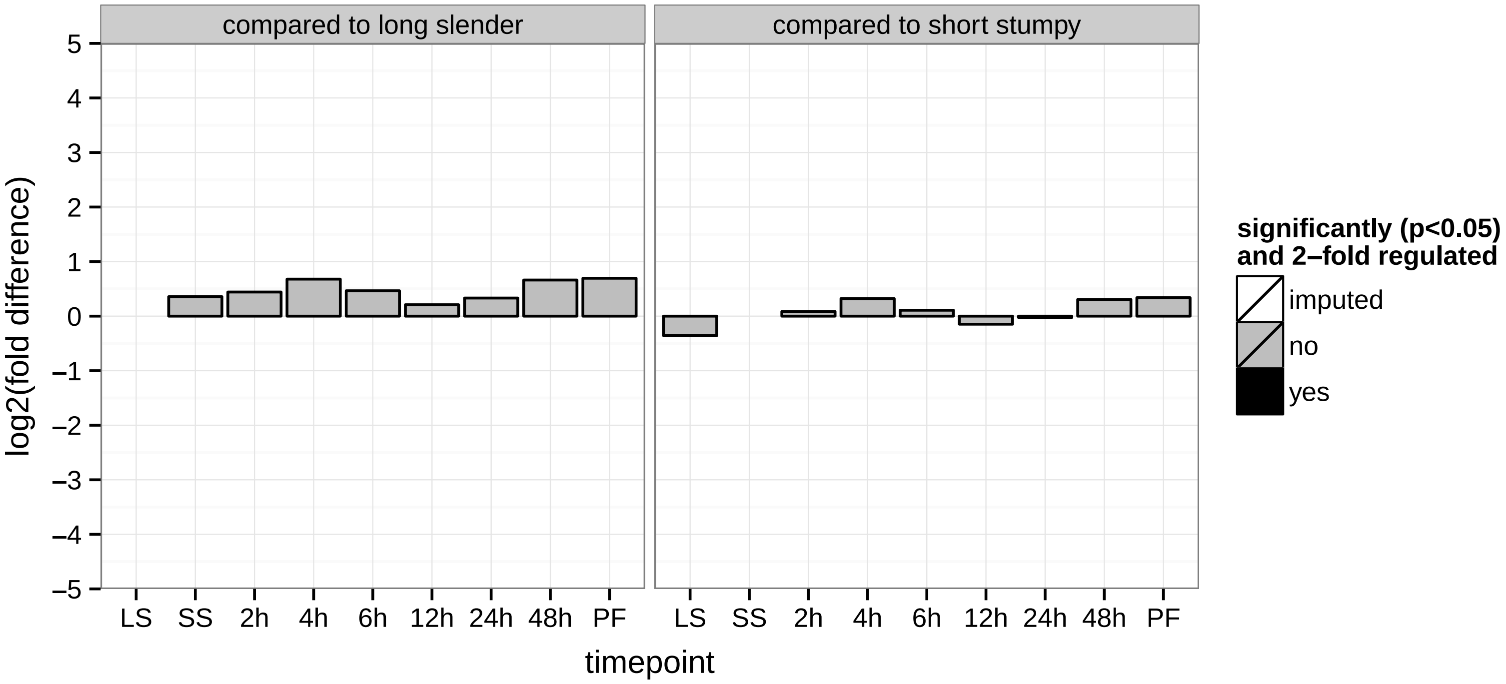
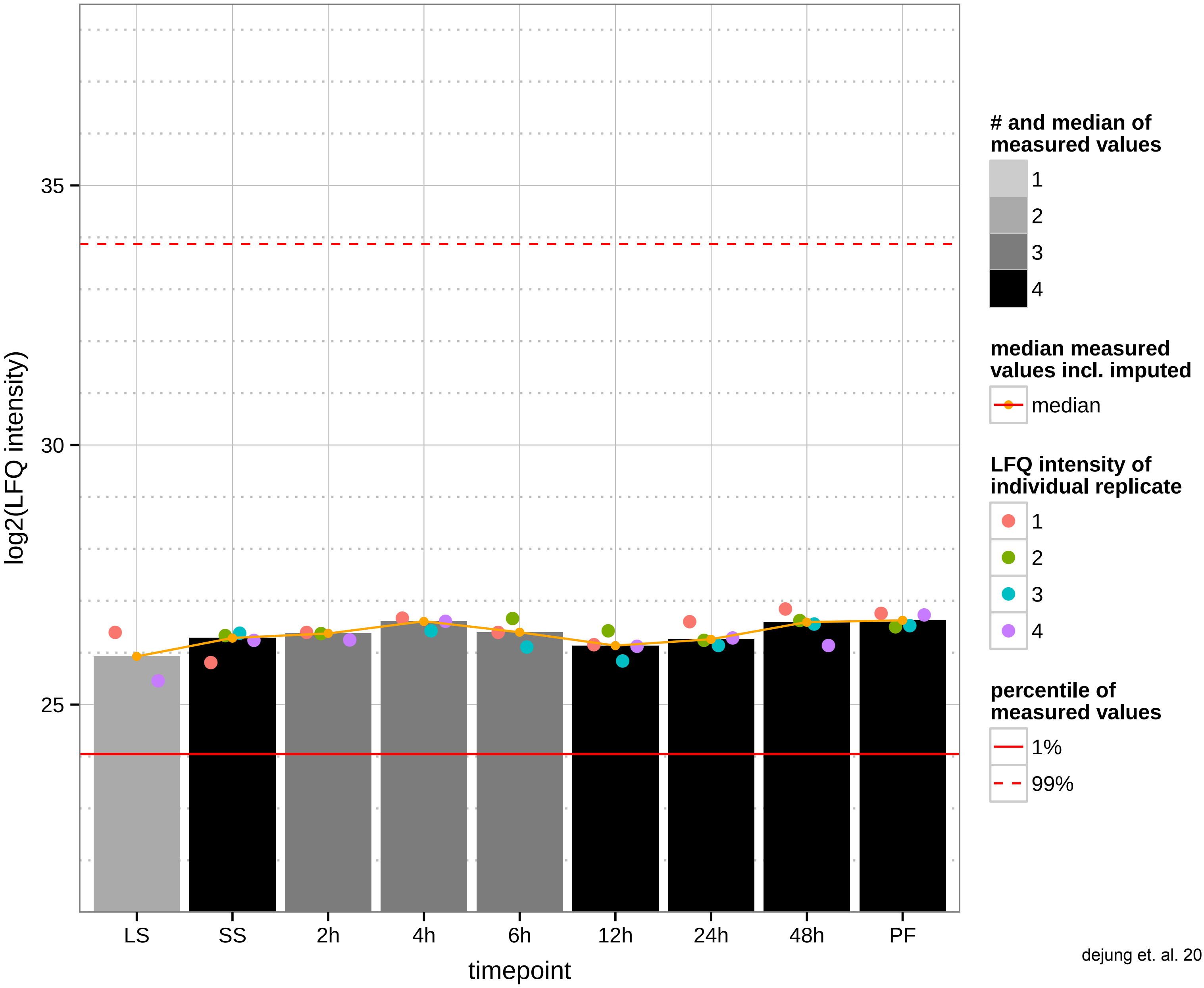
hypothetical protein, conserved
Tb927.7.1100
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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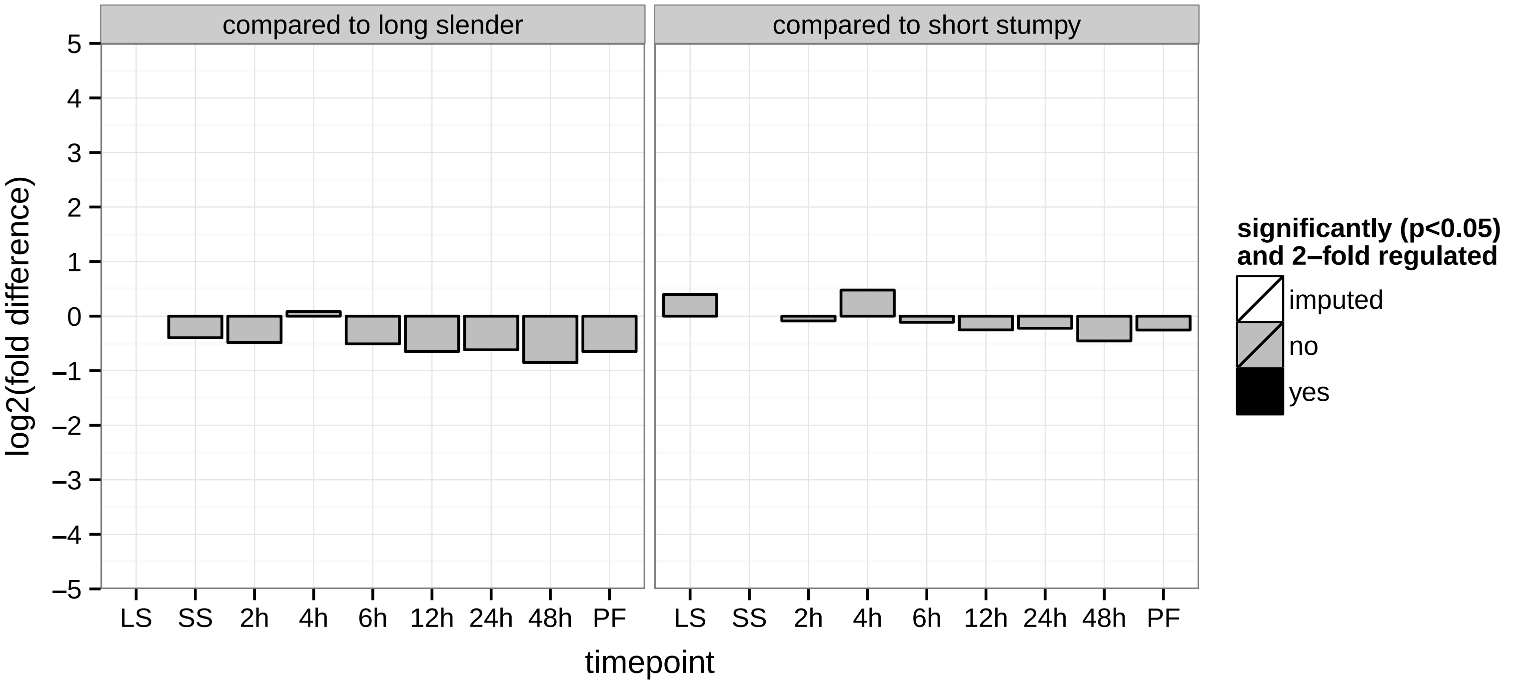
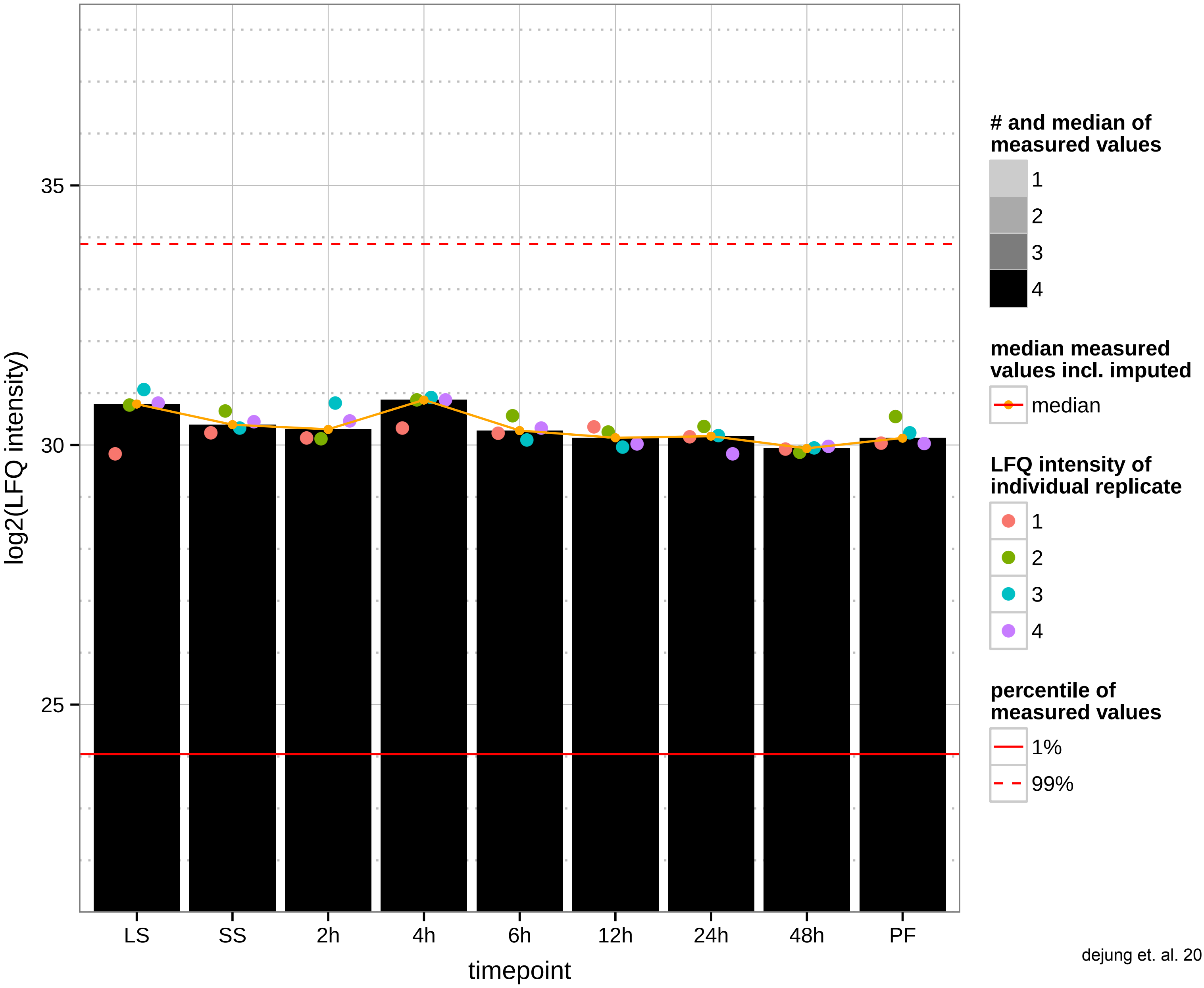
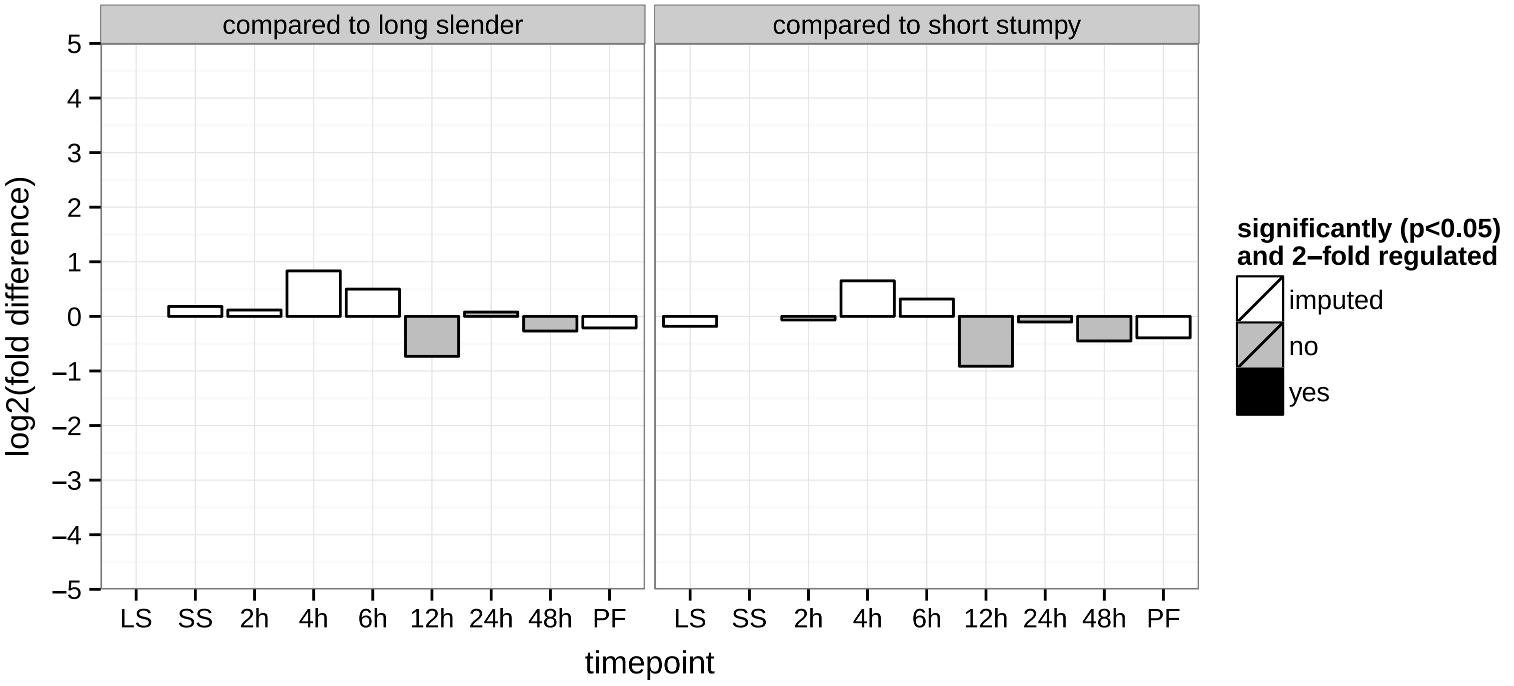
trypanothione/tryparedoxin dependent peroxidase 2, glutathione peroxidase−like 2 (TDPX2)
Tb927.7.1130
AGOF: glutathione peroxidase activity
AGOC: null
AGOP: response to oxidative stress
PGOF: glutathione peroxidase activity
PGOC: null
PGOP: oxidation−reduction process, response to oxidative stress

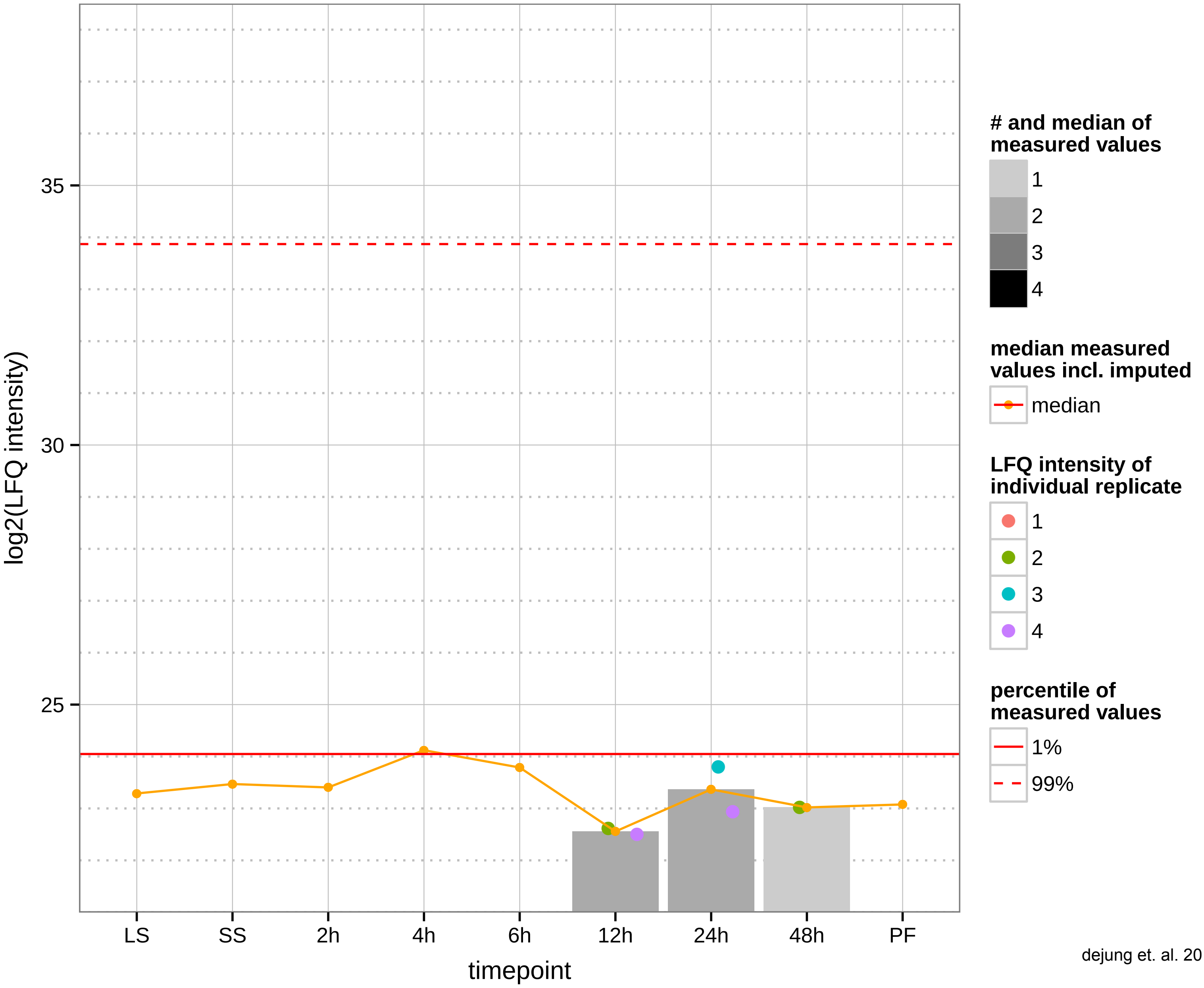




dejung et. al. 2015

regulator of chromosome condensation, putative
Tb927.7.1210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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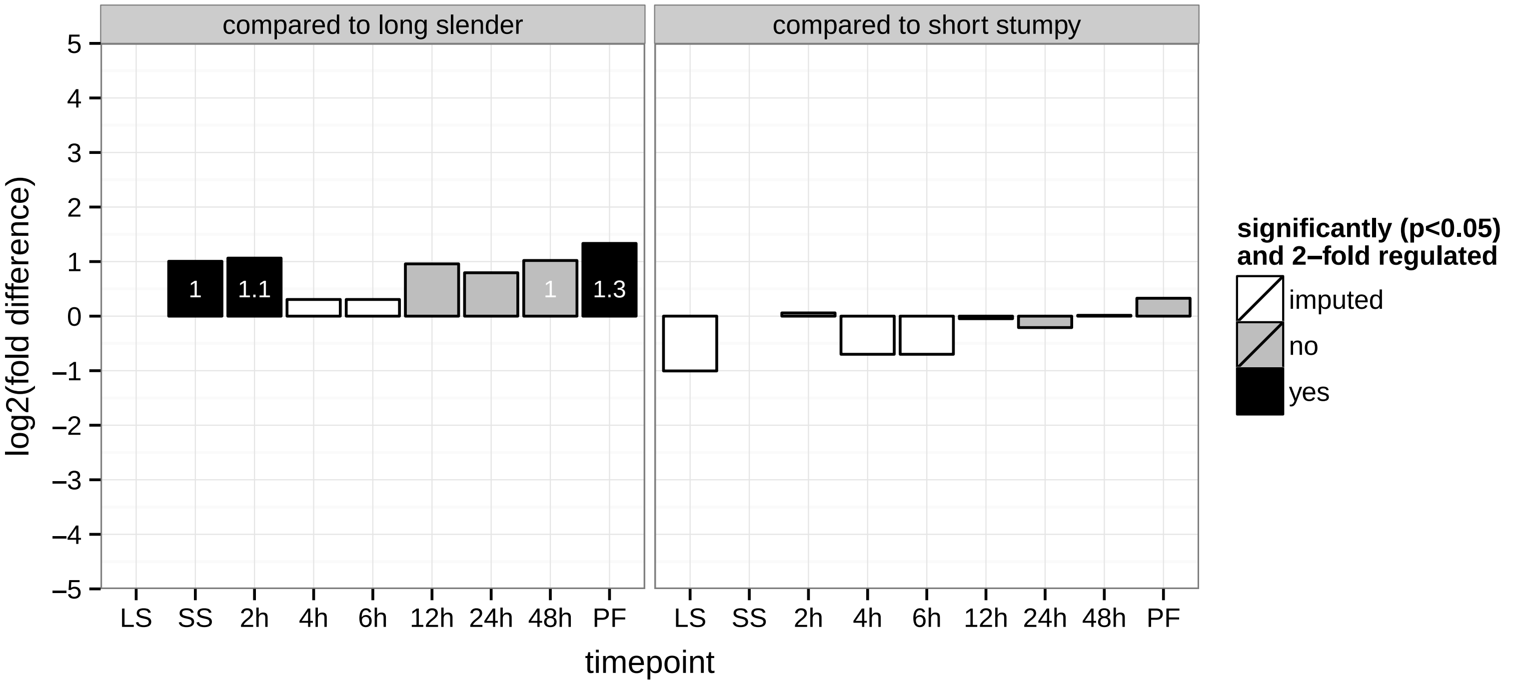
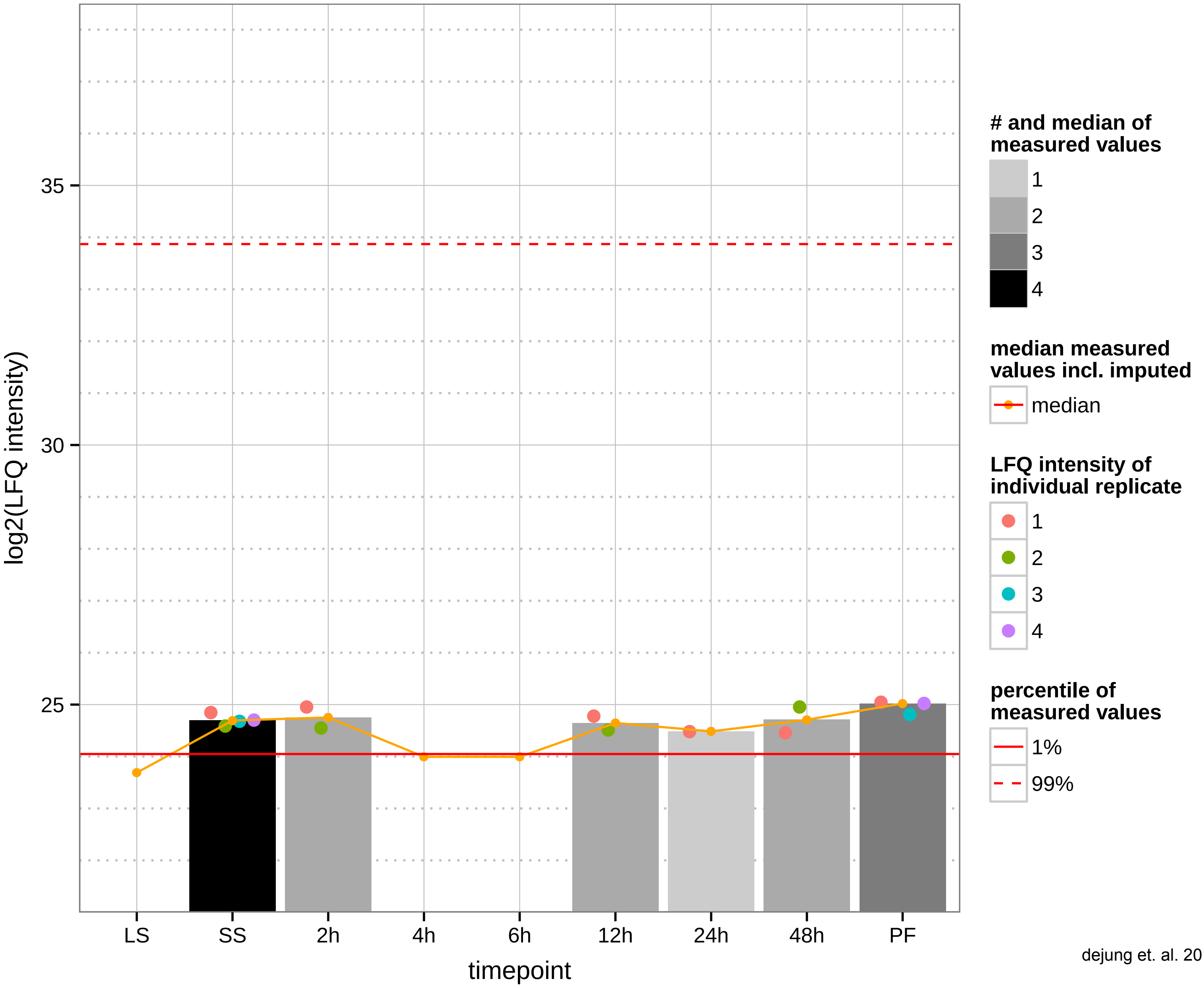
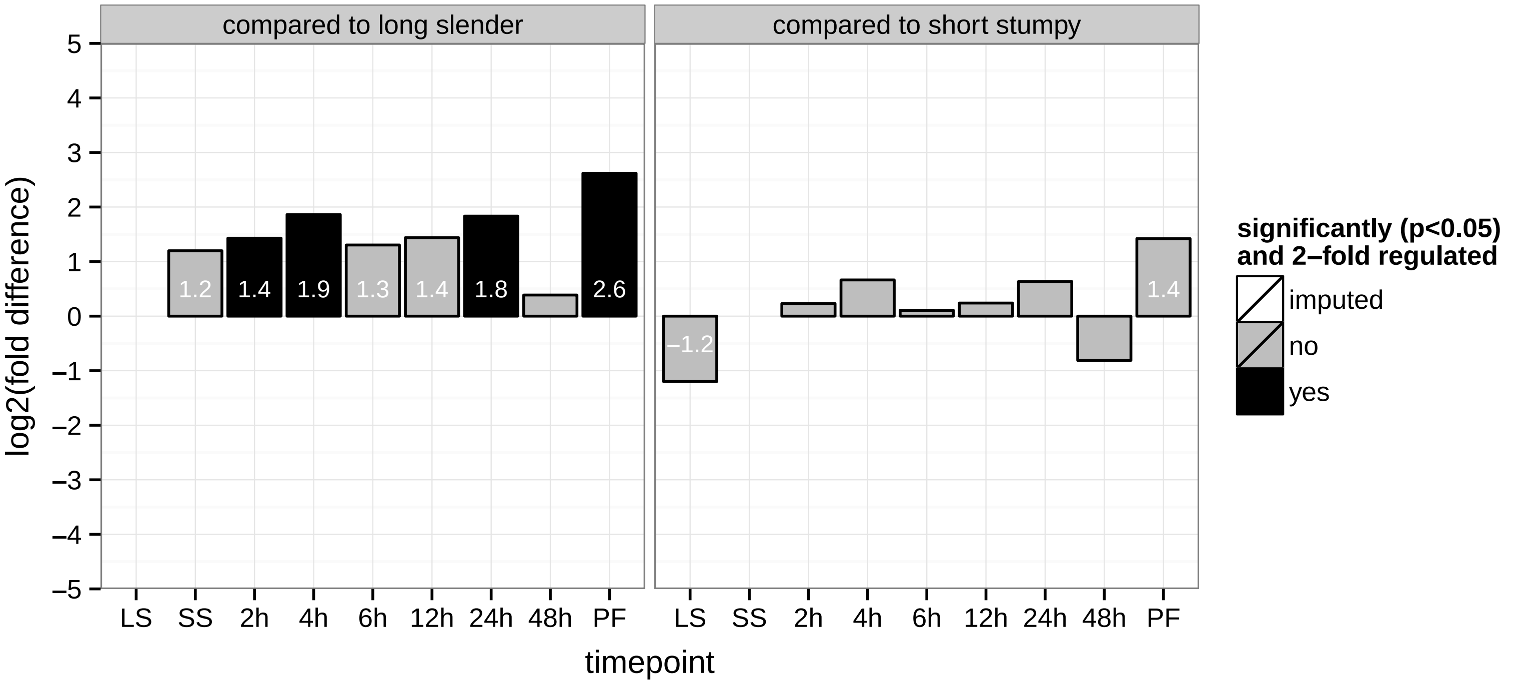
sphingosine kinase A, B, putative
Tb927.7.1240
AGOF: diacylglycerol kinase activity, sphinganine kinase activity
AGOC: cytosol
AGOP: protein kinase C–activating G–protein coupled receptor signaling pathway, sphinganine metabolic process
PGOF: NAD+ kinase activity, diacylglycerol kinase activity
PGOC: null
PGOP: metabolic process, protein kinase C–activating G–protein coupled receptor signaling pathway

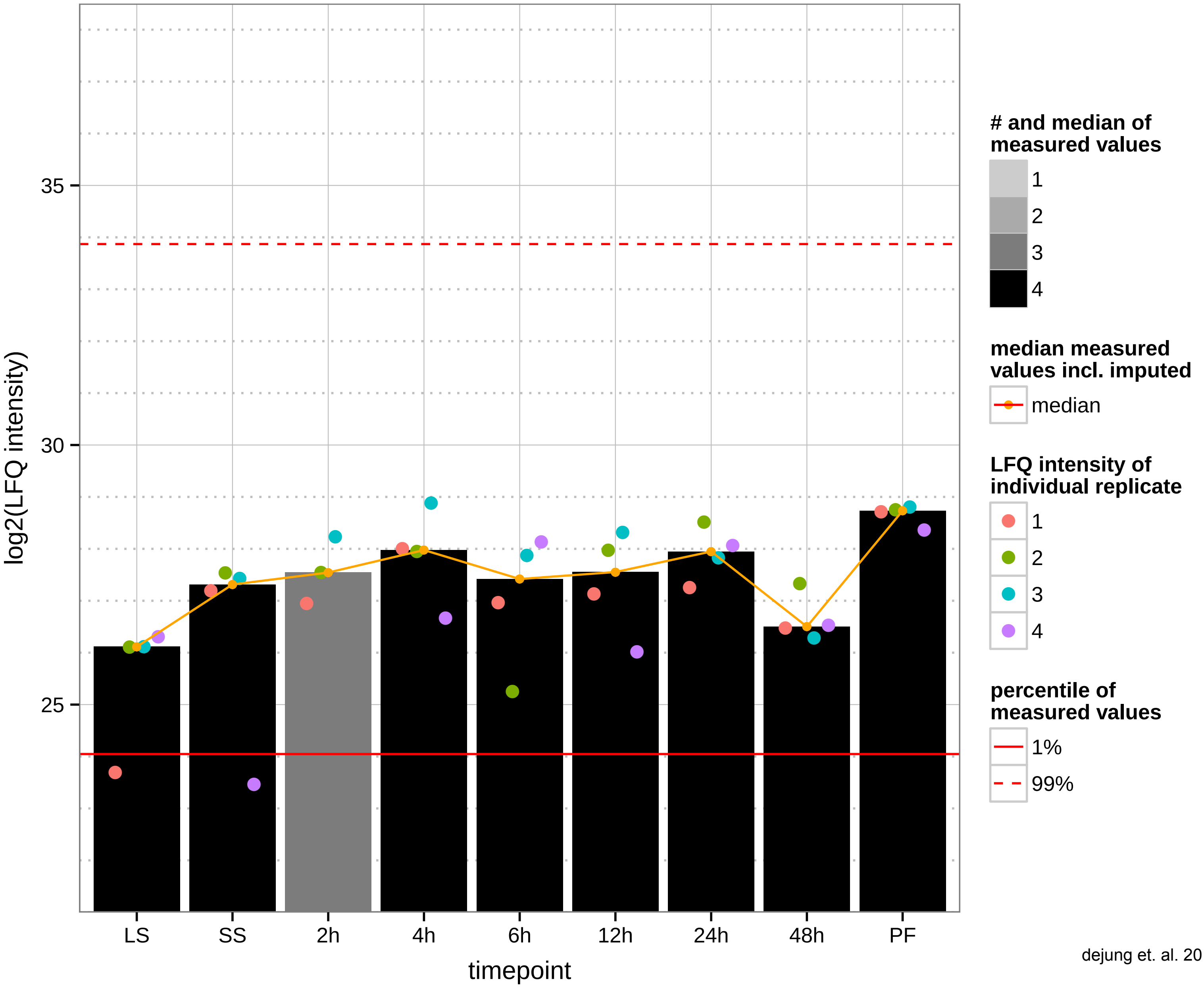




dejung et. al. 2015

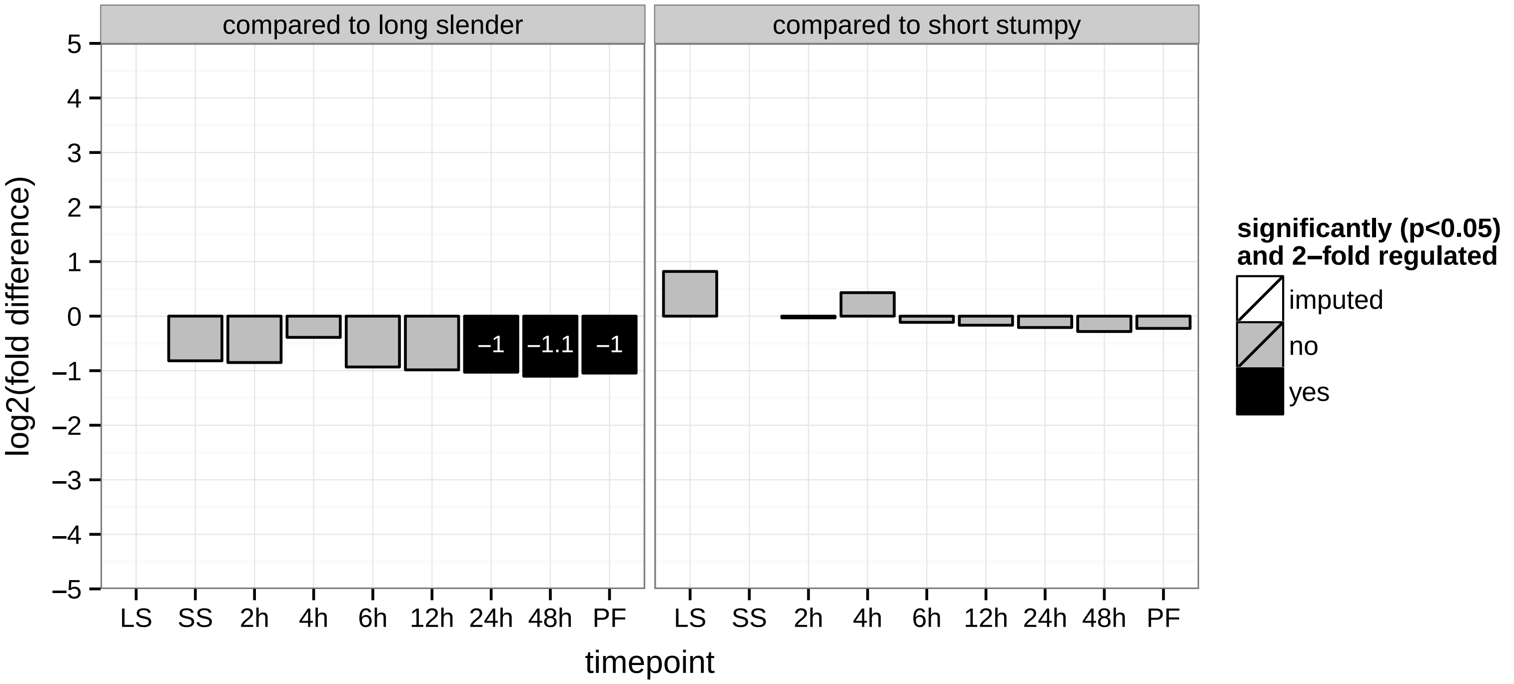
hypothetical protein, conserved
Tb927.7.1290
AGOF: null
AGOC: null
AGOP: null
PGOF: carbohydrate binding
PGOC: null
PGOP: null

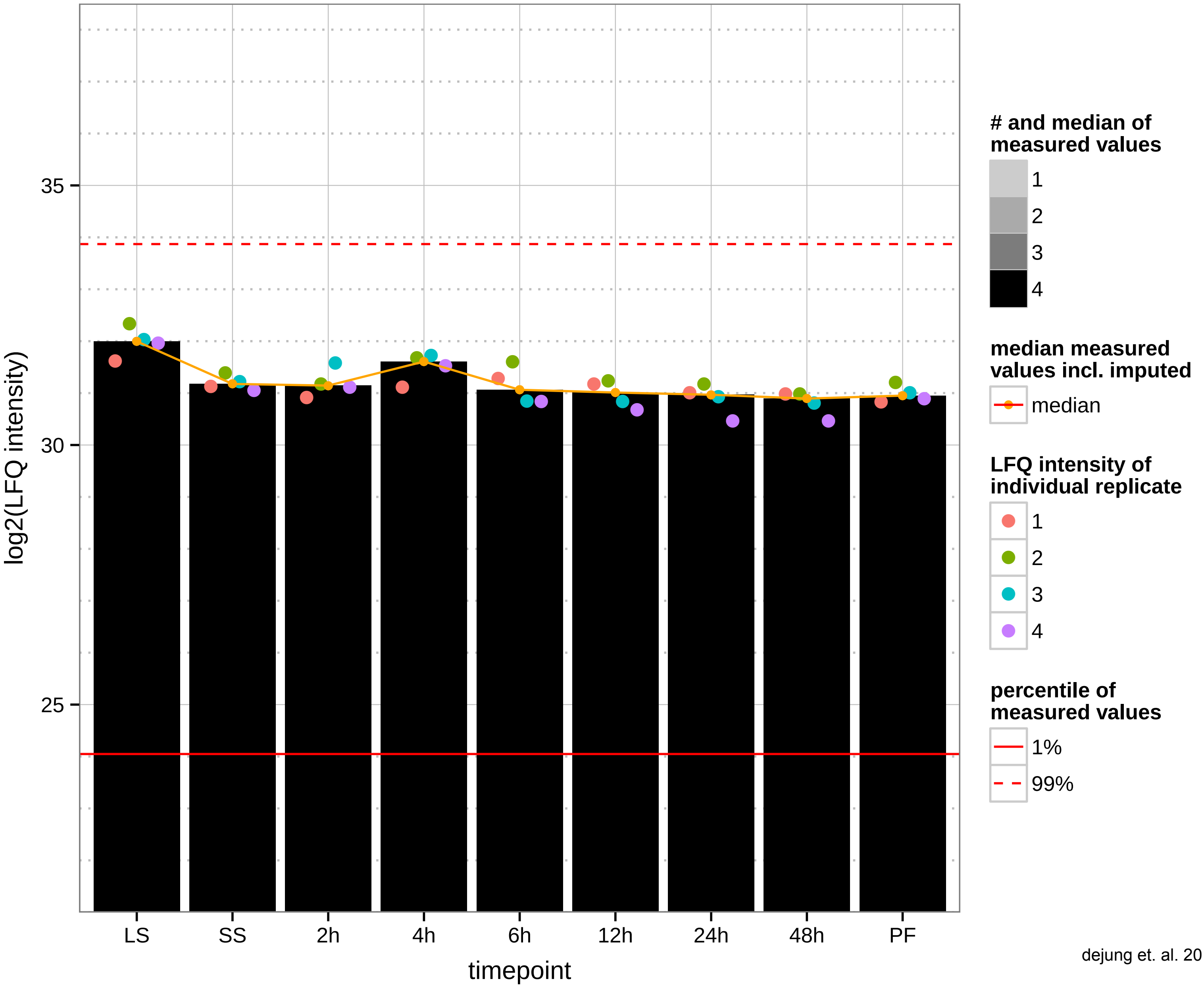




dejung et. al. 2015

protein disulfide isomerase, putative
Tb927.7.1300
AGOF: isomerase activity
AGOC: endoplasmic reticulum
AGOP: cell redox homeostasis
PGOF: isomerase activity
PGOC: endoplasmic reticulum
PGOP: cell redox homeostasis





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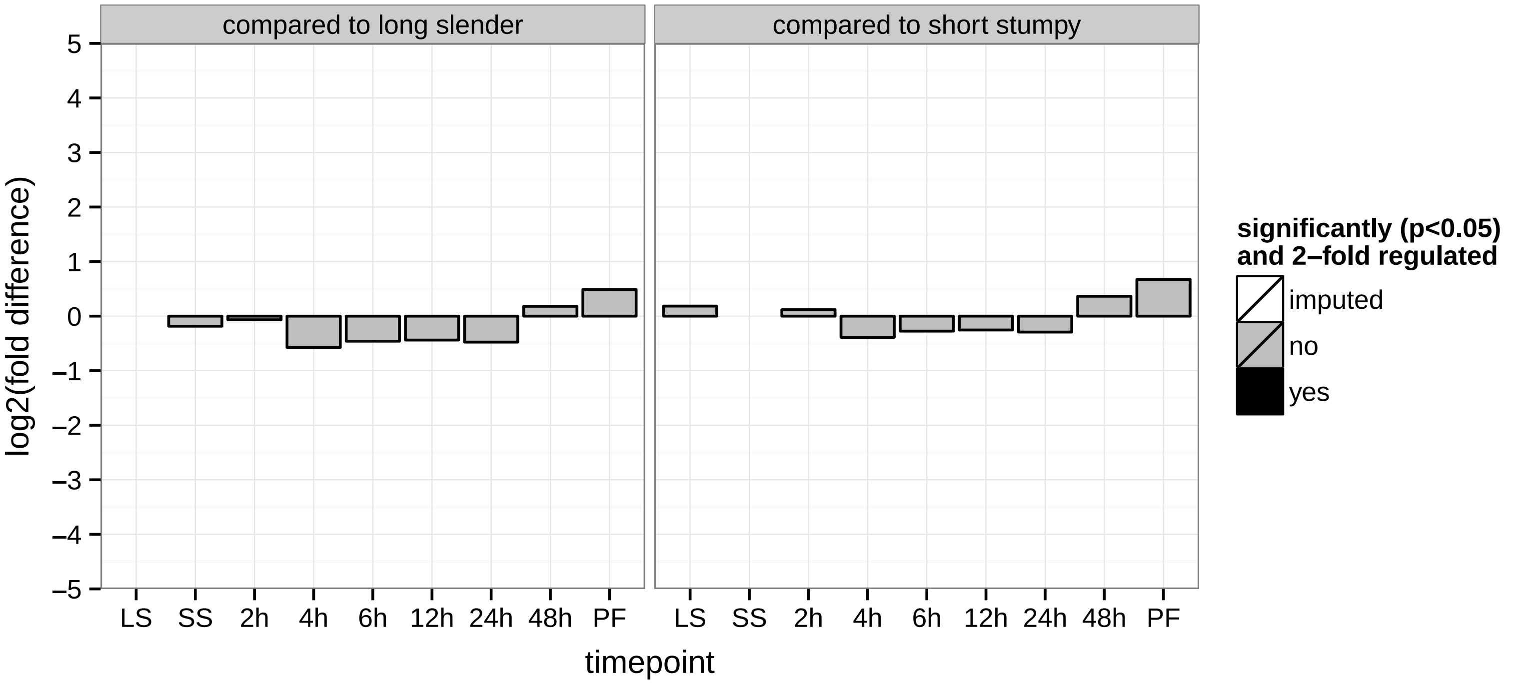
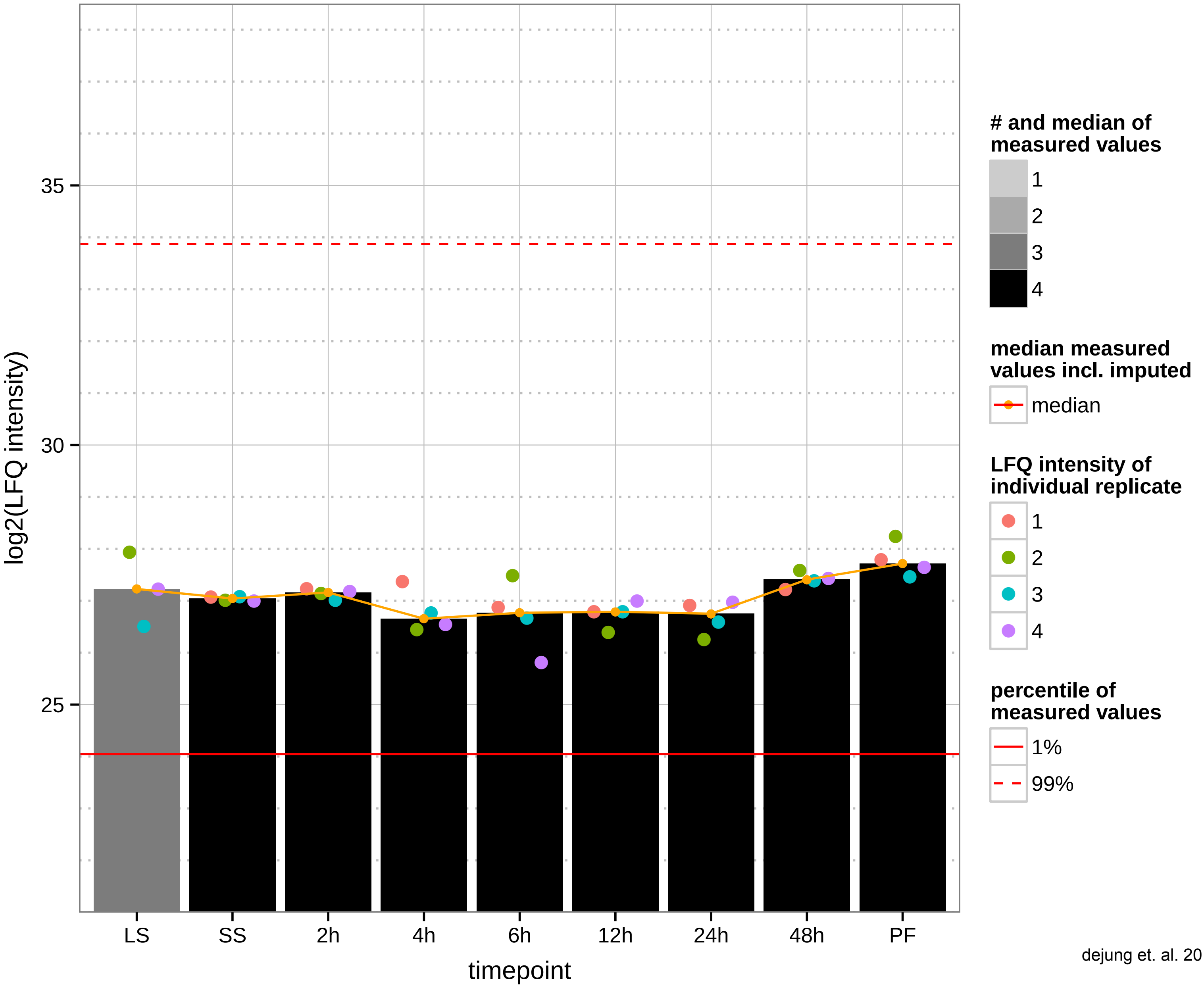
hypothetical protein, conserved
Tb927.7.1310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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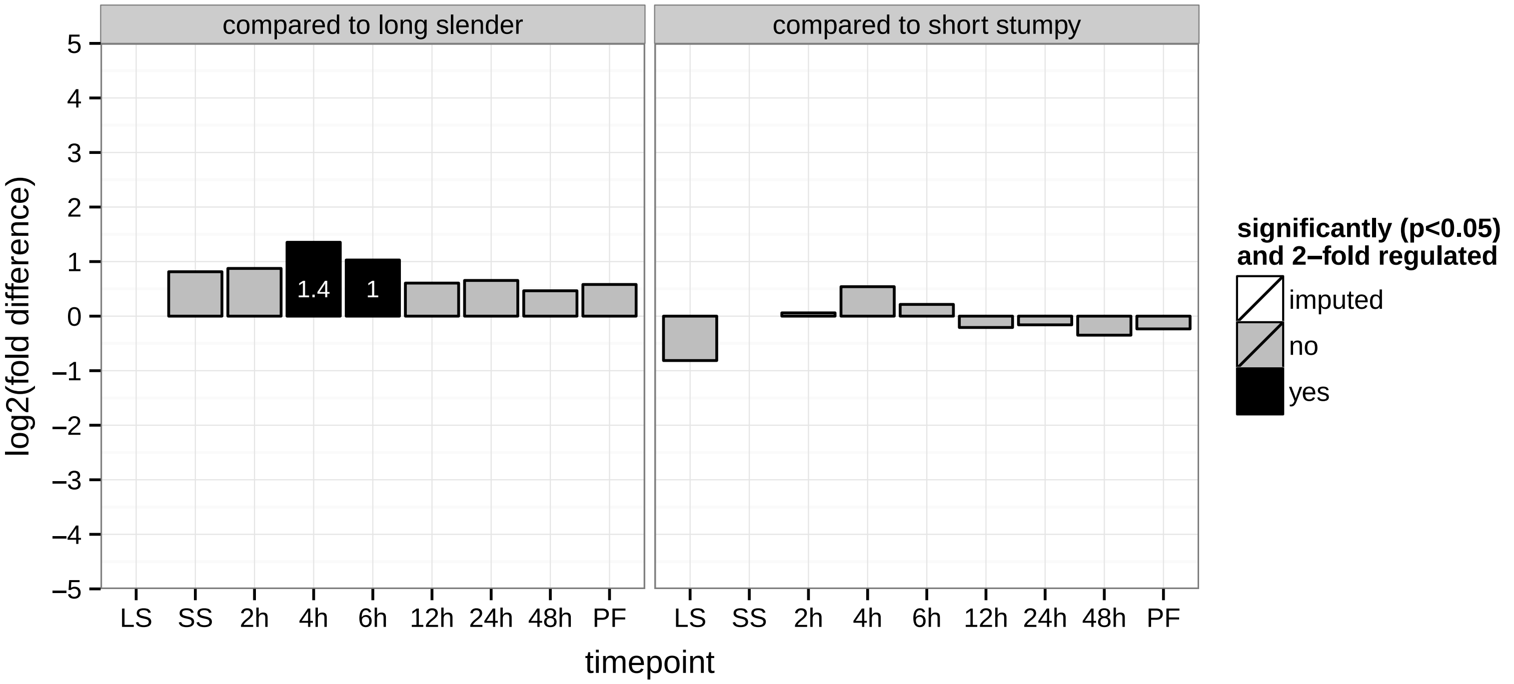
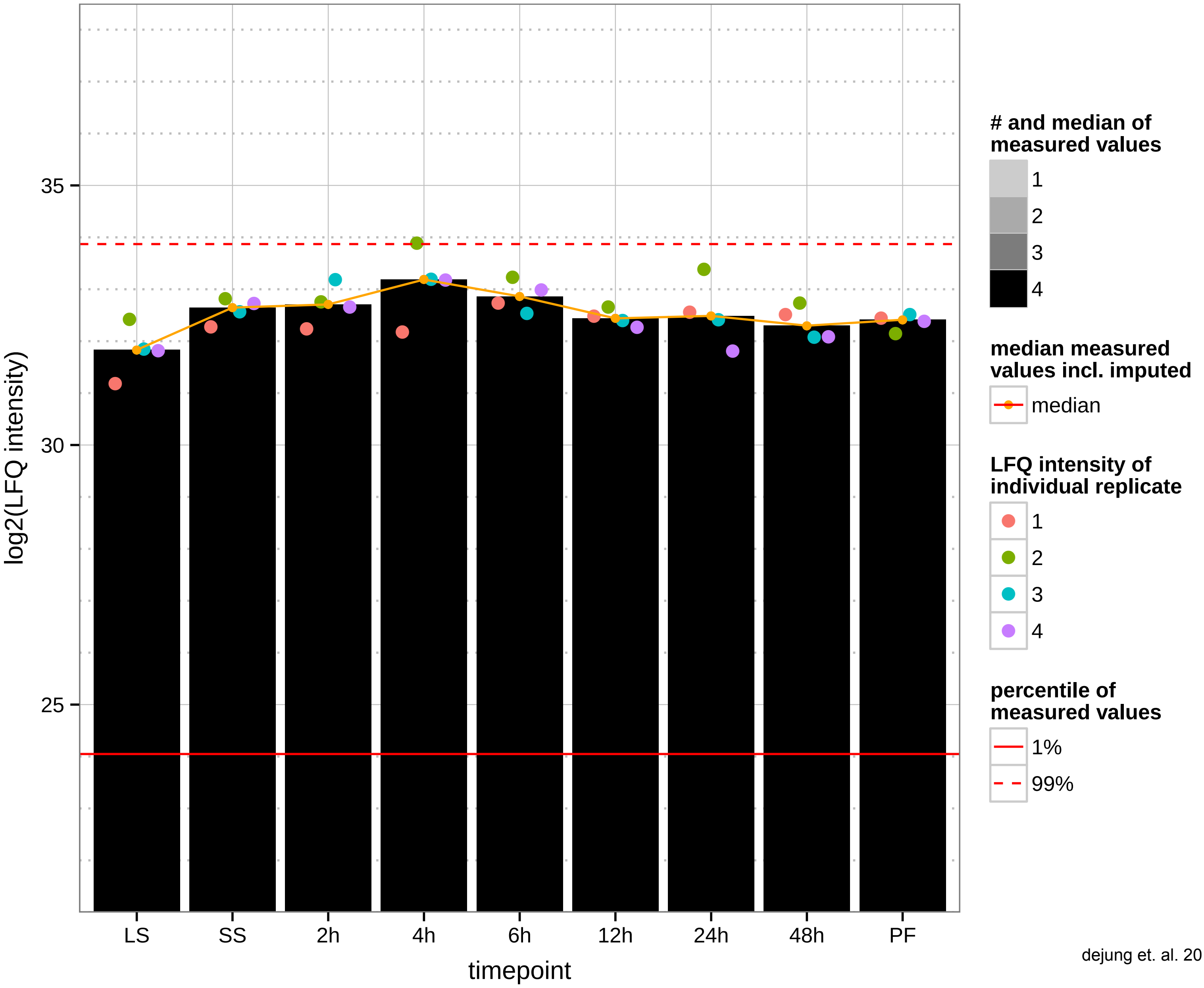
10 kDa heat shock protein, putative (HSP10)
Tb927.7.1340;Tb927.7.1320
AGOF: ATP binding, unfolded protein binding
AGOC: mitochondrial matrix, mitochondrial membrane, mitochondrion
AGOP: protein folding
PGOF: null
PGOC: cytoplasm
PGOP: protein folding





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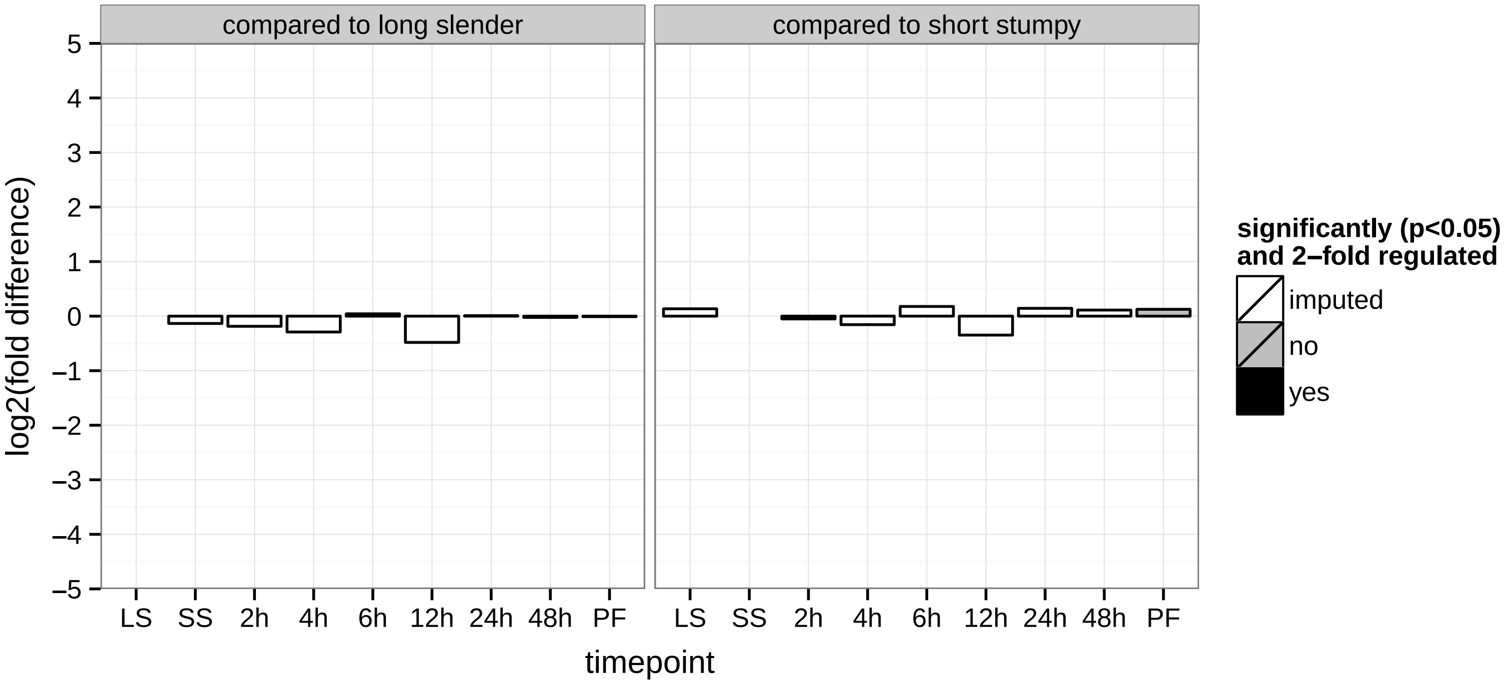
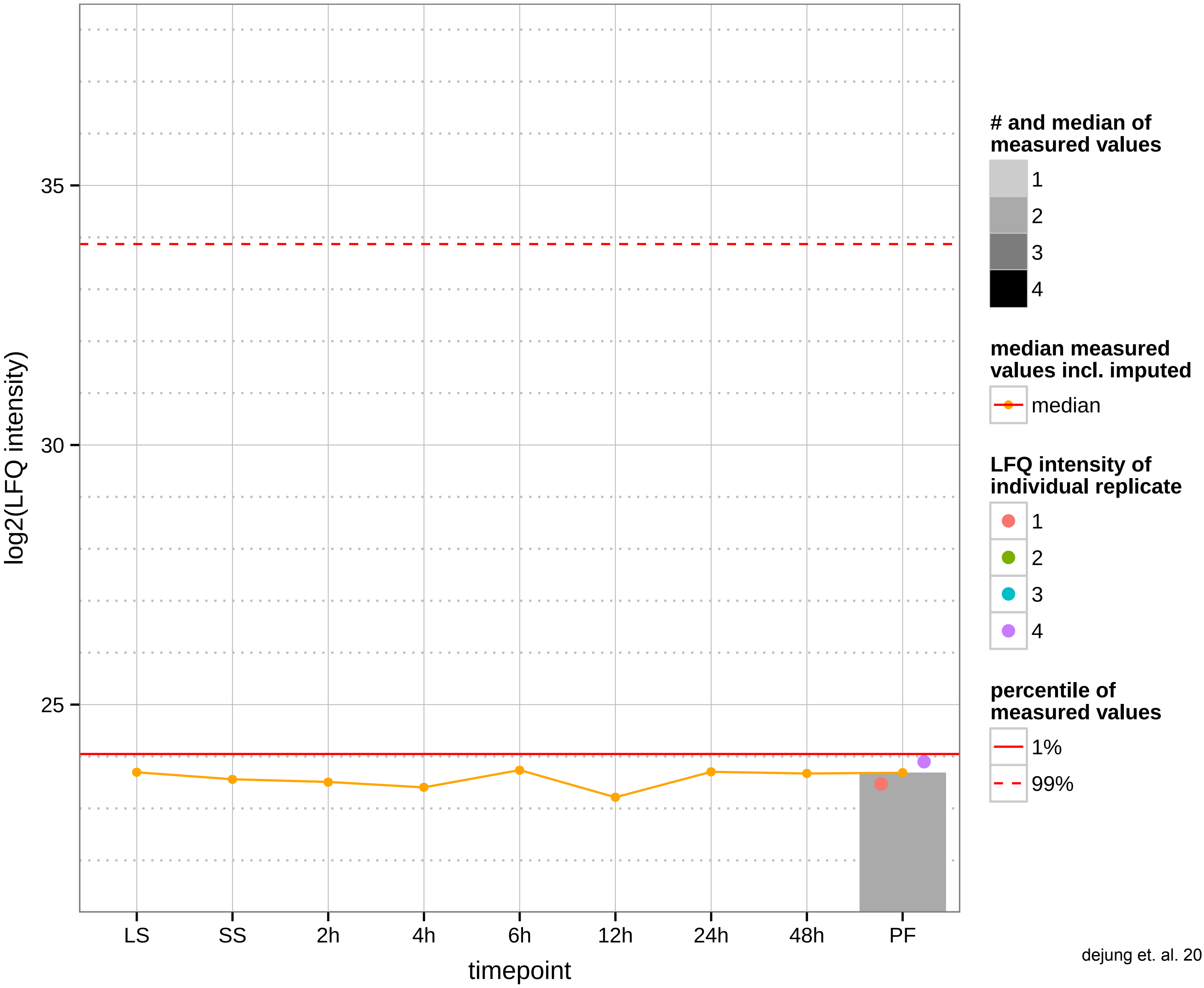
hypothetical protein, conserved
Tb927.7.1350
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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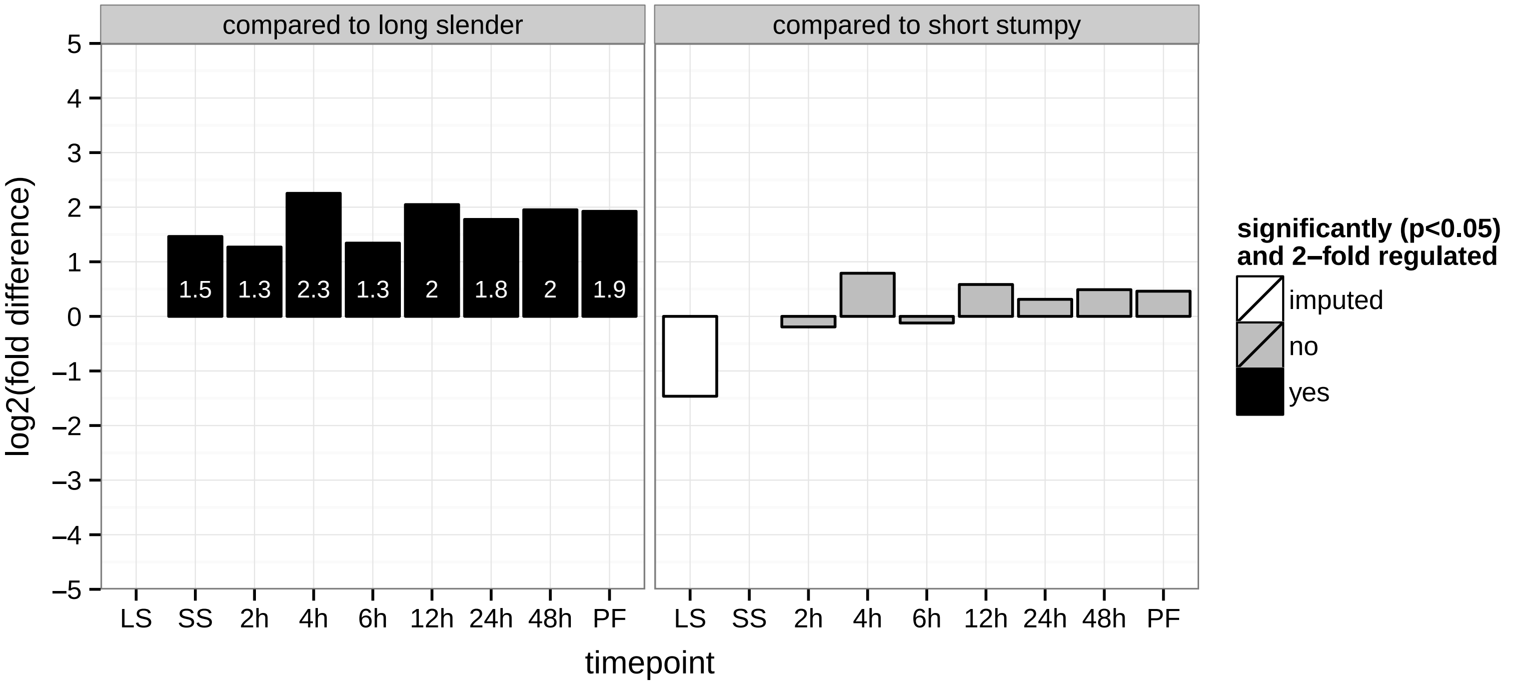
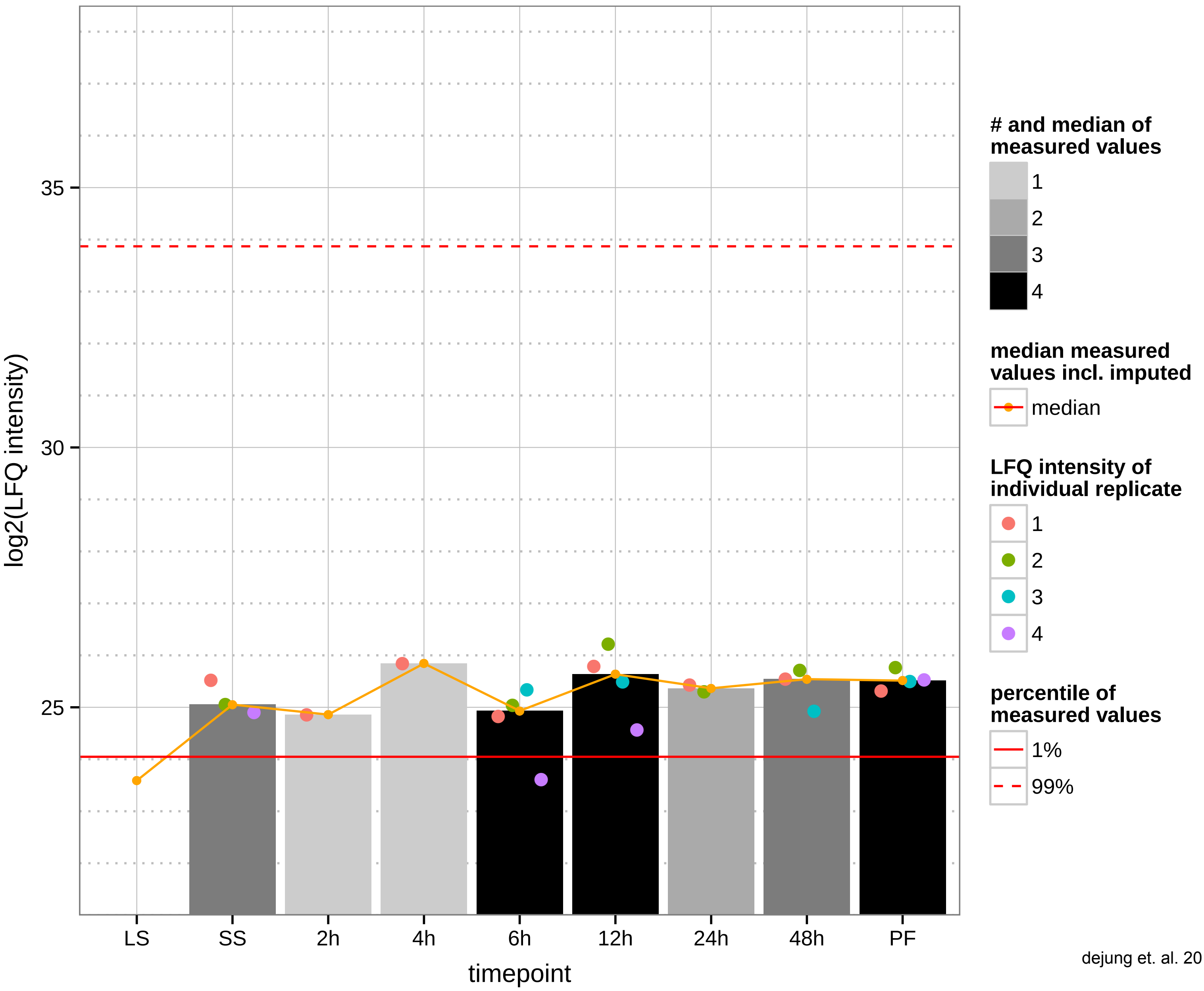
hypothetical protein, conserved
Tb927.7.1380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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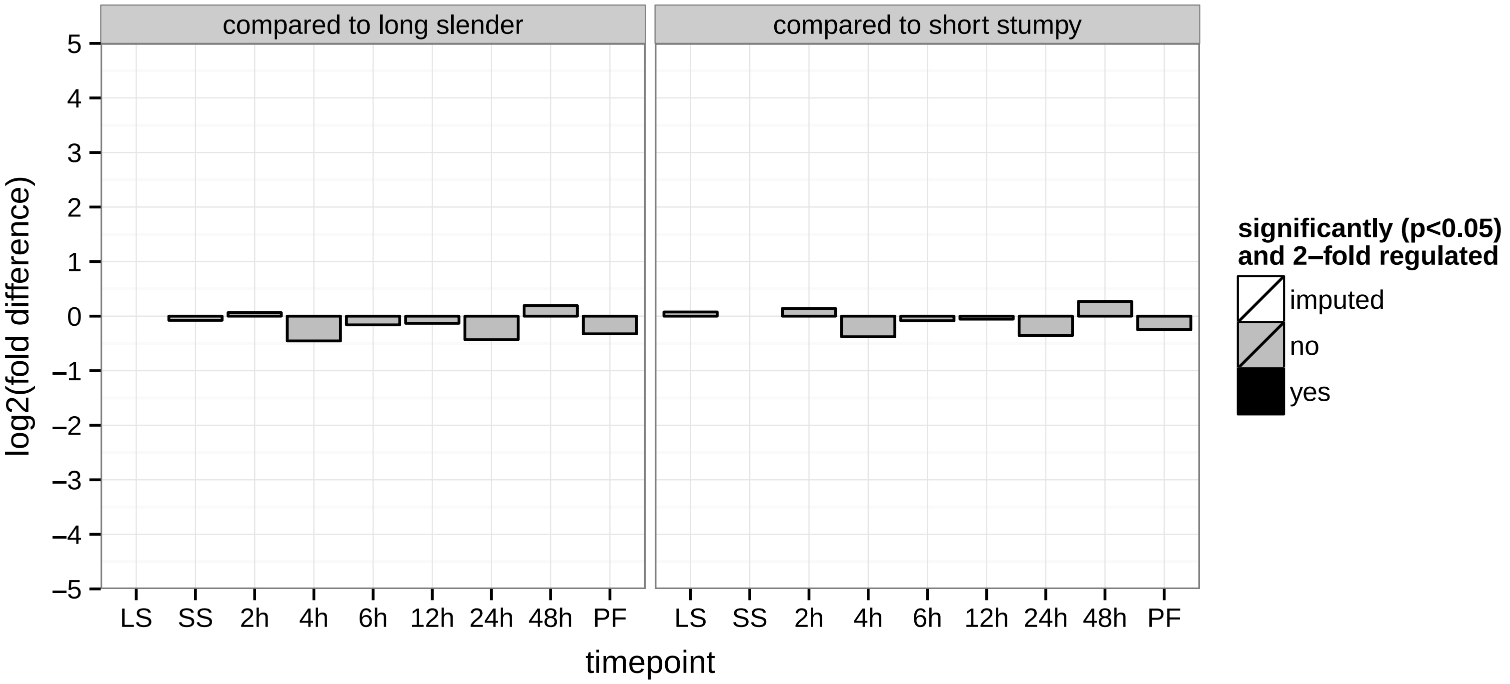
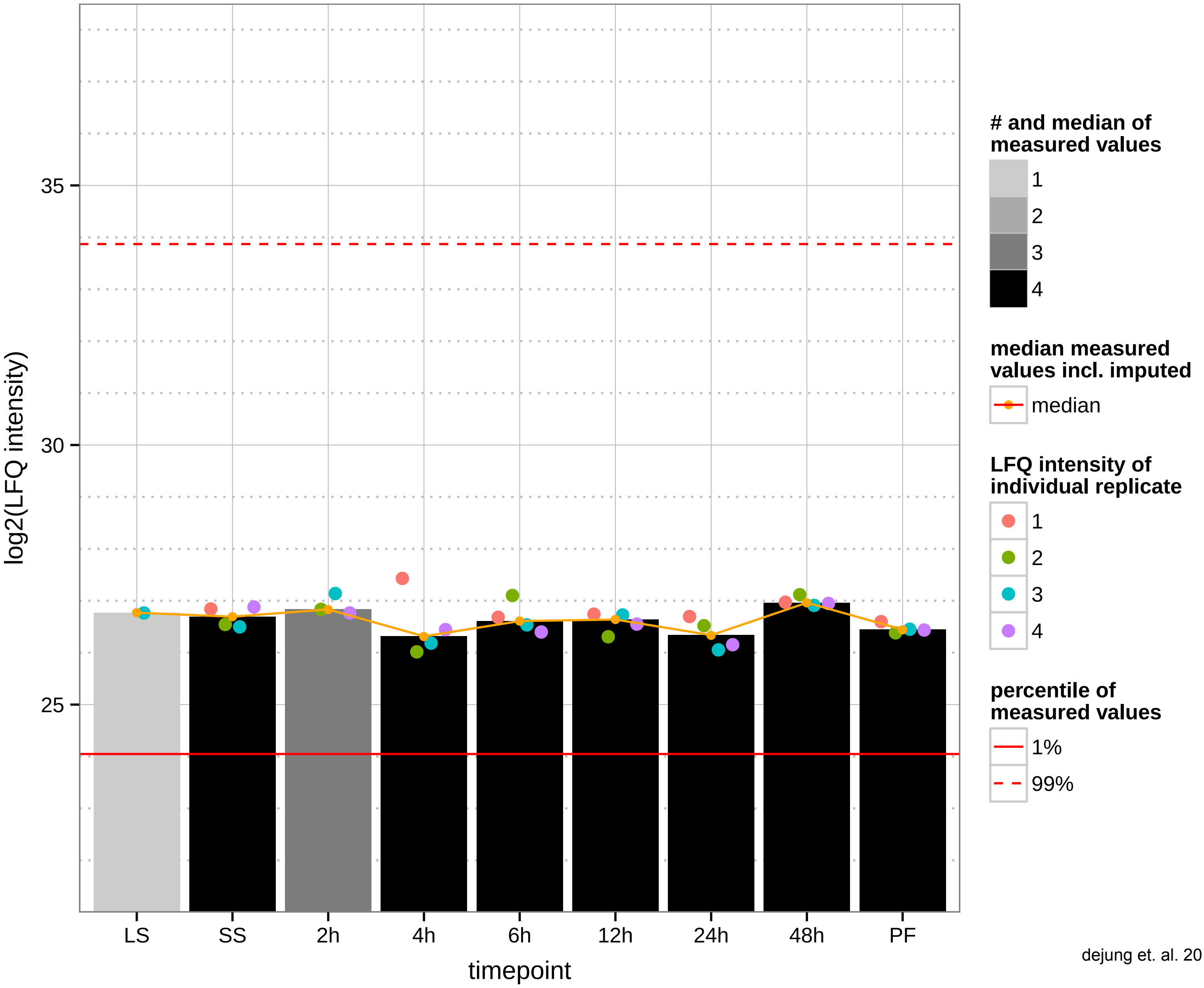
leucine–rich repeat protein (LRRP), putative
Tb927.7.1430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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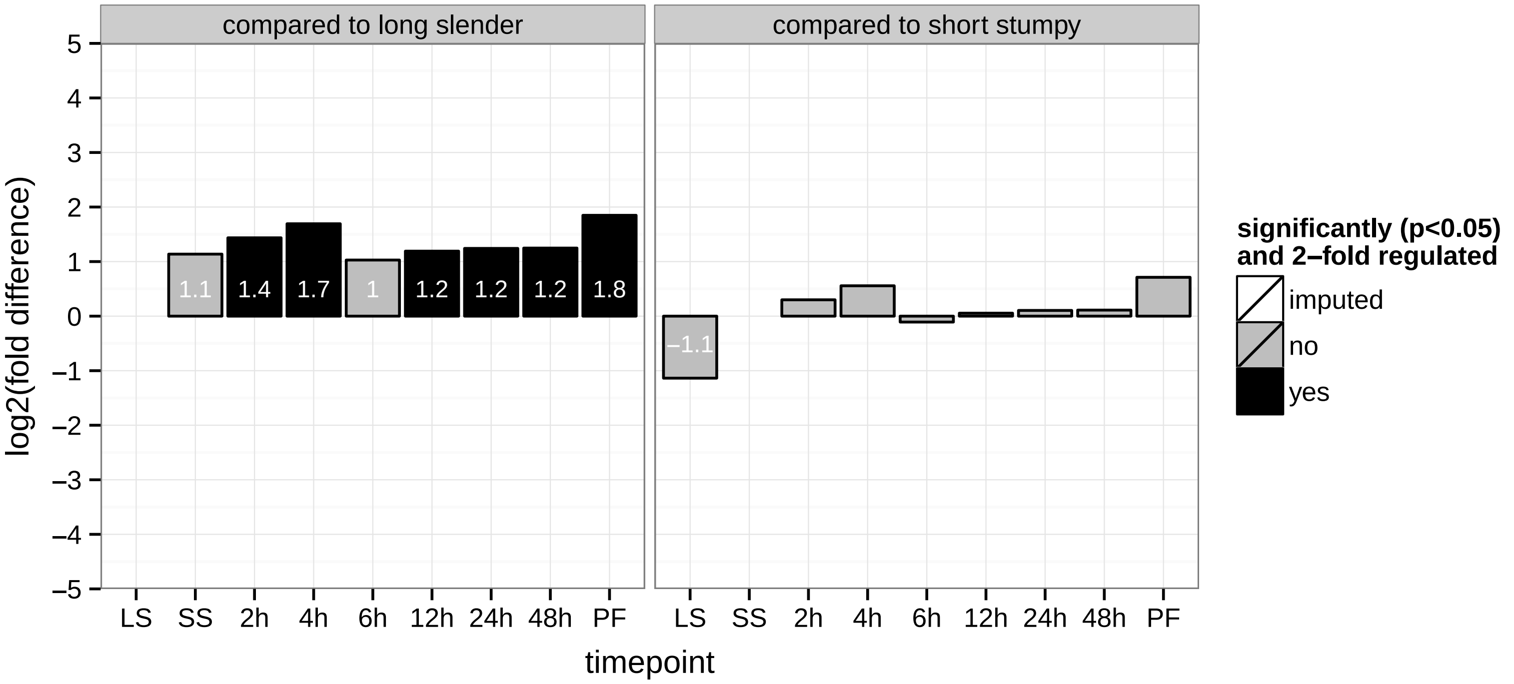
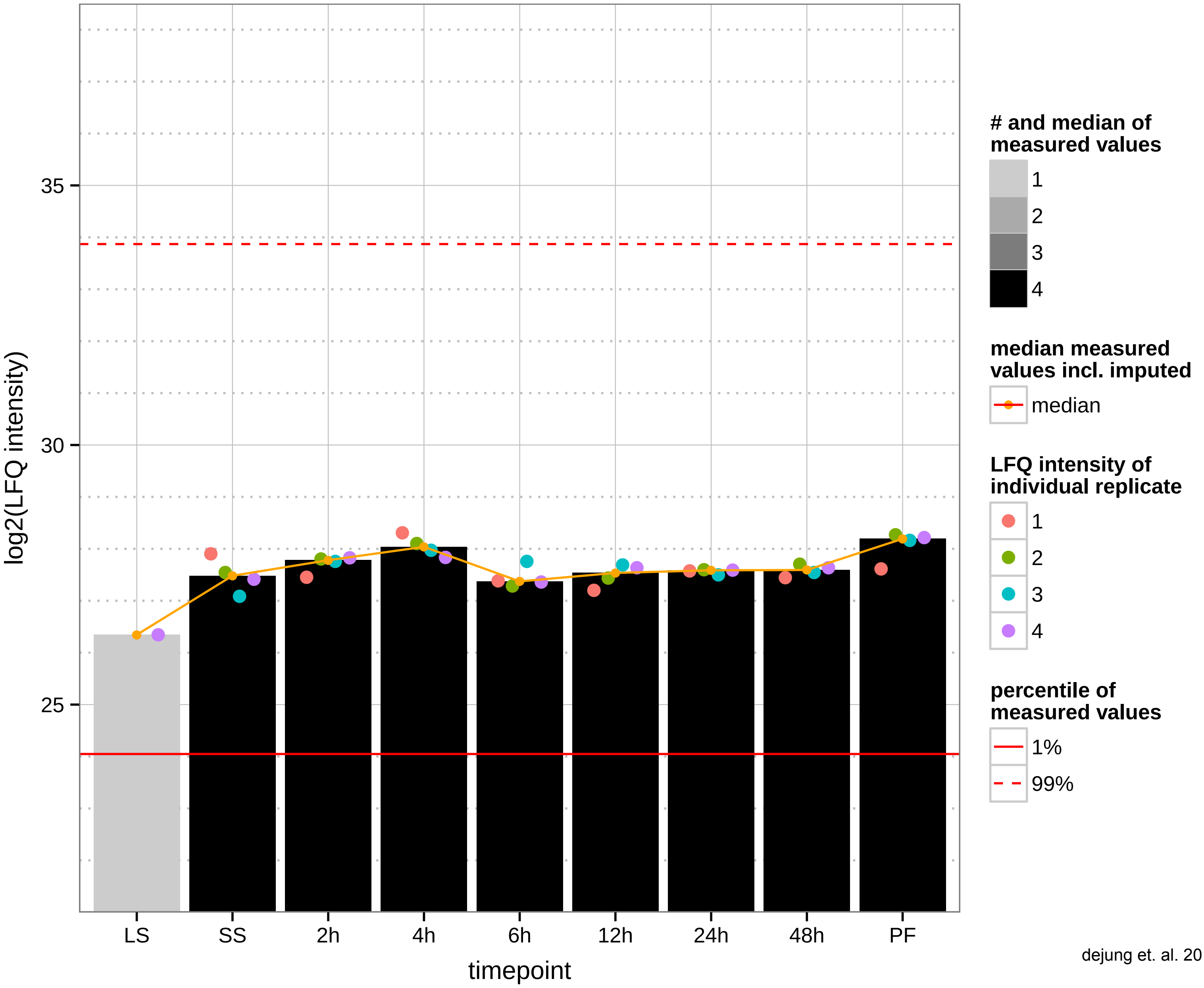
nucleotide binding protein, putative (NBP 2)
Tb927.7.1500
AGOF: nucleotide binding
AGOC: cytosol
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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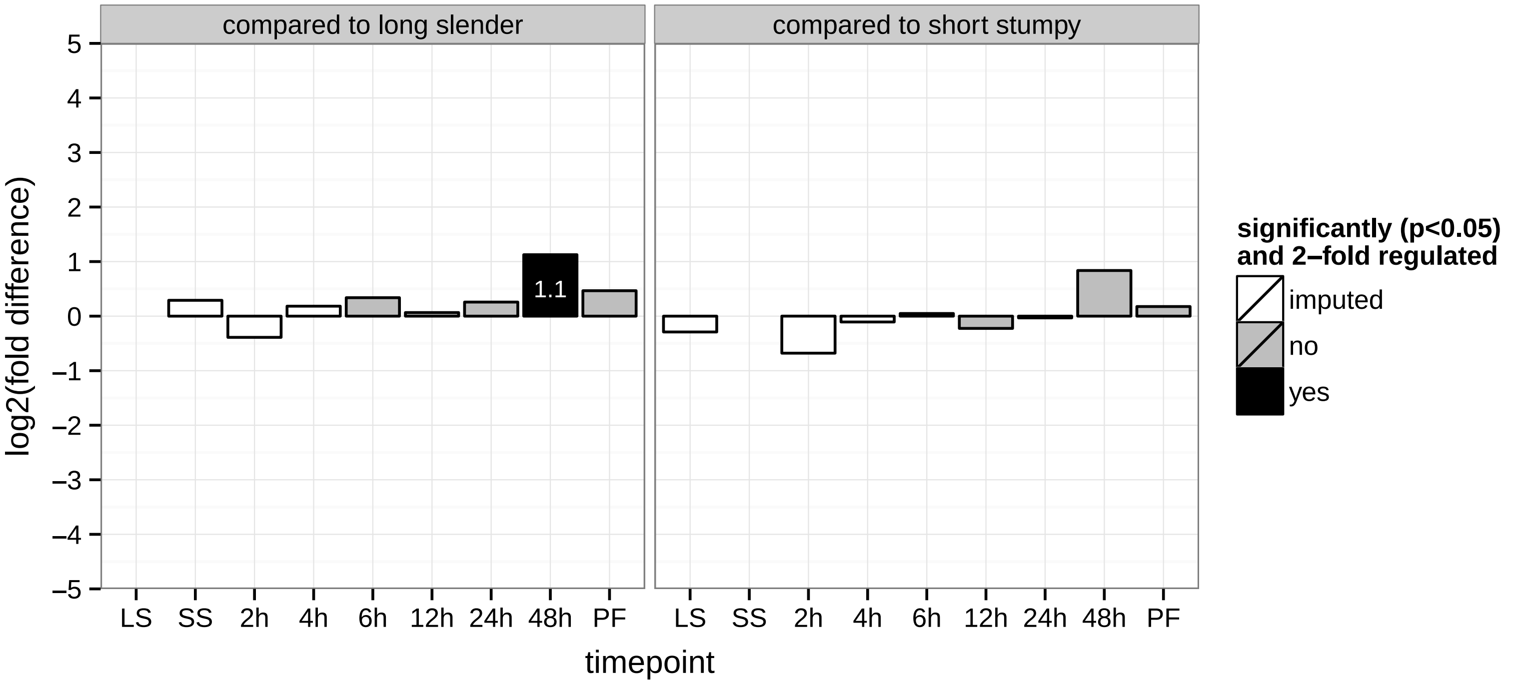
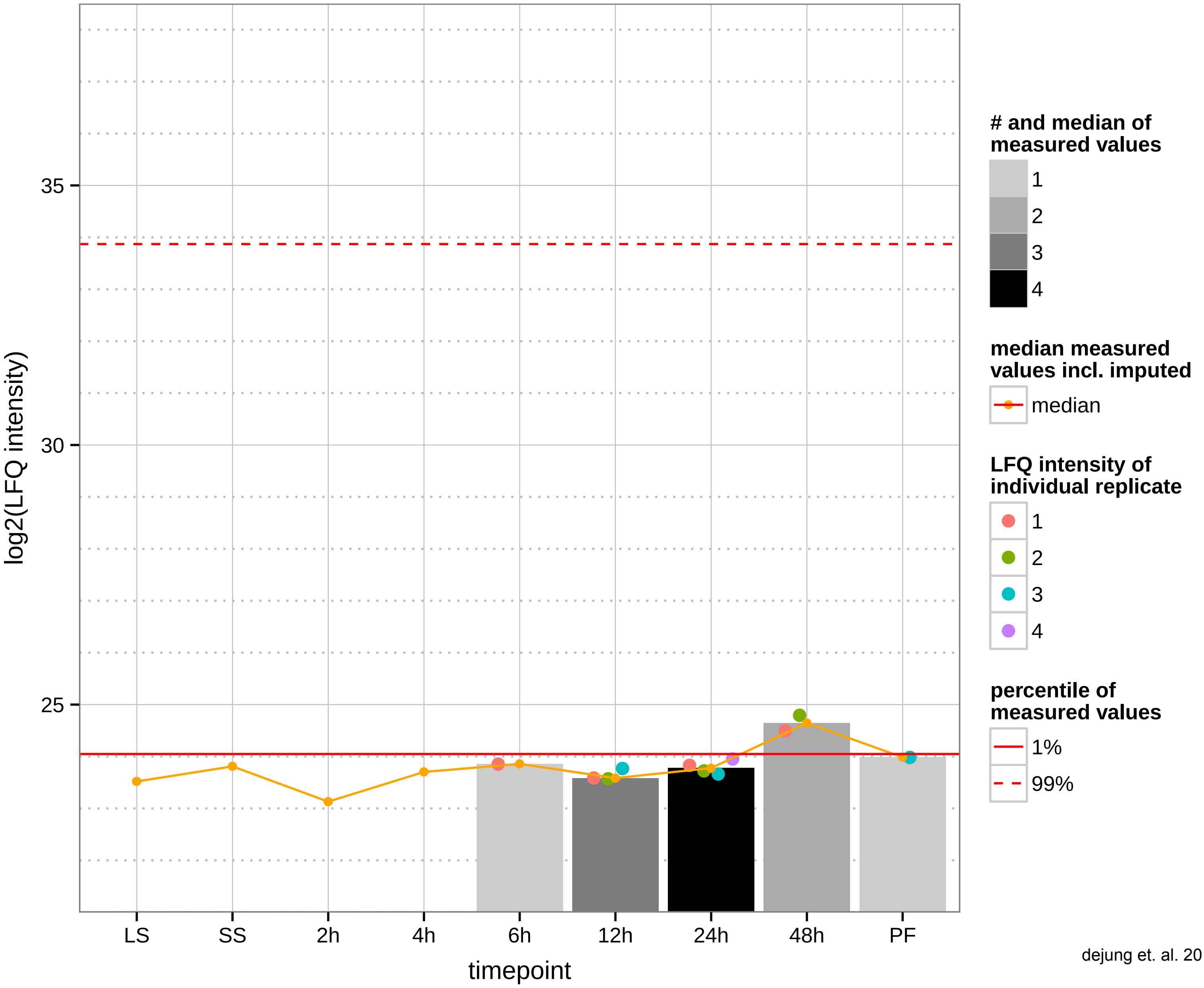
pseudouridylate synthase I, putative
Tb927.7.1510
AGOF: RNA binding, pseudouridine synthase activity
AGOC: null
AGOP: pseudouridine synthesis
PGOF: RNA binding, pseudouridine synthase activity
PGOC: null
PGOP: RNA modification, pseudouridine synthesis





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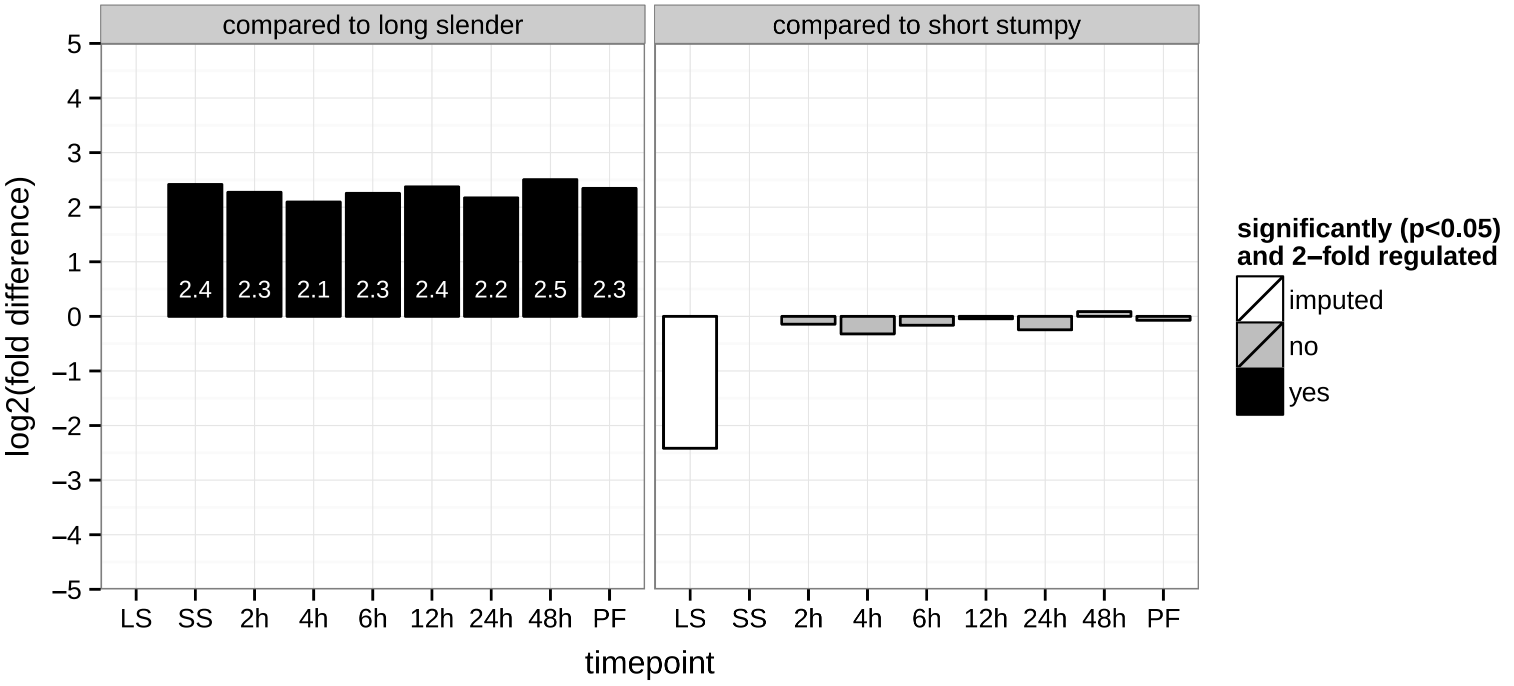
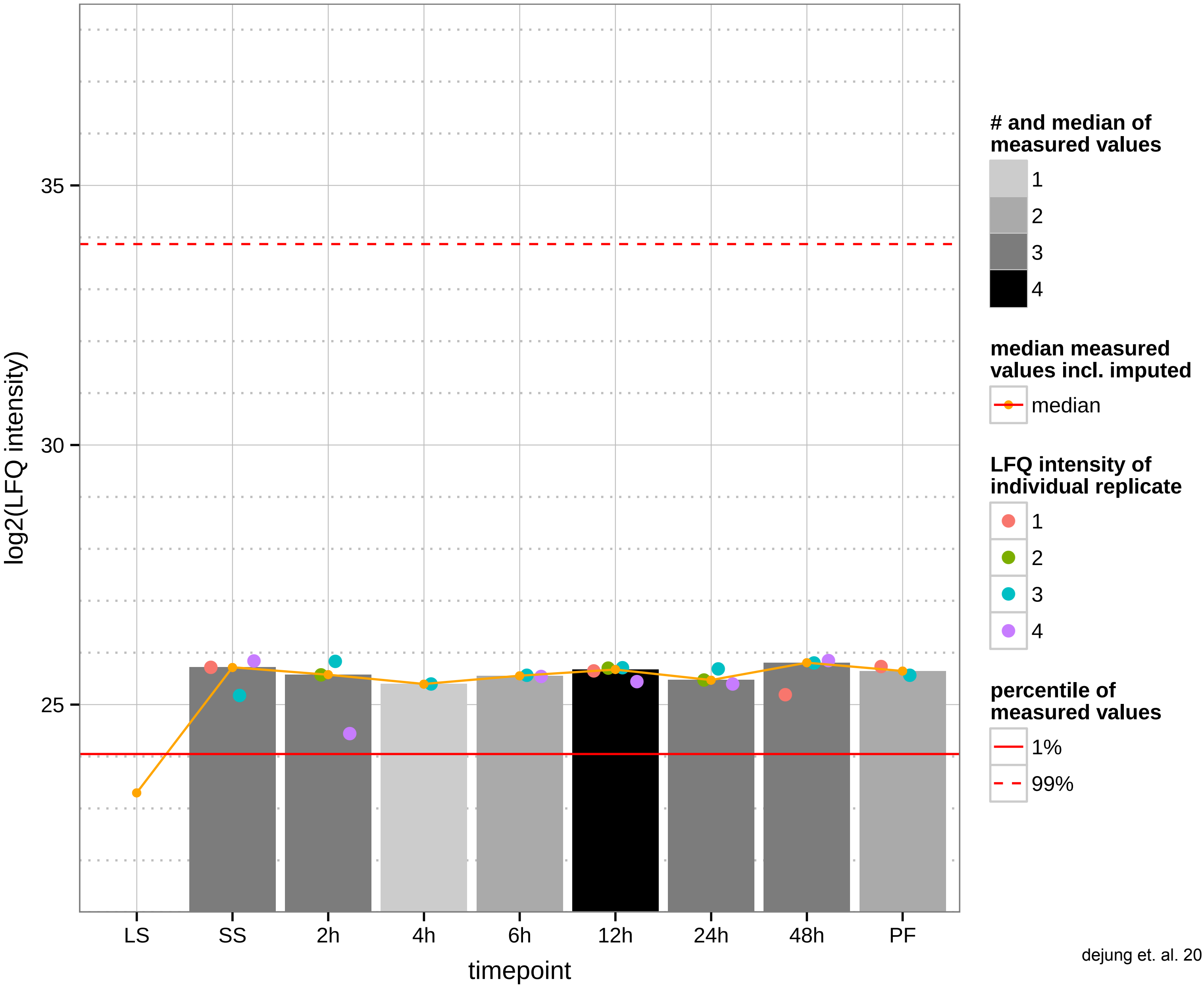
hypothetical protein, conserved
Tb927.7.1630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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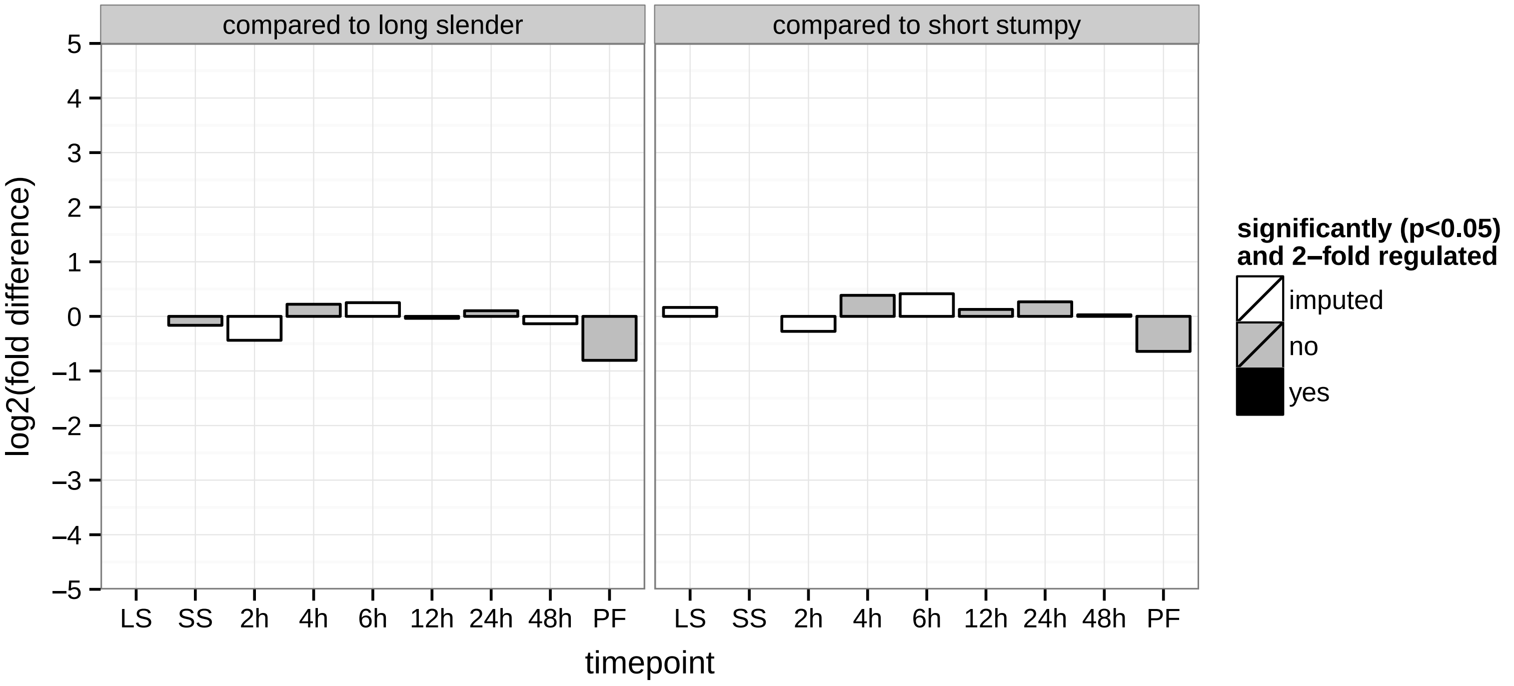
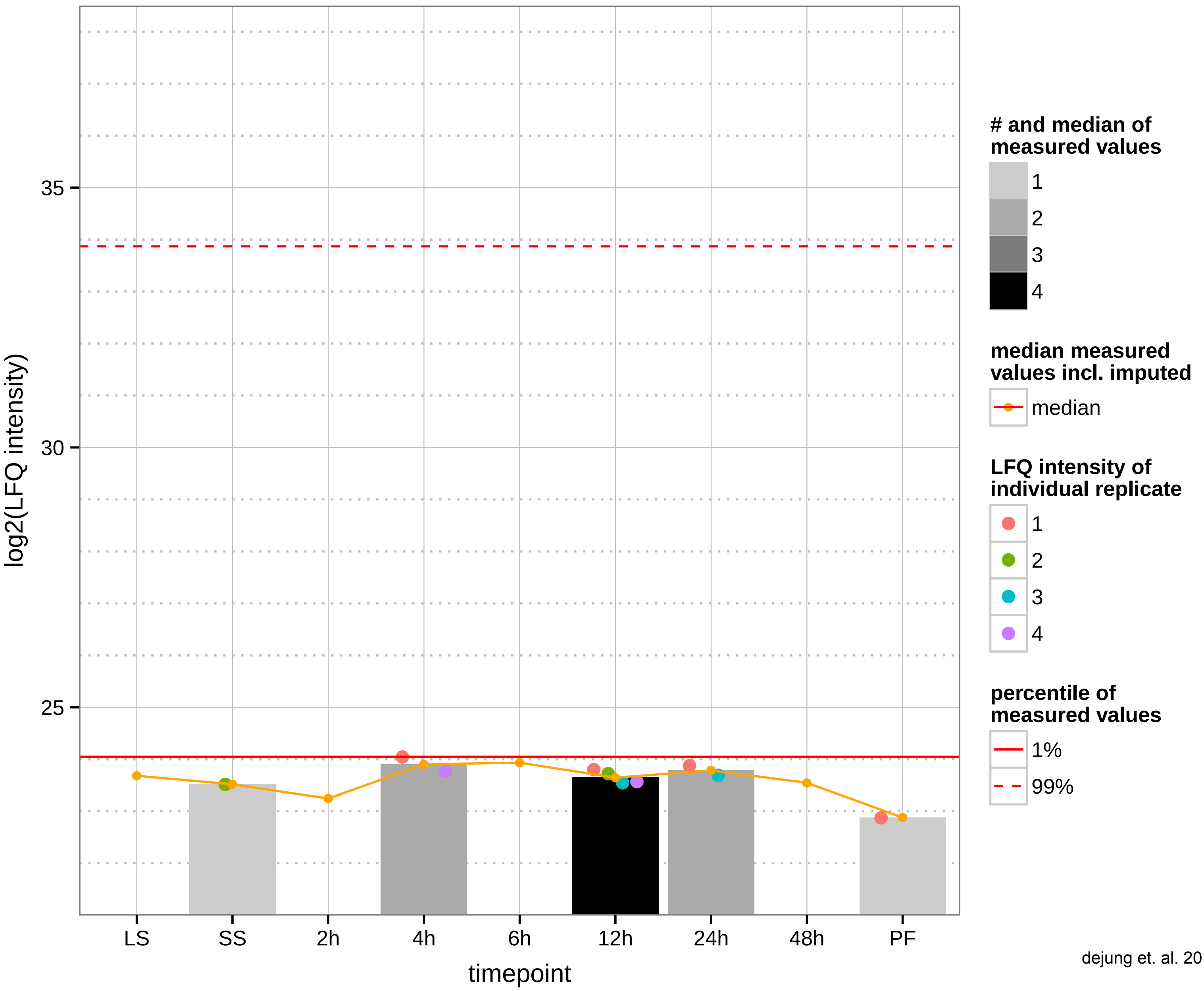
hypothetical protein, conserved
Tb927.7.1650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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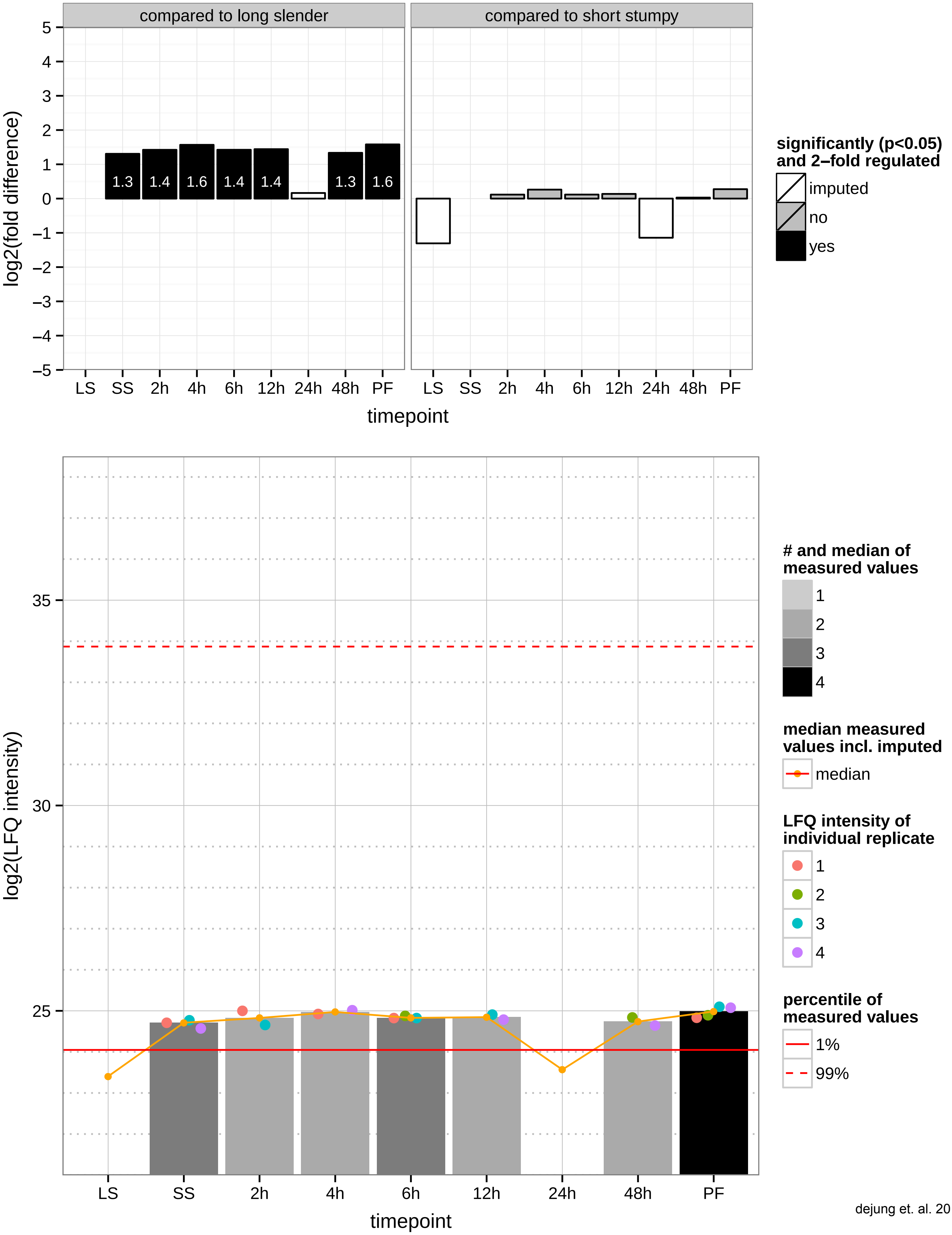
hypothetical protein, conserved
Tb927.7.1770
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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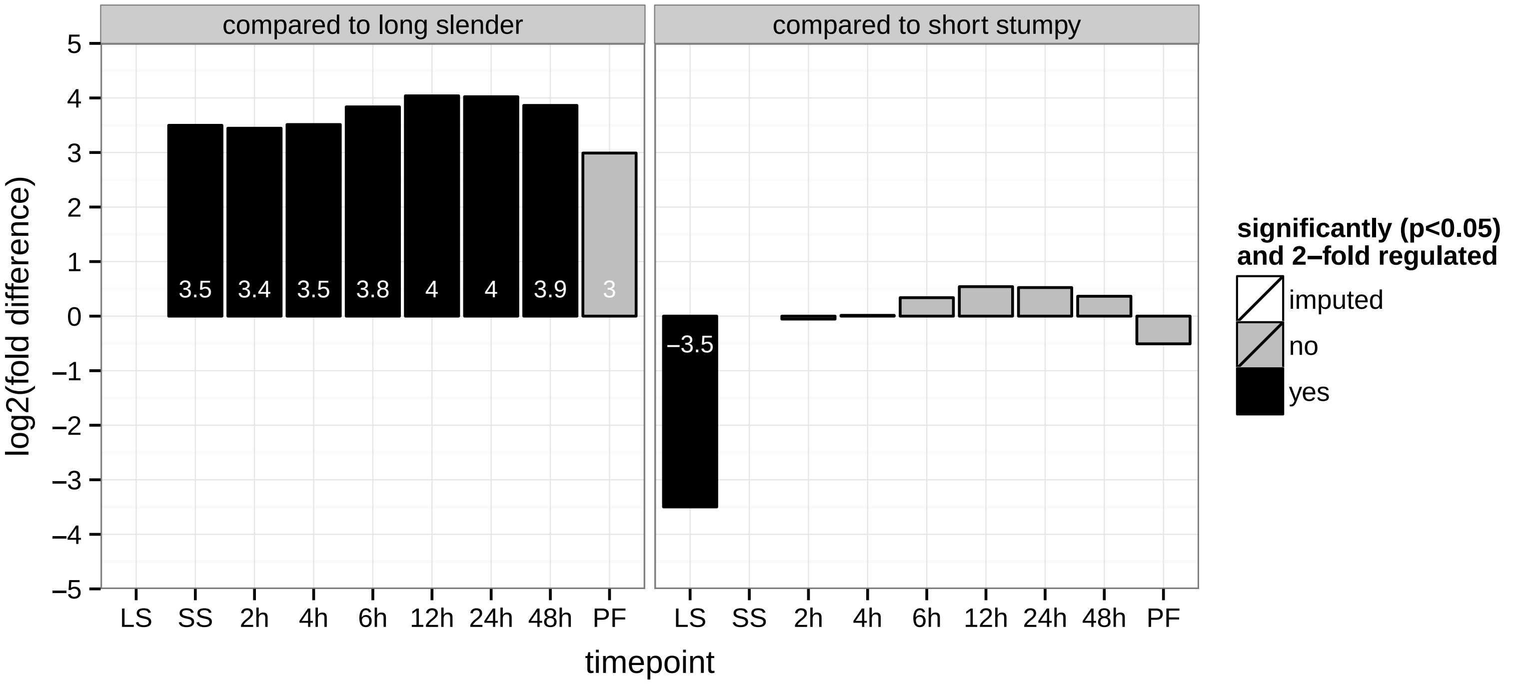
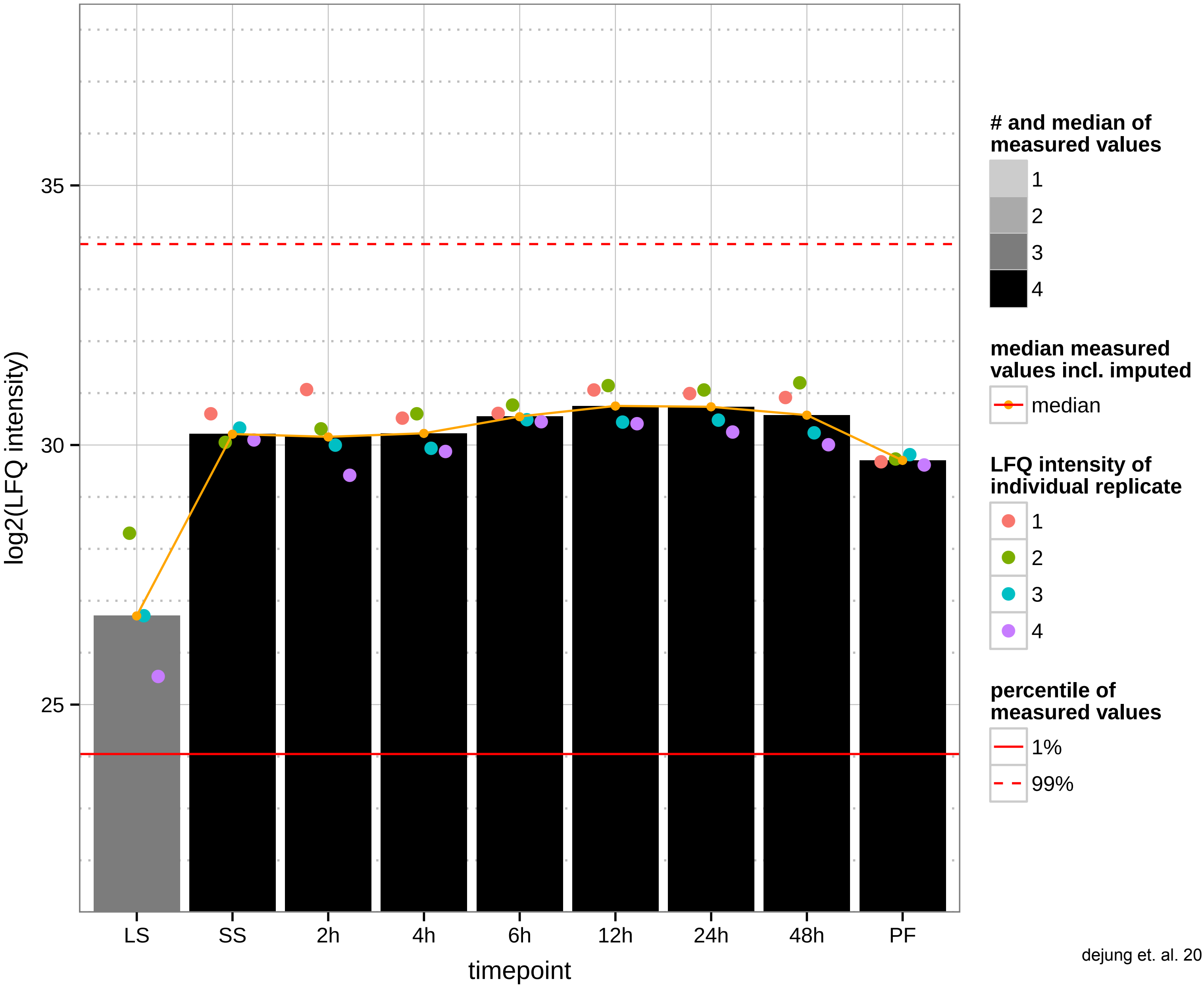
Adenine phosphoribosyltransferase, putative
Tb927.7.1790
AGOF: adenine phosphoribosyltransferase activity
AGOC: null
AGOP: purine ribonucleoside salvage
PGOF: null
PGOC: null
PGOP: nucleoside metabolic process





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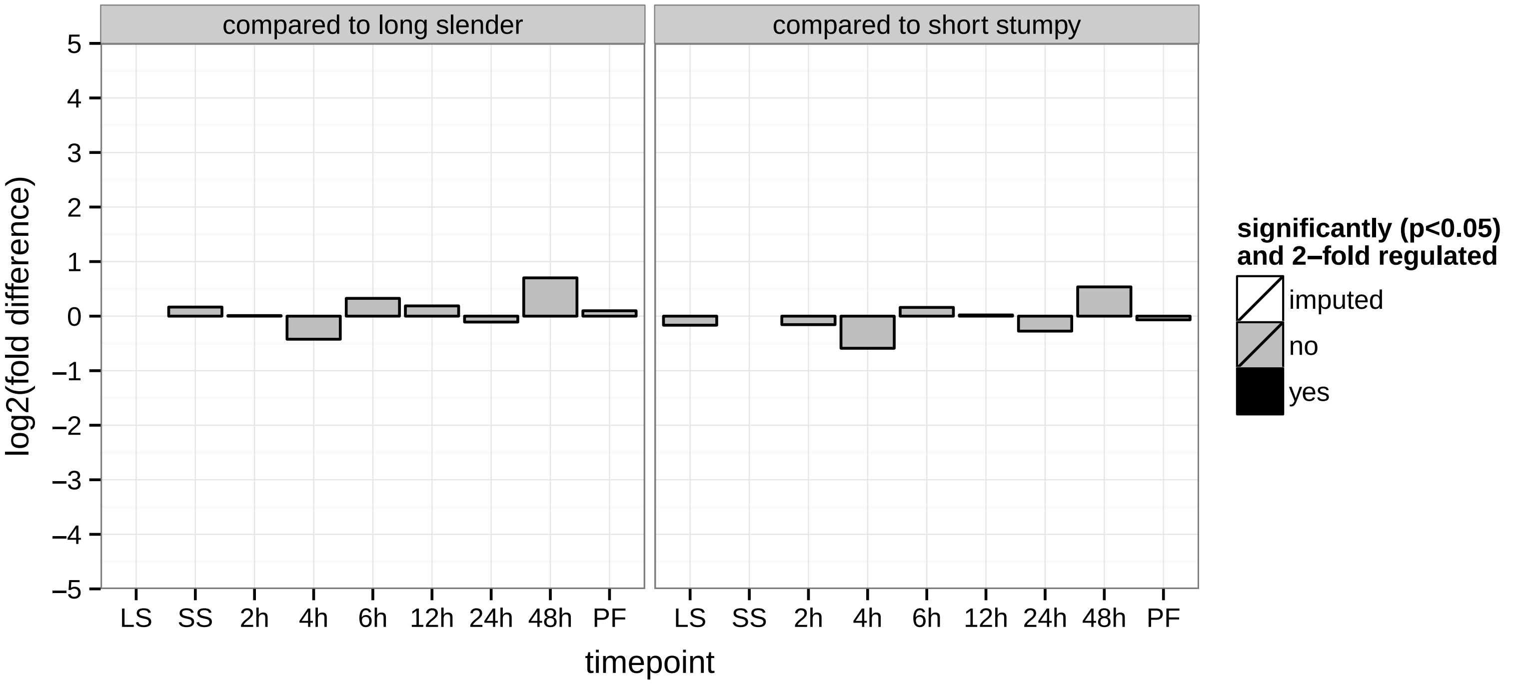
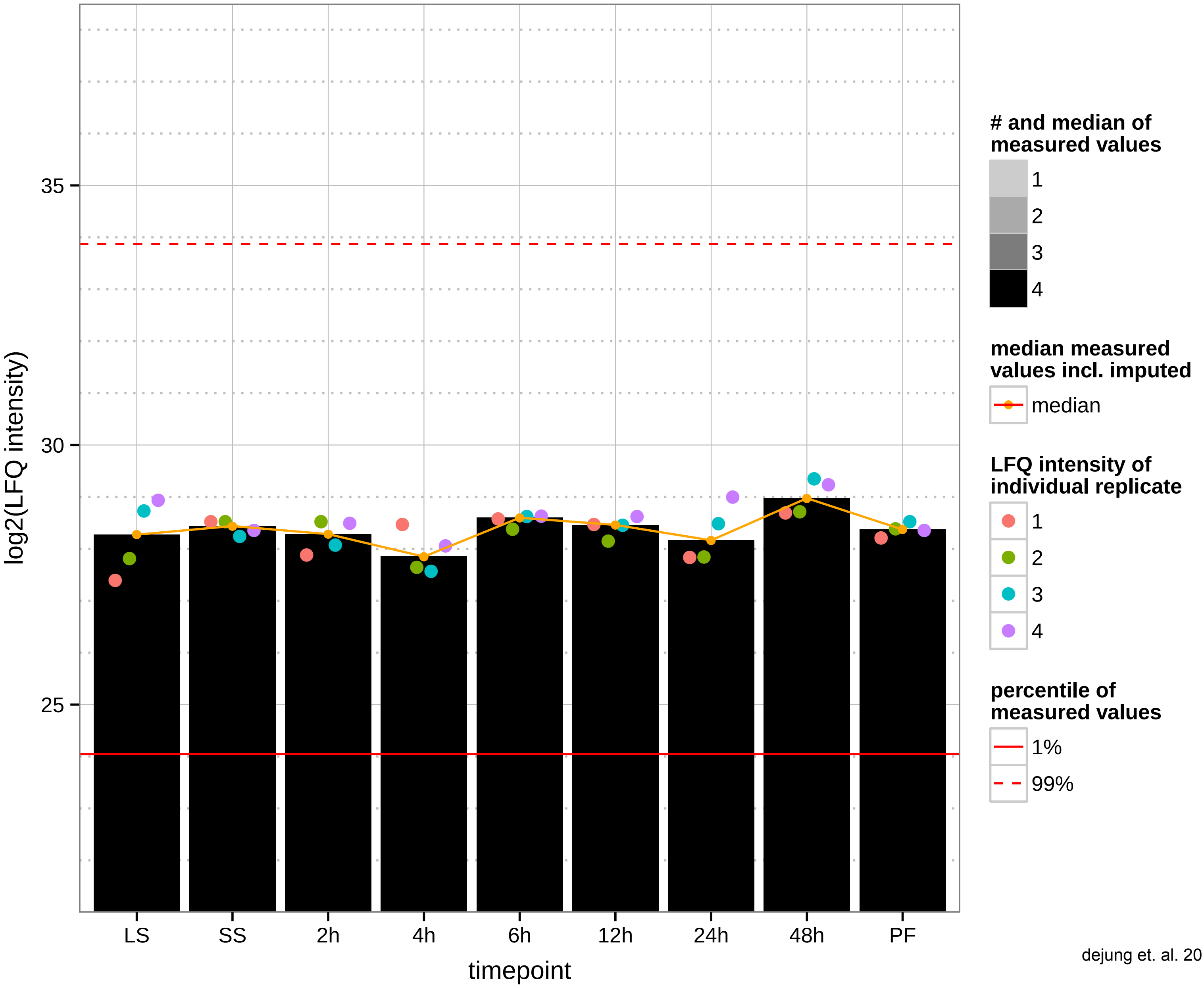
paraflagellar rod component, putative (PFC5)
Tb927.7.1920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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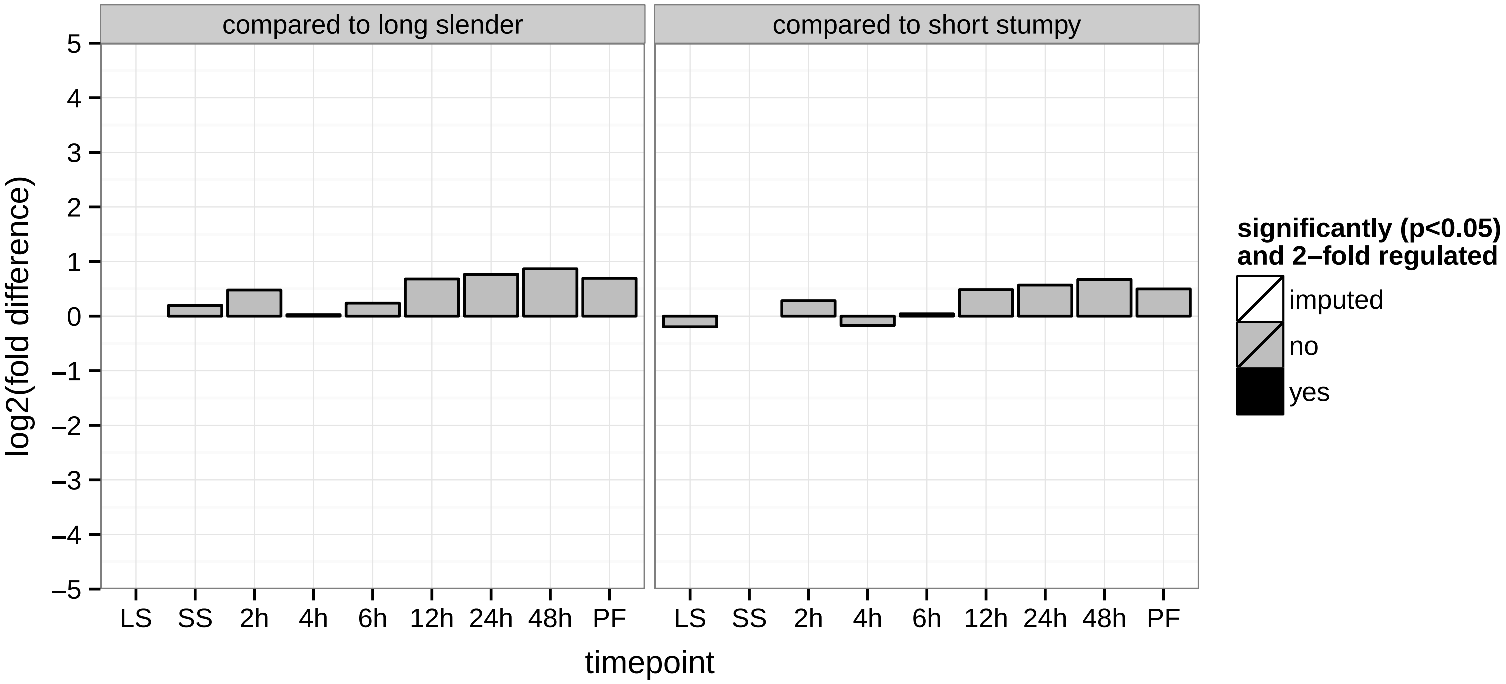
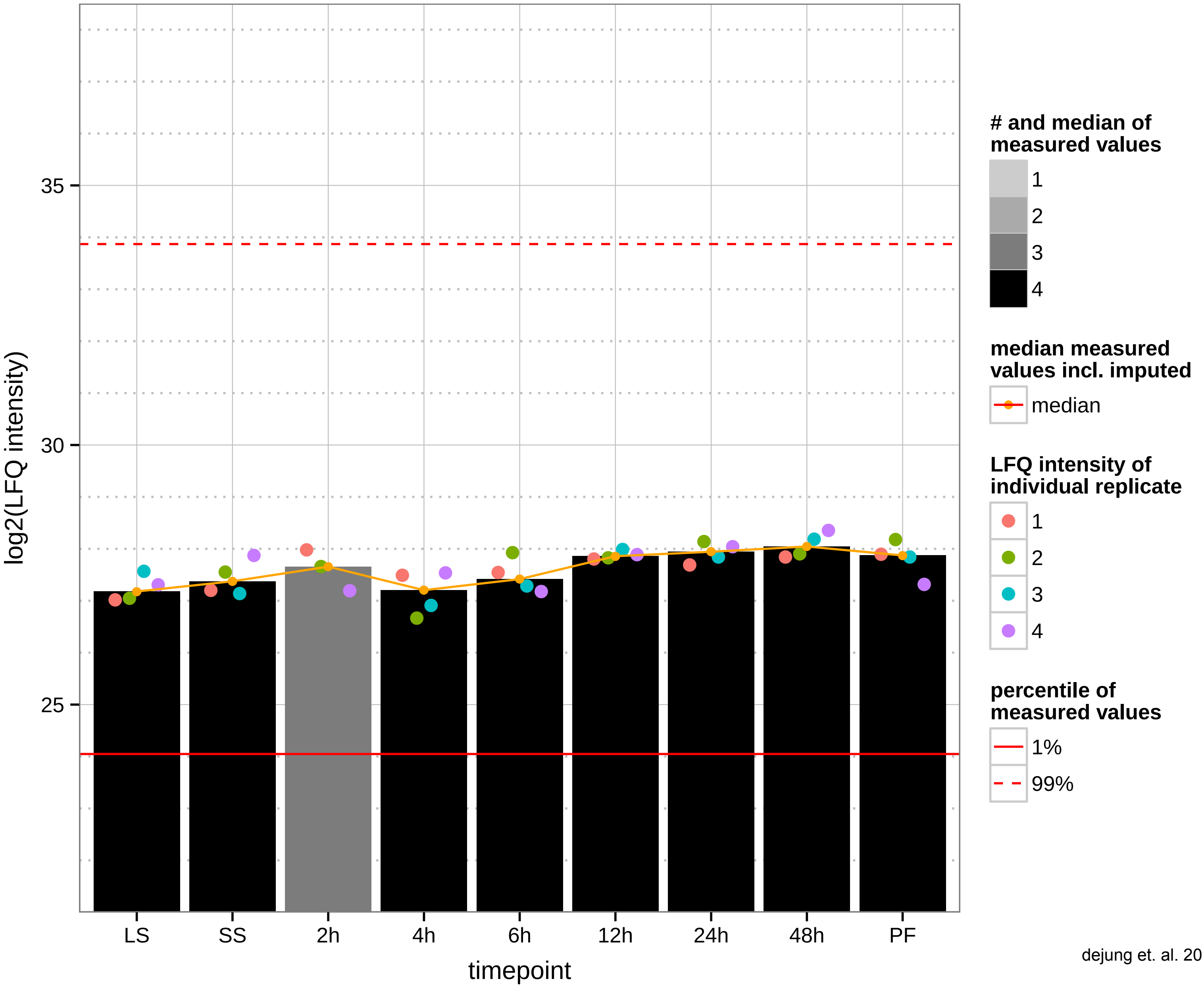
heat shock protein DNAJ, putative
Tb927.7.2070
AGOF: heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding, unfolded protein binding
PGOC: null
PGOP: protein folding





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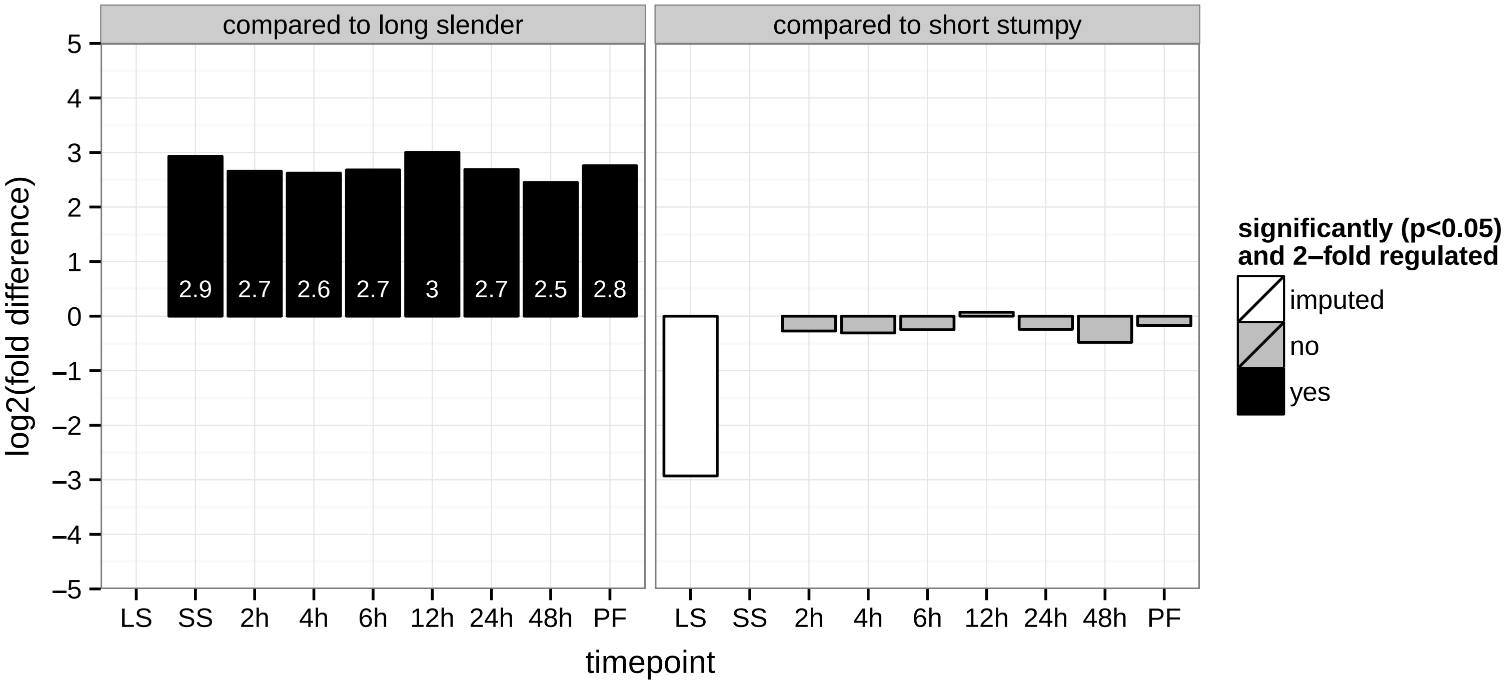
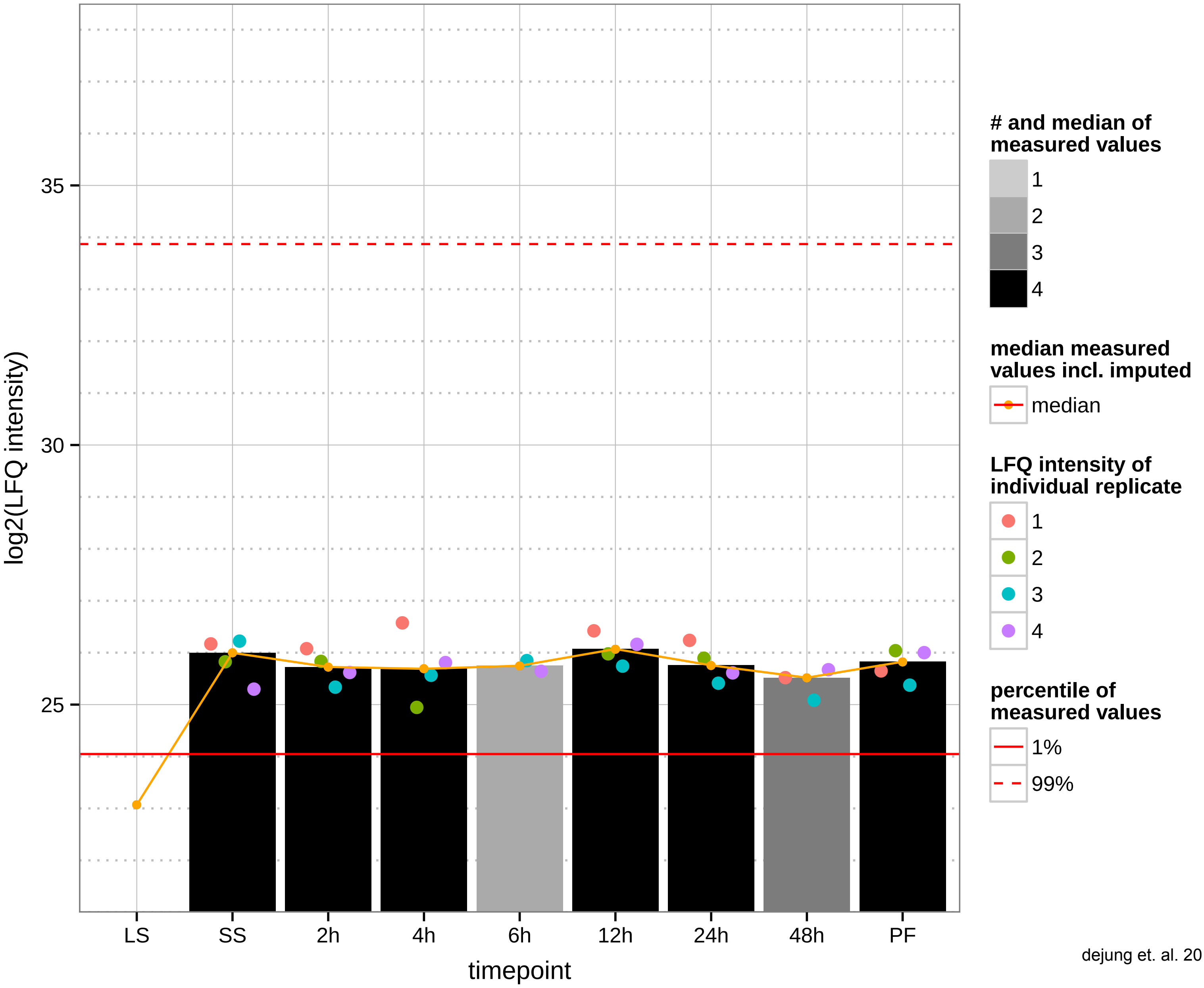
methyltransferase, putative, mRNA cap methyltransferase−like protein
Tb927.7.2080
AGOF: null
AGOC: null
AGOP: 7−methylguanosine mRNA capping
PGOF: mRNA guanylyltransferase activity
PGOC: null
PGOP: 7−methylguanosine mRNA capping





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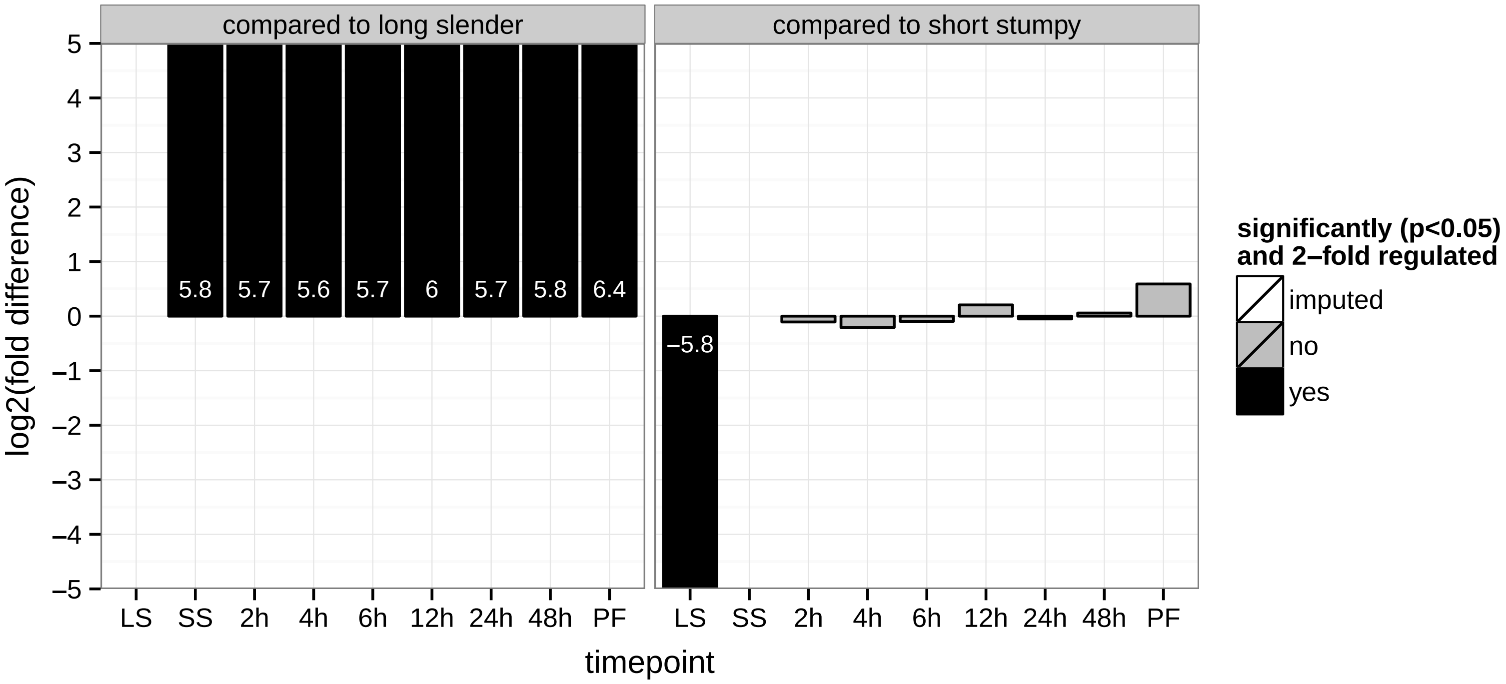
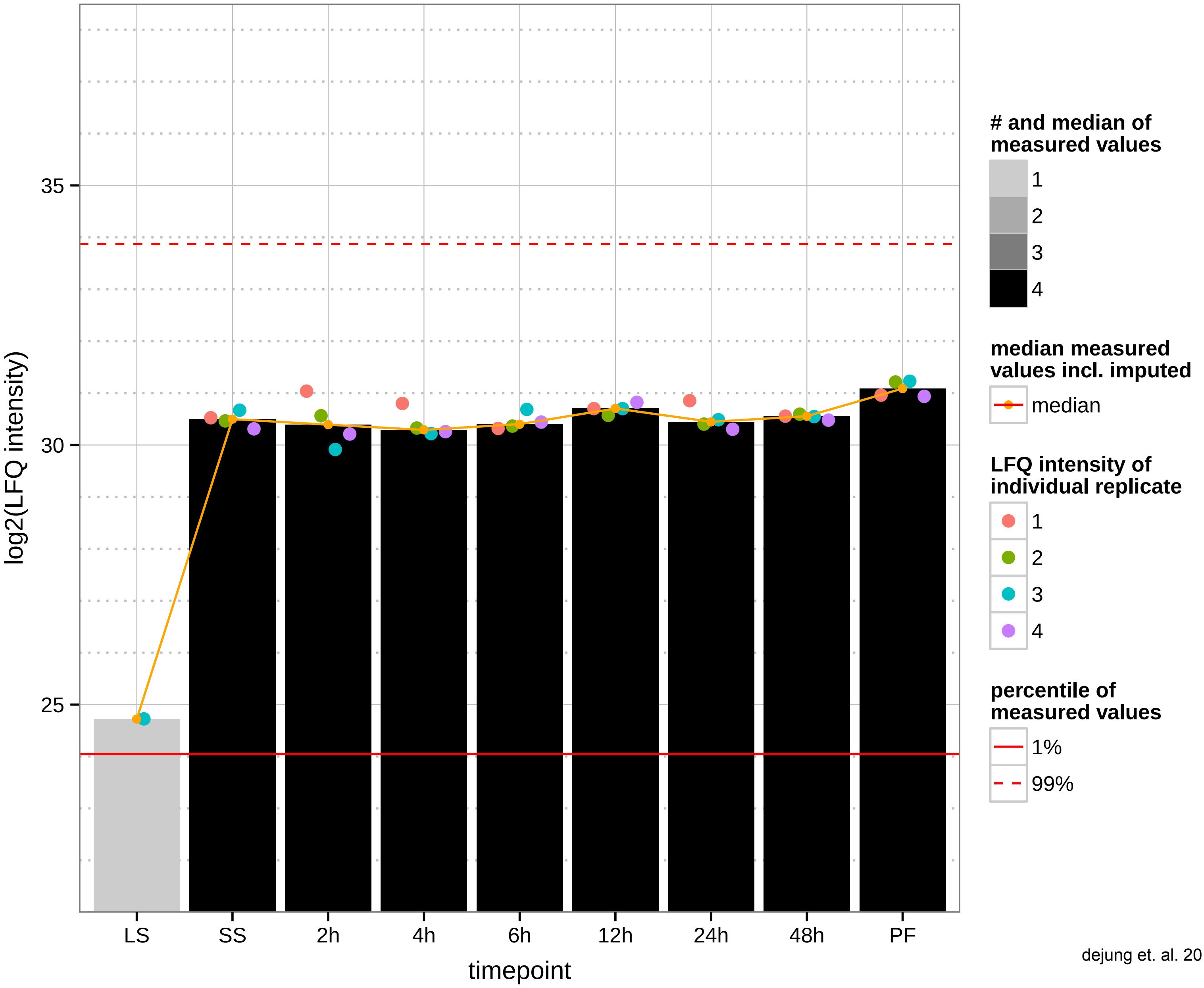
proline dehydrogenase
Tb927.7.210
AGOF: proline dehydrogenase activity
AGOC: null
AGOP: glutamate biosynthetic process, proline catabolic process
PGOF: proline dehydrogenase activity
PGOC: null
PGOP: glutamate biosynthetic process, oxidation–reduction process, proline catabolic process





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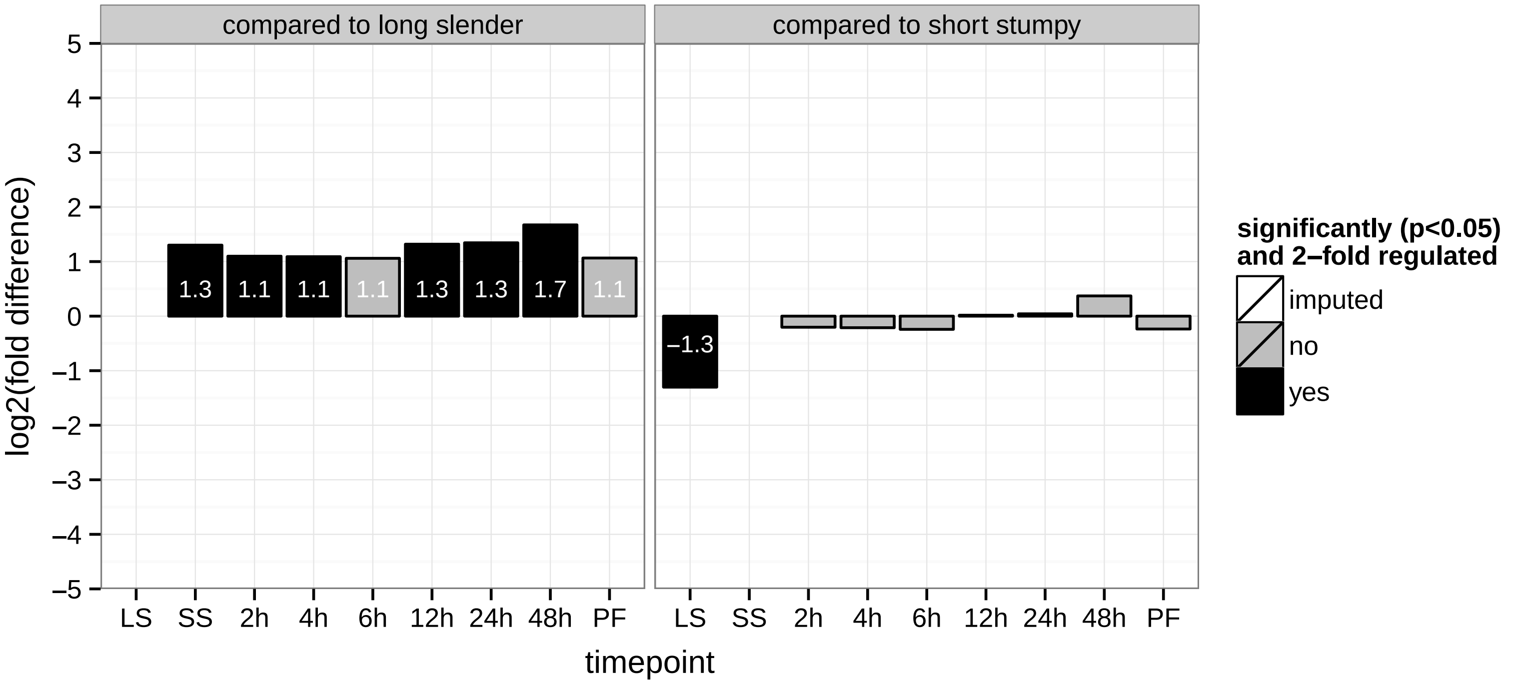
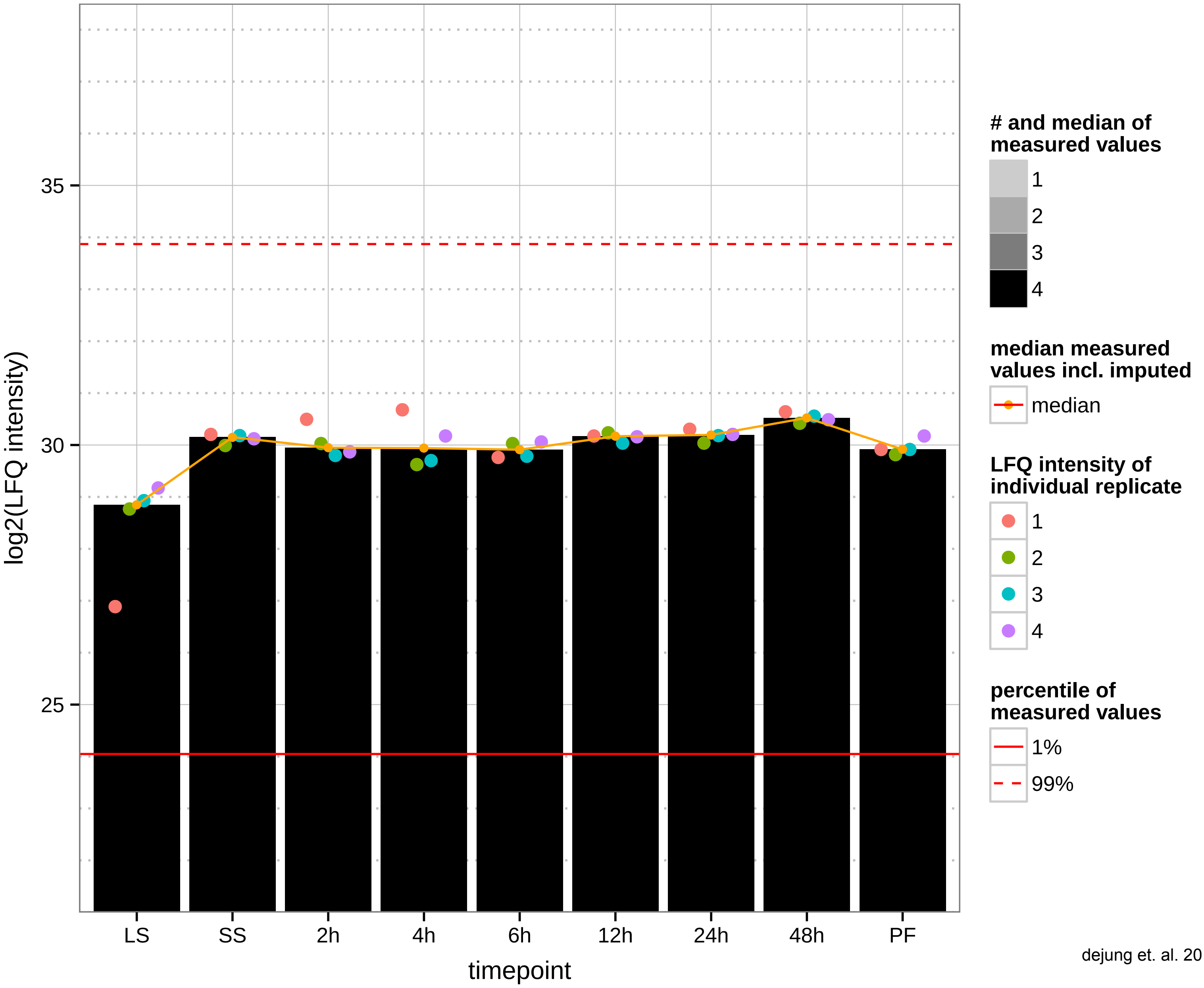
GMP synthase, putative, glutamine amidotransferase
Tb927.7.2100
AGOF: ATP binding, GMP synthase (glutamine−hydrolyzing) activity
AGOC: null
AGOP: GMP biosynthetic process, biosynthetic process, glutamine metabolic process, purine ribonucleotide biosynthetic proc
PGOF: ATP binding, GMP synthase (glutamine−hydrolyzing) activity, pyrophosphatase activity
PGOC: null
PGOP: GMP biosynthetic process, purine nucleotide biosynthetic process





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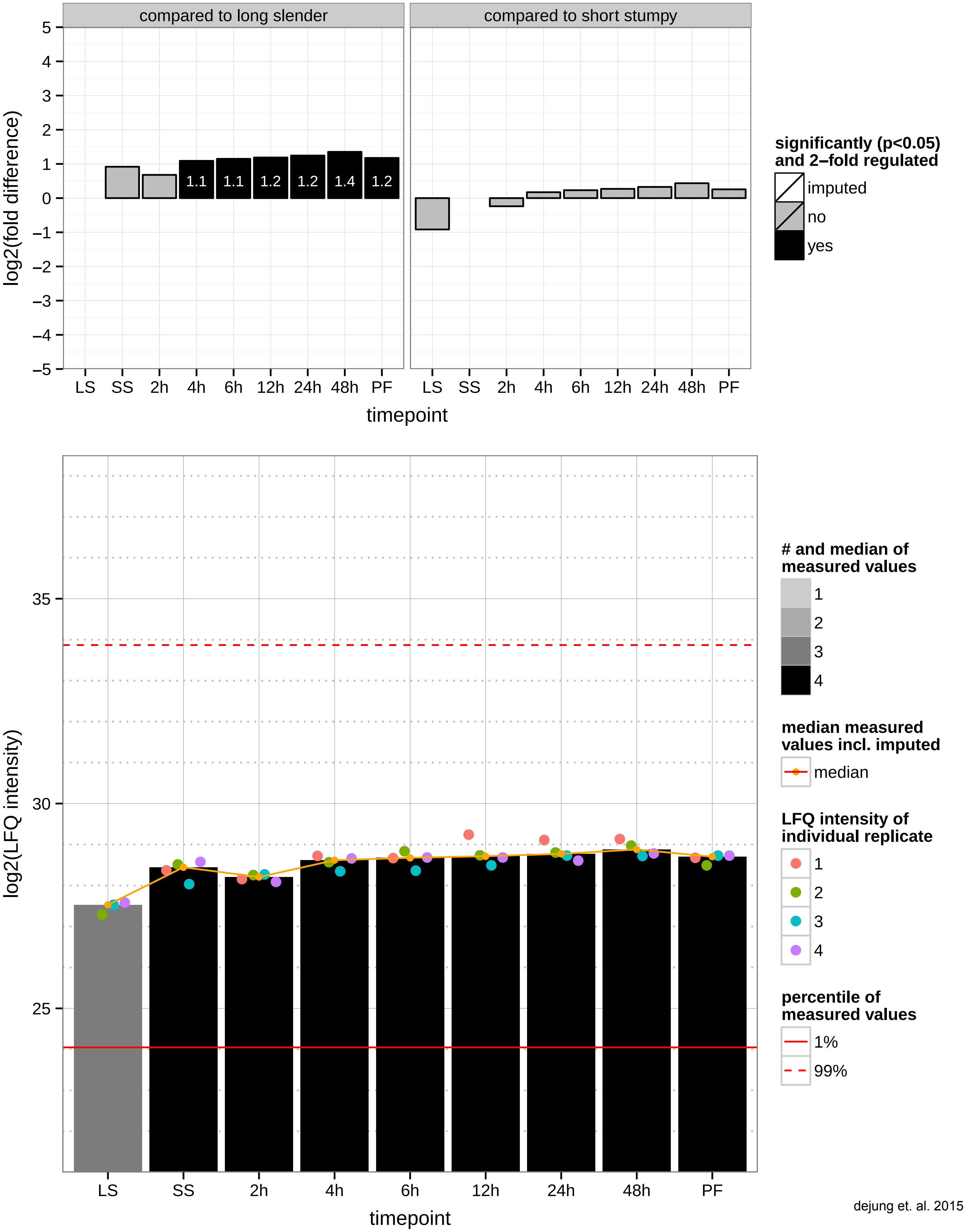
hypothetical protein, conserved
Tb927.7.2120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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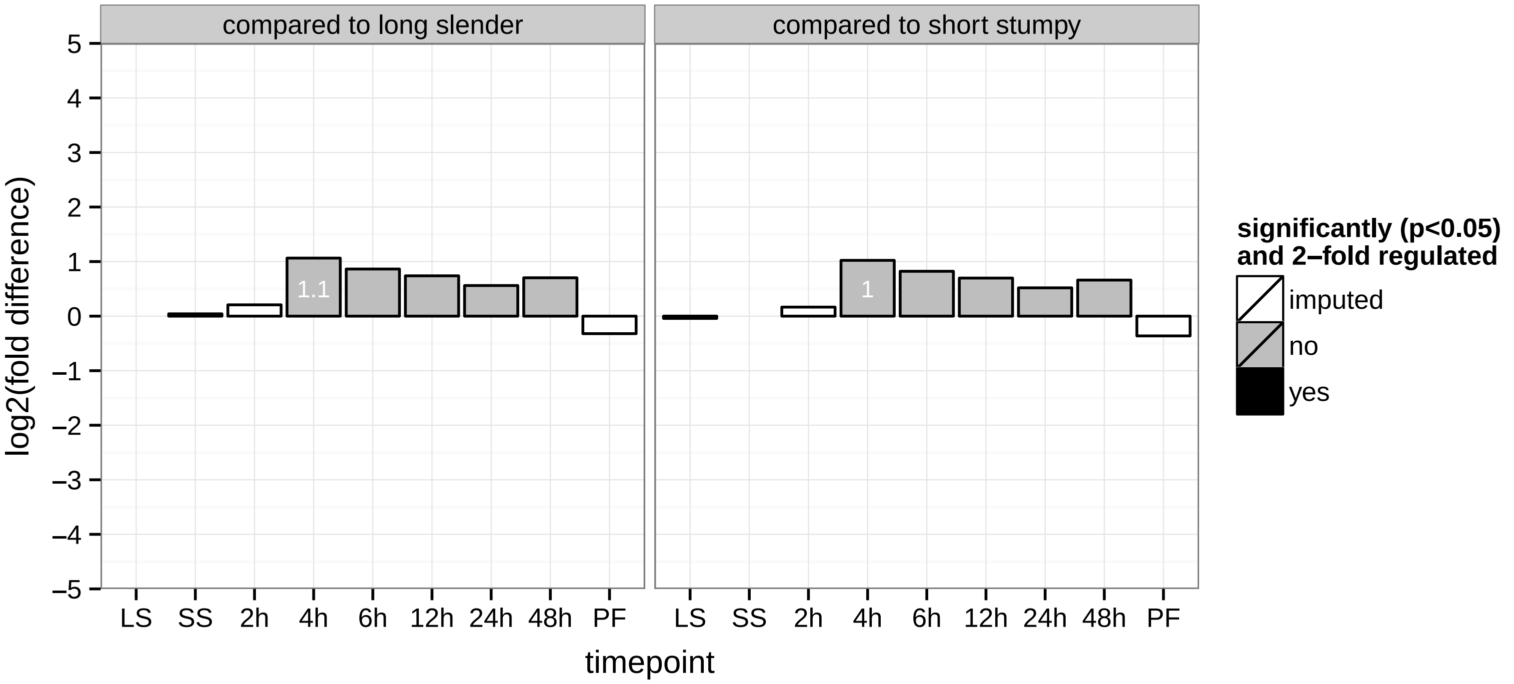
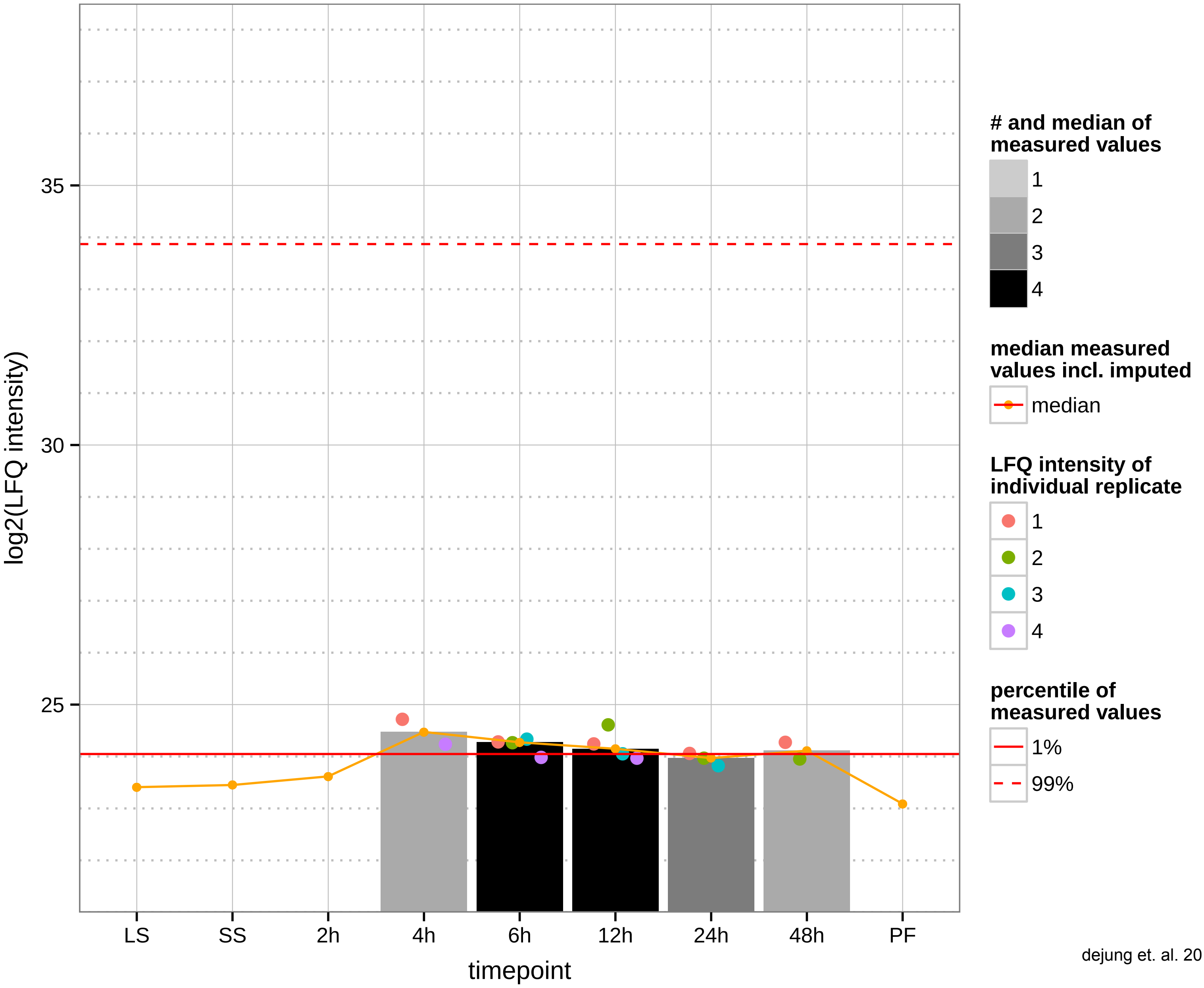
hypothetical protein, conserved
Tb927.7.2130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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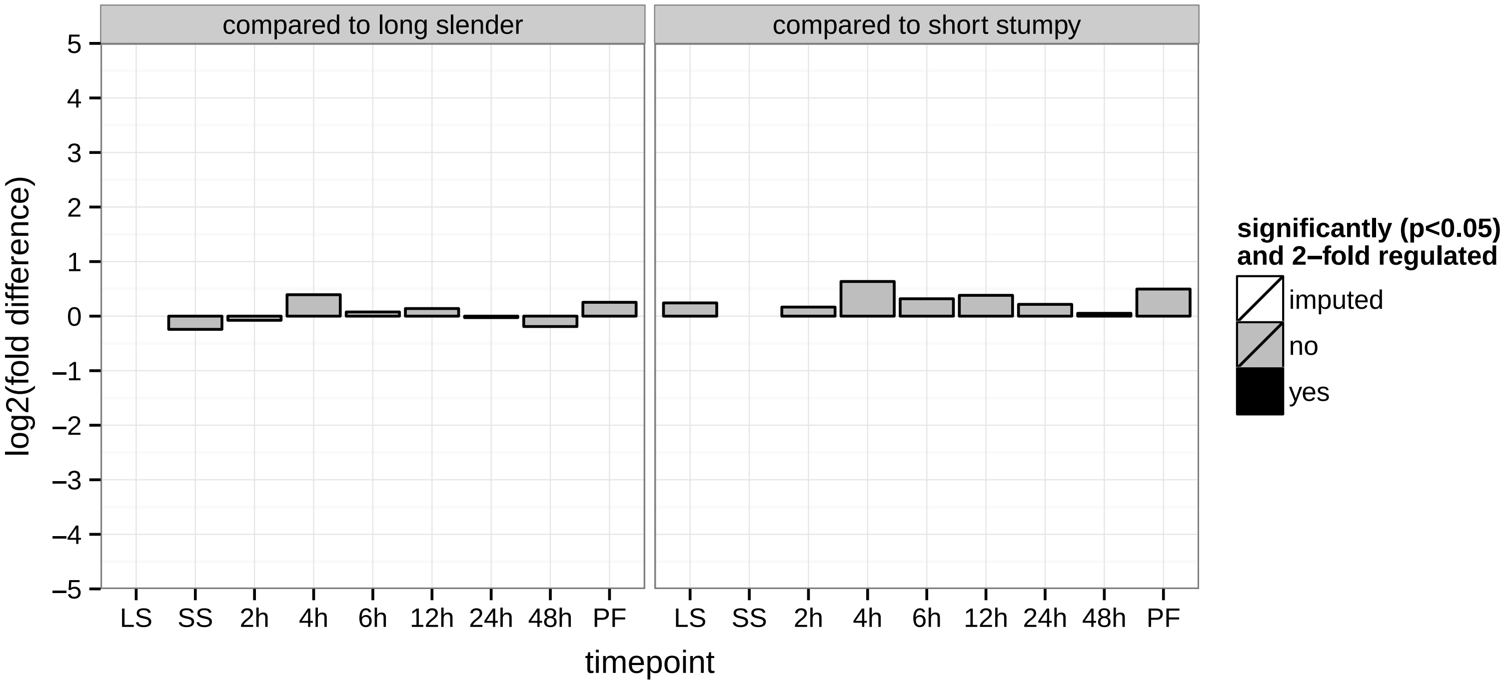
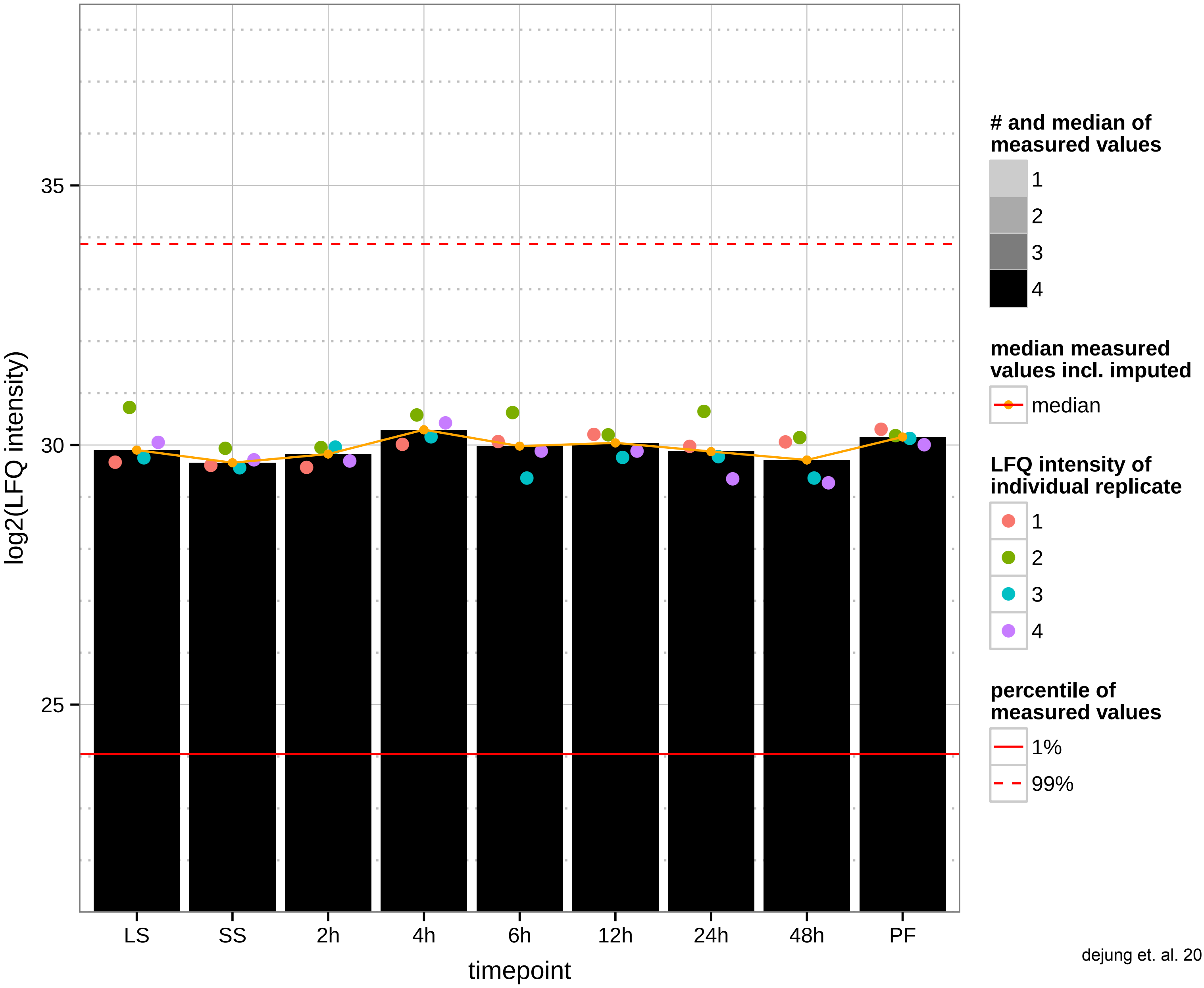
hypothetical protein, conserved
Tb927.7.2190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: endoplasmic reticulum
PGOP: null





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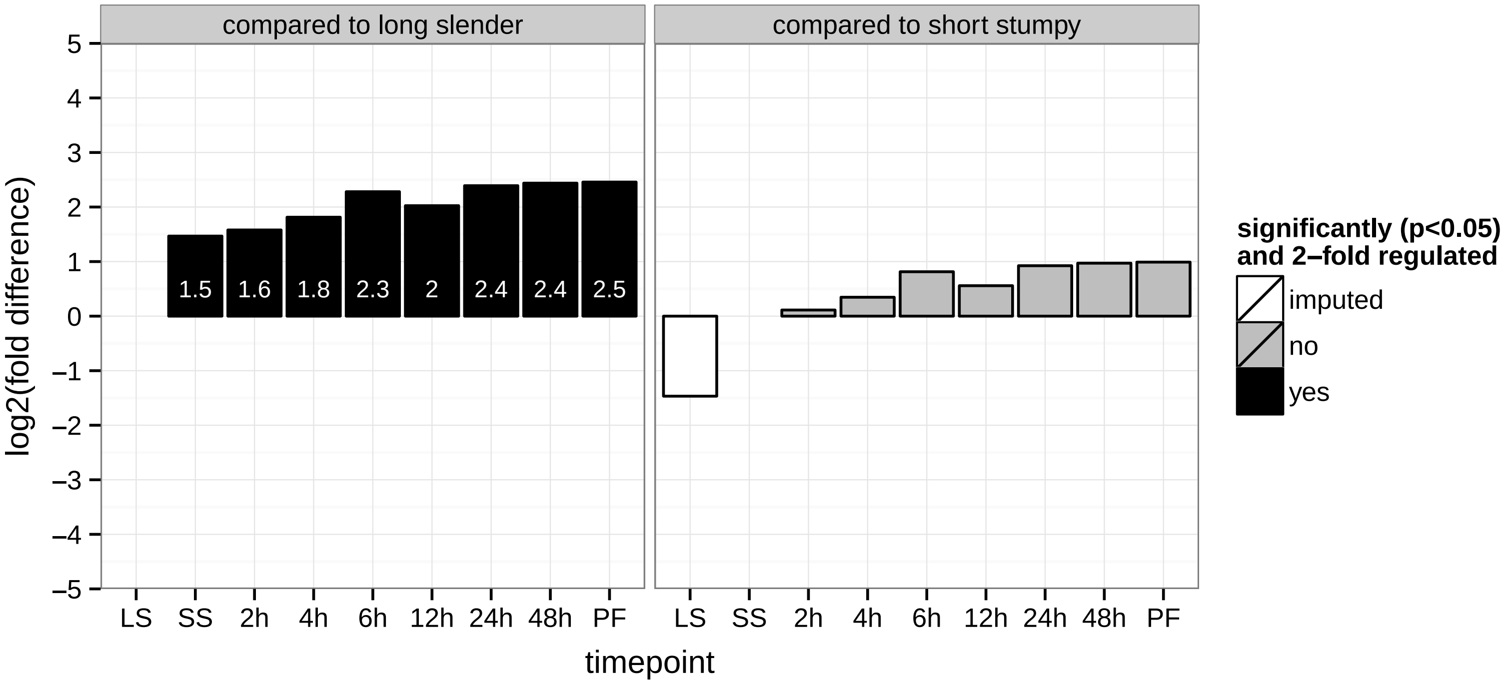
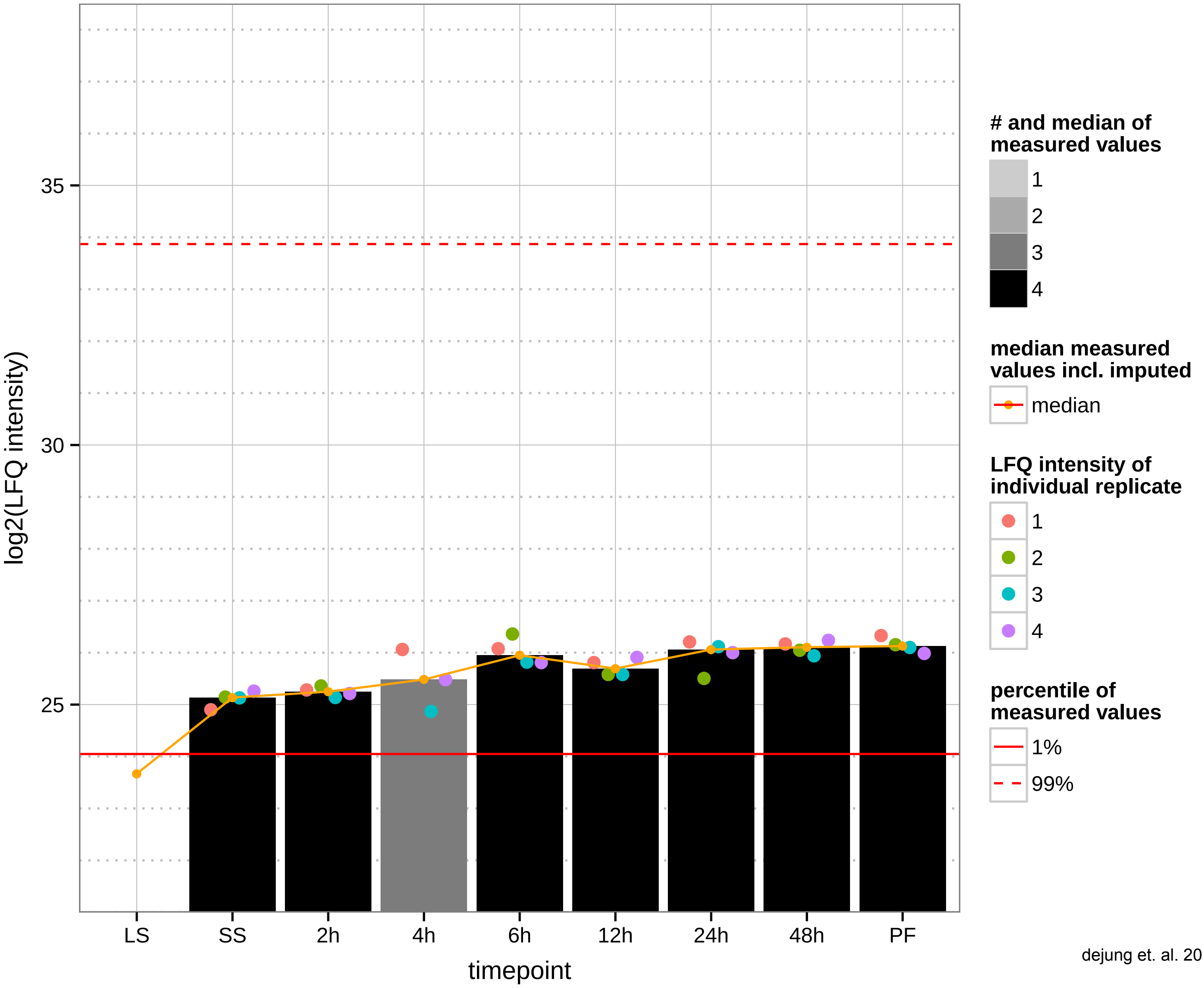
CDP−DAG synthase (CDS)
Tb927.7.220
AGOF: phosphatidate cytidylyltransferase activity, transferase activity, transferring phosphorus−containing groups
AGOC: endoplasmic reticulum membrane, integral to Golgi membrane
AGOP: CDP−diacylglycerol biosynthetic process, phosphatidylglycerol biosynthetic process, phosphatidylinositol metabolic pr
PGOF: phosphatidate cytidylyltransferase activity, transferase activity, transferring phosphorus−containing groups
PGOC: membrane
PGOP: null





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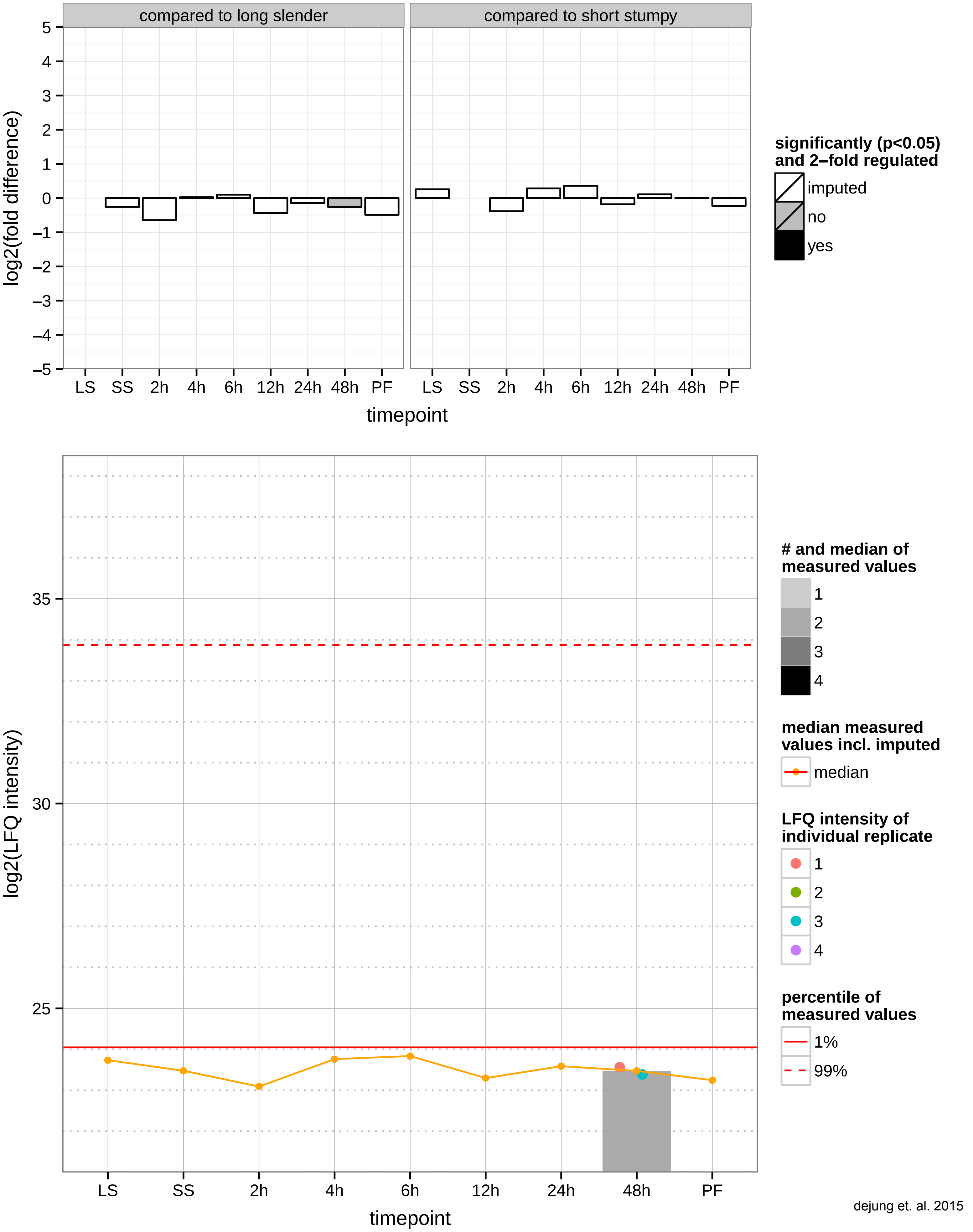
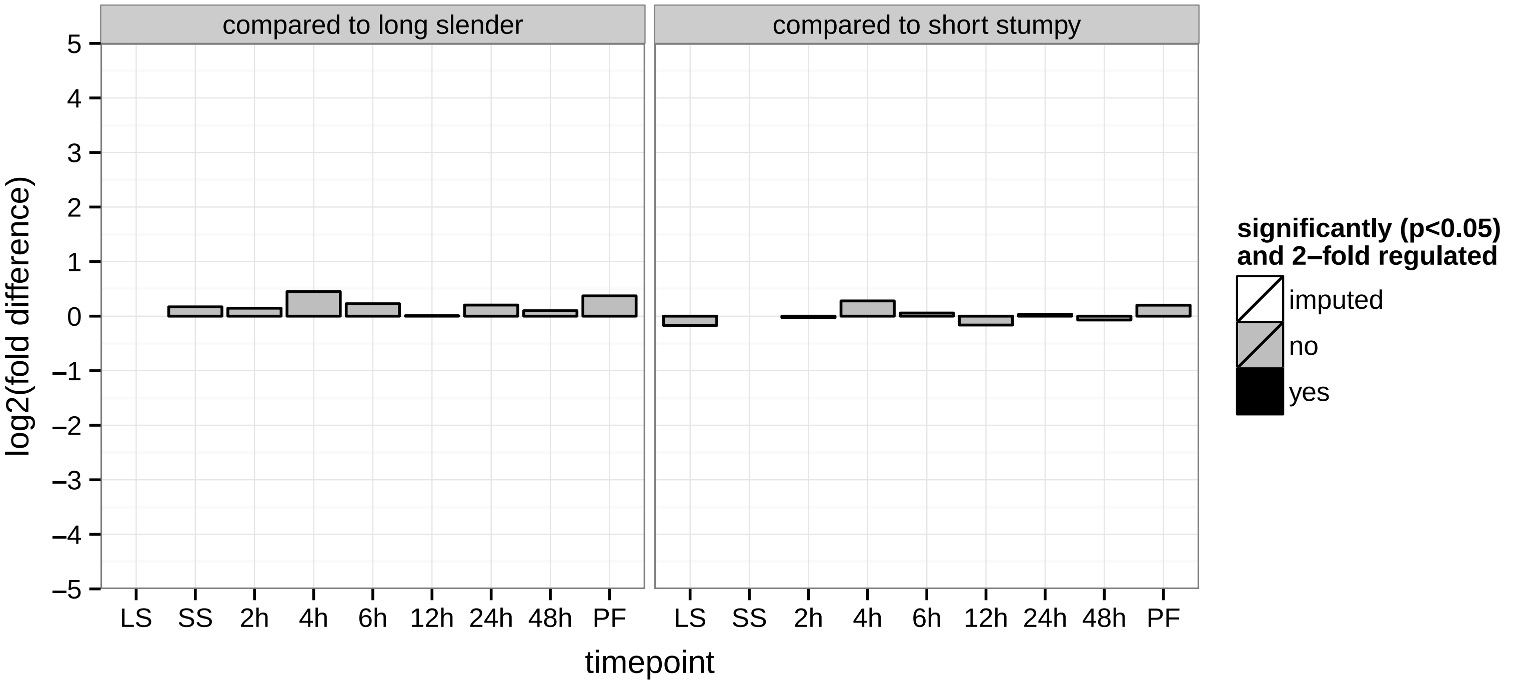
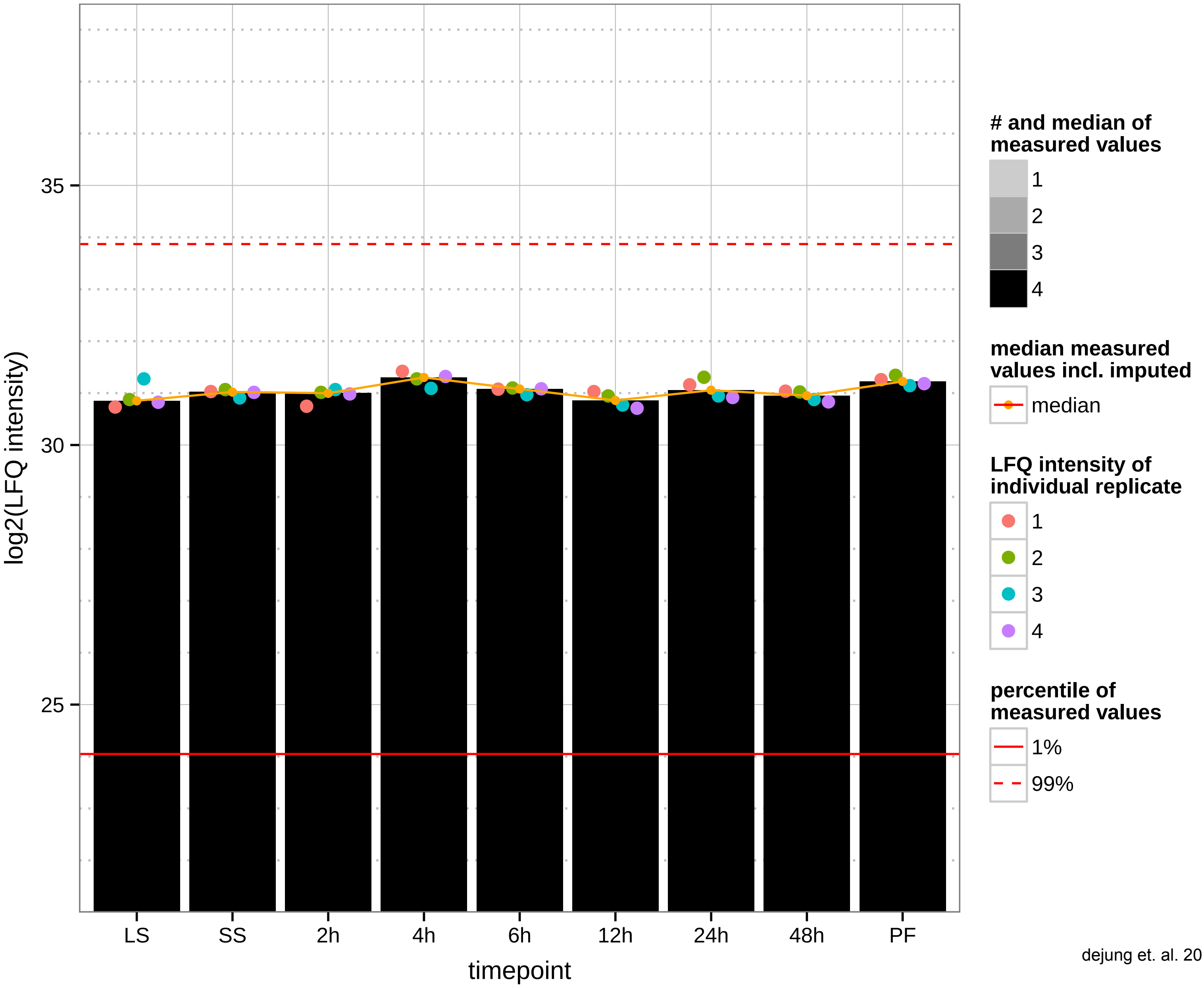
hypothetical protein, conserved
Tb927.7.2230
AGOF: null
AGOC: integral to membrane, membrane
AGOP: transport
PGOF: null
PGOC: null
PGOP: null



hypothetical protein, conserved
Tb927.7.2240
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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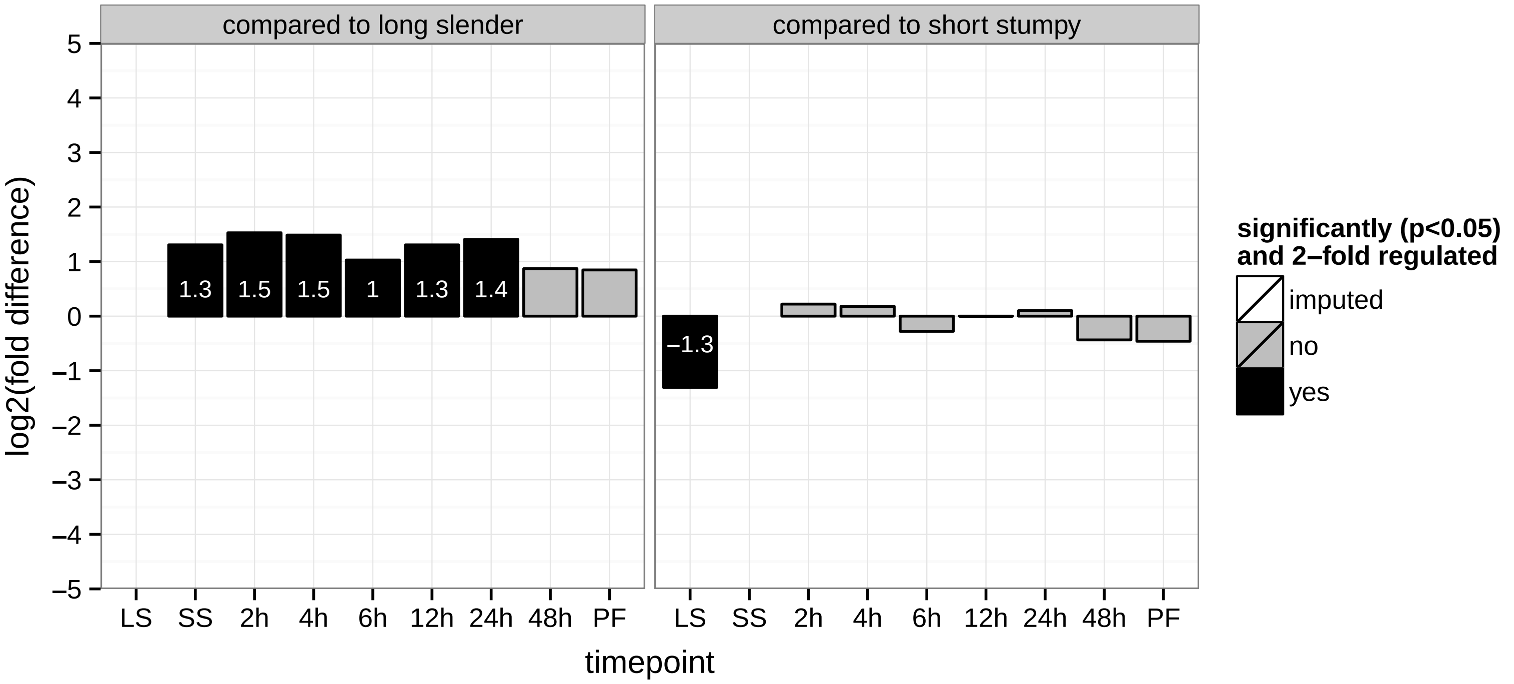
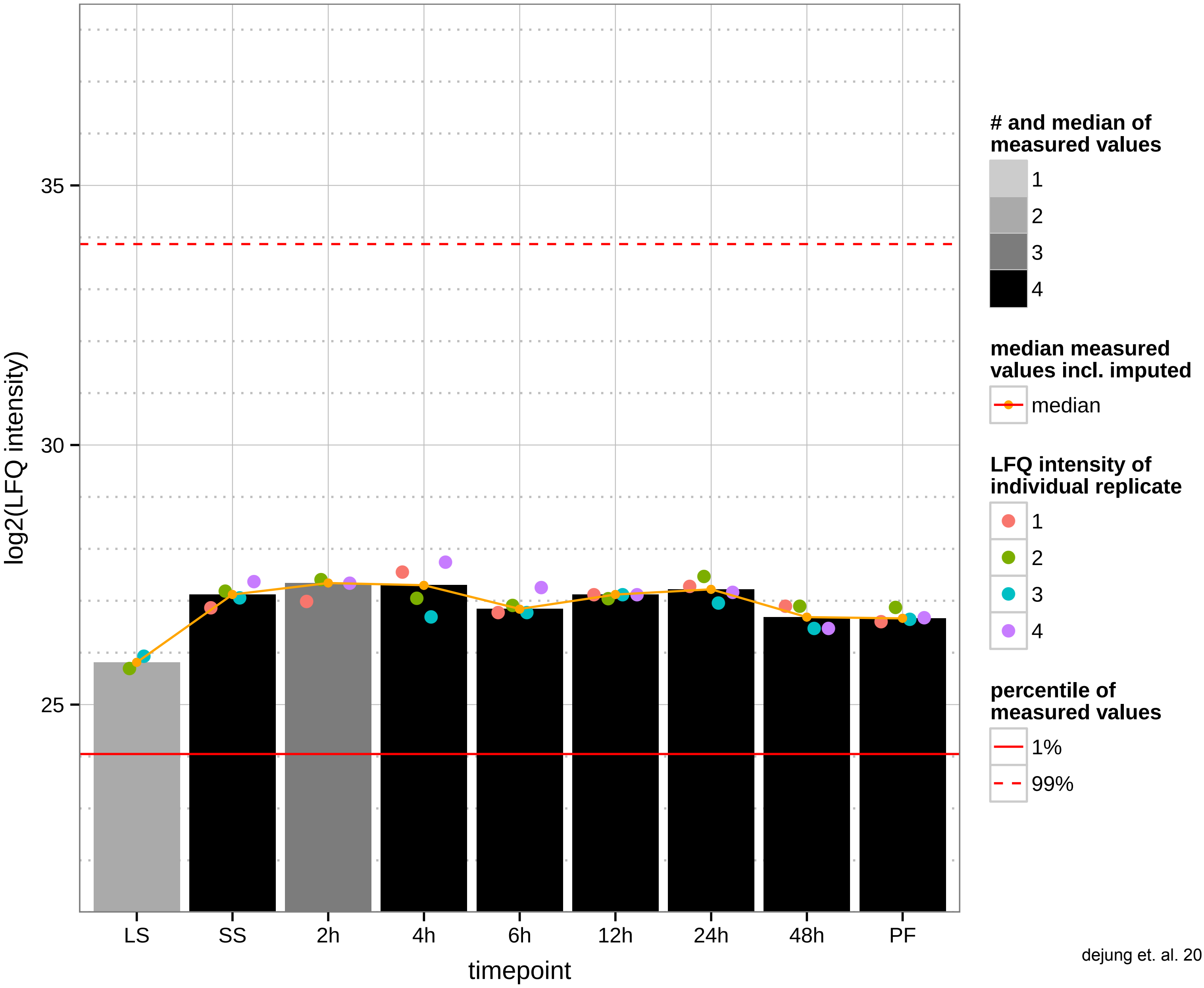
hypothetical protein, conserved
Tb927.7.2260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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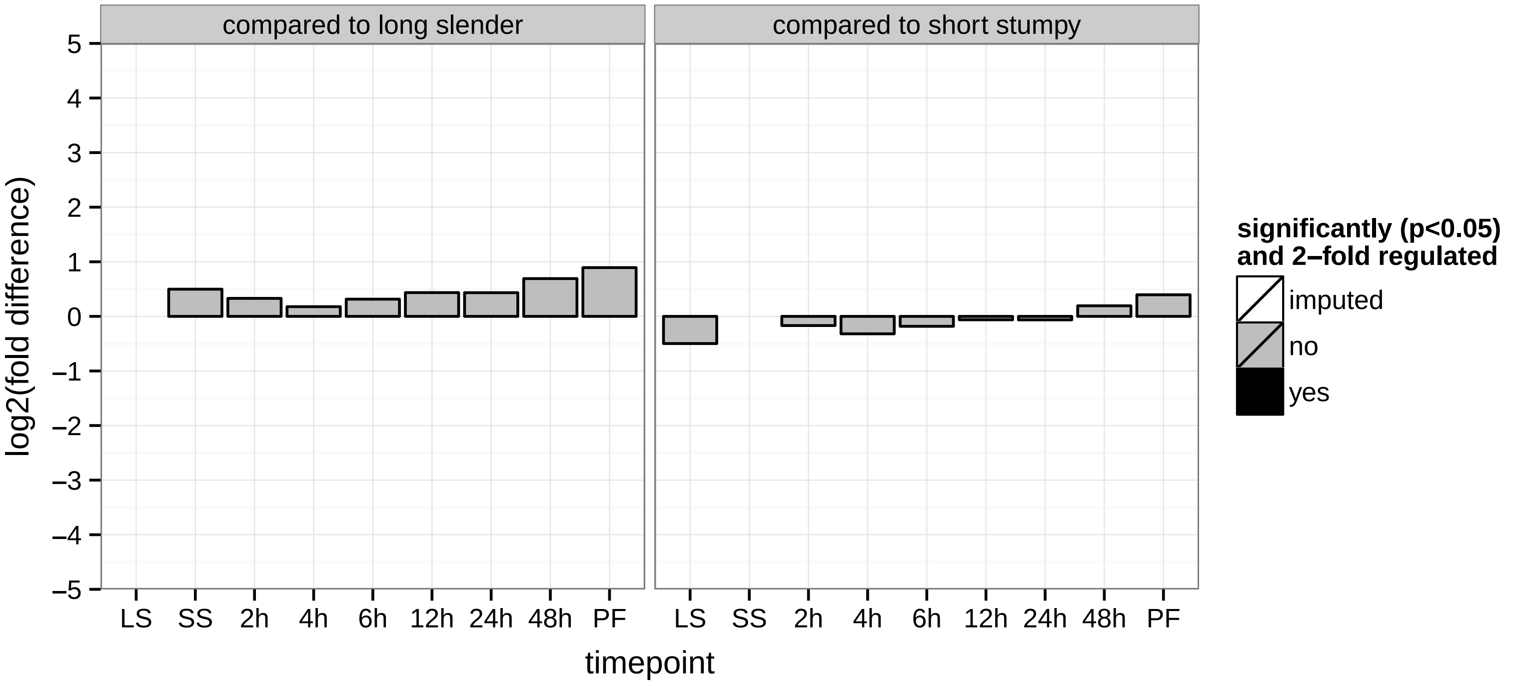
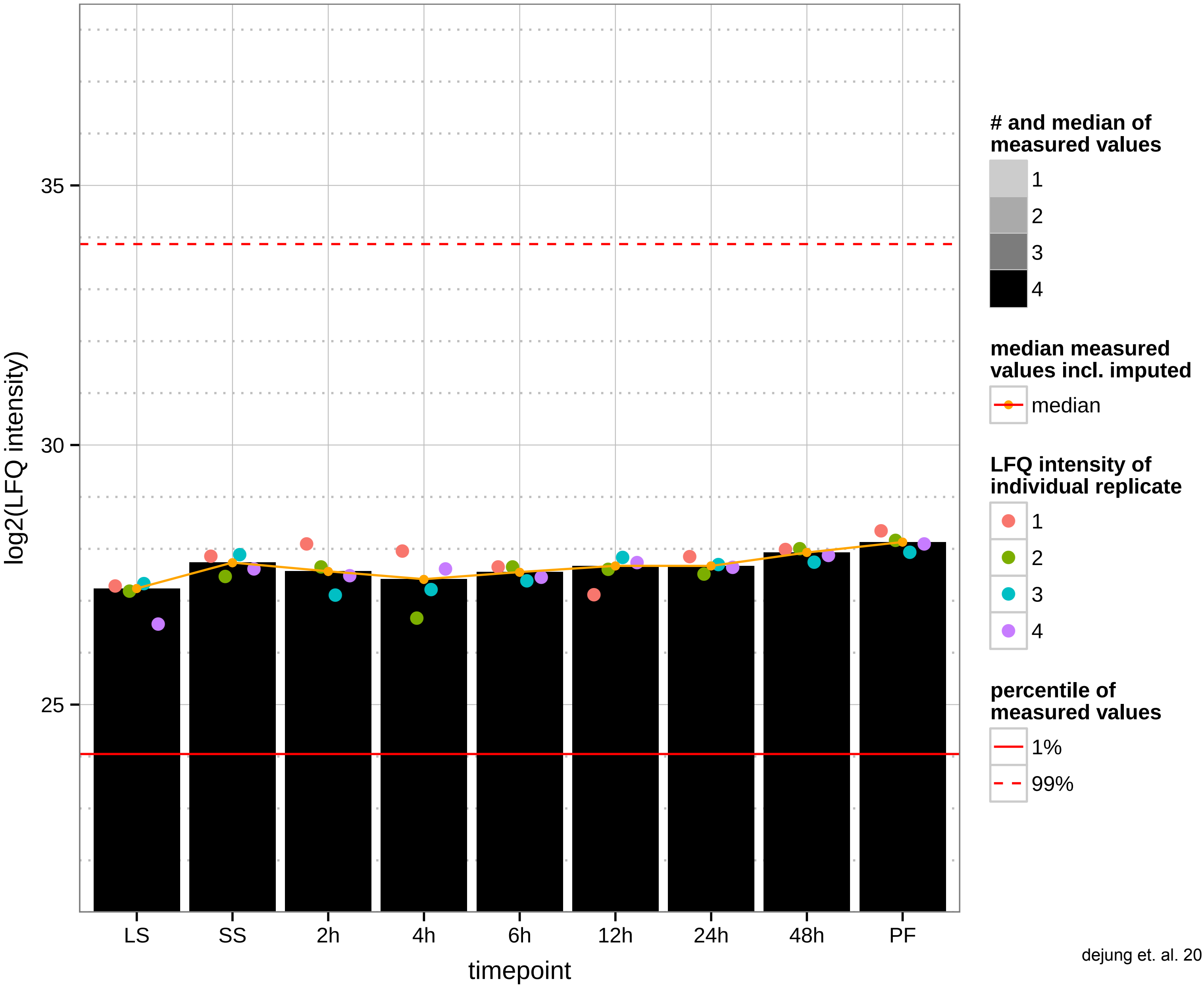
Nucleoporin (TbNup132)
Tb927.7.2300
AGOF: null
AGOC: nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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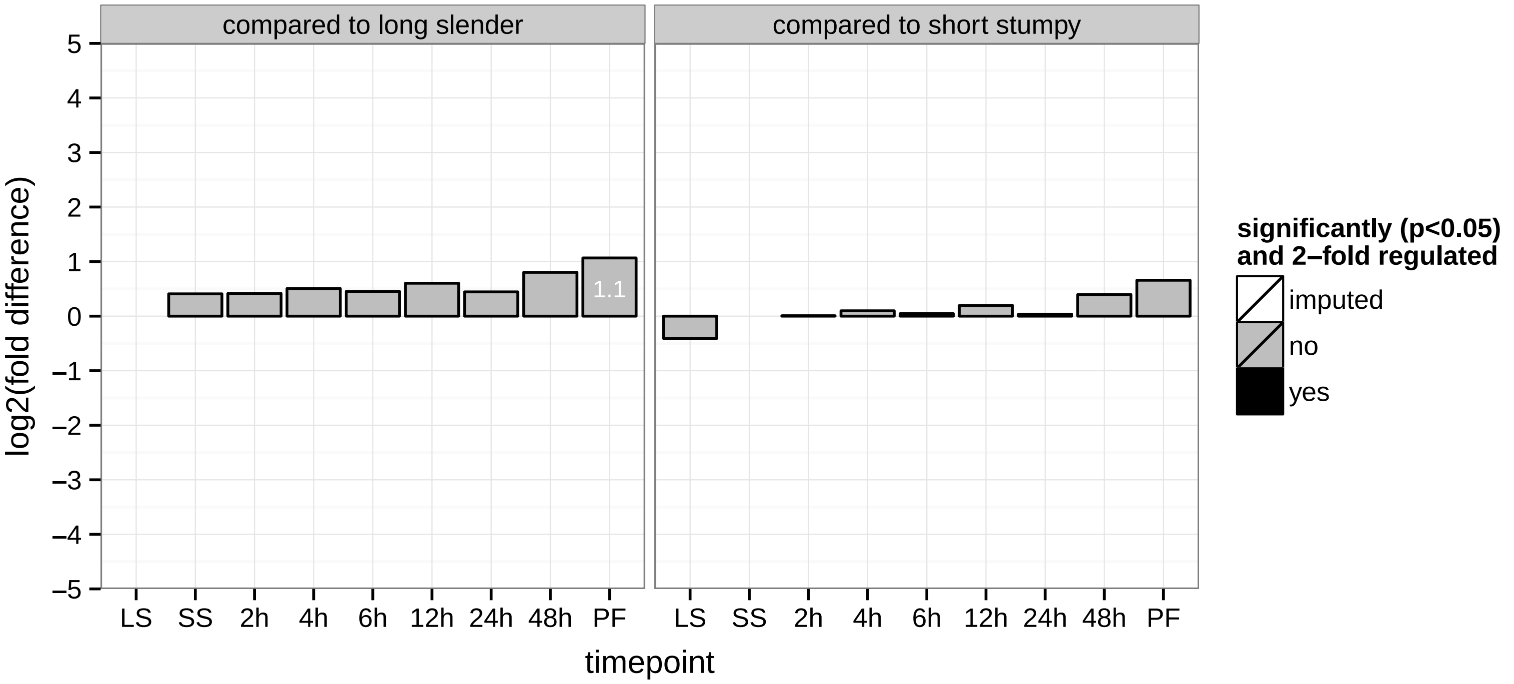
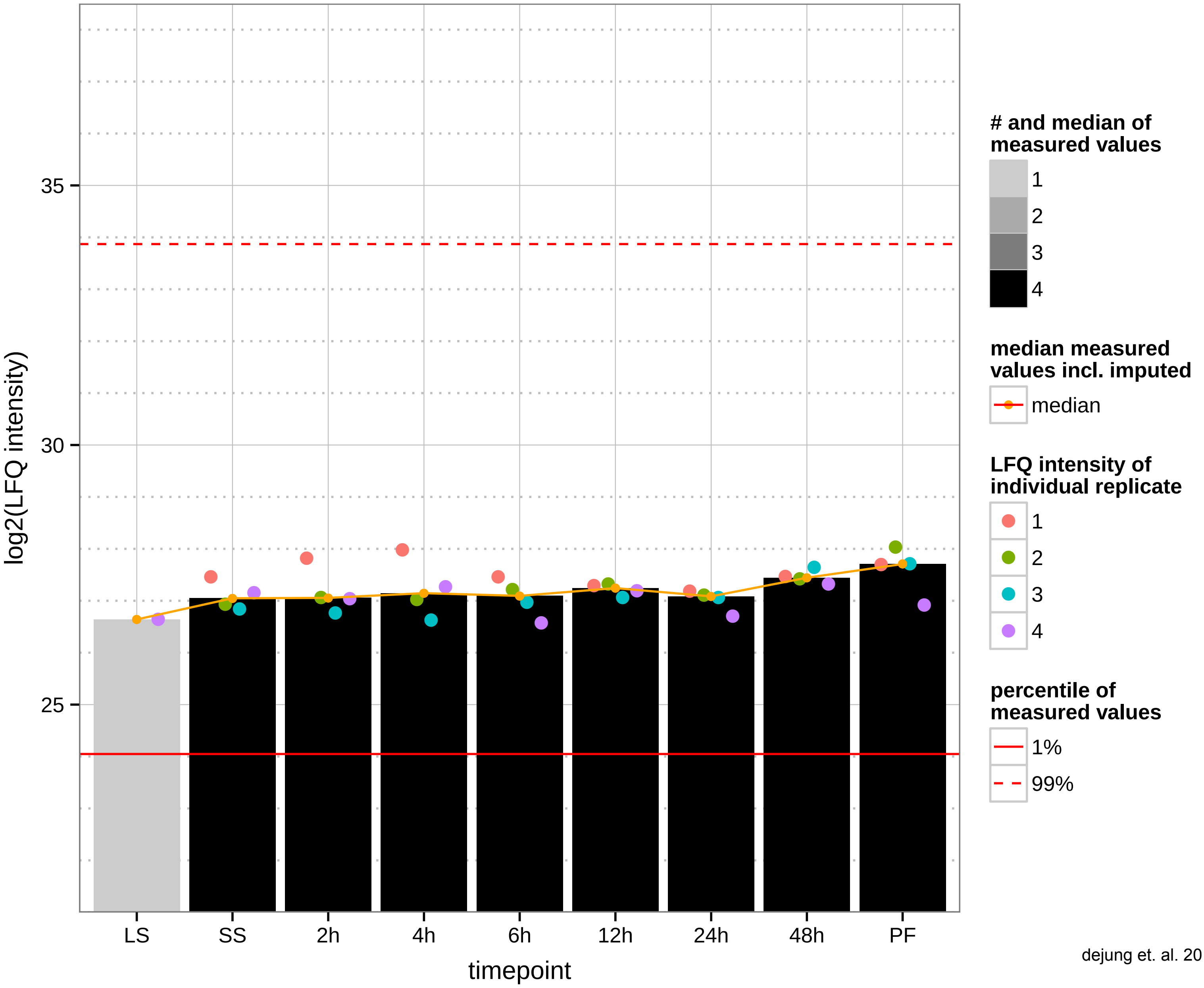
pyrroline−5−carboxylate reductase, putative (P5CR)
Tb927.7.2440
AGOF: pyrroline−5−carboxylate reductase activity
AGOC: null
AGOP: proline biosynthetic process
PGOF: oxidoreductase activity, pyrroline−5−carboxylate reductase activity
PGOC: null
PGOP: oxidation−reduction process, proline biosynthetic process





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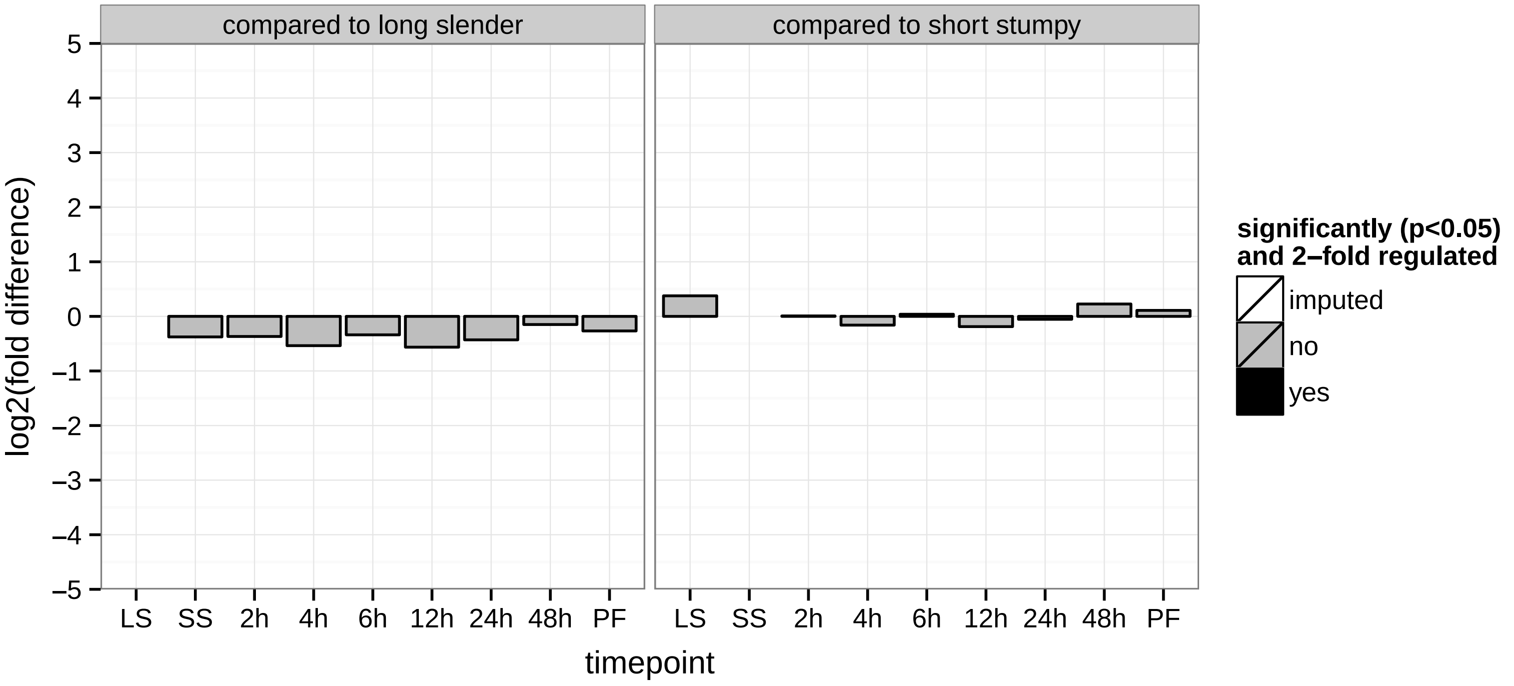
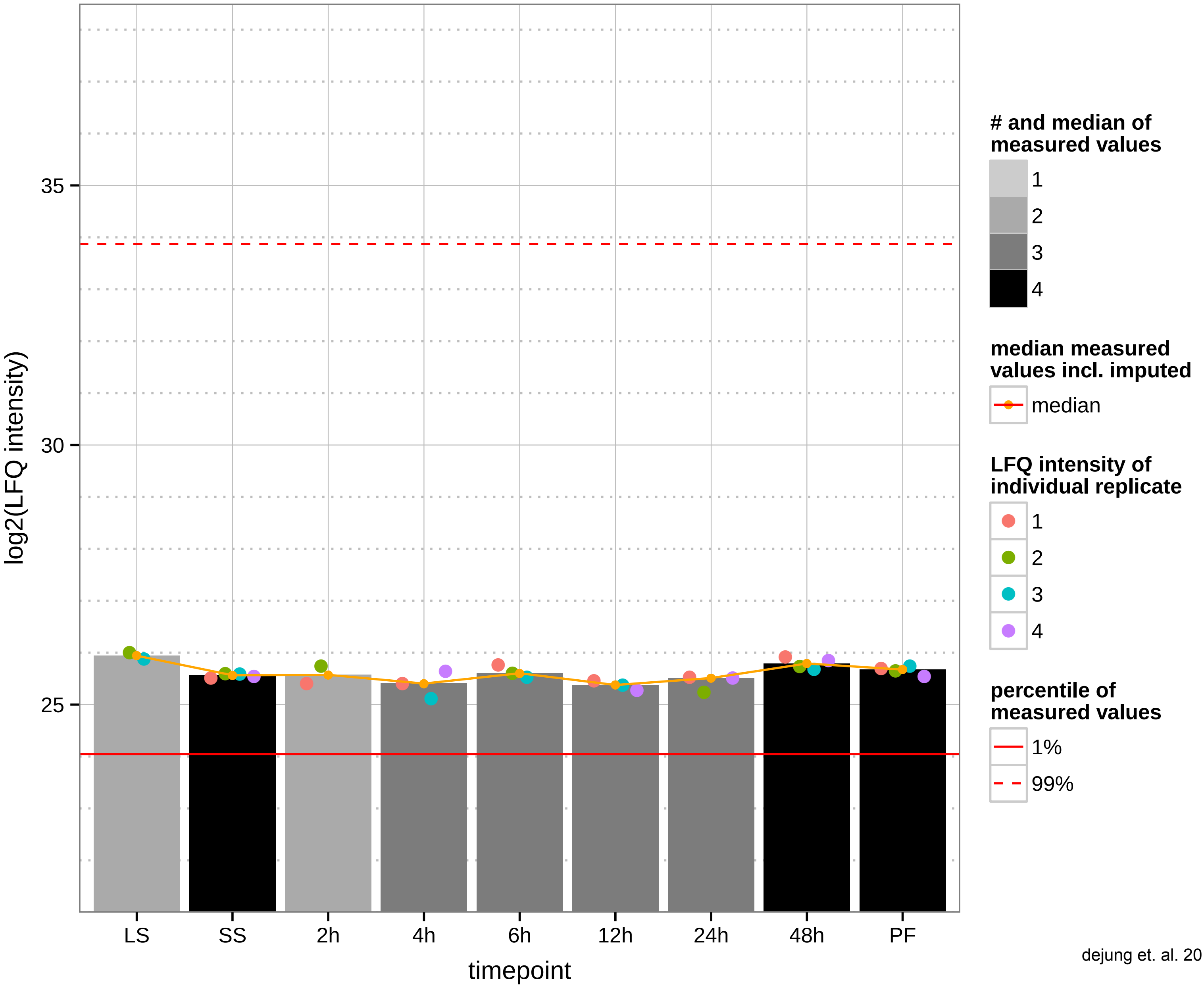
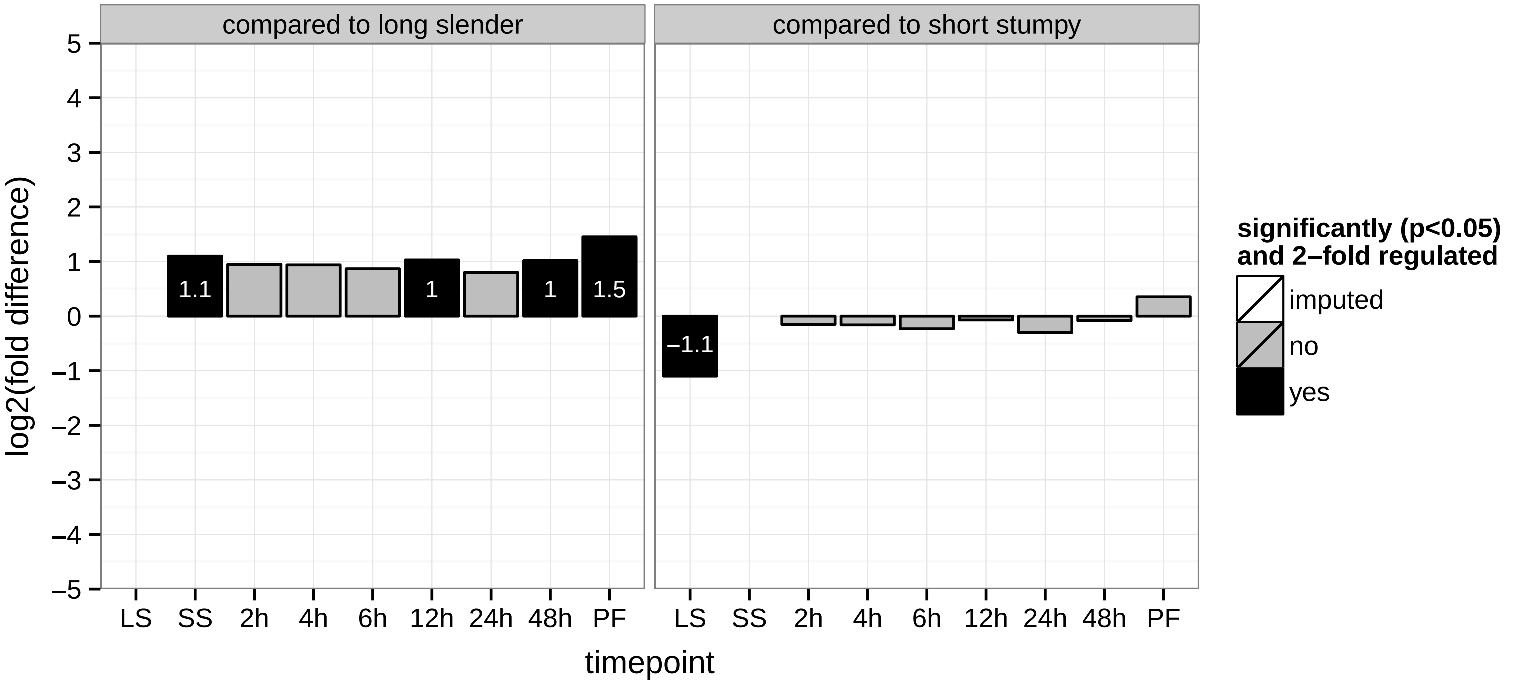
hypothetical protein, conserved
Tb927.7.2450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

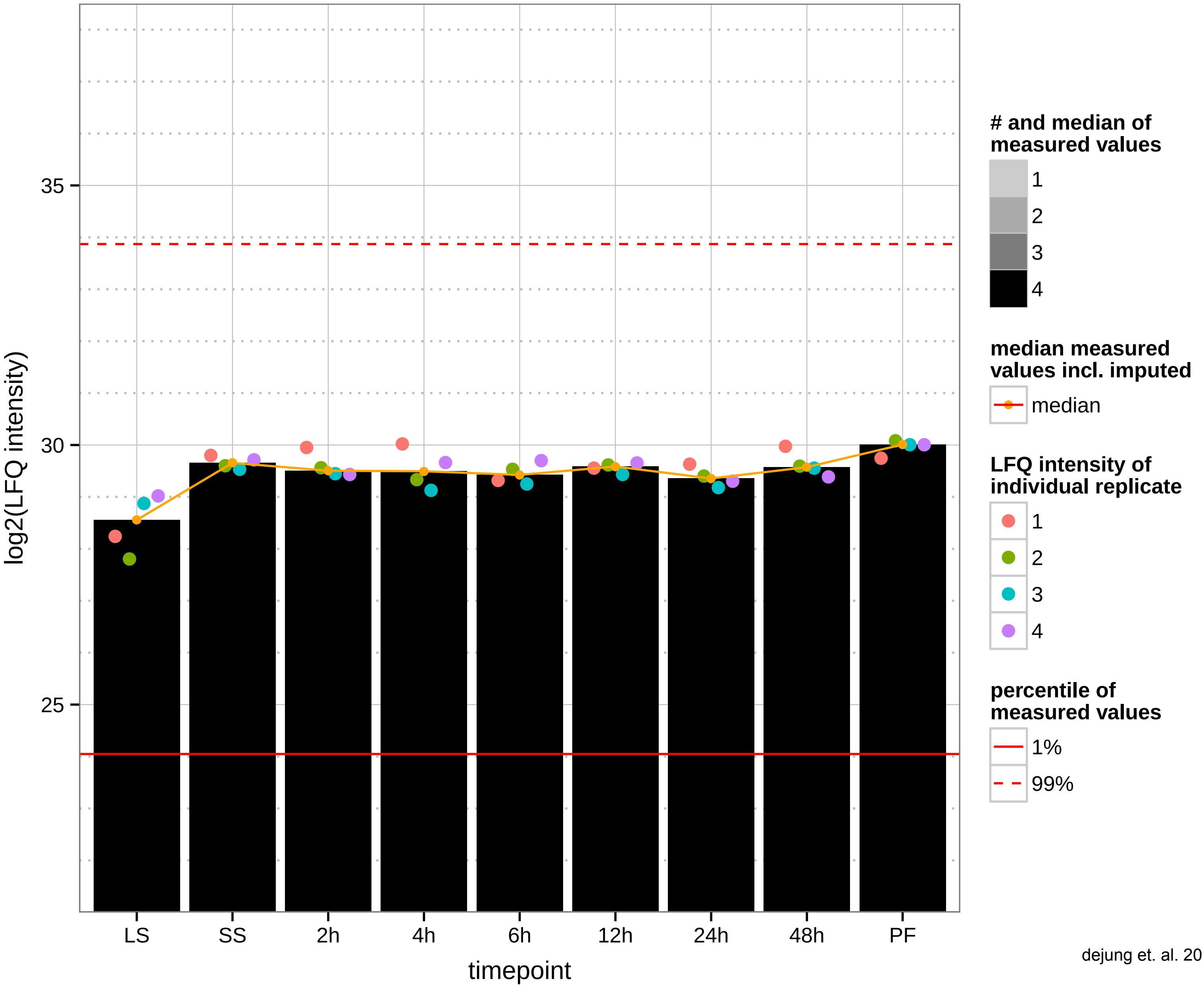




dejung et. al. 2015

proteasome regulatory ATPase subunit 1
Tb927.7.2500
AGOF: ATP binding, nucleoside–triphosphatase activity
AGOC: cytoplasm, nucleus
AGOP: protein catabolic process
PGOF: ATP binding, hydrolase activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: cytoplasm
PGOP: protein catabolic process





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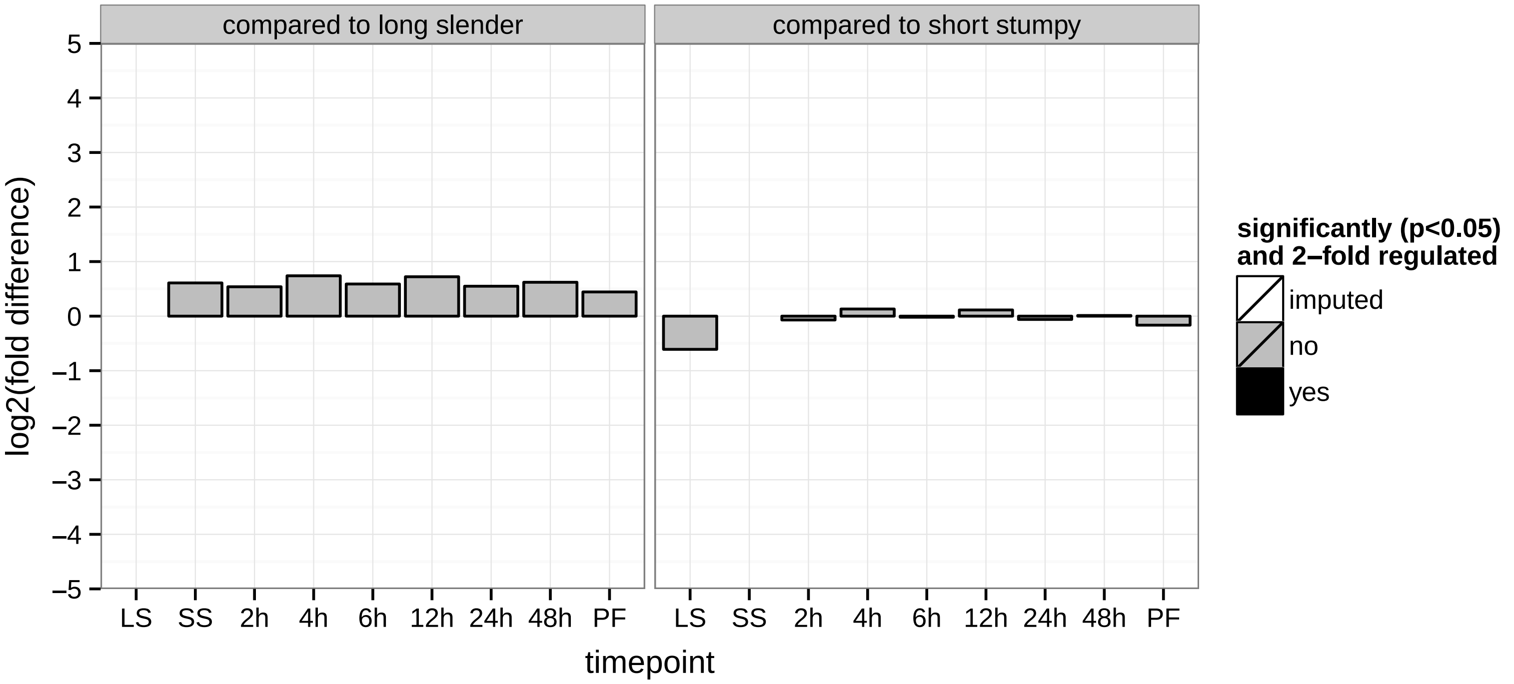
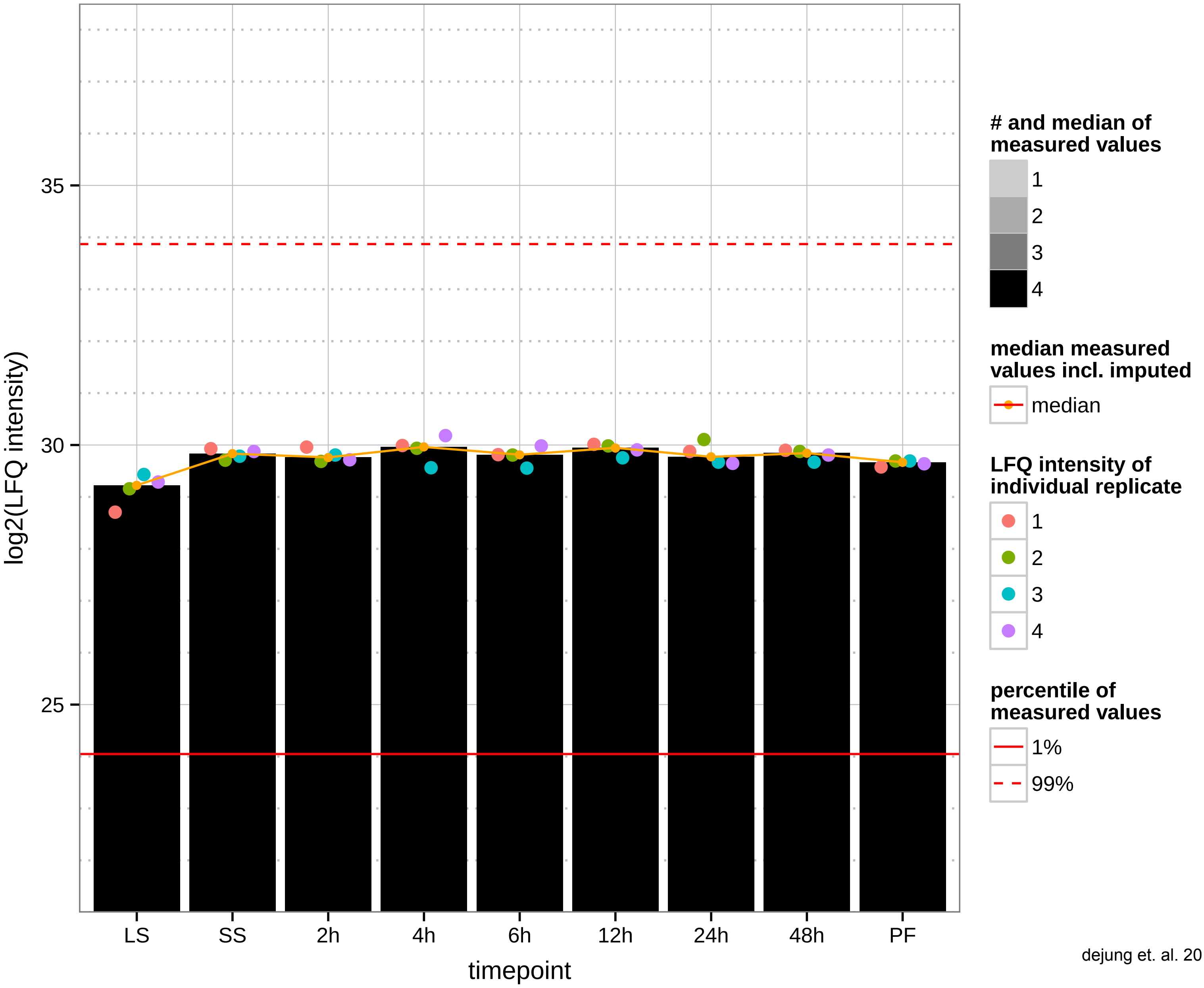
proteasome regulatory ATPase subunit 5 (RPT5)
Tb927.7.2550
AGOF: ATP binding, nucleoside–triphosphatase activity
AGOC: cytoplasm, nucleus
AGOP: protein catabolic process
PGOF: ATP binding, hydrolase activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: cytoplasm
PGOP: protein catabolic process





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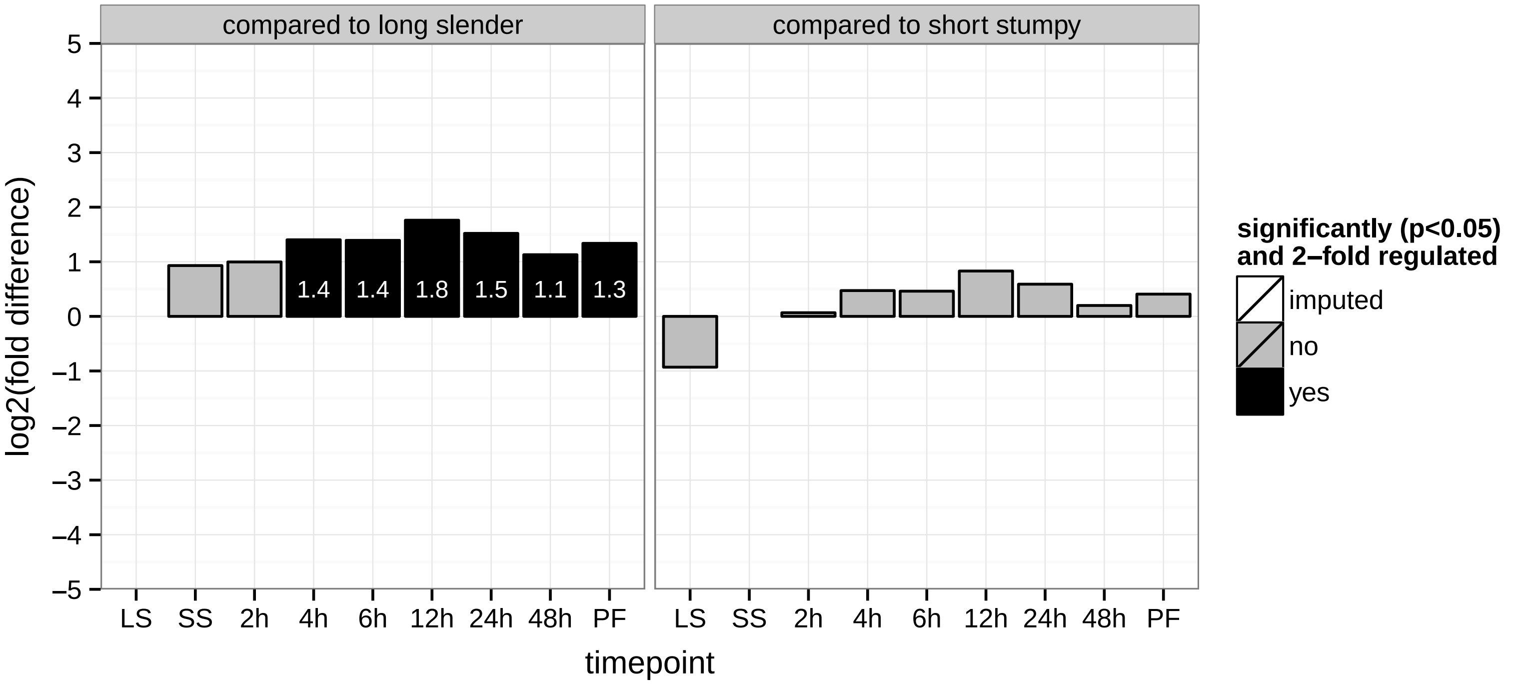
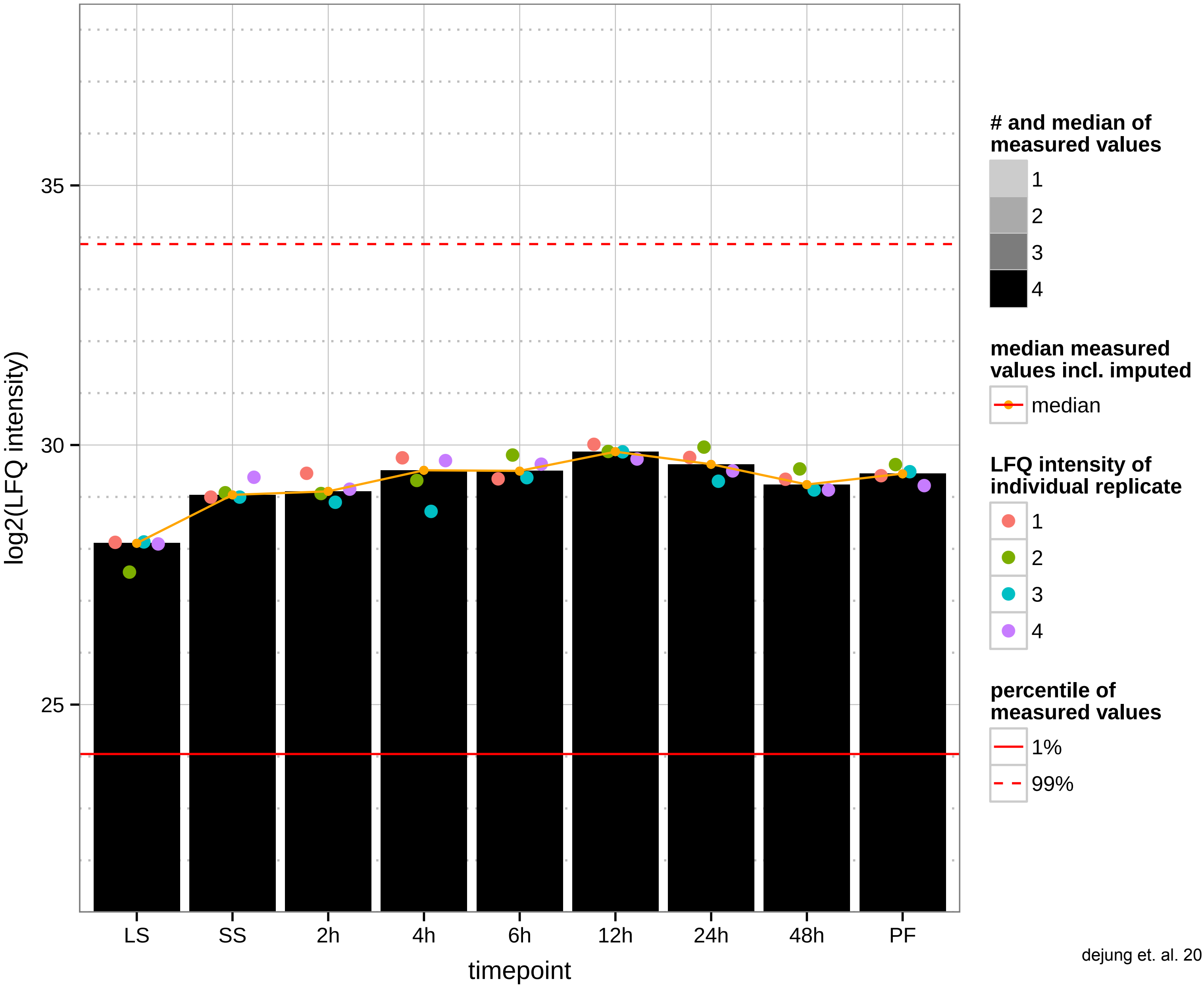
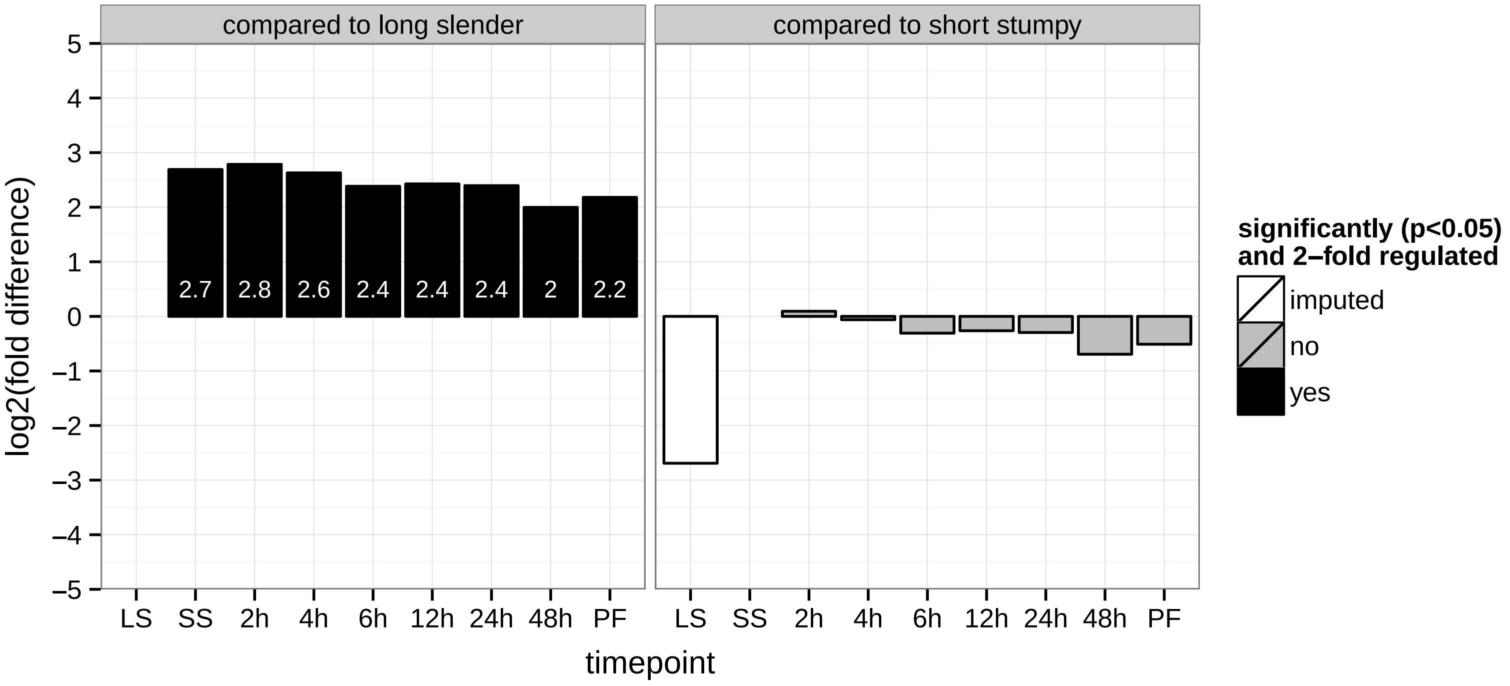
ribosome biogenesis protein, putative
Tb927.7.270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

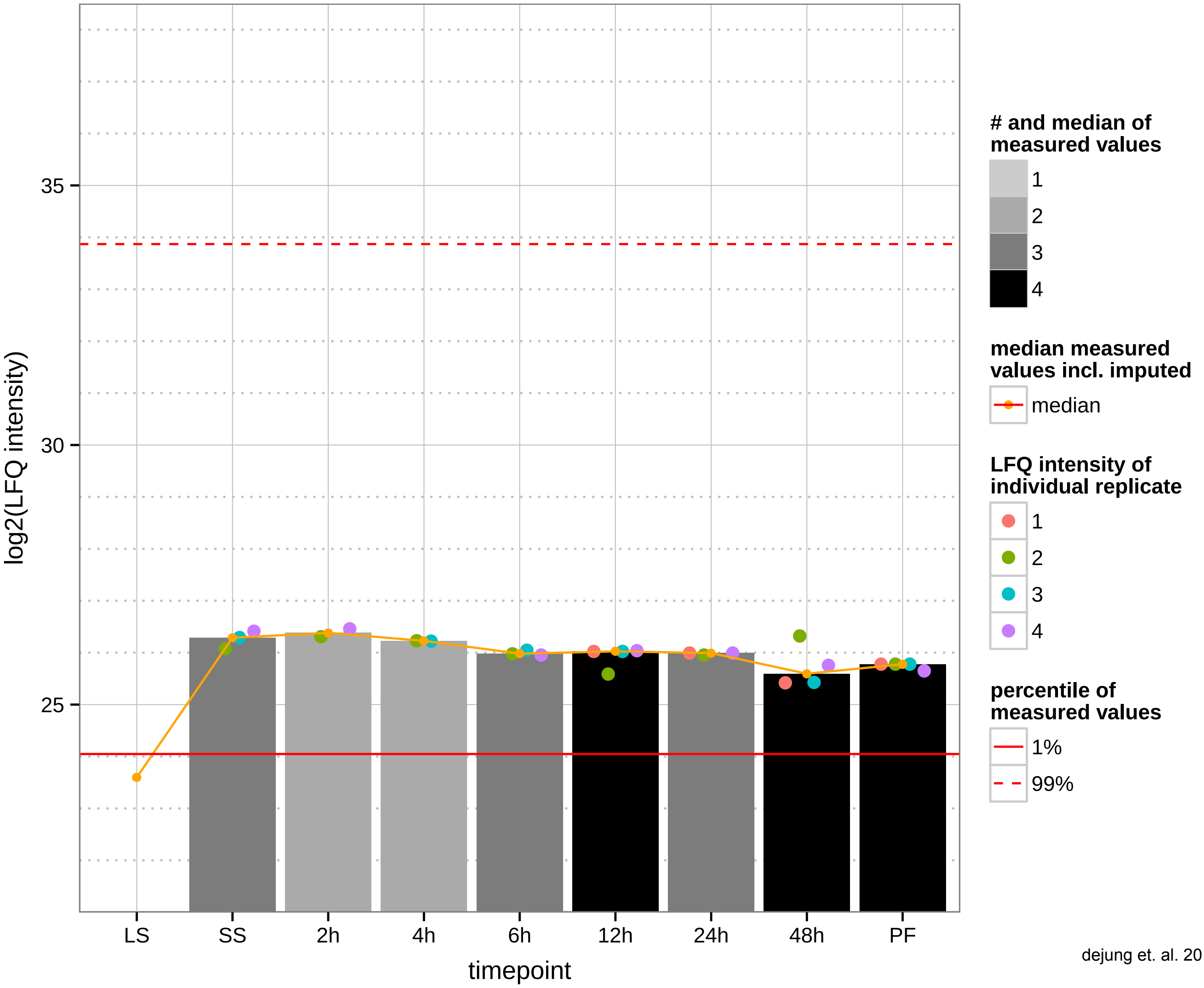




dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.2720
AGOF: RNA binding, translation initiation factor activity
AGOC: null
AGOP: translational initiation
PGOF: RNA binding, translation initiation factor activity
PGOC: null
PGOP: translational initiation





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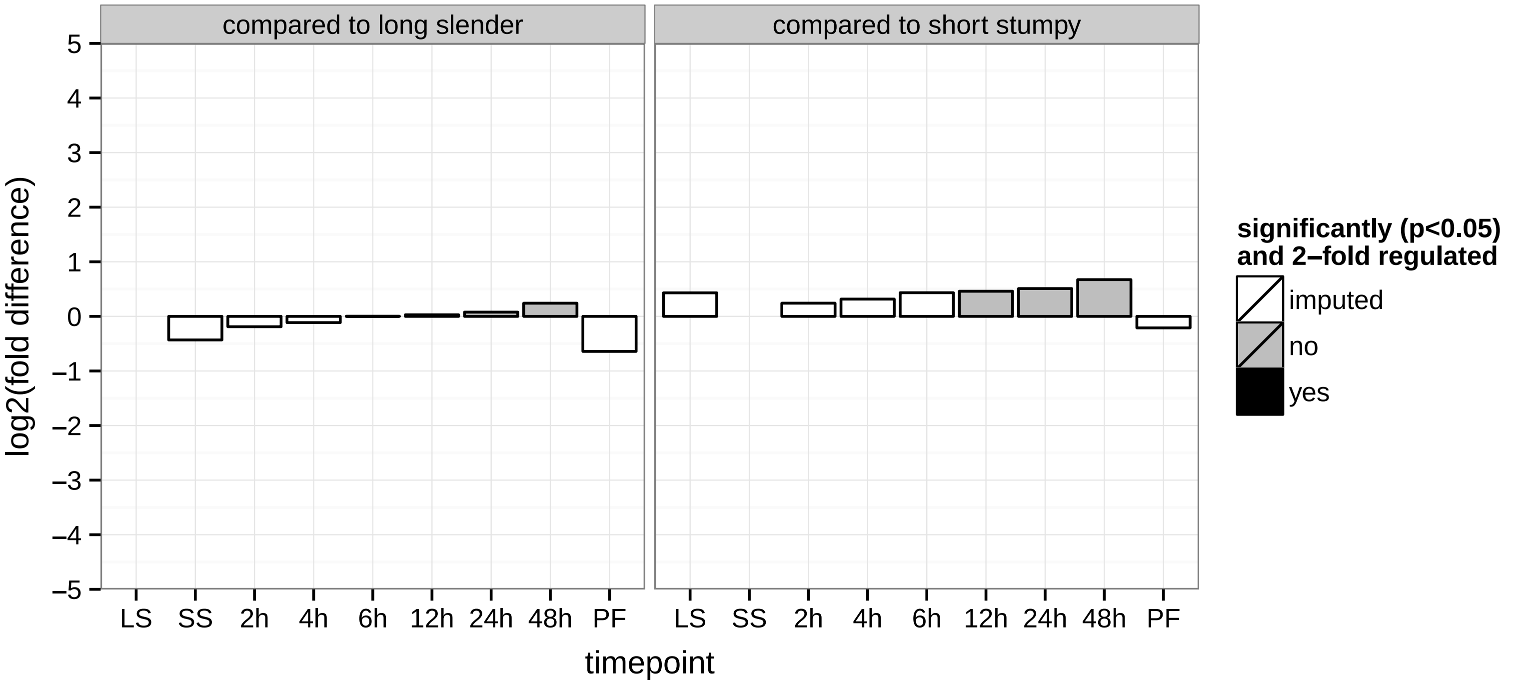
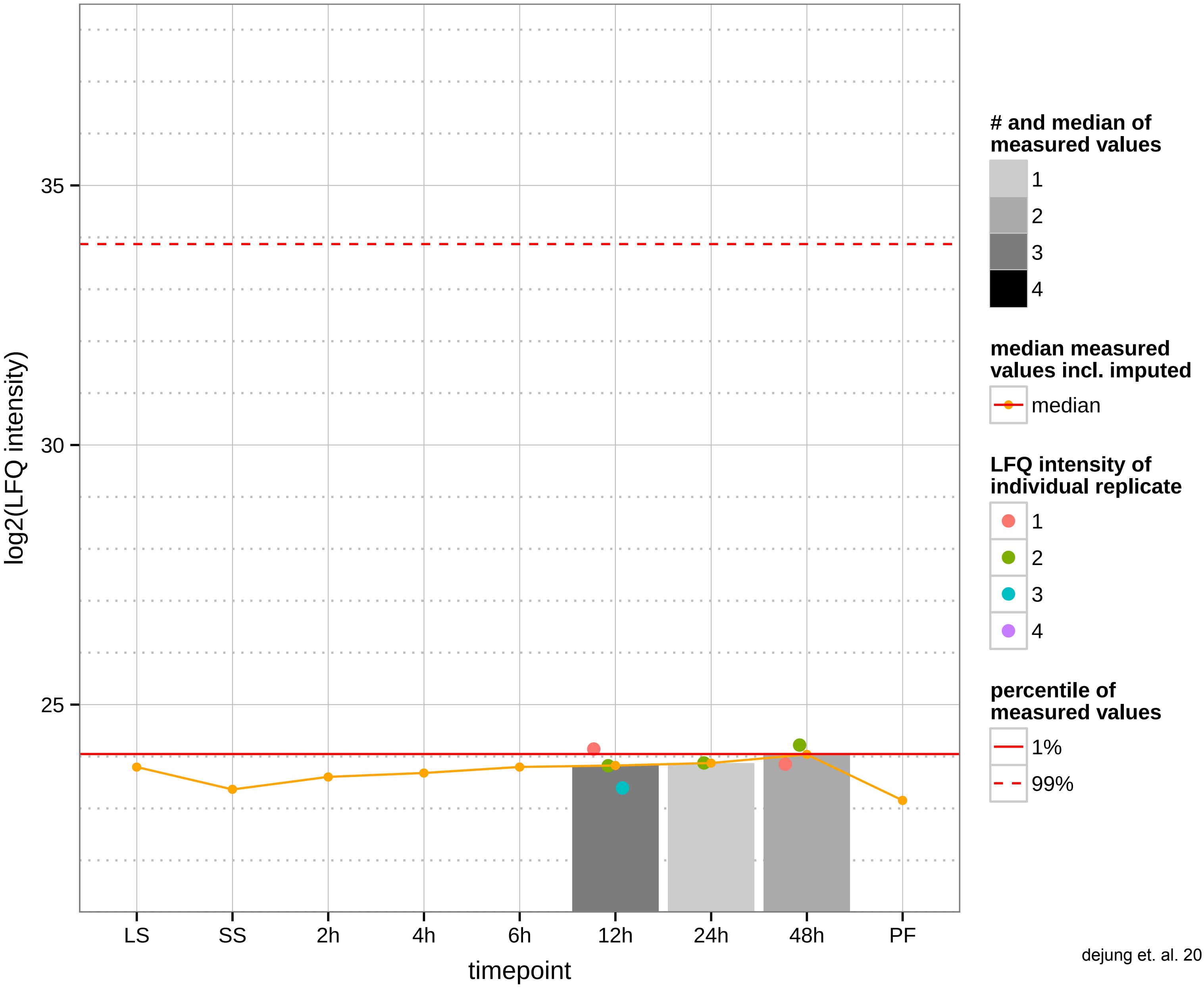
leucine–rich repeat protein (LRRP), putative
Tb927.7.2730
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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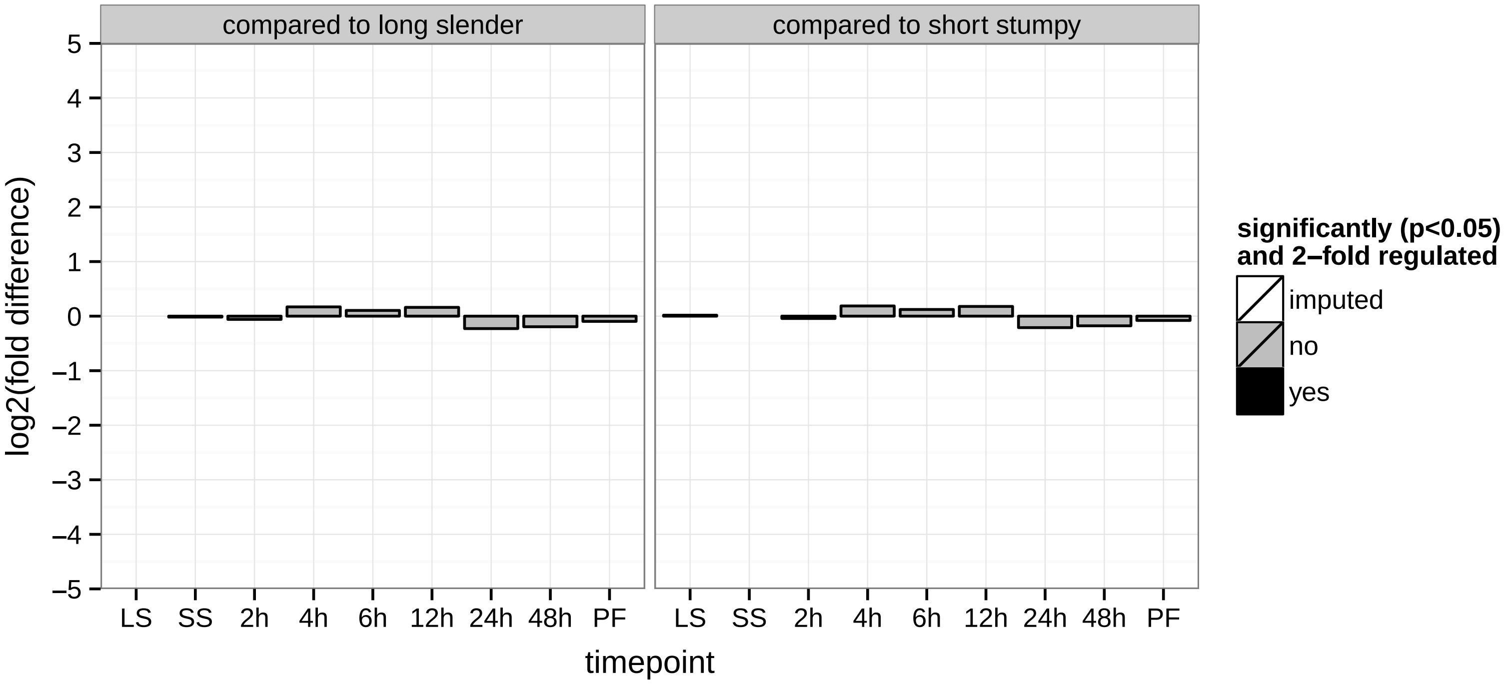
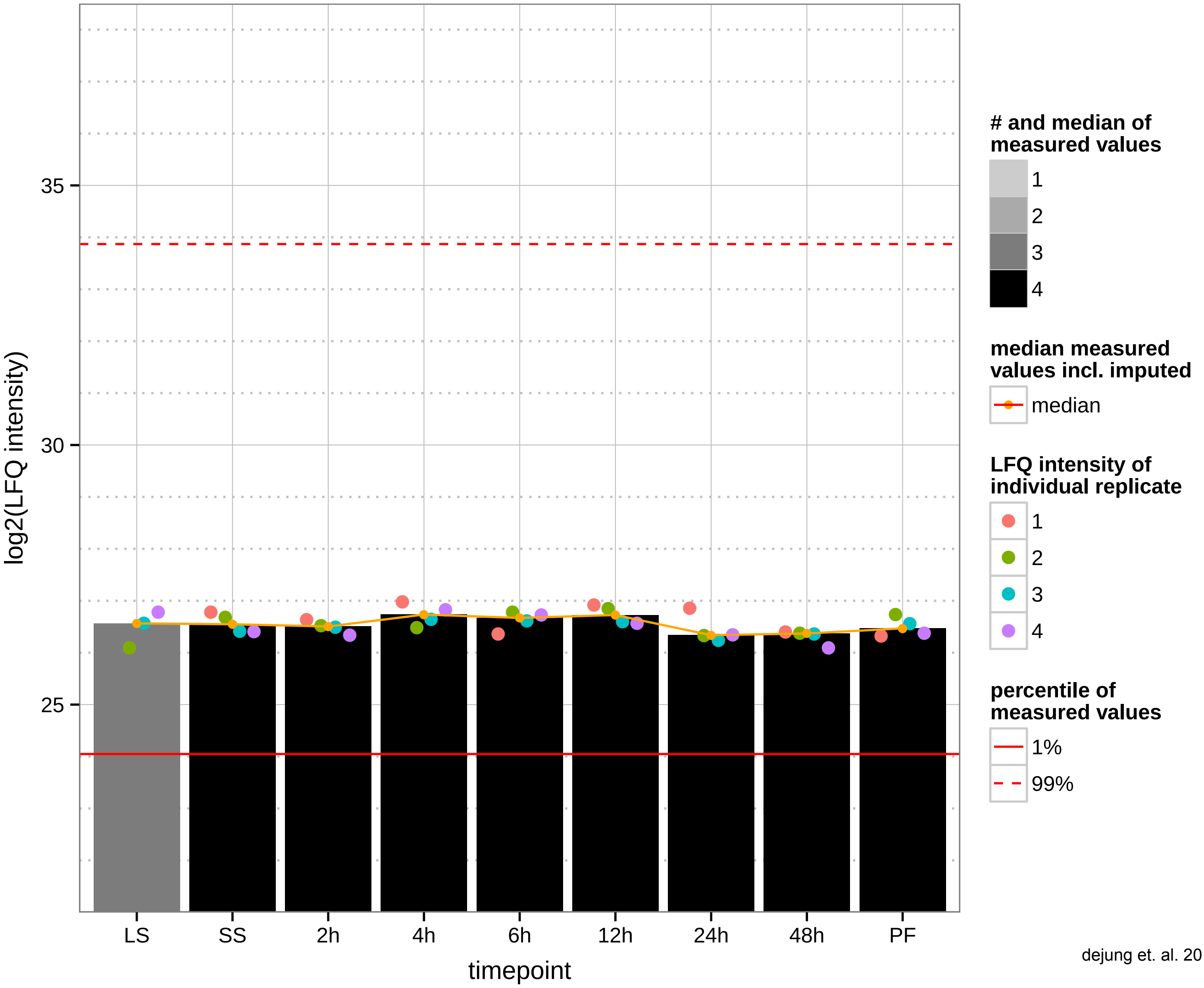
protein kinase, putative
Tb927.7.2750
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: growth, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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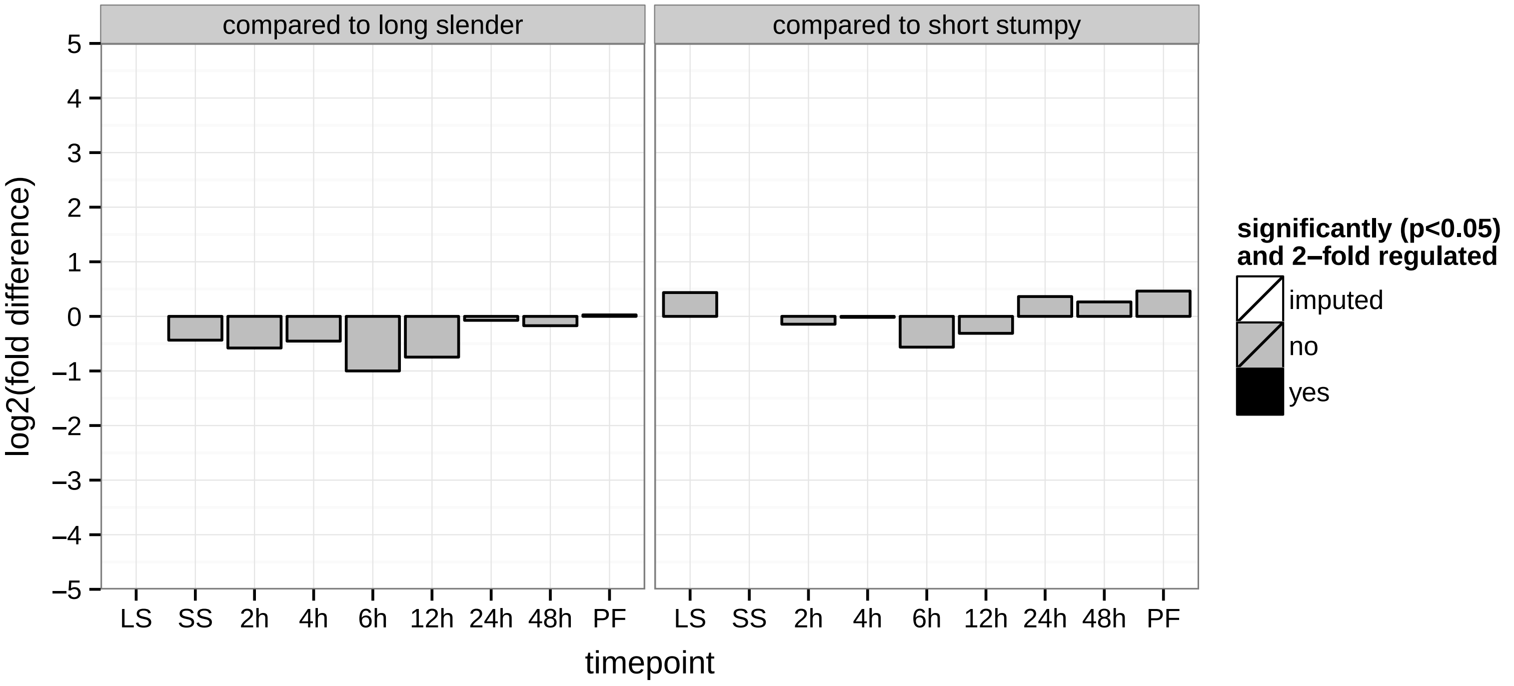
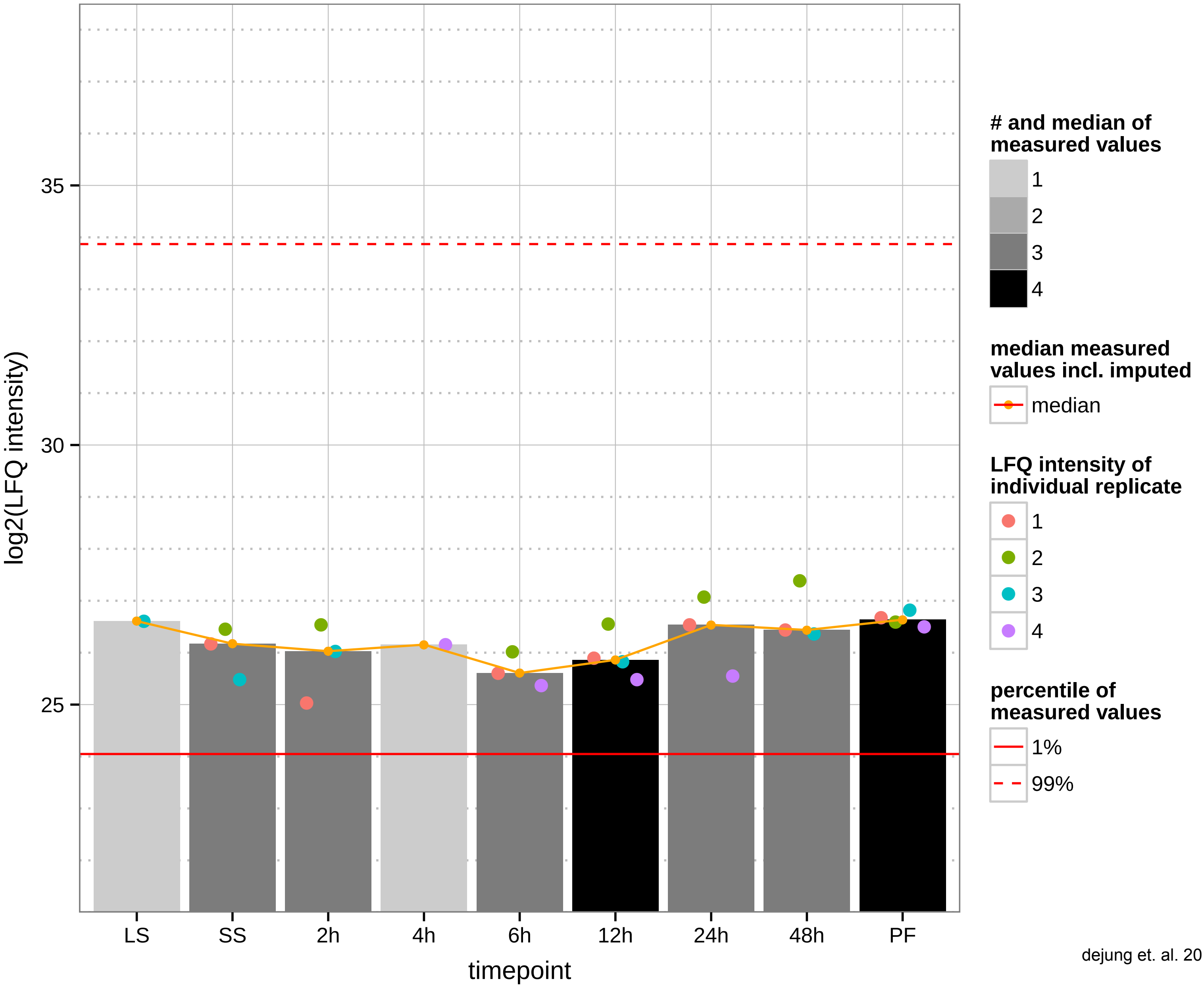
hypothetical protein, conserved
Tb927.7.2780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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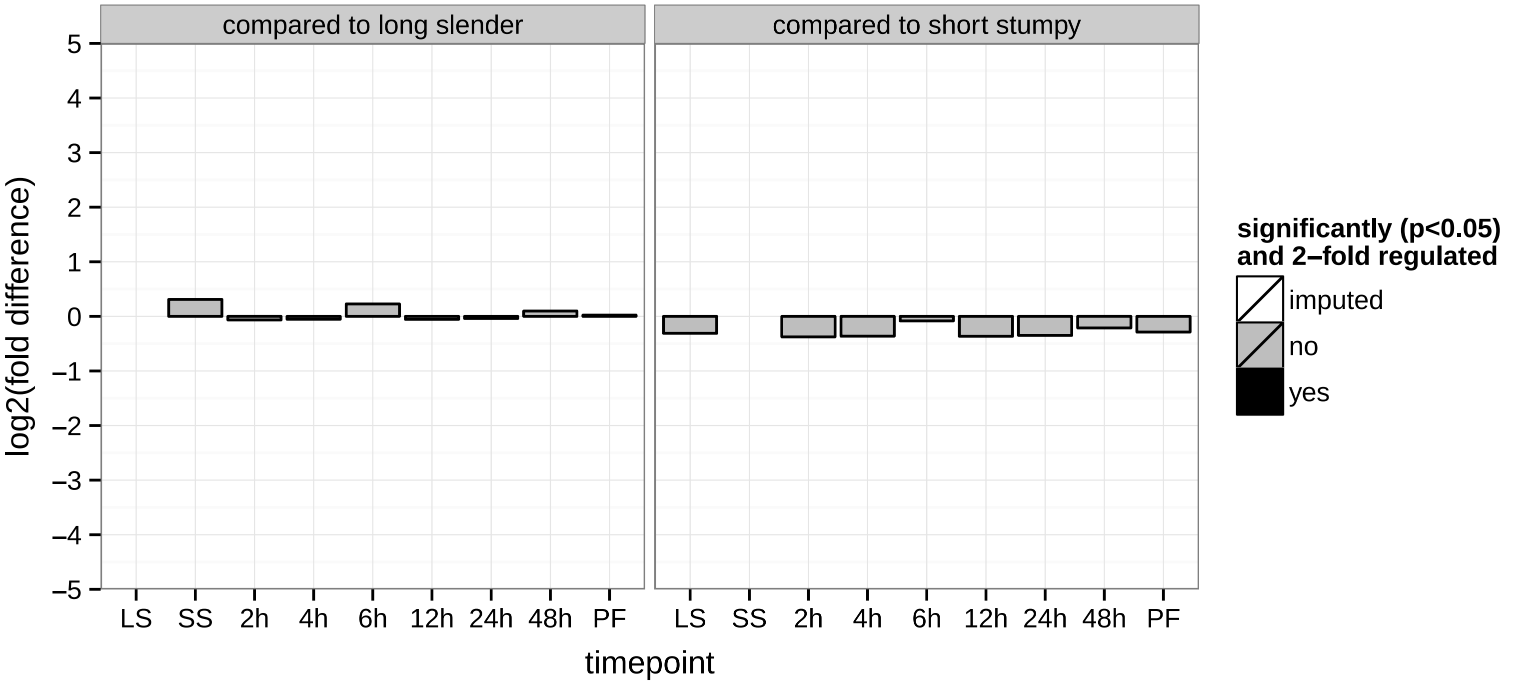
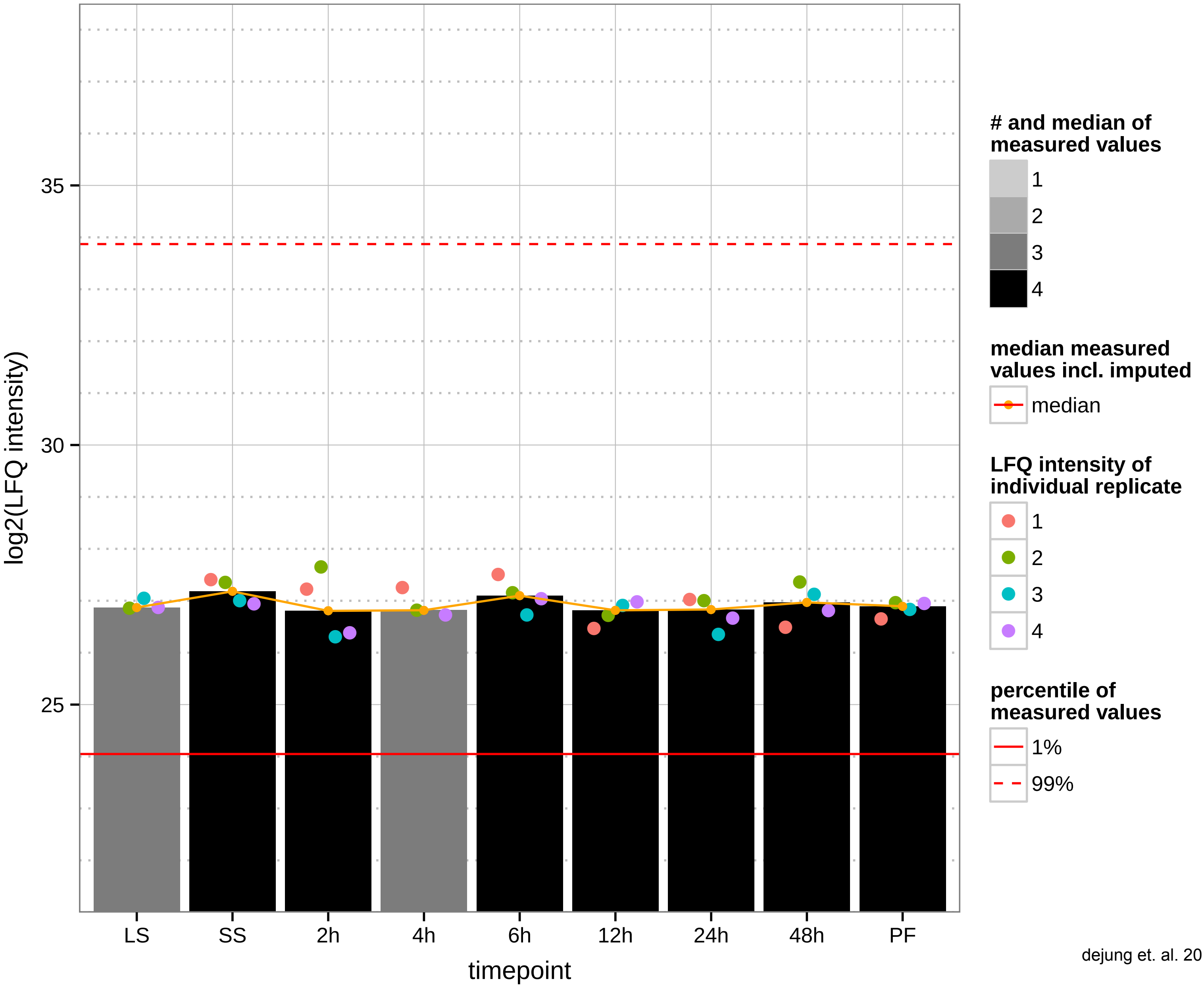
hypothetical protein, conserved
Tb927.7.2790
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null





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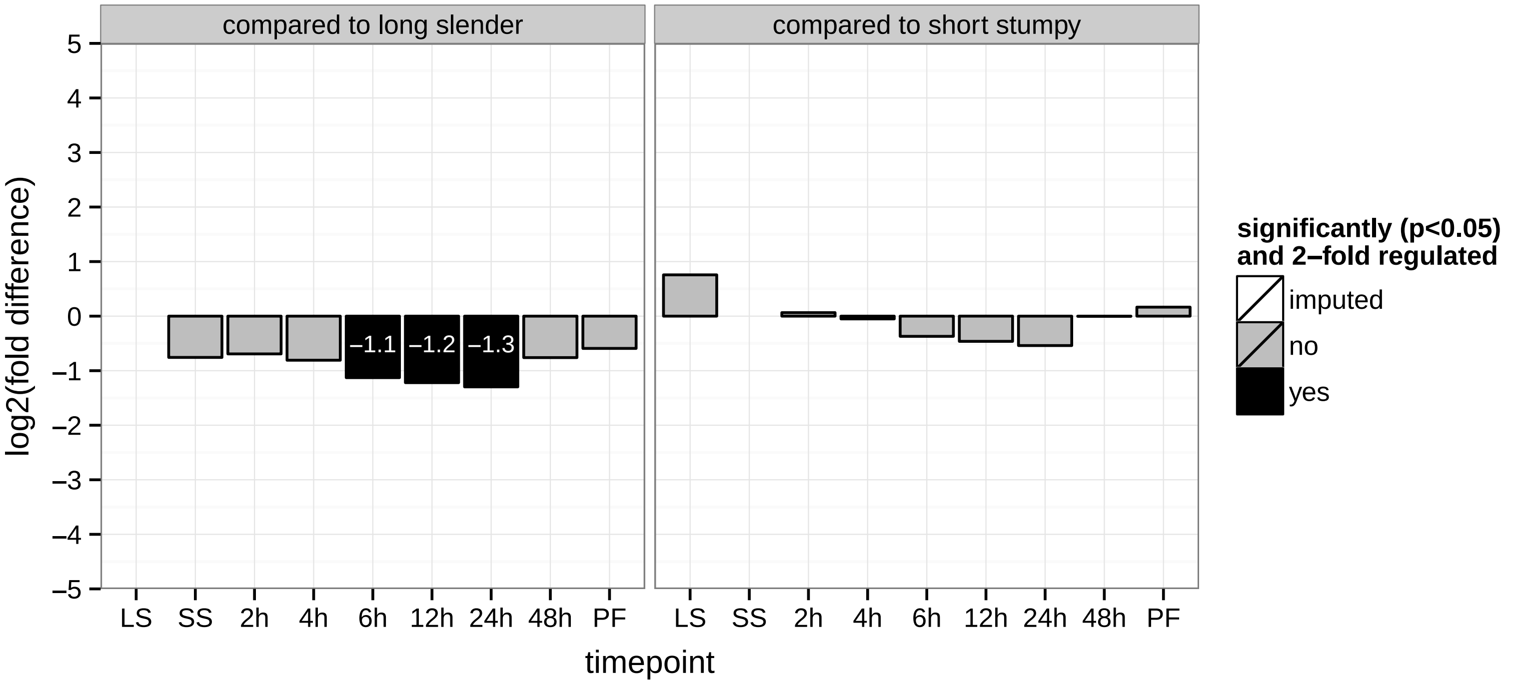
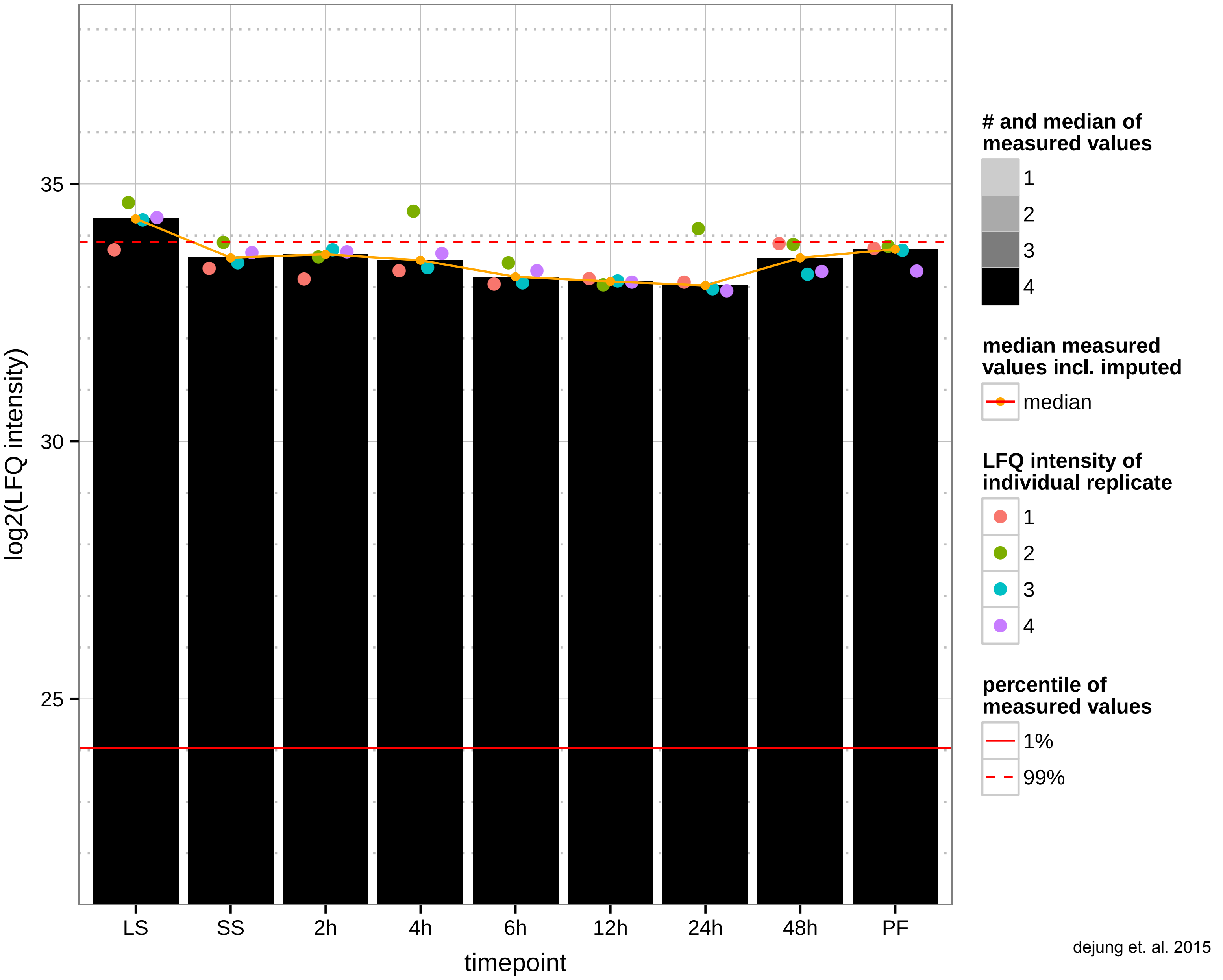
histone H2A, putative
Tb927.7.2940;Tb927.7.2930;Tb927.7.2920;Tb927.7.2910;Tb927.7.2900;Tb927.7.2890;Tb927.7.2880;Tb927.7.2870;Tb927.7
AGOF: DNA binding
AGOC: nucleosome, nucleus
AGOP: chromosome organization, nucleosome assembly
PGOF: DNA binding, null
PGOC: nucleosome, nucleus, null
PGOP: nucleosome assembly, null





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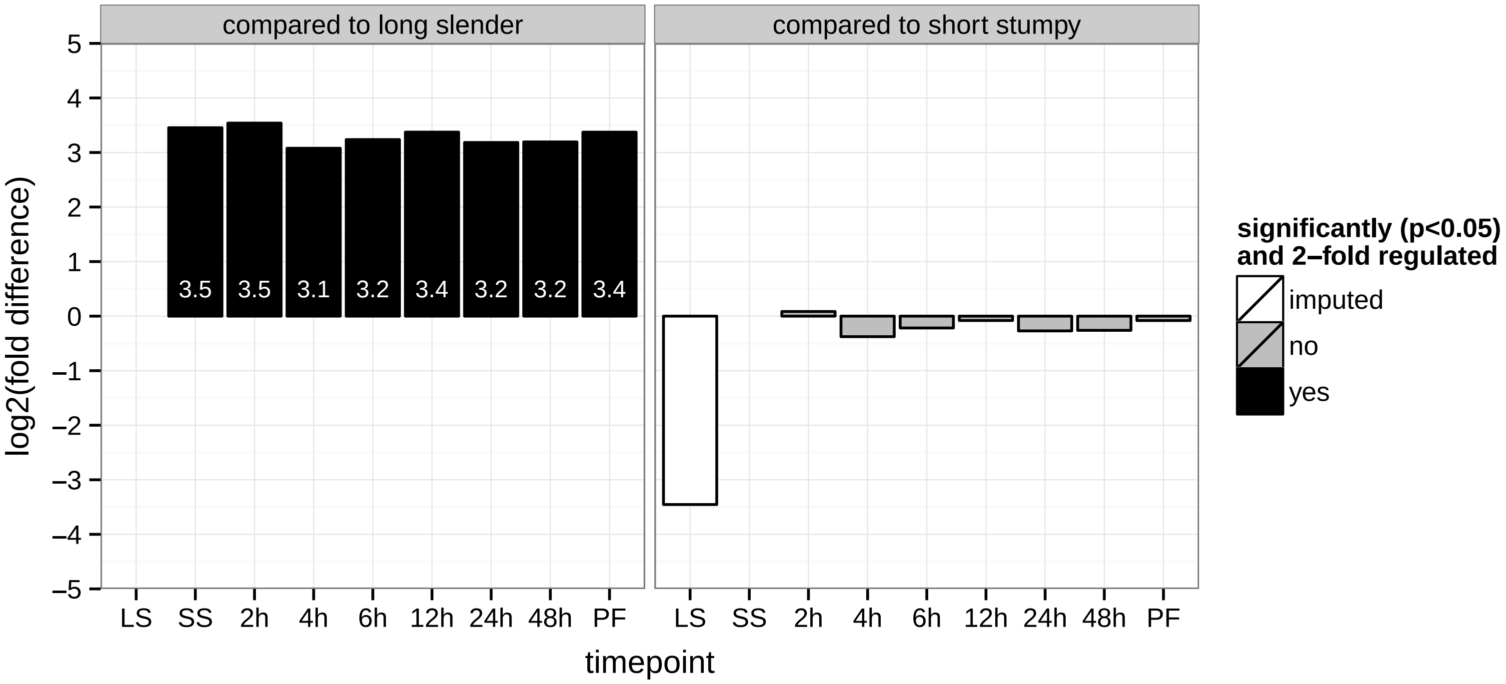
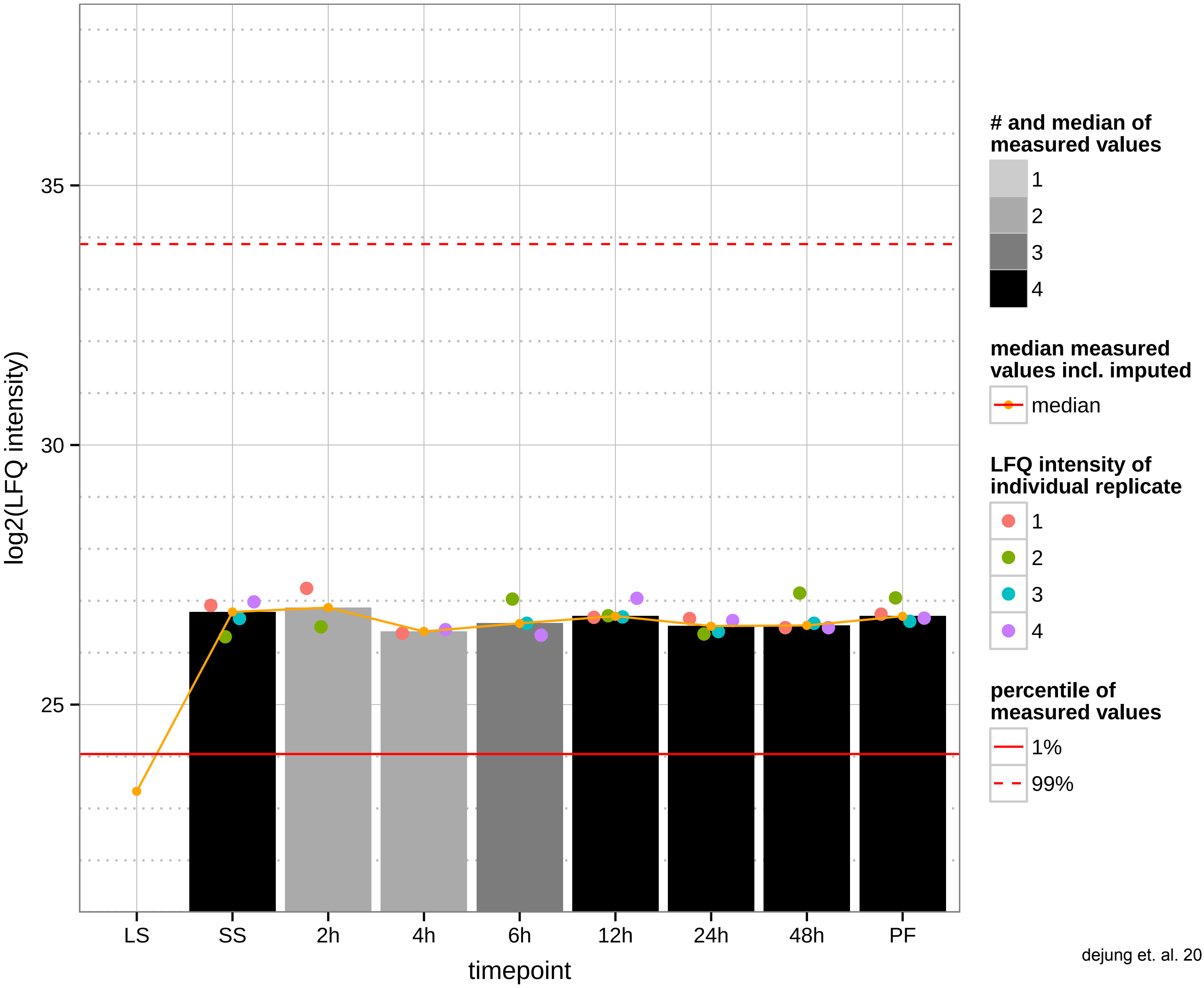
hypothetical protein, conserved
Tb927.7.3080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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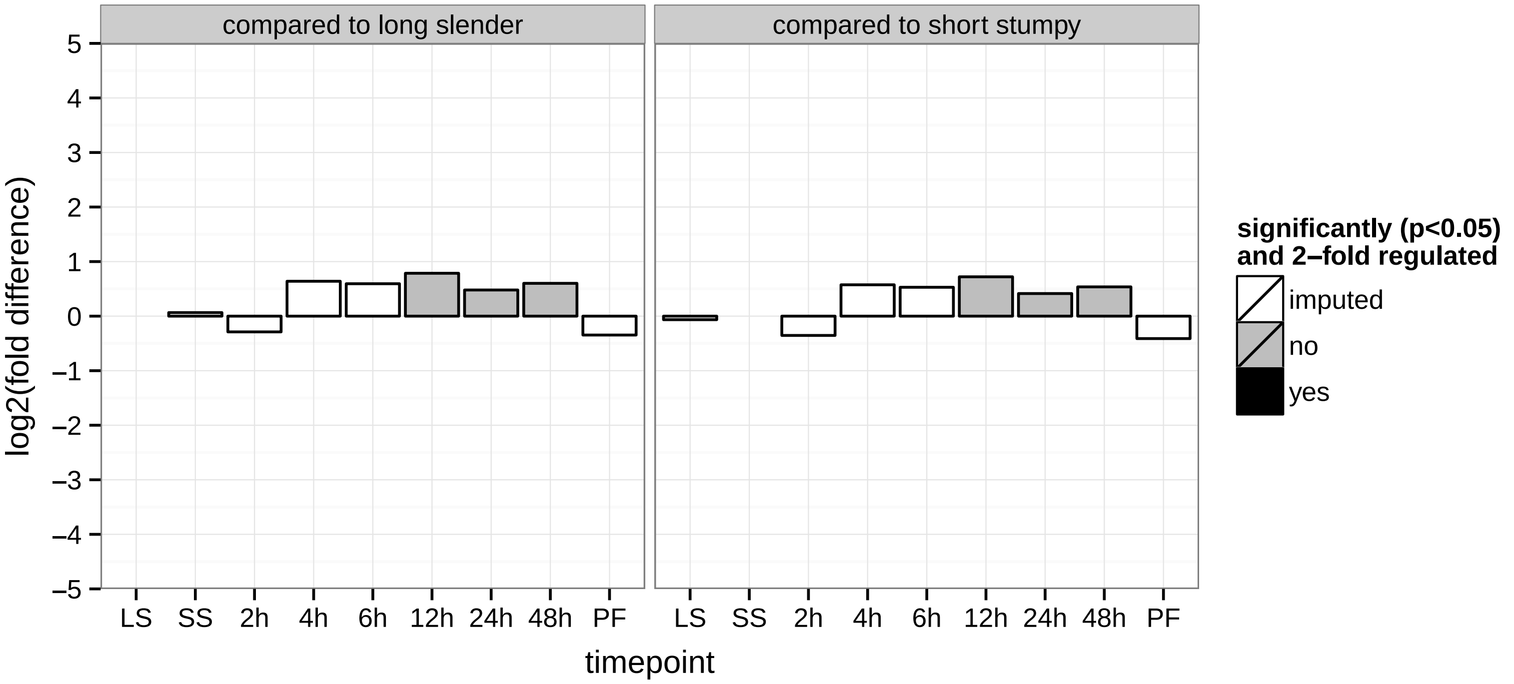
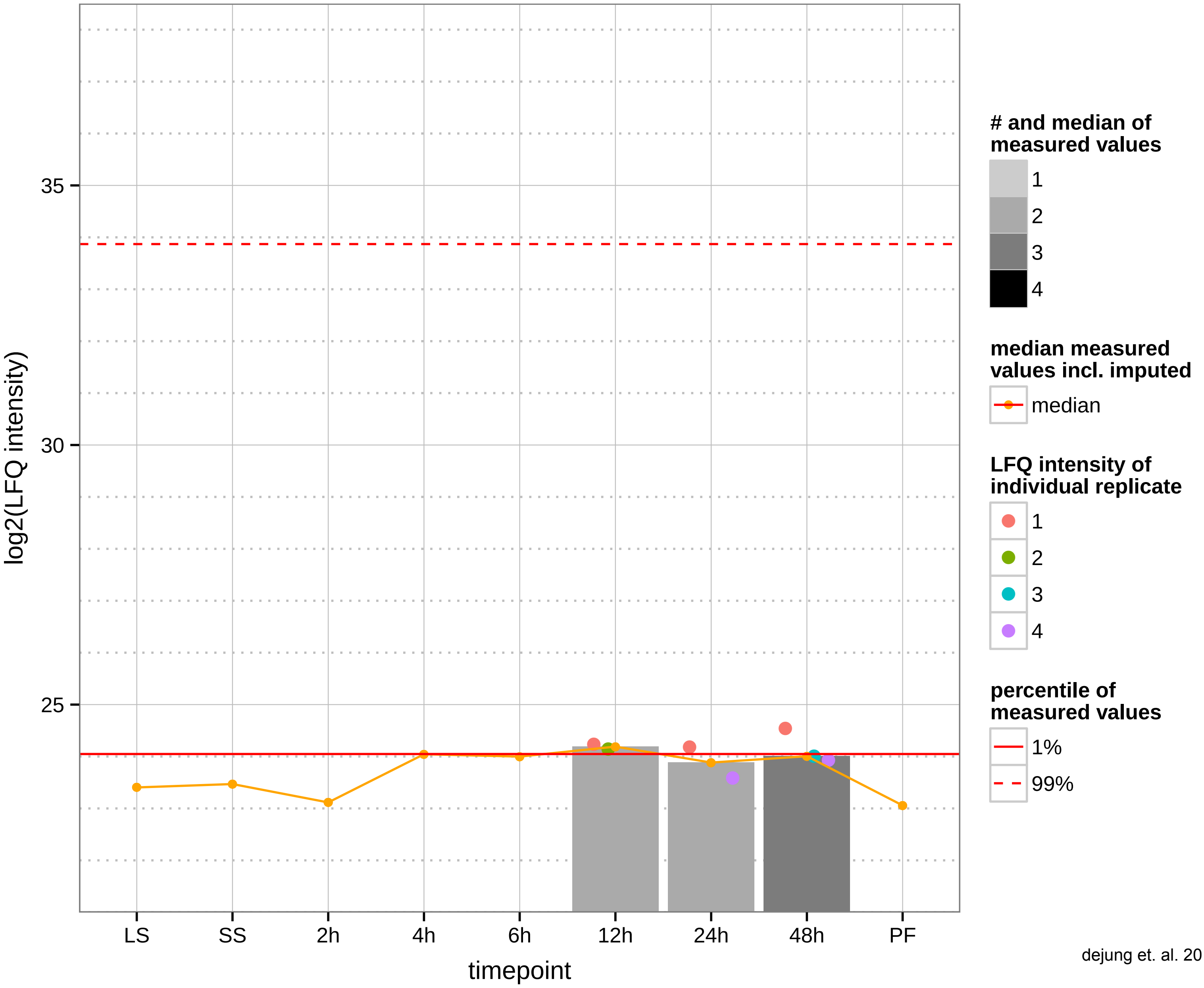
hypothetical protein, conserved
Tb927.7.310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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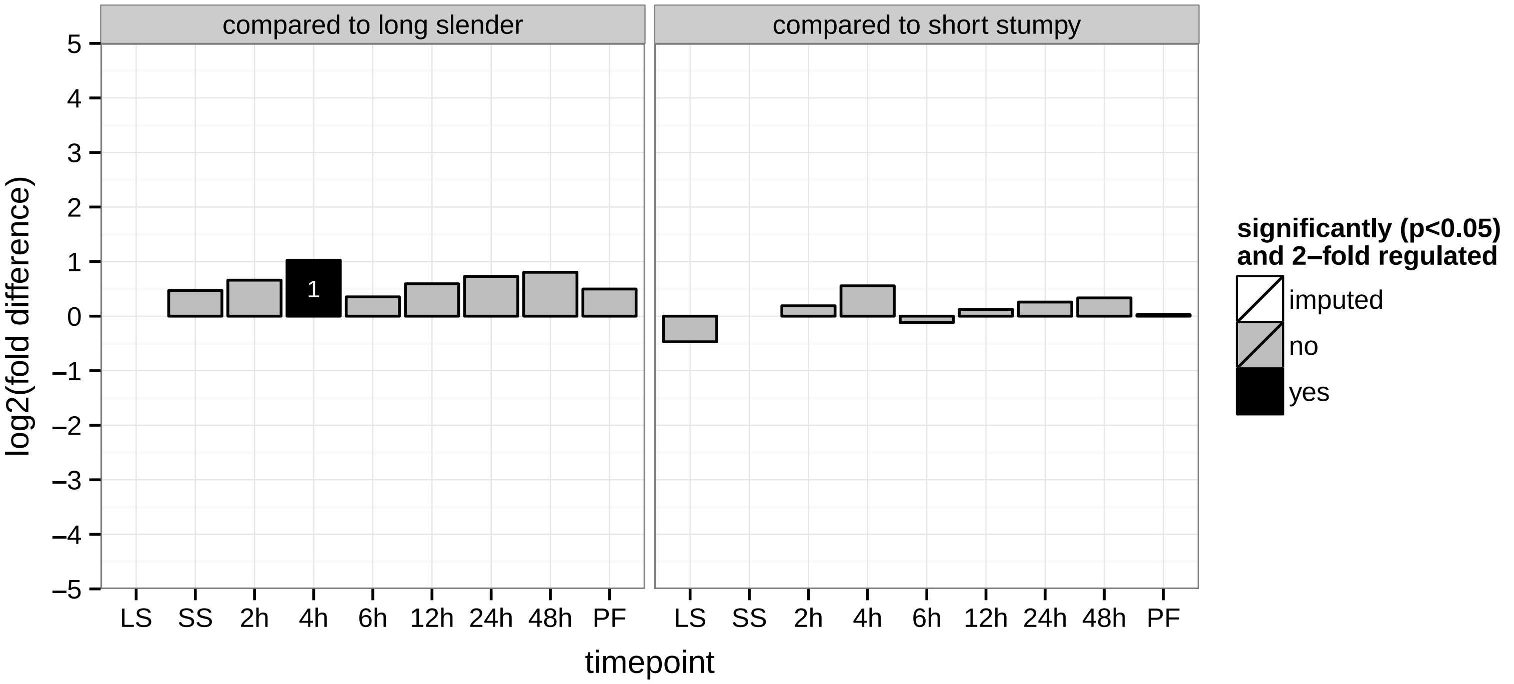
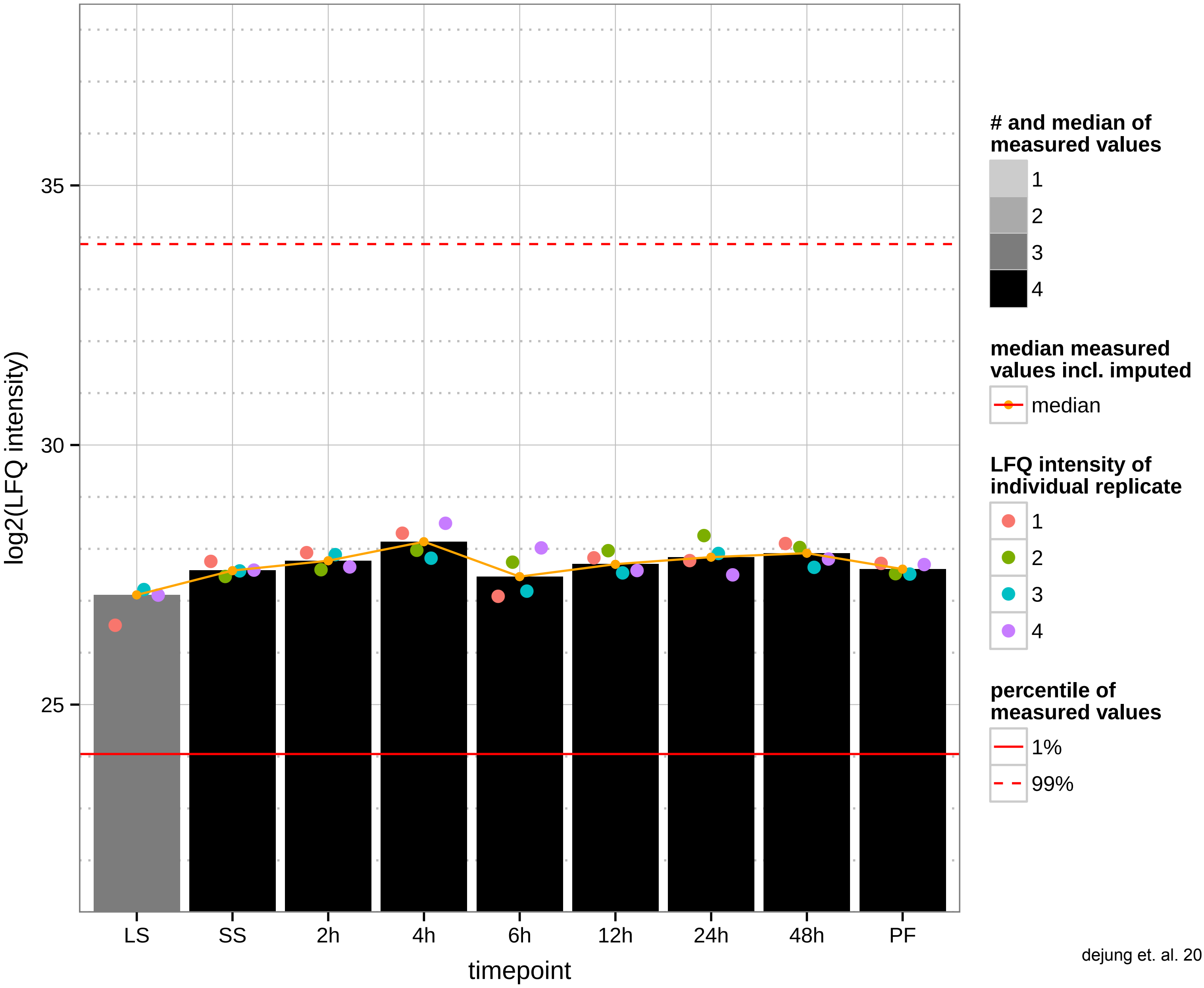
small nuclear ribonucleoprotein SmD1, SmD−1 like small nuclear ribonucleoprotein (Sm−D1)
Tb927.7.3120
AGOF: snRNA binding
AGOC: nucleus, small nuclear ribonucleoprotein complex
AGOP: nuclear mRNA trans splicing, SL addition
PGOF: null
PGOC: null
PGOP: null





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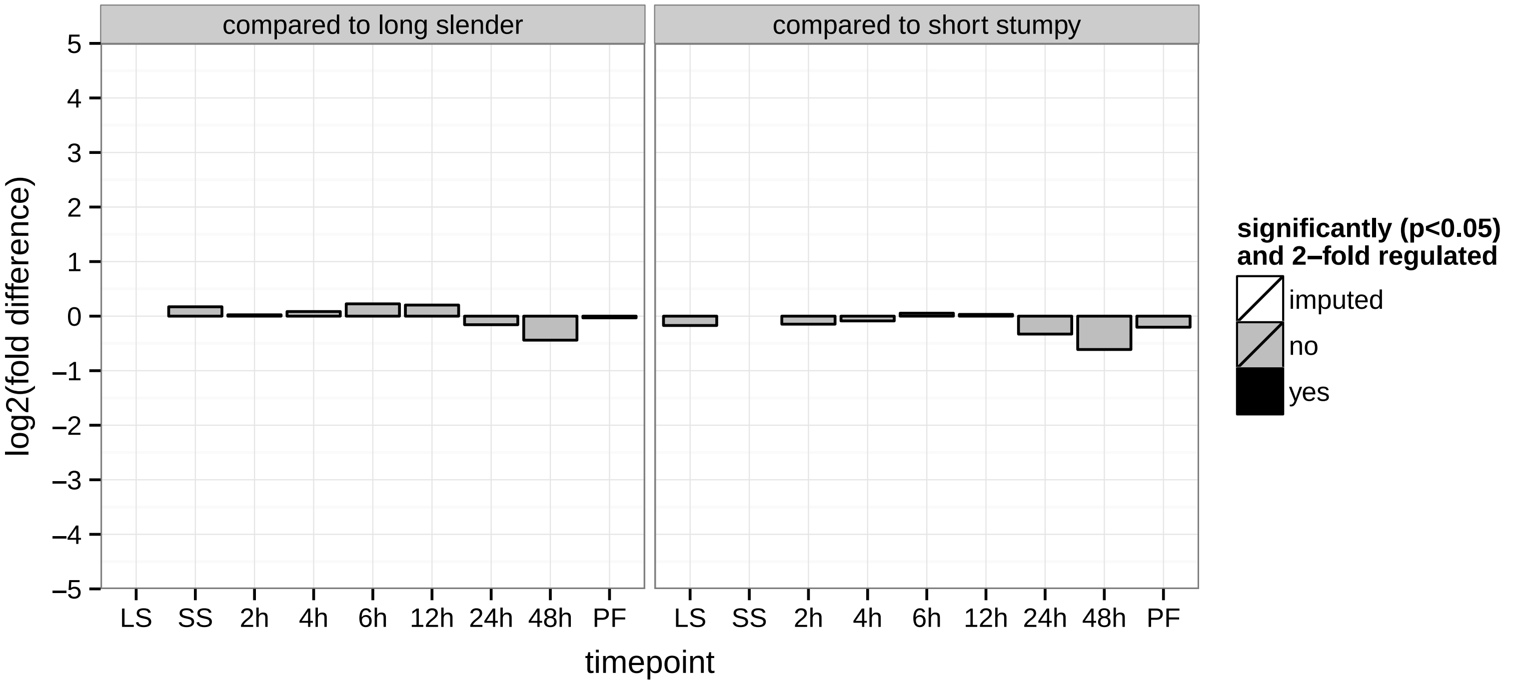
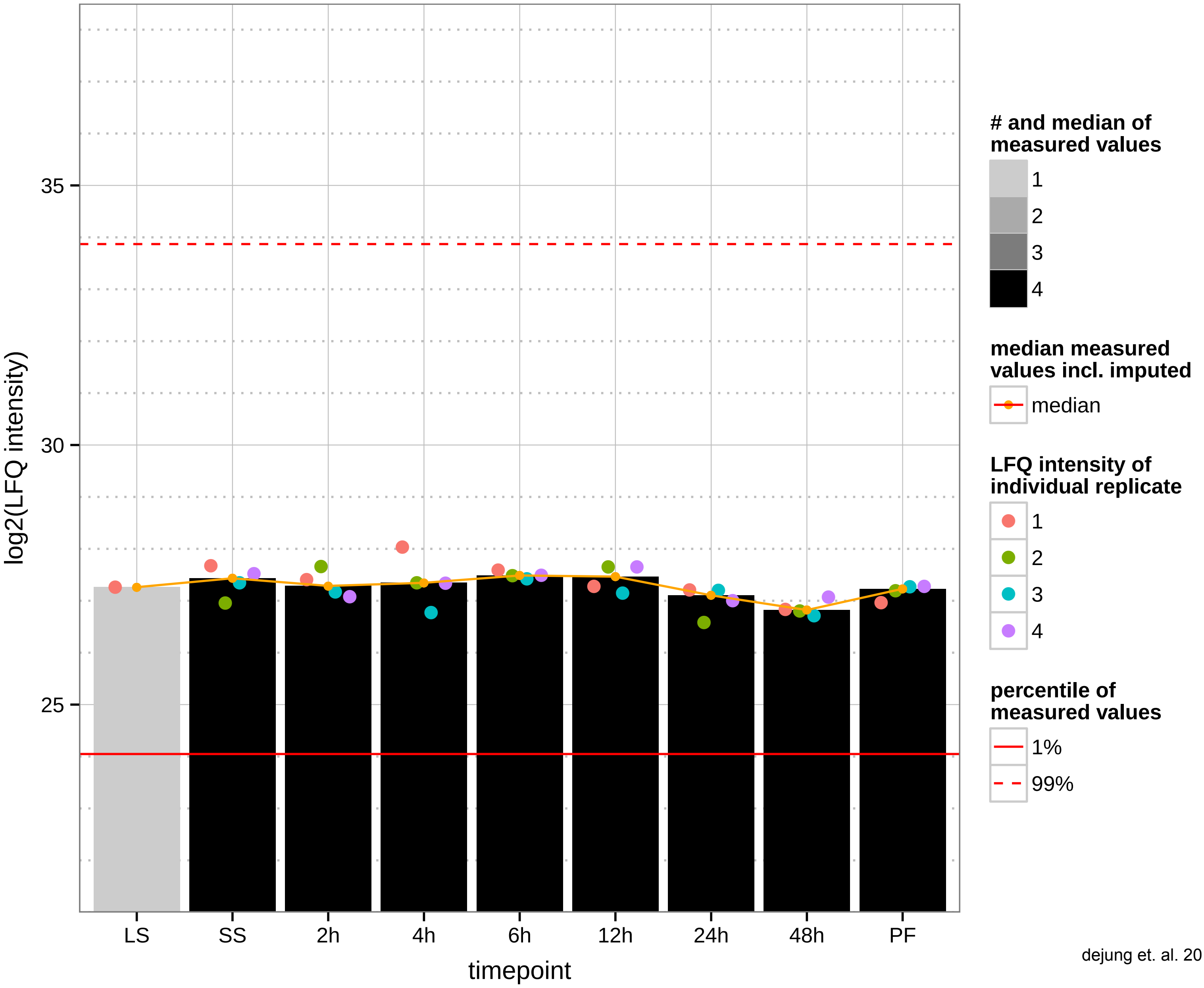
hypothetical protein, conserved
Tb927.7.3170
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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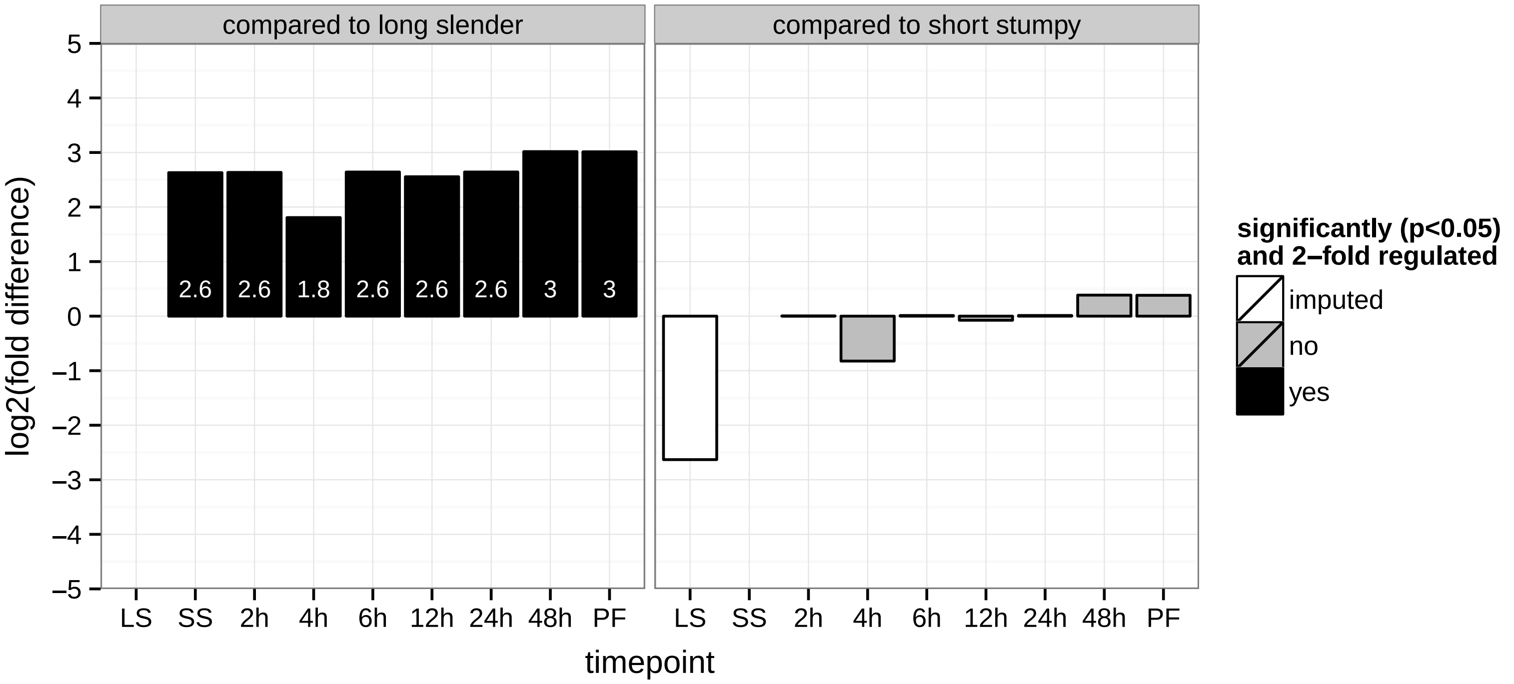
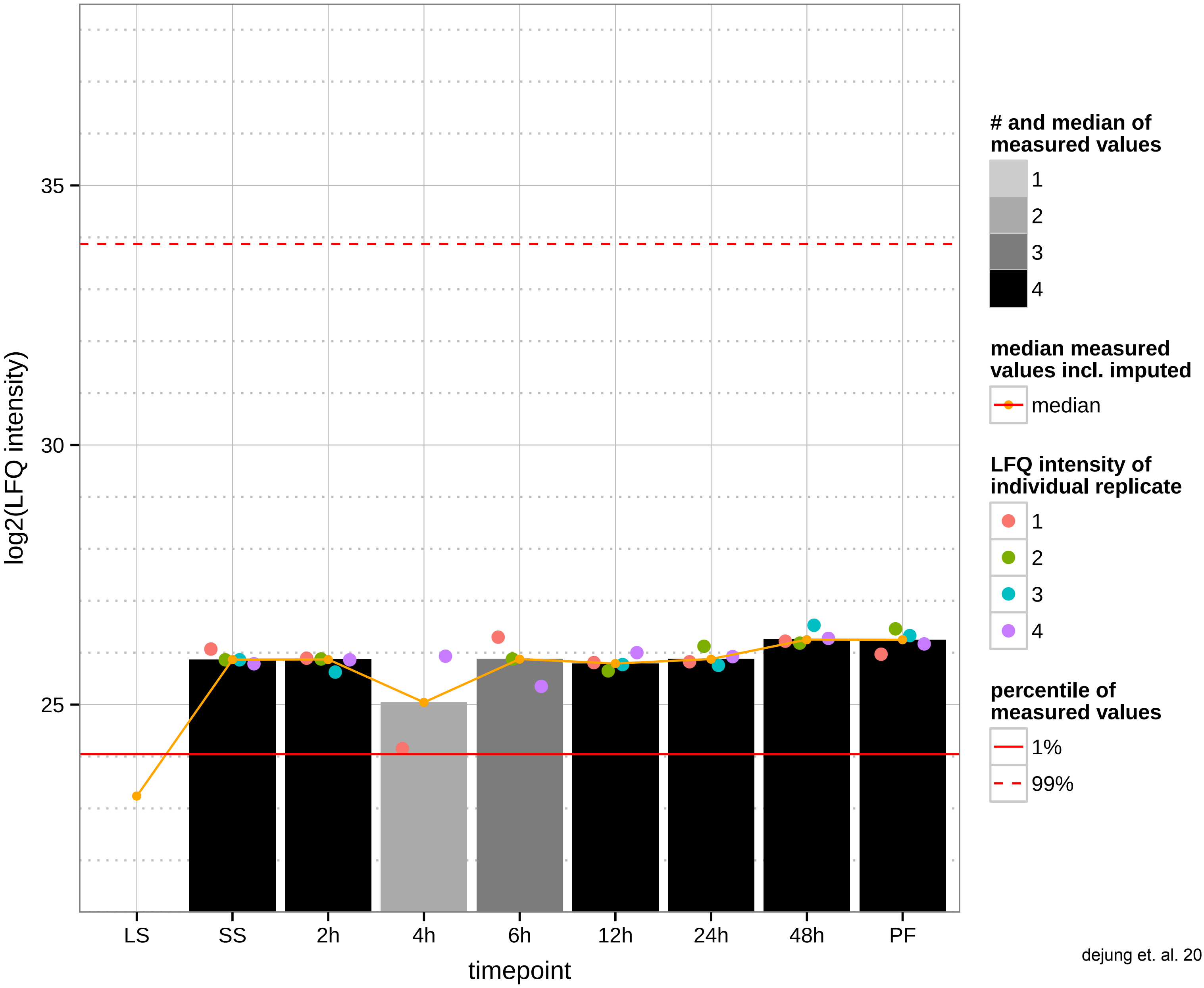
hypothetical protein, conserved
Tb927.7.3290
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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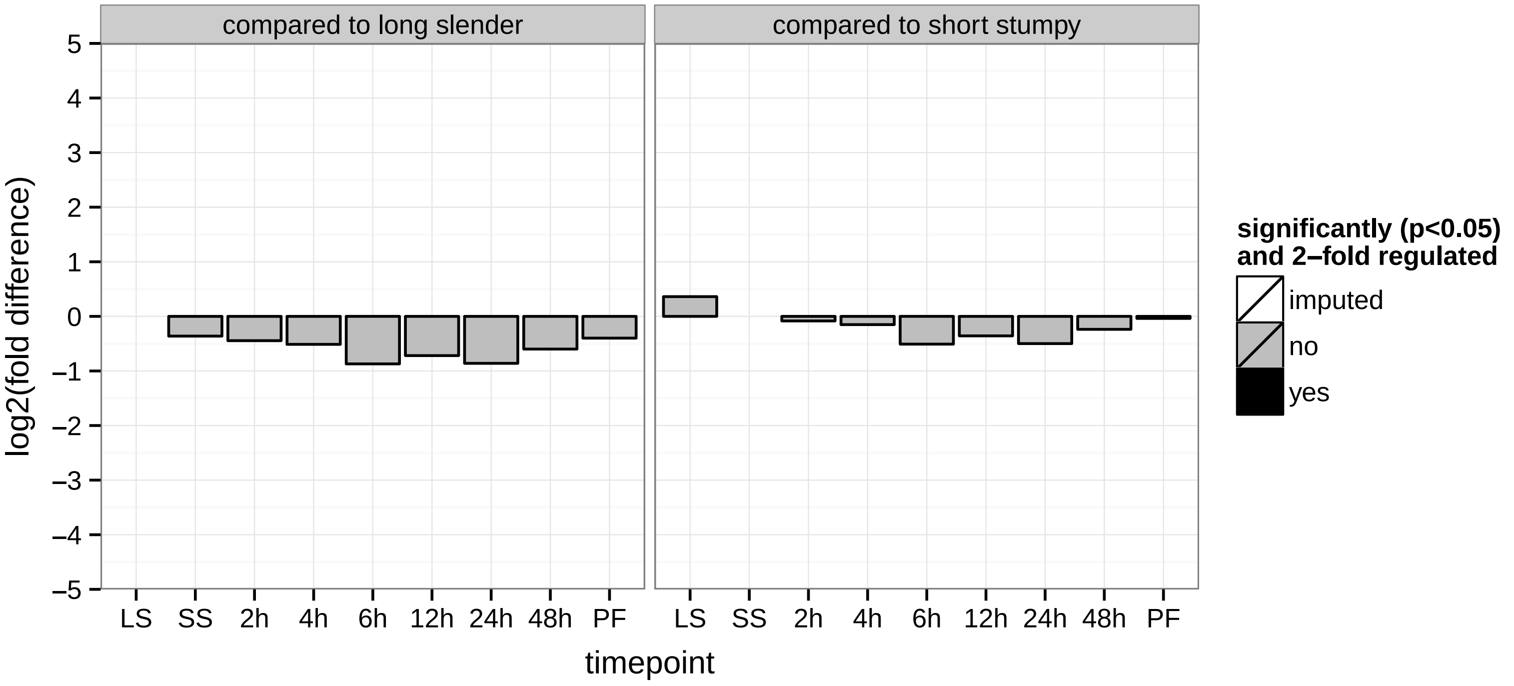
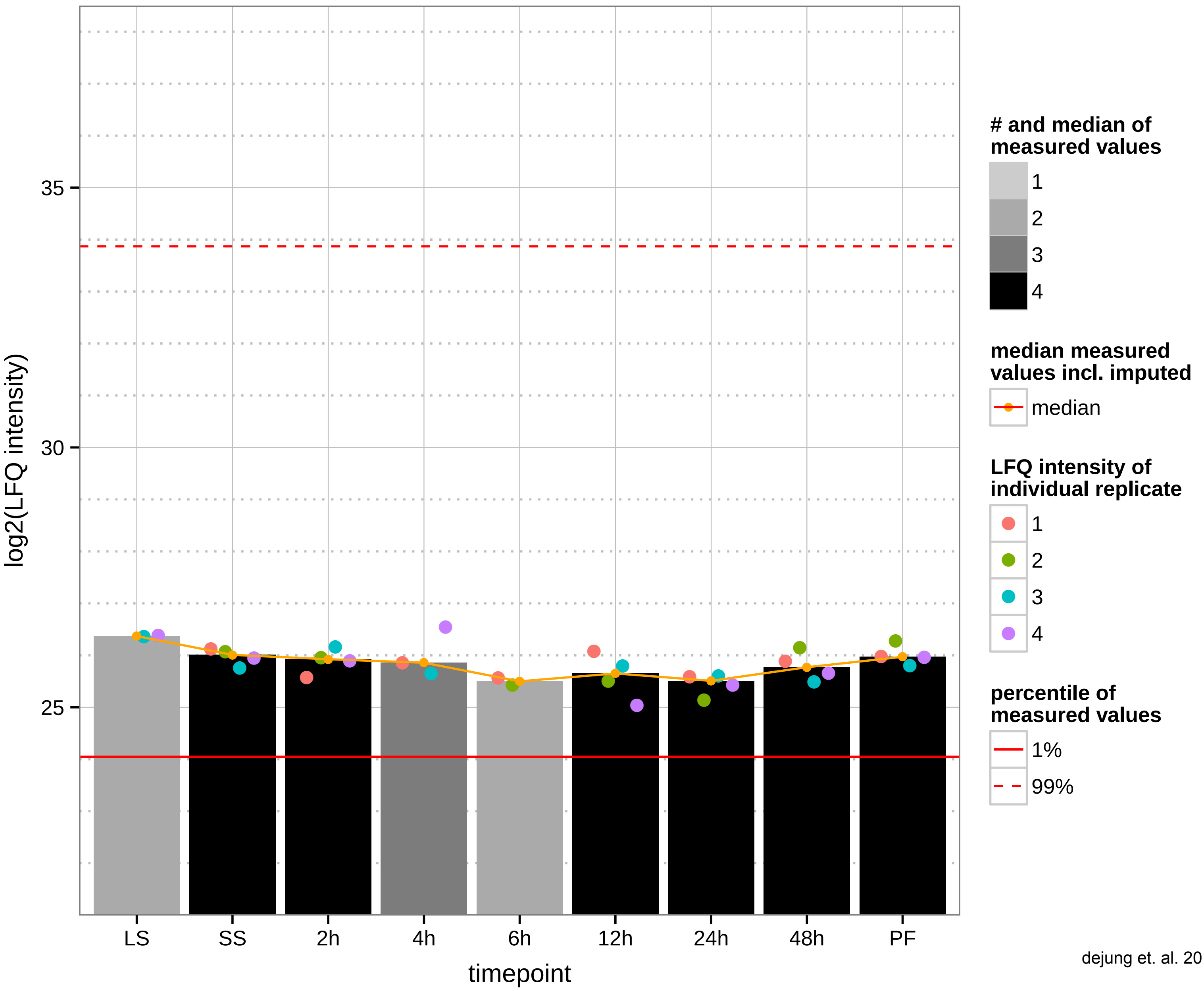
hypothetical protein, conserved
Tb927.7.3310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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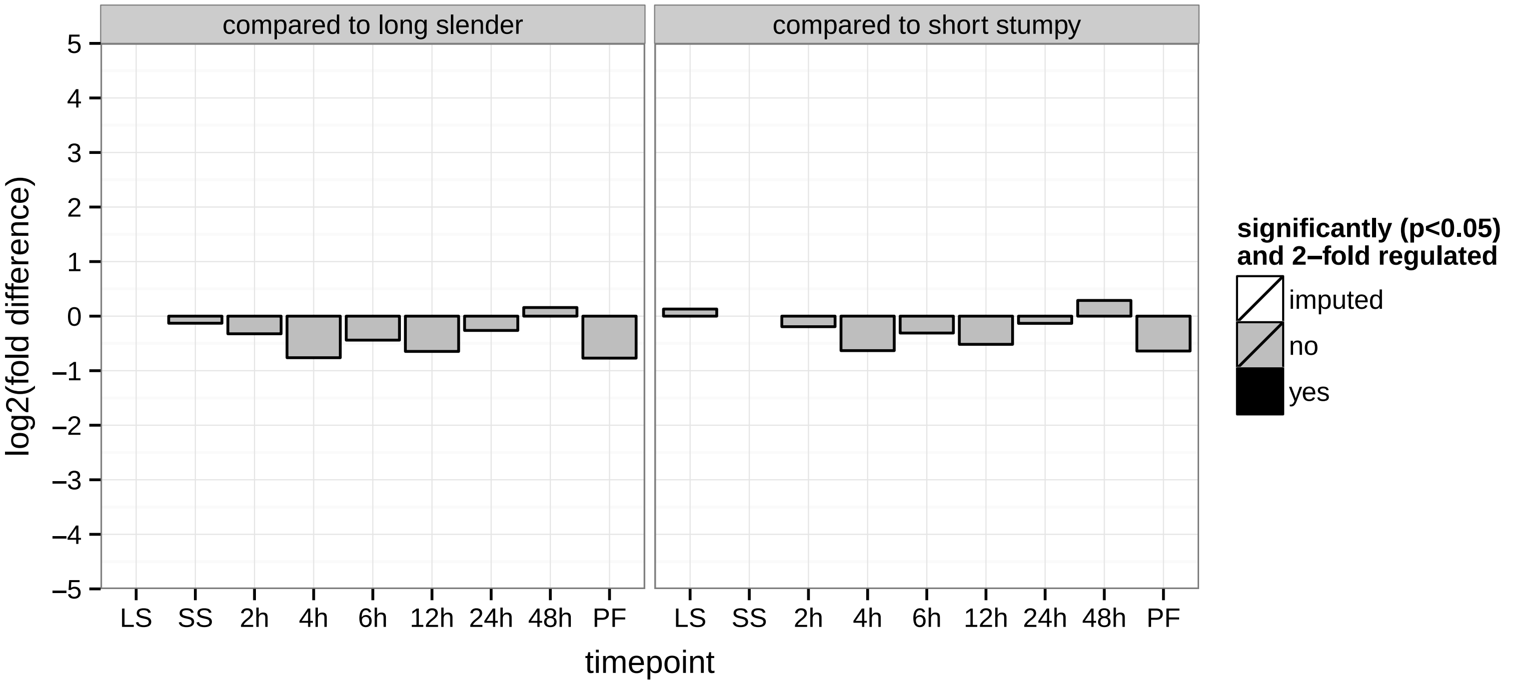
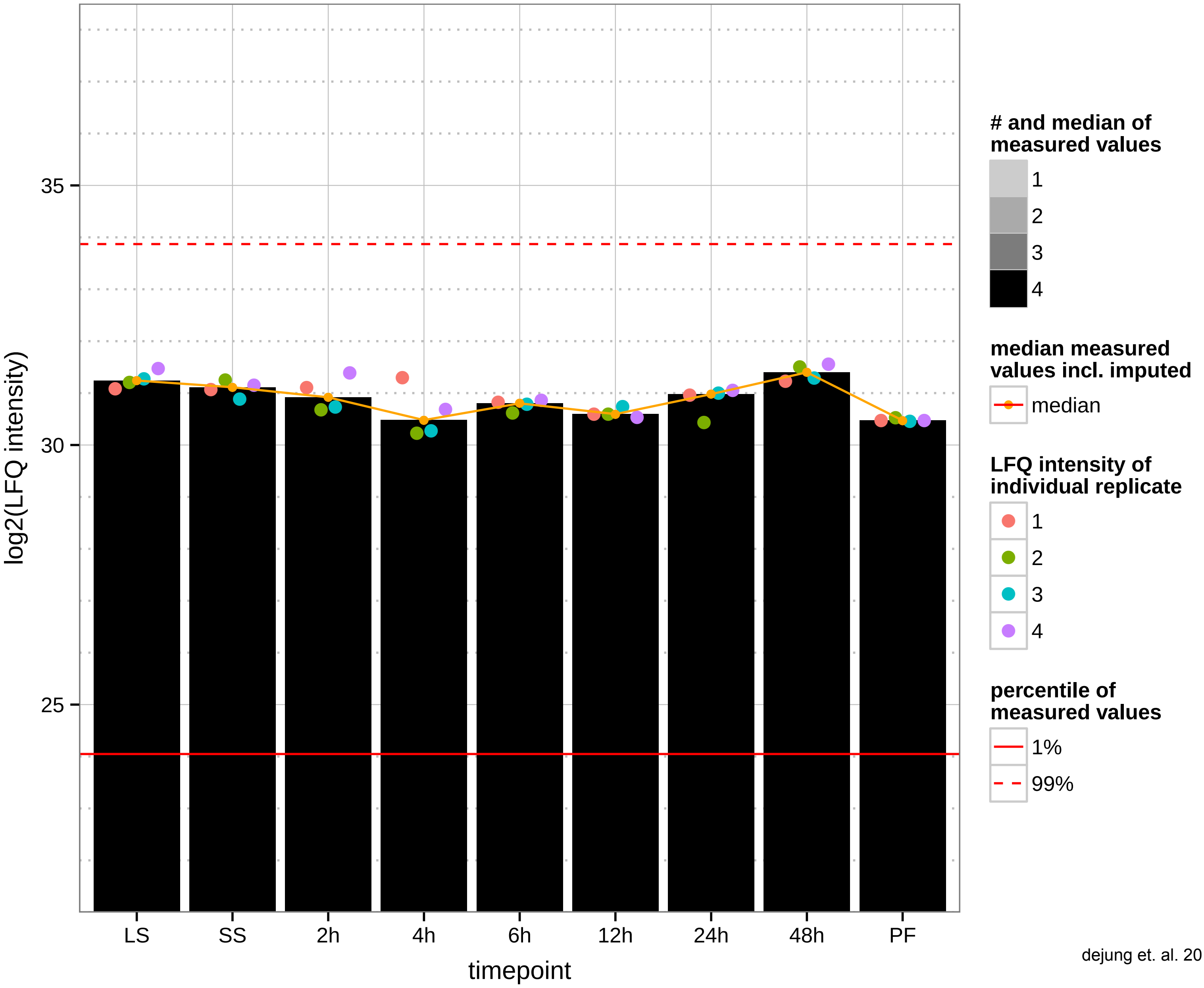
hypothetical protein, conserved
Tb927.7.3330
AGOF: null
AGOC: membrane, nucleus
AGOP: regulation of transcription, DNA−dependent, vesicle−mediated transport
PGOF: null
PGOC: null
PGOP: null





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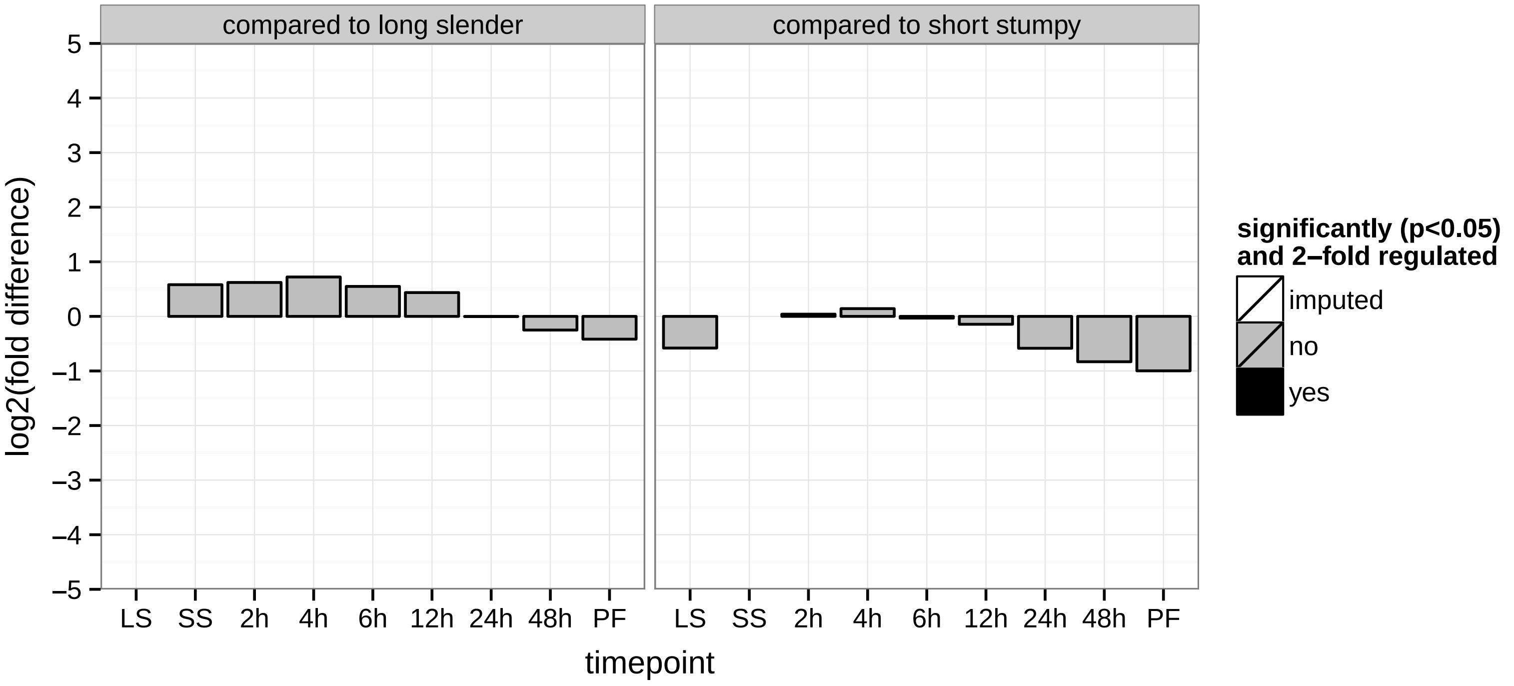
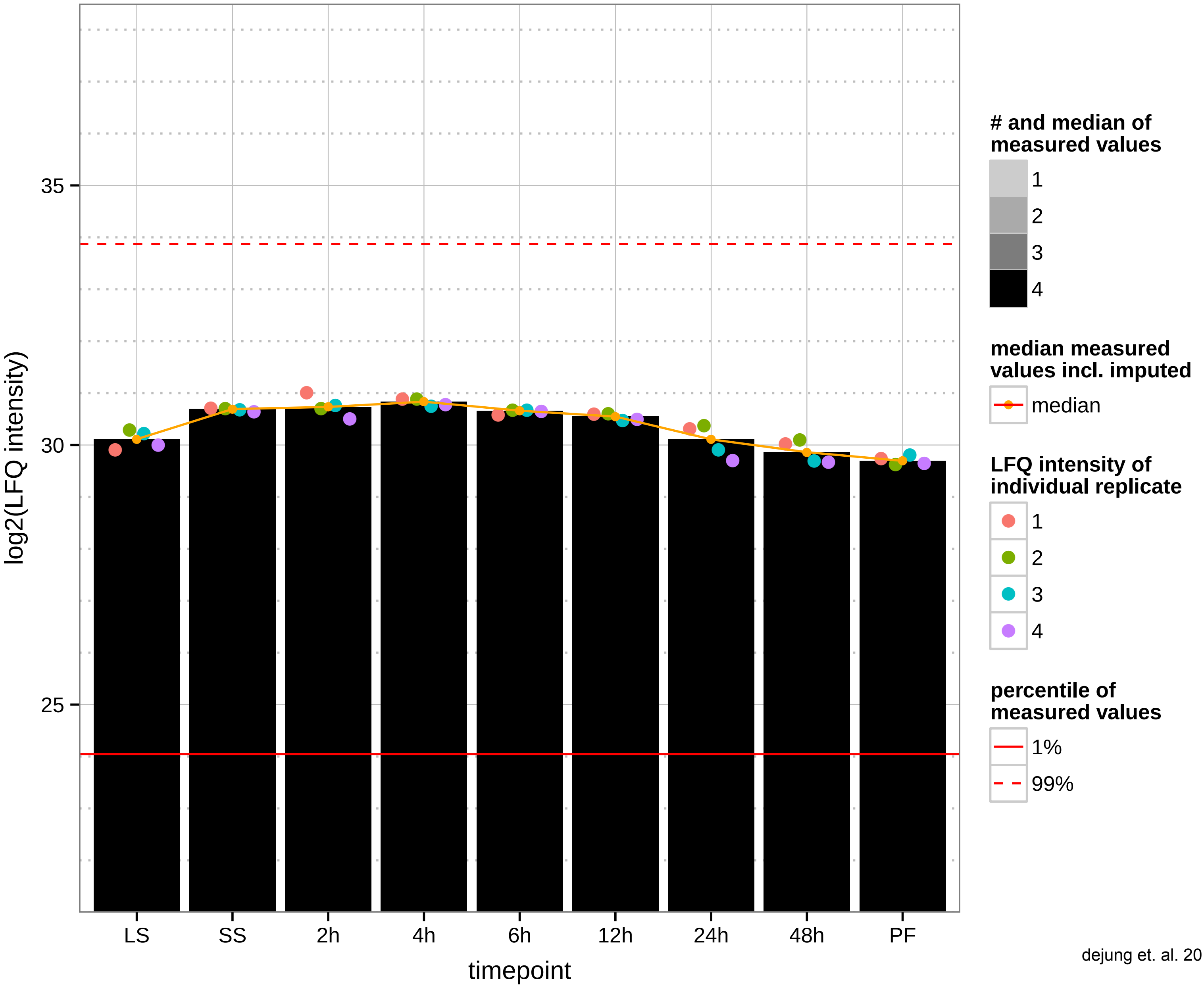
hypothetical protein, conserved
Tb927.7.3370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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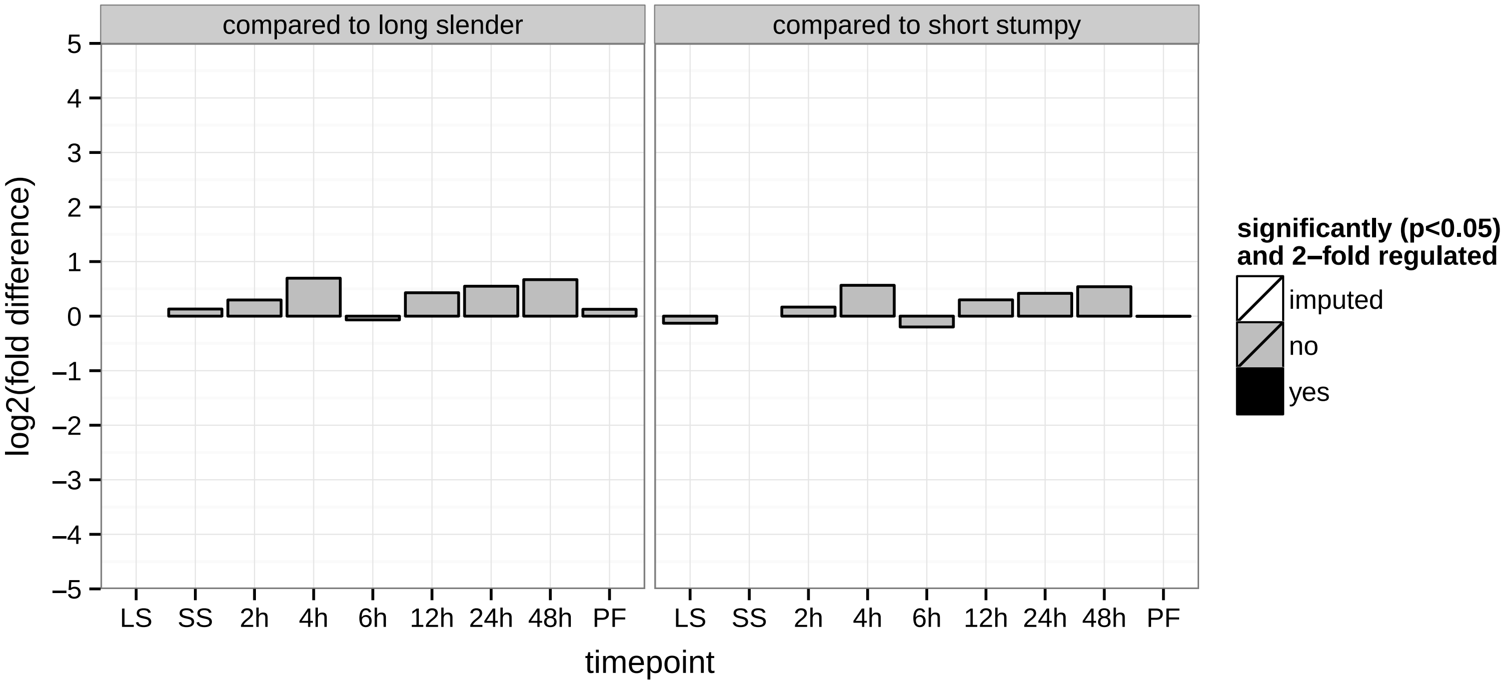
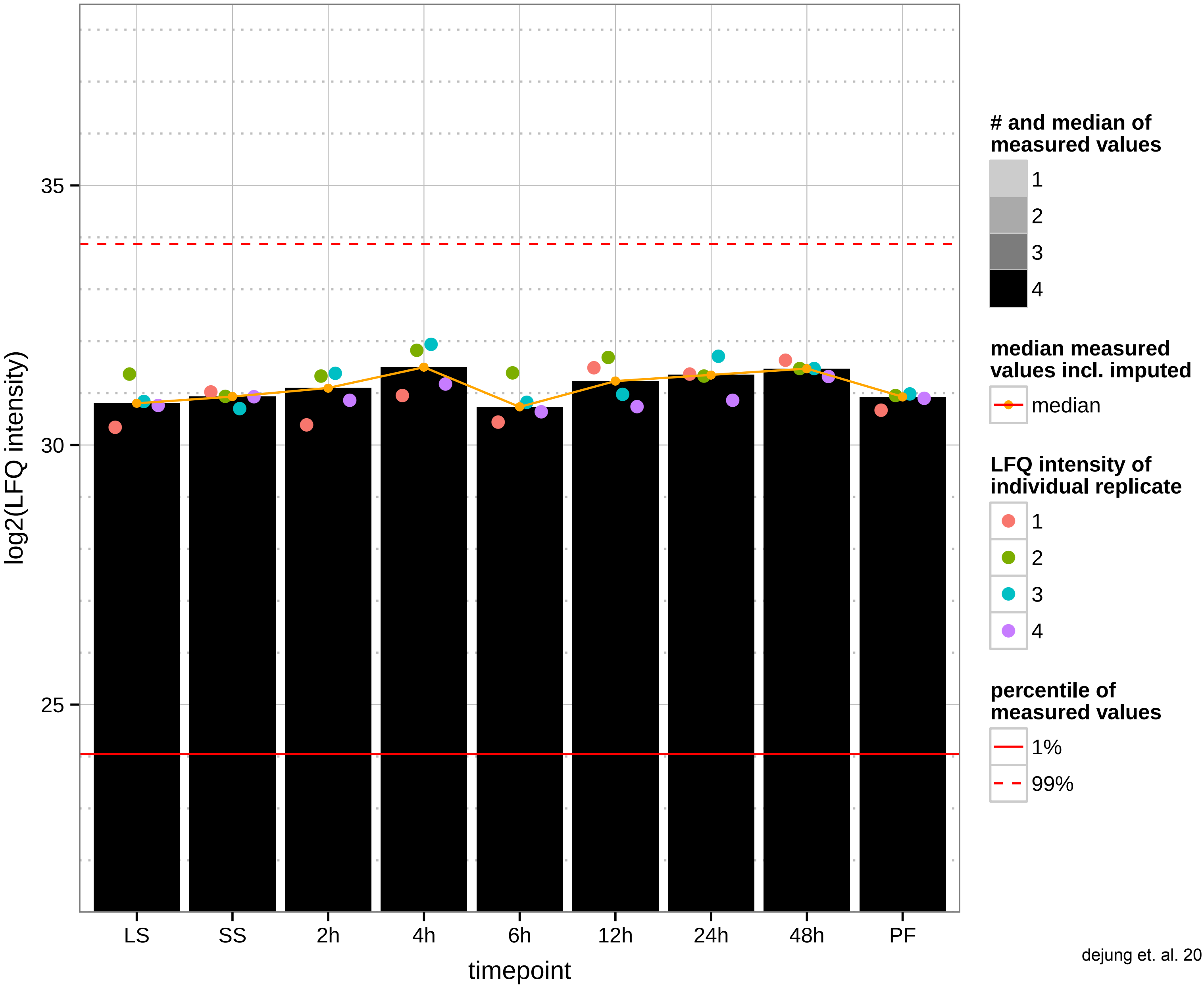
I/6 autoantigen
Tb927.7.3440
AGOF: calcium ion binding, structural constituent of cytoskeleton
AGOC: microtubule cytoskeleton
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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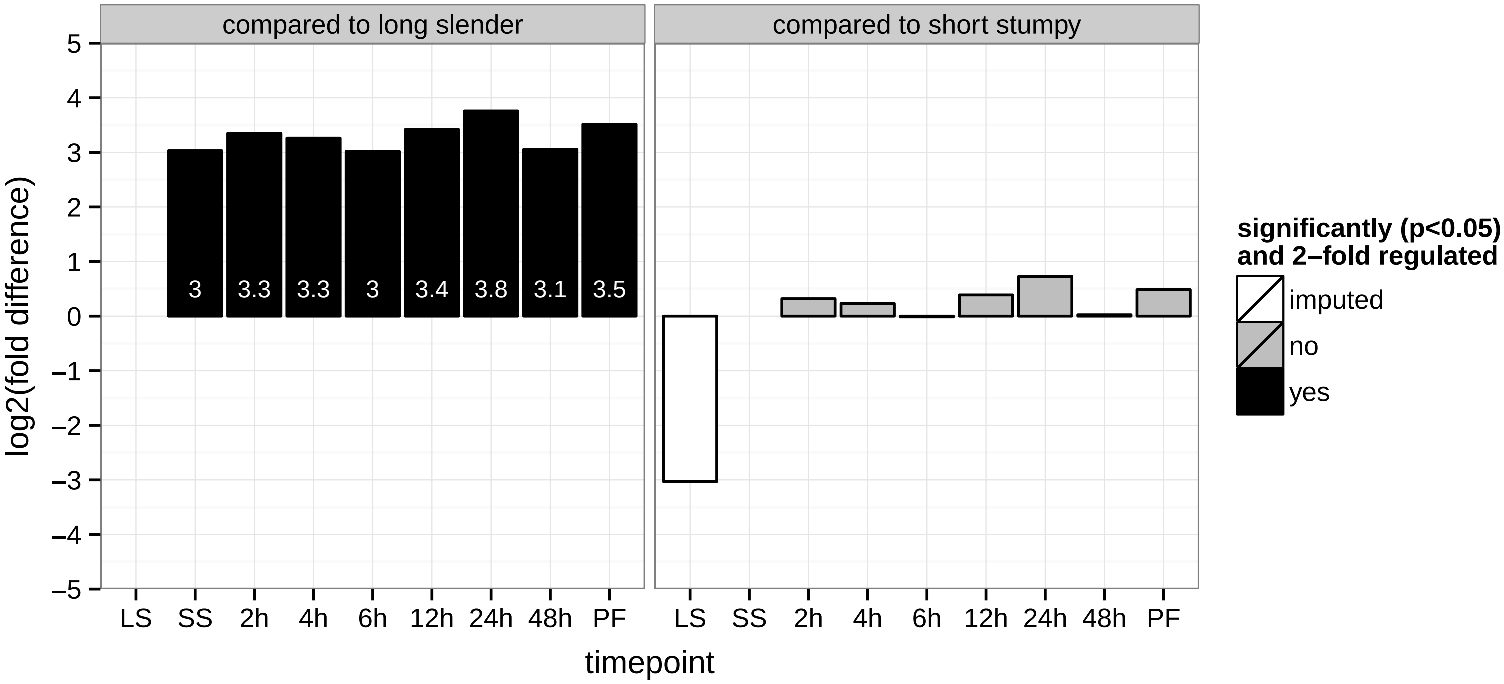
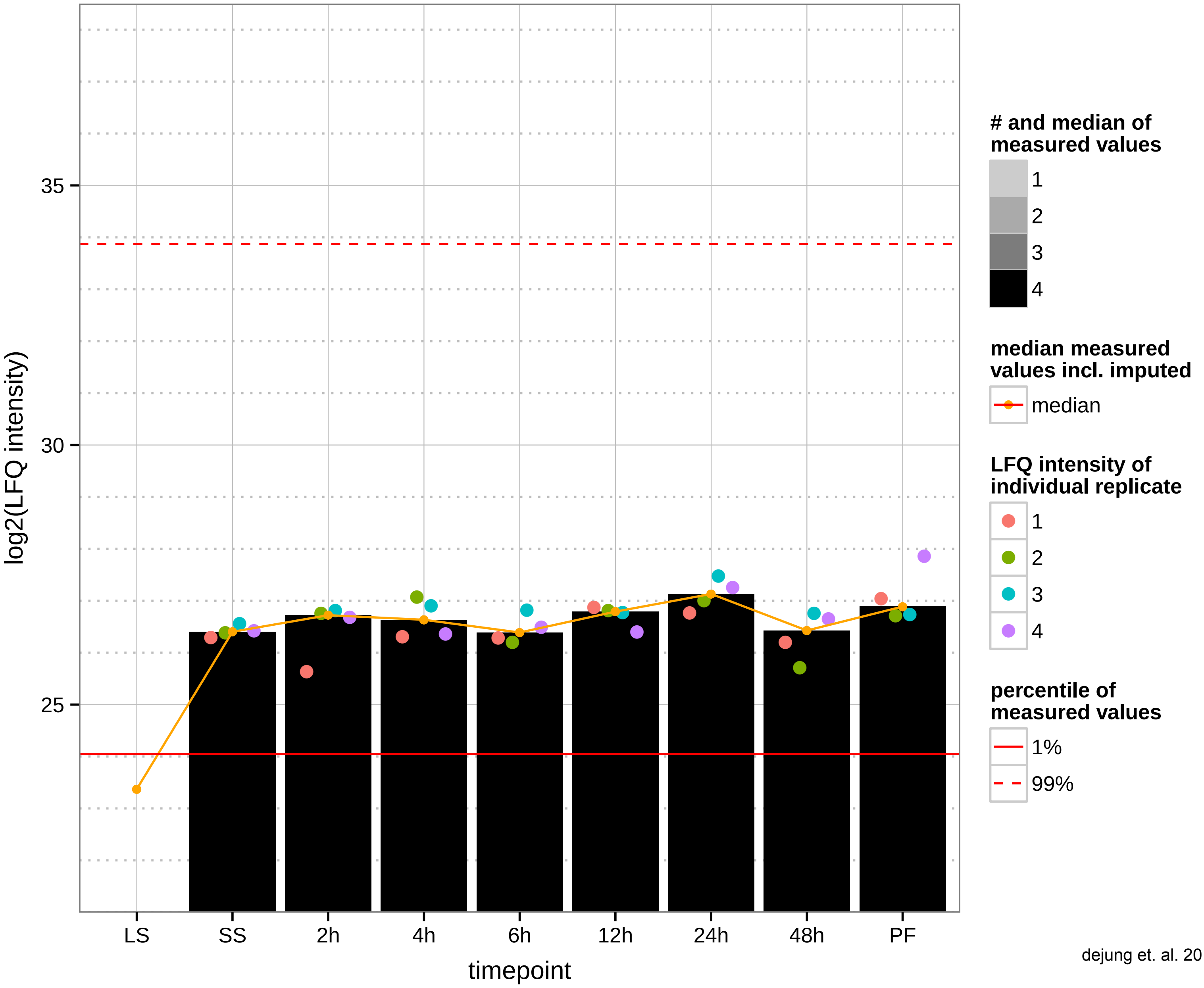
mitochondrial pyruvate carrier protein 2, putative
Tb927.7.3520
AGOF: pyruvate transmembrane transporter activity
AGOC: mitochondrial membrane, mitochondrion
AGOP: pyruvate transport
PGOF: null
PGOC: null
PGOP: null





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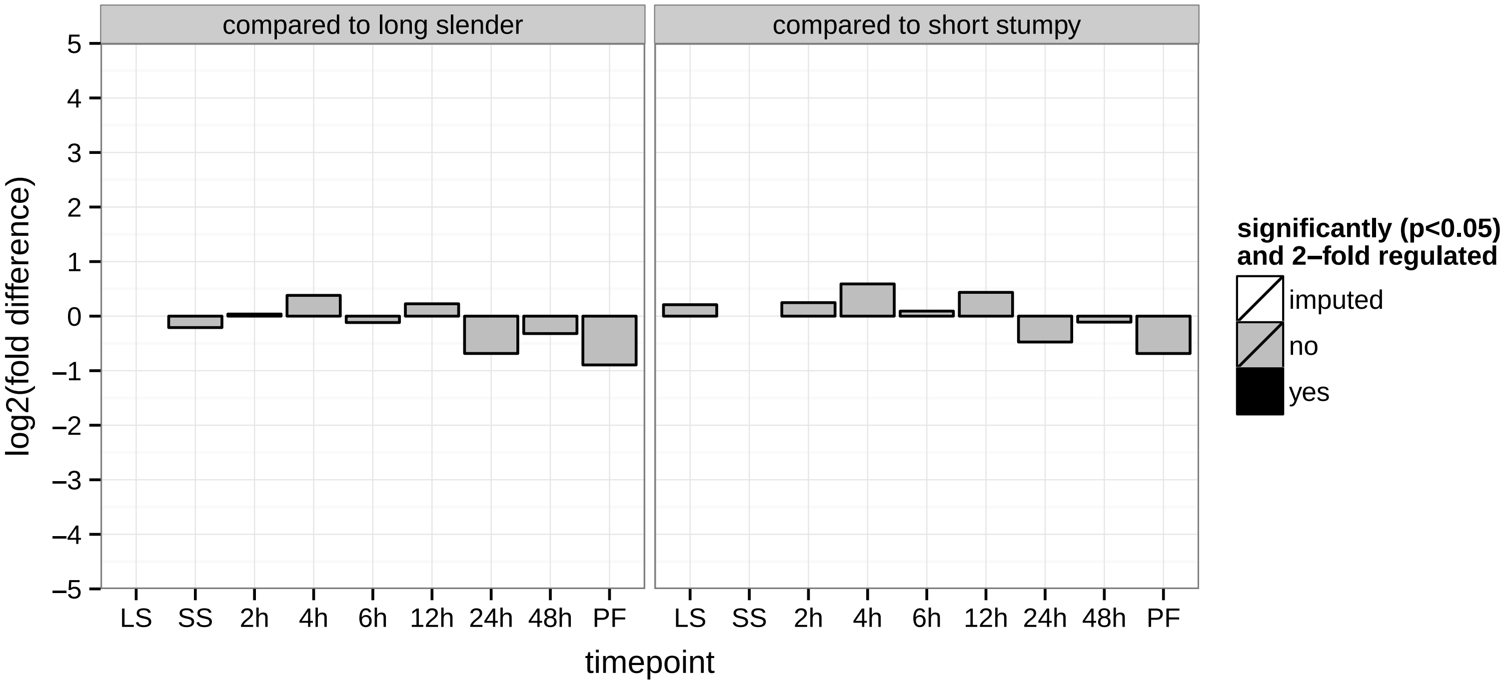
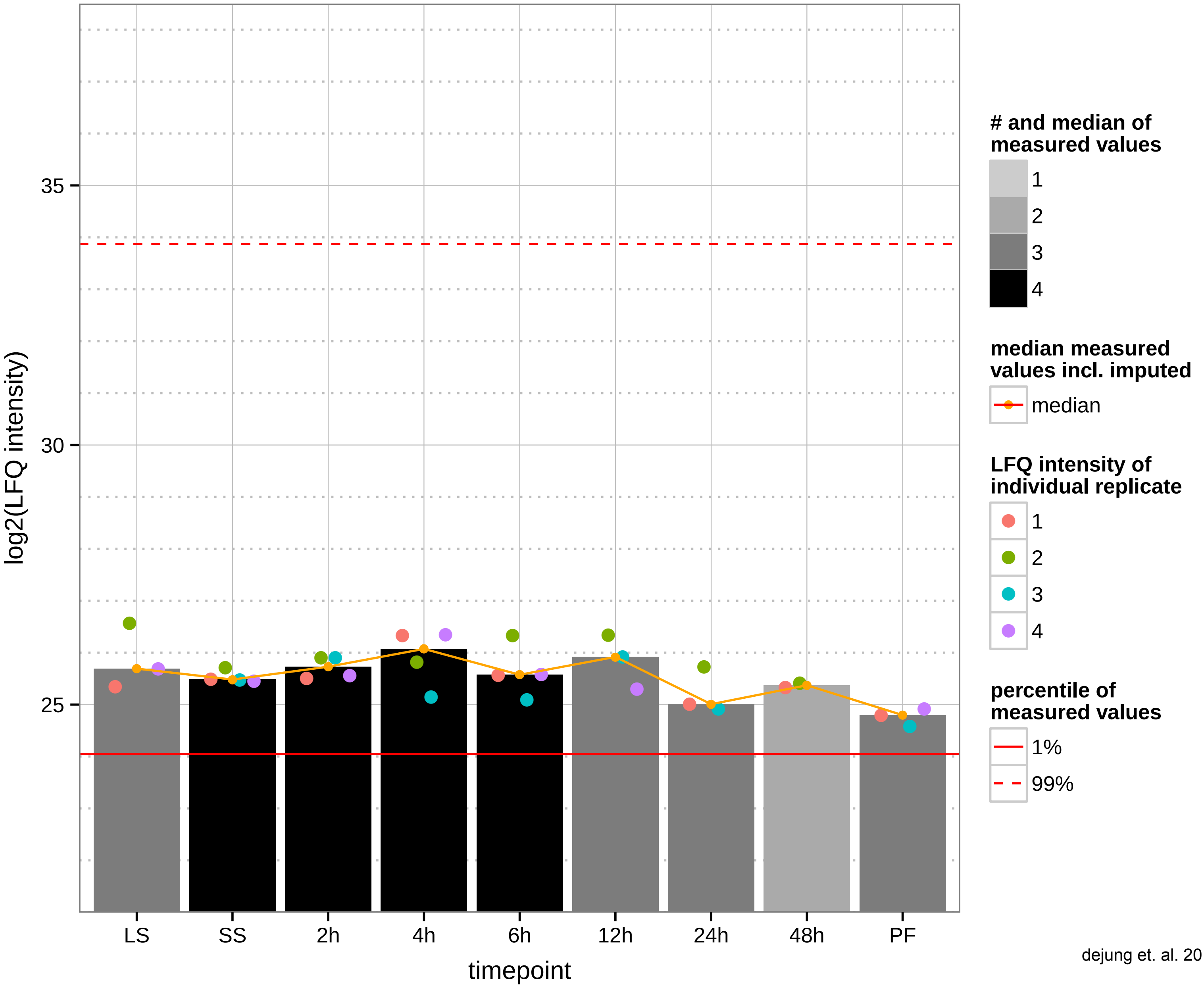
hypothetical protein, conserved
Tb927.7.3540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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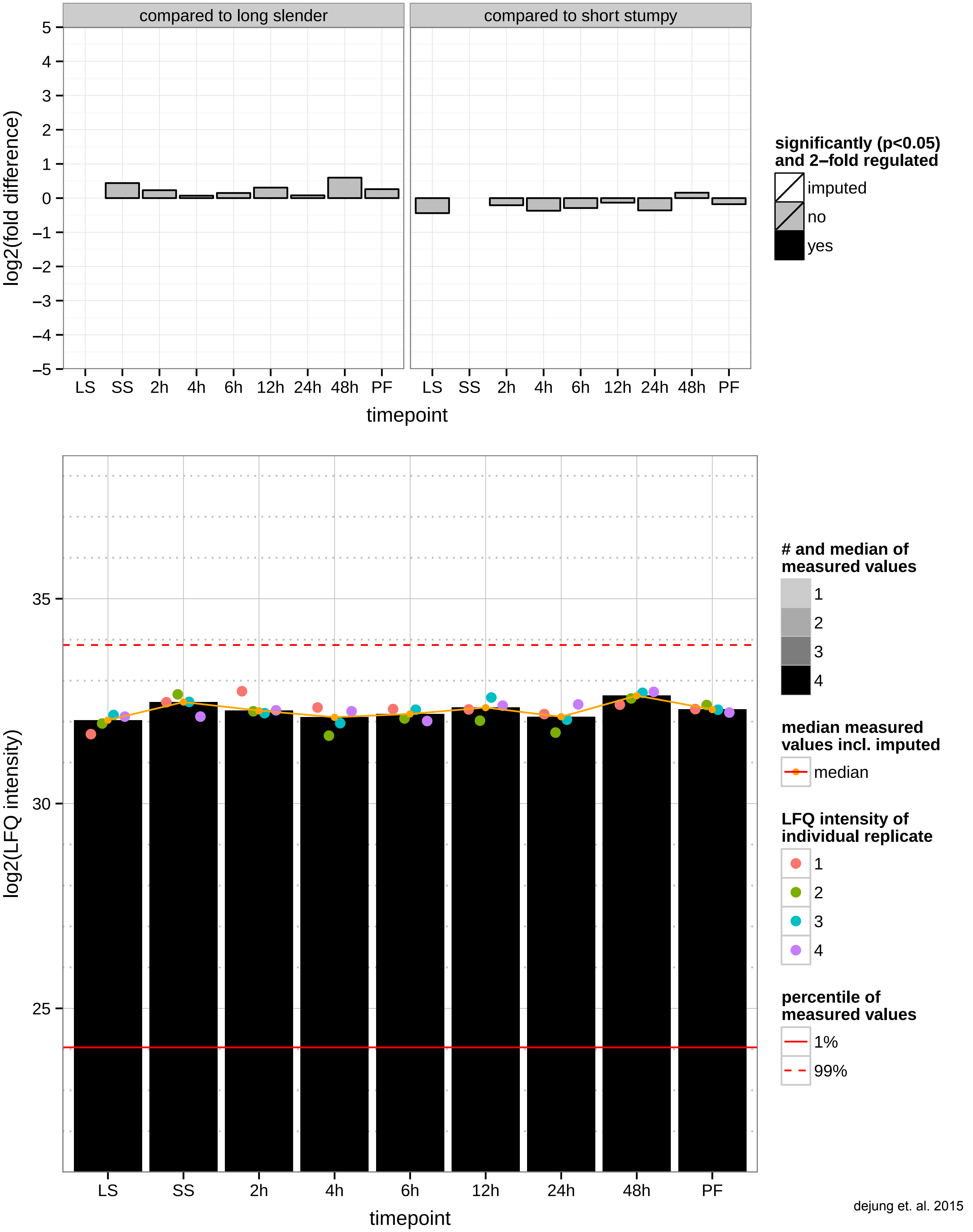
hypothetical protein, conserved
Tb927.7.3550
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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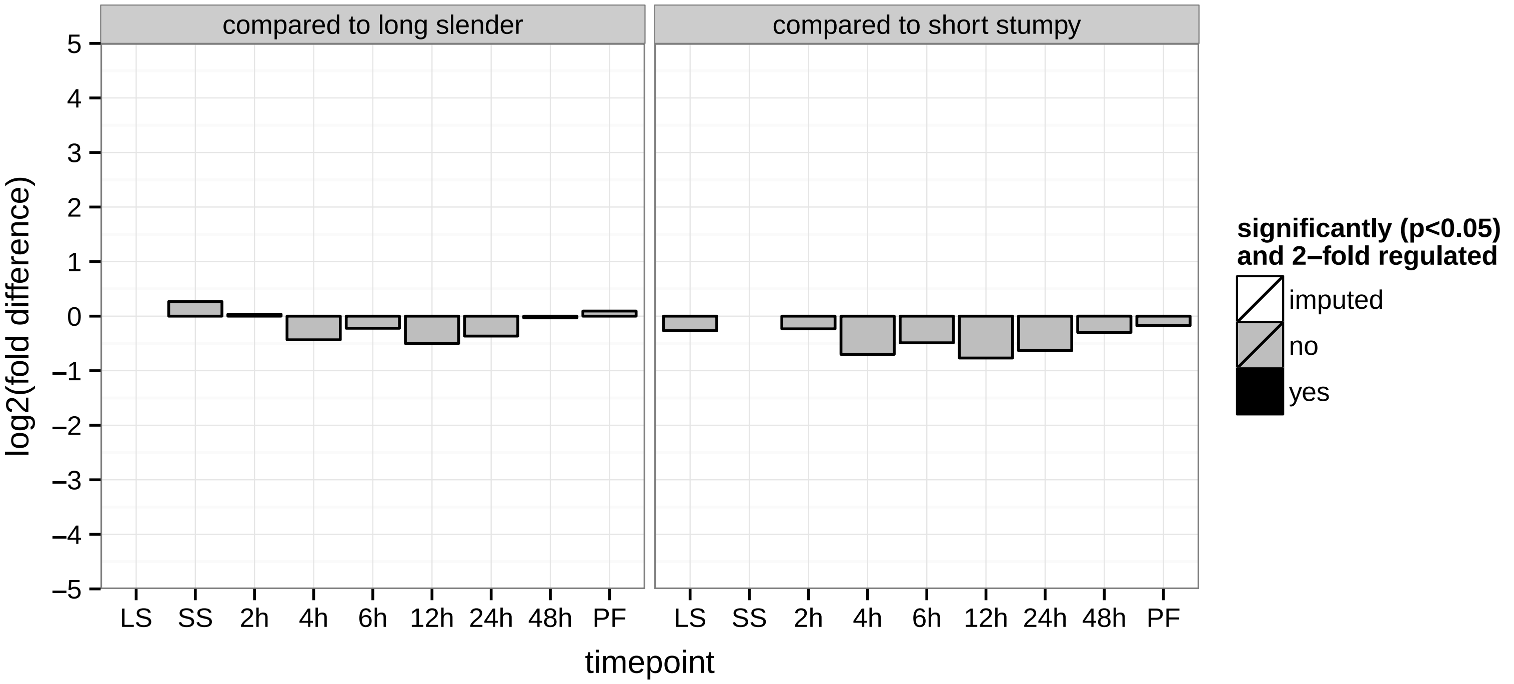
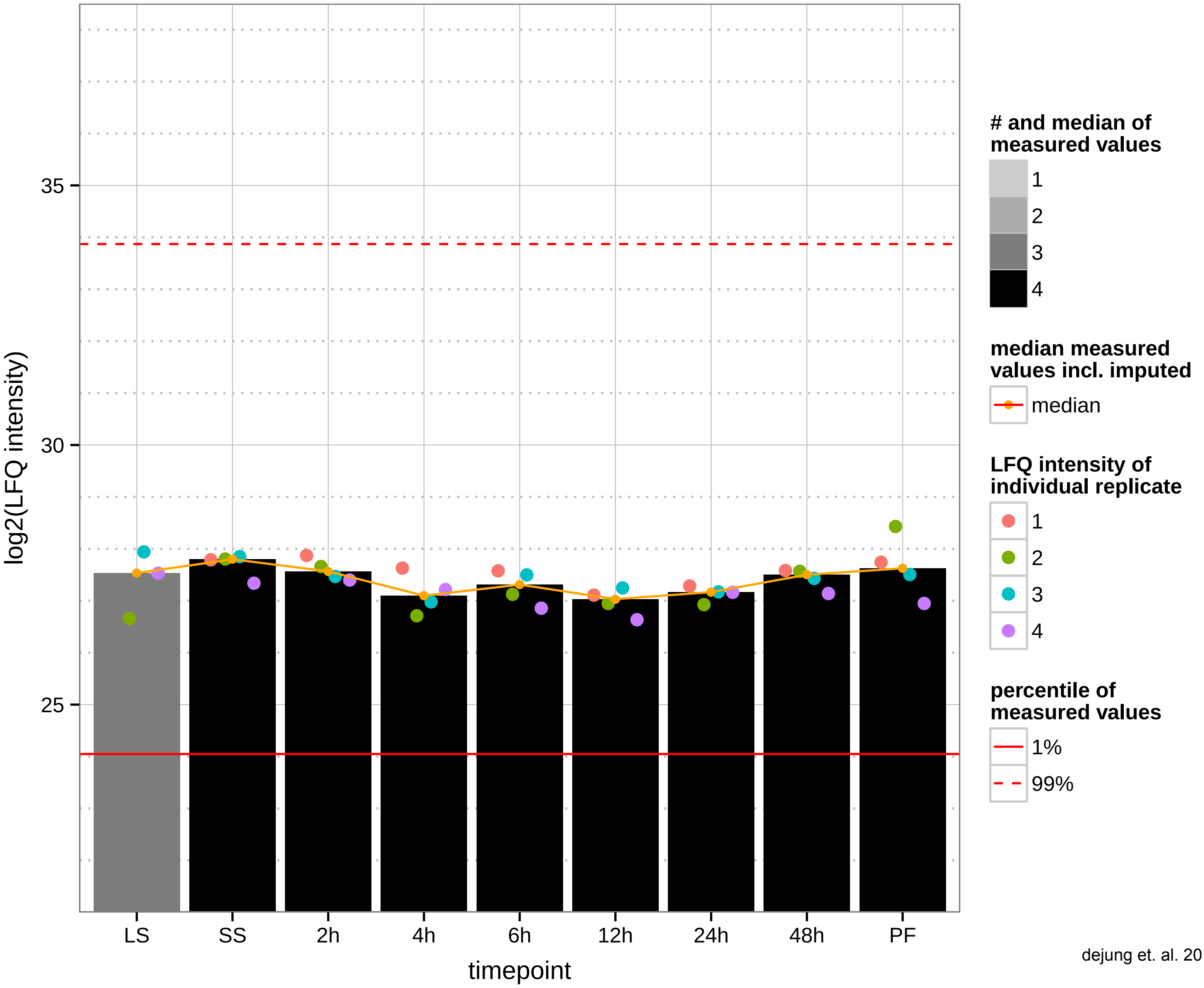
hypothetical protein, conserved
Tb927.7.3560
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null





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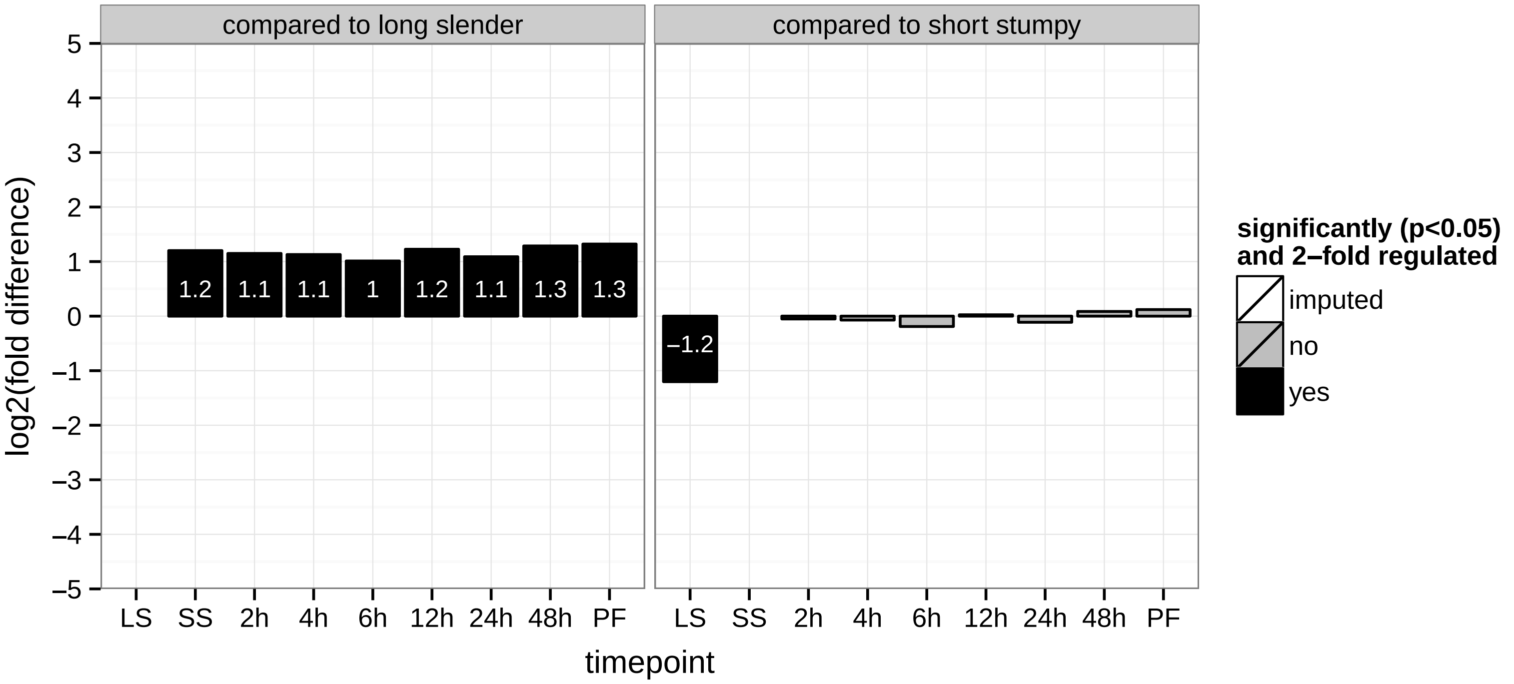
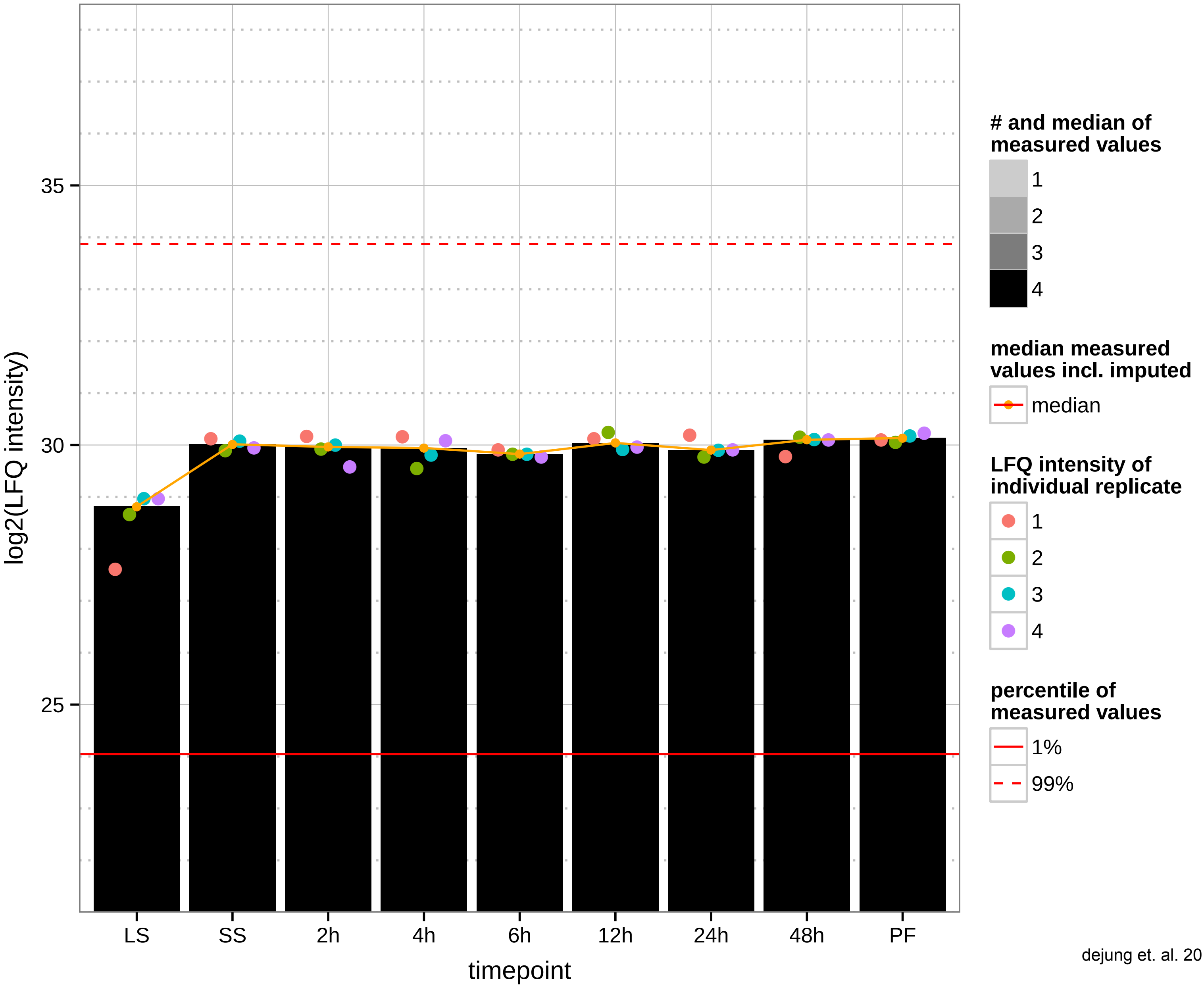
tyrosyl–tRNA synthetase, putative
Tb927.7.3620
AGOF: ATP binding, tyrosine–tRNA ligase activity
AGOC: cytoplasm
AGOP: translation, tyrosyl–tRNA aminoacylation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, nucleotide binding
PGOC: cytoplasm
PGOP: tRNA aminoacylation for protein translation





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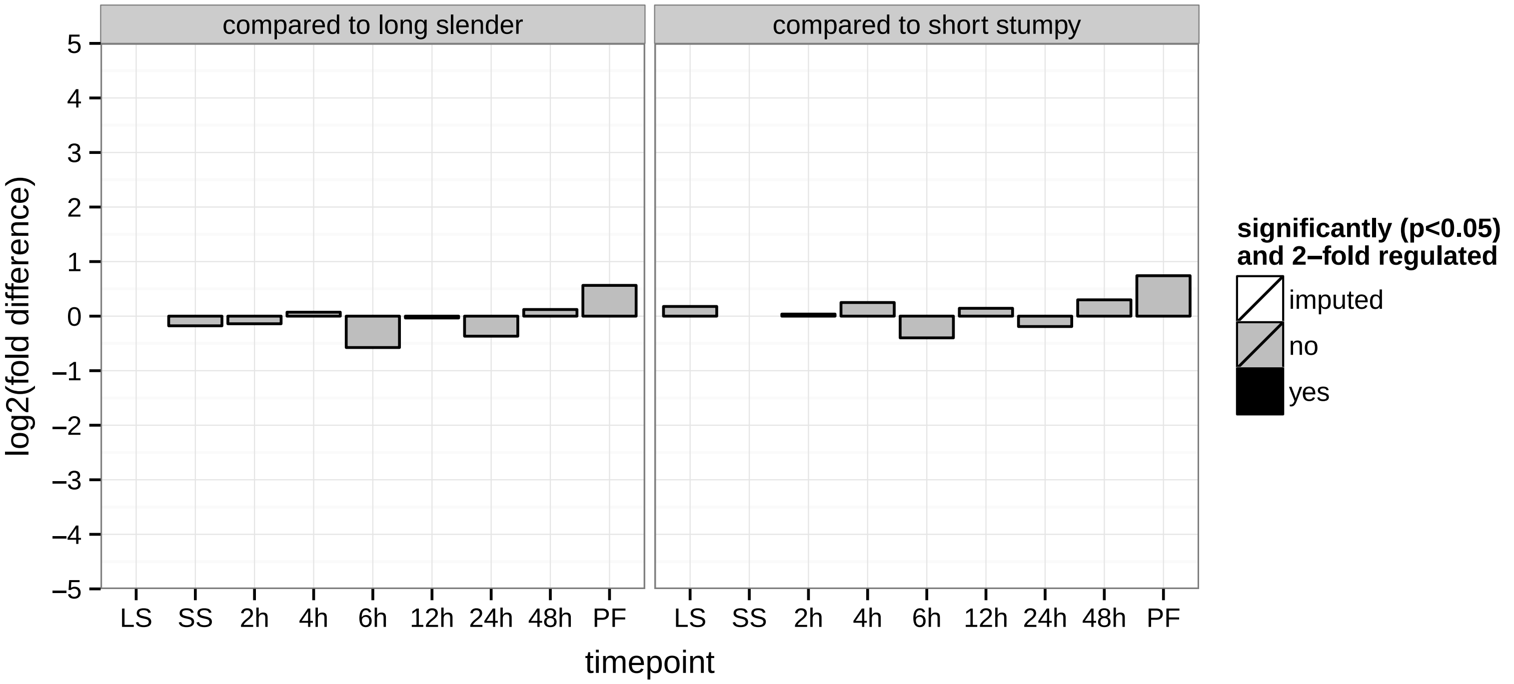
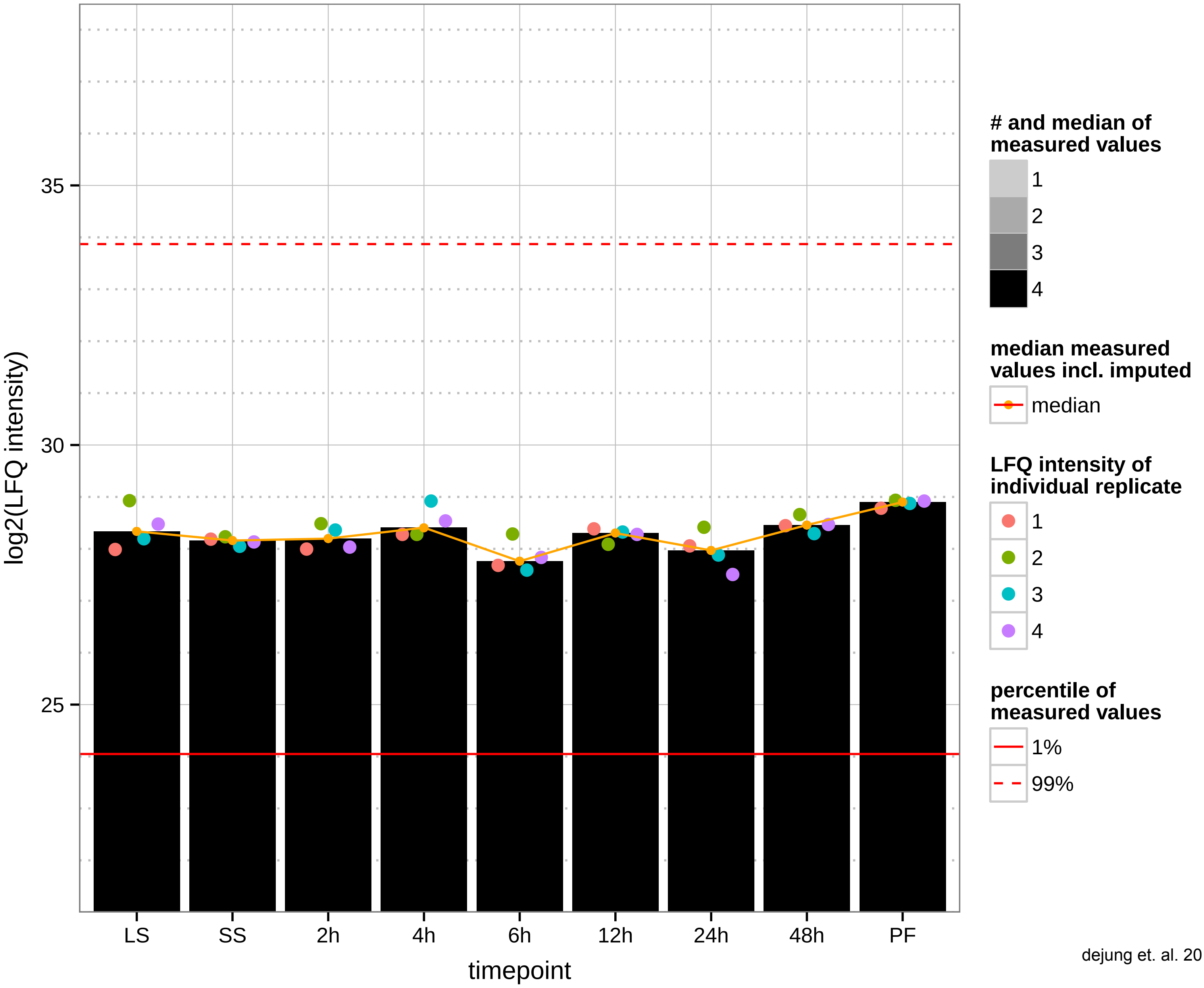
hypothetical protein, conserved
Tb927.7.3740
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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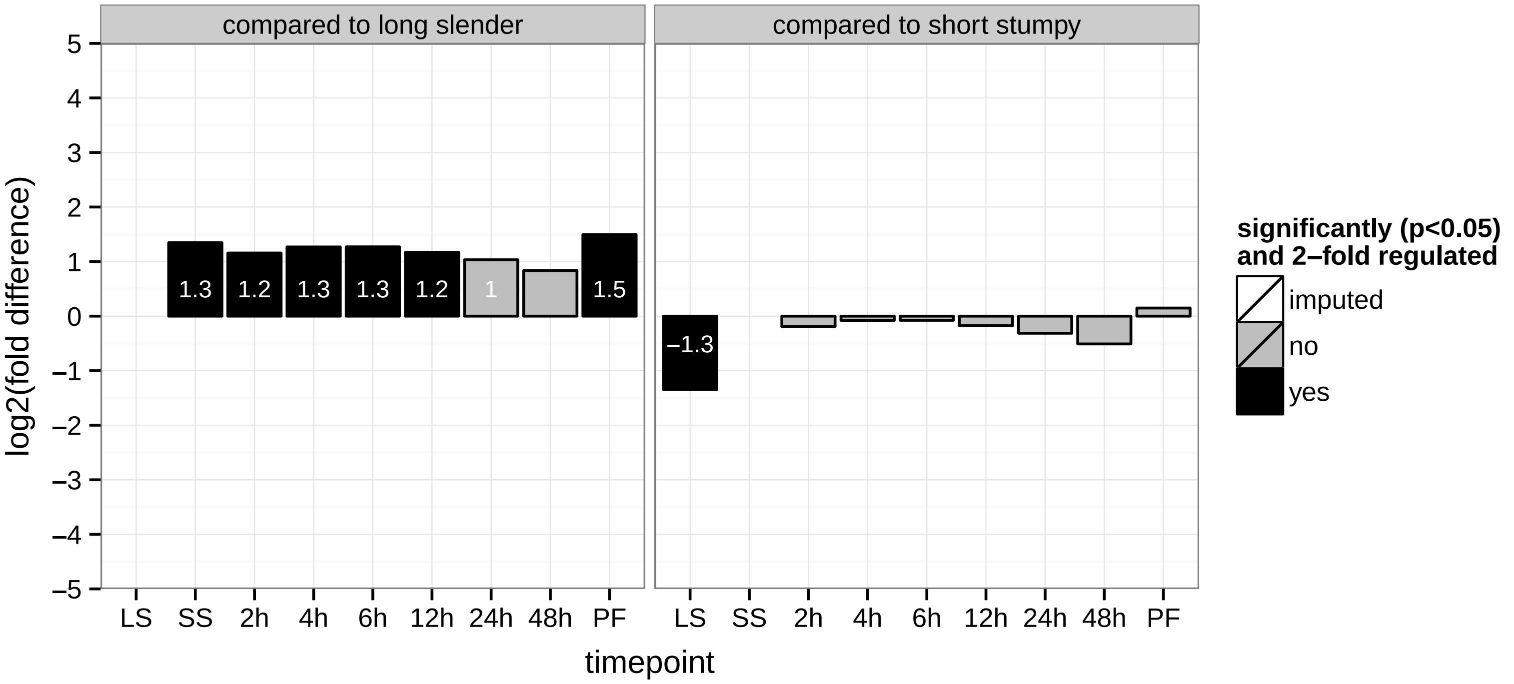
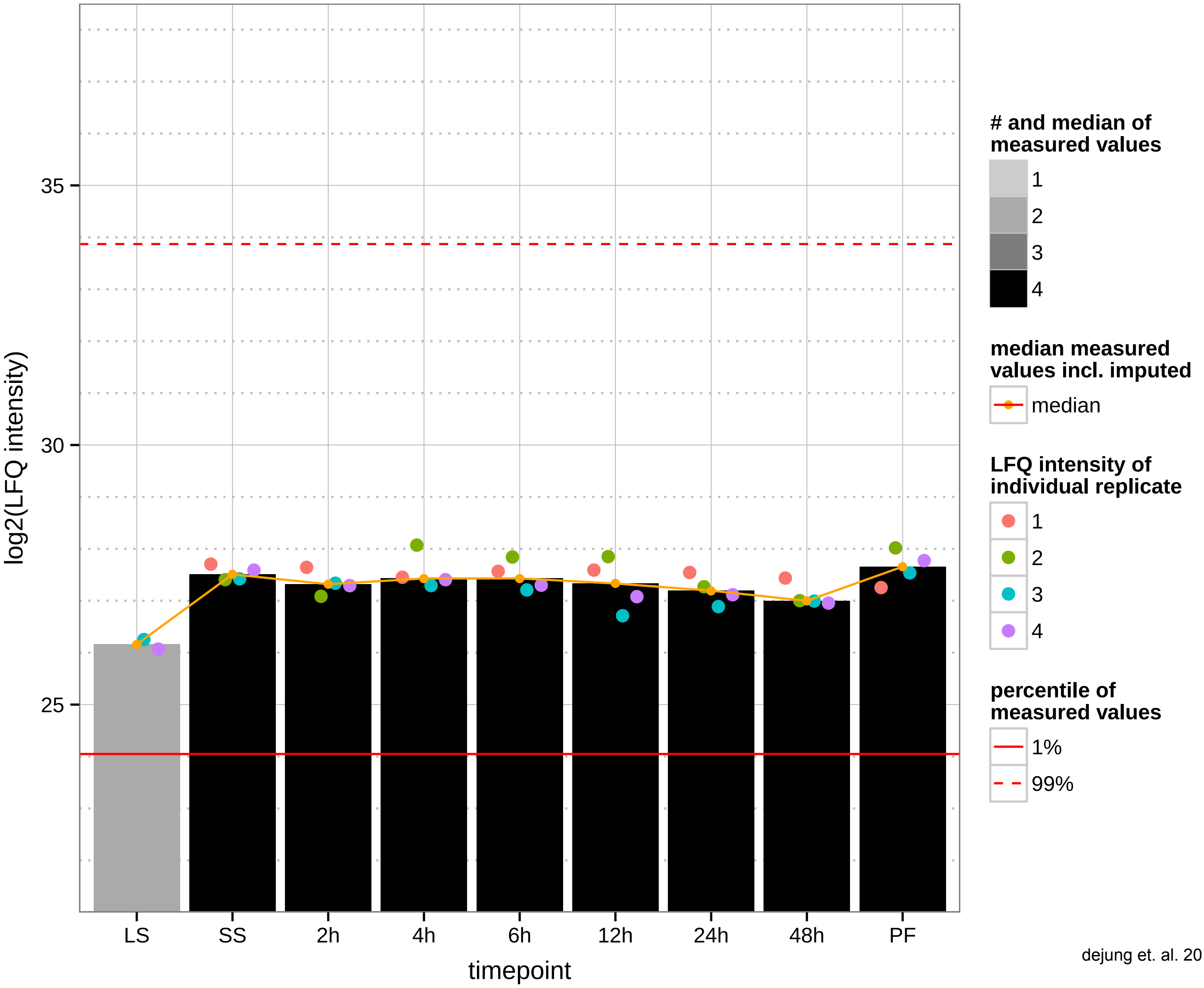
TFIIF–stimulated CTD phosphatase, putative
Tb927.7.3750
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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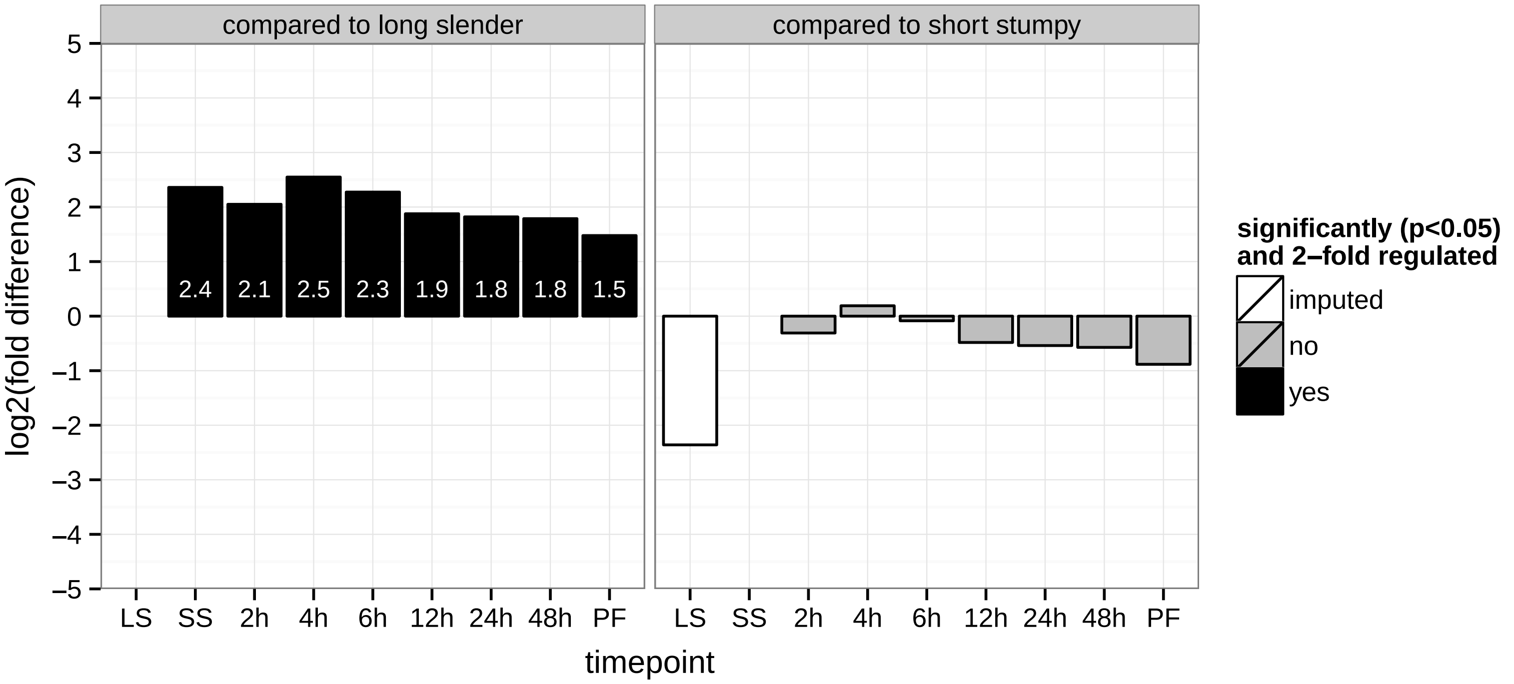
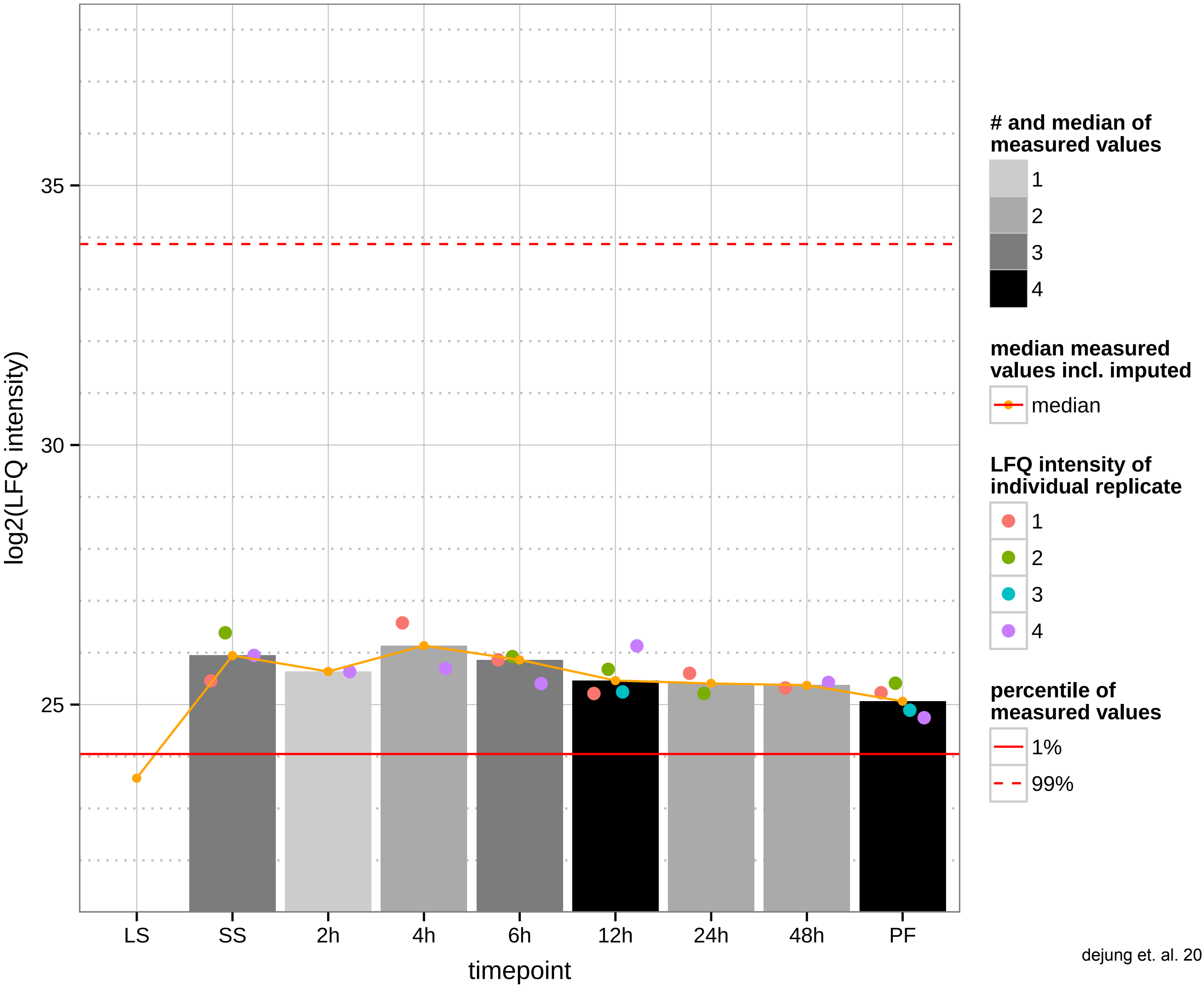
phosphatidylserine synthase, putative
Tb927.7.3760
AGOF: CDP−diacylglycerol−serine O−phosphatidyltransferase activity
AGOC: cellular_component
AGOP: phosphatidylserine biosynthetic process
PGOF: null
PGOC: null
PGOP: phosphatidylserine biosynthetic process





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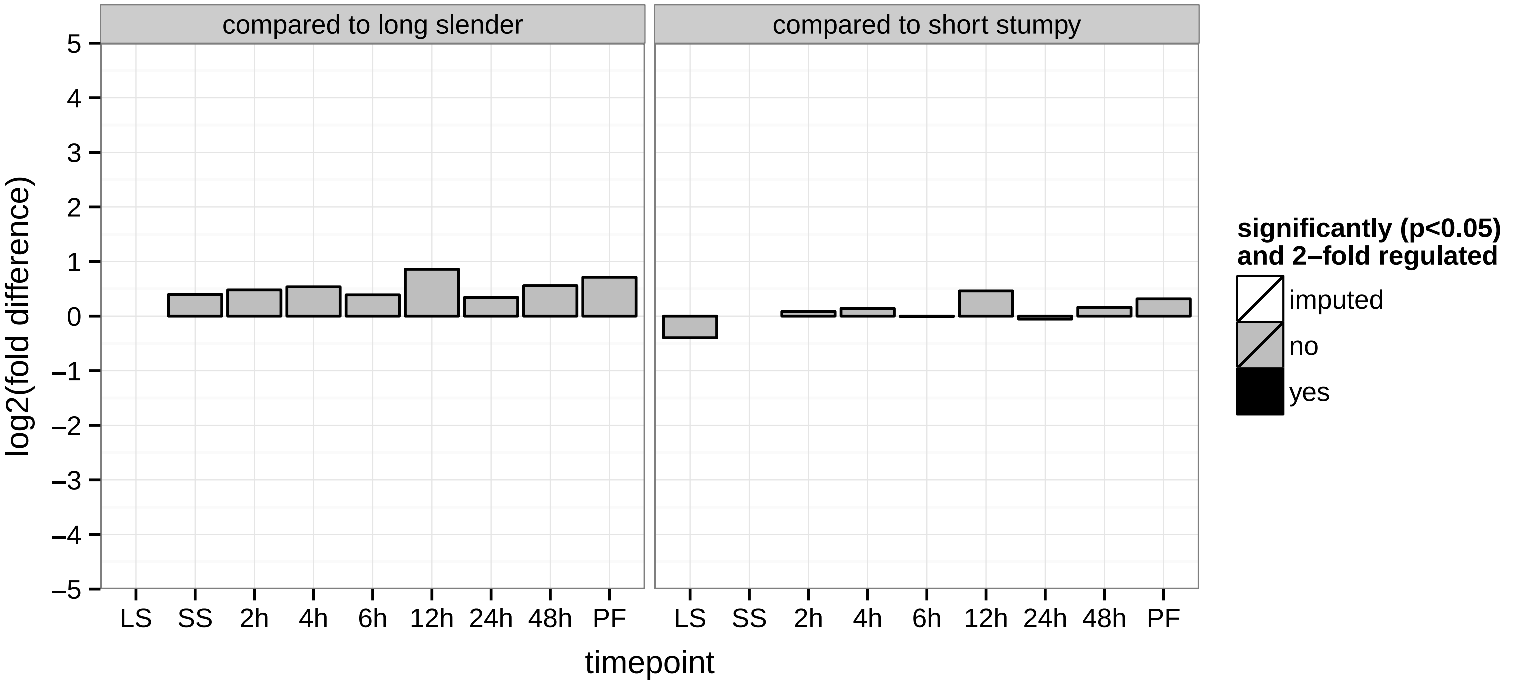
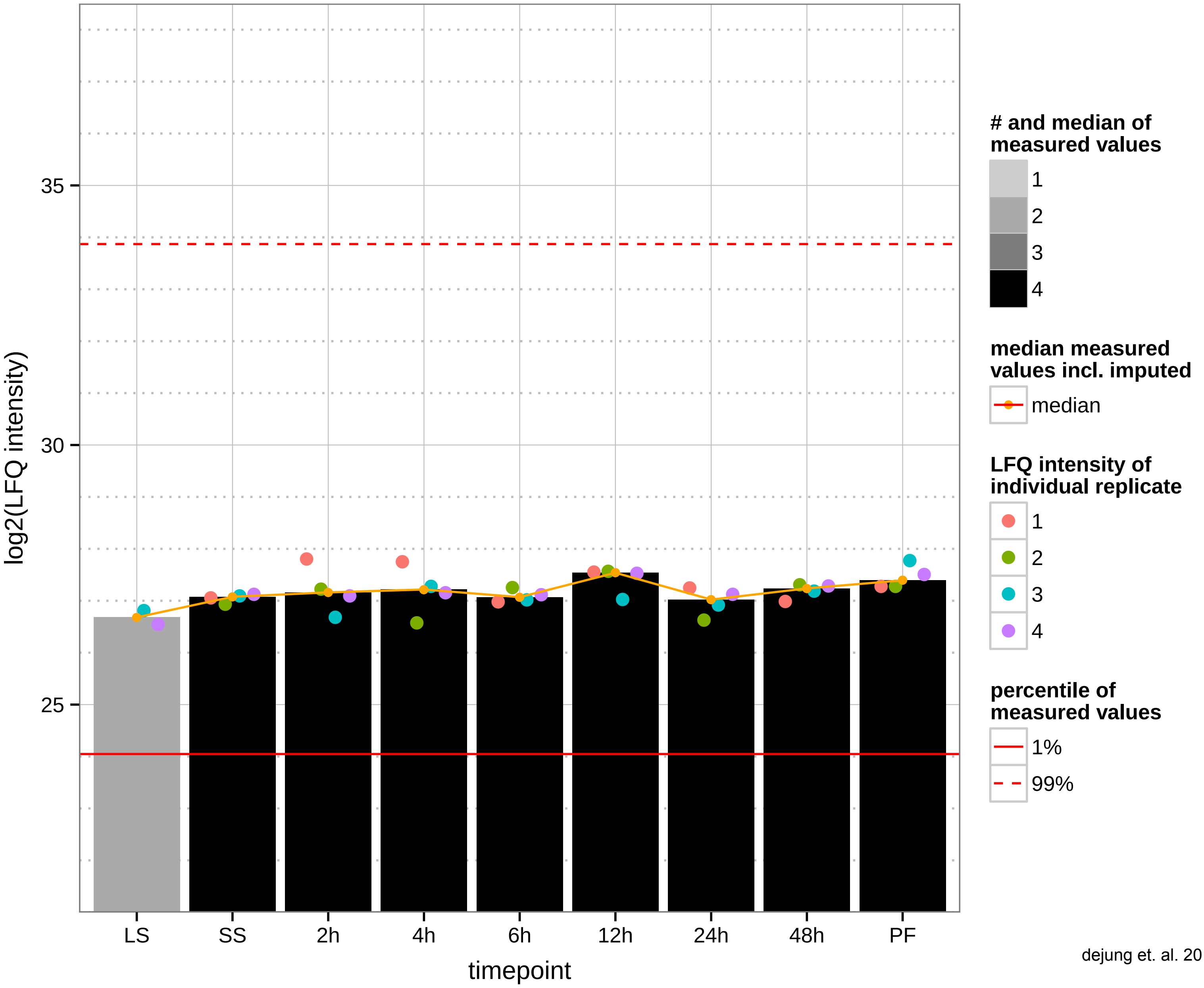
hypothetical protein, conserved
Tb927.7.3770
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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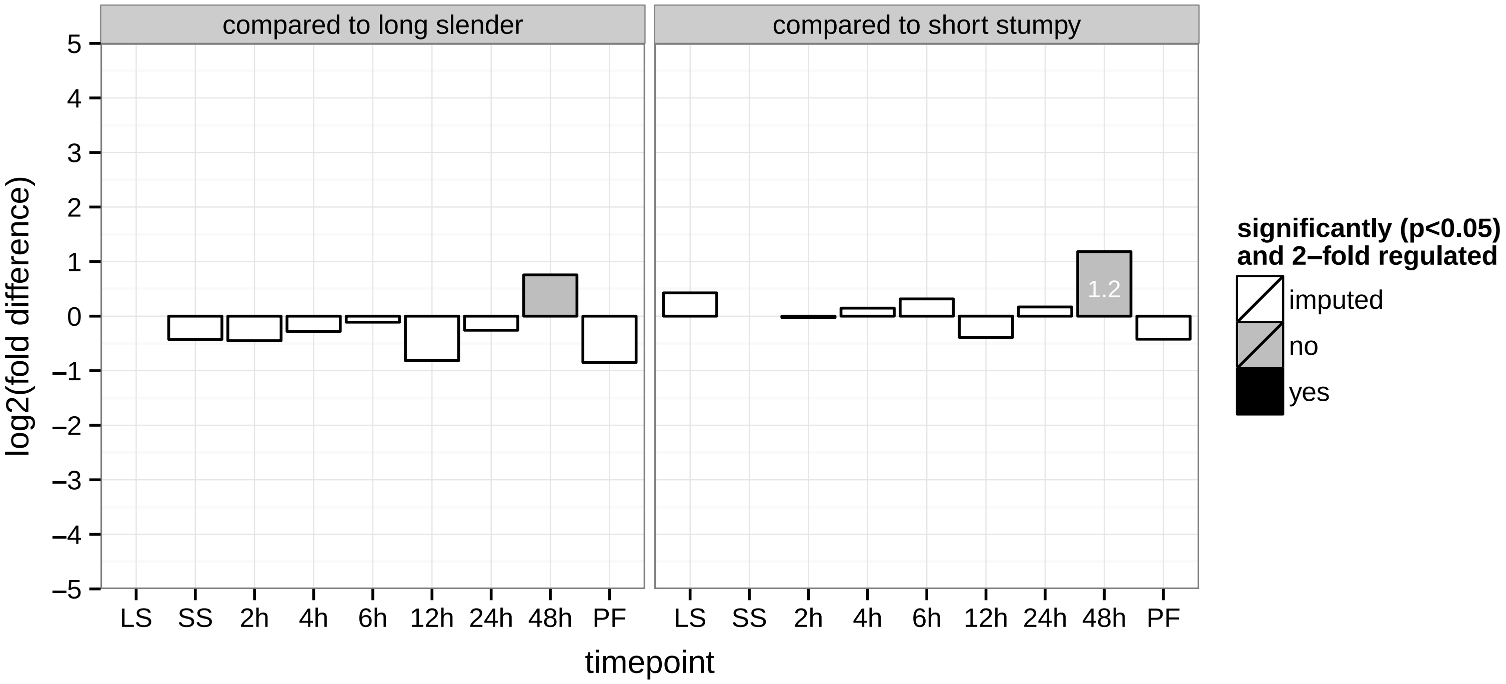
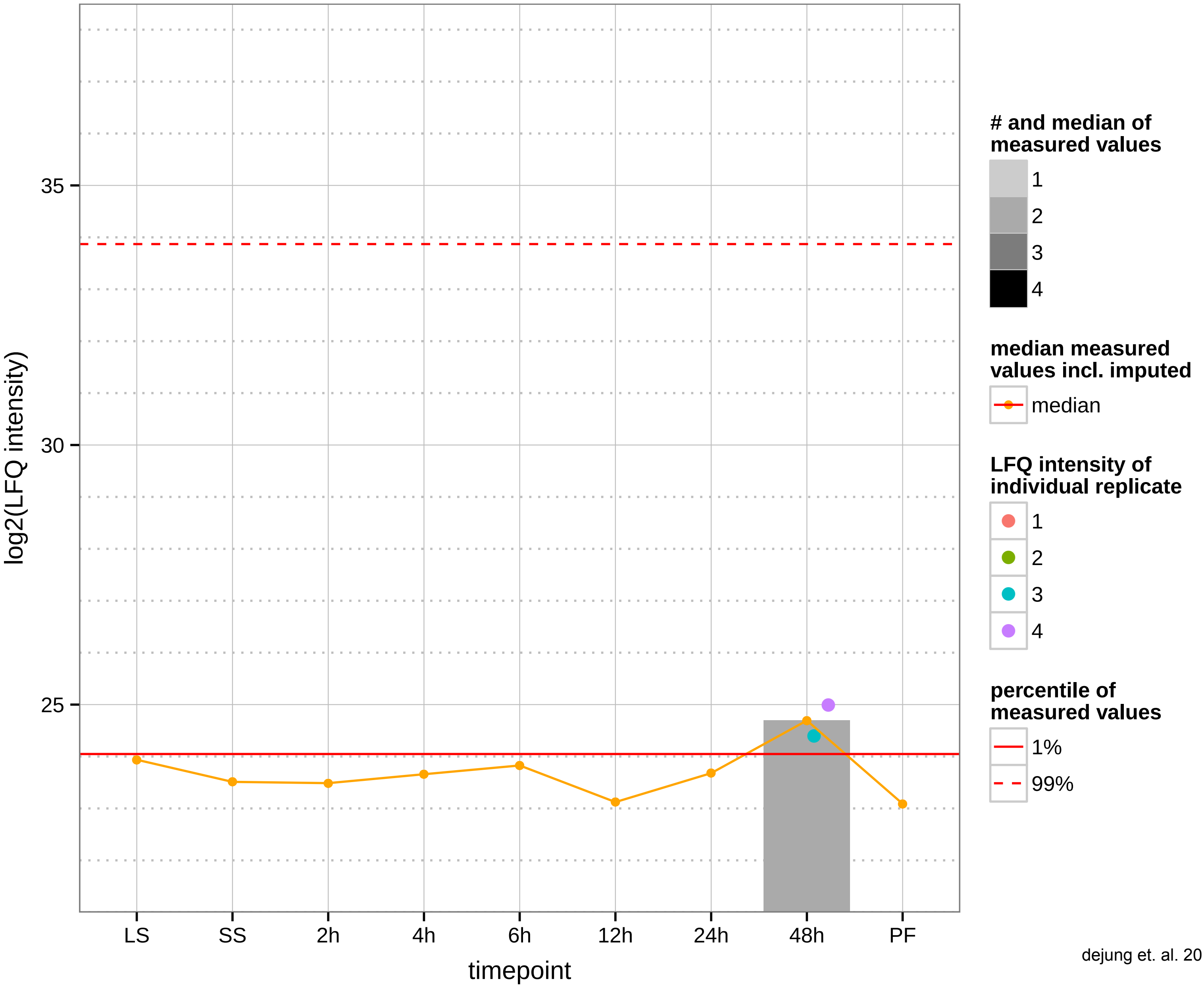
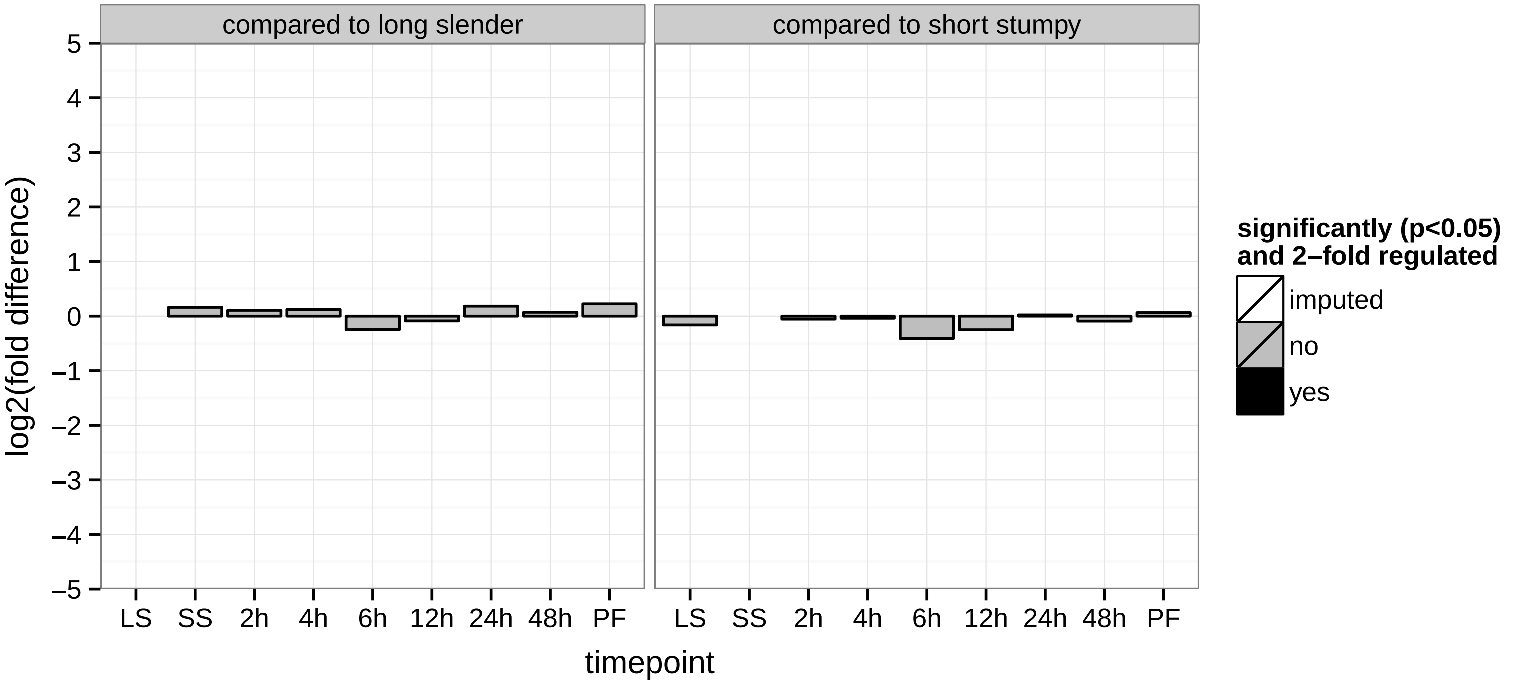
hypothetical protein, conserved
Tb927.7.3820
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

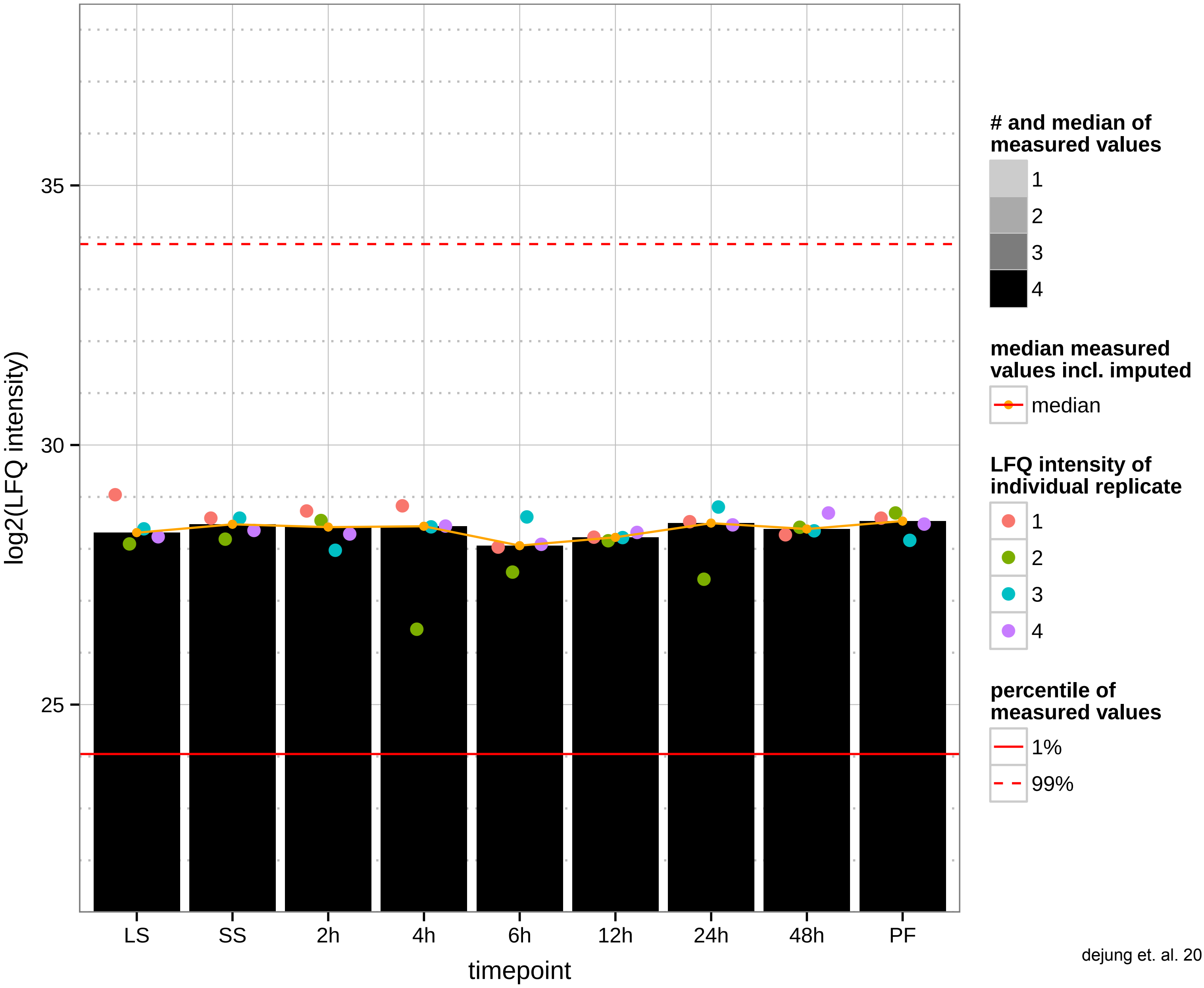




dejung et. al. 2015

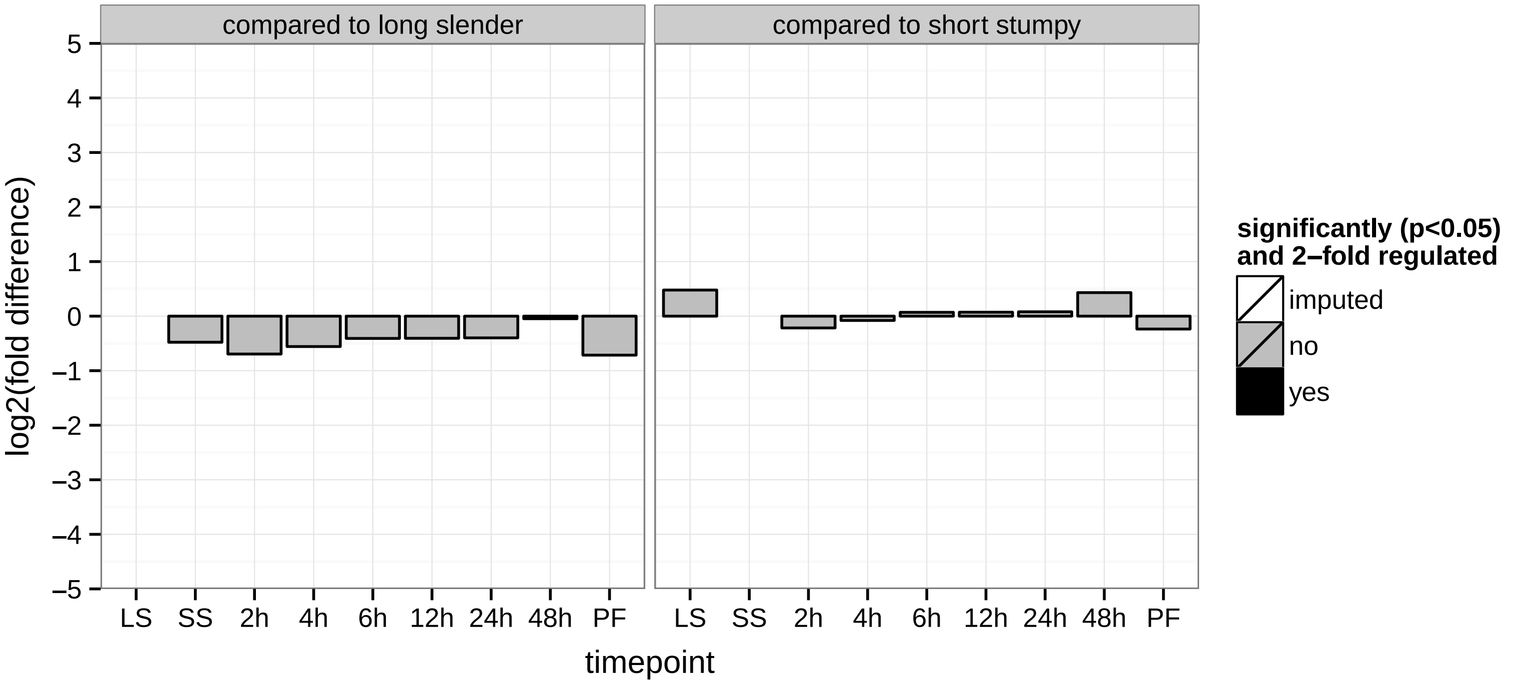
protein kinase, putative
Tb927.7.3880
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

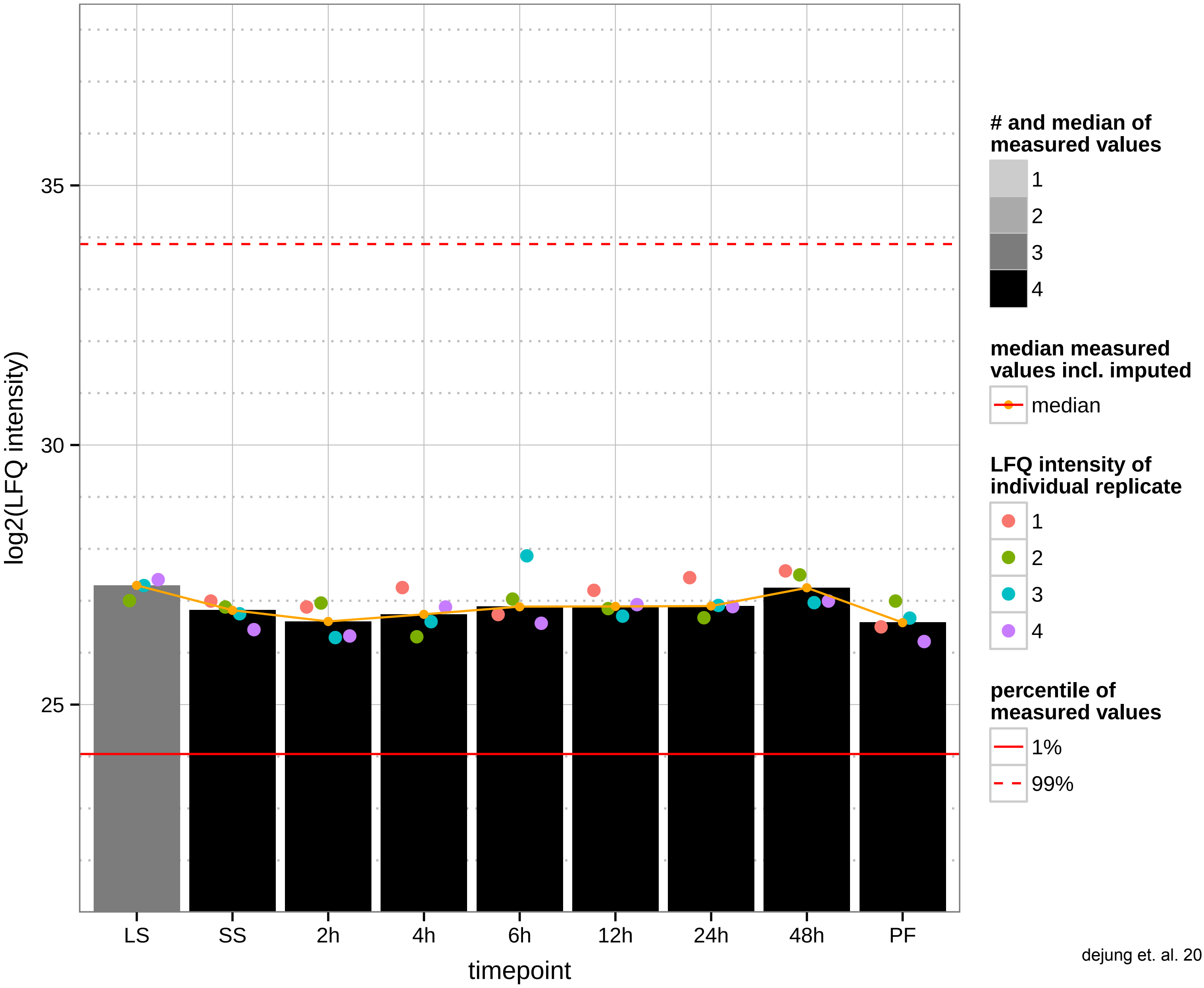




dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.3920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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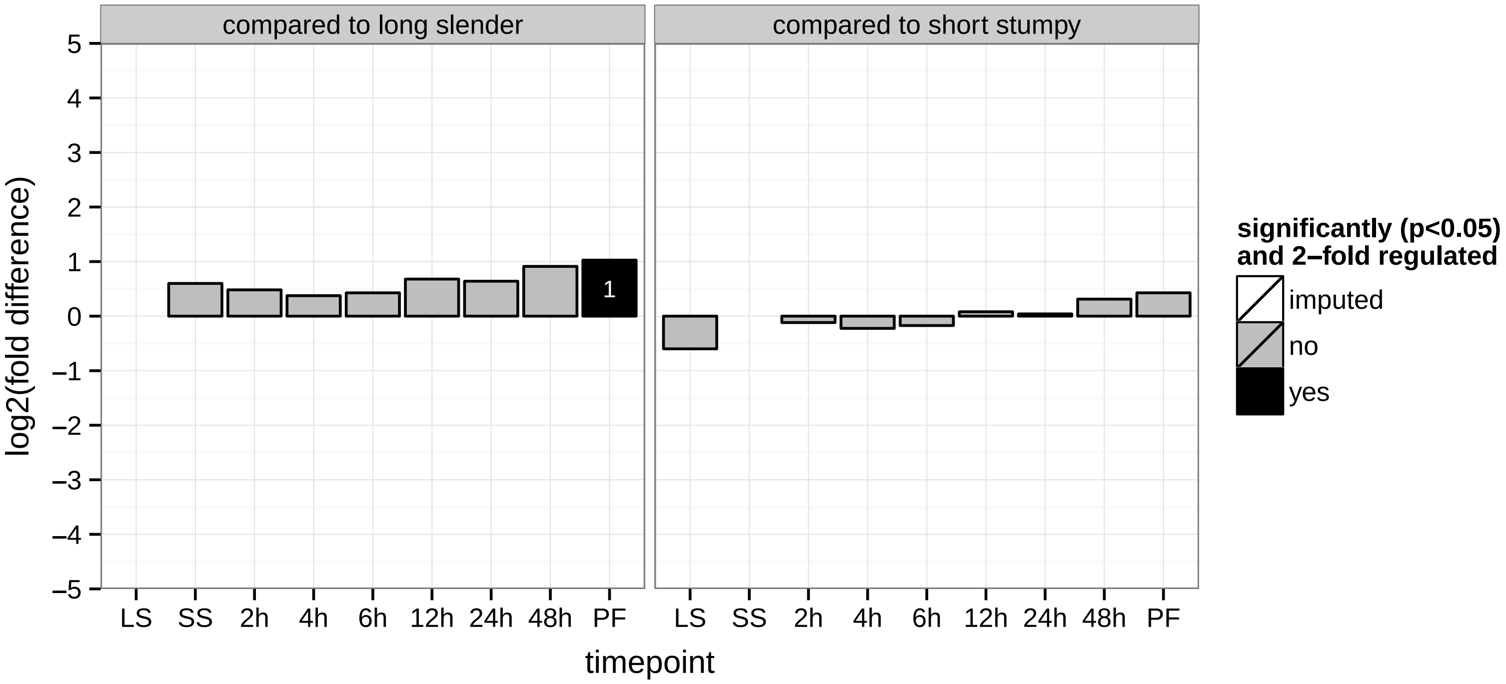
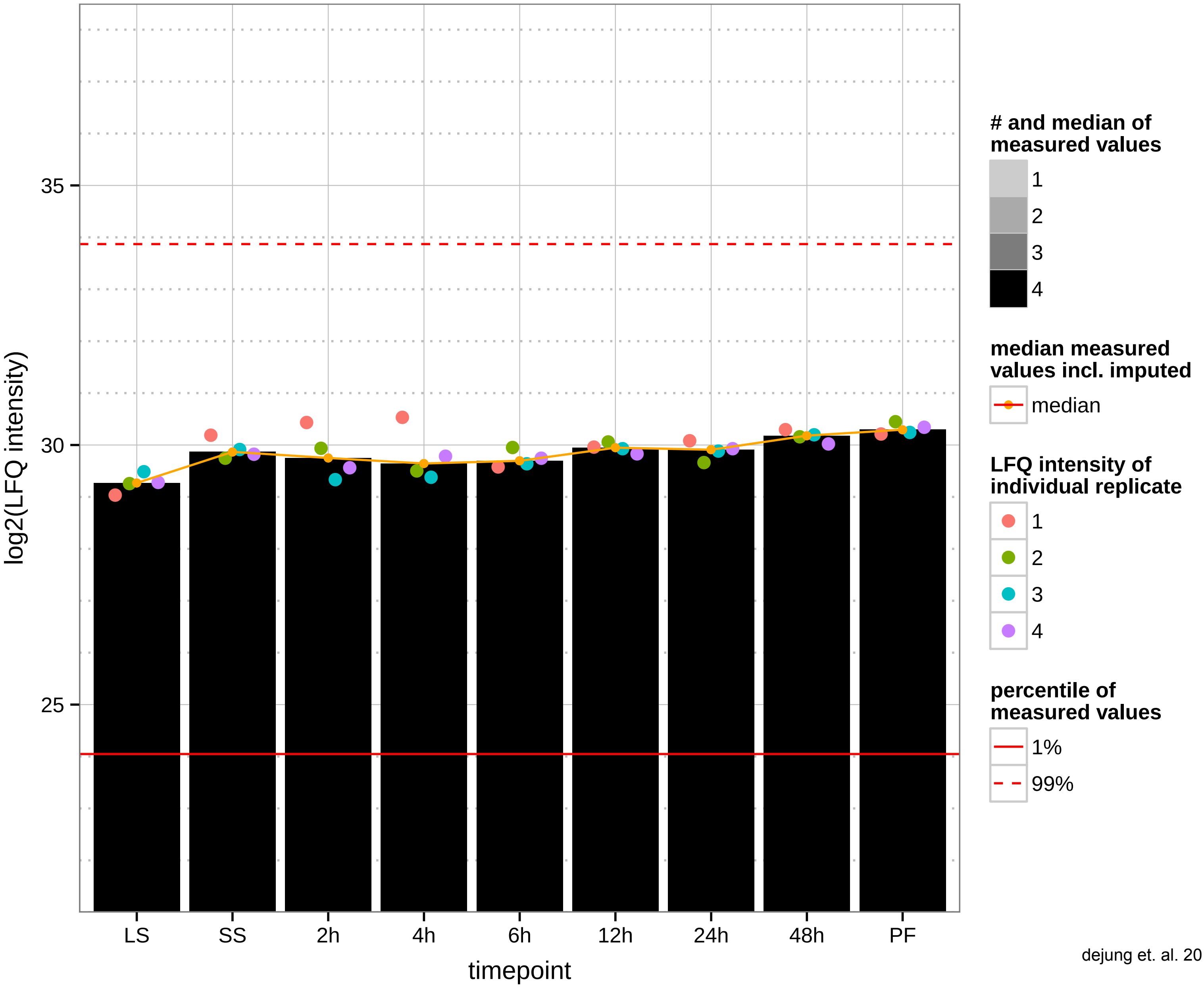
immunodominant antigen, putative, tc40 antigen–like
Tb927.7.3980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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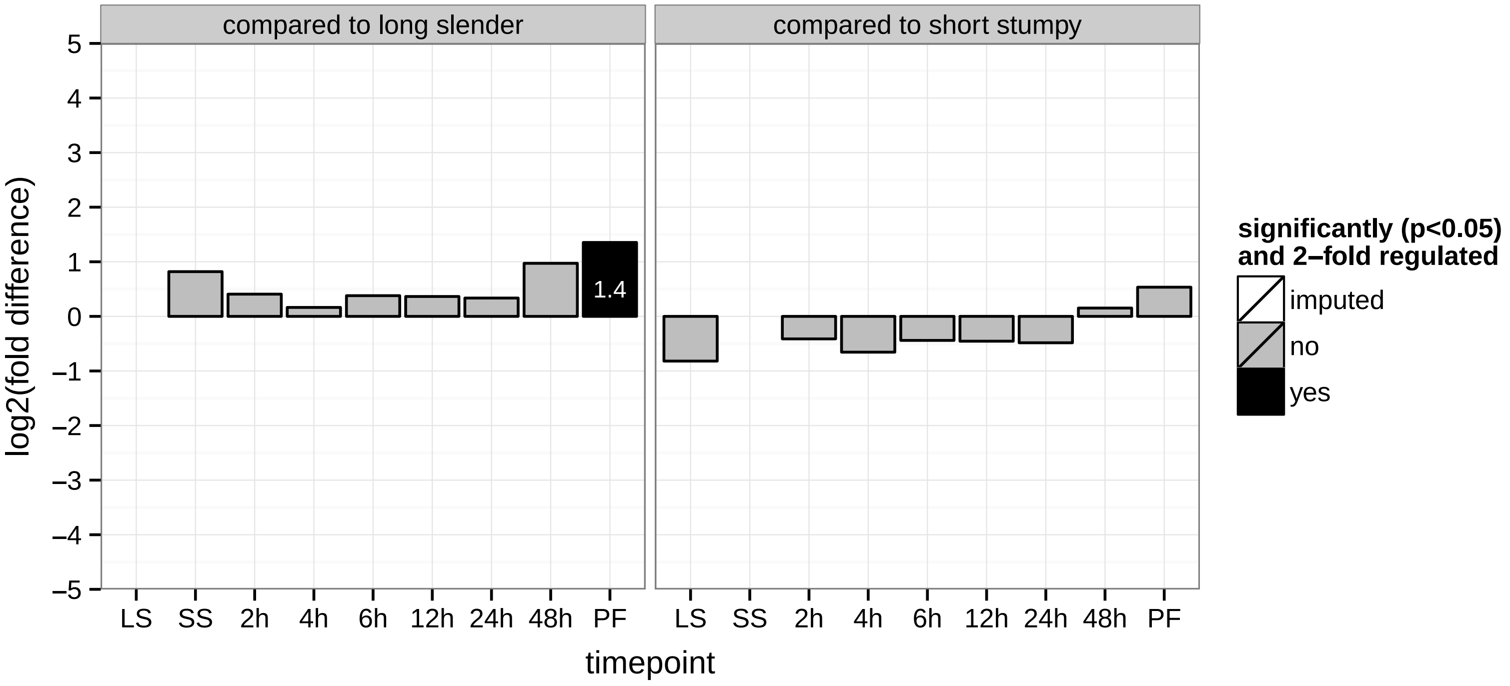
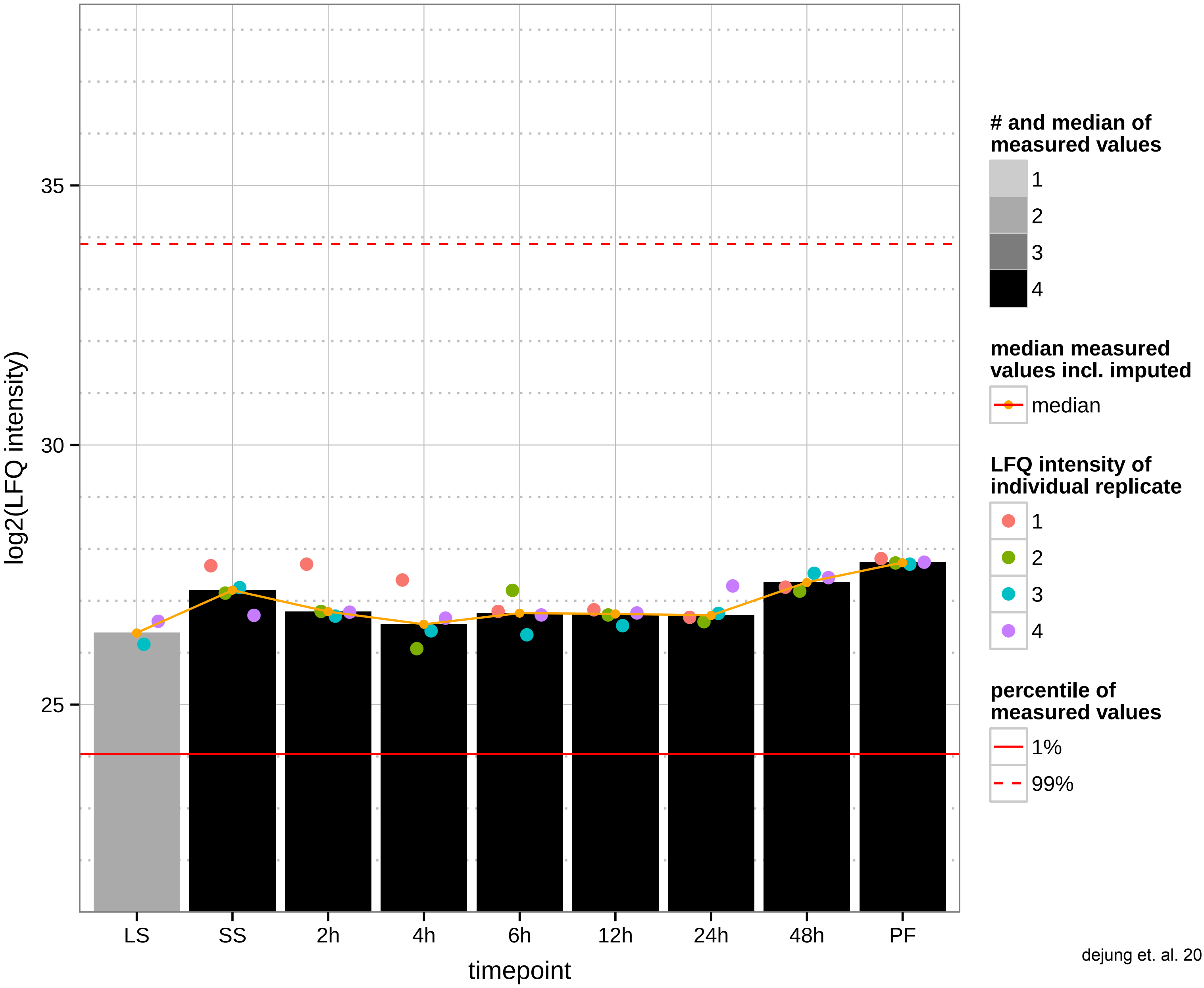
glutathione synthetase, putative
Tb927.7.4000
AGOF: ATP binding, glutathione synthase activity
AGOC: null
AGOP: glutathione biosynthetic process
PGOF: ATP binding, glutathione synthase activity
PGOC: null
PGOP: glutathione biosynthetic process





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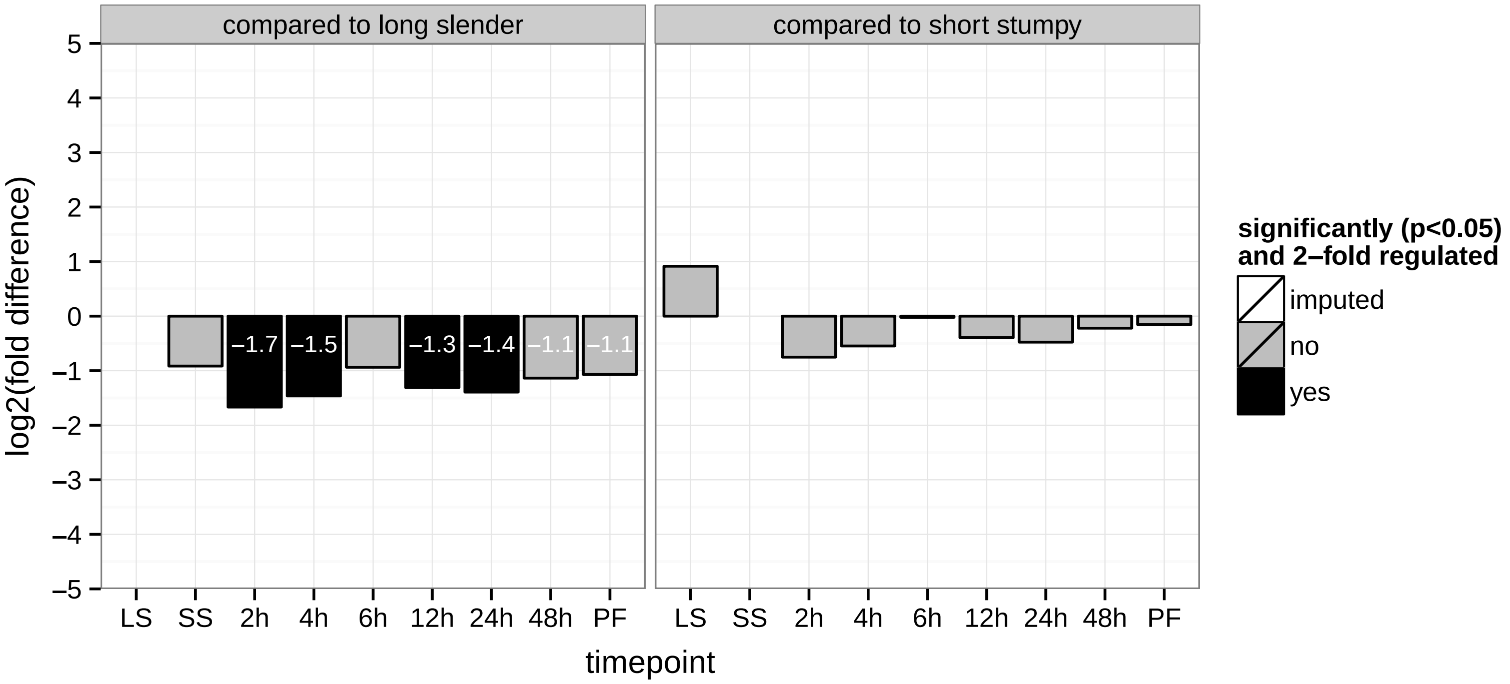
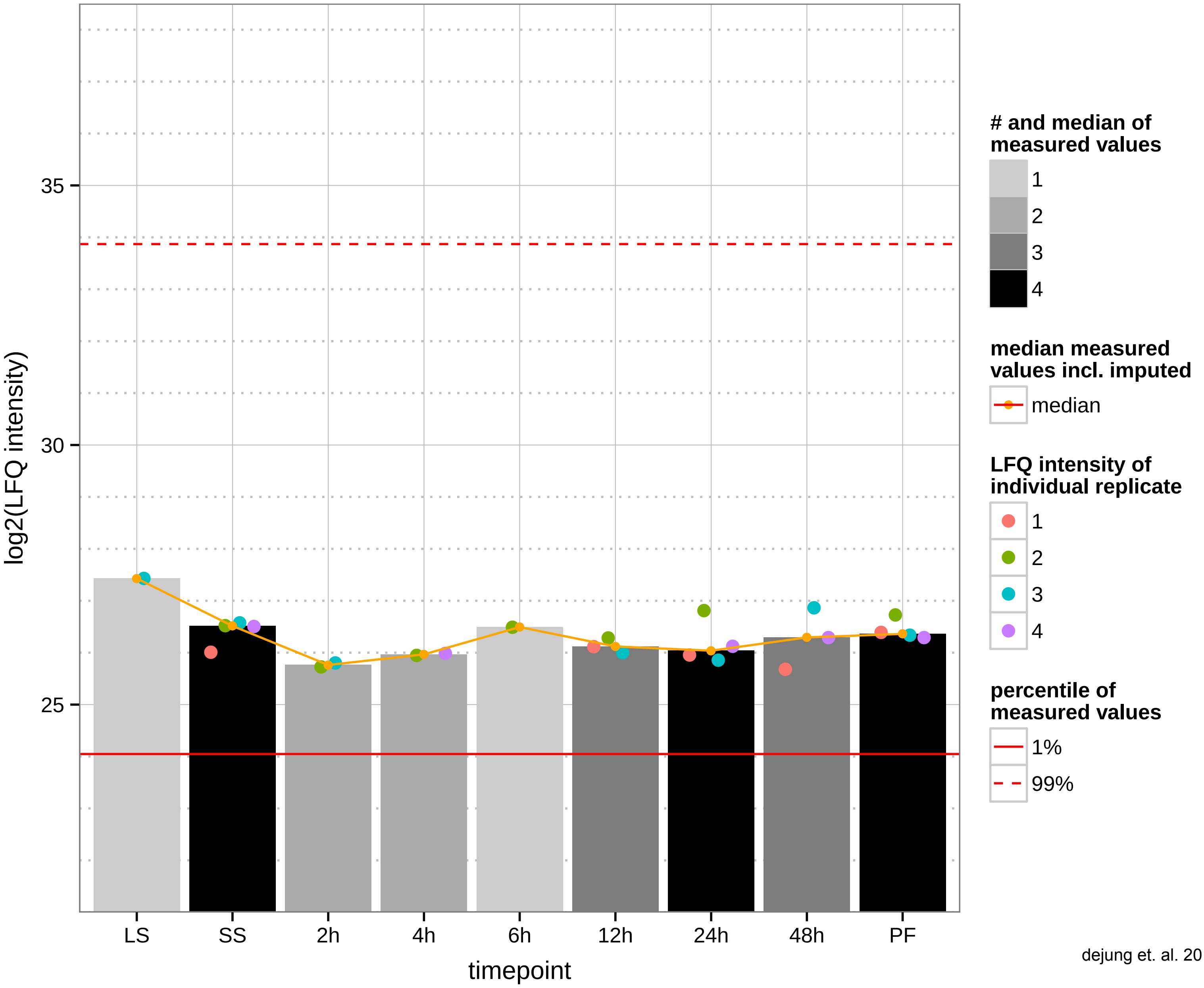
protein phosphatase 2C, putative
Tb927.7.4020
AGOF: phosphatase activity
AGOC: null
AGOP: dephosphorylation
PGOF: catalytic activity
PGOC: null
PGOP: null





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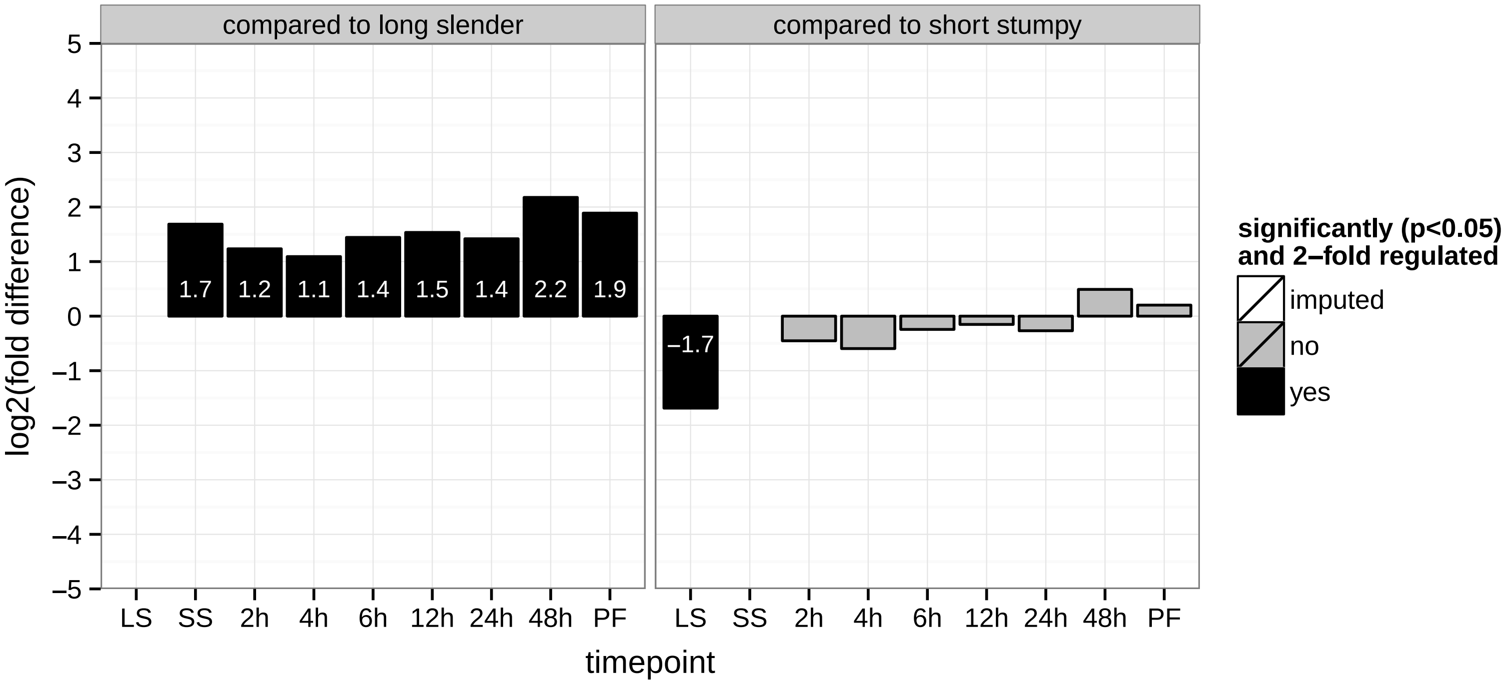
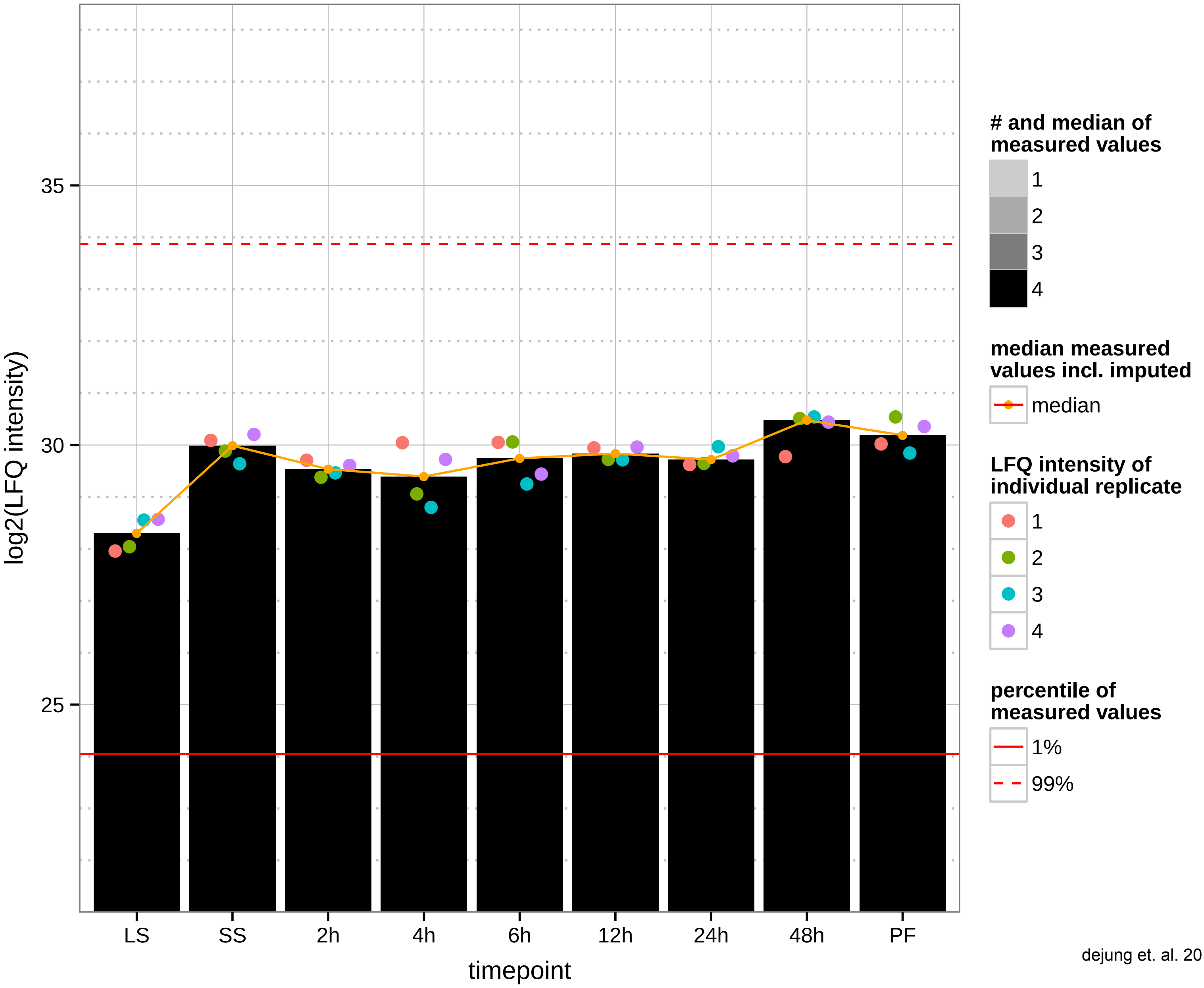
fatty acid elongase, putative
Tb927.7.4180
AGOF: fatty acid elongase activity
AGOC: integral to endoplasmic reticulum membrane
AGOP: long–chain fatty acid biosynthetic process
PGOF: null
PGOC: integral to membrane
PGOP: null





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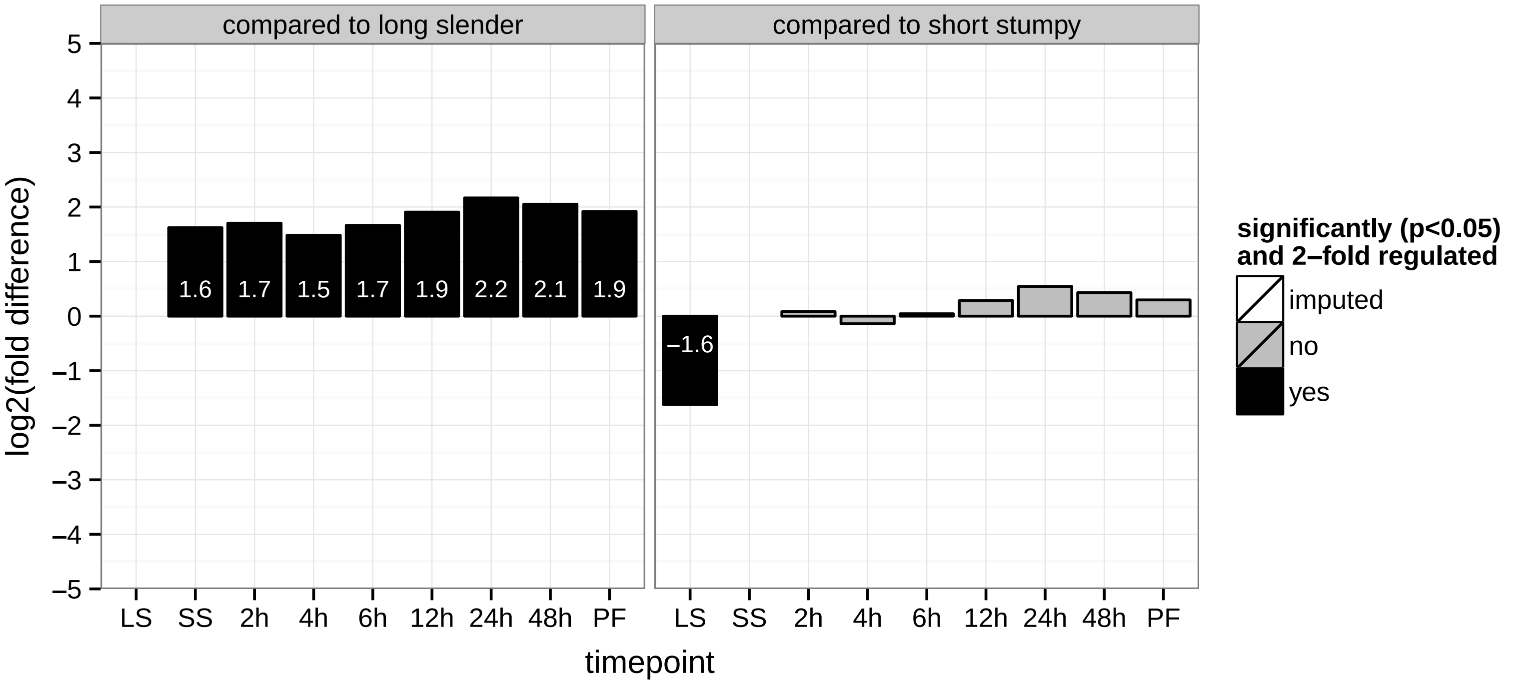
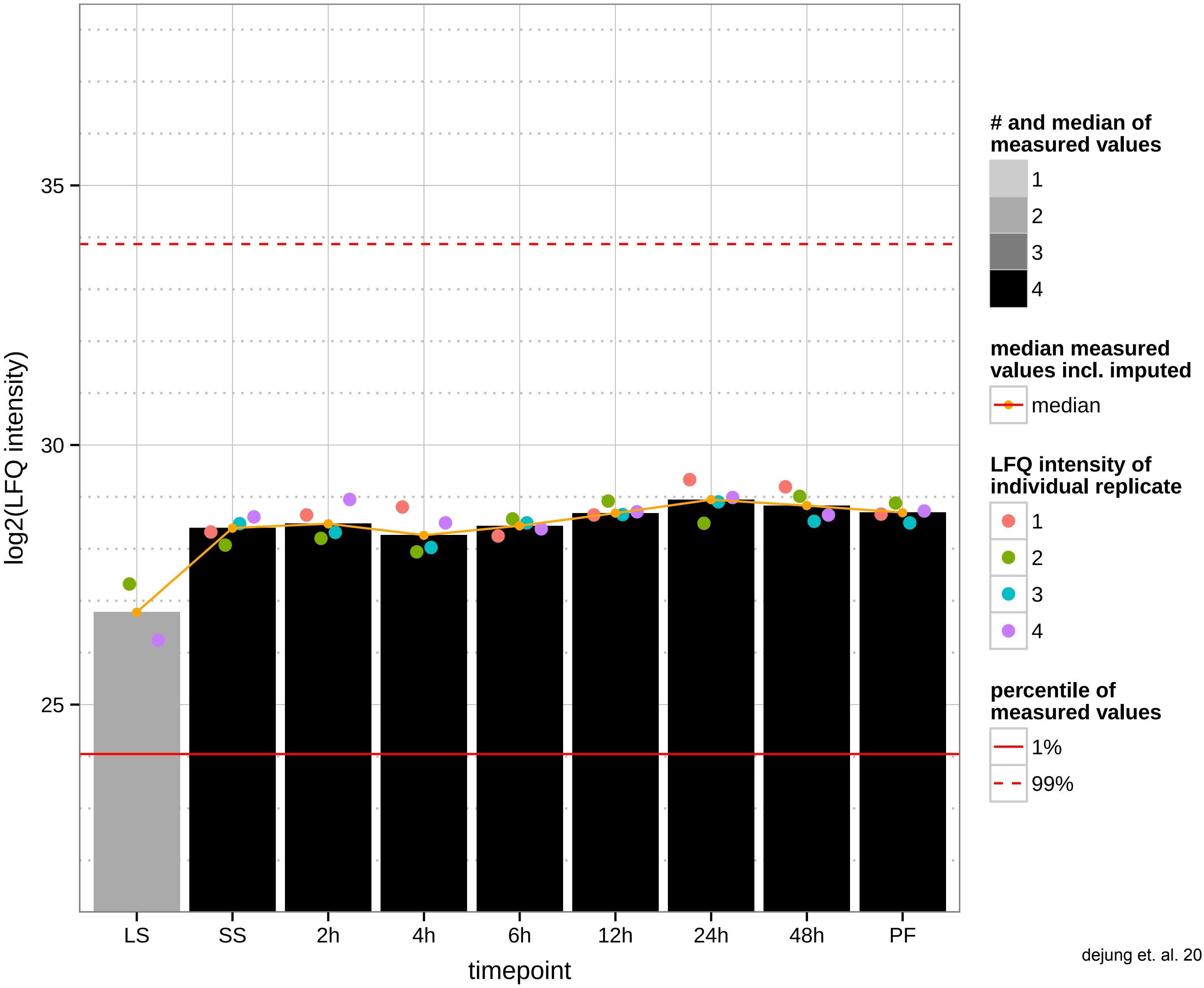
hypothetical protein, conserved
Tb927.7.4220
AGOF: null
AGOC: small–subunit processome
AGOP: rRNA processing
PGOF: protein binding
PGOC: null
PGOP: null





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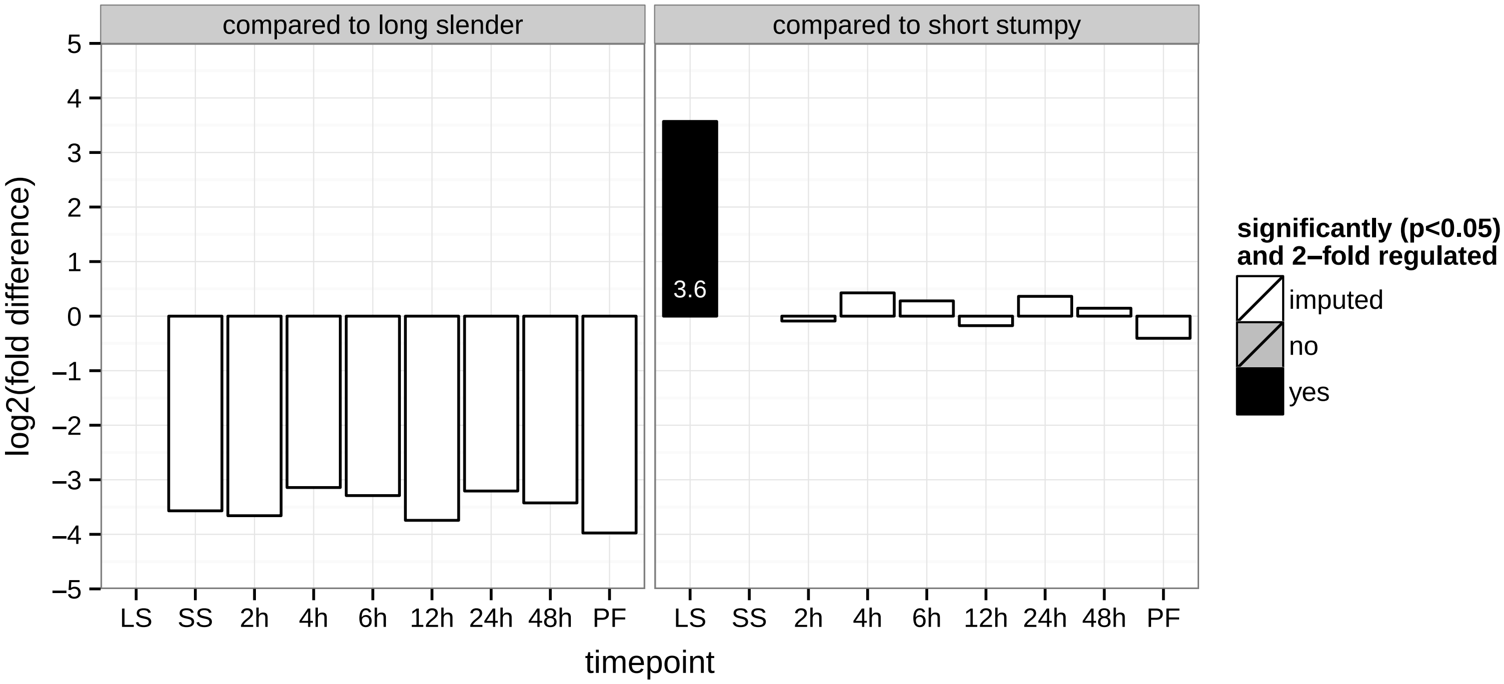
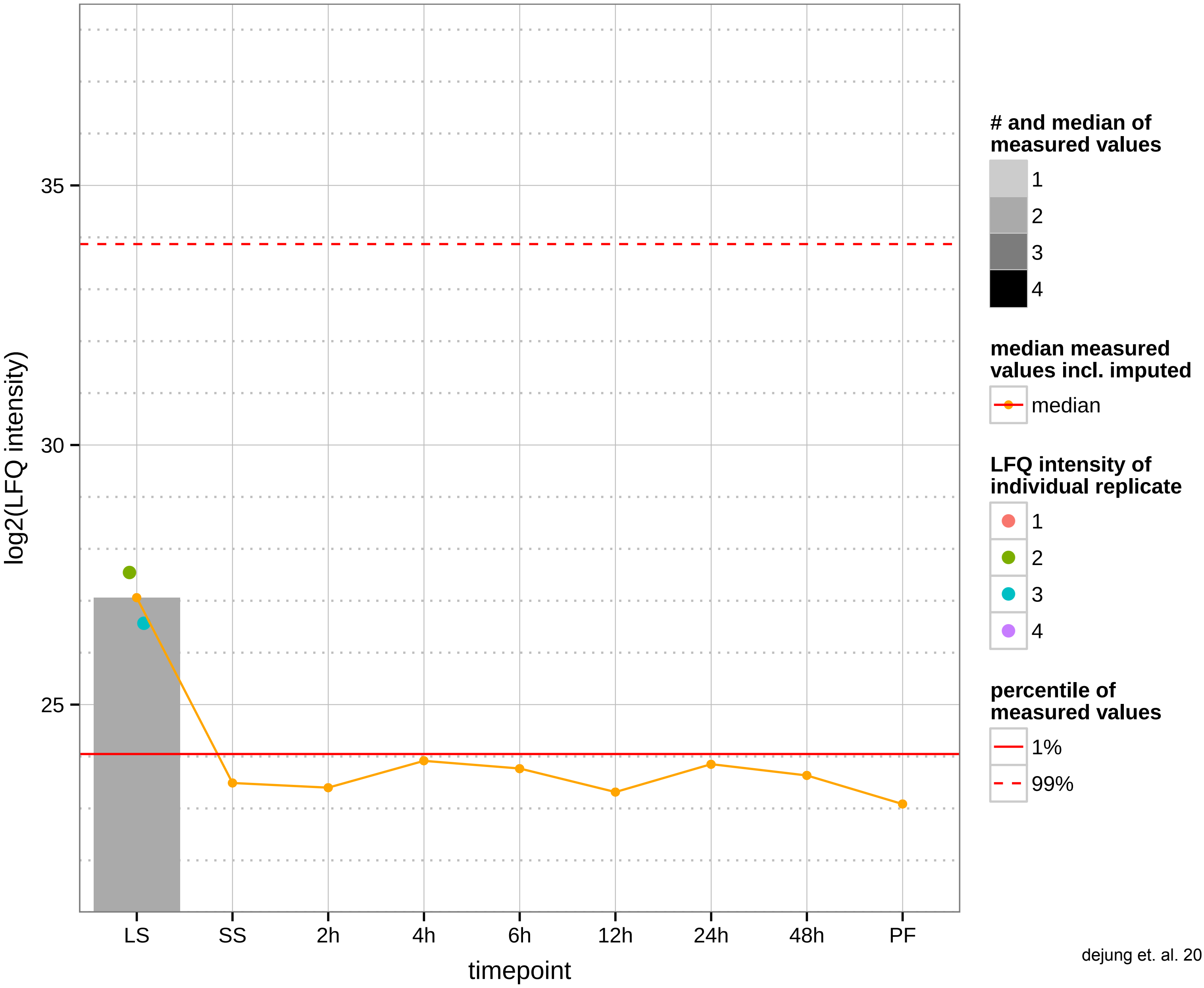
hypothetical protein, conserved
Tb927.7.4230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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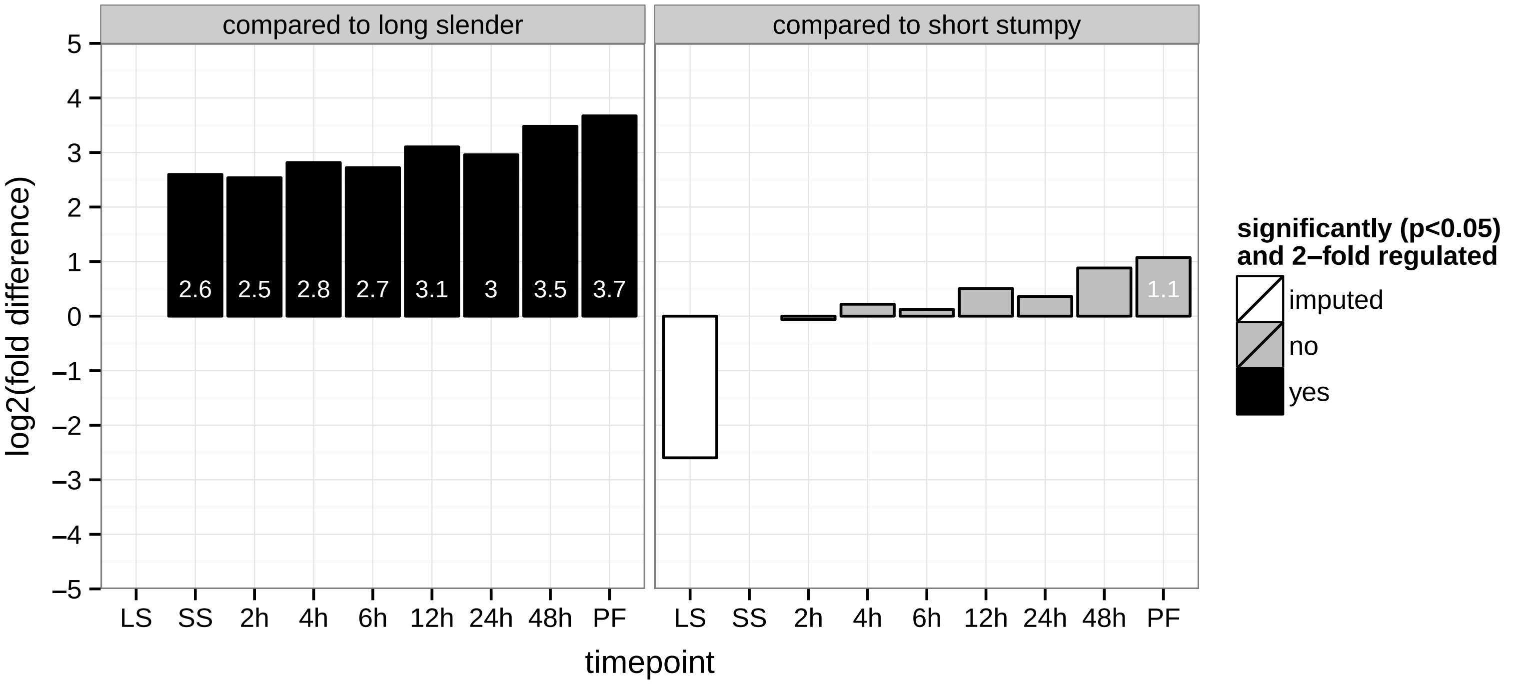
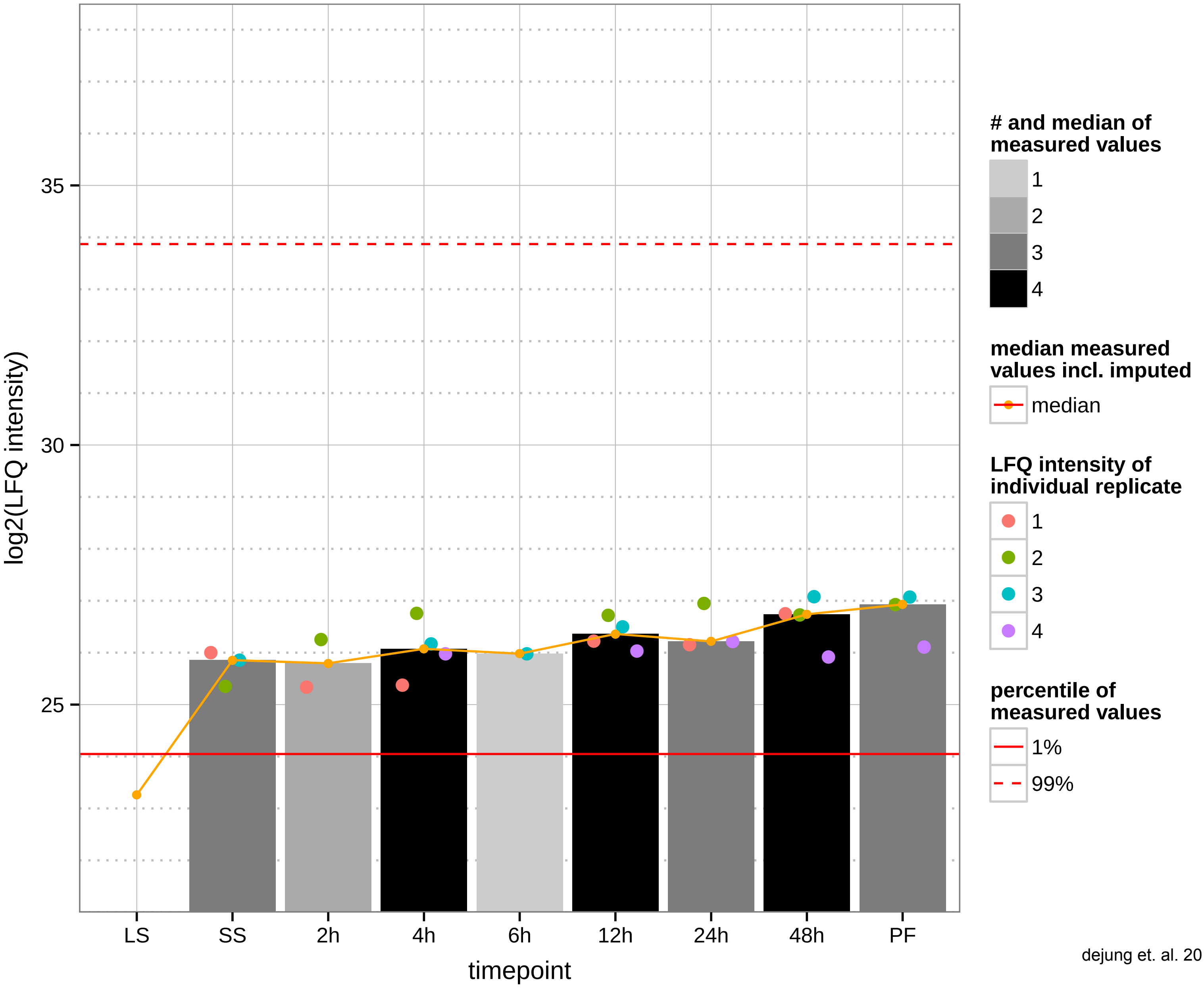
hypothetical protein, conserved
Tb927.7.4250;Tb927.7.4240
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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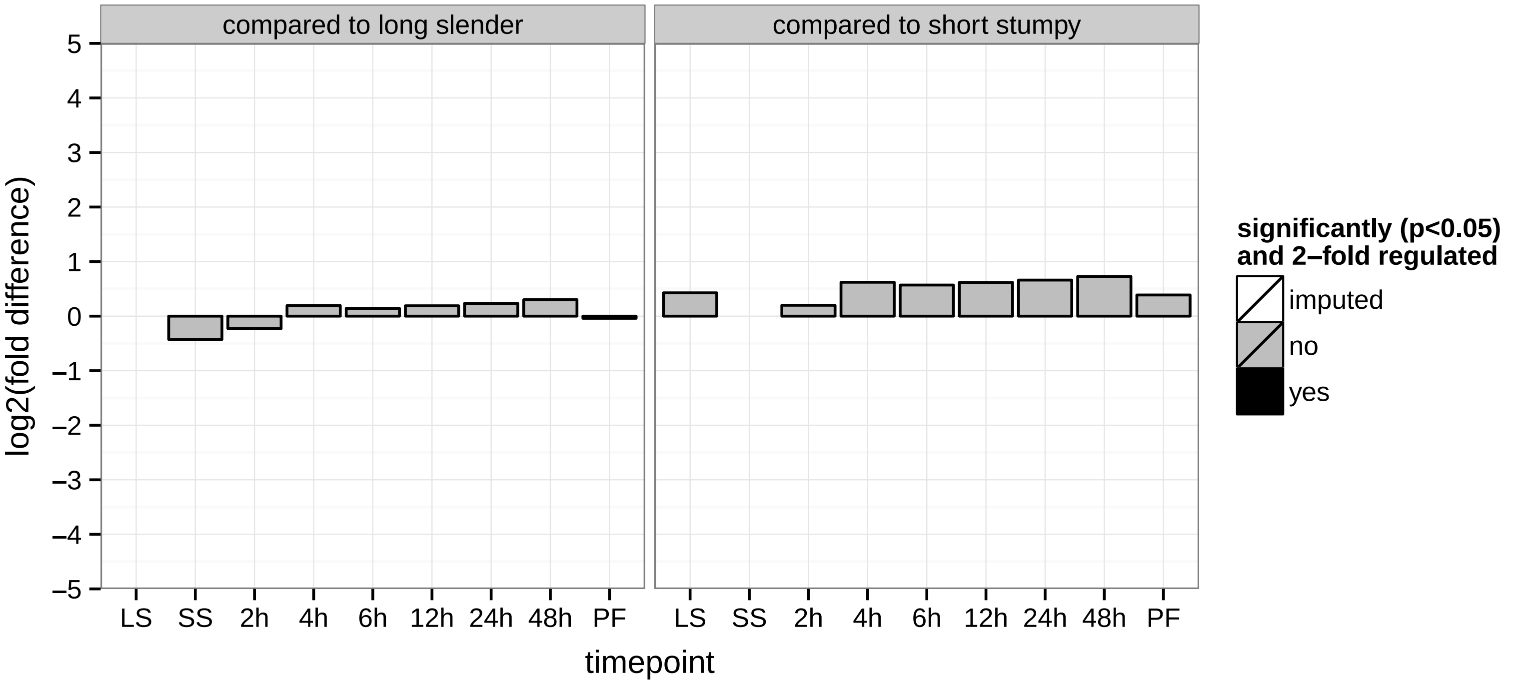
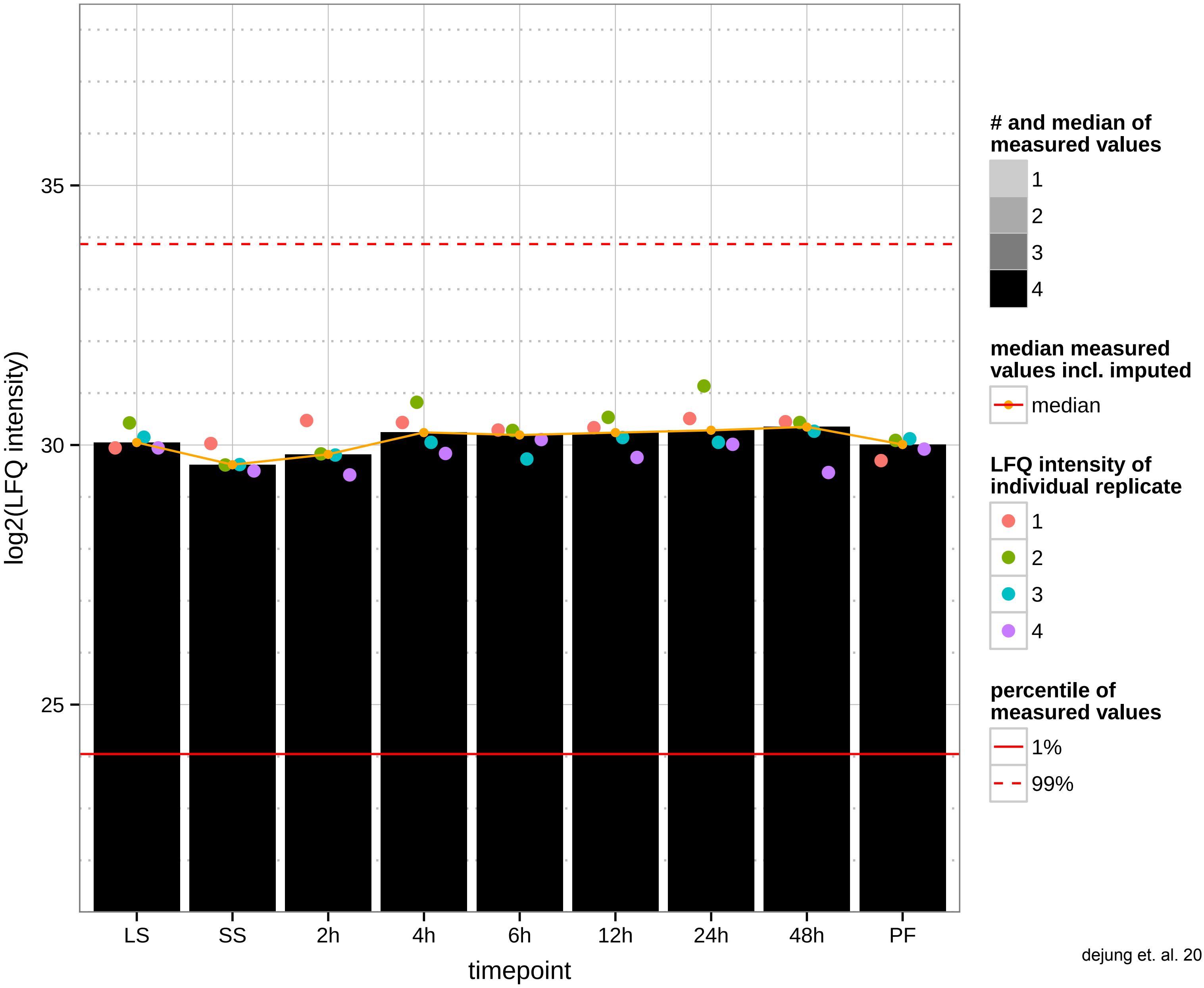
hypothetical protein, conserved
Tb927.7.4290
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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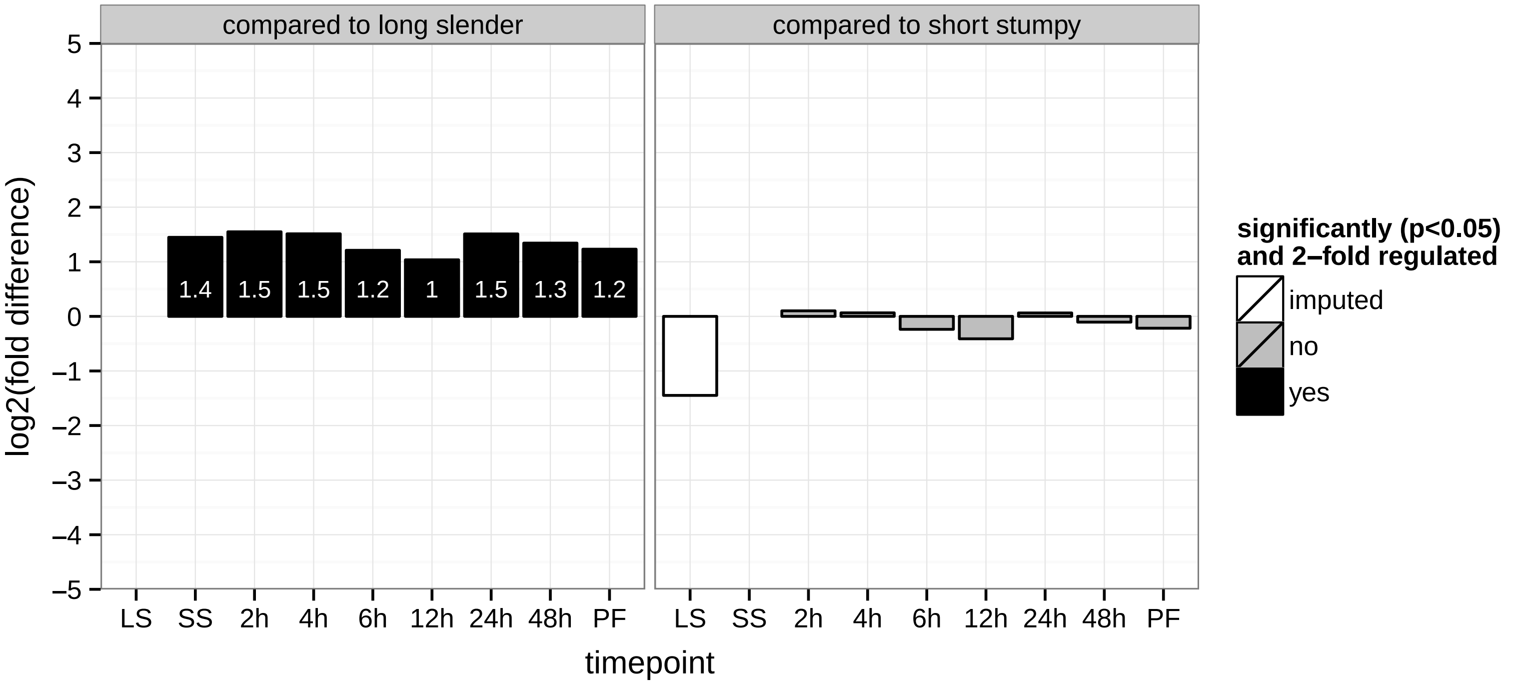
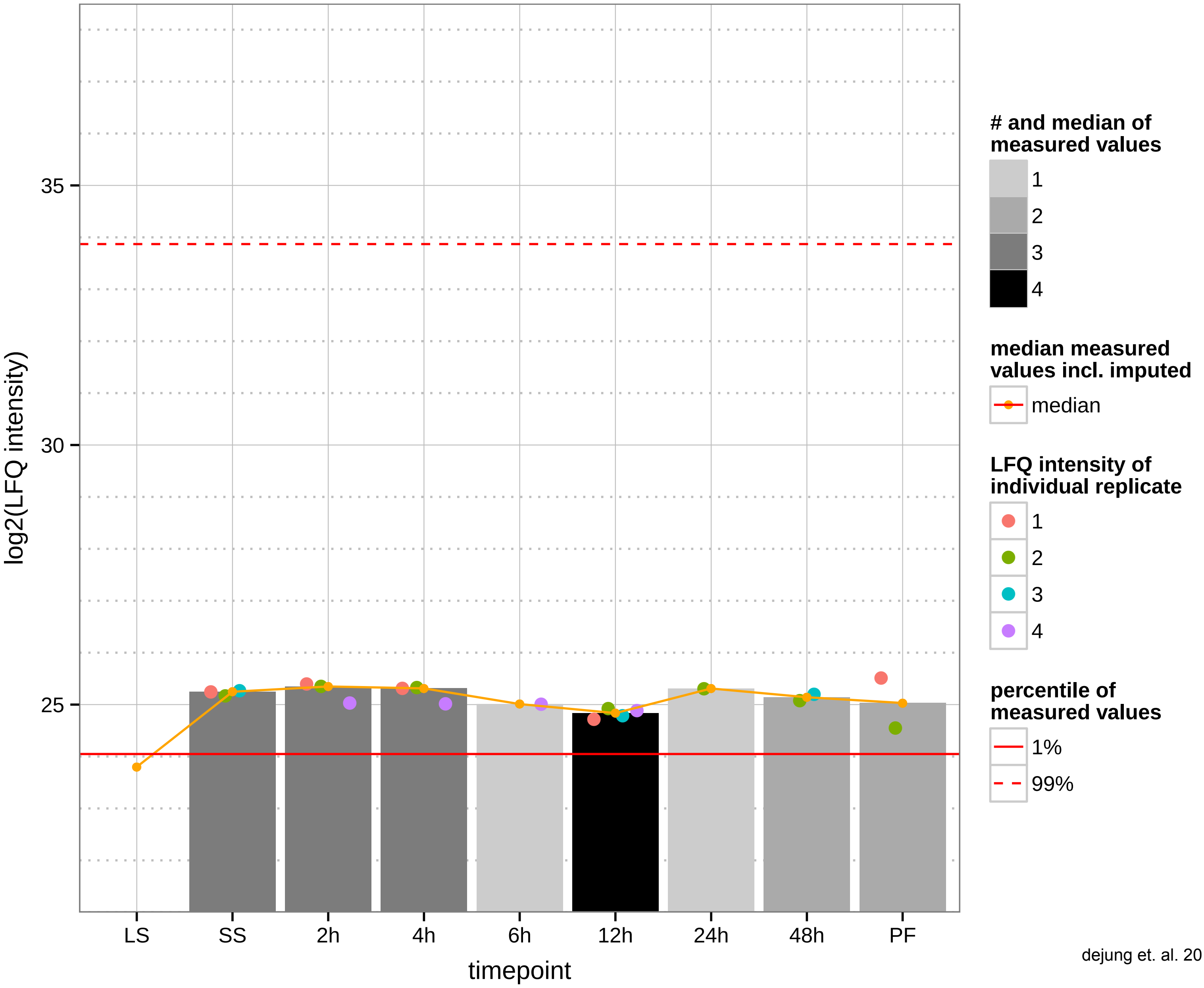
hypothetical protein, conserved
Tb927.7.4320
AGOF: polynucleotide 5'−phosphatase activity
AGOC: mRNA cap methyltransferase complex
AGOP: 7−methylguanosine mRNA capping
PGOF: polynucleotide 5'−phosphatase activity, transferase activity
PGOC: null
PGOP: null





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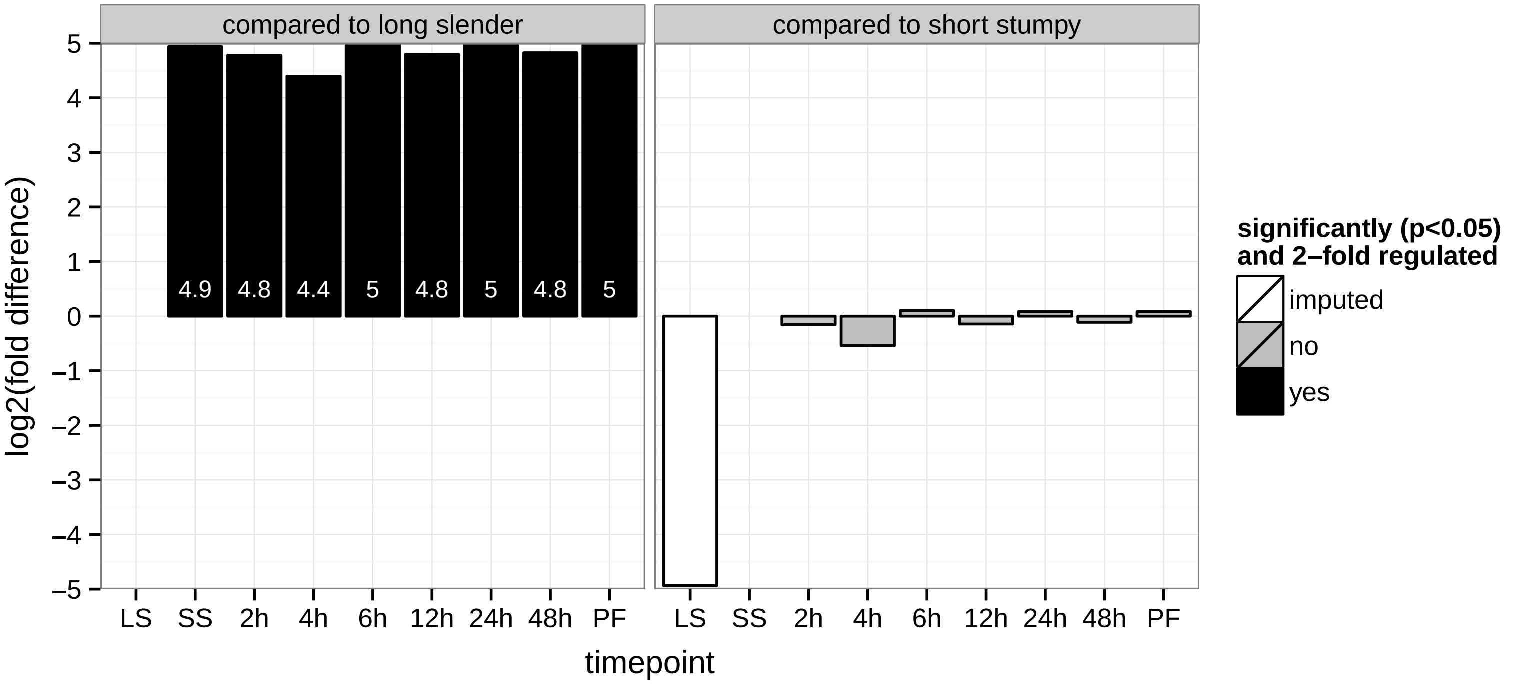
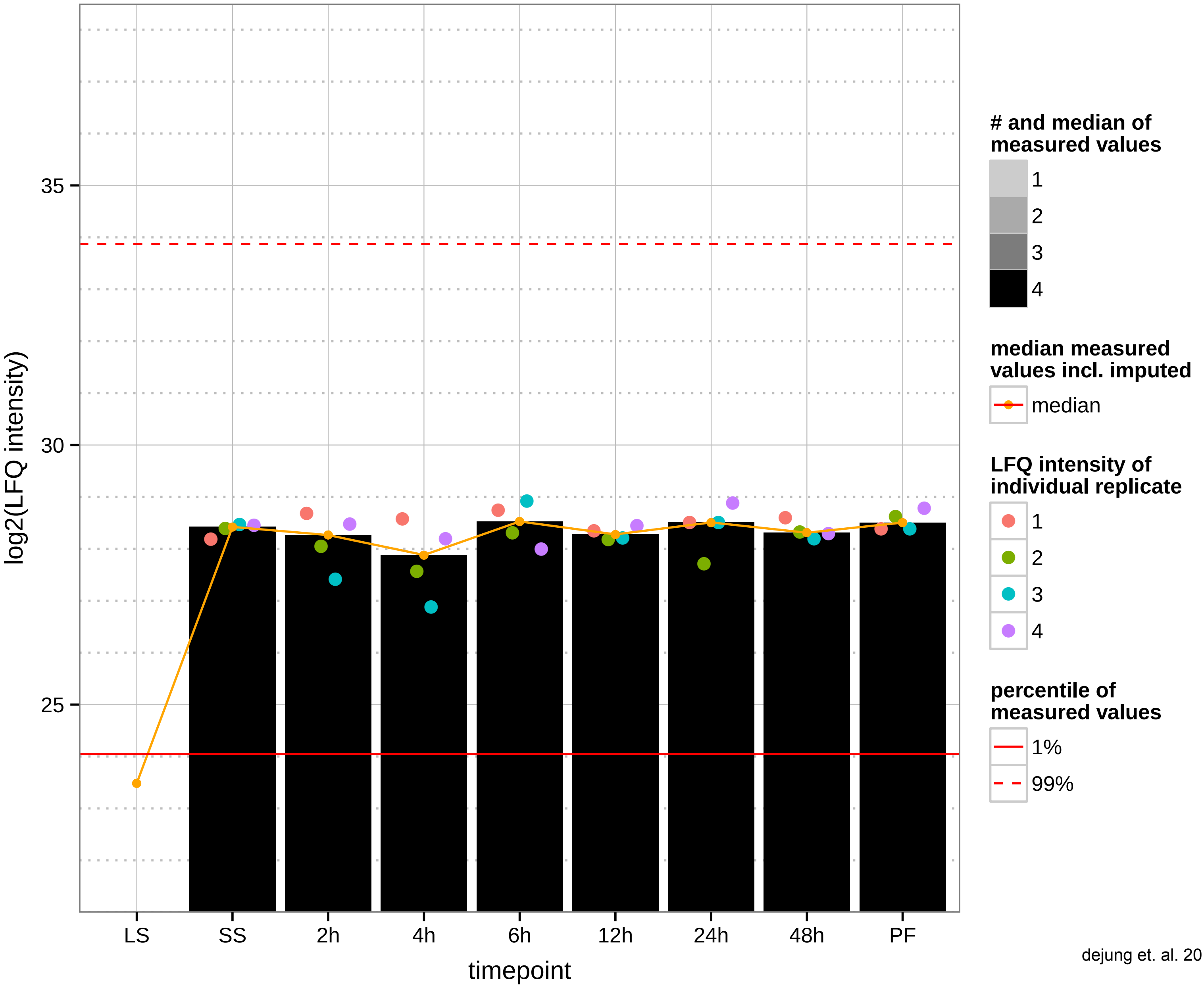
hypothetical protein, conserved
Tb927.7.4340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: nucleus
PGOP: null





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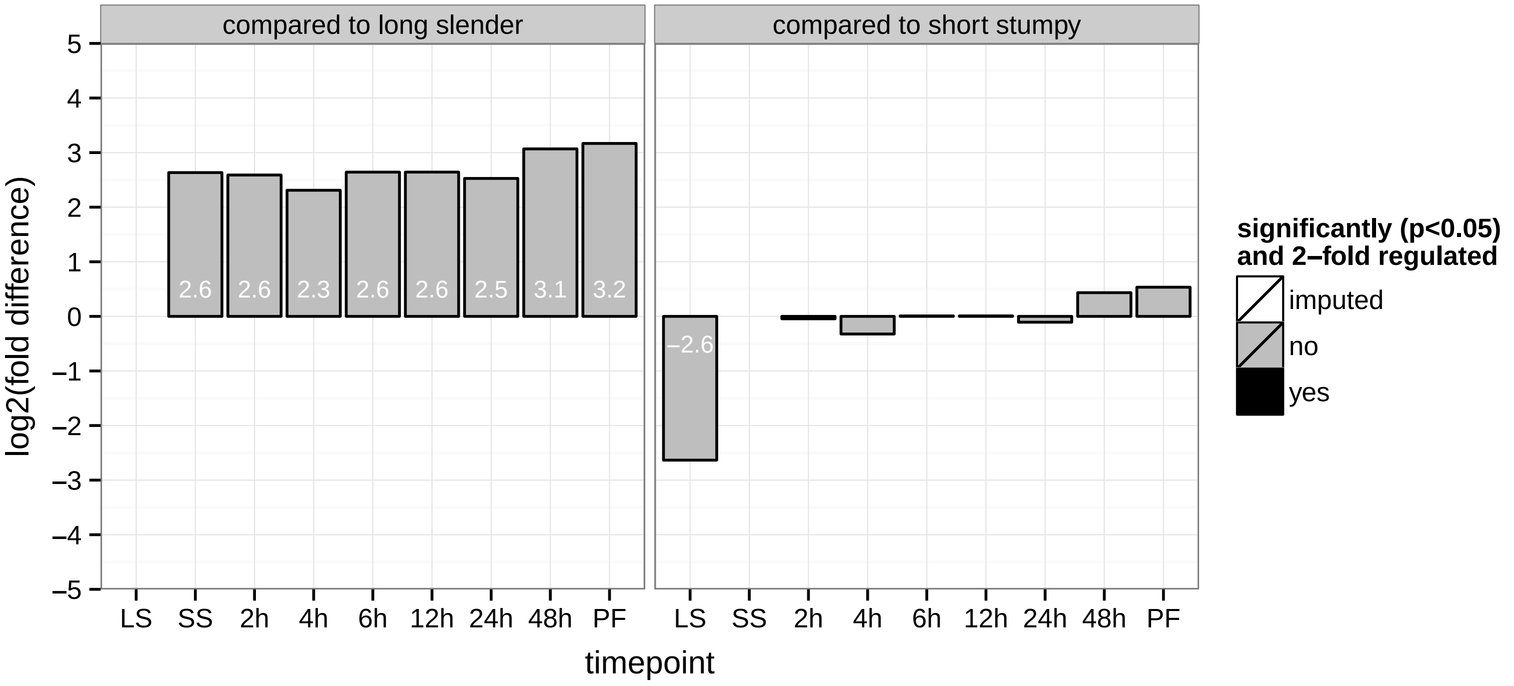
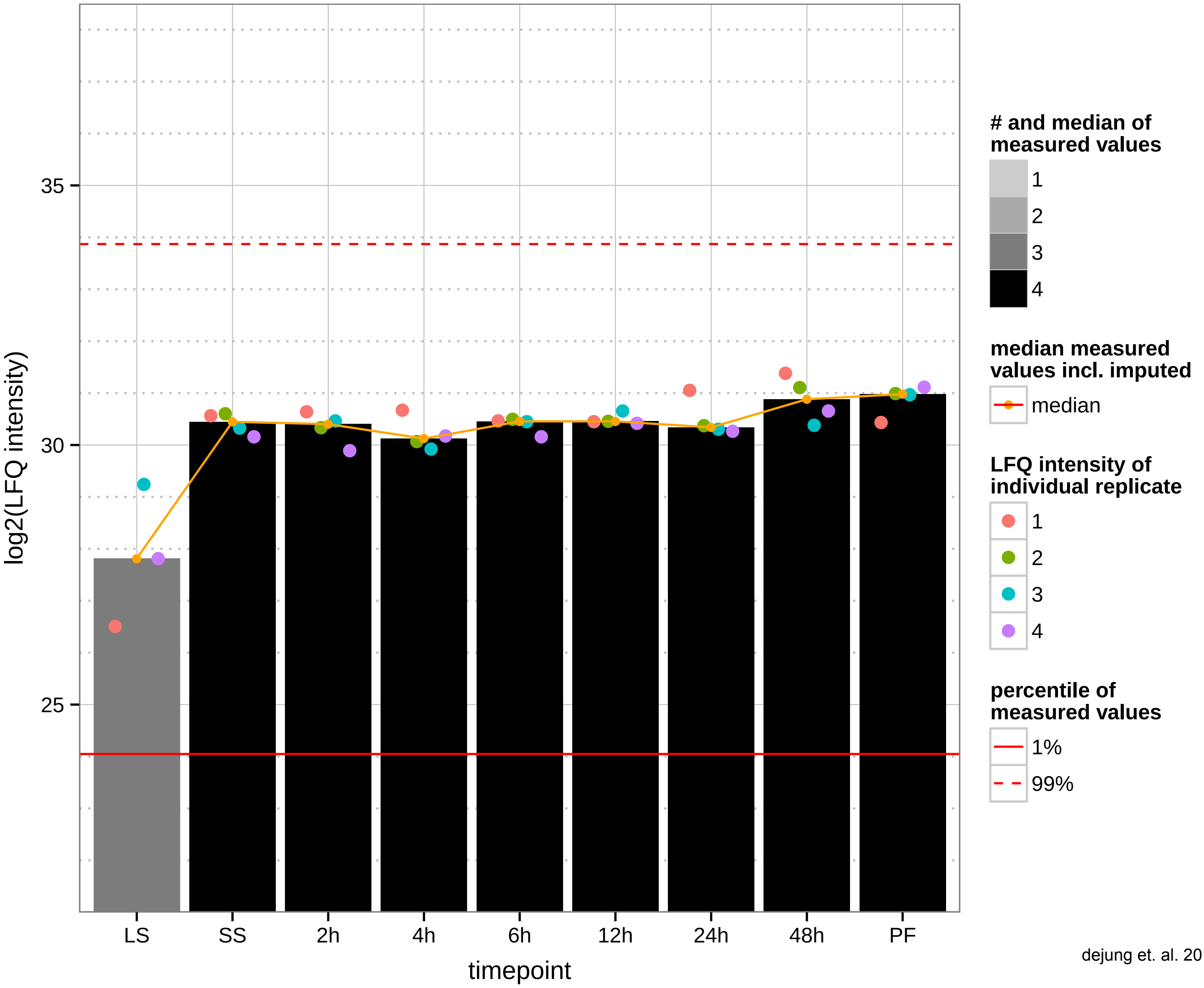
threonine synthase, putative
Tb927.7.4390
AGOF: pyridoxal phosphate binding, threonine synthase activity
AGOC: null
AGOP: threonine biosynthetic process
PGOF: catalytic activity, pyridoxal phosphate binding, threonine synthase activity
PGOC: null
PGOP: metabolic process, threonine biosynthetic process





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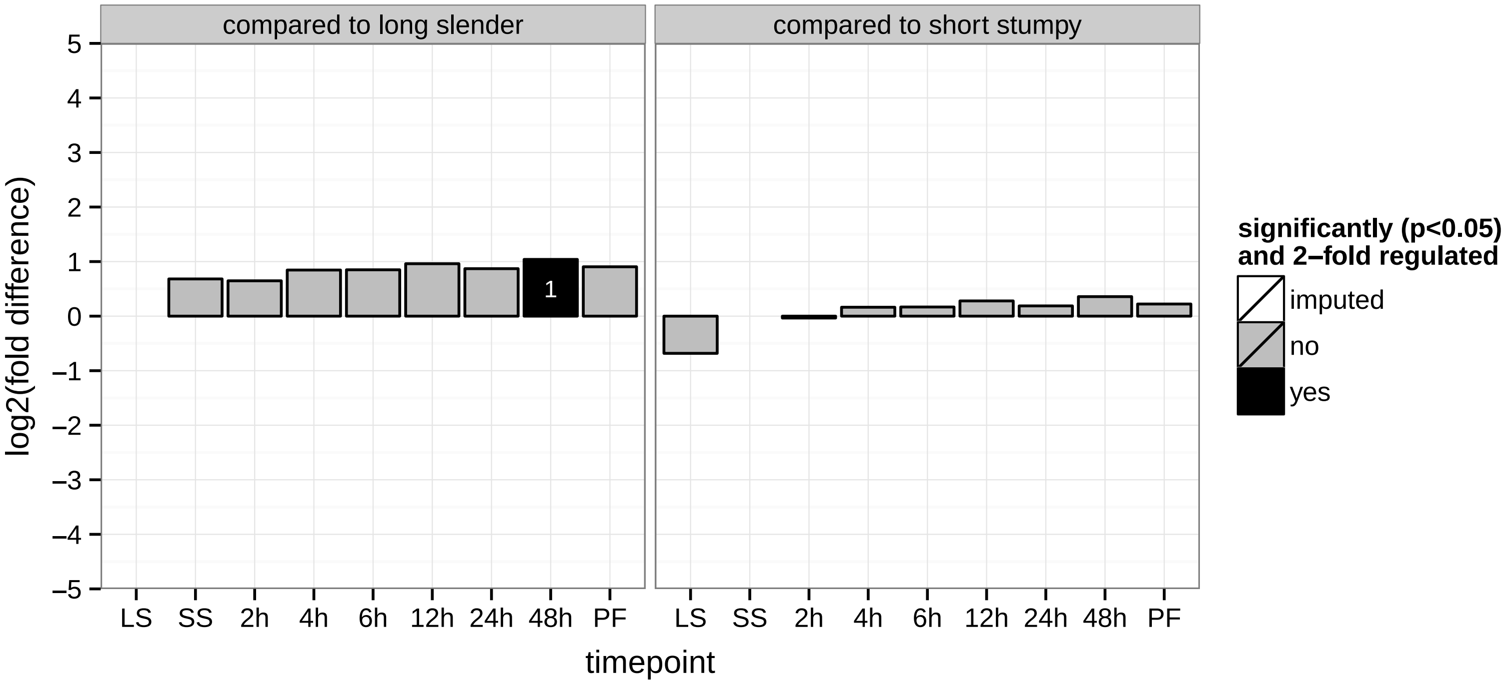
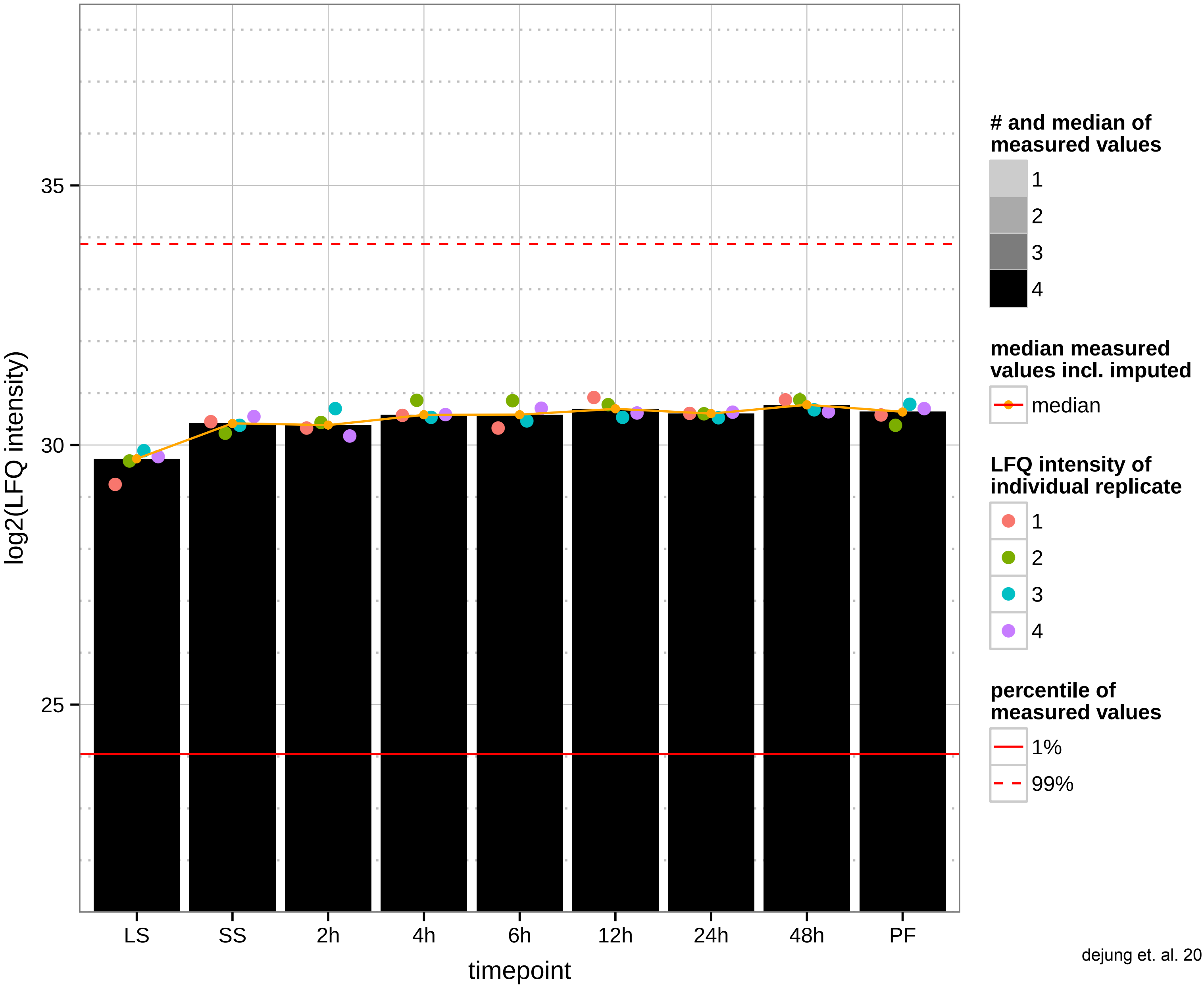
proteasome alpha 3 subunit, putative
Tb927.7.4420
AGOF: endopeptidase activity, threonine–type endopeptidase activity
AGOC: proteasome core complex, proteasome core complex, alpha–subunit complex
AGOP: protein metabolic process, ubiquitin–dependent protein catabolic process
PGOF: endopeptidase activity, threonine–type endopeptidase activity
PGOC: proteasome core complex, proteasome core complex, alpha–subunit complex
PGOP: proteolysis involved in cellular protein catabolic process, ubiquitin–dependent protein catabolic process





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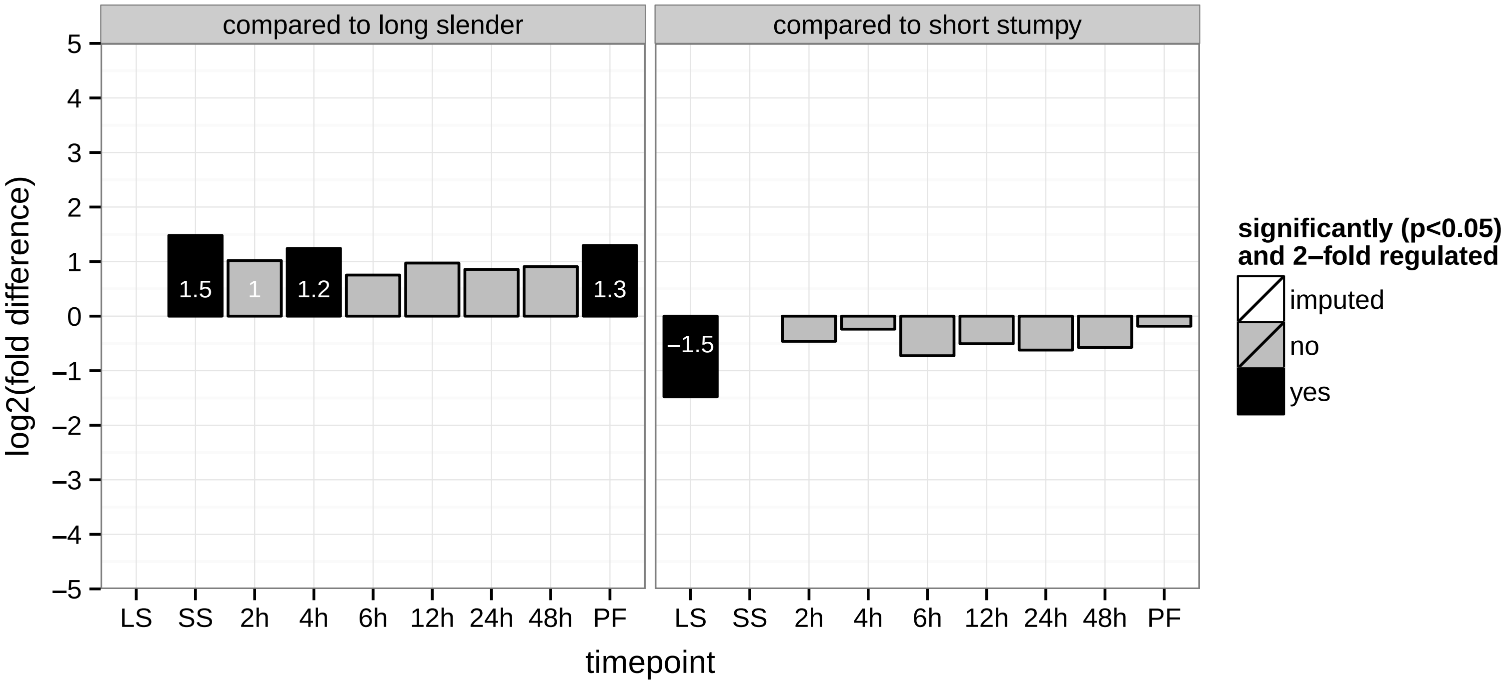
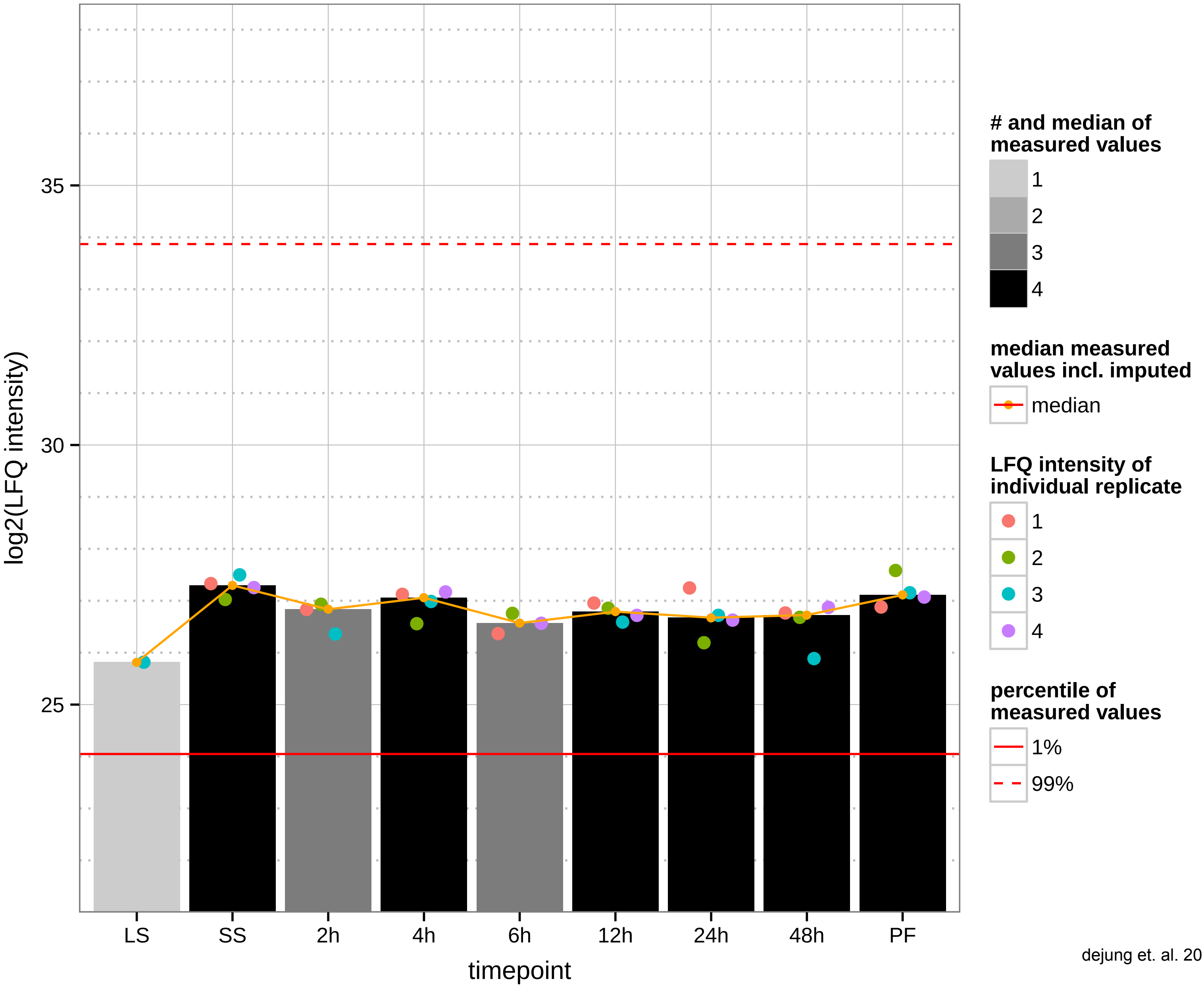
hypothetical protein, conserved
Tb927.7.4440
AGOF: catalytic activity, coenzyme binding
AGOC: mitochondrion
AGOP: cellular metabolic process
PGOF: catalytic activity, coenzyme binding
PGOC: null
PGOP: cellular metabolic process





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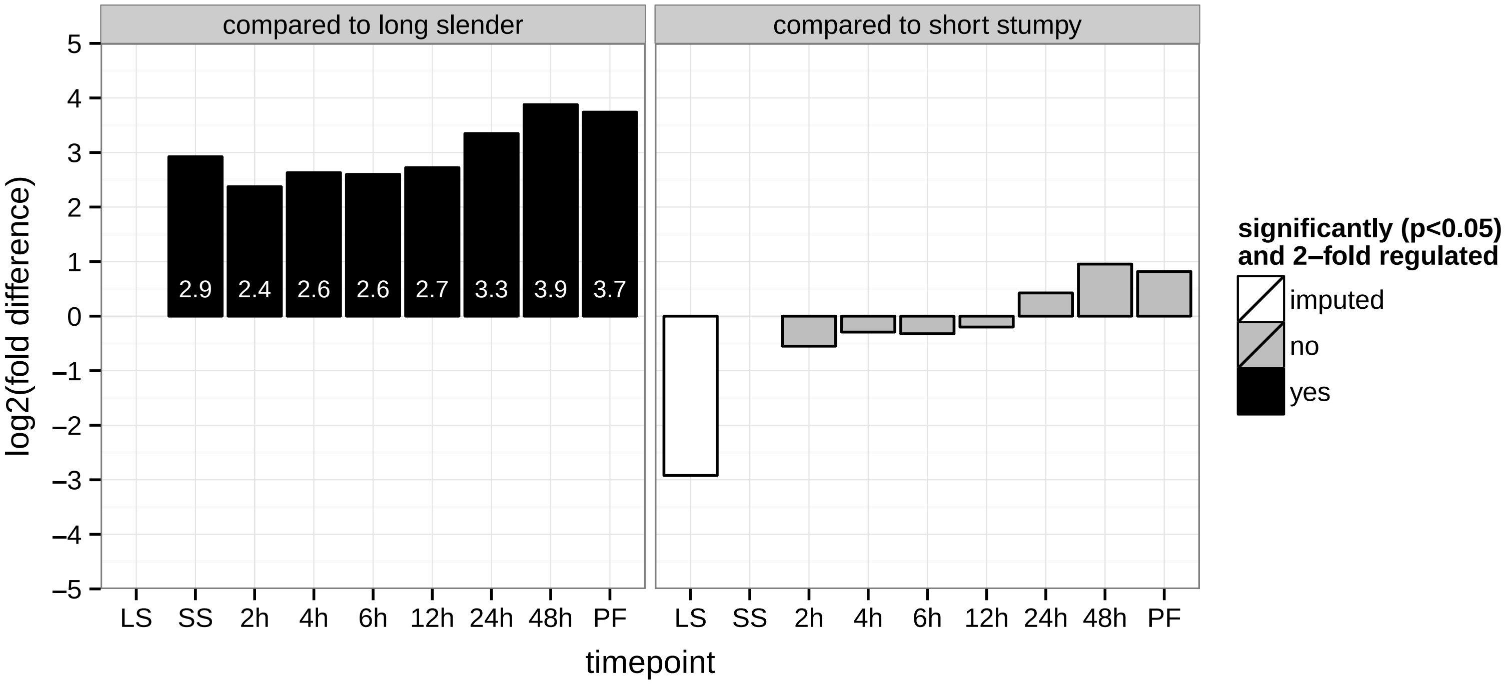
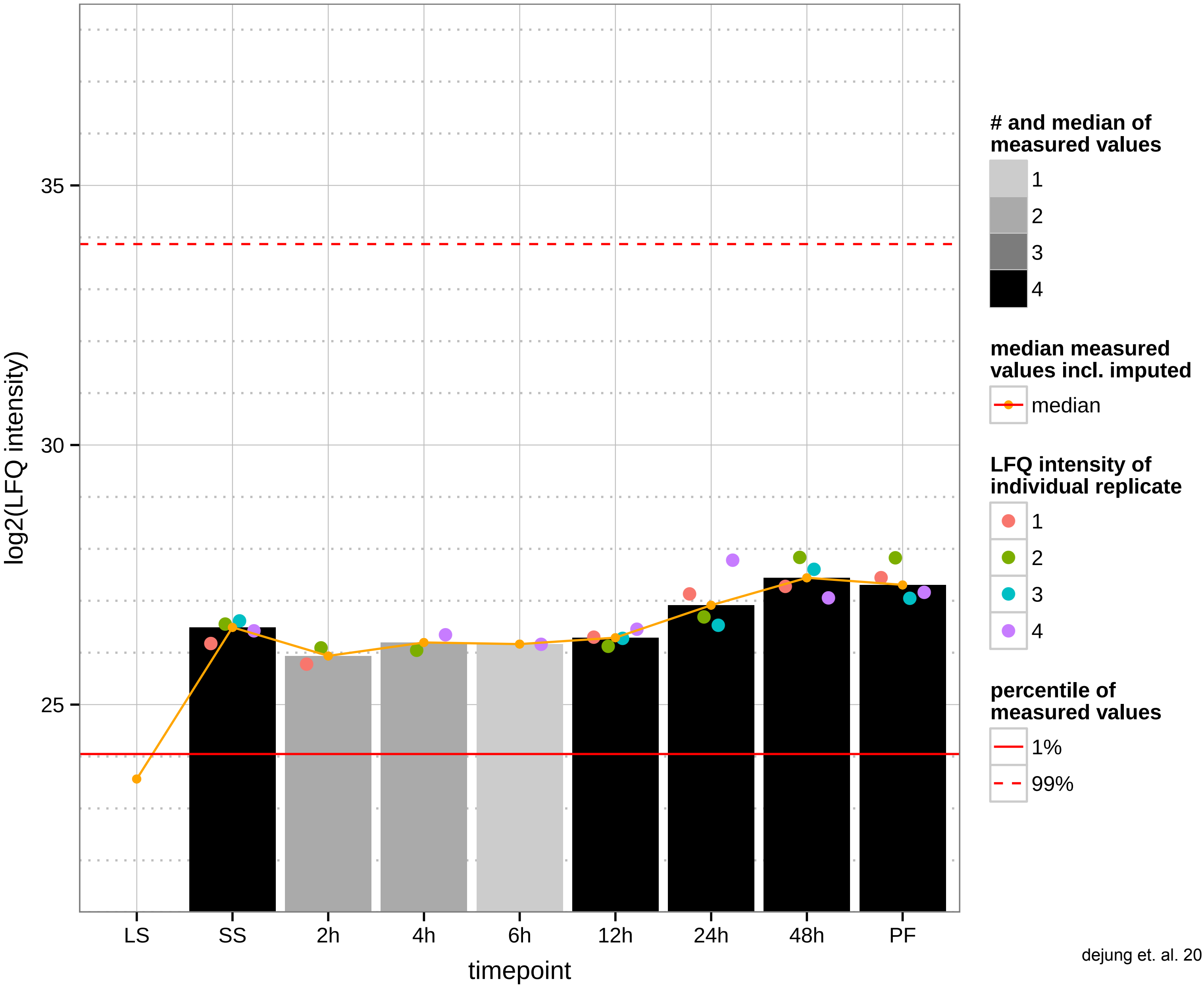
hypothetical protein, conserved
Tb927.7.4450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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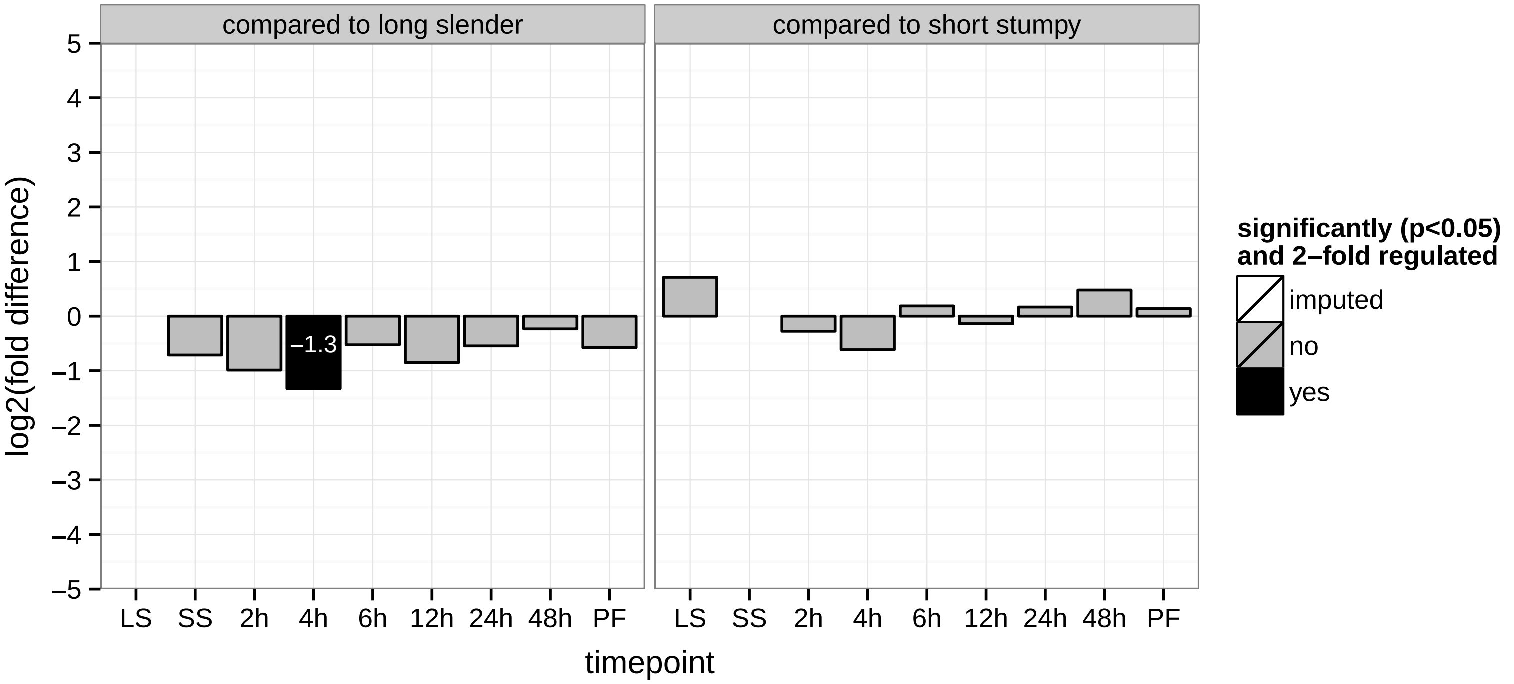
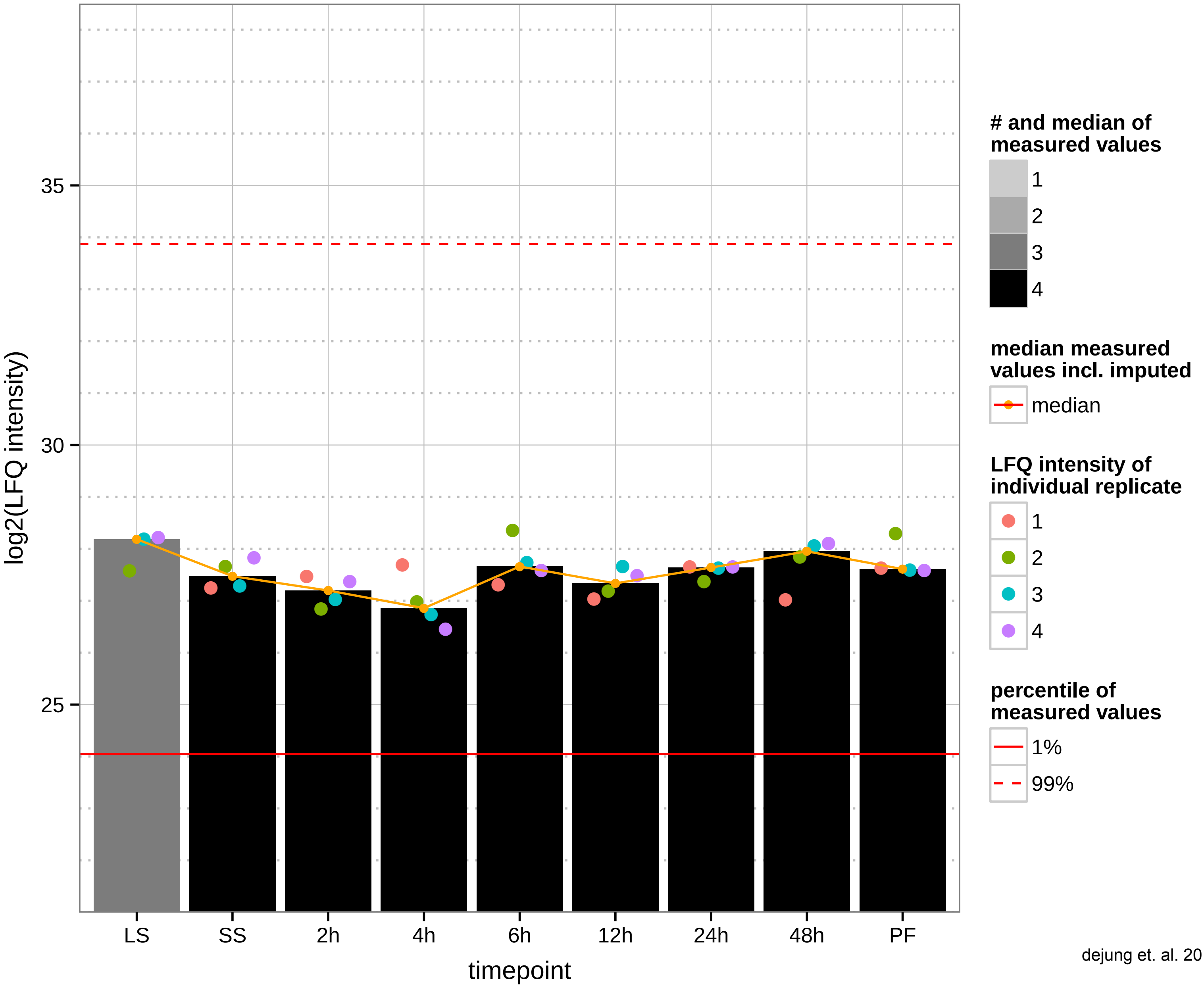
hypothetical protein, conserved
Tb927.7.4460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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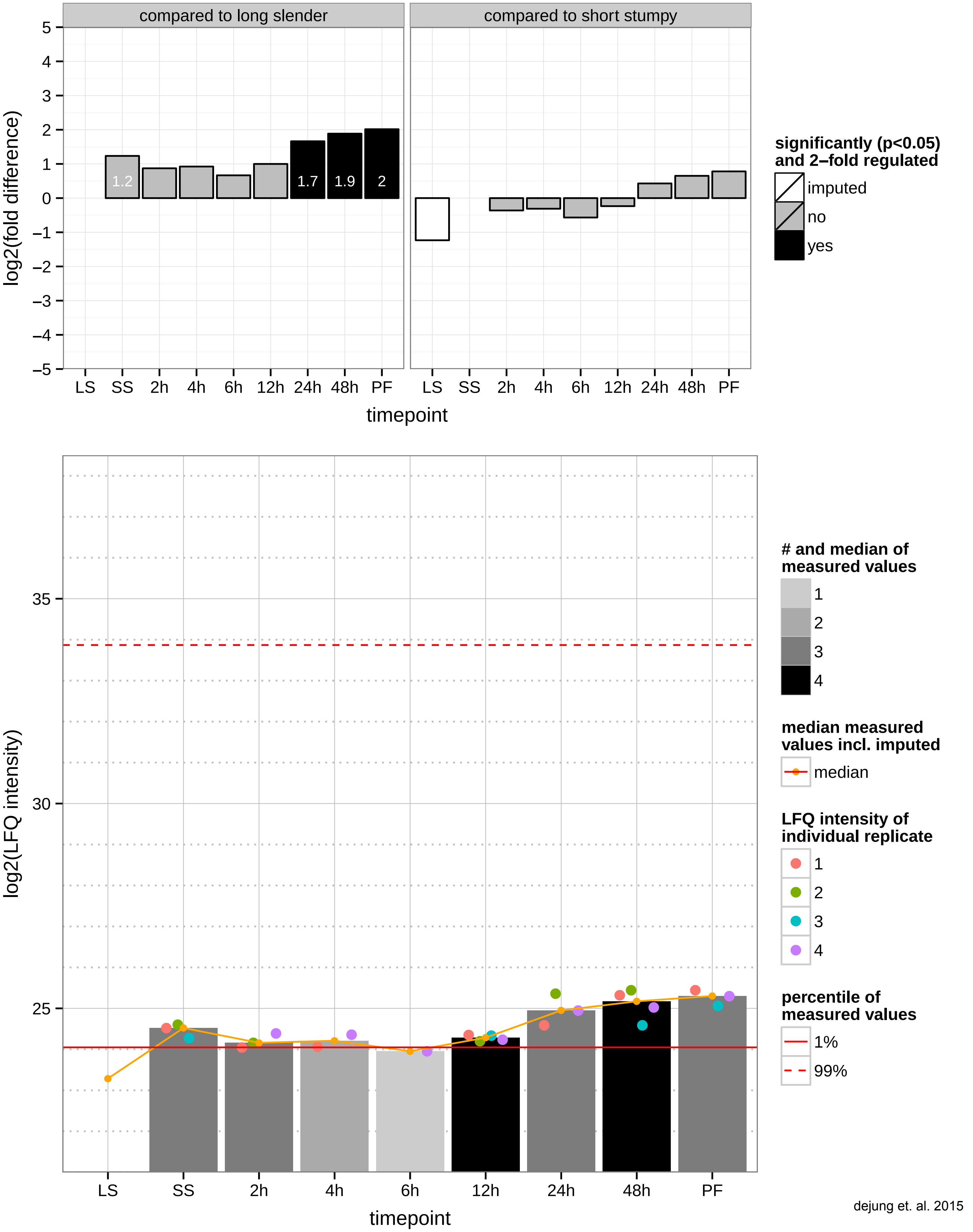
hypothetical protein, conserved
Tb927.7.4620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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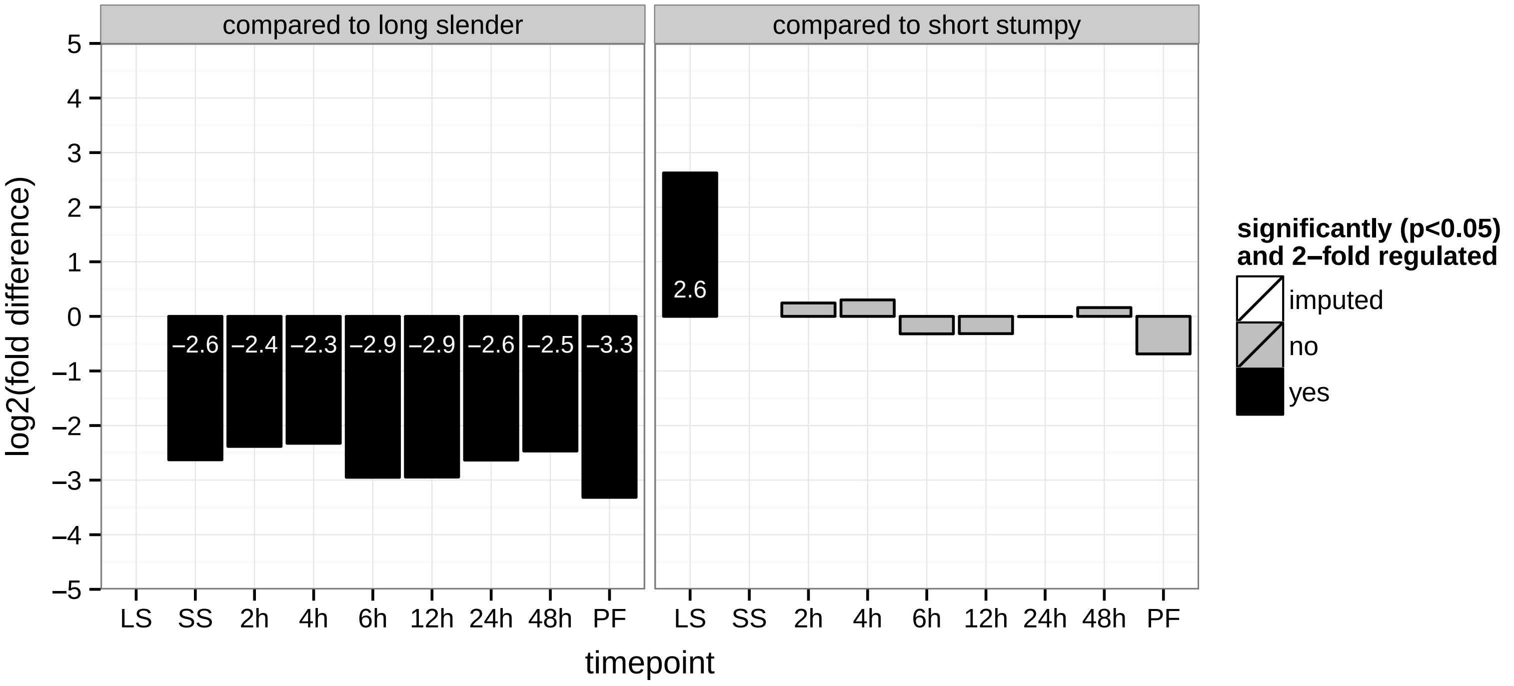
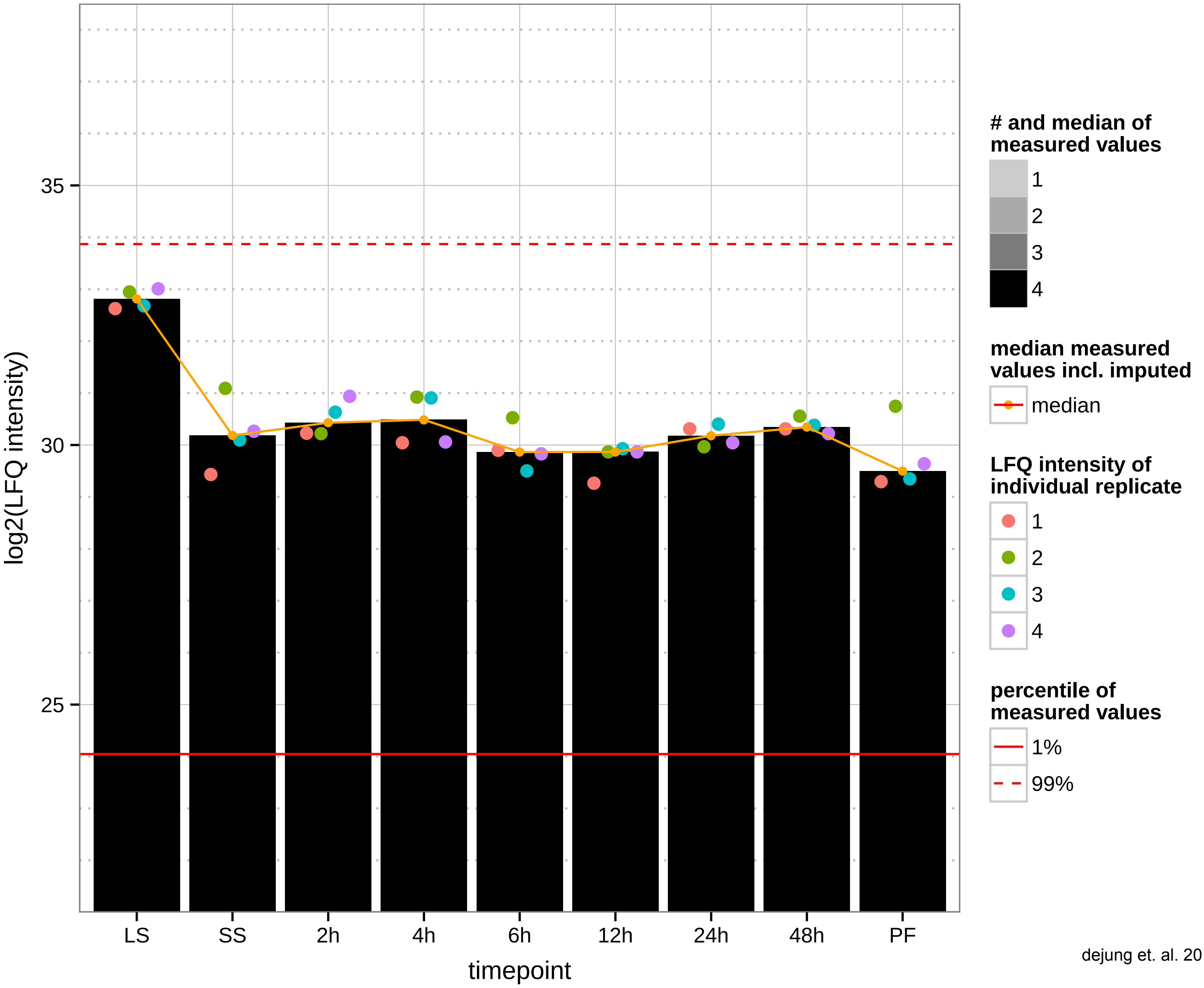
hypothetical protein, conserved
Tb927.7.4760;Tb11.v5.0159
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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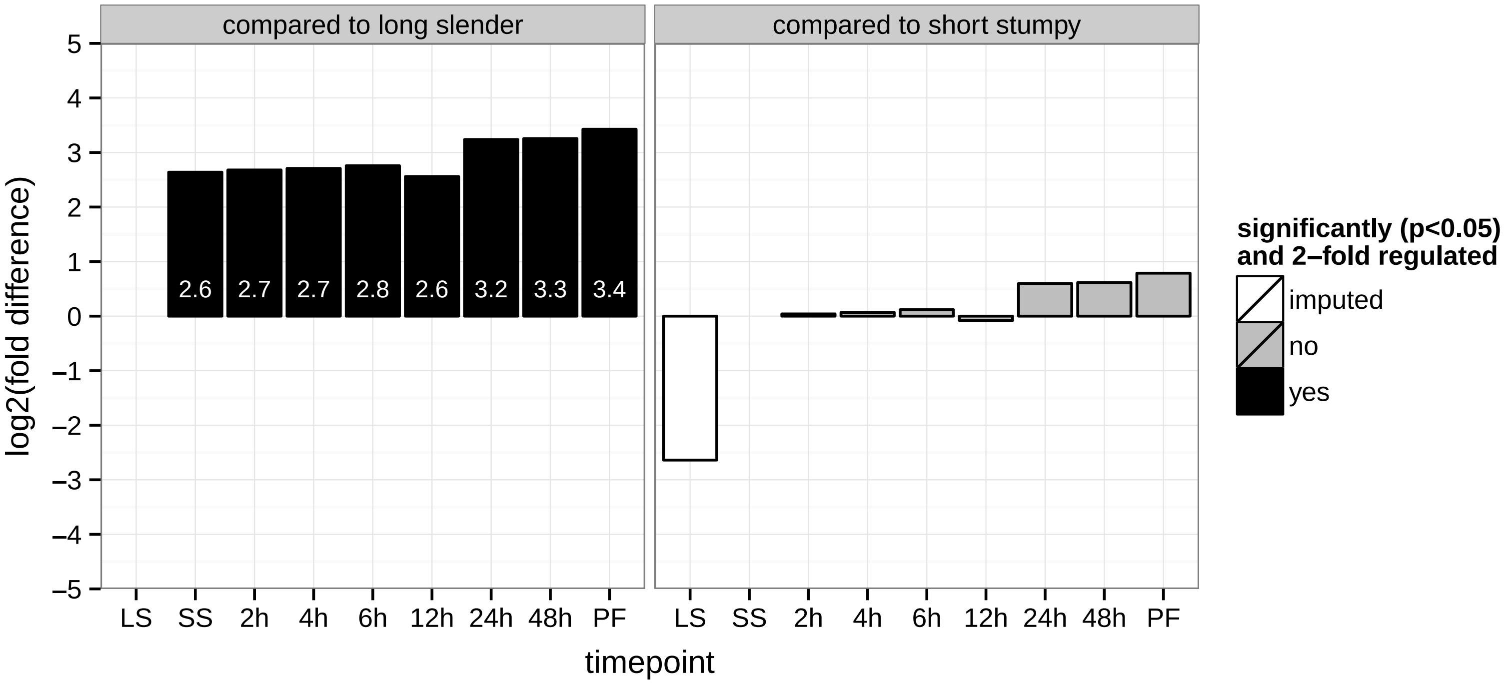
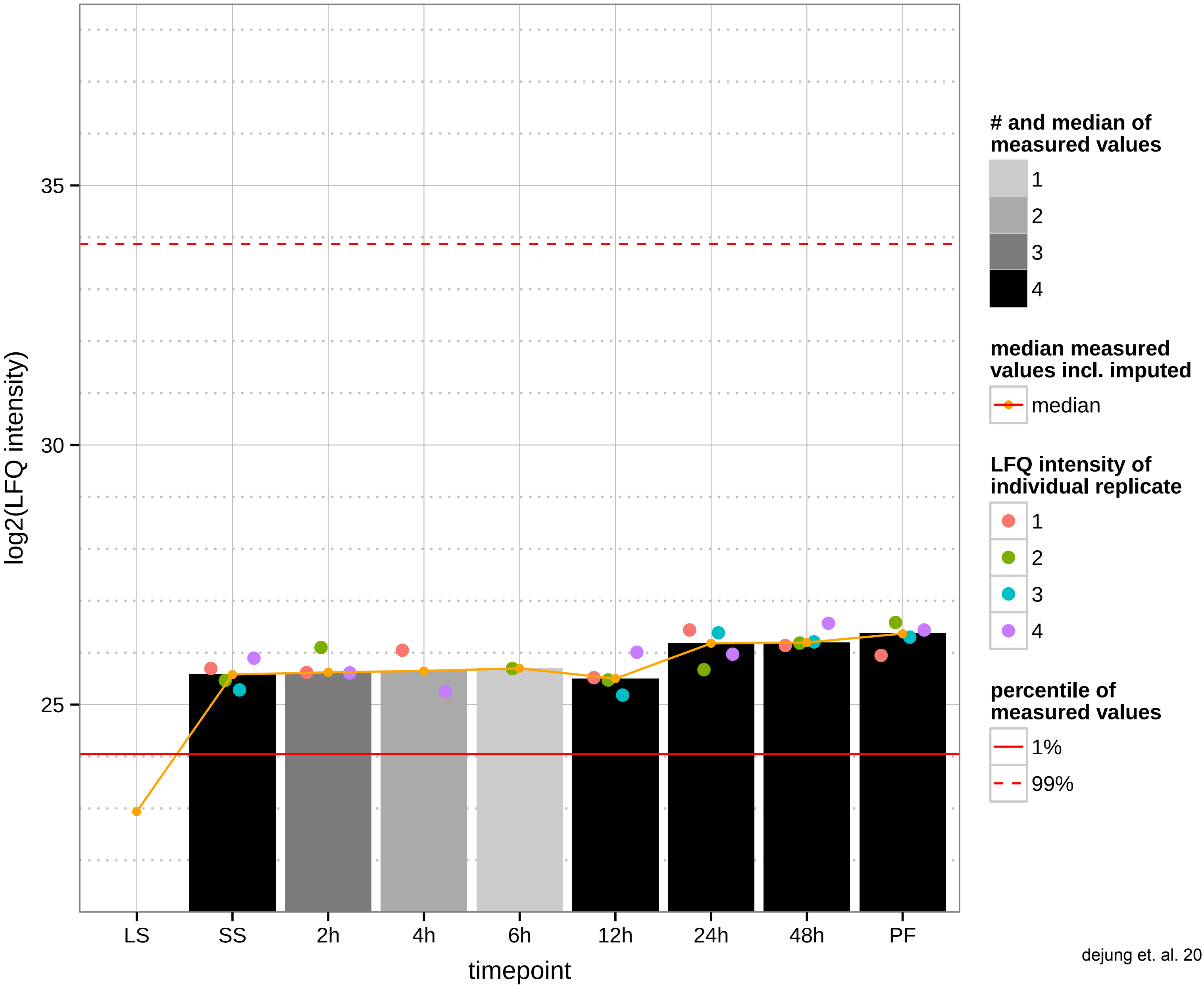
hypothetical protein, conserved
Tb927.7.5110
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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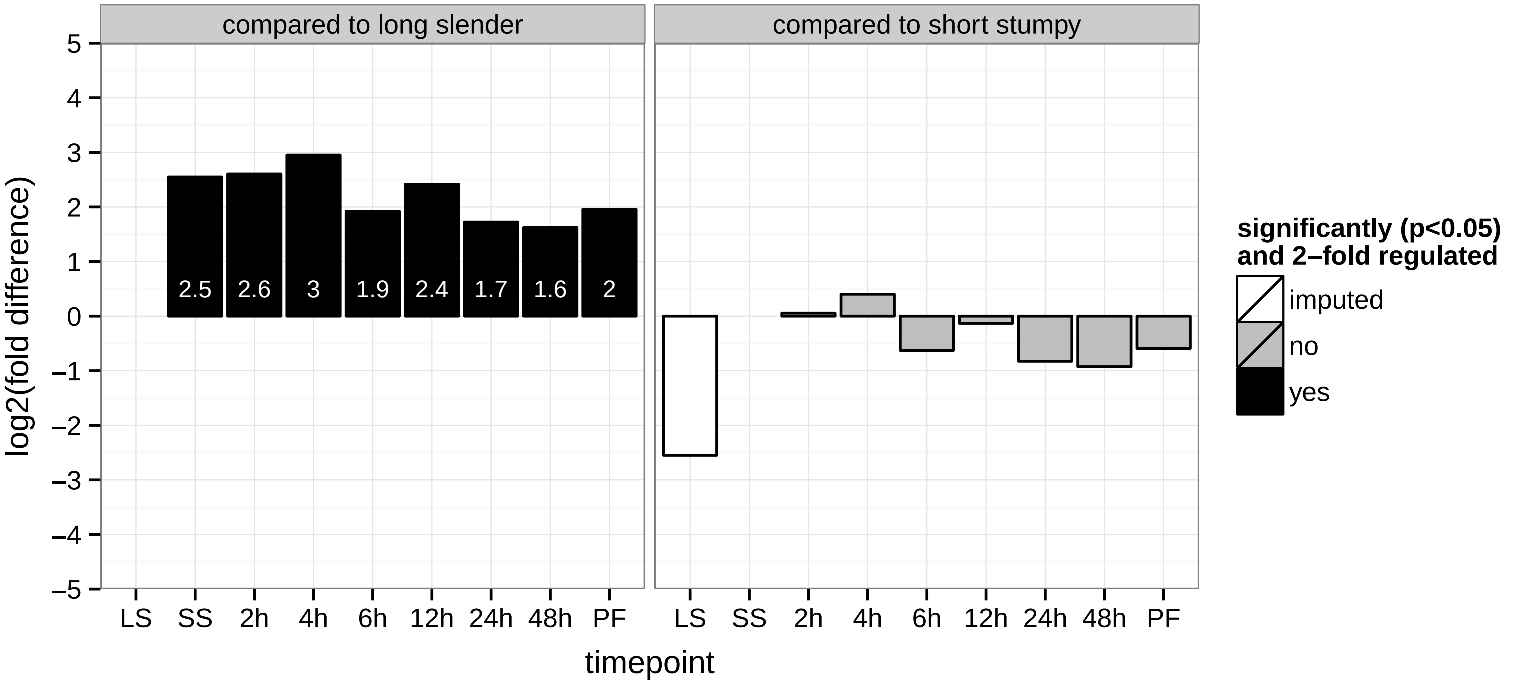
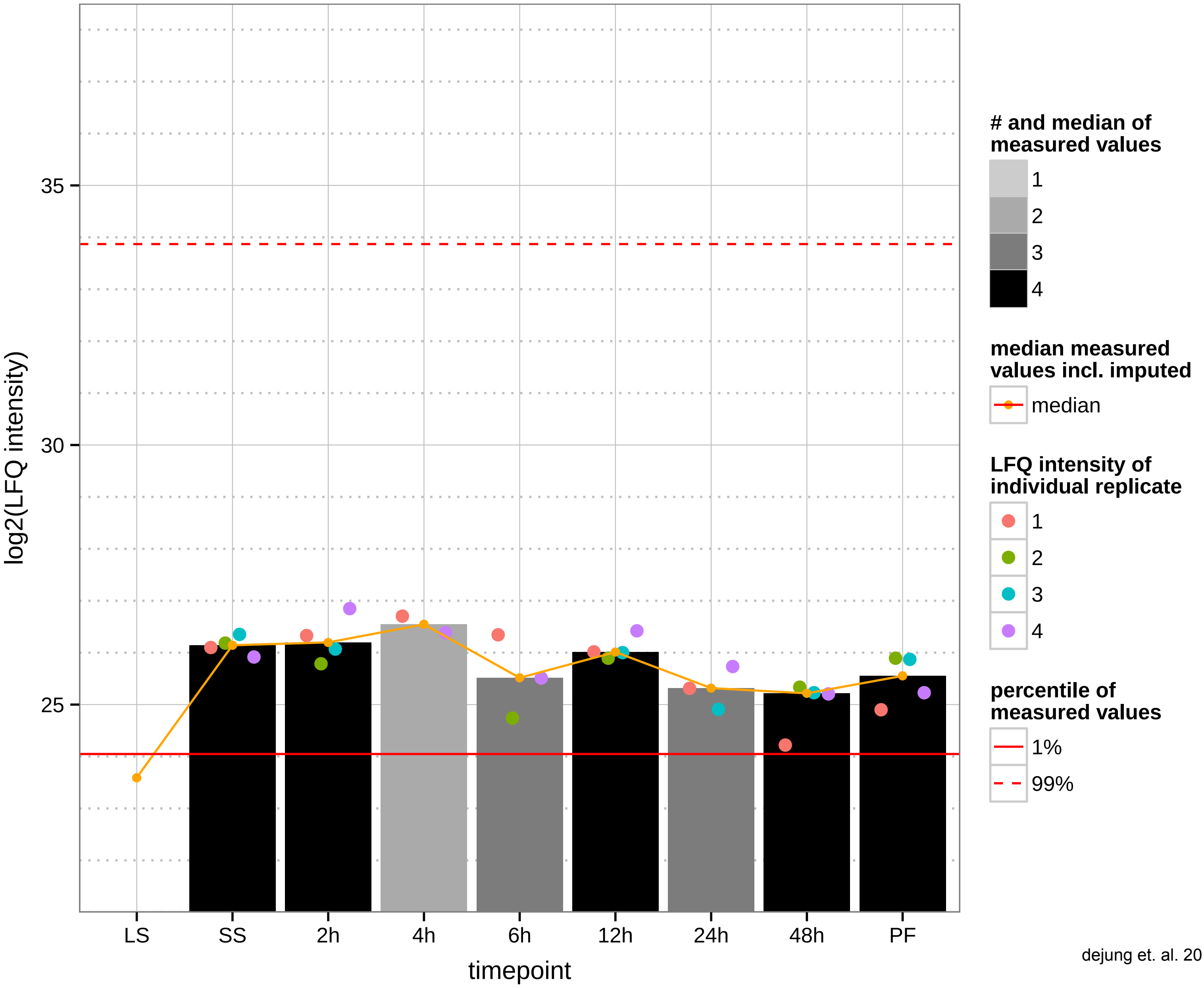
hypothetical protein, conserved
Tb927.7.5290
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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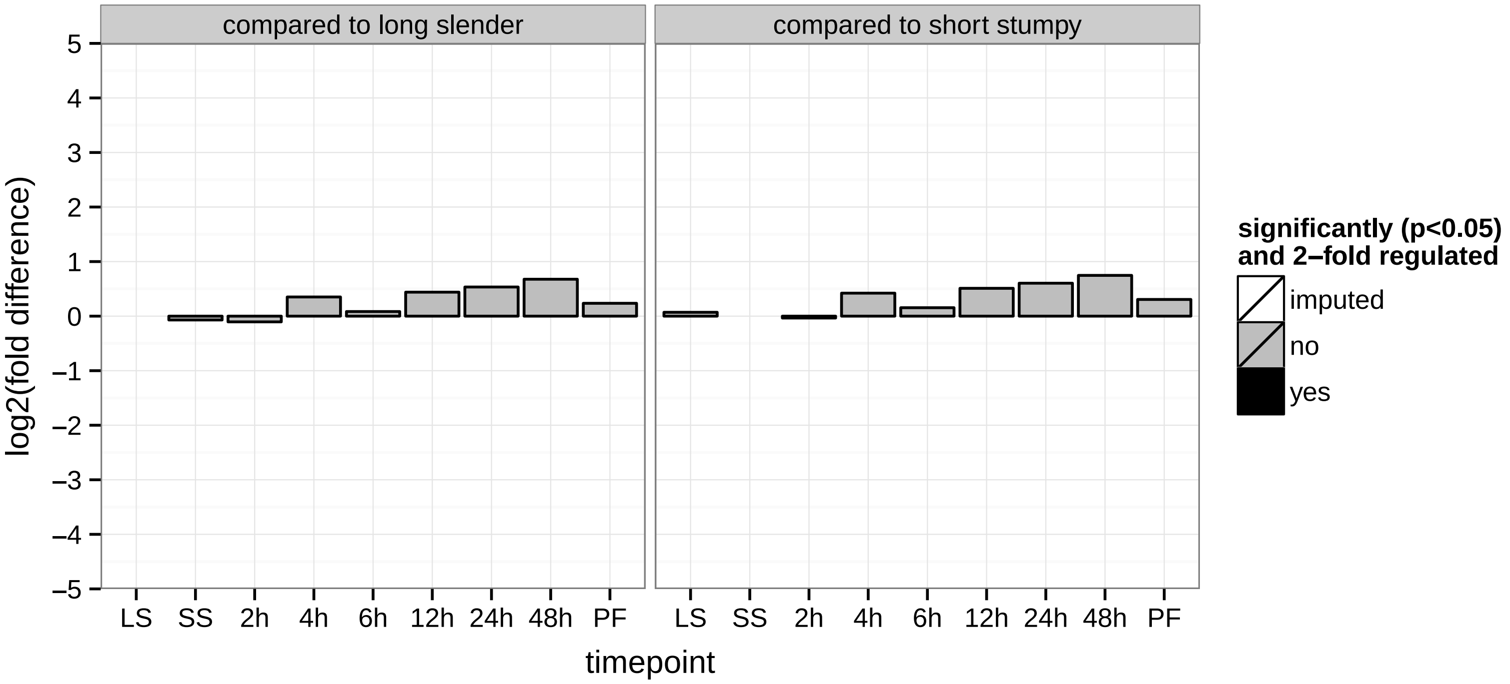
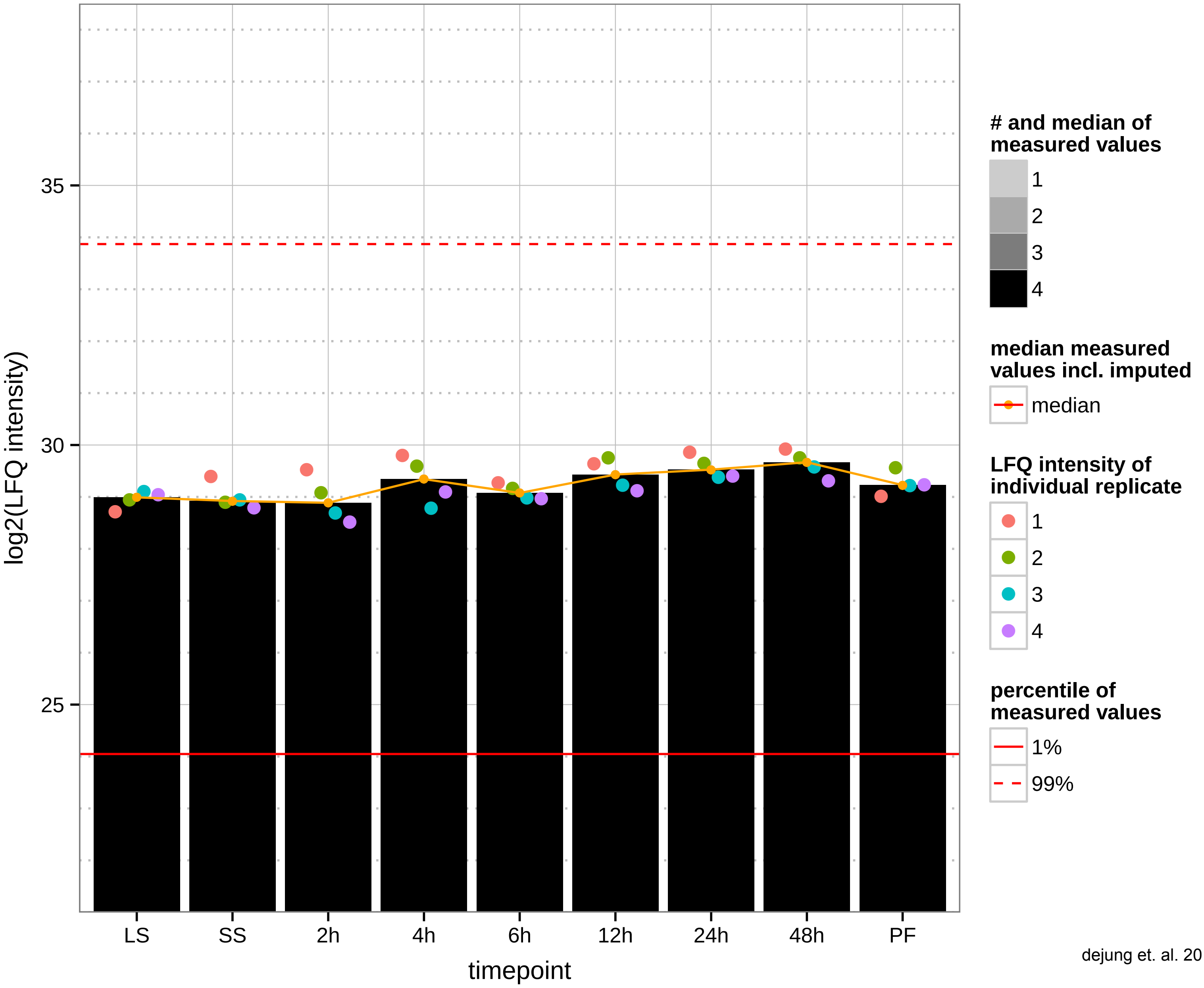
hypothetical protein, conserved
Tb927.7.5340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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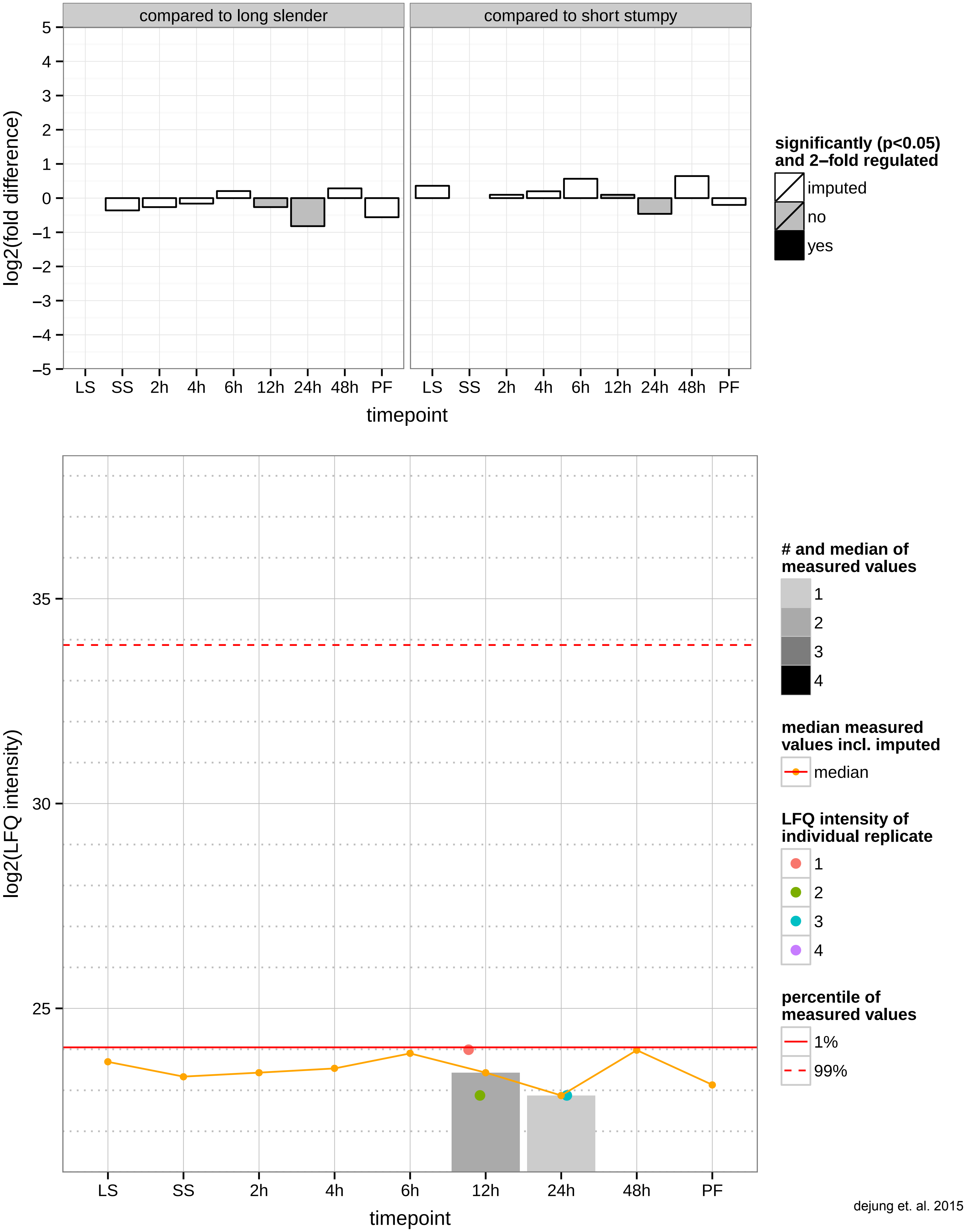
hypothetical protein, conserved
Tb927.7.5440
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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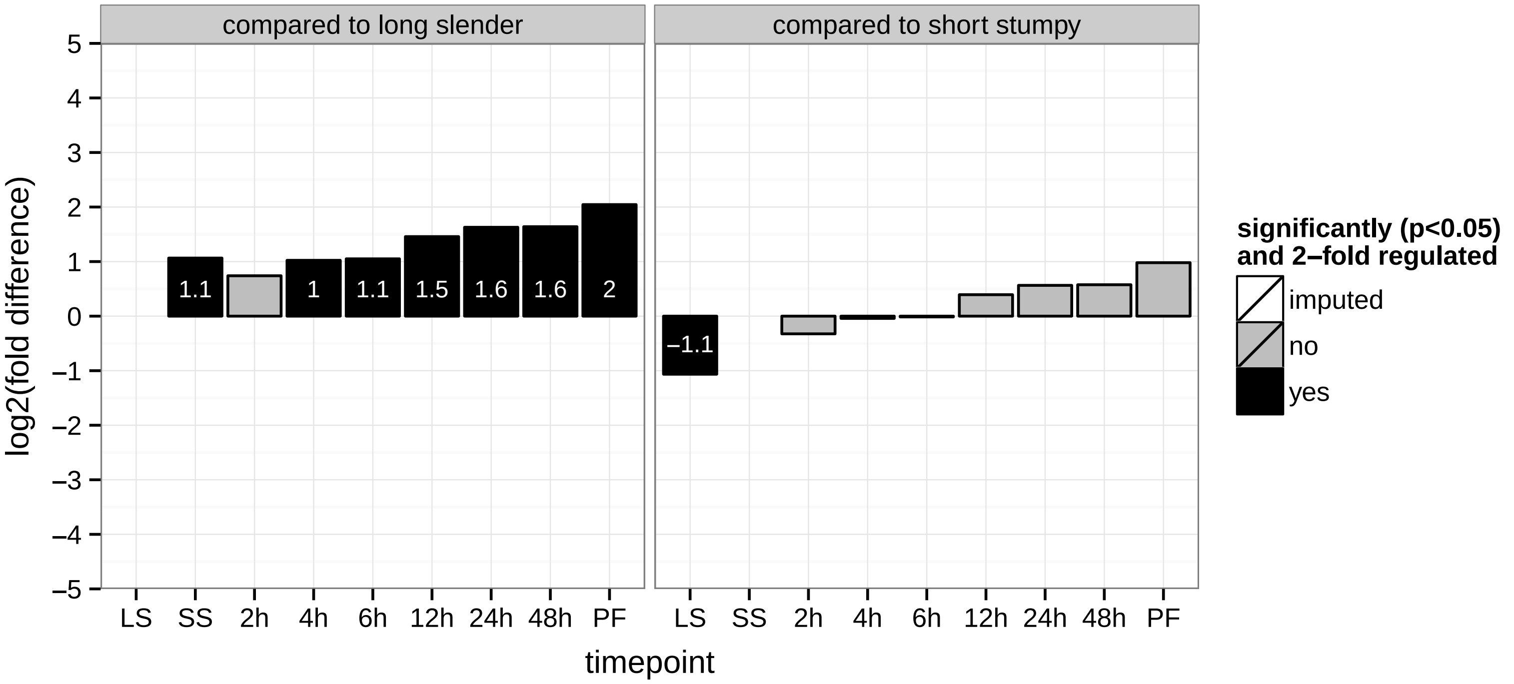
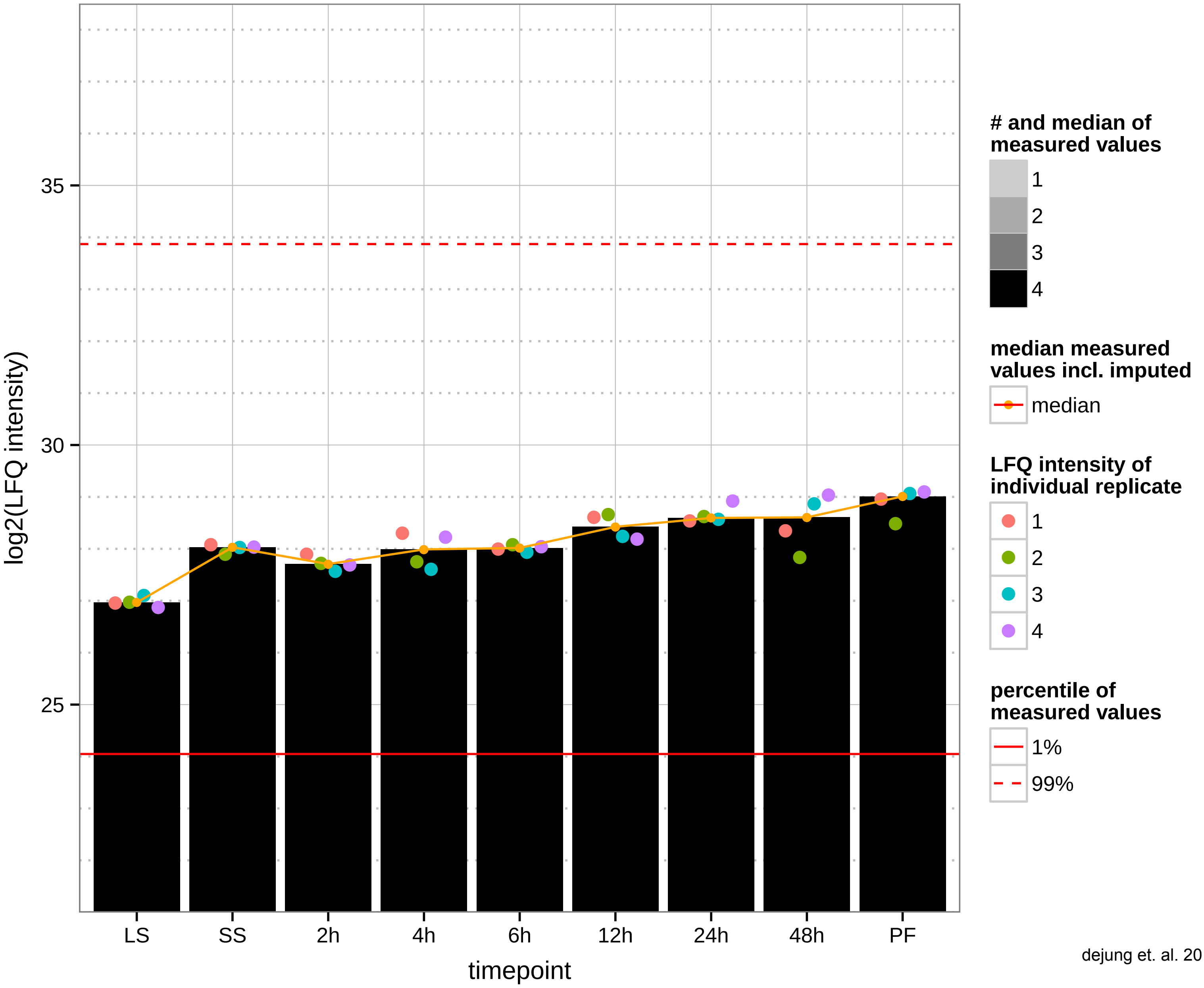
arginine N−methyltransferase, type III (PRMT7)
Tb927.7.5490
AGOF: arginine N−methyltransferase activity
AGOC: cytoplasm
AGOP: histone arginine methylation, peptidyl−arginine methylation
PGOF: protein methyltransferase activity
PGOC: cytoplasm
PGOP: protein methylation





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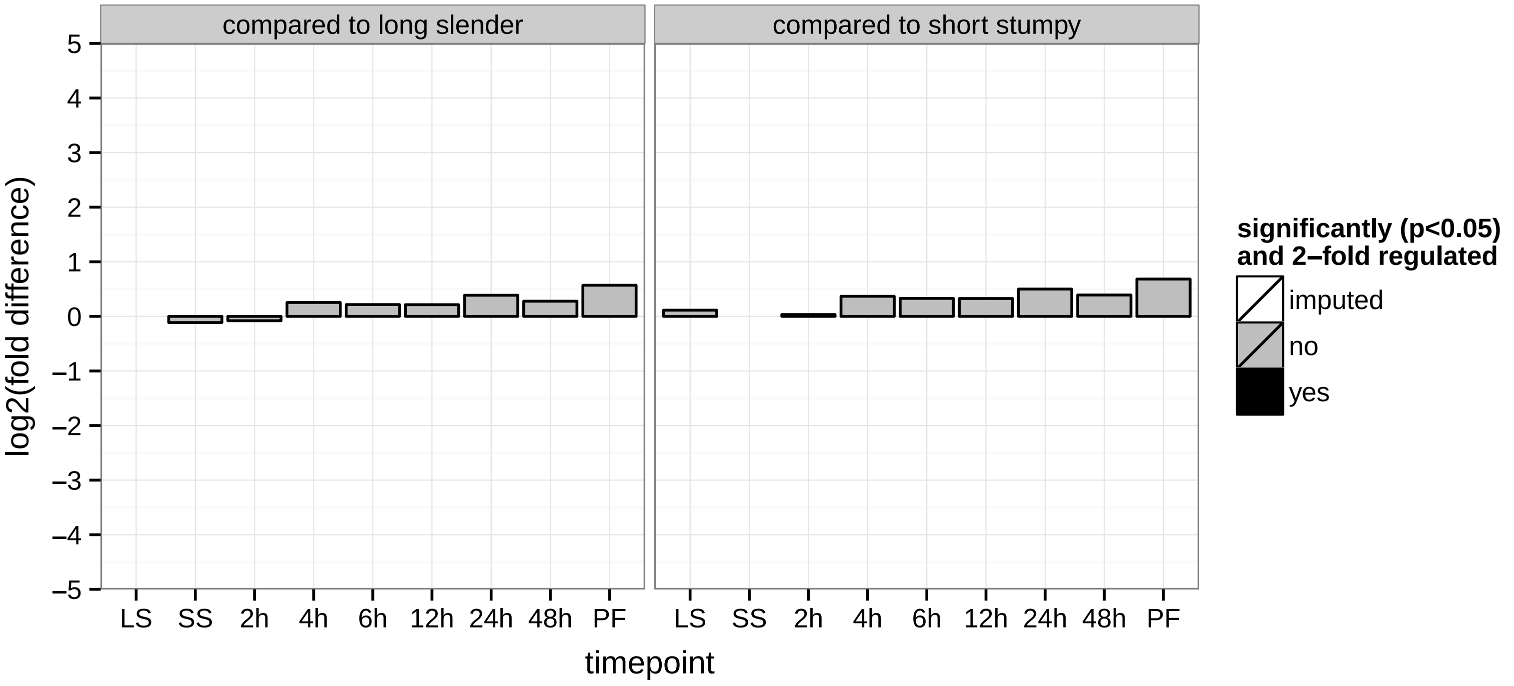
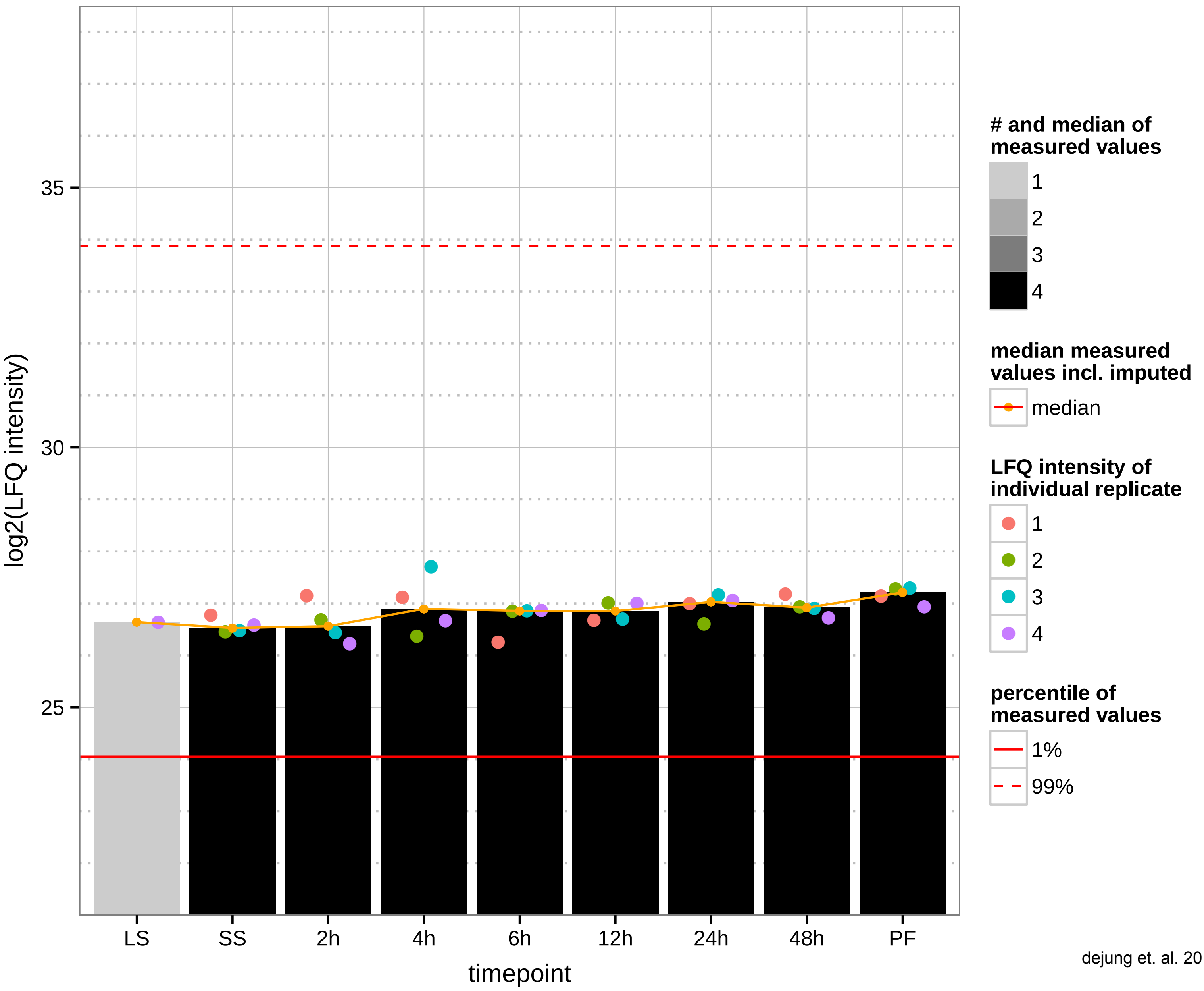
hypothetical protein, conserved
Tb927.7.5530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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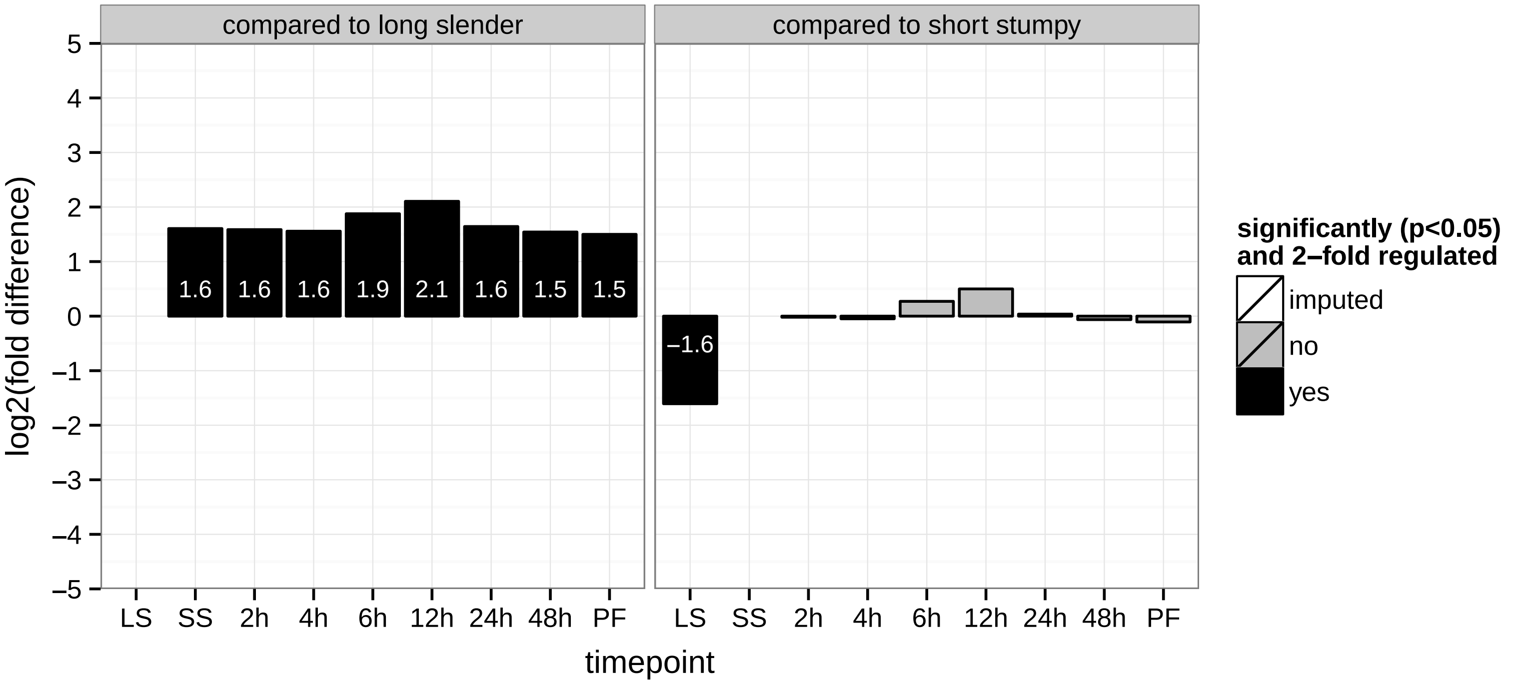
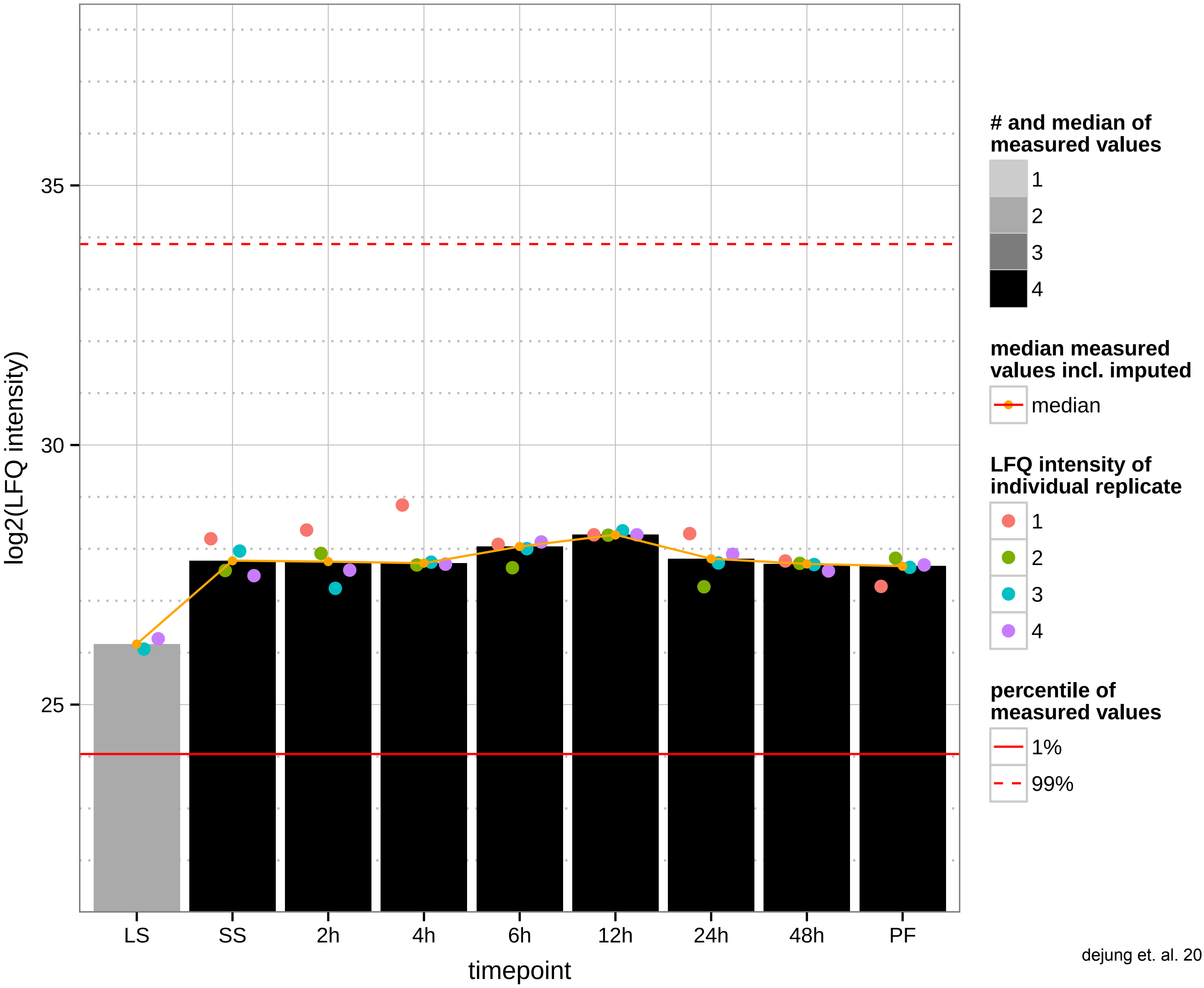
glucosamine–fructose–6–phosphate aminotransferase, putative
Tb927.7.5560
AGOF: carbohydrate binding, glutamine–fructose–6–phosphate transaminase (isomerizing) activity
AGOC: cytoplasm
AGOP: carbohydrate biosynthetic process
PGOF: carbohydrate binding, glutamine–fructose–6–phosphate transaminase (isomerizing) activity
PGOC: cytoplasm
PGOP: carbohydrate biosynthetic process, carbohydrate metabolic process, metabolic process





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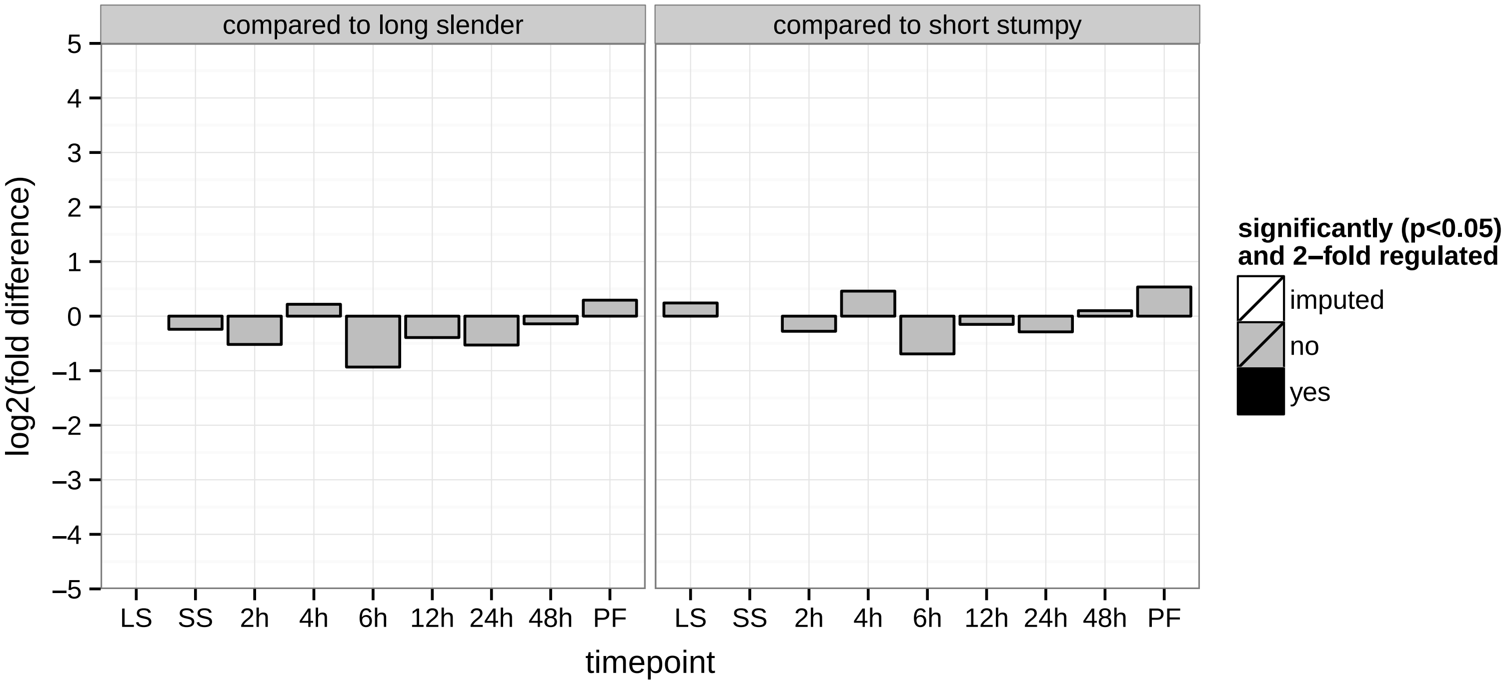
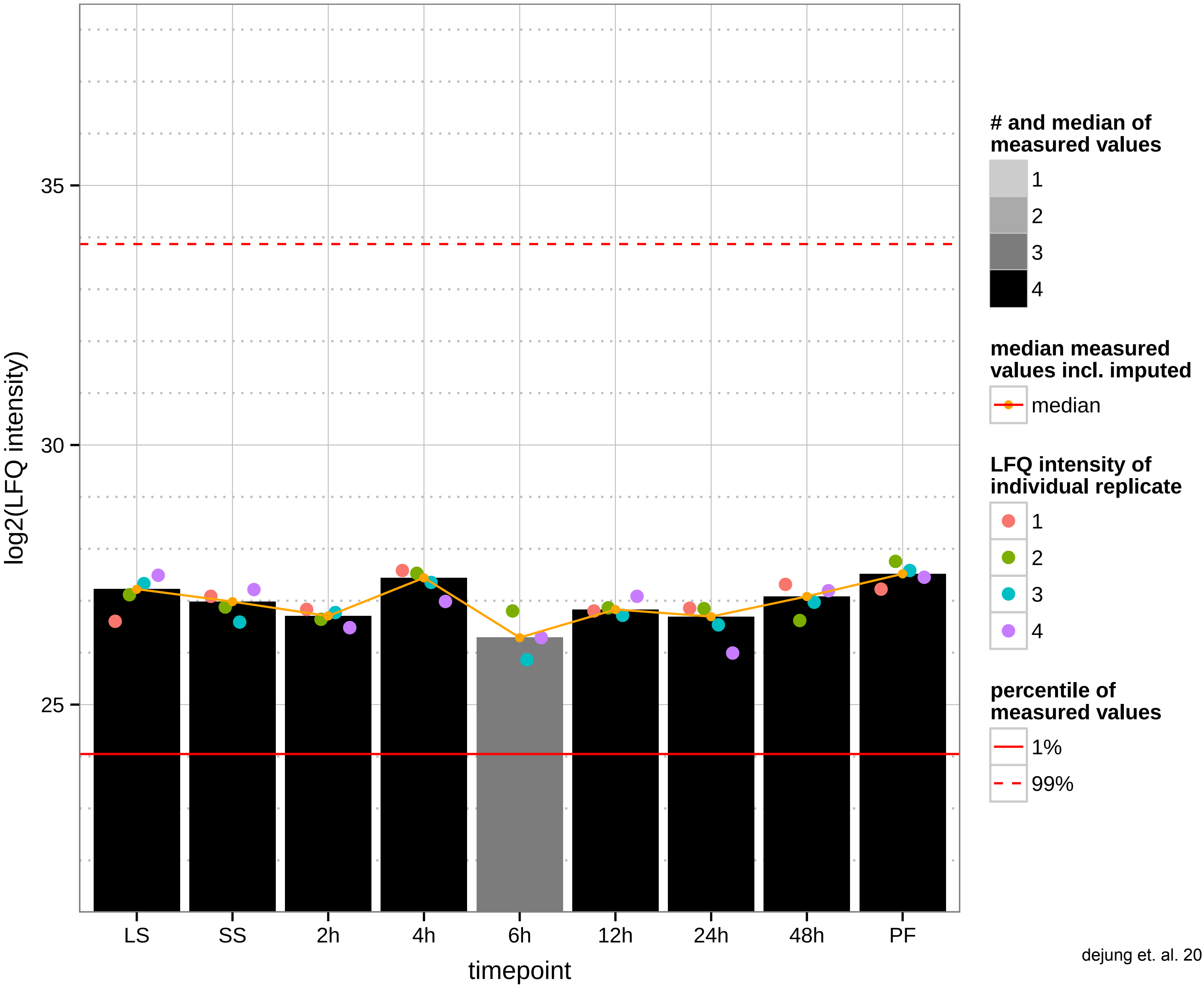
cell cycle associated protein MOB1–A (MOB1A), cell cycle associated protein MOB1–B (MOB1B)
Tb927.7.5570;Tb927.7.5580
AGOF: null
AGOC: cytosol, cytoplasm
AGOP: cell division
PGOF: null
PGOC: null
PGOP: null





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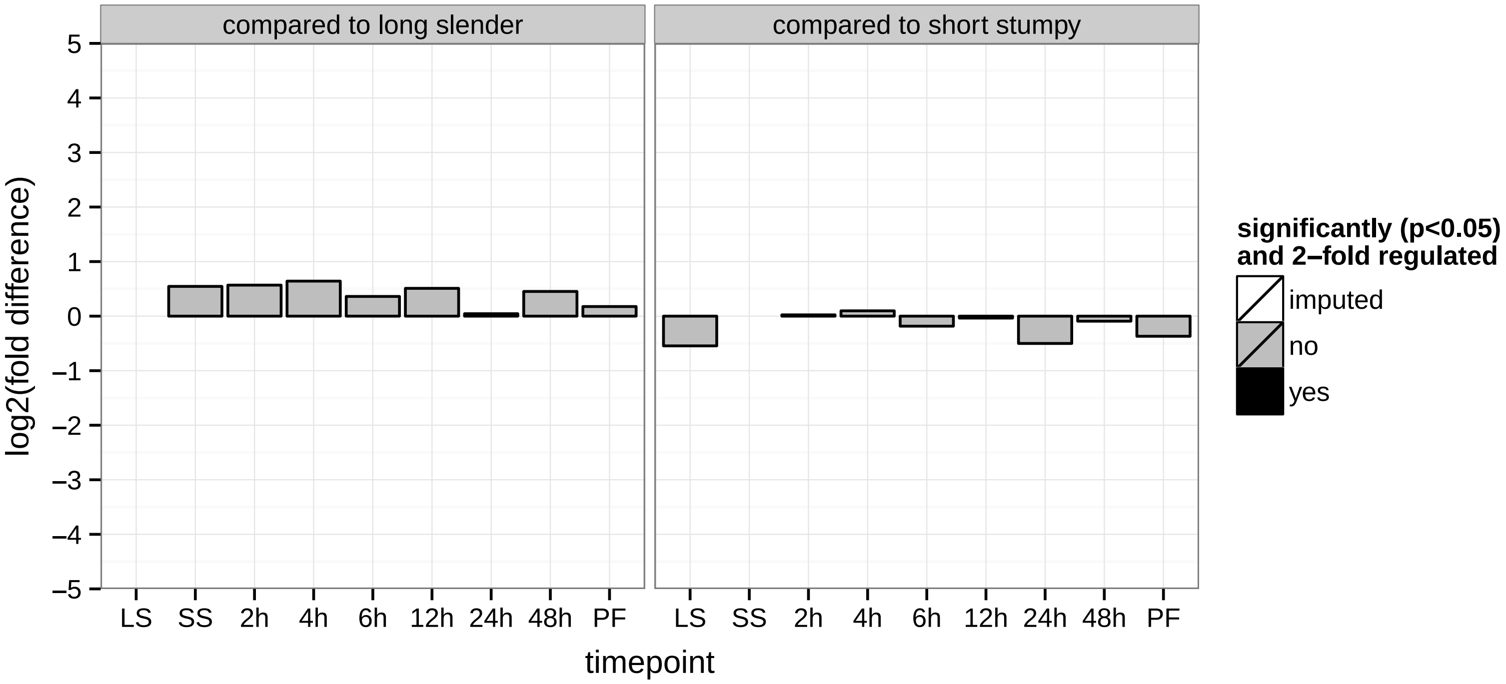
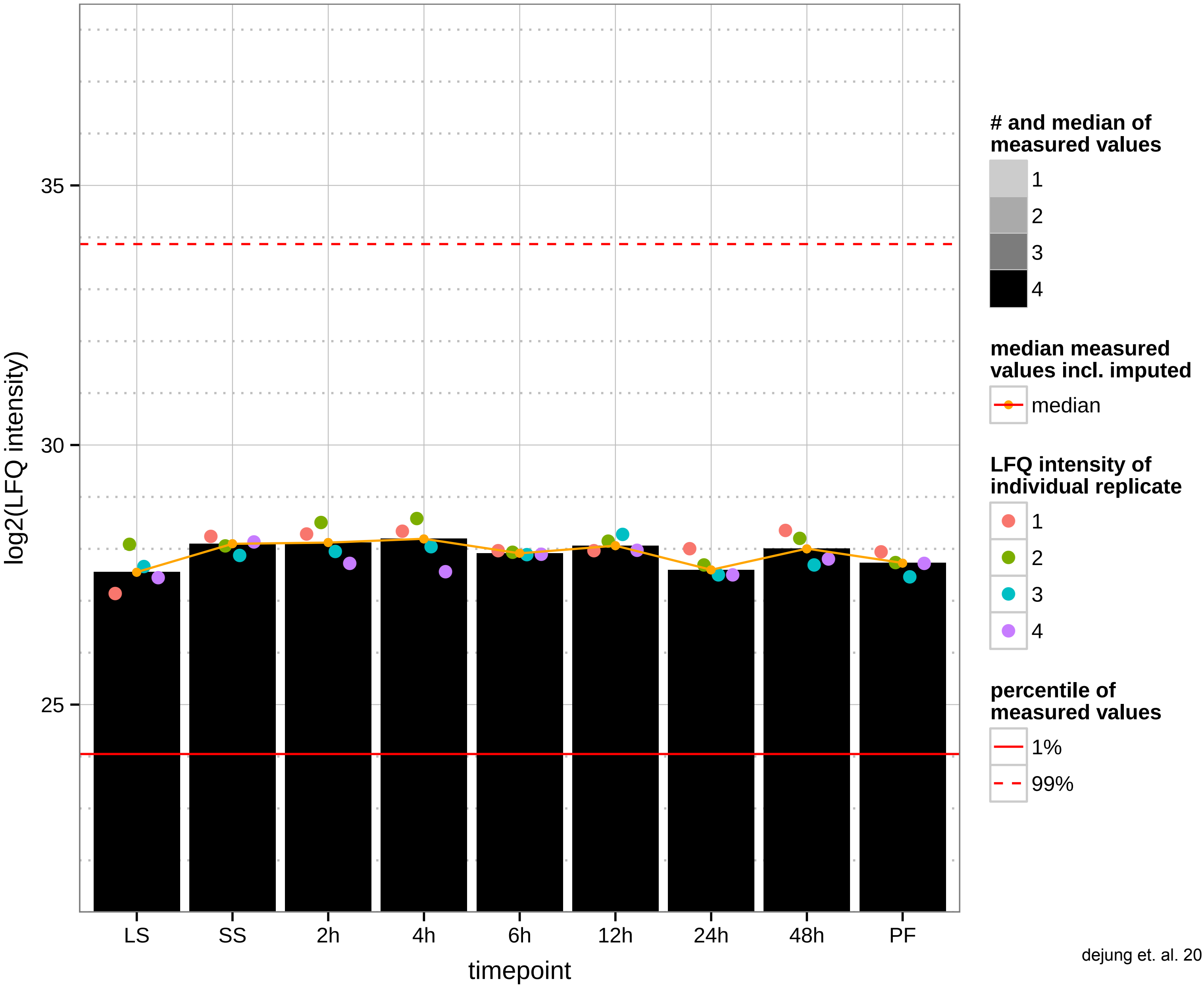
hypothetical protein, conserved
Tb927.7.5660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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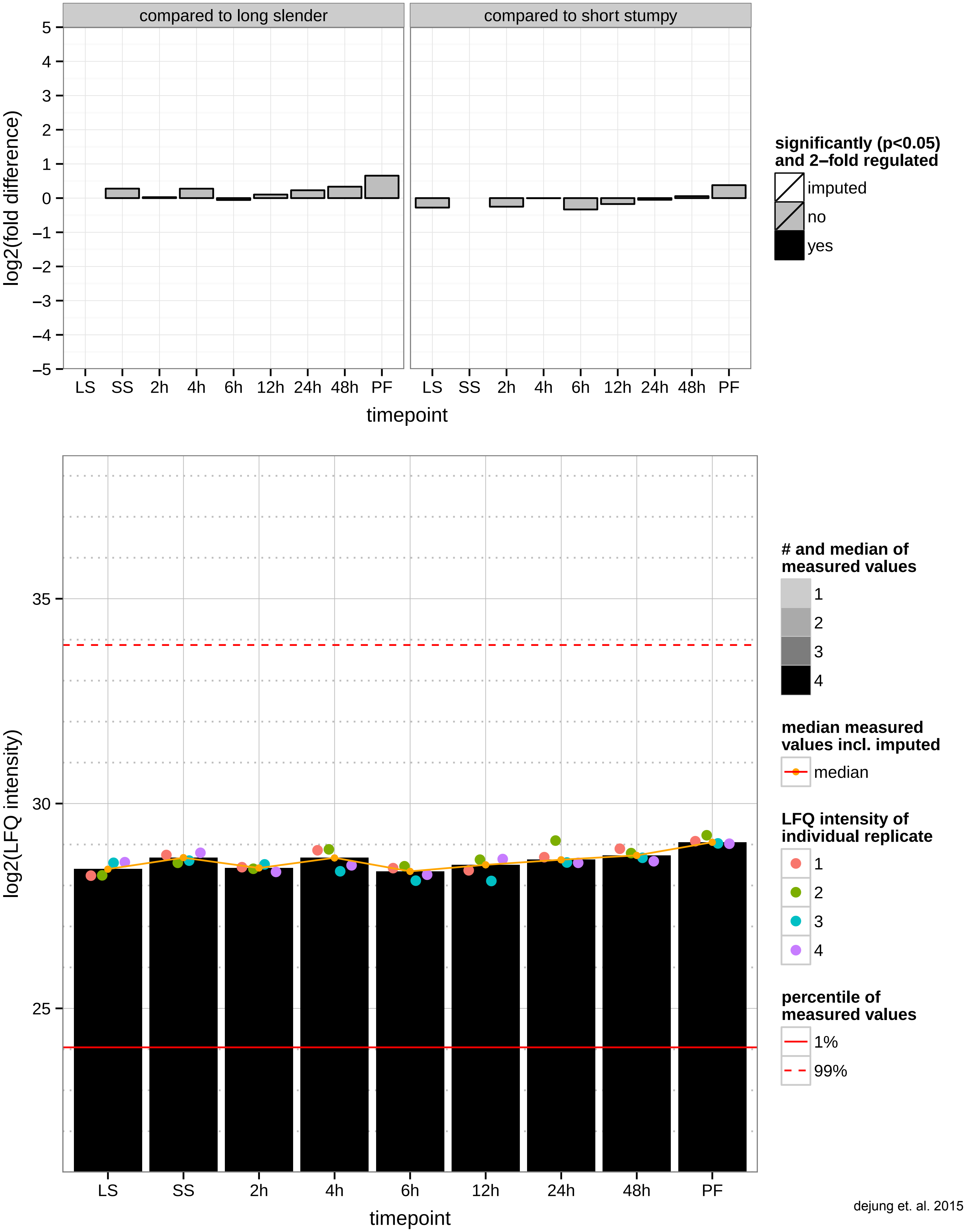
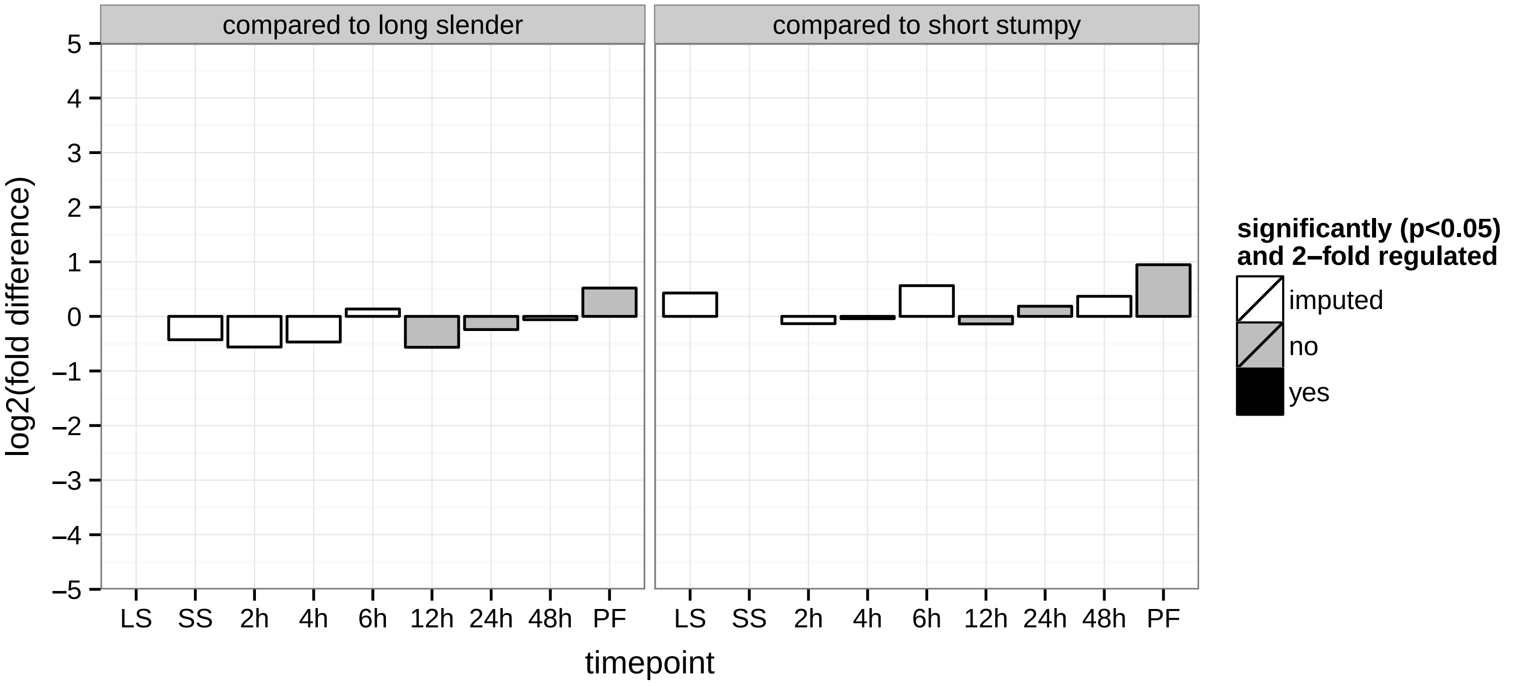
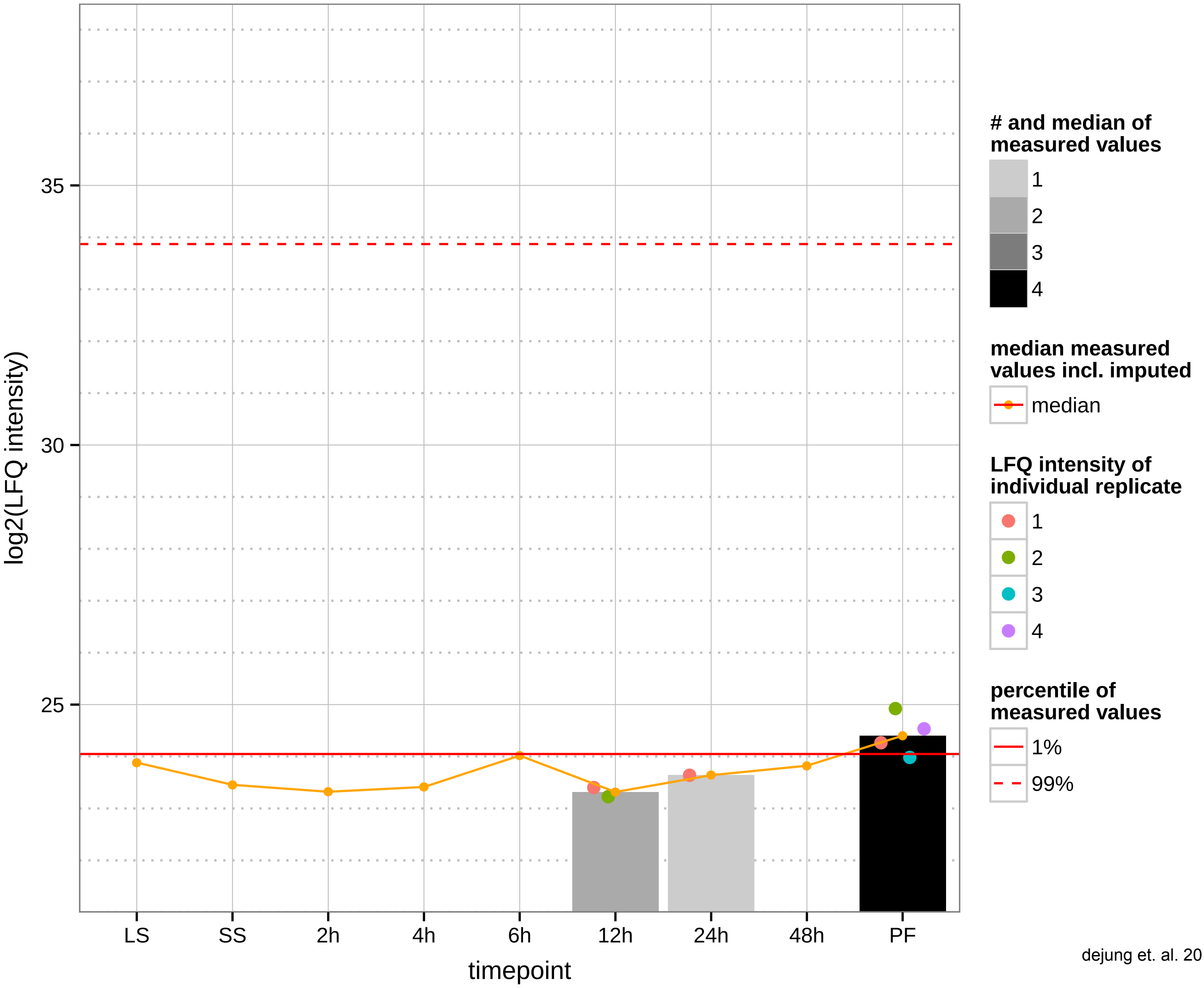
hypothetical protein, conserved
Tb927.7.5700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.5710
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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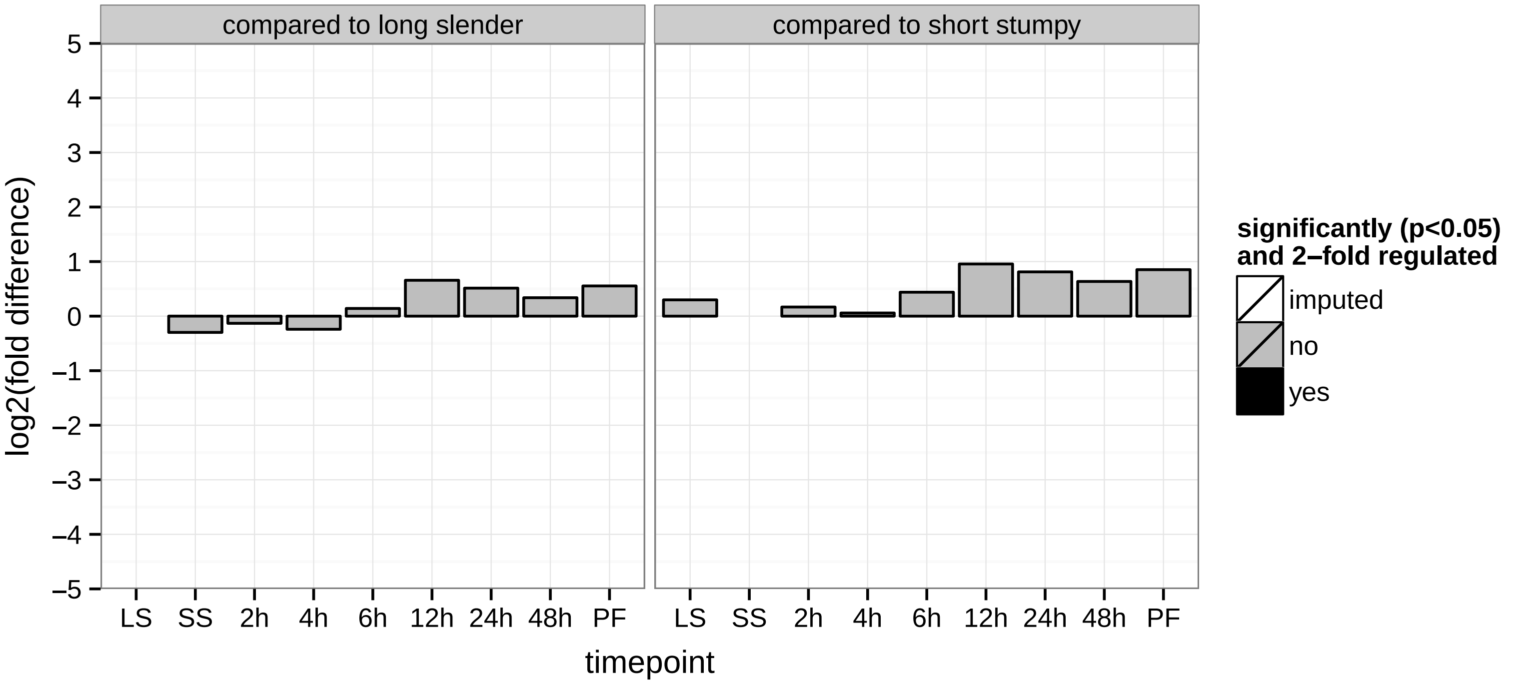
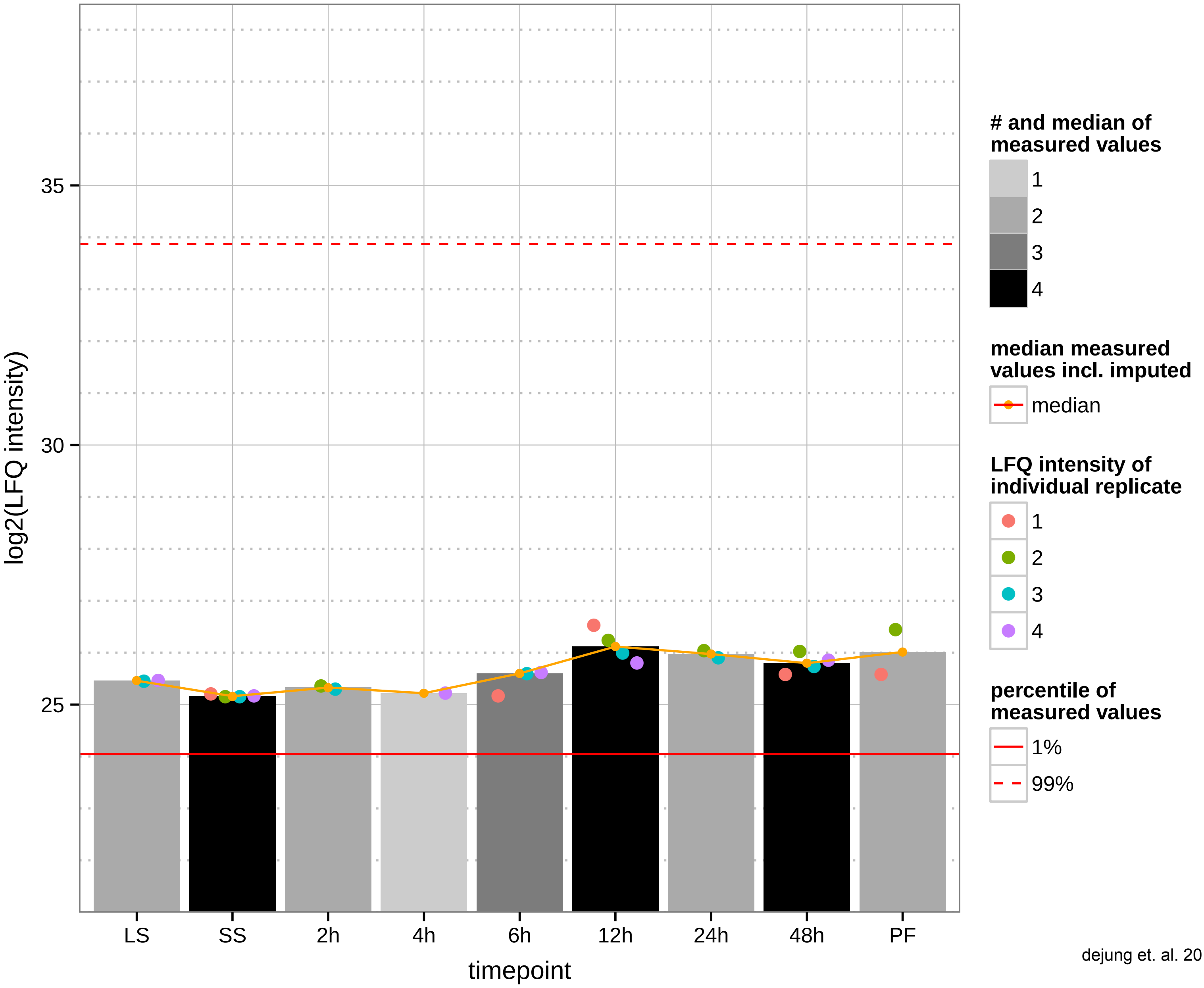
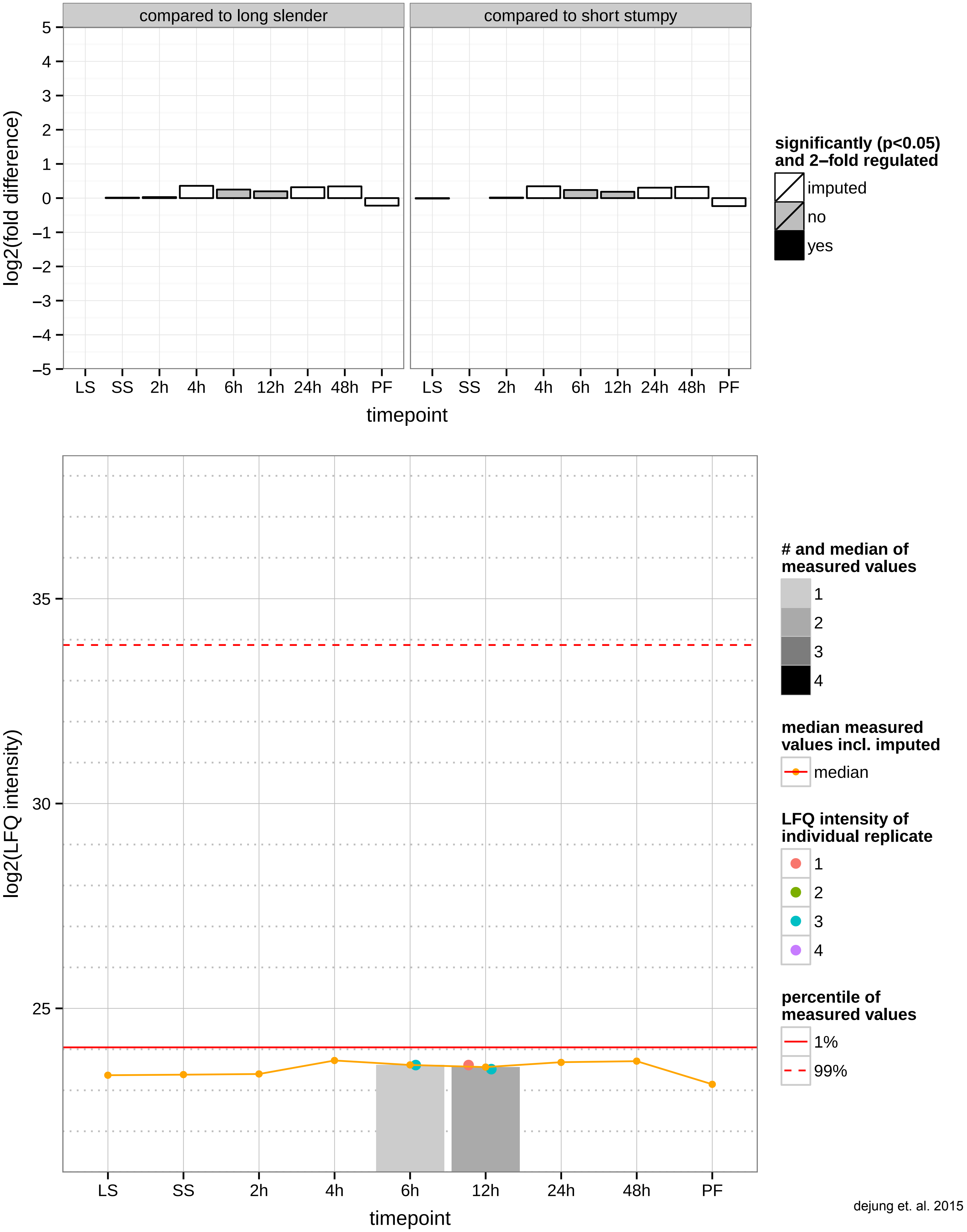
nuclear transport factor 2 protein, putative (NFT2)
Tb927.7.5760
AGOF: null
AGOC: intracellular
AGOP: transport
PGOF: null
PGOC: intracellular
PGOP: transport





dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.5780
AGOF: null
AGOC: null
AGOP: cell redox homeostasis
PGOF: null
PGOC: null
PGOP: cell redox homeostasis



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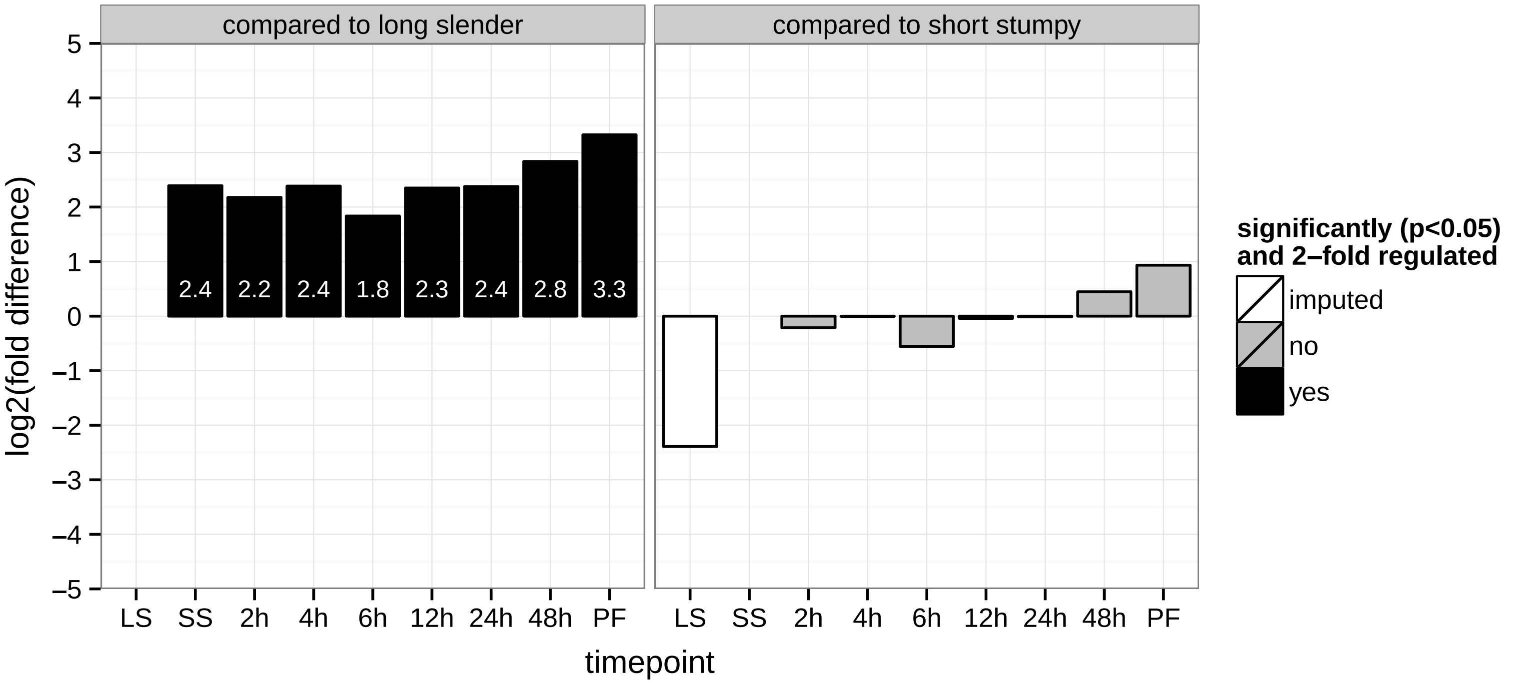
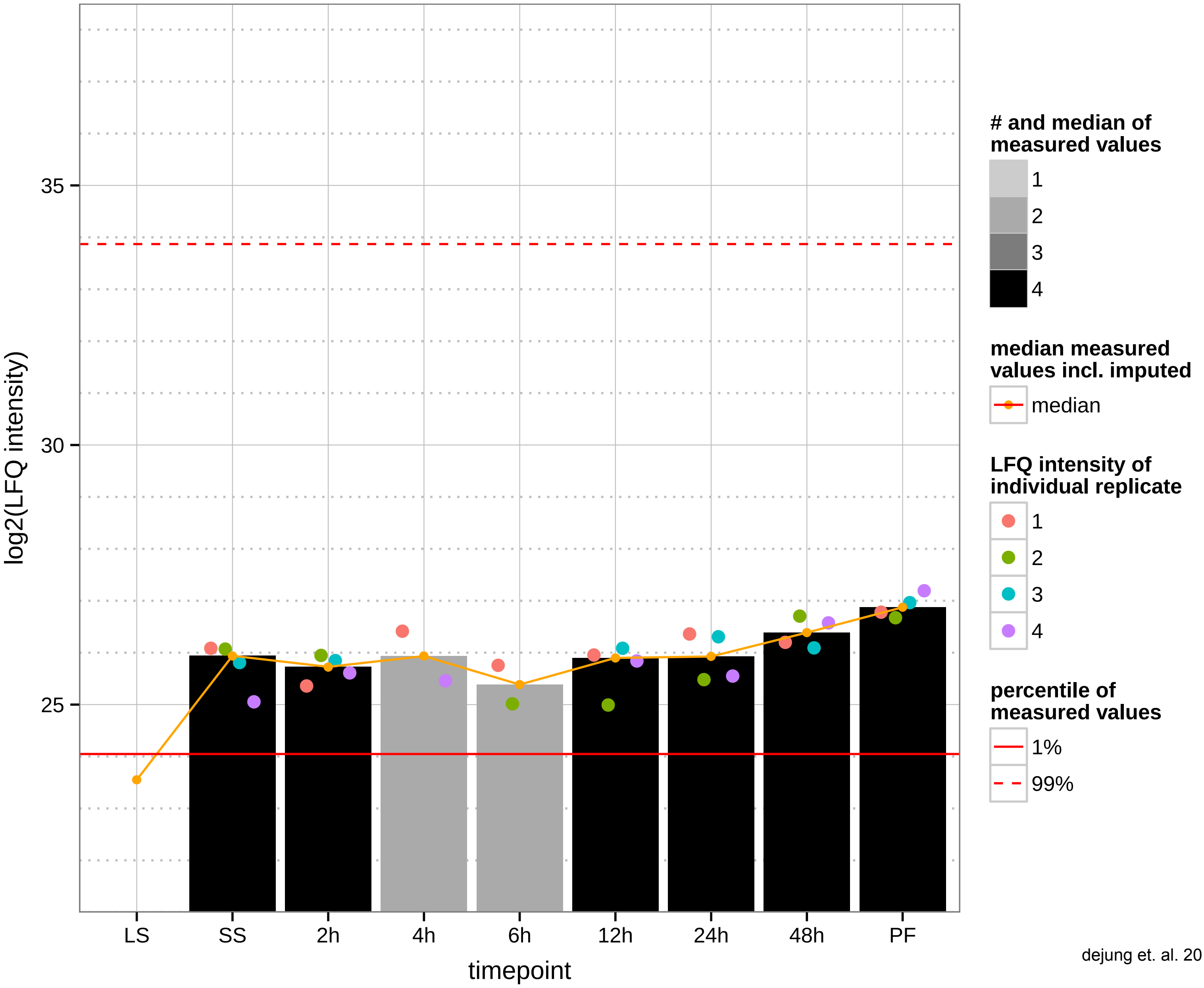
GTP–binding protein, putative
Tb927.7.580
AGOF: GTP binding
AGOC: intracellular
AGOP: null
PGOF: GTP binding
PGOC: null
PGOP: null





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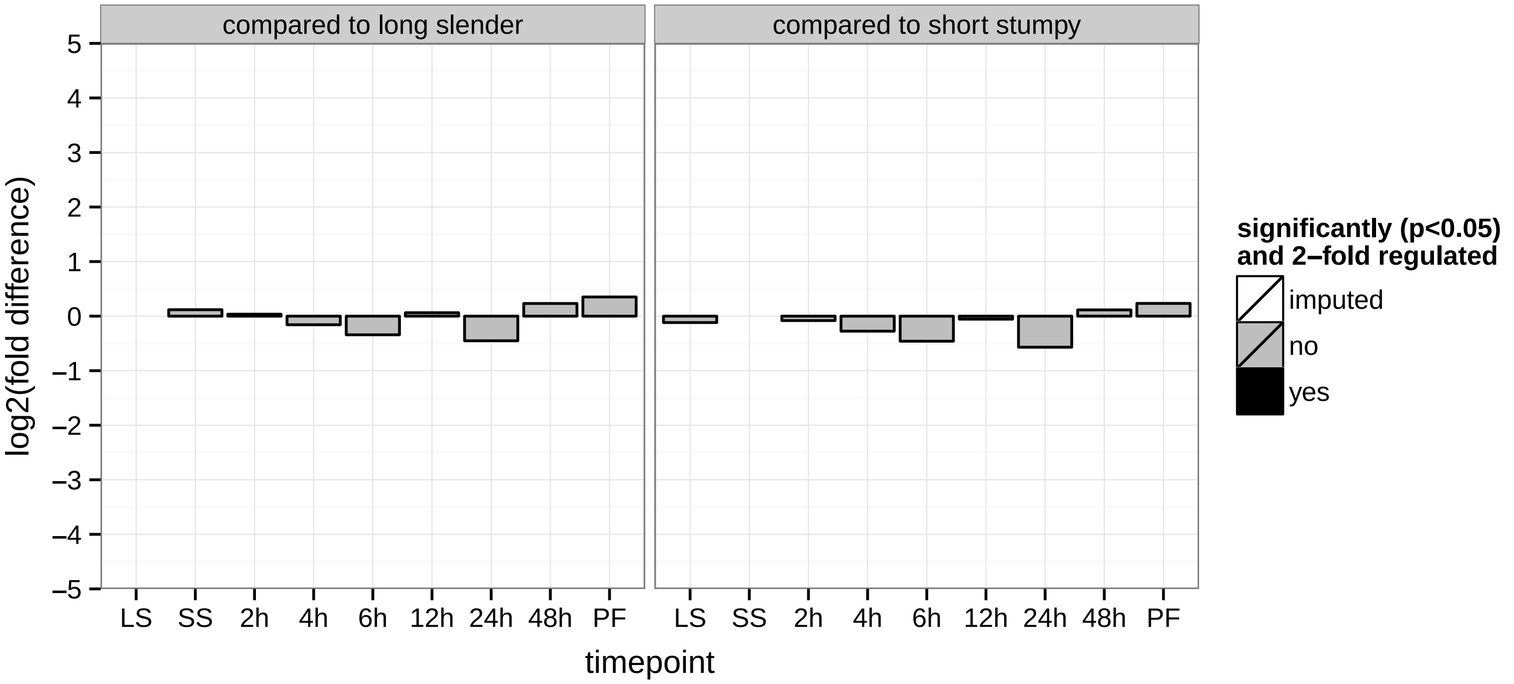
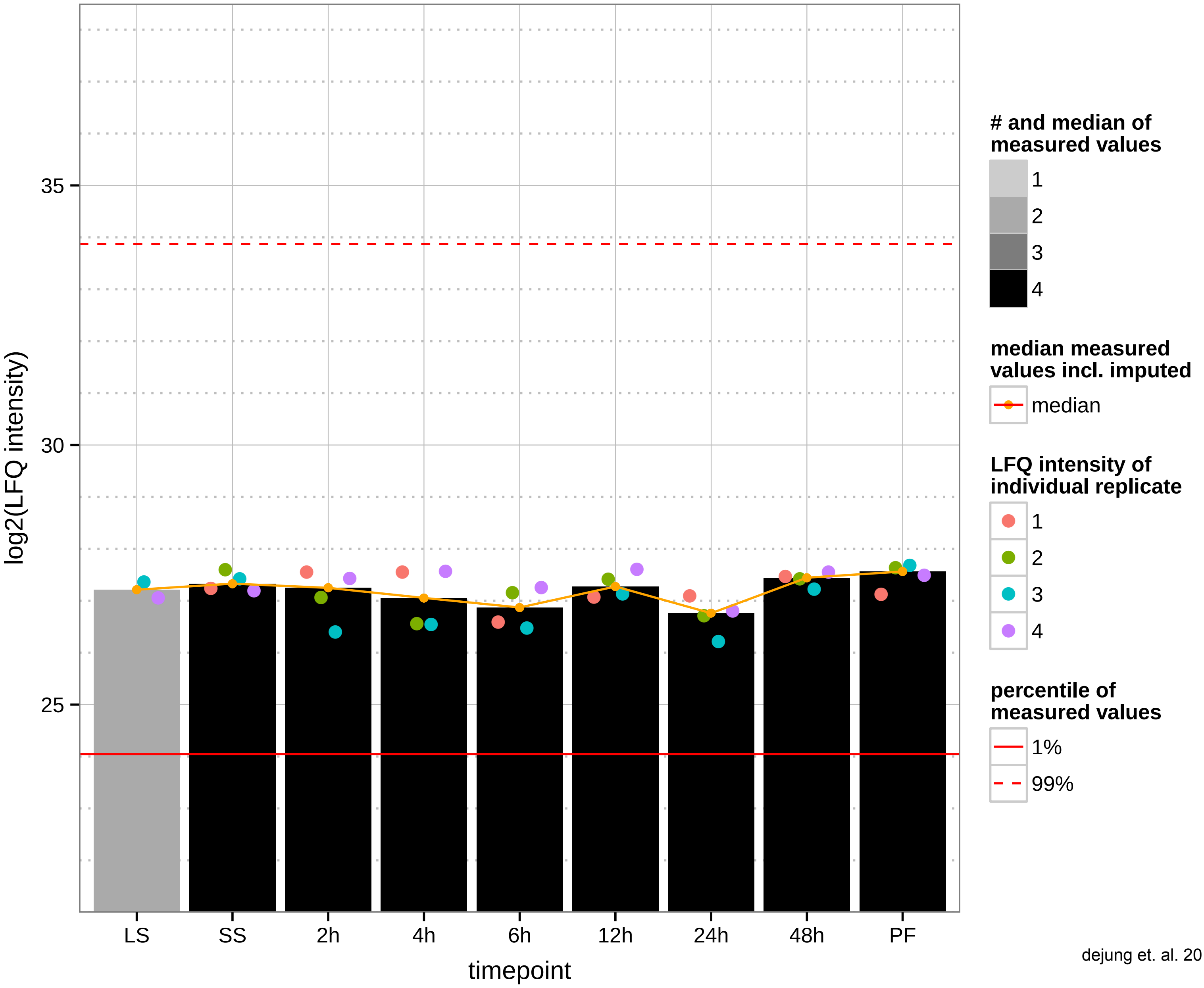
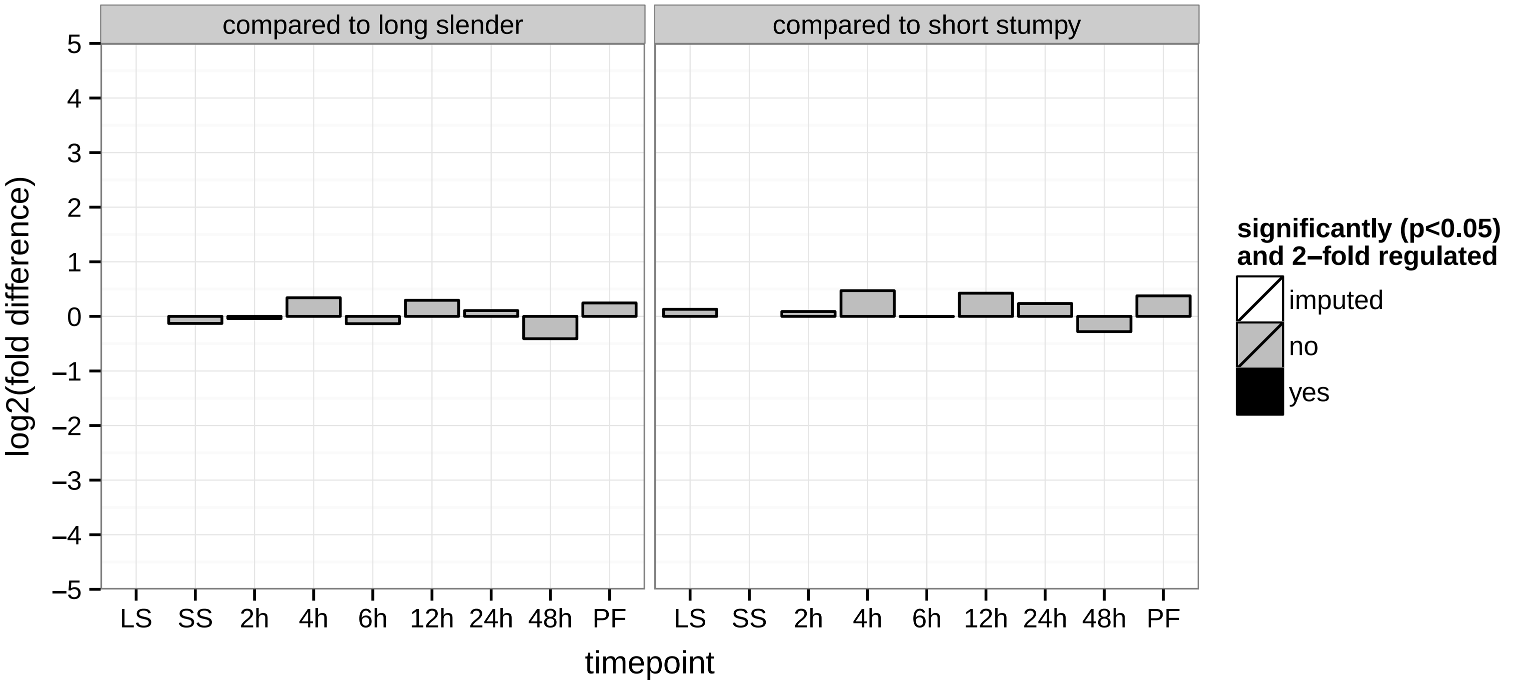
Monooxygenase, putative
Tb927.7.5820
AGOF: monooxygenase activity
AGOC: mitochondrial membrane, mitochondrion
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null

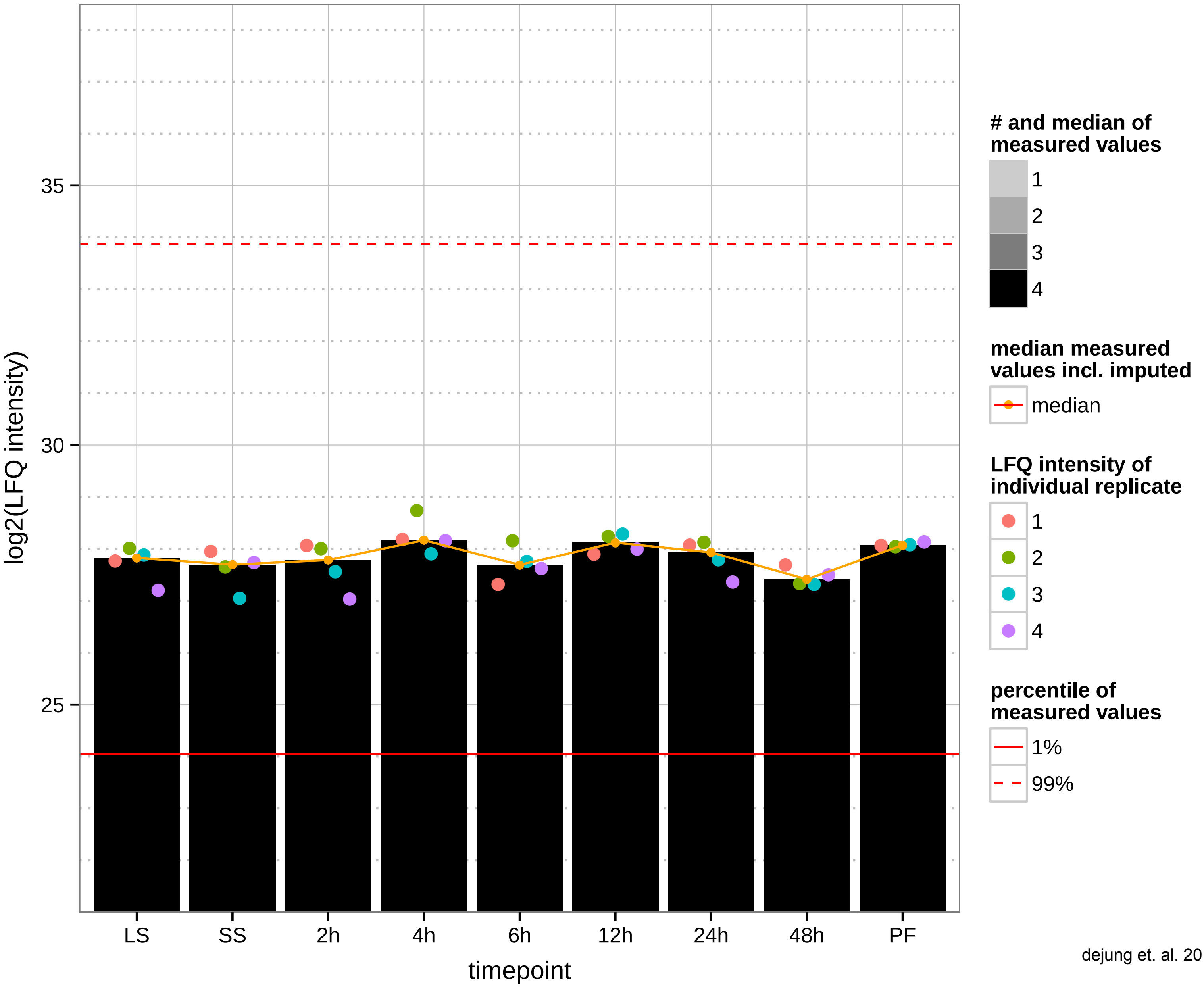




dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.5840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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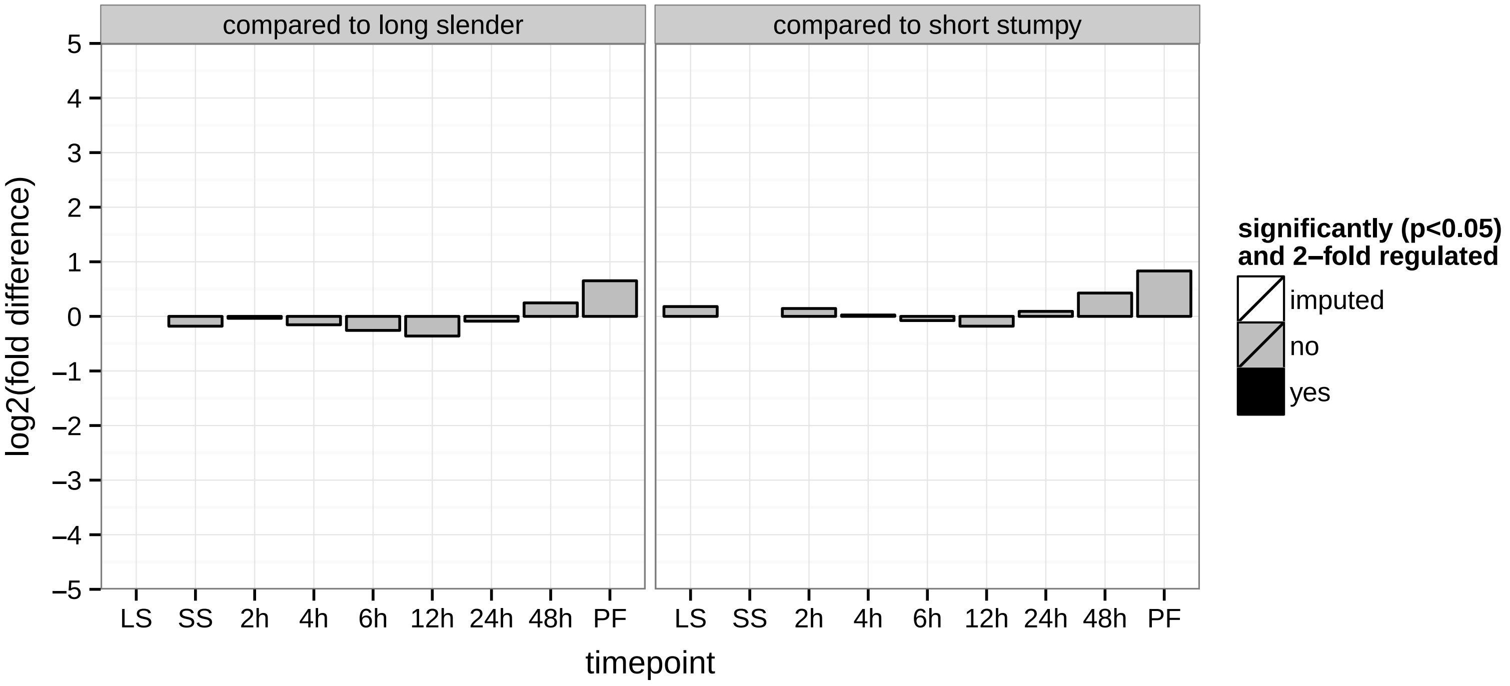
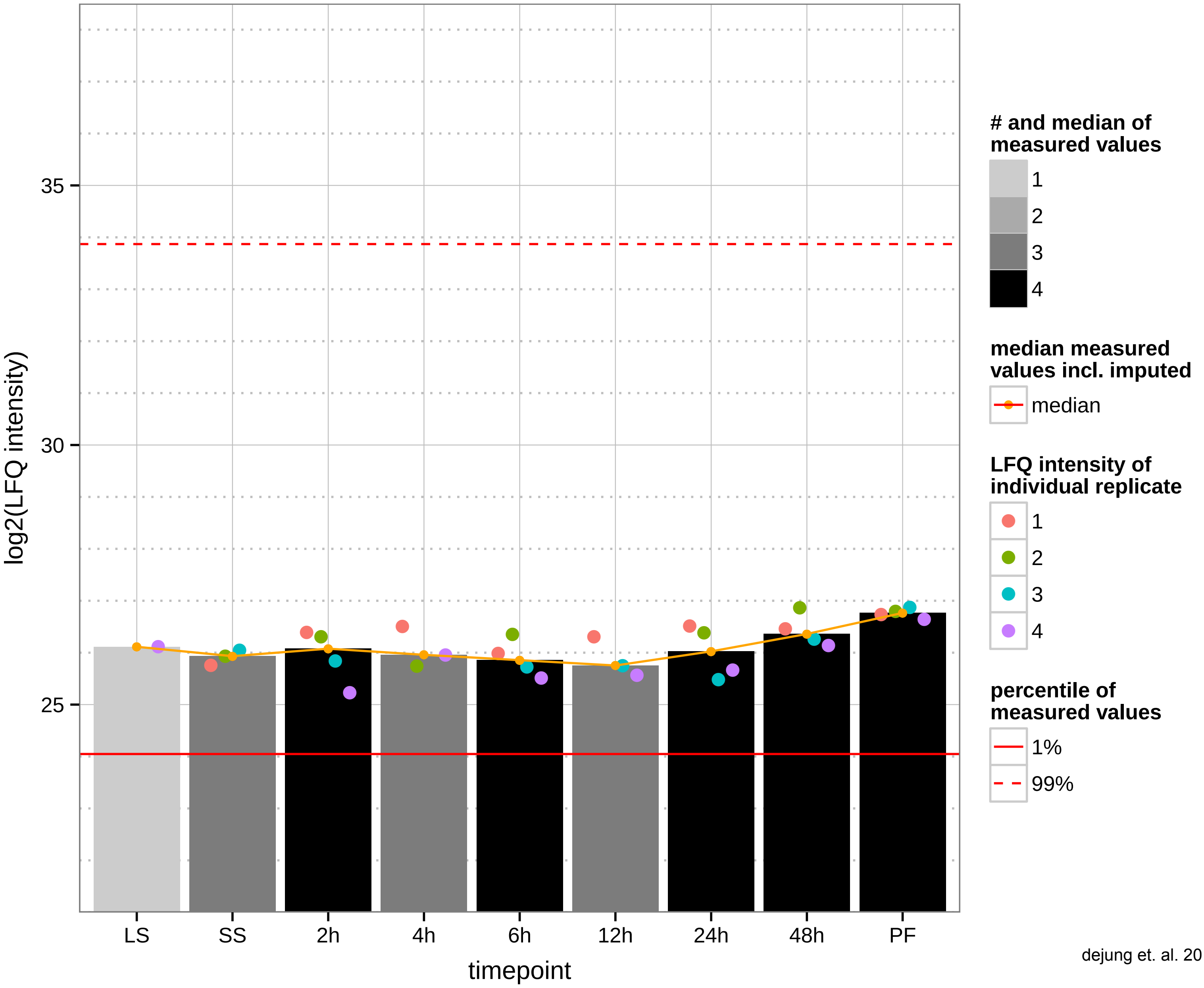
mercaptopyruvate sulfurtransferase, putative (MST)
Tb927.7.5920
AGOF: 3−mercaptopyruvate sulfurtransferase activity
AGOC: cytosol
AGOP: cyanide metabolic process, cysteine biosynthetic process via cystathionine
PGOF: null
PGOC: null
PGOP: null





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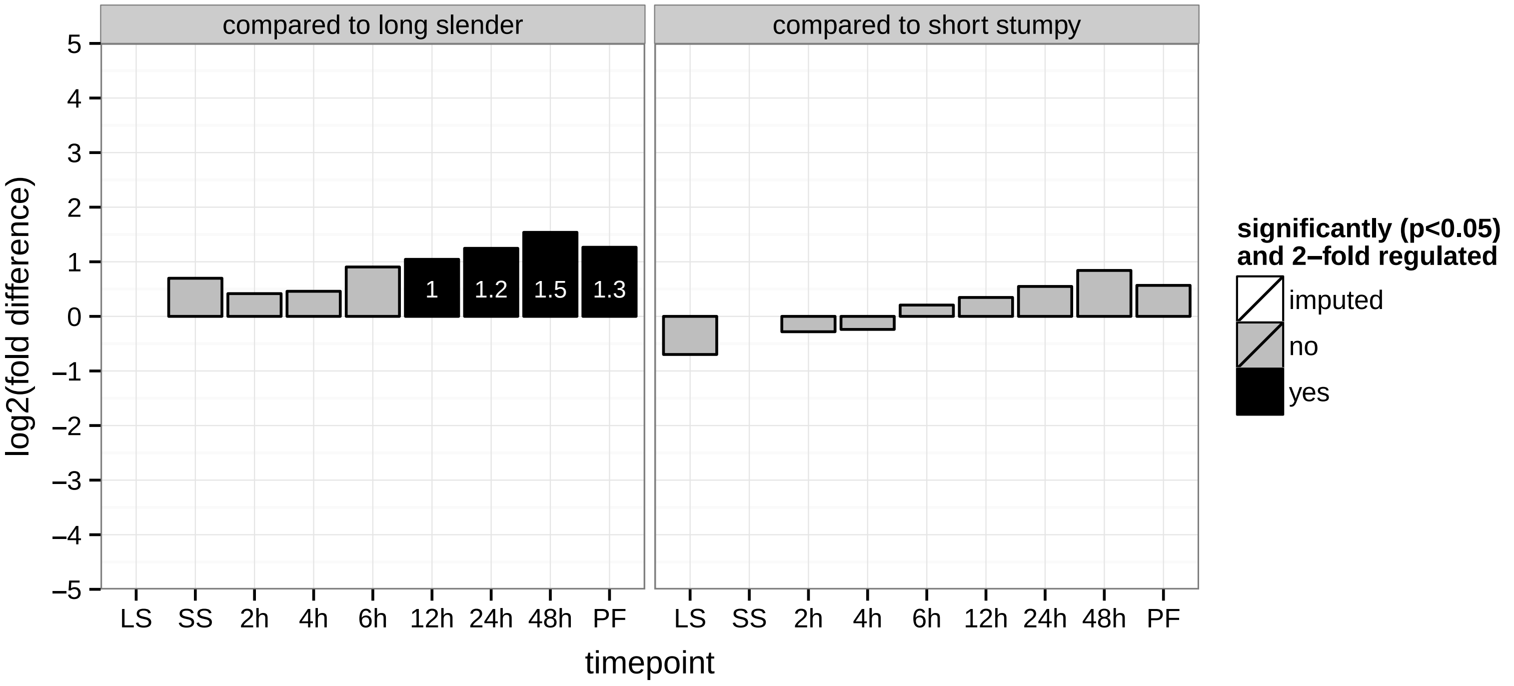
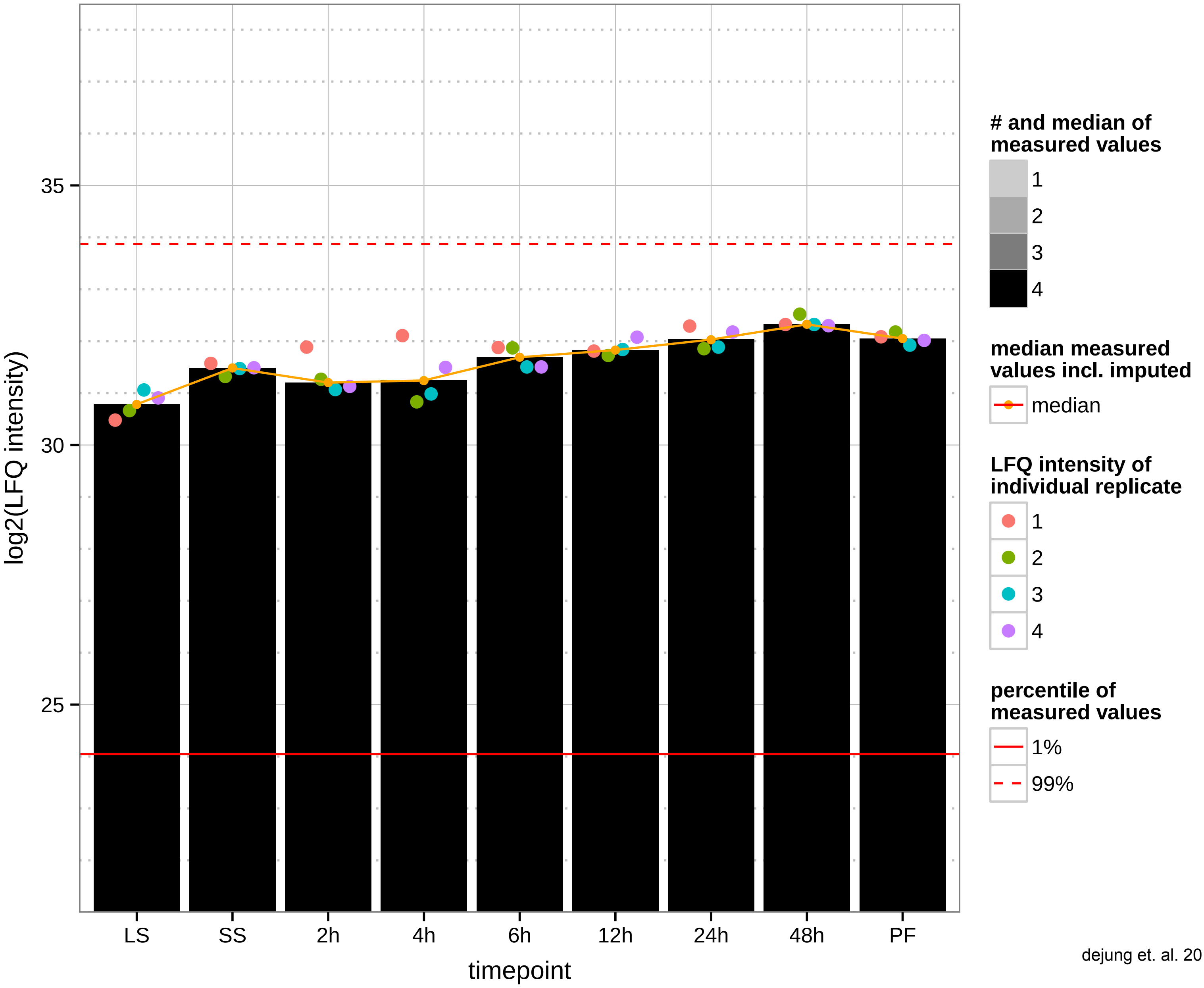
hypothetical protein, conserved
Tb927.7.6090
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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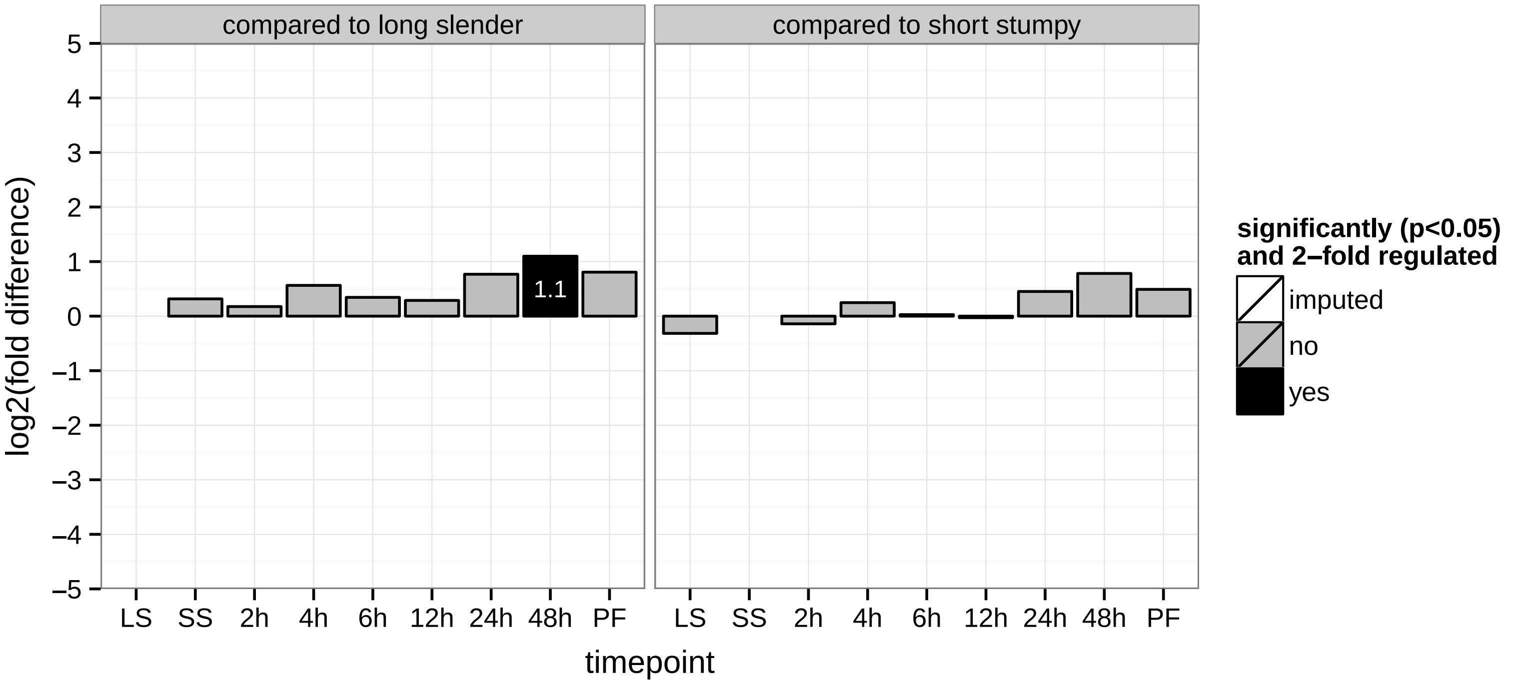
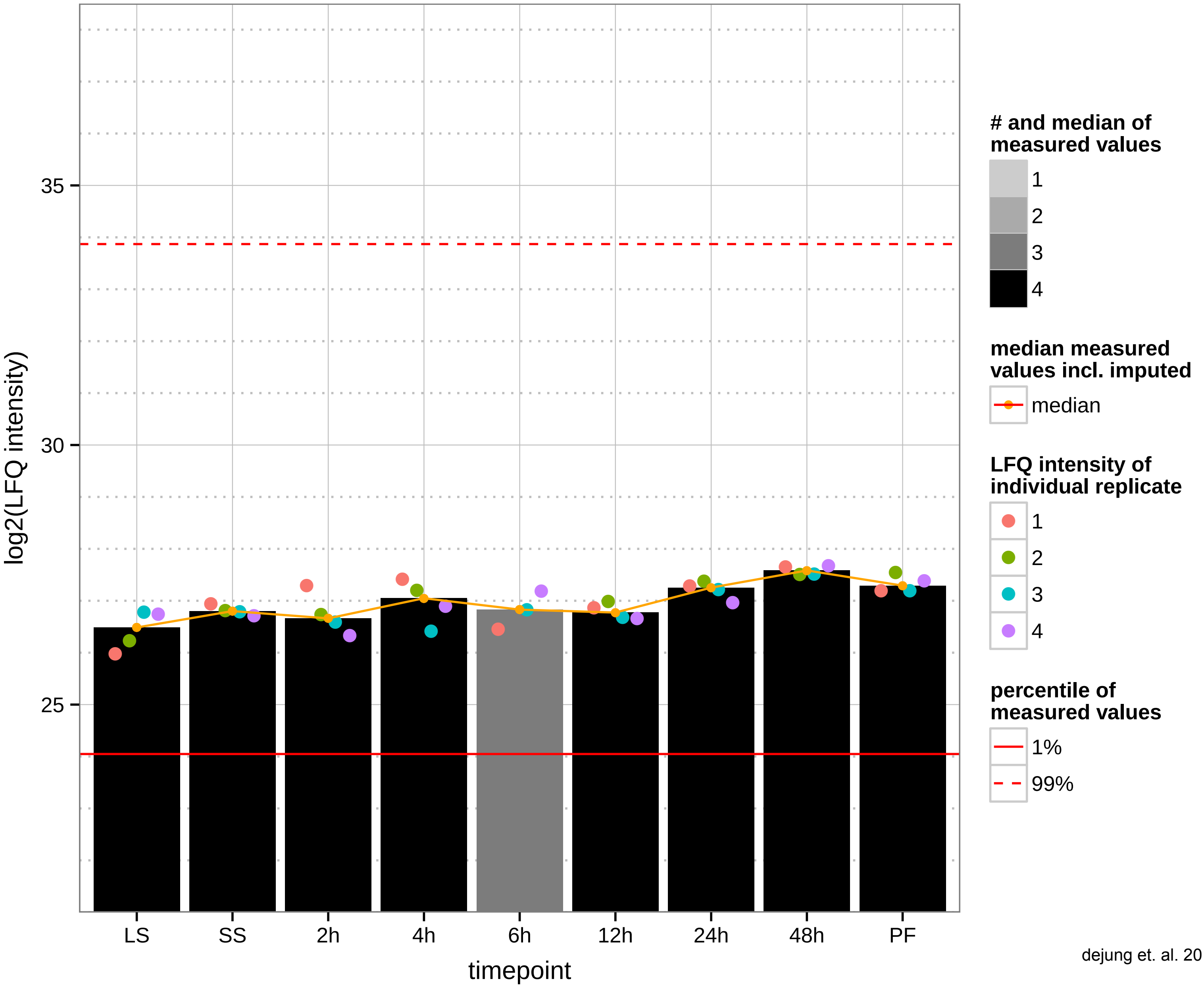
ADP–ribosylation factor, putative (ARF3)
Tb927.7.6230
AGOF: GTP binding
AGOC: intracellular
AGOP: intracellular protein transport, small GTPase mediated signal transduction
PGOF: GTP binding
PGOC: intracellular
PGOP: intracellular protein transport, small GTPase mediated signal transduction





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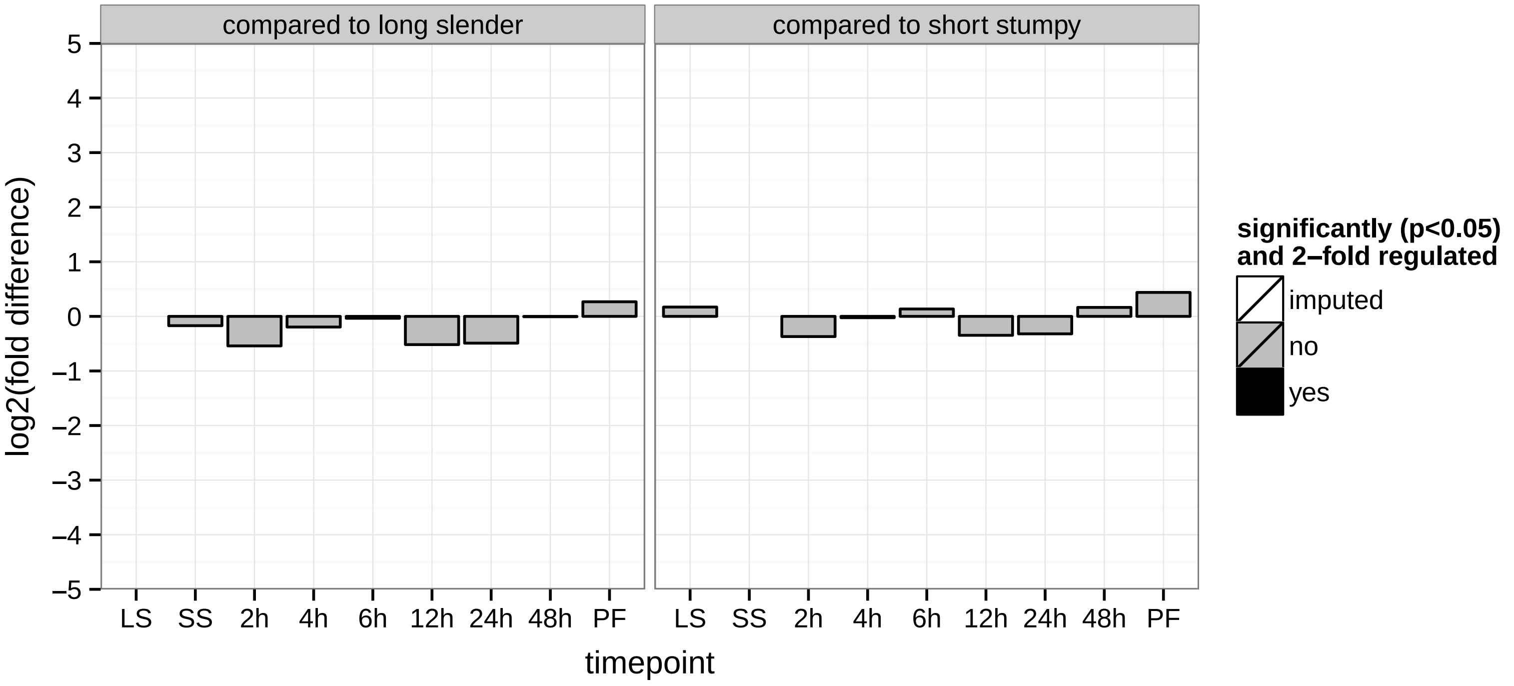
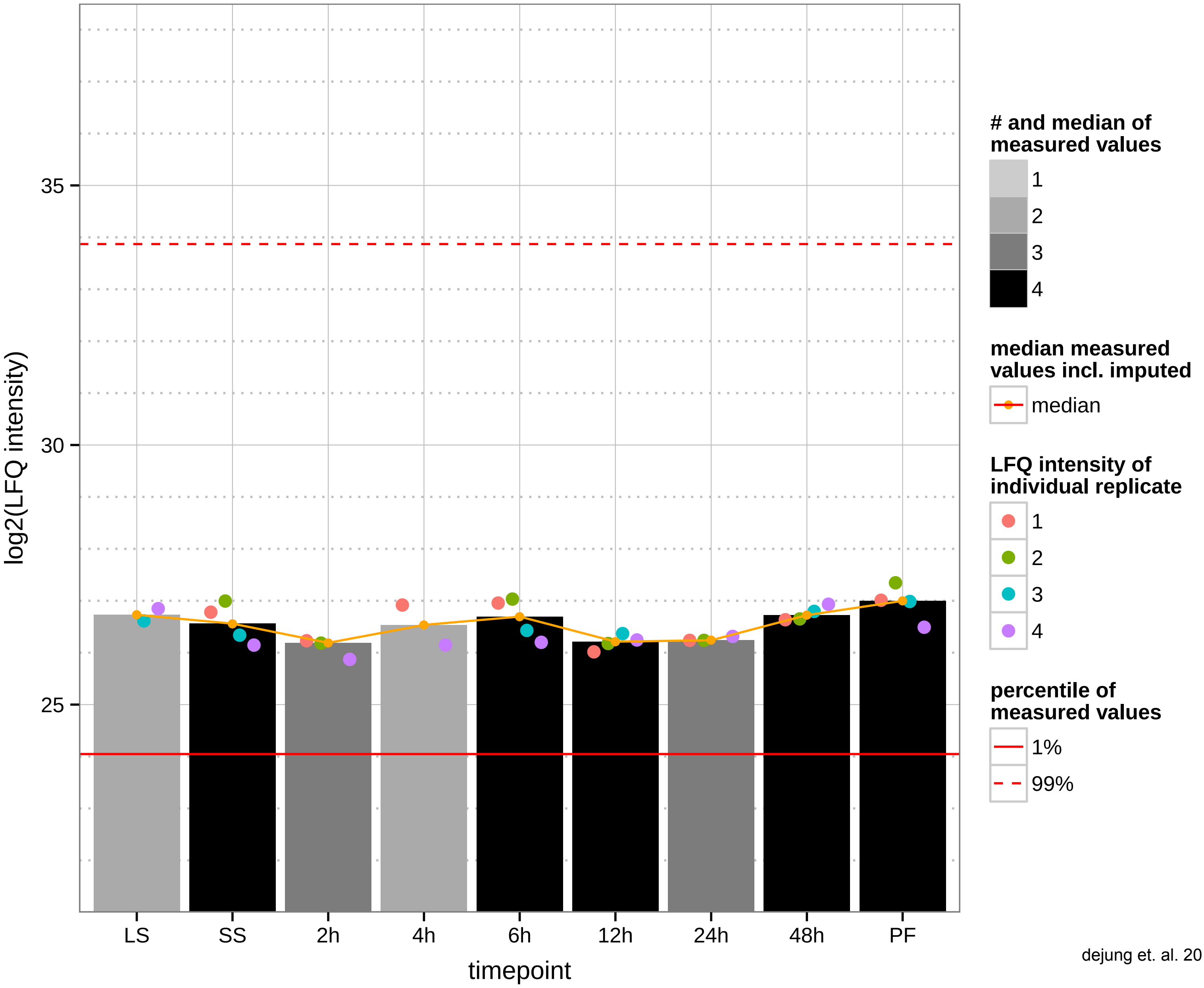
hypothetical protein, conserved
Tb927.7.6280
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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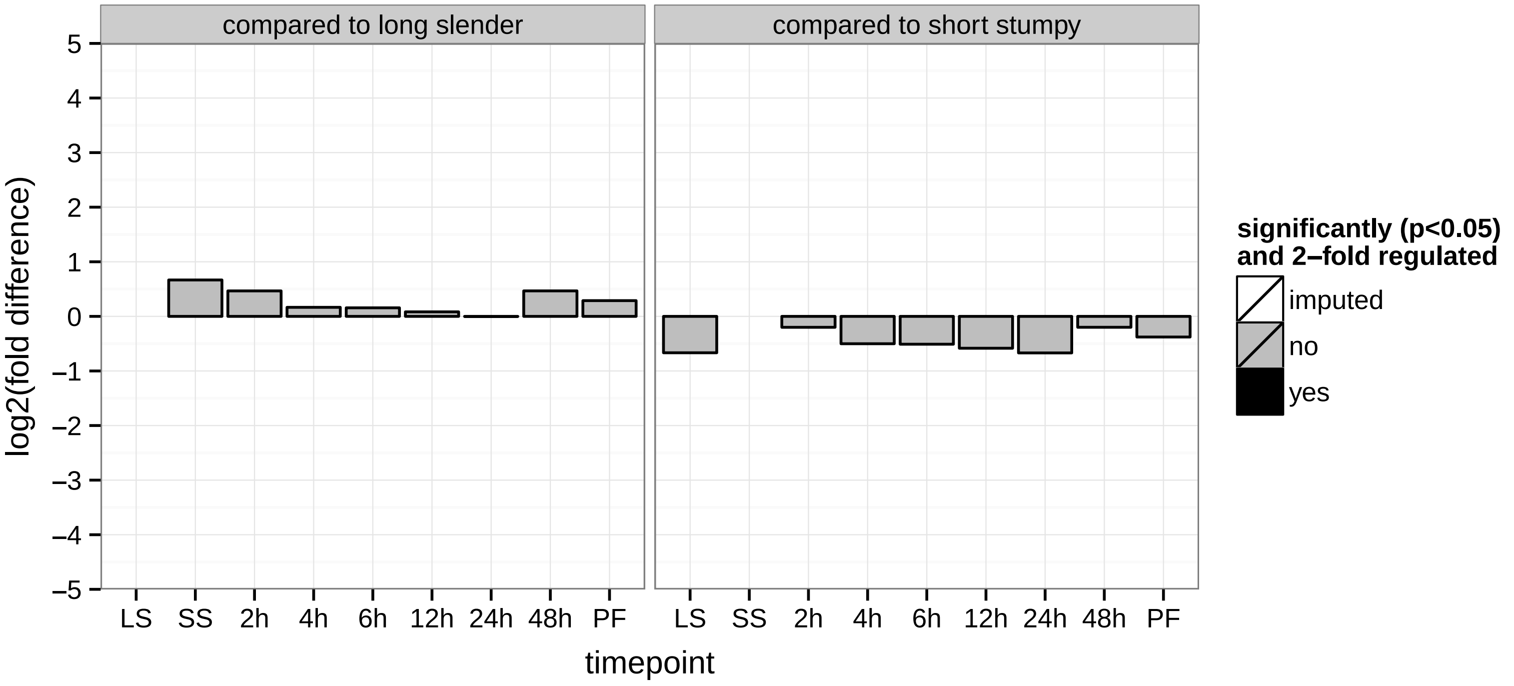
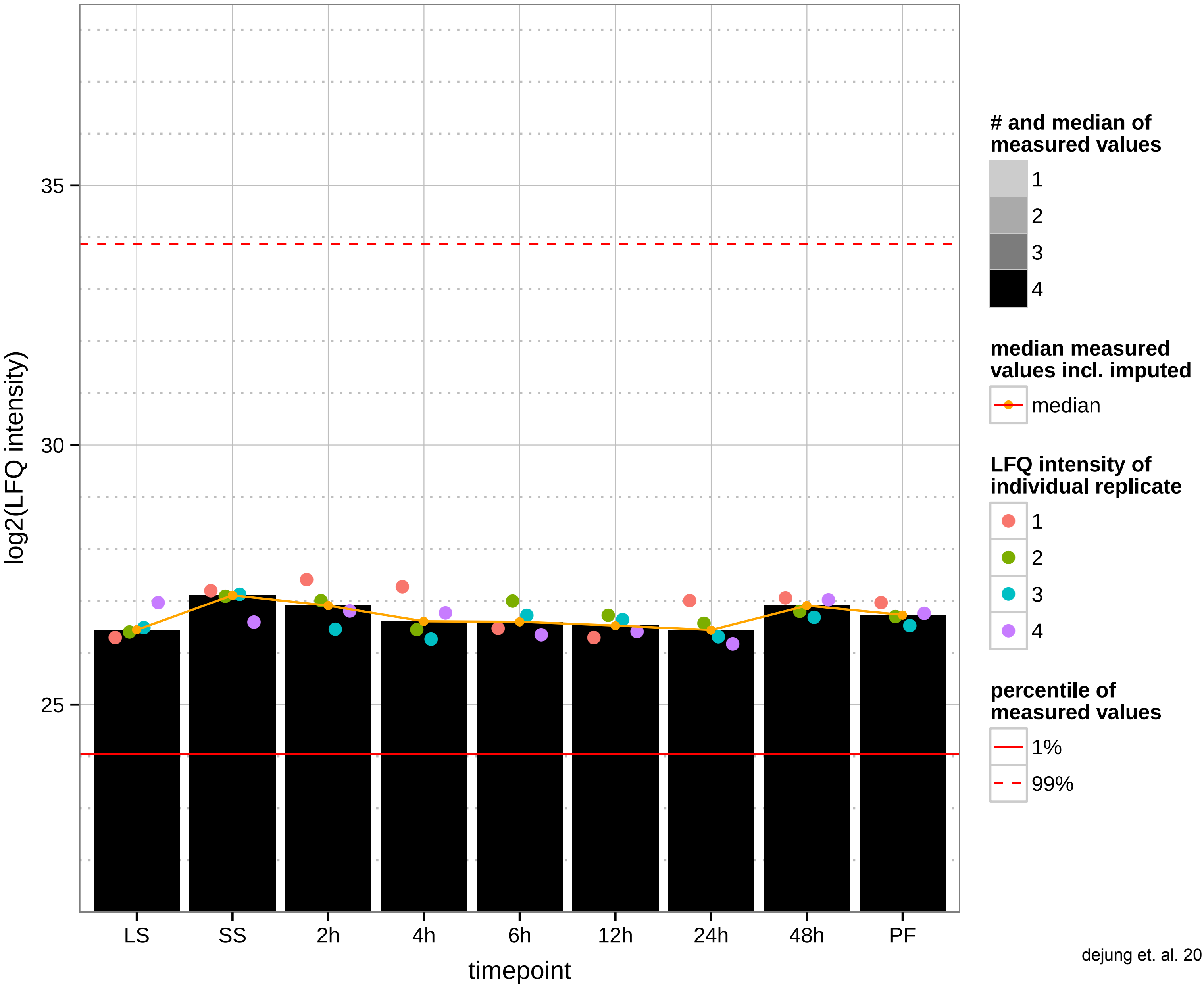
kinesin, putative (TbKIF9A)
Tb927.7.6290
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: axoneme, microtubule associated complex
AGOP: ciliary cell motility, microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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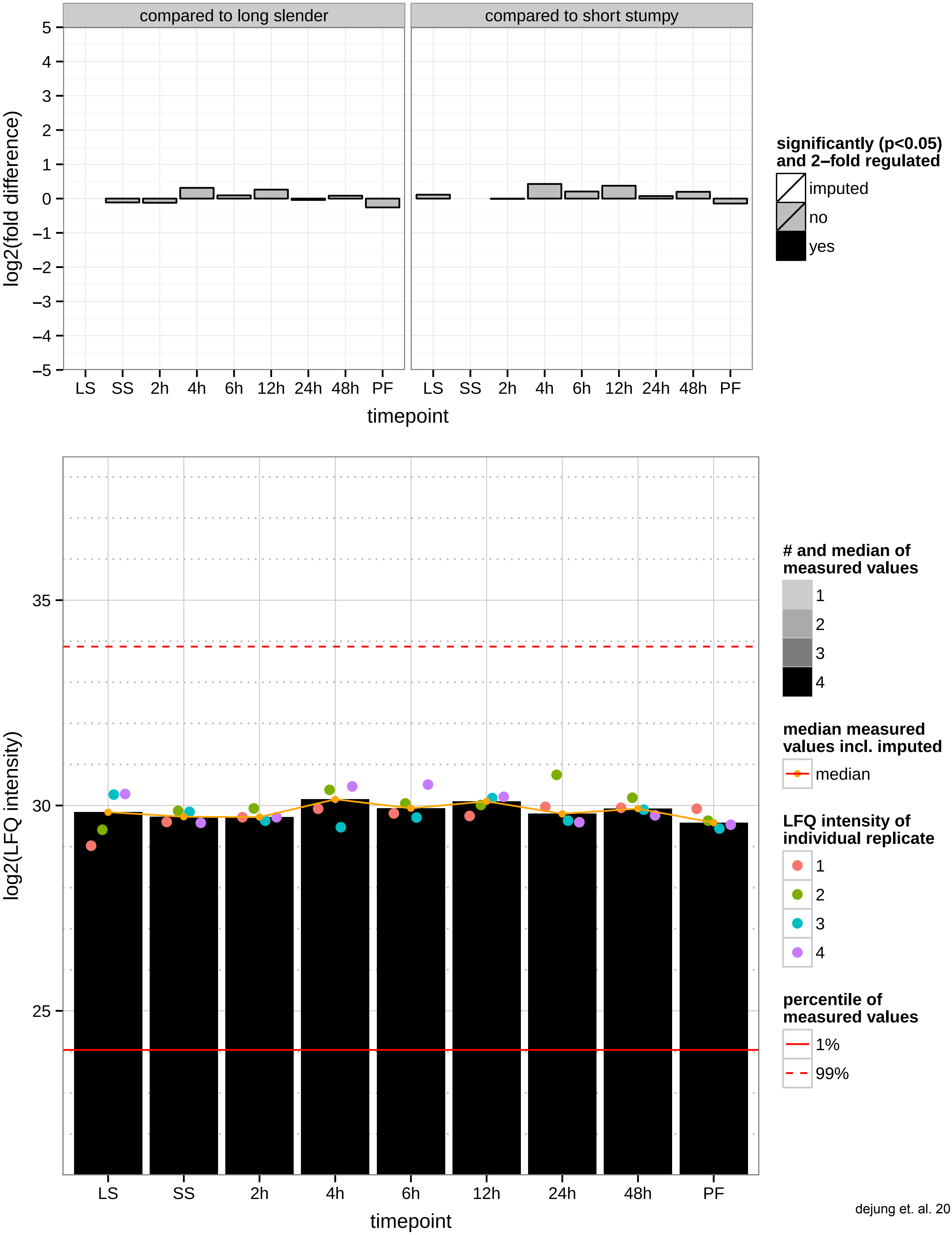
histone H2A variant, H2Az (h2aZ)
Tb927.7.6360
AGOF: DNA binding
AGOC: nucleosome, nucleus
AGOP: chromatin organization, chromosome organization, nucleosome assembly, transcription initiation from RNA polymeras
PGOF: DNA binding
PGOC: nucleosome, nucleus
PGOP: nucleosome assembly



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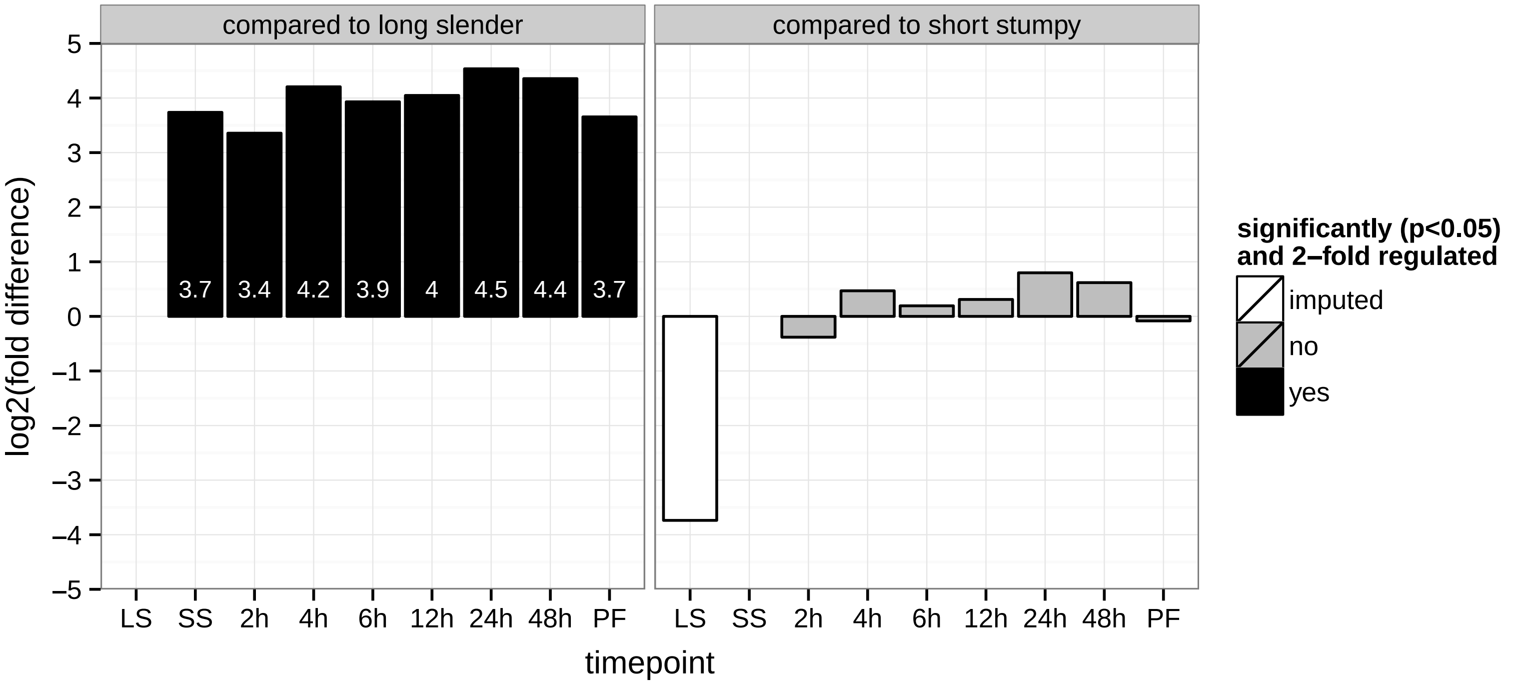
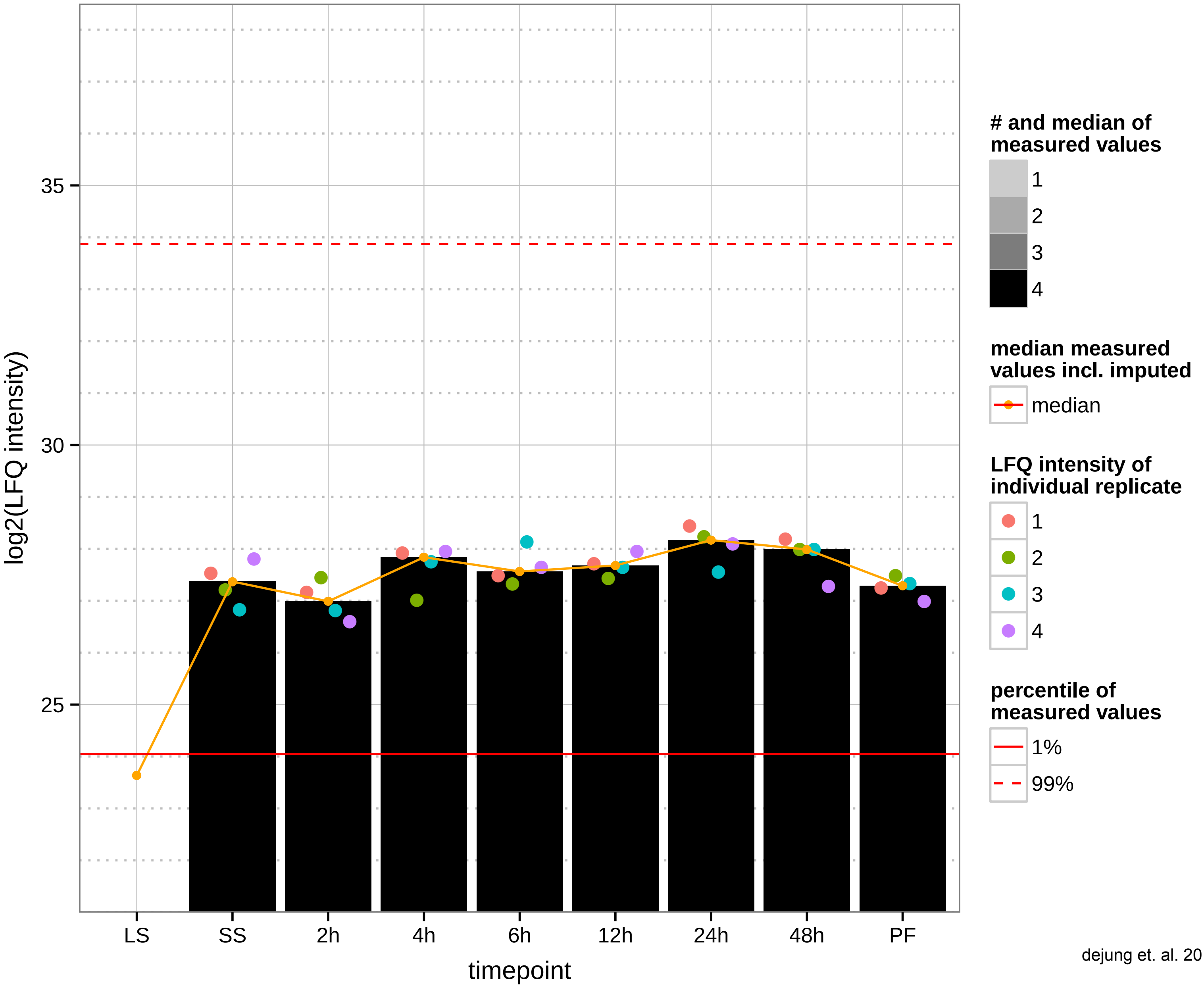
hypothetical protein, conserved
Tb927.7.640
AGOF: null
AGOC: mitochondrial membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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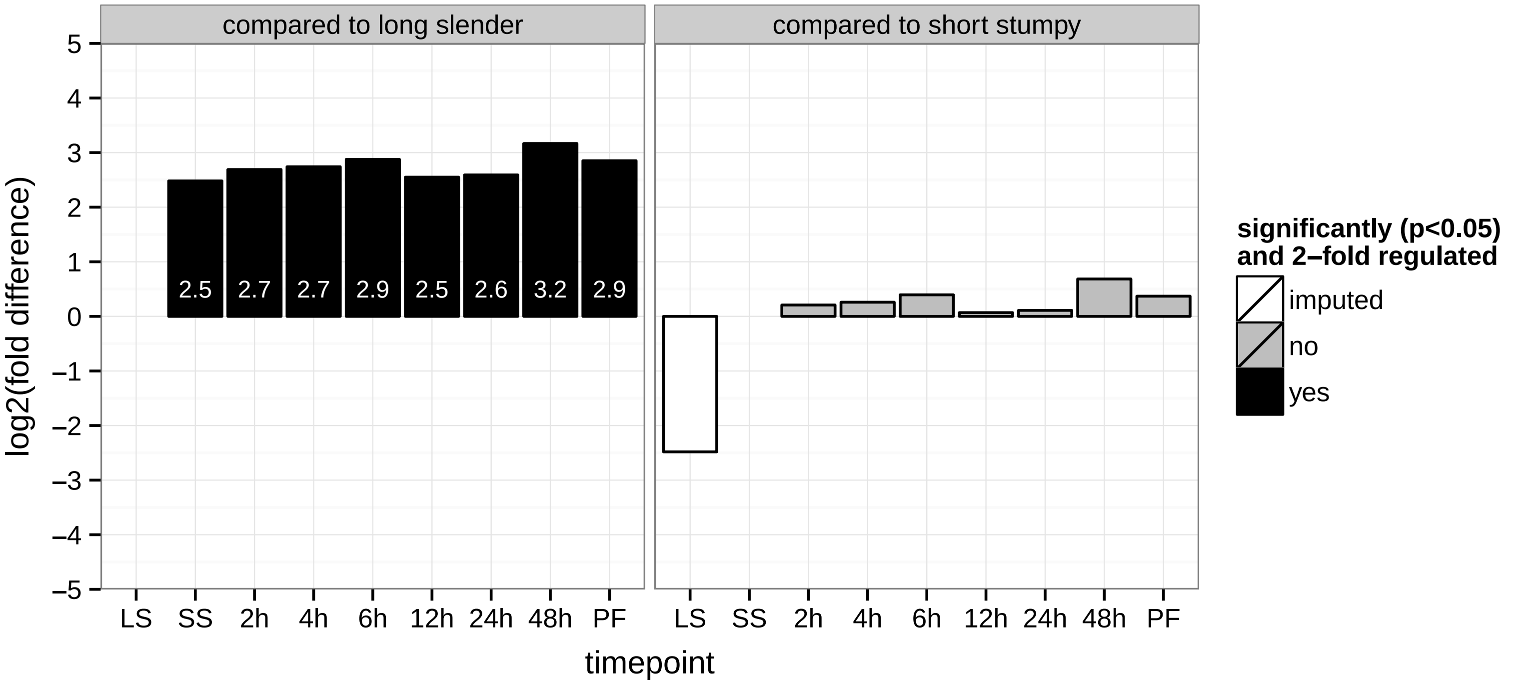
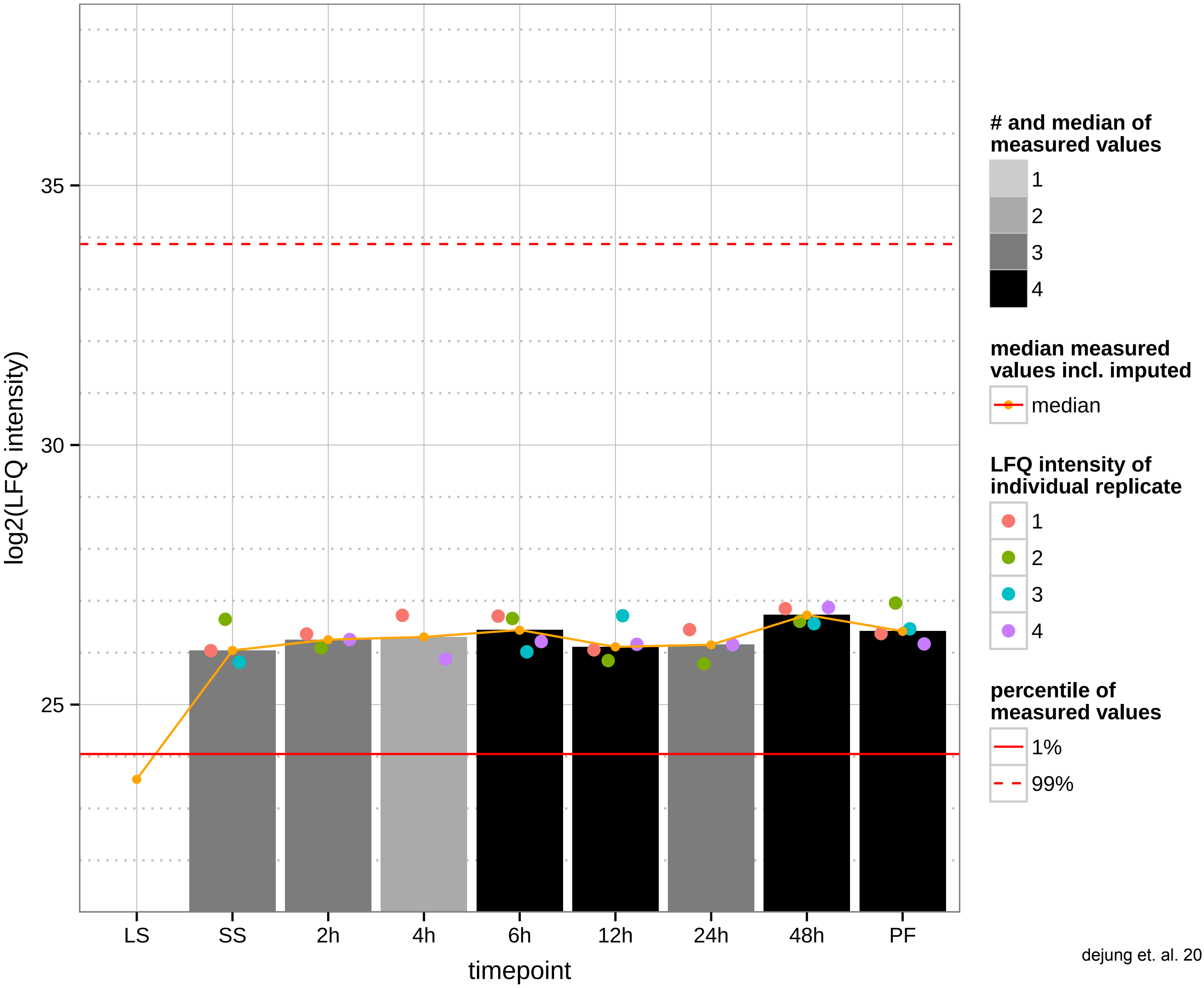
hypothetical protein, conserved
Tb927.7.6640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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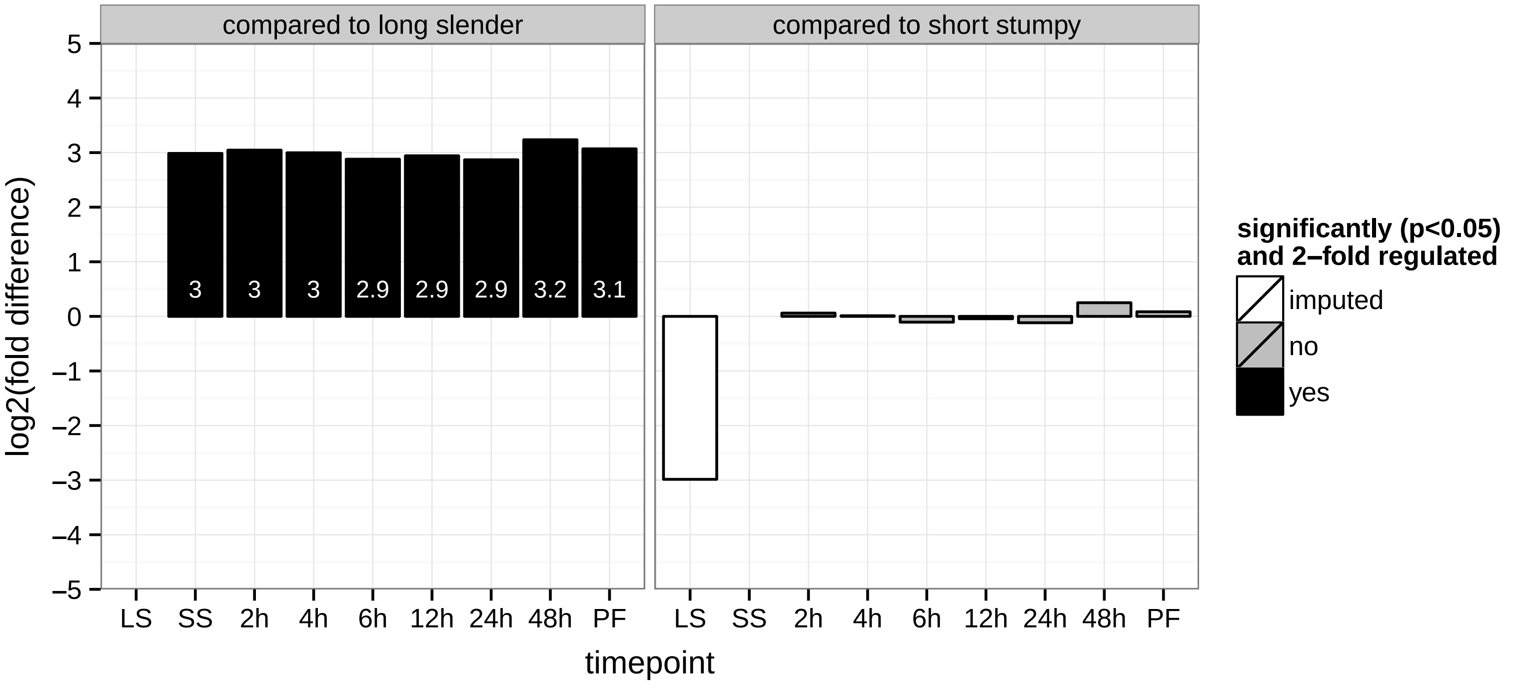
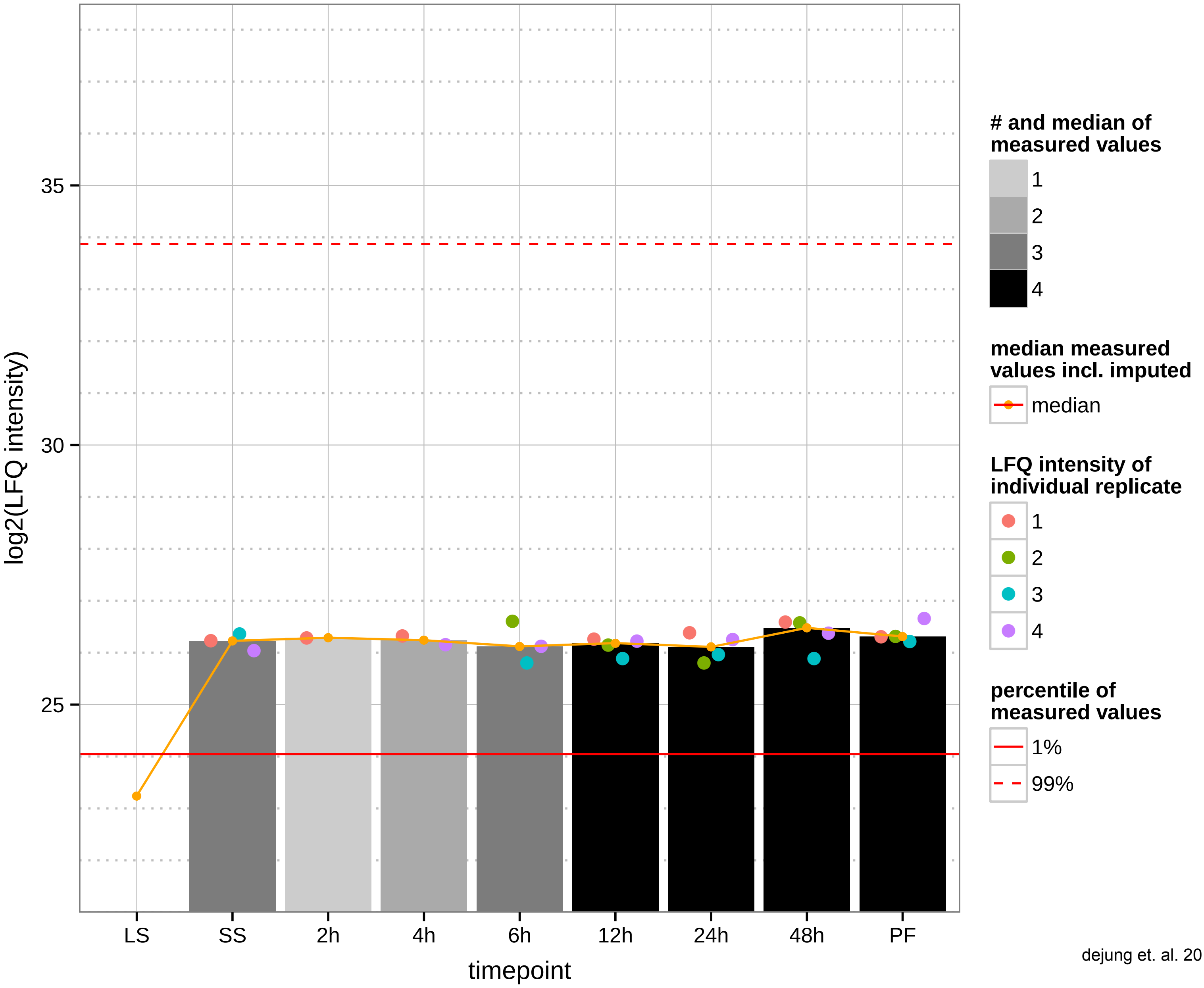
protein kinase, putative
Tb927.7.6680
AGOF: ATP binding, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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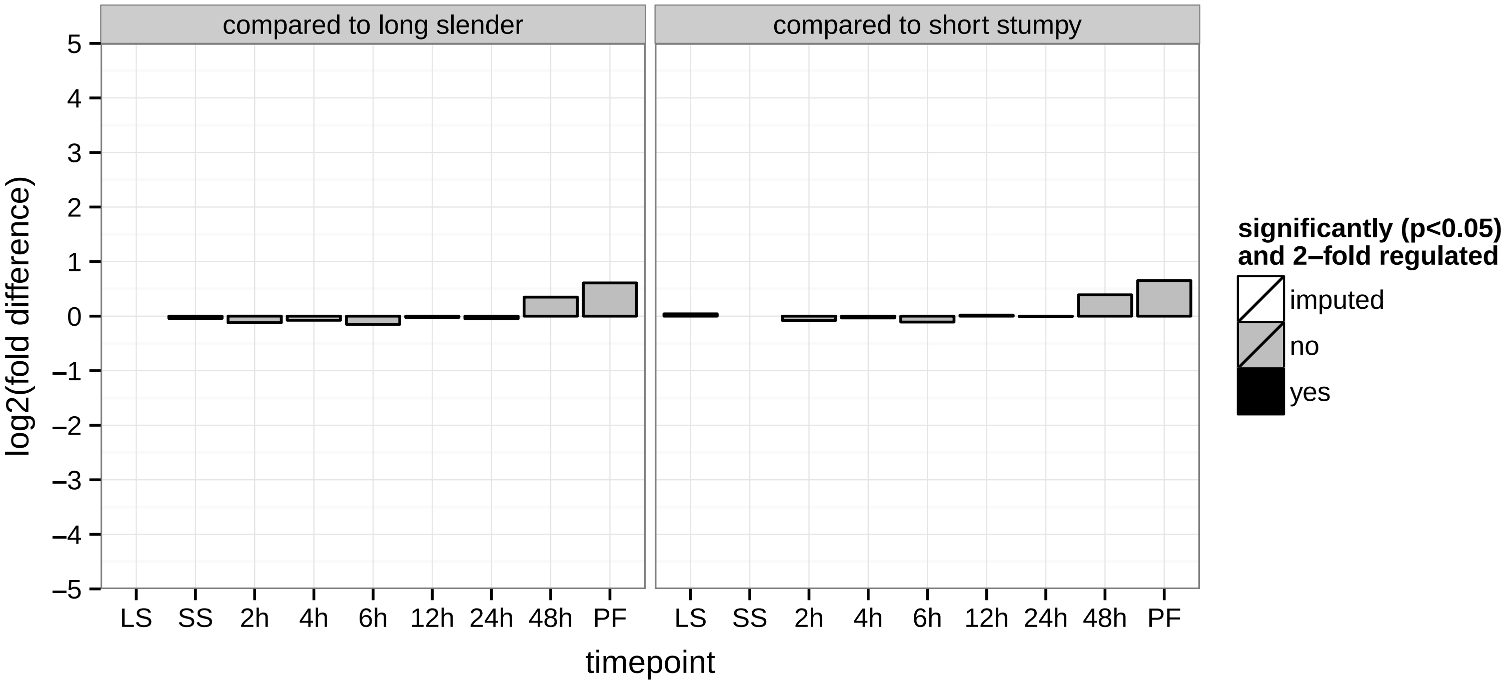
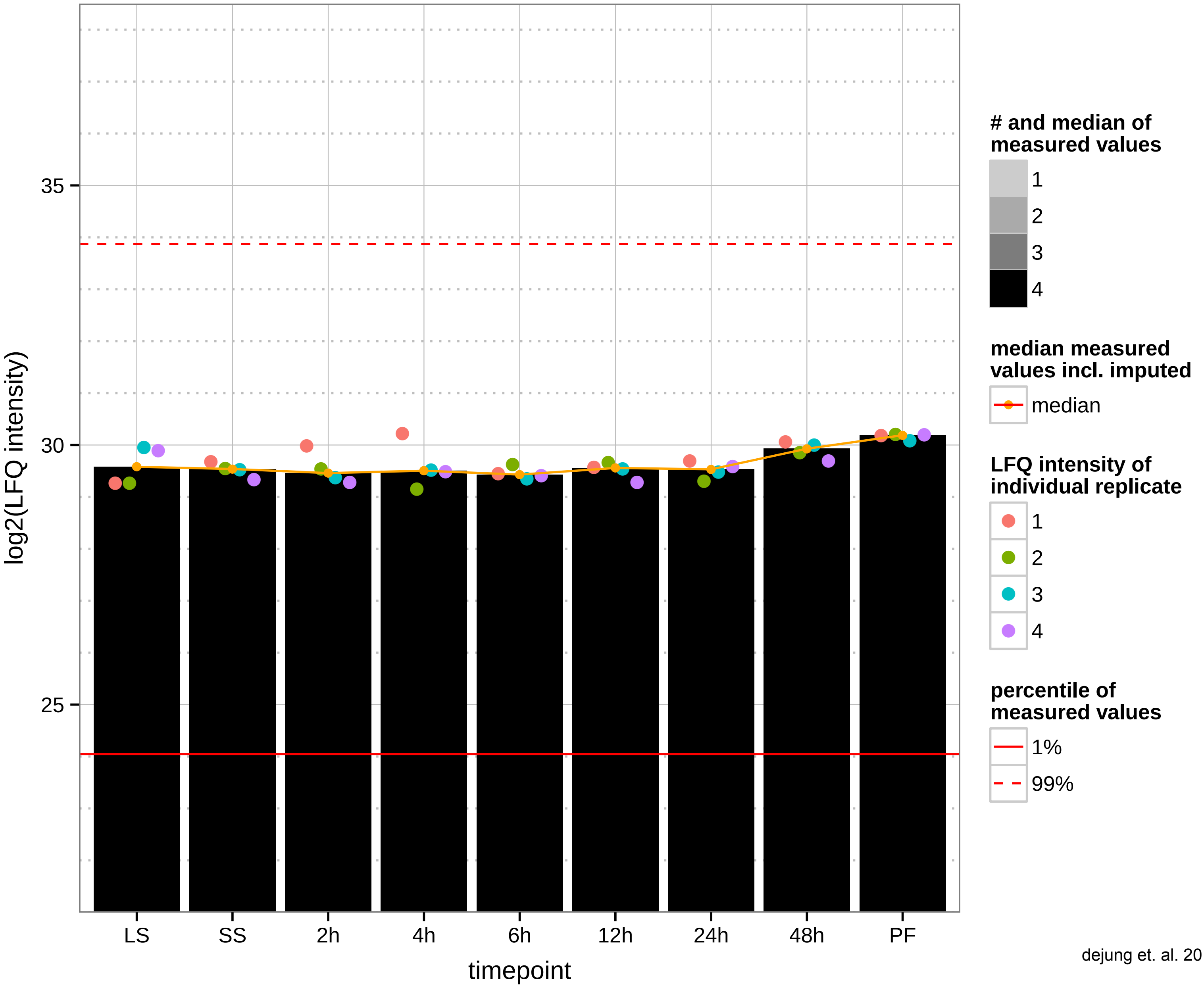
hypothetical protein, conserved
Tb927.7.6910
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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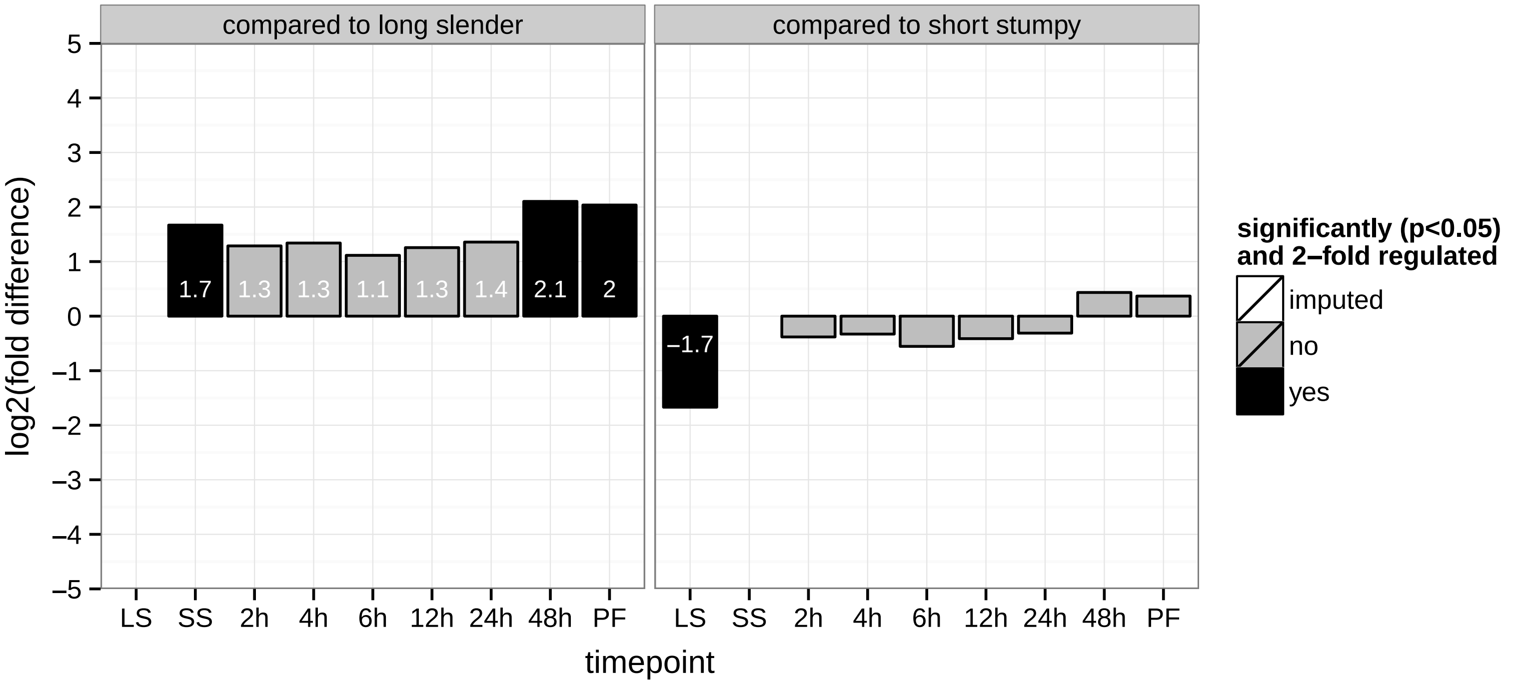
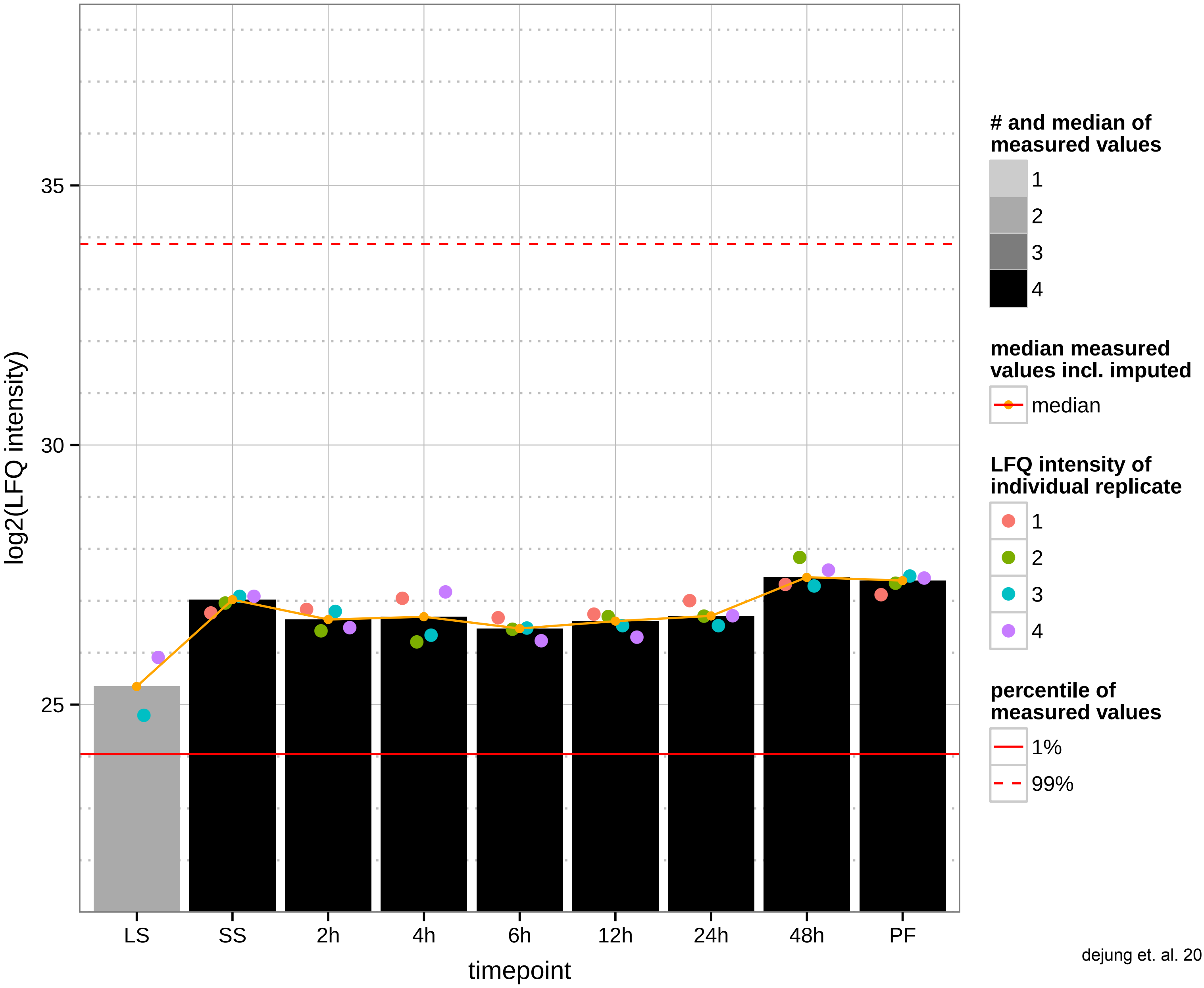
ATPase, putative
Tb927.7.6930
AGOF: ATP binding
AGOC: null
AGOP: null
PGOF: ATP binding
PGOC: null
PGOP: null





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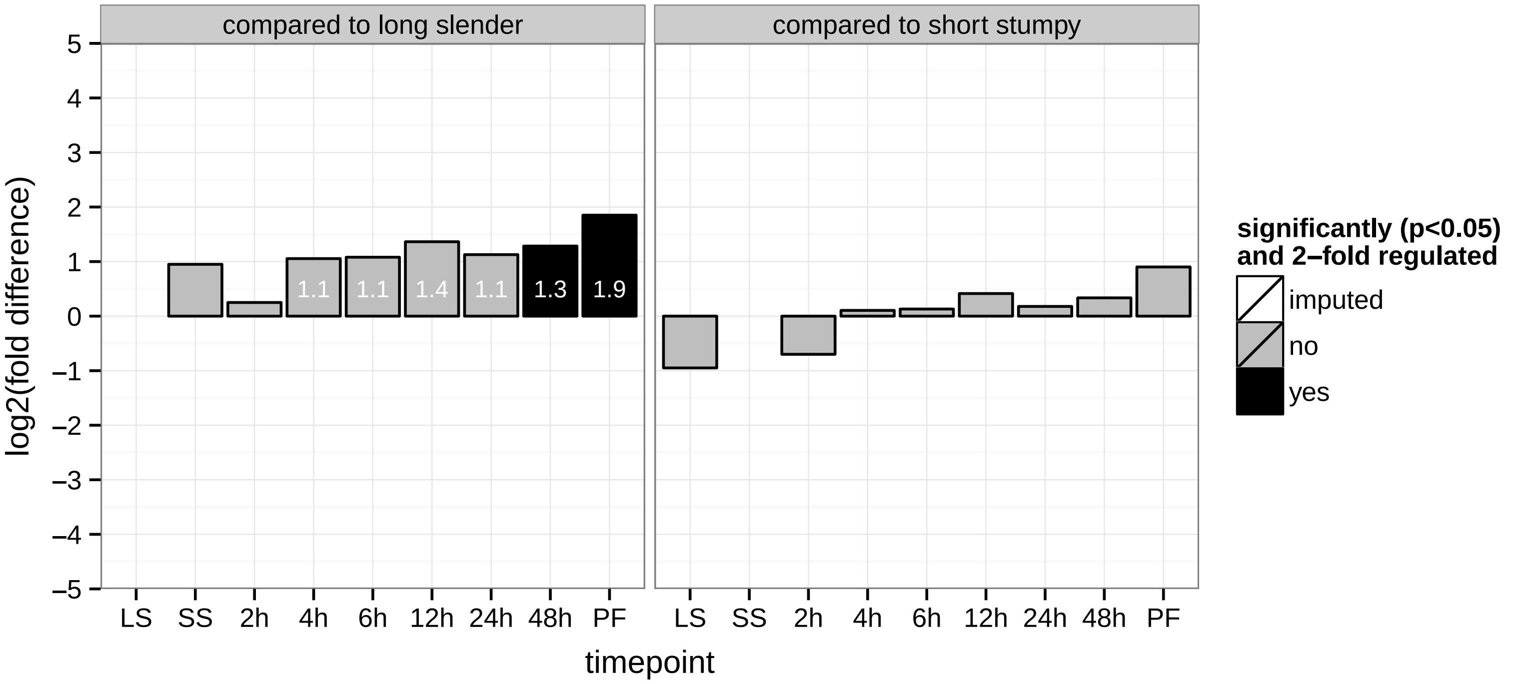
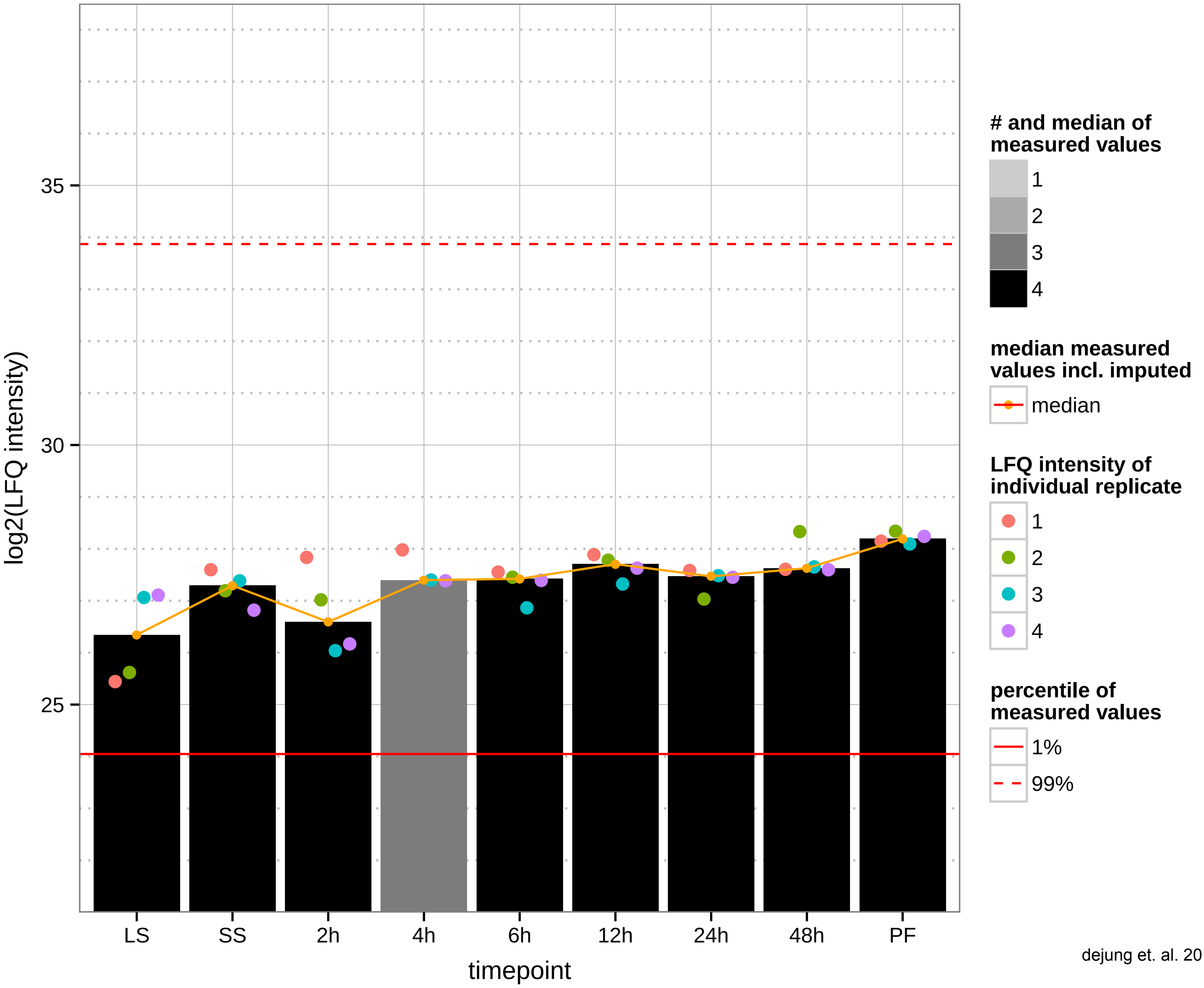
hypothetical protein, conserved
Tb927.7.6980
AGOF: null
AGOC: null
AGOP: null
PGOF: nucleic acid binding
PGOC: nucleus
PGOP: null





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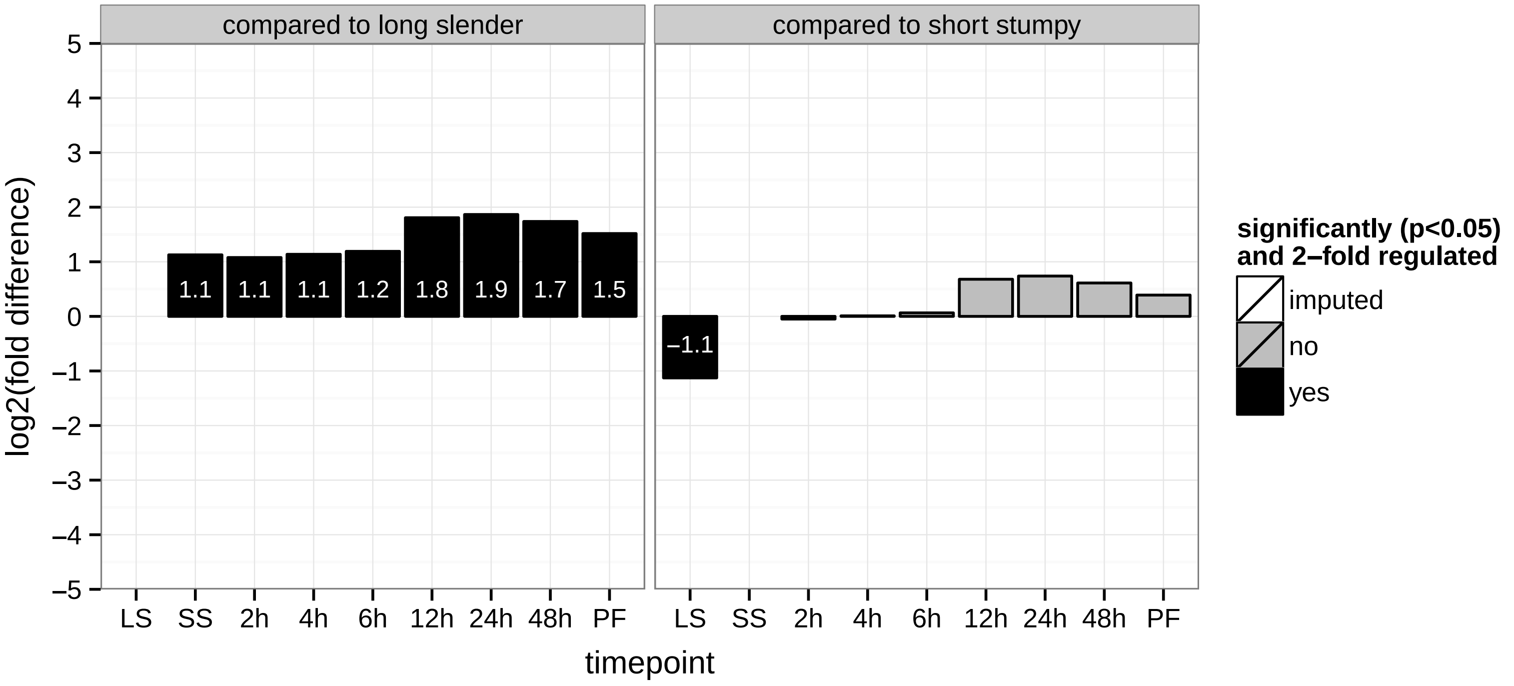
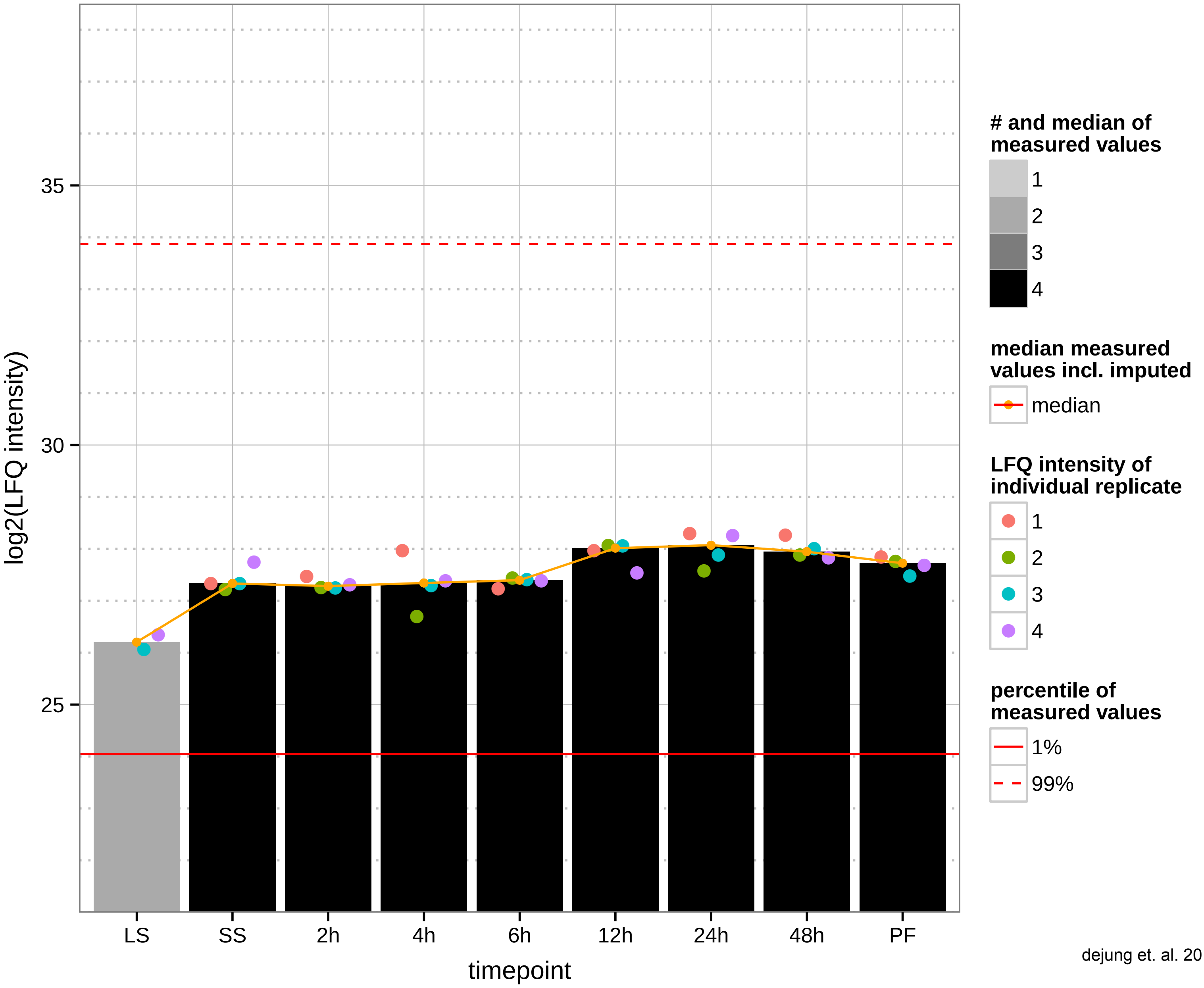
hypothetical protein, conserved
Tb927.7.700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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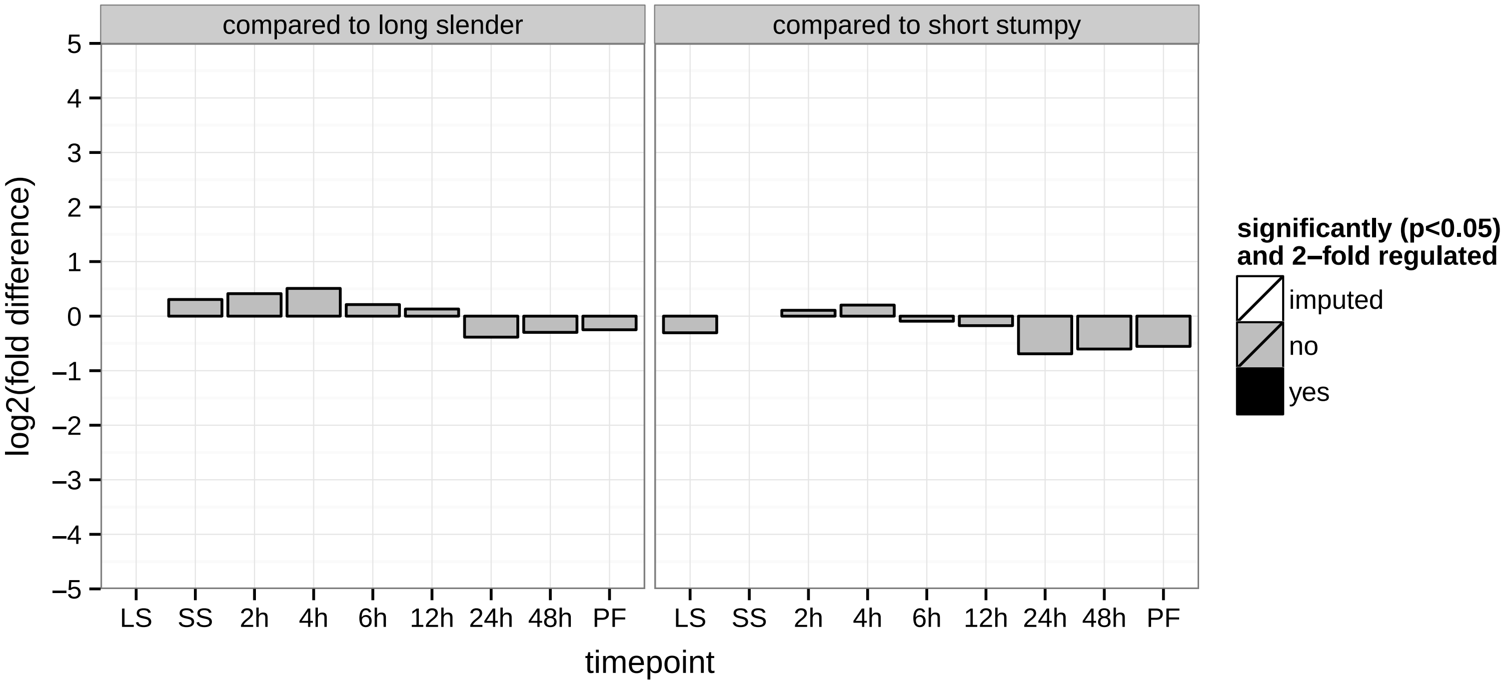
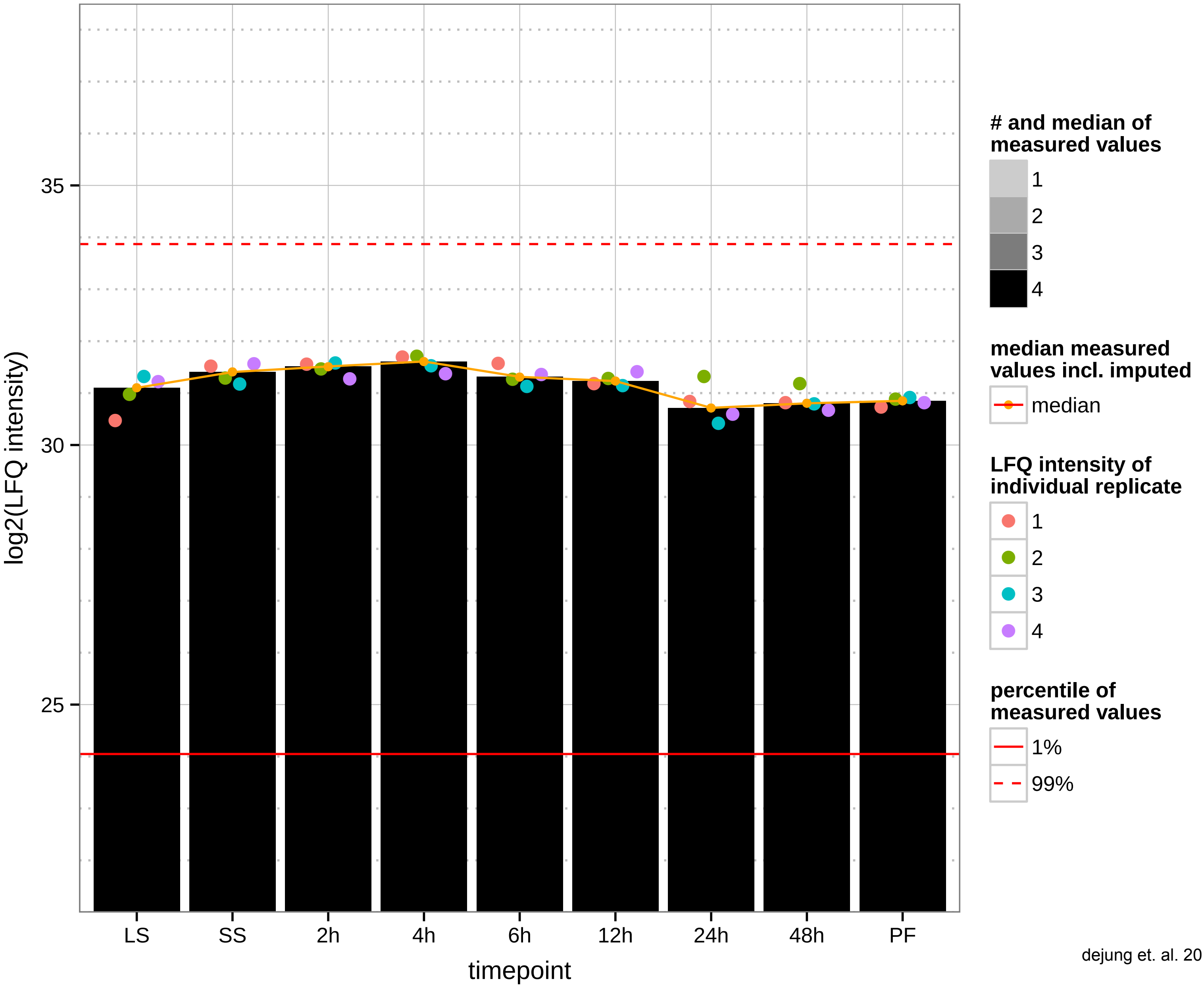
methylthioadenosine phosphorylase, putative (MTAP)
Tb927.7.7040
AGOF: transferase activity, transferring pentosyl groups
AGOC: null
AGOP: nucleoside metabolic process
PGOF: catalytic activity, transferase activity, transferring pentosyl groups
PGOC: null
PGOP: nucleoside metabolic process





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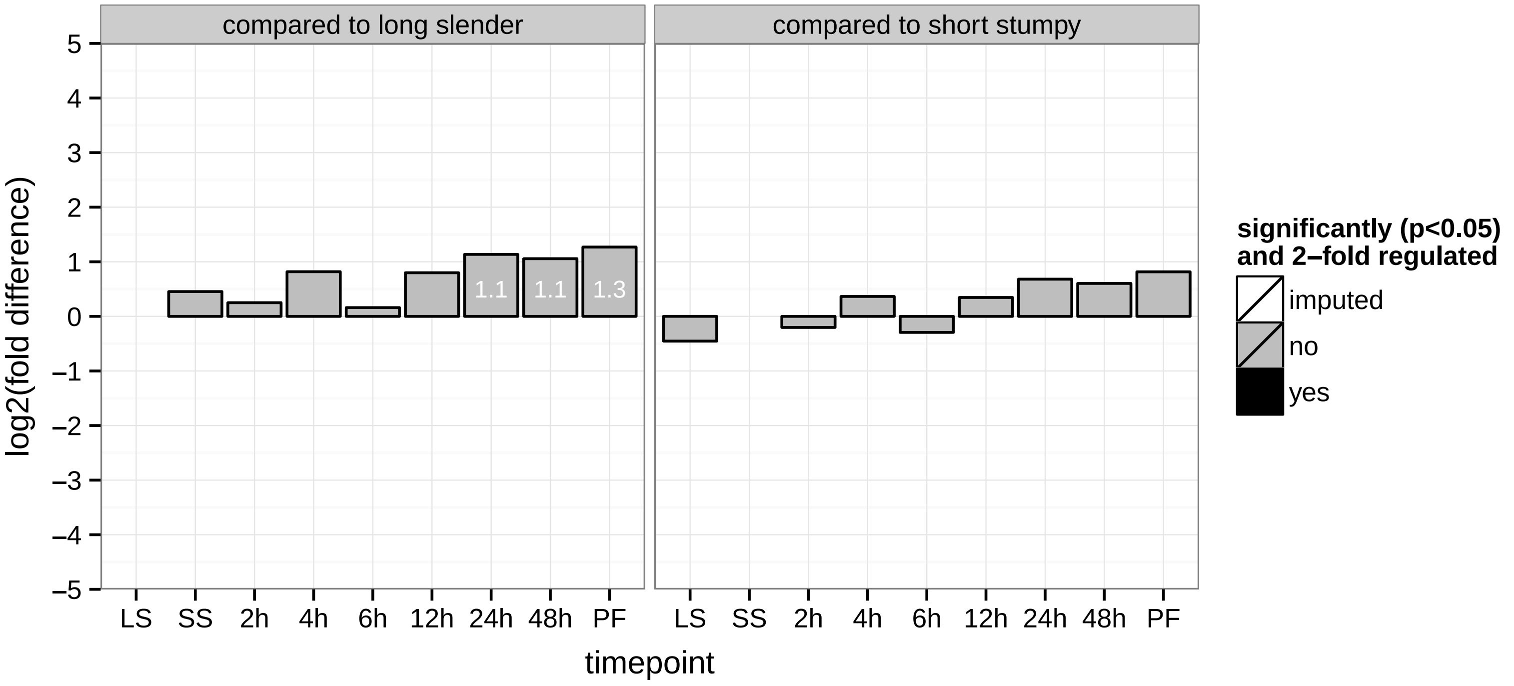
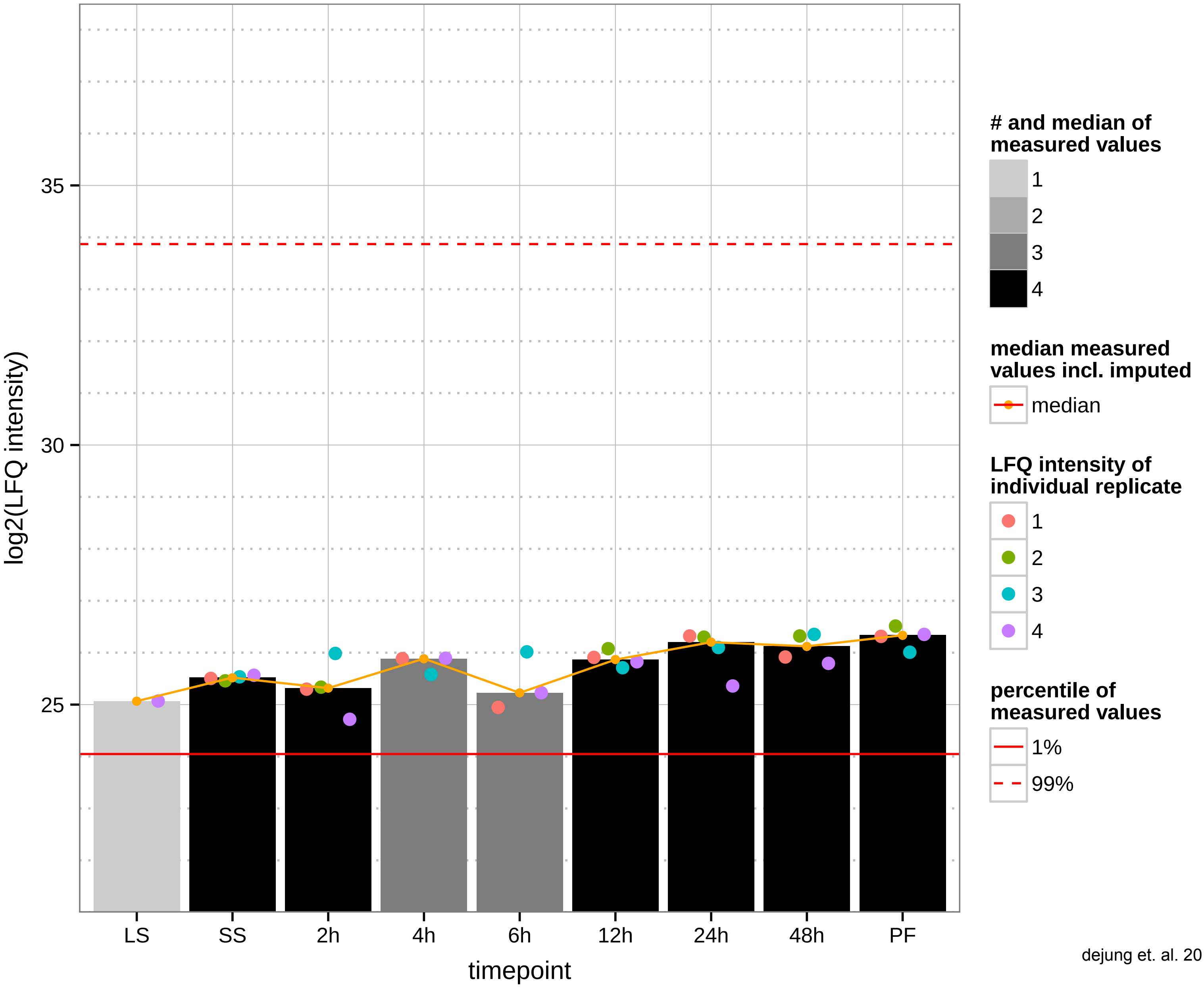
mitochondrial glycoprotein–like protein
Tb927.7.7080
AGOF: null
AGOC: mitochondrial matrix, mitochondrion
AGOP: null
PGOF: null
PGOC: mitochondrial matrix
PGOP: null





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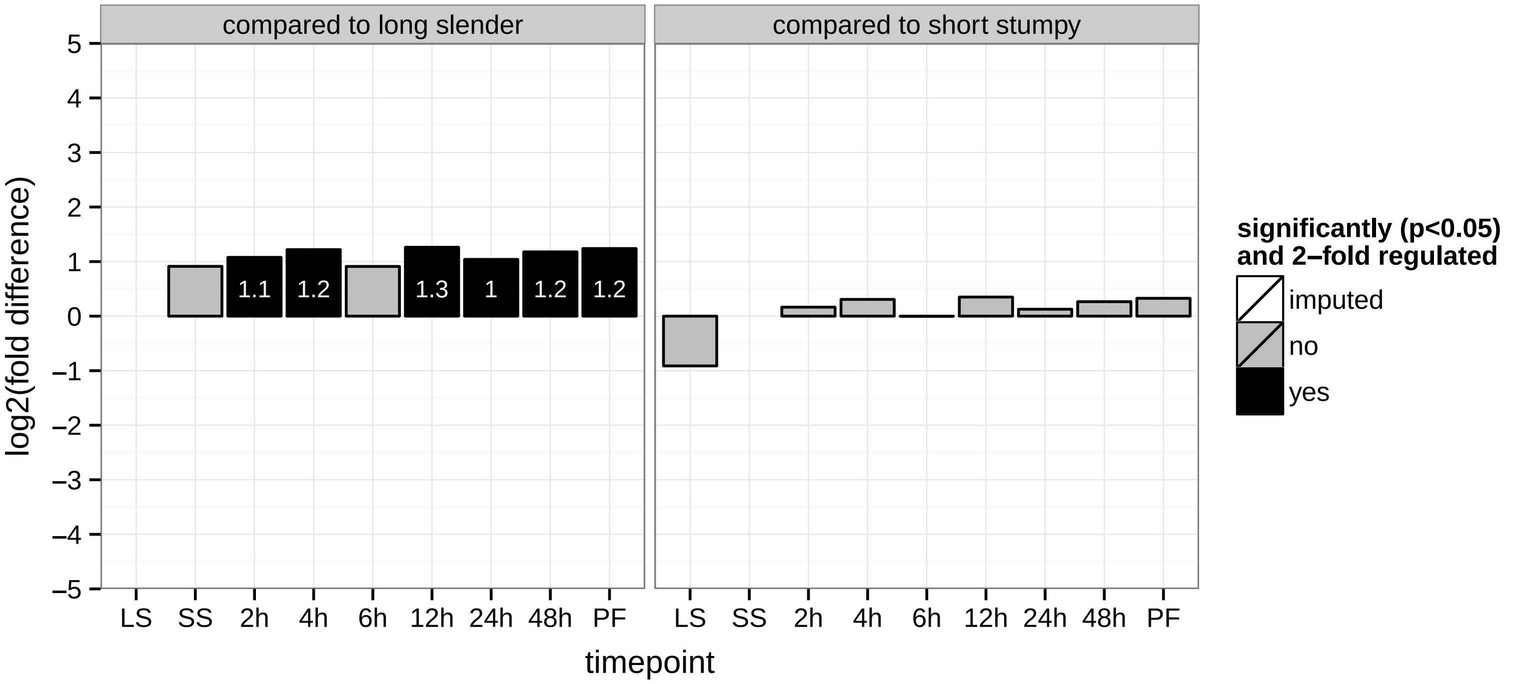
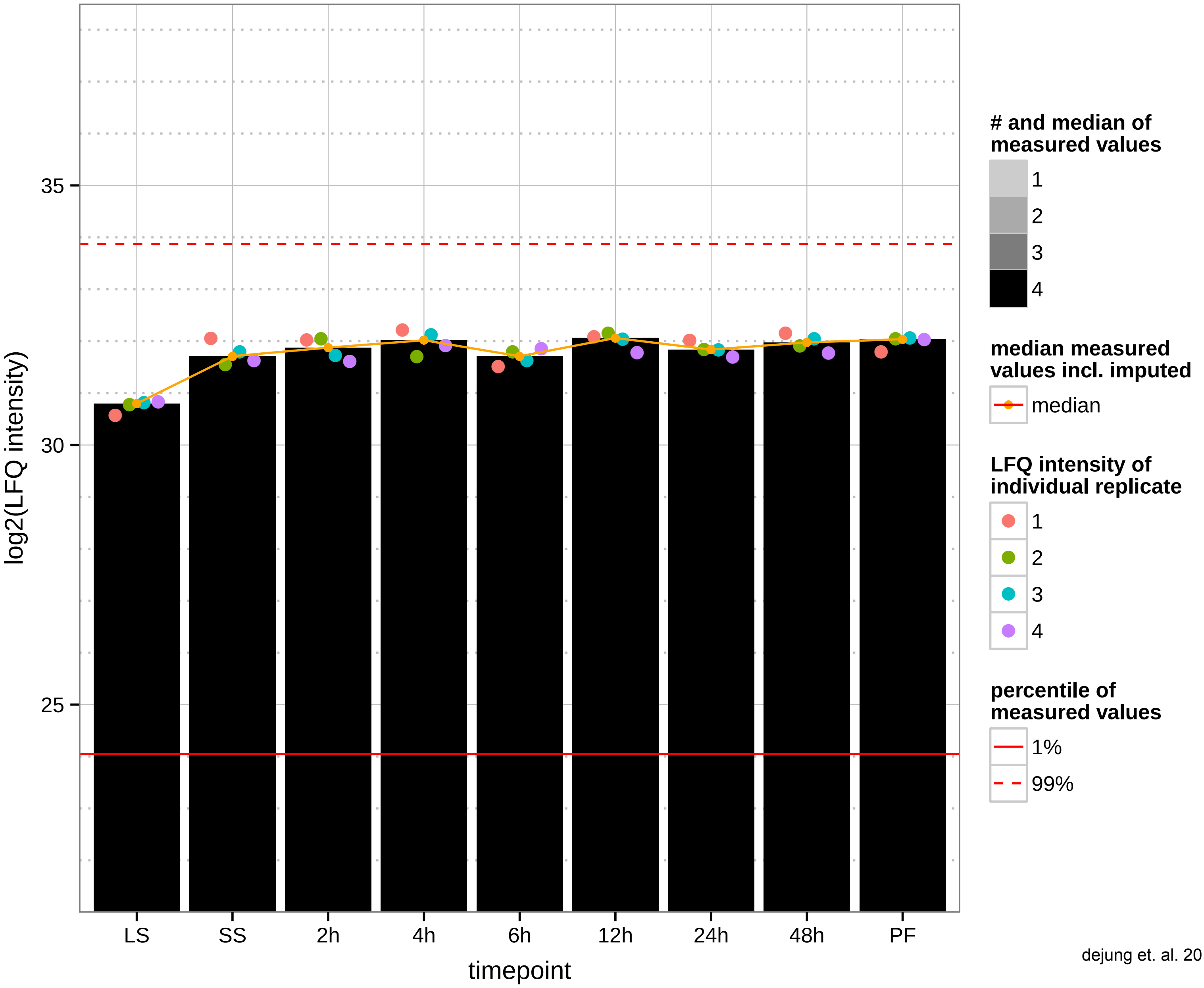
heat shock 70 kDa protein, putative (HSP70)
Tb927.7.710
AGOF: ATP binding
AGOC: null
AGOP: response to stress
PGOF: null
PGOC: null
PGOP: null





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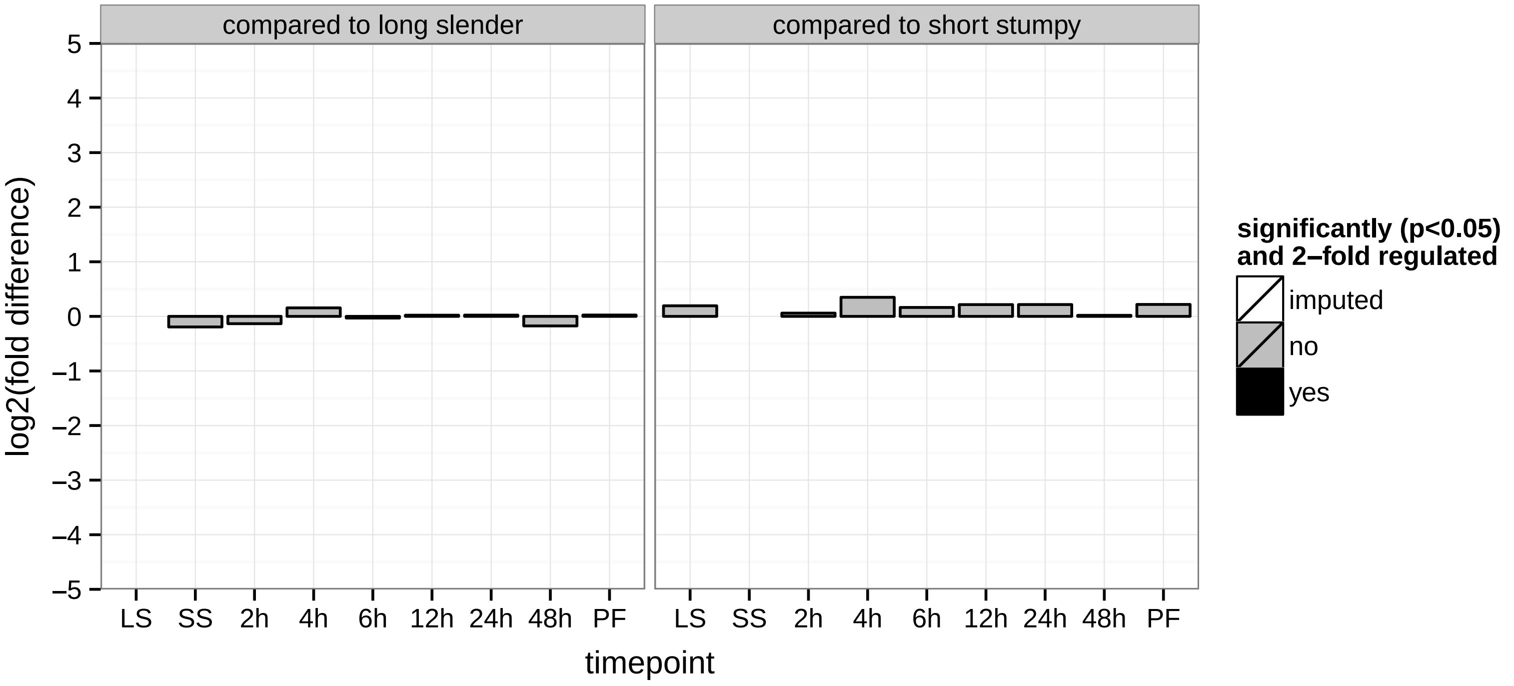
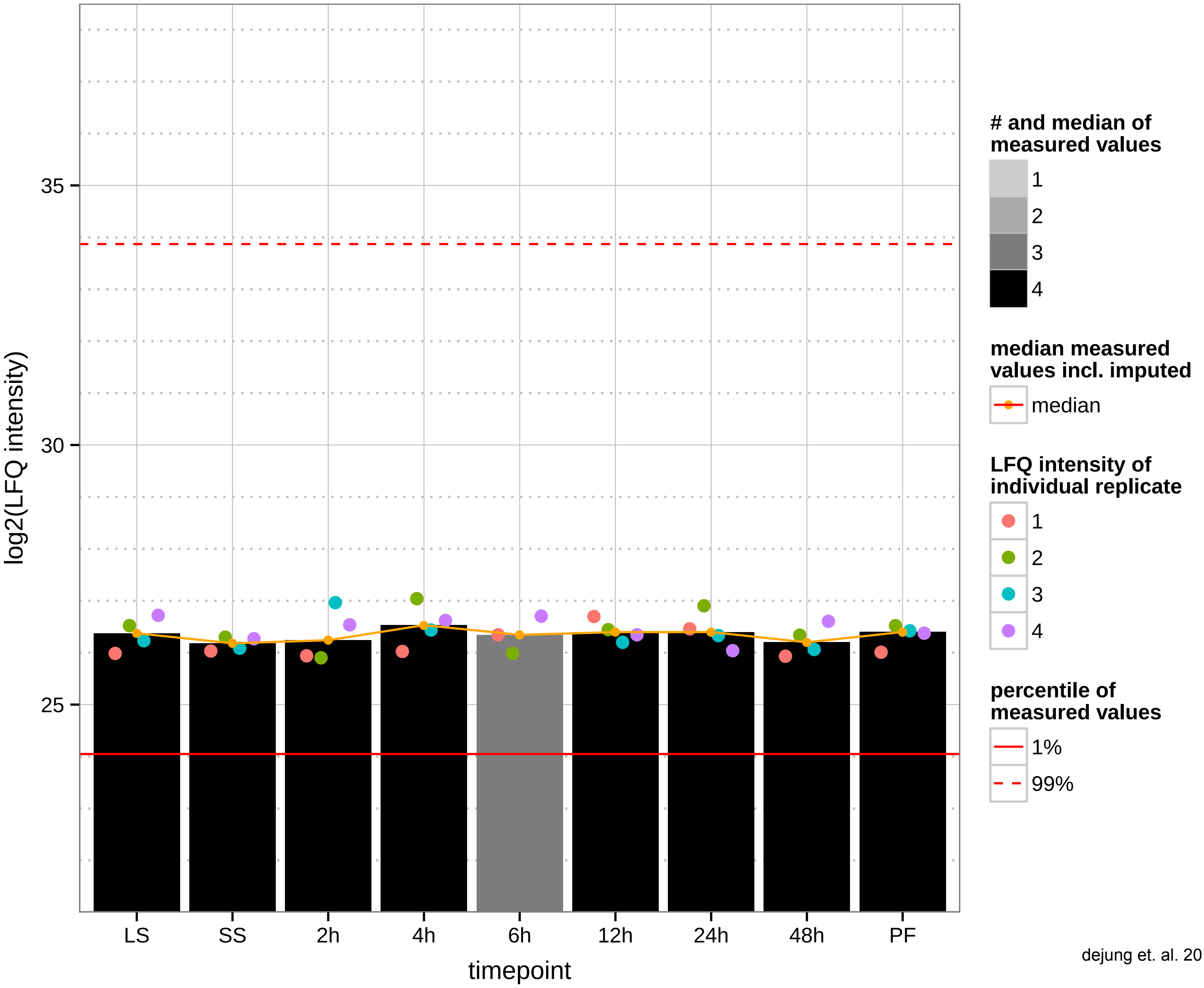
hypothetical protein, conserved
Tb927.7.7140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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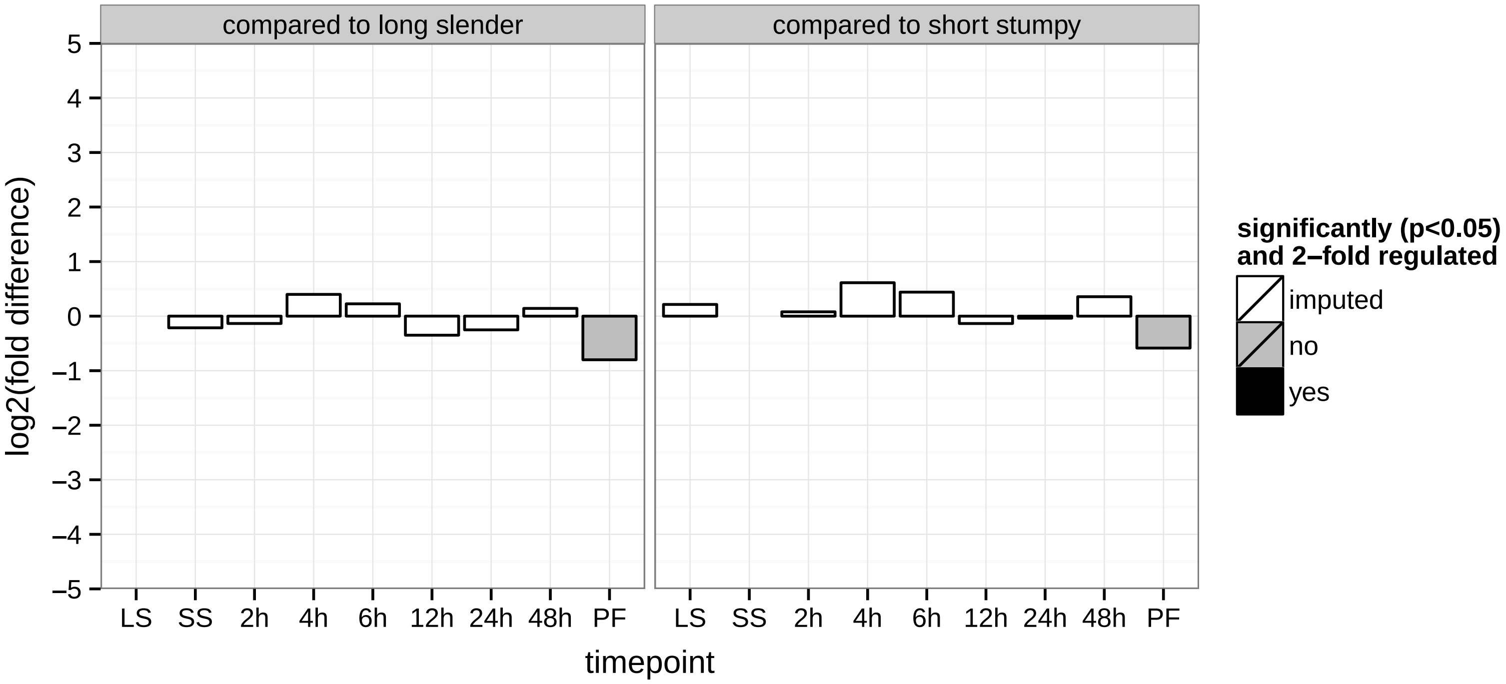
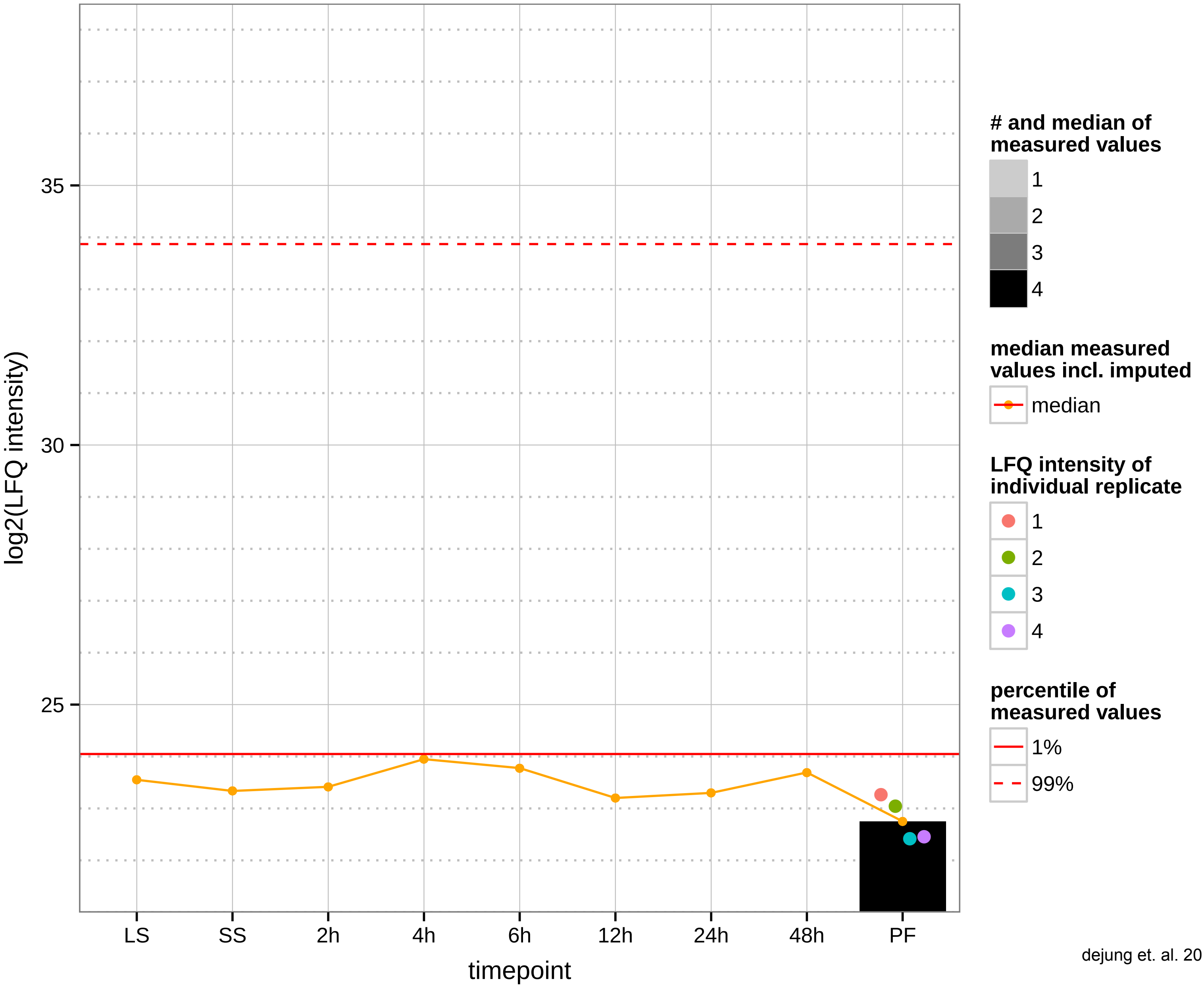
hypothetical protein, conserved
Tb927.7.7190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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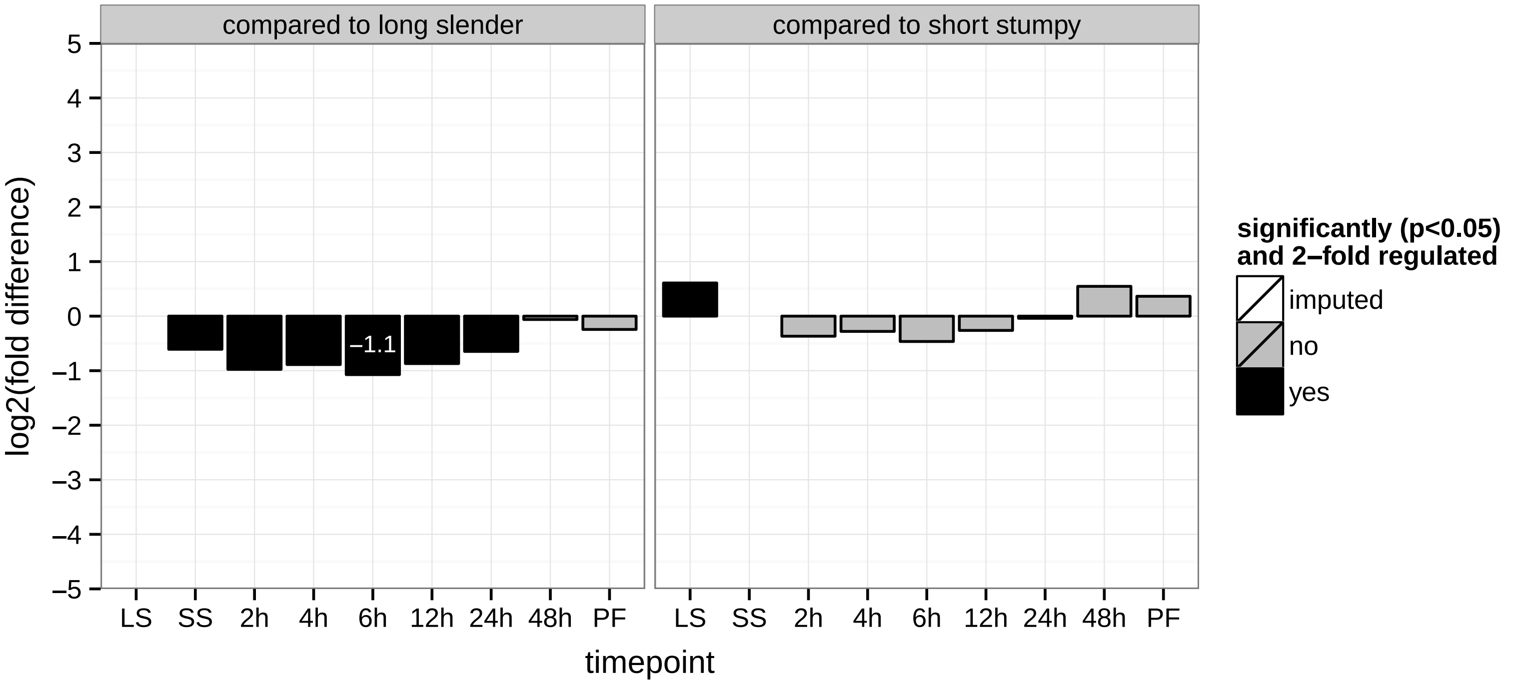
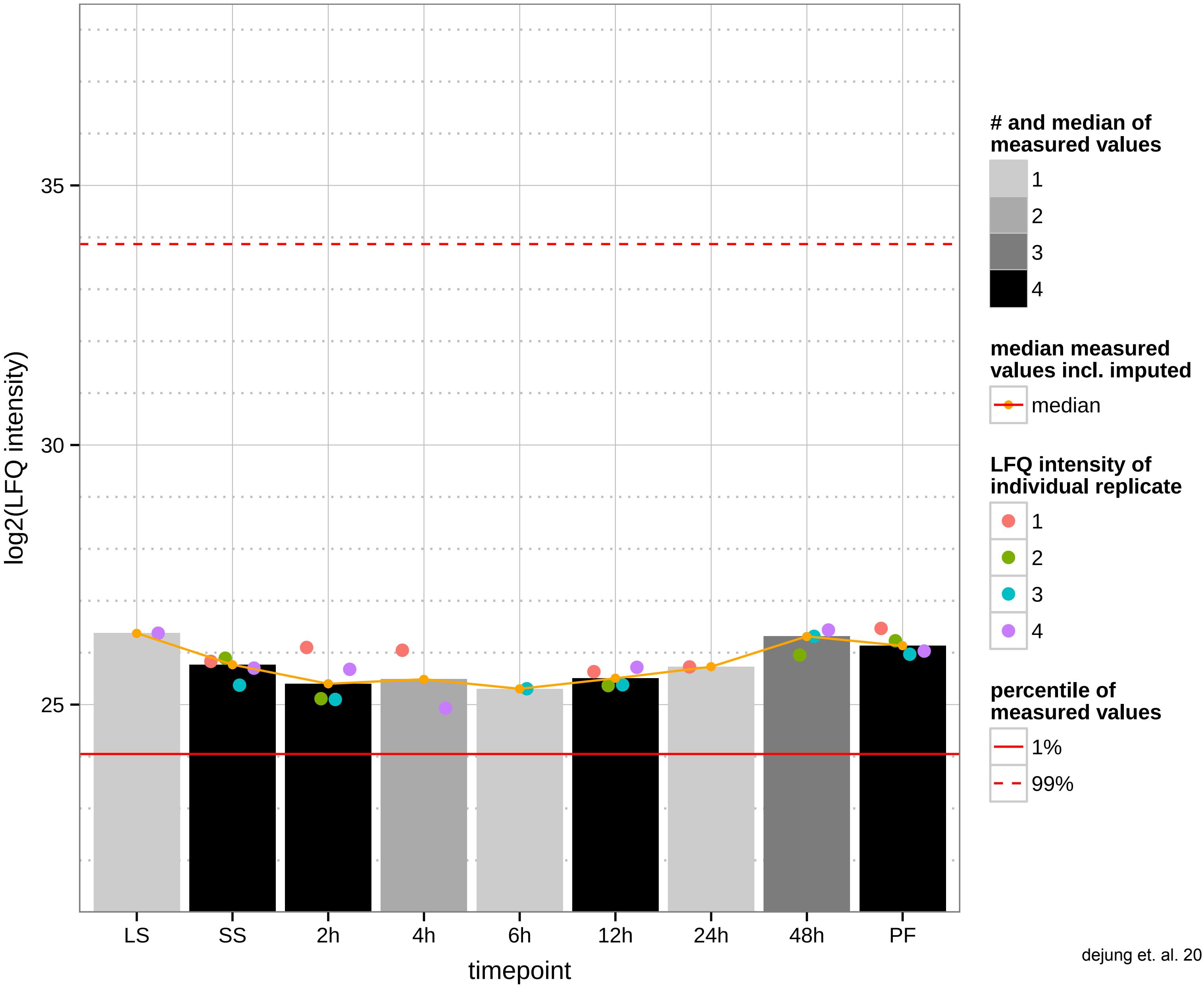
leucine–rich repeat protein (LRRP), putative
Tb927.7.7240
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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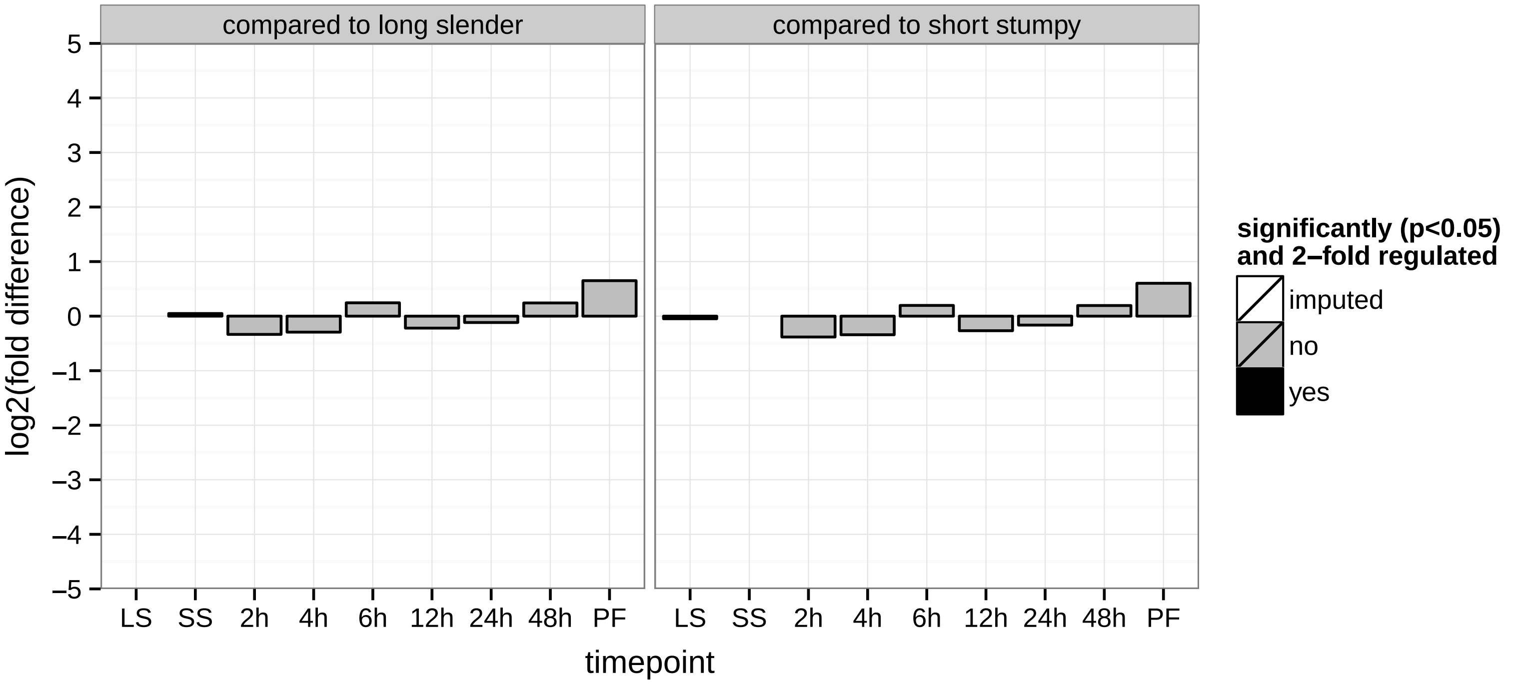
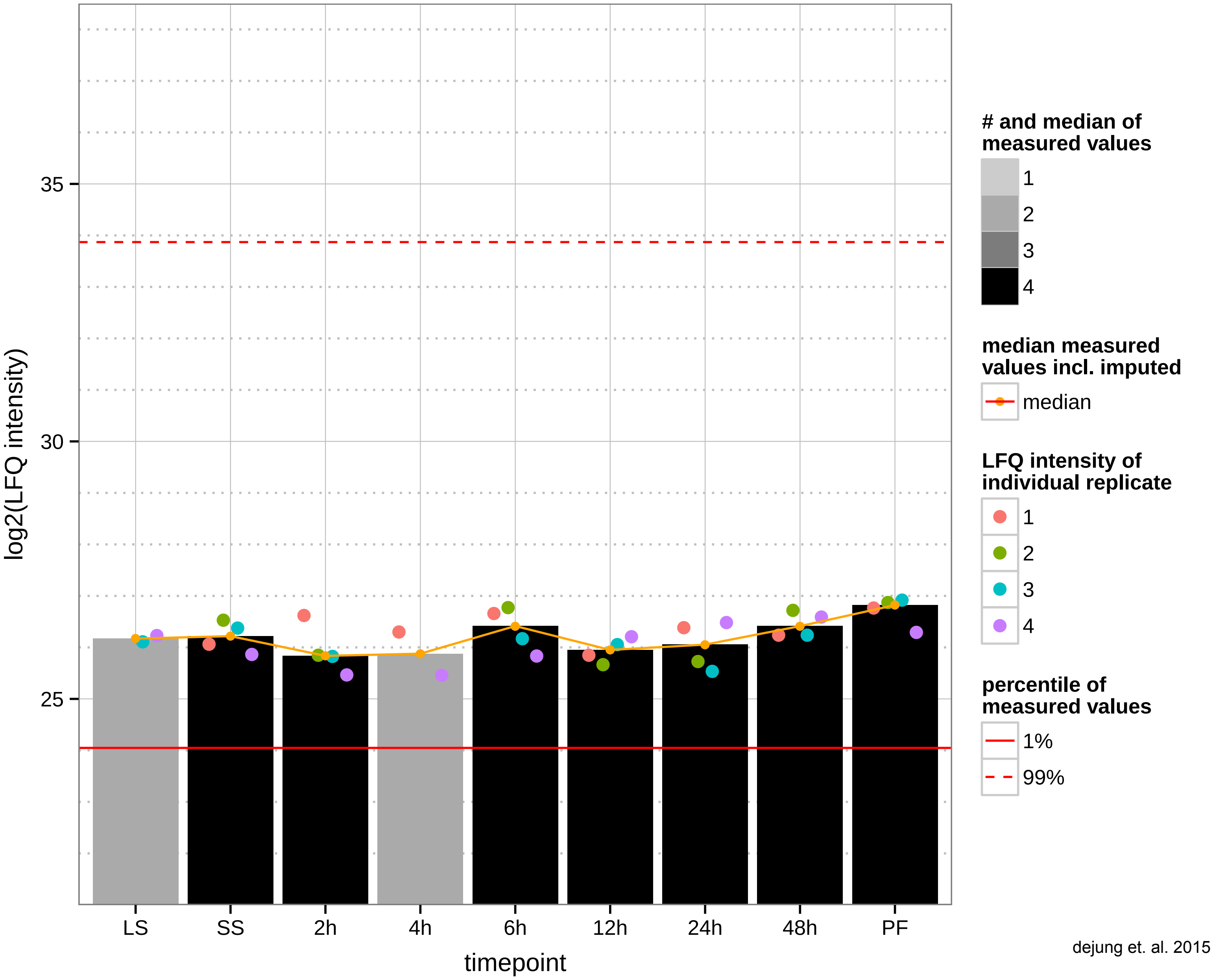
hypothetical protein, conserved
Tb927.7.7250
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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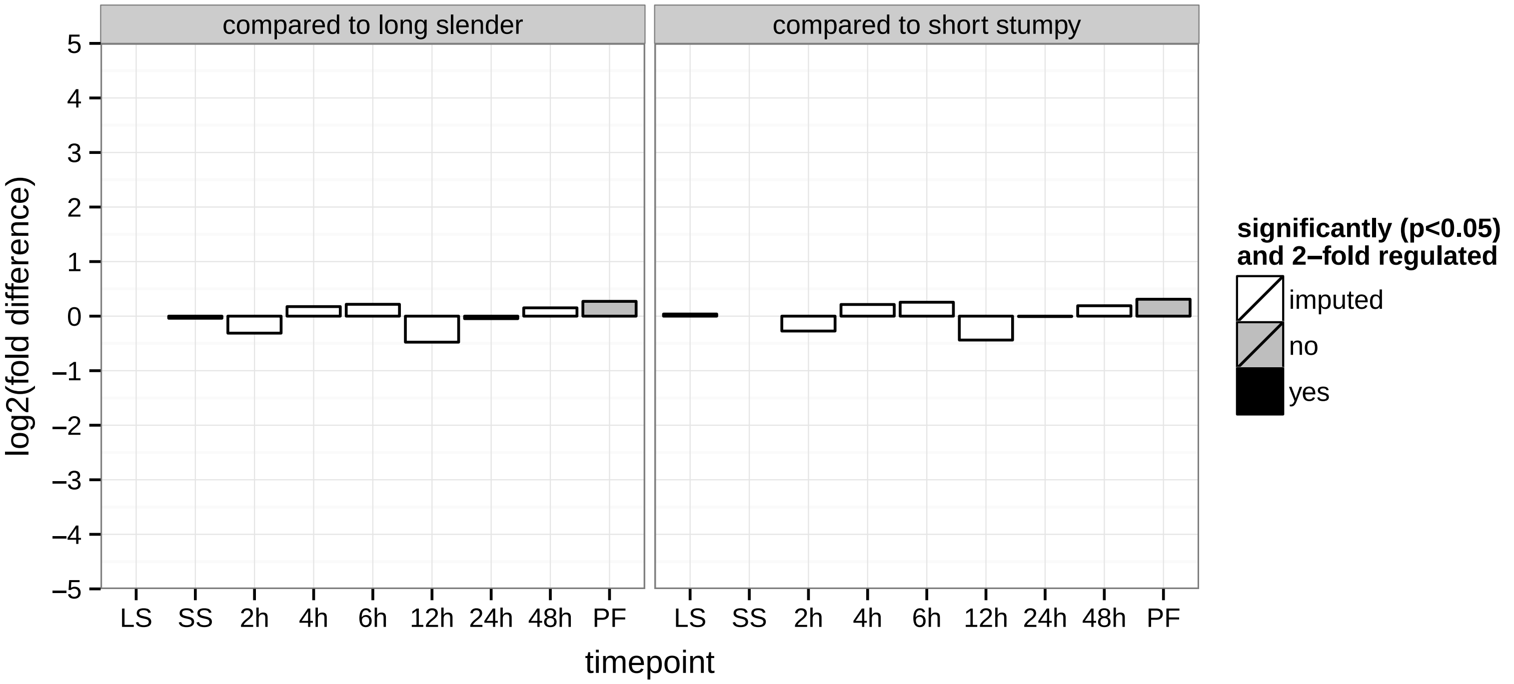
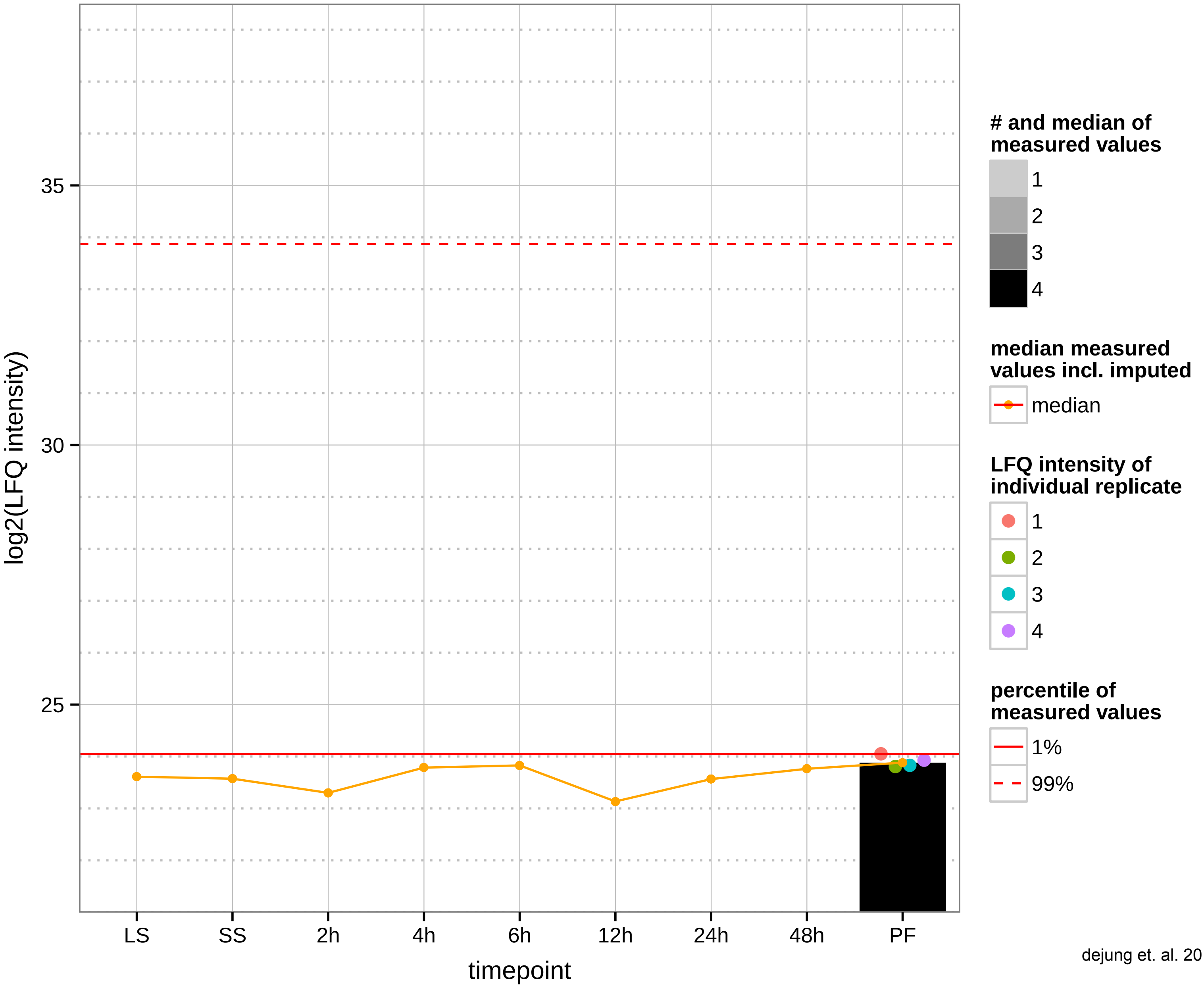
hypothetical protein, conserved
Tb927.7.7290
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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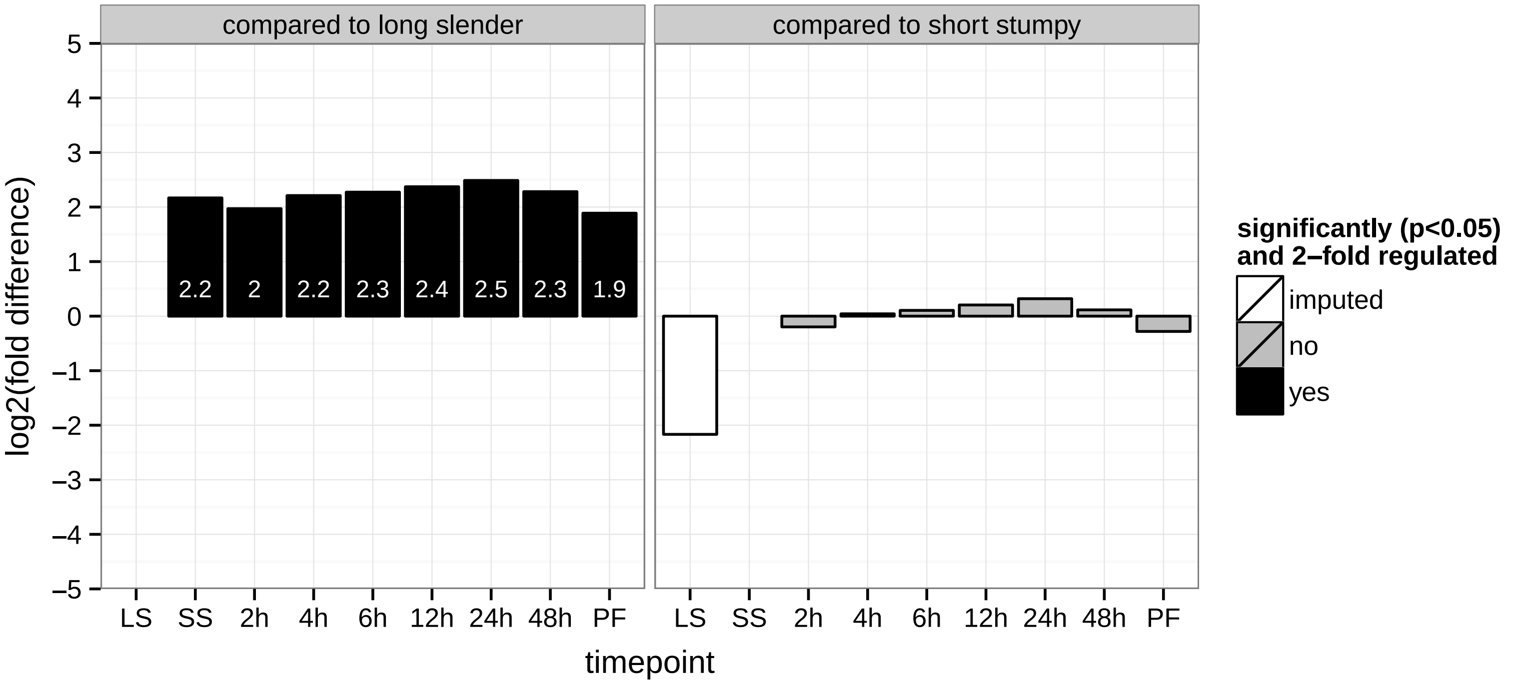
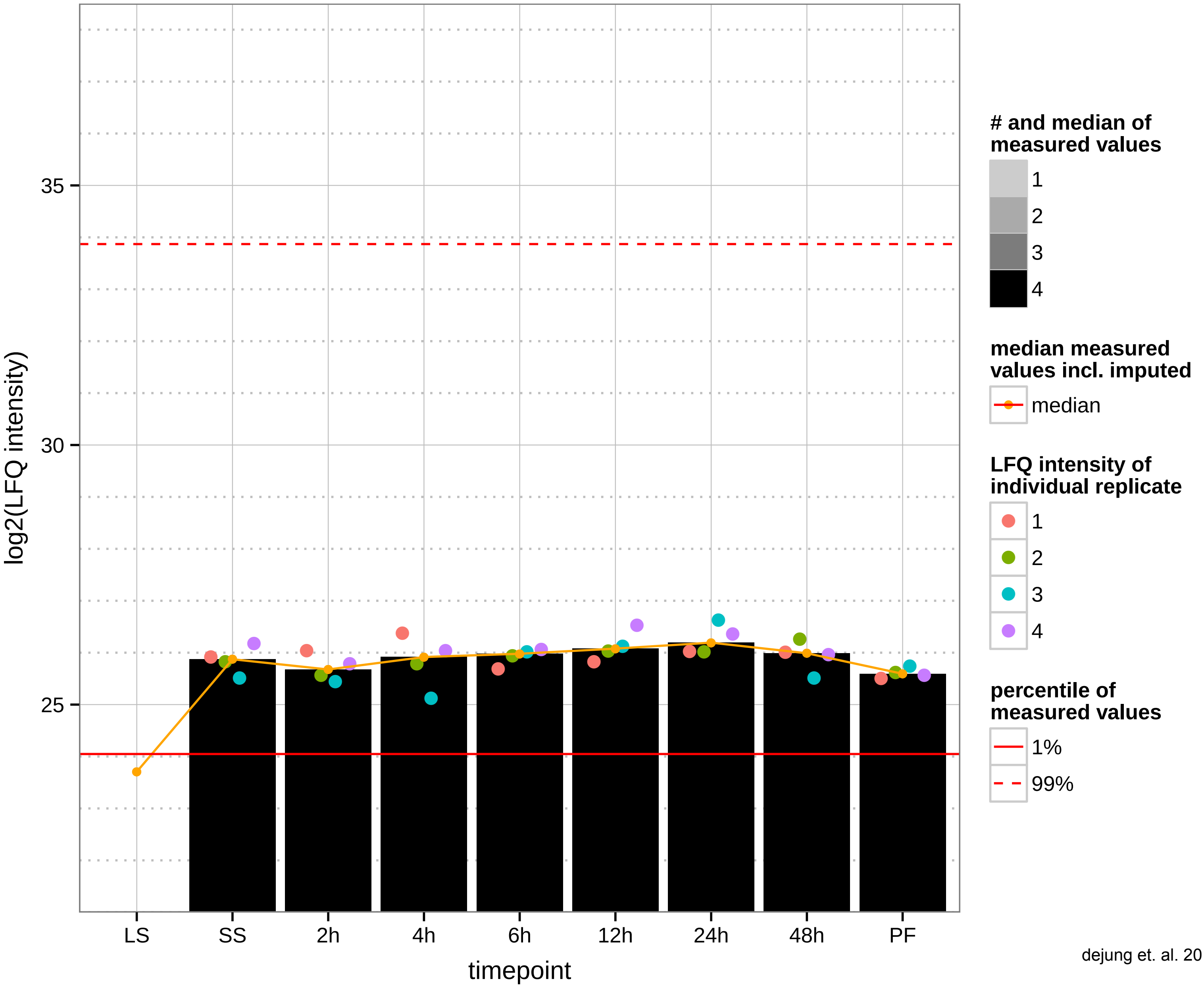
ATP−dependent DEAD/H RNA helicase, putative
Tb927.7.7300
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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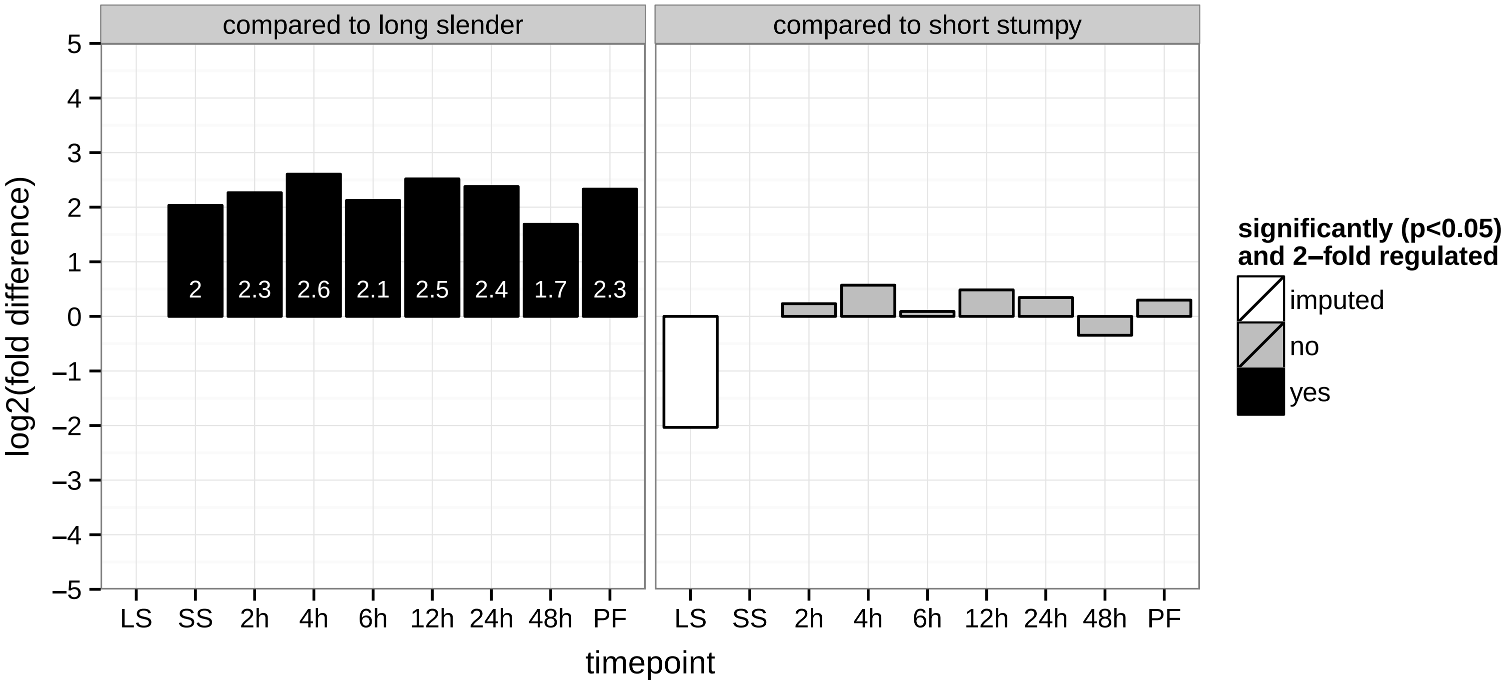
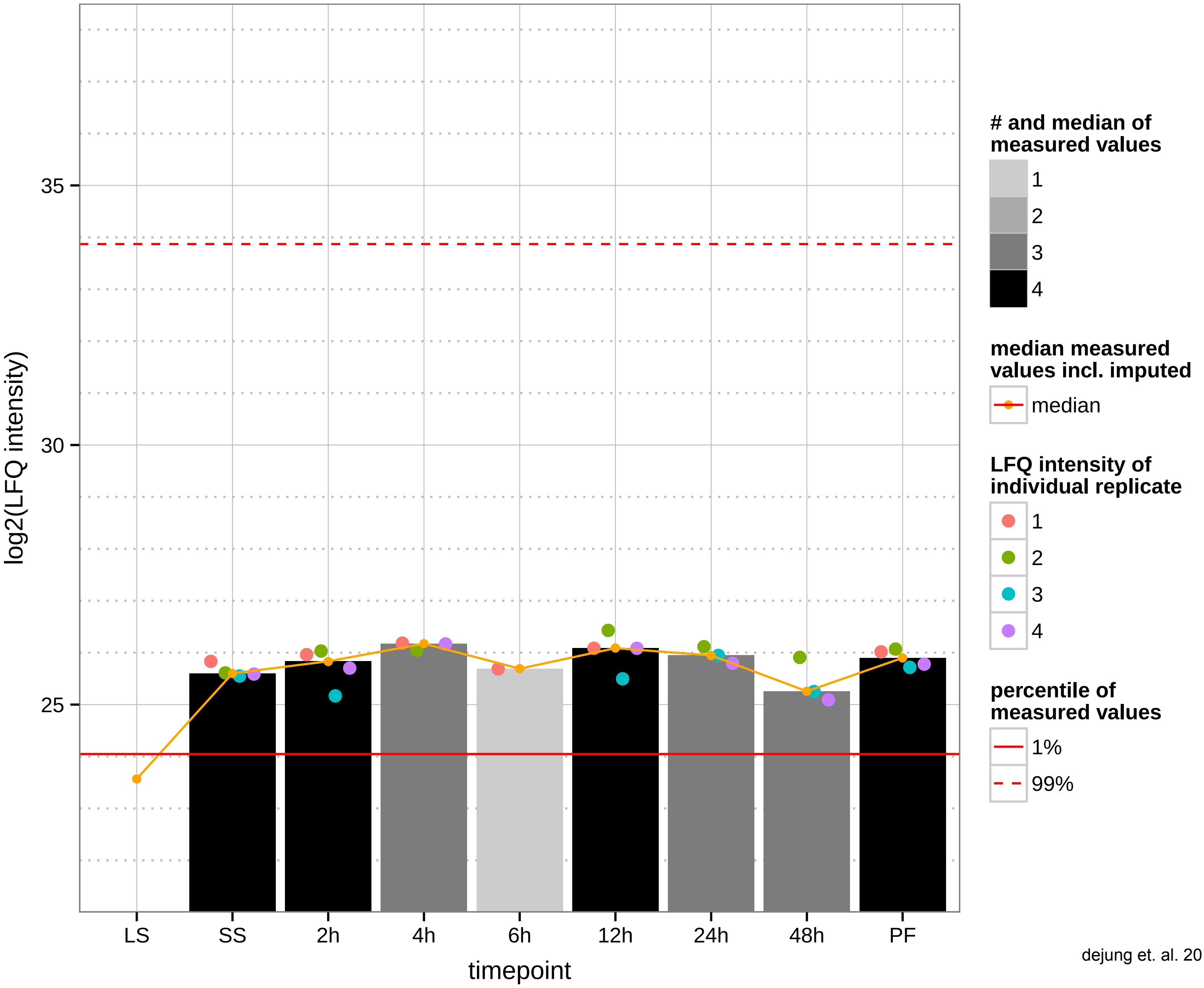
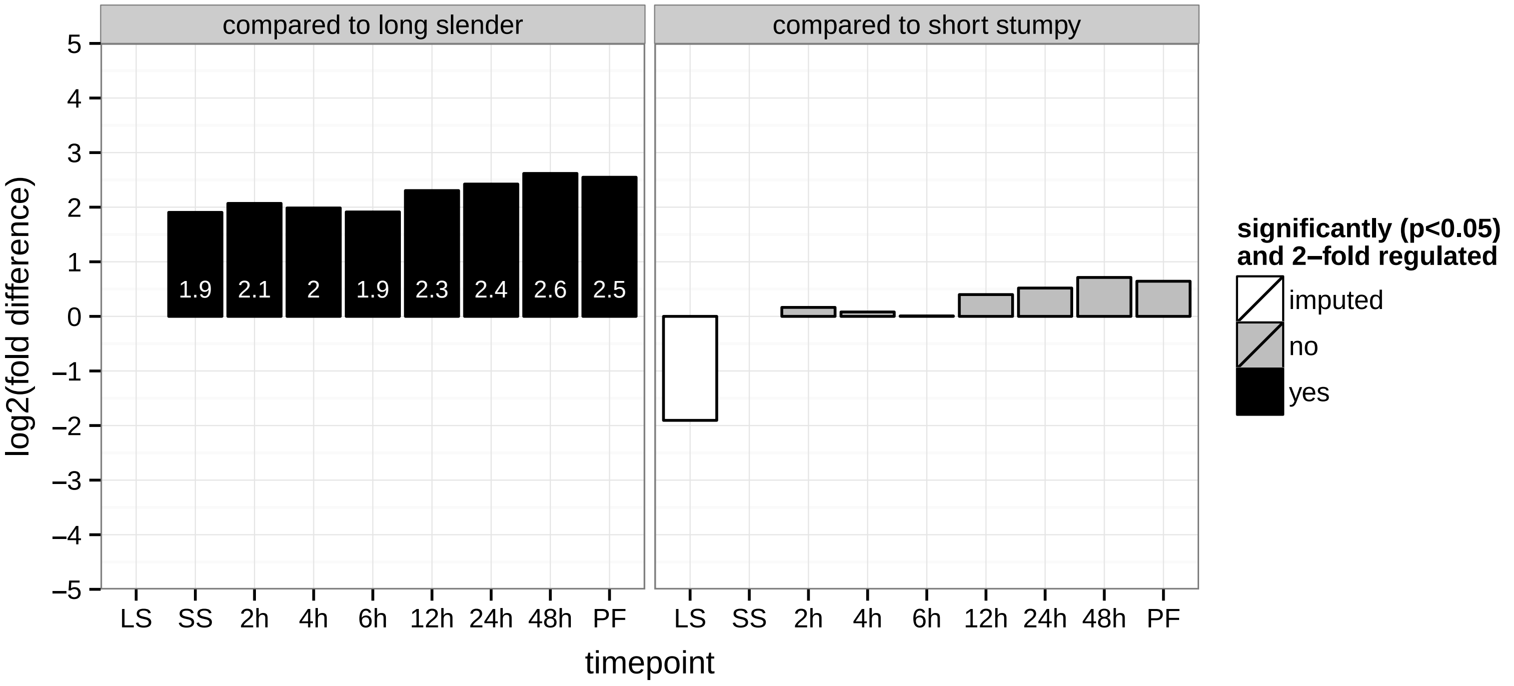
hypothetical protein, conserved
Tb927.7.7320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

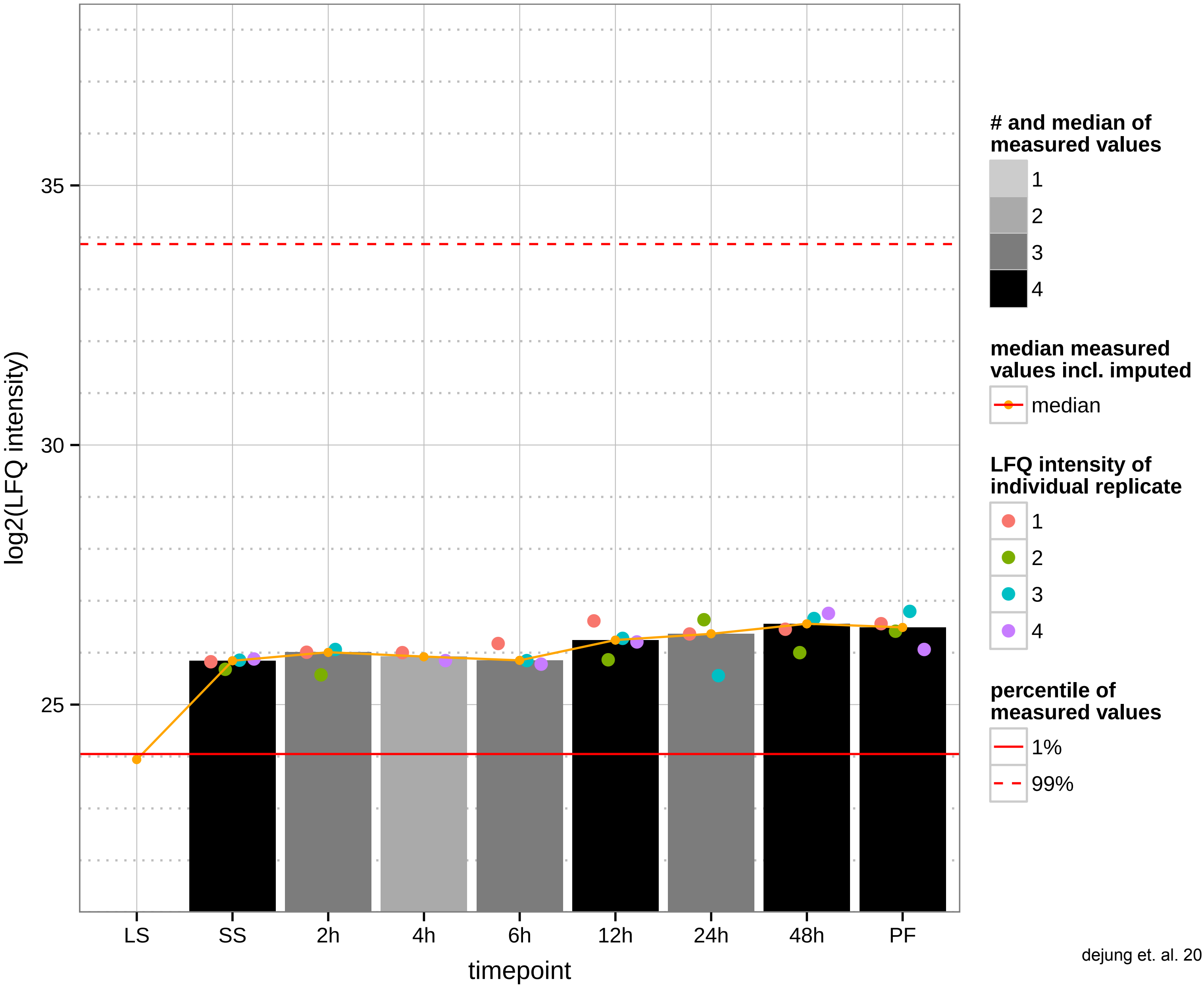




dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.7330
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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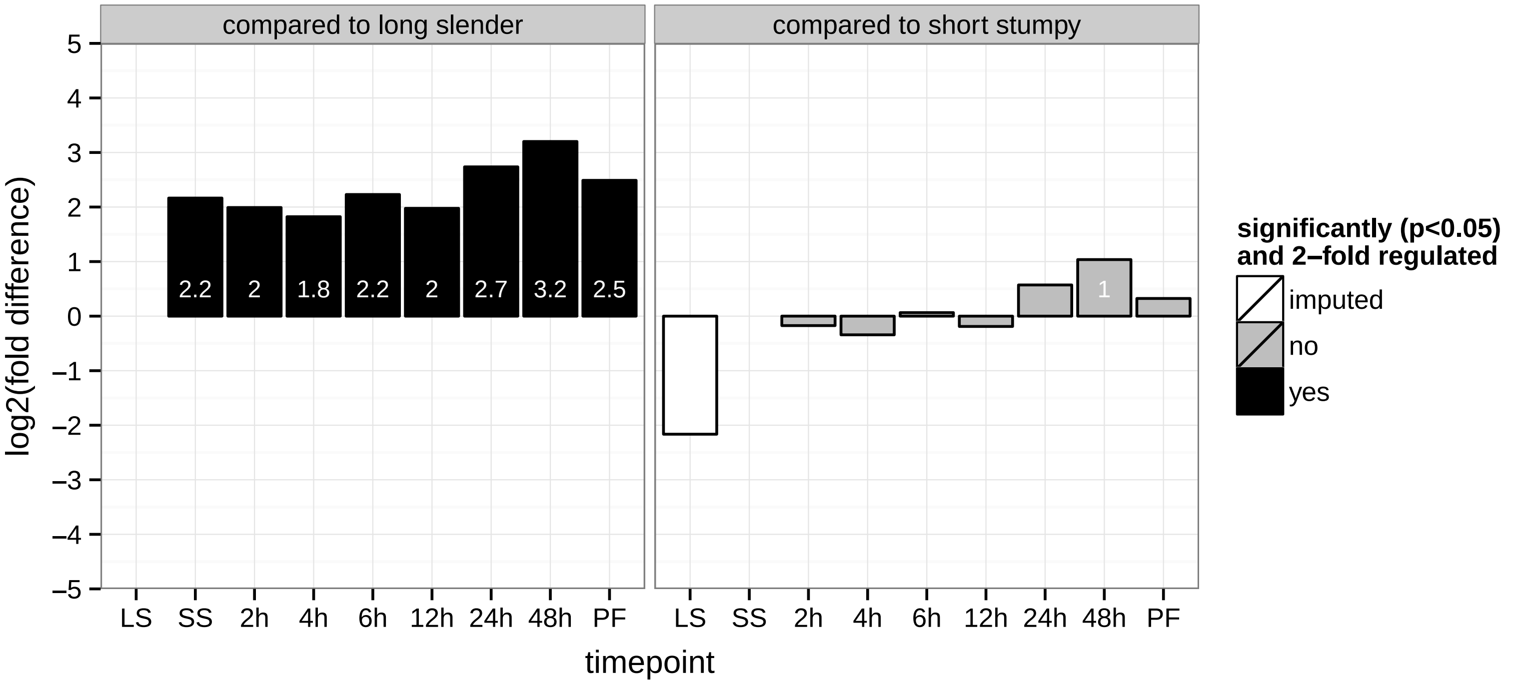
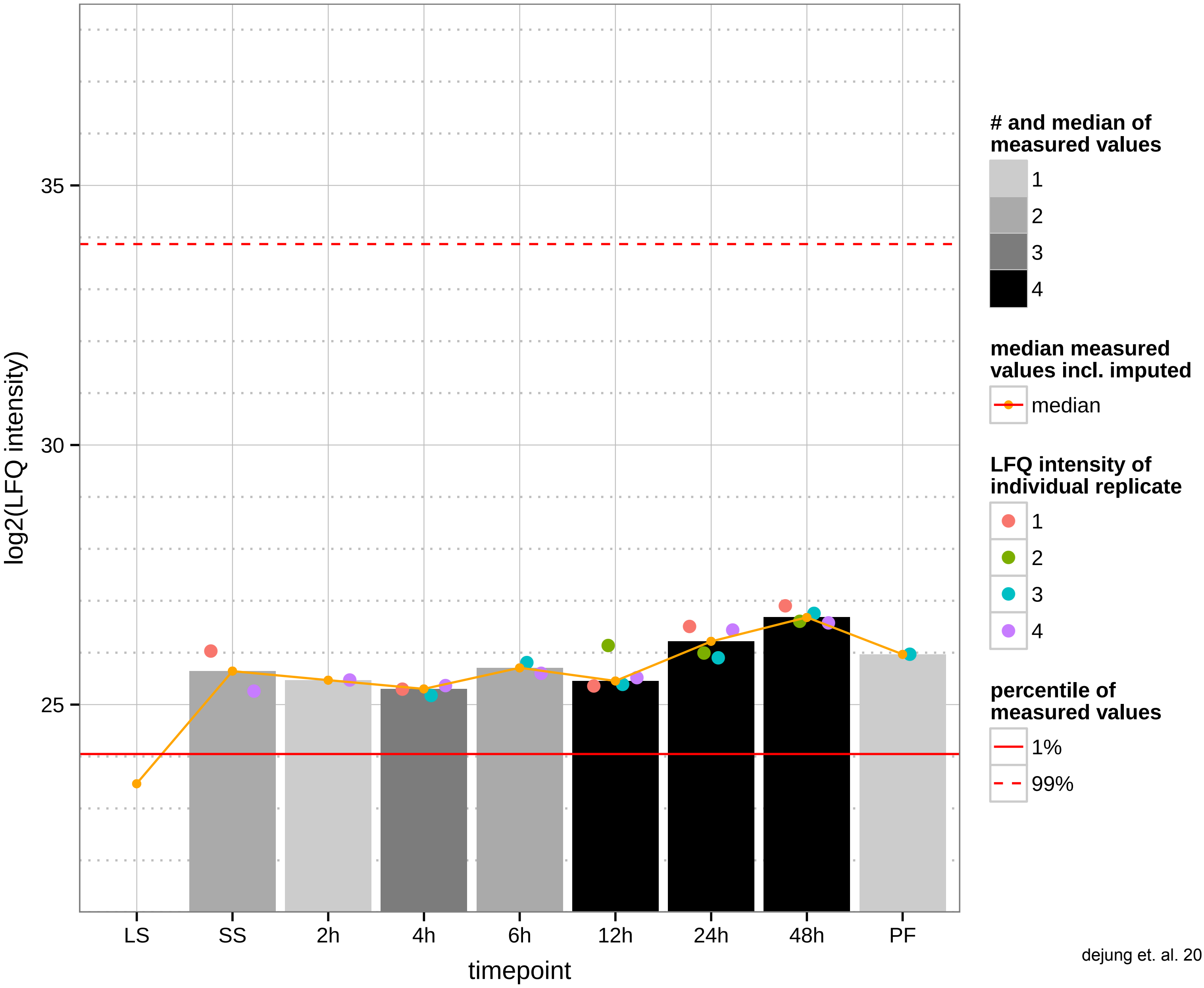
chaperone protein DNAj, putative
Tb927.7.740
AGOF: heat shock protein binding, unfolded protein binding
AGOC: integral to membrane, mitochondrion
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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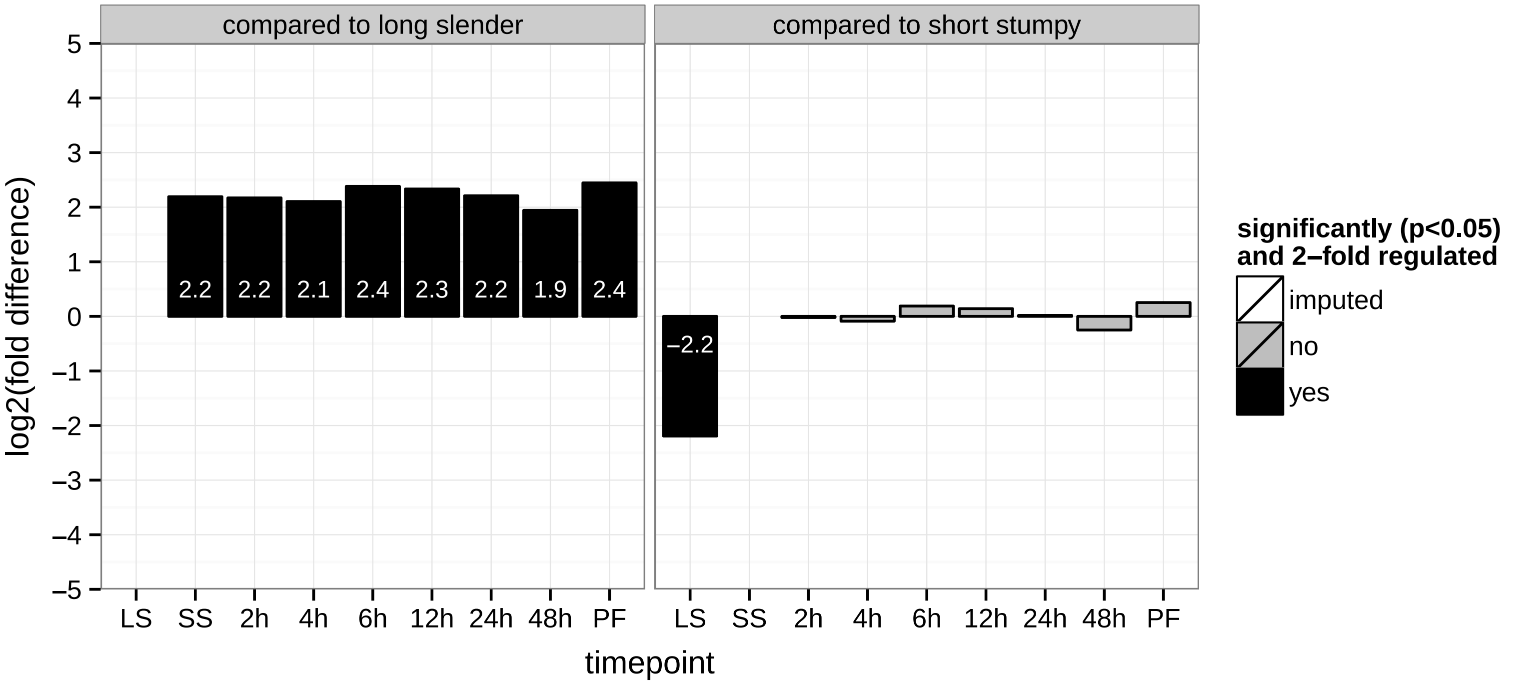
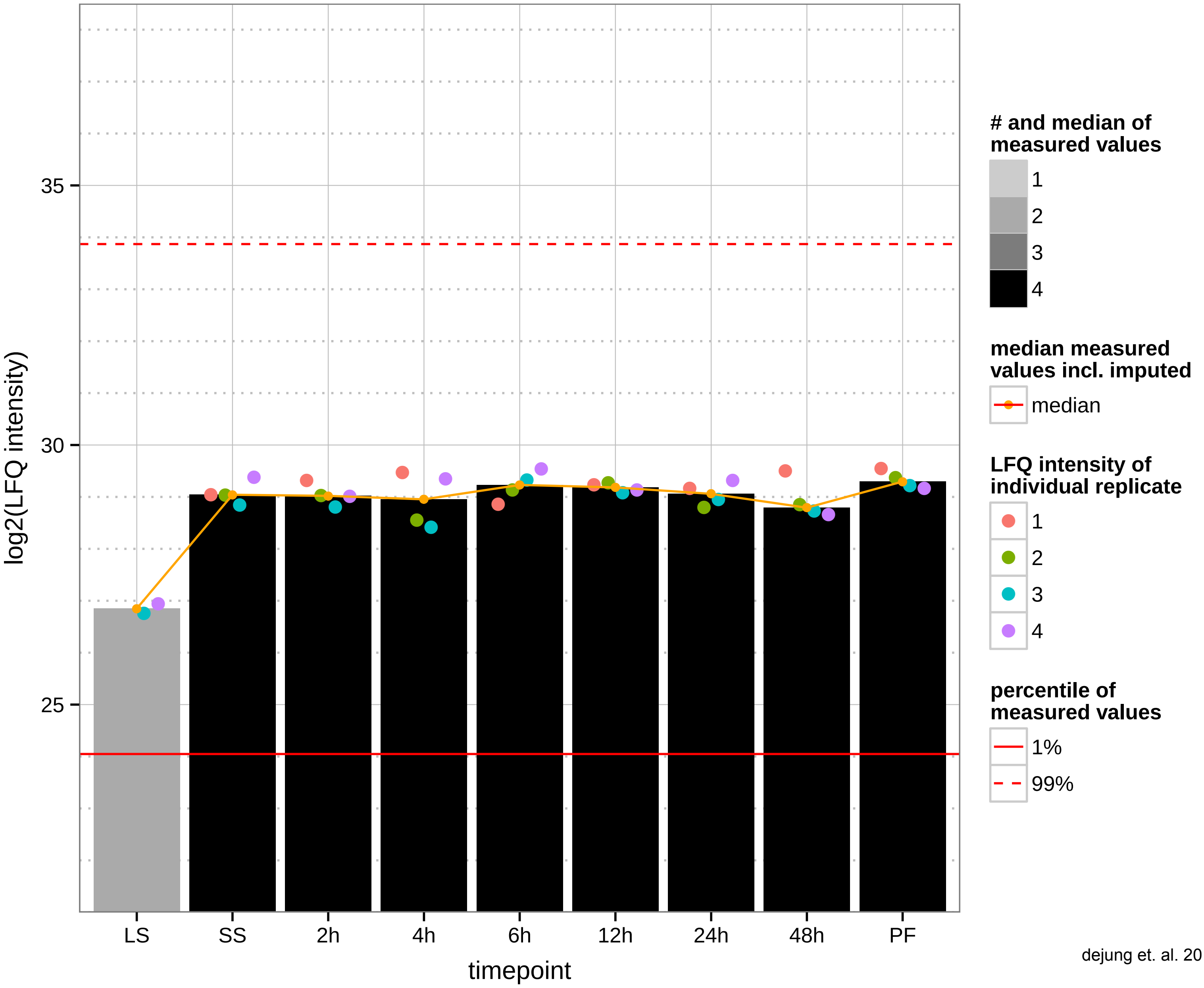
oxidoreductase, putative
Tb927.7.7410
AGOF: oxidoreductase activity, zinc ion binding
AGOC: mitochondrion
AGOP: metabolic process, oxidation–reduction process
PGOF: null
PGOC: null
PGOP: null





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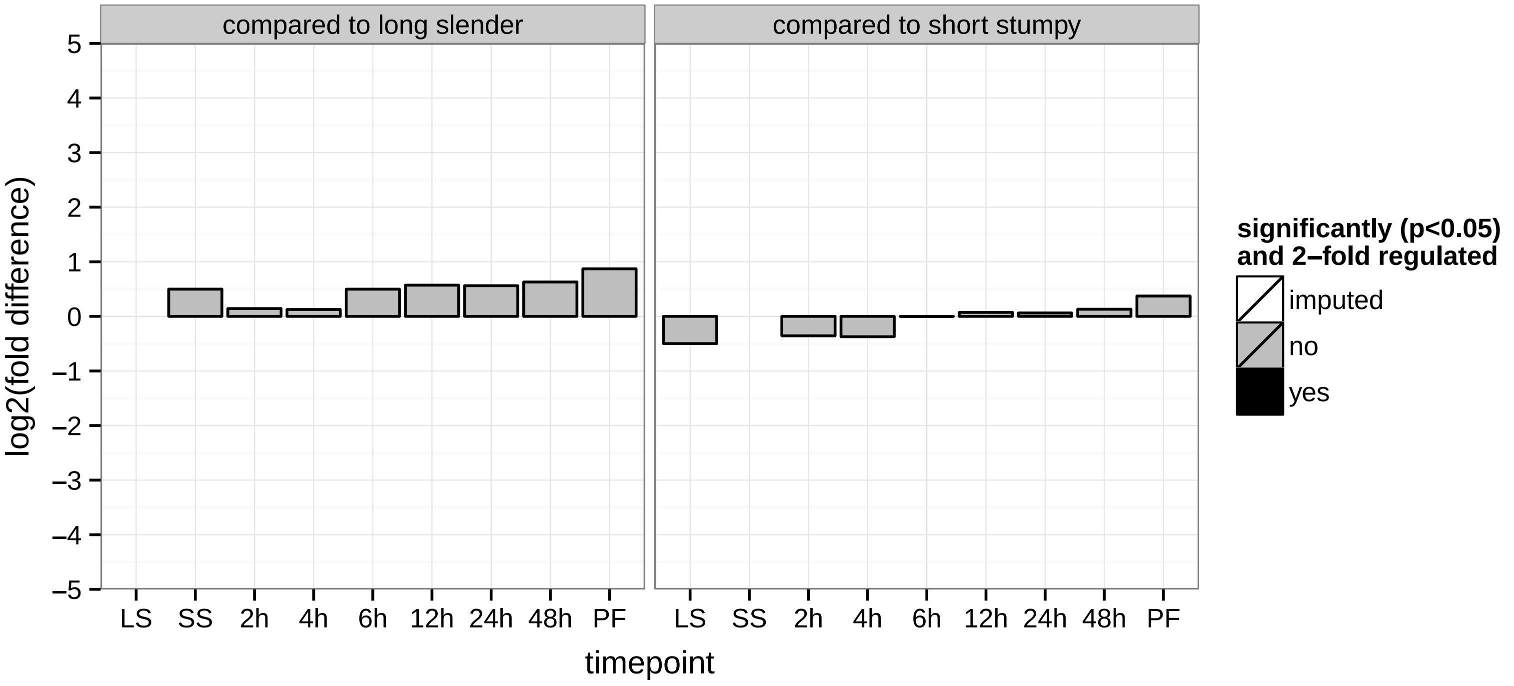
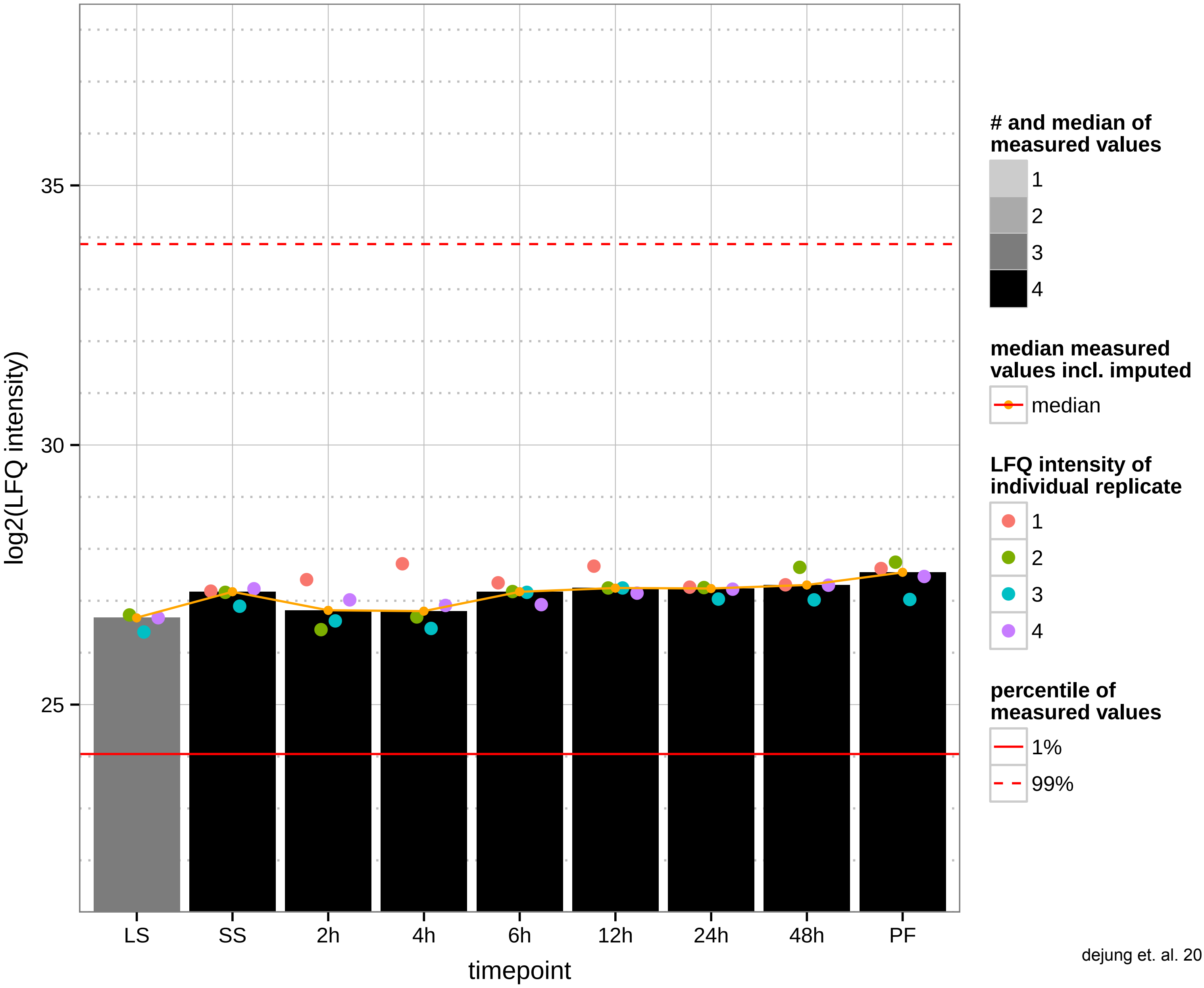
GTP–binding protein, putative
Tb927.7.7450
AGOF: GTP binding
AGOC: intracellular
AGOP: null
PGOF: GTP binding
PGOC: null
PGOP: null





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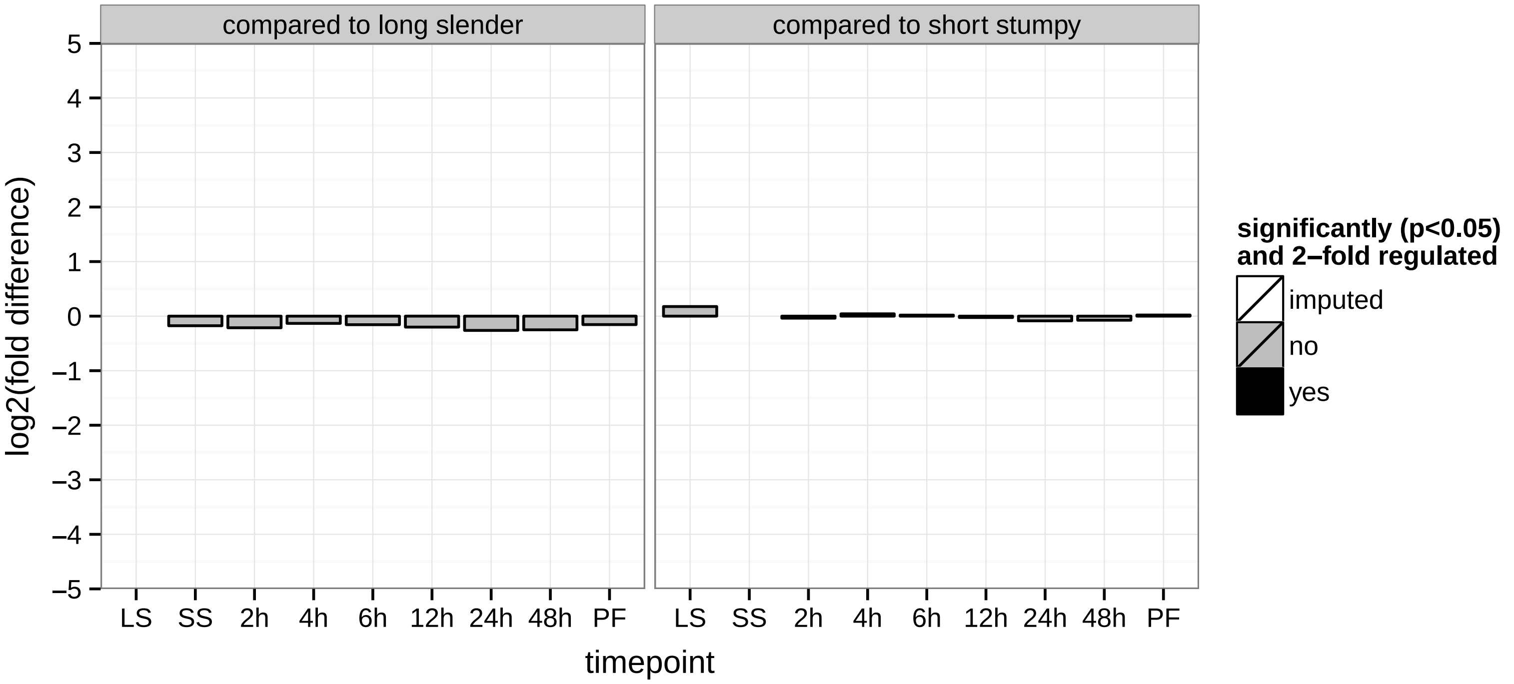
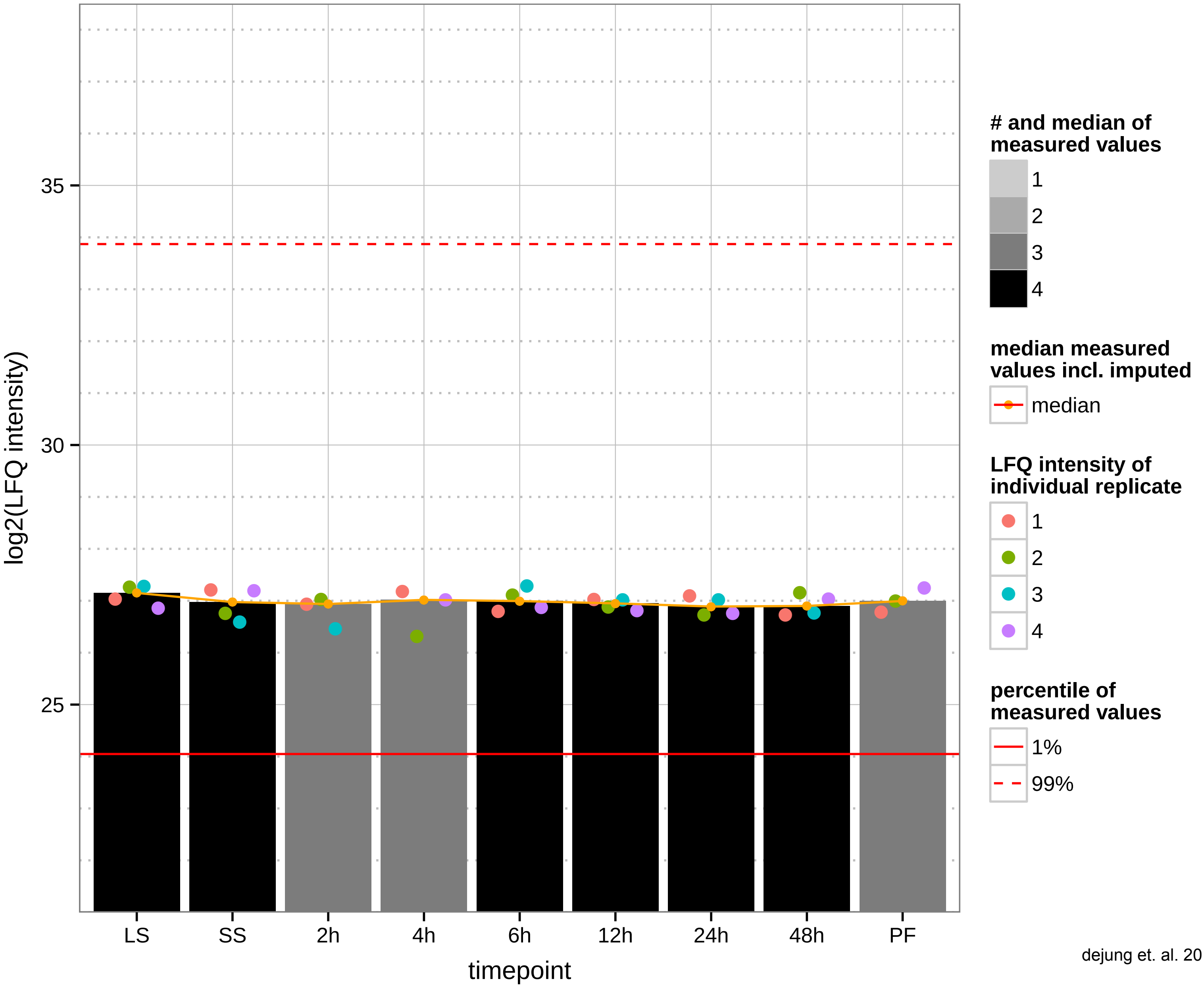
hypothetical protein, conserved
Tb927.7.760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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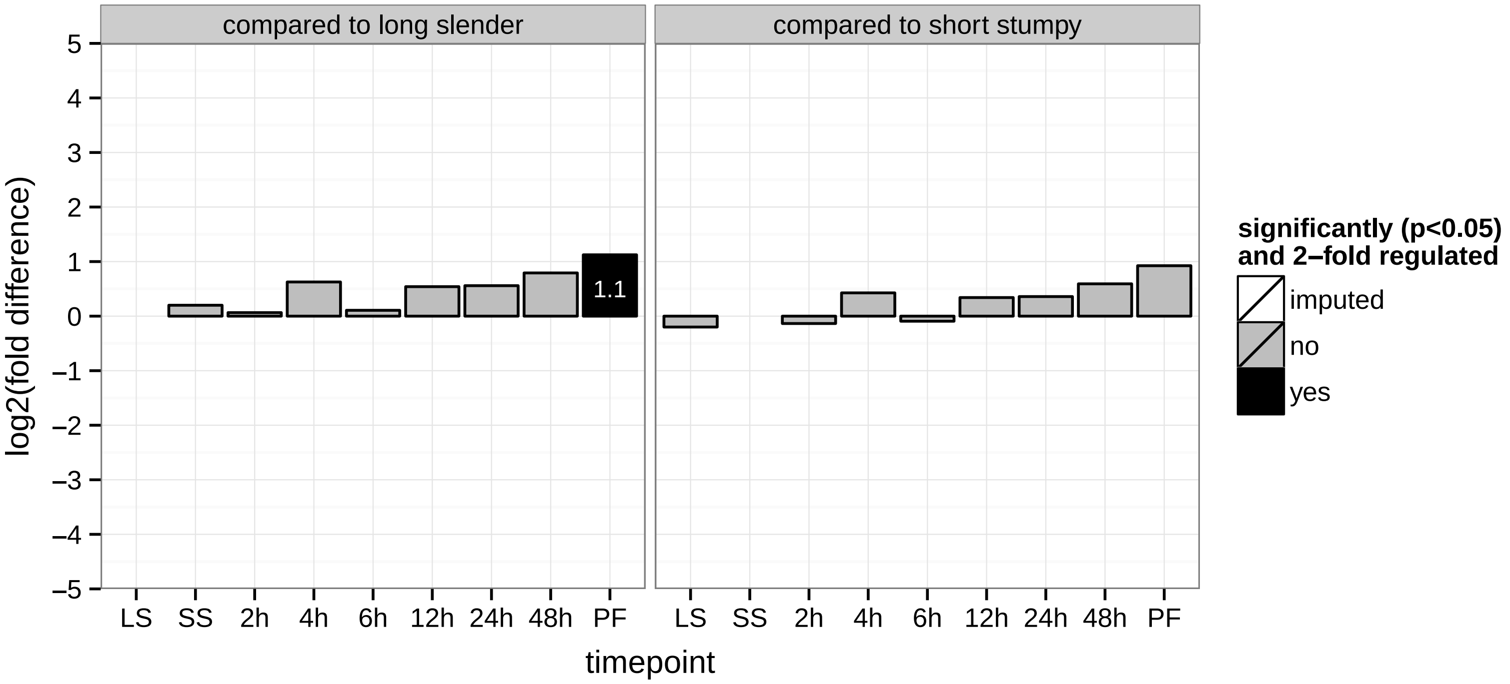
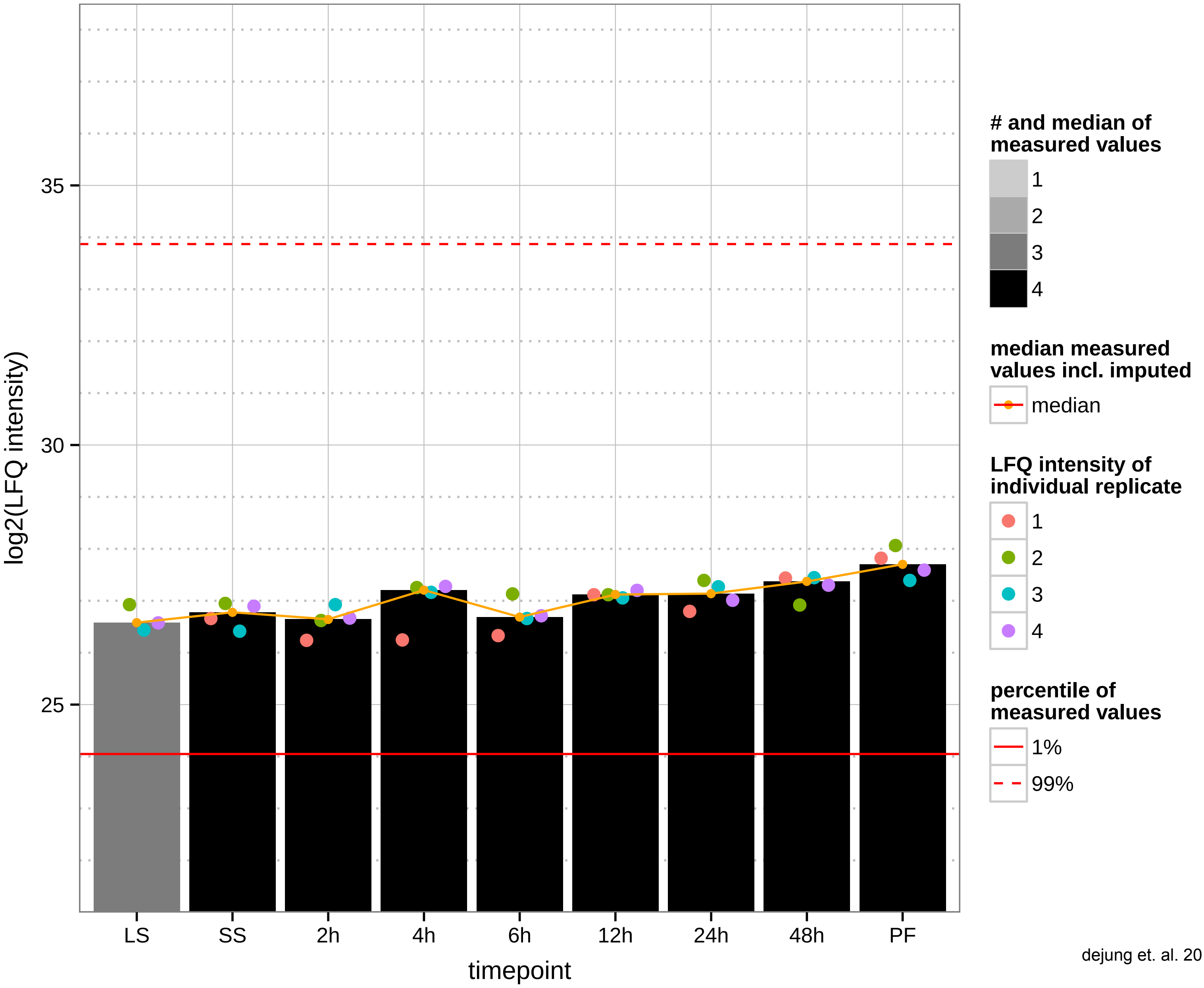
RNA–binding protein, putative (RPB25)
Tb927.7.880
AGOF: RNA binding
AGOC: cytosol, nucleus
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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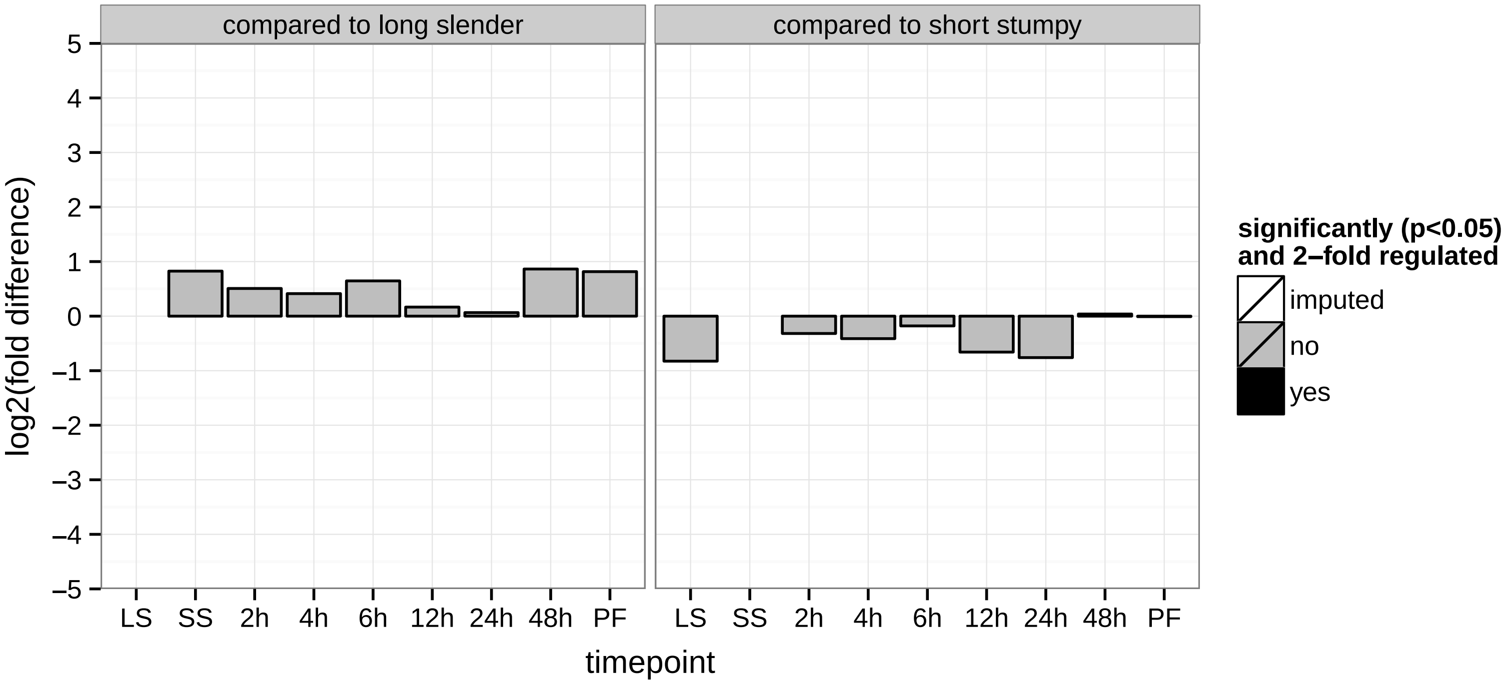
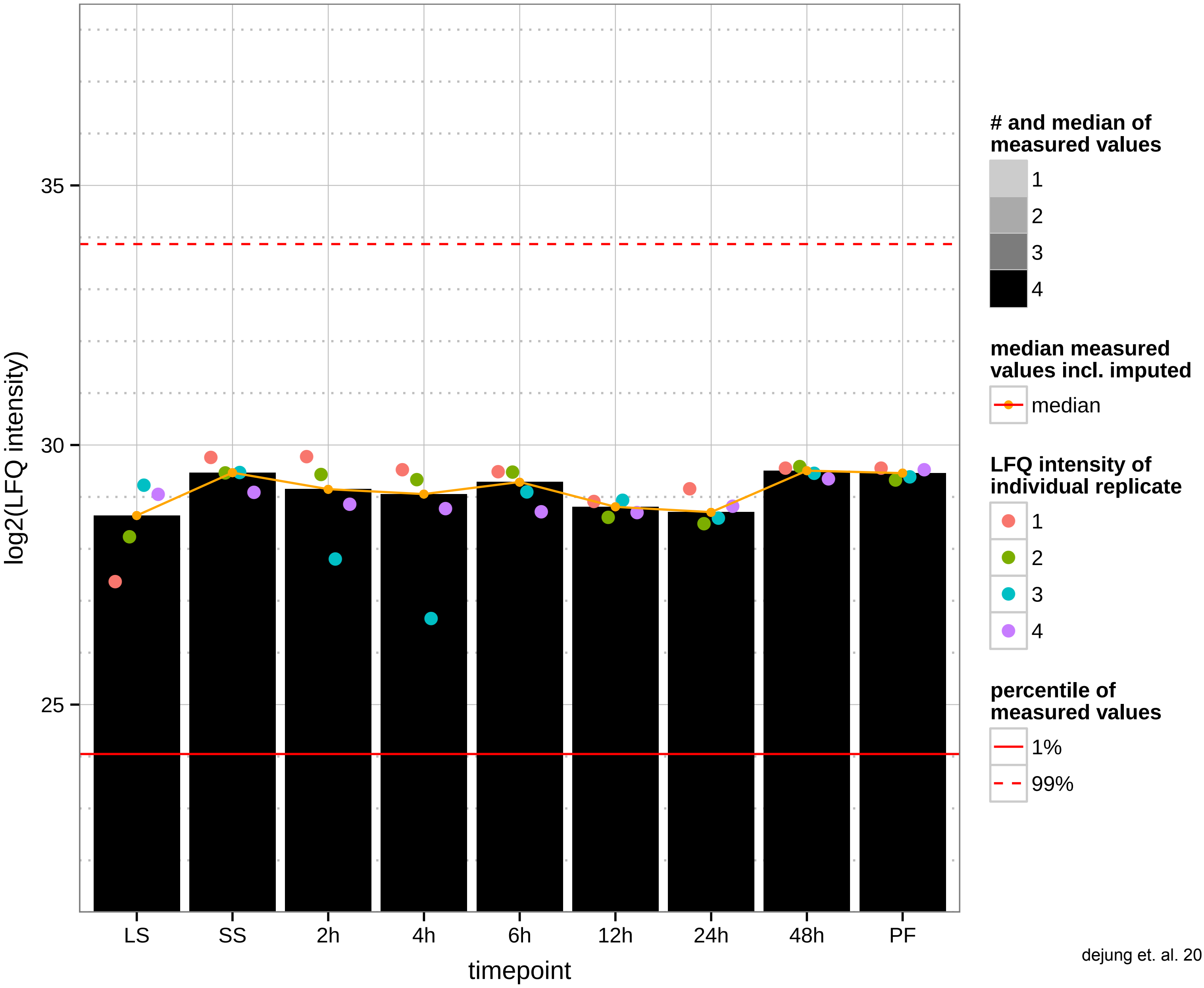
dynein heavy chain, putative
Tb927.7.920
AGOF: null, ATP binding, ATPase activity, microtubule motor activity
AGOC: null, dynein complex
AGOP: null, microtubule–based movement
PGOF: null, microtubule motor activity
PGOC: null, dynein complex
PGOP: null, microtubule–based movement





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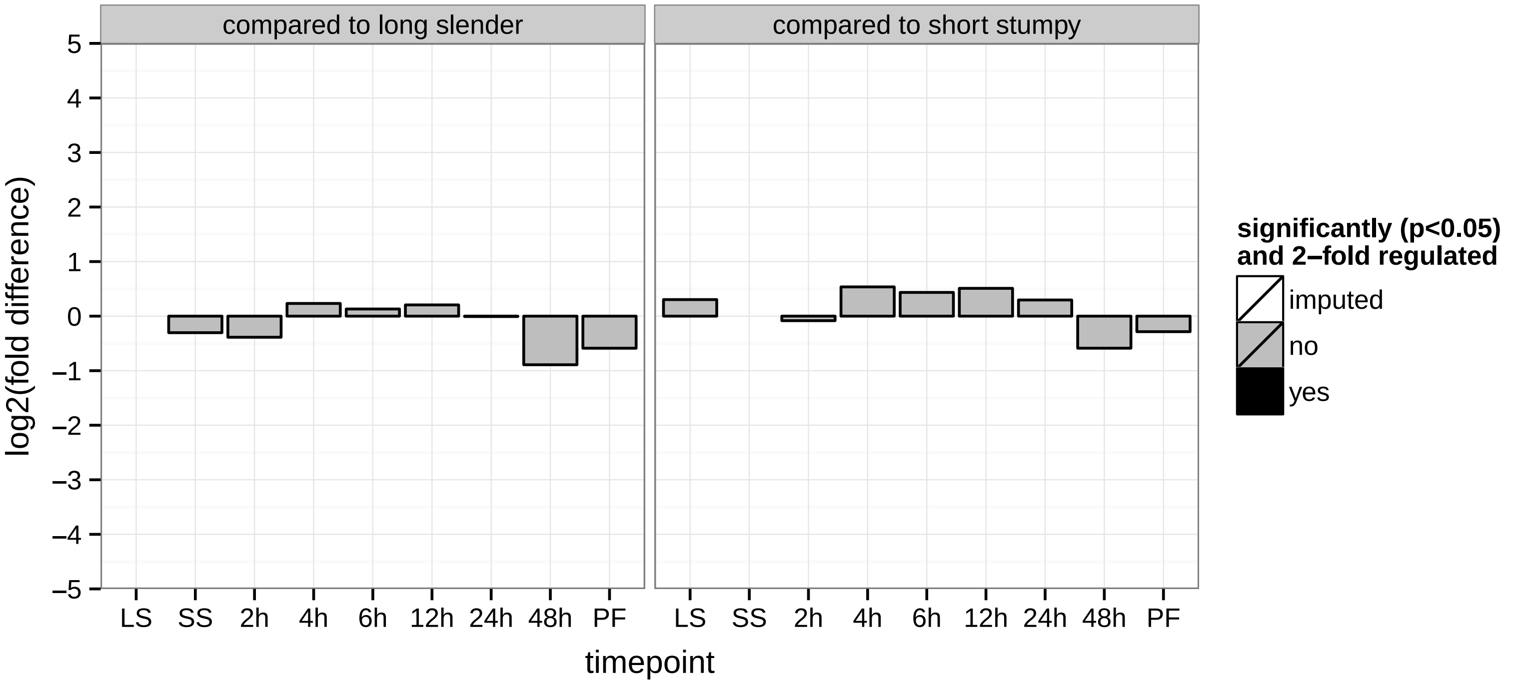
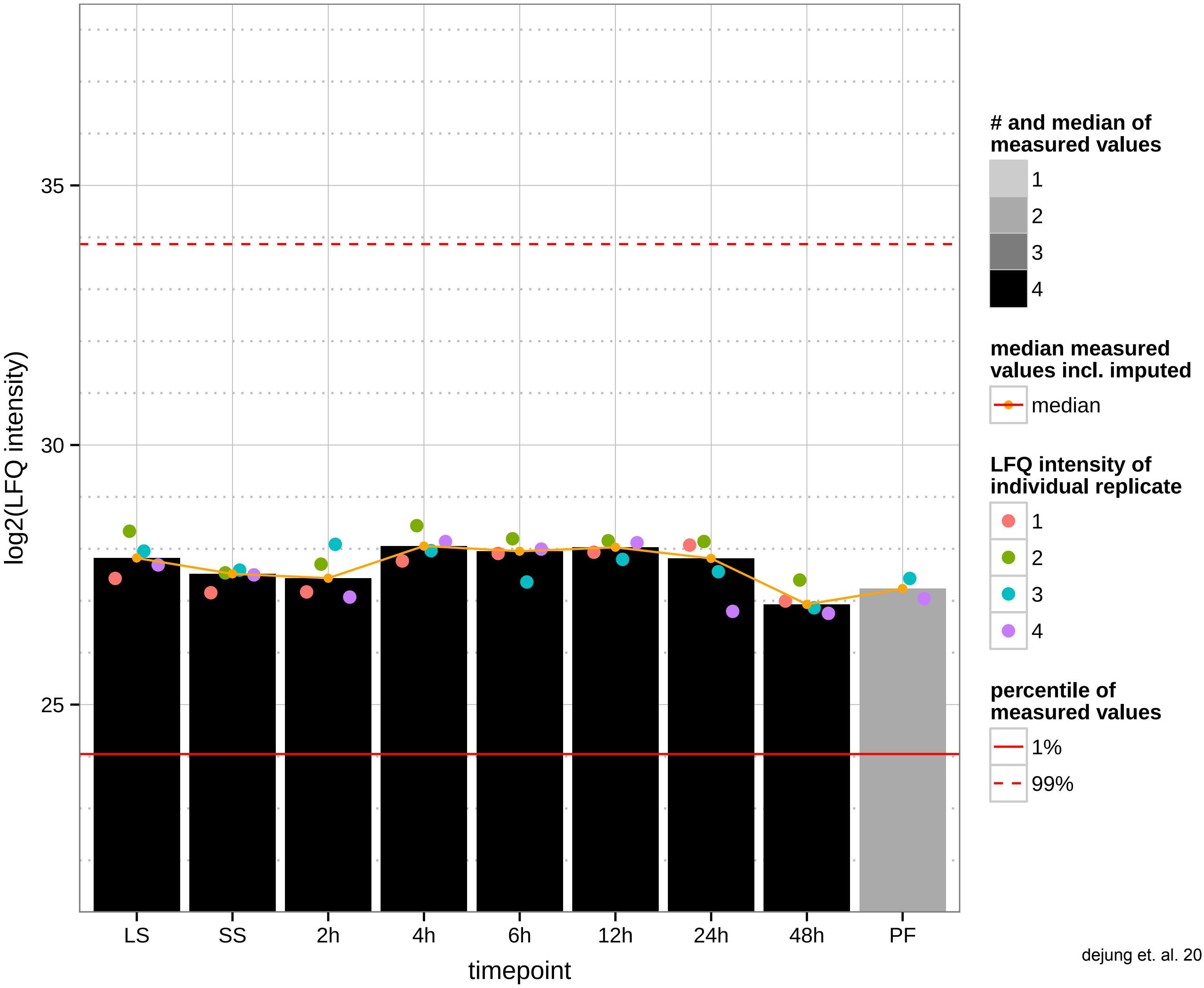
protein kinase C substrate protein, heavy chain, putative, glucosidase II beta subunit
Tb927.7.940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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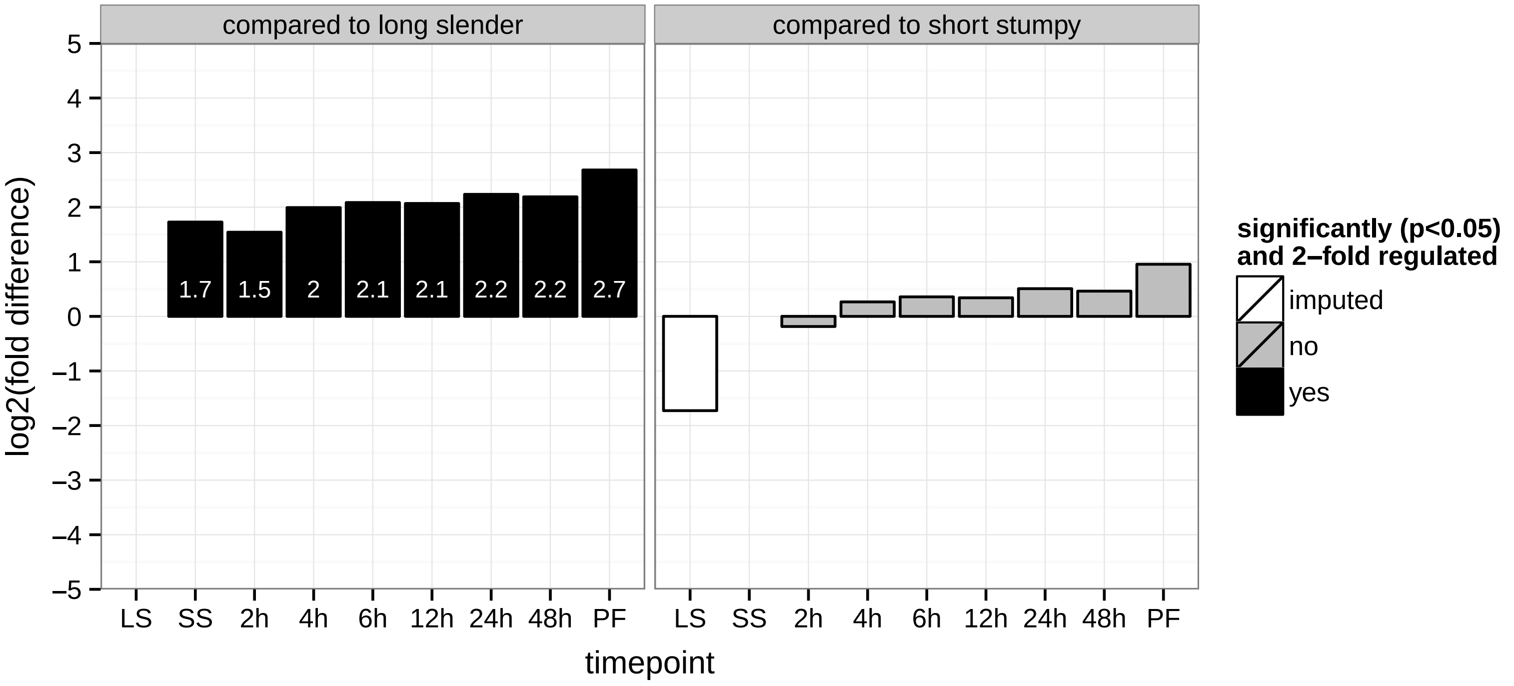
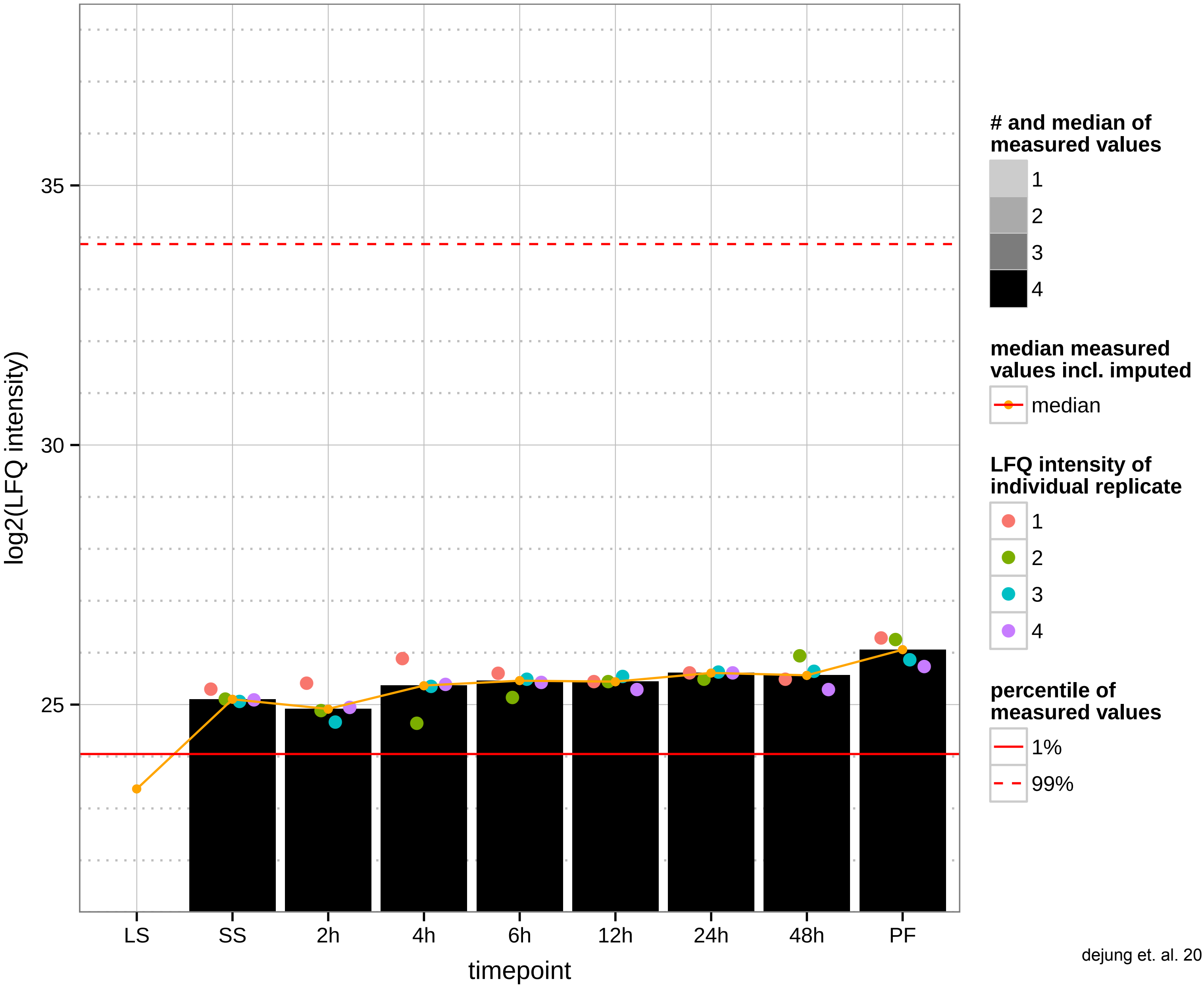
NPAPL, nuclear−poly(A)−polymerase−like (NPAPL)
Tb927.8.1090
AGOF: ATP−dependent RNA helicase activity, nucleic acid binding, nucleotidyltransferase activity
AGOC: nucleus
AGOP: null
PGOF: nucleotidyltransferase activity
PGOC: null
PGOP: null





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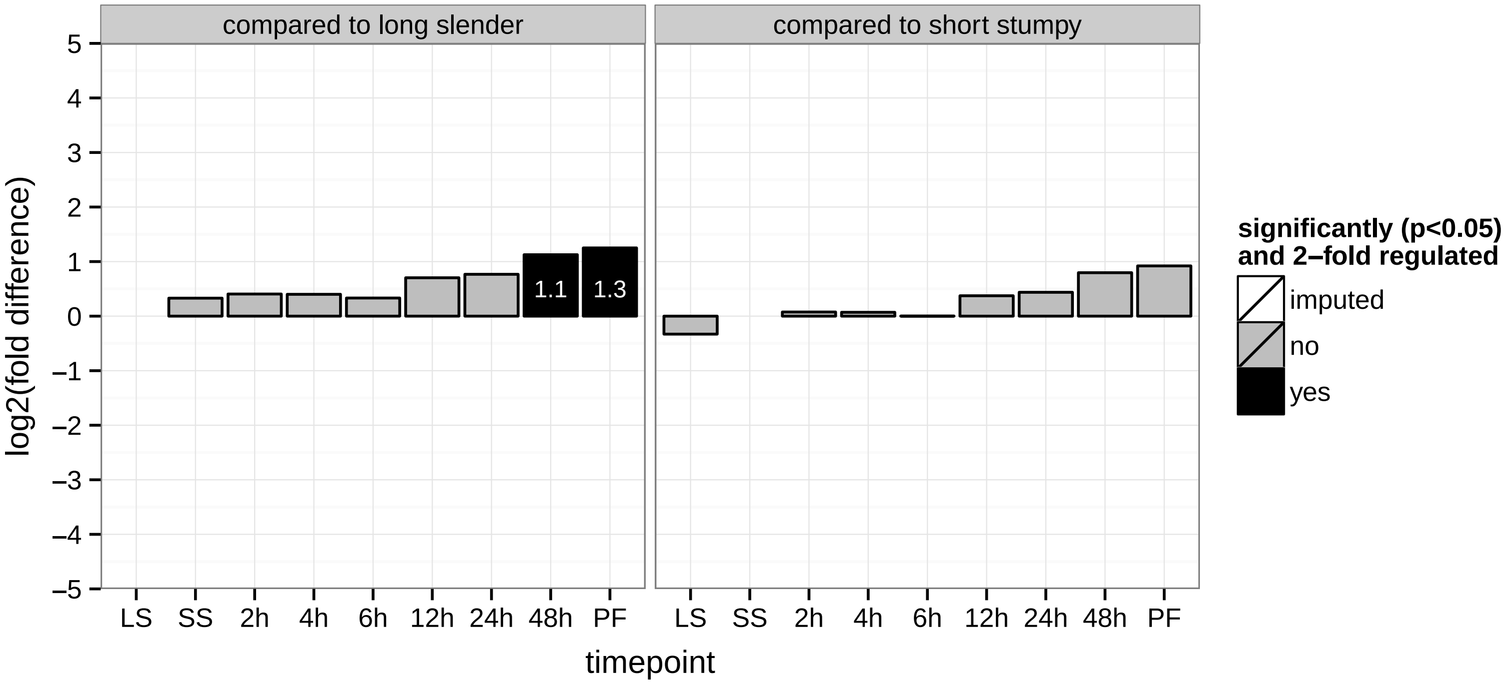
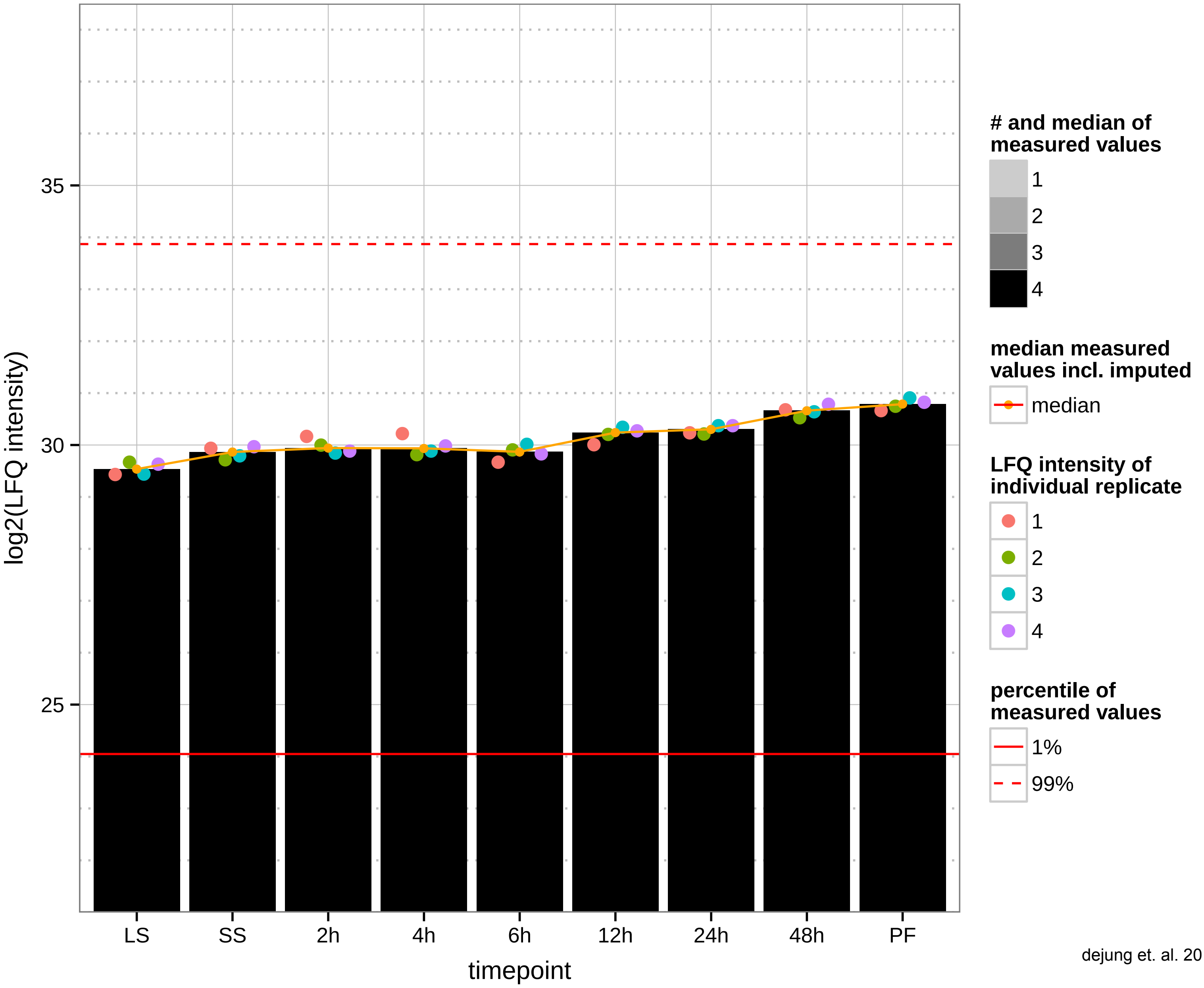
hypothetical protein, conserved
Tb927.8.1190;Tb927.8.1170;Tb11.v5.0871
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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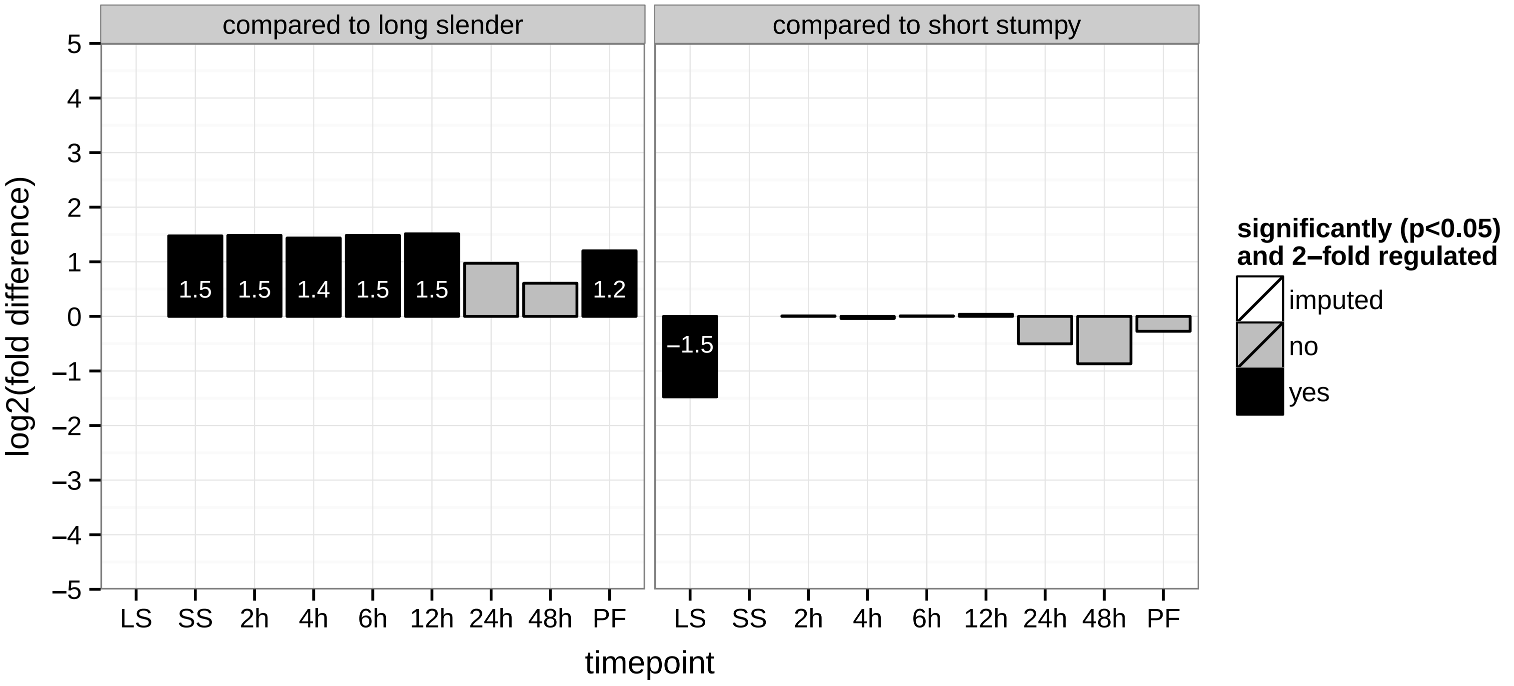
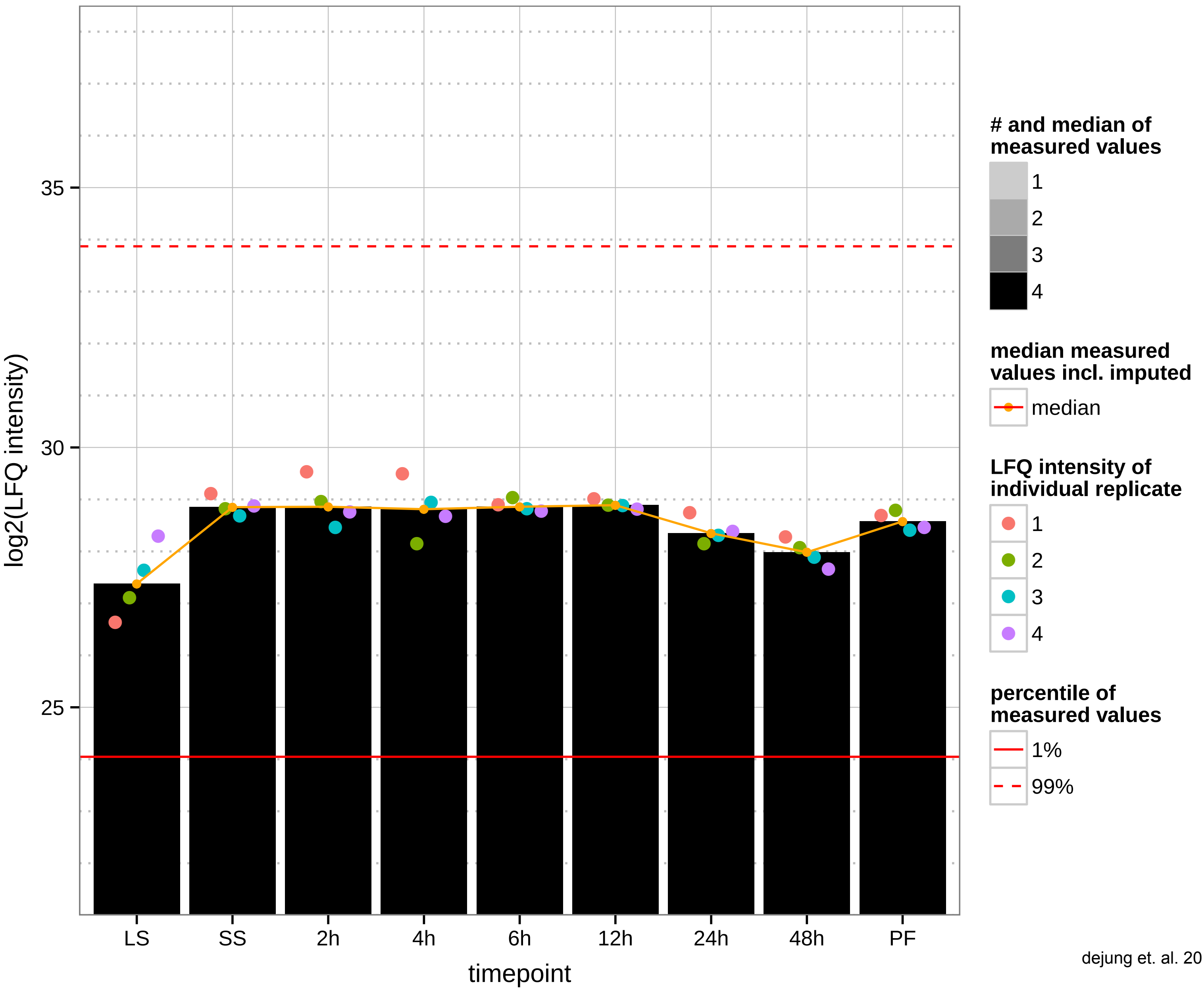
vacuolar–type Ca2+–ATPase 2 (TbA2)
Tb927.8.1200
AGOF: ATP binding, calcium–transporting ATPase activity
AGOC: plasma membrane
AGOP: ATP biosynthetic process, calcium ion transport, cell growth, cellular calcium ion homeostasis, metabolic process
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, calcium–tra
PGOC: membrane
PGOP: ATP biosynthetic process, calcium ion transmembrane transport, cation transport, metabolic process





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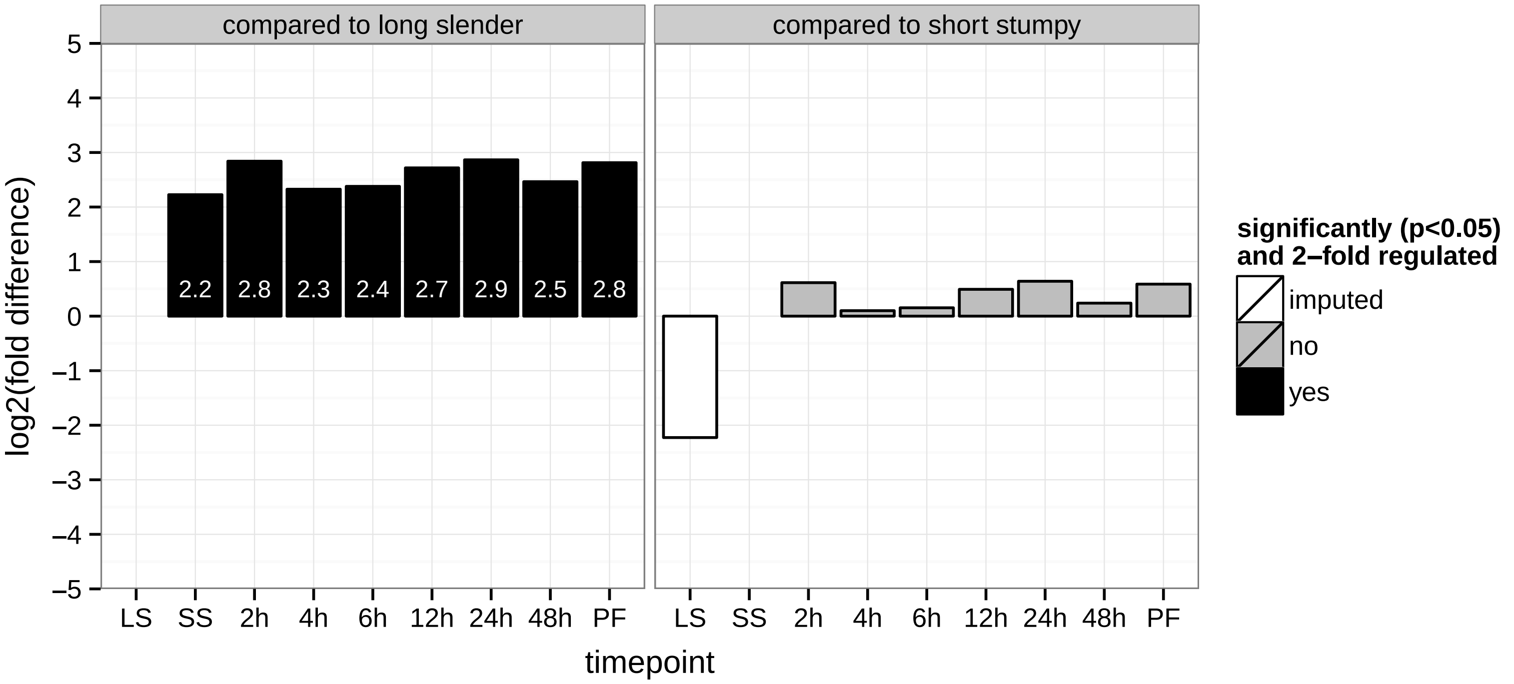
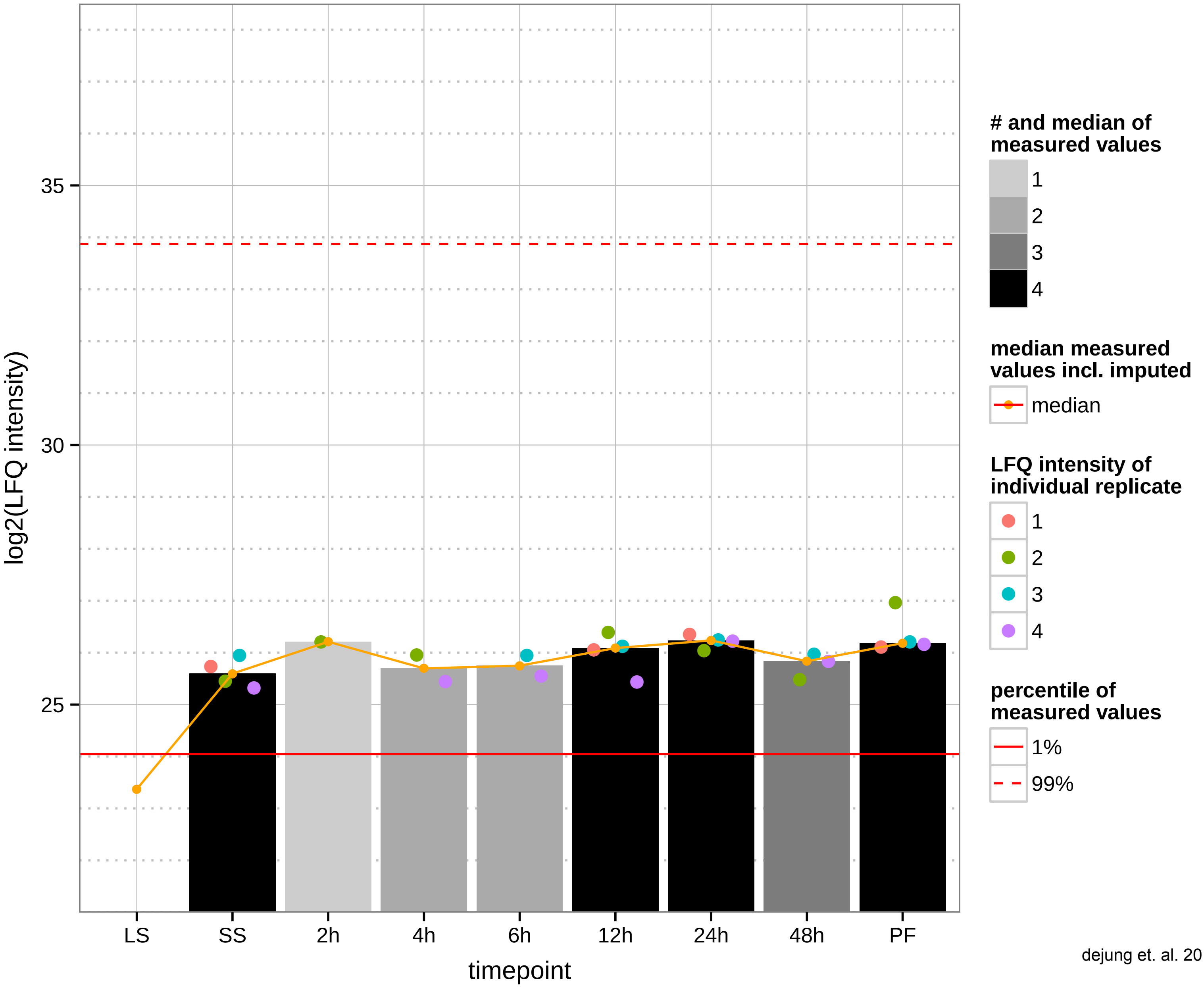
hypothetical protein, conserved (pseudogene)
Tb927.8.1220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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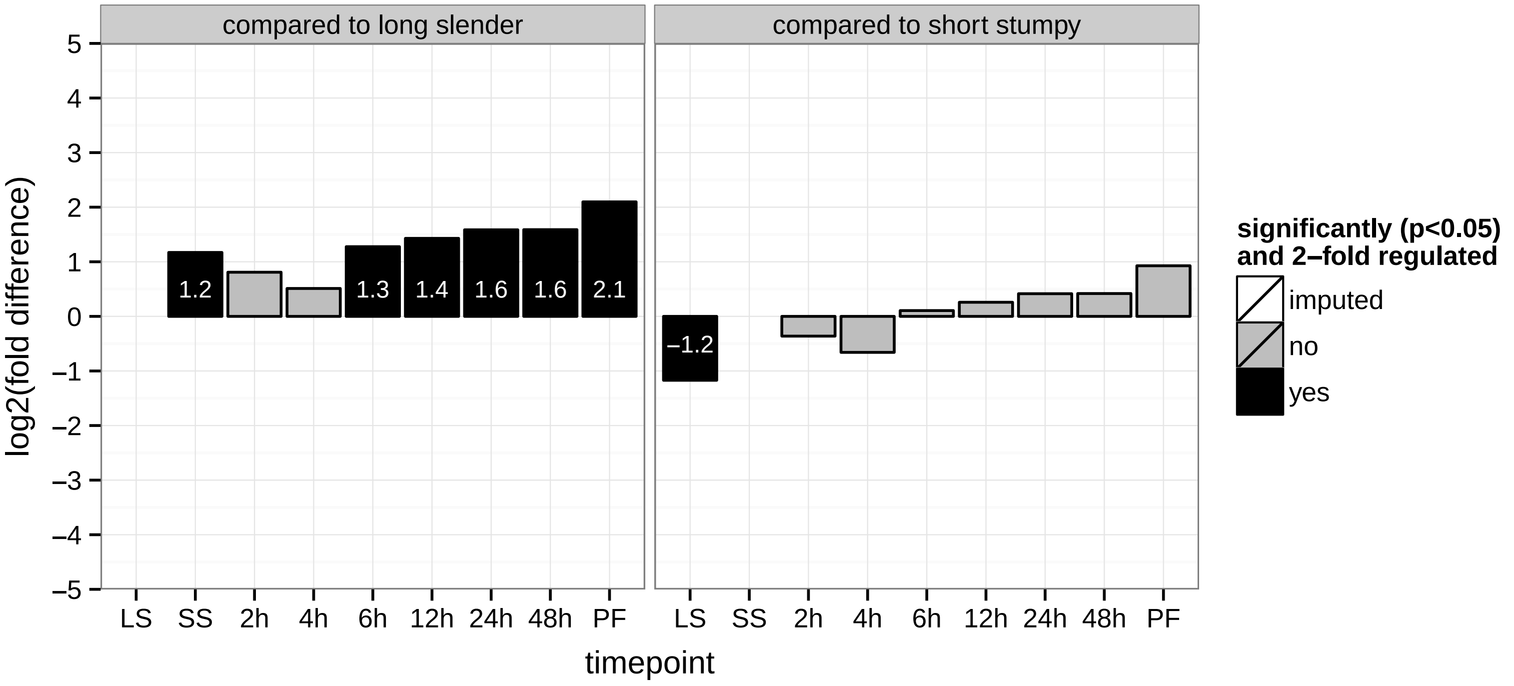
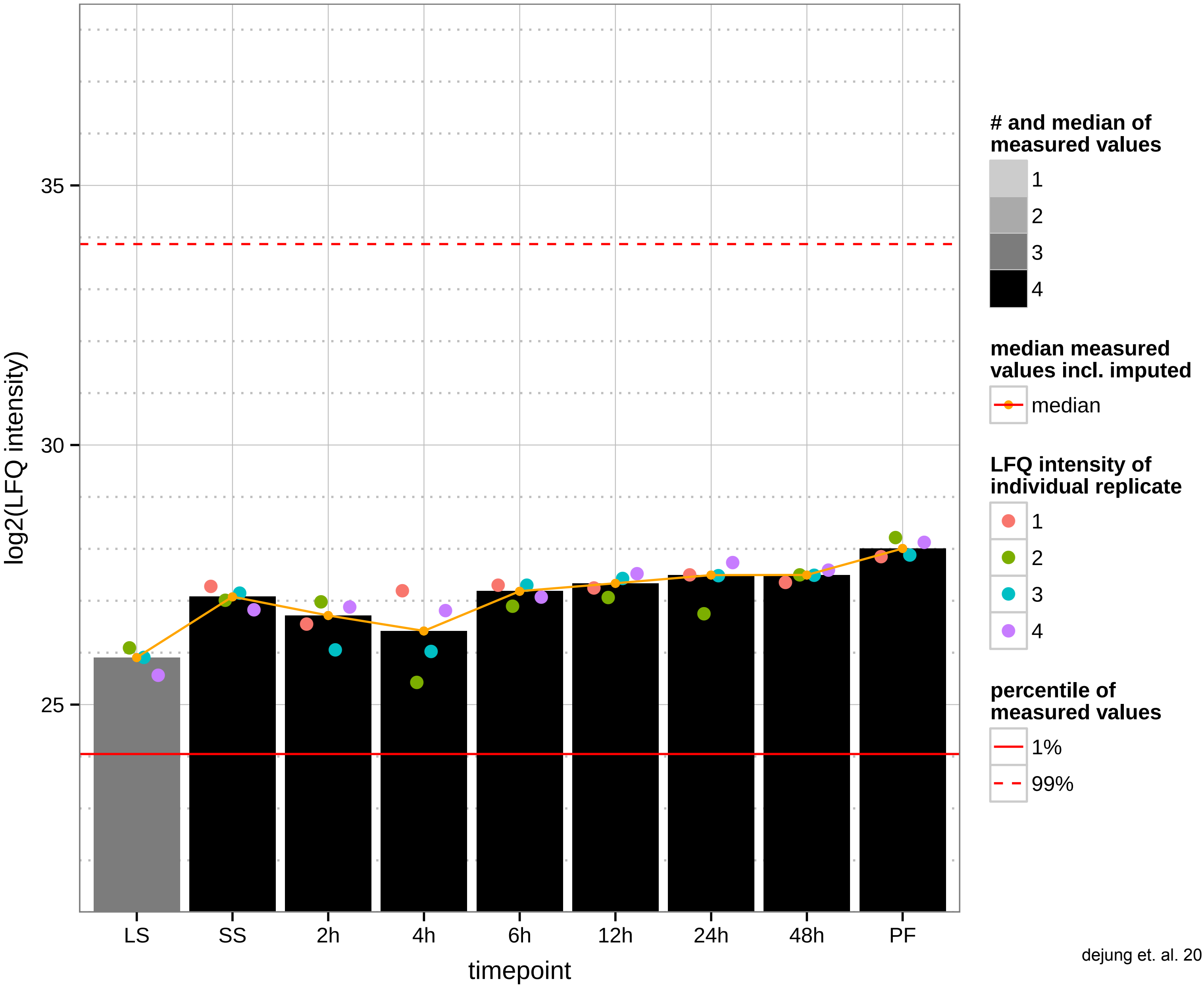
hypothetical protein, conserved, pre−rrna−processing protein tsr1 homolog
Tb927.8.1410;Tb11.v5.0588
AGOF: null
AGOC: null, cytoplasm, nucleolus, nucleus
AGOP: null, ribosome biogenesis
PGOF: null
PGOC: nucleus
PGOP: ribosome biogenesis





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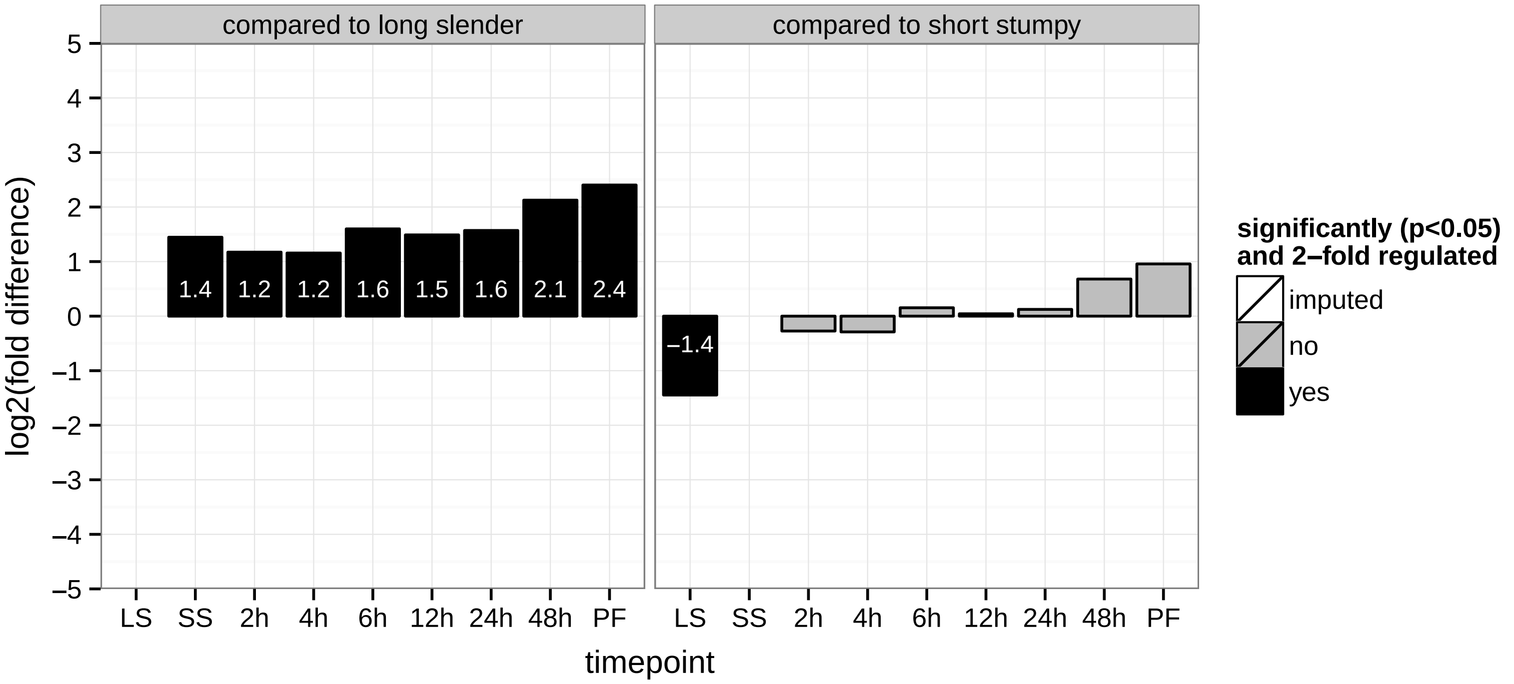
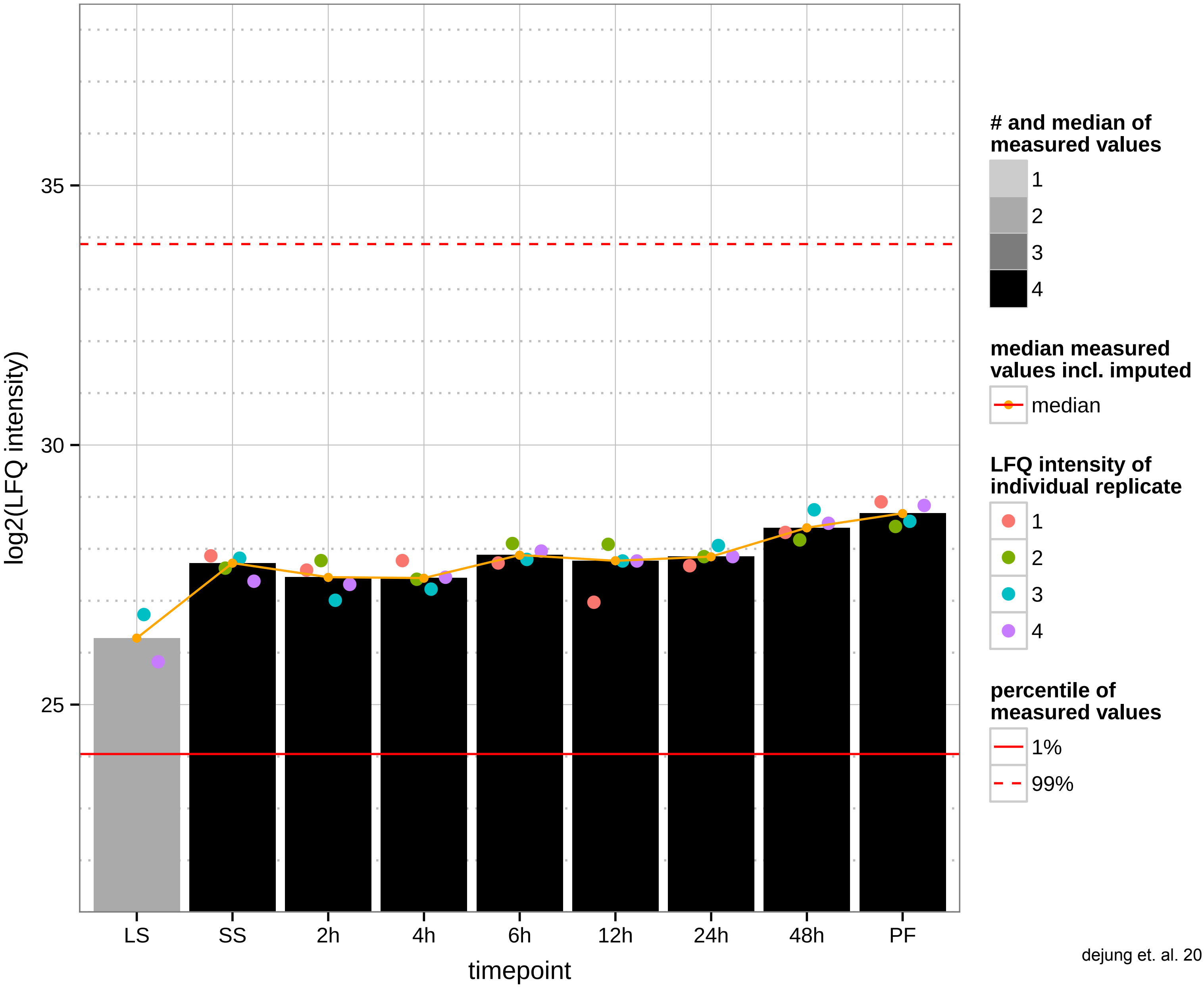
acyl–CoA dehydrogenase, mitochondrial precursor, putative
Tb927.8.1420
AGOF: acyl–CoA dehydrogenase activity
AGOC: mitochondrial membrane, mitochondrion
AGOP: metabolic process
PGOF: acyl–CoA dehydrogenase activity, oxidoreductase activity, acting on the CH–CH group of donors
PGOC: null
PGOP: metabolic process, oxidation–reduction process





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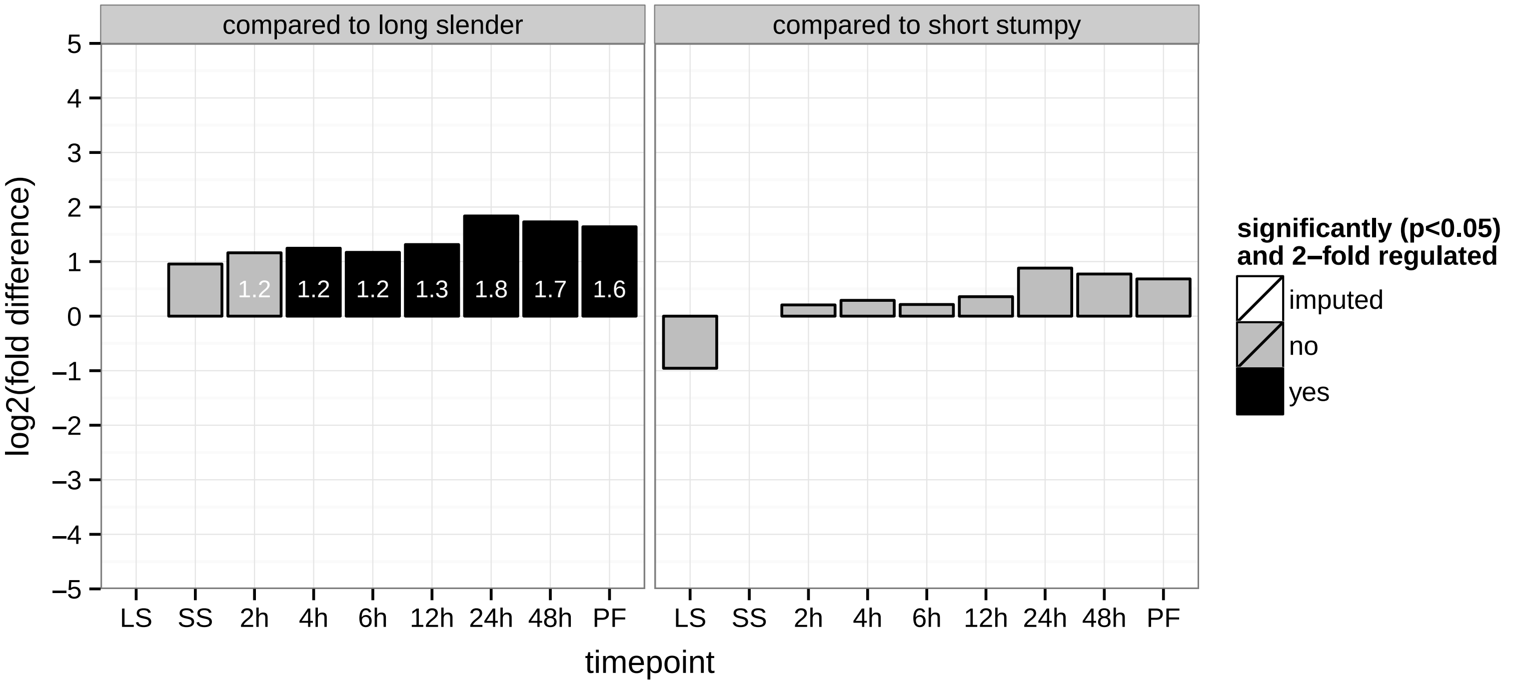
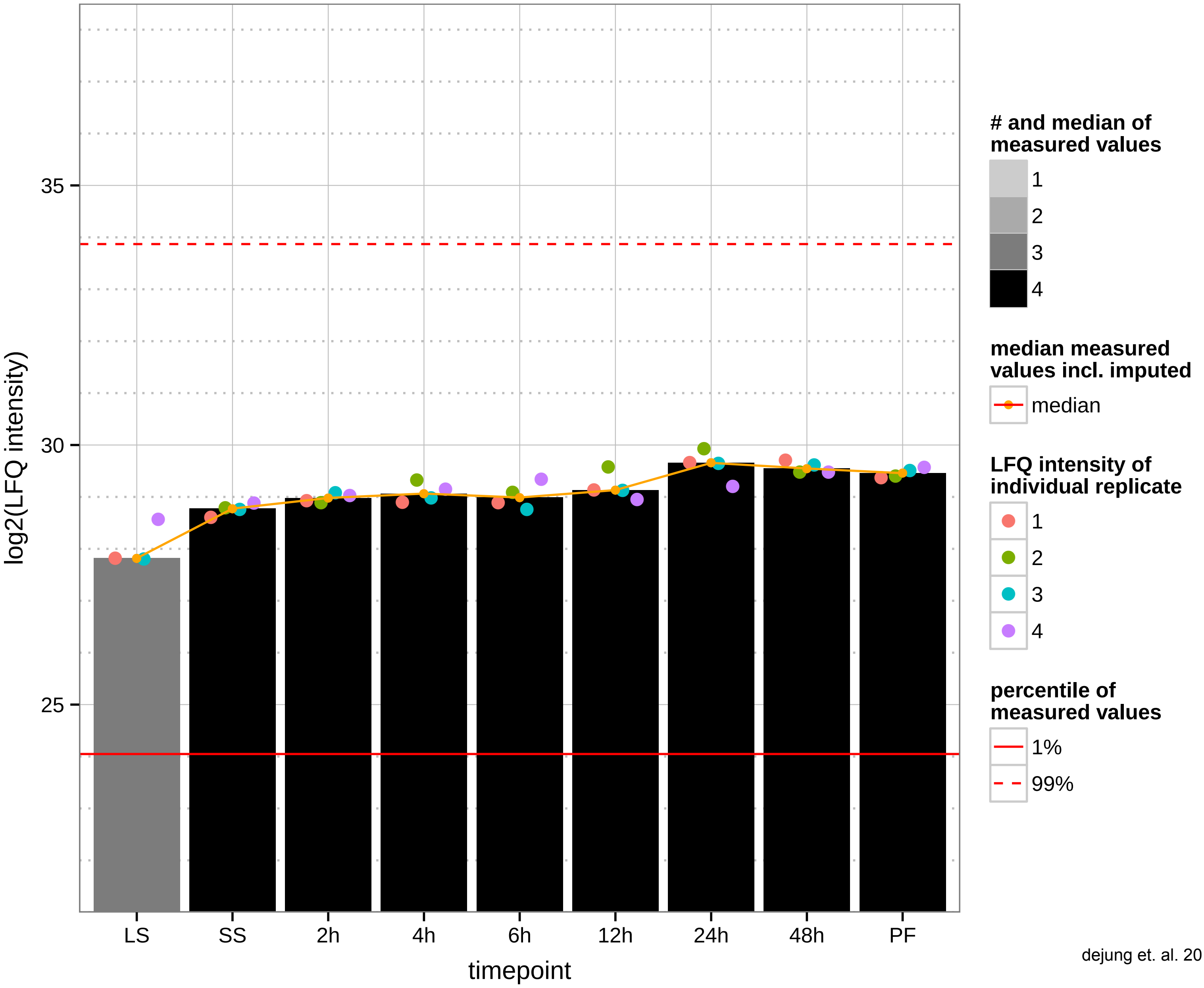
maoC–like dehydratase, putative
Tb927.8.1440
AGOF: fatty acid synthase activity, oxidoreductase activity
AGOC: mitochondrion
AGOP: fatty acid biosynthetic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process





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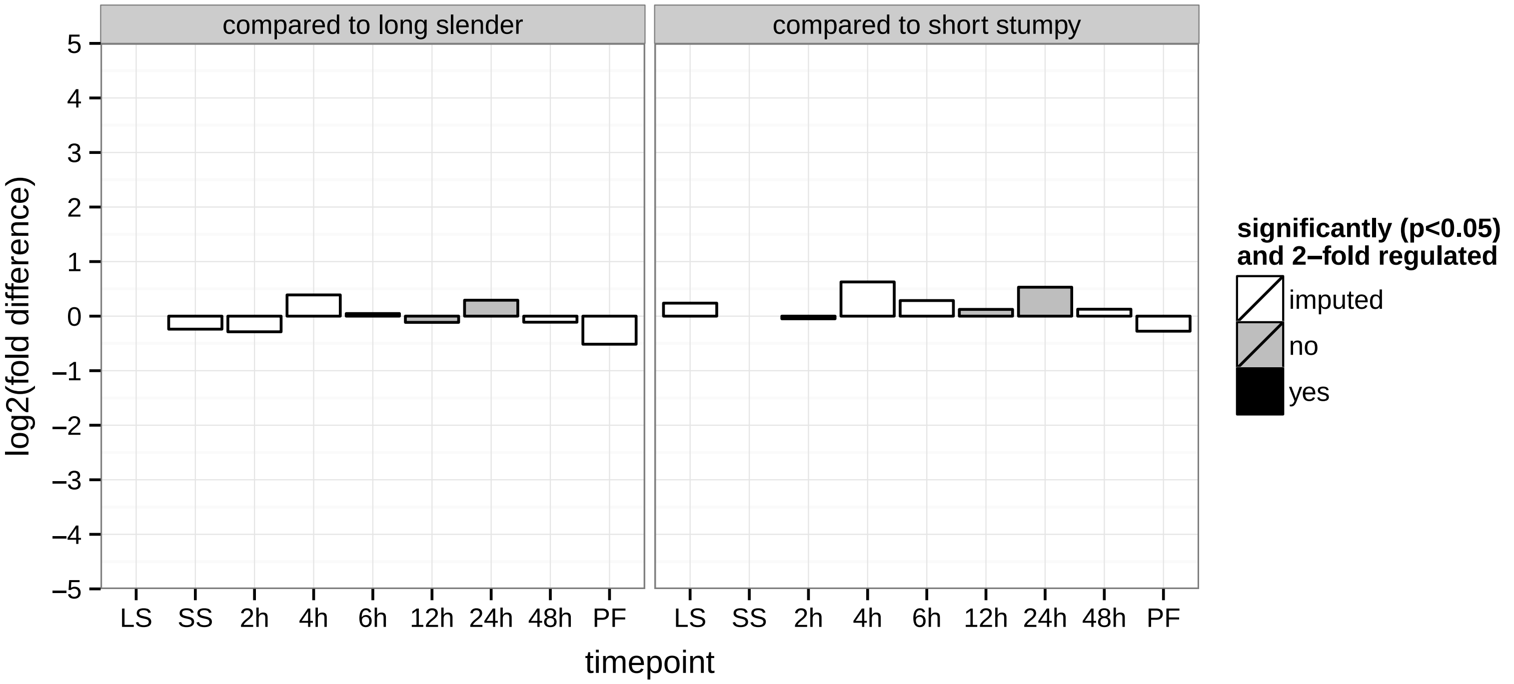
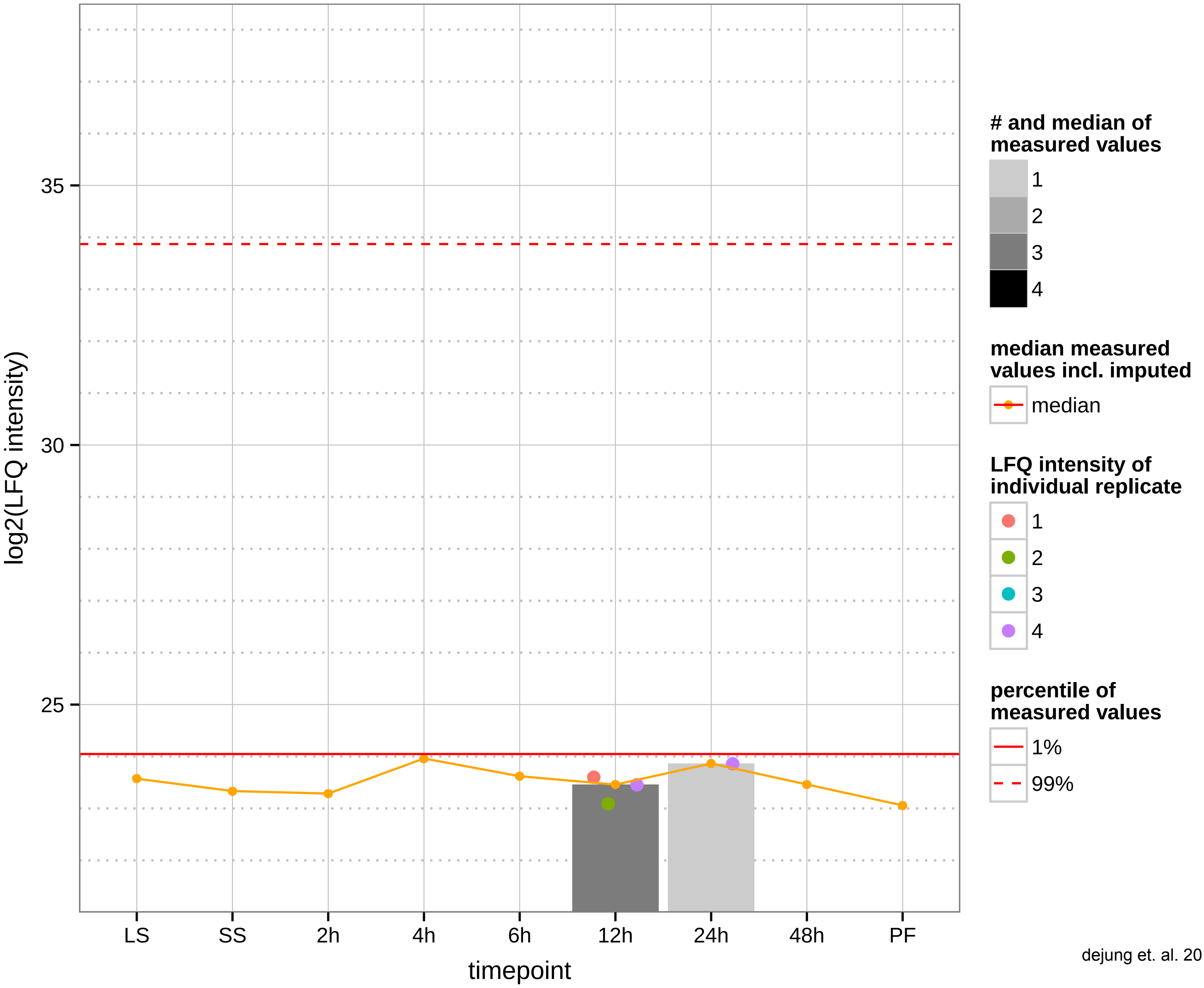
hypothetical protein, conserved
Tb927.8.1470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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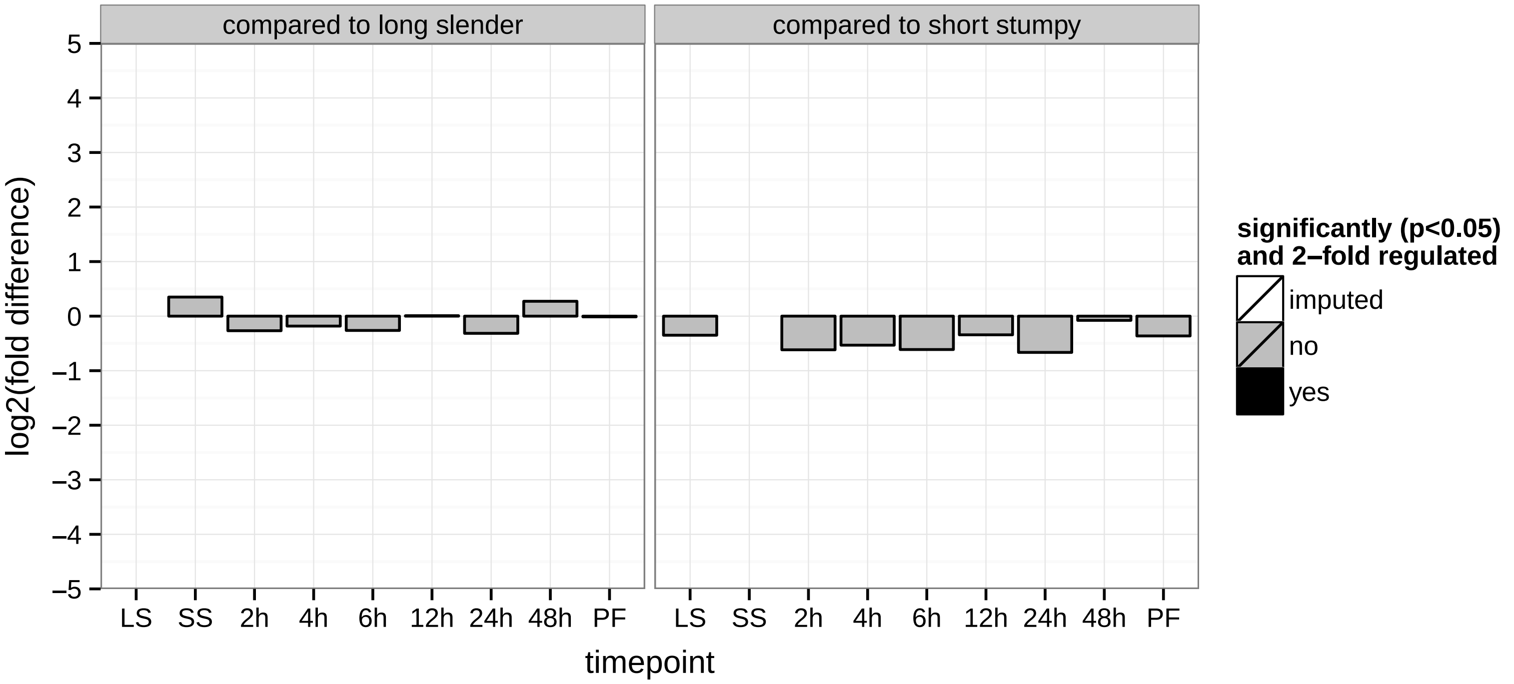
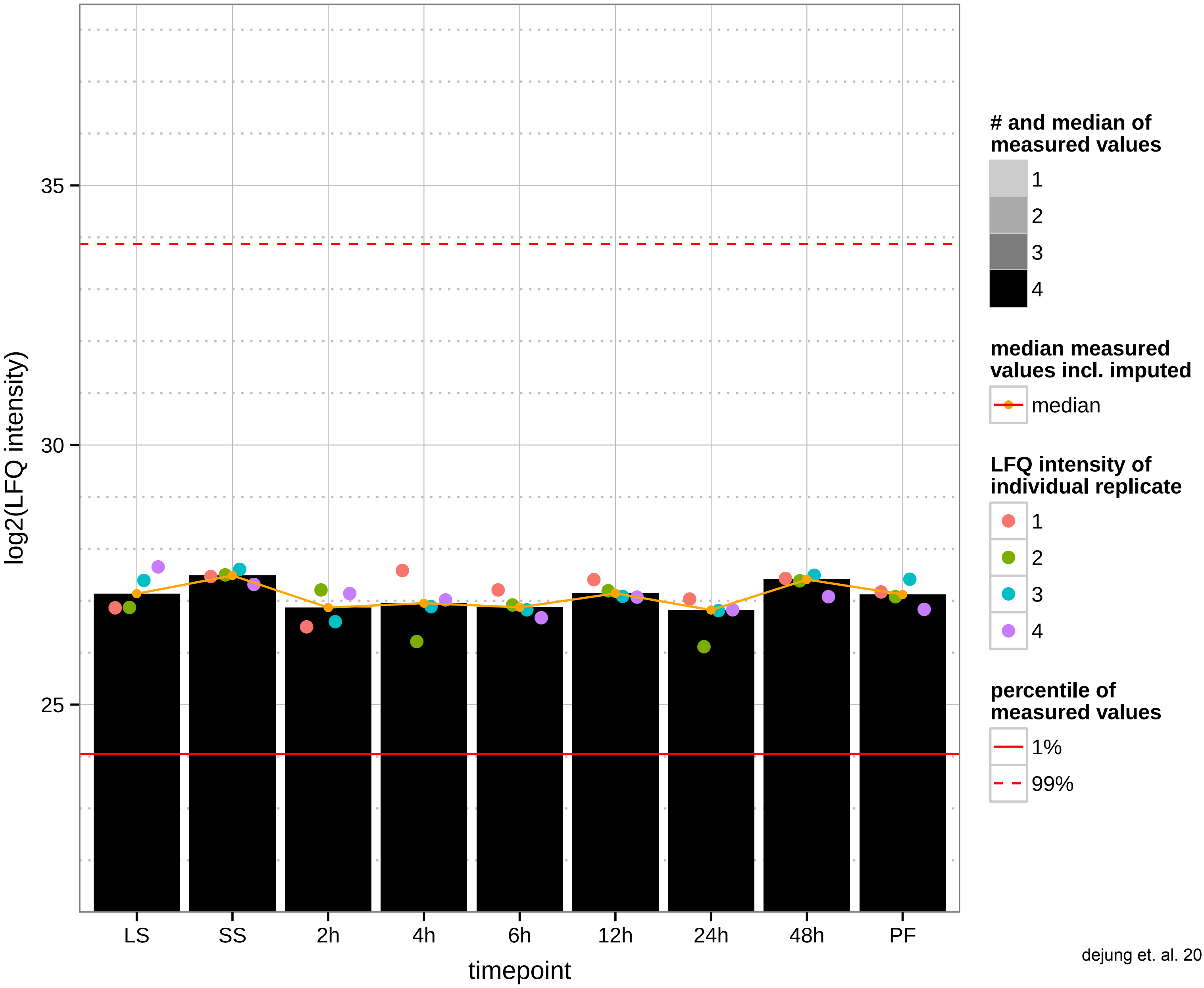
hypothetical protein, conserved
Tb927.8.1540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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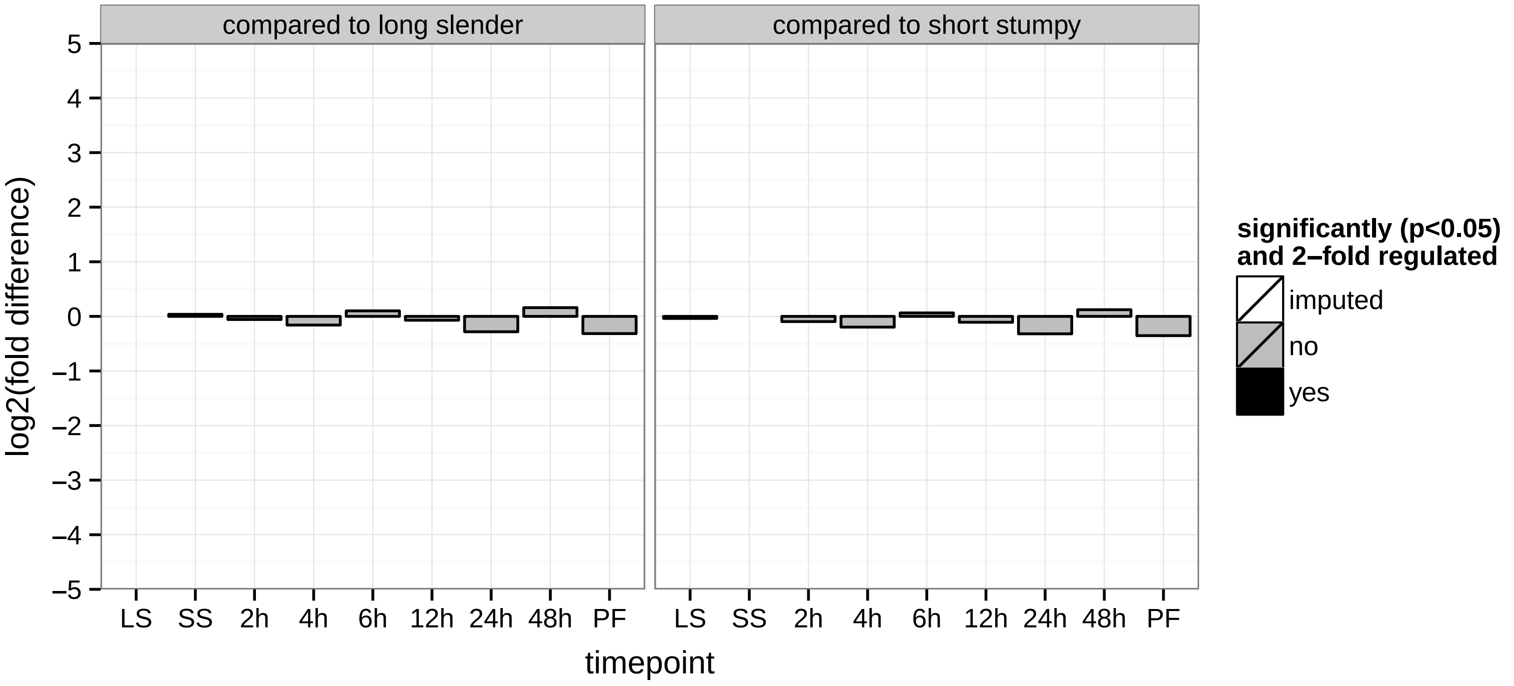
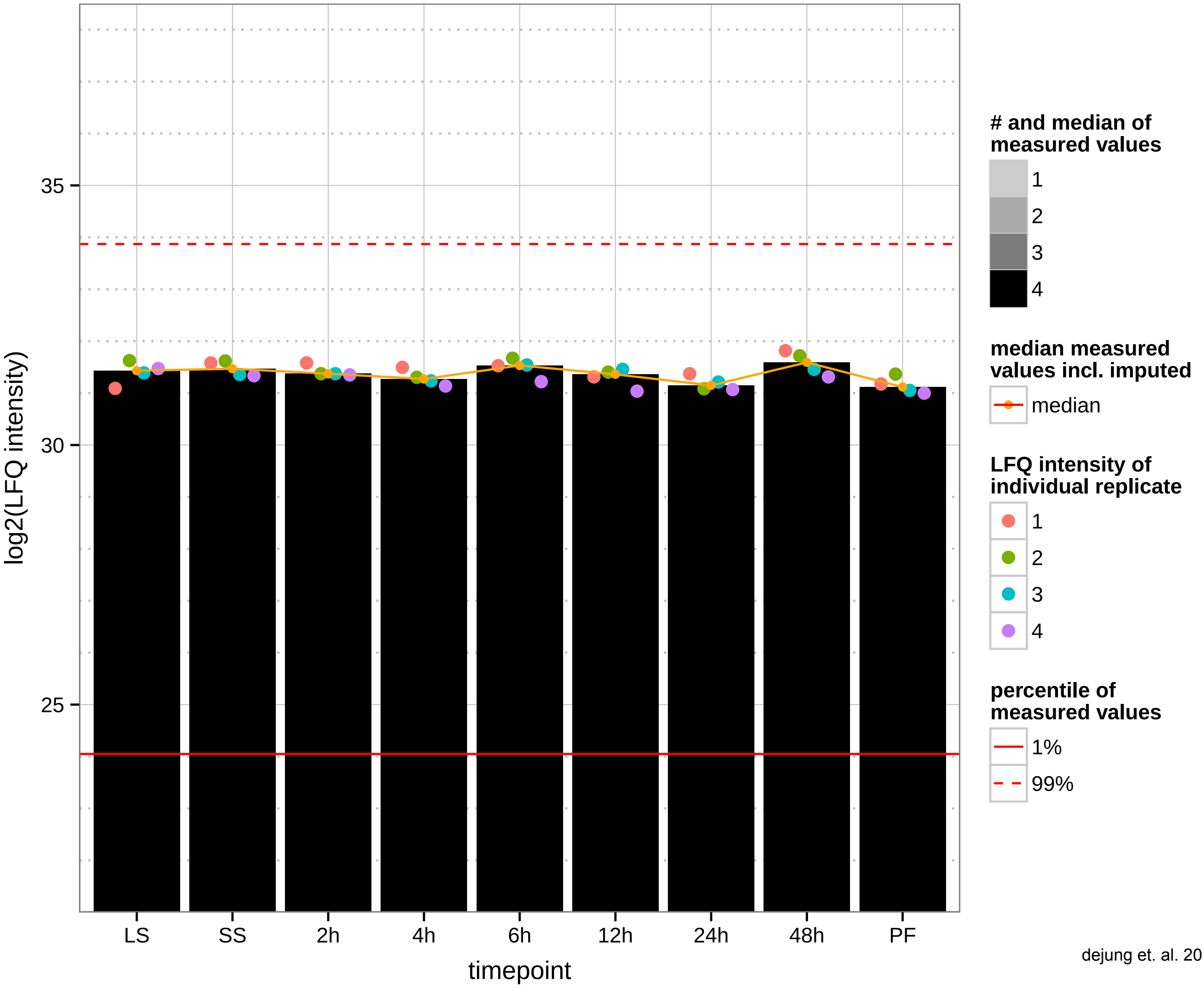
paraflagellar rod component, putative (PFC3)
Tb927.8.1550
AGOF: null
AGOC: null
AGOP: null
PGOF: calmodulin binding
PGOC: microtubule–based flagellum
PGOP: null





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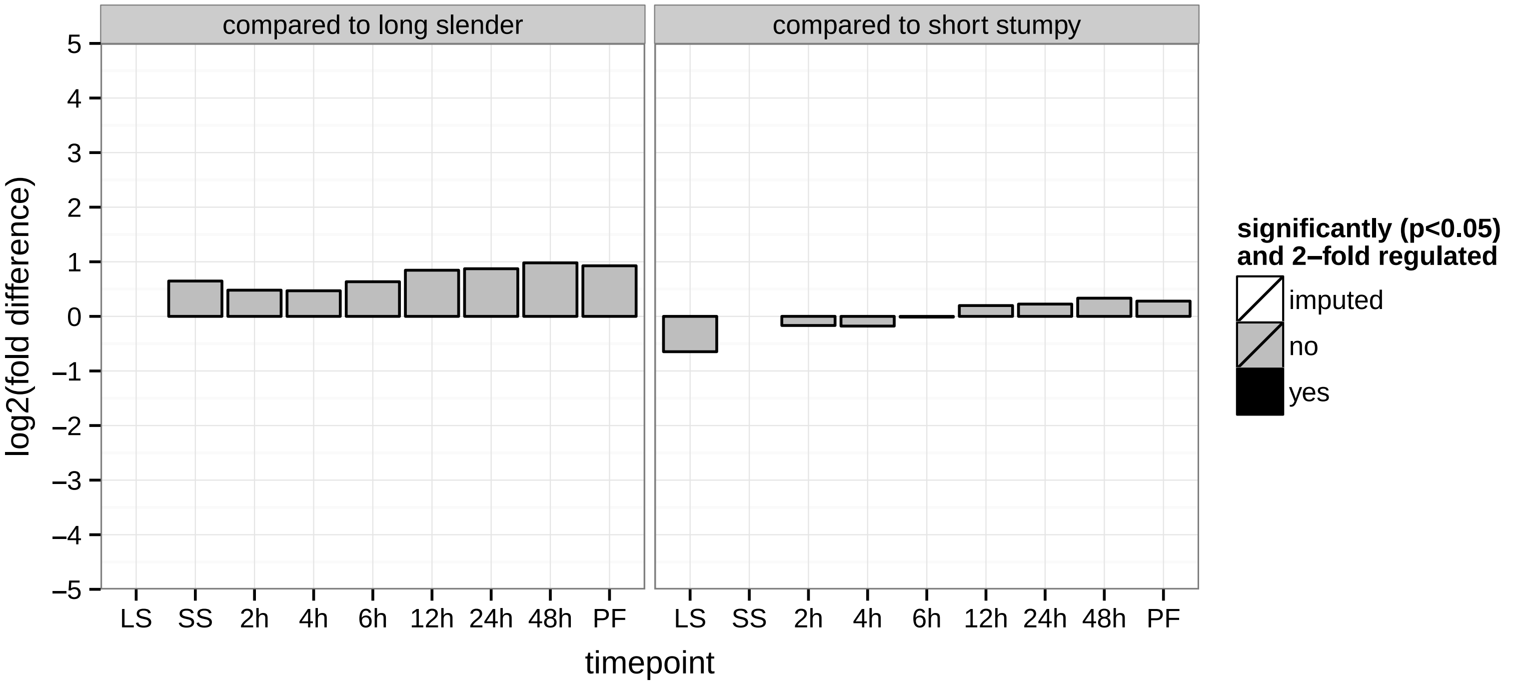
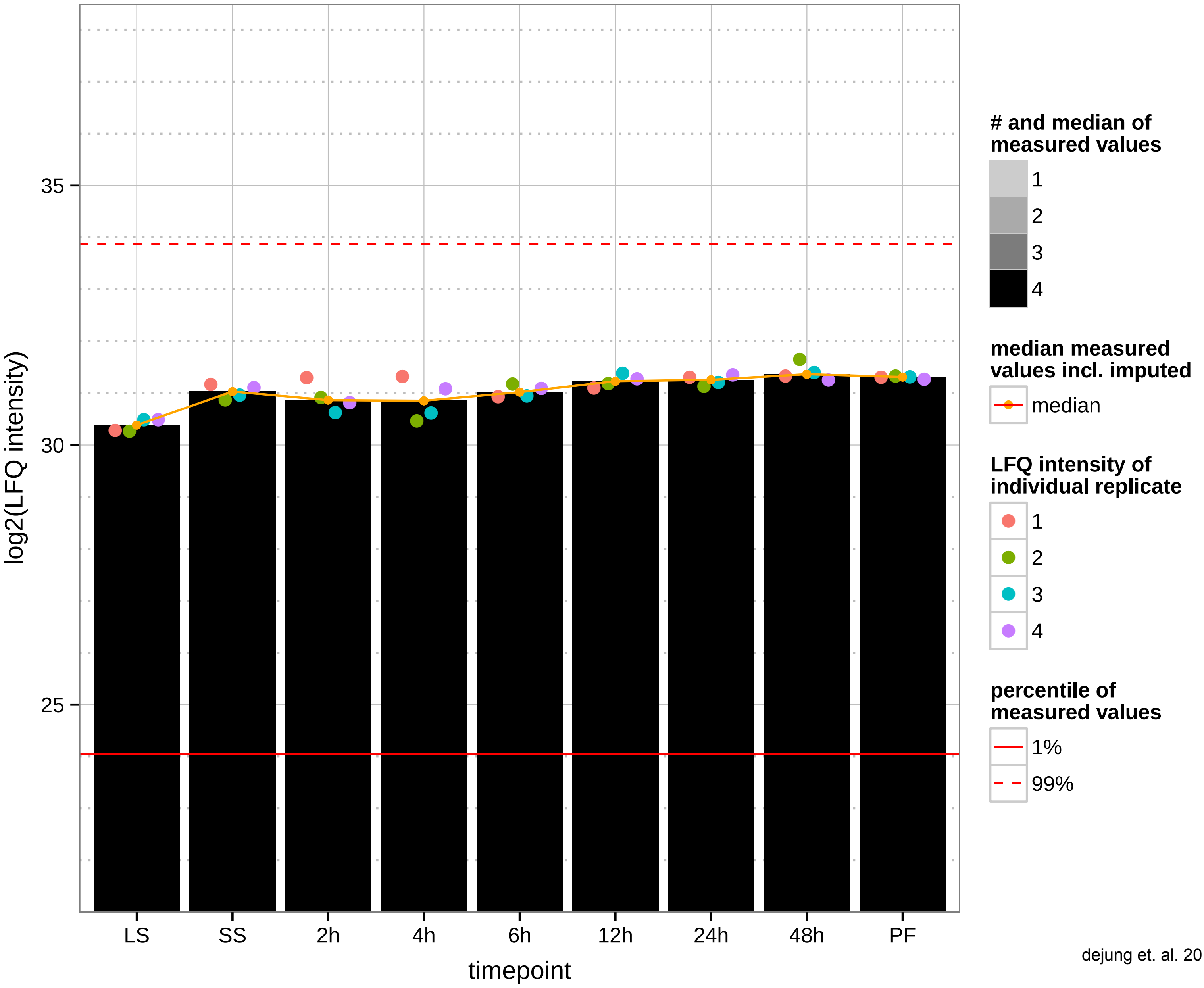
lysyl–tRNA synthetase, putative
Tb927.8.1600
AGOF: ATP binding, lysine–tRNA ligase activity, nucleic acid binding
AGOC: cytoplasm
AGOP: lysyl–tRNA aminoacylation, tRNA aminoacylation for protein translation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, lysine–tRNA ligase activity, nucleic acid binding, nucleotide binding
PGOC: cytoplasm
PGOP: lysyl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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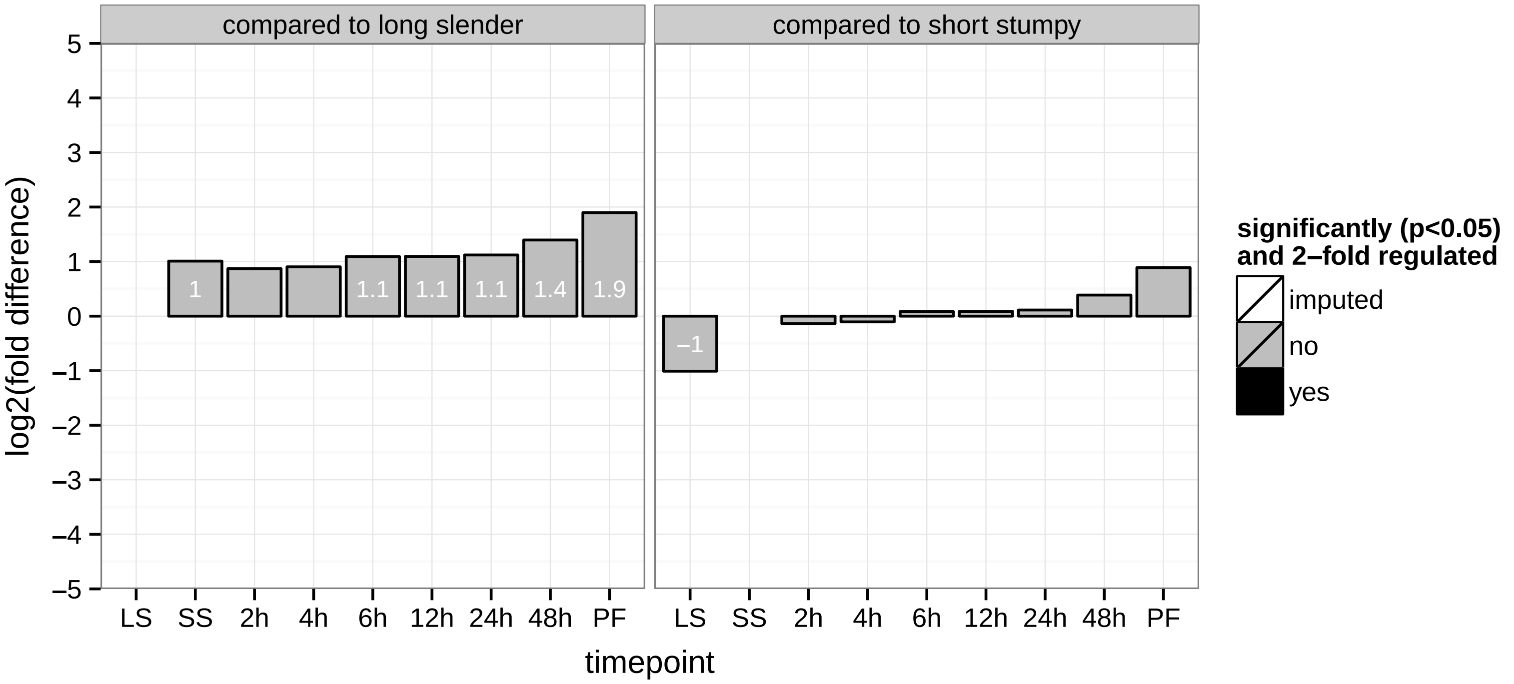
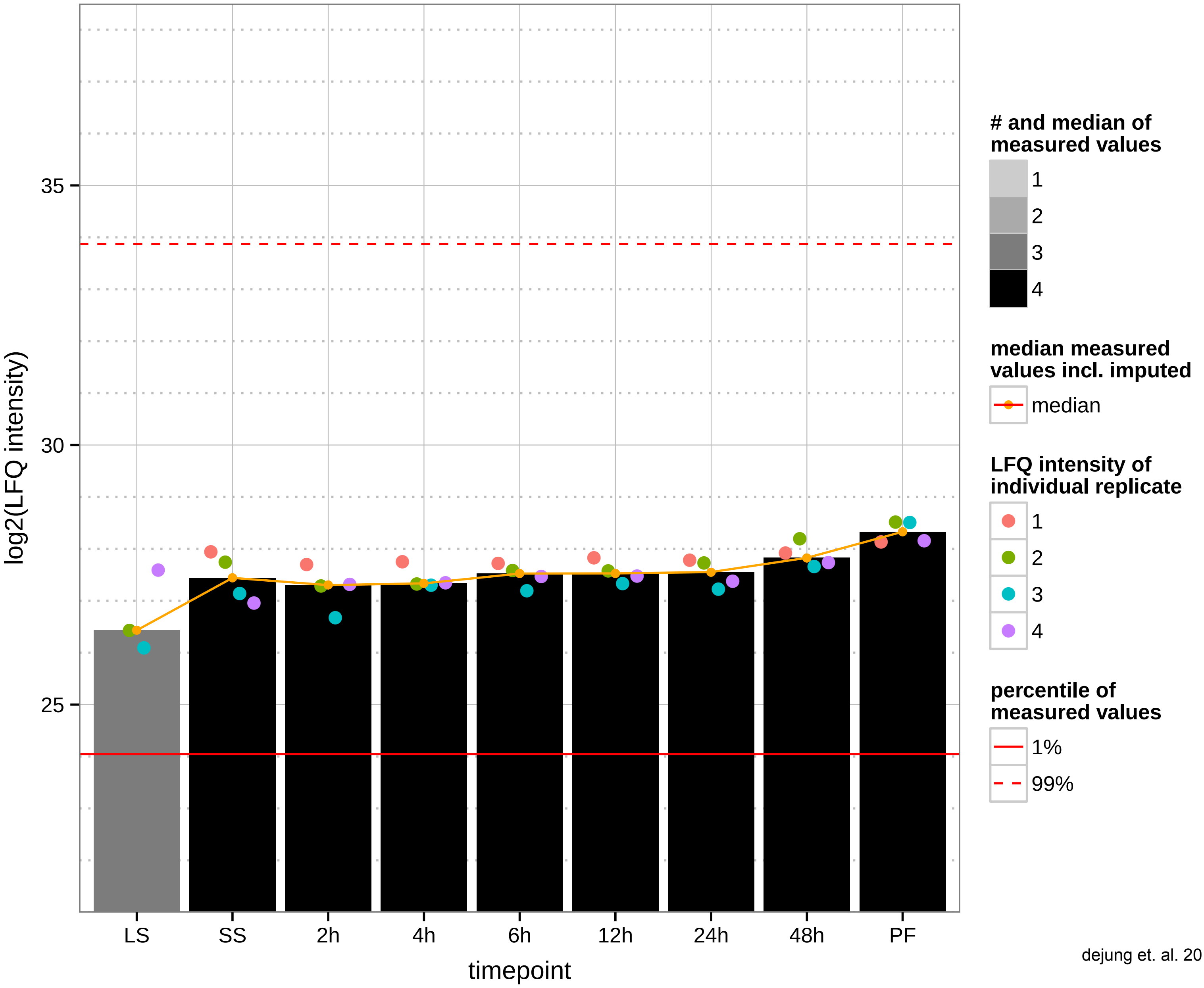
protein phosphatase 2A, regulatory subunit B, putative, phosphotyrosyl phosphate activator protein
Tb927.8.1710
AGOF: phosphatase activator activity
AGOC: null
AGOP: null
PGOF: phosphatase activator activity
PGOC: null
PGOP: null





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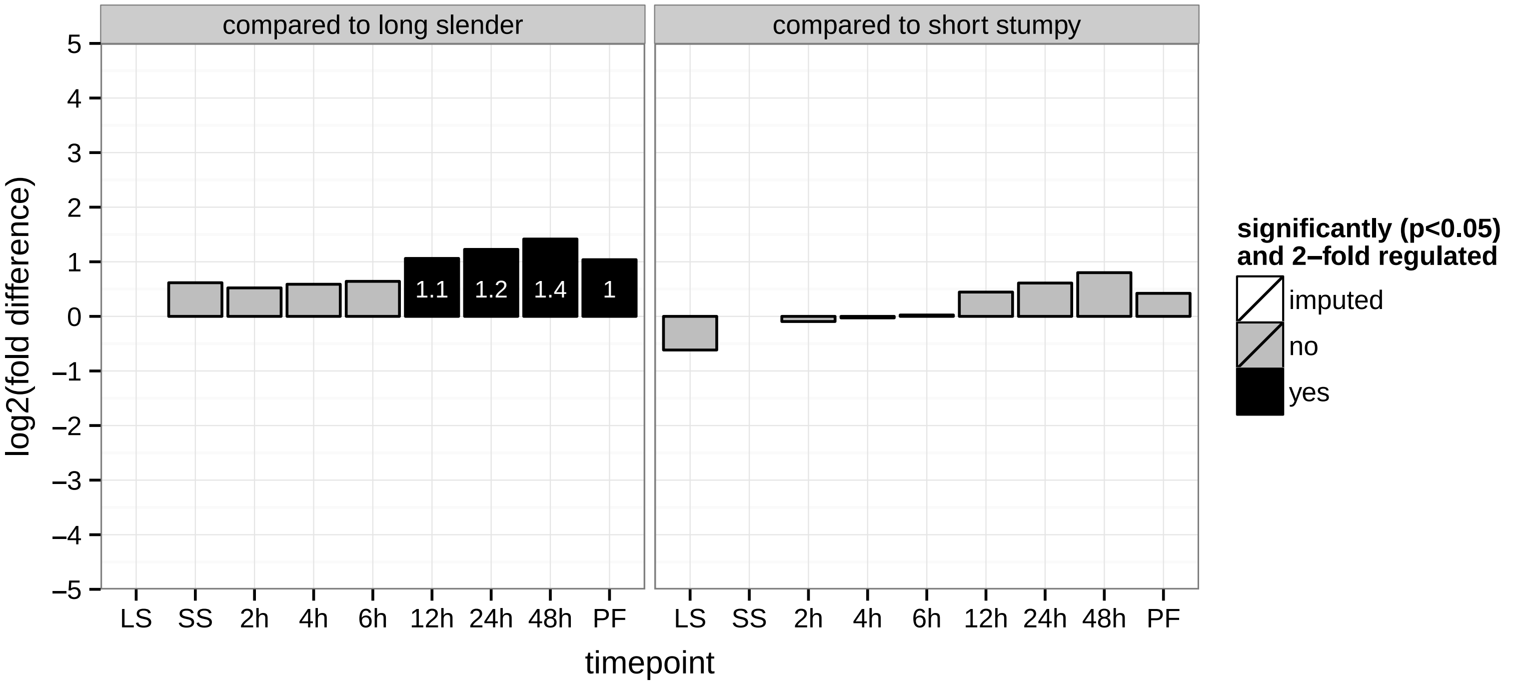
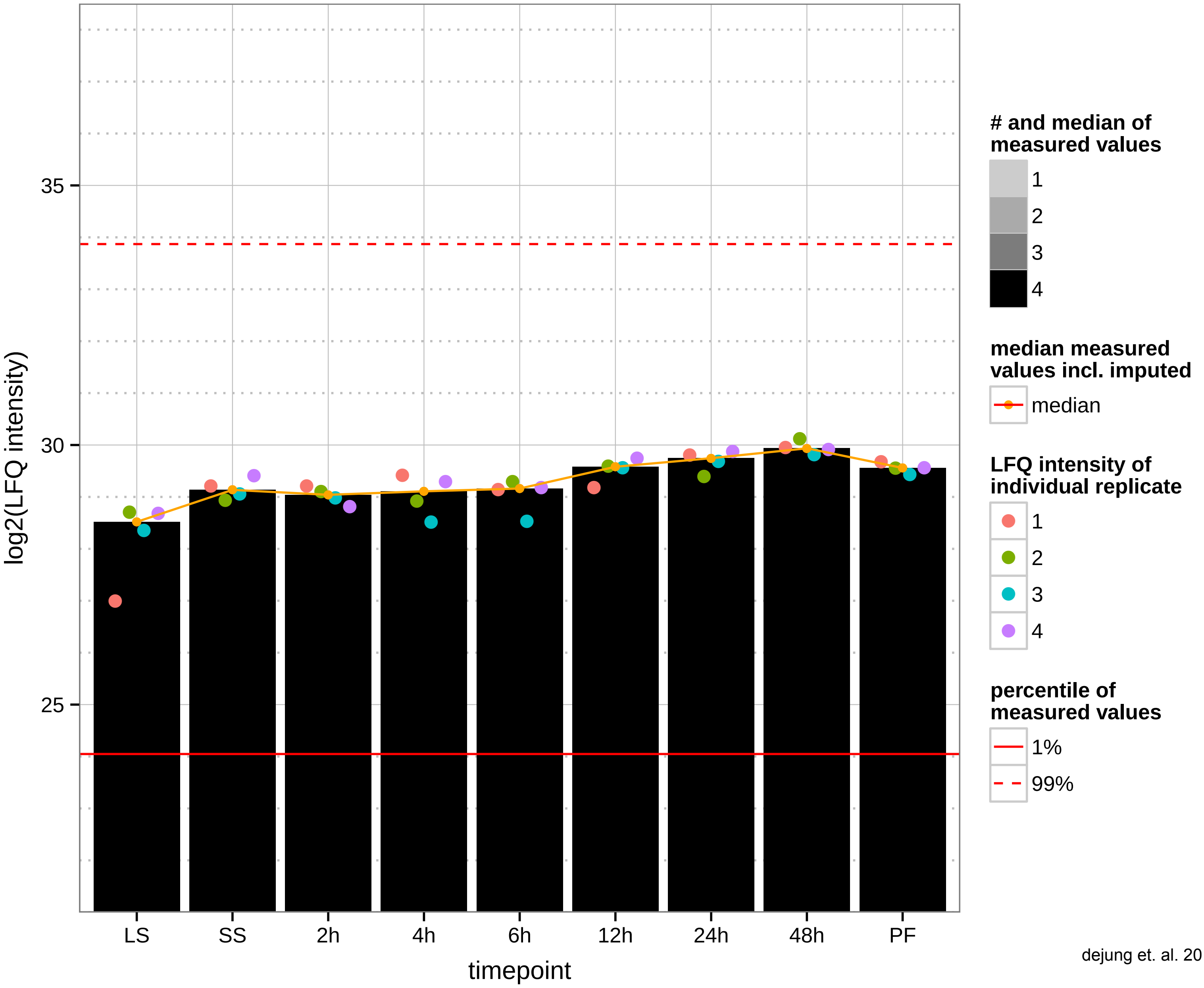
hypothetical protein, conserved
Tb927.8.1740
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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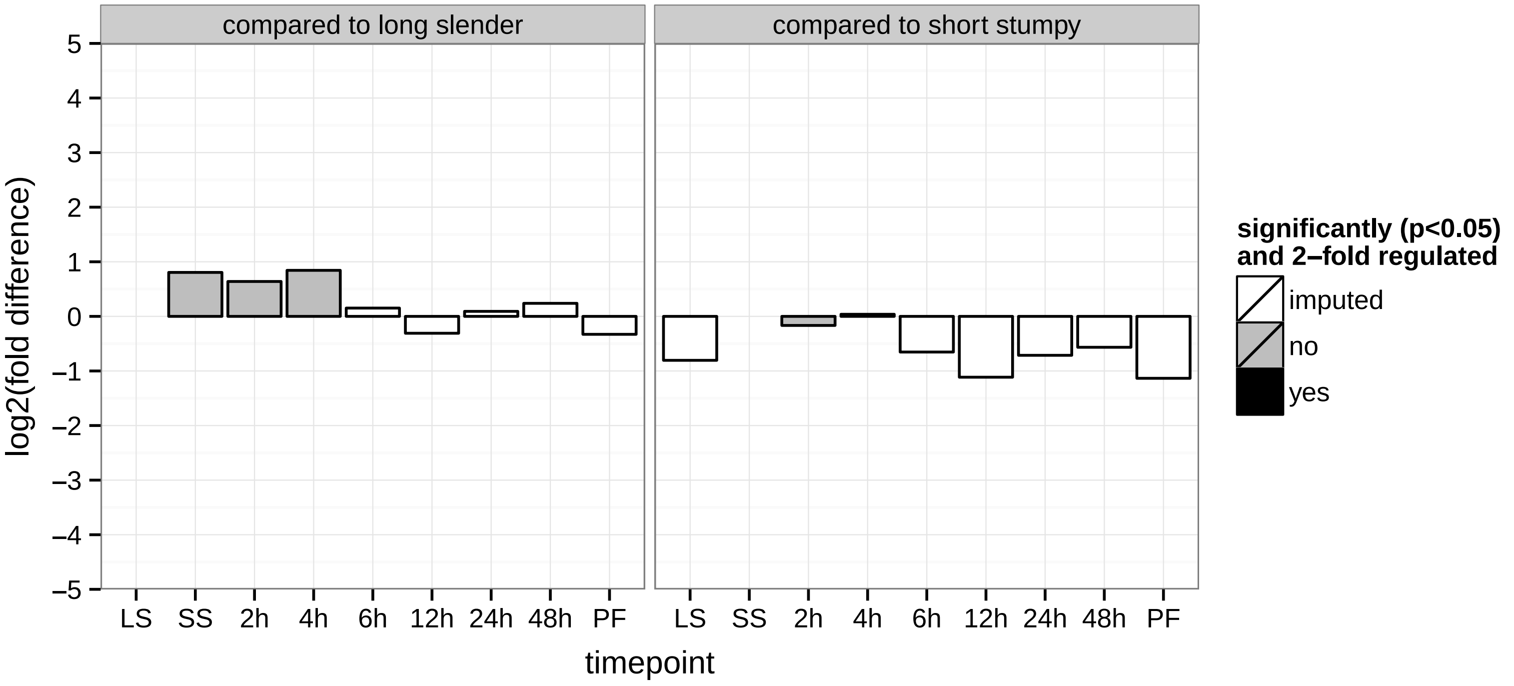
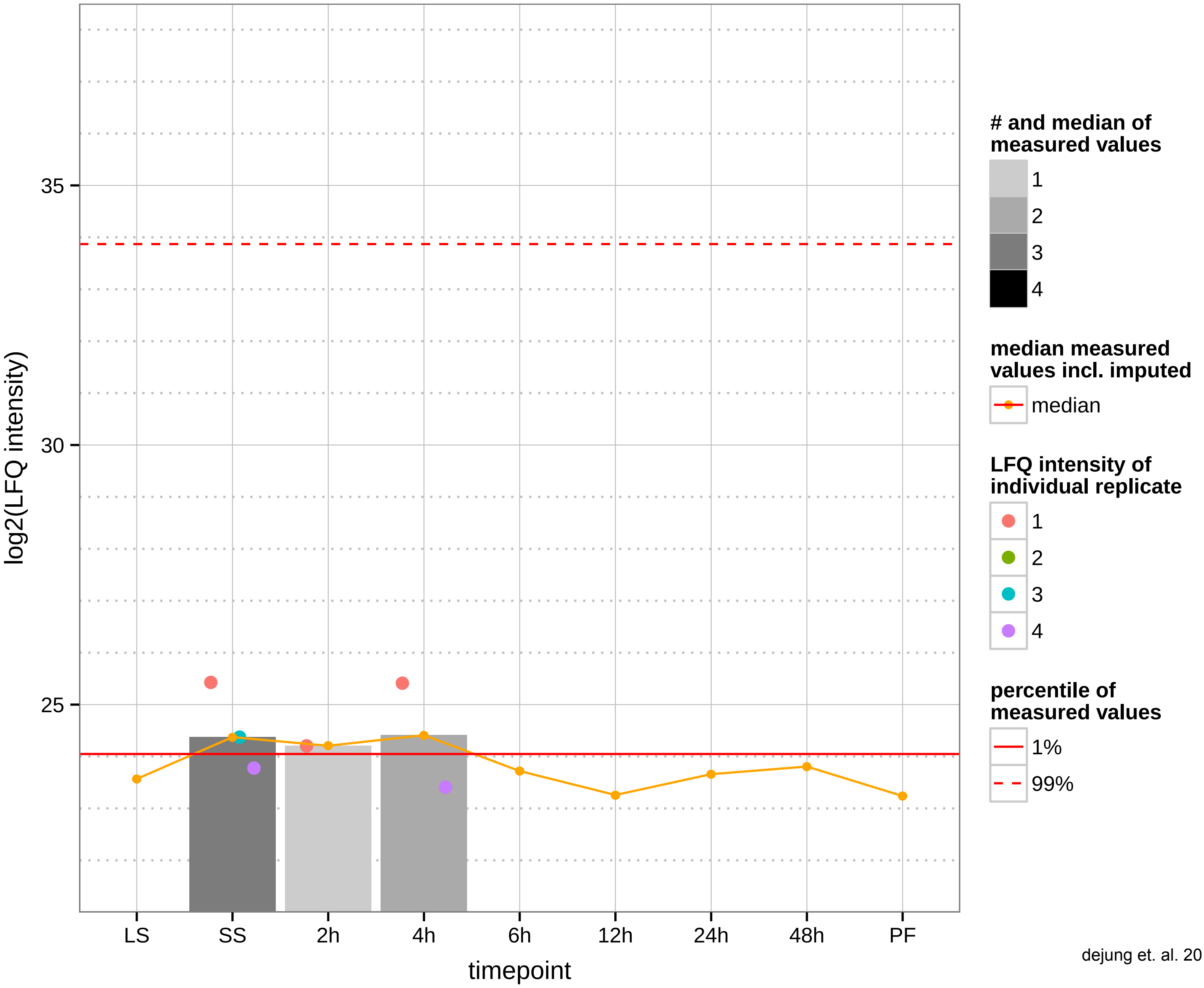
protein kinase, putative
Tb927.8.1780
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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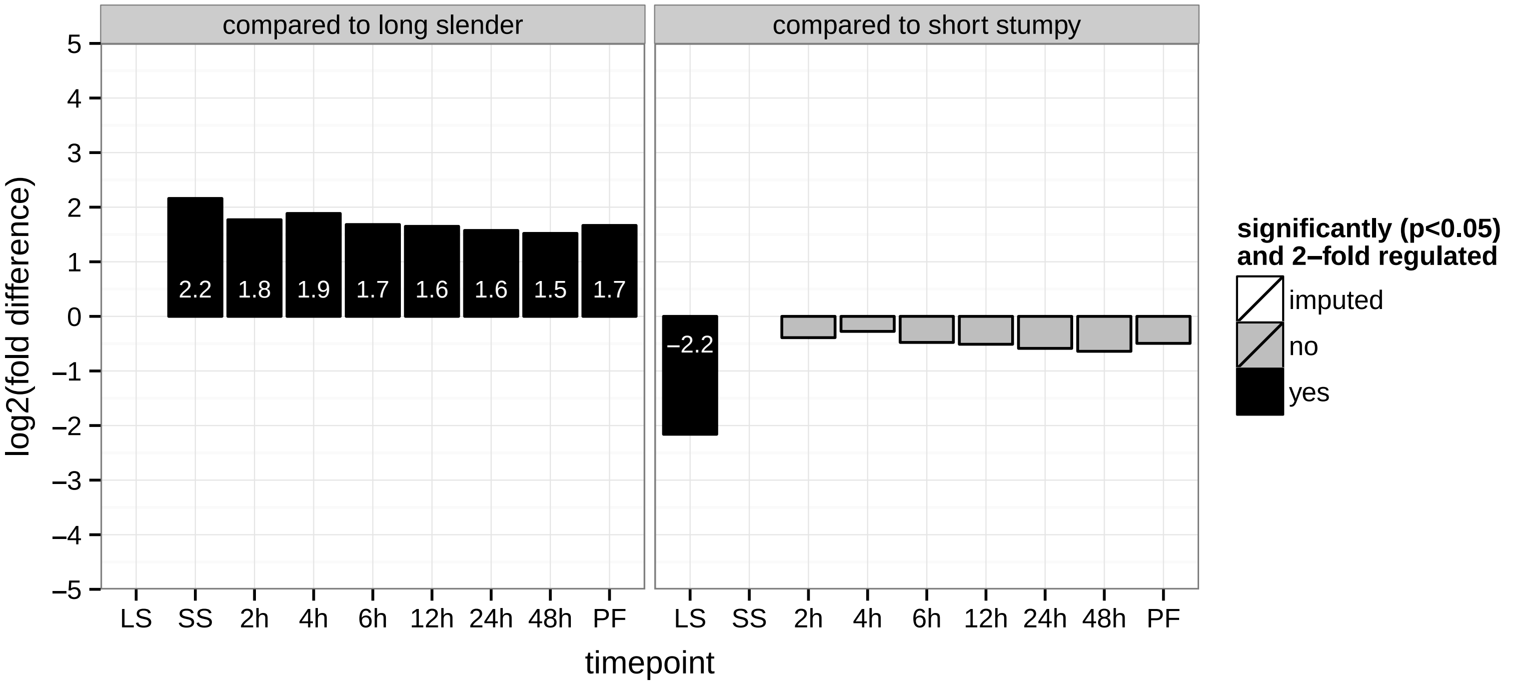
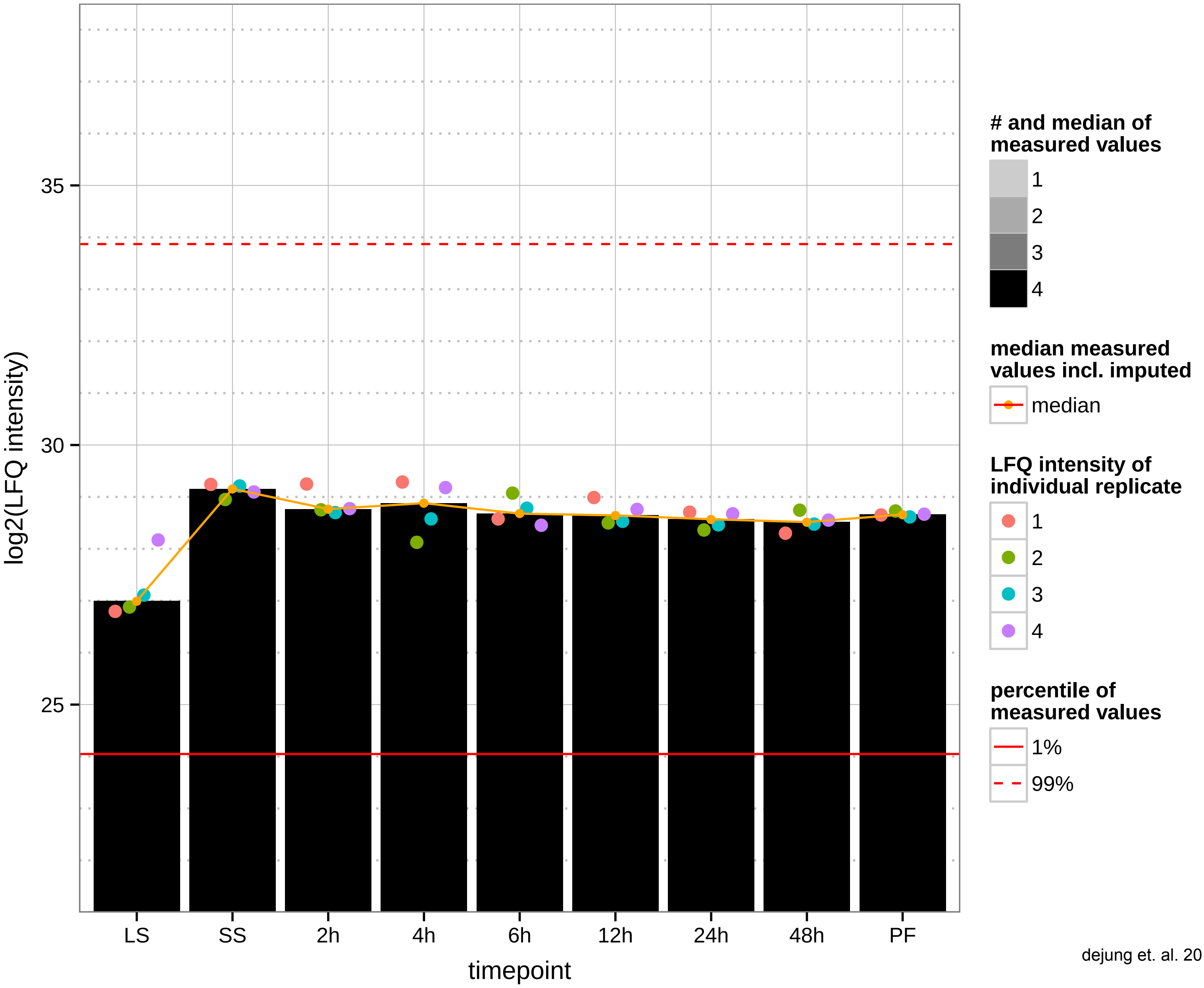
hypothetical protein, conserved
Tb927.8.1840
AGOF: ARF guanyl–nucleotide exchange factor activity
AGOC: intracellular
AGOP: regulation of ARF protein signal transduction
PGOF: ARF guanyl–nucleotide exchange factor activity
PGOC: intracellular
PGOP: regulation of ARF protein signal transduction





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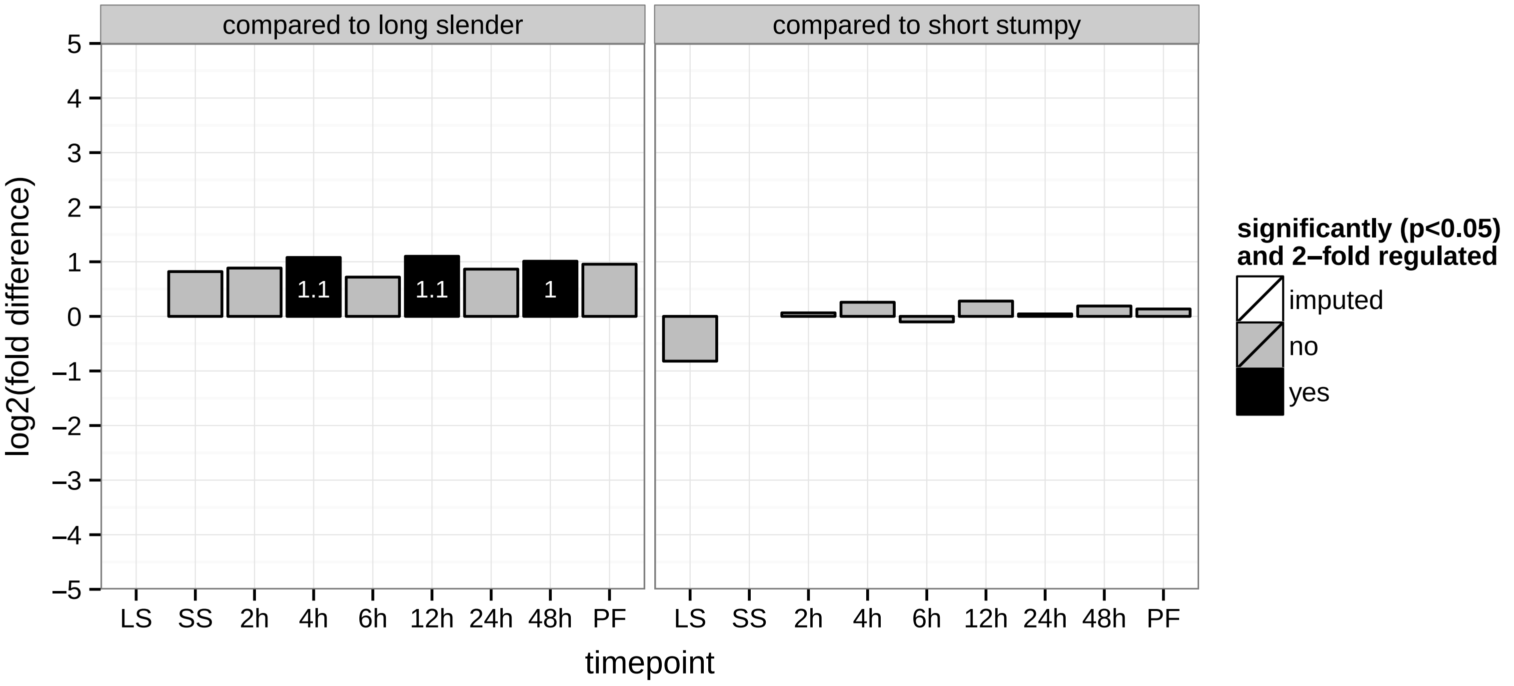
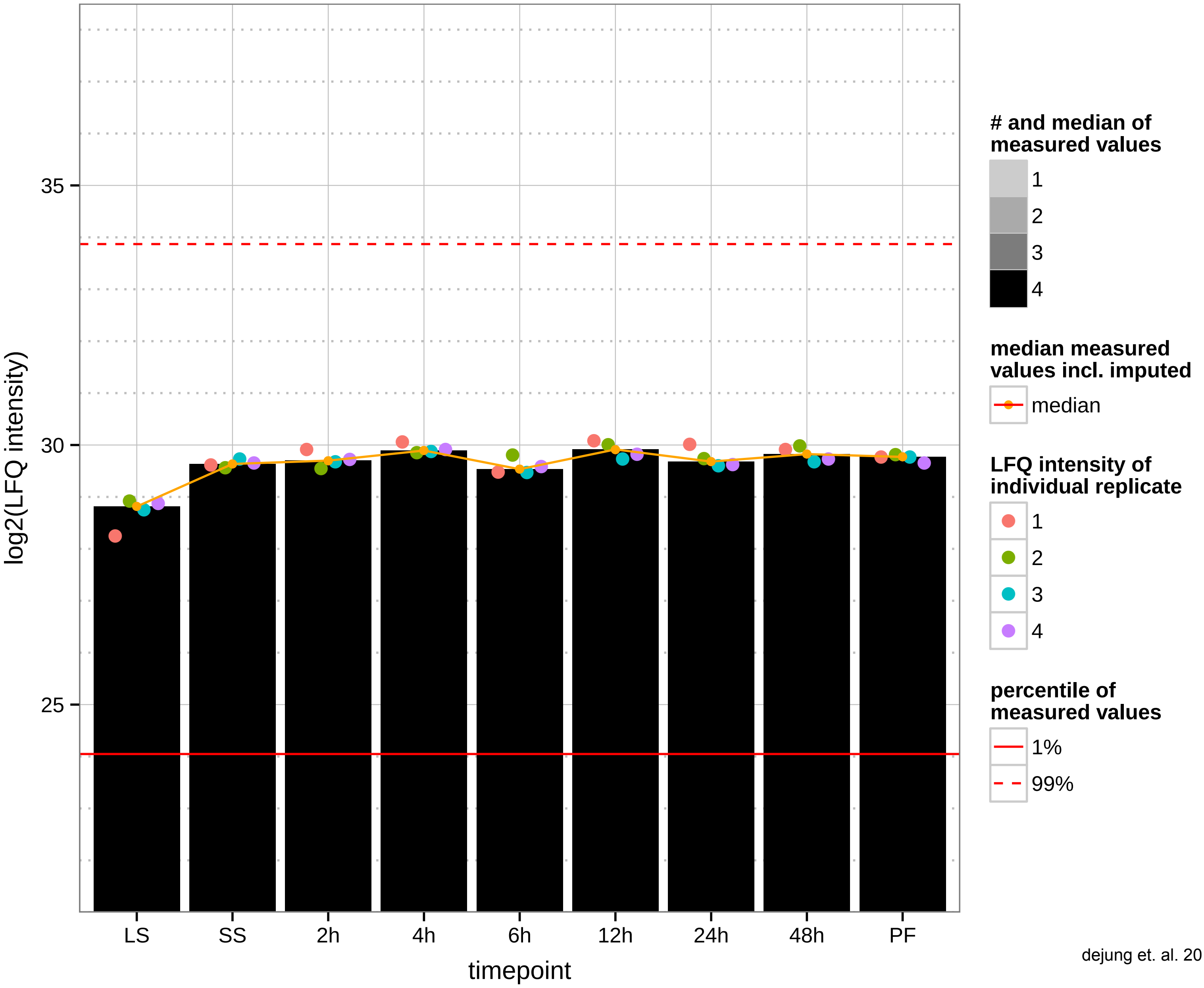
hypothetical protein, conserved
Tb927.8.1960
AGOF: null
AGOC: cytoplasm, nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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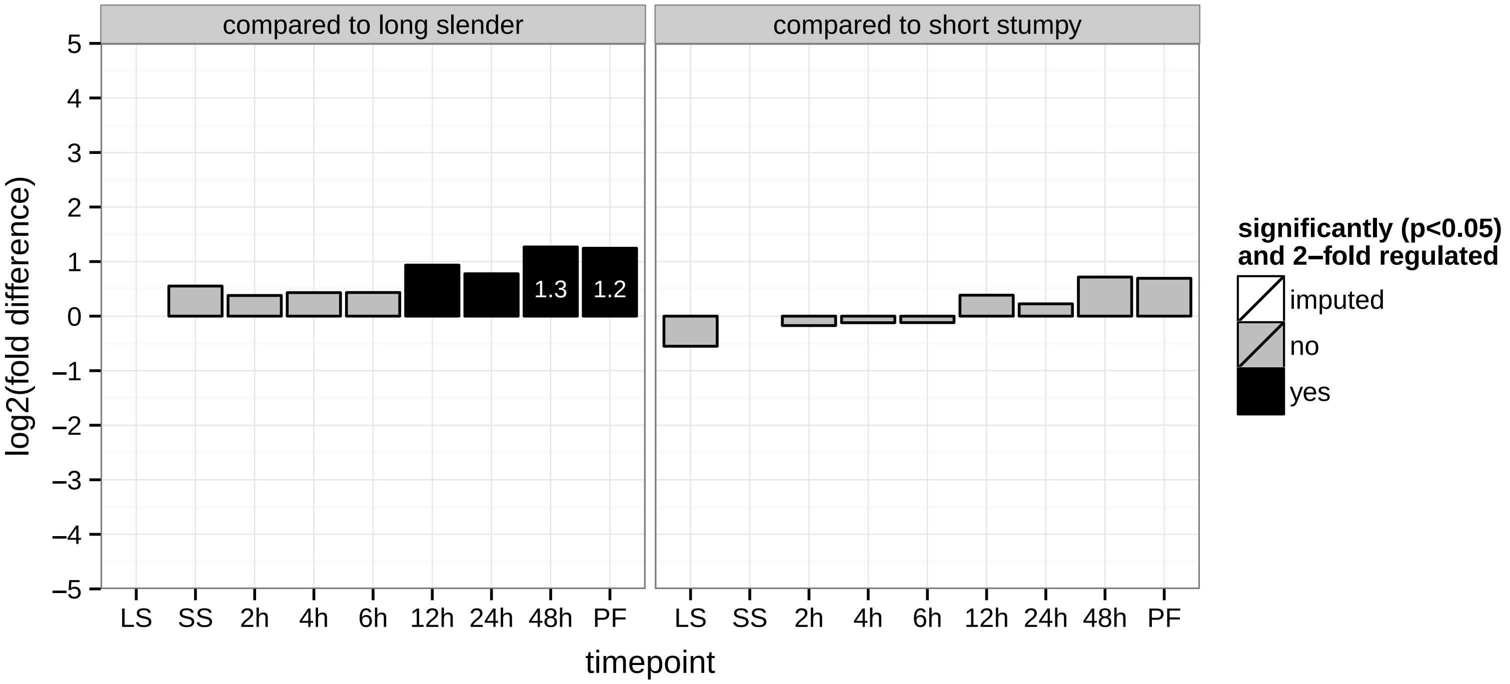
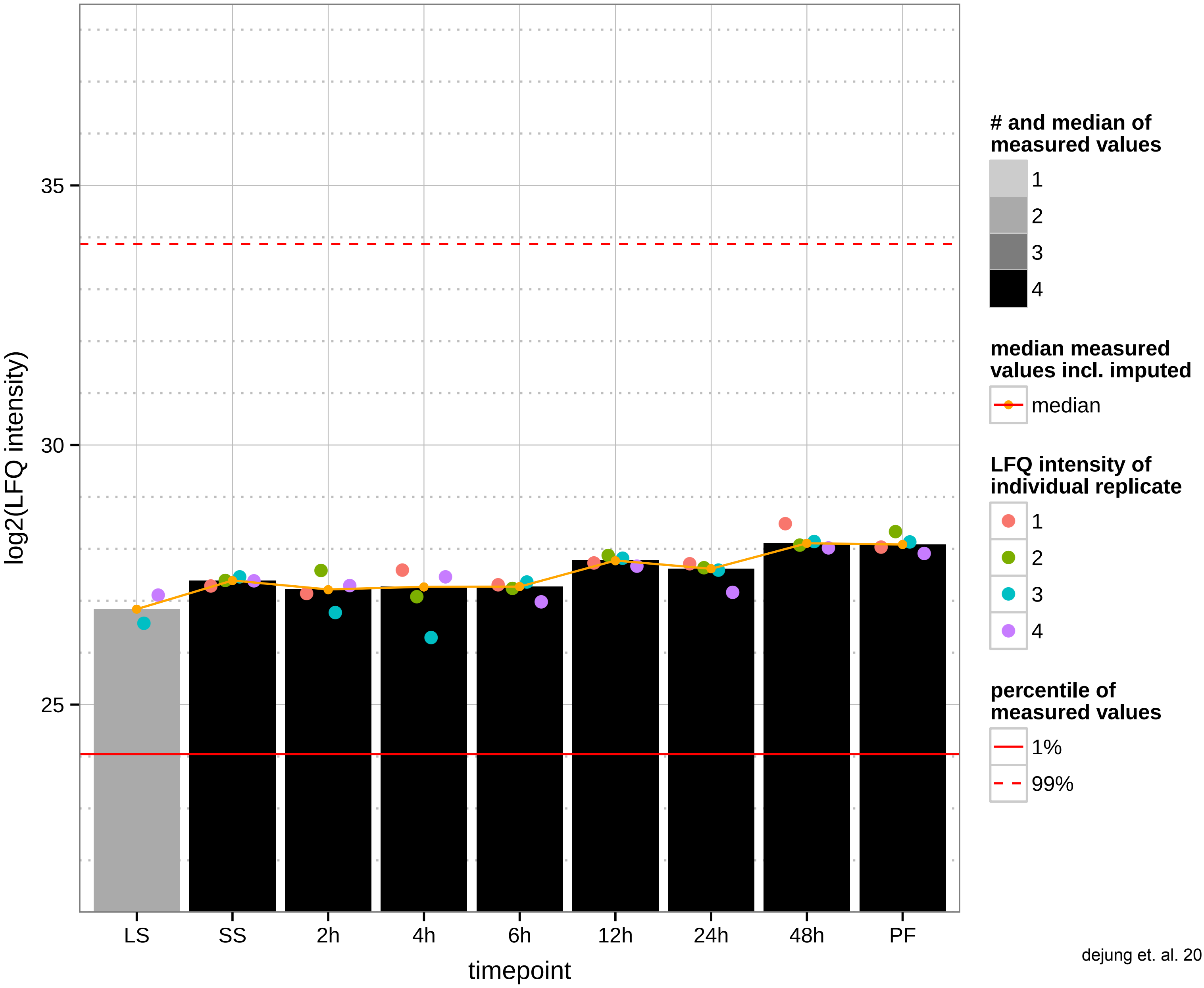
hypothetical protein, conserved
Tb927.8.1980
AGOF: null
AGOC: nucleolus
AGOP: rRNA processing
PGOF: protein binding
PGOC: nucleolus
PGOP: rRNA processing





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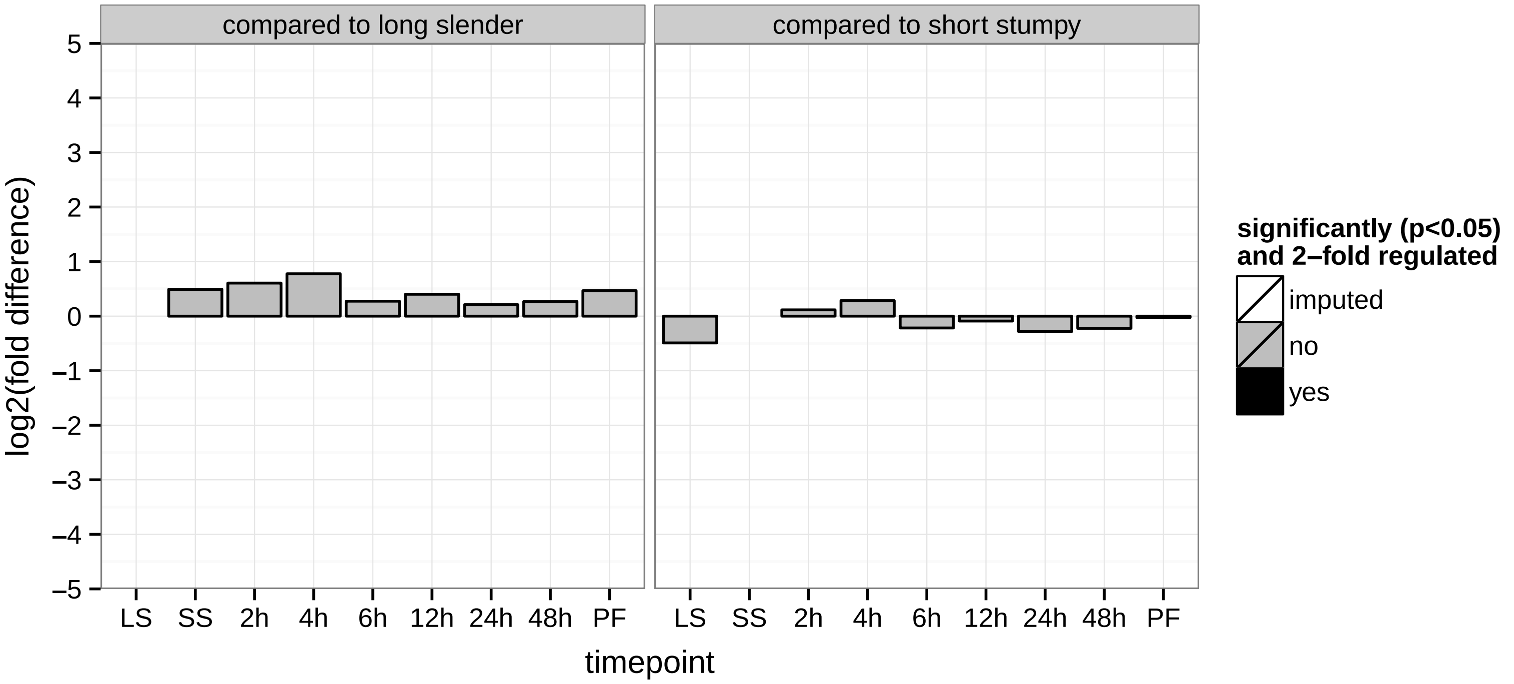
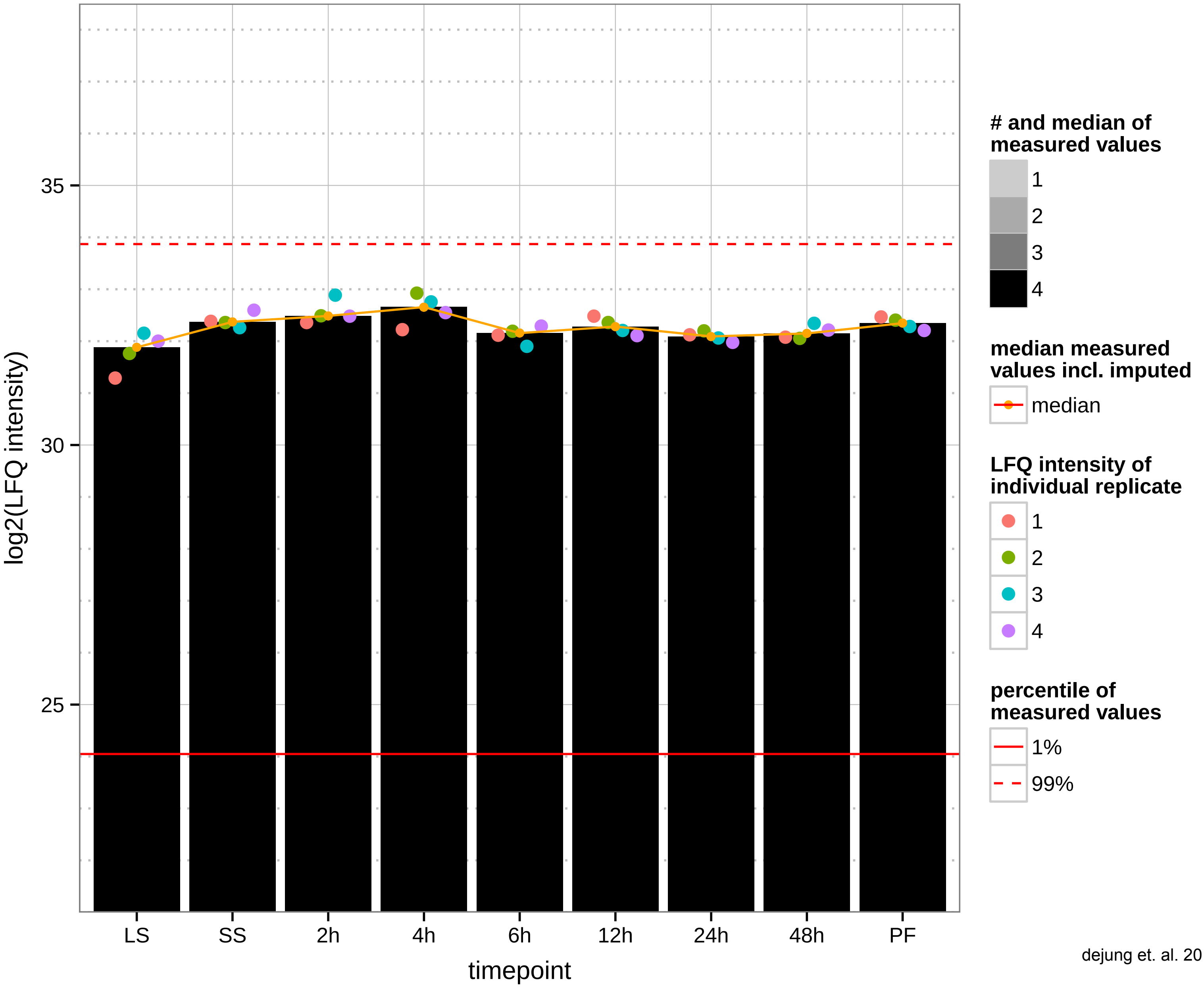
peroxidoxin, tryparedoxin peroxidase (TRYP2)
Tb927.8.1990
AGOF: antioxidant activity, trypanothione–disulfide reductase activity
AGOC: mitochondrion
AGOP: cell redox homeostasis, oxidation–reduction process
PGOF: antioxidant activity, oxidoreductase activity, peroxiredoxin activity
PGOC: null
PGOP: oxidation–reduction process





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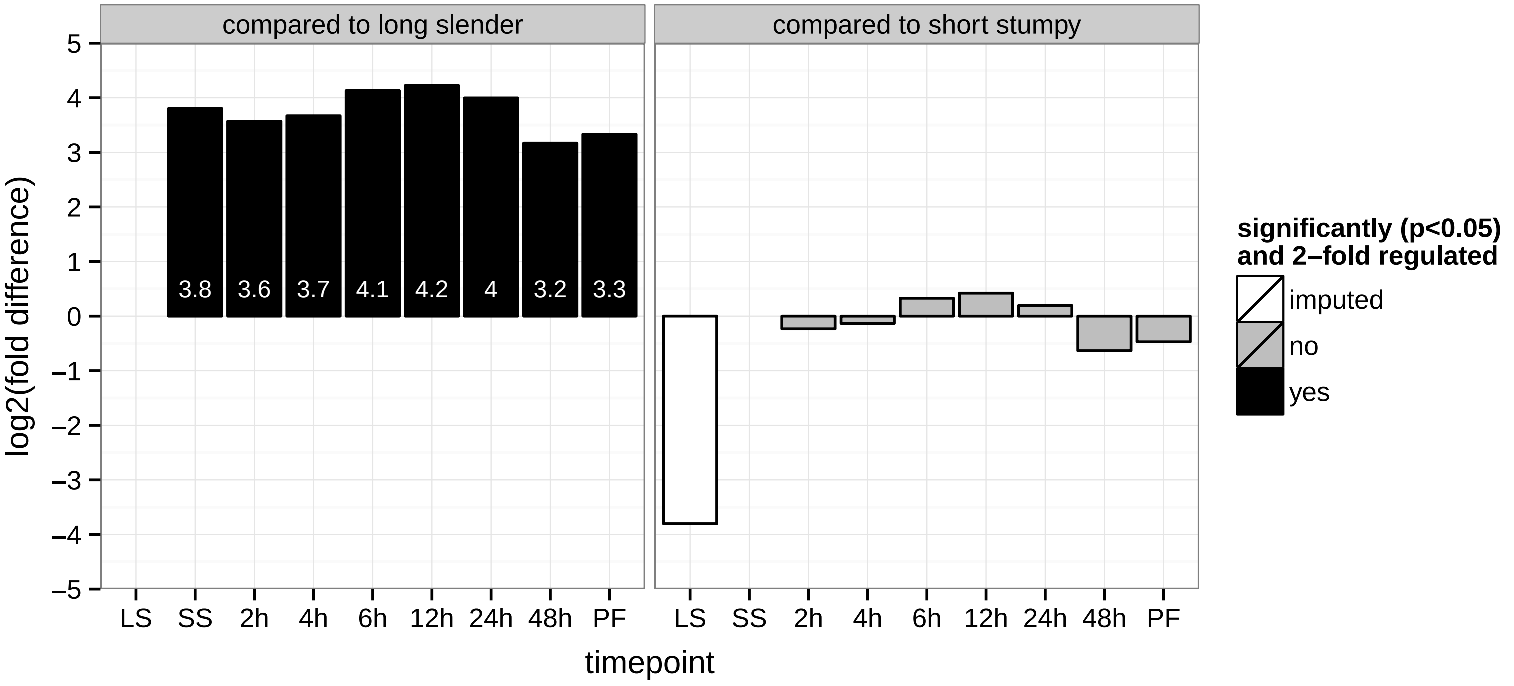
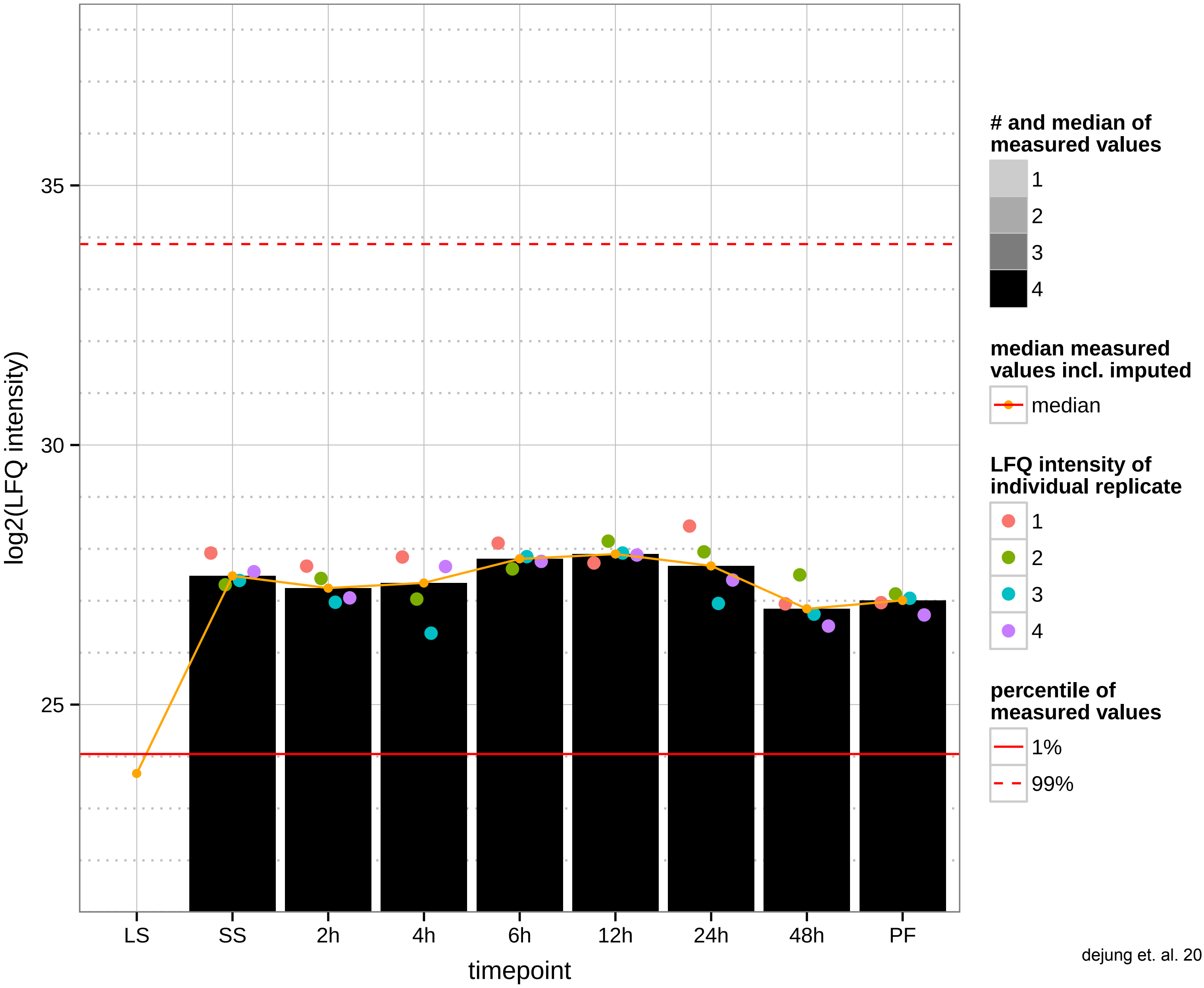
agmatinase, putative
Tb927.8.2020
AGOF: arginase activity, metal ion binding
AGOC: null
AGOP: arginine metabolic process
PGOF: hydrolase activity, acting on carbon–nitrogen (but not peptide) bonds, in linear amidines, metal ion binding
PGOC: null
PGOP: null





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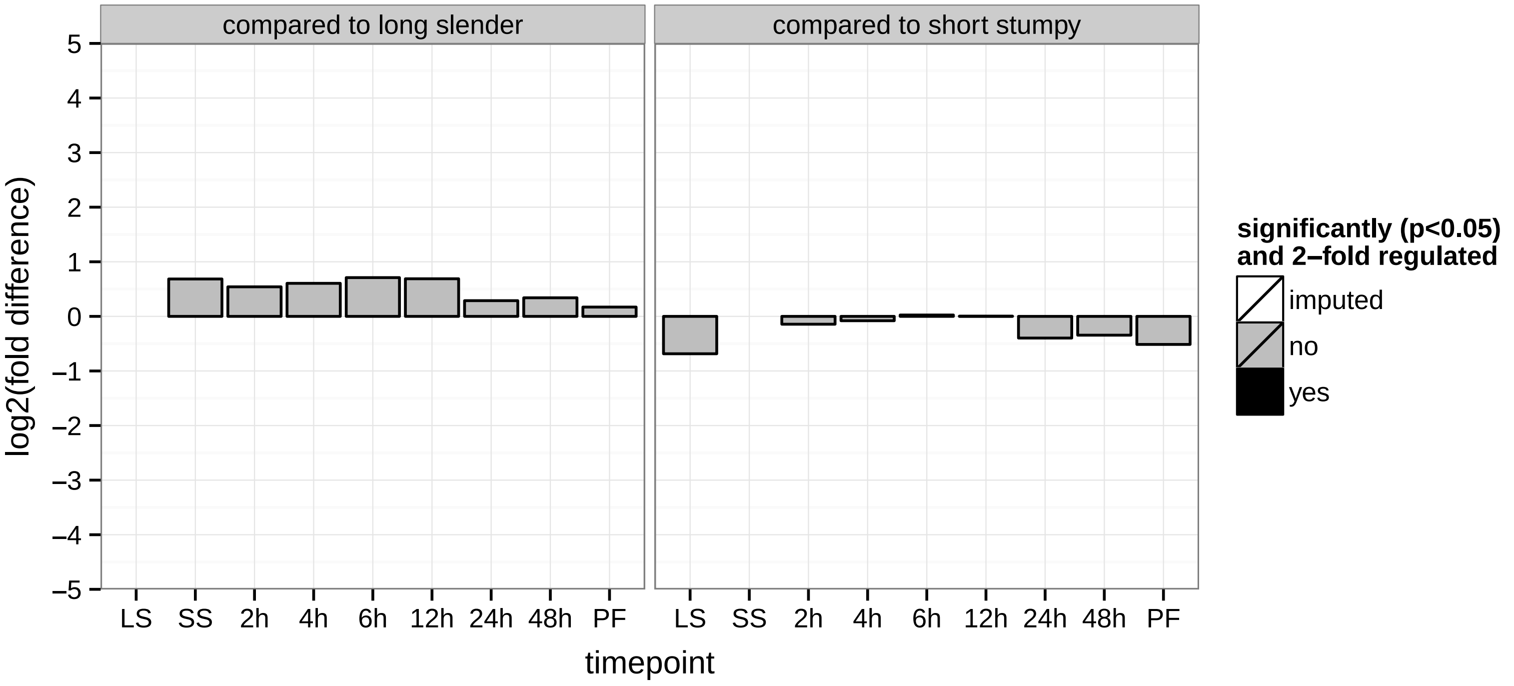
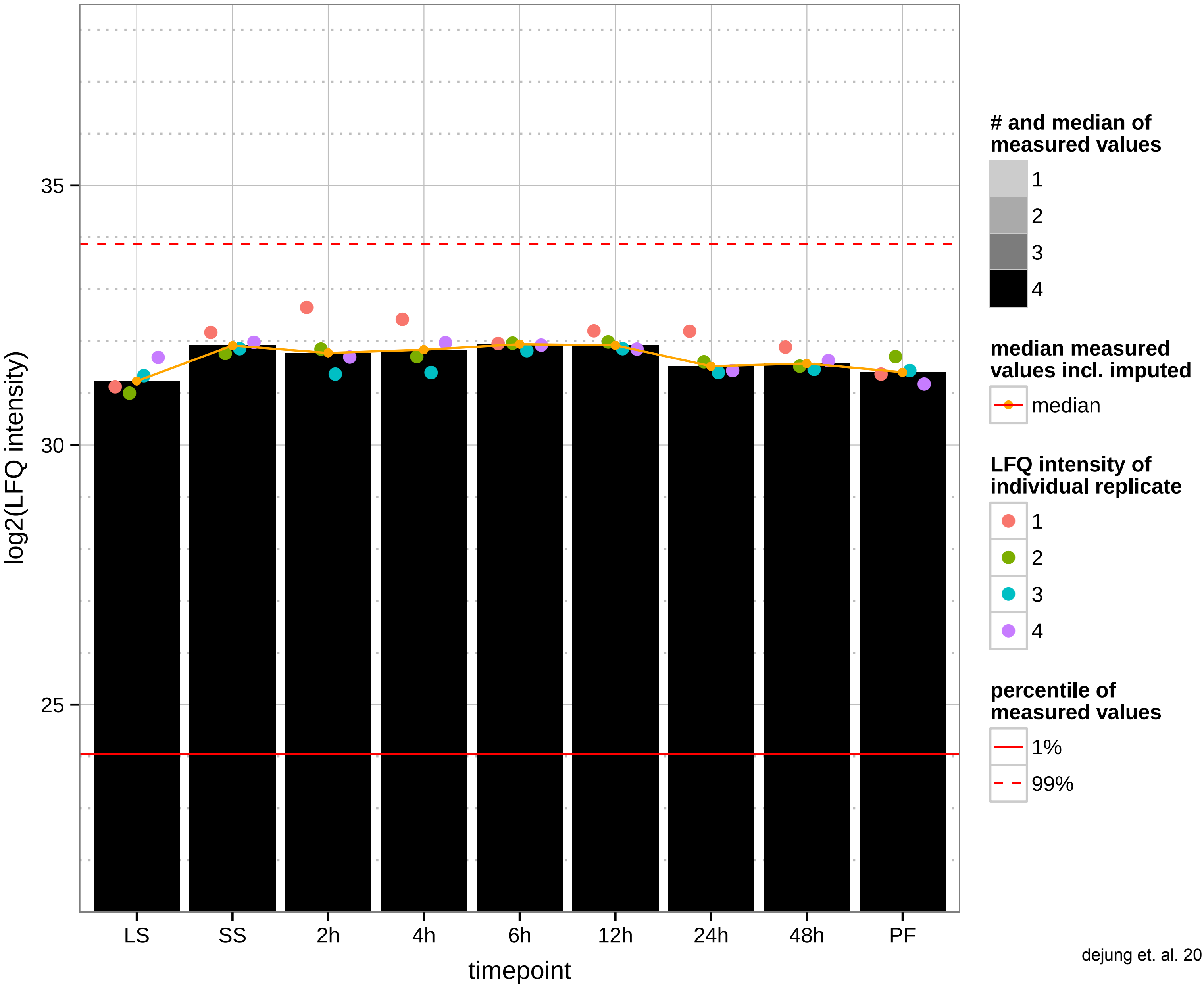
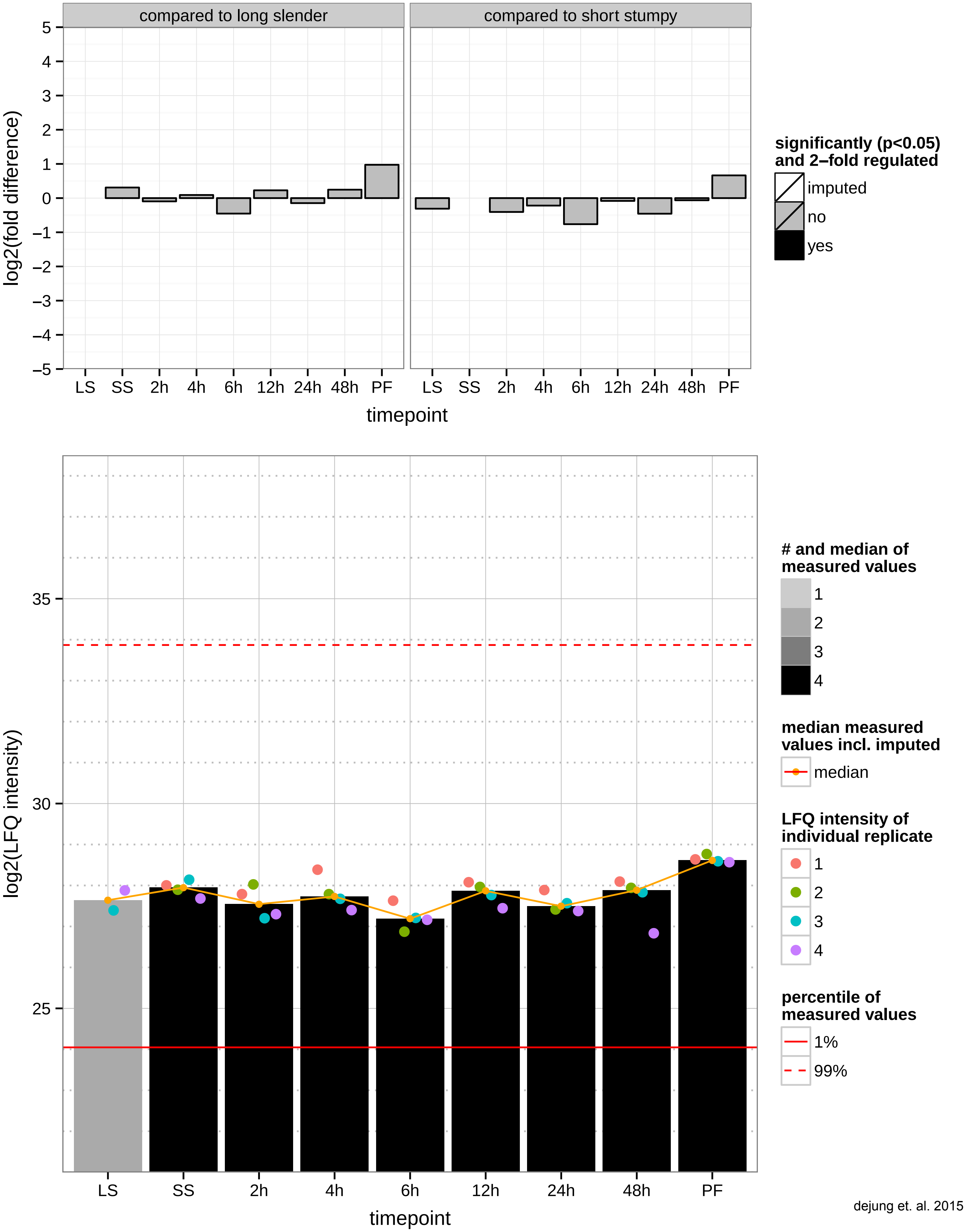
GDP–mannose pyrophosphorylase
Tb927.8.2050
AGOF: mannose–1–phosphate guanylyltransferase activity, nucleotidyltransferase activity
AGOC: cytoplasm
AGOP: GDP–mannose biosynthetic process, protein glycosylation
PGOF: nucleotidyltransferase activity
PGOC: null
PGOP: biosynthetic process





dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.2120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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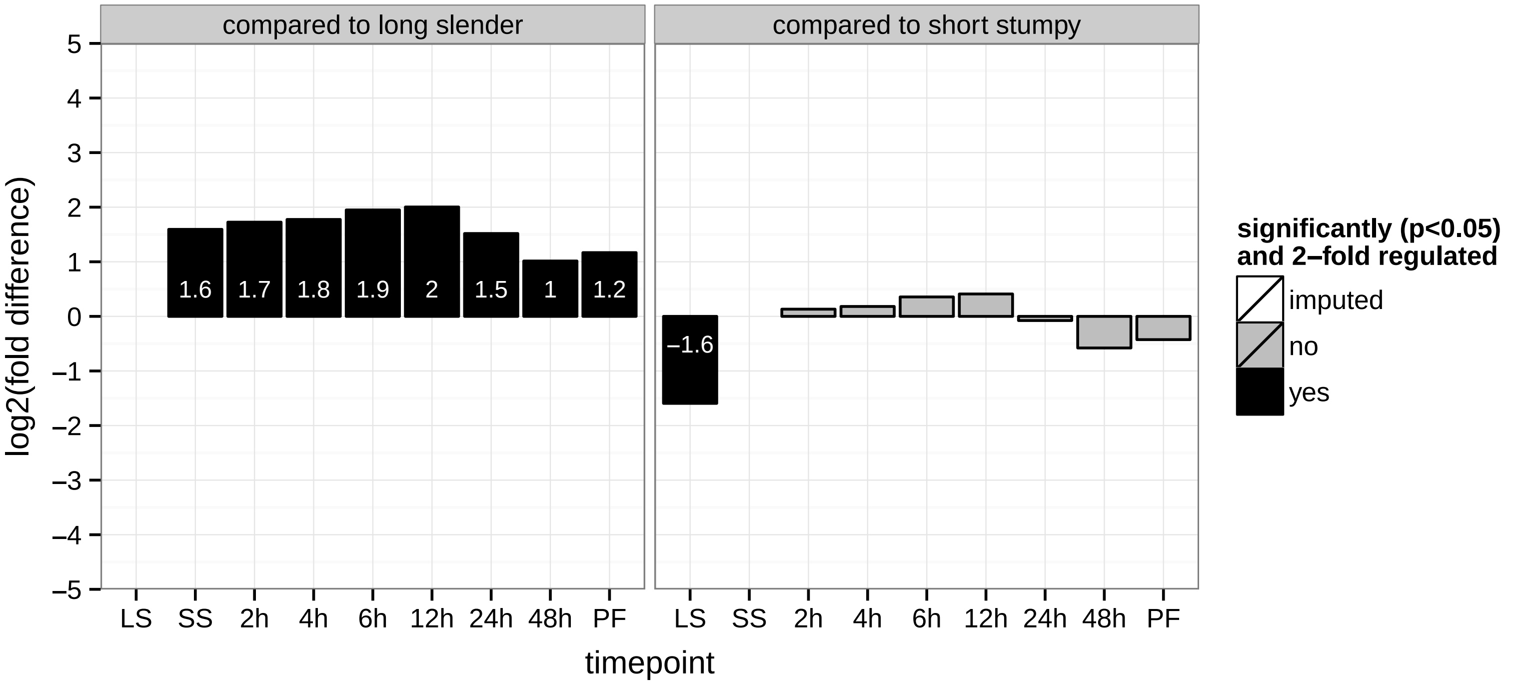
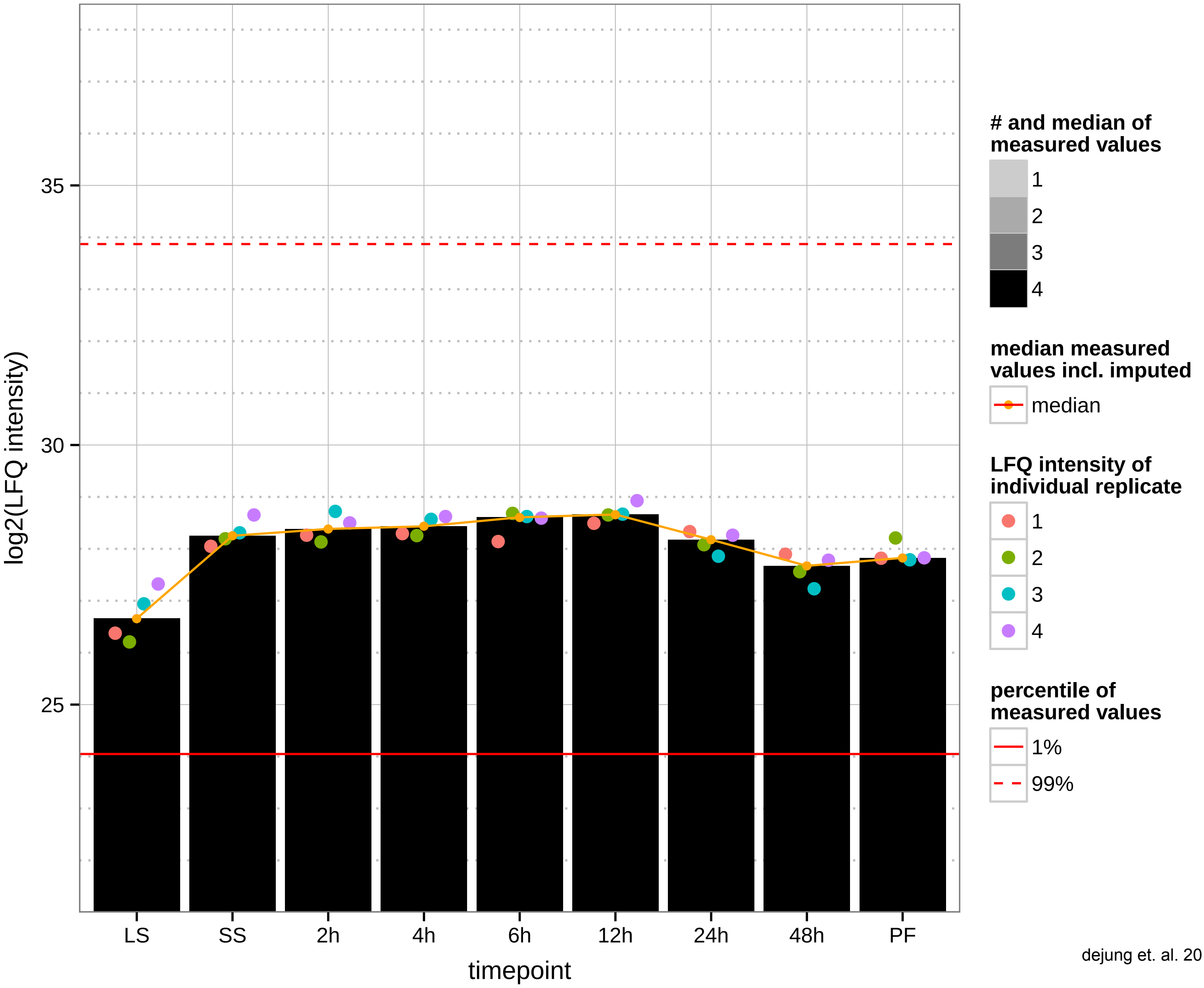
terbinafine resistance locus protein (yip1), putative
Tb927.8.2200
AGOF: null
AGOC: Golgi apparatus, integral to membrane
AGOP: response to drug, vesicle−mediated transport
PGOF: null
PGOC: membrane
PGOP: null





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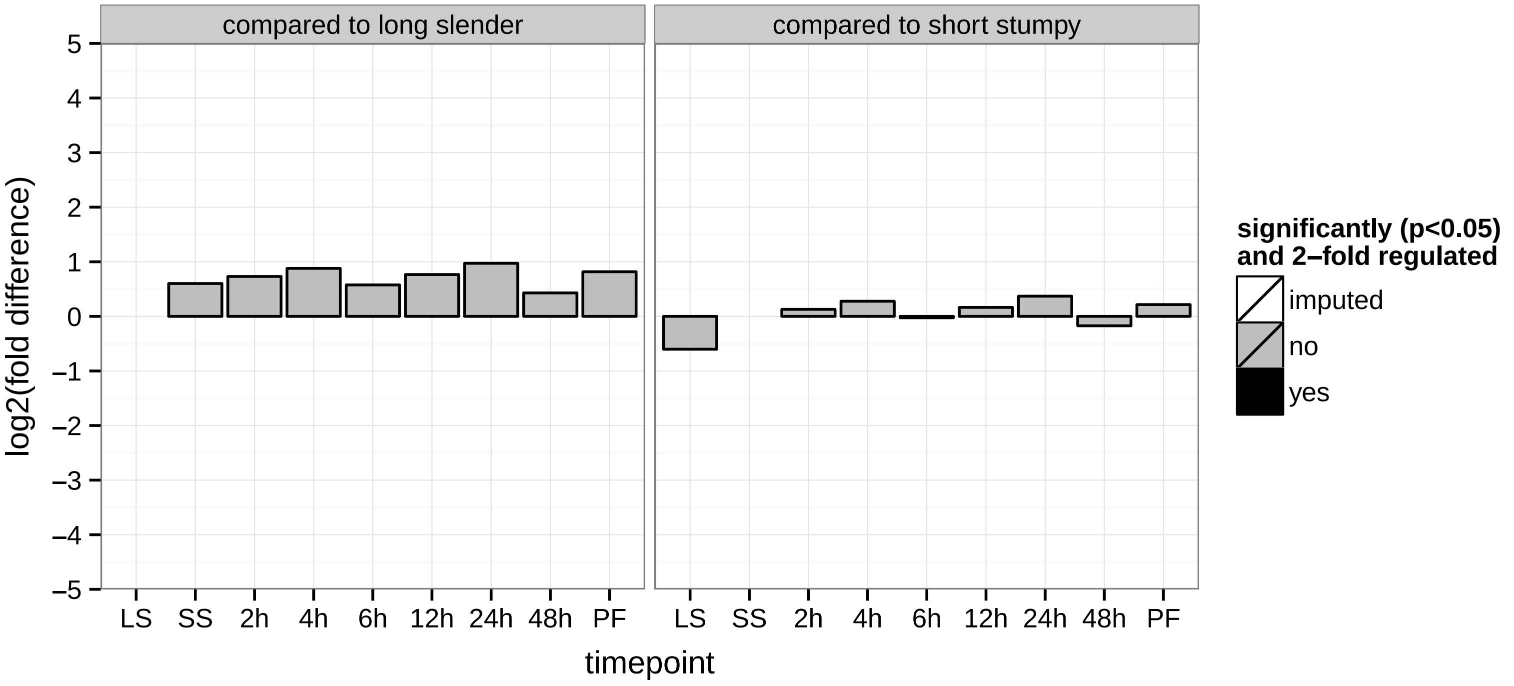
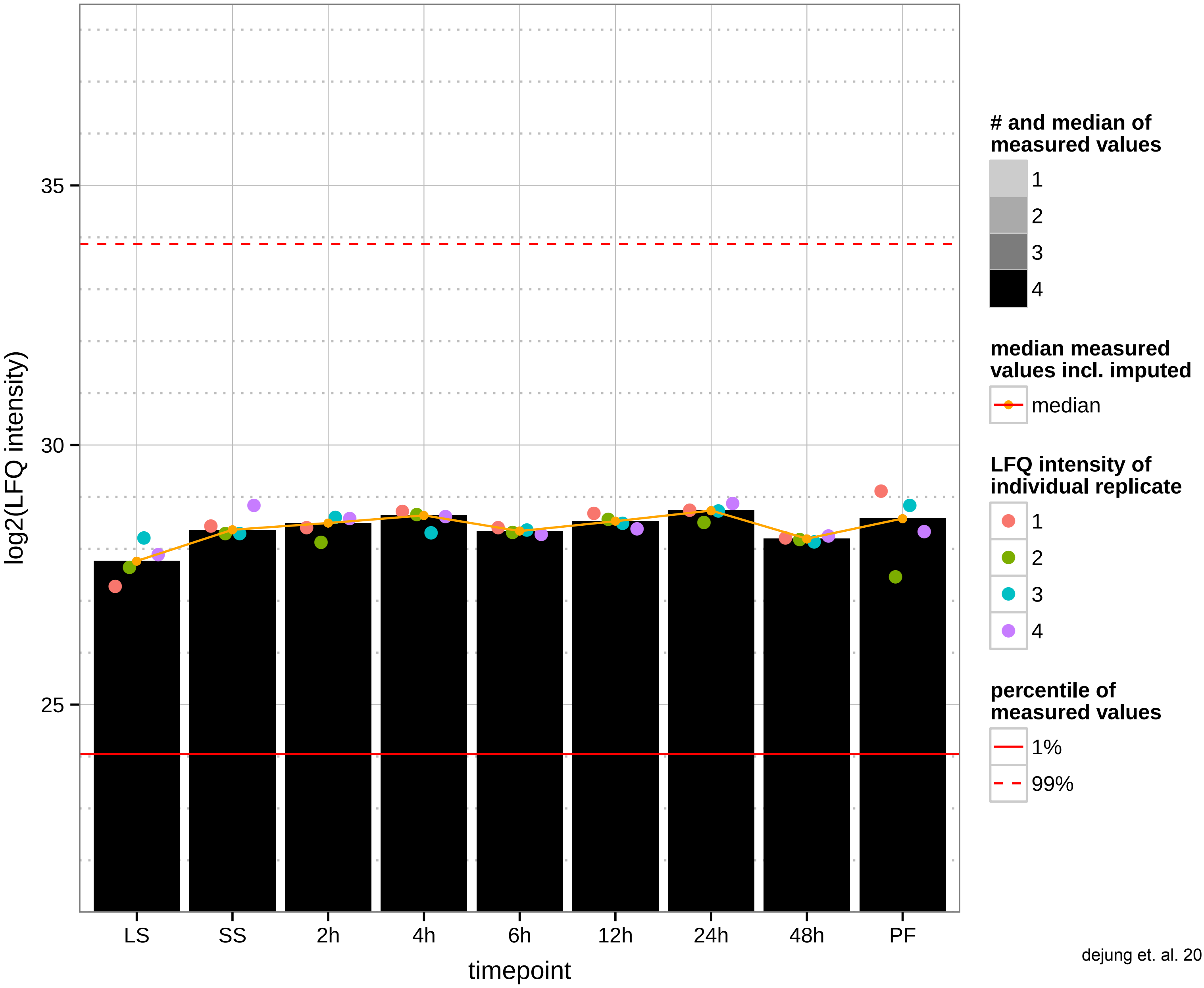
pteridine reductase (PTR1)
Tb927.8.2210
AGOF: oxidoreductase activity, pteridine reductase activity
AGOC: cytosol
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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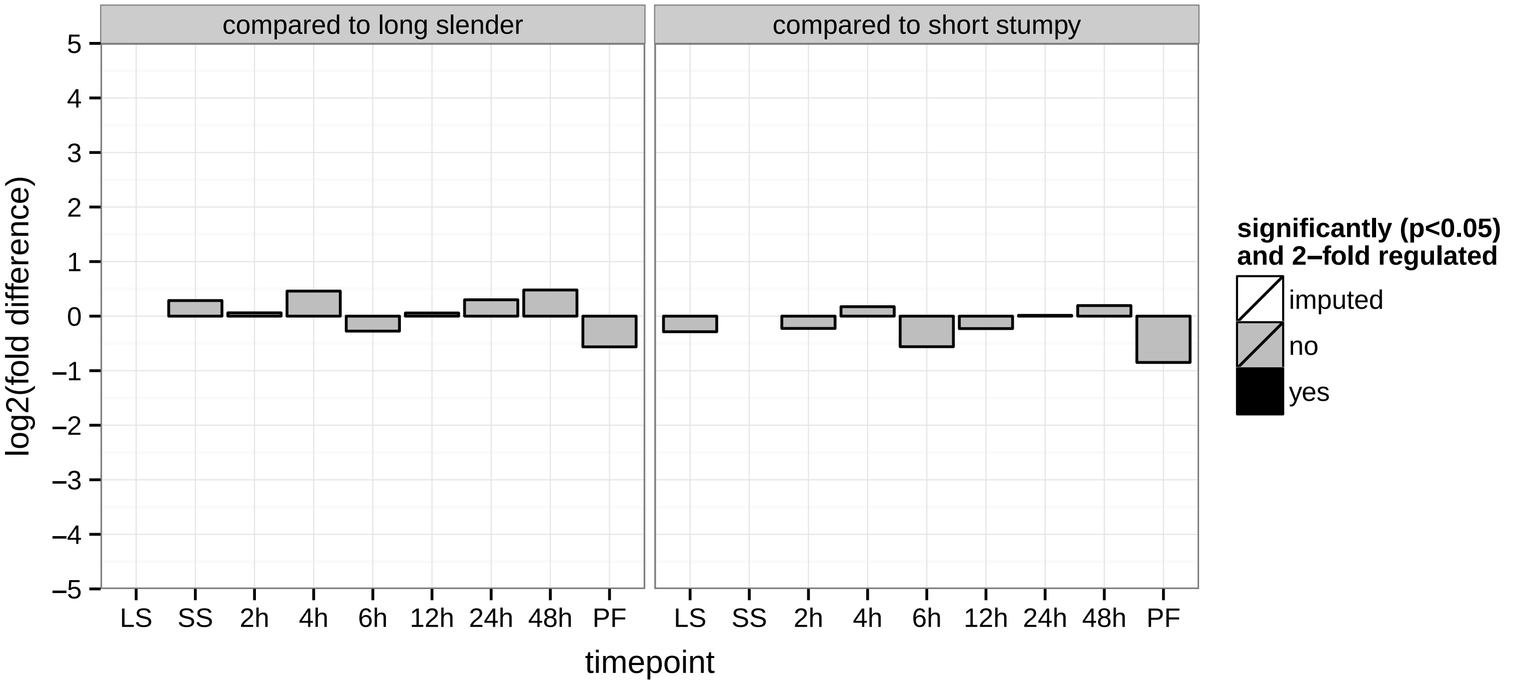
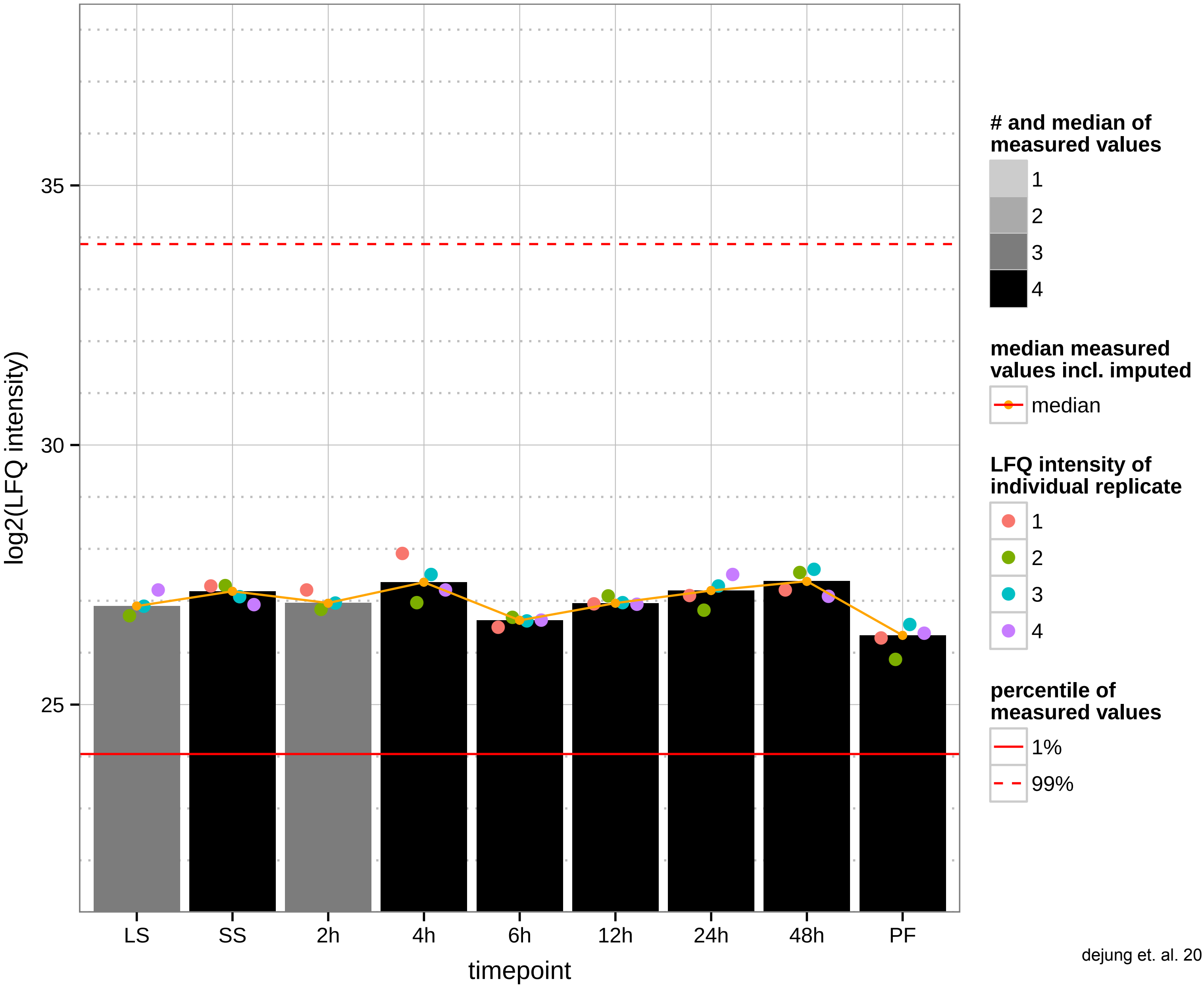
hypothetical protein, conserved
Tb927.8.2290
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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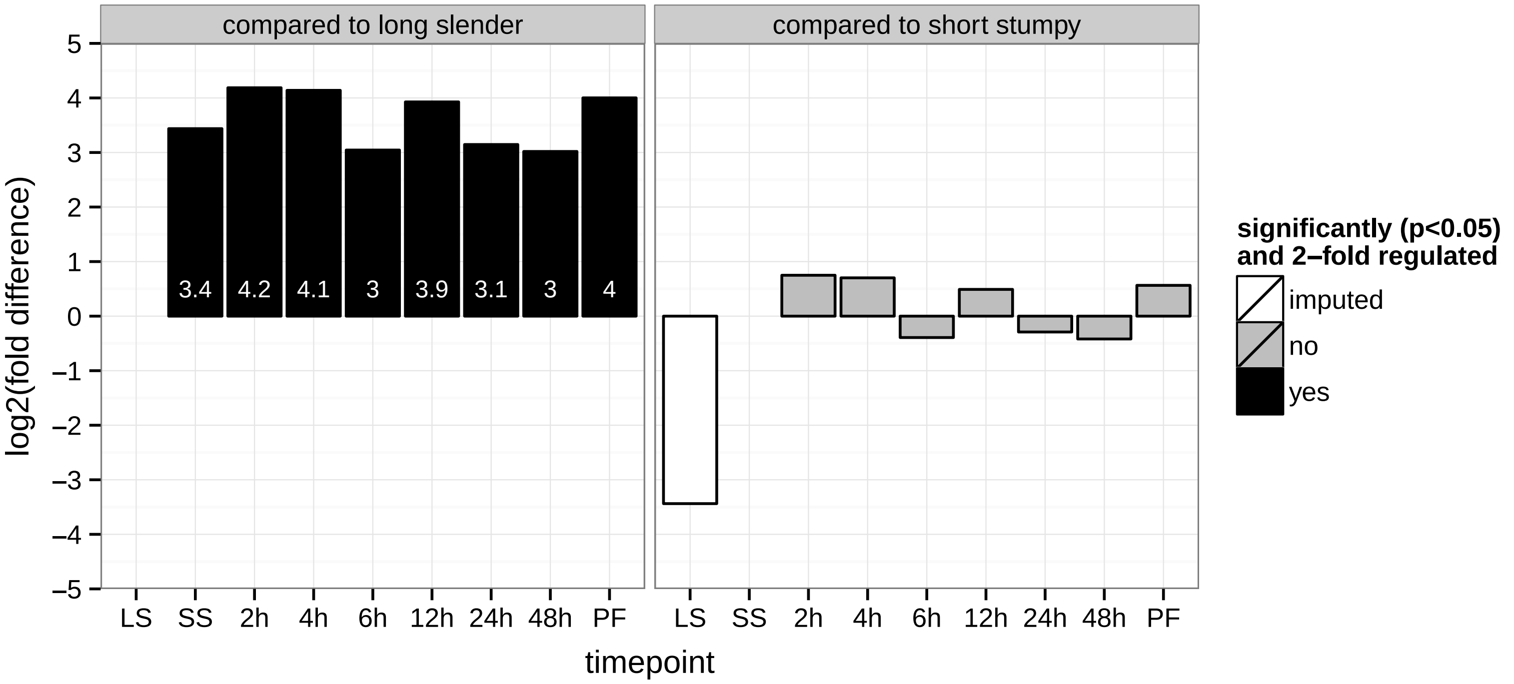
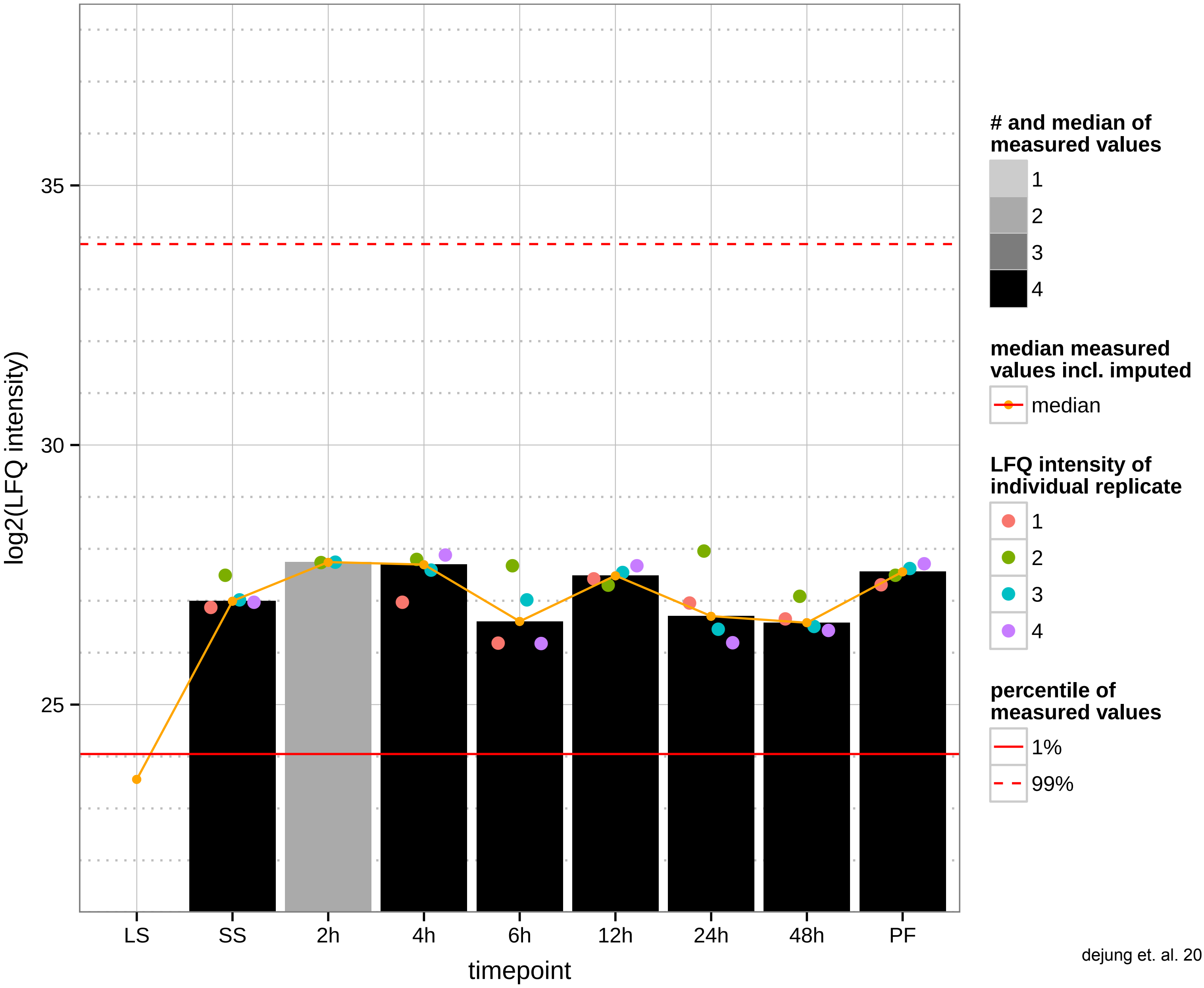
(H+)–ATPase G subunit, putative
Tb927.8.2310
AGOF: ATPase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances
AGOC: myosin complex, vacuolar proton–transporting V–type ATPase complex
AGOP: proton transport, vacuolar acidification
PGOF: hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances
PGOC: vacuolar proton–transporting V–type ATPase complex
PGOP: proton transport





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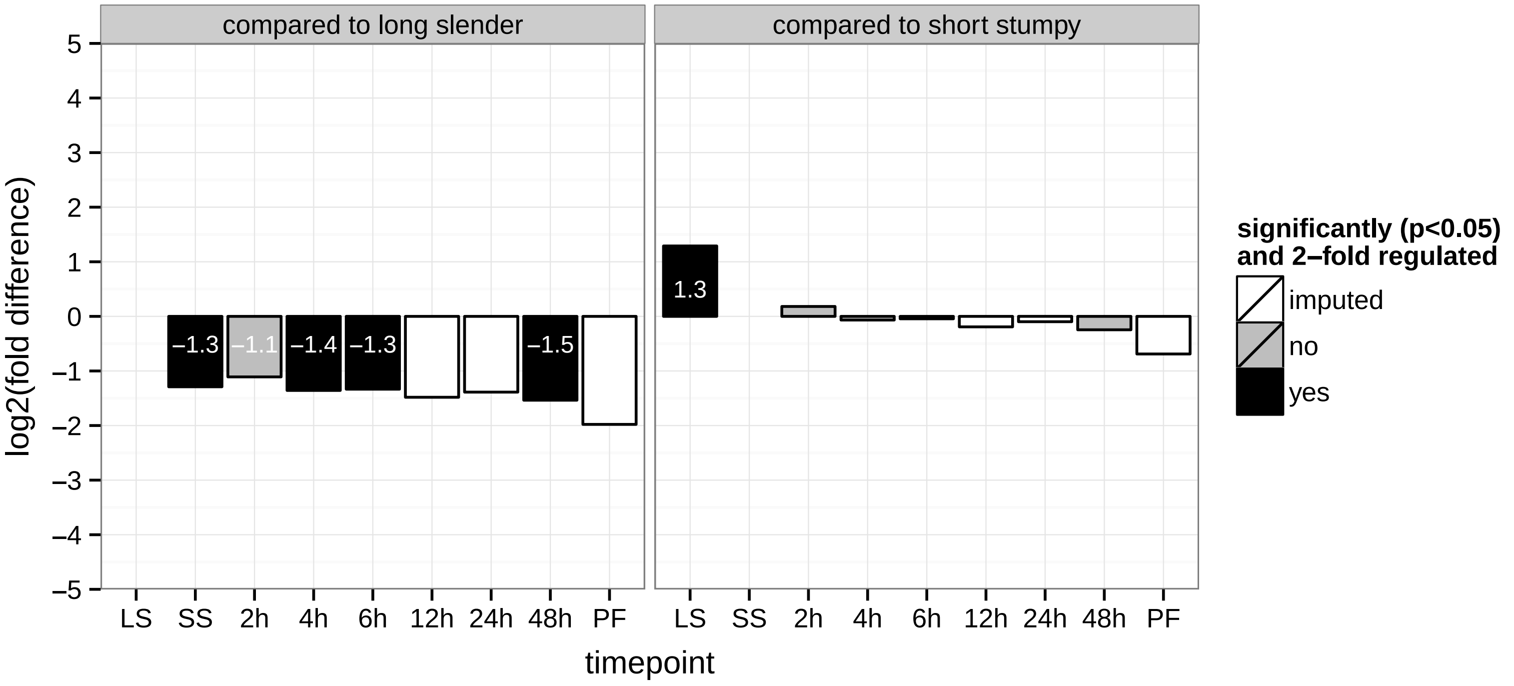
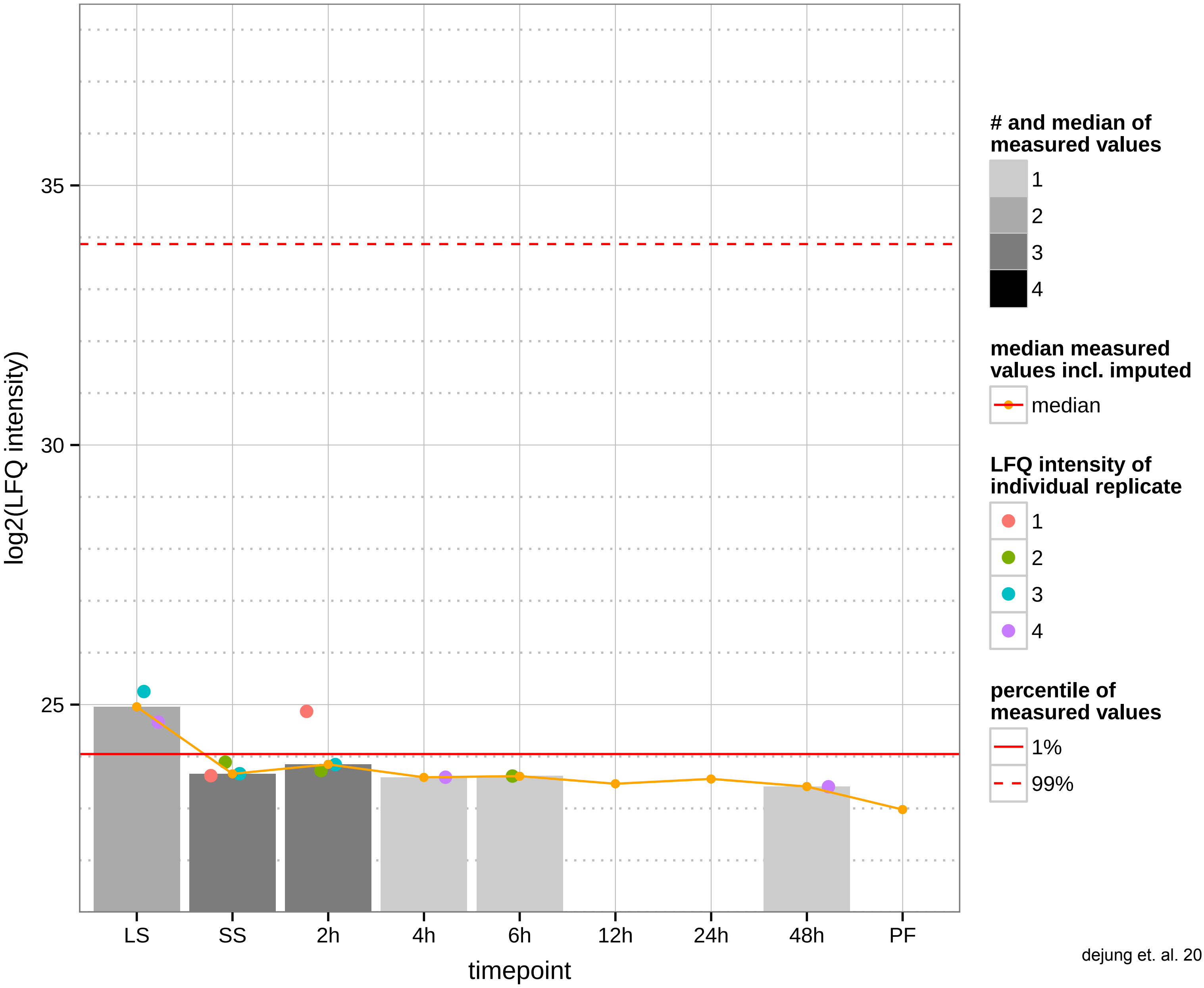
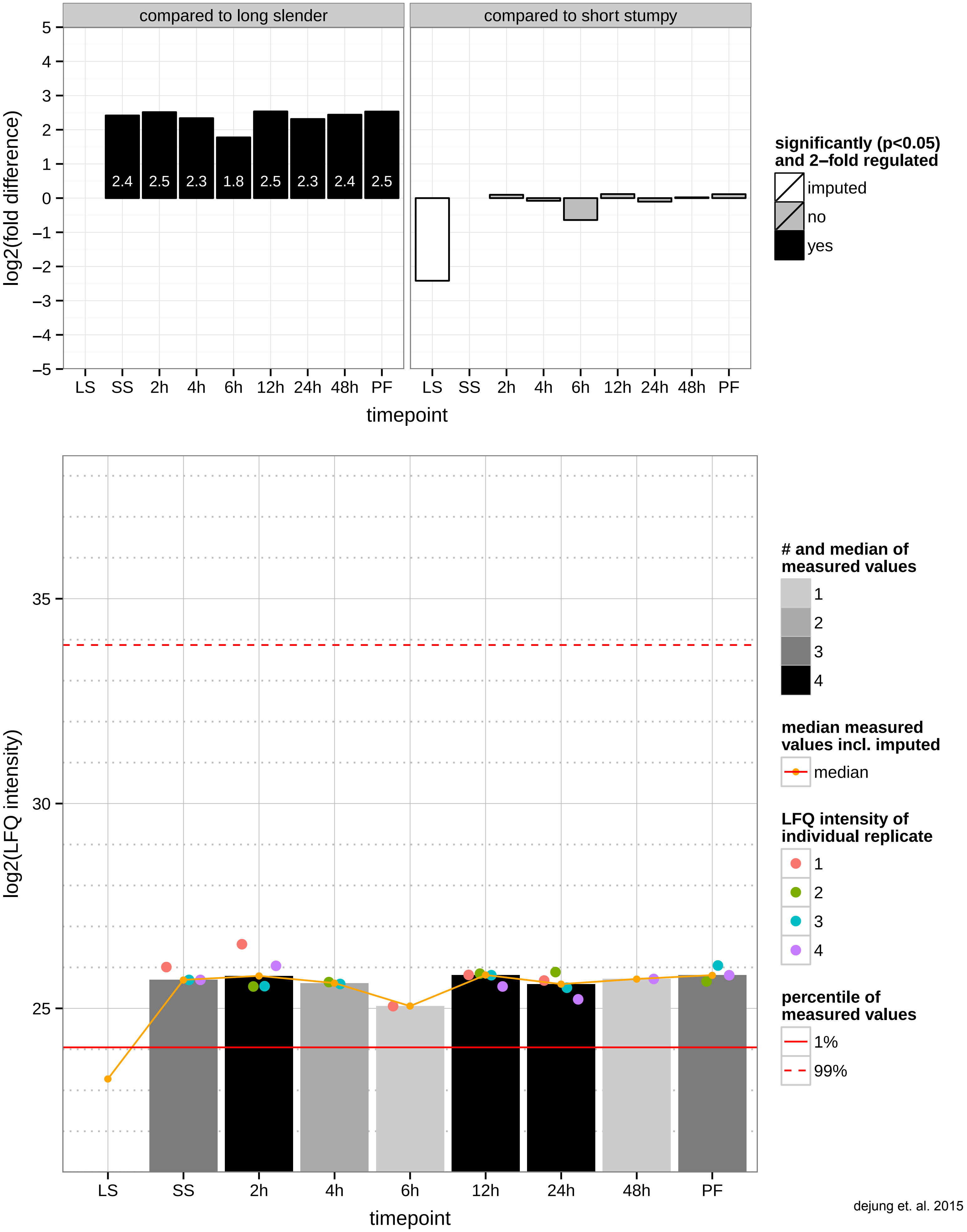
ABC transporter, putative
Tb927.8.2380
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances, heme binding, protein homodimeri
AGOC: flagellar pocket, integral to membrane, membrane, vesicle
AGOP: heme transport
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: membrane
PGOP: null





dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.2450
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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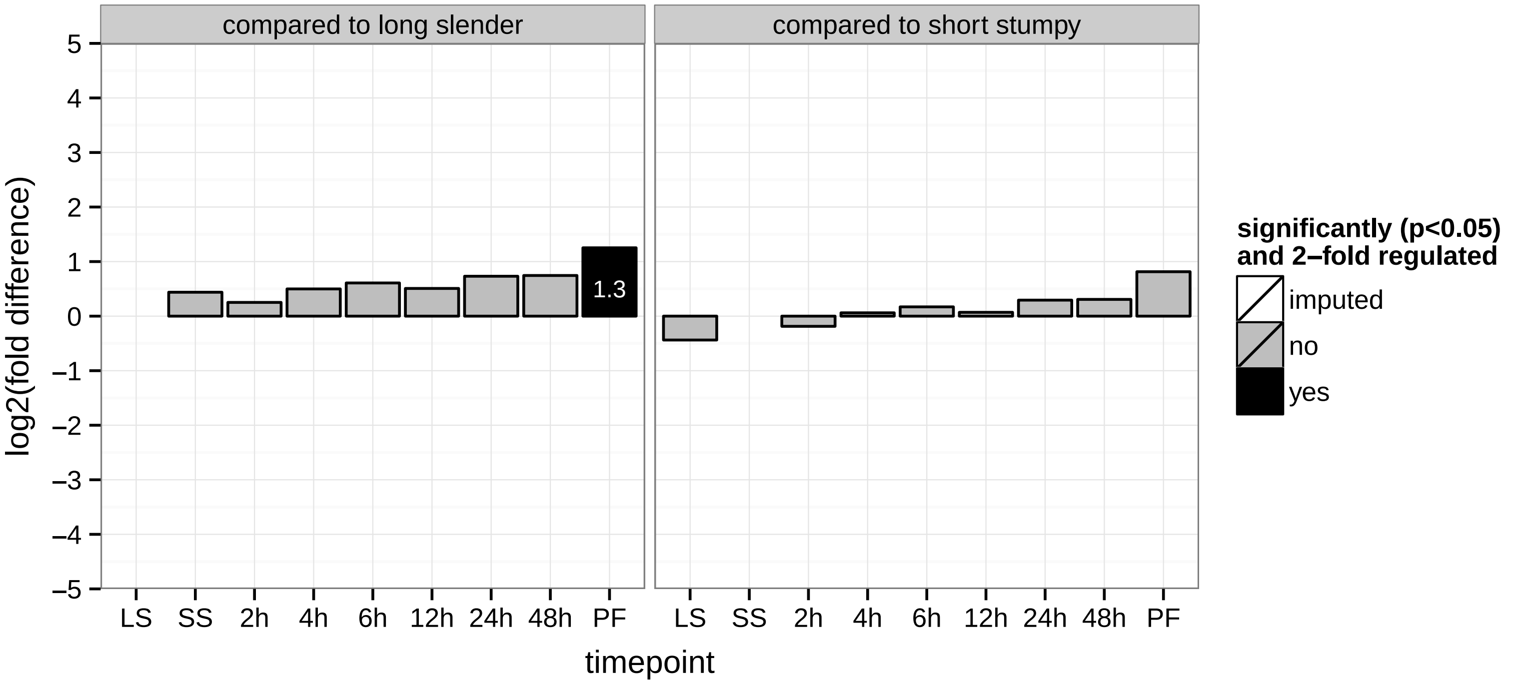
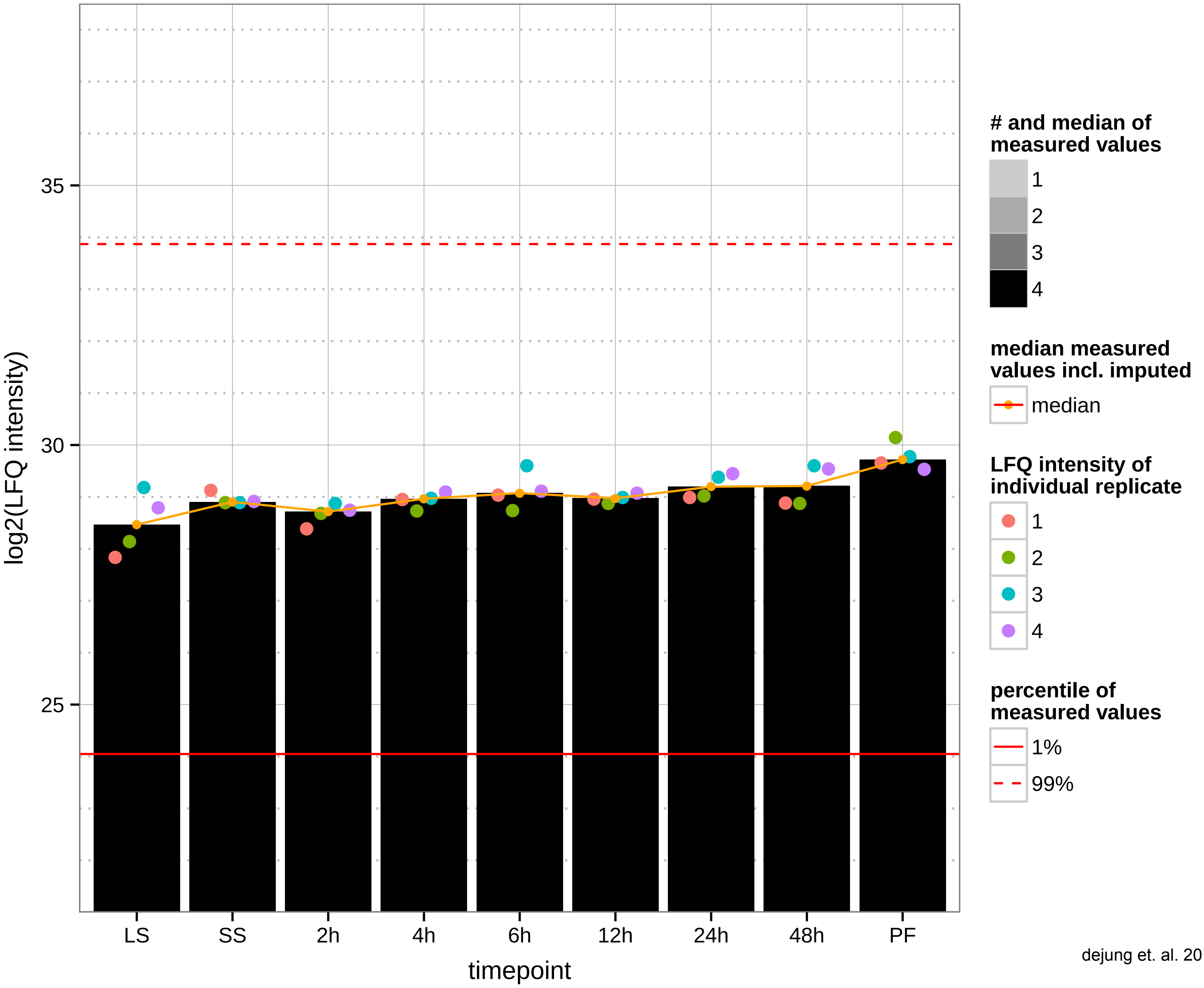
hypothetical protein, conserved
Tb927.8.2460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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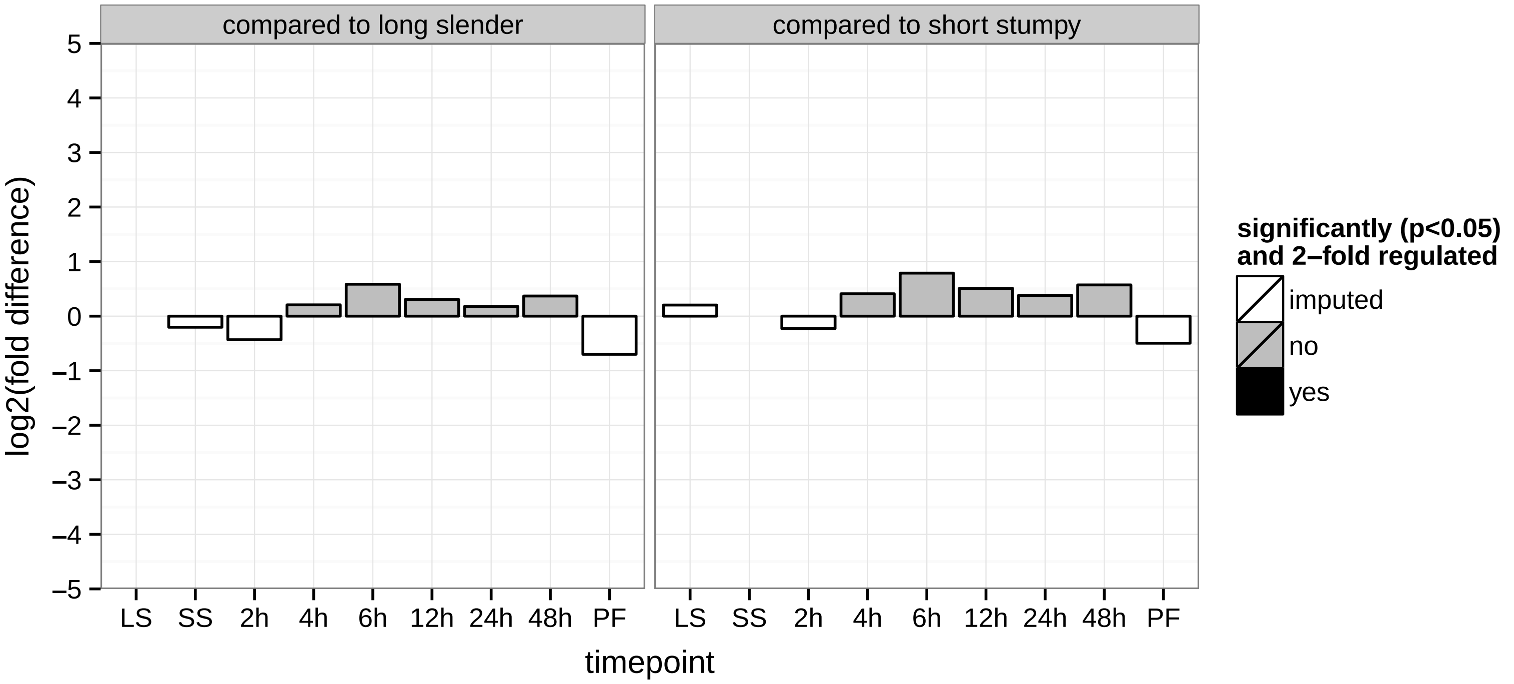
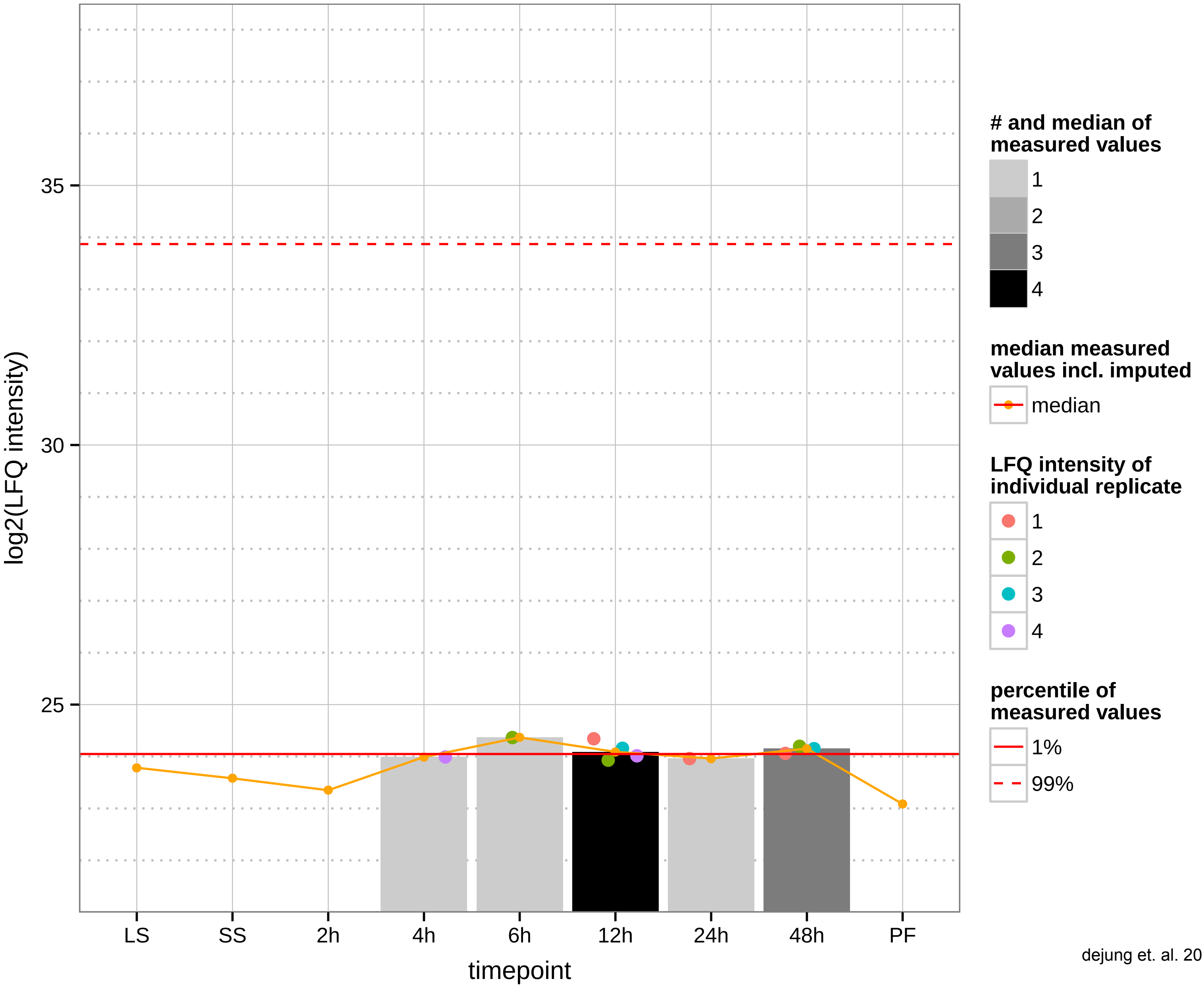
hypothetical protein, conserved
Tb927.8.2590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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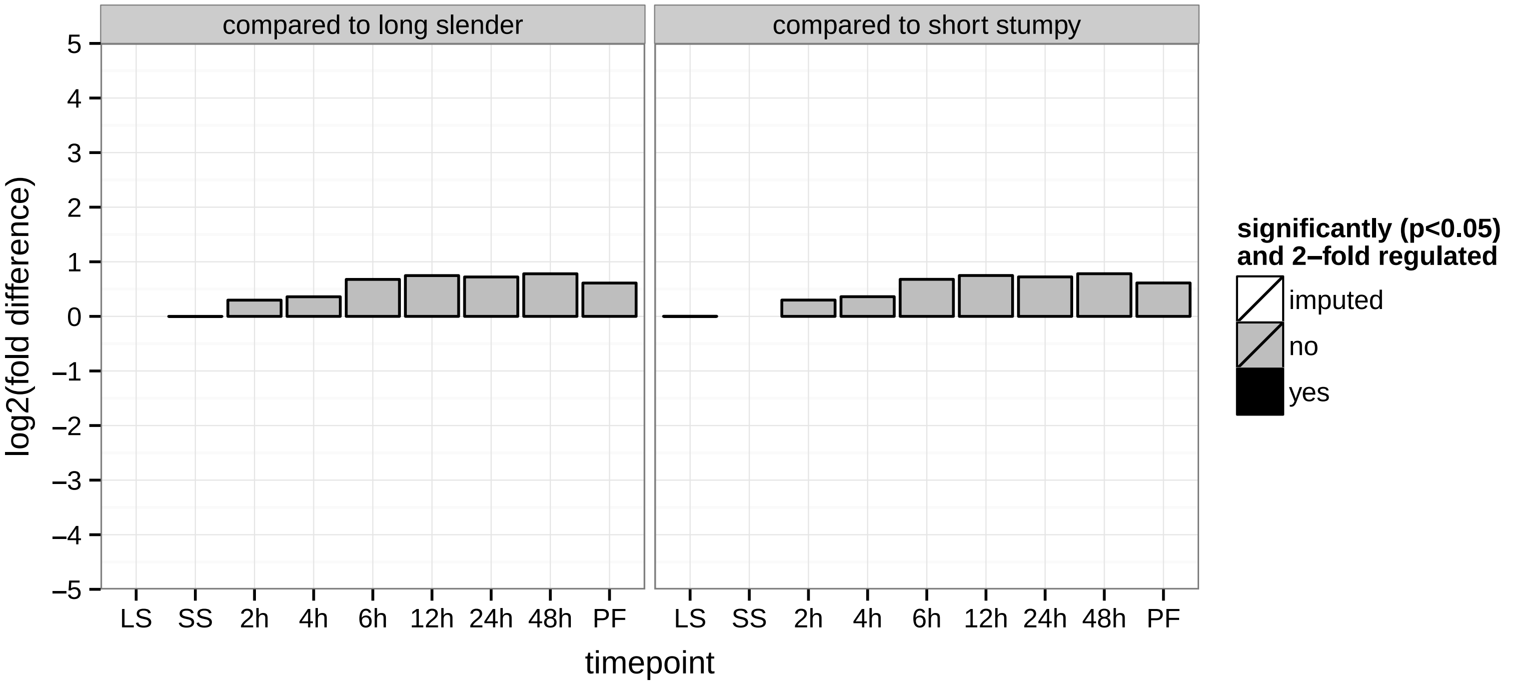
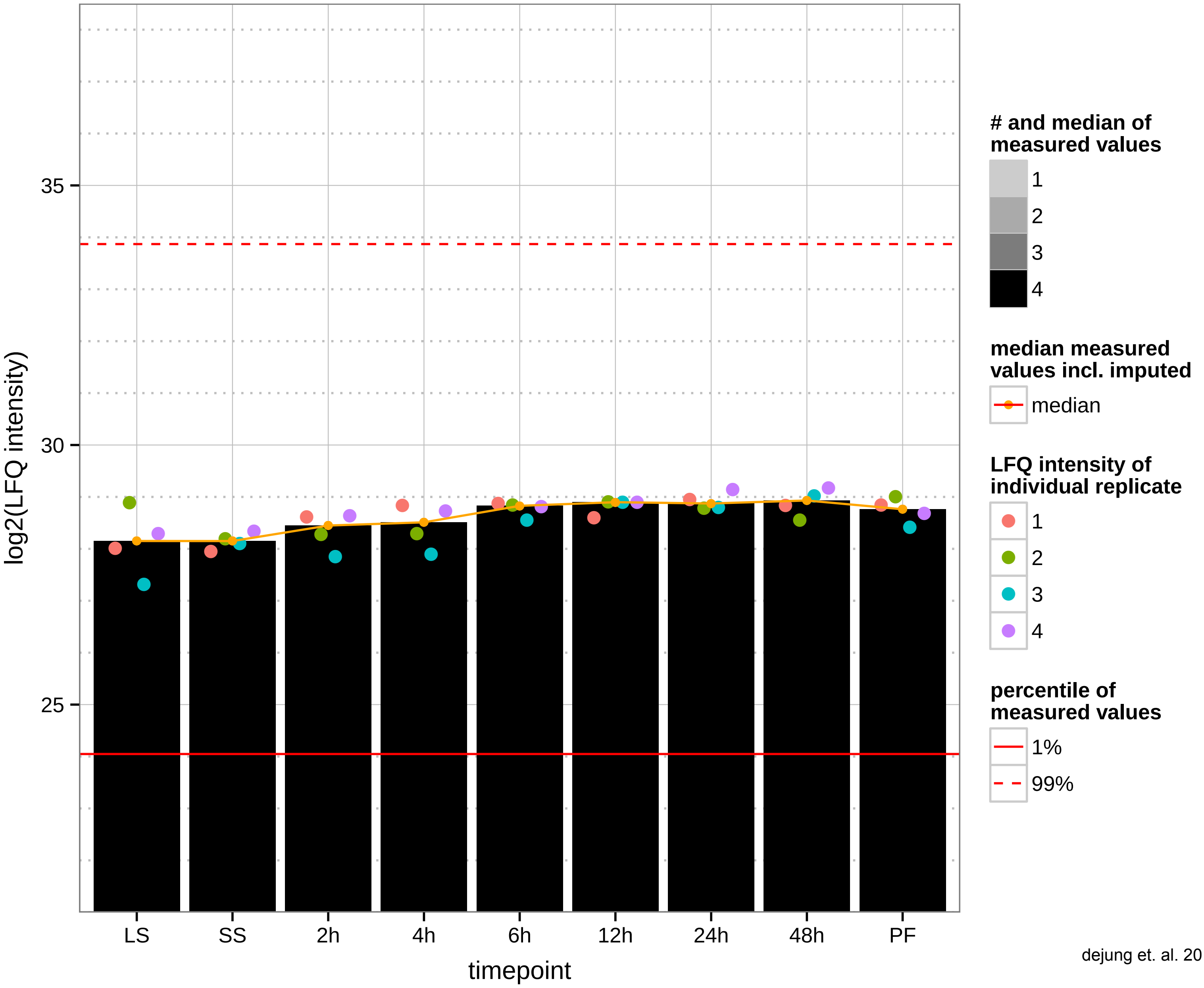
hypothetical protein, conserved
Tb927.8.2600
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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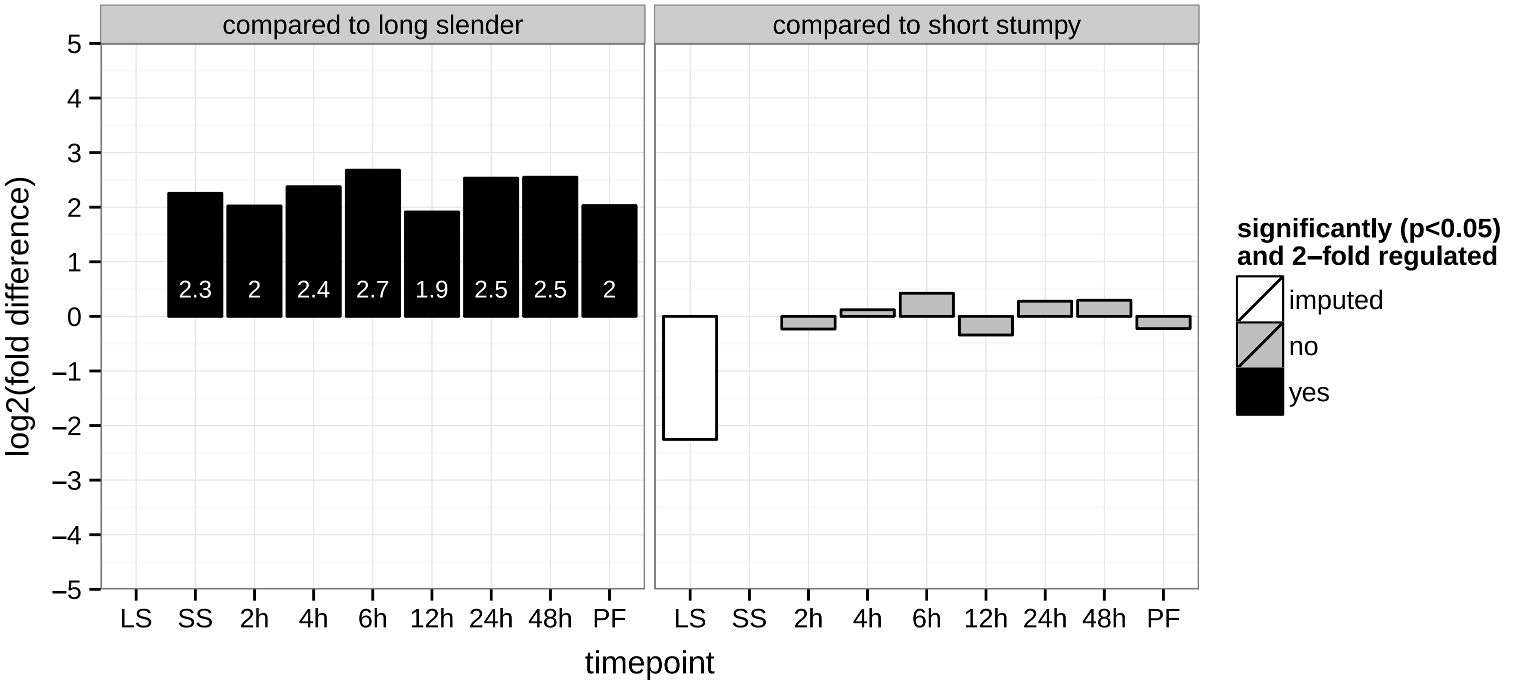
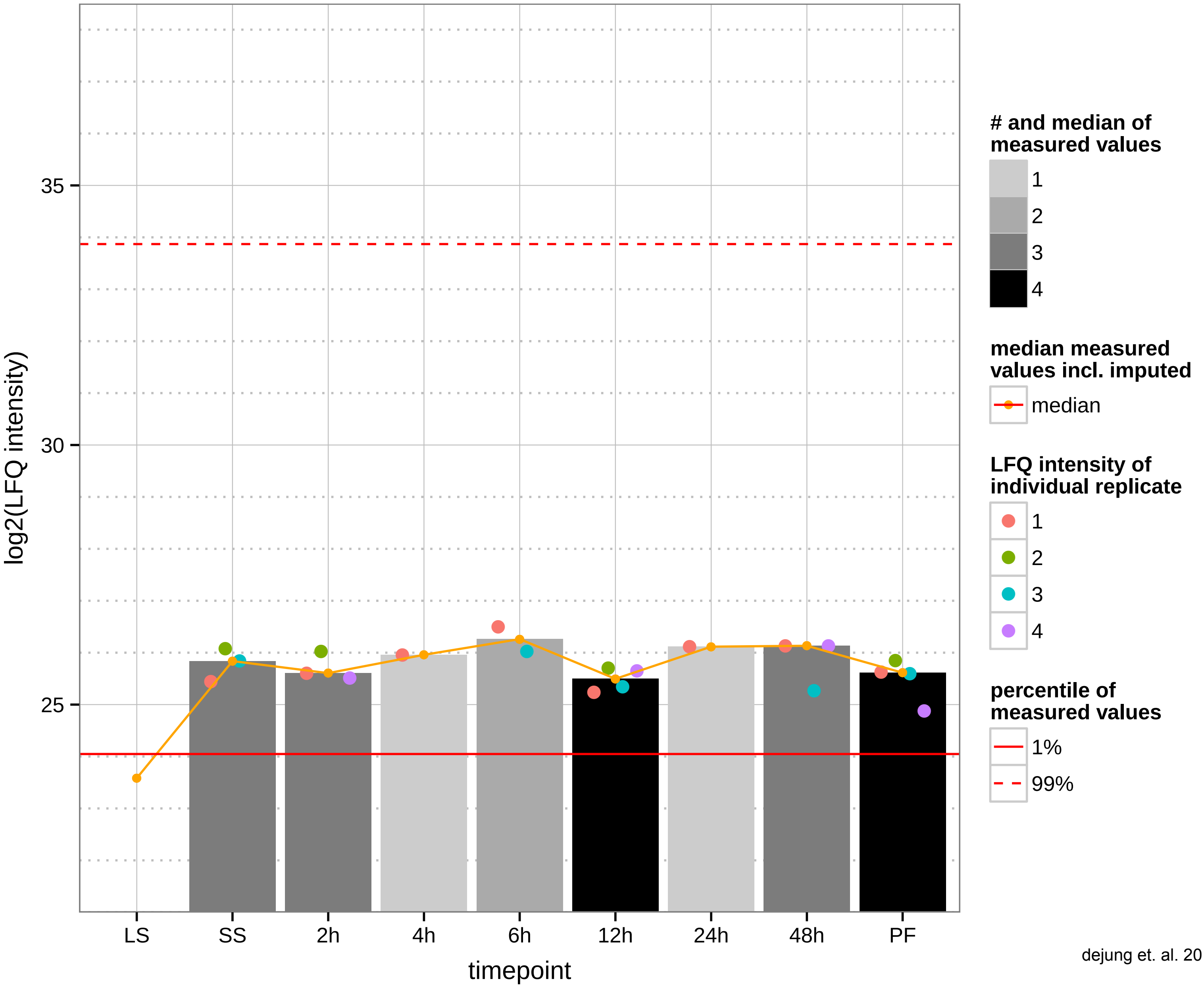
hypothetical protein, conserved
Tb927.8.2620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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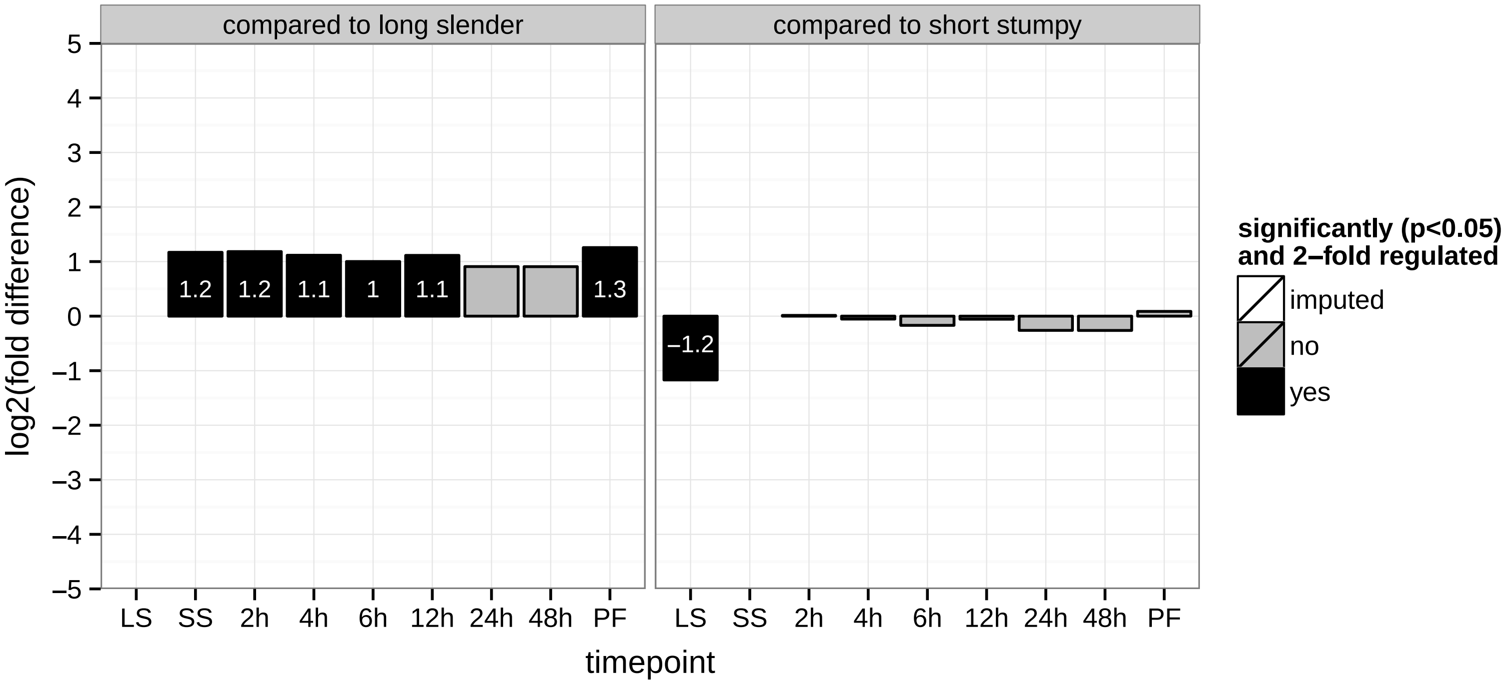
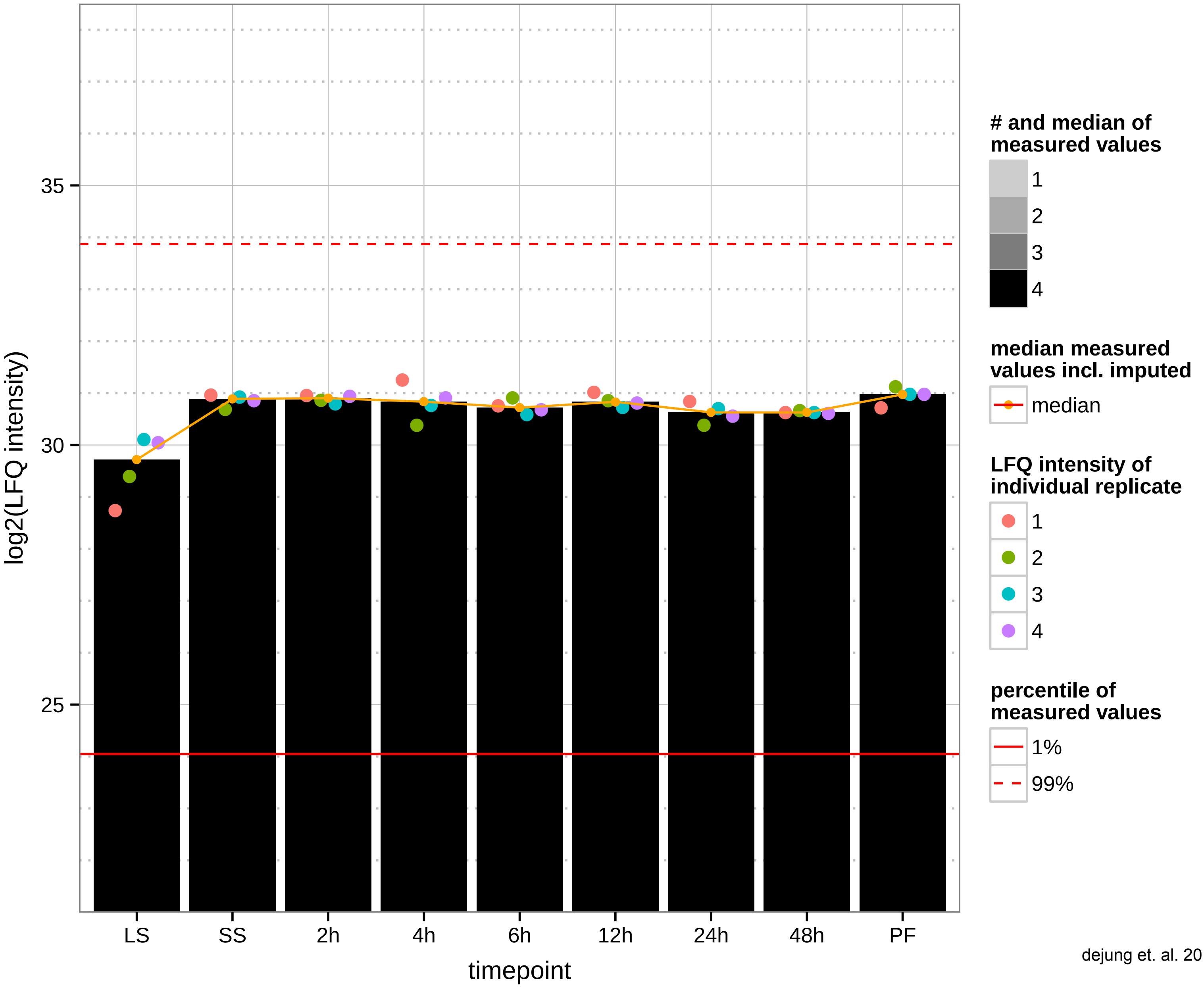
ubiquitin–activating enzyme E1, putative (UBA1)
Tb927.8.2640
AGOF: ATP binding, ubiquitin activating enzyme activity, ubiquitin–protein ligase activity
AGOC: null
AGOP: cellular protein modification process
PGOF: ATP binding, catalytic activity, small protein activating enzyme activity
PGOC: null
PGOP: cellular protein modification process





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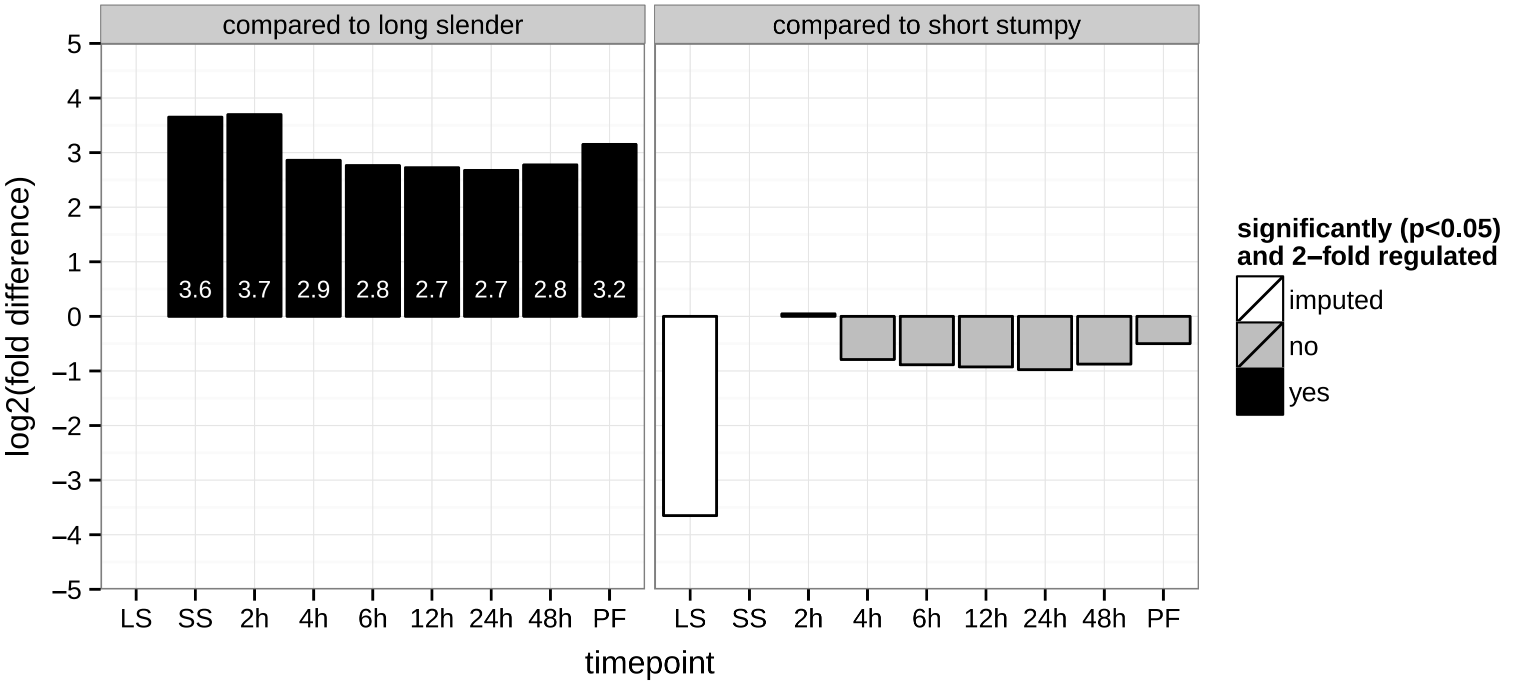
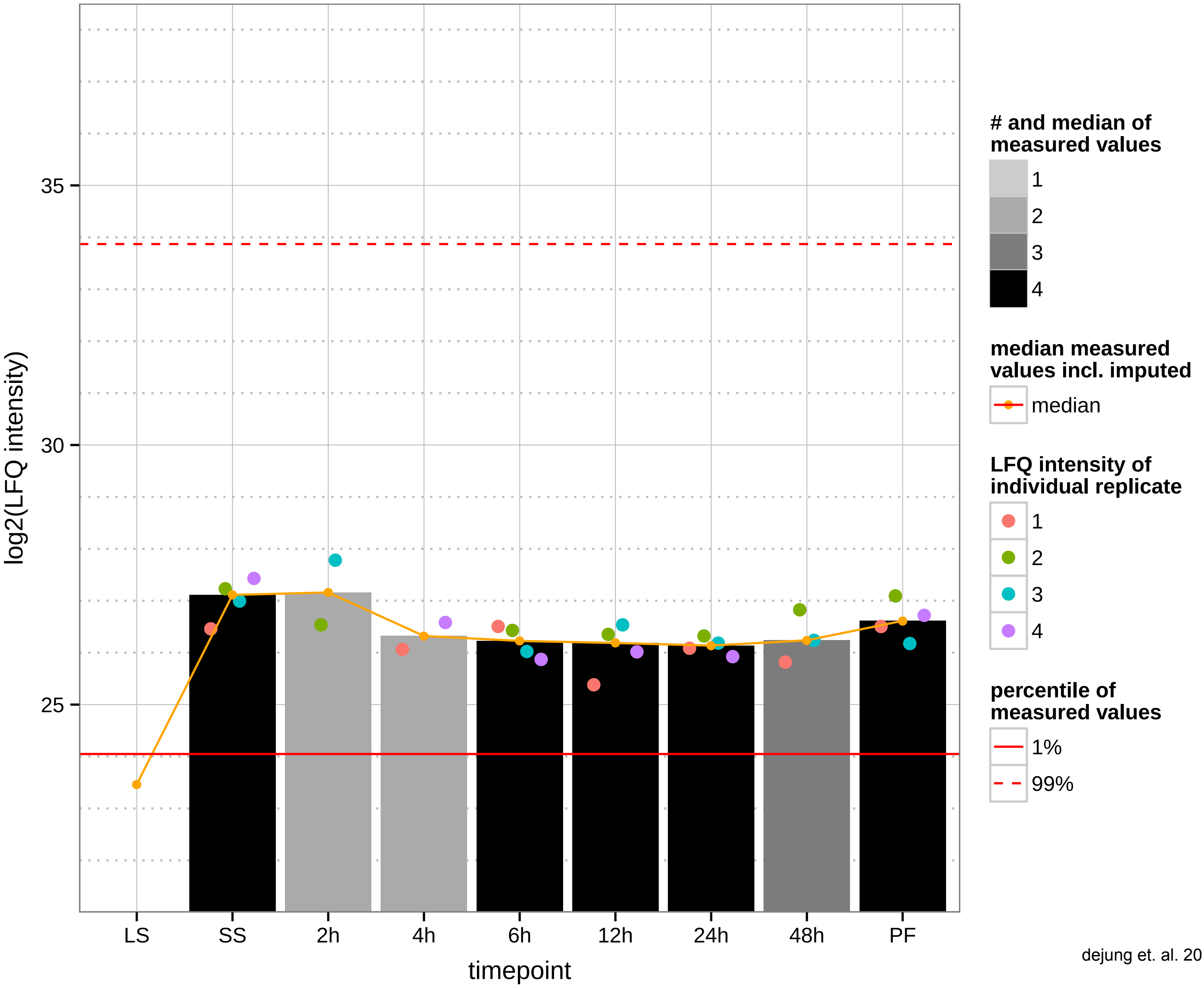
hypothetical protein, conserved
Tb927.8.2670
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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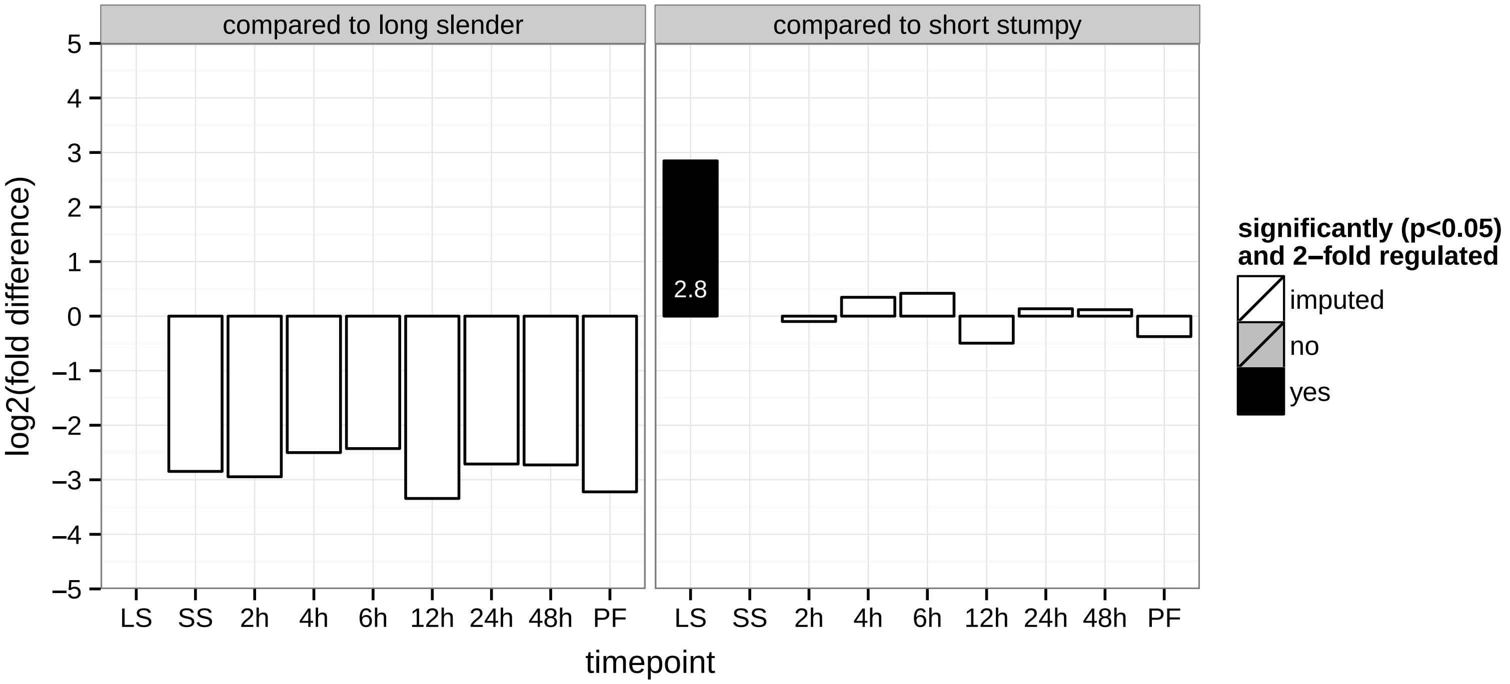
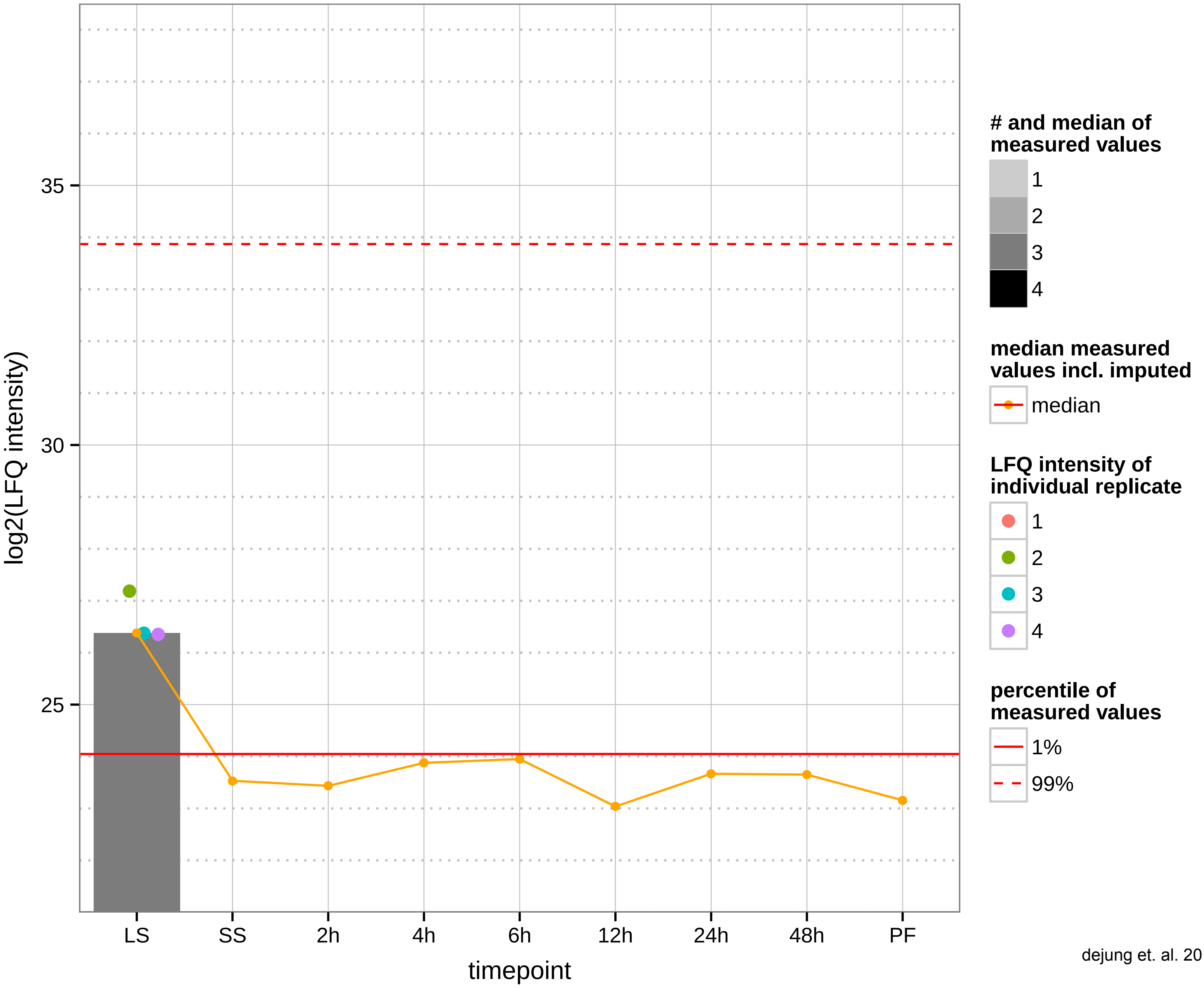
RNA–binding protein RBP10, putative (RBP10)
Tb927.8.2780
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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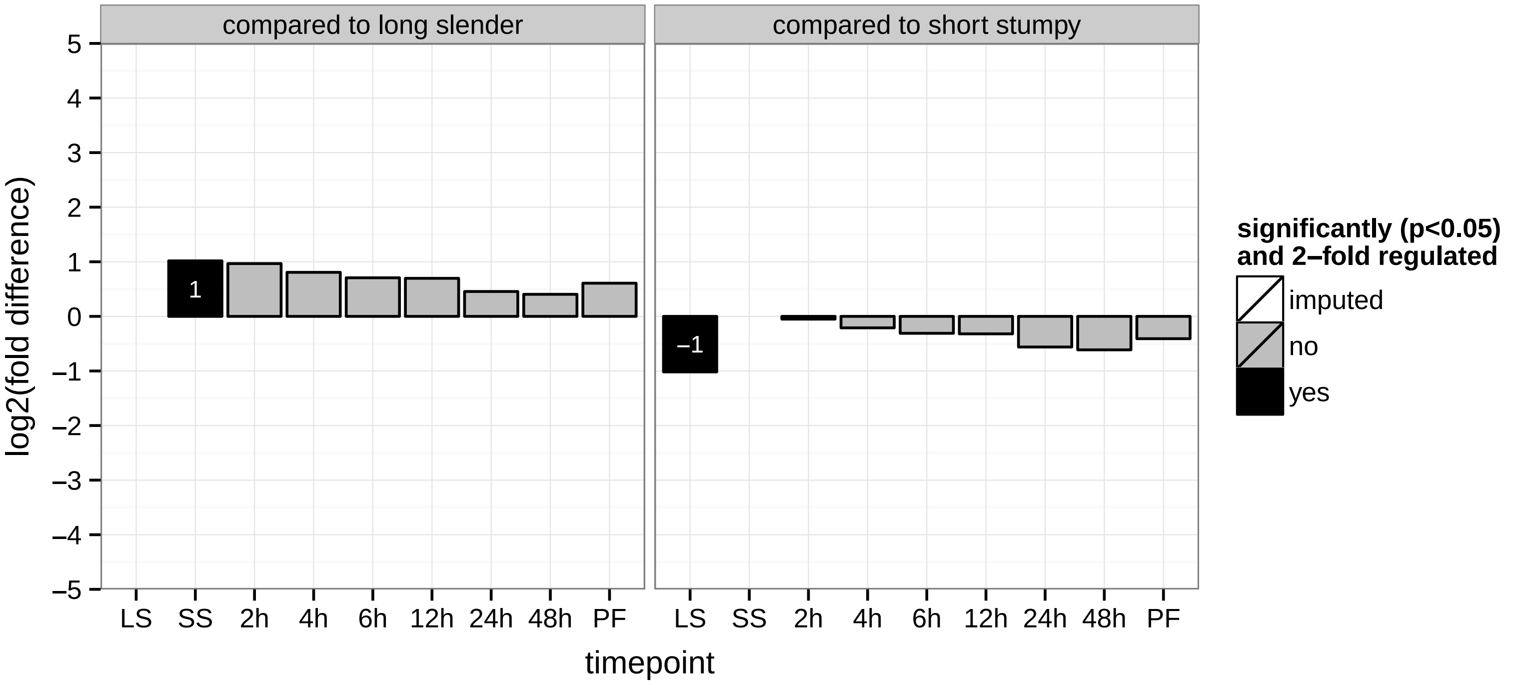
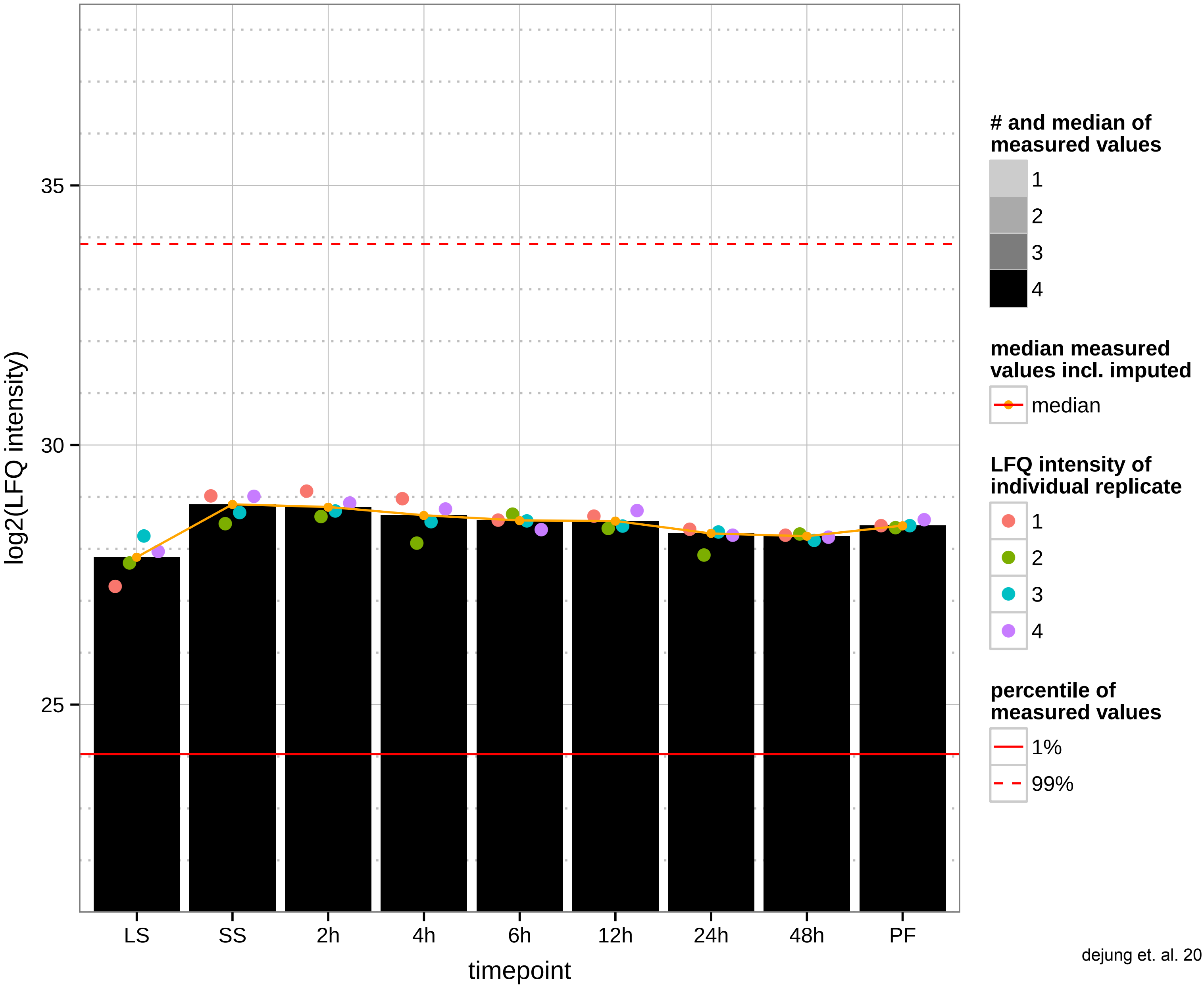
hypothetical protein, conserved
Tb927.8.2820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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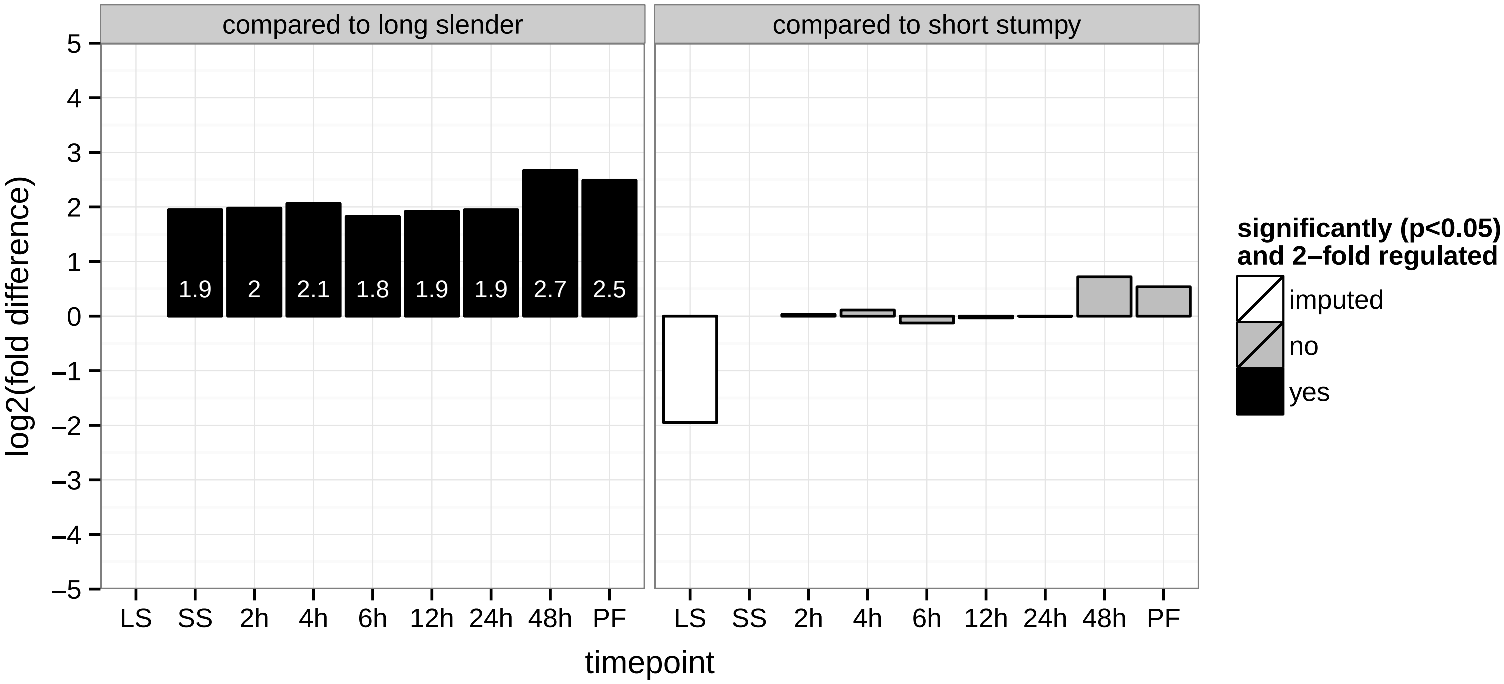
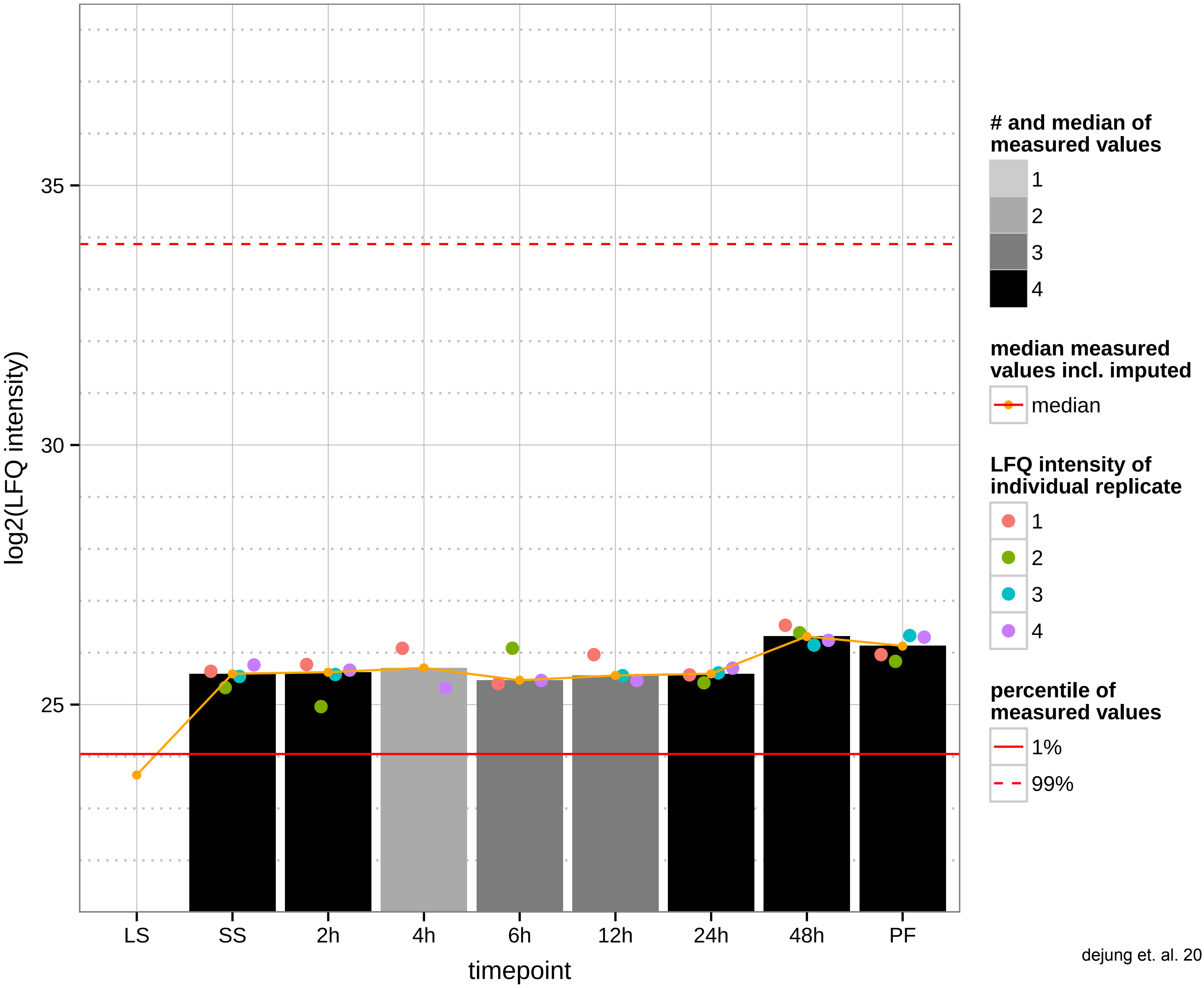
Poly(A)−specific ribonuclease PARN−1
Tb927.8.2850
AGOF: nuclease activity, nucleic acid binding
AGOC: cytoplasm, nucleus
AGOP: null
PGOF: nucleic acid binding
PGOC: nucleus
PGOP: null





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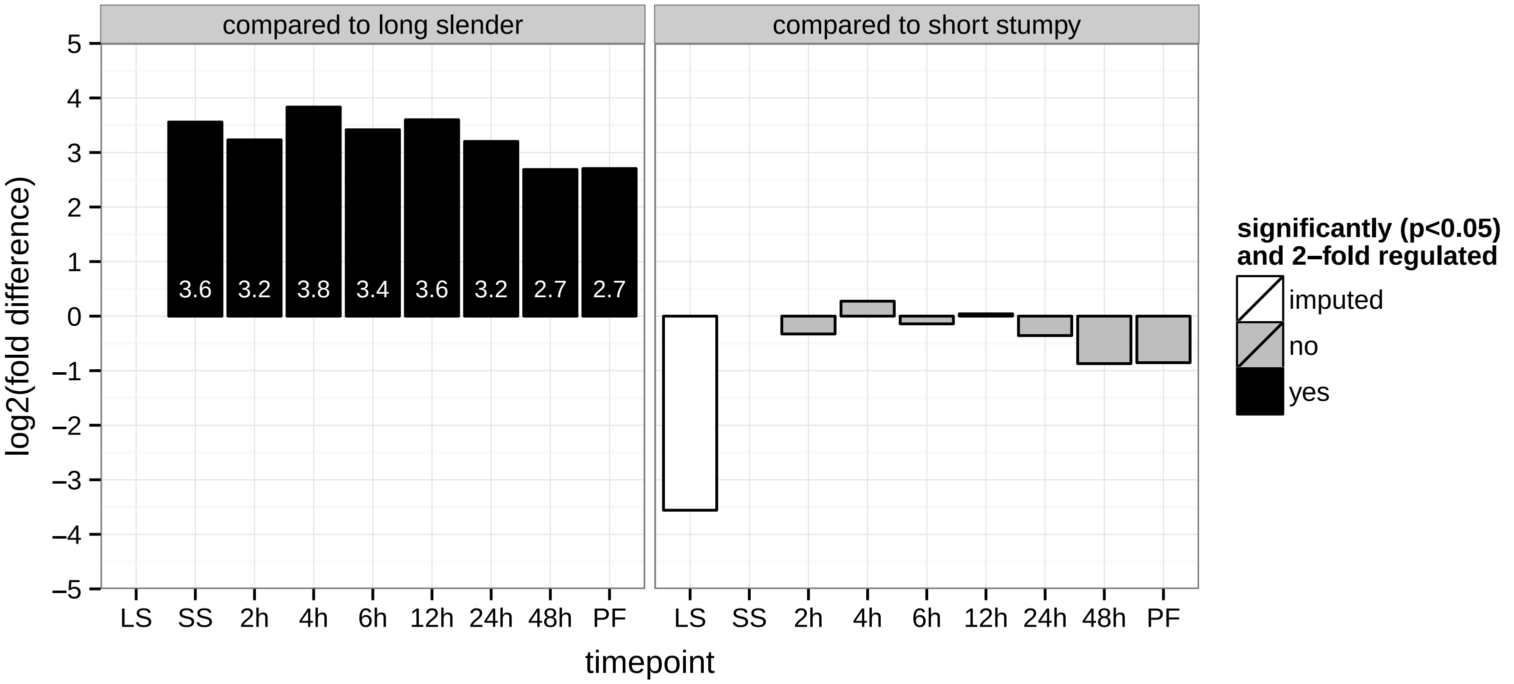
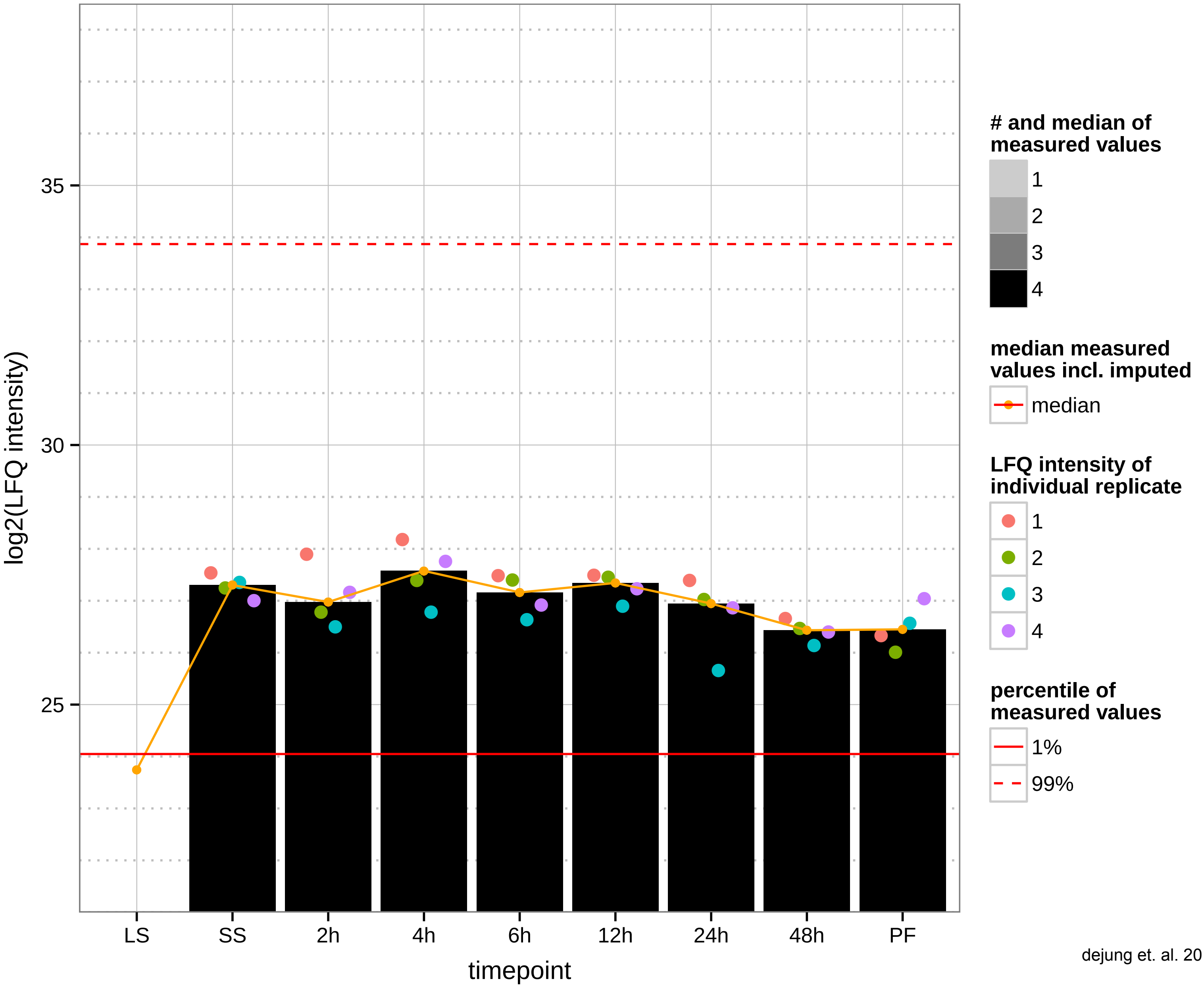
hypothetical protein, conserved
Tb927.8.2970
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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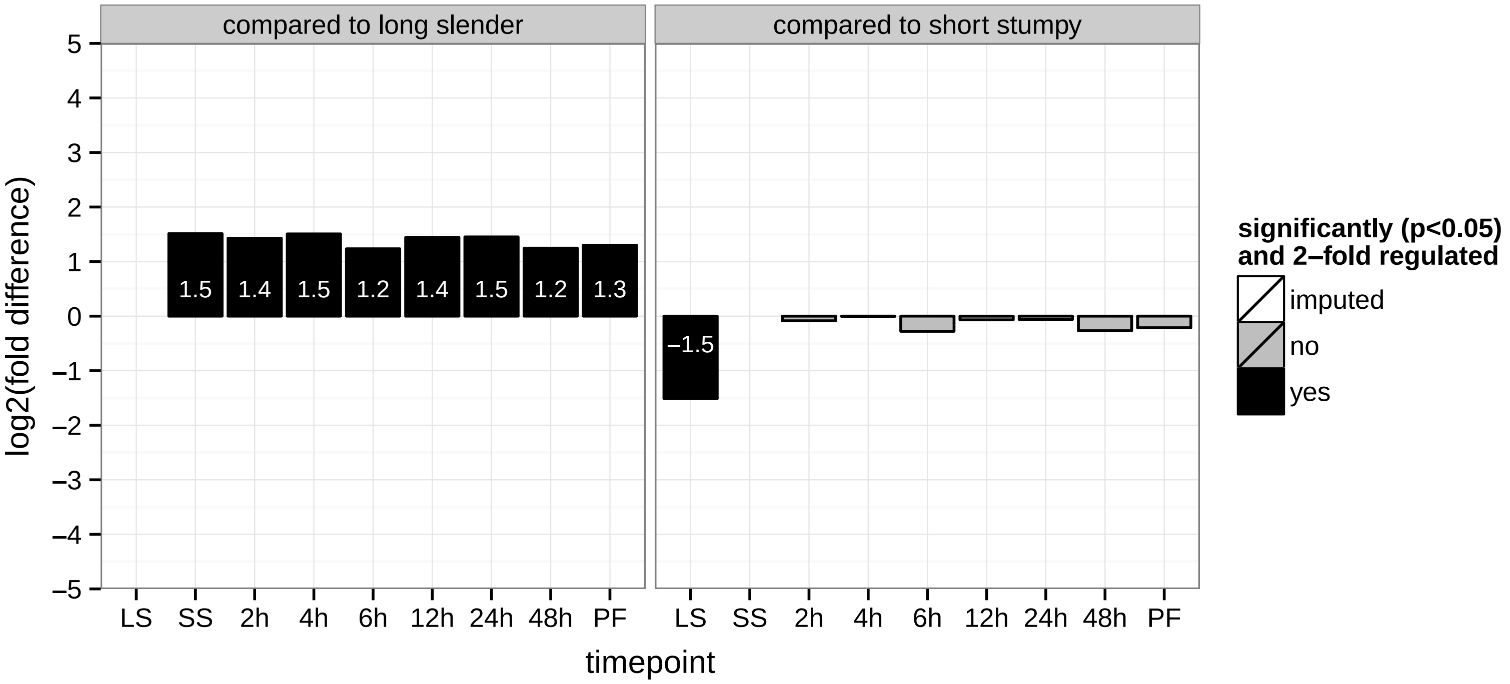
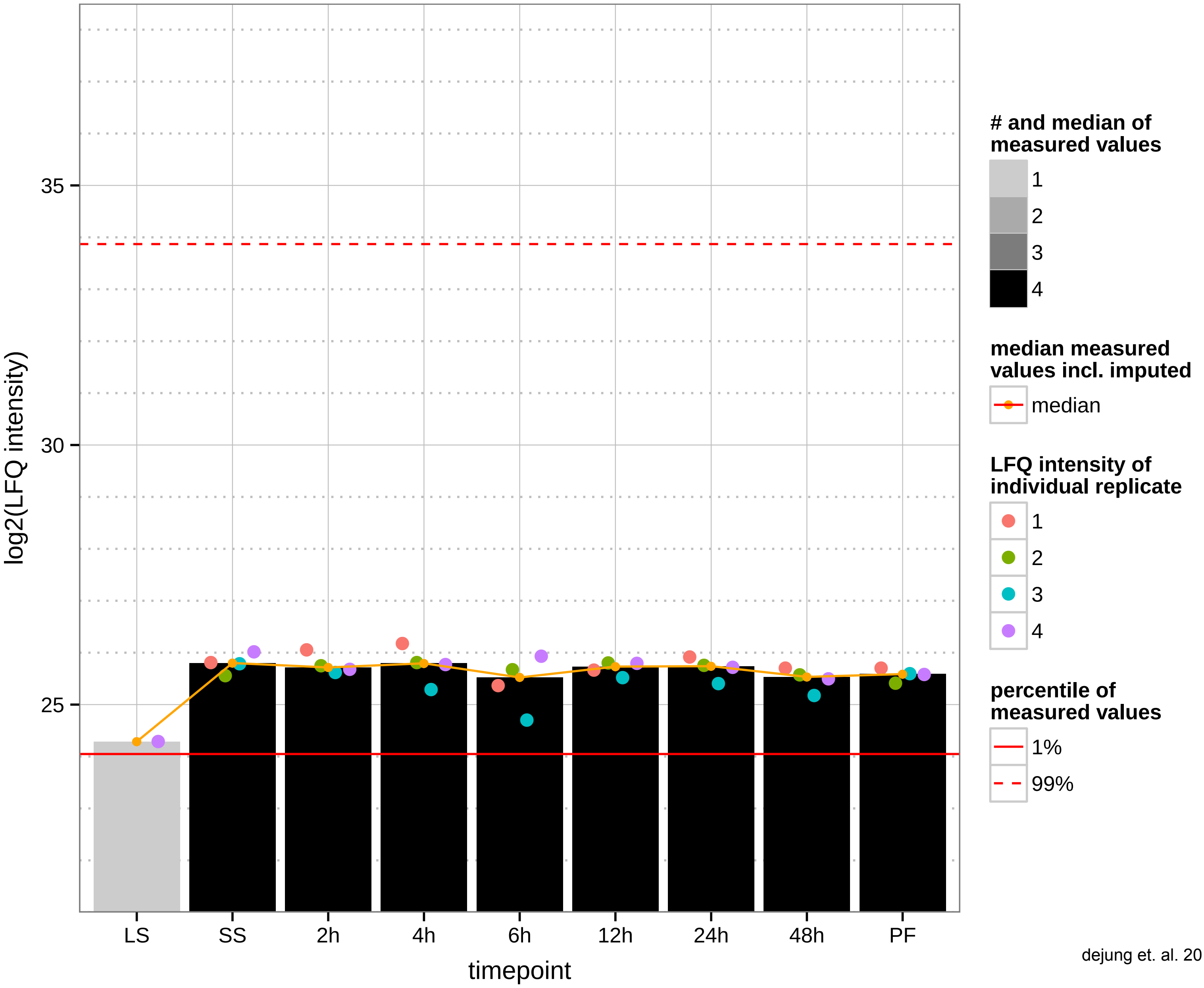
hypothetical protein, conserved
Tb927.8.3020
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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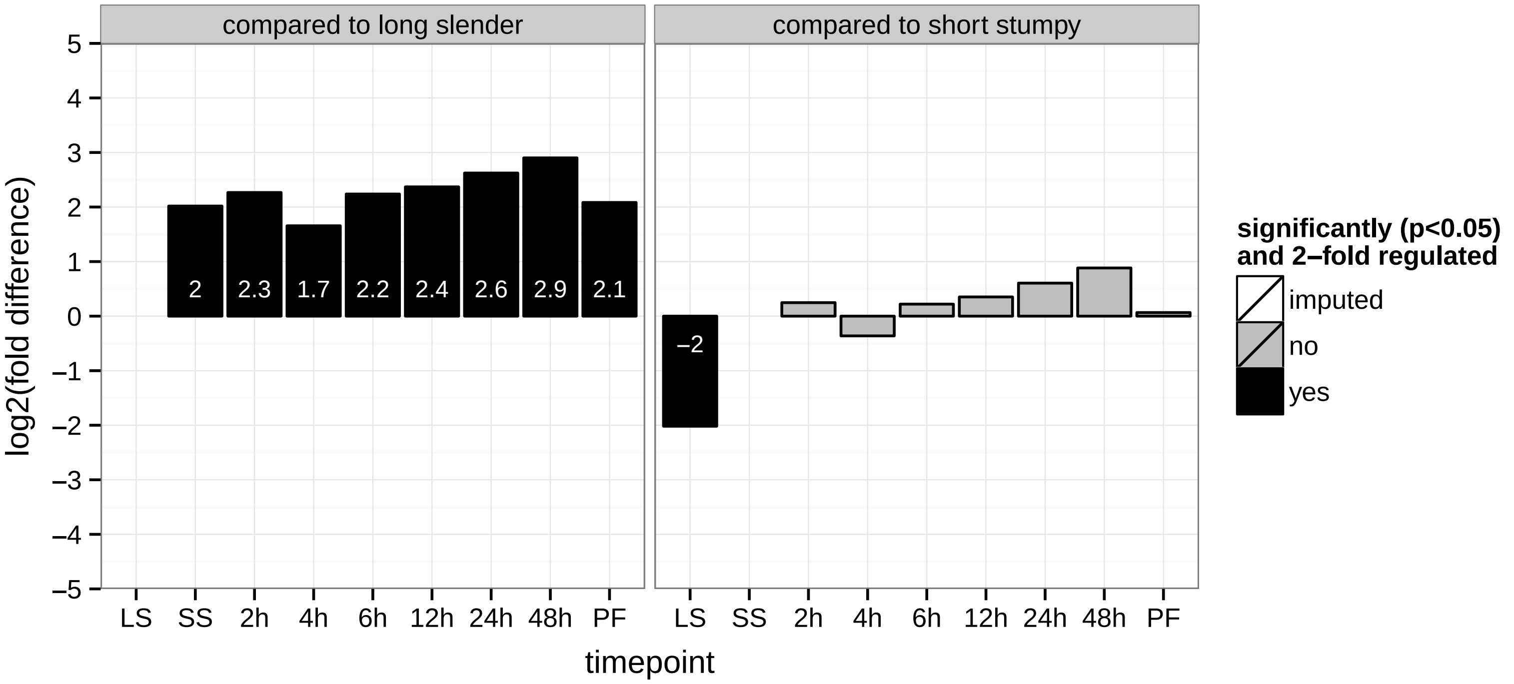
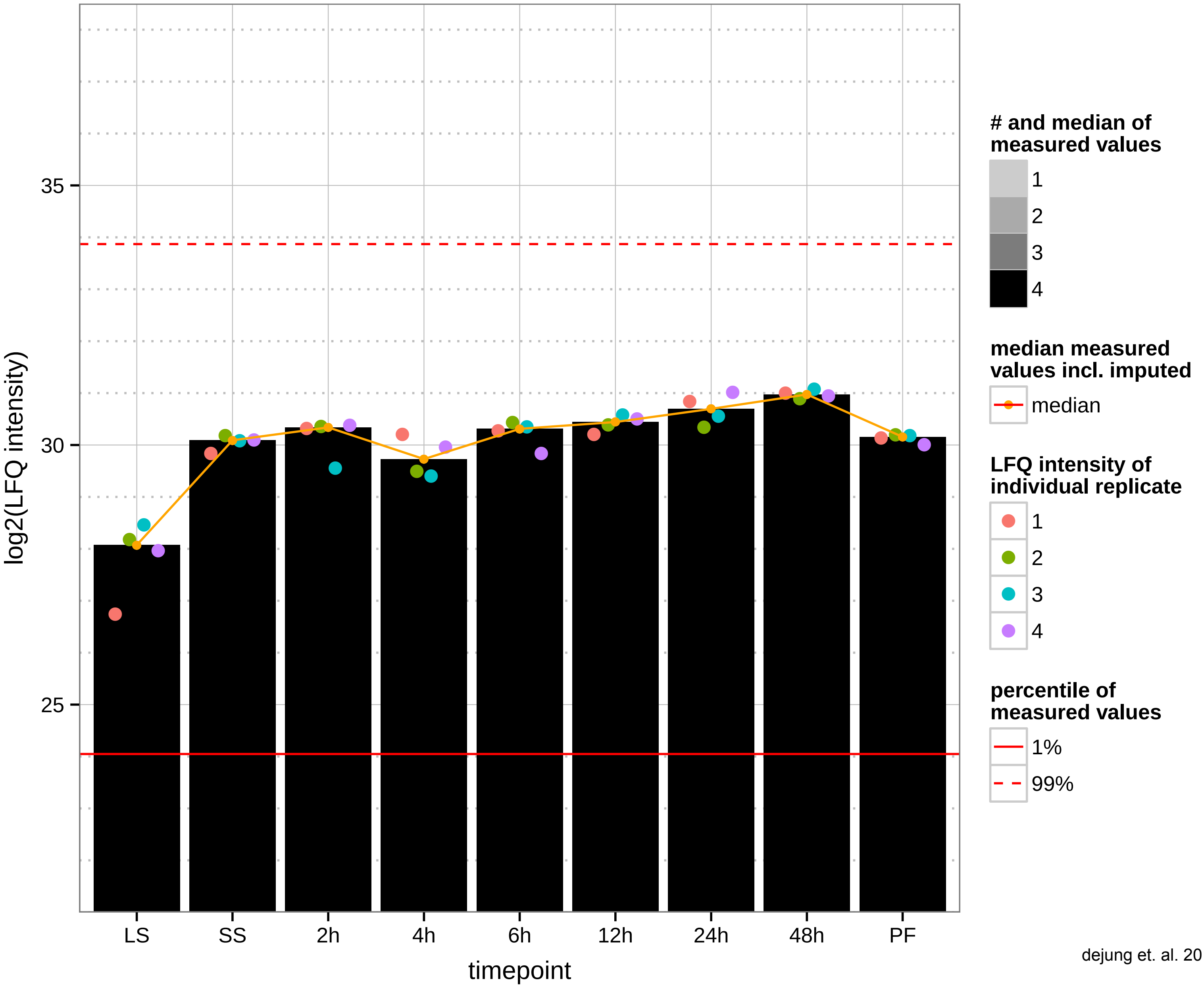
cytosolic leucyl aminopeptidase, putative, metallo–peptidase, Clan MF, Family M17
Tb927.8.3060
AGOF: aminopeptidase activity, manganese ion binding, metalloexopeptidase activity
AGOC: cytoplasm, intracellular
AGOP: protein metabolic process, proteolysis
PGOF: aminopeptidase activity
PGOC: intracellular
PGOP: proteolysis





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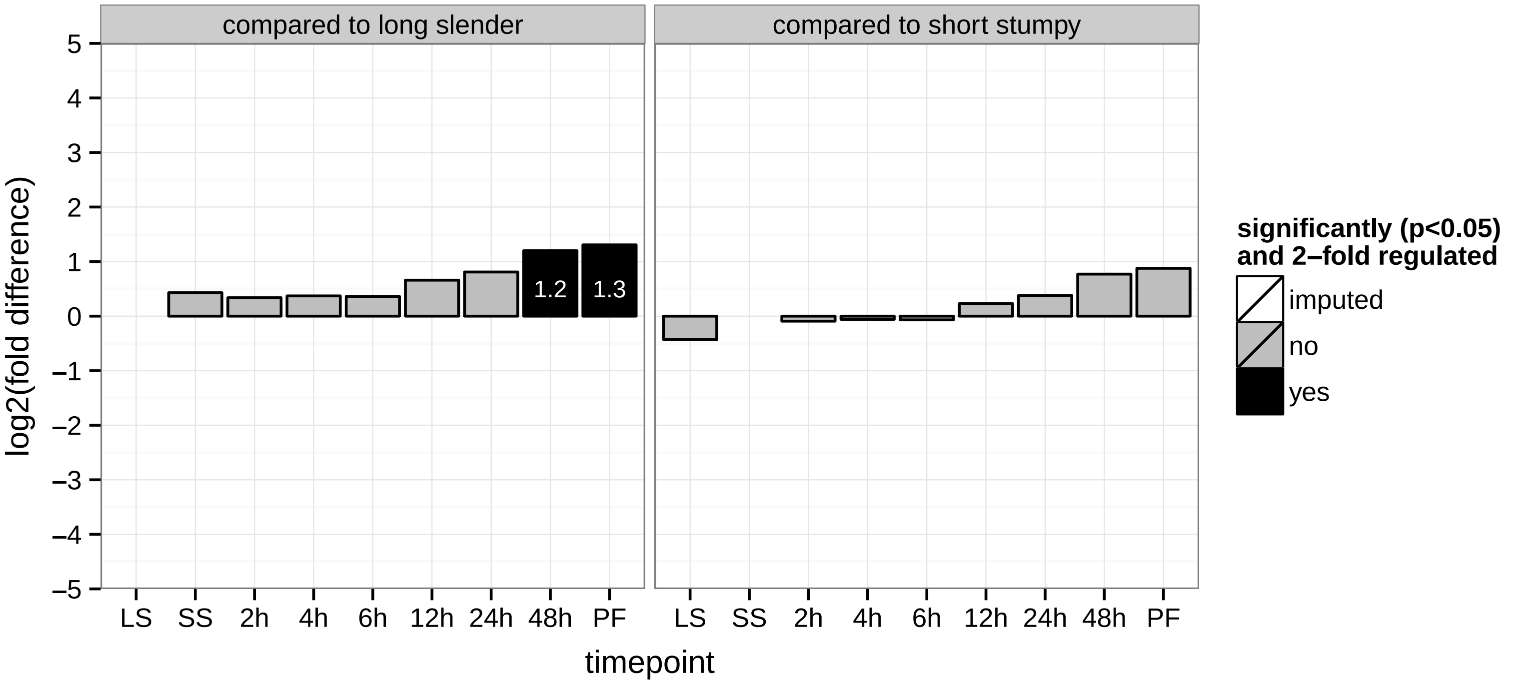
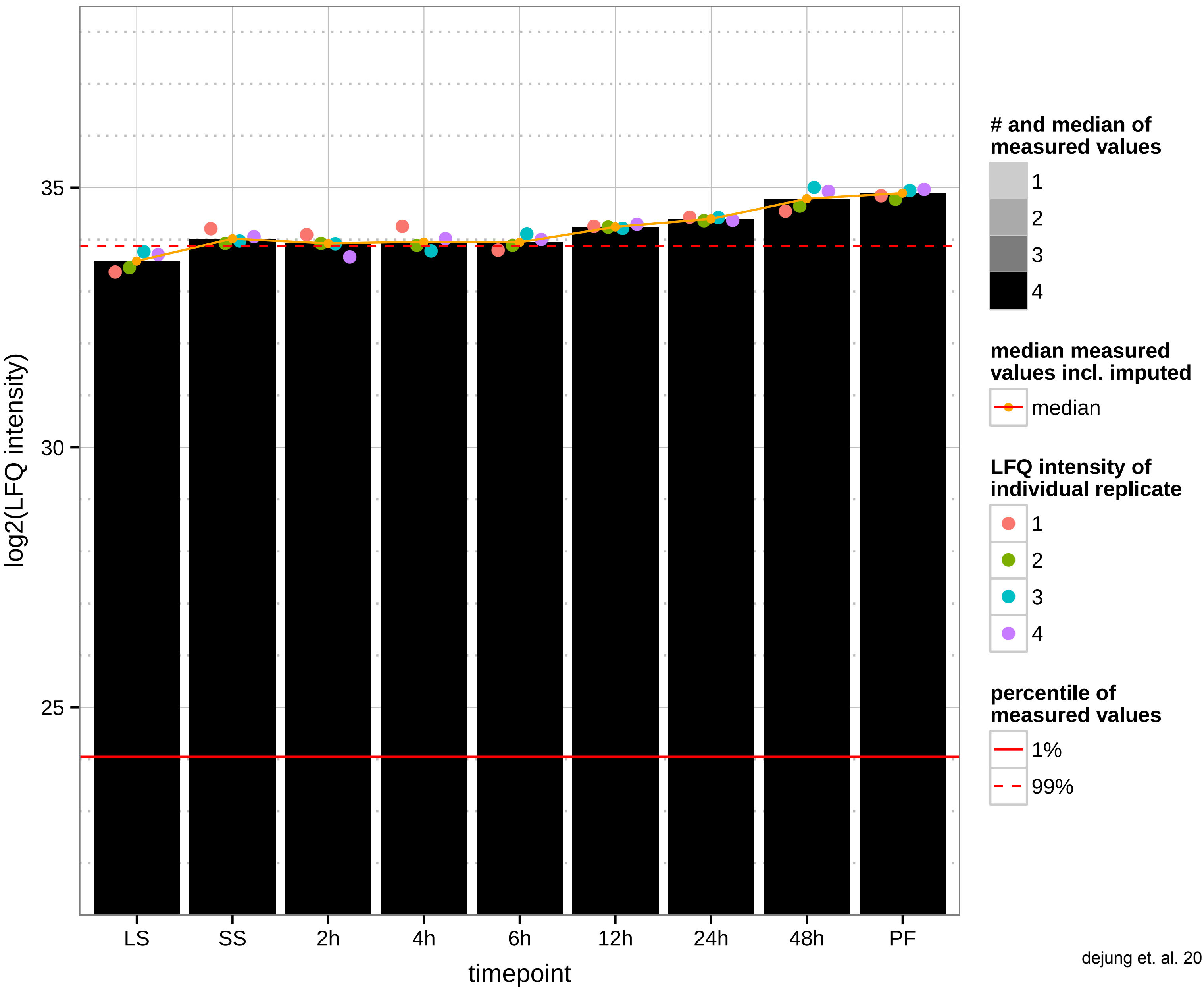
T–complex protein 1, gamma subunit, putative (TCP–1–gamma)
Tb927.8.3150
AGOF: ATP binding, unfolded protein binding
AGOC: chaperonin–containing T–complex
AGOP: protein folding, regulation of cell cycle
PGOF: ATP binding, unfolded protein binding
PGOC: null
PGOP: cellular protein metabolic process, protein folding





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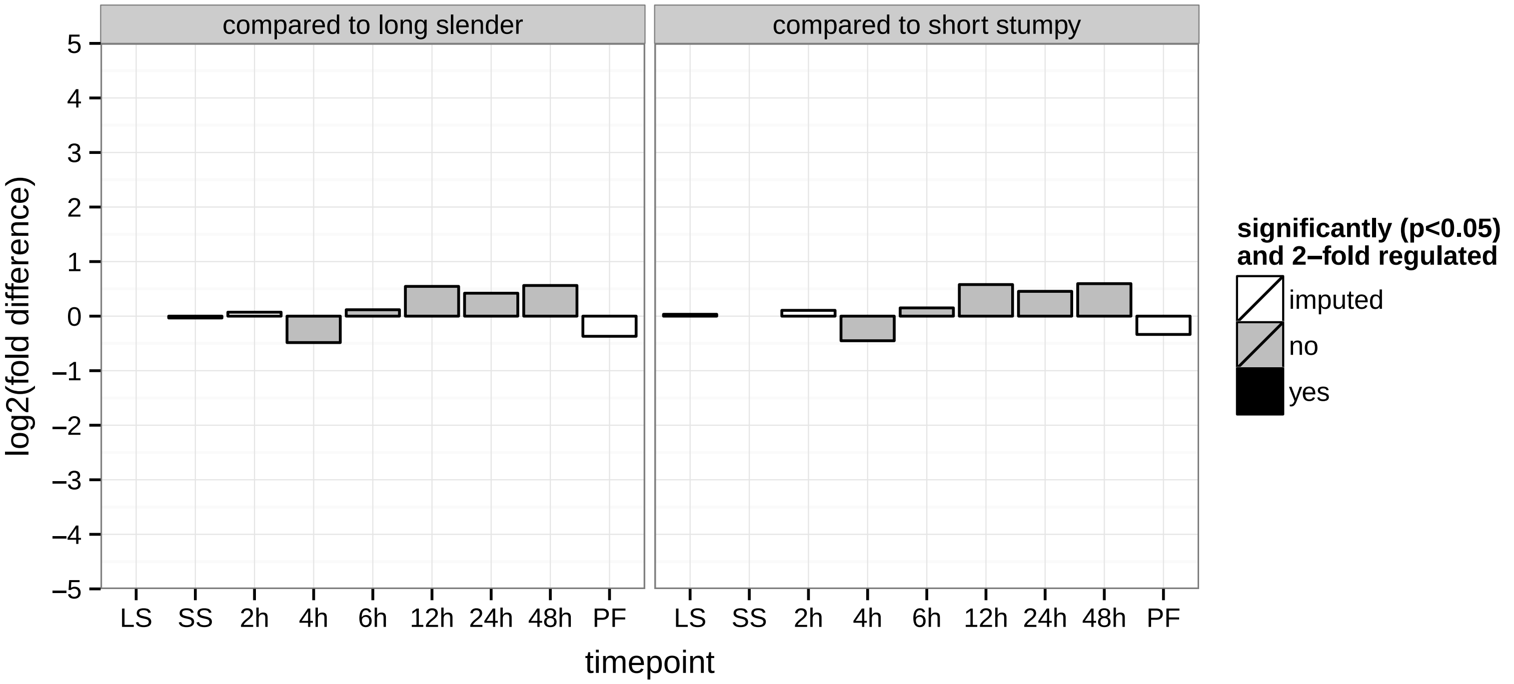
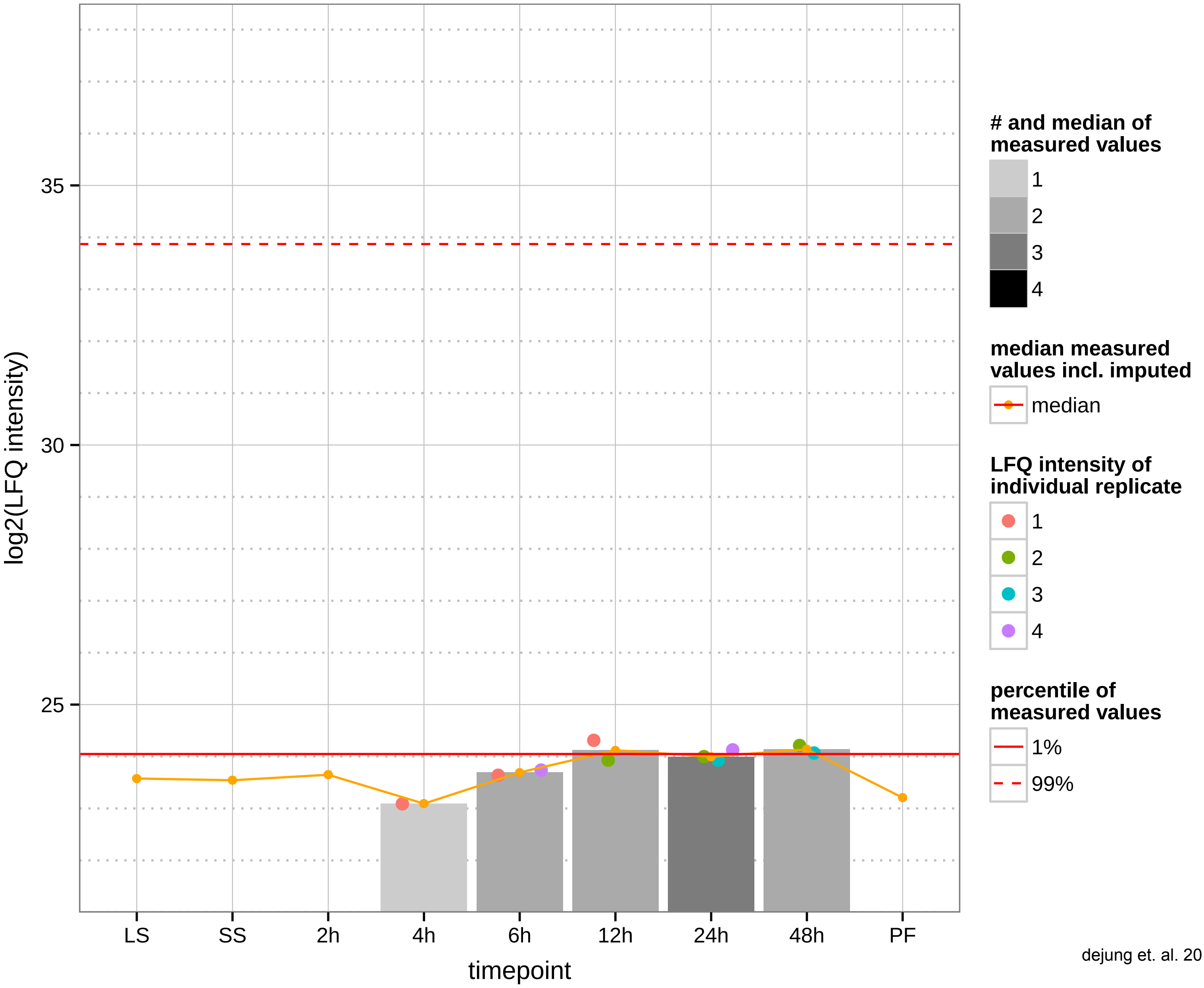
hypothetical protein, conserved
Tb927.8.3170
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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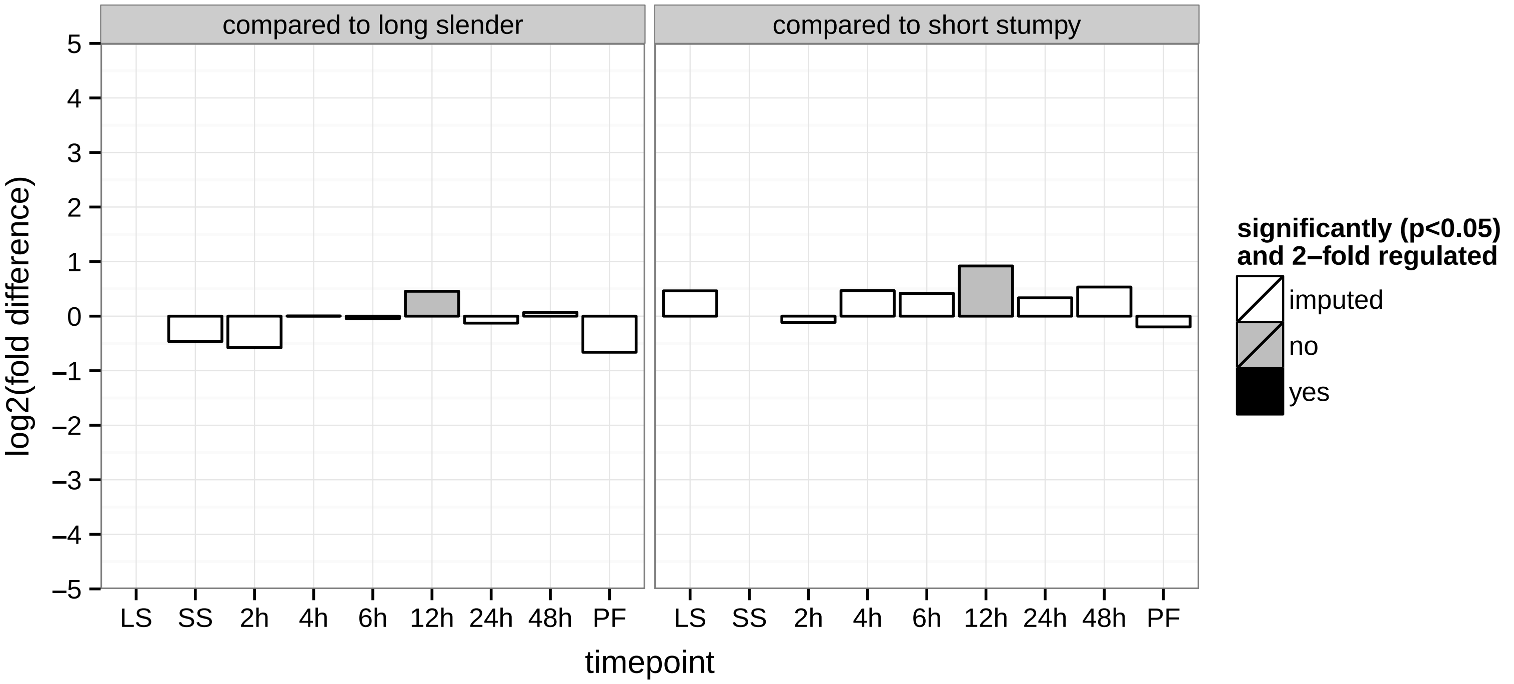
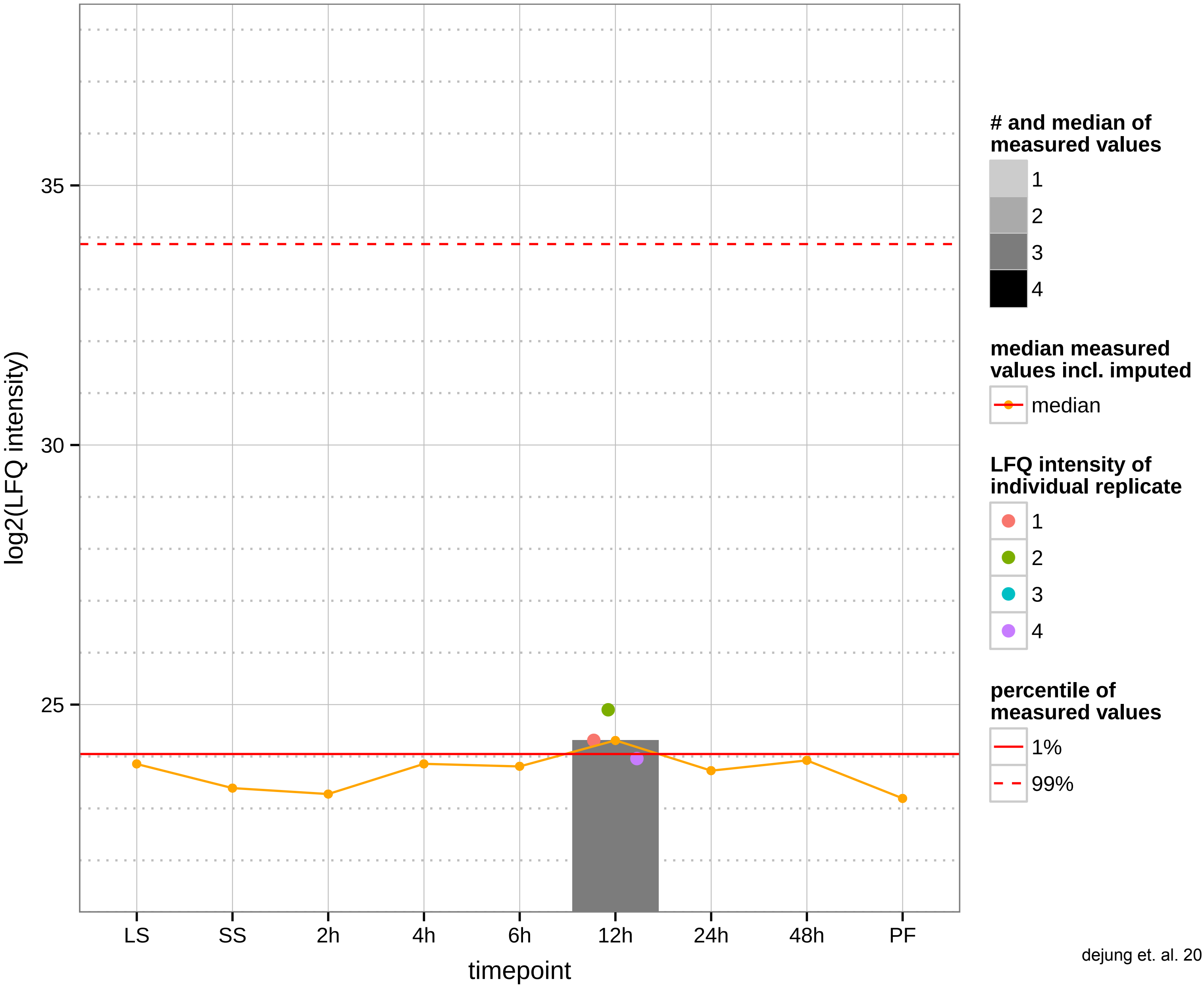
hypothetical protein, conserved
Tb927.8.3200
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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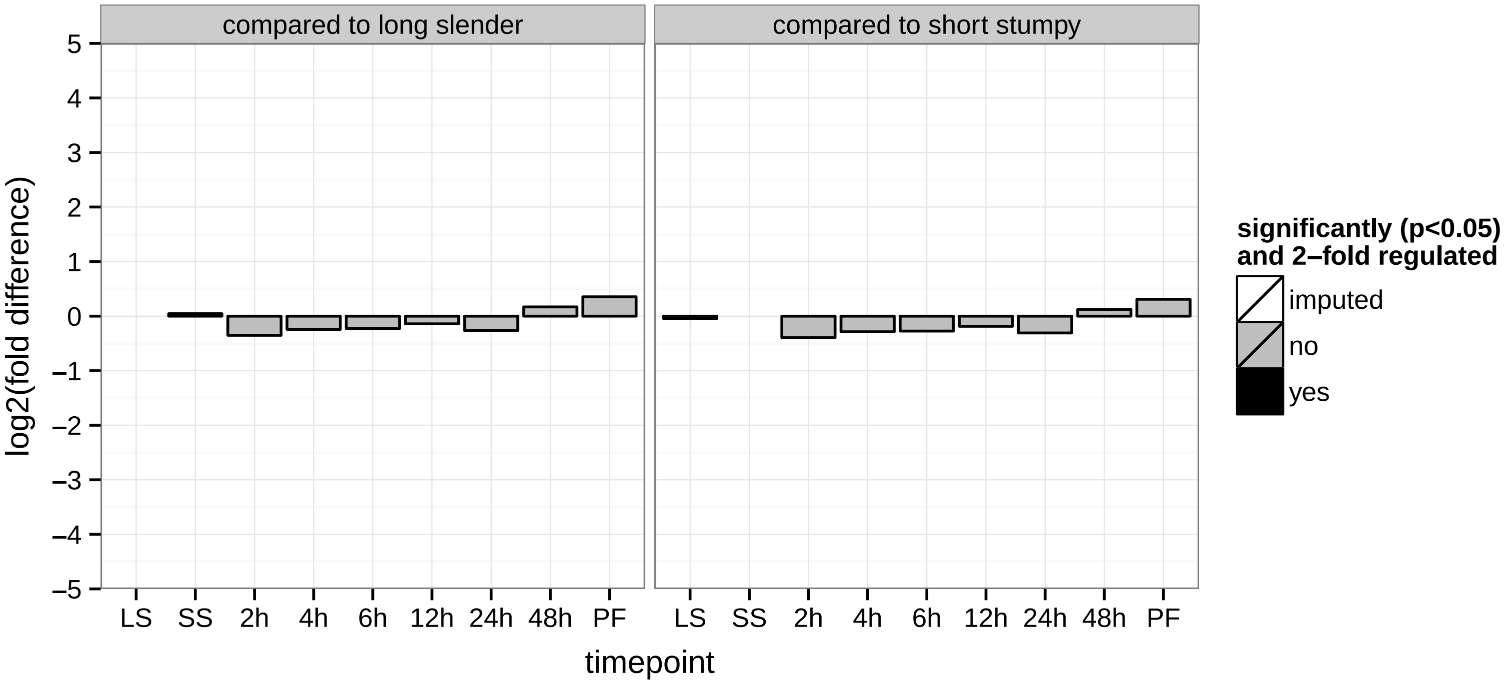
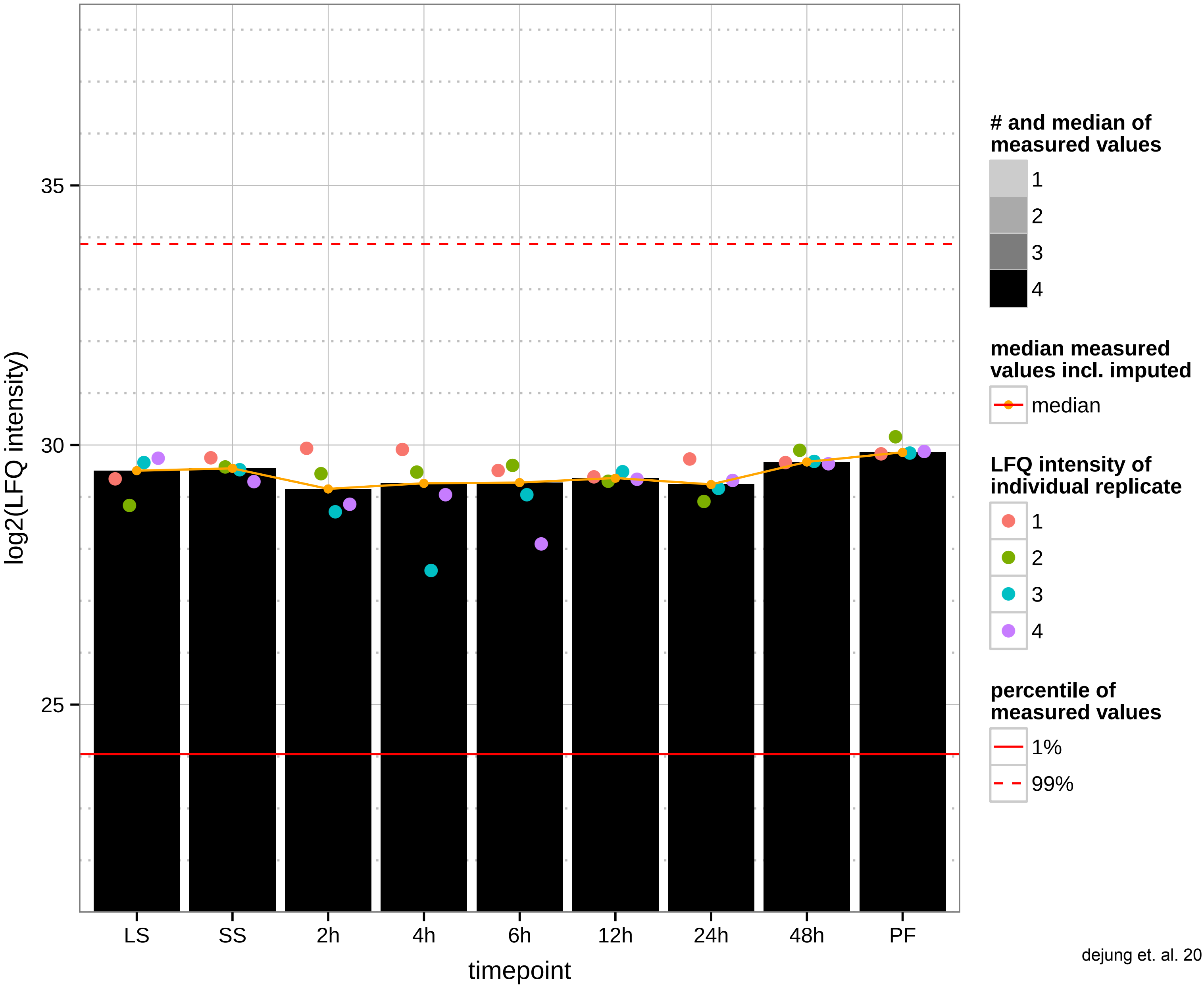
dynein heavy chain, putative
Tb927.8.3250
AGOF: ATP binding, ATPase activity, microtubule motor activity
AGOC: dynein complex
AGOP: microtubule–based movement
PGOF: ATP binding, ATPase activity, microtubule motor activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: dynein complex
PGOP: microtubule–based movement





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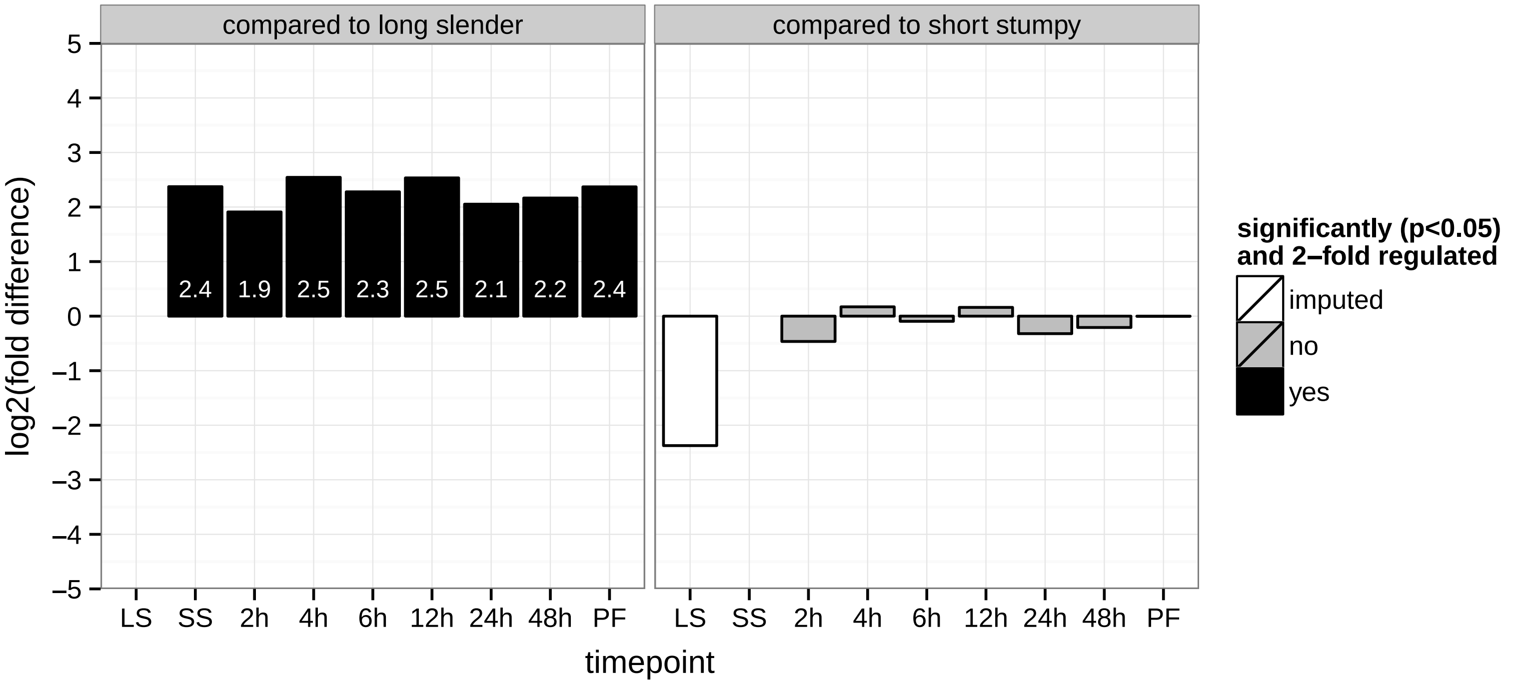
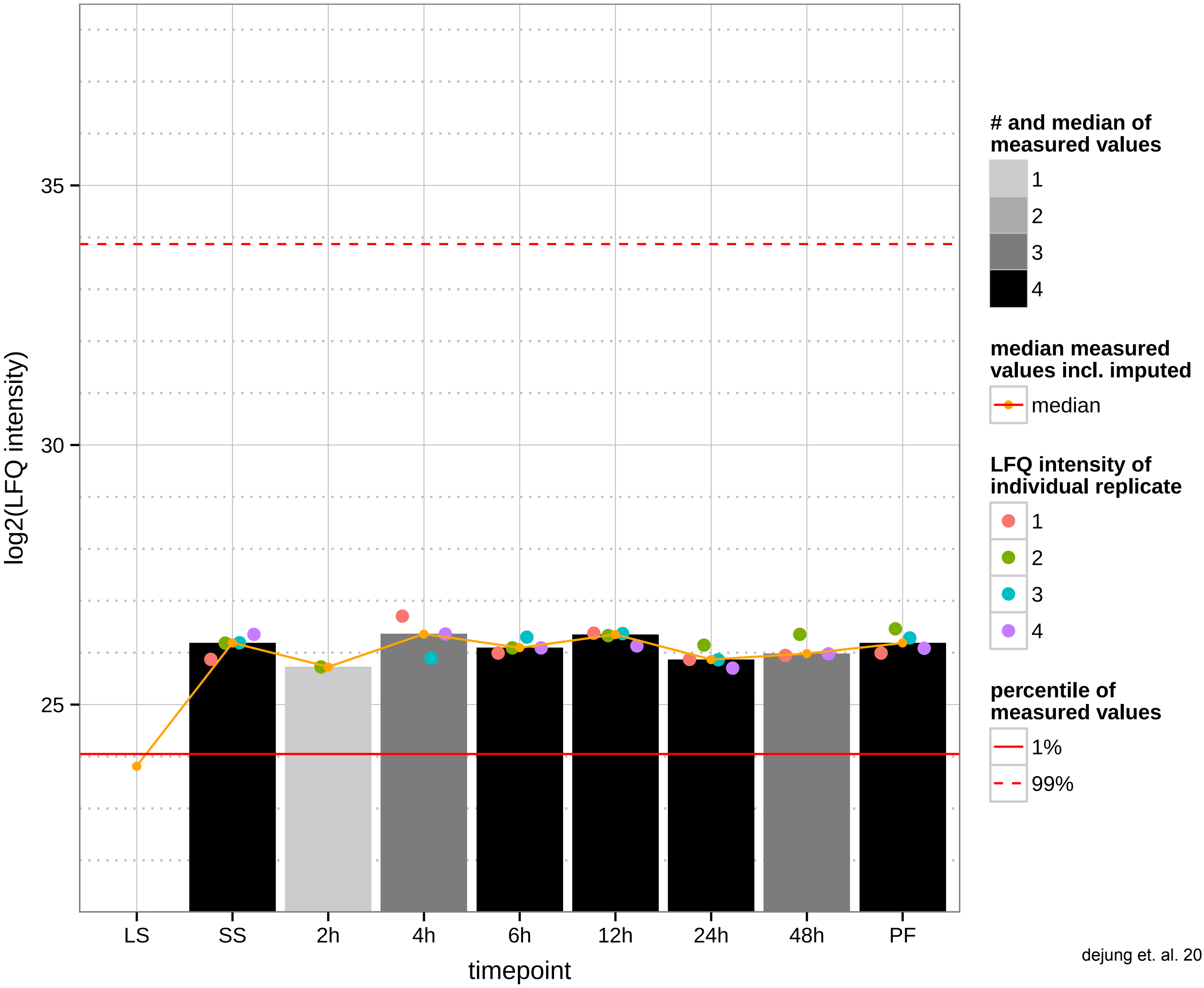
hypothetical protein, conserved
Tb927.8.3280
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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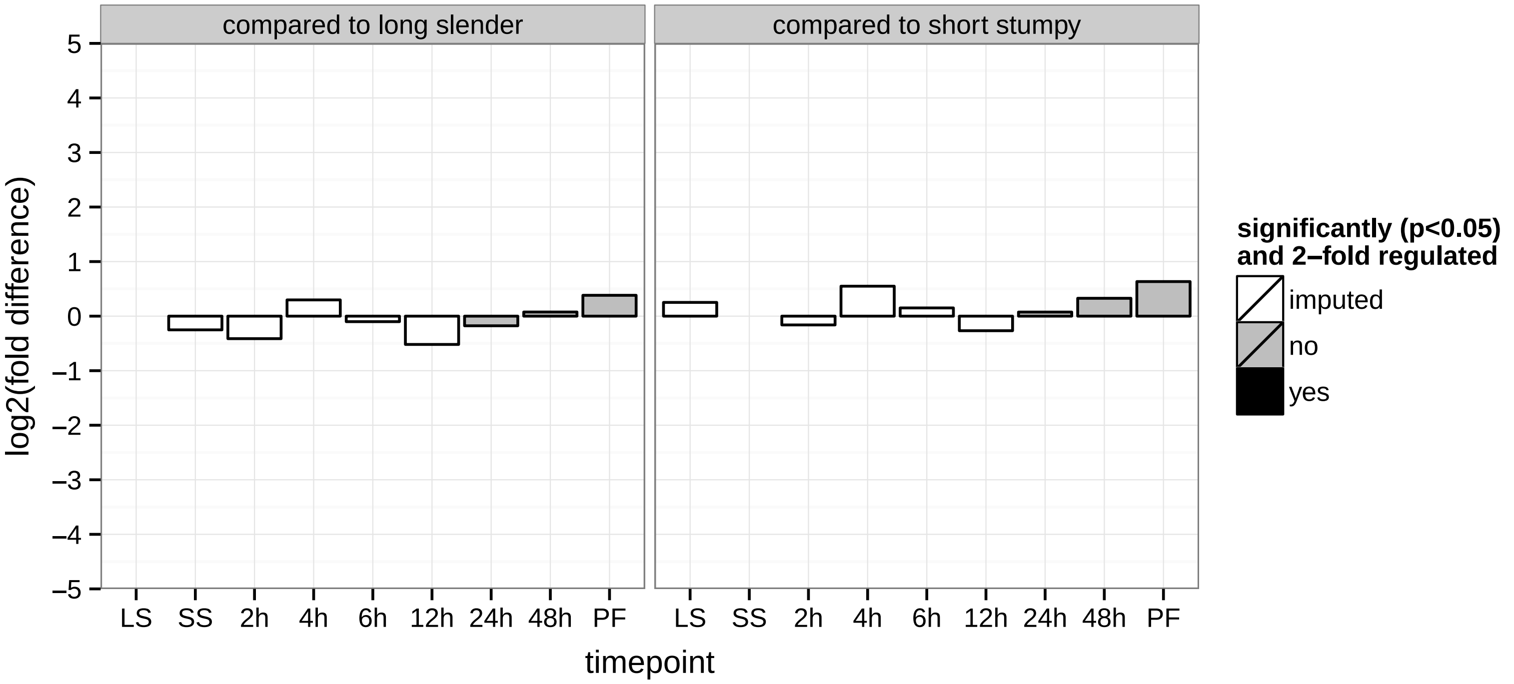
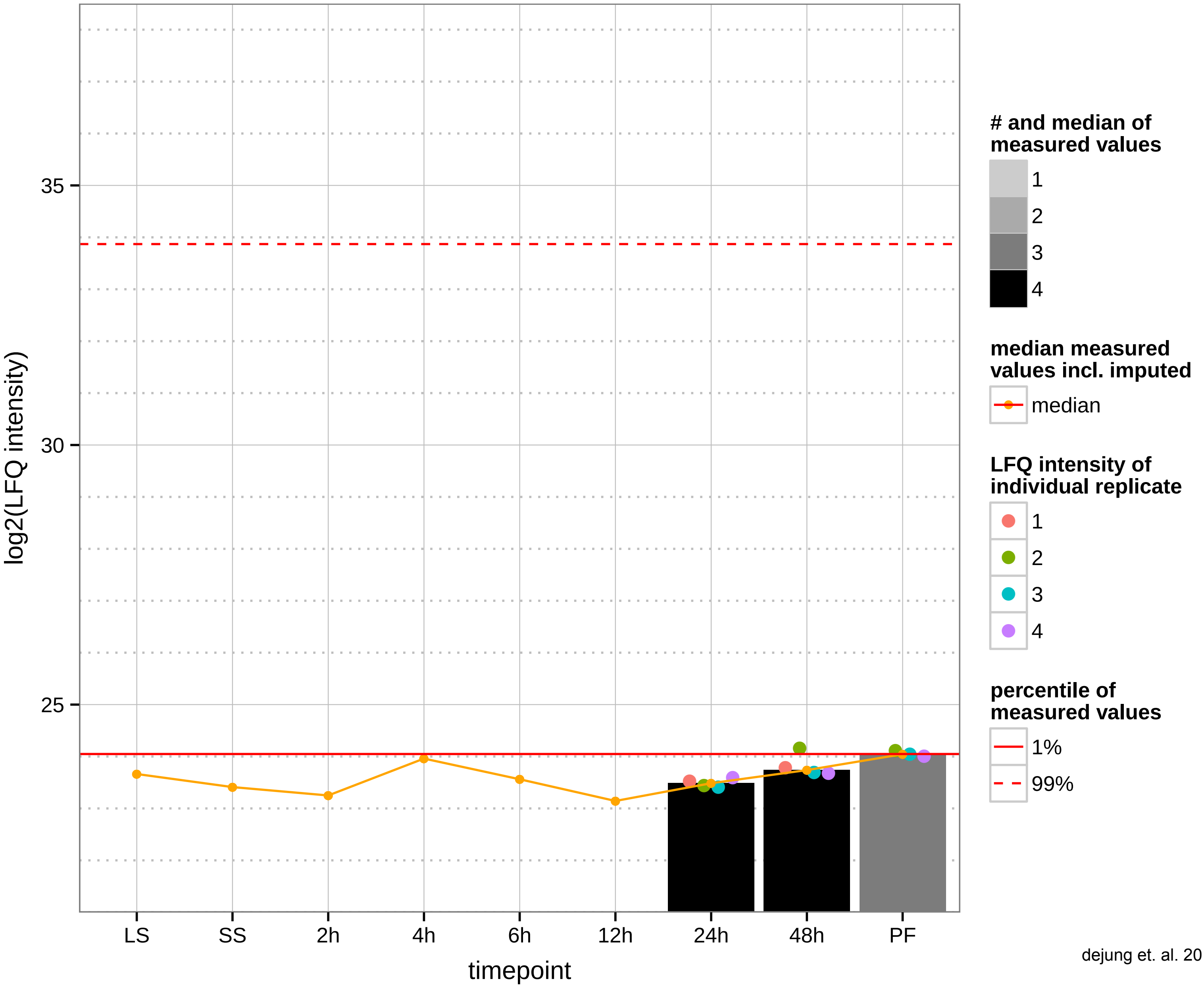
DNA polymerase theta (helicase domain only), putative
Tb927.8.3350;Tb11.v5.0792
AGOF: null, ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: null, nucleobase–containing compound metabolic process
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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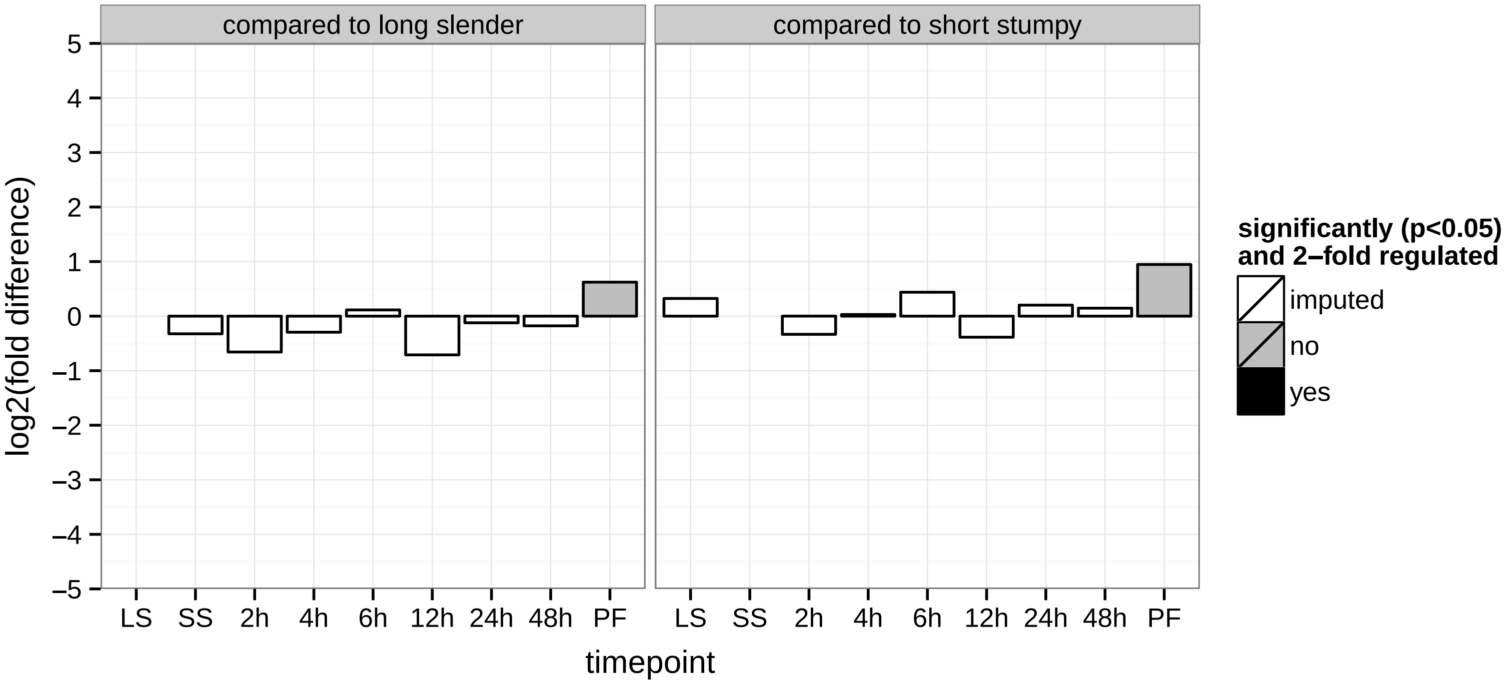
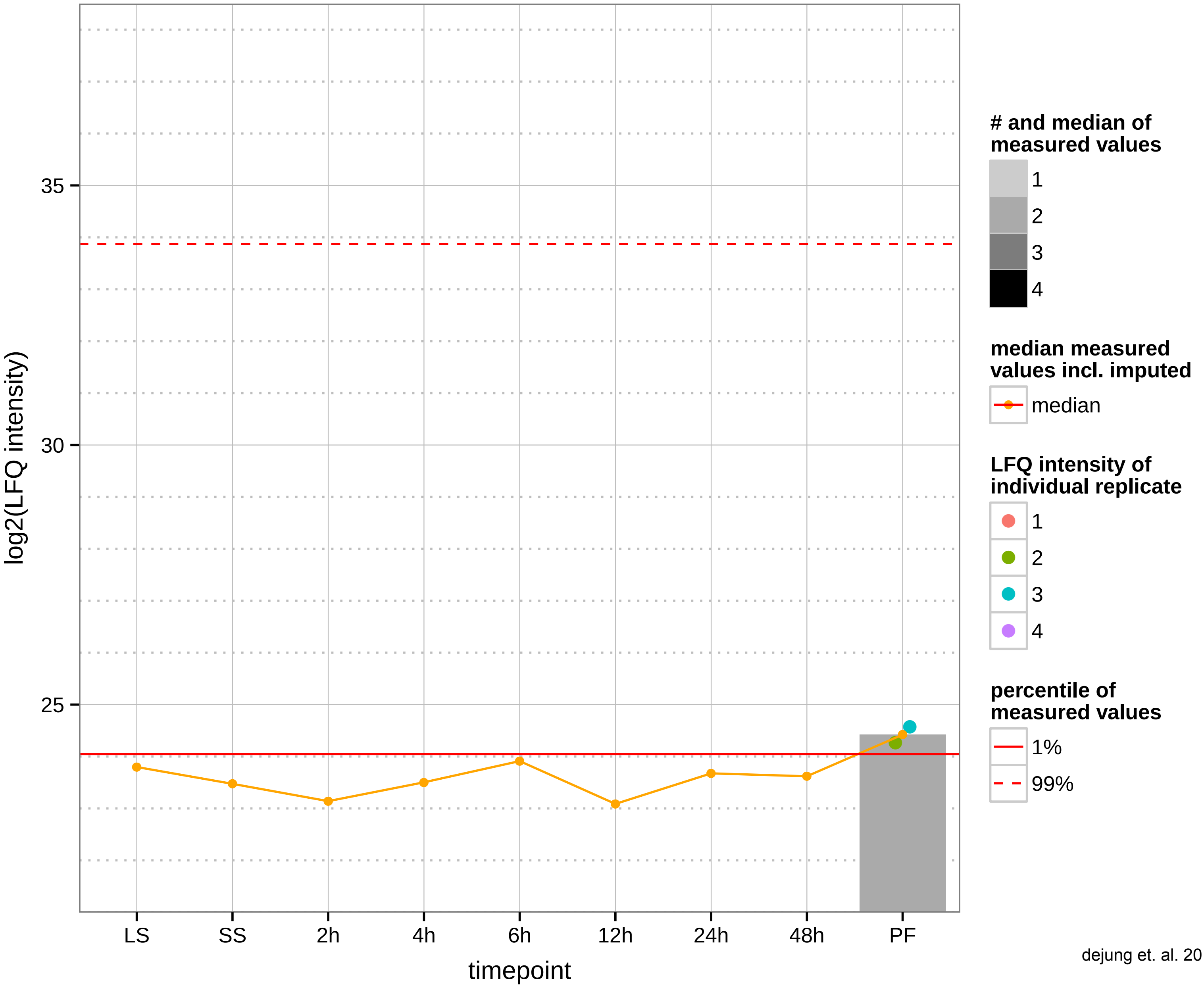
hypothetical protein, conserved
Tb927.8.3460
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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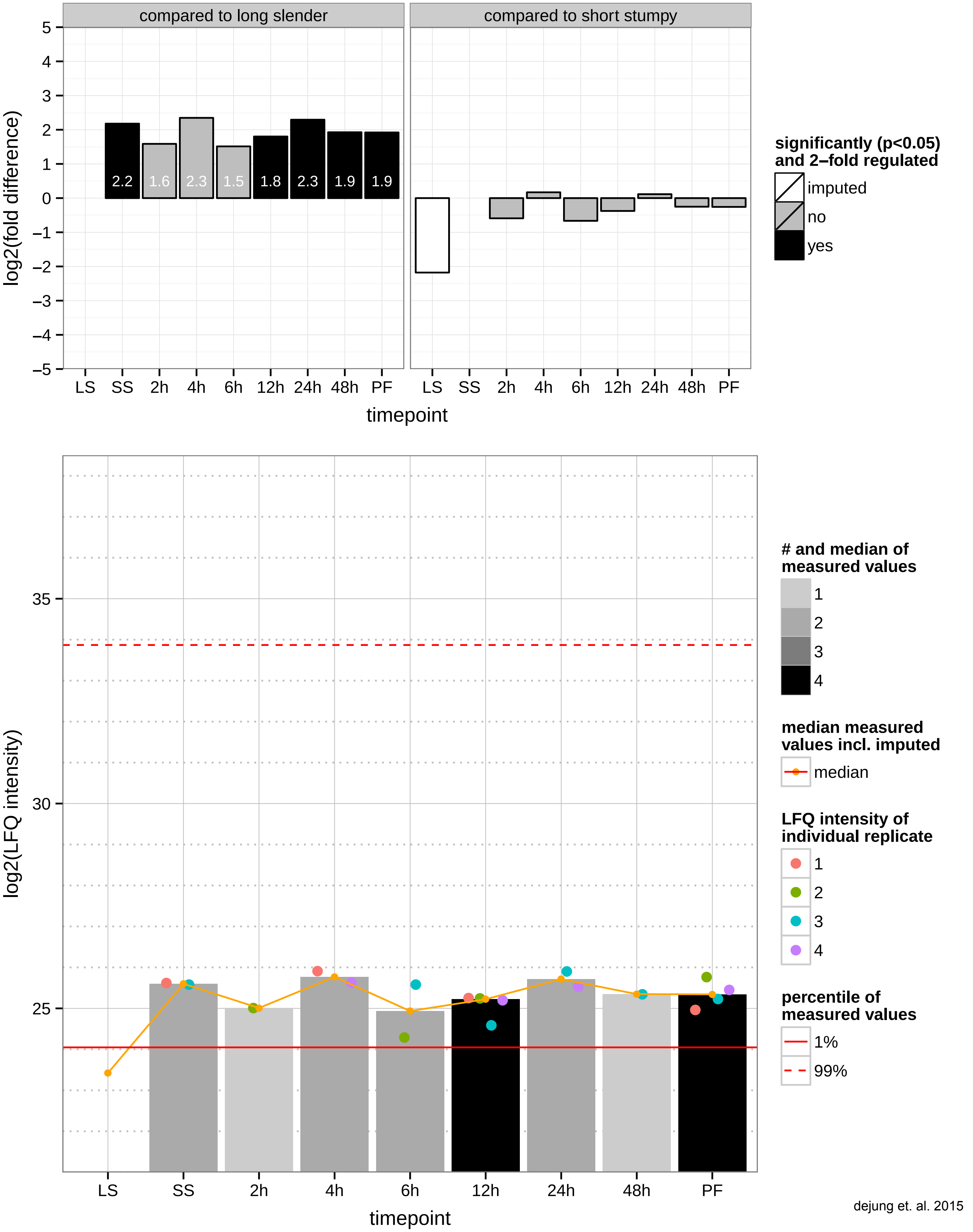
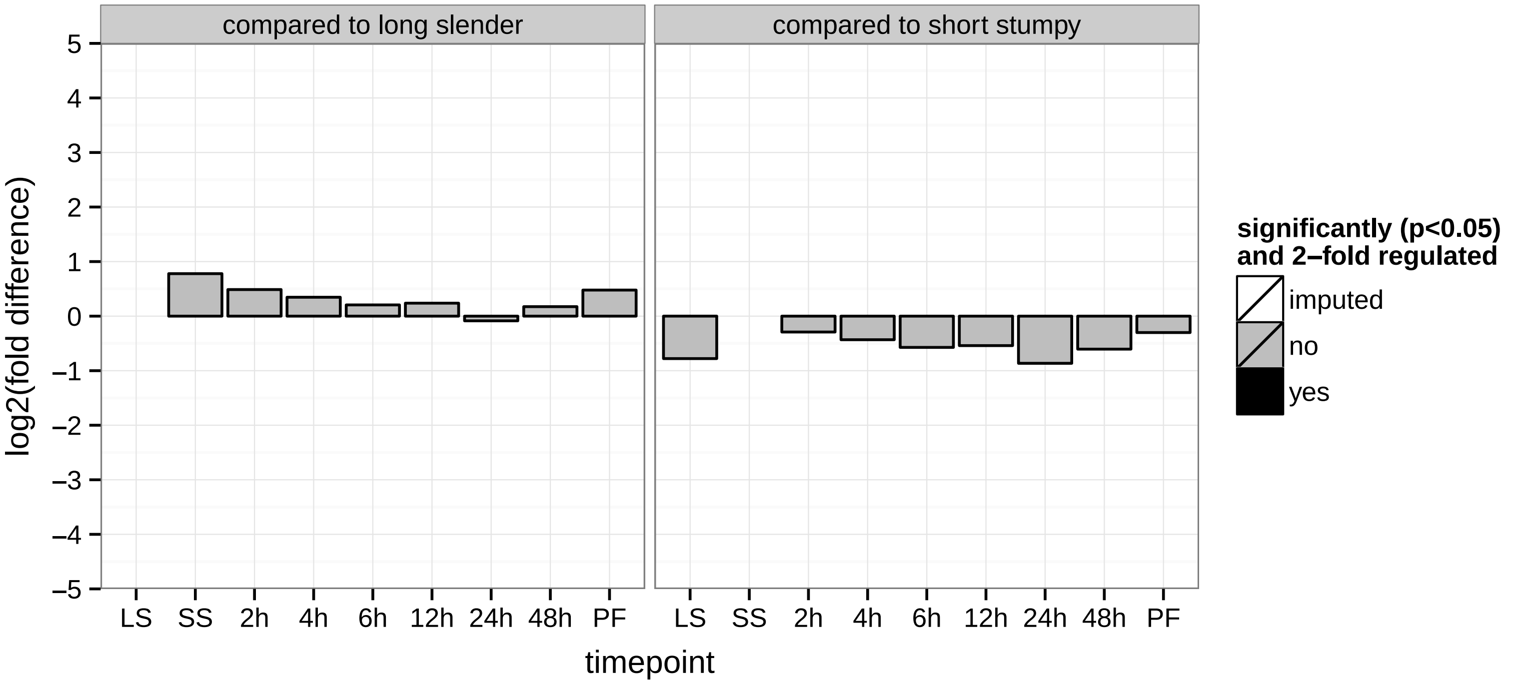
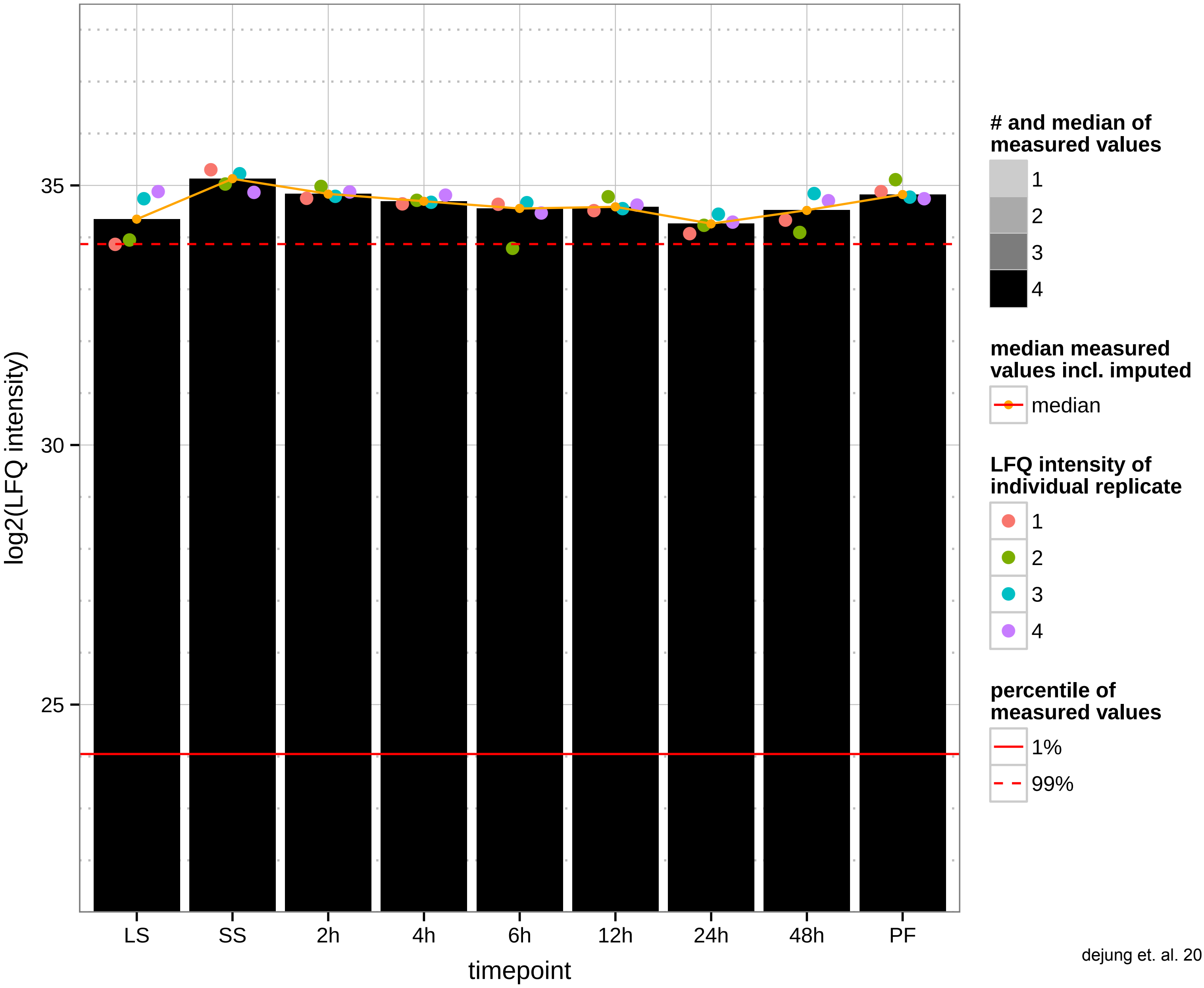
hypothetical protein, conserved
Tb927.8.3920;Tb927.8.3500
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null



glycerol−3−phosphate dehydrogenase [NAD+], glycosomal
Tb927.8.3530
AGOF: NAD binding, glycerol−3−phosphate dehydrogenase [NAD+] activity, protein homodimerization activity
AGOC: cytoplasm, glycerol−3−phosphate dehydrogenase complex, glycosome
AGOP: carbohydrate metabolic process, glycerol−3−phosphate catabolic process, glycerol−3−phosphate metabolic process,
PGOF: NAD binding, glycerol−3−phosphate dehydrogenase [NAD+] activity, oxidoreductase activity, acting on CH−OH group
PGOC: cytoplasm, glycerol−3−phosphate dehydrogenase complex
PGOP: carbohydrate metabolic process, glycerol−3−phosphate catabolic process, glycerol−3−phosphate metabolic process,





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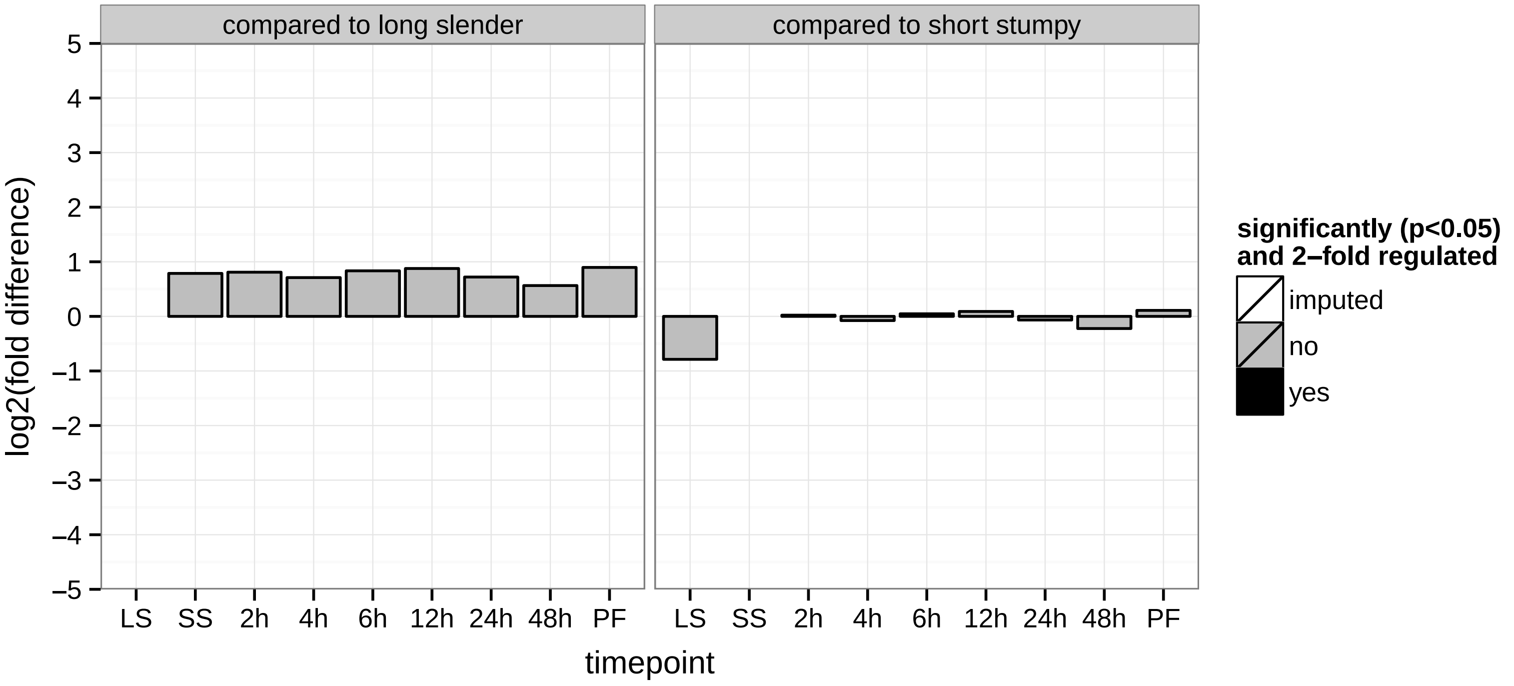
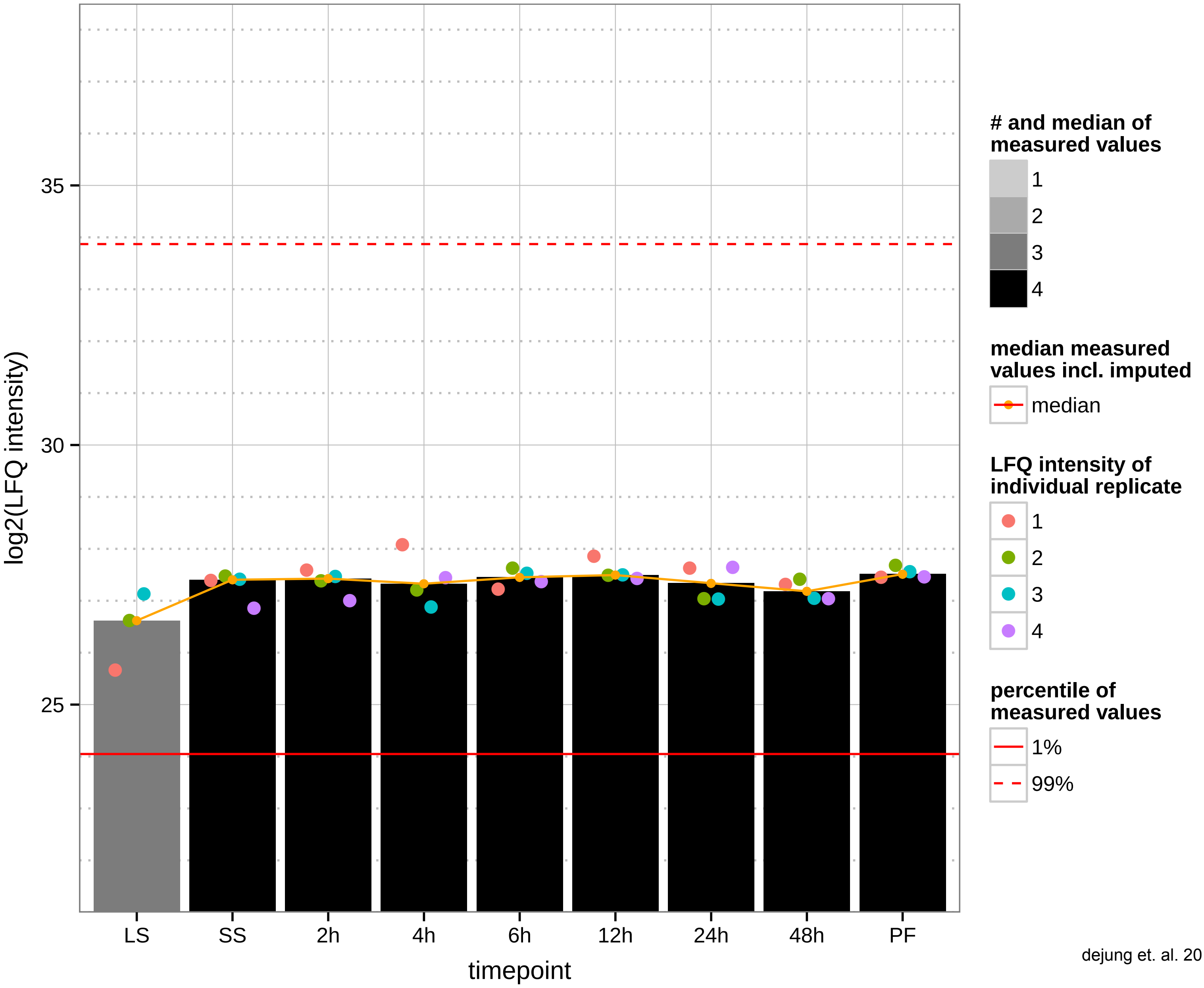
protein transport protein SEC23 (SEC23.1)
Tb927.8.3660
AGOF: GTPase activator activity, protein binding, zinc ion binding
AGOC: COPII vesicle coat
AGOP: ER to Golgi vesicle–mediated transport, intracellular protein transport
PGOF: zinc ion binding
PGOC: COPII vesicle coat
PGOP: ER to Golgi vesicle–mediated transport, intracellular protein transport





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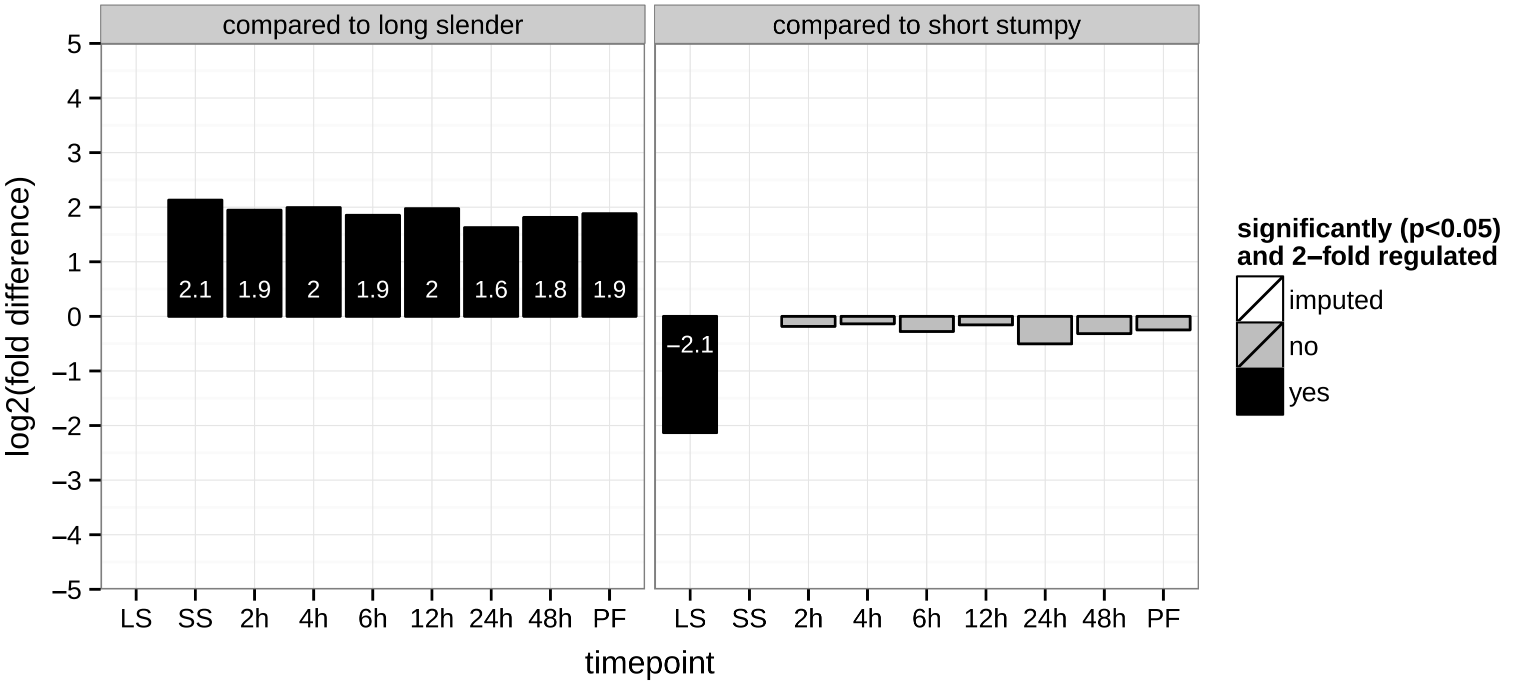
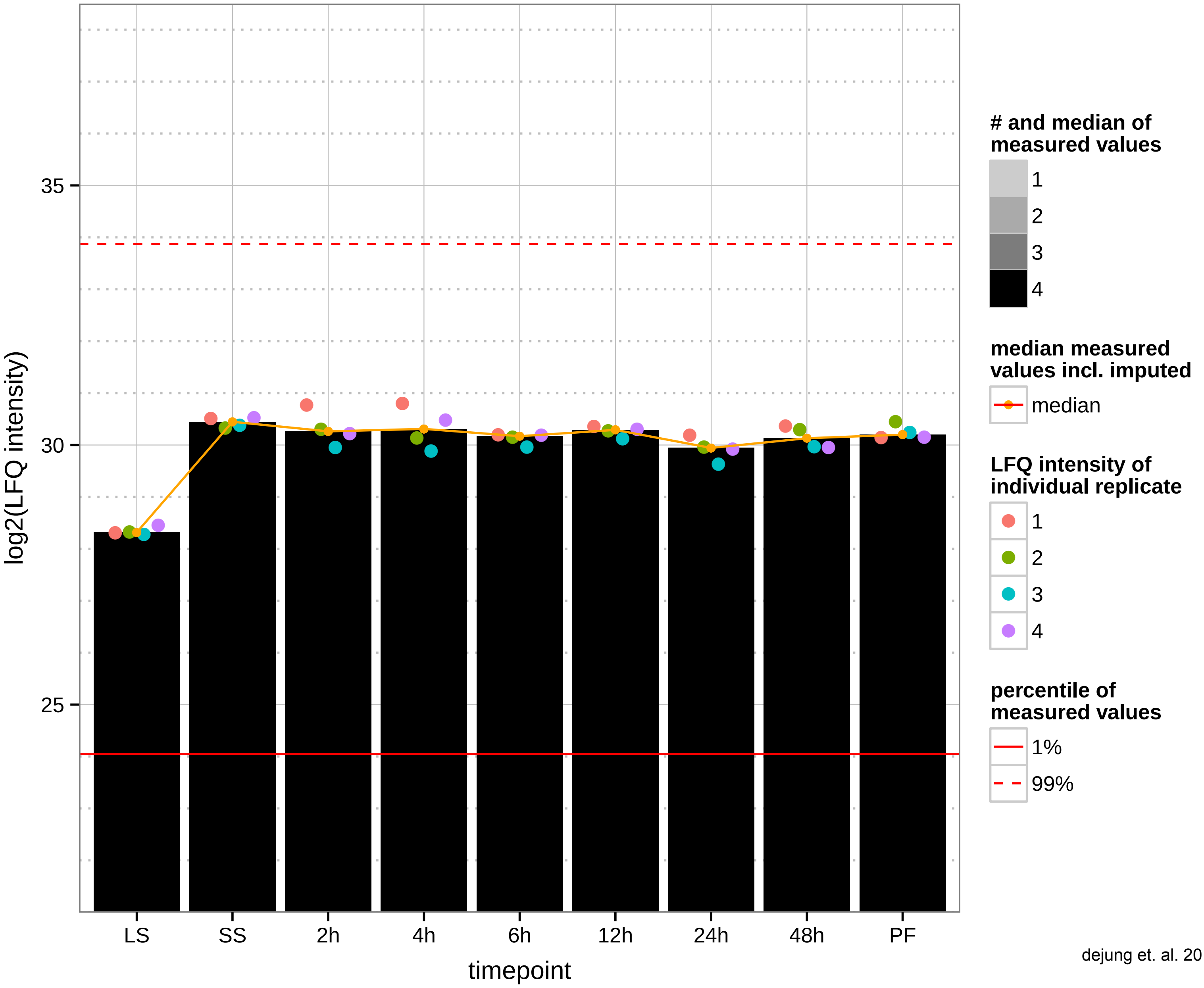
isocitrate dehydrogenase [NADP], mitochondrial precursor, putative (IDH)
Tb927.8.3690
AGOF: NAD binding, isocitrate dehydrogenase (NADP+) activity, magnesium ion binding
AGOC: mitochondrion
AGOP: isocitrate metabolic process, oxidation–reduction process, tricarboxylic acid cycle
PGOF: isocitrate dehydrogenase (NADP+) activity, oxidoreductase activity, acting on the CH–OH group of donors, NAD or NA
PGOC: null
PGOP: isocitrate metabolic process, oxidation–reduction process





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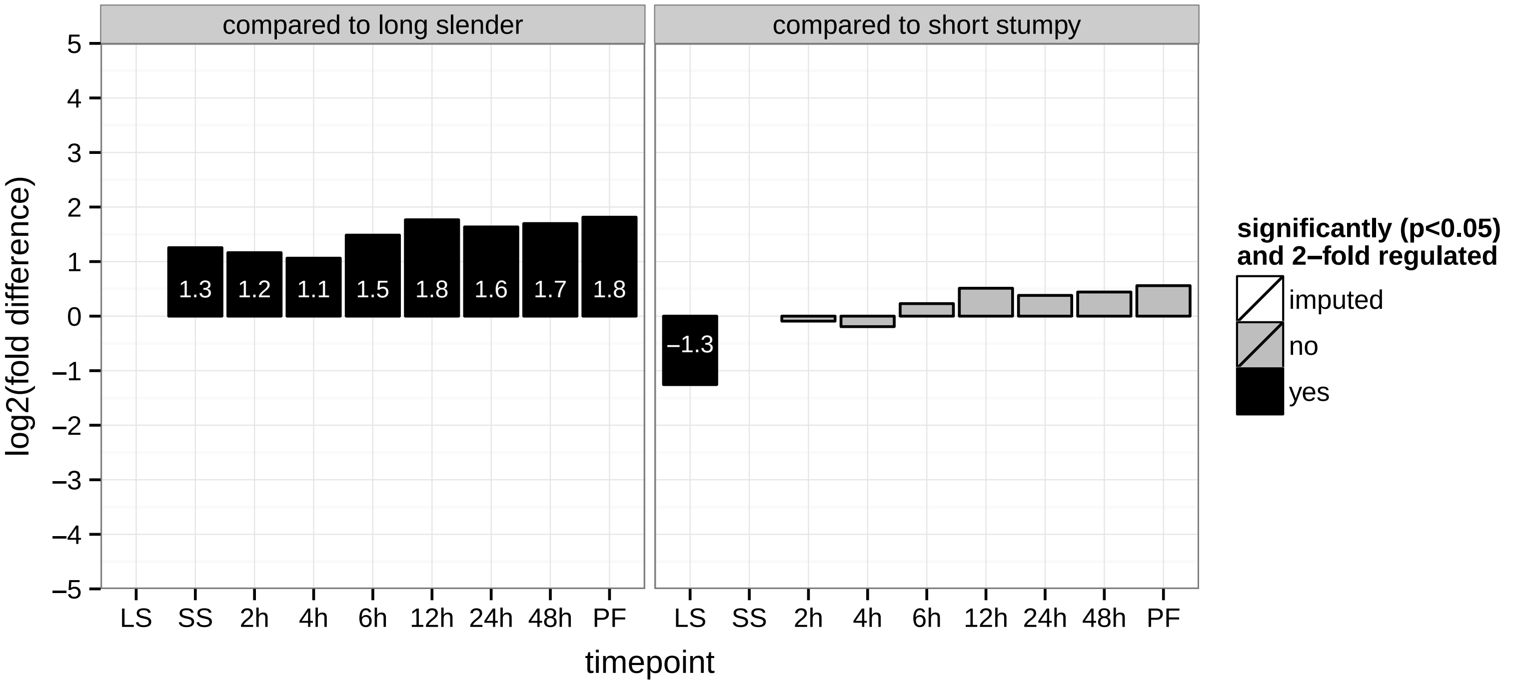
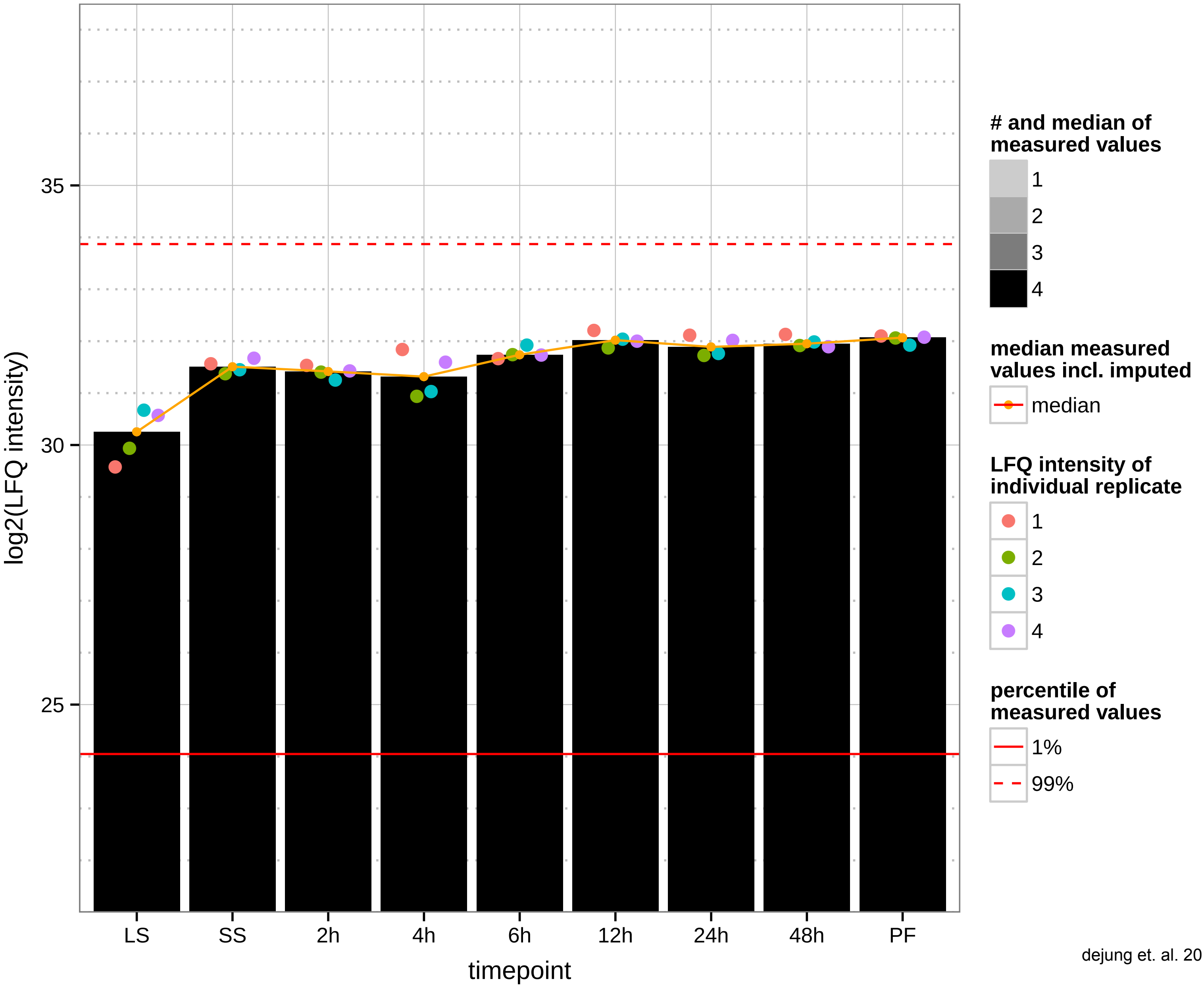
Nucleolar protein 56, putative (NOP56)
Tb927.8.3750
AGOF: snoRNA binding
AGOC: box C/D snoRNP complex, small−subunit processome
AGOP: nuclear mRNA splicing, via spliceosome, rRNA processing
PGOF: null
PGOC: null
PGOP: null





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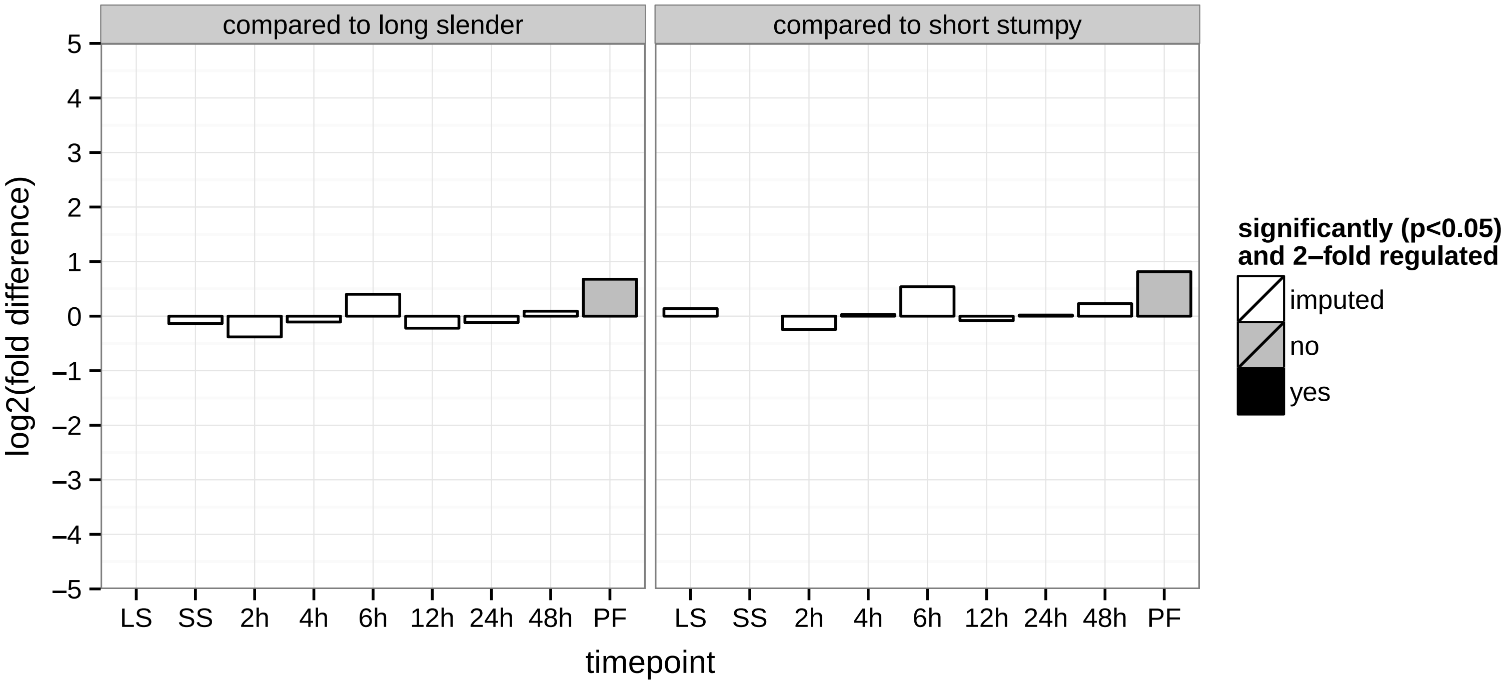
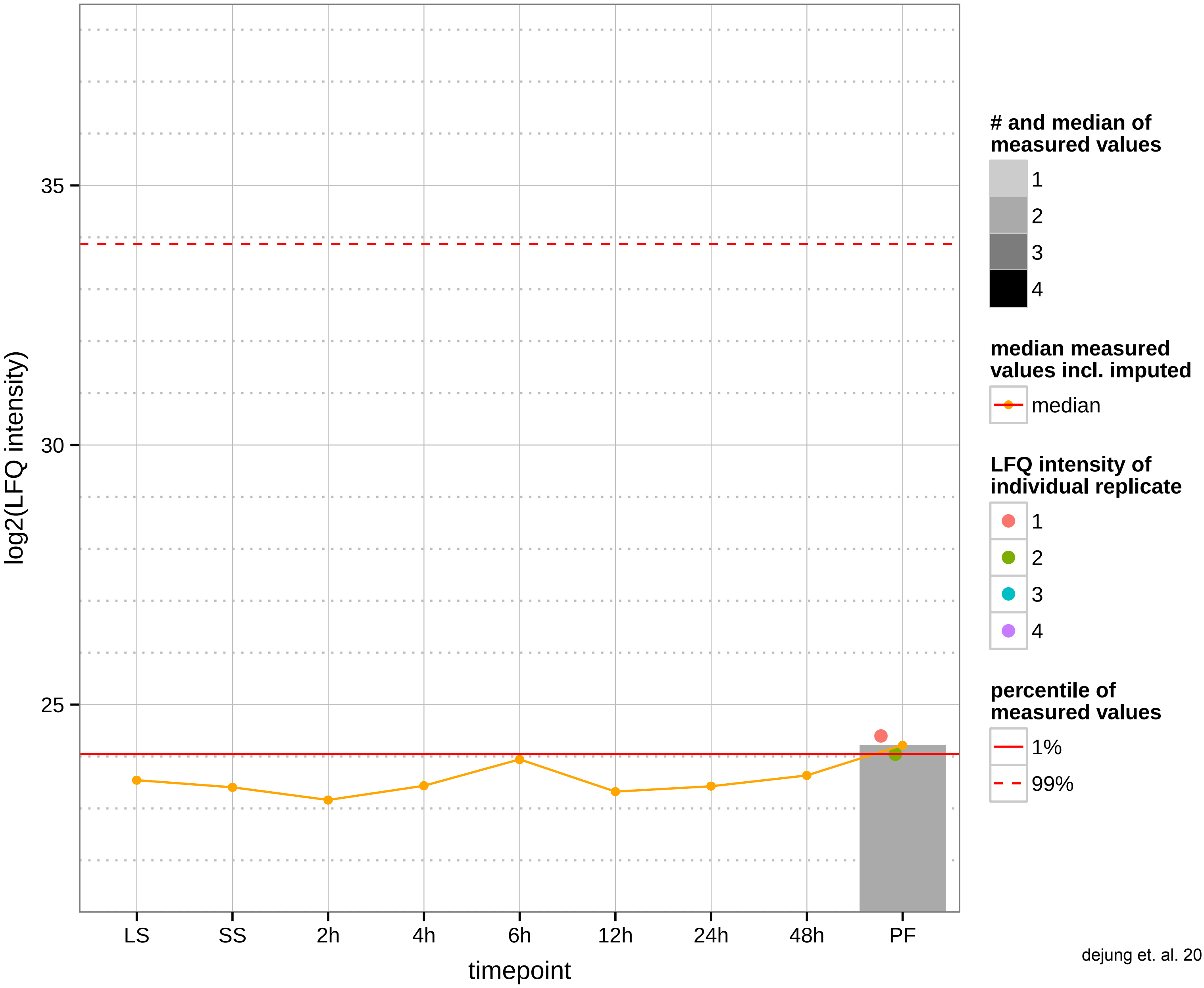
hypothetical protein, conserved
Tb927.8.3780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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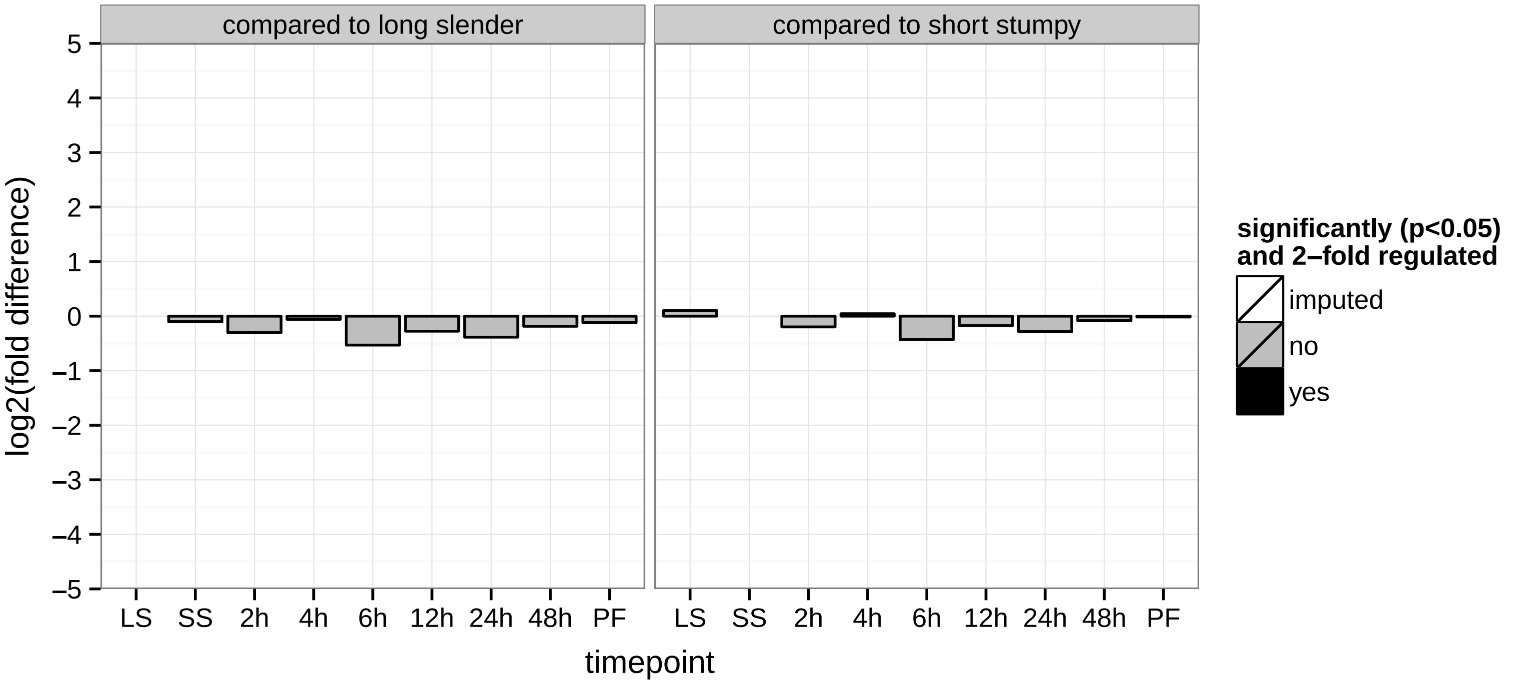
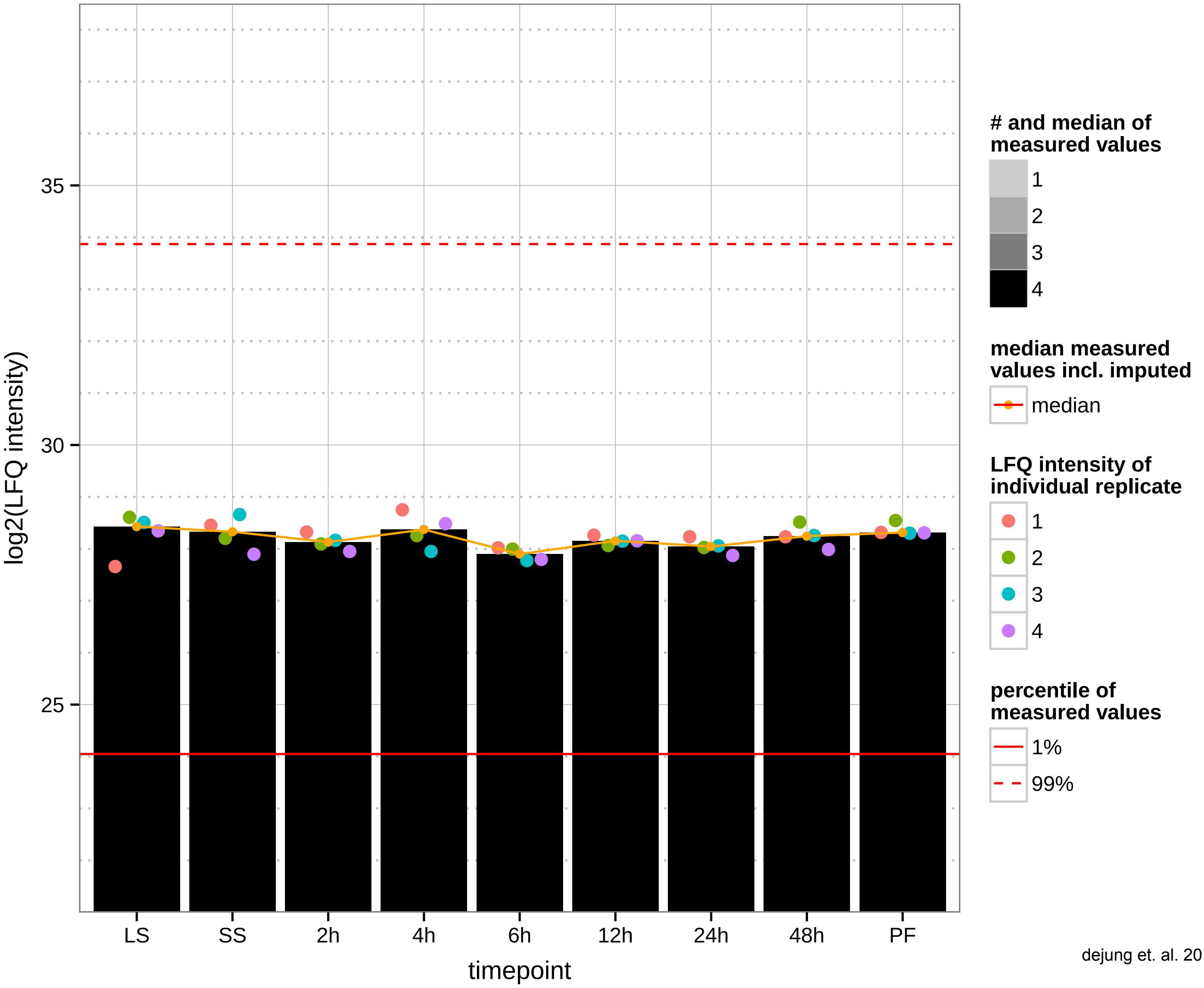
paraflagellar rod component, putative (PFC2)
Tb927.8.3790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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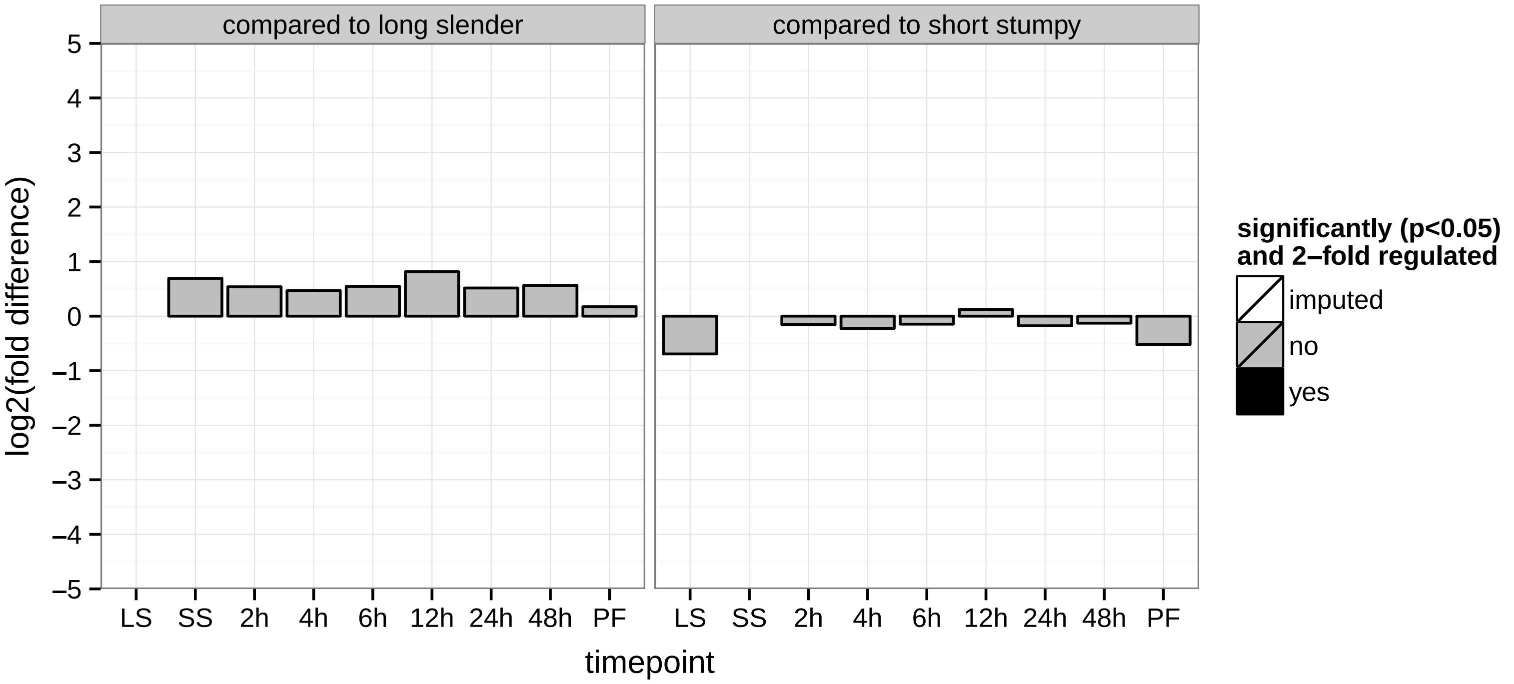
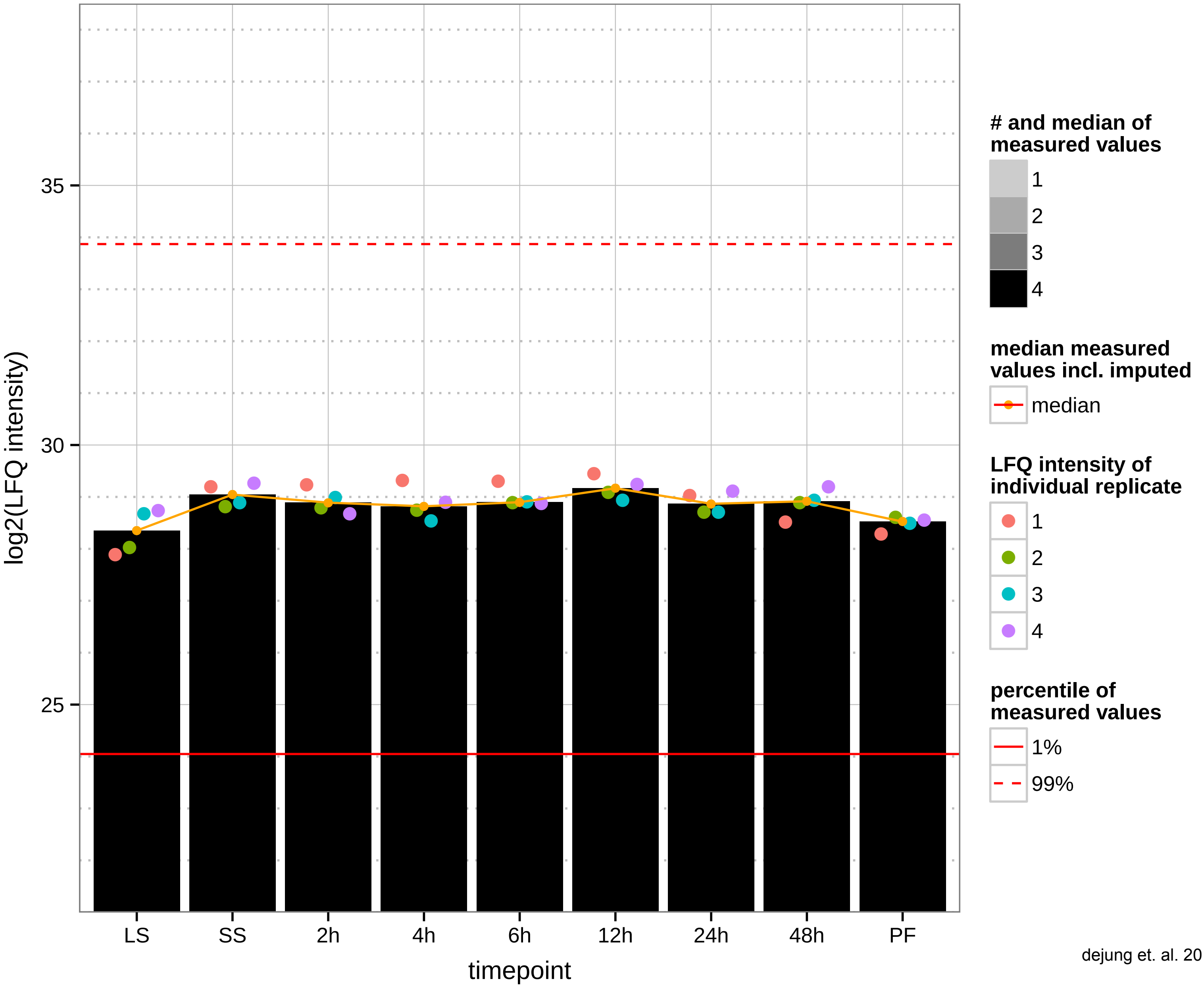
variant surface glycoprotein (VSG), putative, hypothetical protein, conserved
Tb927.8.3840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: evasion or tolerance of host immune response, null





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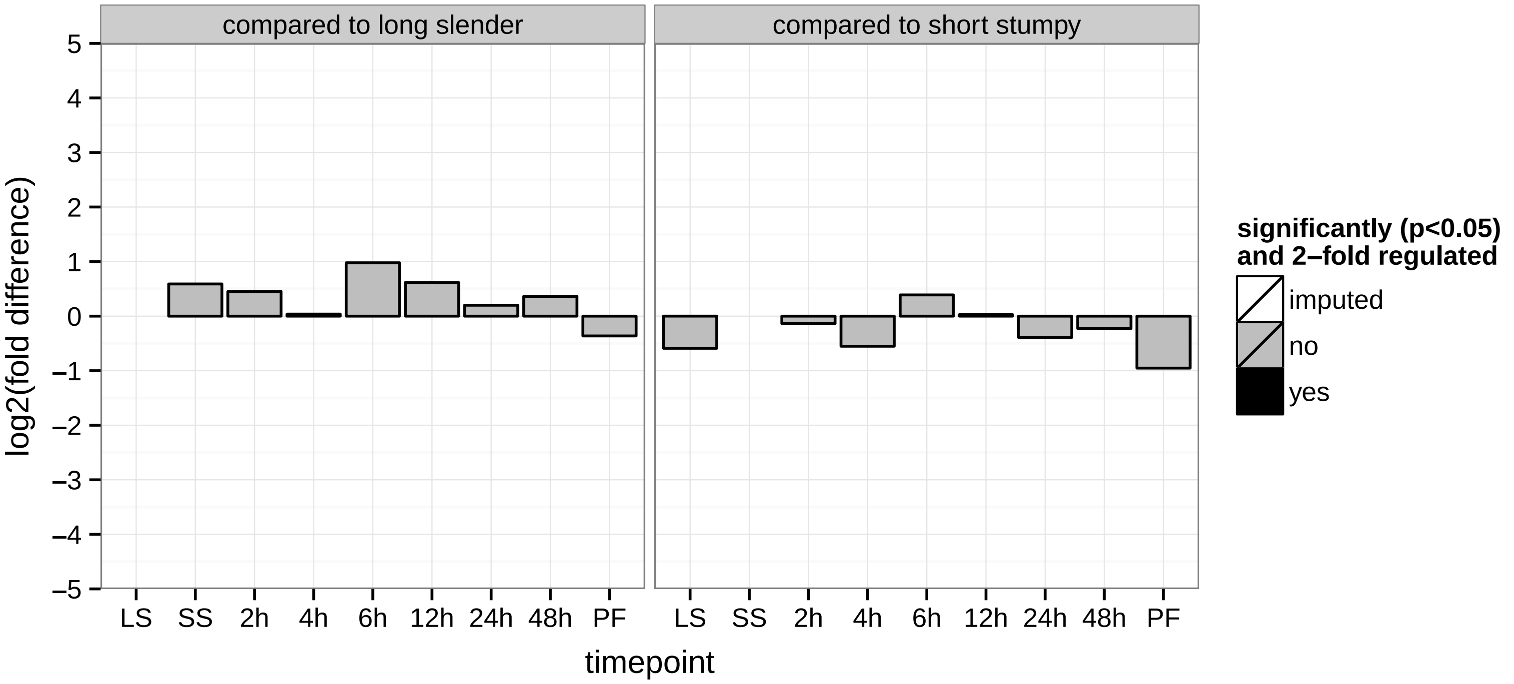
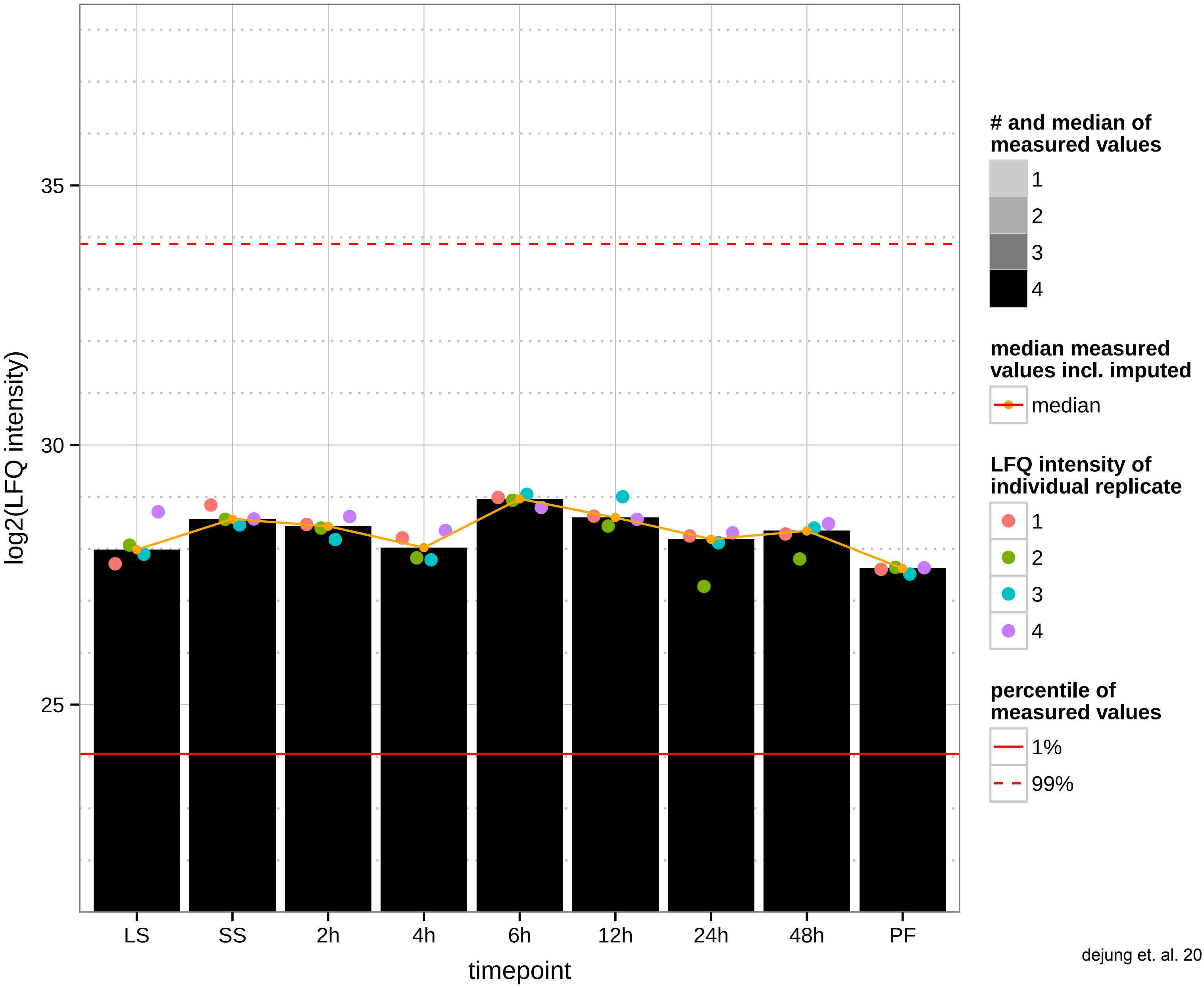
hypothetical protein, conserved
Tb927.8.3870;Tb11.v5.0681
AGOF: null, structural constituent of cell wall
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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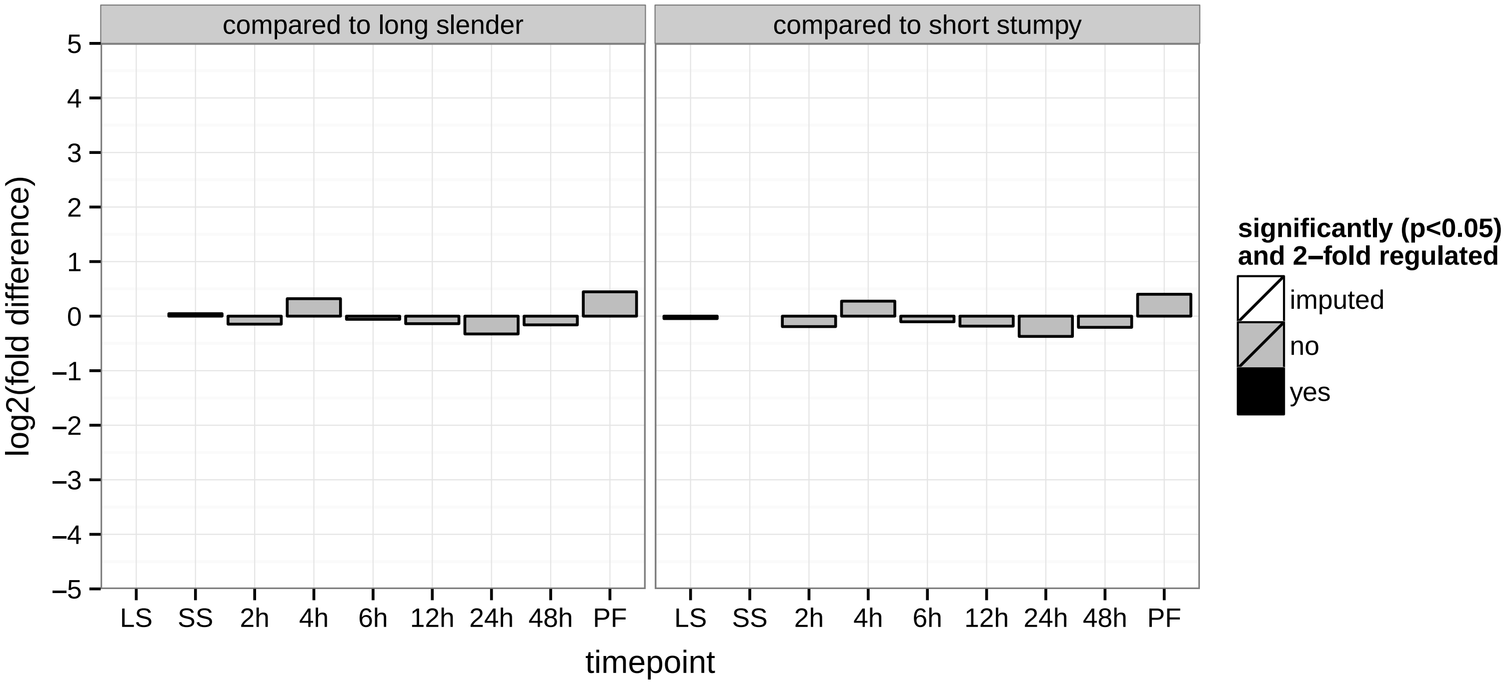
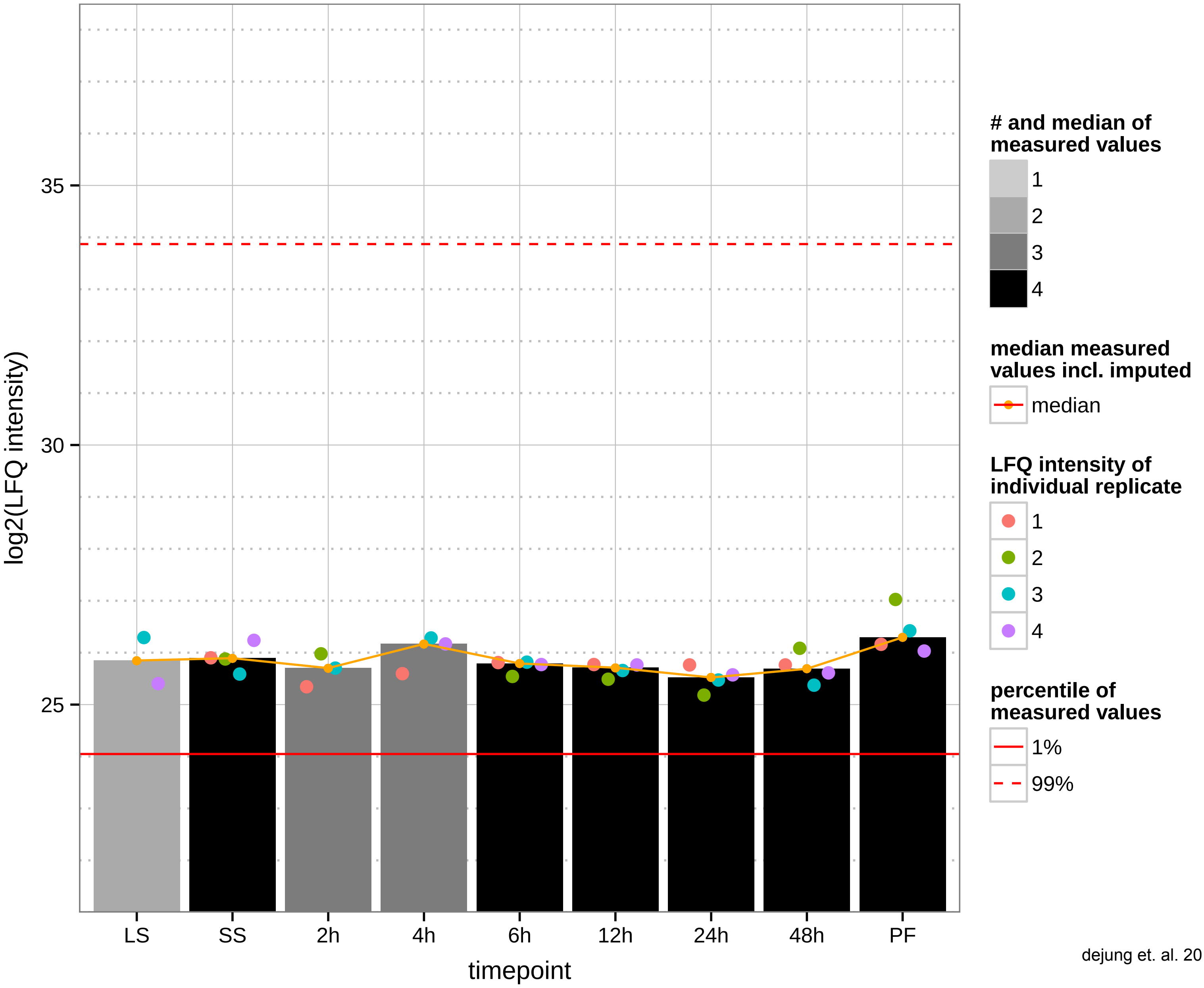
hypothetical protein, conserved
Tb927.8.3950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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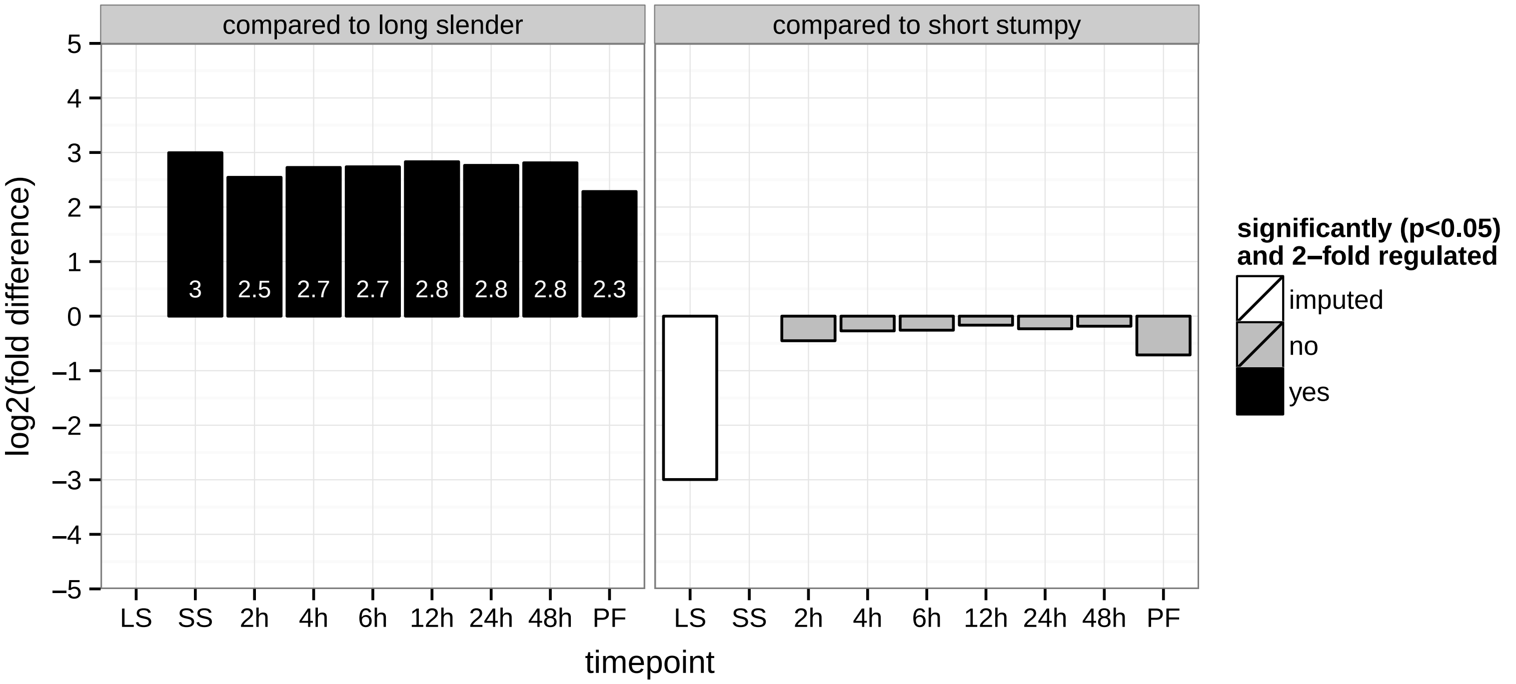
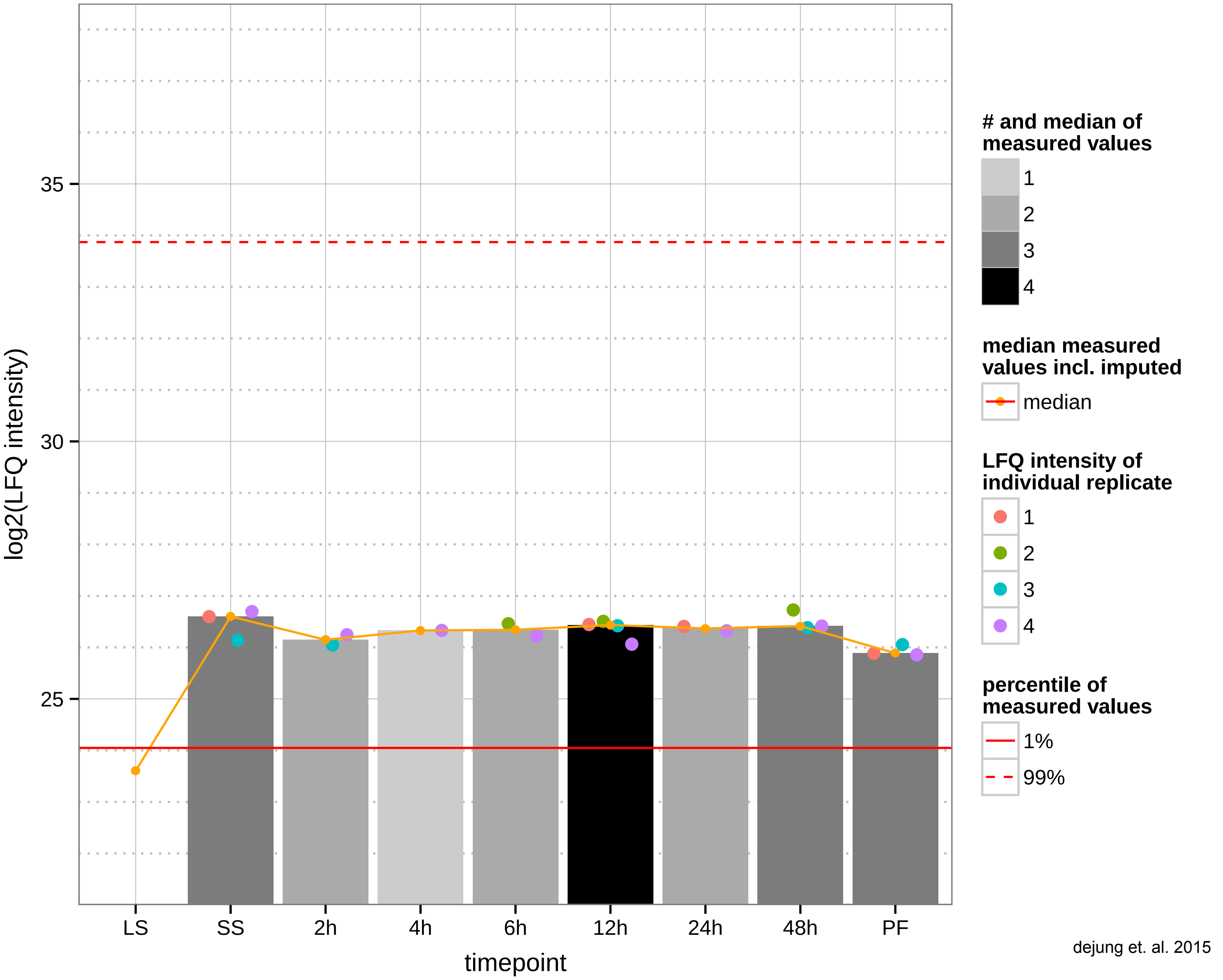
oxidoreductase, putative
Tb927.8.3970
AGOF: alcohol dehydrogenase activity, zinc–dependent, oxidoreductase activity, zinc ion binding
AGOC: null
AGOP: metabolic process, oxidation–reduction process
PGOF: oxidoreductase activity, transferase activity, transferring acyl groups other than amino–acyl groups, zinc ion binding
PGOC: null
PGOP: oxidation–reduction process





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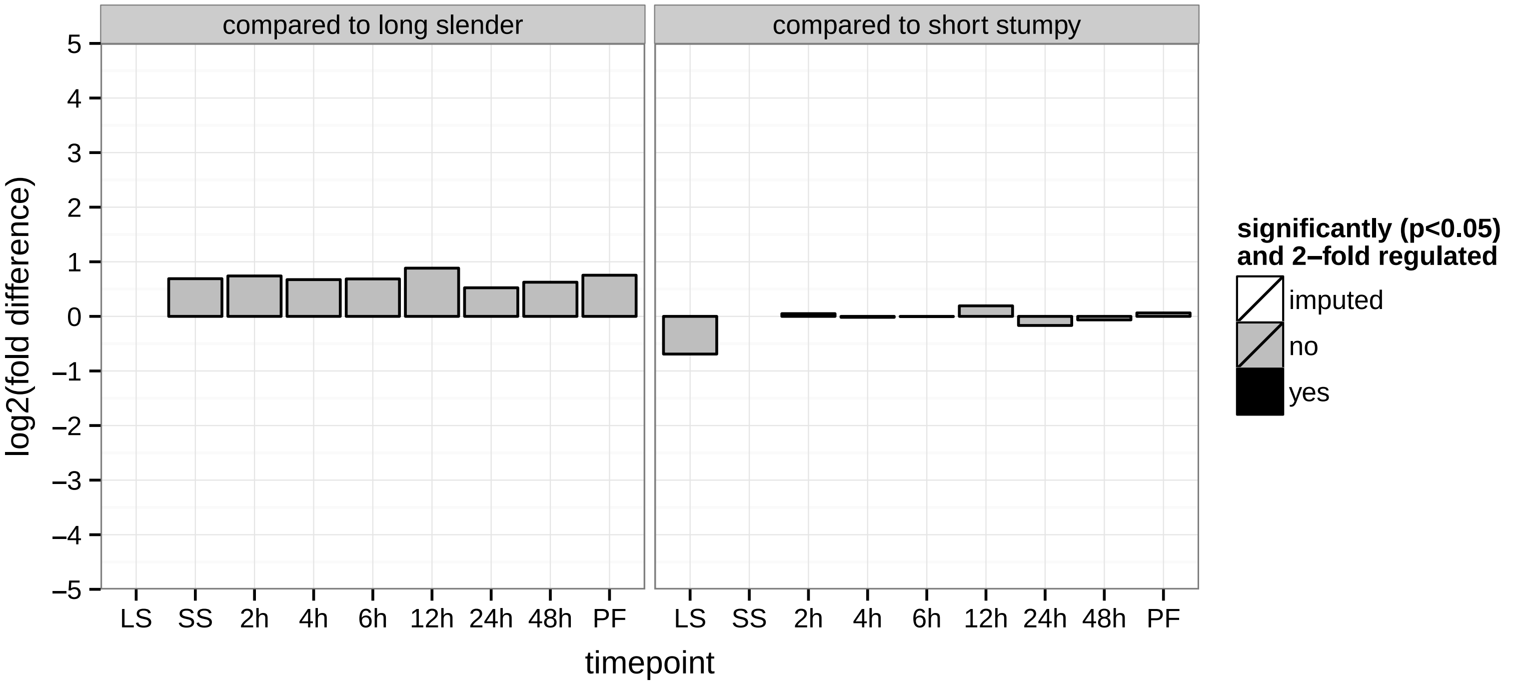
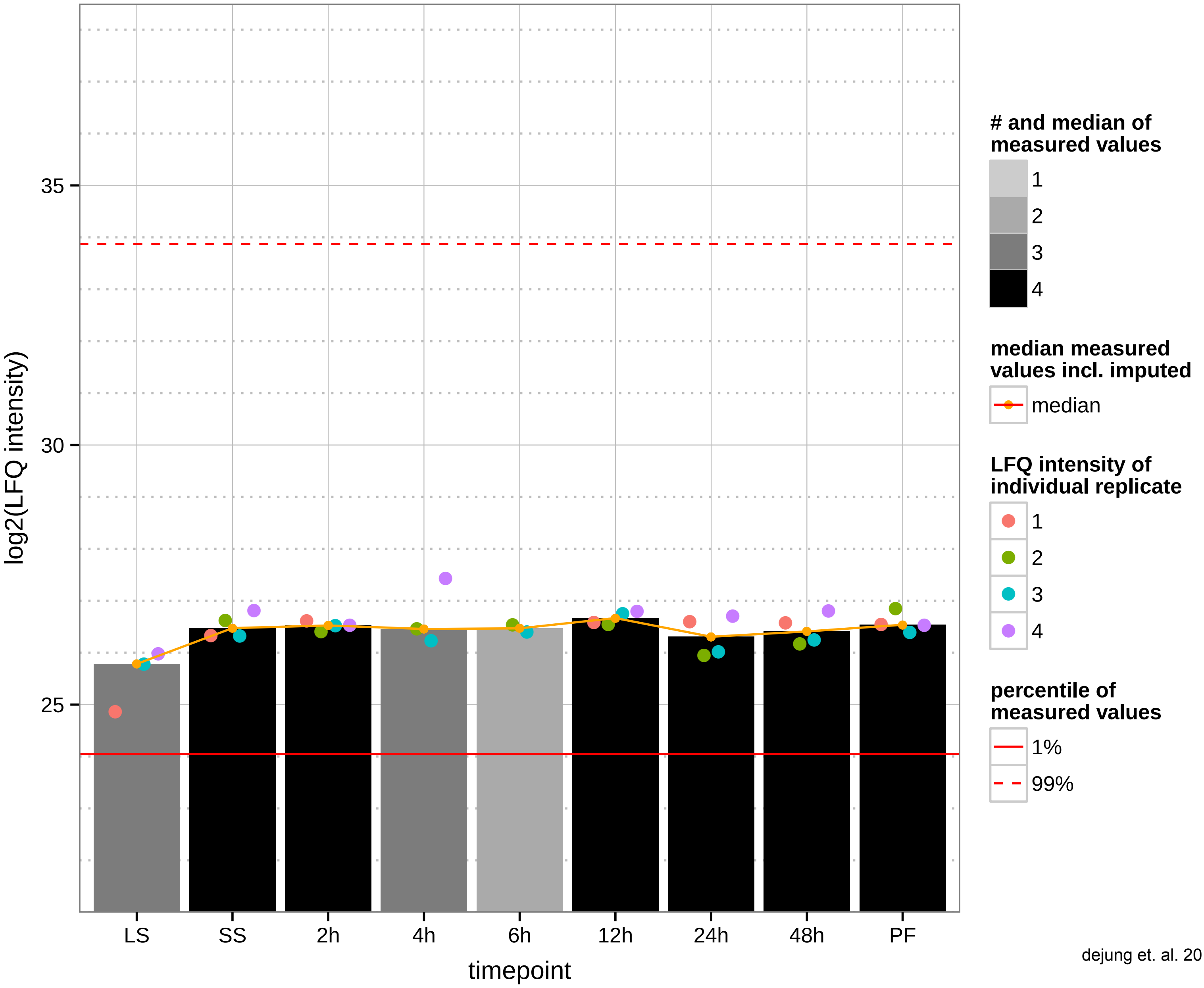
class I transcription factor A, subunit 5b (CITFA−5b)
Tb927.8.4130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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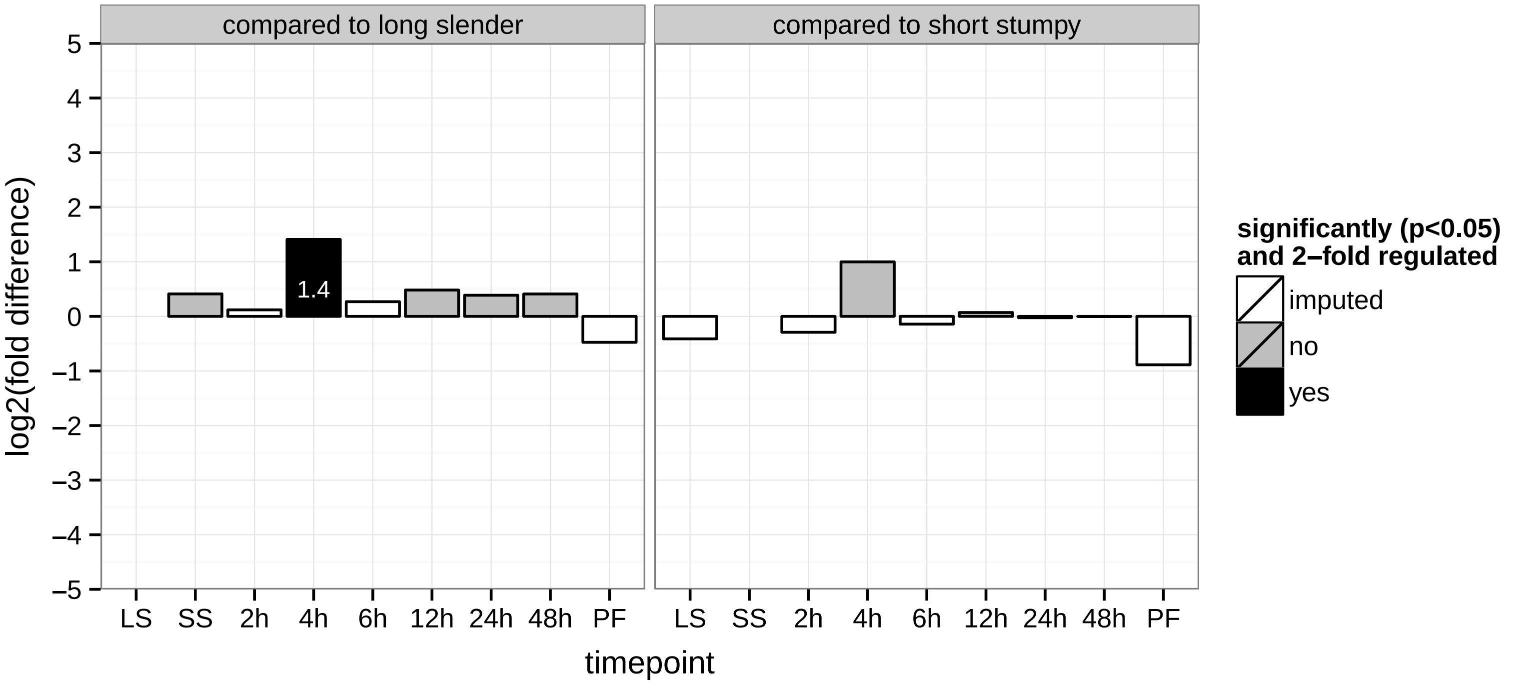
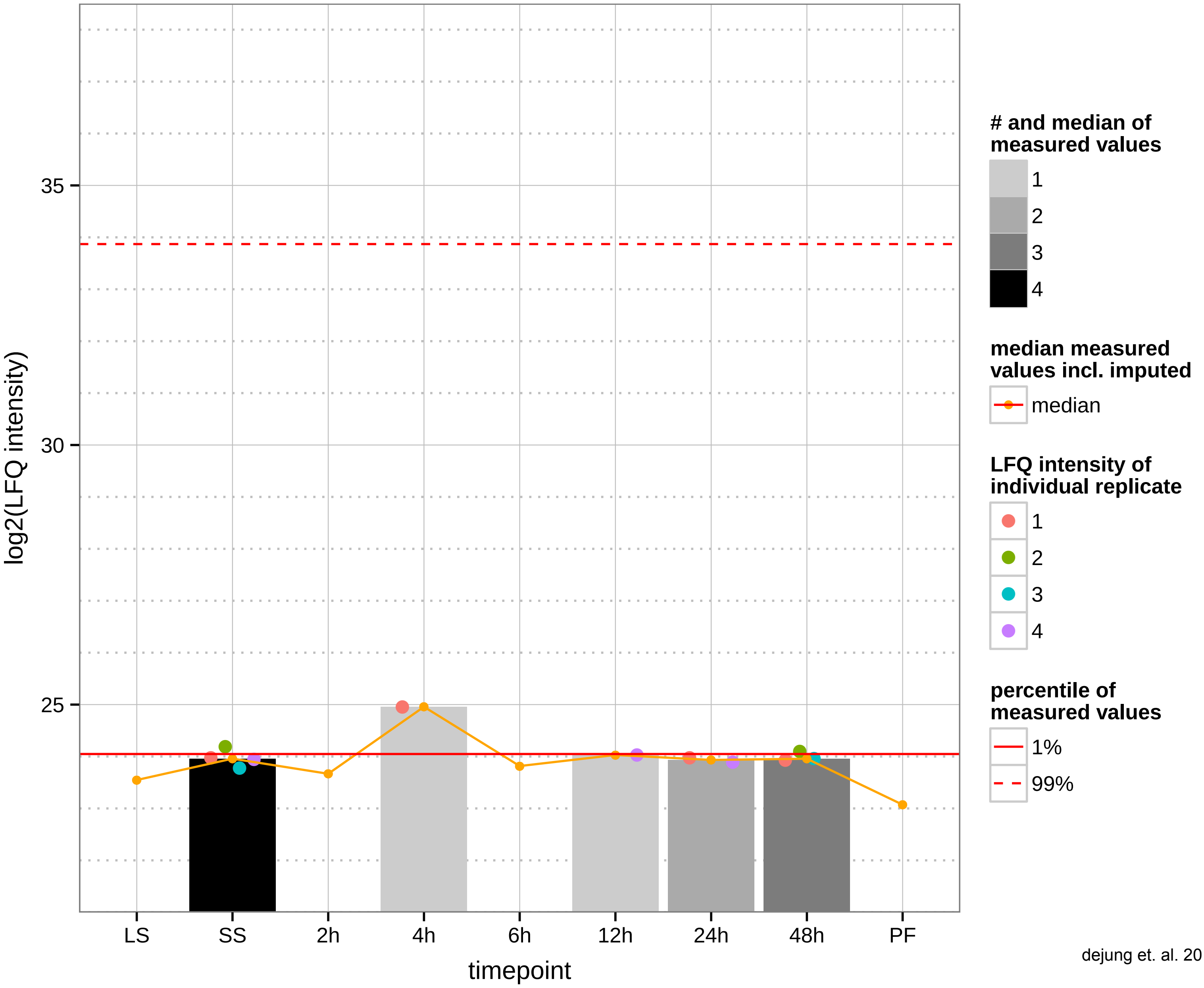
hypothetical protein, conserved
Tb927.8.4160
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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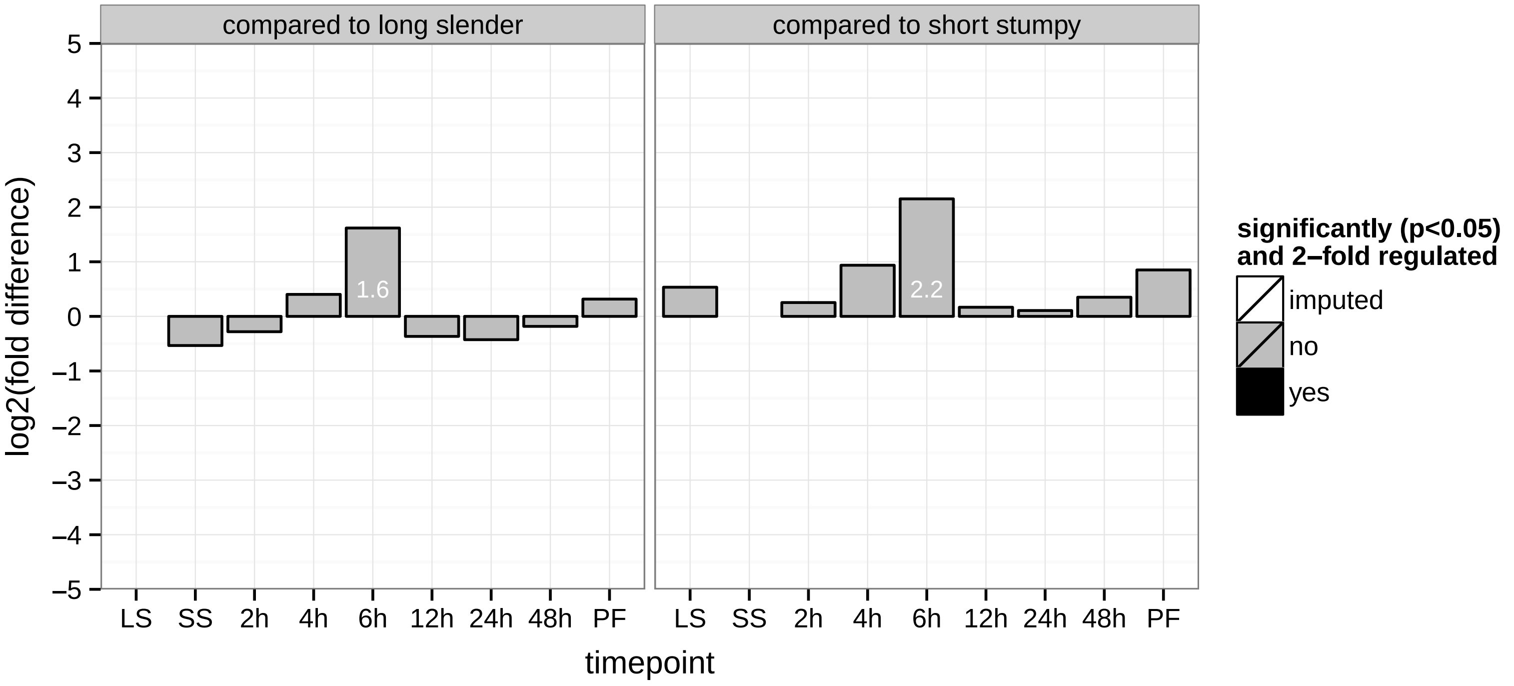
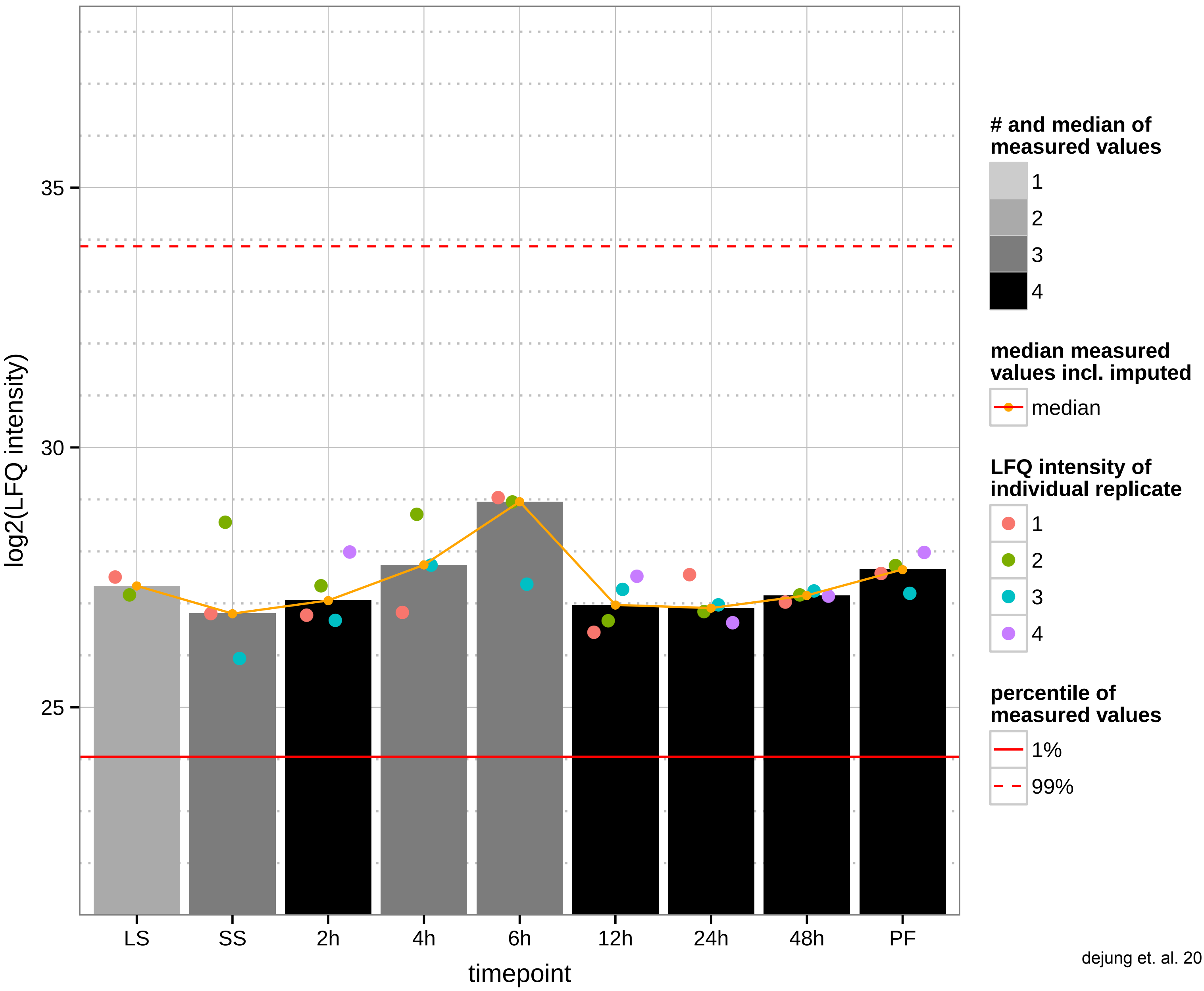
RNA–binding protein, putative (MRD1)
Tb927.8.4170
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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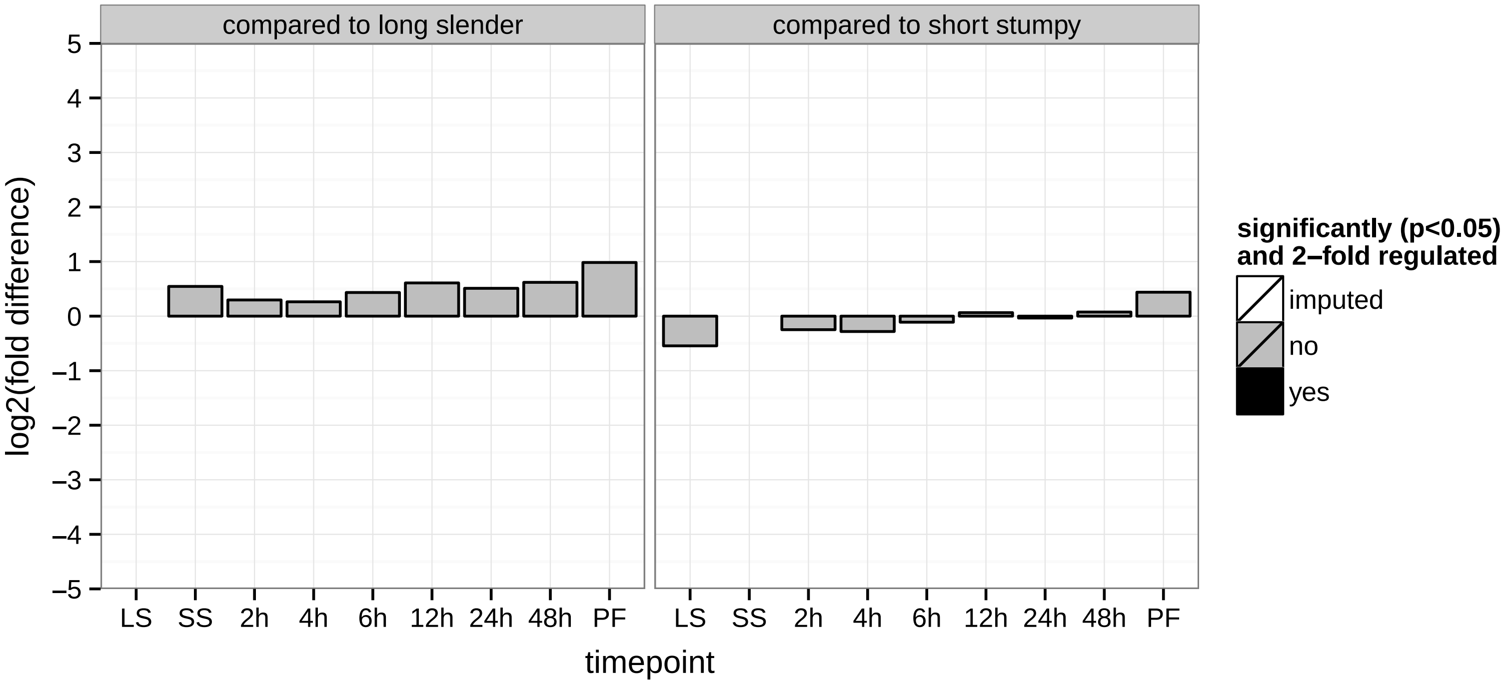
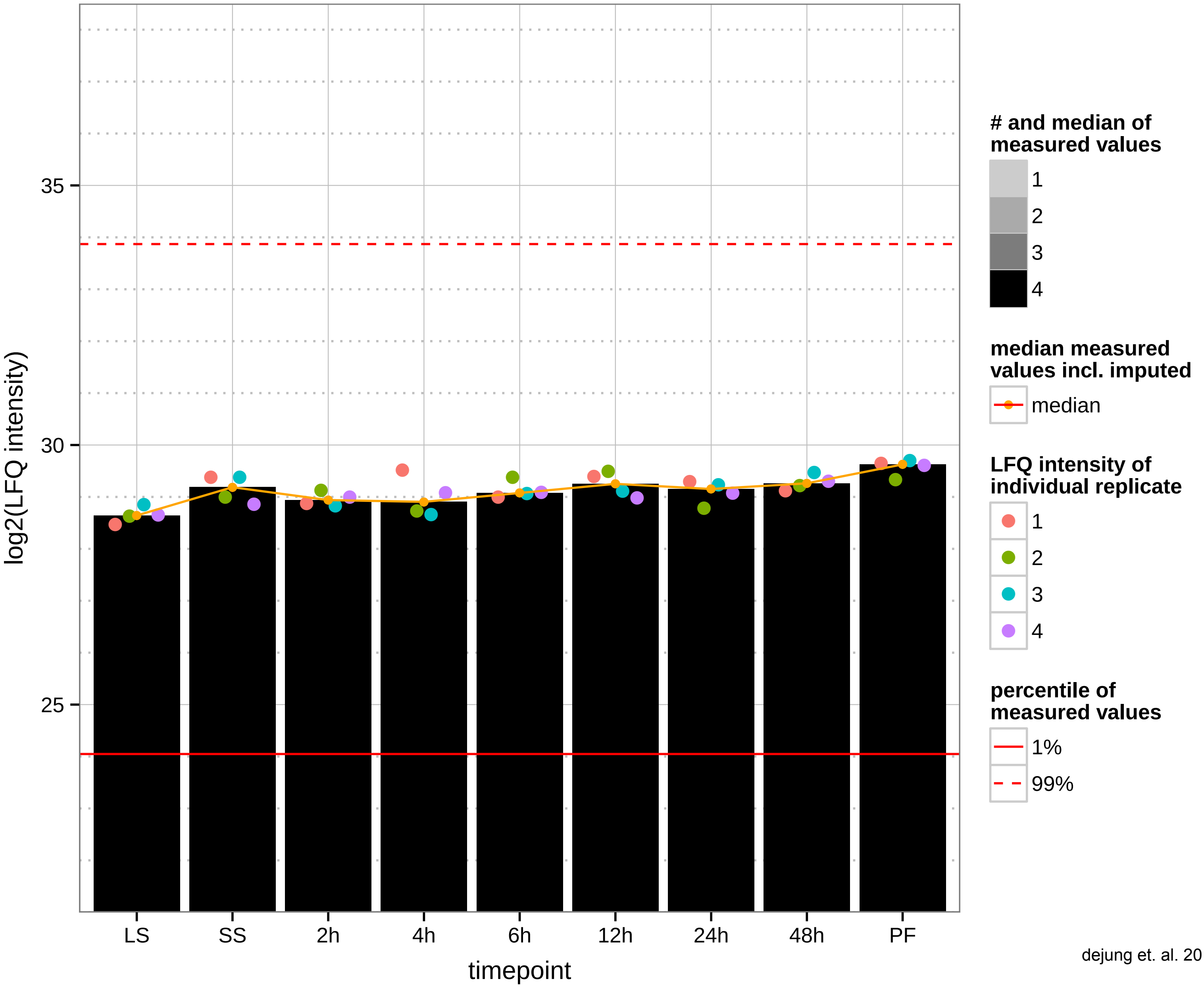
hypothetical protein, conserved
Tb927.8.4210
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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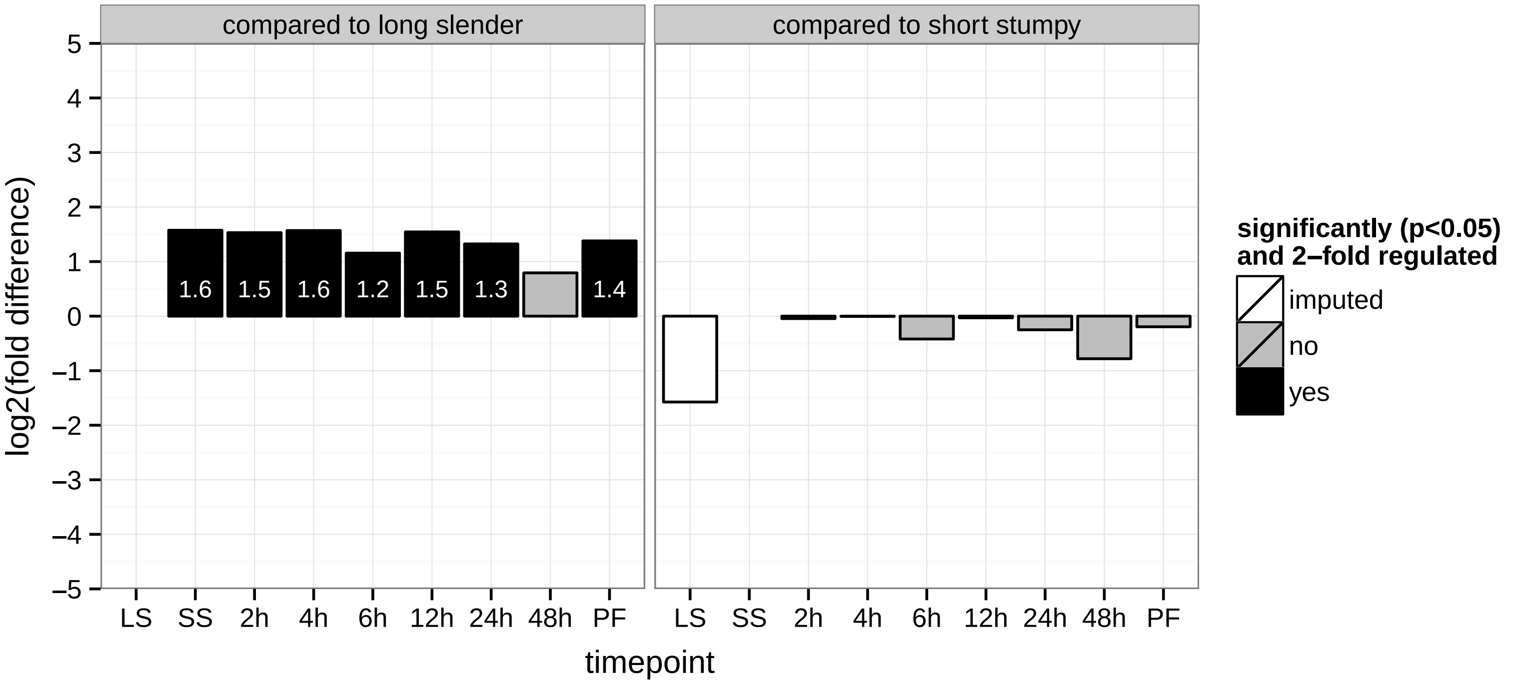
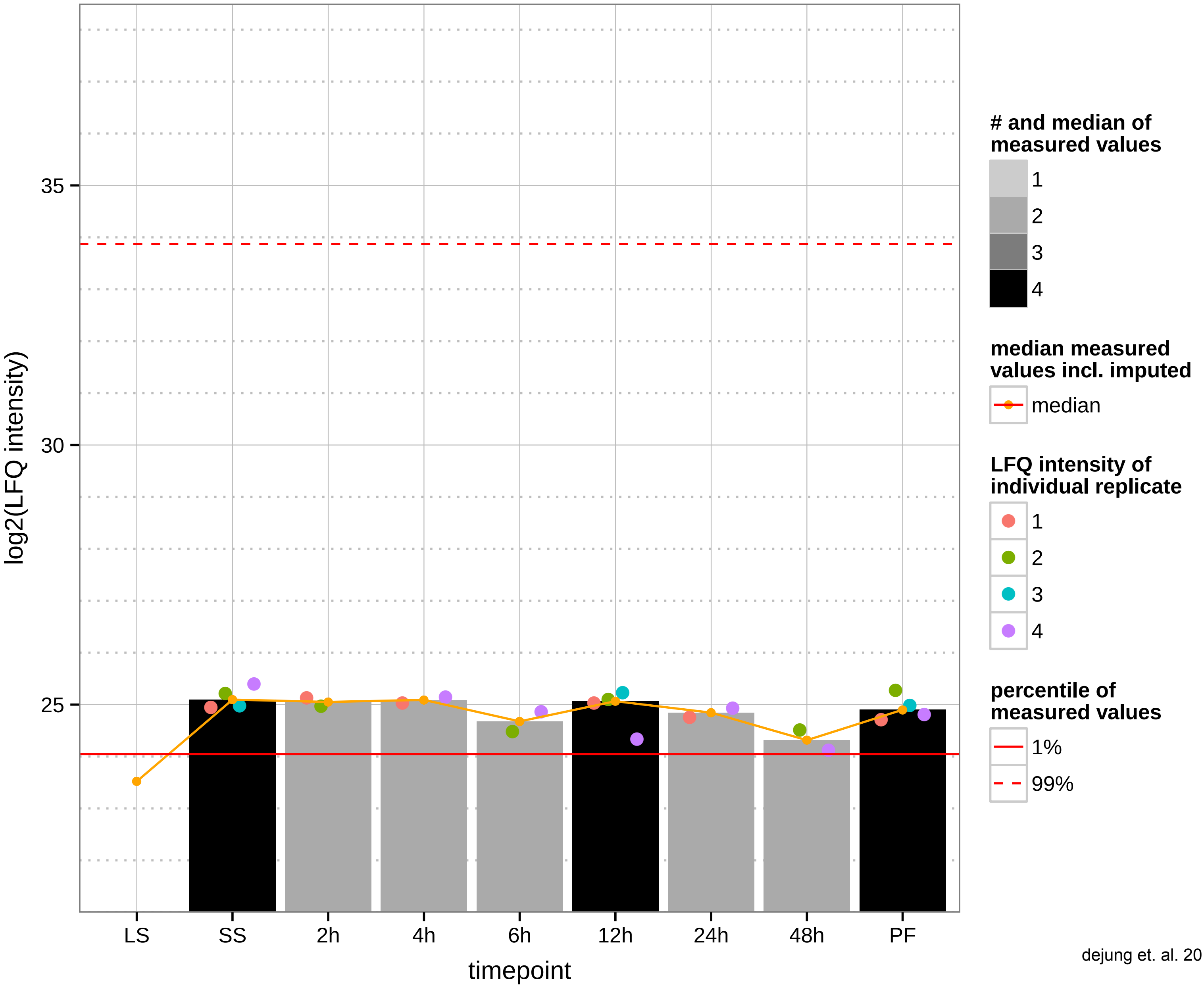
hypothetical protein, conserved
Tb927.8.4270
AGOF: deaminase activity
AGOC: null
AGOP: purine ribonucleoside monophosphate biosynthetic process
PGOF: null
PGOC: null
PGOP: null





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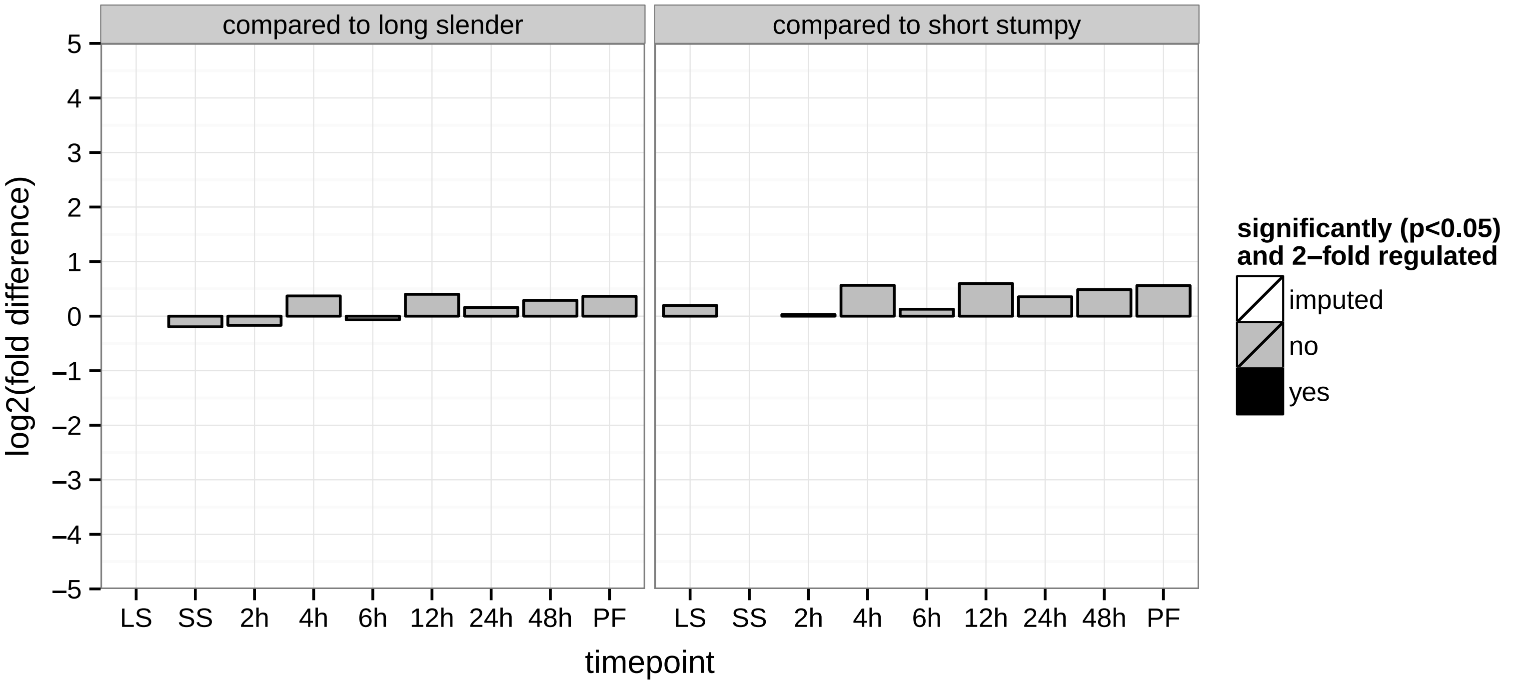
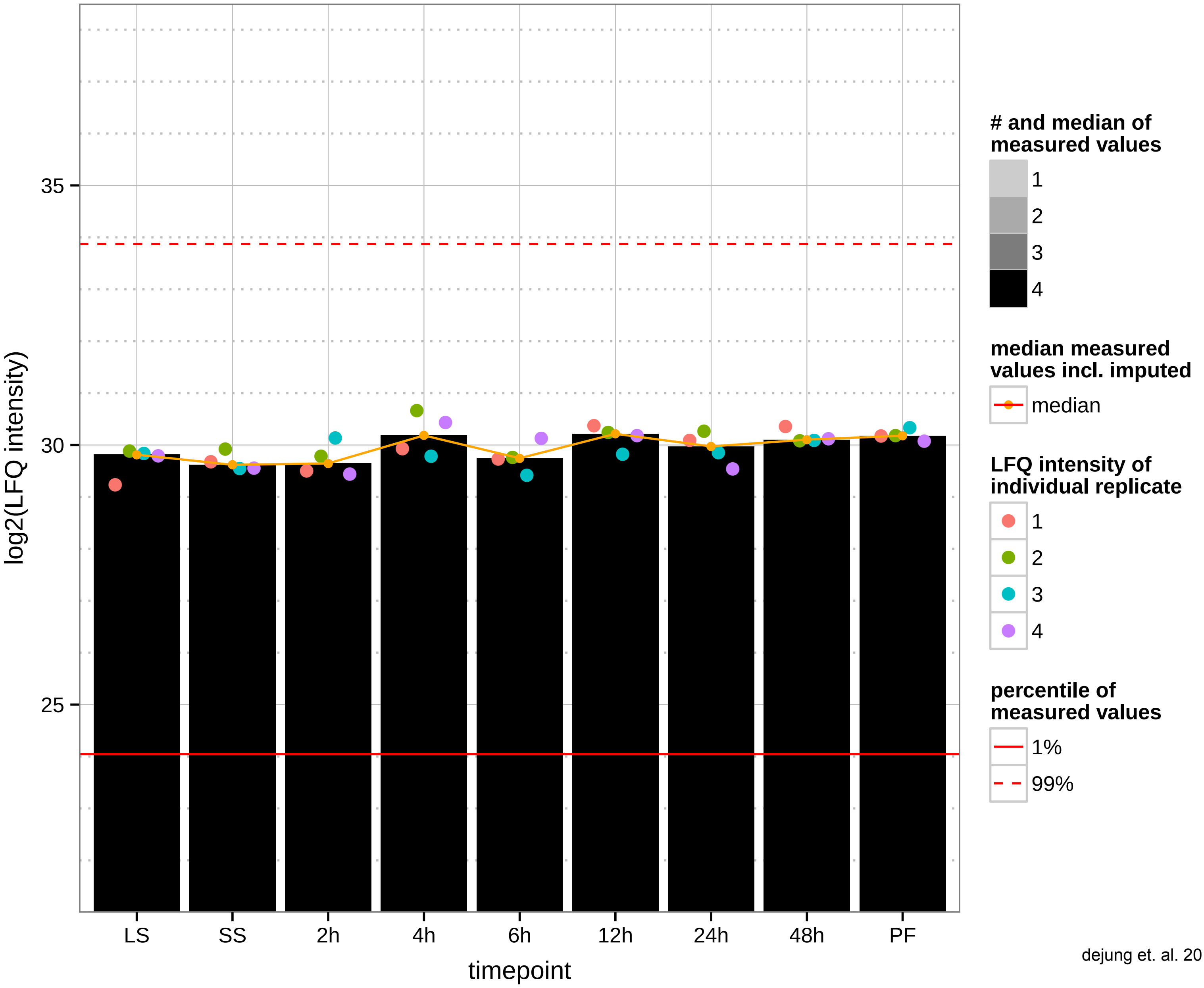
nuclear transport factor 2, putative
Tb927.8.4280
AGOF: protein transporter activity
AGOC: intracellular, nucleus
AGOP: protein import into nucleus
PGOF: null
PGOC: intracellular
PGOP: transport





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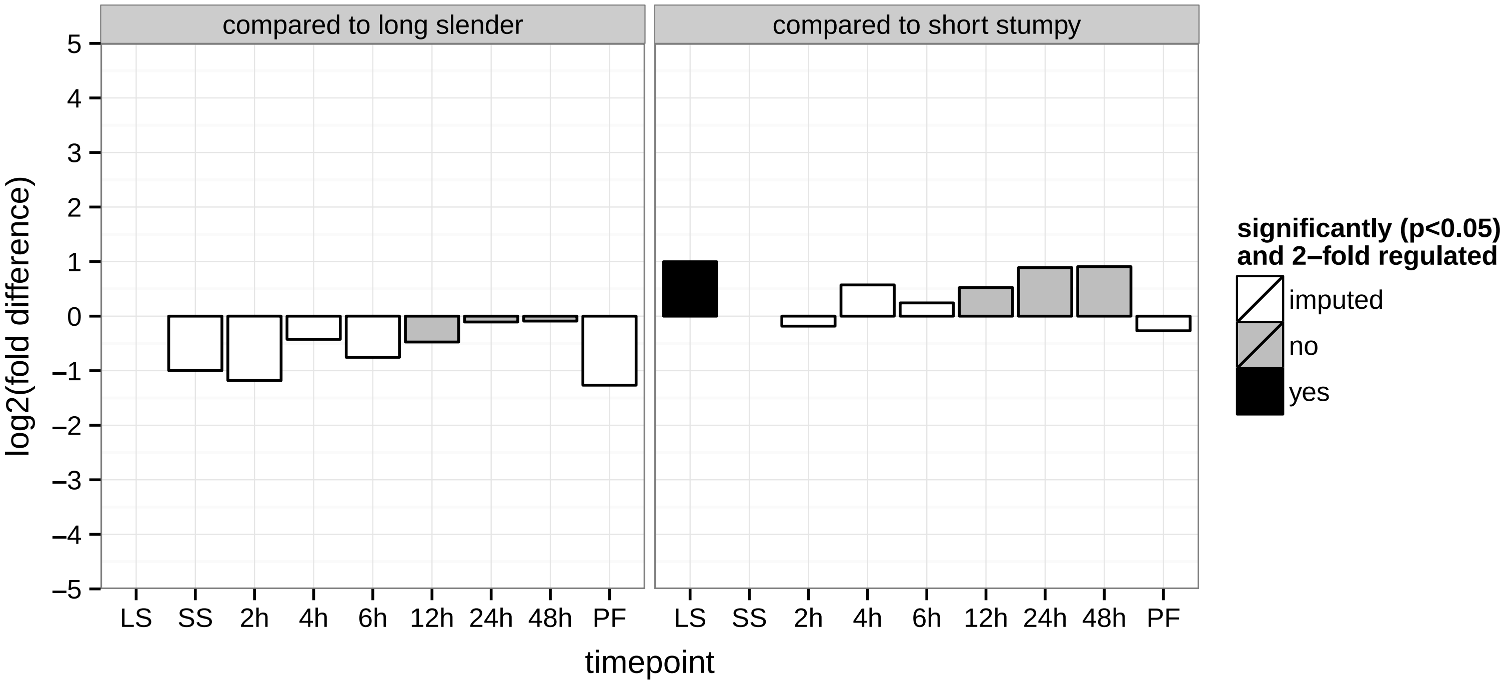
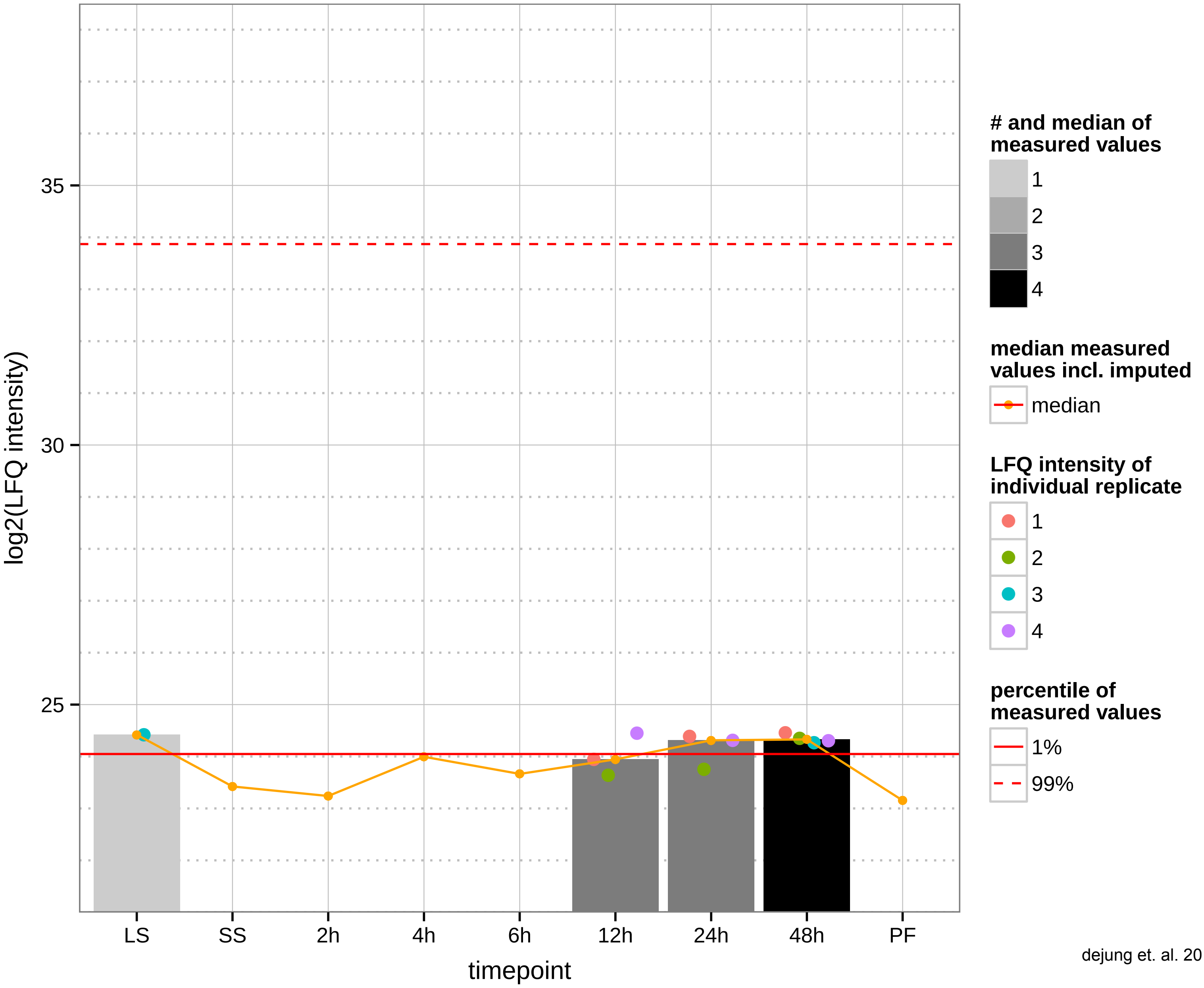
hypothetical protein, conserved
Tb927.8.4320
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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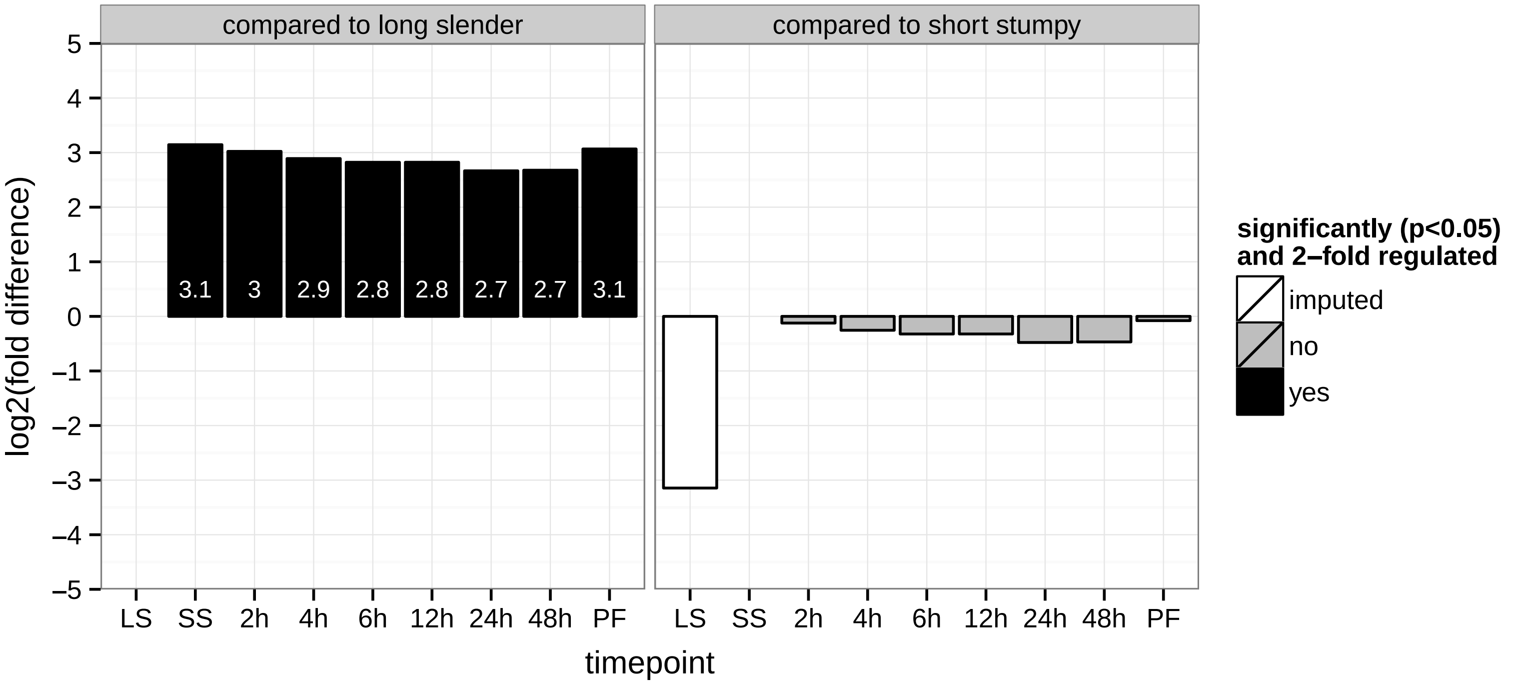
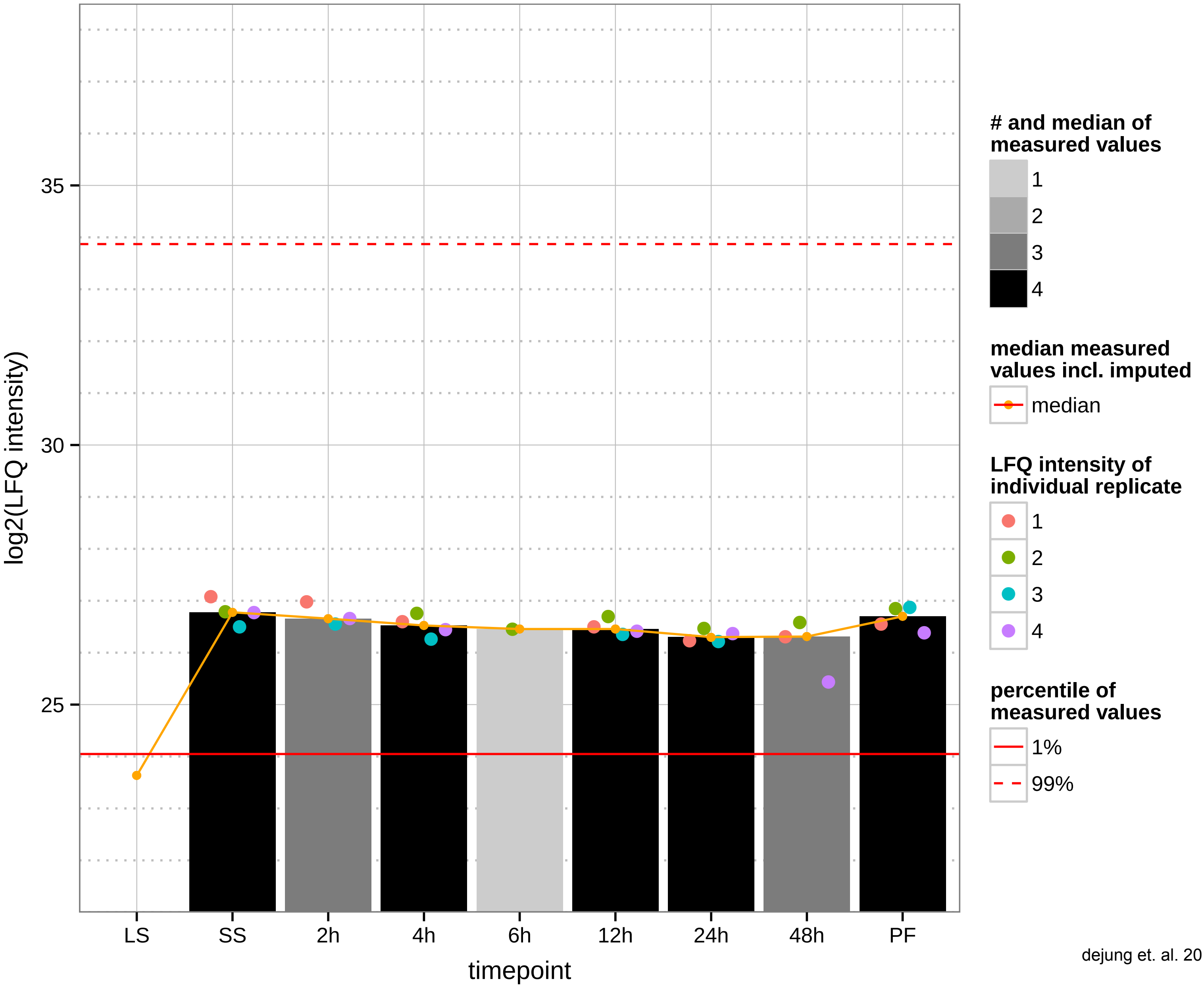
hypothetical protein, conserved
Tb927.8.4370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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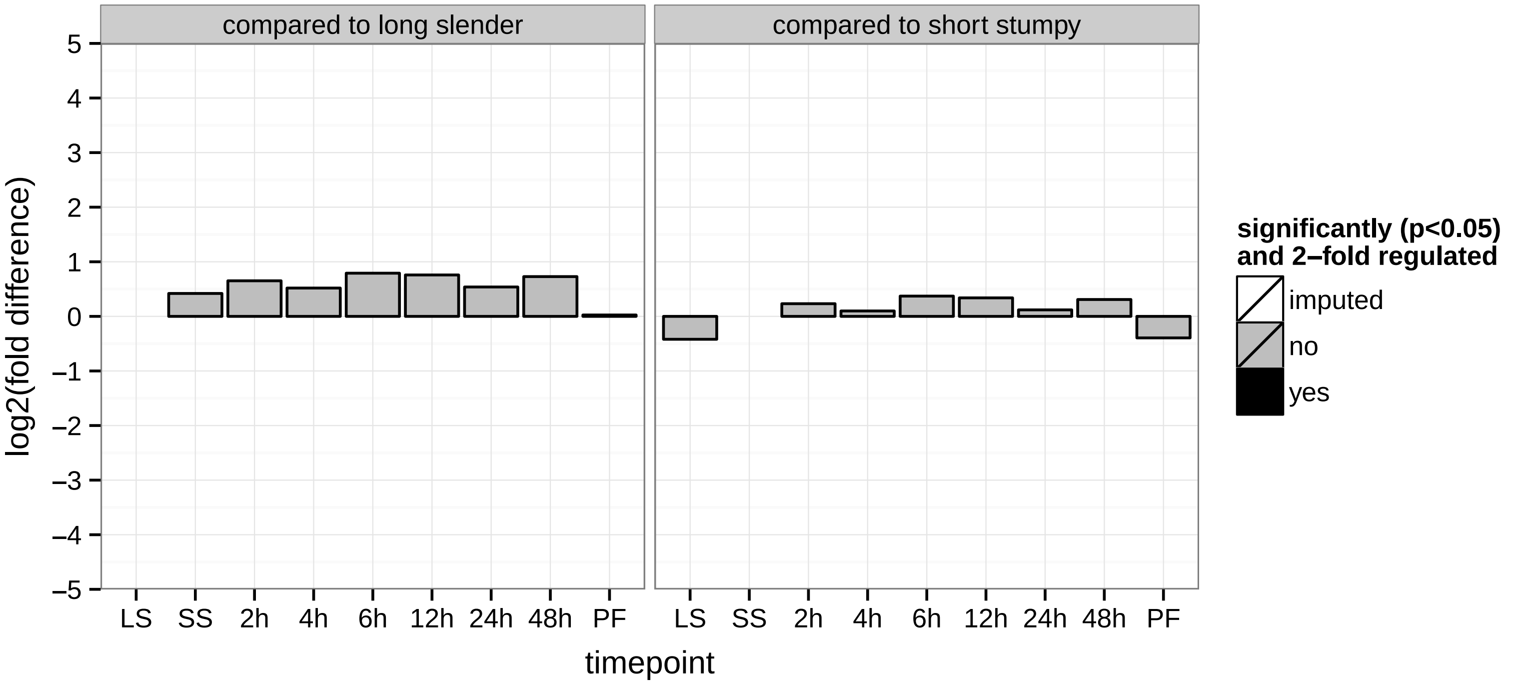
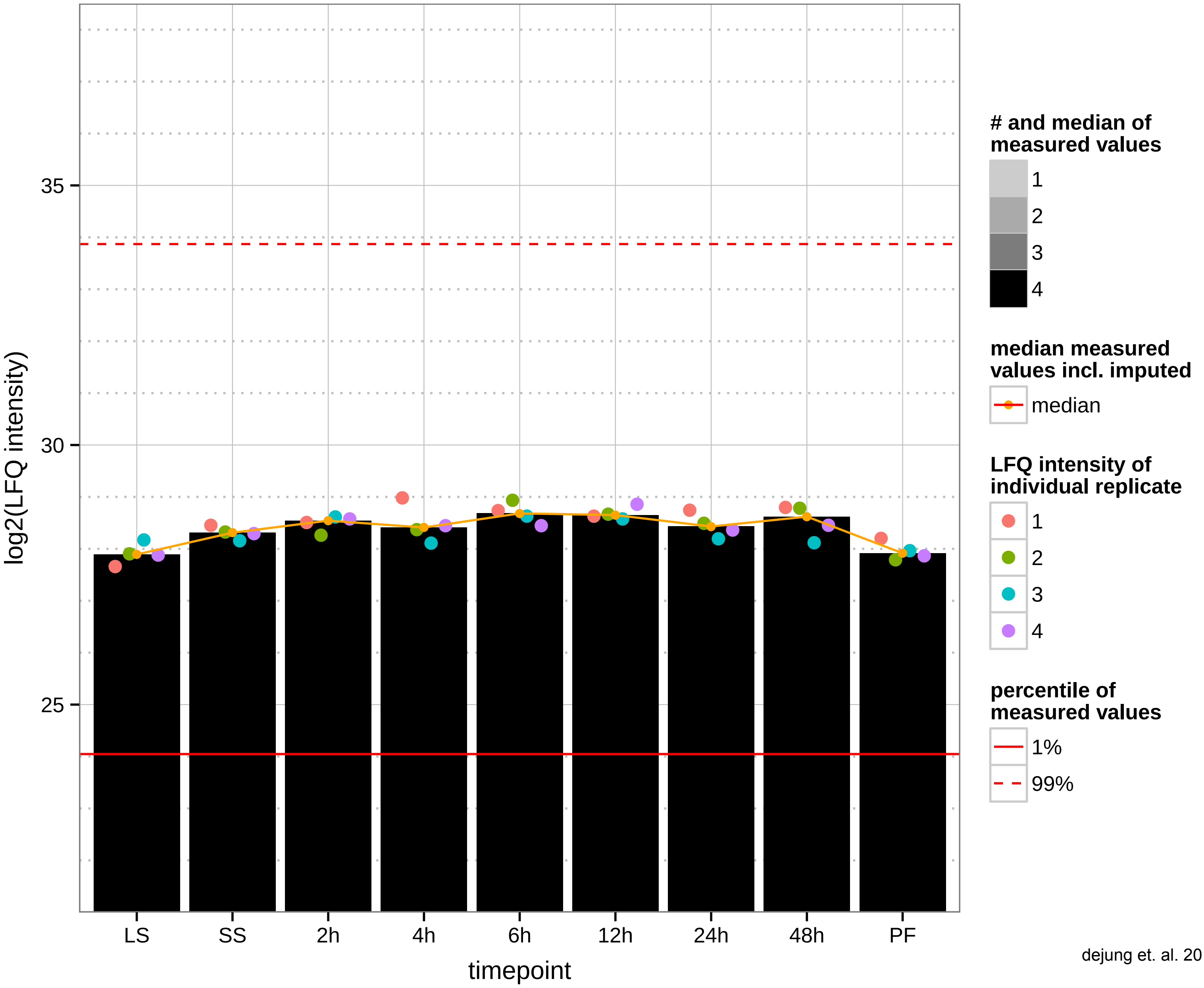
hypothetical protein, conserved
Tb927.8.4400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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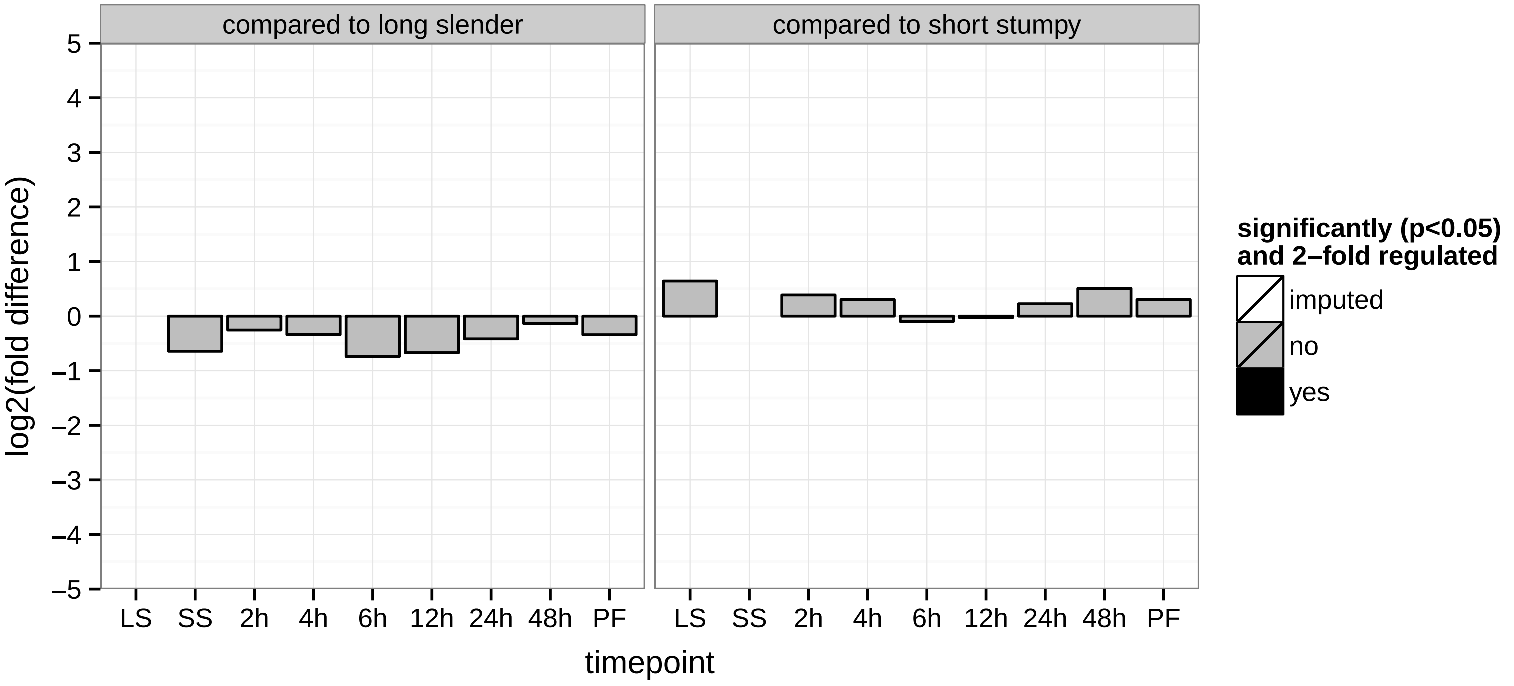
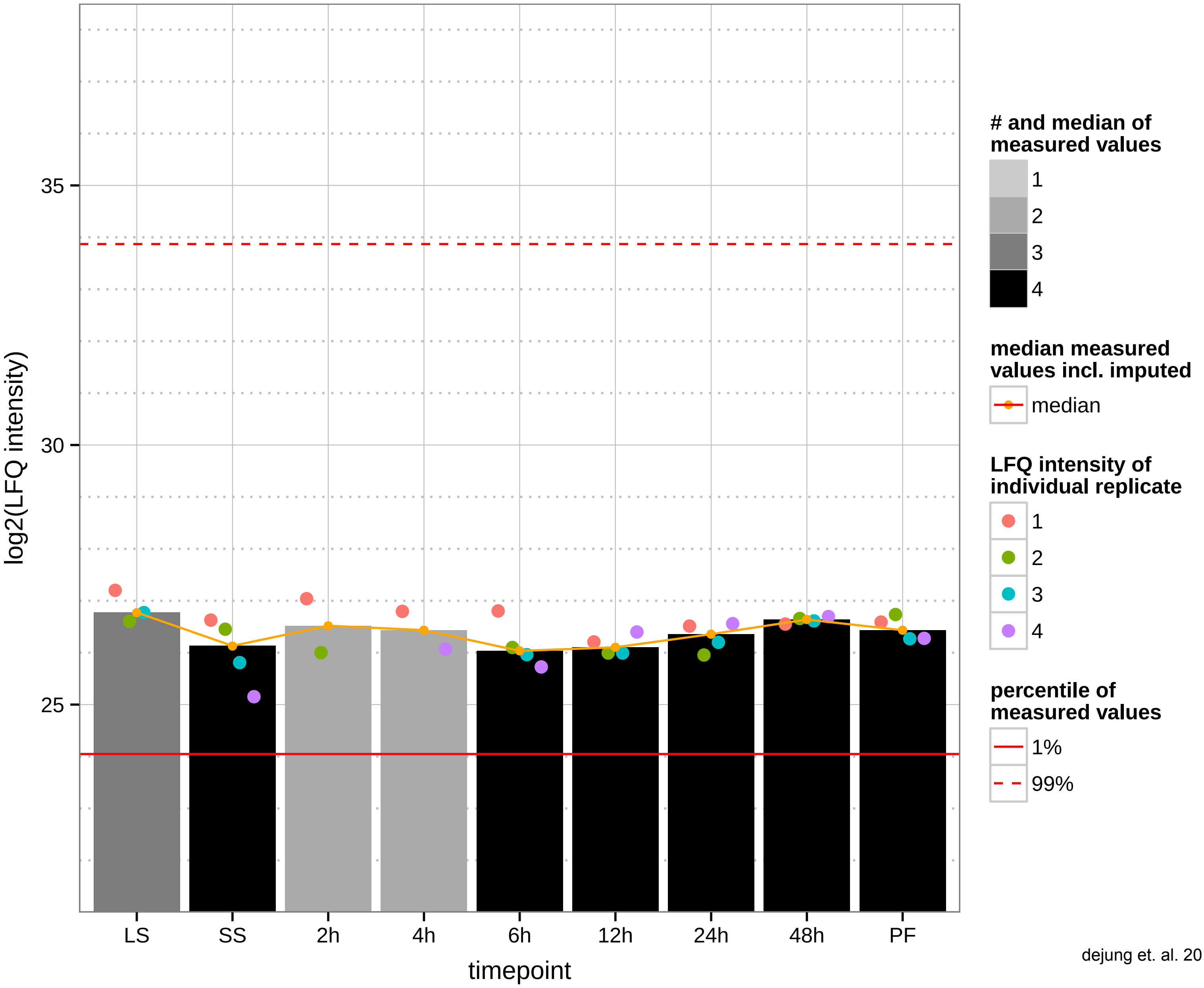
hypothetical protein, conserved
Tb927.8.4460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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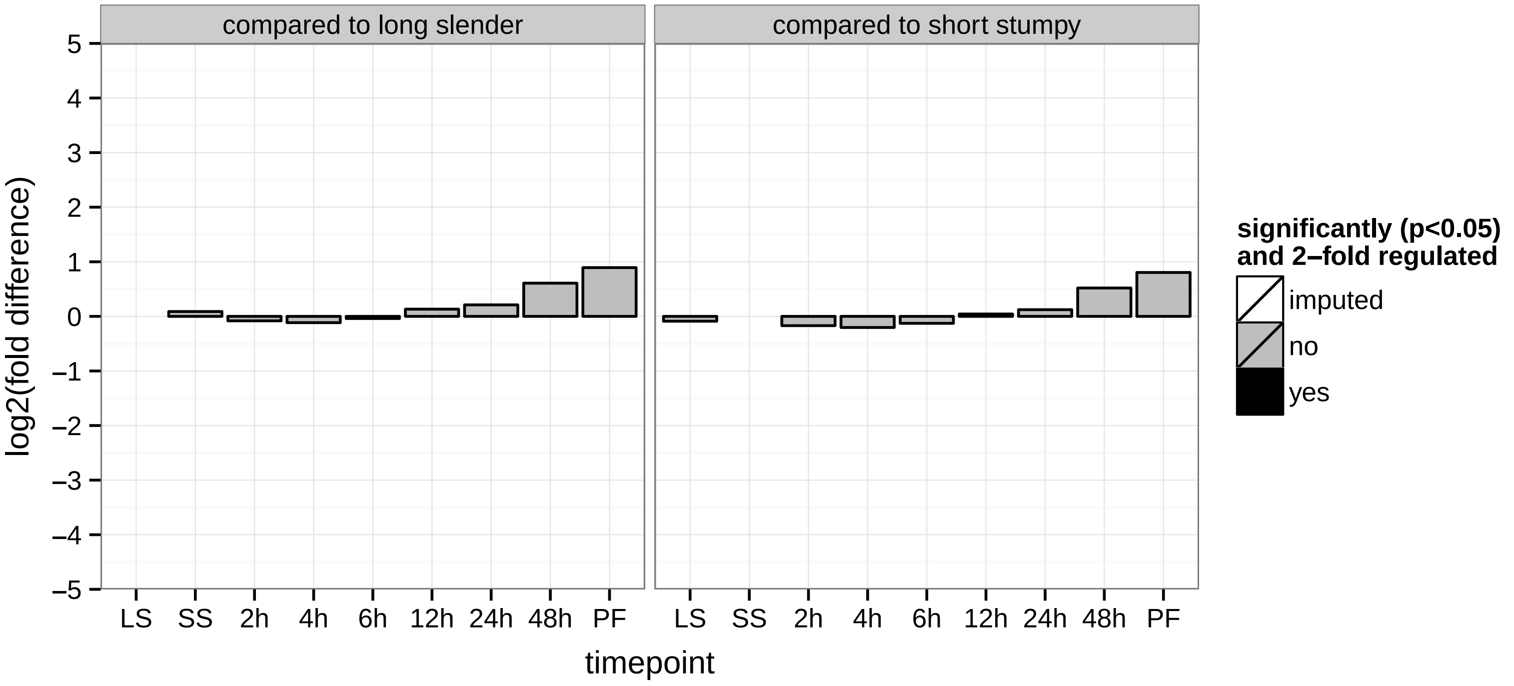
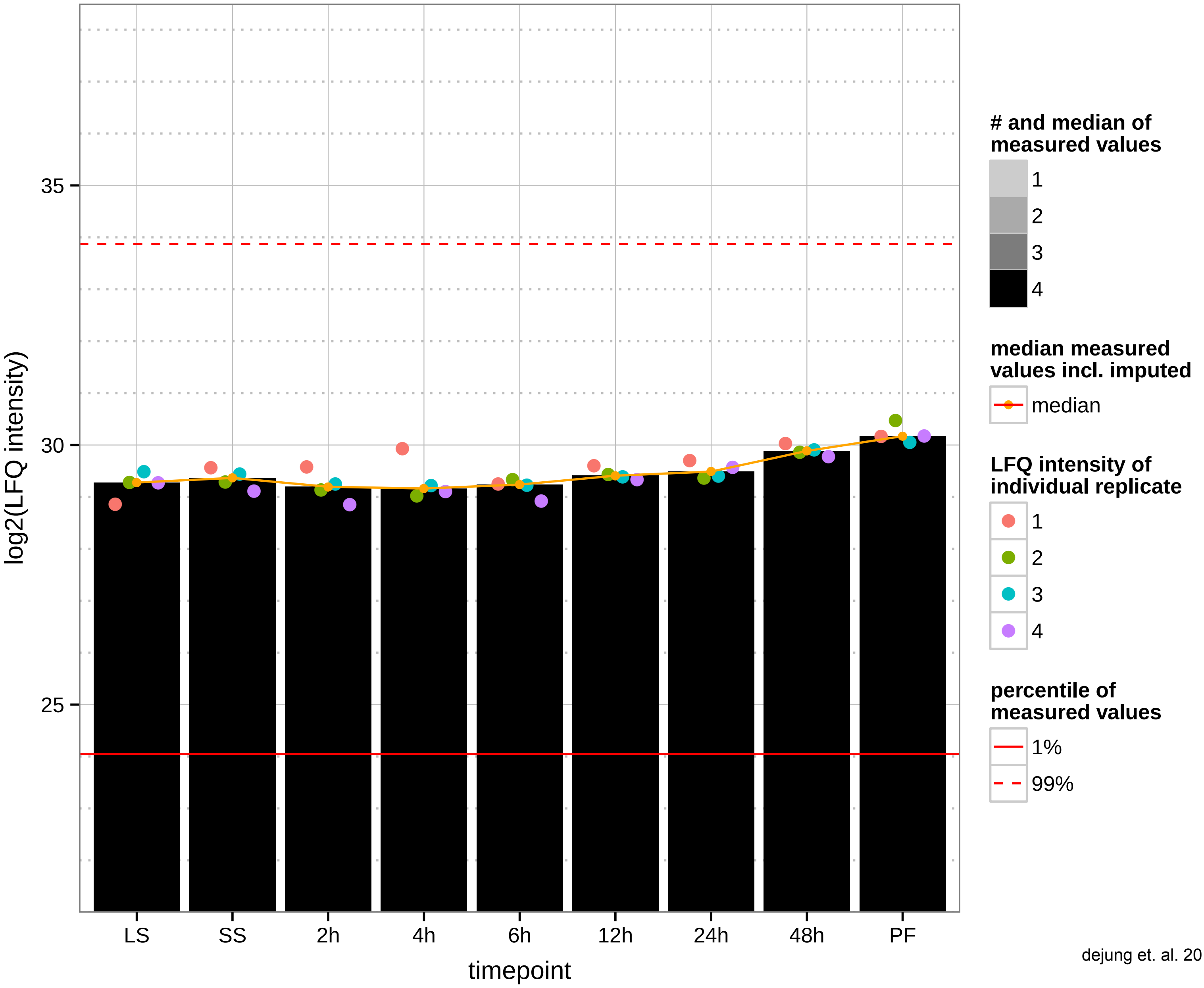
hypothetical protein, conserved, Eukaryotic translation initiation factor 4 gamma type 5 (eif4g5)
Tb927.8.4500;Tb11.v5.0763
AGOF: null, RNA binding, protein binding
AGOC: null, eukaryotic translation initiation factor 4F complex
AGOP: null, RNA metabolic process, translation
PGOF: DNA binding, RNA binding, binding, protein binding
PGOC: null
PGOP: null





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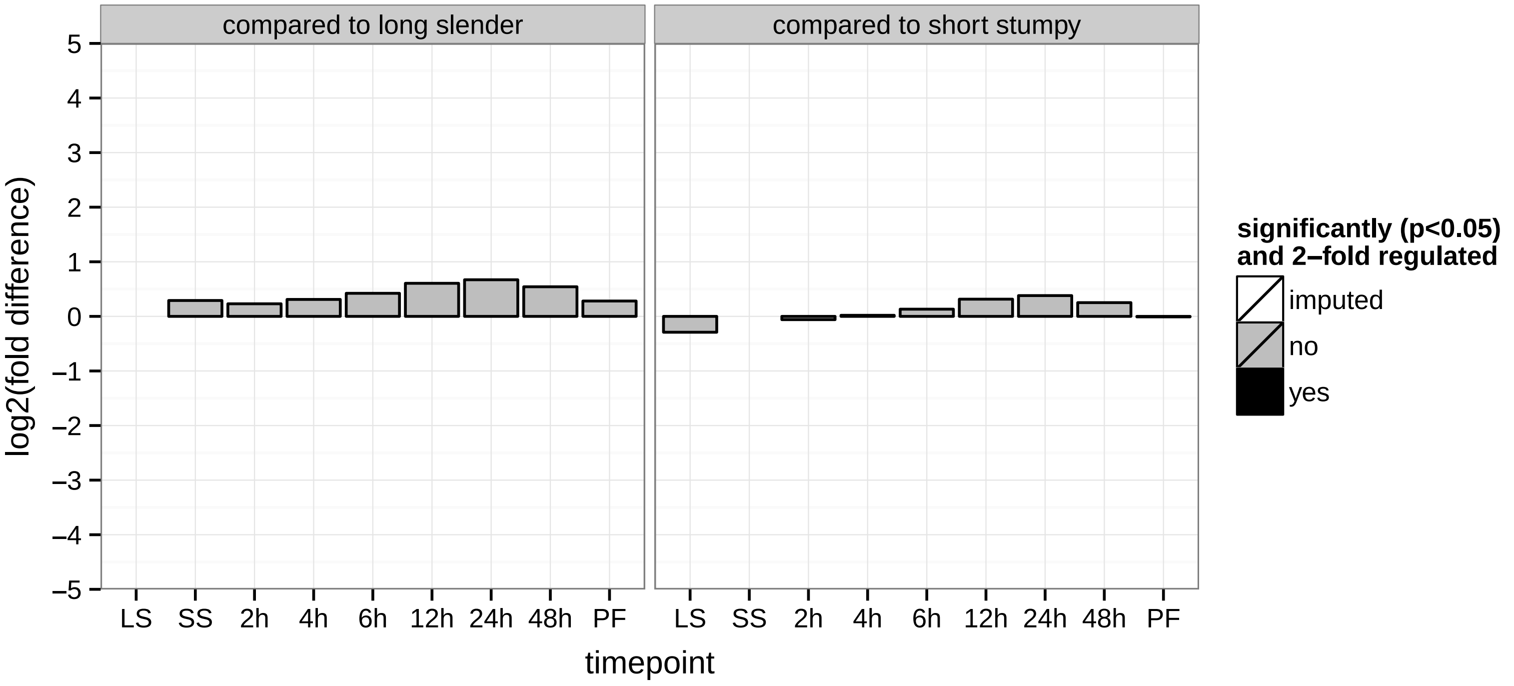
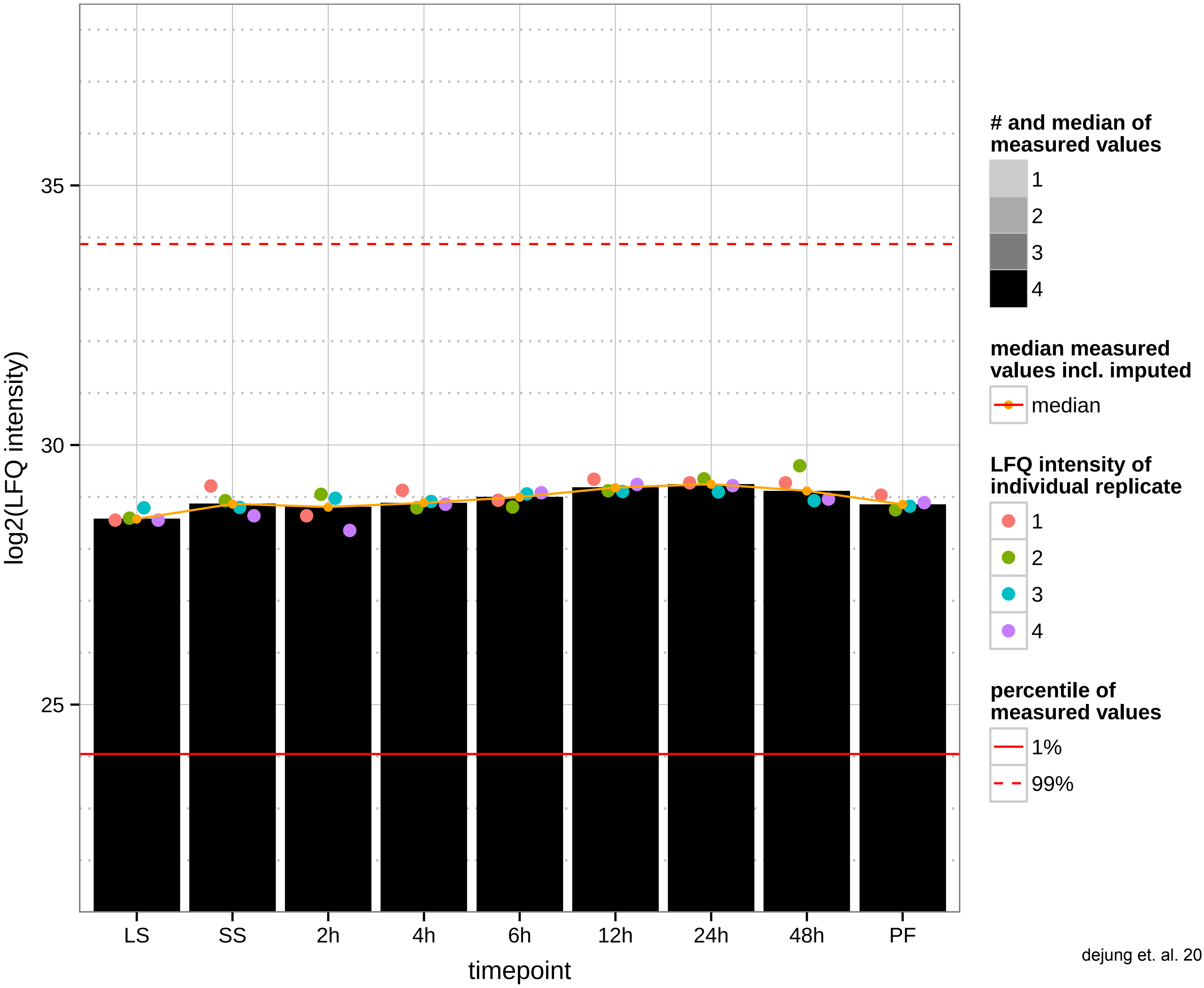
PAB1–binding protein, putative (PBP1)
Tb927.8.4540
AGOF: null
AGOC: cytoplasmic stress granule, polysome
AGOP: positive regulation of translation, stress granule assembly
PGOF: null
PGOC: null
PGOP: null





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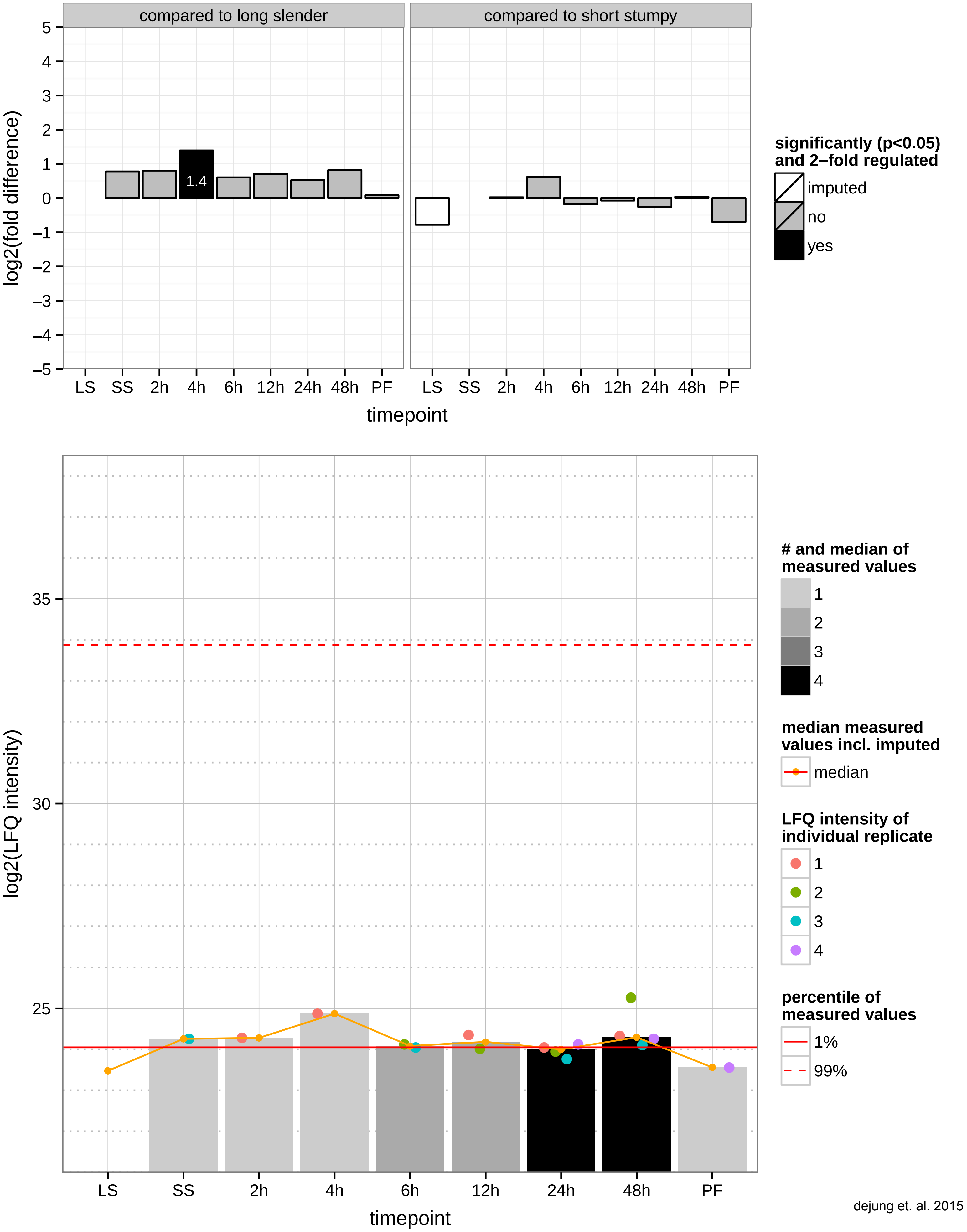
hypothetical protein, conserved
Tb927.8.4560
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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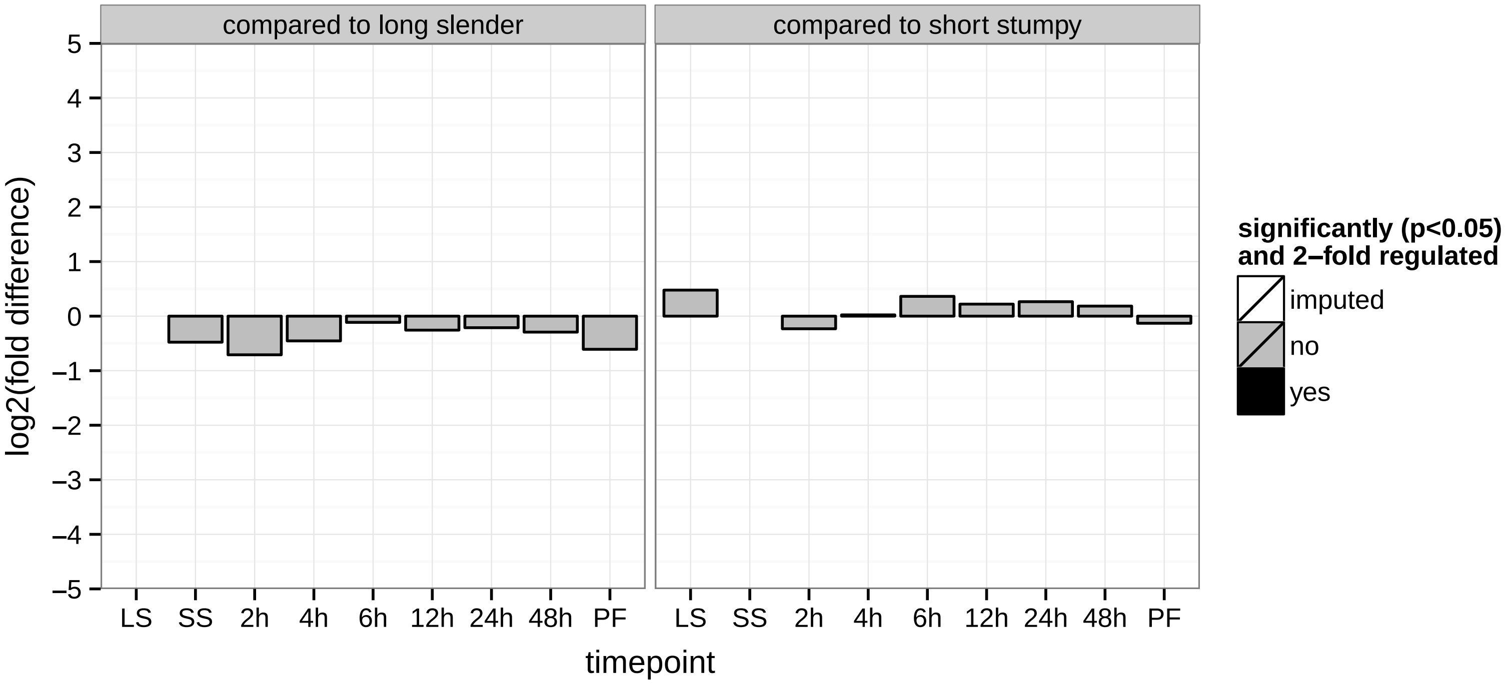
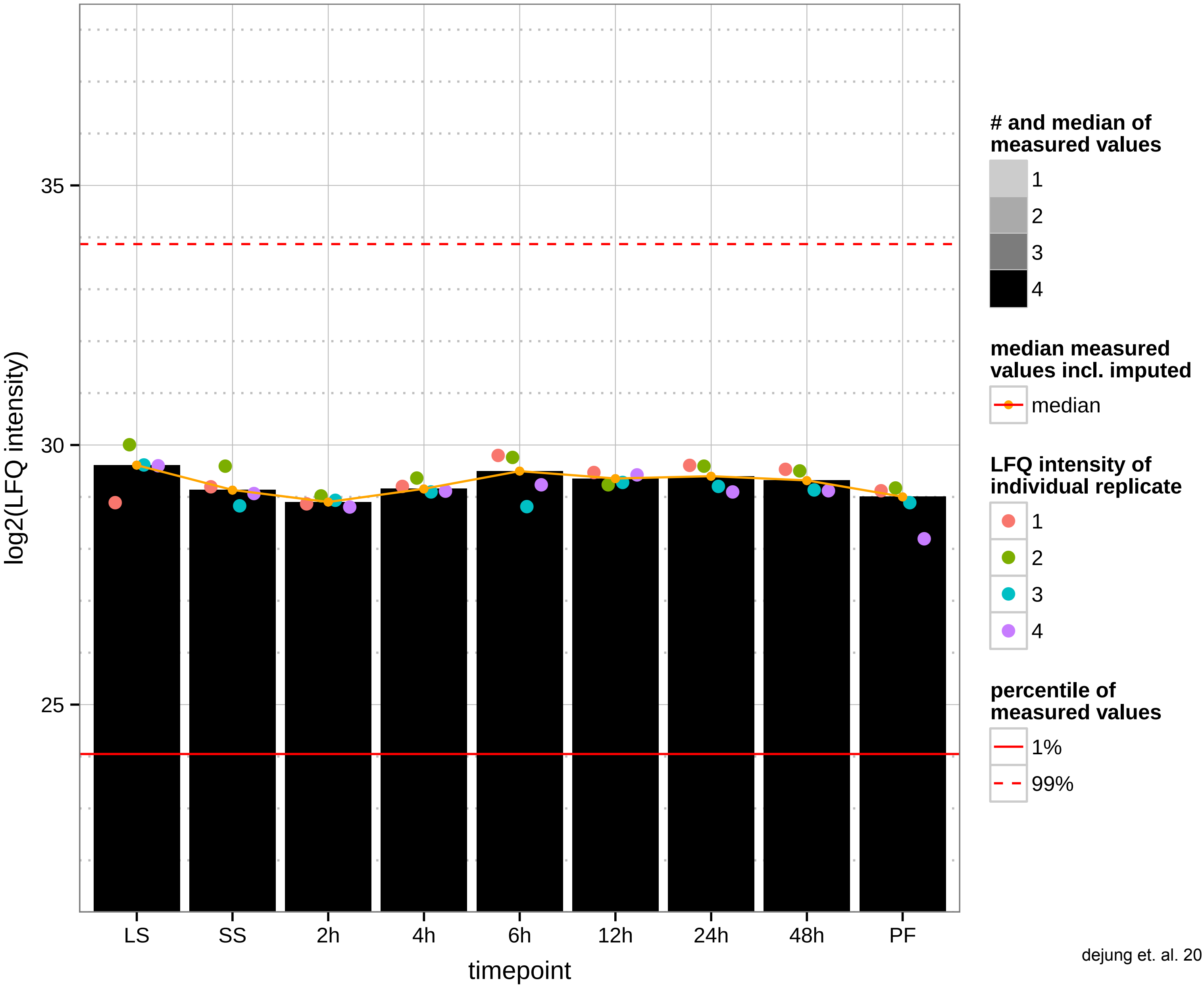
hypothetical protein, conserved
Tb927.8.4580
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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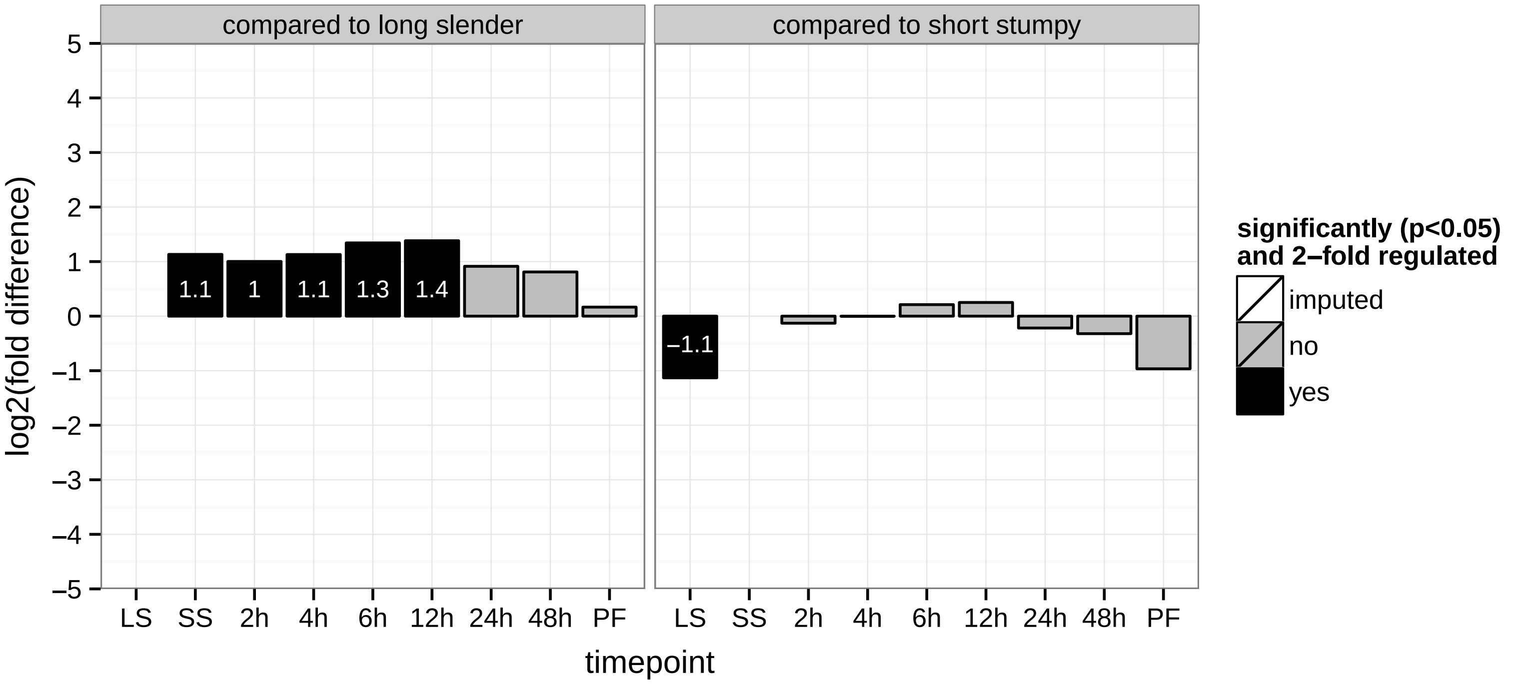
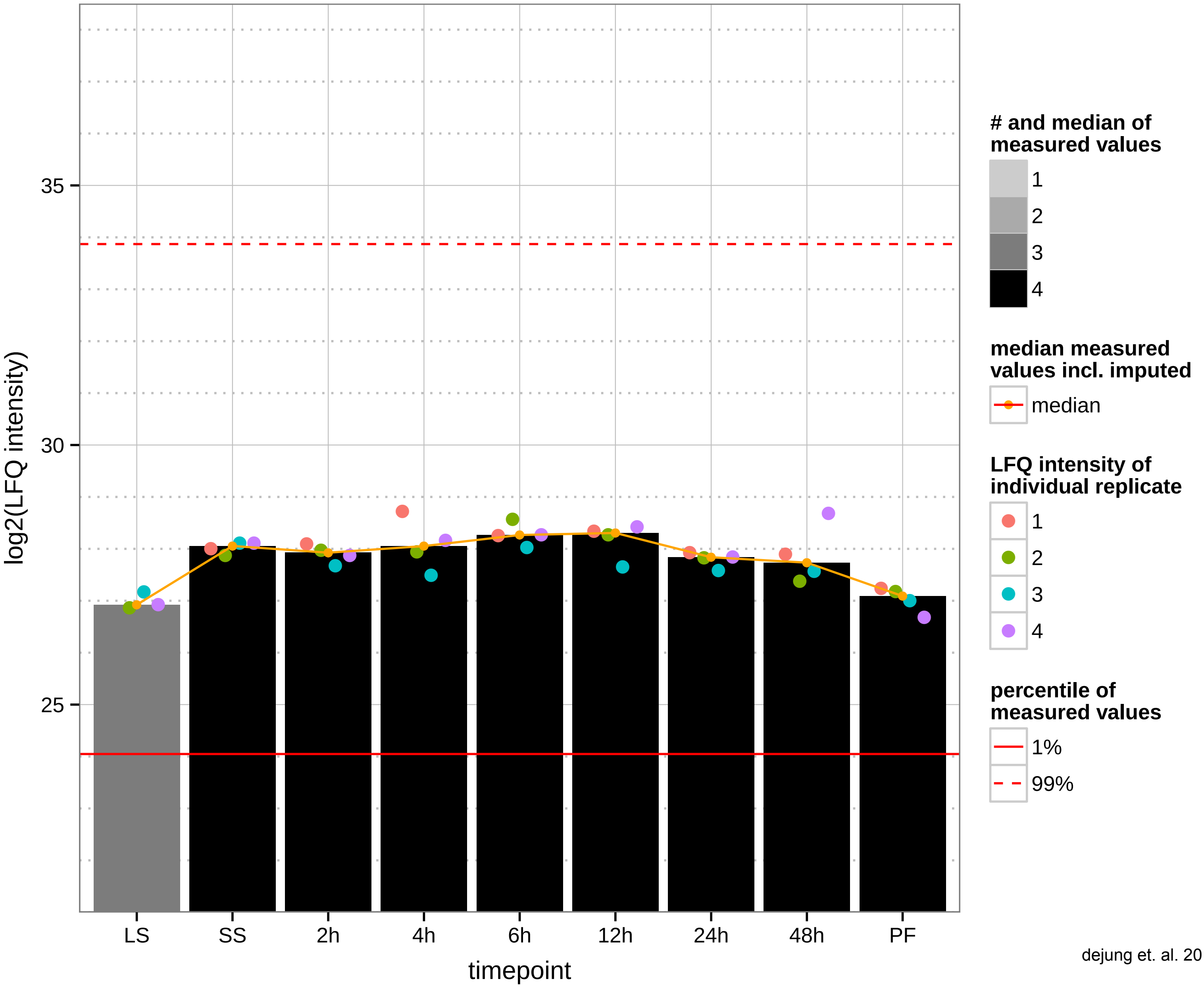
Ras−related protein RabX1 (RABX1)
Tb927.8.4610
AGOF: GTP binding, GTPase activity
AGOC: endoplasmic reticulum, integral to membrane, intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti





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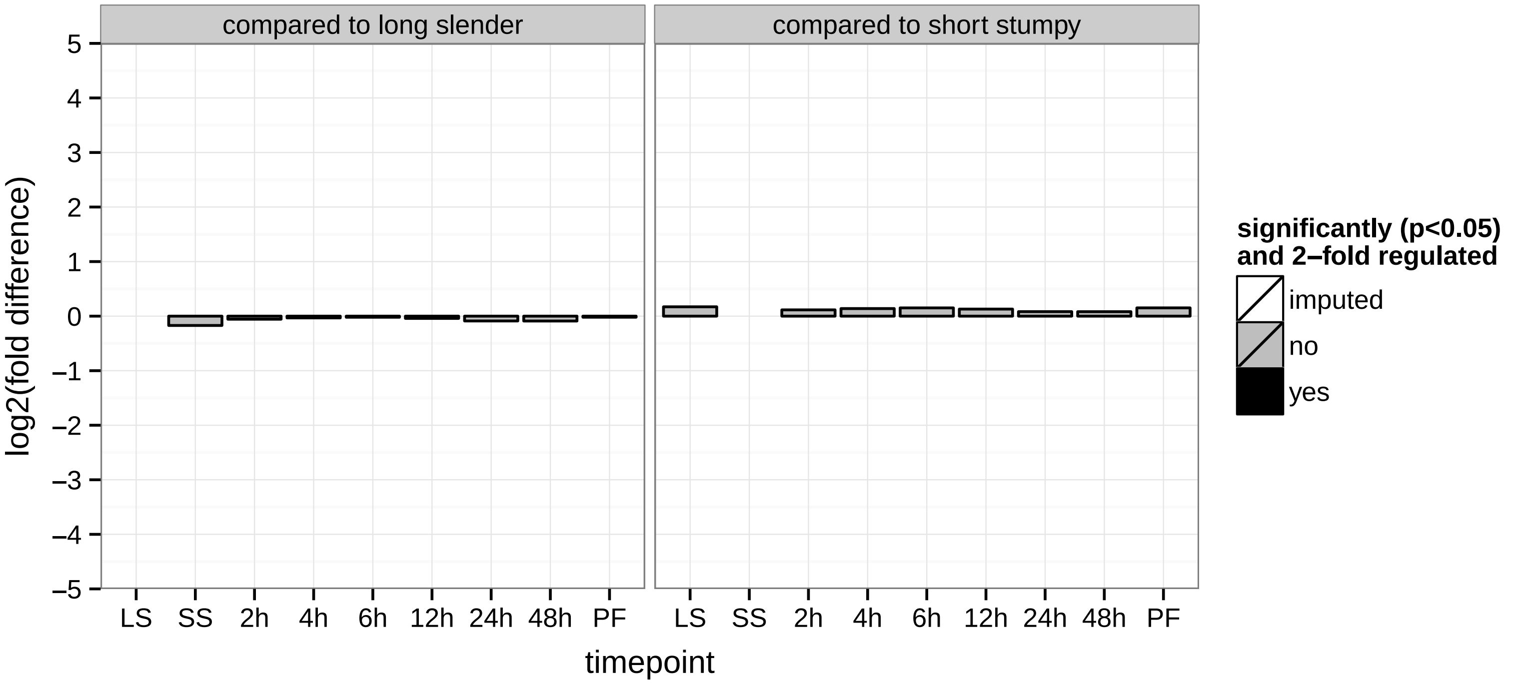
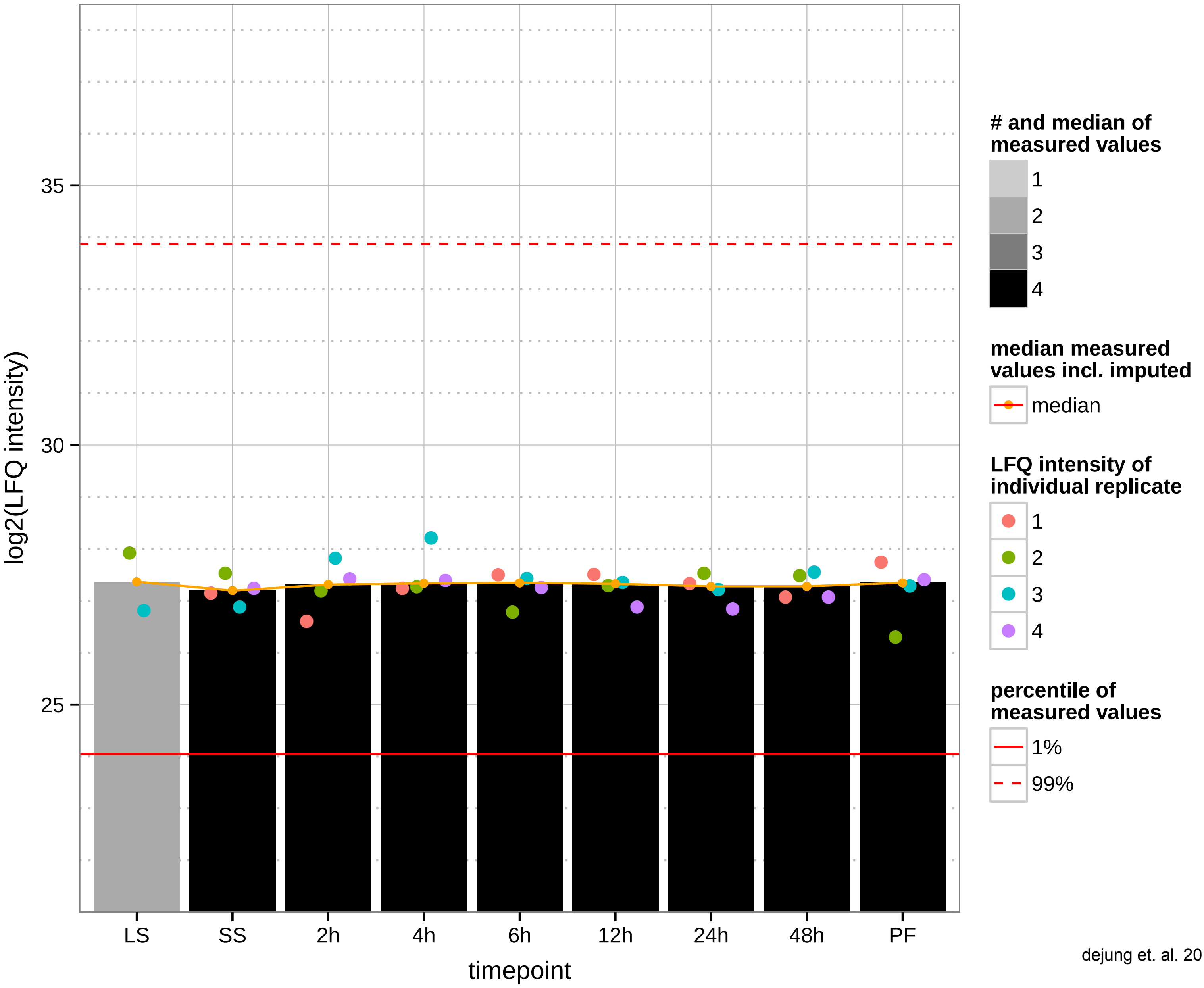
flagellar protofilament ribbon protein, putative
Tb927.8.4640
AGOF: null
AGOC: cilium
AGOP: ciliary or flagellar motility, negative regulation of microtubule depolymerization
PGOF: null
PGOC: null
PGOP: null





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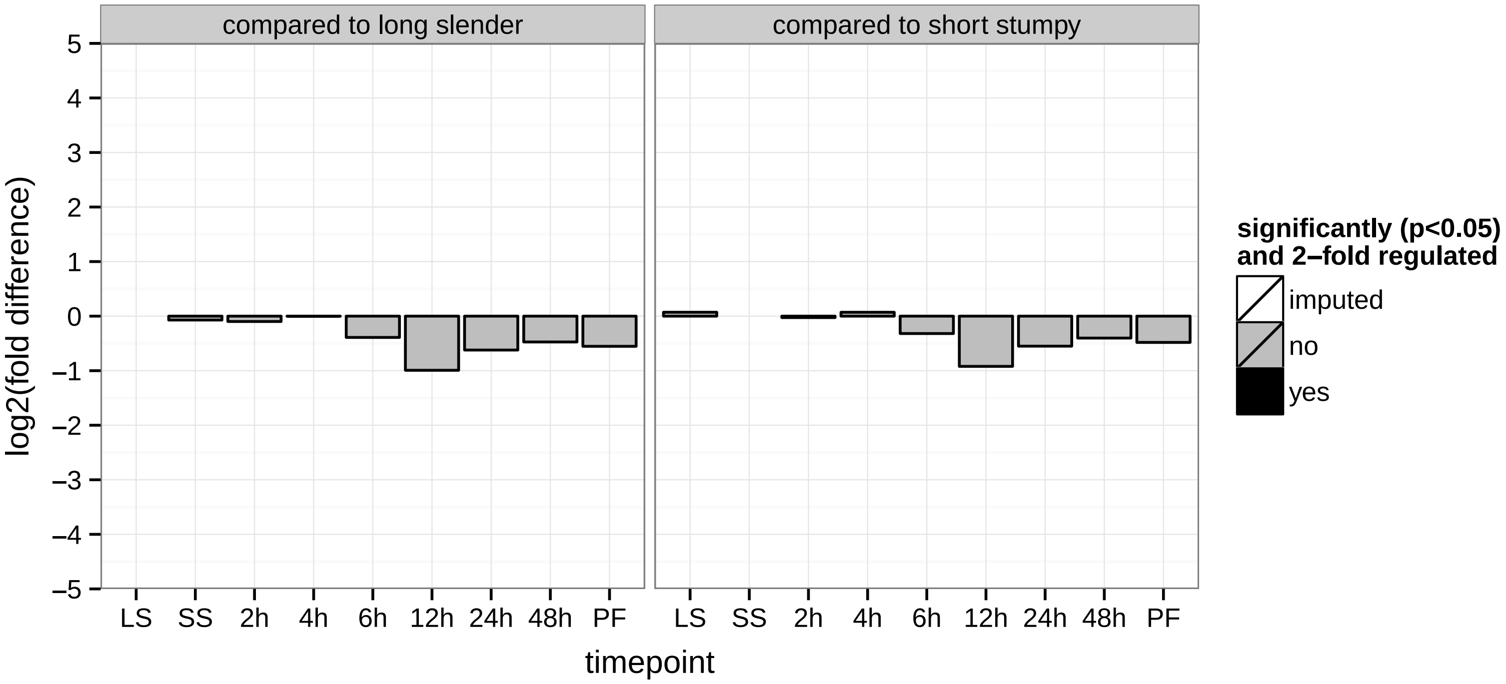
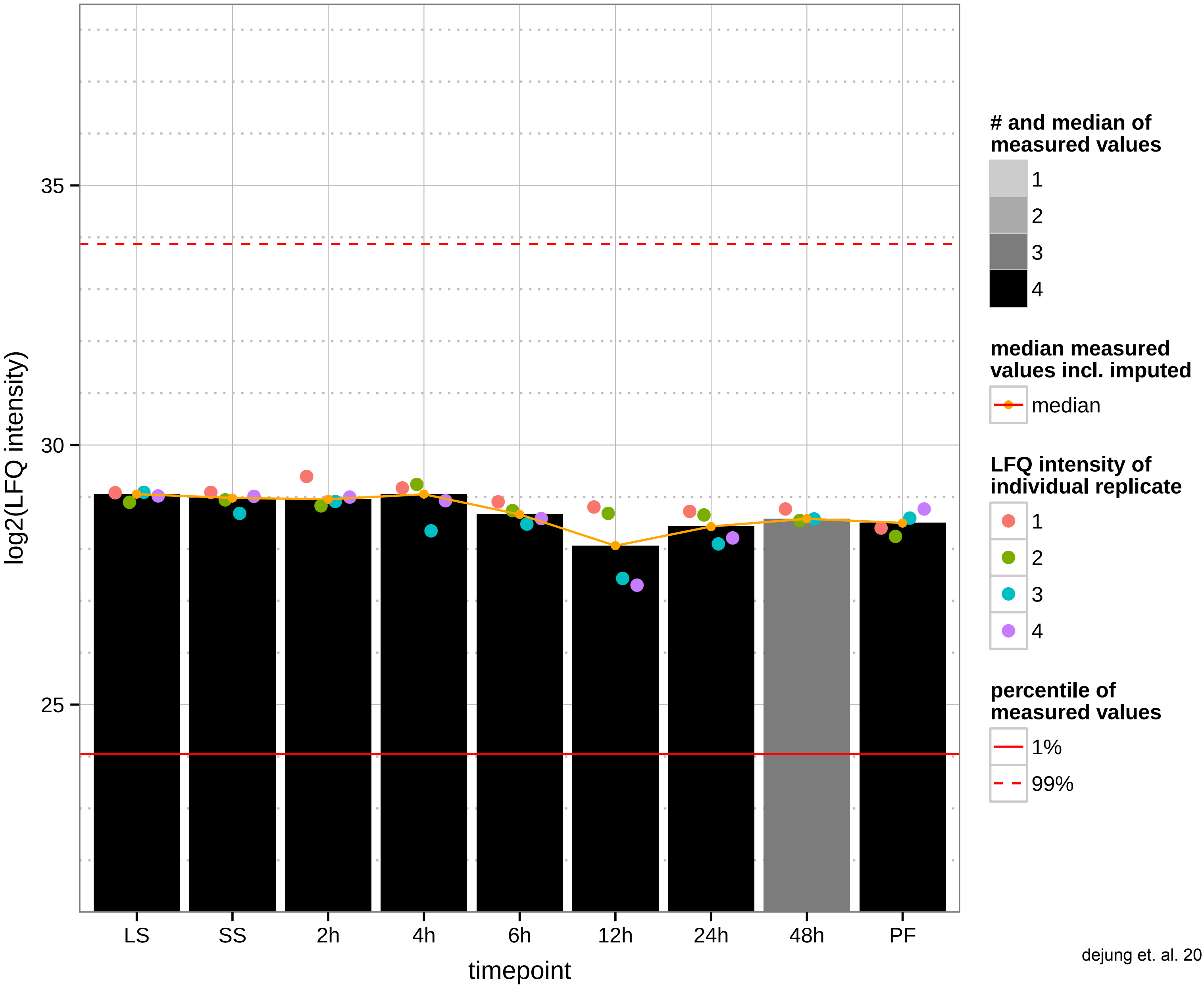
small GTP–binding protein Rab18 (TbRAB18)
Tb927.8.4770
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: protein transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, protein transport, signal transduction, small GTPase mediated signal transduction





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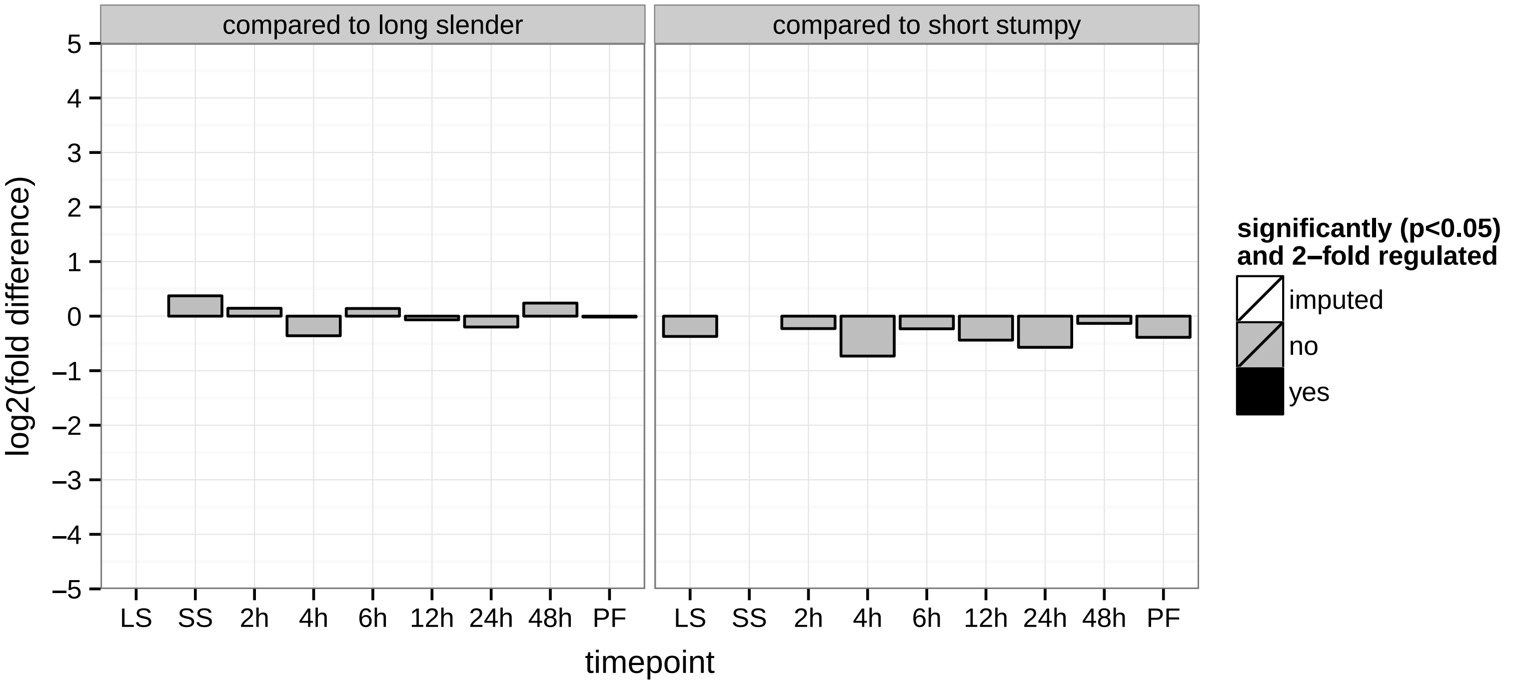
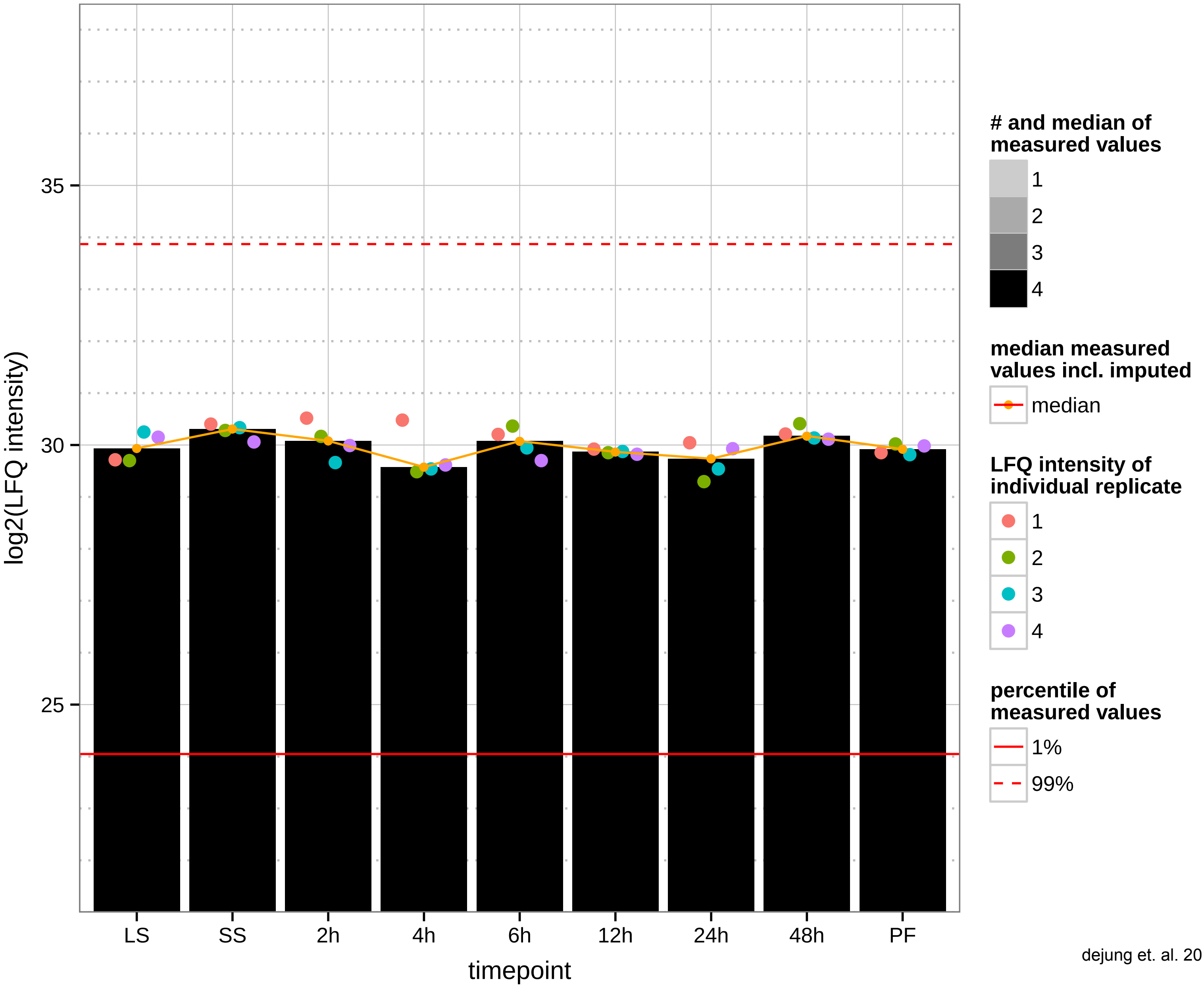
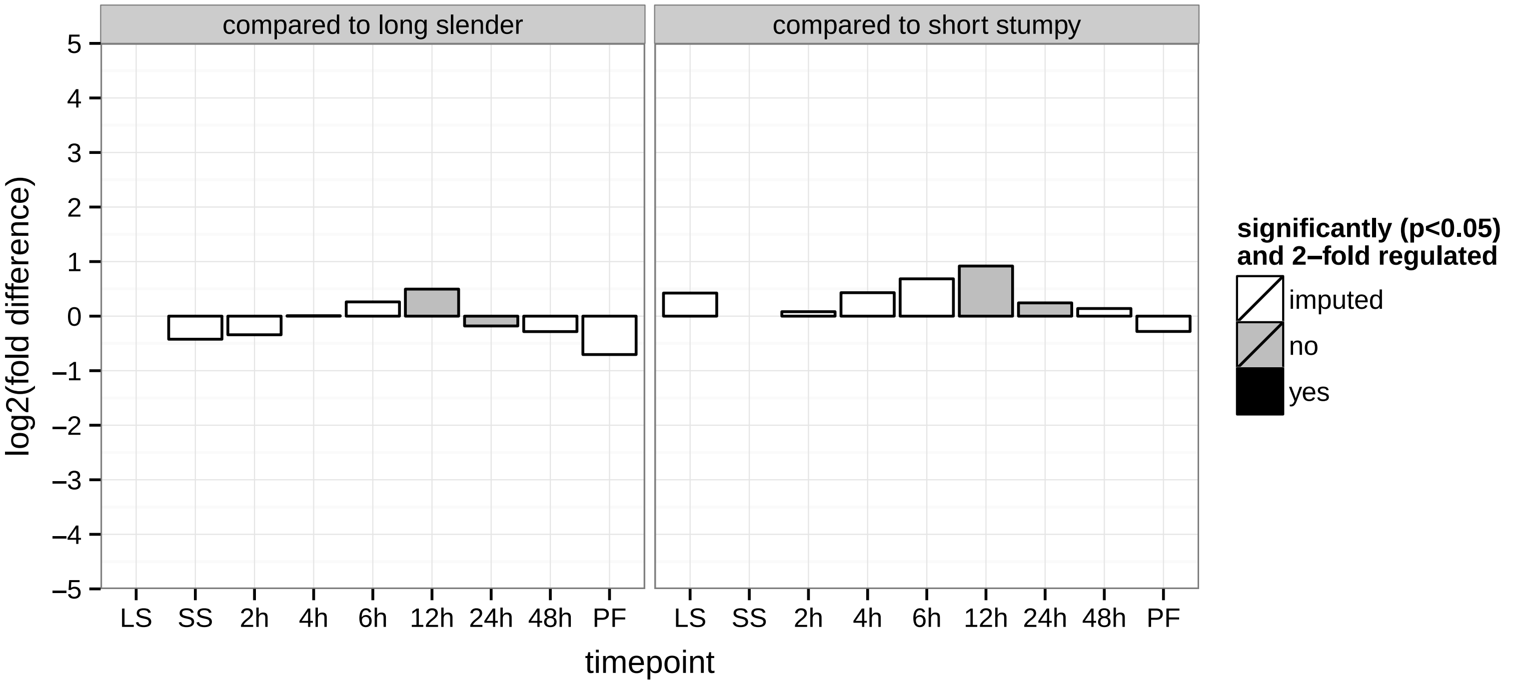
hypothetical protein, conserved
Tb927.8.4780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

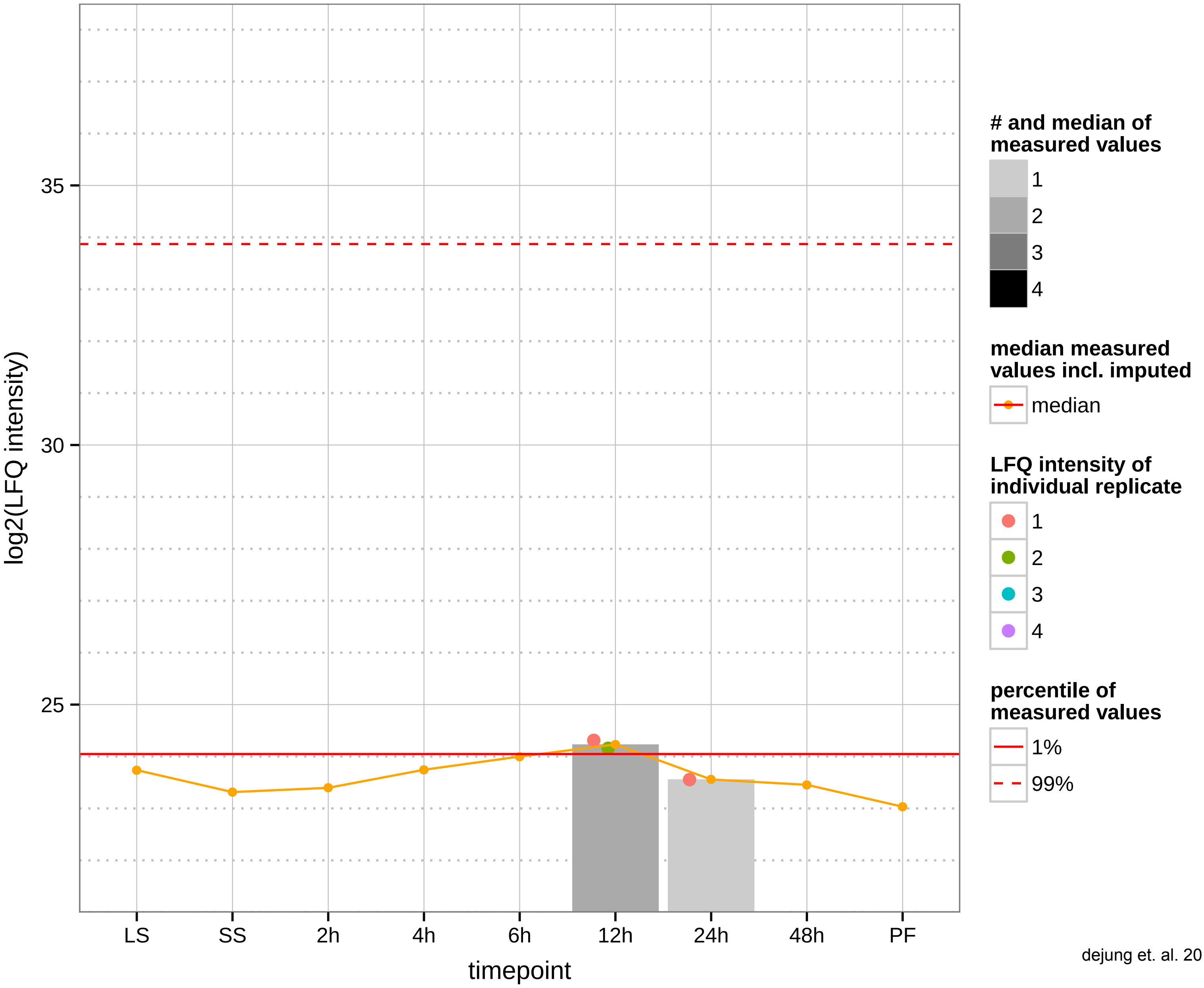




dejung et. al. 2015

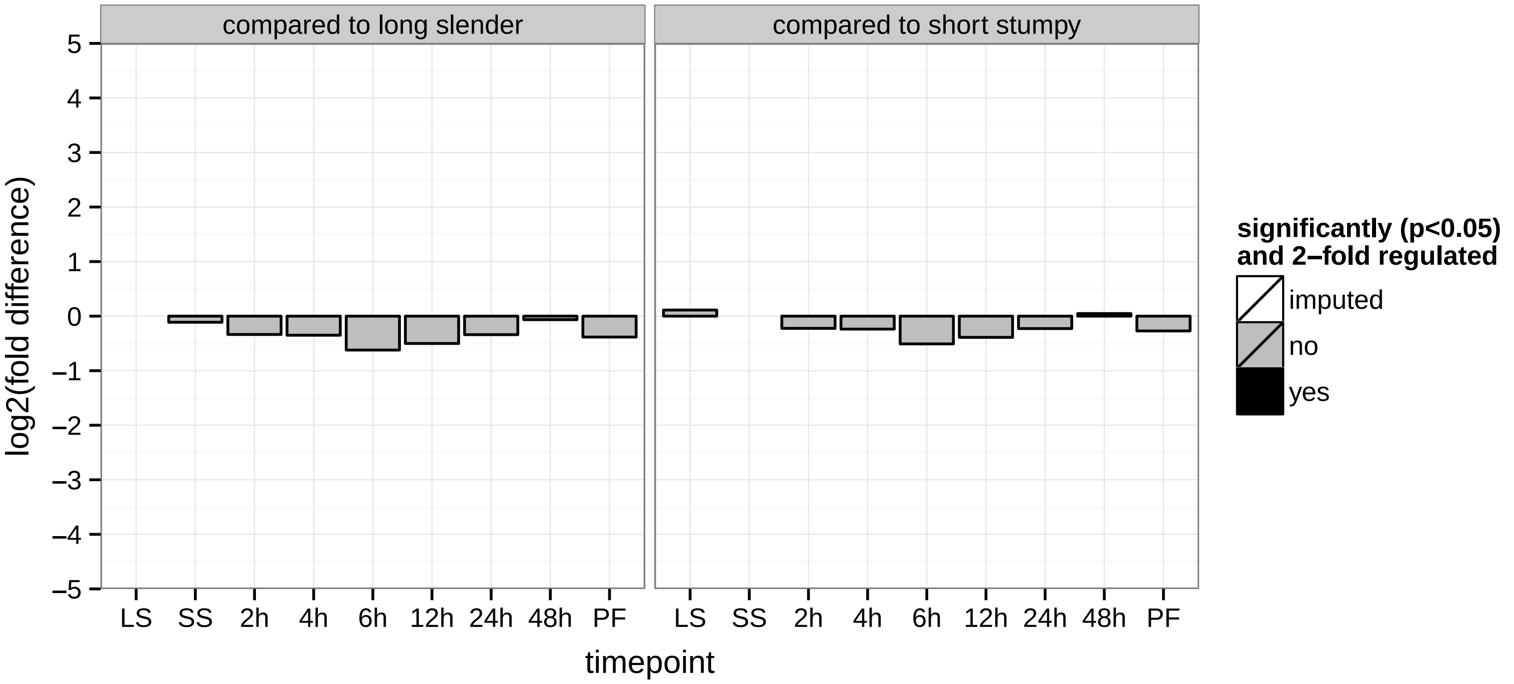
kinesin, putative
Tb927.8.4840
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: kinesin complex, microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement

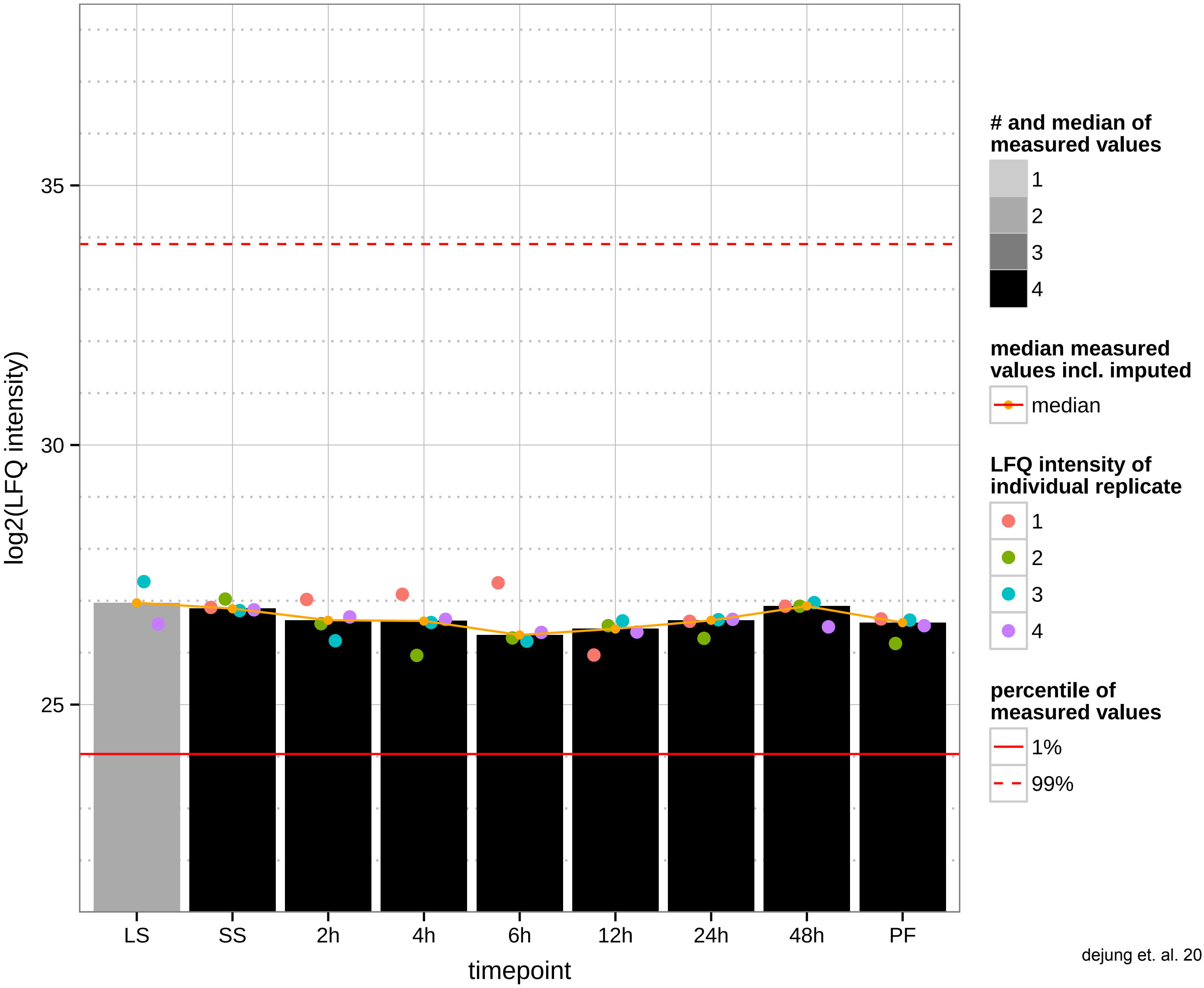




dejung et. al. 2015

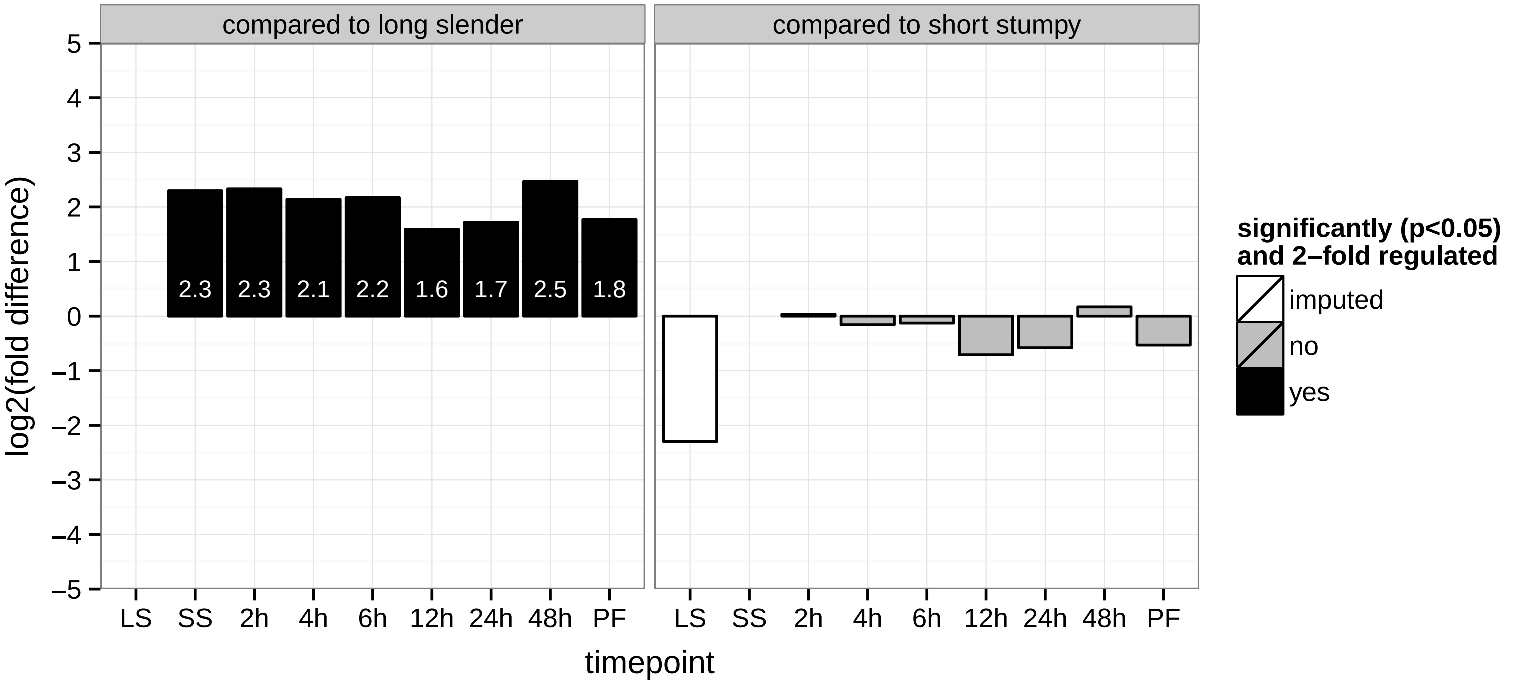
DIGIT, flagellar component
Tb927.8.4870
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null

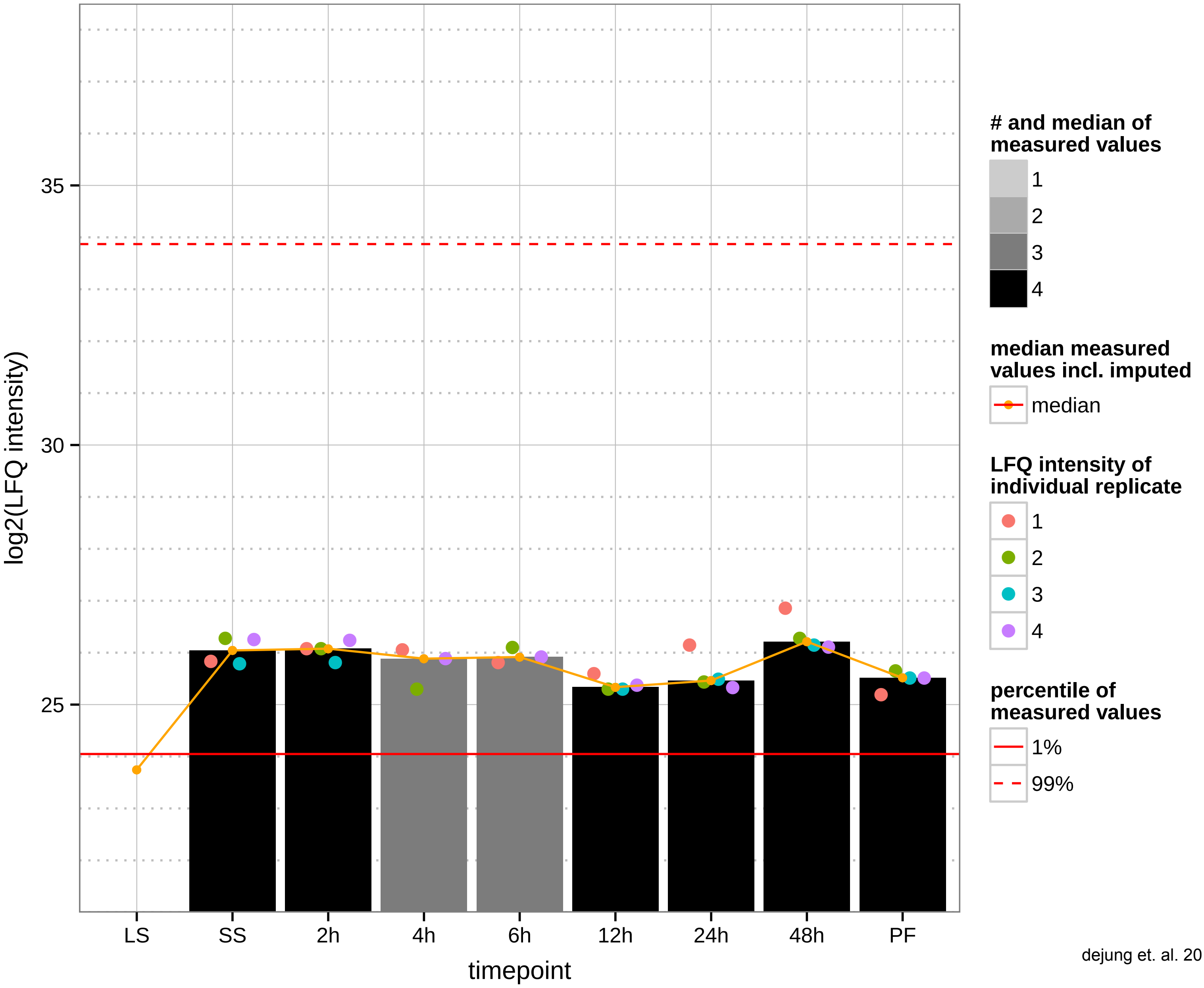




dejung et. al. 2015

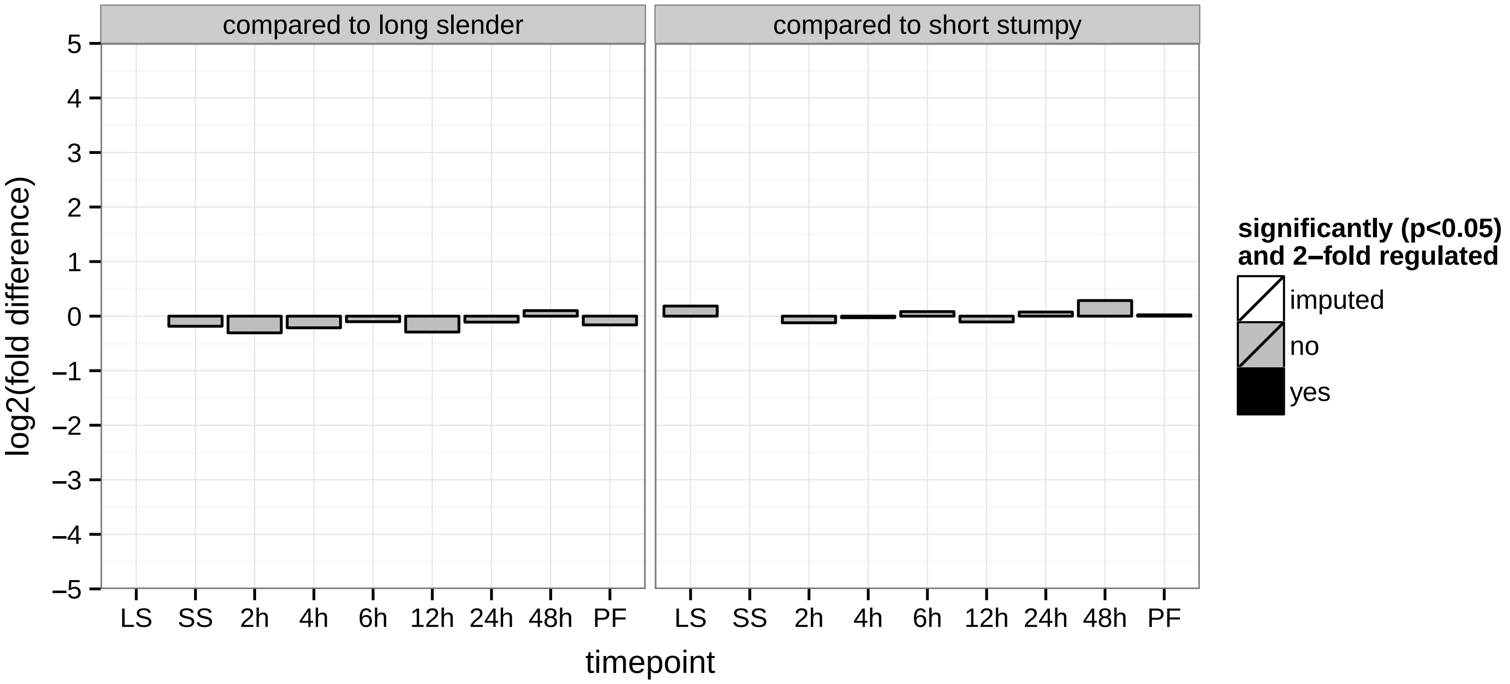
hypothetical protein, conserved
Tb927.8.4940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

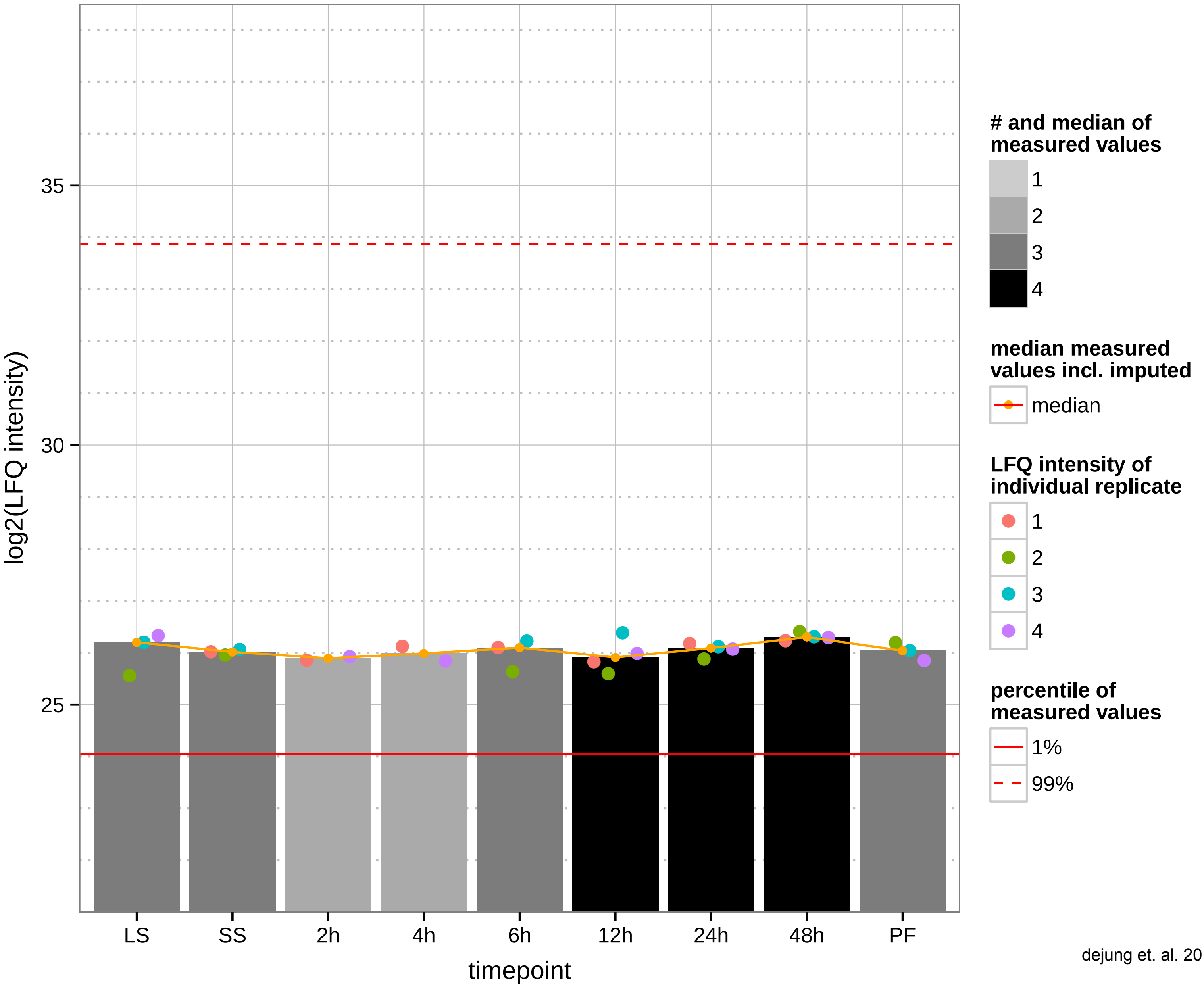




dejung et. al. 2015

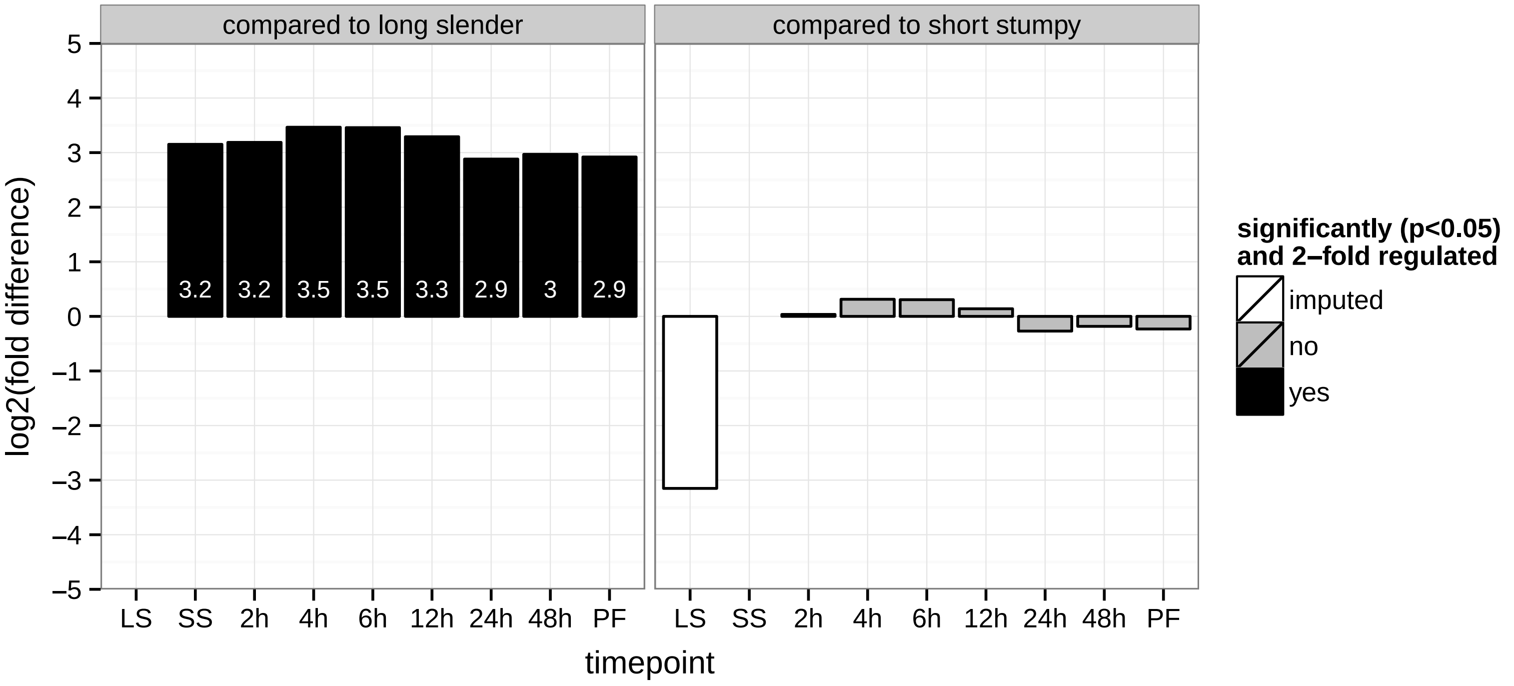
hypothetical protein, conserved
Tb927.8.5020
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

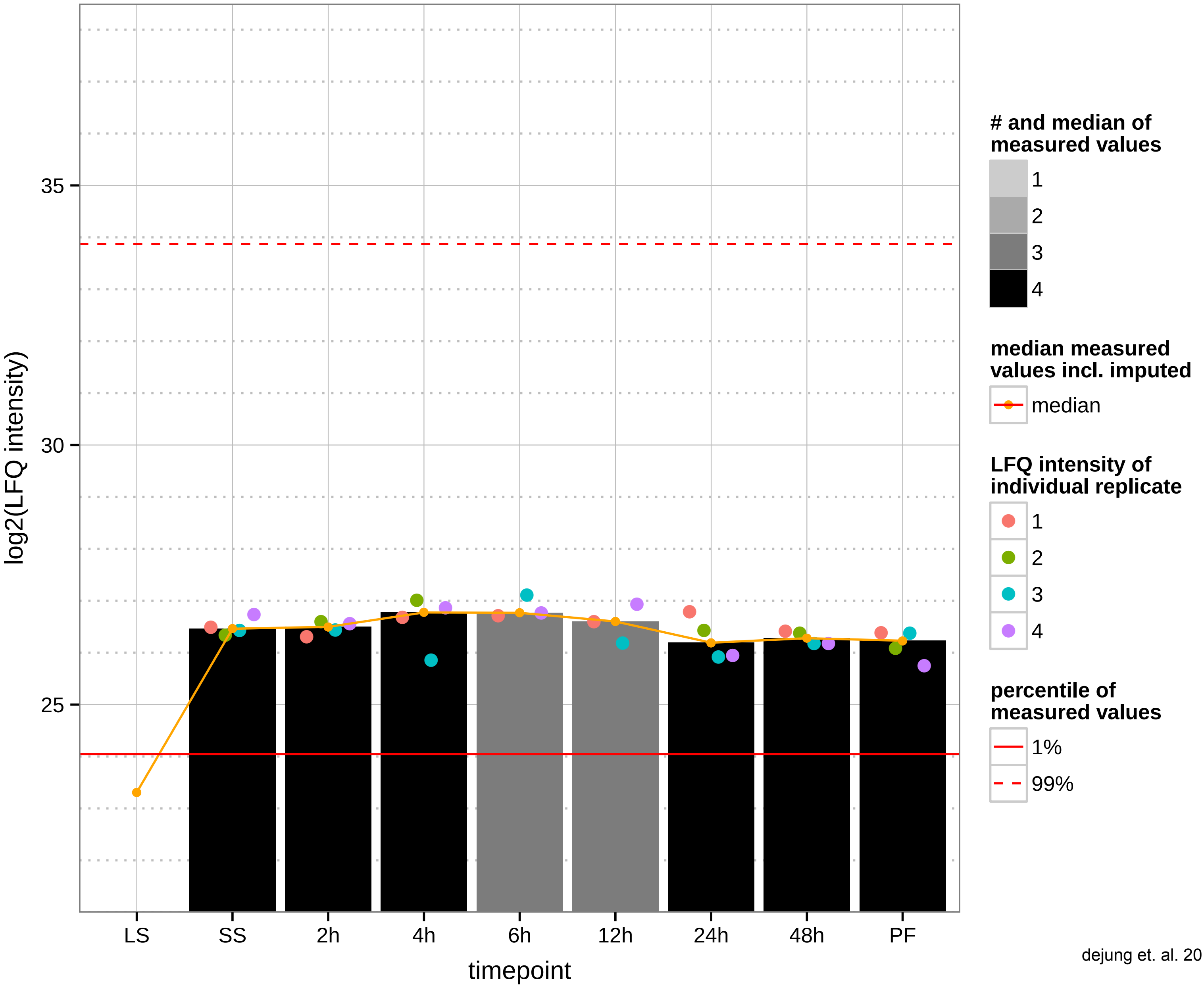




dejung et. al. 2015

ADP–ribosylation factor, putative, small GTPase
Tb927.8.5060
AGOF: GTP binding
AGOC: intracellular
AGOP: intracellular protein transport, small GTPase mediated signal transduction
PGOF: GTP binding
PGOC: intracellular
PGOP: intracellular protein transport, small GTPase mediated signal transduction





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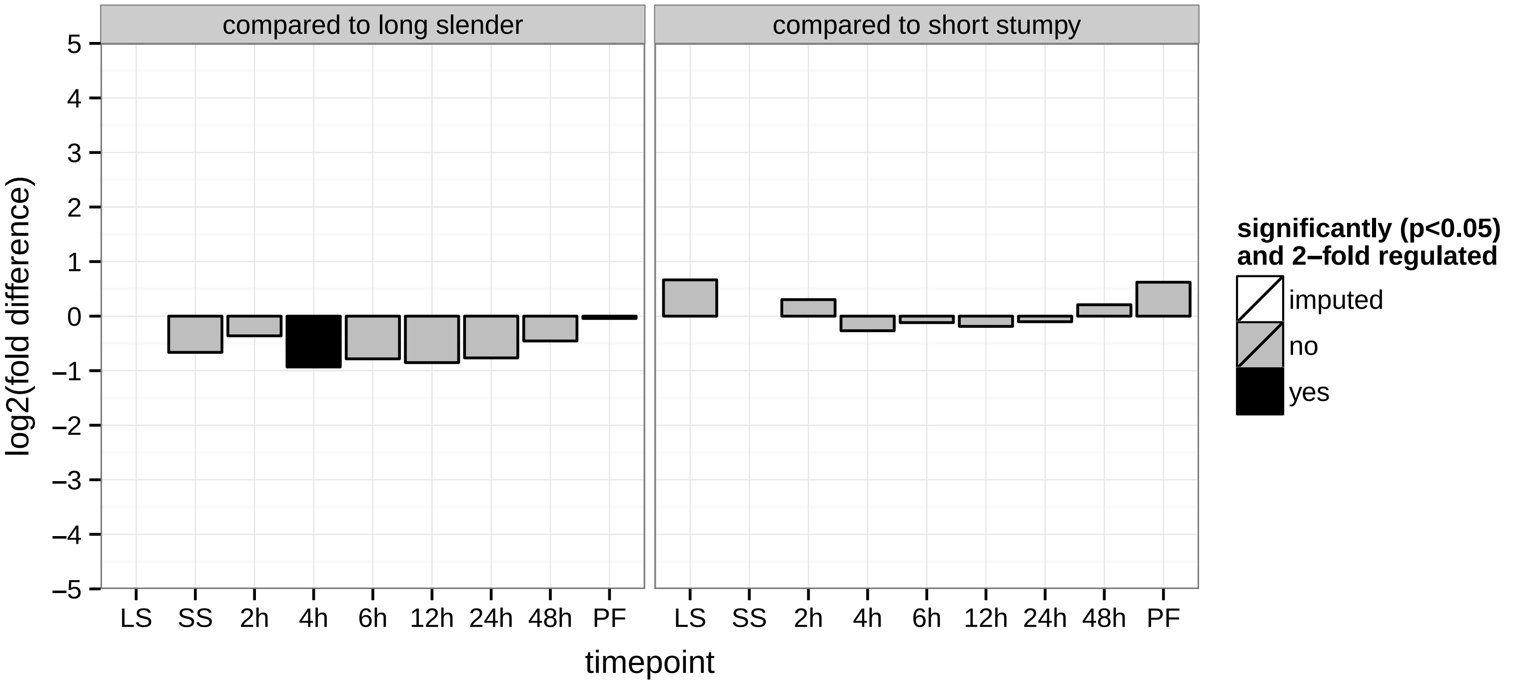
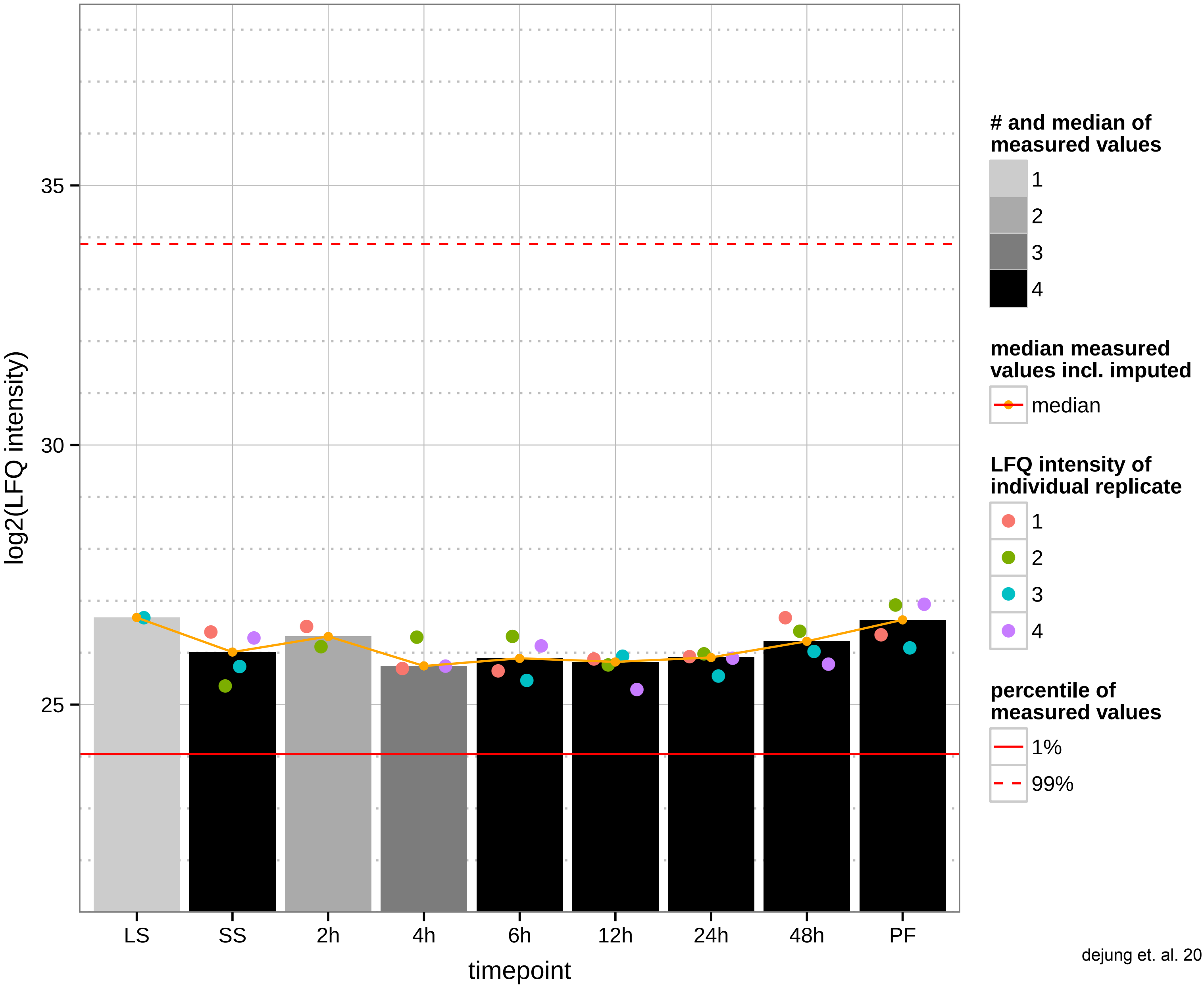
cyclophilin–type peptidyl–prolyl cis–trans isomerase, putative, PPIase, rotamase, cyclophilin, putative (PPIase)
Tb927.8.5230
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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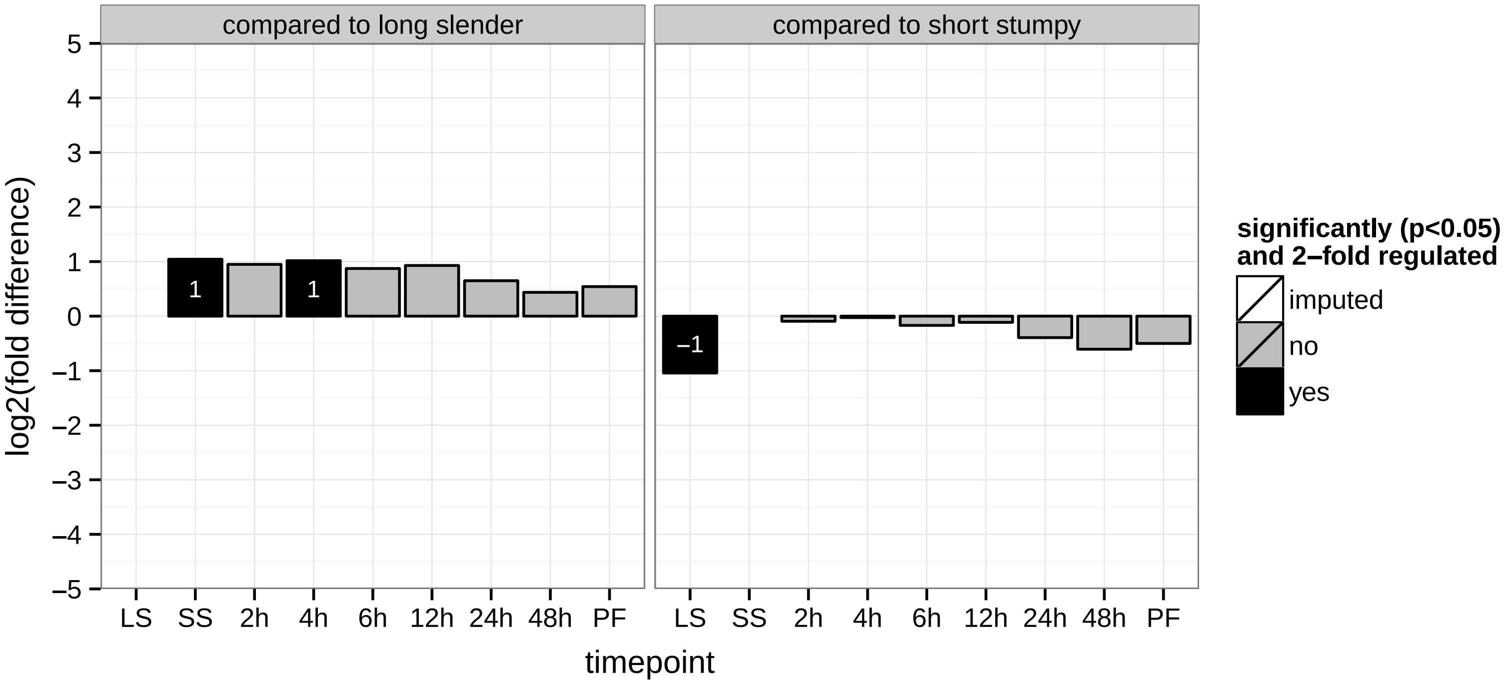
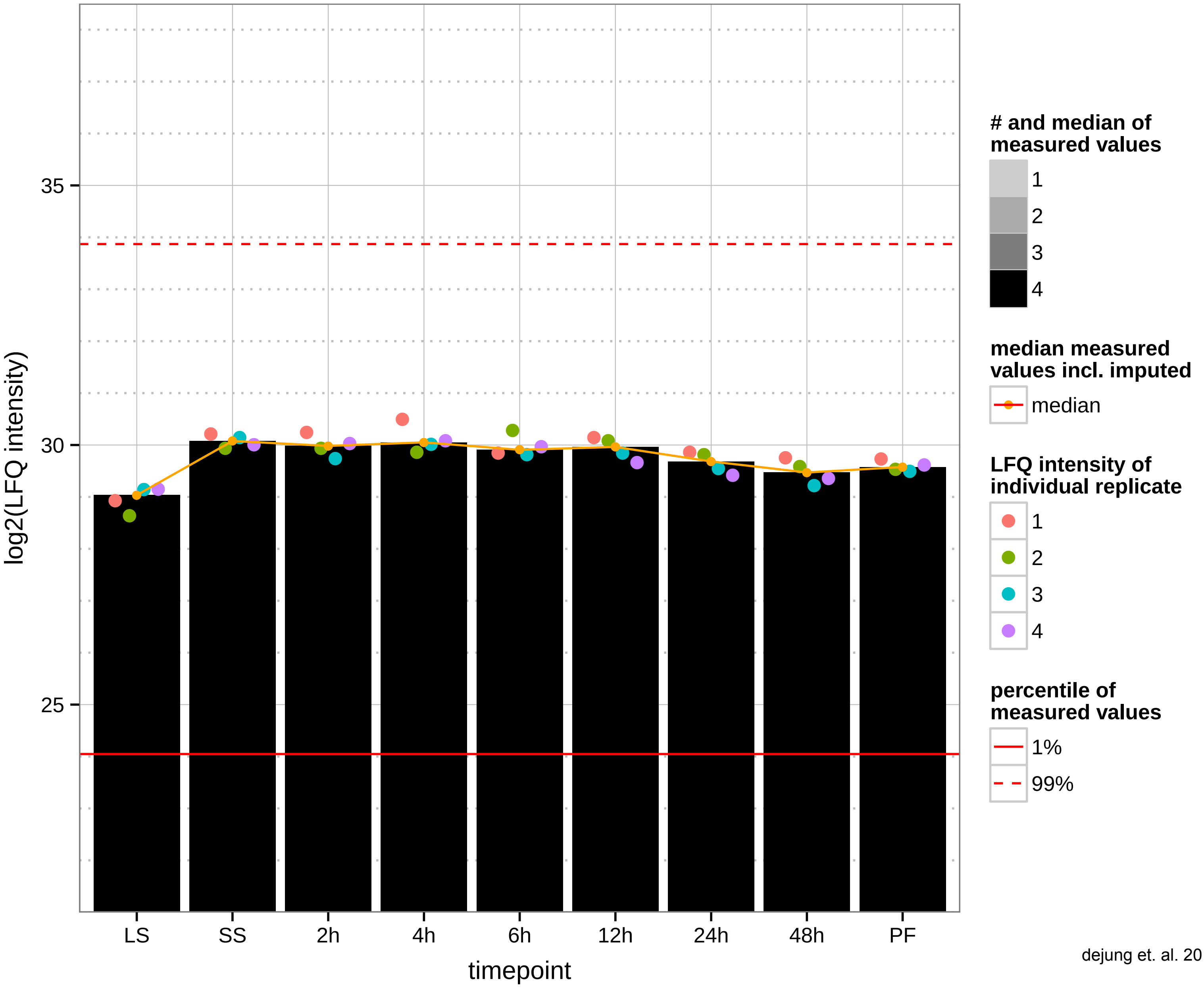
coatomer delta subunit, putative, delta–COP, delta–coat protein
Tb927.8.5250
AGOF: null
AGOC: clathrin adaptor complex, cytoplasm
AGOP: intracellular protein transport, vesicle–mediated transport
PGOF: protein binding
PGOC: clathrin adaptor complex
PGOP: intracellular protein transport, transport, vesicle–mediated transport





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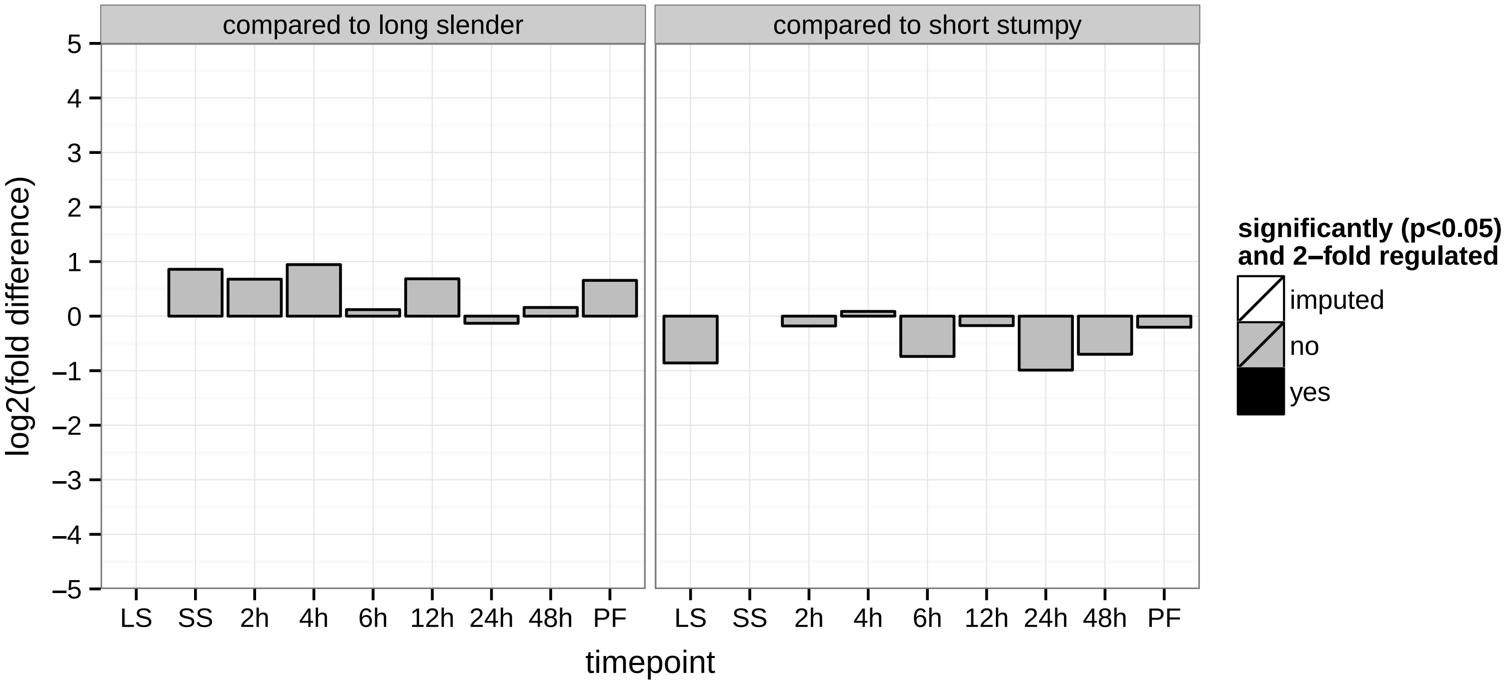
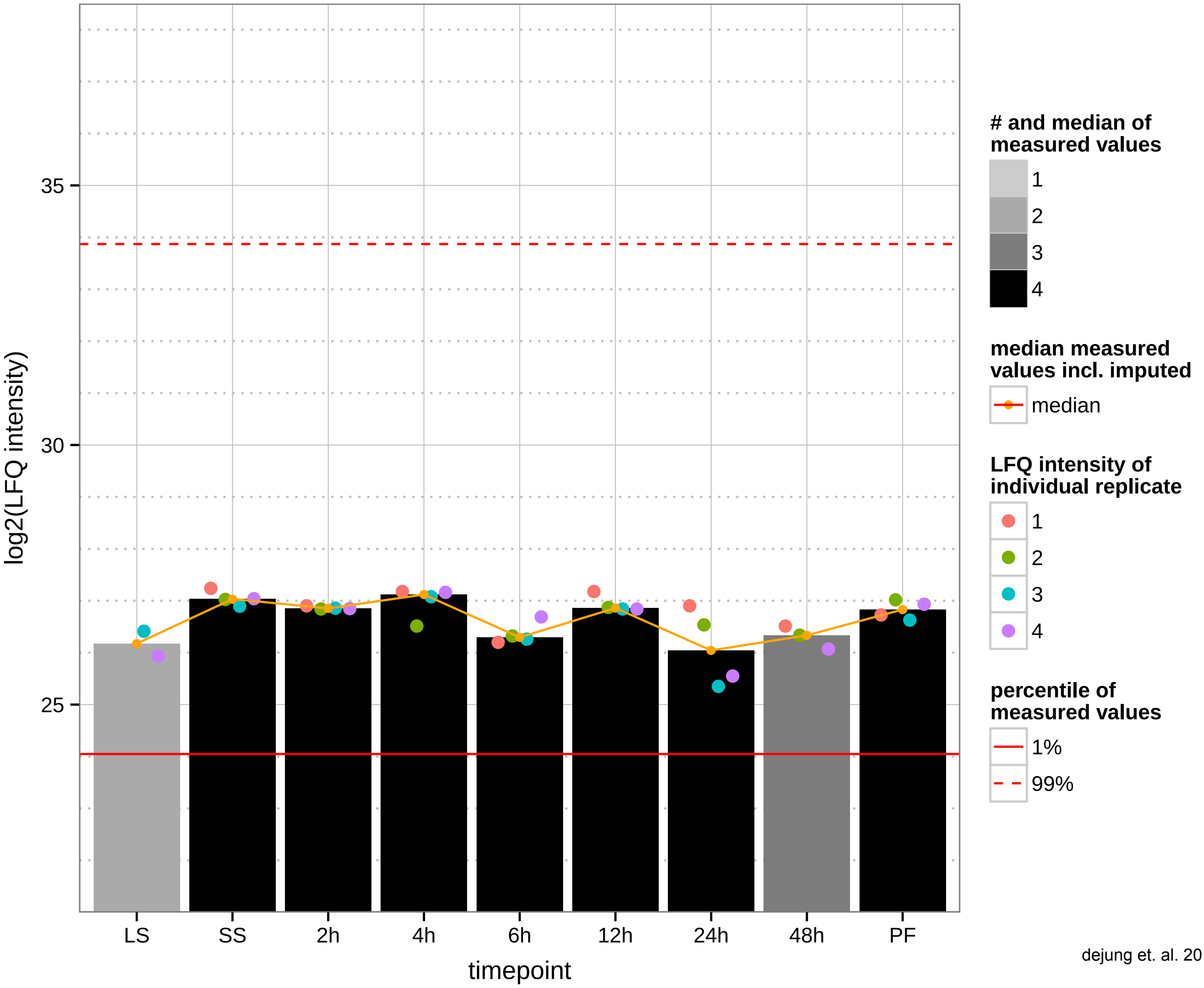
hypothetical protein, conserved
Tb927.8.5290
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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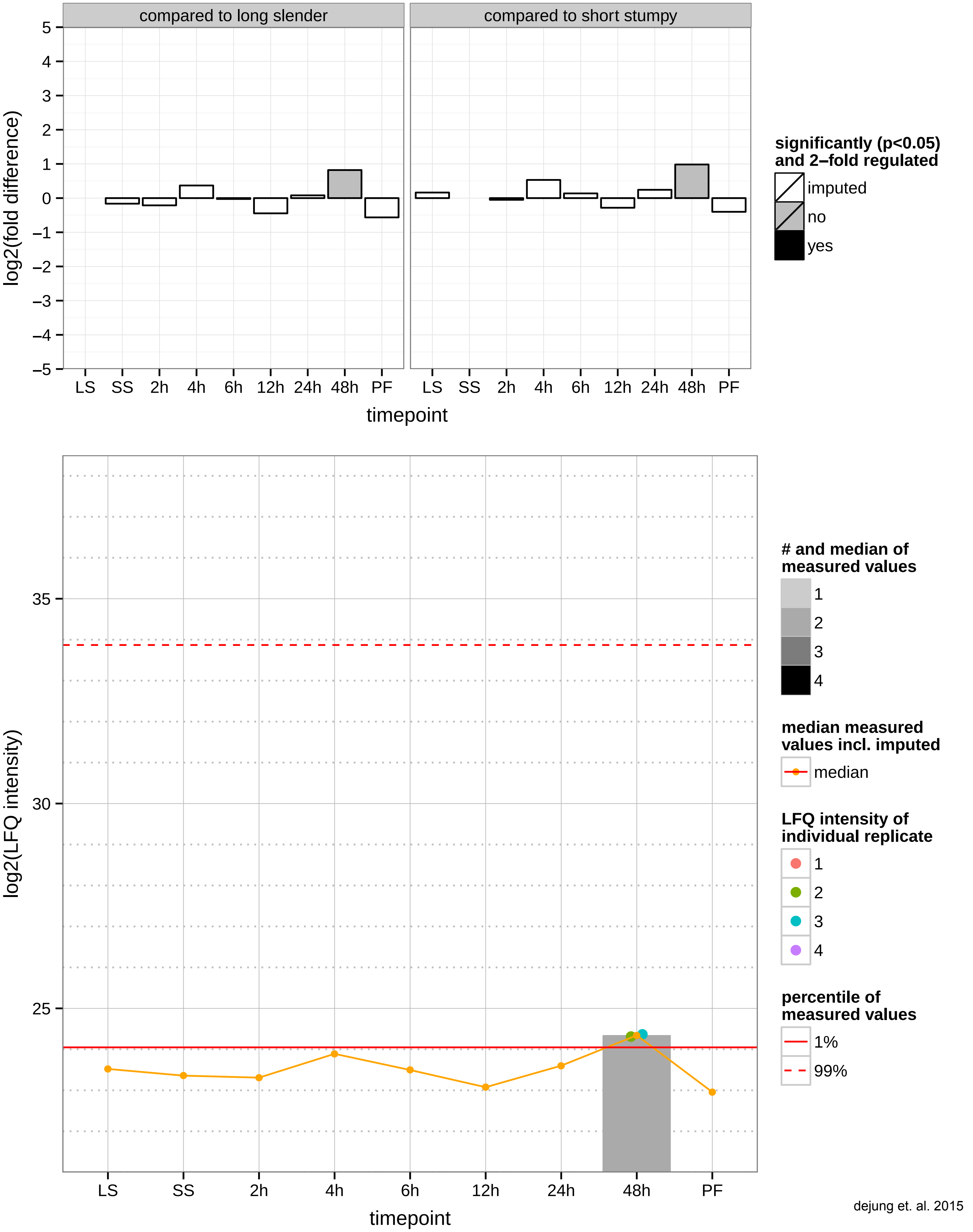
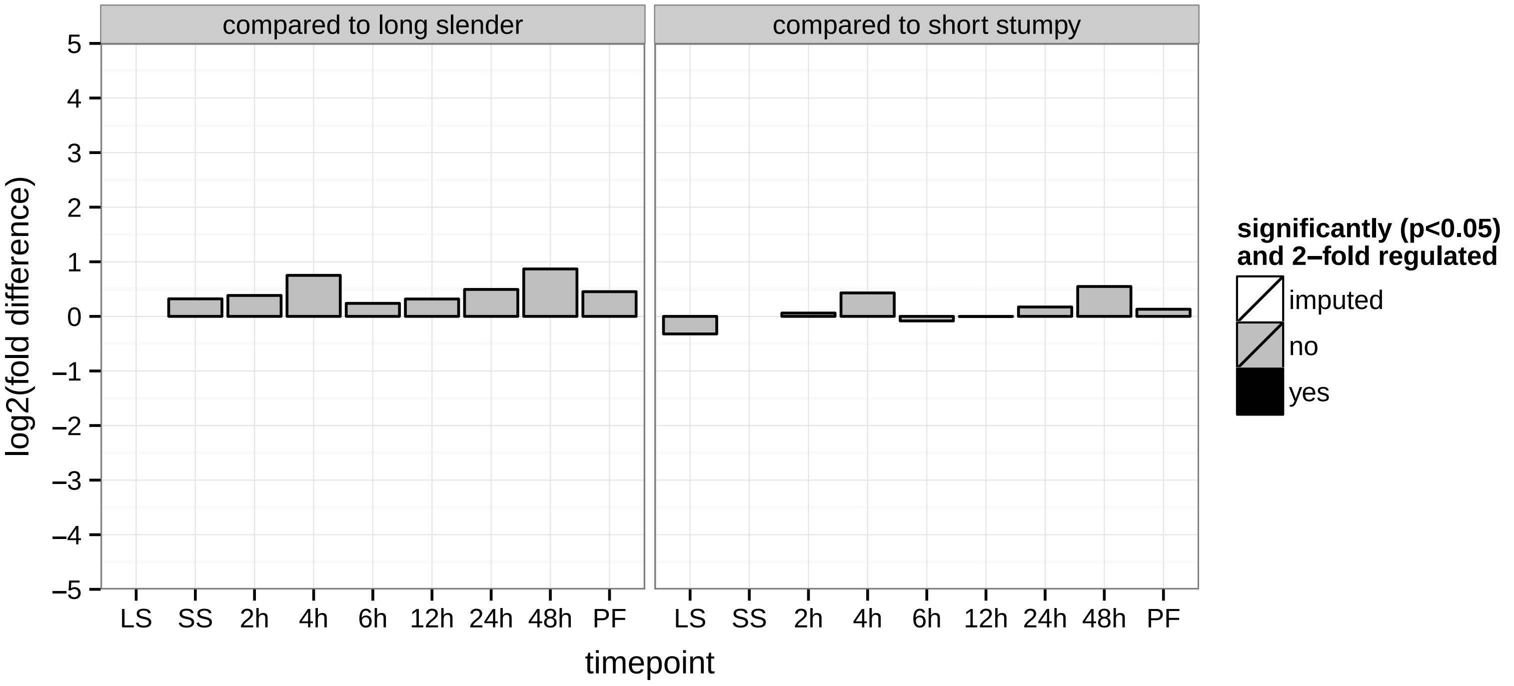
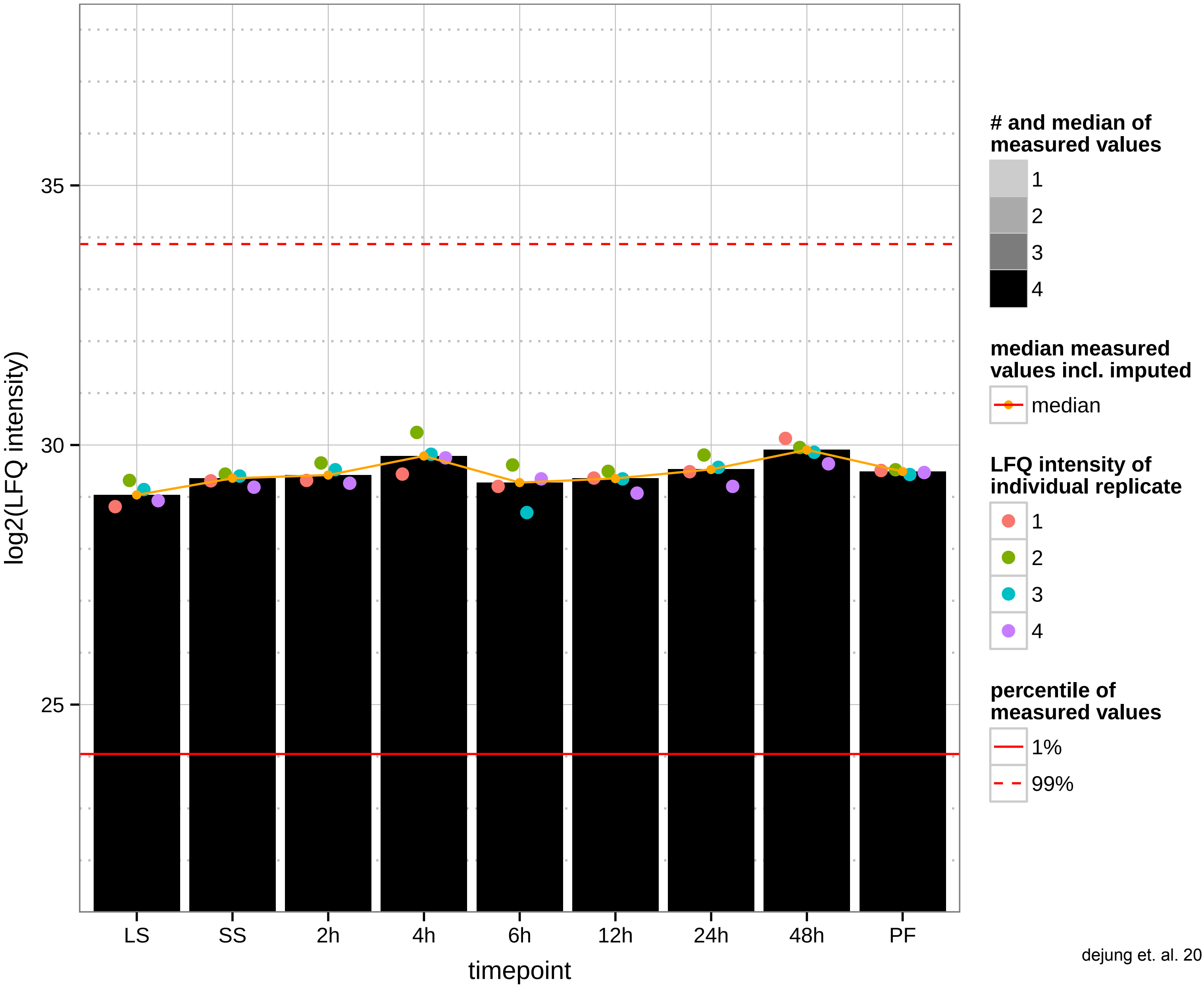
hypothetical protein, conserved
Tb927.8.5310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



tyrosyl/methionyl–tRNA synthetase, putative
Tb927.8.5330
AGOF: tRNA binding
AGOC: null
AGOP: tRNA aminoacylation
PGOF: tRNA binding
PGOC: null
PGOP: null





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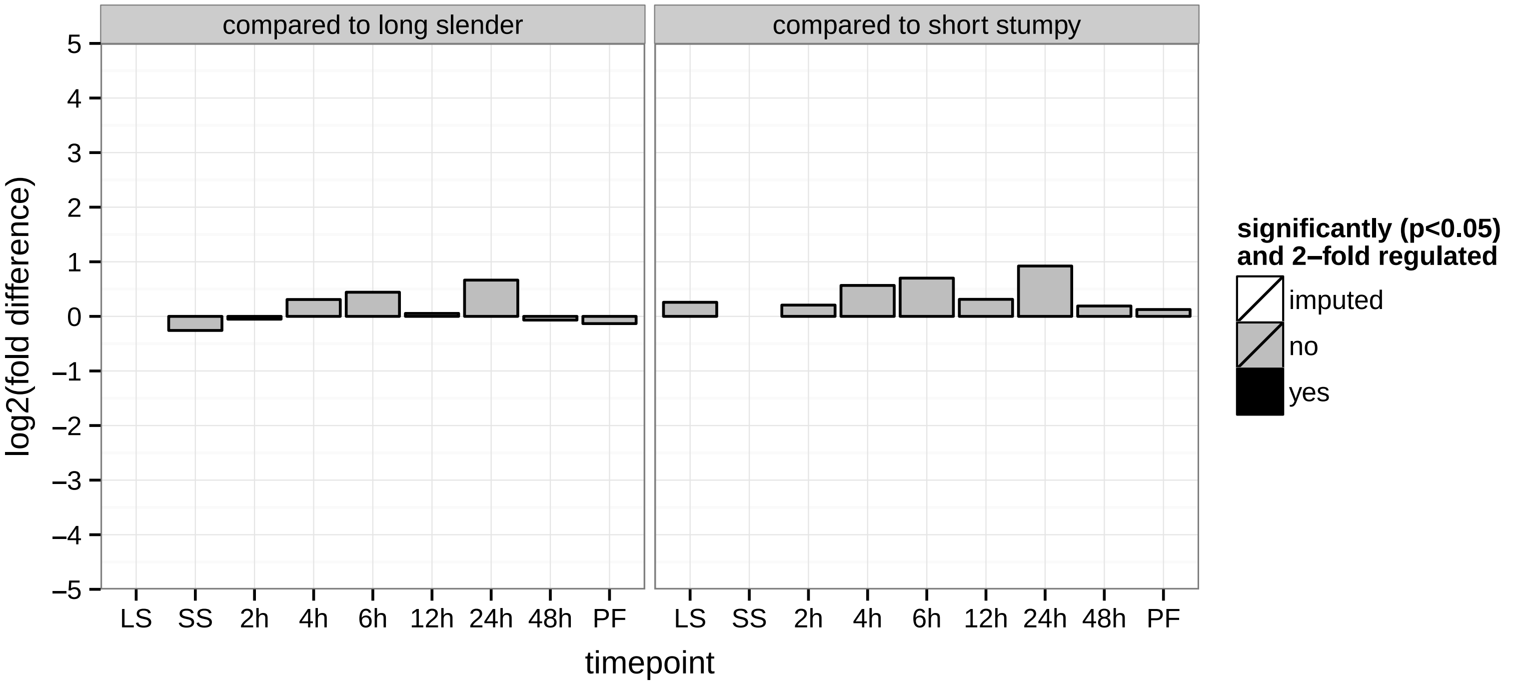
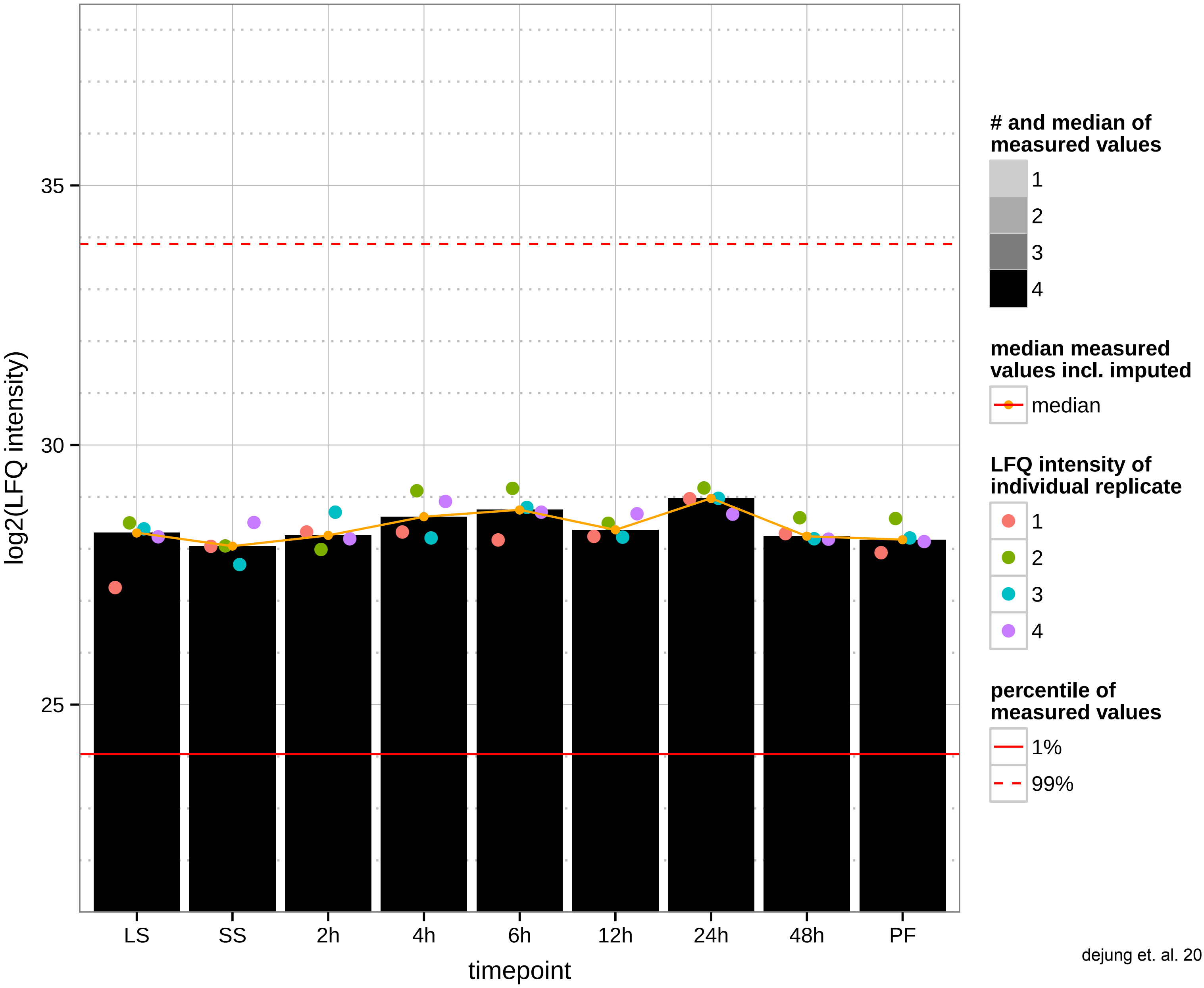
ubiquitin fold modifier protein, putative (UFM1)
Tb927.8.5380
AGOF: null
AGOC: mitochondrion
AGOP: protein modification by small protein conjugation
PGOF: null
PGOC: null
PGOP: null





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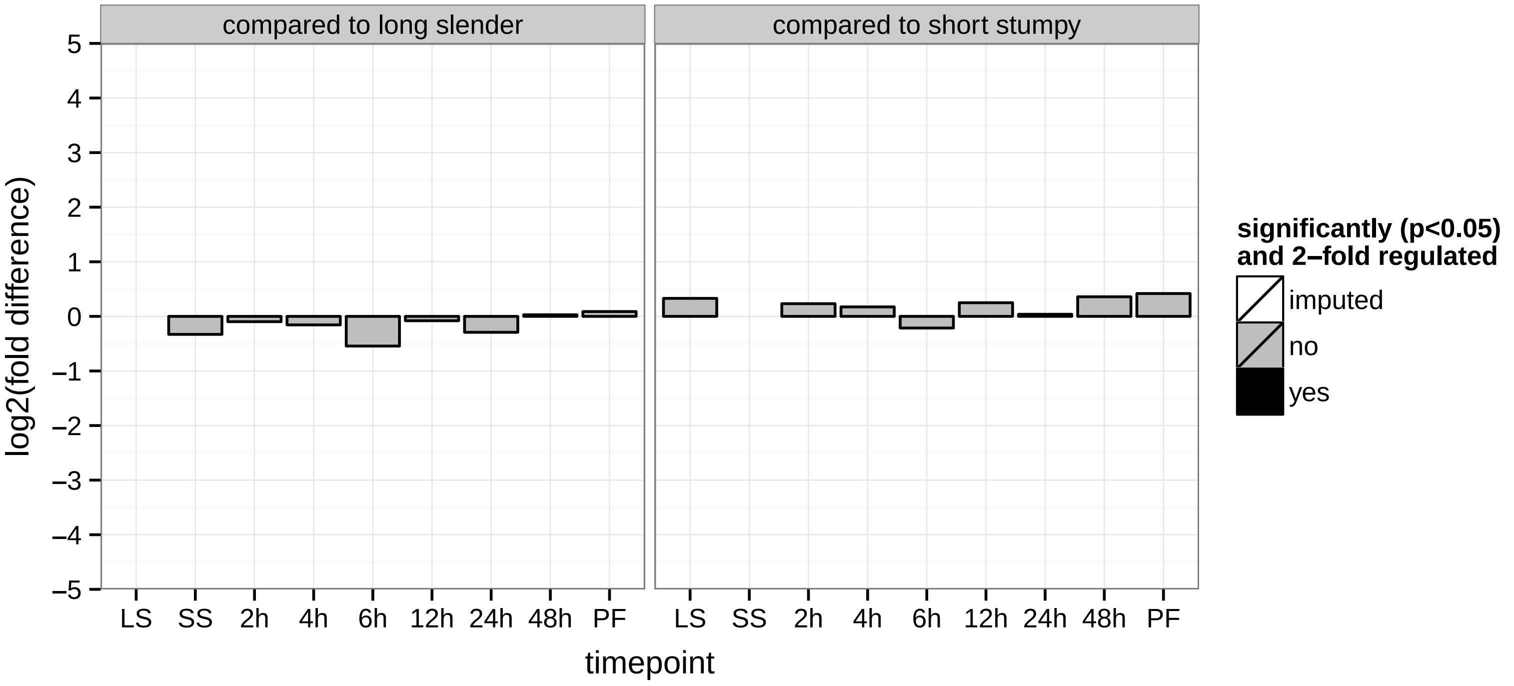
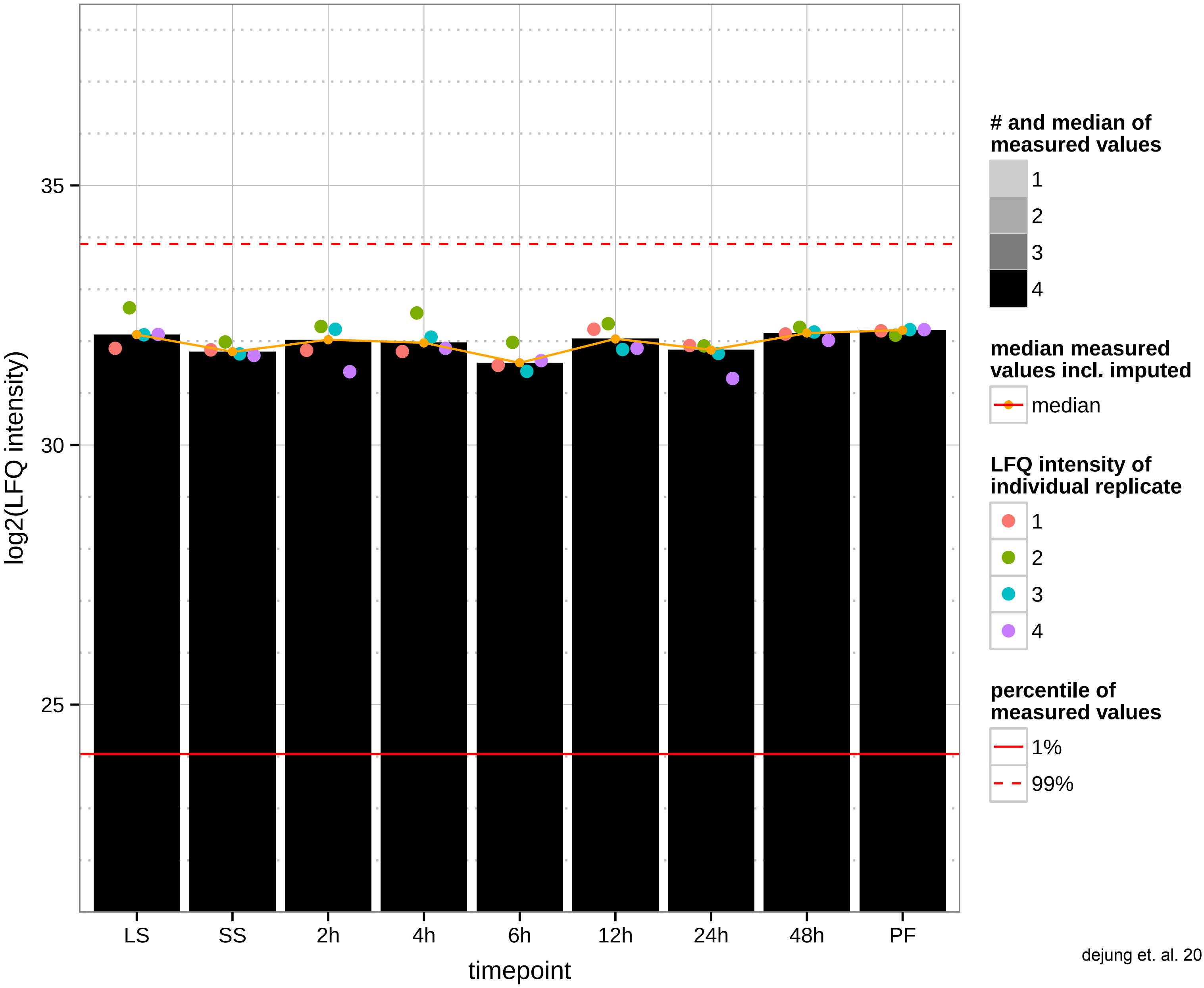
flagellar calcium–binding protein, 24 kDa calflagin, 24 kDa calcimedin (Tb–24), 44 kDa calflagin, 44 kDa calcimedin (Tb–44),
Tb927.8.5460;Tb11.v5.0797;Tb927.8.5465;Tb11.v5.0798
AGOF: null, calcium ion binding
AGOC: null, bacterial–type flagellum, cilium, motile cilium
AGOP: null, ciliary or flagellar motility, calcium ion transport, ciliary or flagellar motility
PGOF: calcium ion binding
PGOC: null
PGOP: null





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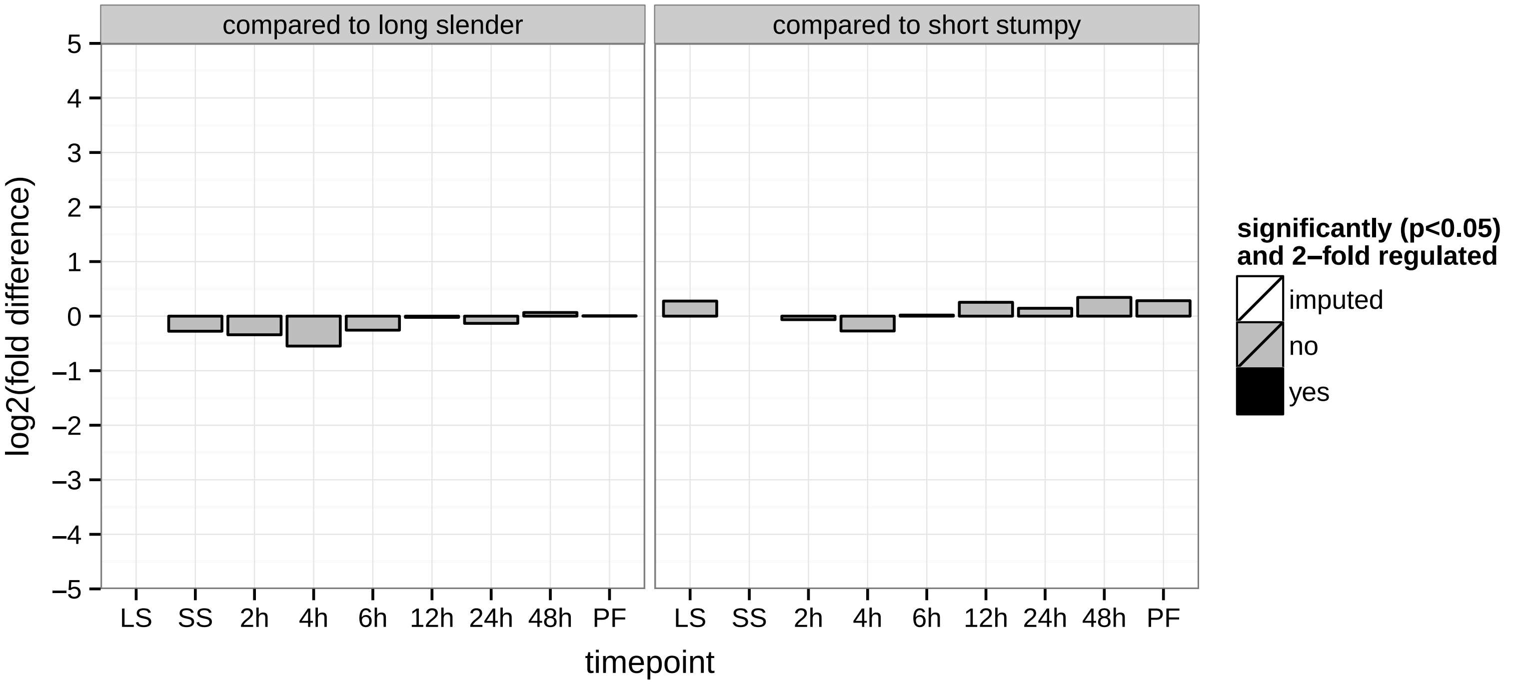
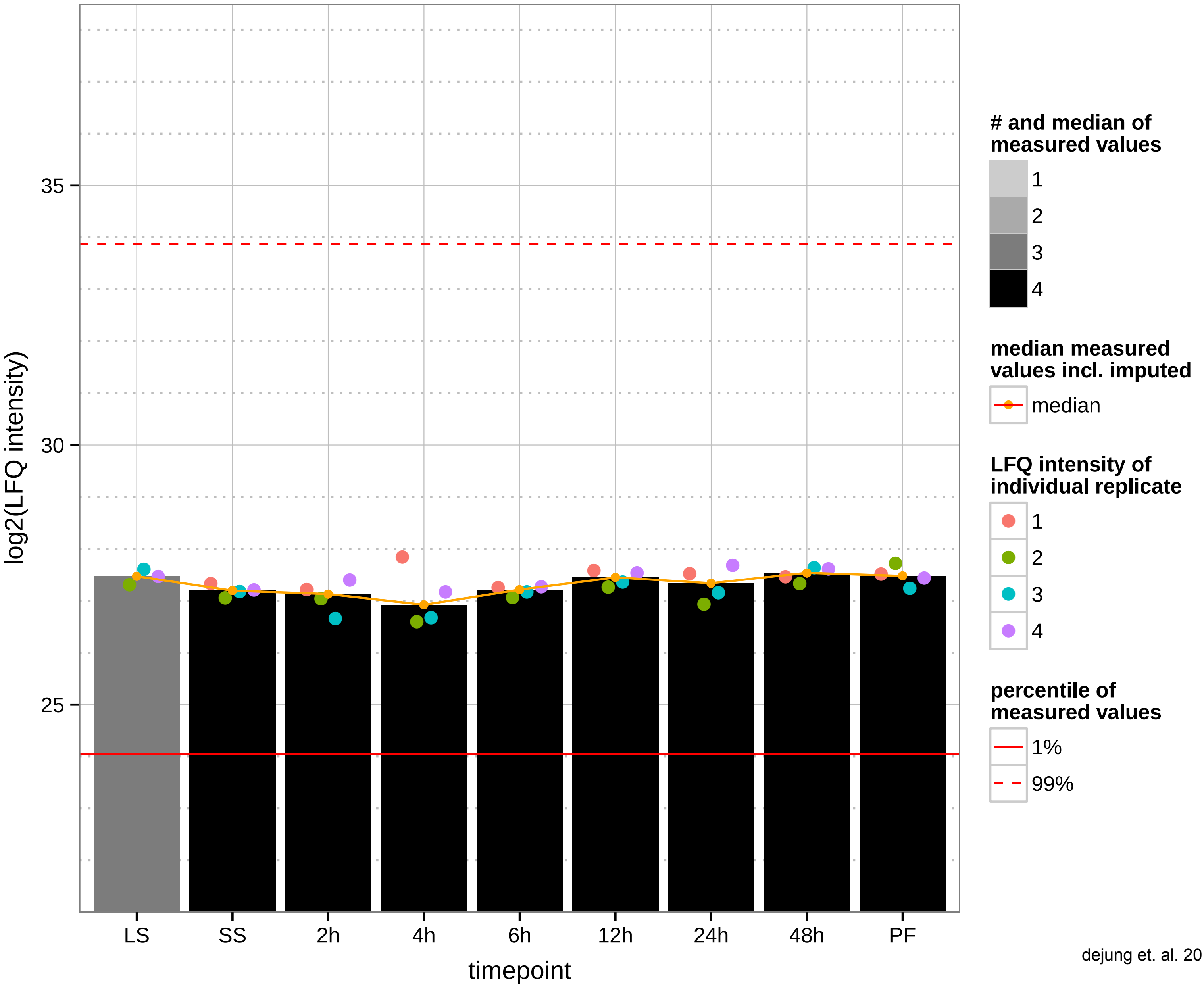
apurinic/apyrimidinic endonuclease, putative
Tb927.8.5510
AGOF: nuclease activity
AGOC: null
AGOP: DNA repair
PGOF: nuclease activity
PGOC: null
PGOP: DNA repair





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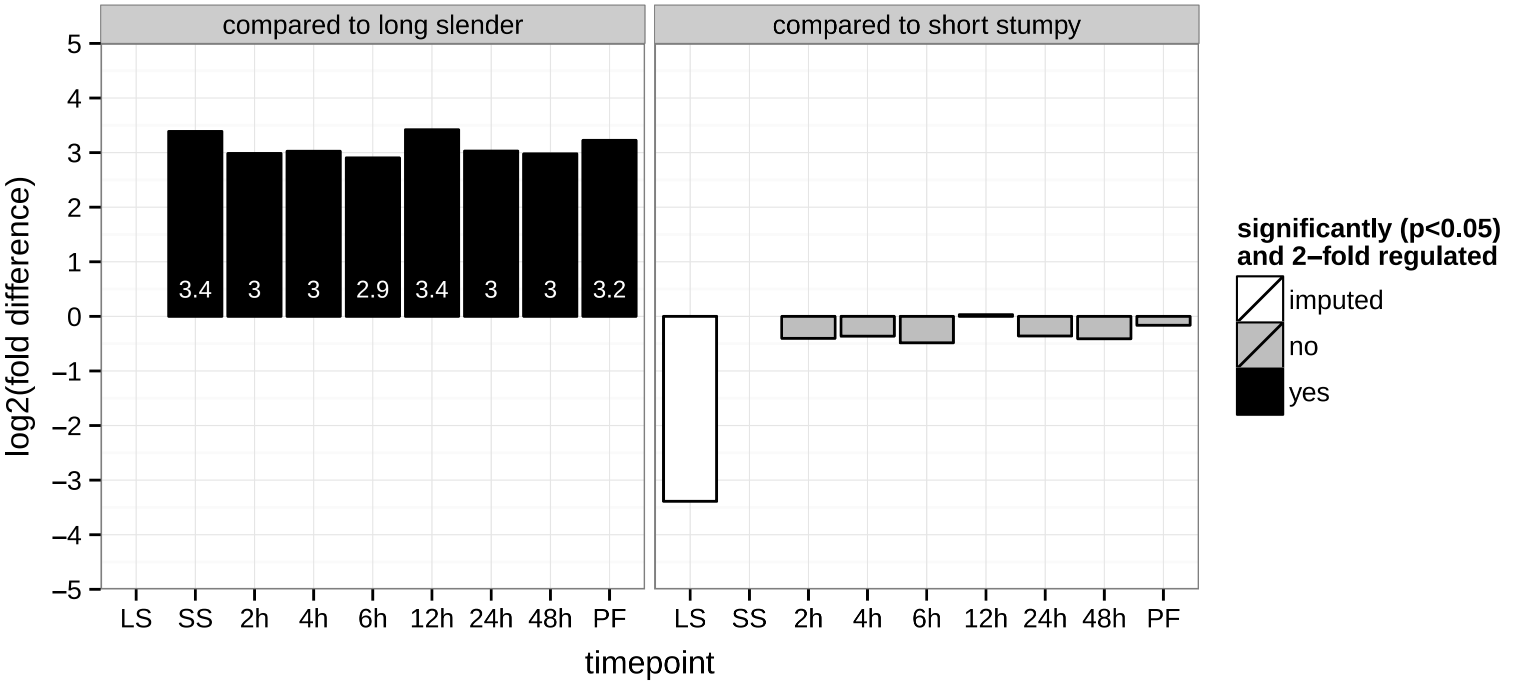
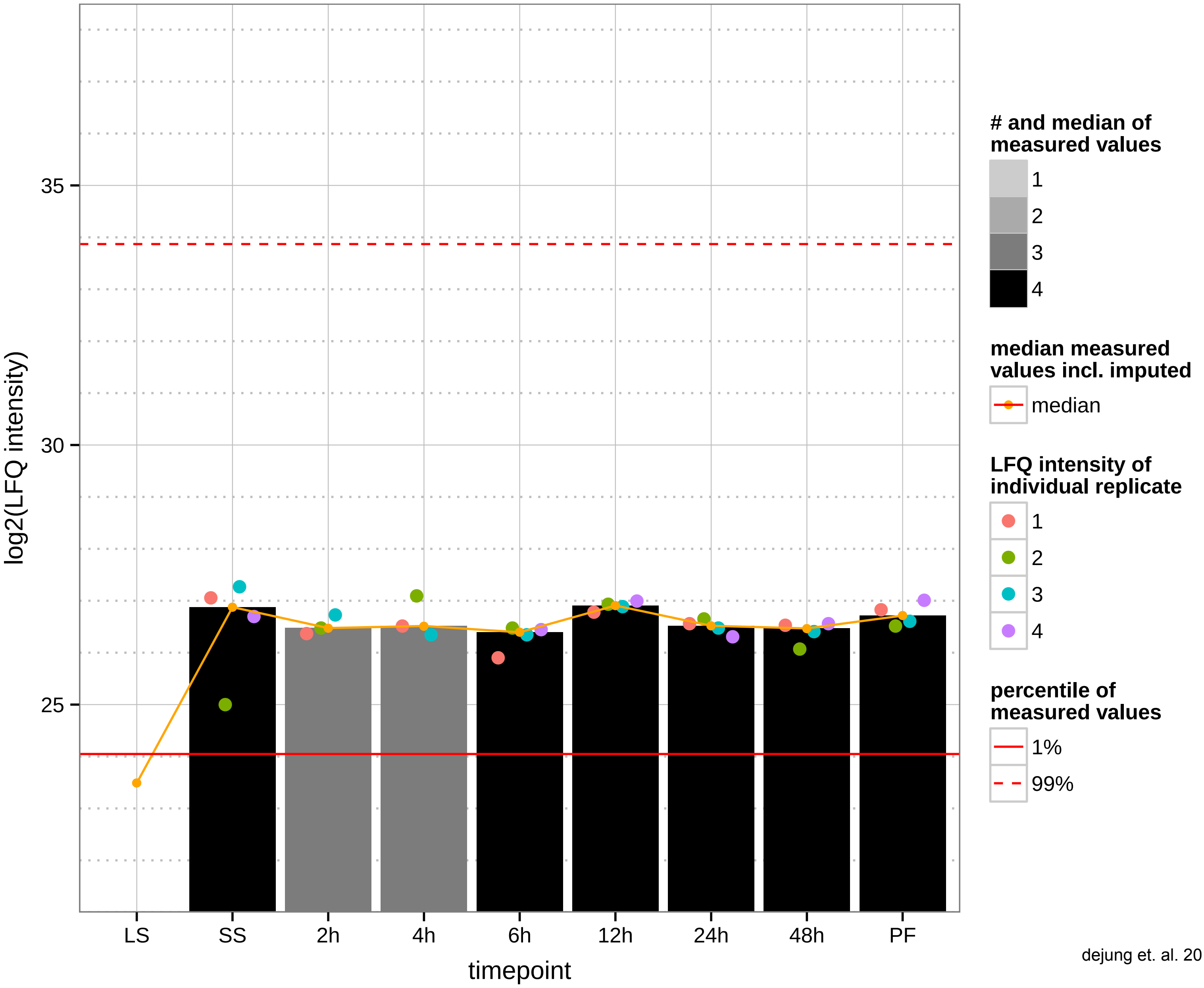
hypothetical protein, conserved
Tb927.8.5520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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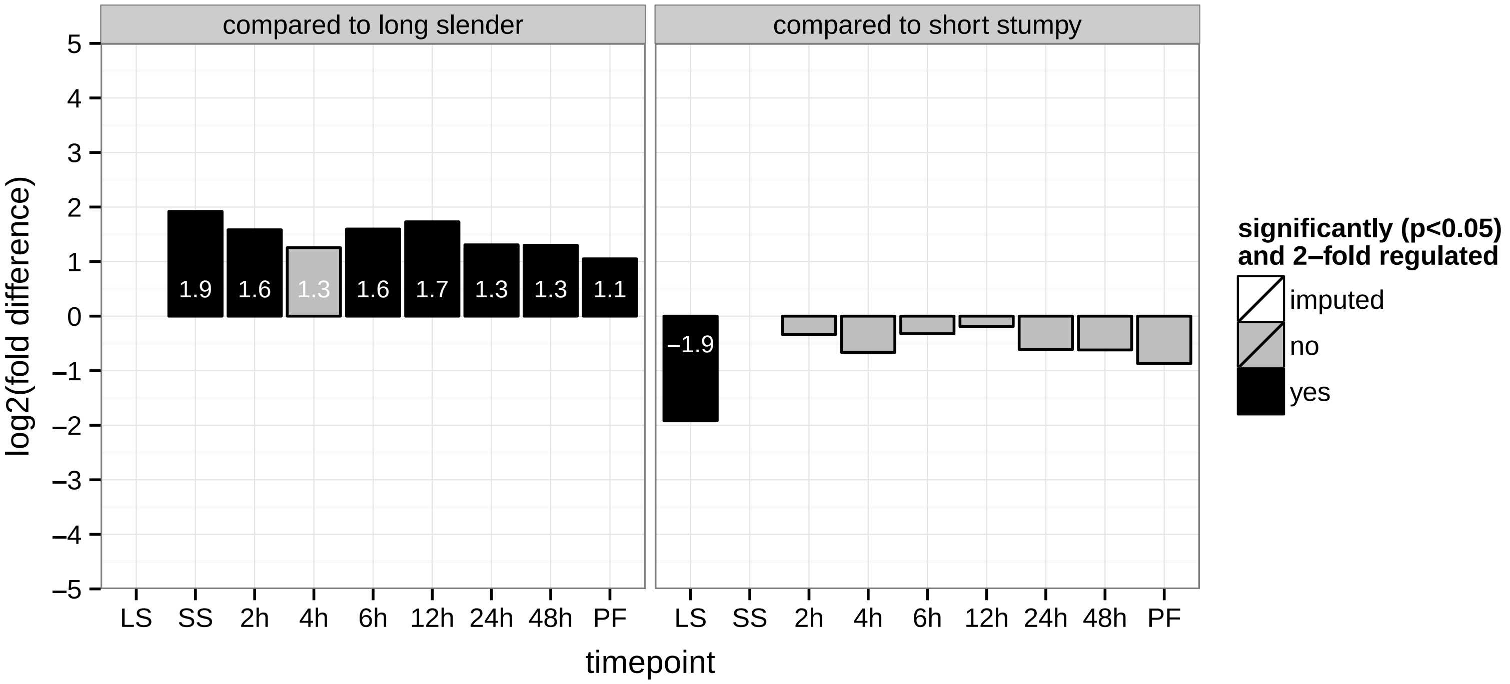
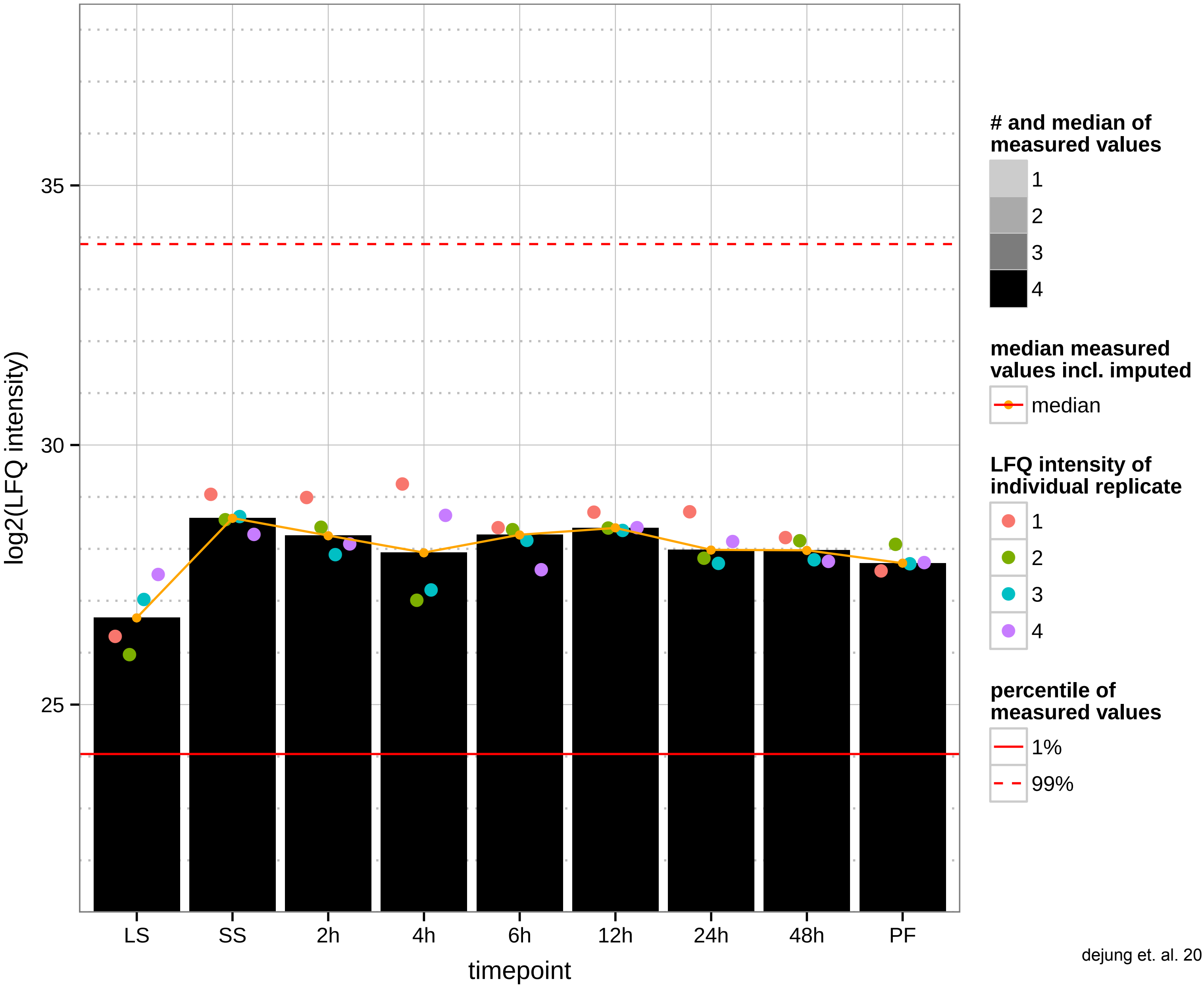
hypothetical protein, conserved
Tb927.8.5580
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: integral to membrane
PGOP: null





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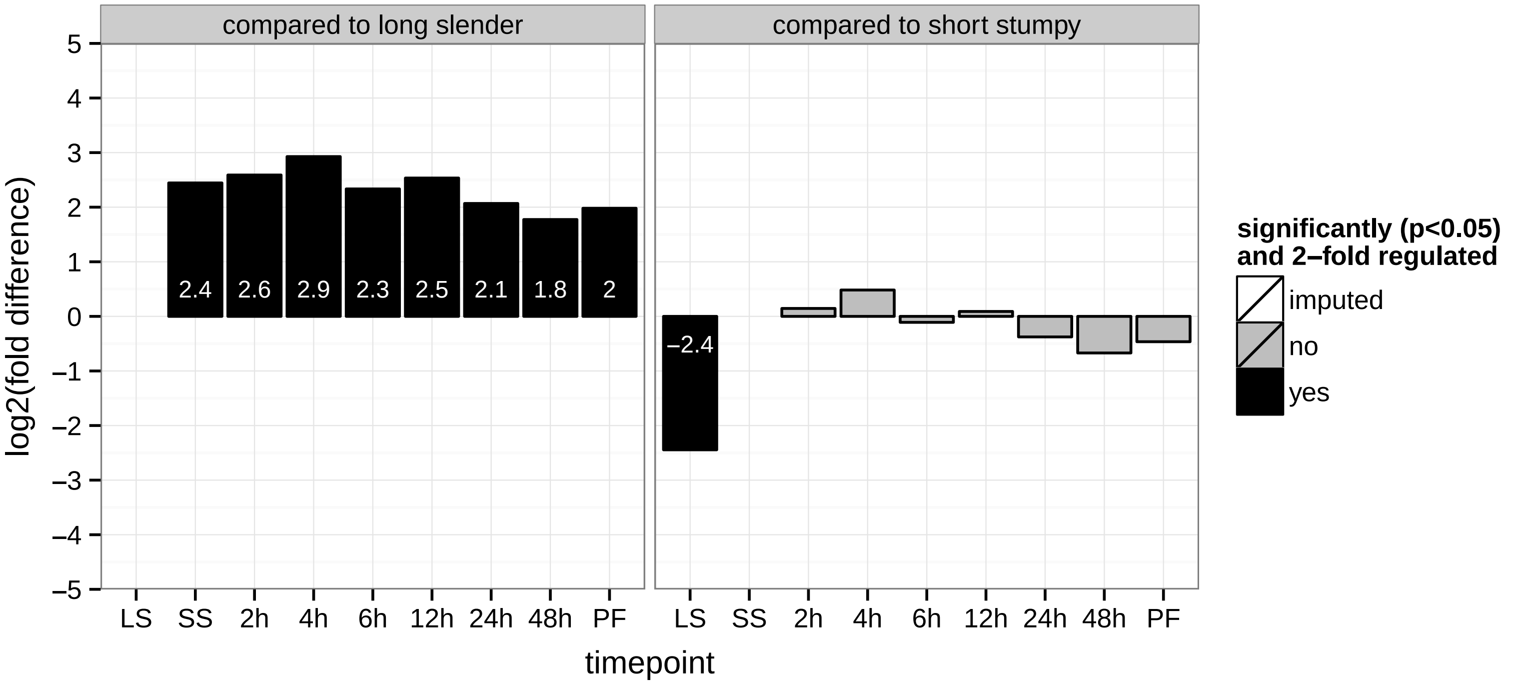
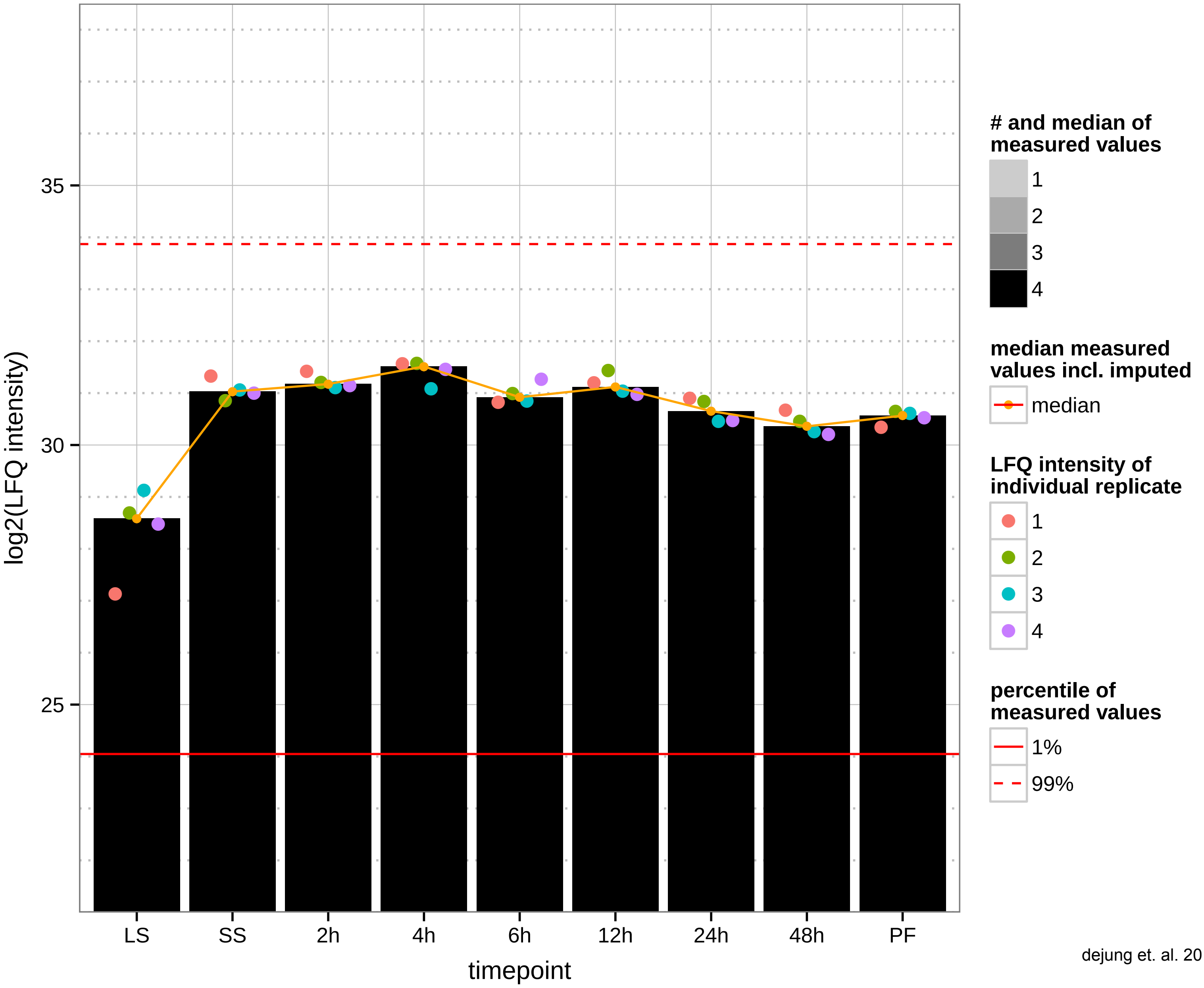
transaldolase, putative
Tb927.8.5600
AGOF: sedoheptulose−7−phosphate:D−glyceraldehyde−3−phosphate glyceronetransferase activity
AGOC: cytoplasm
AGOP: pentose−phosphate shunt
PGOF: sedoheptulose−7−phosphate:D−glyceraldehyde−3−phosphate glyceronetransferase activity
PGOC: cytoplasm
PGOP: carbohydrate metabolic process, pentose−phosphate shunt





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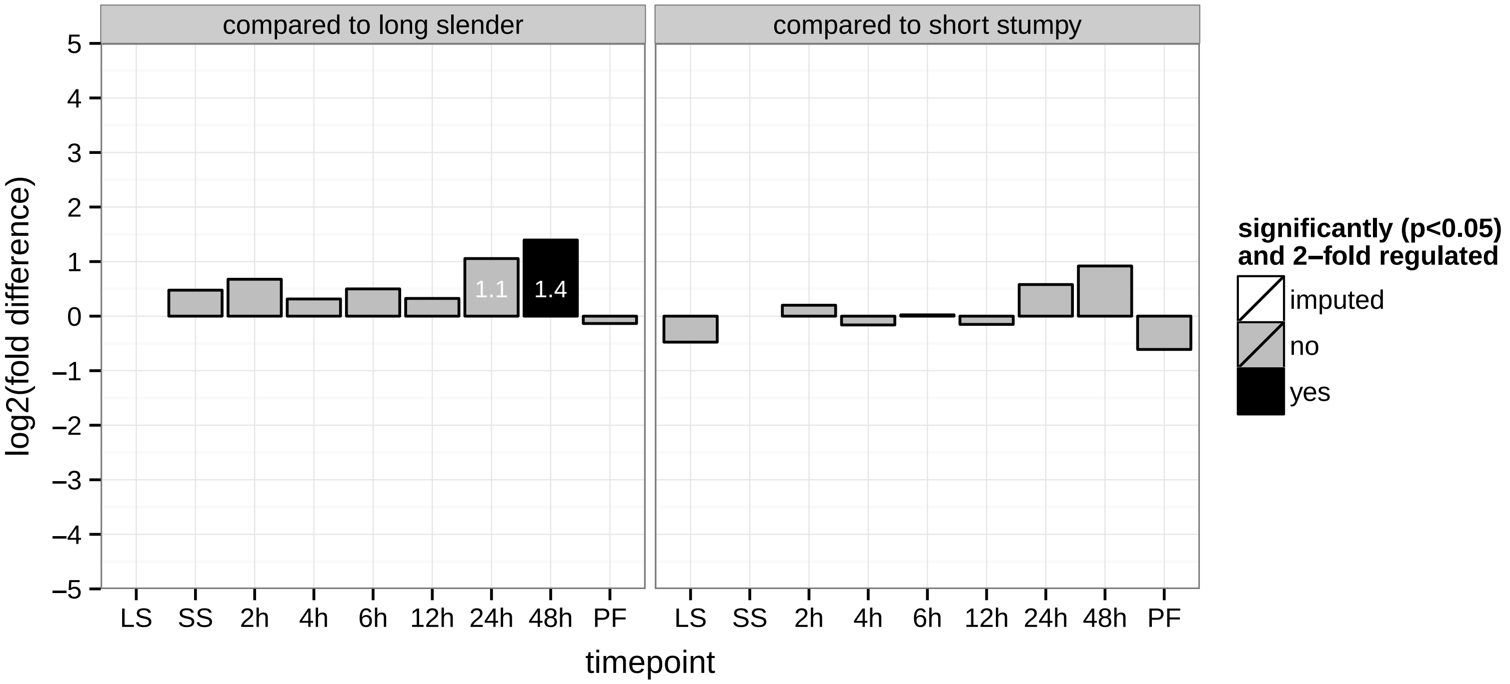
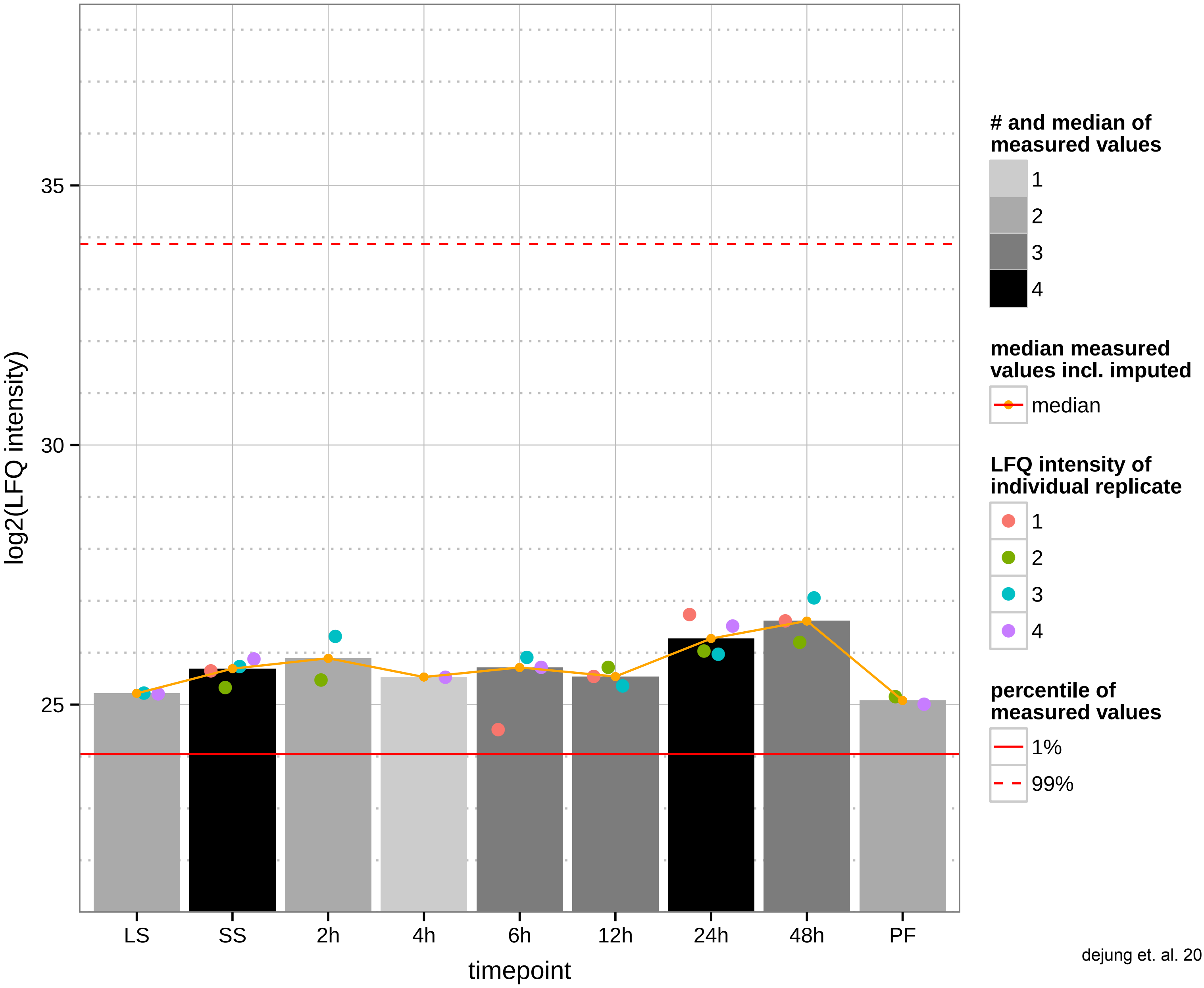
dihydroorotase, putative
Tb927.8.5630
AGOF: hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds, in cyclic amides
AGOC: null
AGOP: pyrimidine nucleobase biosynthetic process
PGOF: hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
PGOC: null
PGOP: null





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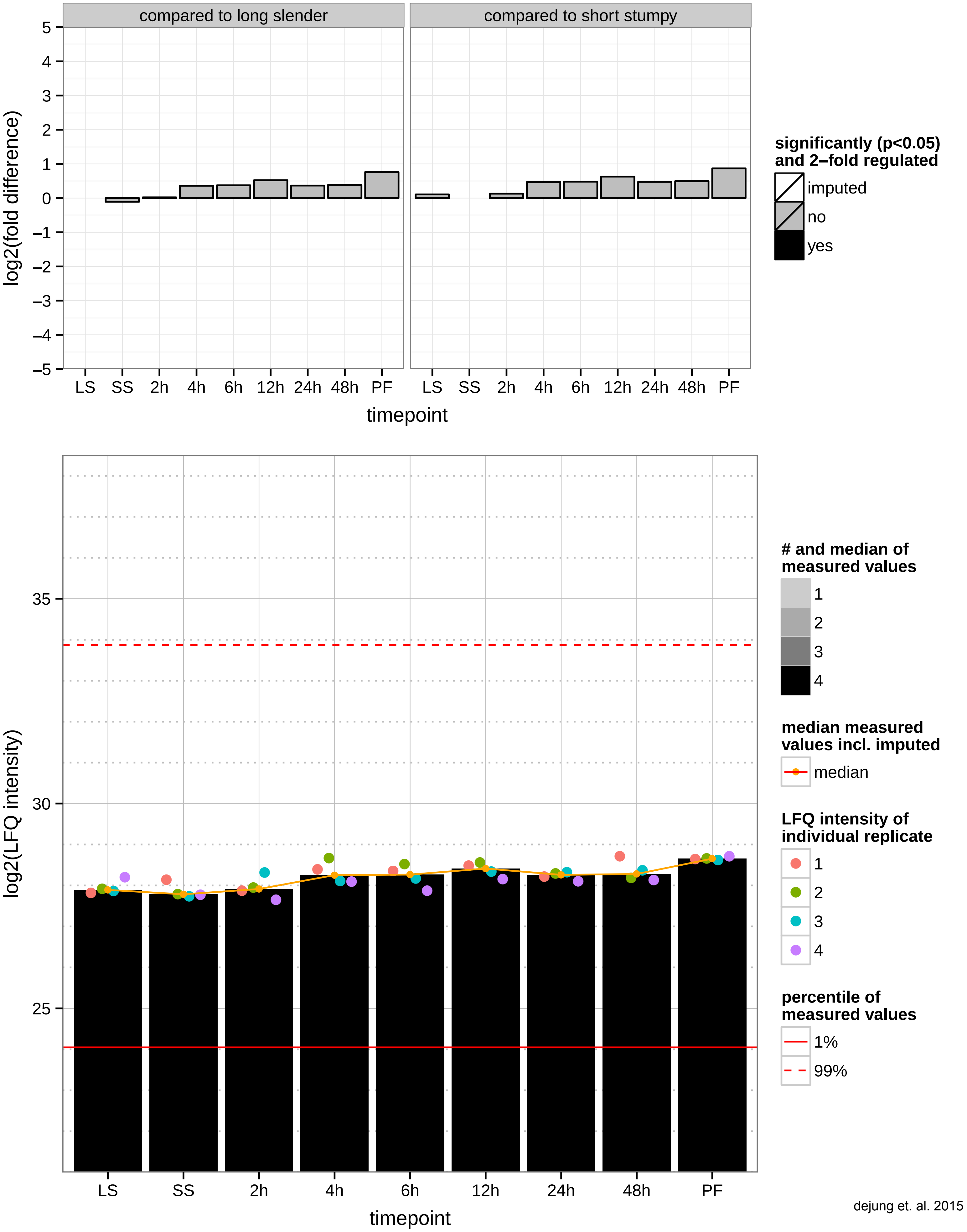
proteasome regulatory non–ATP–ase subunit 10
Tb927.8.570
AGOF: null
AGOC: proteasome complex
AGOP: cell growth, ubiquitin–dependent protein catabolic process
PGOF: protein binding
PGOC: null
PGOP: null



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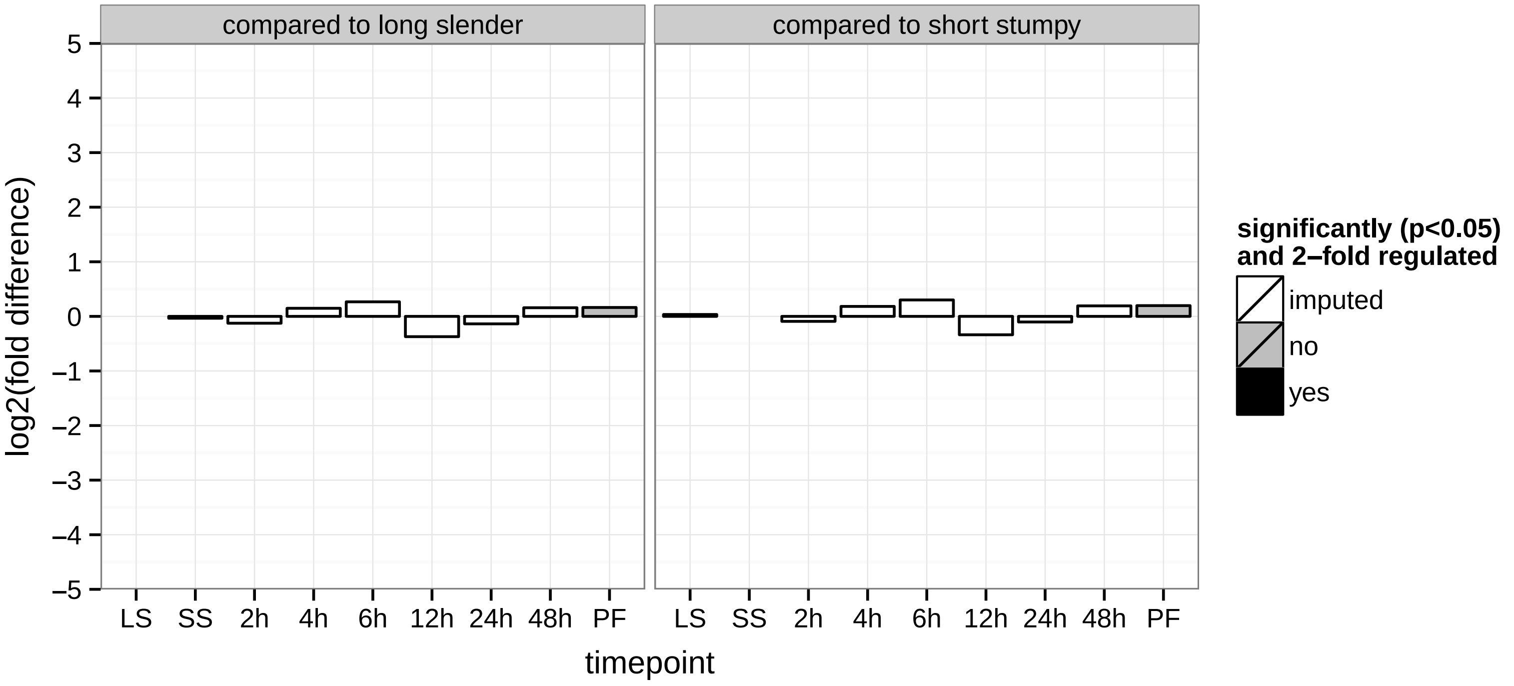
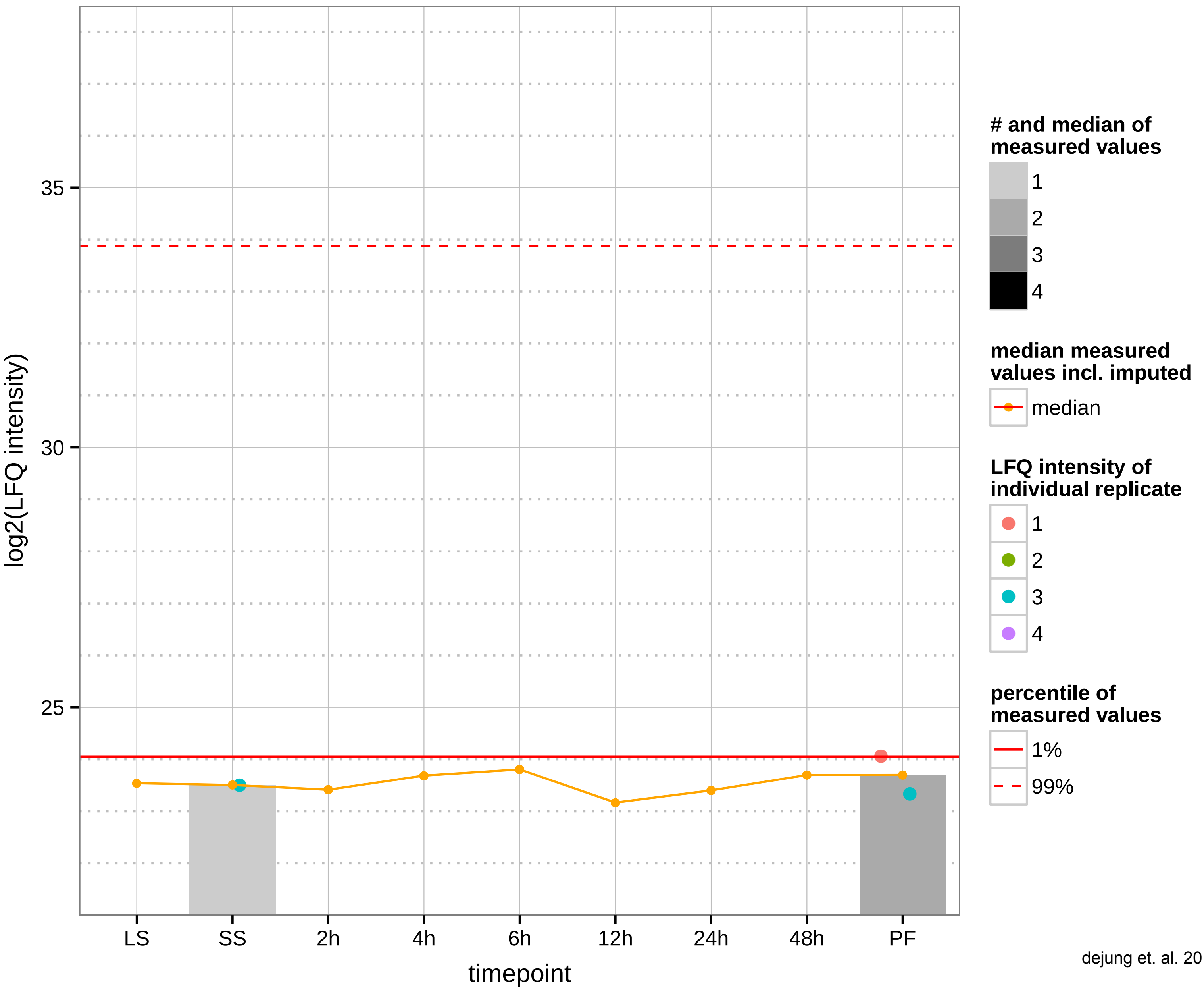
protein kinase, putative
Tb927.8.5730
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: growth, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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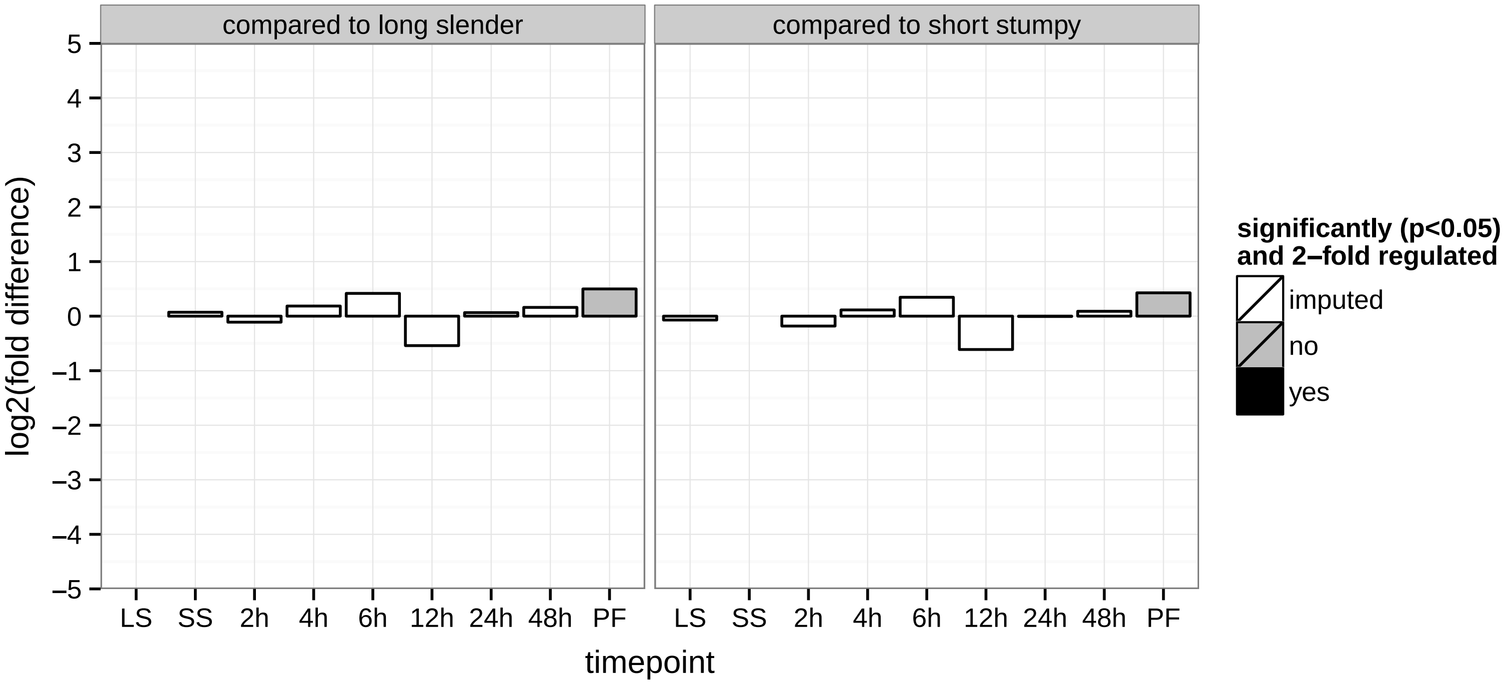
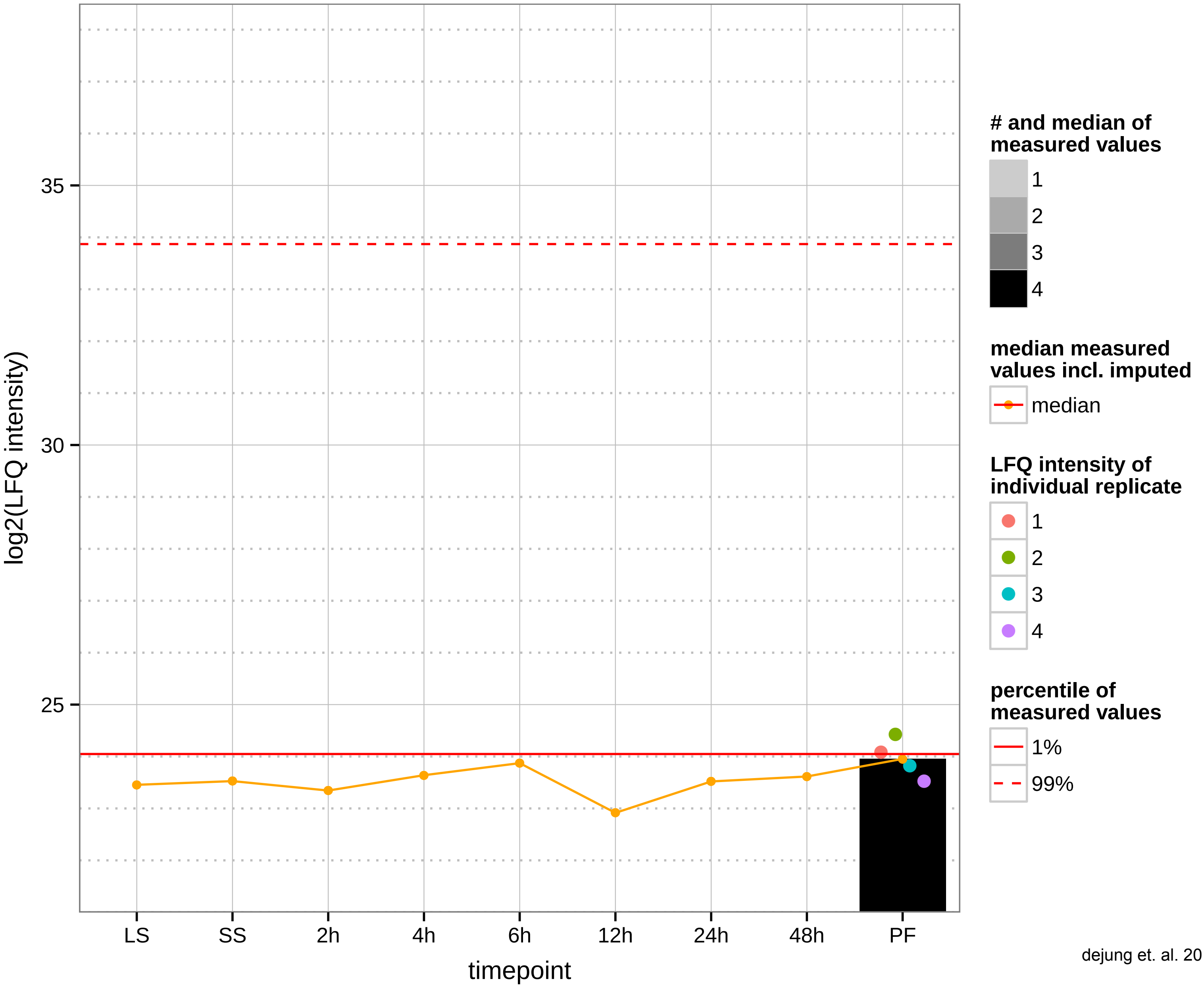
hypothetical protein, conserved
Tb927.8.5820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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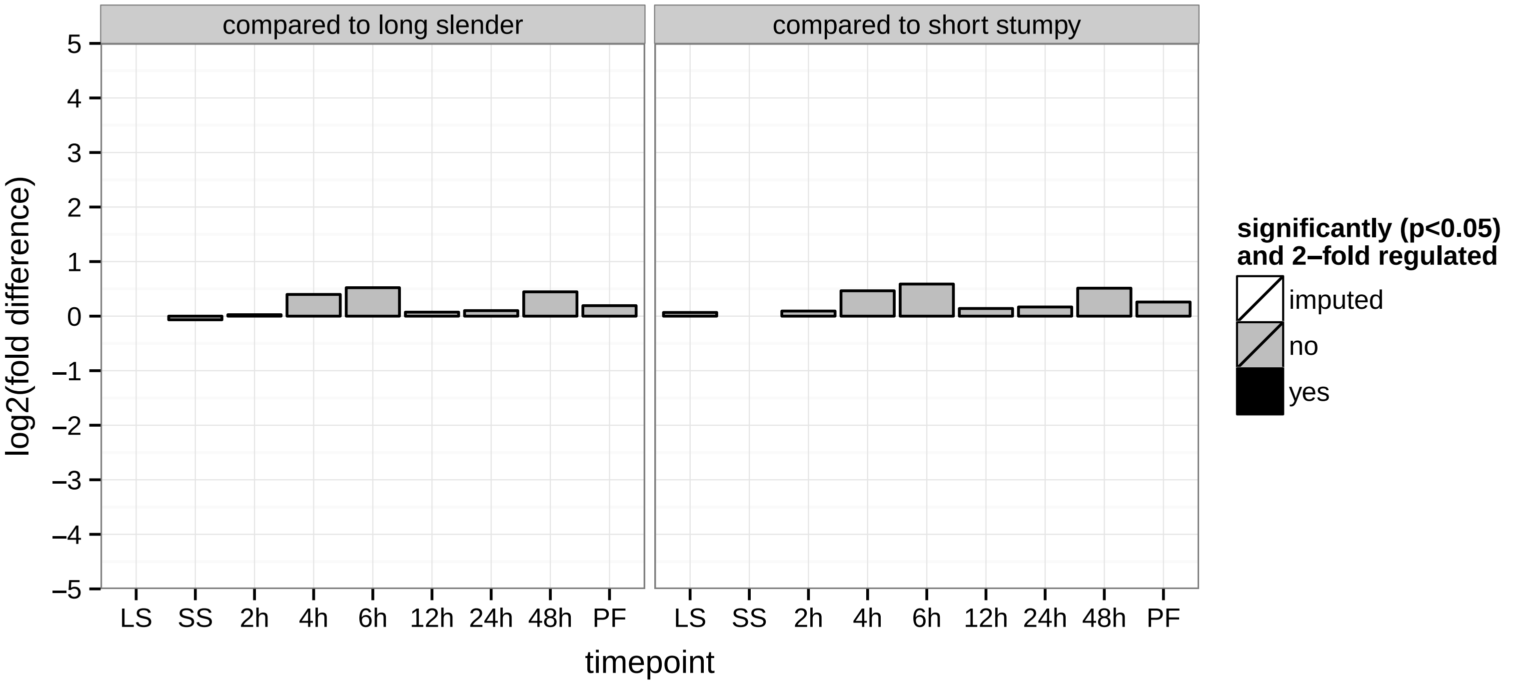
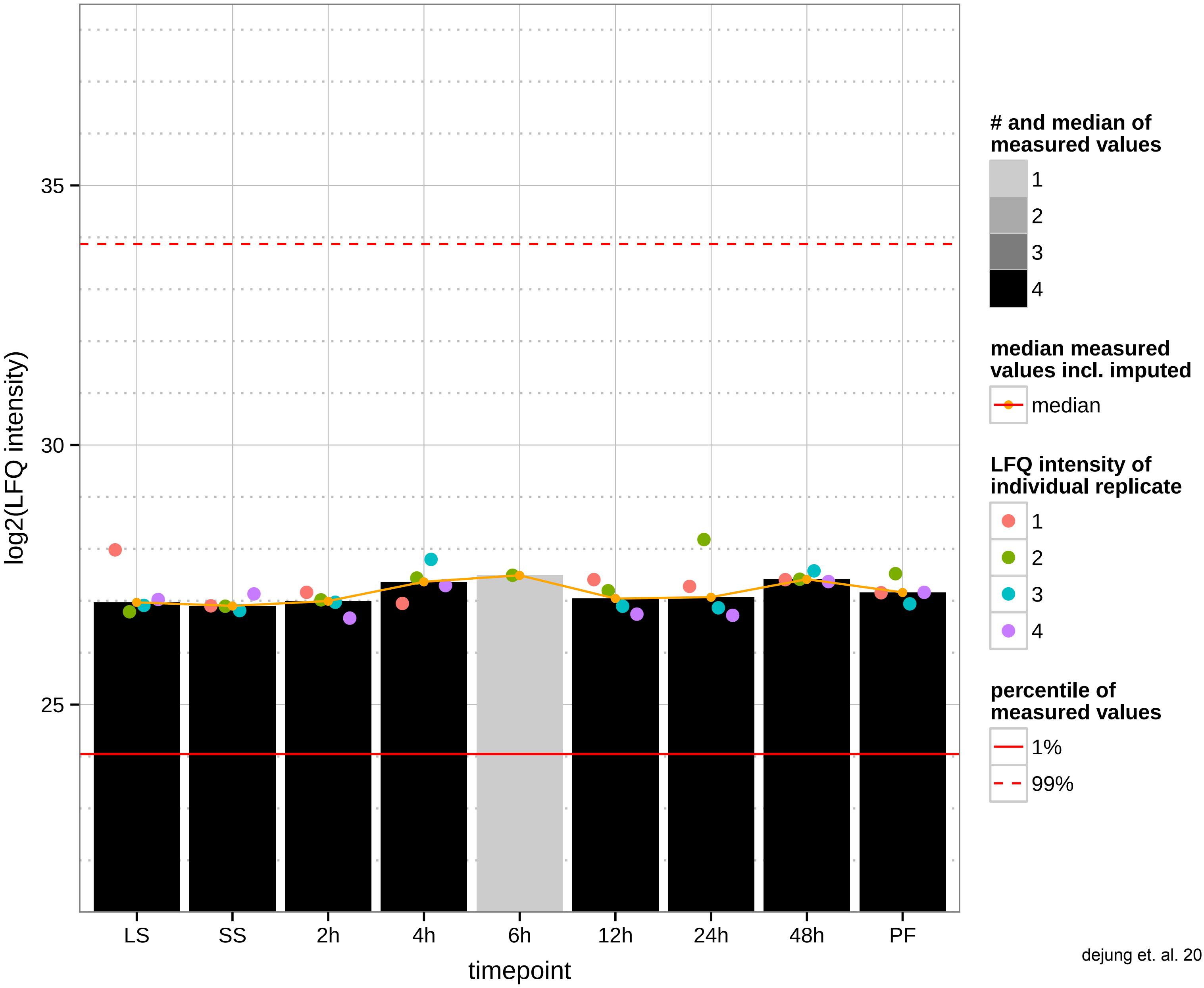
hypothetical protein, conserved
Tb927.8.5830
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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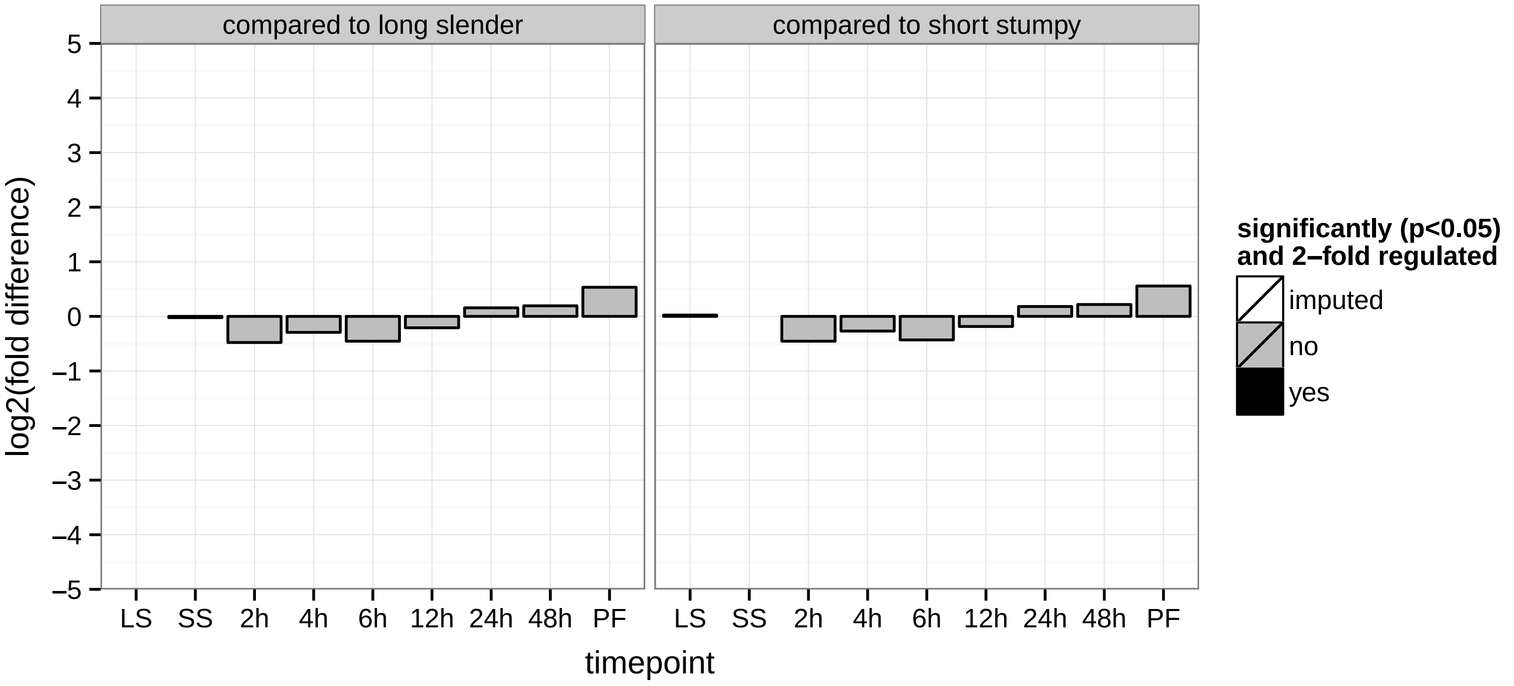
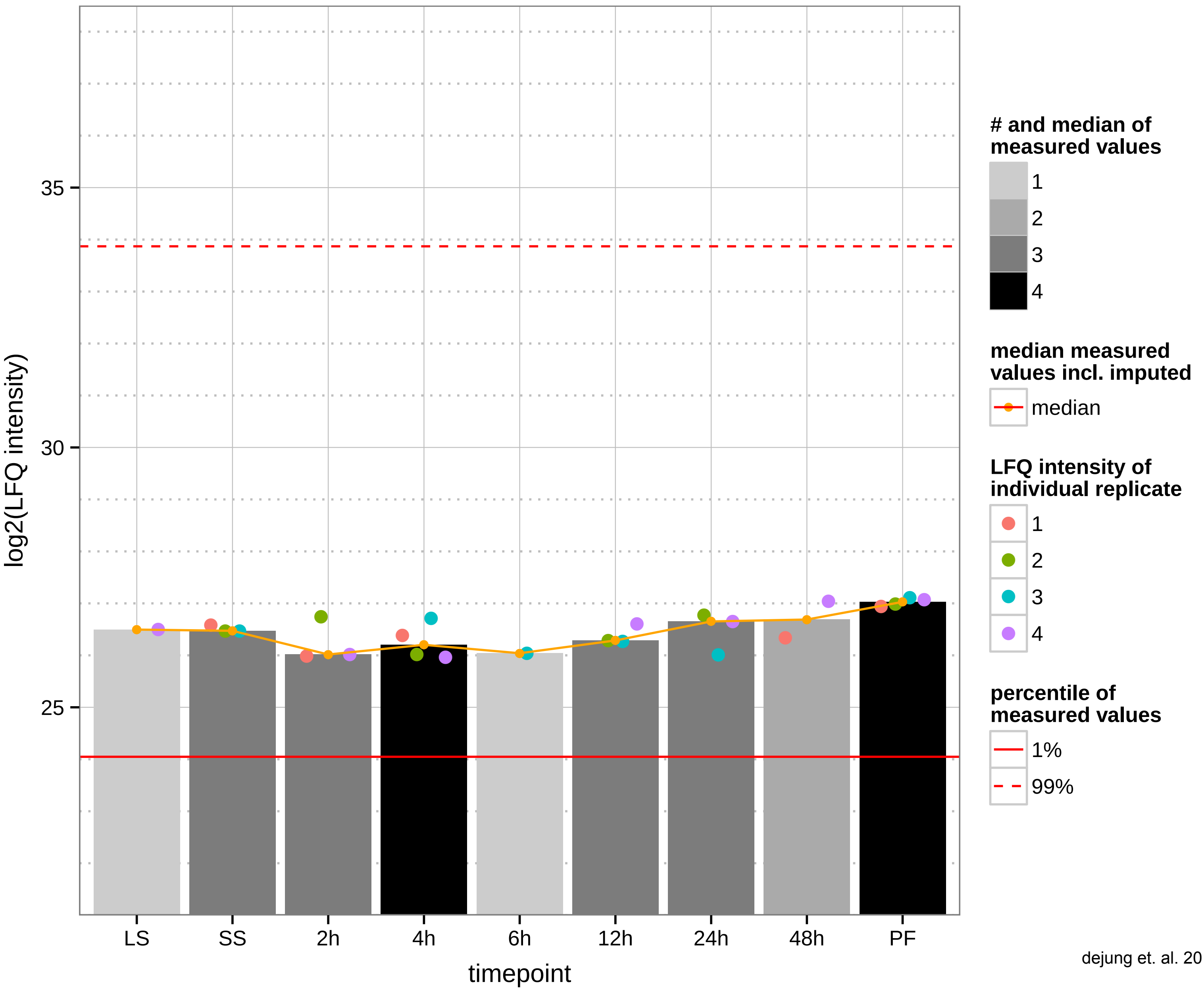
hypothetical protein, conserved
Tb927.8.5890
AGOF: null
AGOC: nucleus
AGOP: chromatin assembly or disassembly
PGOF: null
PGOC: nucleus
PGOP: chromatin assembly or disassembly





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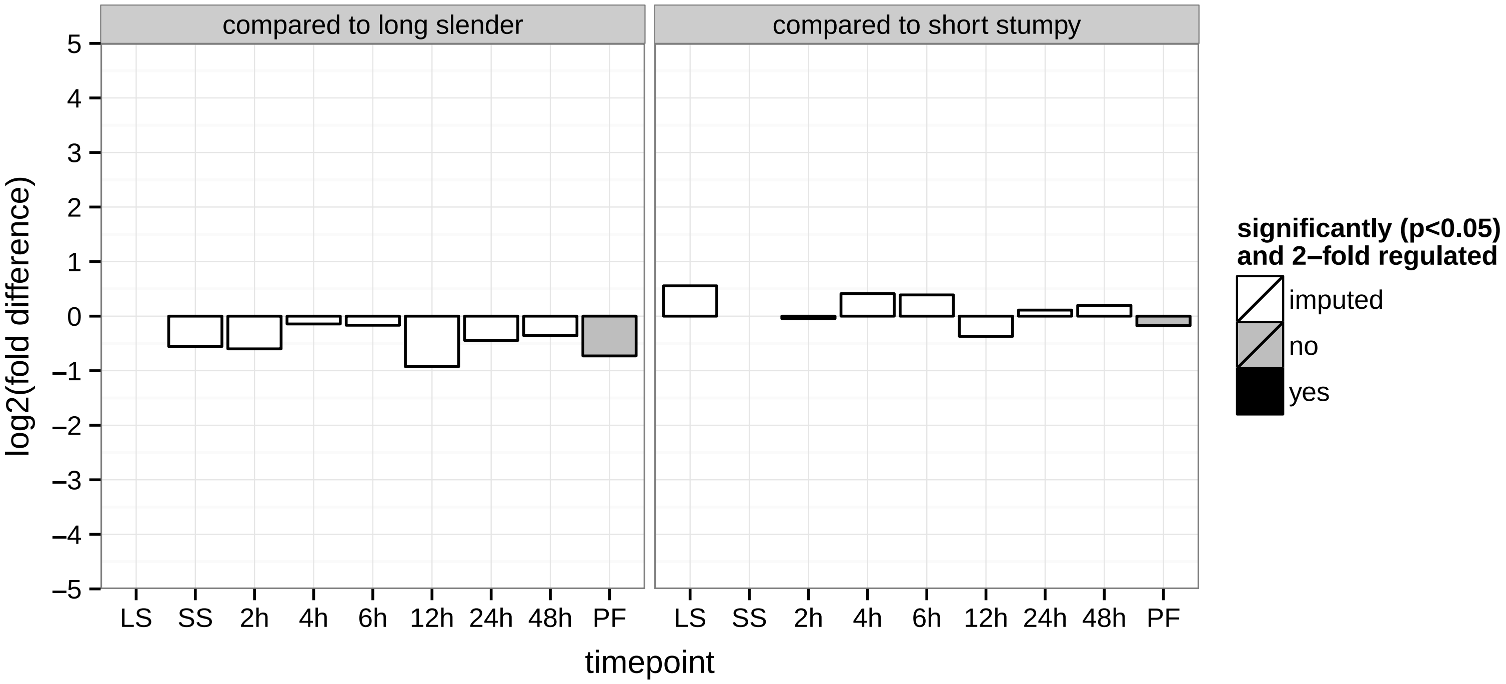
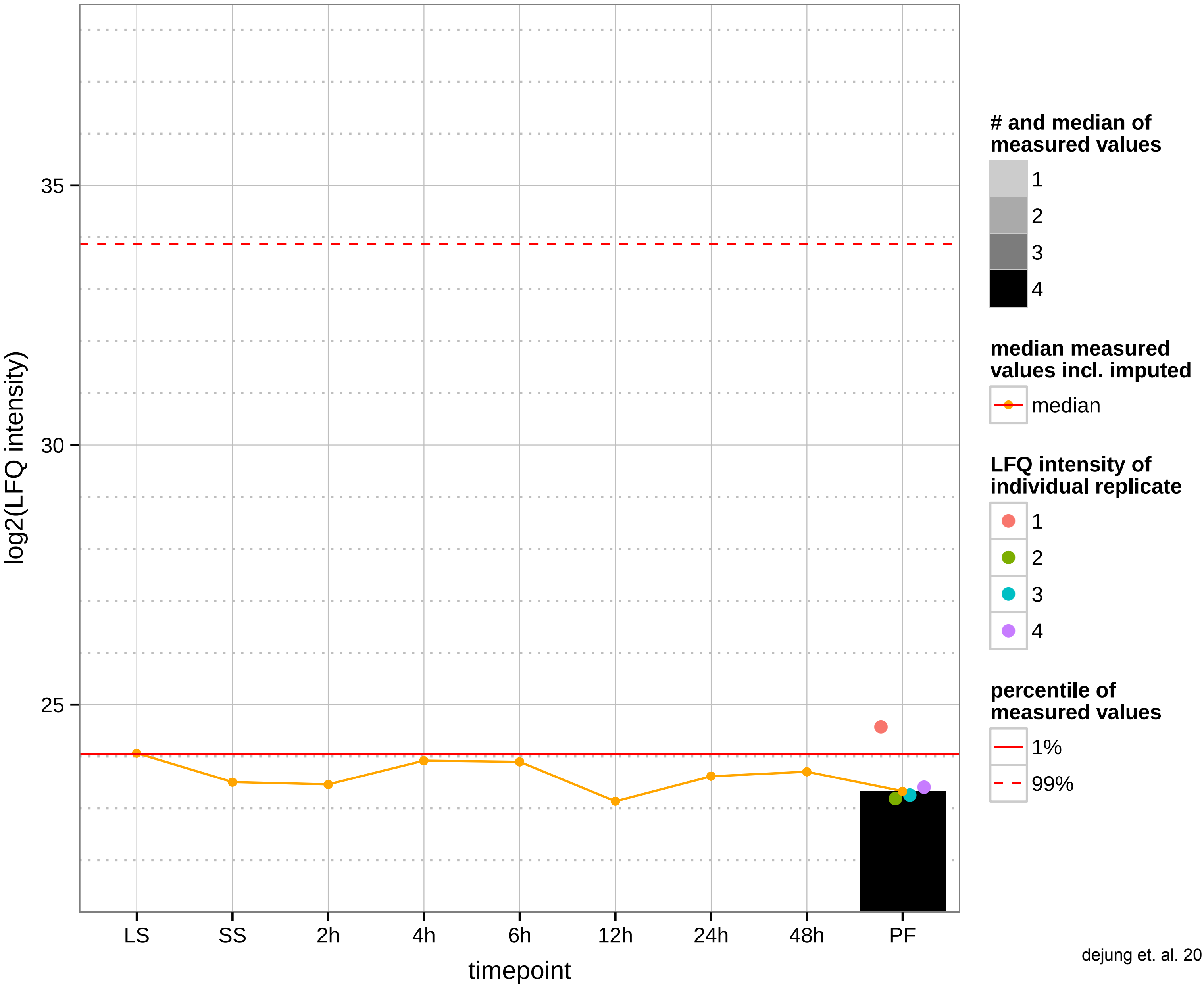
carnitine O–palmitoyltransferase, putative
Tb927.8.590
AGOF: carnitine O–acetyltransferase activity
AGOC: mitochondrion
AGOP: generation of precursor metabolites and energy
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: null





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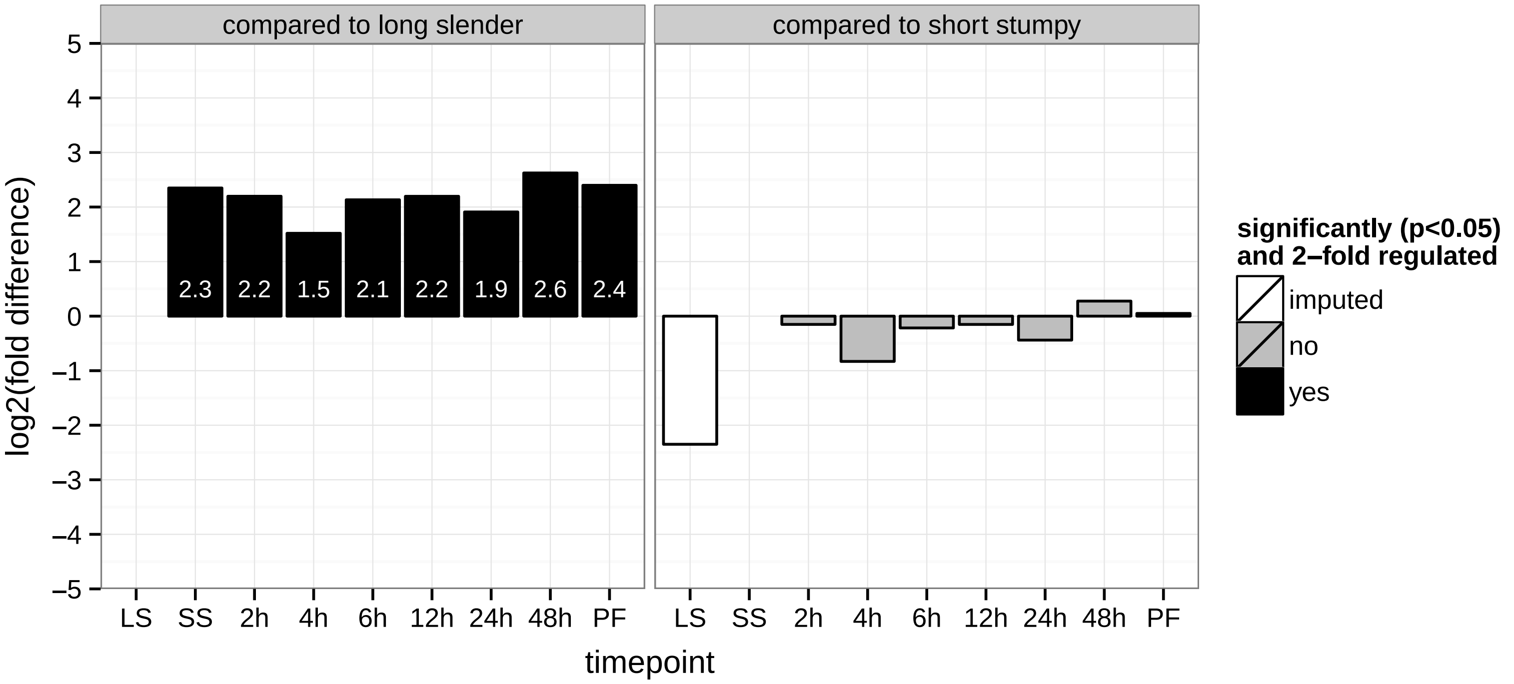
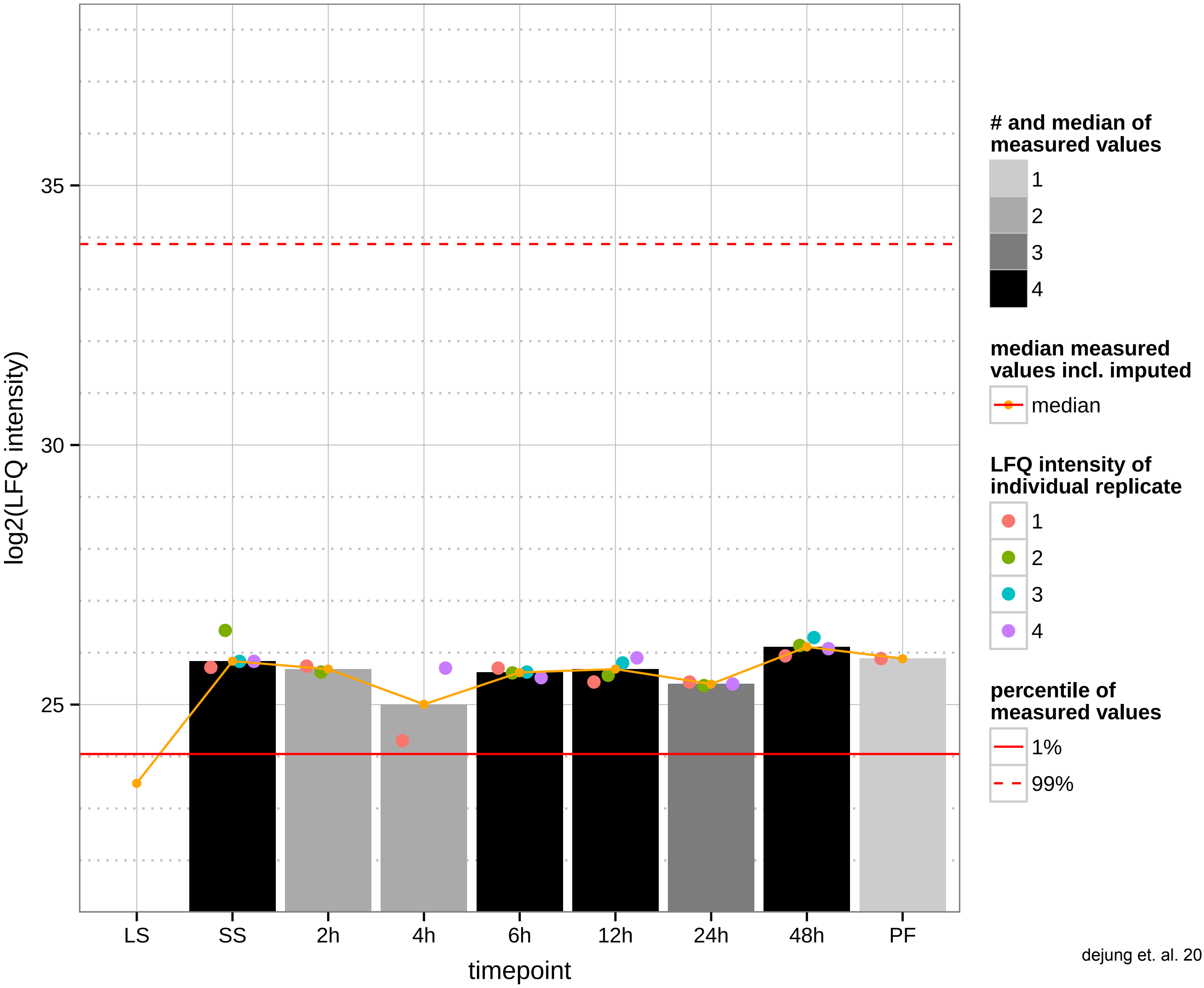
hypothetical protein, conserved
Tb927.8.5940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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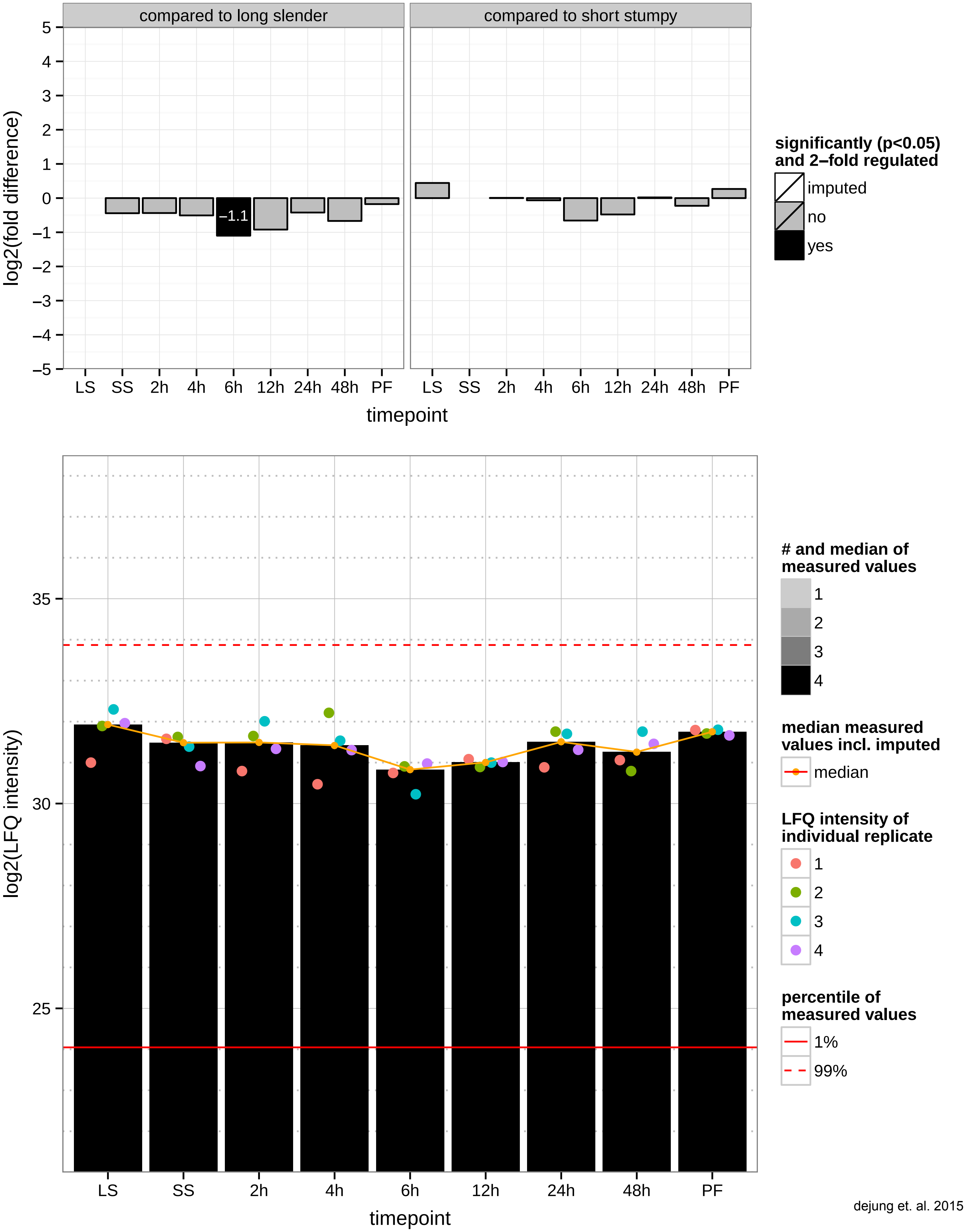
60S ribosomal protein L12, putative
Tb927.8.6030;Tb927.9.14000
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: ribosome
PGOP: translation



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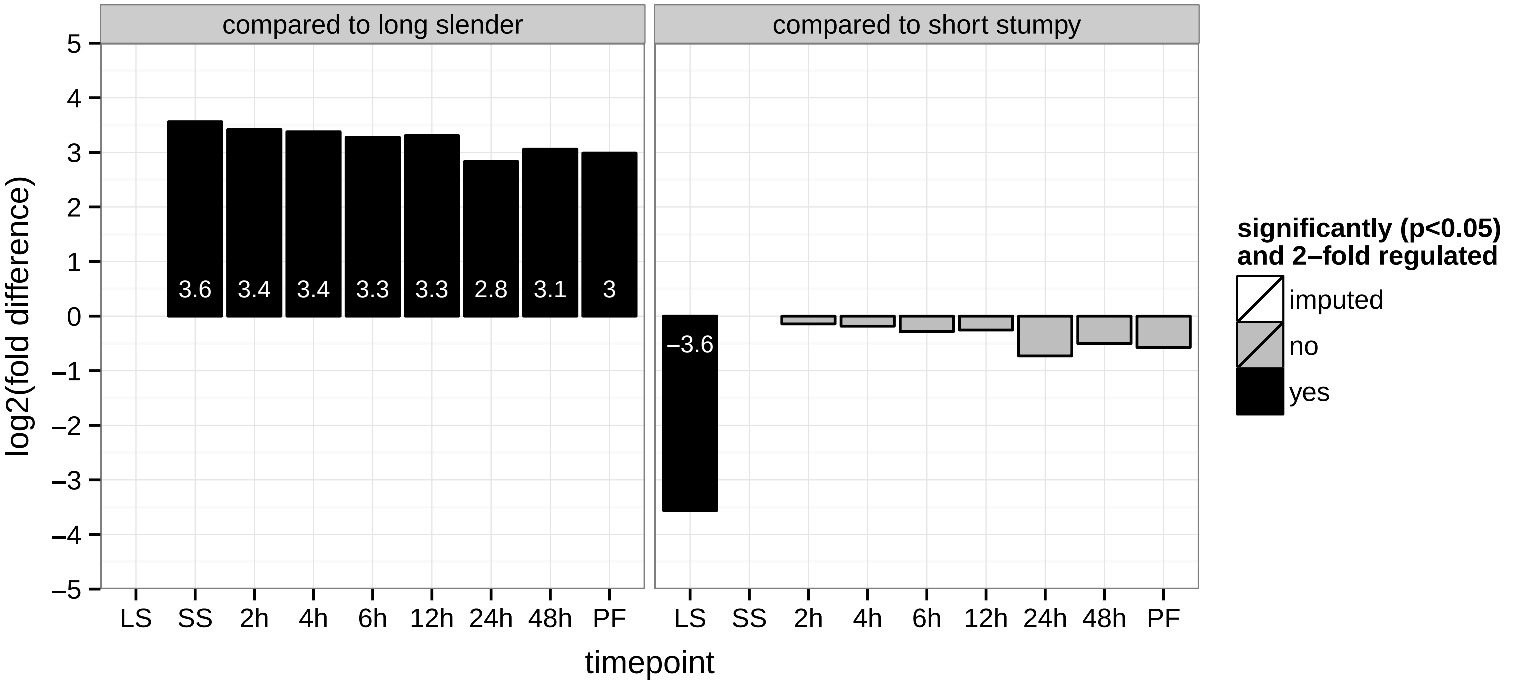
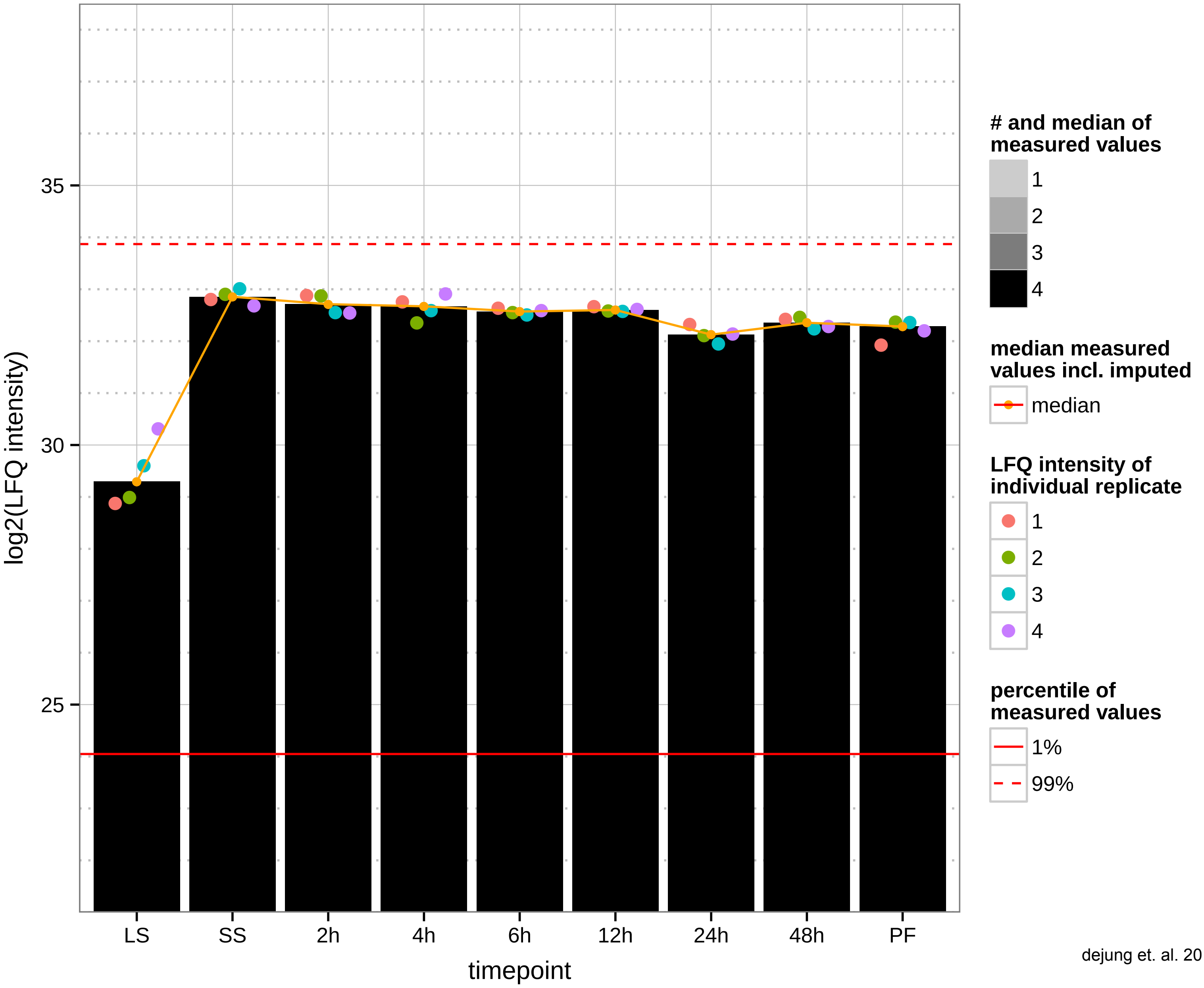
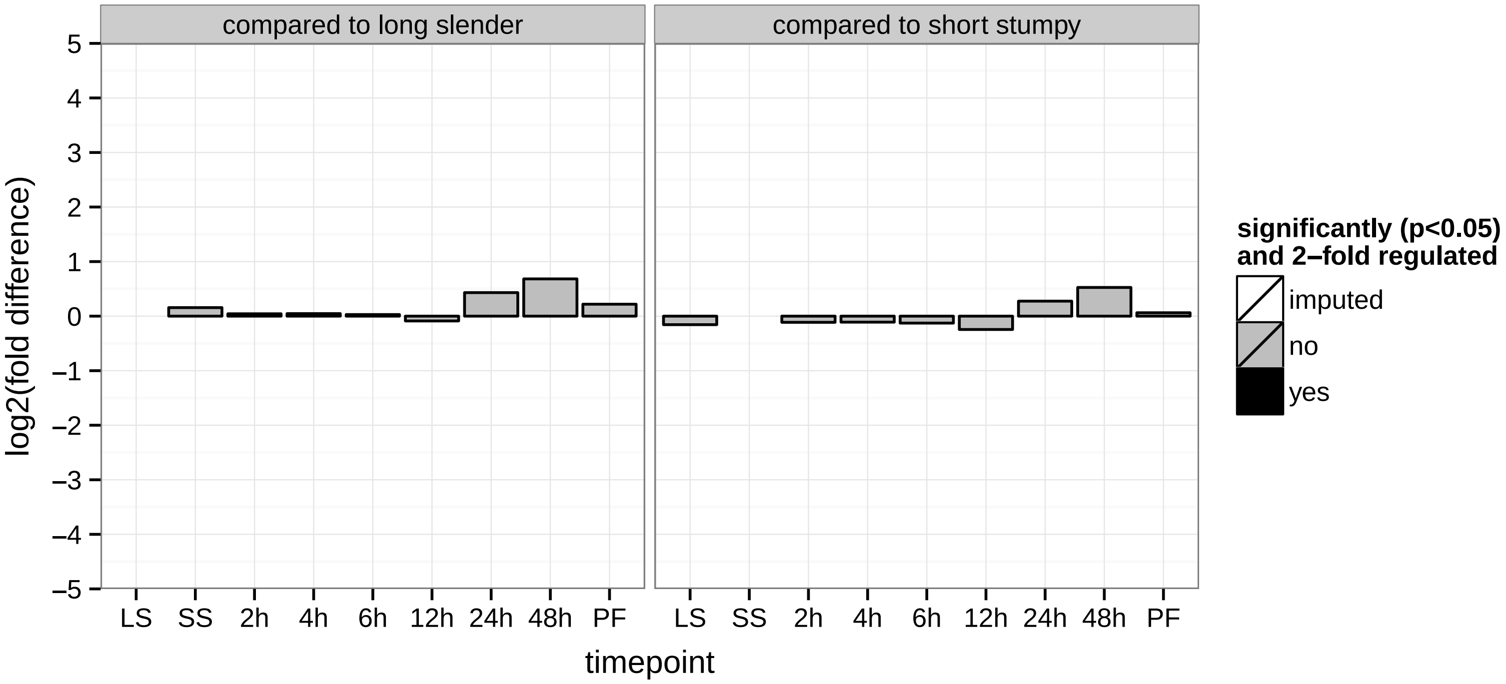
2–amino–3–ketobutyrate coenzyme A ligase, putative, glycine acetyltransferase
Tb927.8.6060
AGOF: glycine C–acetyltransferase activity, pyridoxal phosphate binding, transferase activity, transferring nitrogenous groups
AGOC: mitochondrion
AGOP: biosynthetic process, threonine catabolic process
PGOF: glycine C–acetyltransferase activity, pyridoxal phosphate binding, transferase activity
PGOC: null
PGOP: biosynthetic process

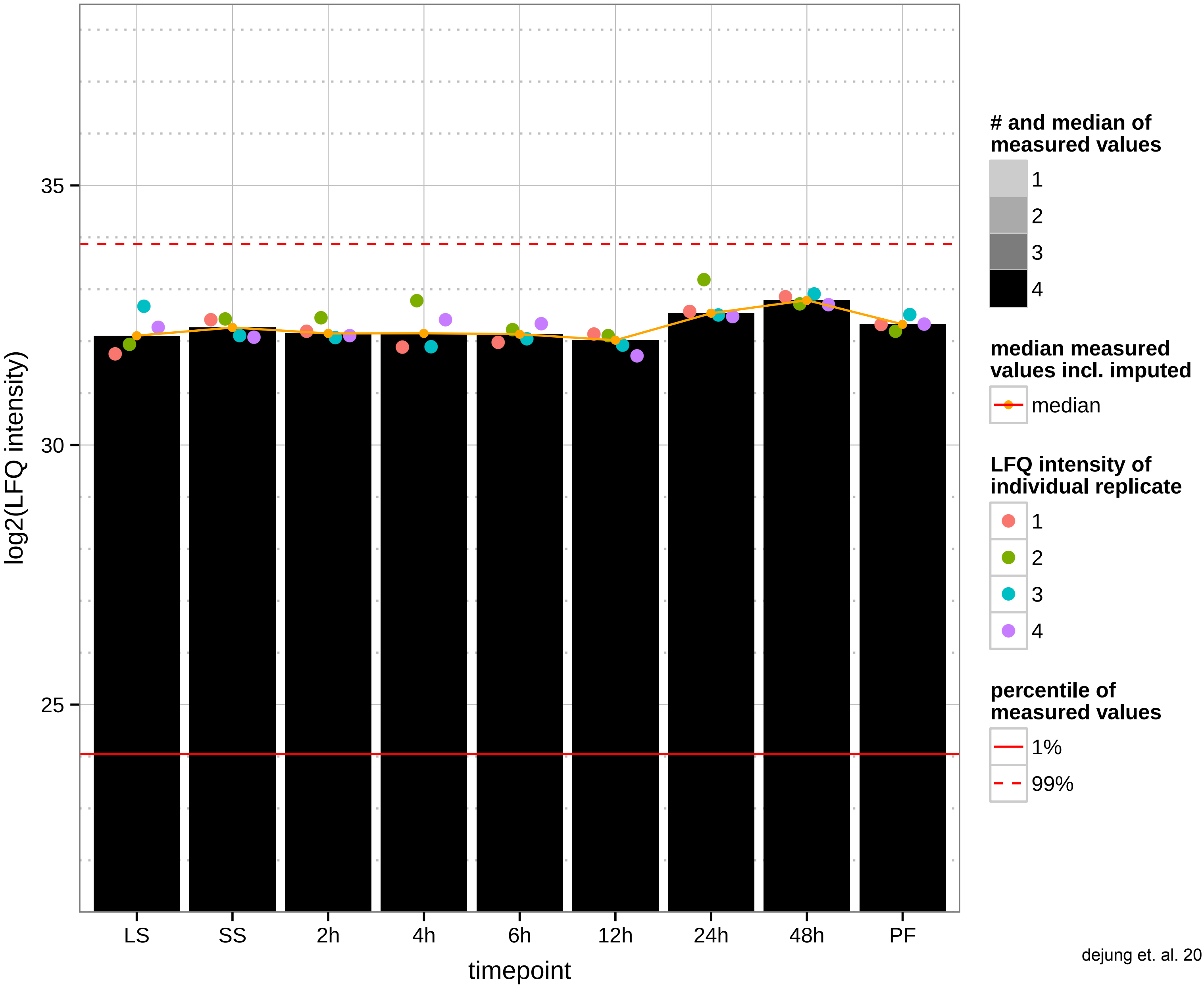




dejung et. al. 2015

40S ribosomal protein S8, putative
Tb927.8.6160;Tb927.8.6150
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome, null
PGOC: intracellular, ribosome, null
PGOP: translation, null





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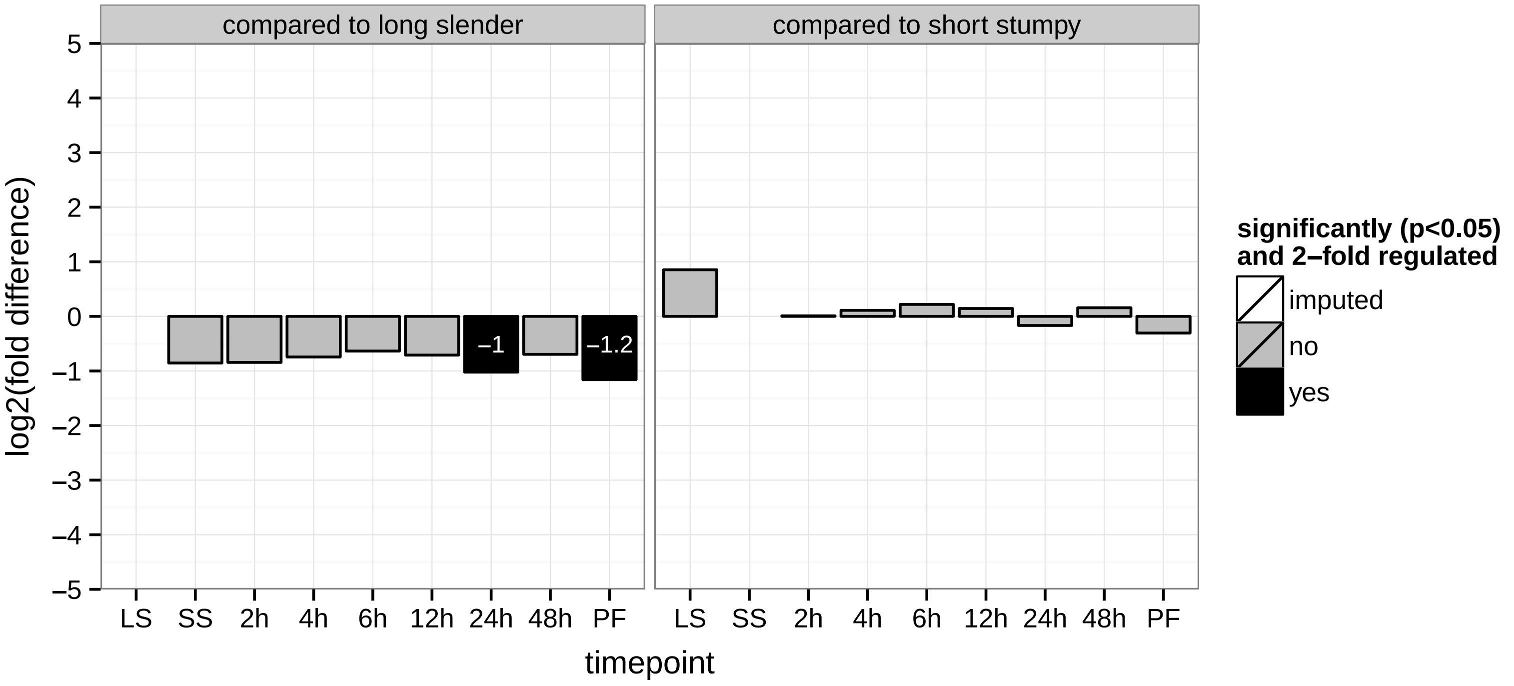
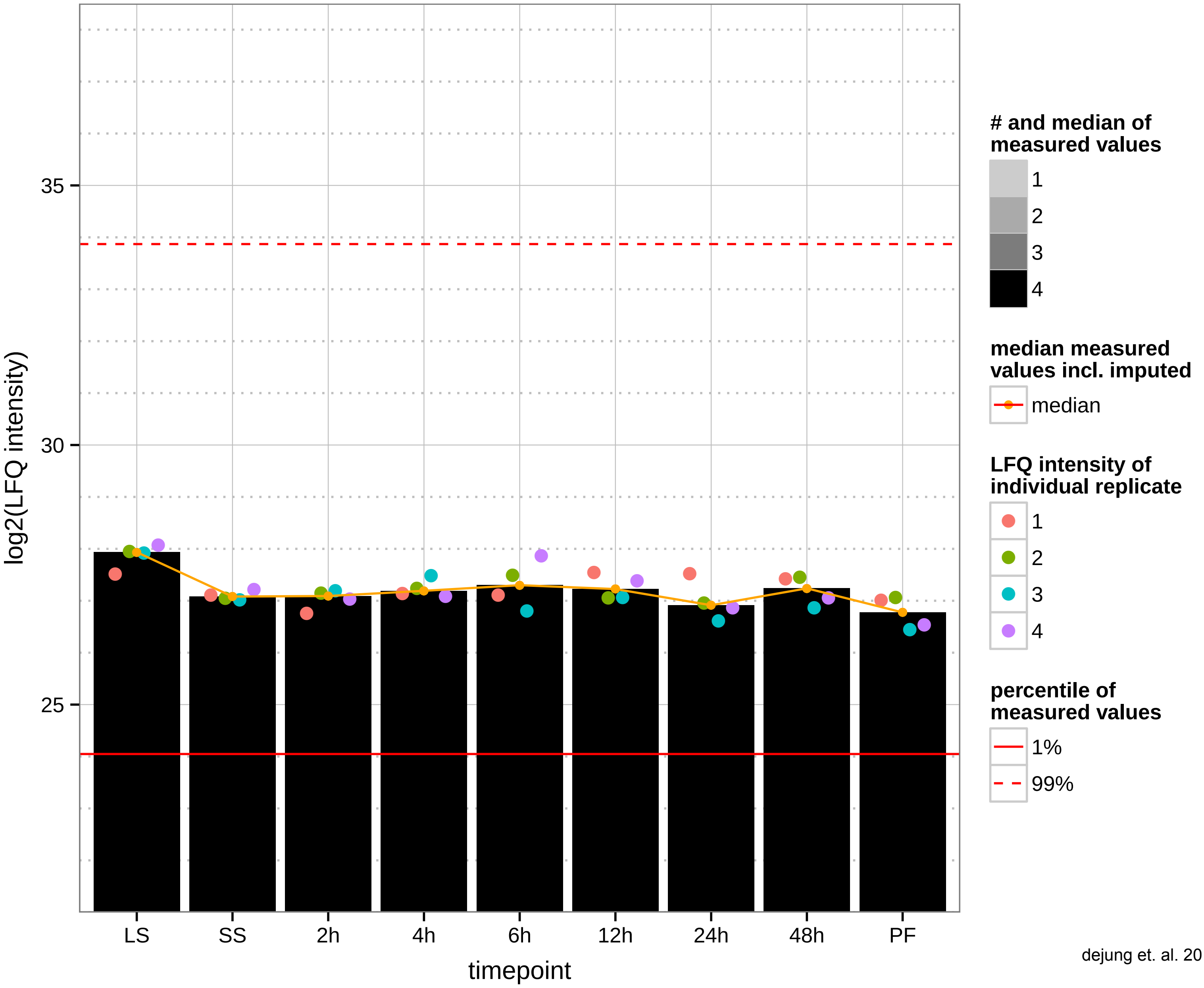
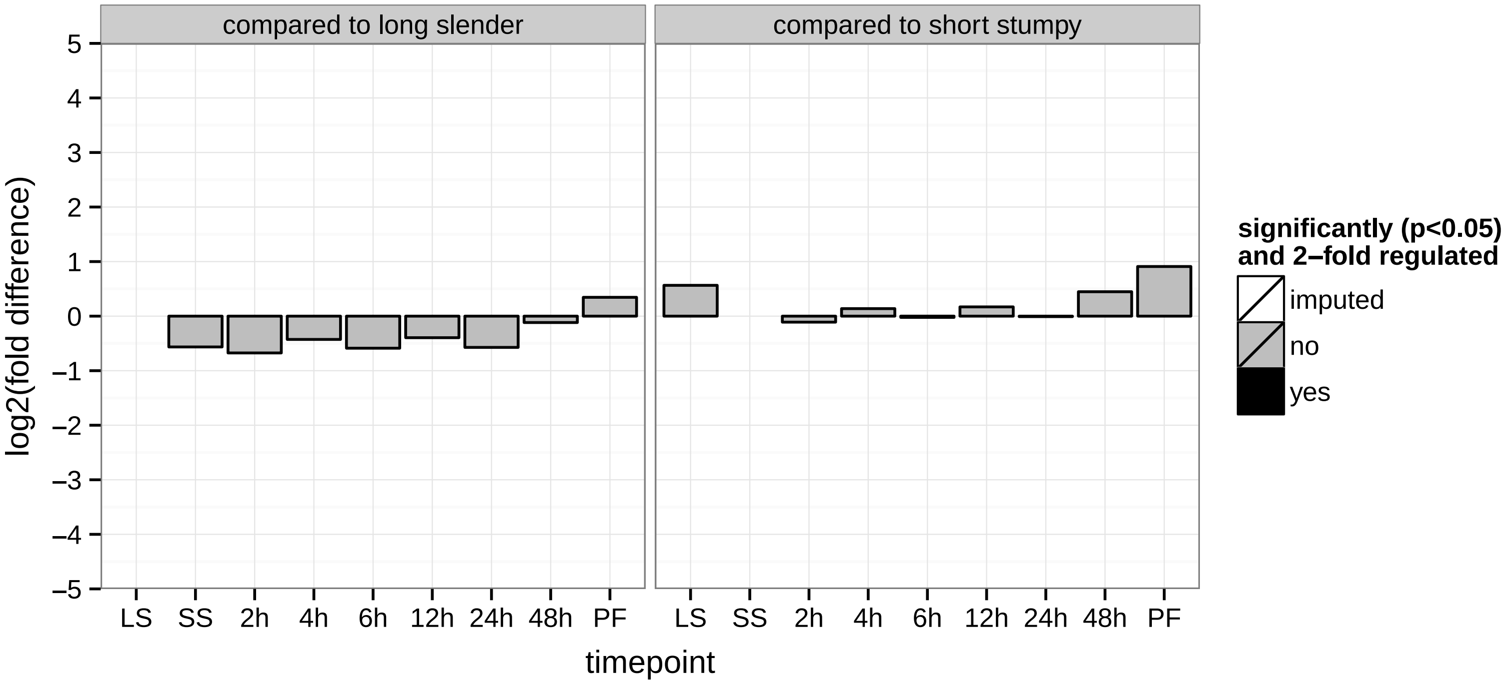
hypothetical protein, conserved
Tb927.8.6230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

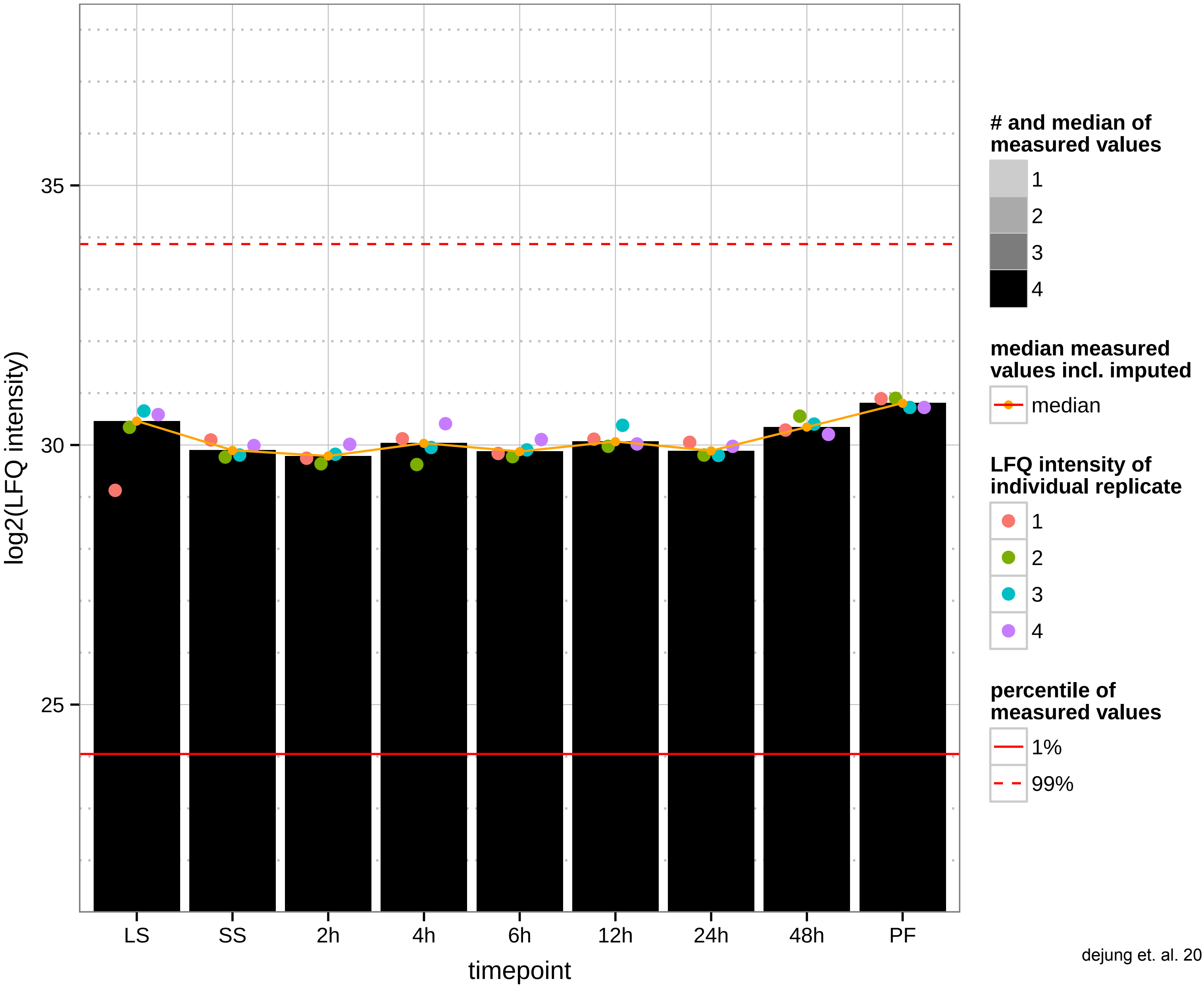




dejung et. al. 2015

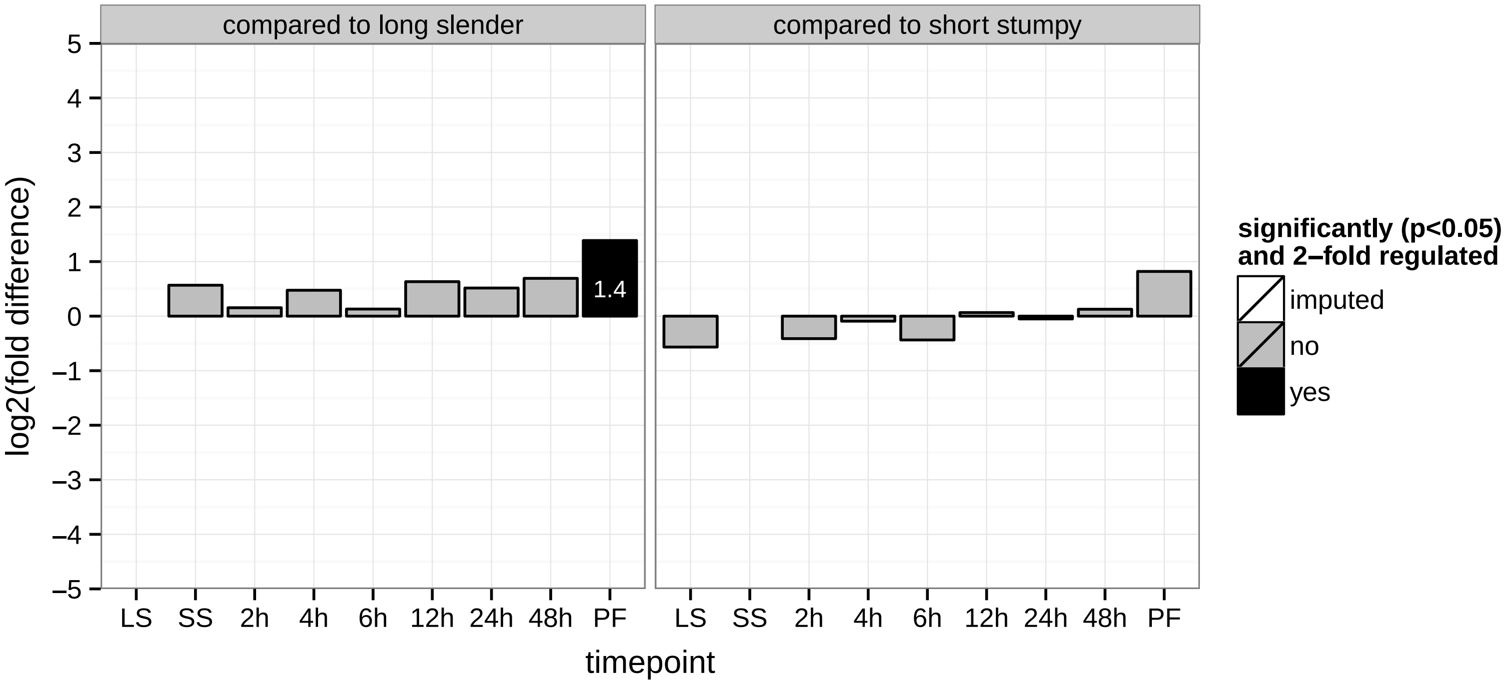
STOP axonemal protein
Tb927.8.6240
AGOF: microtubule binding
AGOC: cytoskeleton
AGOP: microtubule anchoring
PGOF: null
PGOC: null
PGOP: null

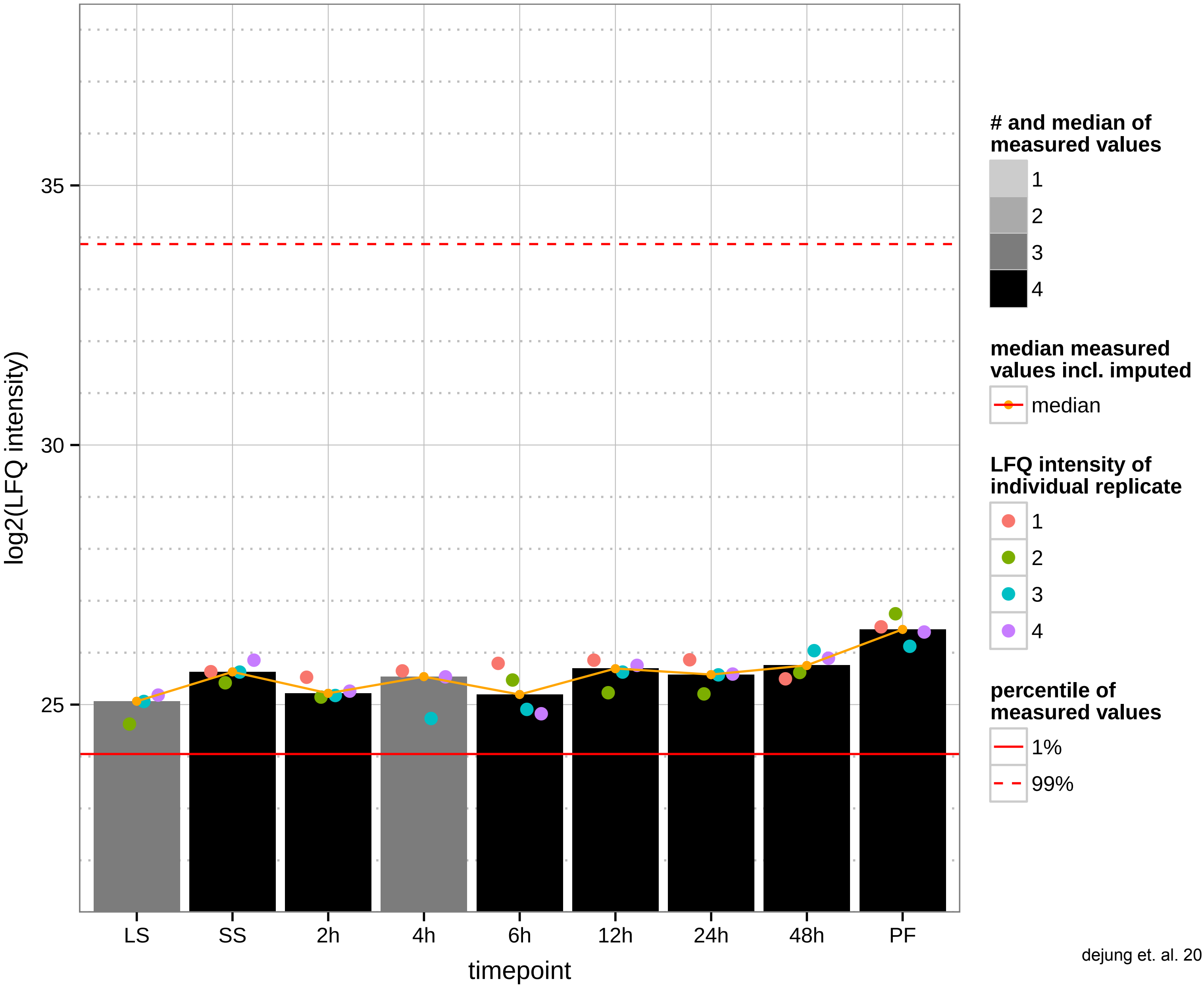




dejung et. al. 2015

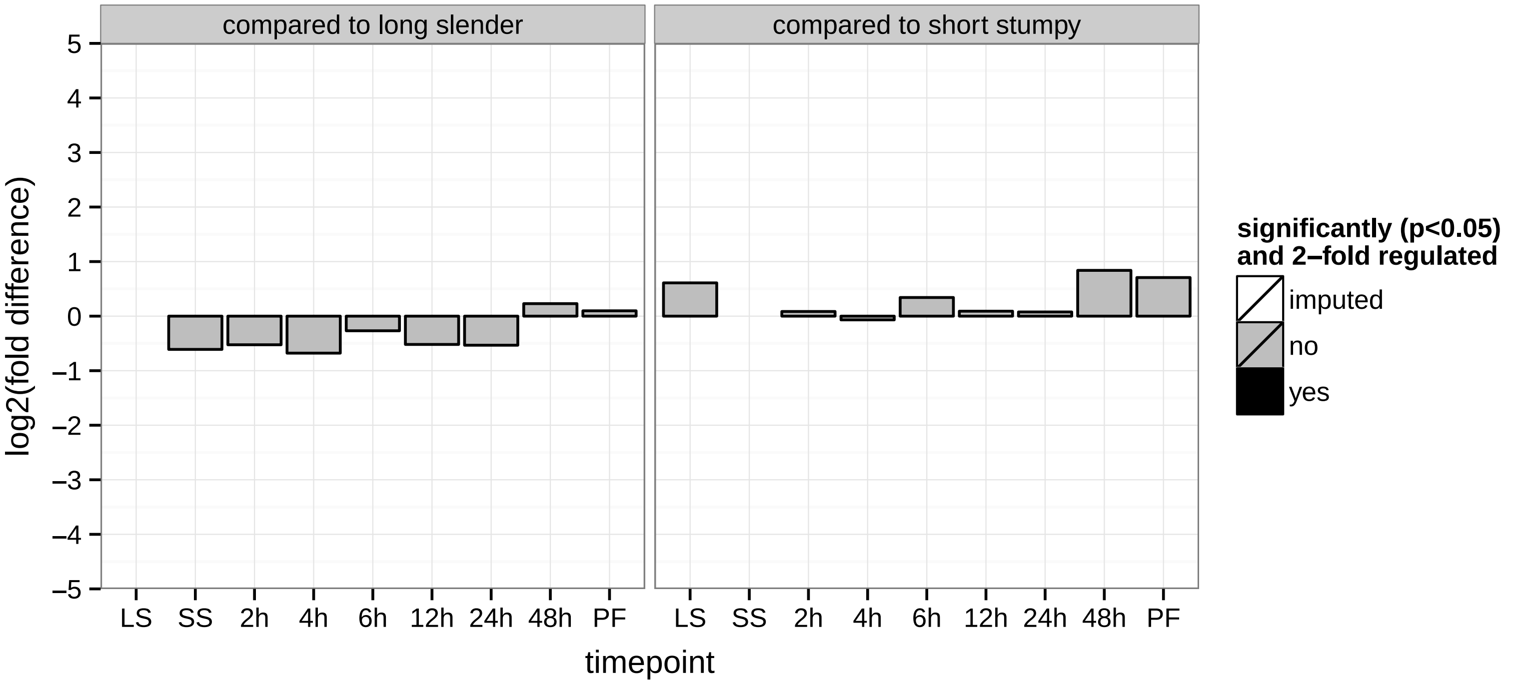
hypothetical protein, conserved
Tb927.8.6250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

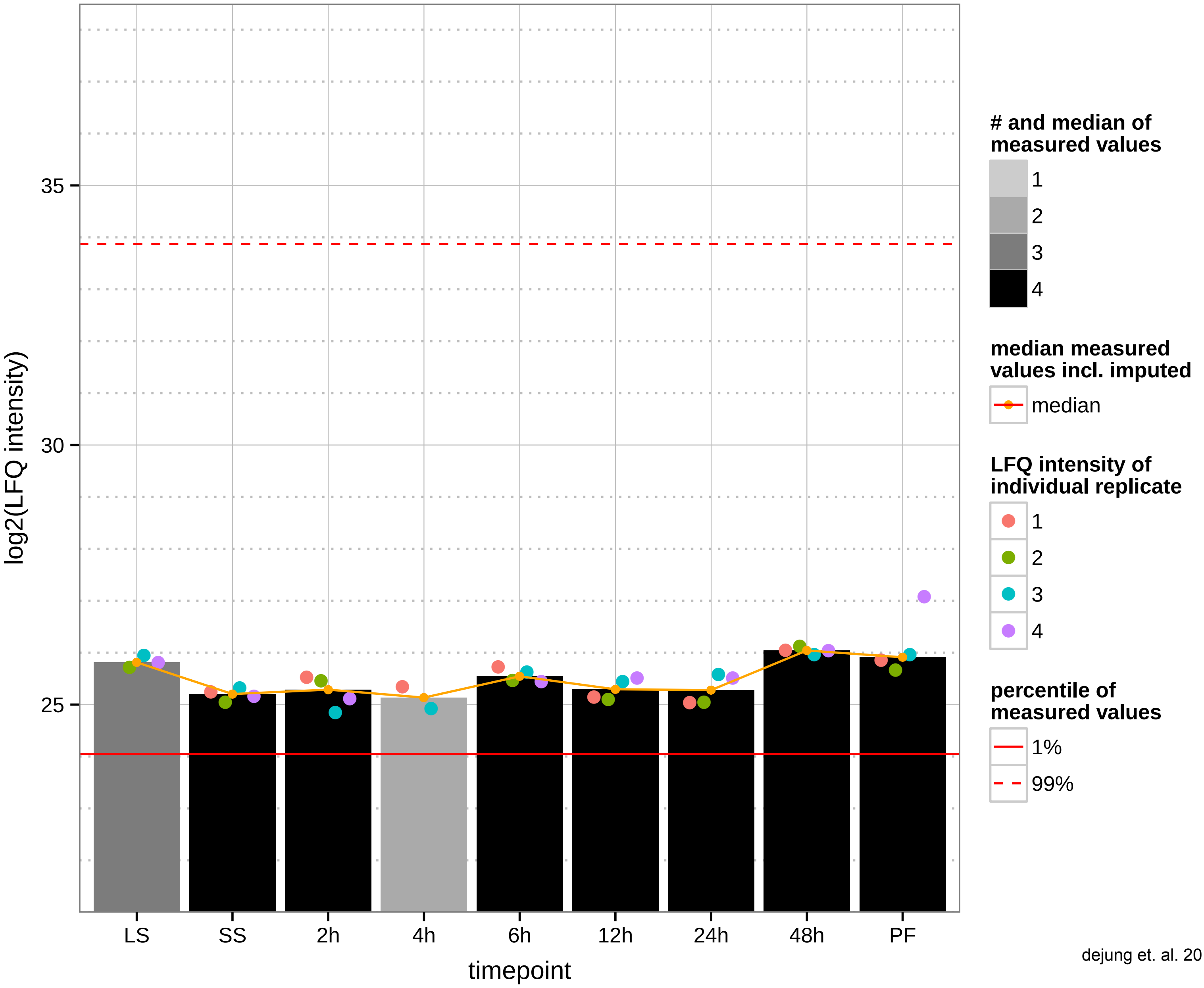




dejung et. al. 2015

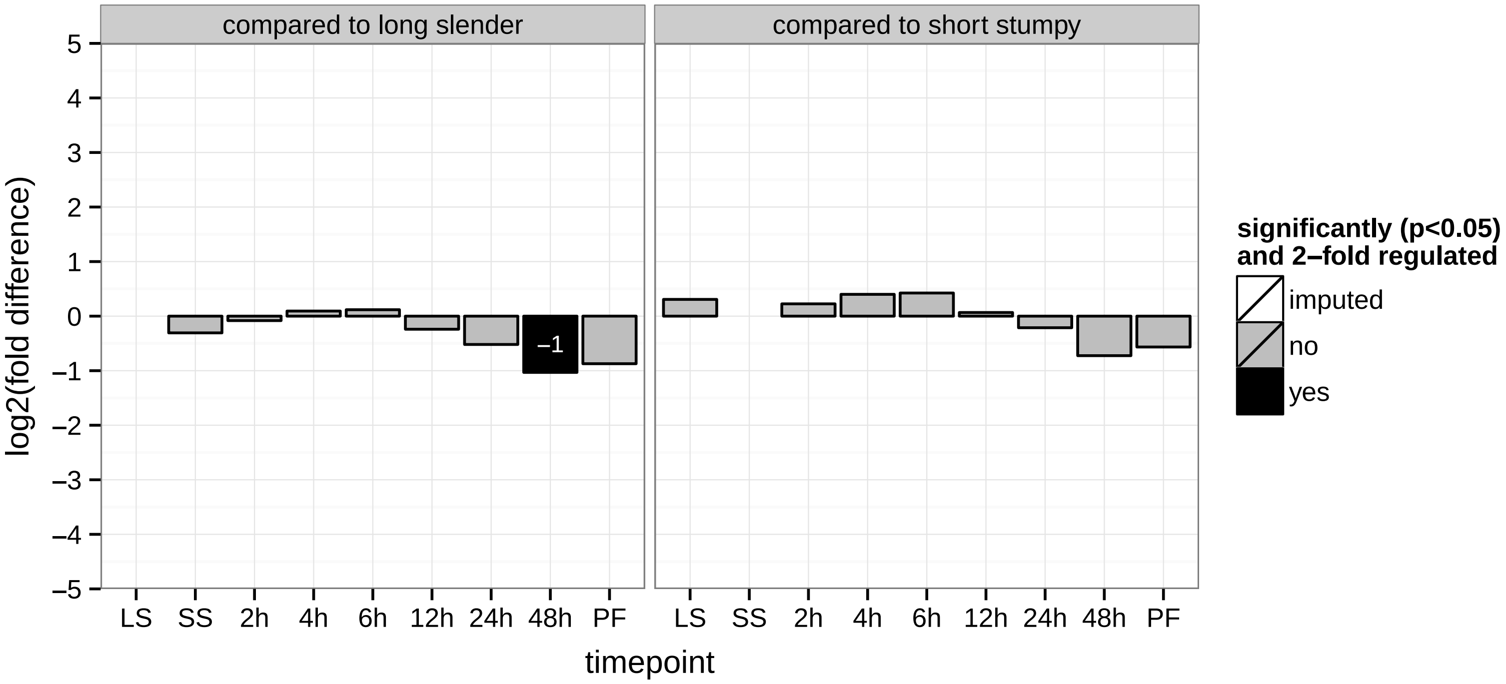
hypothetical protein, conserved
Tb927.8.6270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

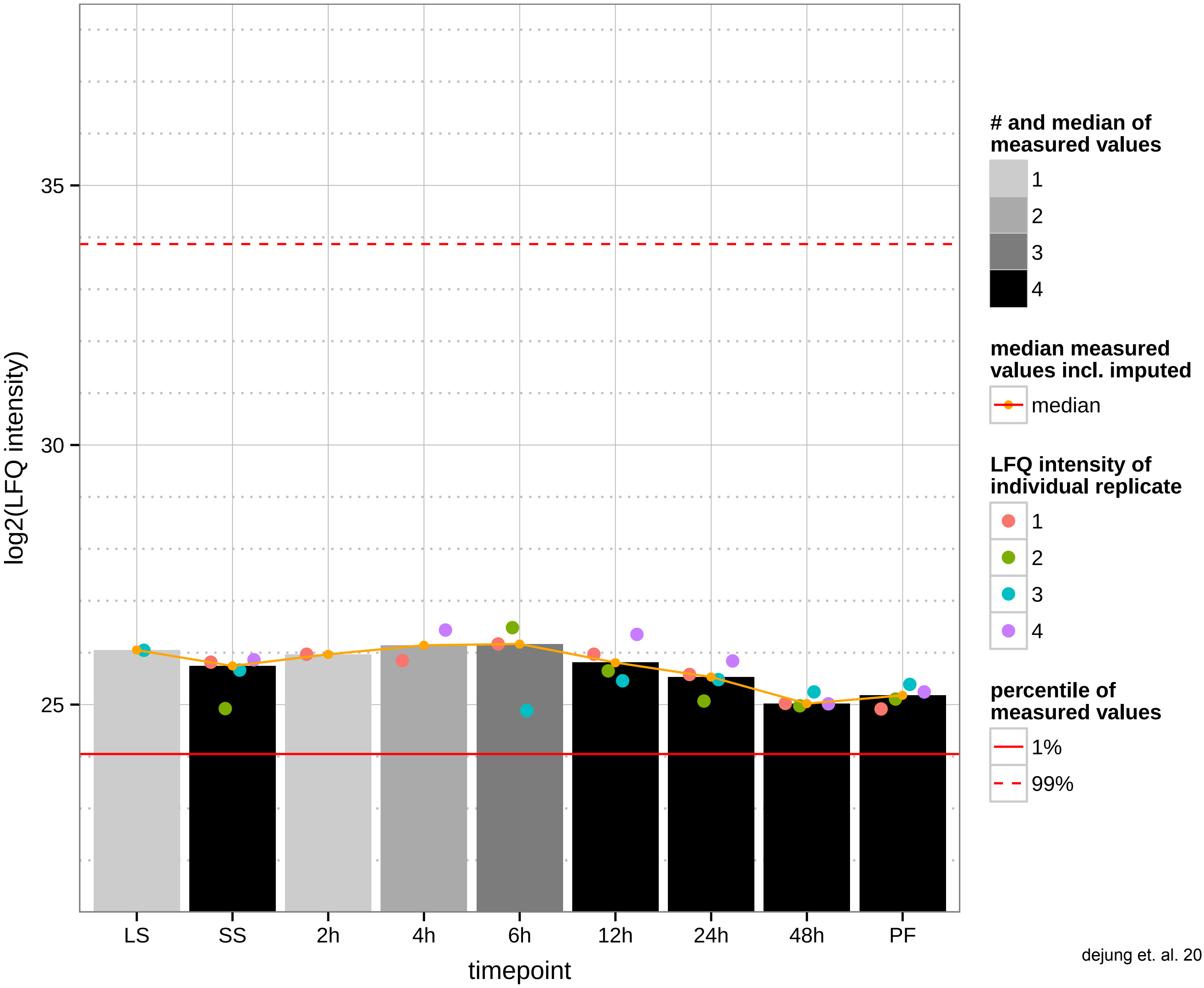




dejung et. al. 2015

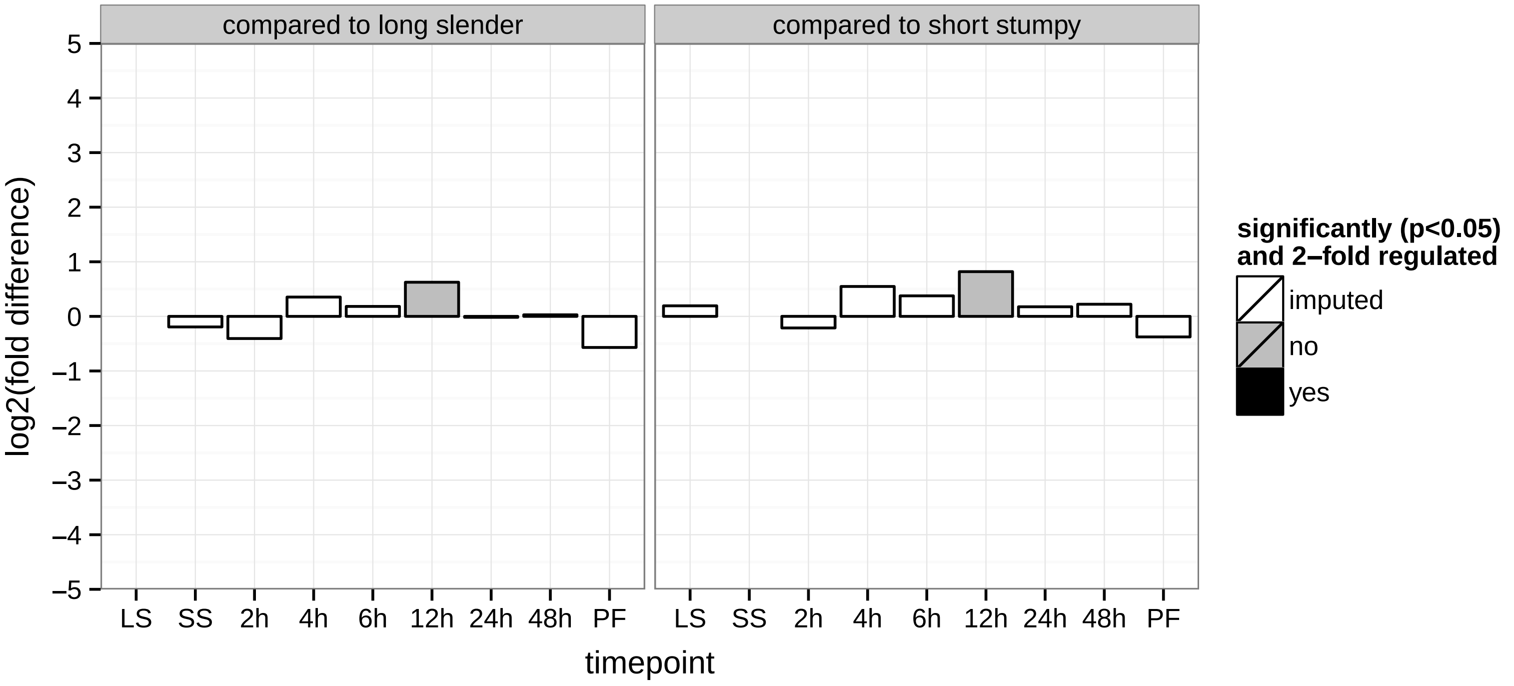
hypothetical protein, conserved
Tb927.8.6290
AGOF: ATP binding, inositol tetrakisphosphate 1–kinase activity, magnesium ion binding
AGOC: intracellular
AGOP: inositol trisphosphate metabolic process
PGOF: null
PGOC: null
PGOP: null

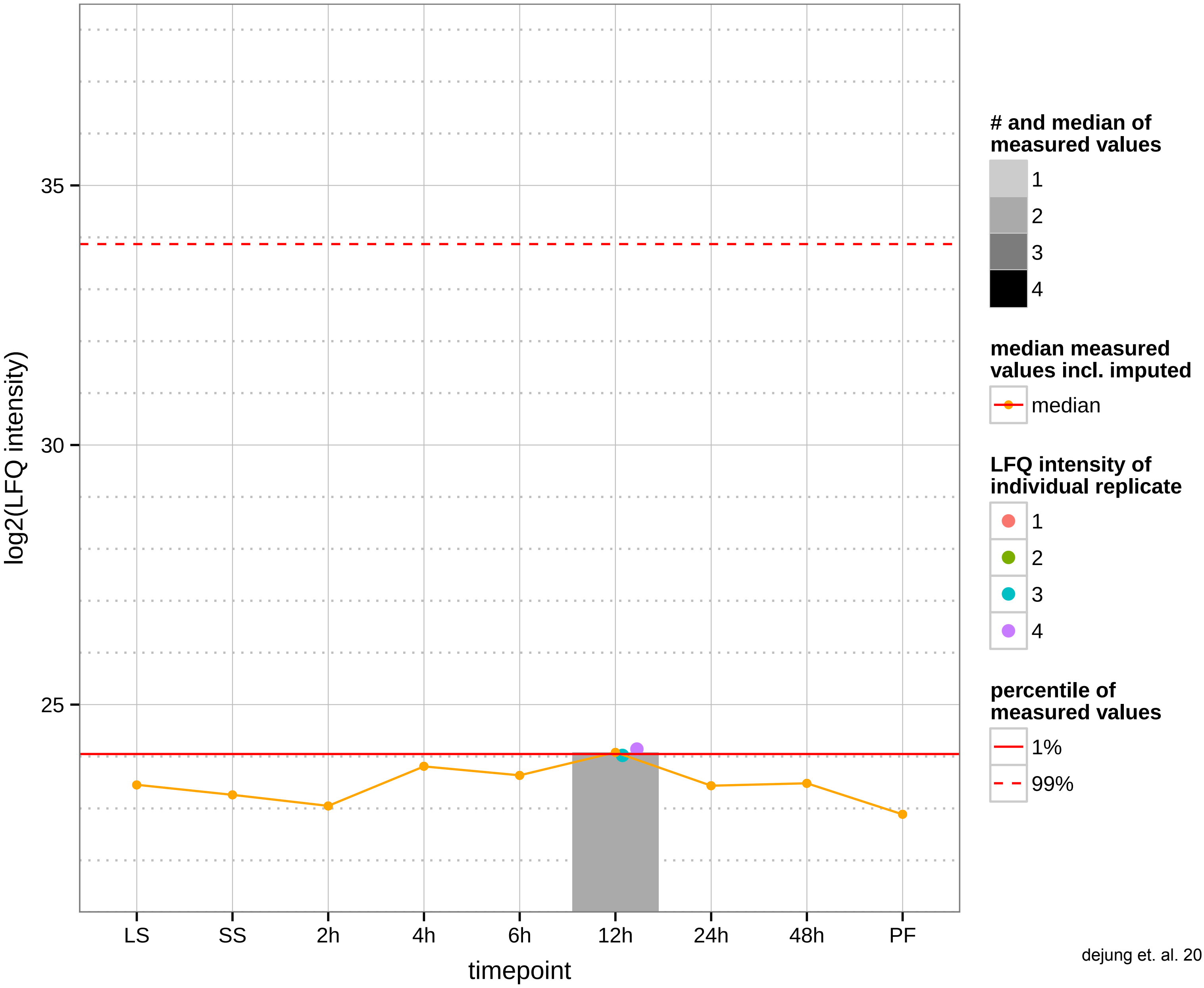




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.6360
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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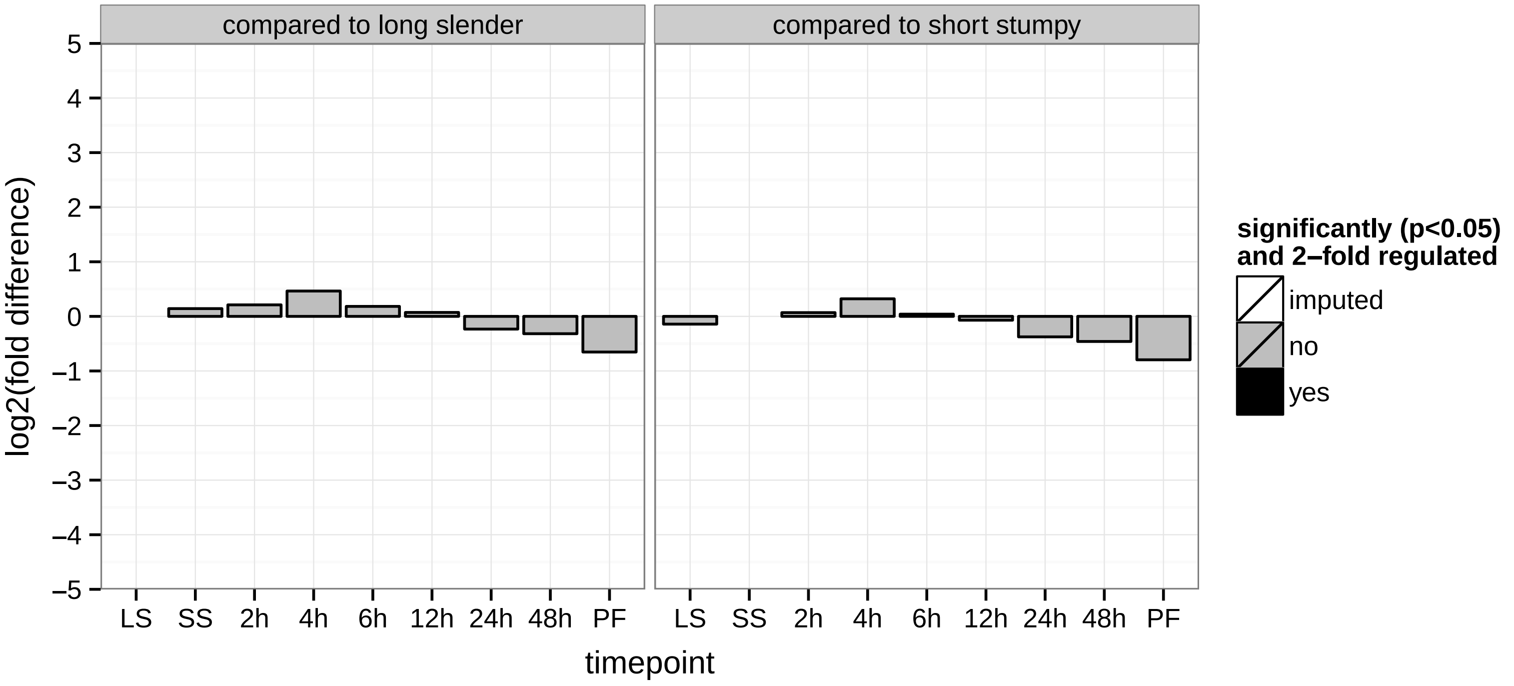
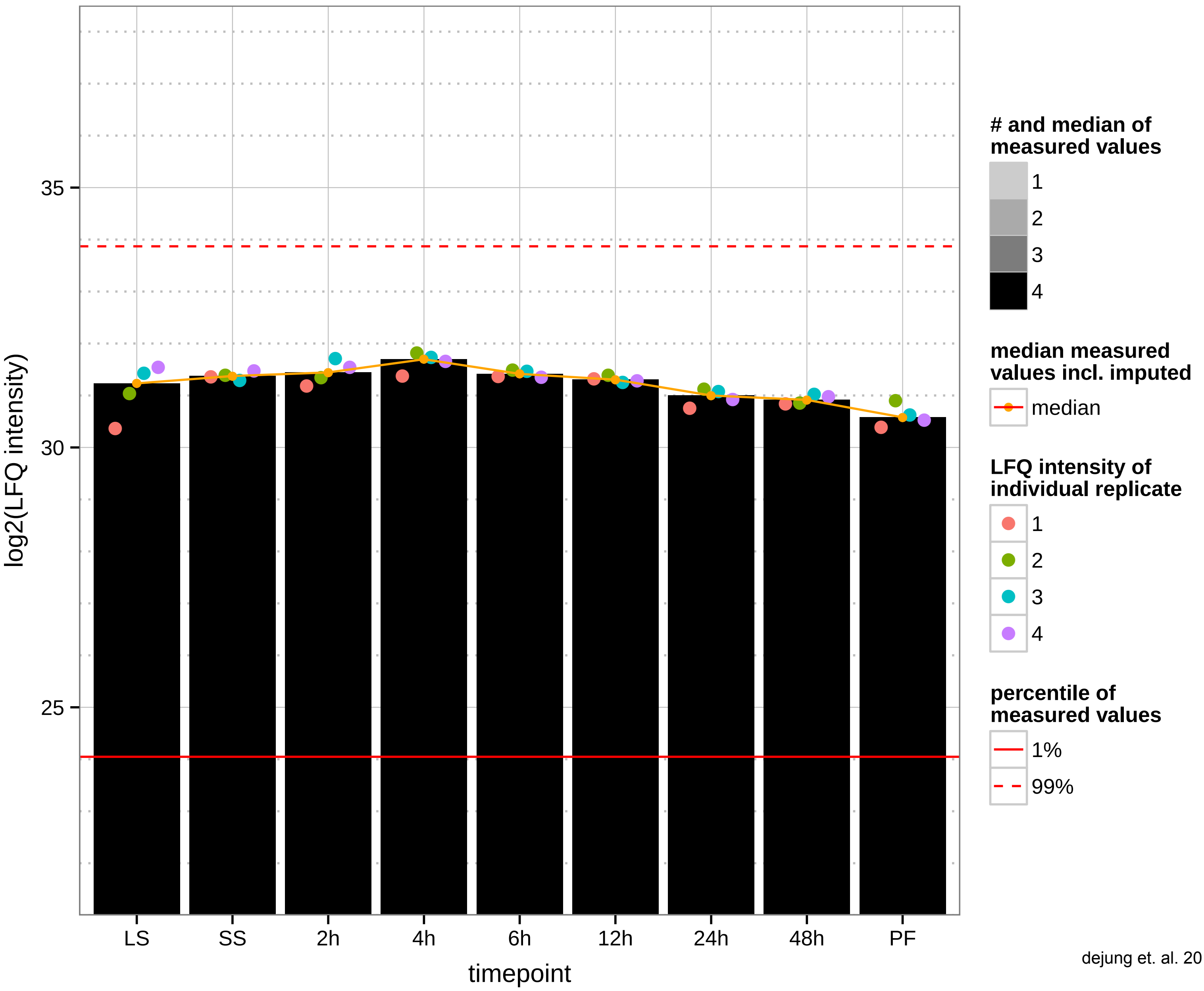
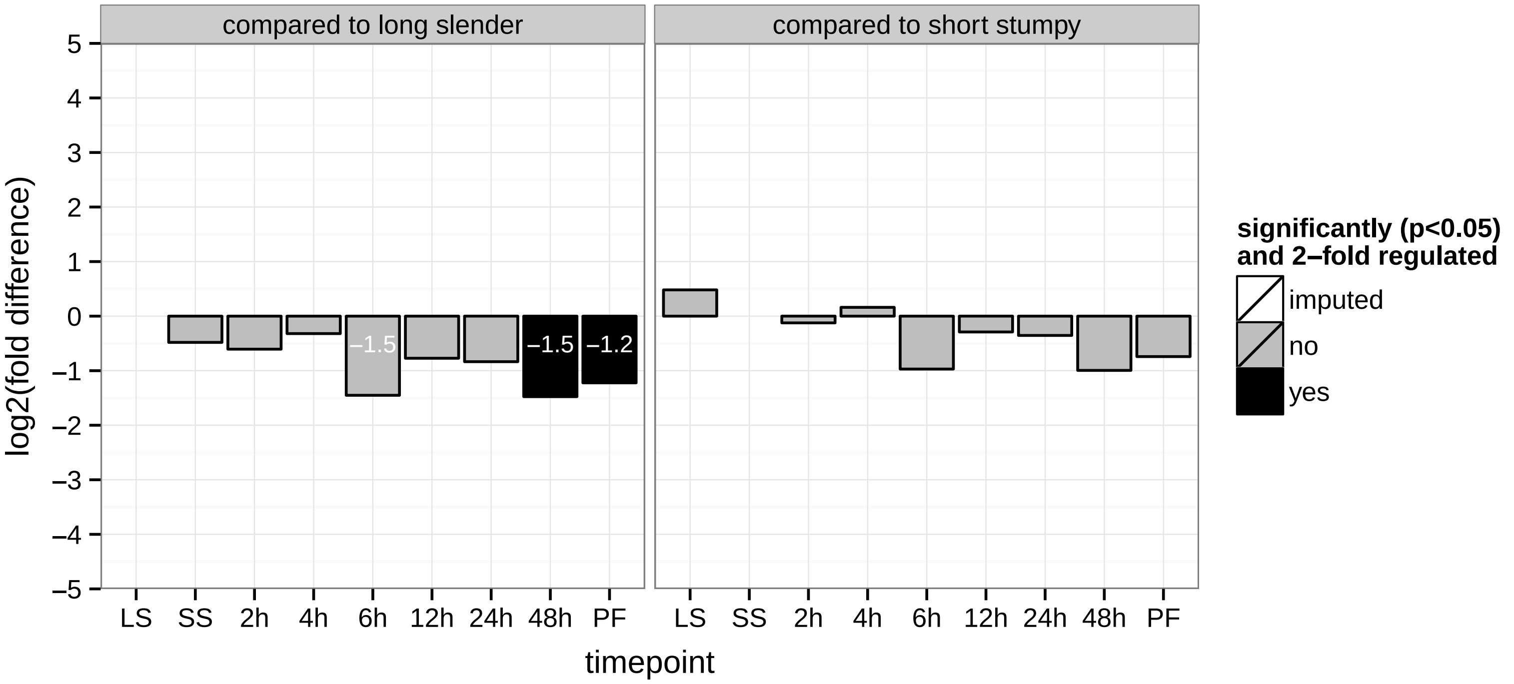
lysophospholipase, putative, alpha/beta hydrolase, putative (TbLysoPLA)
Tb927.8.6390
AGOF: hydrolase activity, acting on ester bonds
AGOC: null
AGOP: metabolic process
PGOF: hydrolase activity
PGOC: null
PGOP: null

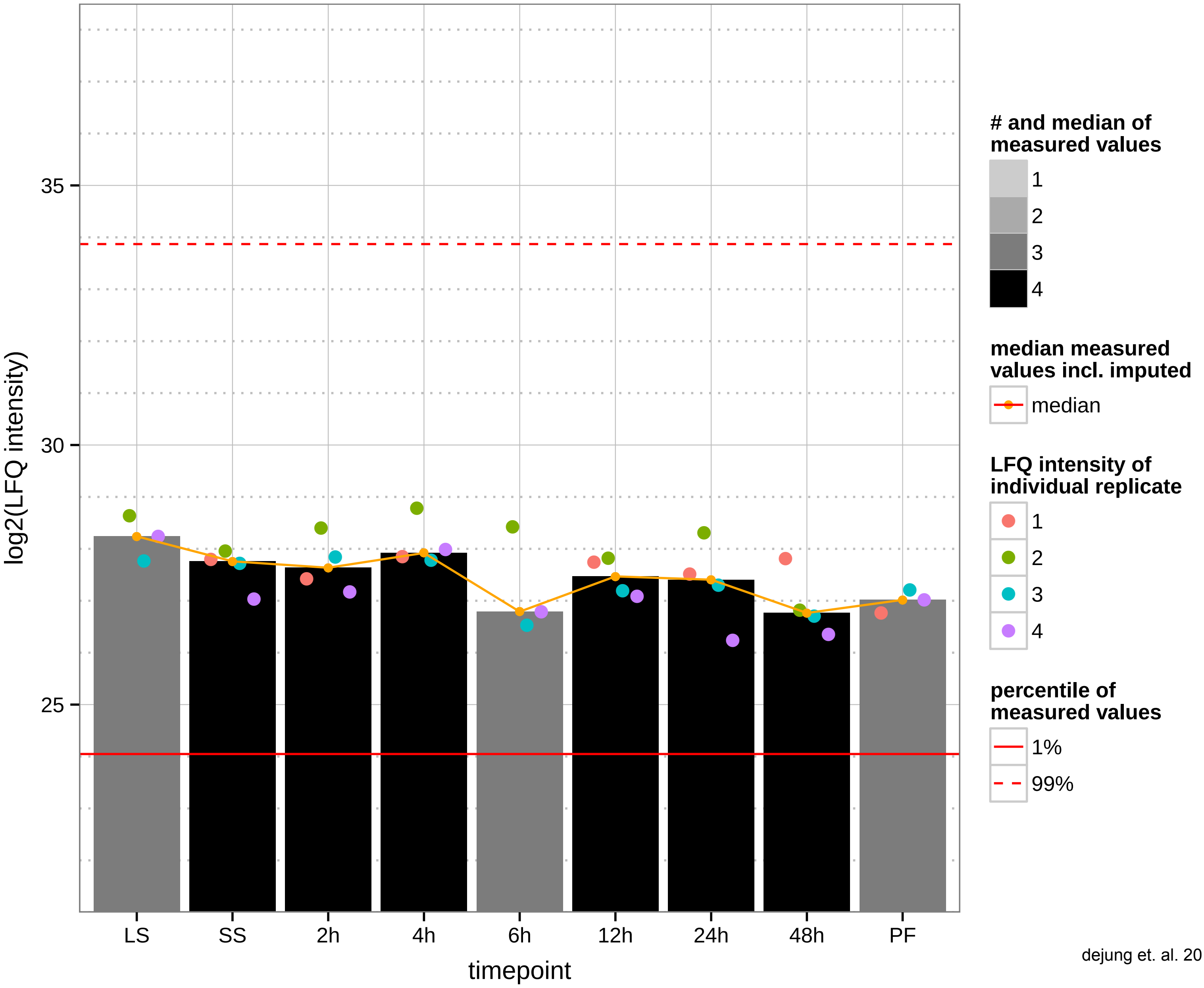




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.6430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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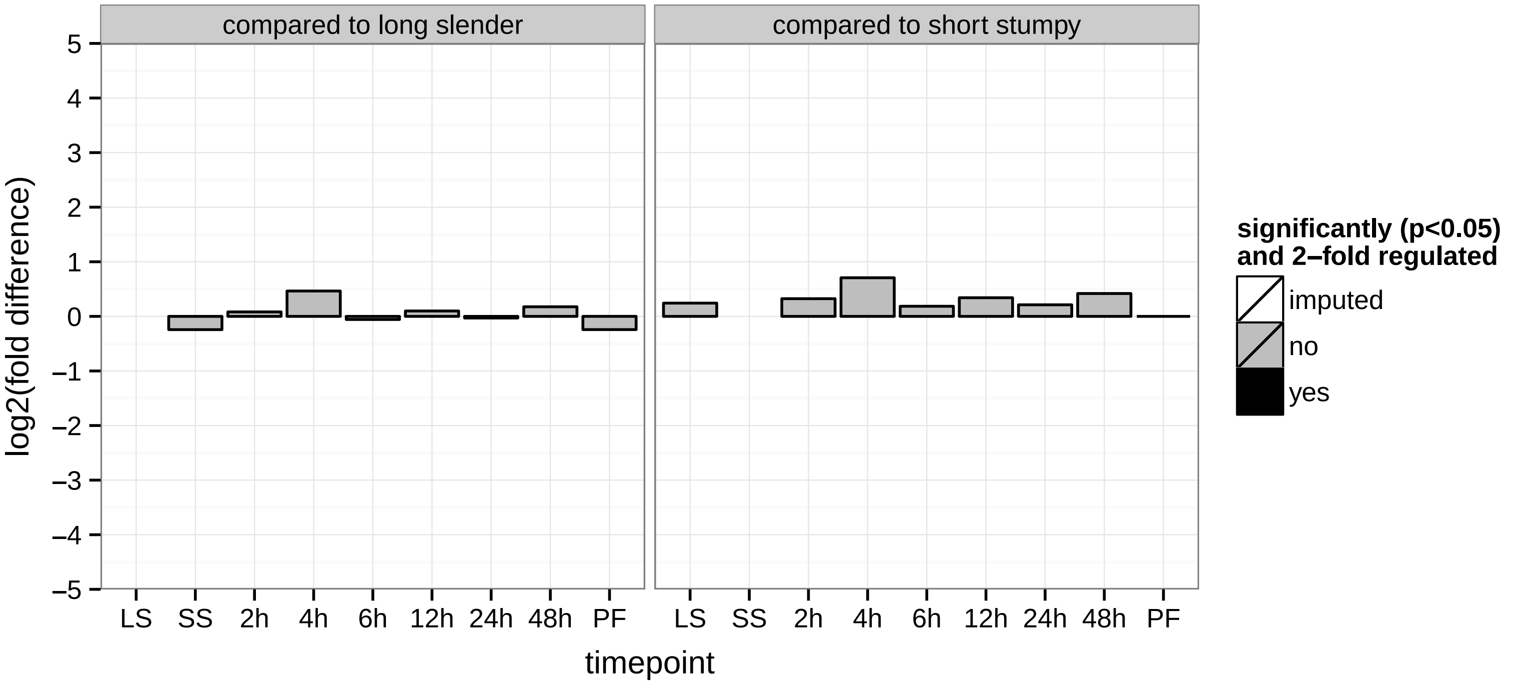
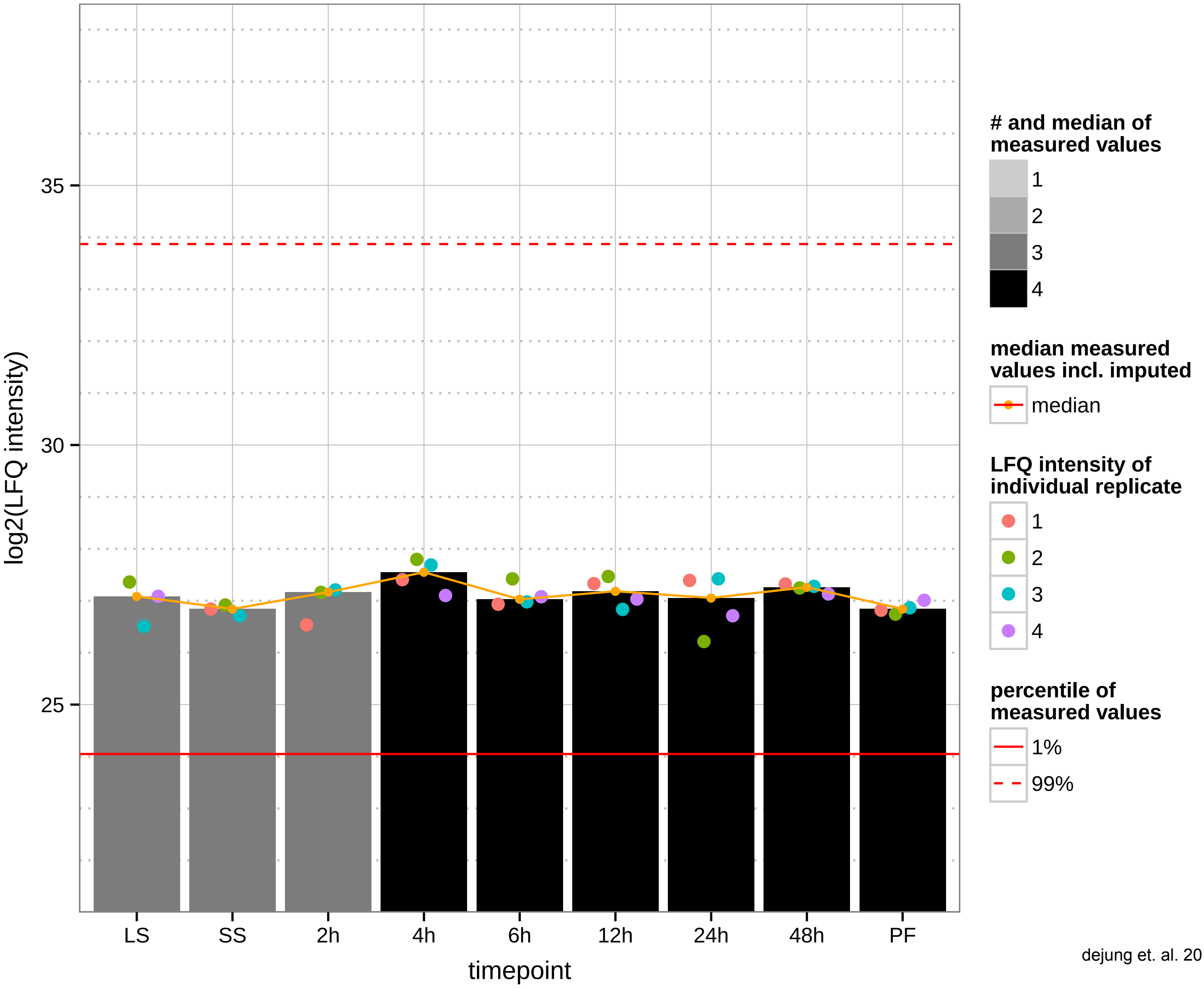
RNA–binding protein, putative (RPB20)
Tb927.8.6440
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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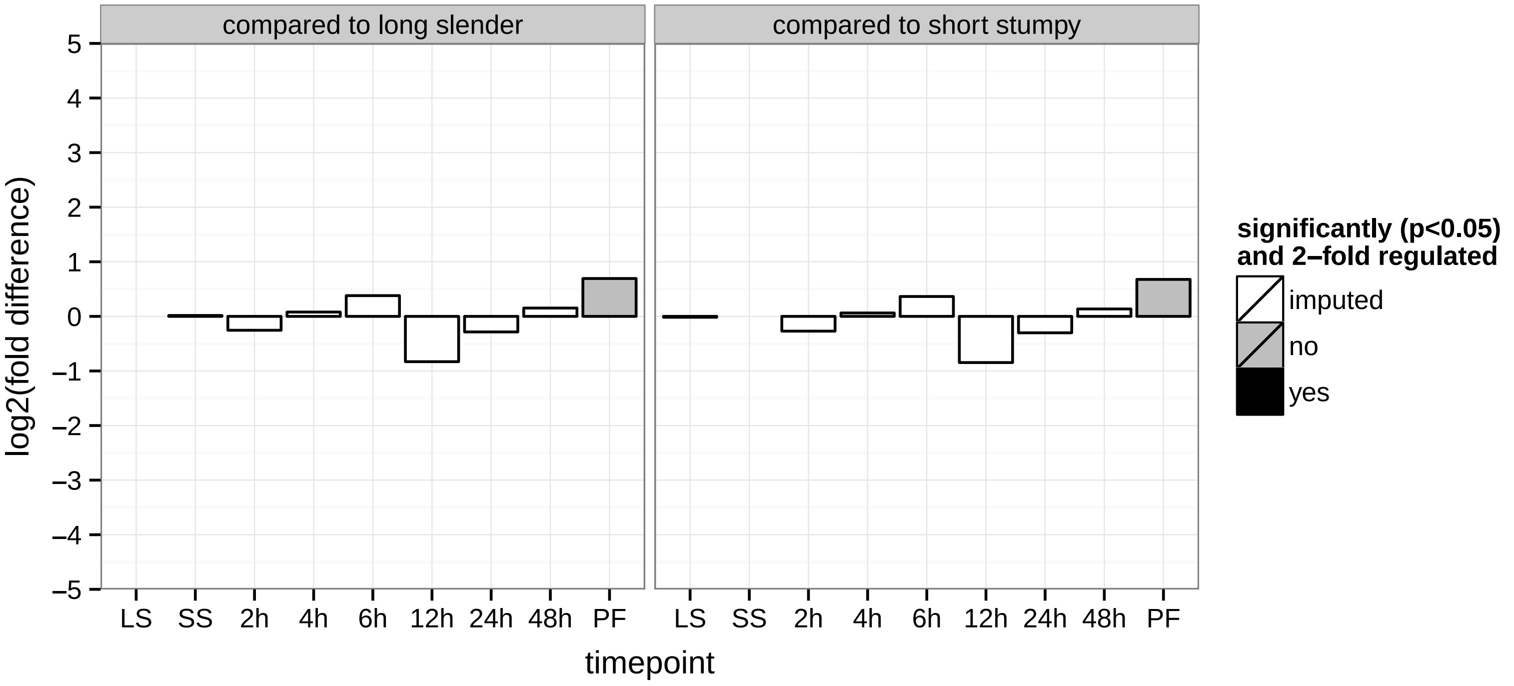
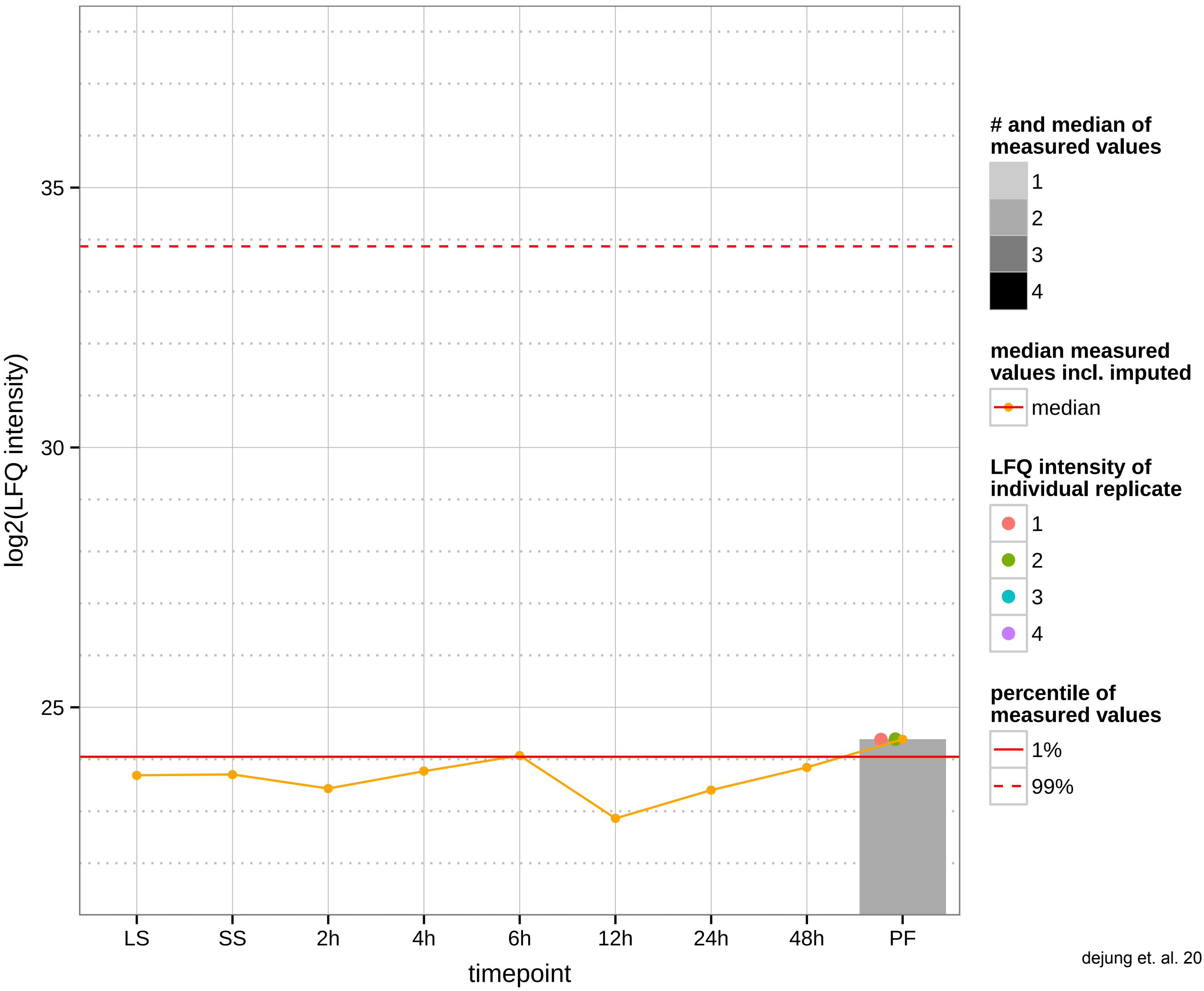
hypothetical protein, conserved
Tb927.8.6530
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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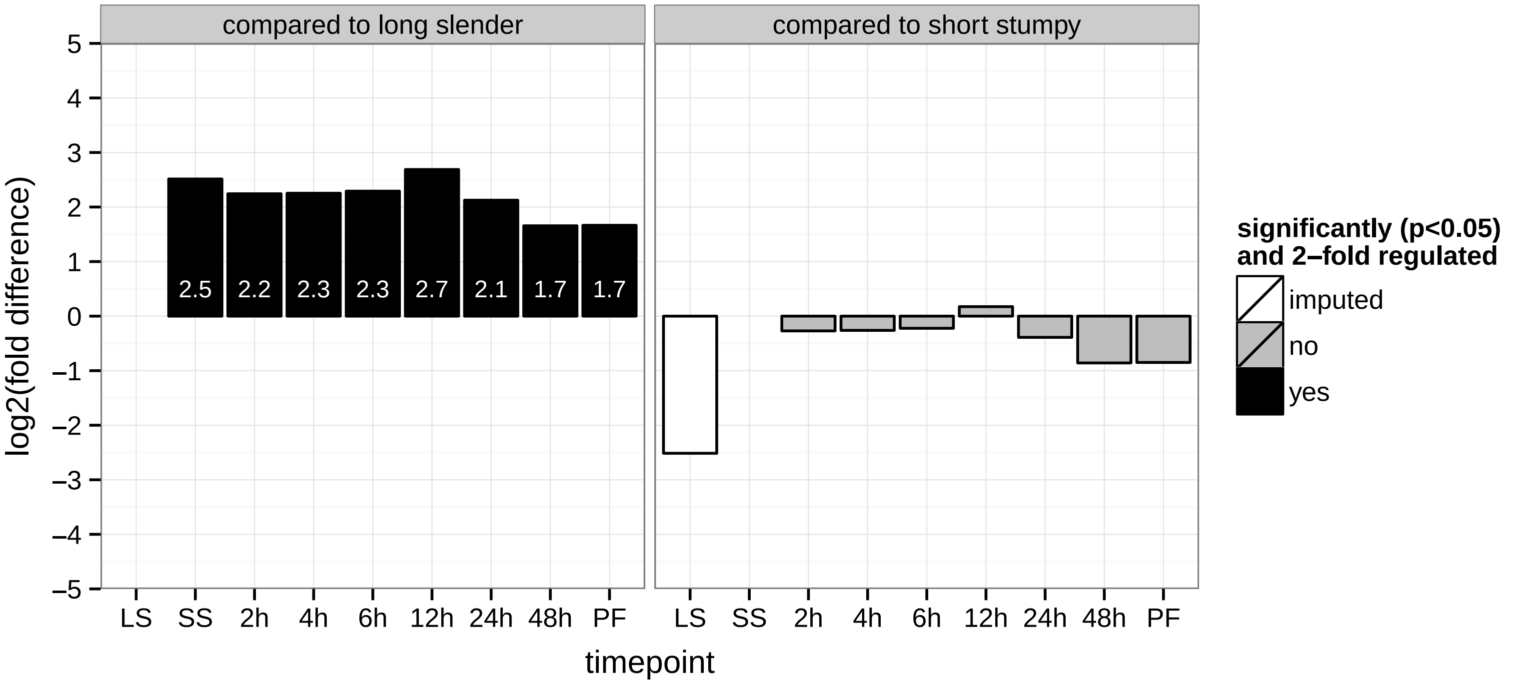
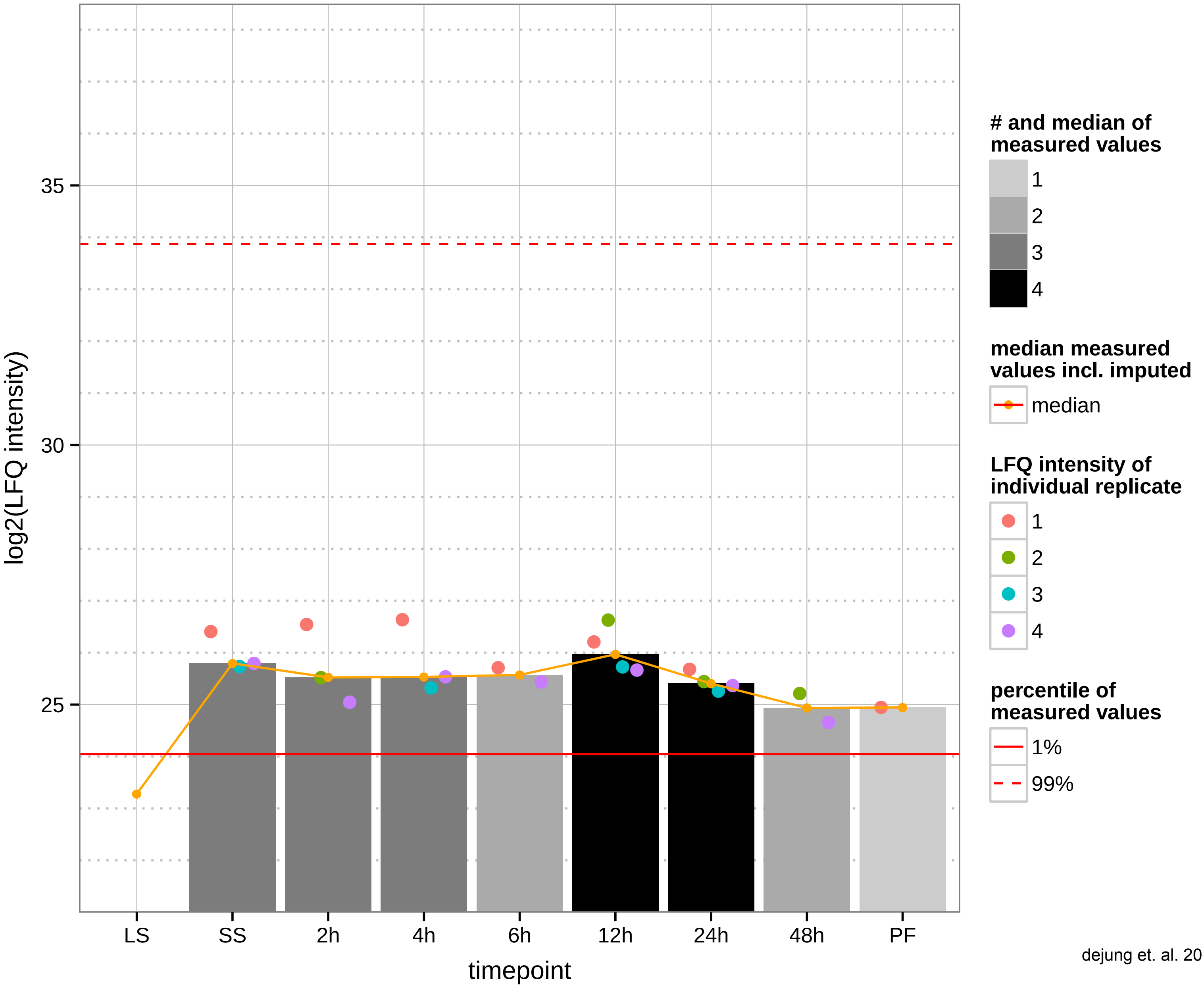
hypothetical protein, conserved
Tb927.8.6600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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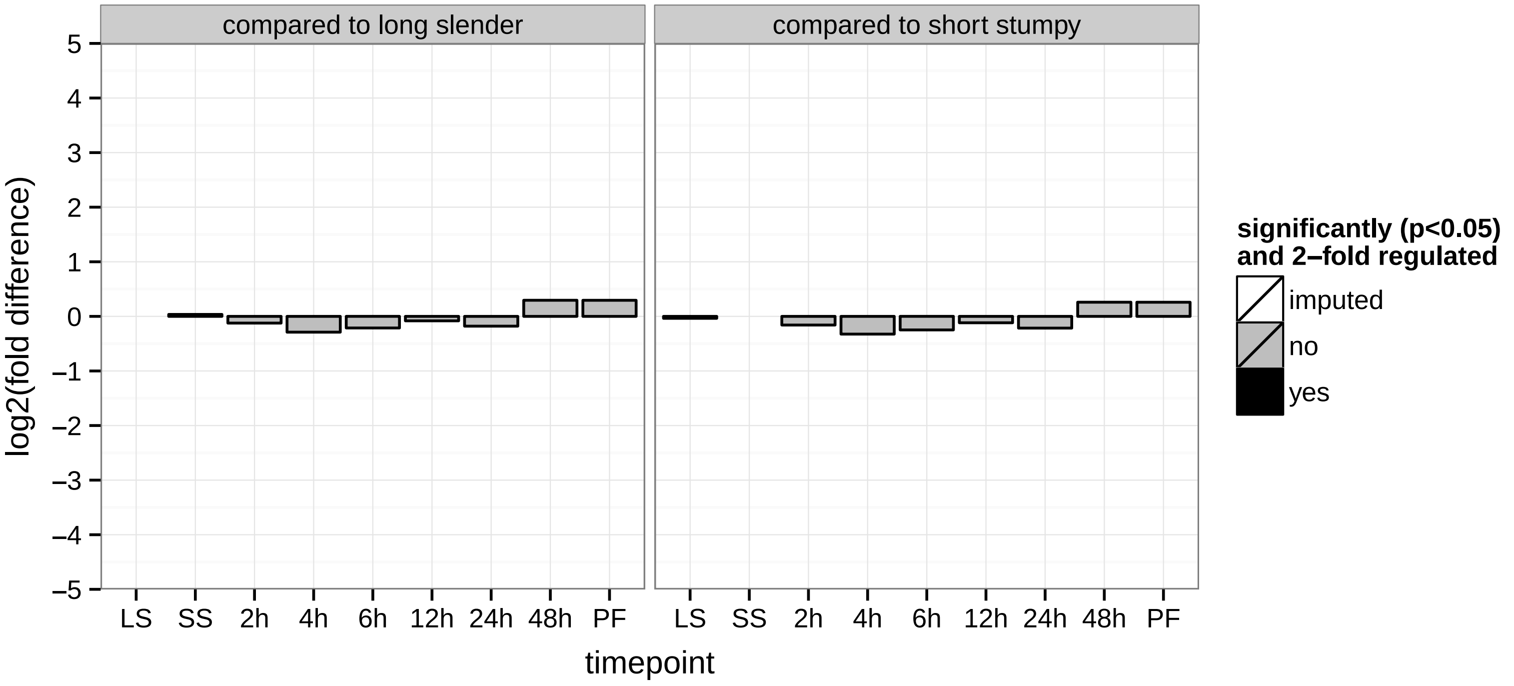
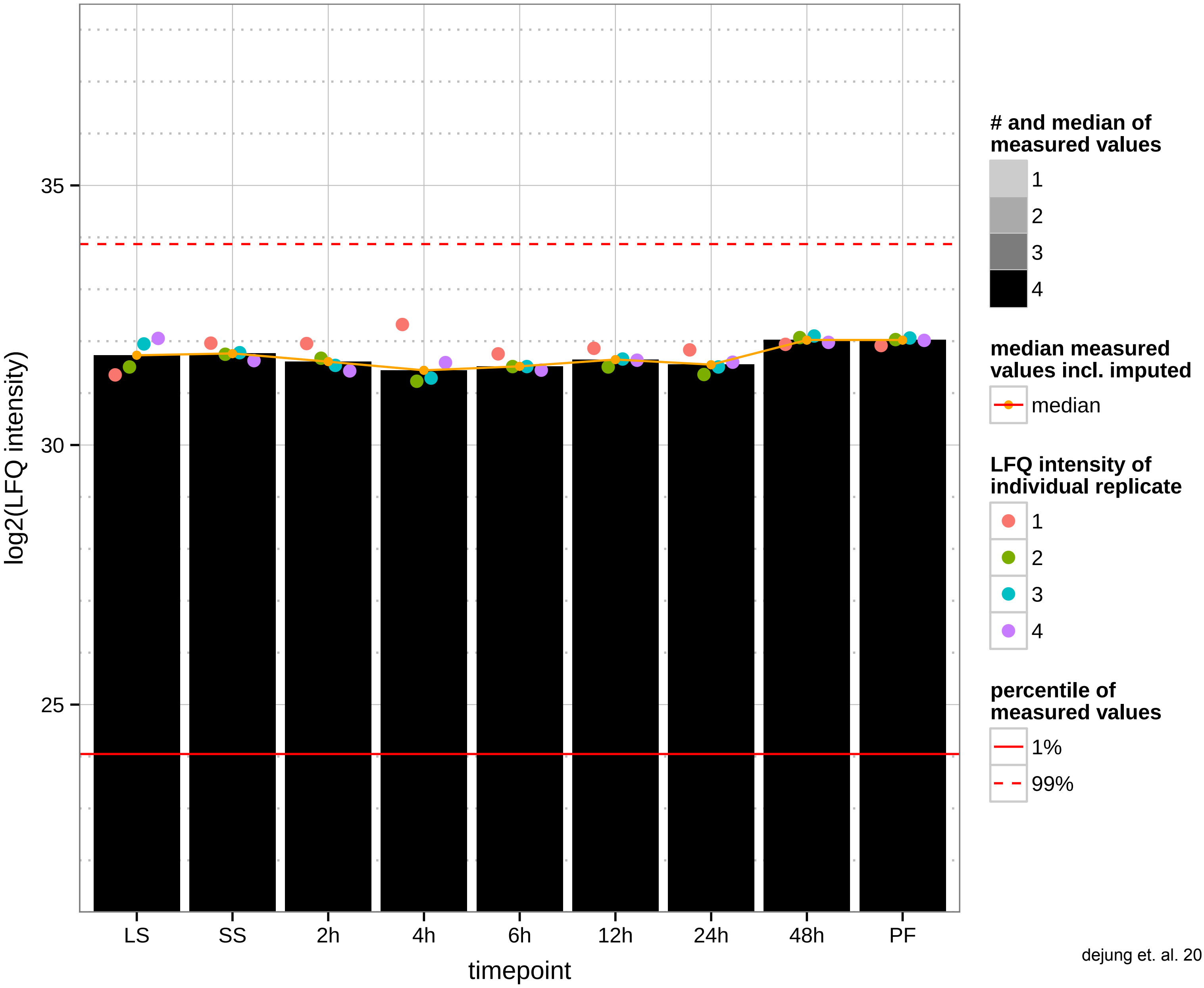
paraflagellar rod component, putative (PFC1)
Tb927.8.6660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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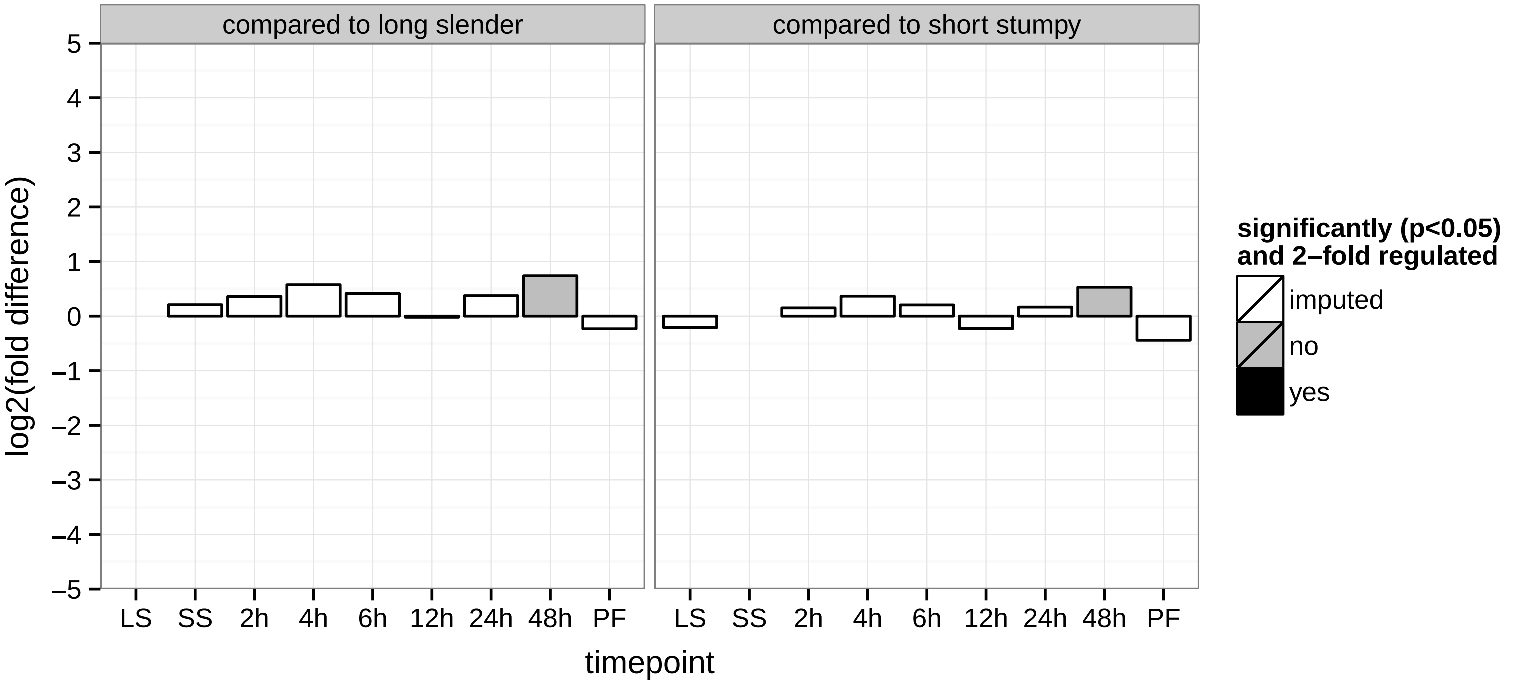
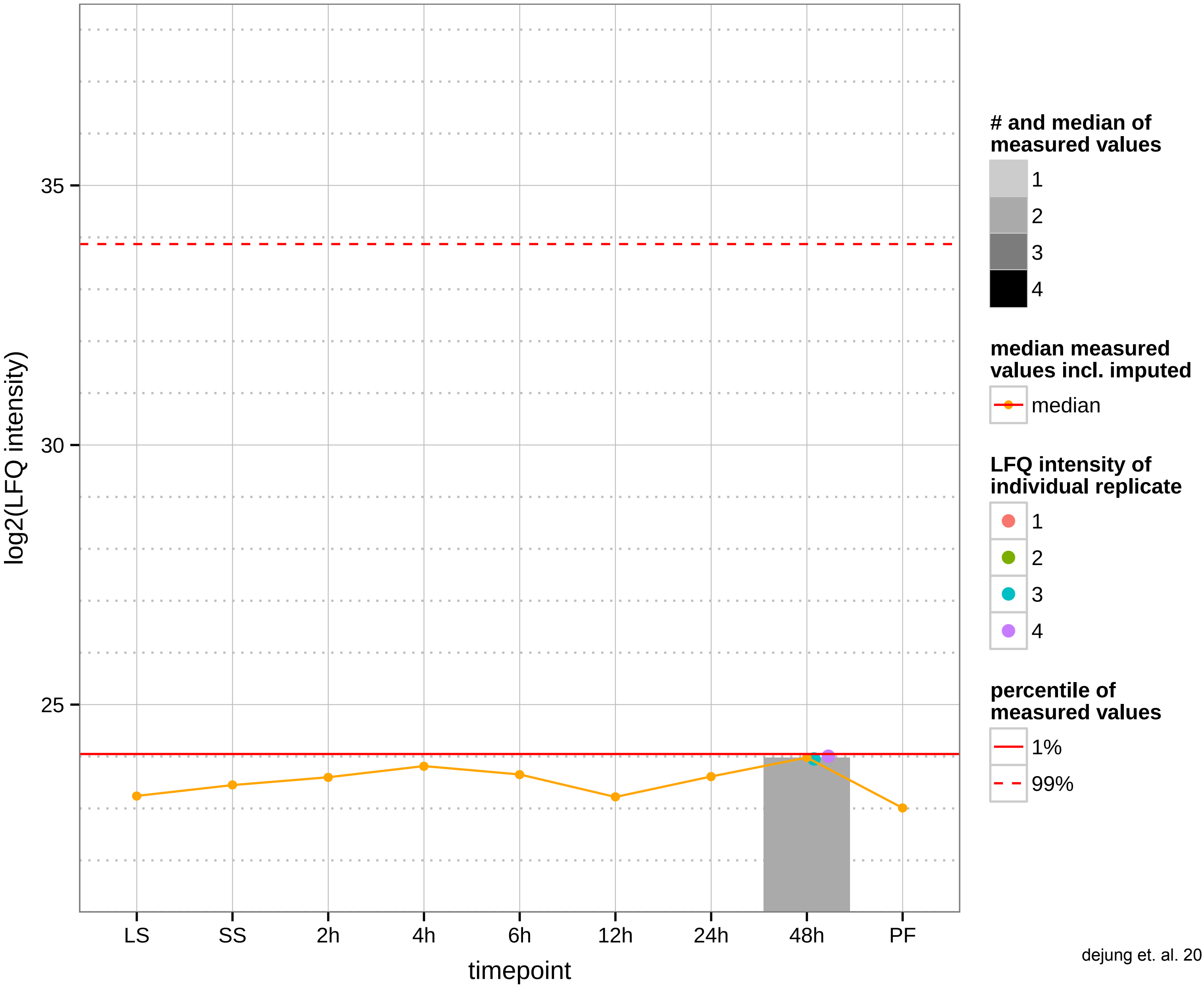
hypothetical protein, conserved
Tb927.8.6870
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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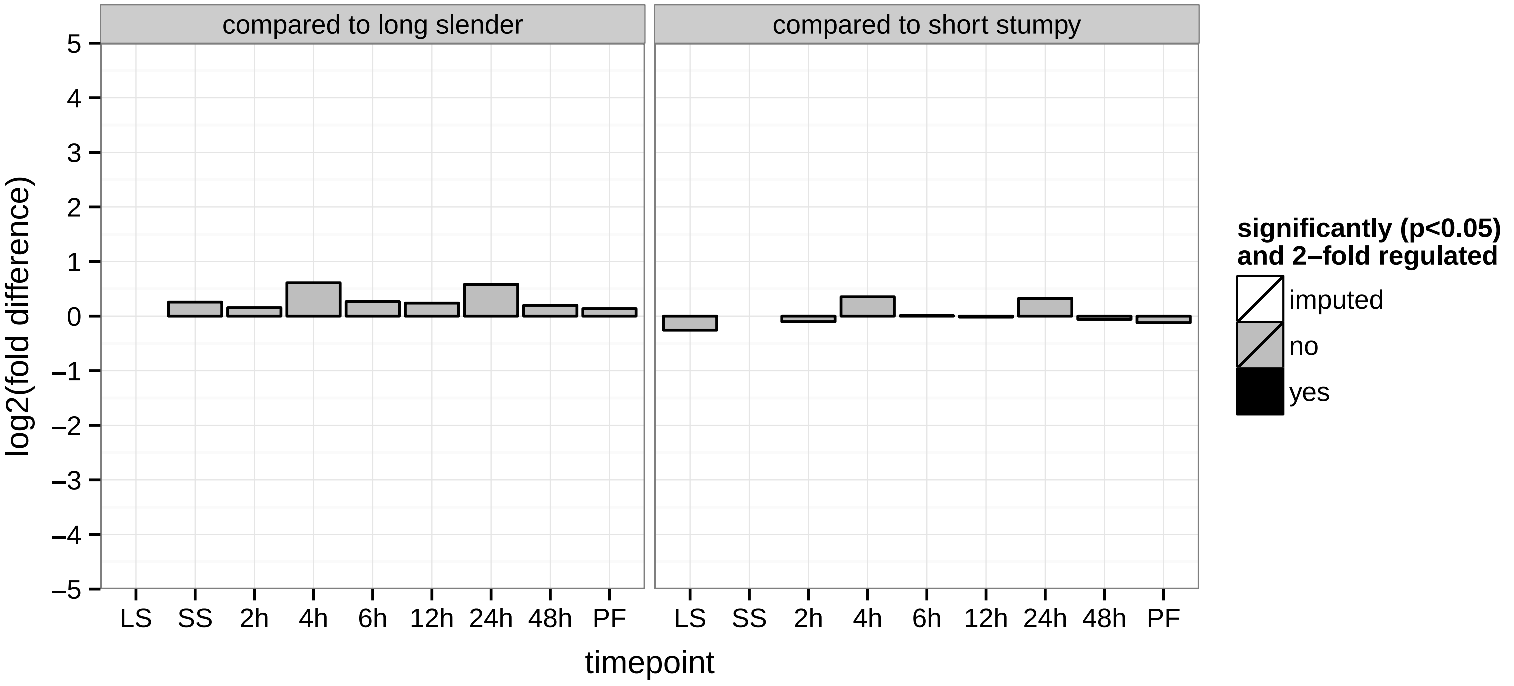
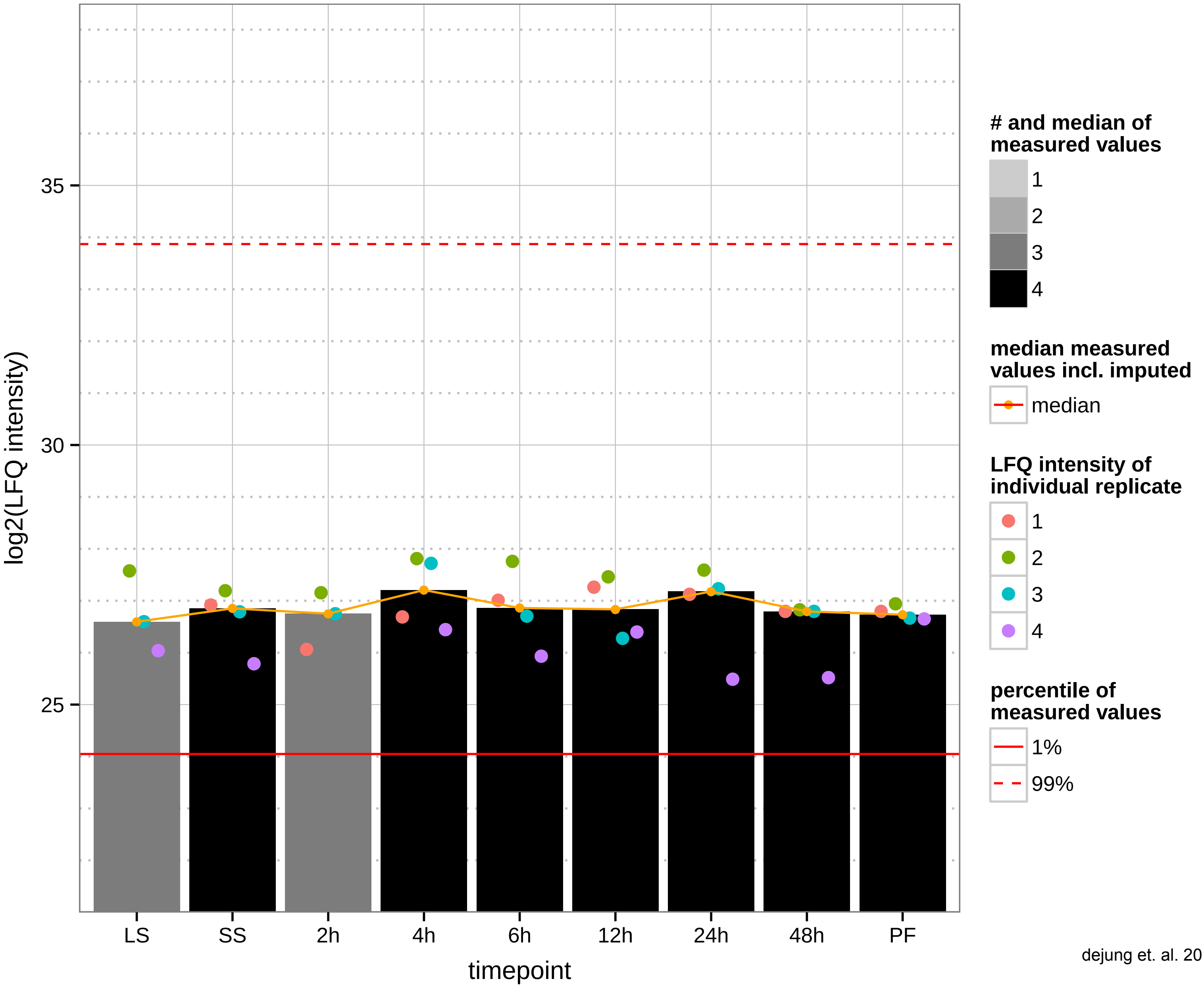
peptidyl–prolyl cis–trans isomerase/rotamase, putative, PPIase, parvulin (PIN1)
Tb927.8.690
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: isomerase activity
PGOC: null
PGOP: null





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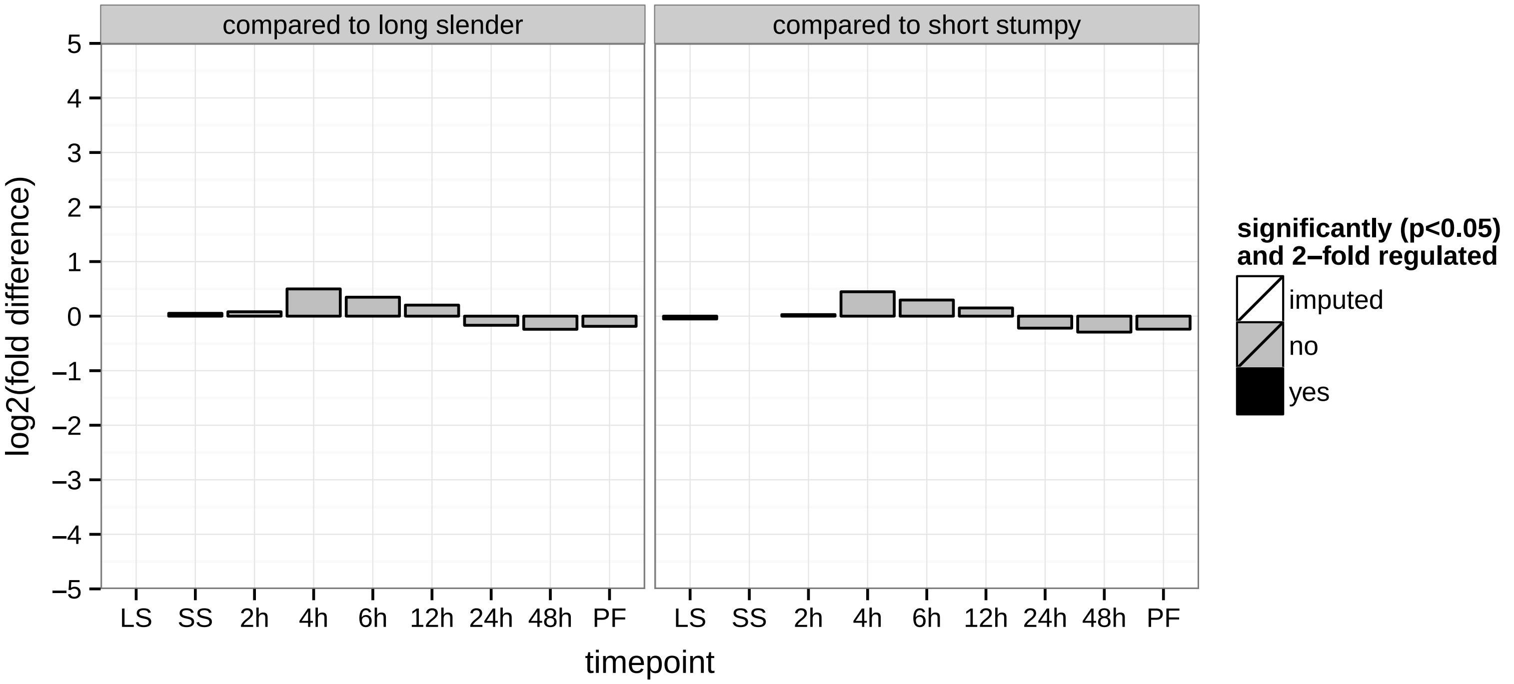
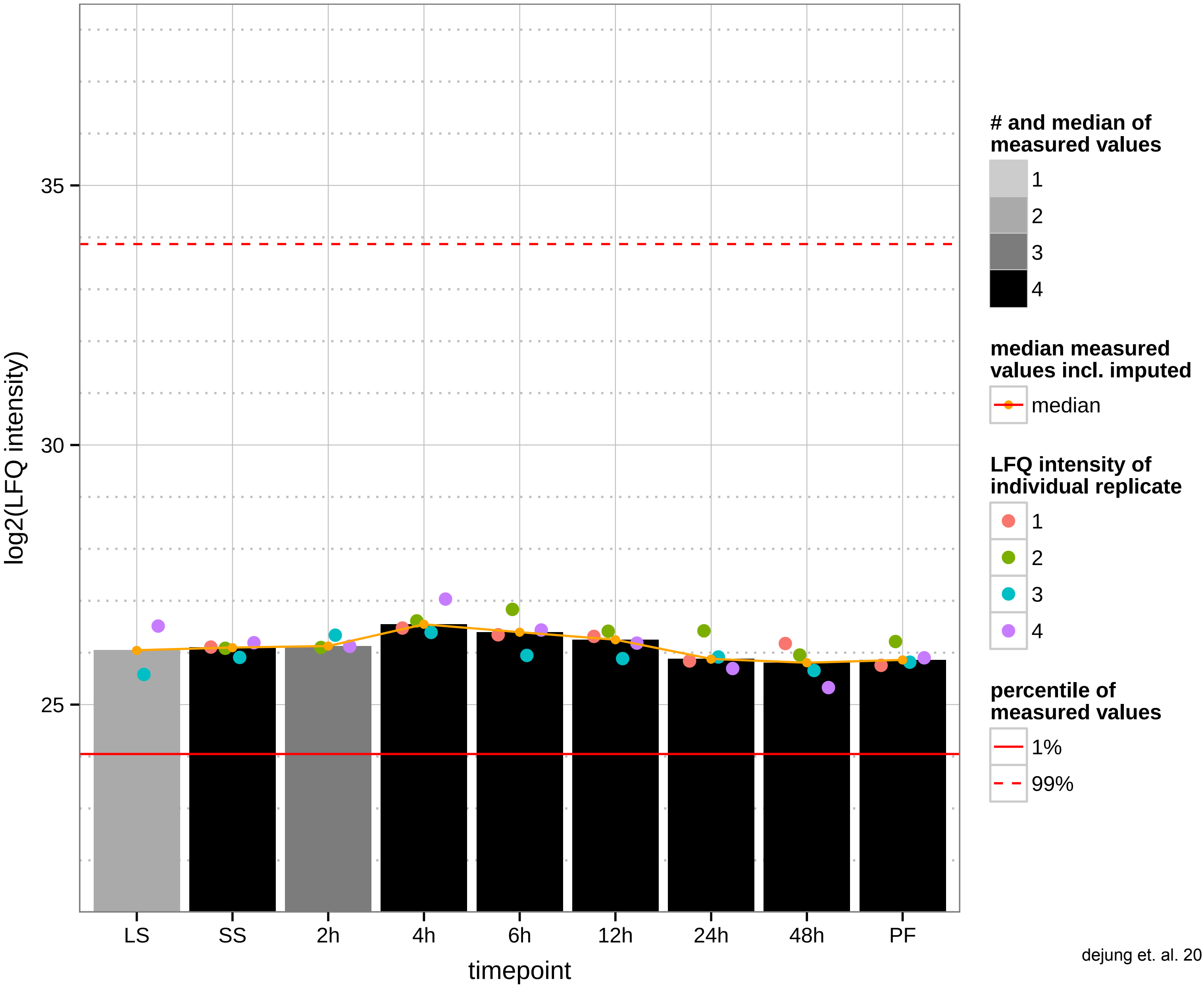
hypothetical protein, conserved
Tb927.8.6900
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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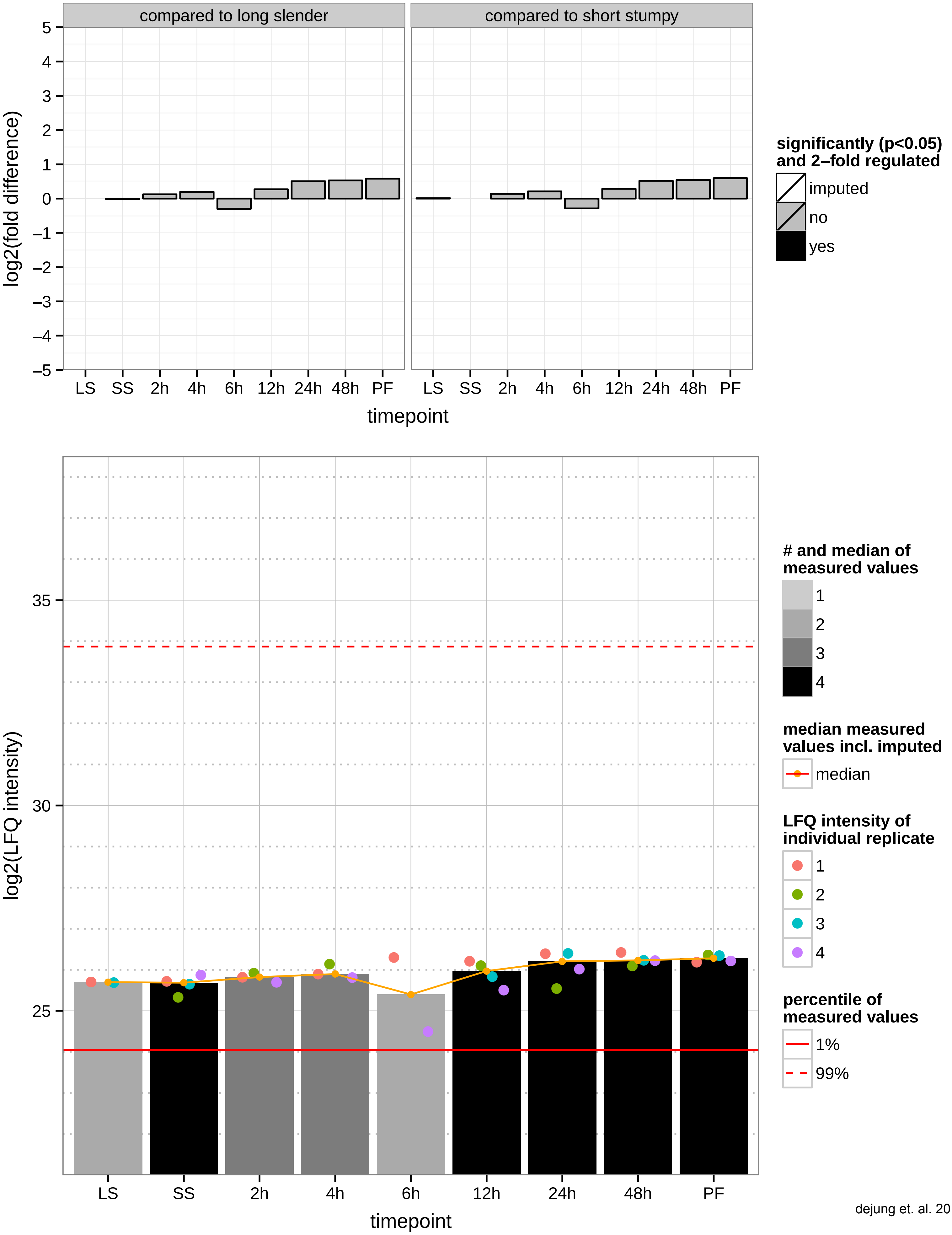
cyclophilin, putative
Tb927.8.6910
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding



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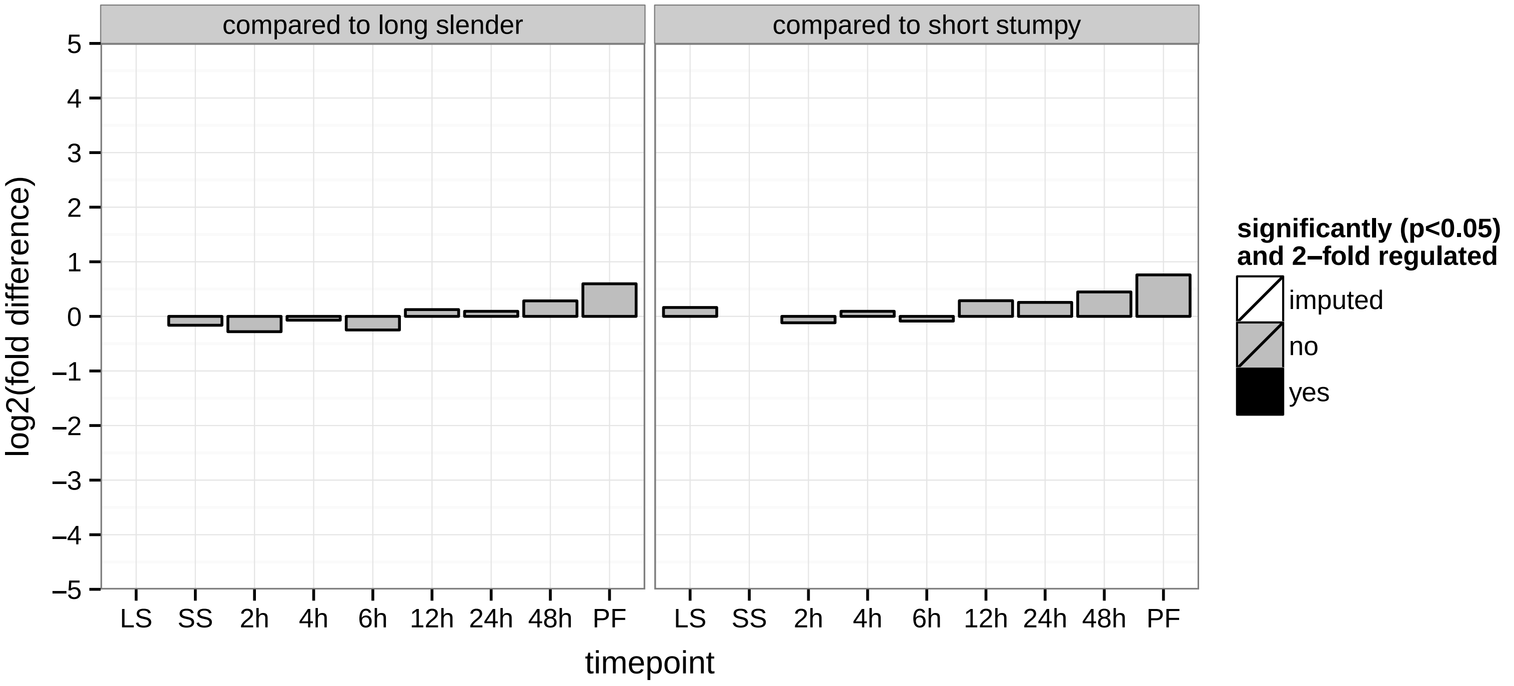
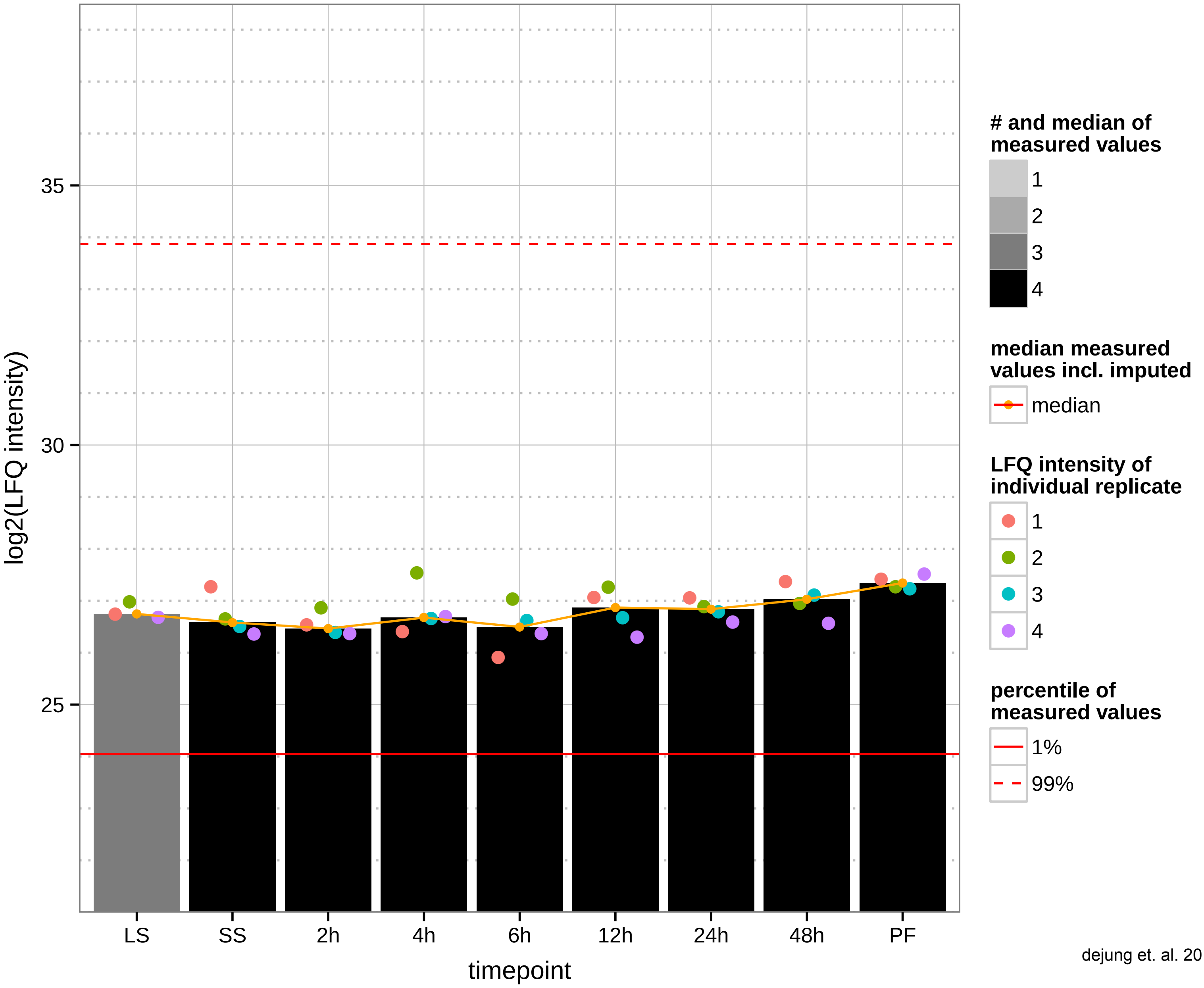
hypothetical protein, conserved
Tb927.8.6920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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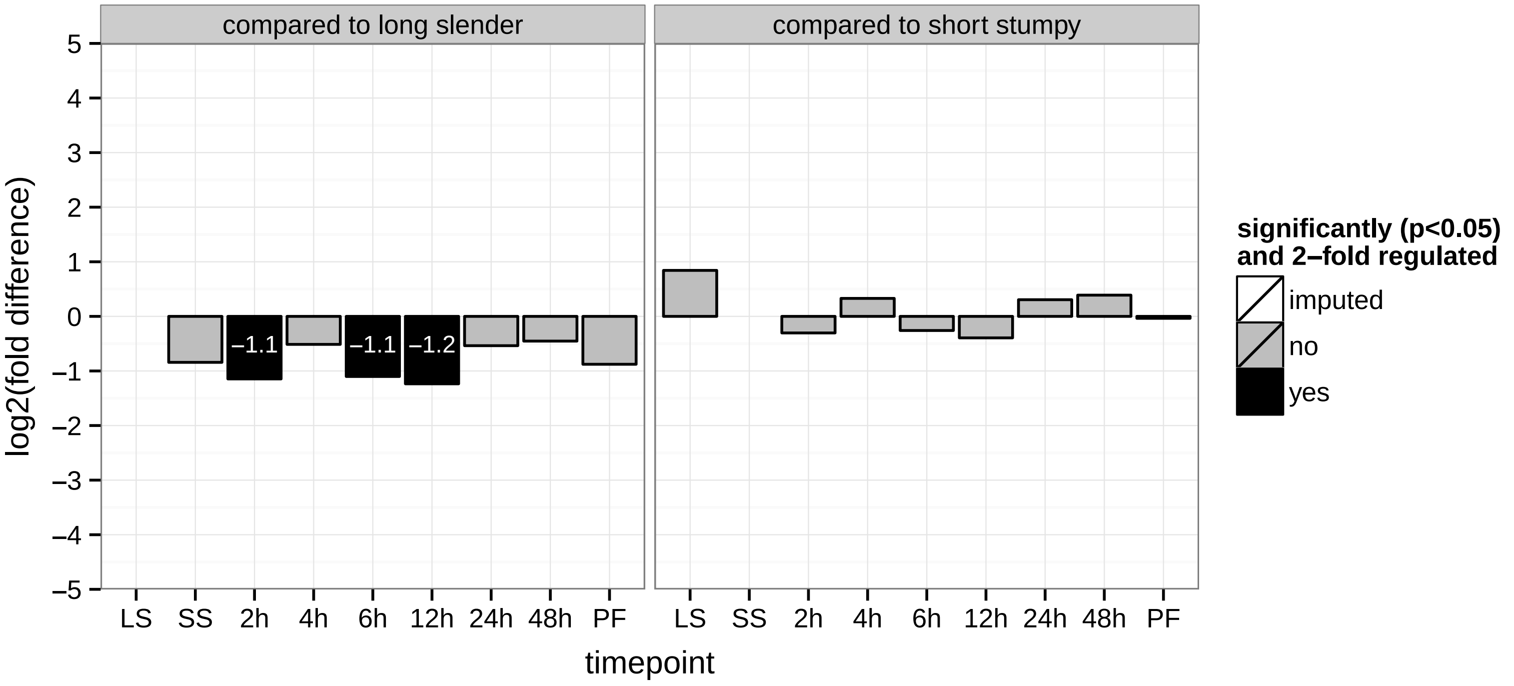
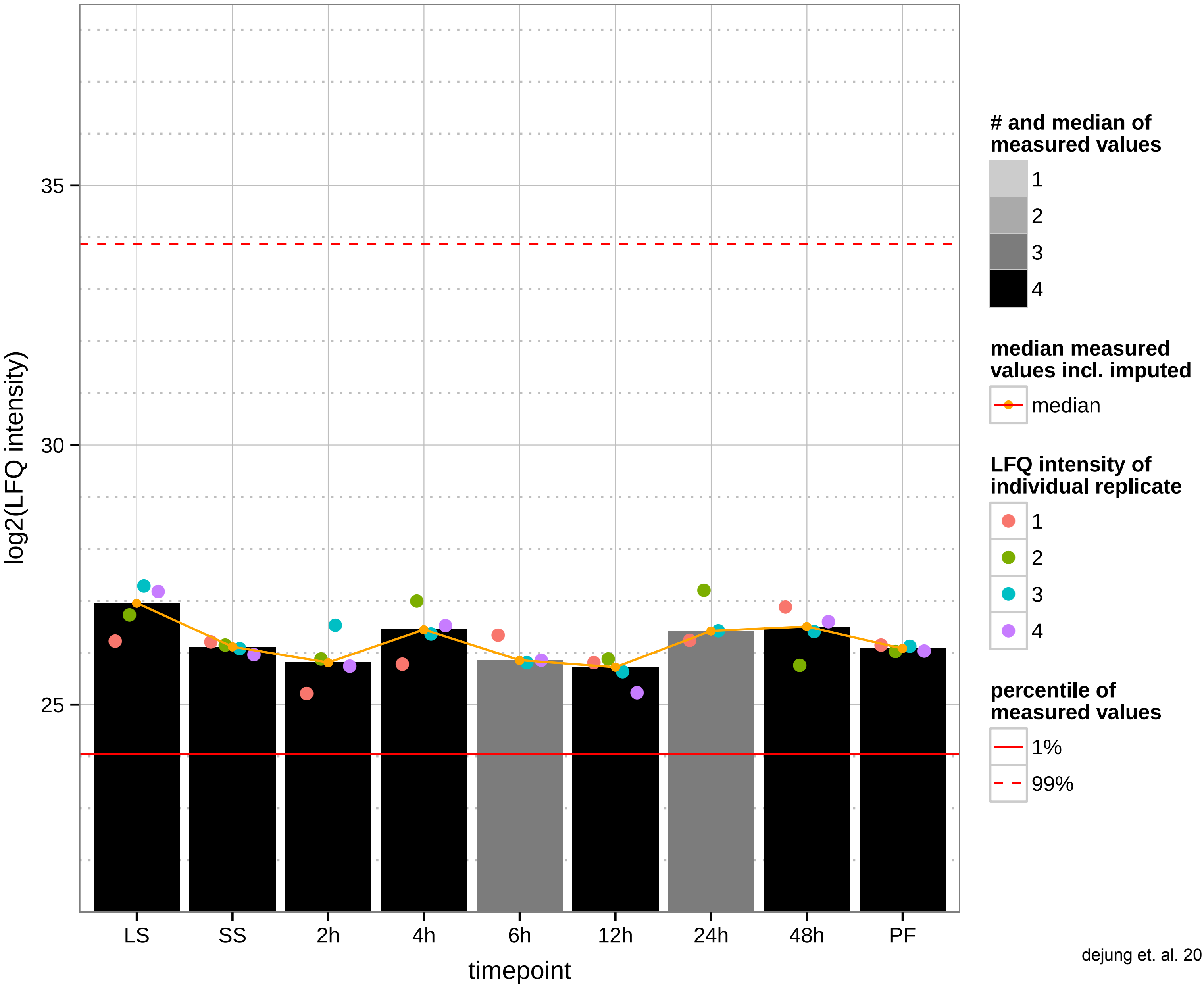
dynein light chain 2B, cytoplasmic, putative, predicted dynein modulator, roadblock/LC7 family member
Tb927.8.6950;Tb927.4.5370
AGOF: null, microtubule motor activity
AGOC: null, cytoplasmic dynein complex
AGOP: ciliary or flagellar motility, microtubule–based movement
PGOF: null
PGOC: null
PGOP: null





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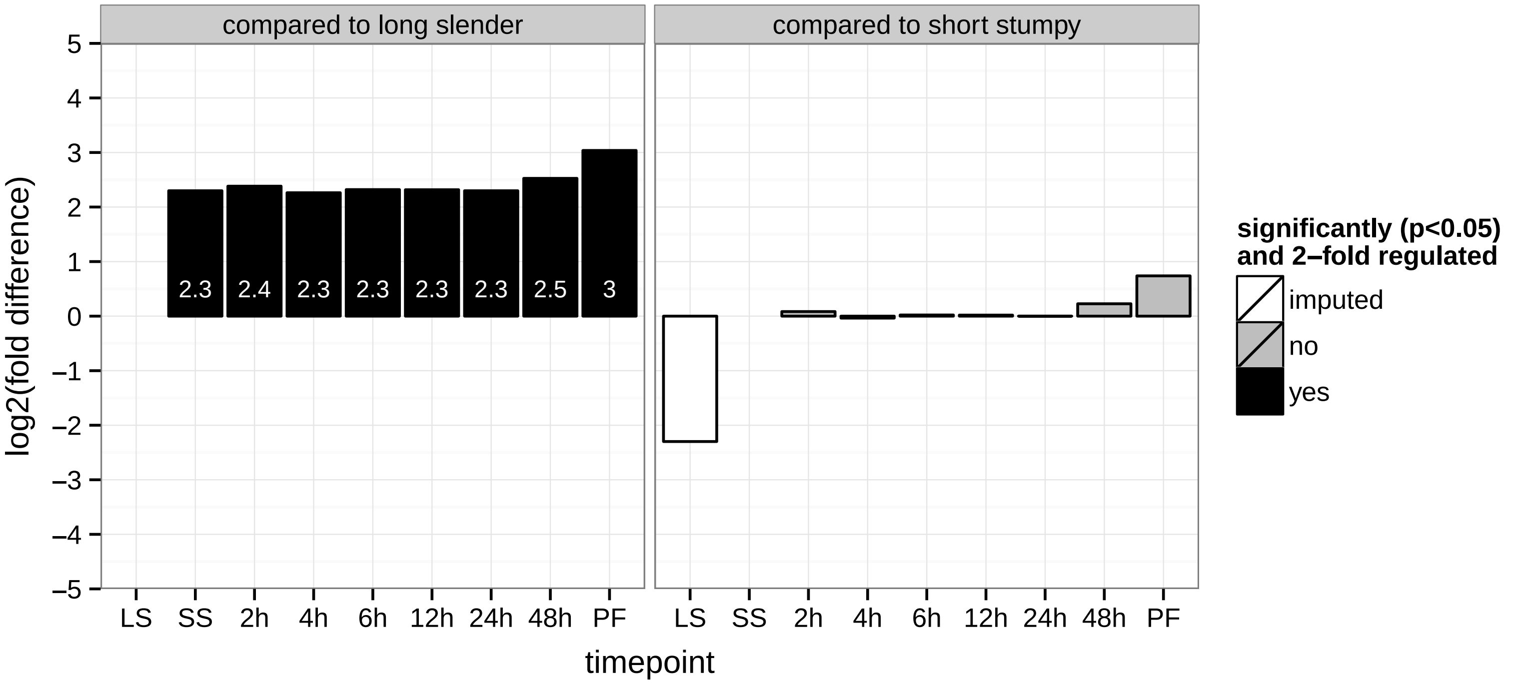
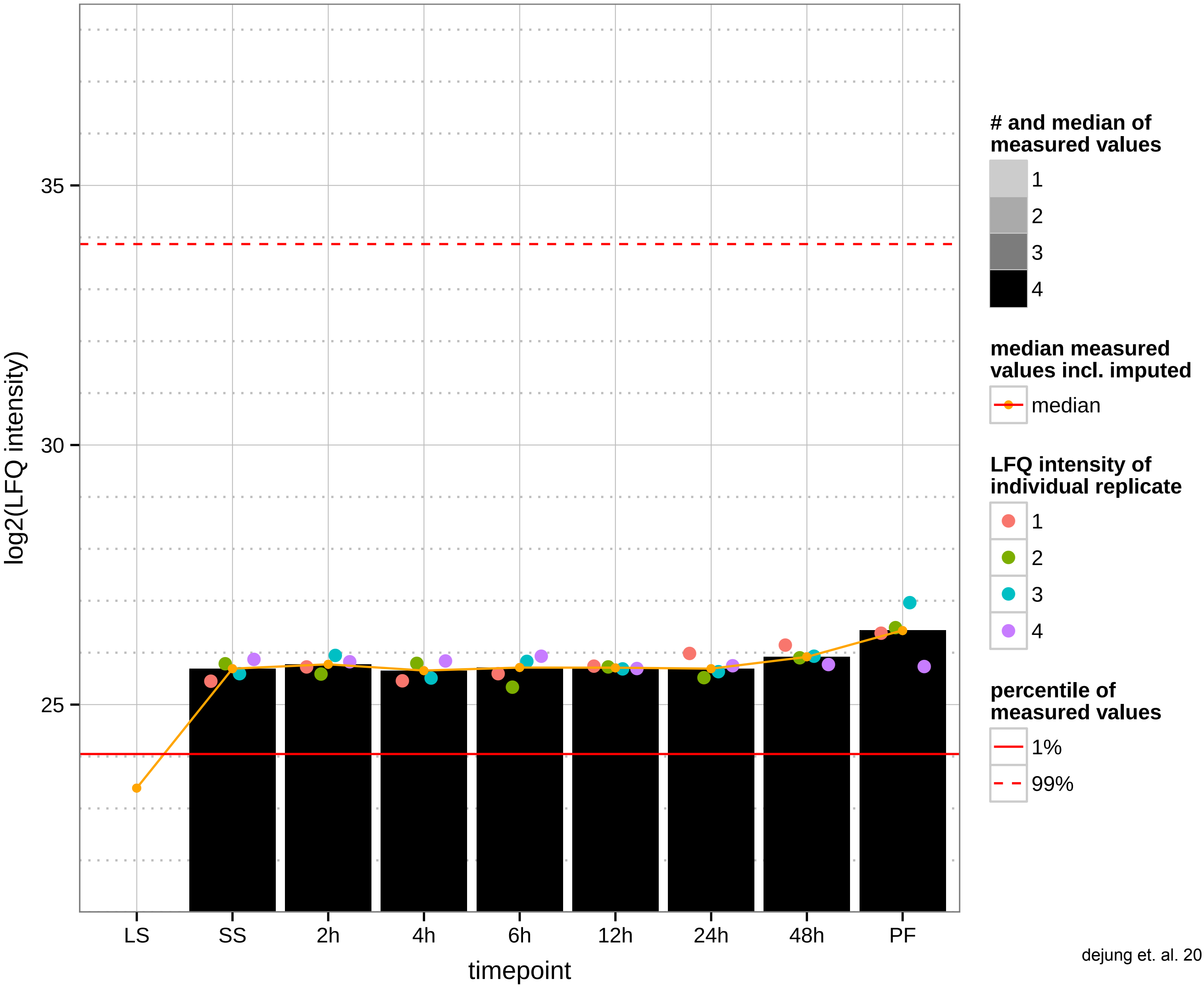
hypothetical protein, conserved
Tb927.8.6980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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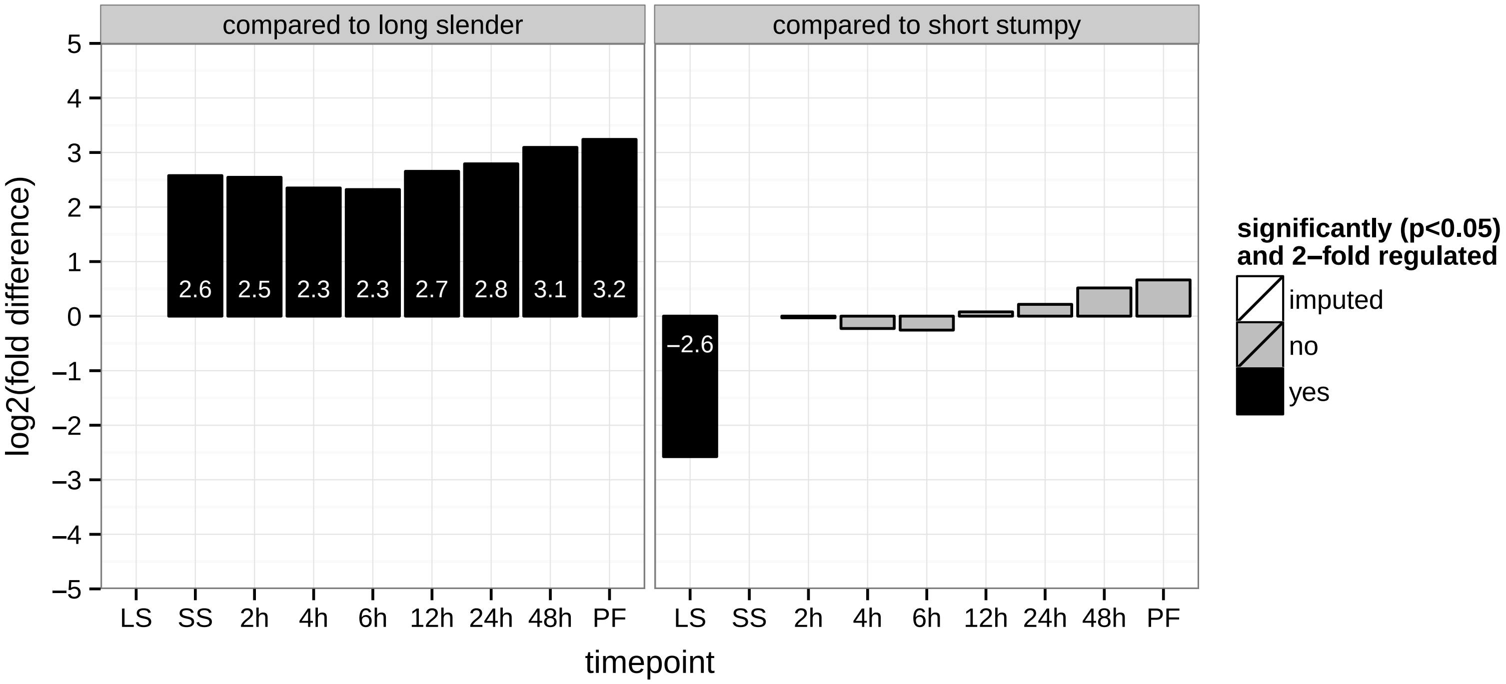
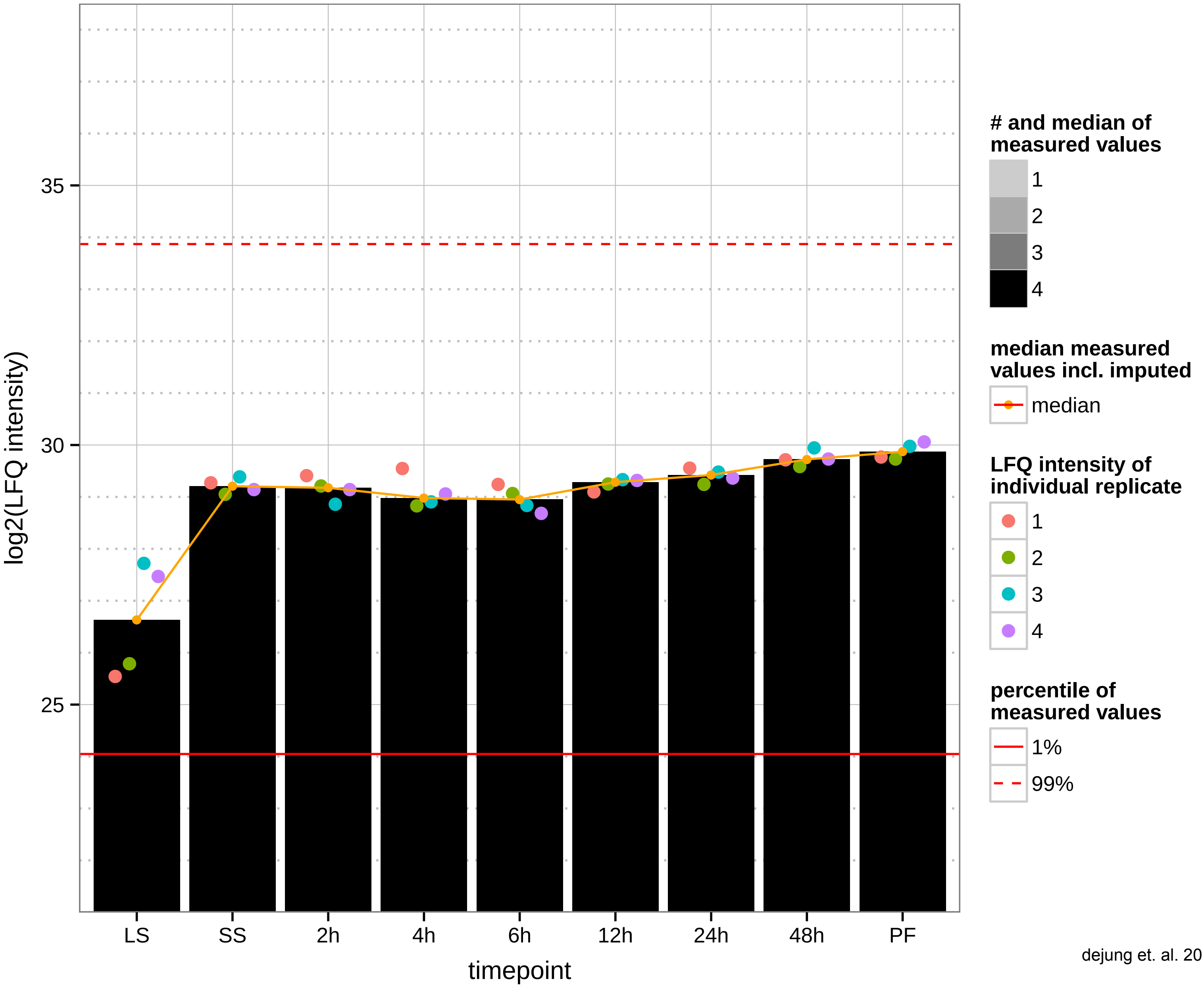
peptidase, putative, metallo–peptidase, Clan ME, Family M16
Tb927.8.7020
AGOF: catalytic activity, metalloendopeptidase activity, zinc ion binding
AGOC: null
AGOP: proteolysis
PGOF: catalytic activity, metal ion binding, metalloendopeptidase activity, zinc ion binding
PGOC: null
PGOP: proteolysis





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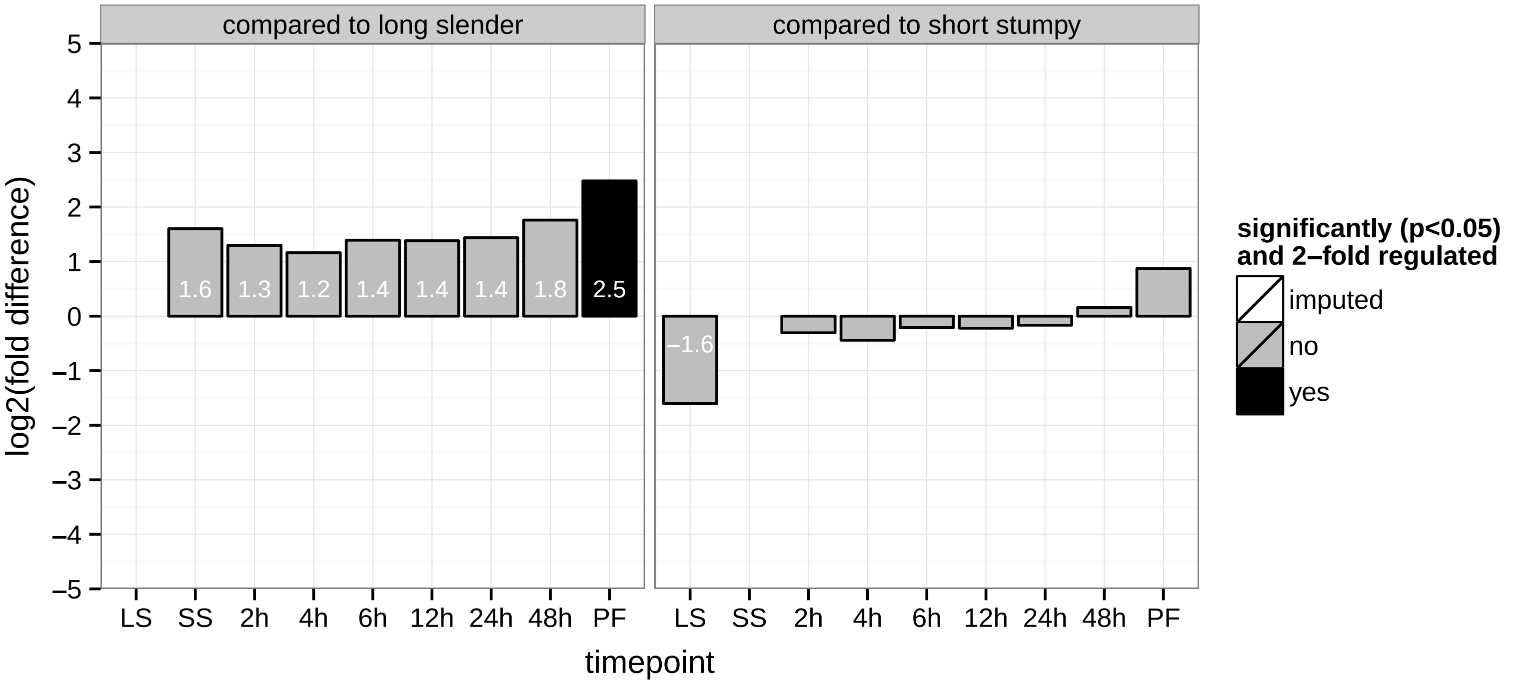
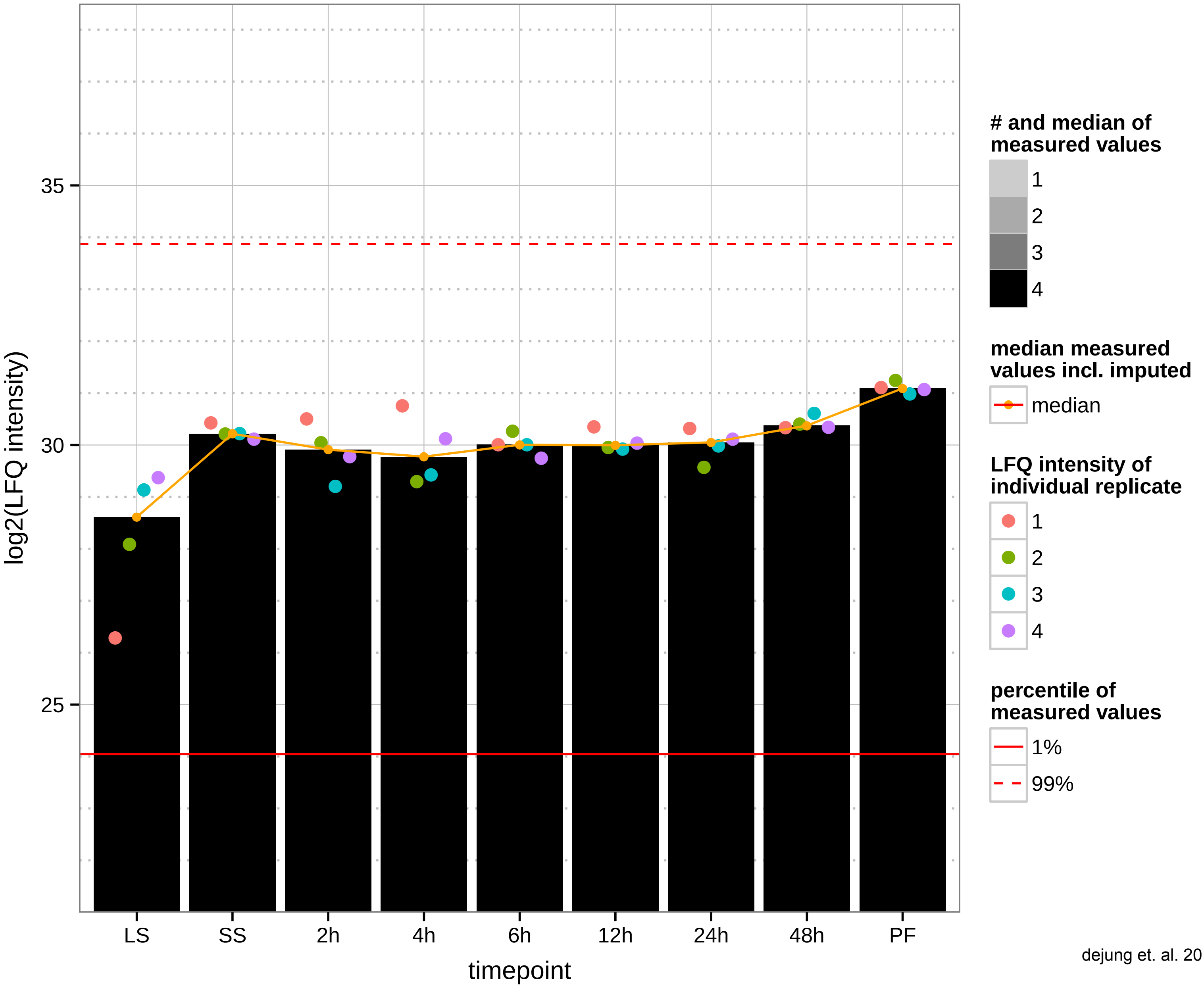
acetyl–CoA carboxylase
Tb927.8.7100
AGOF: ATP binding, acetyl–CoA carboxylase activity, biotin binding, biotin carboxylase activity
AGOC: biotin carboxylase complex, cytoplasm, mitochondrion
AGOP: fatty acid biosynthetic process, fatty acid elongation, quorum sensing
PGOF: ATP binding, acetyl–CoA carboxylase activity, biotin carboxylase activity, catalytic activity, ligase activity, metal ion binc
PGOC: null
PGOP: fatty acid biosynthetic process, metabolic process





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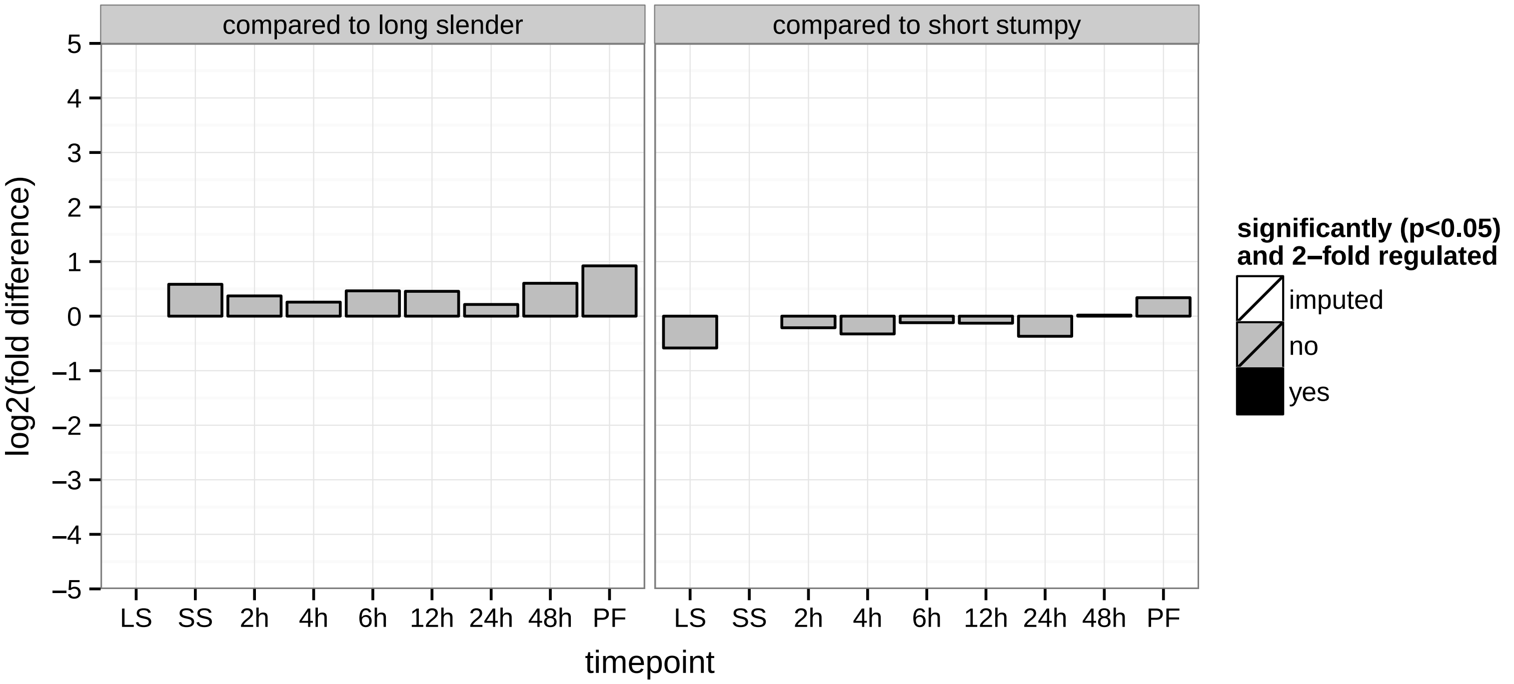
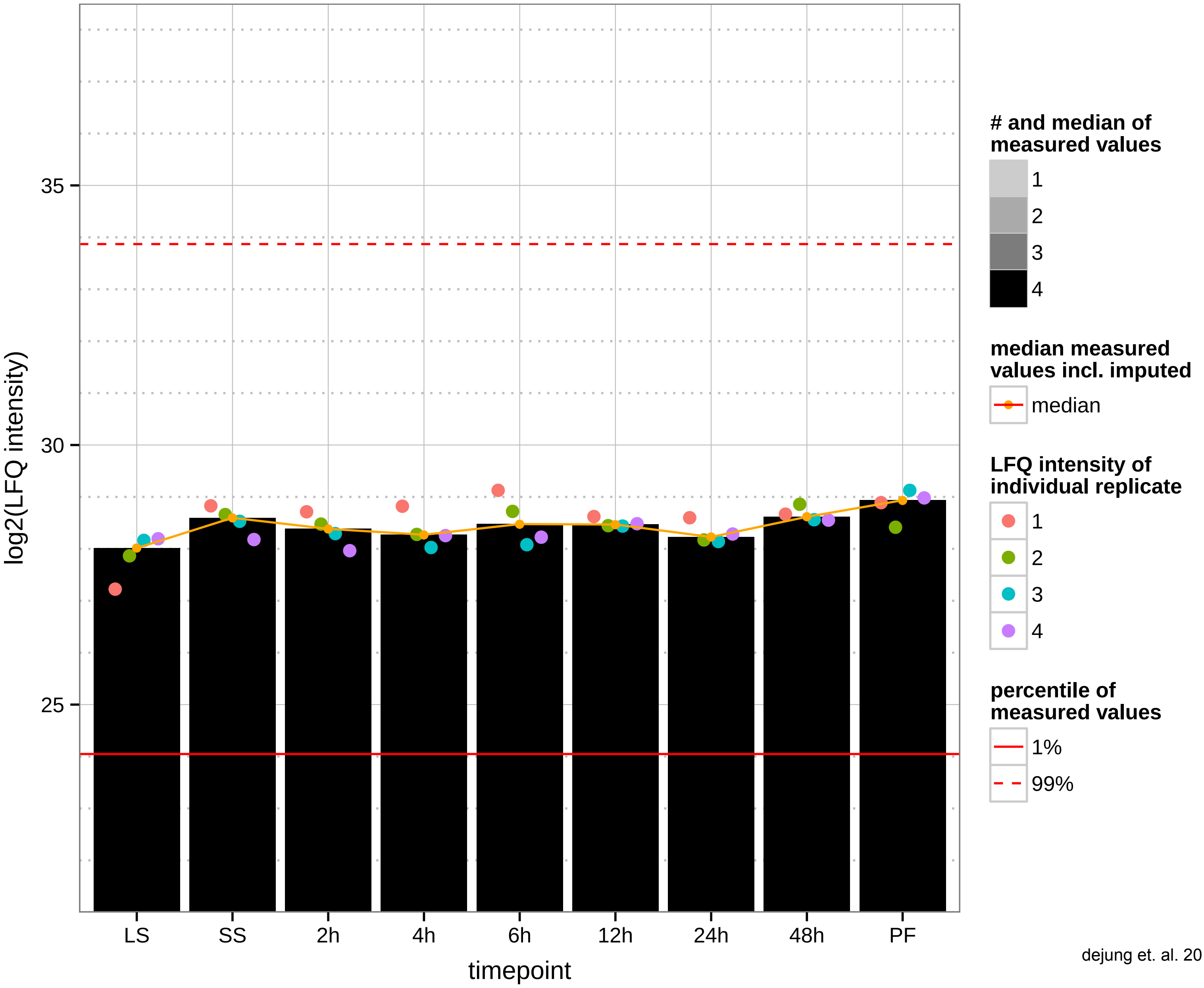
inositol polyphosphate 1‒phosphatase, putative
Tb927.8.7170
AGOF: null
AGOC: mitochondrion
AGOP: phosphatidylinositol phosphorylation
PGOF: null
PGOC: null
PGOP: phosphatidylinositol phosphorylation





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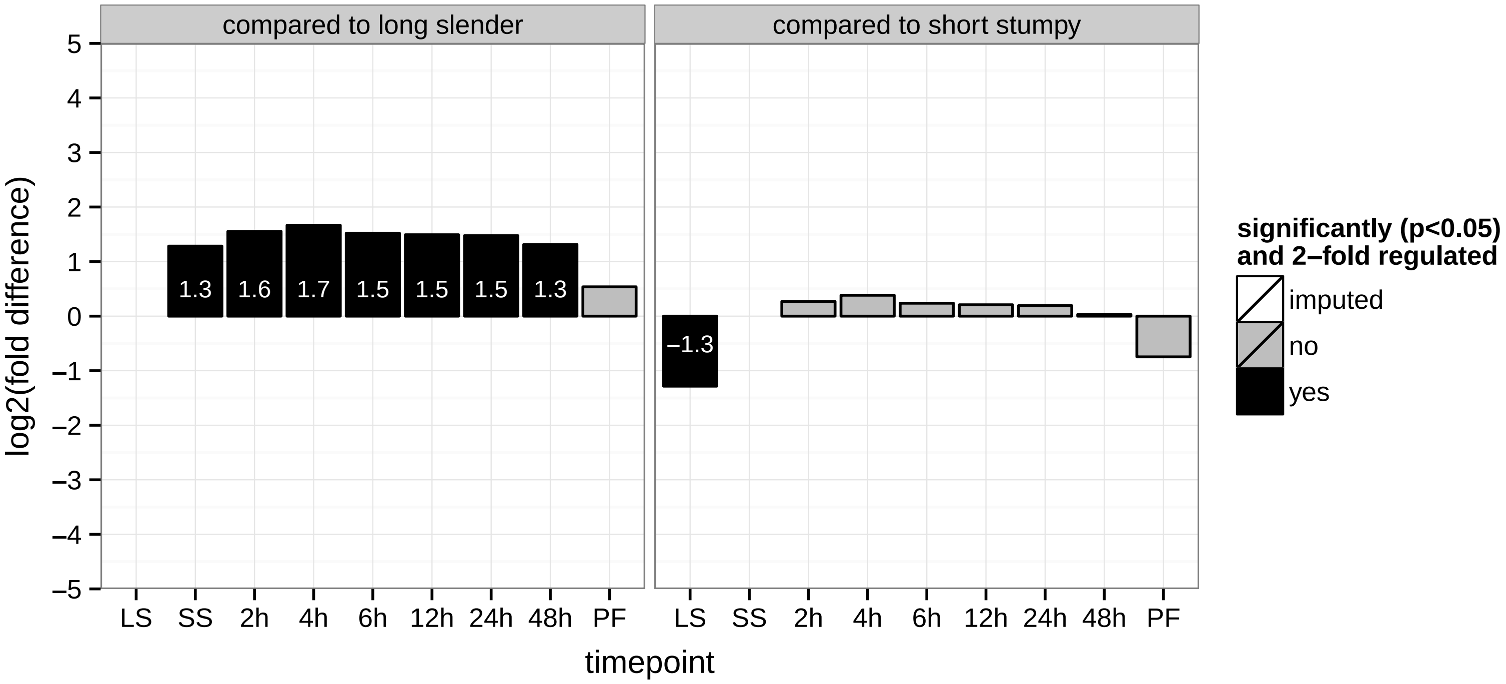
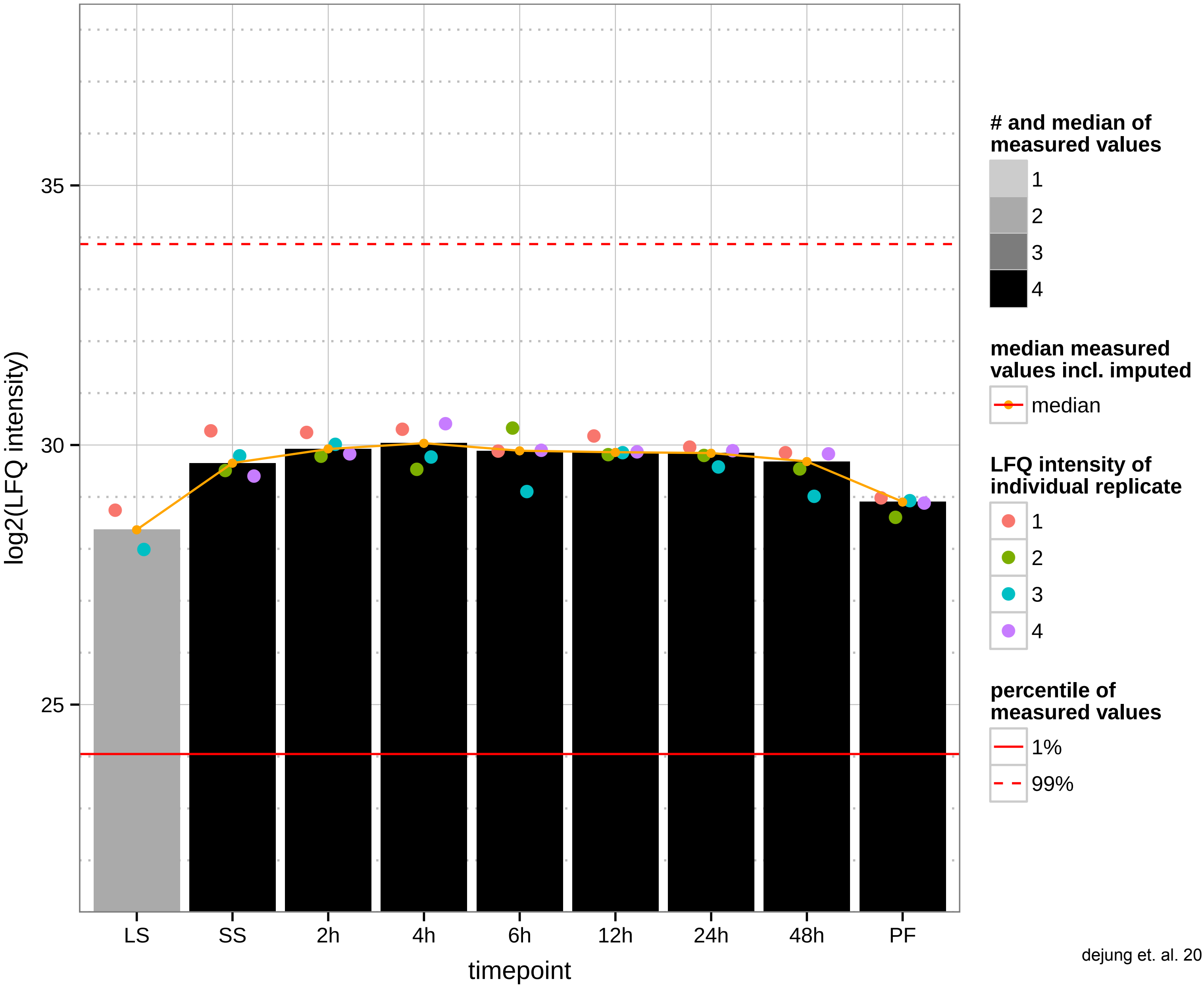
nucleolar RNA–binding protein, putative
Tb927.8.730
AGOF: RNA binding
AGOC: nucleolus
AGOP: RNA metabolic process
PGOF: null
PGOC: null
PGOP: null





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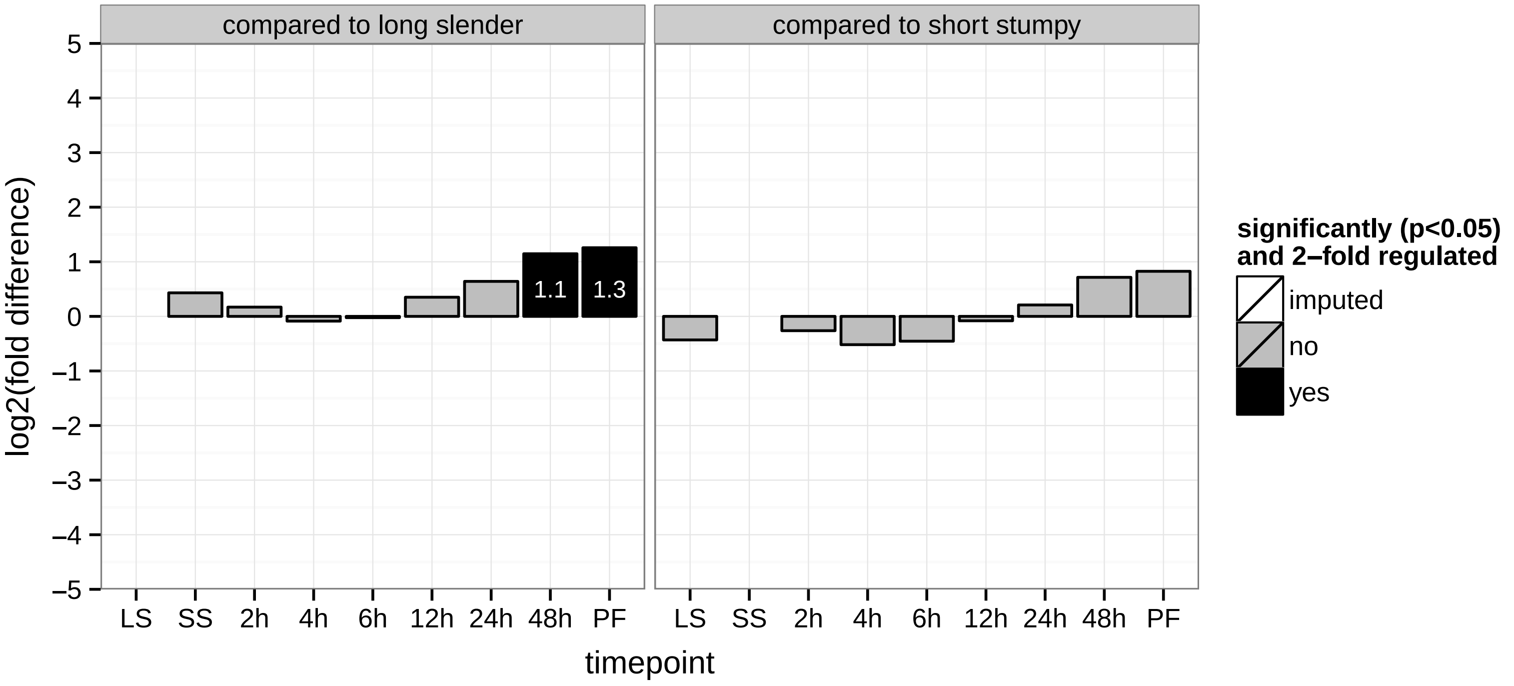
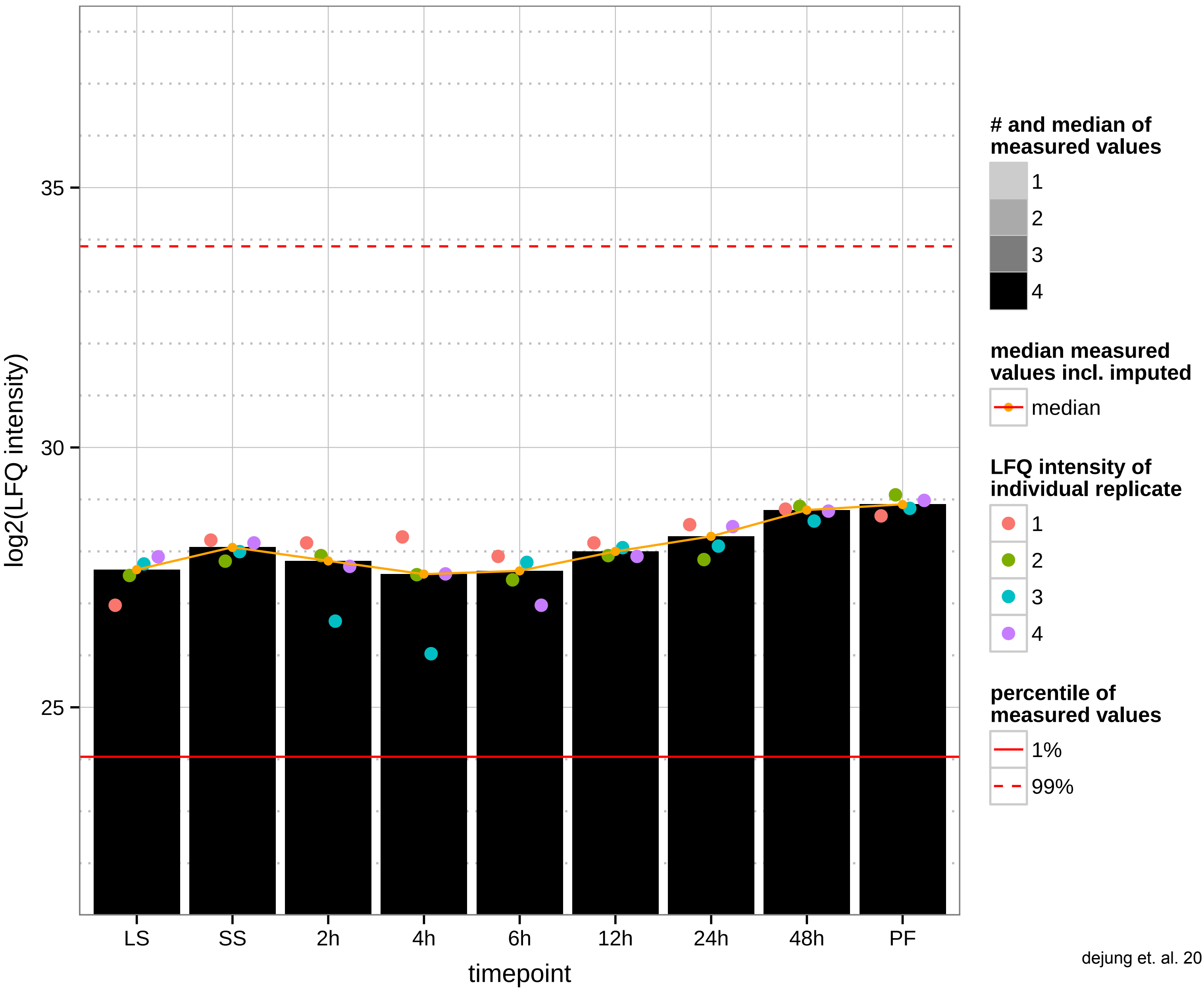
RNA polymerase IIA largest subunit, putative, RNA polymerase IIA largest subunit (RPB1)
Tb927.8.7400;Tb927.4.5020;Tb11.v5.0504
AGOF: null, DNA binding, DNA–directed RNA polymerase activity
AGOC: null, nucleus
AGOP: null, transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA–dependent





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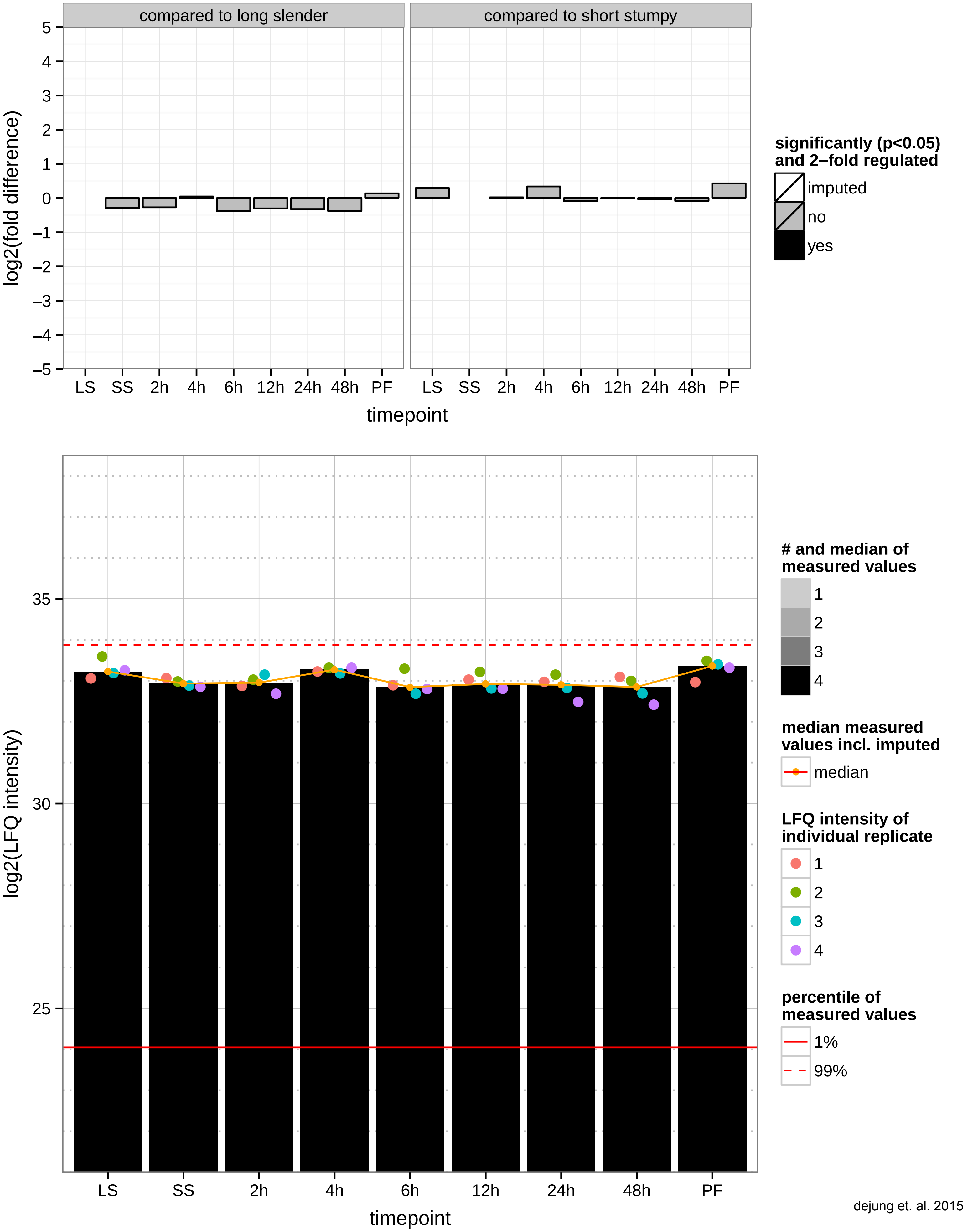
calreticulin, putative
Tb927.8.7410
AGOF: calcium ion binding, carbohydrate binding, glucosidase activity, transferase activity, transferring glycosyl groups, unfolc
AGOC: endoplasmic reticulum, integral to membrane
AGOP: protein folding
PGOF: calcium ion binding, unfolded protein binding
PGOC: endoplasmic reticulum
PGOP: protein folding



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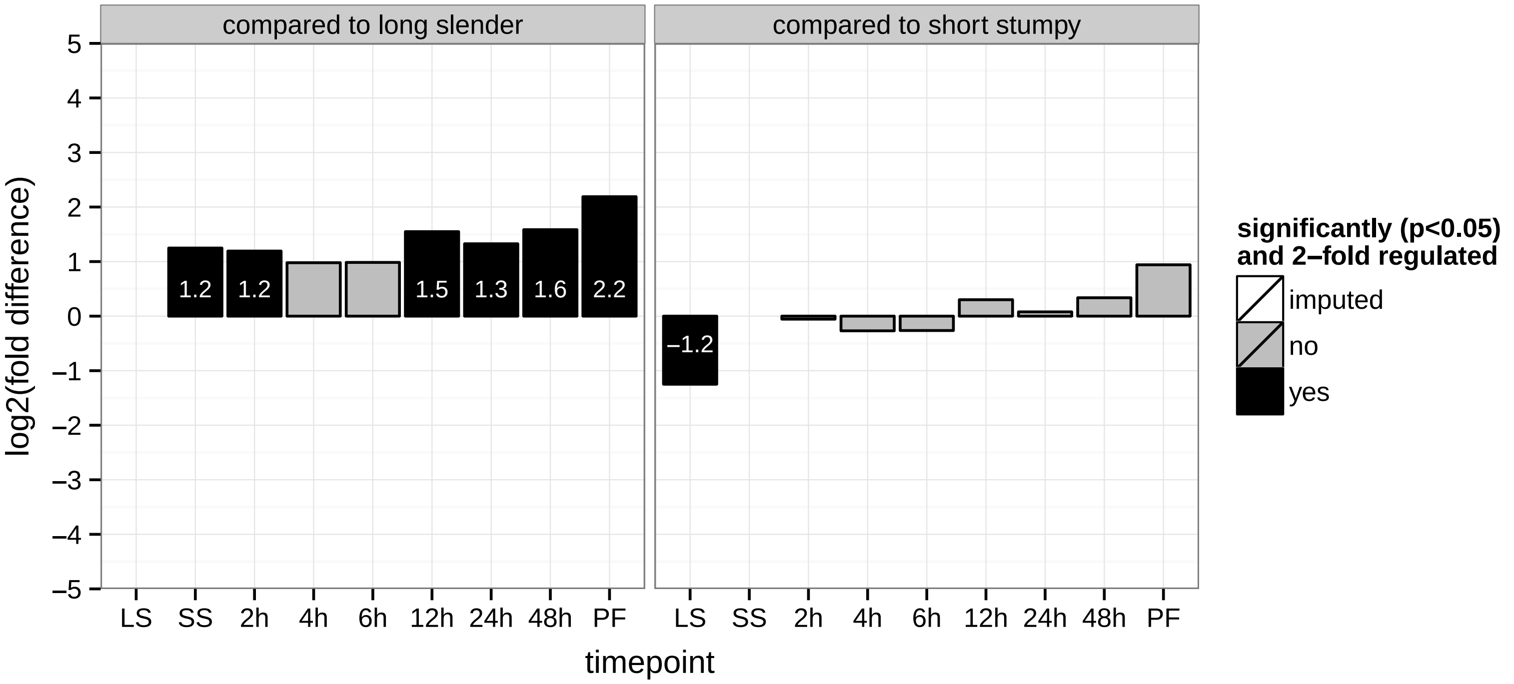
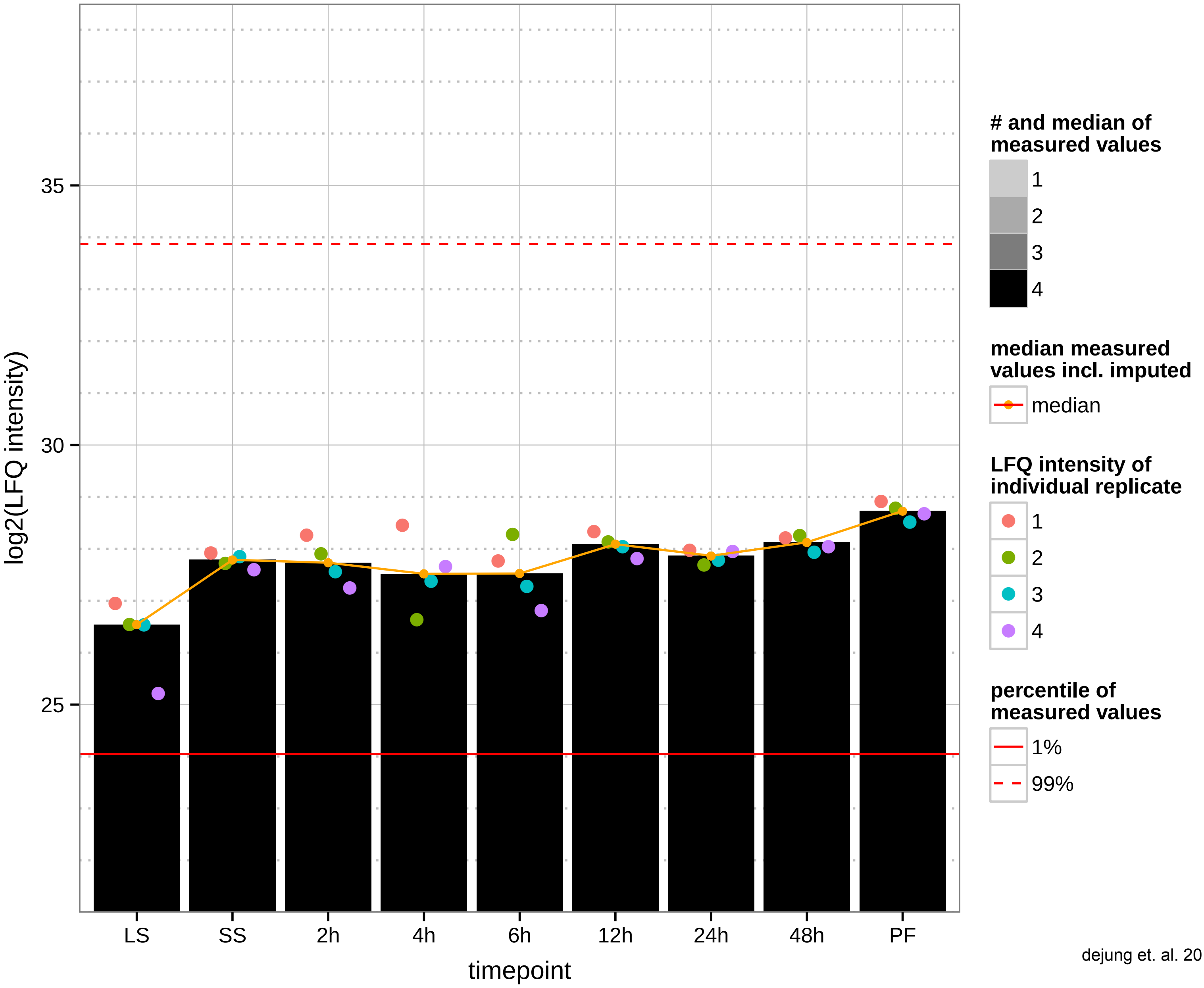
hypothetical protein, conserved
Tb927.8.7490
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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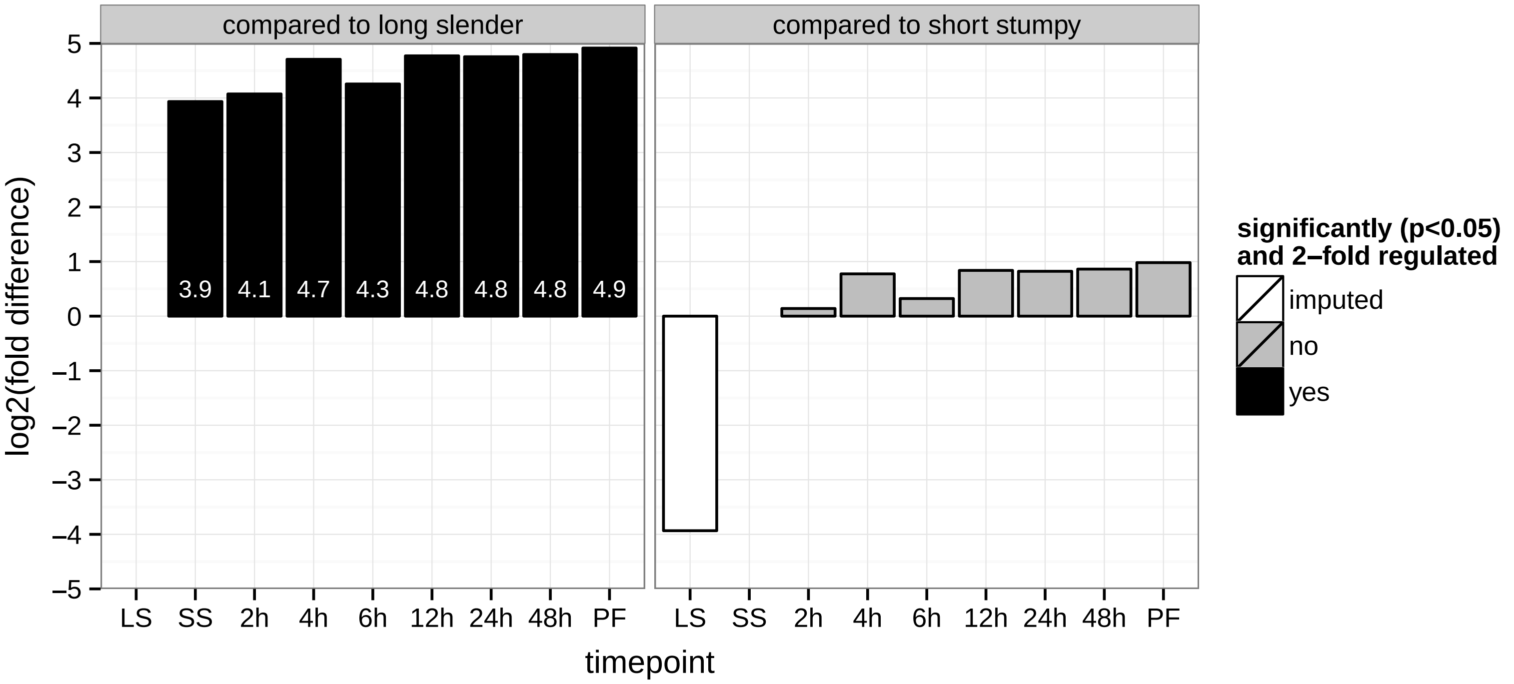
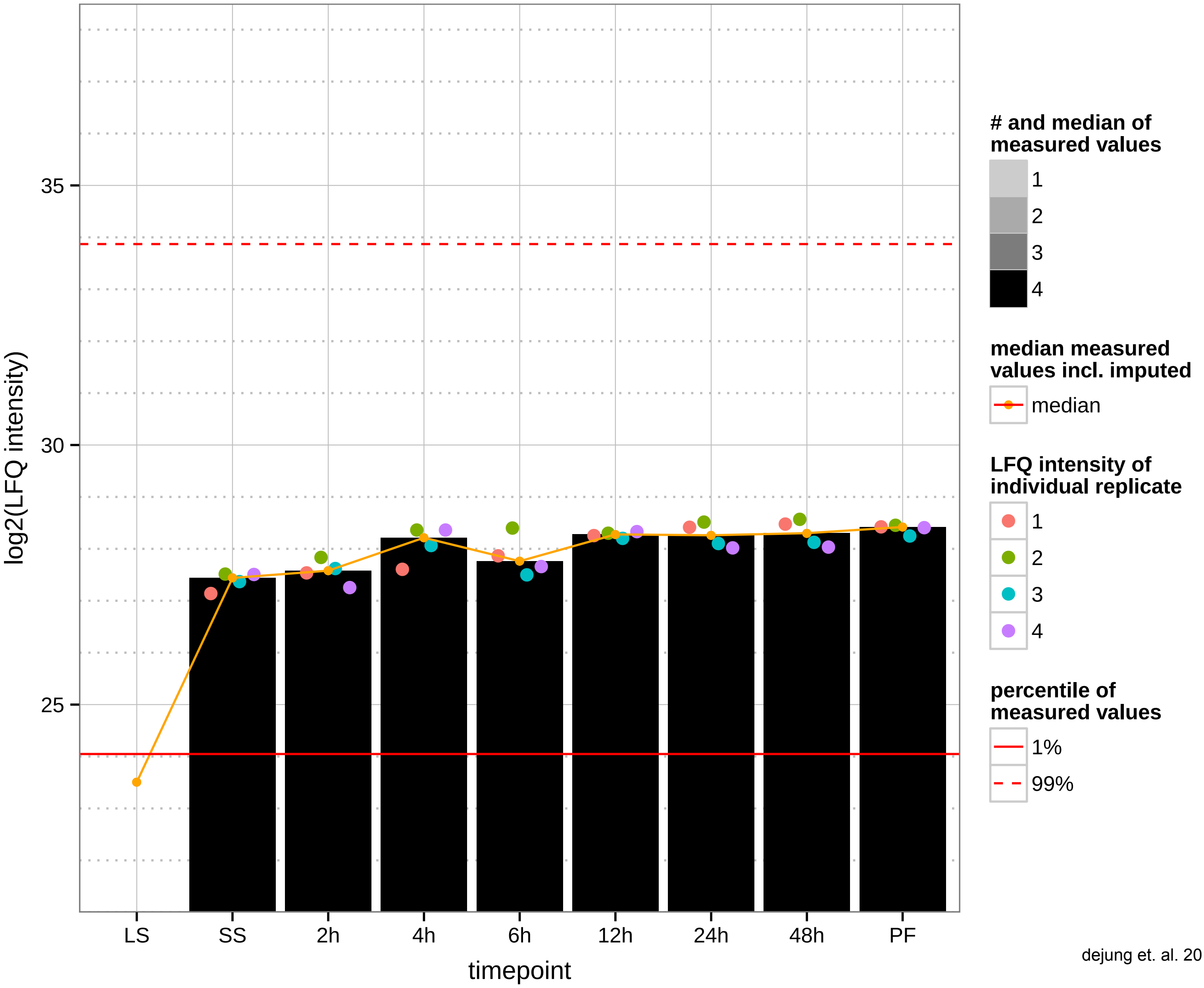
nucleolar RNA−binding protein, putative
Tb927.8.750
AGOF: RNA binding
AGOC: nucleolus
AGOP: RNA metabolic process
PGOF: null
PGOC: null
PGOP: null





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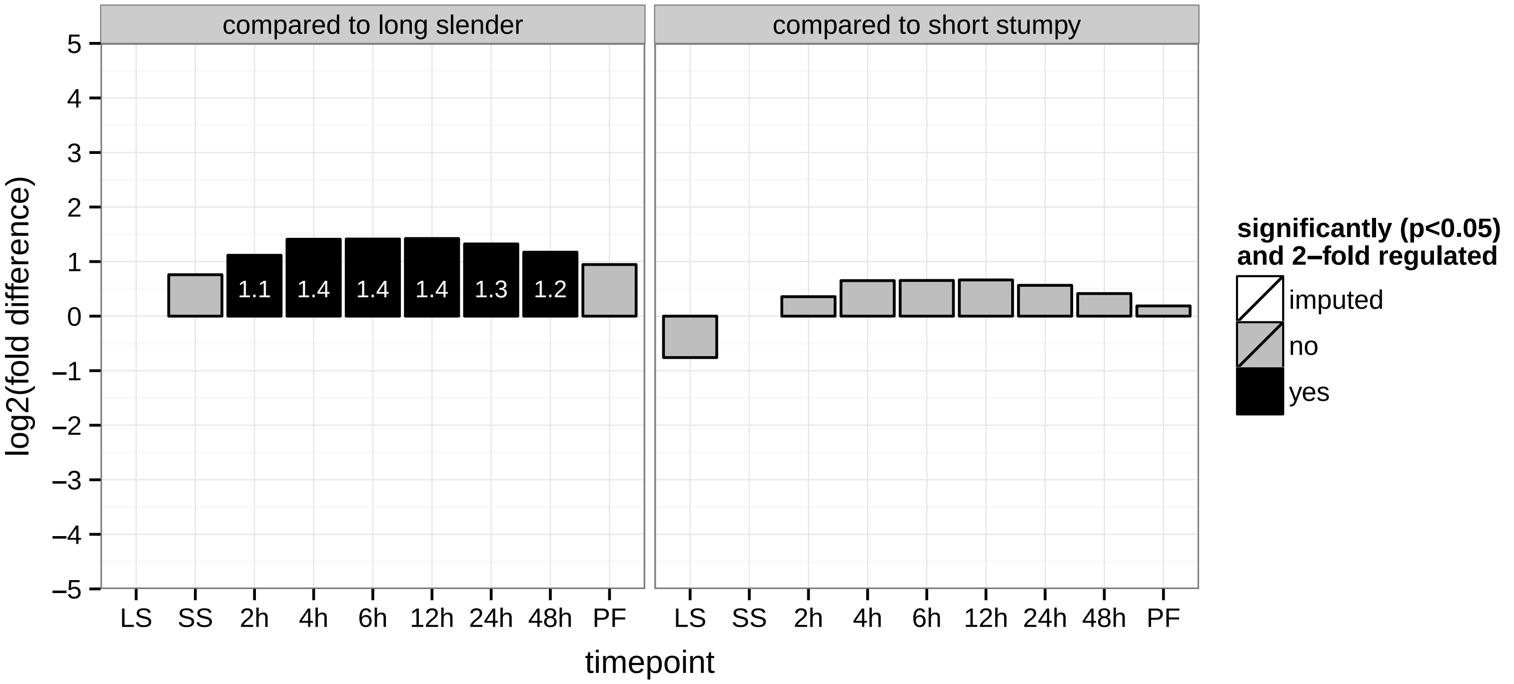
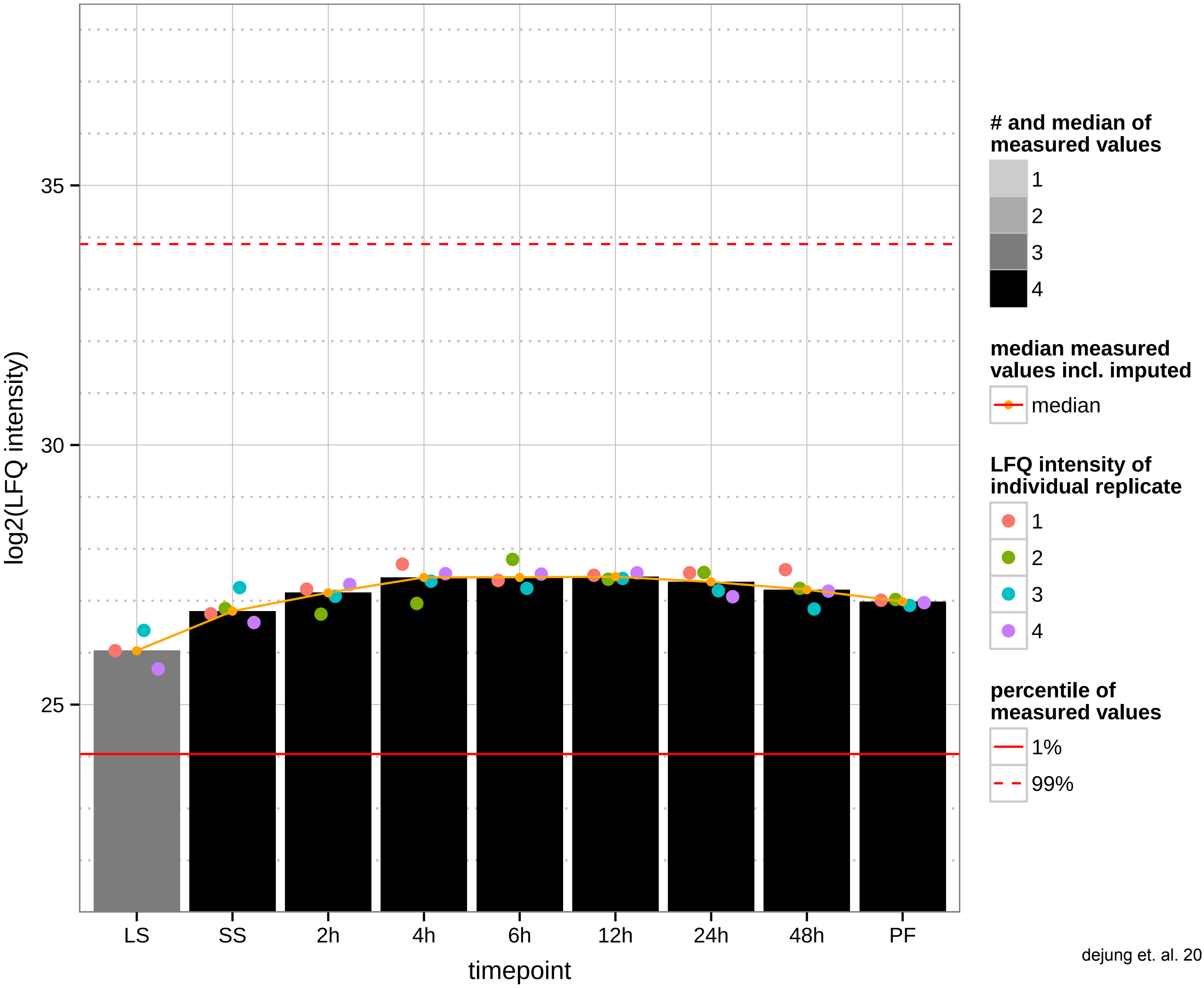
p–nitrophenylphosphatase, putative
Tb927.8.7510
AGOF: phosphatase activity
AGOC: null
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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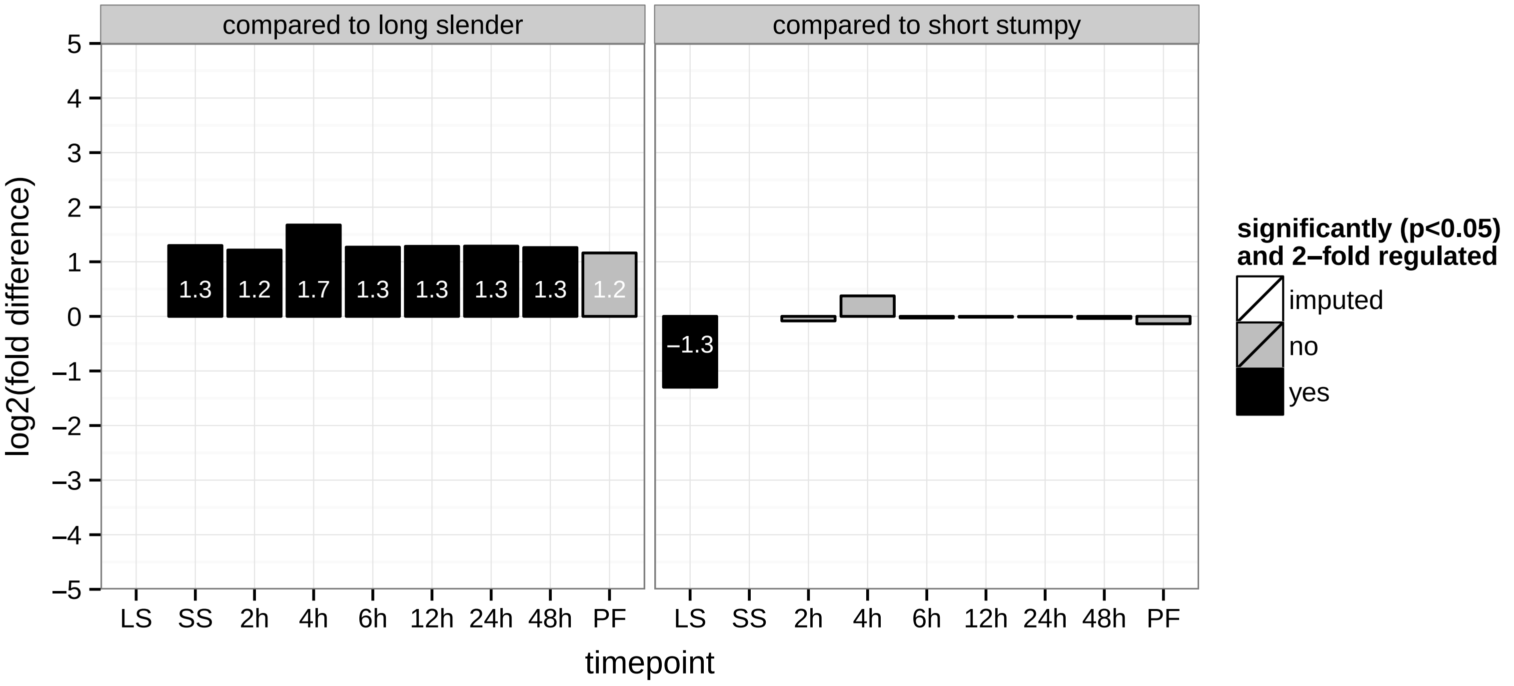
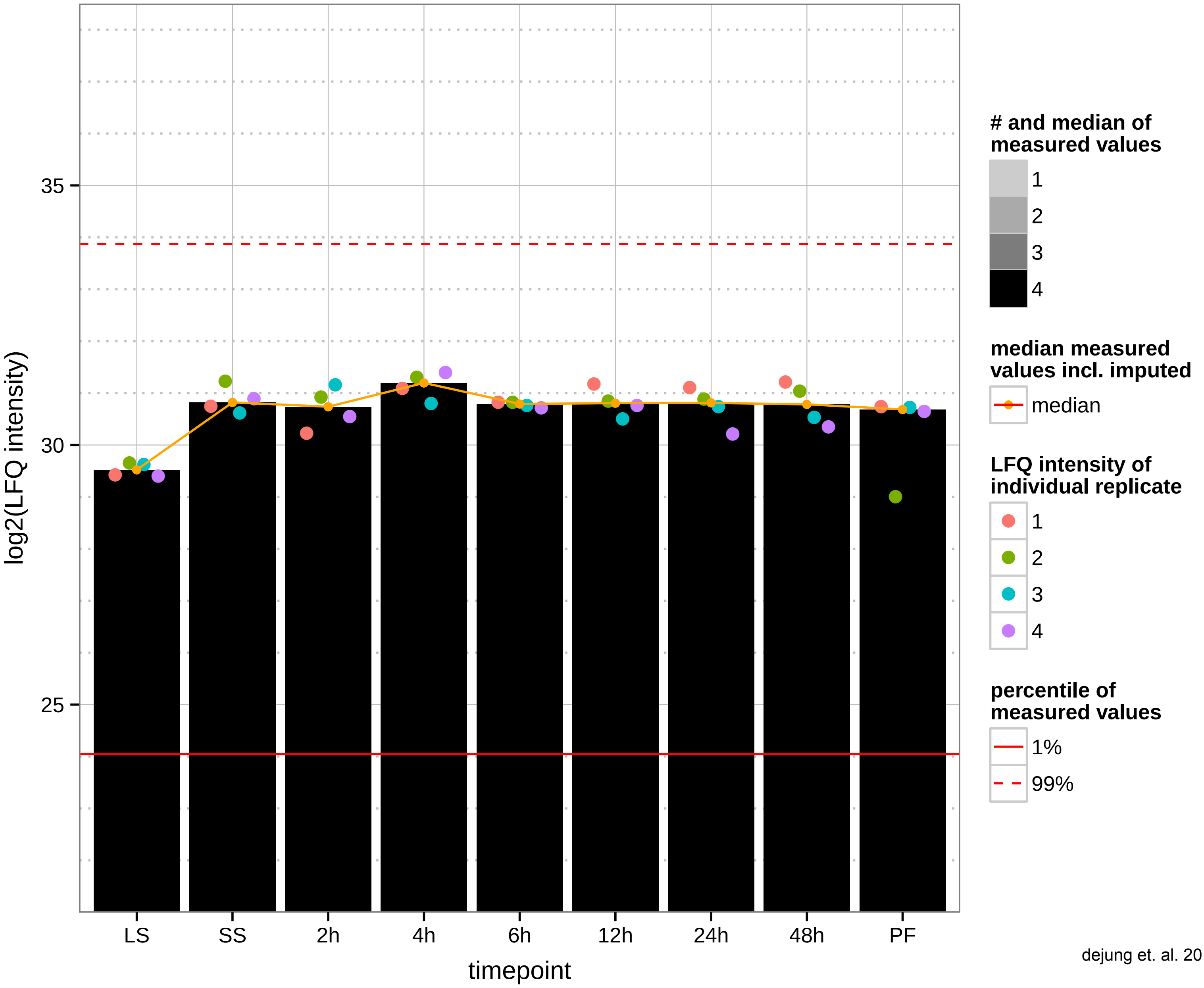
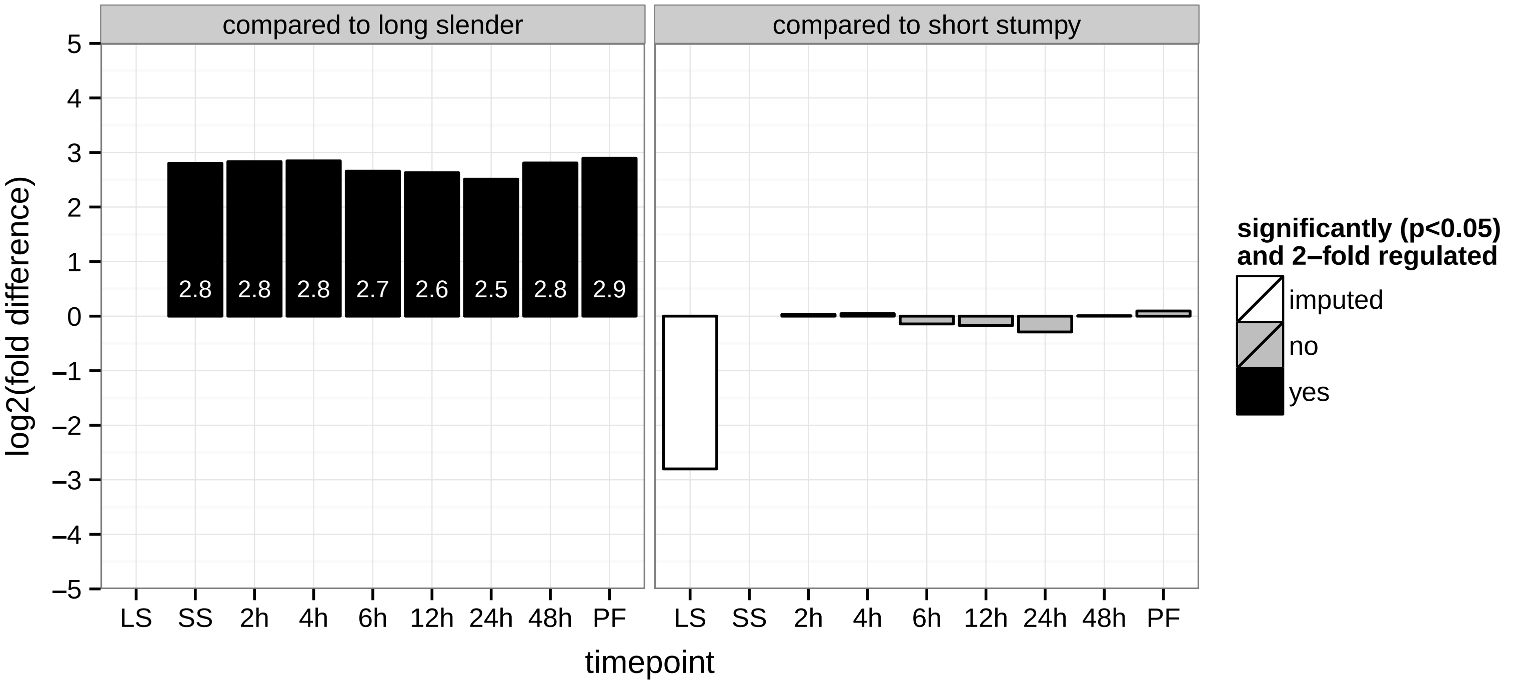
nucleolar RNA–binding protein, truncated, nucleolar RNA–binding protein (Nopp44/46)
Tb927.8.760;Tb927.8.740
AGOF: RNA binding, nucleic acid binding, protein binding, protein serine/threonine/tyrosine kinase activity
AGOC: nucleolus
AGOP: null, RNA metabolic process
PGOF: null
PGOC: null
PGOP: null

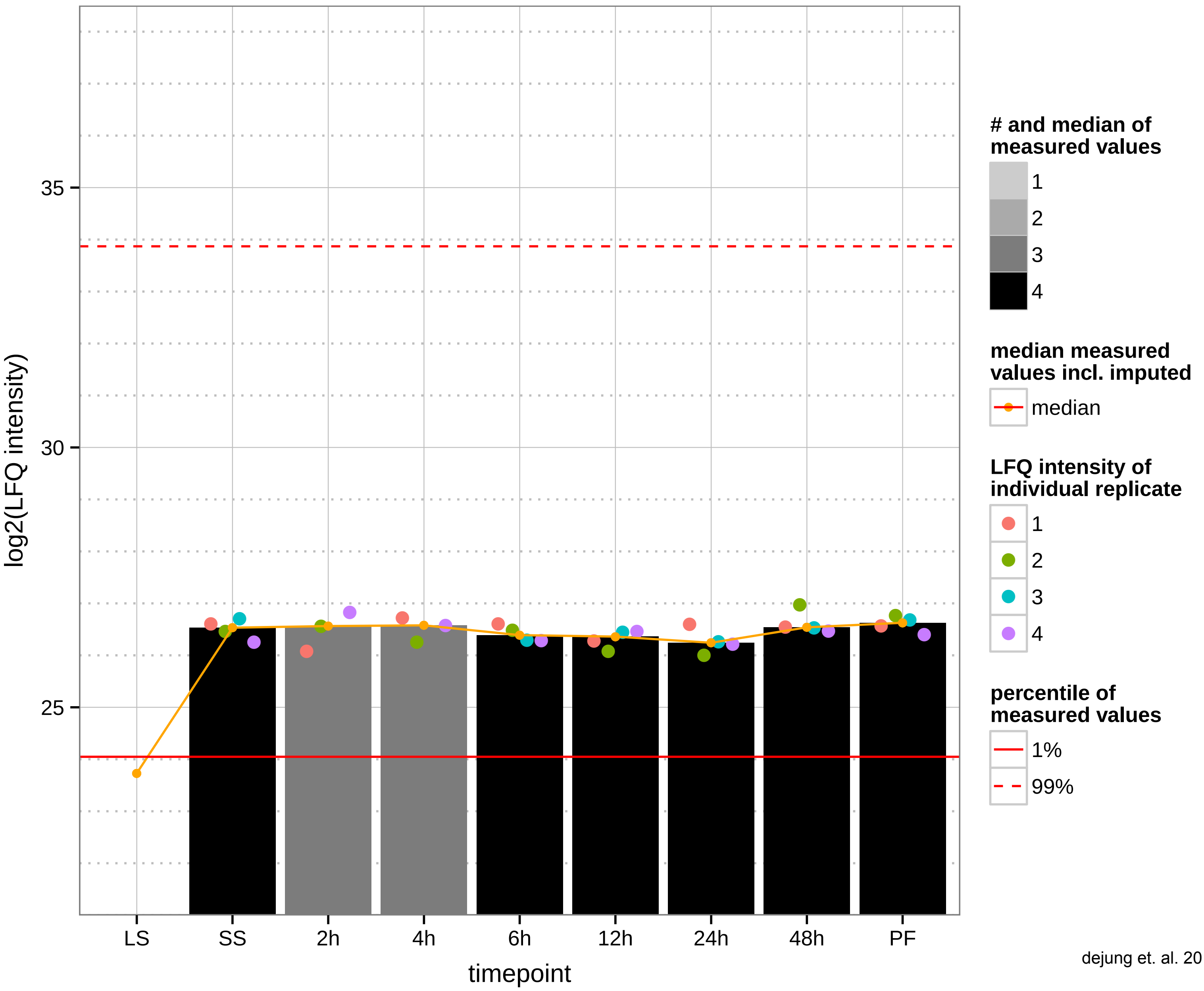




dejung et. al. 2015

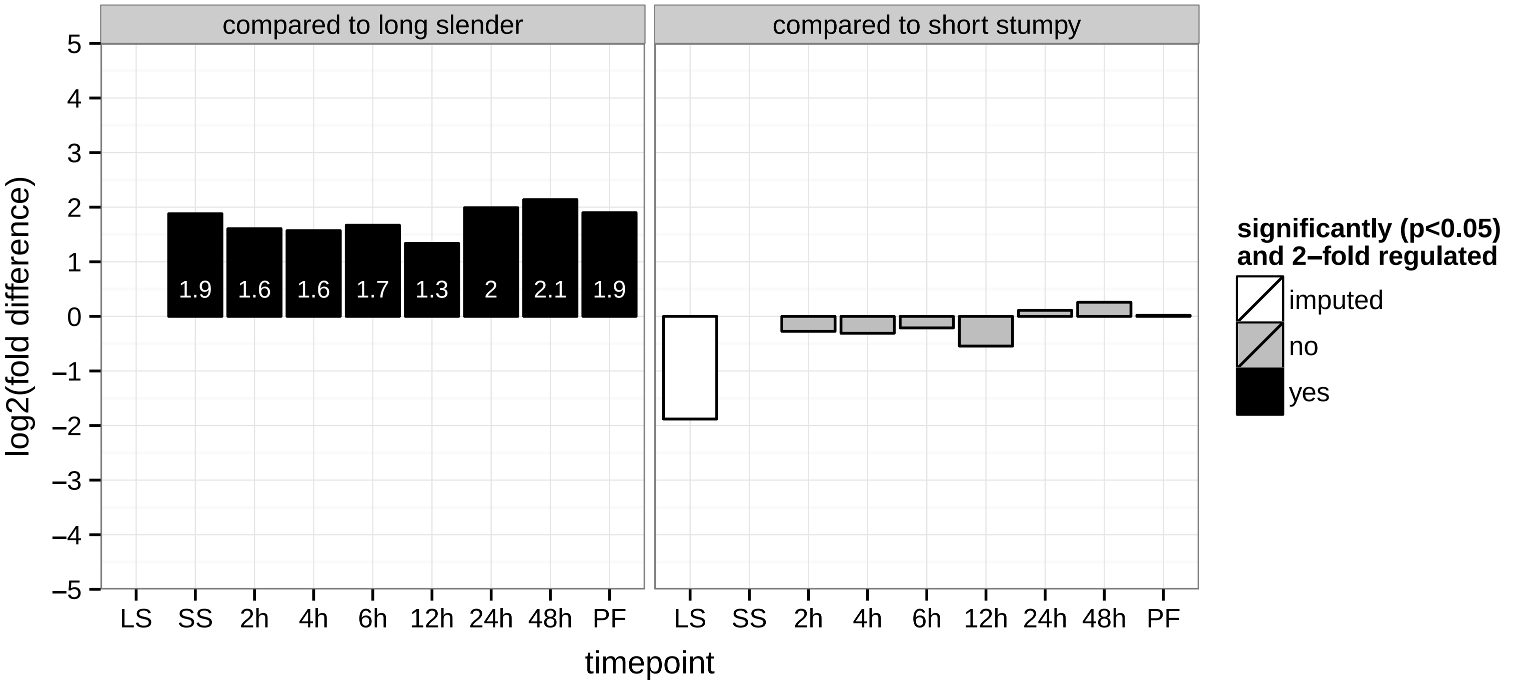
hypothetical protein, conserved
Tb927.8.7950
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

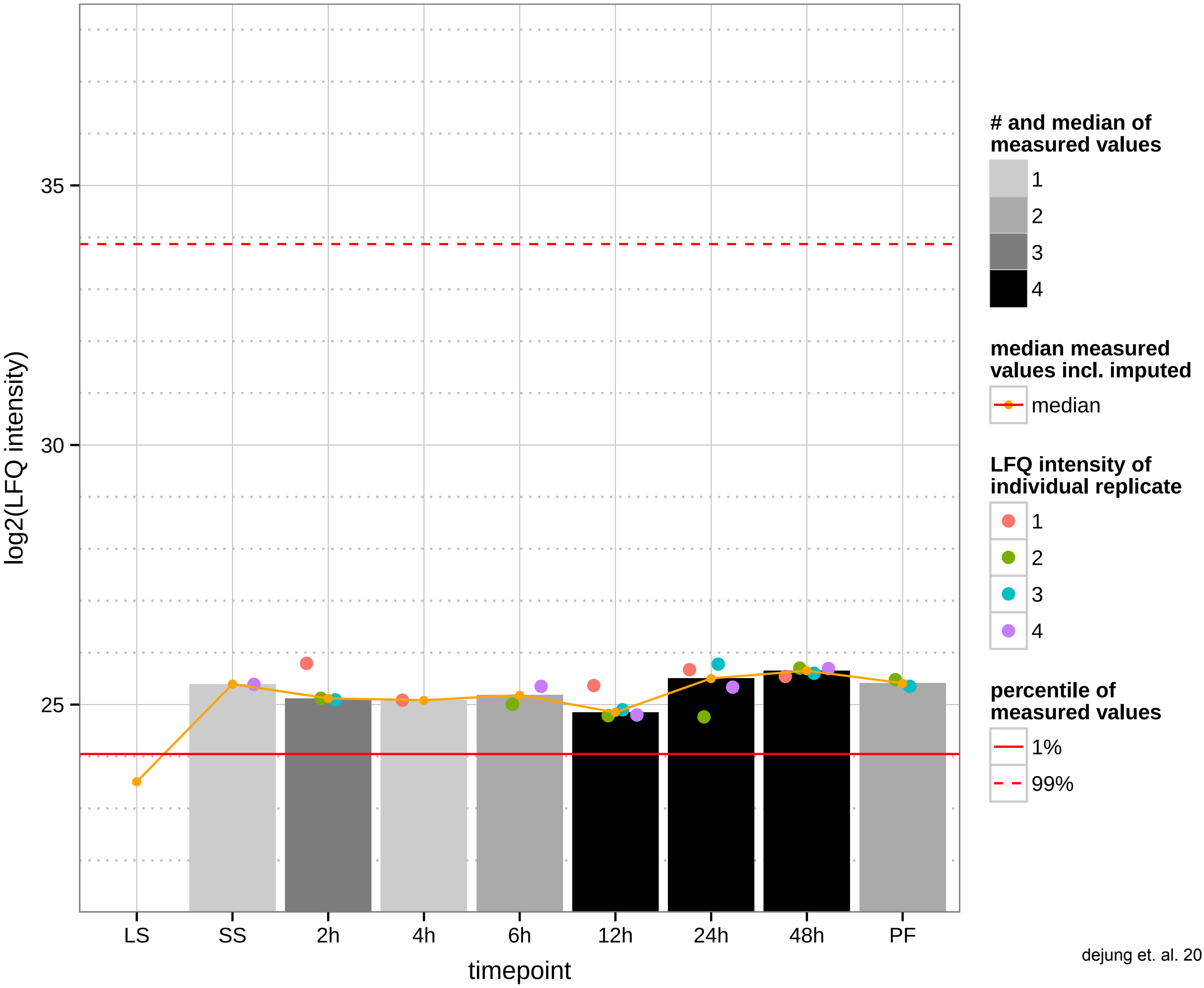




dejung et. al. 2015

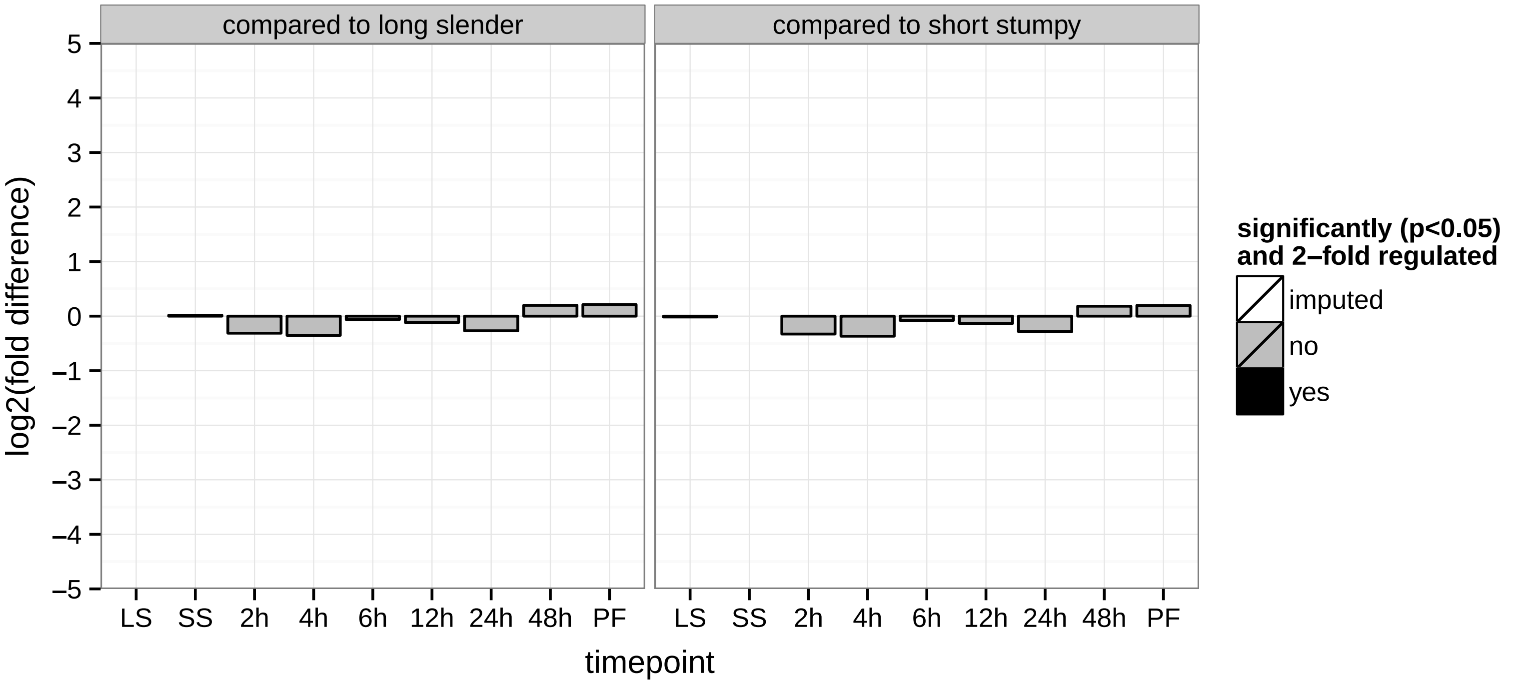
monoglyceride lipase, putative
Tb927.8.8020
AGOF: hydrolase activity
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

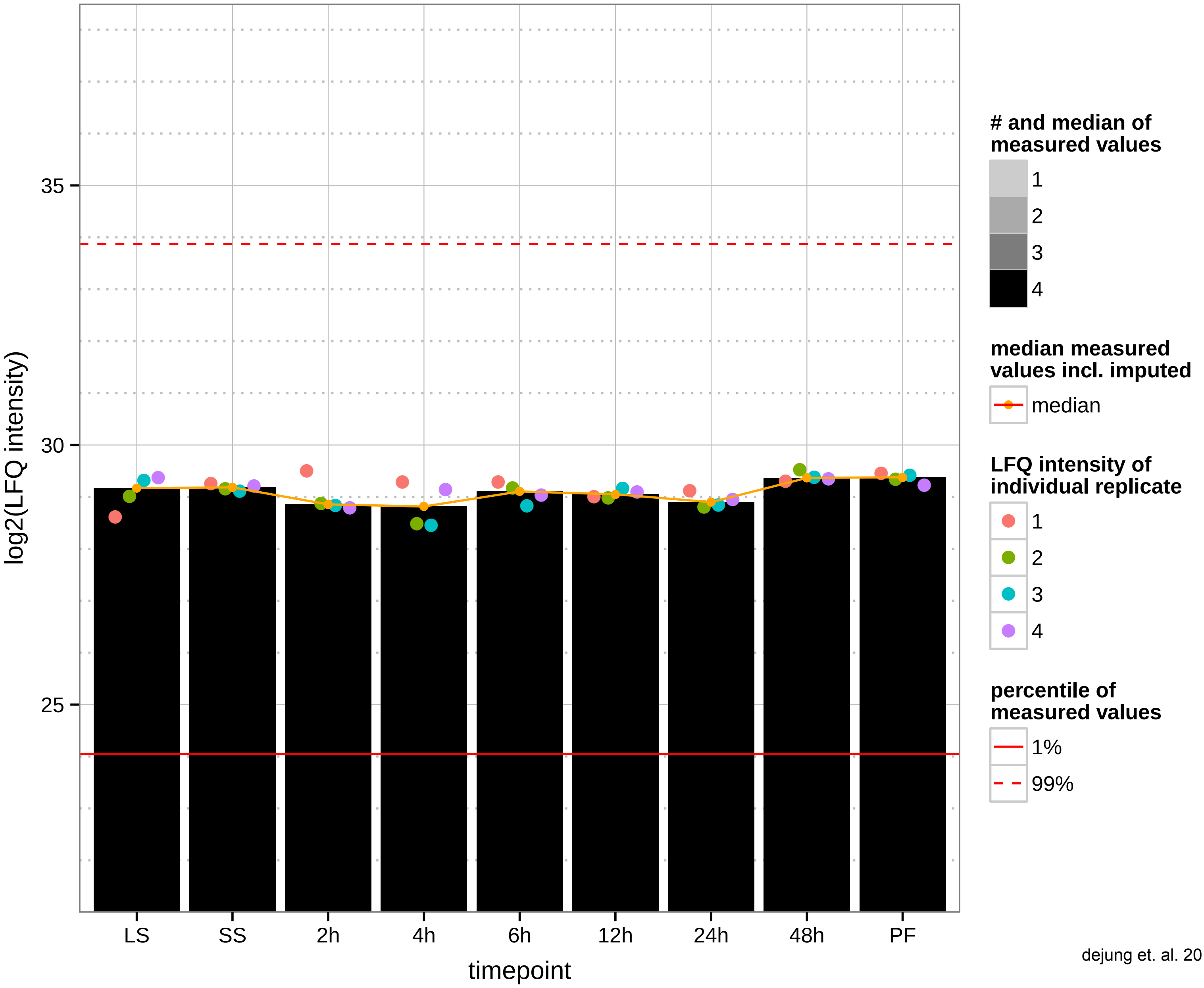




dejung et. al. 2015

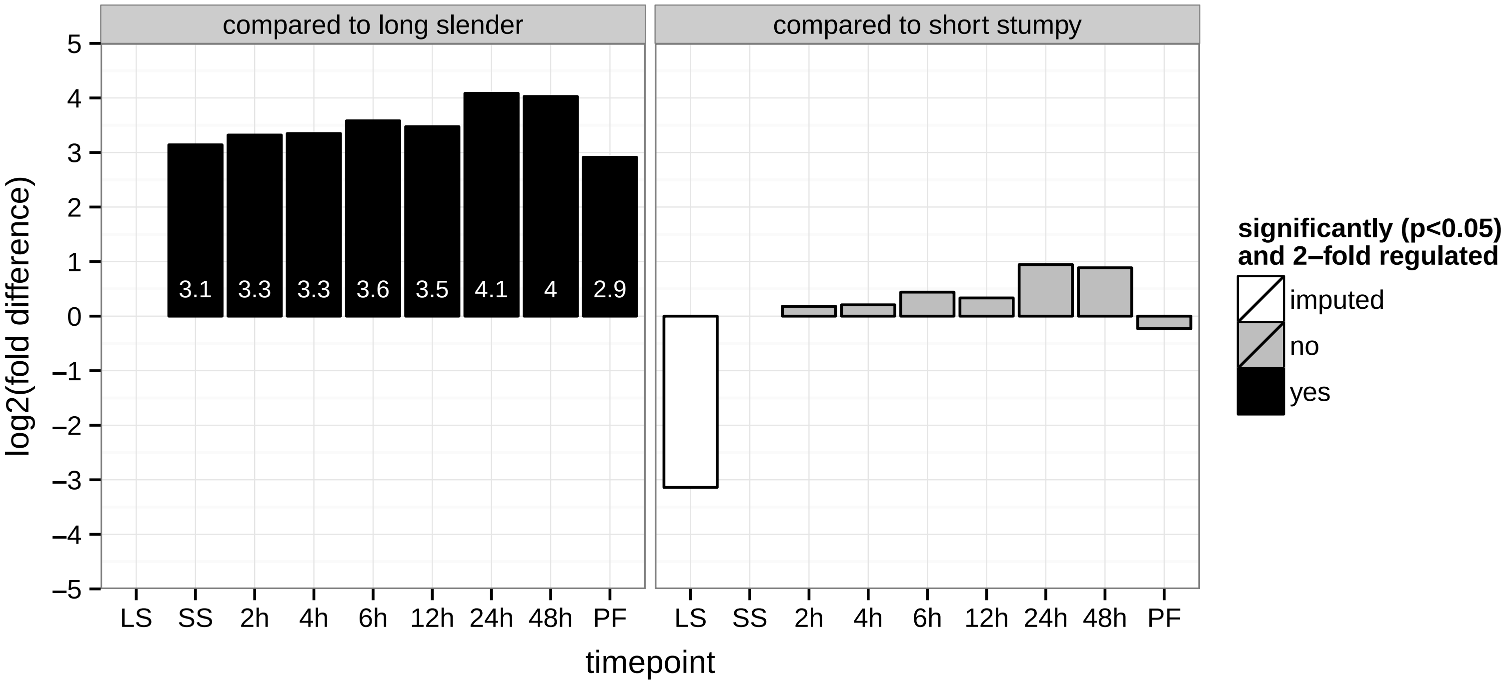
radial spoke protein RSP9, putative
Tb927.8.810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

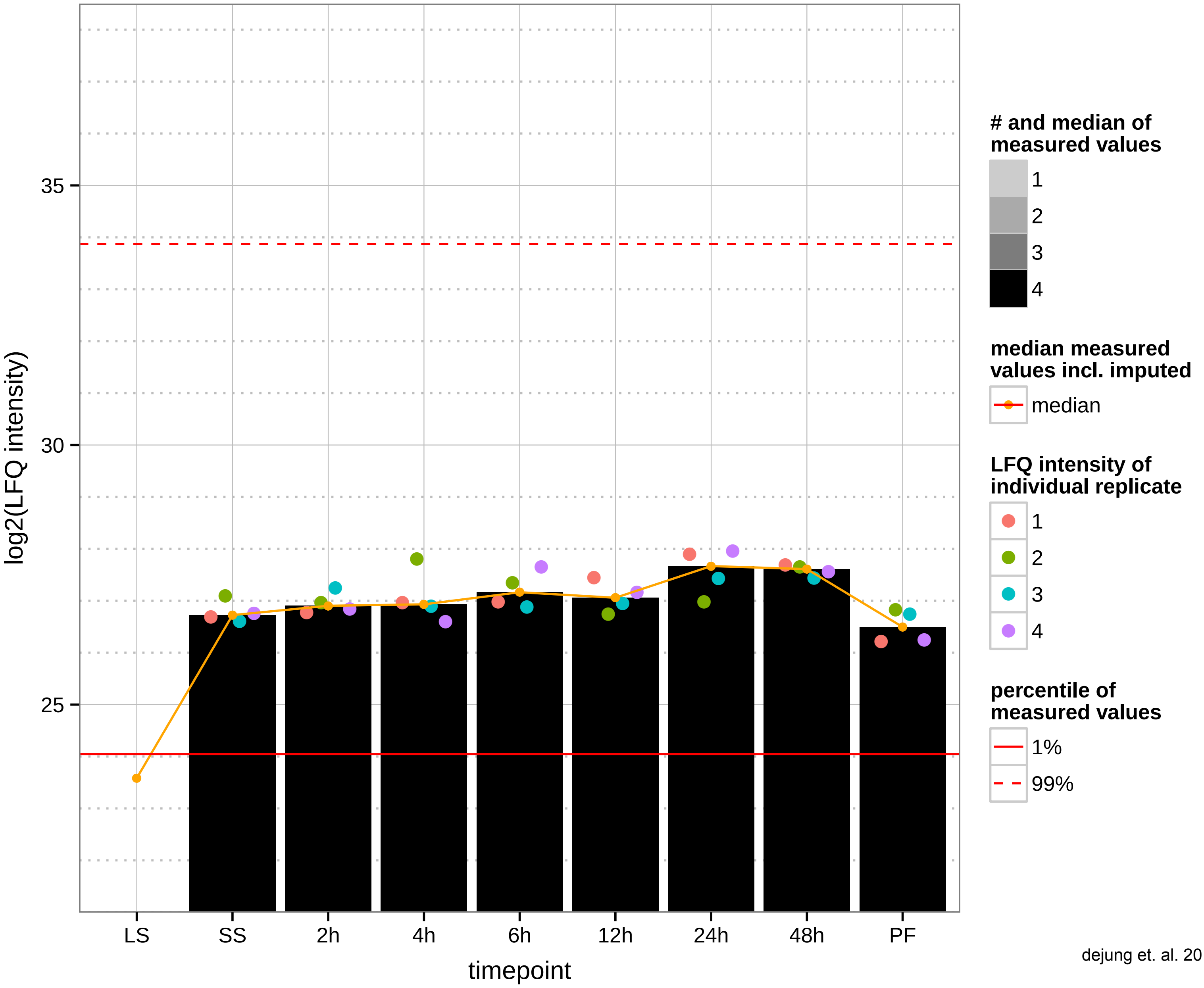




dejung et. al. 2015

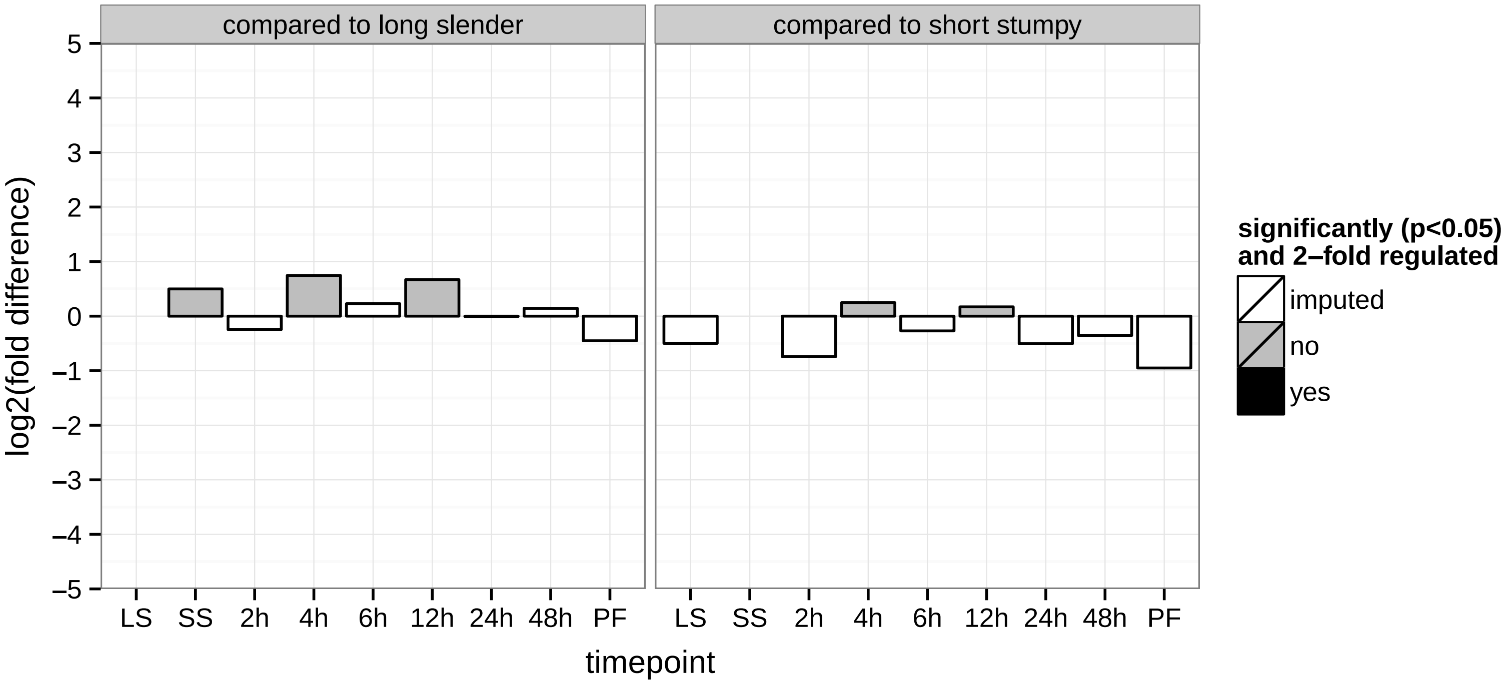
mitochondrial RNA binding protein 1, putative (MRB8170)
Tb927.8.8170
AGOF: RNA binding
AGOC: mitochondrion
AGOP: RNA biosynthetic process
PGOF: null
PGOC: null
PGOP: null

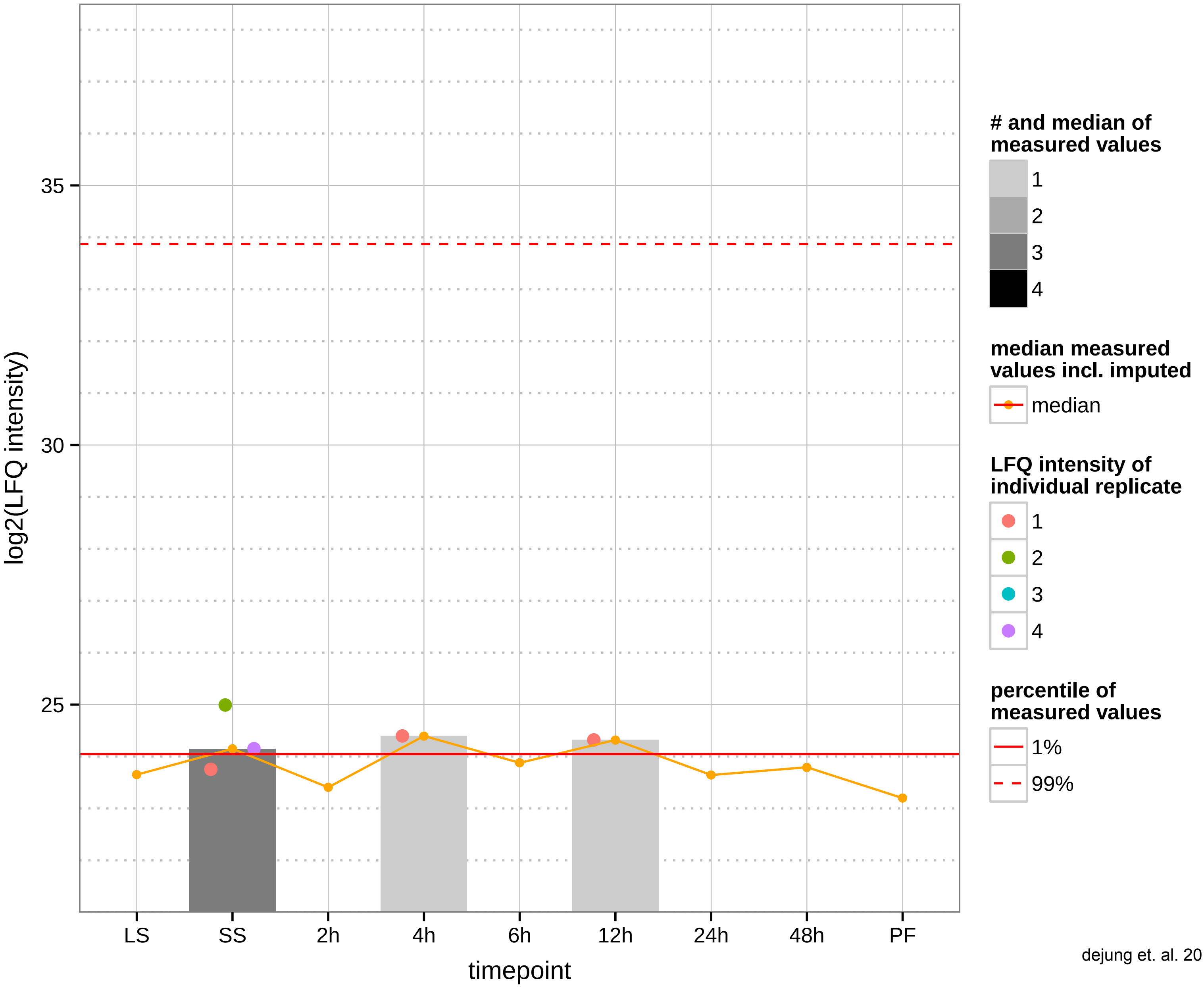




dejung et. al. 2015

amino acid transporter, putative
Tb927.8.8250;Tb927.8.8260
AGOF: amine transmembrane transporter activity
AGOC: integral to membrane
AGOP: amino acid transport
PGOF: null
PGOC: null
PGOP: null





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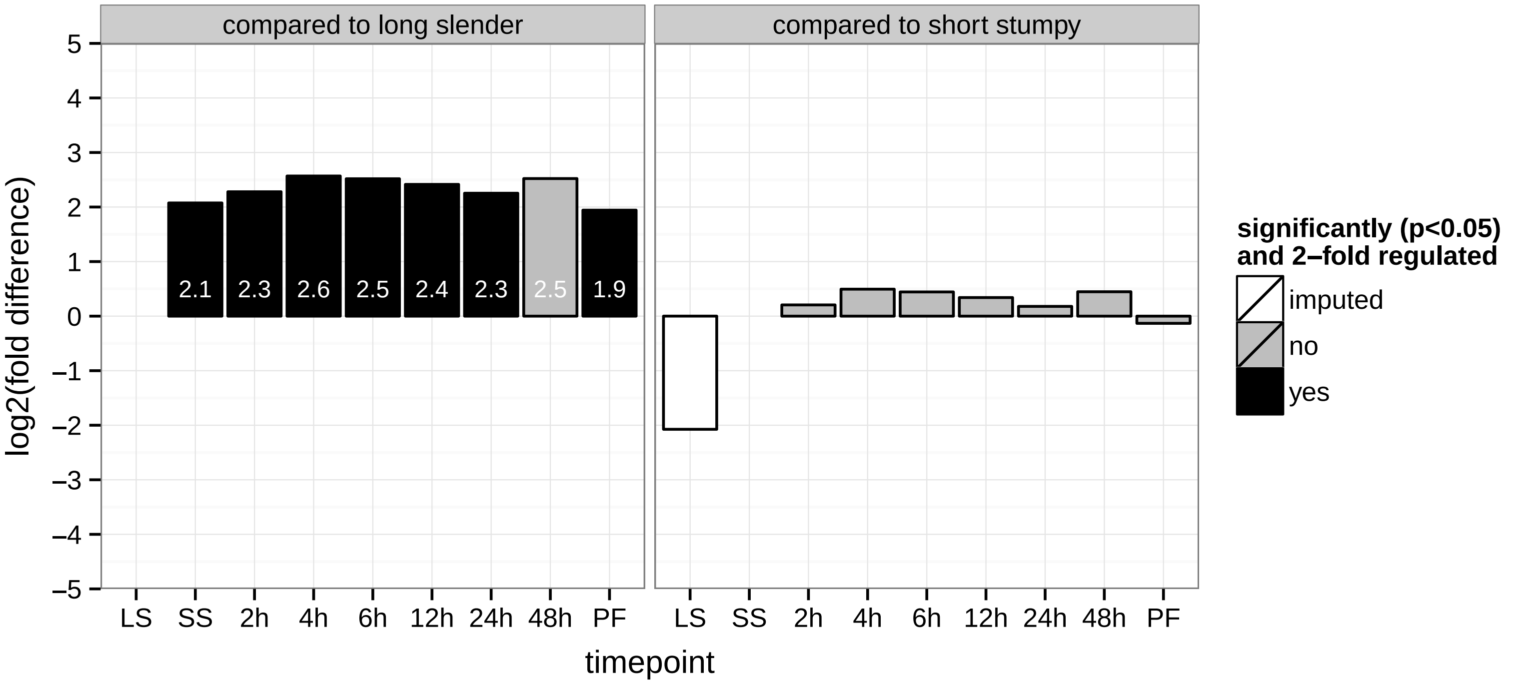
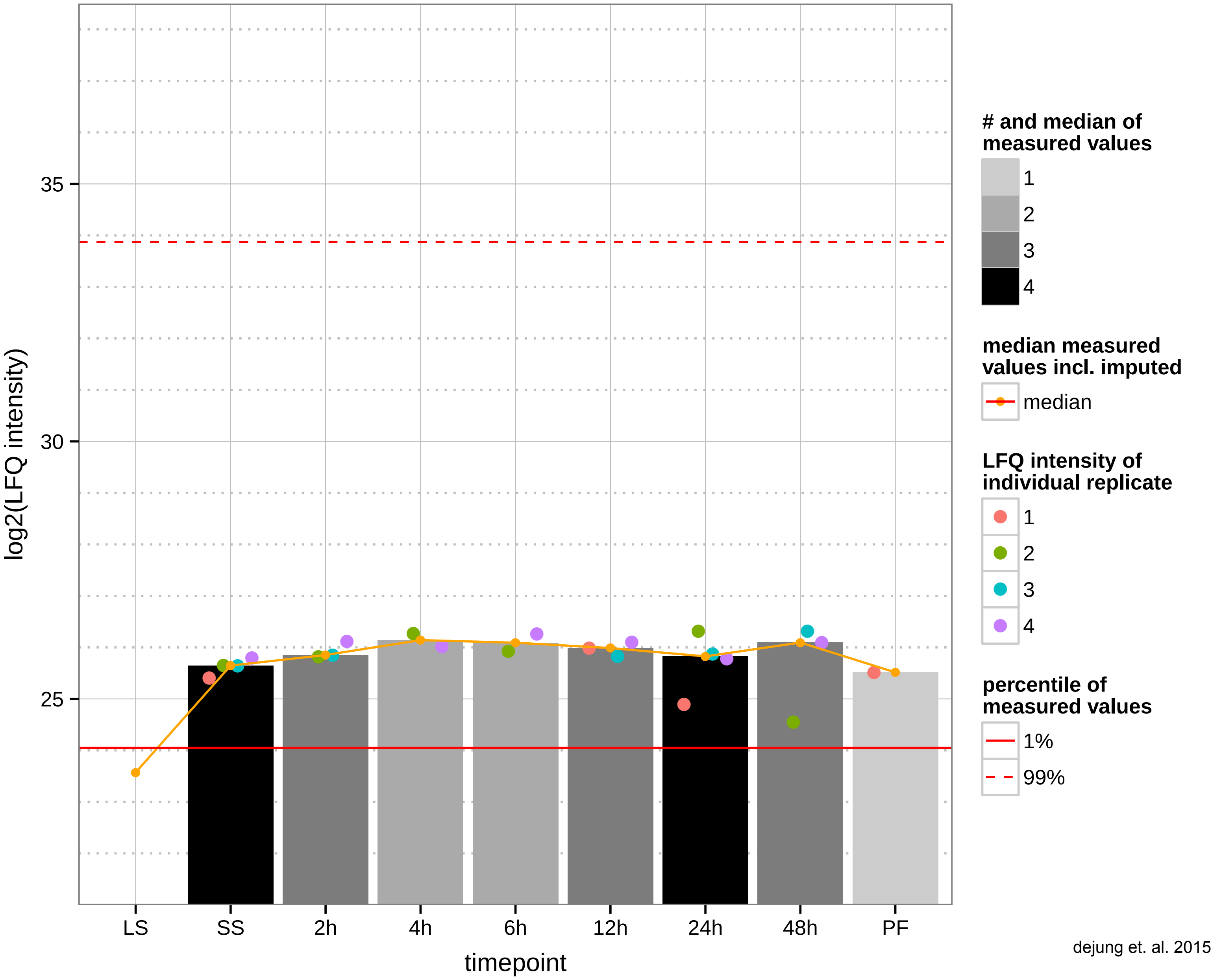
ubiquitin–conjugating enzyme E2, putative, ubiquitin–protein ligase, ubiquitin carrier protein, putative (PEX4)
Tb927.8.920
AGOF: ubiquitin–protein ligase activity
AGOC: null
AGOP: cellular protein modification process, post–translational protein modification, regulation of protein metabolic process
PGOF: acid–amino acid ligase activity
PGOC: null
PGOP: null





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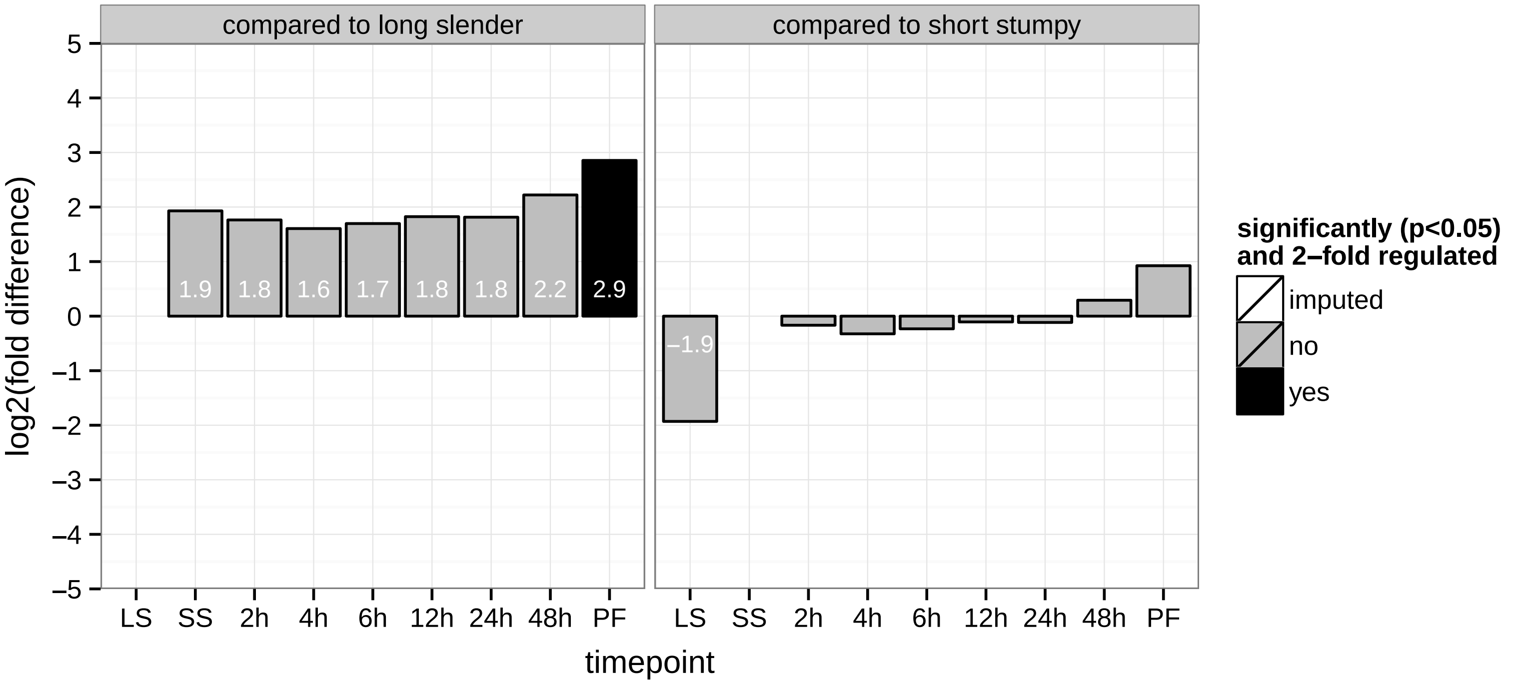
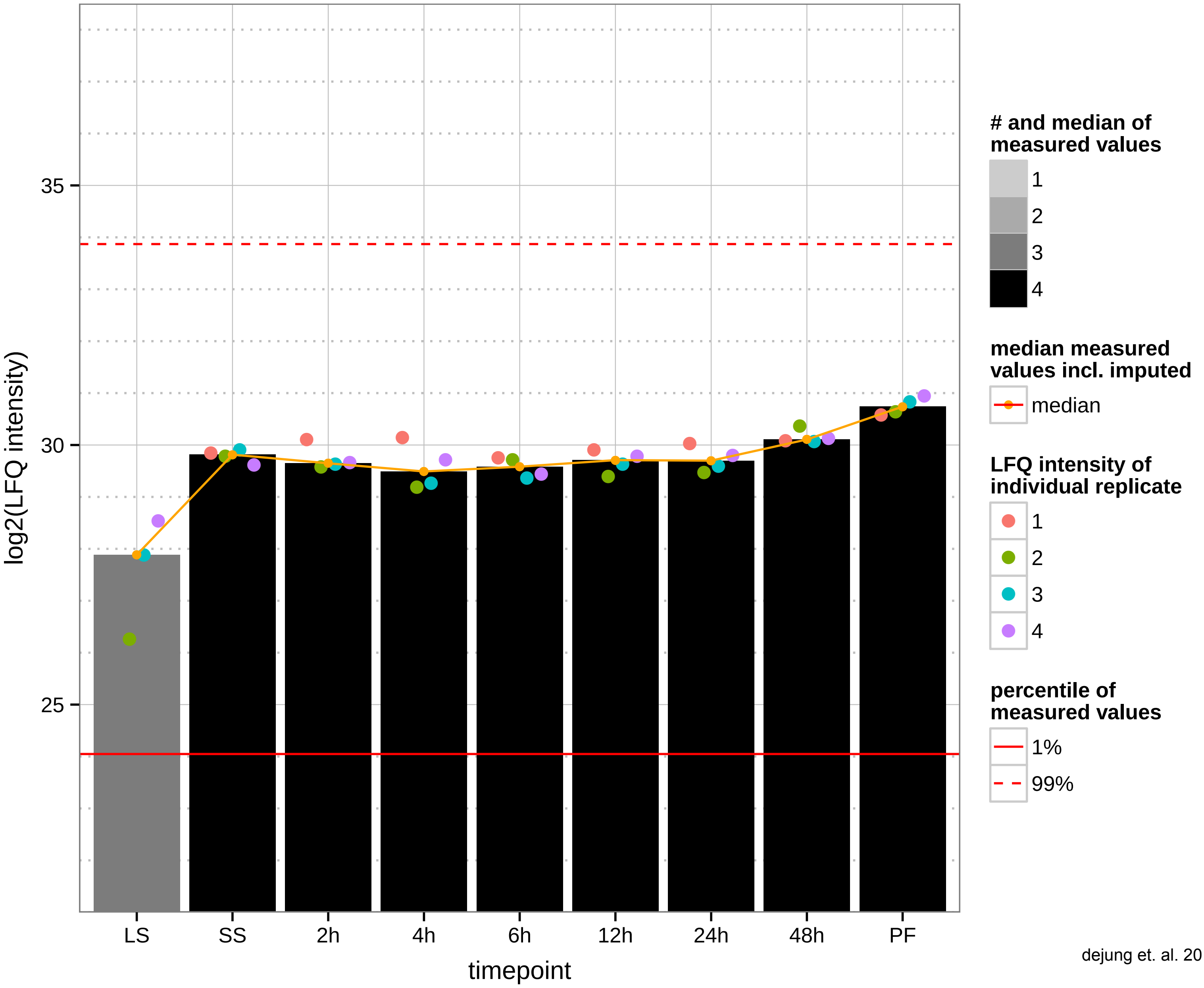
phosphoacetylglucosamine mutase, putative, acetylglucosaminephosphomutase, N−acetylglucosamine−phosphate mutase
Tb927.8.980
AGOF: phosphoacetylglucosamine mutase activity
AGOC: null
AGOP: carbohydrate metabolic process, glucosamine metabolic process
PGOF: intramolecular transferase activity, phosphotransferases, phosphoacetylglucosamine mutase activity
PGOC: null
PGOP: carbohydrate metabolic process





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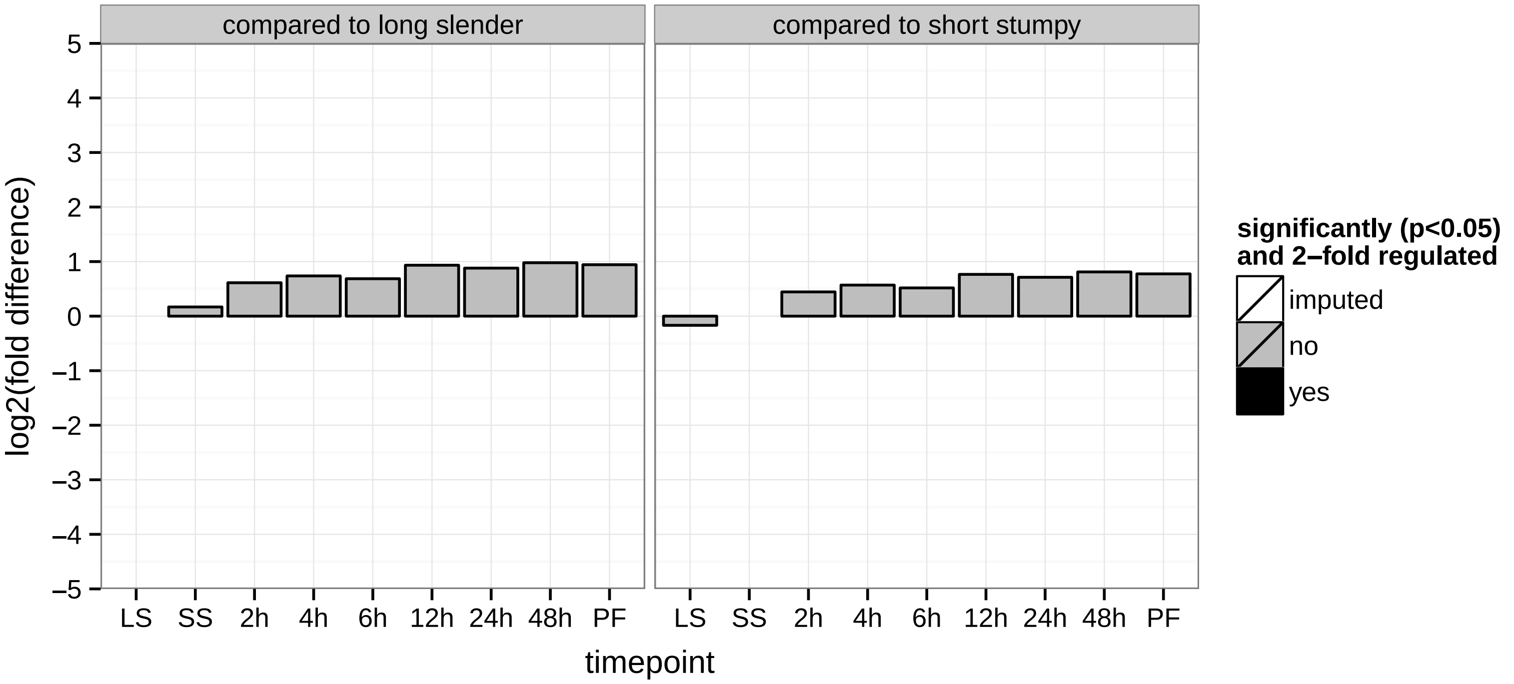
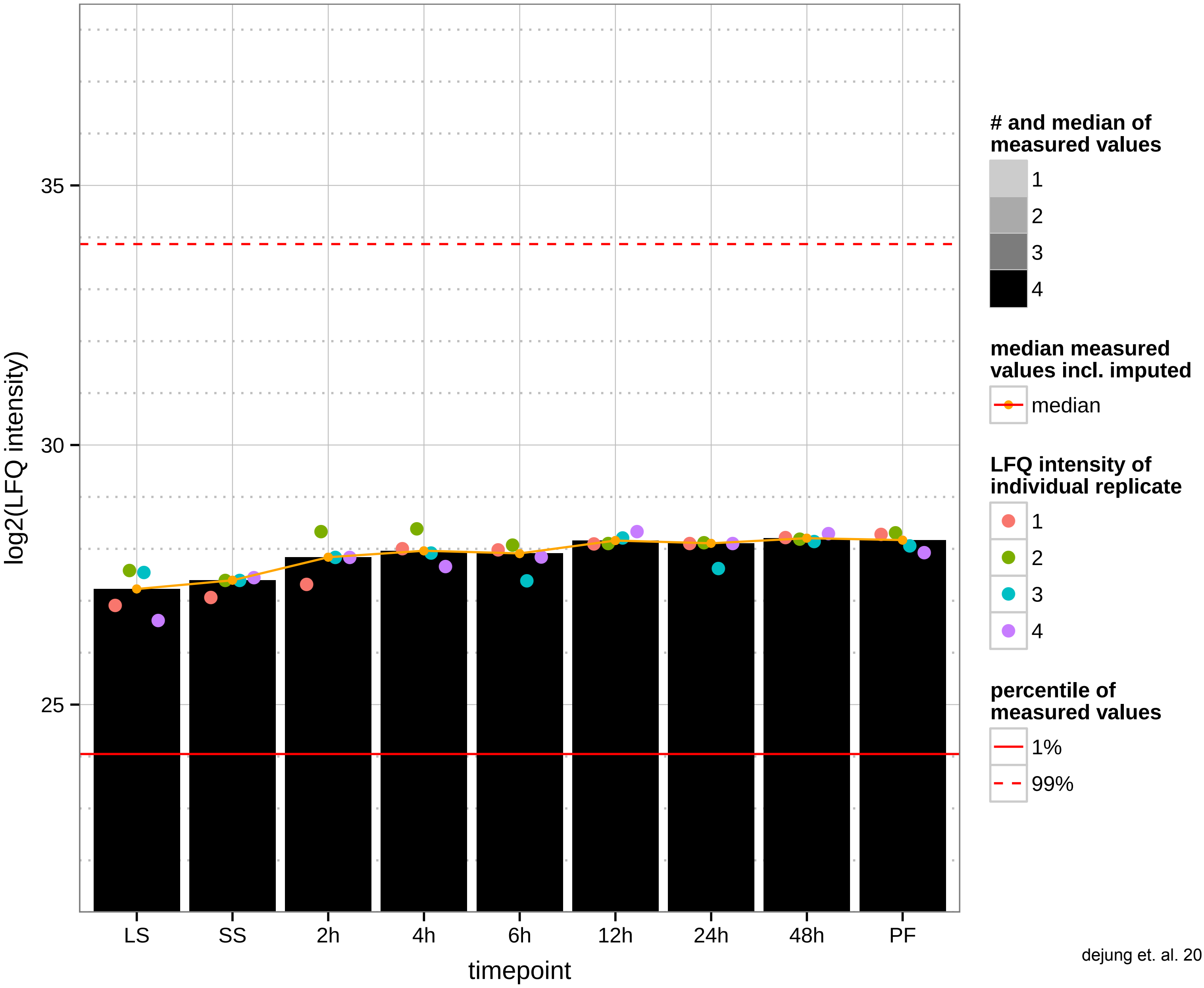
RNA–binding protein 33 (RNA–binding motif protein 33) (RBP33)
Tb927.8.990
AGOF: RNA binding, mRNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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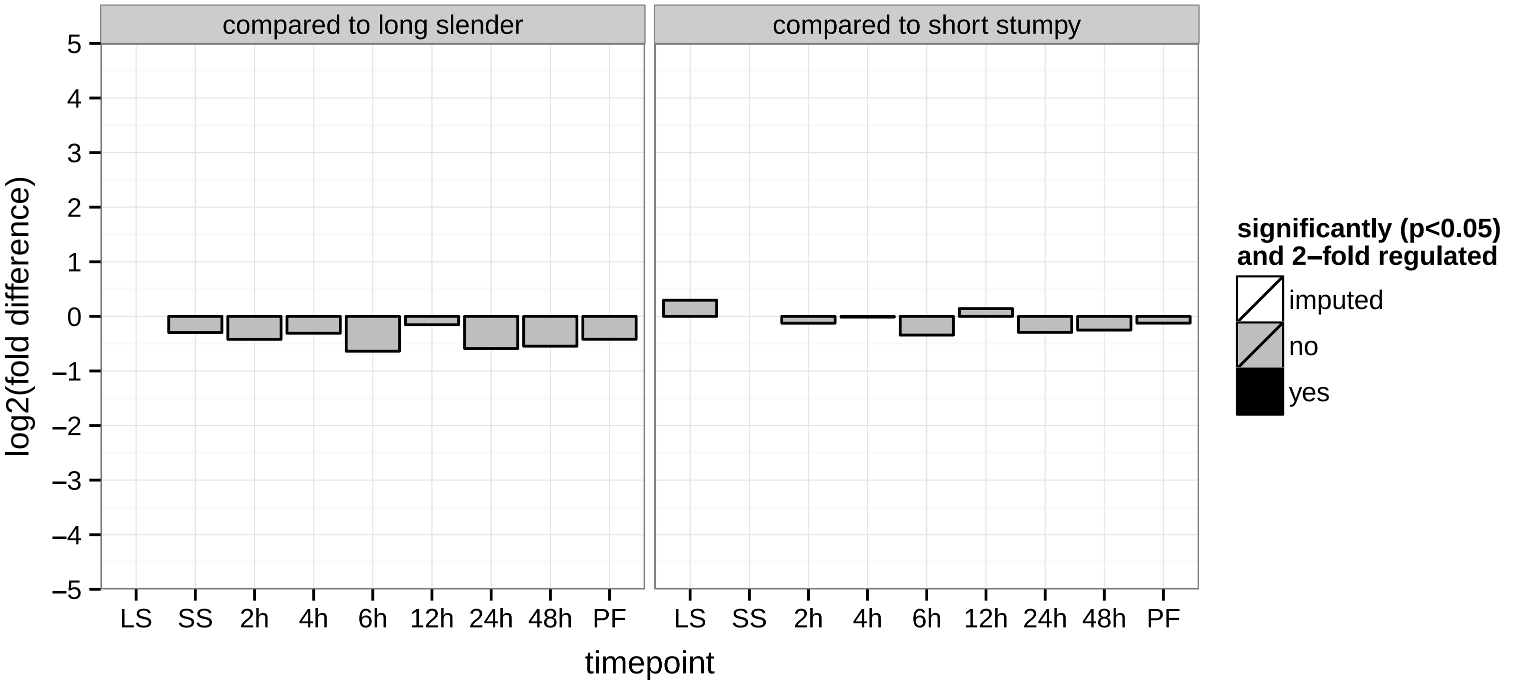
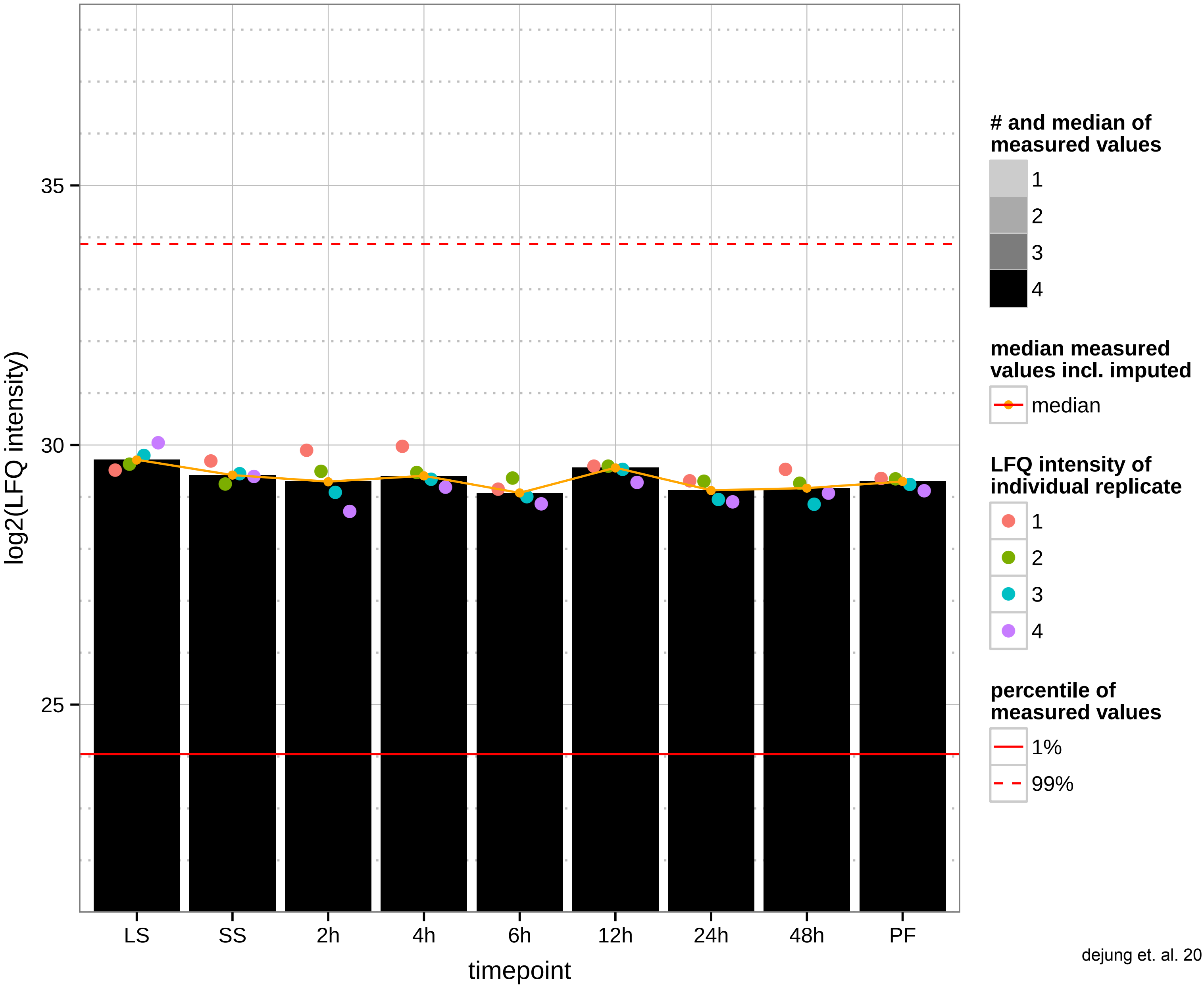
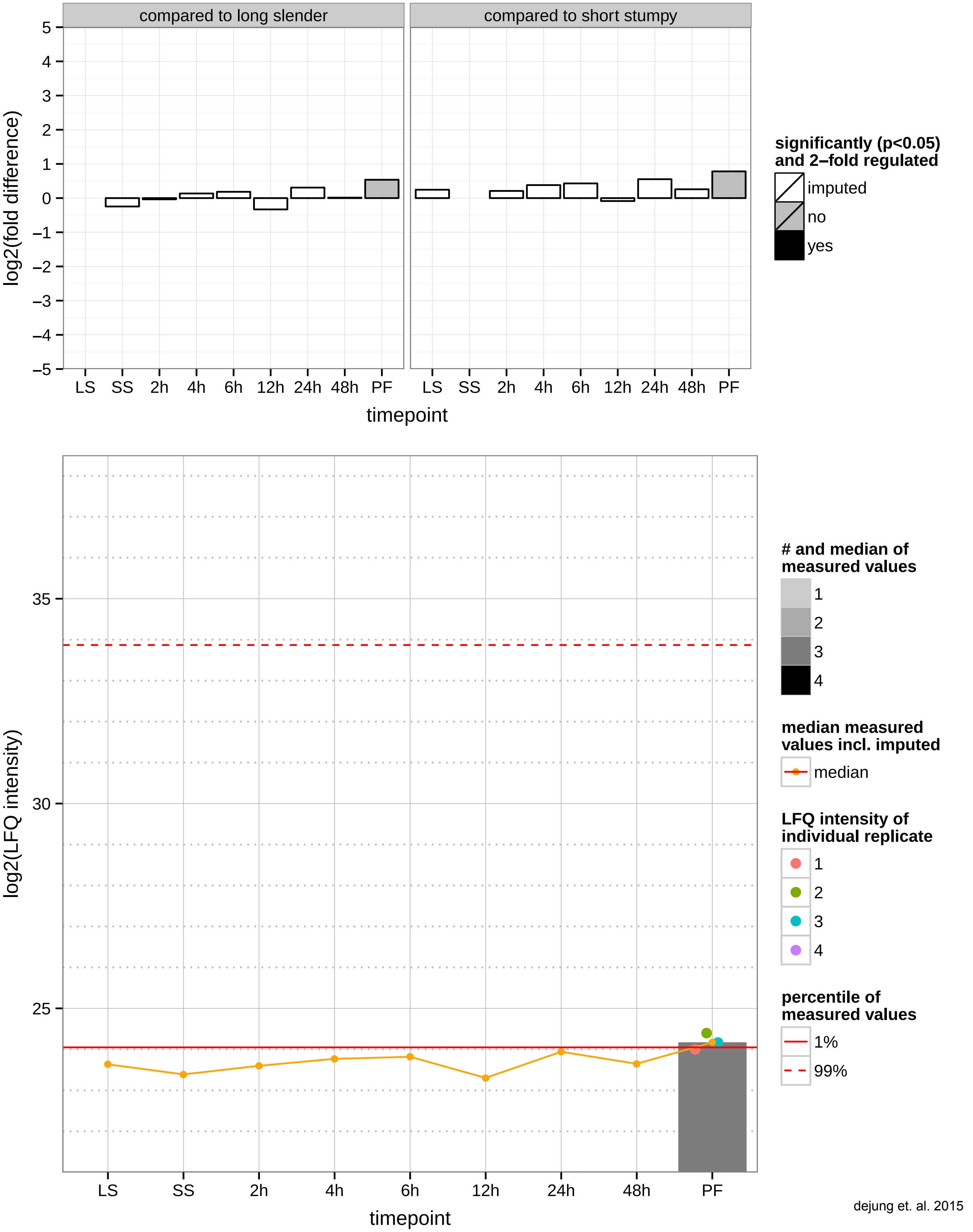
chaperone protein DNAj, putative
Tb927.9.10010
AGOF: heat shock protein binding, unfolded protein binding
AGOC: integral to membrane, mitochondrial inner membrane
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.10070
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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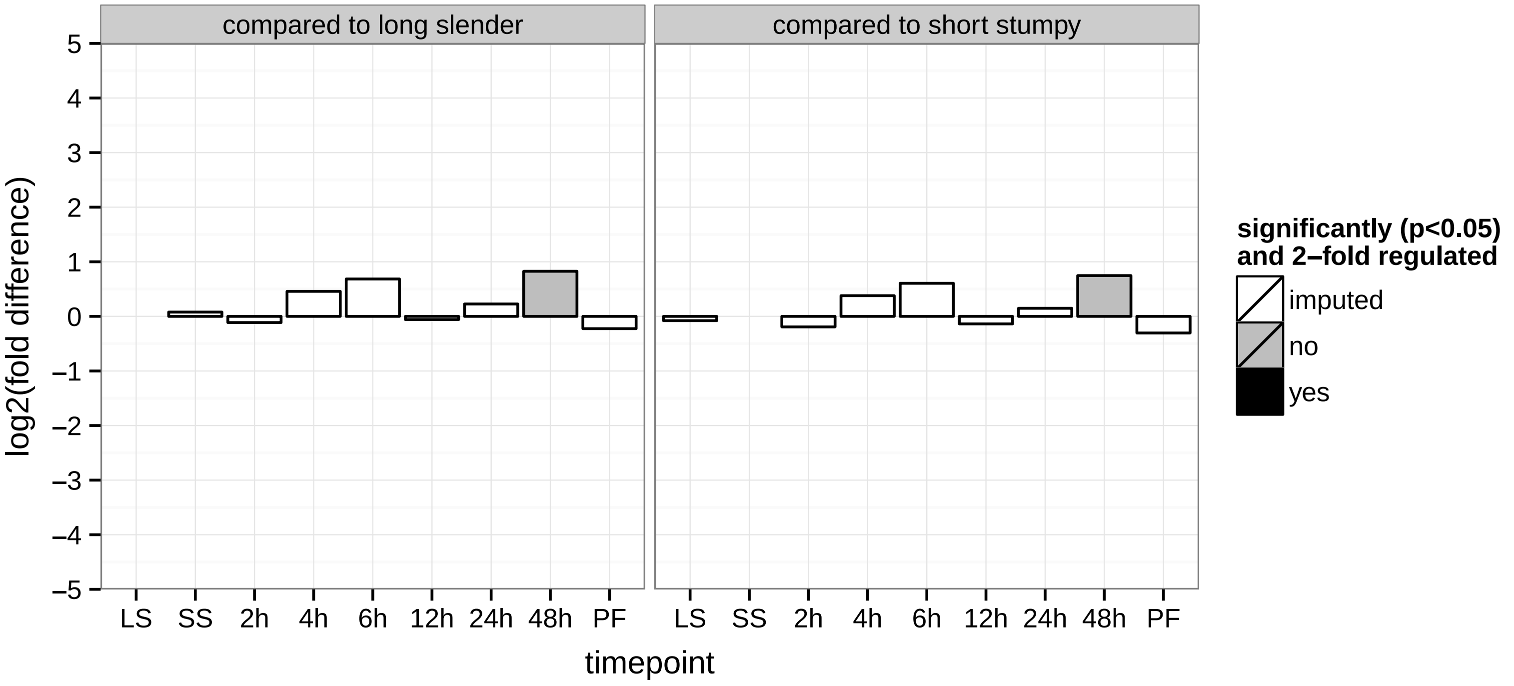
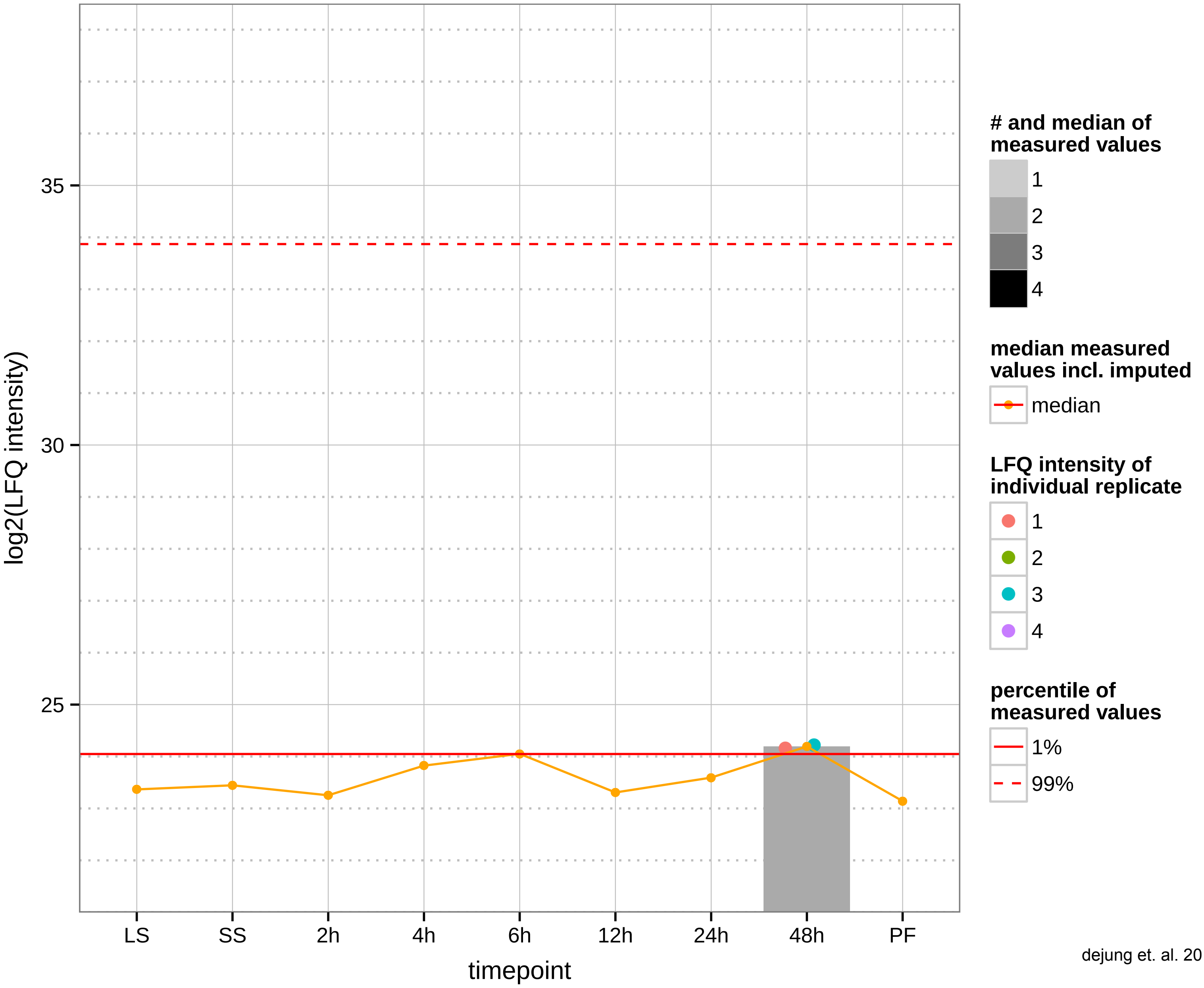
phosphatidylserine decarboxylase, putative
Tb927.9.10080
AGOF: phosphatidylserine decarboxylase activity
AGOC: mitochondrion
AGOP: phosphatidylserine catabolic process, phospholipid biosynthetic process
PGOF: phosphatidylserine decarboxylase activity
PGOC: null
PGOP: phospholipid biosynthetic process





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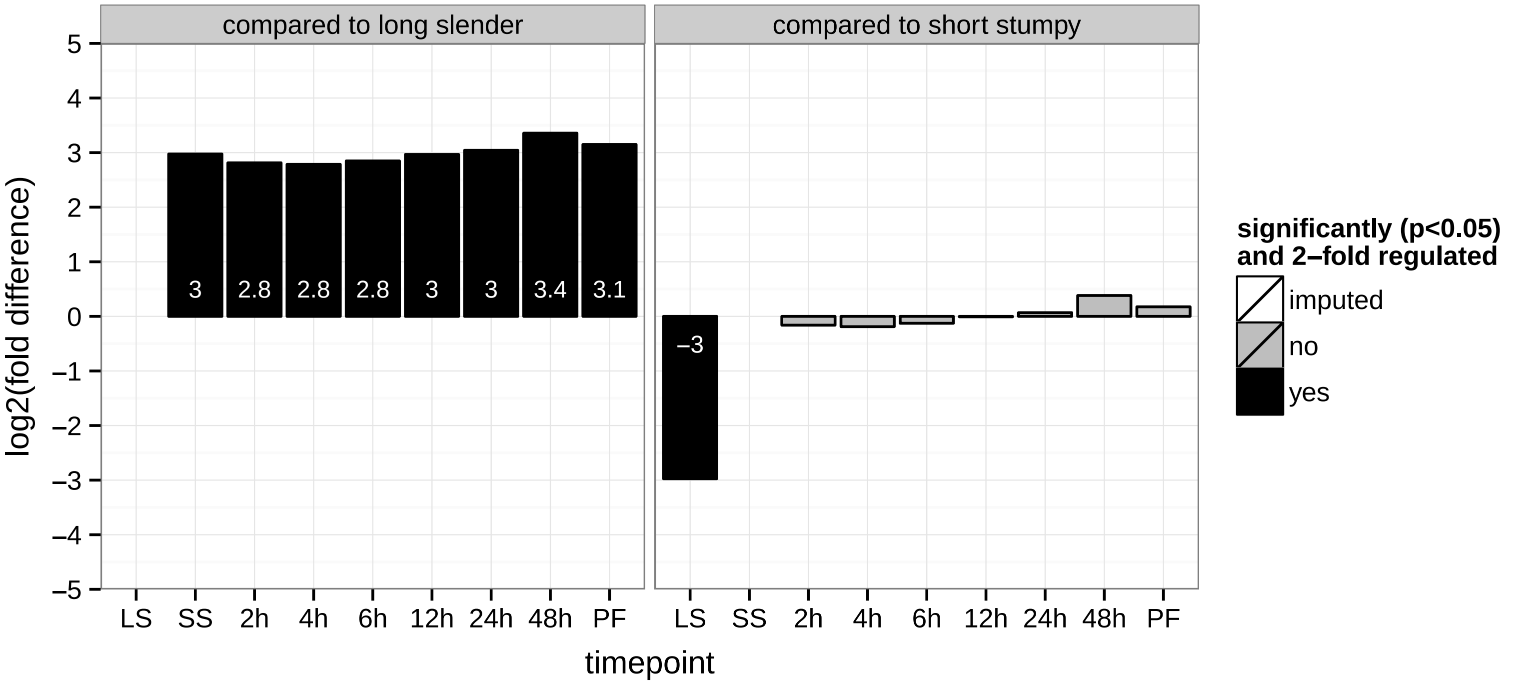
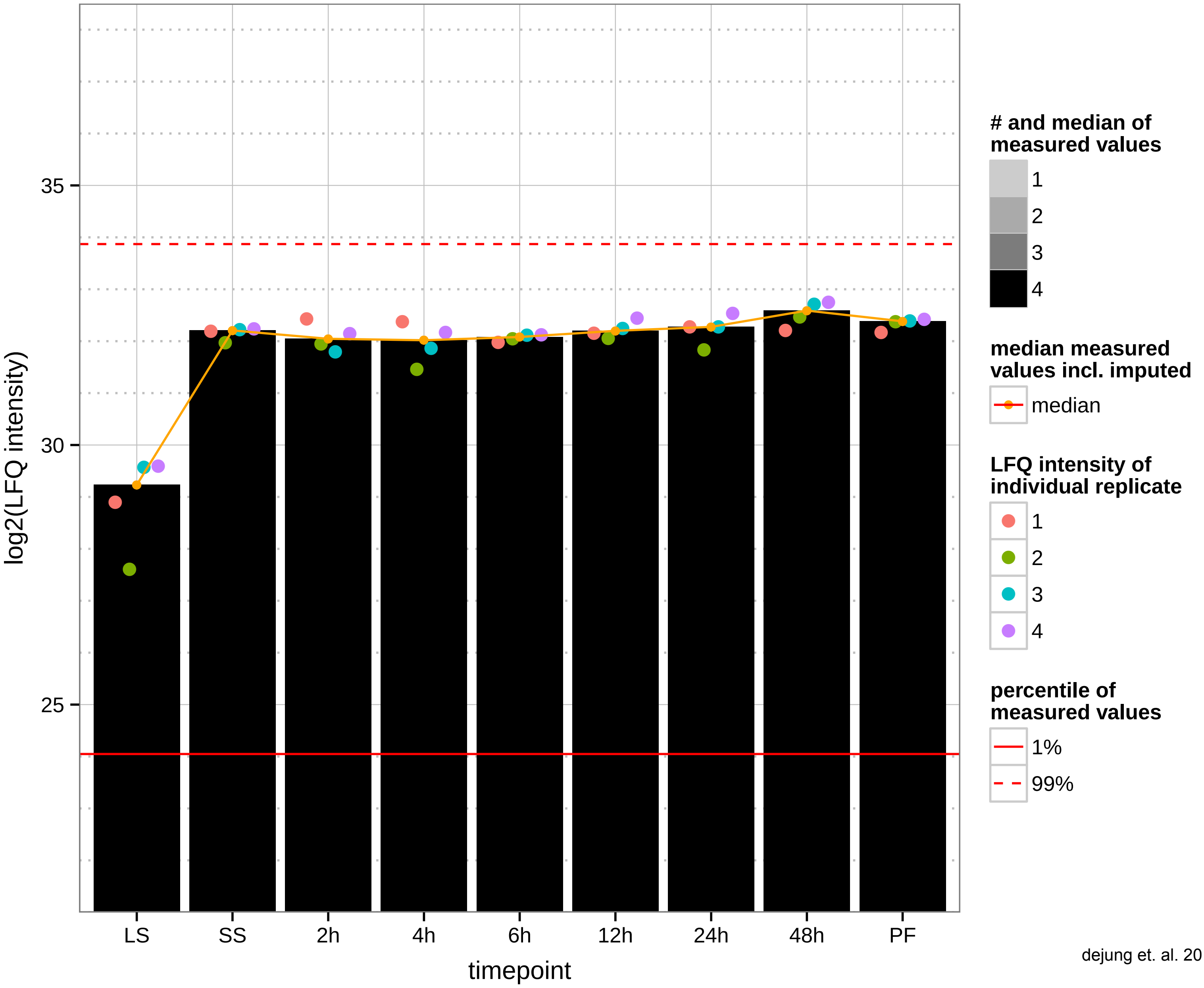
hypothetical protein, conserved
Tb927.9.10100
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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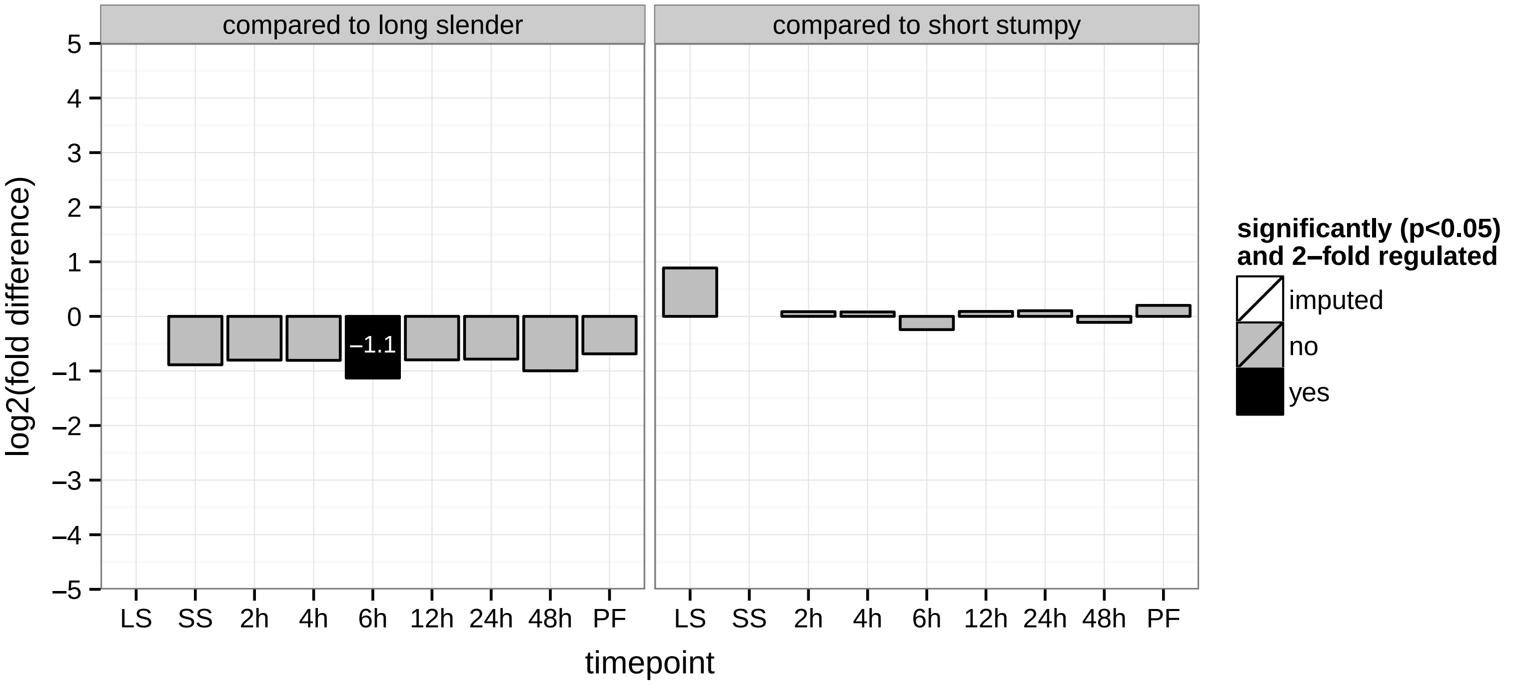
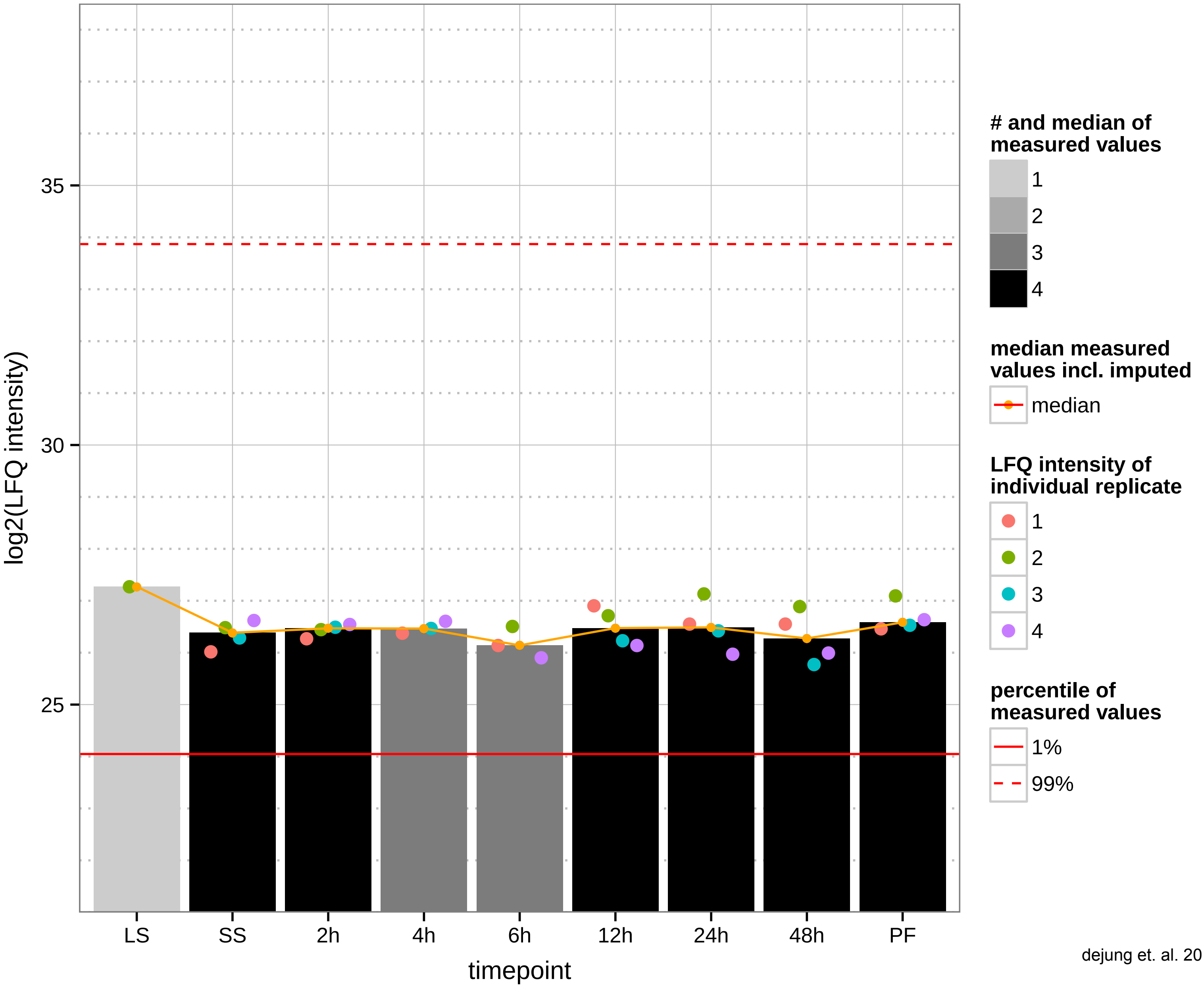
hypothetical protein, conserved
Tb927.9.10160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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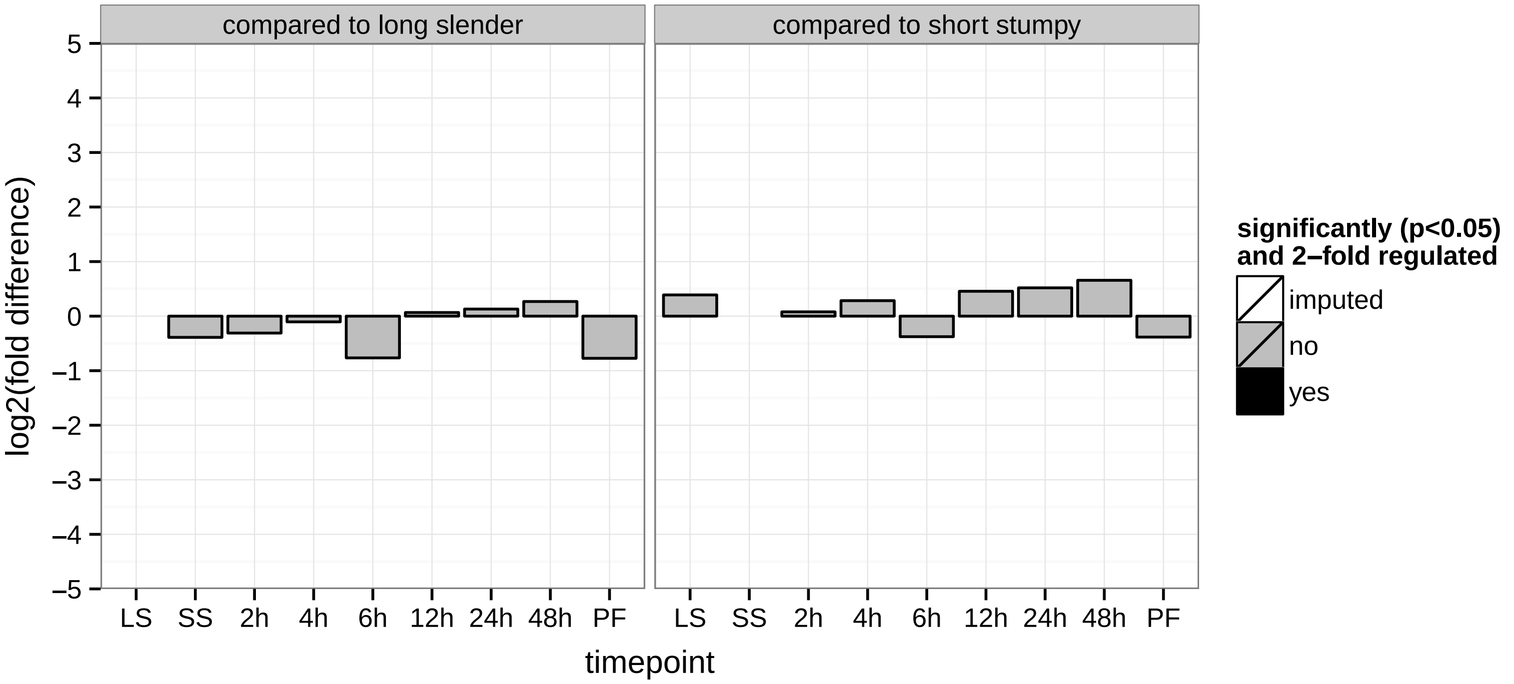
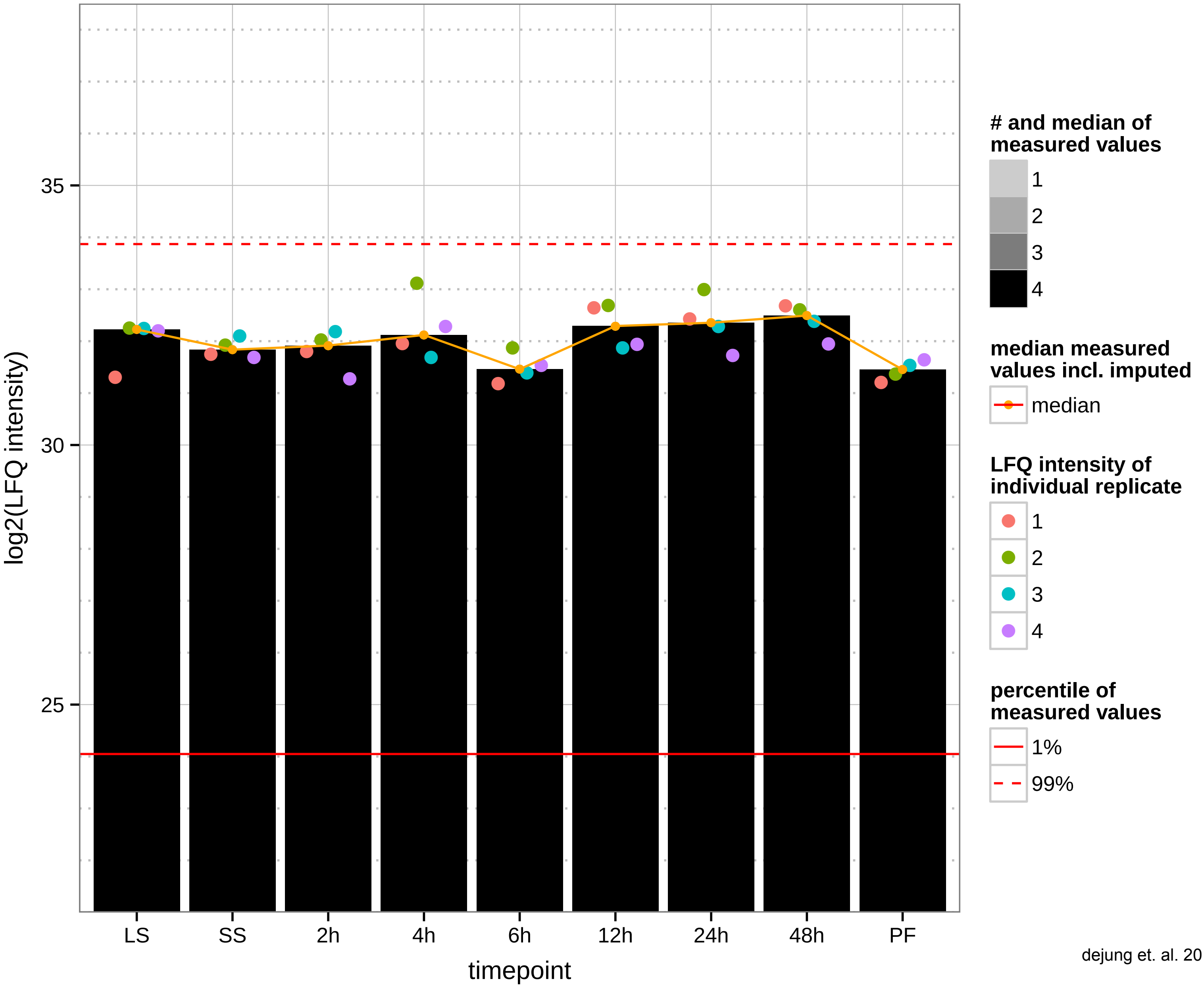
hypothetical protein, conserved
Tb927.9.10230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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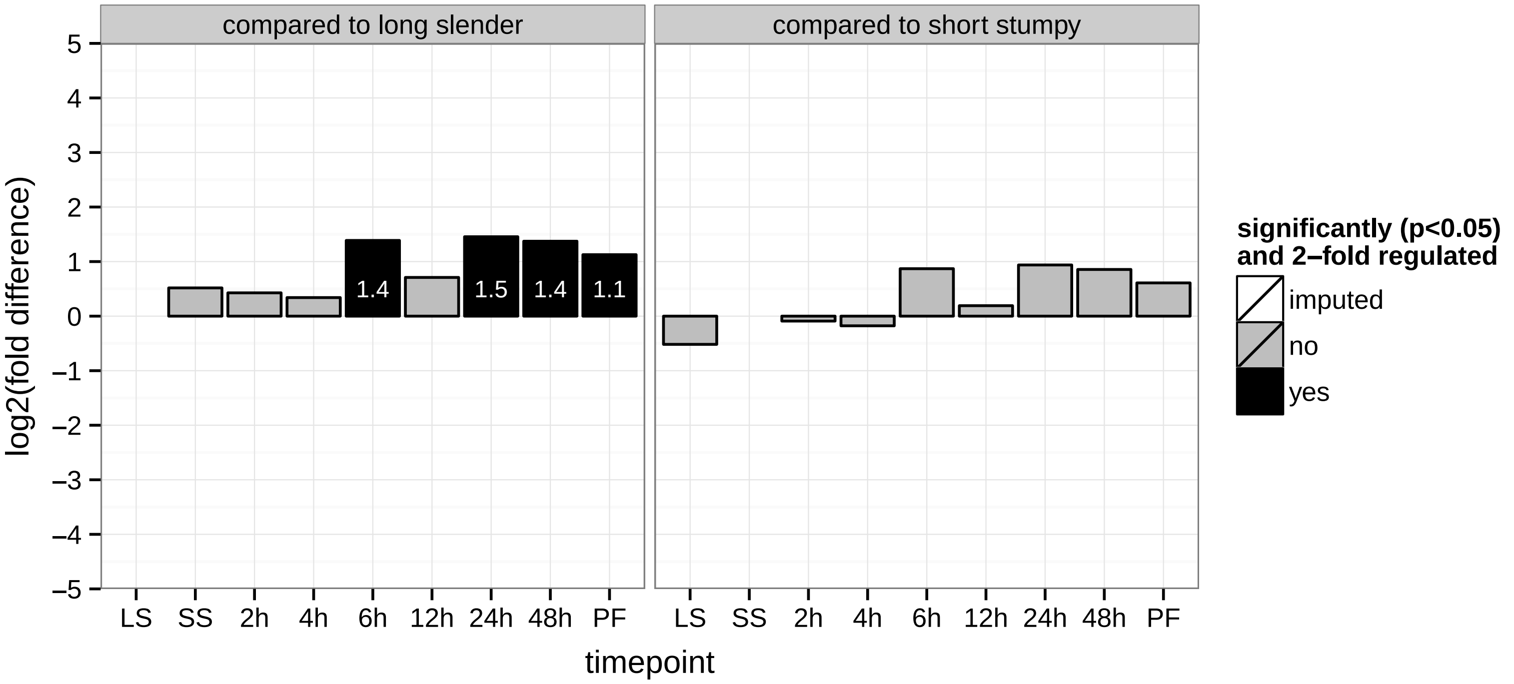
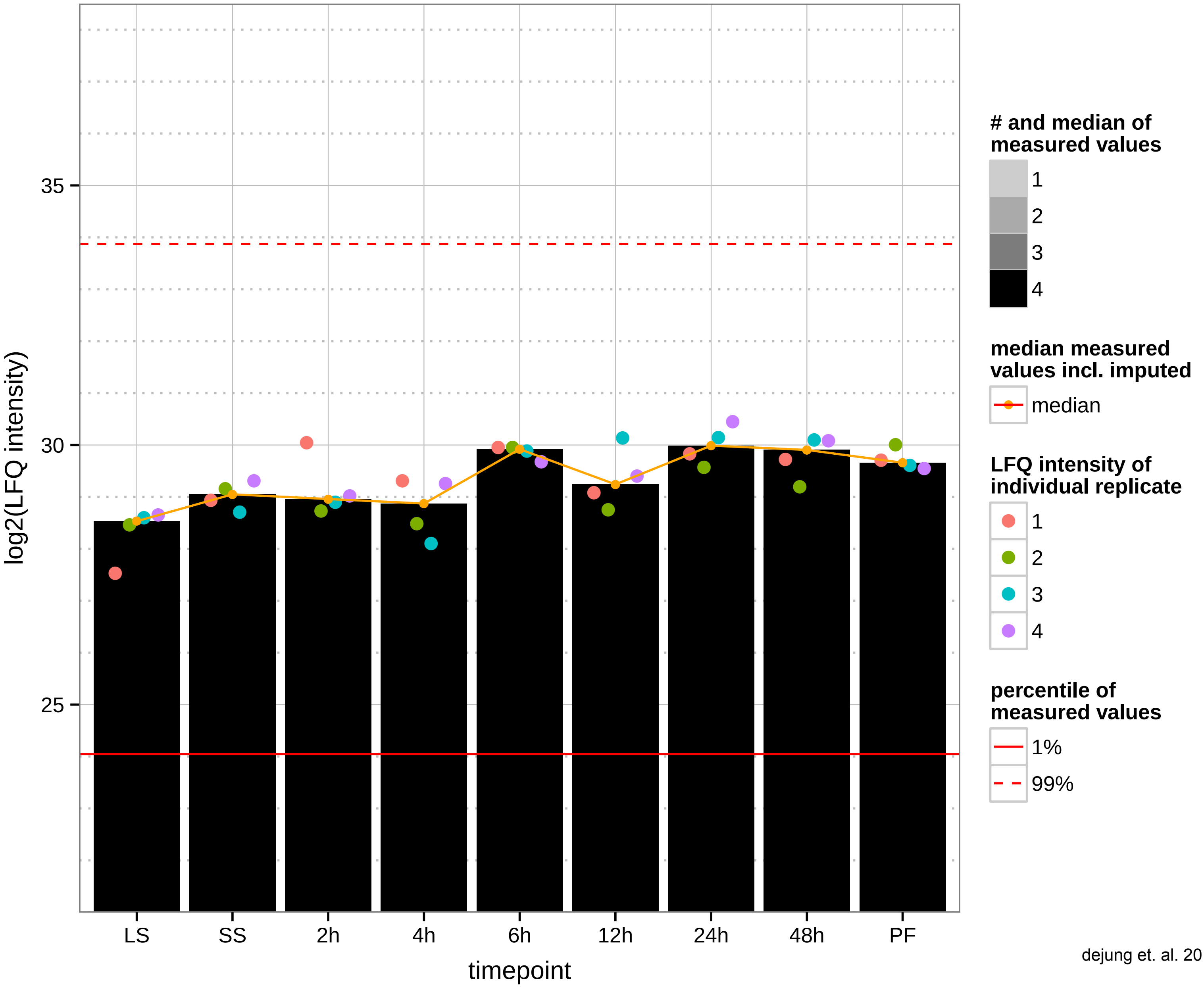
hypothetical protein, conserved
Tb927.9.10400
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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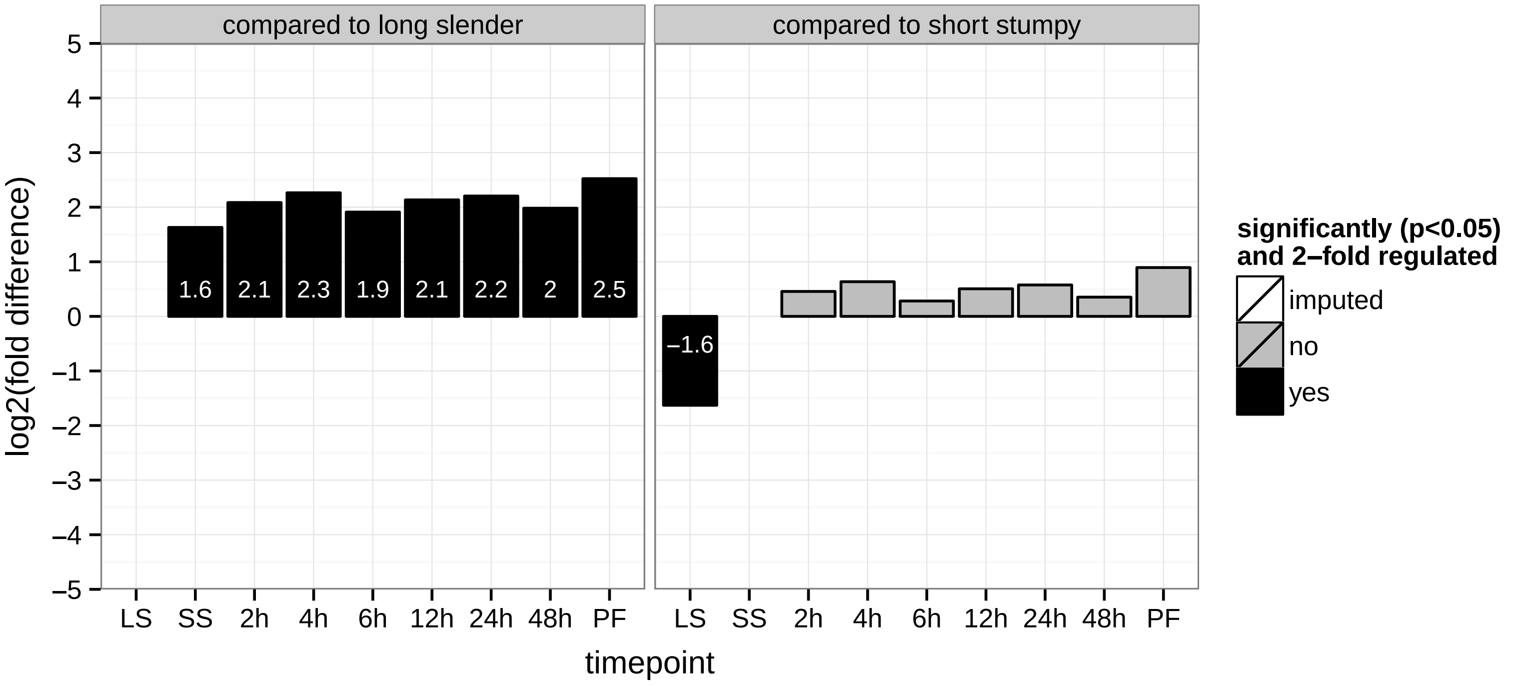
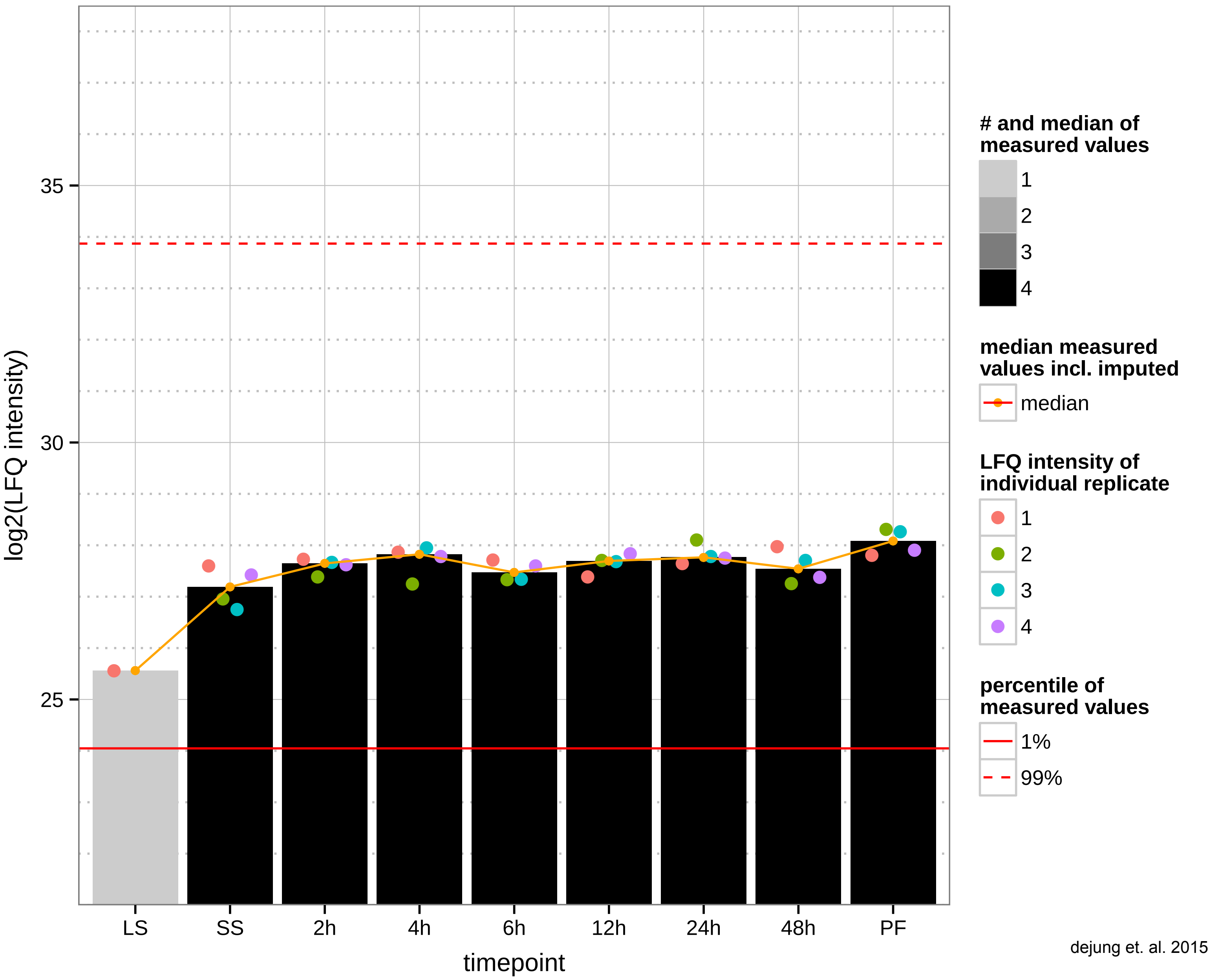
hypothetical protein, conserved
Tb927.9.10500
AGOF: hydrolase activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: hydrolase activity
PGOC: null
PGOP: metabolic process





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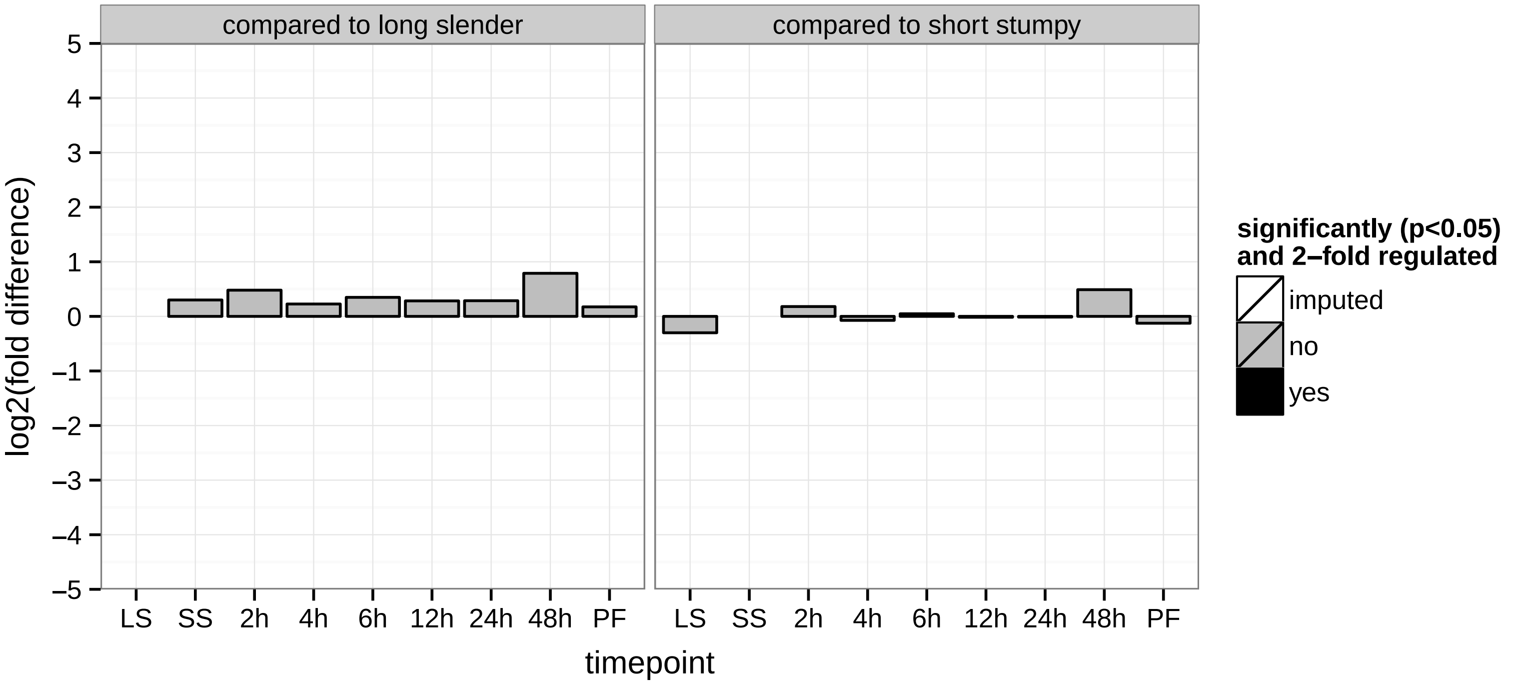
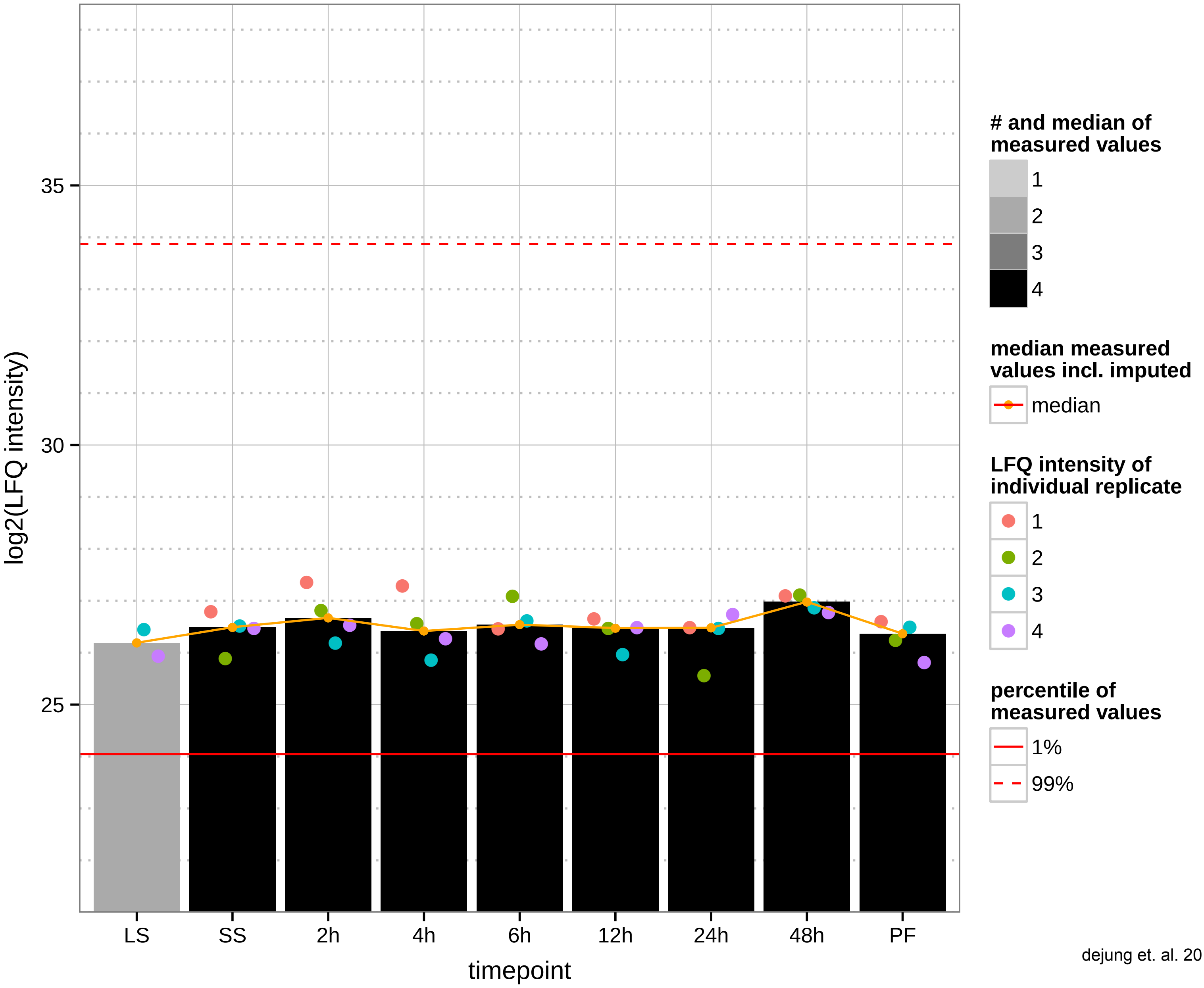
hypothetical protein, conserved
Tb927.9.10530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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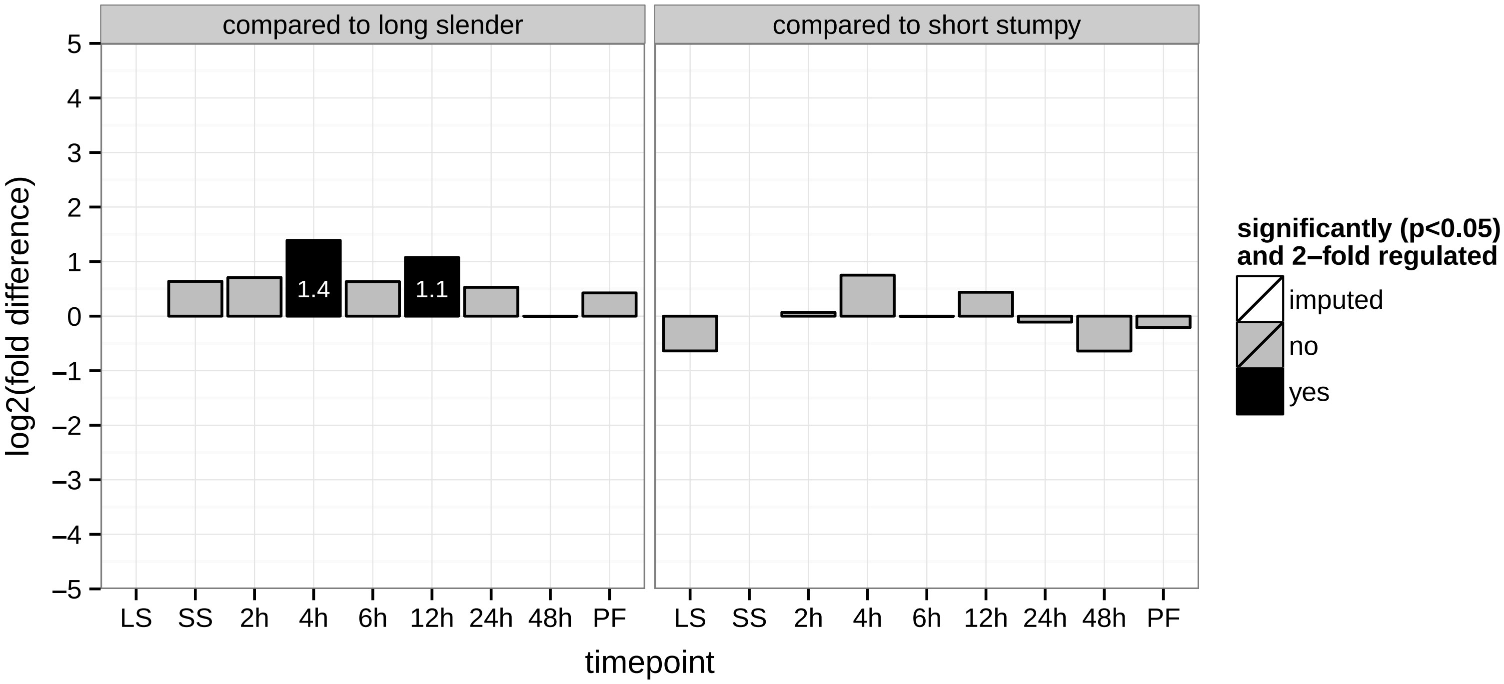
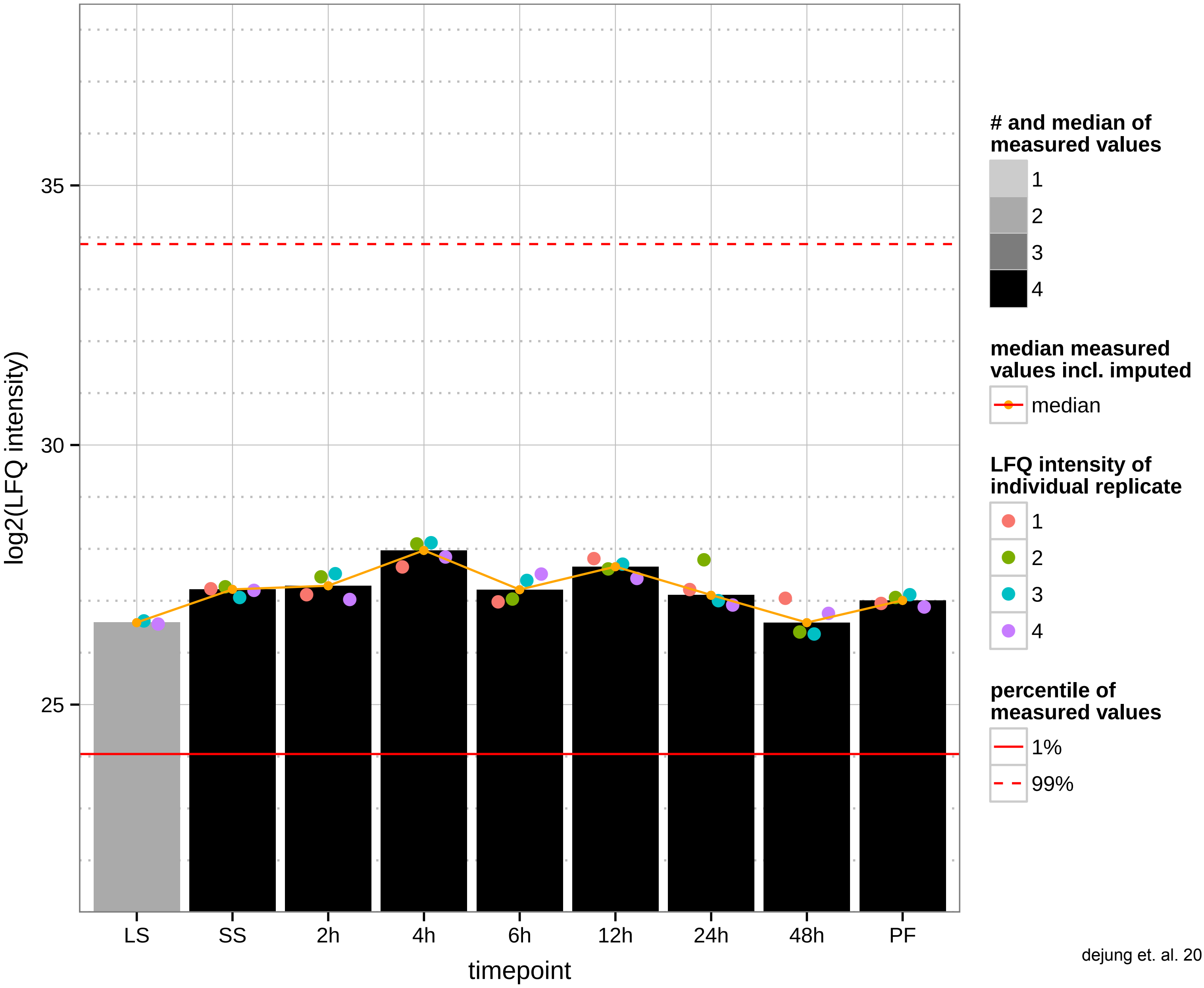
predicted zinc finger protein
Tb927.9.10570
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: metal ion binding
PGOC: null
PGOP: null





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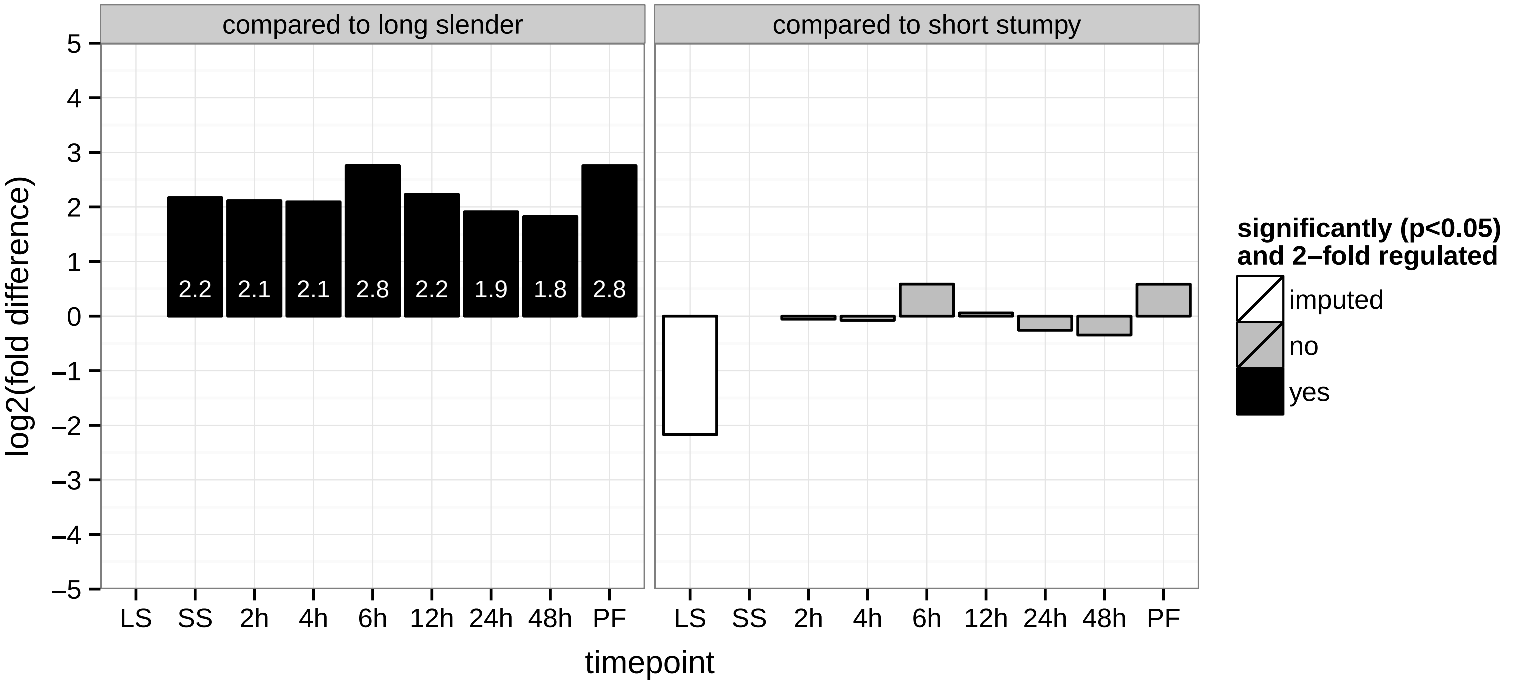
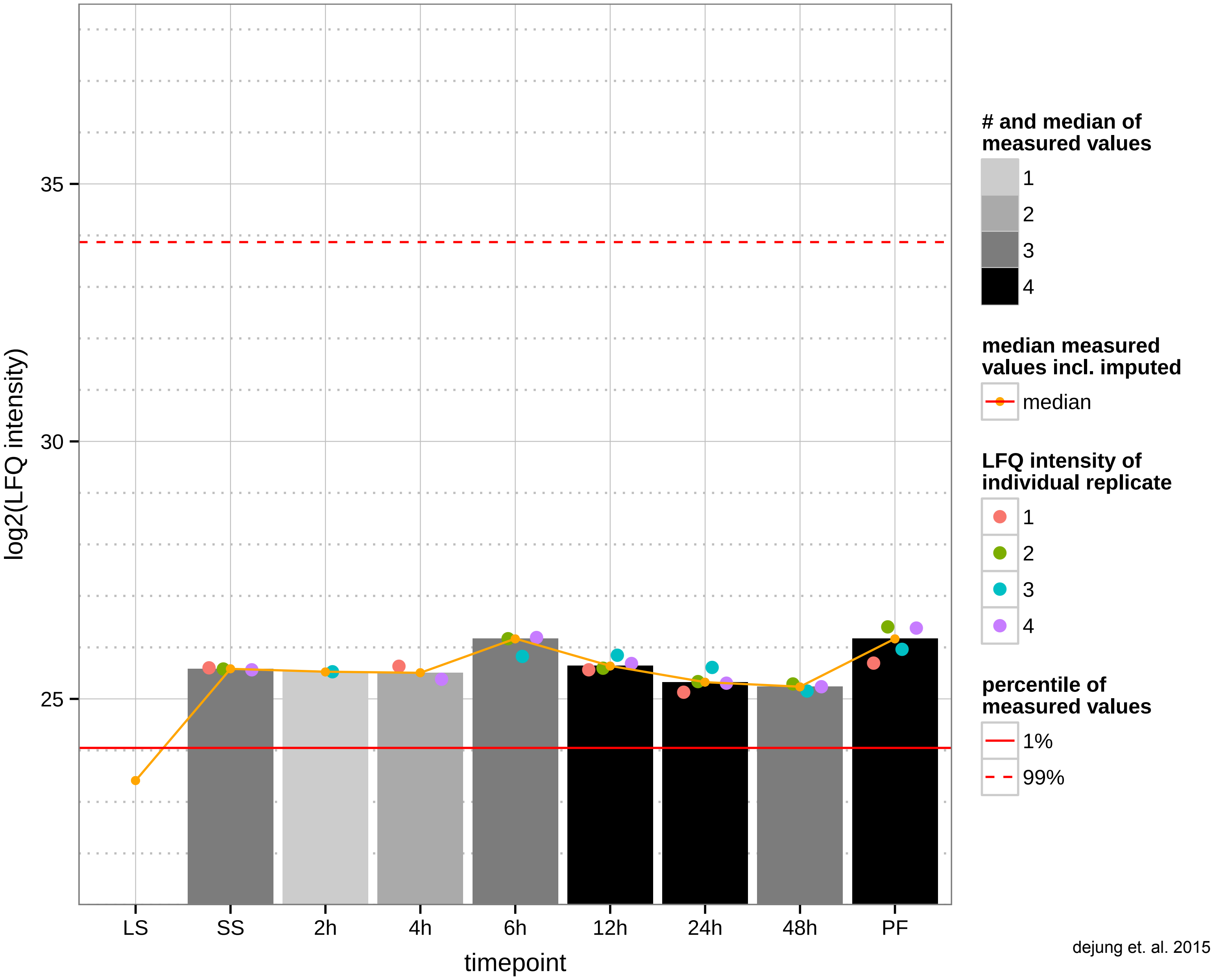
3–demethylubiquinone–9 3–methyltransferase, putative
Tb927.9.10580
AGOF: 2–polyprenyl–6–methoxy–1, 4–benzoquinone methyltransferase activity, hexaprenyldihydroxybenzoate methyltransfera
AGOC: mitochondrial membrane, mitochondrion
AGOP: ubiquinone biosynthetic process, ubiquinone metabolic process
PGOF: 2–polyprenyl–6–methoxy–1, 4–benzoquinone methyltransferase activity
PGOC: null
PGOP: ubiquinone biosynthetic process





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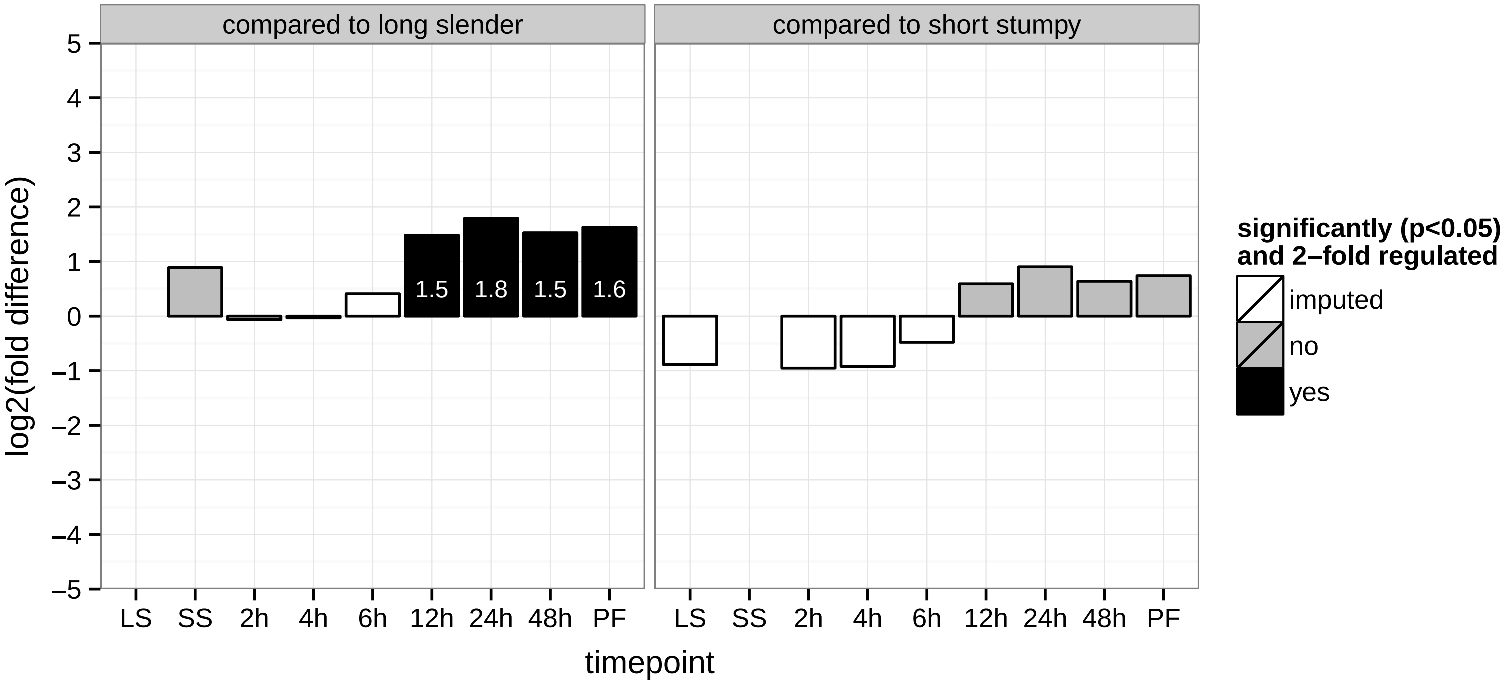
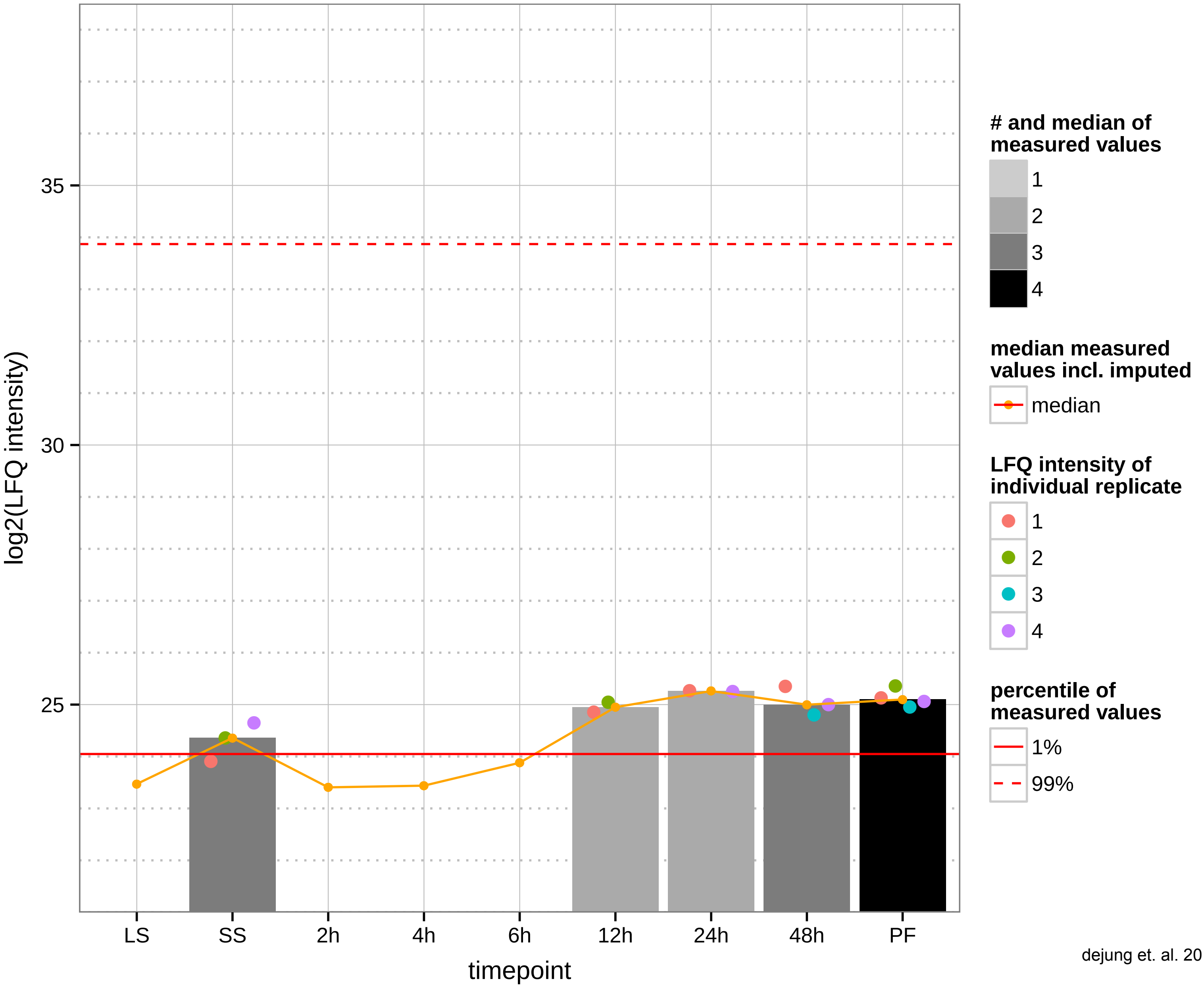
hypothetical protein, conserved
Tb927.9.10680
AGOF: null
AGOC: null
AGOP: null
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: DNA–directed RNA polymerase III complex
PGOP: transcription from RNA polymerase III promoter





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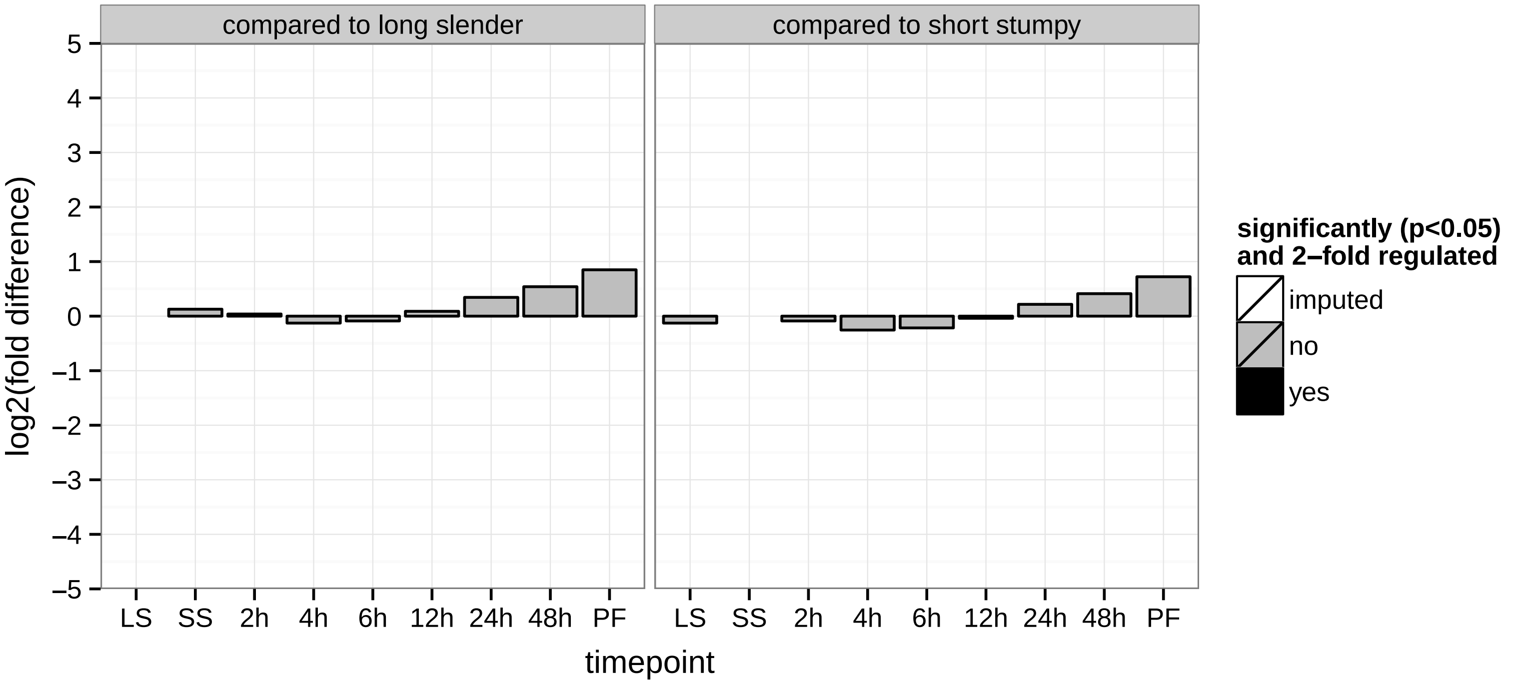
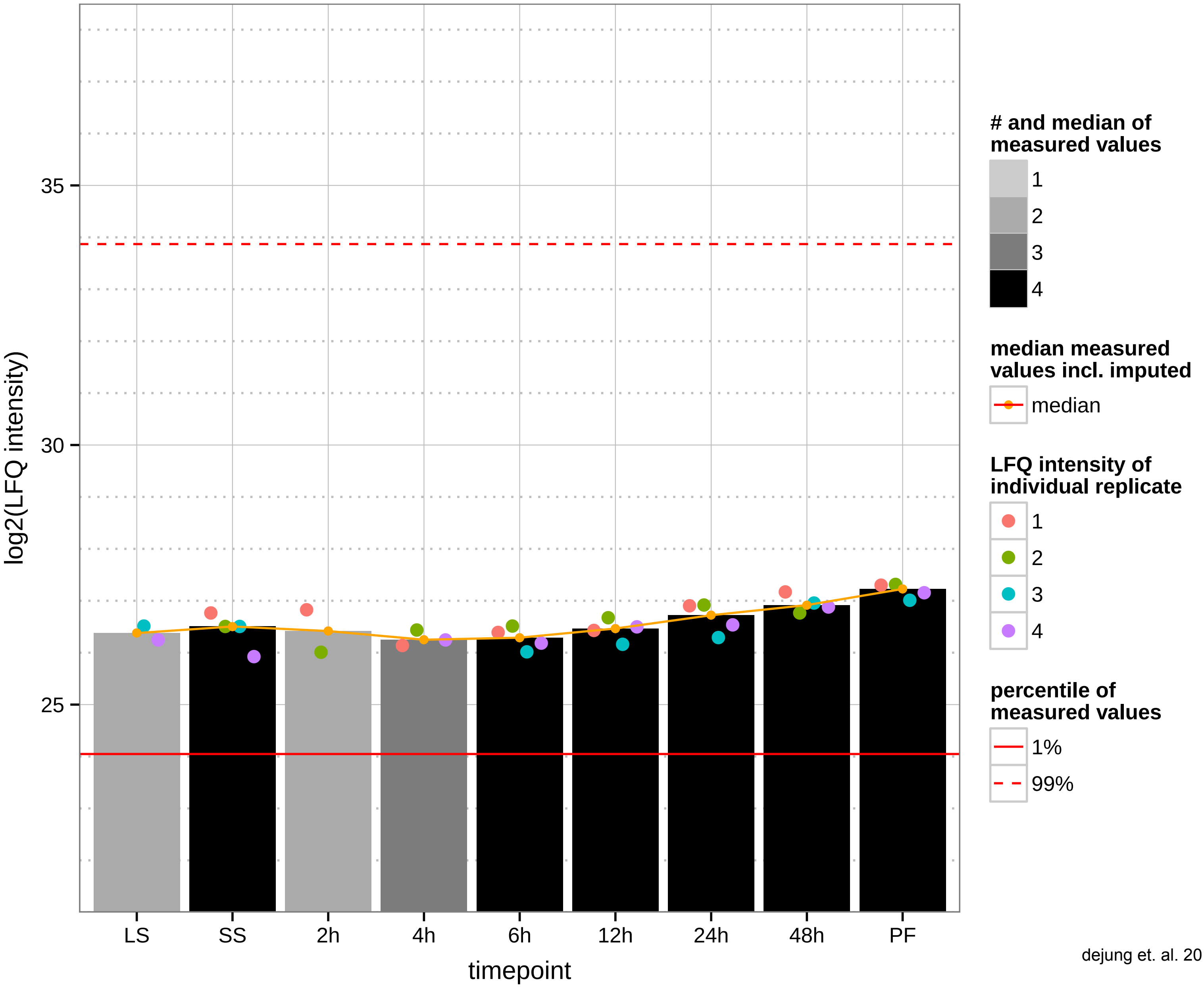
hypothetical protein, conserved
Tb927.9.10690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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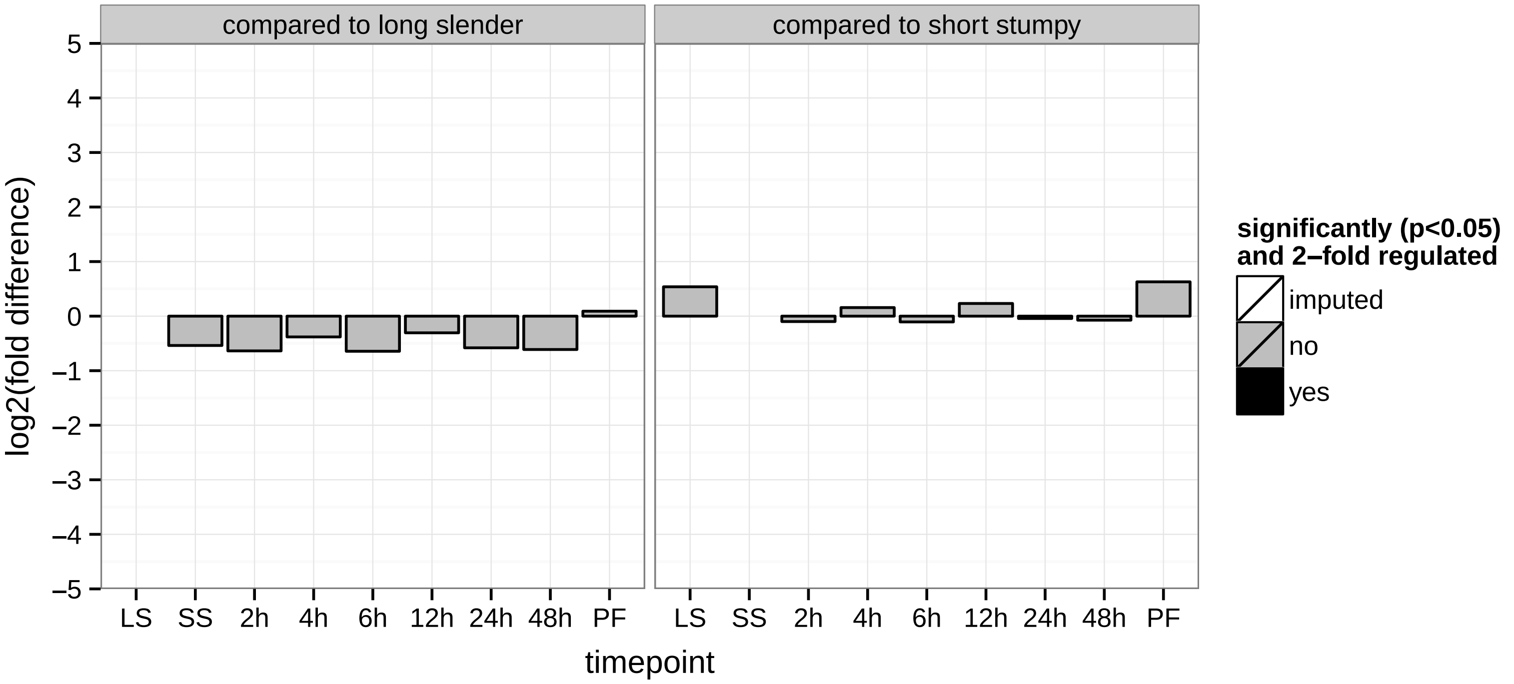
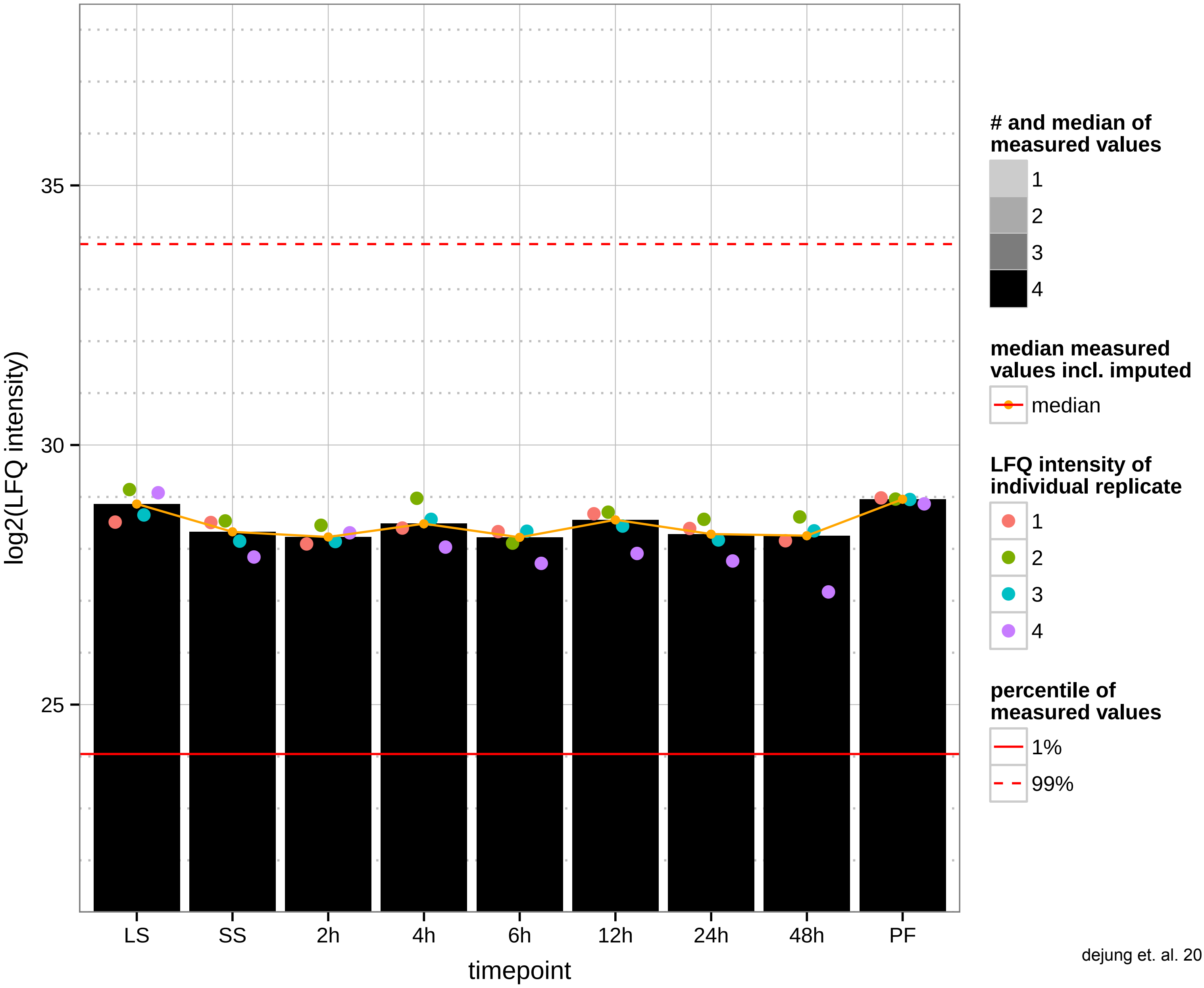
hypothetical protein, conserved
Tb927.9.10890
AGOF: cAMP−dependent protein kinase regulator activity
AGOC: null
AGOP: signal transduction
PGOF: cAMP−dependent protein kinase regulator activity
PGOC: null
PGOP: signal transduction





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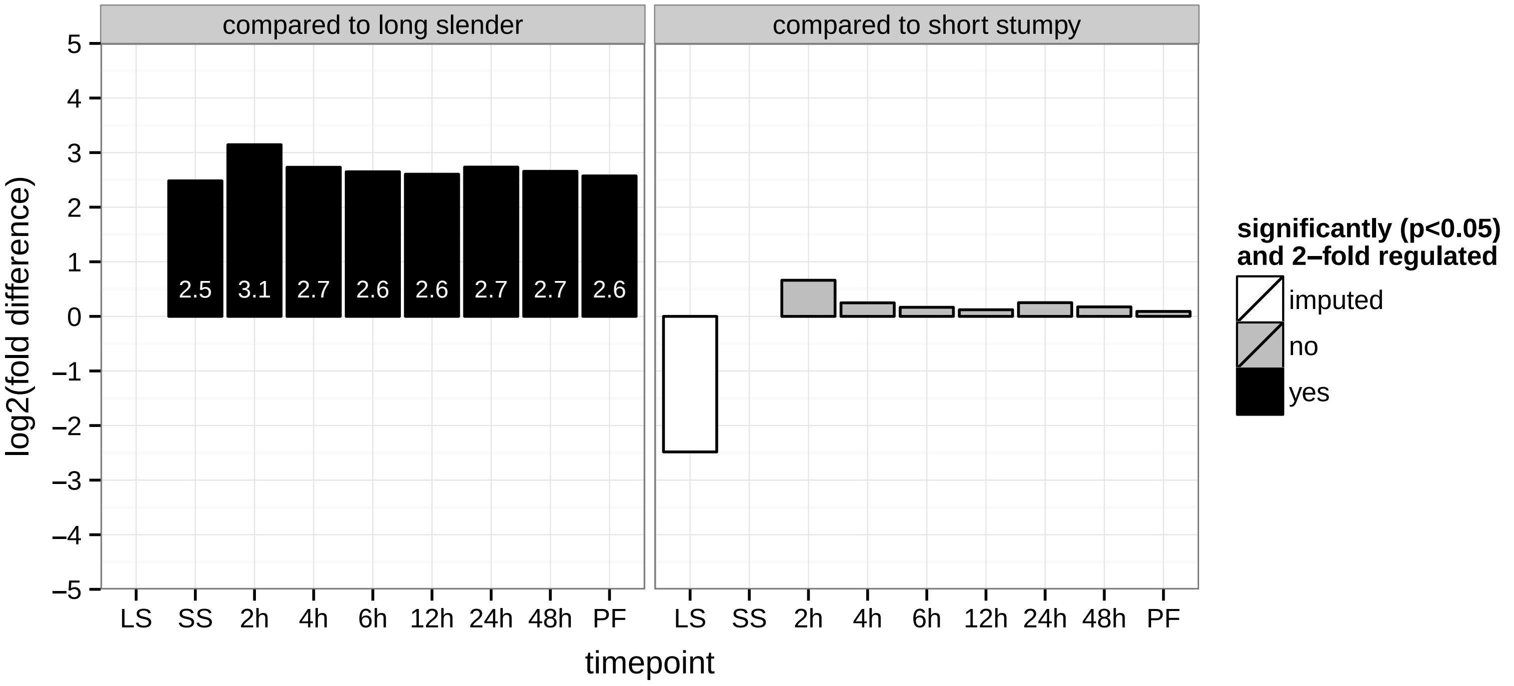
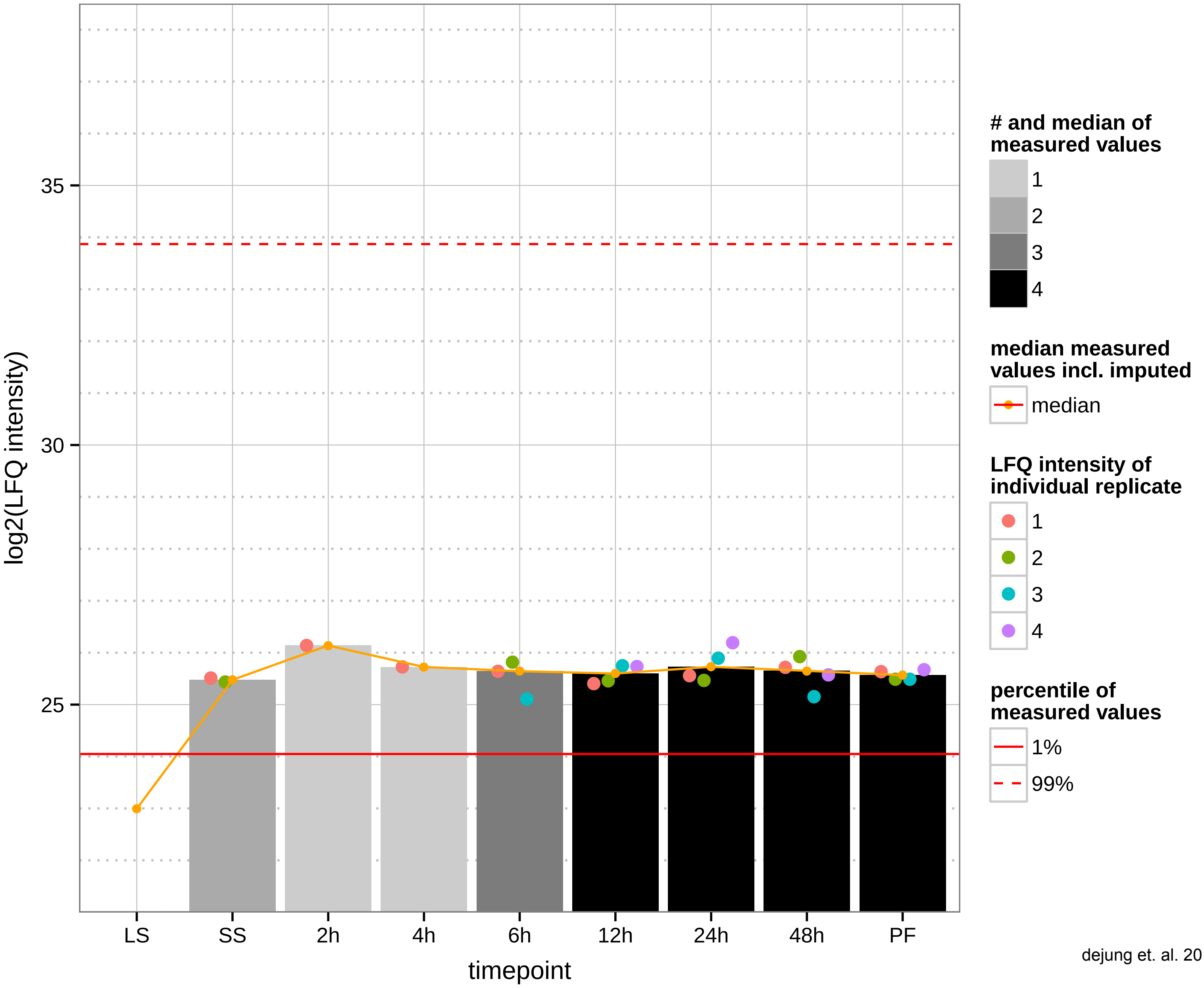
ATP–dependent DEAD/H RNA helicase, putative
Tb927.9.10960
AGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase–containing compound metabolic process
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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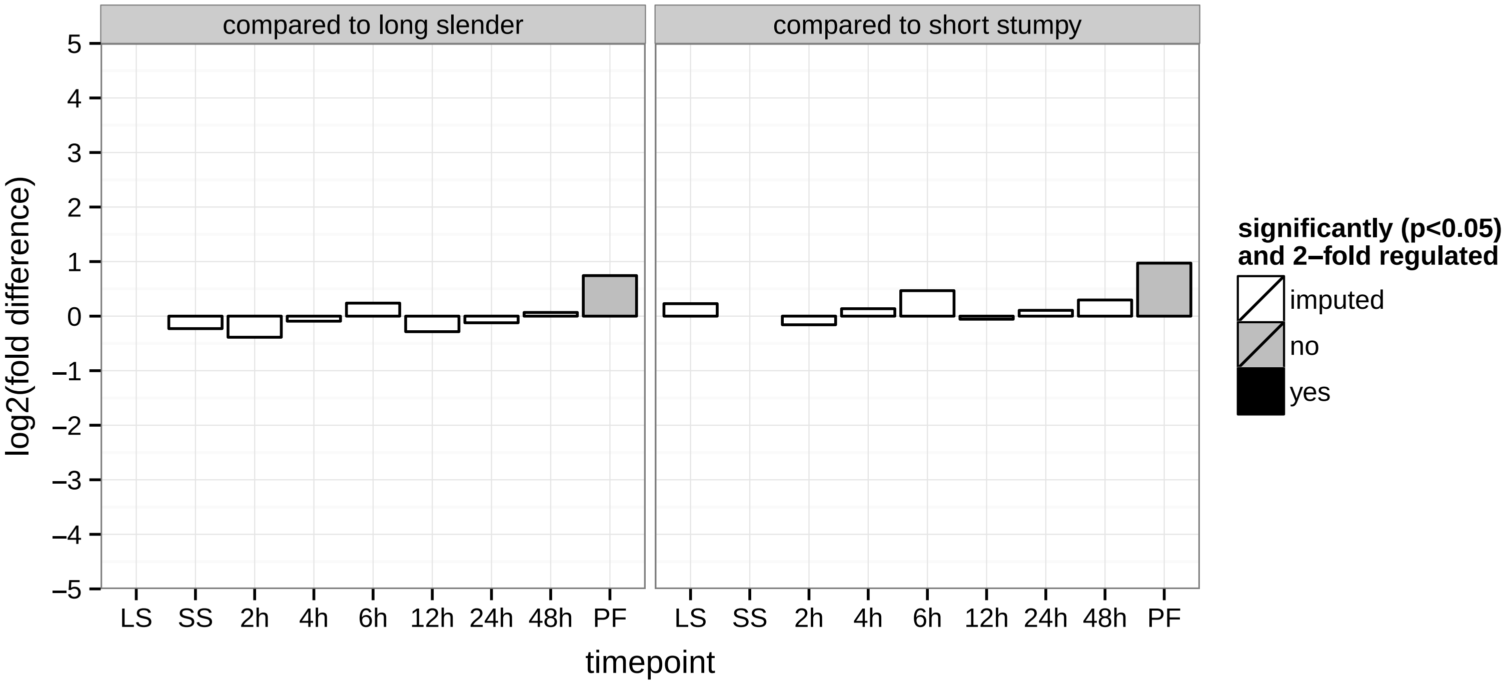
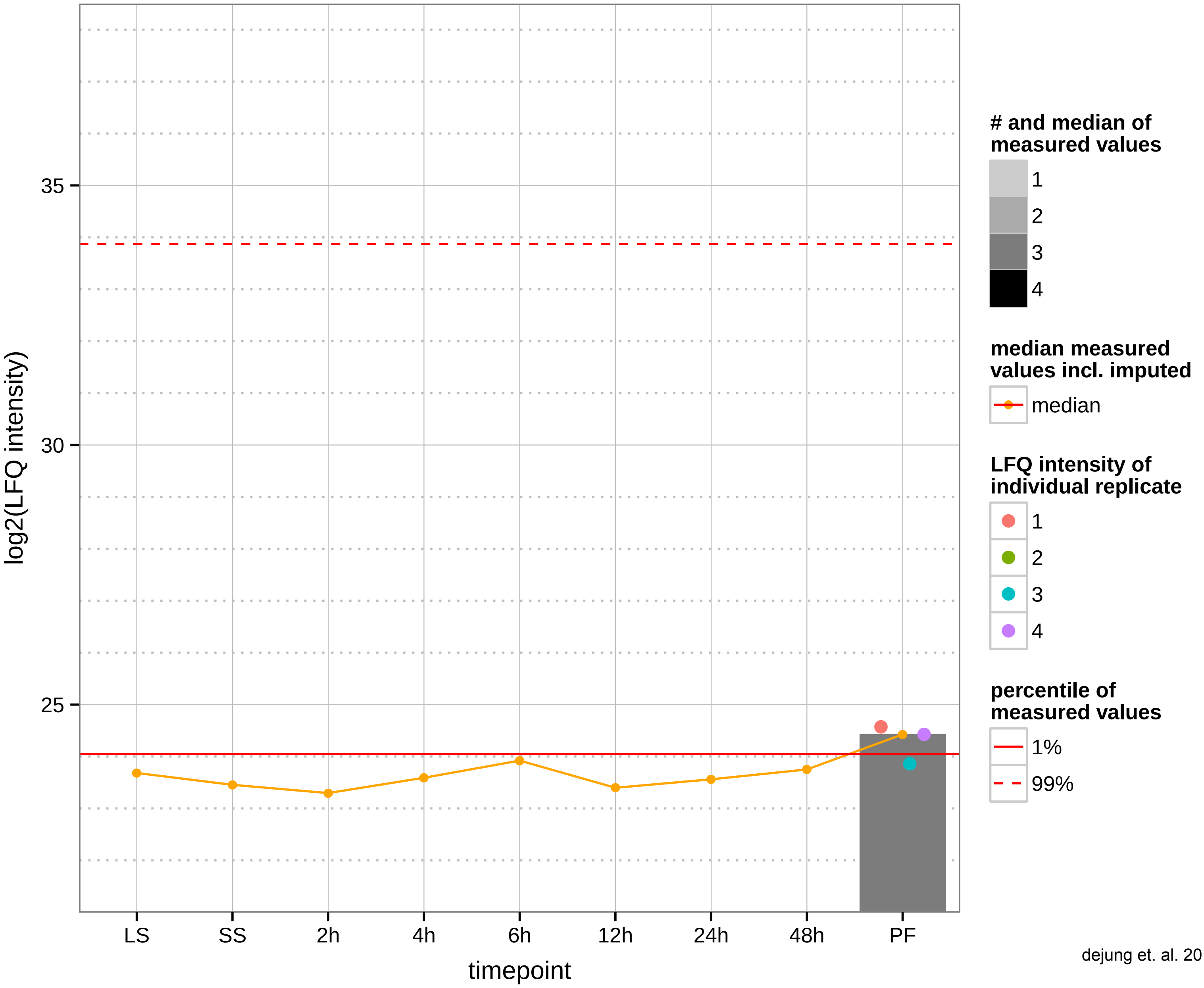
mitochondrial carrier protein (MCP3)
Tb927.9.11040
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrial part
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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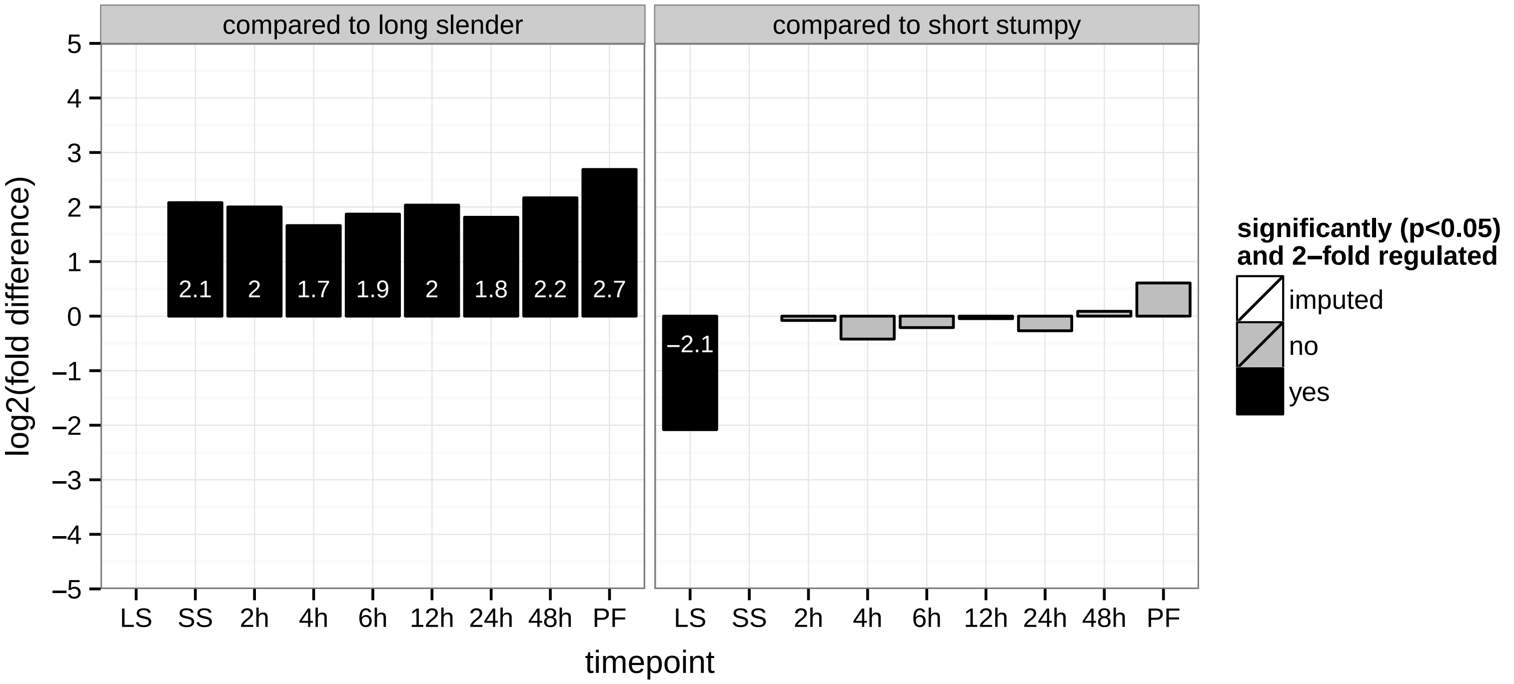
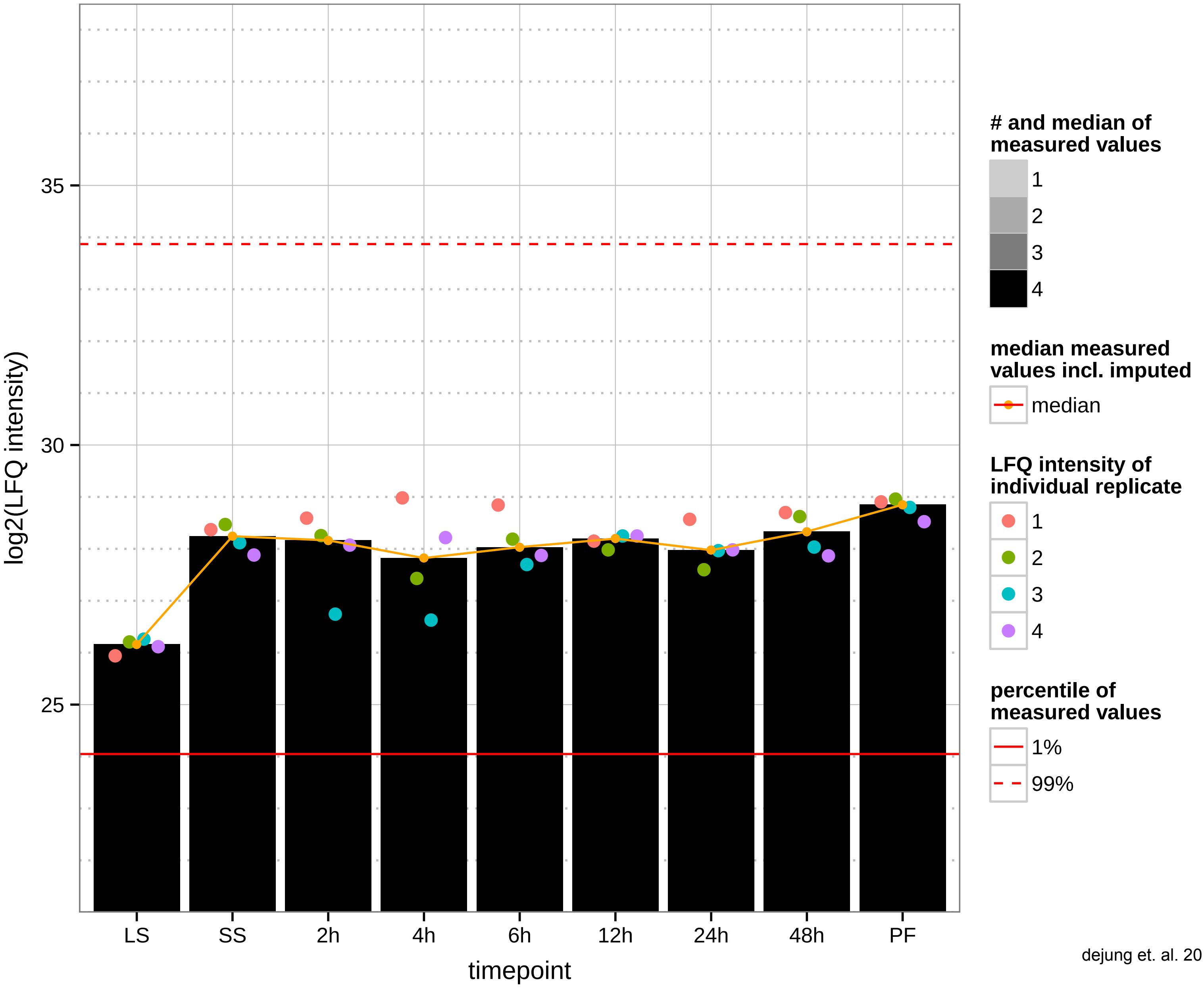
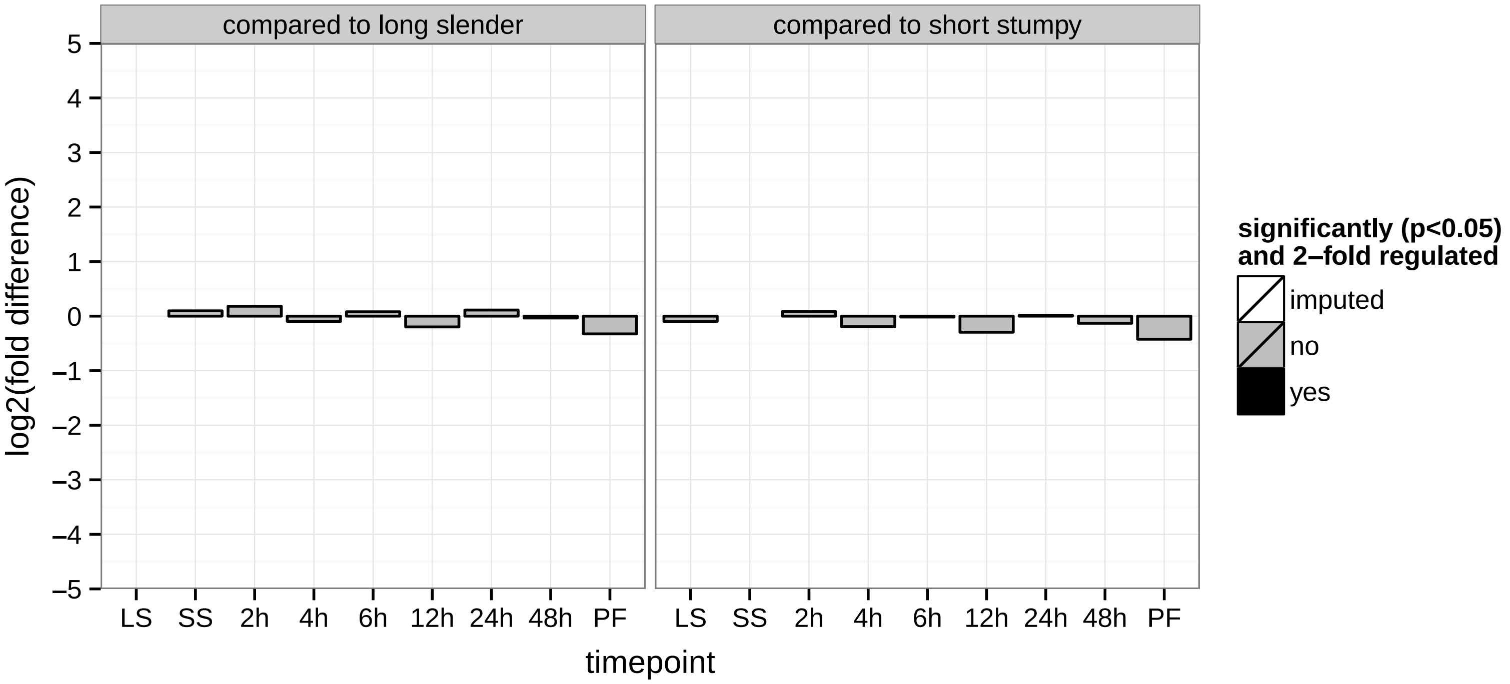
PRP8 protein homologue, U5 snRNA–associated splicing factor
Tb927.9.11110
AGOF: null
AGOC: spliceosomal complex
AGOP: nuclear mRNA splicing, via spliceosome
PGOF: nucleic acid binding, protein binding
PGOC: spliceosomal complex
PGOP: nuclear mRNA splicing, via spliceosome

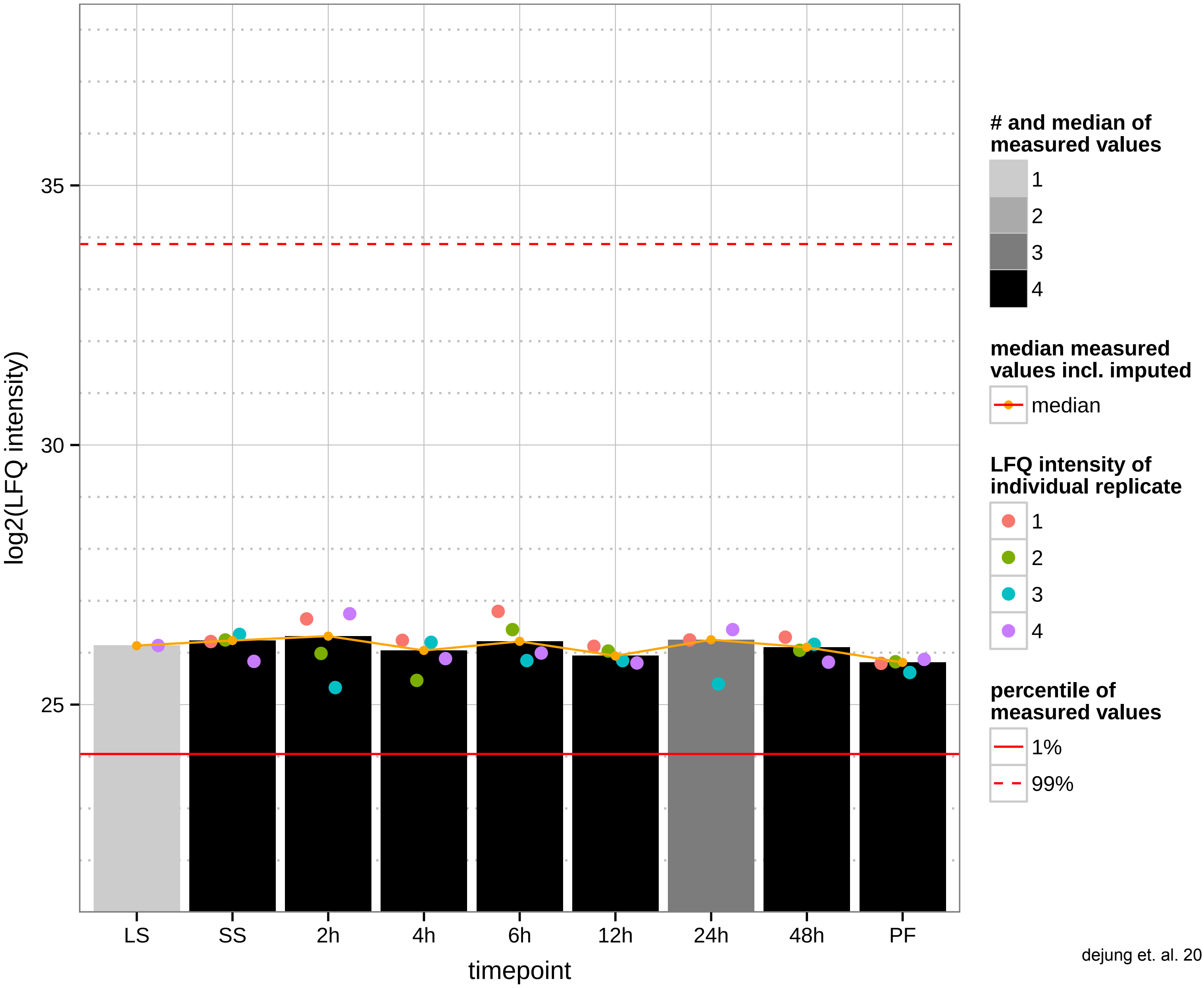




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.11140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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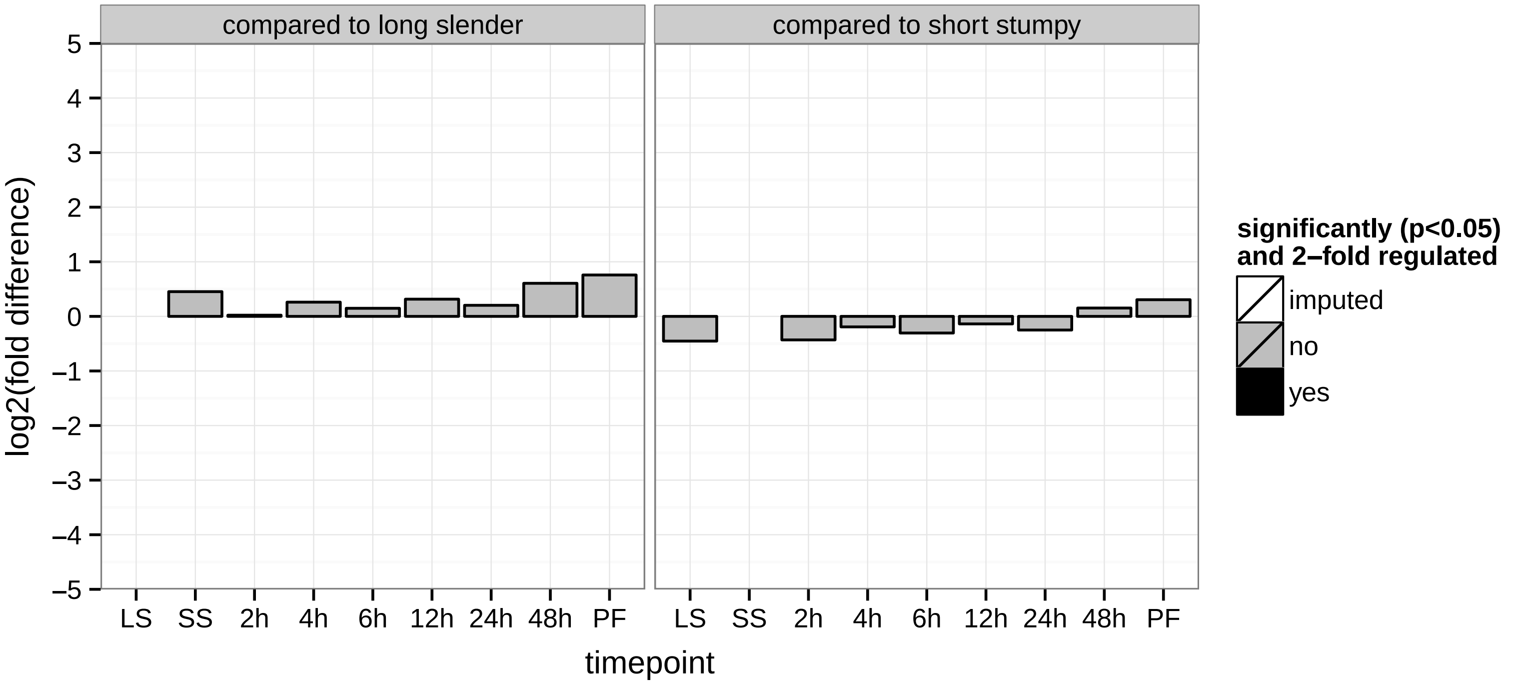
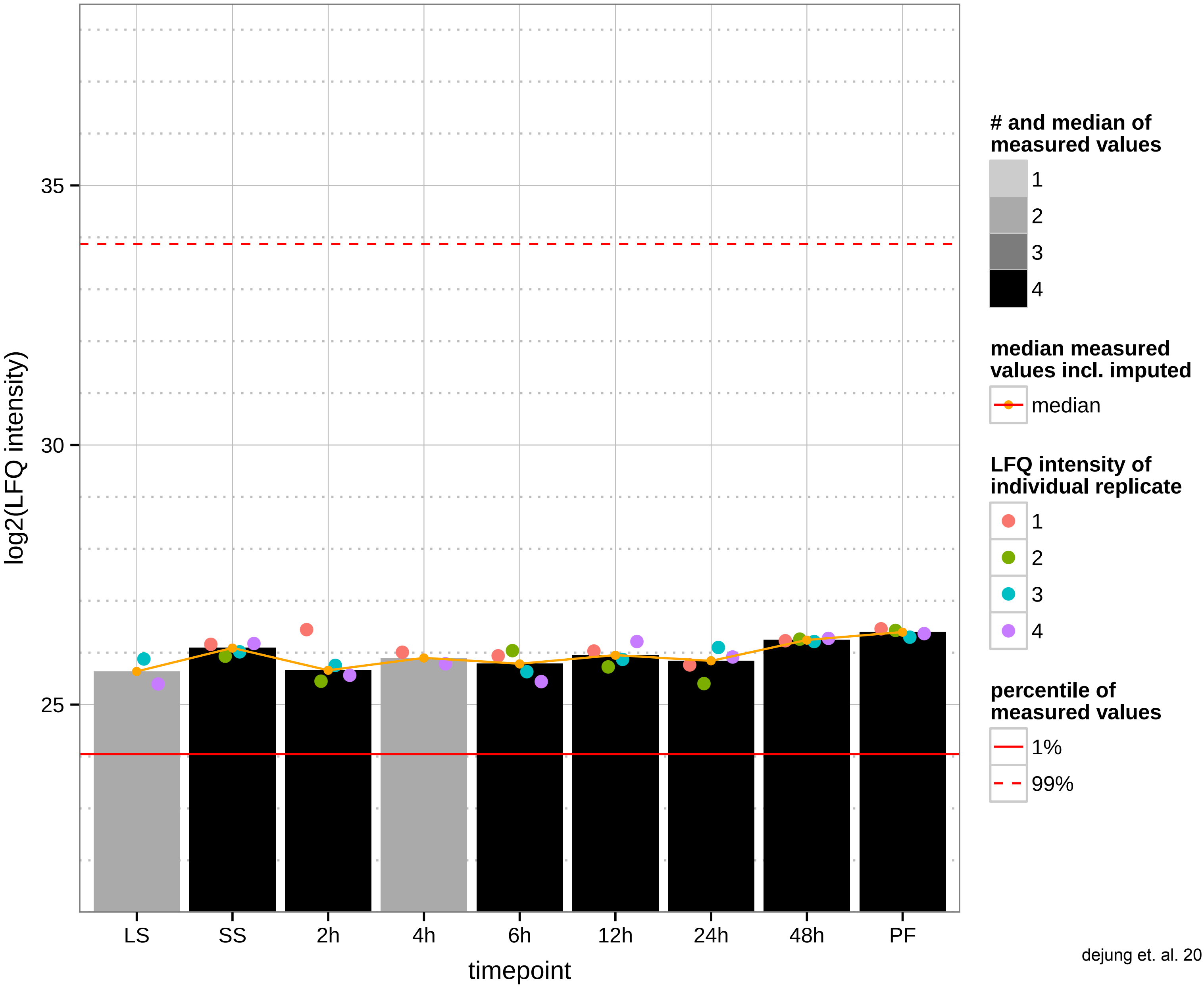
hypothetical protein, conserved
Tb927.9.11150
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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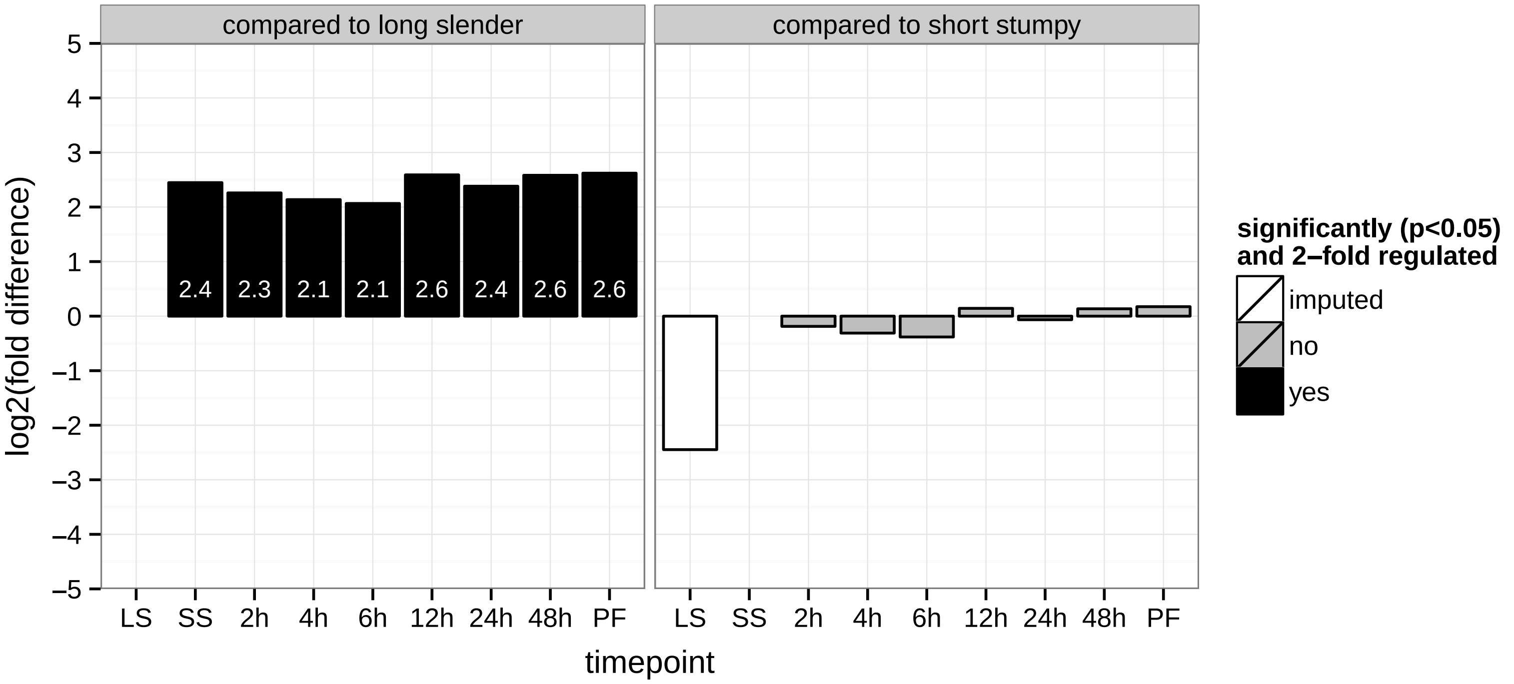
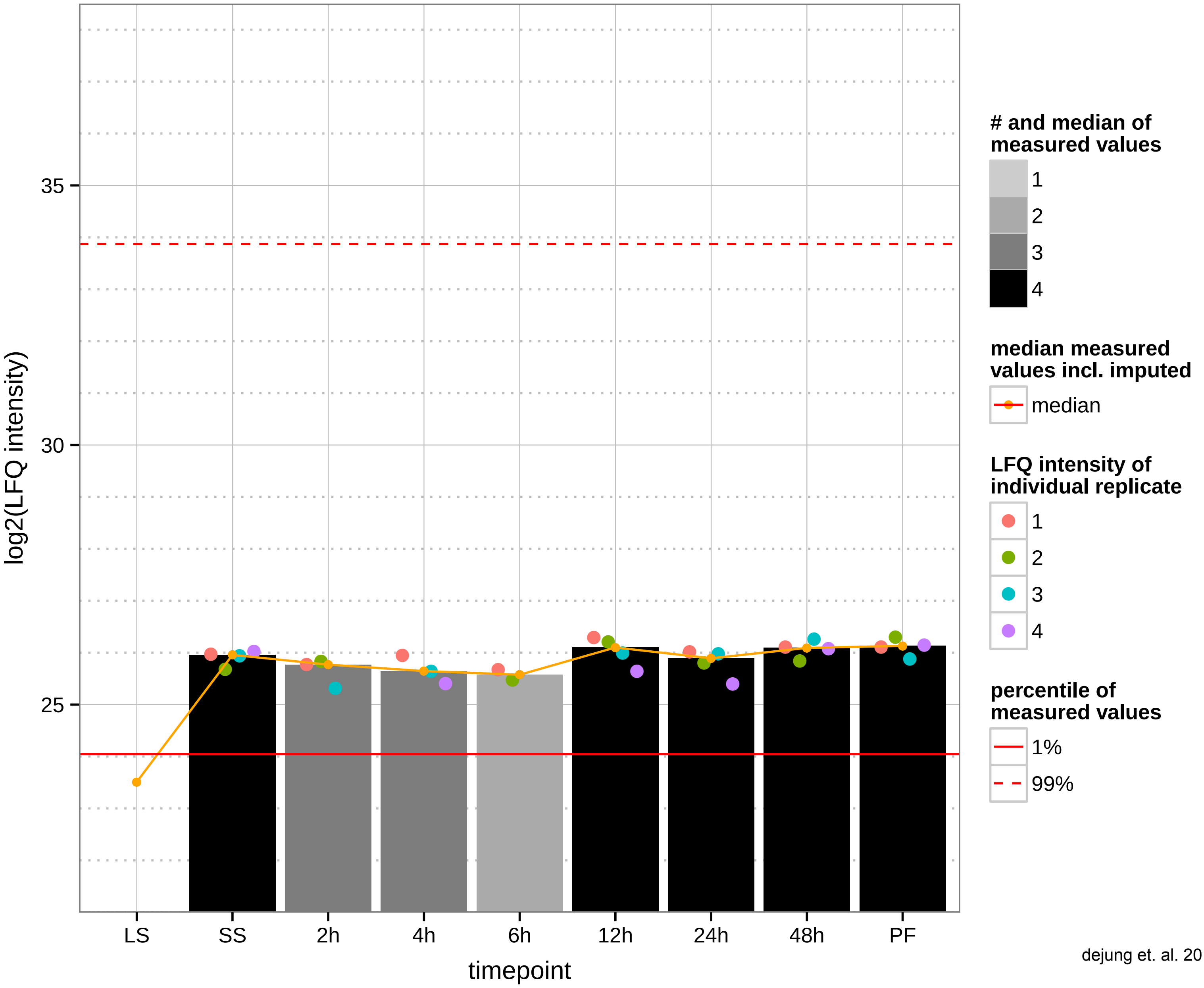
predicted WD40 repeat protein
Tb927.9.11250
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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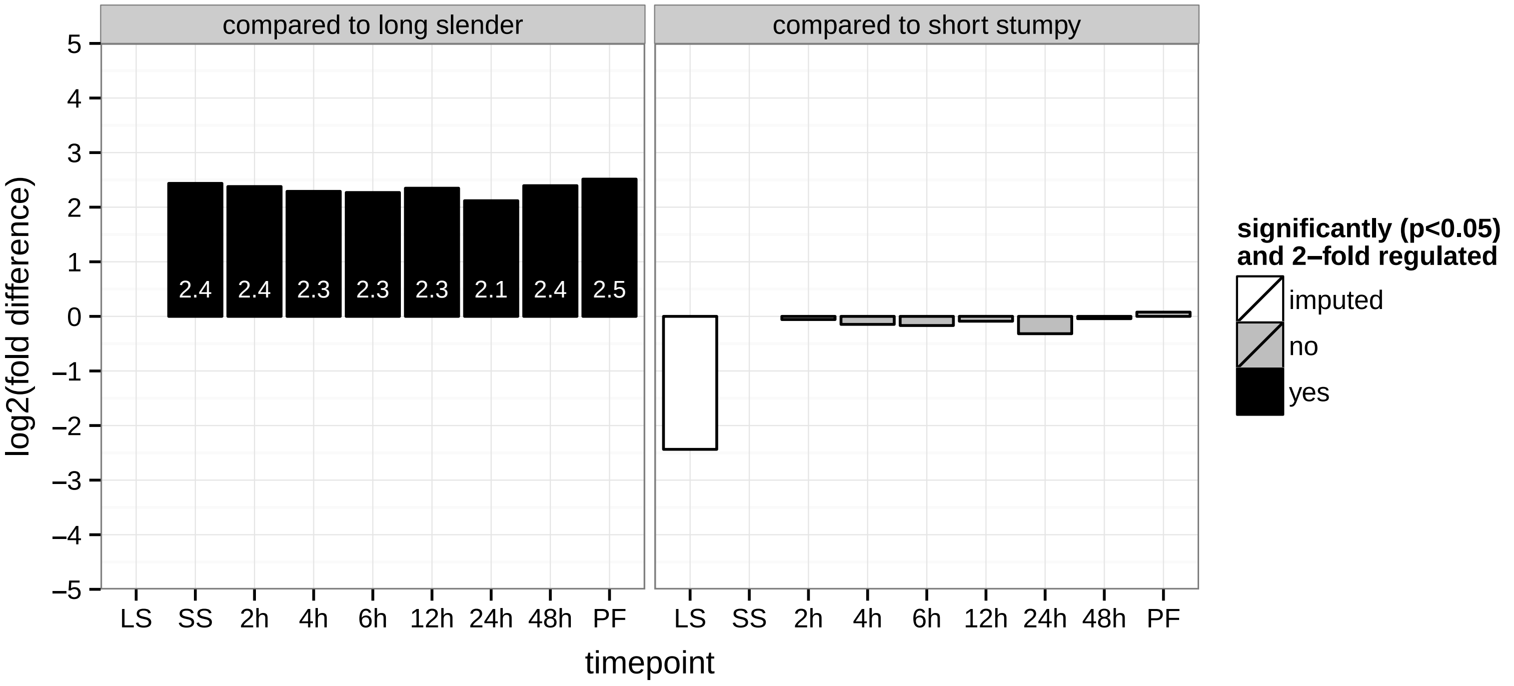
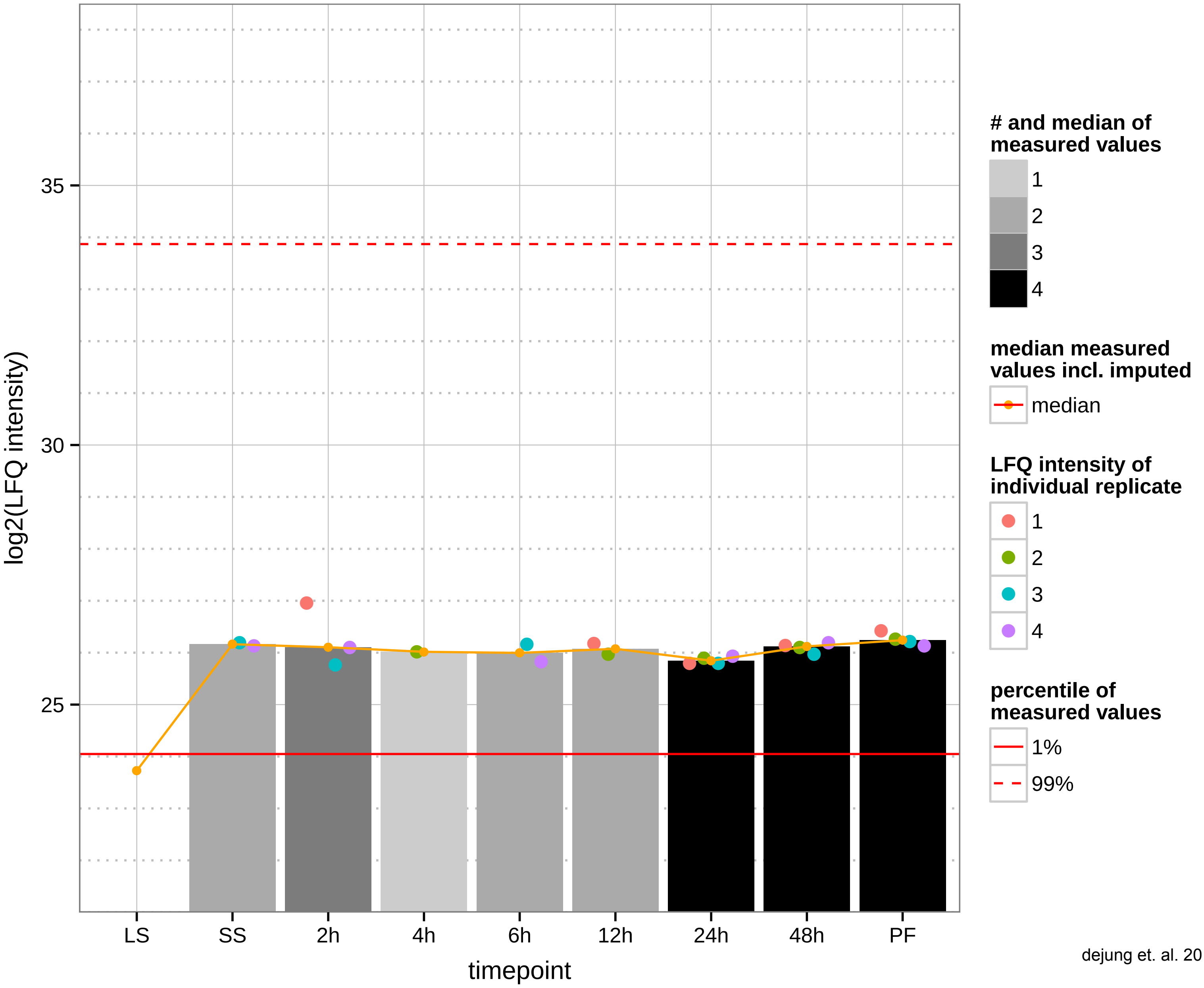
nucleoside diphosphate kinase, putative
Tb927.9.11260
AGOF: ATP binding, nucleoside diphosphate kinase activity
AGOC: cilium
AGOP: CTP biosynthetic process, GTP biosynthetic process, UTP biosynthetic process, ciliary or flagellar motility
PGOF: ATP binding, nucleoside diphosphate kinase activity
PGOC: null
PGOP: CTP biosynthetic process, GTP biosynthetic process, UTP biosynthetic process, nucleoside diphosphate phosphoryla





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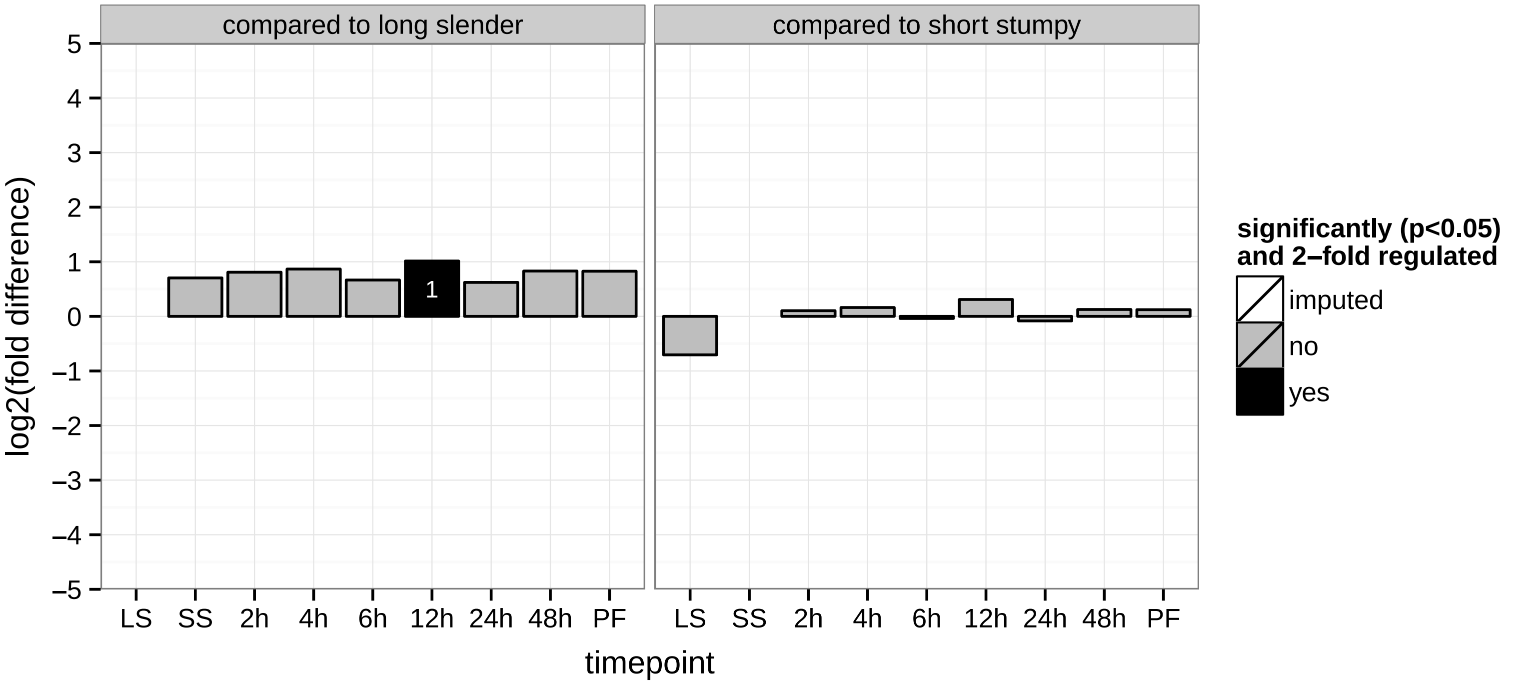
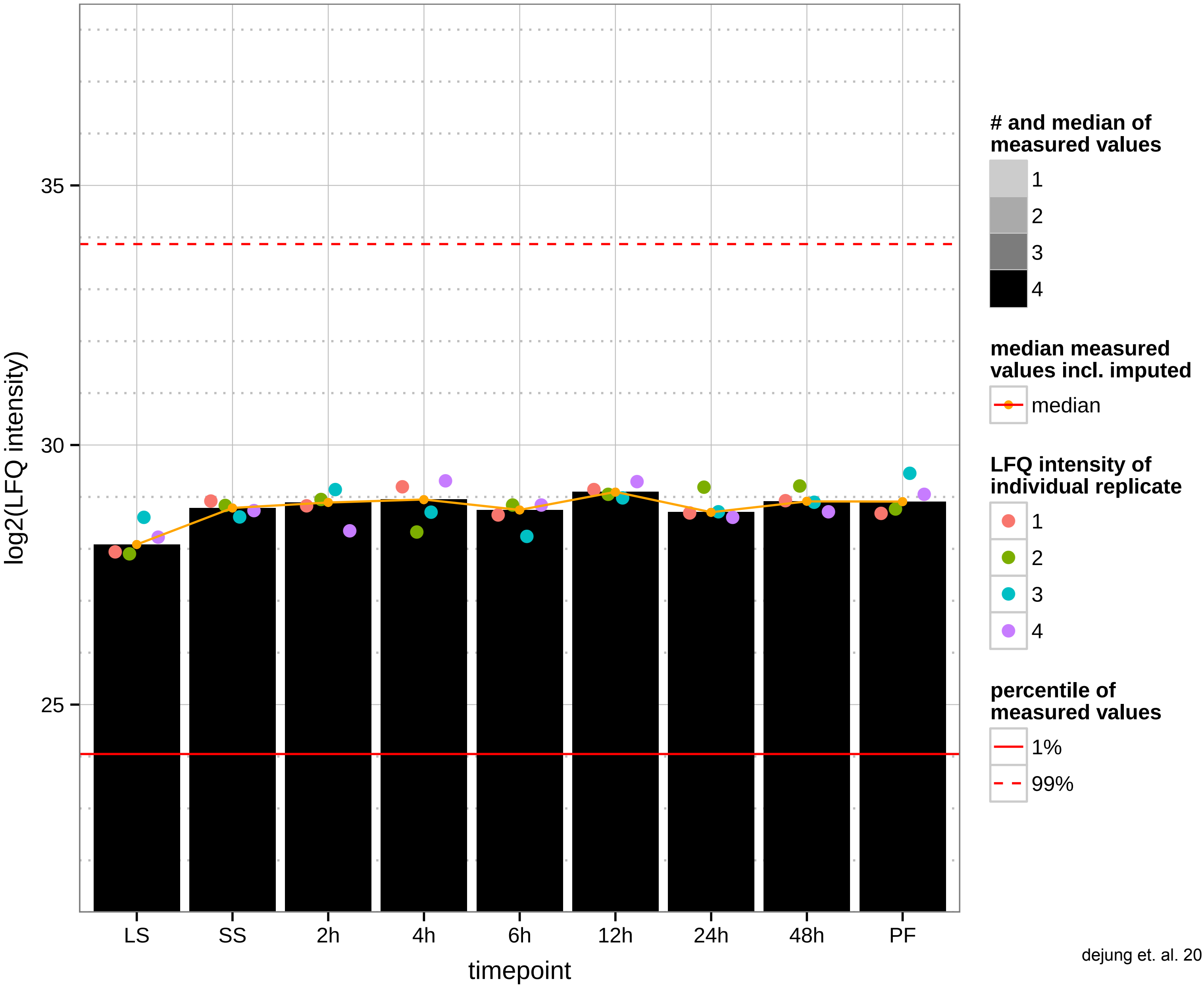
unspecified product
Tb927.9.11310
AGOF: null
AGOC: null
AGOP: null
PGOF: threonine–type endopeptidase activity
PGOC: proteasome core complex
PGOP: proteolysis involved in cellular protein catabolic process





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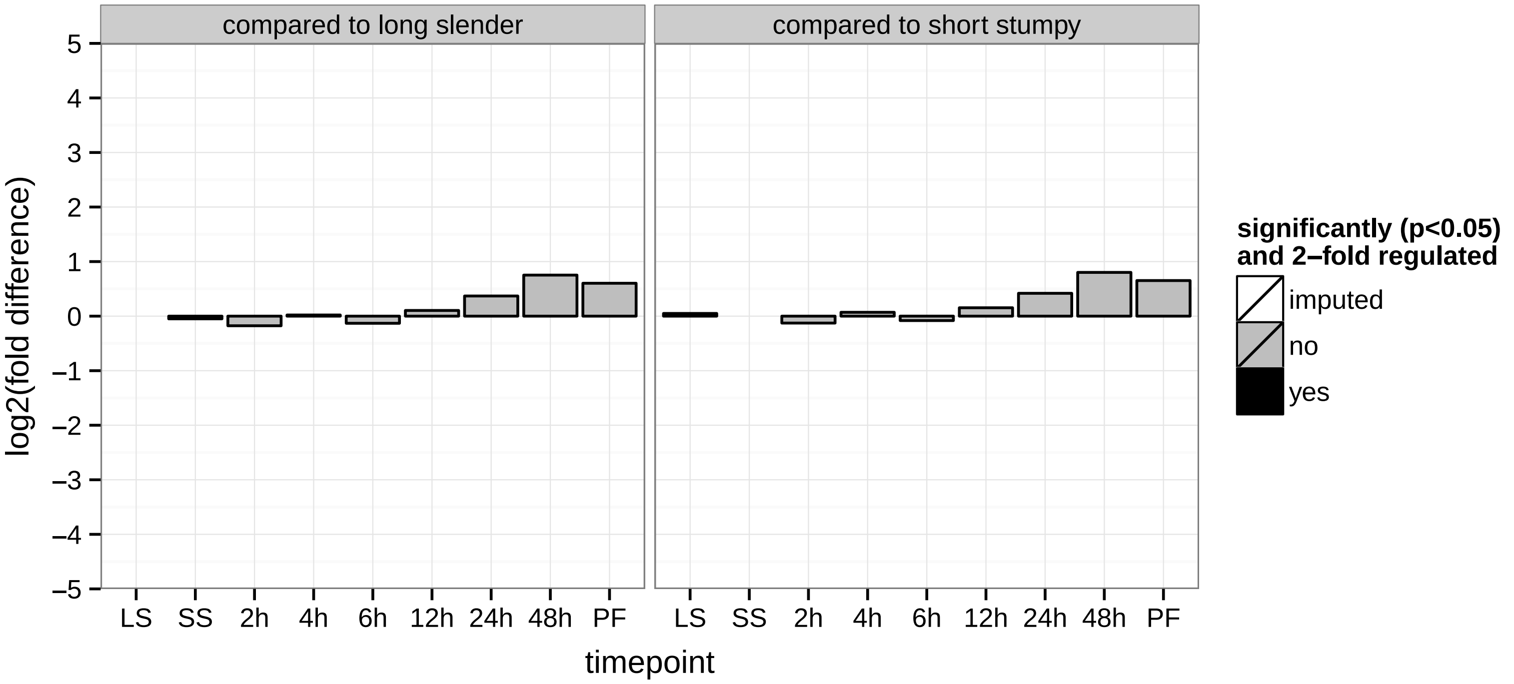
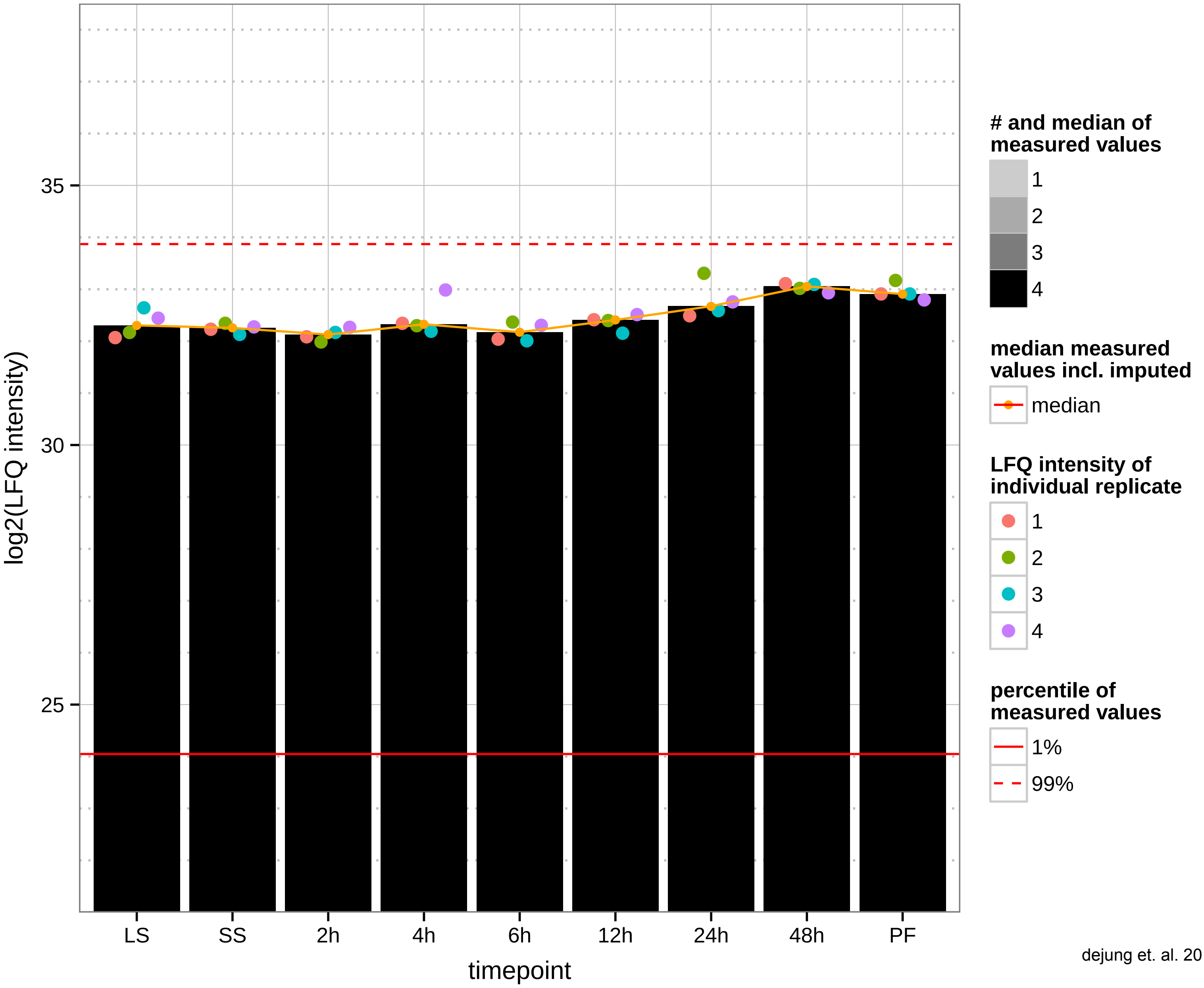
unspecified product
Tb927.9.11410;Tb927.9.11380
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null, structural constituent of ribosome
PGOC: null, ribosome
PGOP: null, translation





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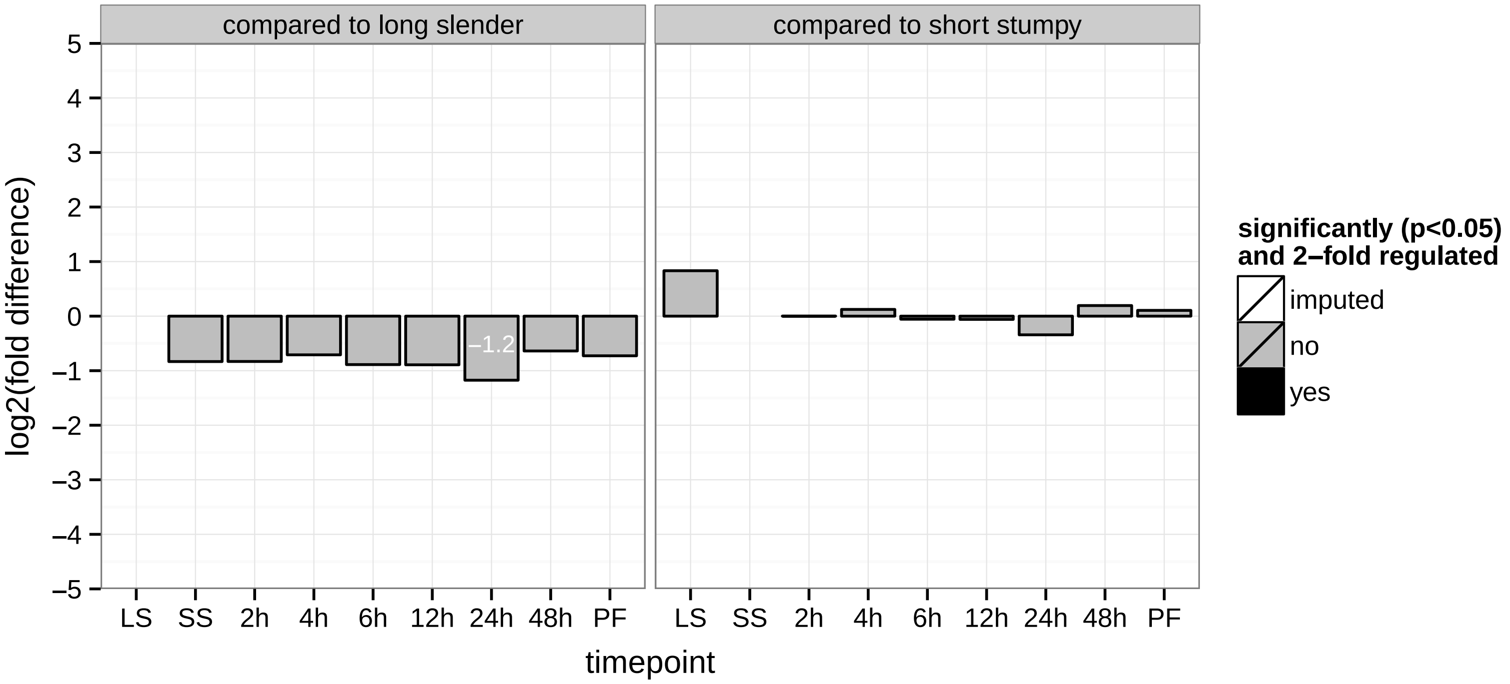
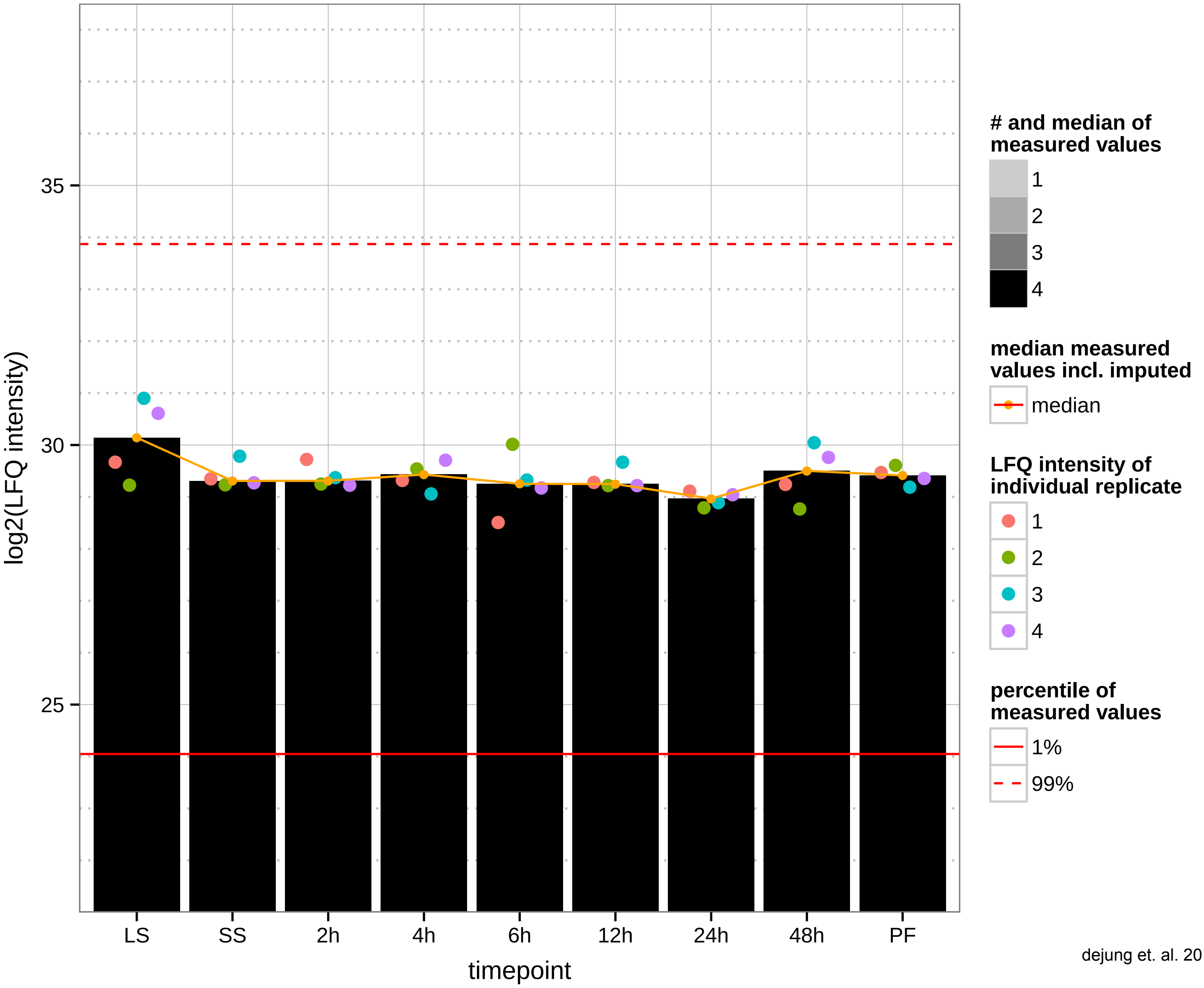
Gim5A protein, glycosomal membrane protein (gim5A)
Tb927.9.11580
AGOF: null
AGOC: glycosome membrane
AGOP: null
PGOF: null
PGOC: integral to peroxisomal membrane
PGOP: peroxisome fission





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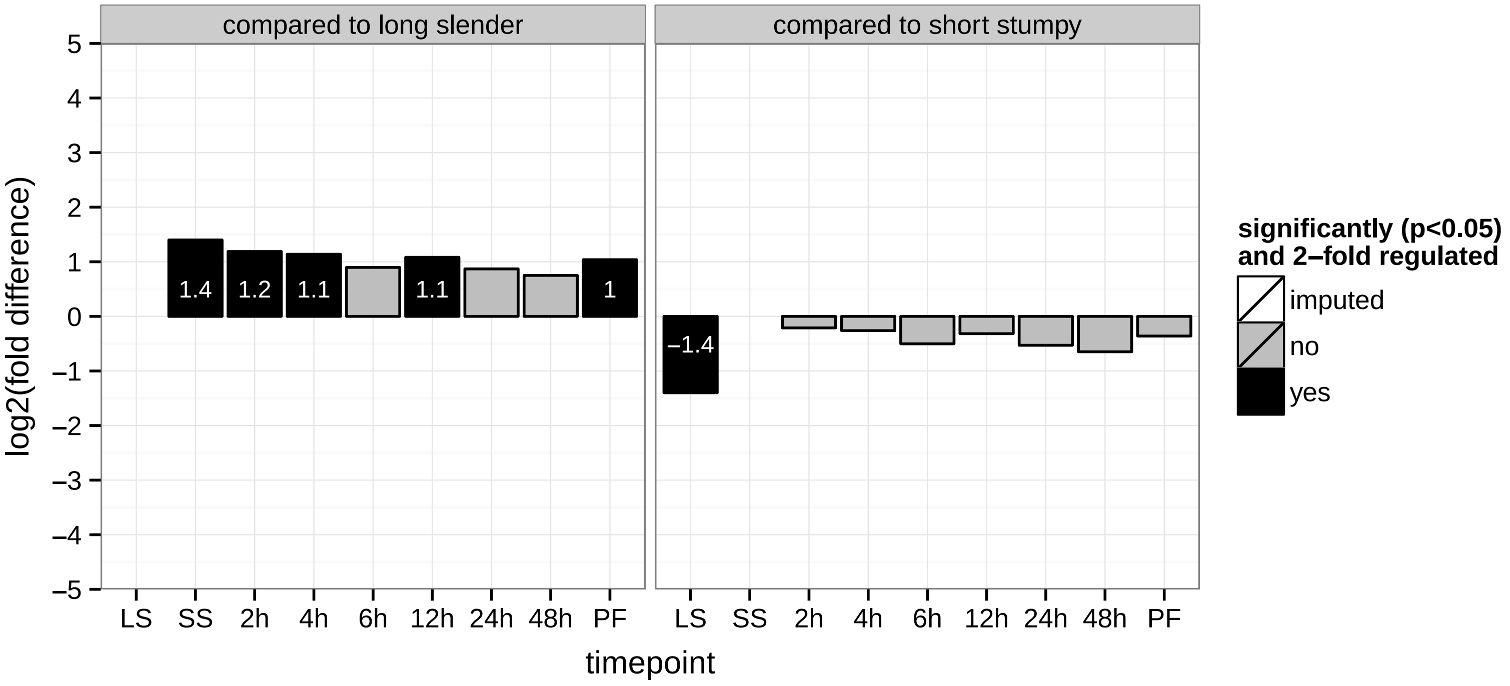
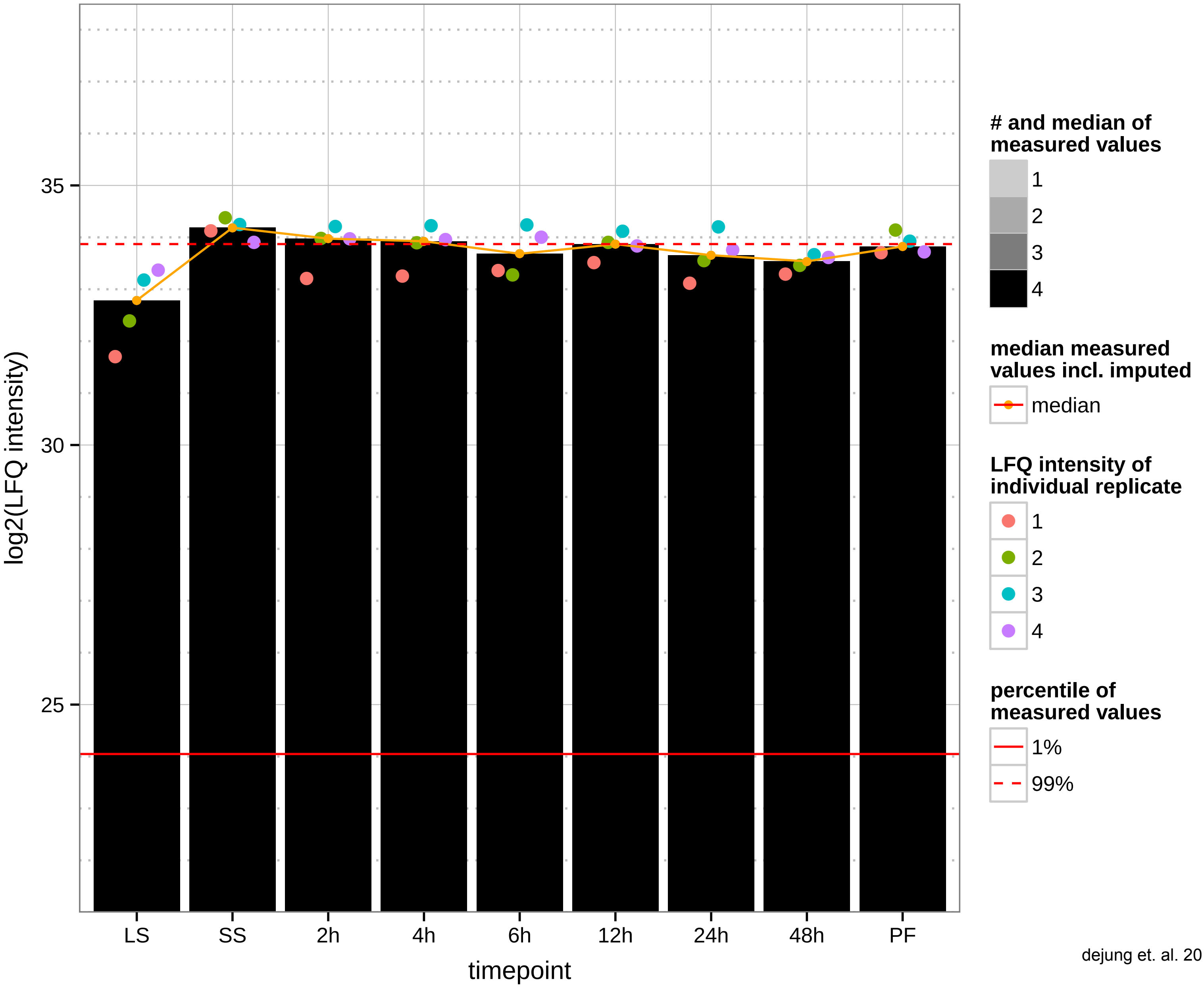
unspecified product (gim5B)
Tb927.9.11600
AGOF: null
AGOC: glycosome membrane
AGOP: null
PGOF: null
PGOC: integral to peroxisomal membrane
PGOP: peroxisome fission





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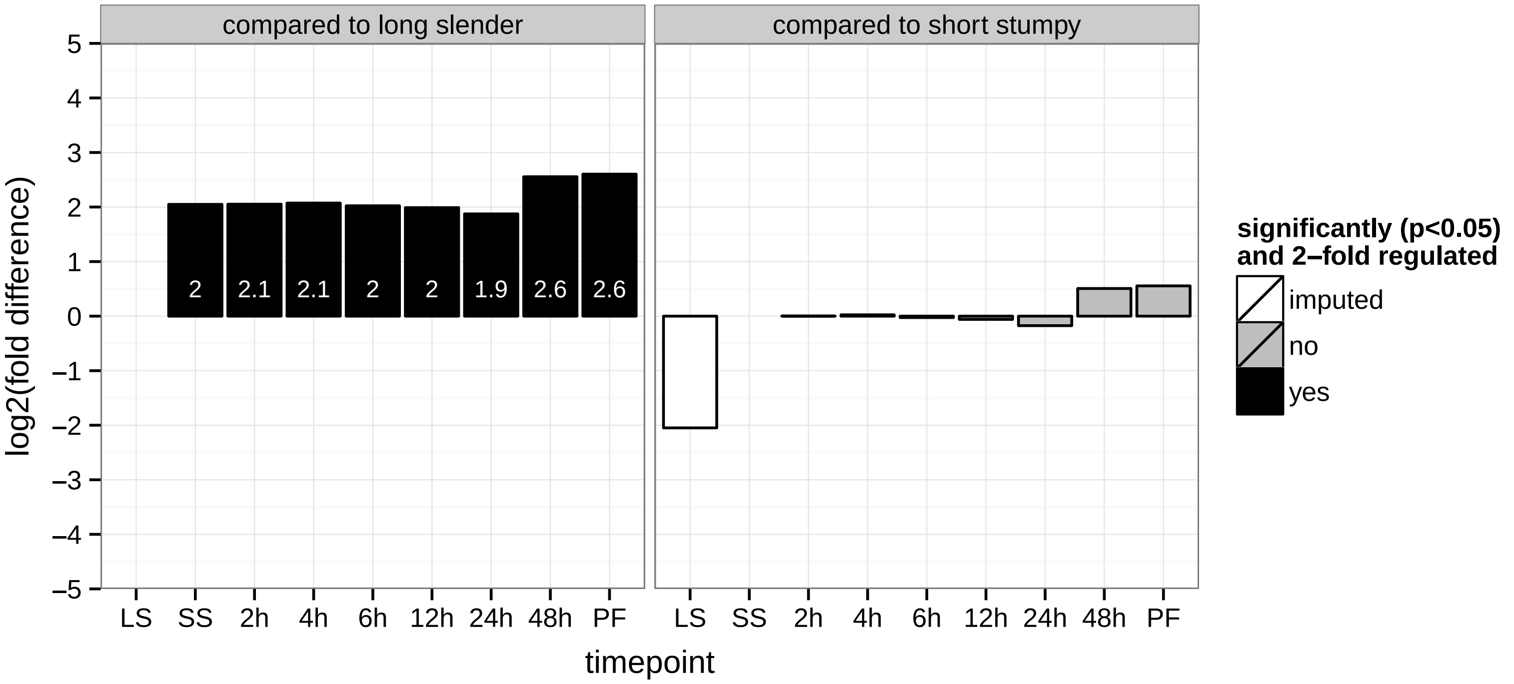
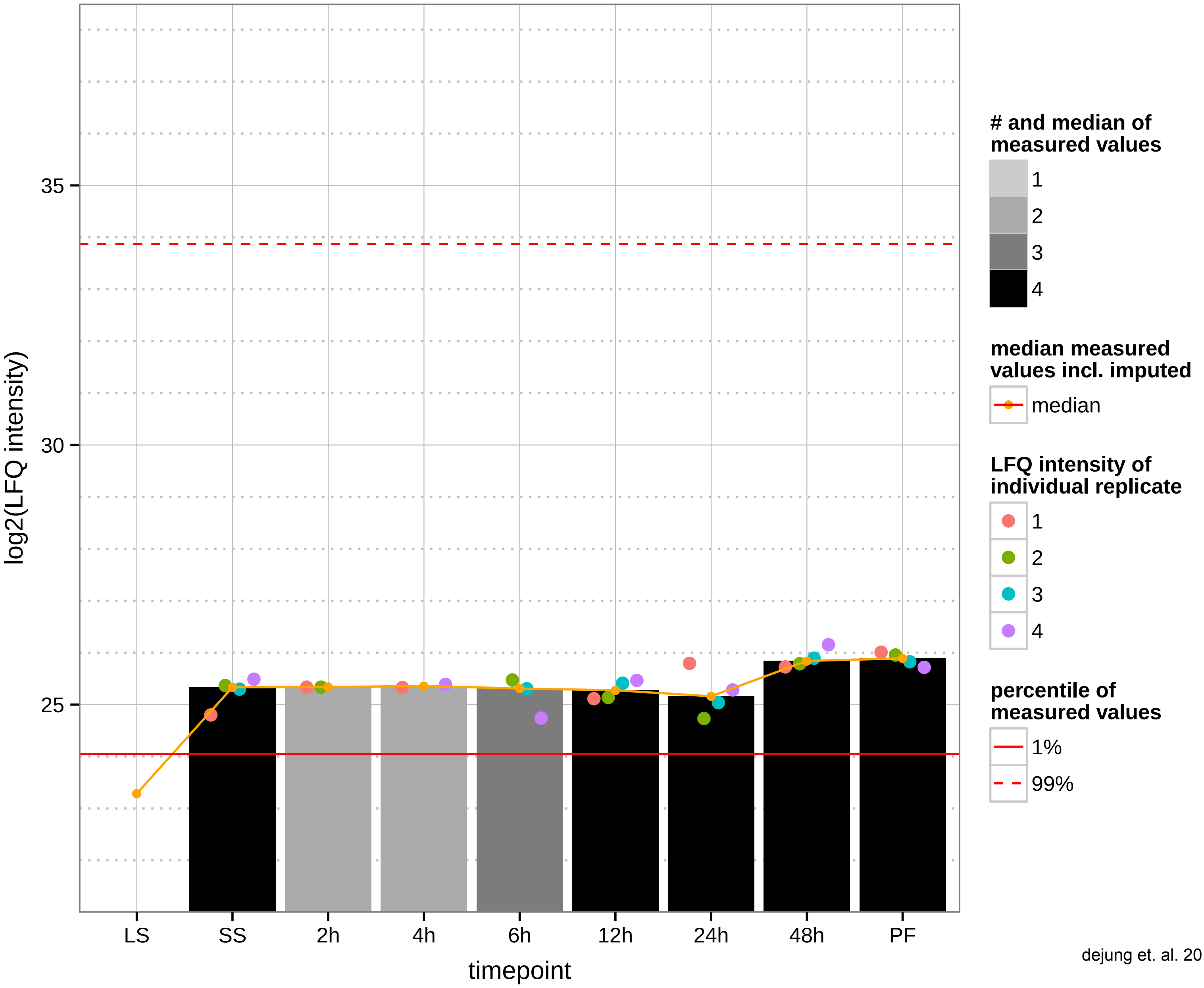
hypothetical protein, conserved
Tb927.9.11770
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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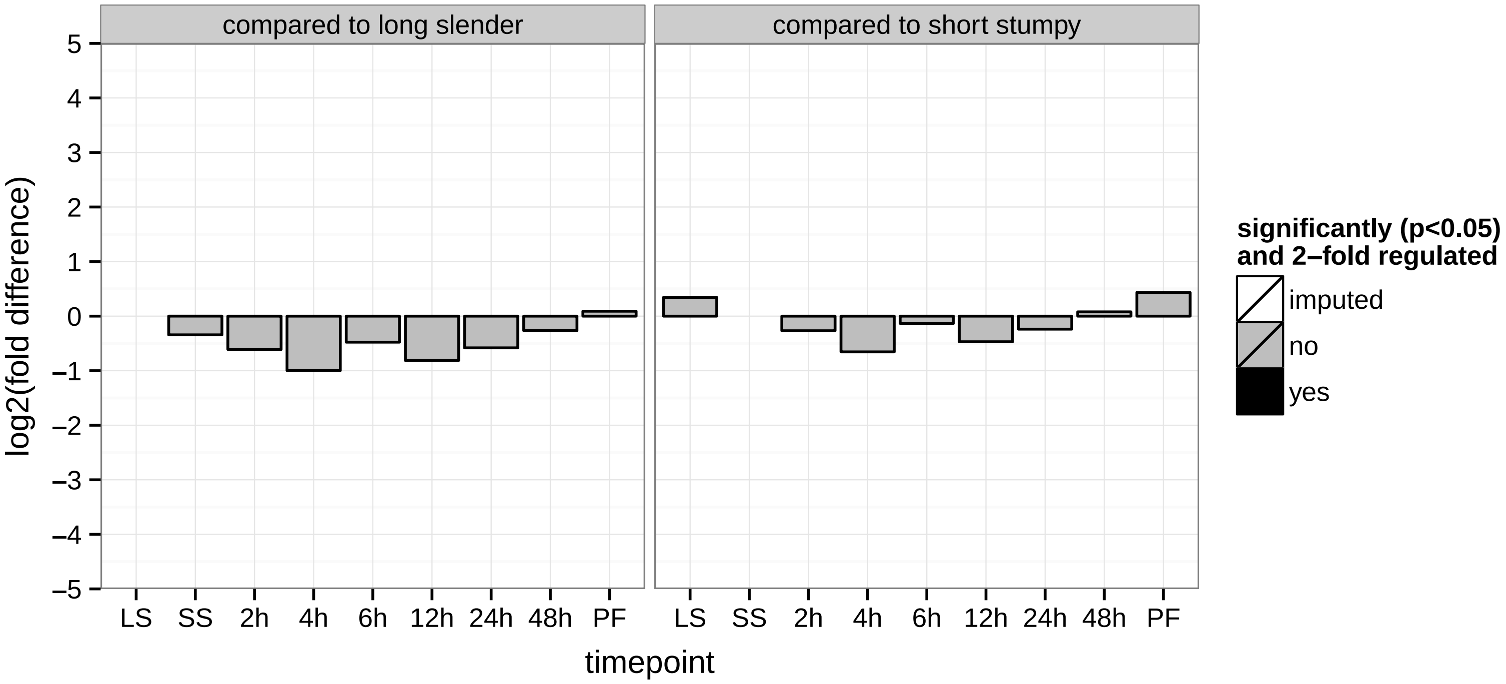
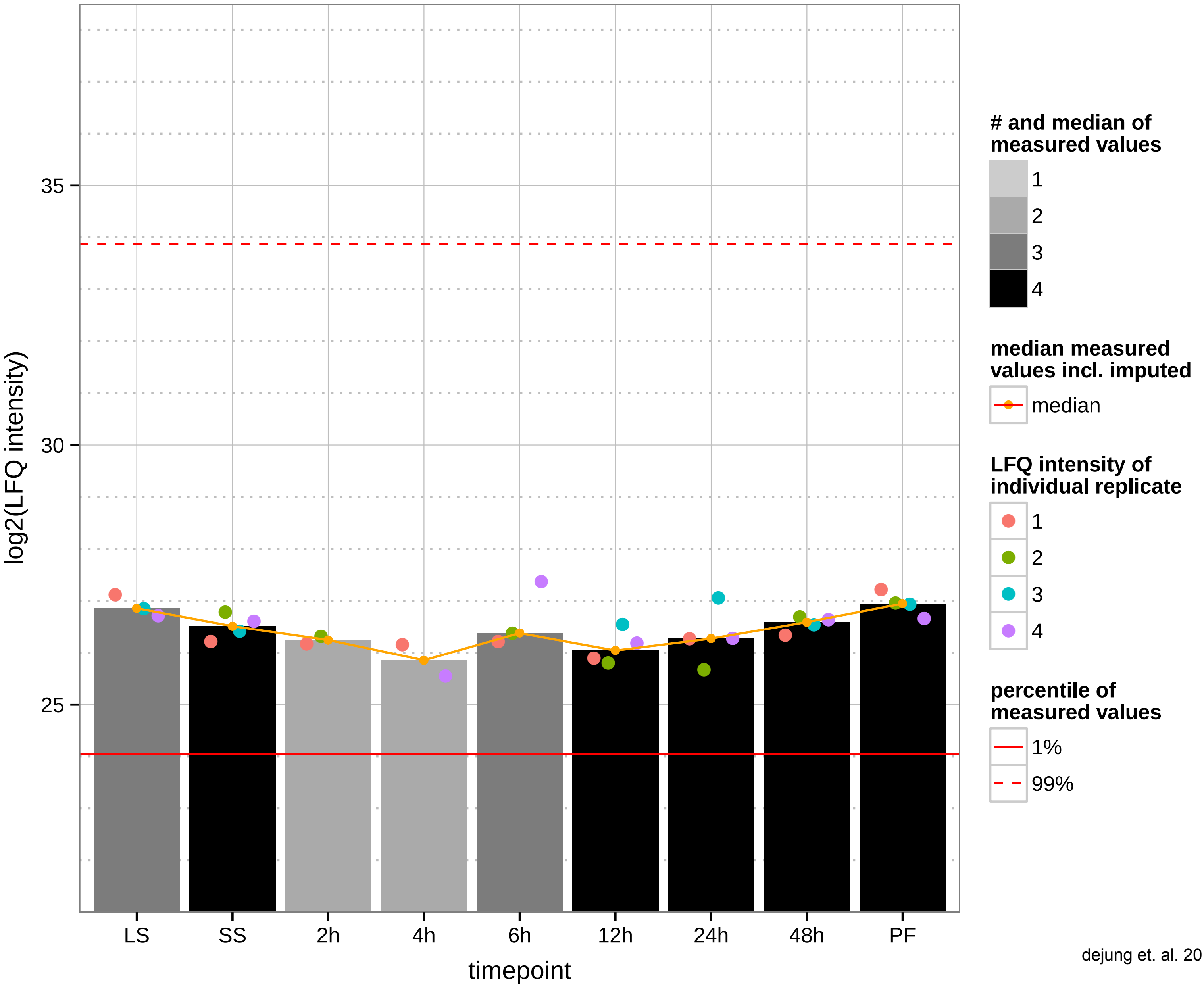
structural maintenance of chromosome 1, putative (SMC1)
Tb927.9.11850
AGOF: ATP binding
AGOC: chromosome, condensin complex, nucleus
AGOP: chromosome organization, chromosome segregation, mitotic sister chromatid segregation
PGOF: ATP binding, protein binding
PGOC: chromosome
PGOP: DNA recombination, DNA repair, chromosome condensation, chromosome organization, sister chromatid cohesion





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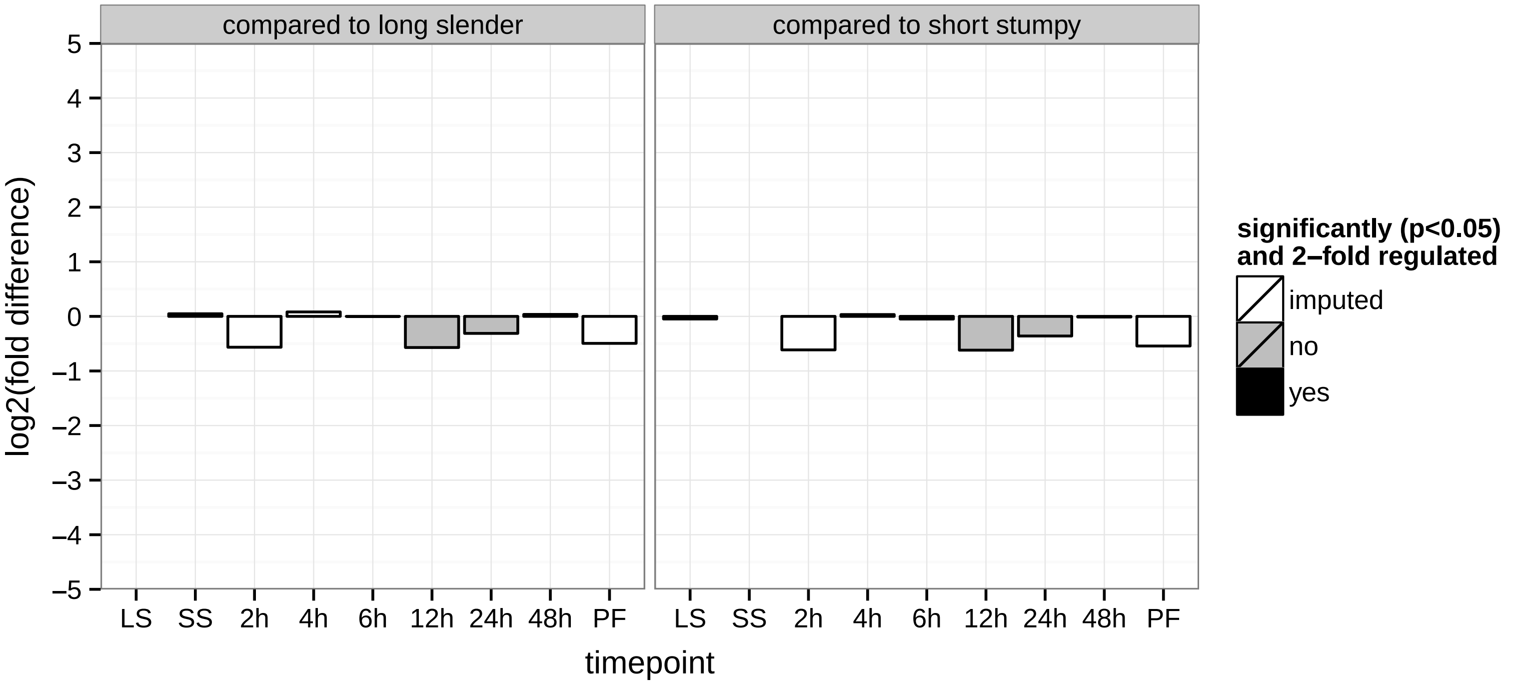
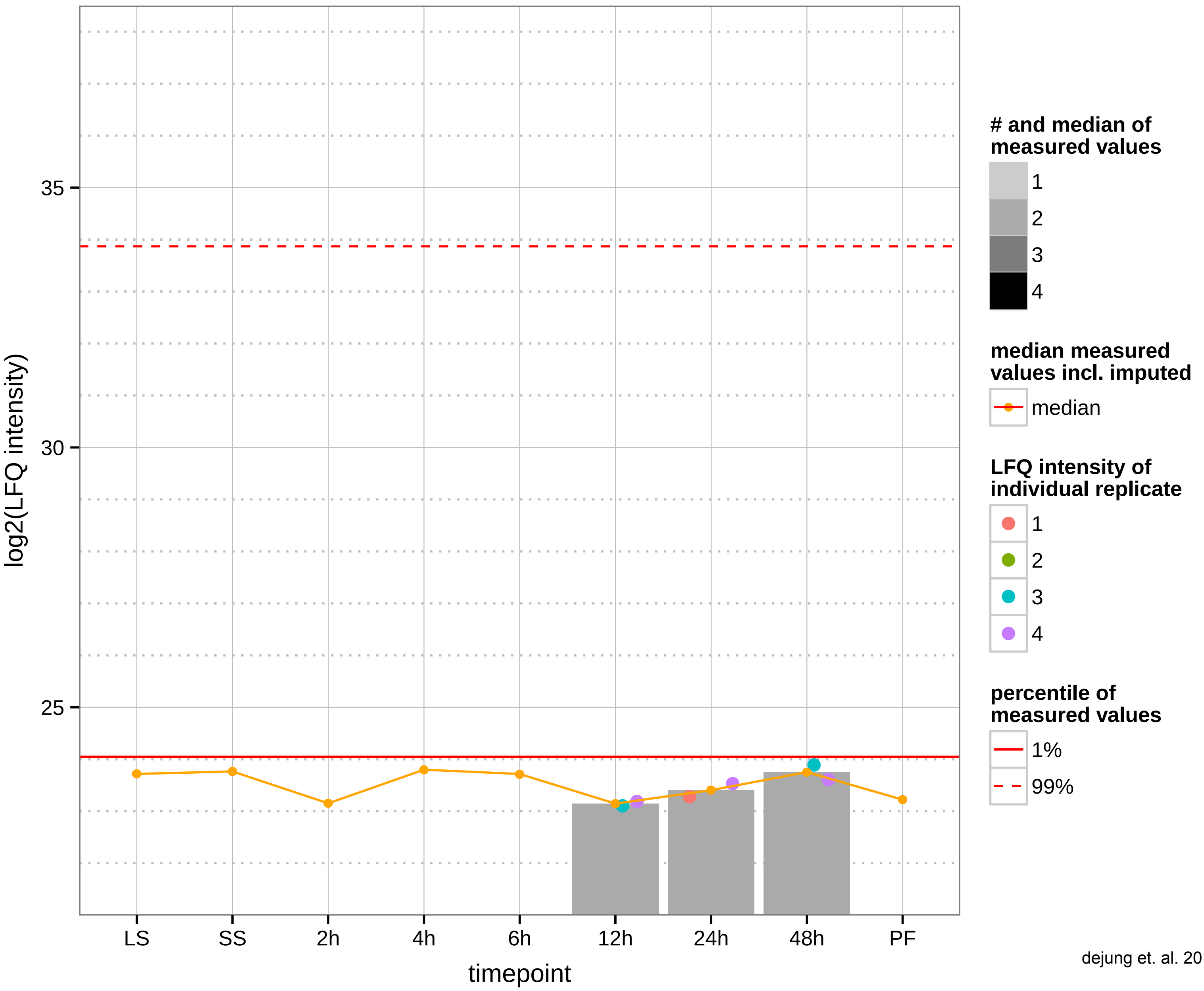
acyl transferase–like protein
Tb927.9.11900
AGOF: transferase activity
AGOC: null
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: metabolic process





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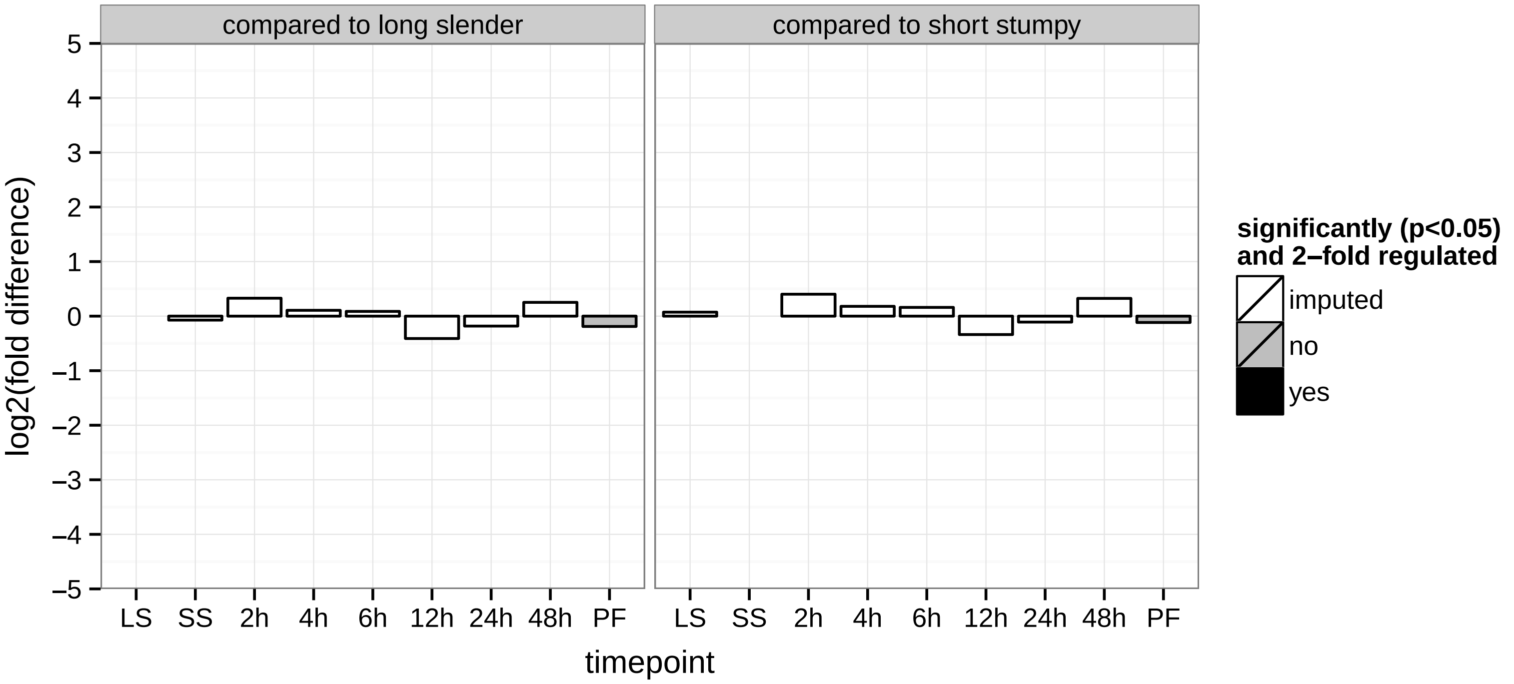
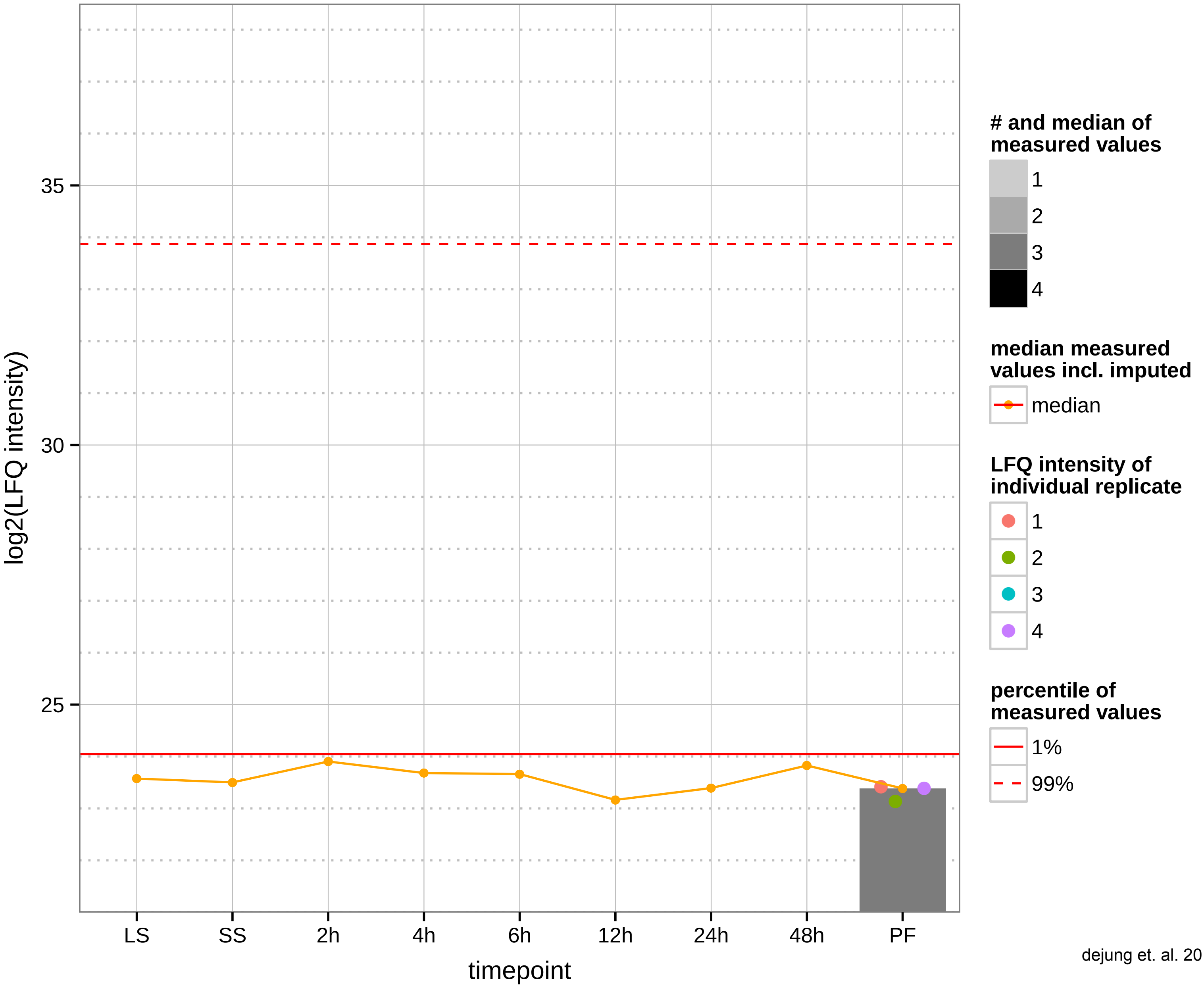
hypothetical protein, conserved
Tb927.9.12100
AGOF: methyltransferase activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: methyltransferase activity
PGOC: null
PGOP: metabolic process





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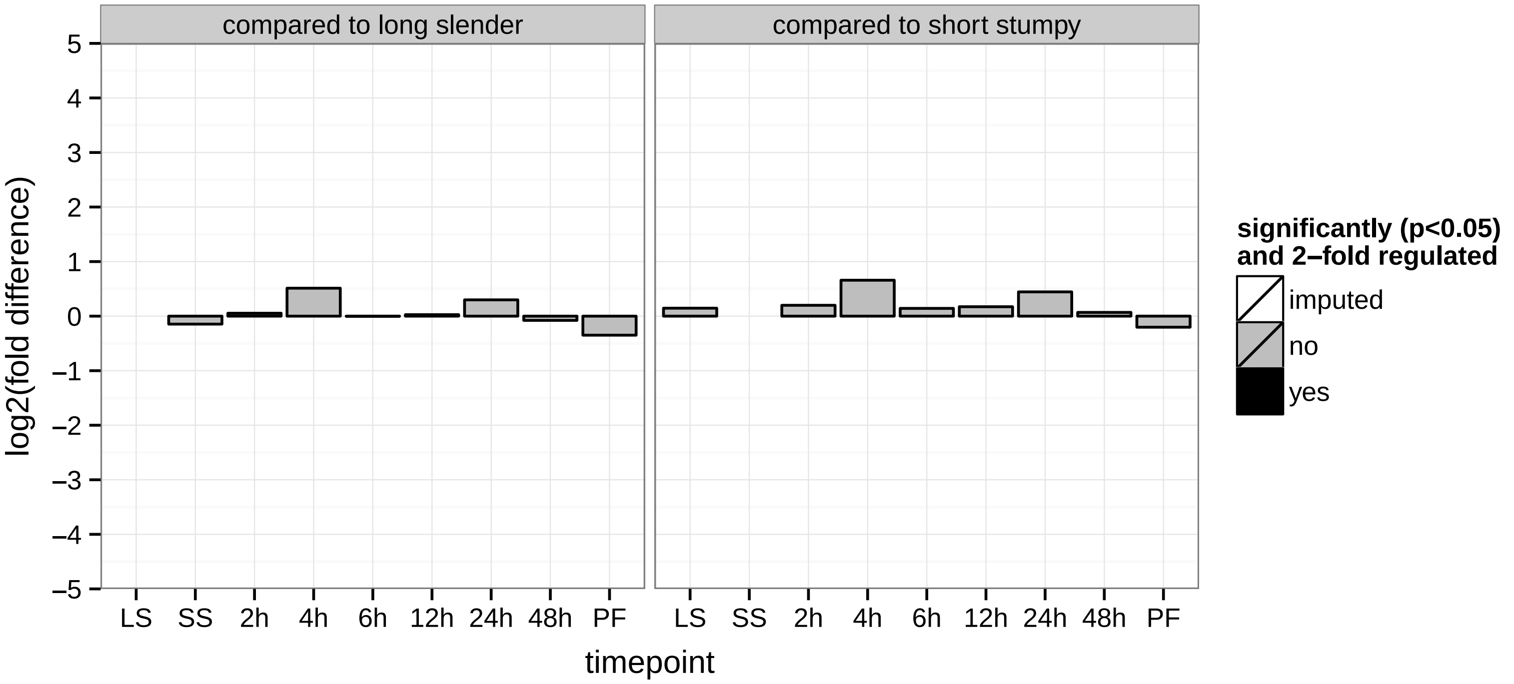
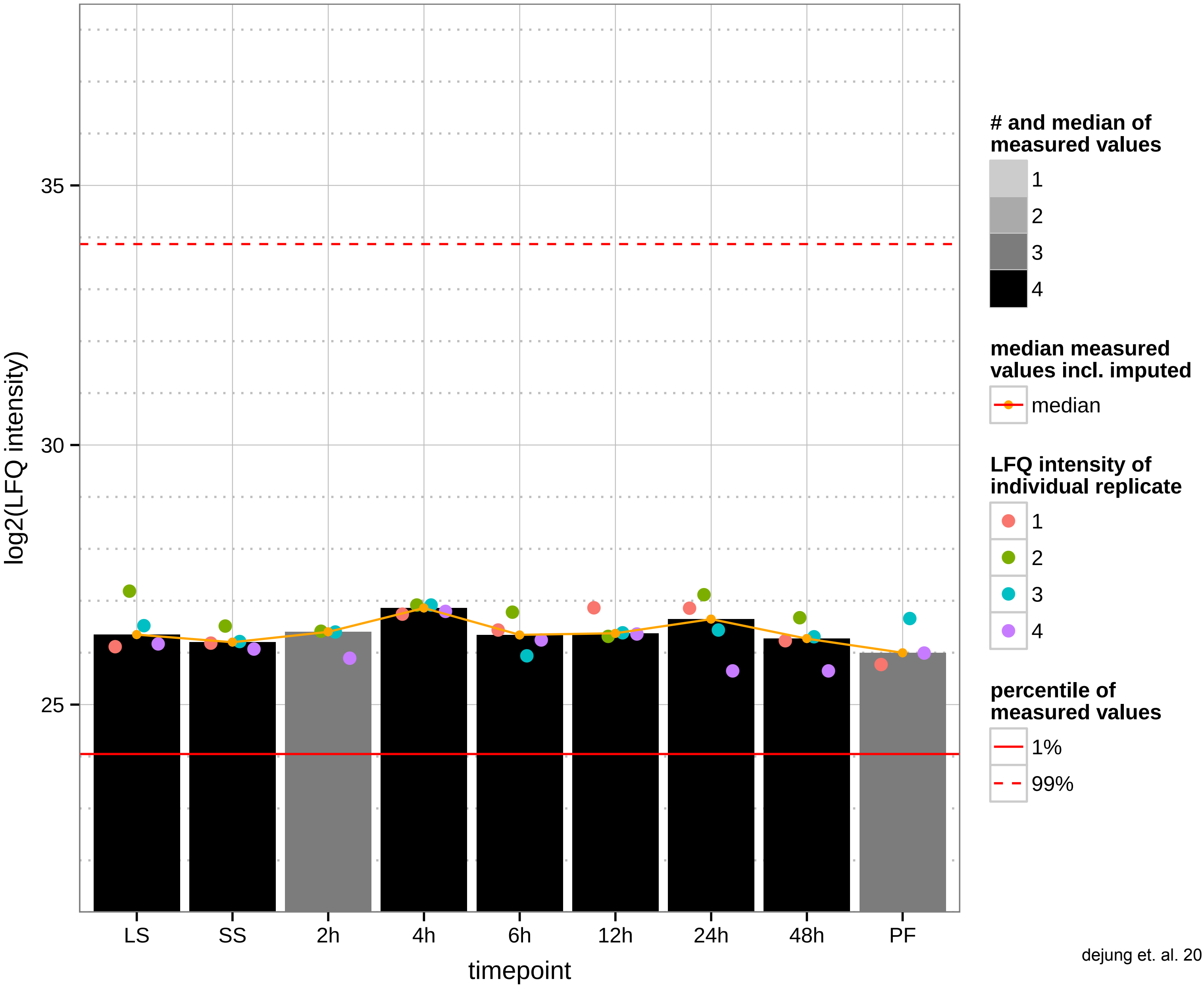
transport protein particle (TRAPP) subunit, putative
Tb927.9.12150
AGOF: null
AGOC: TRAPP complex, membrane
AGOP: ER to Golgi vesicle–mediated transport
PGOF: null
PGOC: null
PGOP: null





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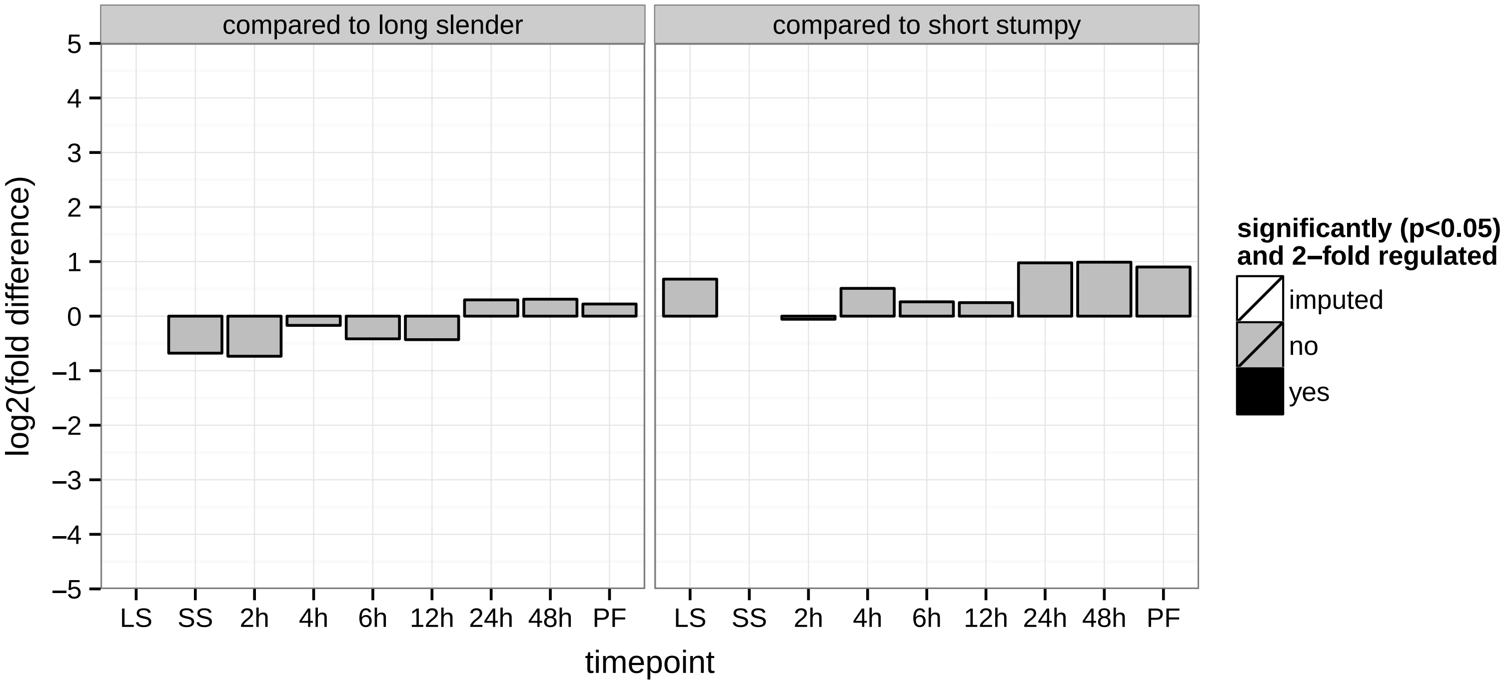
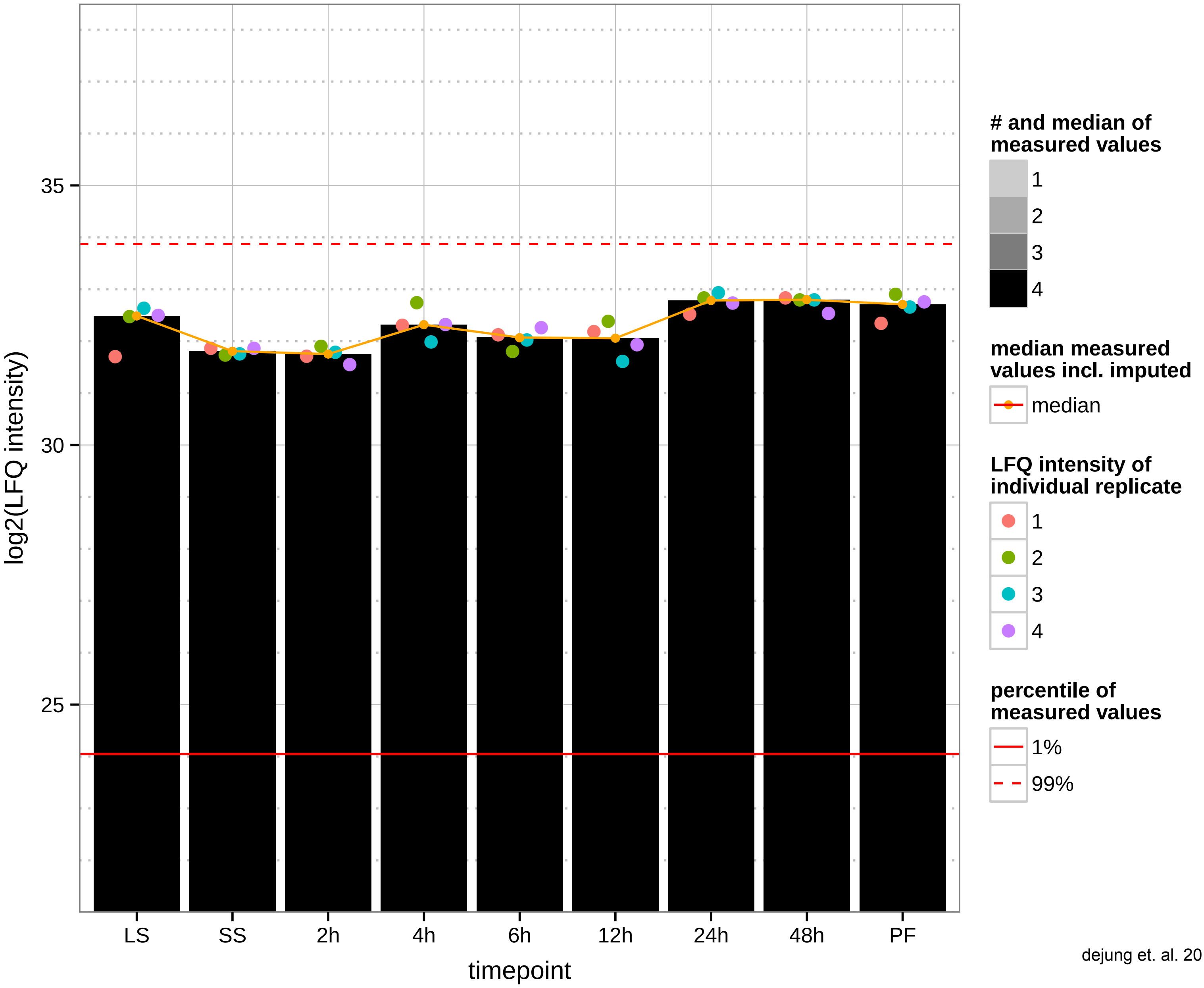
unspecified product
Tb927.9.12240;Tb927.9.12200
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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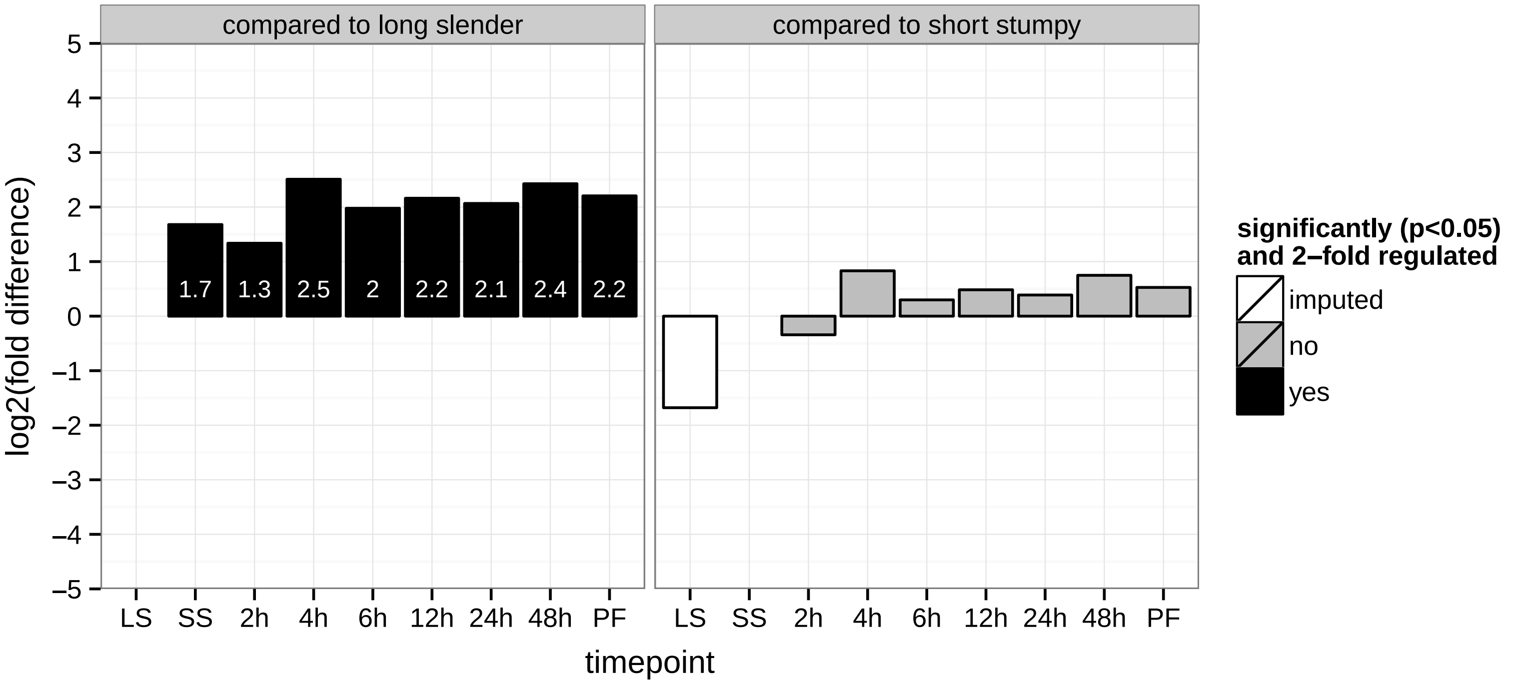
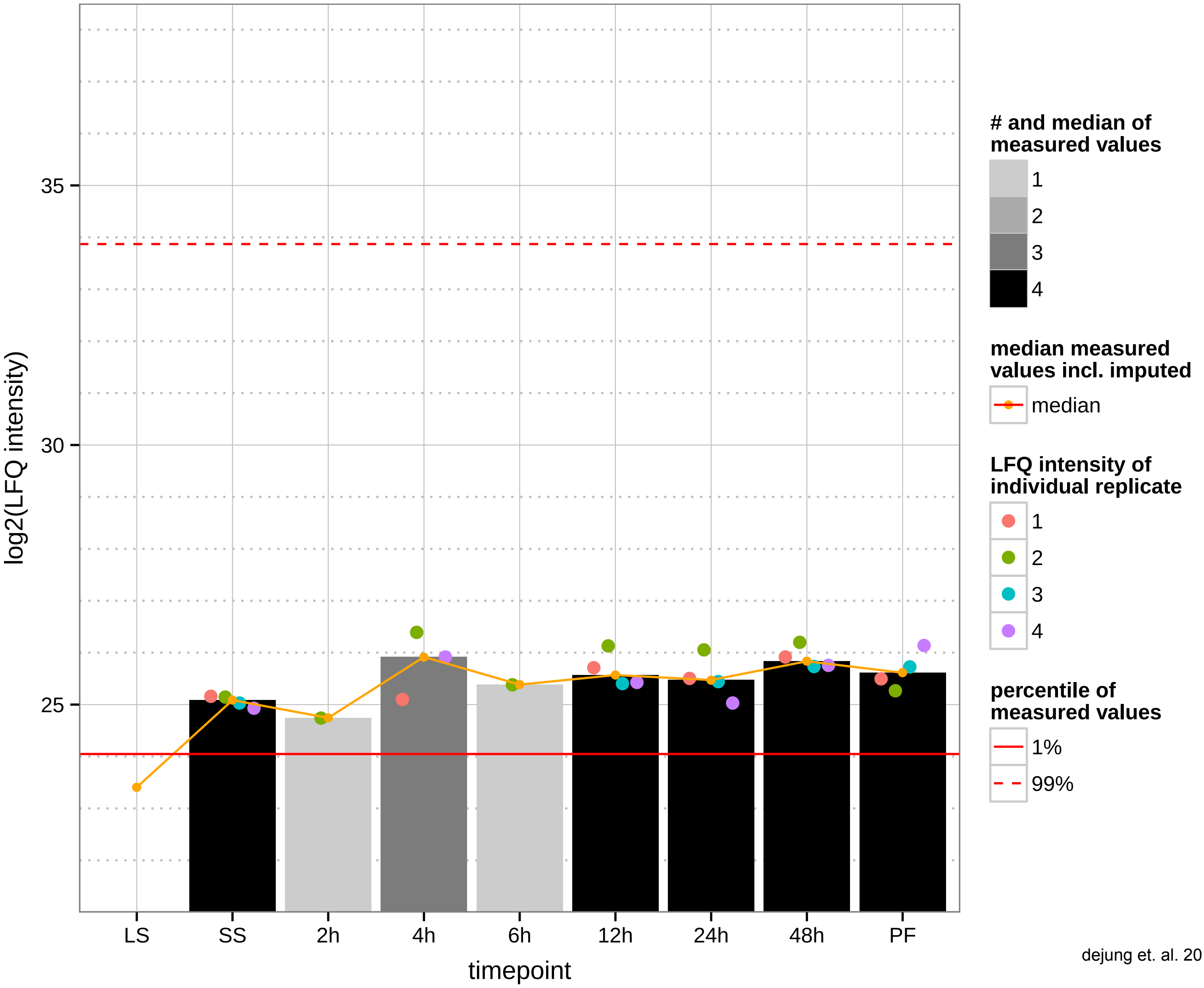
Peroxin 19
Tb927.9.12290
AGOF: null
AGOC: peroxisome
AGOP: null
PGOF: null
PGOC: peroxisome
PGOP: null





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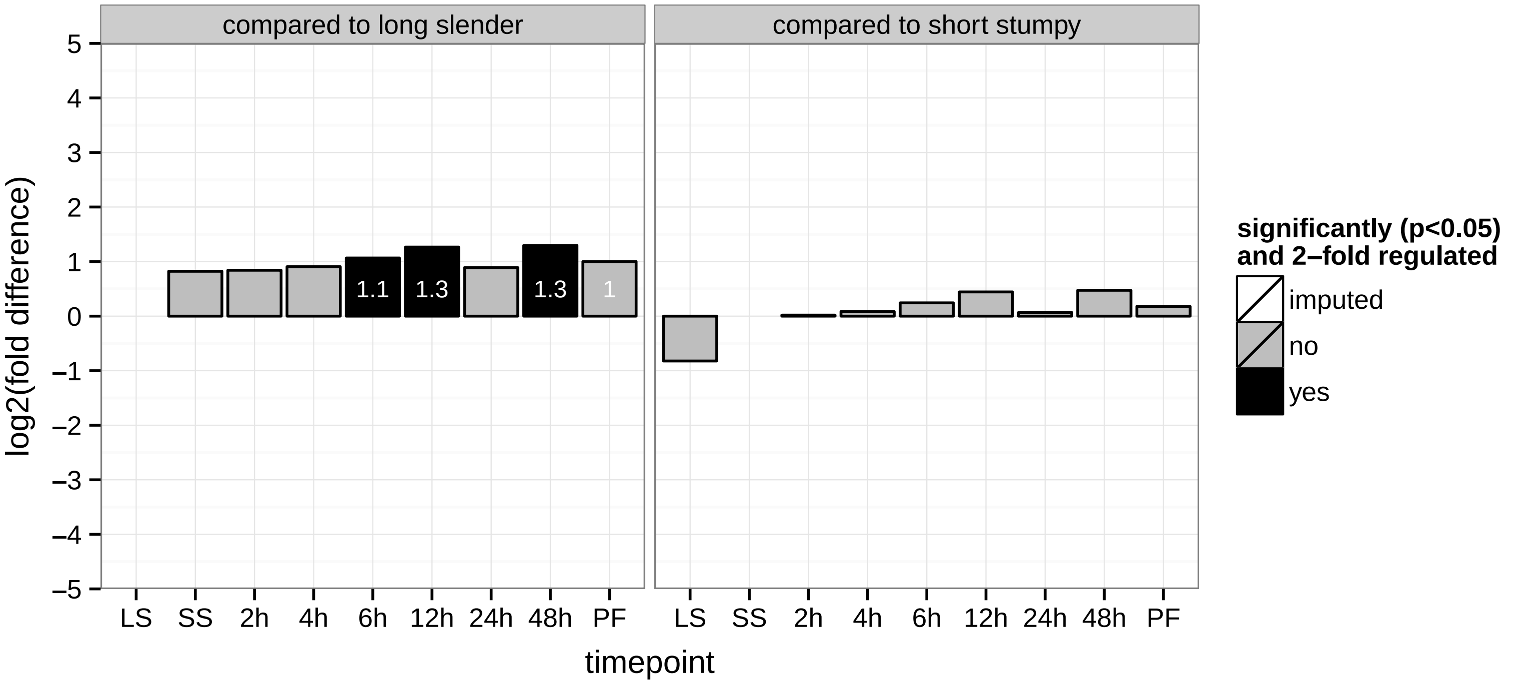
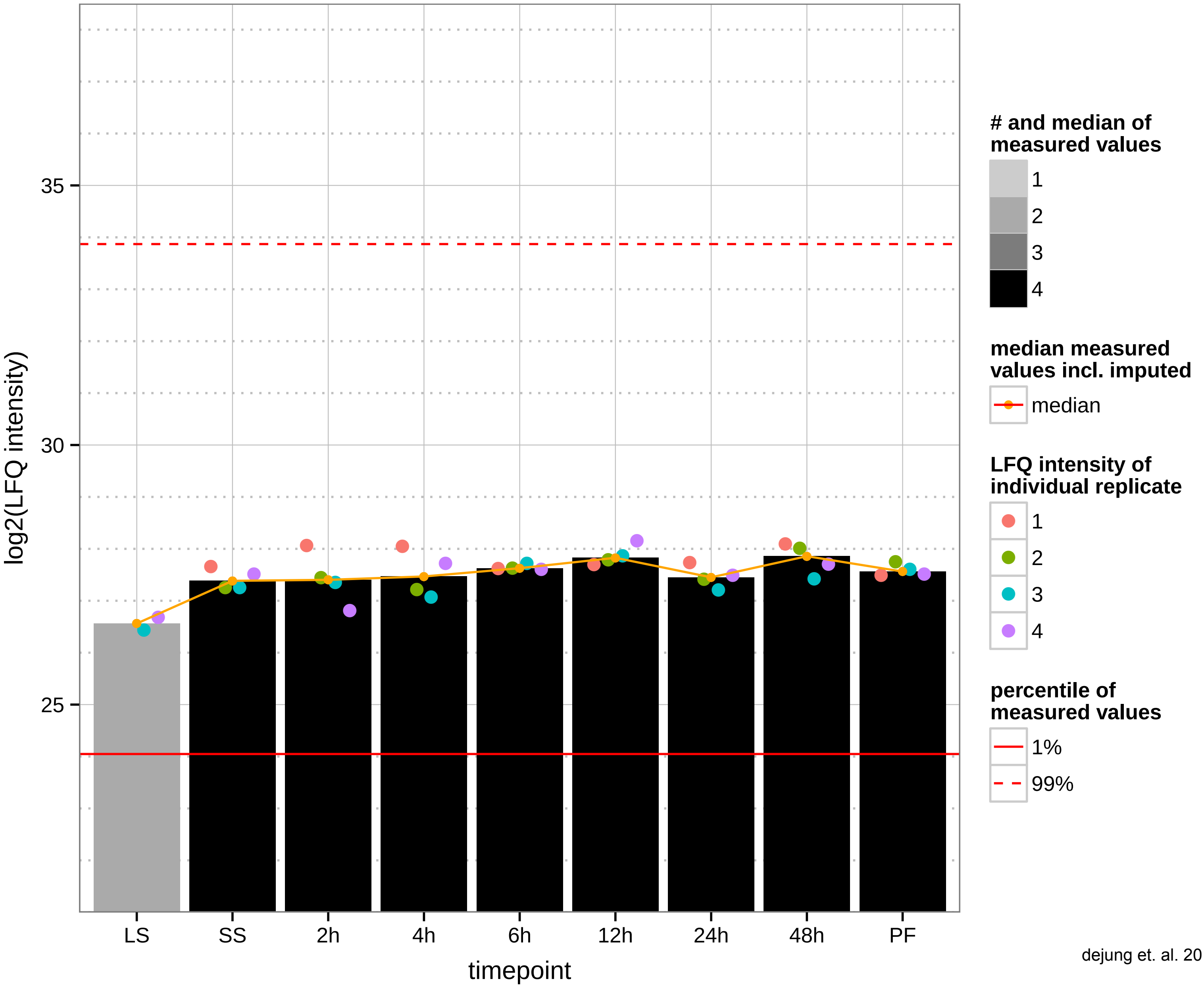
replication factor C, subunit 3, putative
Tb927.9.12300
AGOF: ATP binding, DNA binding, DNA clamp loader activity
AGOC: DNA replication factor C complex
AGOP: DNA replication
PGOF: ATP binding, DNA binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: DNA replication





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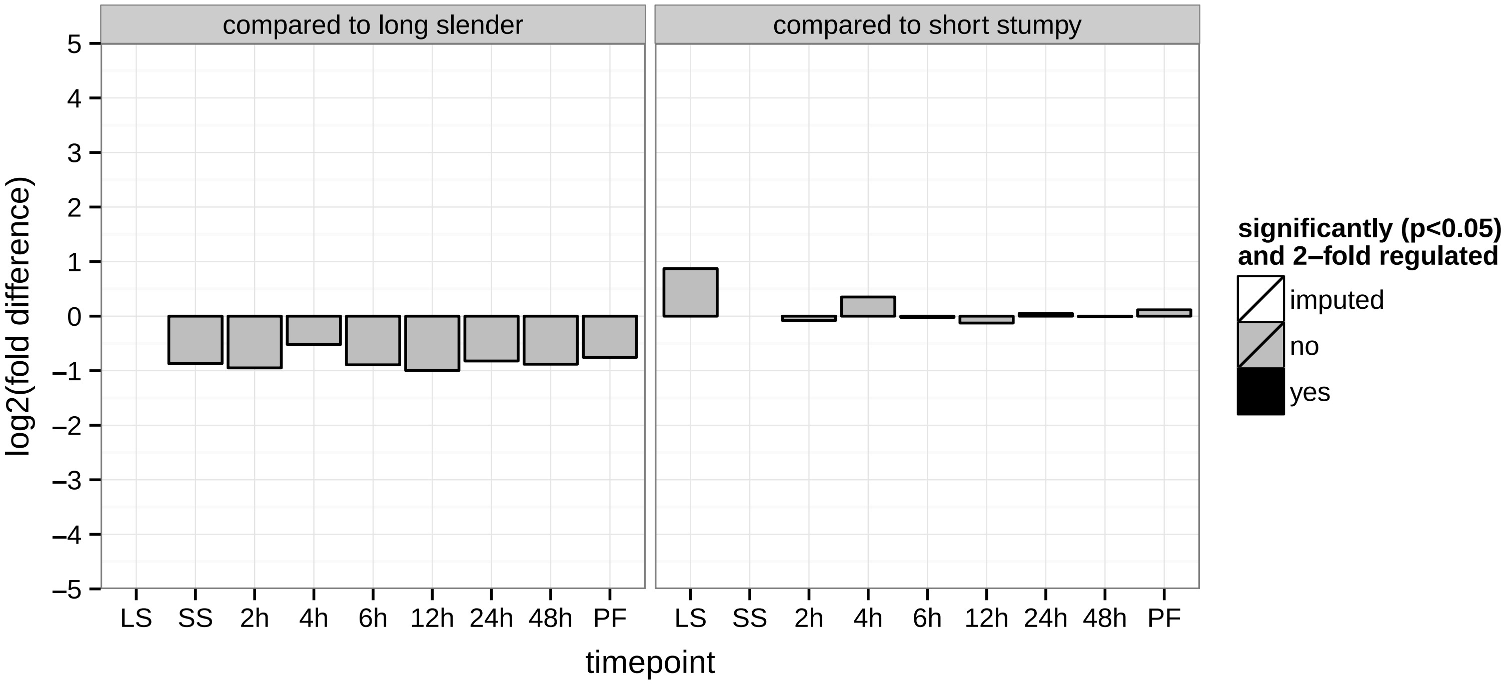
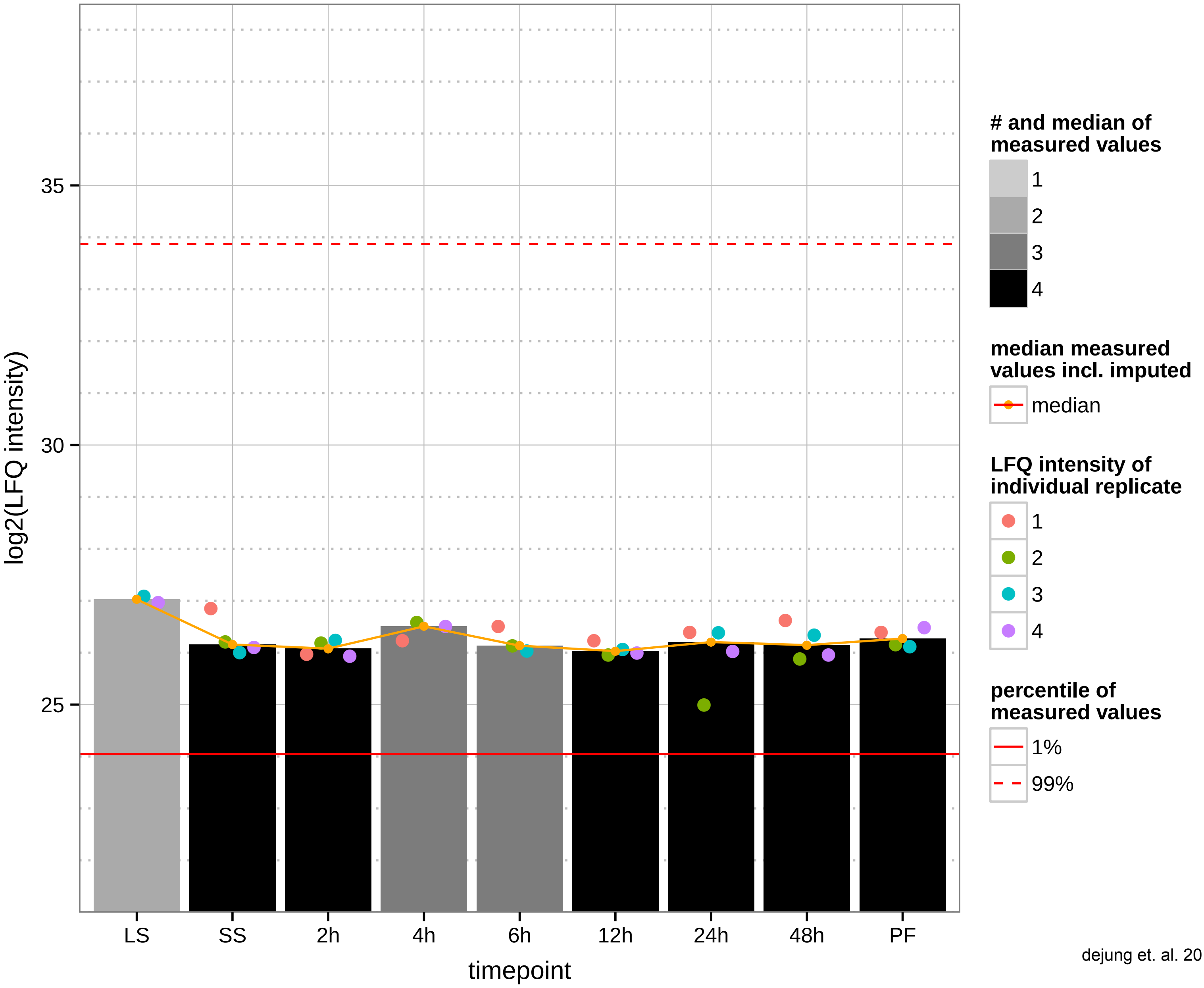
hypothetical protein, conserved
Tb927.9.12480
AGOF: microtubule motor activity
AGOC: microtubule associated complex, mitochondrion
AGOP: microtubule–based process
PGOF: null
PGOC: microtubule associated complex
PGOP: microtubule–based process





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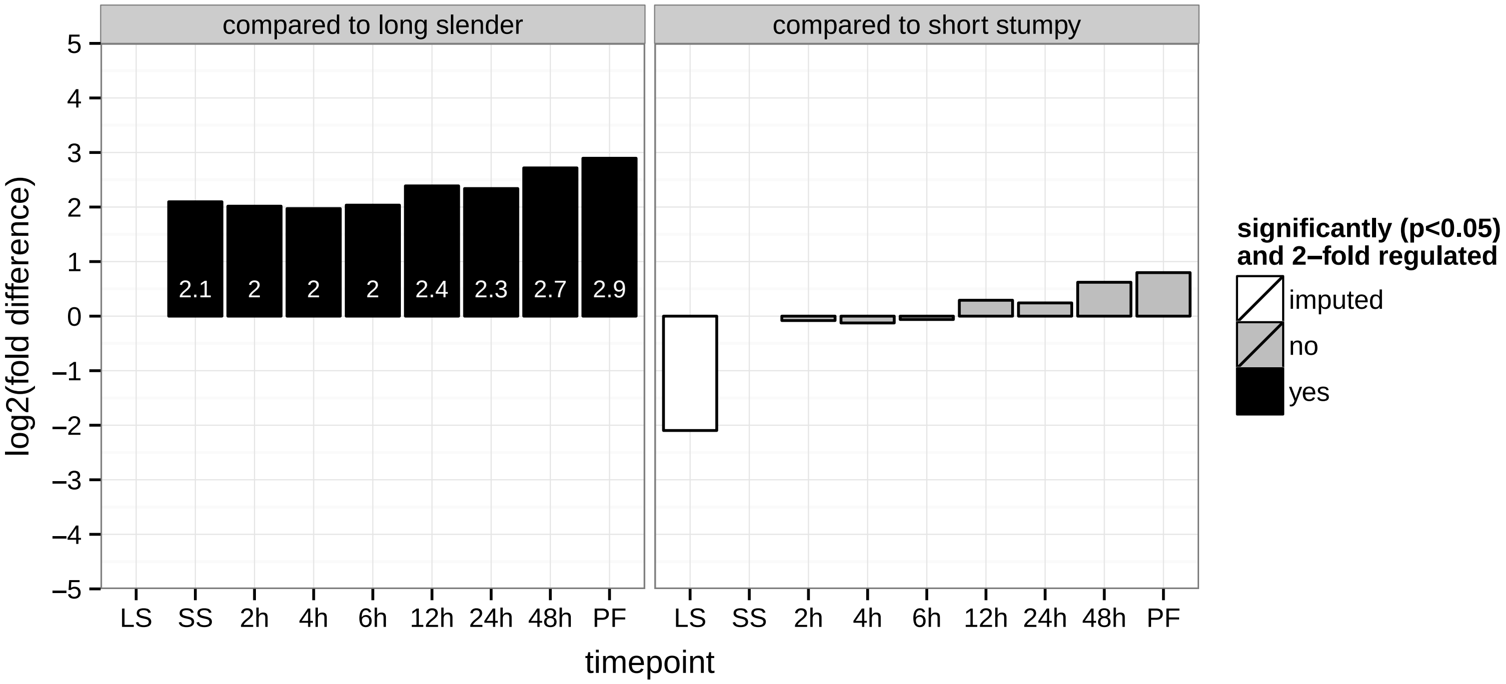
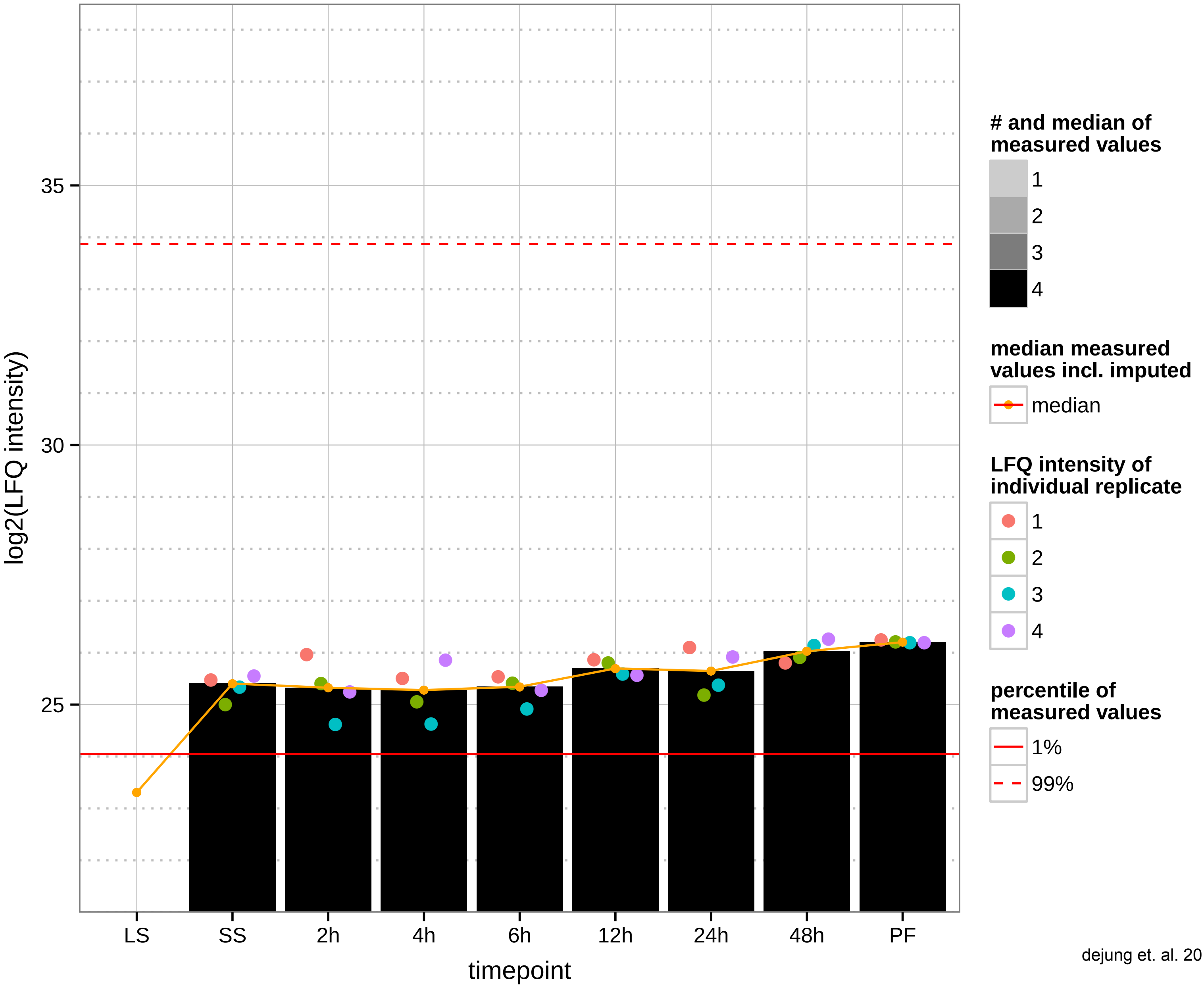
hypothetical protein, conserved
Tb927.9.12500
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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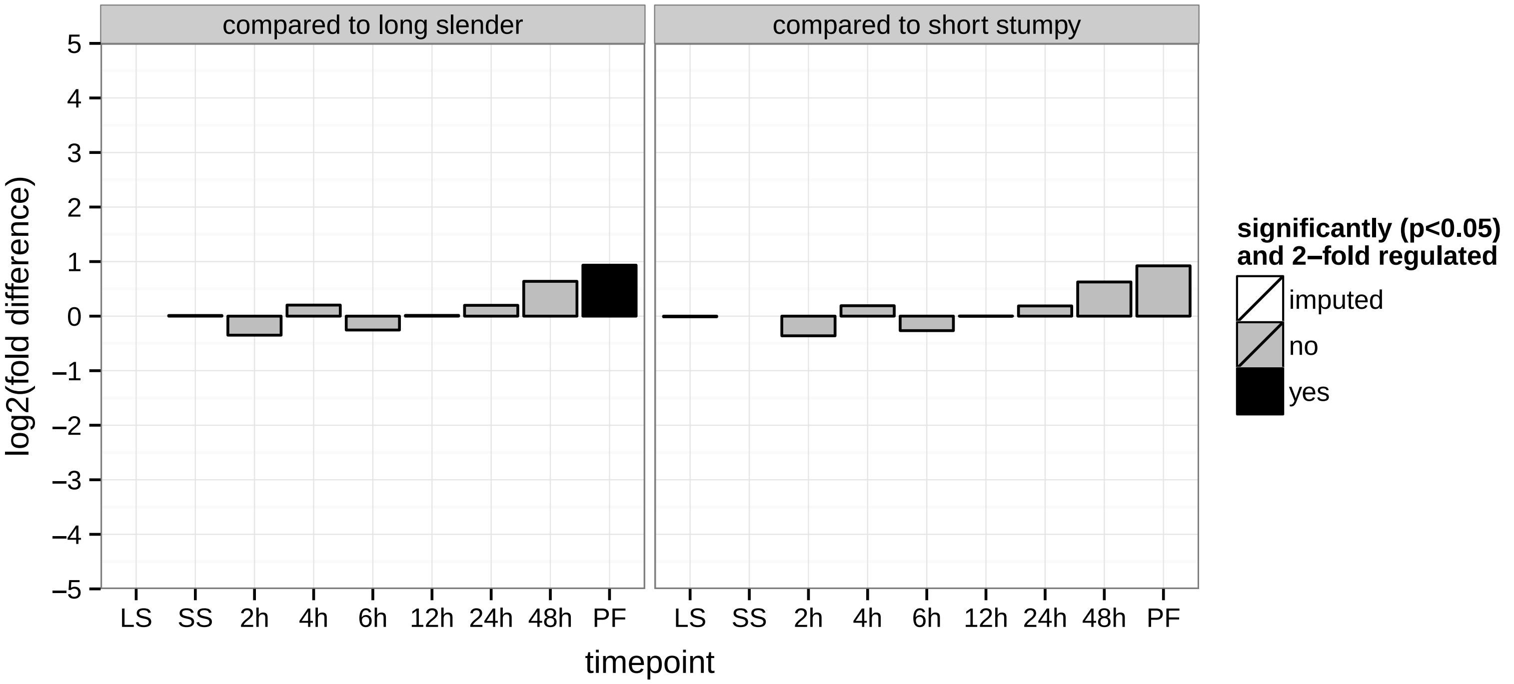
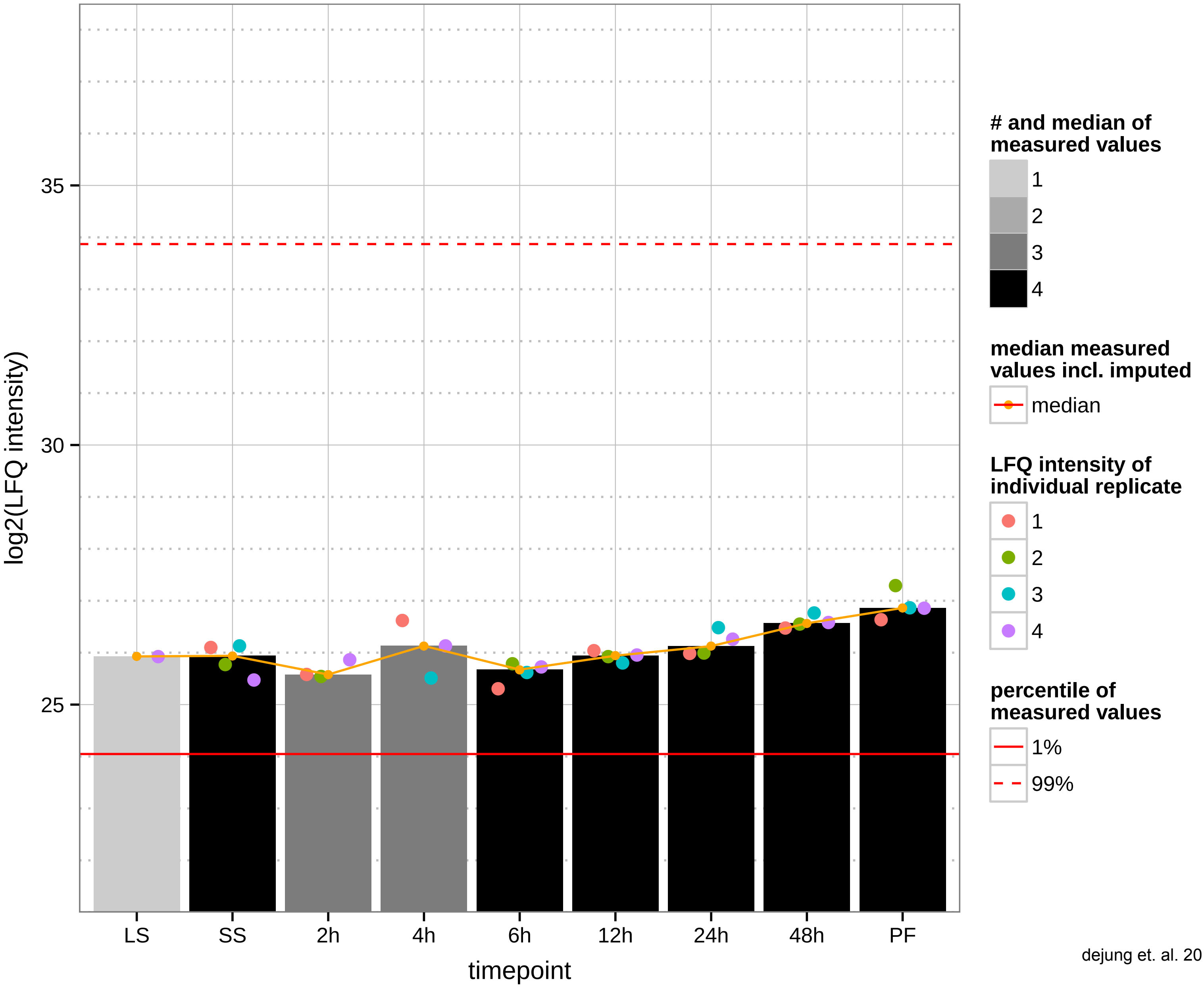
phospholipase A1, putative
Tb927.9.12700
AGOF: 1–alkyl–2–acetylglycerophosphocholine esterase activity, phosphatidylcholine 1–acylhydrolase activity
AGOC: extracellular region
AGOP: lipid catabolic process
PGOF: 1–alkyl–2–acetylglycerophosphocholine esterase activity
PGOC: null
PGOP: lipid catabolic process





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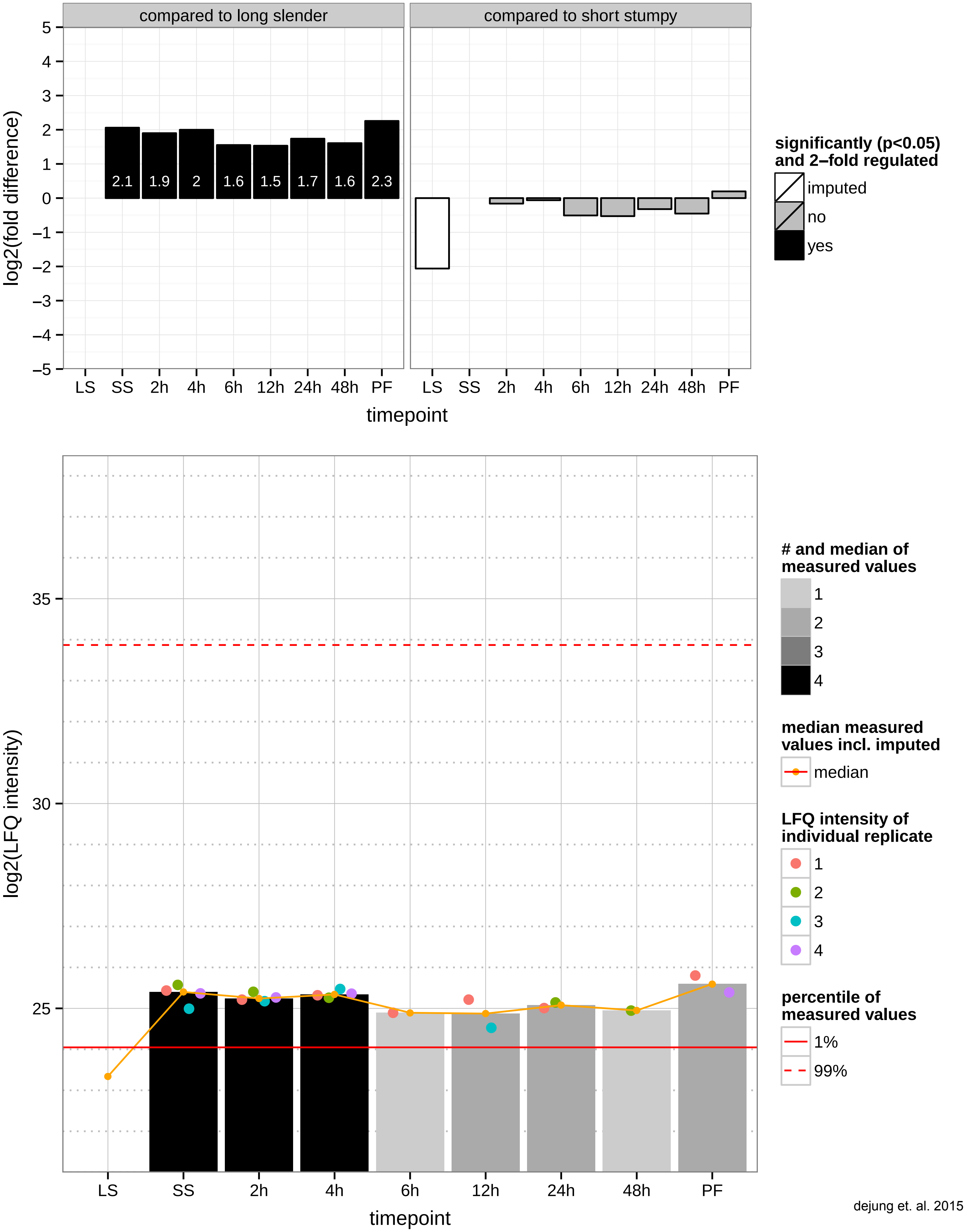
hypothetical protein, conserved
Tb927.9.12710
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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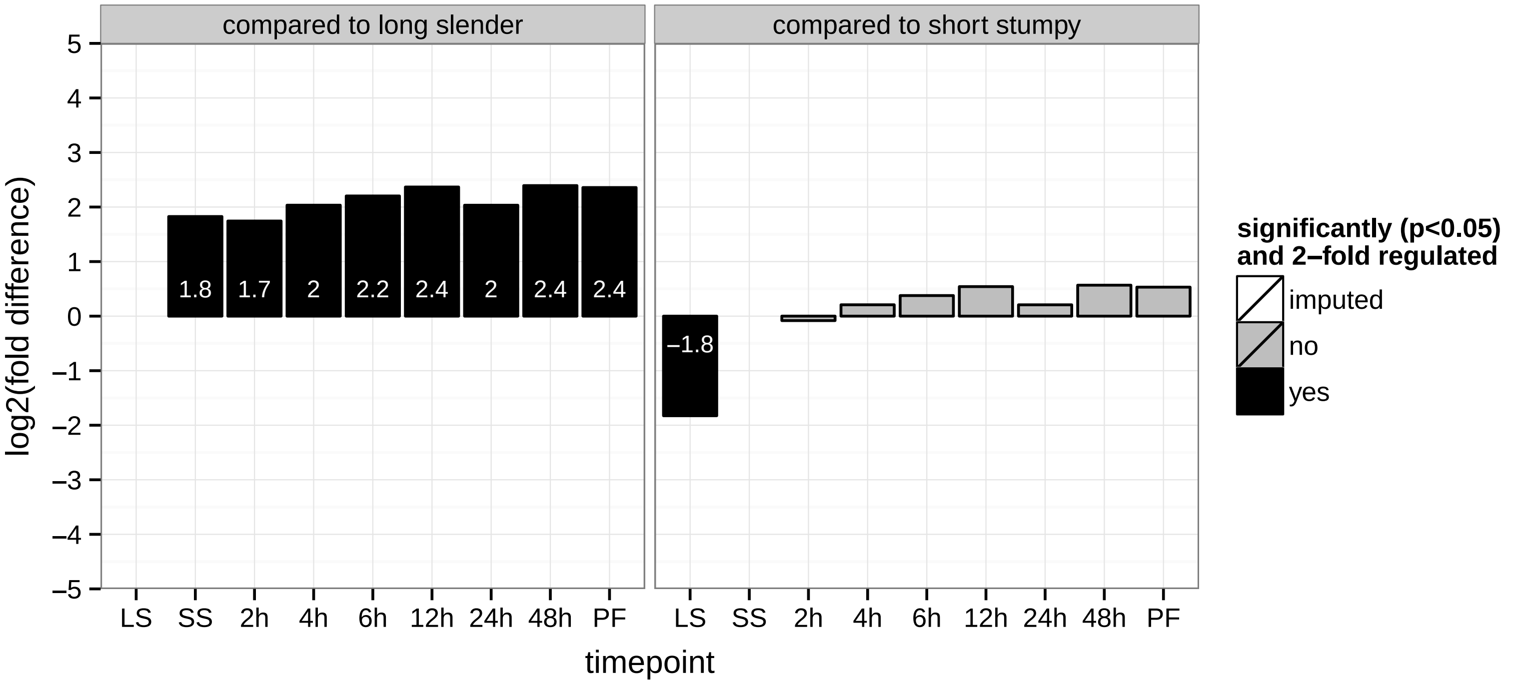
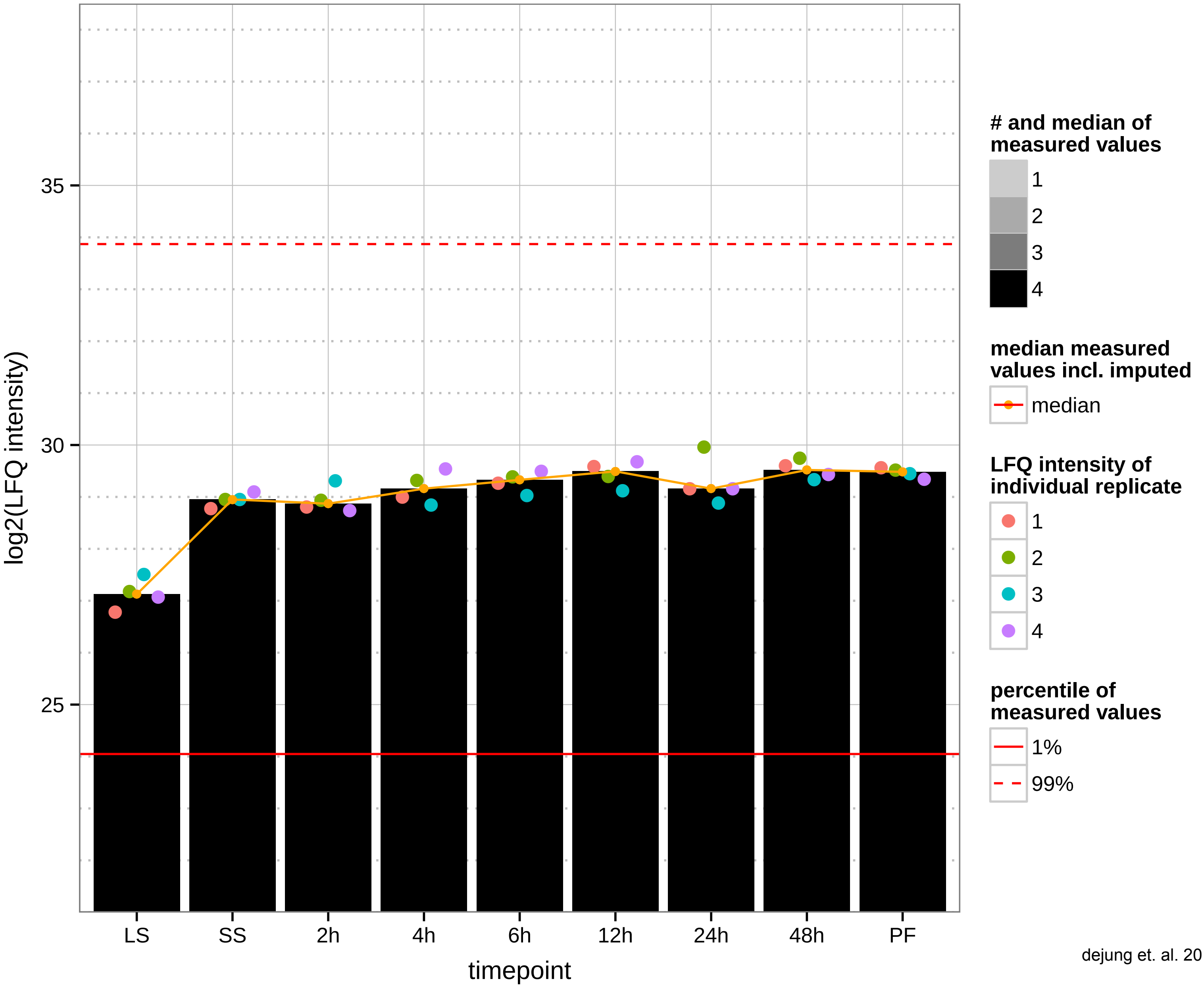
chaperone protein DNAj, putative
Tb927.9.12730
AGOF: chaperone binding, heat shock protein binding, unfolded protein binding
AGOC: mitochondrion
AGOP: protein folding
PGOF: heat shock protein binding, unfolded protein binding
PGOC: null
PGOP: protein folding





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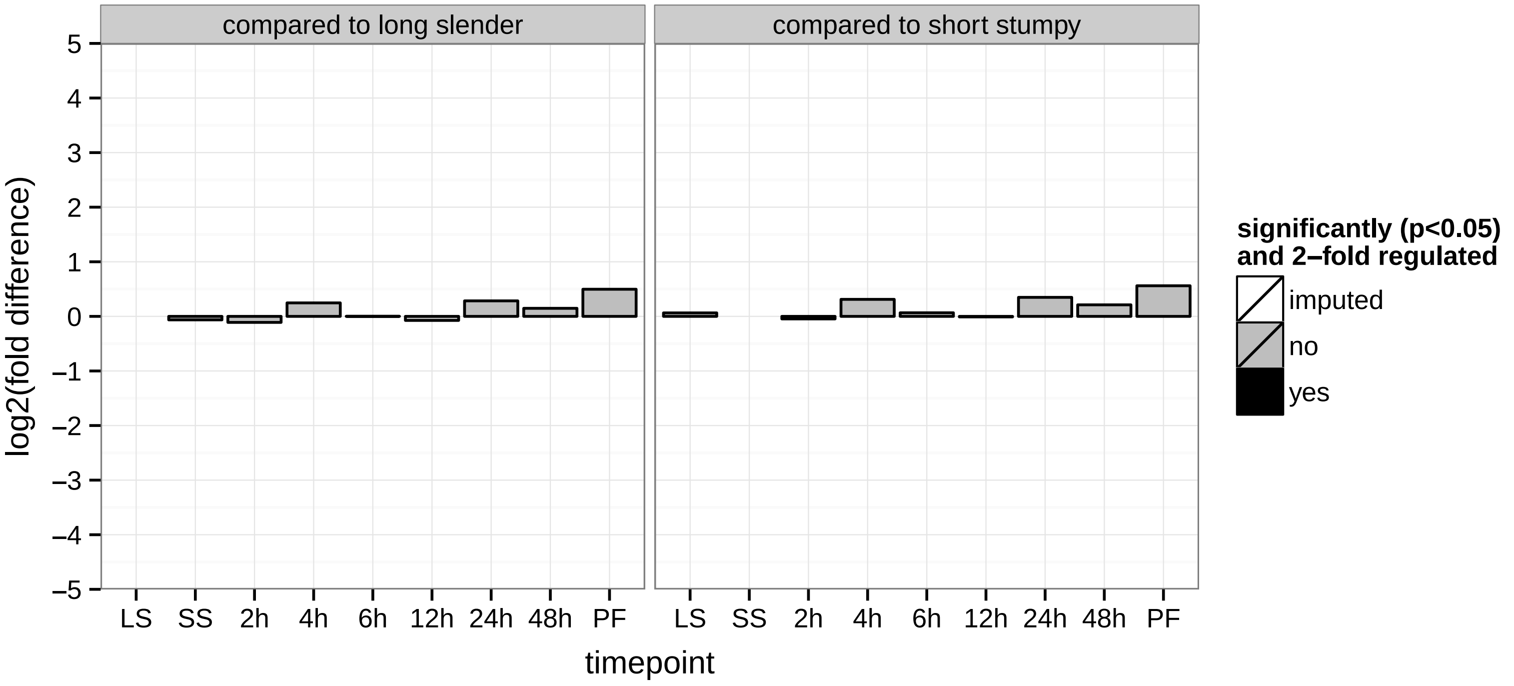
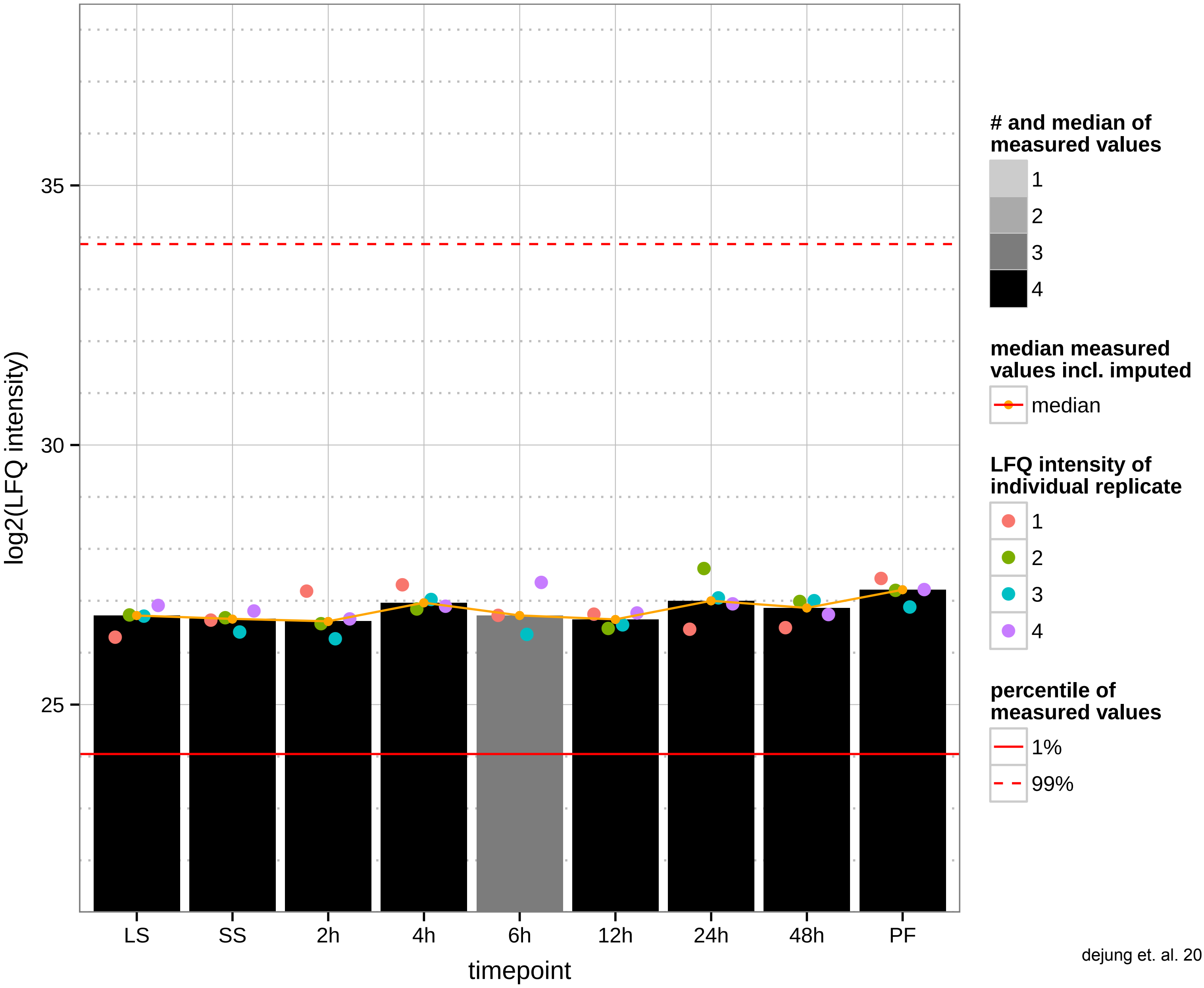
dynein light chain, putative, dynein Tctex2 family
Tb927.9.12820
AGOF: ATPase activity, coupled
AGOC: dynein complex
AGOP: microtubule–based movement
PGOF: null
PGOC: null
PGOP: null





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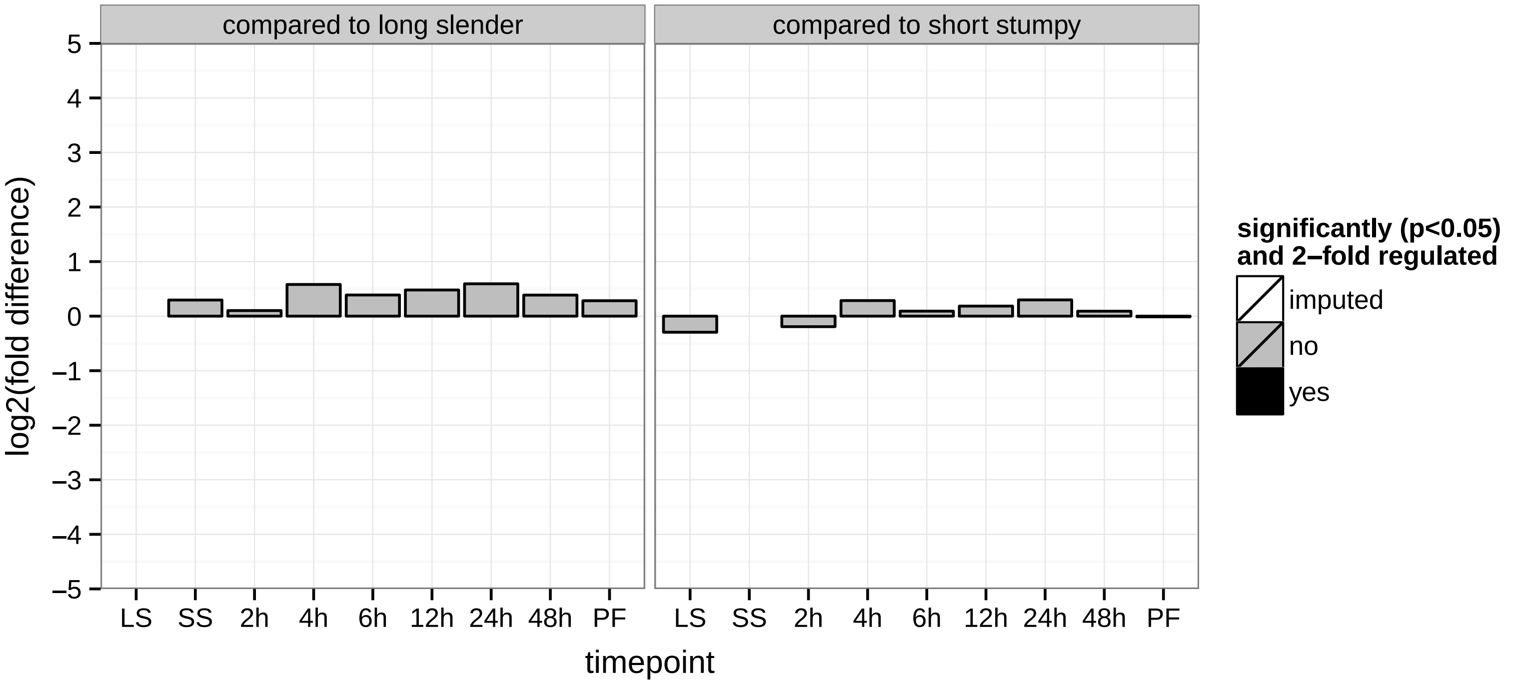
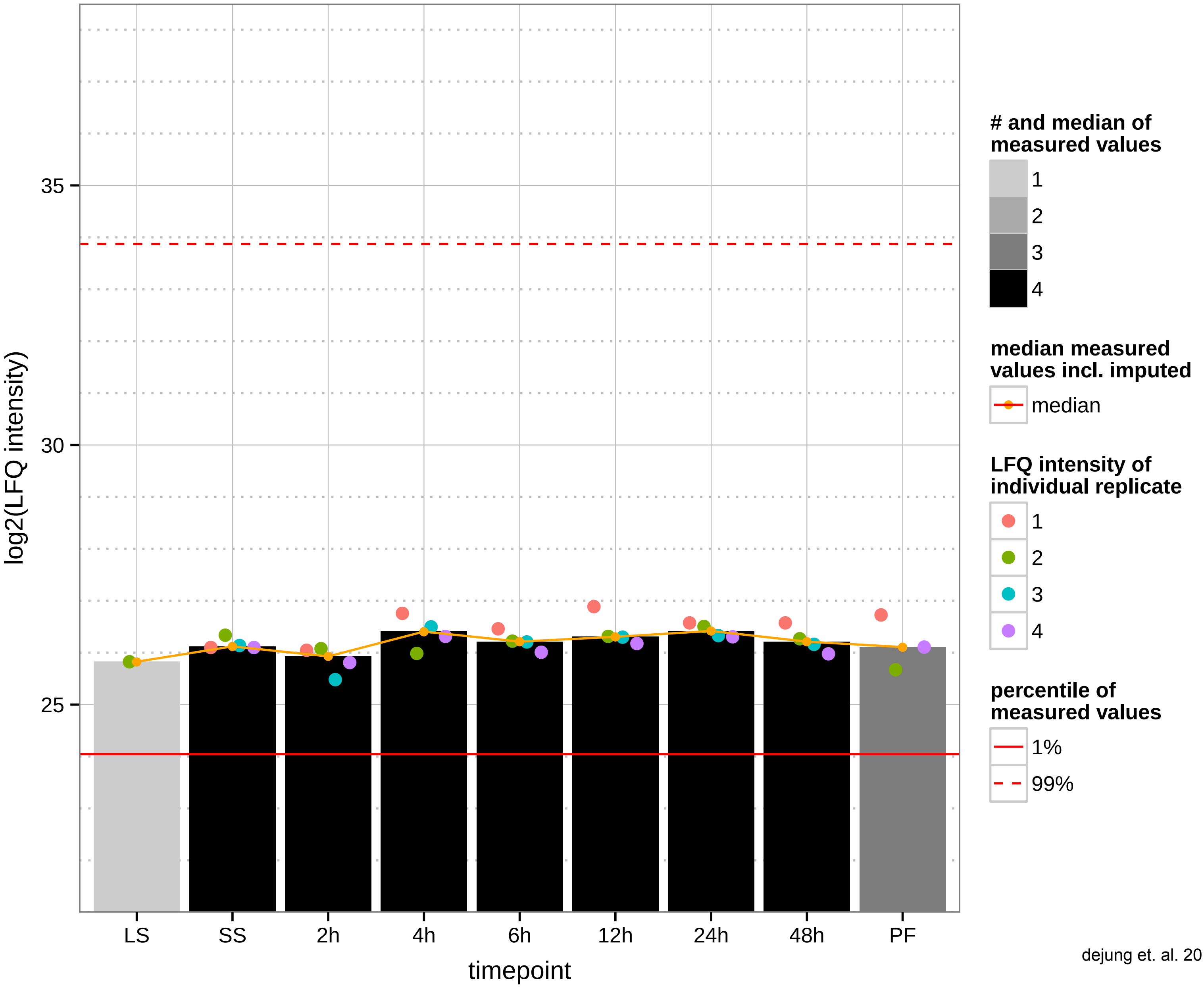
RNA polymerase–associated protein LEO1, putative
Tb927.9.12900
AGOF: RNA binding
AGOC: Cdc73/Paf1 complex
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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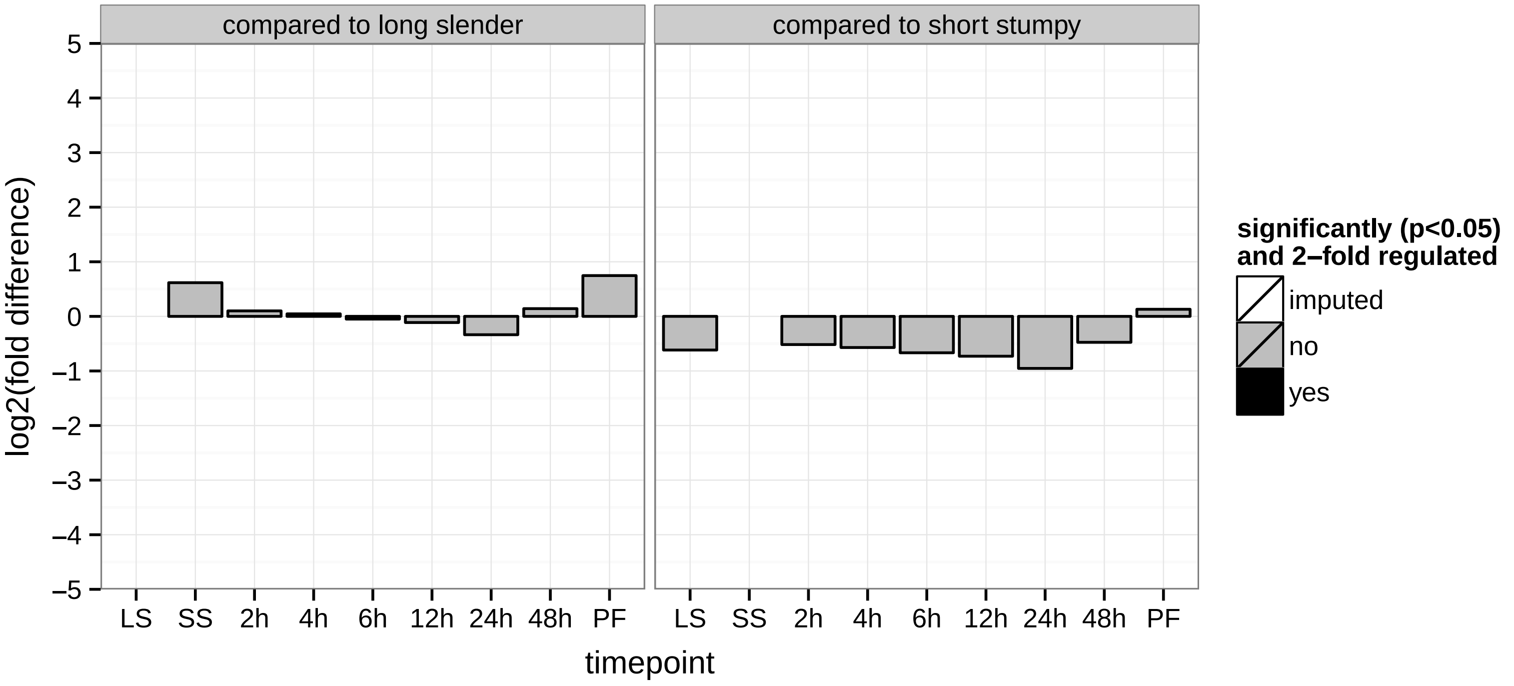
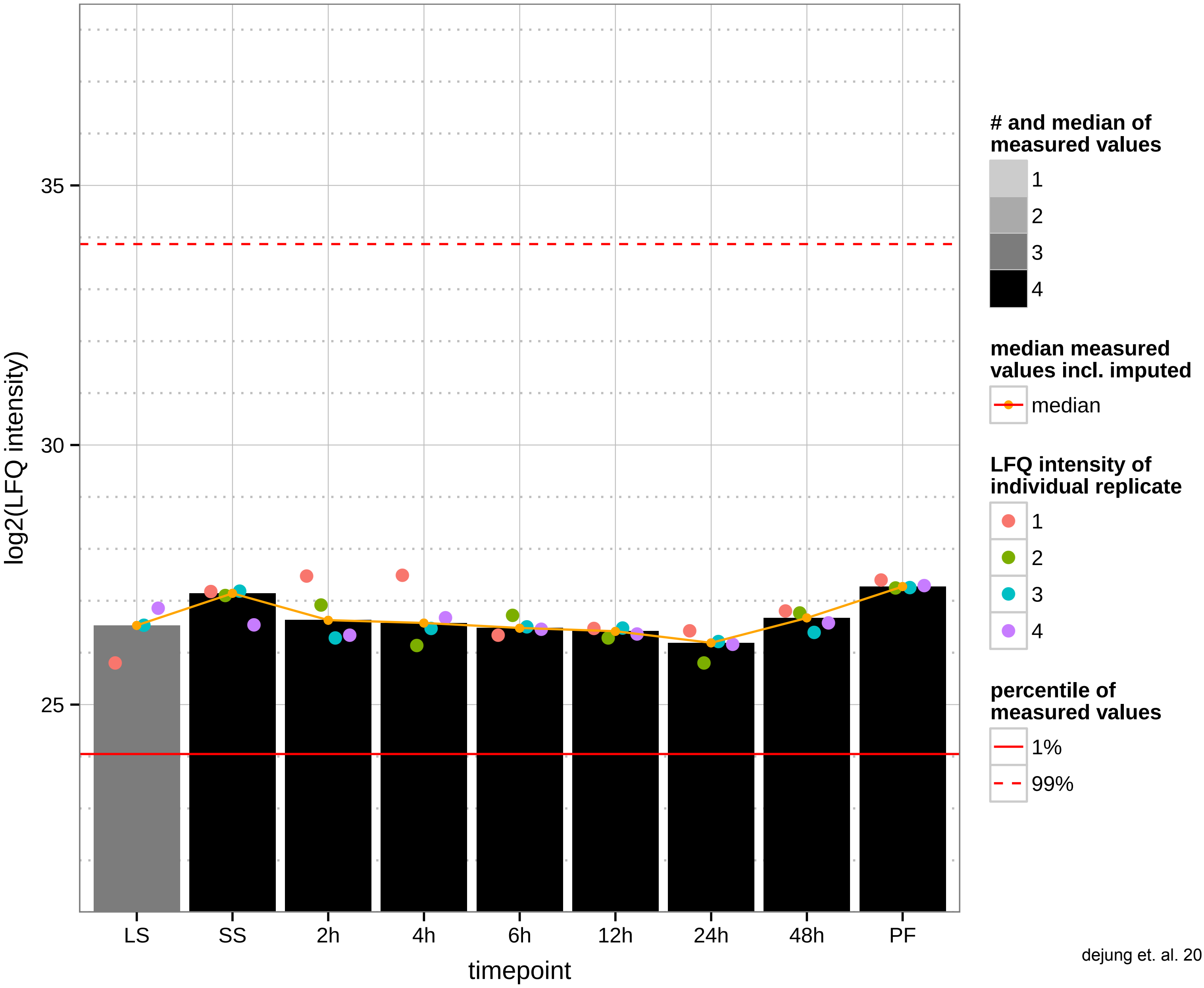
hypothetical protein, conserved
Tb927.9.12990
AGOF: null
AGOC: null
AGOP: null
PGOF: null, protein binding
PGOC: null
PGOP: null





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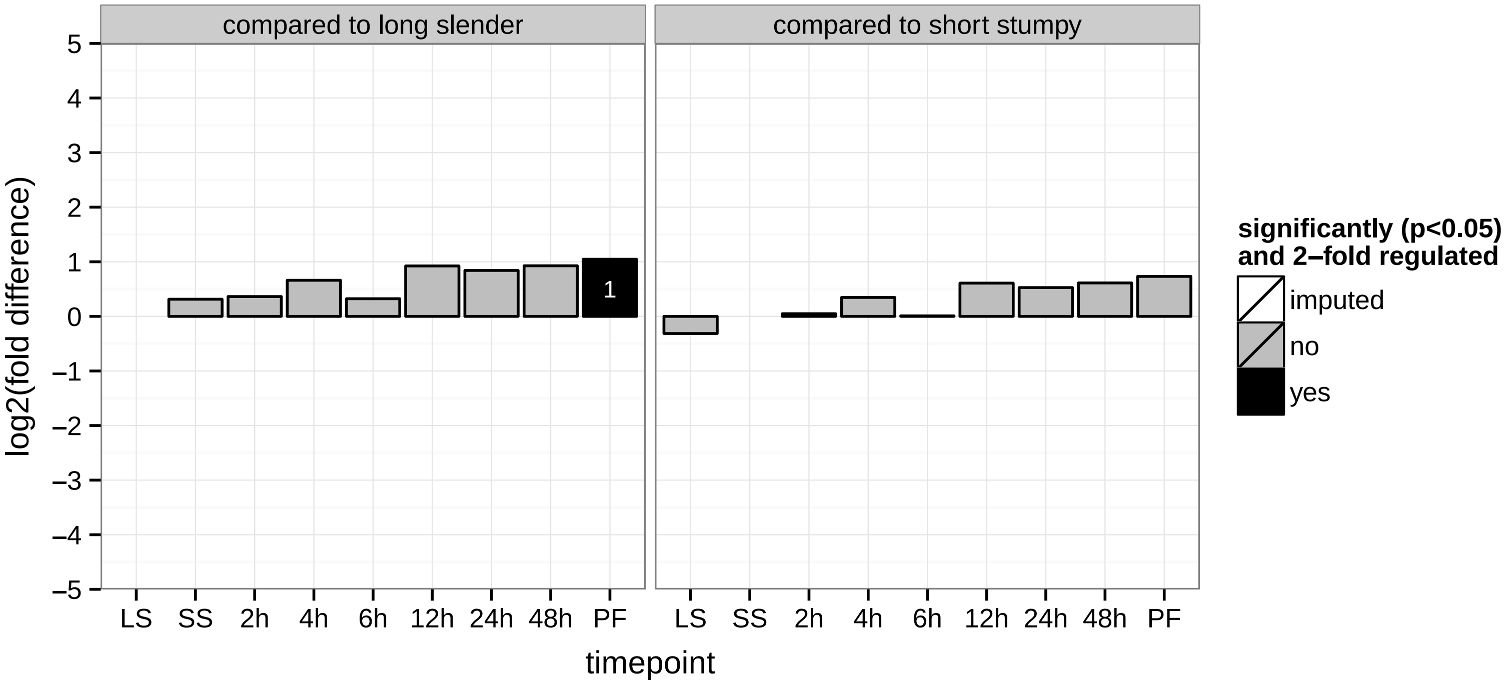
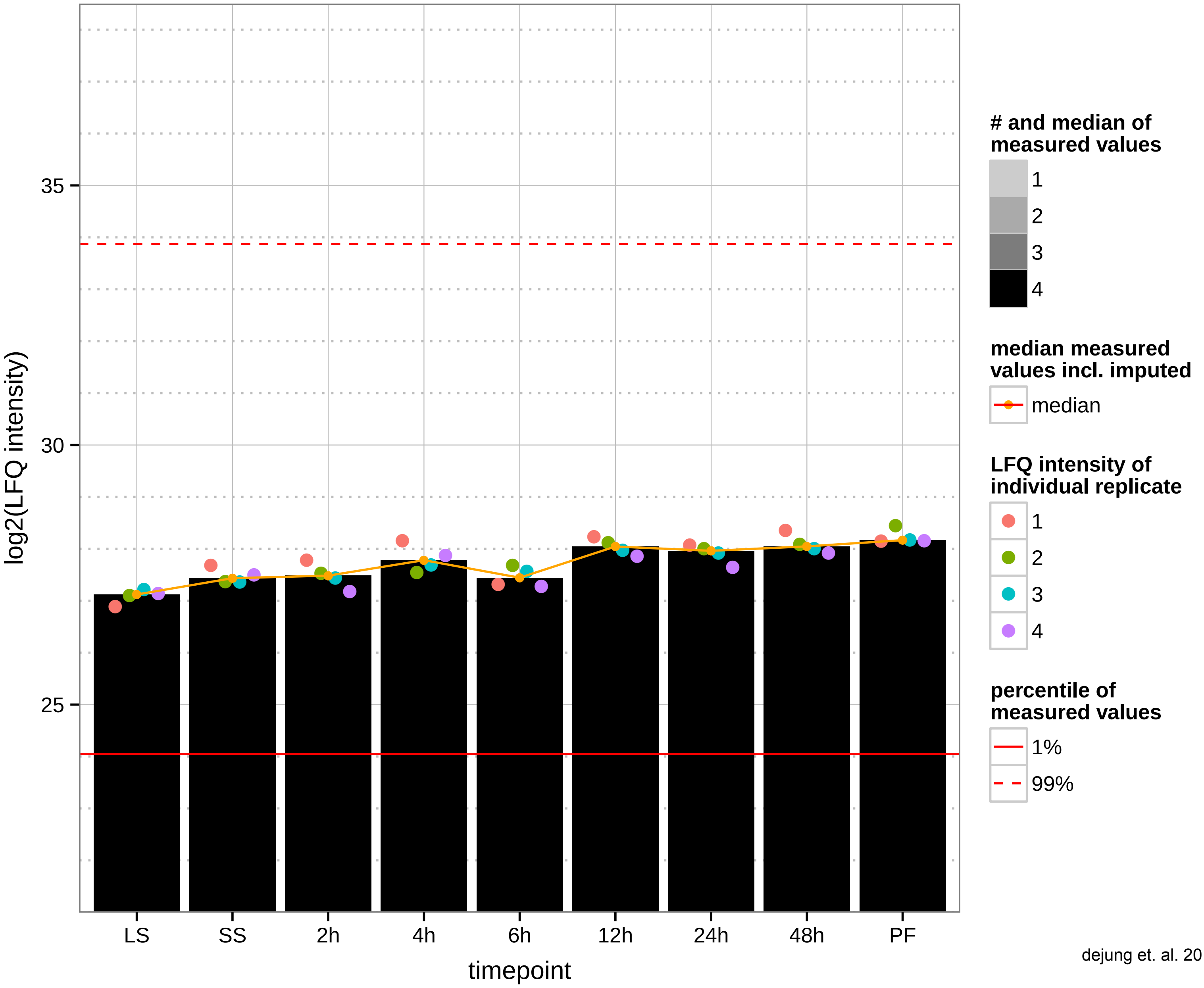
hypothetical protein, conserved
Tb927.9.13320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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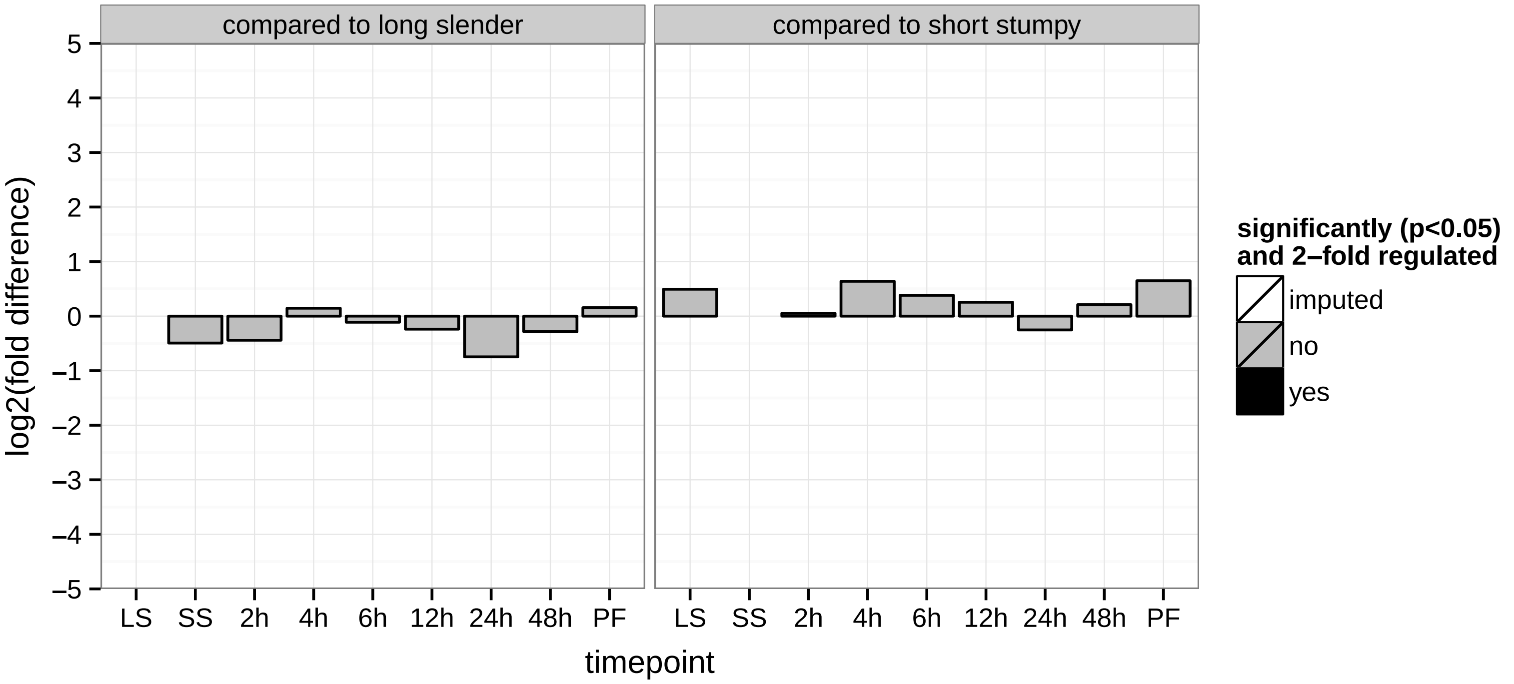
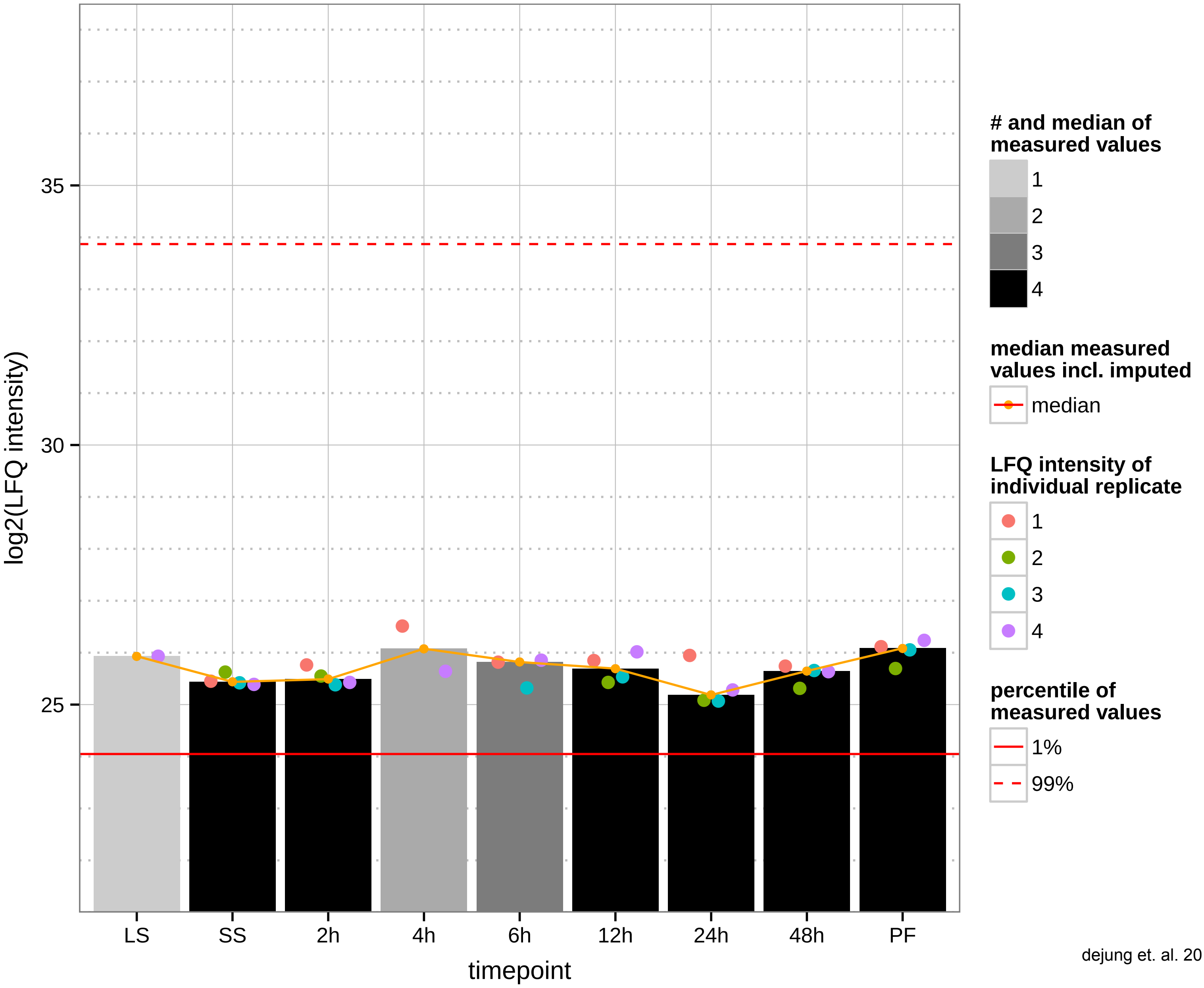
hypothetical protein, conserved
Tb927.9.13330
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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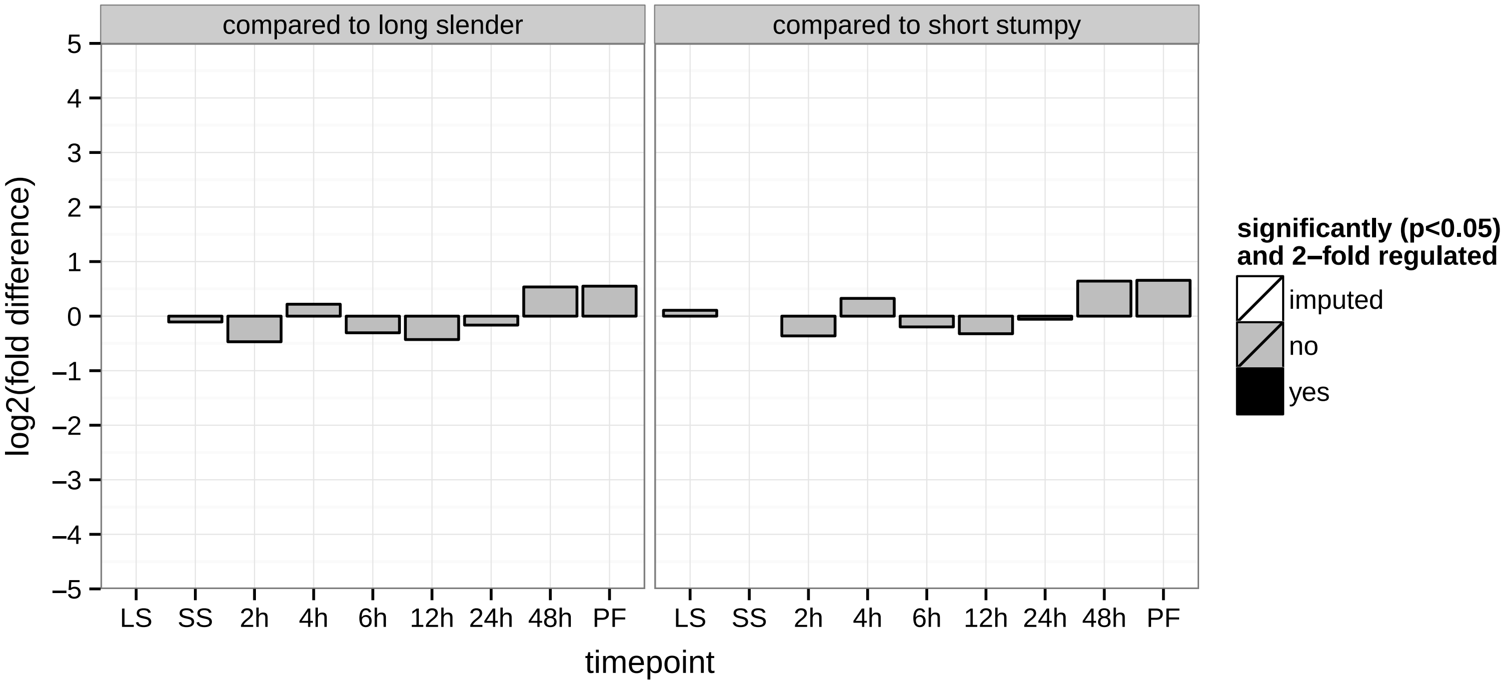
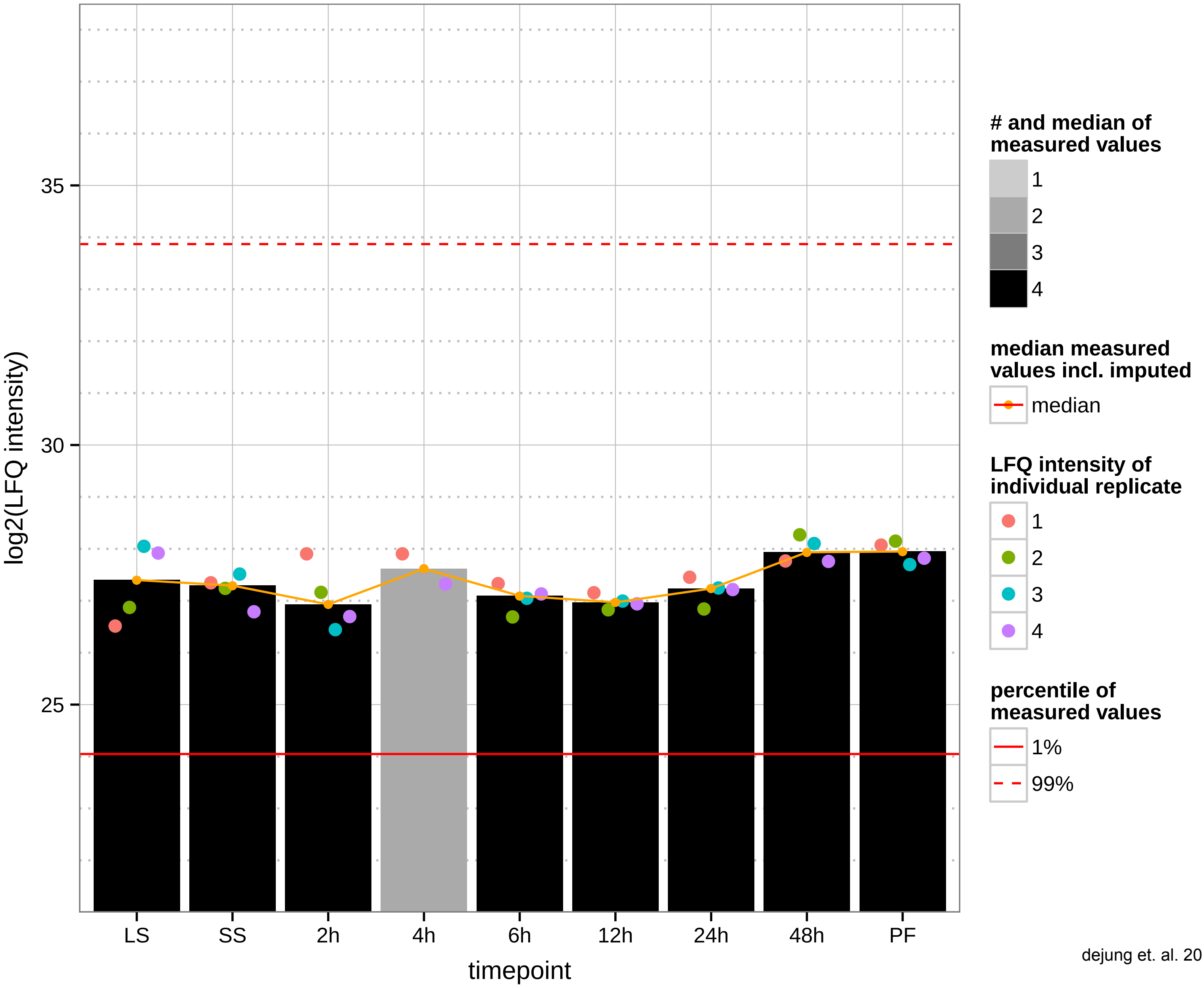
hypothetical protein, conserved
Tb927.9.13440
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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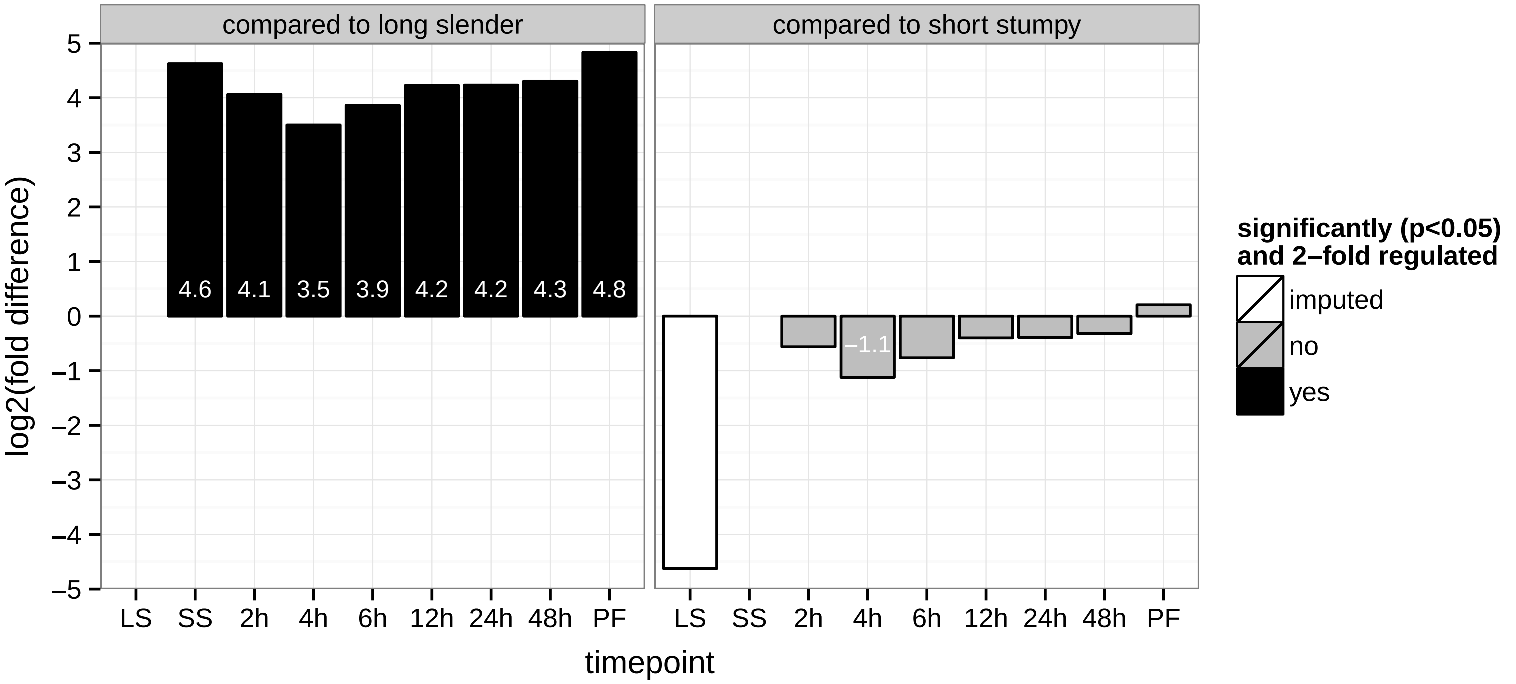
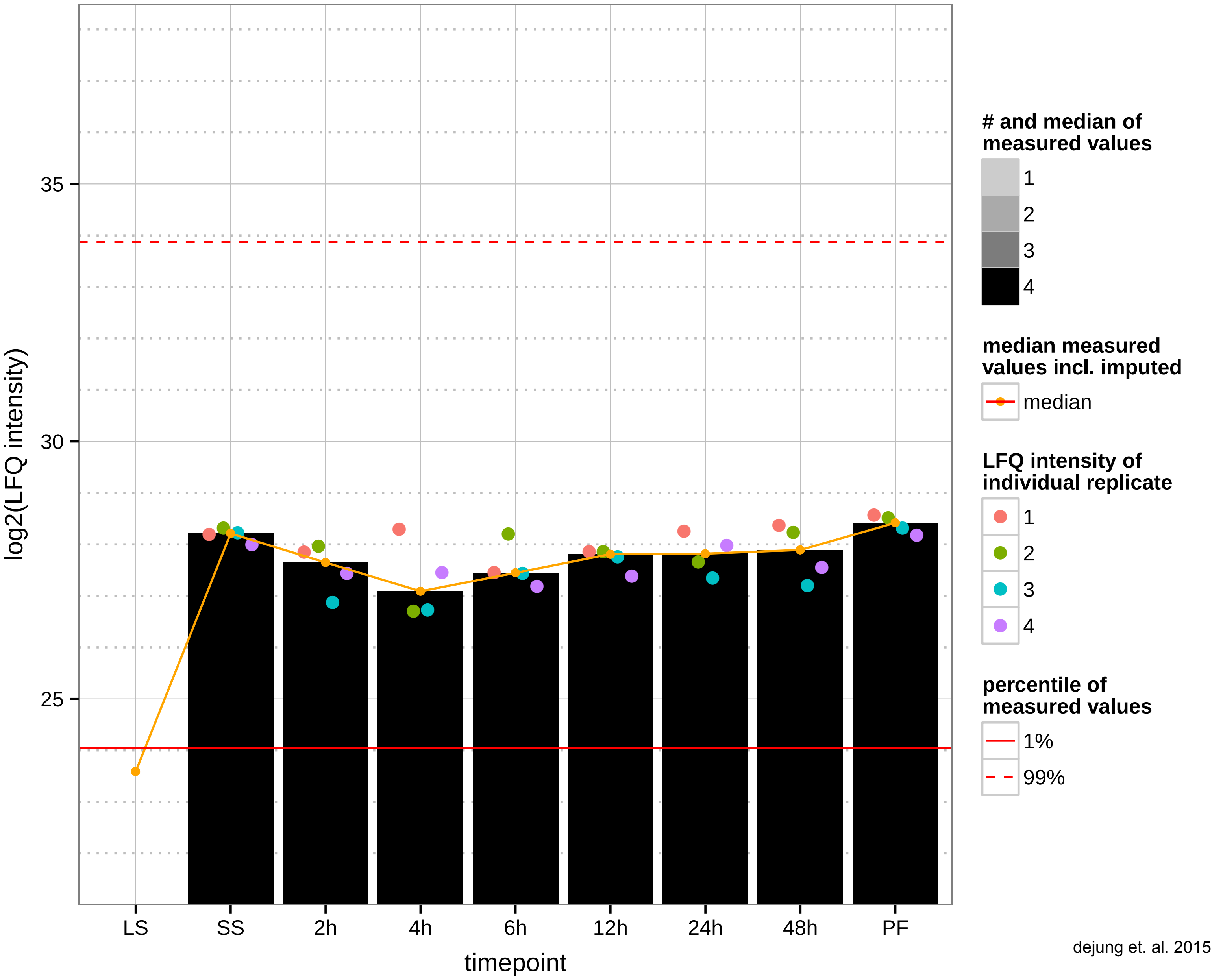
hypothetical protein, conserved
Tb927.9.1350
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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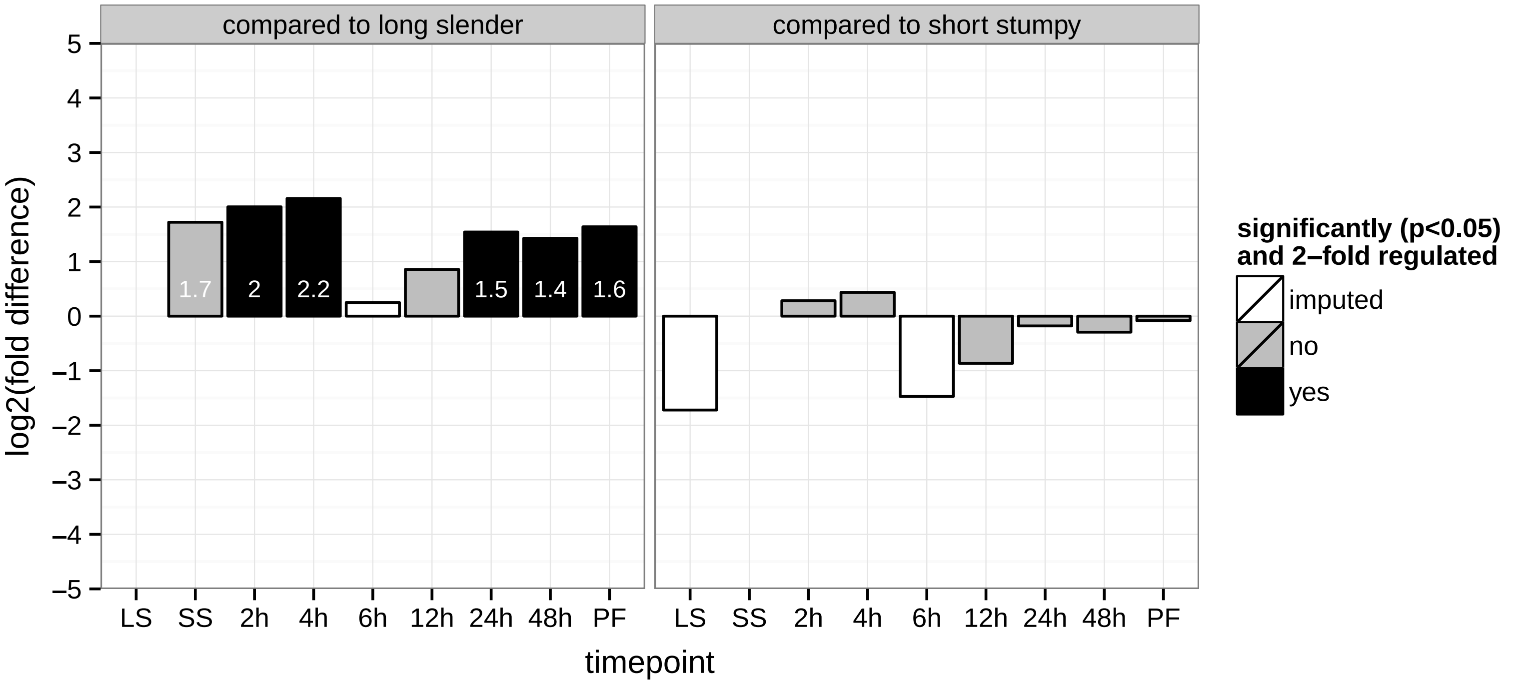
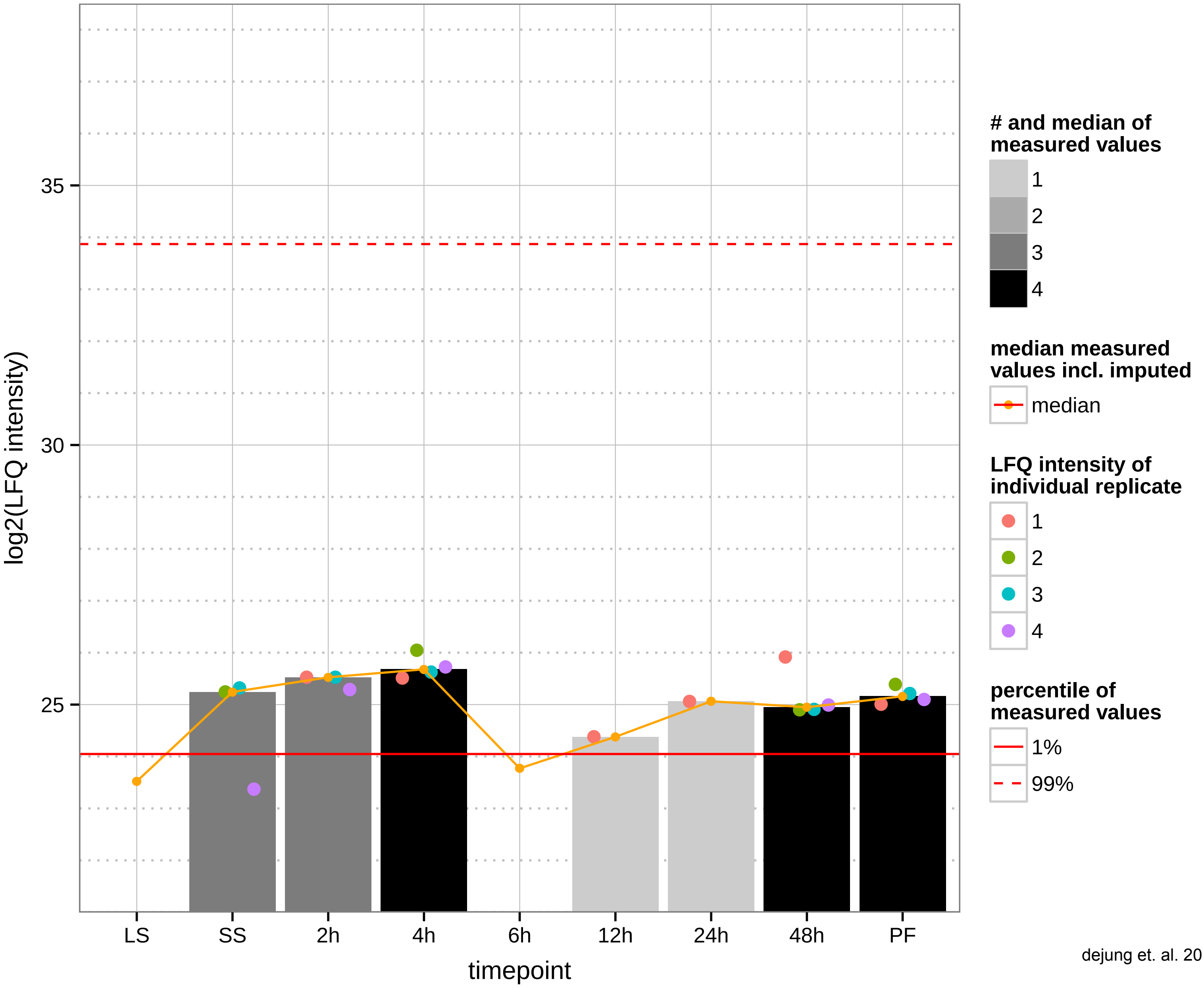
hypothetical protein, conserved
Tb927.9.13540
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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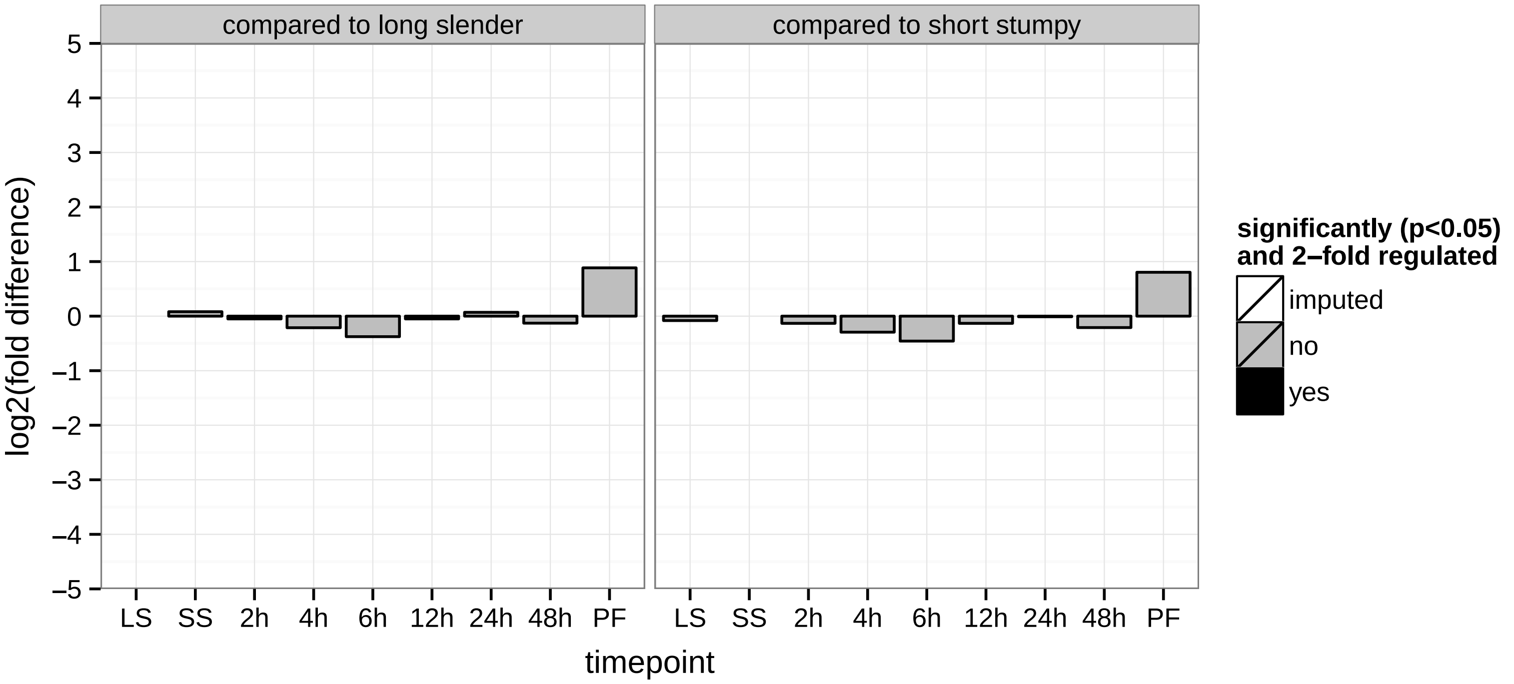
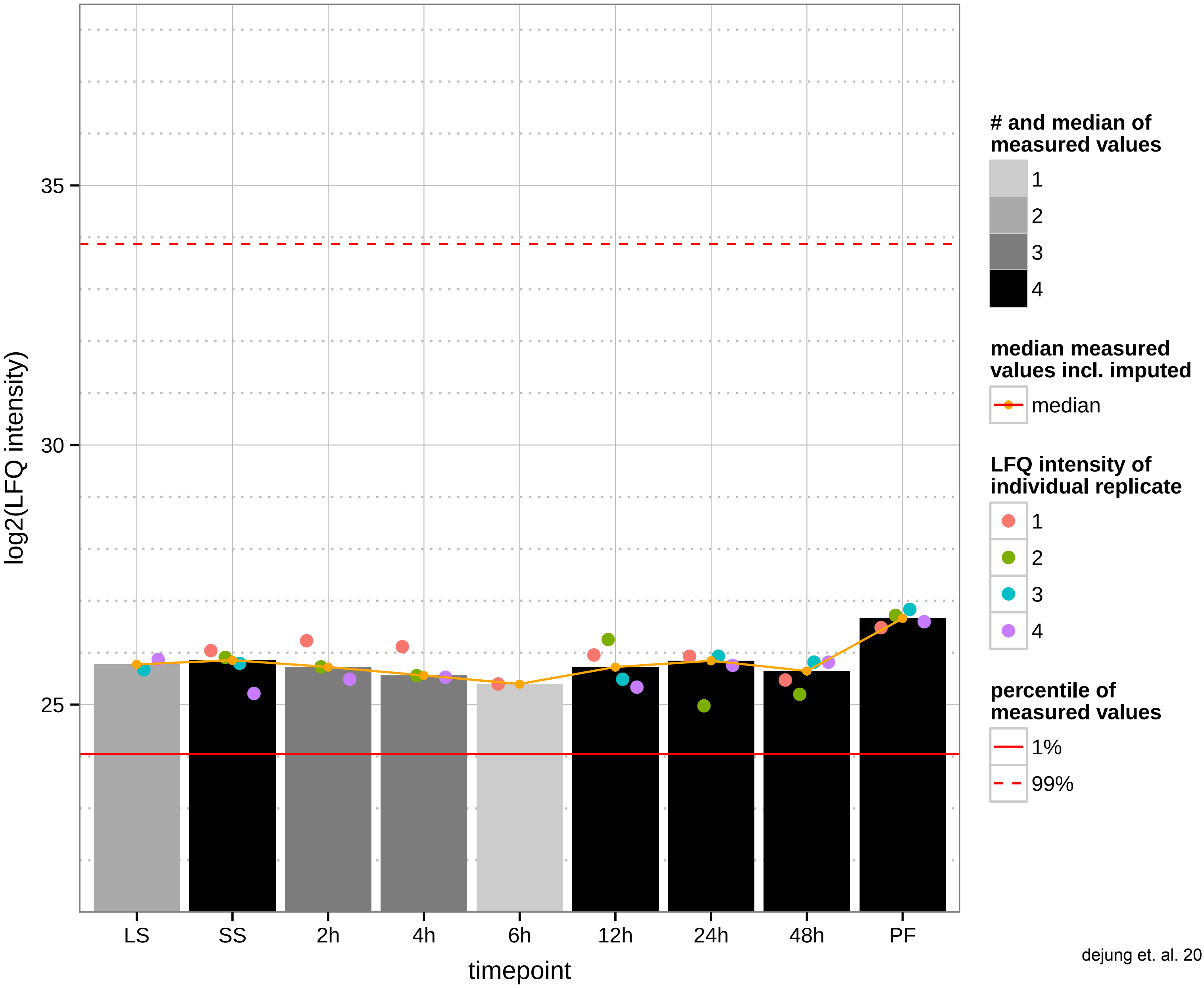
helicase, putative
Tb927.9.13610
AGOF: ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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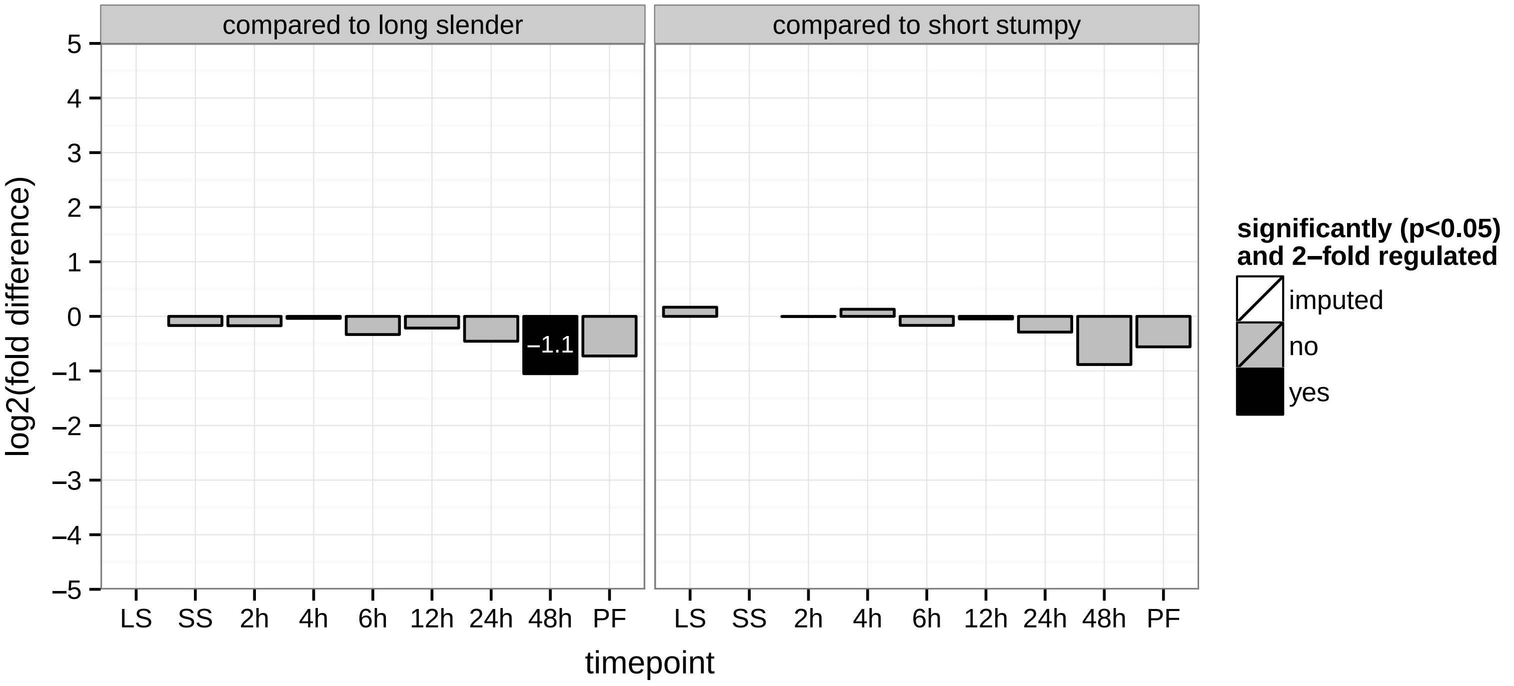
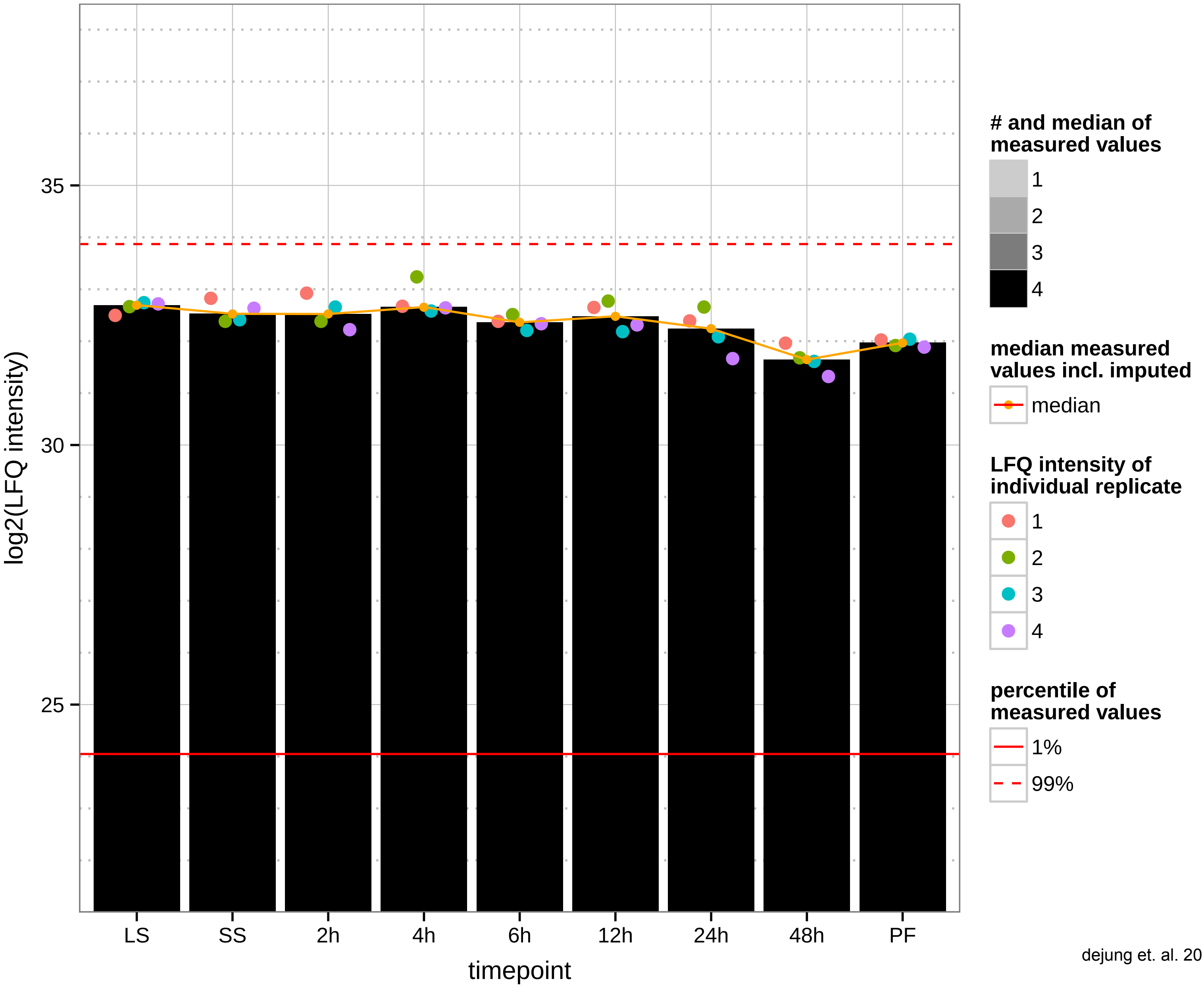
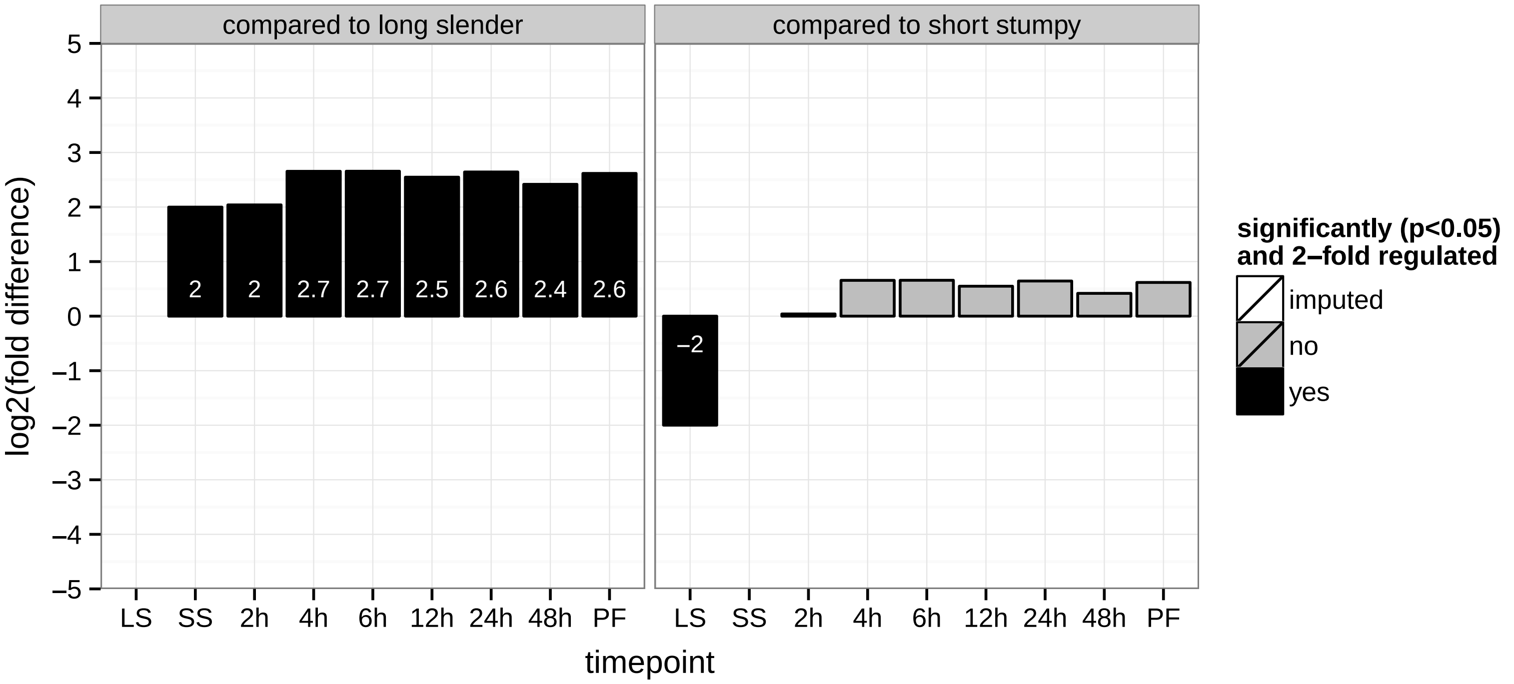
ADP–ribosylation factor, putative
Tb927.9.13740;Tb927.9.13710;Tb927.9.13680;Tb927.9.13650
AGOF: GTP binding
AGOC: intracellular
AGOP: intracellular protein transport, small GTPase mediated signal transduction
PGOF: GTP binding, null
PGOC: intracellular, null
PGOP: intracellular protein transport, protein transport, small GTPase mediated signal transduction, null

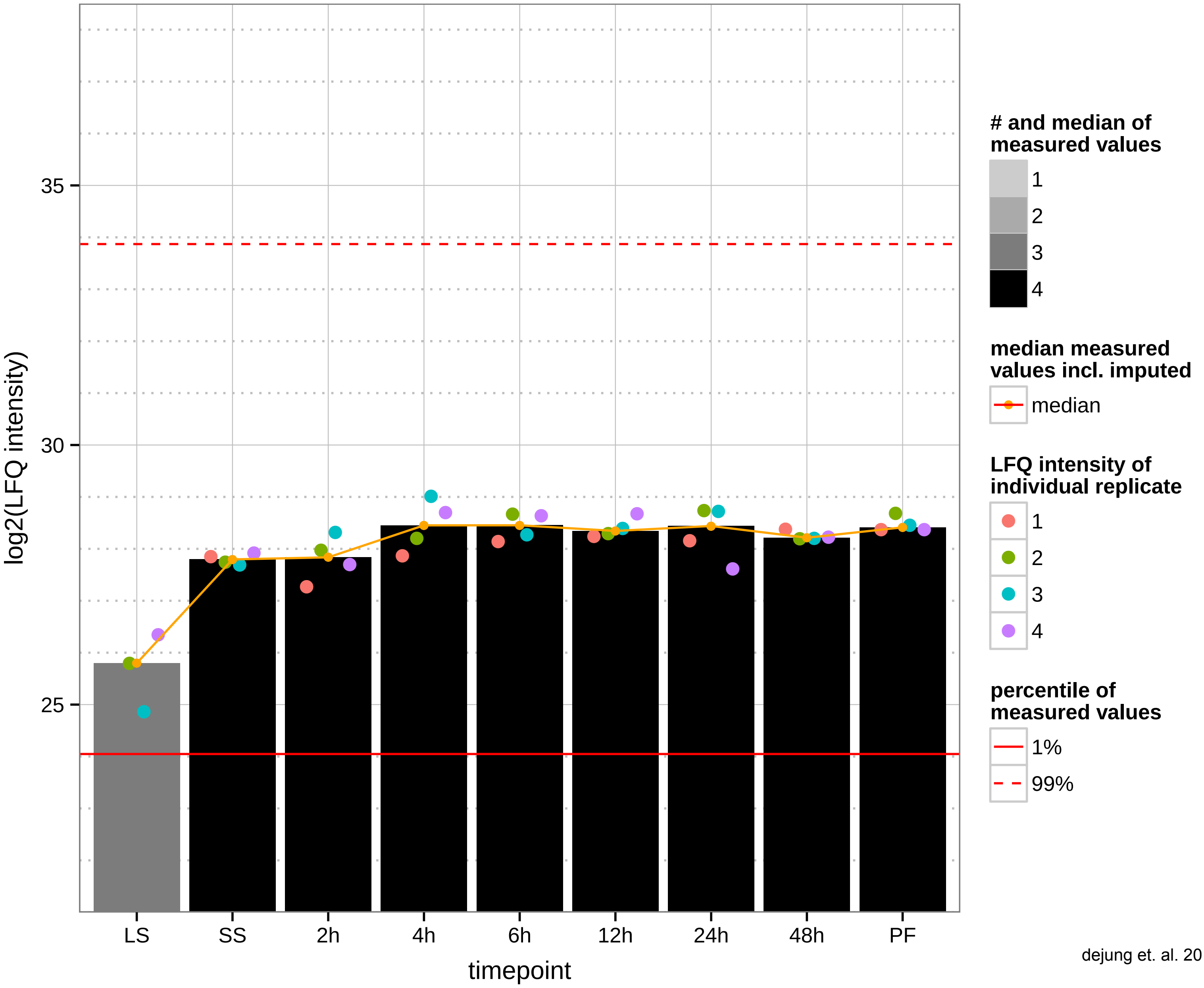




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.1380
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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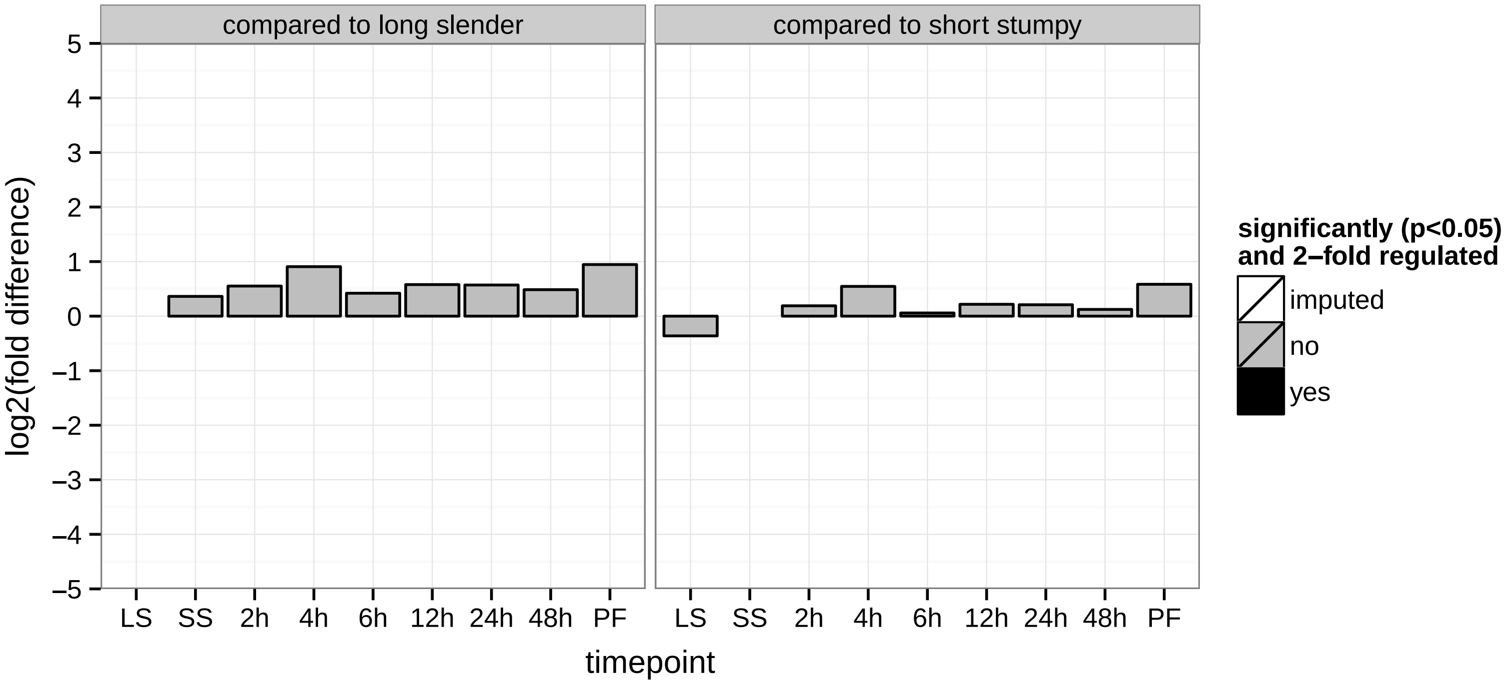
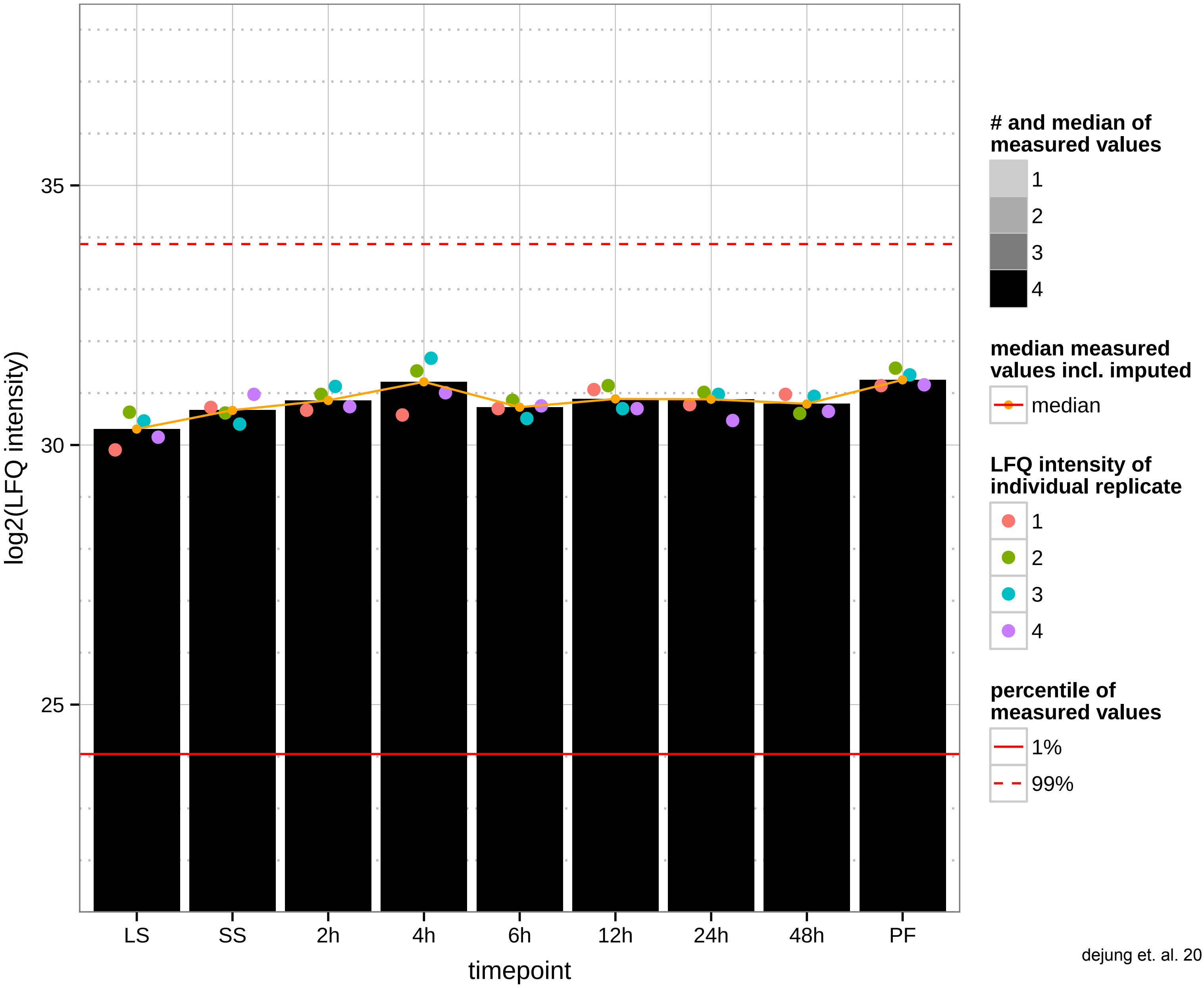
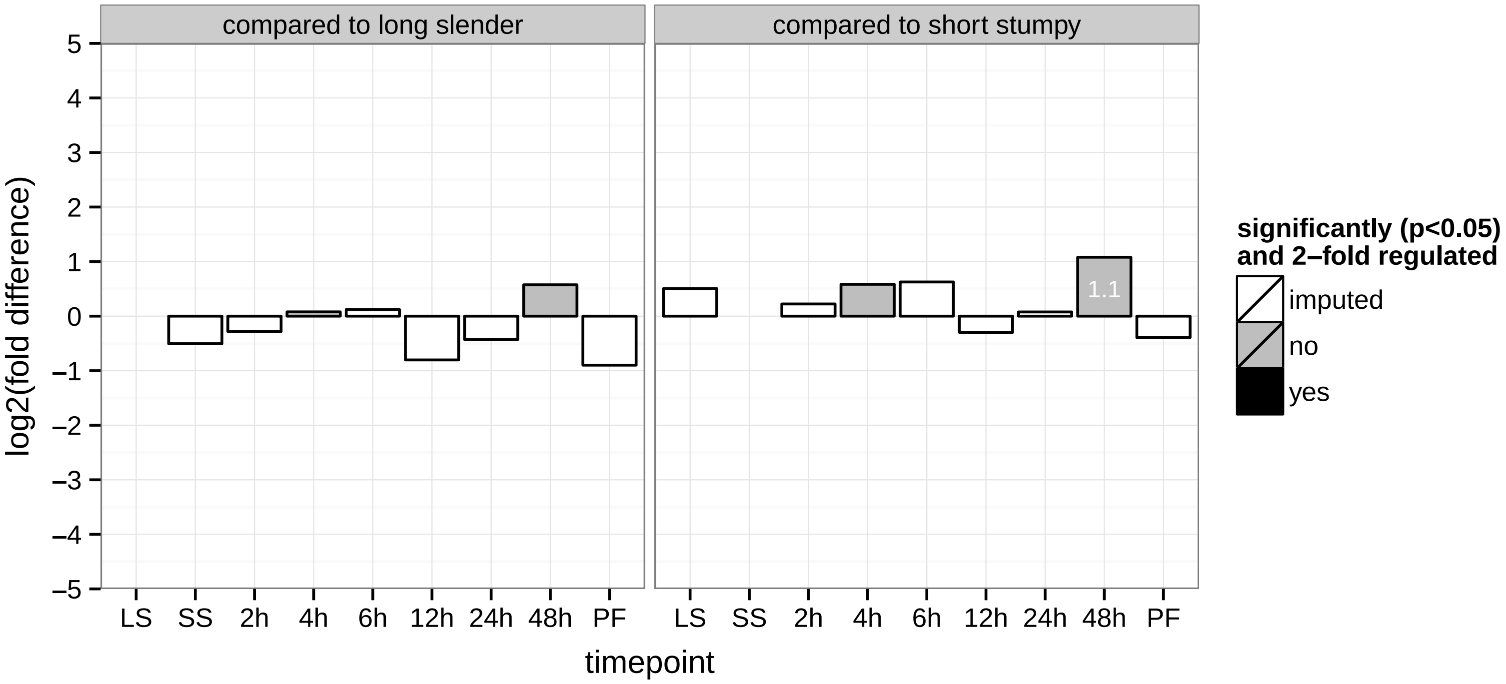
RNA–binding protein, putative (DRBD2)
Tb927.9.13990
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null

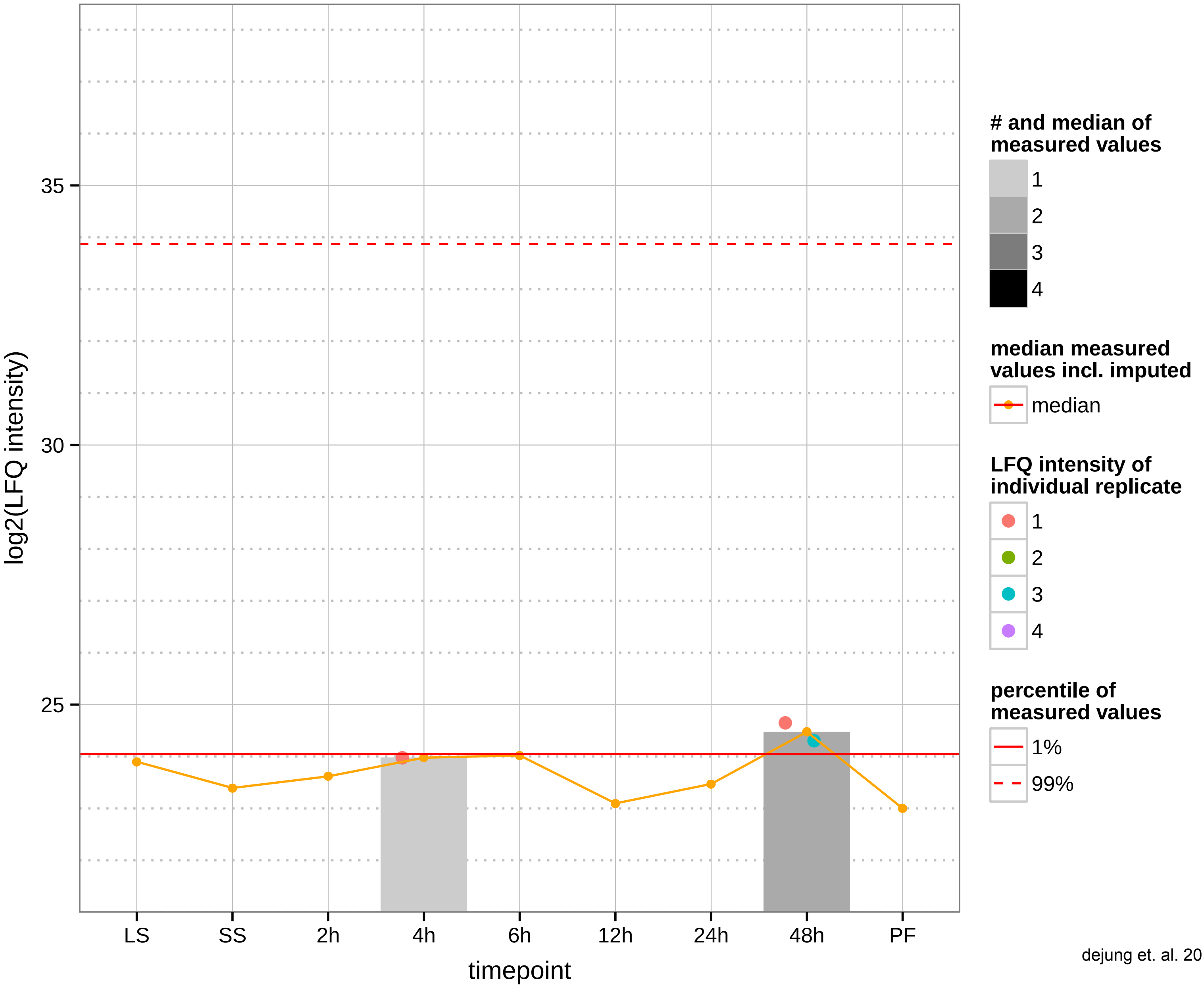




dejung et. al. 2015

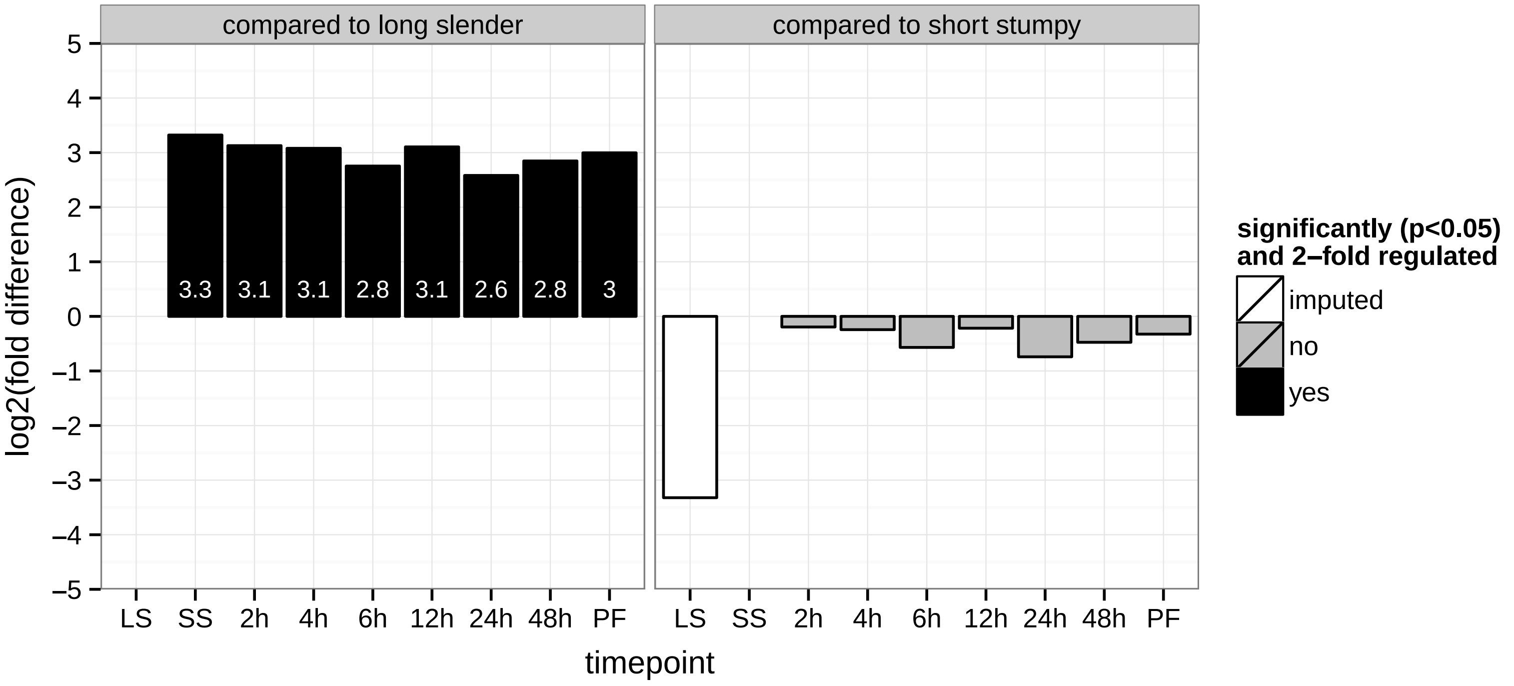
Monooxygenase, putative
Tb927.9.1400
AGOF: monooxygenase activity
AGOC: null
AGOP: cellular aromatic compound metabolic process
PGOF: null
PGOC: null
PGOP: null

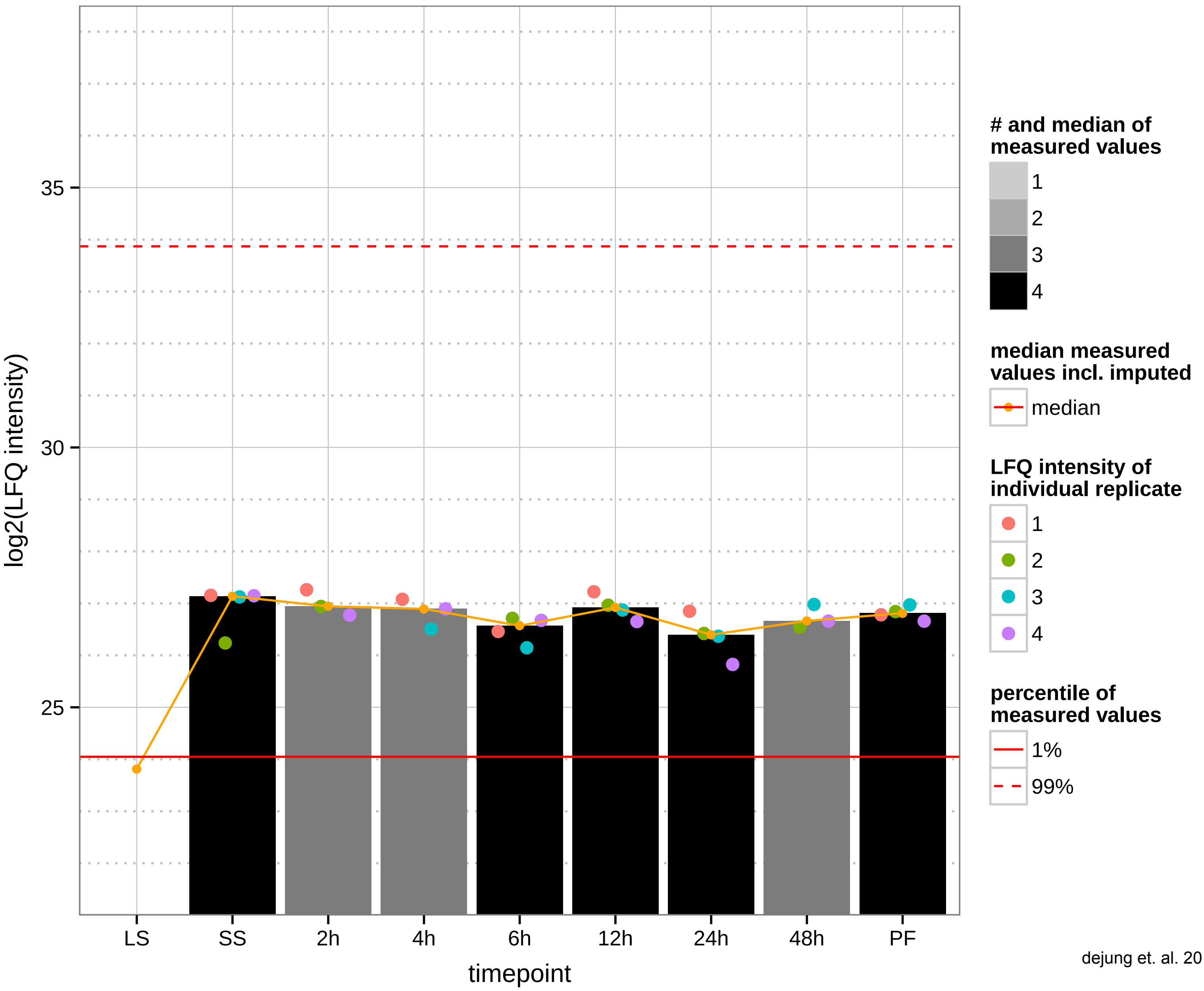




dejung et. al. 2015

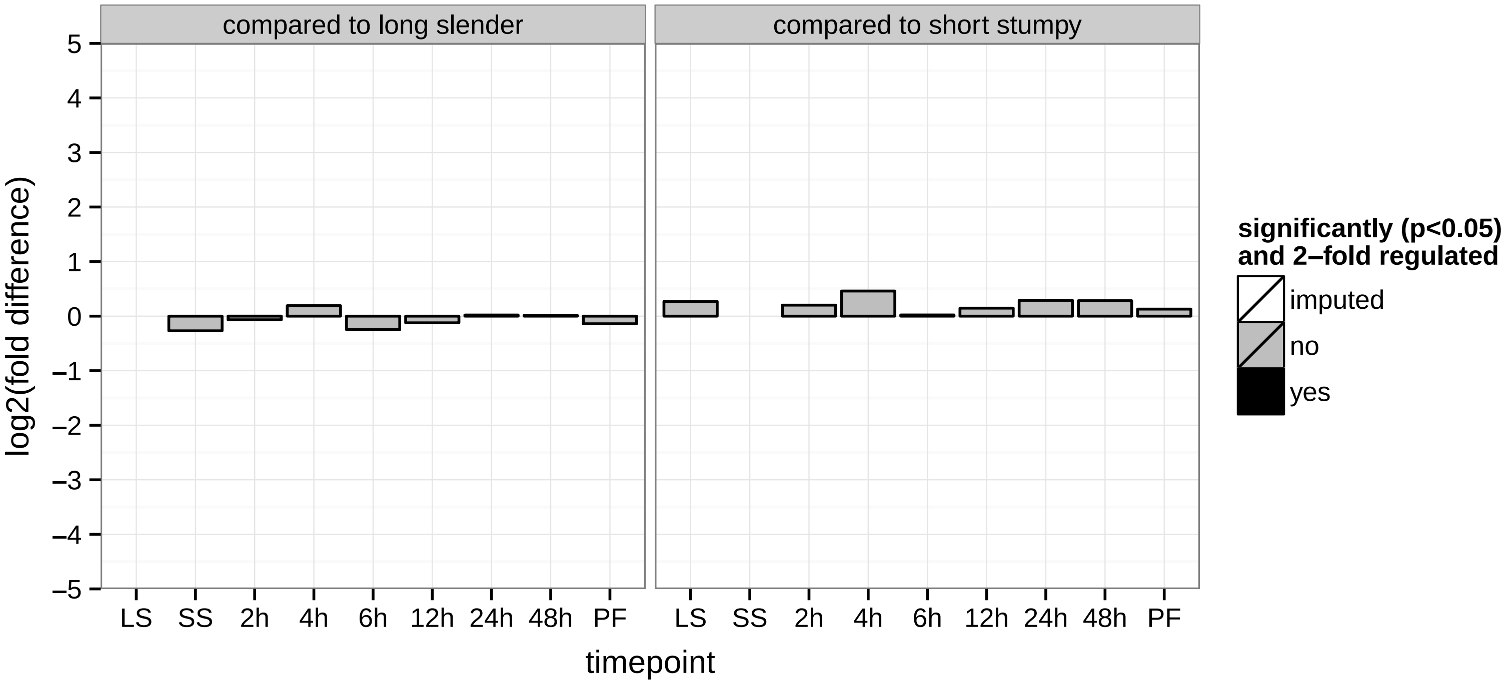
short–chain dehydrogenase, putative
Tb927.9.14070
AGOF: oxidoreductase activity
AGOC: null
AGOP: metabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process

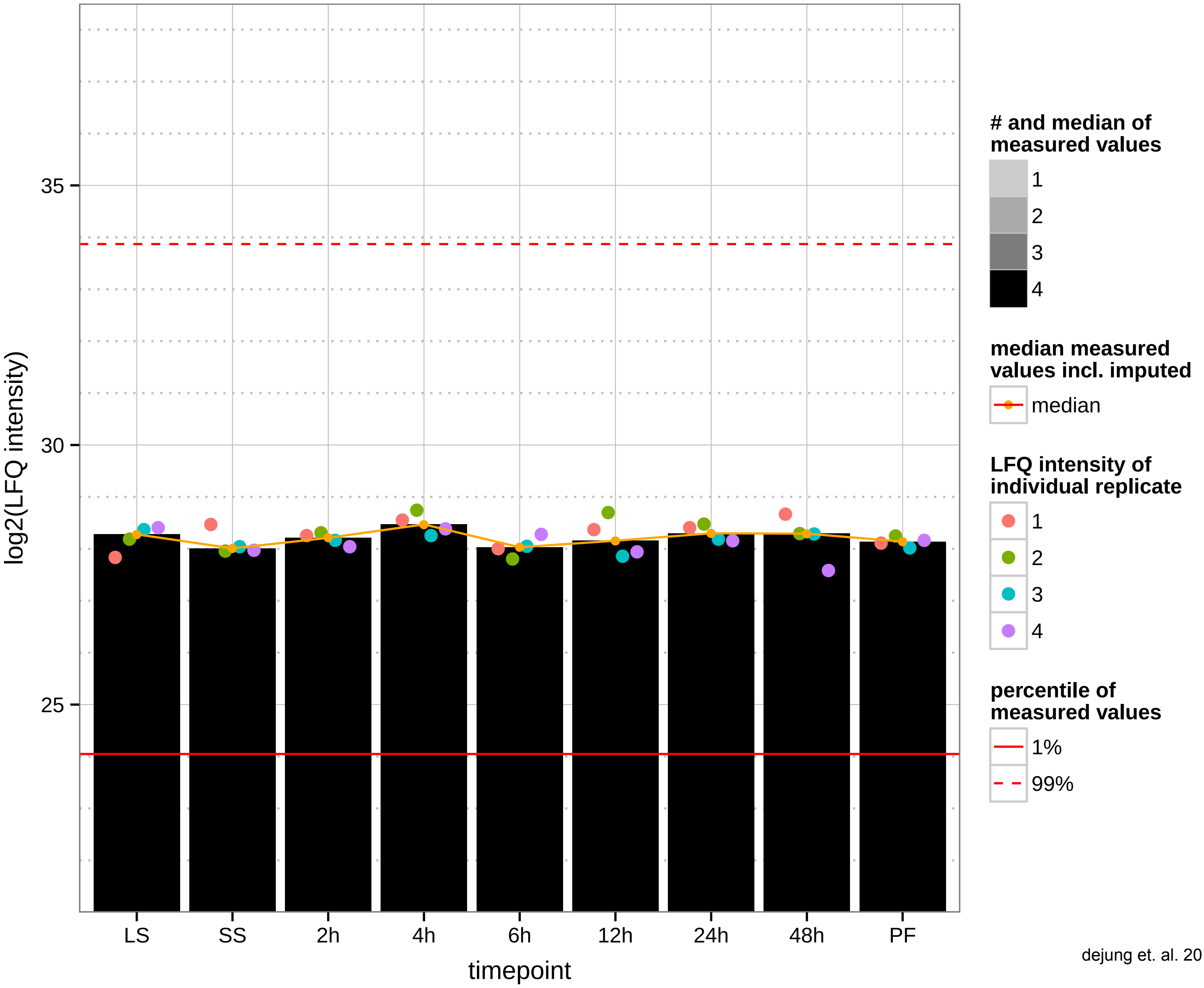




dejung et. al. 2015

vesicle–associated membrane protein, putative
Tb927.9.14080
AGOF: null
AGOC: integral to membrane
AGOP: vesicle–mediated transport
PGOF: null
PGOC: integral to membrane
PGOP: transport, vesicle–mediated transport





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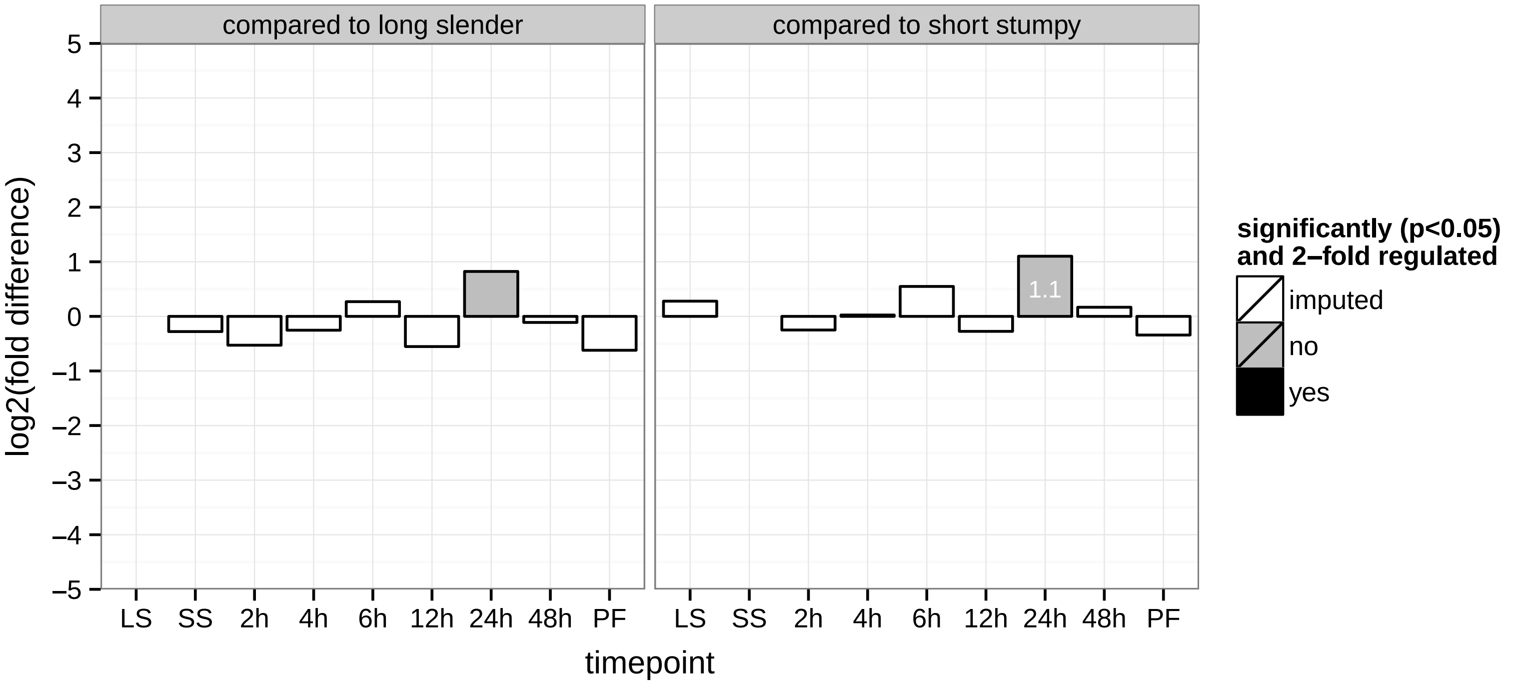
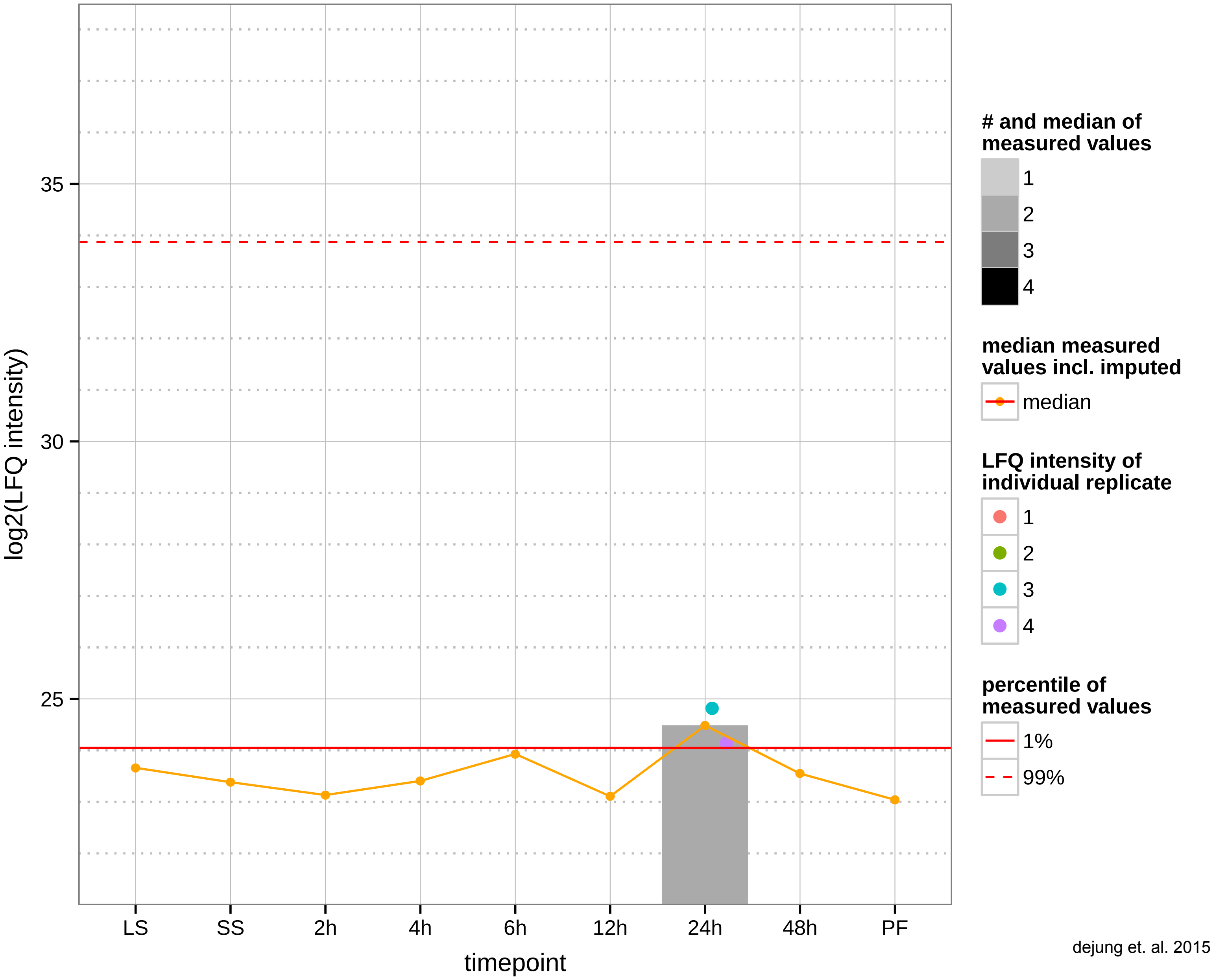
hypothetical protein, conserved
Tb927.9.14230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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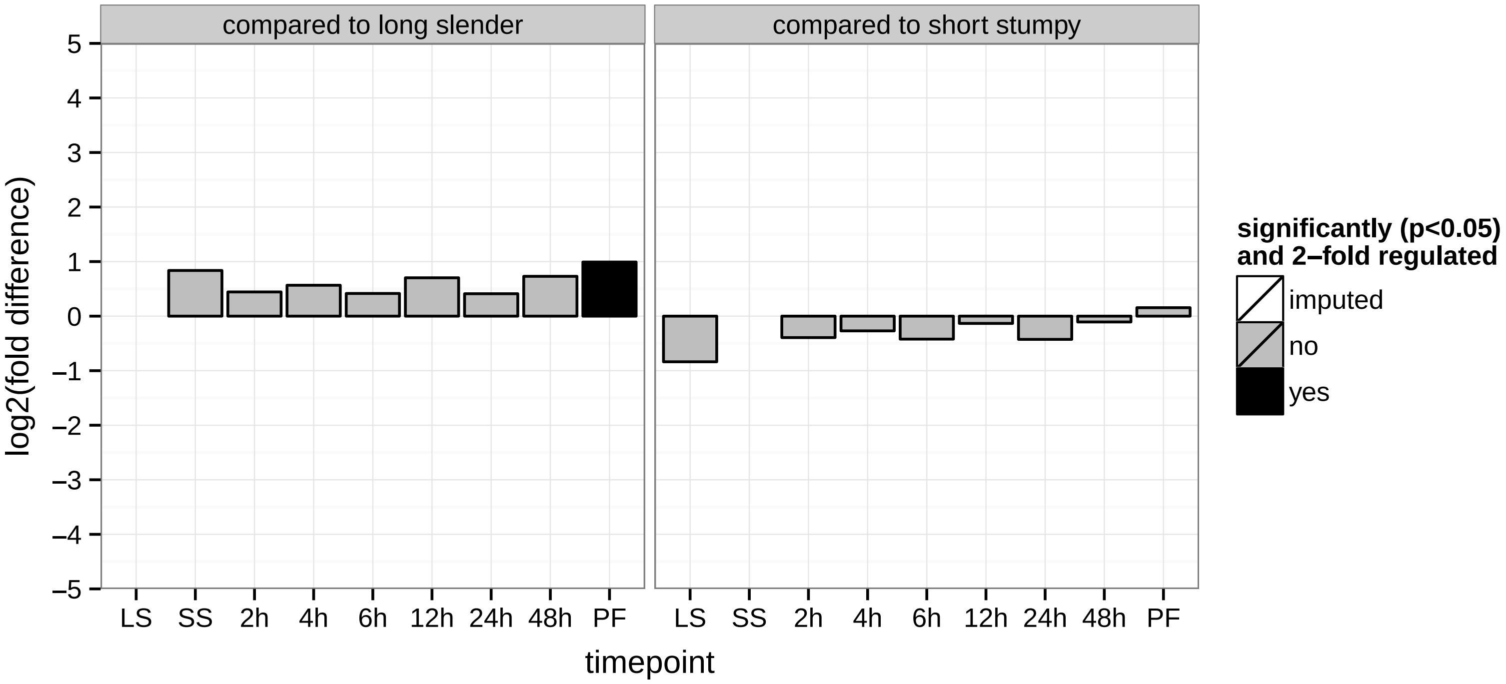
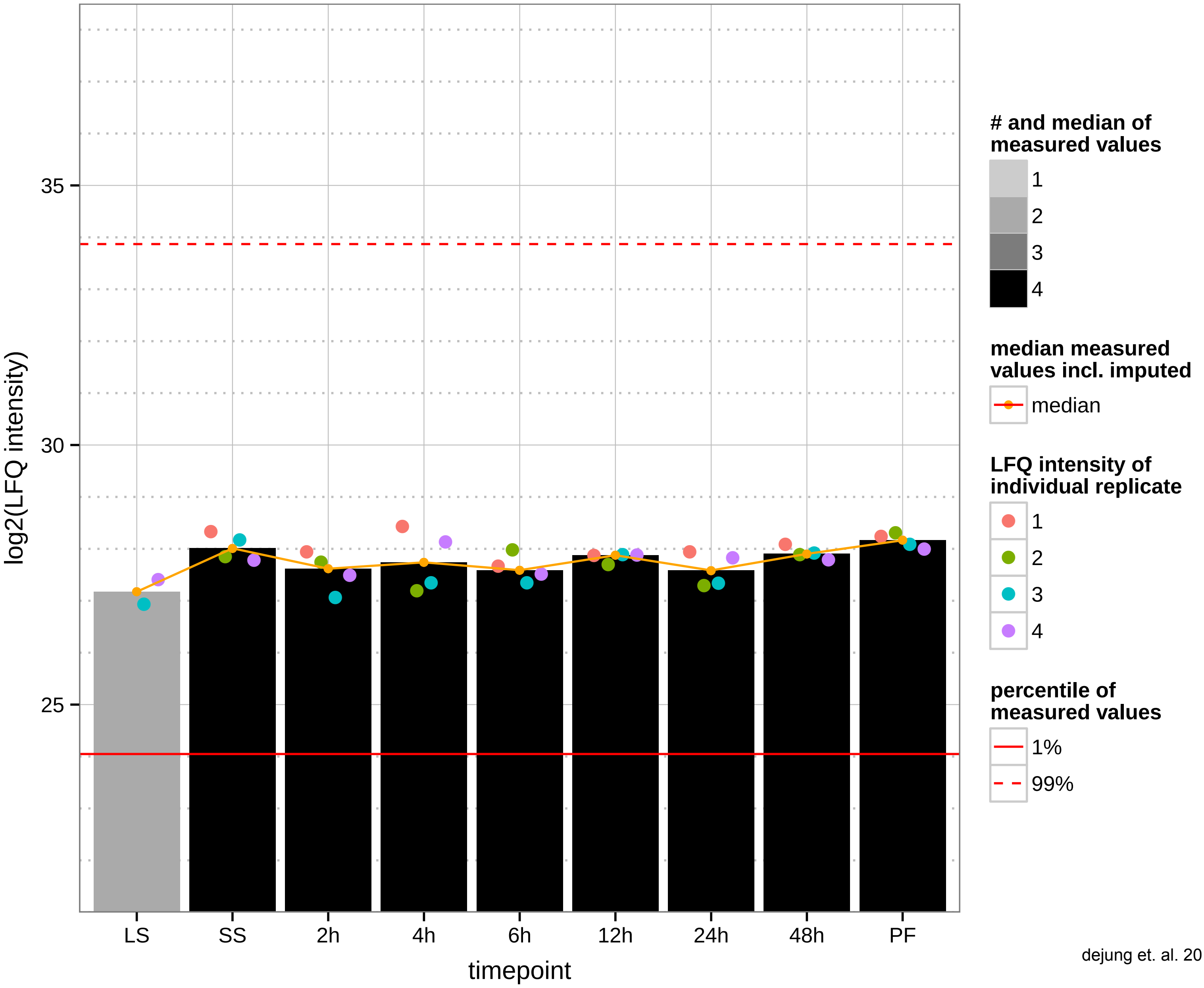
hypothetical protein, conserved, Nucleoporin (Nup82)
Tb927.9.14240;Tb11.v5.0621
AGOF: null
AGOC: null, nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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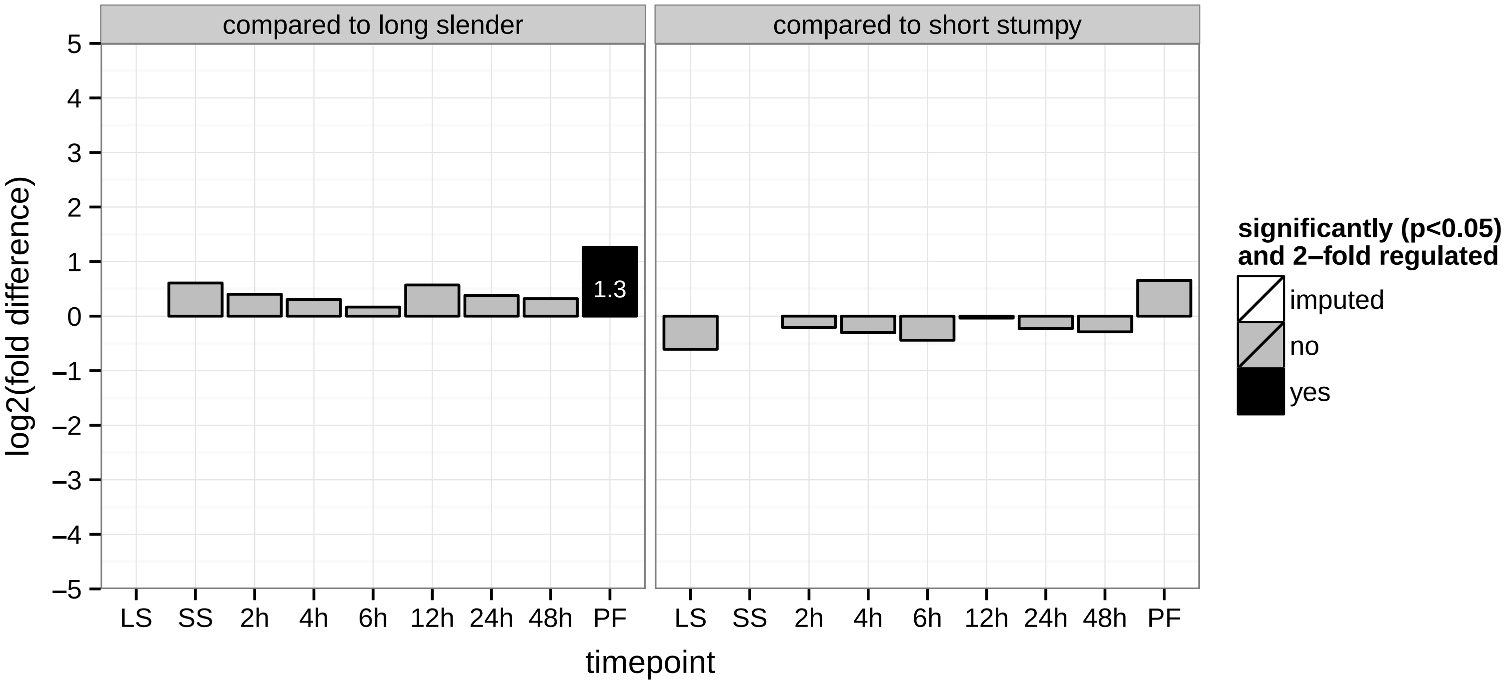
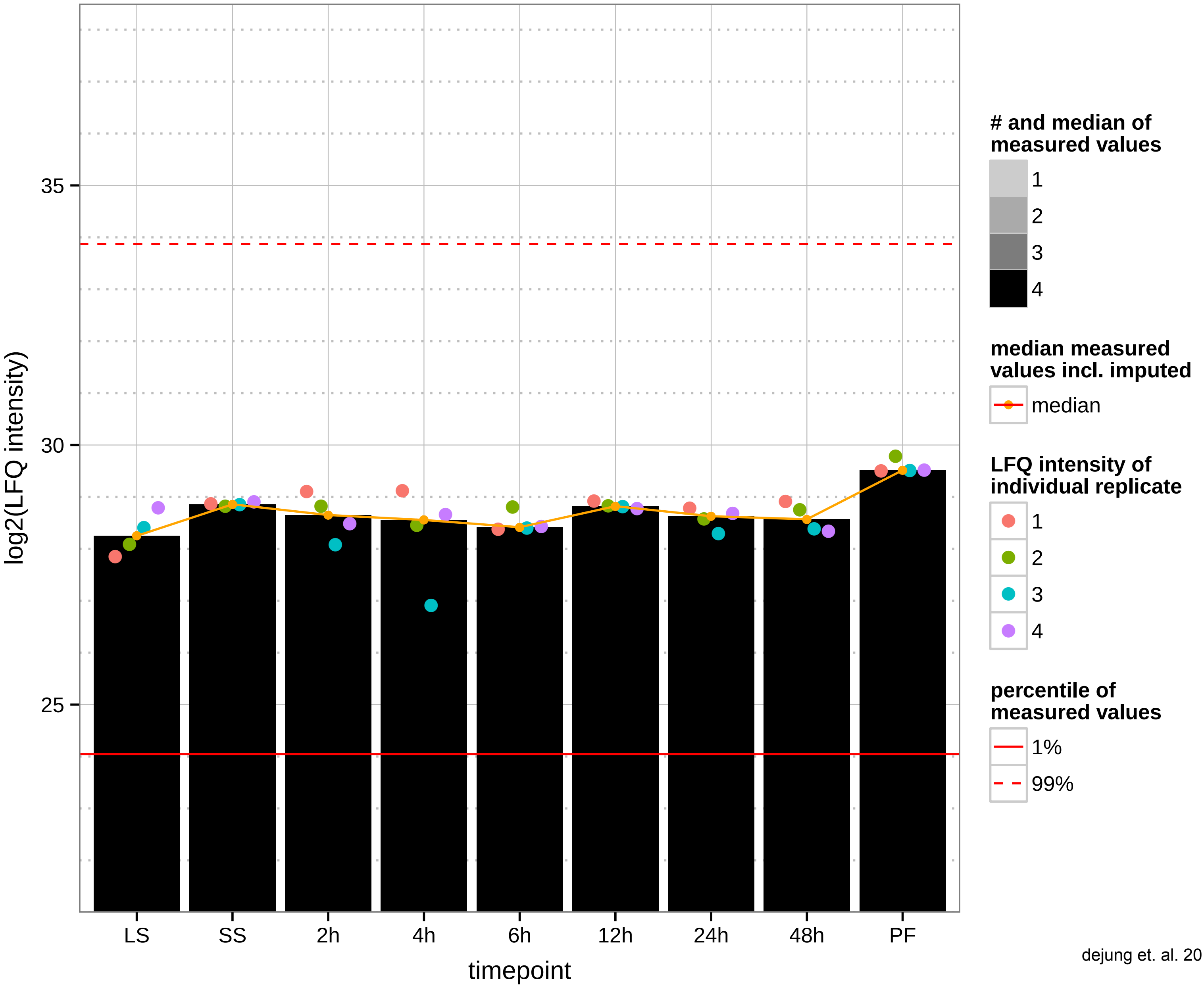
casein kinase II, putative
Tb927.9.14430
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: nucleolus
AGOP: growth, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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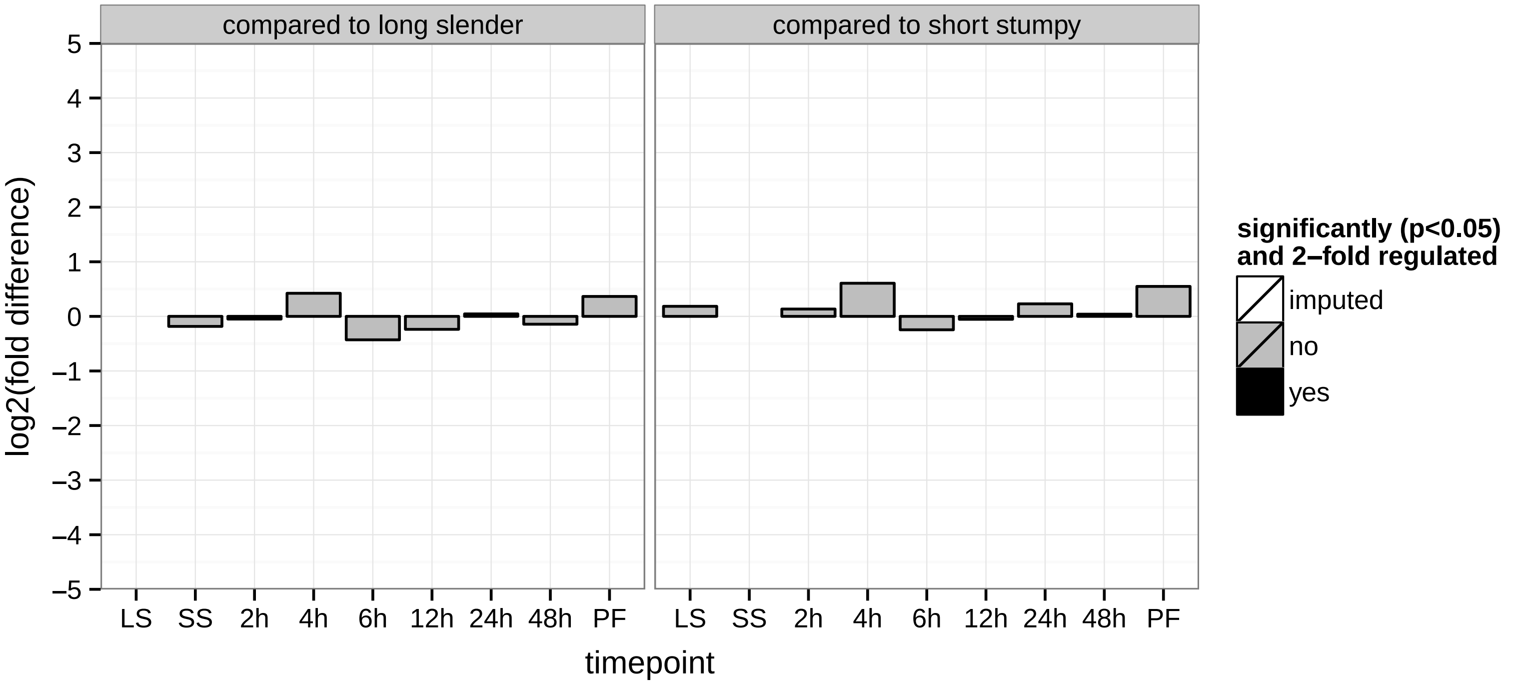
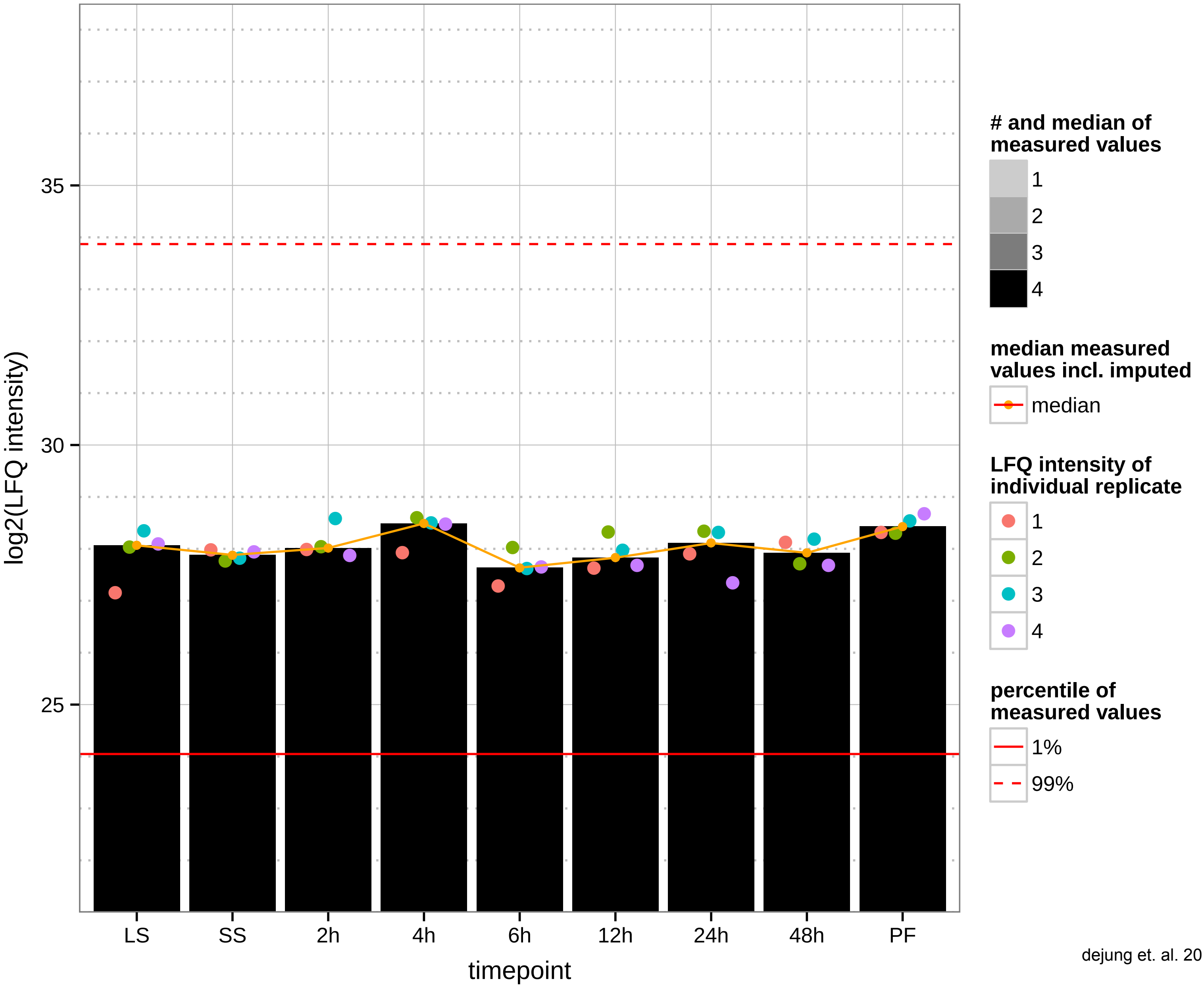
dynein–associated protein, putative
Tb927.9.14480
AGOF: null
AGOC: null
AGOP: microtubule–based movement
PGOF: null
PGOC: null
PGOP: null





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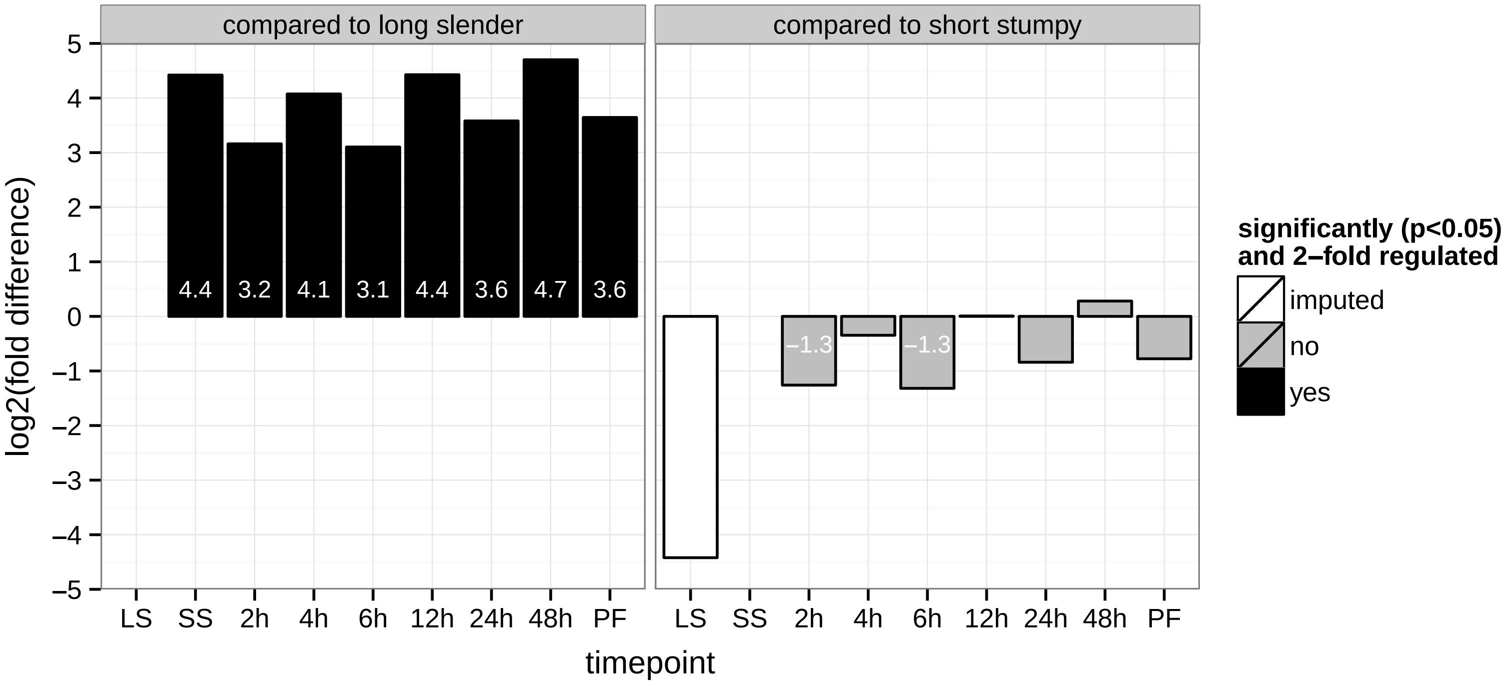
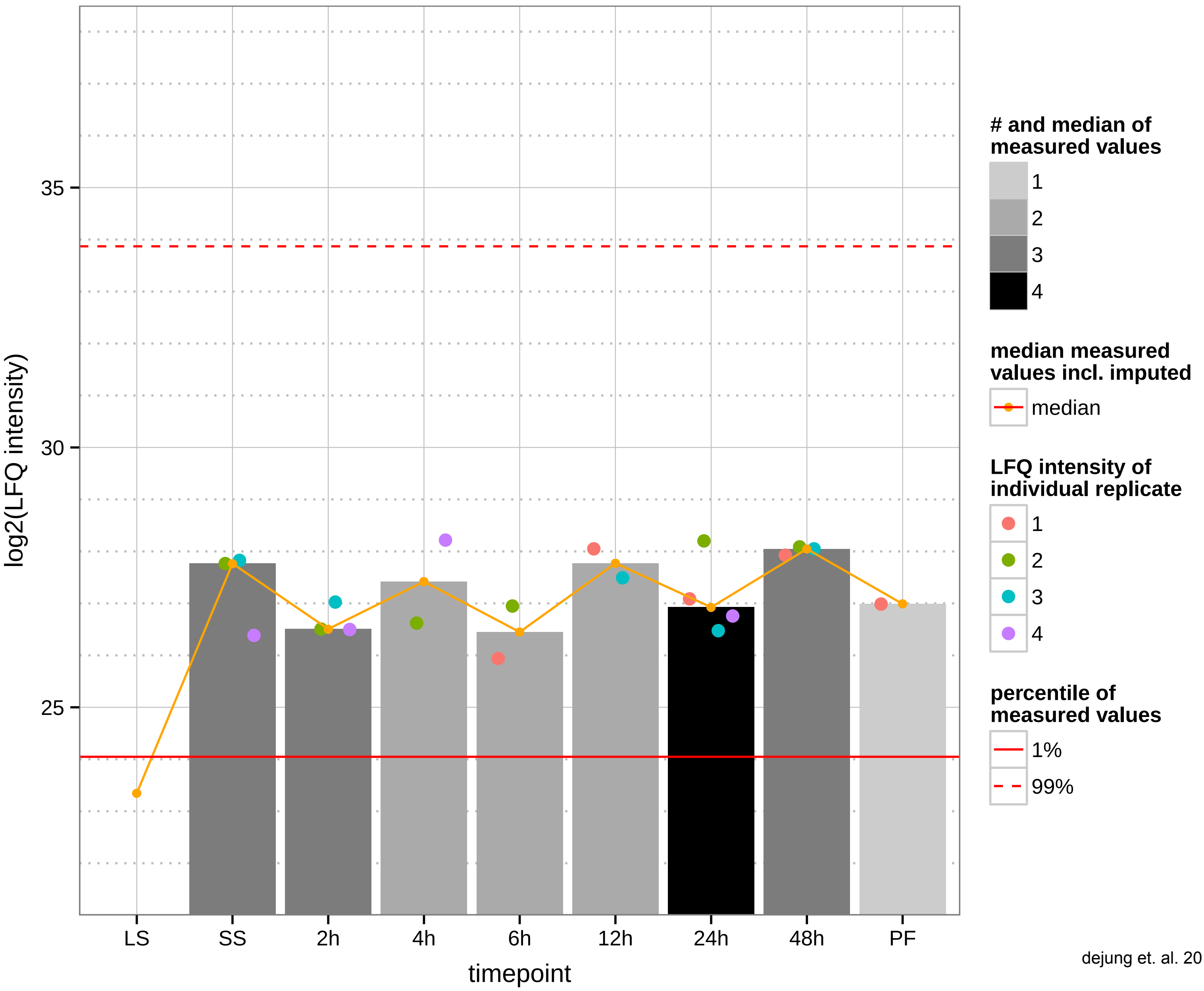
hypothetical protein, conserved
Tb927.9.1470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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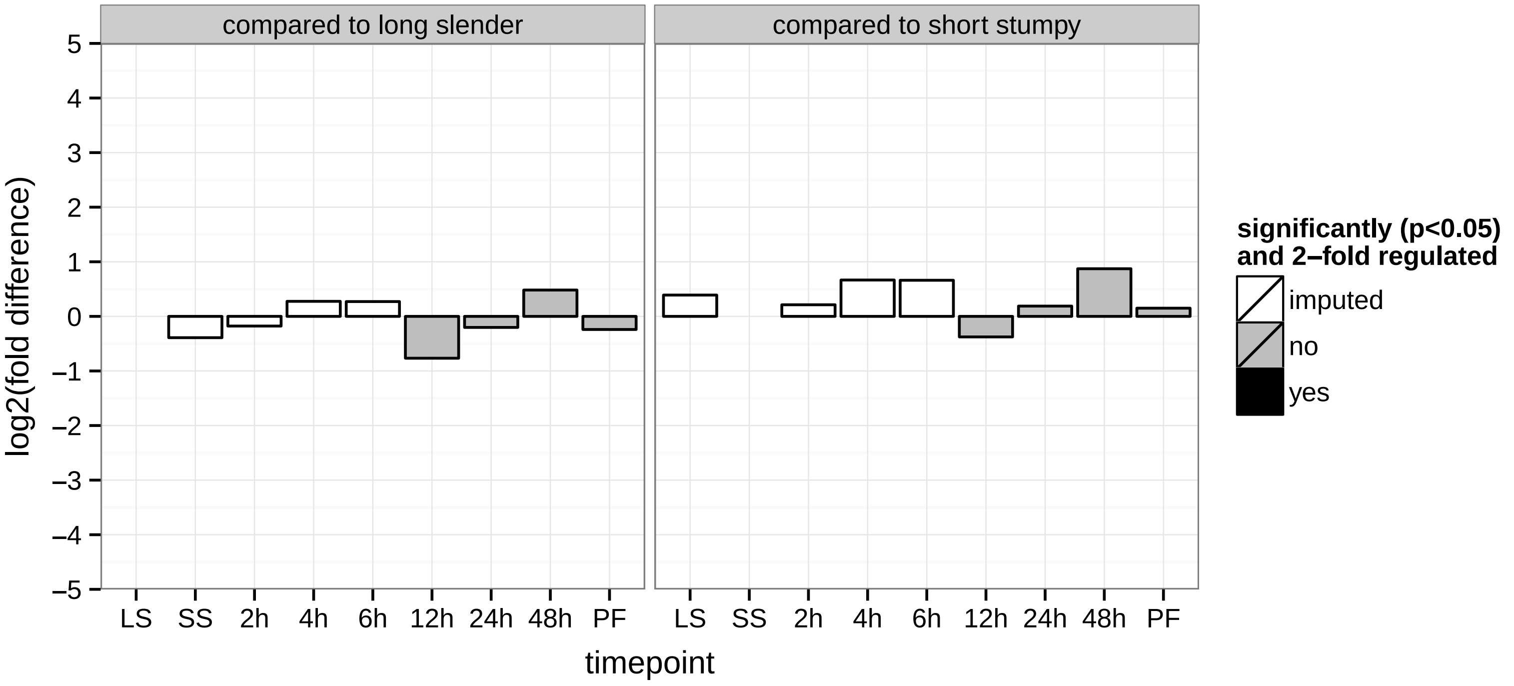
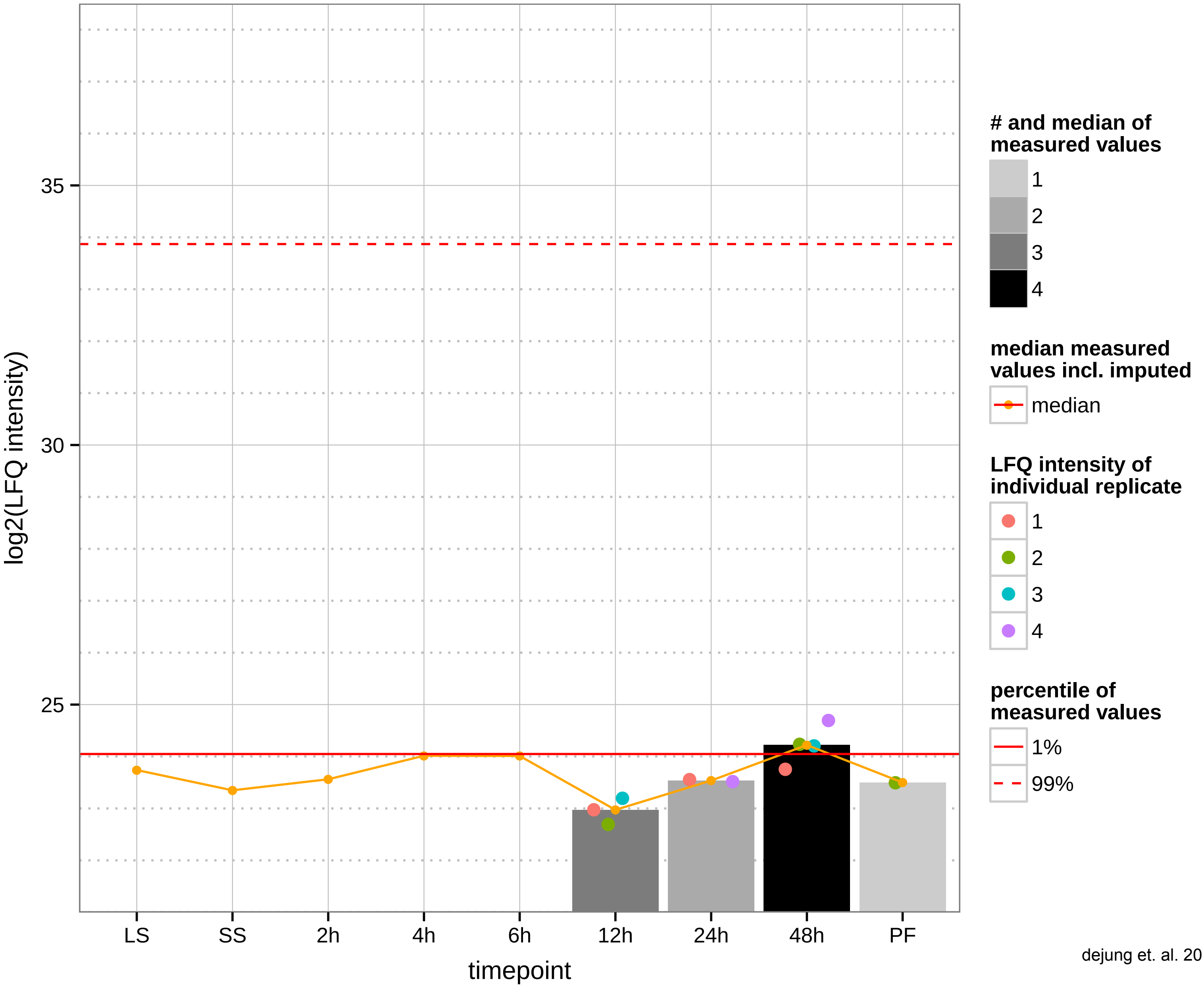
DNA polymerase epsilon subunit b, putative
Tb927.9.15030
AGOF: DNA binding, DNA−directed DNA polymerase activity
AGOC: nucleus
AGOP: DNA−dependent DNA replication
PGOF: DNA binding, DNA−directed DNA polymerase activity
PGOC: nucleus
PGOP: DNA replication, DNA−dependent DNA replication





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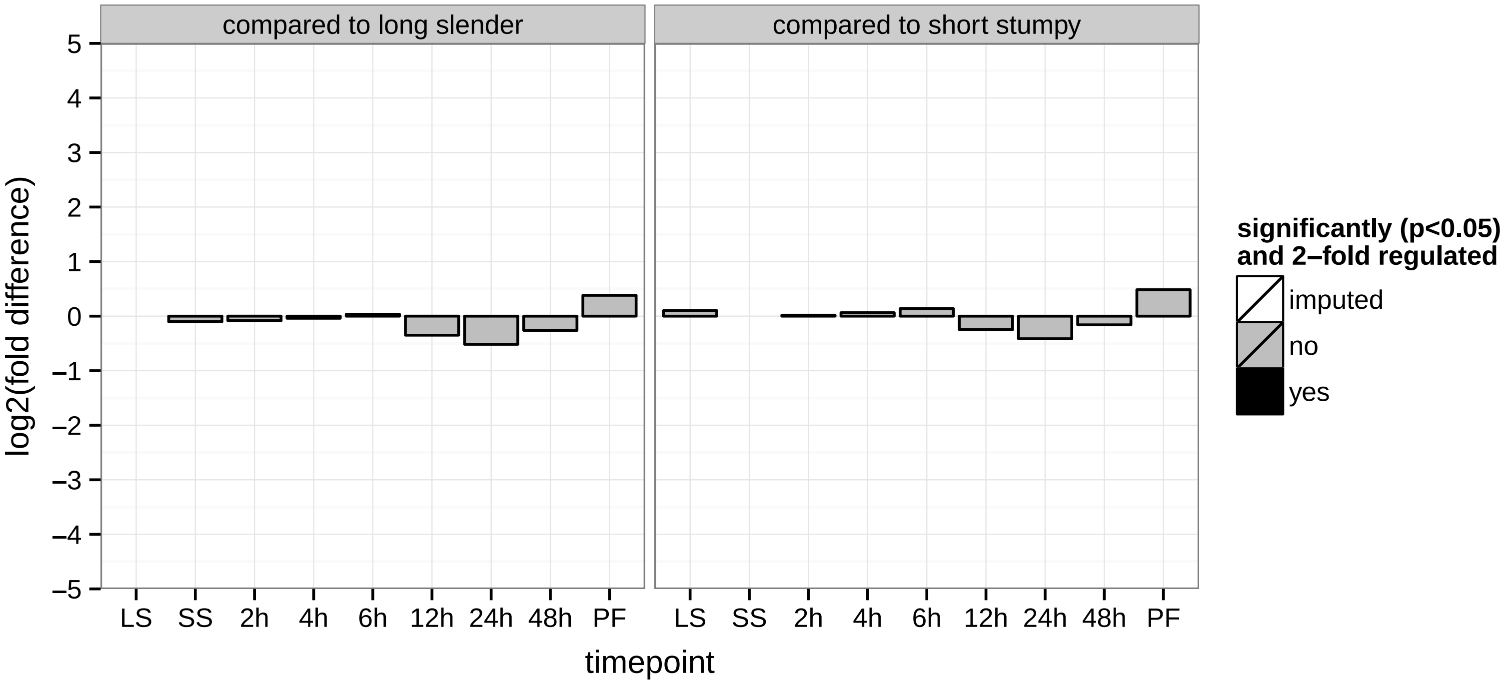
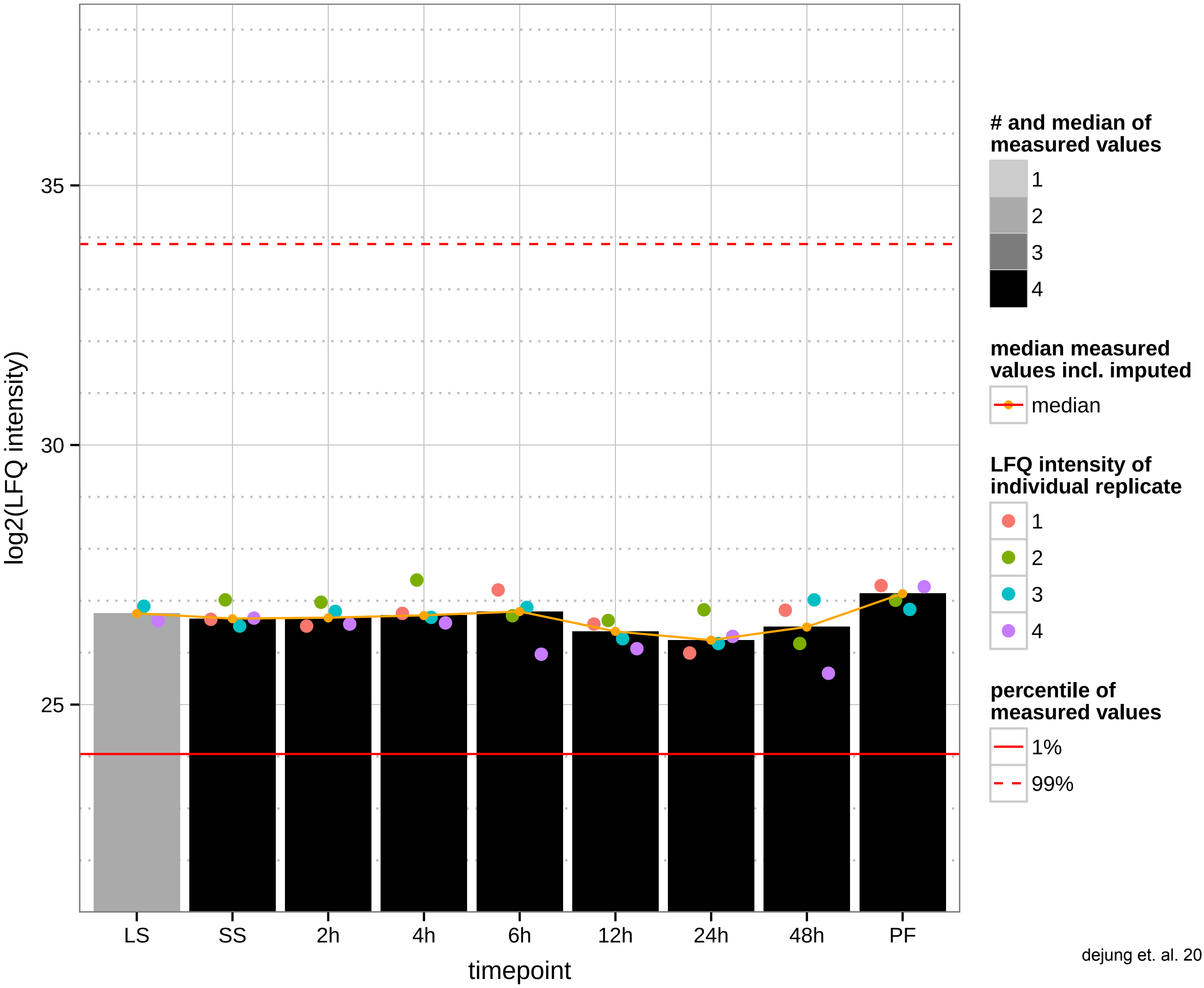
trypanin–related protein, putative
Tb927.9.15050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: microtubule–based flagellum
PGOP: cell motility





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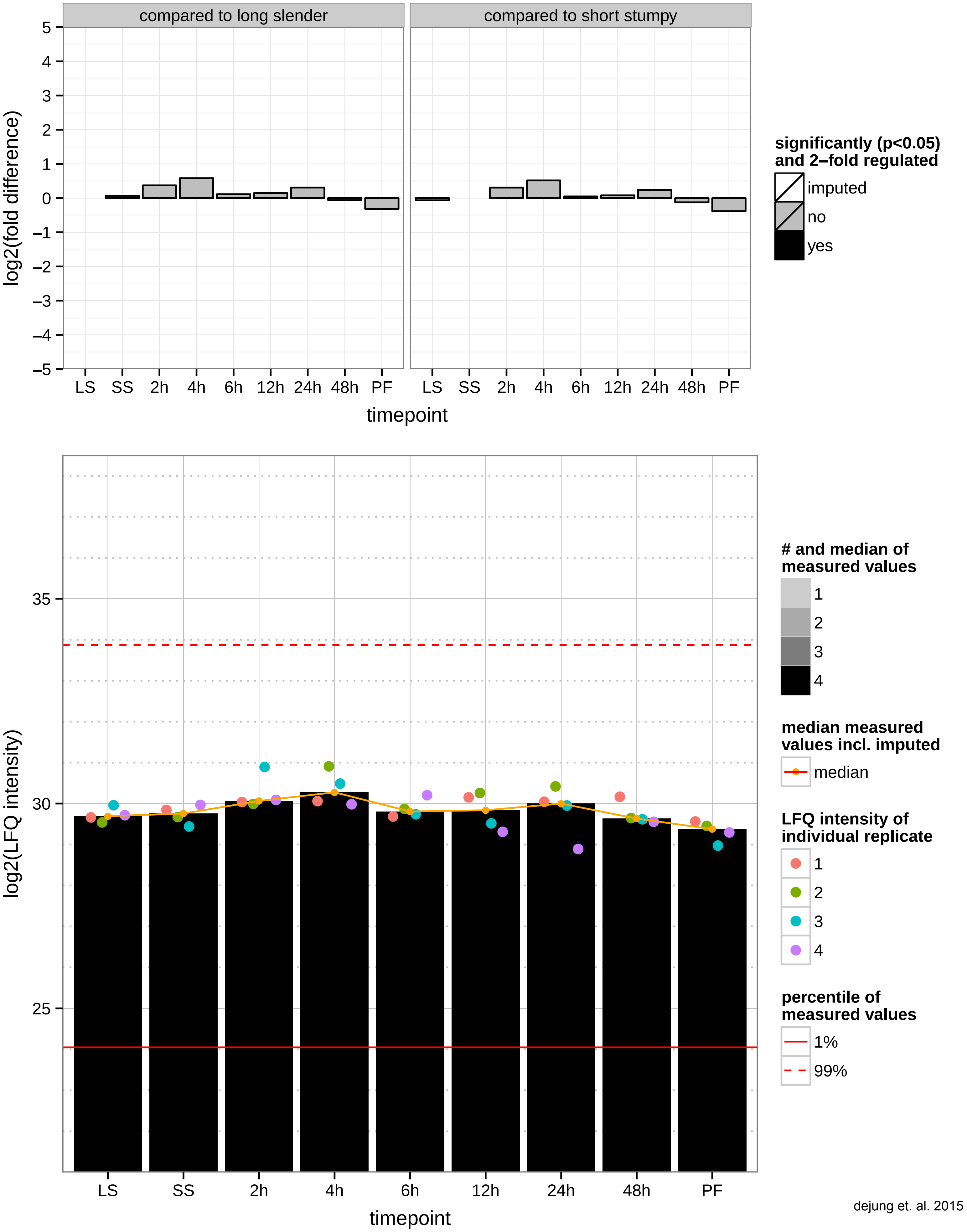
rRNA processing protein, putative
Tb927.9.15060
AGOF: null
AGOC: nucleus
AGOP: ribosome biogenesis
PGOF: null
PGOC: null
PGOP: null



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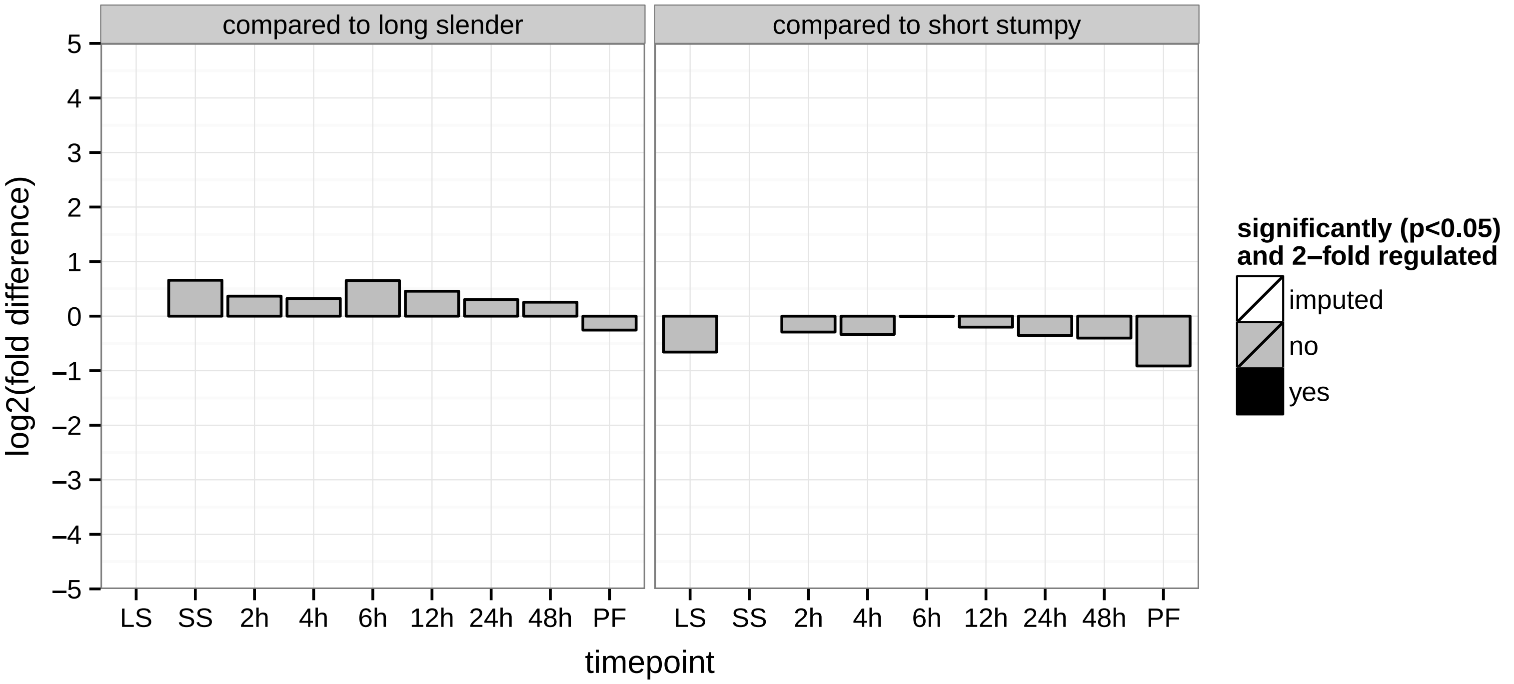
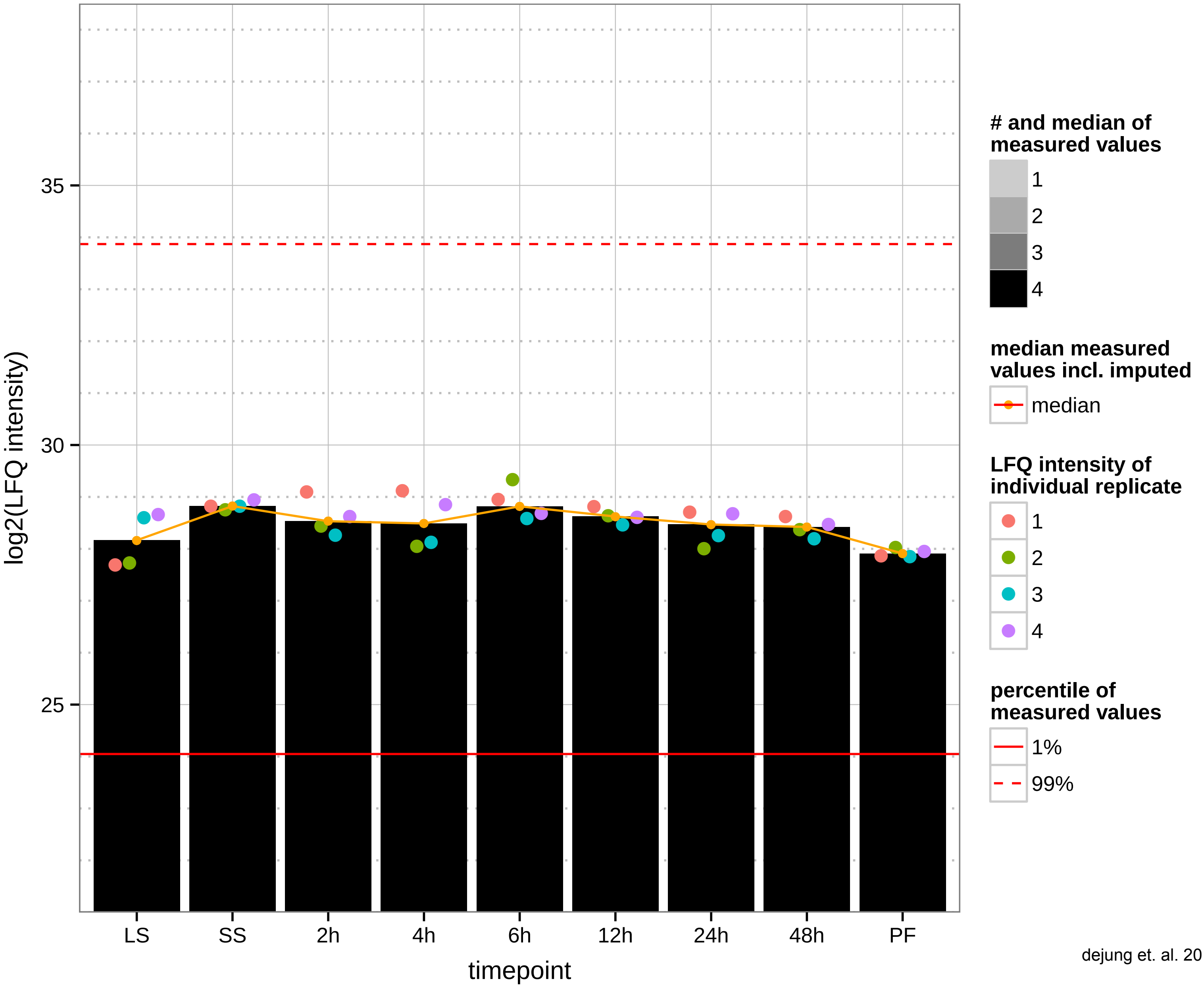
hypothetical protein, conserved
Tb927.9.15070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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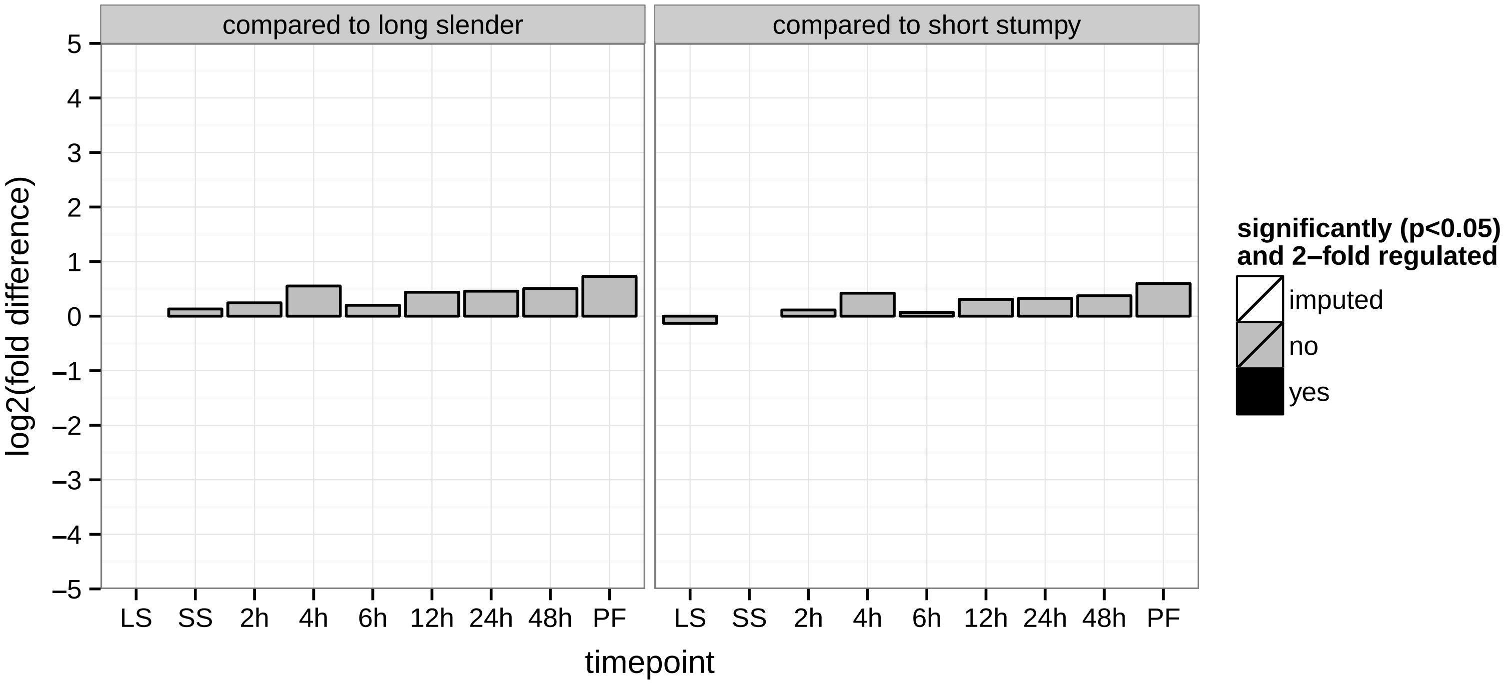
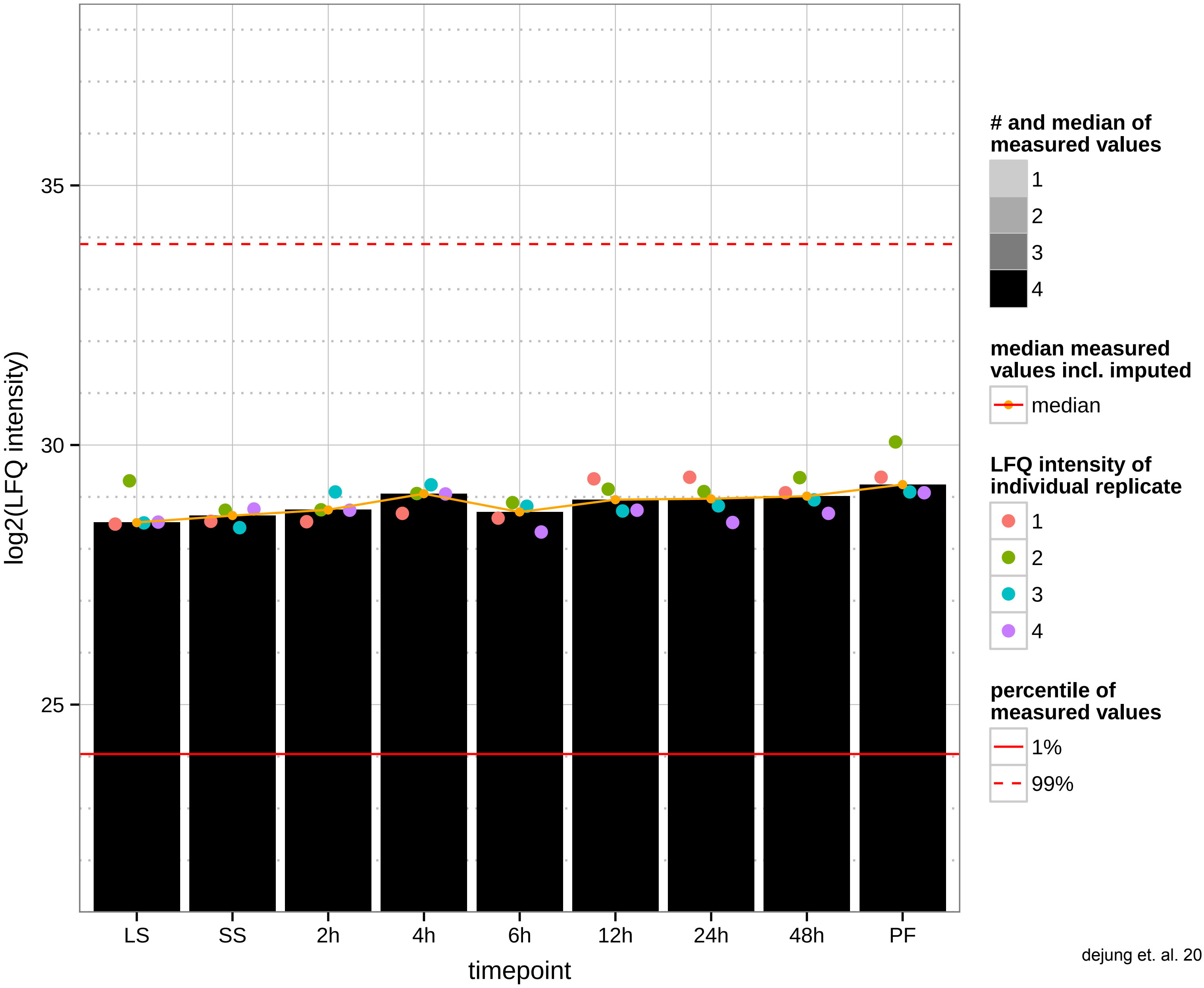
cytosolic coat protein, putative
Tb927.9.15090
AGOF: protein transmembrane transporter activity
AGOC: ER to Golgi transport vesicle membrane, integral to membrane
AGOP: transport
PGOF: null
PGOC: integral to membrane
PGOP: transport





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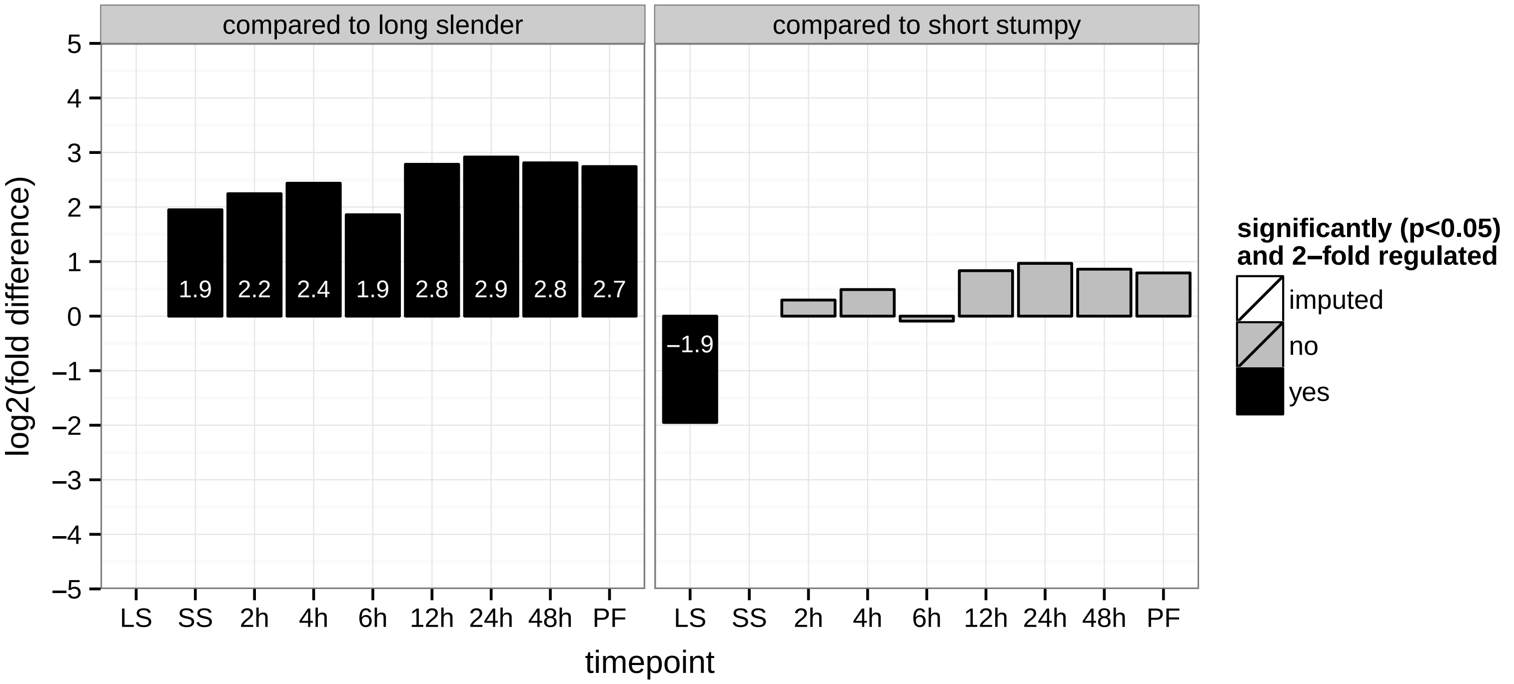
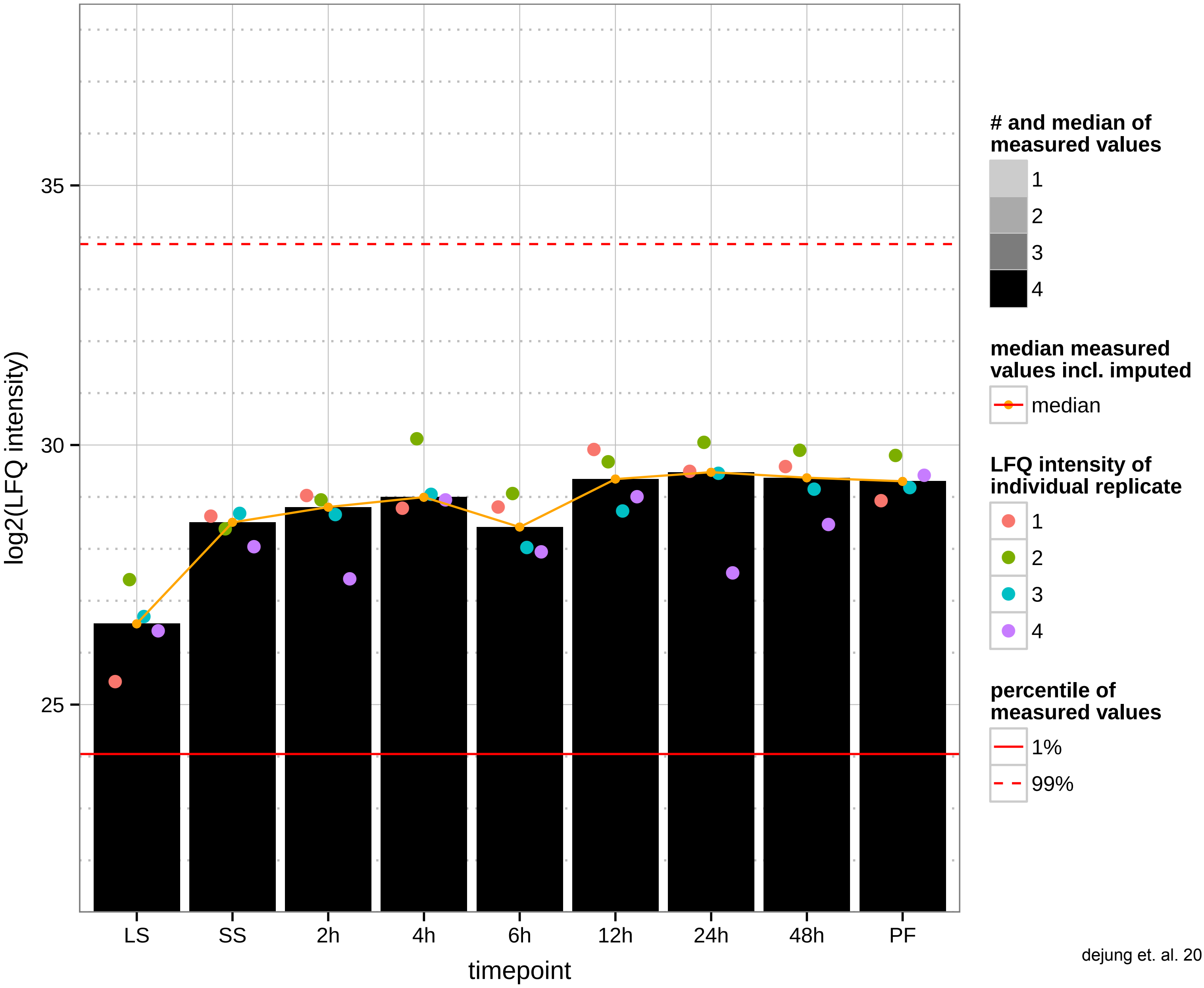
hypothetical protein, conserved
Tb927.9.1520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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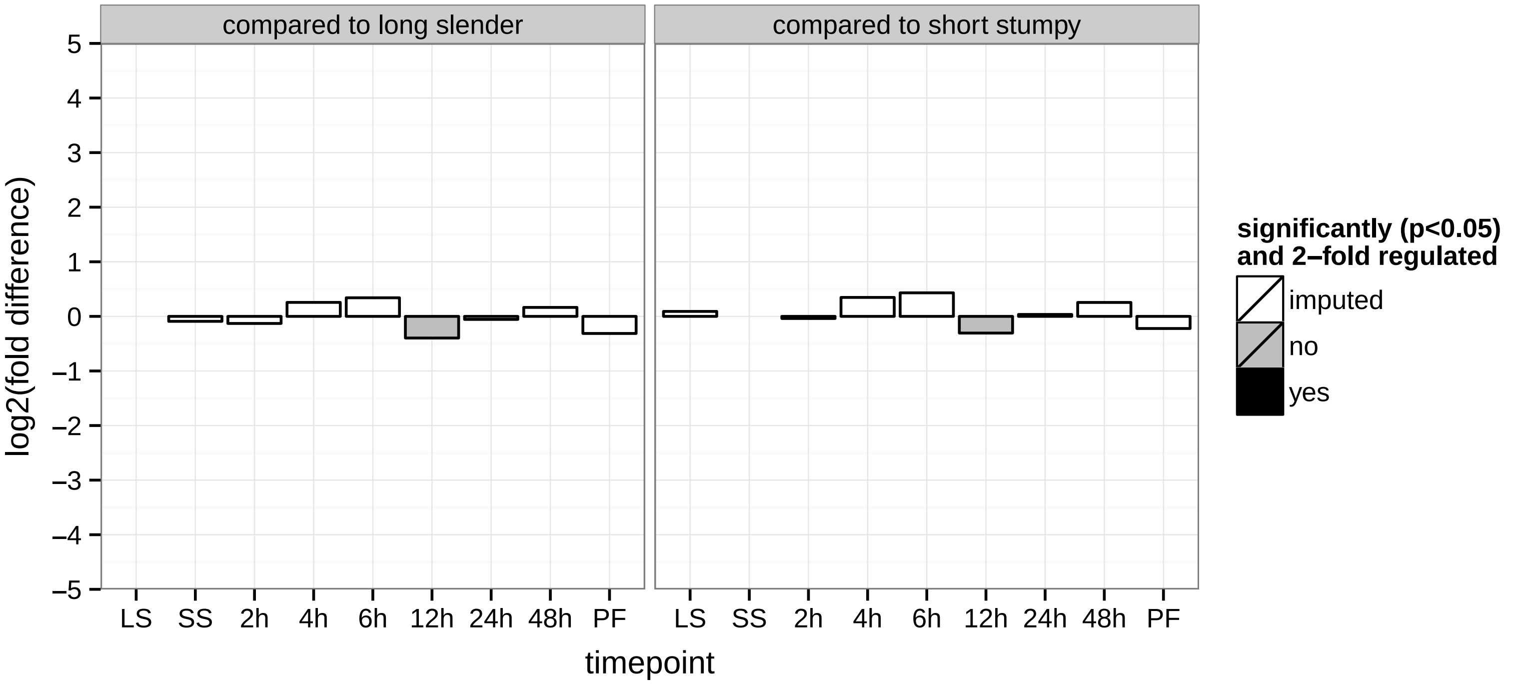
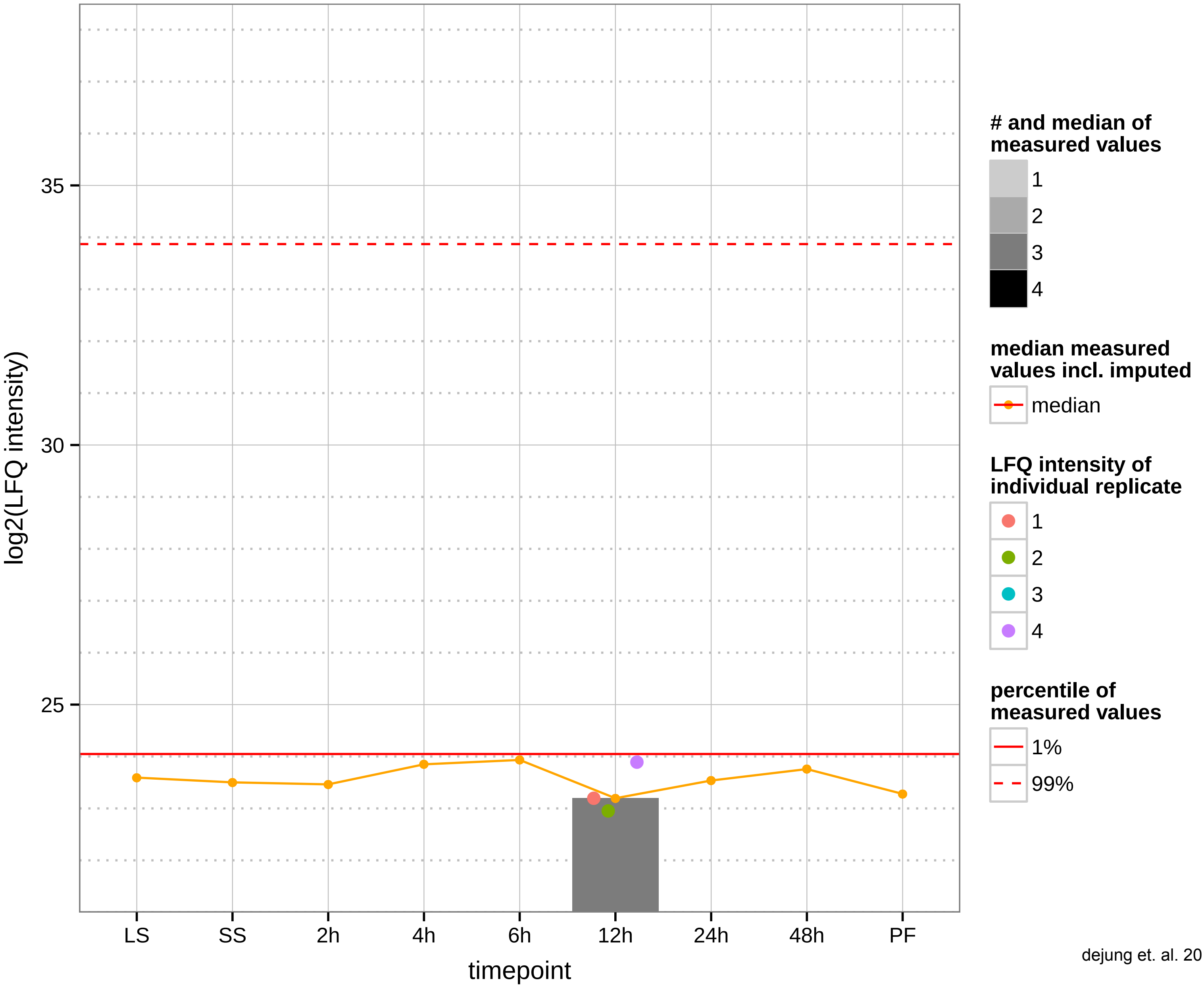
hypothetical protein, conserved
Tb927.9.1530
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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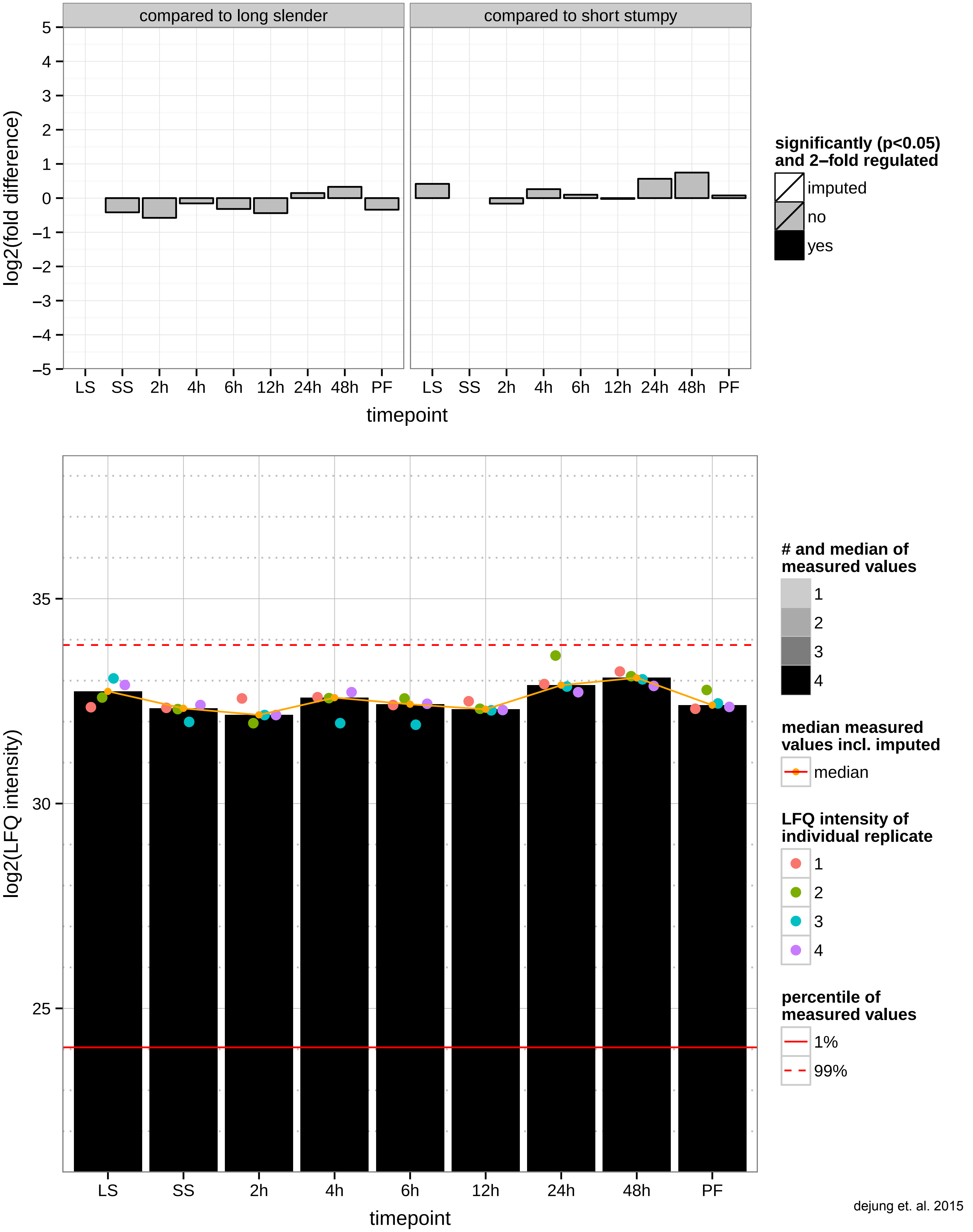
40S ribosomal protein S6, putative
Tb927.9.15360
AGOF: null
AGOC: intracellular, ribosome
AGOP: regulation of cell growth, regulation of cell proliferation, translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation



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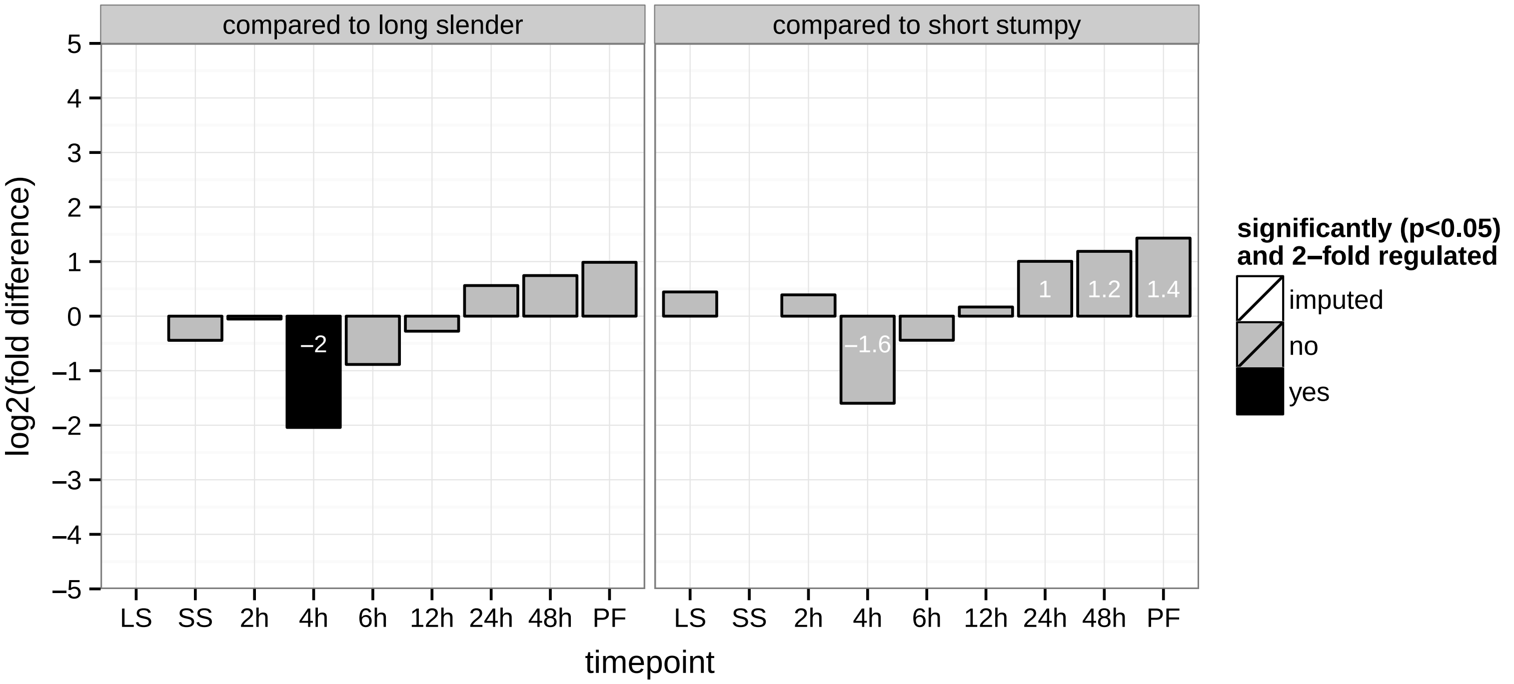
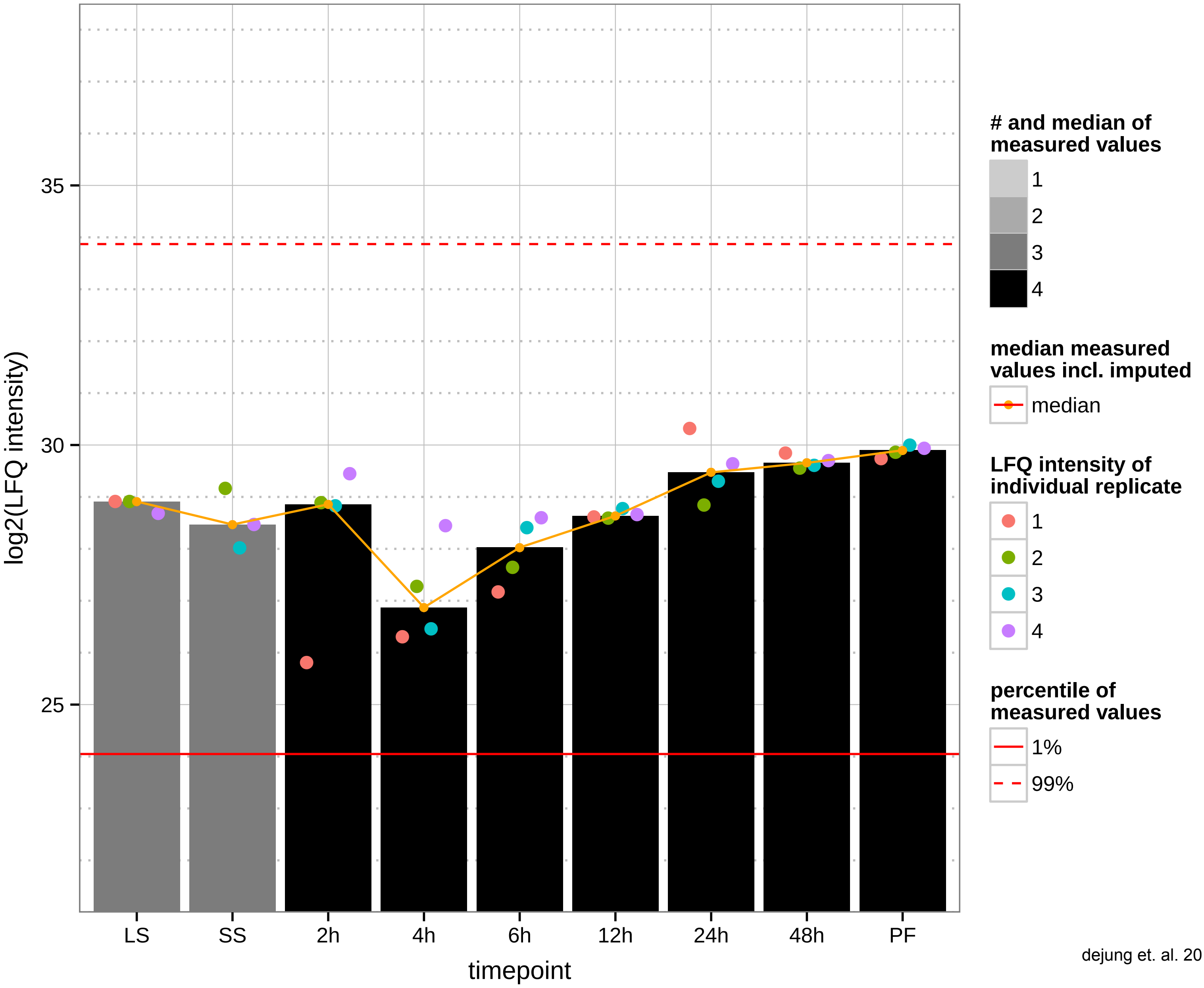
kinesin, putative
Tb927.9.15470
AGOF: null, ATP binding, microtubule motor activity, motor activity
AGOC: null, microtubule associated complex
AGOP: null, microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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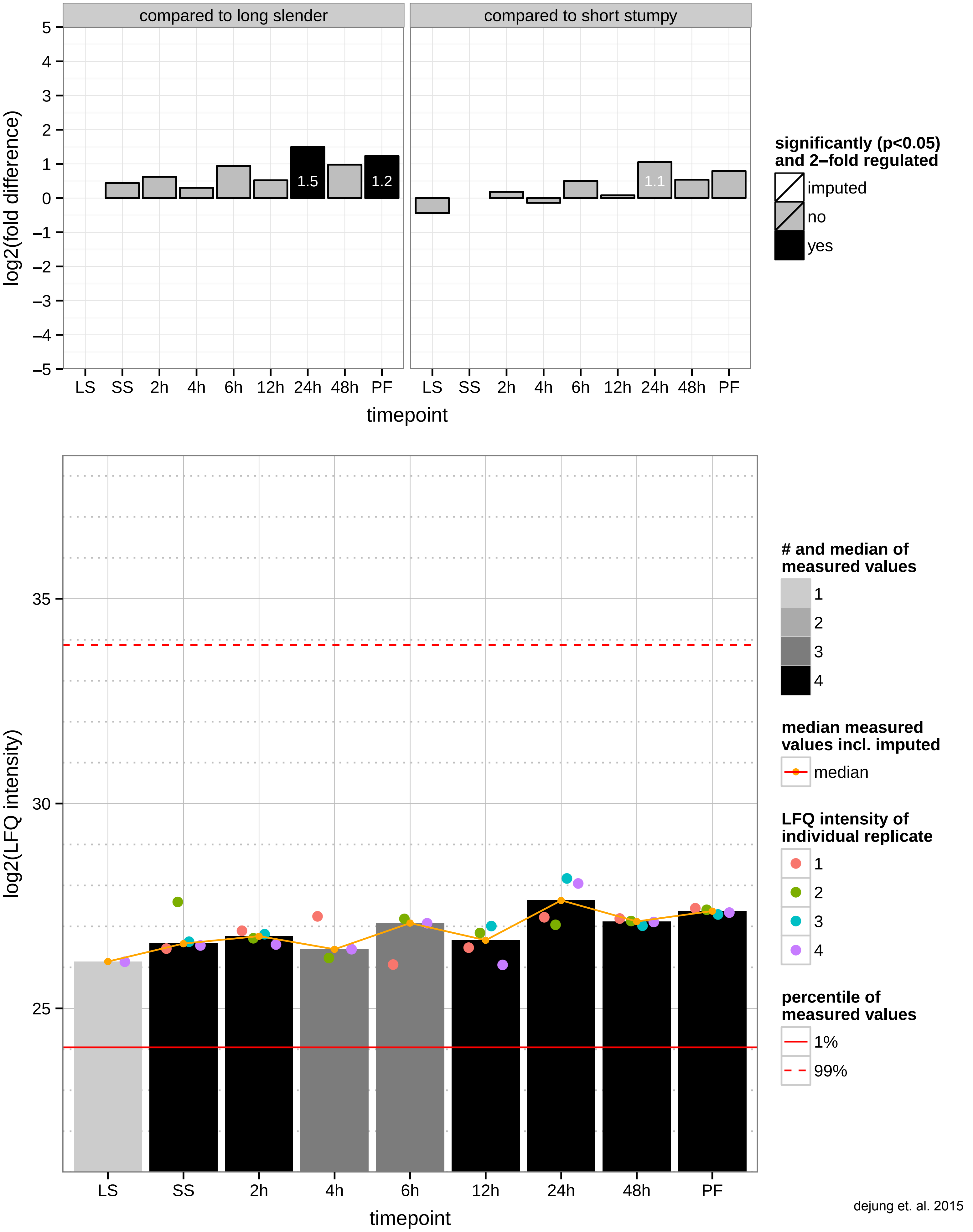
hypothetical protein, conserved
Tb927.9.1560
AGOF: heat shock protein binding
AGOC: null
AGOP: null
PGOF: heat shock protein binding
PGOC: null
PGOP: null



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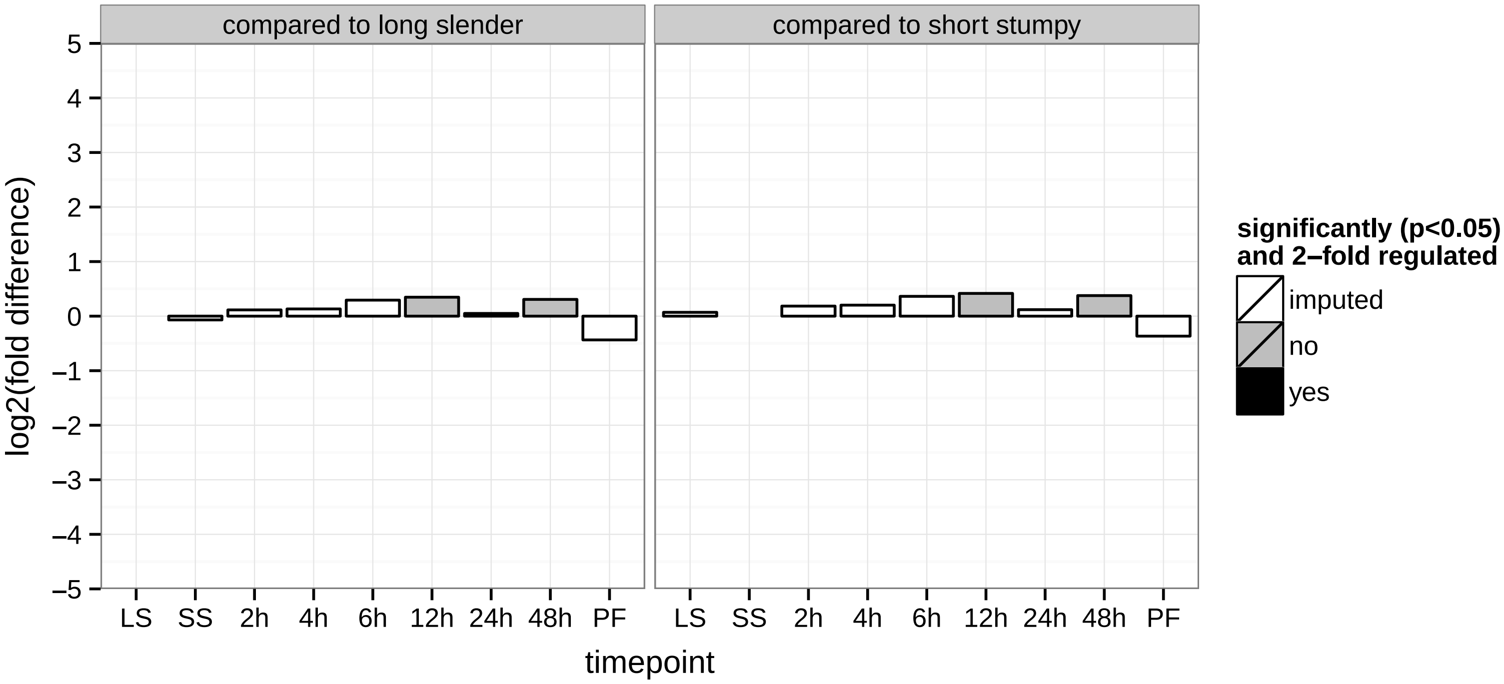
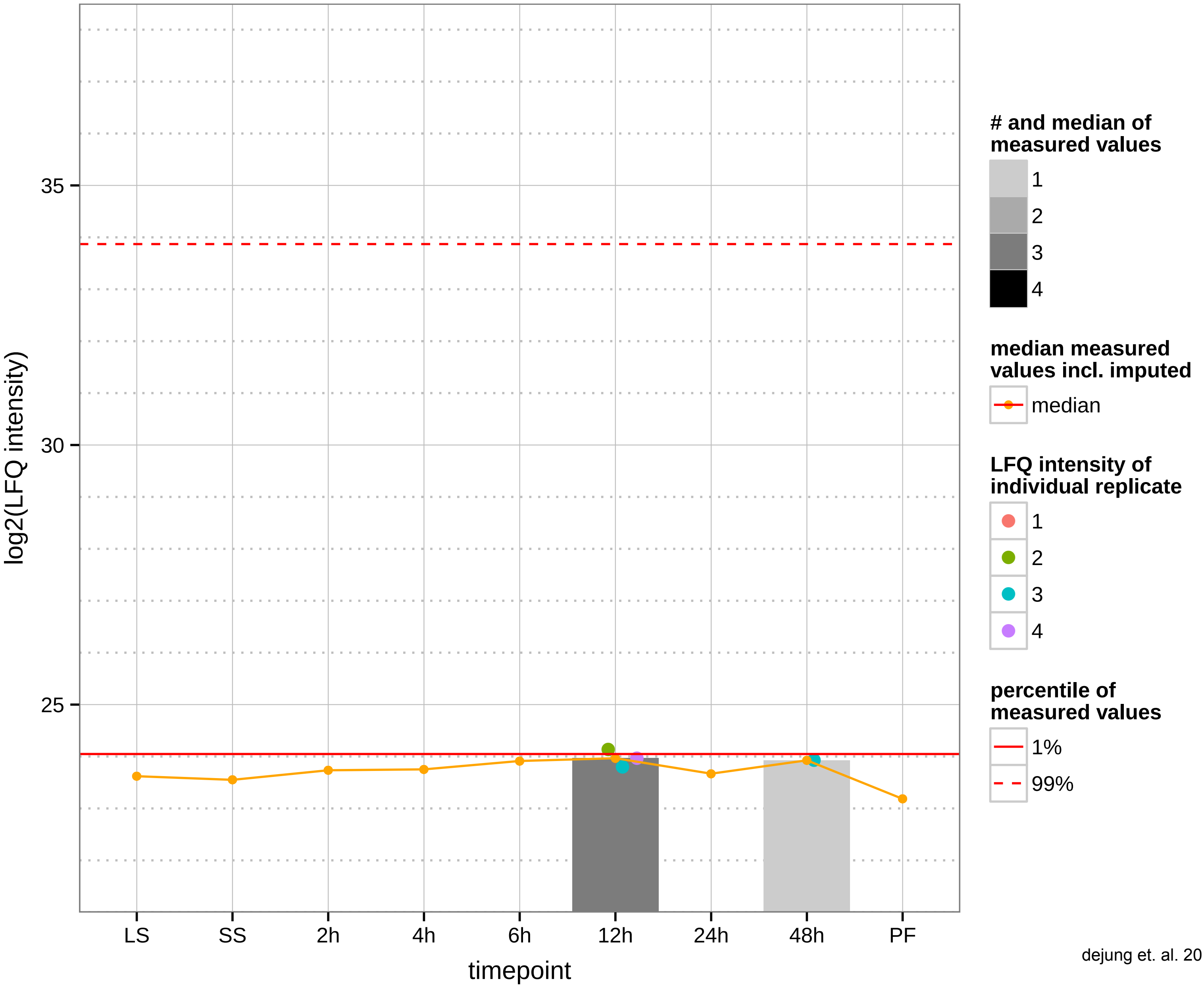
hypothetical protein, conserved
Tb927.9.1660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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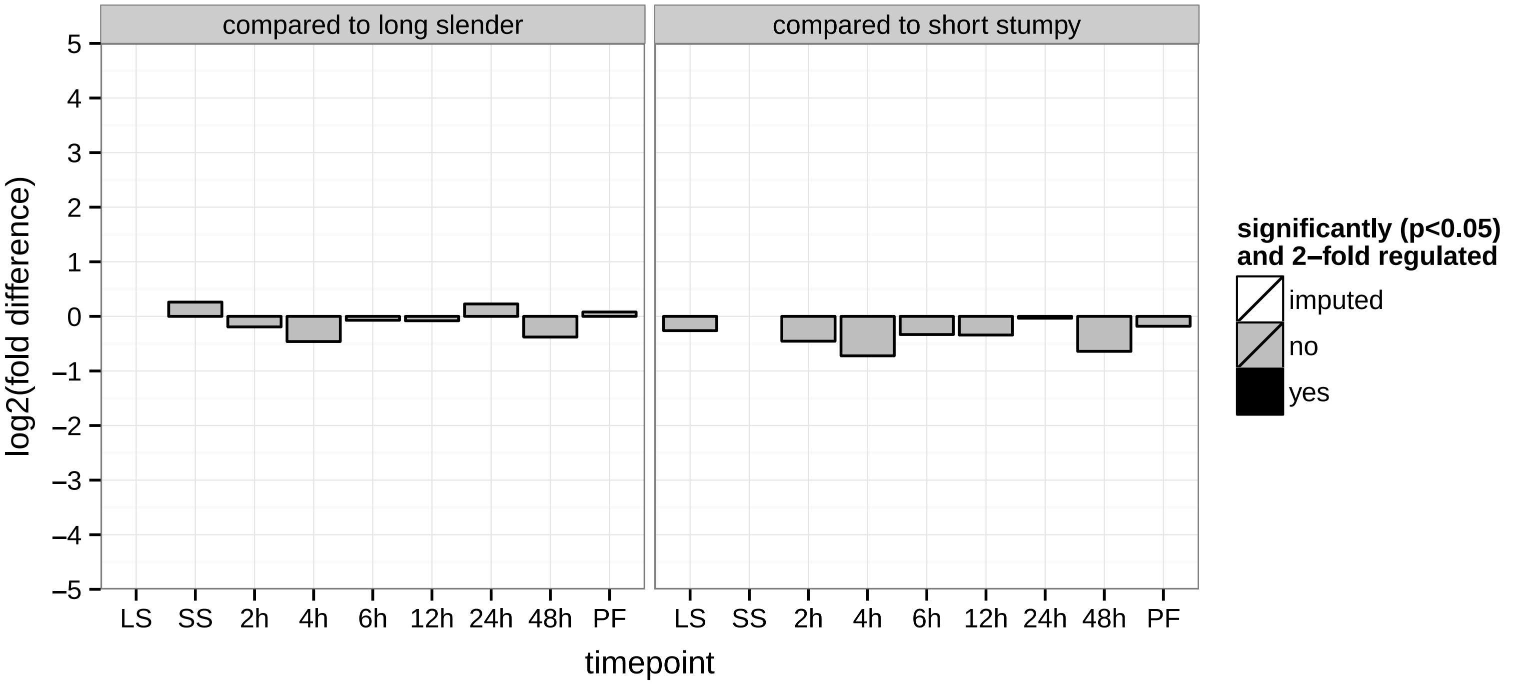
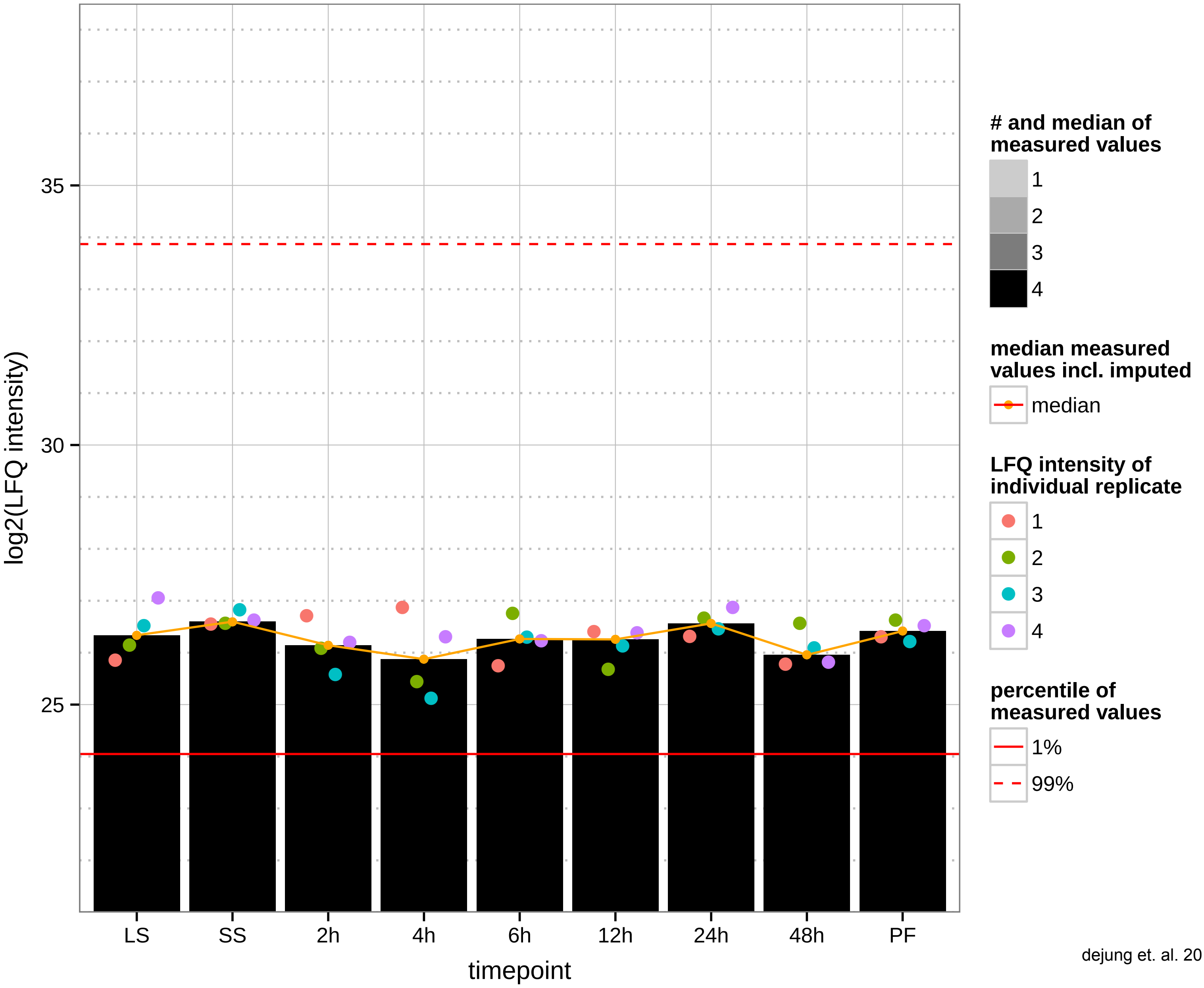
hypothetical protein, conserved
Tb927.9.1700
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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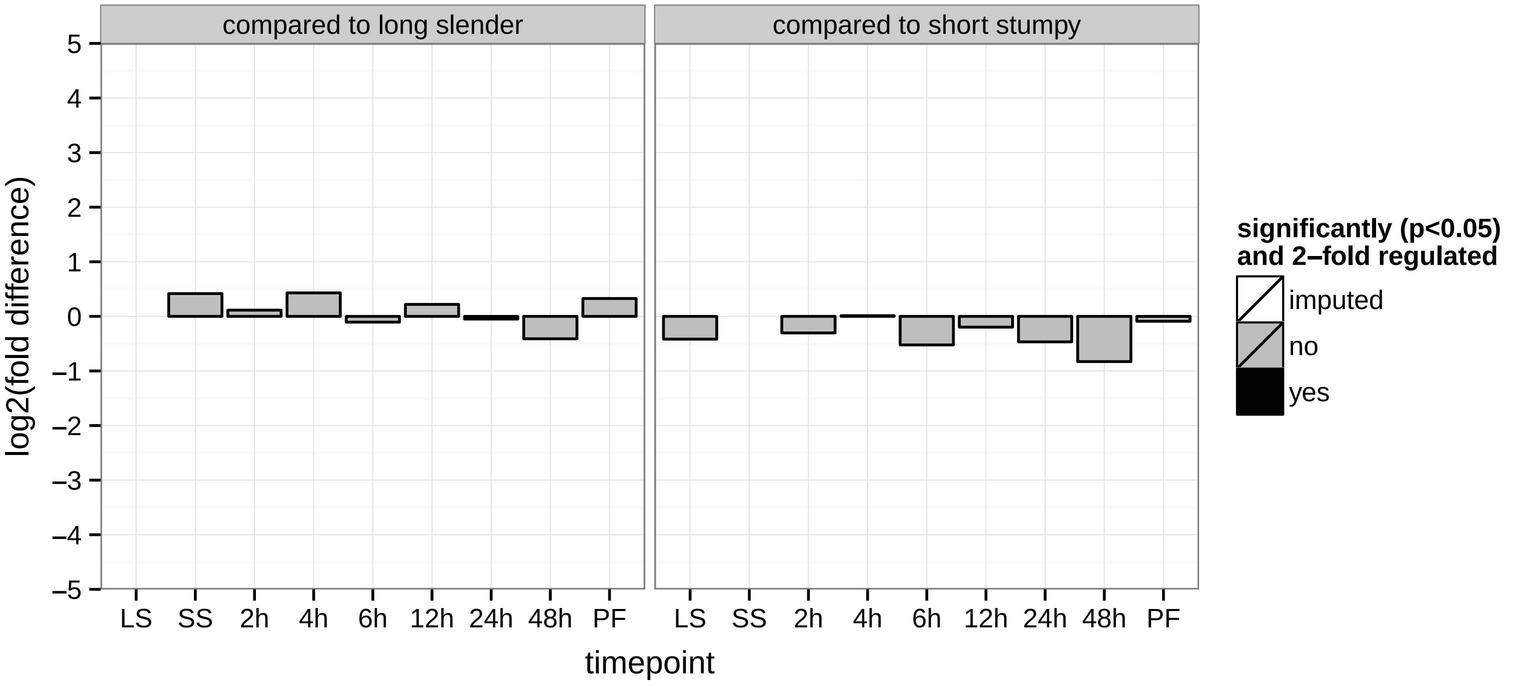
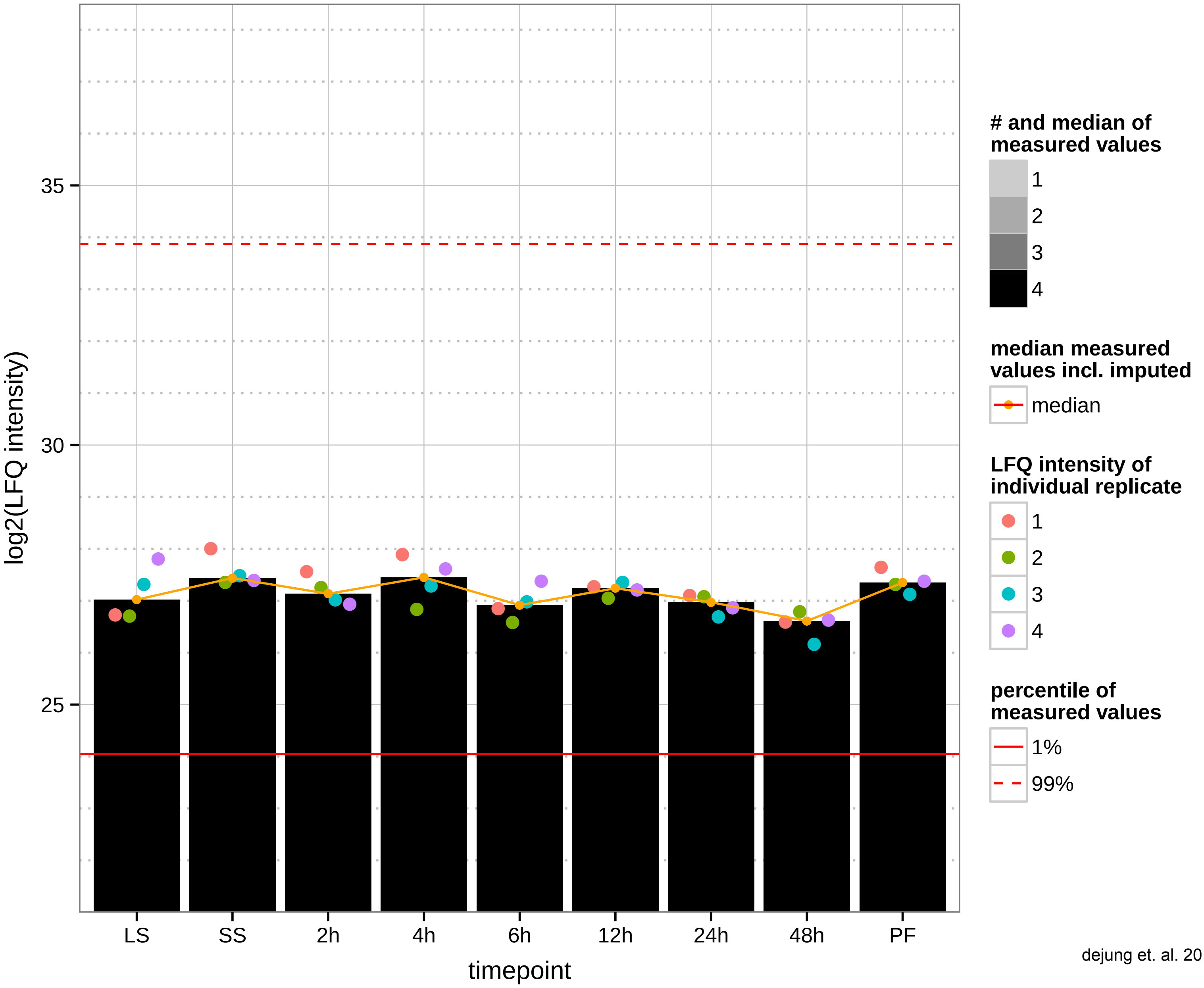
peroxisomal membrane protein 4, putative
Tb927.9.1720
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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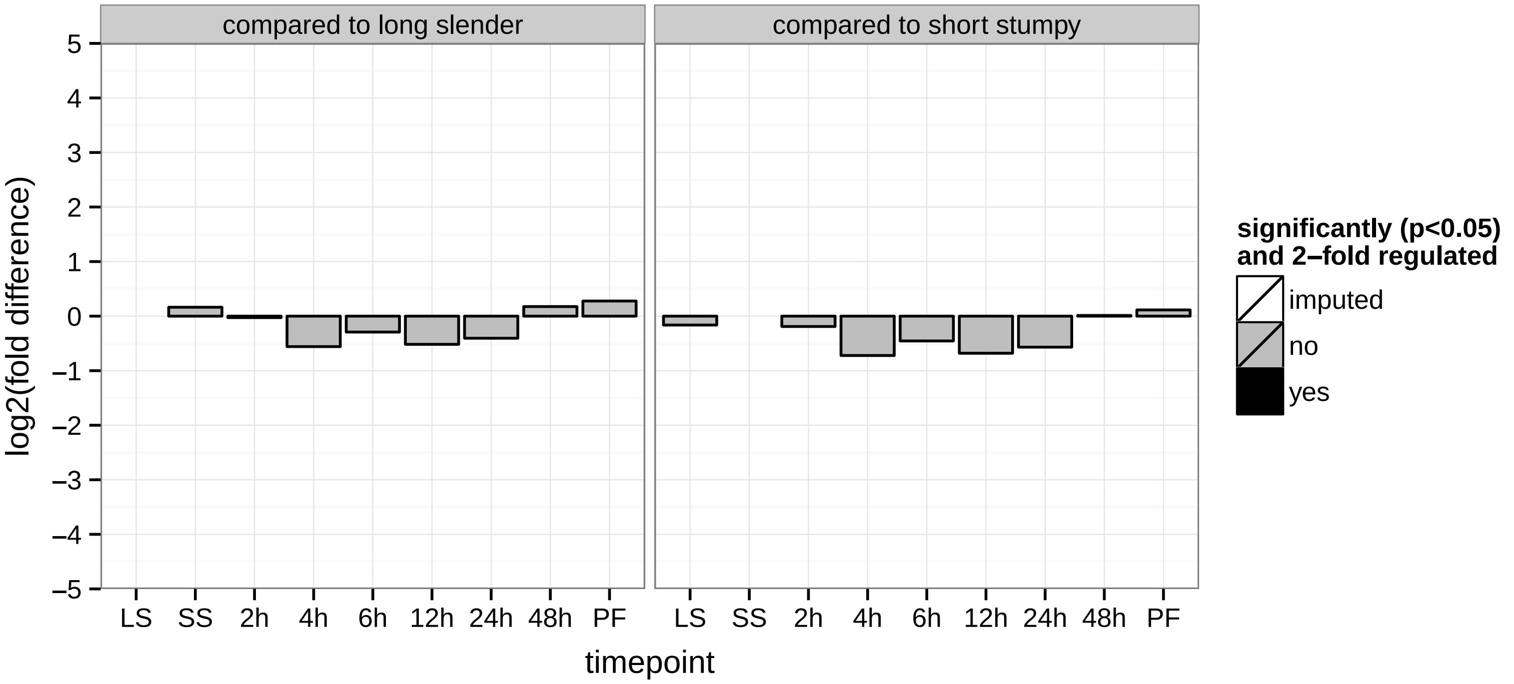
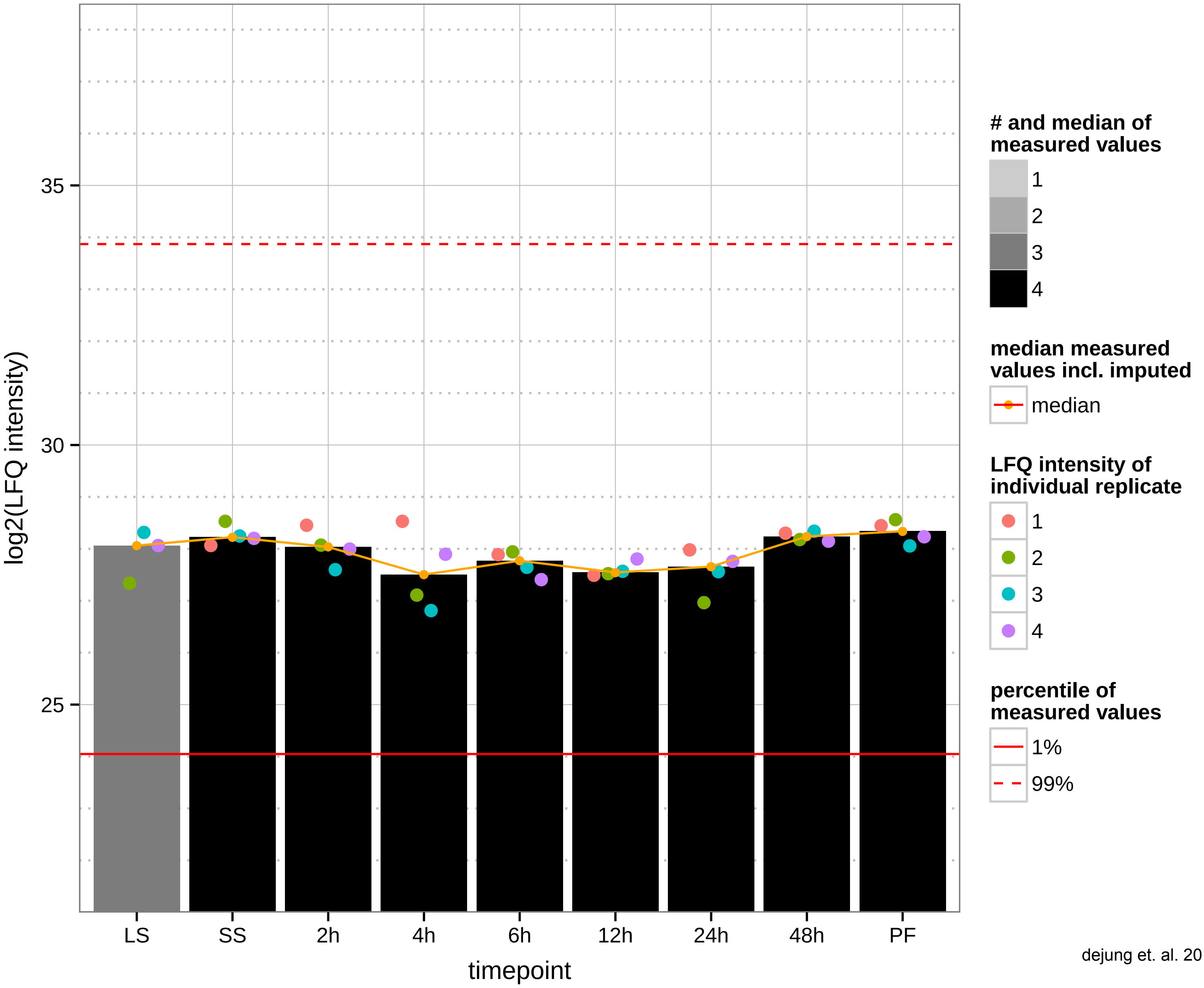
hypothetical protein, conserved
Tb927.9.1750
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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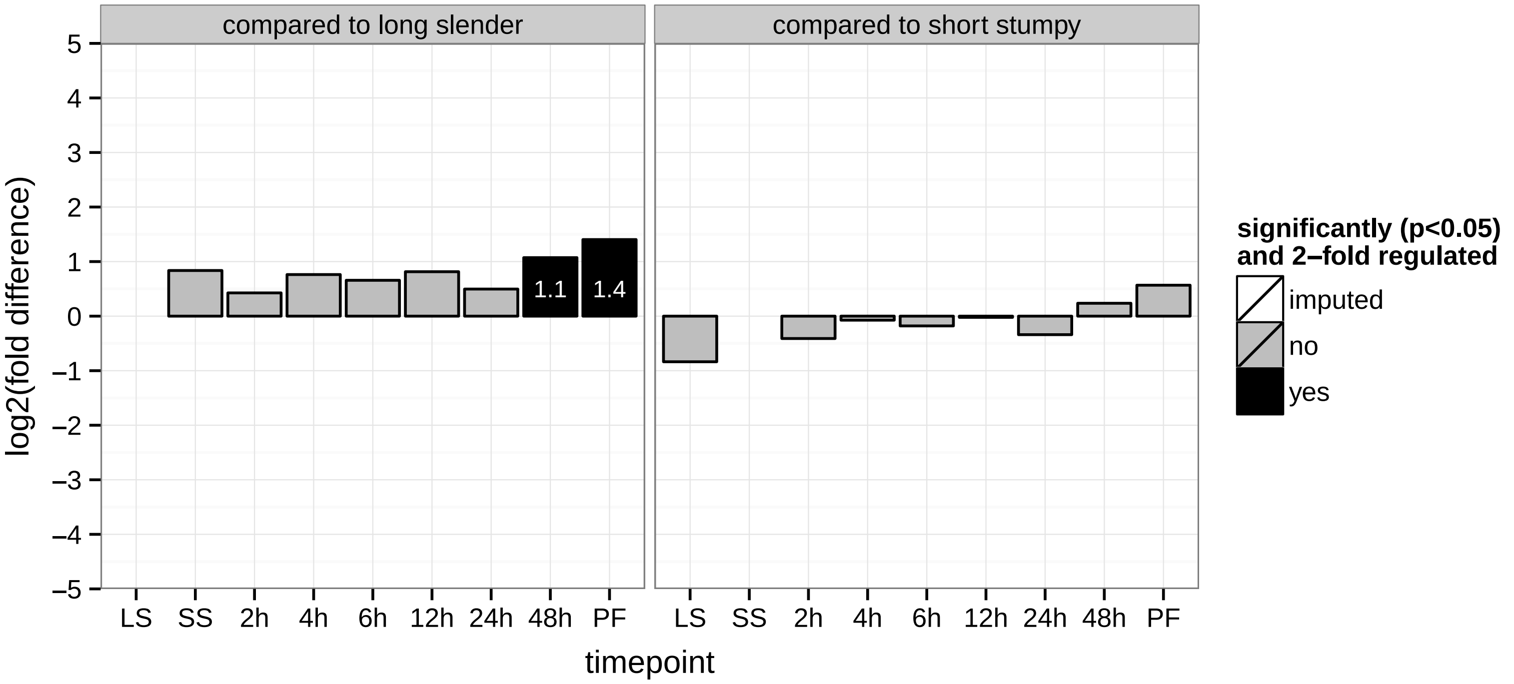
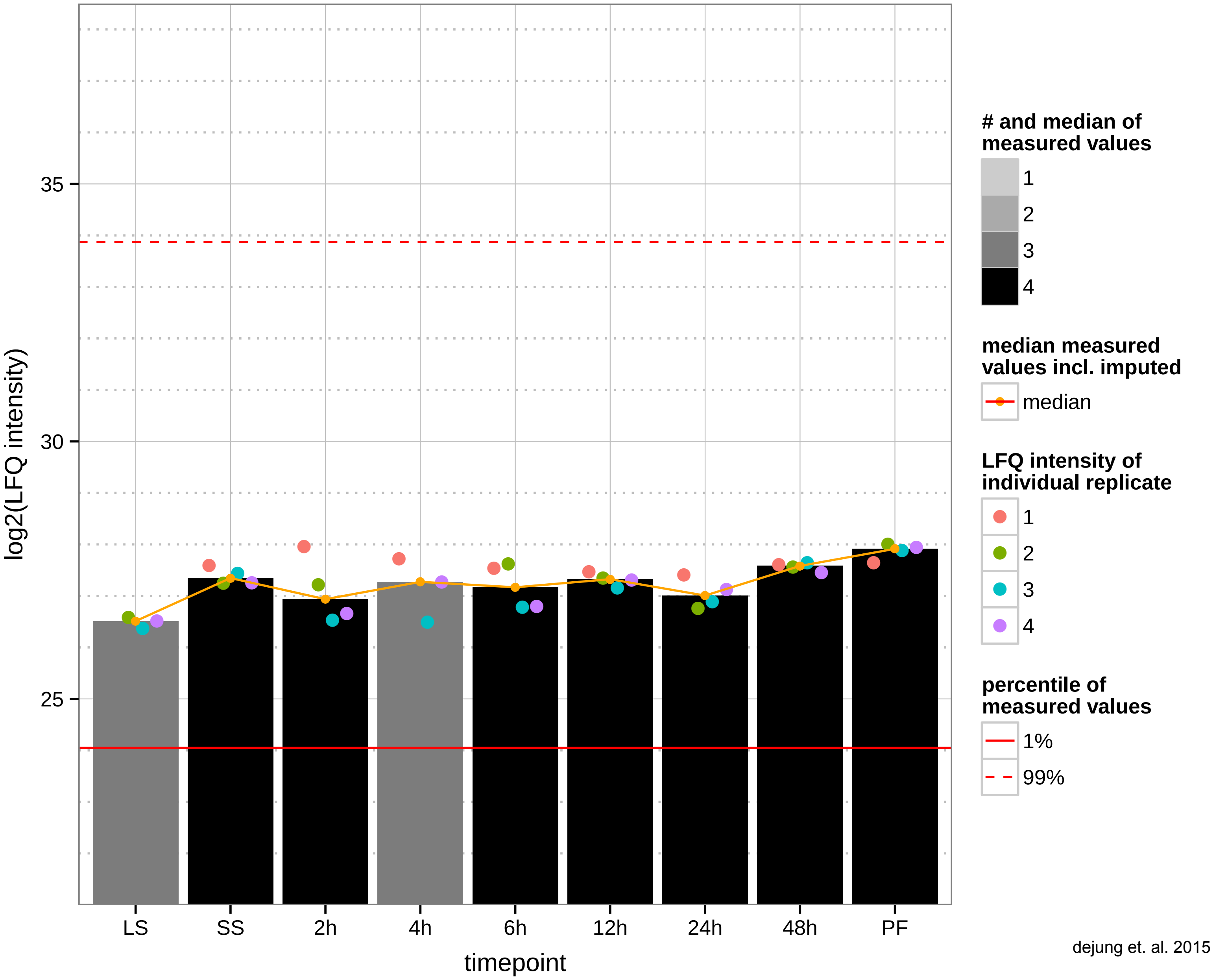
hypothetical protein, conserved
Tb927.9.1770
AGOF: acid–amino acid ligase activity, zinc ion binding
AGOC: intracellular
AGOP: cellular protein modification process
PGOF: acid–amino acid ligase activity, protein binding, zinc ion binding
PGOC: intracellular
PGOP: cellular protein modification process





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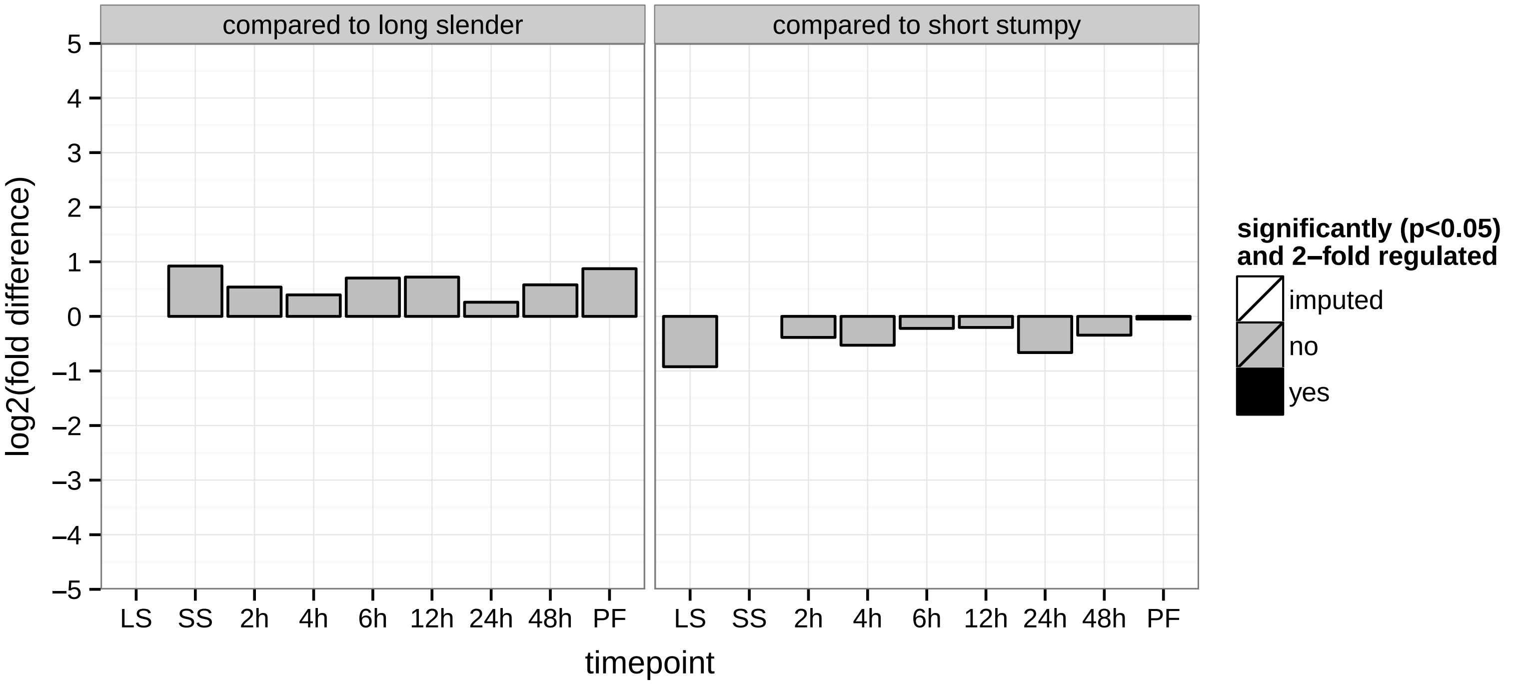
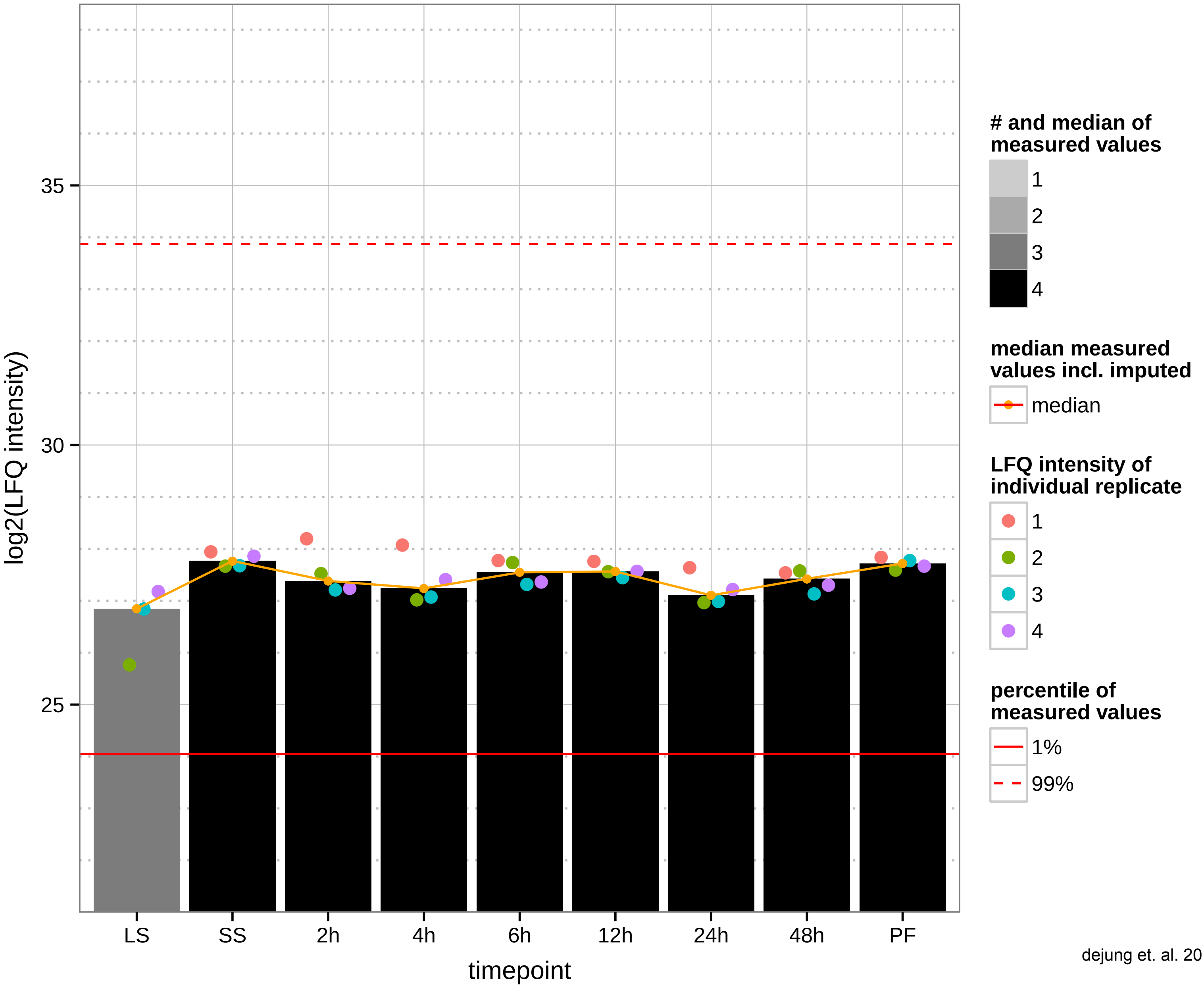
sec1 family transport protein, putative (SLY1)
Tb927.9.1780
AGOF: protein transporter activity
AGOC: mitochondrion
AGOP: protein secretion, vesicle docking involved in exocytosis, vesicle–mediated transport
PGOF: null
PGOC: null
PGOP: vesicle docking involved in exocytosis, vesicle–mediated transport





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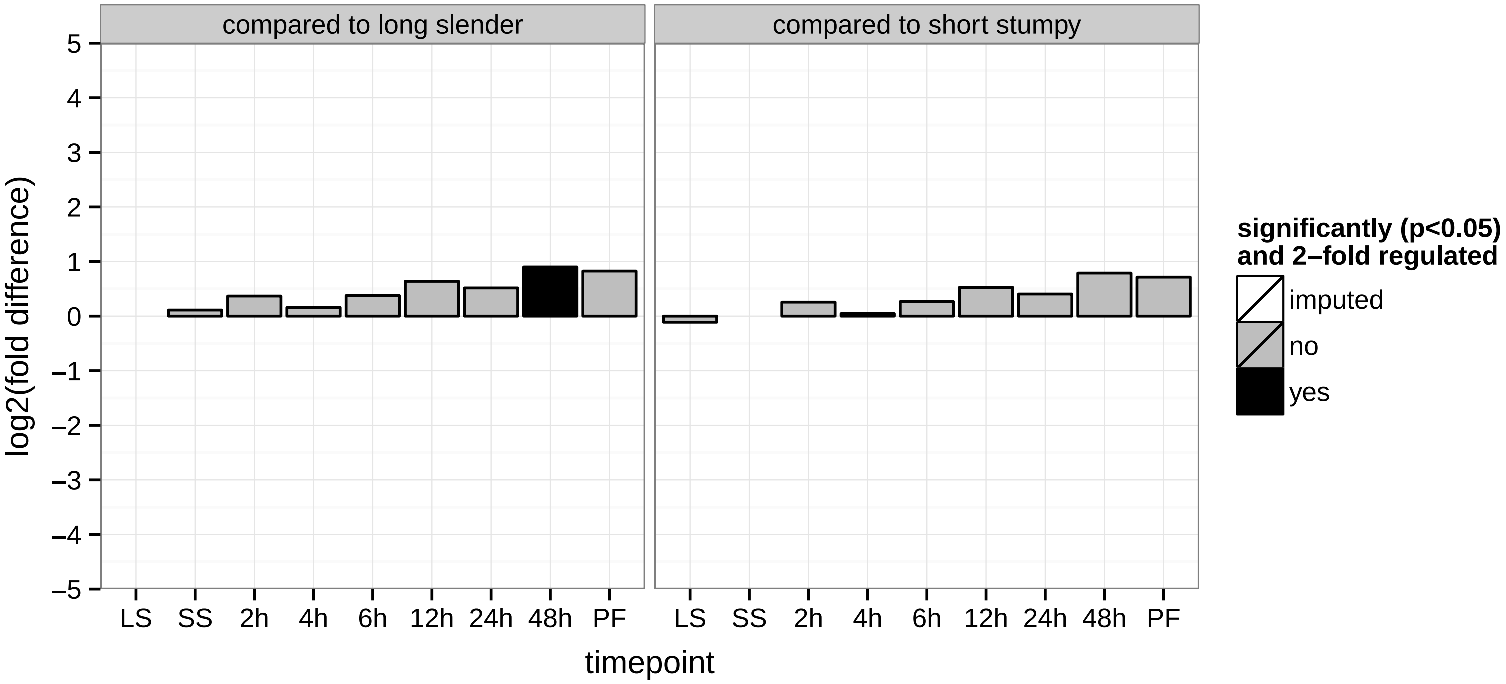
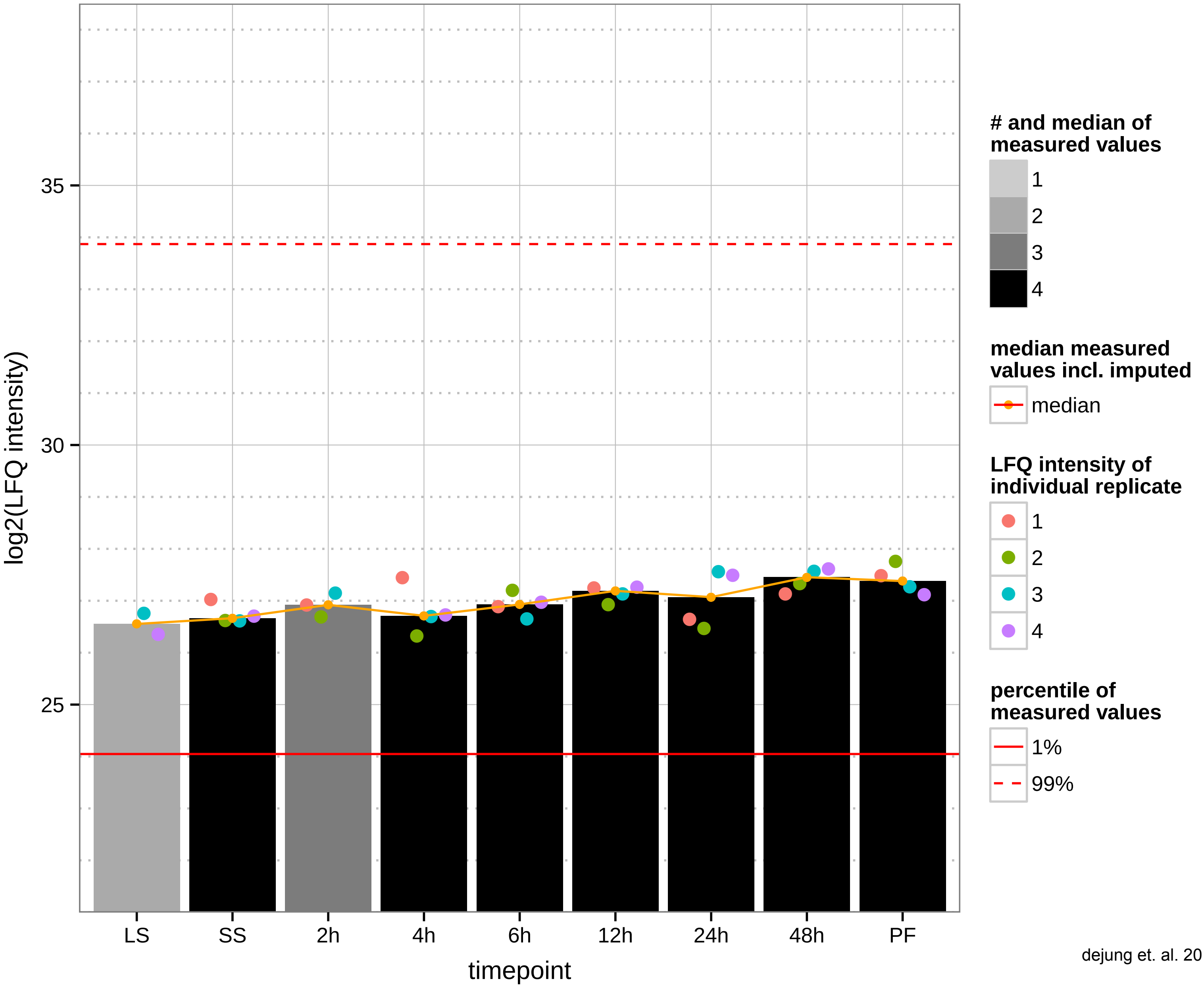
hypothetical protein, conserved
Tb927.9.1880
AGOF: null
AGOC: null
AGOP: null
PGOF: binding, protein binding
PGOC: null
PGOP: null





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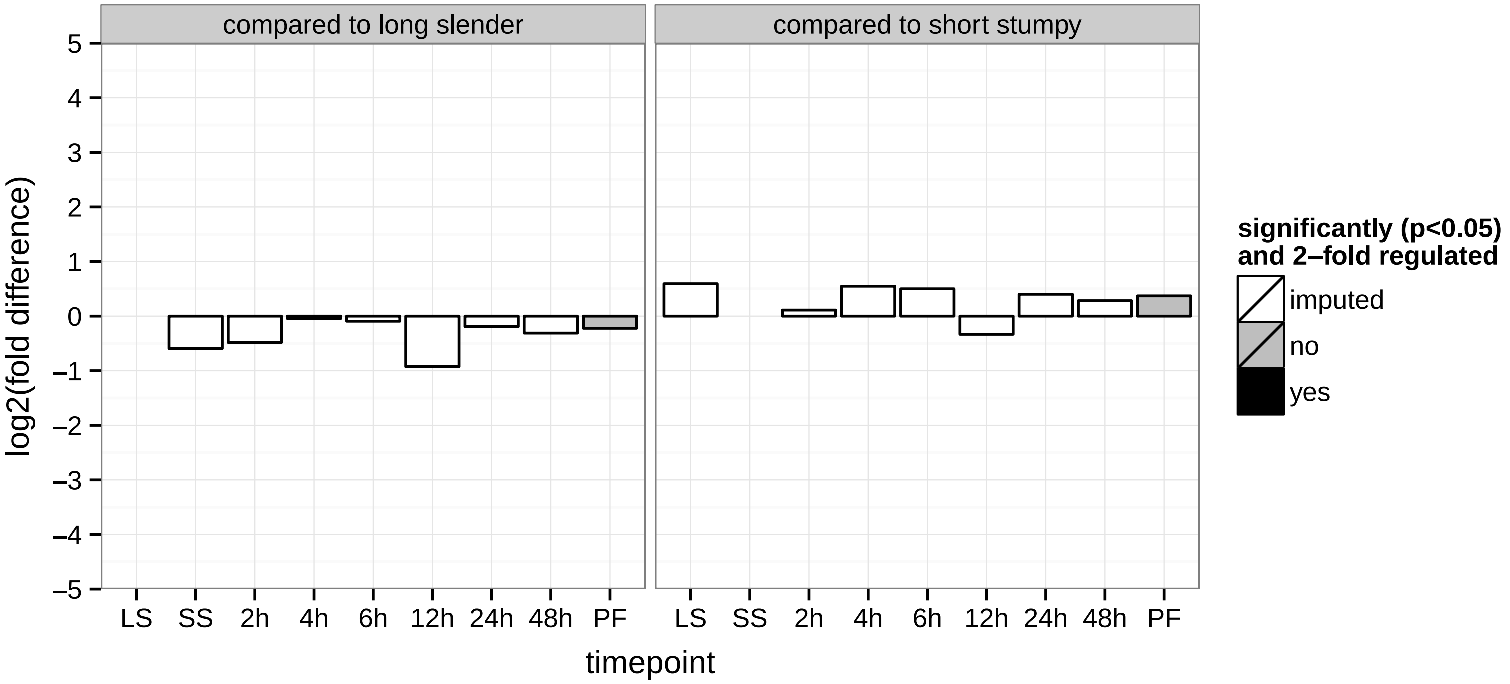
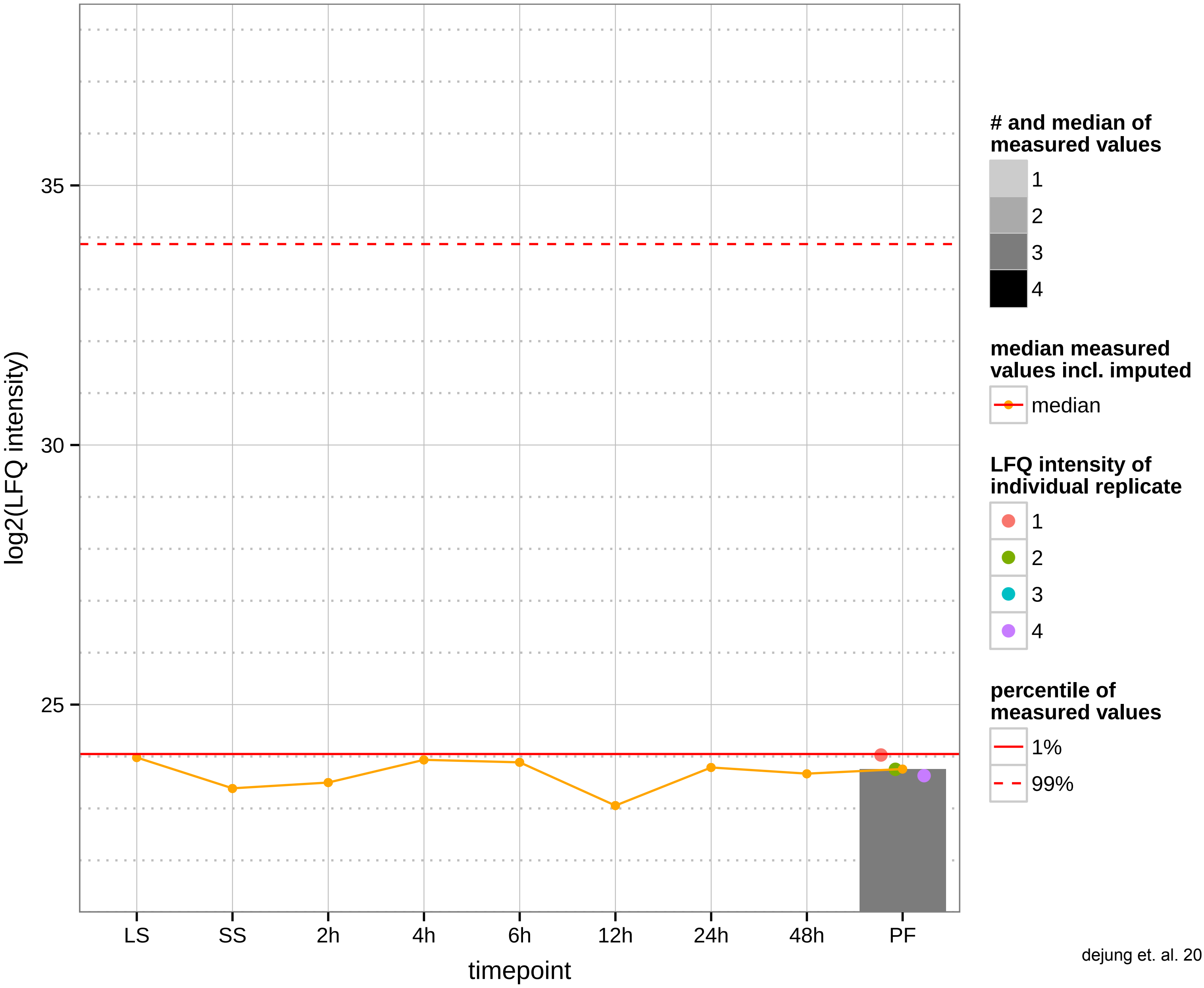
hypothetical protein, conserved
Tb927.9.1950
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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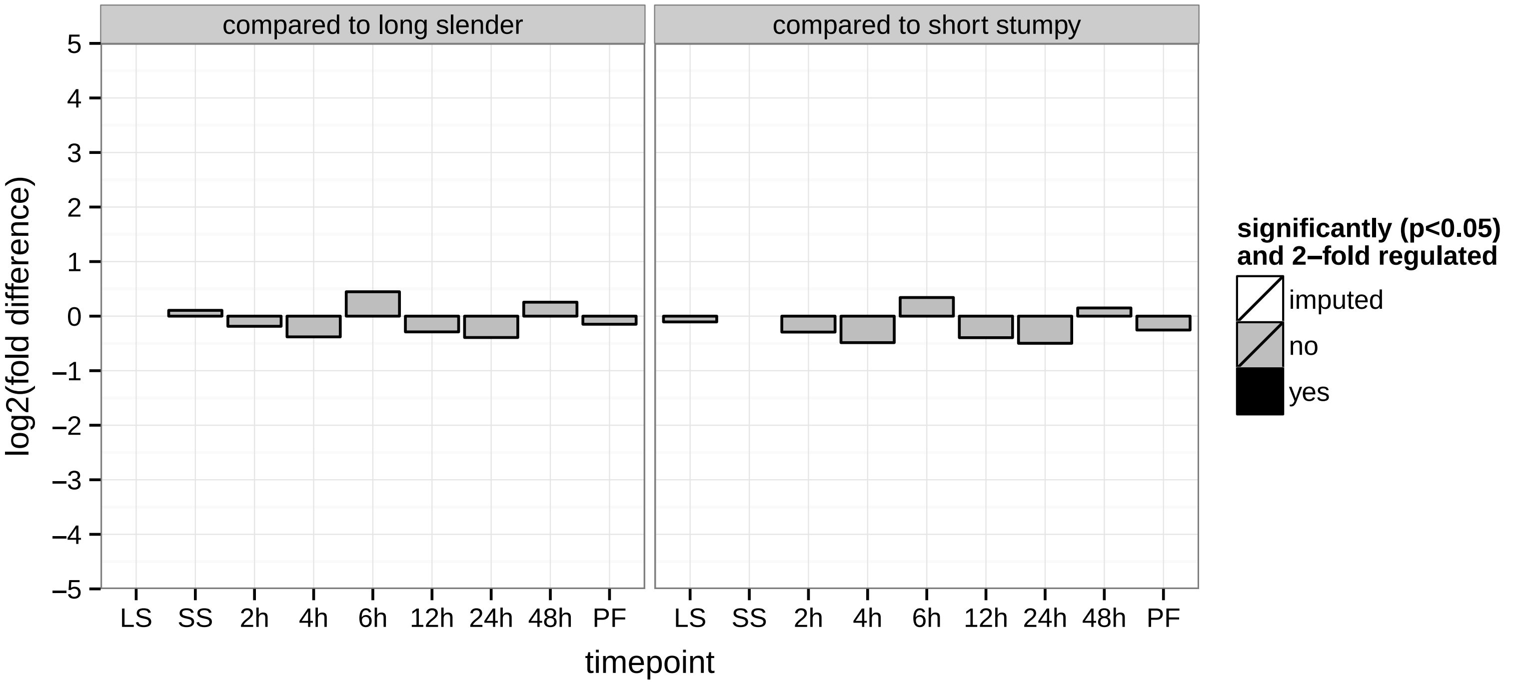
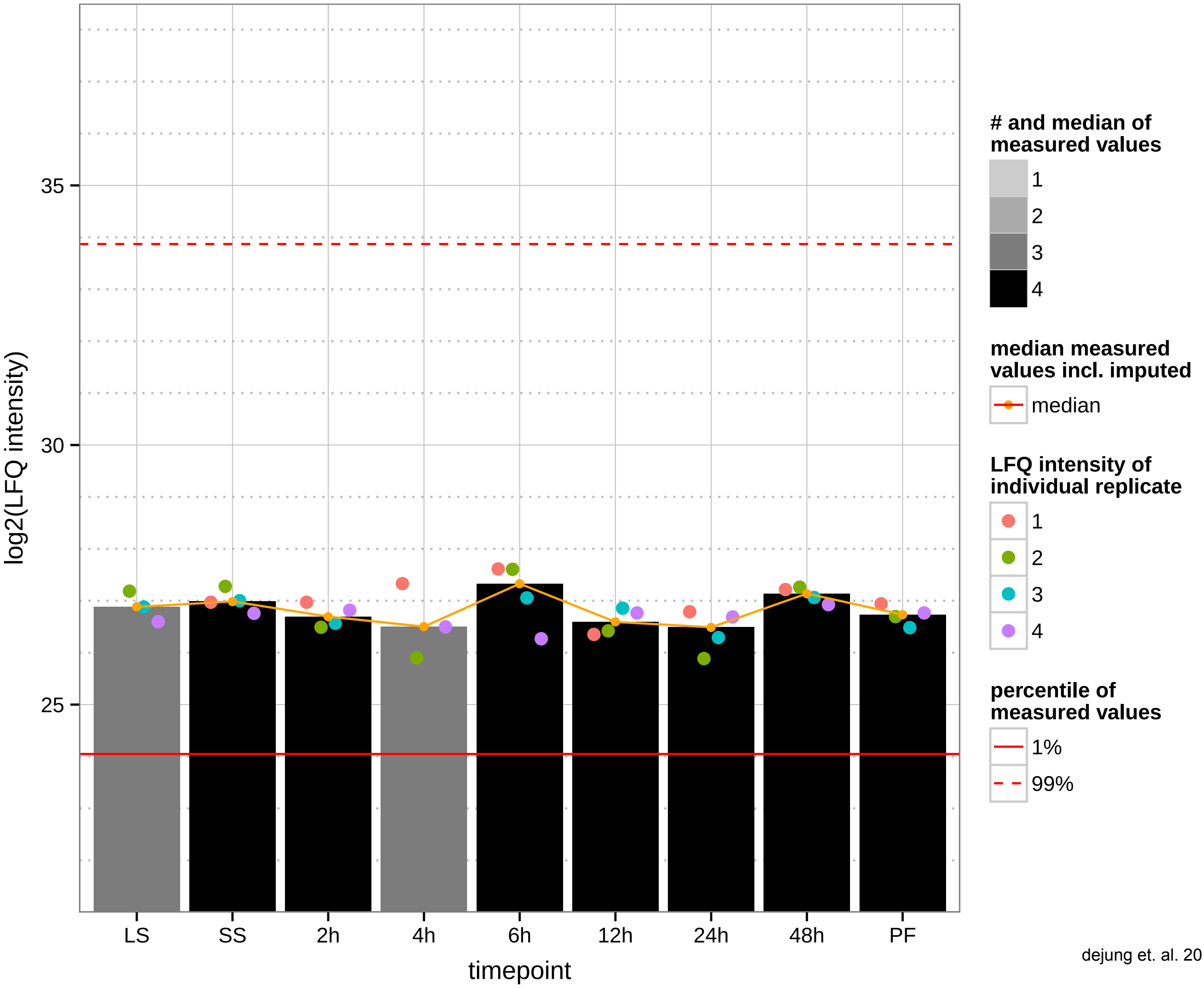
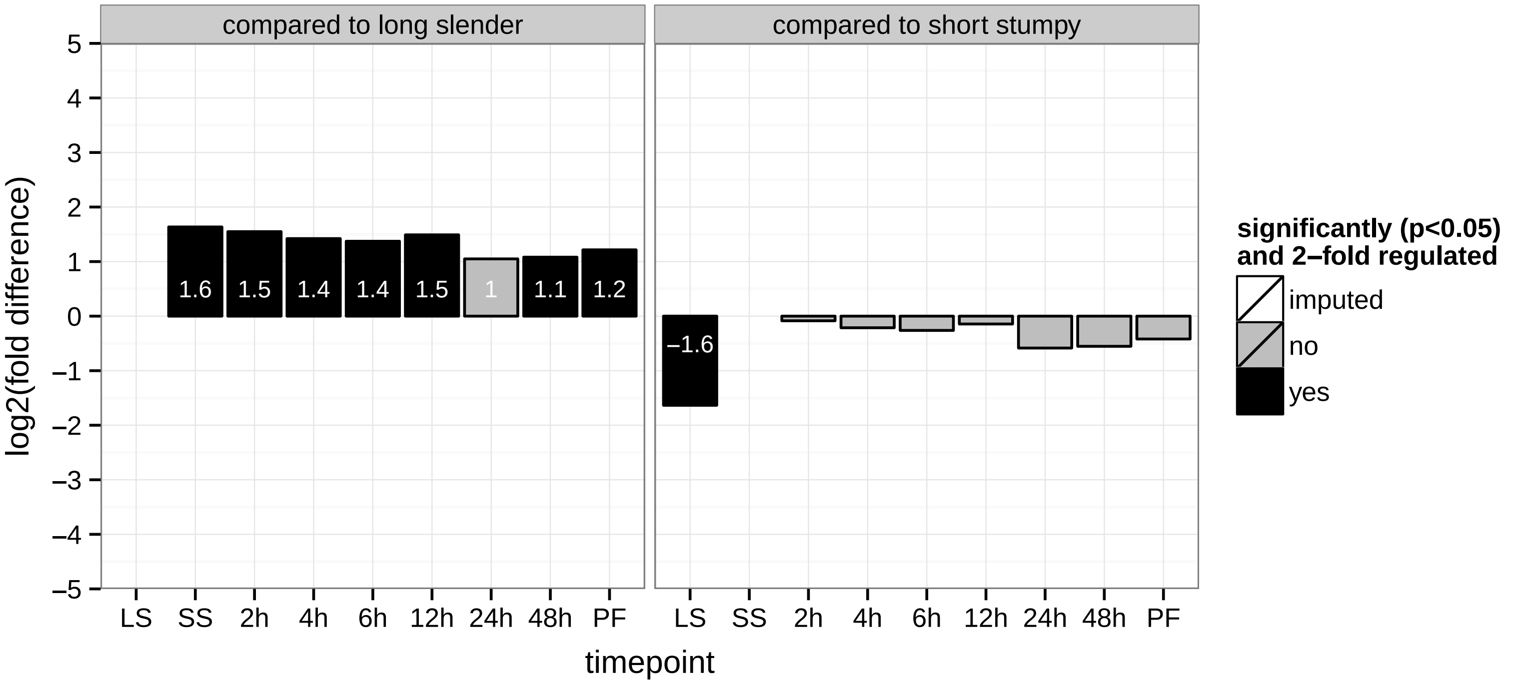
hypothetical protein, conserved
Tb927.9.1980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

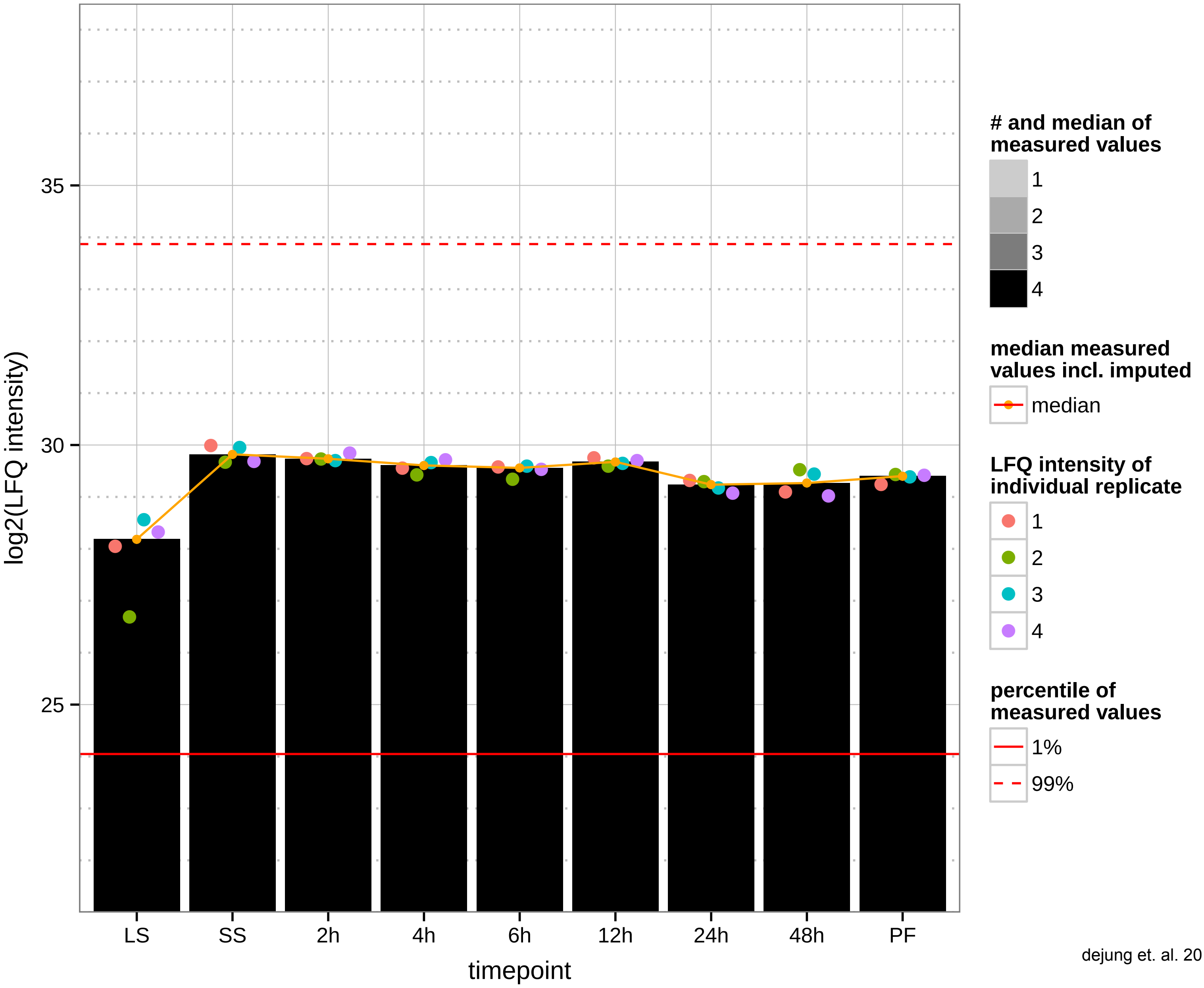




dejung et. al. 2015

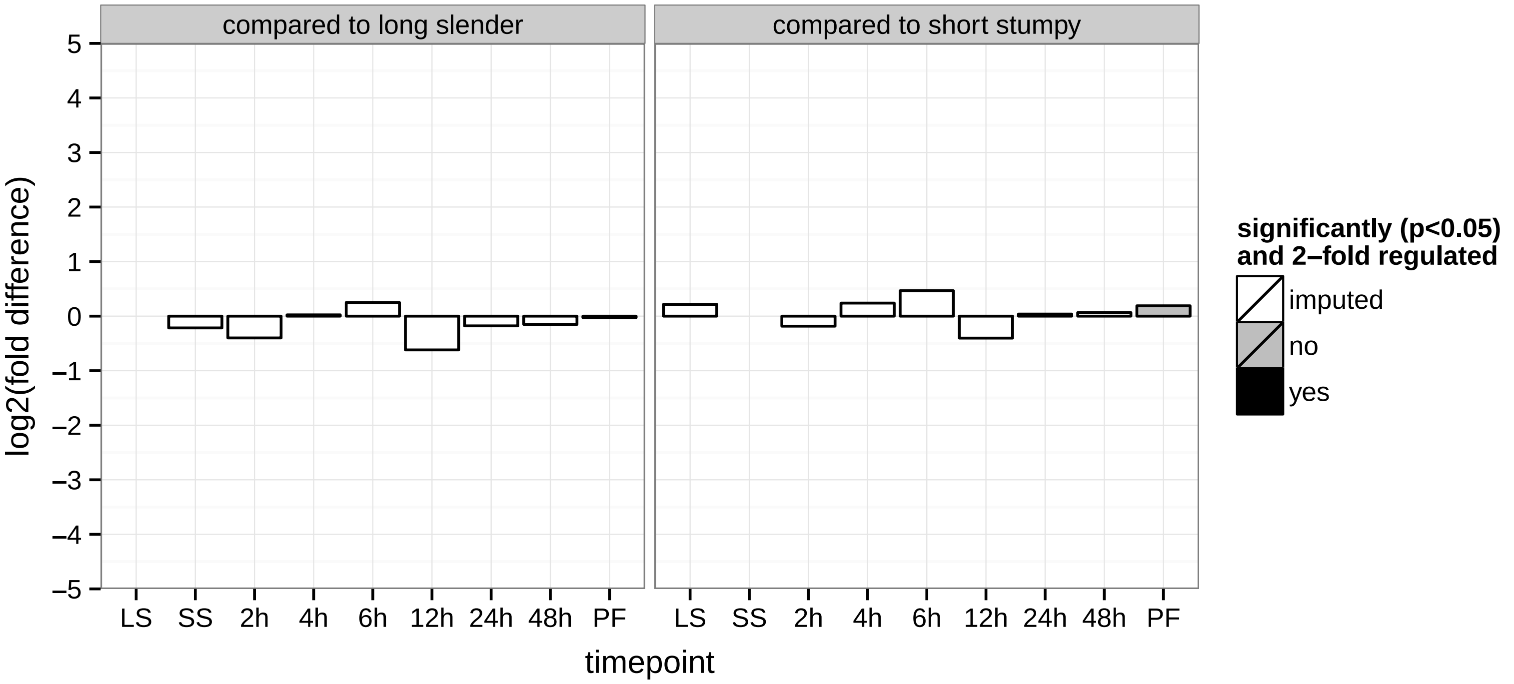
kynureninase, putative
Tb927.9.2010
AGOF: kynureninase activity, pyridoxal phosphate binding
AGOC: cytoplasm
AGOP: NAD biosynthetic process, tryptophan catabolic process
PGOF: kynureninase activity, pyridoxal phosphate binding
PGOC: cytoplasm
PGOP: NAD biosynthetic process, metabolic process, tryptophan catabolic process

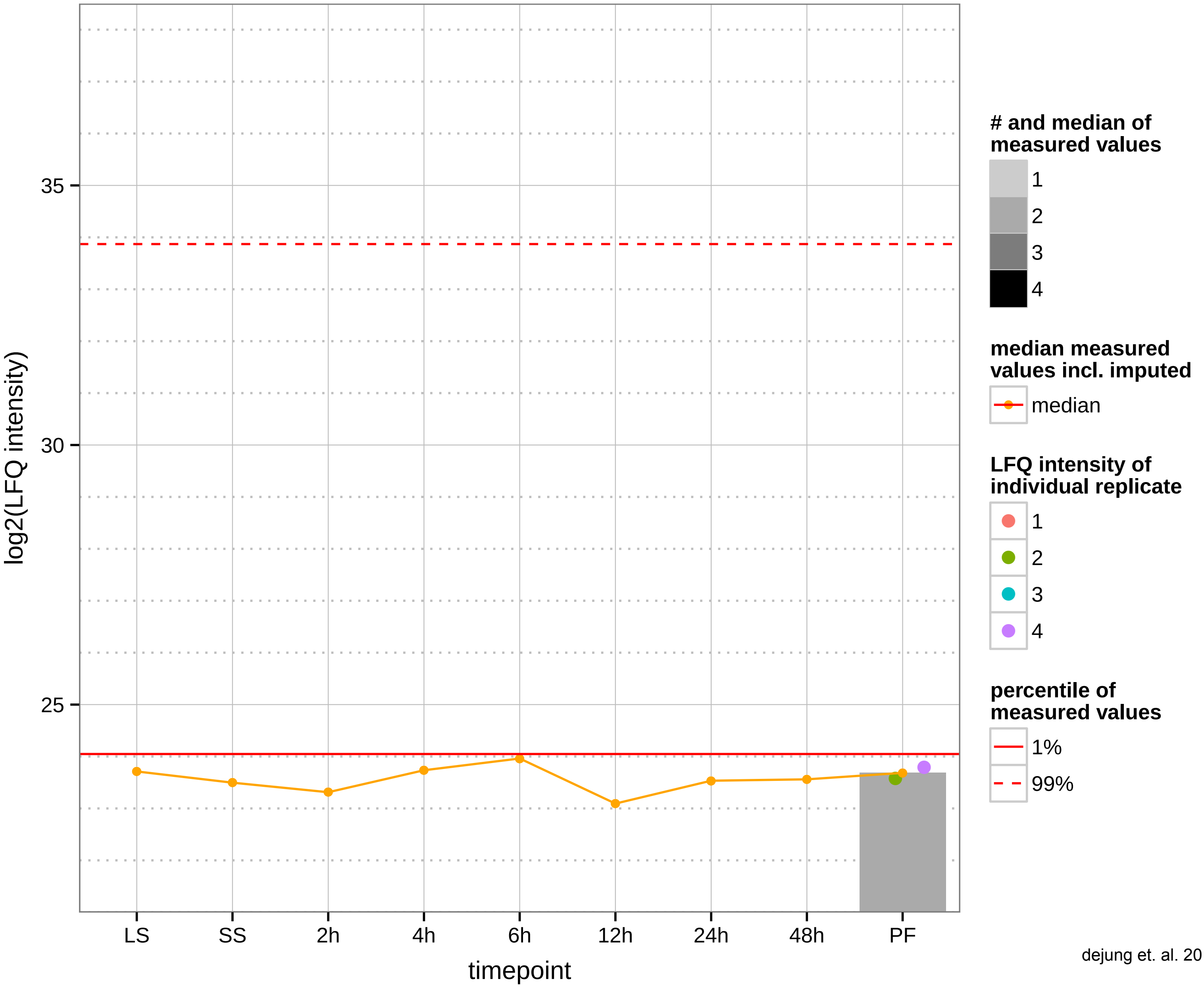




dejung et. al. 2015

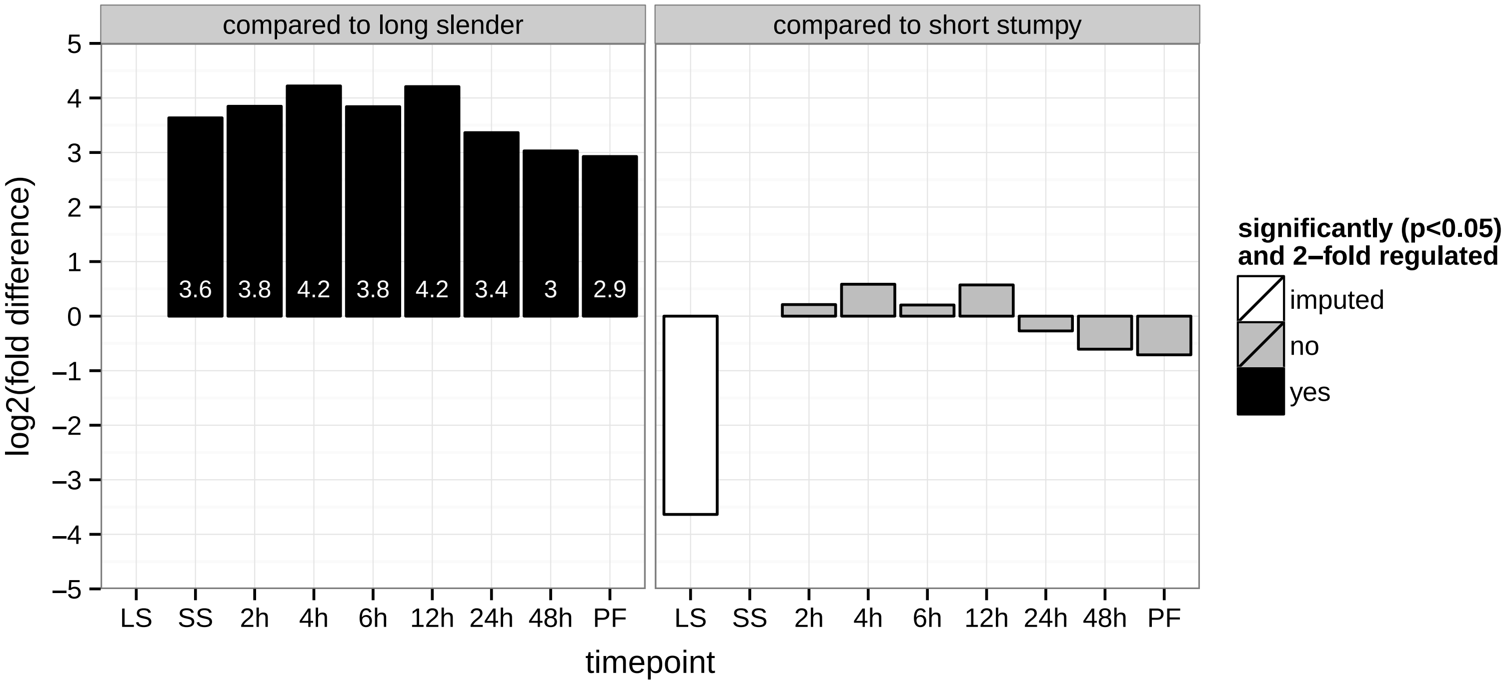
hypothetical protein, conserved
Tb927.9.2130
AGOF: null
AGOC: null
AGOP: null
PGOF: transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: null

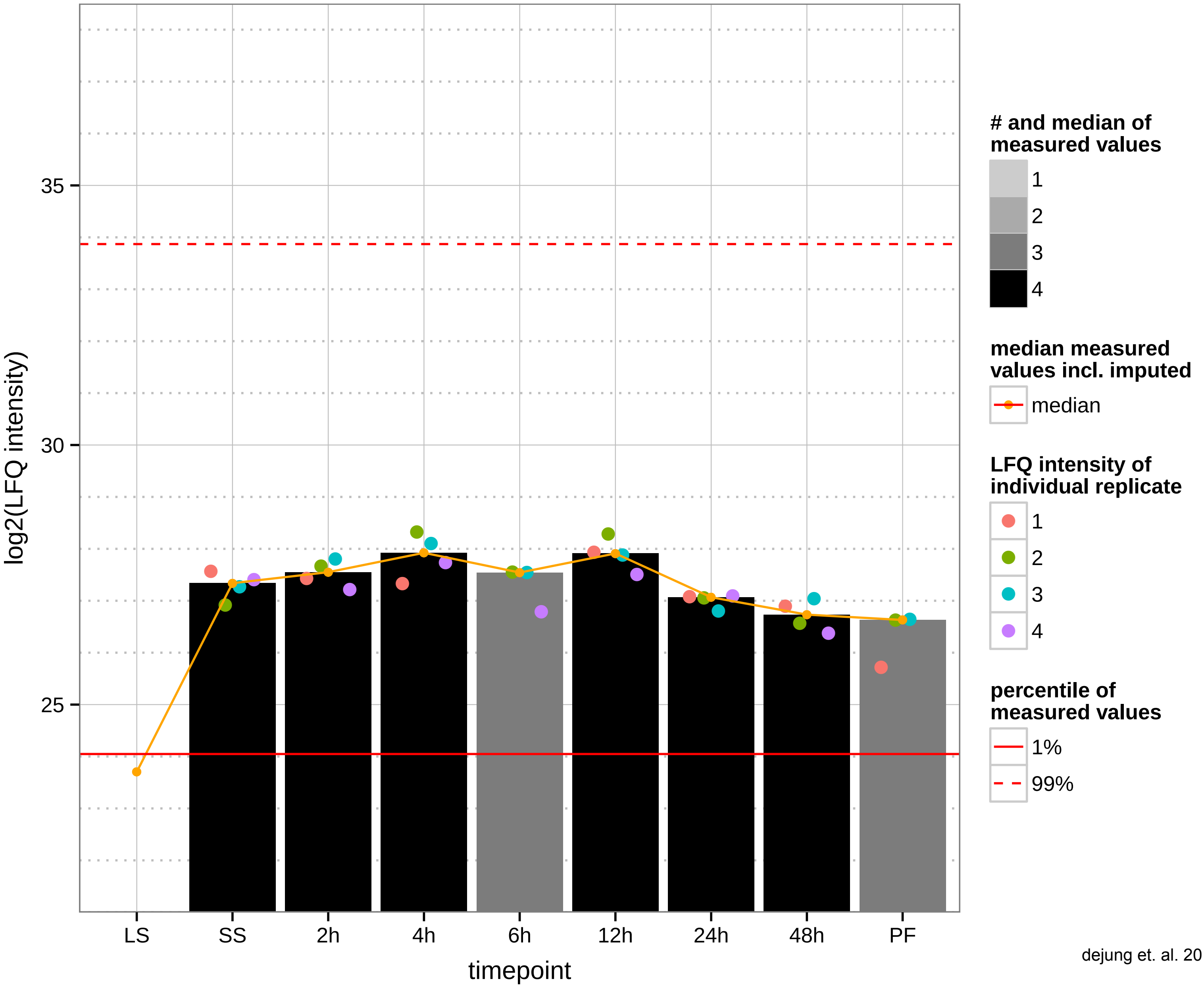




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.2420
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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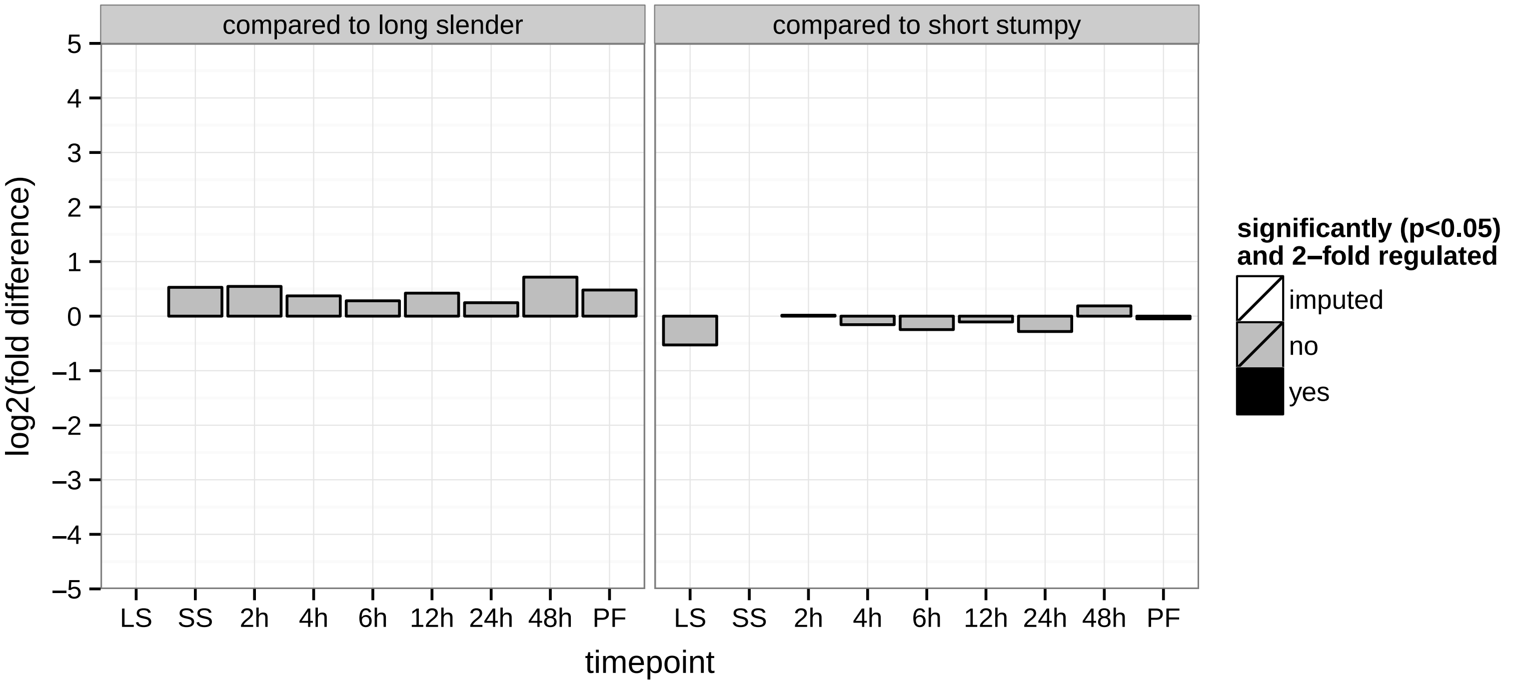
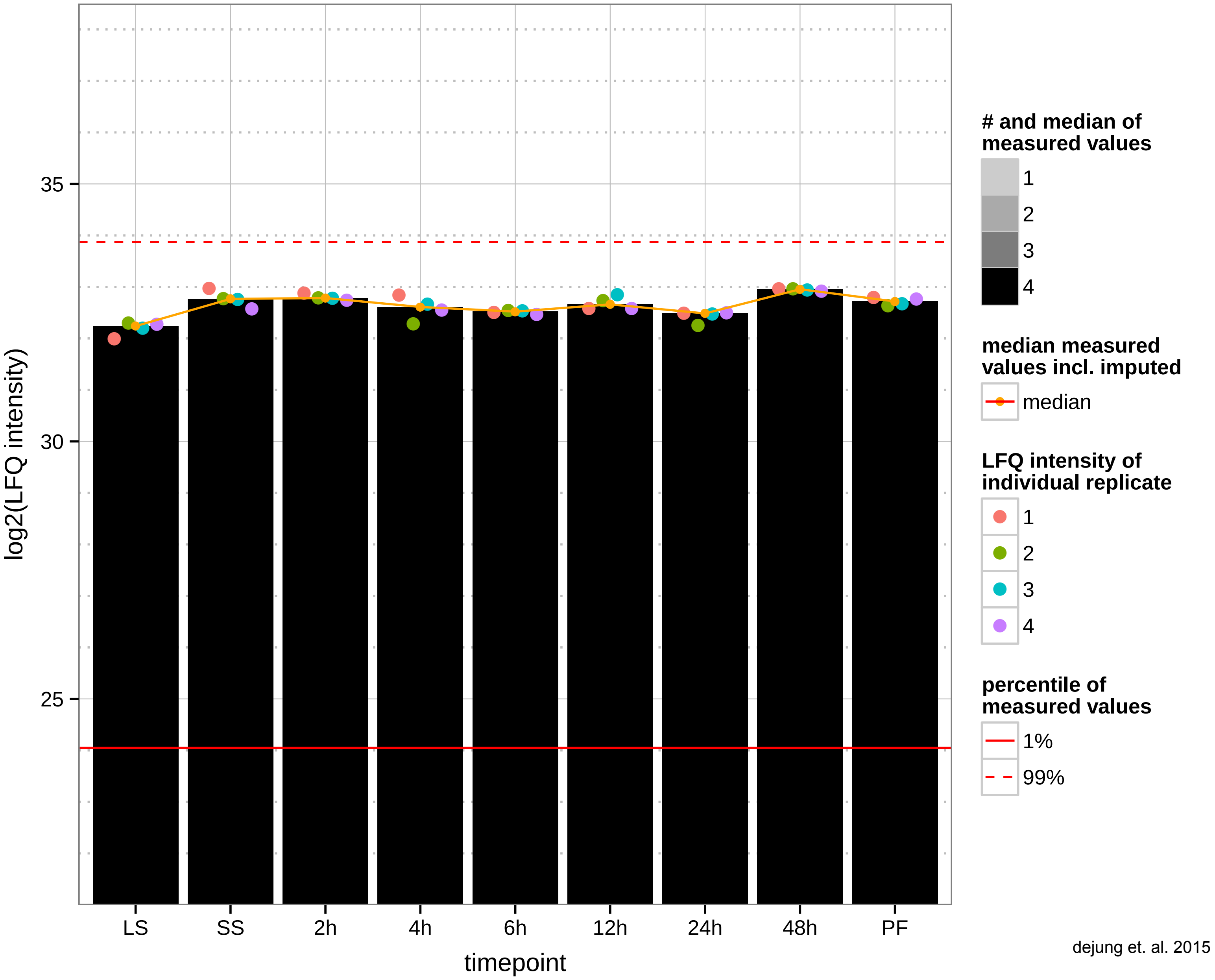
nucleolar protein (NOP86)
Tb927.9.2470
AGOF: null
AGOC: nucleolus
AGOP: G2/M transition of mitotic cell cycle
PGOF: null
PGOC: null
PGOP: null





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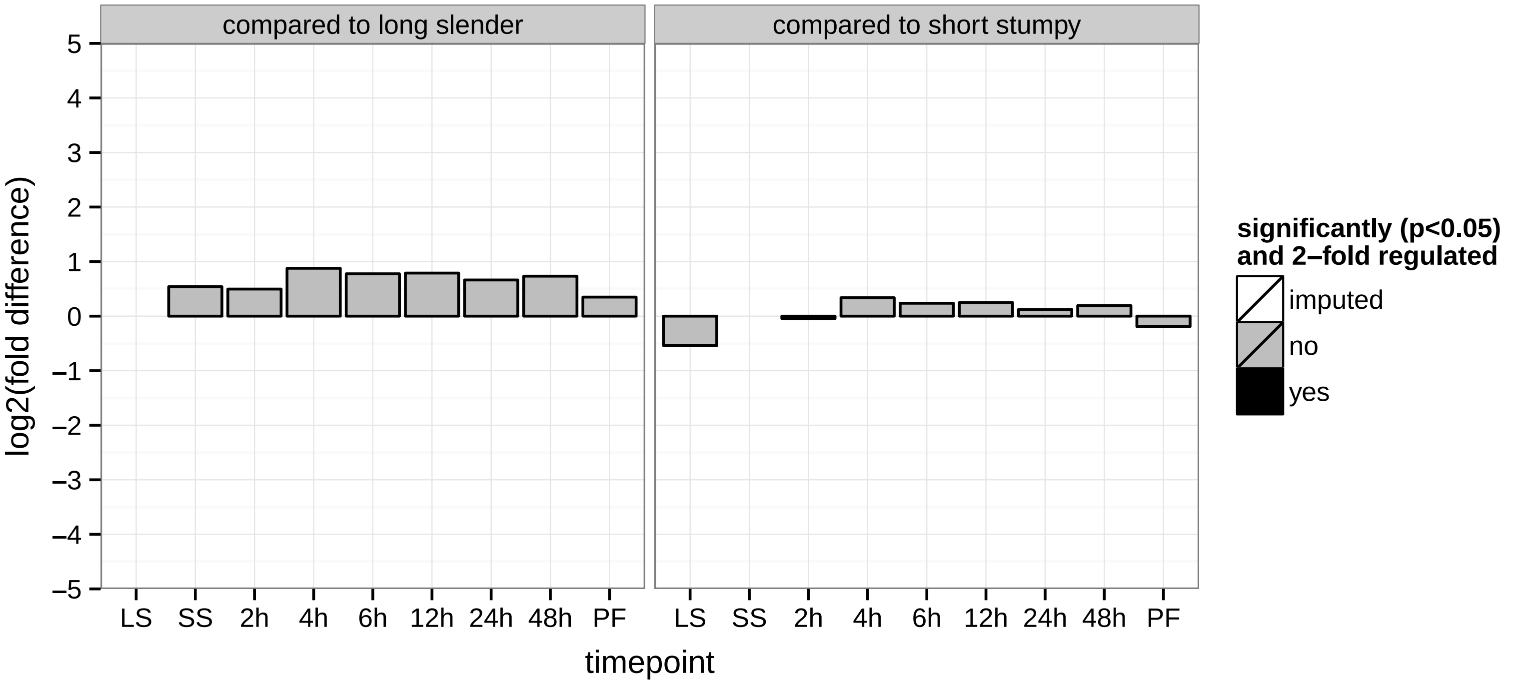
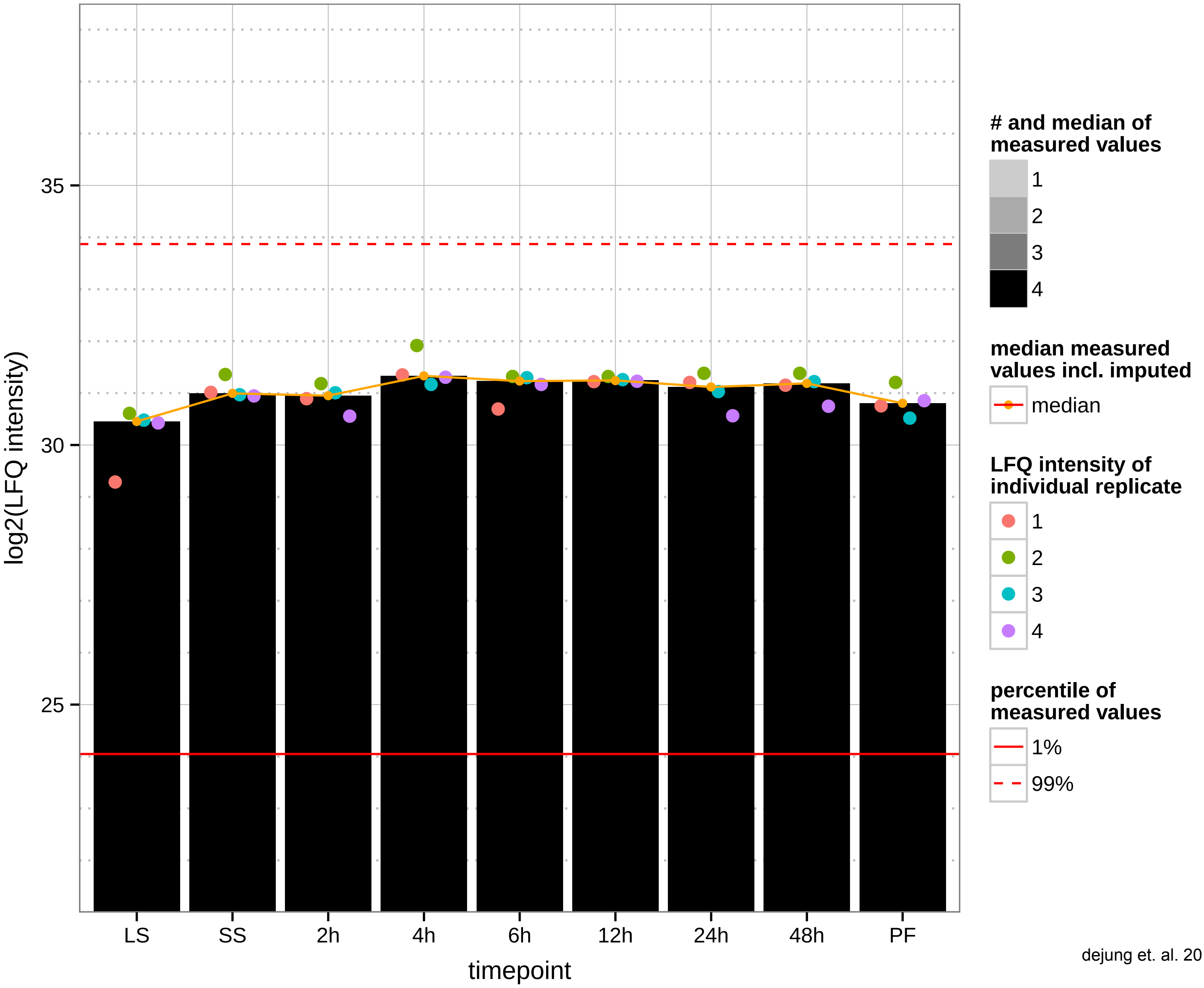
mitotubule–associated protein Gb4, putative, microtubule–associated protein (GB4)
Tb927.9.2520;Tb11.v5.0868
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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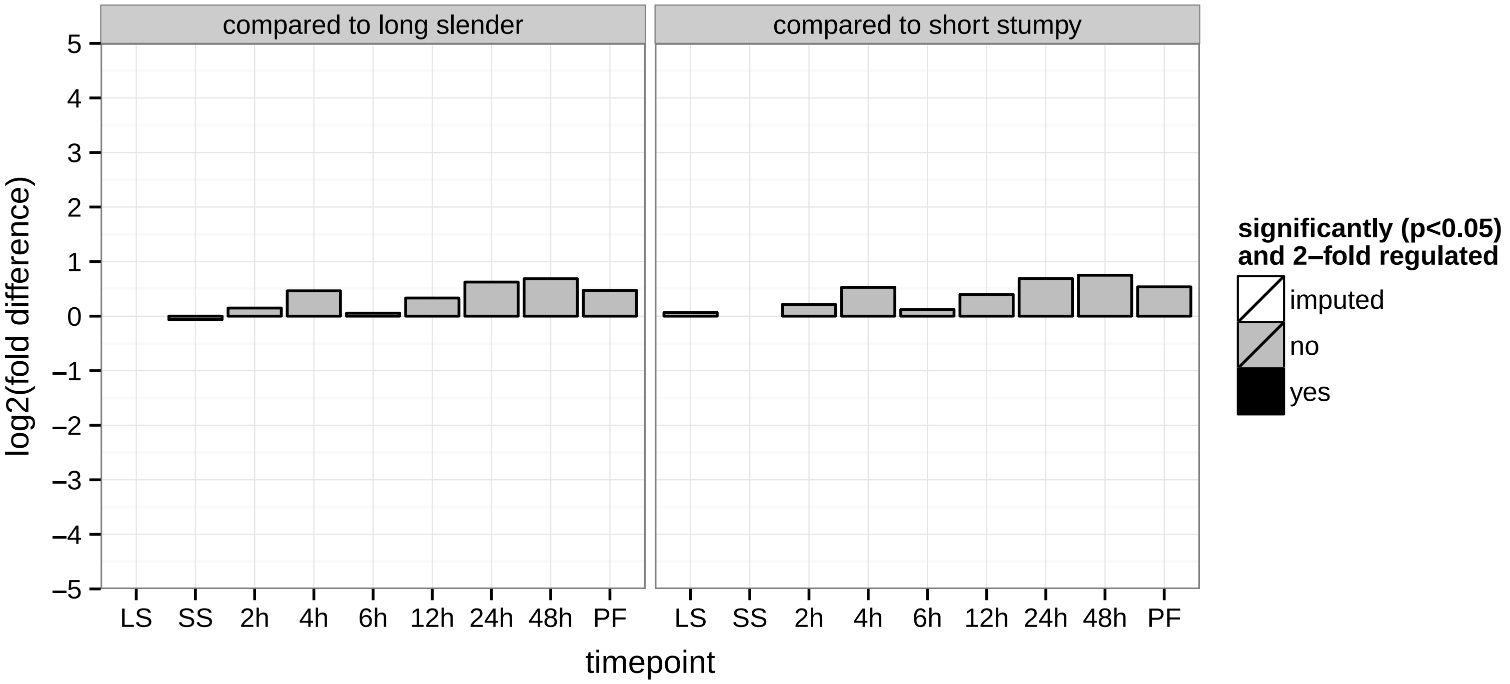
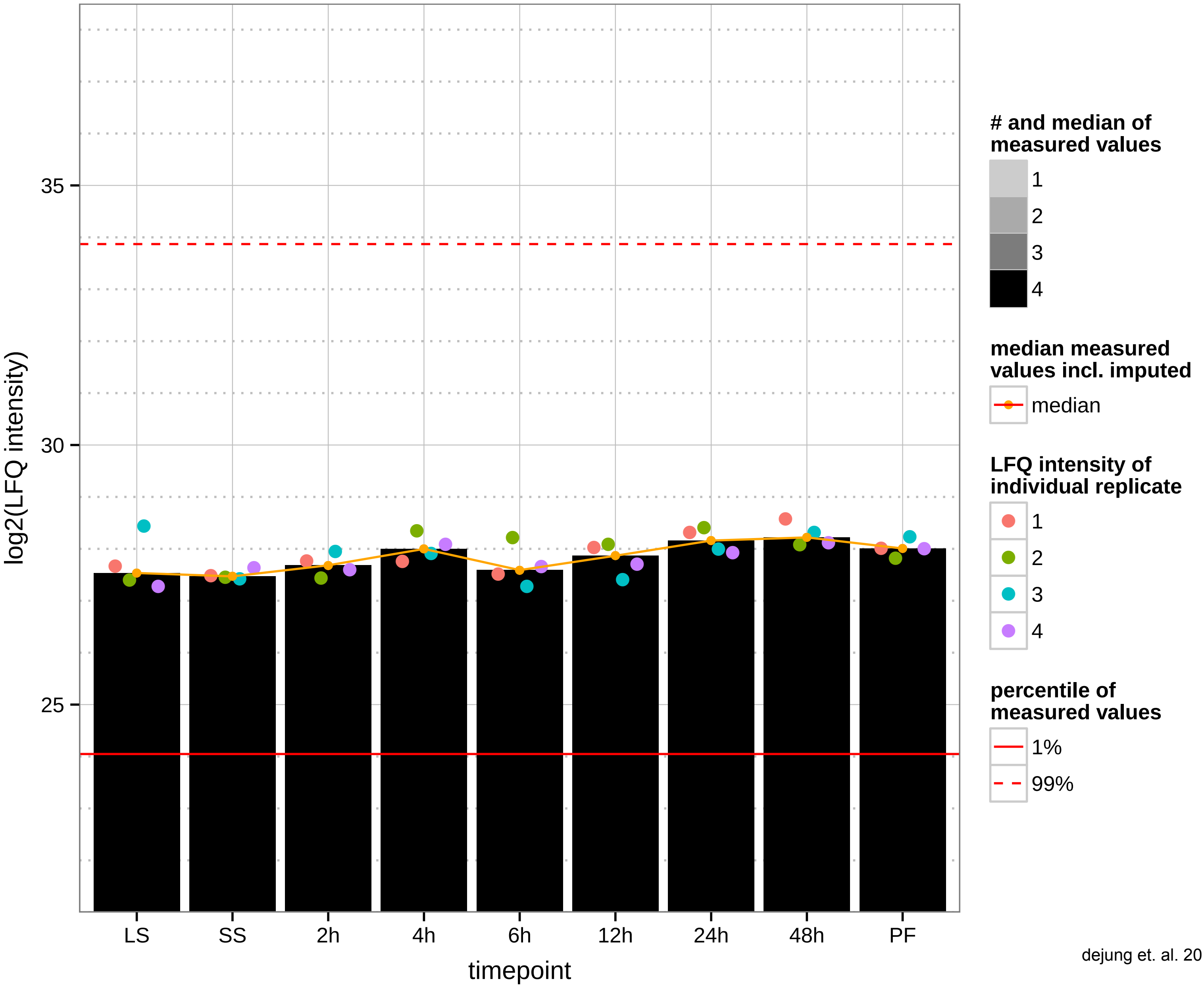
deoxyhypusine hydroxylase, putative
Tb927.9.2580
AGOF: deoxyhypusine monooxygenase activity
AGOC: null
AGOP: peptidyl–lysine modification to hypusine
PGOF: binding
PGOC: null
PGOP: null





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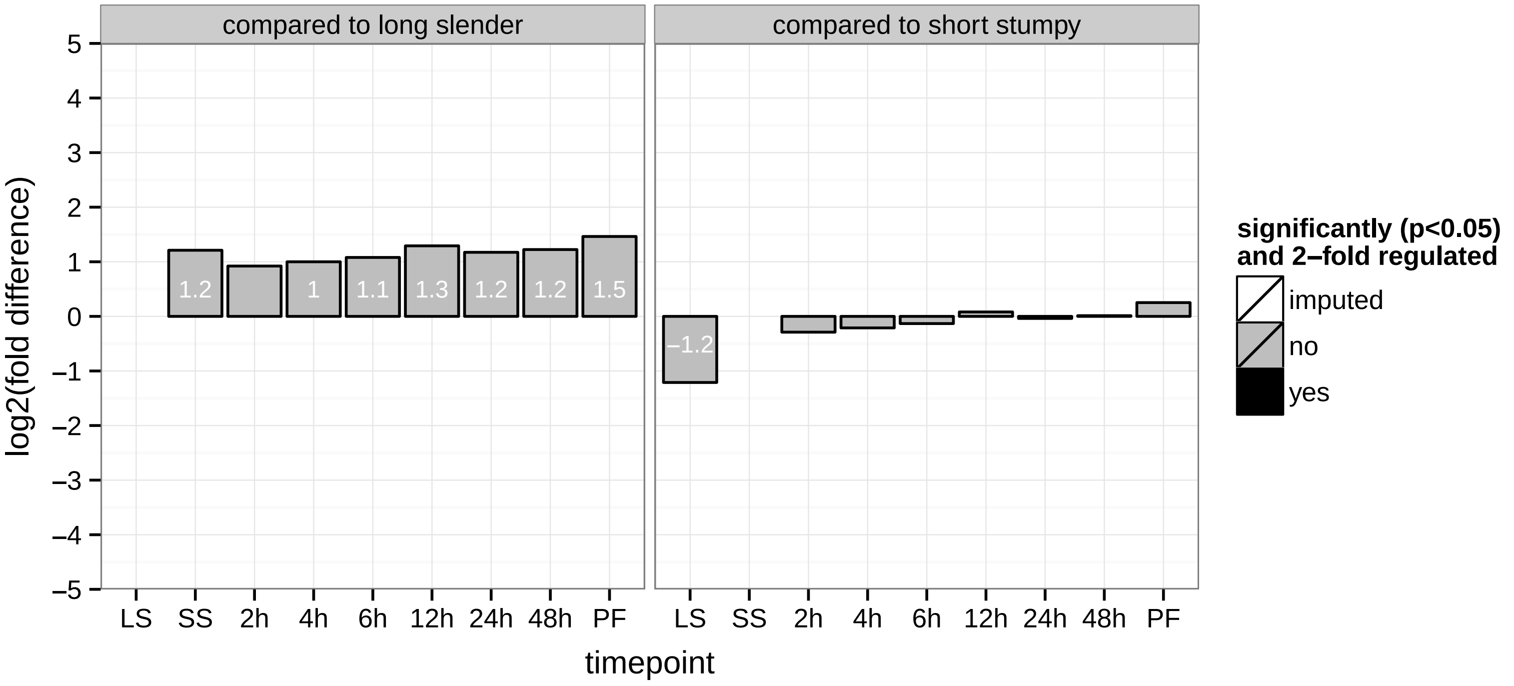
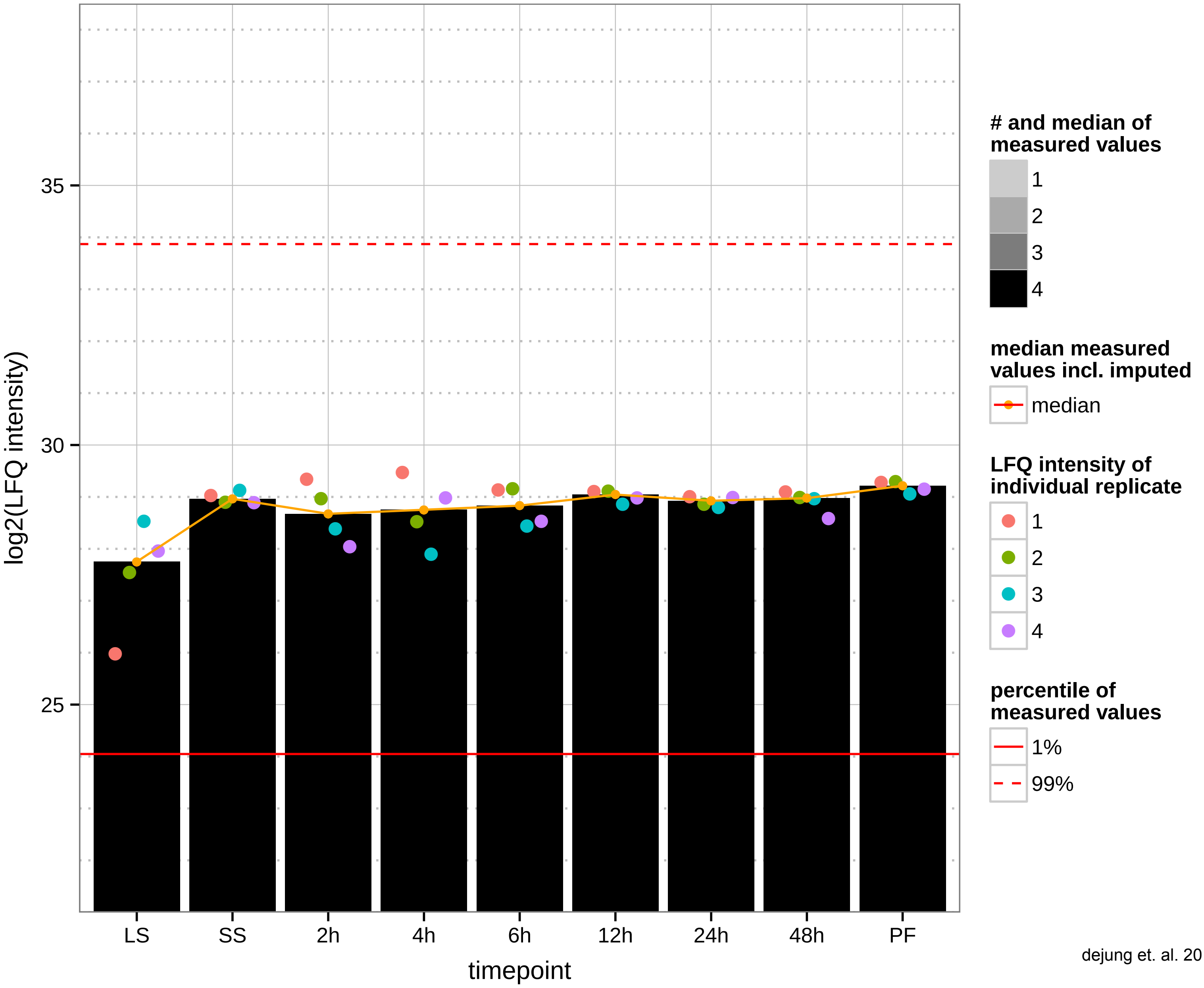
hypothetical protein, conserved
Tb927.9.2590
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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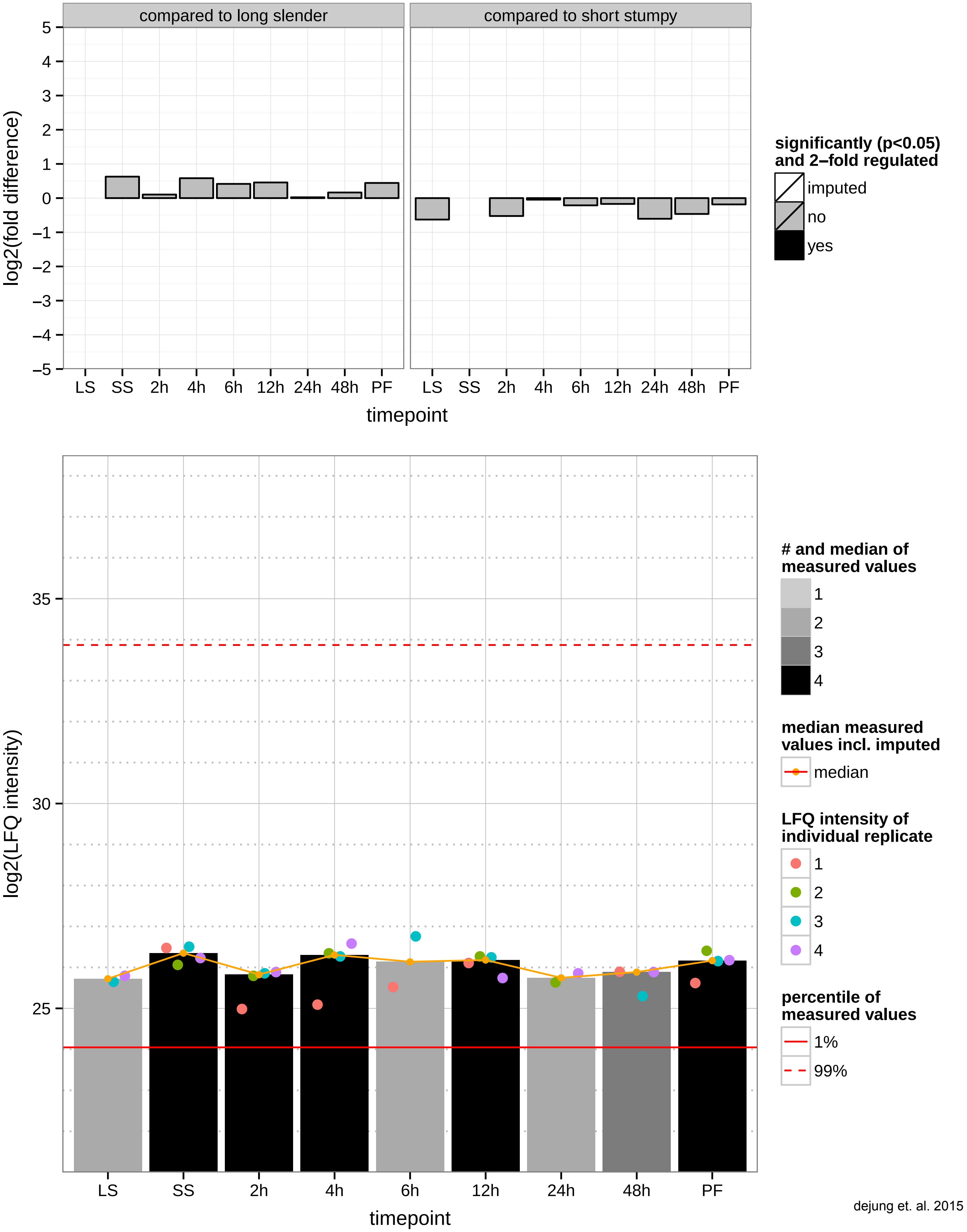
hypothetical protein, conserved
Tb927.9.2600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: intracellular
PGOP: ER to Golgi vesicle–mediated transport



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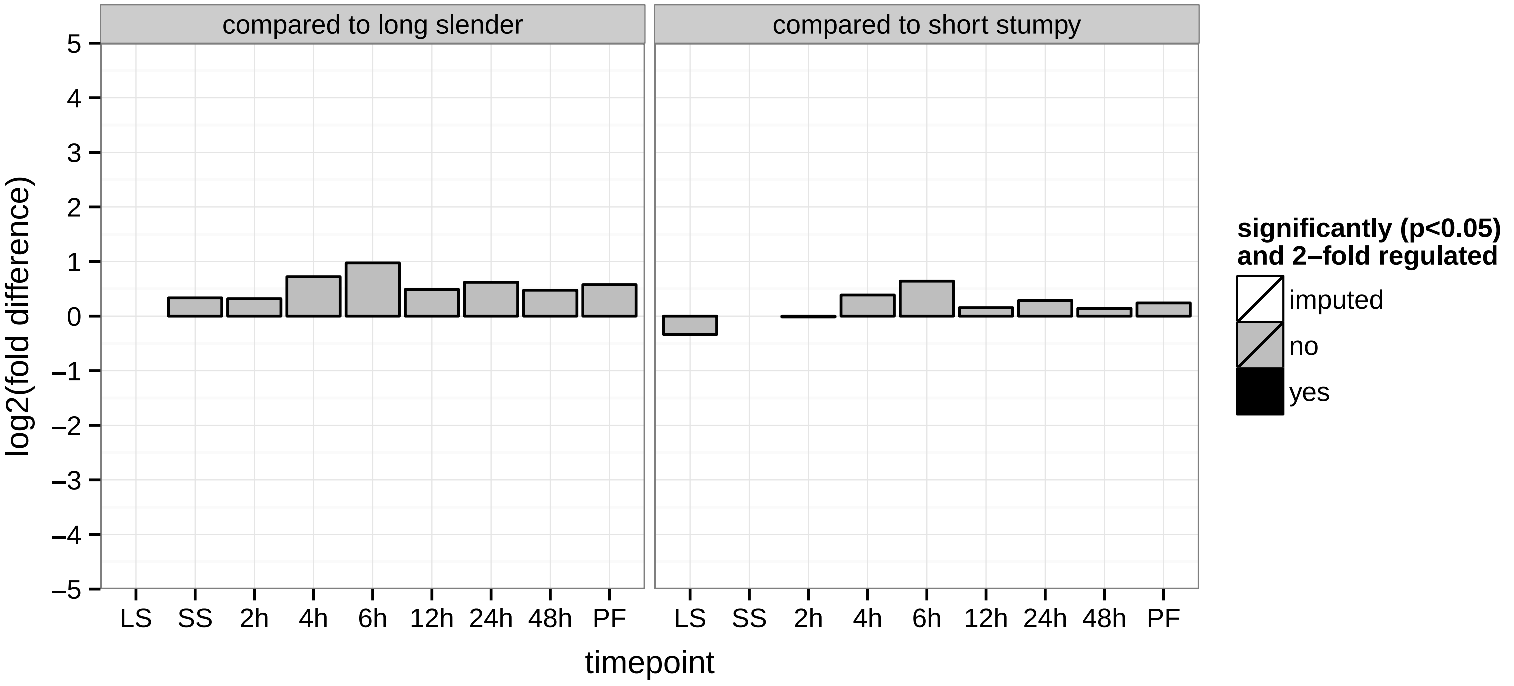
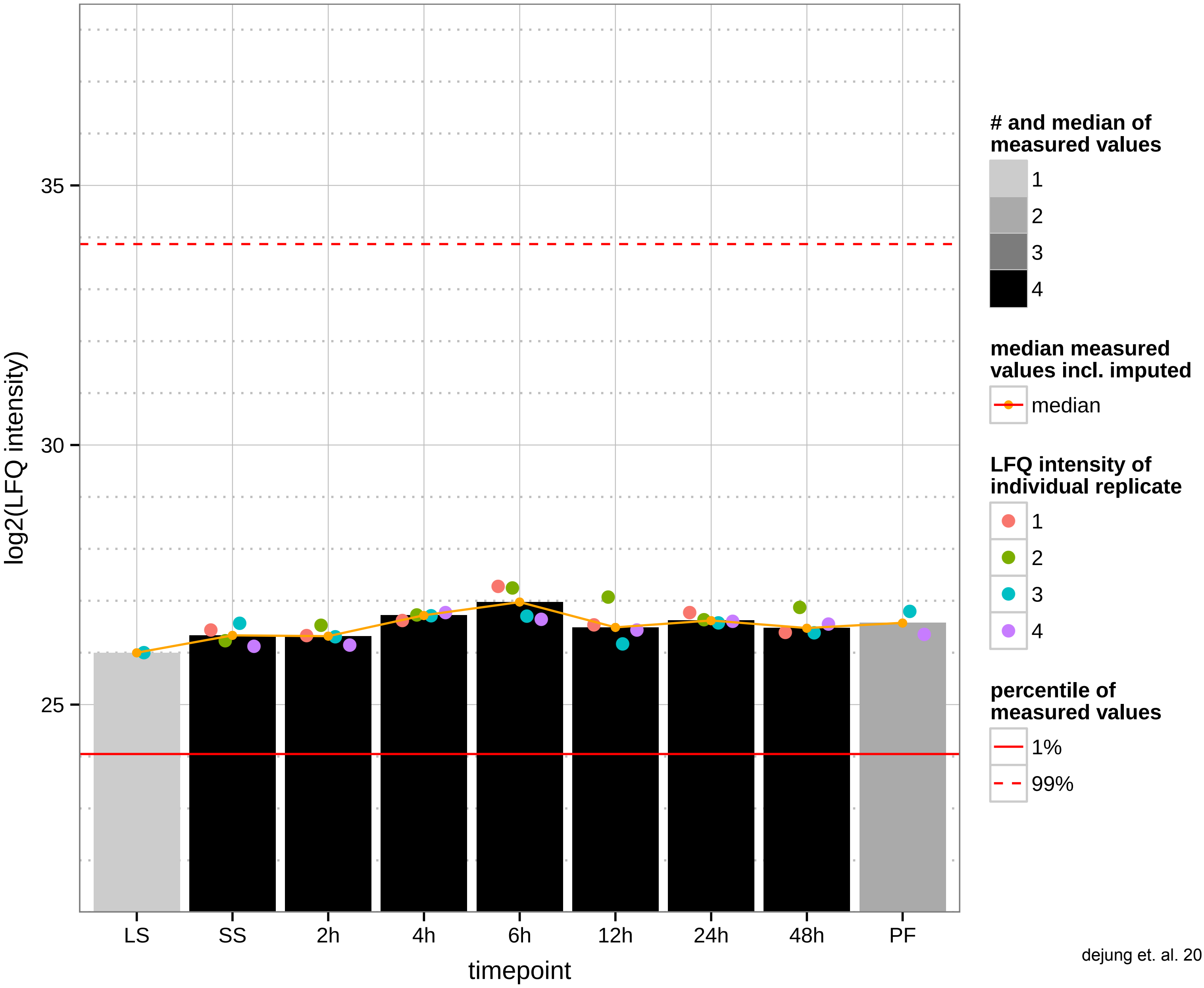
hypothetical protein, conserved
Tb927.9.2650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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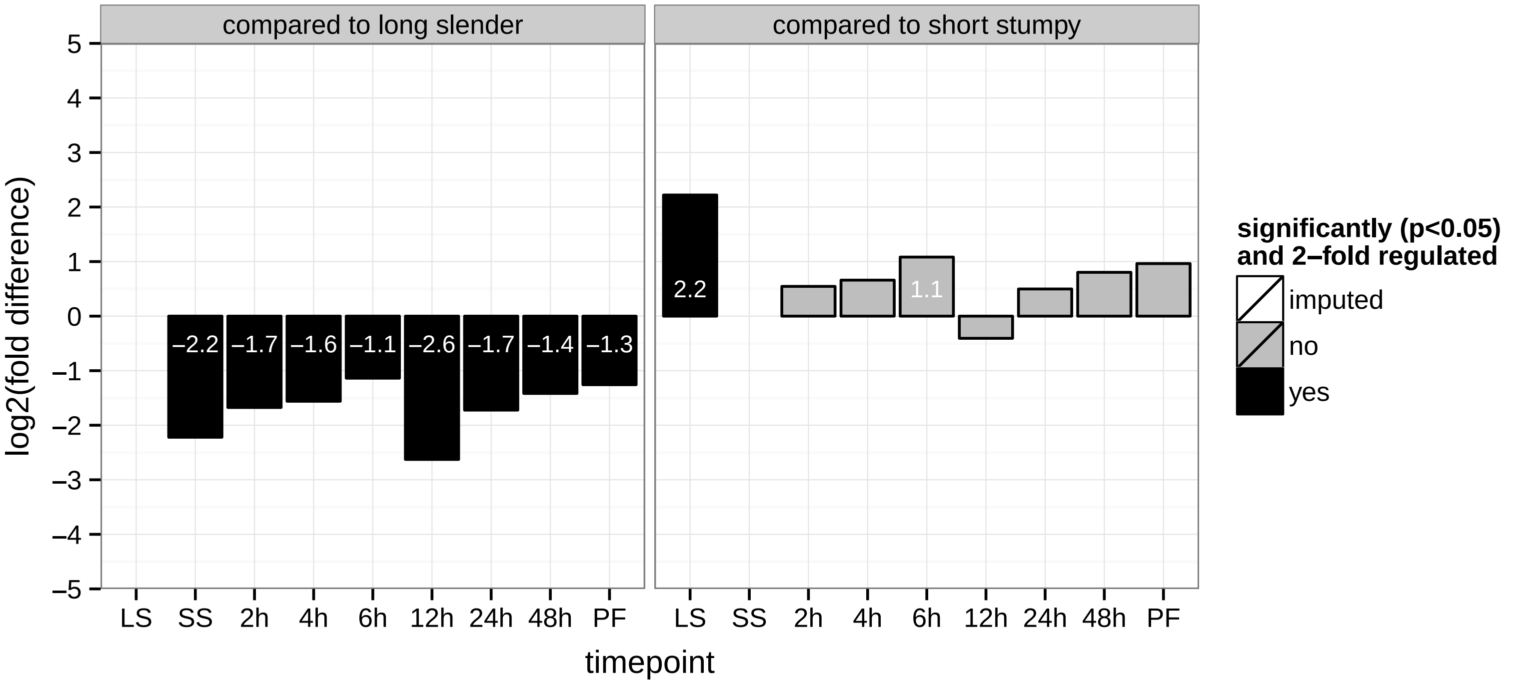
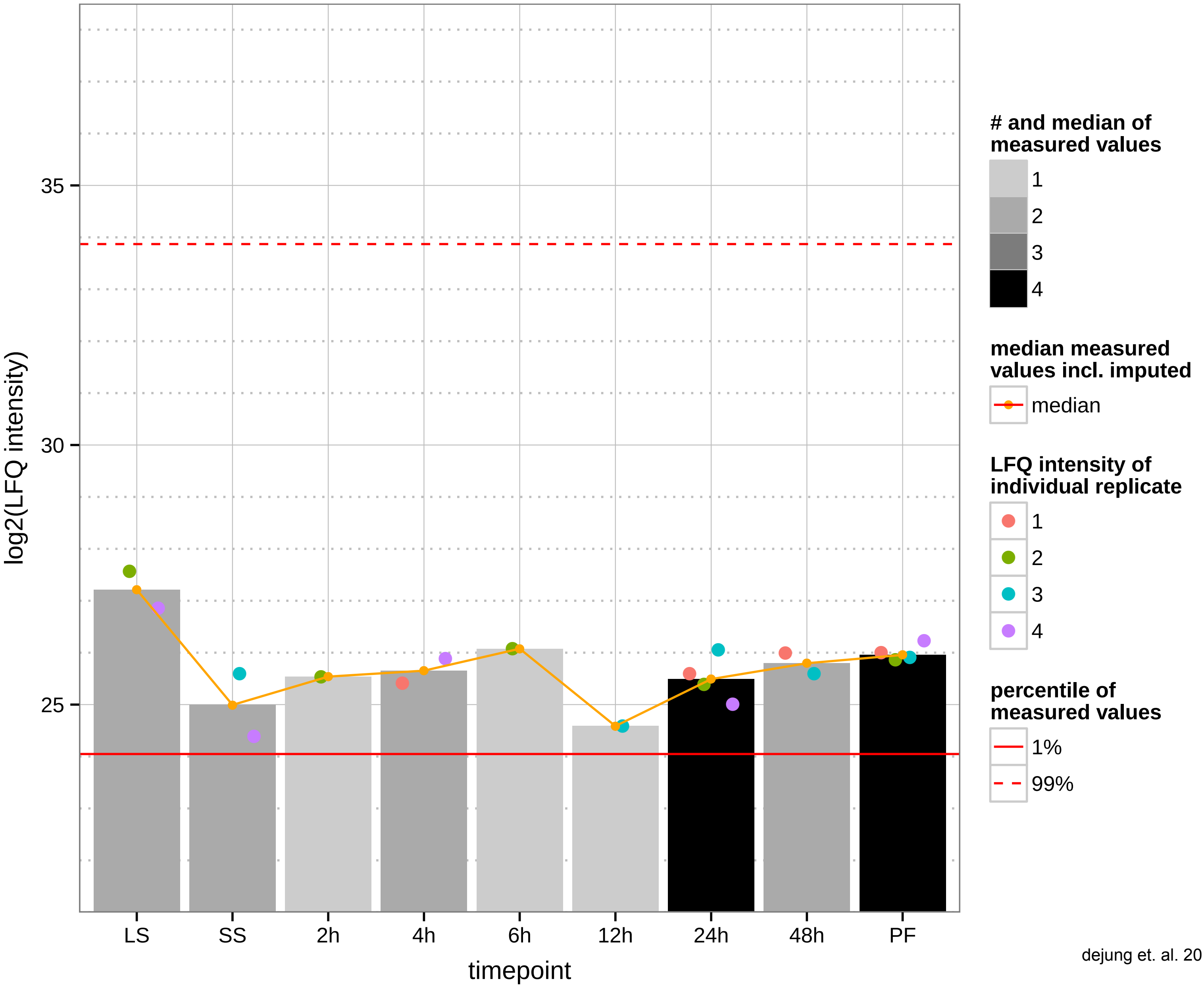
hypothetical protein, conserved
Tb927.9.2980
AGOF: null
AGOC: null
AGOP: null
PGOF: cAMP−dependent protein kinase regulator activity
PGOC: null
PGOP: signal transduction





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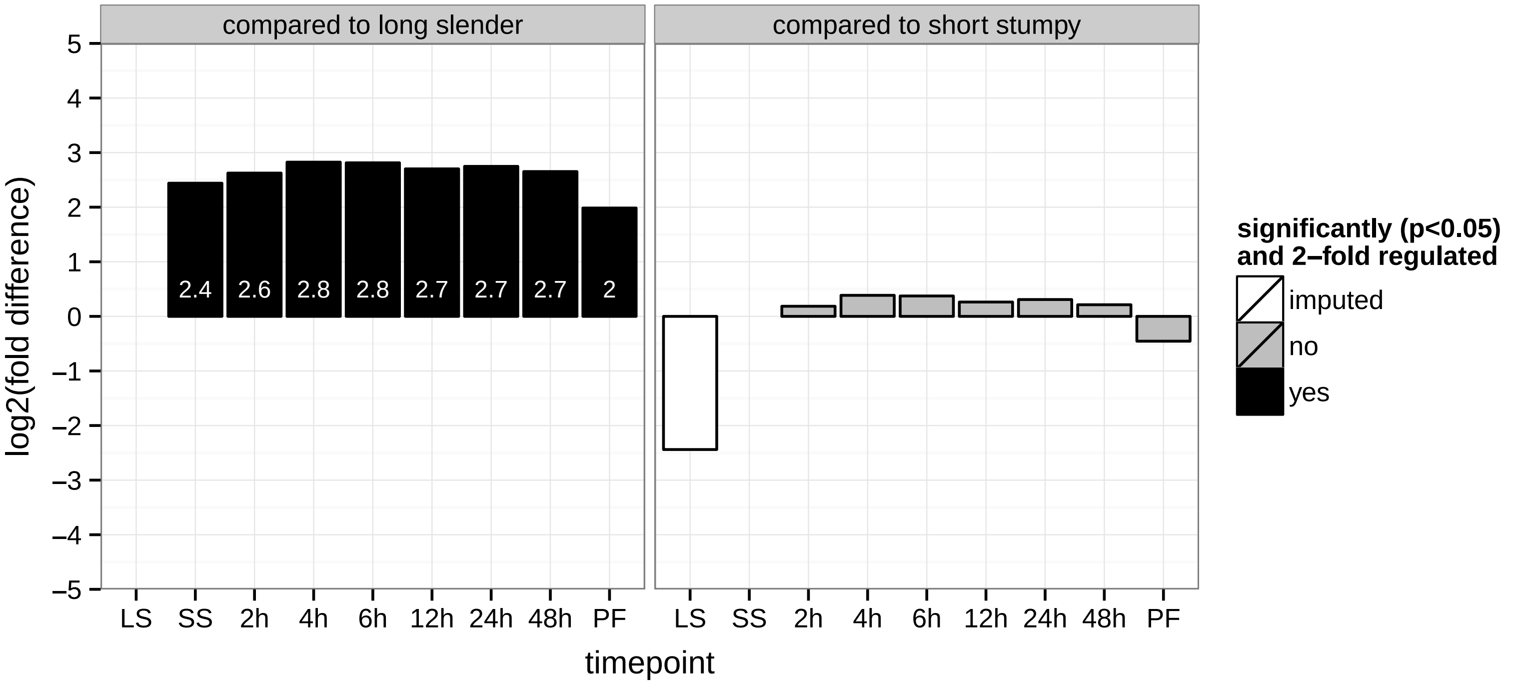
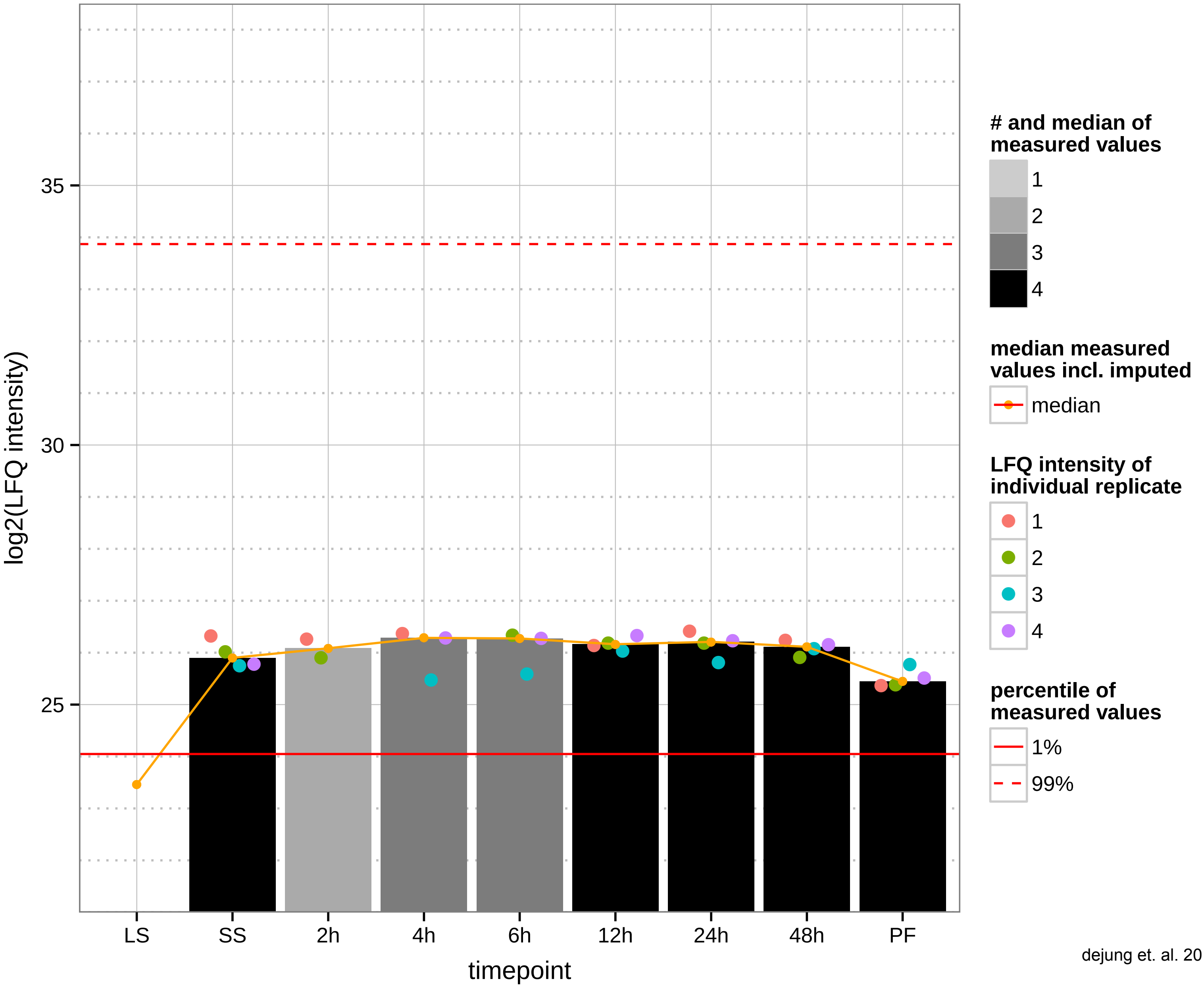
cytidine deaminase, putative
Tb927.9.3000
AGOF: cytidine deaminase activity, hydrolase activity, zinc ion binding
AGOC: null
AGOP: cytidine metabolic process
PGOF: catalytic activity, hydrolase activity, zinc ion binding
PGOC: null
PGOP: null





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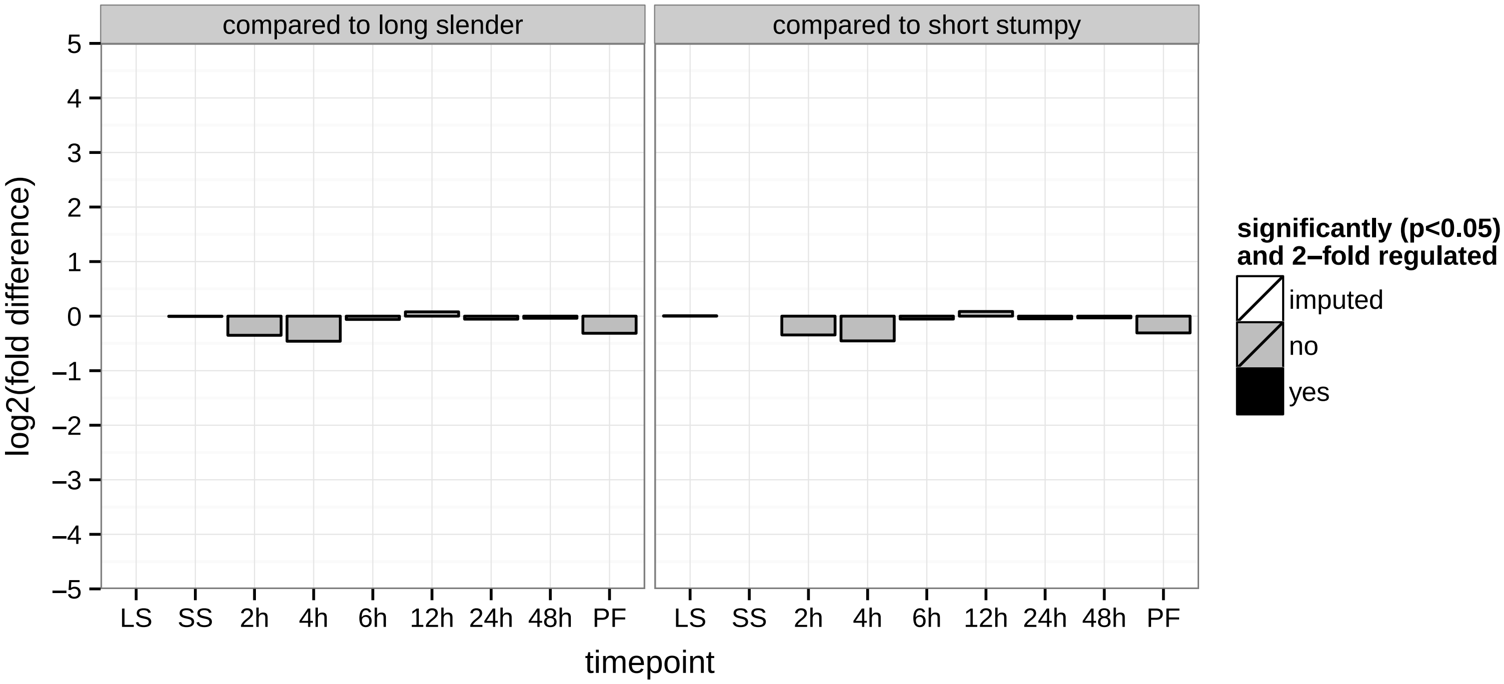
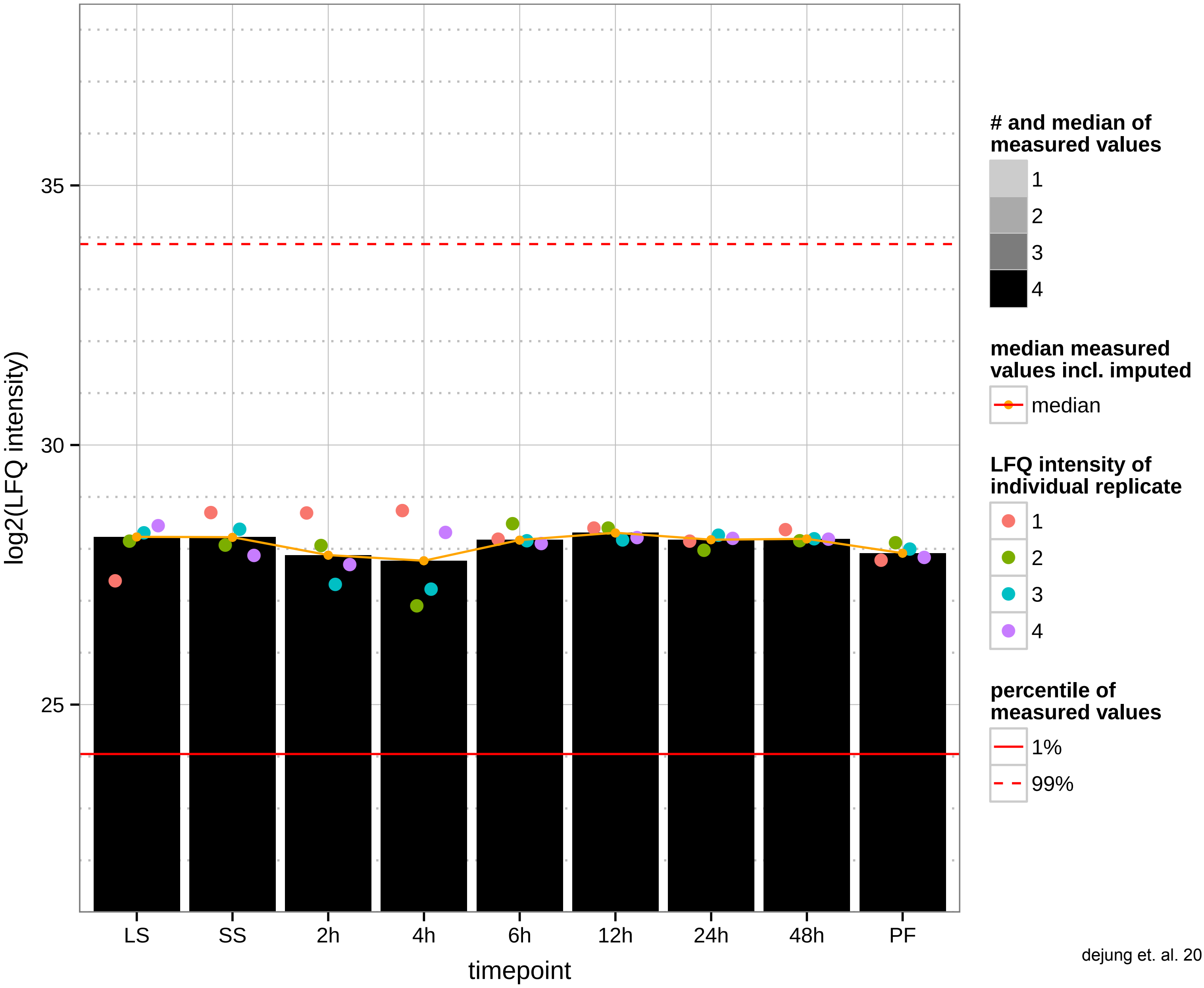
acidocalcisomal exopolyphosphatase
Tb927.9.3280
AGOF: exopolyphosphatase activity, manganese ion binding
AGOC: cytoplasm
AGOP: polyphosphate metabolic process
PGOF: hydrolase activity, manganese ion binding, pyrophosphatase activity
PGOC: cytoplasm
PGOP: null





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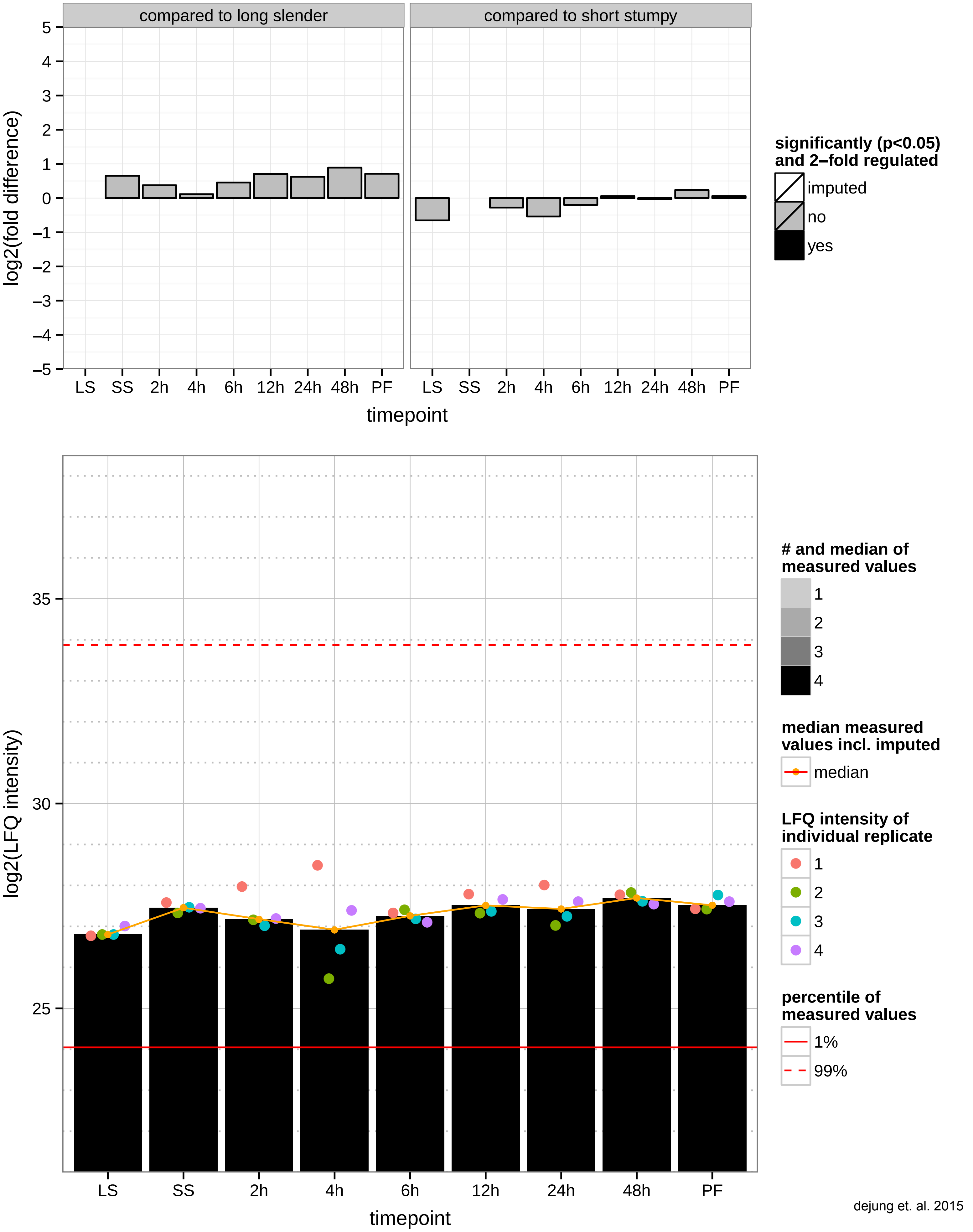
endo–beta–N–acetylglucosaminidase, putative
Tb927.9.3400
AGOF: hydrolase activity, acting on glycosyl bonds, mannosyl–glycoprotein endo–beta–N–acetylglucosaminidase activity
AGOC: cytoplasm
AGOP: null
PGOF: mannosyl–glycoprotein endo–beta–N–acetylglucosaminidase activity
PGOC: cytoplasm
PGOP: null



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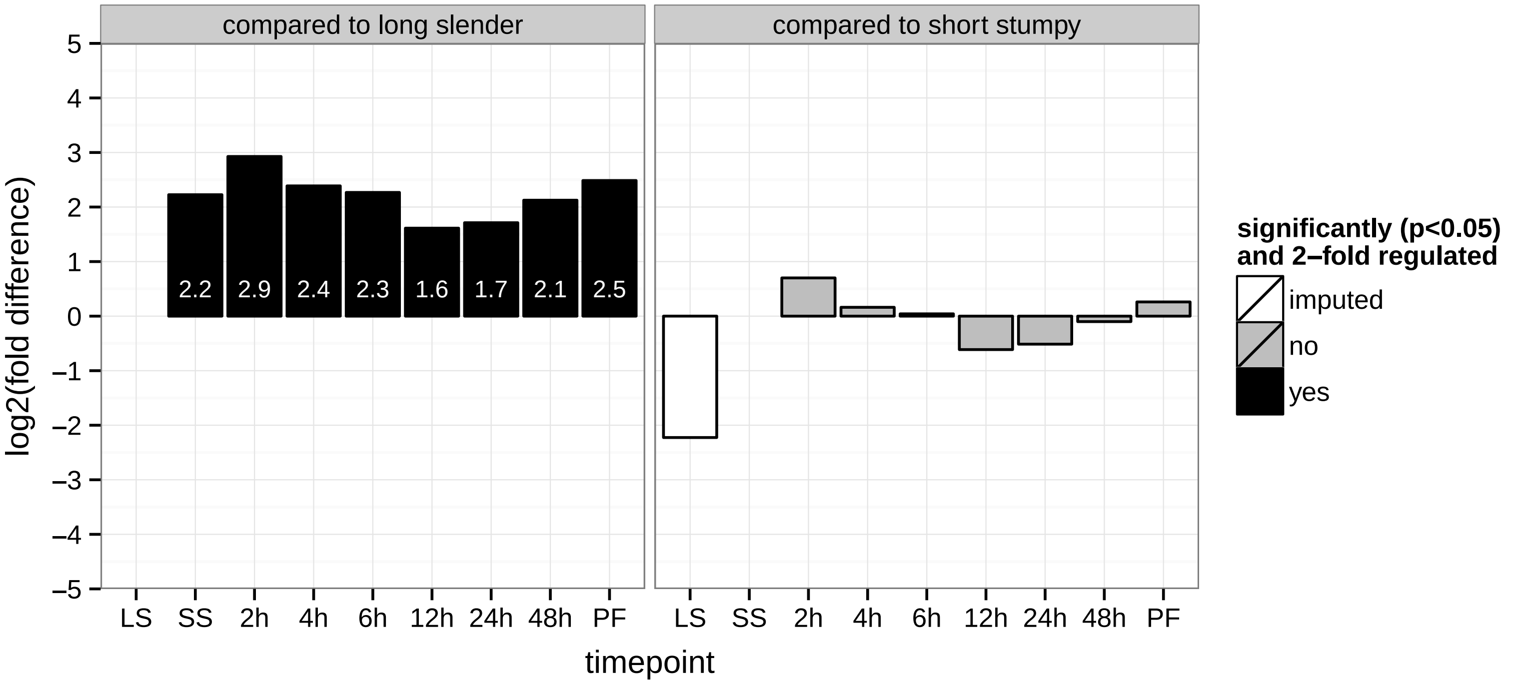
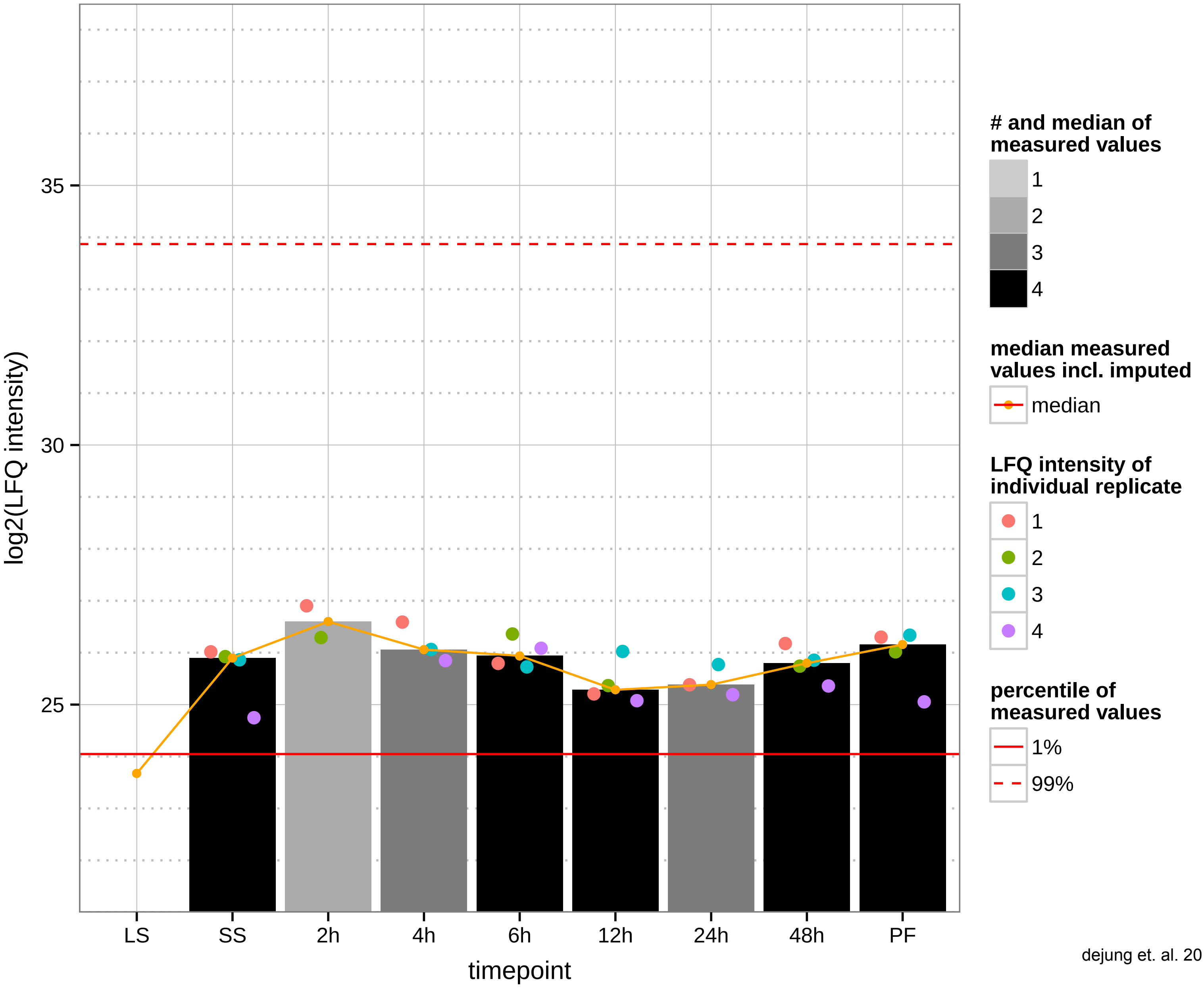
cyclophilin type peptidyl–prolyl cis–trans isomerase, putative
Tb927.9.3440
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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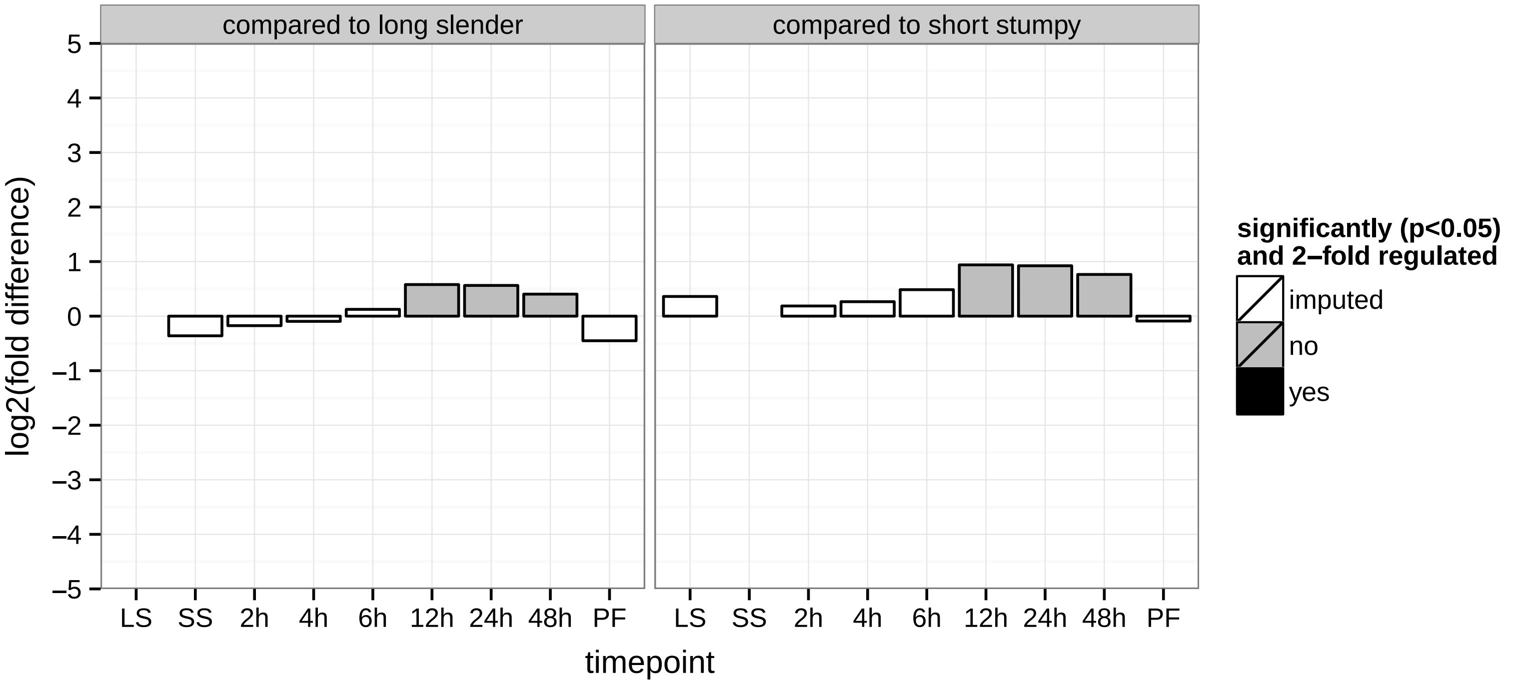
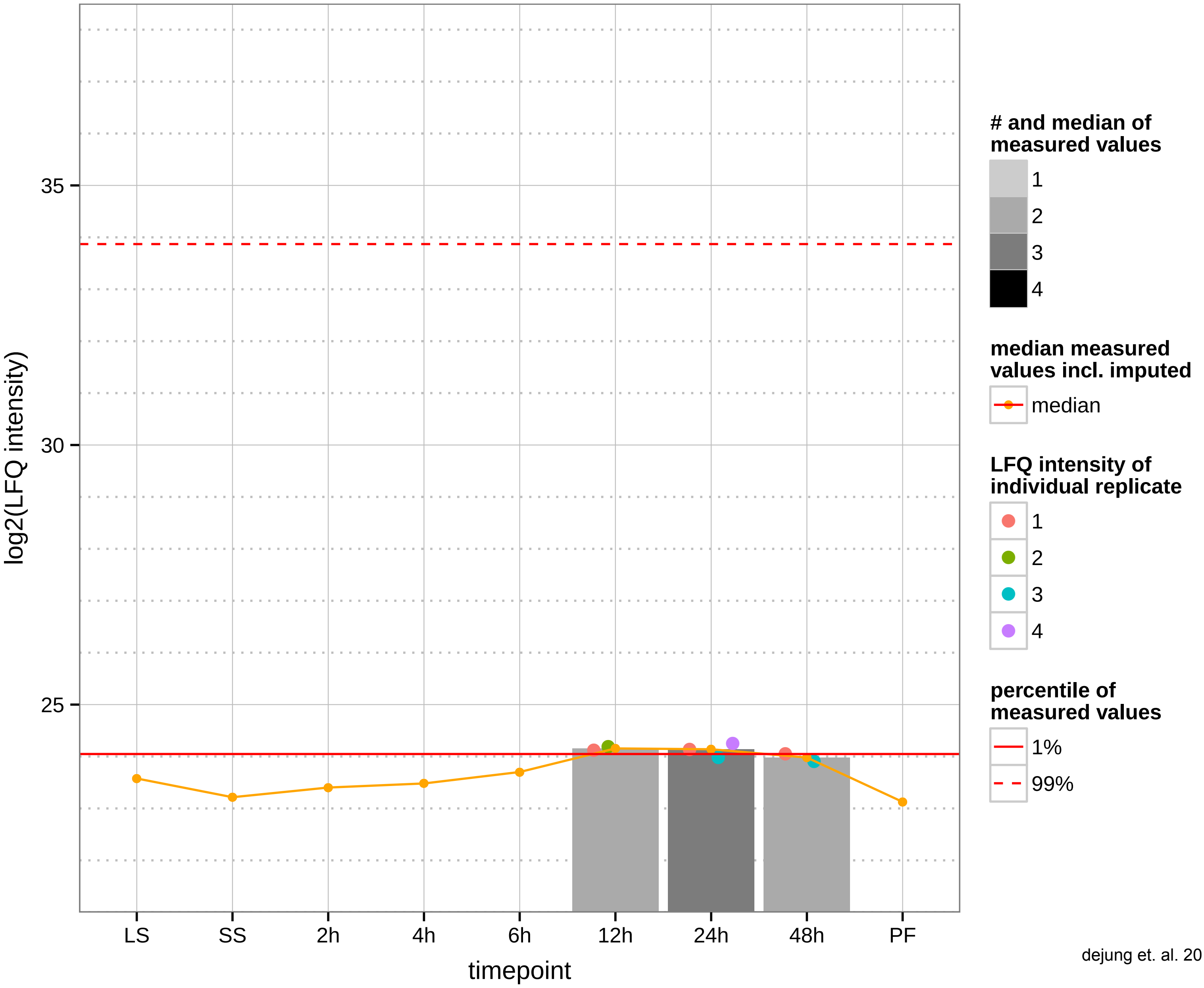
low molecular weight protein tyrosine phosphatase, putative
Tb927.9.3470
AGOF: protein tyrosine phosphatase activity
AGOC: mitochondrion
AGOP: protein dephosphorylation
PGOF: null
PGOC: null
PGOP: null





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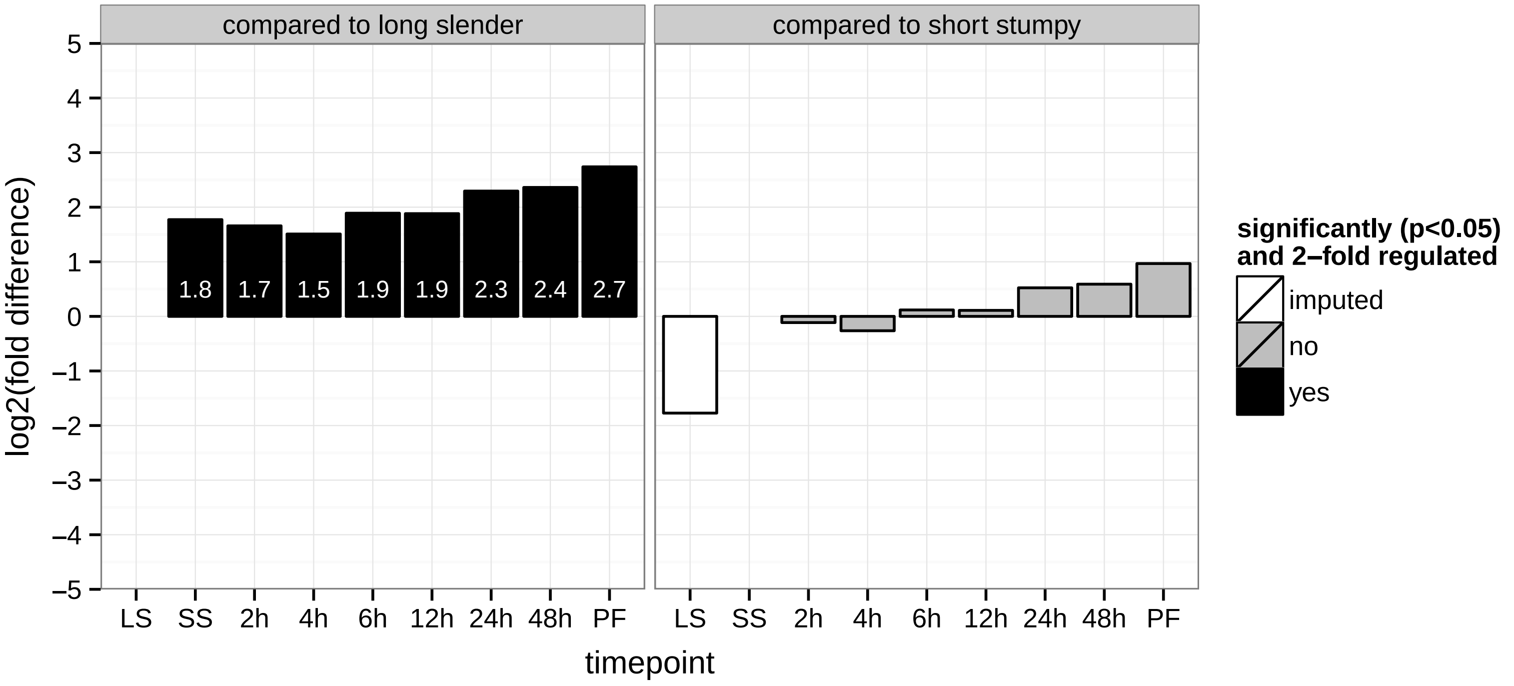
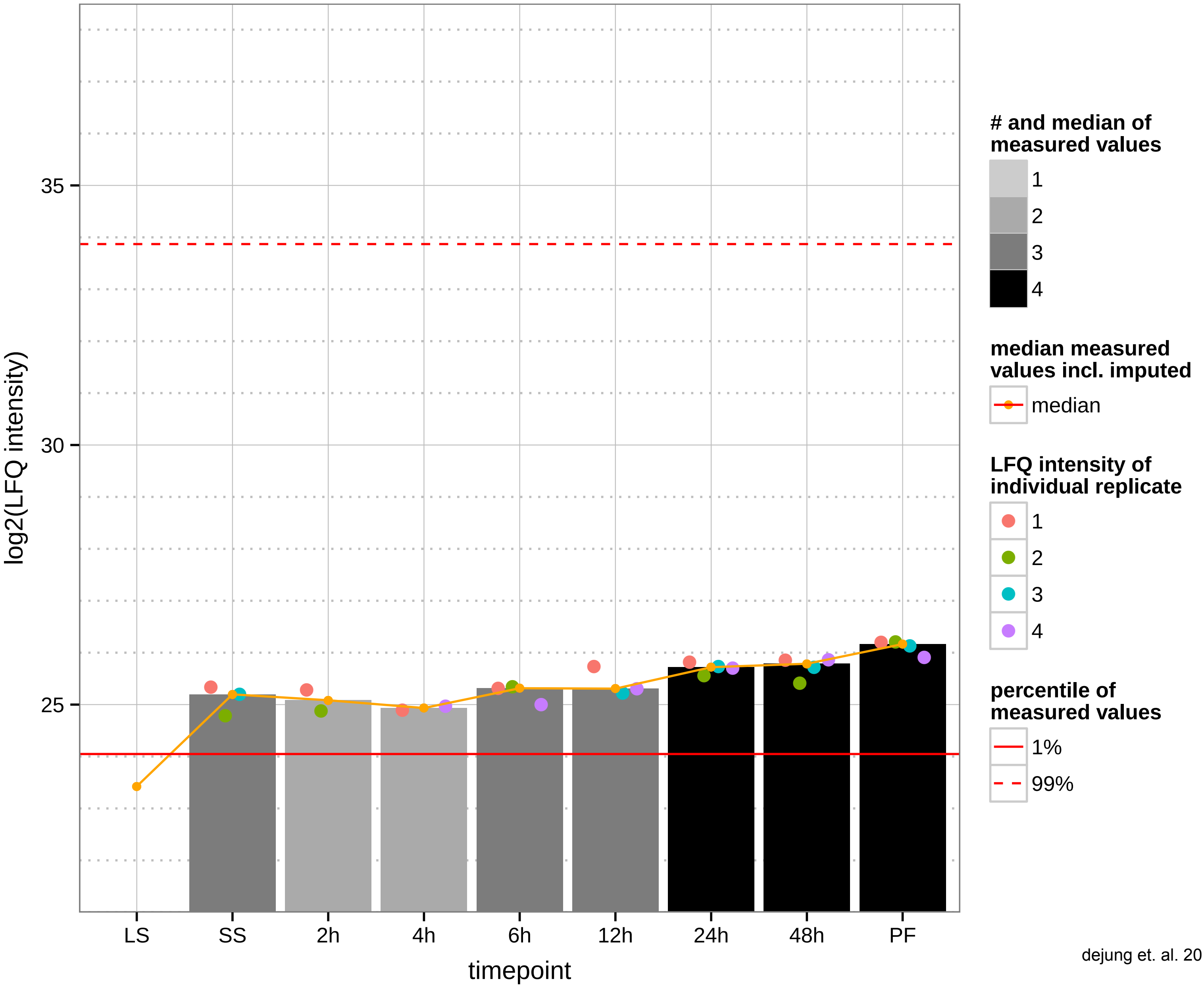
hypothetical protein, conserved
Tb927.9.3620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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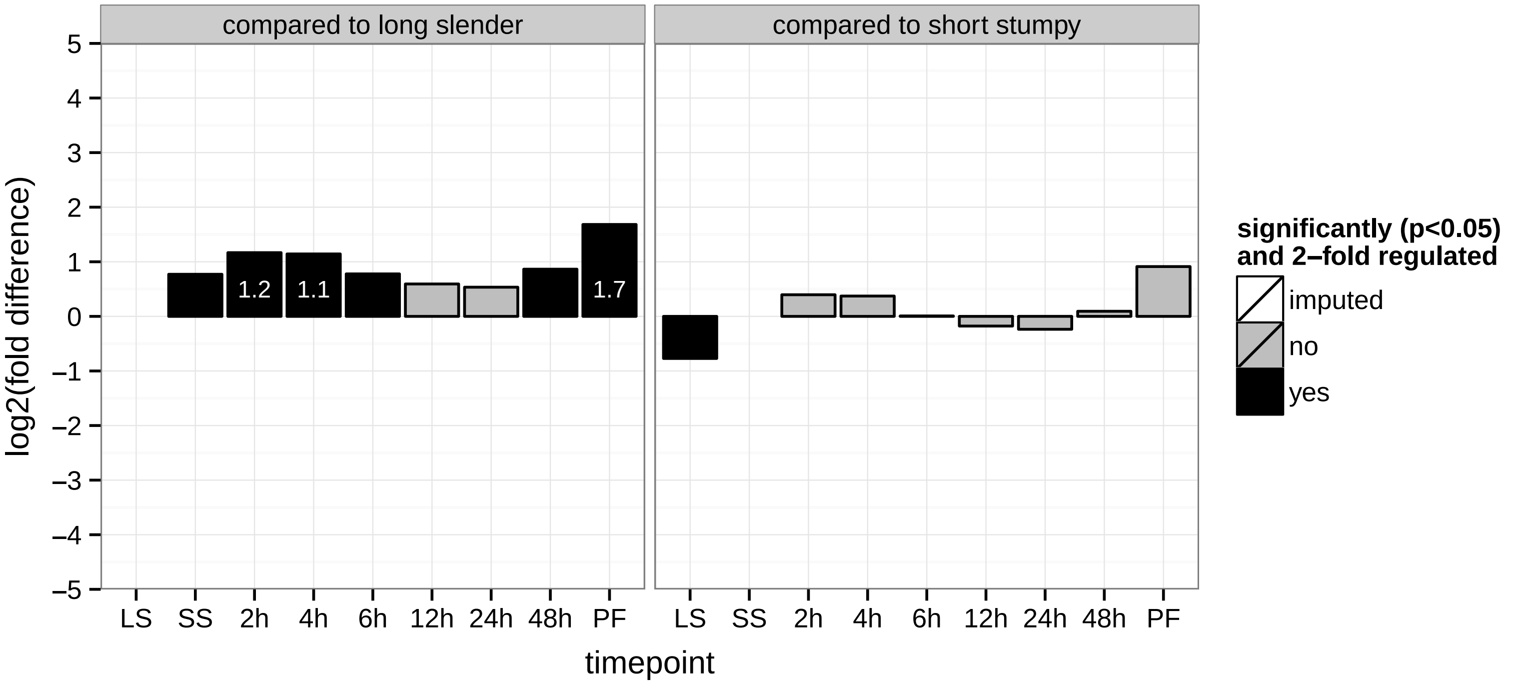
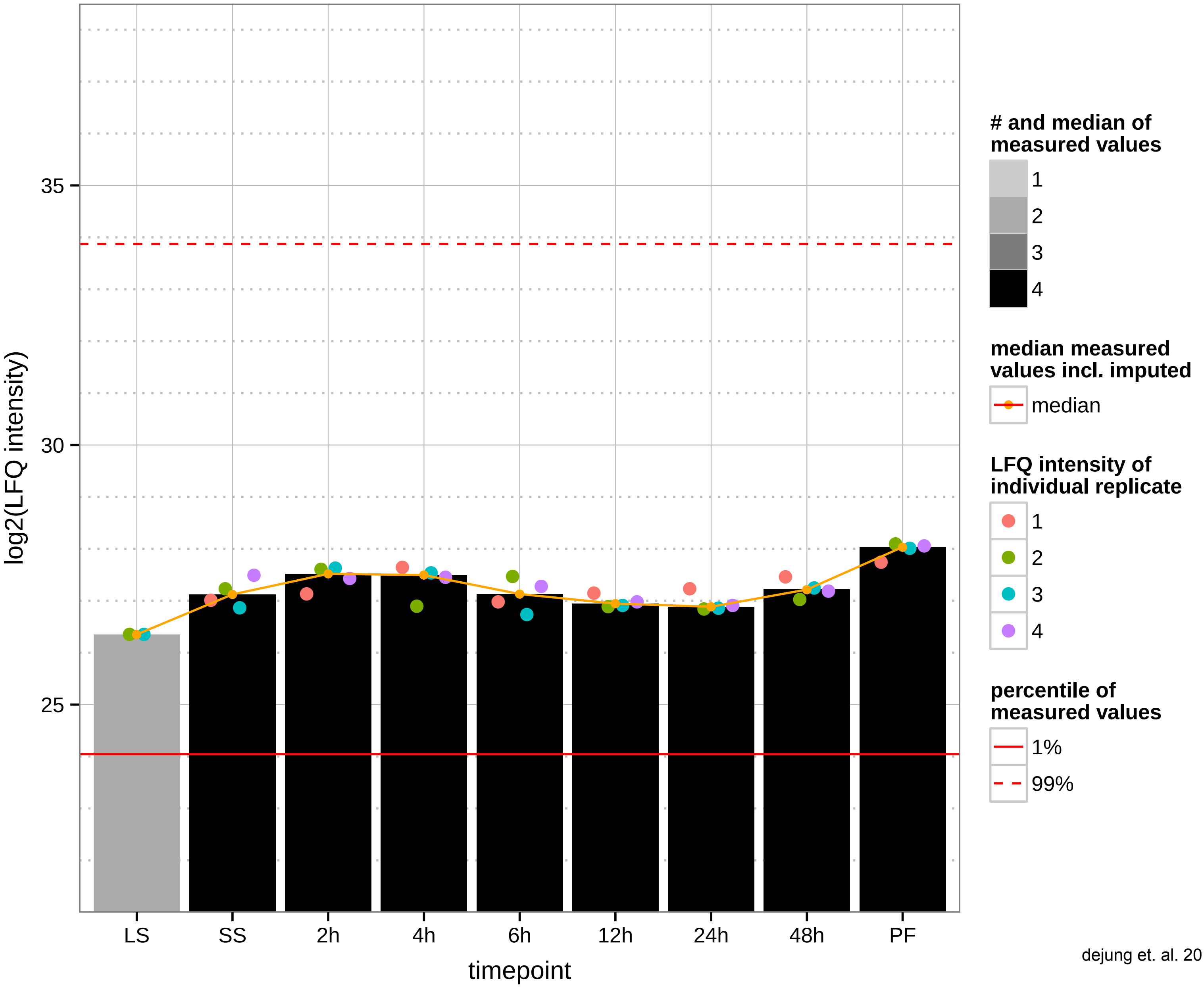
hypothetical protein, conserved
Tb927.9.3630;Tb11.v5.0530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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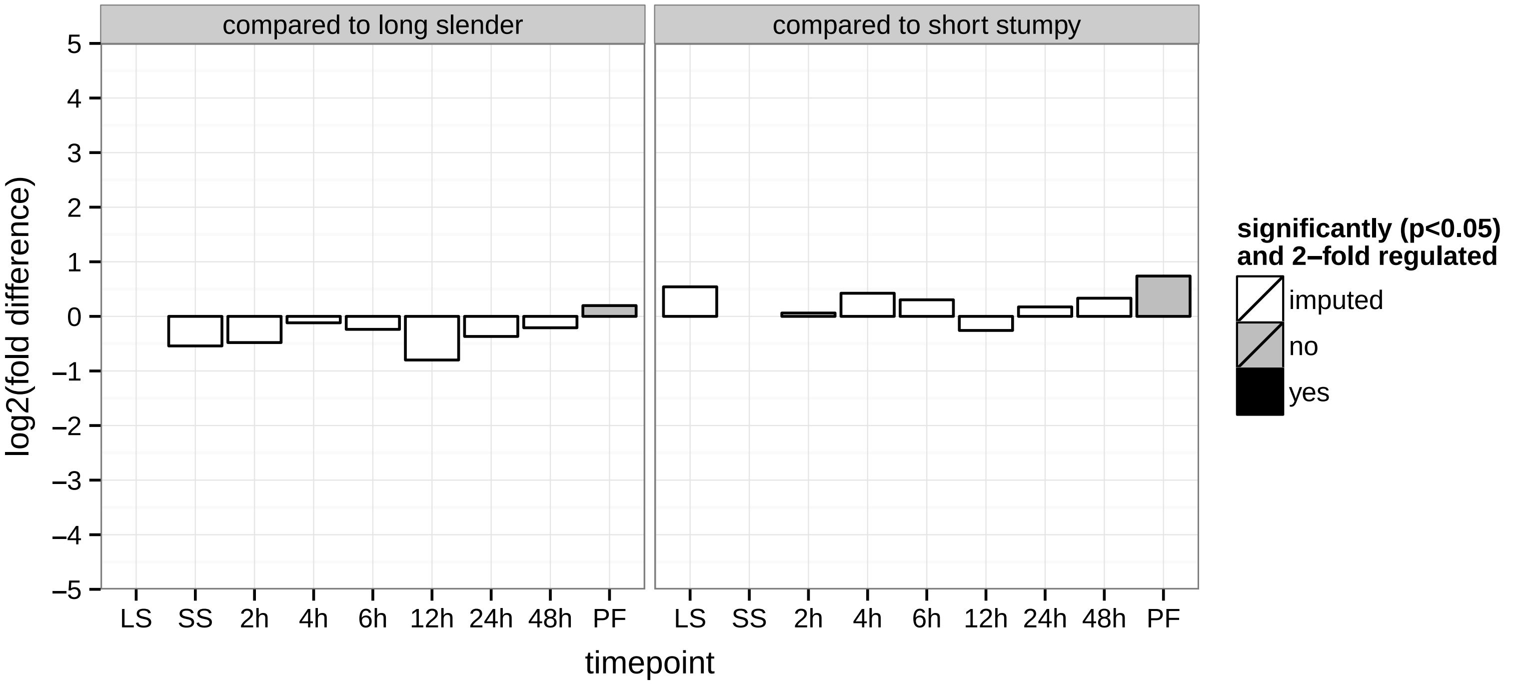
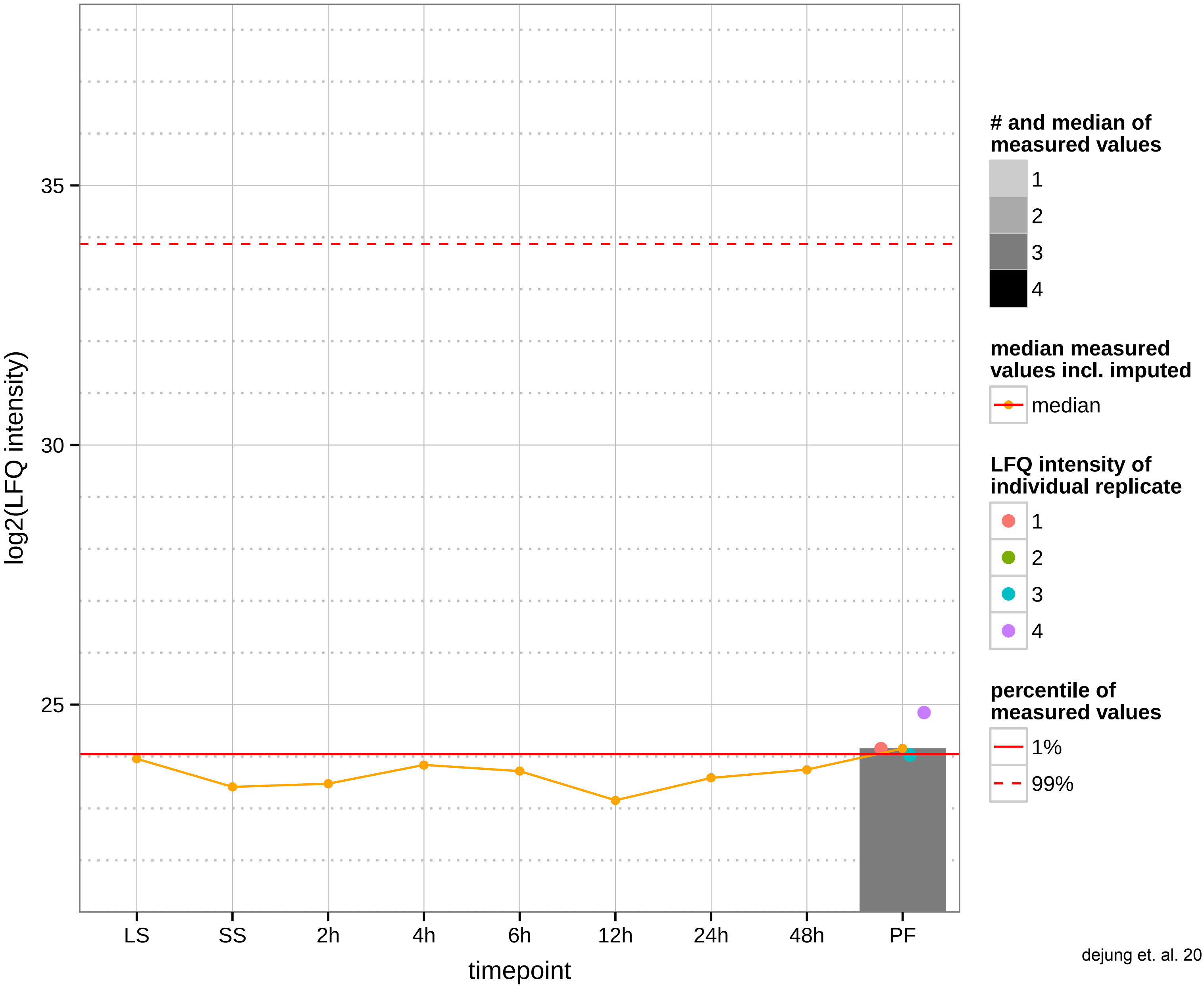
hypothetical protein, conserved
Tb927.9.3670
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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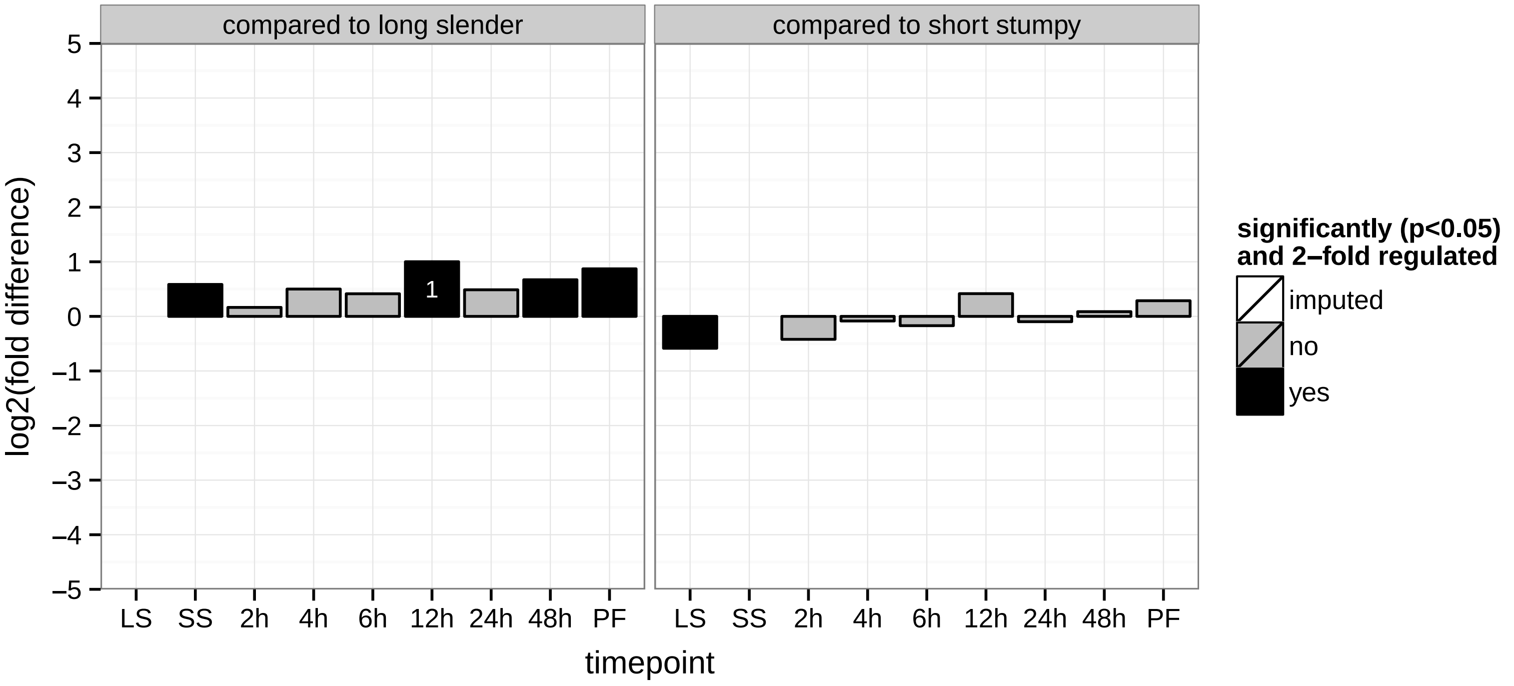
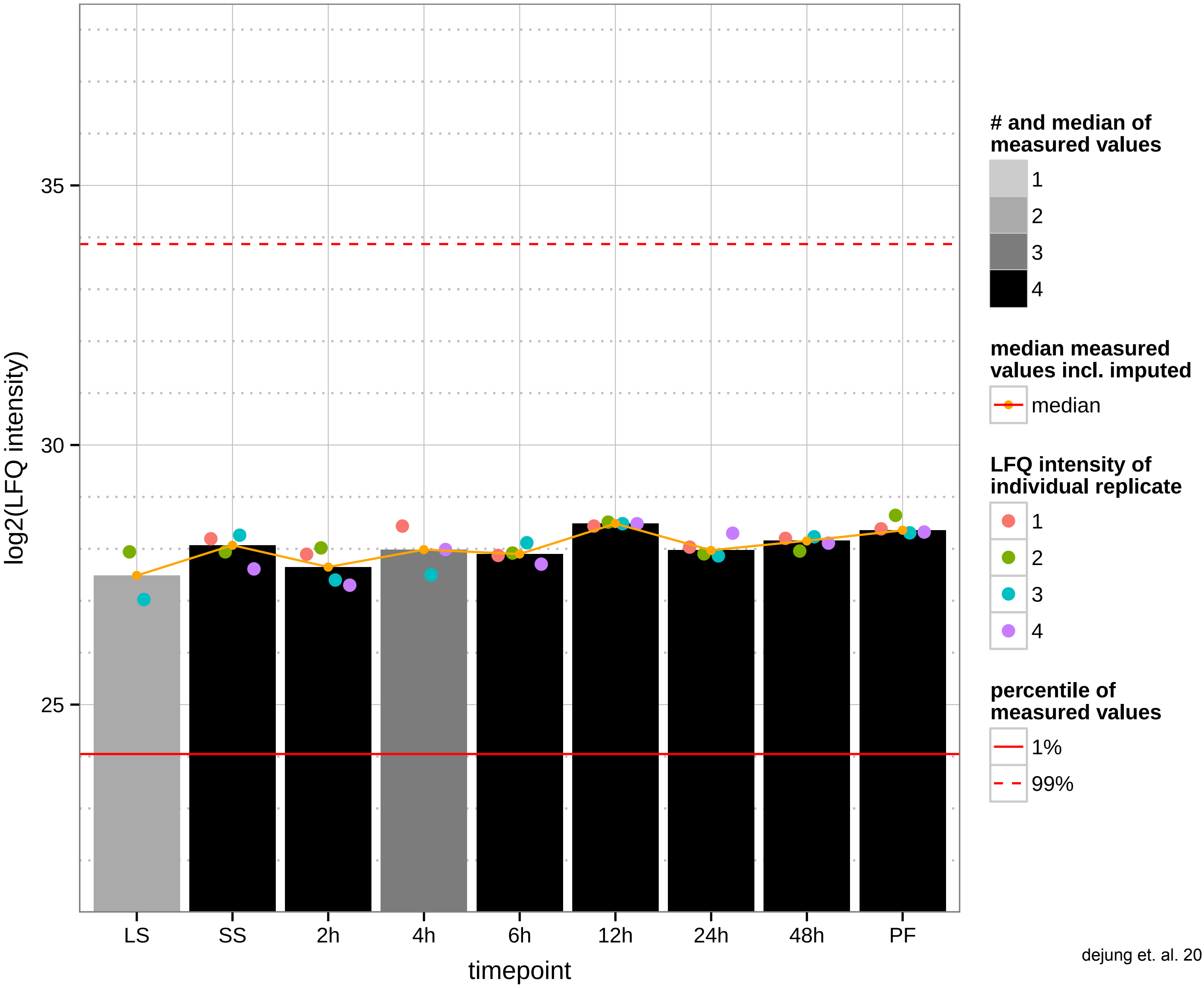
poly(A) export protein, putative (TbGLE2)
Tb927.9.3760
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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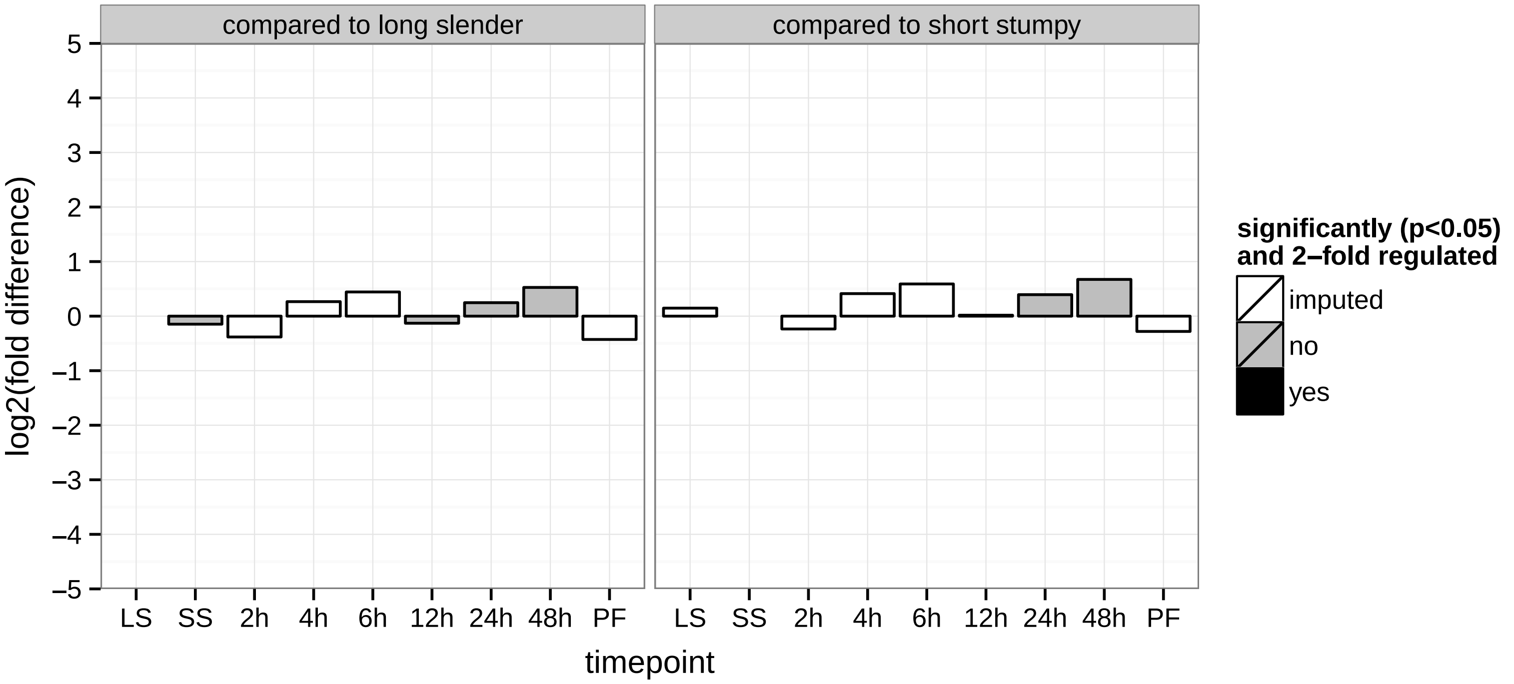
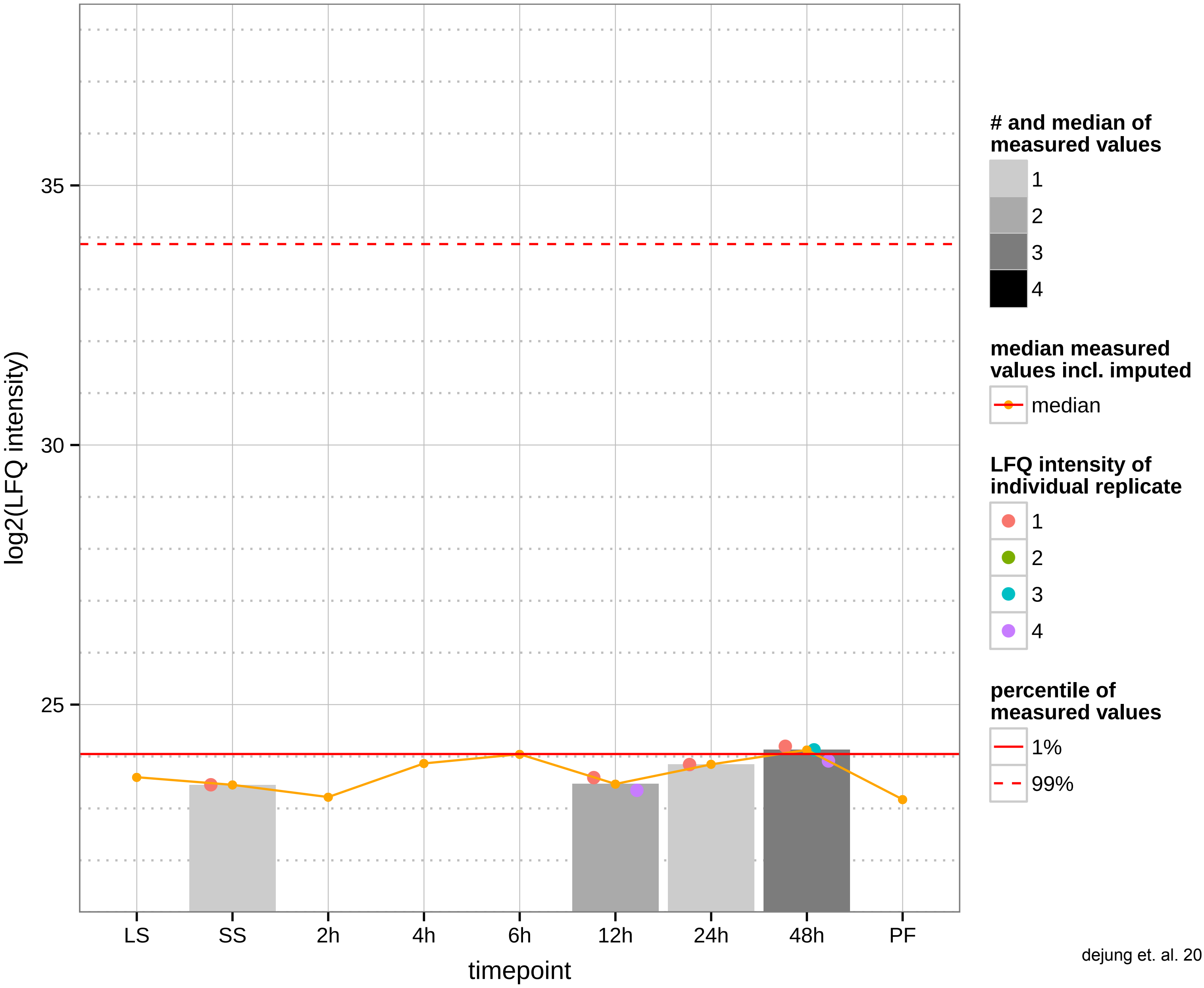
hypothetical protein, conserved
Tb927.9.3870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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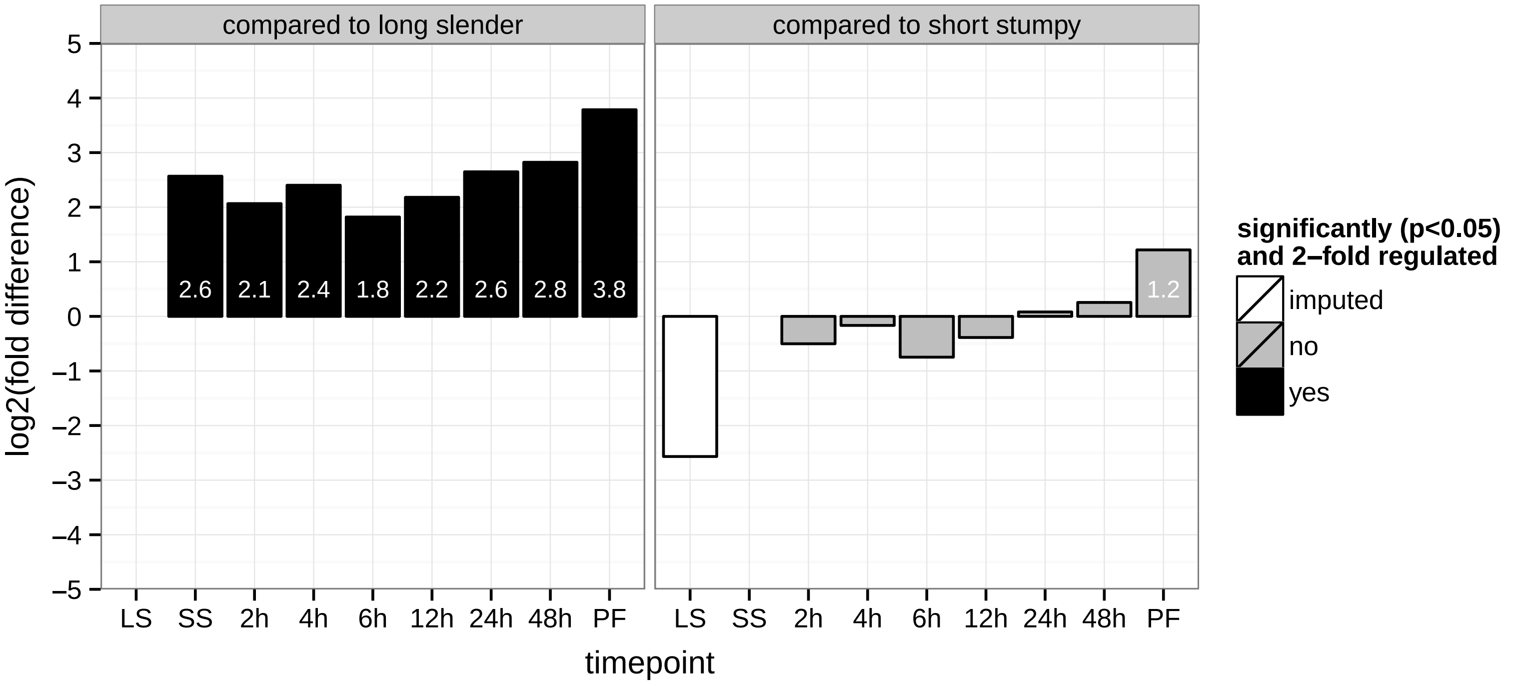
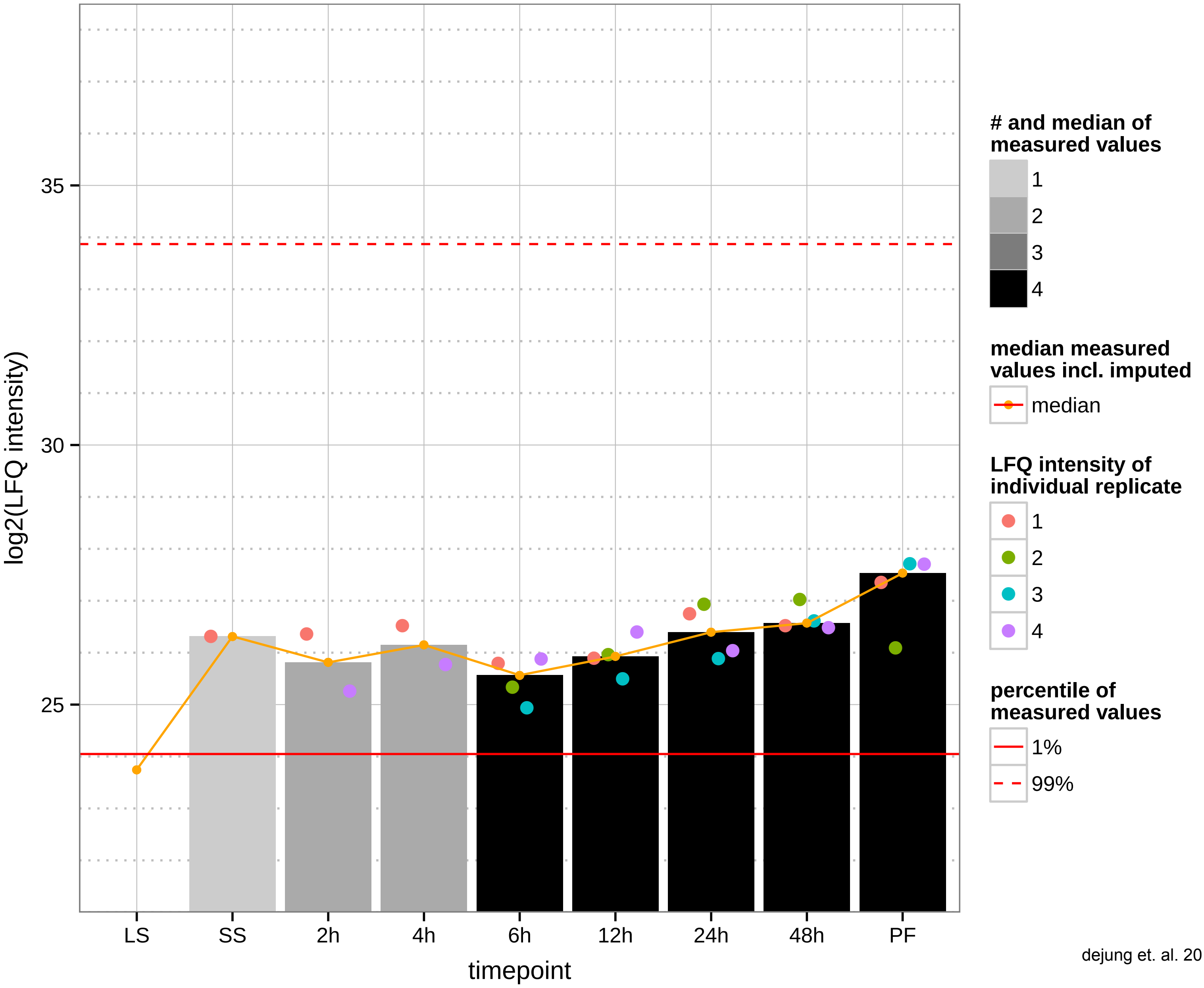
nicotinamidase, putative (PNC1)
Tb927.9.4040;Tb927.9.3970
AGOF: hydrolase activity, nicotinamidase activity
AGOC: cytosol
AGOP: NAD biosynthetic process, metabolic process
PGOF: null, catalytic activity
PGOC: null
PGOP: null, metabolic process





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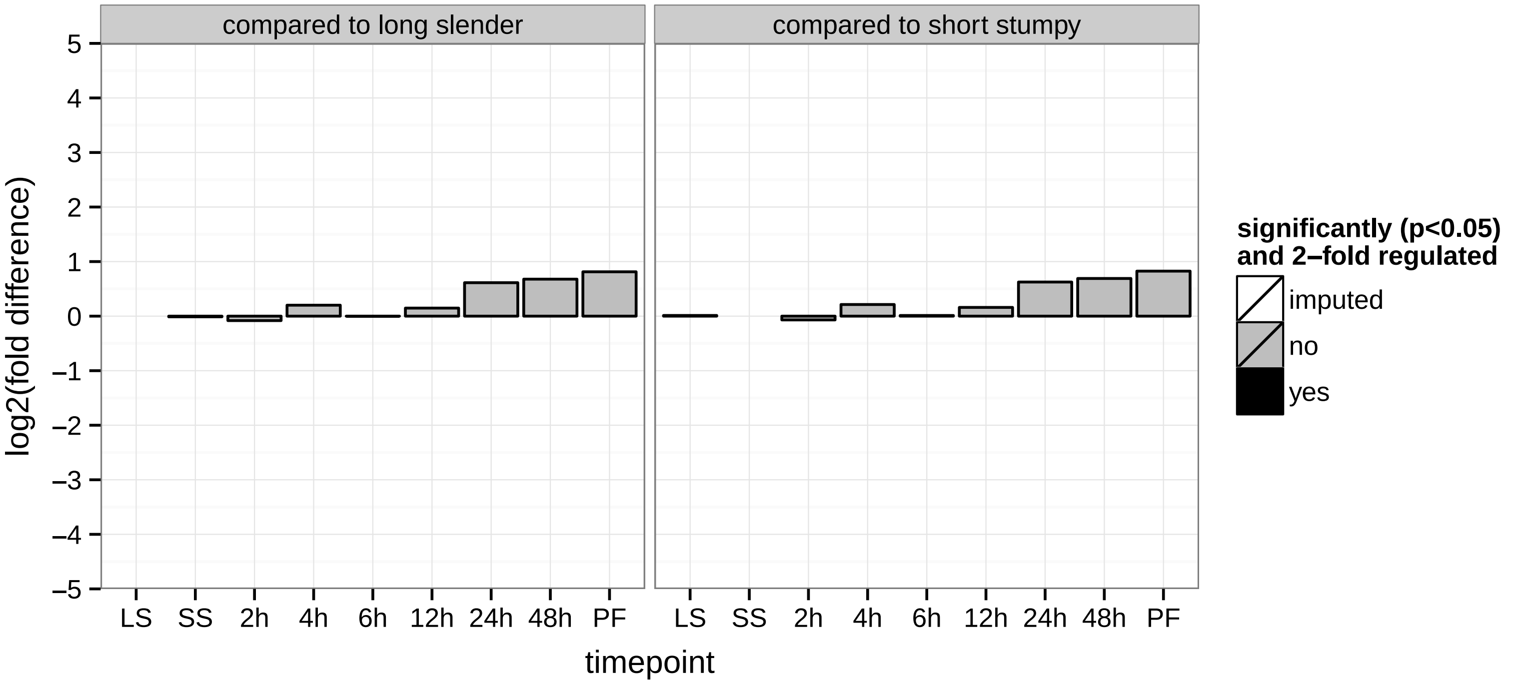
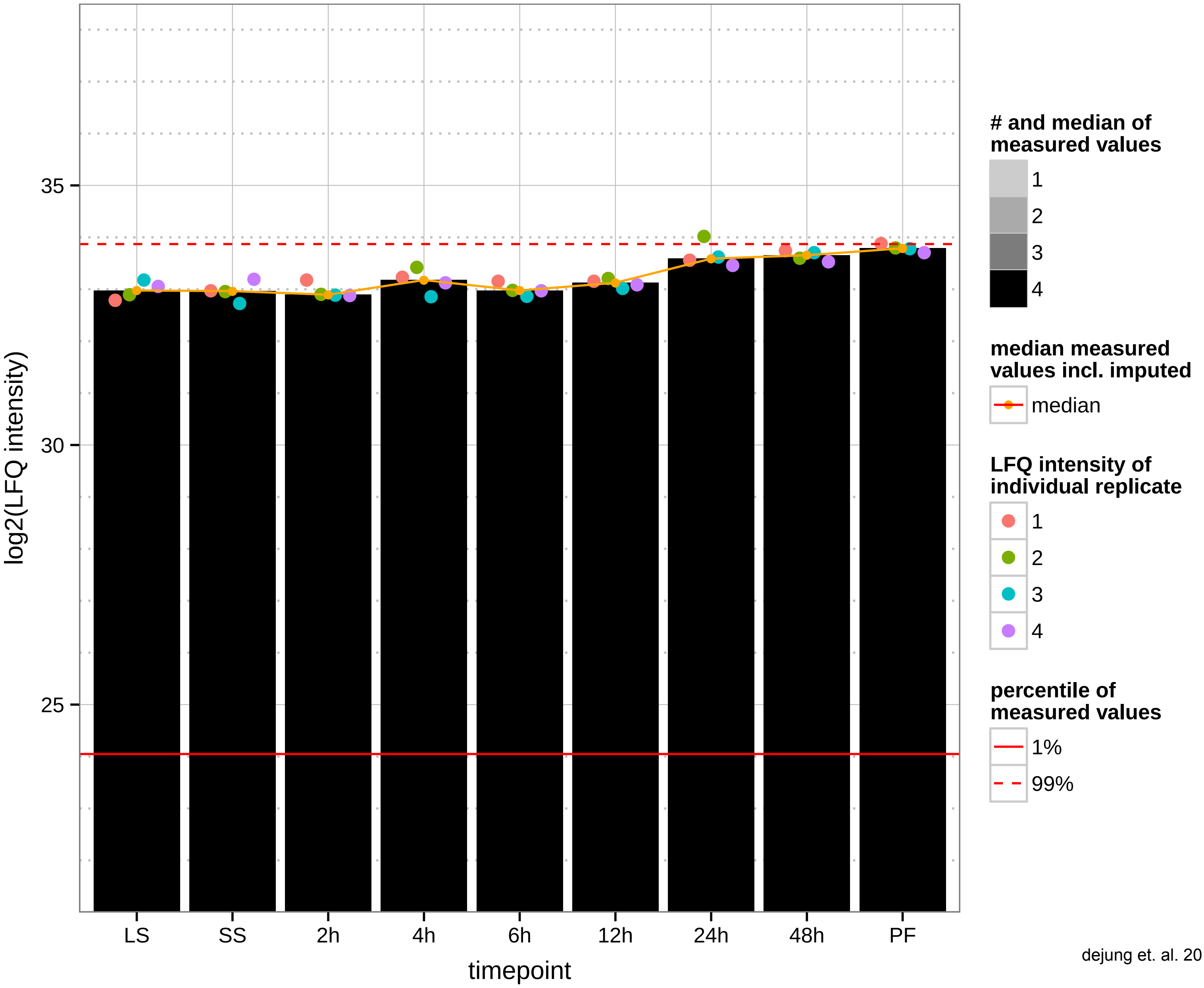
ribosomal protein S7, putative
Tb927.9.3990;Tb927.9.3920
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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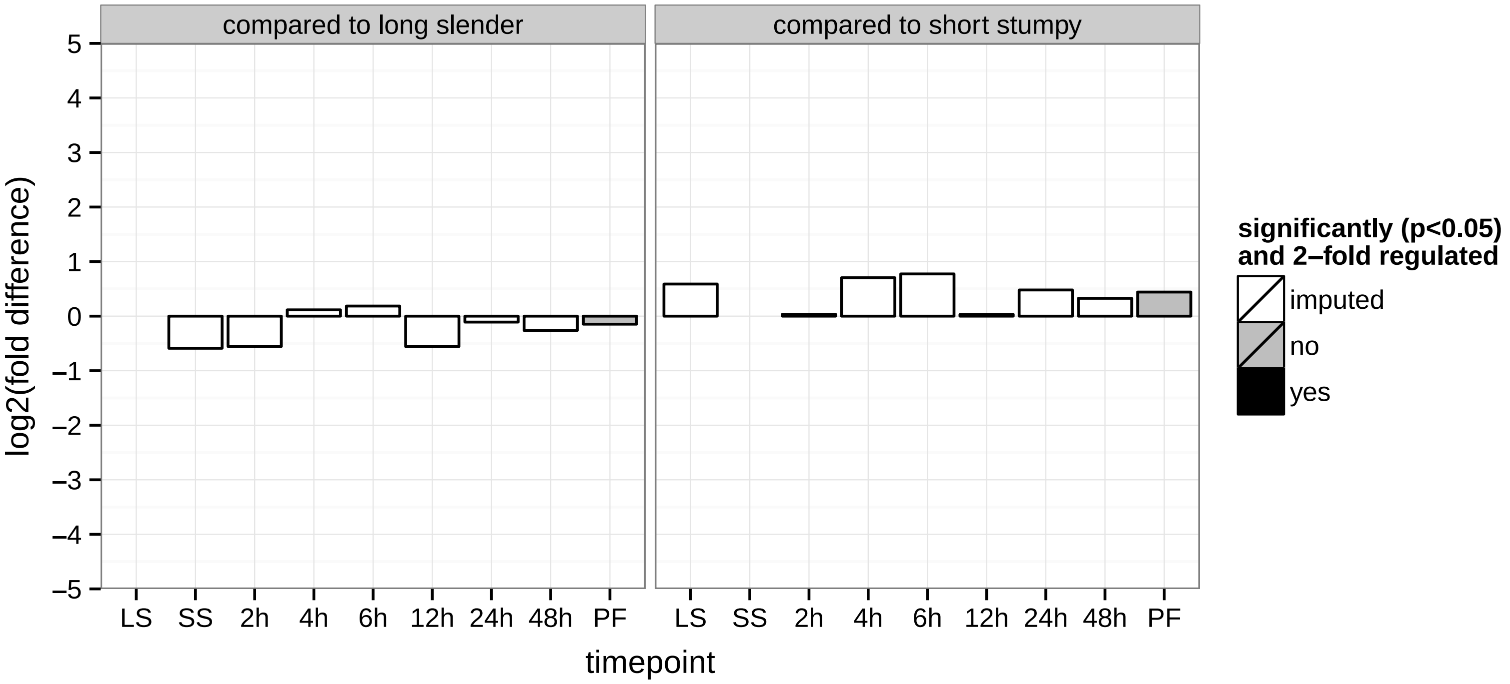
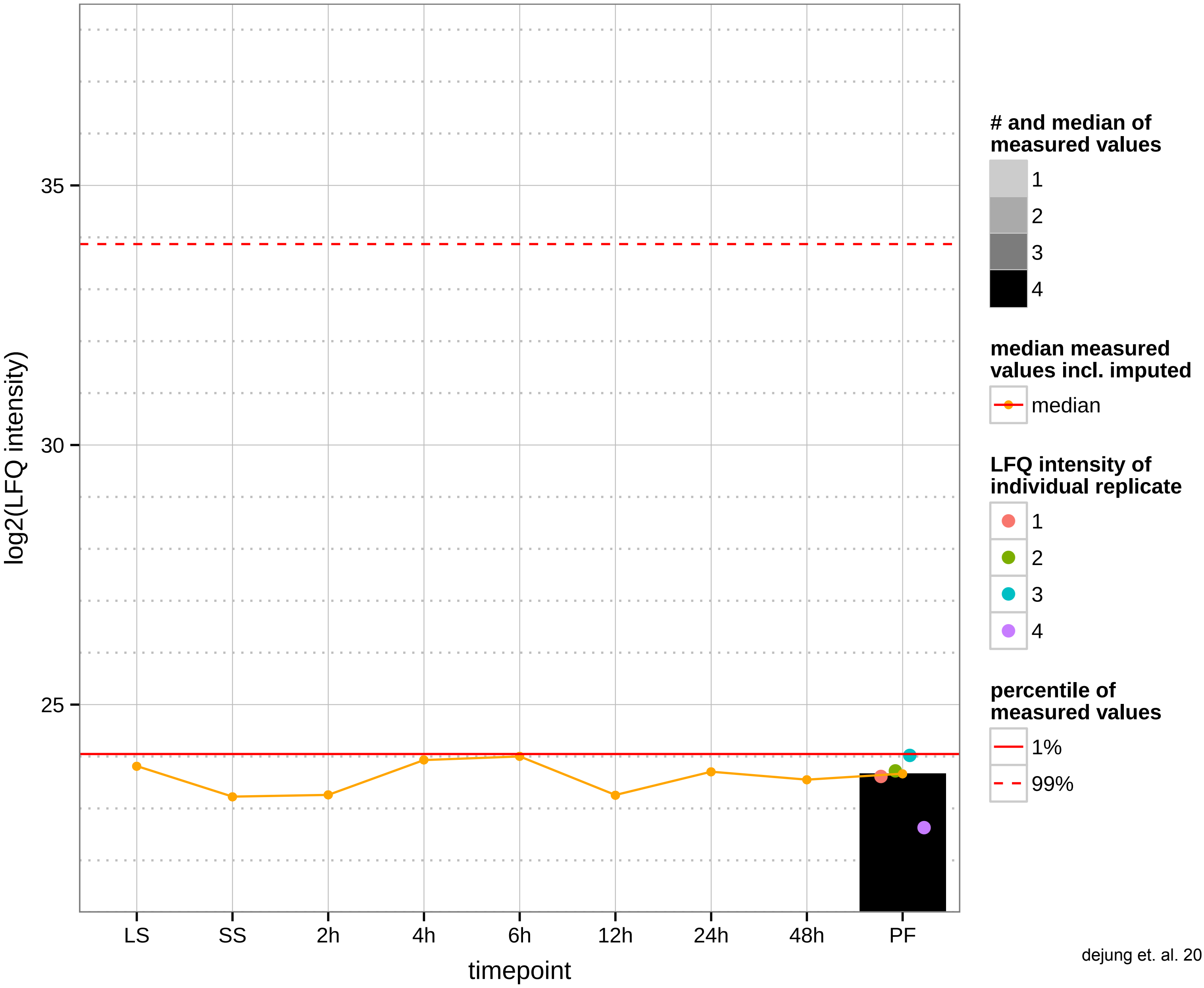
hypothetical protein, conserved
Tb927.9.4050
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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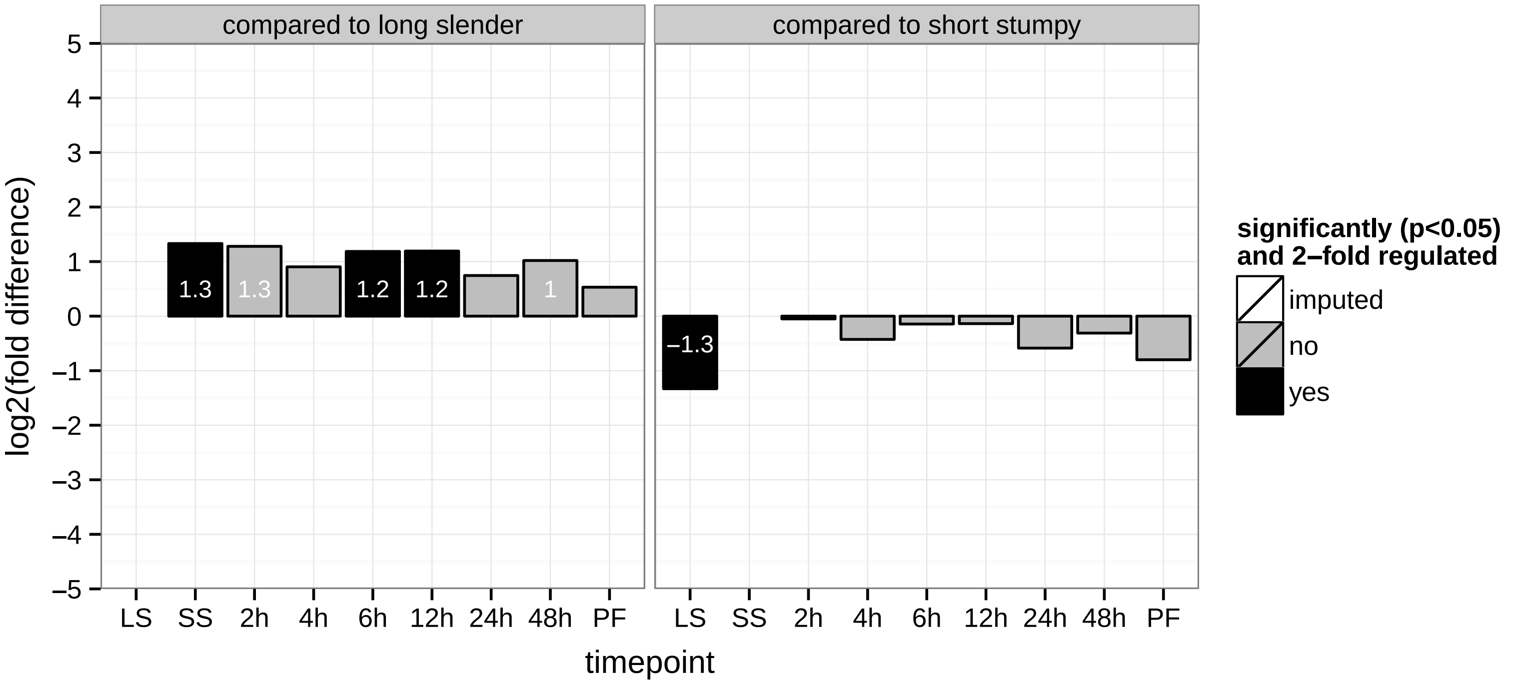
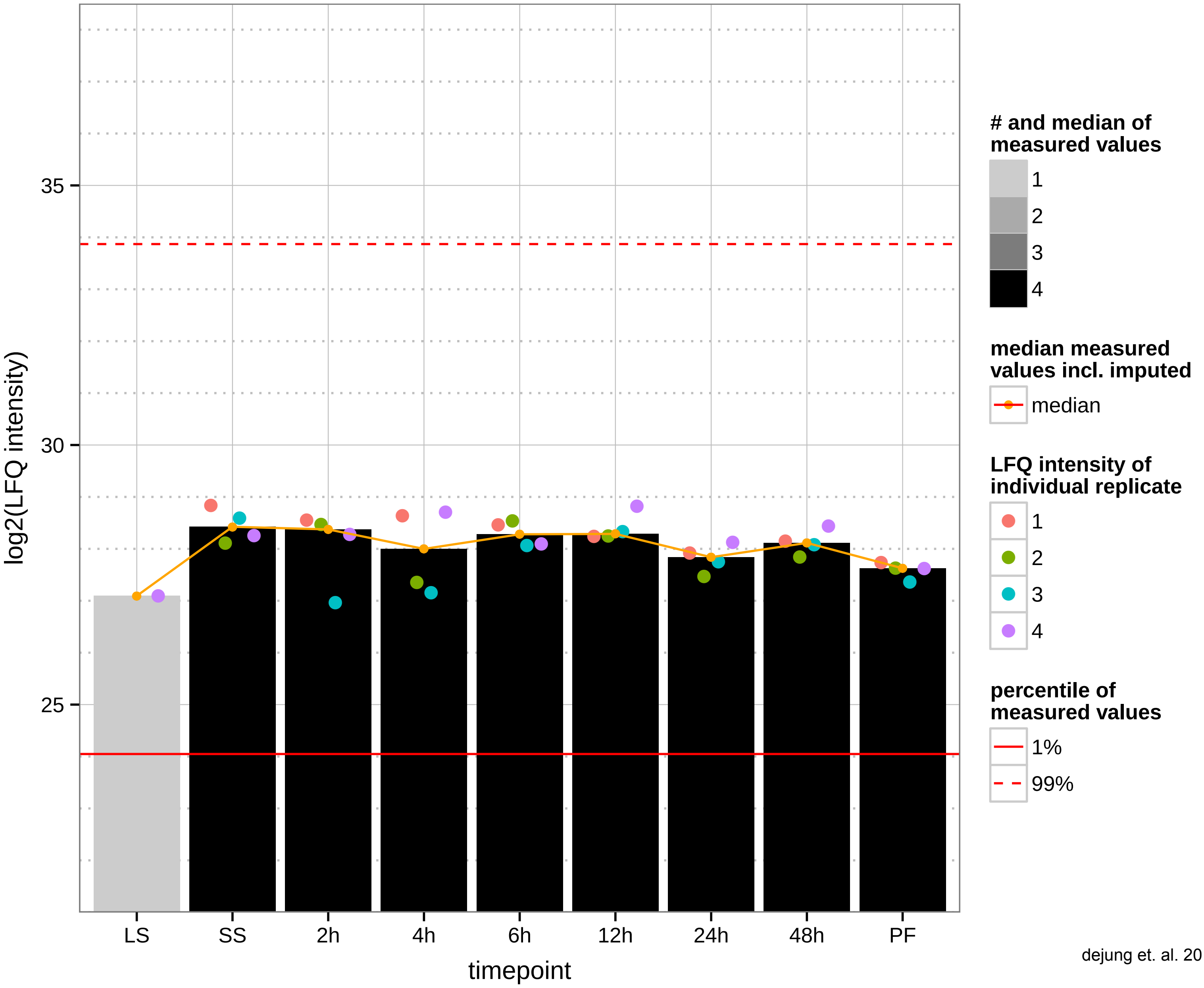
conserved protein
Tb927.9.4080
AGOF: zinc ion binding
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, quorum sensing involved in interaction with ho
PGOF: zinc ion binding
PGOC: null
PGOP: null





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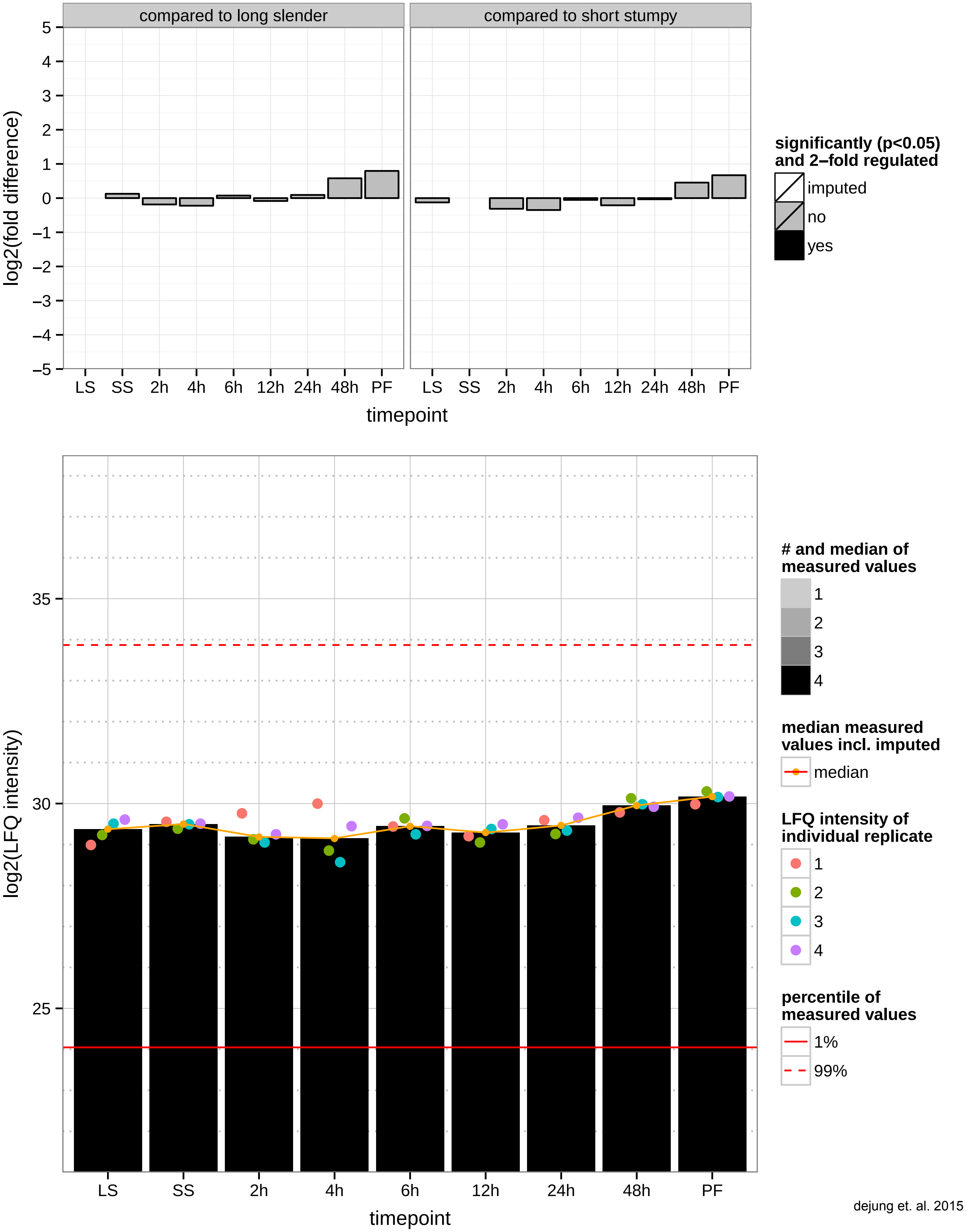
fatty acyl CoA syntetase 1 (ACS1)
Tb927.9.4190
AGOF: fatty–acyl–CoA synthase activity
AGOC: membrane
AGOP: fatty acid metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process



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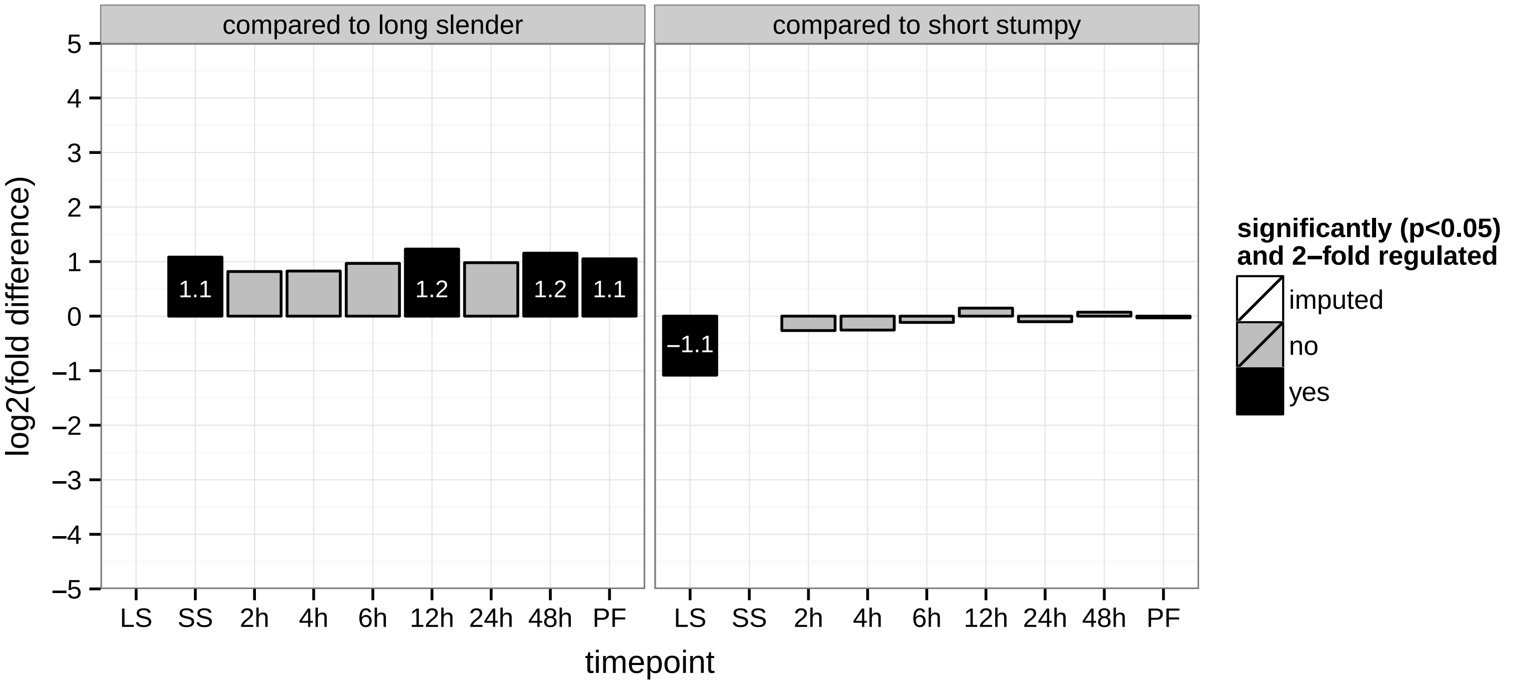
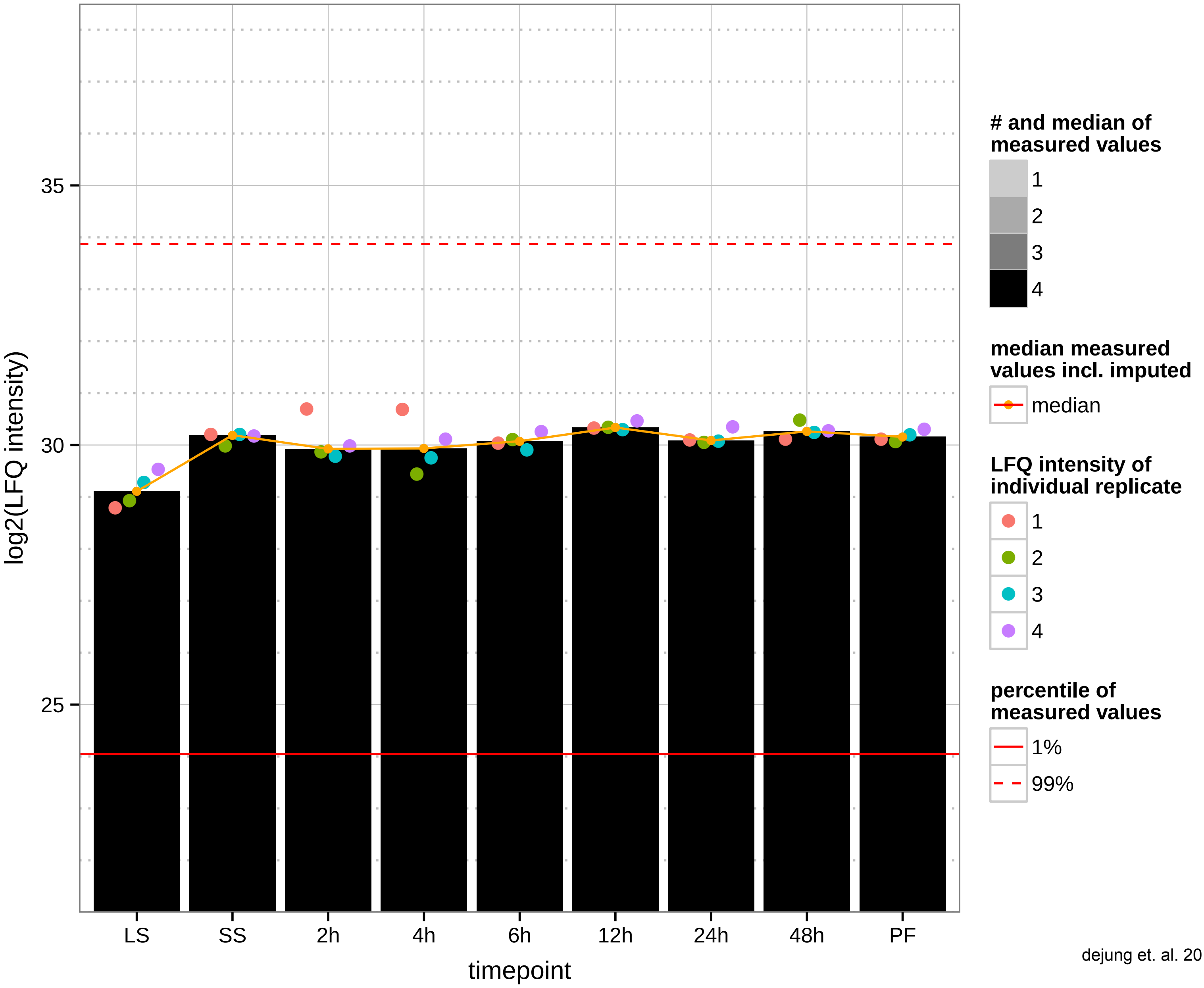
fatty acyl CoA synthetase 4 (ACS4)
Tb927.9.4230
AGOF: fatty–acyl–CoA synthase activity
AGOC: membrane
AGOP: fatty acid metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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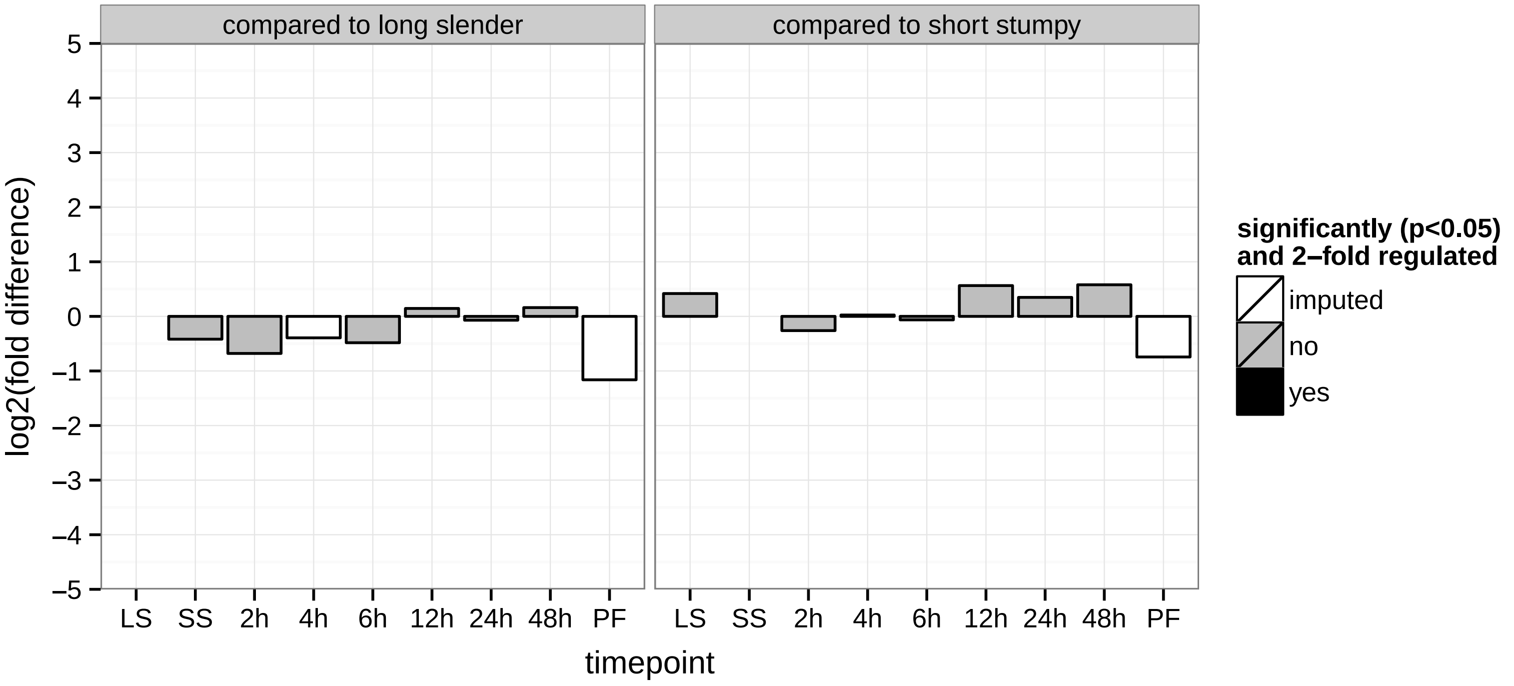
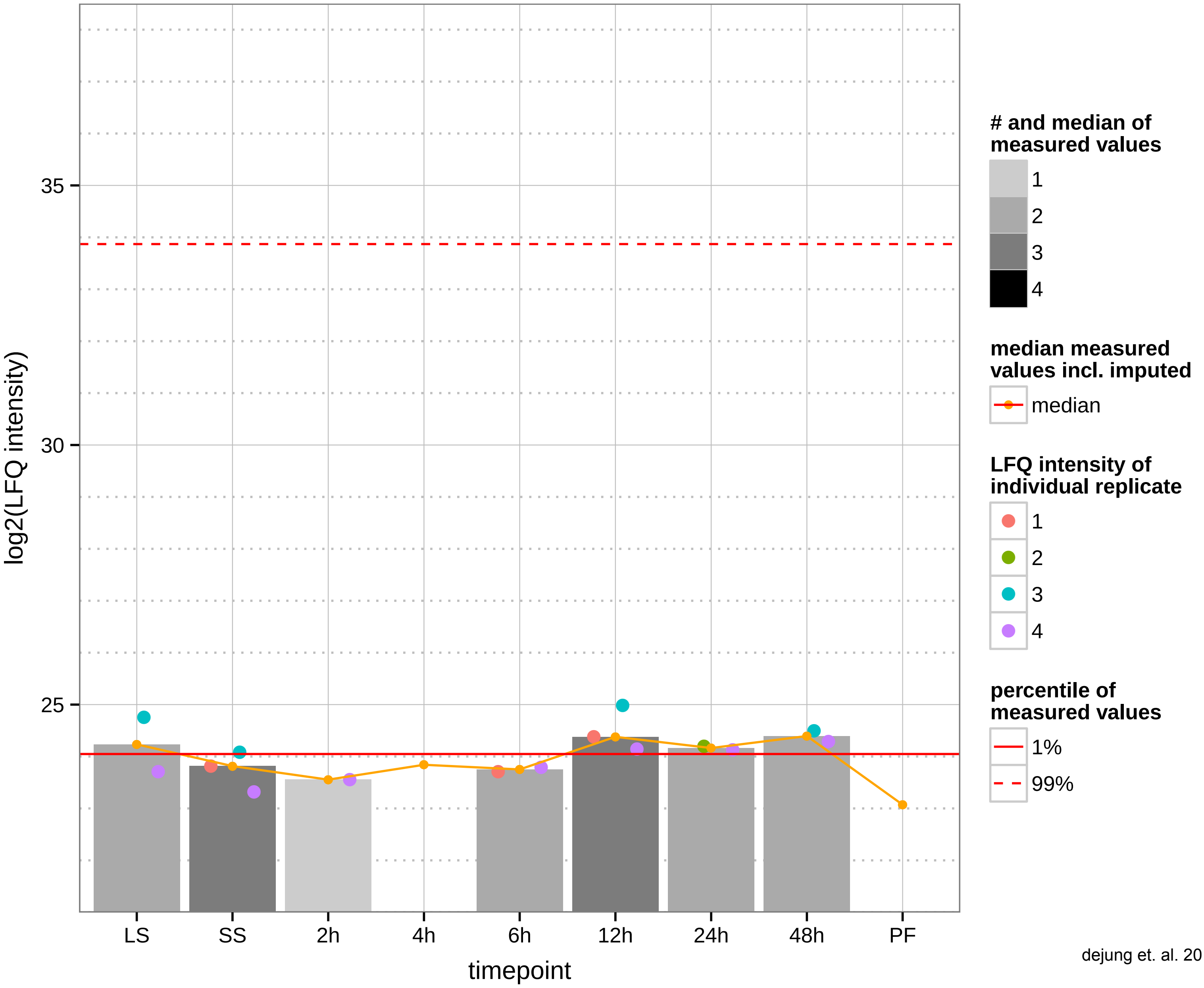
hypothetical protein, conserved
Tb927.9.4250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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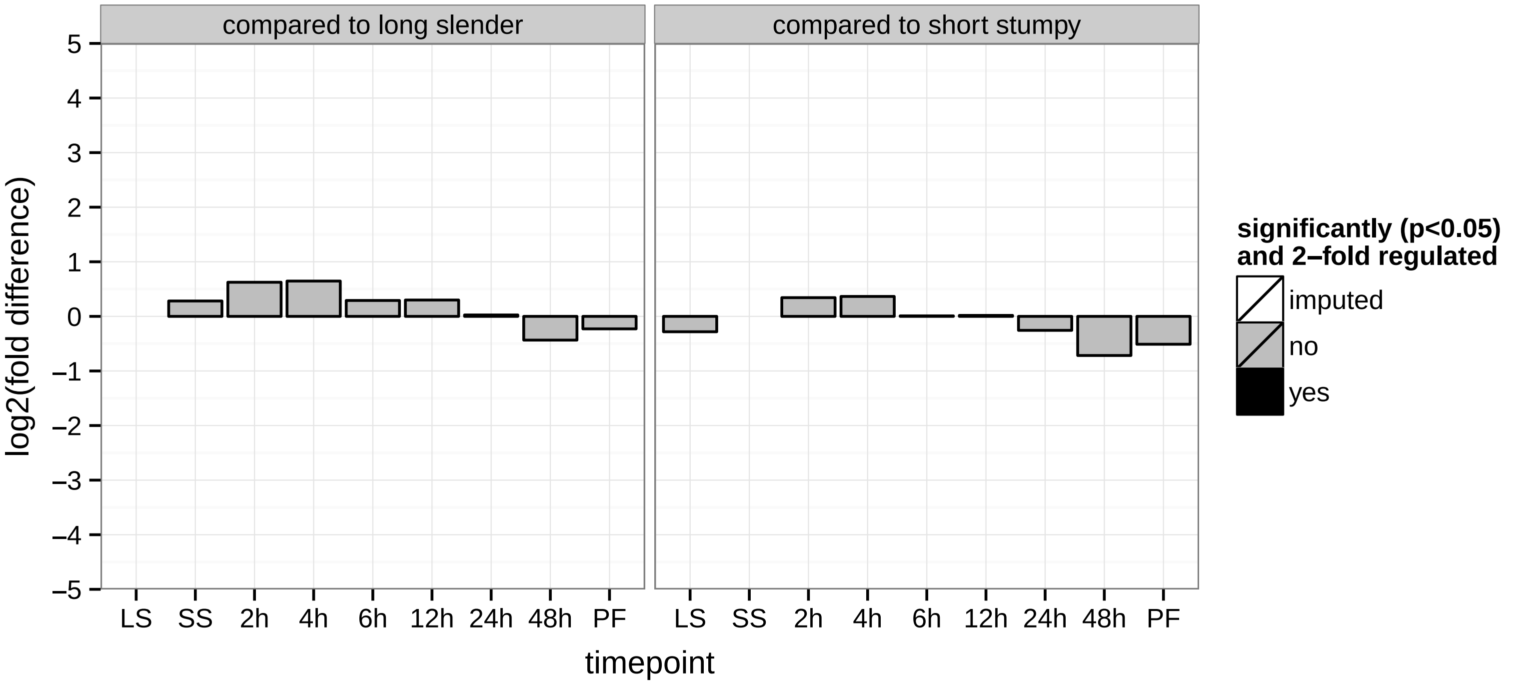
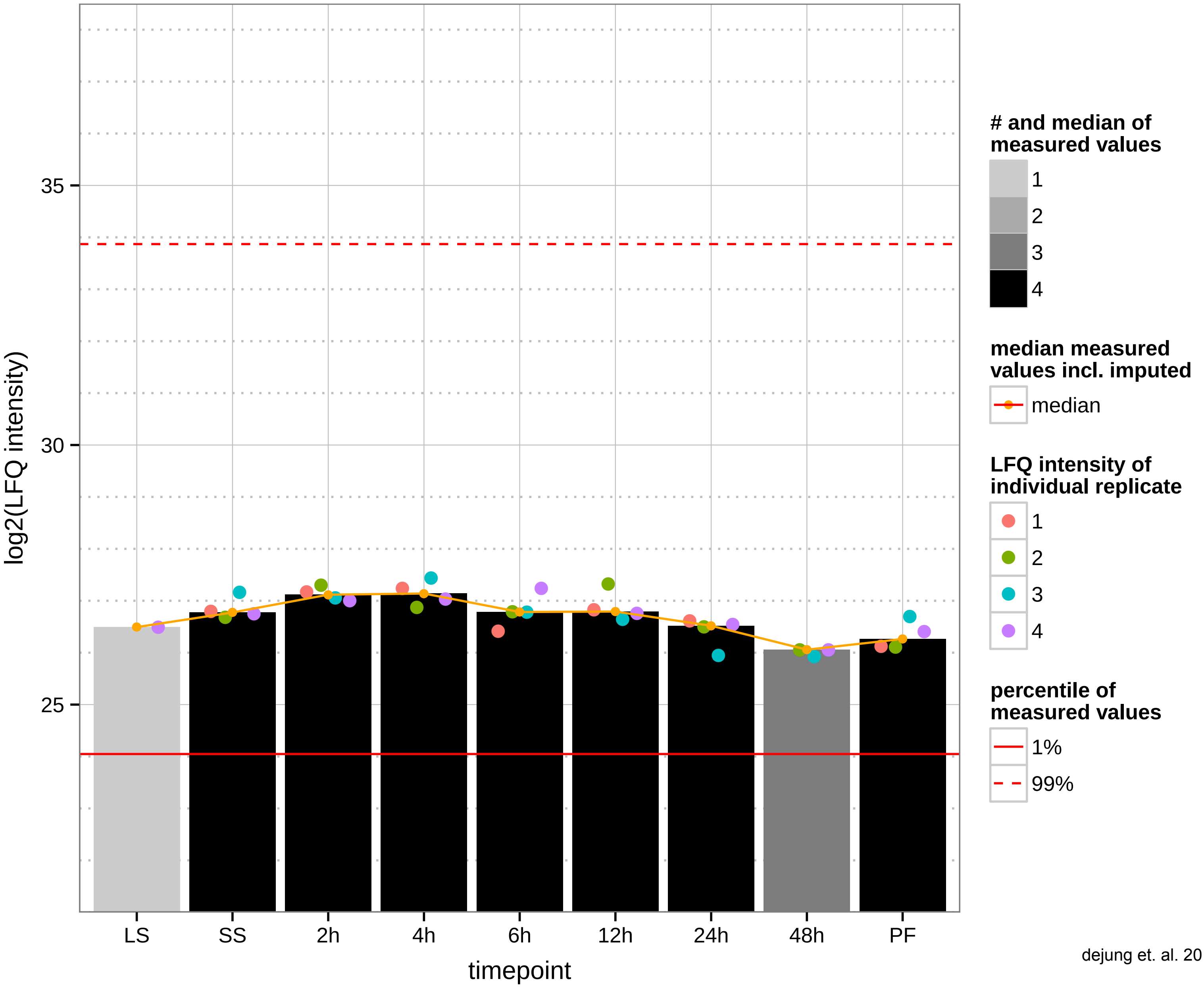
DNA–damage inducible protein DDI1–like protein
Tb927.9.4390
AGOF: aspartic–type endopeptidase activity
AGOC: null
AGOP: nucleotide–excision repair, proteolysis
PGOF: aspartic–type endopeptidase activity, protein binding
PGOC: null
PGOP: proteolysis





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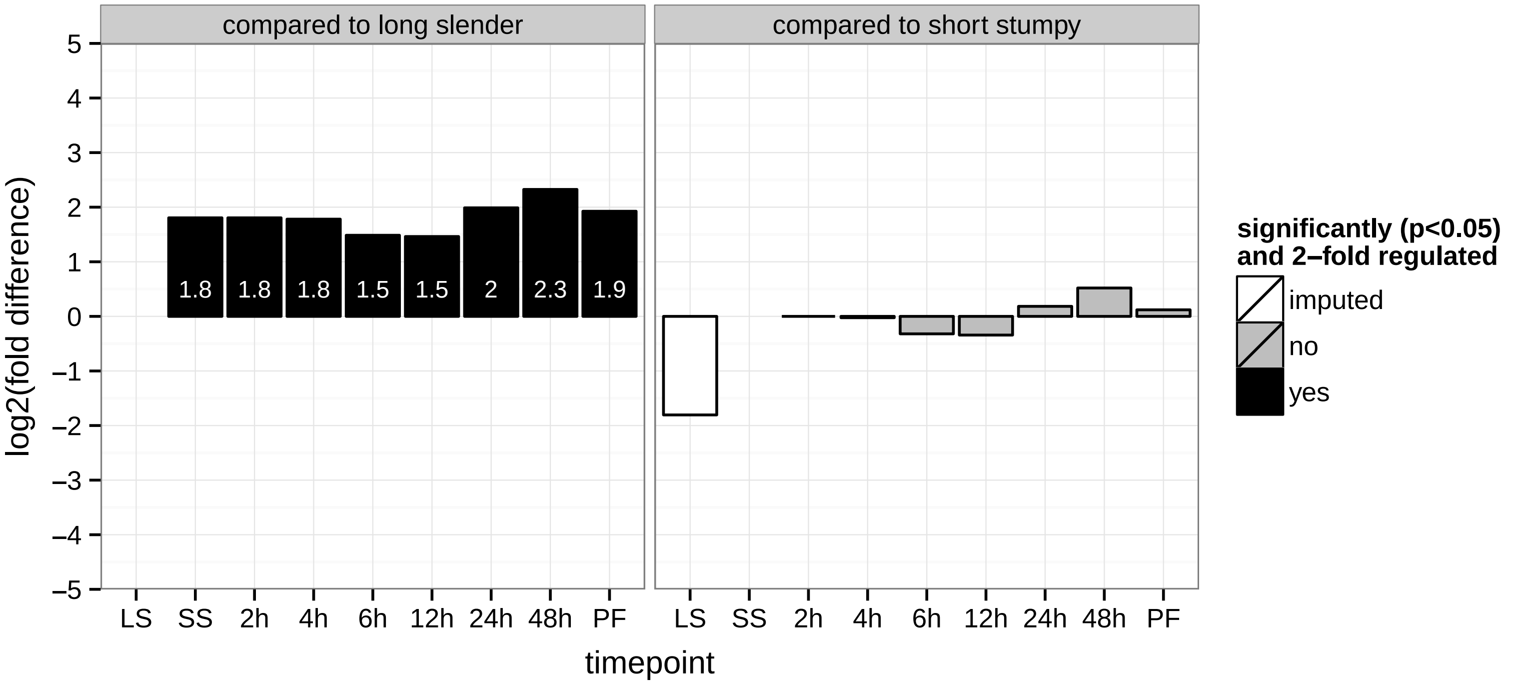
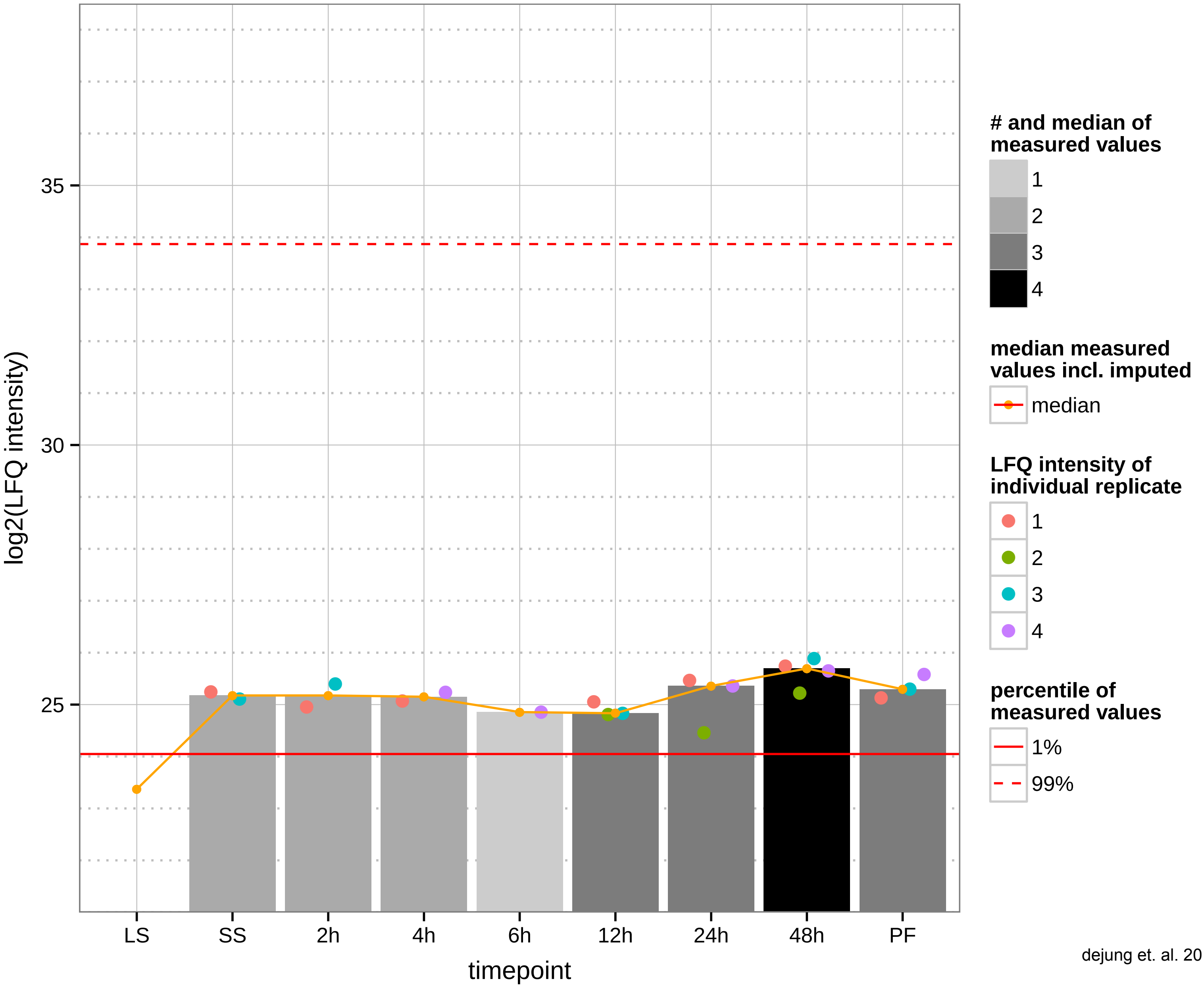
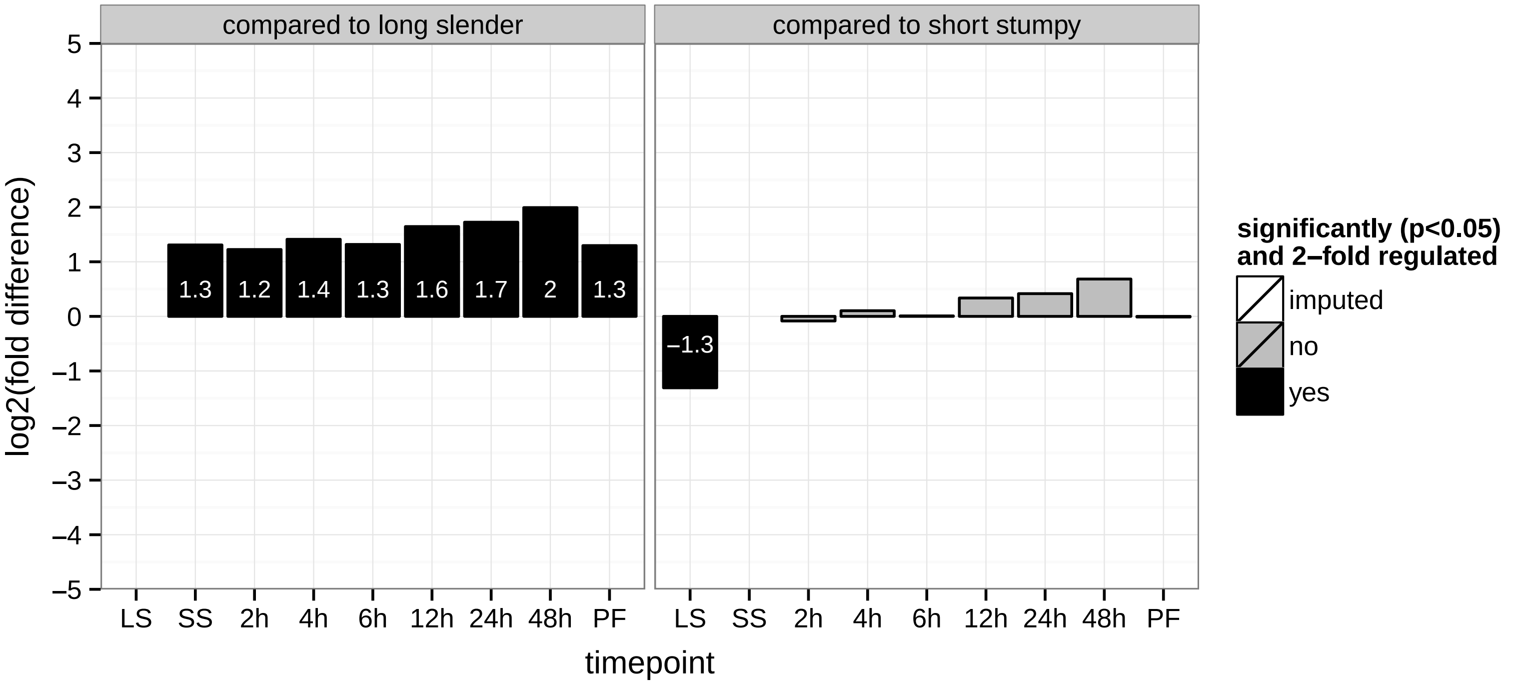
hypothetical protein, conserved
Tb927.9.4420
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

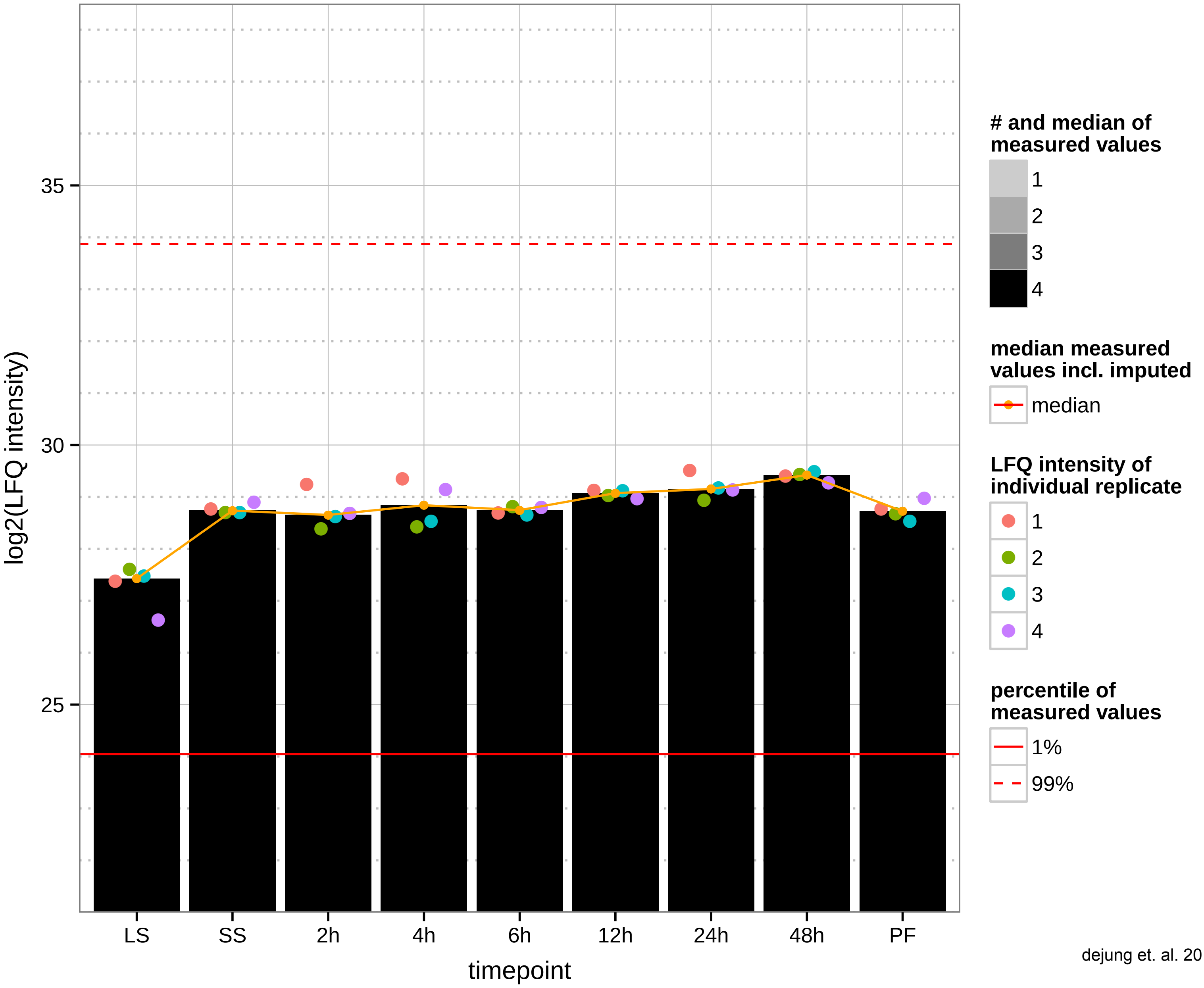




dejung et. al. 2015

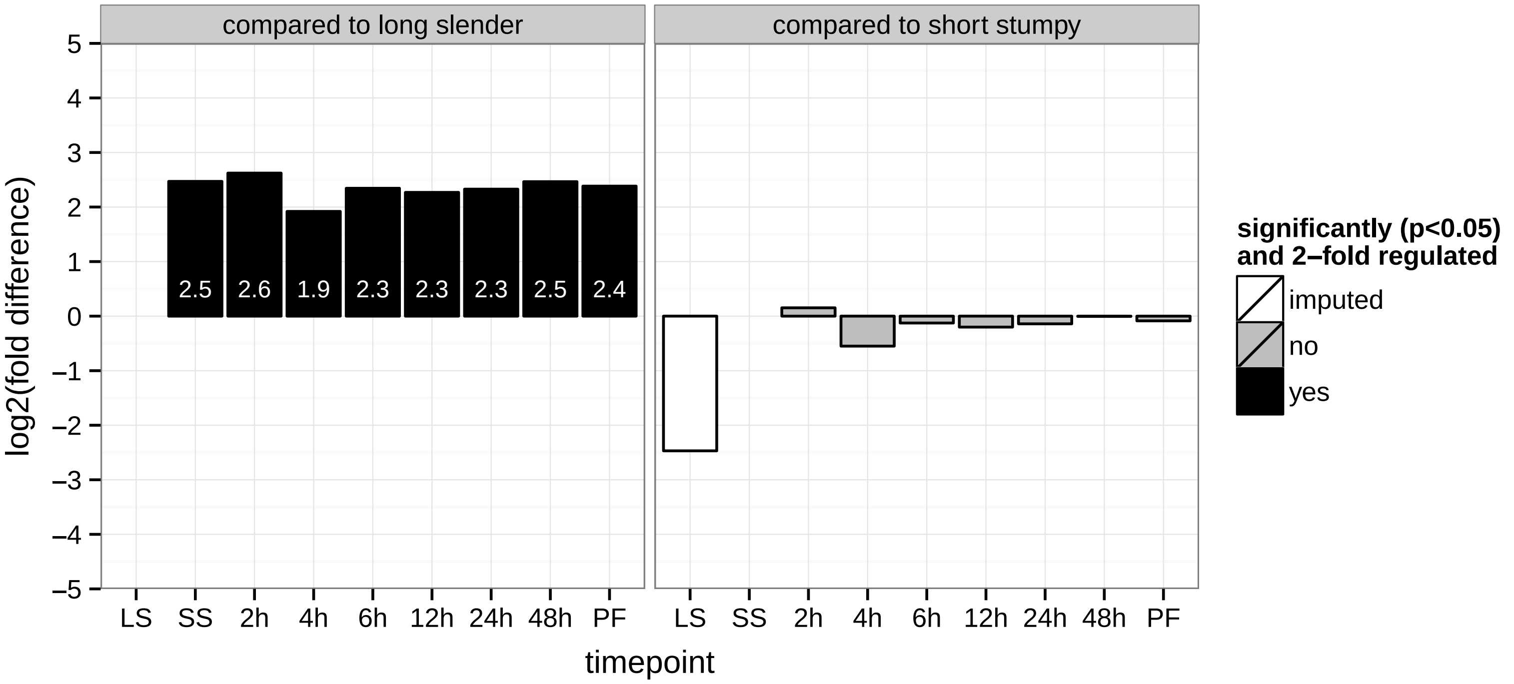
mitochondrial processing peptide beta subunit, putative, metallo–peptidase, Clan ME, Family M16
Tb927.9.4520
AGOF: catalytic activity, metalloendopeptidase activity, zinc ion binding
AGOC: mitochondrial processing peptidase complex, mitochondrion
AGOP: protein processing involved in protein targeting to mitochondrion, proteolysis
PGOF: catalytic activity, metal ion binding, metalloendopeptidase activity, zinc ion binding
PGOC: null
PGOP: proteolysis

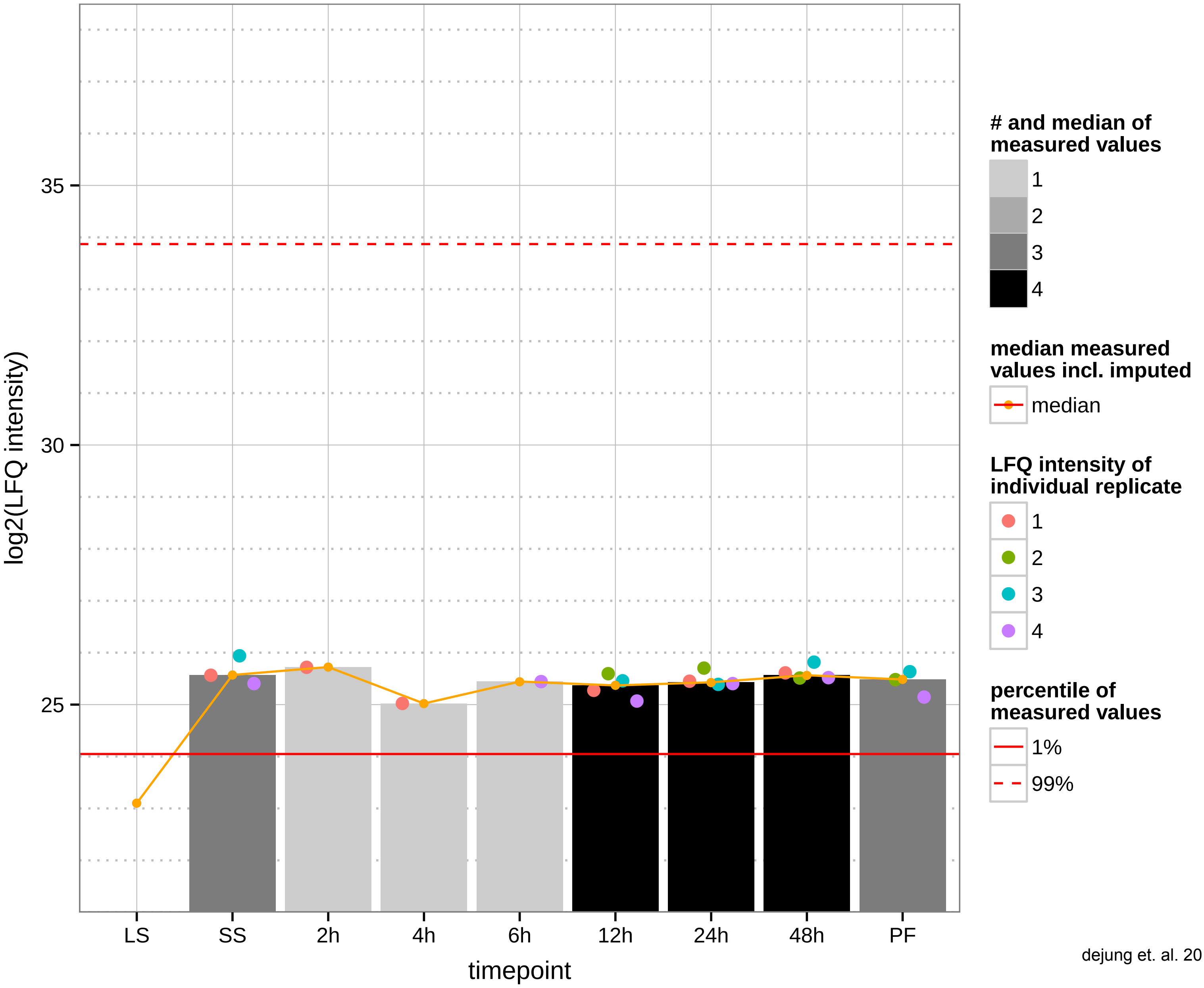




dejung et. al. 2015

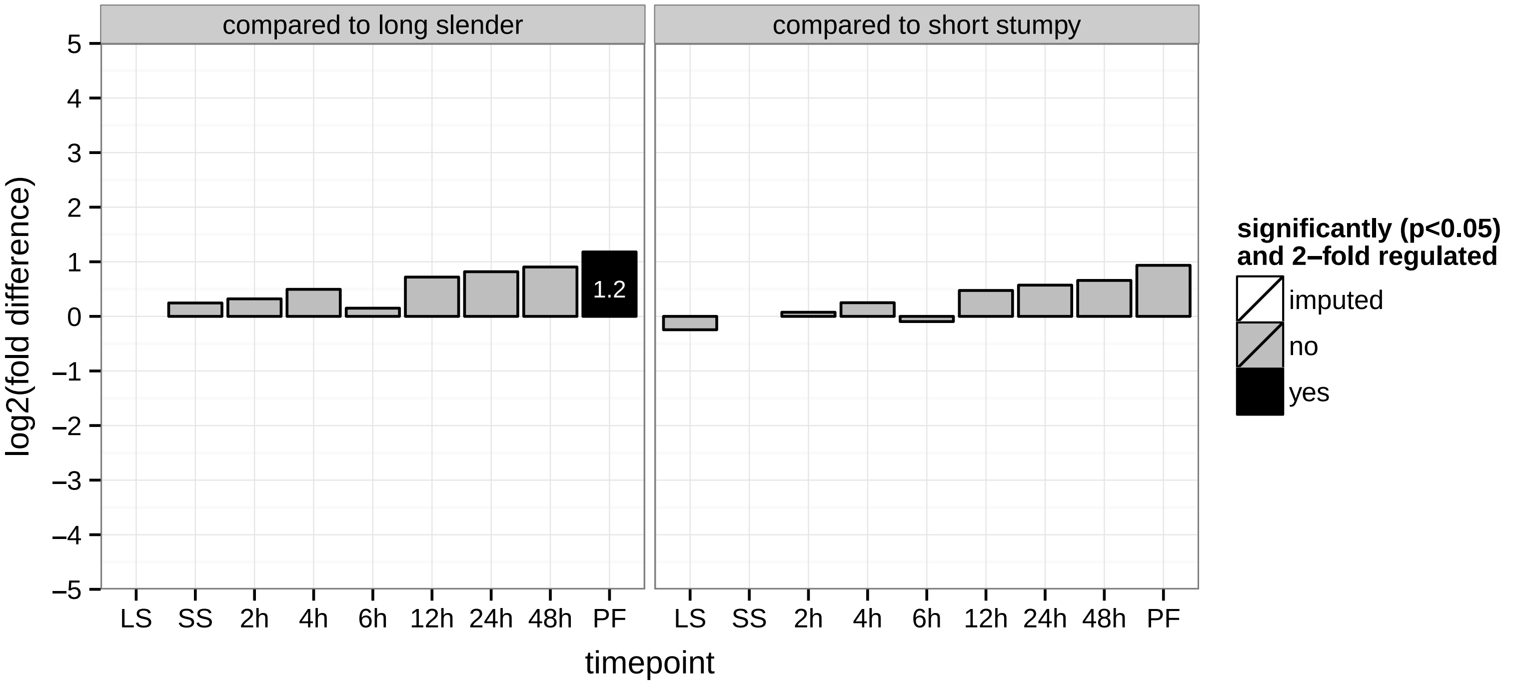
hypothetical protein, conserved
Tb927.9.4660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

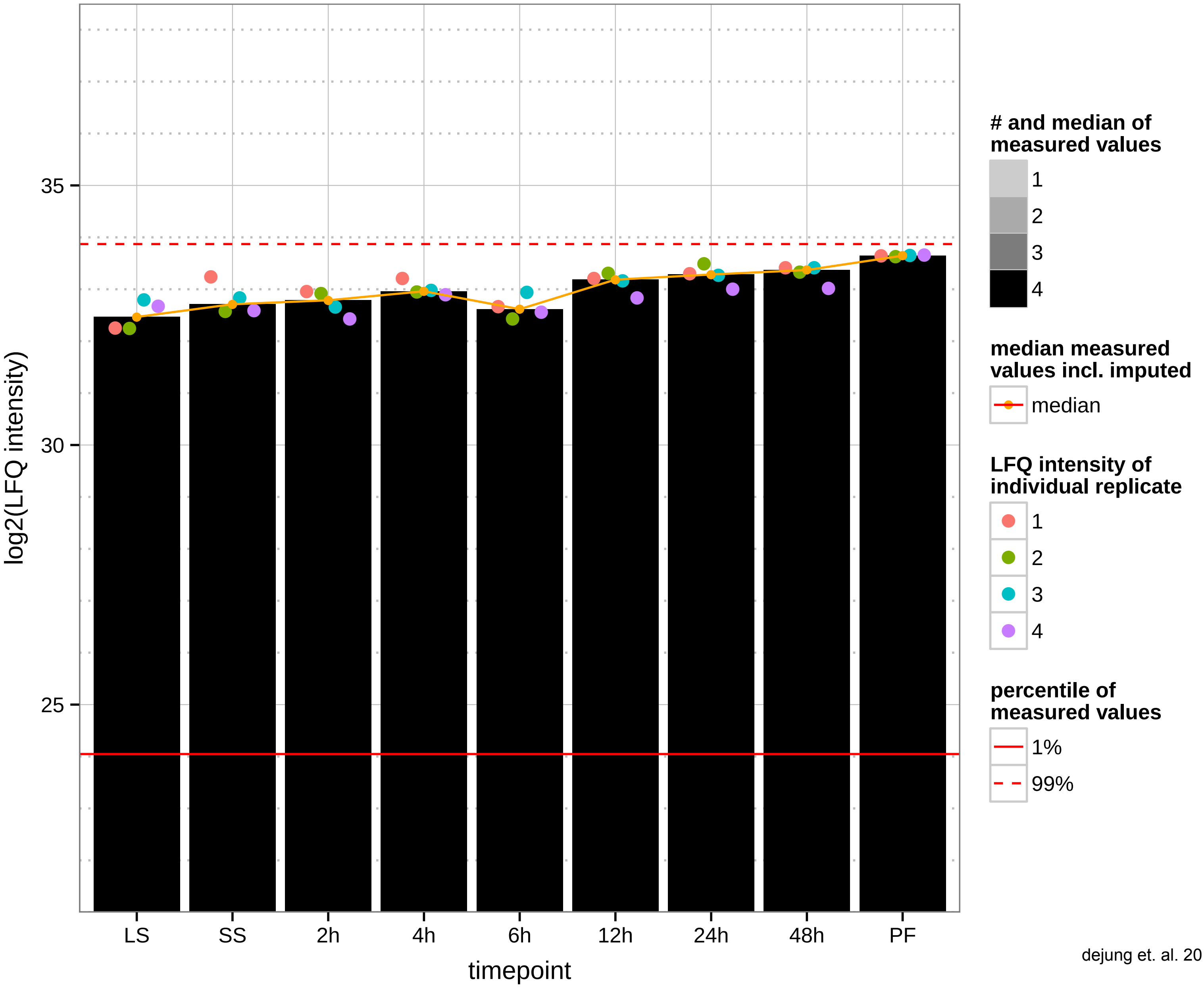




dejung et. al. 2015

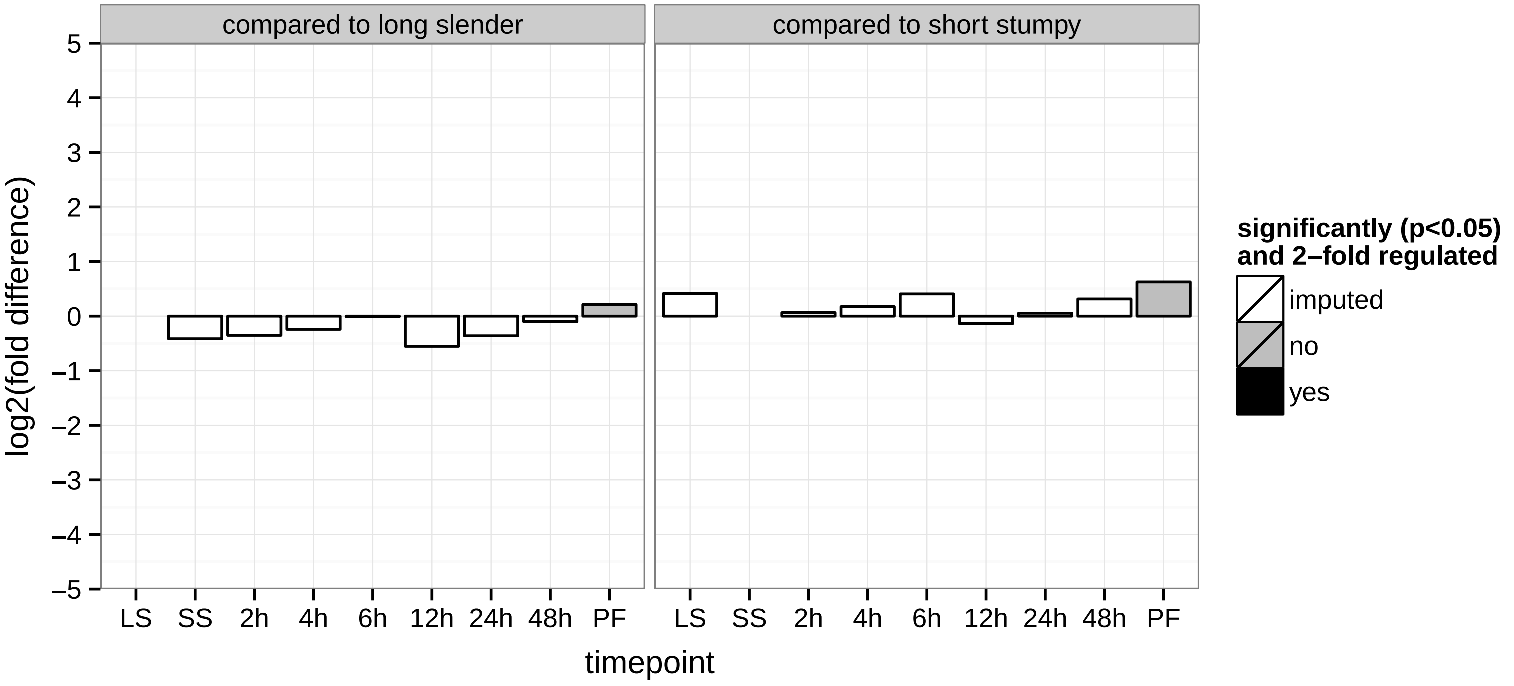
ATP−dependent DEAD box helicase, putative, eukaryotic initiation factor 4a
Tb927.9.4680
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: cytosol
AGOP: nucleobase−containing compound metabolic process, translation
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null

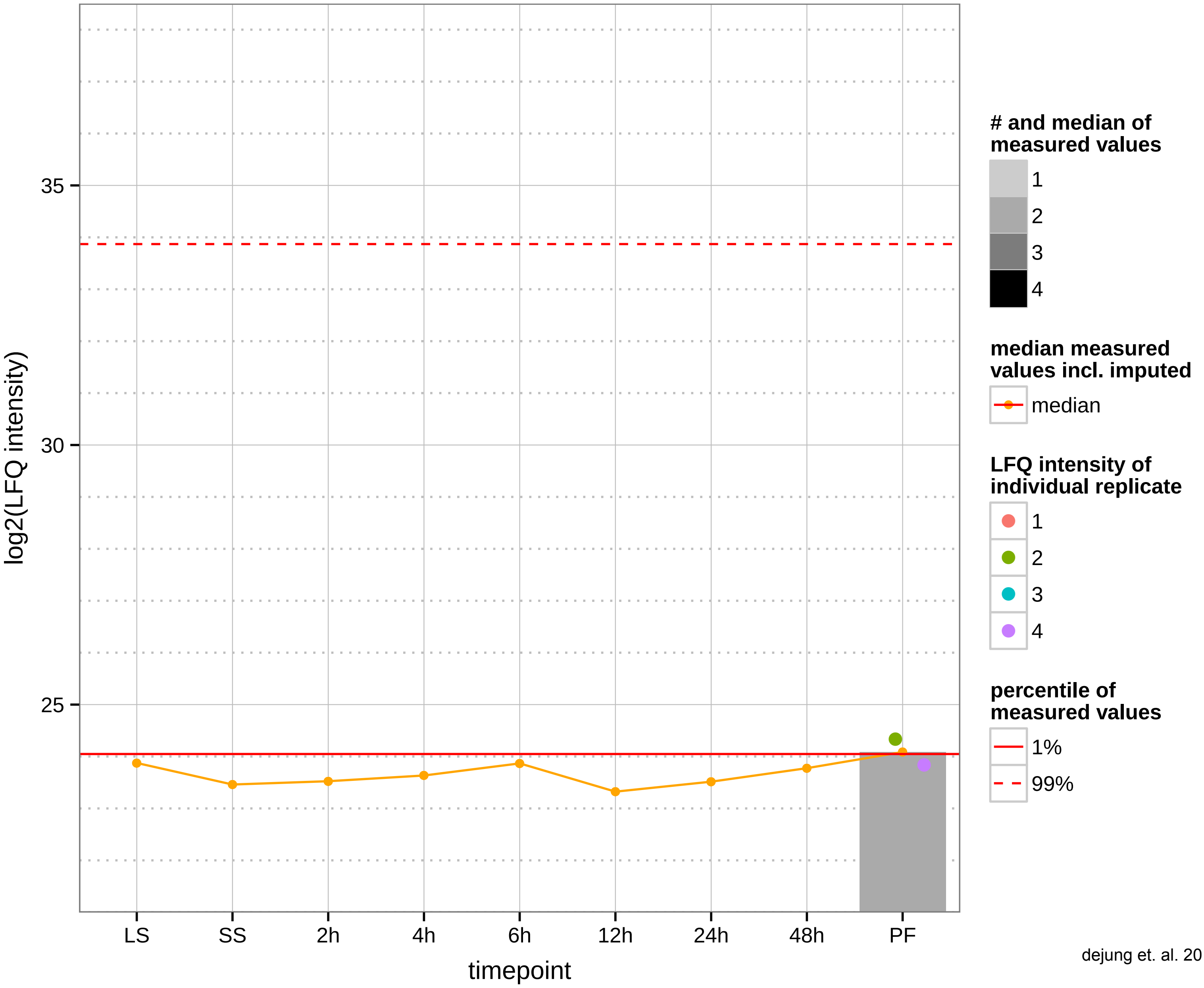




dejung et. al. 2015

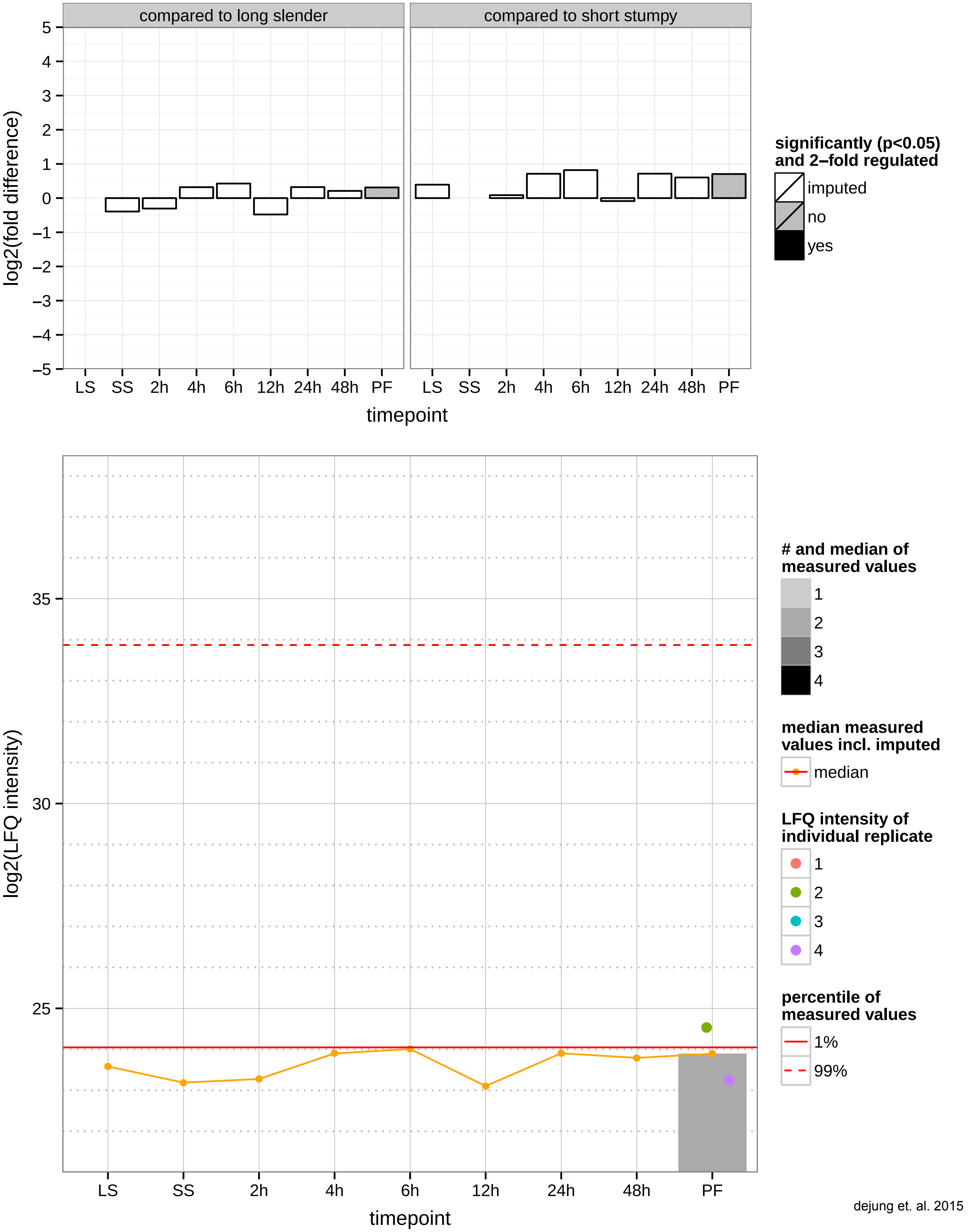
hypothetical protein, conserved
Tb927.9.5000
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.5020
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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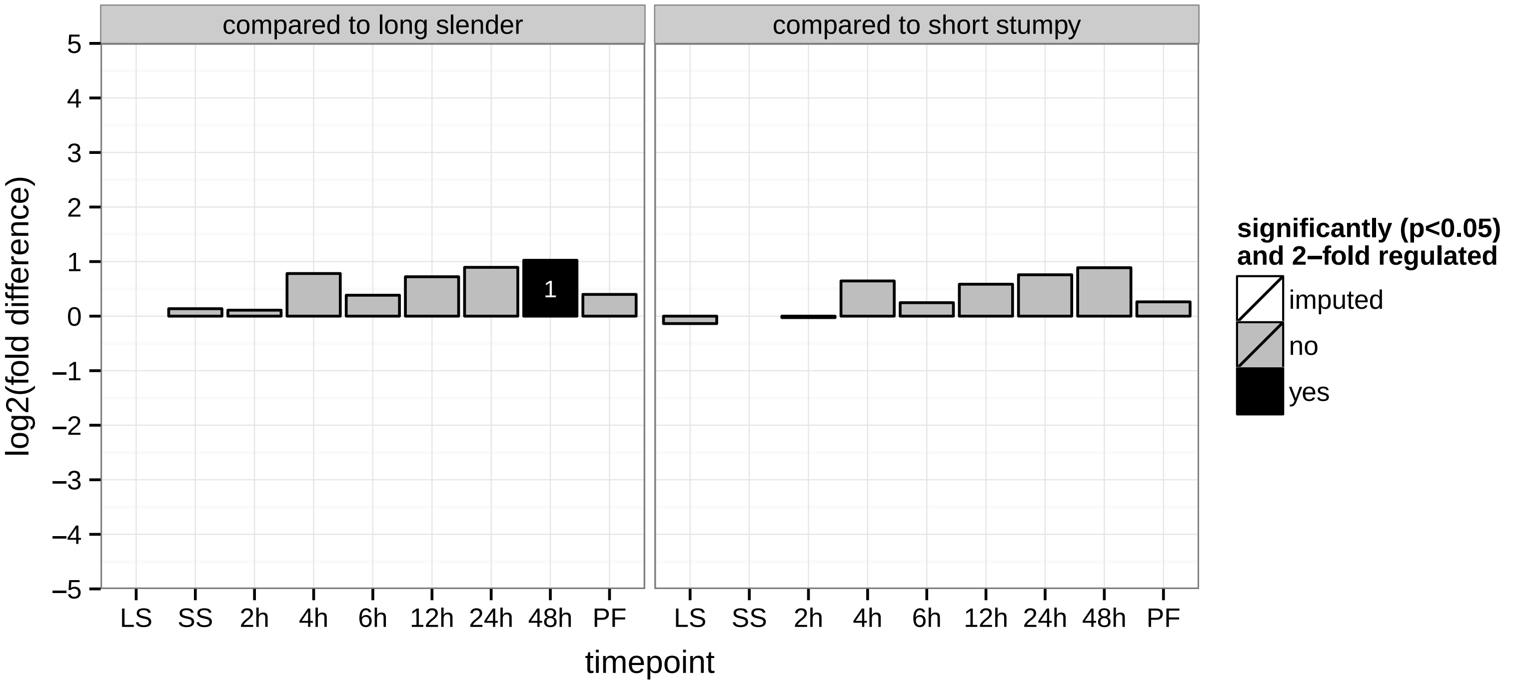
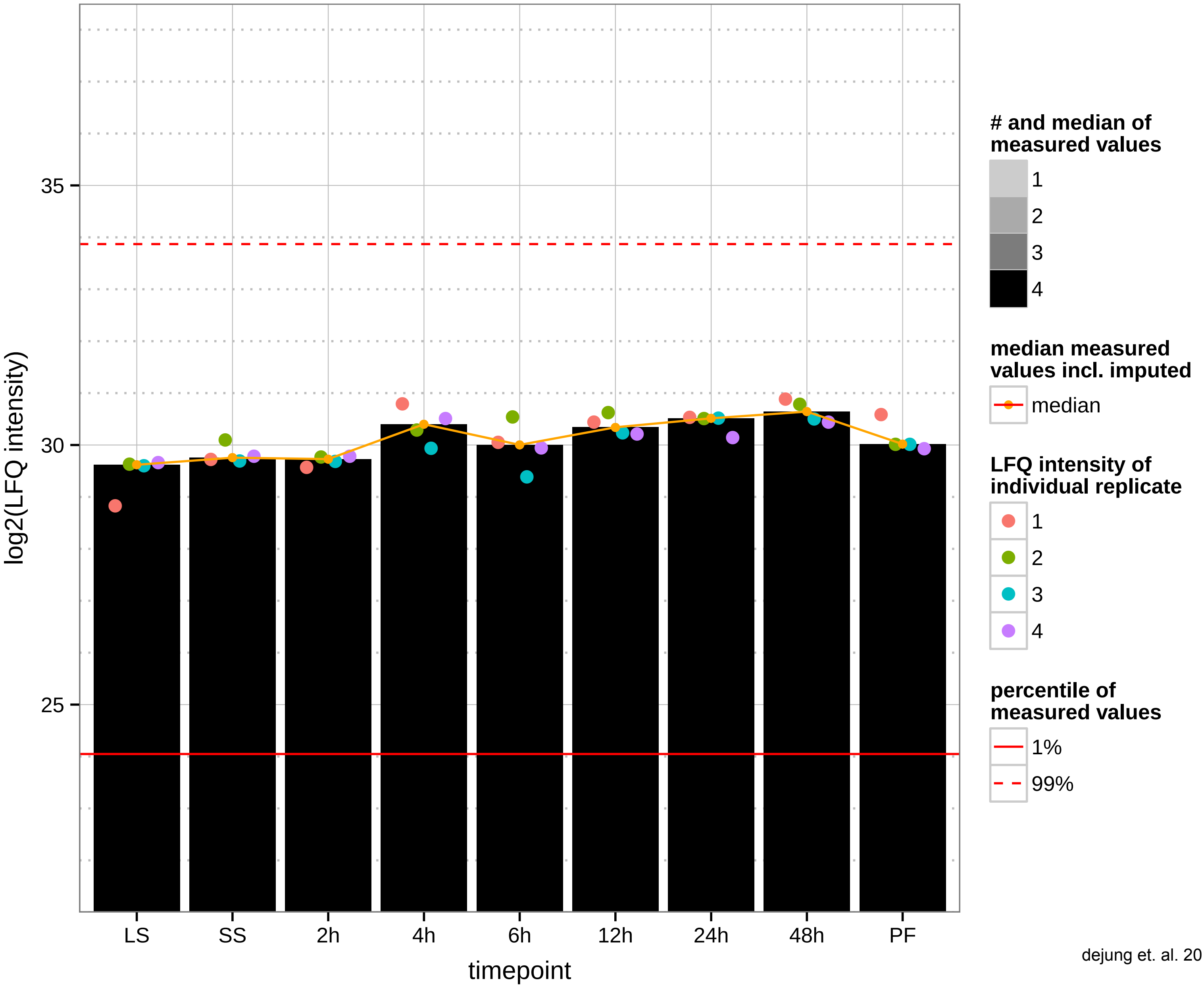
ribosomal protein S6, putative, NHP2/RS6–like protein (NHP2)
Tb927.9.5150
AGOF: structural constituent of ribosome
AGOC: ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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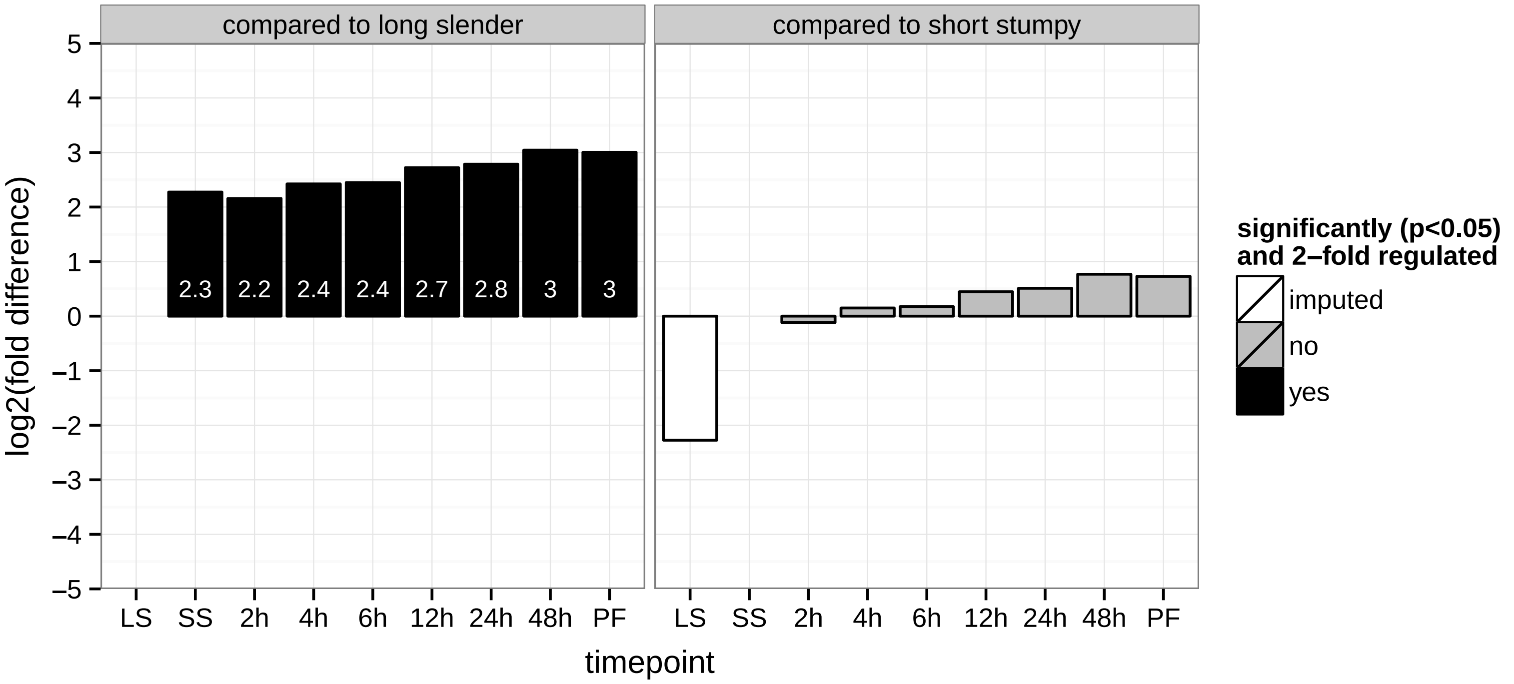
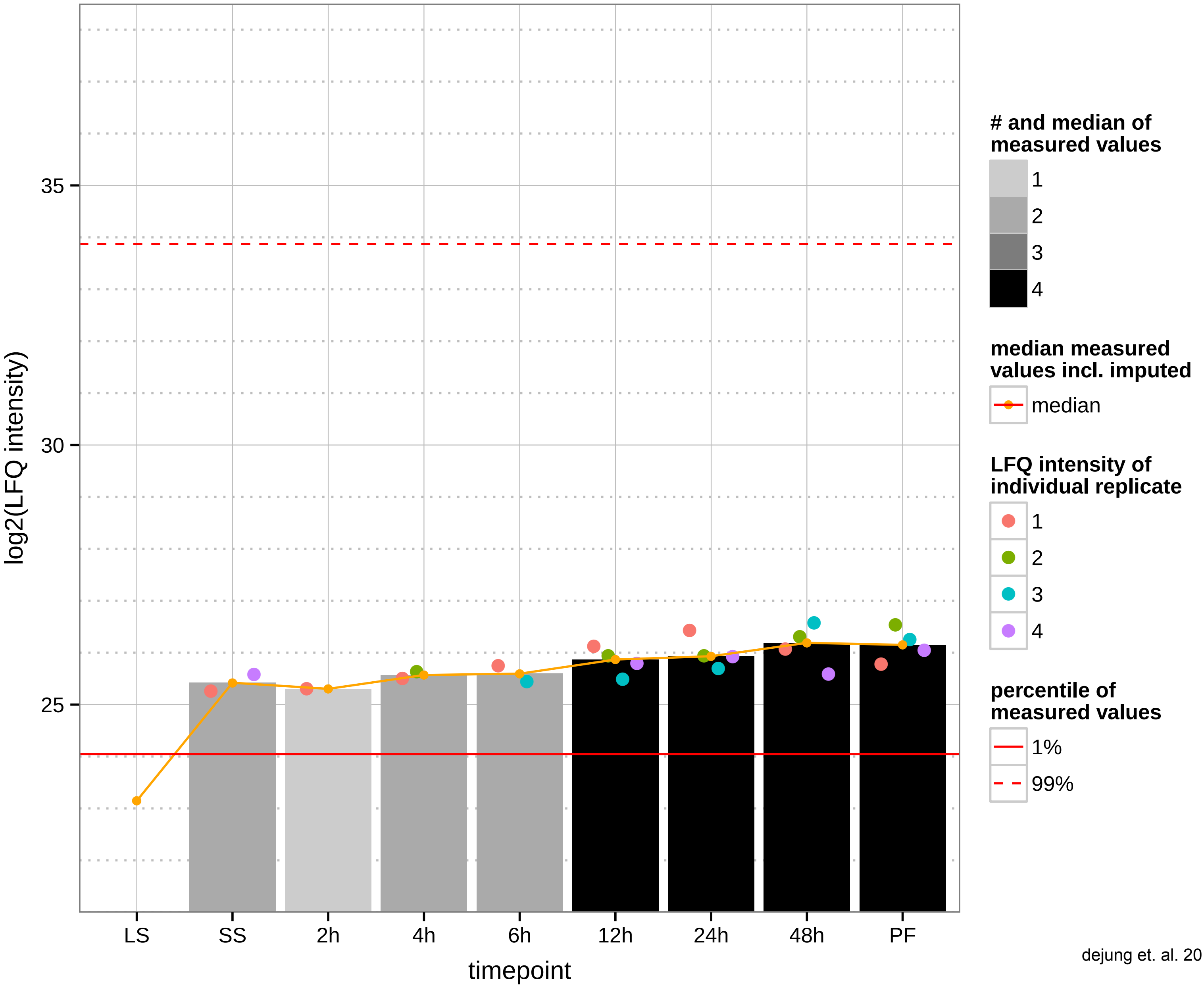
phosphomevalonate kinase protein, putative
Tb927.9.5170
AGOF: ATP binding, phosphomevalonate kinase activity
AGOC: cytoplasm, nucleus
AGOP: ergosterol biosynthetic process, farnesyl diphosphate biosynthetic process, mevalonate pathway, isopentenyl diphosp
PGOF: ATP binding
PGOC: null
PGOP: null





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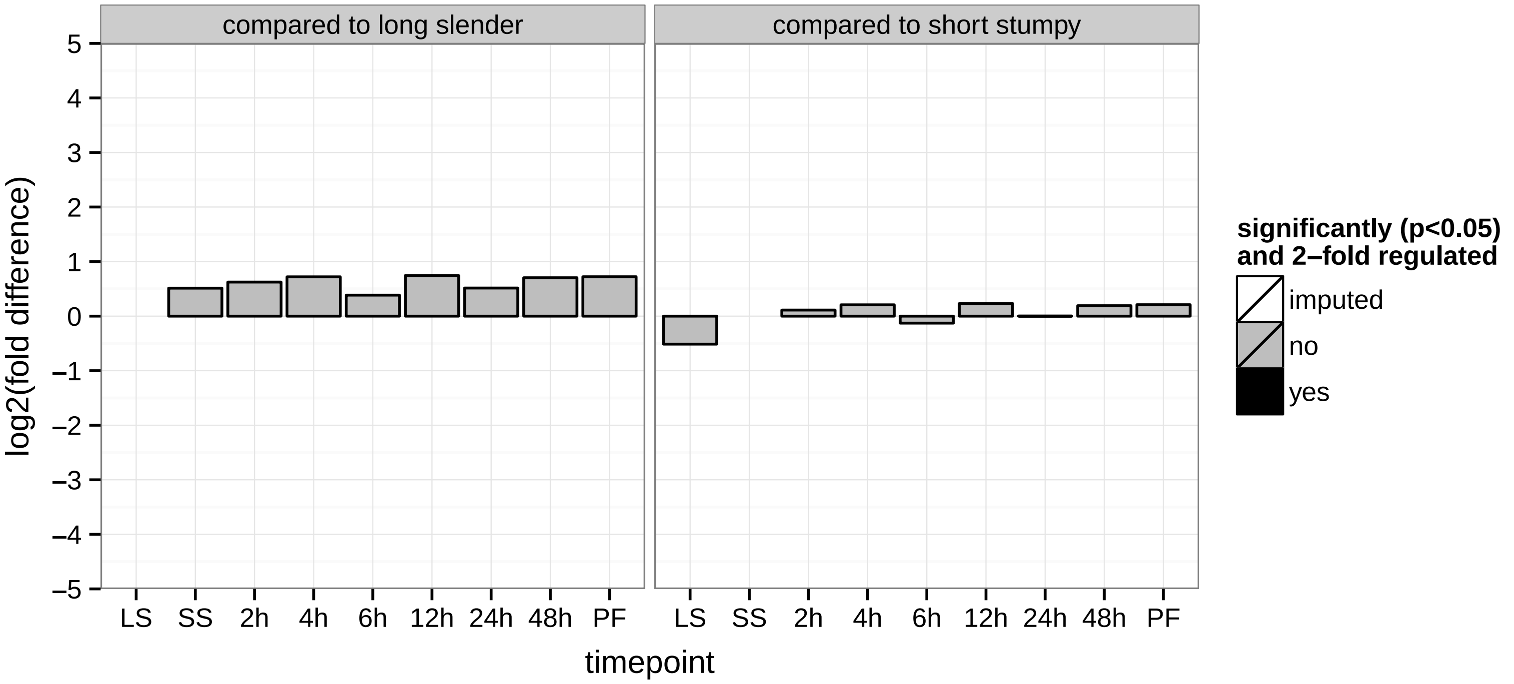
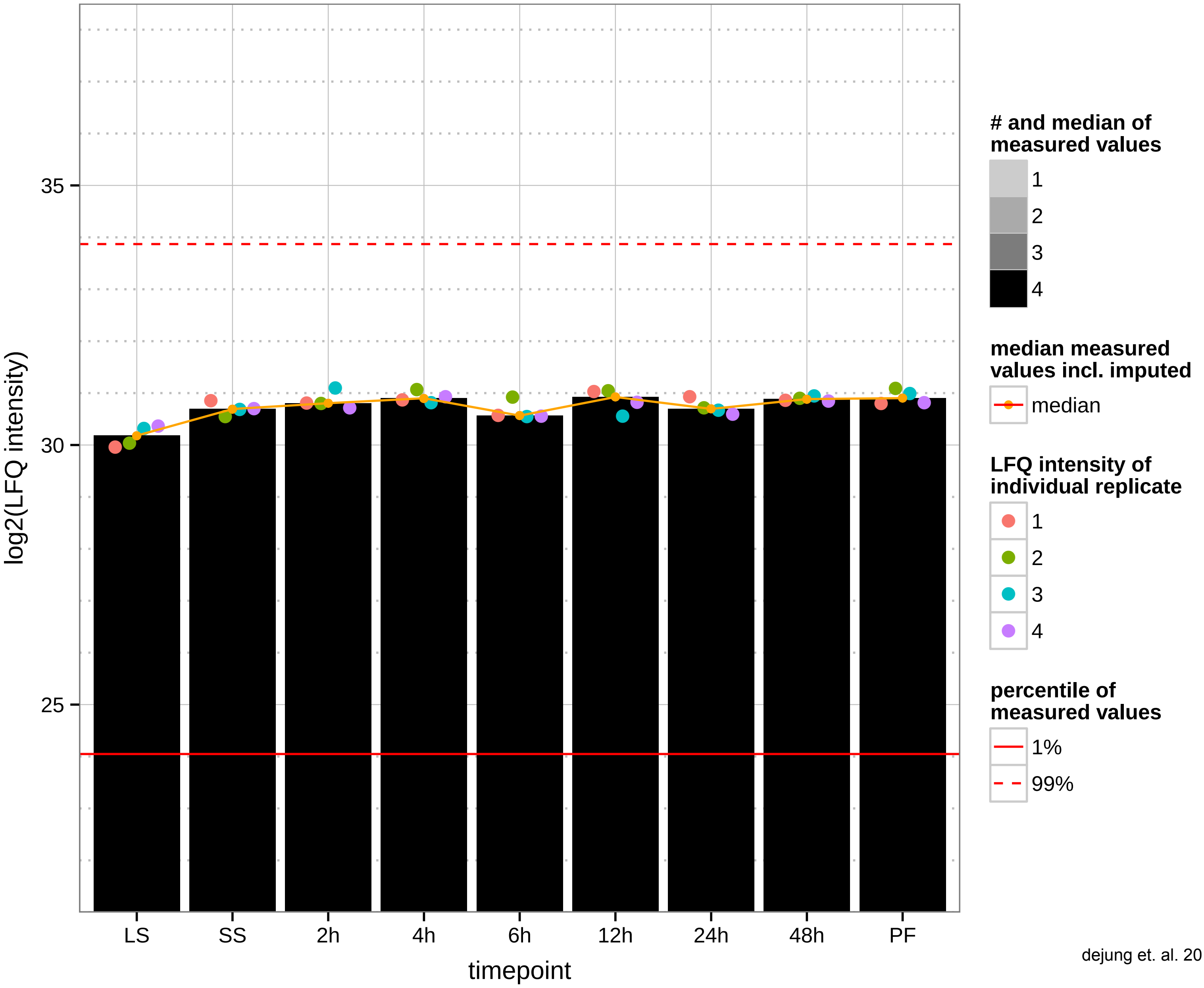
proliferative cell nuclear antigen (PCNA), putative
Tb927.9.5190
AGOF: DNA binding, DNA polymerase processivity factor activity
AGOC: PCNA complex
AGOP: regulation of DNA replication
PGOF: DNA binding, DNA polymerase processivity factor activity
PGOC: PCNA complex
PGOP: regulation of DNA replication





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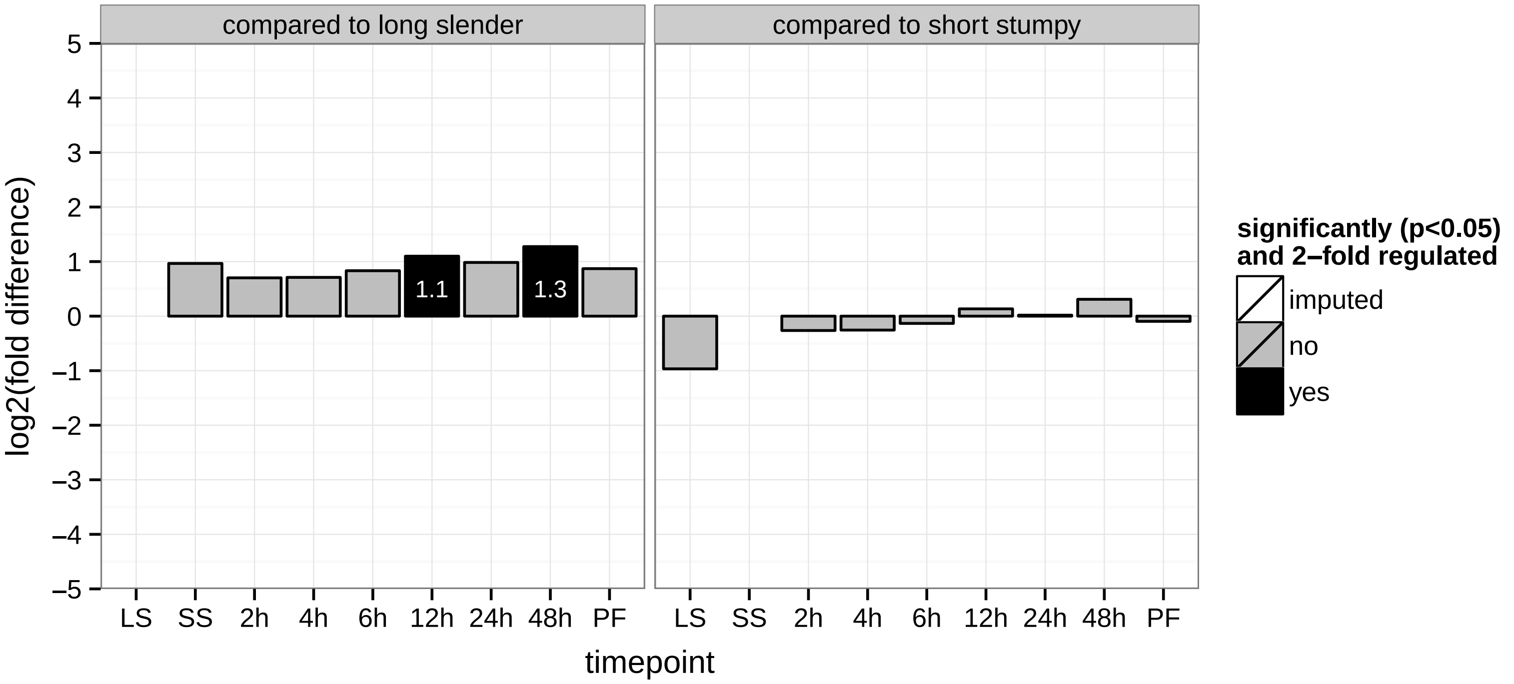
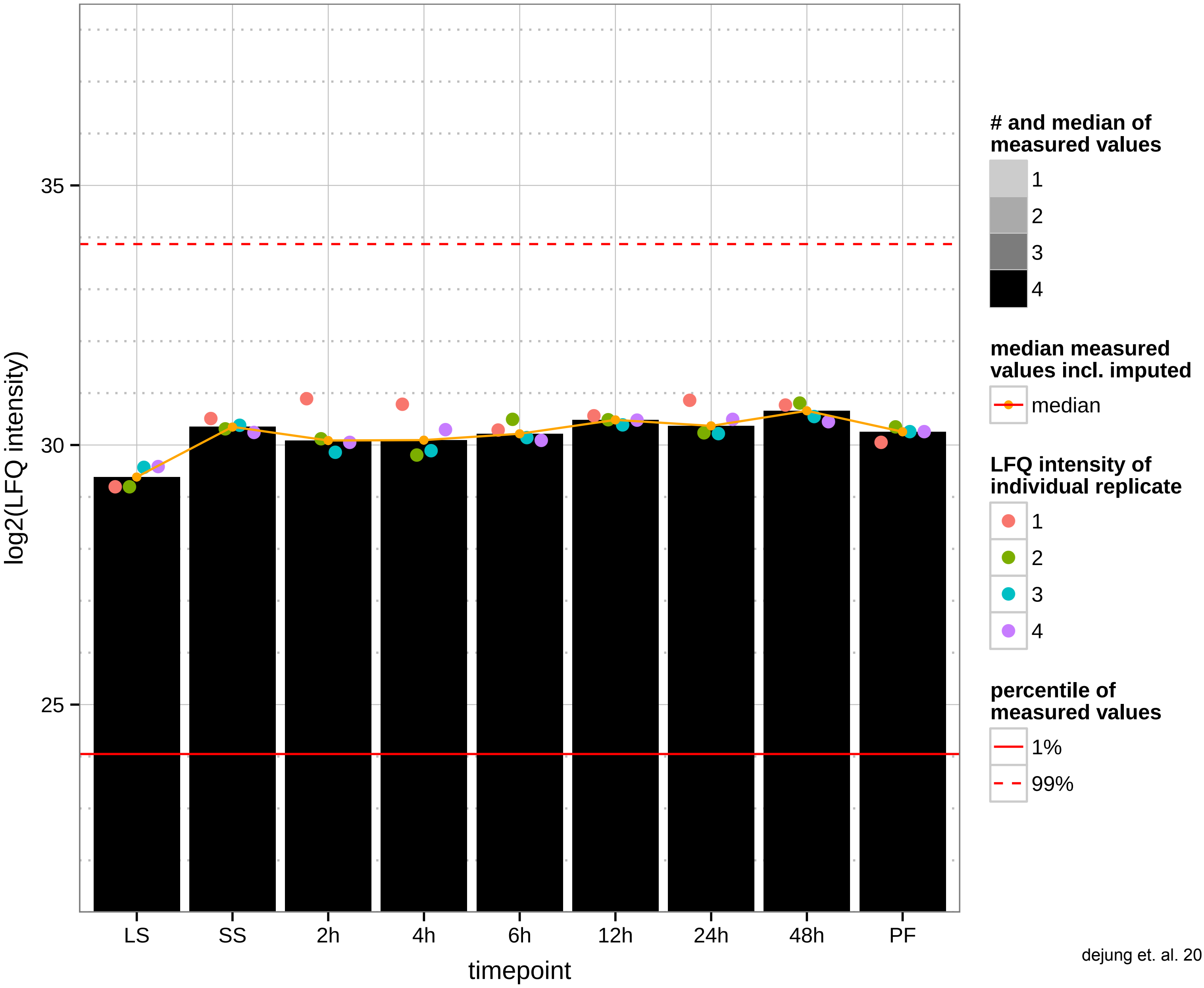
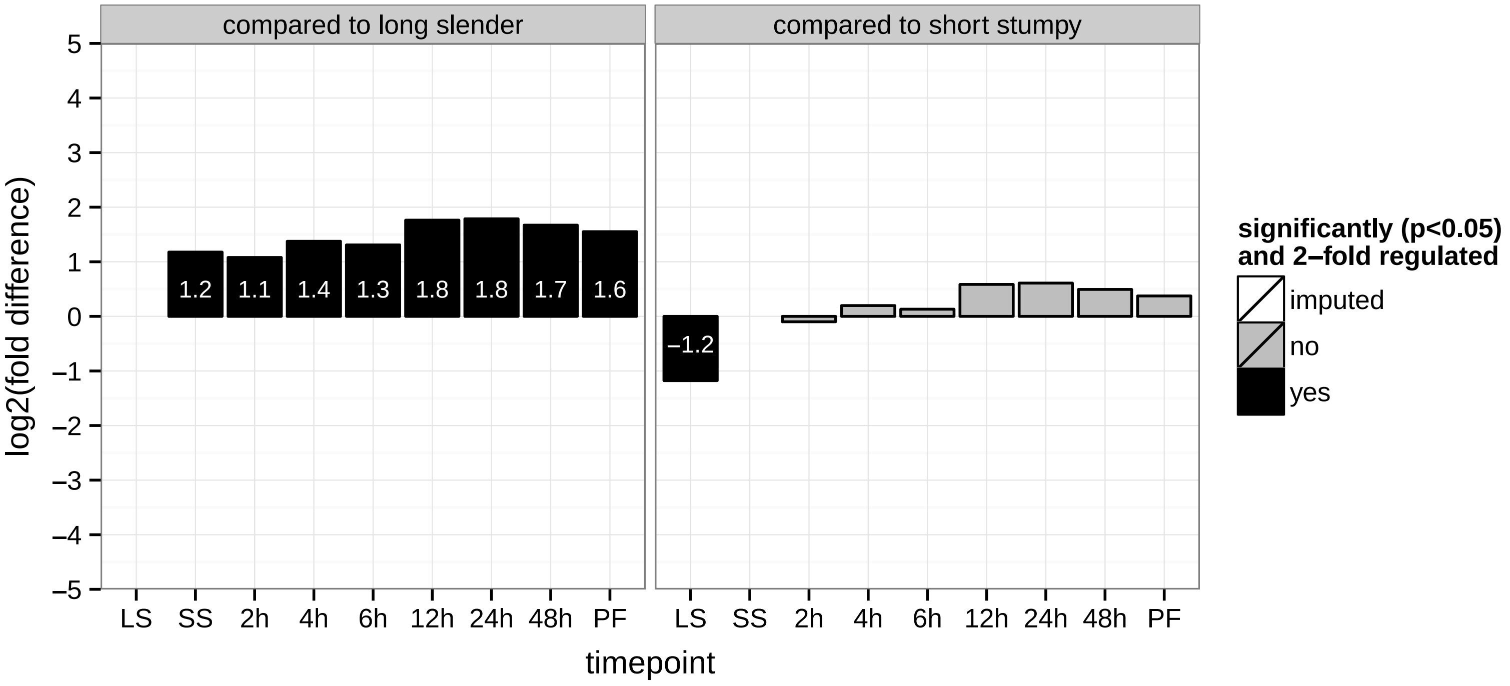
glutaminyl–tRNA synthetase, putative
Tb927.9.5210
AGOF: ATP binding, glutamine–tRNA ligase activity
AGOC: cytoplasm
AGOP: glutaminyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, glutamine–tRNA ligase activity, ligase activity, forming aminoacyl–tRNA a
PGOC: cytoplasm
PGOP: glutaminyl–tRNA aminoacylation, tRNA aminoacylation, tRNA aminoacylation for protein translation, translation

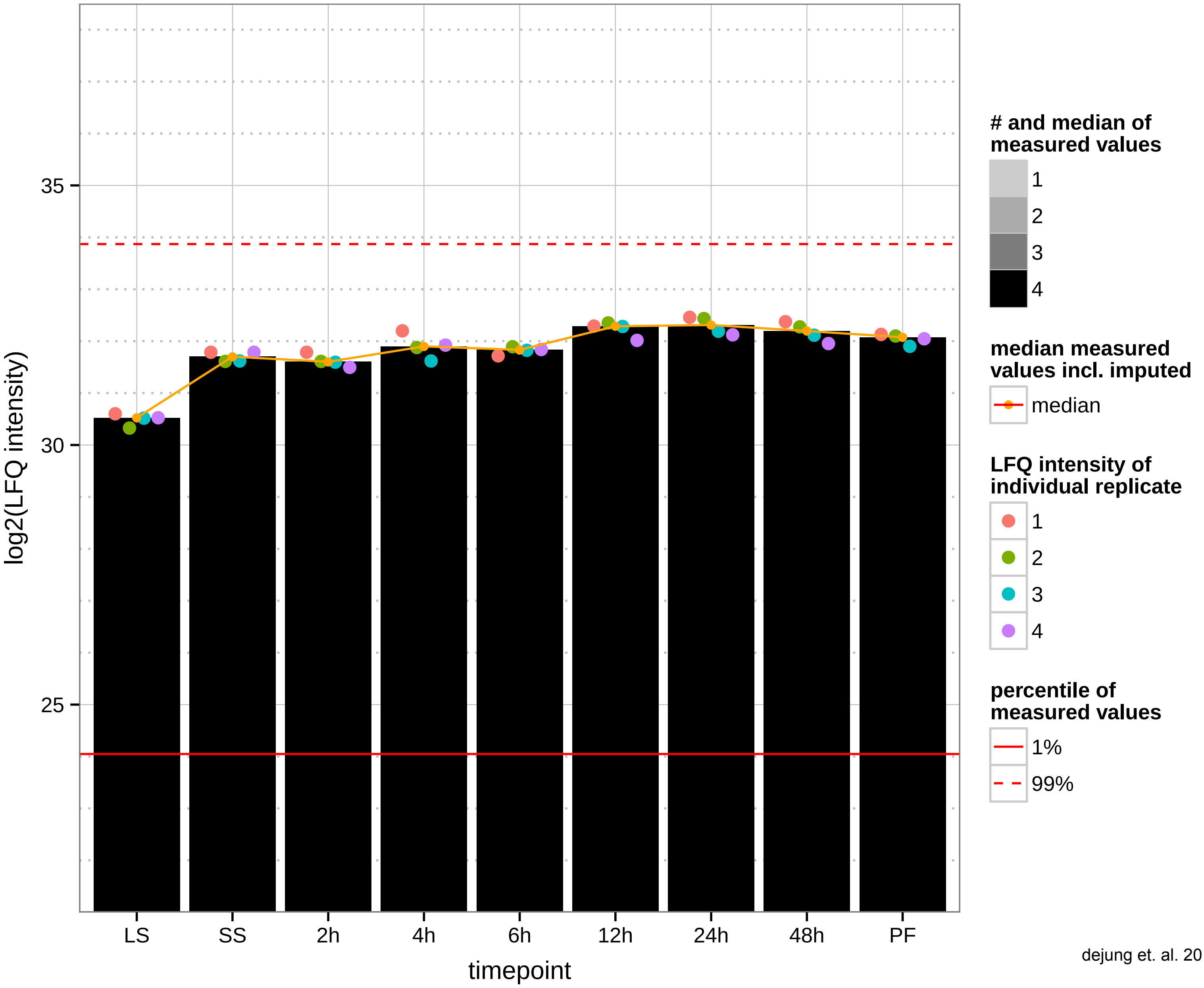




dejung et. al. 2015

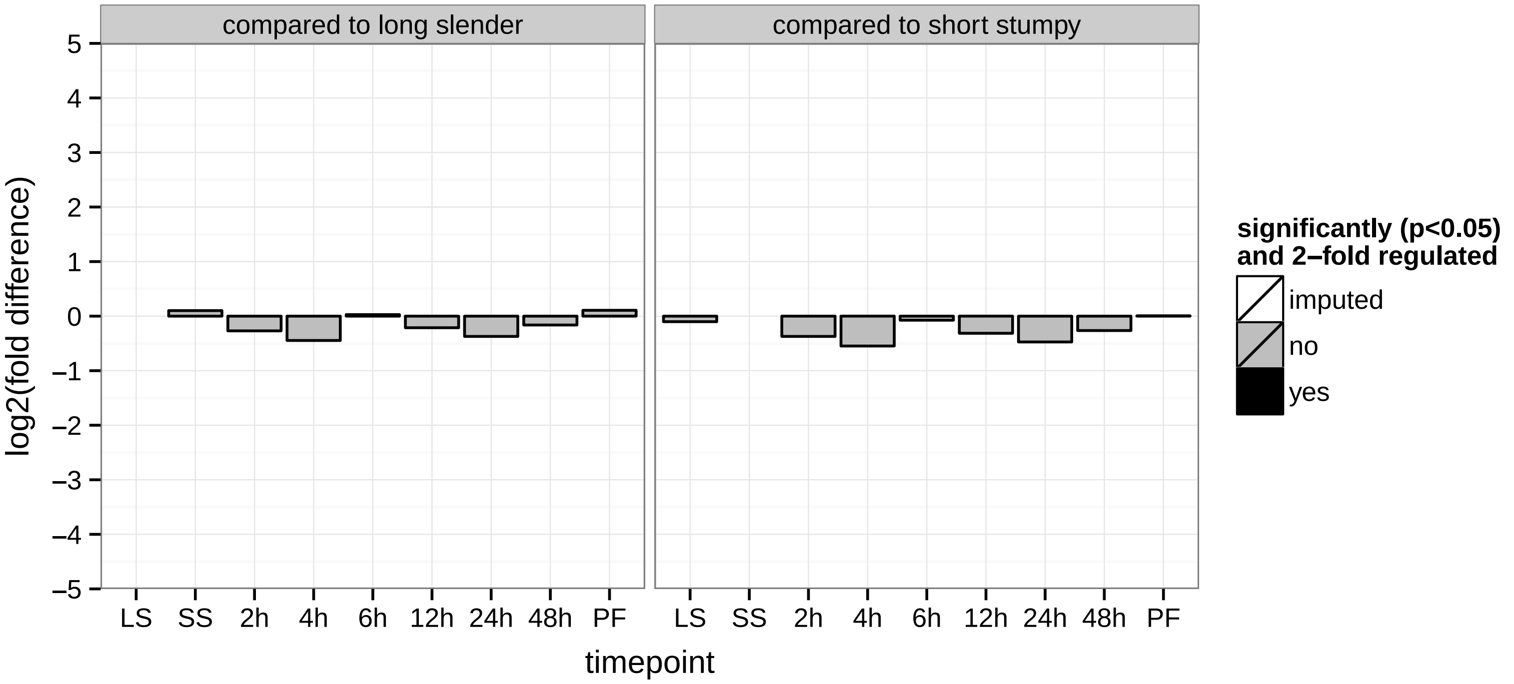
nucleolar RNA binding protein, putative
Tb927.9.5320
AGOF: snoRNA binding
AGOC: null
AGOP: nuclear mRNA splicing, via spliceosome
PGOF: null
PGOC: null
PGOP: null

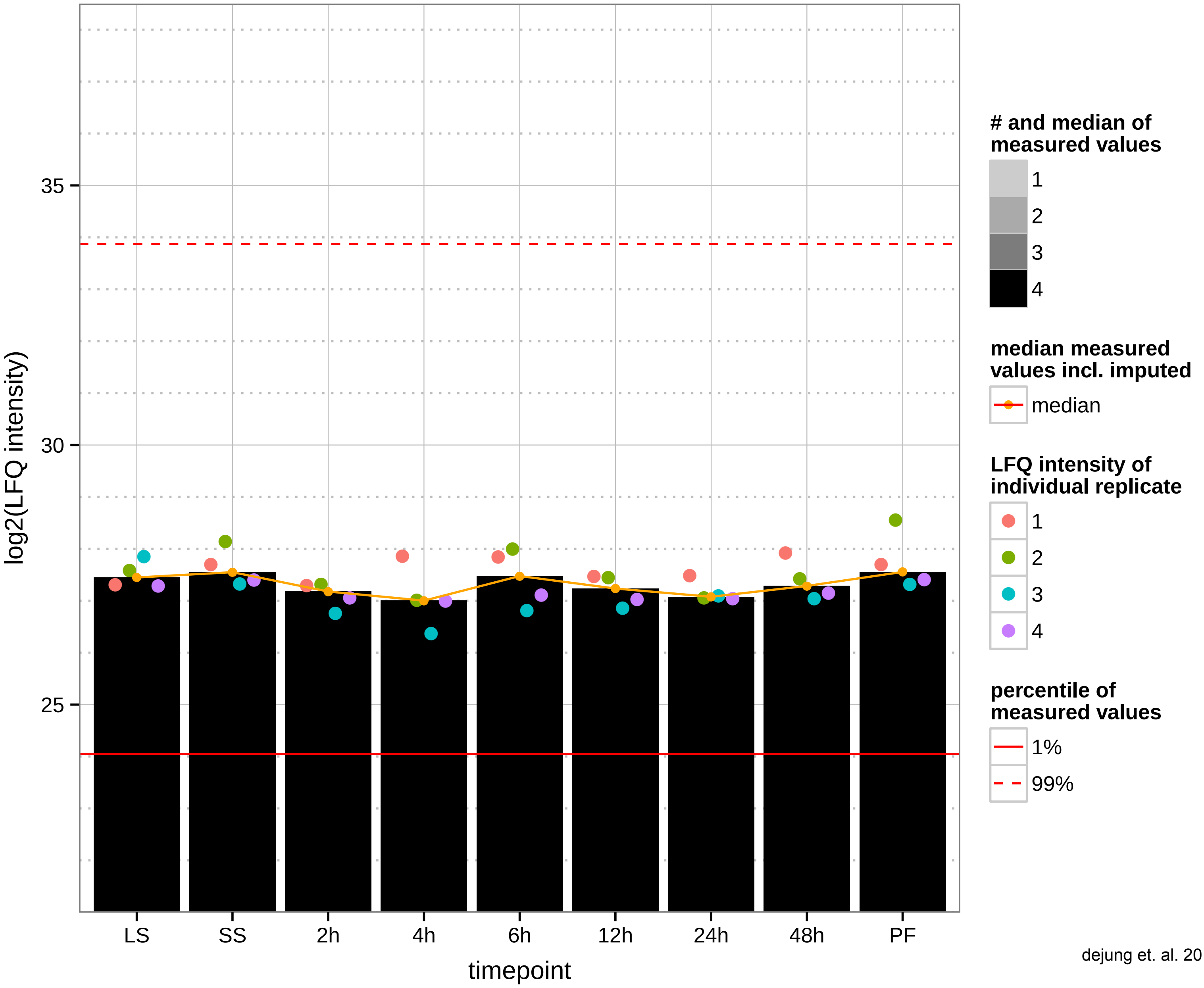




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.5410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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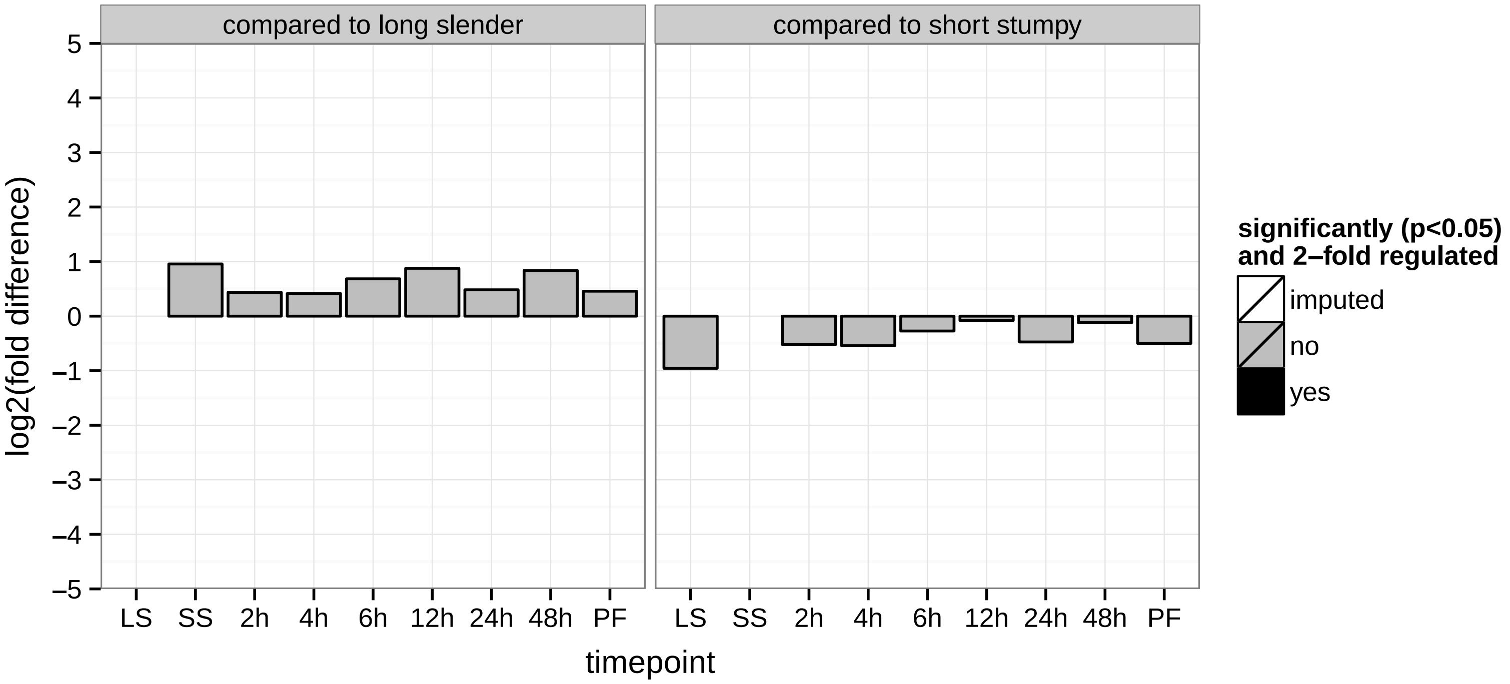
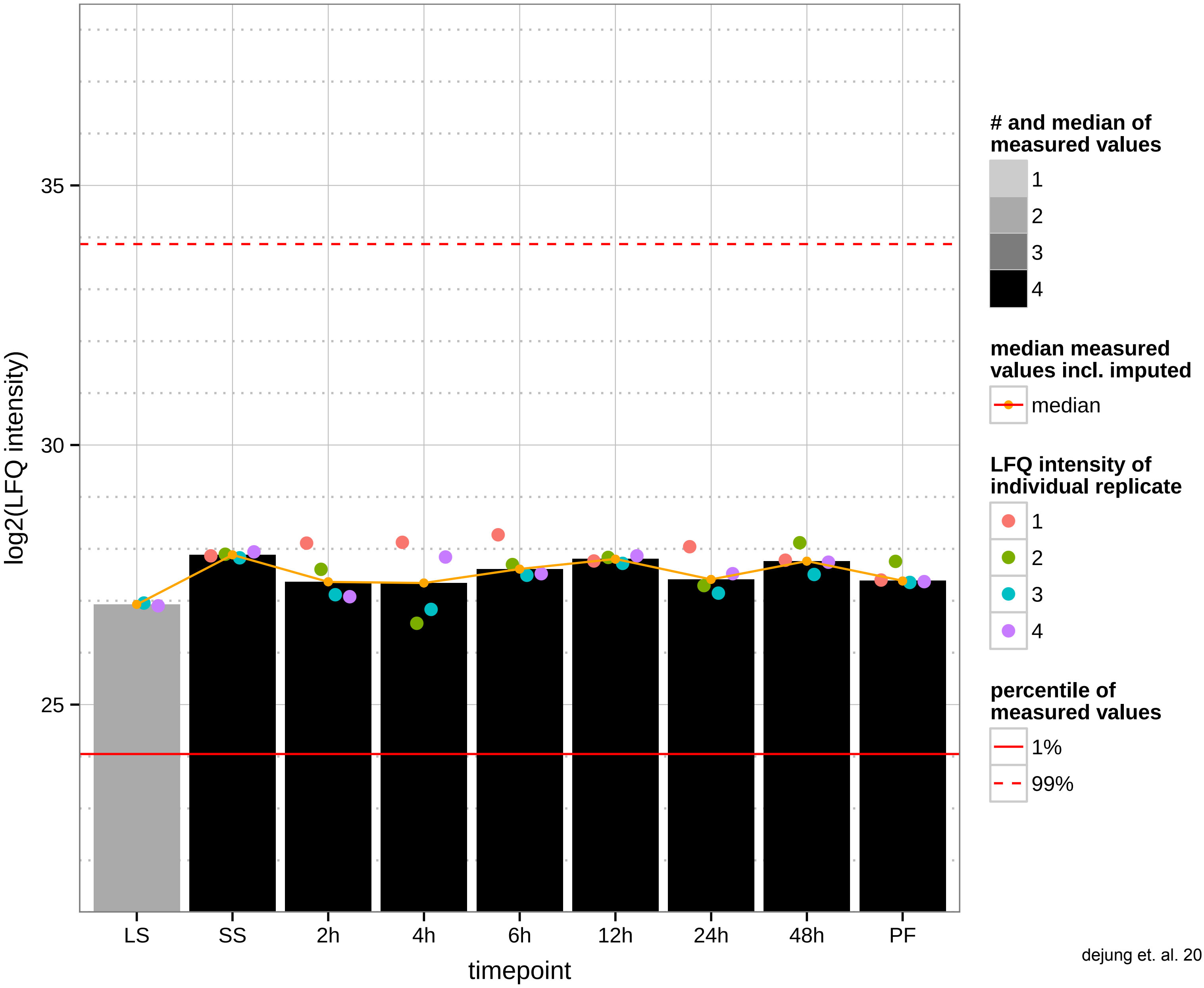
Eukaryotic translation initiation factor 4 gamma type 2 (eif4g2)
Tb927.9.5460
AGOF: RNA binding, nucleic acid binding, protein binding
AGOC: eukaryotic translation initiation factor 4F complex
AGOP: RNA metabolic process, nucleobase‒containing compound metabolic process, translation
PGOF: DNA binding, RNA binding, binding, protein binding
PGOC: null
PGOP: null





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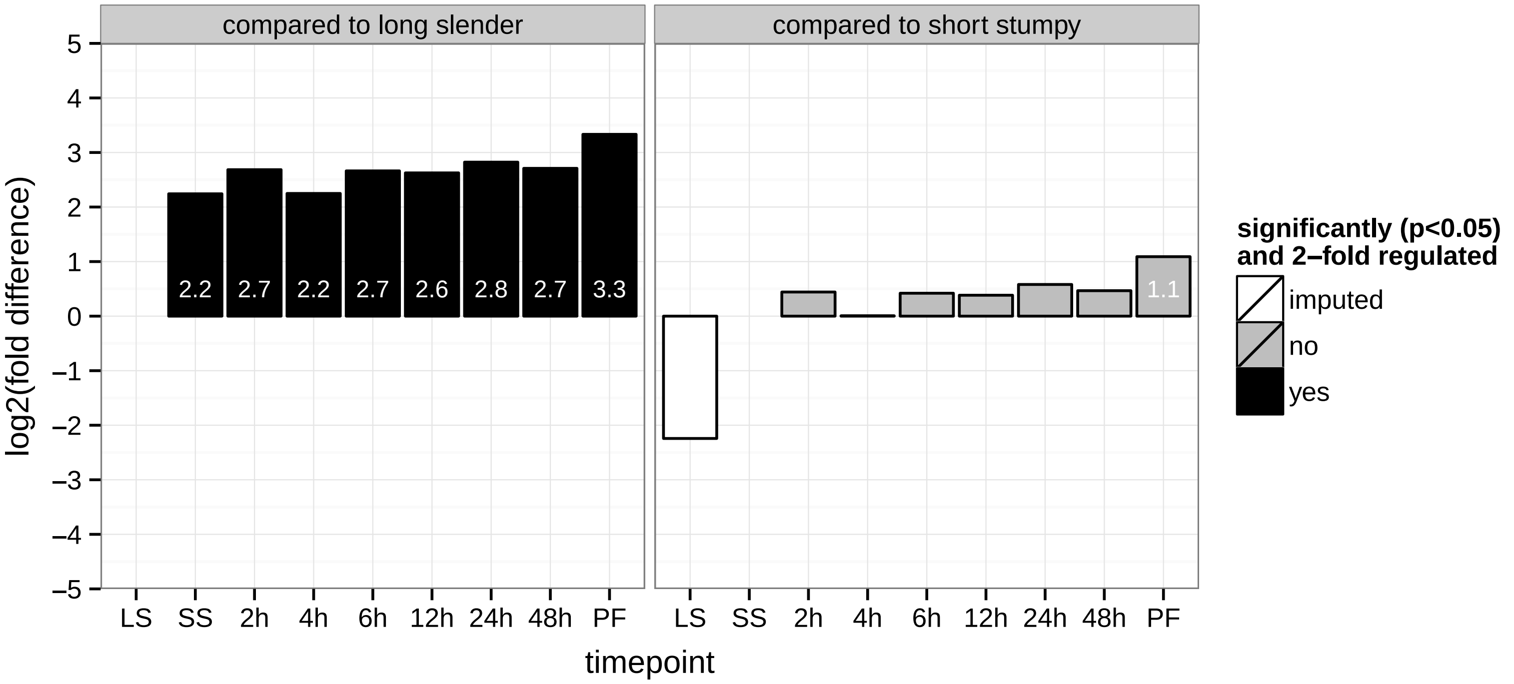
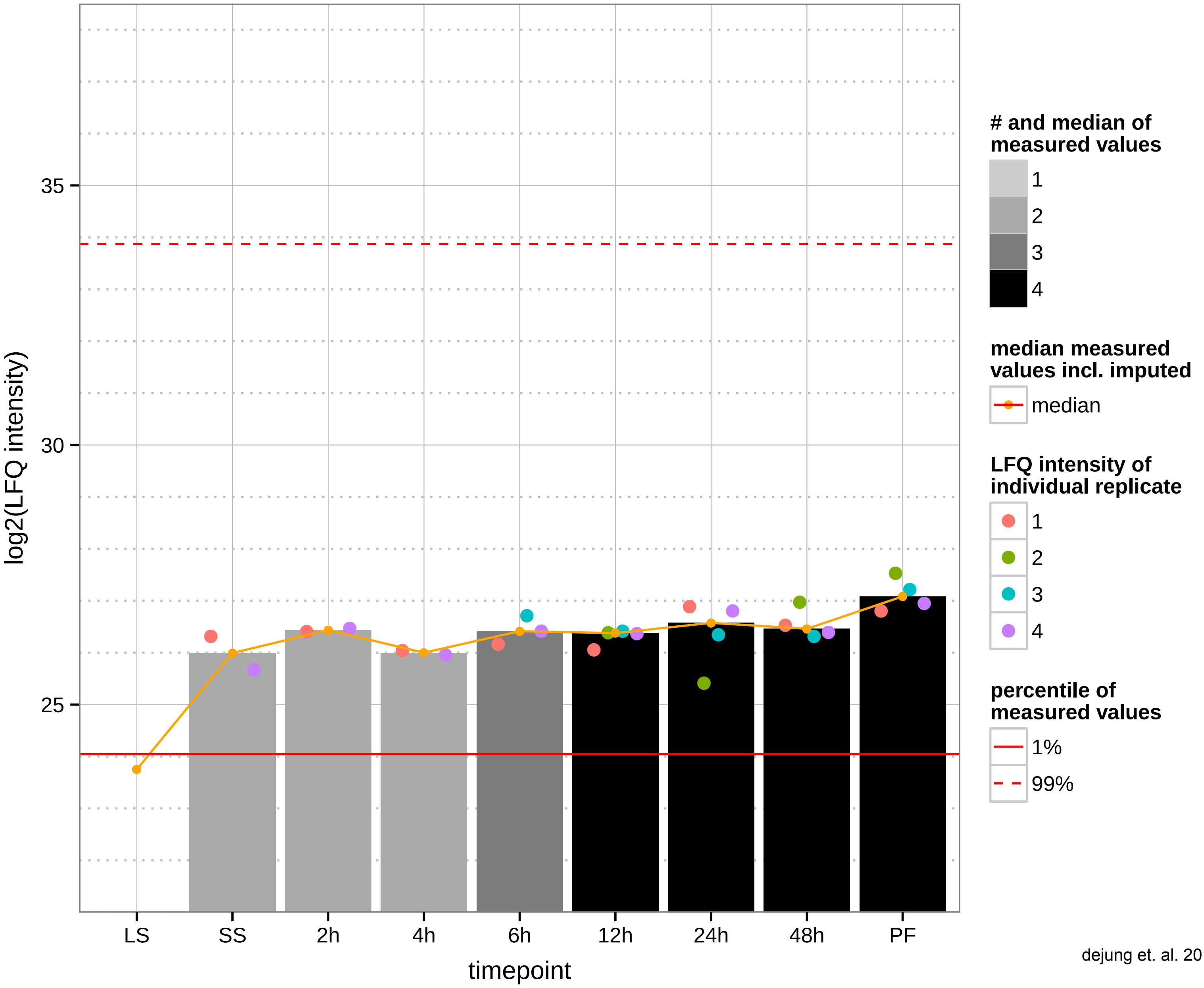
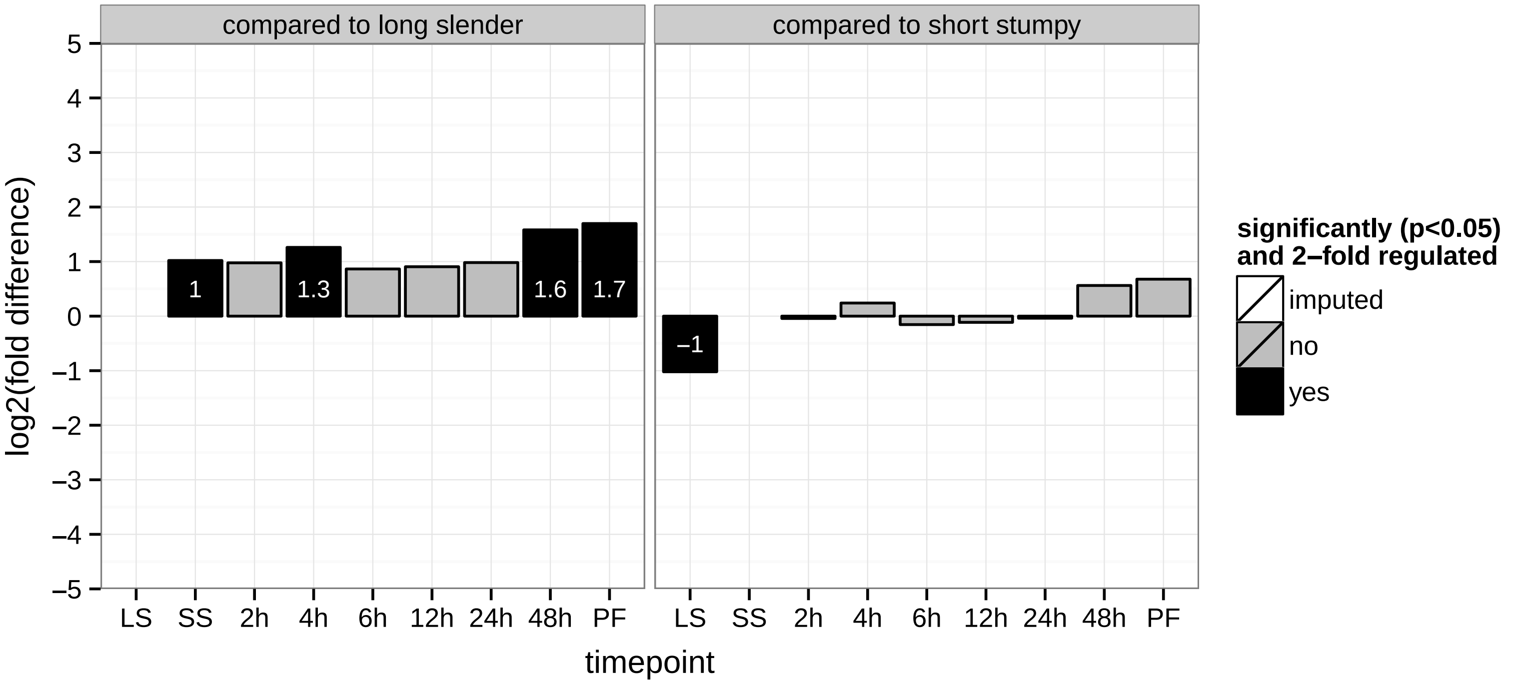
DNA topoisomerase ii (TOP2)
Tb927.9.5590
AGOF: ATP binding, DNA topoisomerase (ATP−hydrolyzing) activity
AGOC: chromosome, mitochondrion, nucleus
AGOP: DNA topological change
PGOF: ATP binding, DNA binding, DNA topoisomerase (ATP−hydrolyzing) activity
PGOC: chromosome
PGOP: DNA topological change

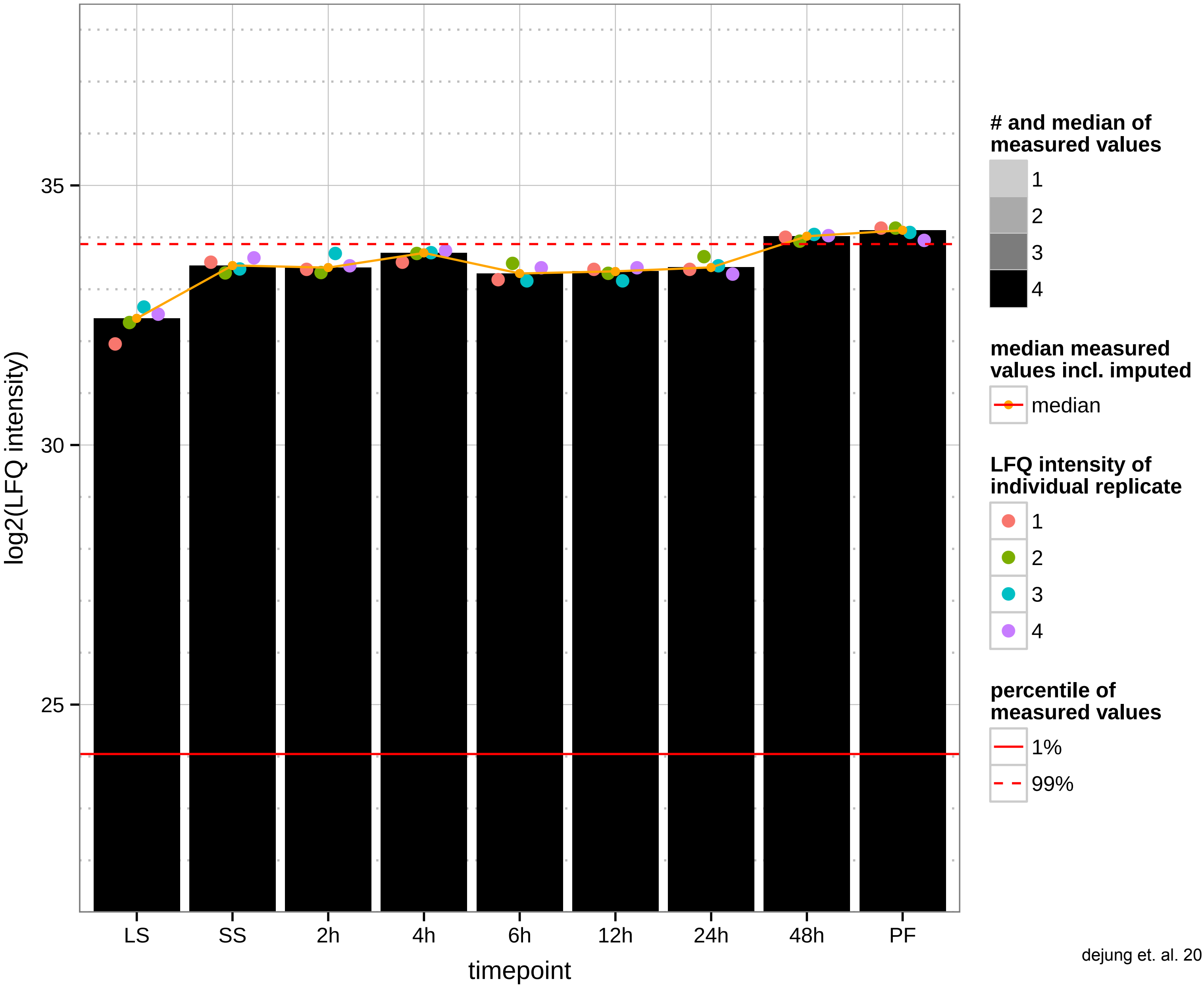




dejung et. al. 2015

unspecified product
Tb927.9.5840;Tb927.9.5750
AGOF: null
AGOC: null
AGOP: null
PGOF: antioxidant activity, oxidoreductase activity, peroxiredoxin activity
PGOC: null
PGOP: oxidation–reduction process





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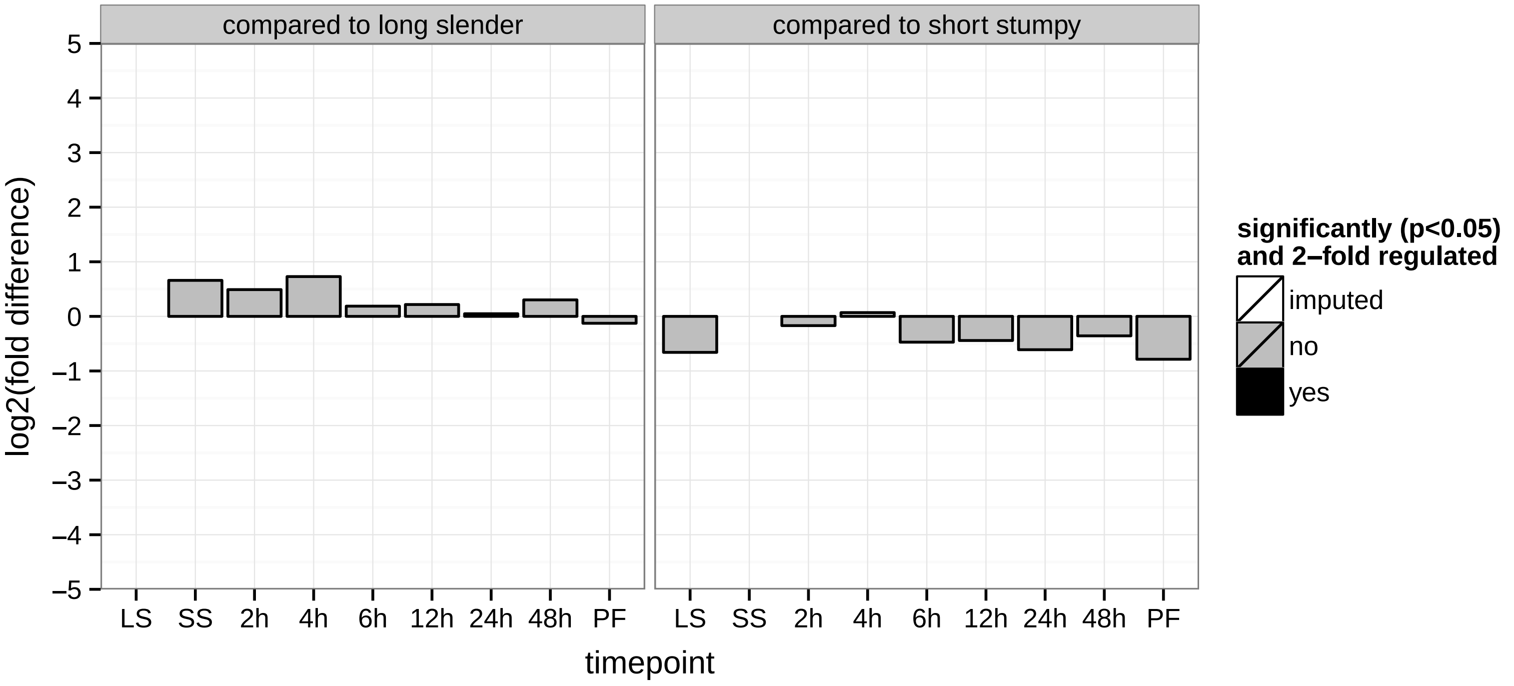
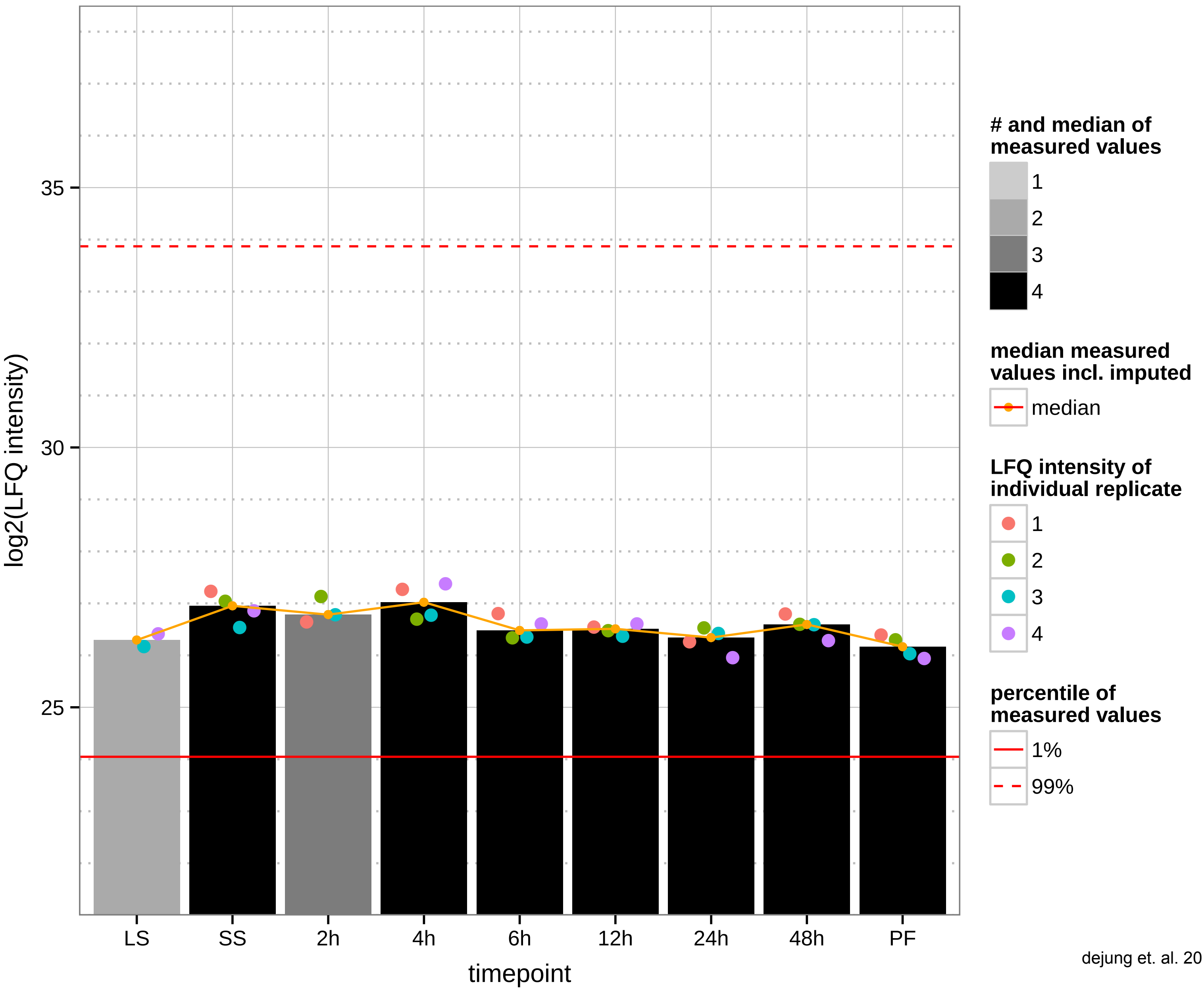
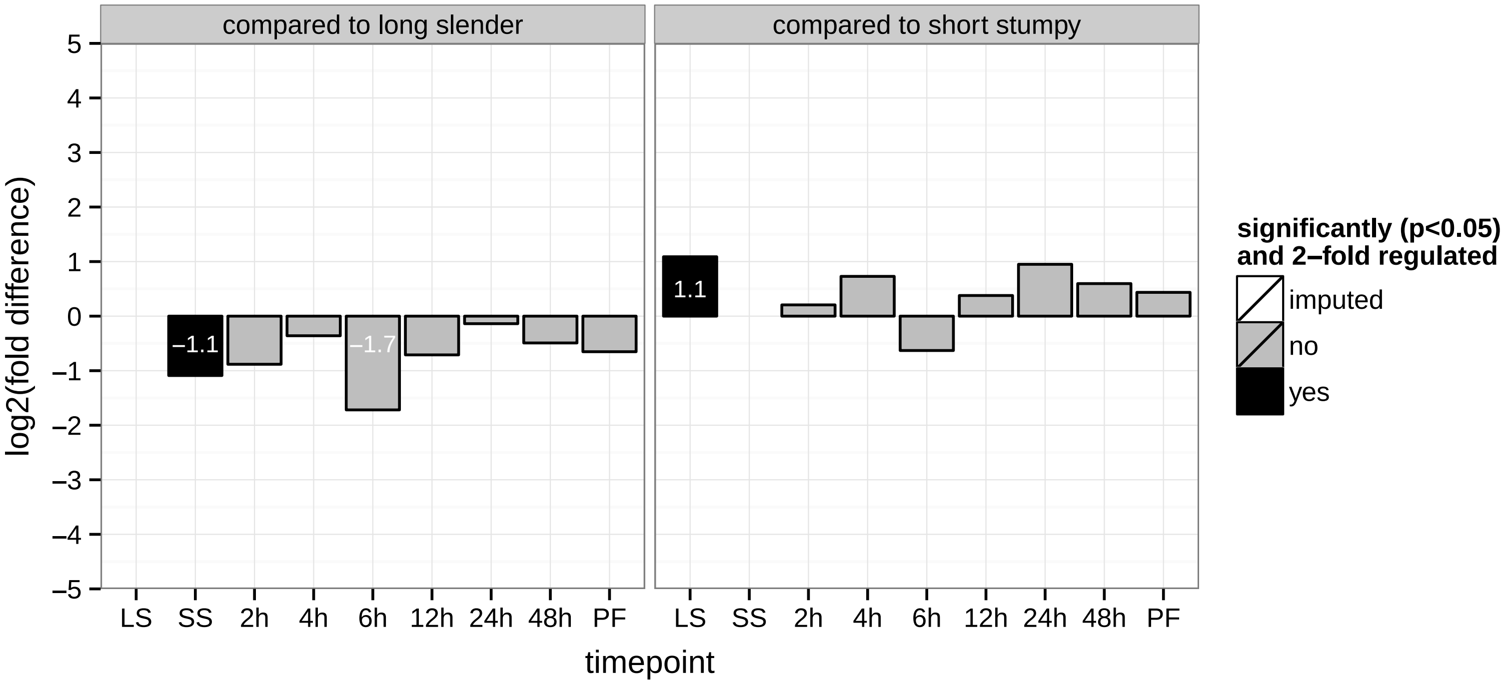
E1–like ubiquitin–activating enzyme, putative (UBA5)
Tb927.9.6040
AGOF: catalytic activity, small conjugating protein binding, small protein activating enzyme activity
AGOC: mitochondrion
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null

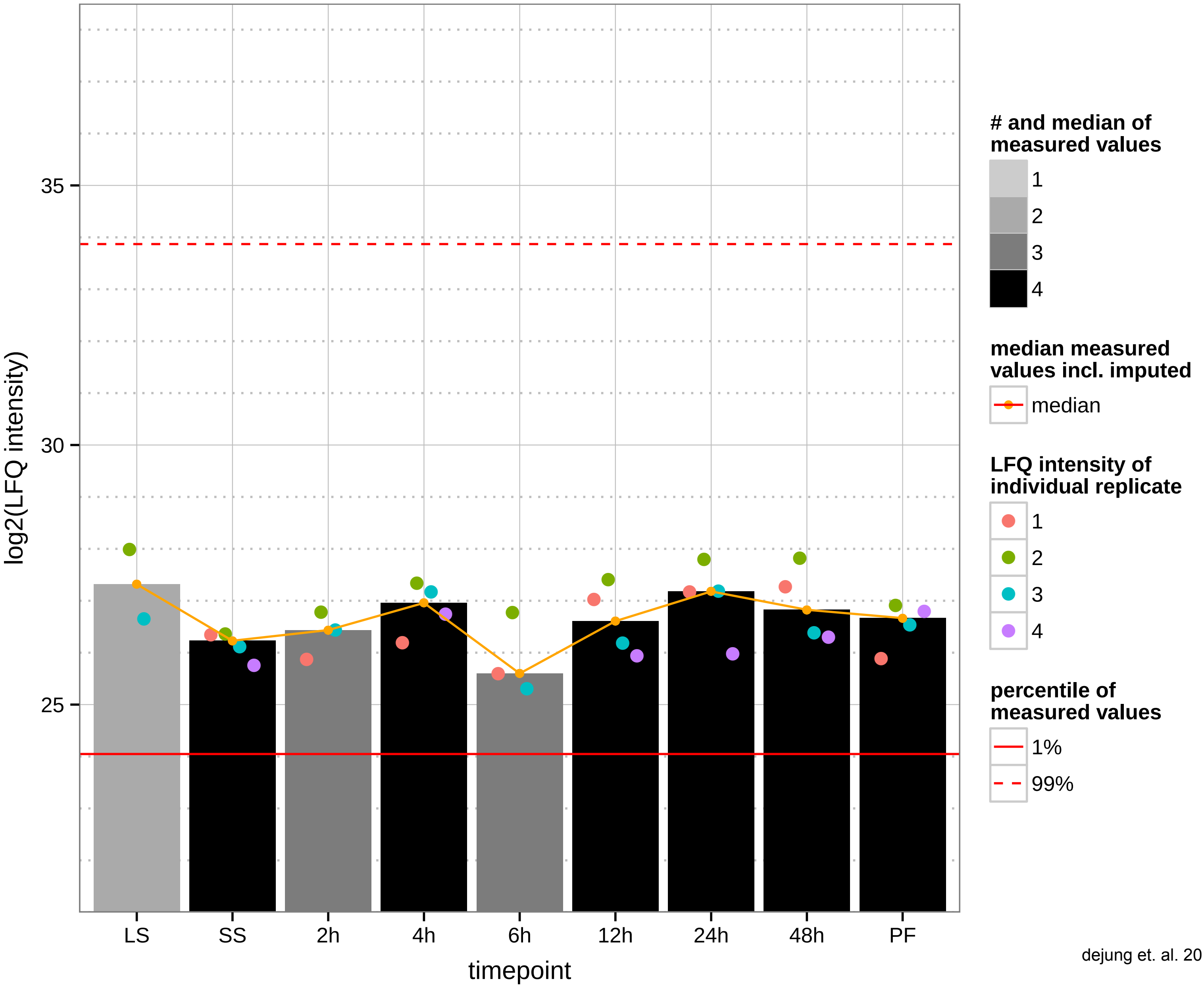




dejung et. al. 2015

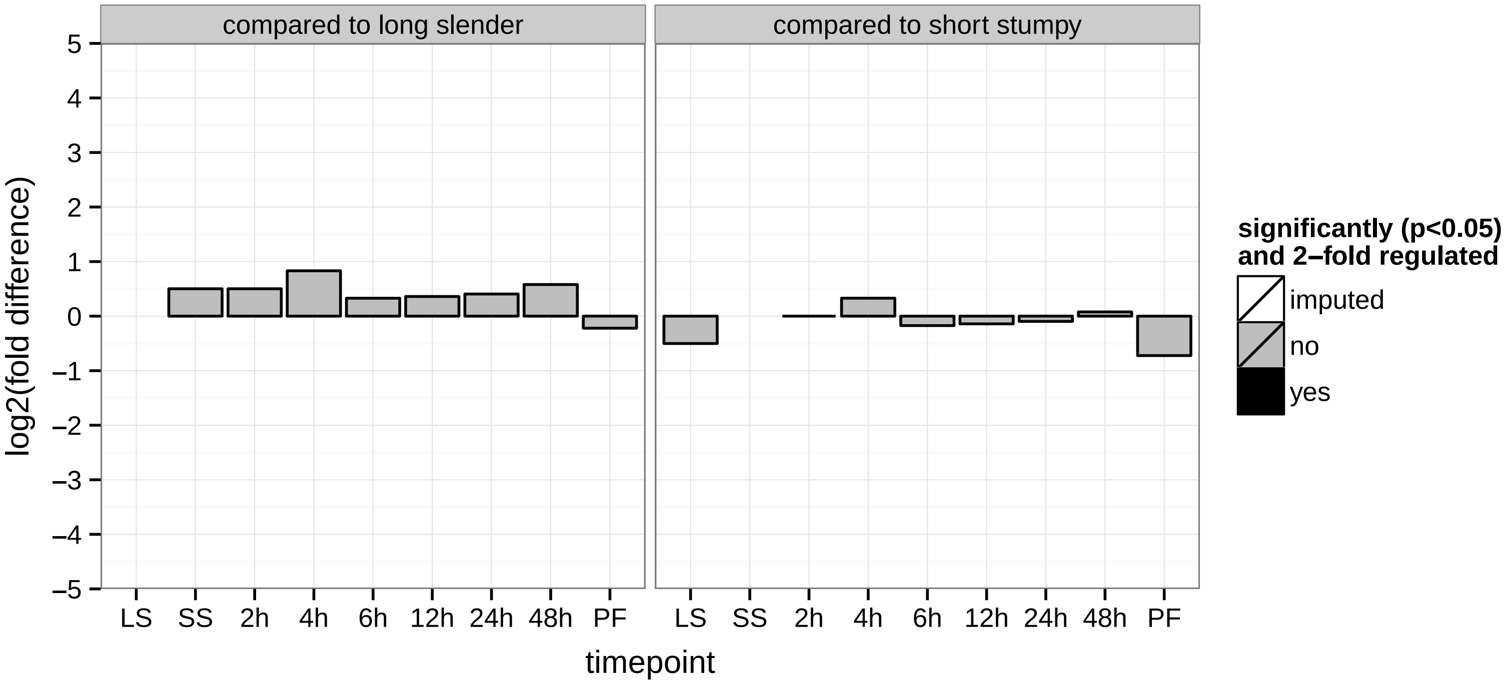
calmodulin, putative
Tb927.9.6130
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null

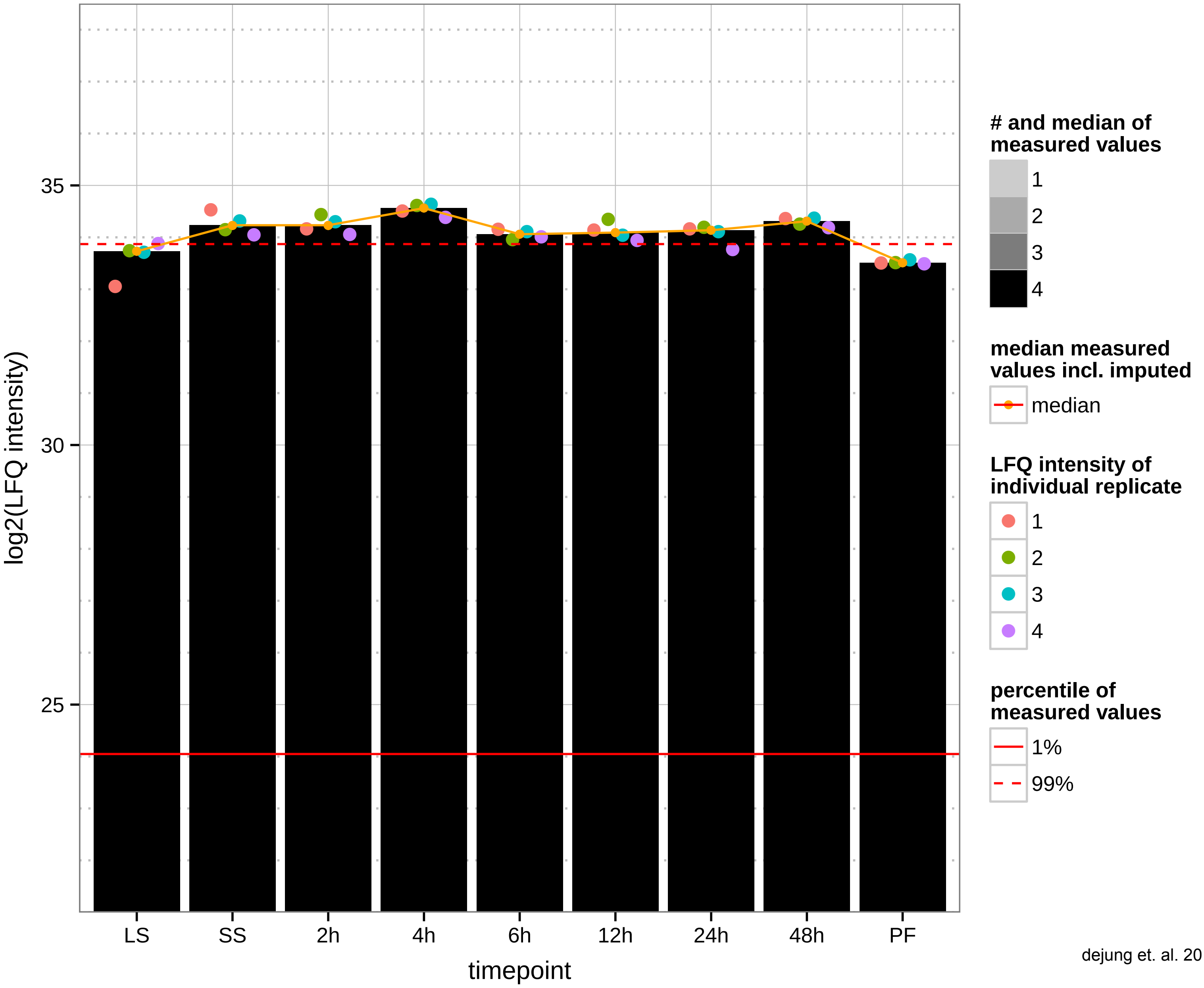




dejung et. al. 2015

unspecified product
Tb927.9.6230;Tb927.9.6170
AGOF: null
AGOC: null
AGOP: null
PGOF: kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: null





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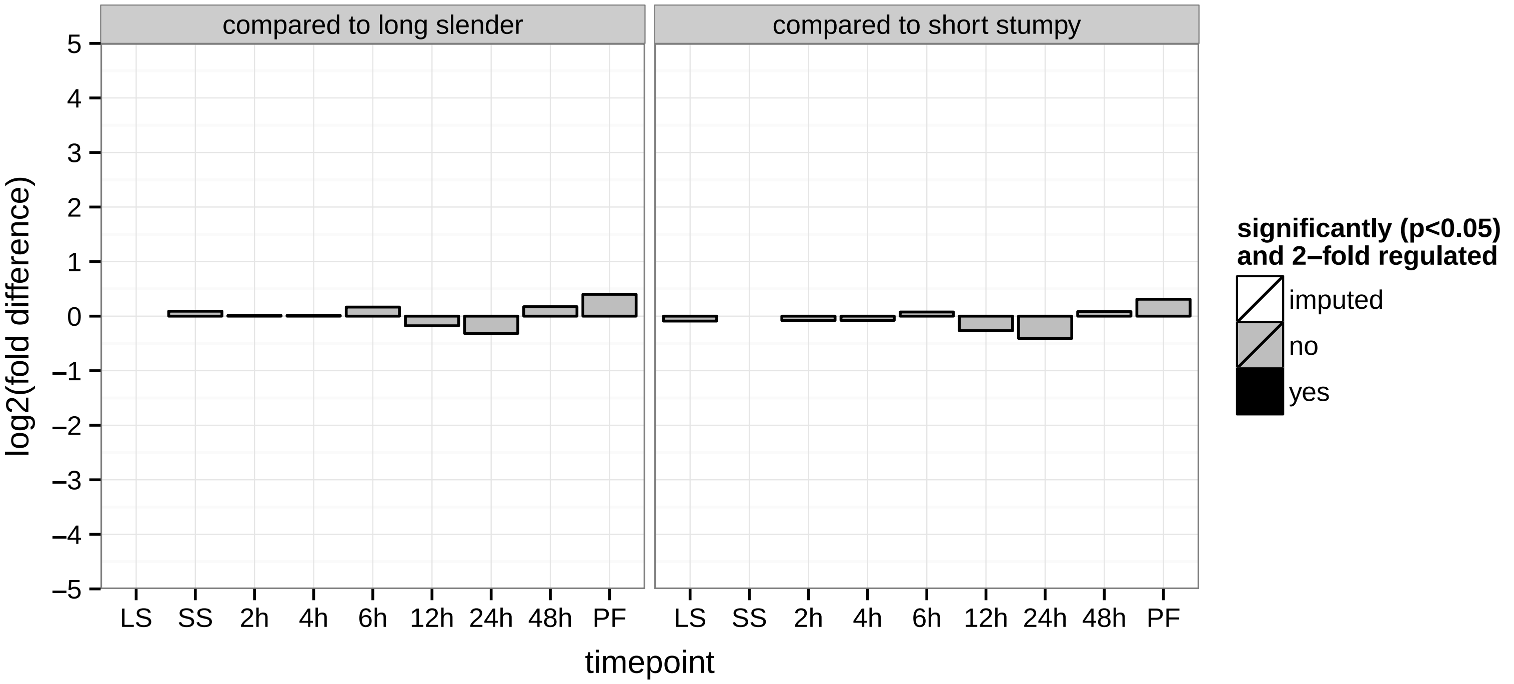
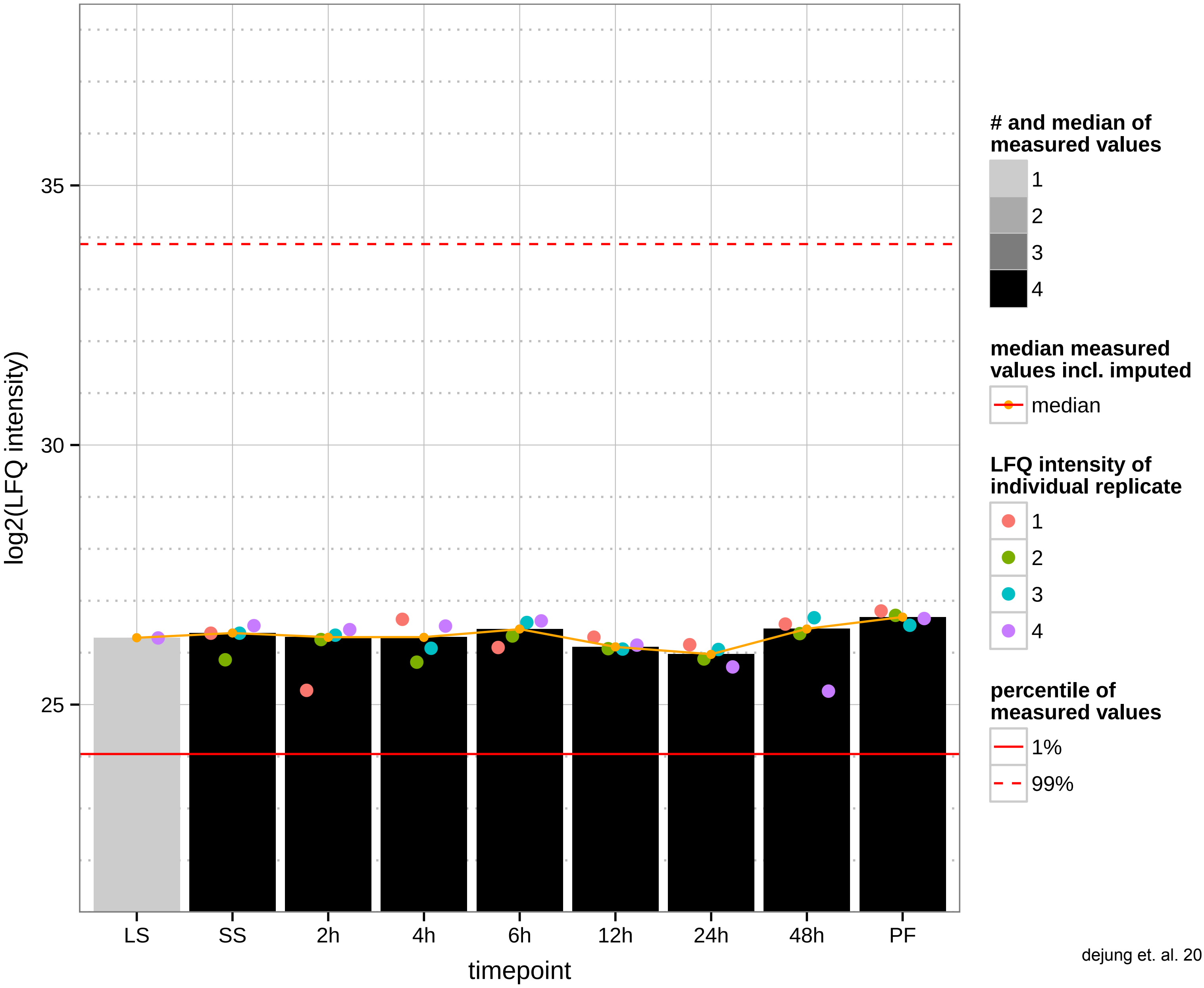
Rab geranylgeranyl transferase component A, putative, Rab escort protein 1
Tb927.9.6430
AGOF: Rab GTPase binding
AGOC: Rab−protein geranylgeranyltransferase complex
AGOP: regulation of GTPase activity, vesicle−mediated transport
PGOF: null
PGOC: null
PGOP: null





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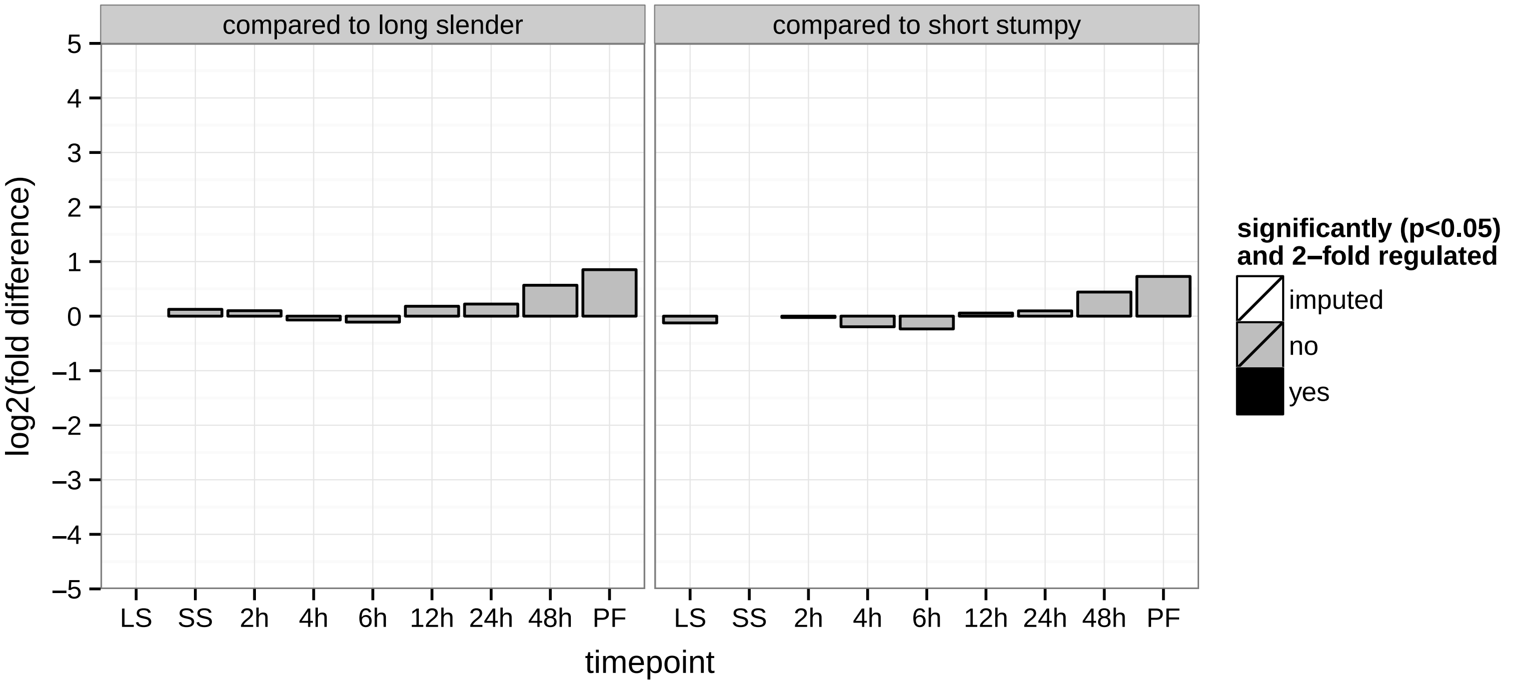
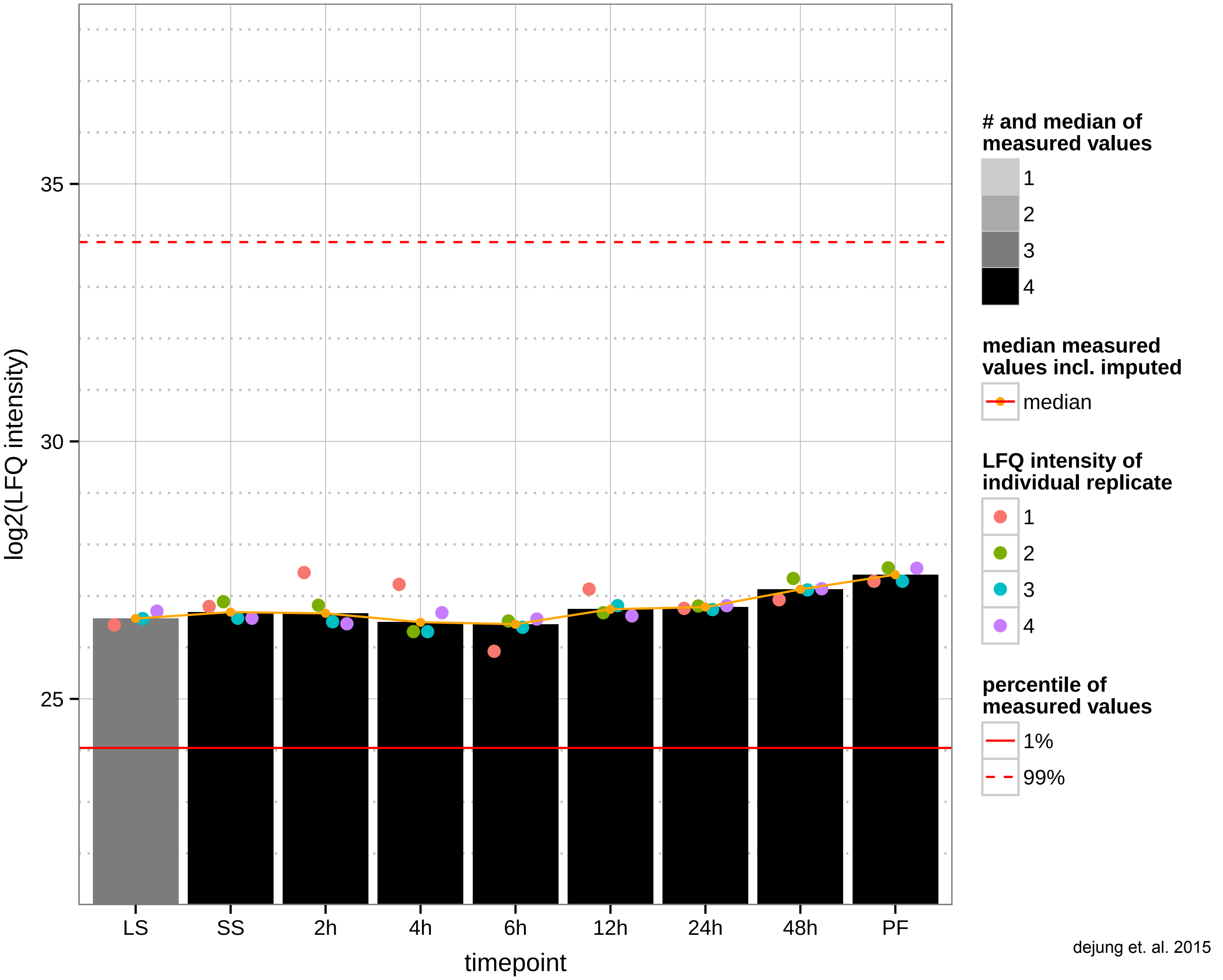
hypothetical protein, conserved
Tb927.9.6450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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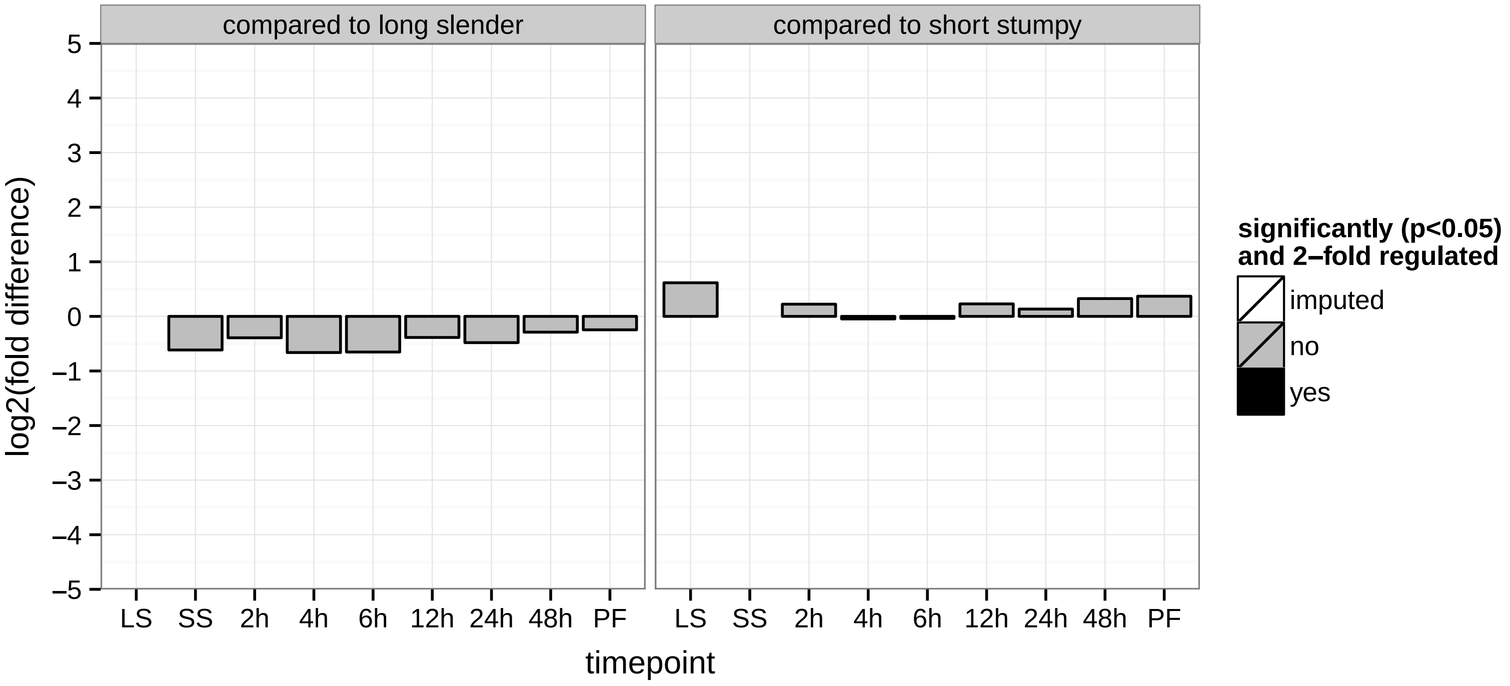
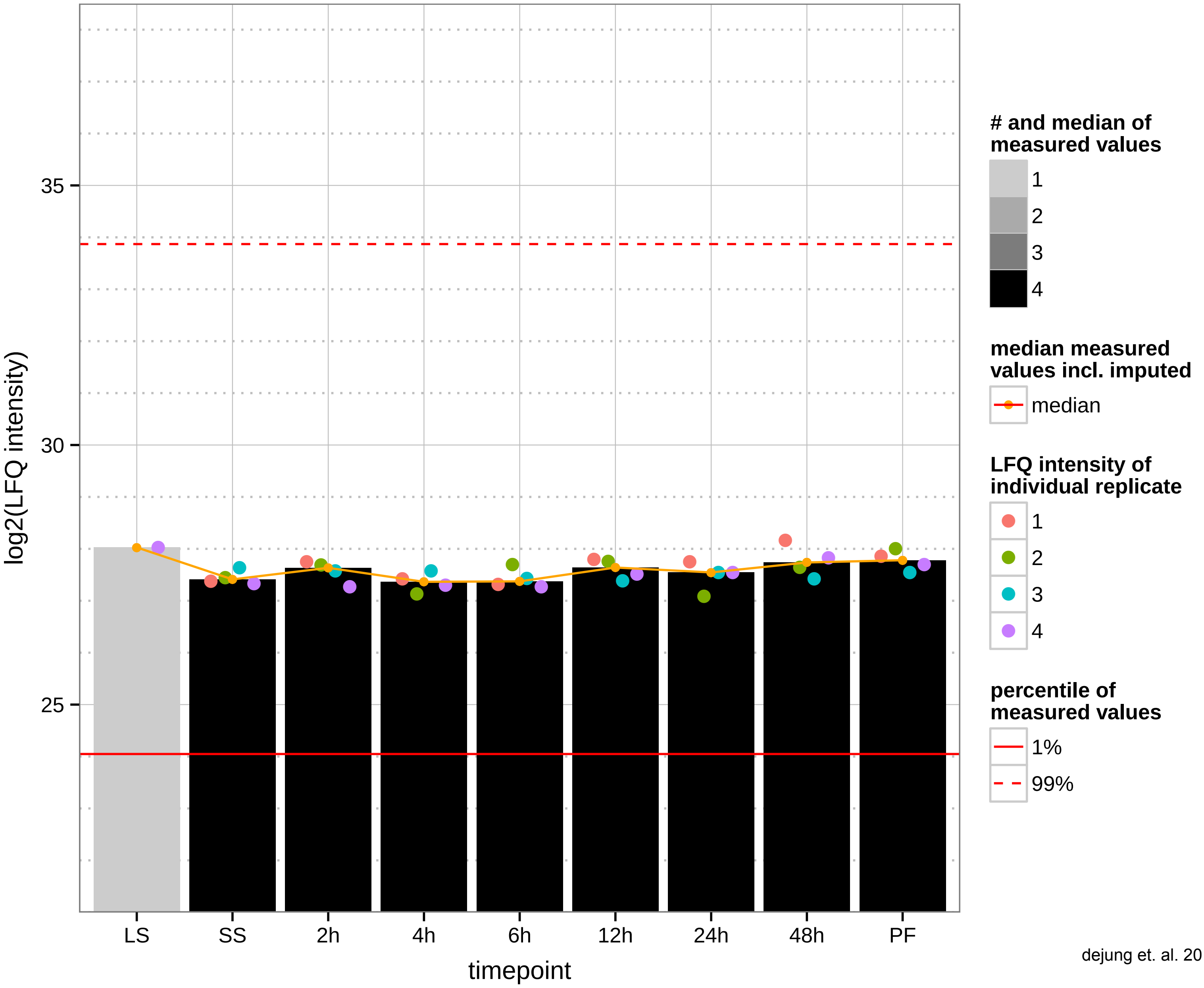
hypothetical protein, conserved
Tb927.9.6460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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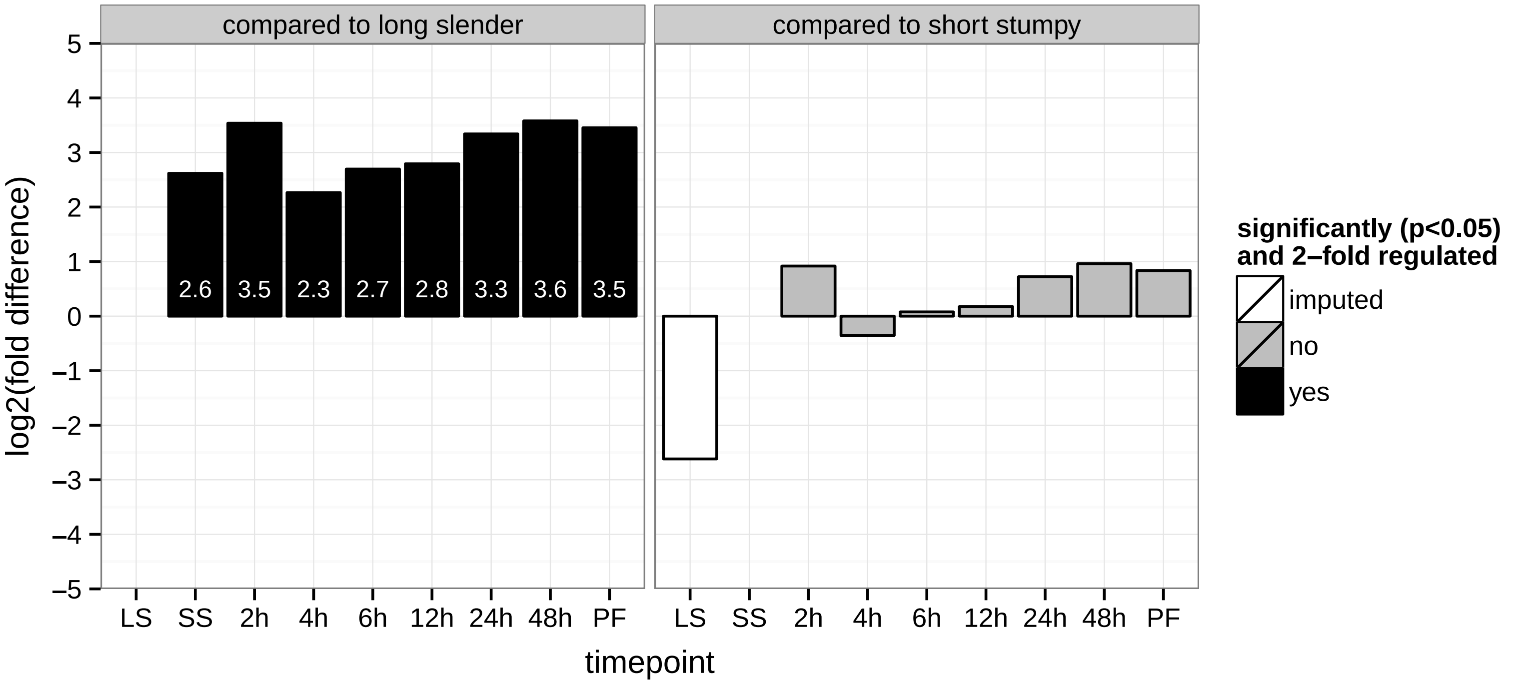
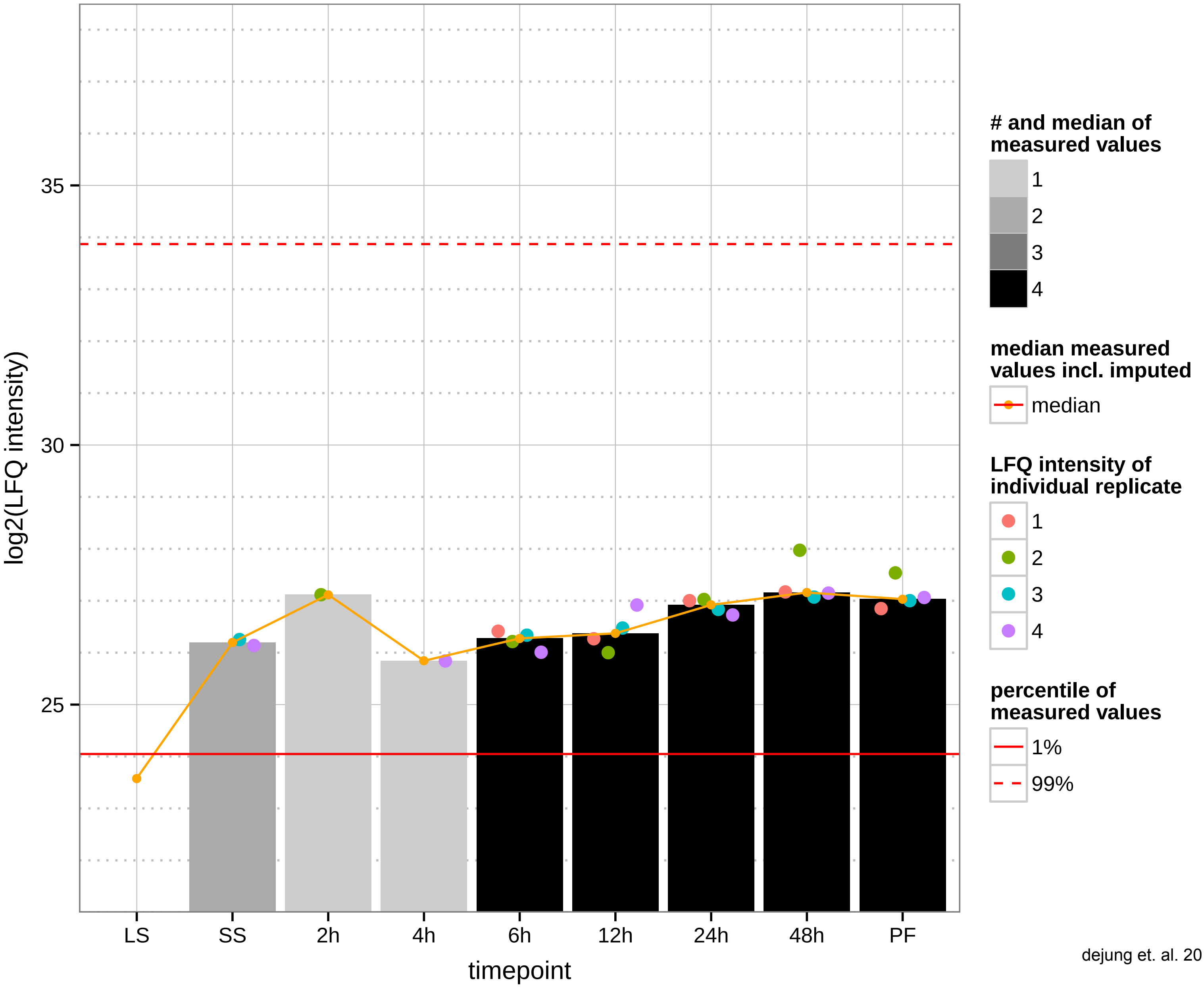
hypothetical protein, conserved
Tb927.9.6510
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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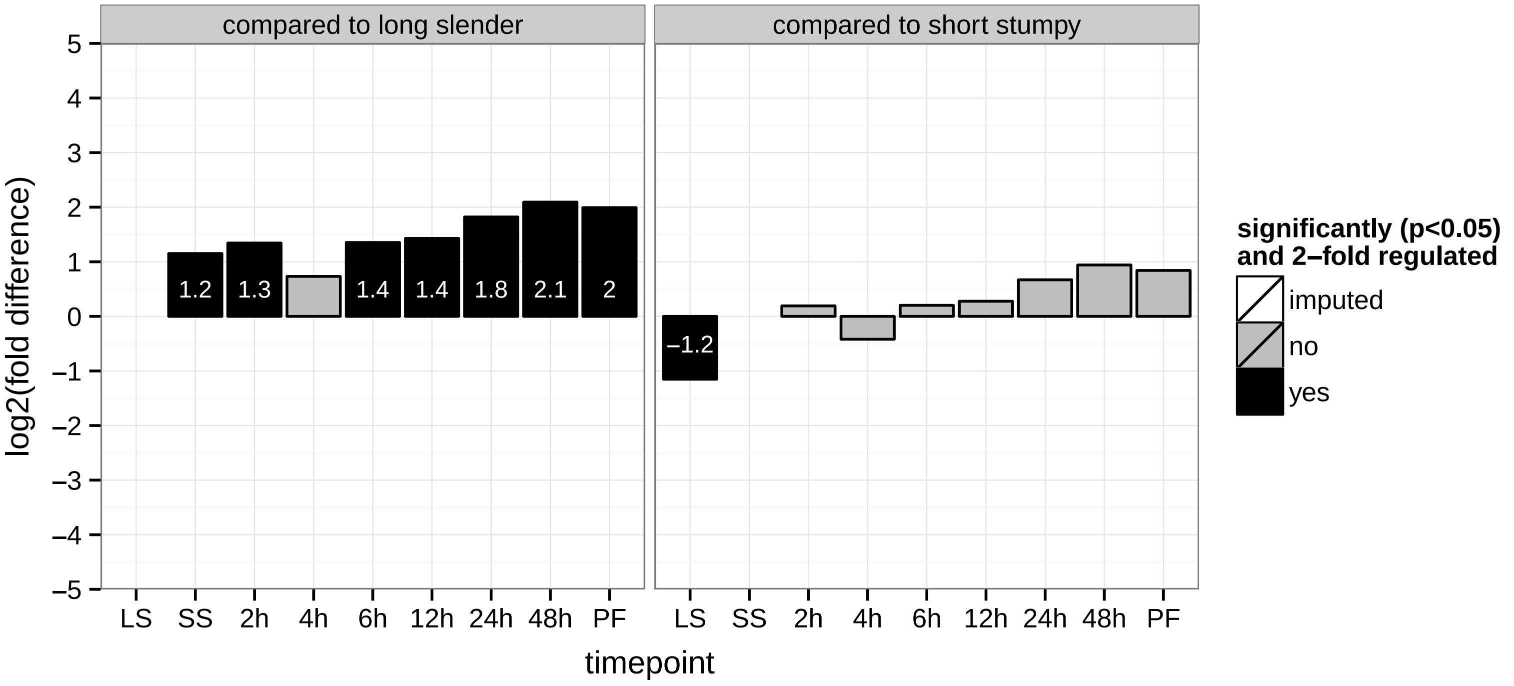
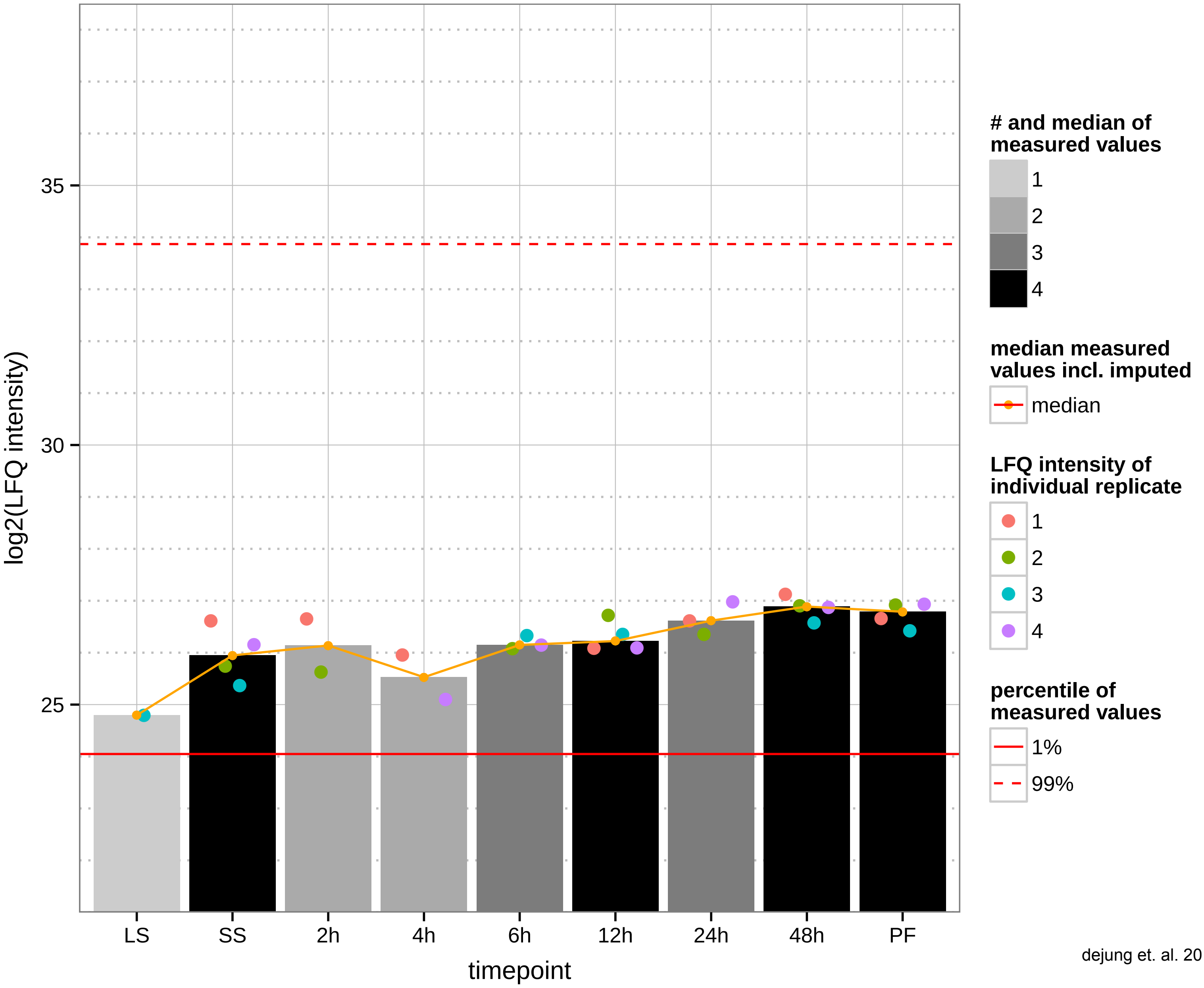
hypothetical protein, conserved
Tb927.9.6580
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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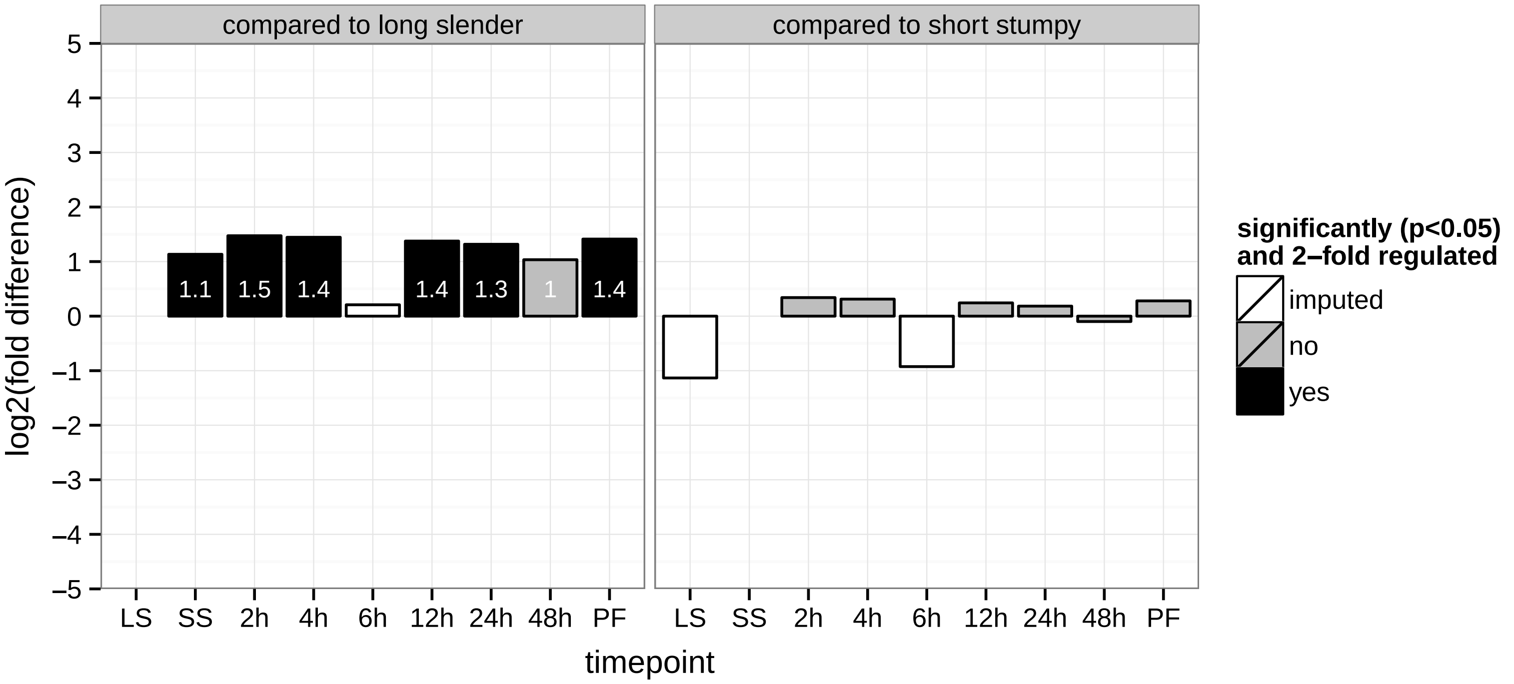
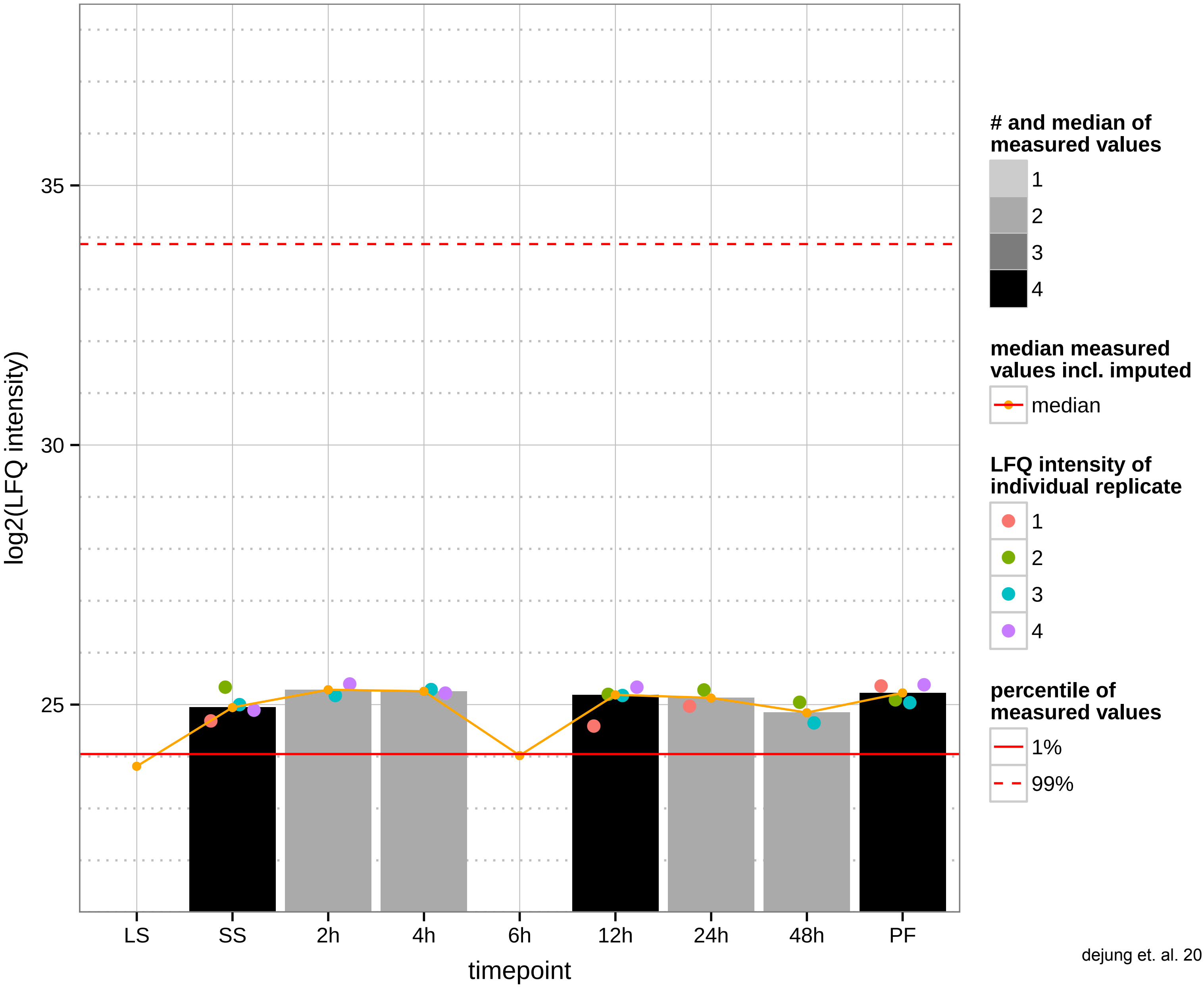
hypothetical protein, conserved
Tb927.9.6760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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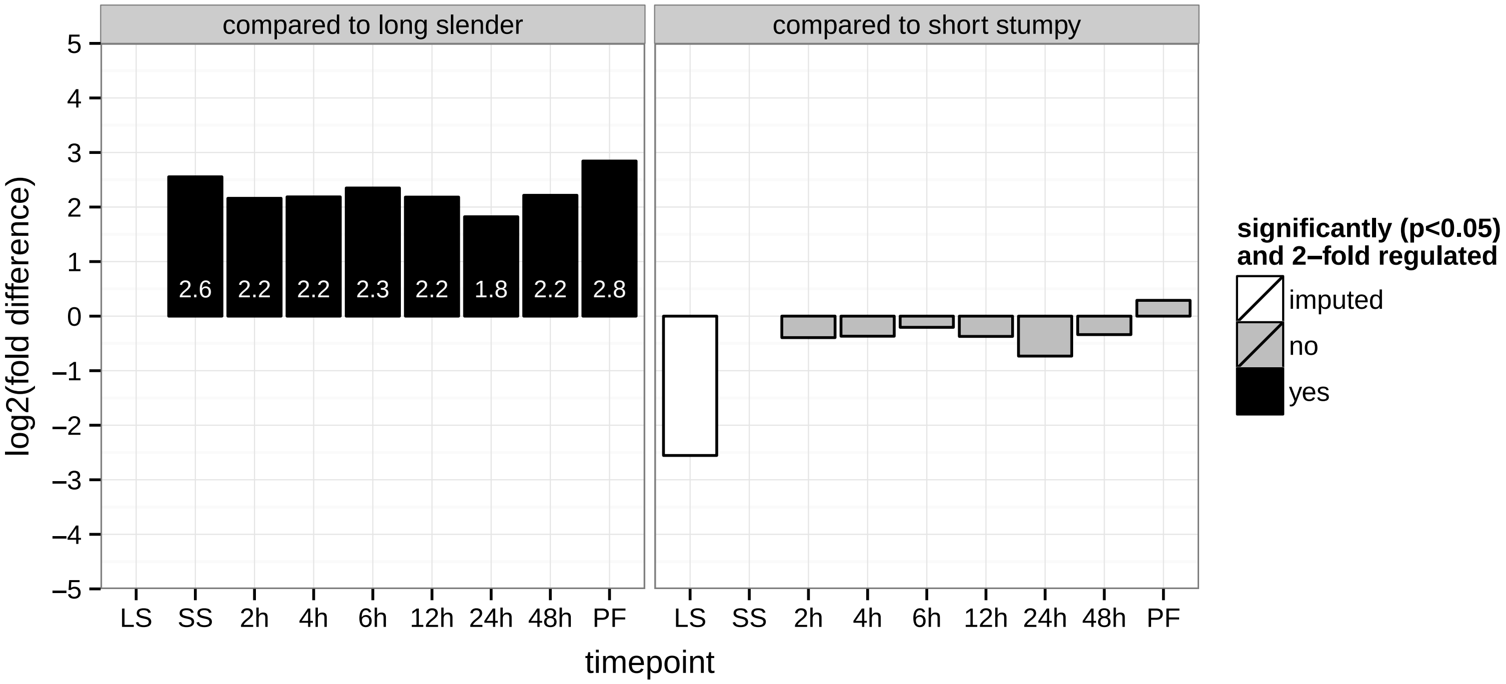
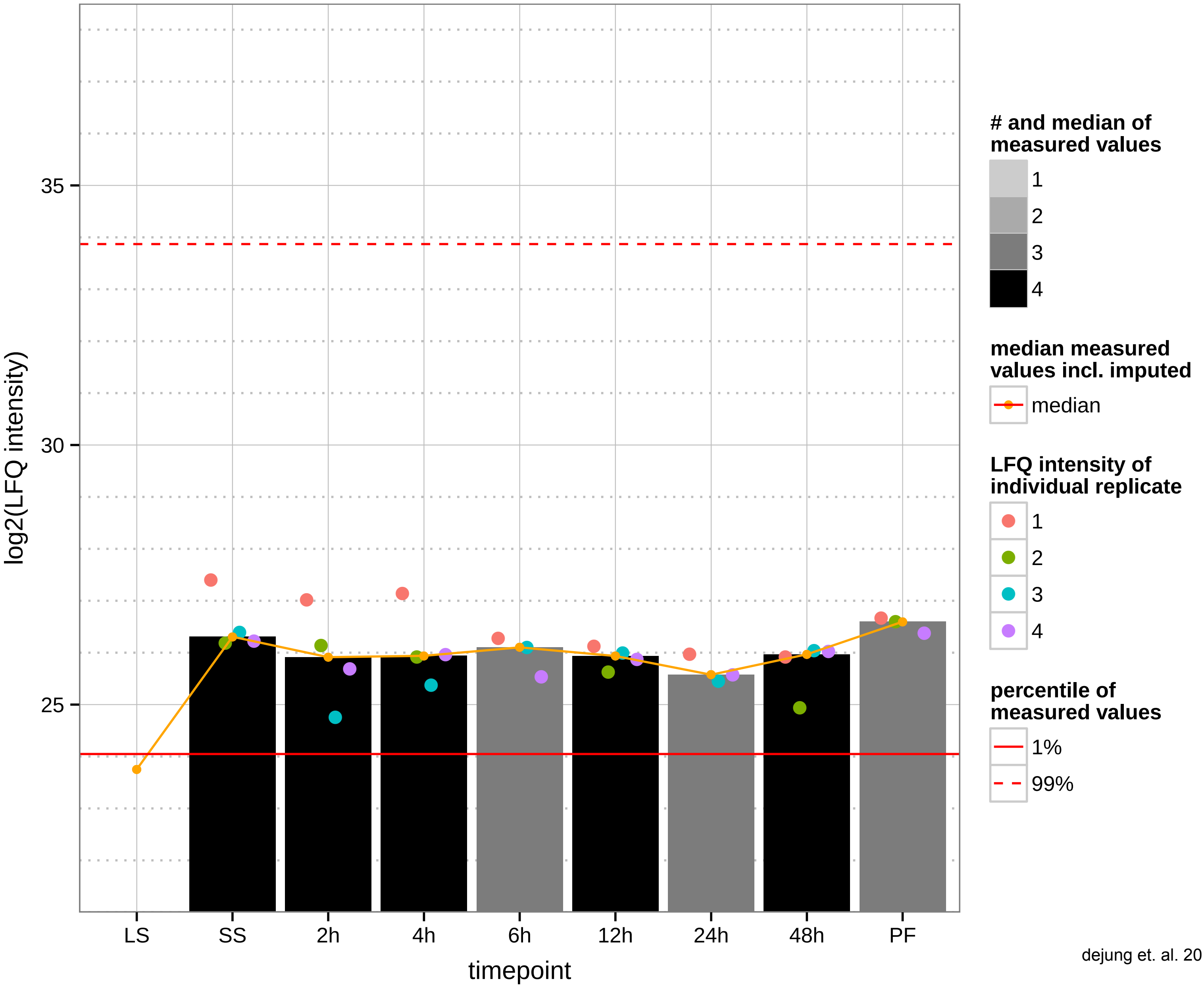
cAMP–specific phosphodiesterase, putative
Tb927.9.6880
AGOF: 3', 5'–cyclic–AMP phosphodiesterase activity
AGOC: null
AGOP: signal transduction
PGOF: 3', 5'–cyclic–nucleotide phosphodiesterase activity
PGOC: null
PGOP: signal transduction





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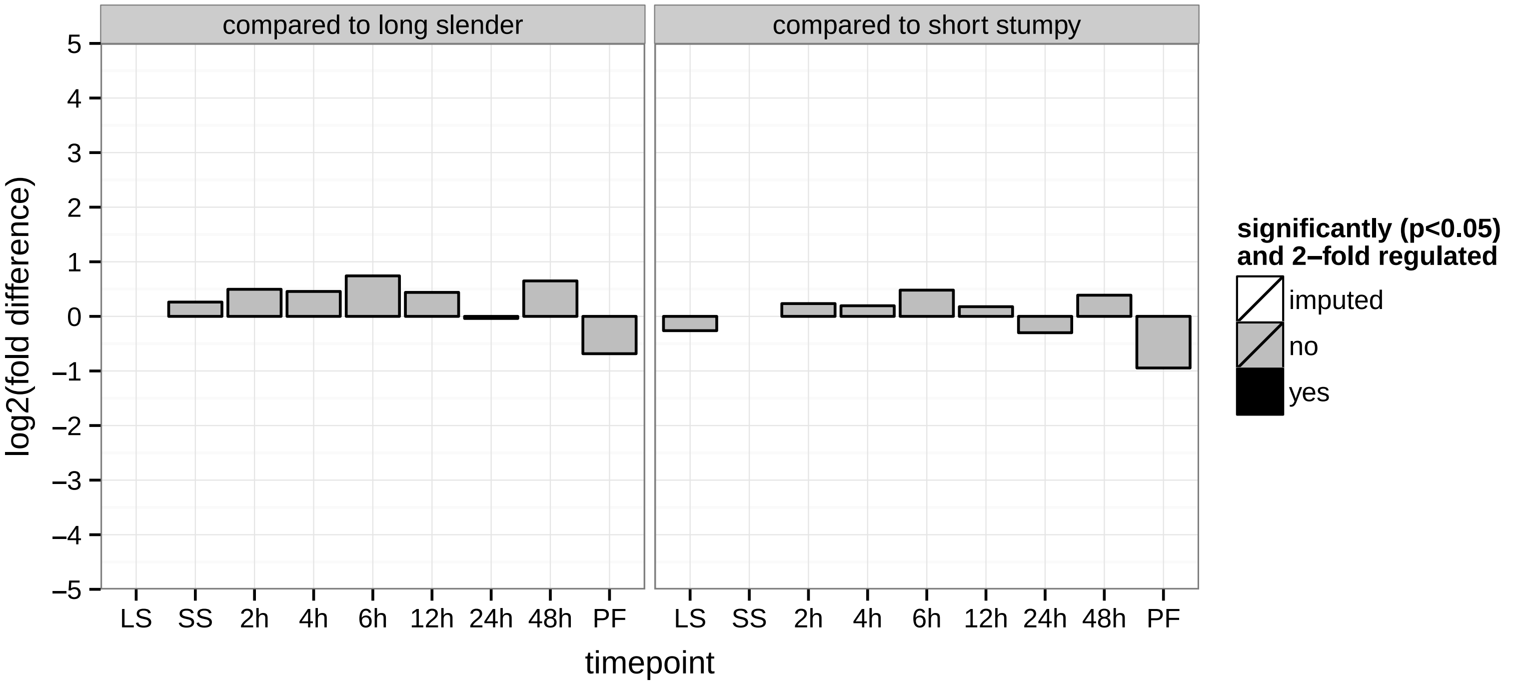
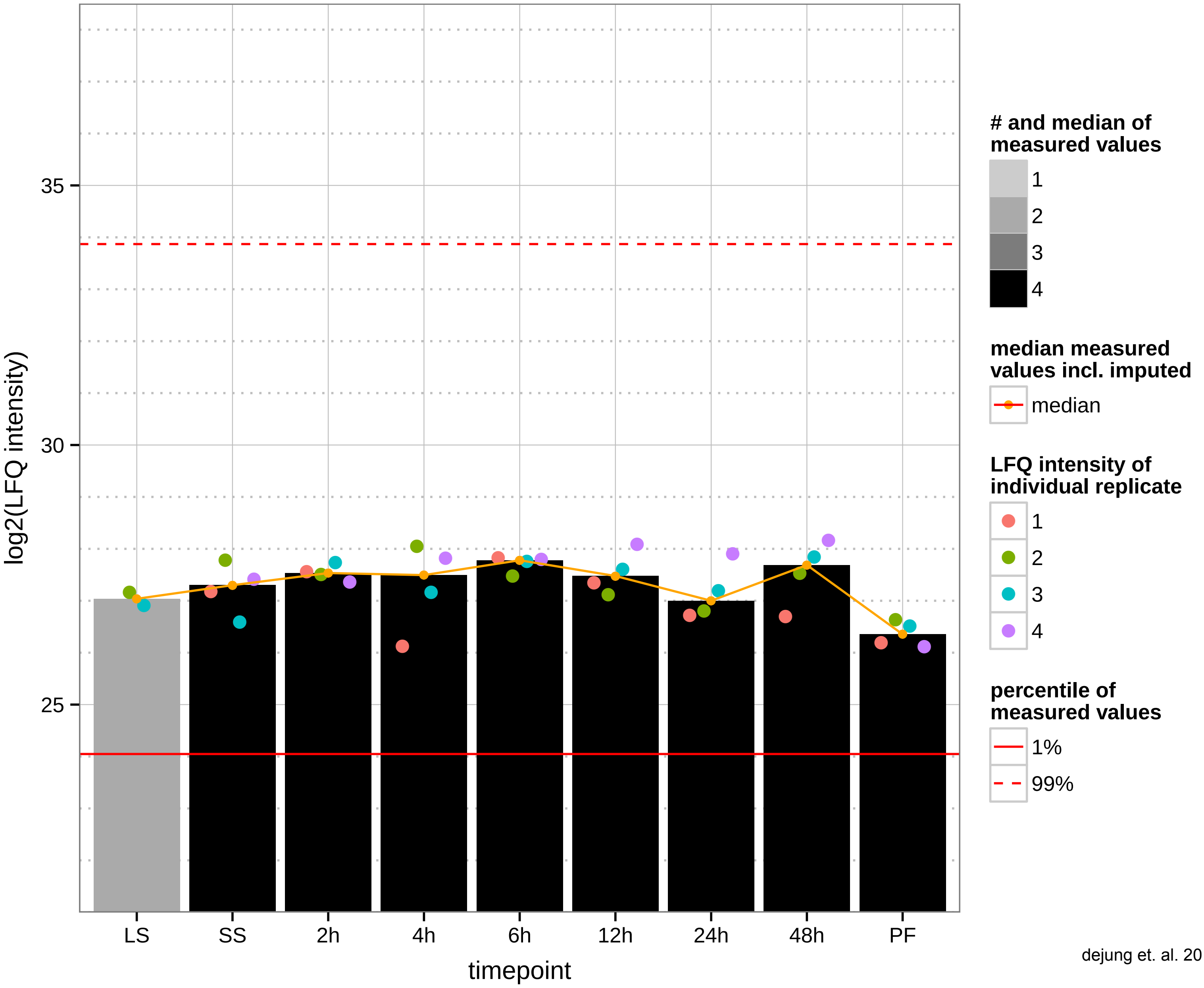
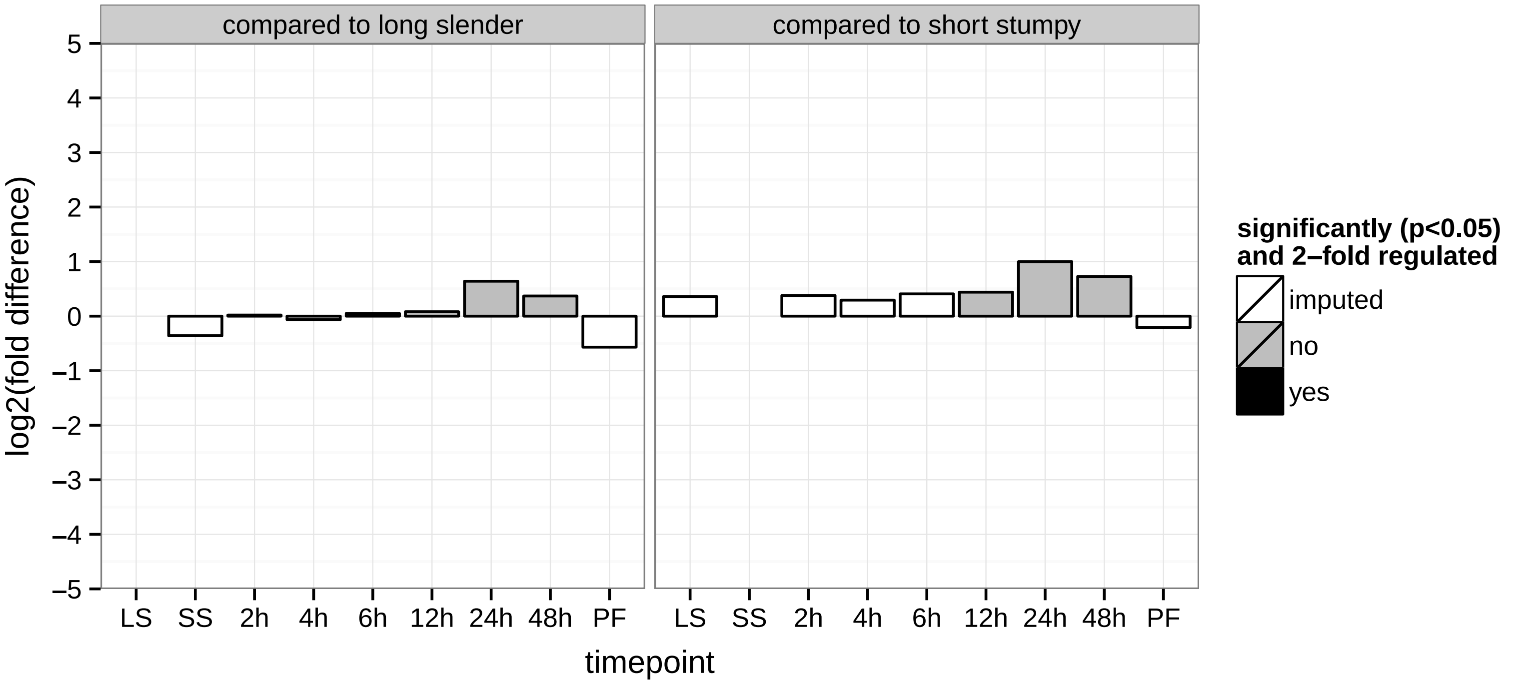
DNA topoisomerase type IB small subunit
Tb927.9.6940
AGOF: ATP binding, DNA topoisomerase type I activity, magnesium ion binding
AGOC: nucleus
AGOP: DNA topological change, chromatin assembly or disassembly
PGOF: DNA binding
PGOC: null
PGOP: null

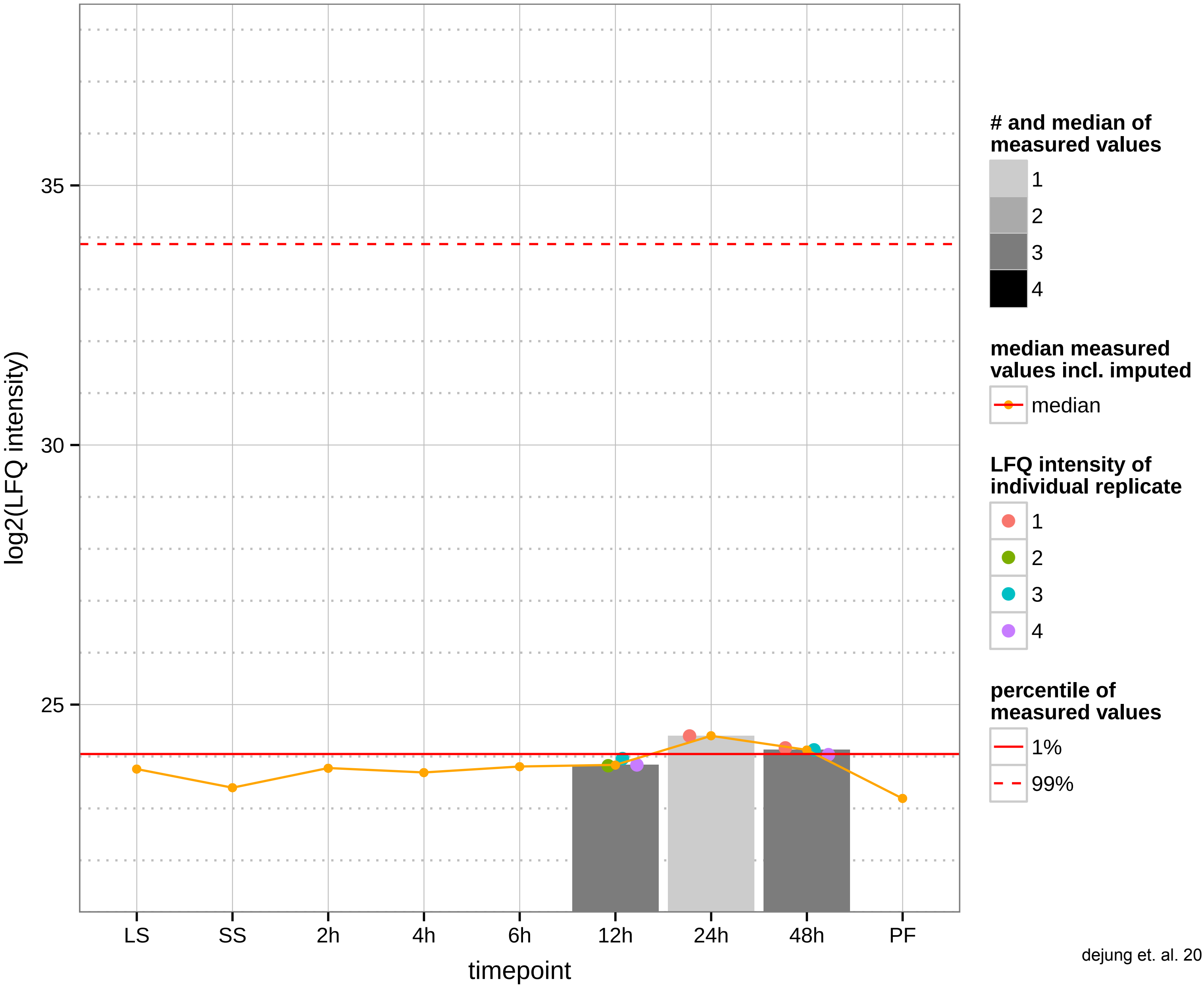




dejung et. al. 2015

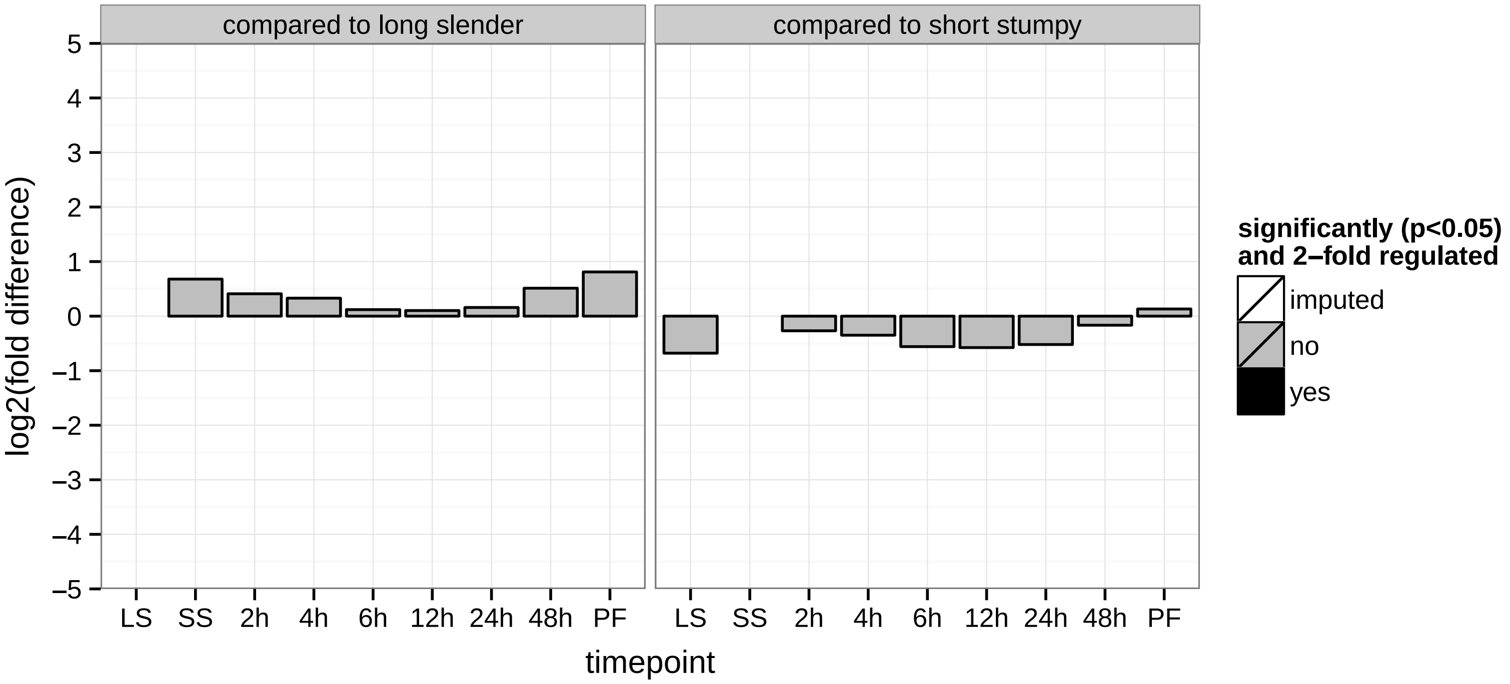
RNA pseudouridylate synthase protein, putative
Tb927.9.7150
AGOF: RNA binding, pseudouridine synthase activity
AGOC: null
AGOP: RNA processing, pseudouridine synthesis
PGOF: RNA binding, pseudouridine synthase activity
PGOC: null
PGOP: RNA modification, pseudouridine synthesis

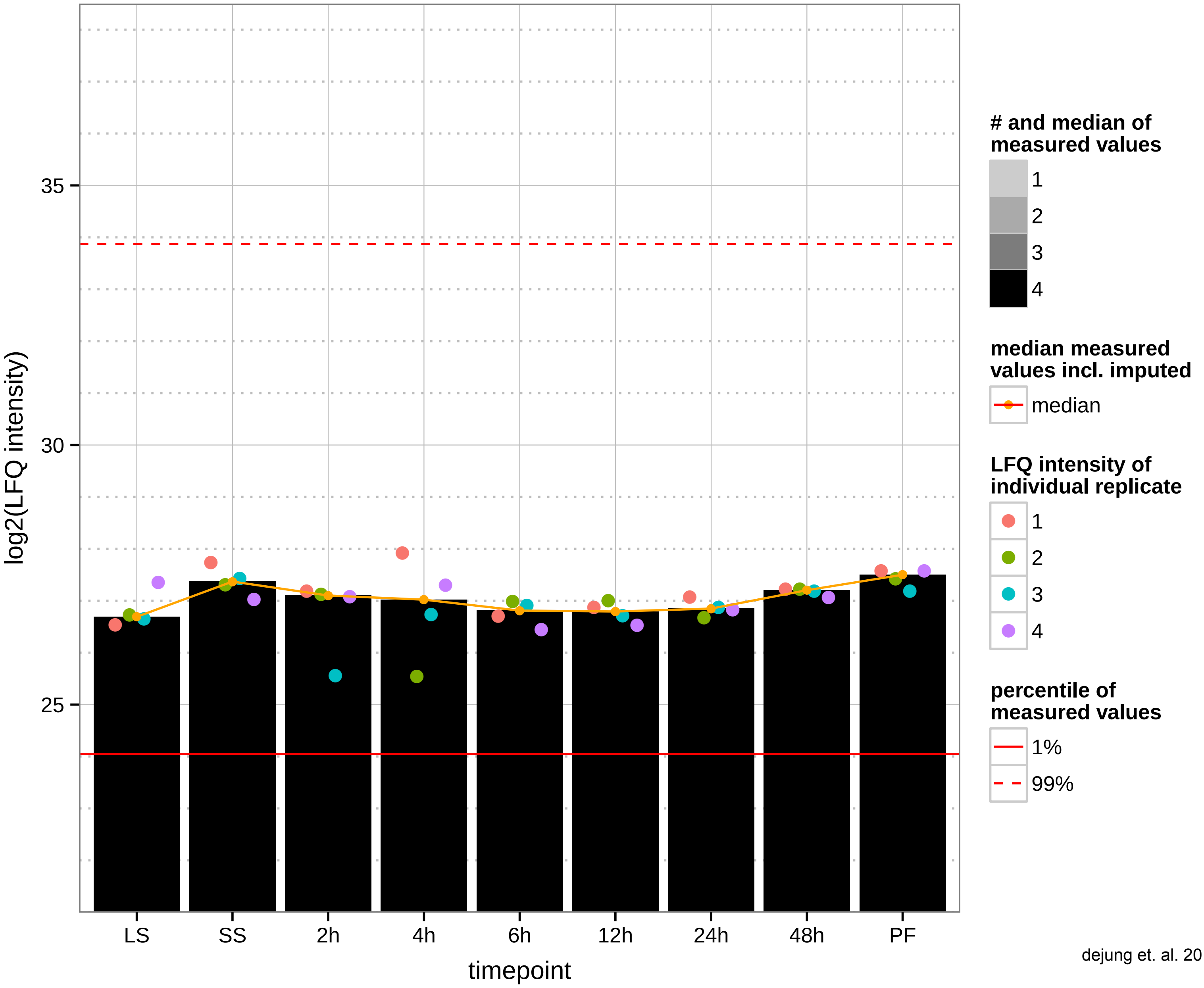




dejung et. al. 2015

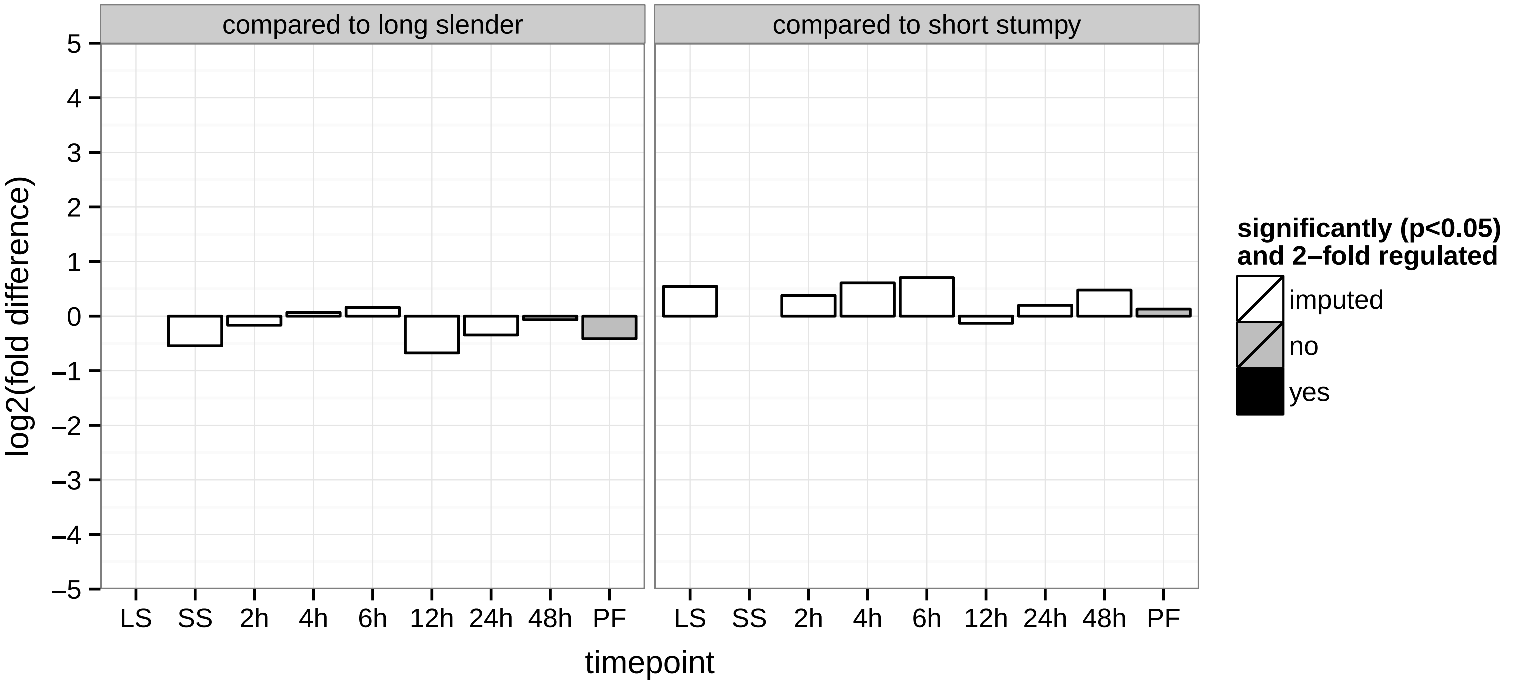
adenosine monophosphate deaminase, putative, AMP deaminase
Tb927.9.7180
AGOF: AMP deaminase activity
AGOC: null
AGOP: purine ribonucleoside monophosphate biosynthetic process
PGOF: deaminase activity
PGOC: null
PGOP: purine ribonucleoside monophosphate biosynthetic process

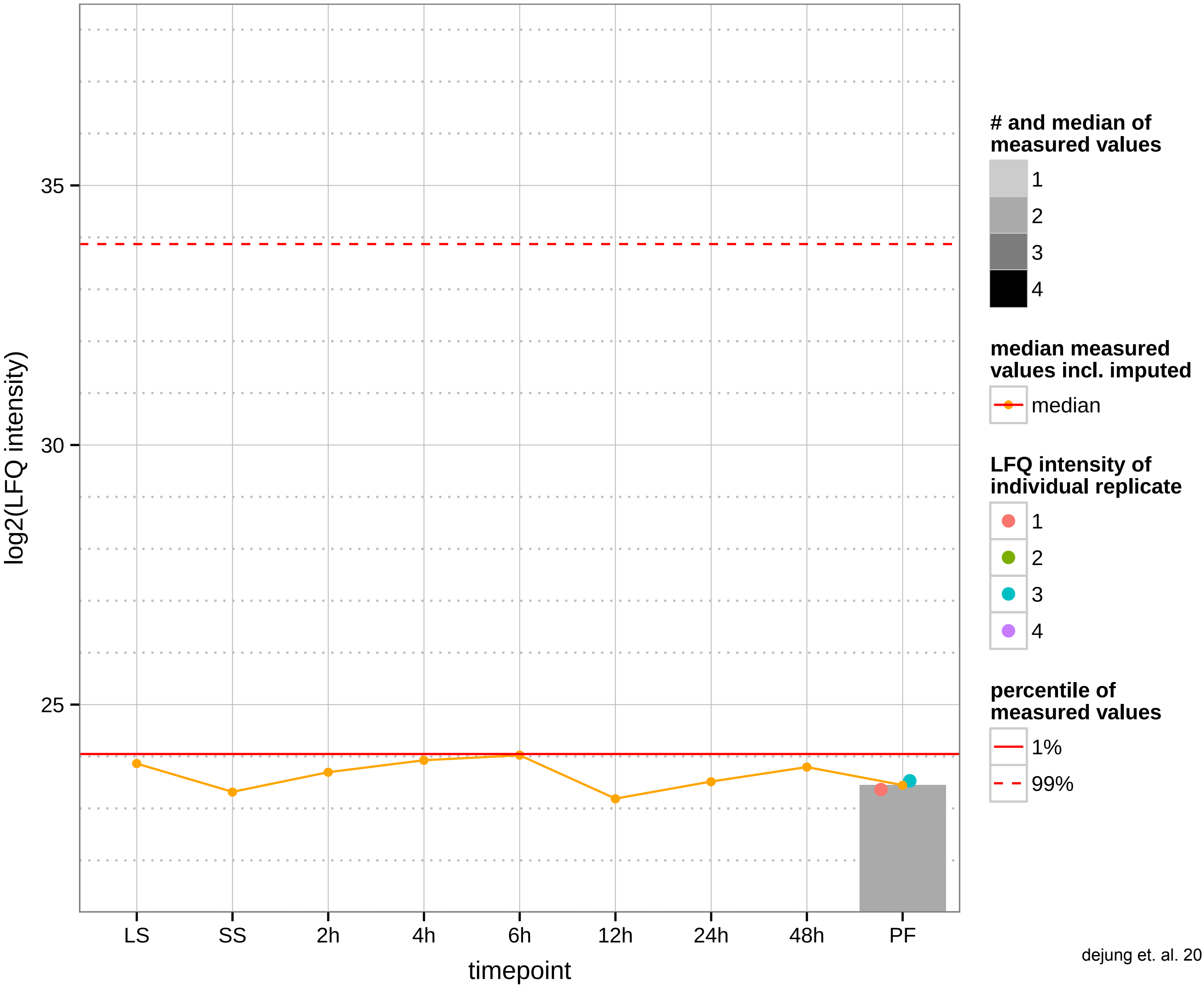




dejung et. al. 2015

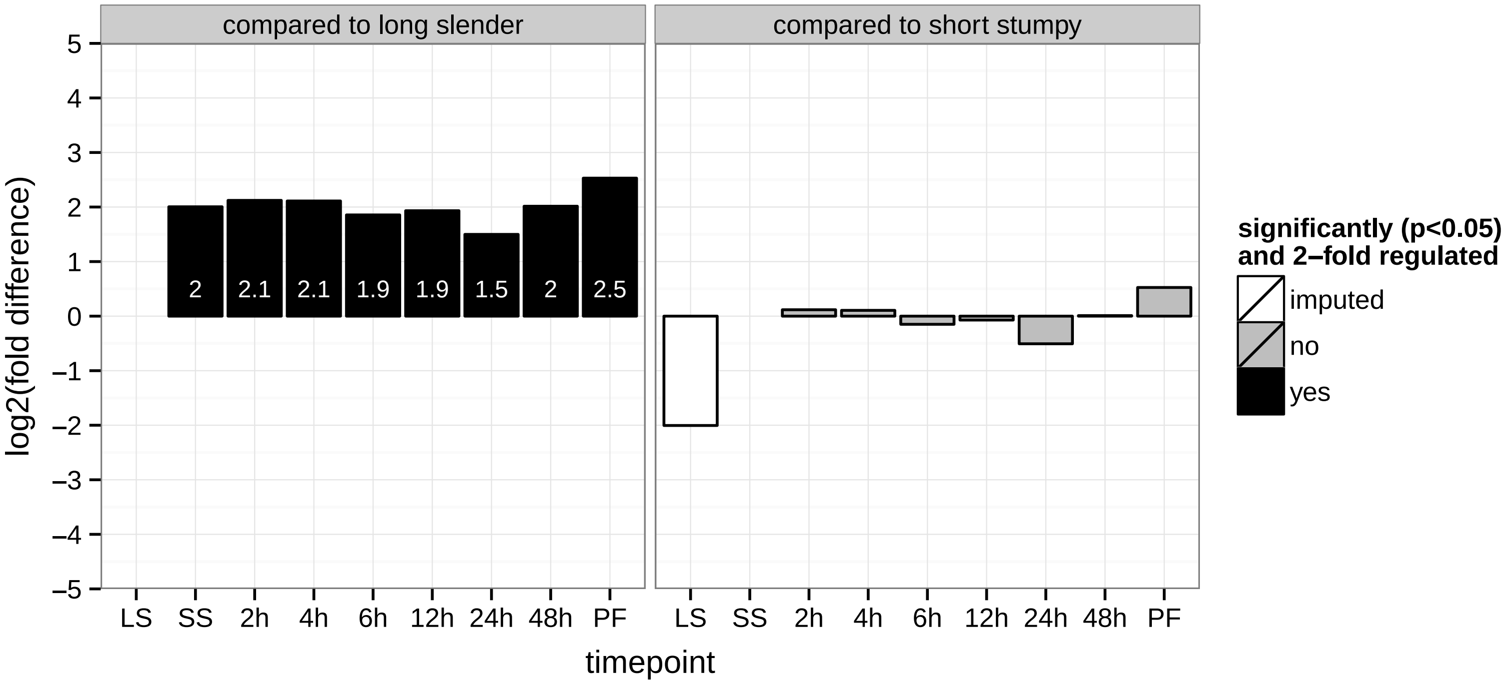
mitochondrial exoribonuclease DSS−1, exoribonuclease DSS−1 (EMBL:AY233297)
Tb927.9.7210
AGOF: RNA binding, exoribonuclease activity
AGOC: mitochondrion
AGOP: mitochondrial RNA 5'−end processing
PGOF: RNA binding, ribonuclease activity
PGOC: null
PGOP: null

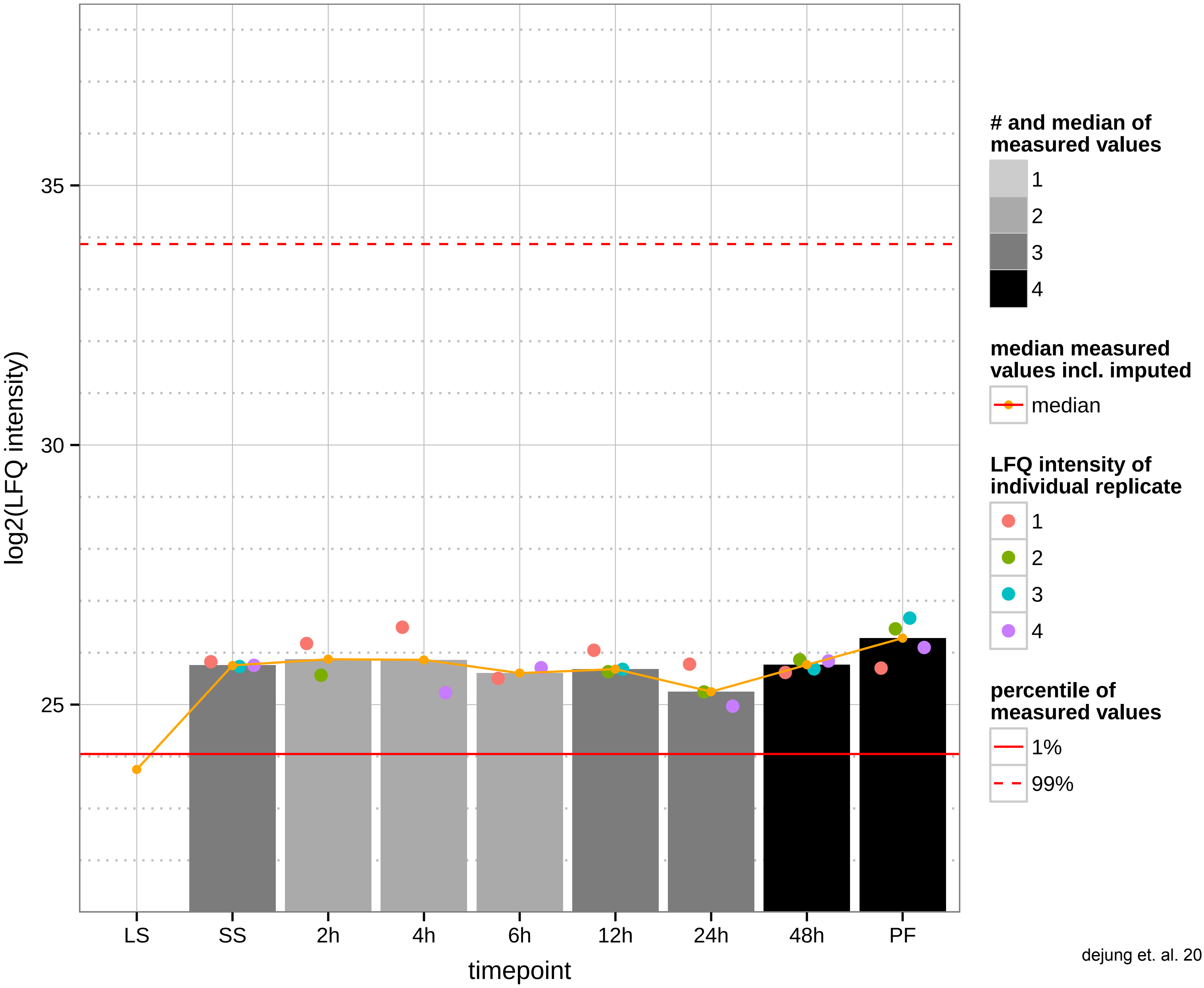




dejung et. al. 2015

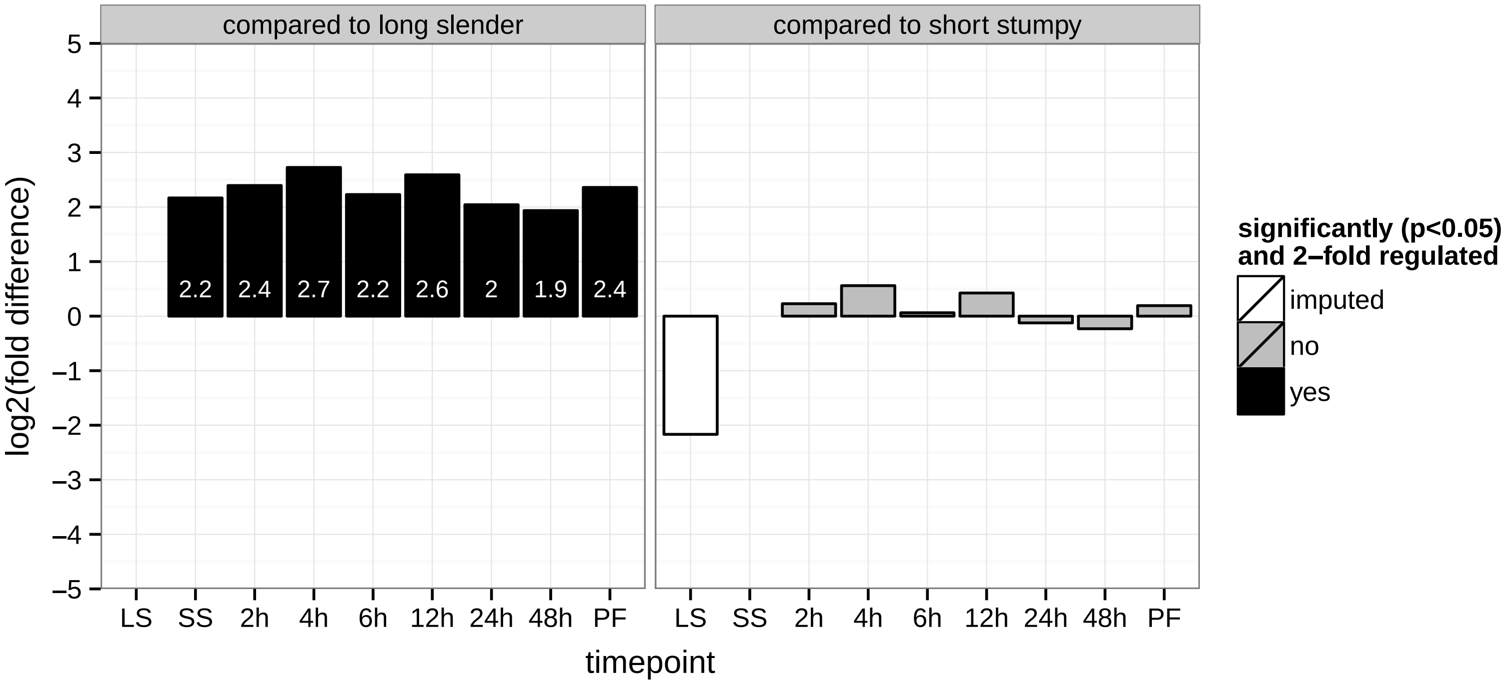
calpain–like cysteine peptidase, putative, cysteine peptidase, Clan CA, family C2
Tb927.9.7540
AGOF: calcium–dependent cysteine–type endopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: calcium–dependent cysteine–type endopeptidase activity
PGOC: intracellular
PGOP: proteolysis

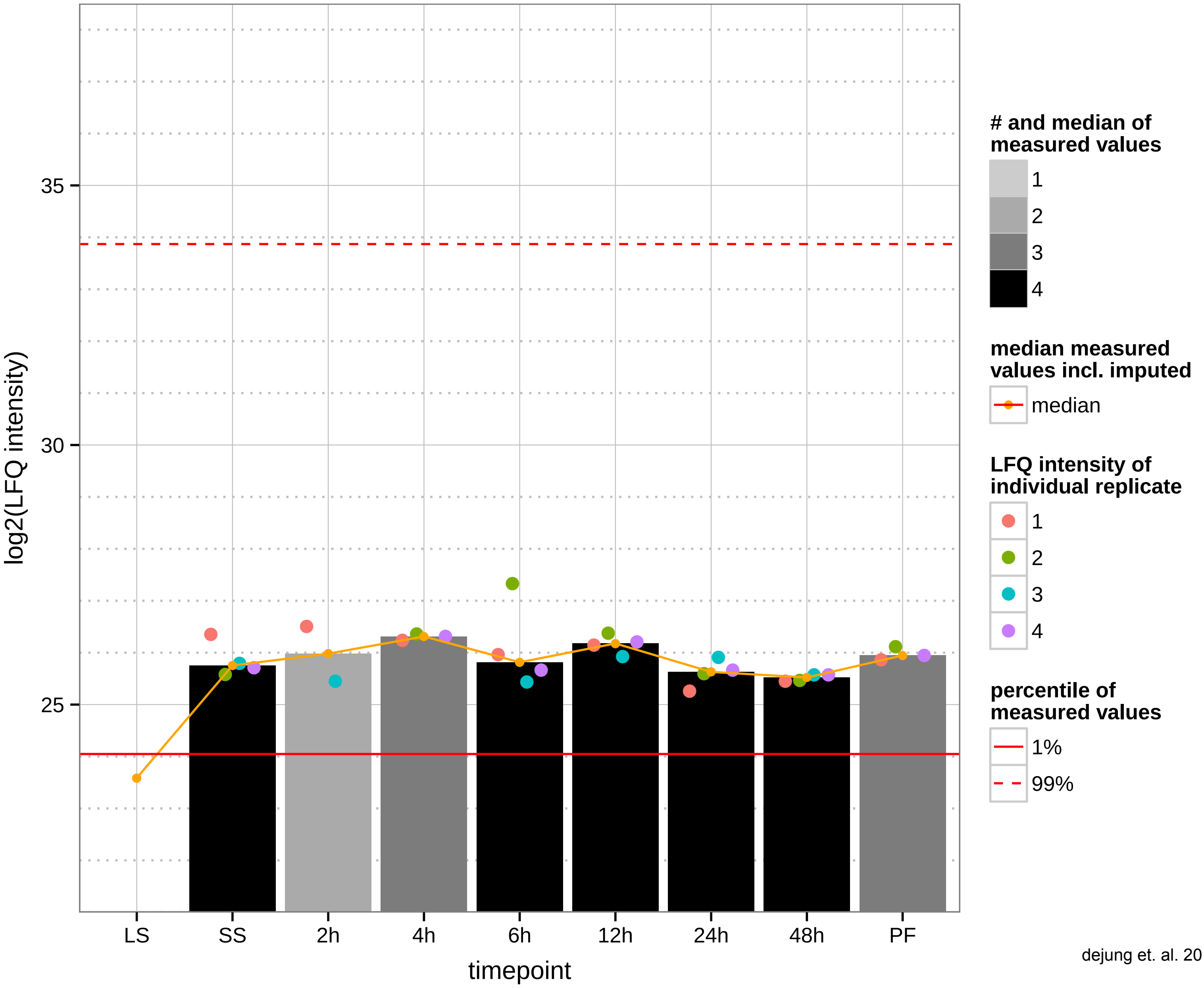




dejung et. al. 2015

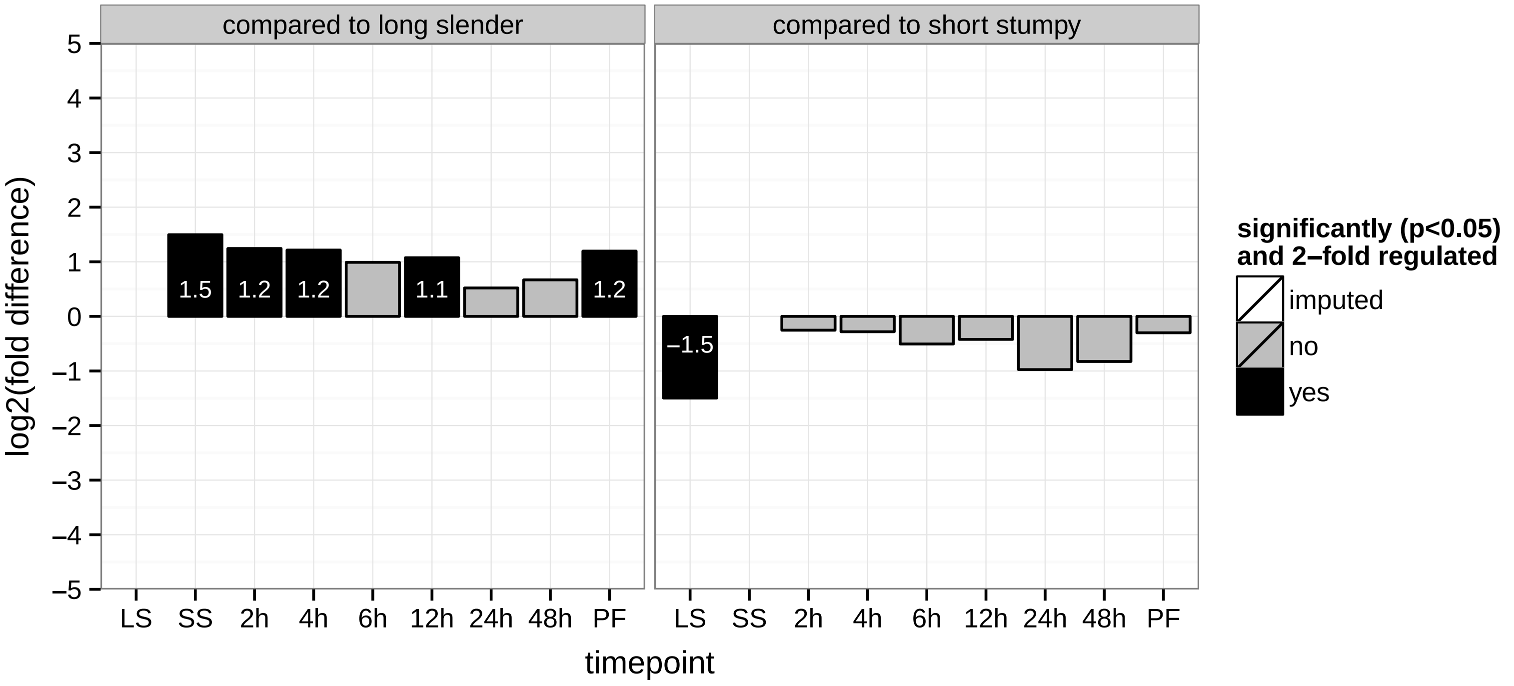
ADP–ribosylation factor, putative
Tb927.9.7650
AGOF: GTP binding
AGOC: intracellular
AGOP: intracellular protein transport, small GTPase mediated signal transduction
PGOF: GTP binding
PGOC: intracellular
PGOP: intracellular protein transport, small GTPase mediated signal transduction

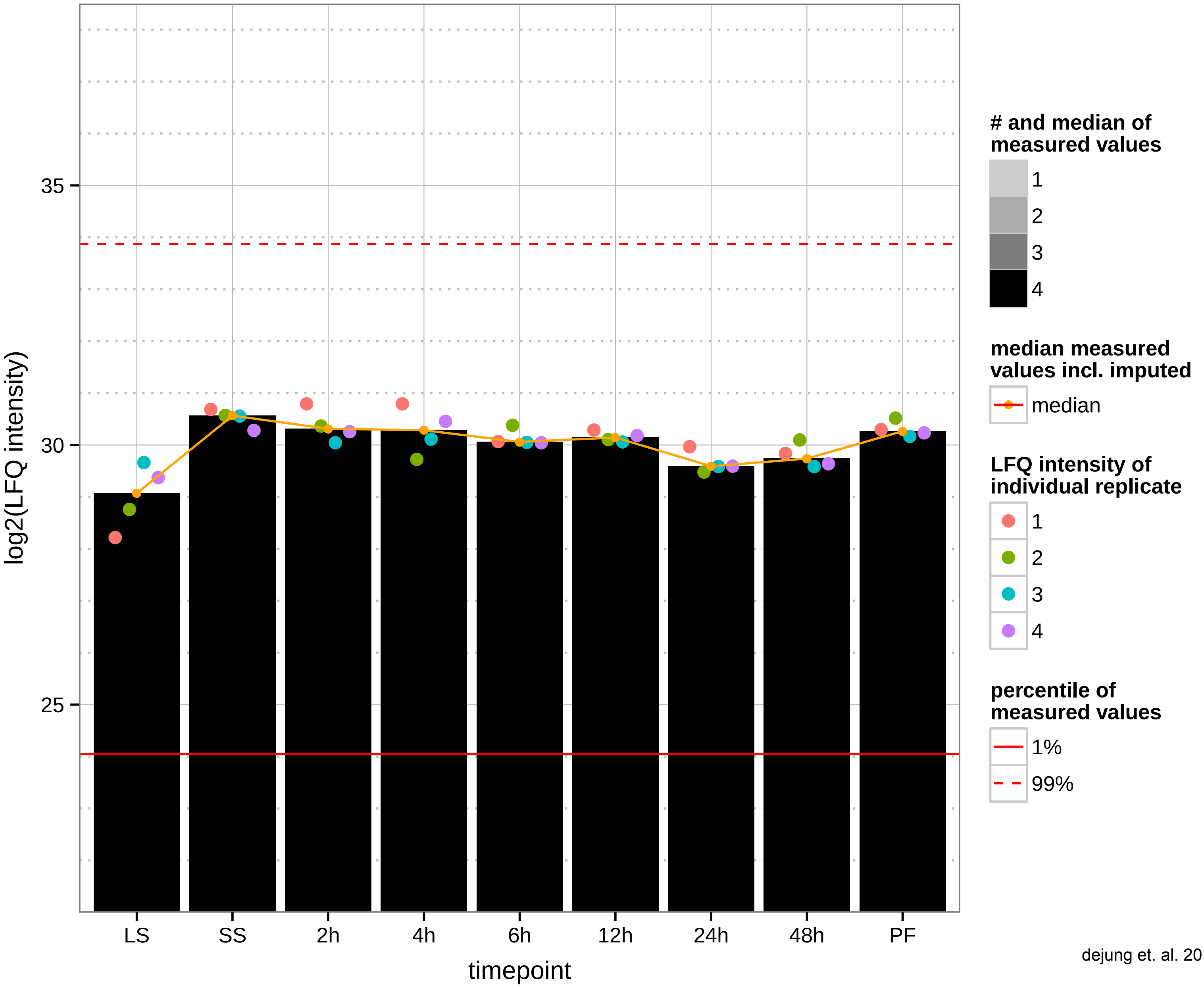




dejung et. al. 2015

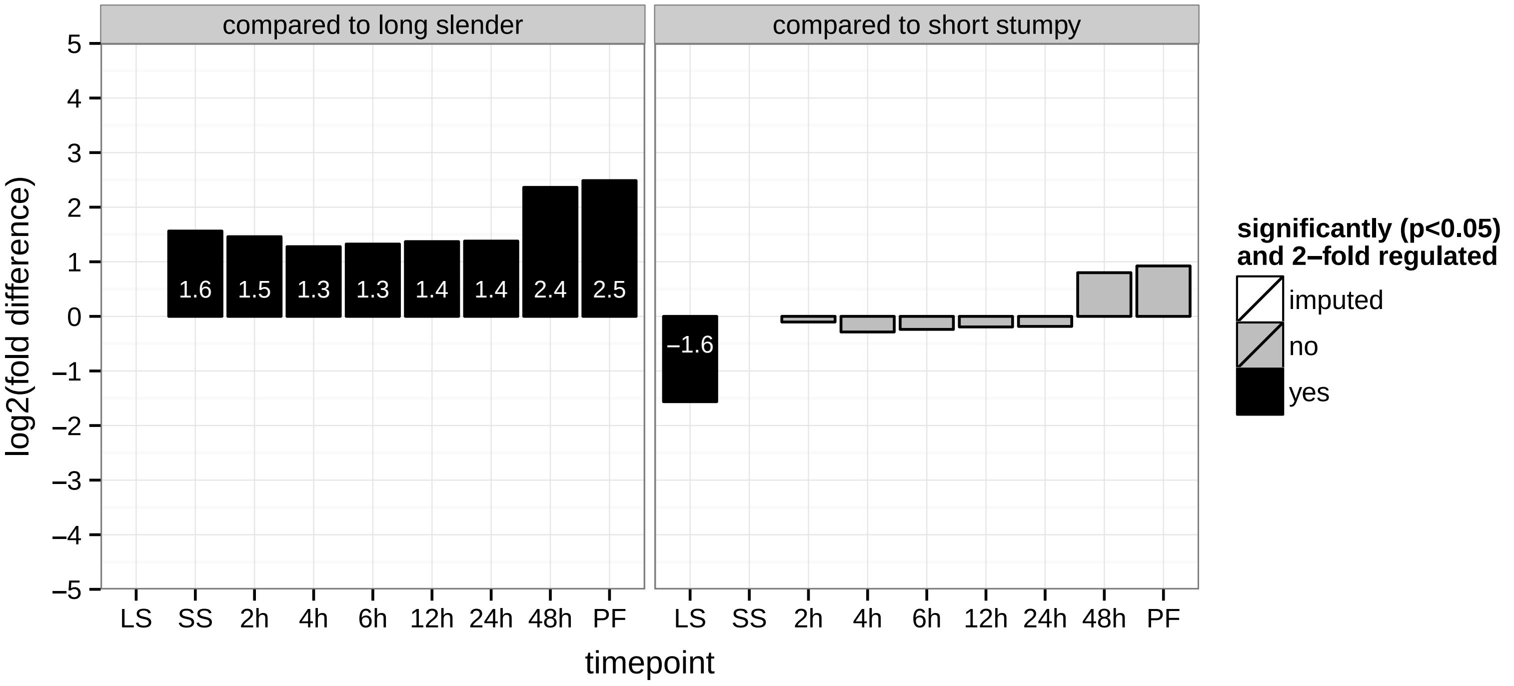
predicted tetratricopeptide repeat protein
Tb927.9.7720
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

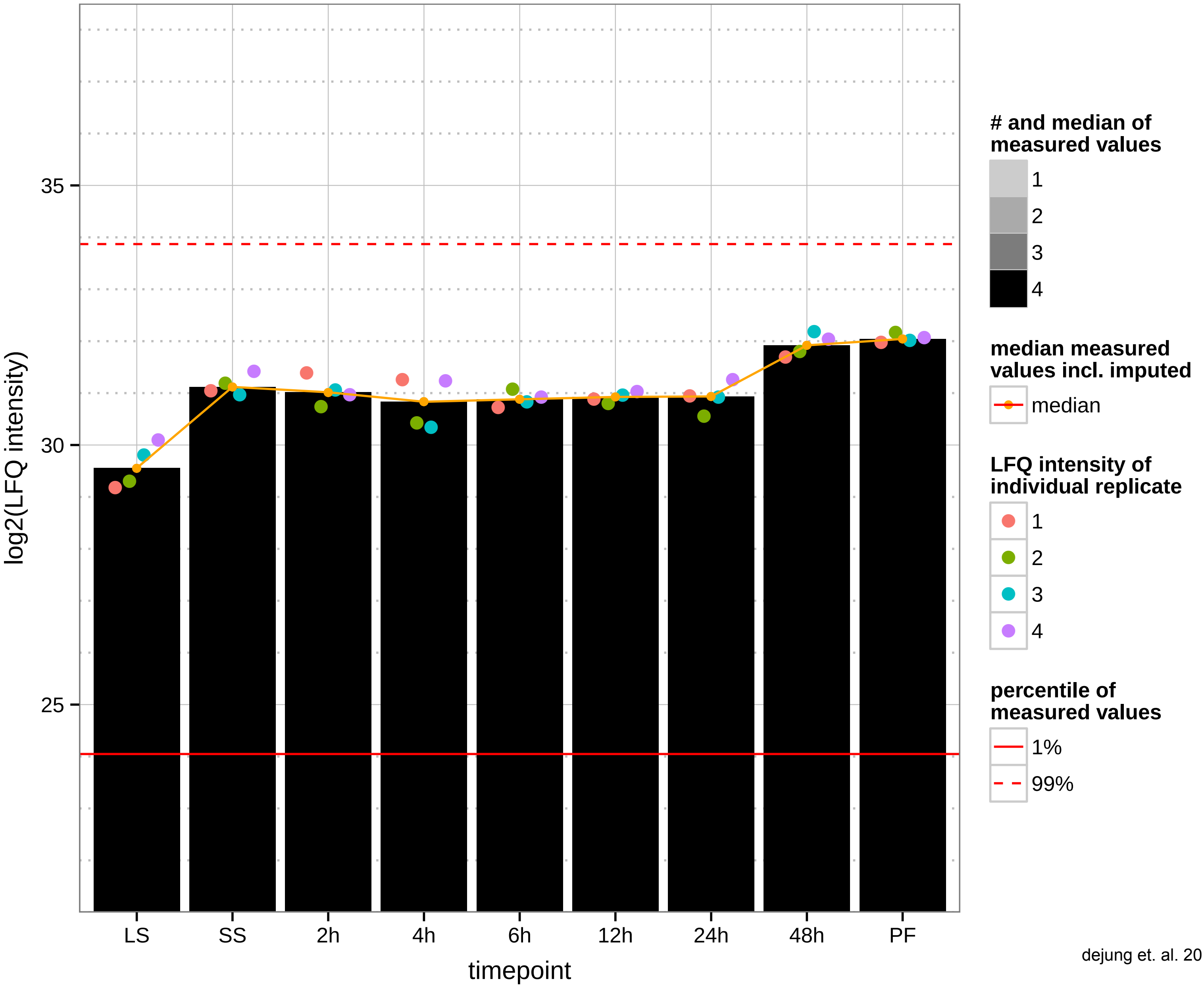




dejung et. al. 2015

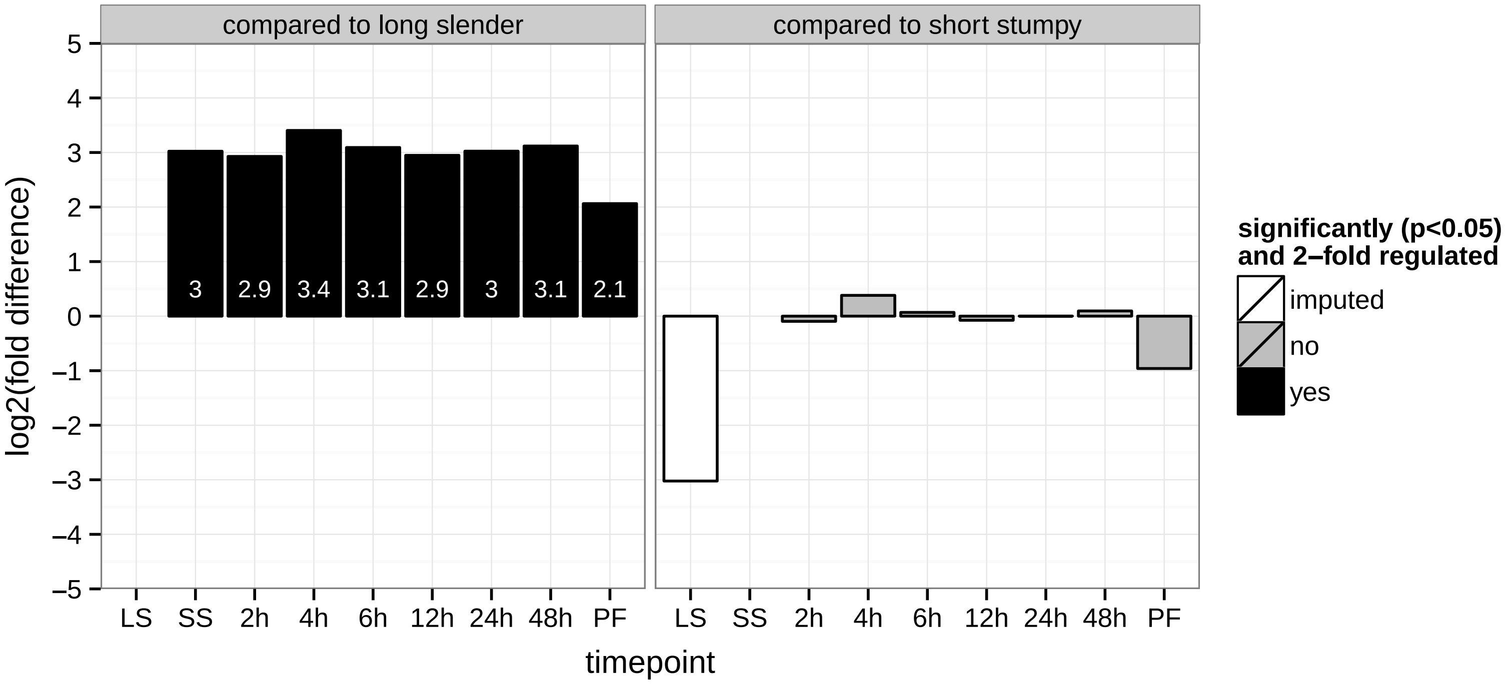
spermidine synthase, SPDSYN (SpSyn)
Tb927.9.7770
AGOF: spermidine synthase activity
AGOC: null
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null

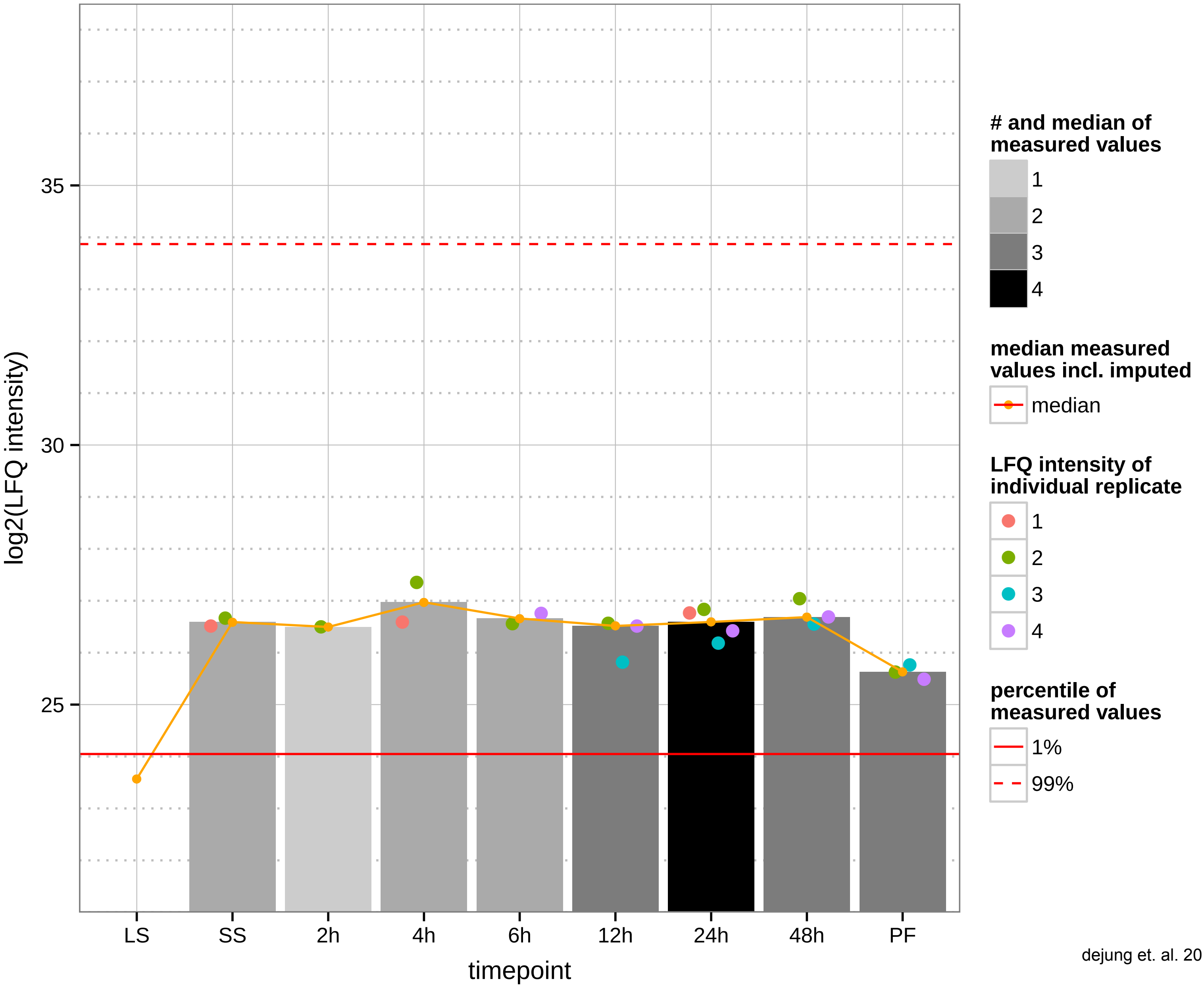




dejung et. al. 2015

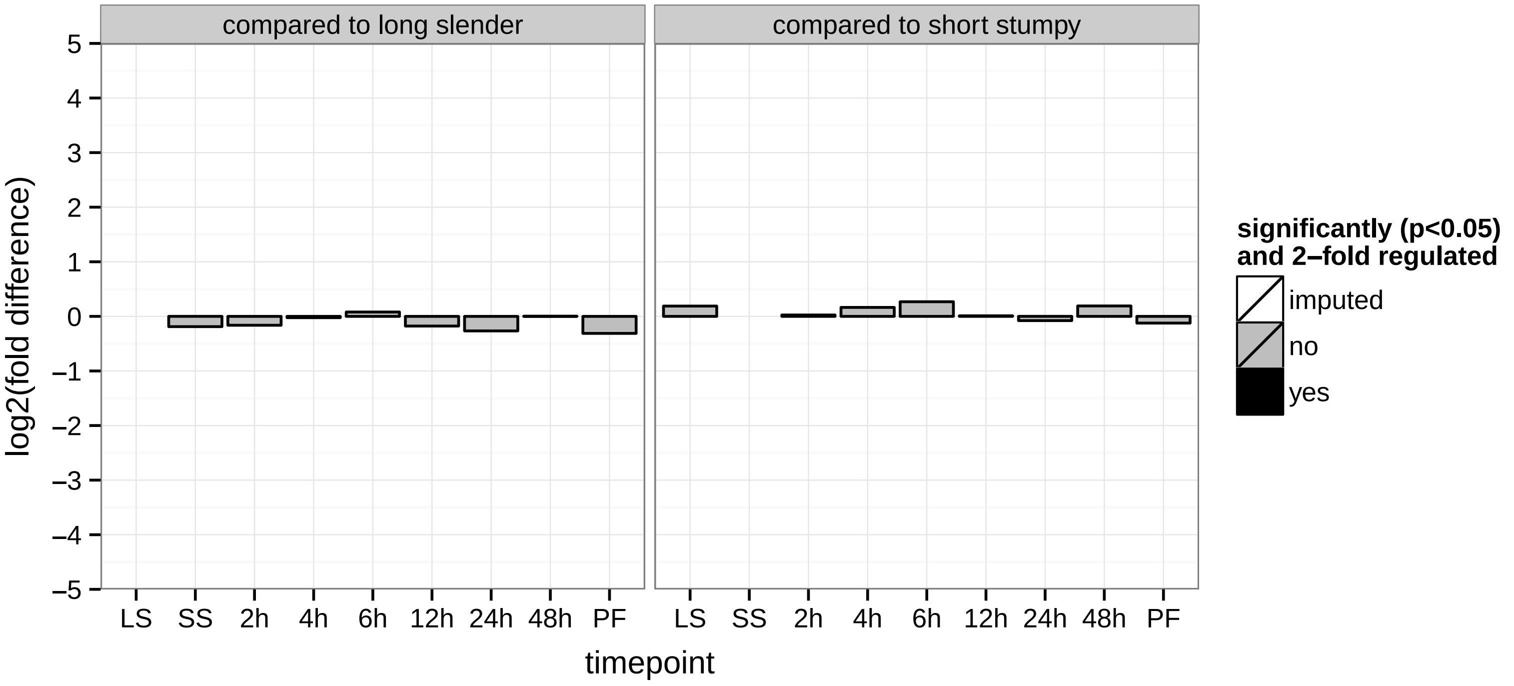
hypothetical protein, conserved
Tb927.9.7800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

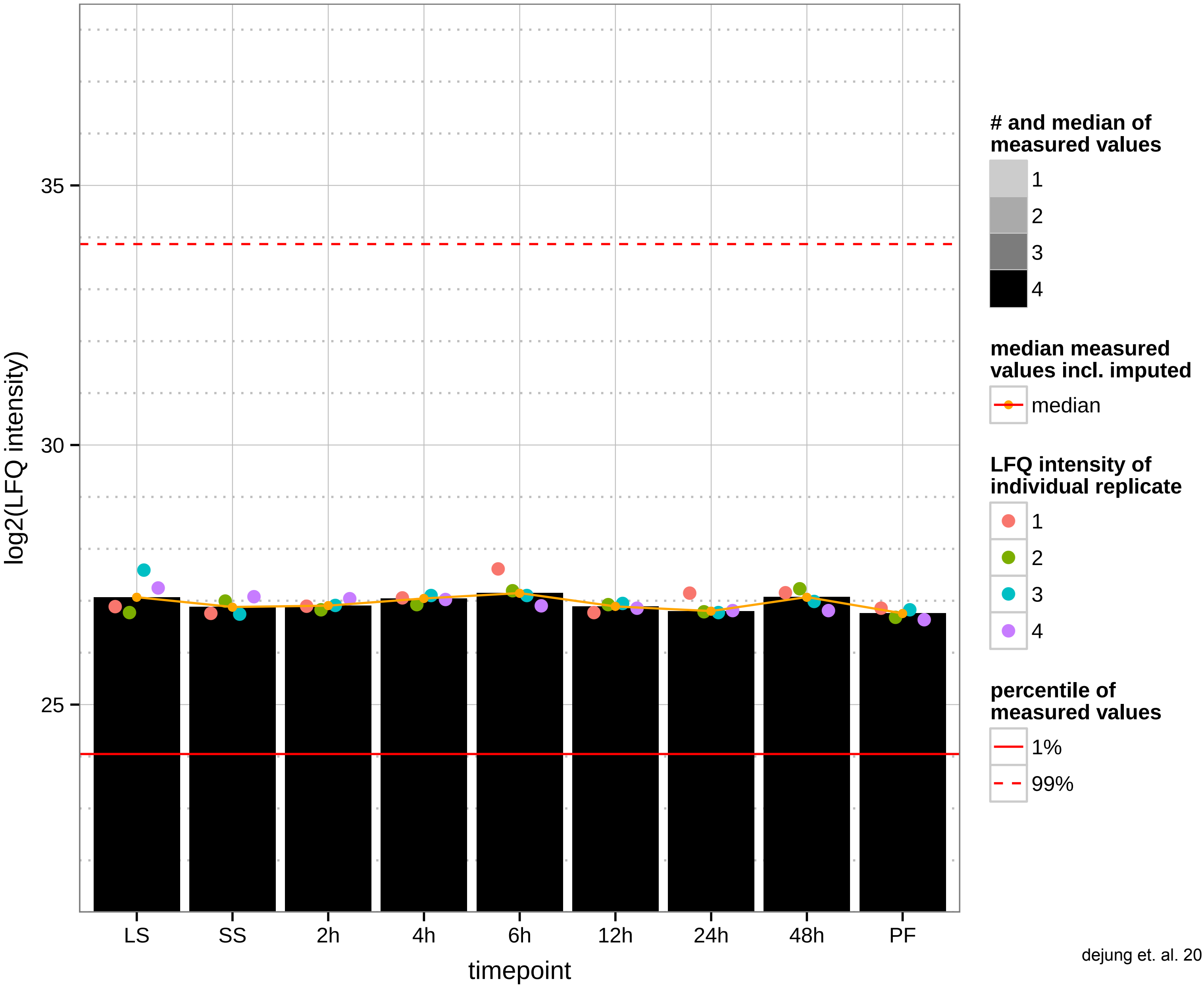




dejung et. al. 2015

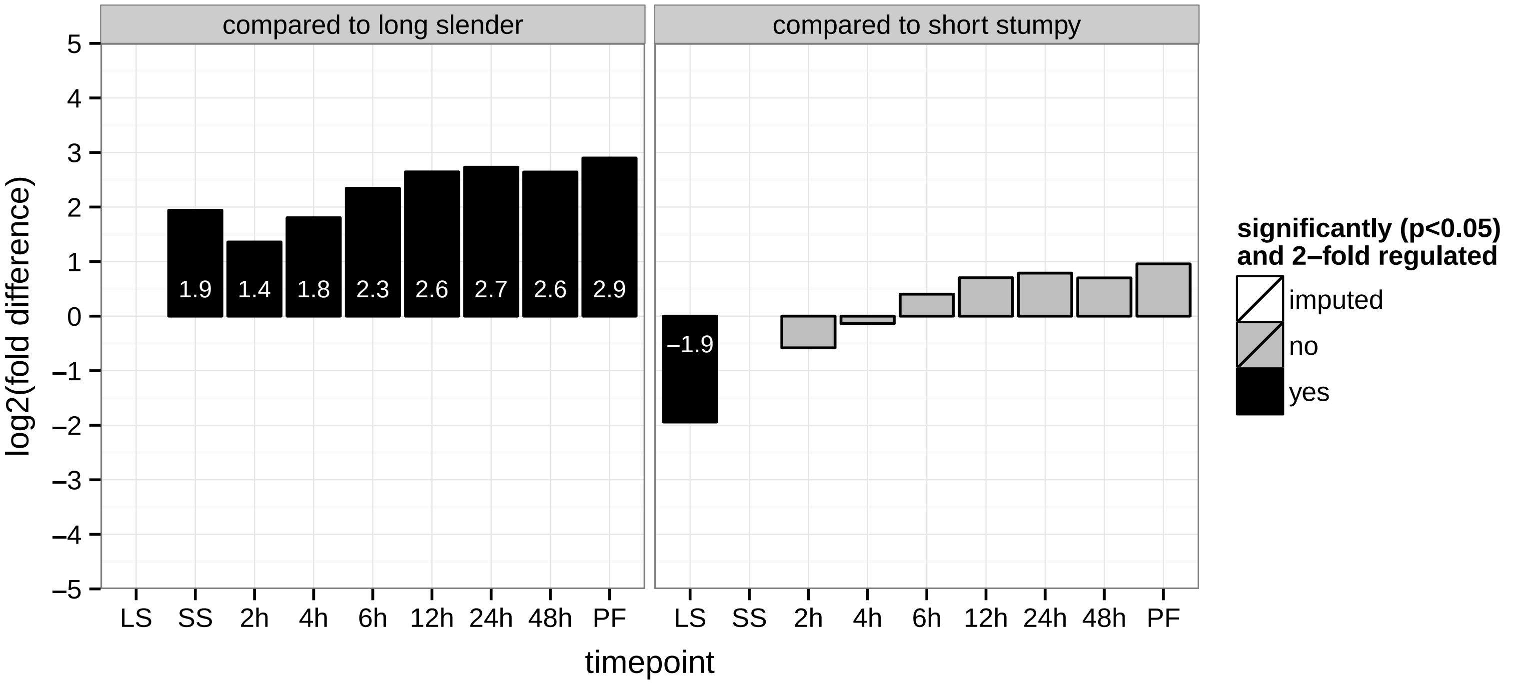
hypothetical protein, conserved
Tb927.9.8190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

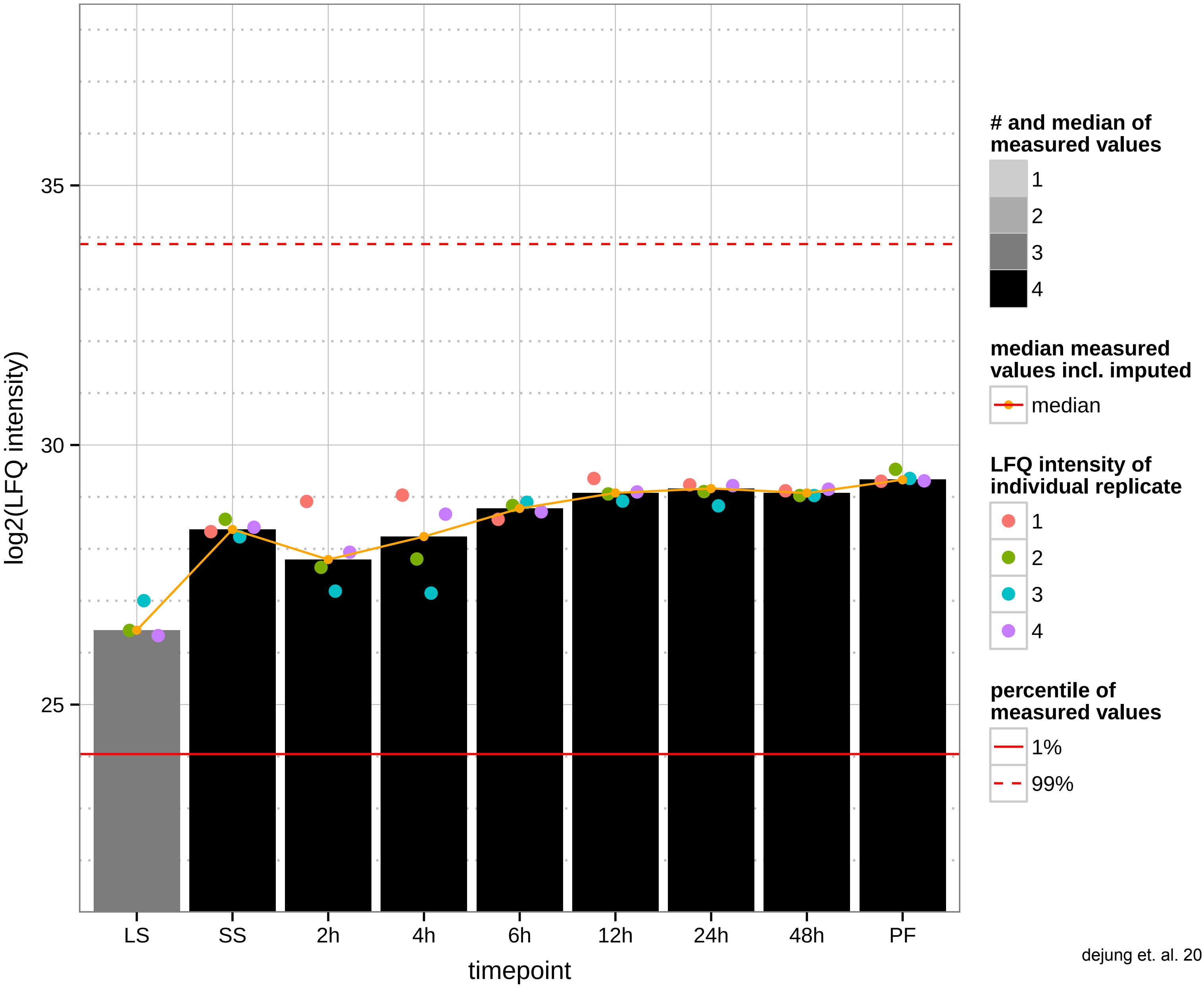




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.8200;Tb11.v5.0687
AGOF: null
AGOC: null, intracellular, nucleolus
AGOP: null, cell proliferation
PGOF: null
PGOC: nucleolus
PGOP: ribosome biogenesis





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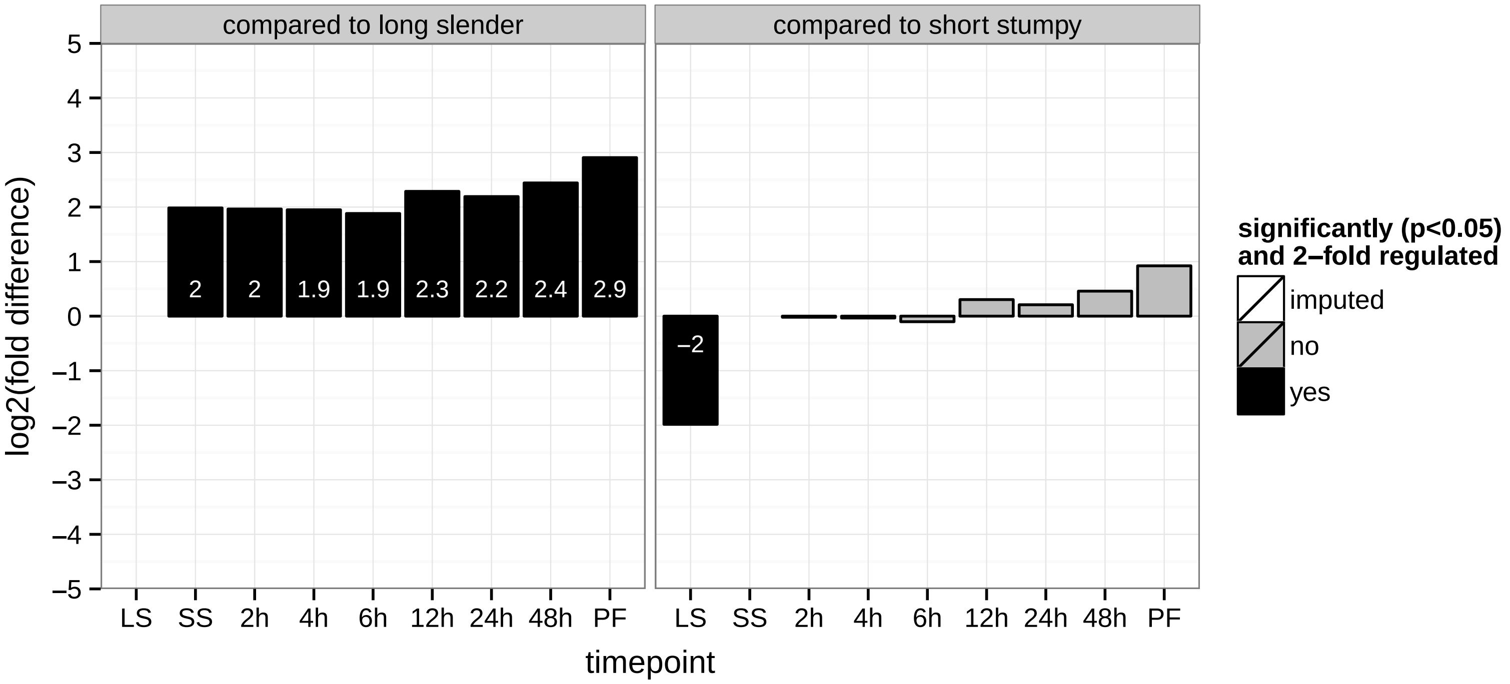
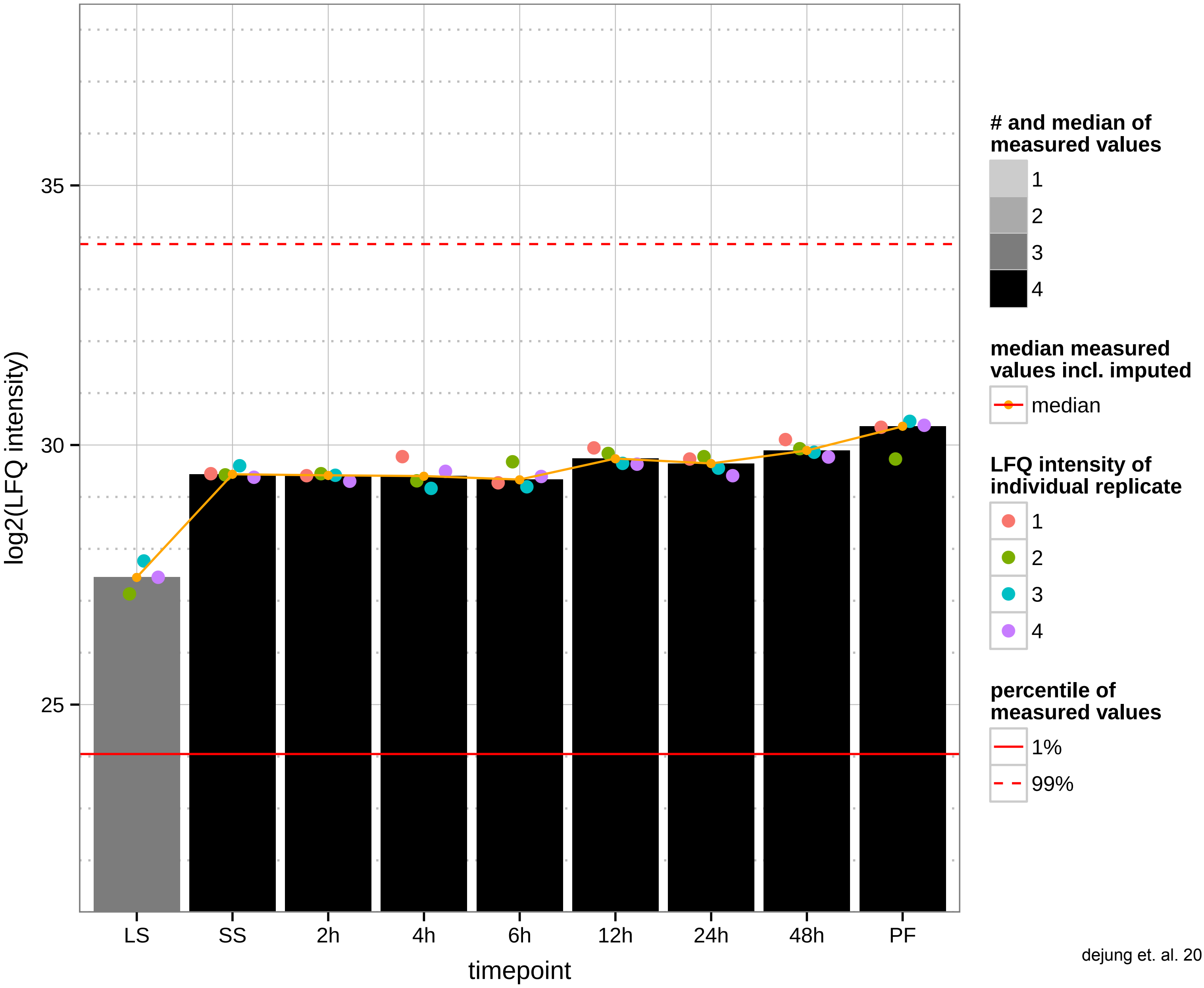
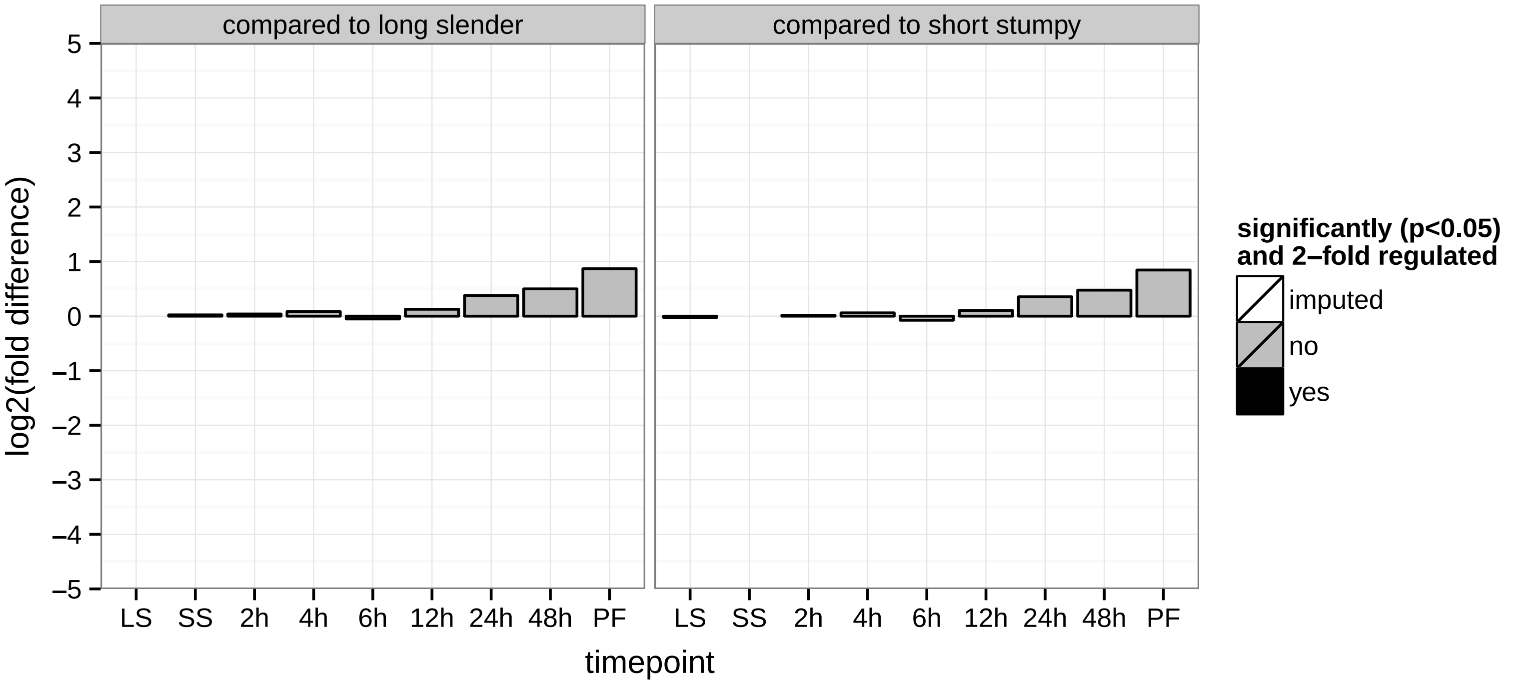
chaperone protein DNAj, putative
Tb927.9.8410
AGOF: heat shock protein binding, unfolded protein binding
AGOC: mitochondrion
AGOP: protein folding
PGOF: heat shock protein binding, unfolded protein binding
PGOC: null
PGOP: protein folding

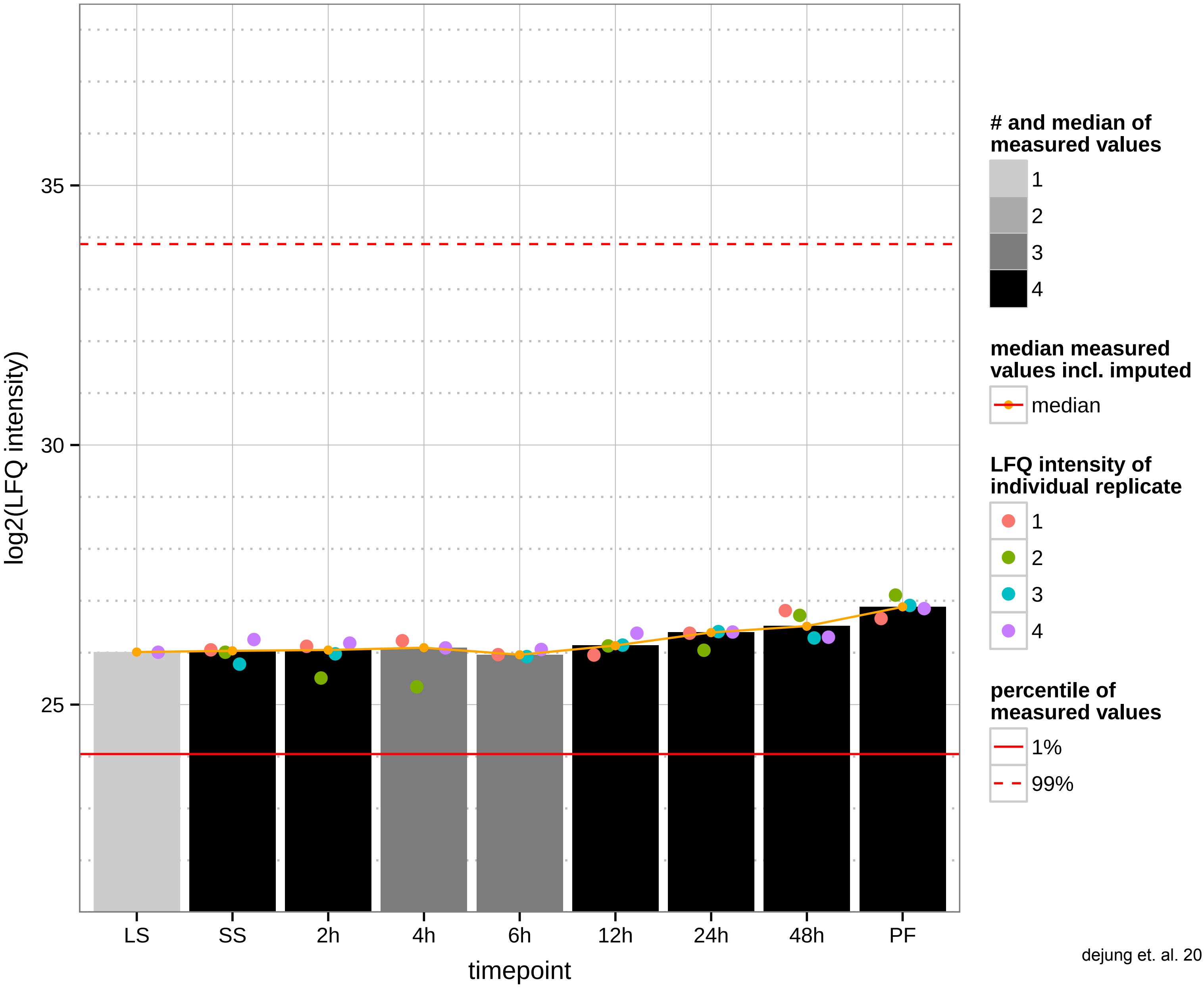




dejung et. al. 2015

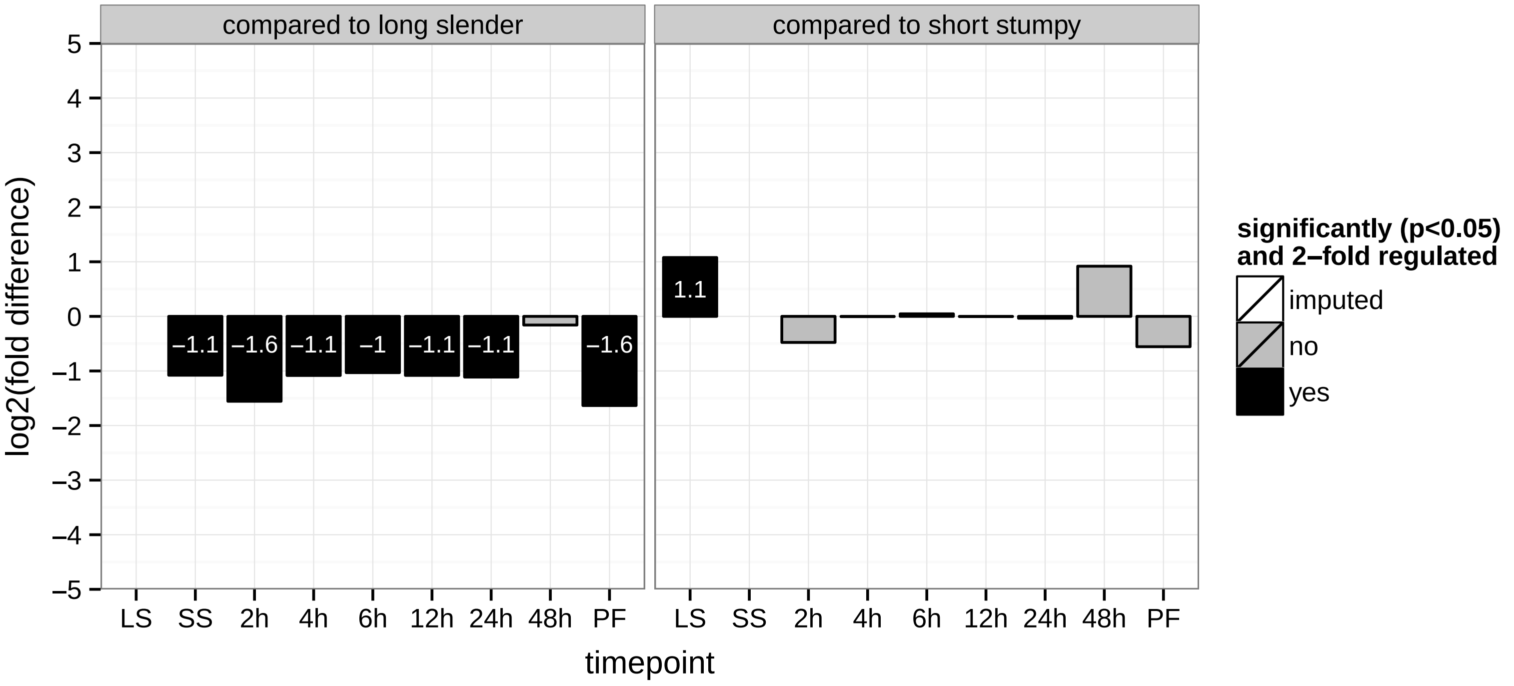
tRNA nucleotidyltransferase, putative
Tb927.9.8780
AGOF: RNA binding, nucleotidyltransferase activity
AGOC: null
AGOP: RNA processing
PGOF: RNA binding, nucleotidyltransferase activity
PGOC: null
PGOP: RNA processing

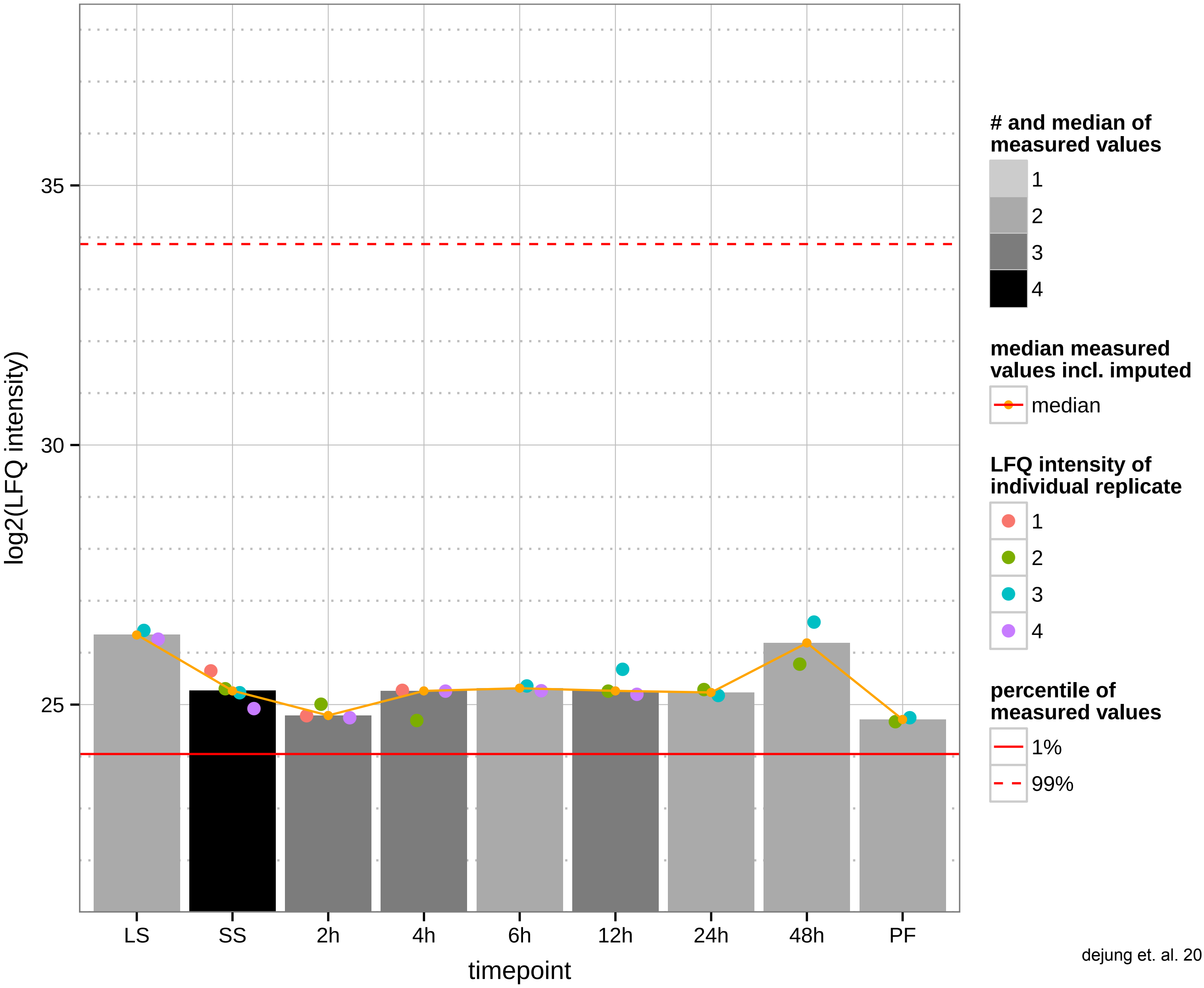




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.8810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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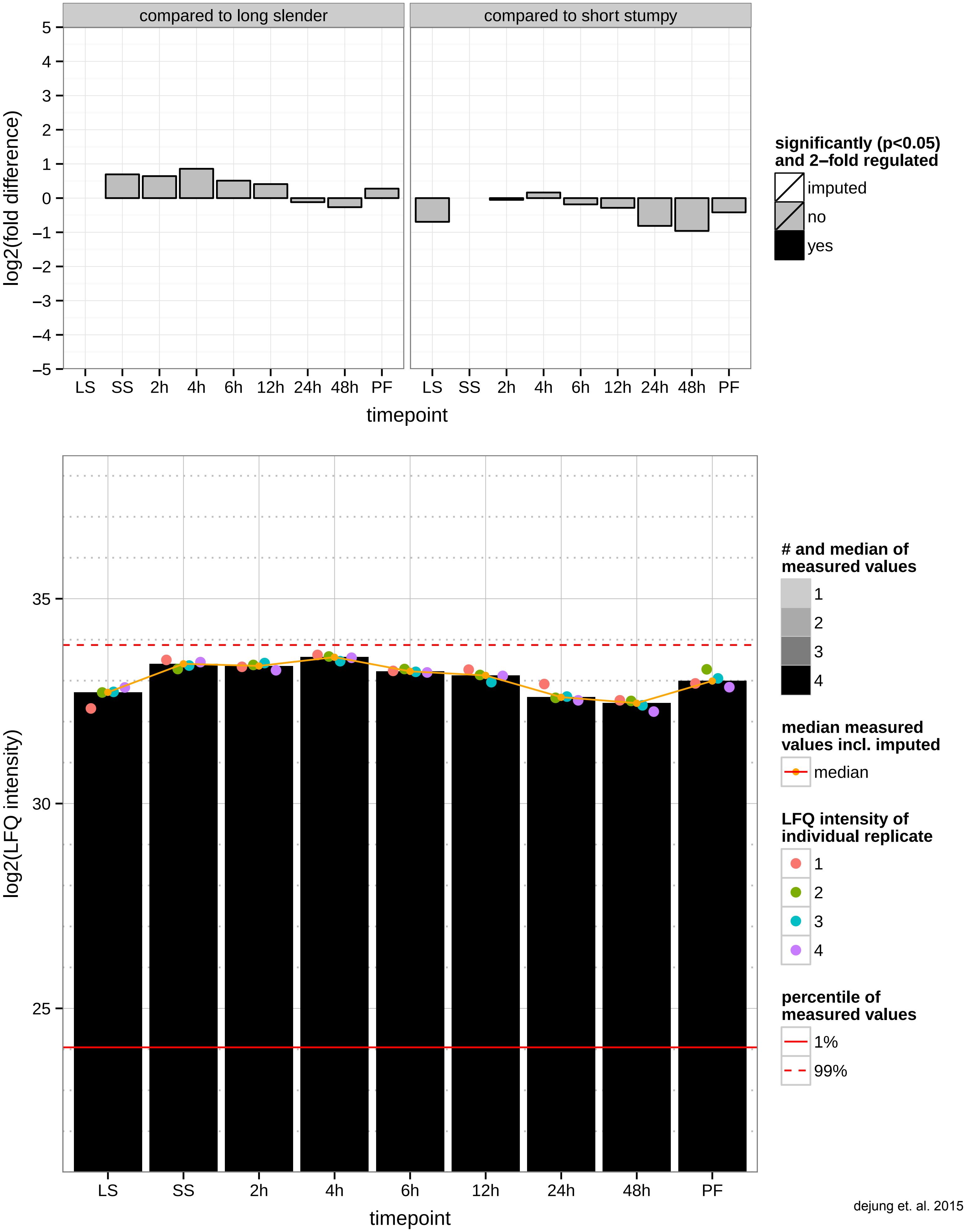
actin A
Tb927.9.8880;Tb927.9.8850
AGOF: structural constituent of cytoskeleton
AGOC: actin cytoskeleton, cytoplasm
AGOP: cytoskeleton organization
PGOF: null
PGOC: null
PGOP: null



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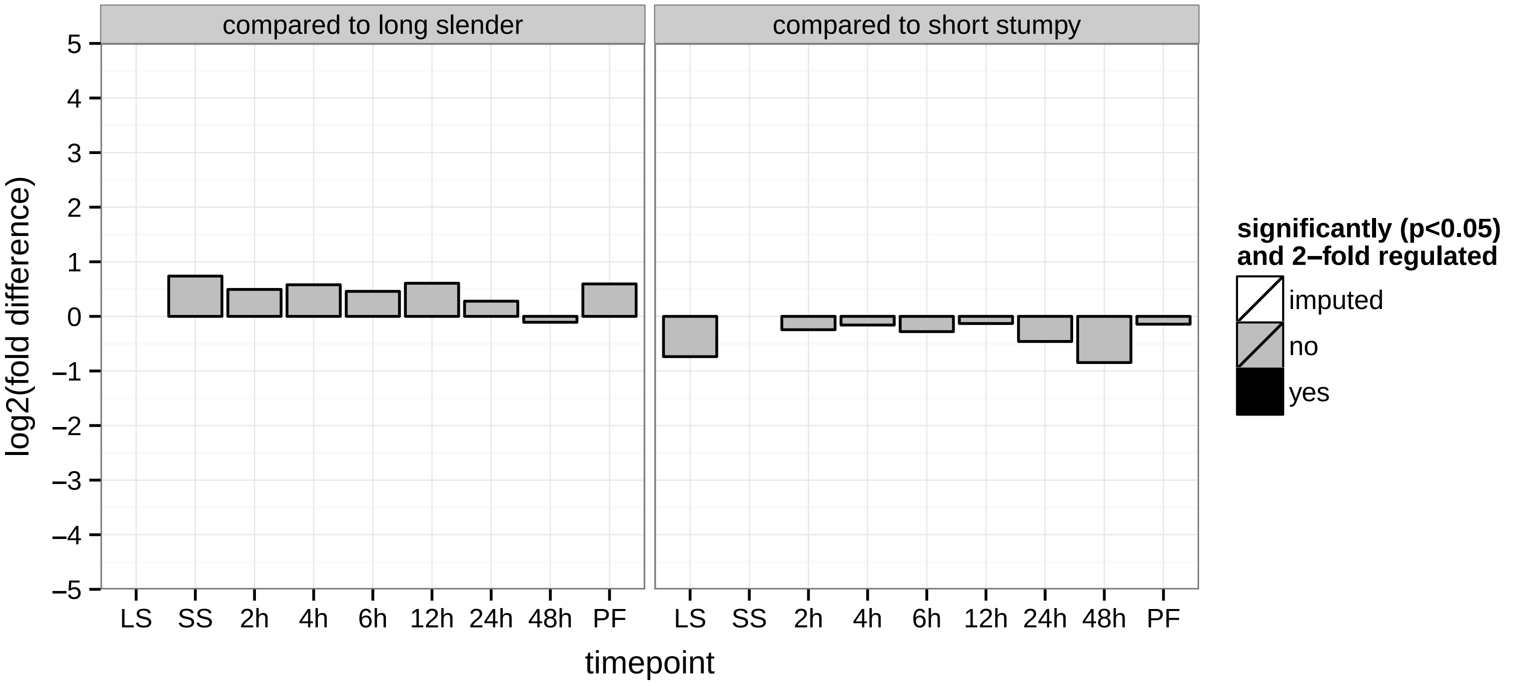
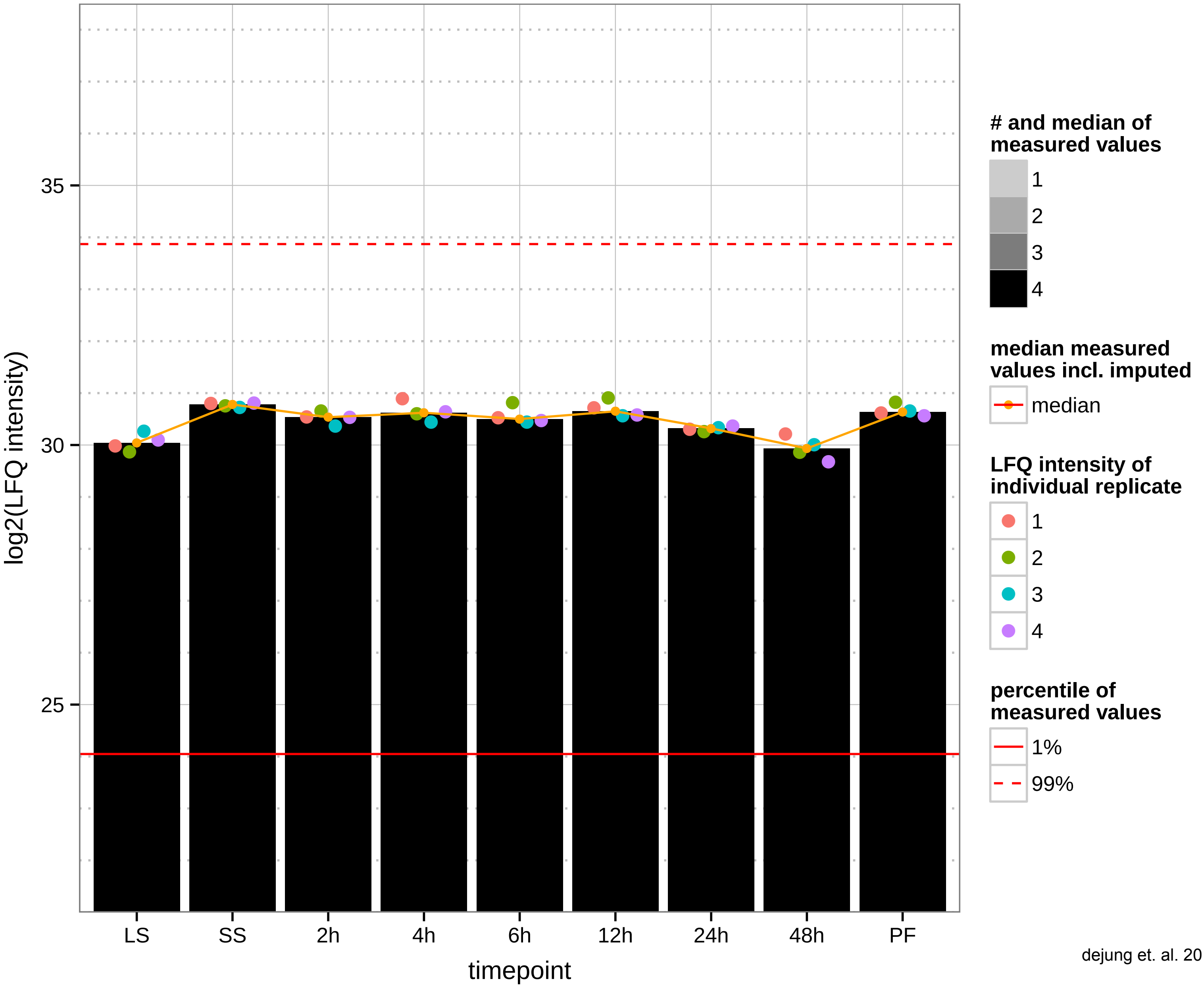
CAAX prenyl protease 1, putative, metallo– peptidase, Clan M– Family M48
Tb927.9.8950
AGOF: metalloendopeptidase activity
AGOC: membrane, mitochondrial inner membrane
AGOP: proteolysis
PGOF: metalloendopeptidase activity
PGOC: membrane
PGOP: proteolysis





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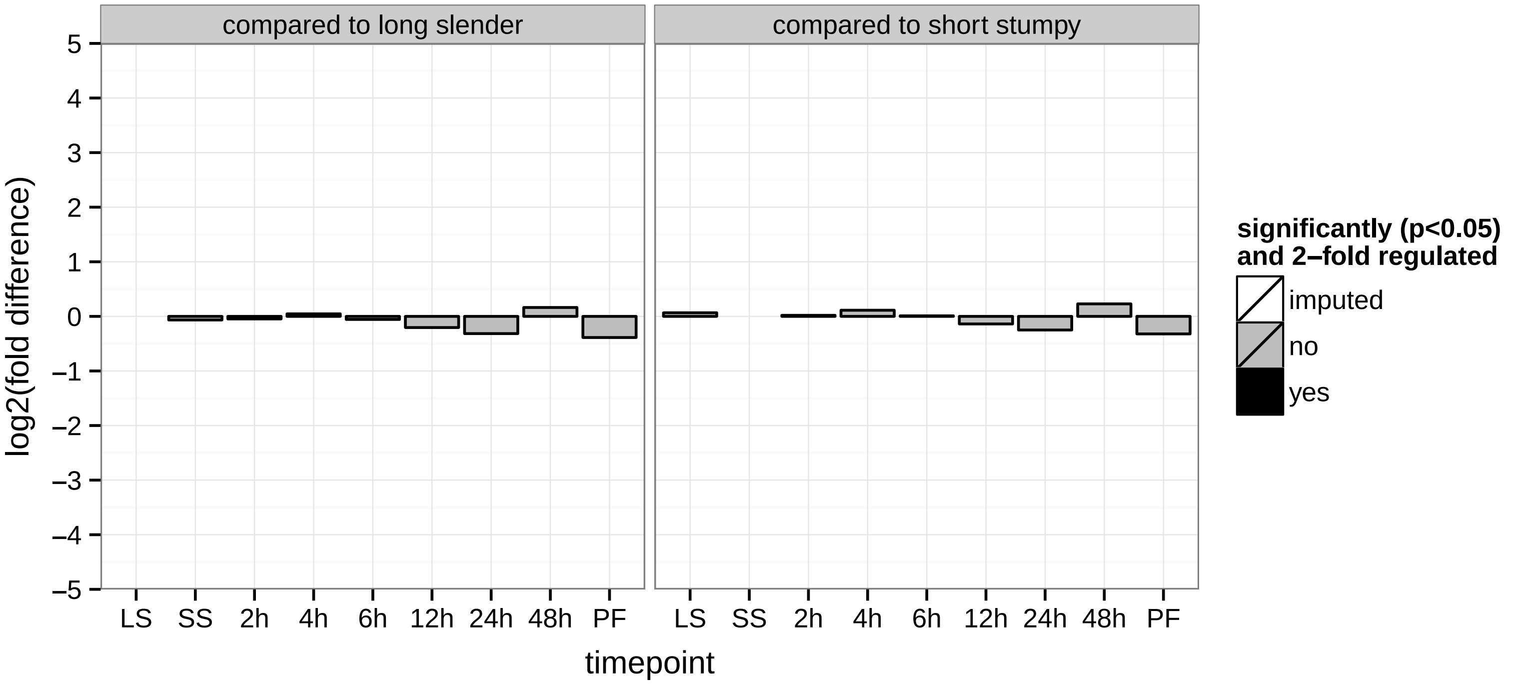
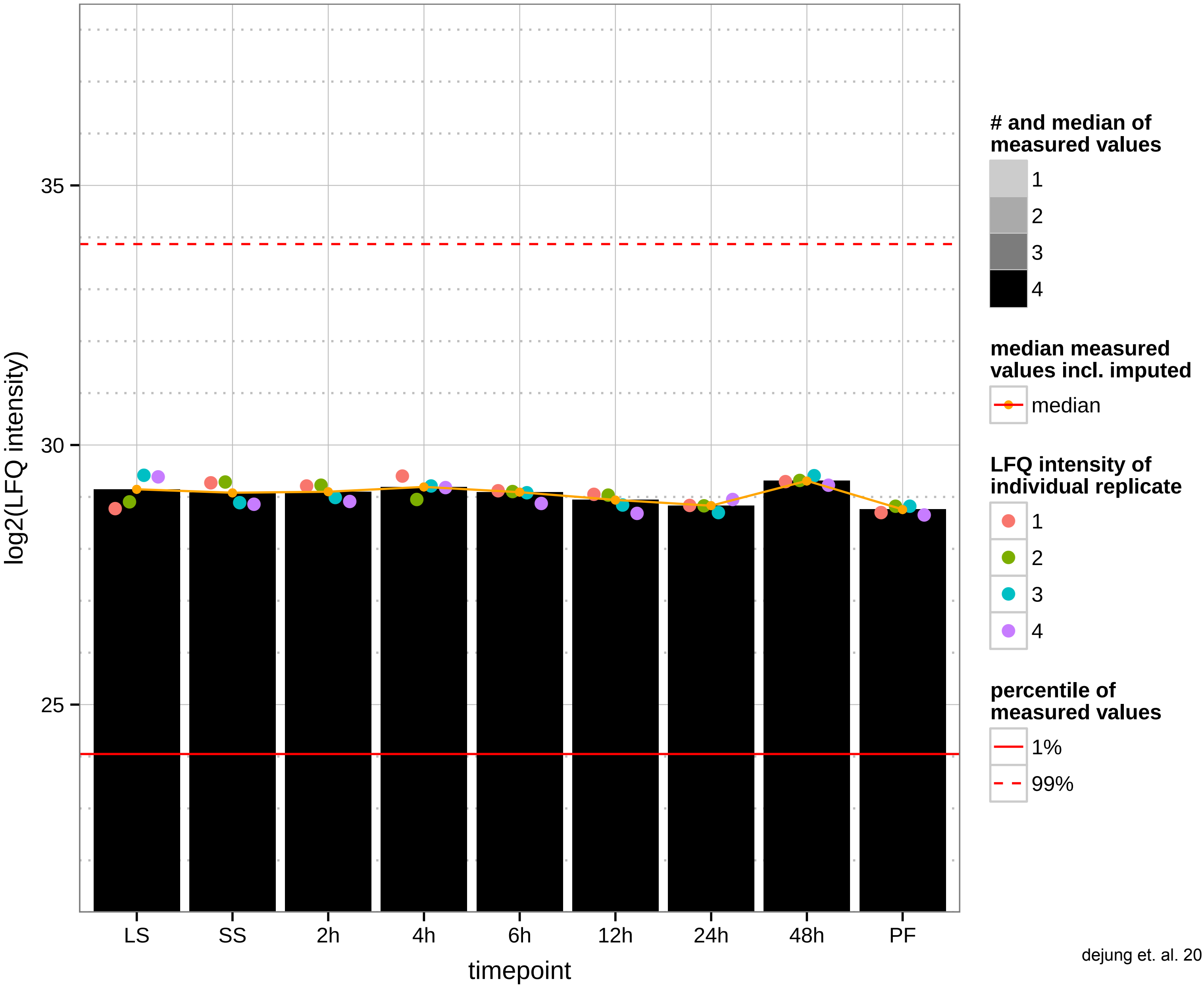
hypothetical protein, conserved
Tb927.9.8990
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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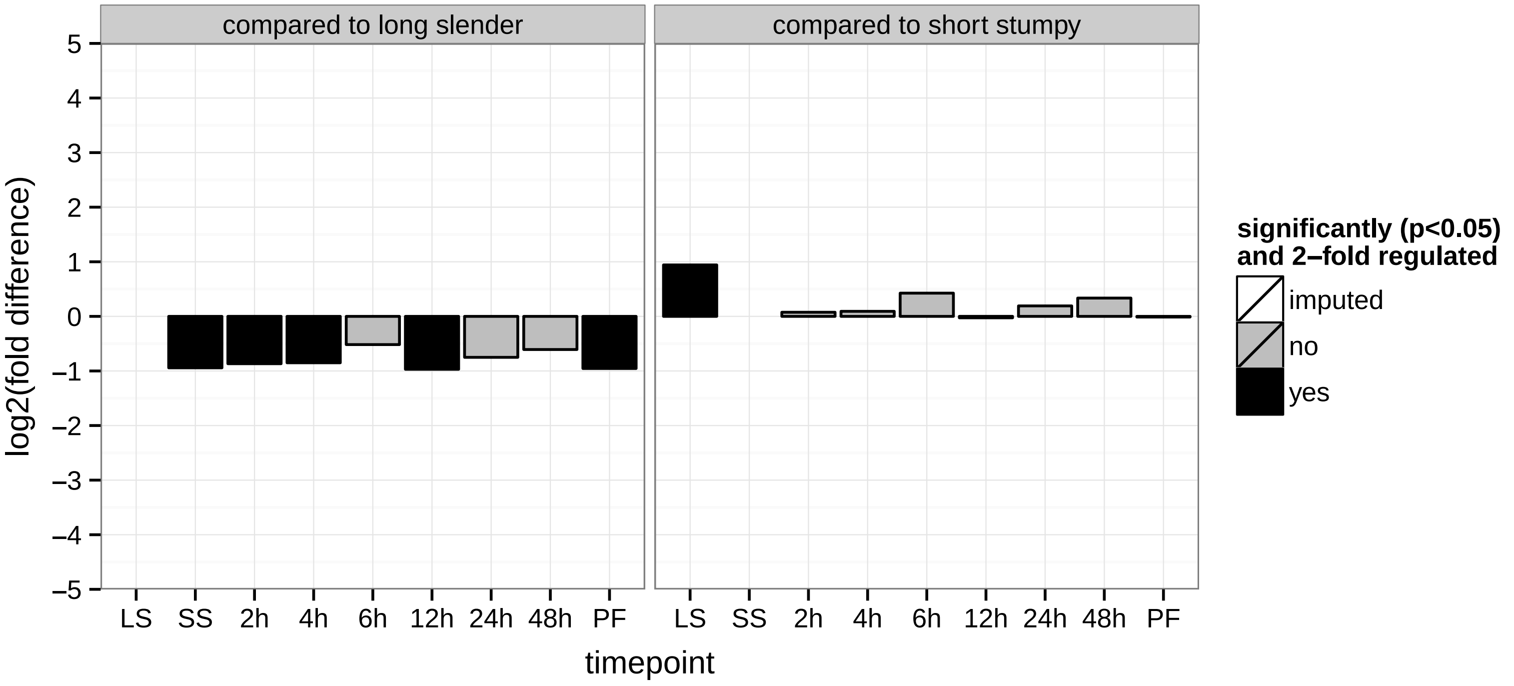
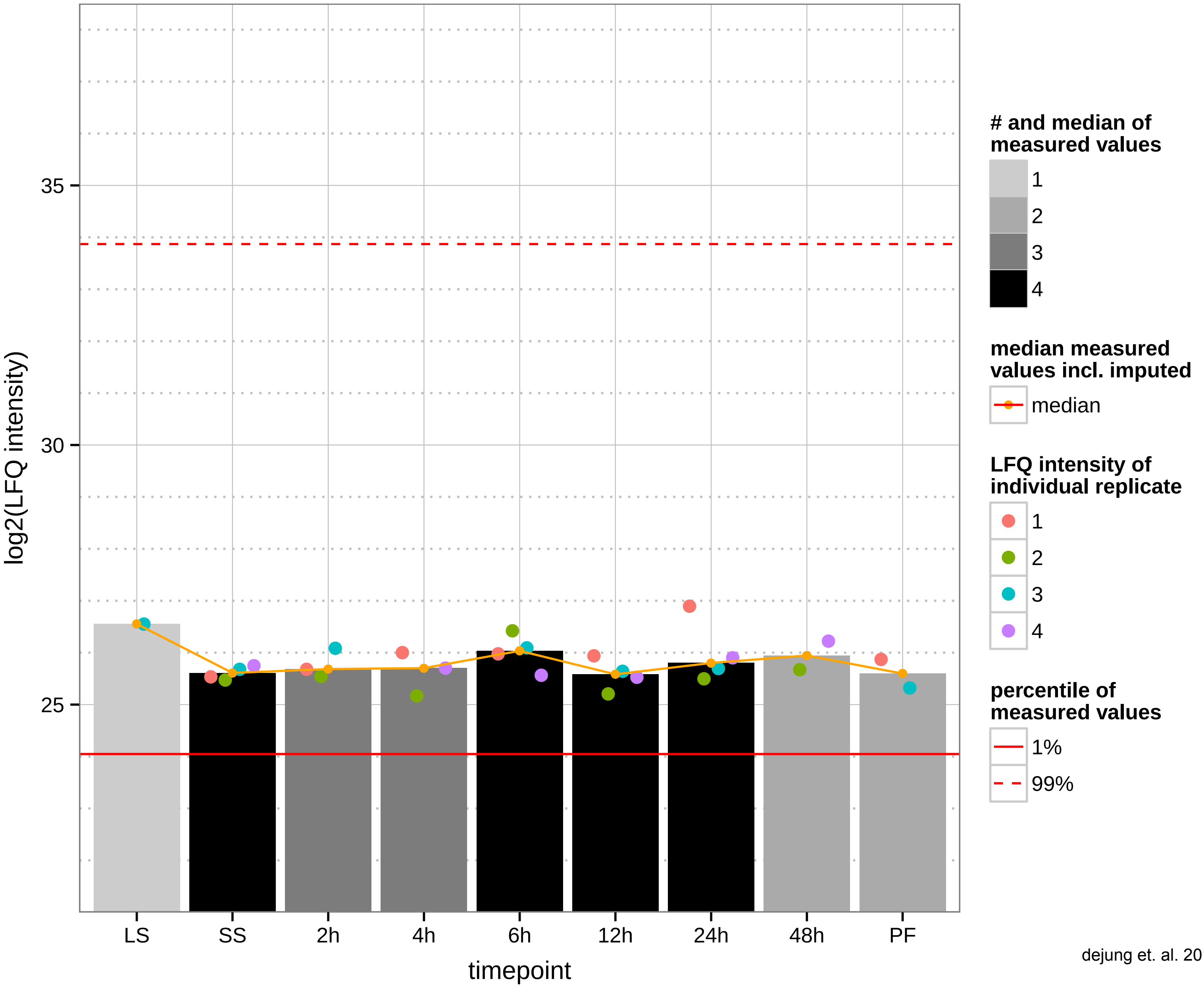
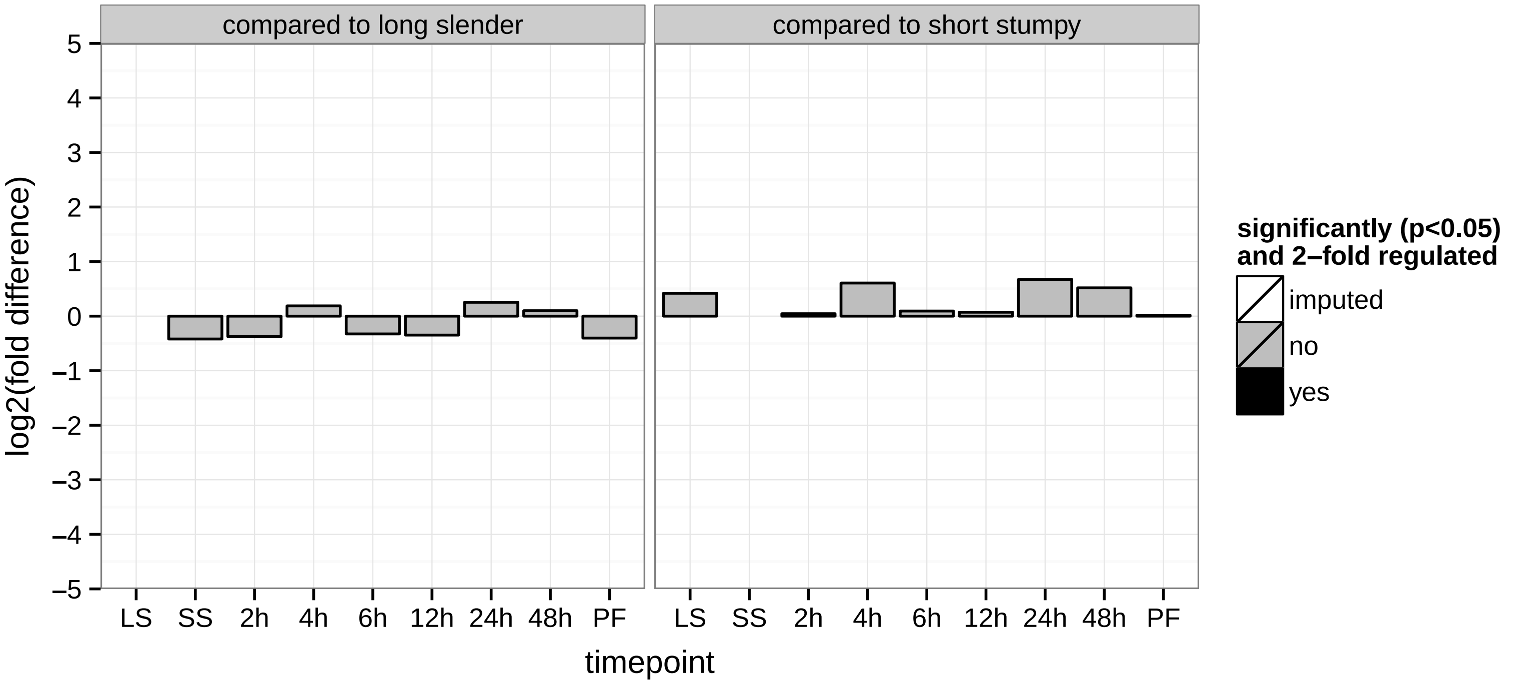
hypothetical protein, conserved
Tb927.9.9010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

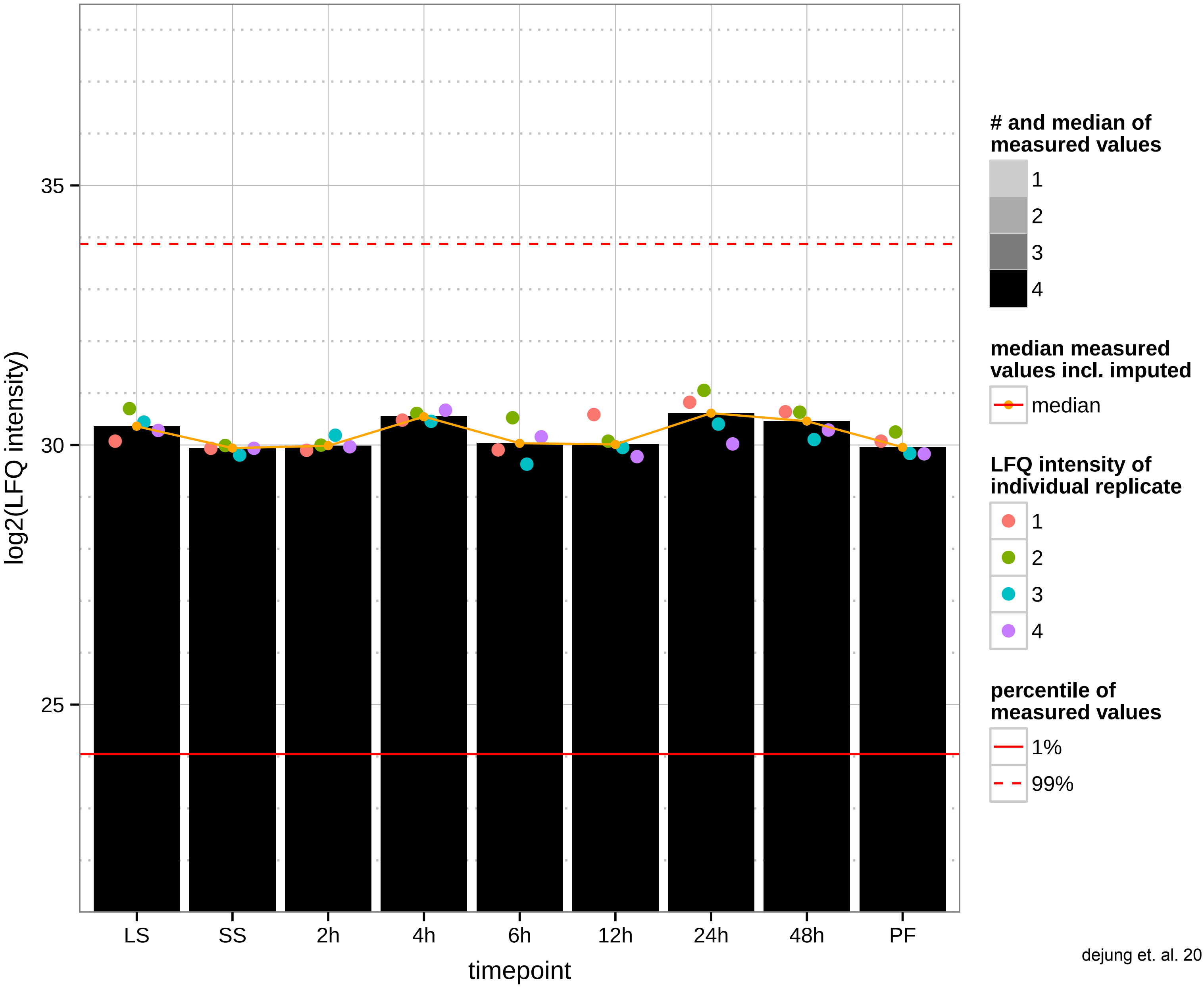




dejung et. al. 2015

Lsm12 protein, putative
Tb927.9.9060
AGOF: null
AGOC: cytoplasmic stress granule
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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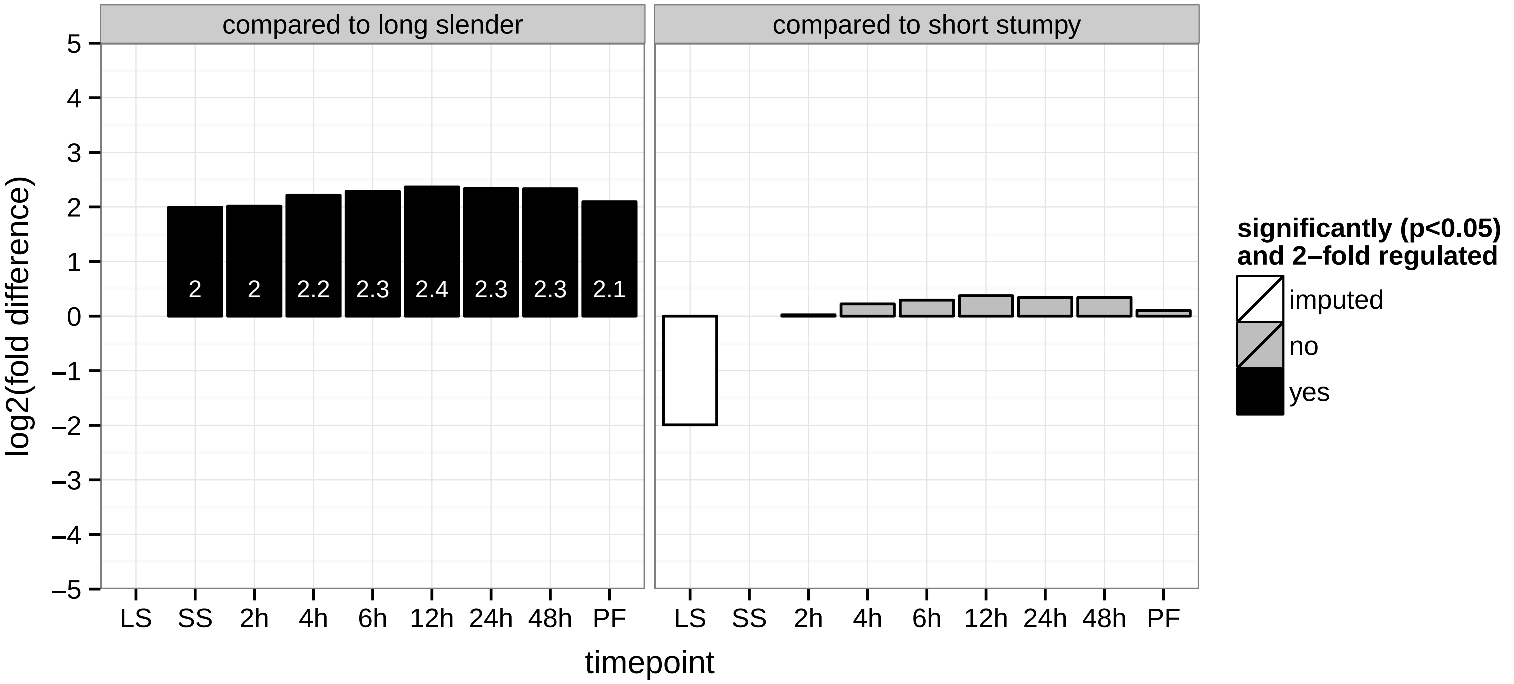
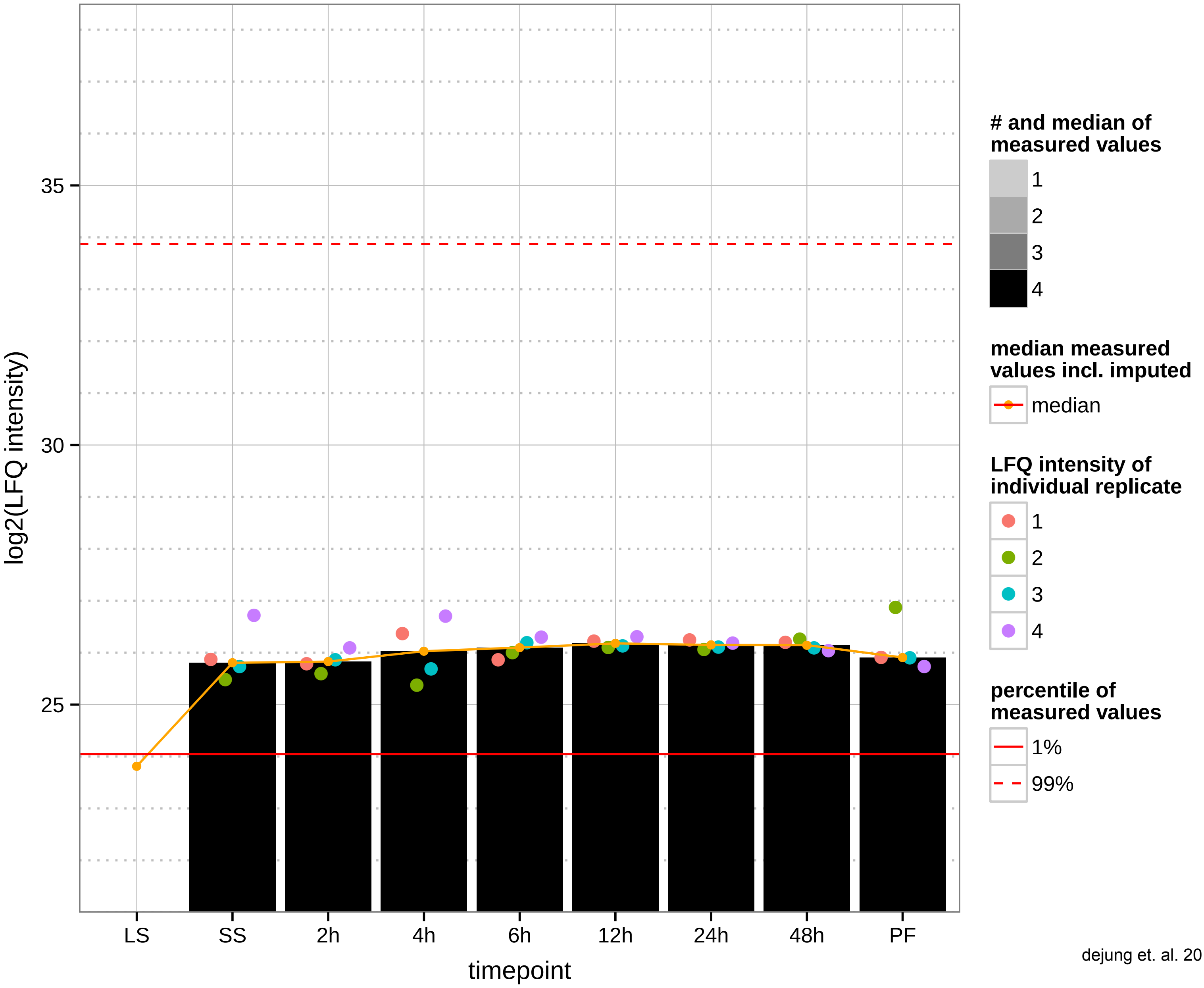
tRNA (guanine–N(7)–)–methyltransferase, putative, methyltransferase
Tb927.9.9120
AGOF: tRNA (guanine–N7–)–methyltransferase activity
AGOC: null
AGOP: tRNA modification
PGOF: tRNA (guanine–N7–)–methyltransferase activity
PGOC: null
PGOP: tRNA modification





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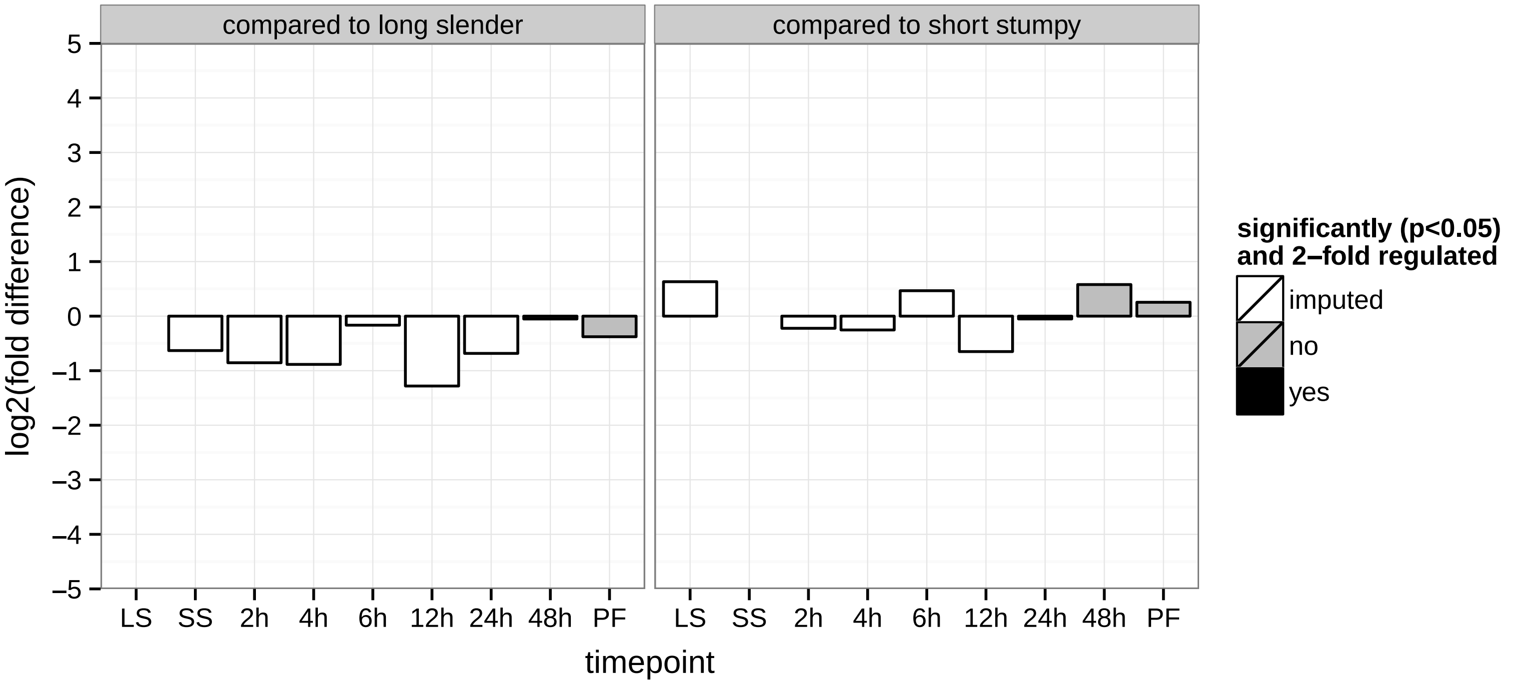
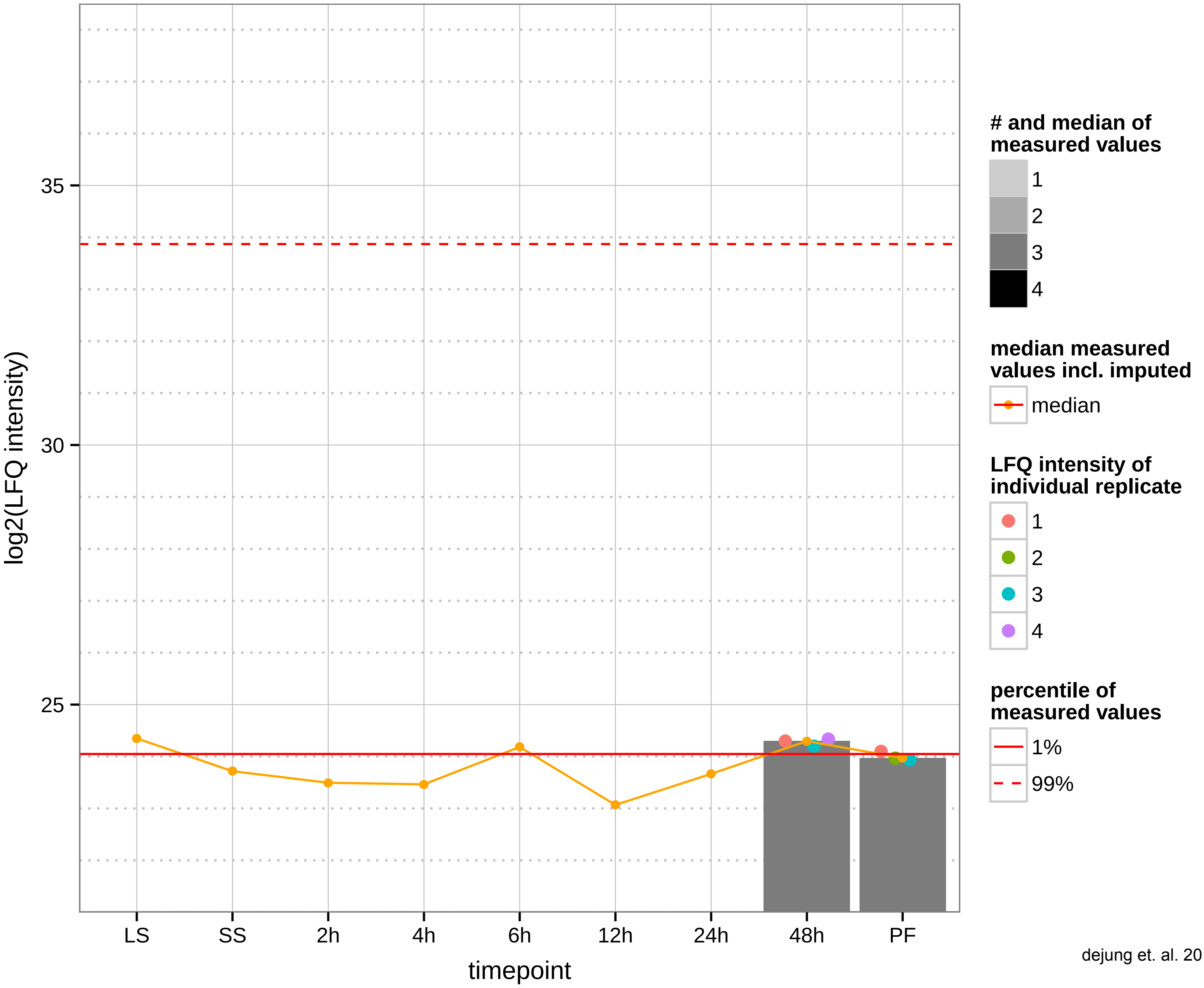
GTP–binding protein, putative
Tb927.9.9150
AGOF: GTP binding
AGOC: null
AGOP: null
PGOF: GTP binding
PGOC: null
PGOP: null





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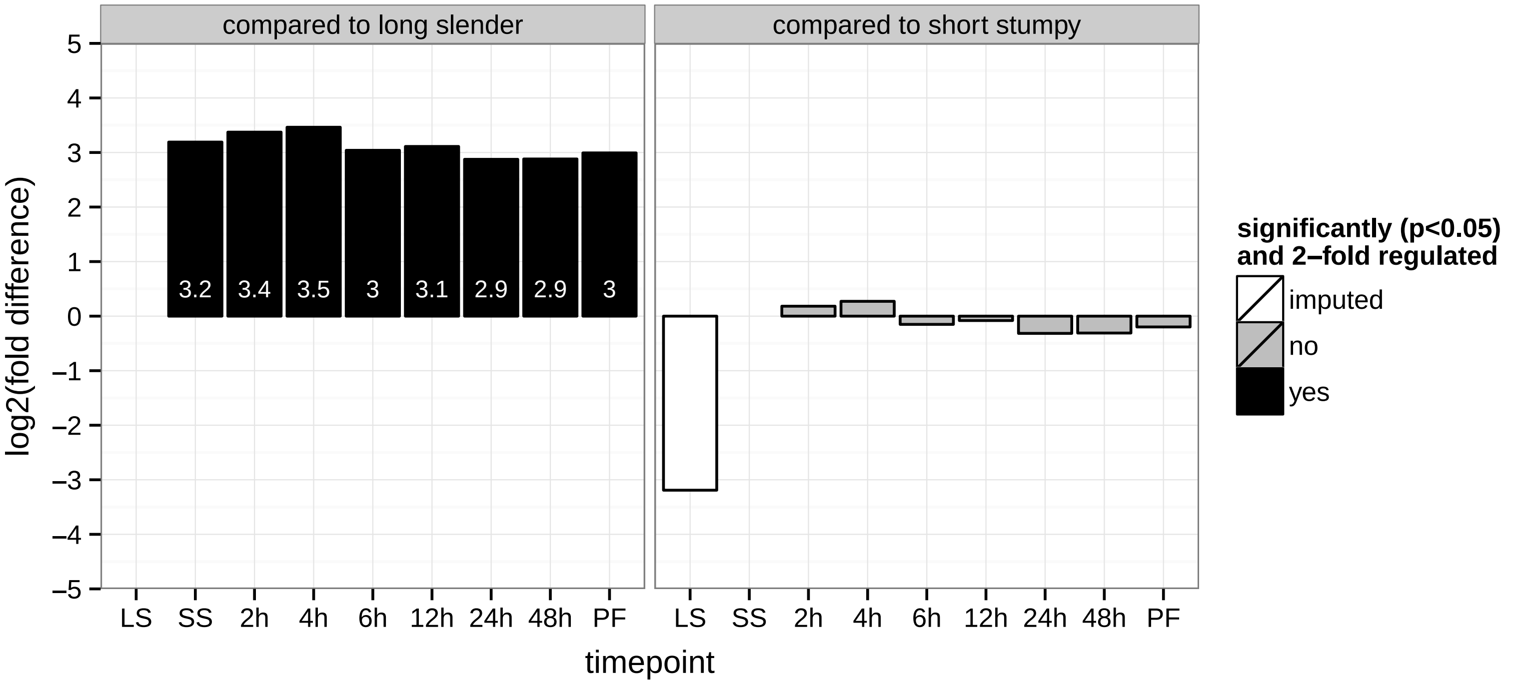
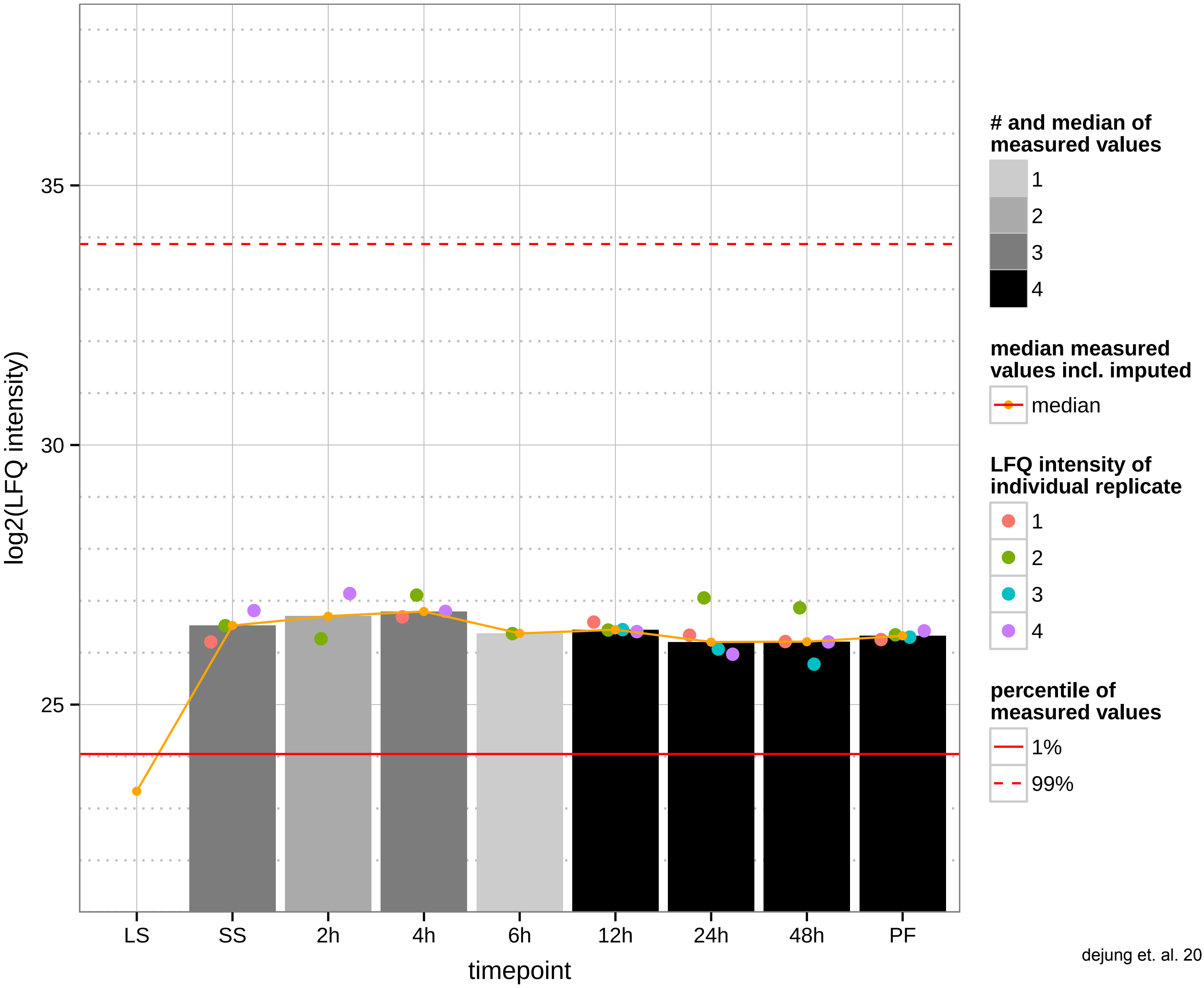
hypothetical protein, conserved
Tb927.9.9260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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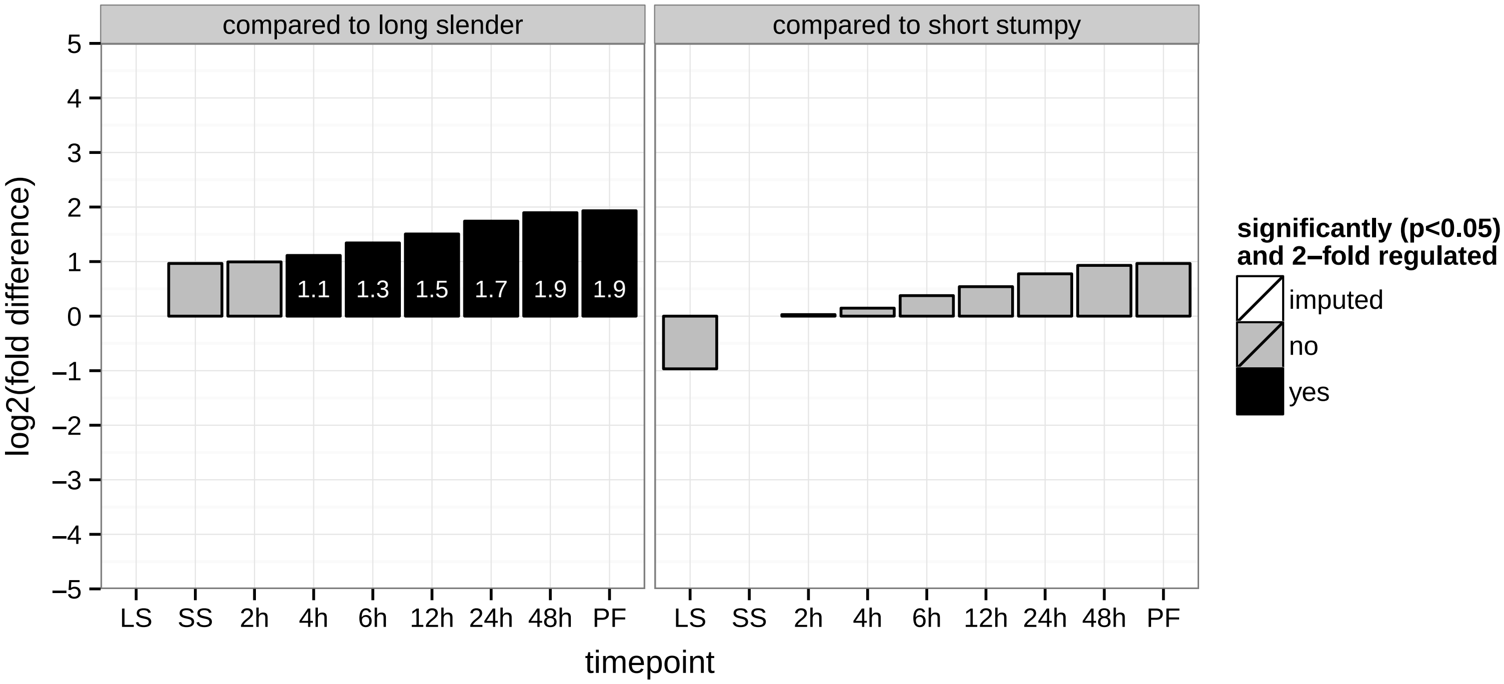
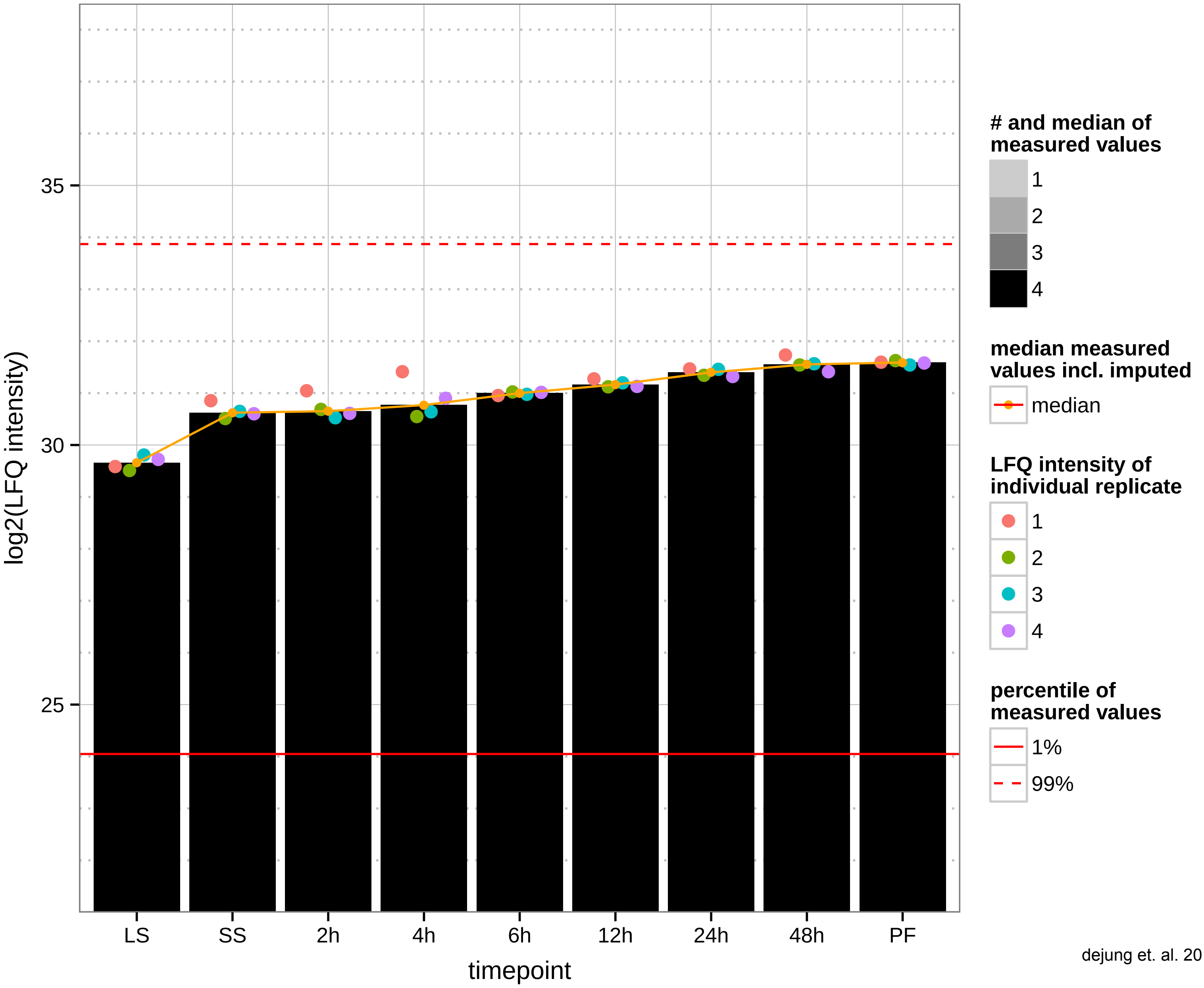
Polyadenylate–binding protein 1 (Poly(A)–binding protein 1) (PABP 1) (PABP1)
Tb927.9.9290
AGOF: RNA binding, poly(A) RNA binding
AGOC: cytoplasm, nucleus
AGOP: RNA processing, regulation of translational initiation
PGOF: RNA binding, nucleic acid binding
PGOC: null
PGOP: null





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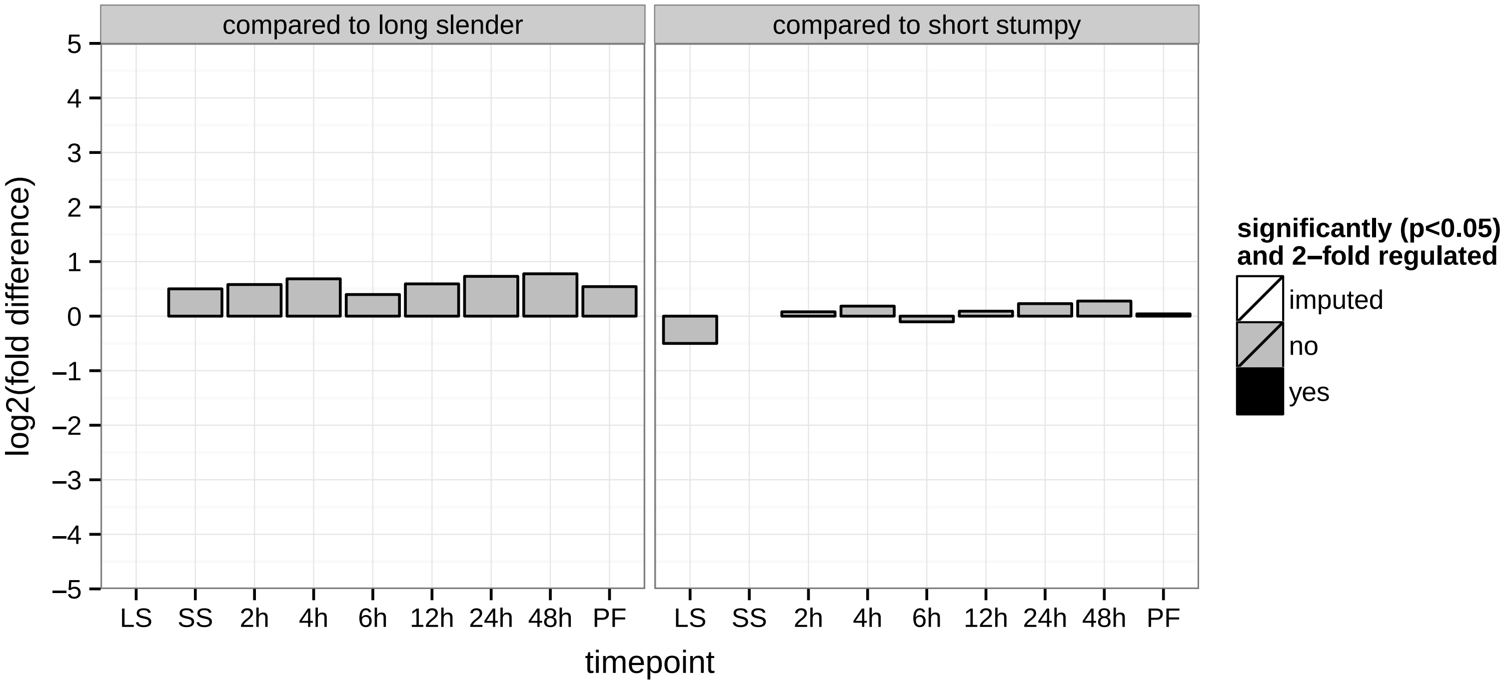
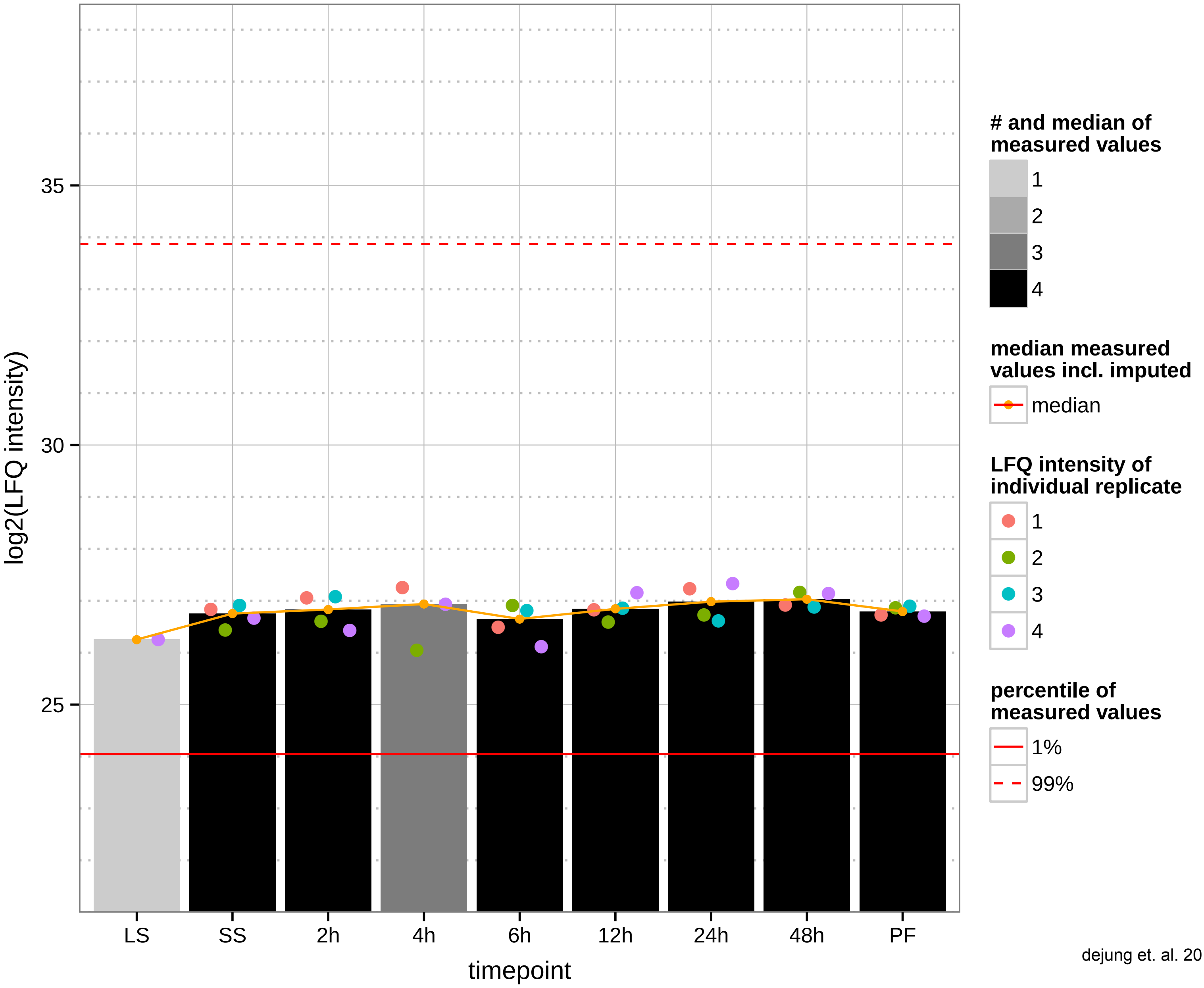
tubulin tyrosine ligase protein, putative
Tb927.9.9580
AGOF: null
AGOC: null
AGOP: cellular protein modification process
PGOF: tubulin−tyrosine ligase activity
PGOC: null
PGOP: cellular protein modification process





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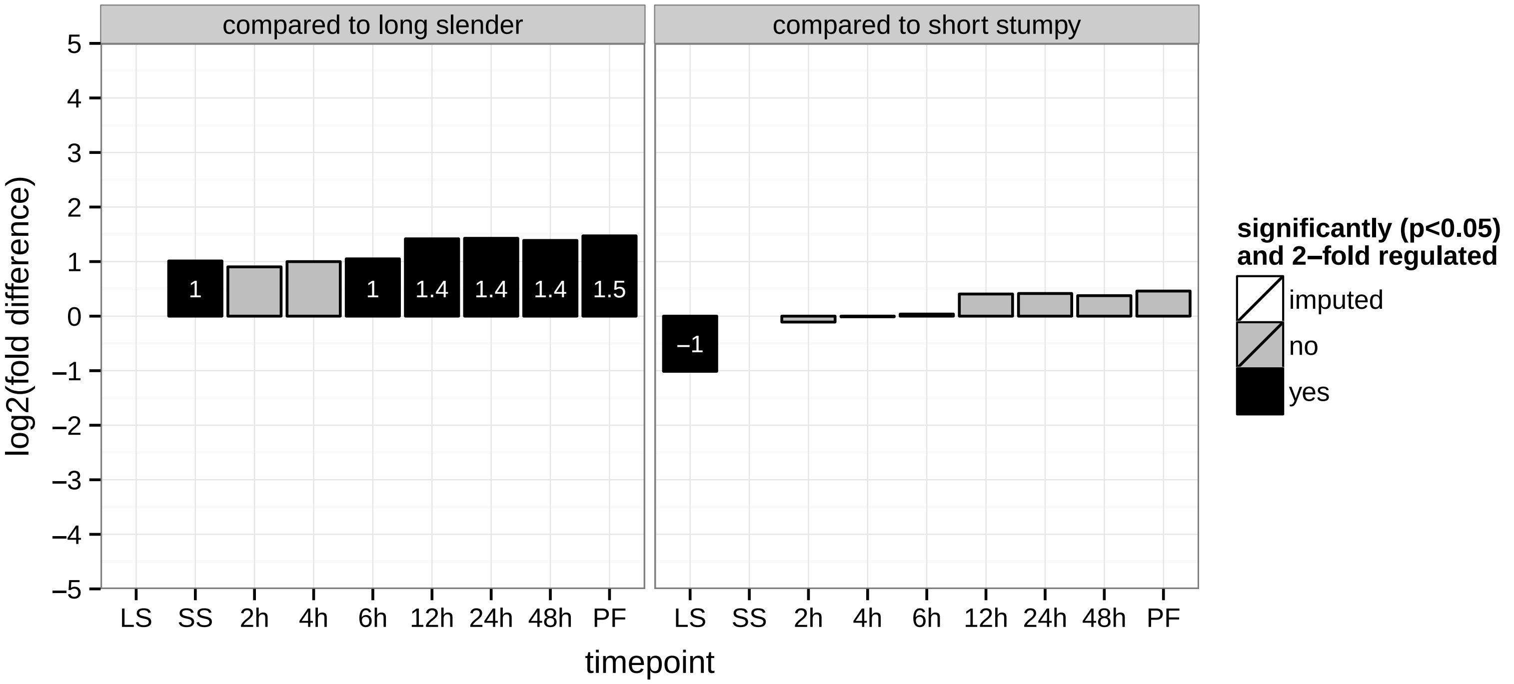
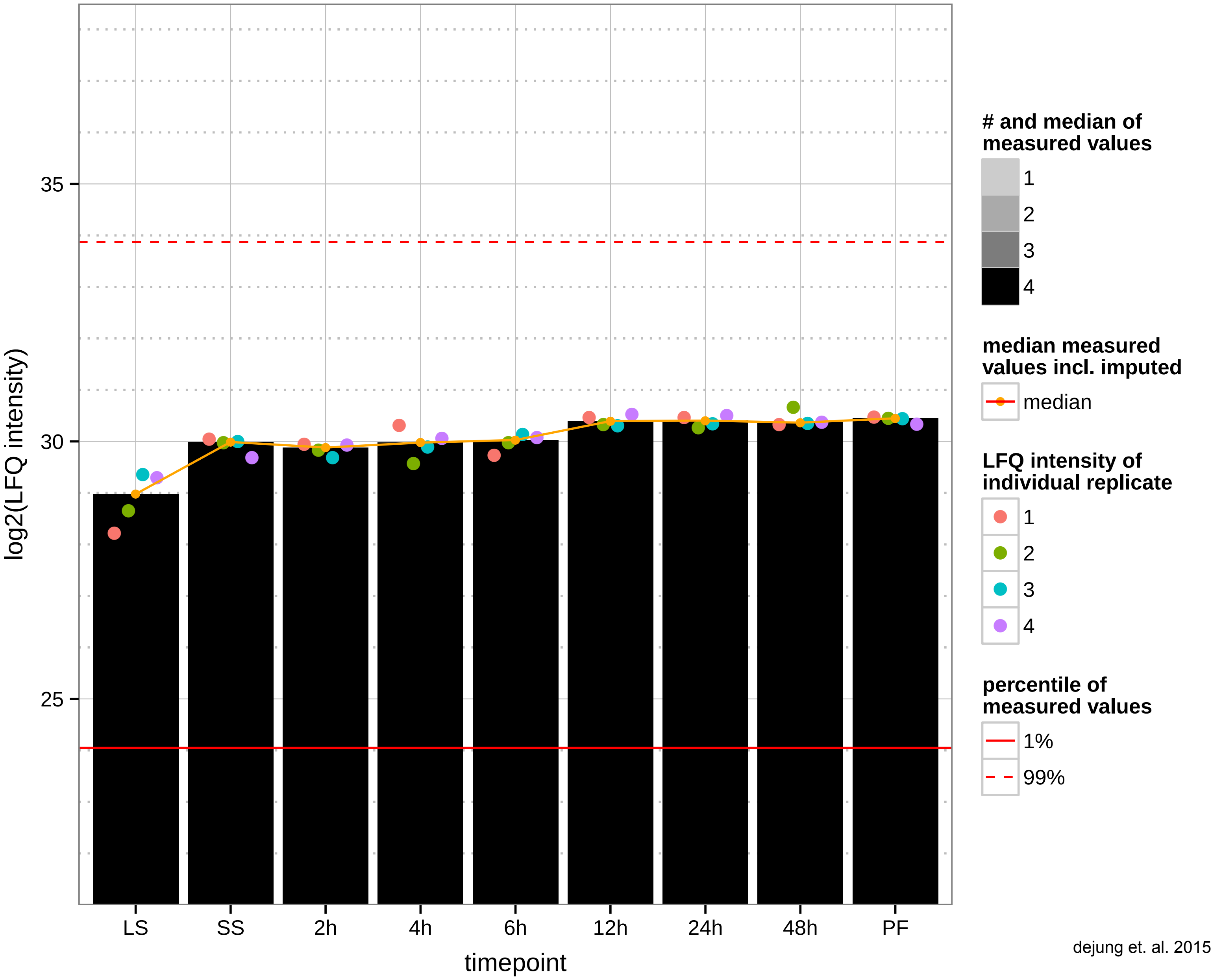
proteasome alpha 1 subunit, putative, 20S proteasome subunit alpha–6, (putative) (TbPSA6)
Tb927.9.9670
AGOF: endopeptidase activity, threonine–type endopeptidase activity
AGOC: proteasome core complex
AGOP: ubiquitin–dependent protein catabolic process
PGOF: endopeptidase activity, threonine–type endopeptidase activity
PGOC: proteasome core complex, proteasome core complex, alpha–subunit complex
PGOP: proteolysis involved in cellular protein catabolic process, ubiquitin–dependent protein catabolic process





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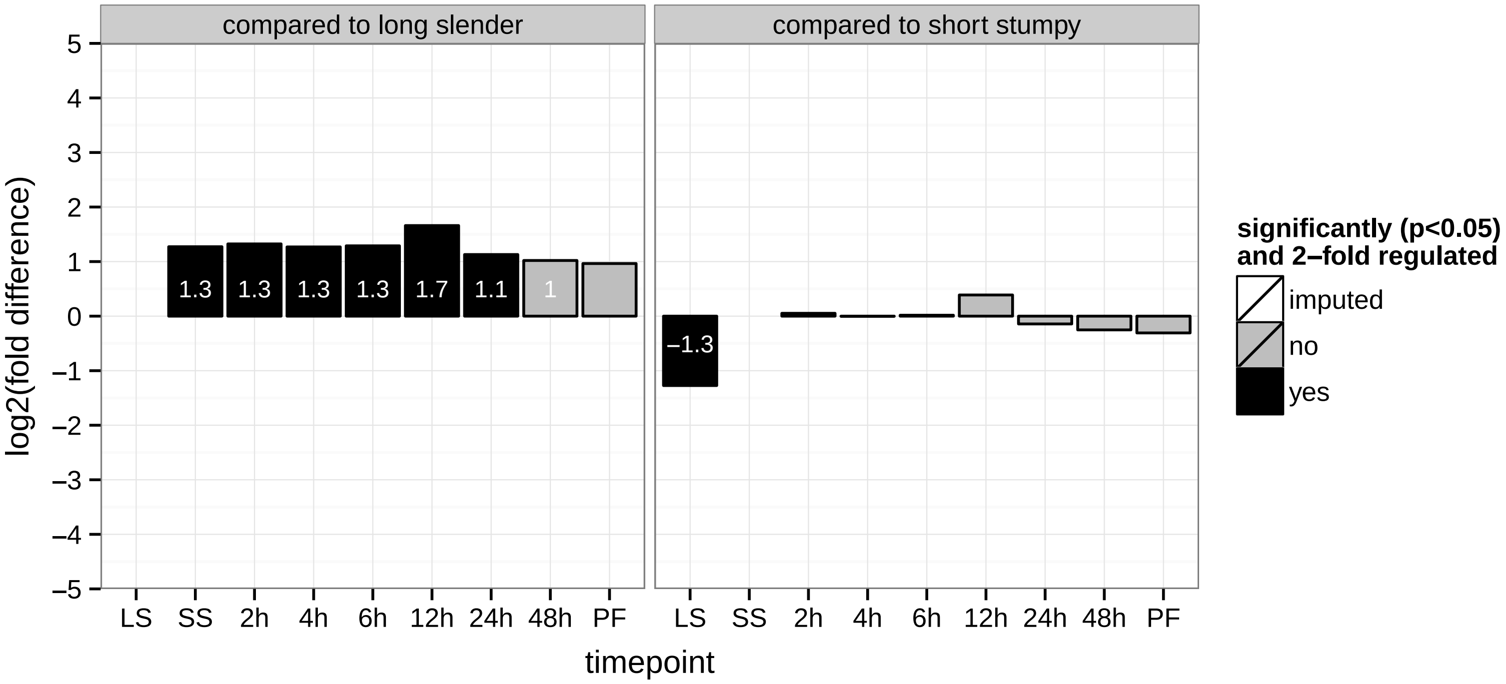
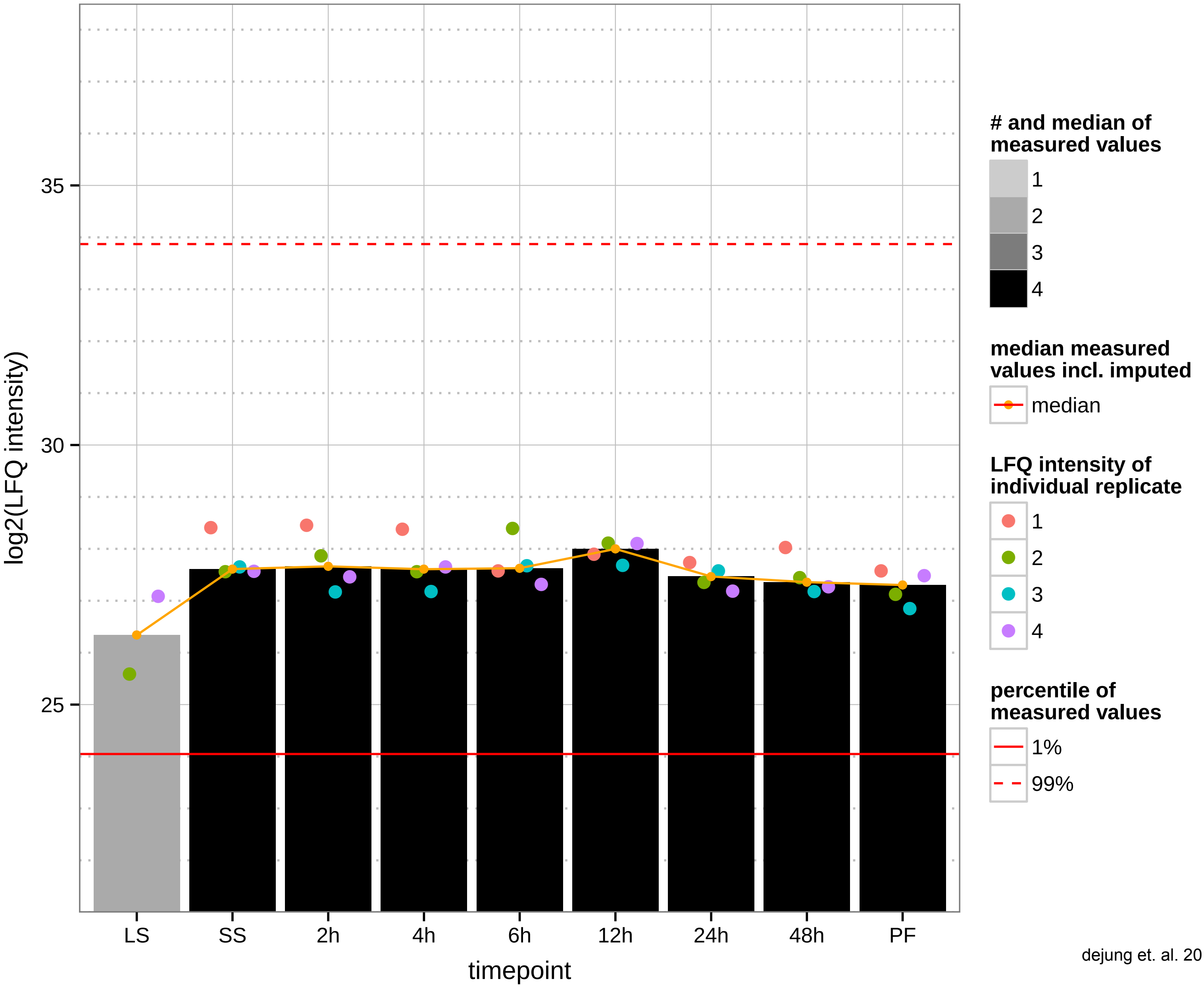
hypothetical protein, conserved
Tb927.9.9710
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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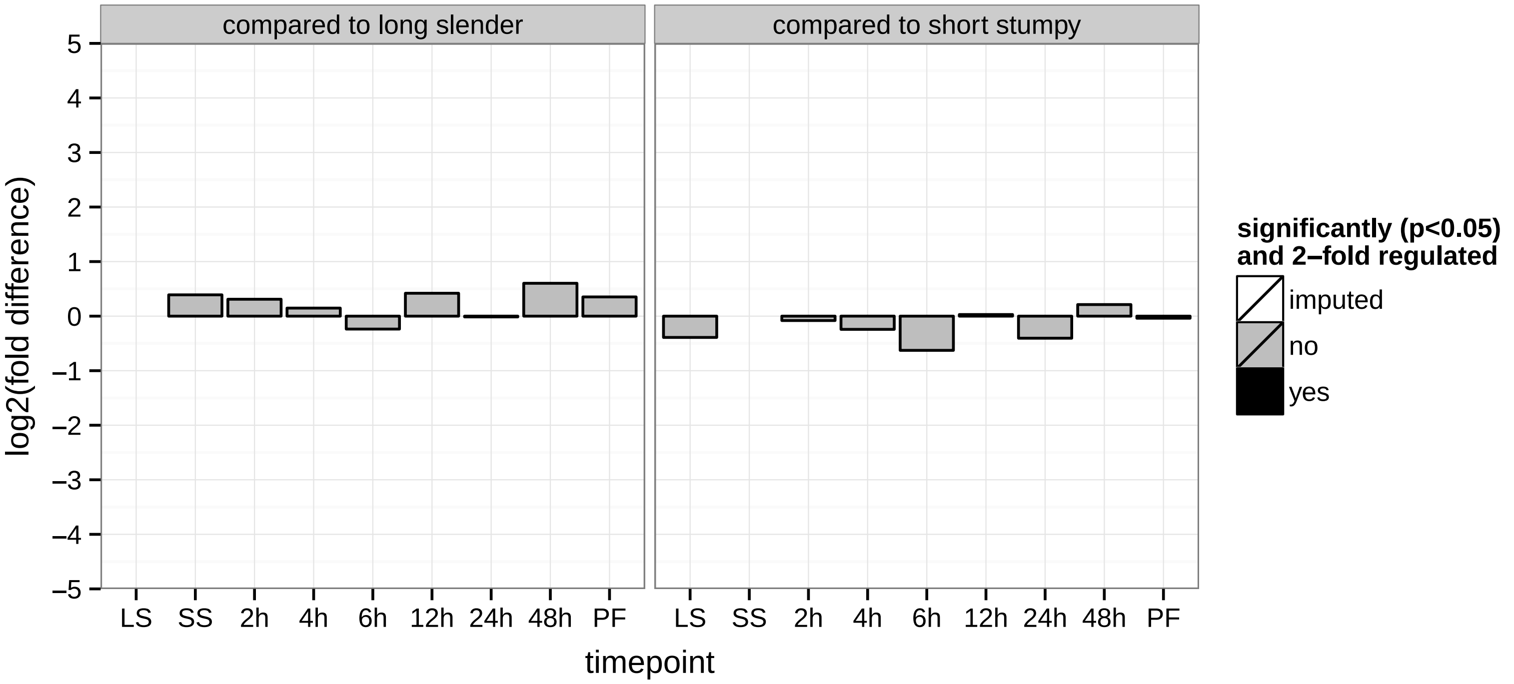
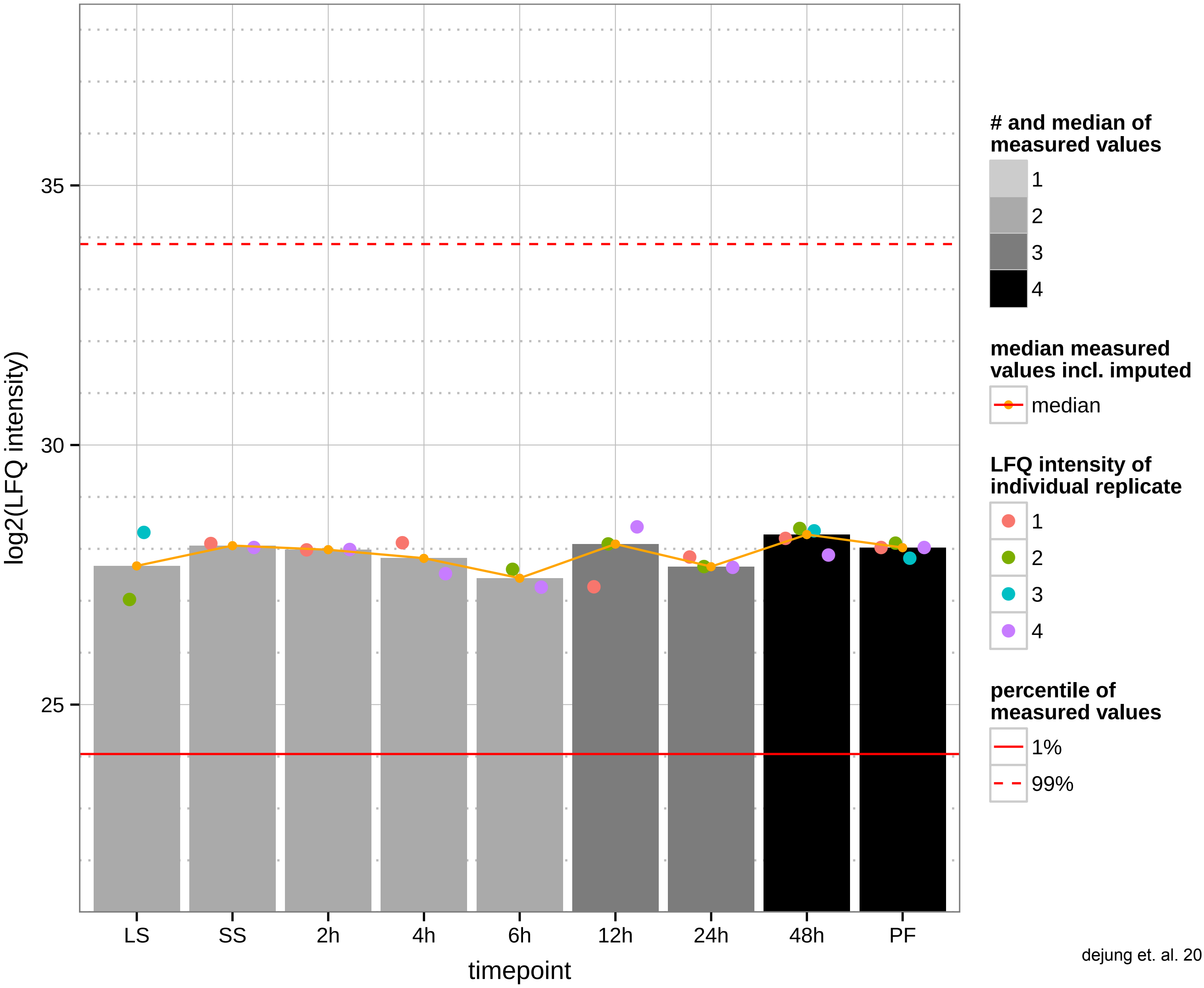
AMP deaminase, putative
Tb927.9.9740
AGOF: AMP deaminase activity
AGOC: mitochondrion
AGOP: purine ribonucleoside monophosphate biosynthetic process
PGOF: deaminase activity
PGOC: null
PGOP: purine ribonucleoside monophosphate biosynthetic process





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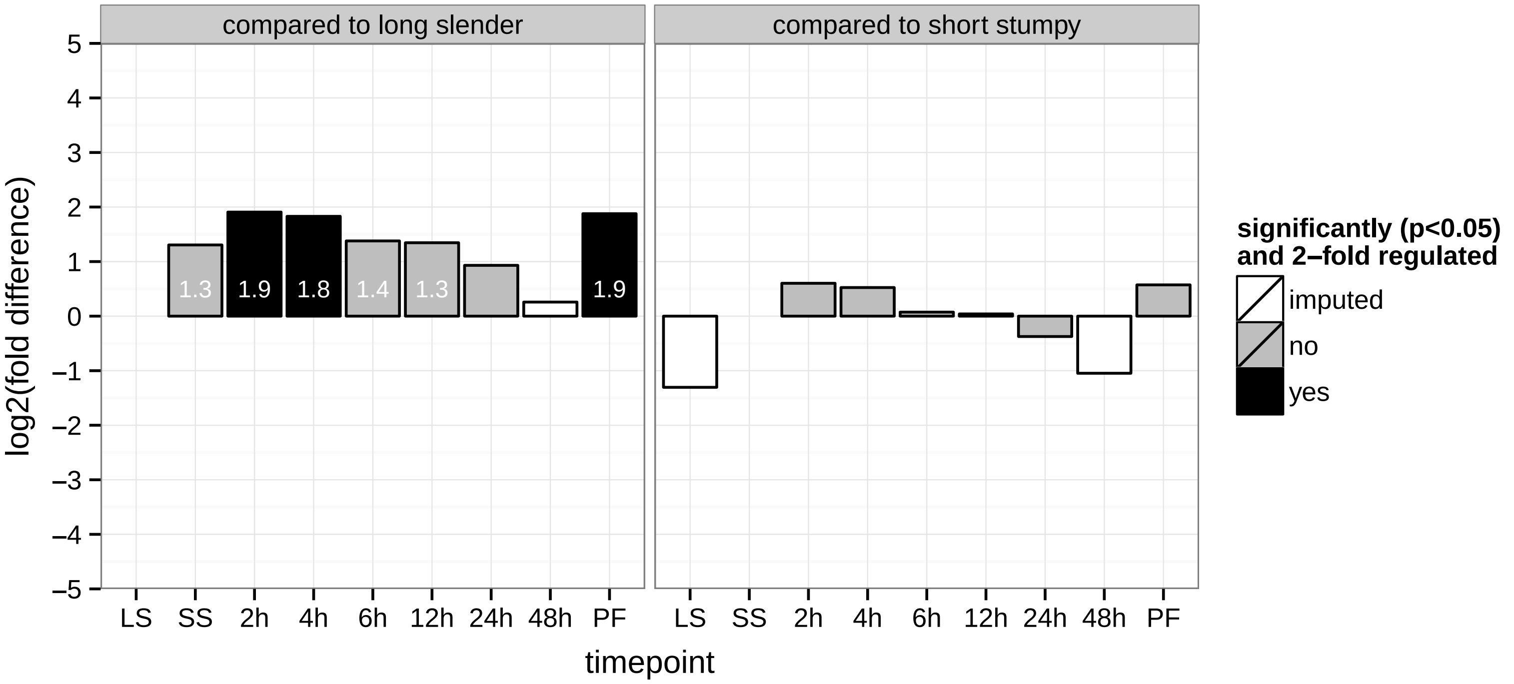
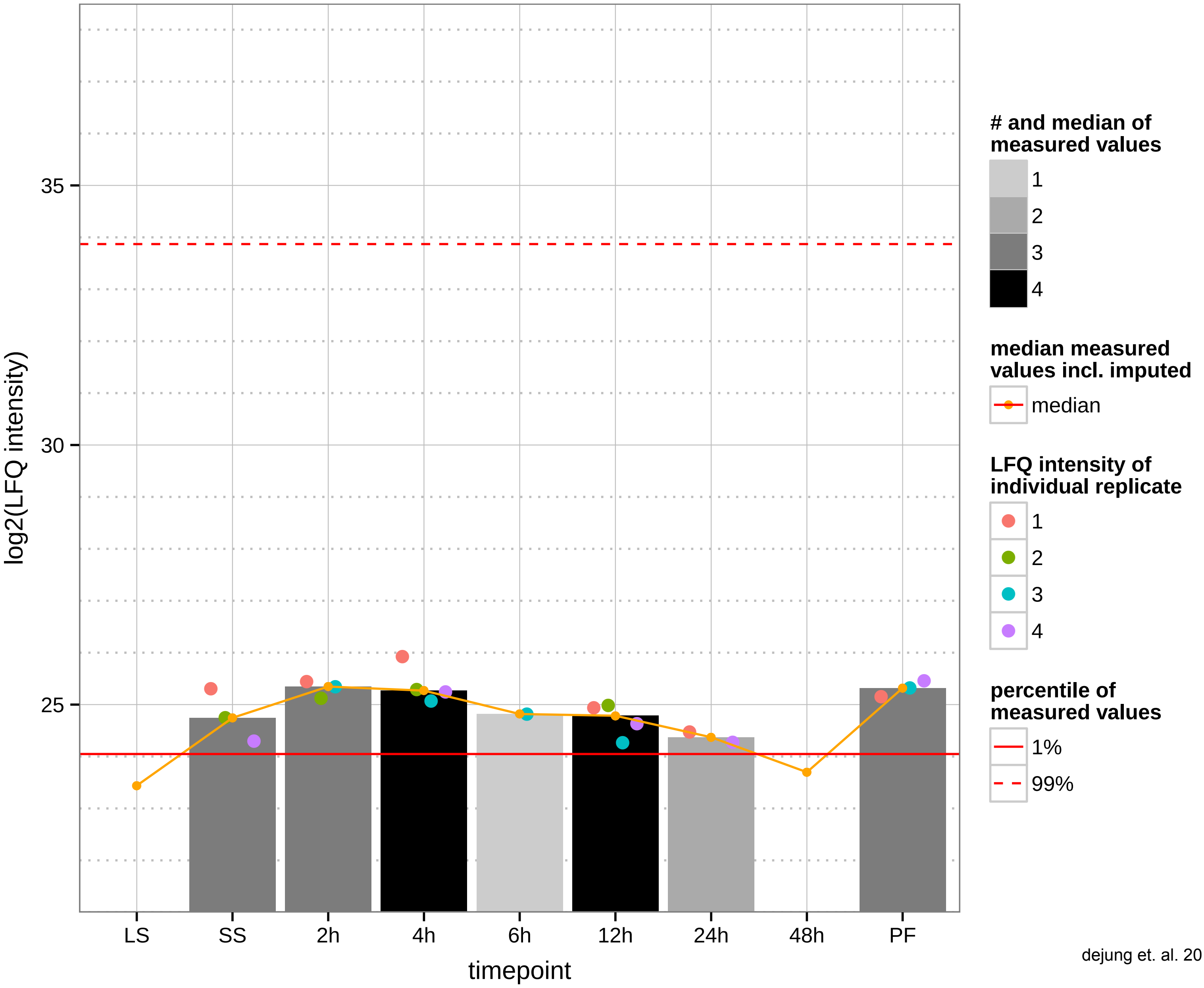
membrane– trafficking protein, putative
Tb927.9.9750
AGOF: null
AGOC: integral to membrane
AGOP: protein transport
PGOF: null
PGOC: integral to membrane
PGOP: protein transport





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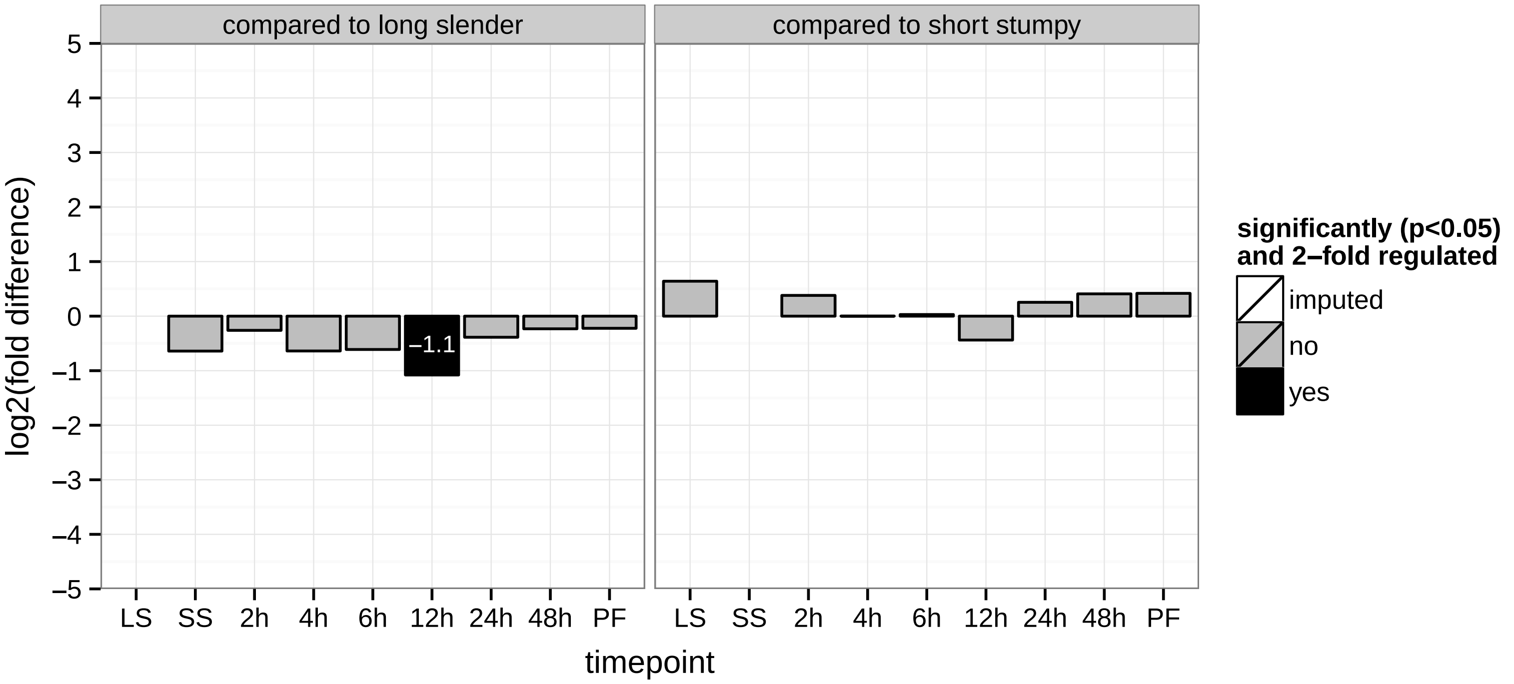
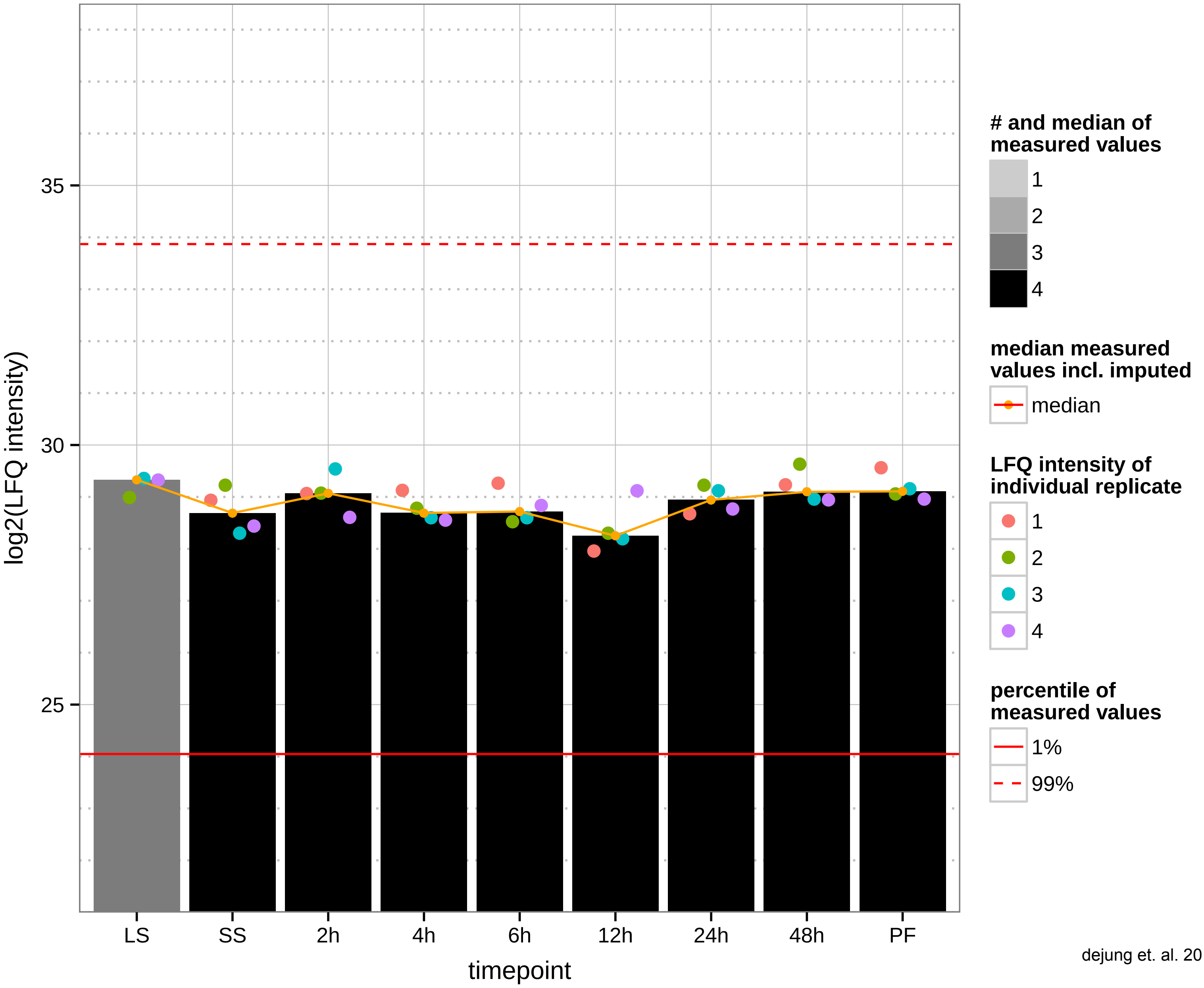
hypothetical protein, conserved
Tb927.9.9810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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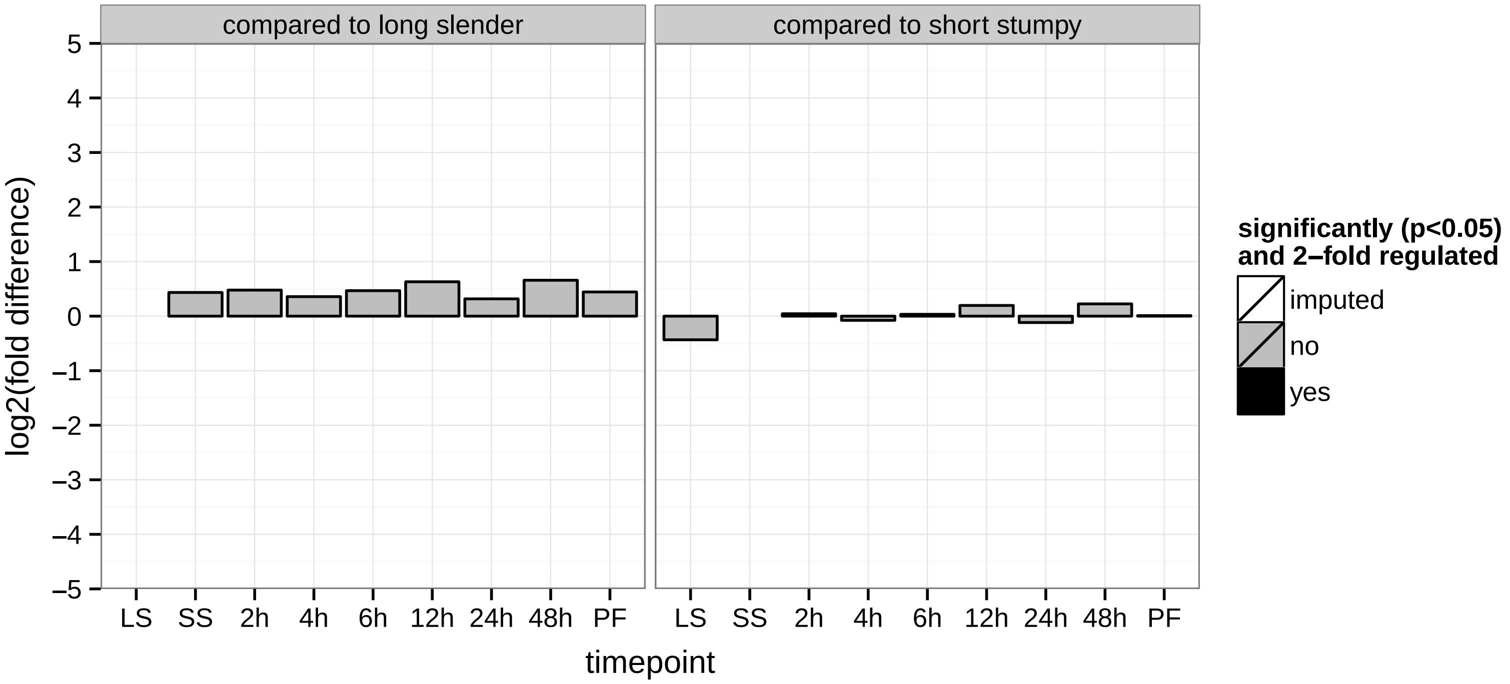
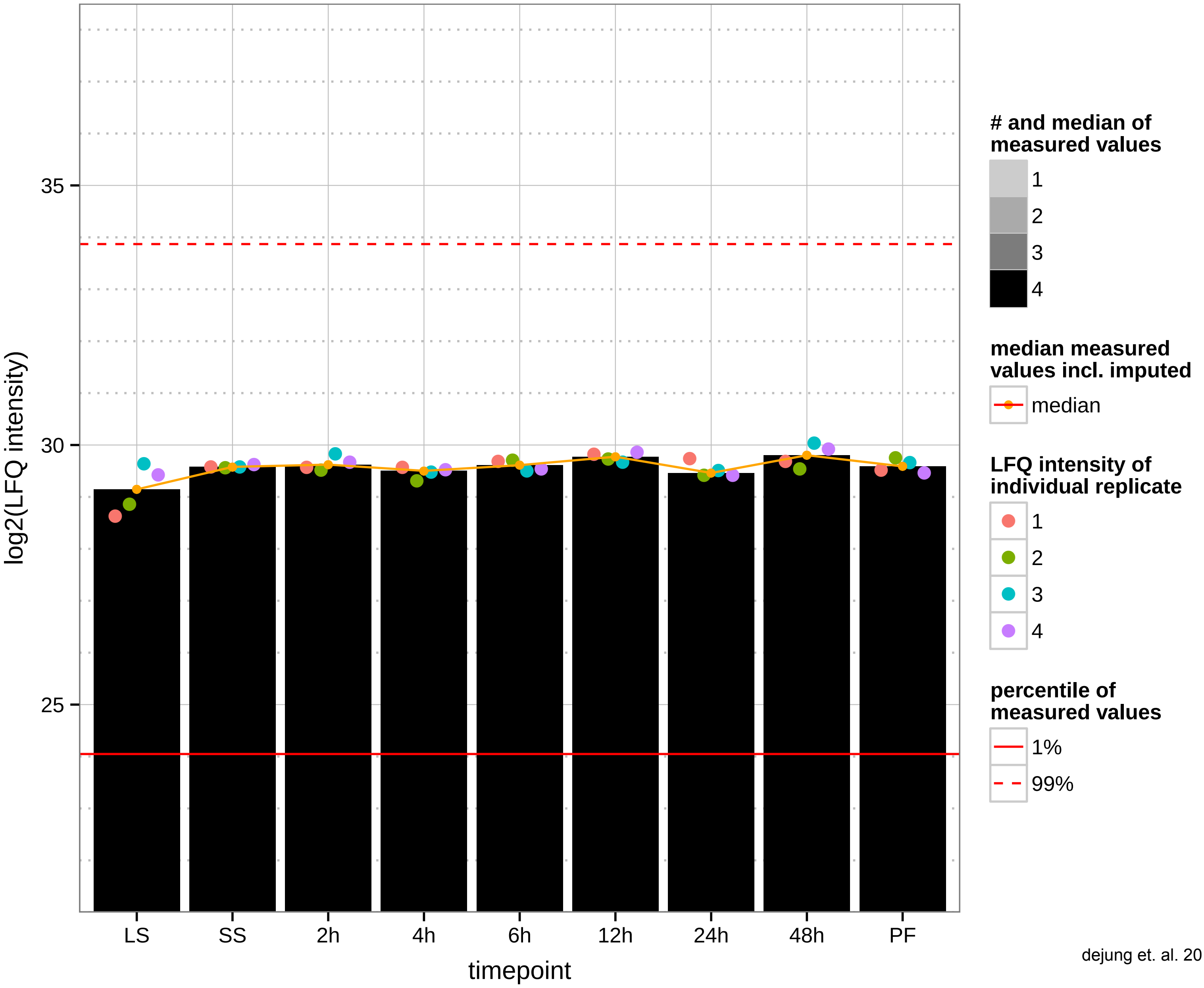
glyceraldehyde−3−phosphate dehydrogenase, putative
Tb927.9.9820
AGOF: NAD binding, glyceraldehyde−3−phosphate dehydrogenase (NAD+) (phosphorylating) activity
AGOC: null
AGOP: glycolysis
PGOF: oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
PGOC: null
PGOP: oxidation−reduction process





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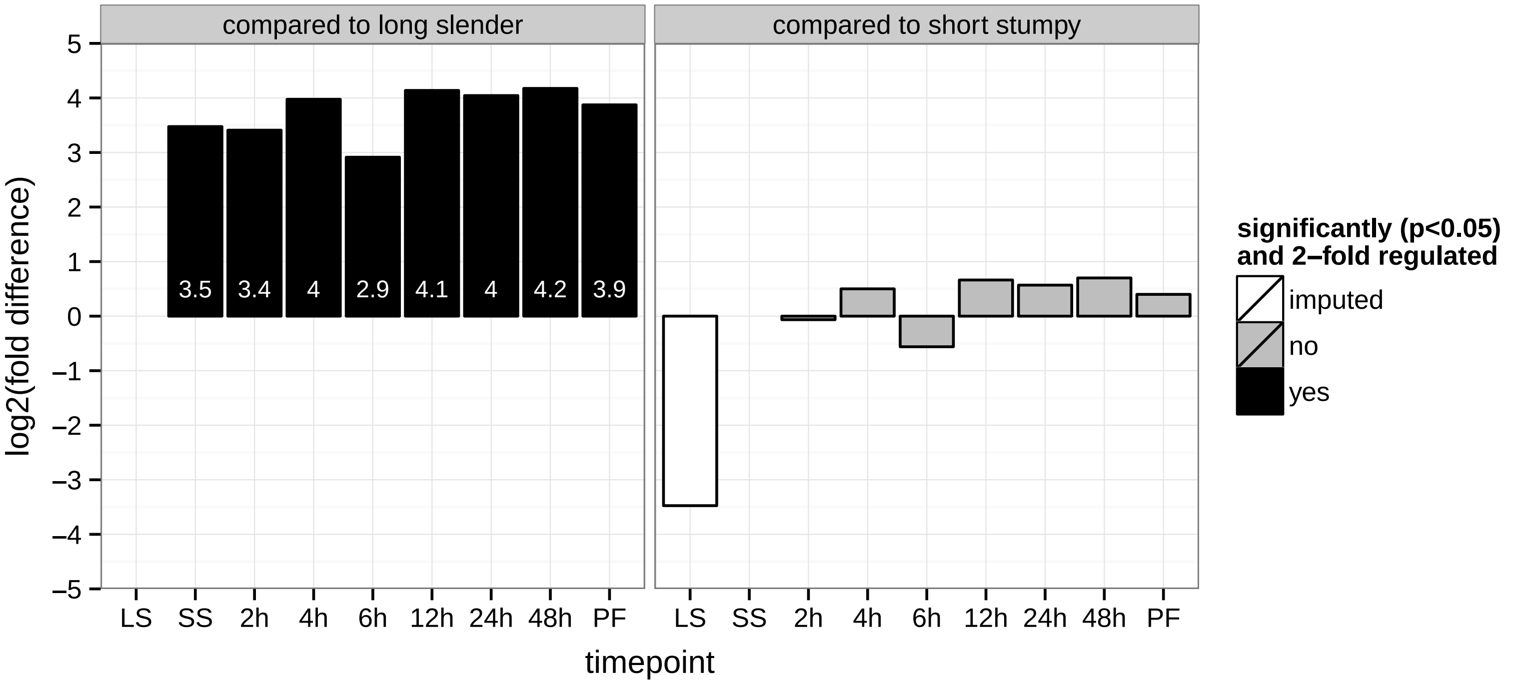
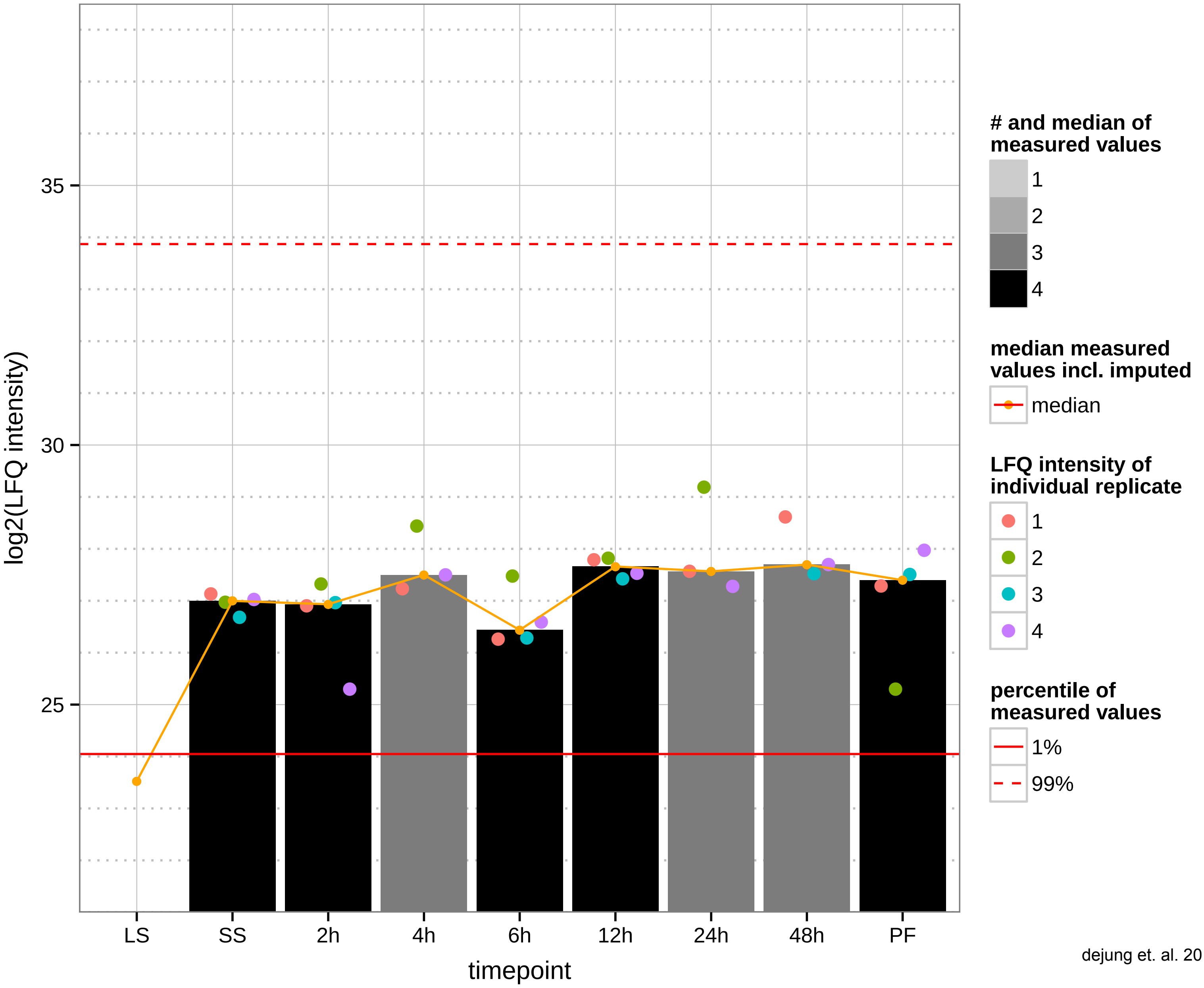
lipoic acid containing carrier protein, putative (GCVH)
Tb927.9.9840
AGOF: null
AGOC: glycine cleavage complex, mitochondrion
AGOP: glycine catabolic process
PGOF: null
PGOC: glycine cleavage complex
PGOP: glycine catabolic process, glycine decarboxylation via glycine cleavage system





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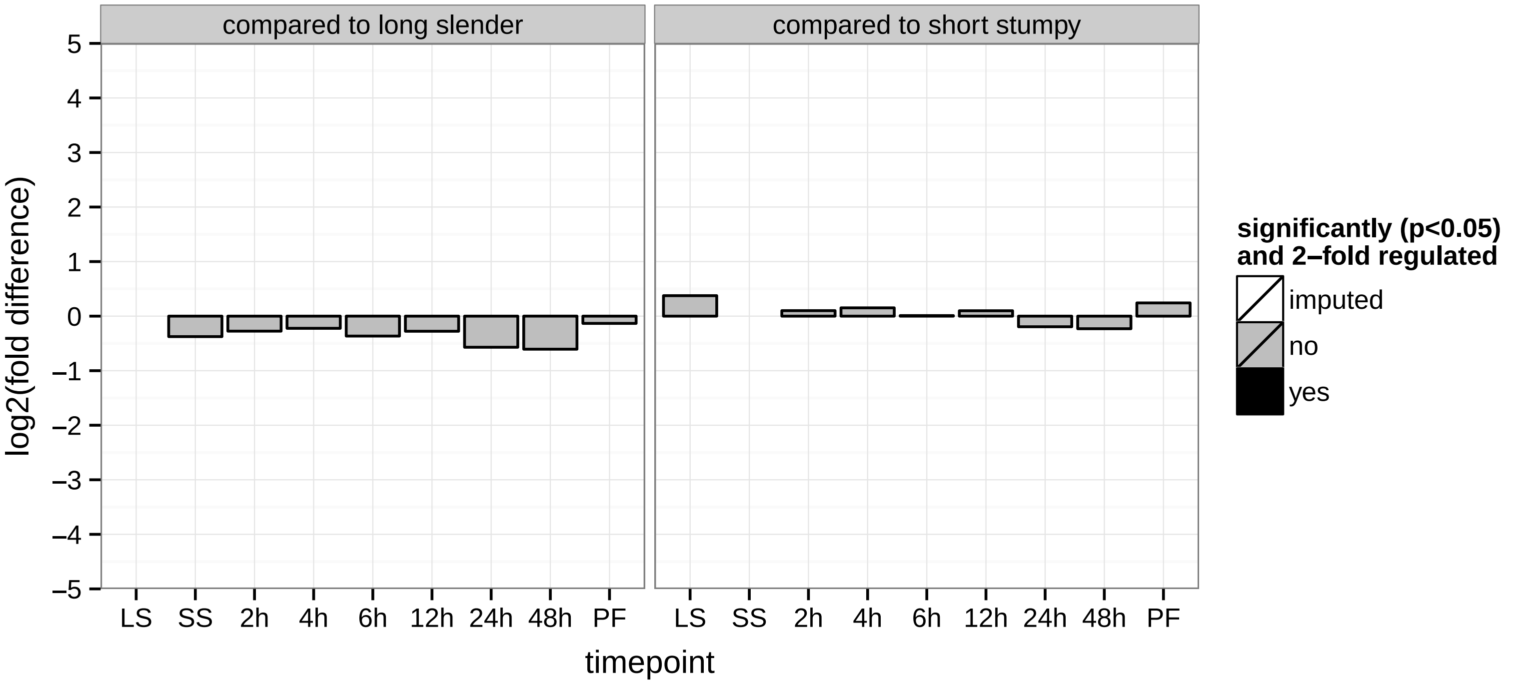
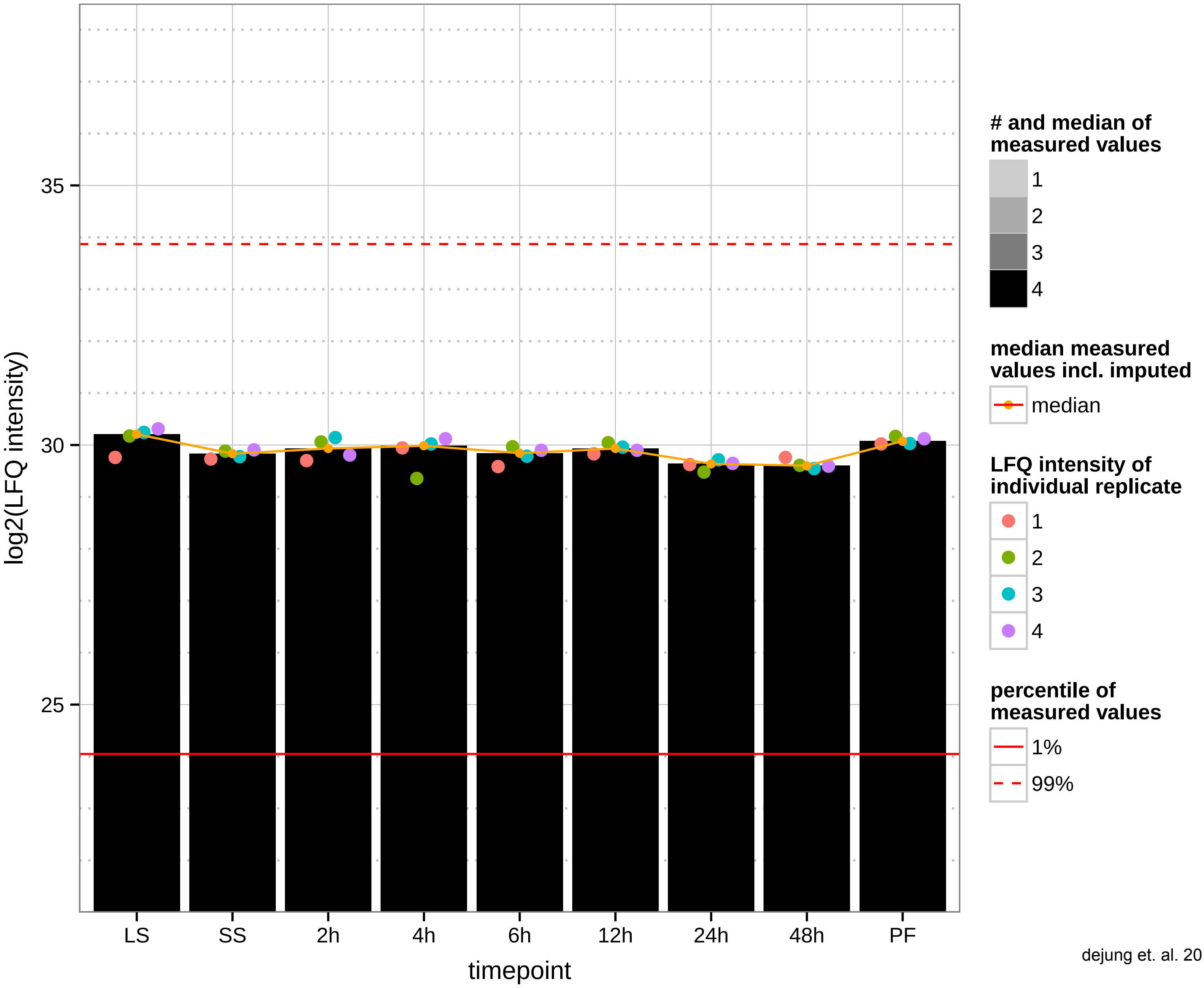
hypothetical protein, conserved
Tb927.9.9860
AGOF: ATP binding
AGOC: null
AGOP: protein folding
PGOF: null
PGOC: null
PGOP: null





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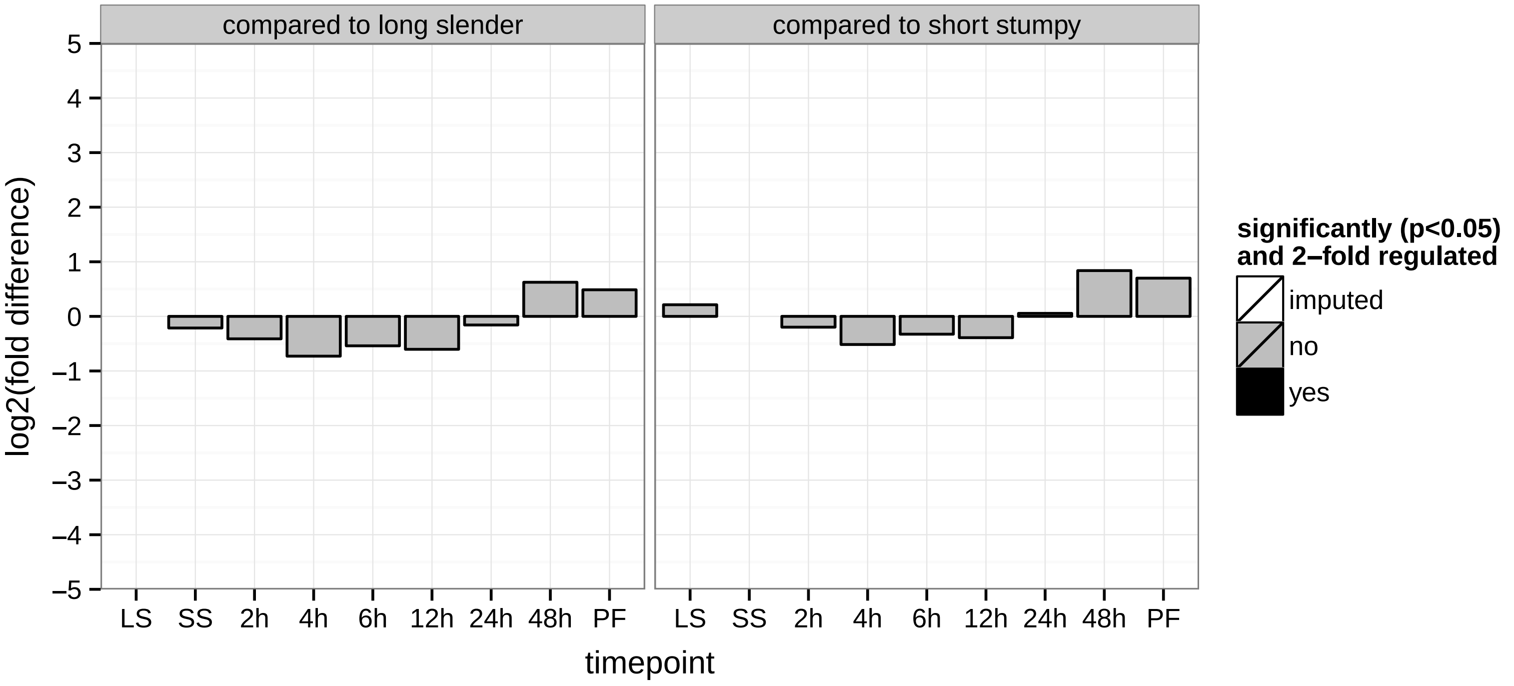
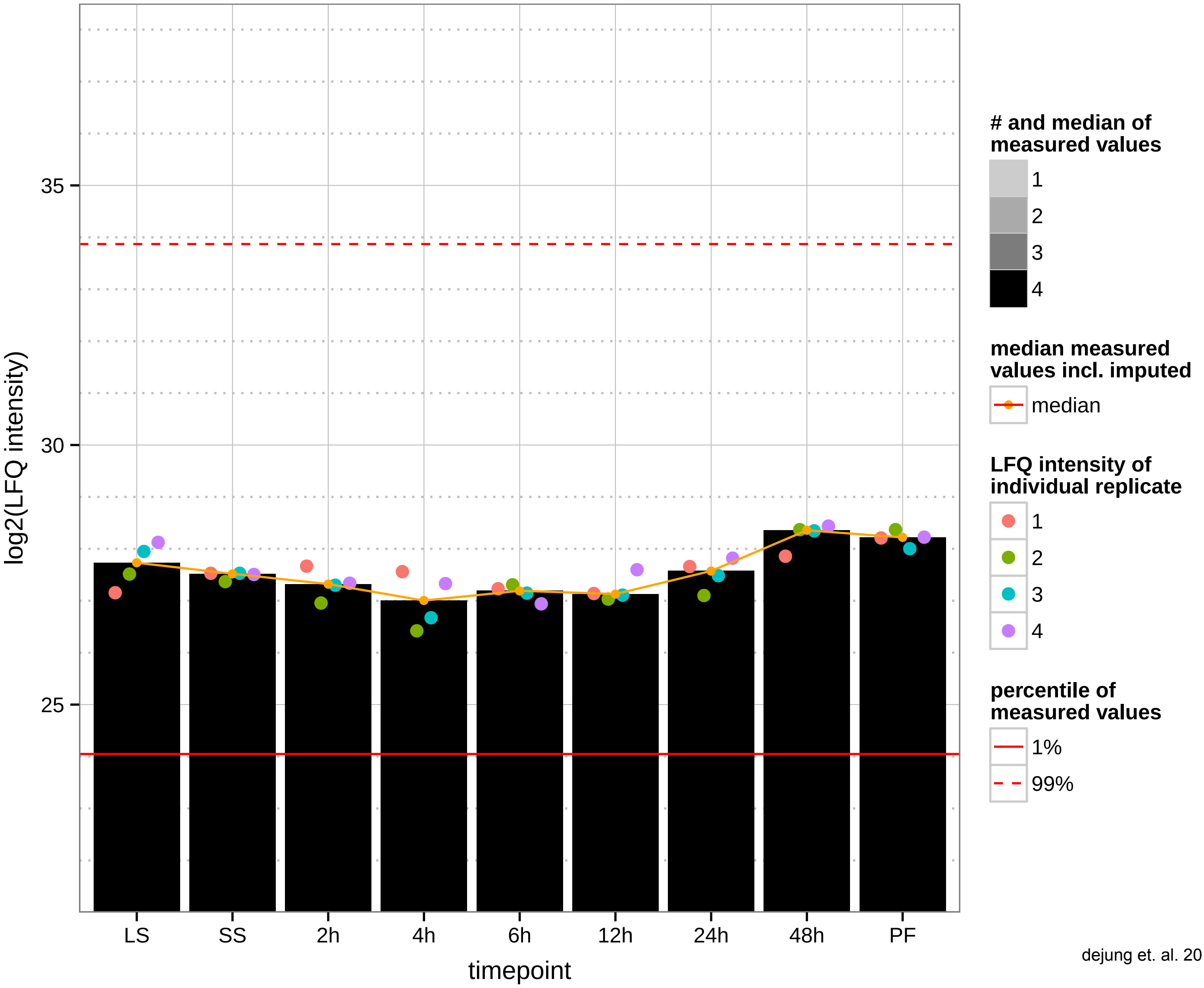
MCAK–like kinesin, putative
Tb927.9.9870
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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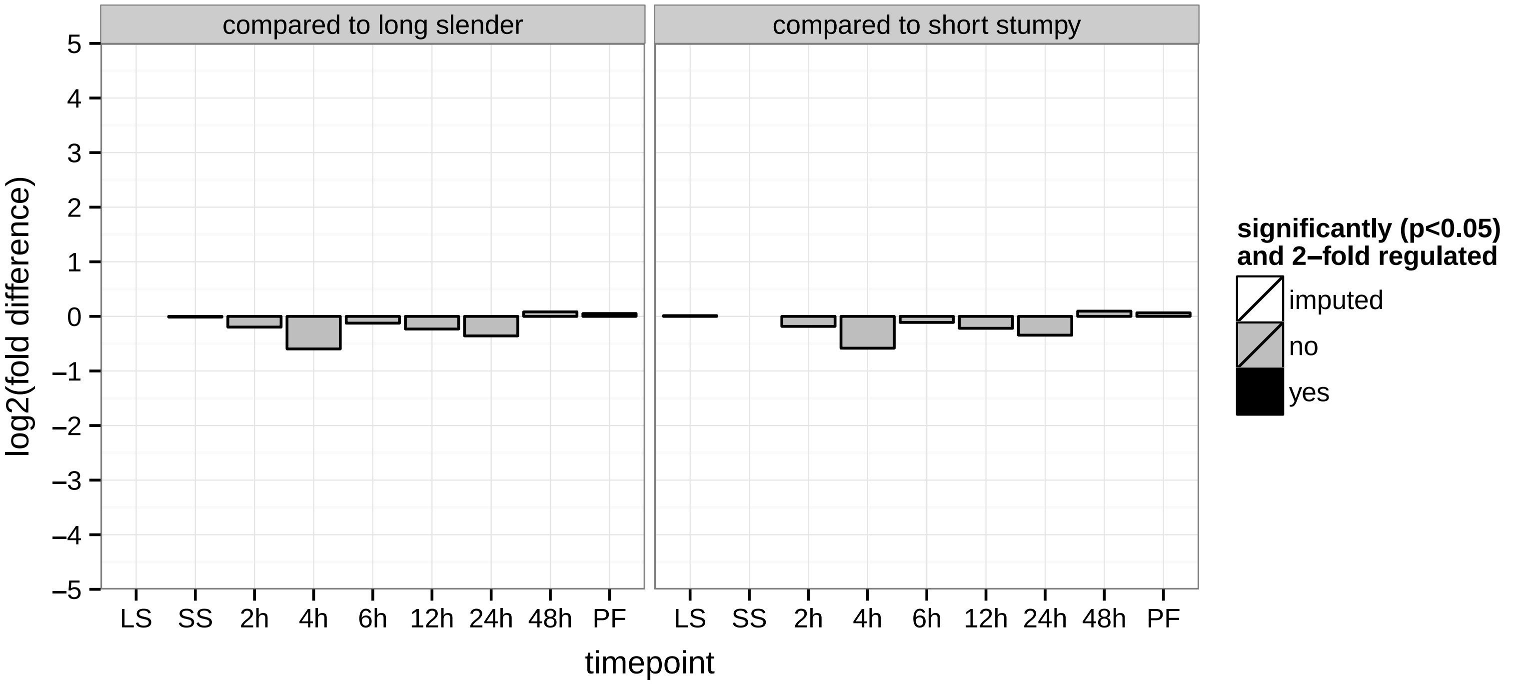
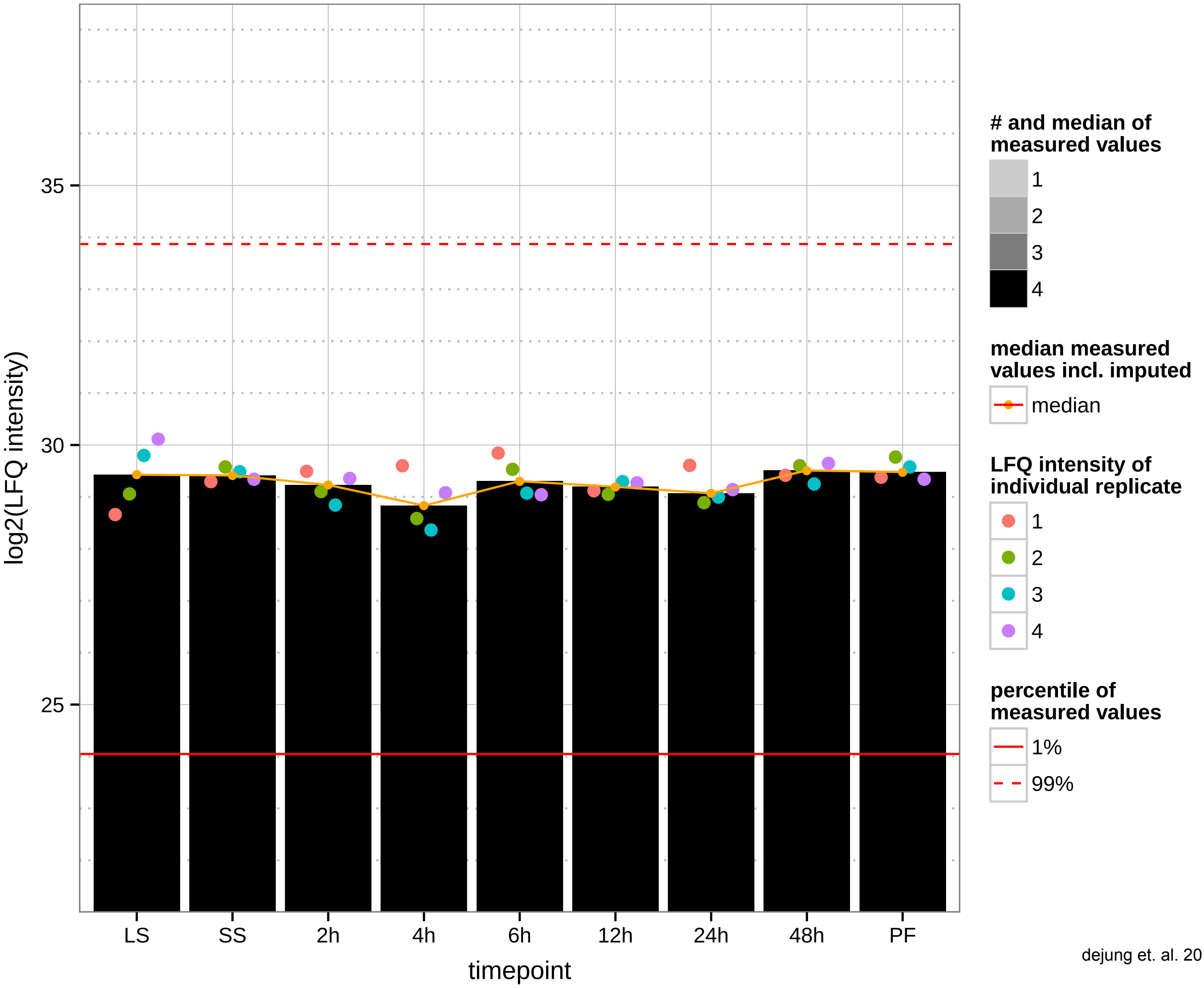
PACRGB
Tb927.9.9940
AGOF: null
AGOC: cilium part
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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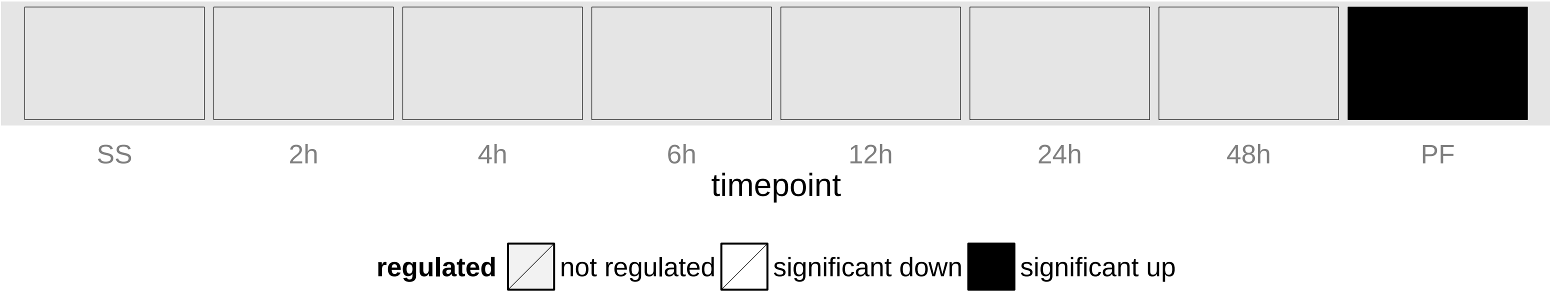

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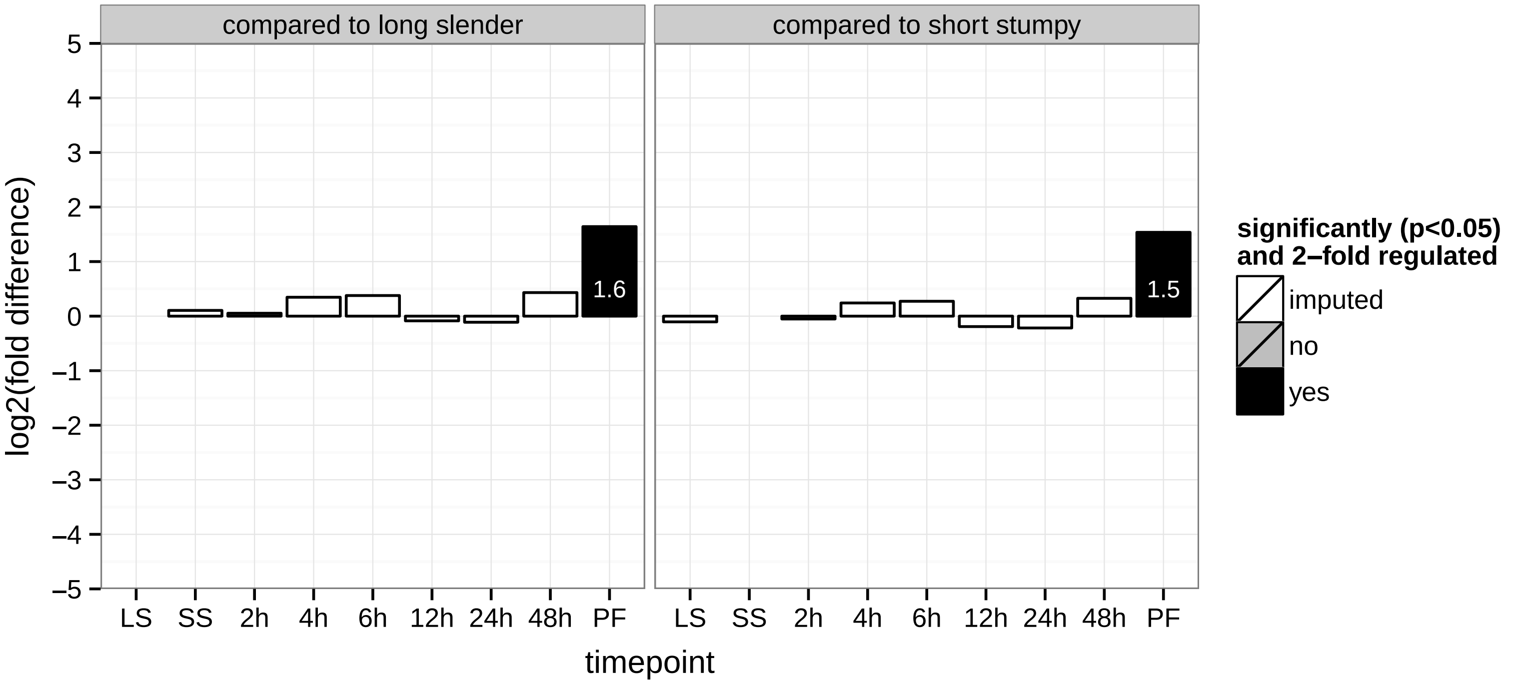
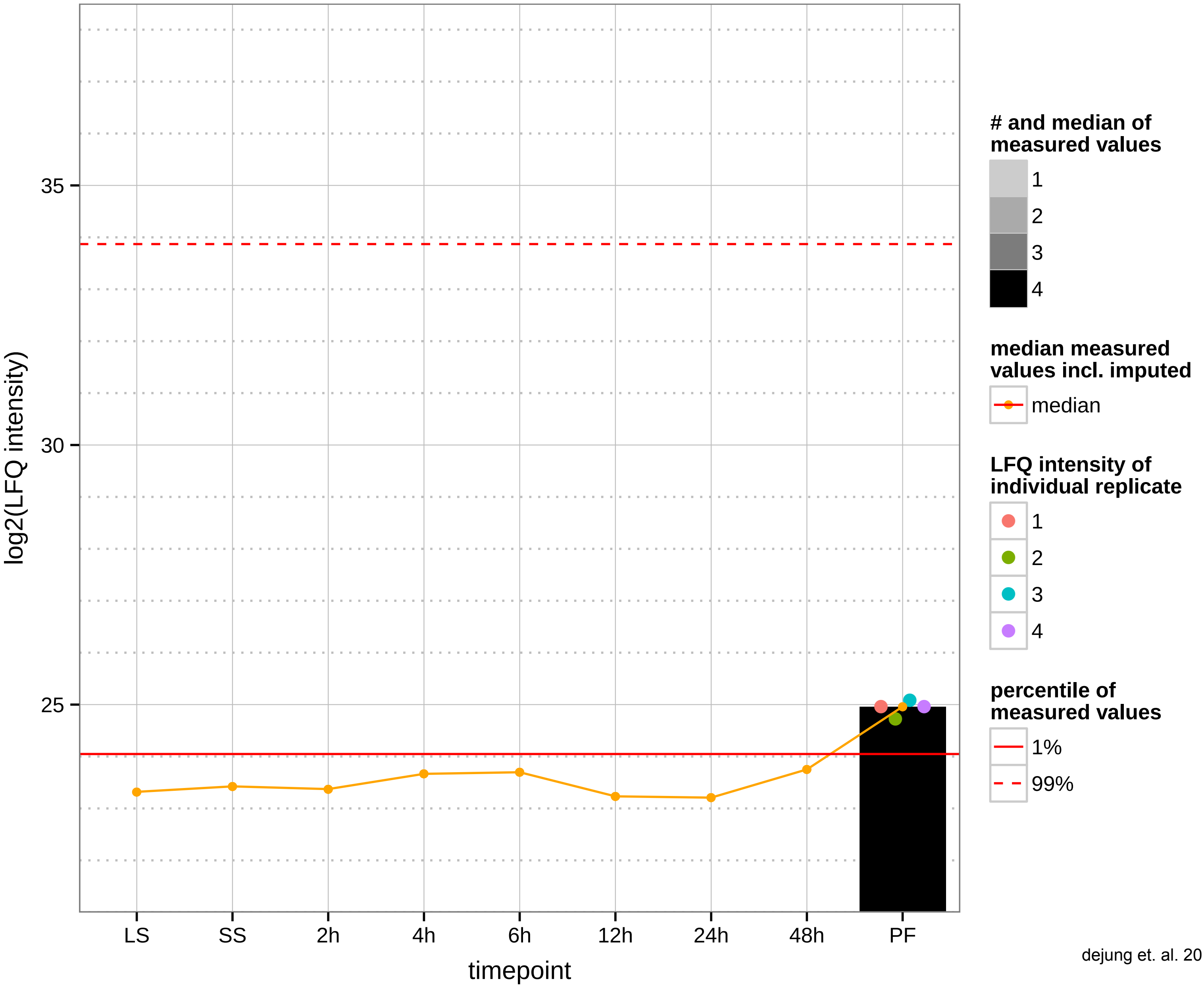
hypothetical protein, conserved, BAC from homologous region on chr5
Tb927.5.4470;Tb05.5K5.120
AGOF: phosphorus–oxygen lyase activity
AGOC: null
AGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction
PGOF: phosphorus–oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction





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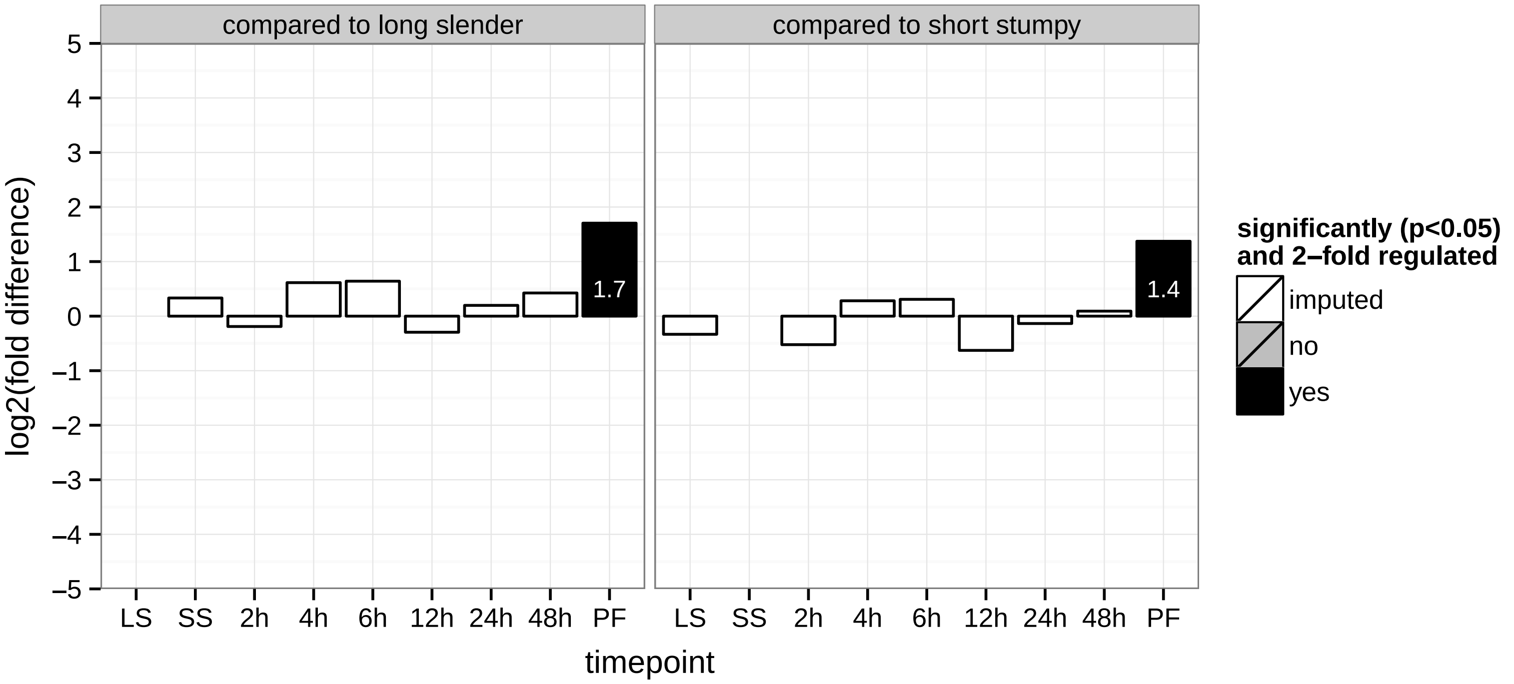
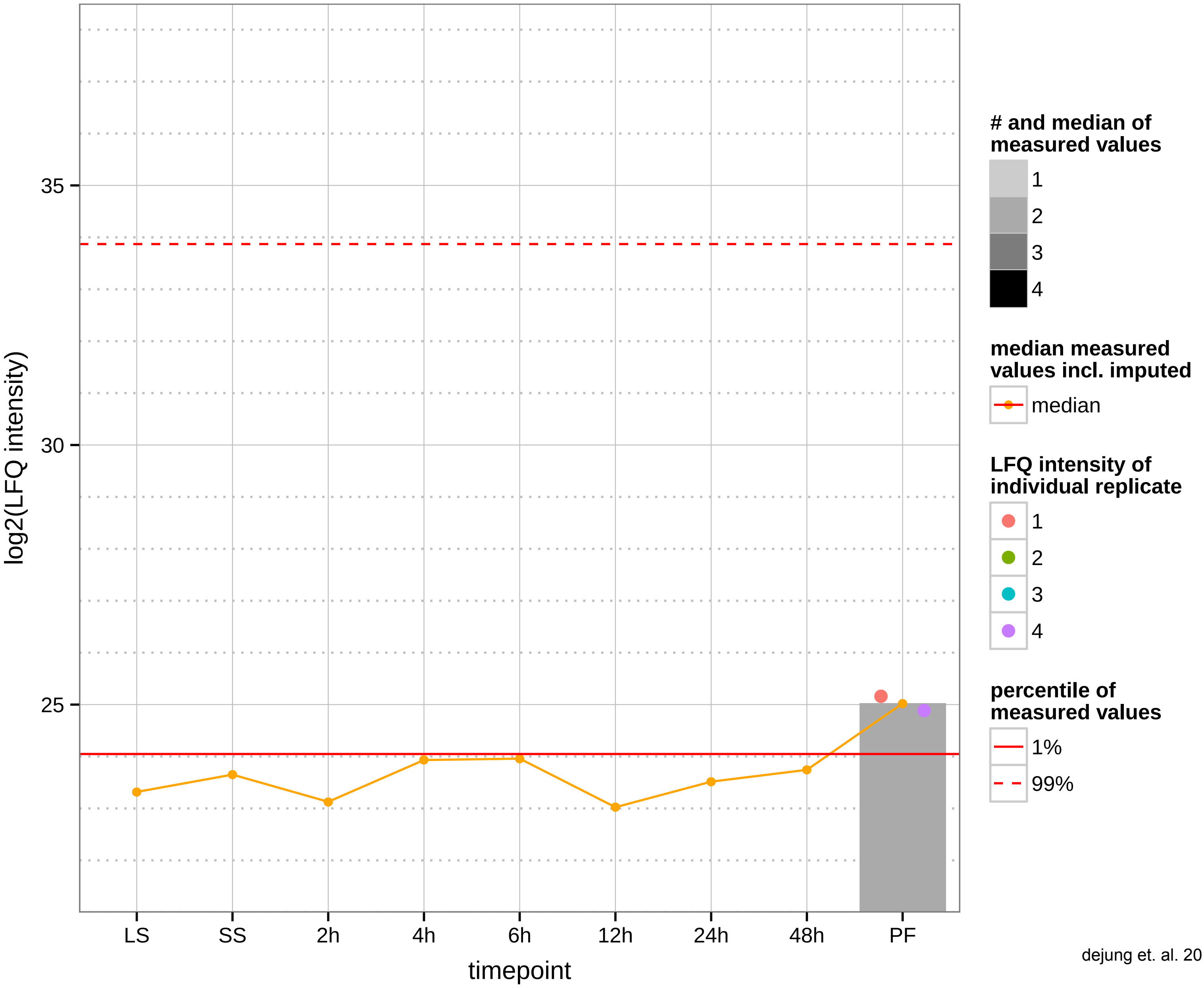
hypothetical protein, conserved
Tb11.02.5360b;Tb11.02.5360
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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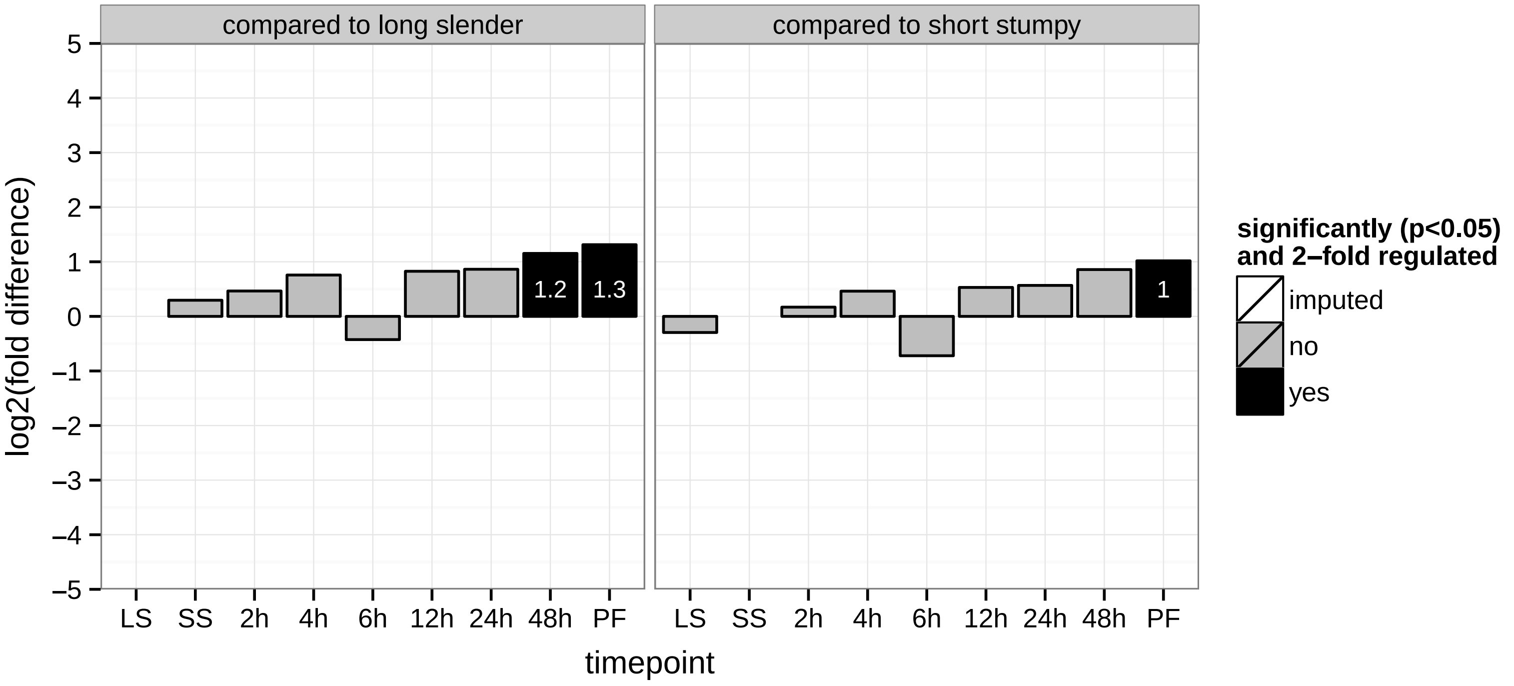
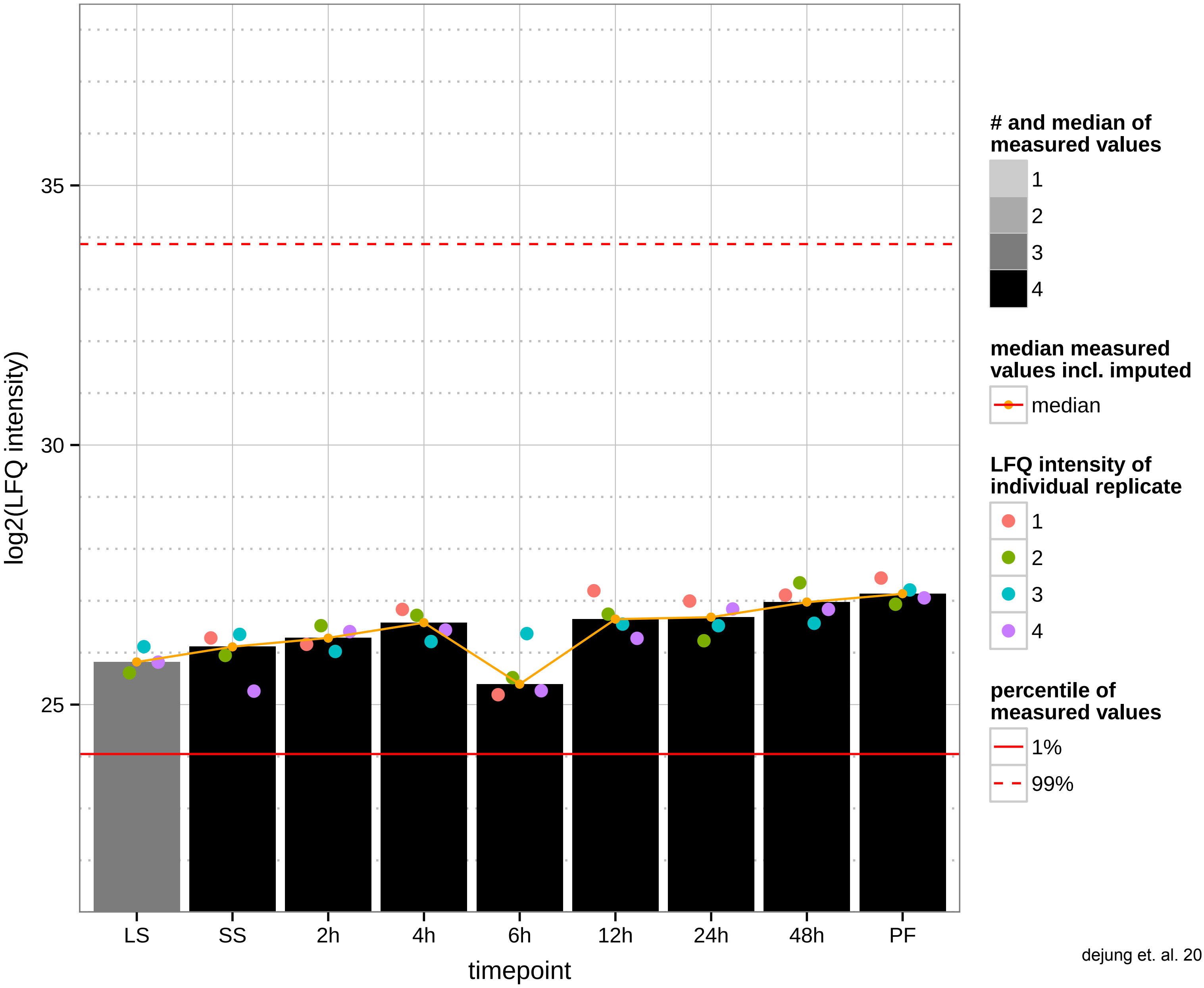
exosome complex exonuclease RRP44p homologue (RRP44), exosome complex exonuclease RRP44p homologue, putative
Tb11.02.5380b;Tb11.02.5380
AGOF: RNA binding, guanyl–nucleotide exchange factor activity, ribonuclease activity
AGOC: exosome (RNase complex), mitochondrion
AGOP: rRNA processing
PGOF: RNA binding, ribonuclease activity
PGOC: null
PGOP: null





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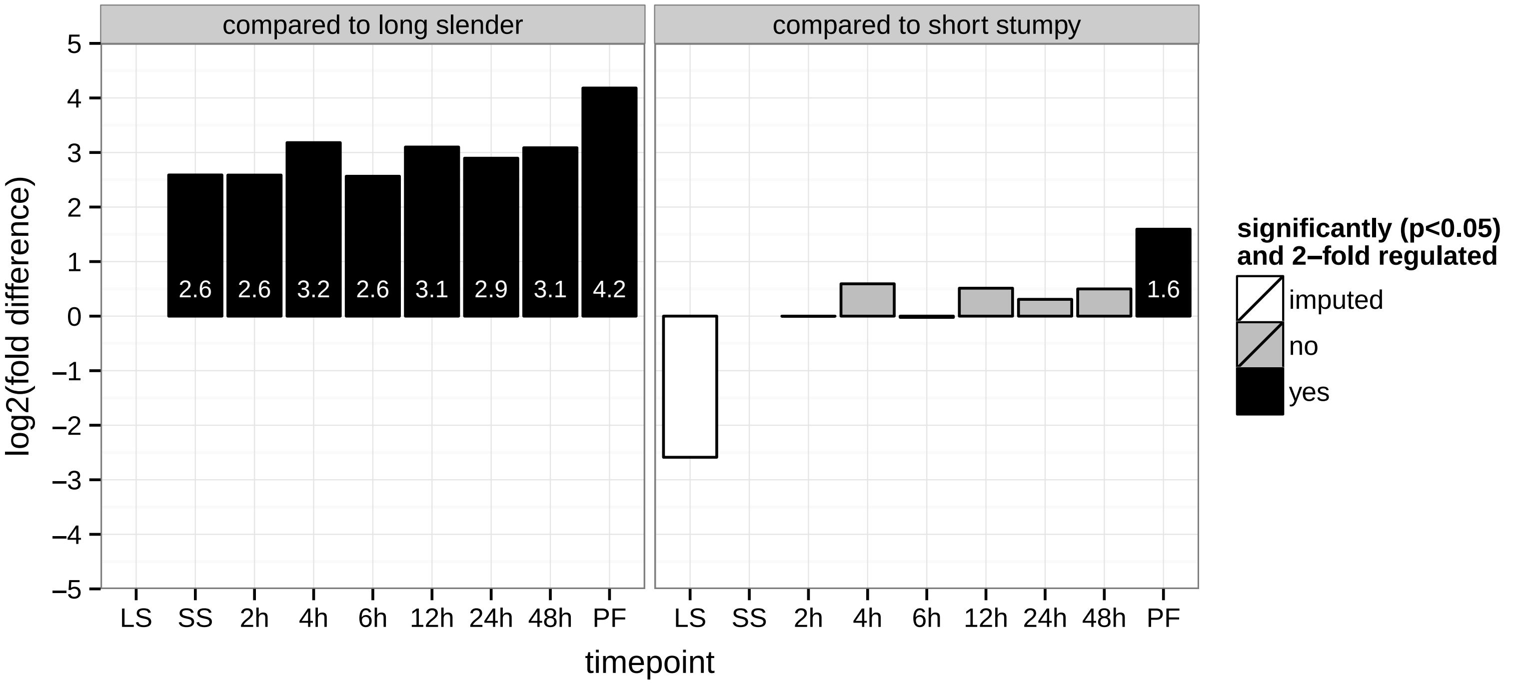
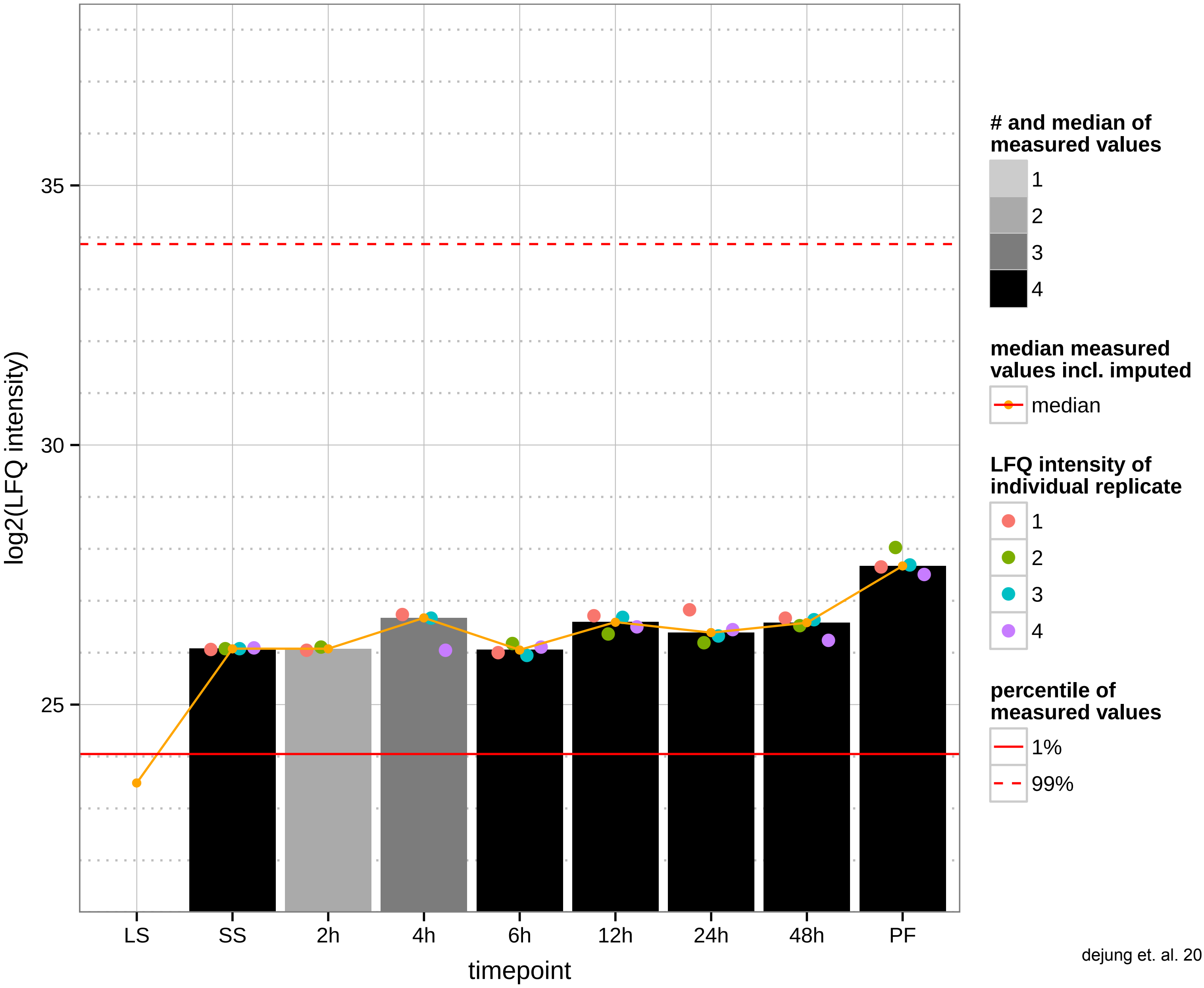
mRNA processing protein, putative
Tb11.02.5390b;Tb11.02.5390
AGOF: mRNA binding
AGOC: mitochondrion
AGOP: mitochondrial RNA processing
PGOF: null
PGOC: null
PGOP: null





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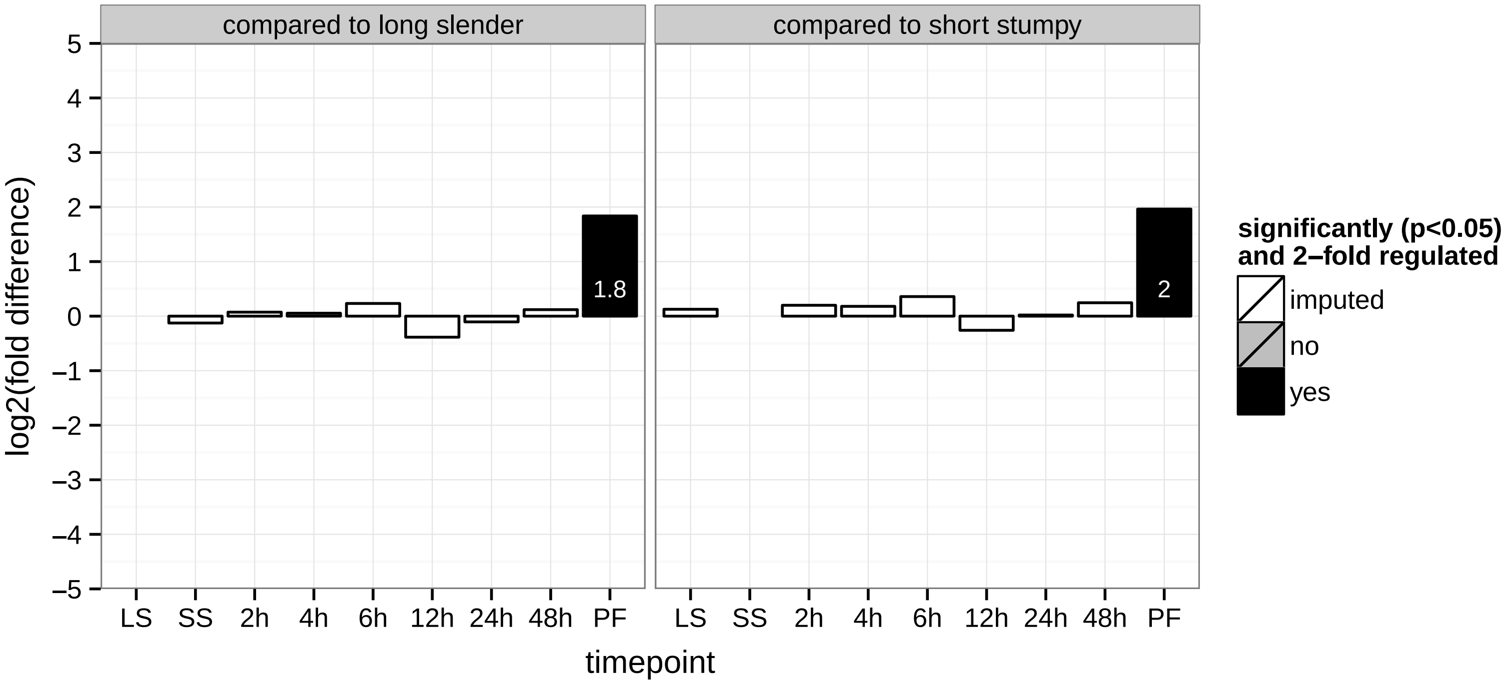
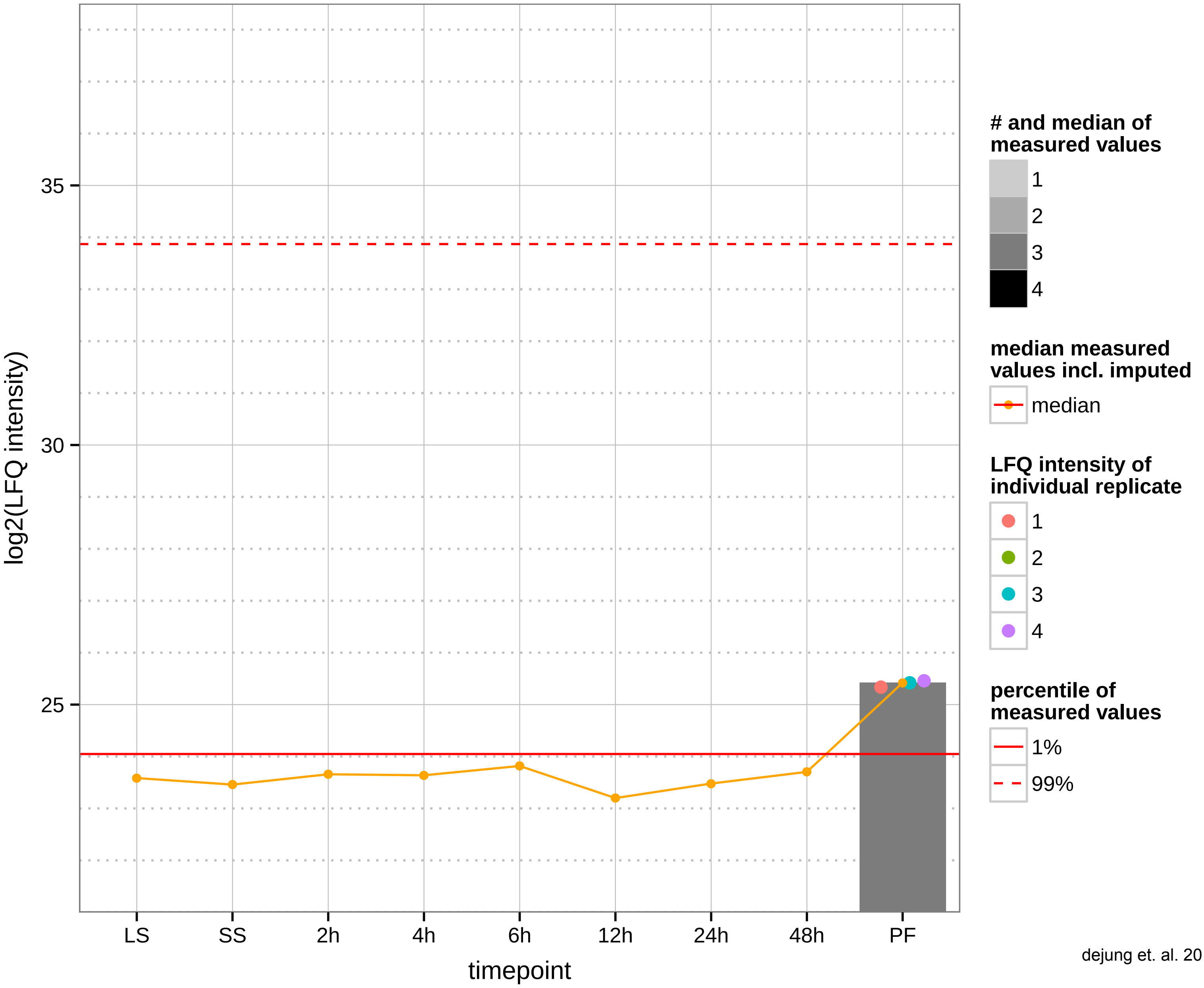
ribonuclease H1, putative
Tb927.7.4930;Tb11.v5.0174
AGOF: null, magnesium ion binding, nucleic acid binding, ribonuclease H activity
AGOC: null
AGOP: null
PGOF: magnesium ion binding, nucleic acid binding, ribonuclease H activity
PGOC: null
PGOP: null





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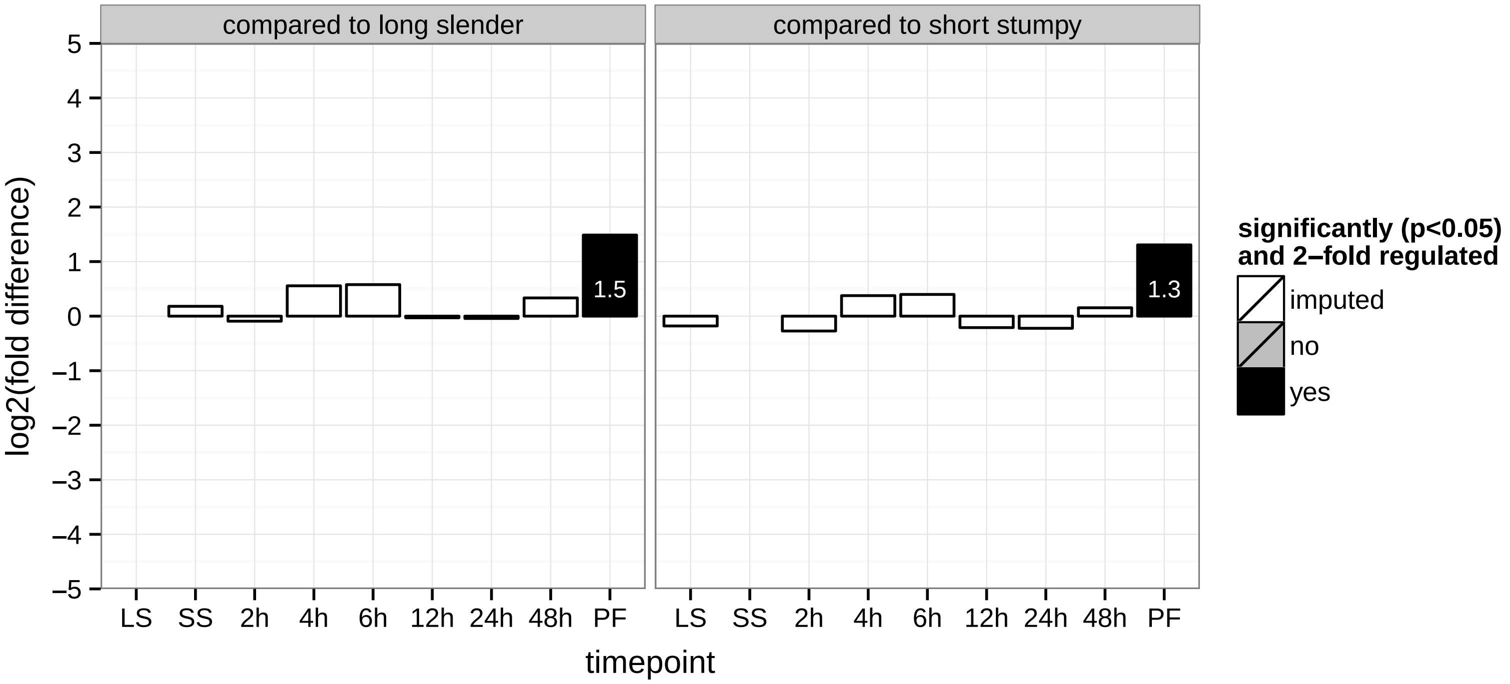
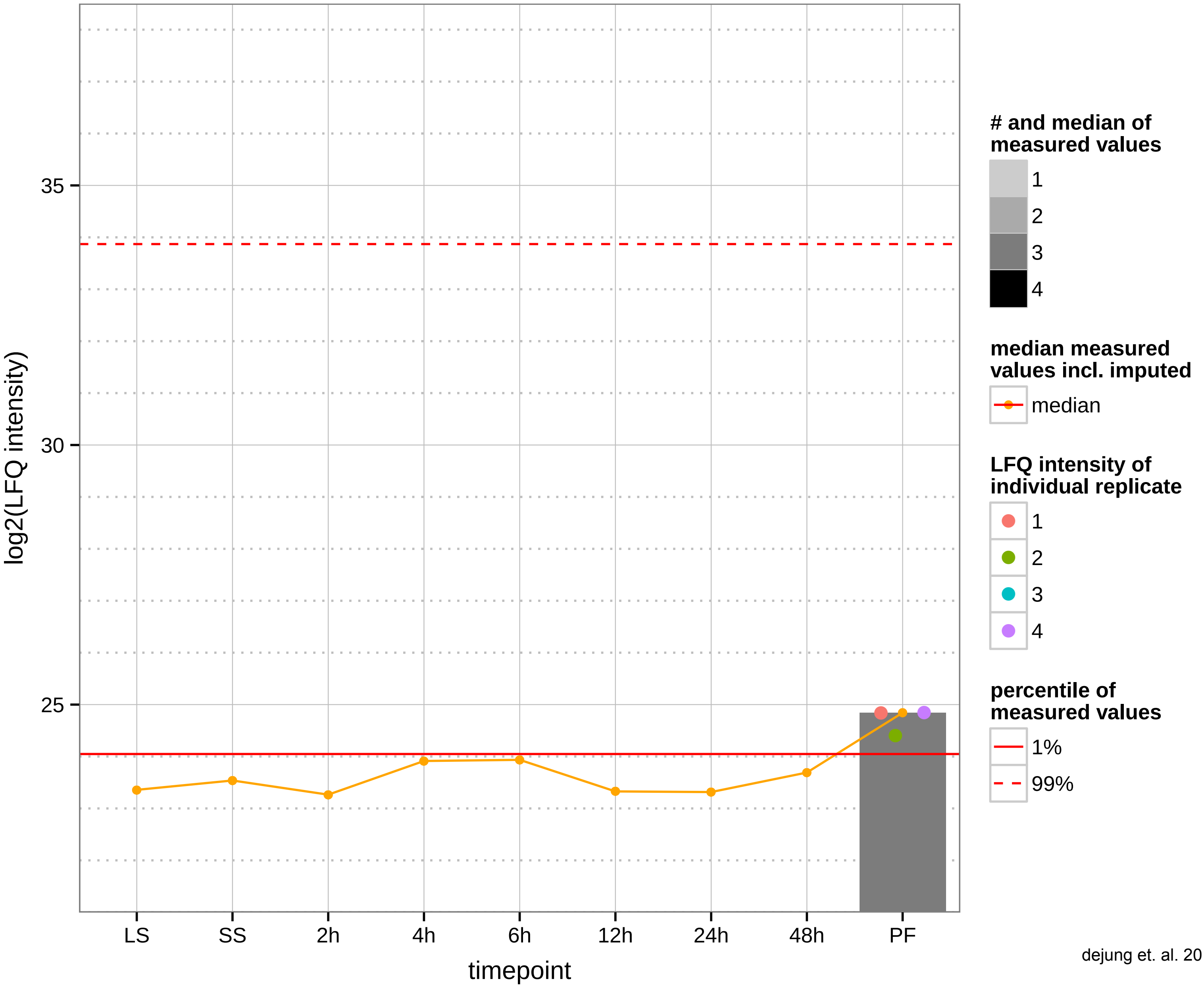
hypothetical protein, conserved
Tb927.10.5200;Tb11.v5.0237
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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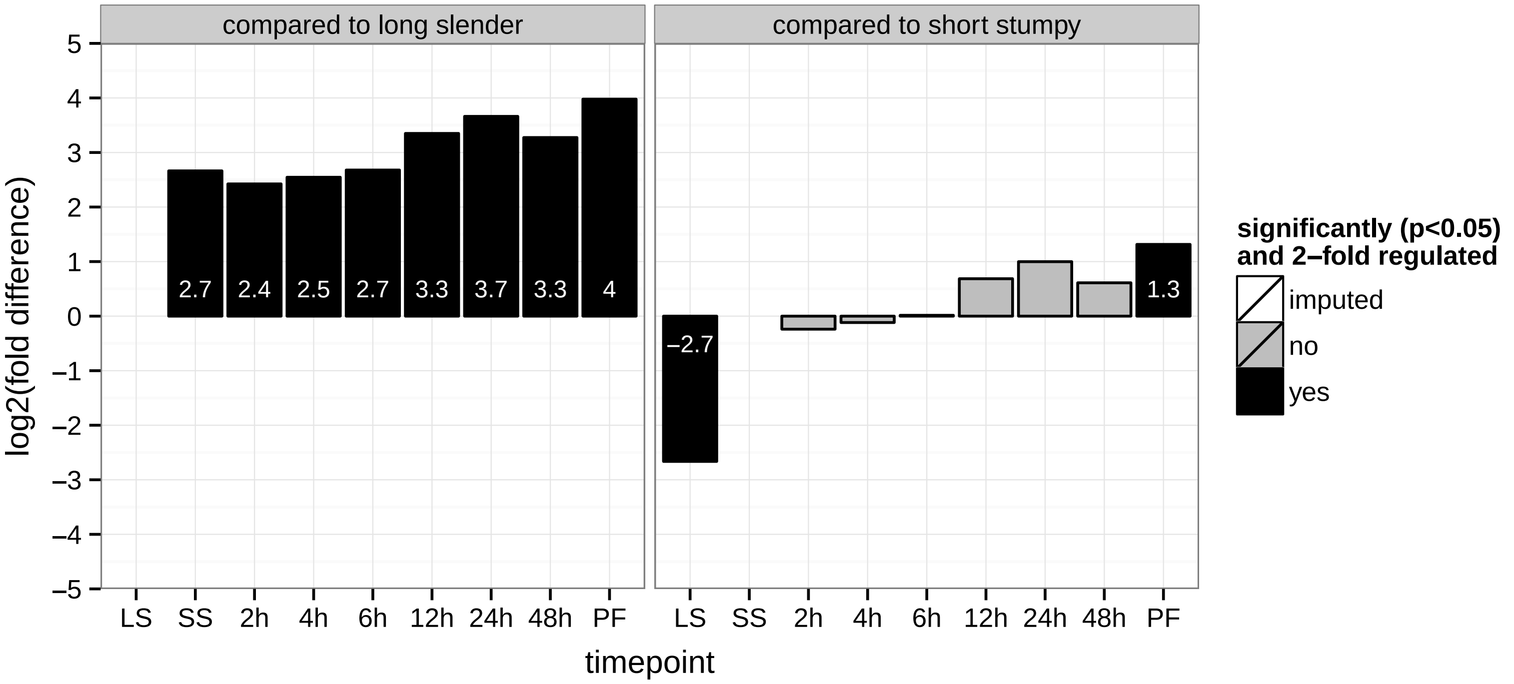
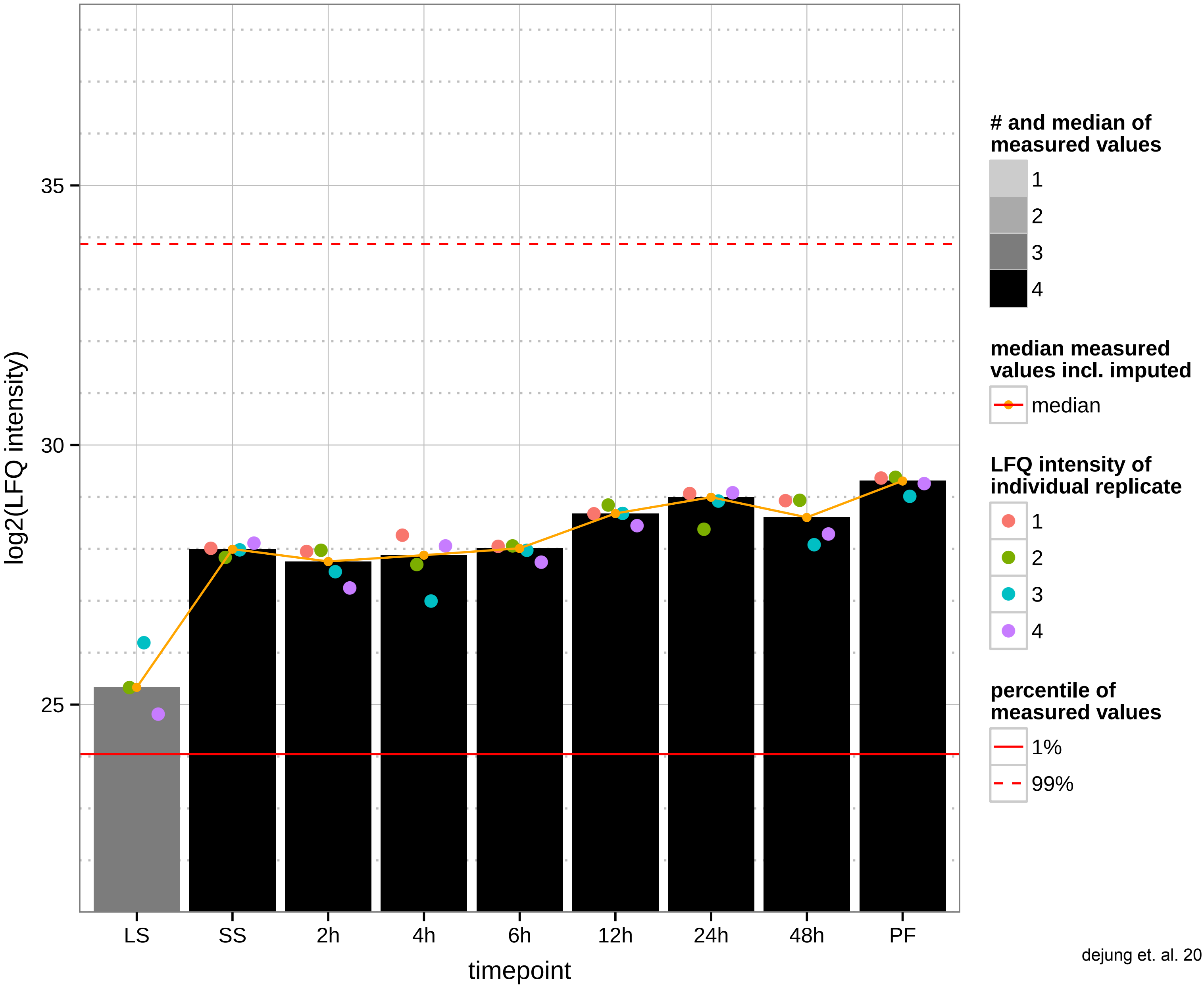
hypothetical protein, conserved
Tb927.10.6320;Tb11.v5.0274
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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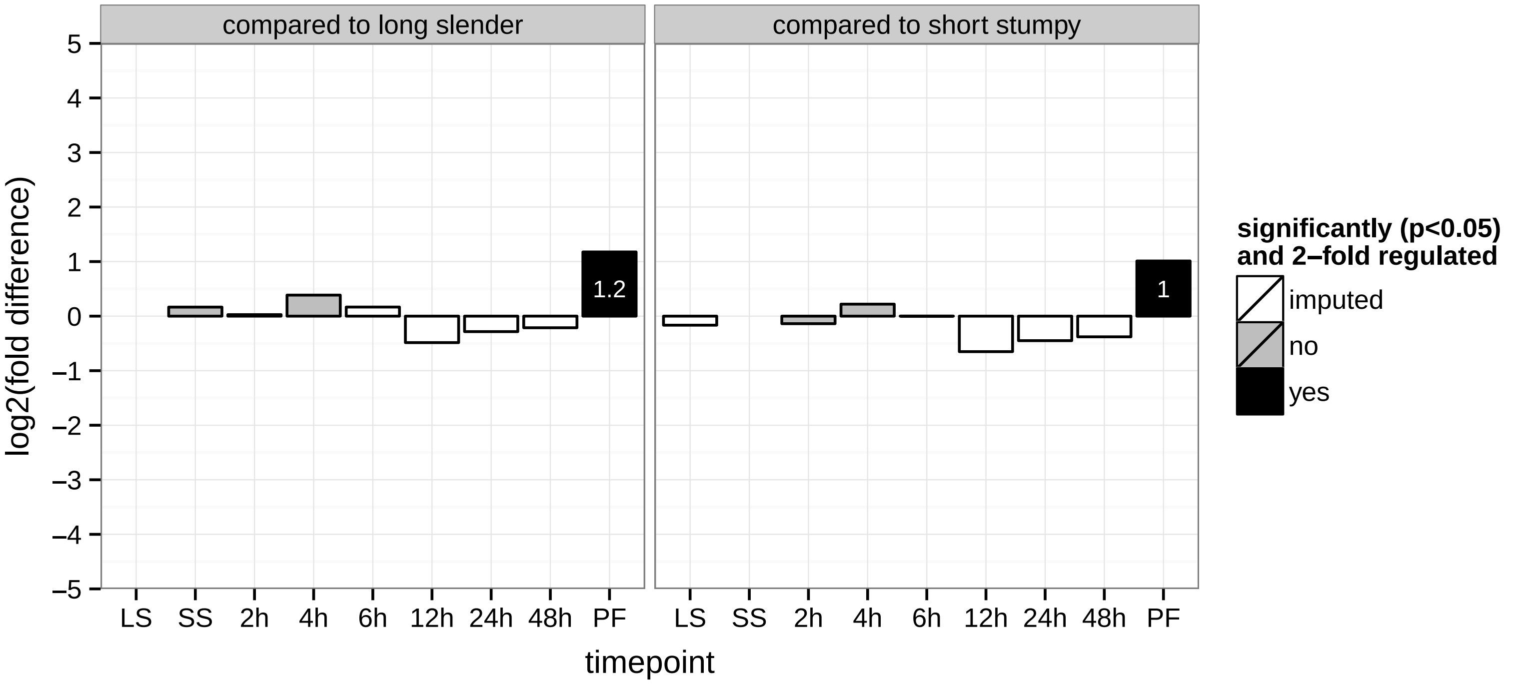
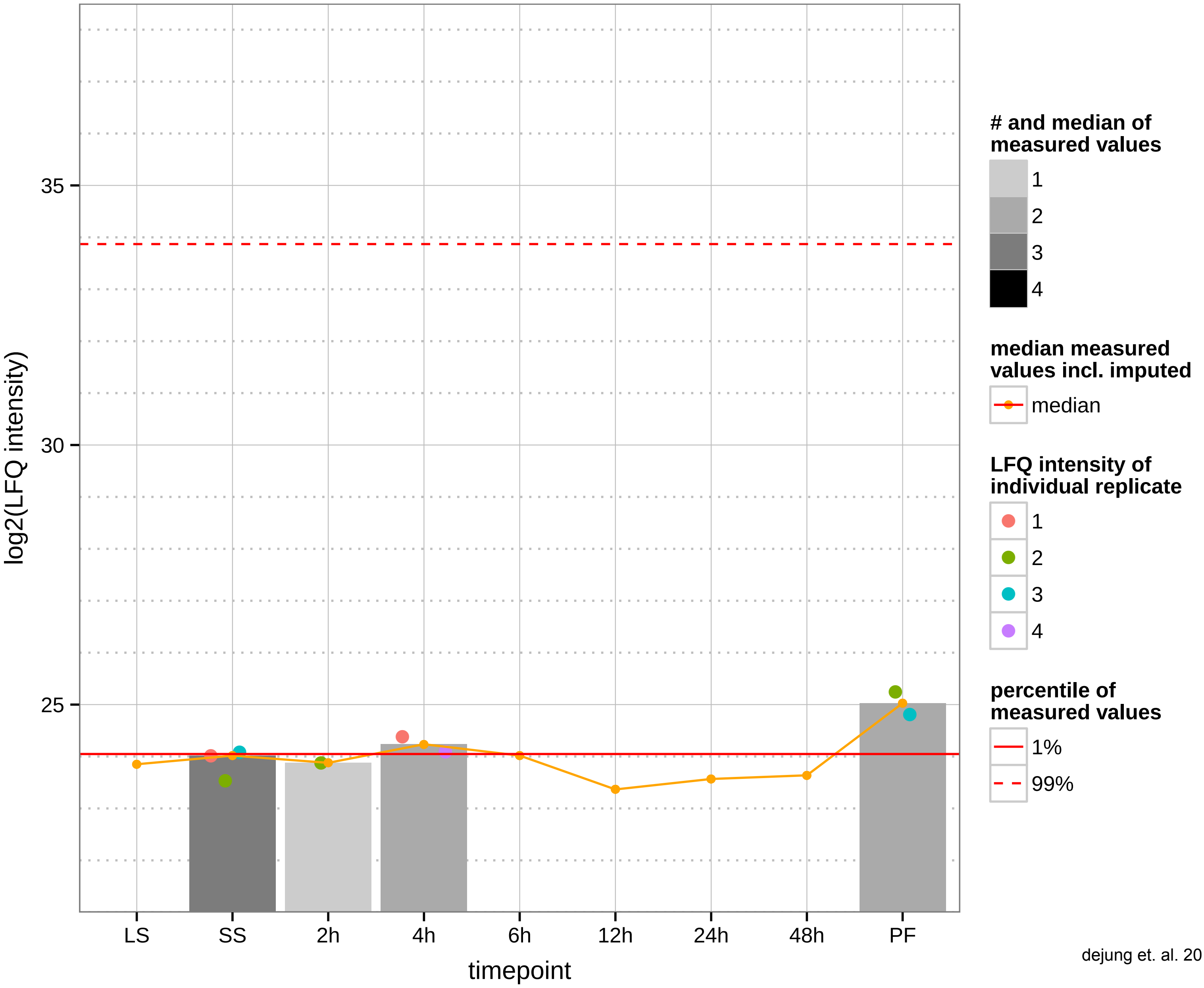
cation transporter, putative
Tb927.10.15940;Tb11.v5.0304
AGOF: null, cation transmembrane transporter activity
AGOC: null, membrane, mitochondrion
AGOP: null, cation transport
PGOF: cation transmembrane transporter activity
PGOC: integral to membrane
PGOP: cation transport, transmembrane transport





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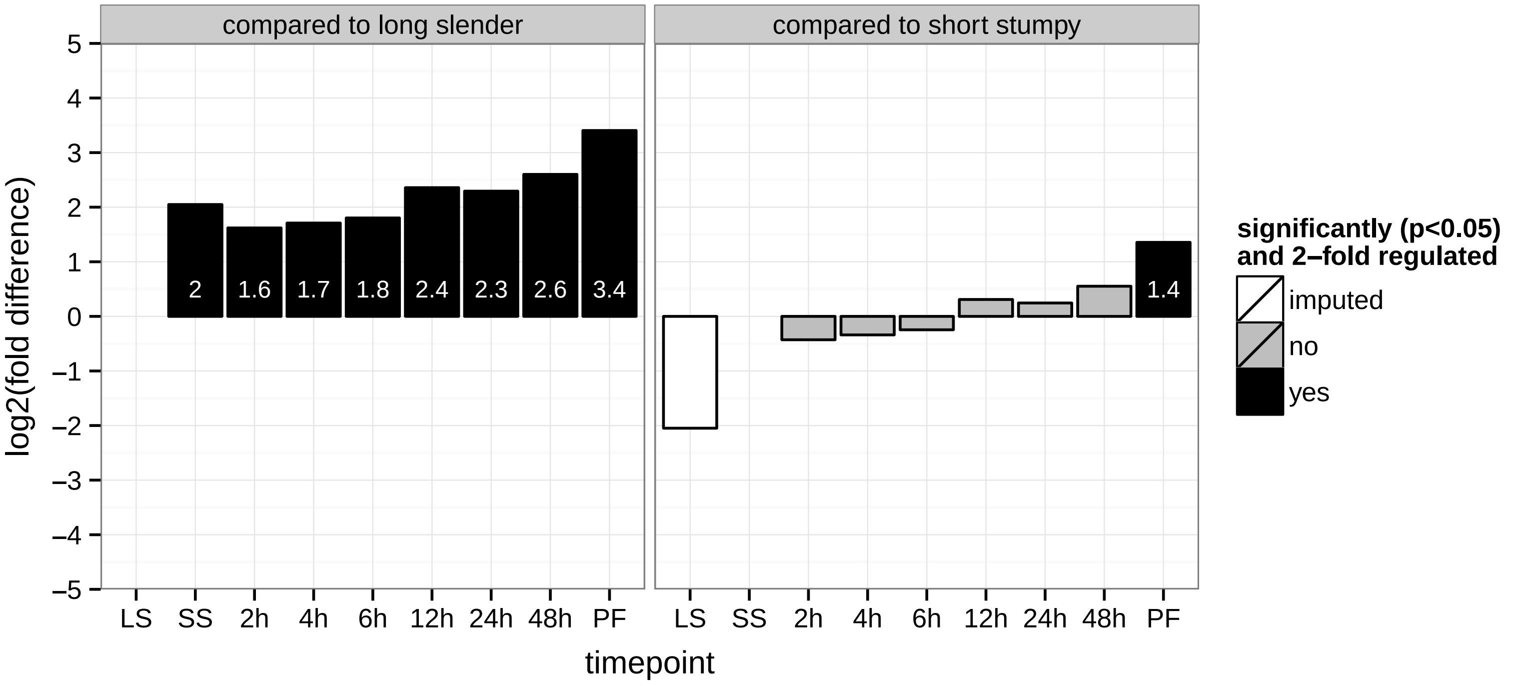
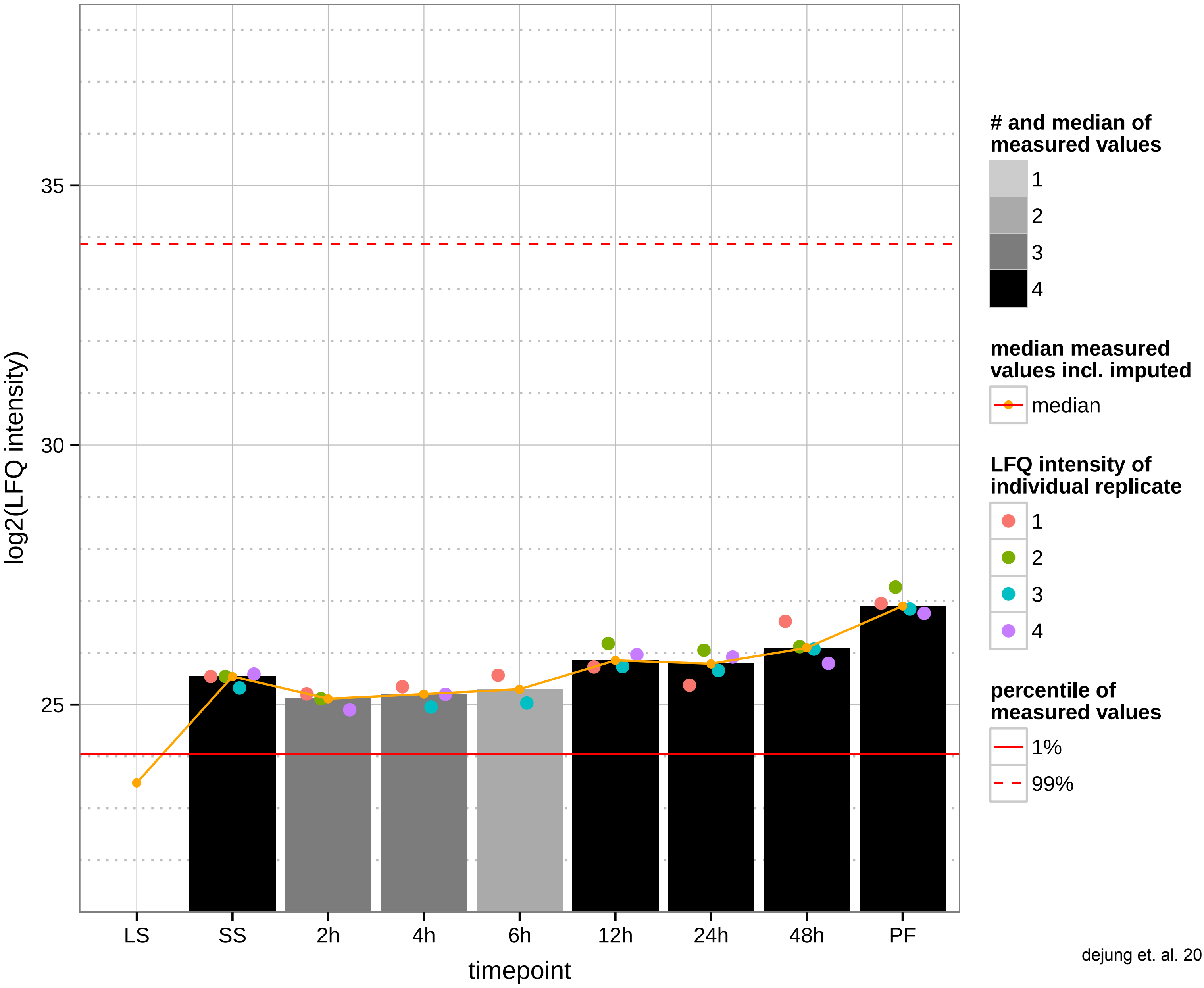
hypothetical protein, conserved, Mitochondrial Editosome−like Complex TUTase (MEAT1)
Tb927.1.1330;Tb11.v5.0371
AGOF: null, RNA uridylyltransferase activity
AGOC: null, mitochondrion
AGOP: null, transcription, DNA−dependent
PGOF: null
PGOC: null
PGOP: null





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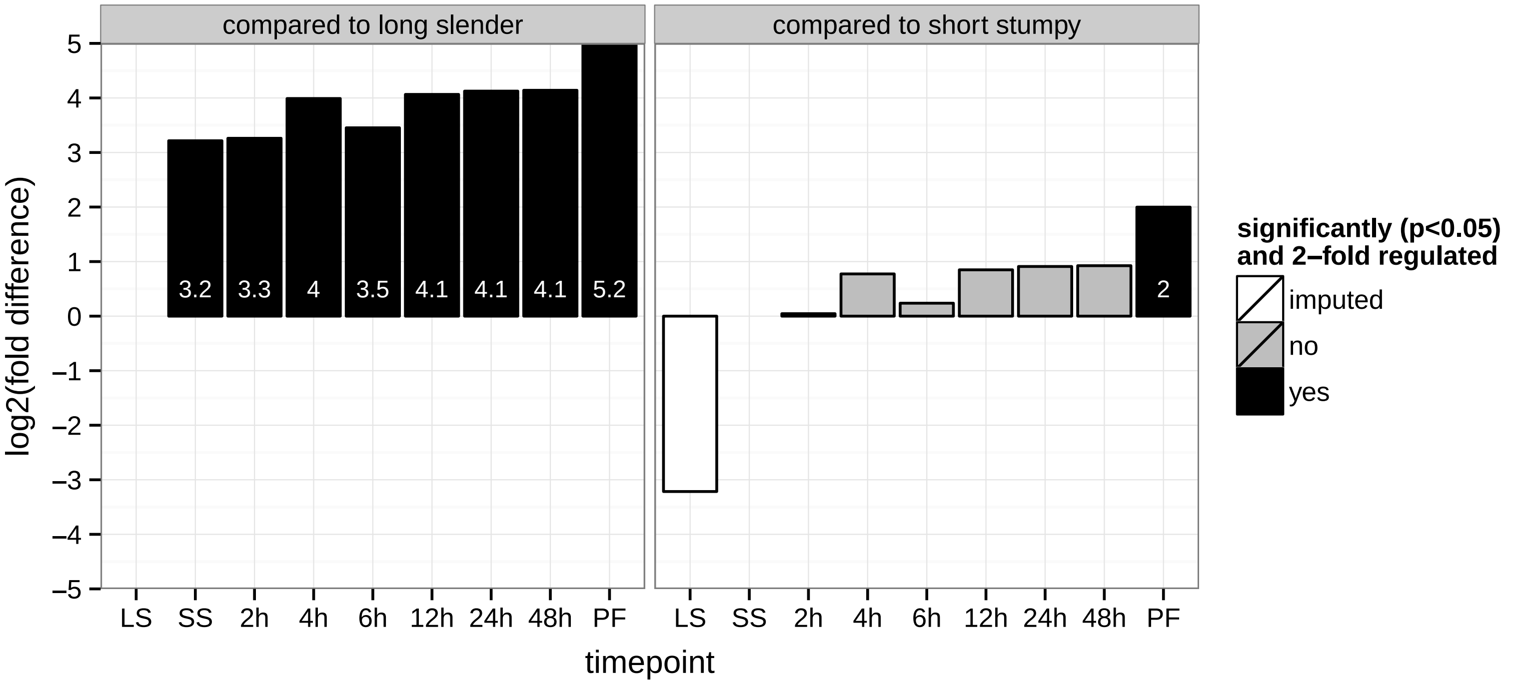
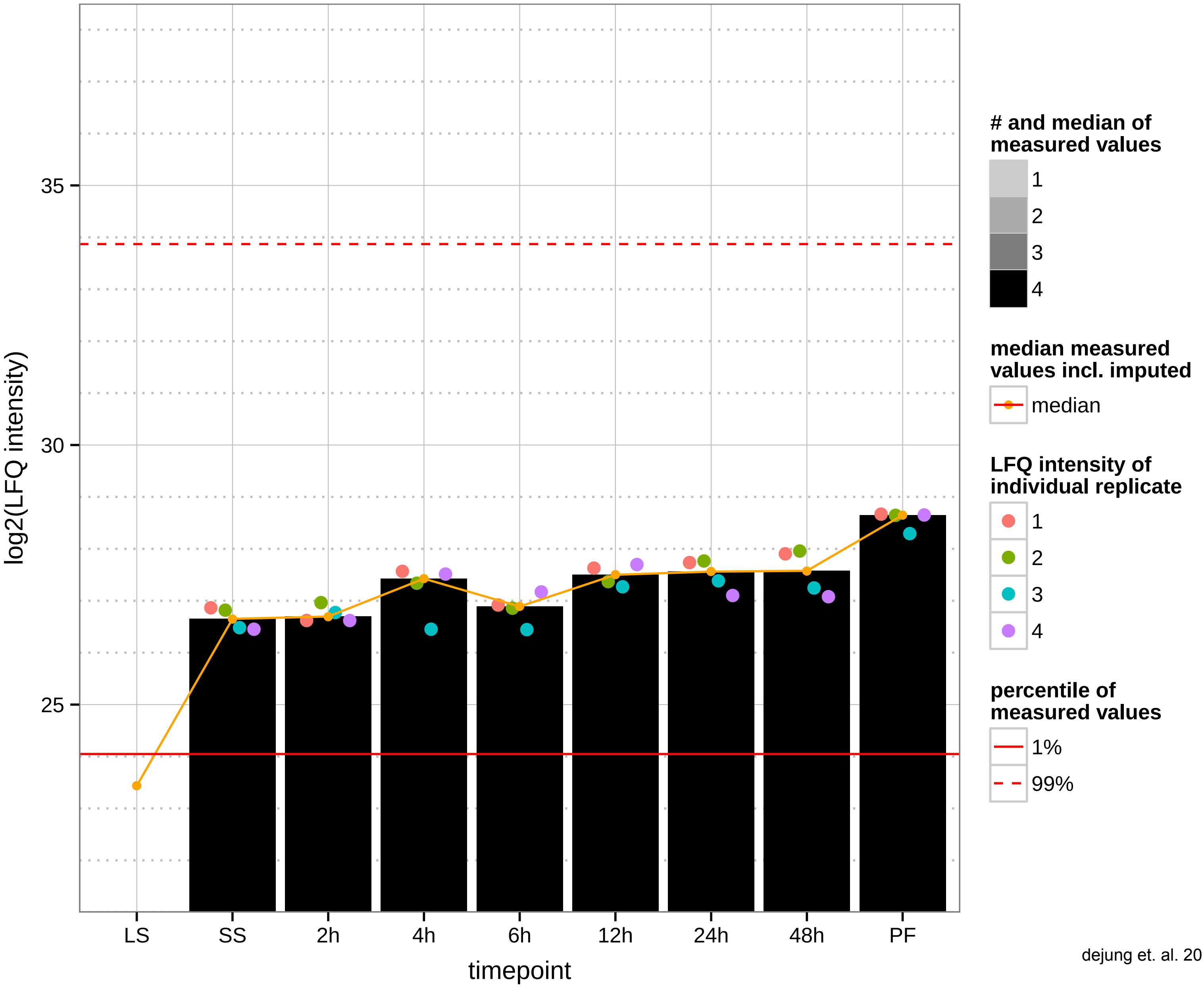
ATP−dependent zinc metallopeptidase, putative, metallo−peptidase, Clan MA(E) Family M41
Tb927.10.16150;Tb11.v5.0397
AGOF: null, ATP binding, metalloendopeptidase activity, nucleoside−triphosphatase activity
AGOC: null, mitochondrion
AGOP: null, proteolysis
PGOF: ATP binding, metalloendopeptidase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: proteolysis





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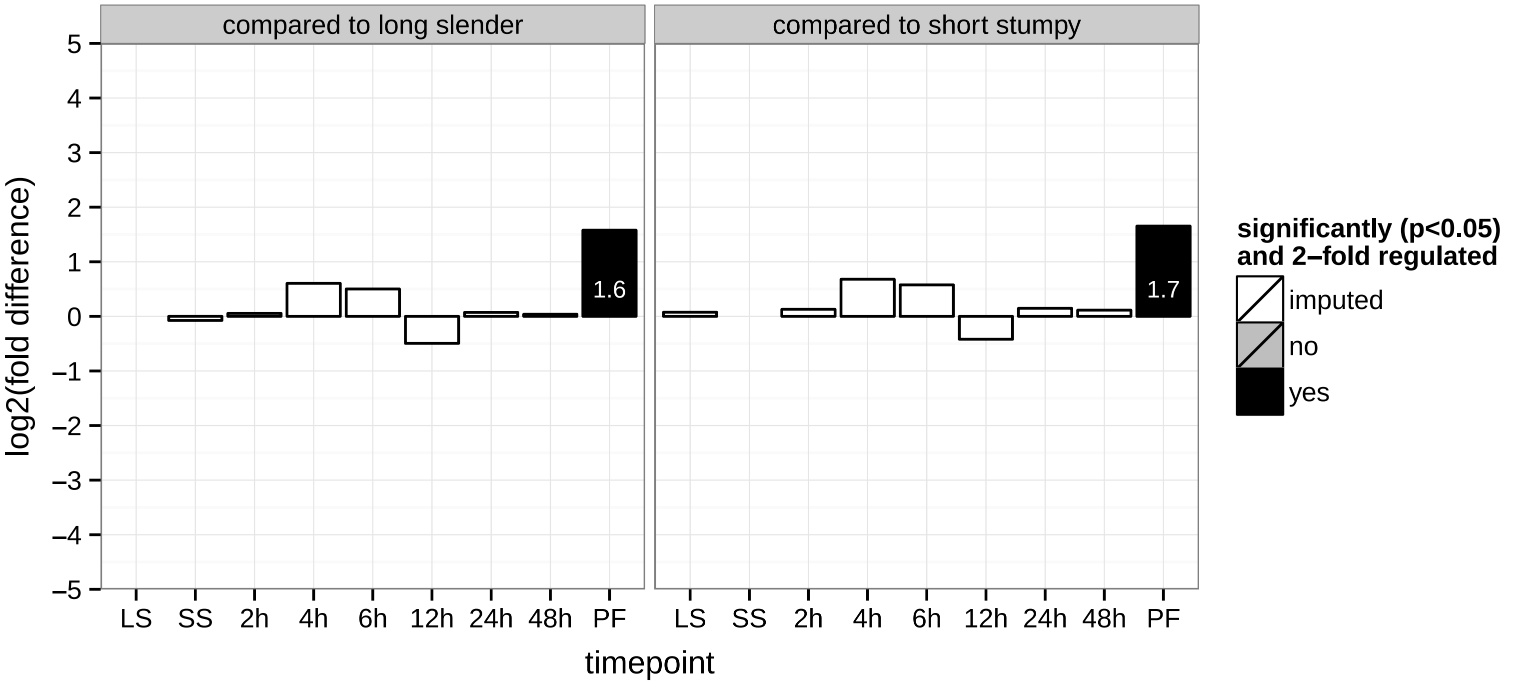
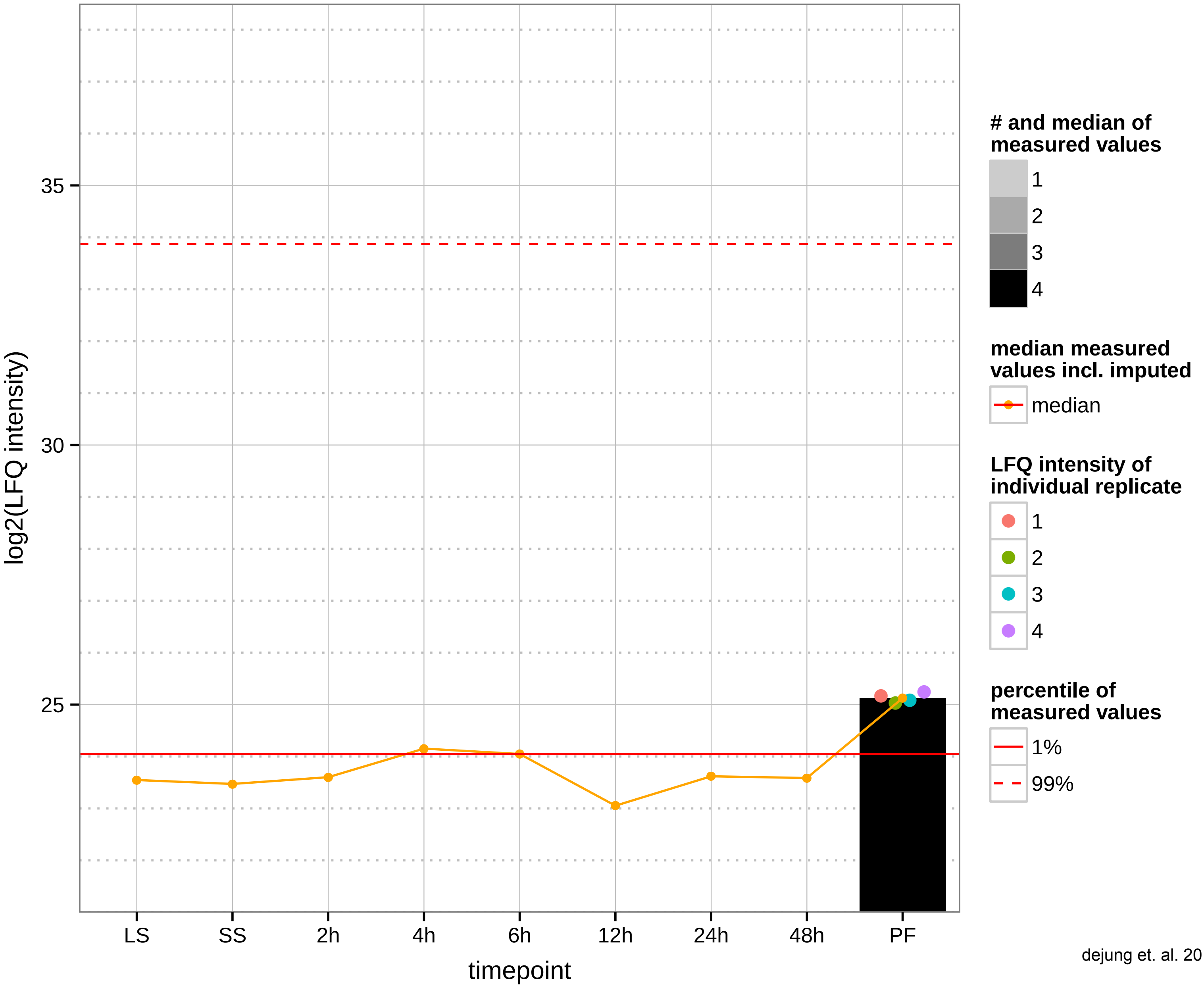
hypothetical protein, conserved
Tb11.v5.0517;Tb927.11.4050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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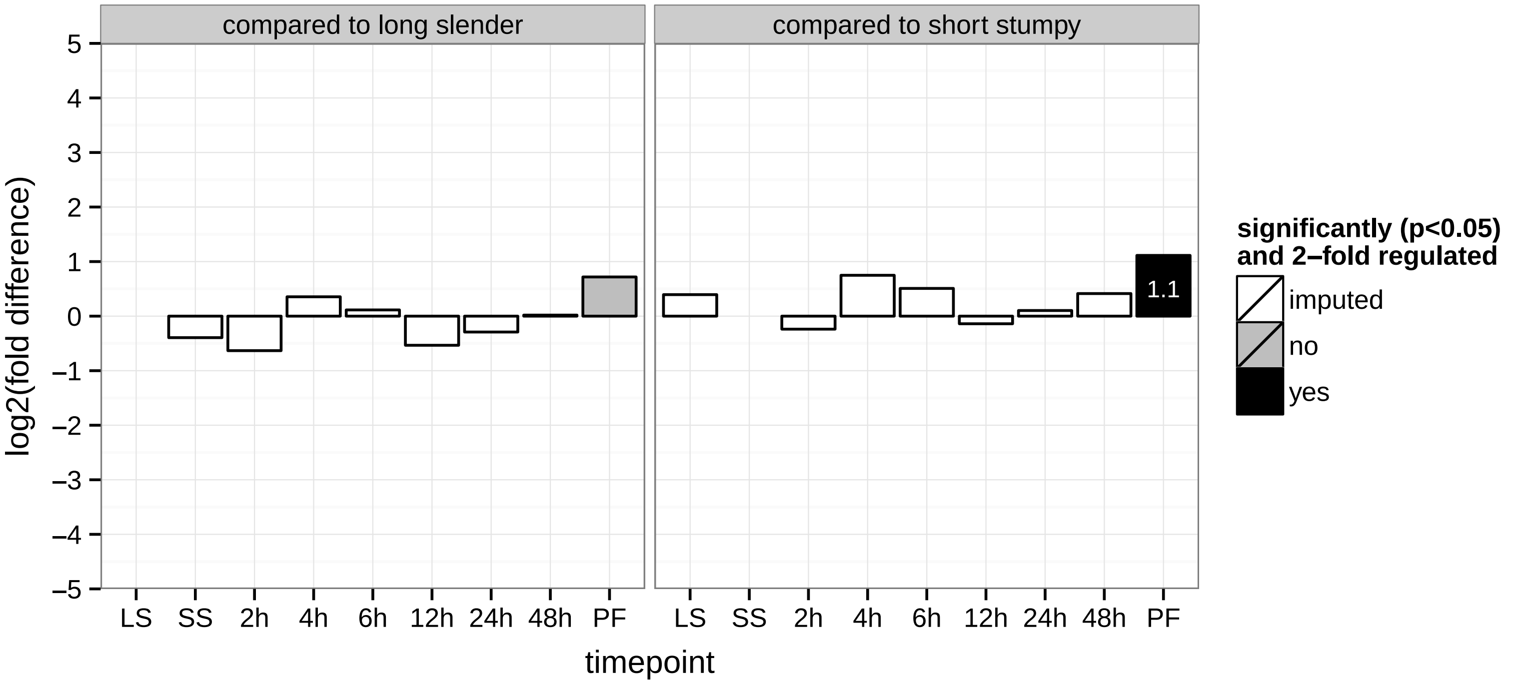
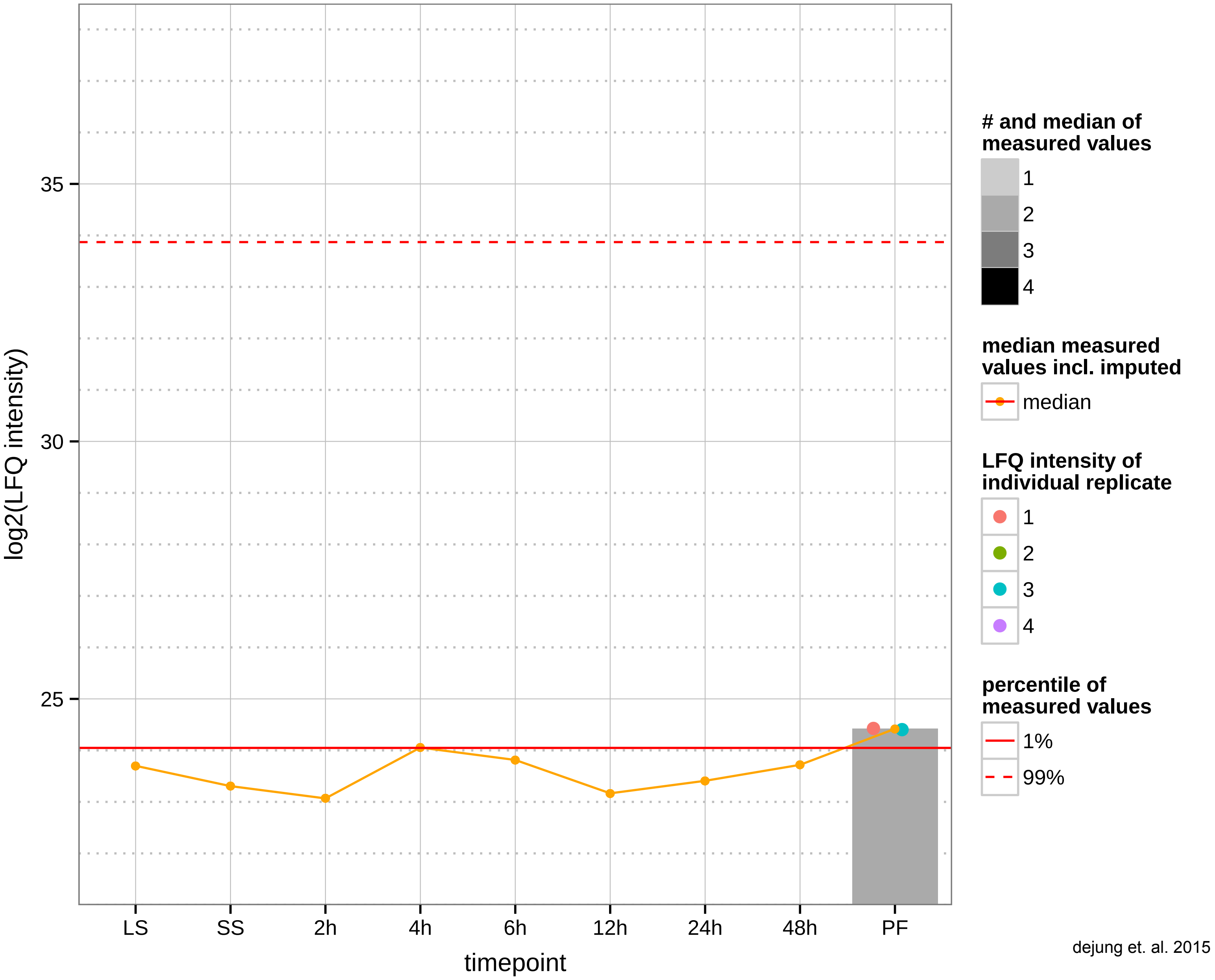
hypothetical protein, conserved
Tb927.8.3320;Tb11.v5.0519
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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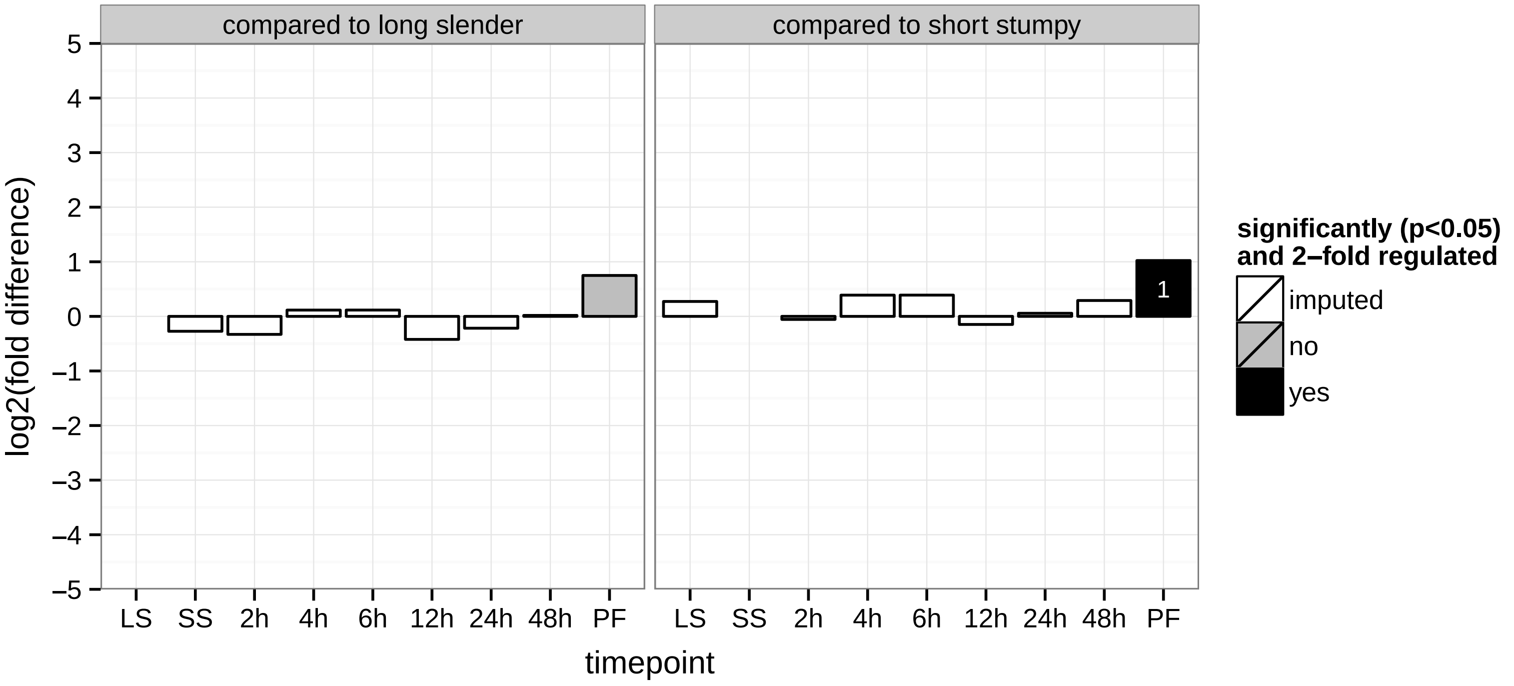
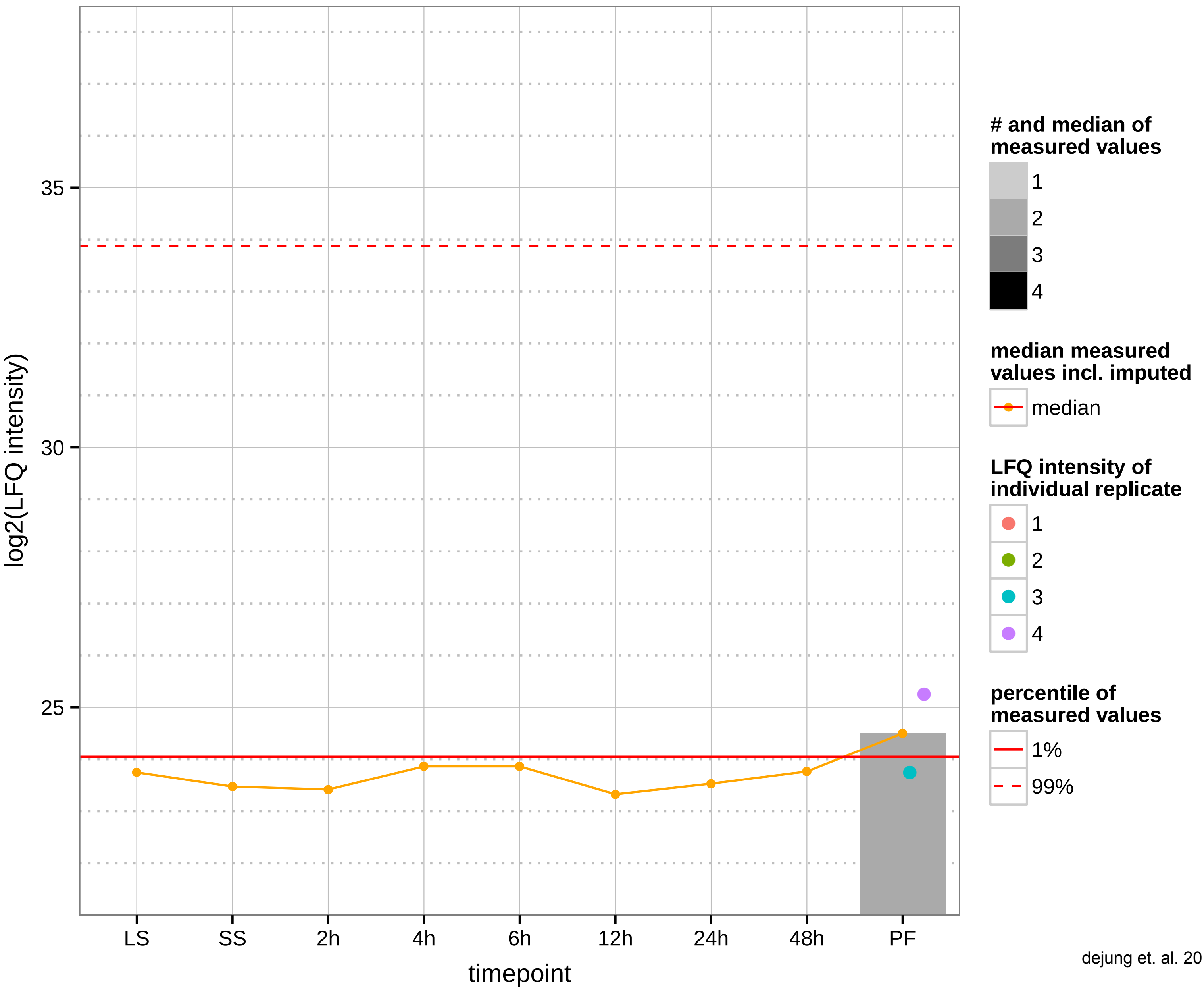
hypothetical protein, conserved, leucine−rich repeat−containing protein
Tb927.1.780;Tb11.v5.0523
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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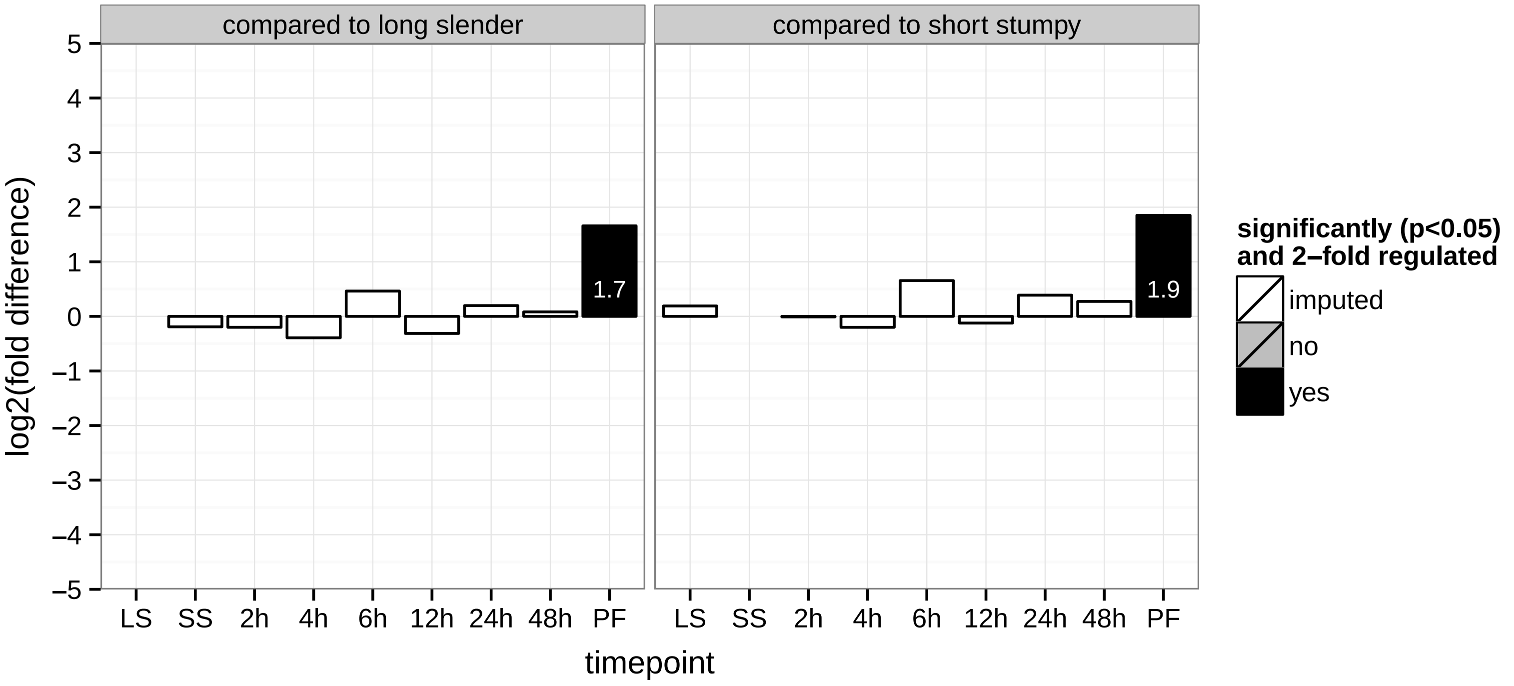
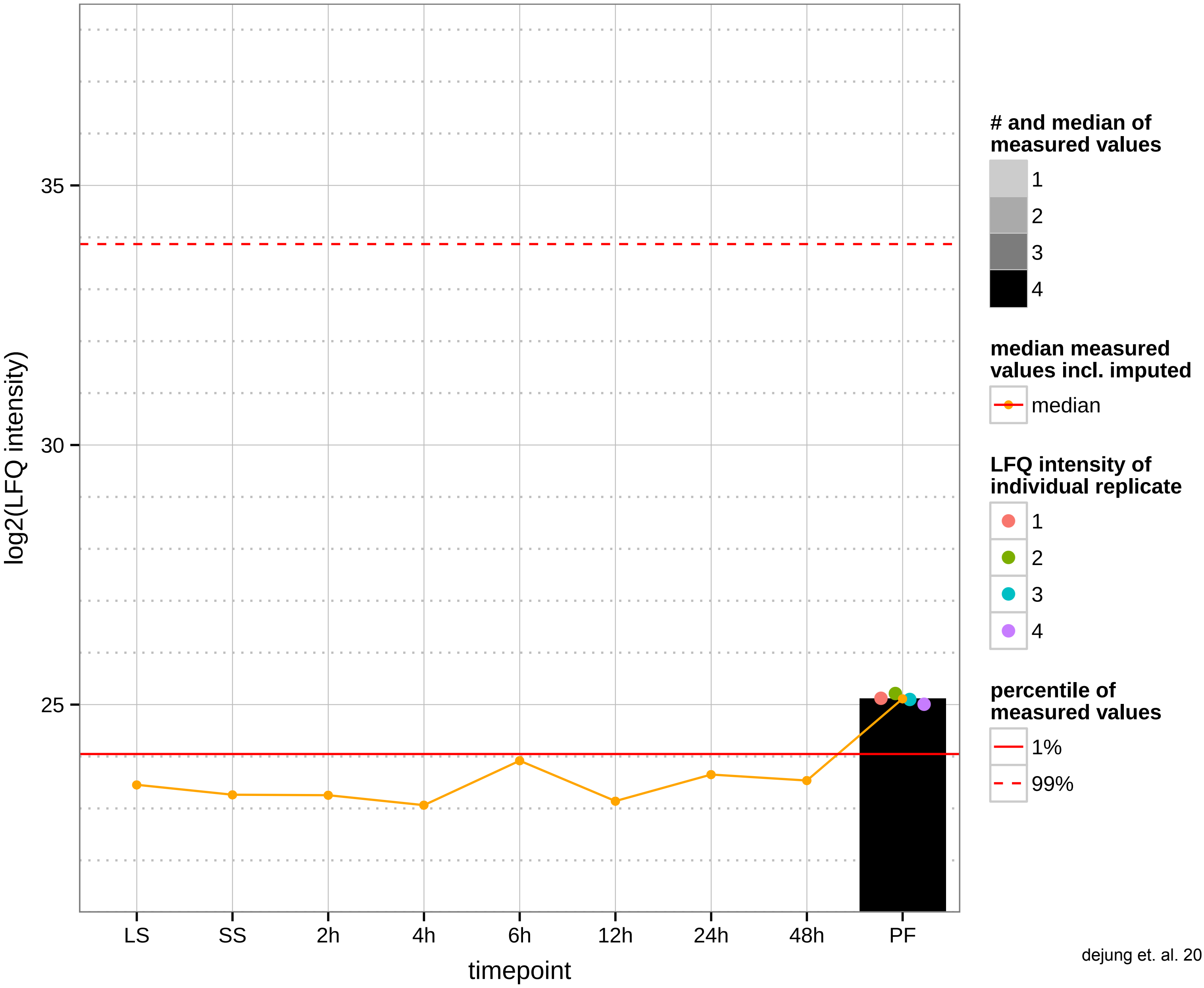
protein kinase, putative
Tb927.7.3210;Tb11.v5.0652
AGOF: null, ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null, growth, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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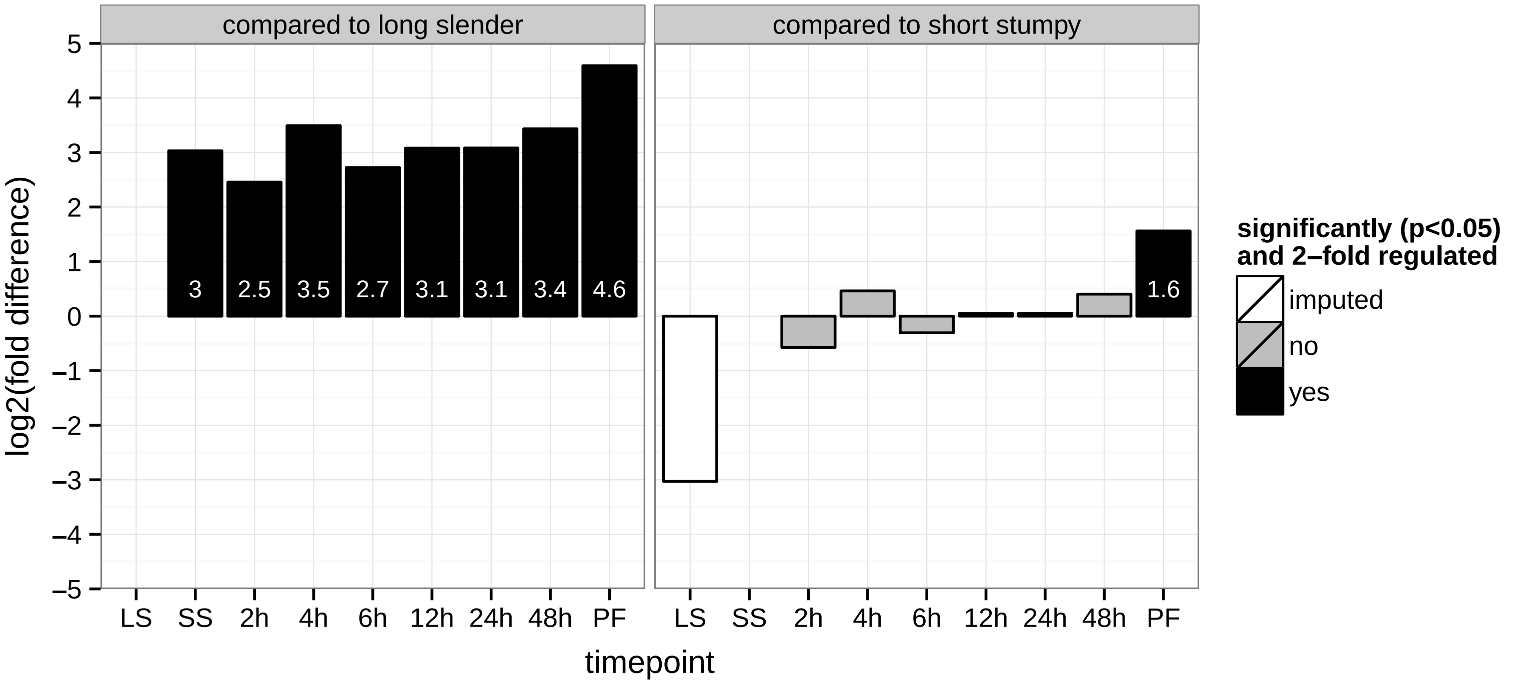
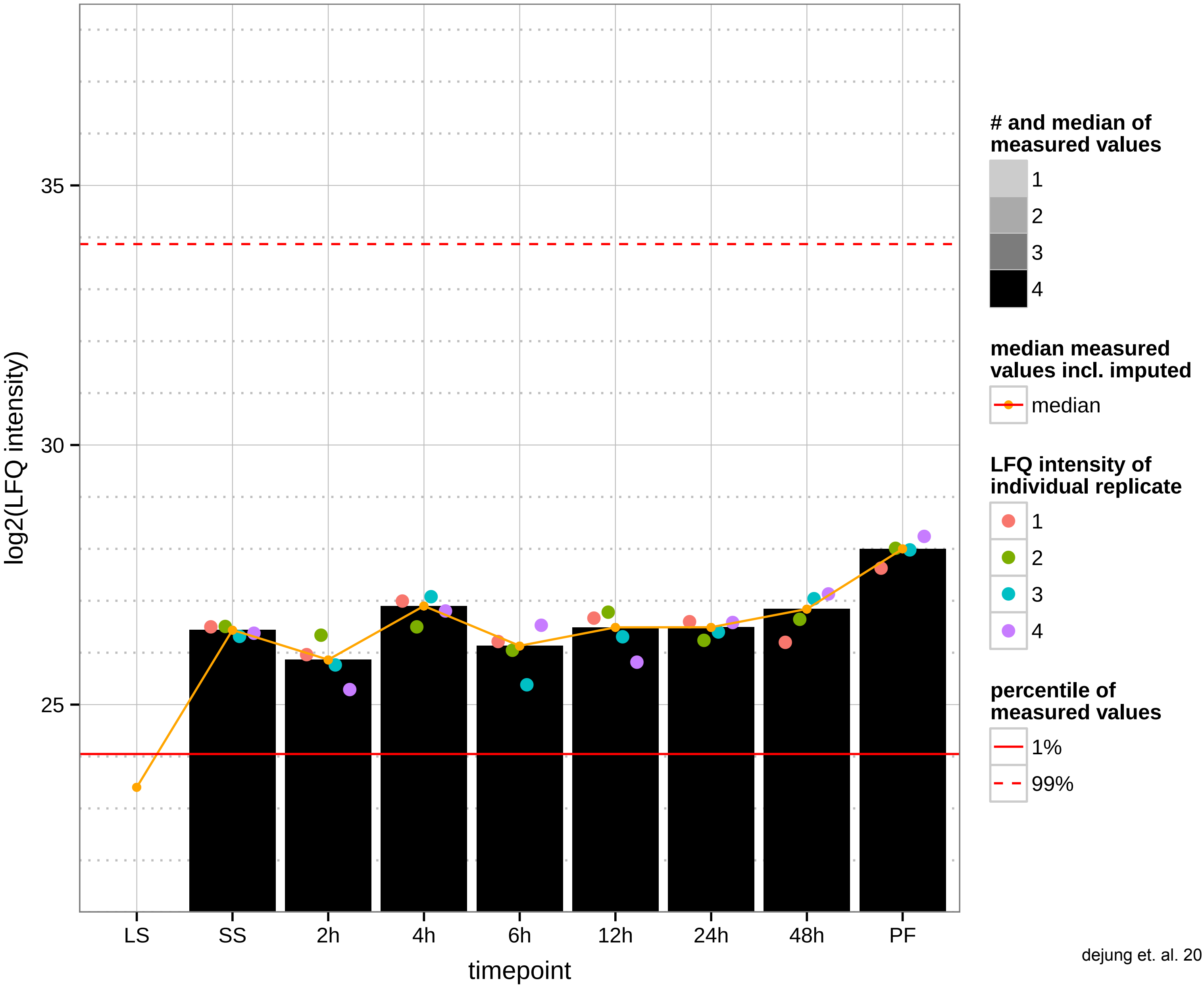
tatD related deoxyribonuclease, putative
Tb927.11.6090;Tb11.v5.0746
AGOF: null, deoxyribonuclease activity, endodeoxyribonuclease activity, producing 5'−phosphomonoesters
AGOC: null
AGOP: null, metabolic process
PGOF: endodeoxyribonuclease activity, producing 5'−phosphomonoesters
PGOC: null
PGOP: null





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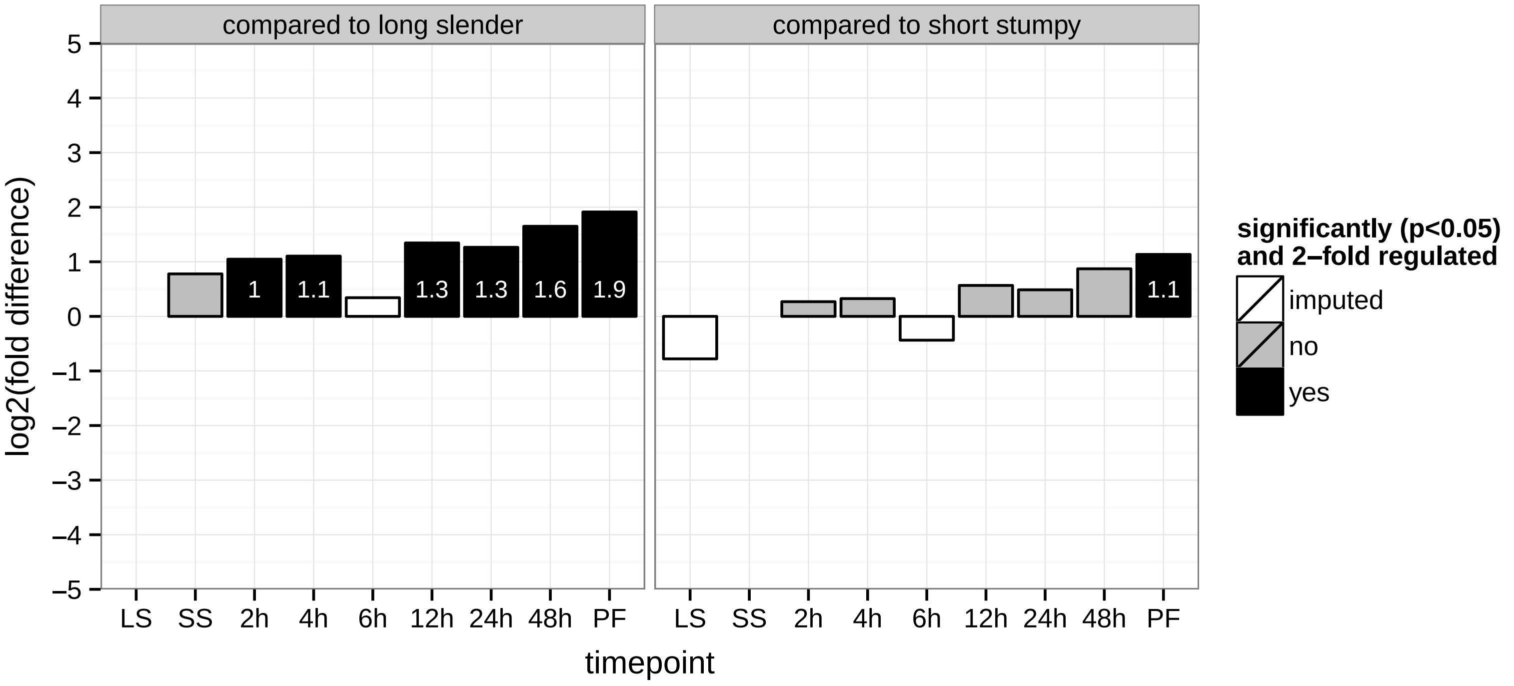
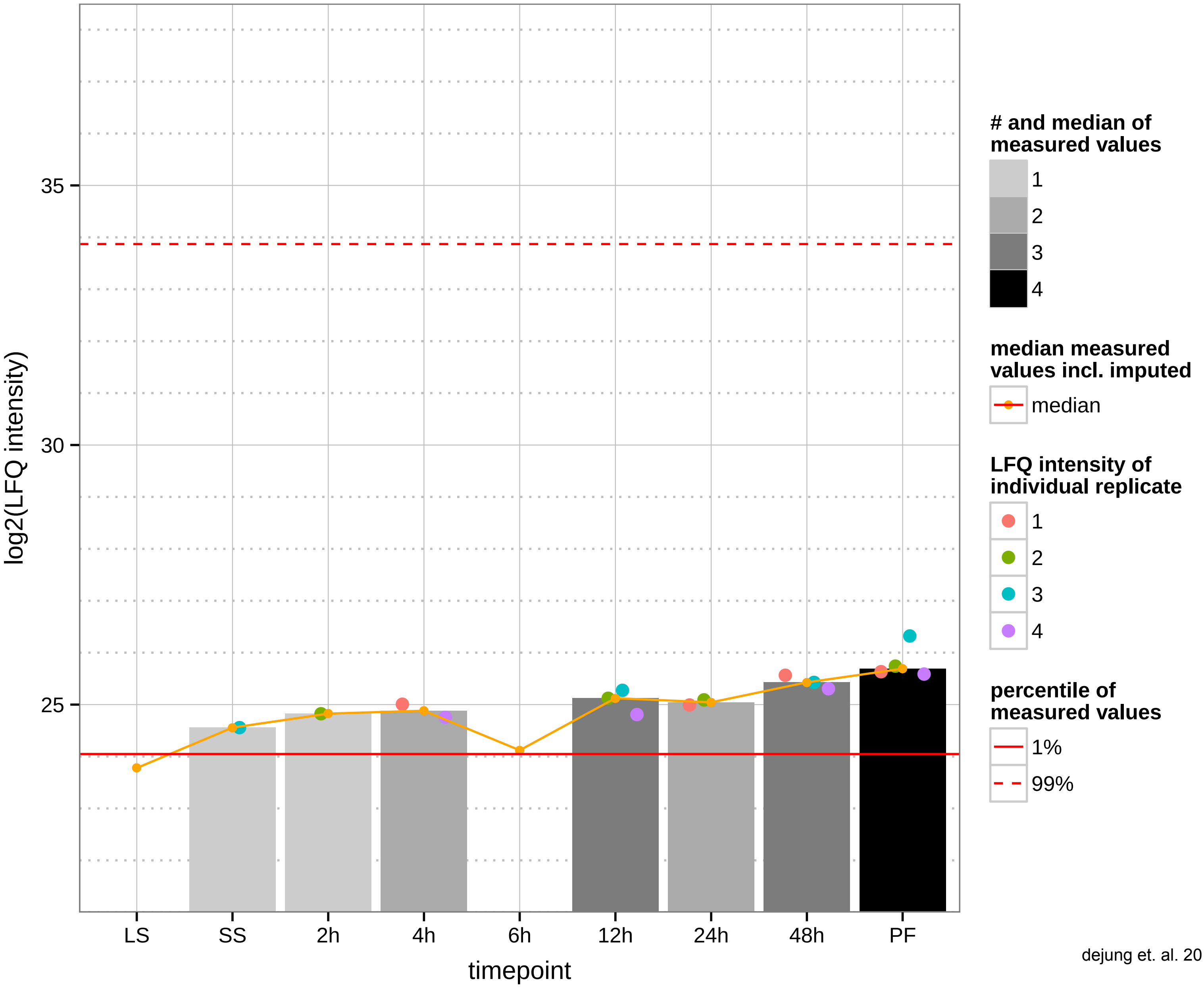
UDP–Gal or UDP–GlcNAc–dependent glycosyltransferase, putative
Tb927.4.5300;Tb11.v5.0880;Tb927.4.5290;Tb927.4.5270;Tb927.4.5260;Tb927.4.5250;Tb927.4.5280
AGOF: null, UDP–glycosyltransferase activity, galactosyltransferase activity
AGOC: null, integral to membrane, membrane, membrane
AGOP: null, GPI anchor biosynthetic process, protein glycosylation
PGOF: galactosyltransferase activity, null
PGOC: membrane, null
PGOP: protein glycosylation, null





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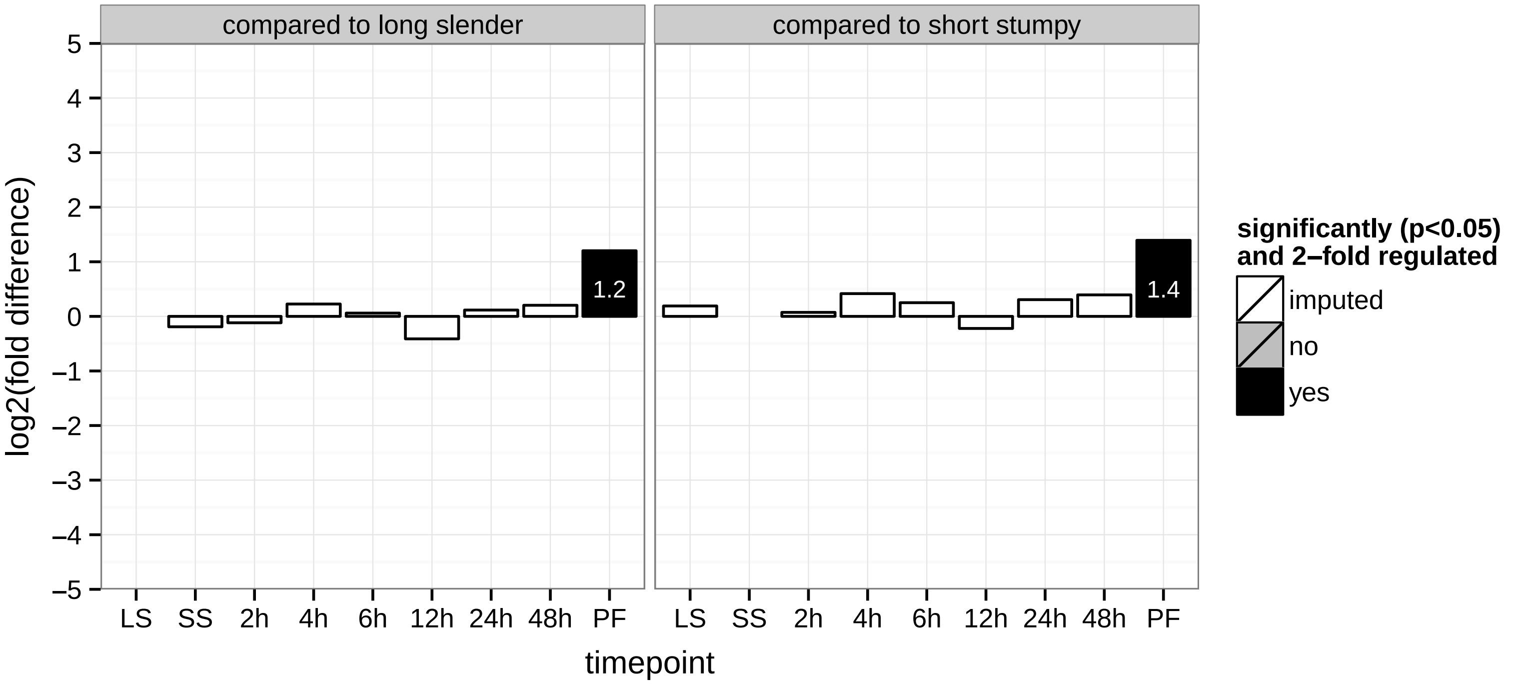
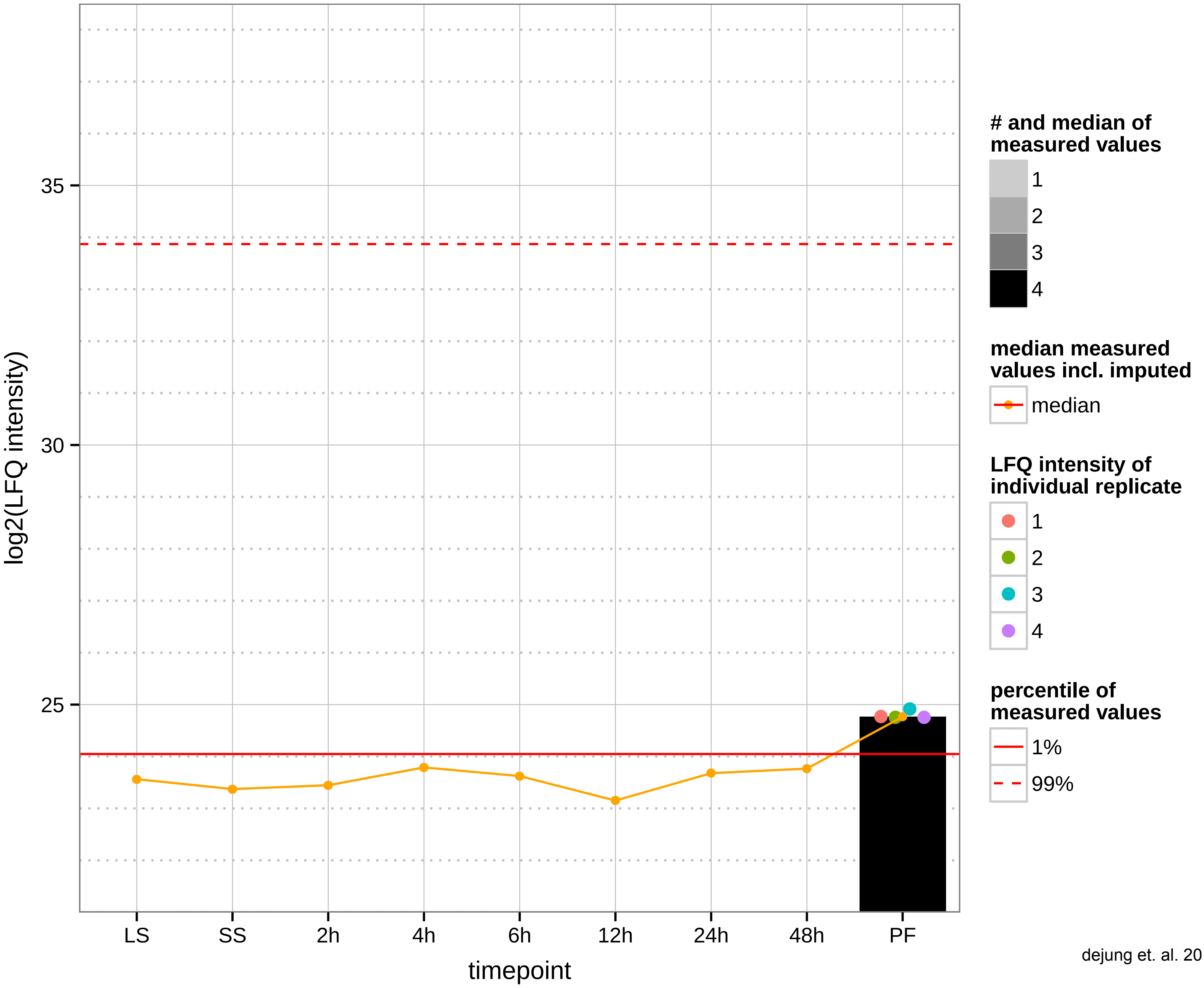
hypothetical protein, conserved
Tb927.4.3080;Tb11.v5.0963
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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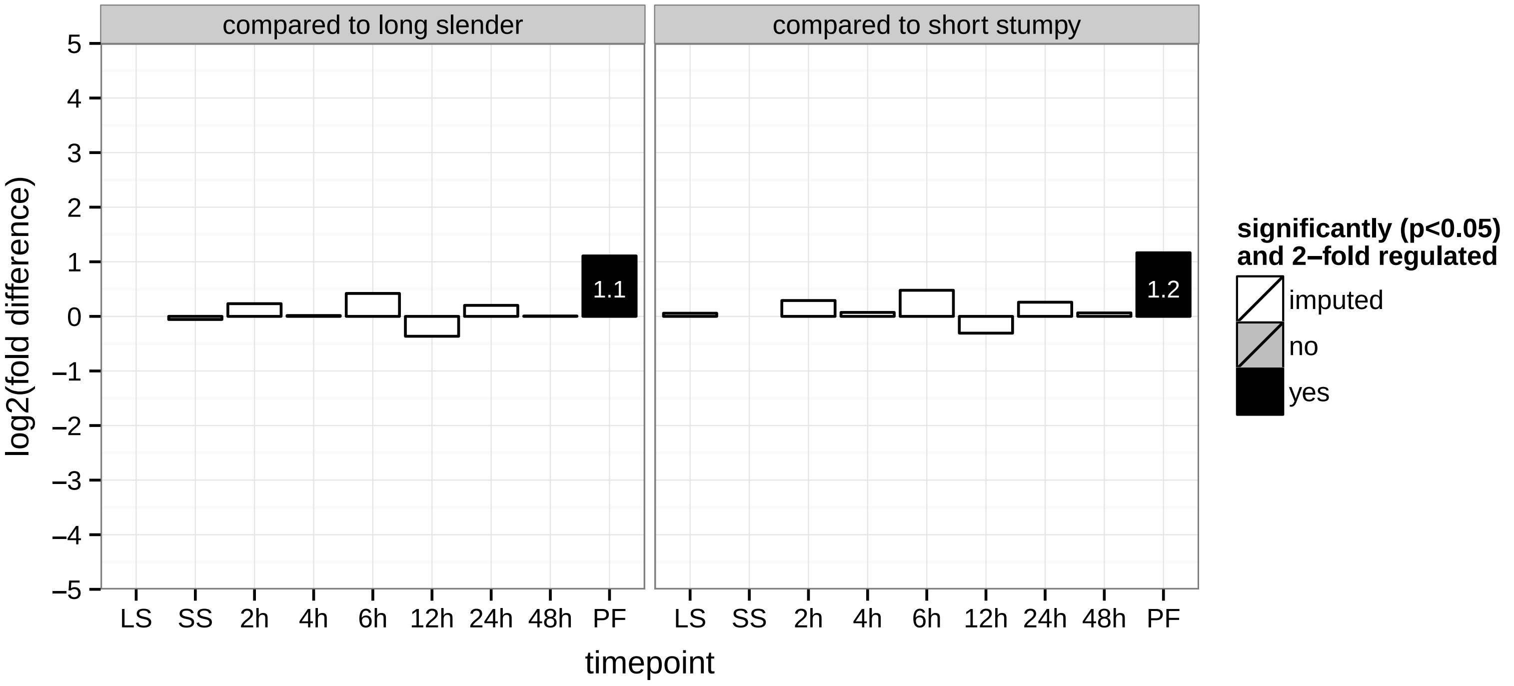
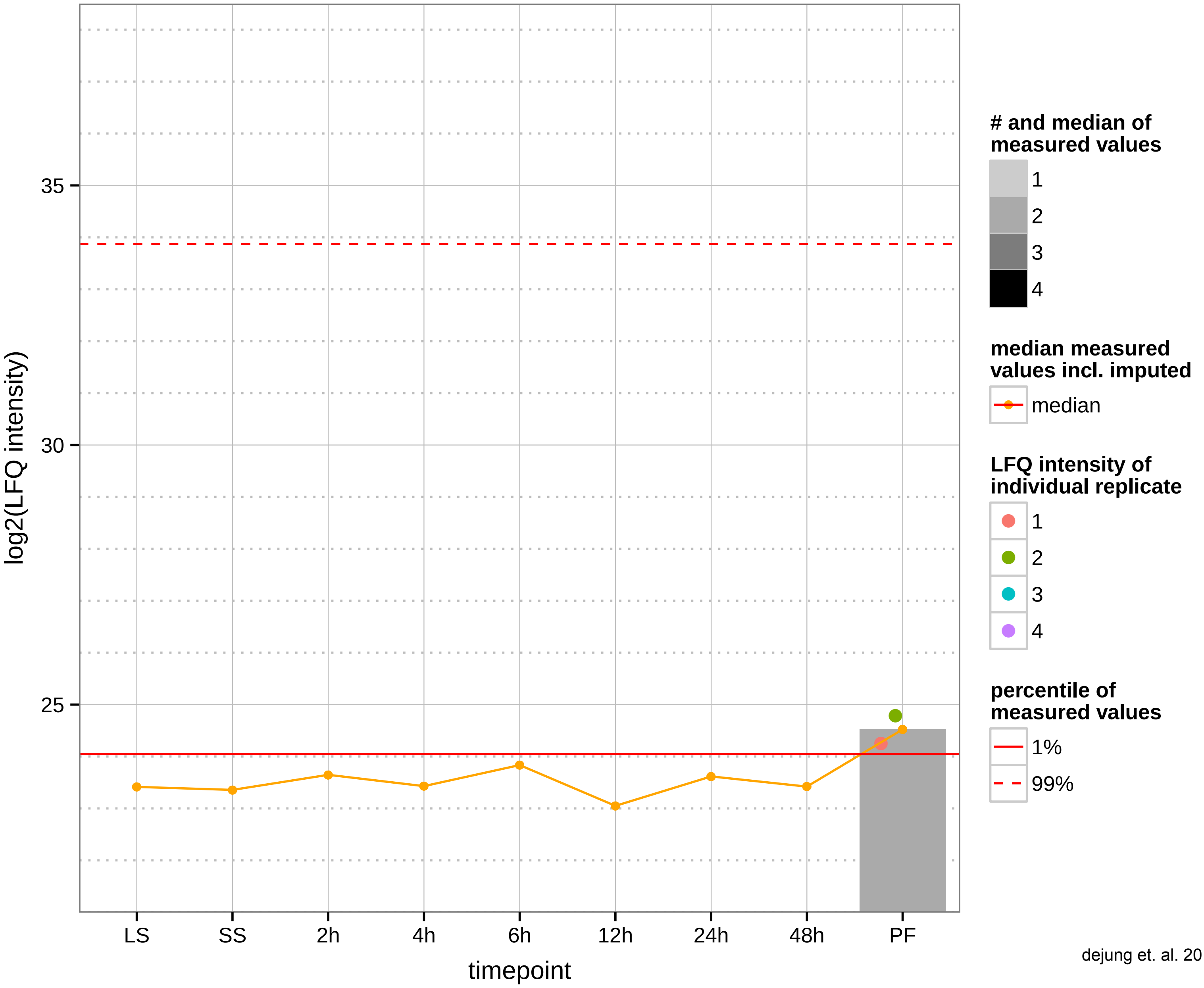
hypothetical protein, conserved
Tb927.4.2990;Tb11.v5.0968
AGOF: null, phosphorus–oxygen lyase activity
AGOC: null
AGOP: null, cyclic nucleotide biosynthetic process, intracellular signal transduction
PGOF: phosphorus–oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction





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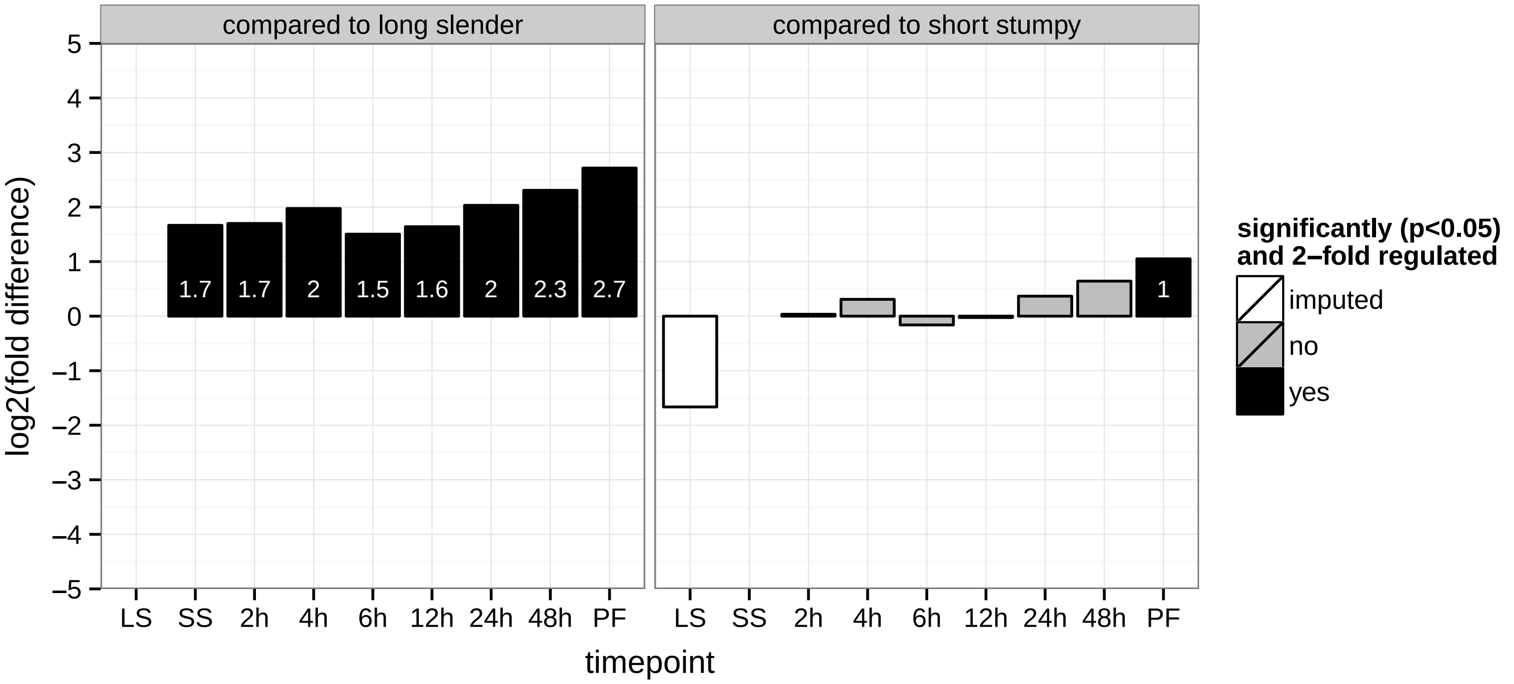
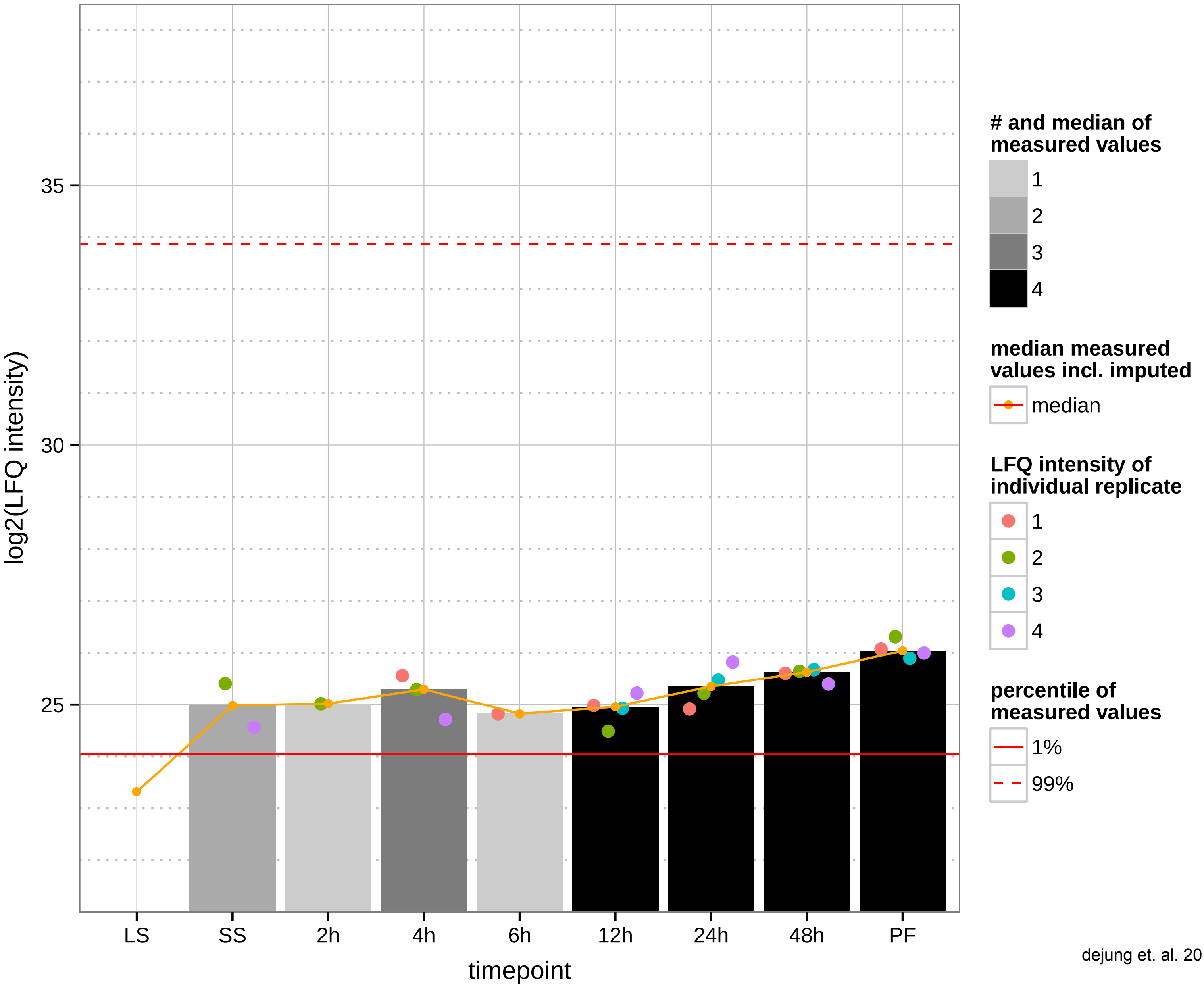
protein kinase, putative
Tb927.10.3340;Tb11.v5.1022
AGOF: null, ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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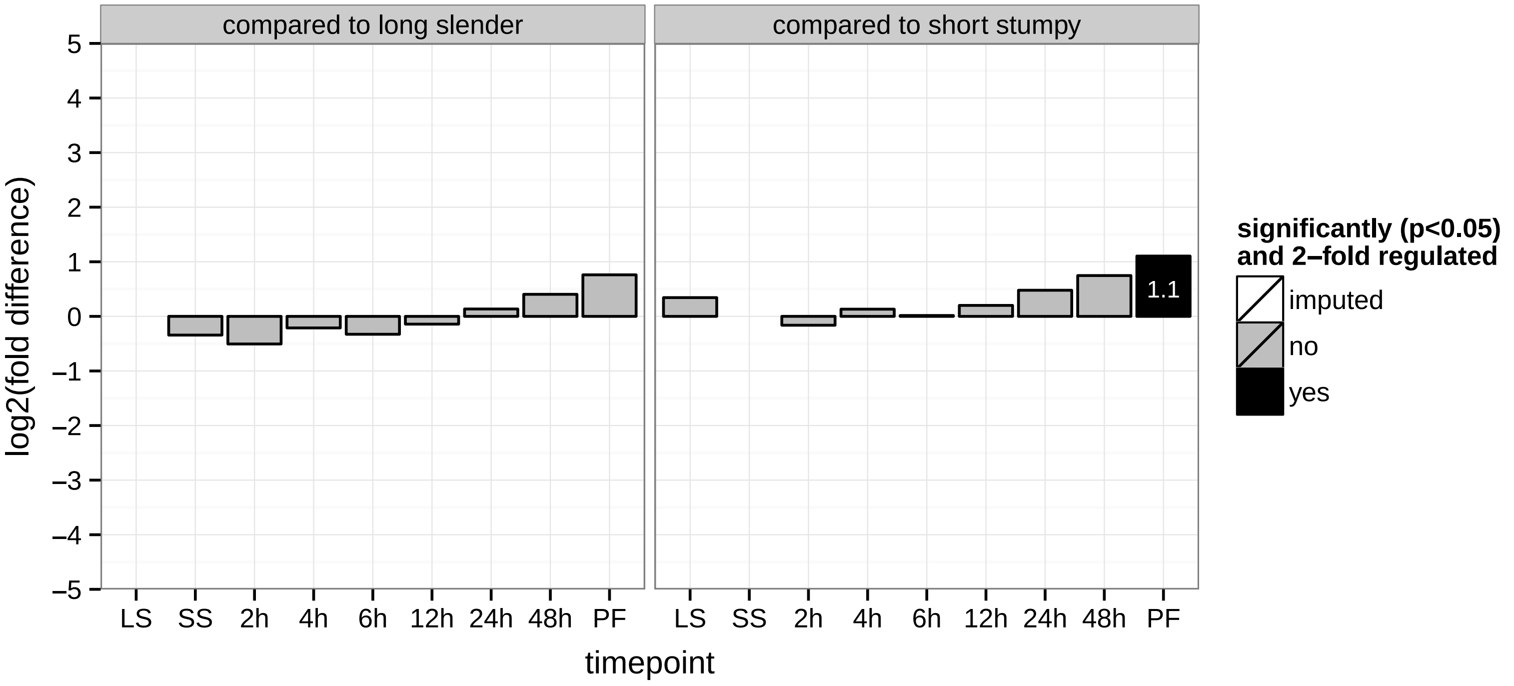
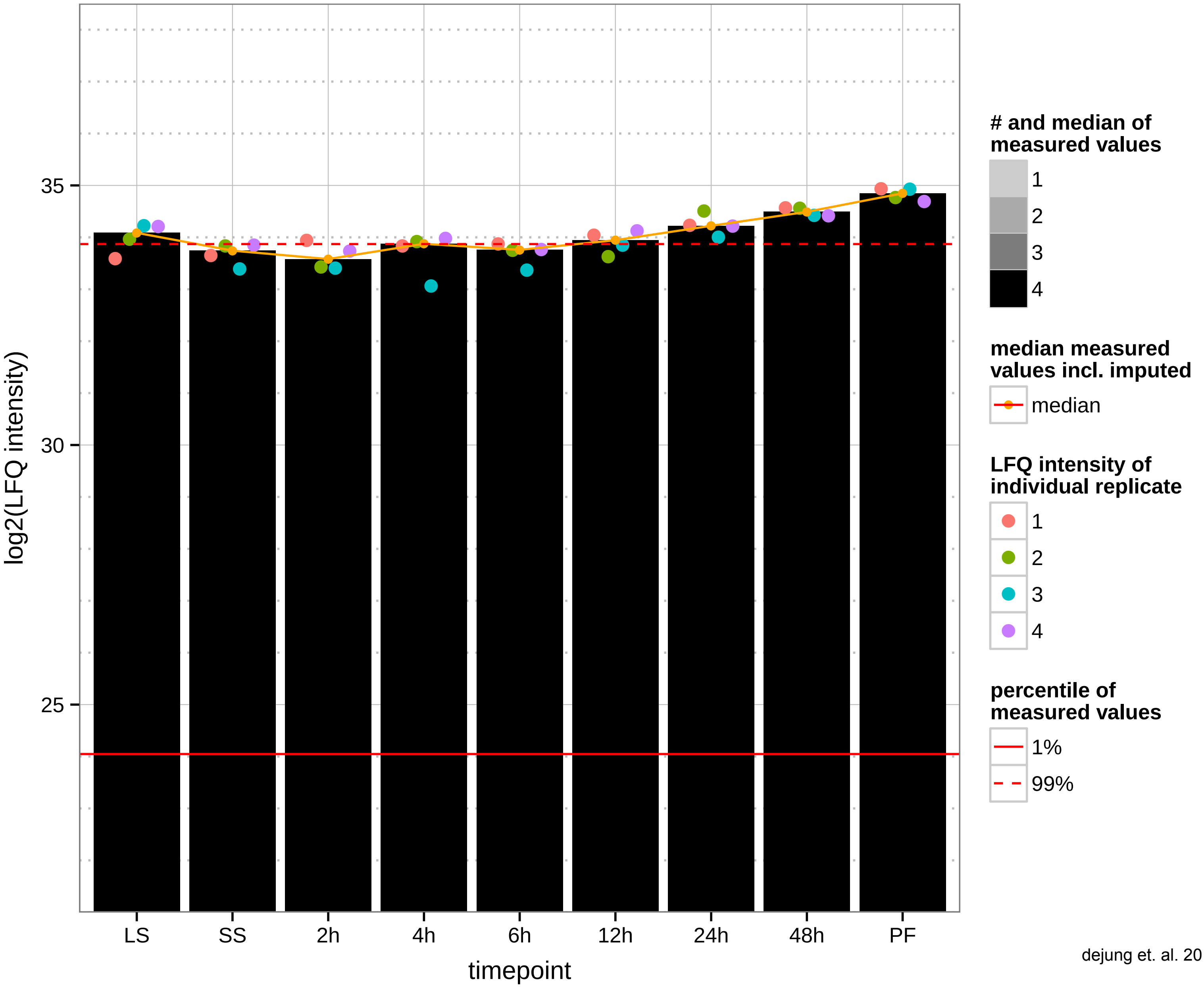
40S ribosomal protein S4, putative
Tb927.11.3600;Tb927.11.3590;Tb11.v5.1059
AGOF: null, RNA binding, structural constituent of ribosome
AGOC: null, intracellular, ribosome
AGOP: null, translation
PGOF: RNA binding, structural constituent of ribosome, null
PGOC: intracellular, ribosome, null
PGOP: translation, null





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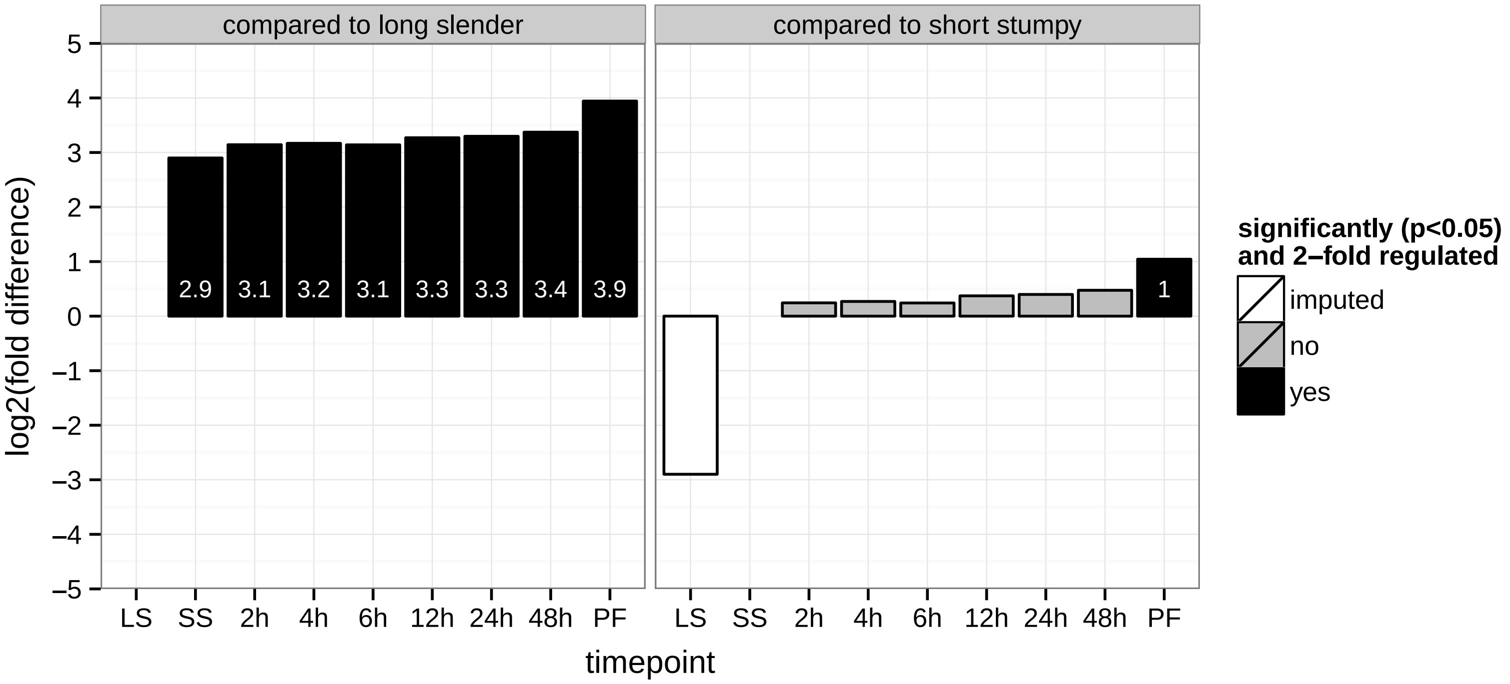
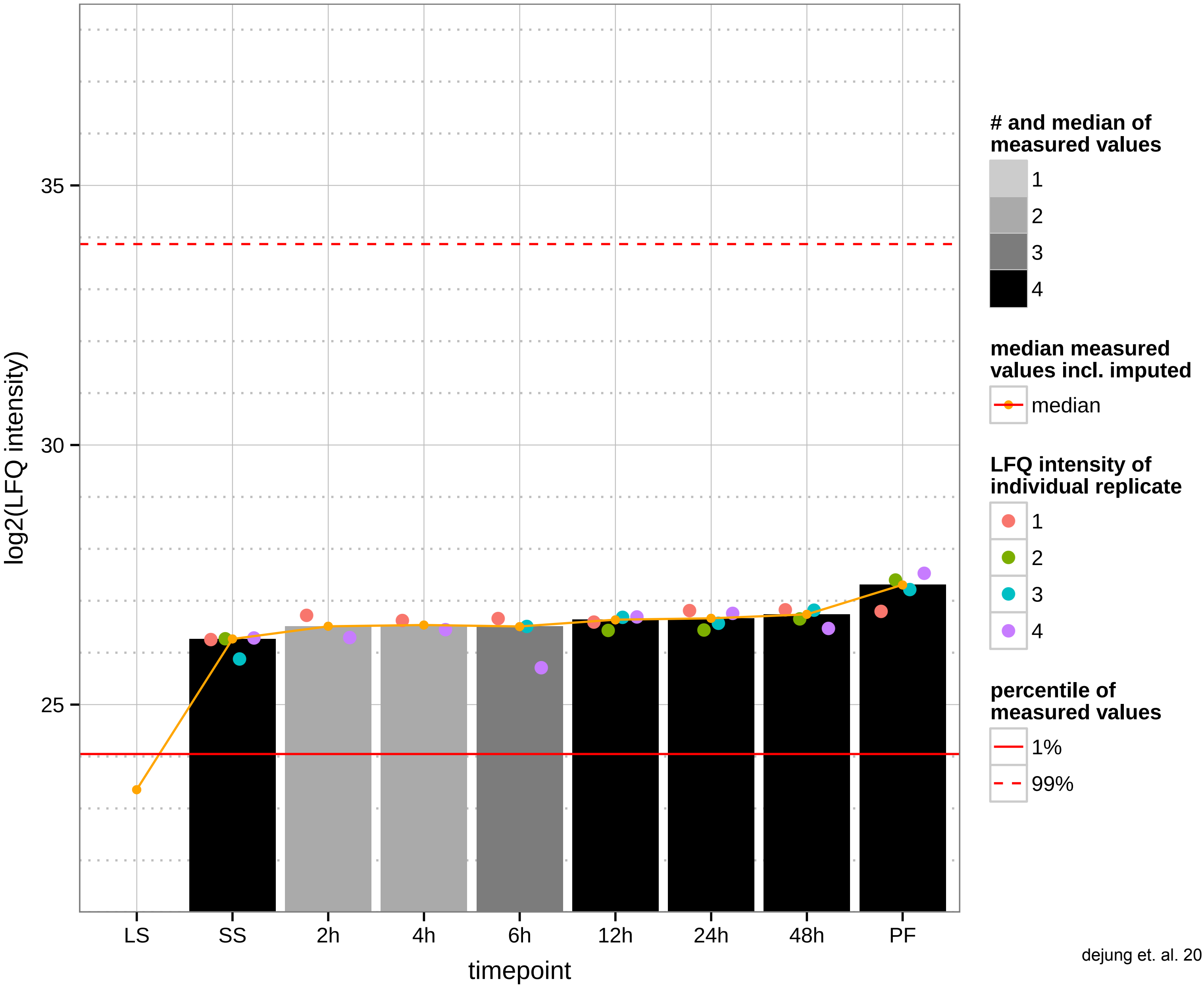
Tubulin/FtsZ family, putative
Tb927.1.1540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: protein complex
PGOP: protein polymerization





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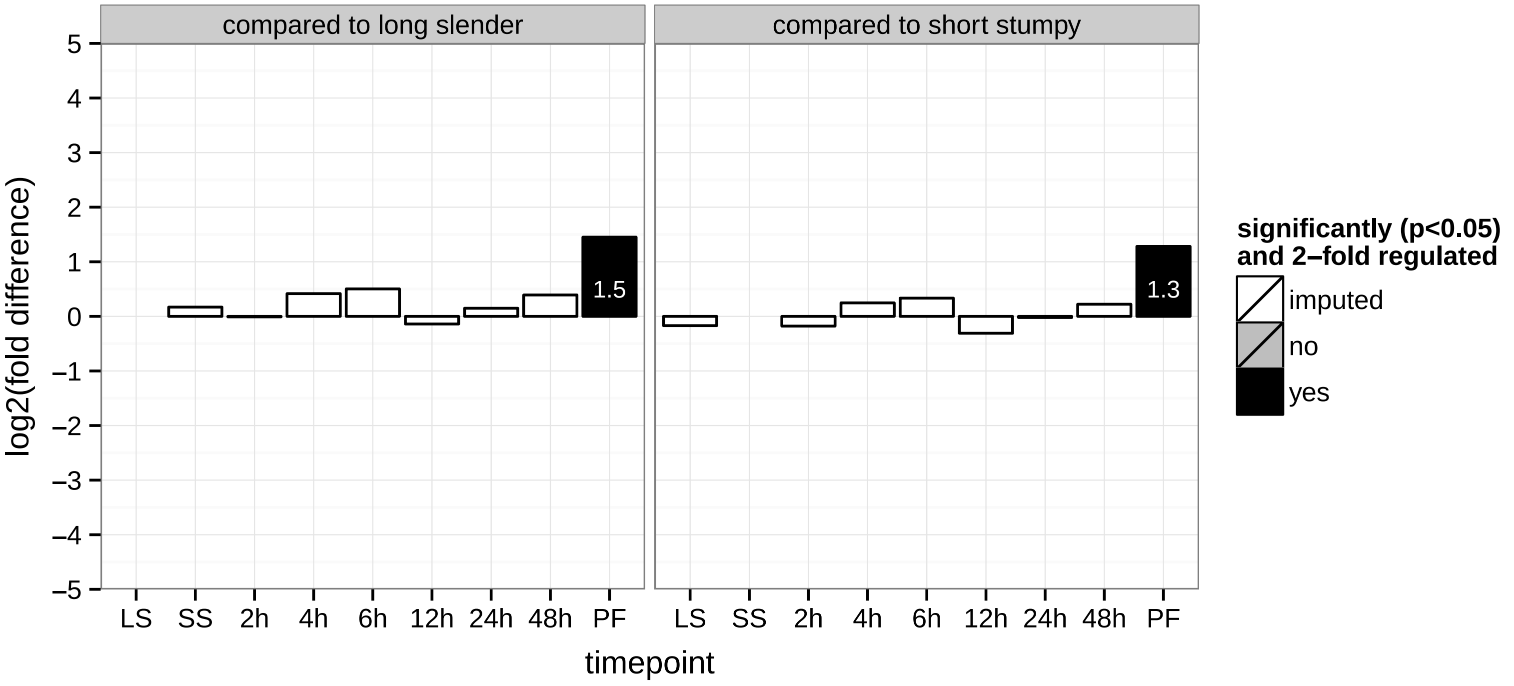
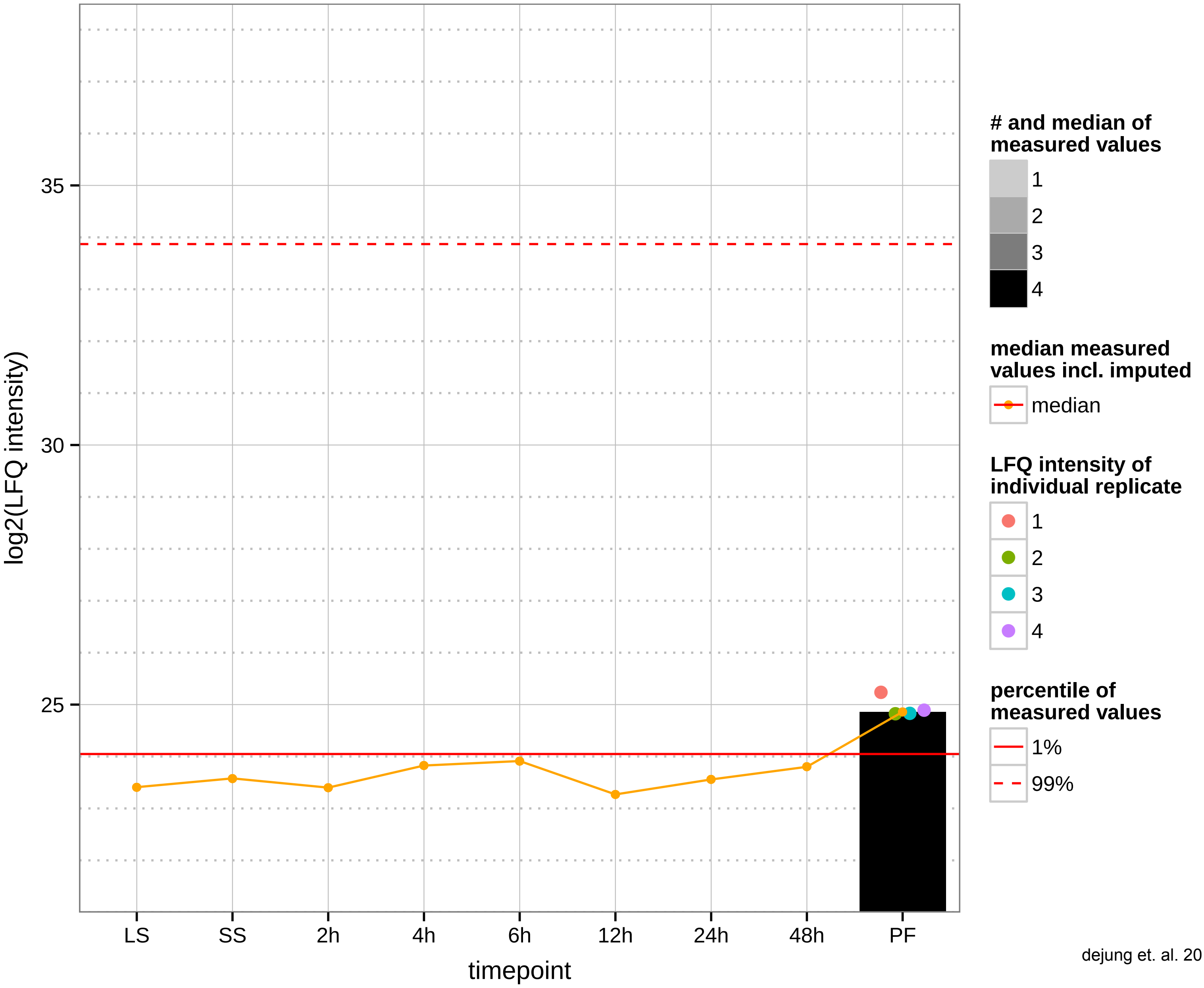
tubulin–tyrosine ligase, putative
Tb927.1.1550
AGOF: tubulin–tyrosine ligase activity
AGOC: null
AGOP: cellular protein modification process
PGOF: tubulin–tyrosine ligase activity
PGOC: null
PGOP: cellular protein modification process





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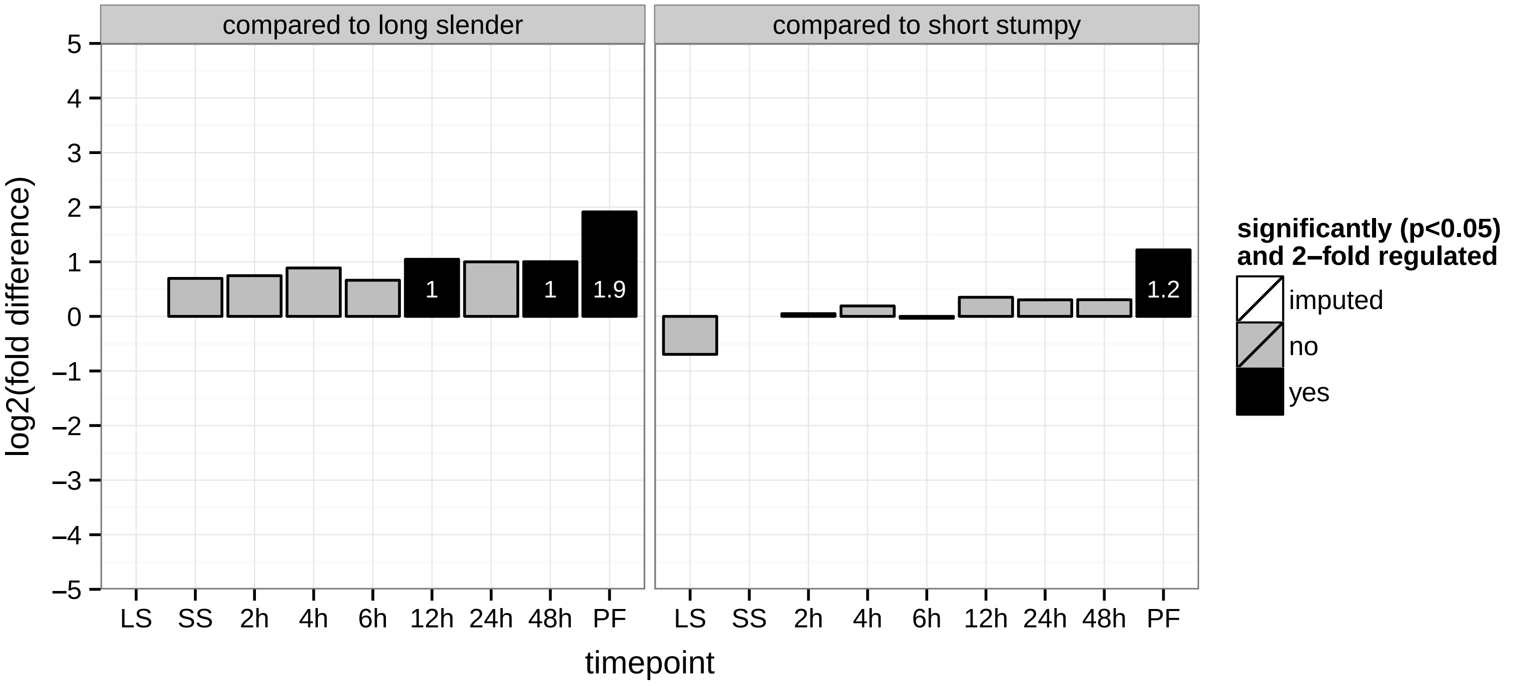
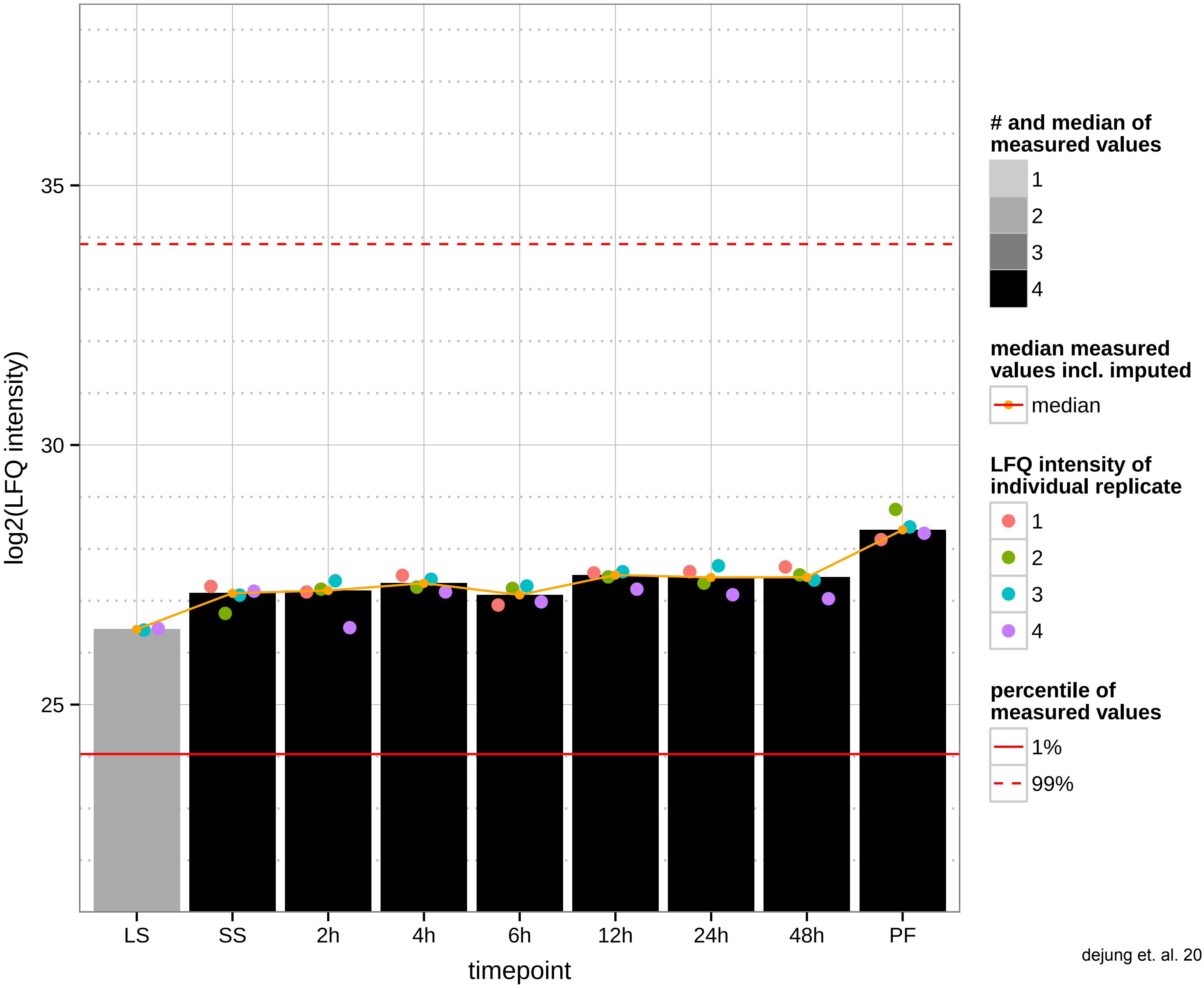
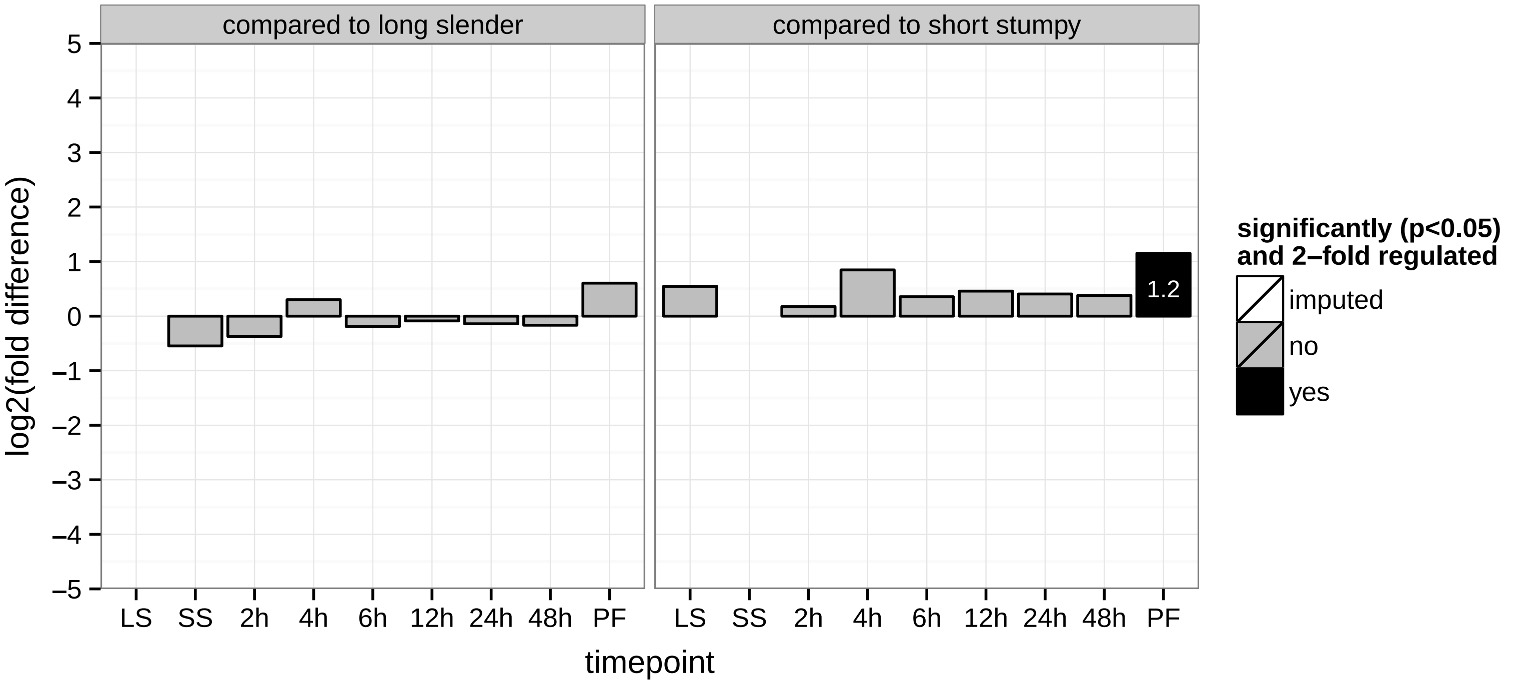
RNasePH–like protein, exosome–associated protein 1, Rrp42 homologue (TbEAP1)
Tb927.1.2580
AGOF: 3'–5'–exoribonuclease activity, RNA binding
AGOC: null
AGOP: RNA processing
PGOF: null
PGOC: null
PGOP: null

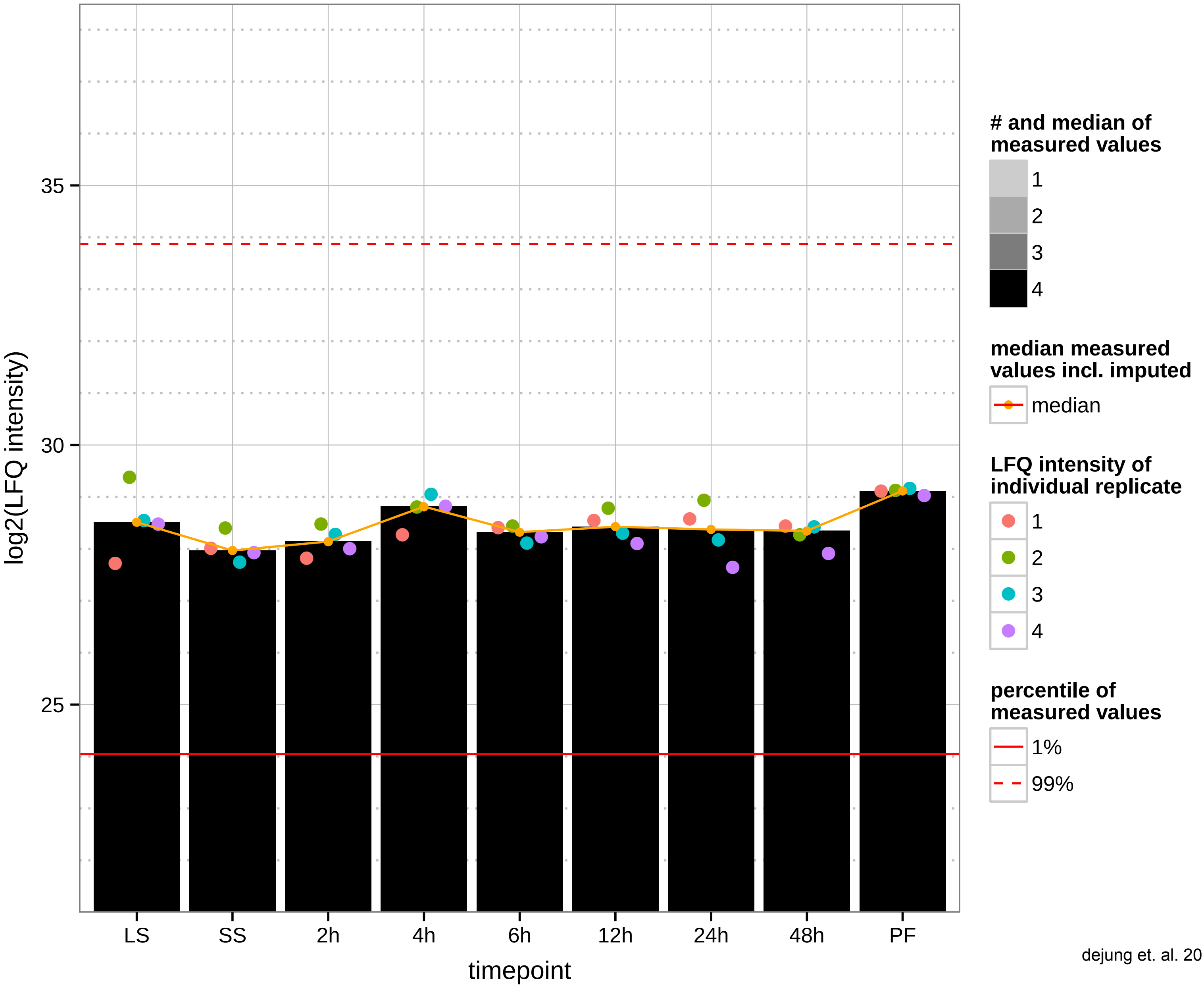




dejung et. al. 2015

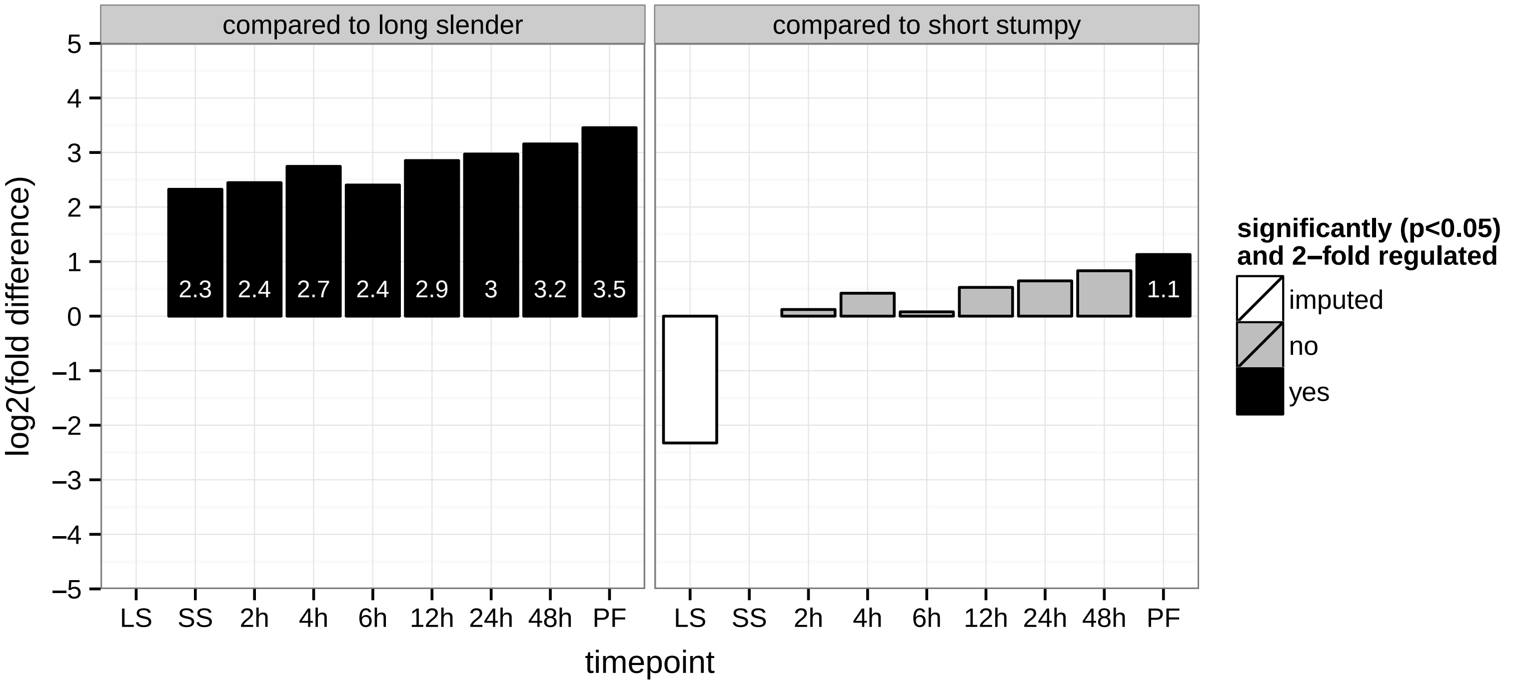
hypothetical protein, conserved
Tb927.1.2750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

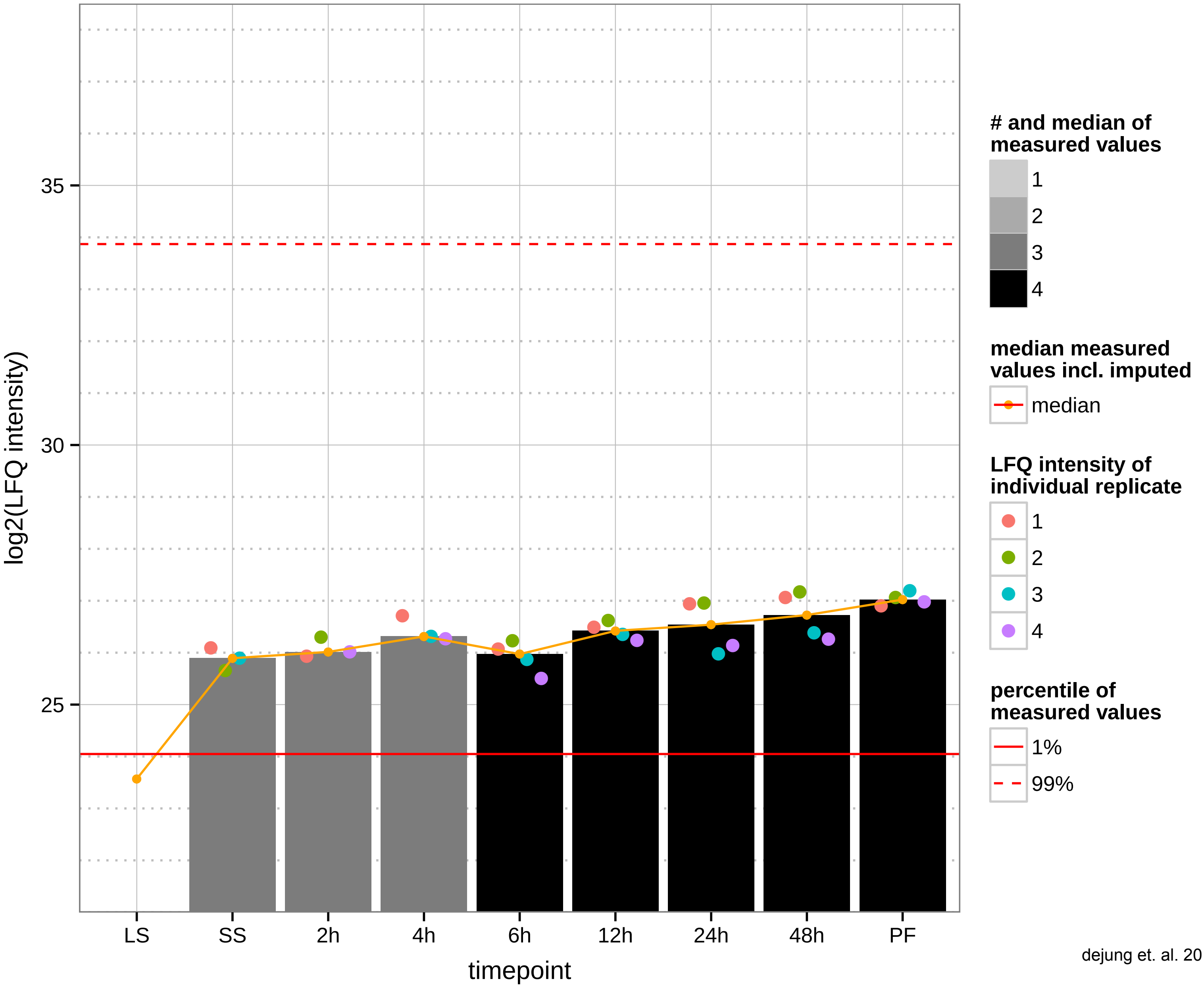




dejung et. al. 2015

mRNA processing protein, putative
Tb927.1.3010
AGOF: mRNA binding
AGOC: mitochondrion
AGOP: mRNA processing
PGOF: null
PGOC: null
PGOP: null





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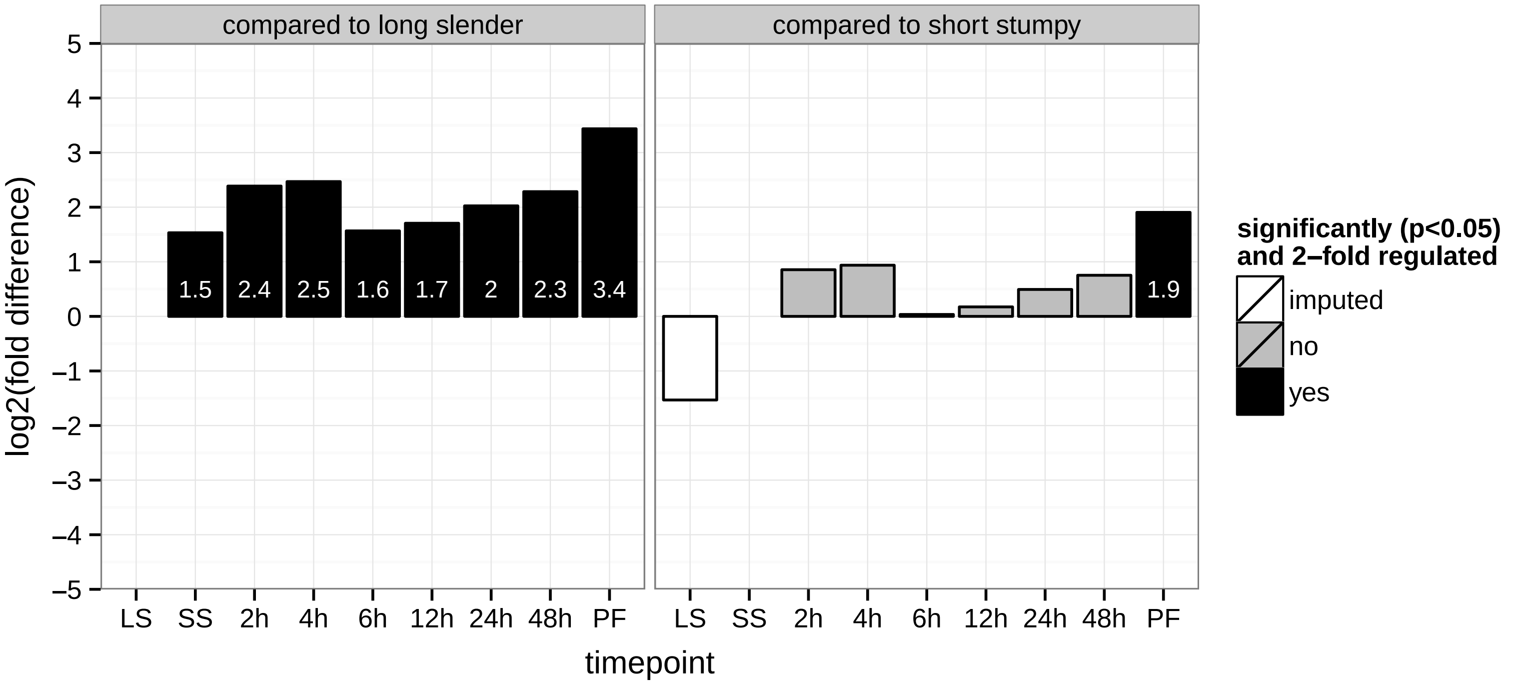
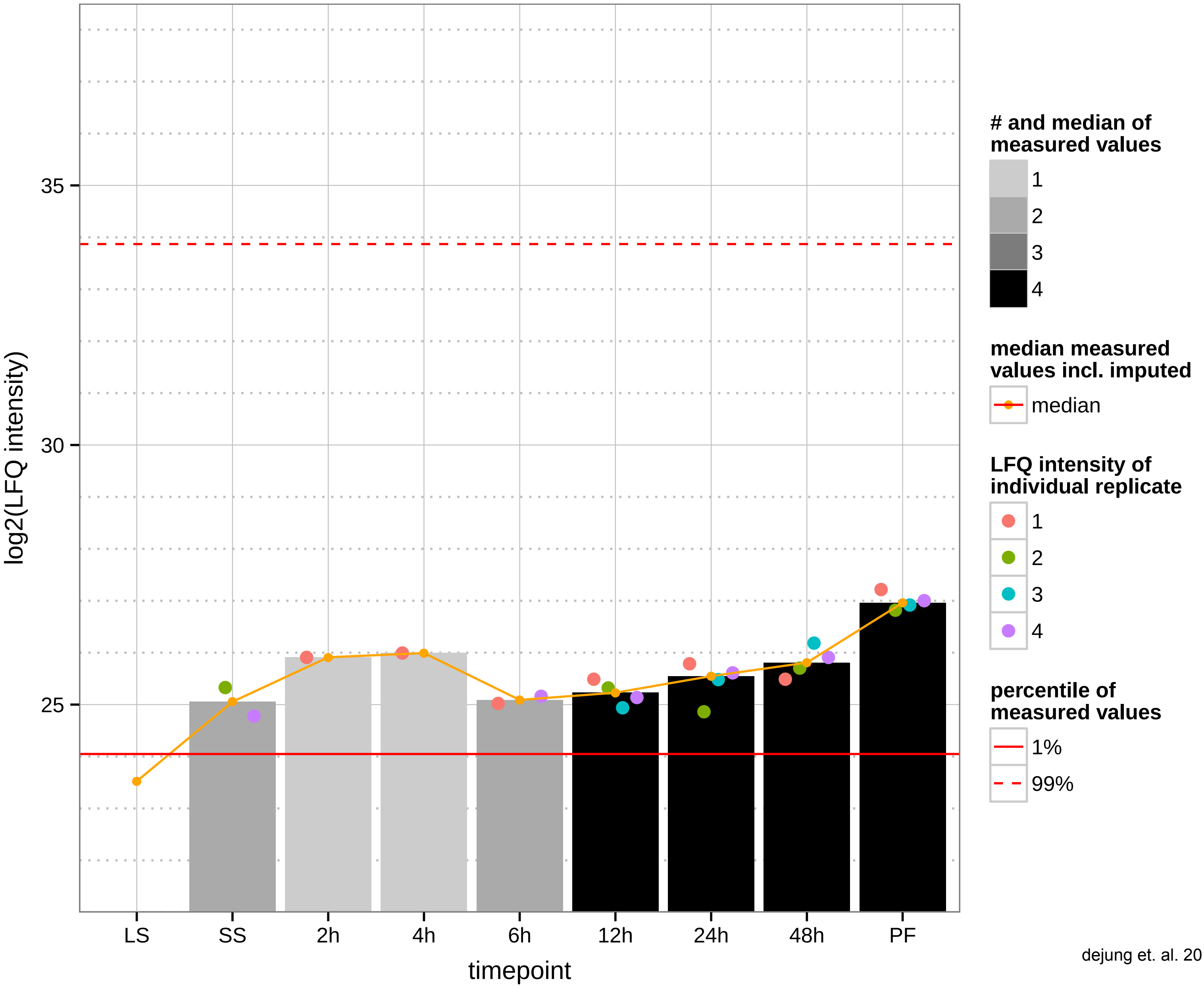
hypothetical protein, conserved
Tb927.1.3050
AGOF: methyltransferase activity
AGOC: null
AGOP: metabolic process
PGOF: RNA methyltransferase activity
PGOC: null
PGOP: RNA processing





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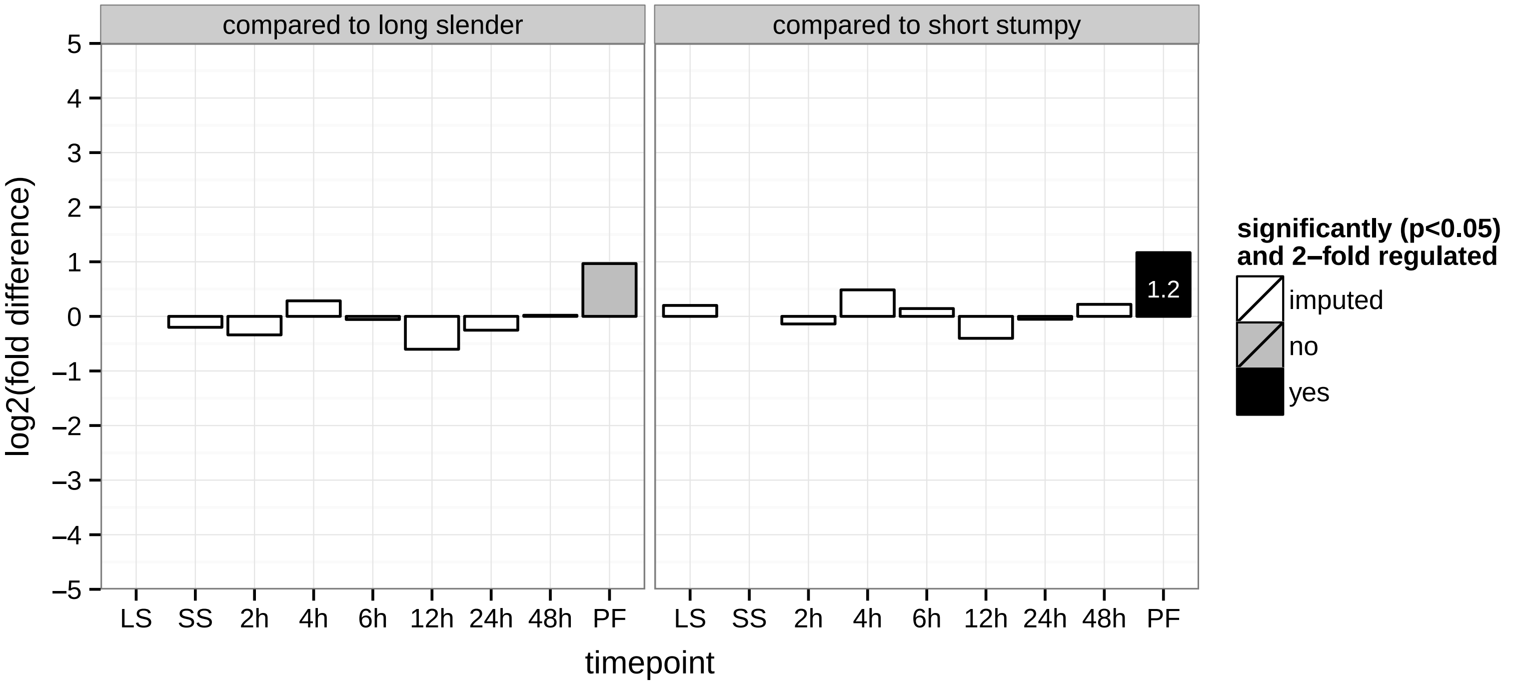
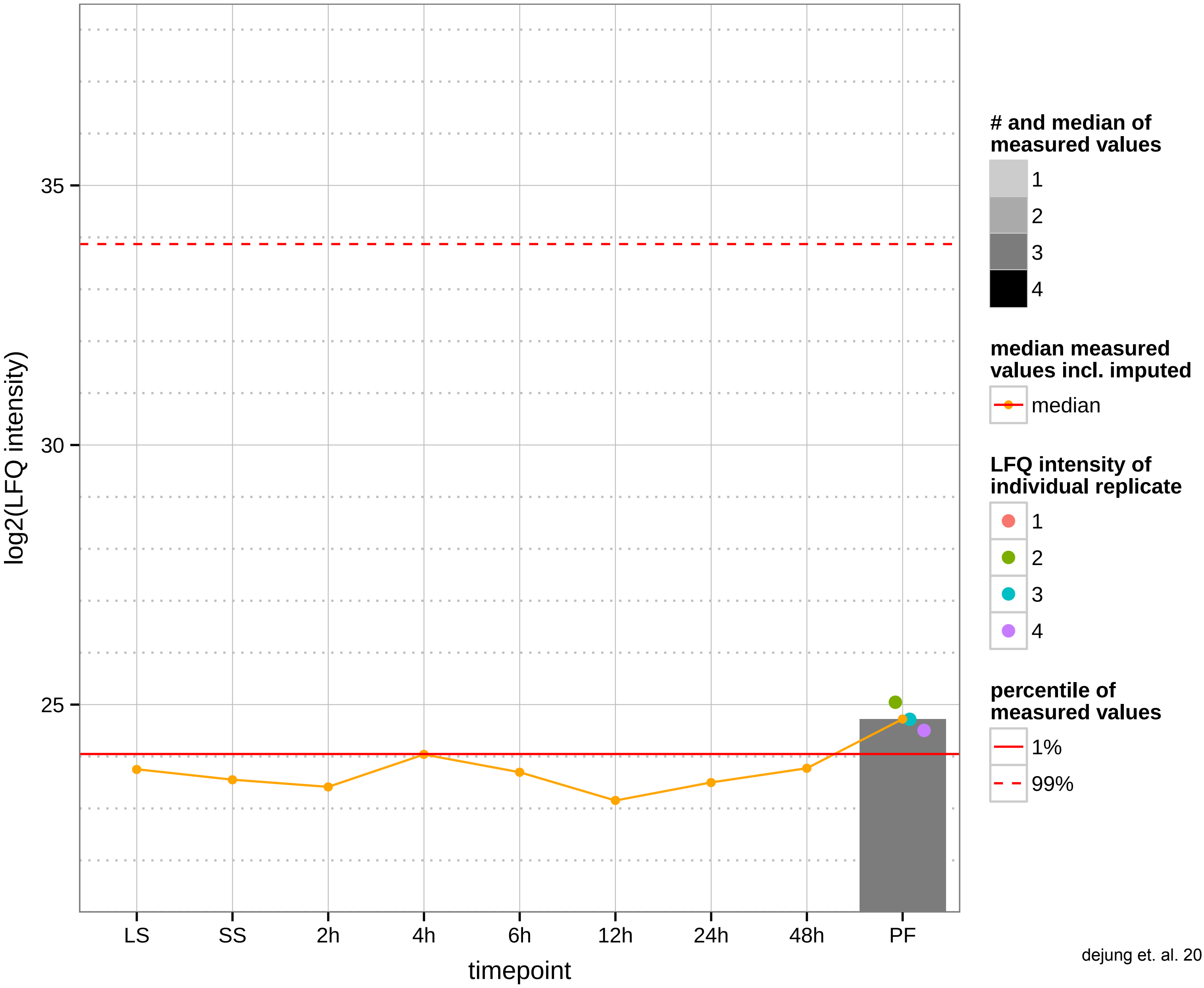
conserved protein, unknown function
Tb927.1.650
AGOF: null
AGOC: null
AGOP: chromatin organization
PGOF: null
PGOC: null
PGOP: null





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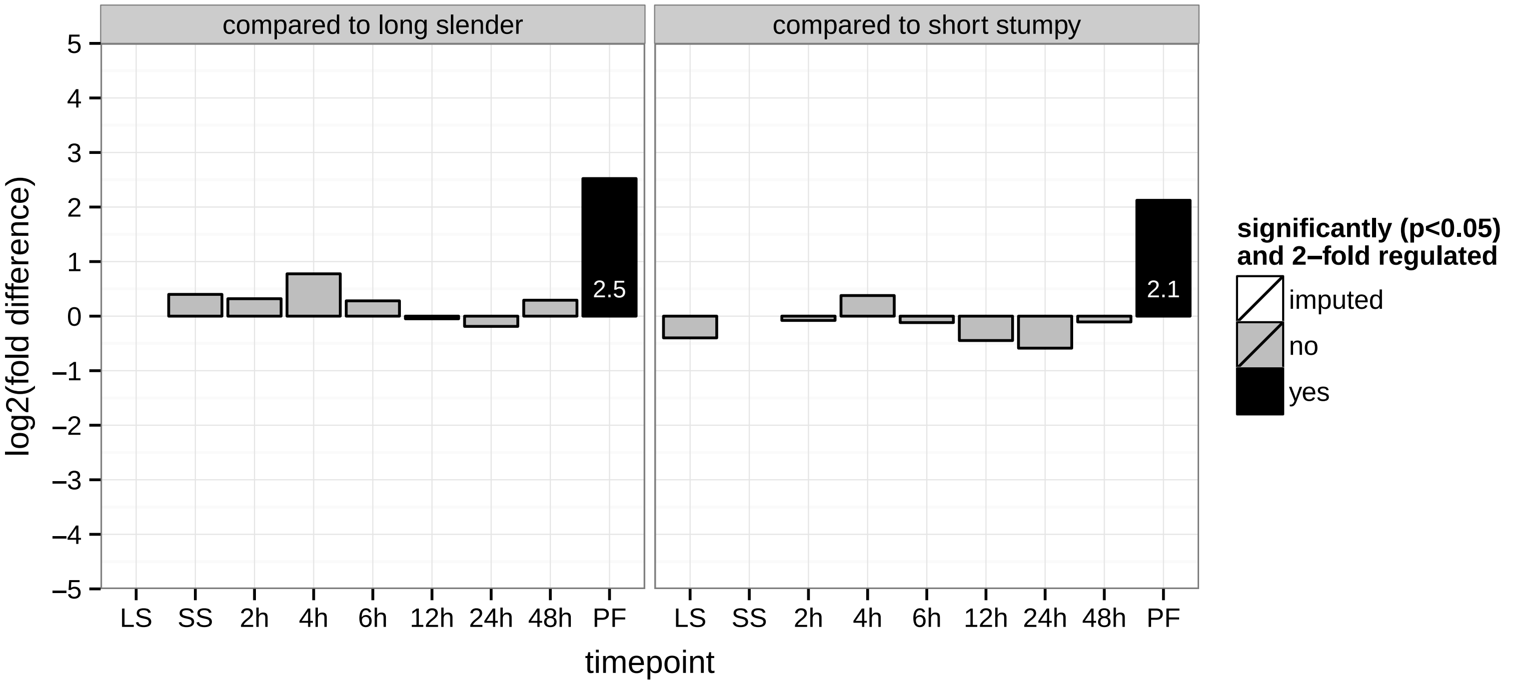
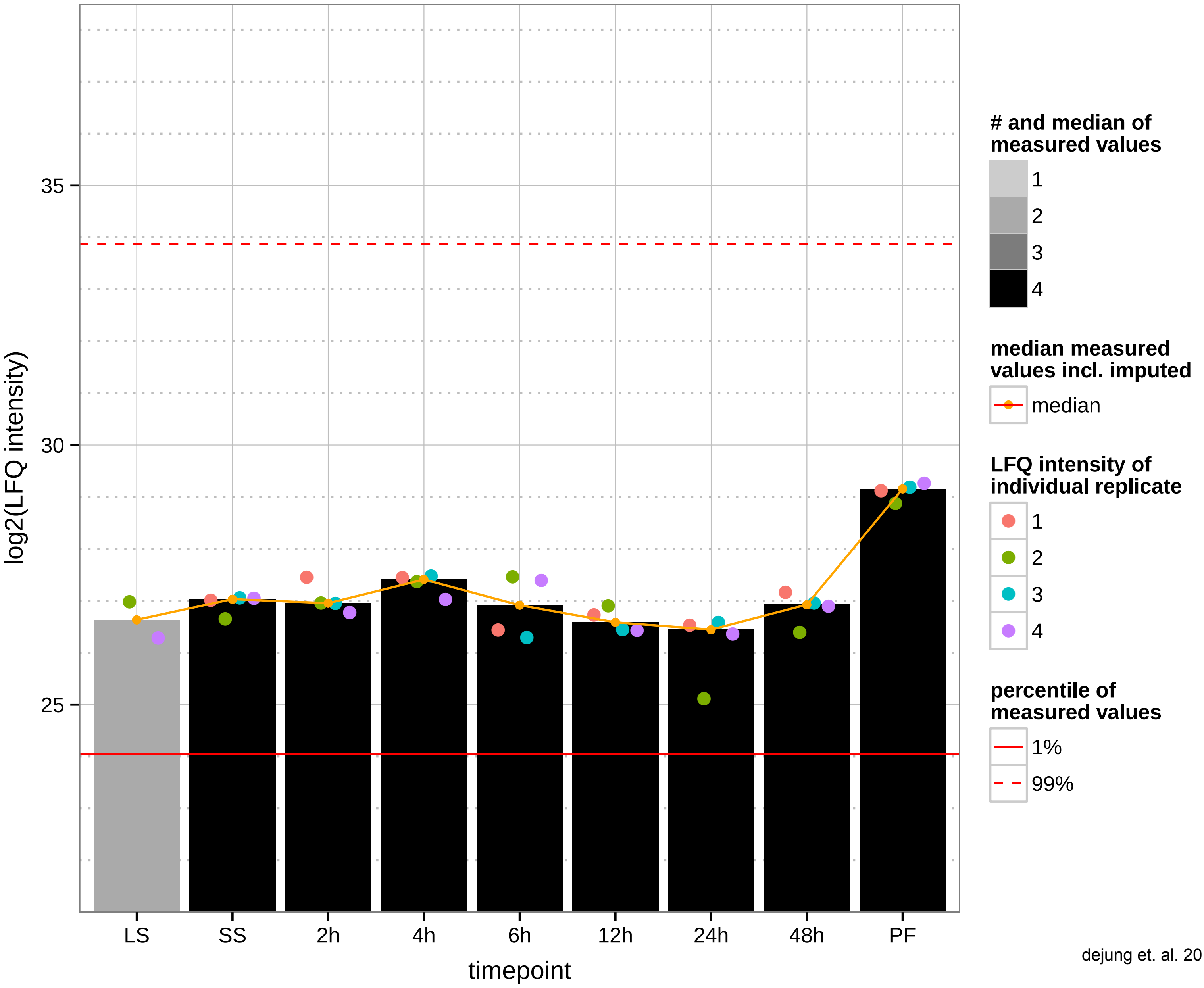
phosphoglycerate kinase (PGKA)
Tb927.1.720
AGOF: phosphoglycerate kinase activity
AGOC: glycosome
AGOP: glycolysis
PGOF: phosphoglycerate kinase activity
PGOC: null
PGOP: glycolysis





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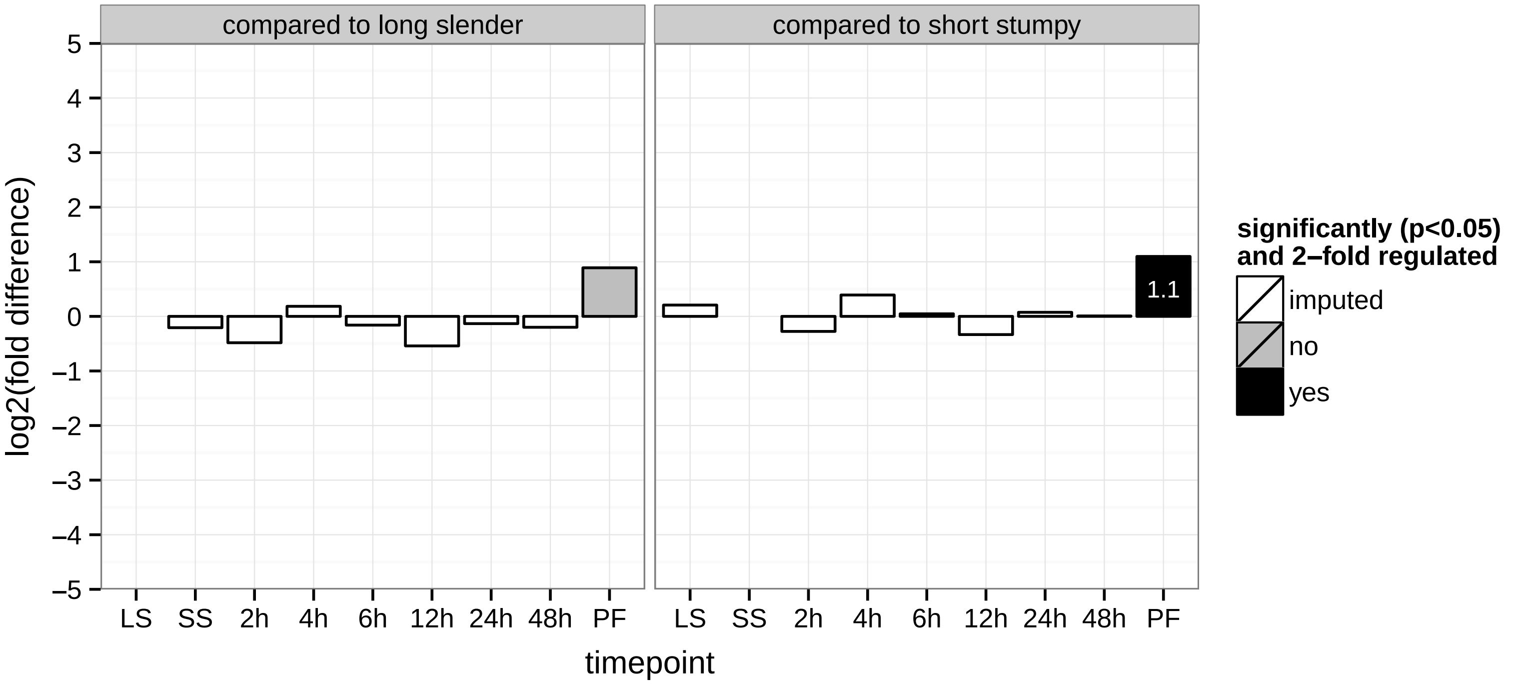
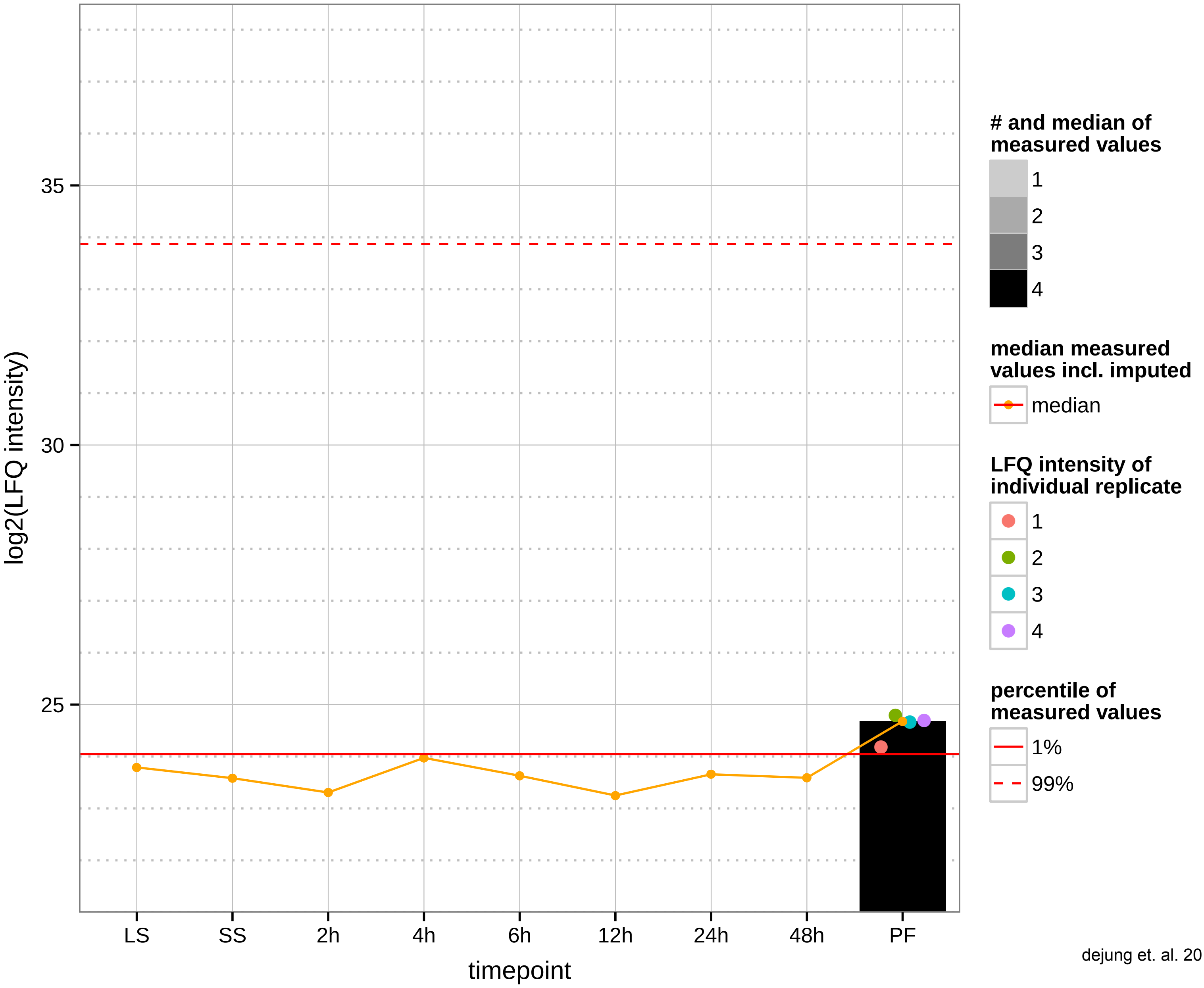
predicted WD40 repeat protein
Tb927.10.10170
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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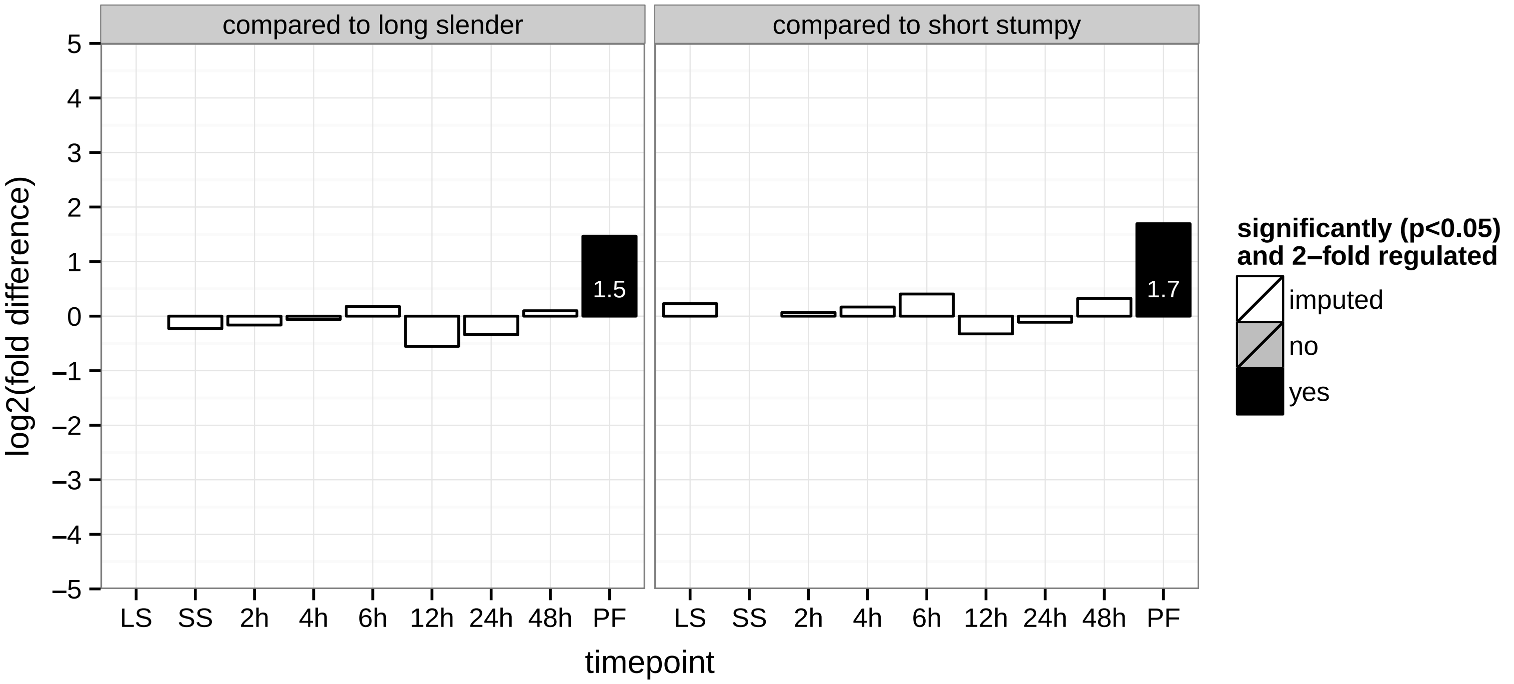
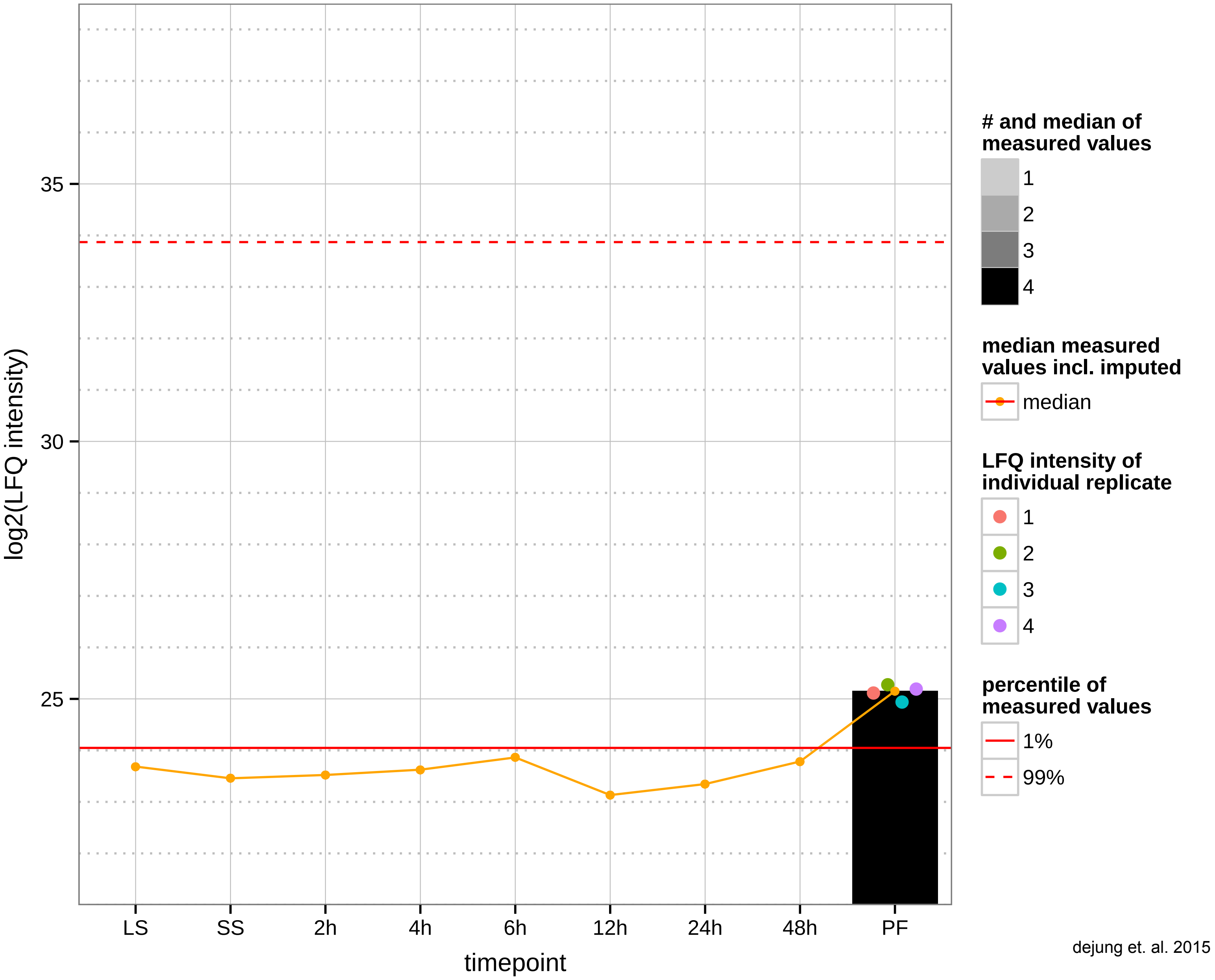
hypothetical protein, conserved
Tb927.10.10690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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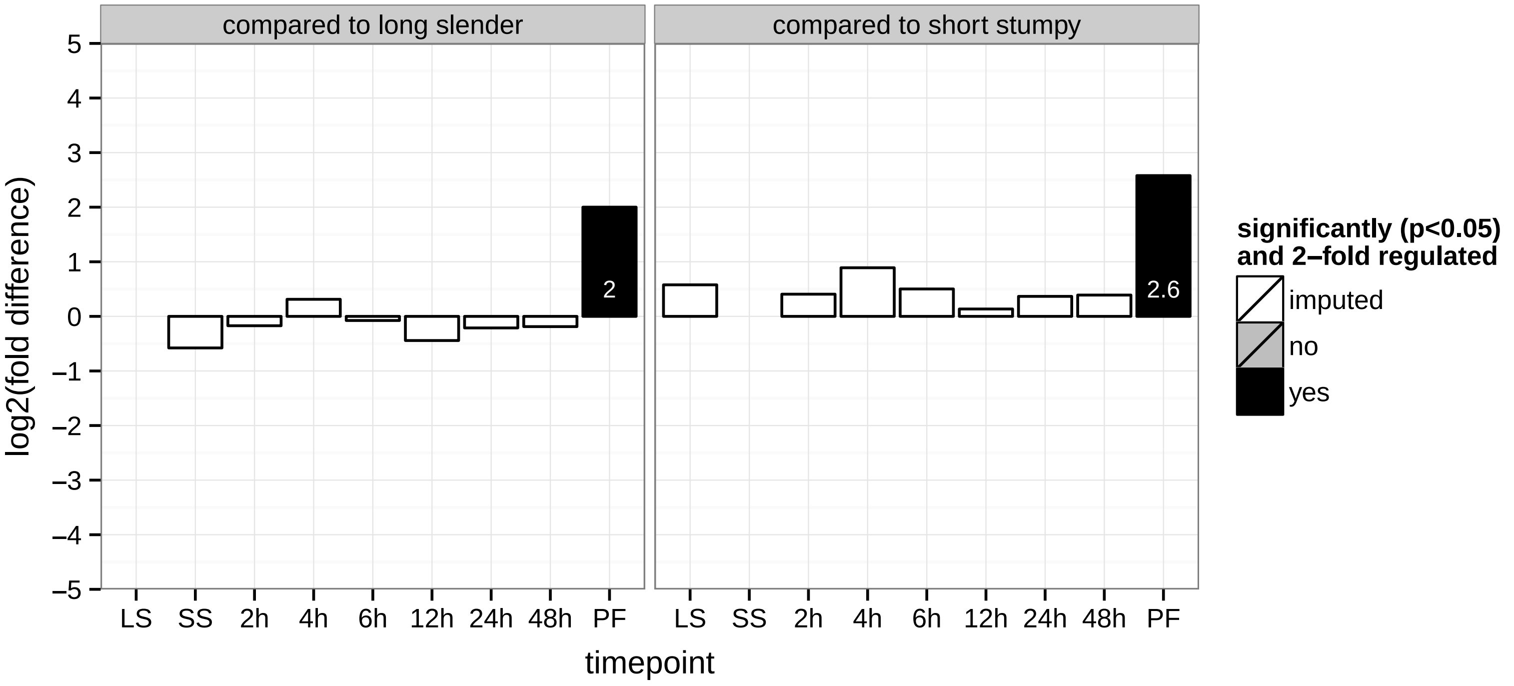
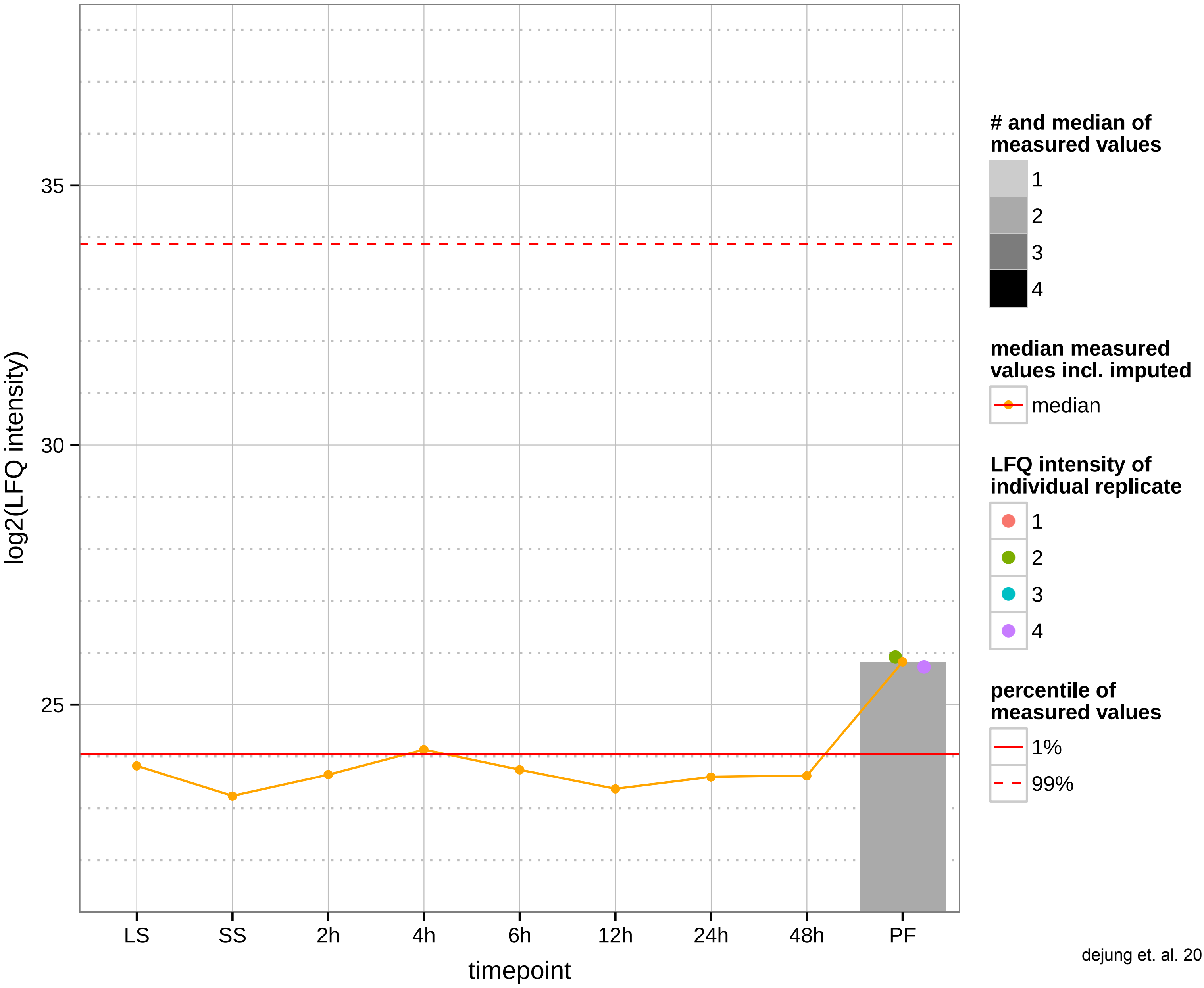
hypothetical protein, conserved
Tb927.10.11230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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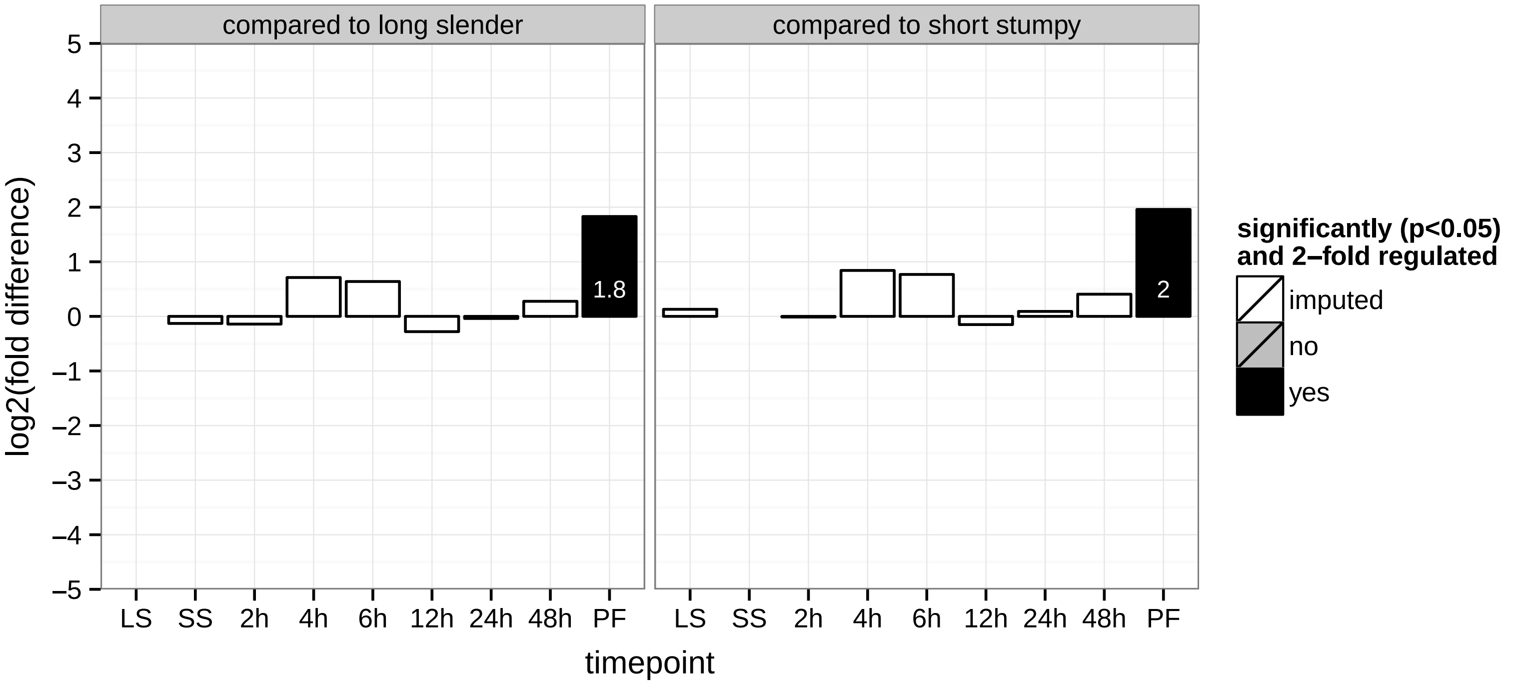
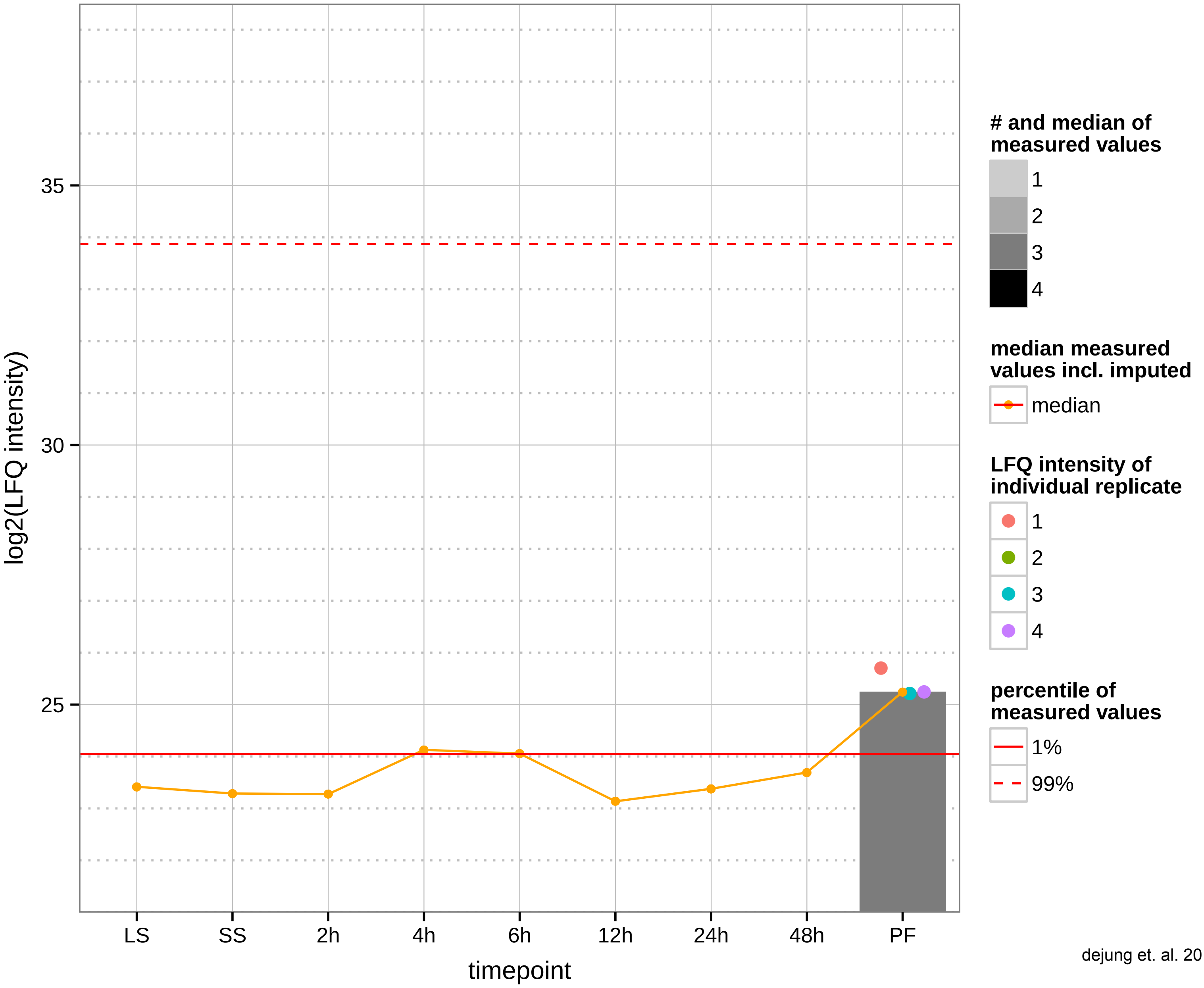
hypothetical protein, conserved
Tb927.10.11340;Tb11.v5.0604
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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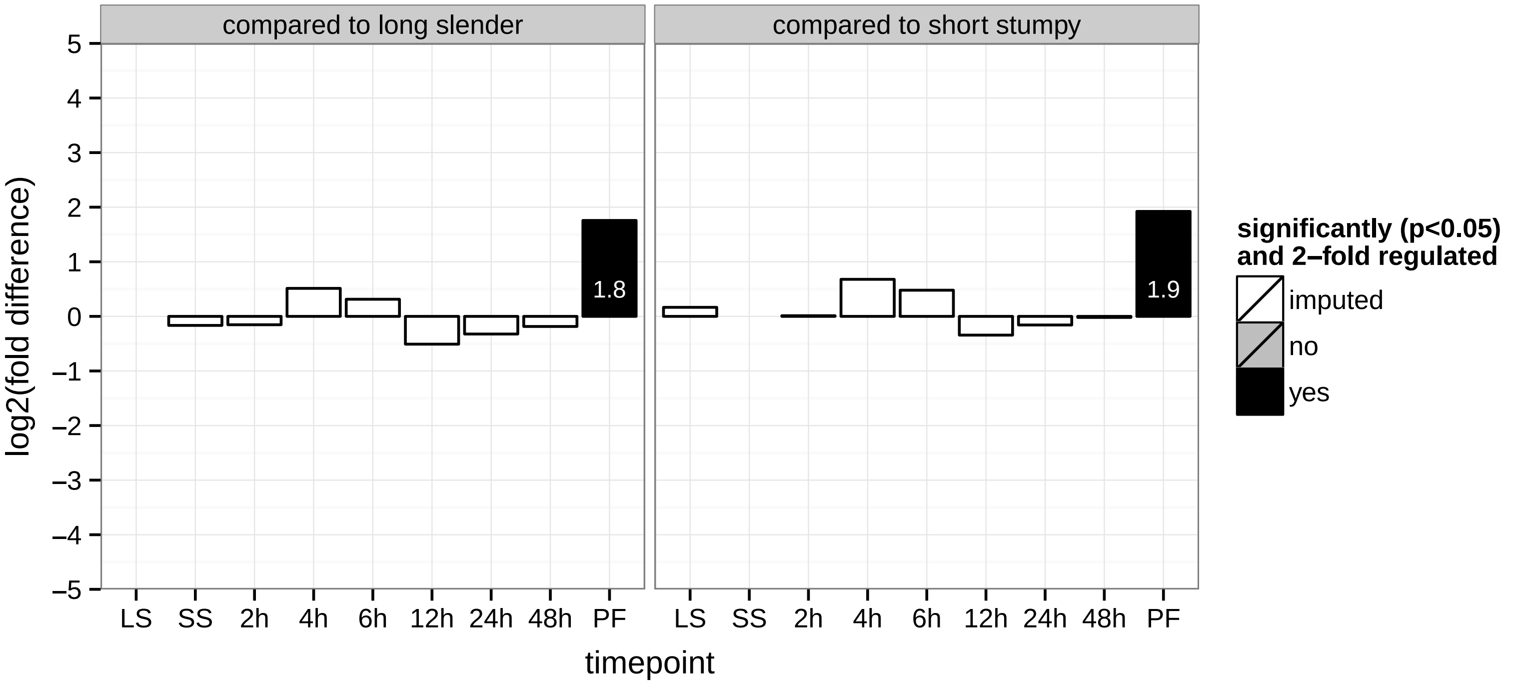
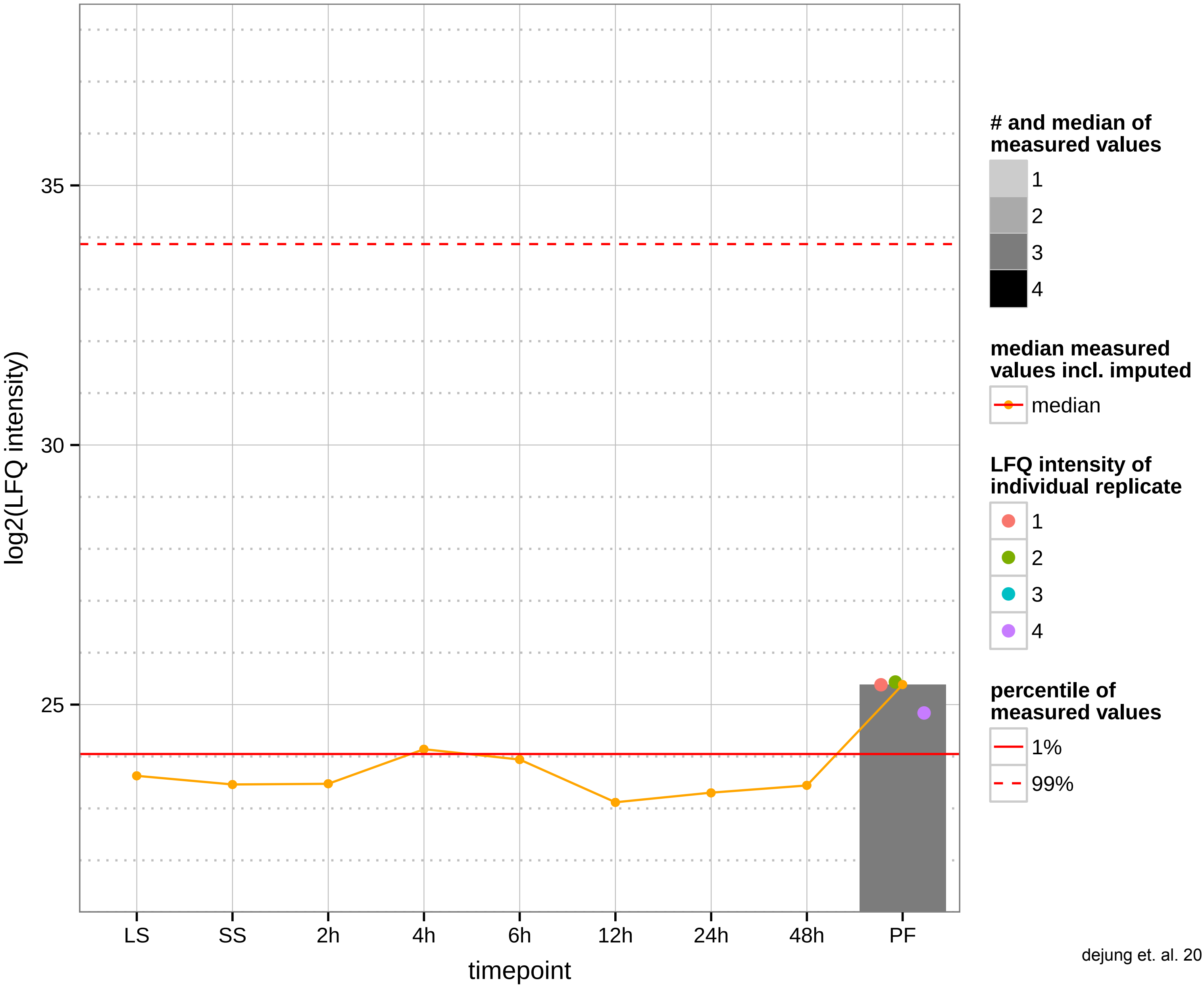
hypothetical protein, conserved
Tb927.10.11410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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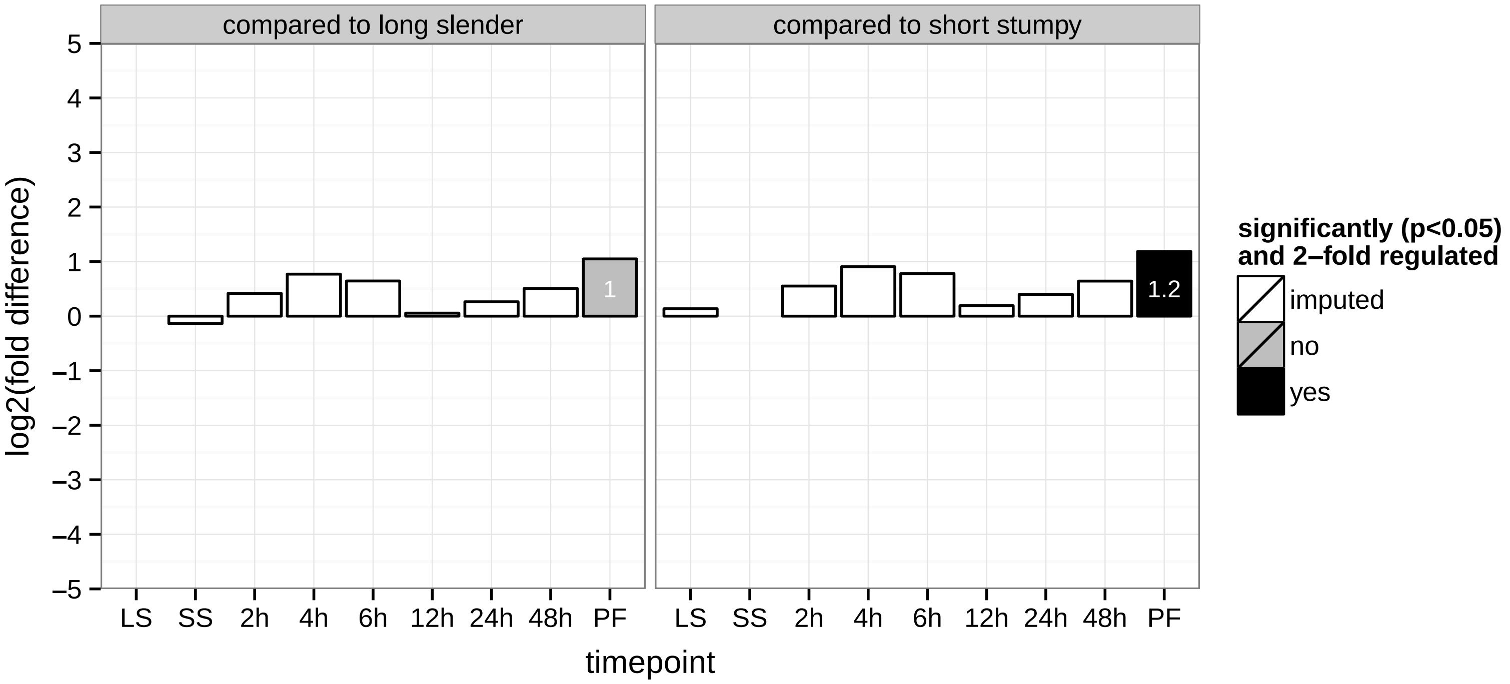
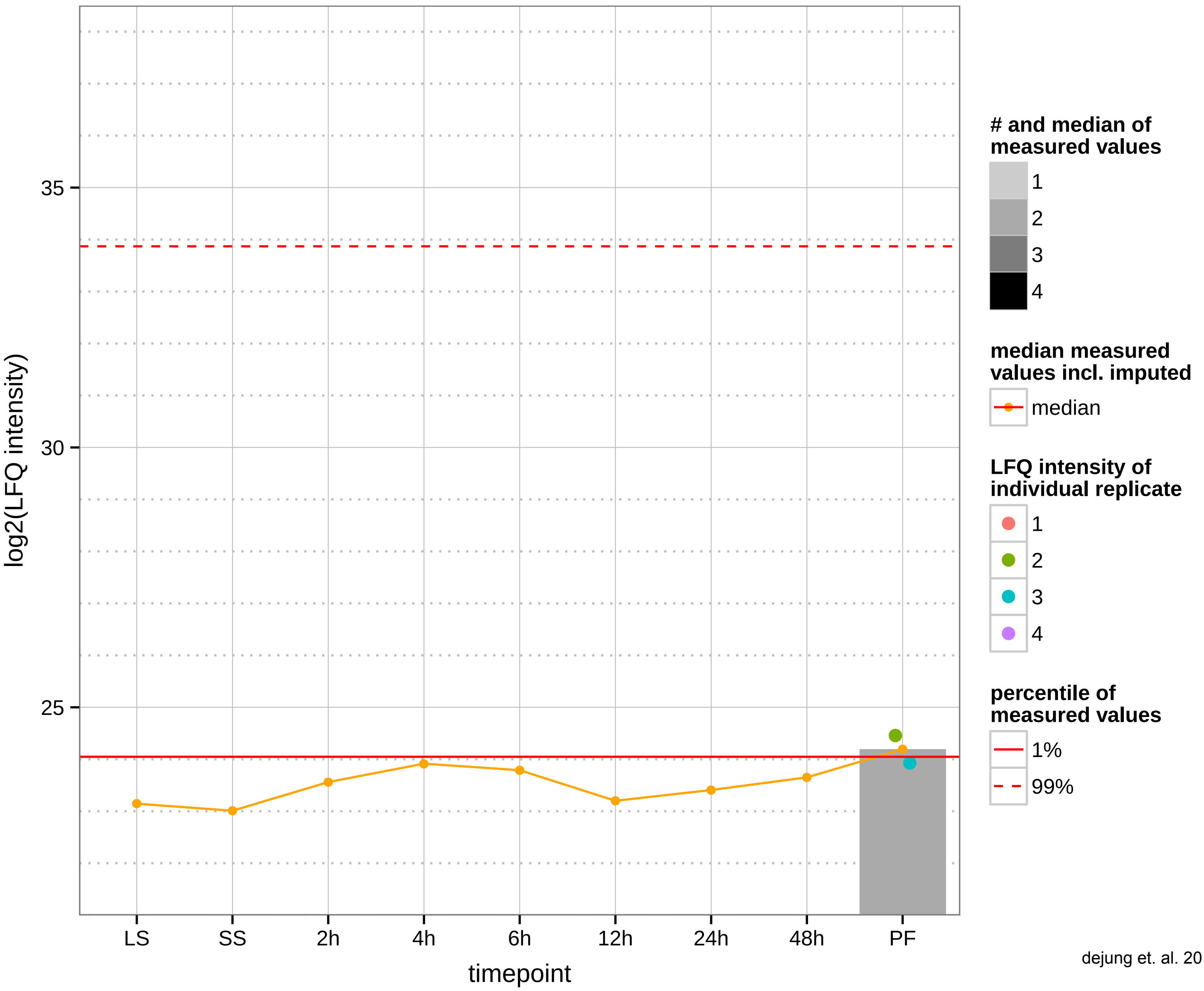
hypothetical protein, conserved
Tb927.10.11810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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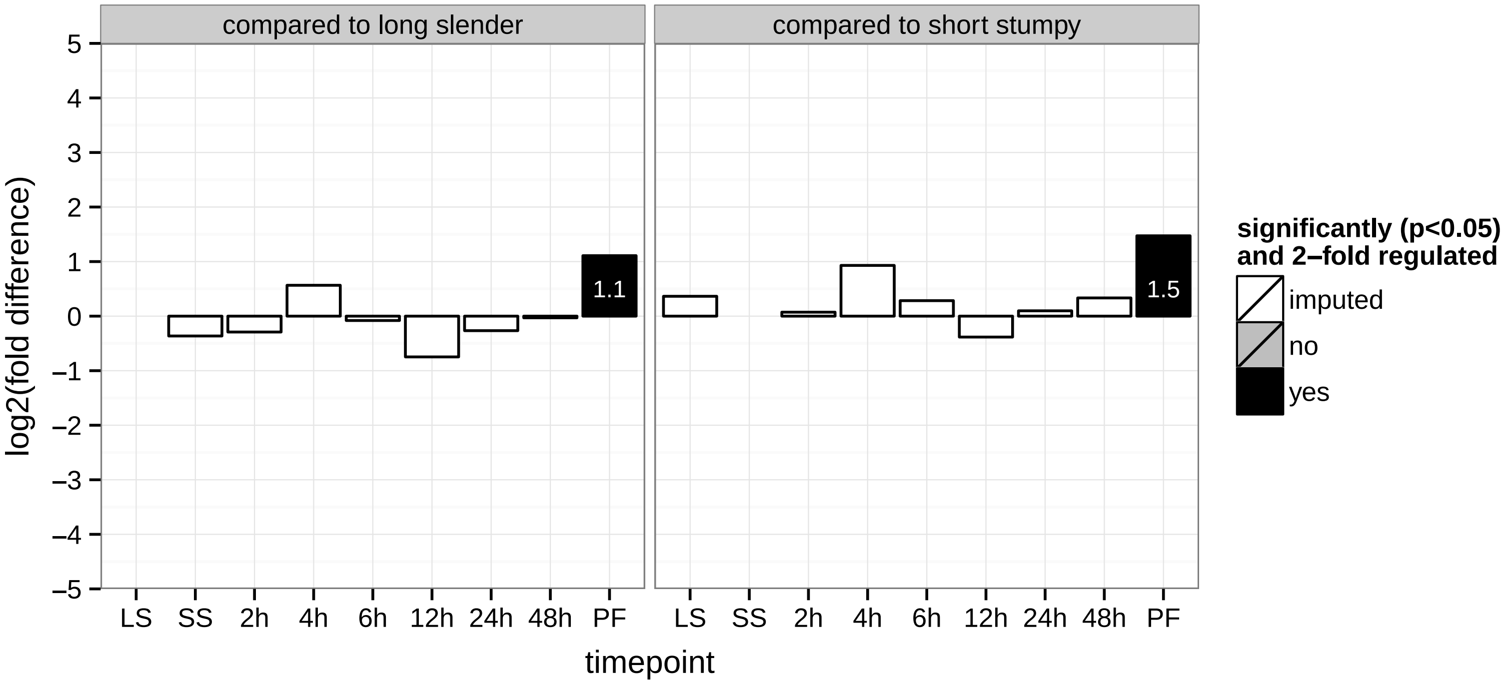
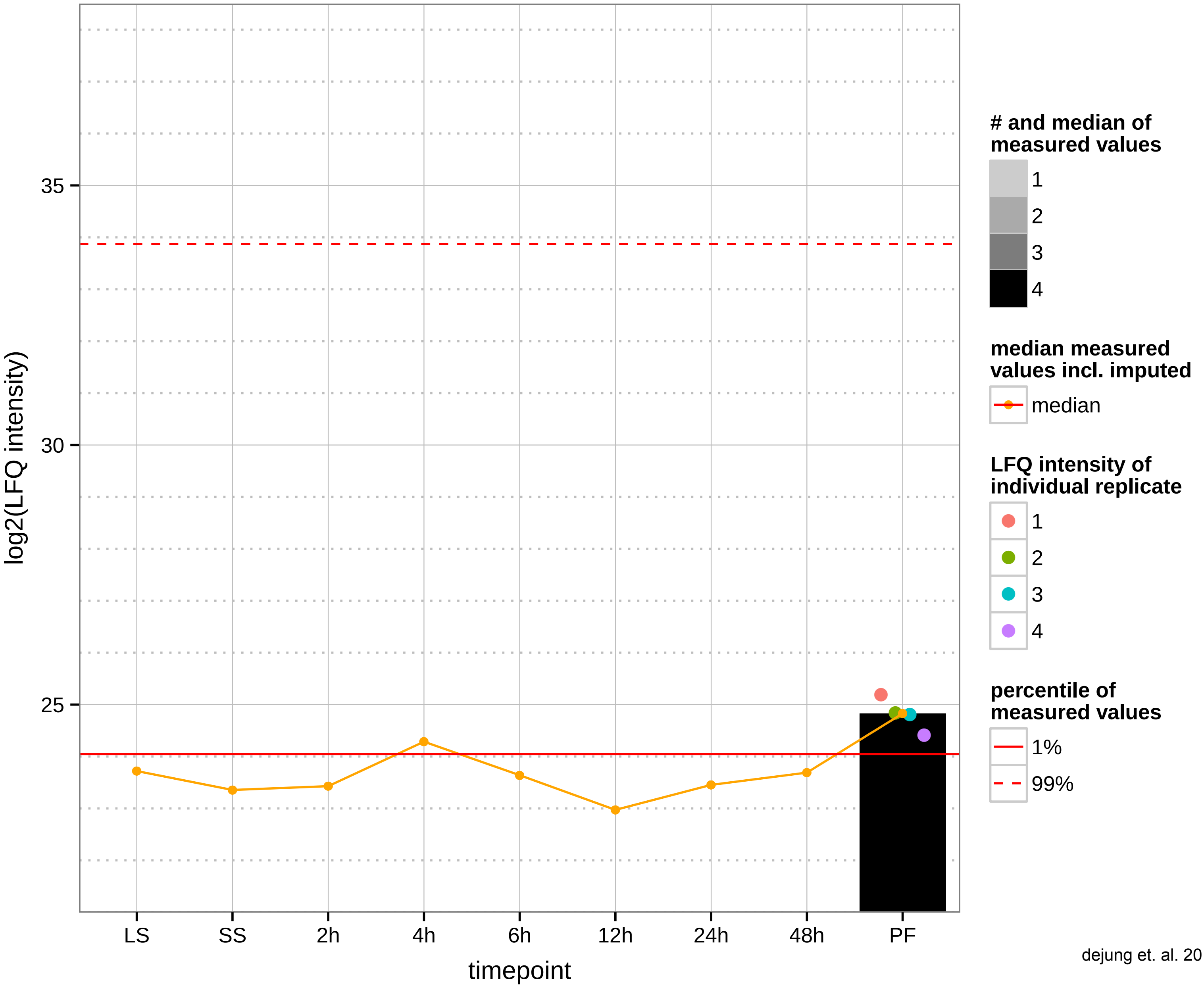
hypothetical protein
Tb927.10.11840
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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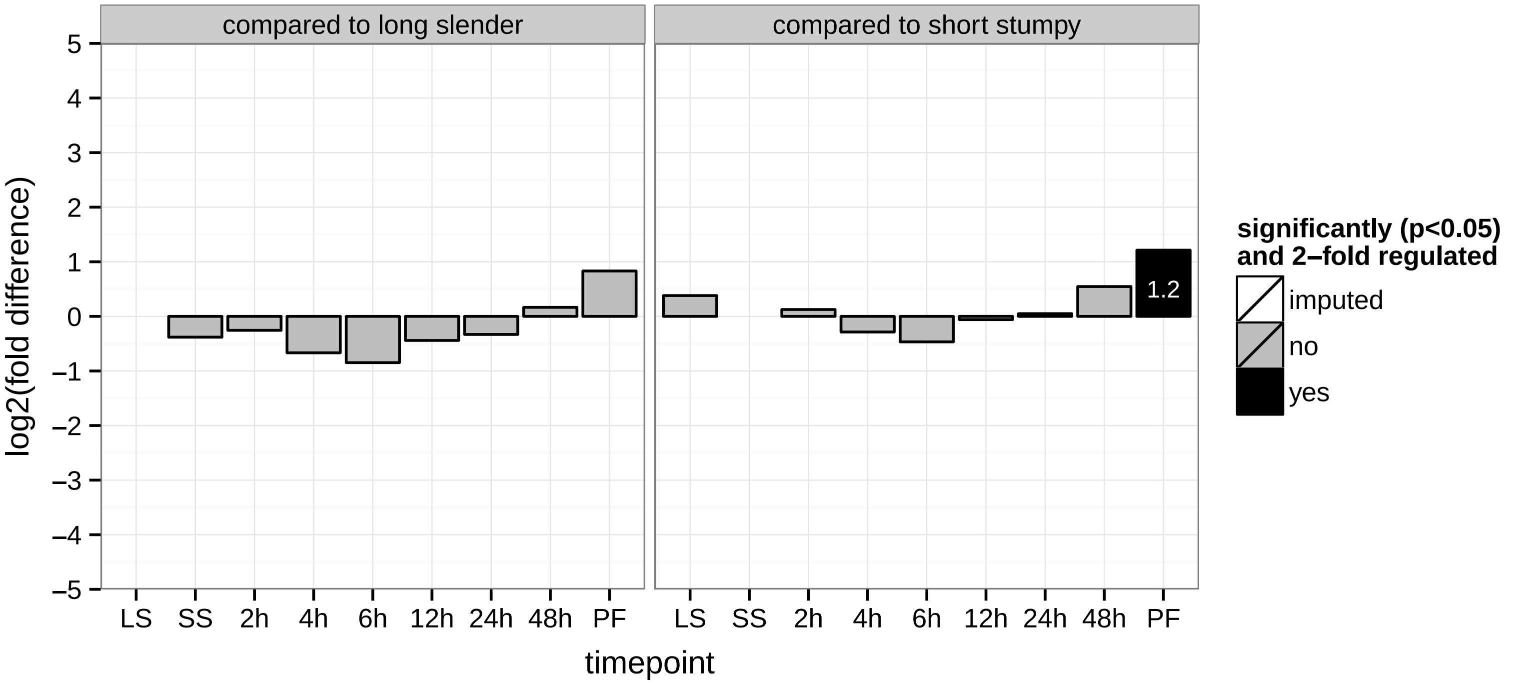
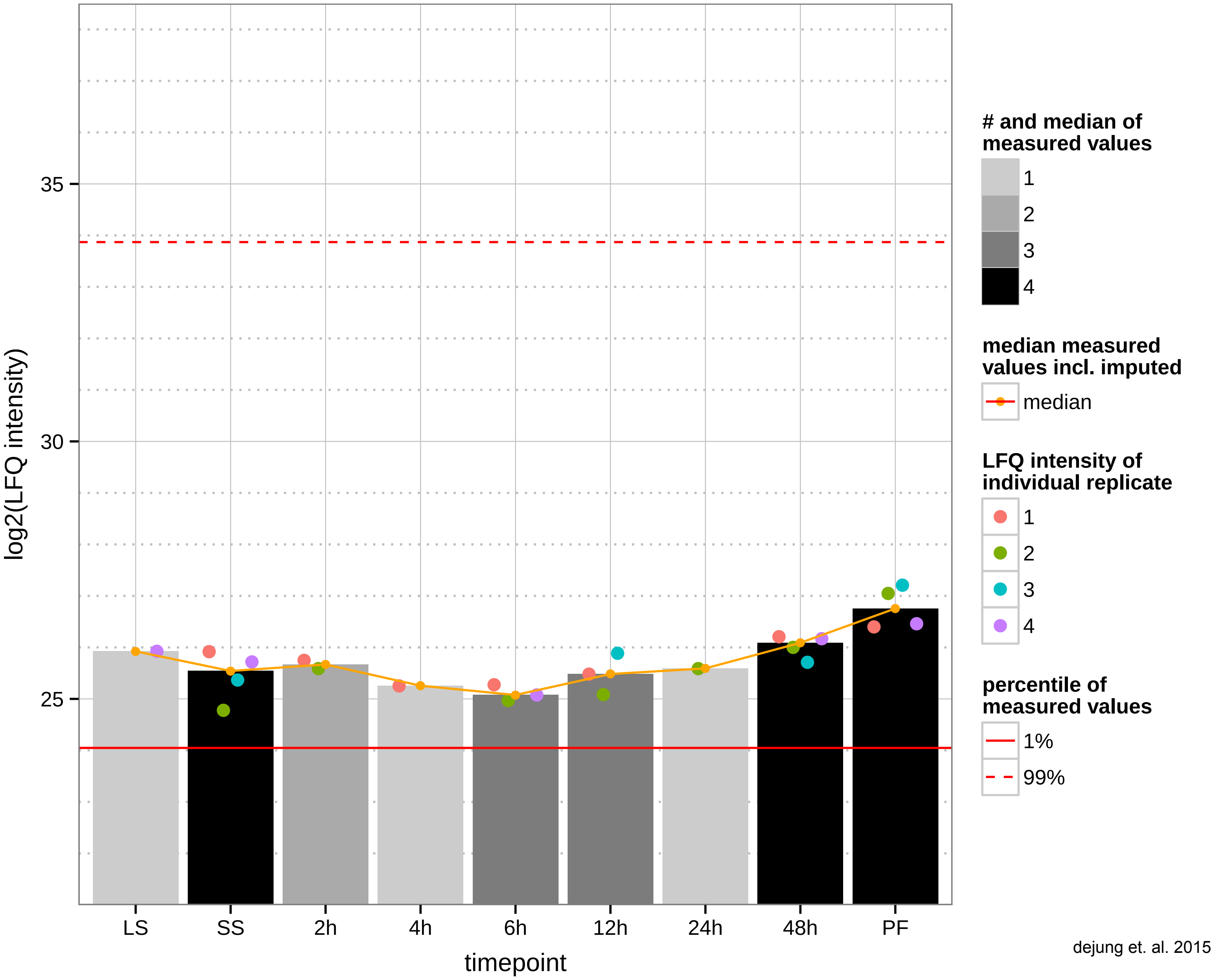
hypothetical protein, conserved
Tb927.10.12180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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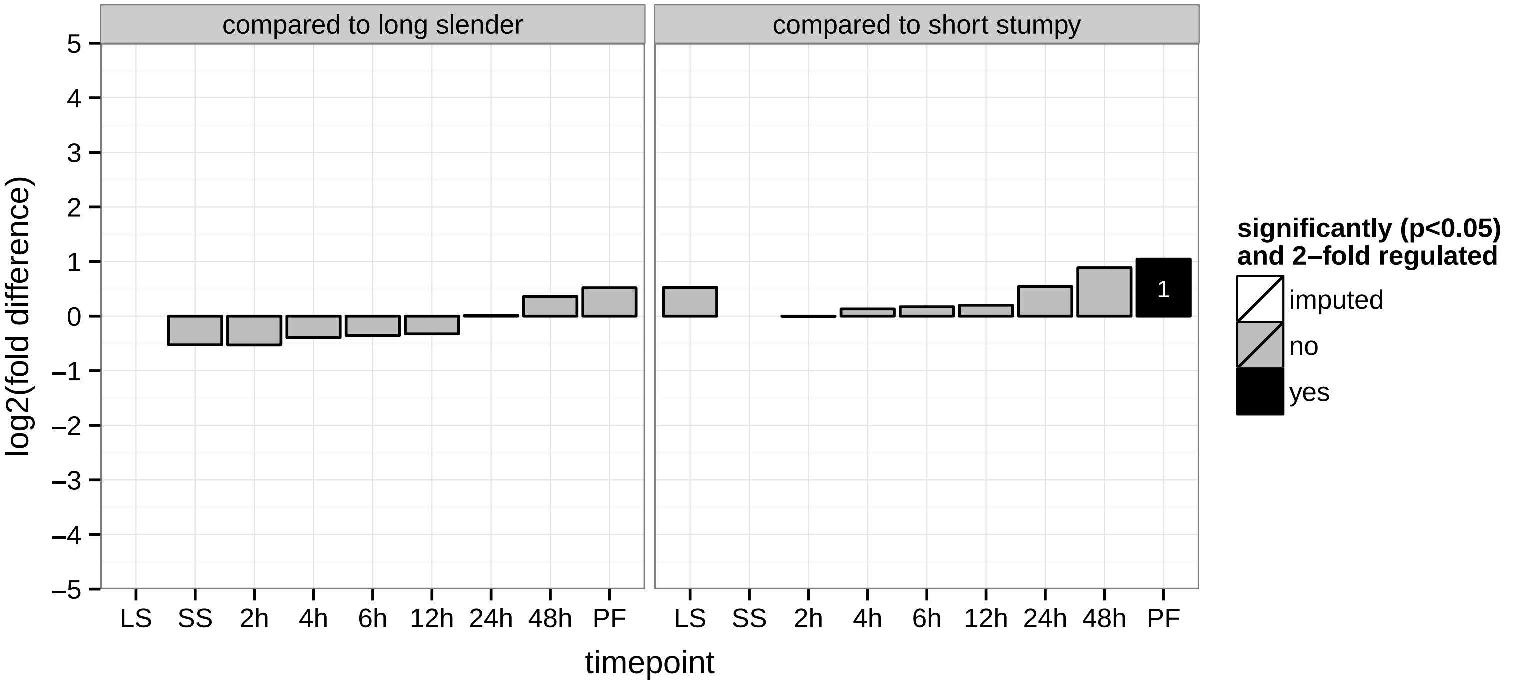
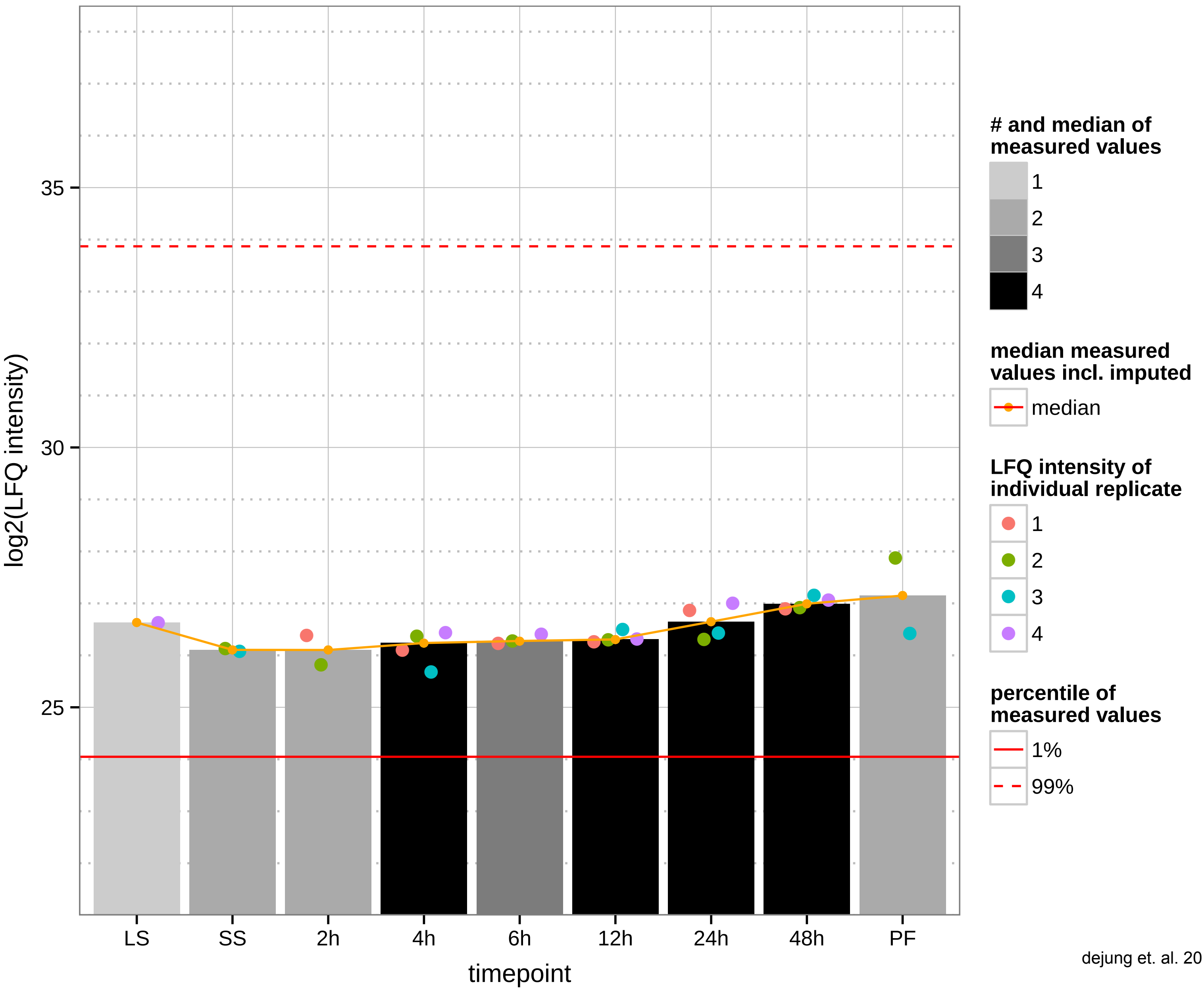
hypothetical protein, conserved
Tb927.10.12930
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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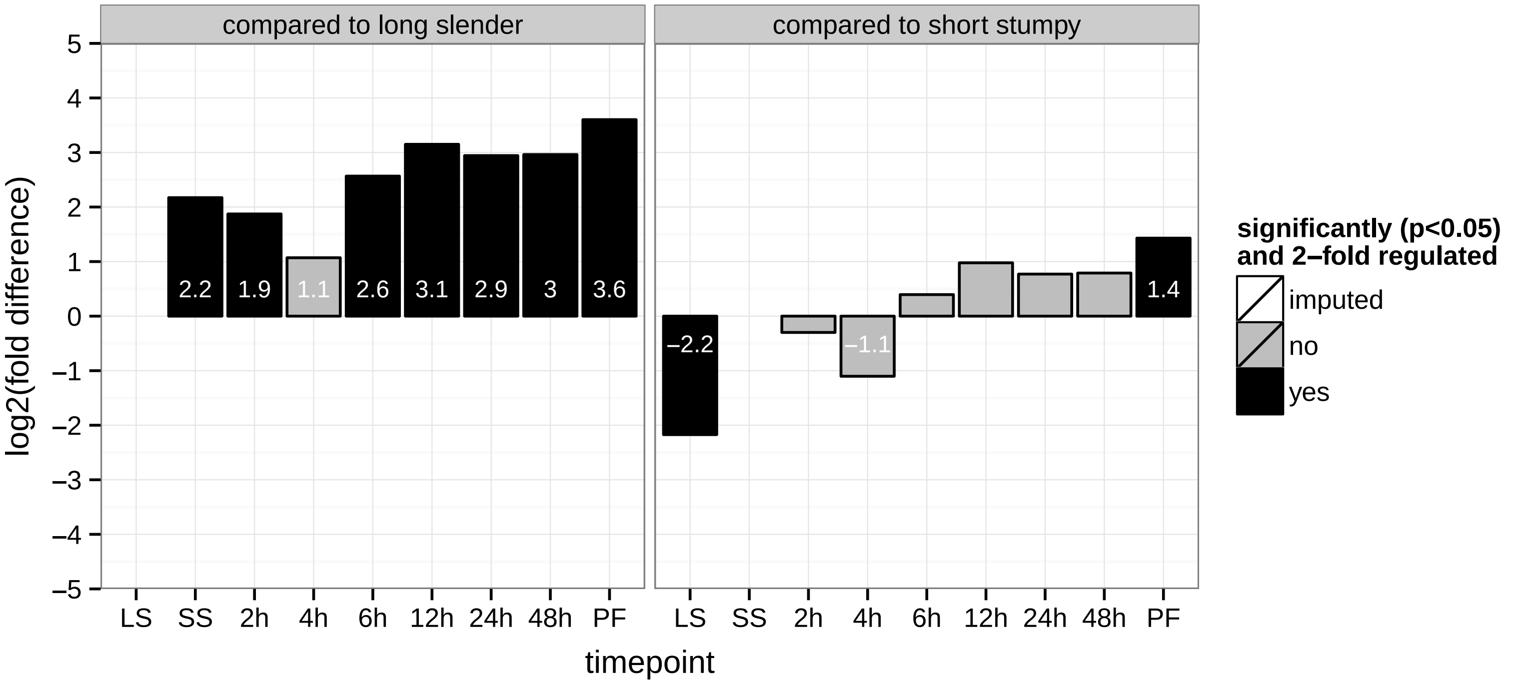
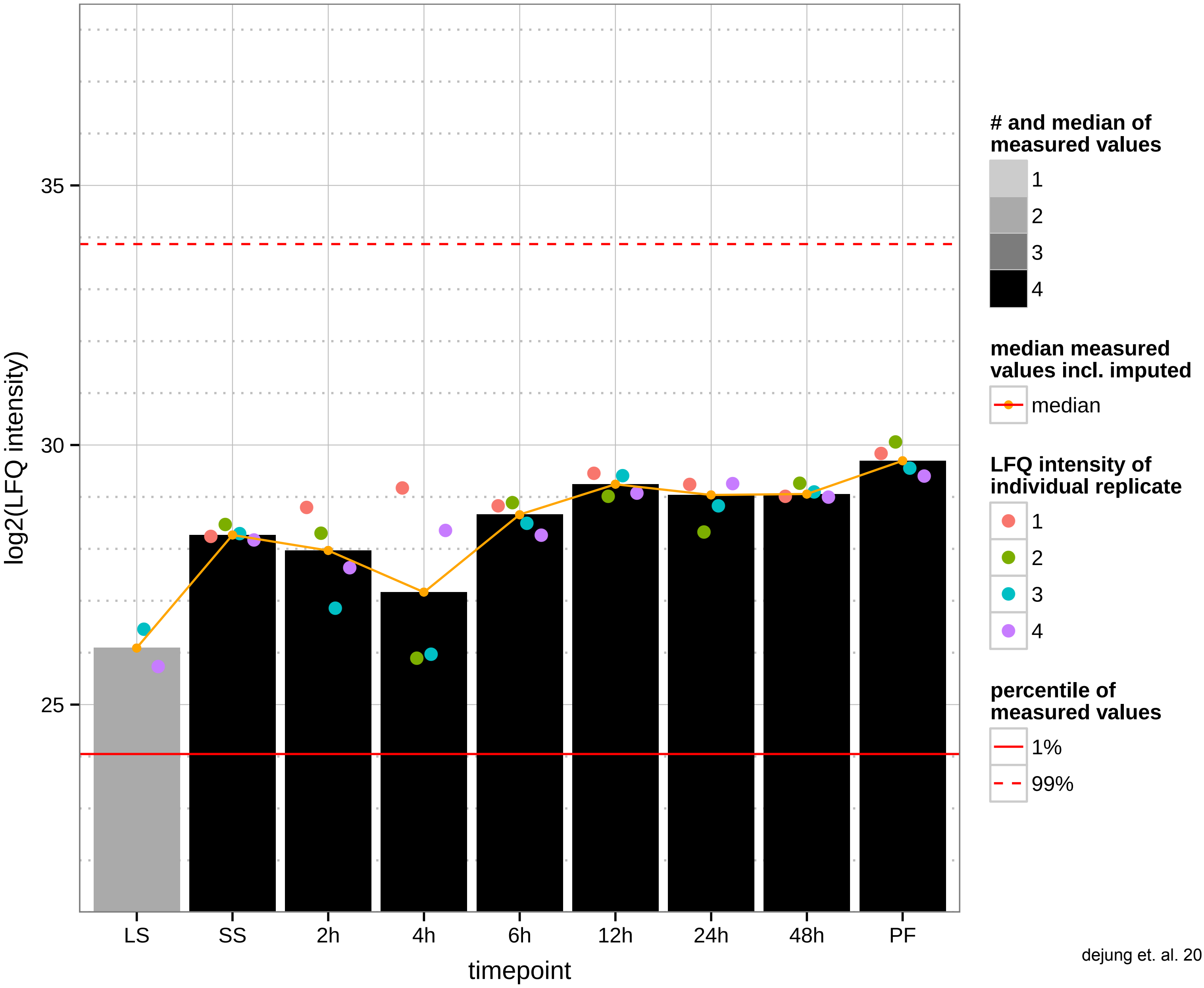
hypothetical protein, conserved
Tb927.10.13180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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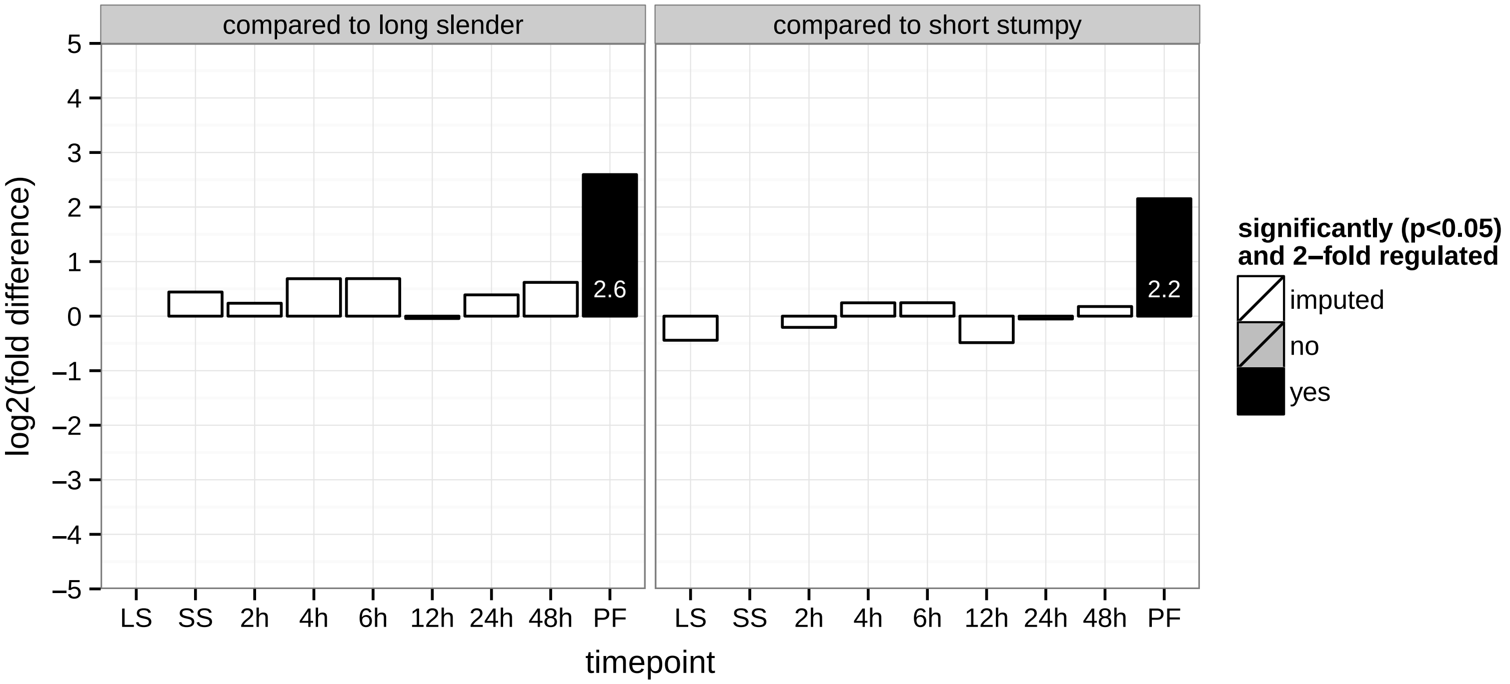
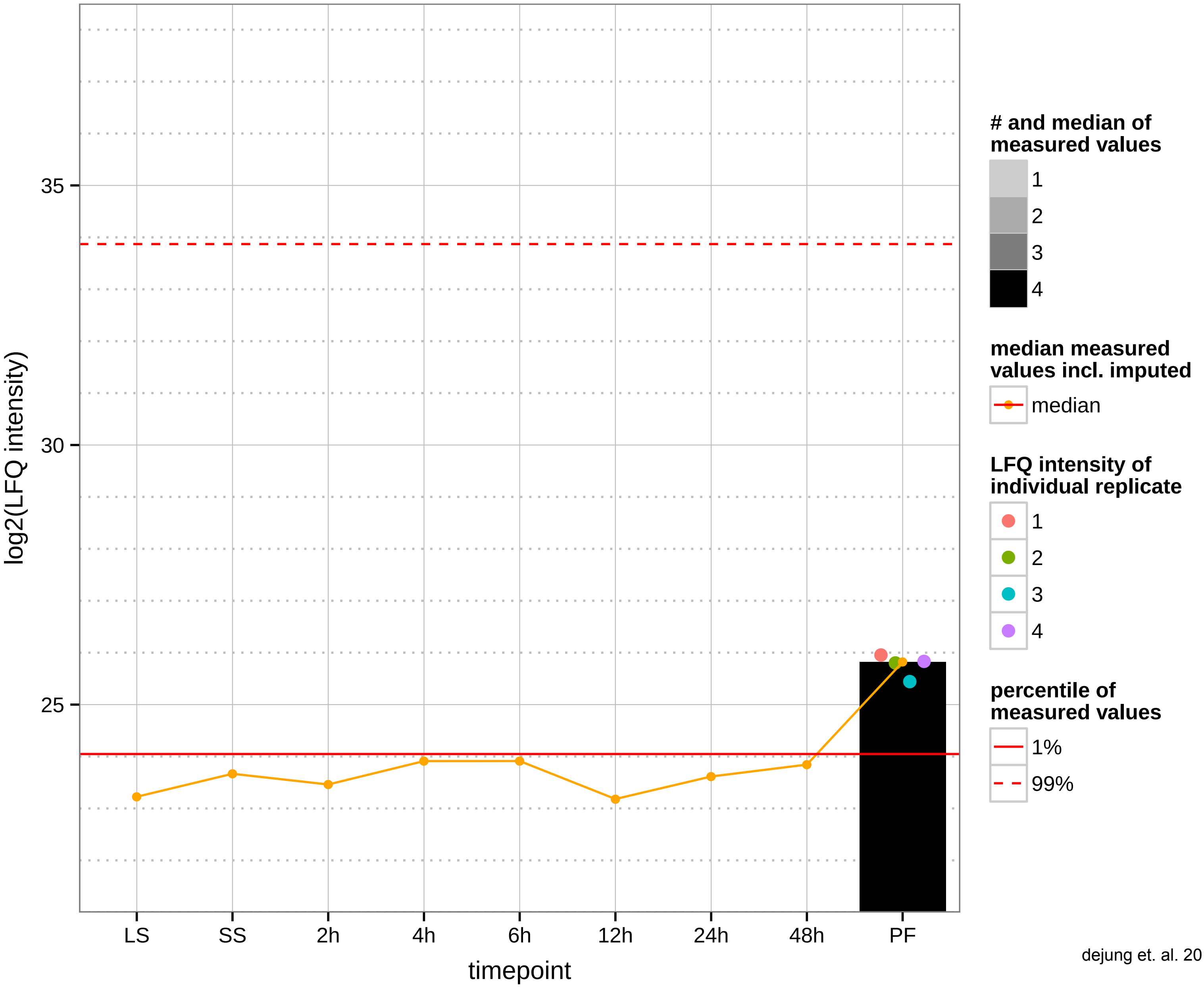
hypothetical protein, conserved
Tb927.10.13230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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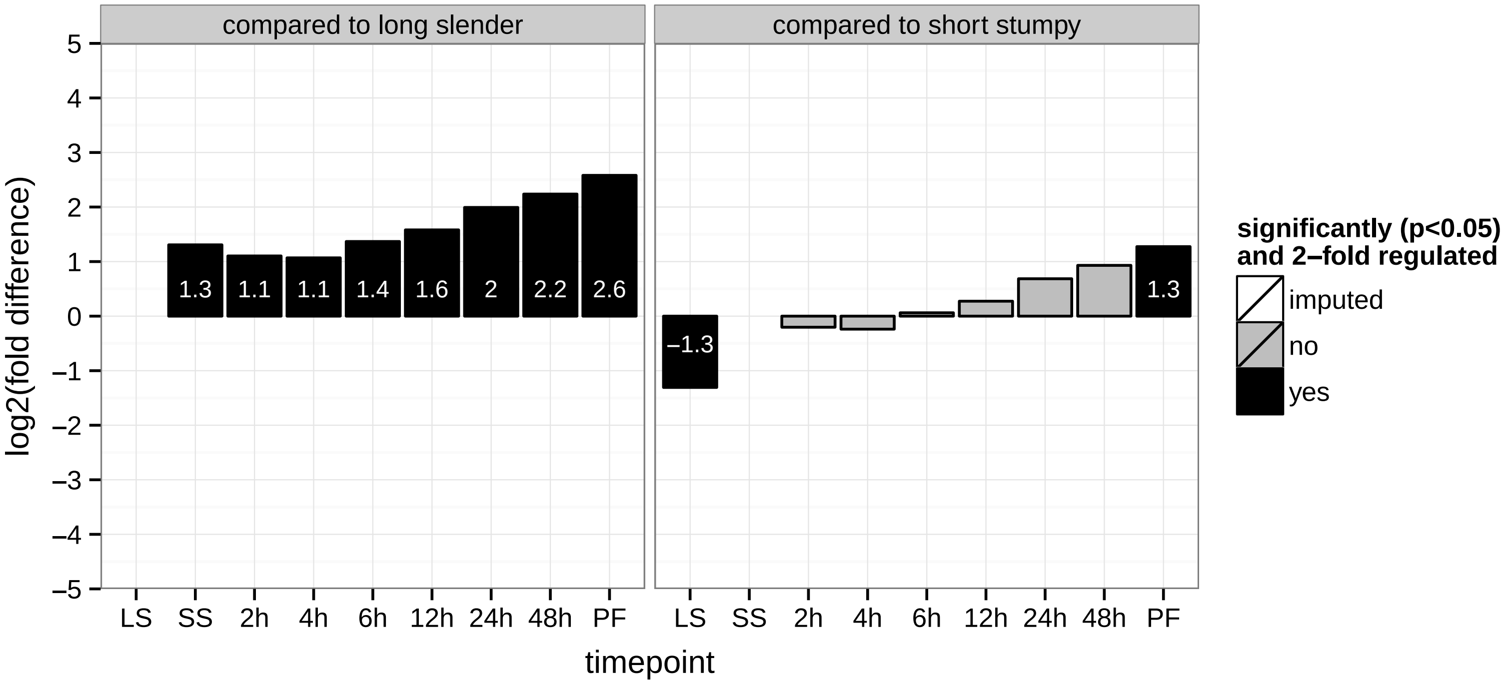
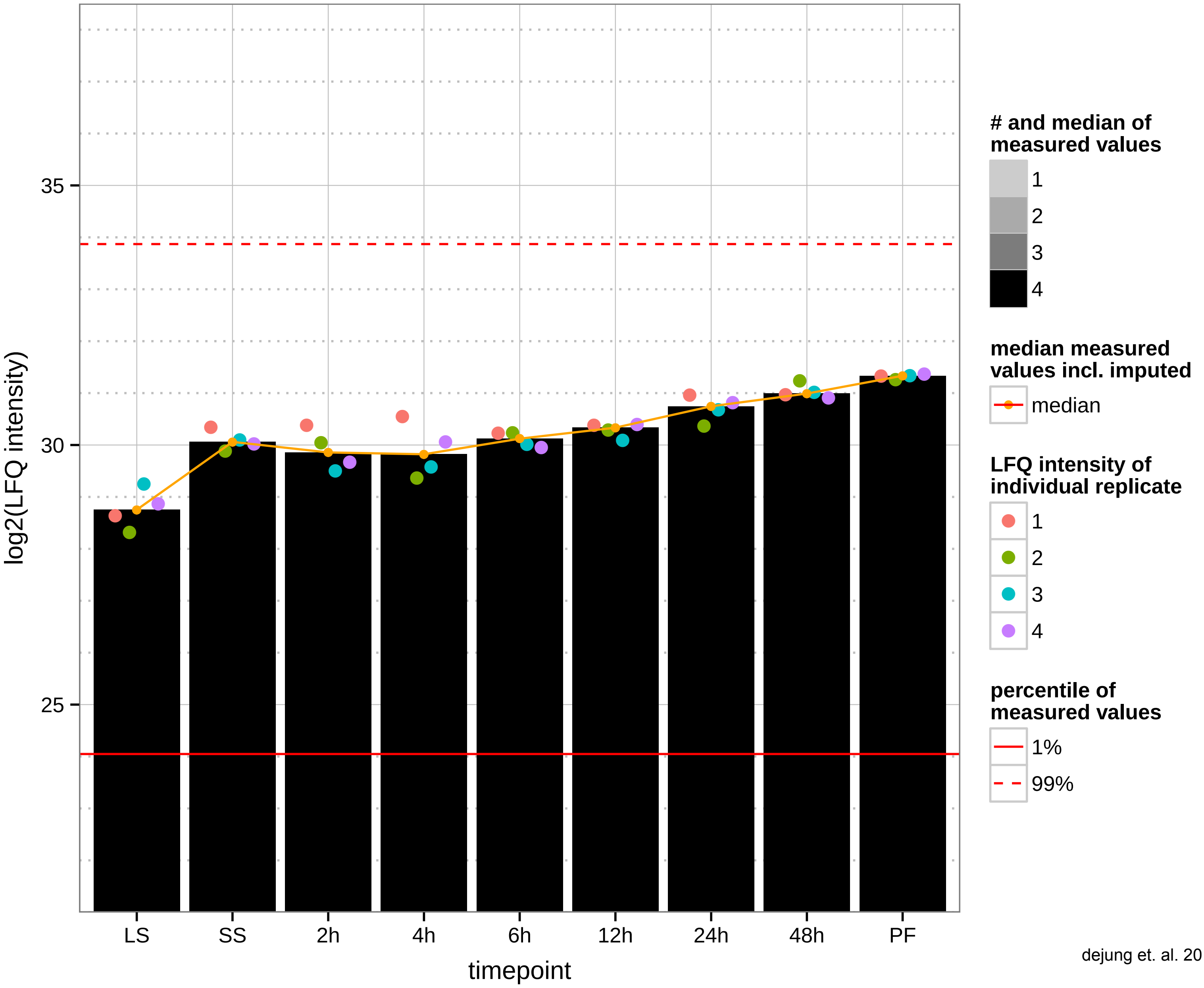
hypothetical protein, conserved
Tb927.10.13280
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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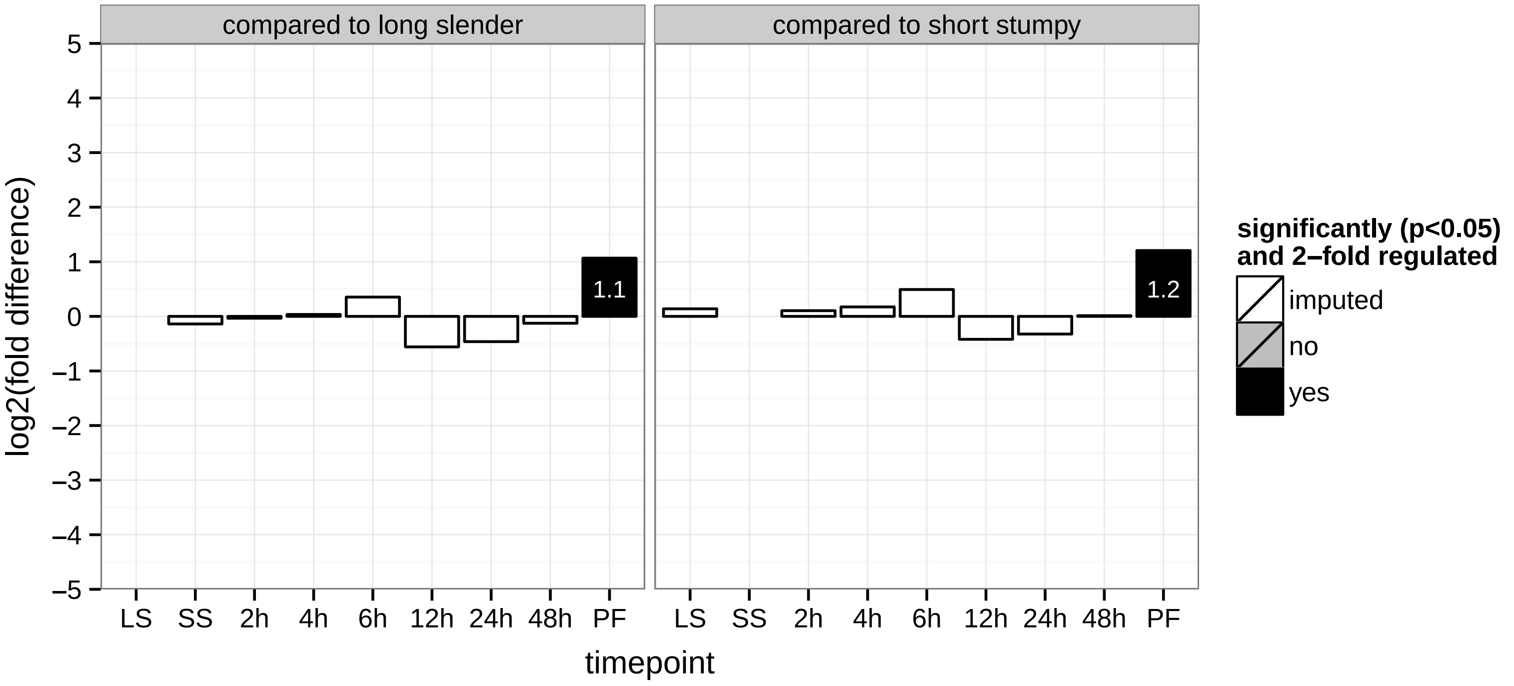
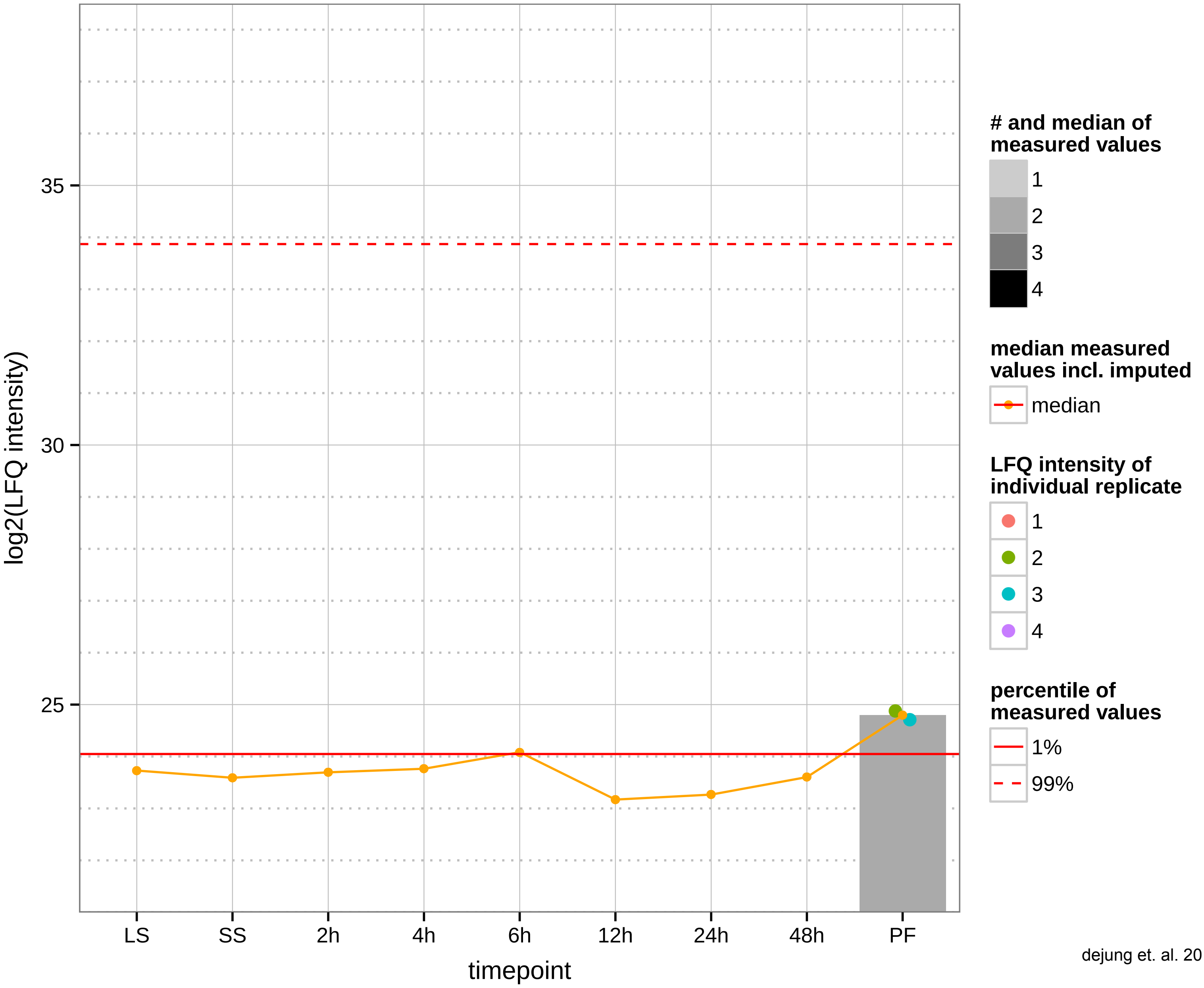
Dynein light chain Tctex−type, putative
Tb927.10.13370
AGOF: microtubule motor activity
AGOC: cytoplasmic dynein complex
AGOP: microtubule−based process
PGOF: null
PGOC: null
PGOP: null





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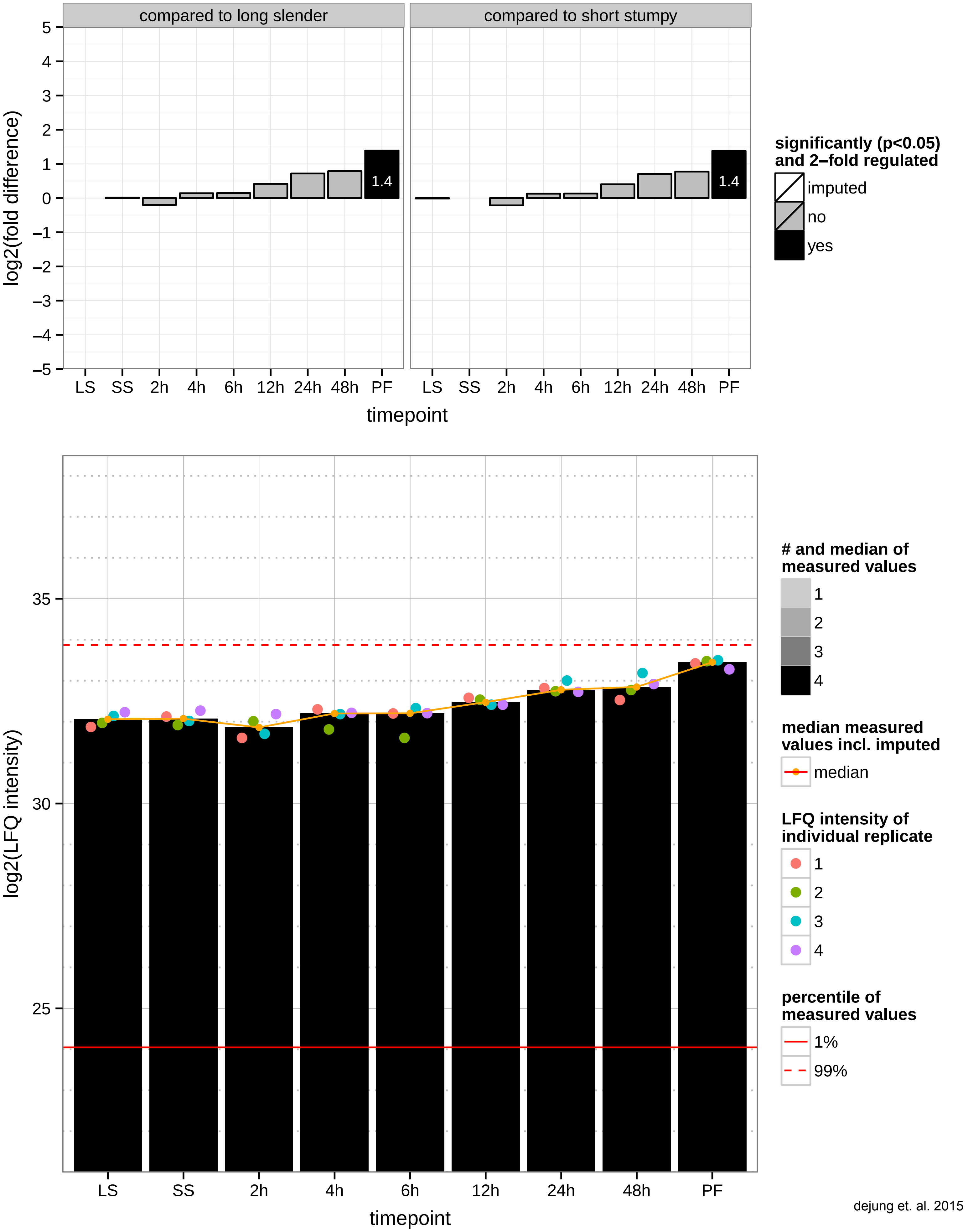
60S ribosomal protein L10a, putative (RPL10A)
Tb927.11.9710;Tb927.10.13500
AGOF: RNA binding, structural constituent of ribosome
AGOC: ribosome, large ribosomal subunit
AGOP: RNA processing, translation
PGOF: RNA binding, structural constituent of ribosome
PGOC: large ribosomal subunit
PGOP: translation



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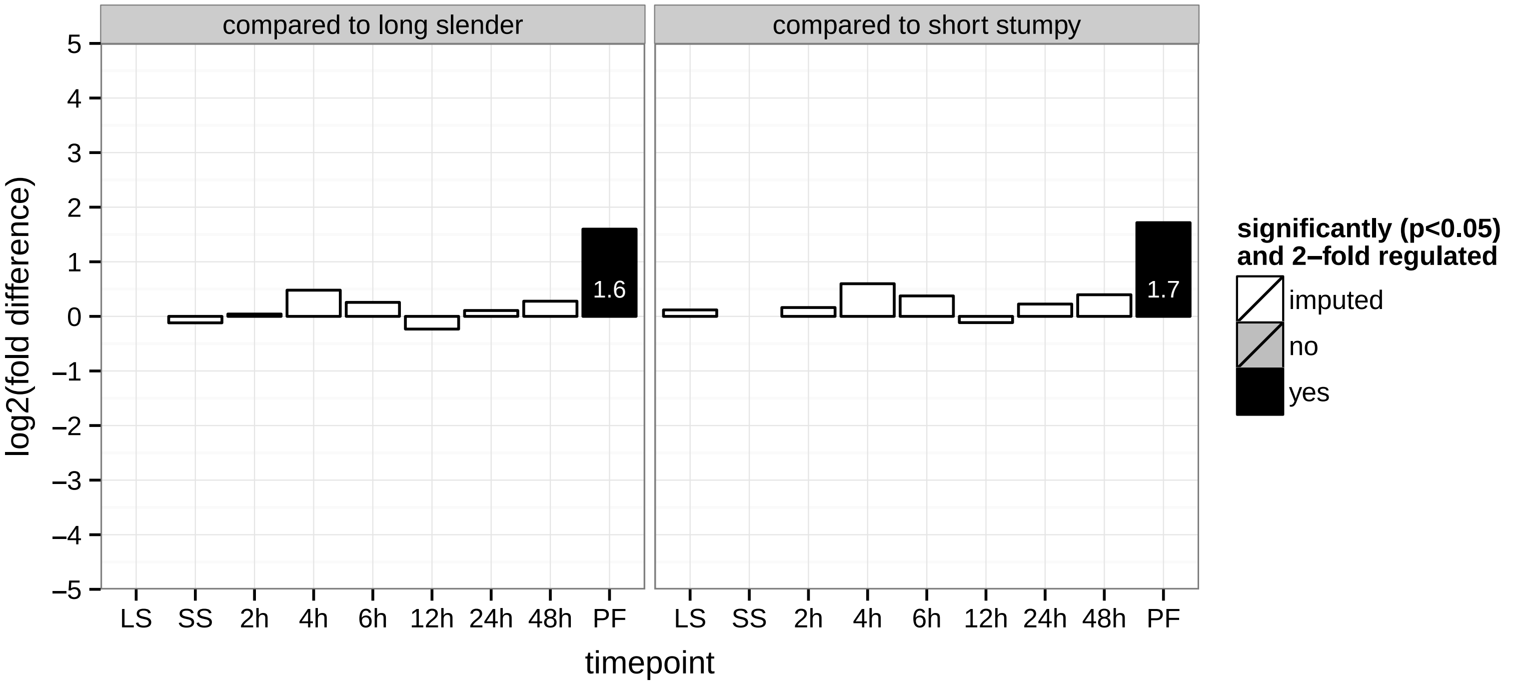
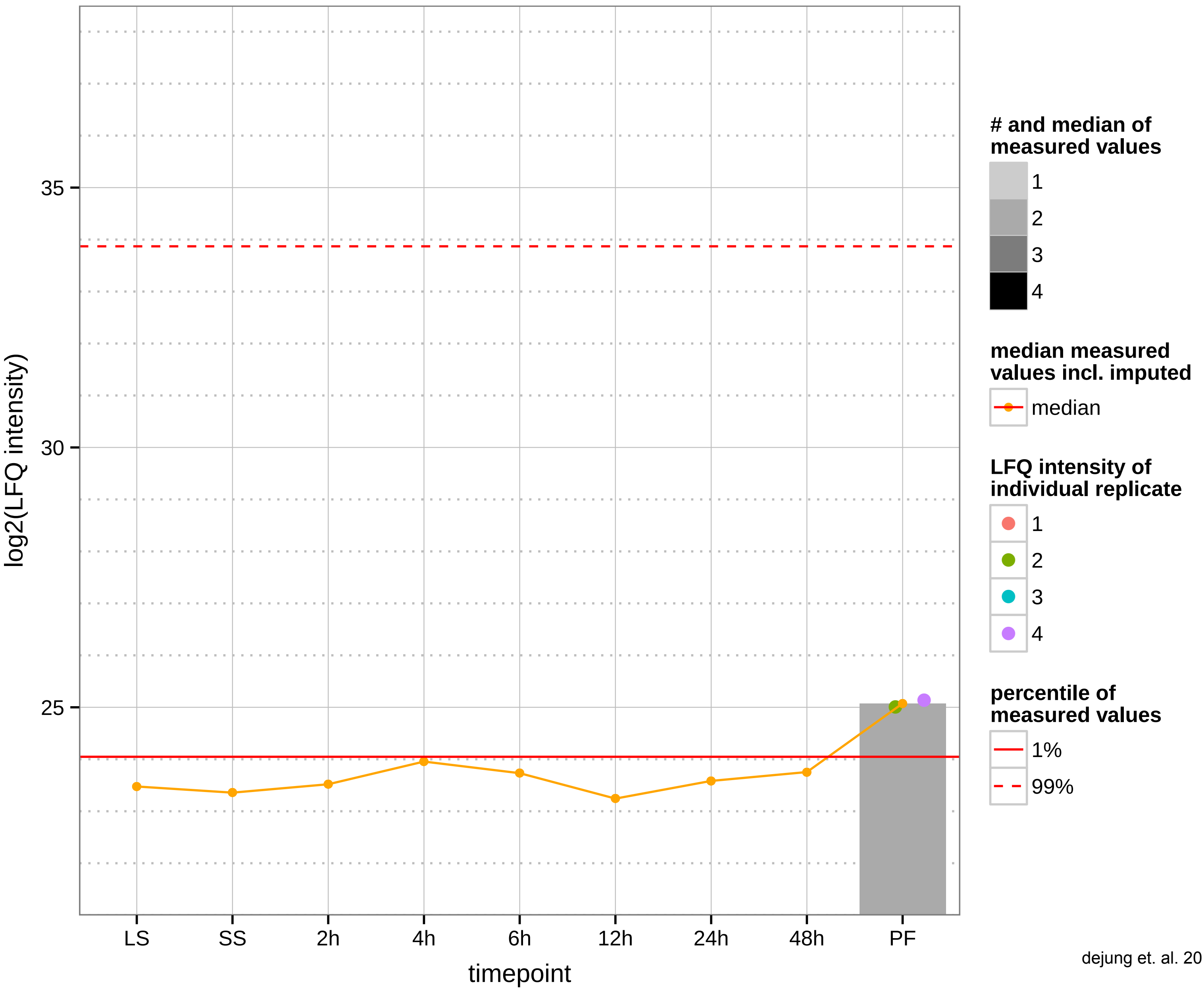
hypothetical protein, conserved
Tb927.10.13660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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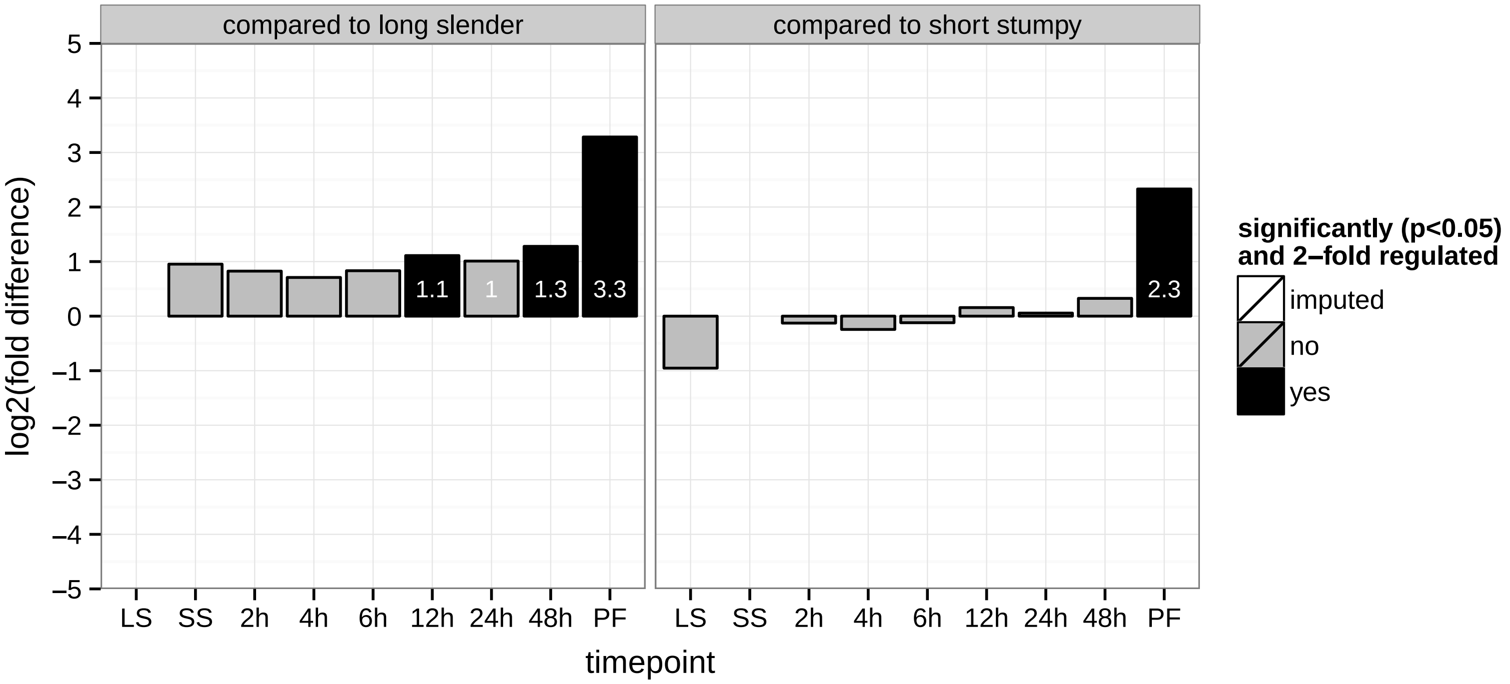
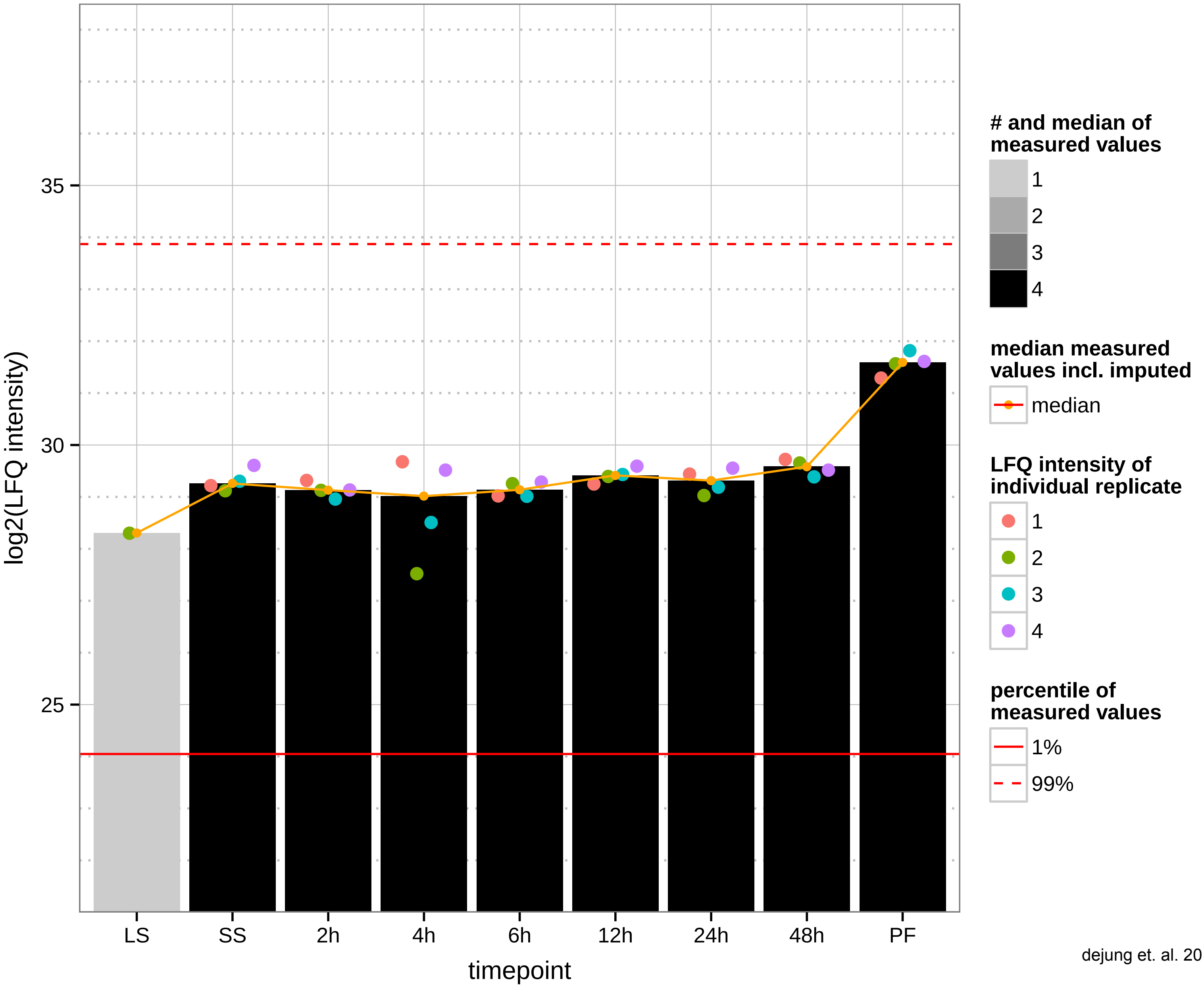
NA, aconitase (ACO)
Tb927.10.14000
AGOF: NA, aconitate hydratase activity
AGOC: NA, cytosol, mitochondrion
AGOP: NA, tricarboxylic acid cycle
PGOF: NA, 4 iron, 4 sulfur cluster binding
PGOC: NA, null
PGOP: NA, metabolic process





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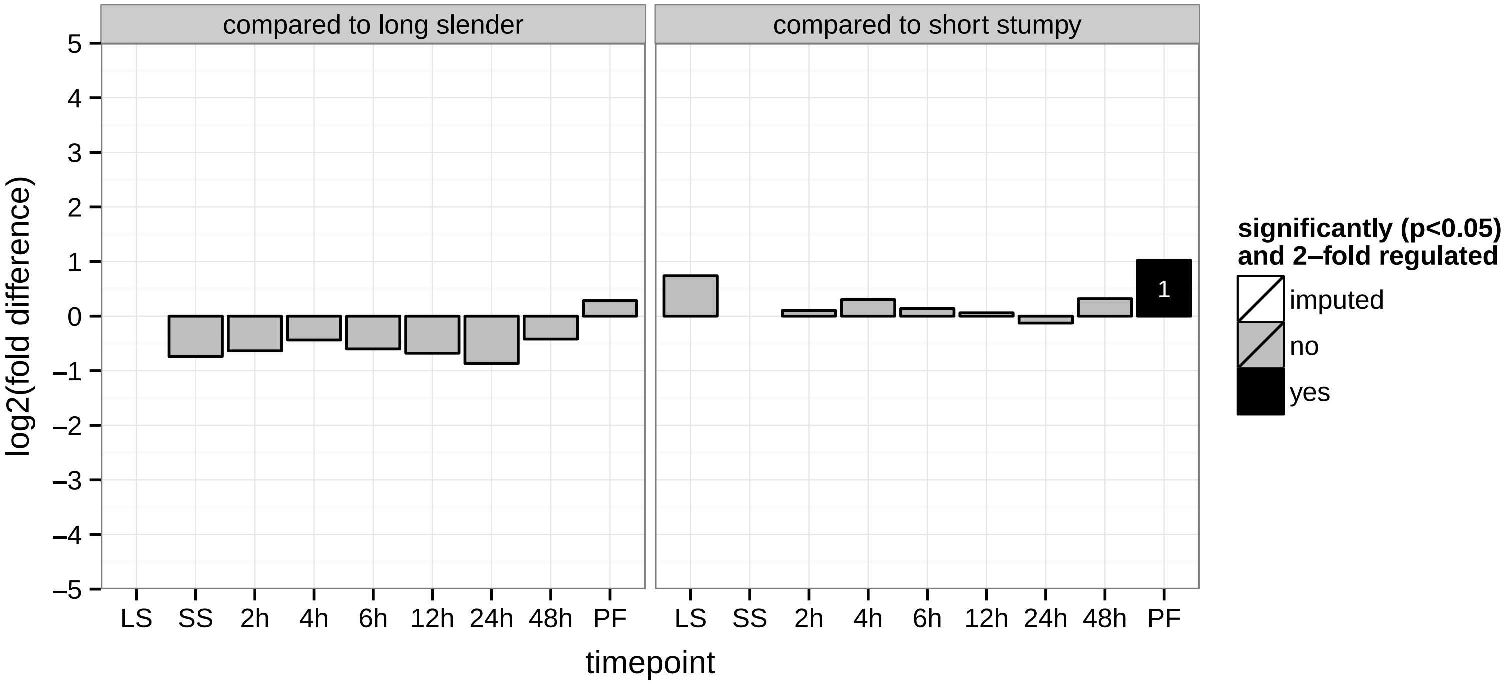
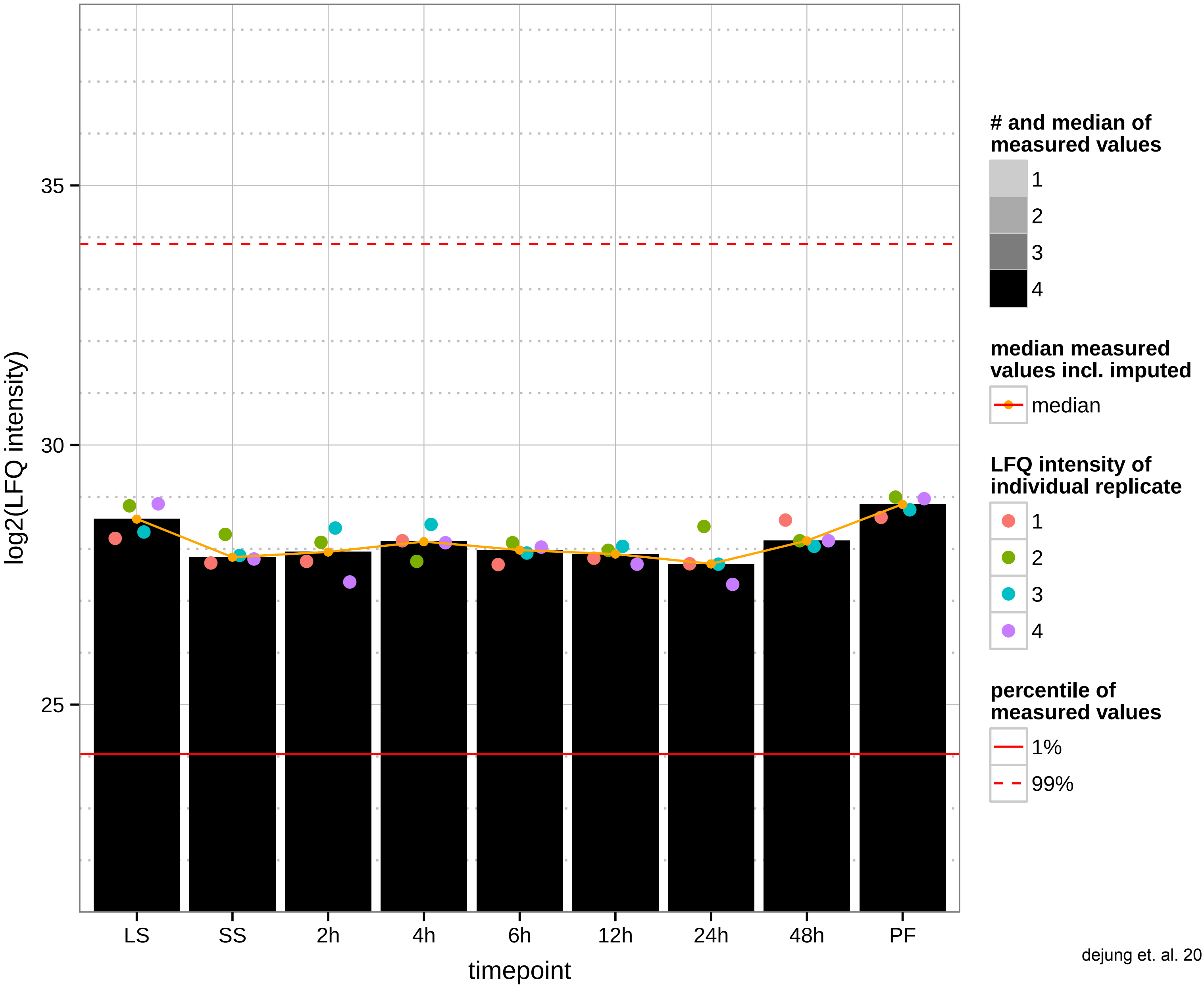
hypothetical protein, conserved
Tb927.10.14030
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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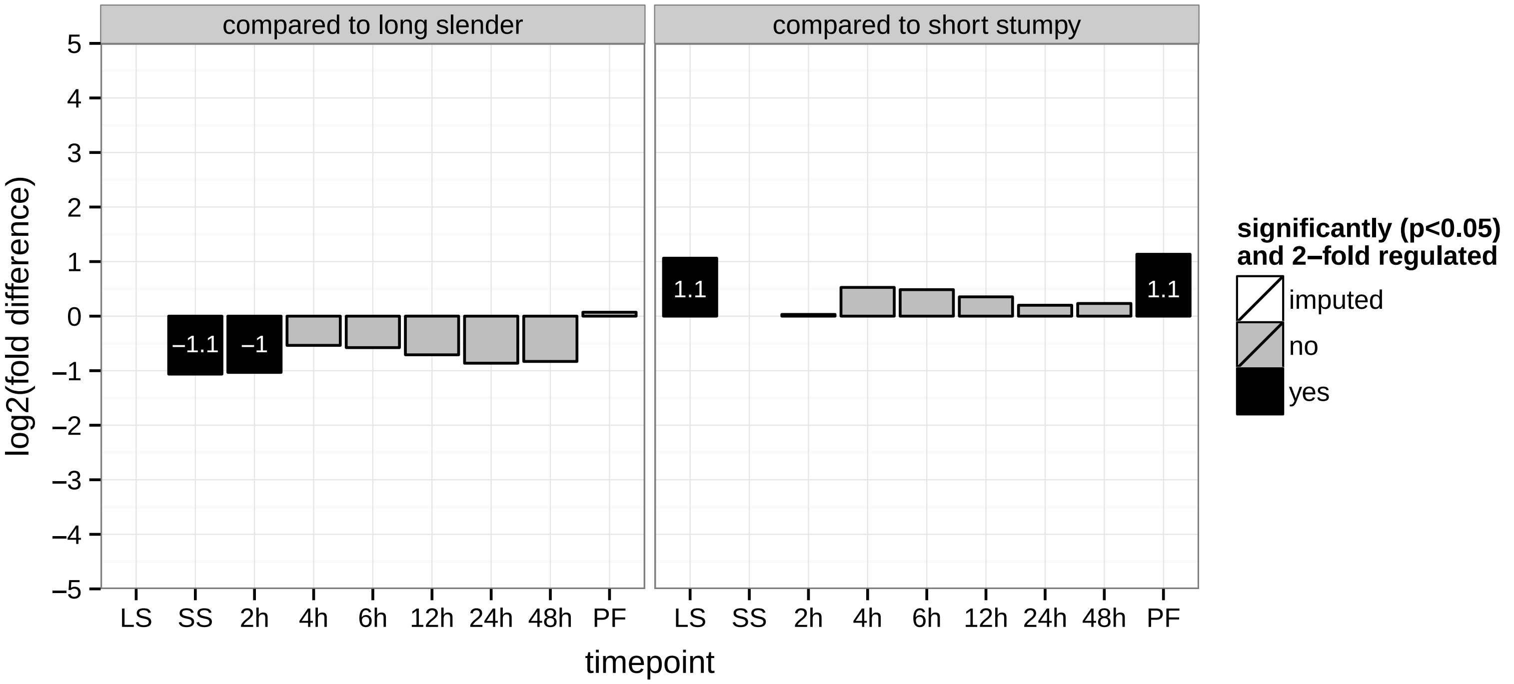
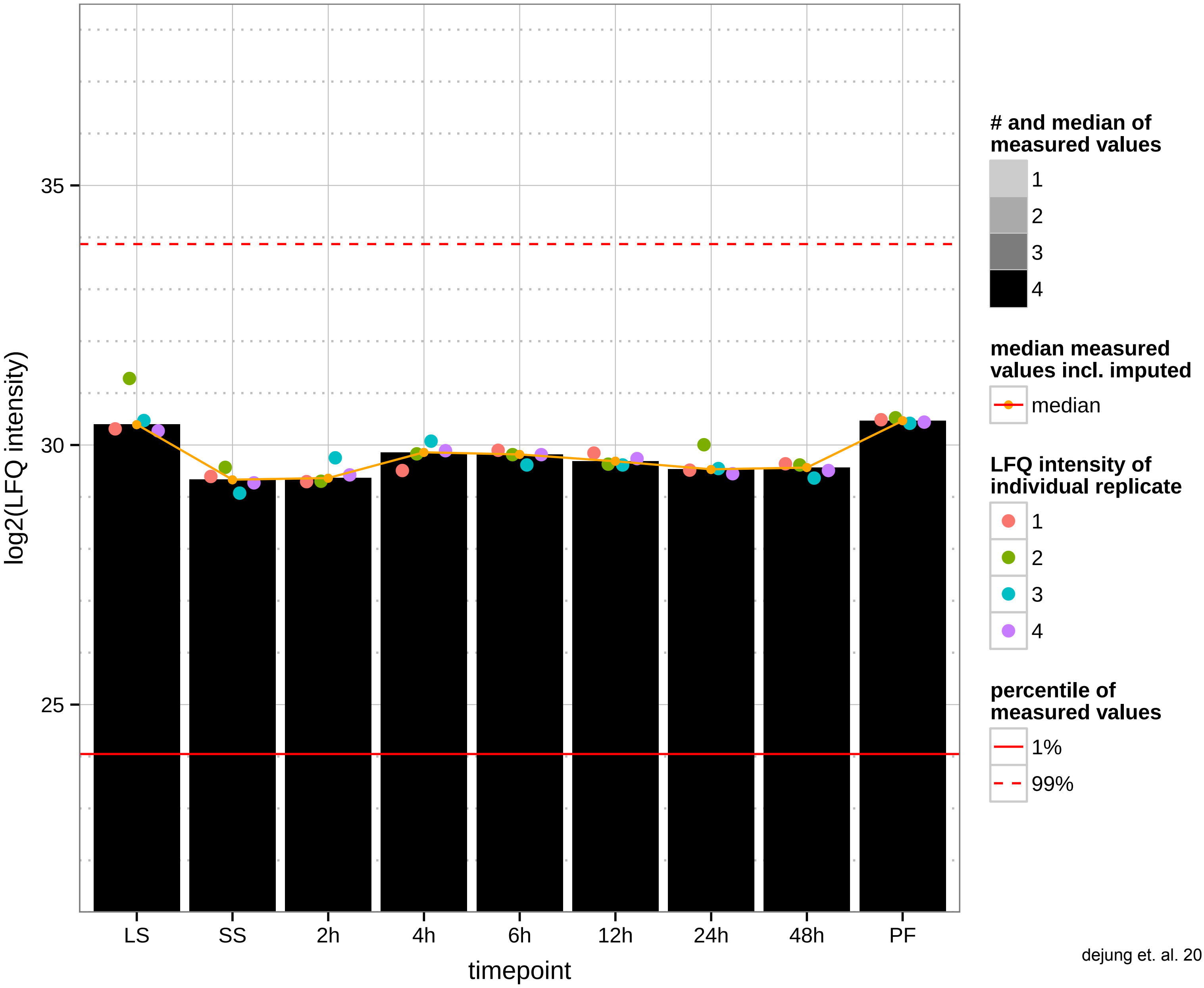
nuclear segregation protein, putative
Tb927.10.14150
AGOF: RNA binding
AGOC: nuclear outer membrane–endoplasmic reticulum membrane network, polysome, ribonucleoprotein complex
AGOP: chromosome segregation, meiosis, regulation of mitosis
PGOF: null
PGOC: null
PGOP: null





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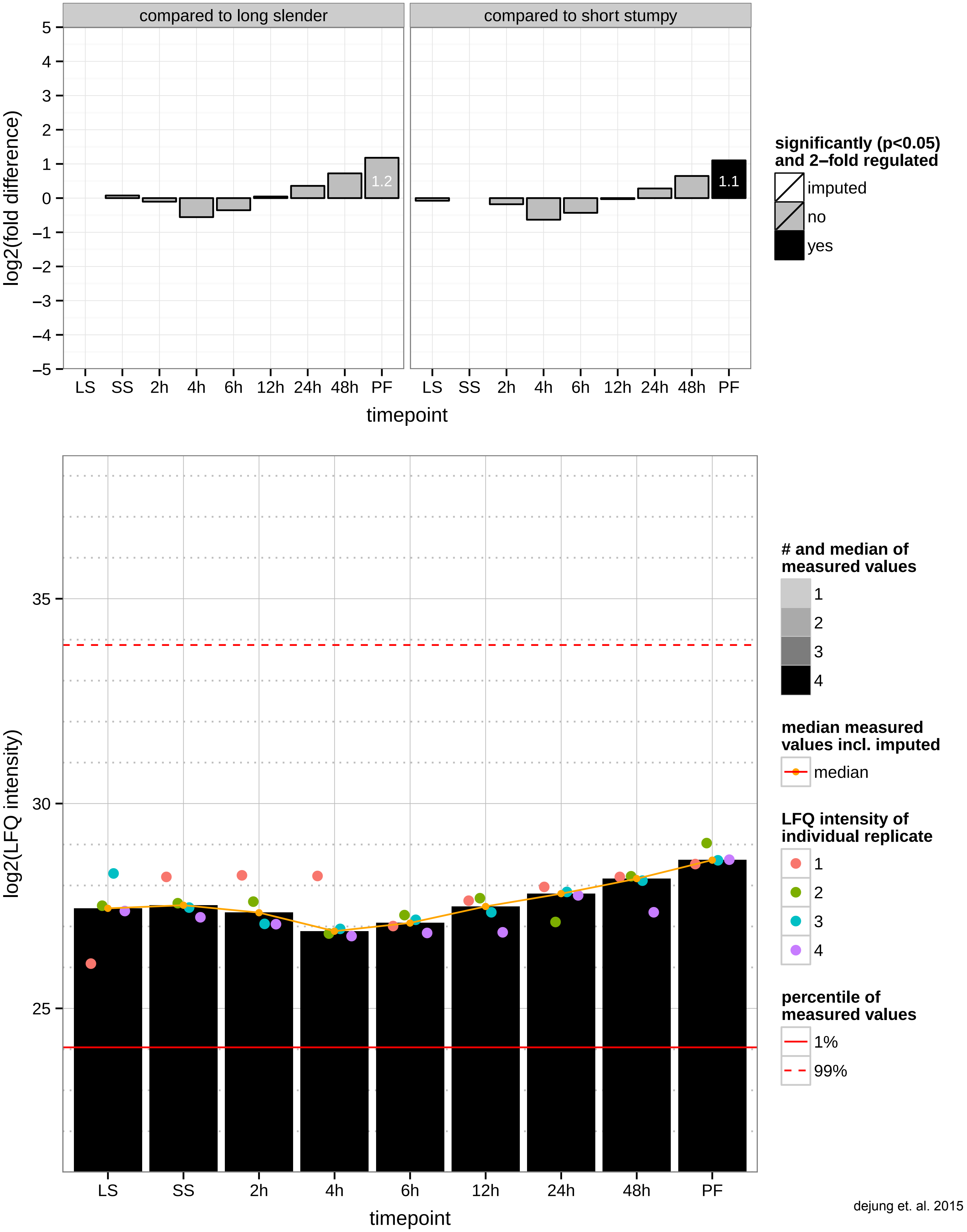
hypothetical protein, conserved
Tb927.10.14320
AGOF: null
AGOC: null
AGOP: null
PGOF: binding, protein binding
PGOC: null
PGOP: null



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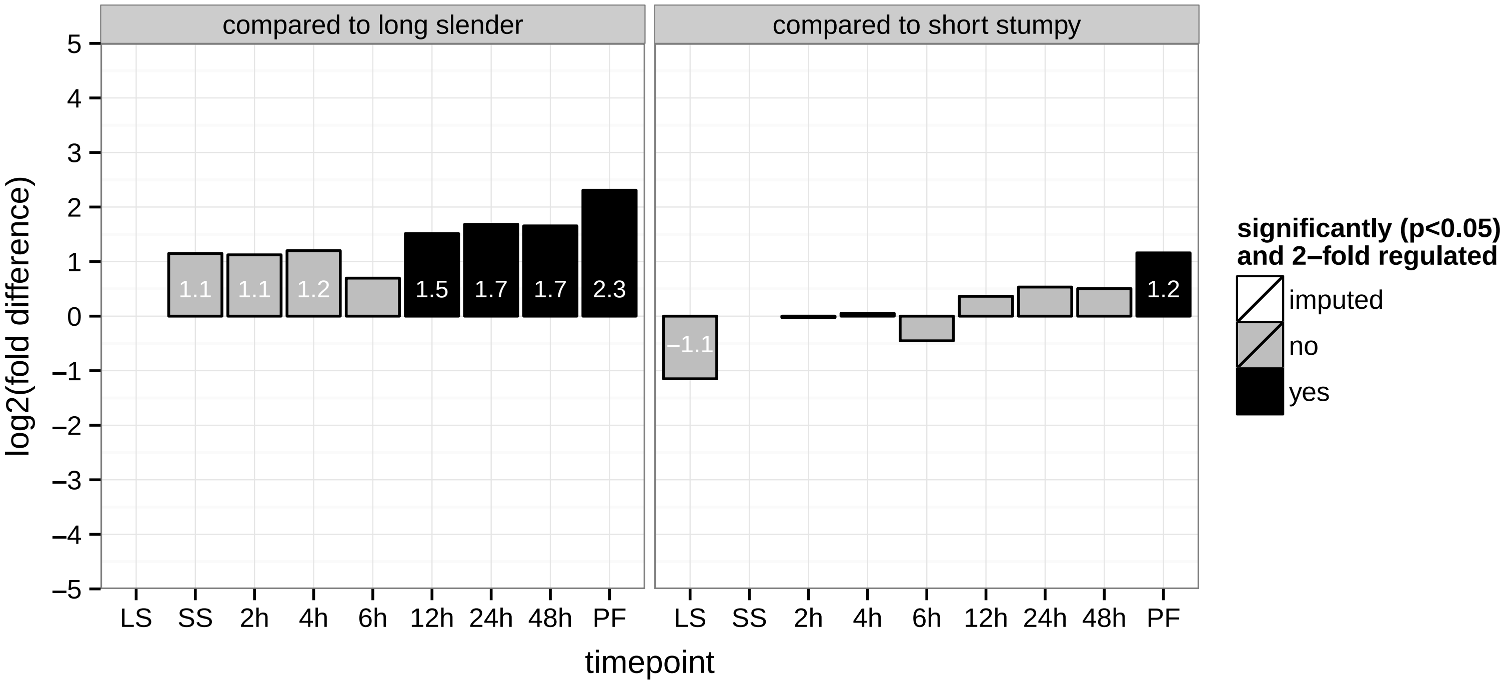
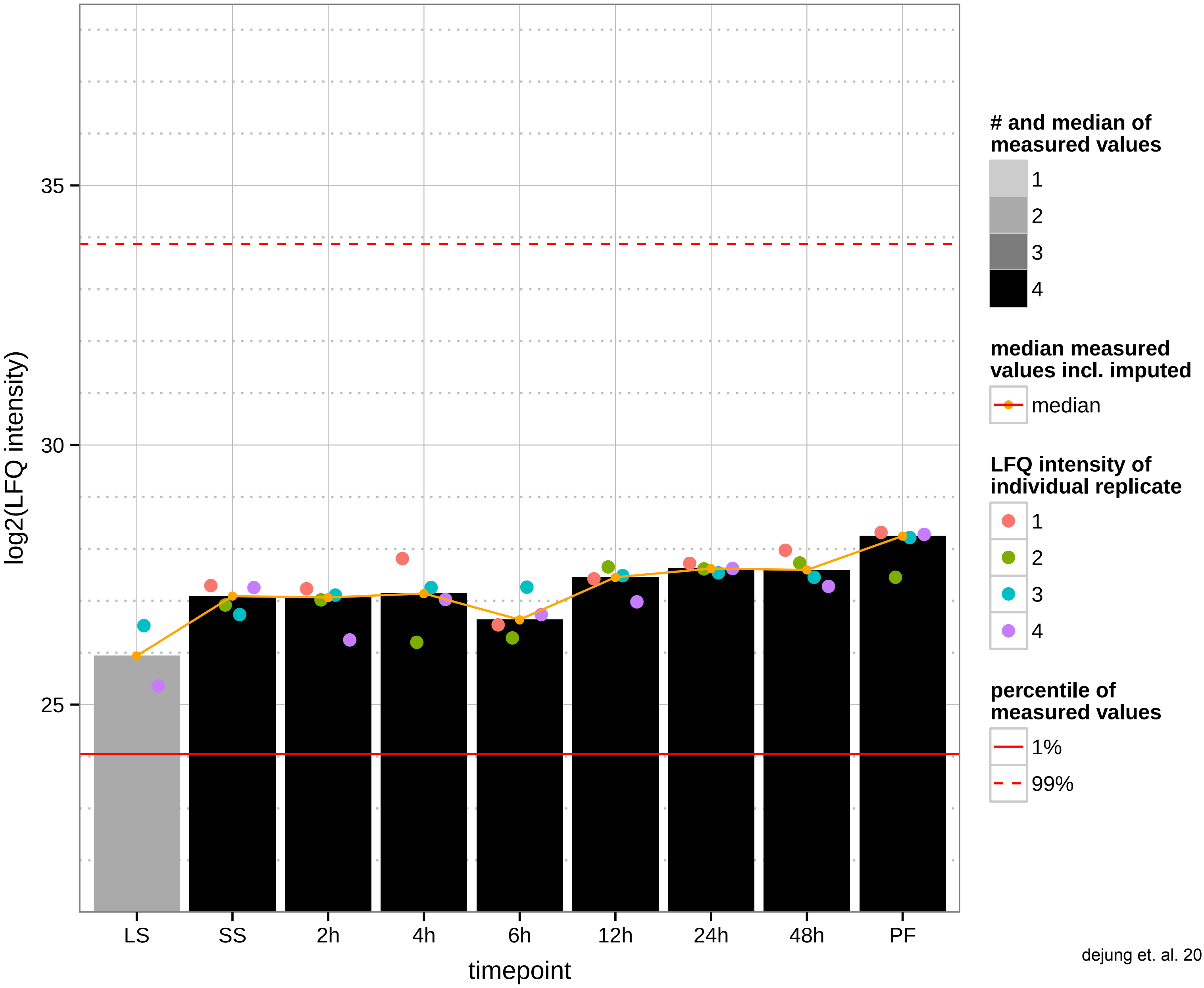
hypothetical protein, conserved
Tb927.10.14380
AGOF: ATP binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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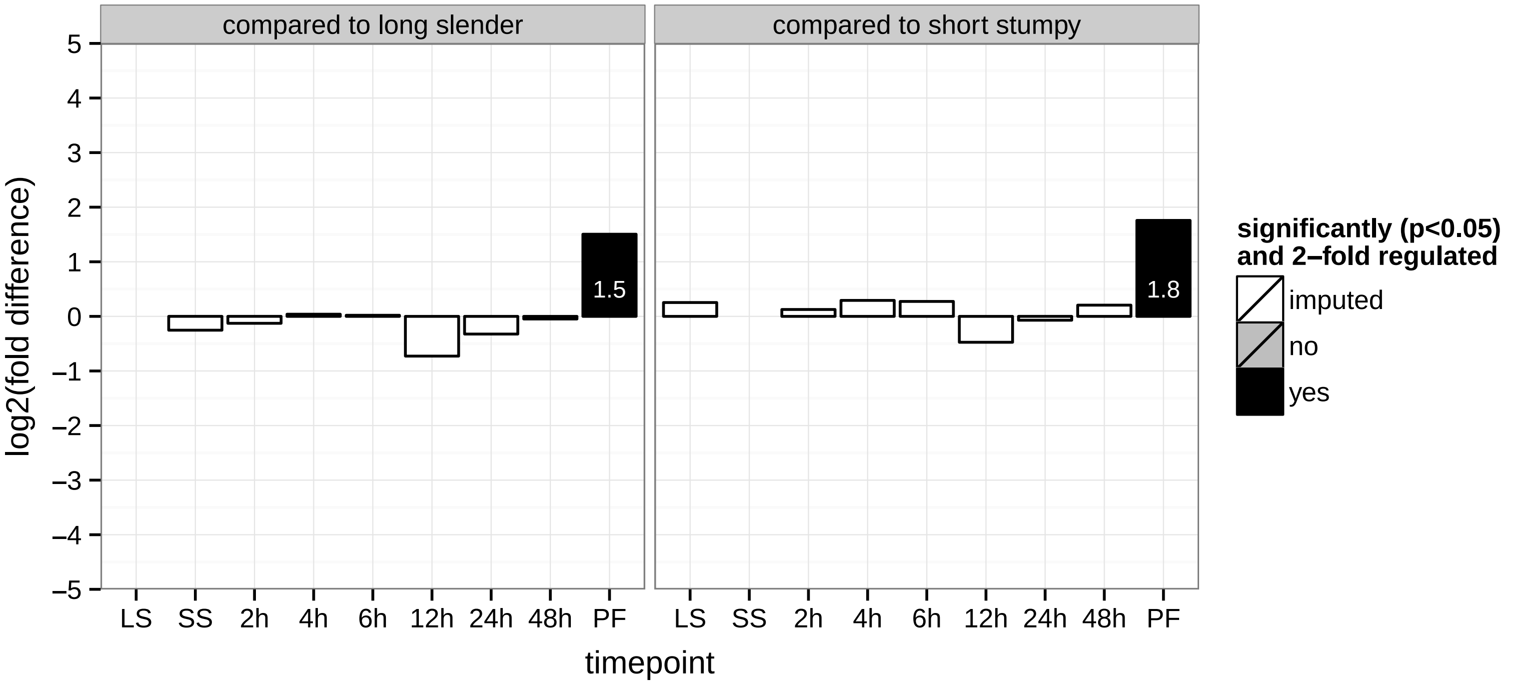
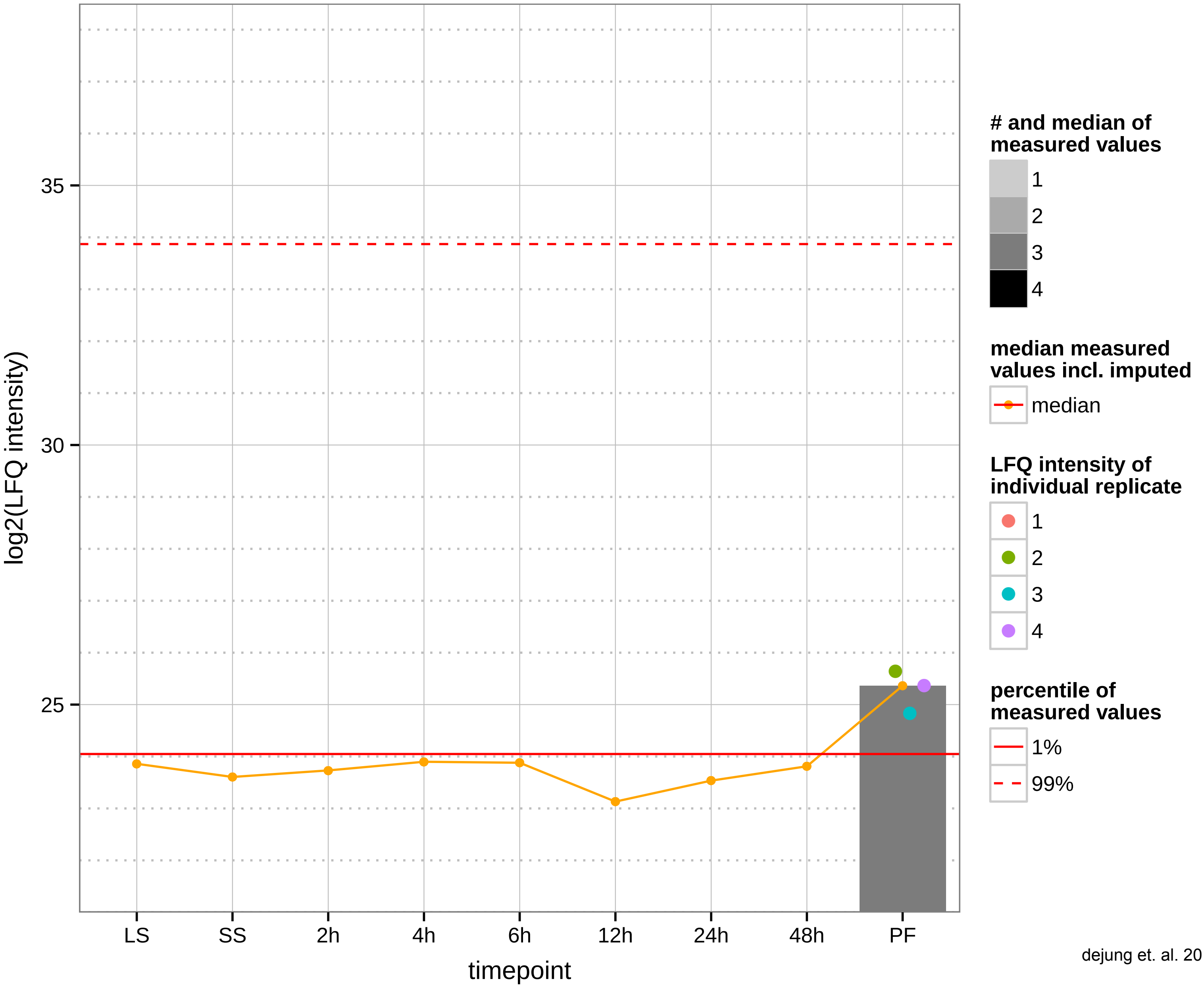
hypothetical protein, conserved
Tb927.10.14430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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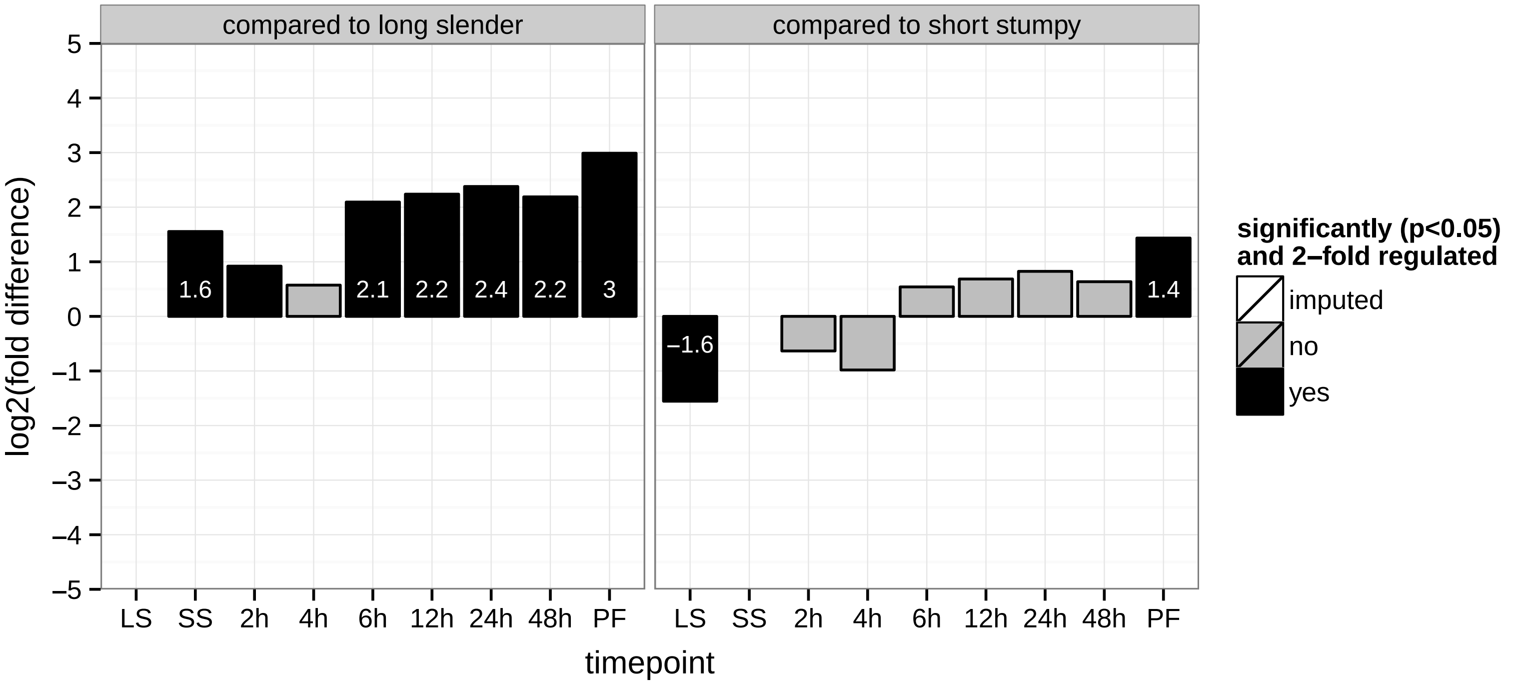
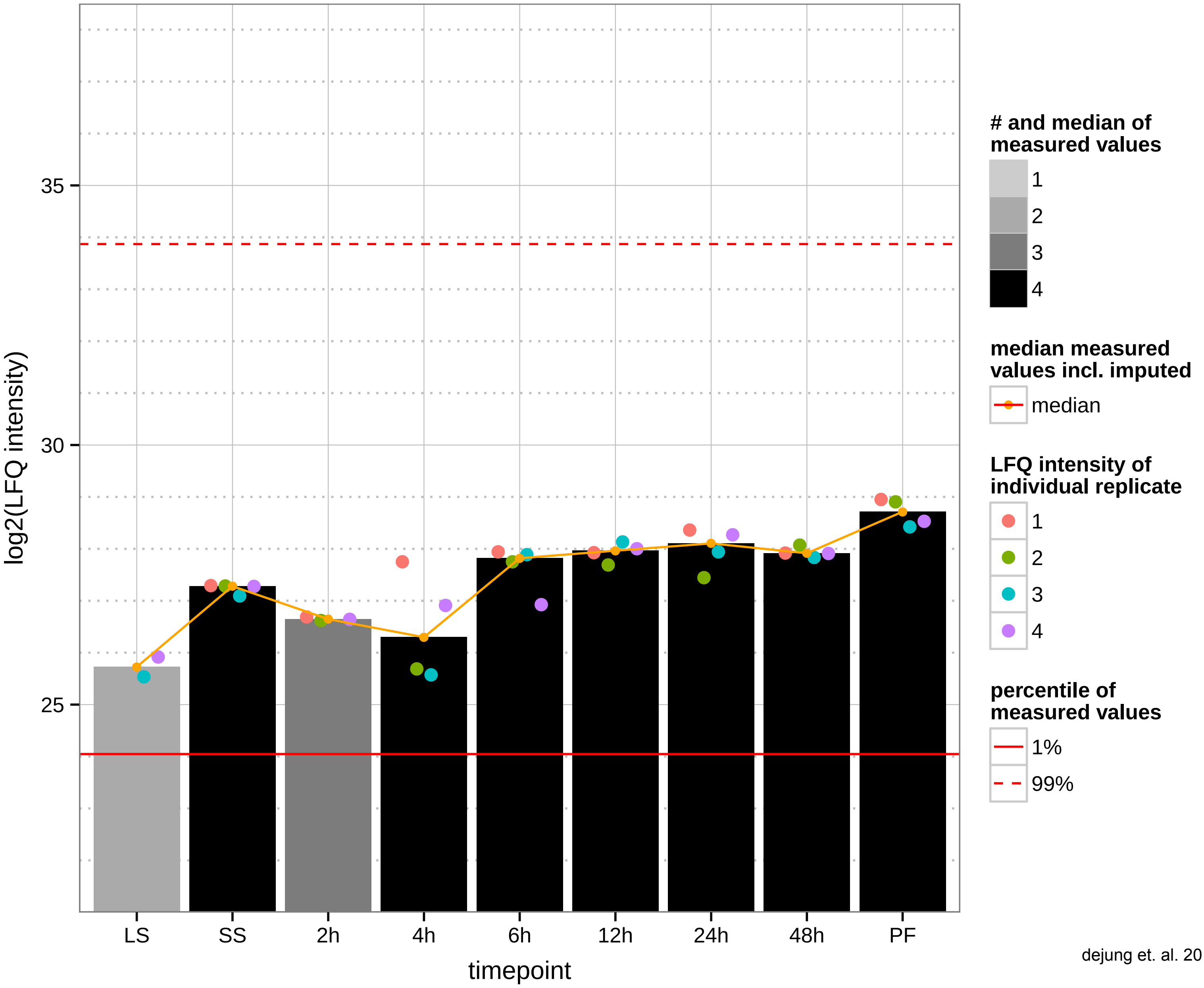
hypothetical protein, conserved
Tb927.10.14870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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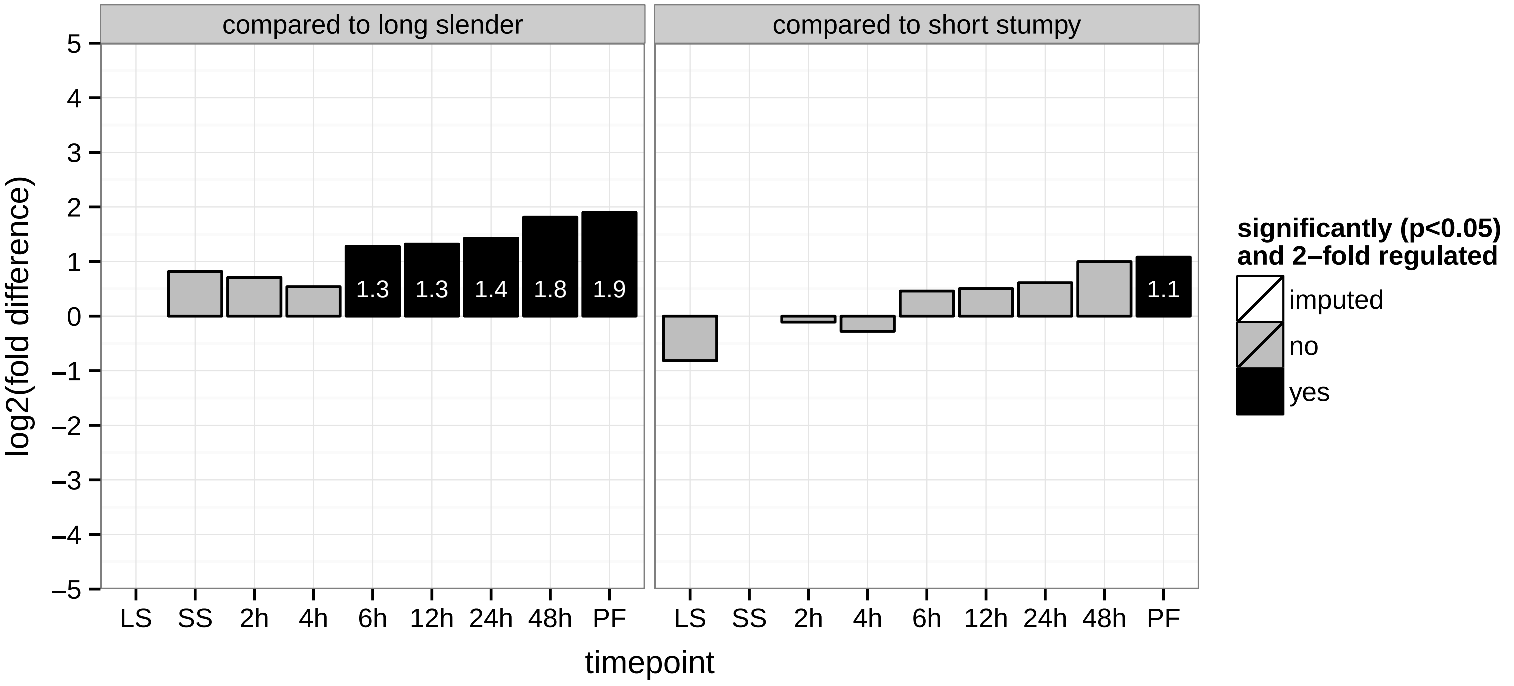
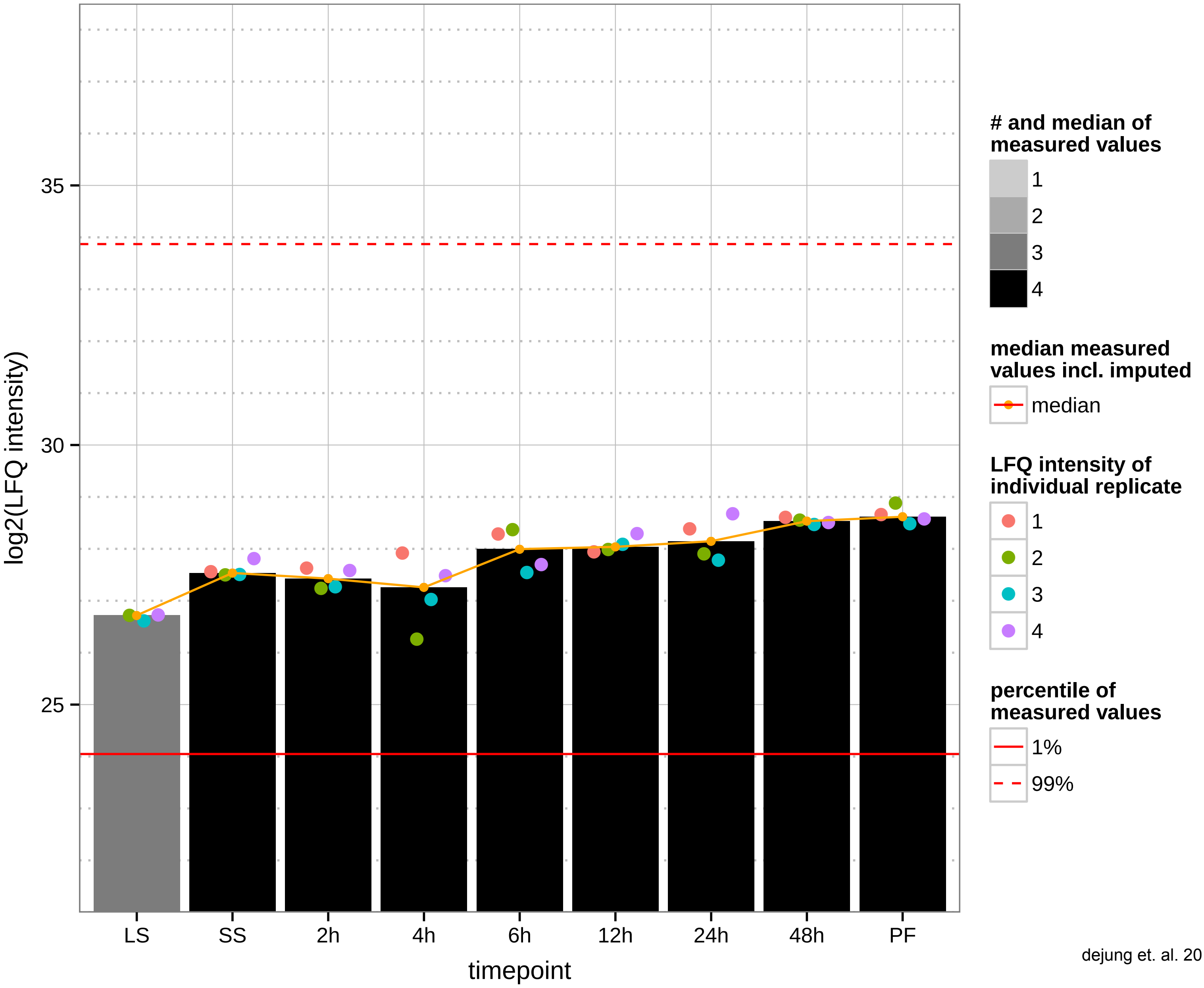
ATP−dependent DEAD/H RNA helicase, putative
Tb927.10.1720
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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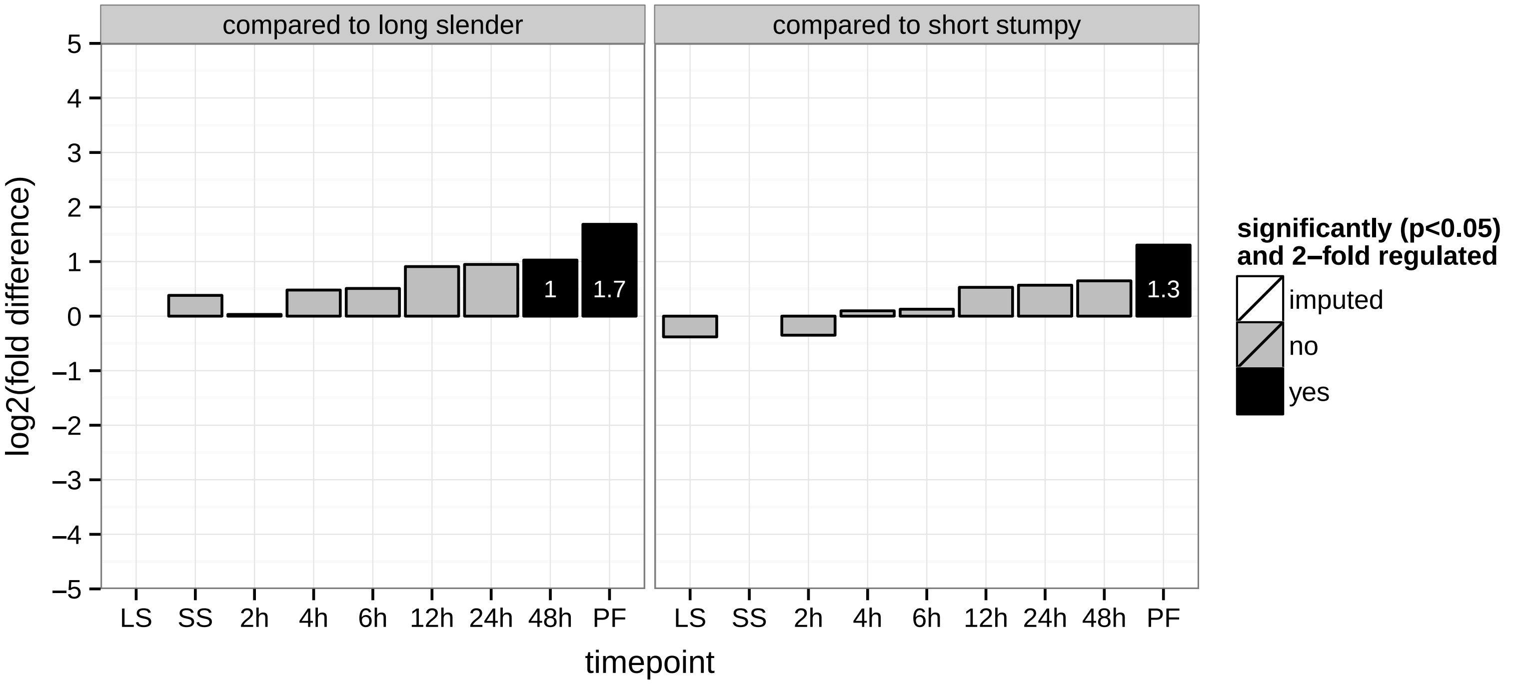
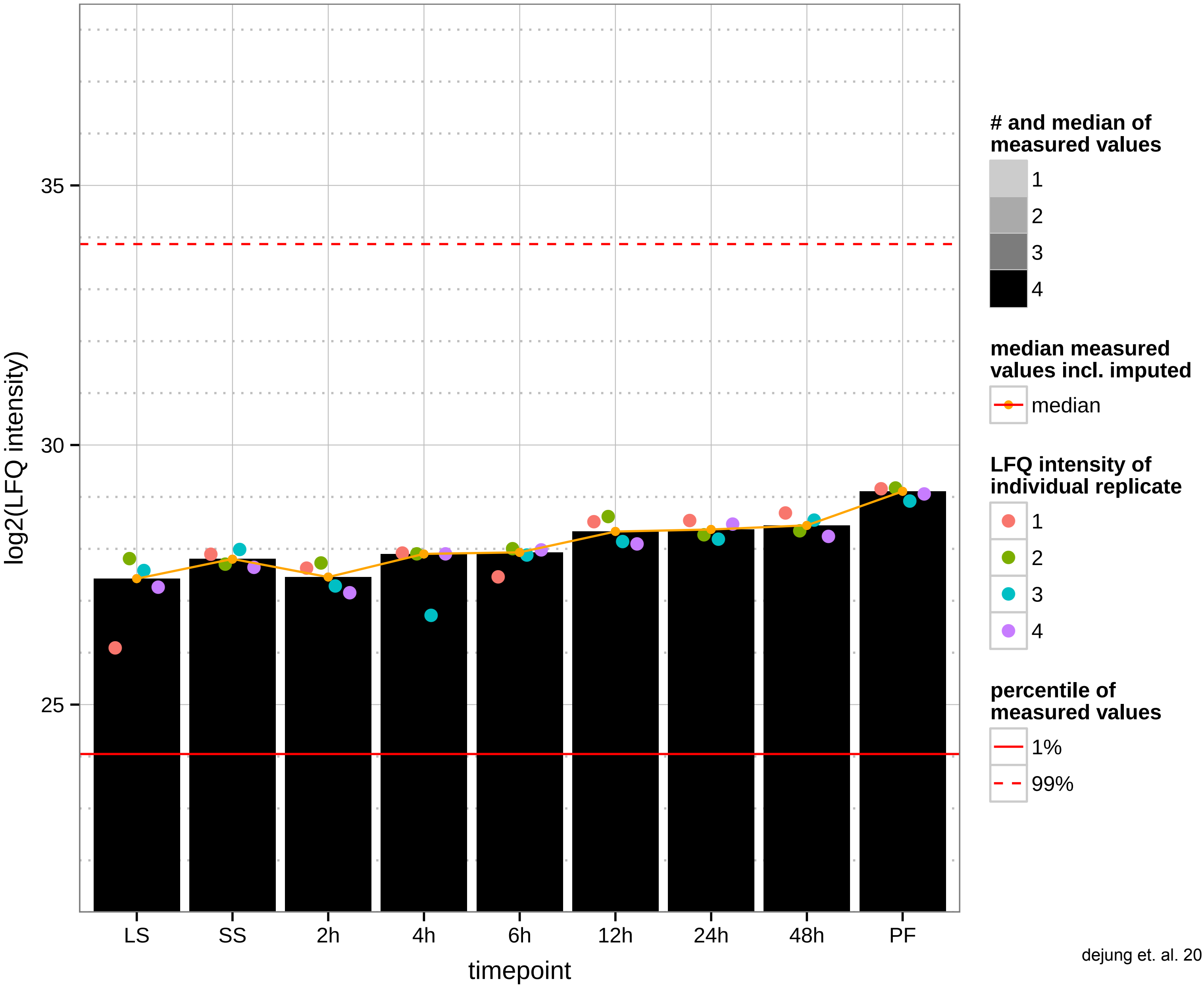
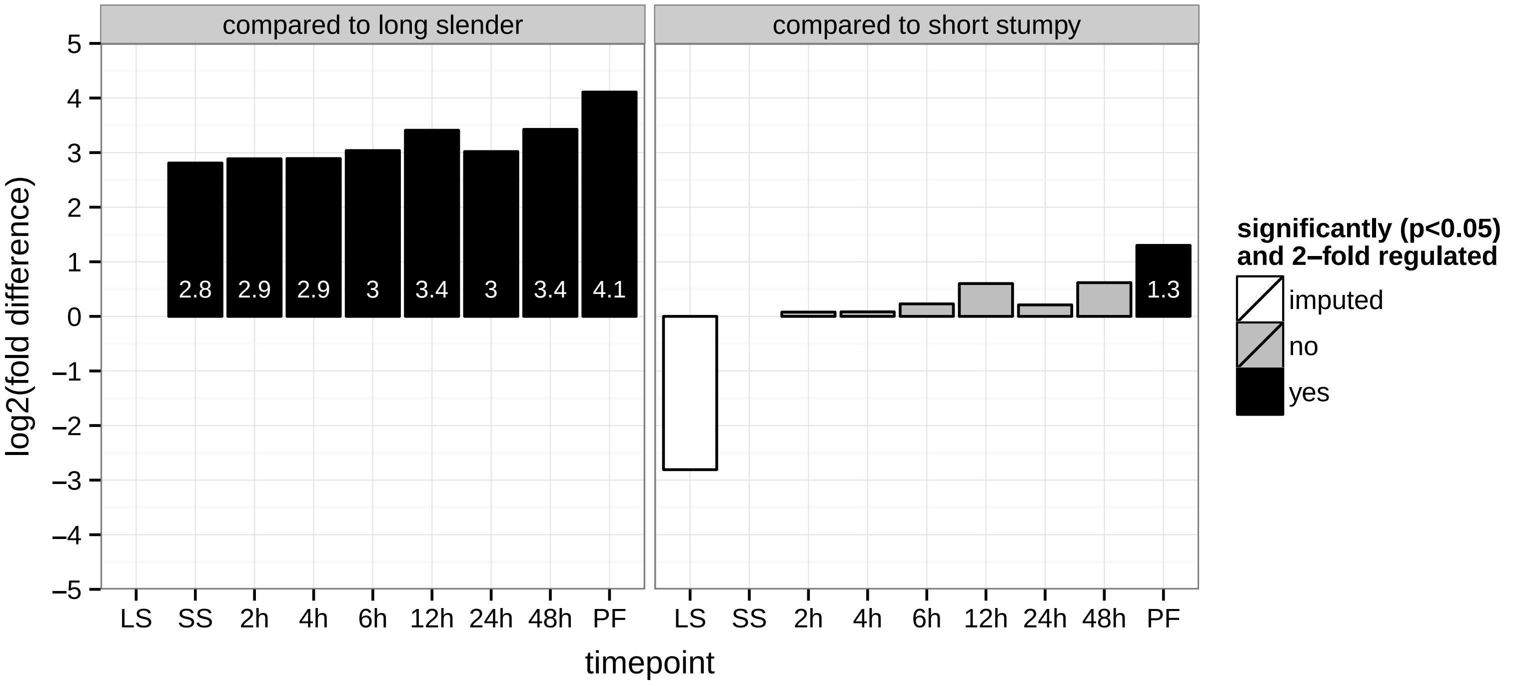
chaperone protein DNAj, putative
Tb927.10.2290
AGOF: chaperone binding, heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding, unfolded protein binding
PGOC: null
PGOP: protein folding

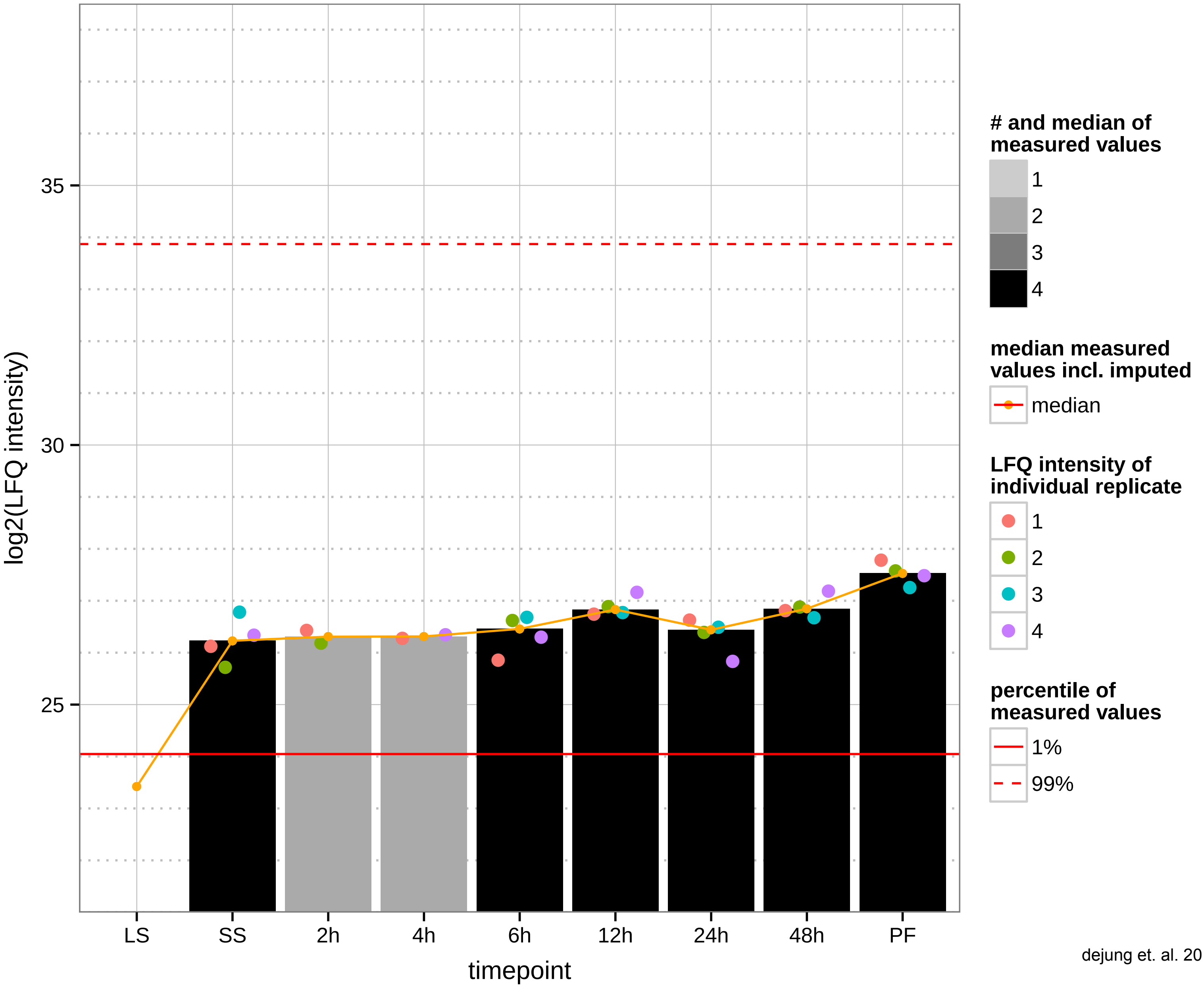




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.2320
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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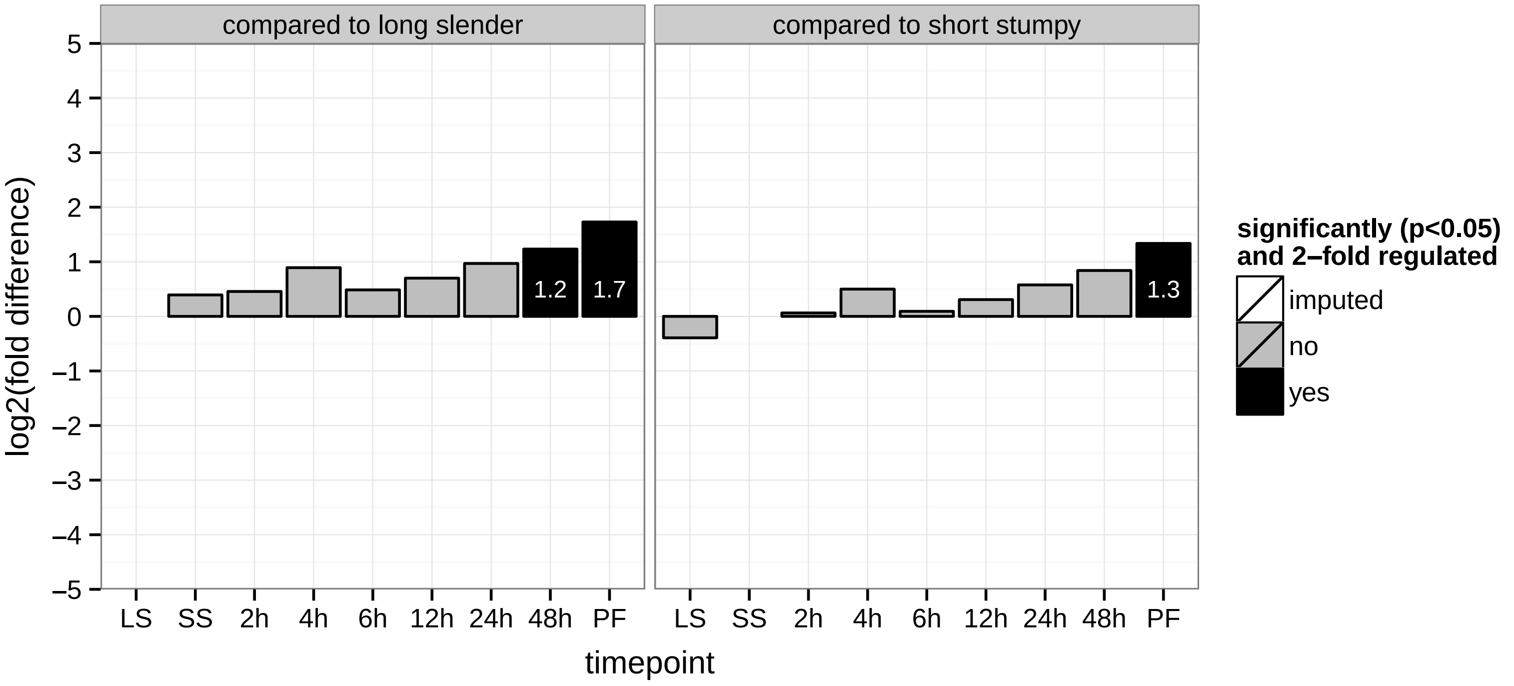
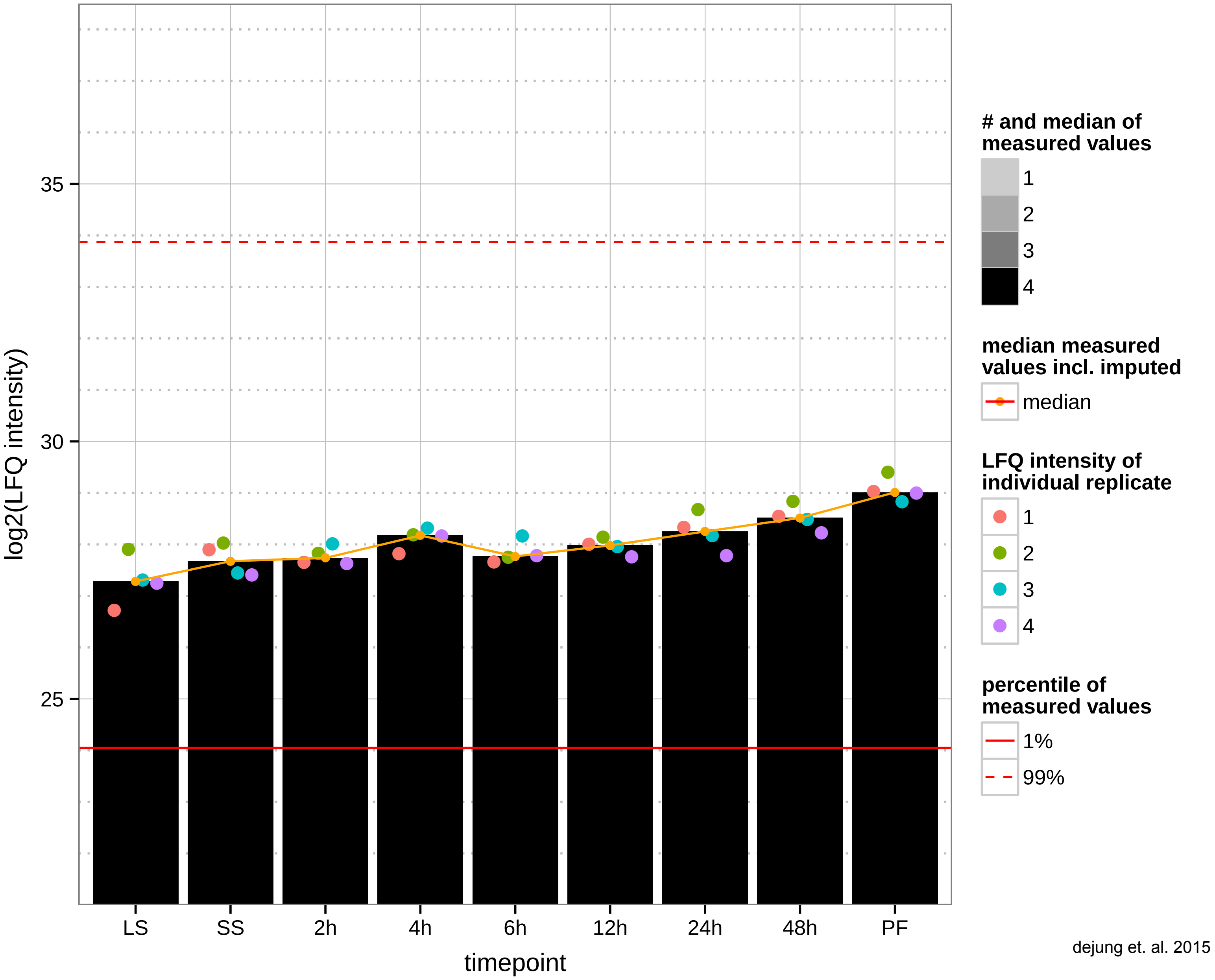
peroxin 14, putative (PEX14)
Tb927.10.240
AGOF: null
AGOC: glycosome membrane, peroxisome
AGOP: protein targeting to vacuole
PGOF: null
PGOC: null
PGOP: null





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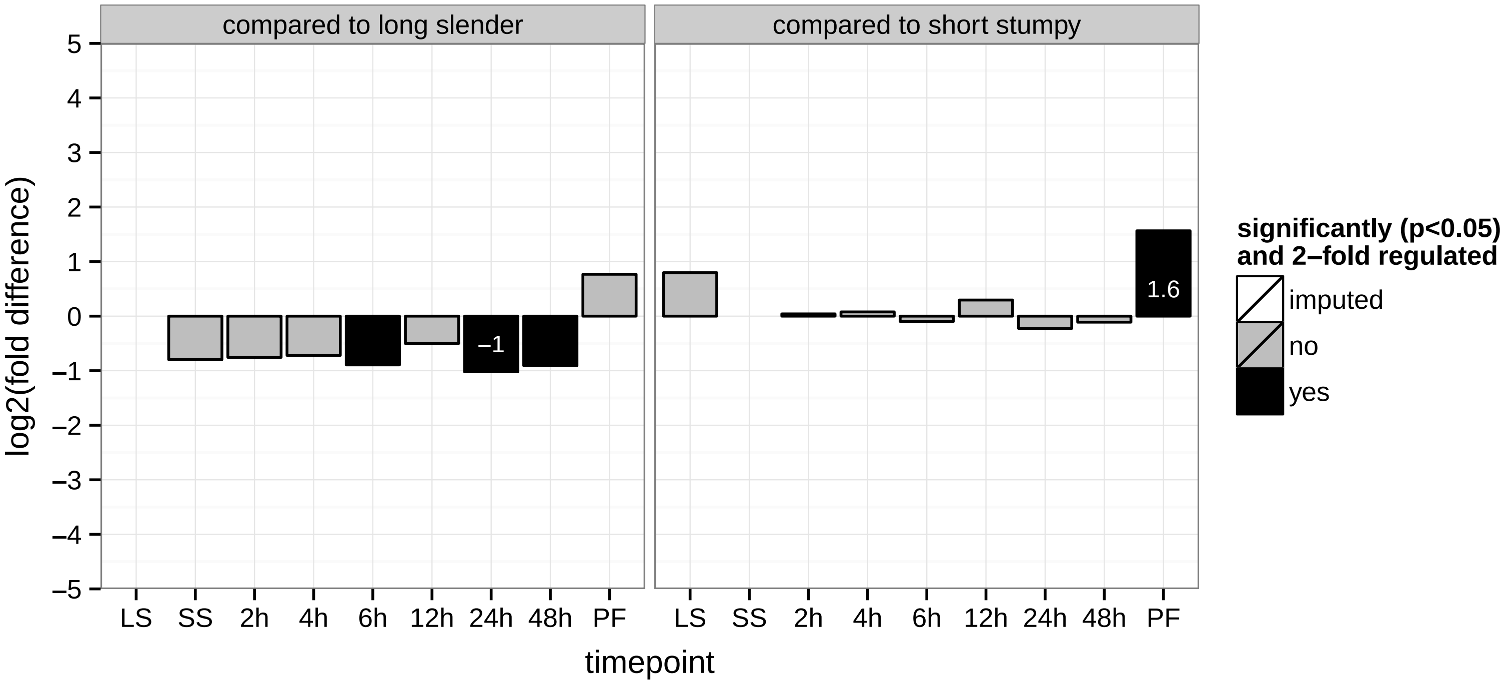
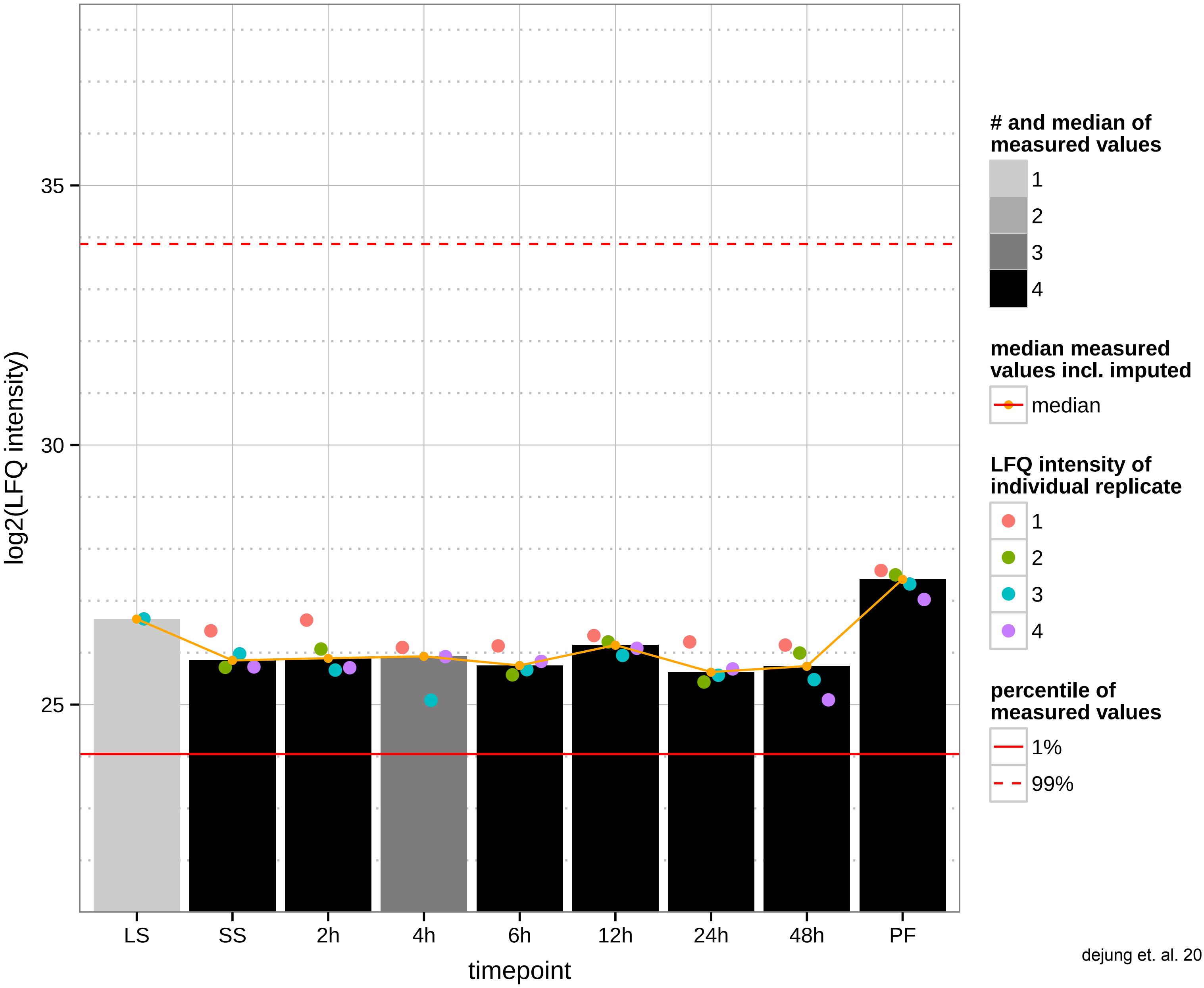
nuclear cap binding complex subunit CBP110, putative, hypothetical protein, conserved (CBP110), nuclear cap binding compl
Tb927.10.2990;Tb11.v5.1039
AGOF: null
AGOC: nuclear cap binding complex
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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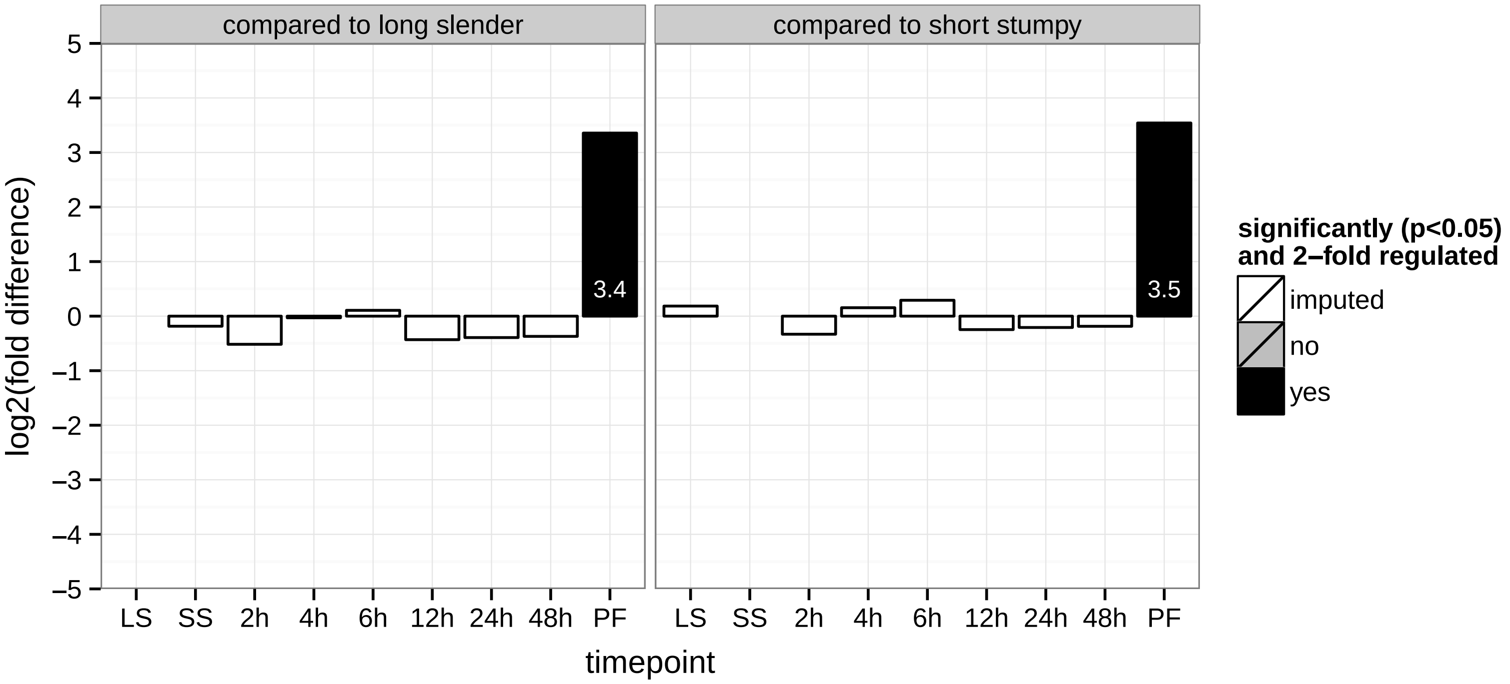
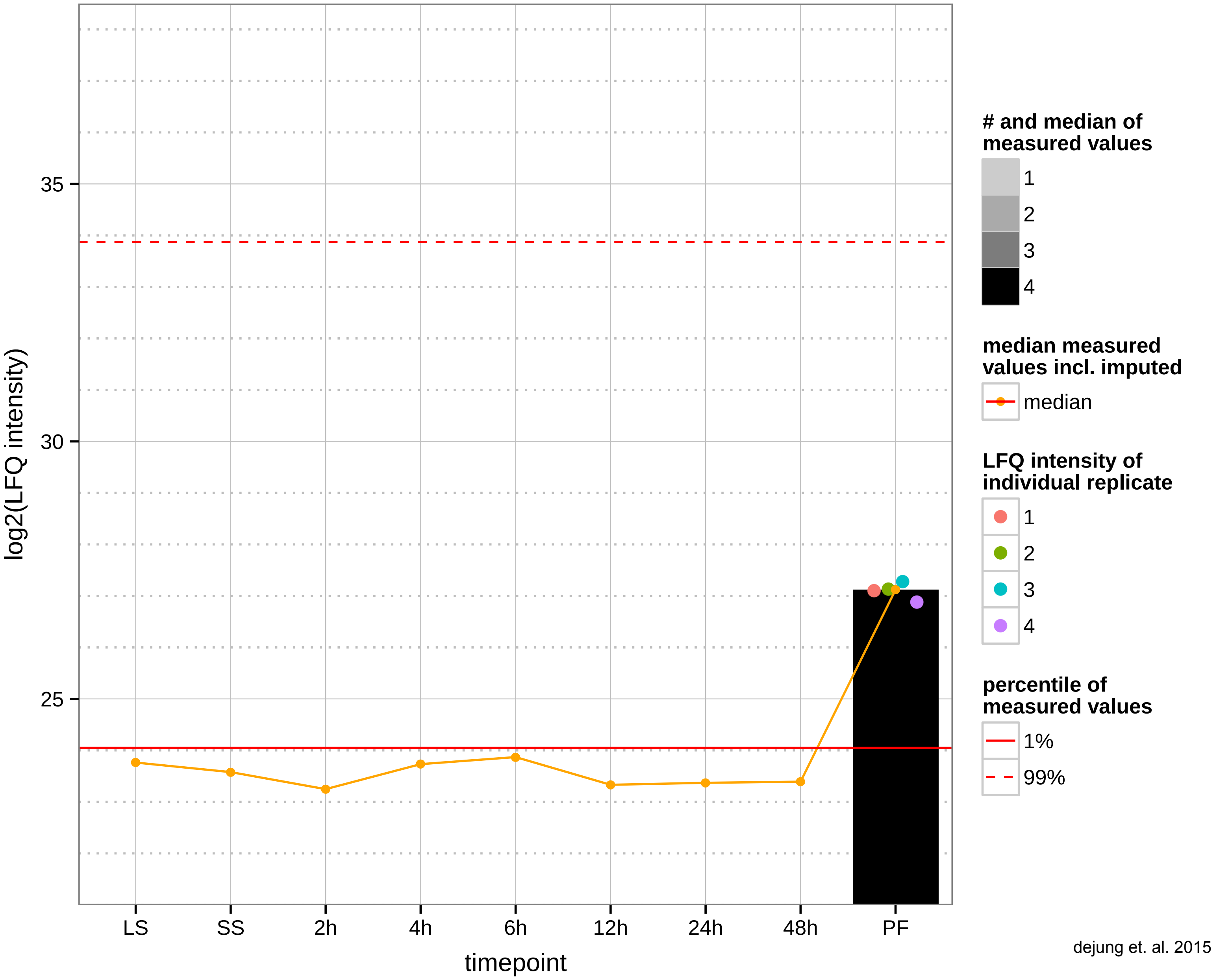
cytochrome c oxidase assembly protein, putative
Tb927.10.3120
AGOF: copper ion binding
AGOC: mitochondrion
AGOP: aerobic respiration
PGOF: copper ion binding
PGOC: null
PGOP: null





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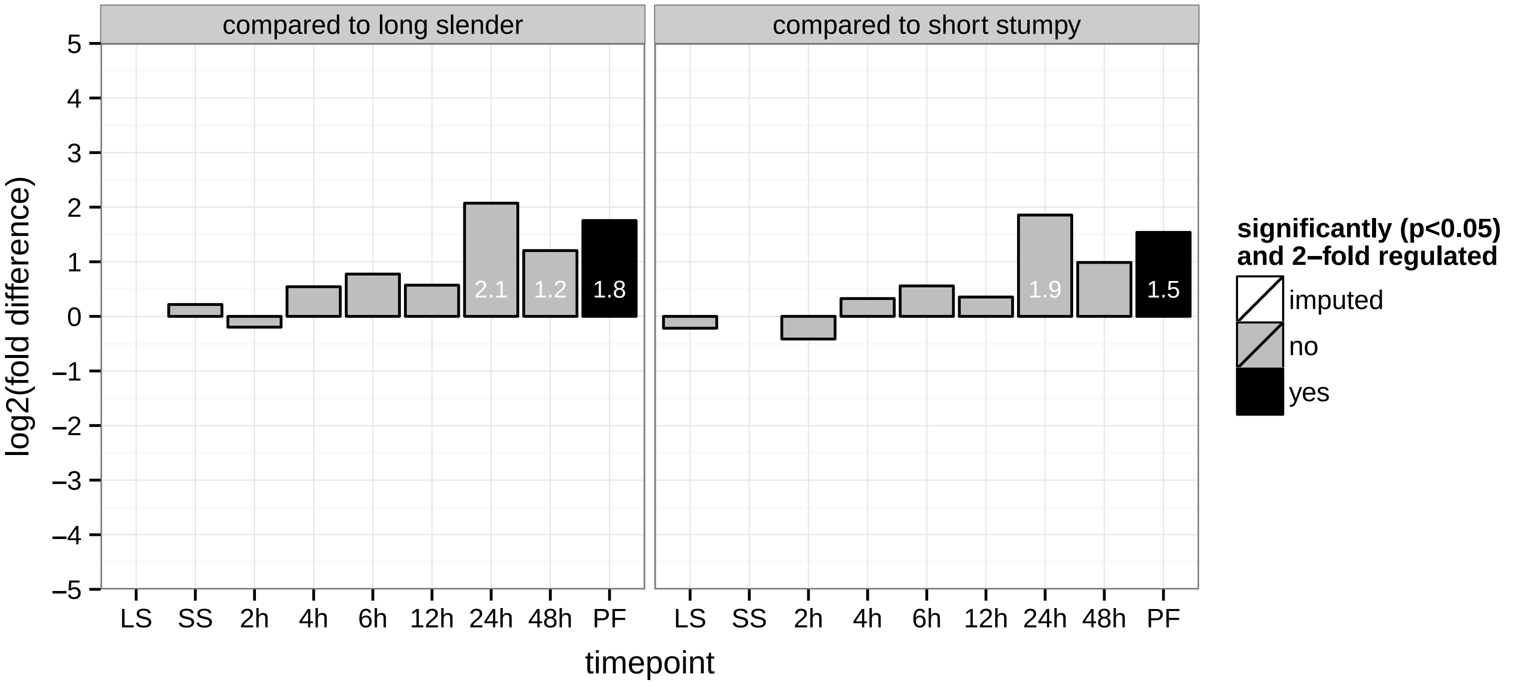
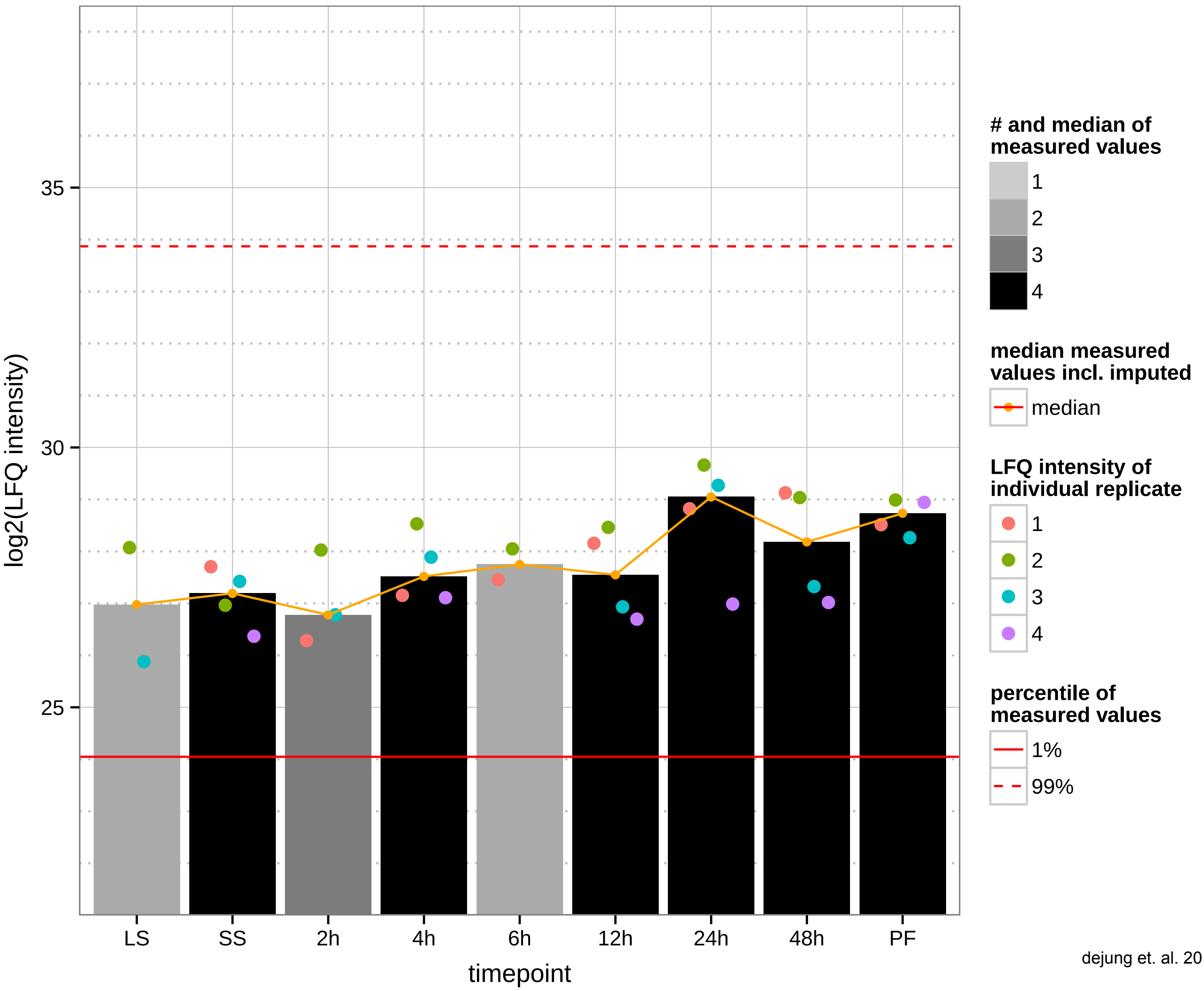
60S acidic ribosomal protein P2, putative
Tb927.10.3380;Tb927.10.3370
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation, translational elongation
PGOF: null, structural constituent of ribosome
PGOC: null, intracellular, ribosome
PGOP: null, translational elongation





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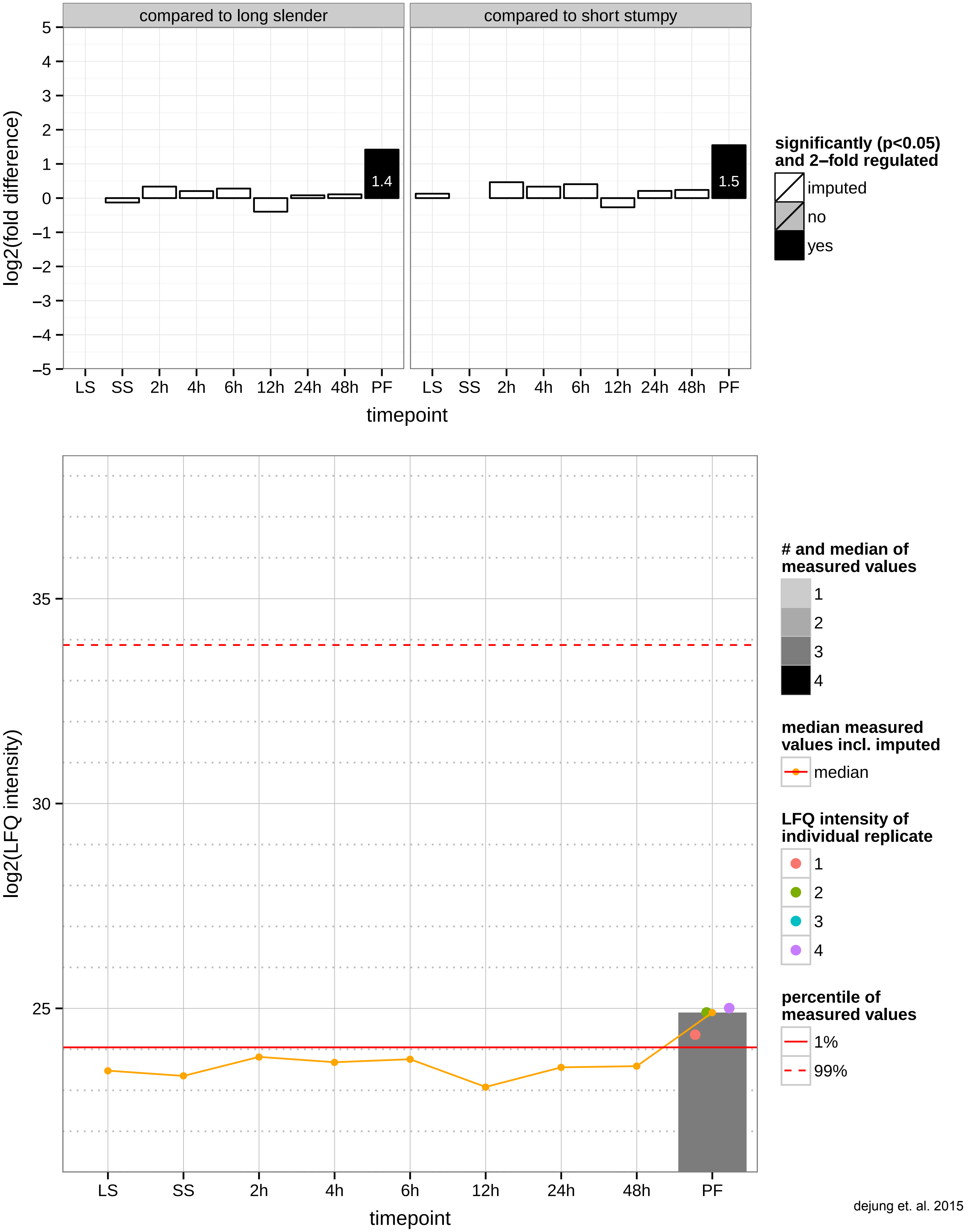
hypothetical protein, conserved
Tb927.10.3430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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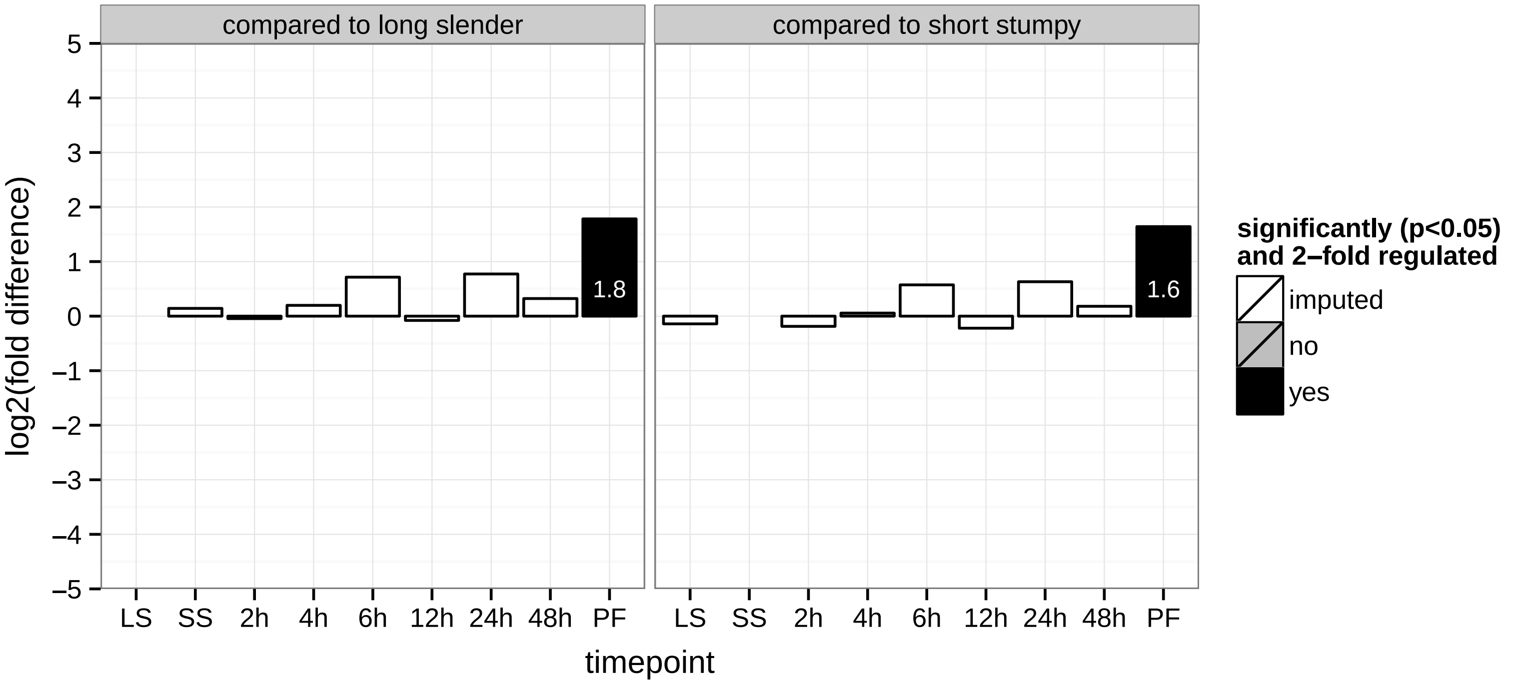
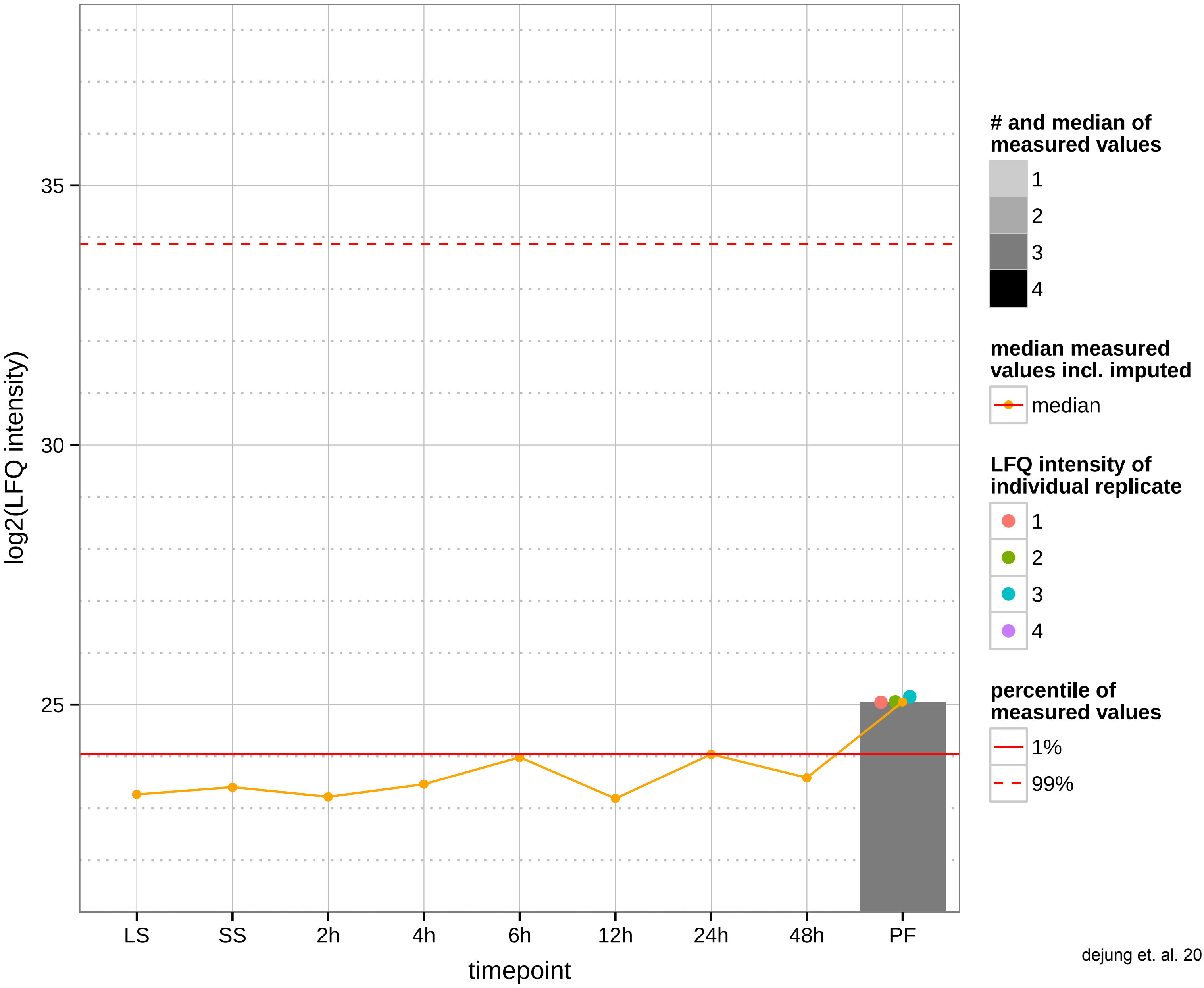
serine palmitoyltransferase, putative
Tb927.10.4050;Tb11.v5.0649
AGOF: null, pyridoxal phosphate binding, serine C−palmitoyltransferase activity, transferase activity, transferring nitrogenous g
AGOC: null
AGOP: null, biosynthetic process
PGOF: pyridoxal phosphate binding, transferase activity
PGOC: null
PGOP: biosynthetic process





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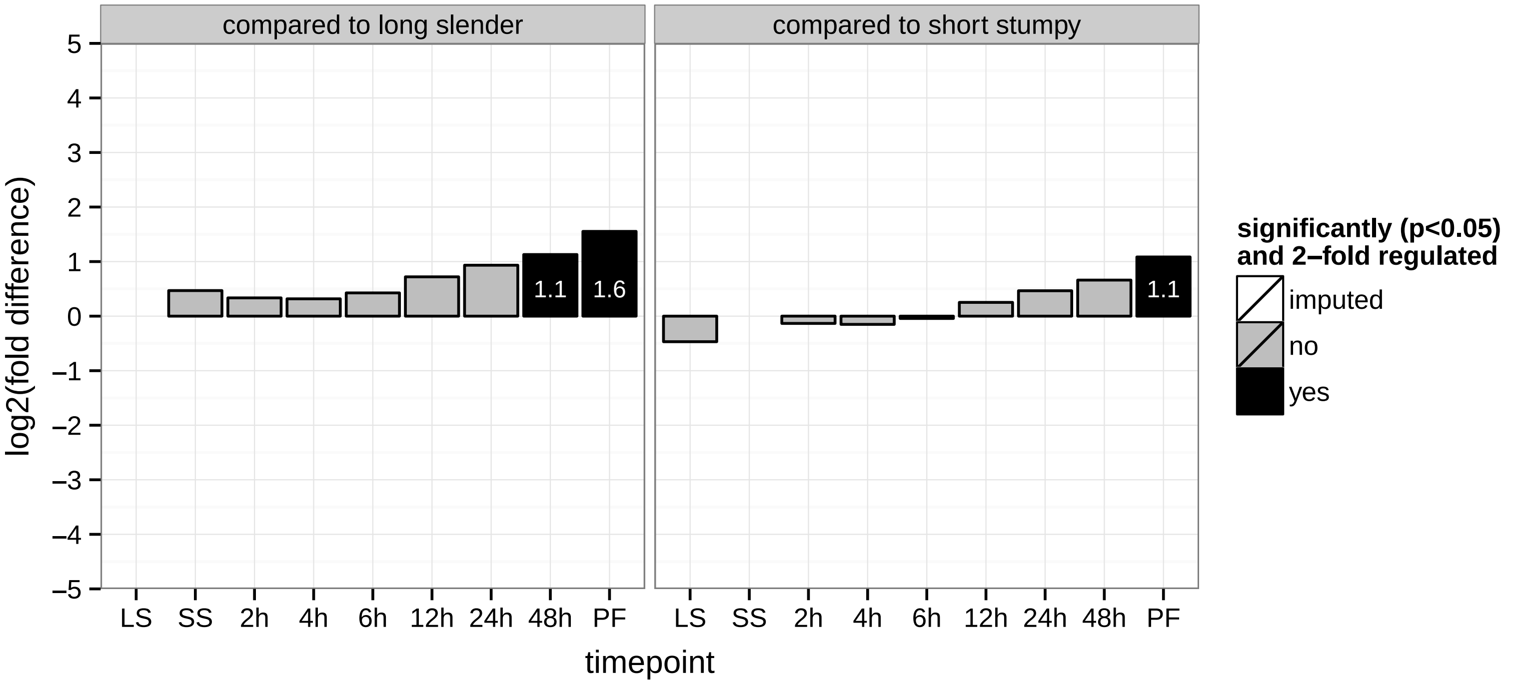
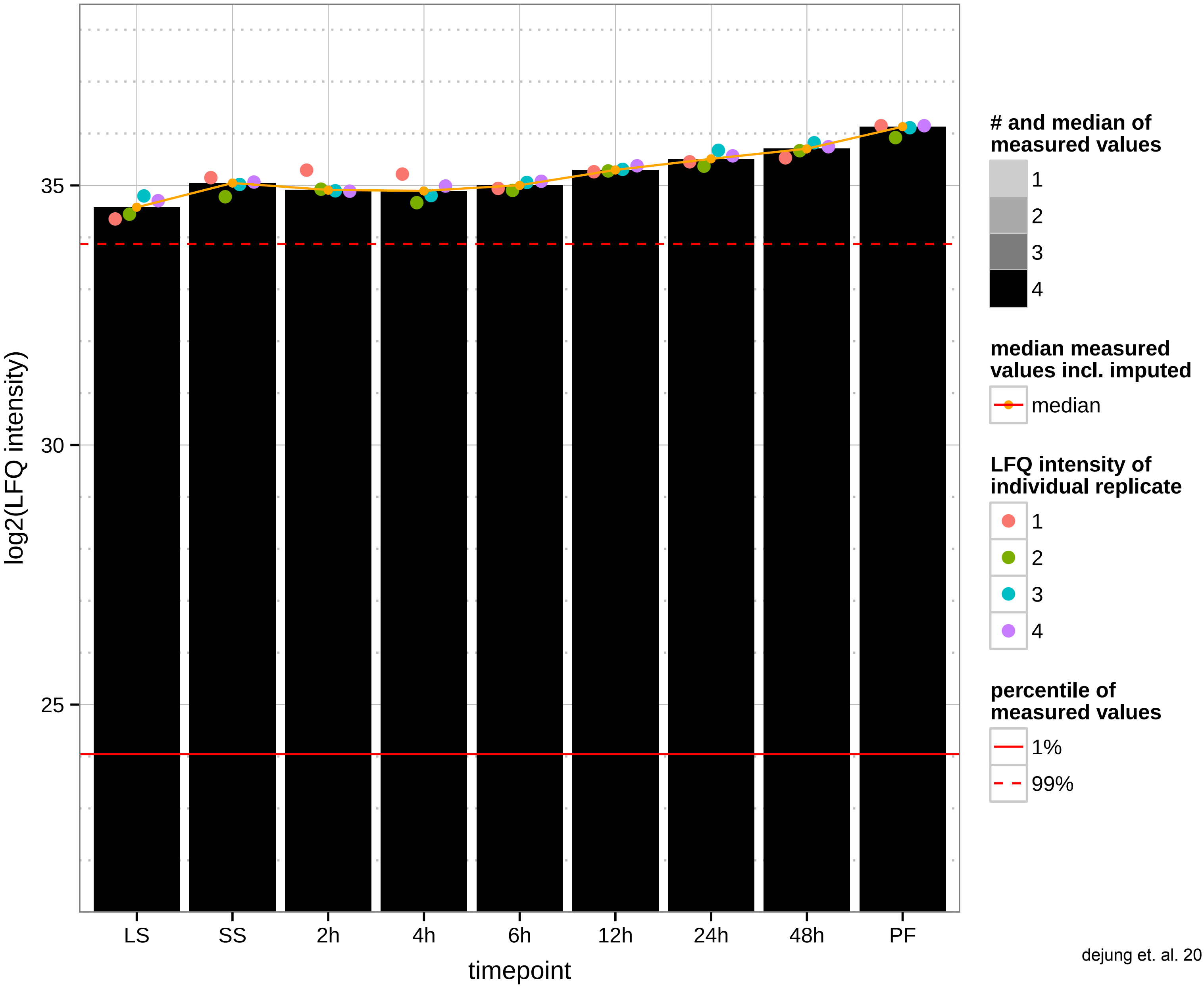
elongation factor 2
Tb927.10.4570;Tb927.10.4560
AGOF: GTP binding, GTPase activity
AGOC: null
AGOP: translation
PGOF: null, GTP binding, GTPase activity
PGOC: null
PGOP: null





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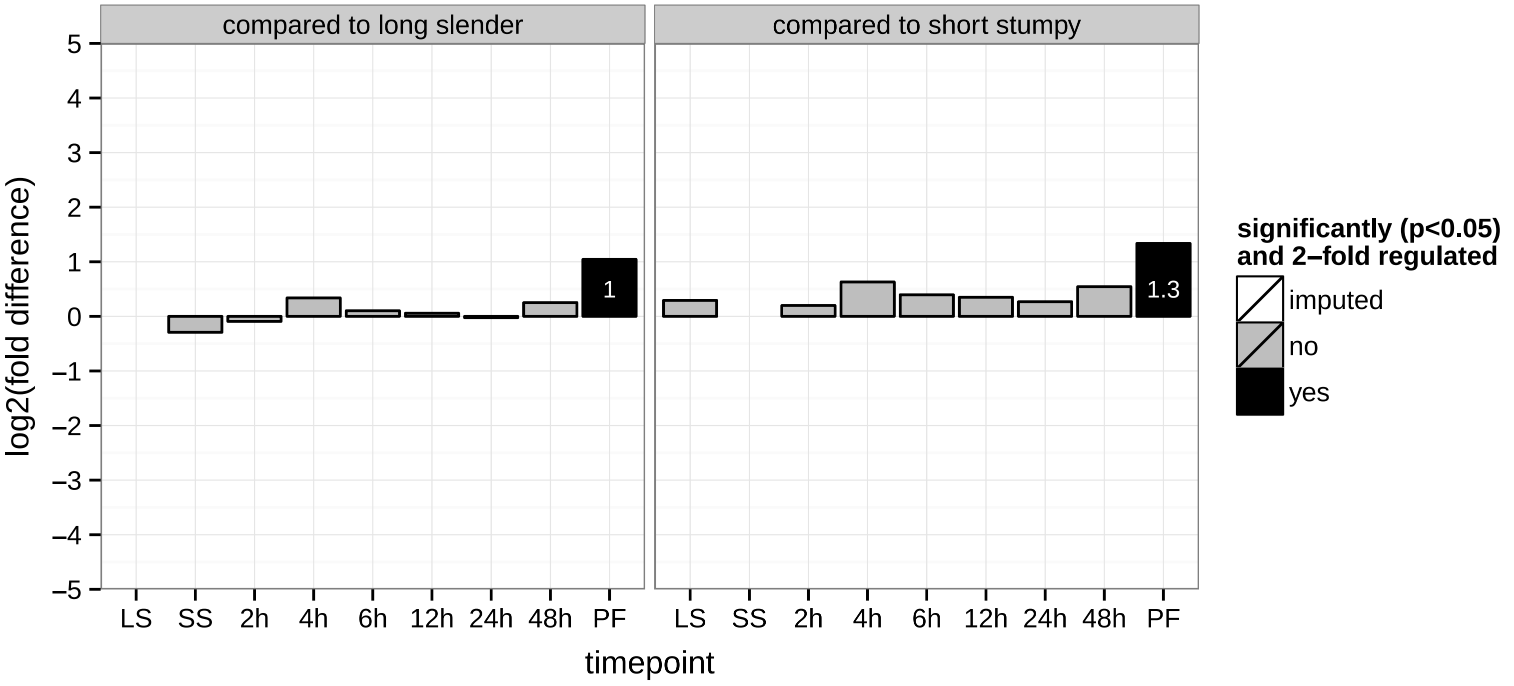
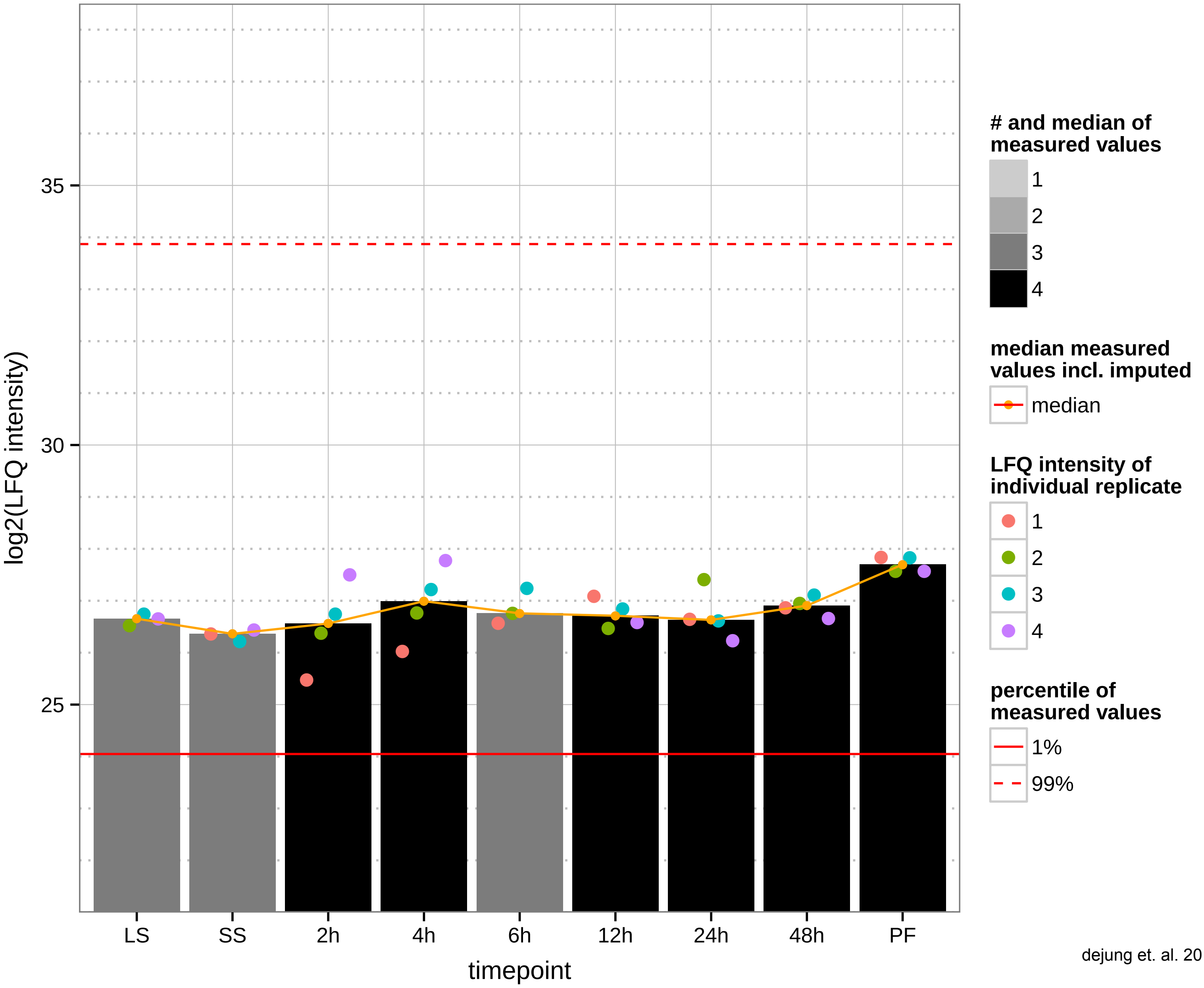
nucleolar RNA–binding protein, putative
Tb927.10.4740
AGOF: RNA binding
AGOC: nucleolus
AGOP: rRNA metabolic process
PGOF: null
PGOC: null
PGOP: null





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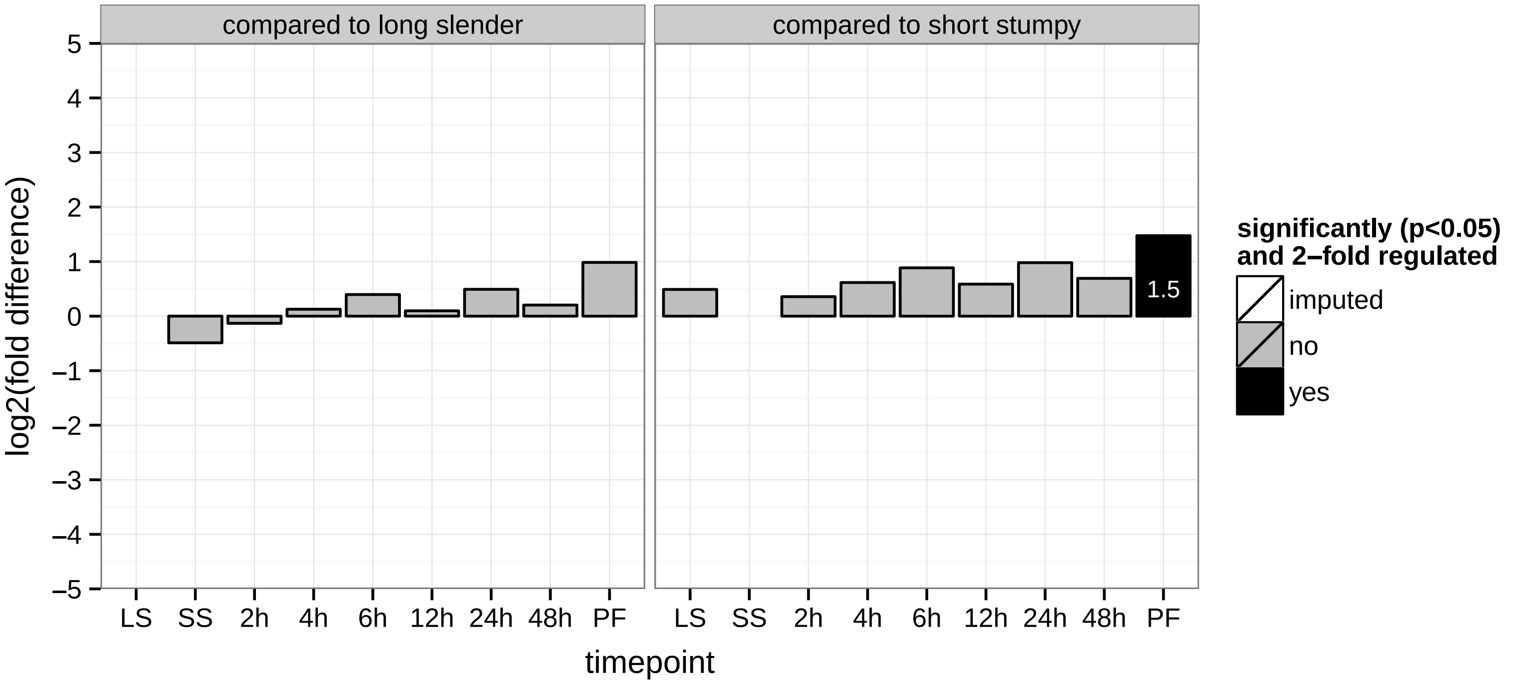
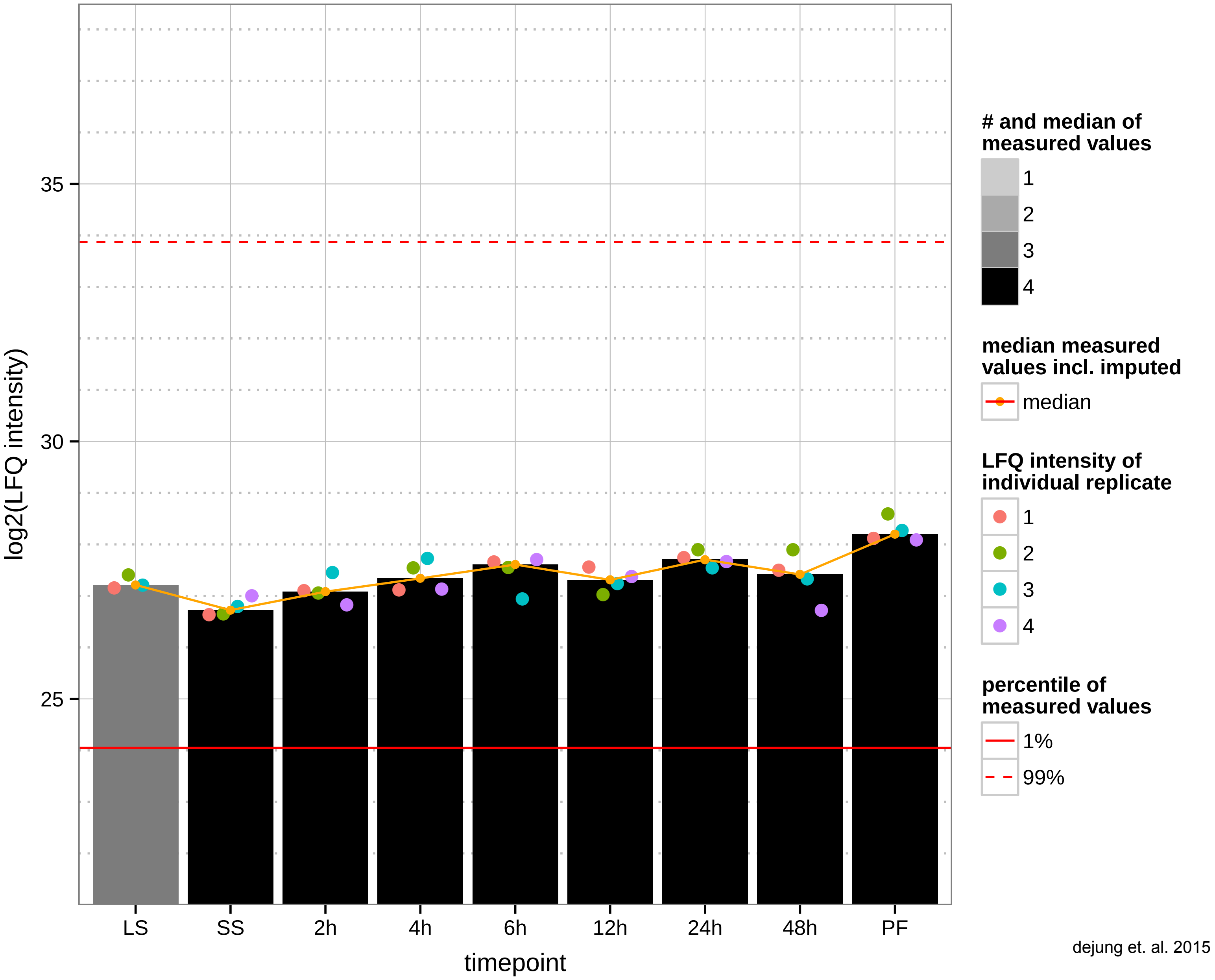
hypothetical protein, conserved
Tb927.10.4760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: membrane
PGOP: null





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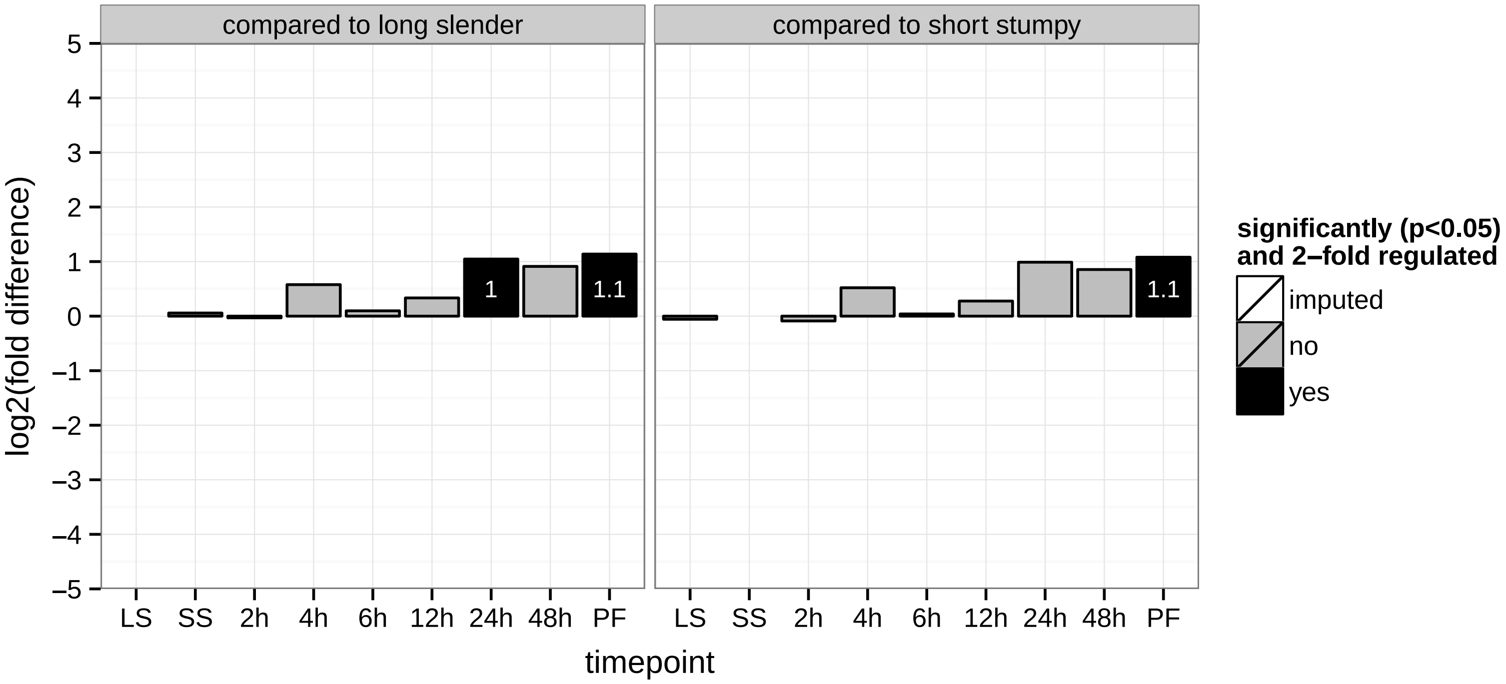
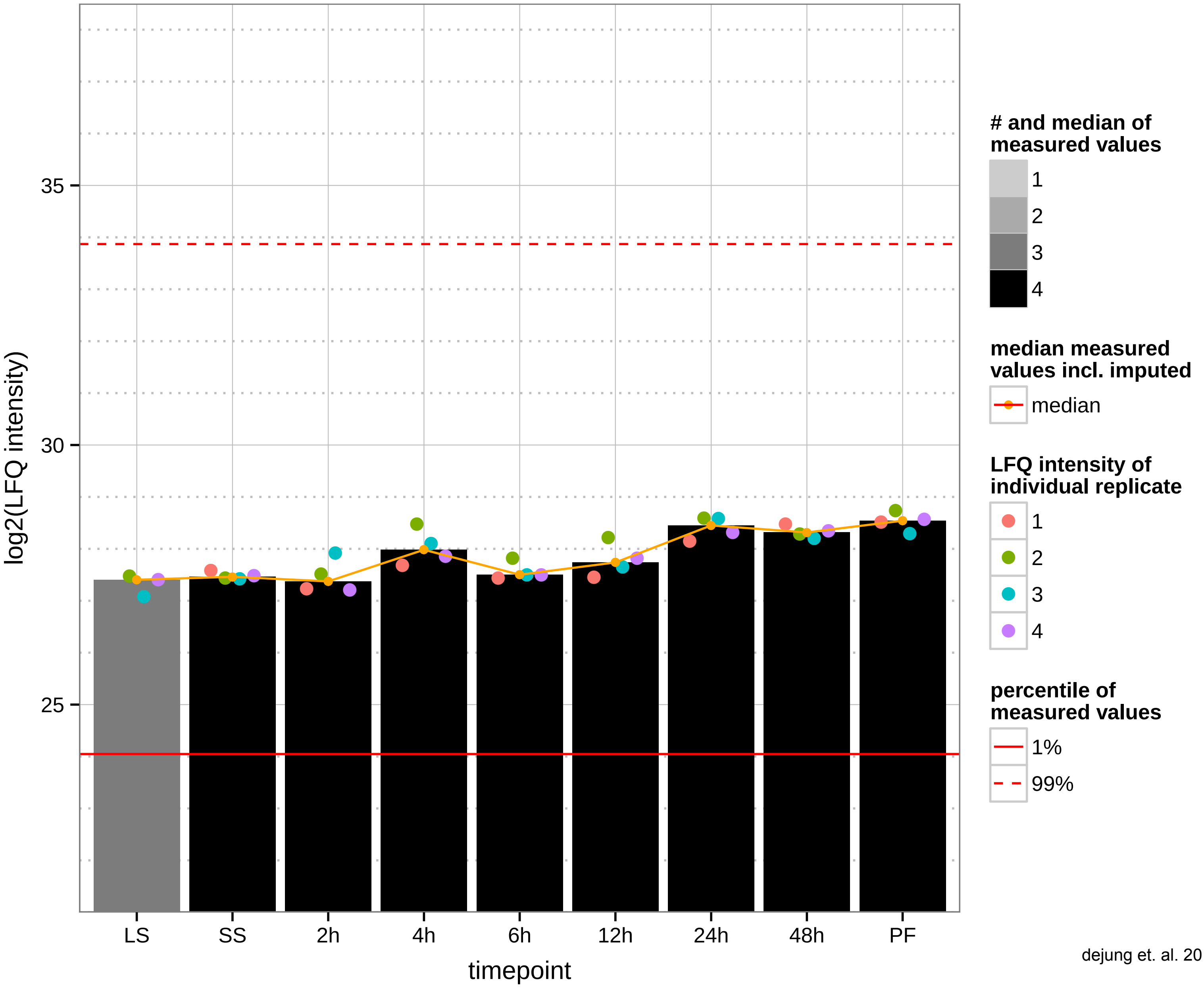
Eukaryotic translation initiation factor 4E type 5 (eif4e5)
Tb927.10.5020
AGOF: RNA 7−methylguanosine cap binding, RNA cap 4 binding, protein binding, translation initiation factor activity
AGOC: cytoplasm, eukaryotic translation initiation factor 4F complex
AGOP: cell motility, translation, translational initiation
PGOF: RNA binding, translation initiation factor activity
PGOC: cytoplasm
PGOP: translational initiation





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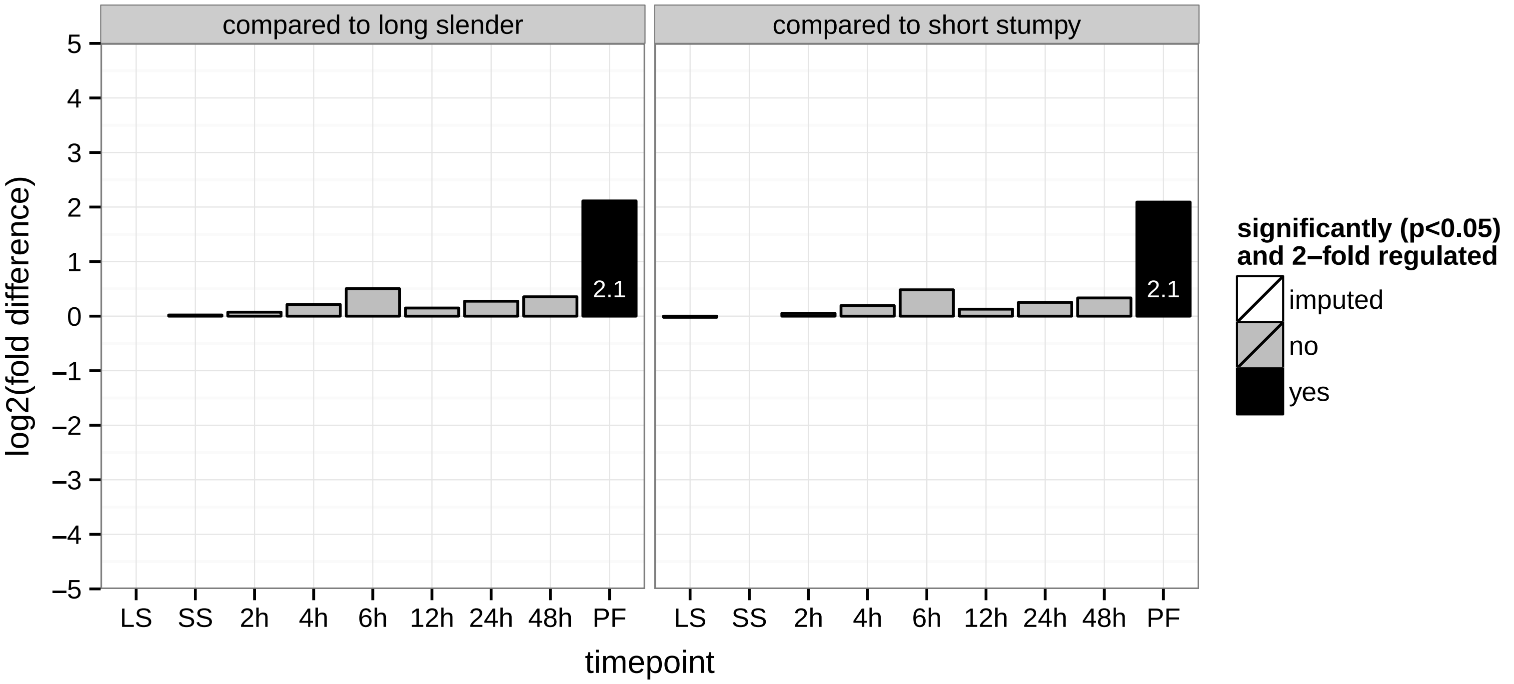
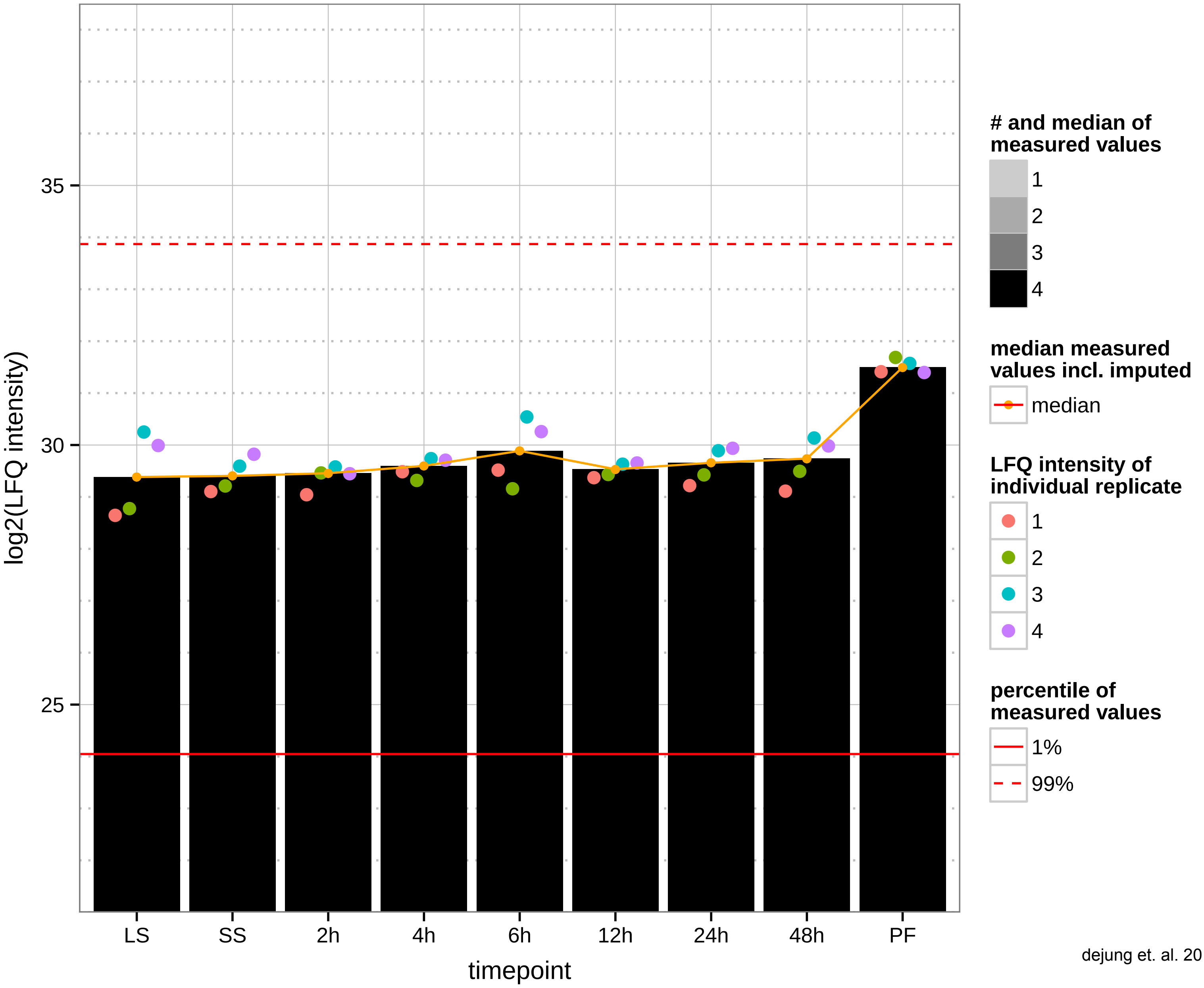
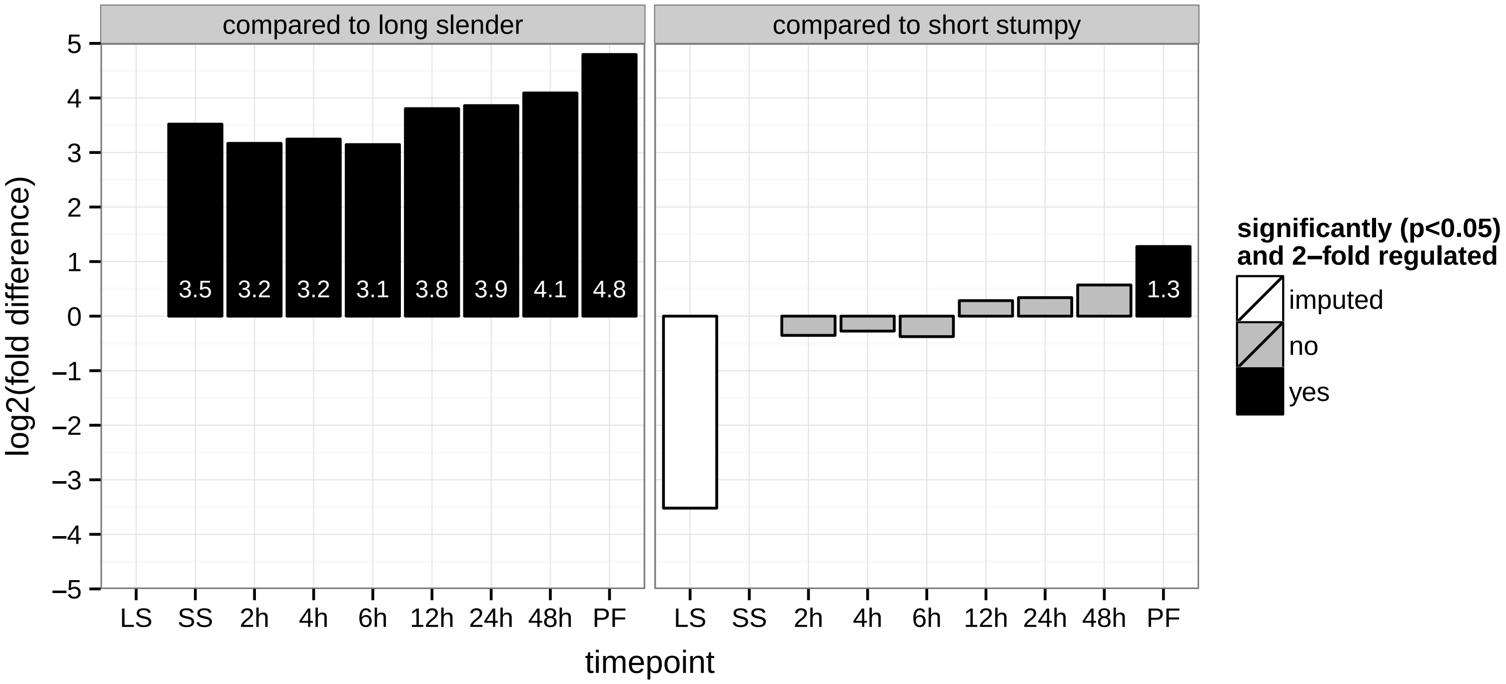
ubiquitin/ribosomal protein S27a, putative
Tb927.10.5030;Tb927.7.3680
AGOF: heme binding, structural constituent of ribosome, structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: ribosome biogenesis, translation, translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation

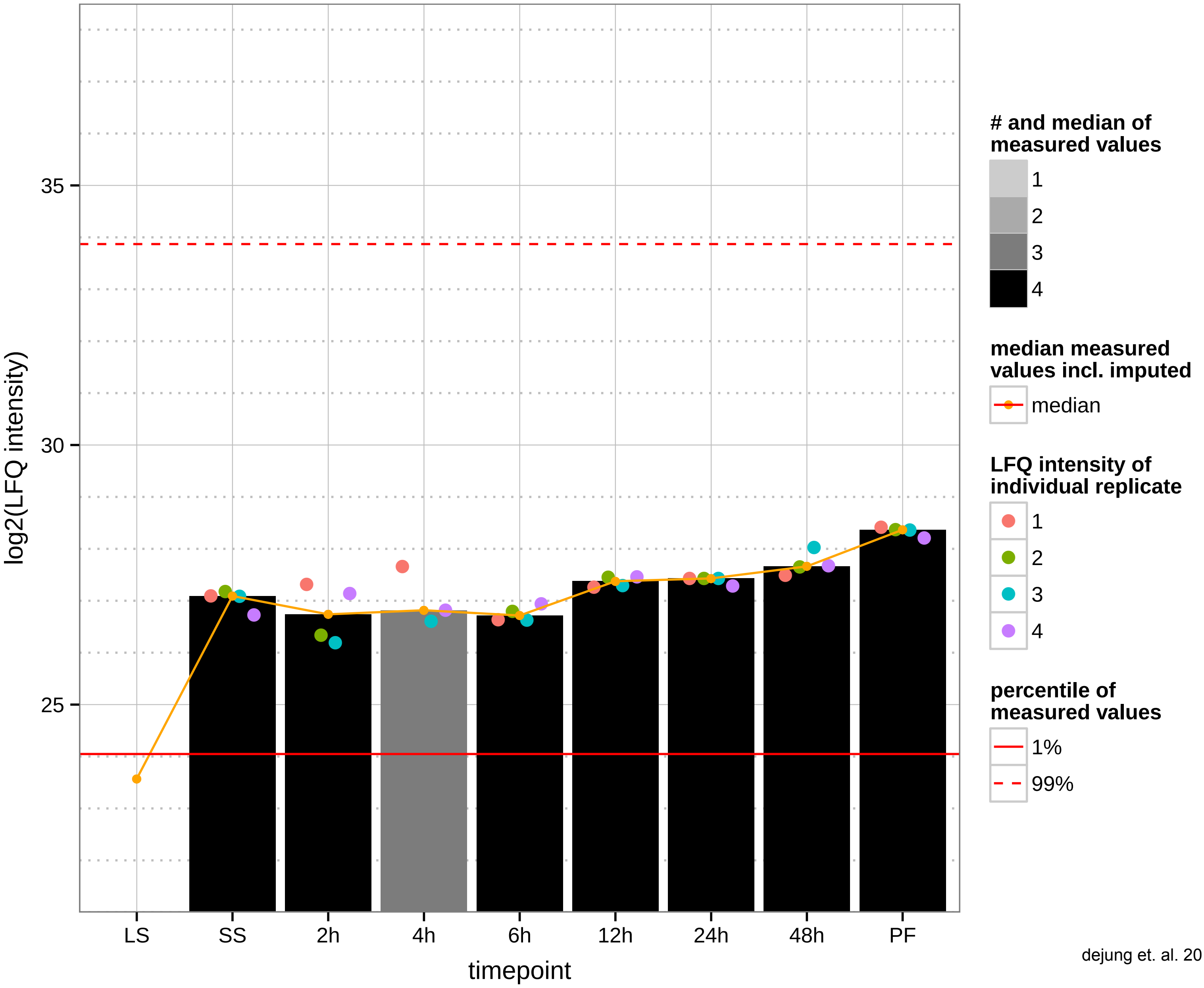




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.510;Tb11.v5.0374
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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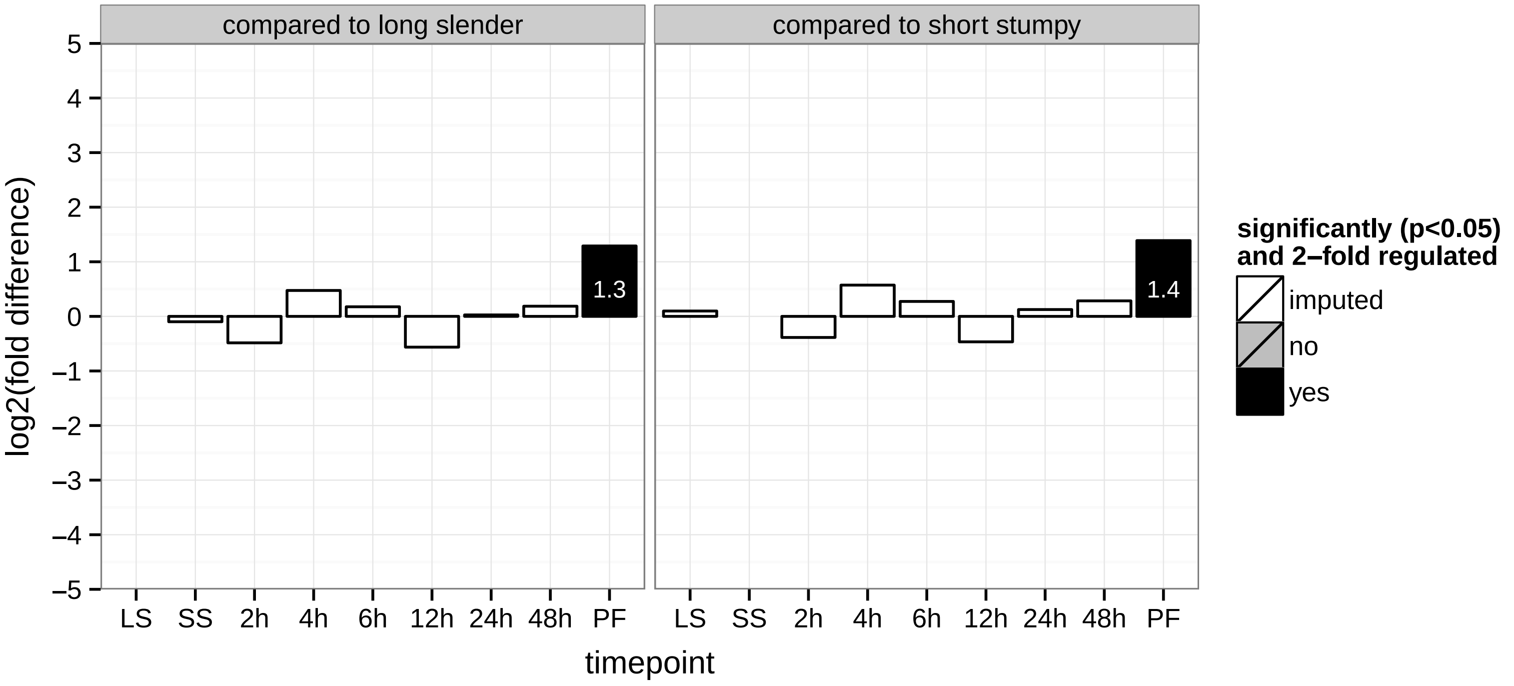
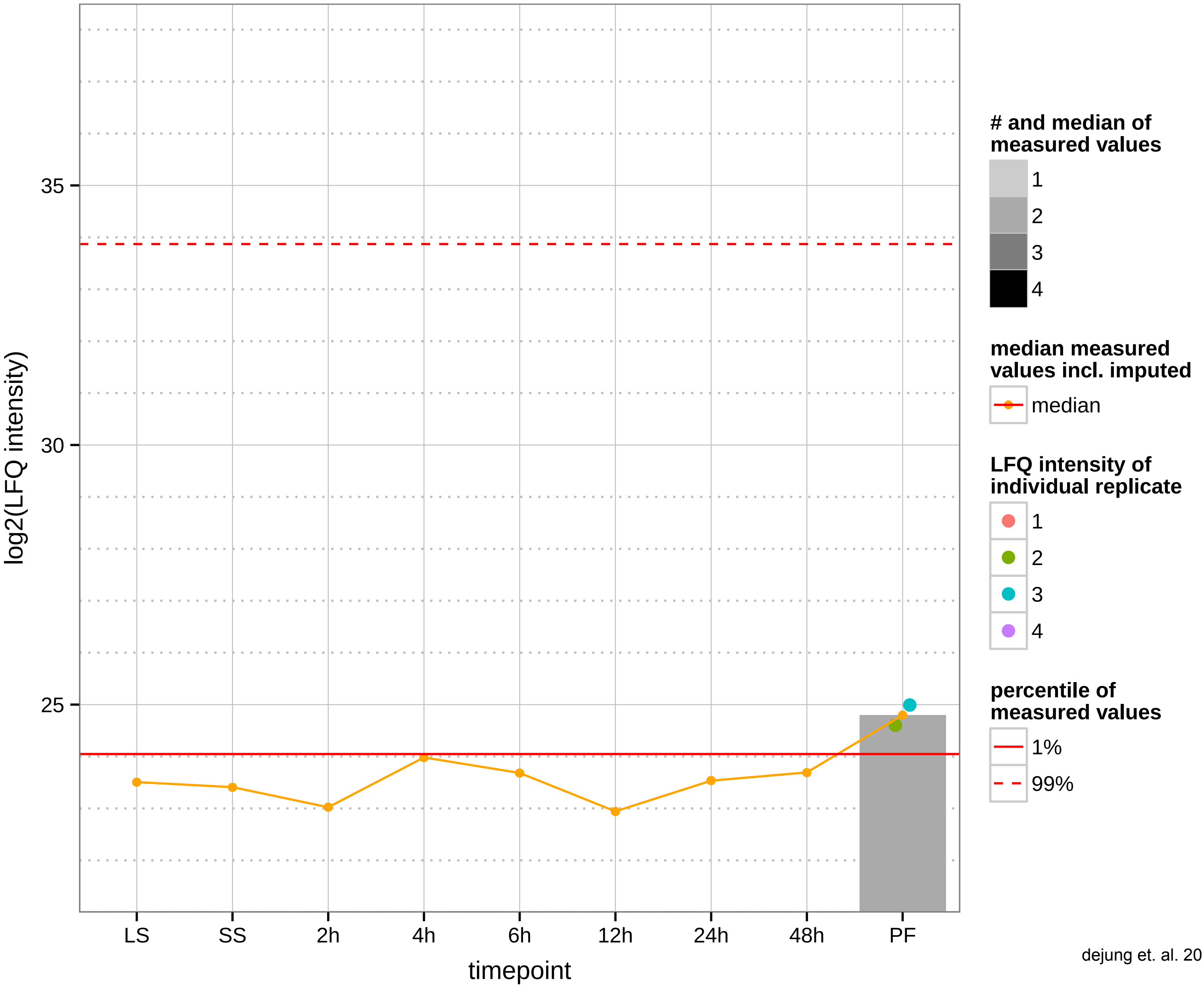
hypothetical protein, conserved
Tb927.10.5260;Tb11.v5.0497
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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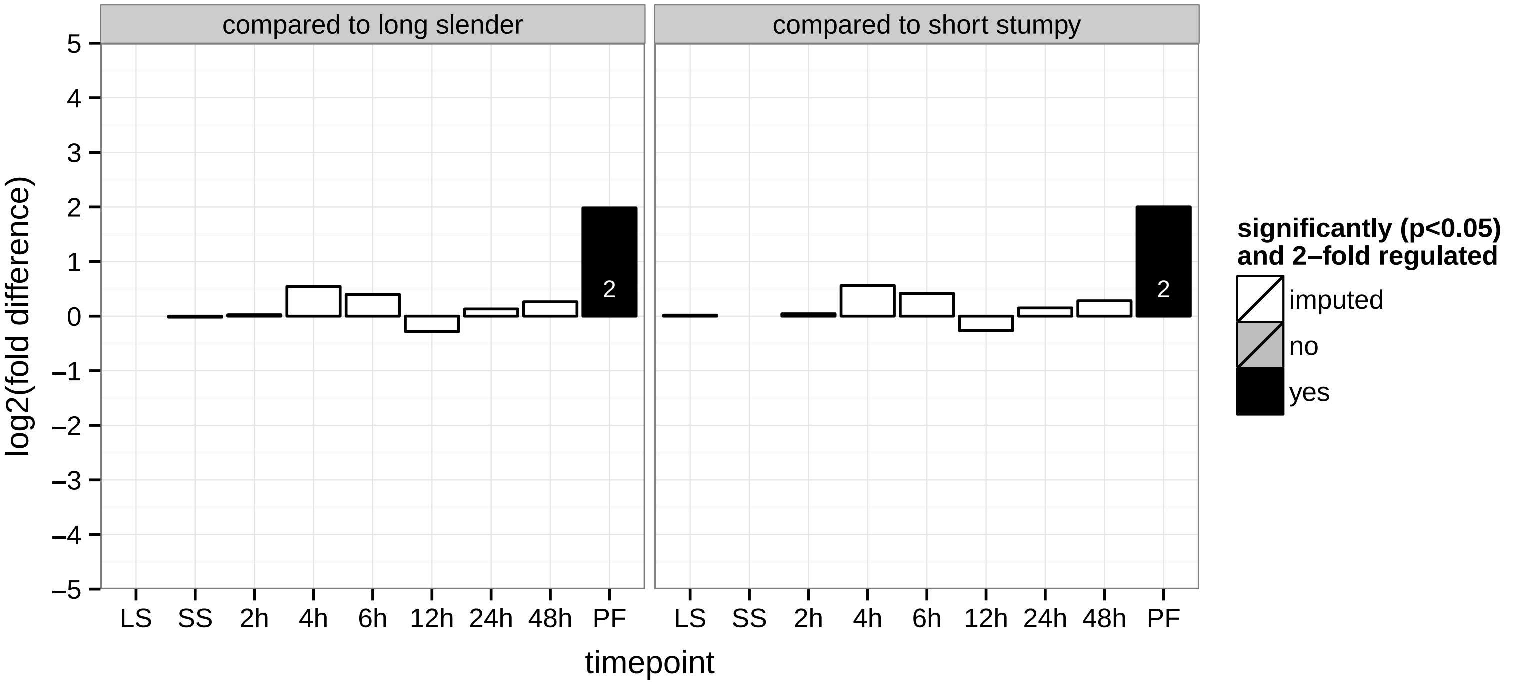
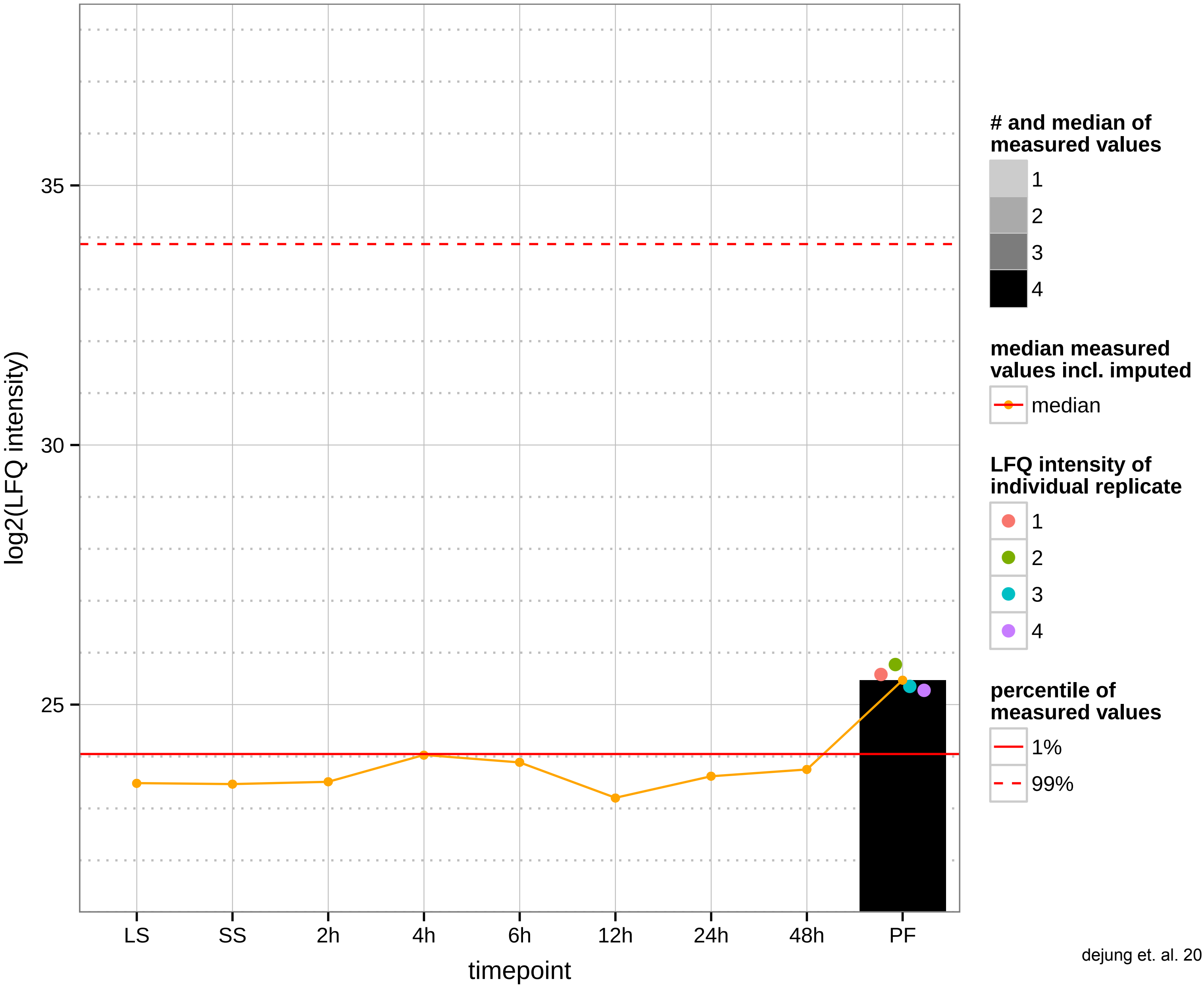
heat shock protein, putative
Tb927.10.5660
AGOF: heat shock protein binding
AGOC: mitochondrion
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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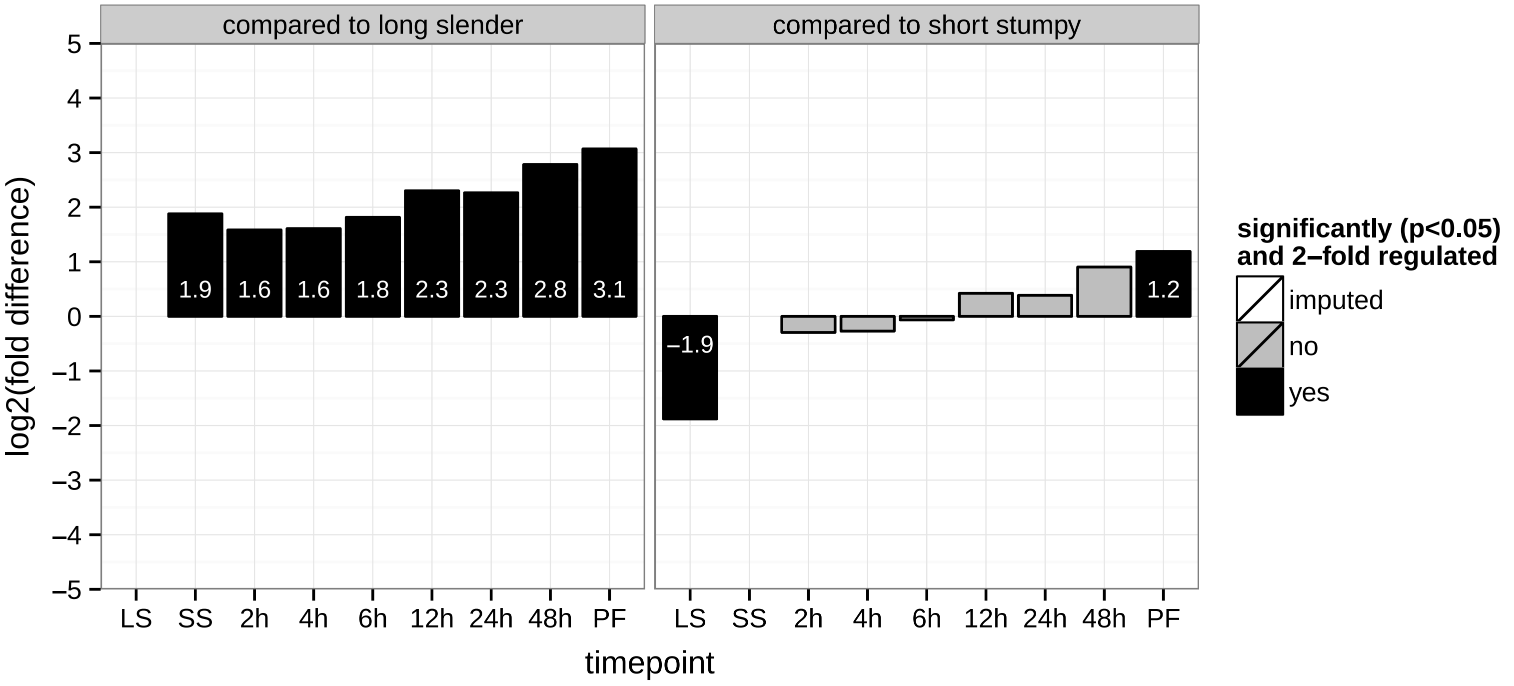
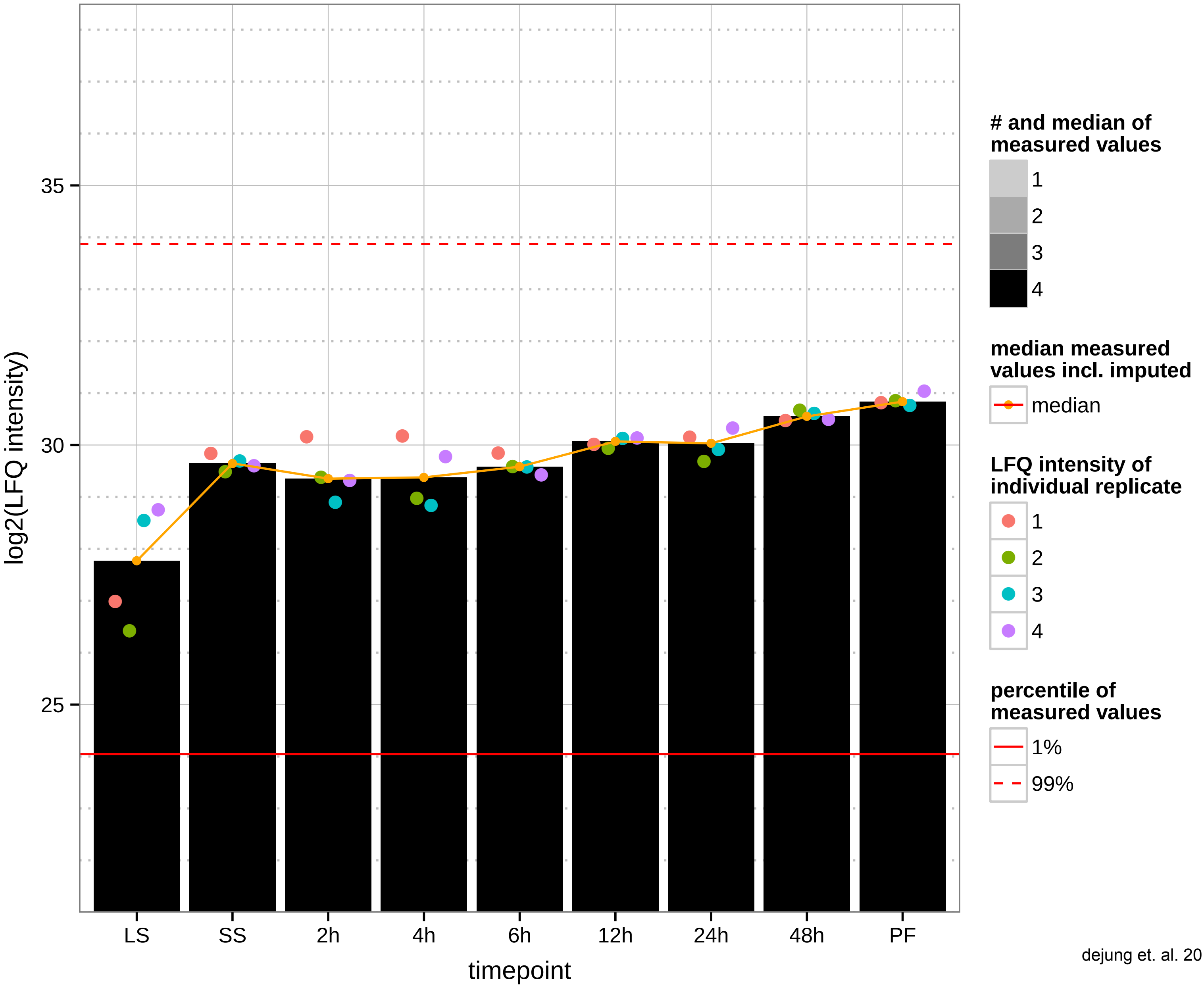
N–acetyltransferase subunit Nat1, putative (NAT1)
Tb927.10.5670
AGOF: N–acetyltransferase activity
AGOC: null
AGOP: cellular protein modification process
PGOF: protein binding
PGOC: null
PGOP: null





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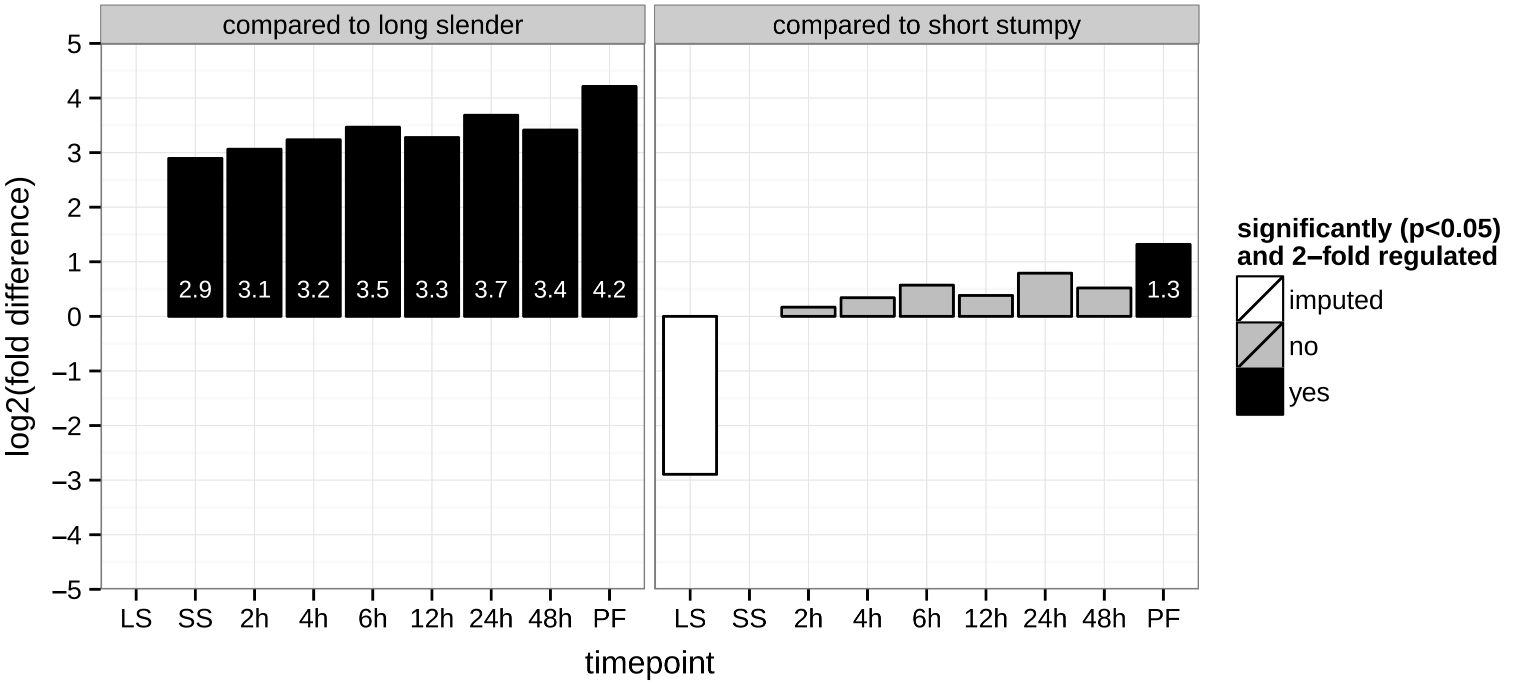
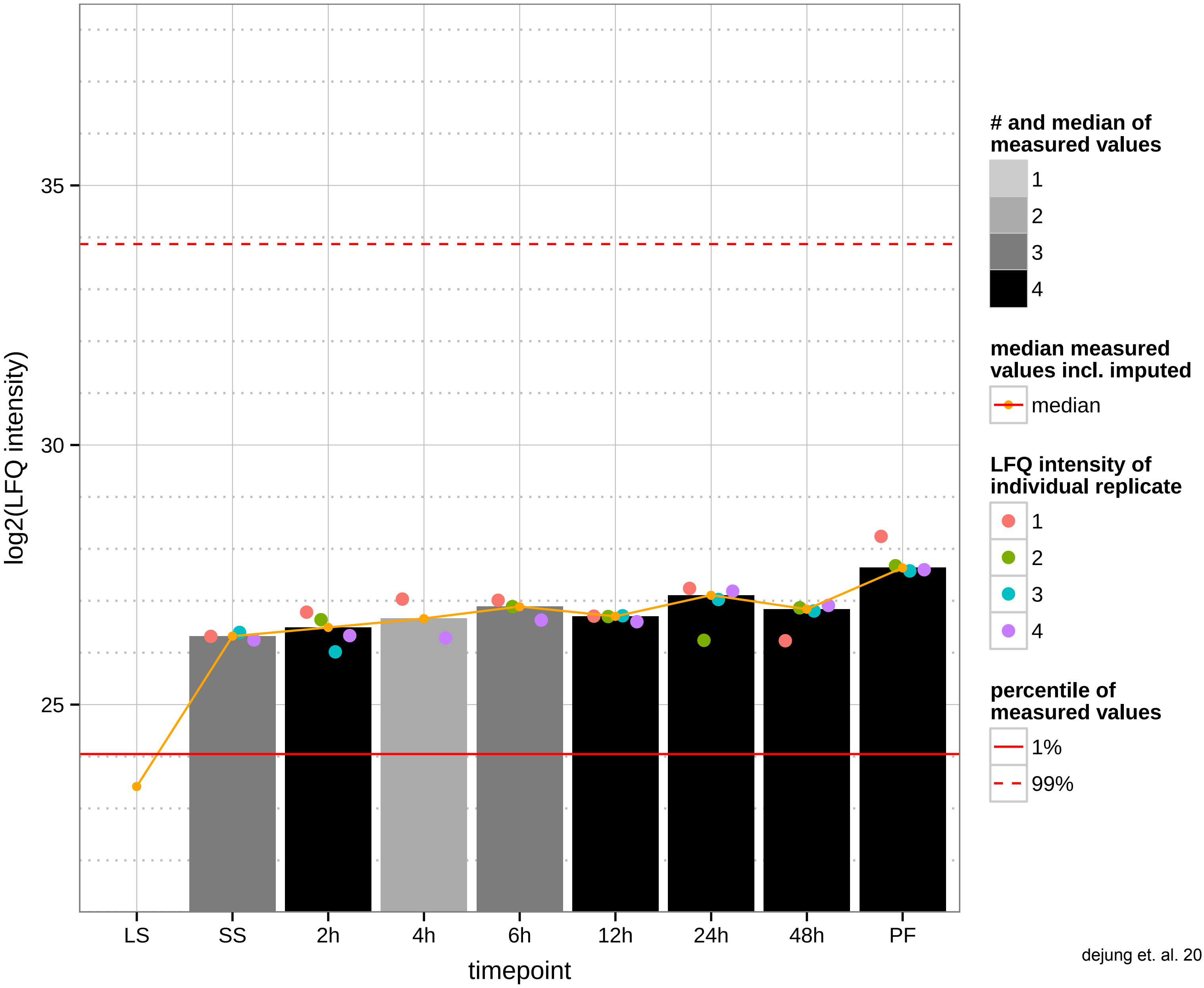
hypothetical protein, conserved
Tb927.10.5920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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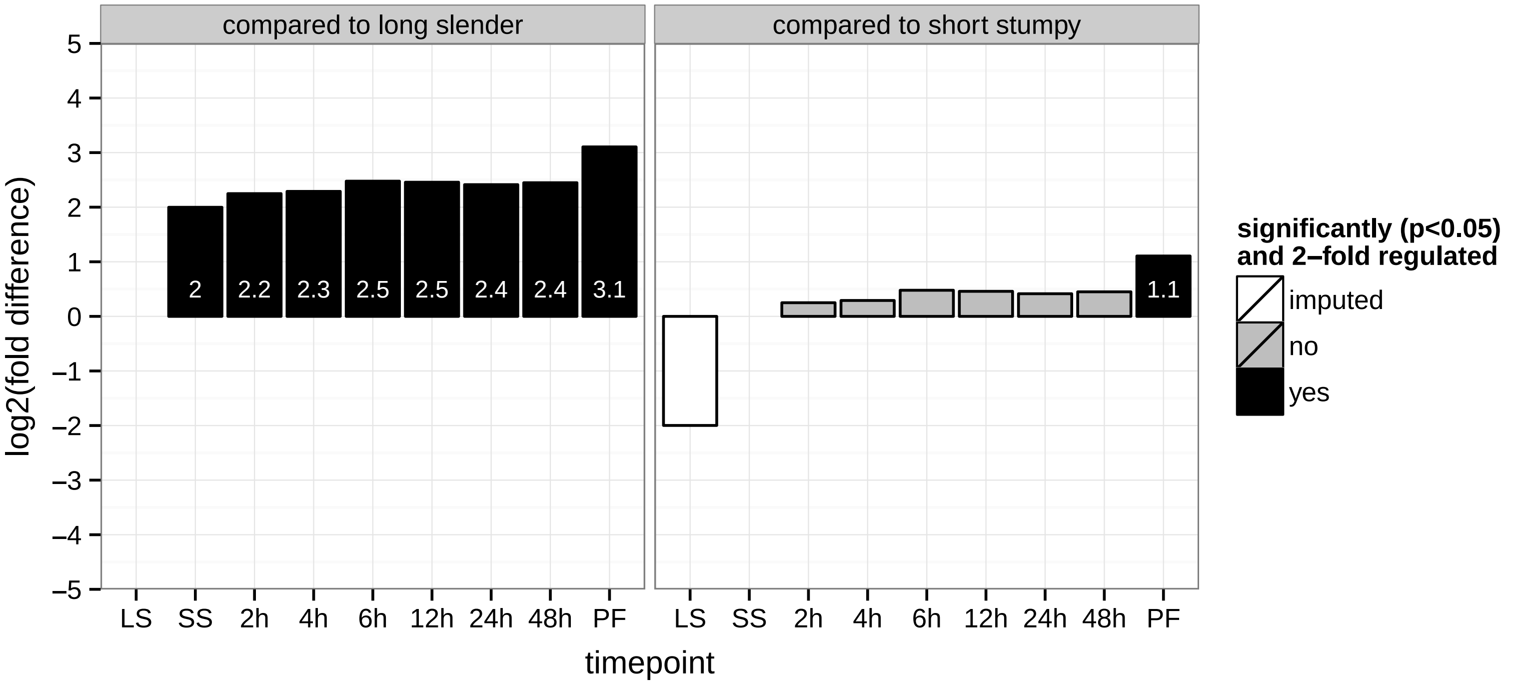
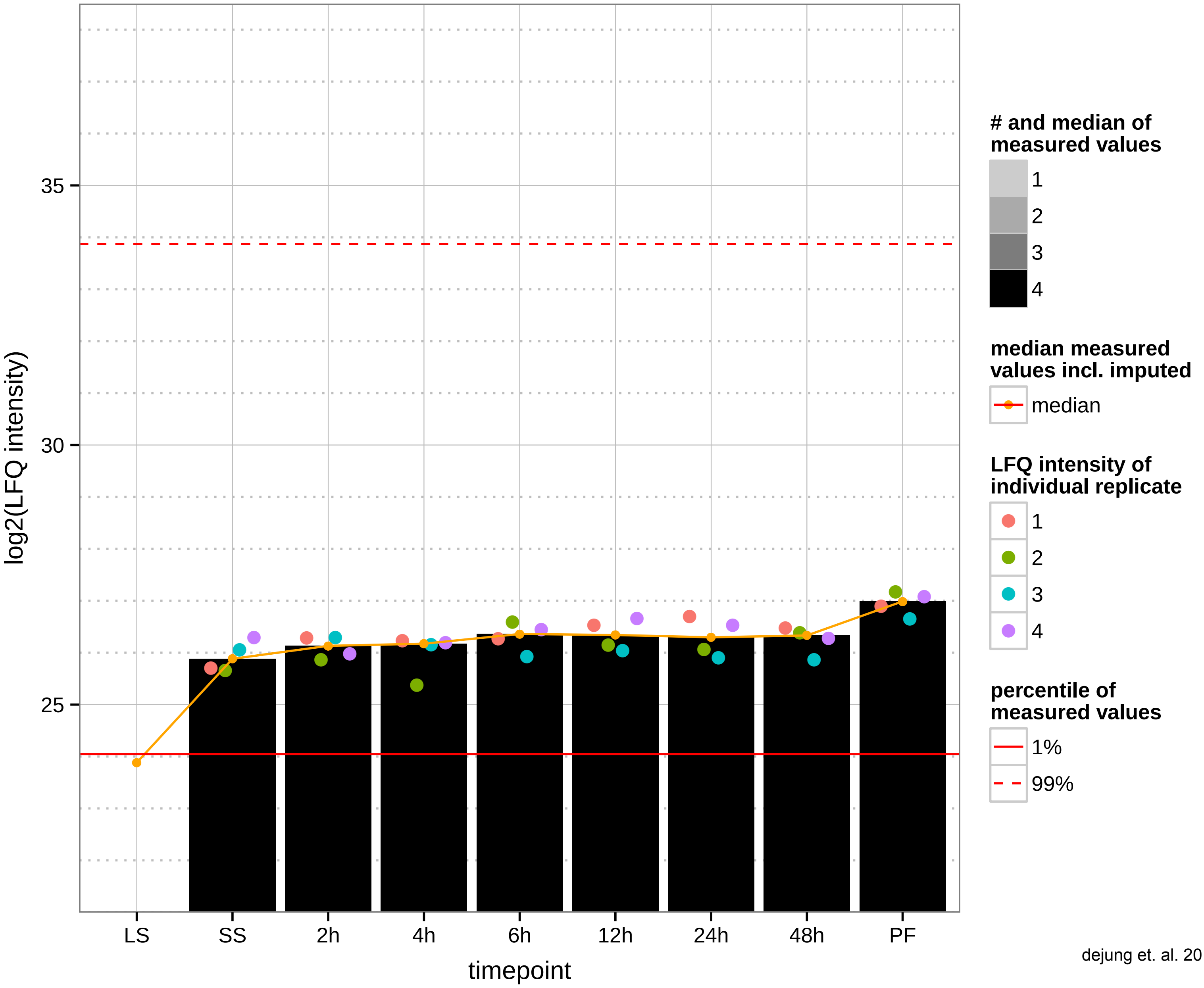
hypothetical protein, conserved
Tb927.10.6180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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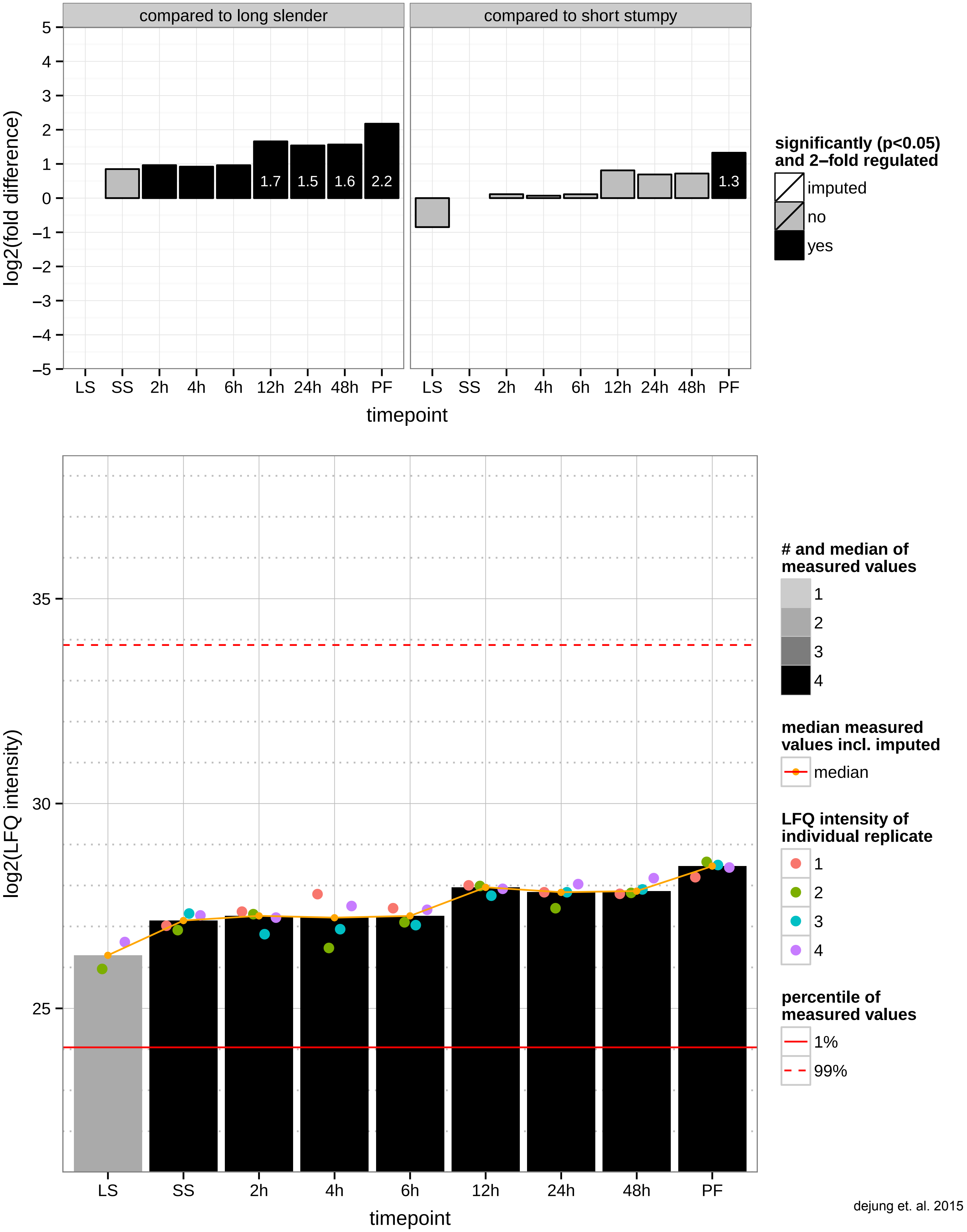
member of the NOL1/NOP2/sun family of proteins
Tb927.10.6680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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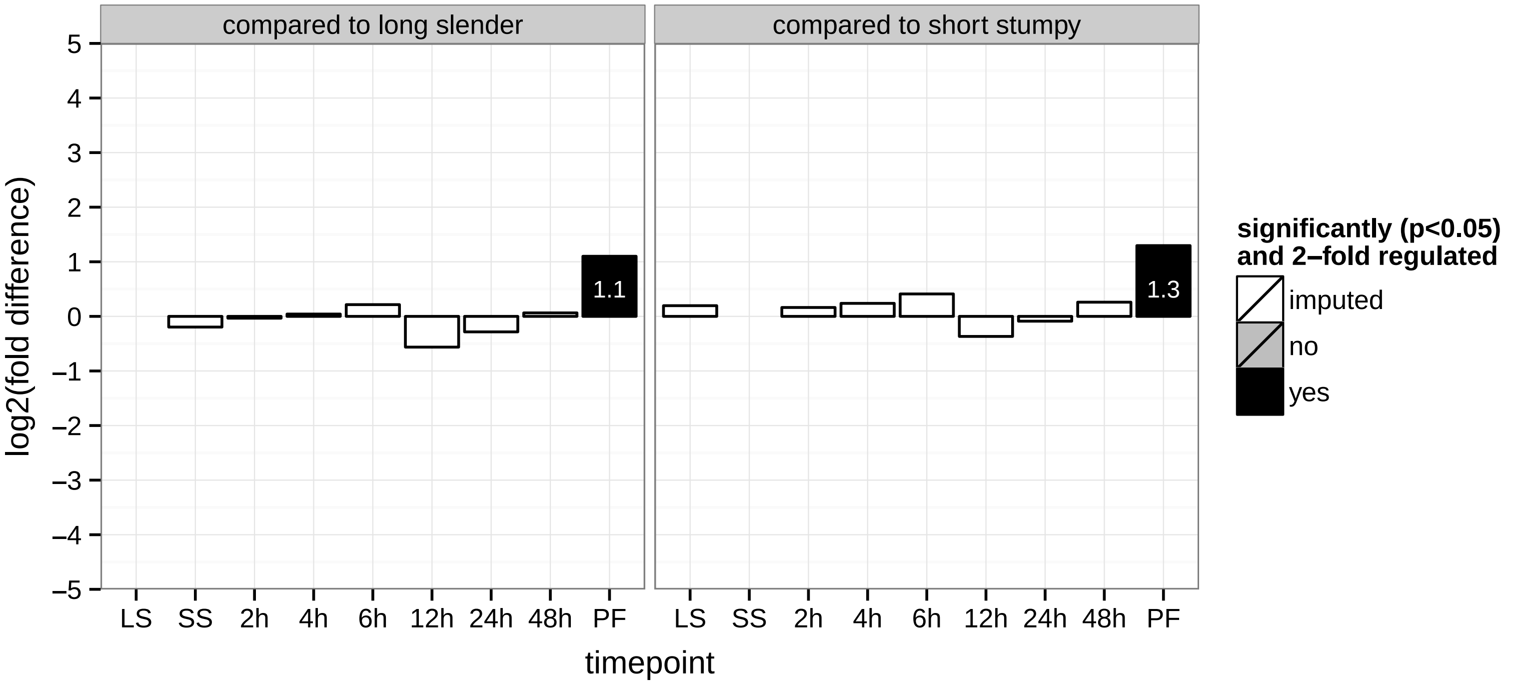
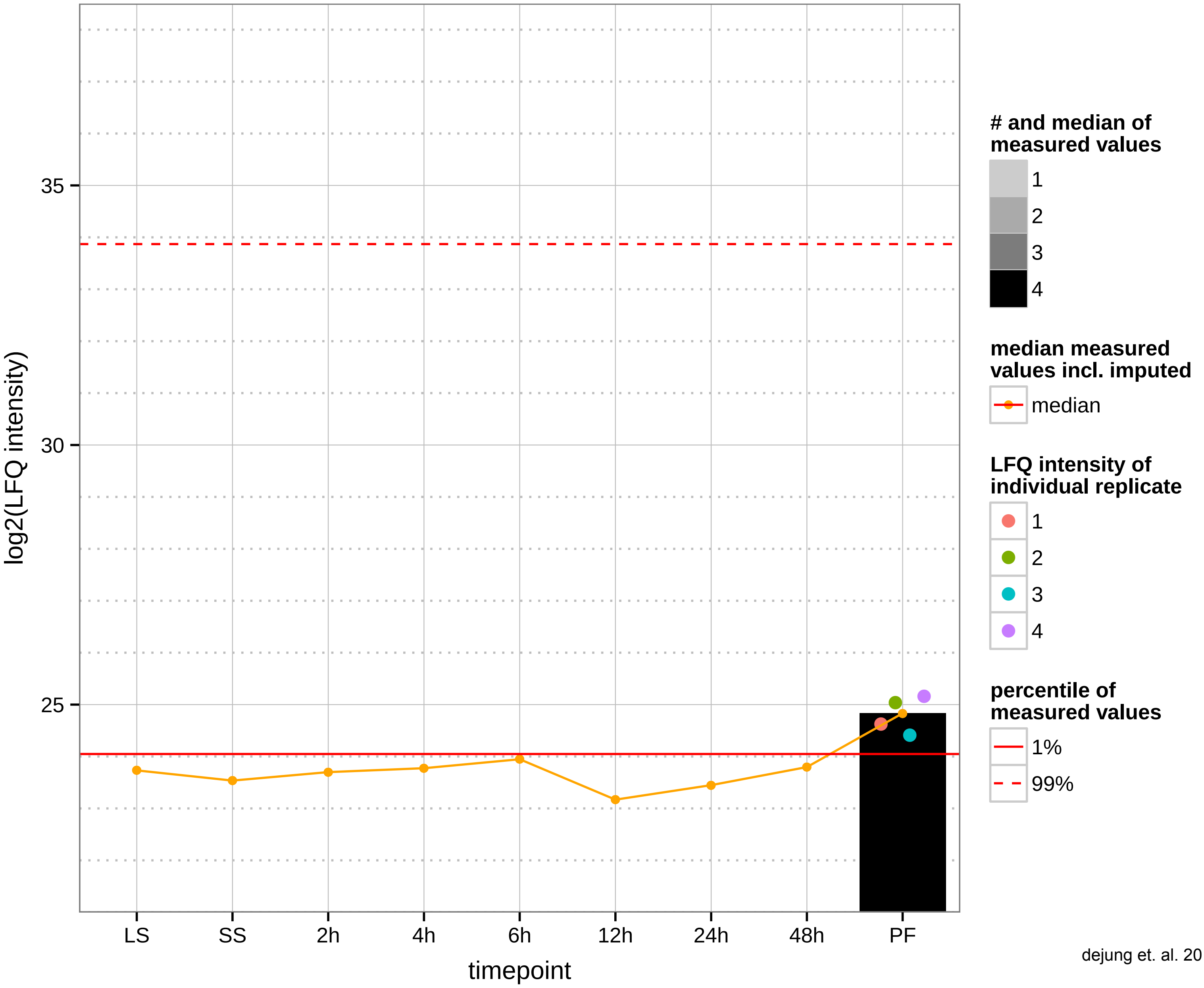
hypothetical protein, conserved
Tb927.10.6710
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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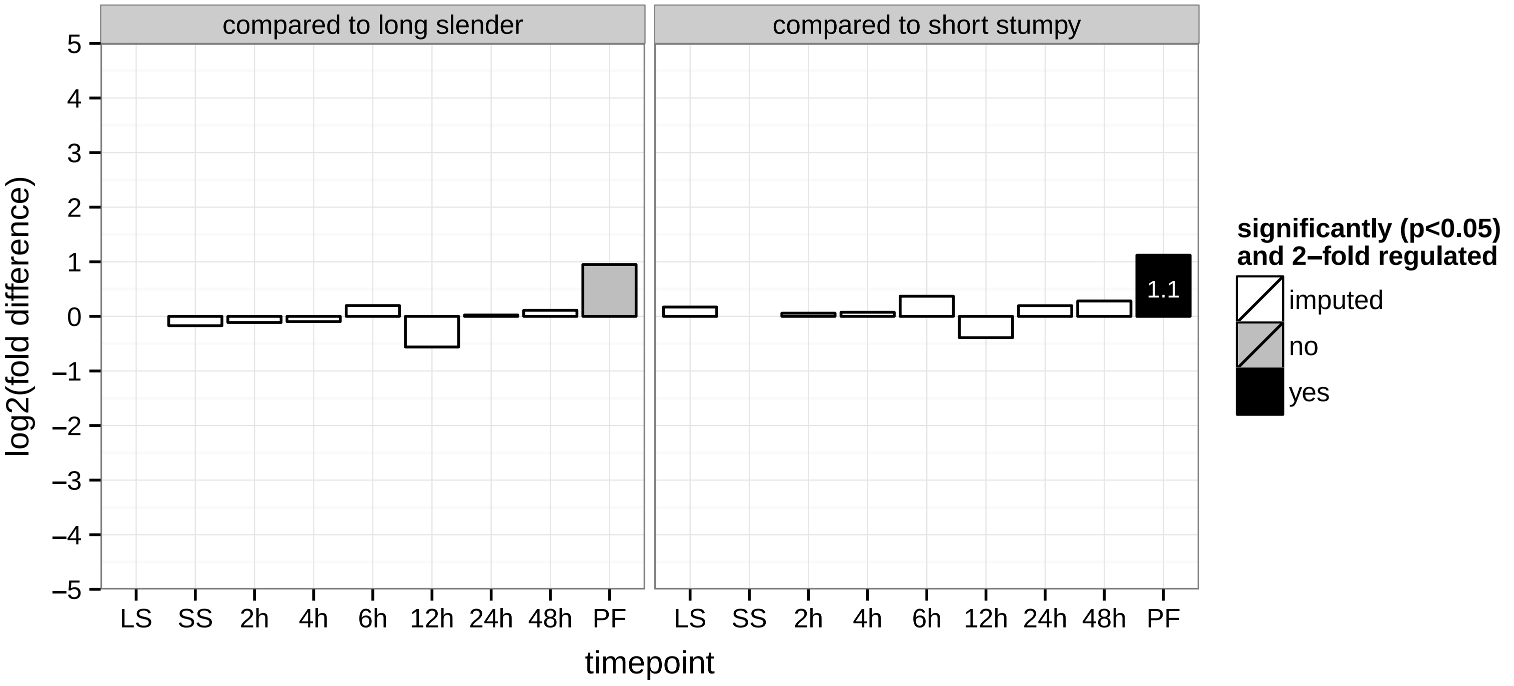
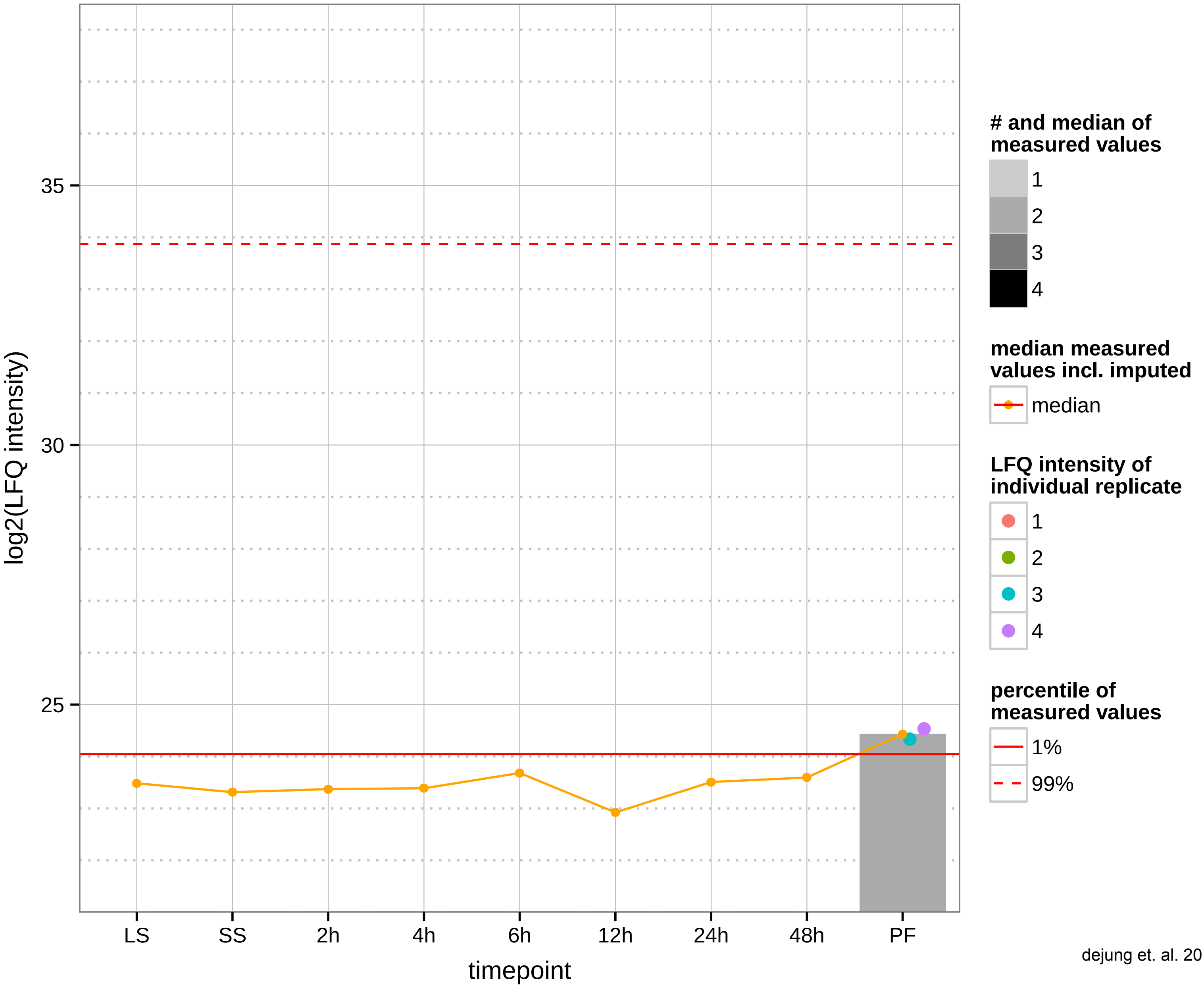
chromatin assembly factor 1 subunit B, putative
Tb927.10.7050
AGOF: histone binding, unfolded protein binding
AGOC: null
AGOP: chromatin assembly, chromatin assembly or disassembly, nucleosome assembly
PGOF: protein binding
PGOC: null
PGOP: null





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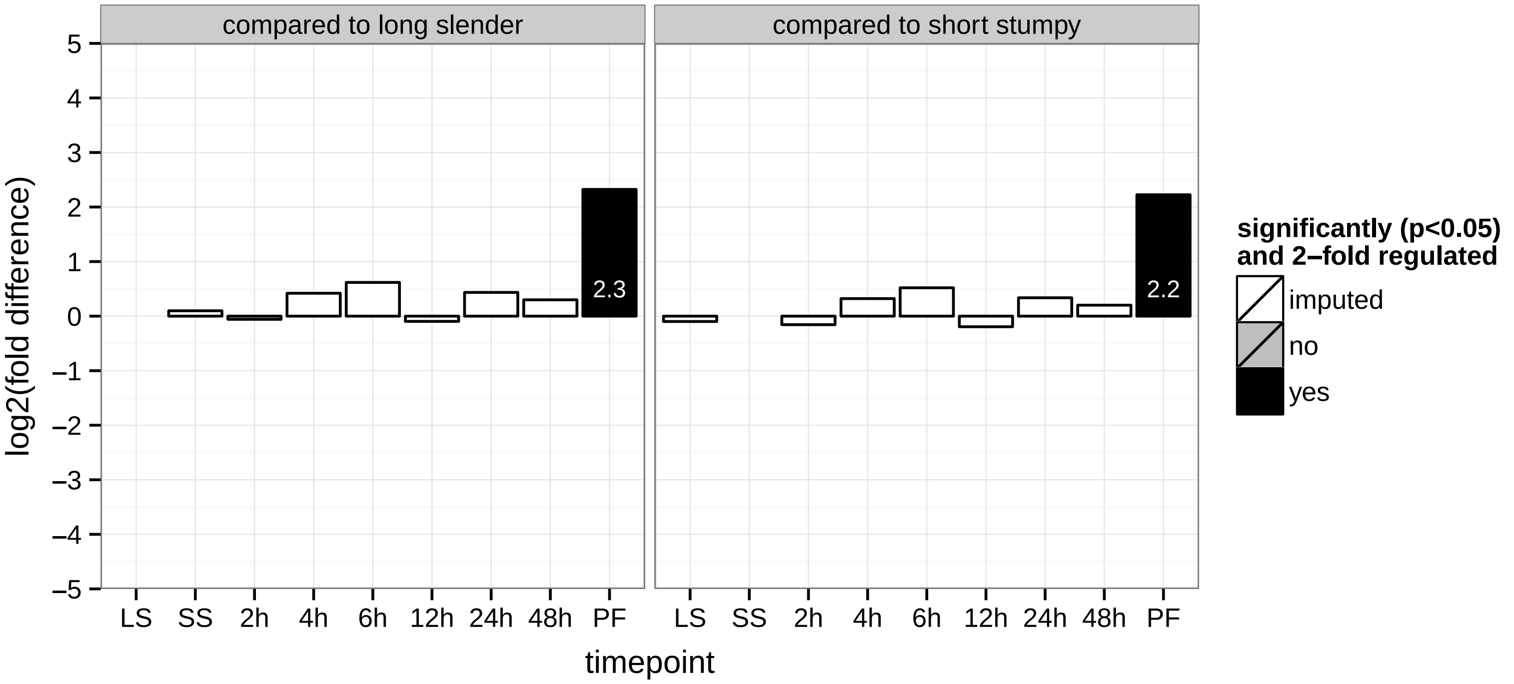
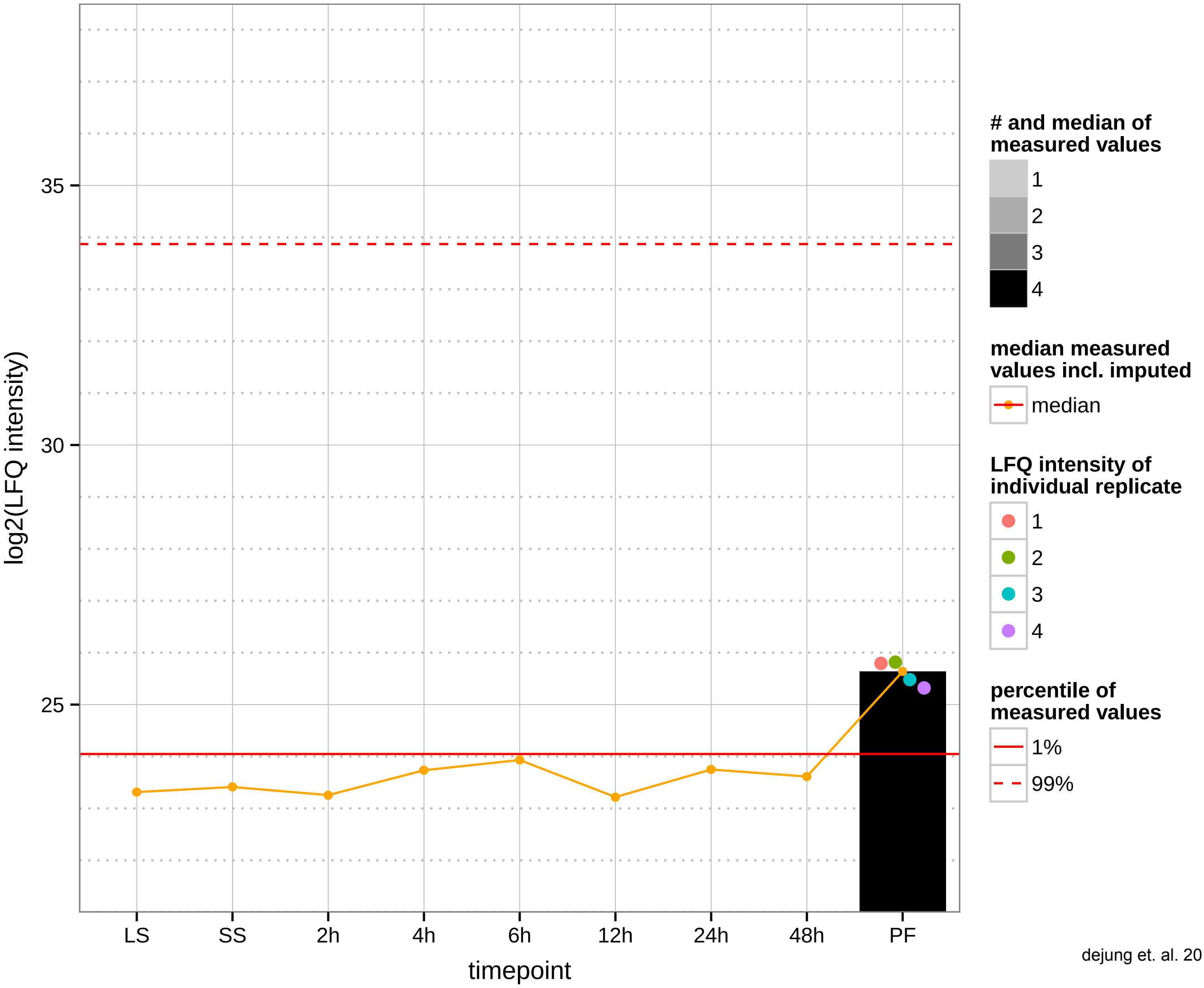
hypothetical protein, conserved
Tb927.10.7270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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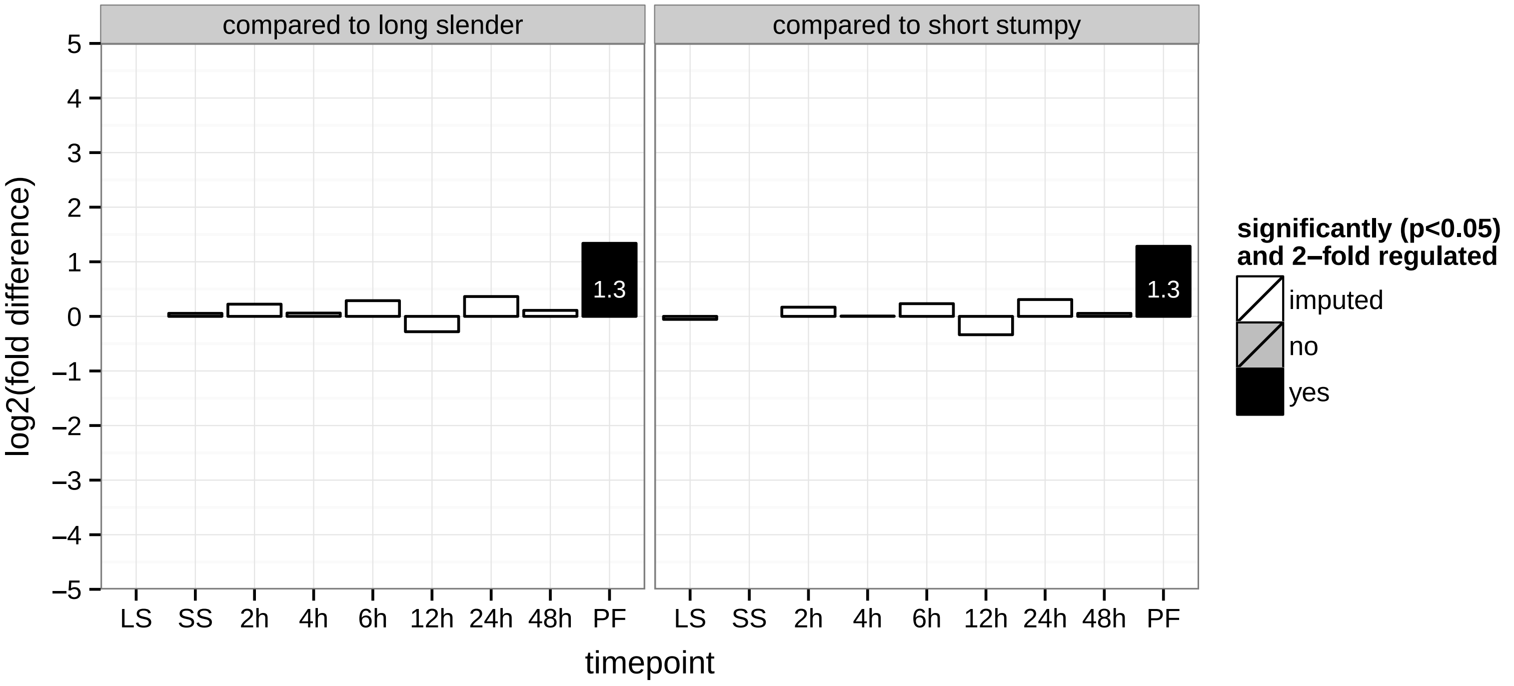
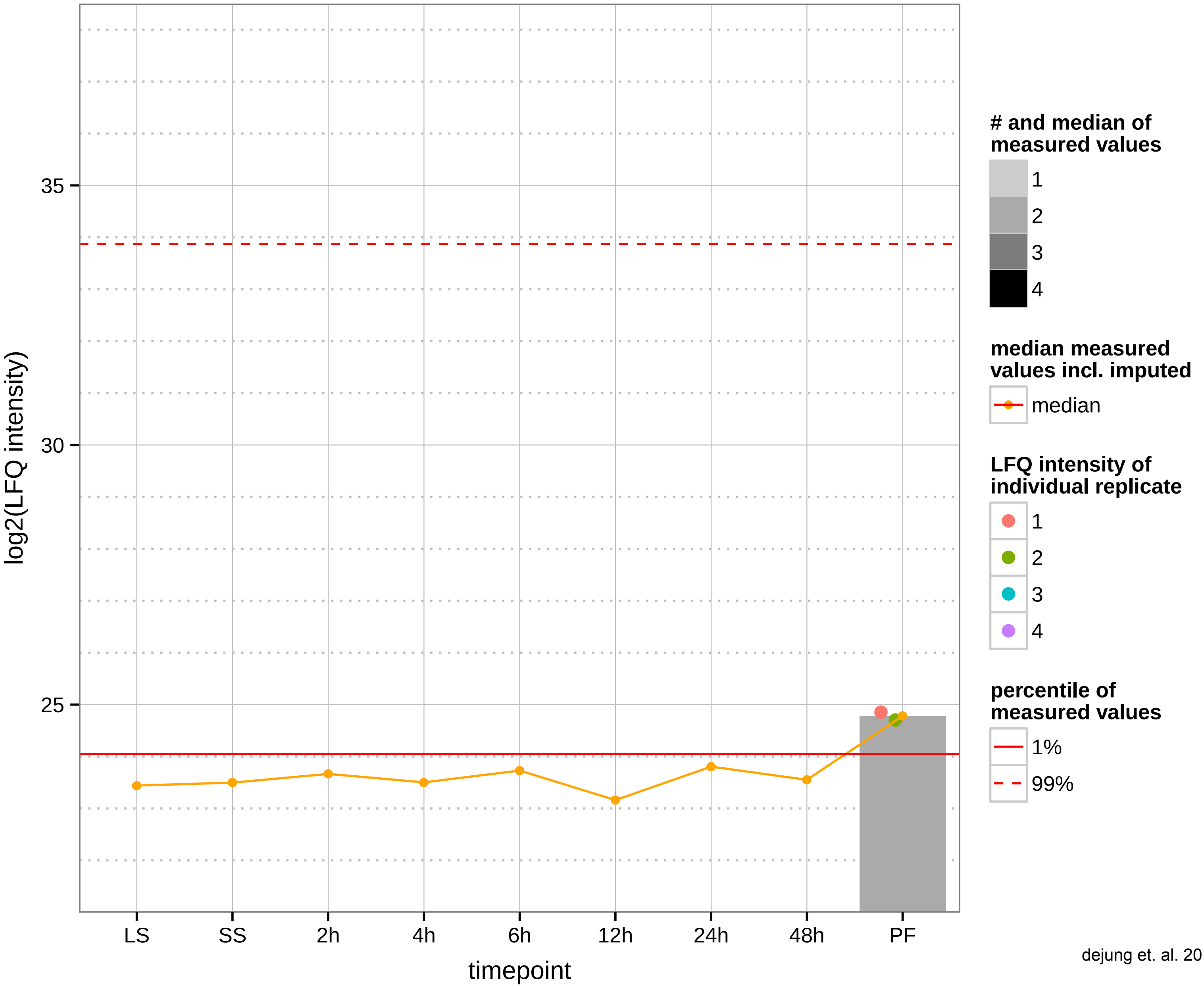
terminal uridylyltransferase 3, putative (TUT3)
Tb927.10.7310
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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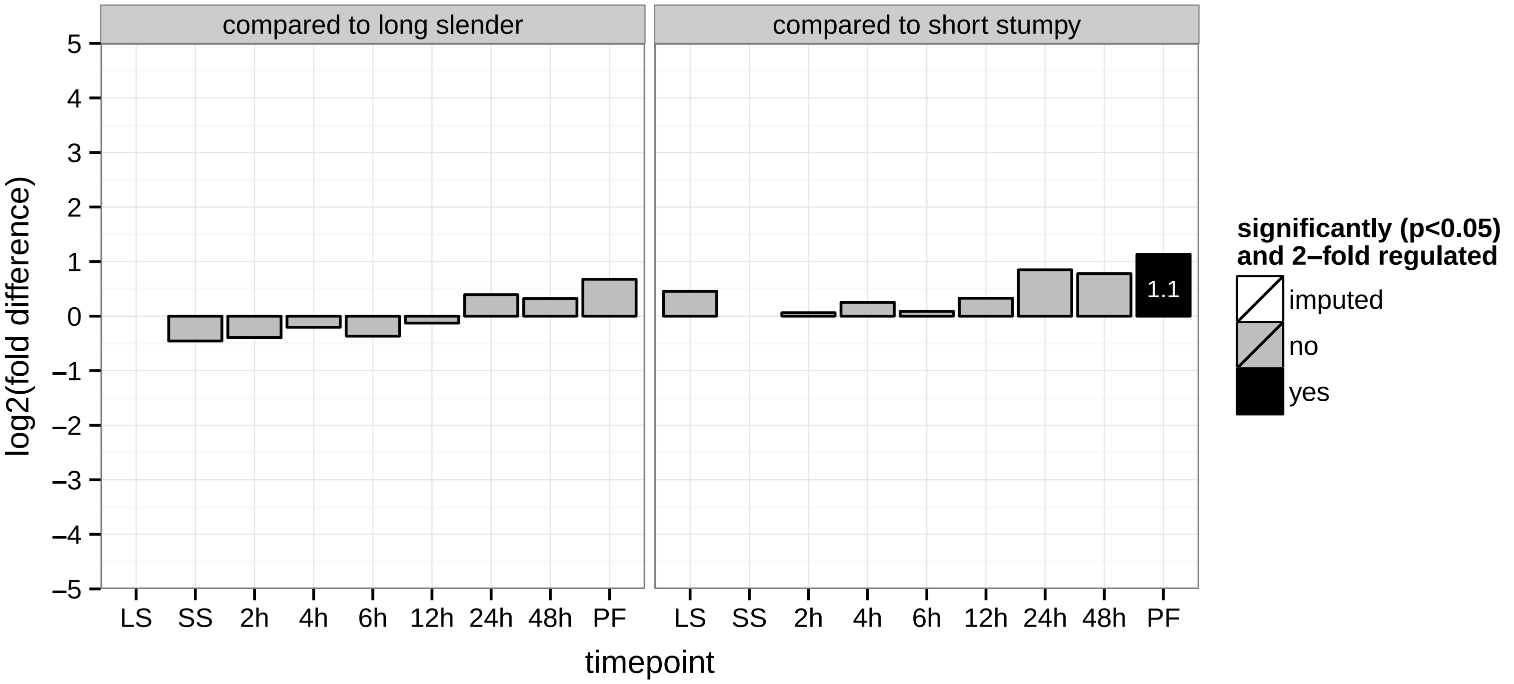
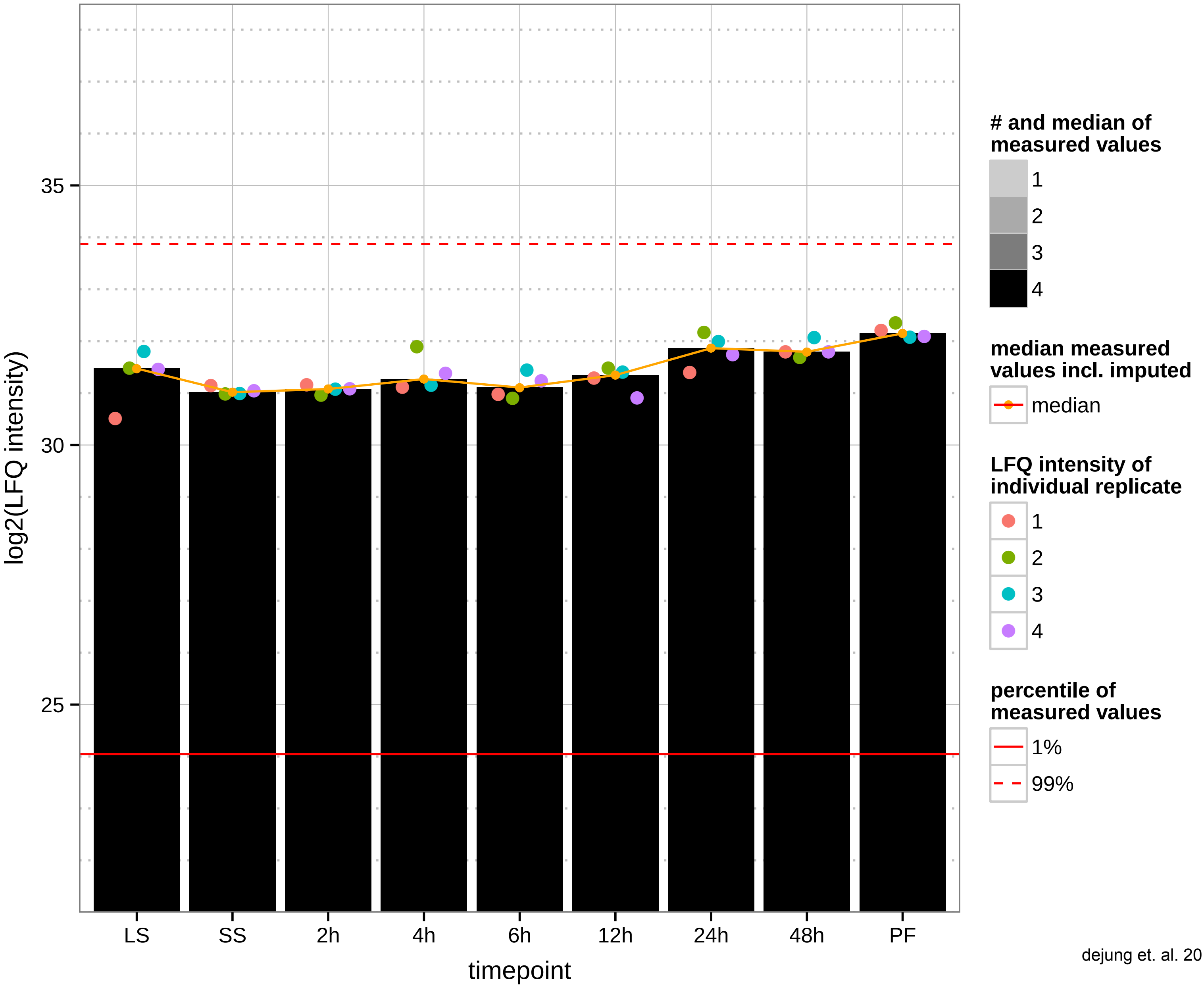
40S ribosomal protein S24E, putative
Tb927.10.7340;Tb927.10.7330
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null, structural constituent of ribosome
PGOC: null, intracellular, ribosome
PGOP: null, translation





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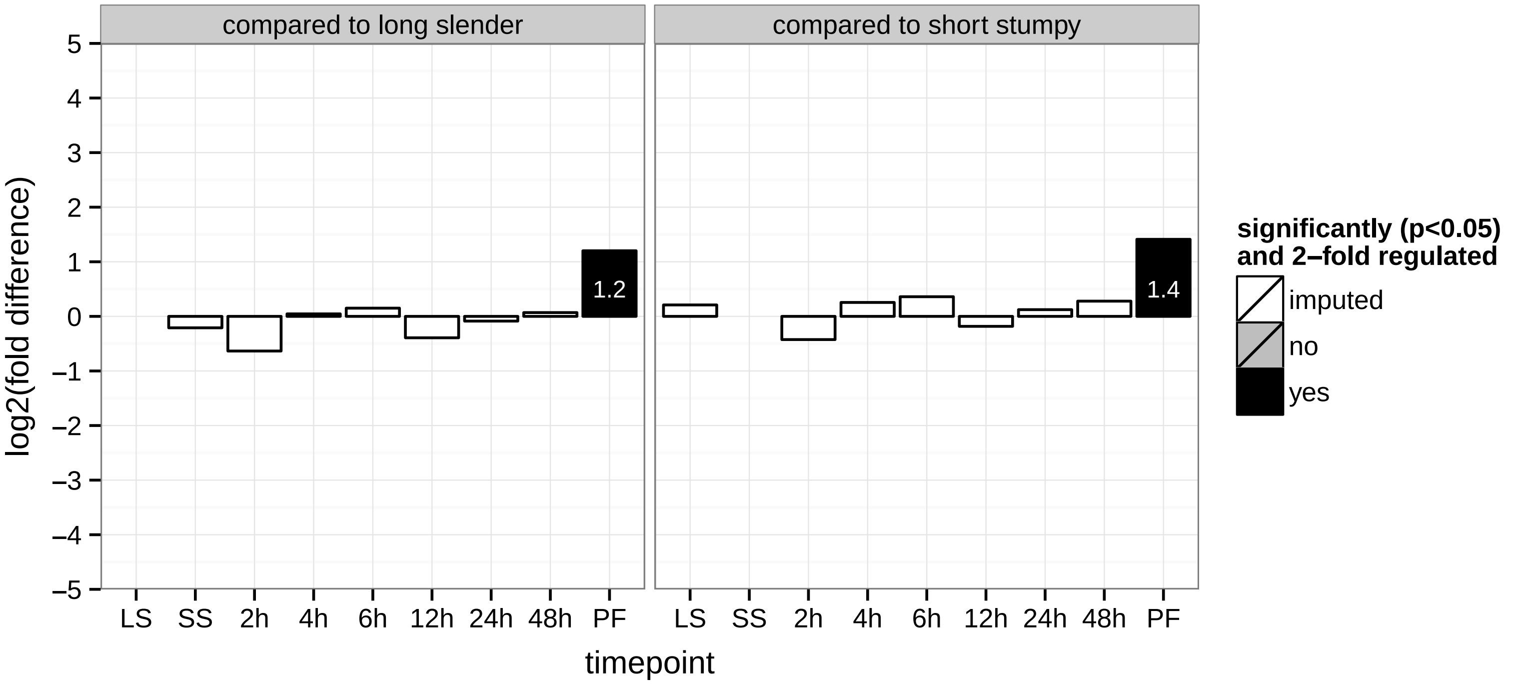
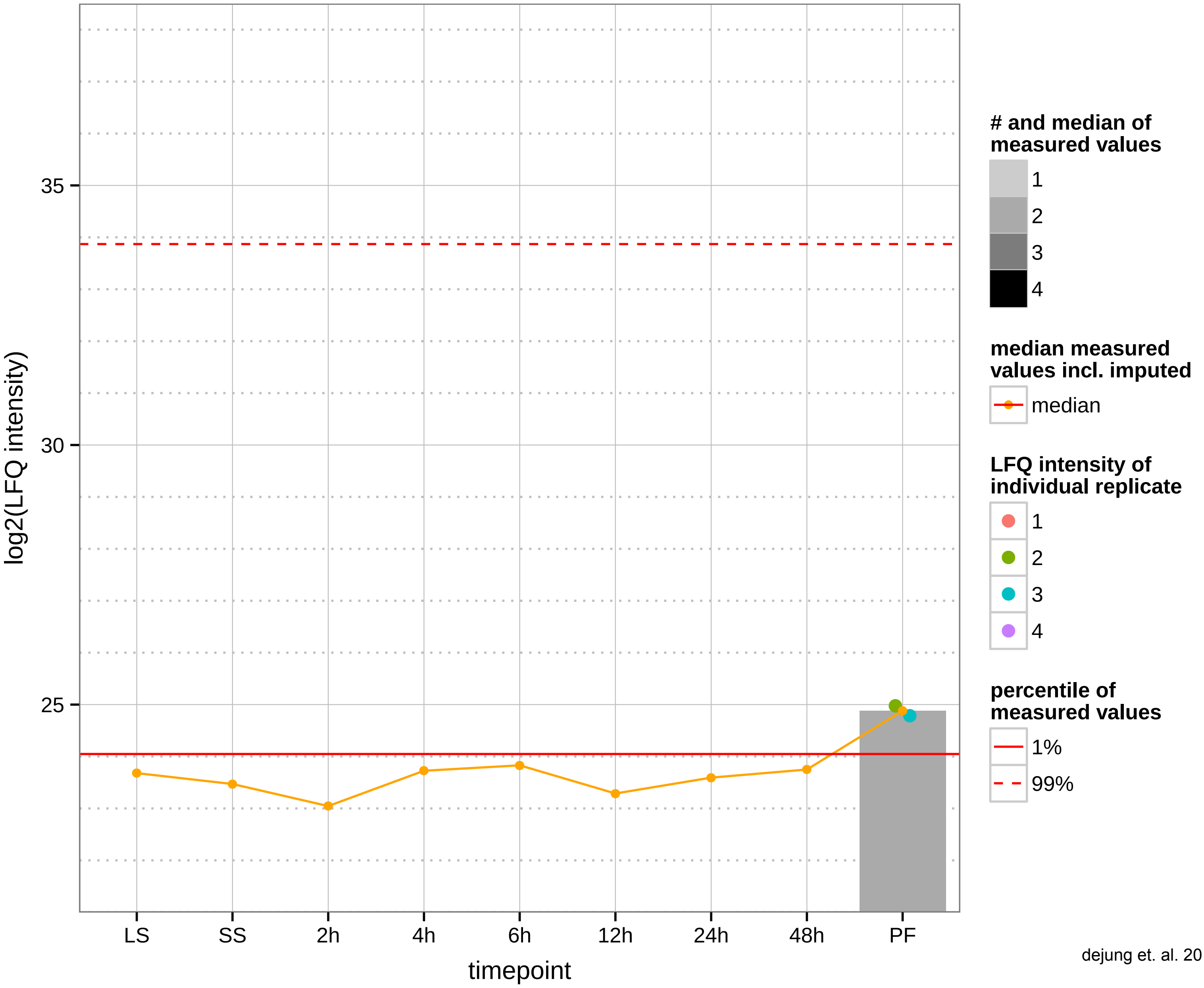
hypothetical protein, conserved
Tb927.10.7600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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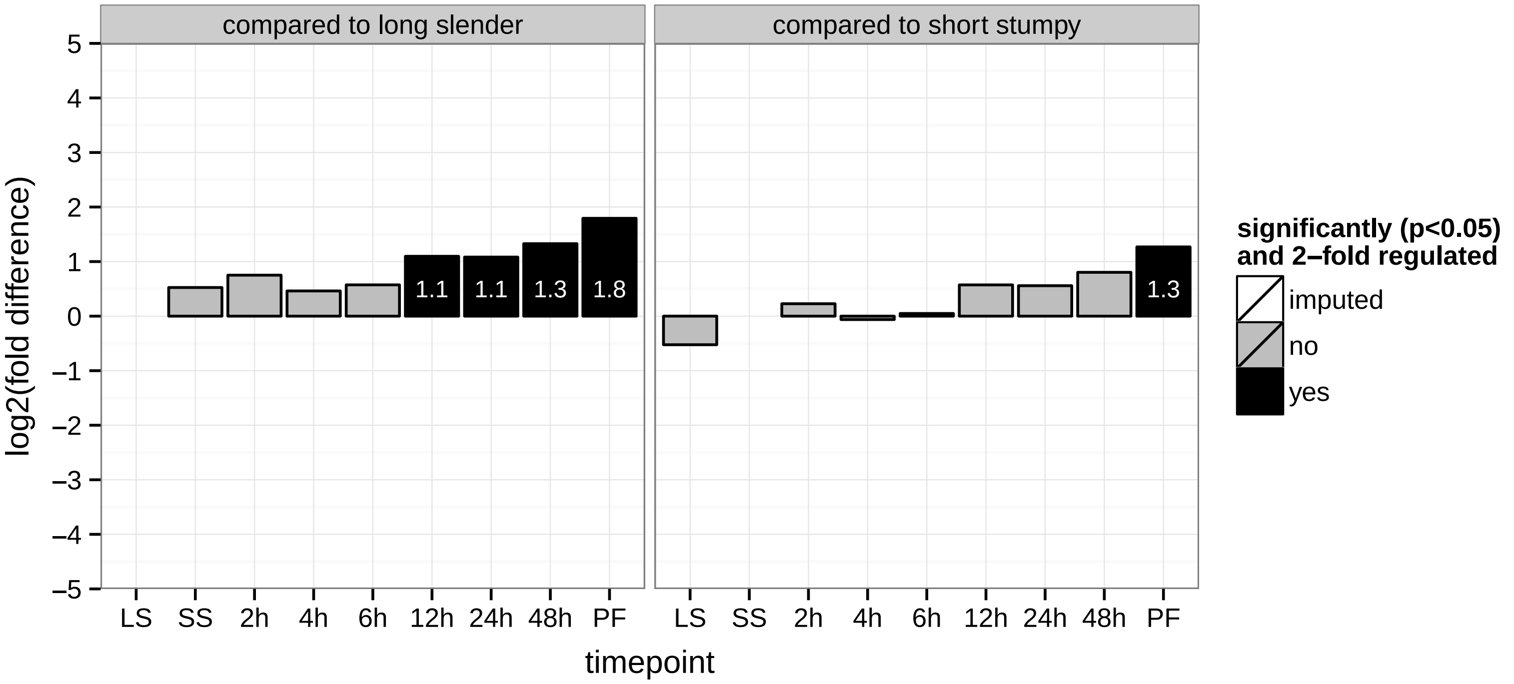
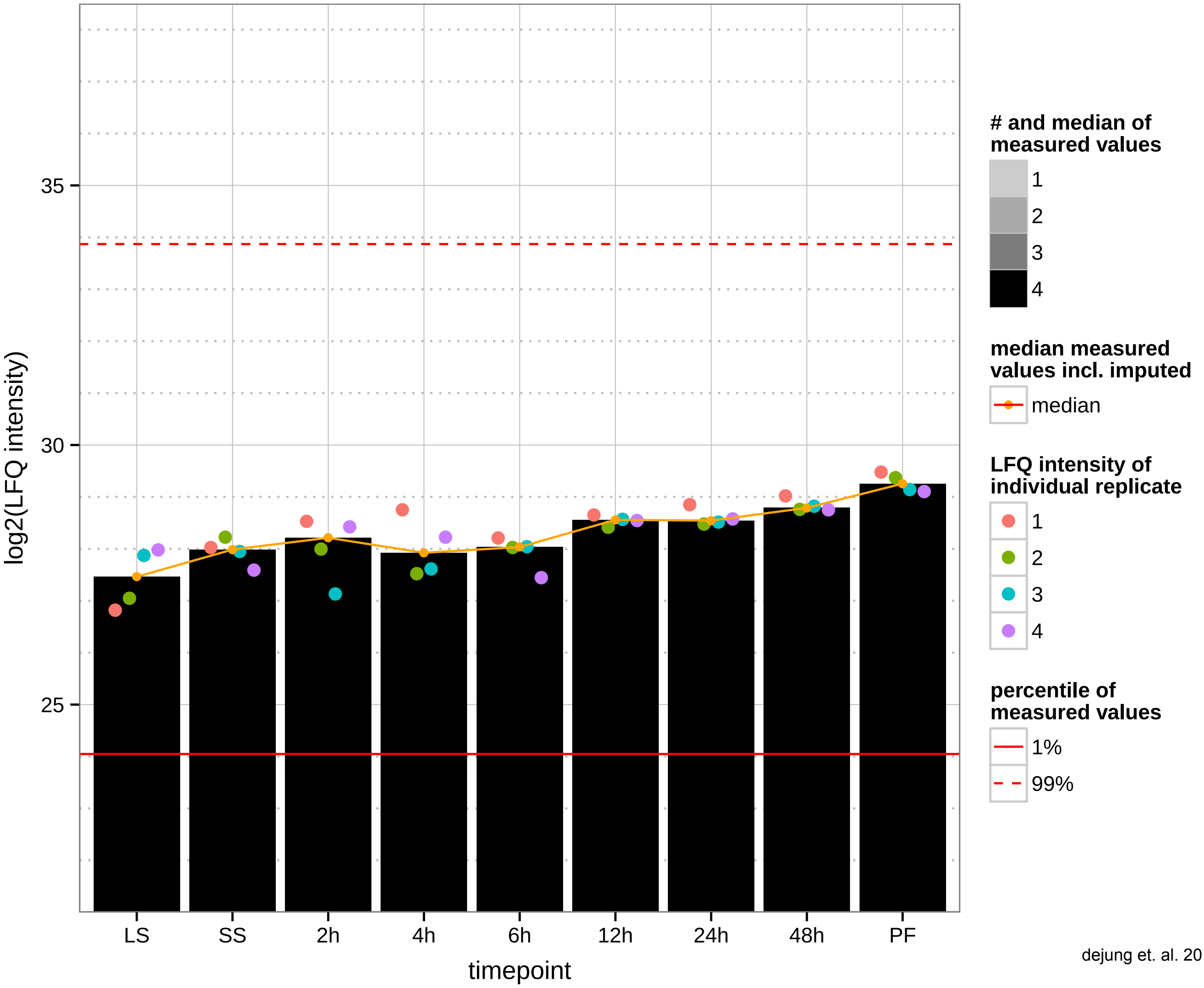
GTPase activating protein, putative
Tb927.10.7680
AGOF: Rab GTPase activator activity
AGOC: intracellular
AGOP: regulation of Rab GTPase activity
PGOF: Rab GTPase activator activity
PGOC: intracellular
PGOP: regulation of Rab GTPase activity





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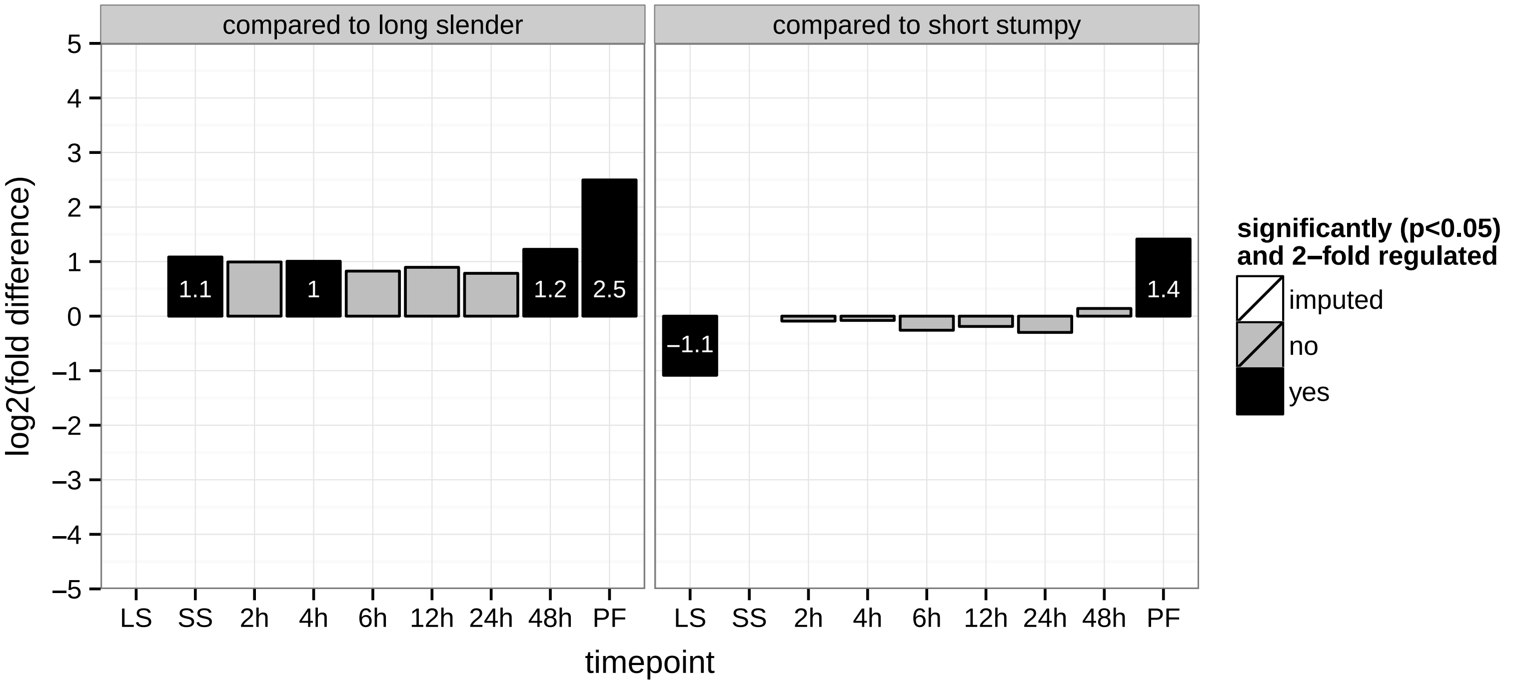
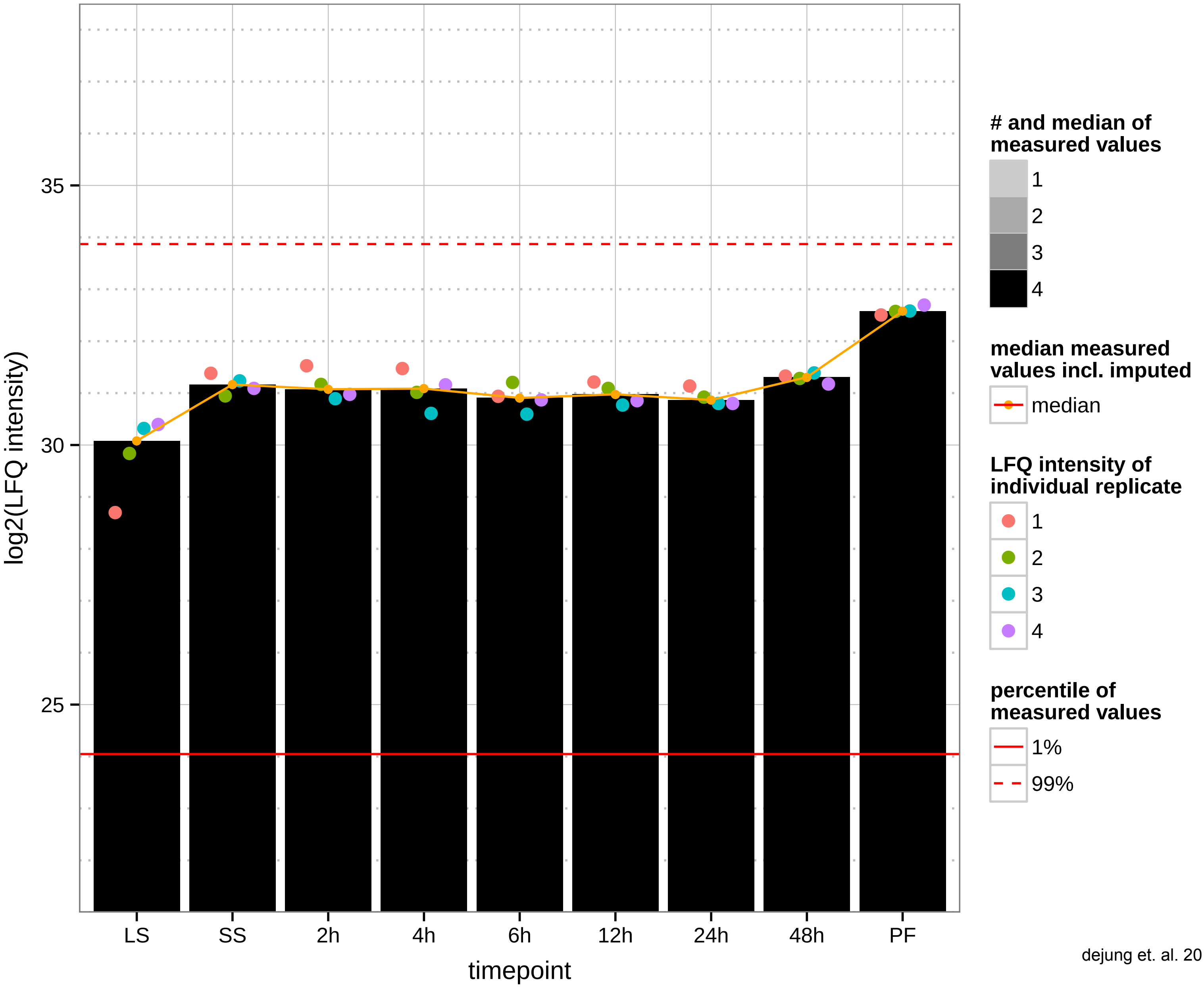
prolyl oligopeptidase, putative, serine peptidase clan SC, family S9A, putative (POP)
Tb927.10.8020
AGOF: APG8–specific protease activity, oligopeptidase activity, serine–type endopeptidase activity
AGOC: cytoplasm, nucleus
AGOP: proteolysis
PGOF: serine–type endopeptidase activity, serine–type peptidase activity
PGOC: null
PGOP: proteolysis





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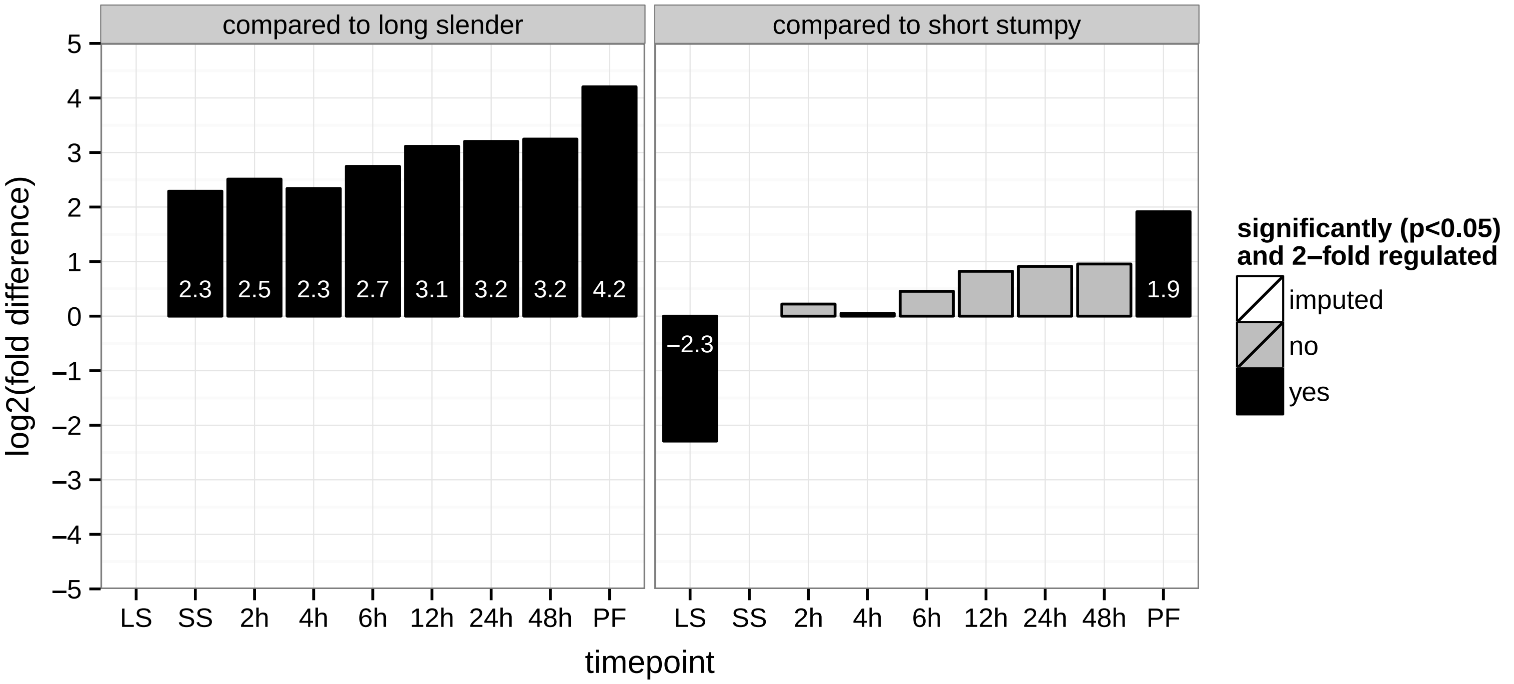
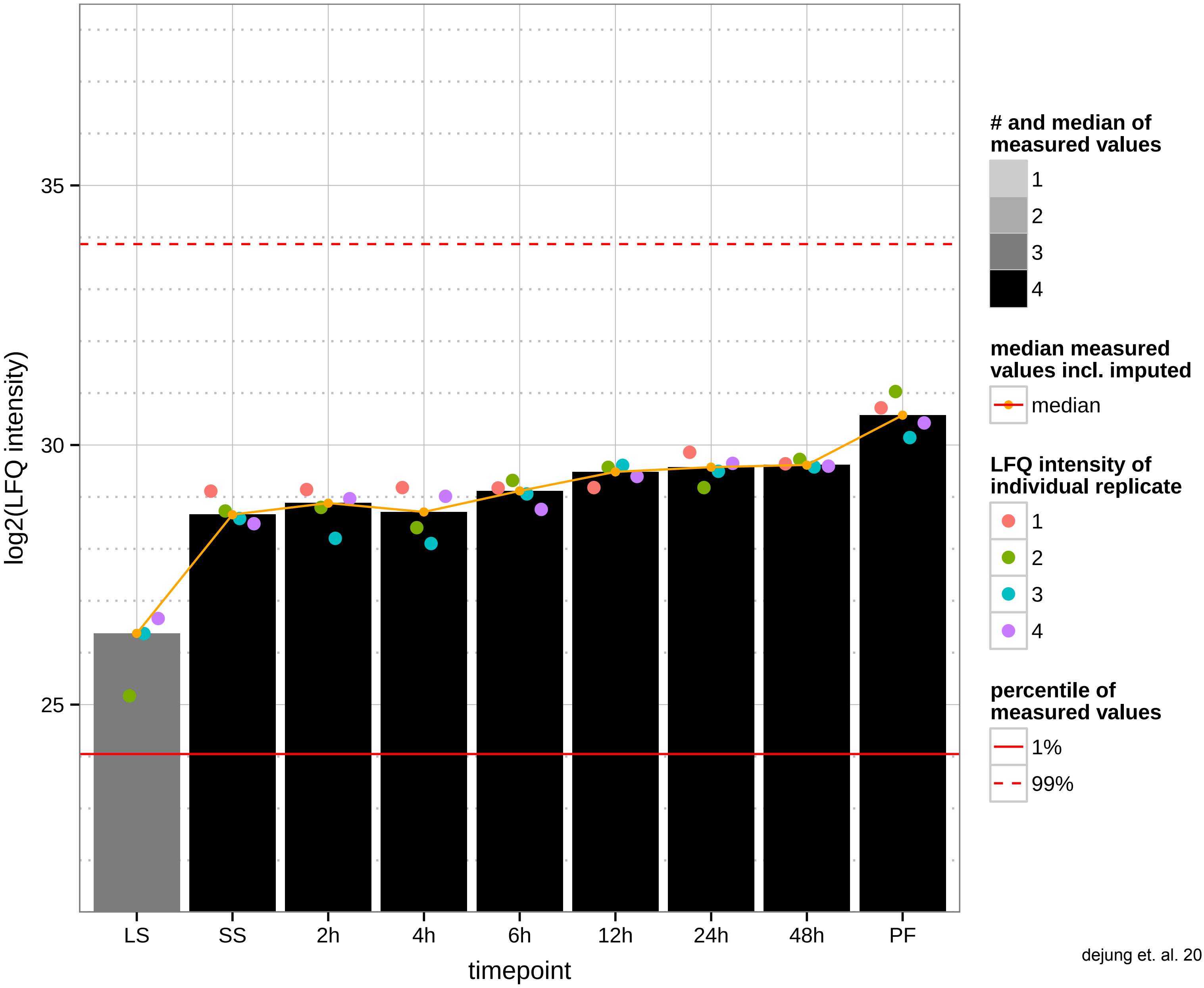
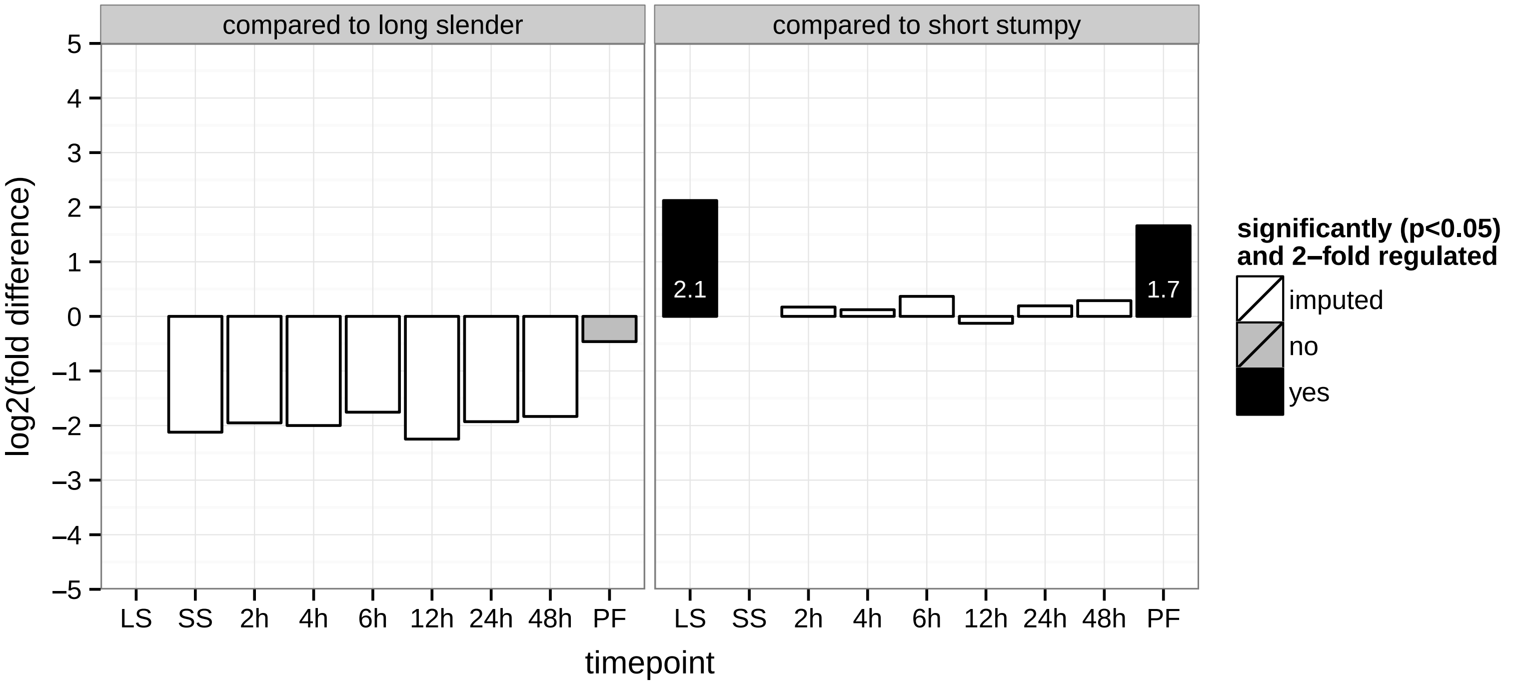
hypothetical protein, conserved
Tb927.10.8200
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: RNA binding, structural constituent of ribosome
PGOC: large ribosomal subunit
PGOP: translation

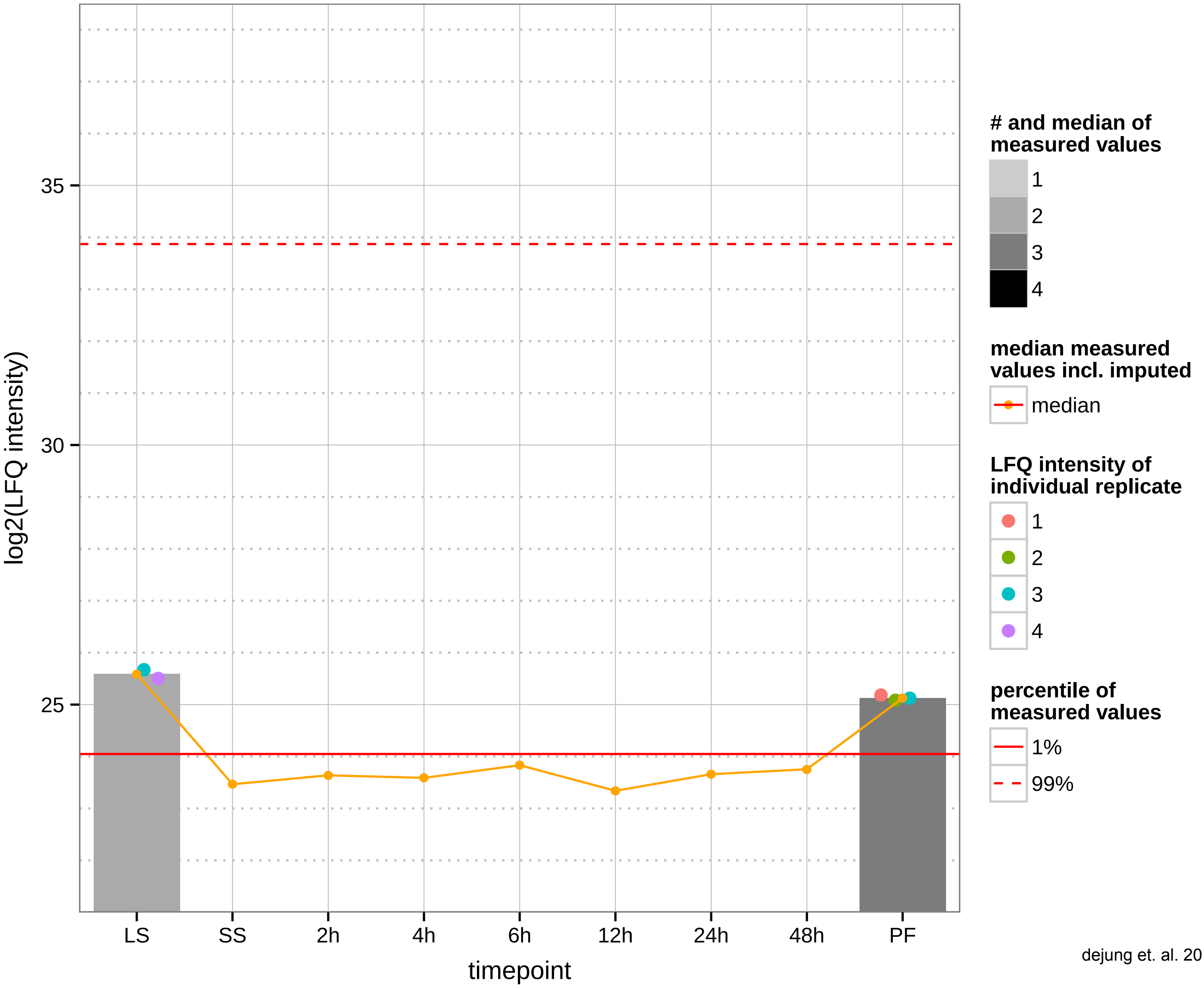




dejung et. al. 2015

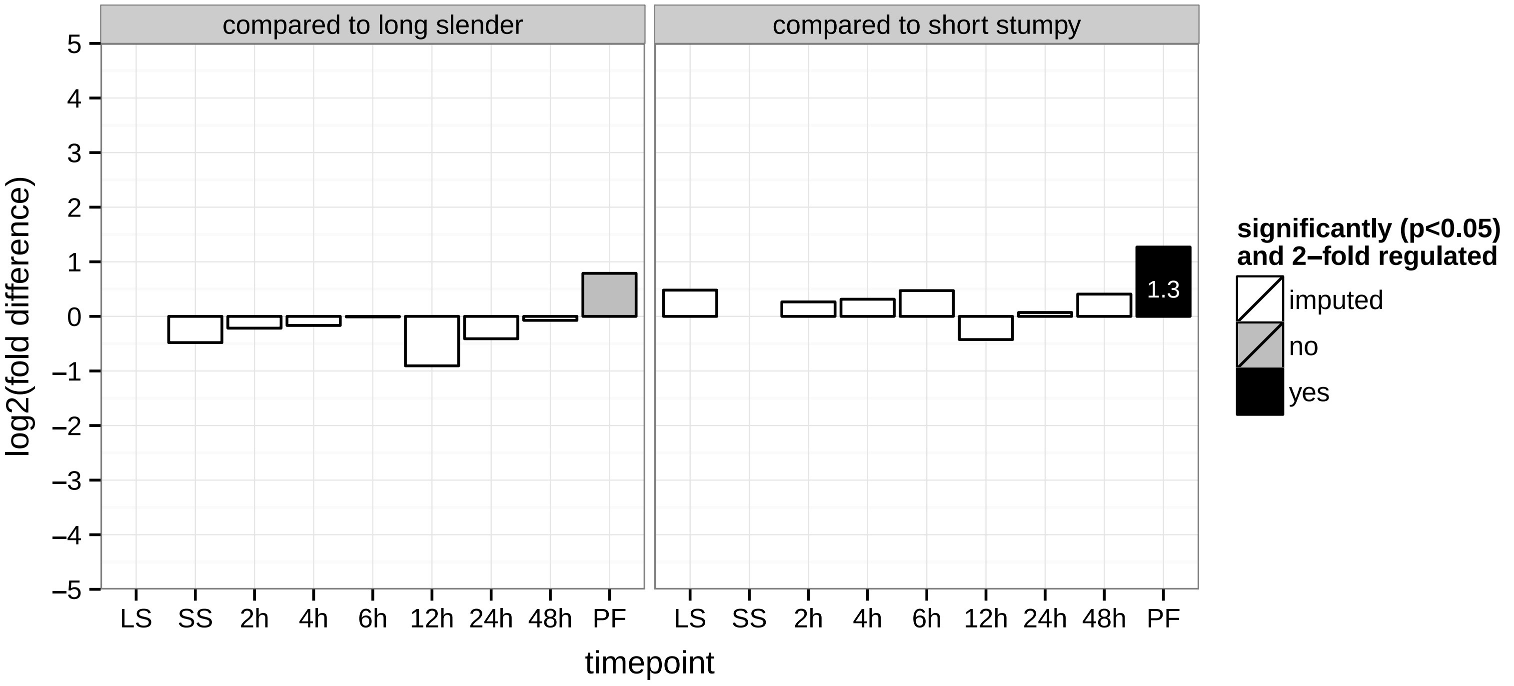
S. cerevisiae PSP1 homologue, putative
Tb927.10.8330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

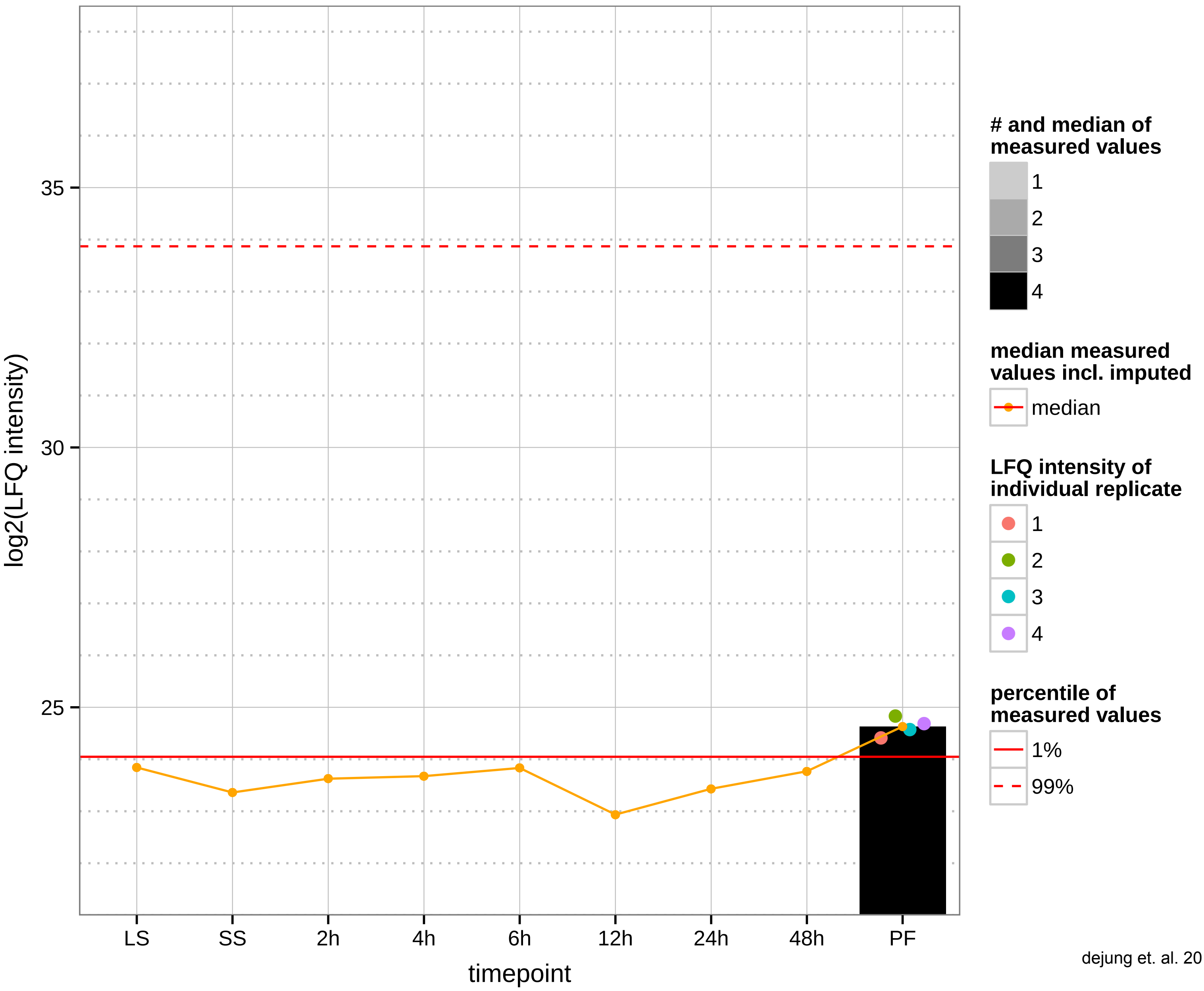




dejung et. al. 2015

ADP−ribosylation factor 3, putative, ADP−ribosylation factor−like protein, putative (ARL3)
Tb927.10.8580
AGOF: GTP binding
AGOC: intracellular
AGOP: intracellular protein transport, small GTPase mediated signal transduction
PGOF: GTP binding
PGOC: intracellular
PGOP: intracellular protein transport, protein transport, small GTPase mediated signal transduction





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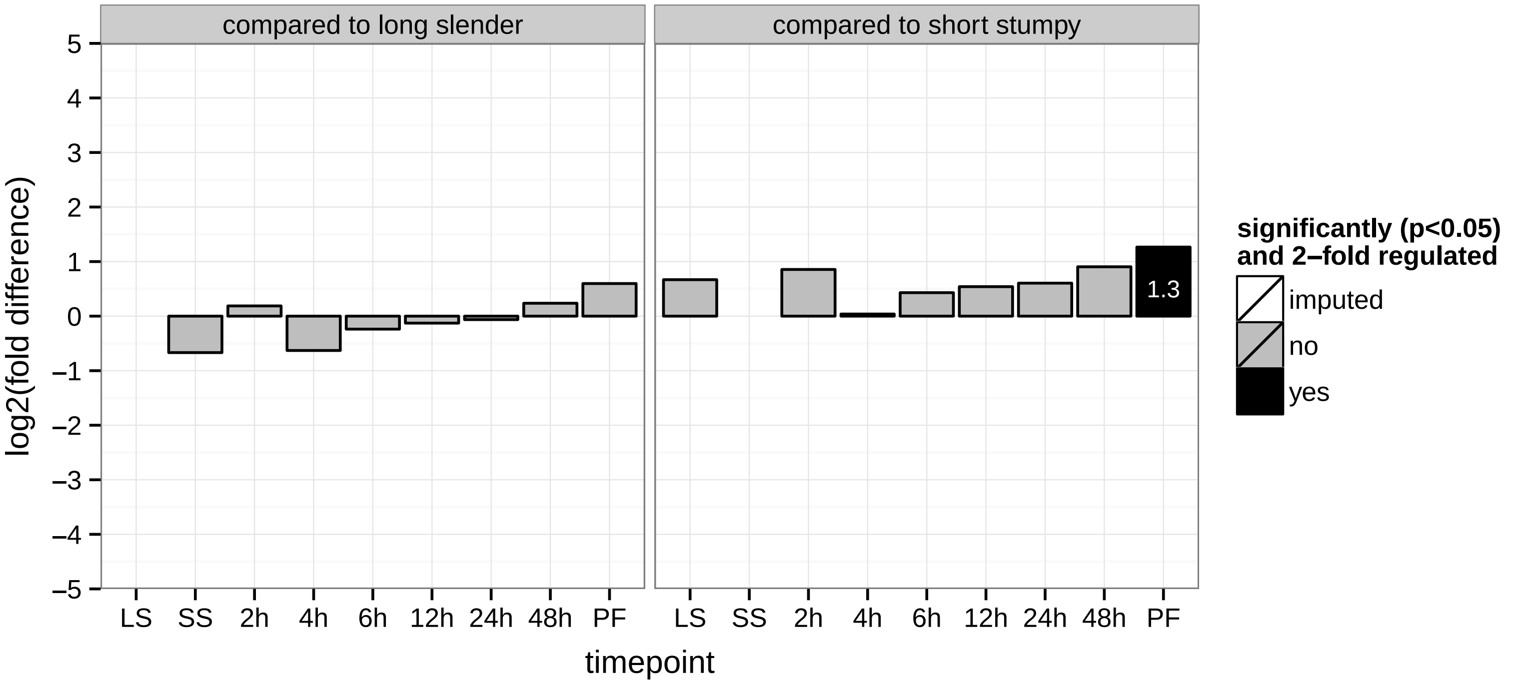
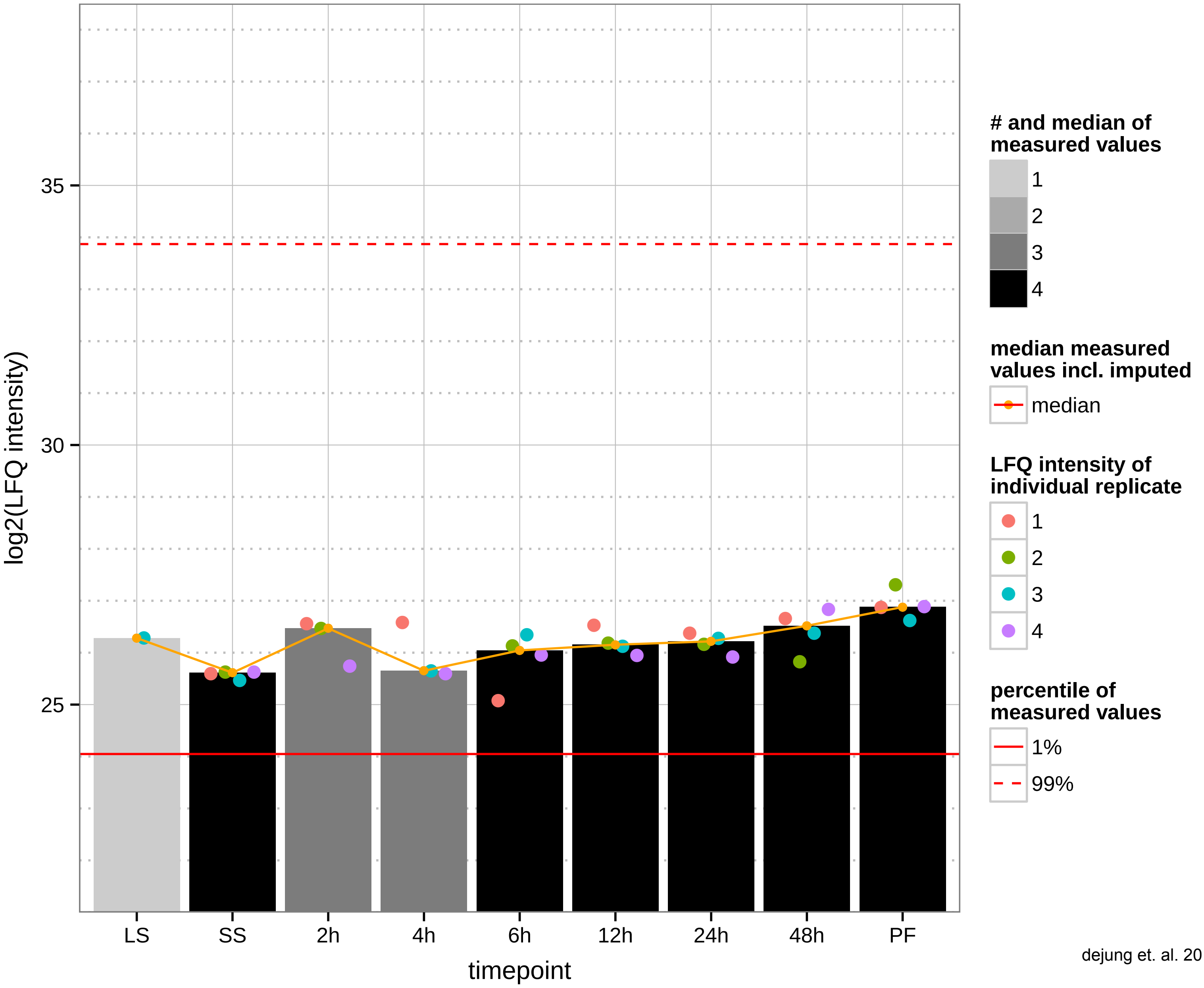
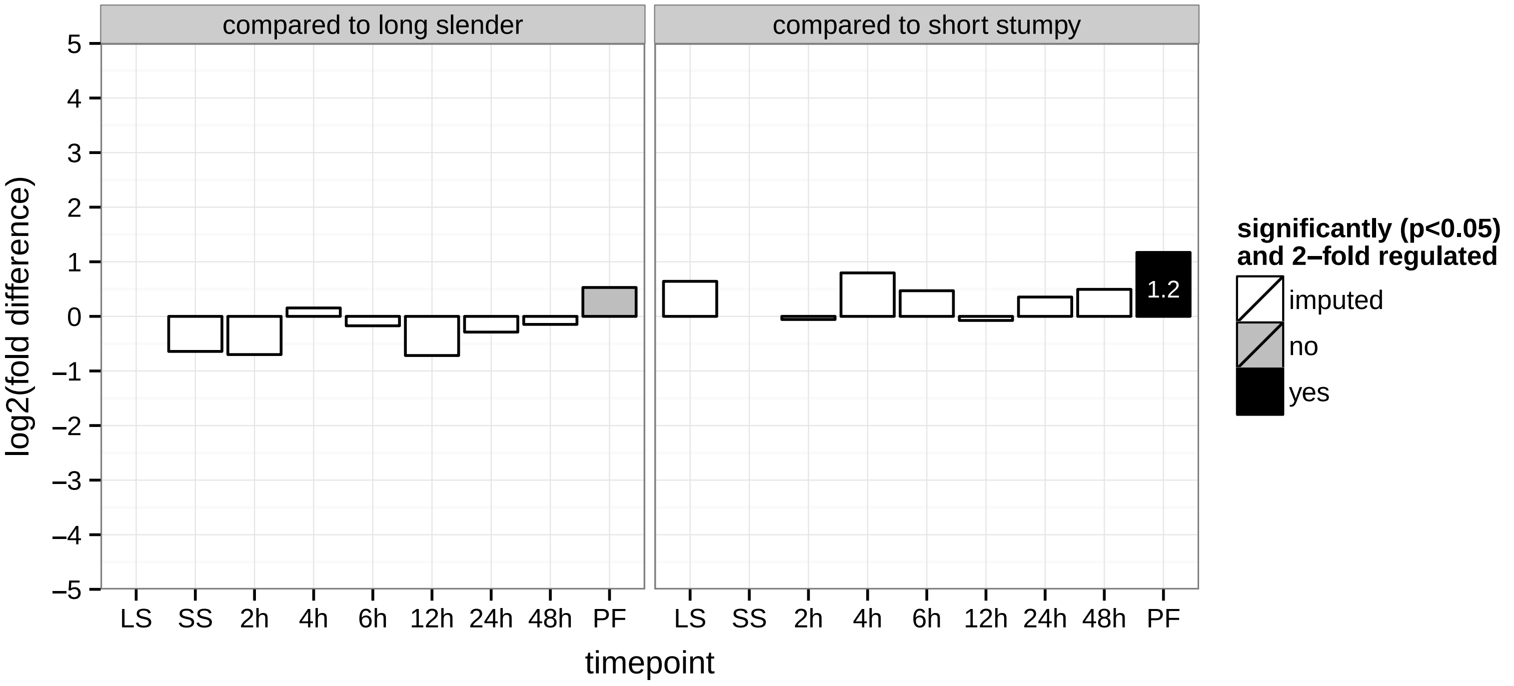
nucleoporin, putative (Nup181)
Tb927.10.8910
AGOF: null
AGOC: nuclear pore
AGOP: intracellular transport
PGOF: null
PGOC: null
PGOP: null

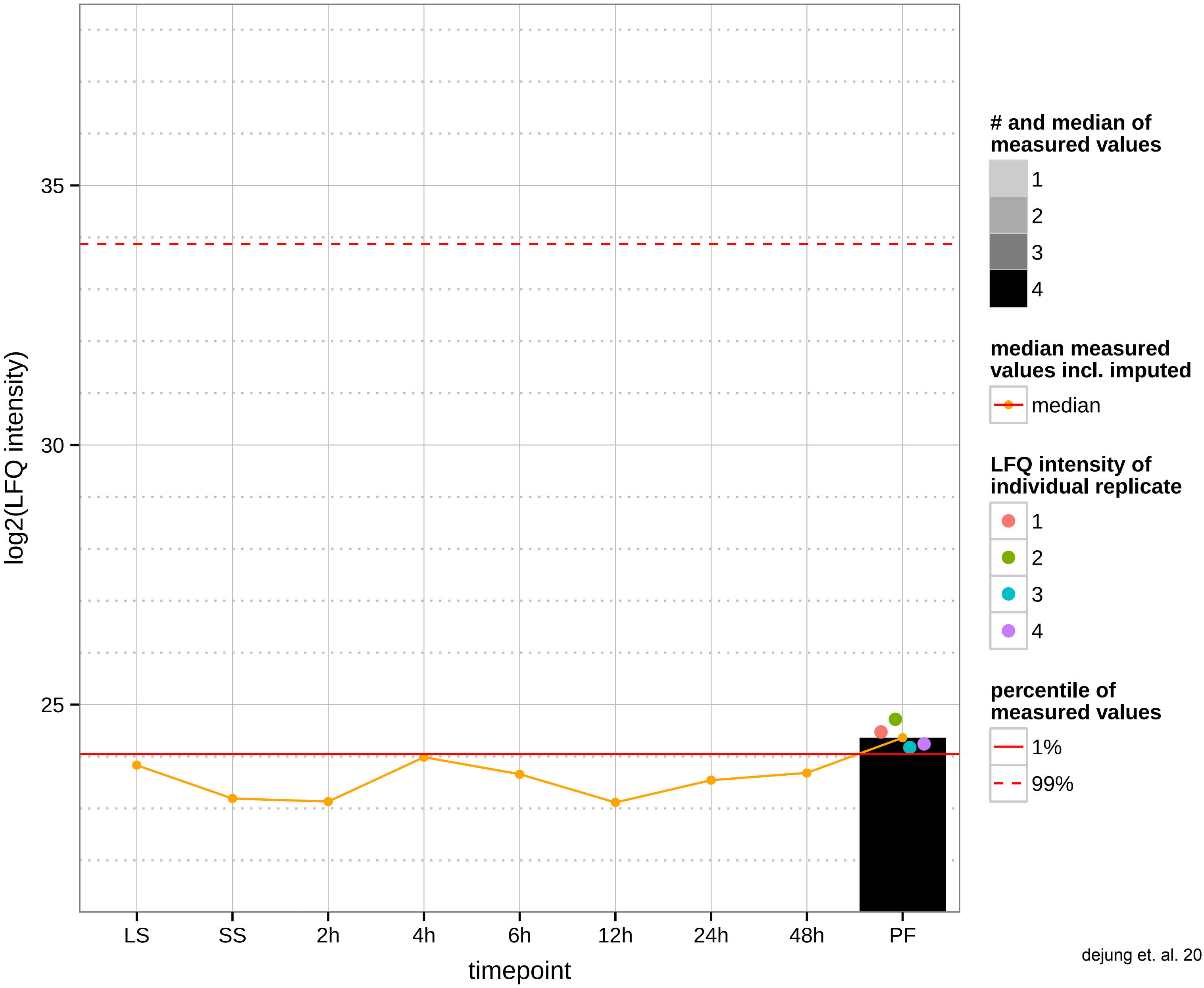




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.9070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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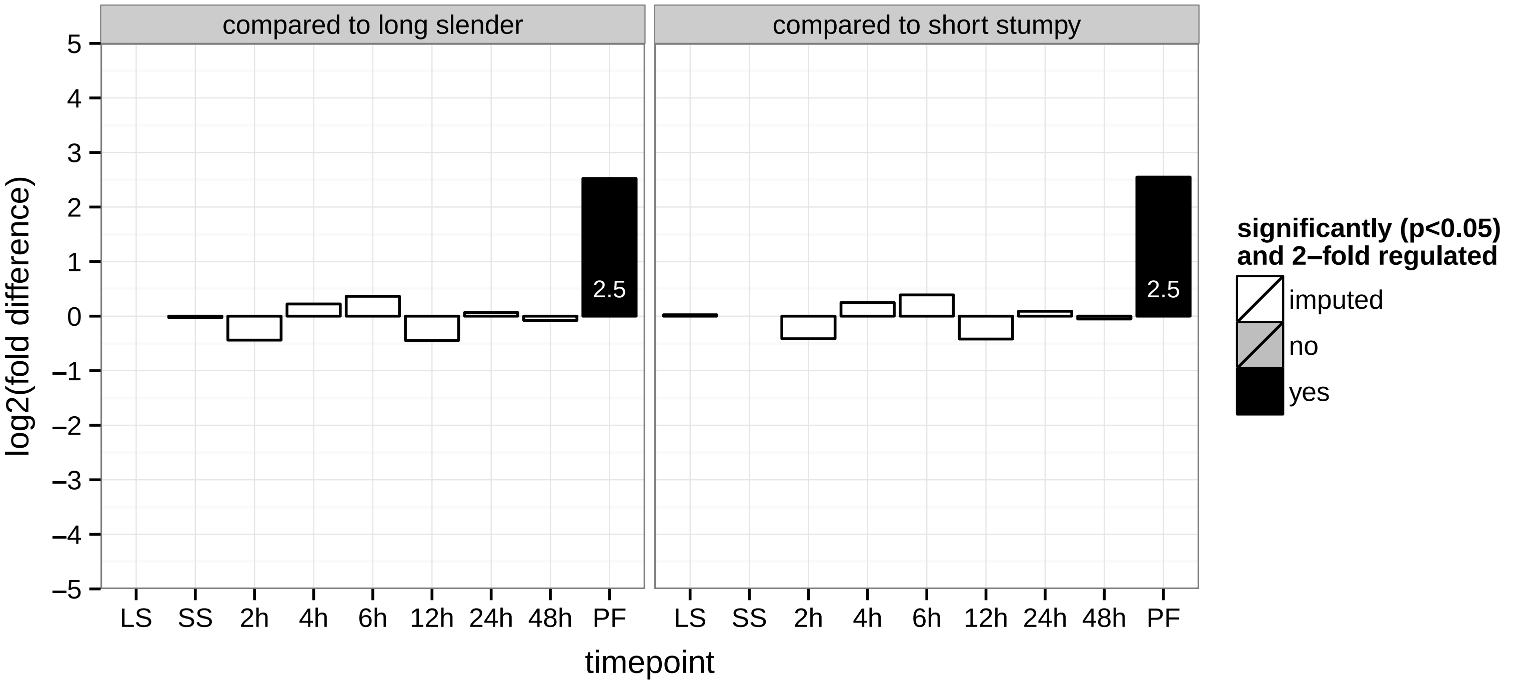
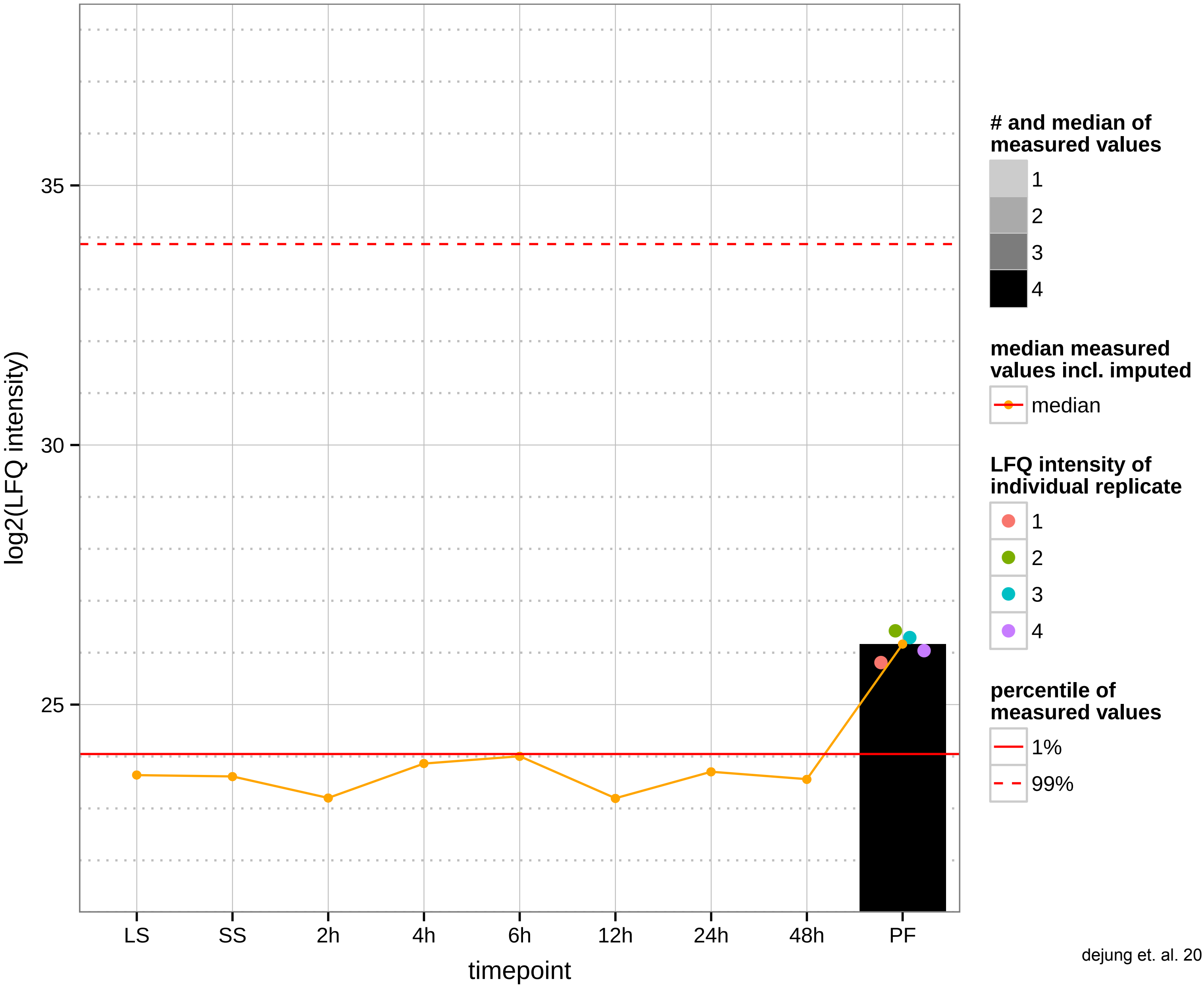
hypothetical protein, conserved
Tb927.10.9120
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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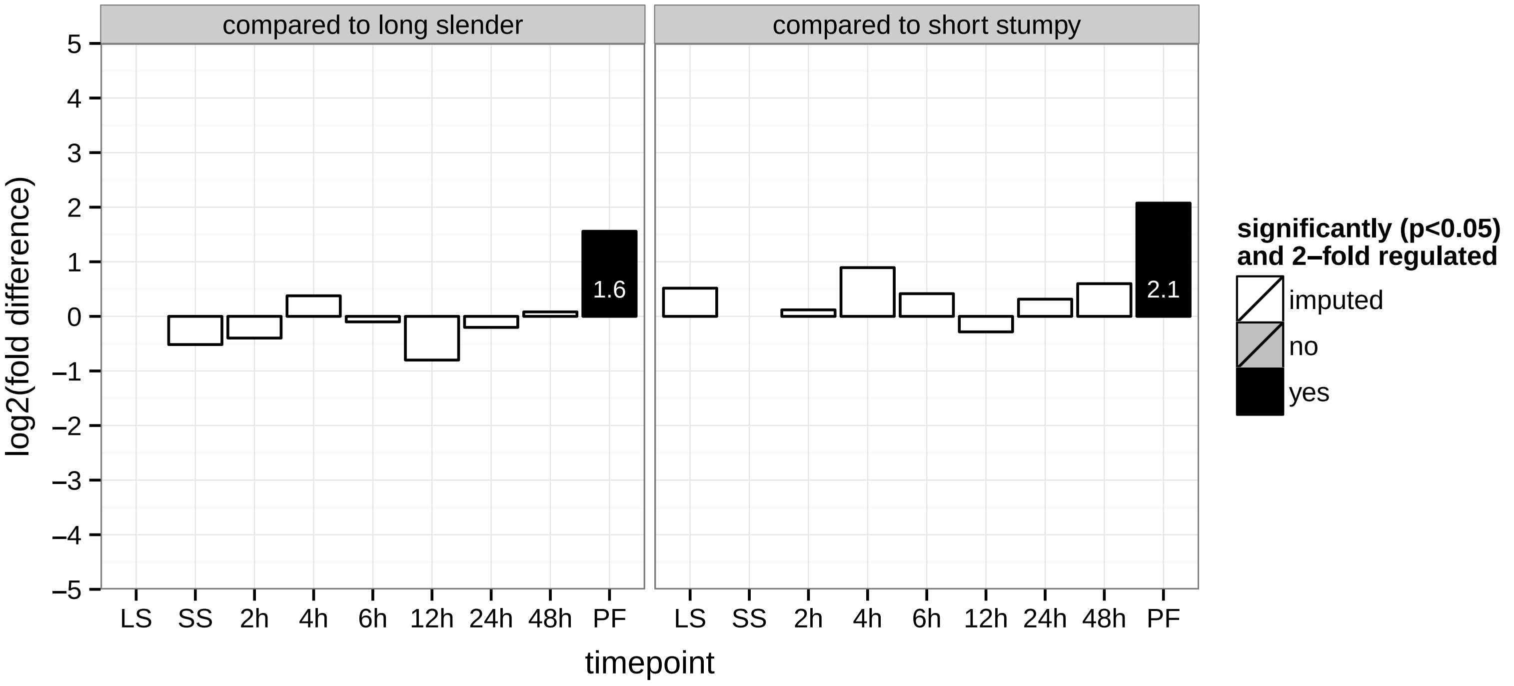
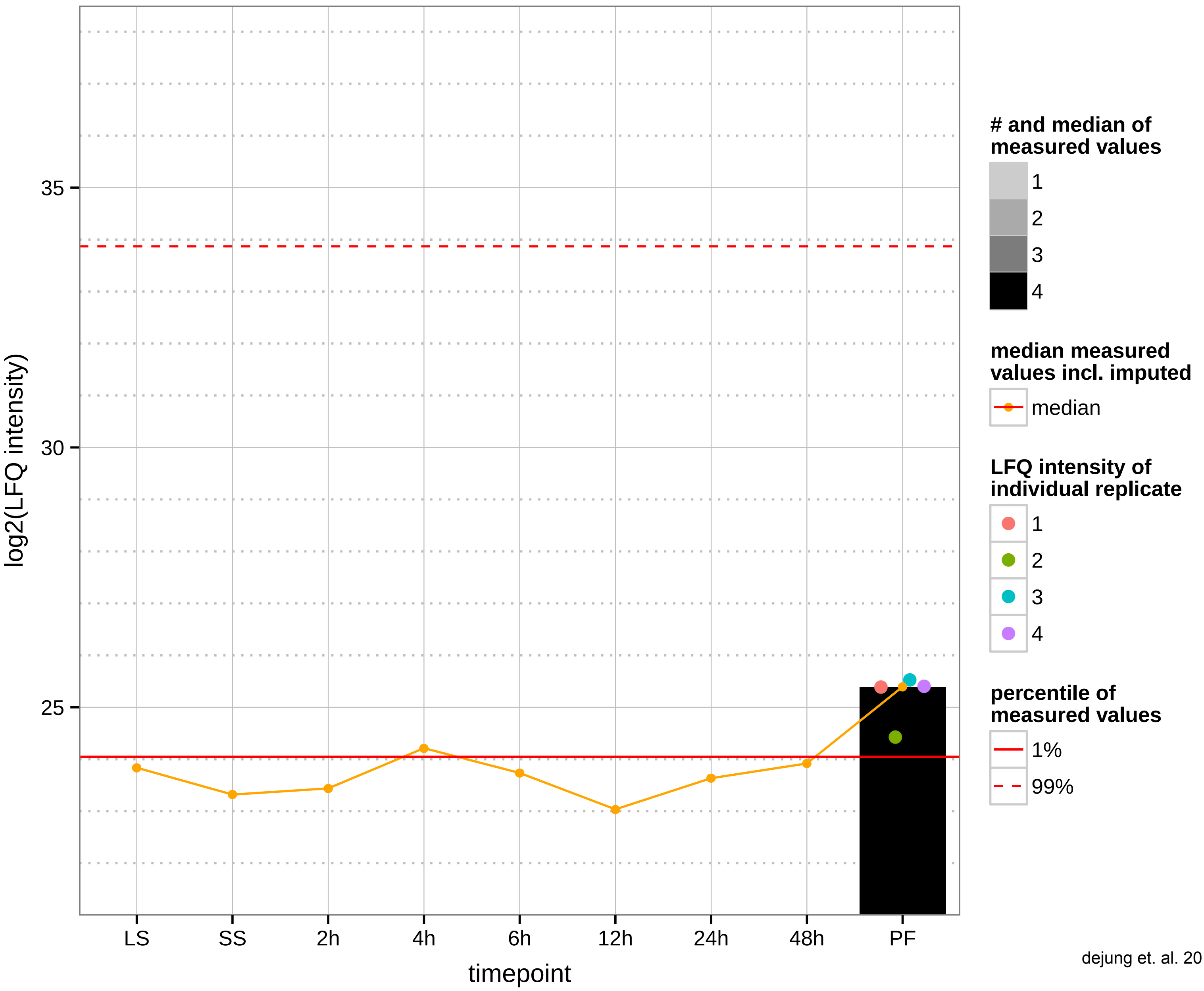
hypothetical protein, conserved
Tb927.10.9150
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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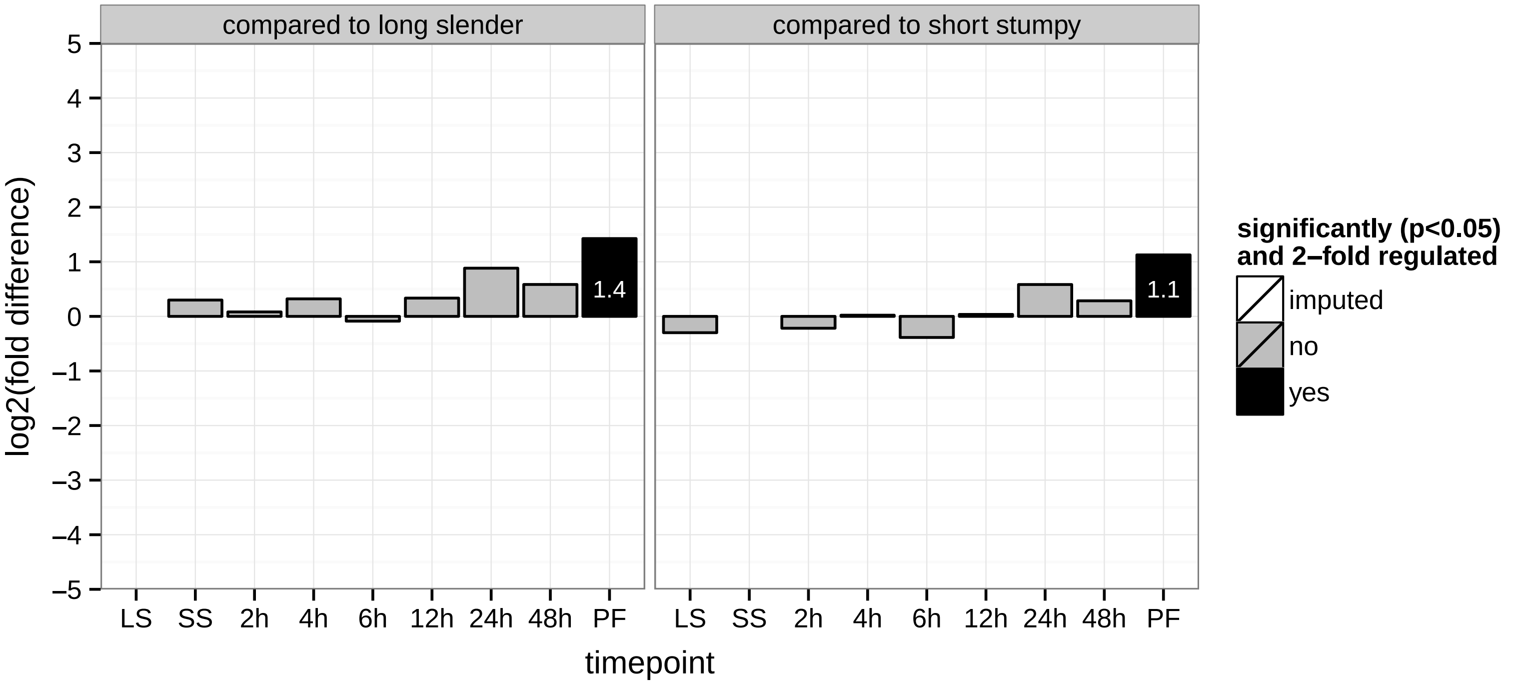
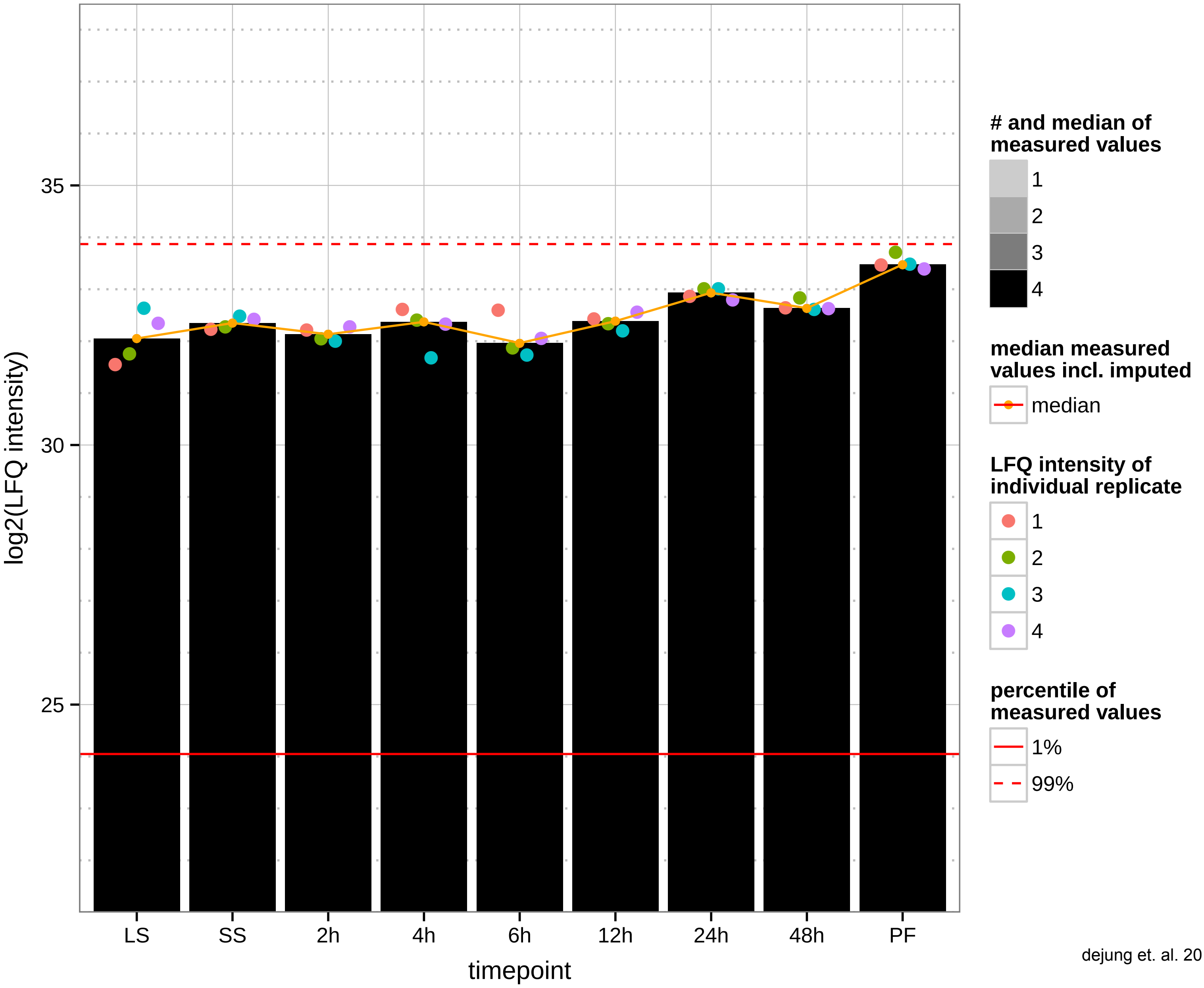
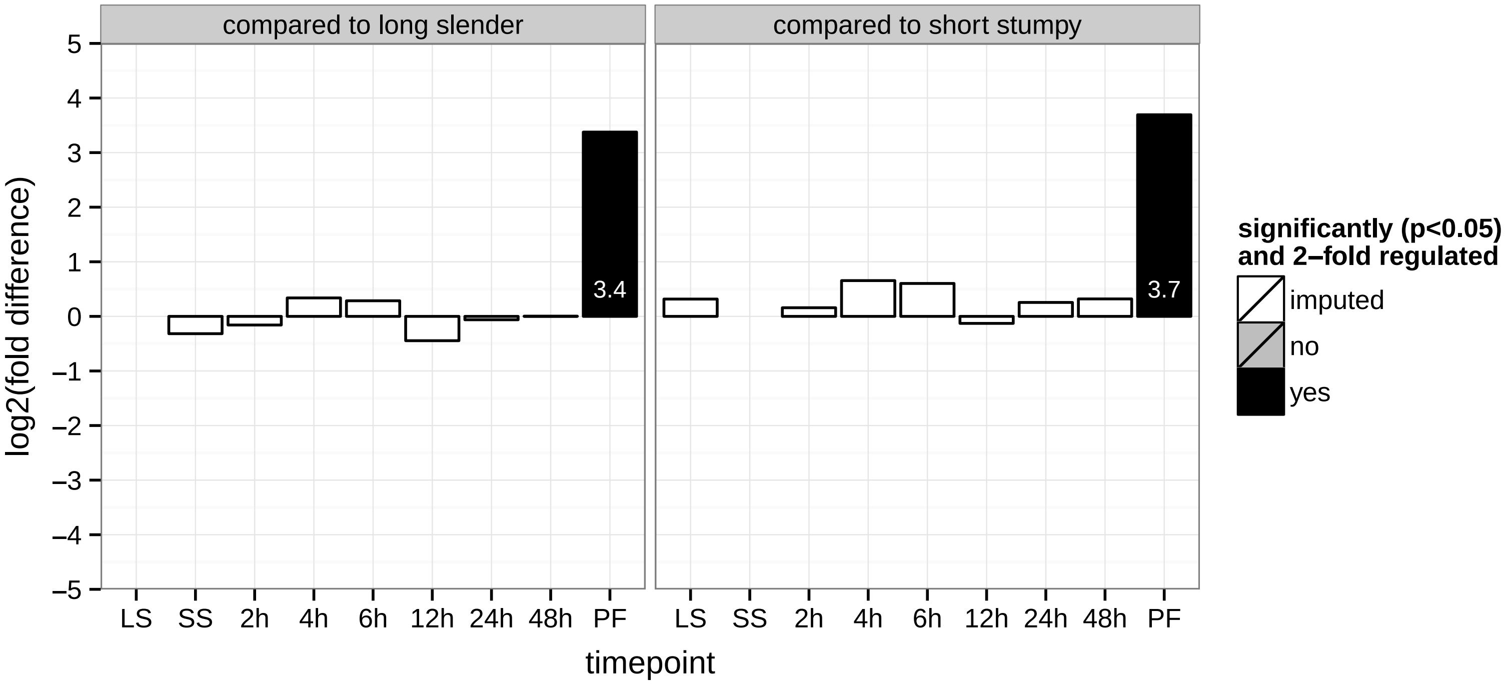
60S ribosomal protein L18, putative (TbL18LP), putative (RPL18)
Tb927.11.4300;Tb927.10.9880
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation, null
PGOF: null
PGOC: null
PGOP: null

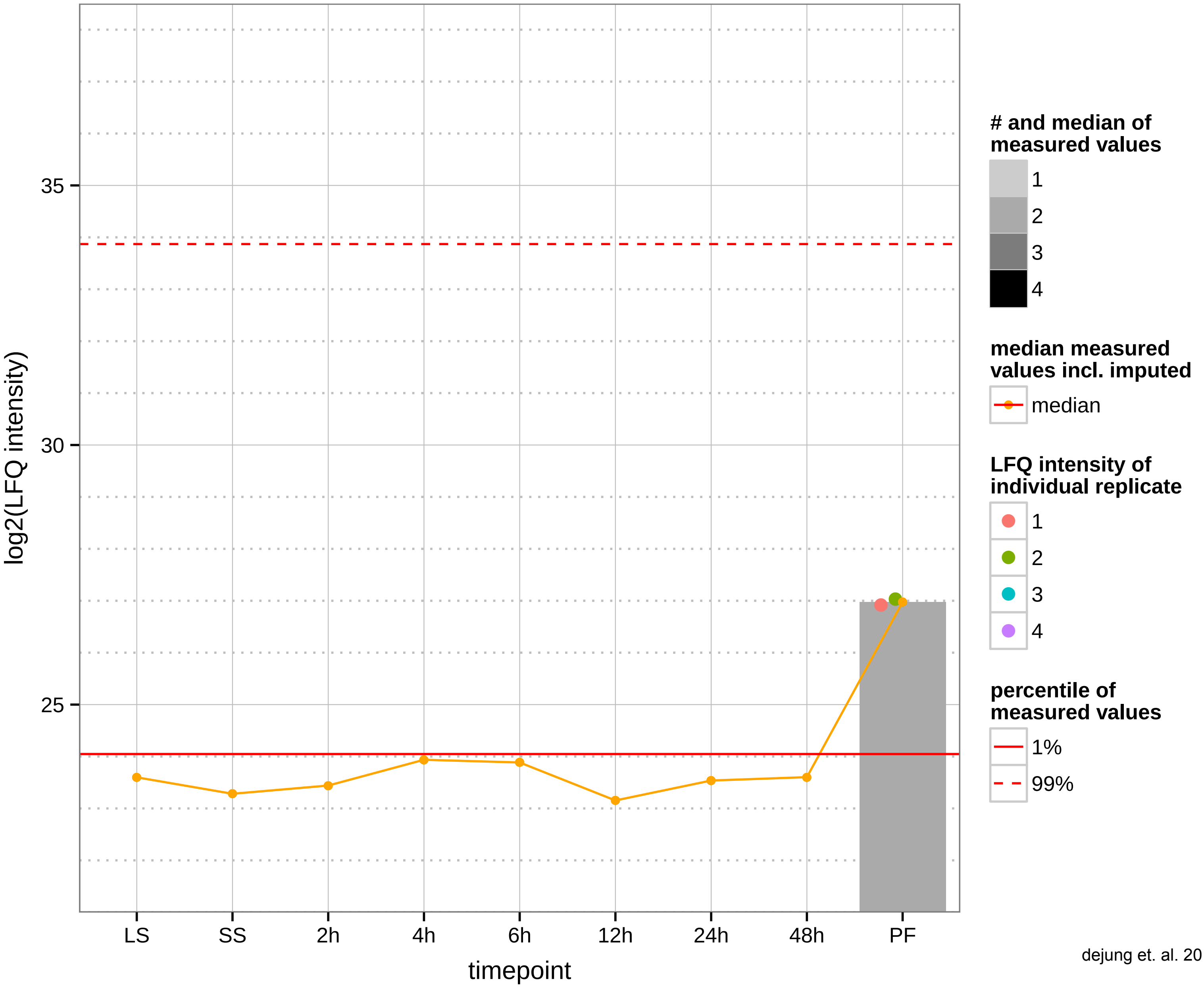




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.9960
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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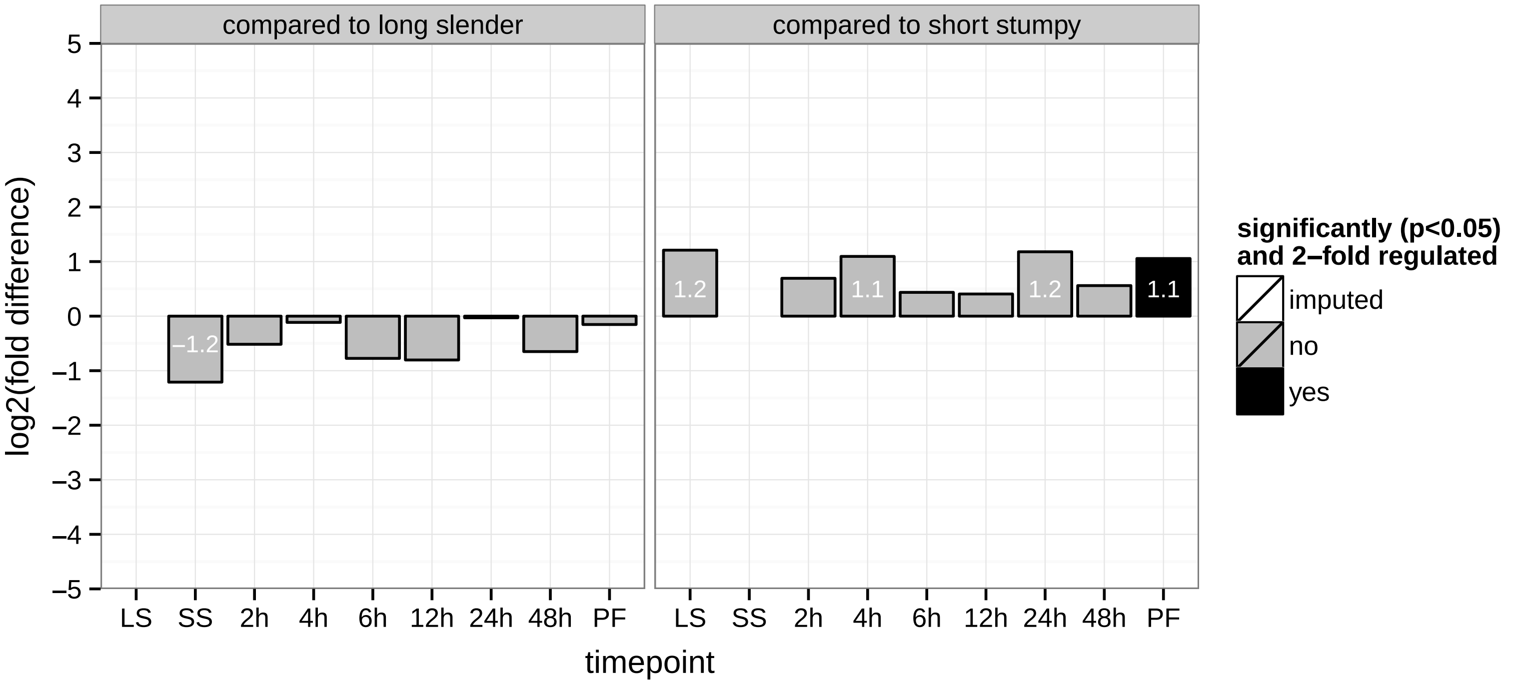
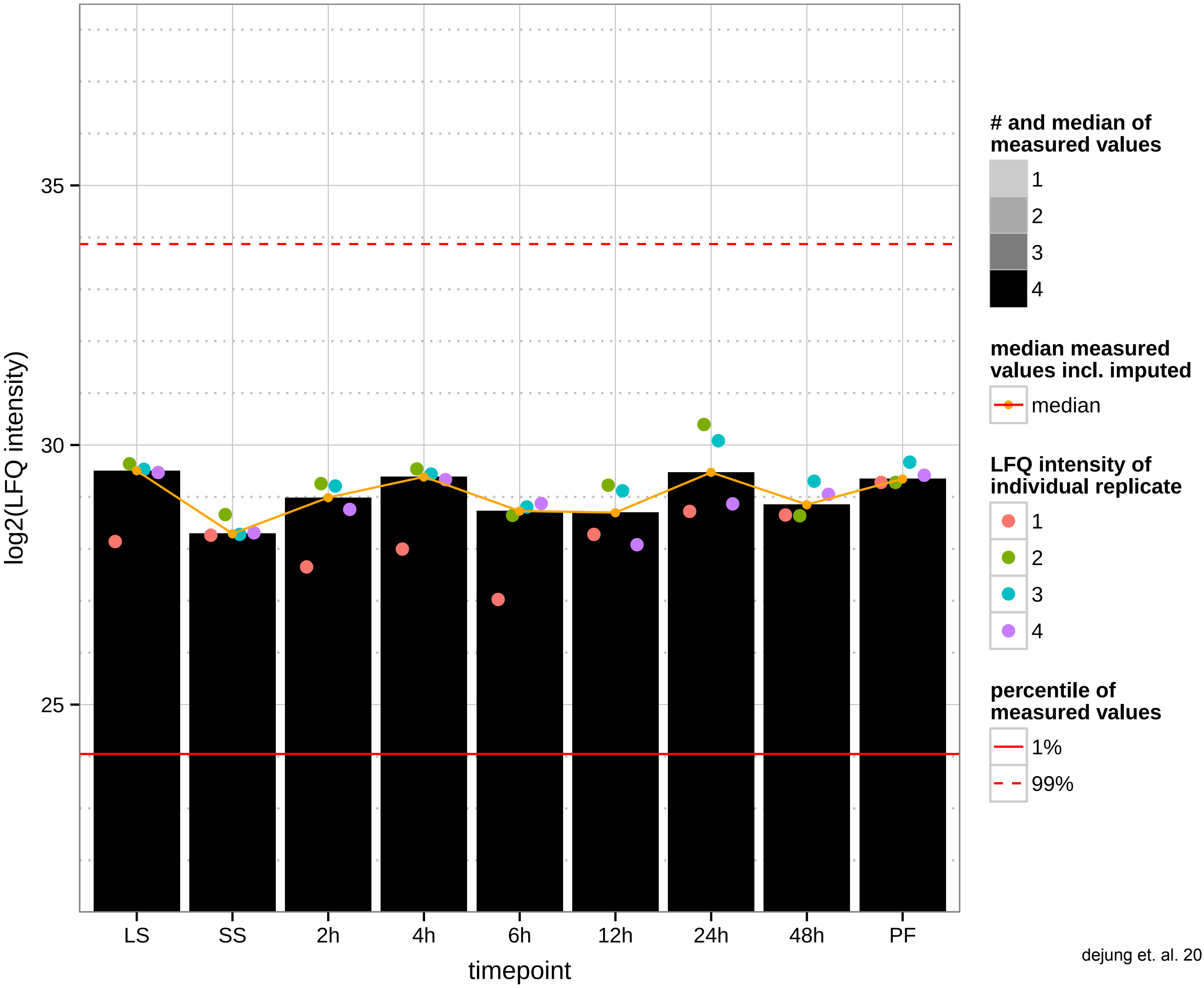
60S ribosomal protein L29, putative
Tb927.11.10030
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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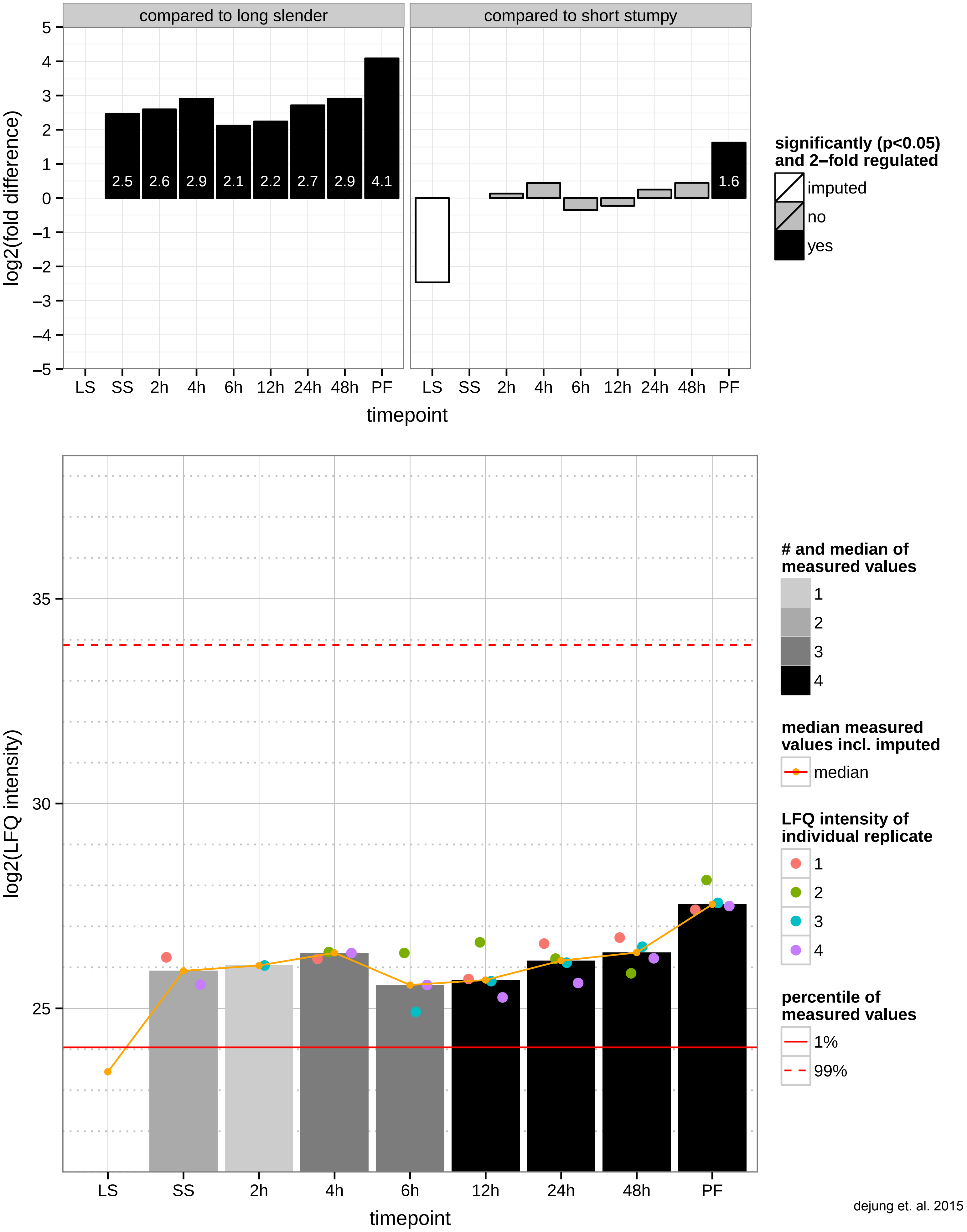
hypothetical protein, conserved
Tb927.11.10080
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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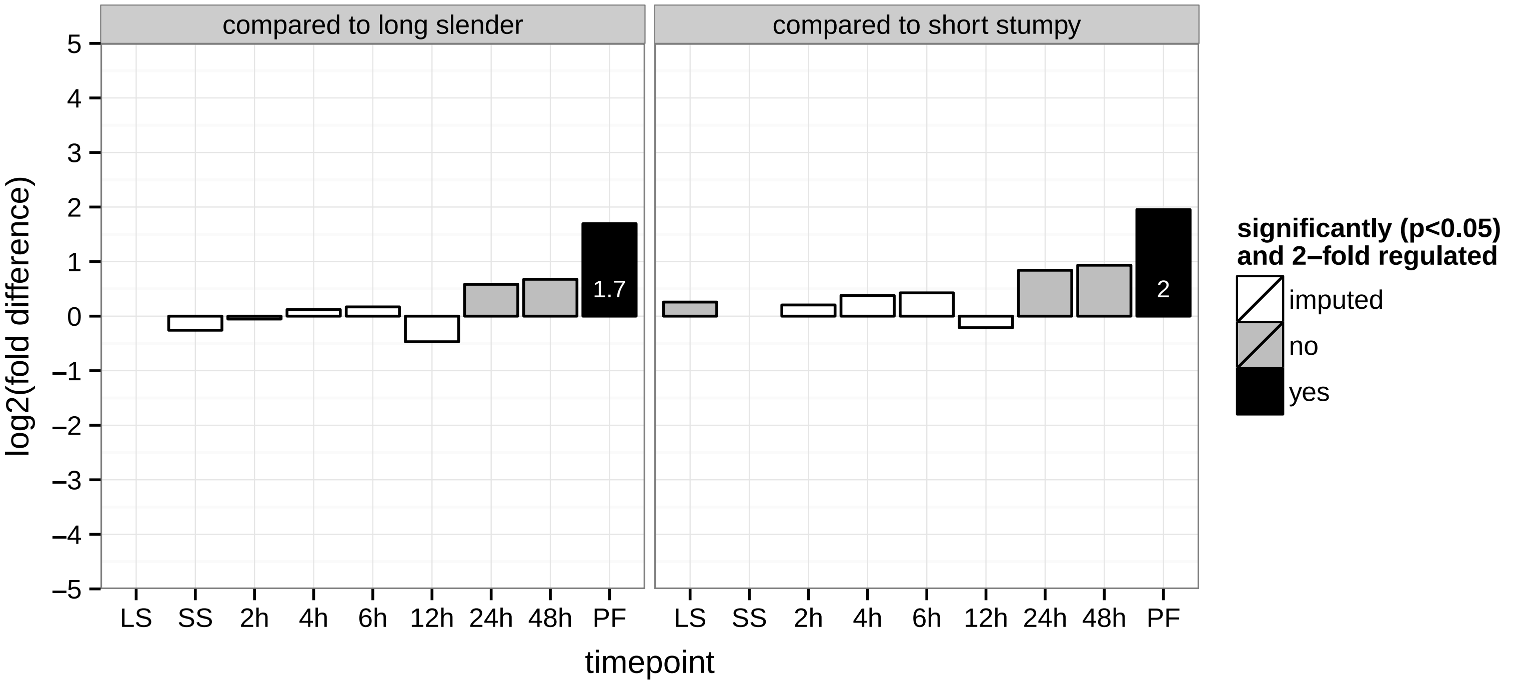
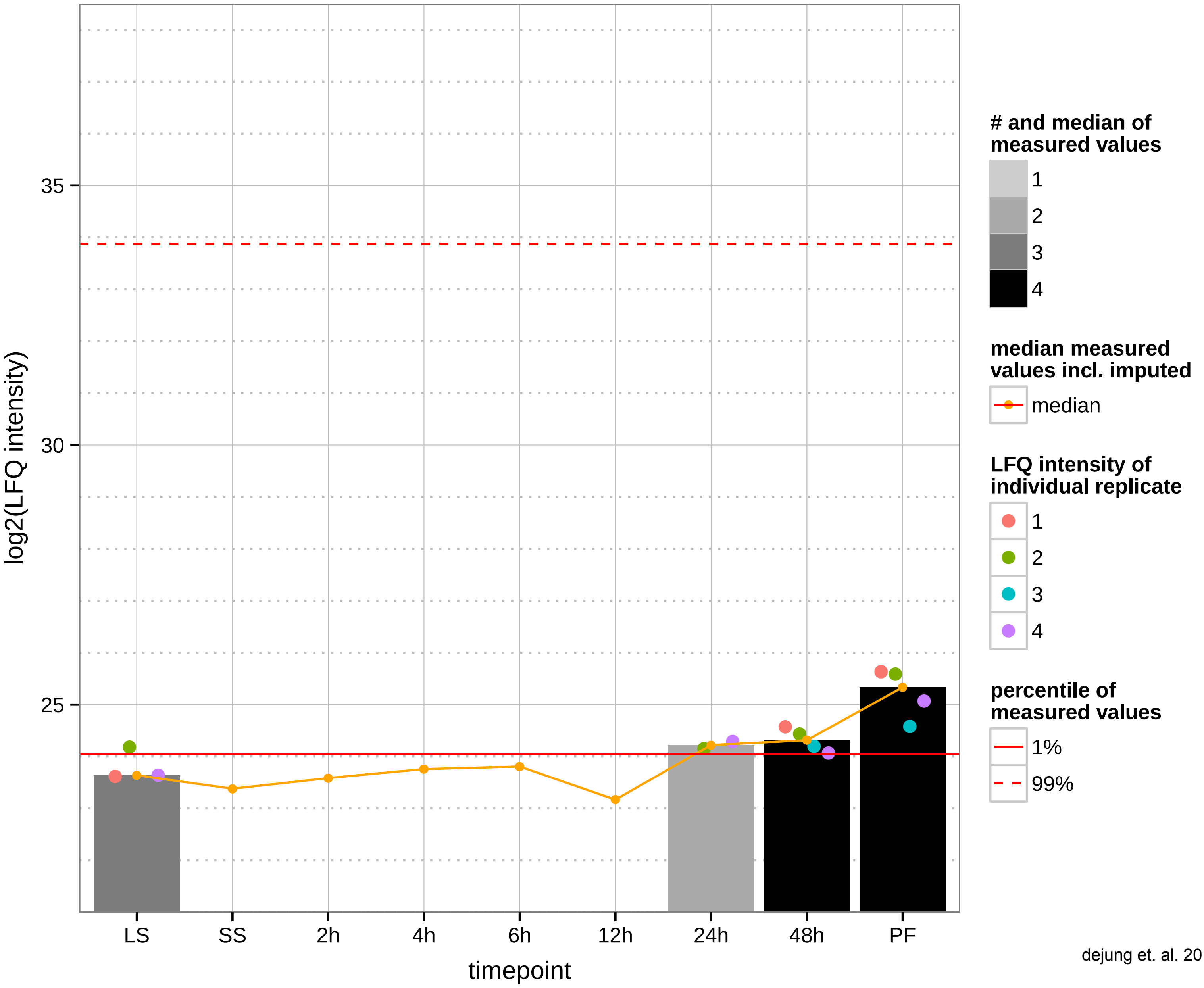
hypothetical protein, conserved
Tb927.11.1040
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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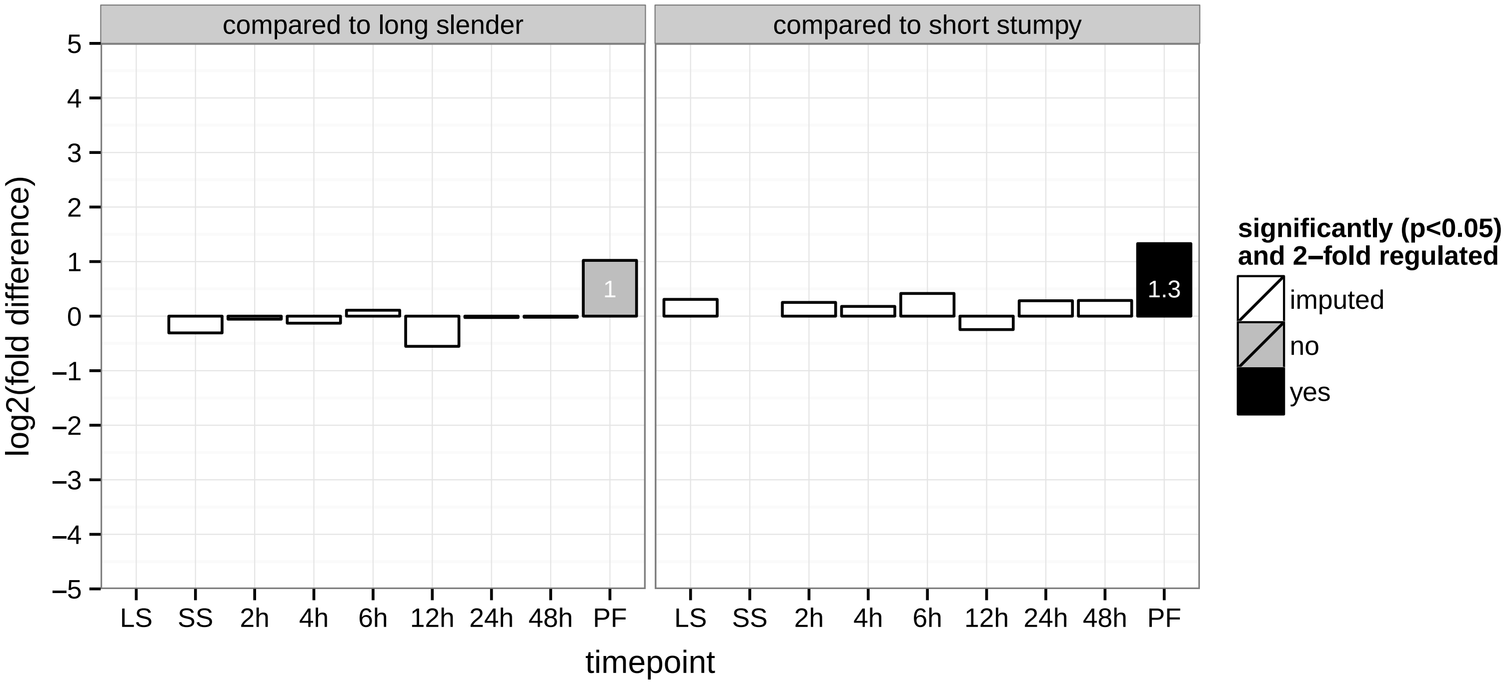
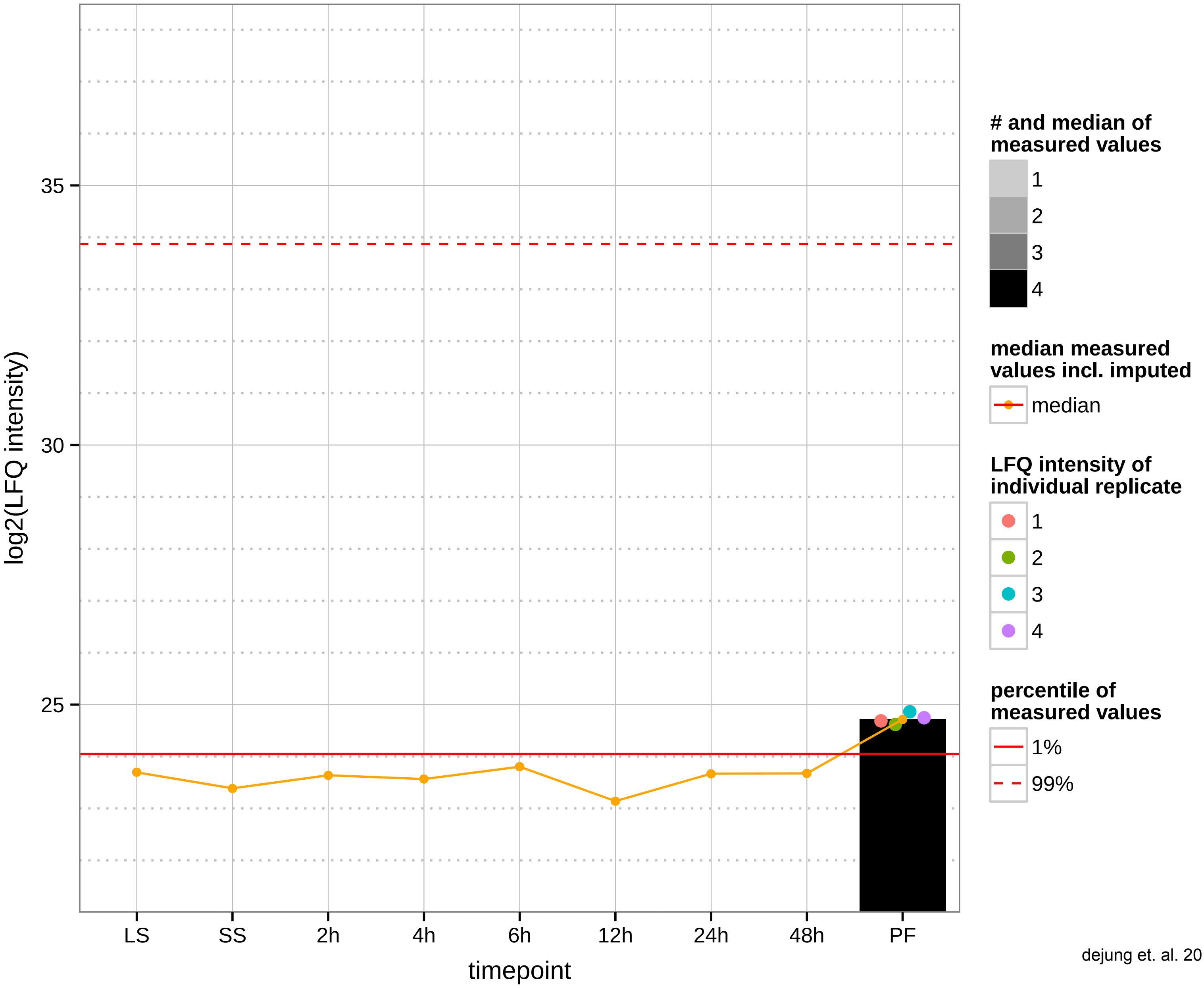
hypothetical protein, conserved
Tb927.11.10460
AGOF: null
AGOC: nucleus
AGOP: DNA replication
PGOF: null
PGOC: null
PGOP: null





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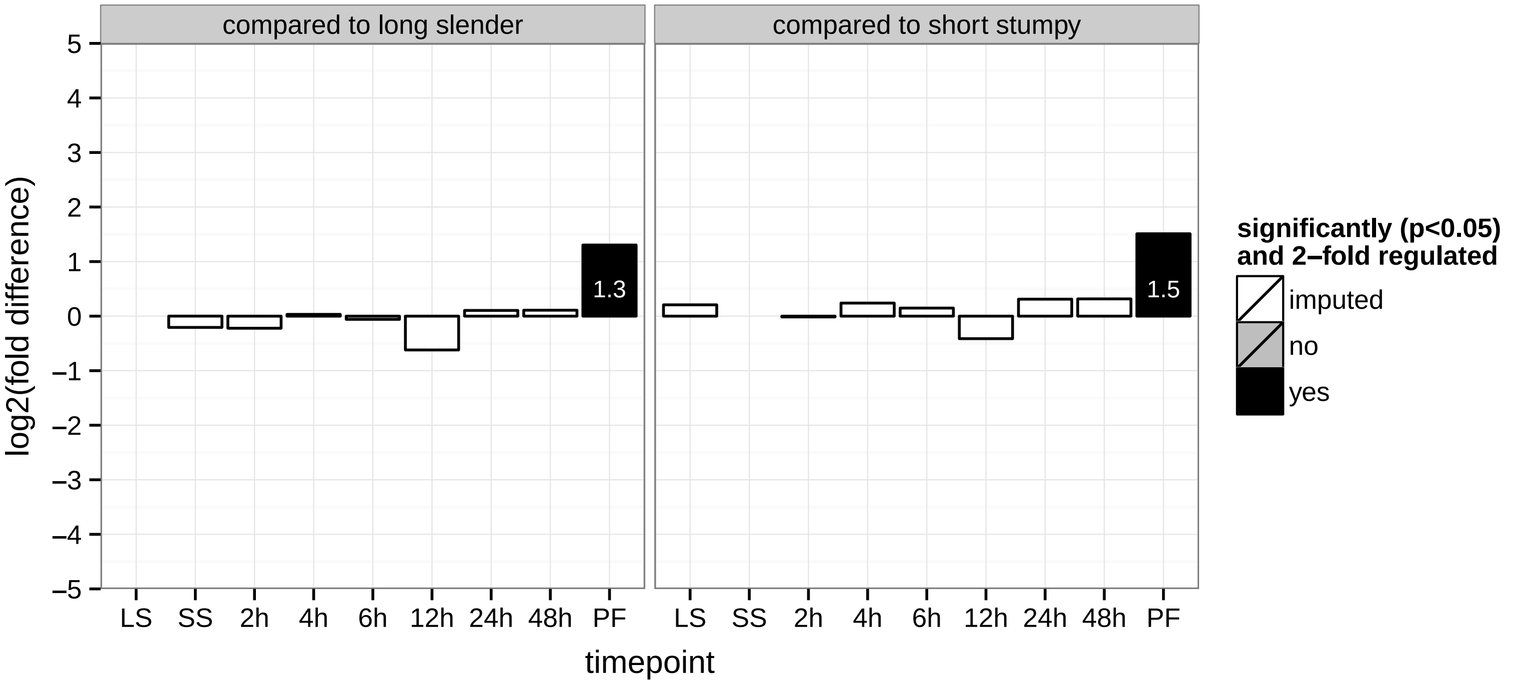
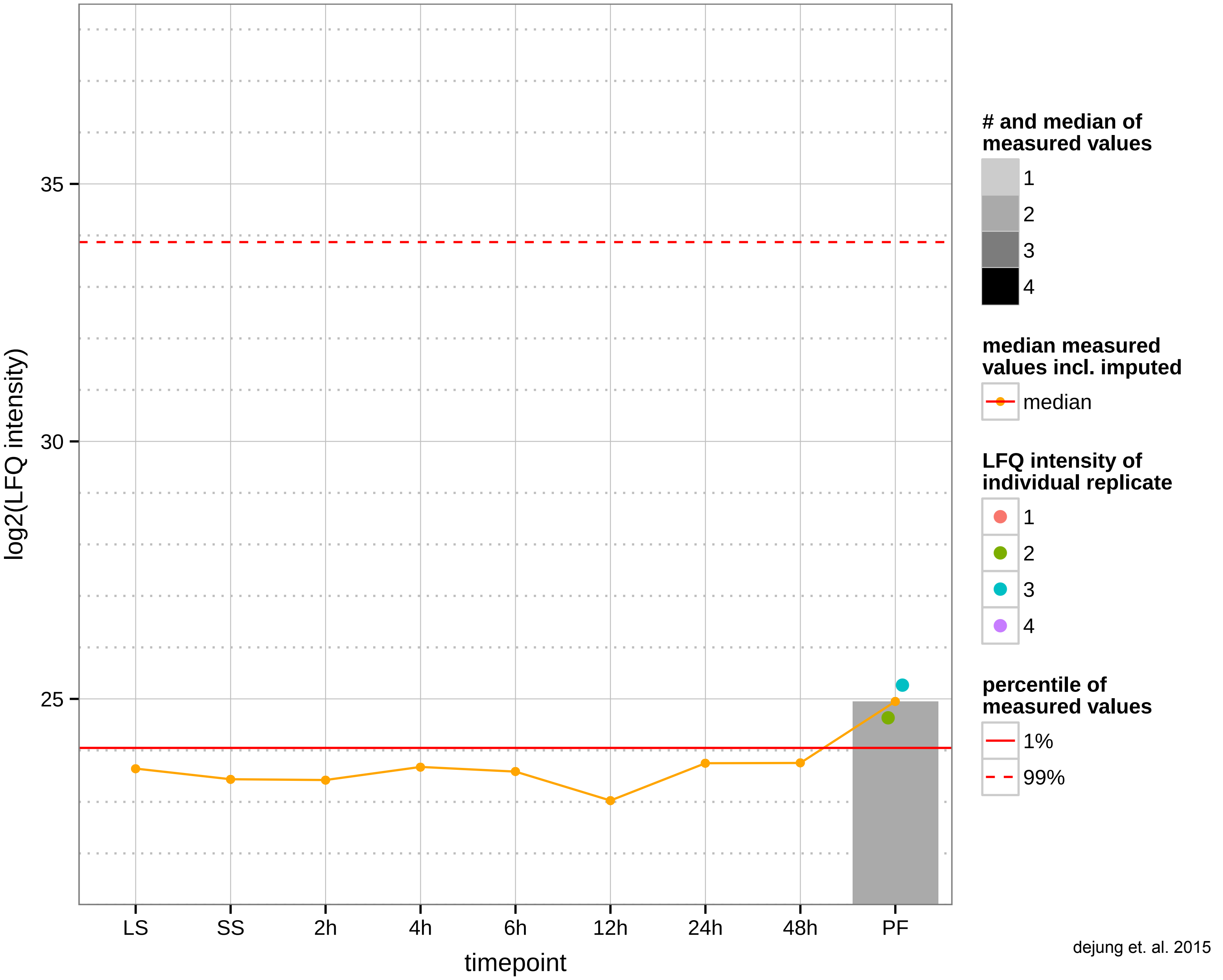
hypothetical protein, conserved
Tb927.11.10470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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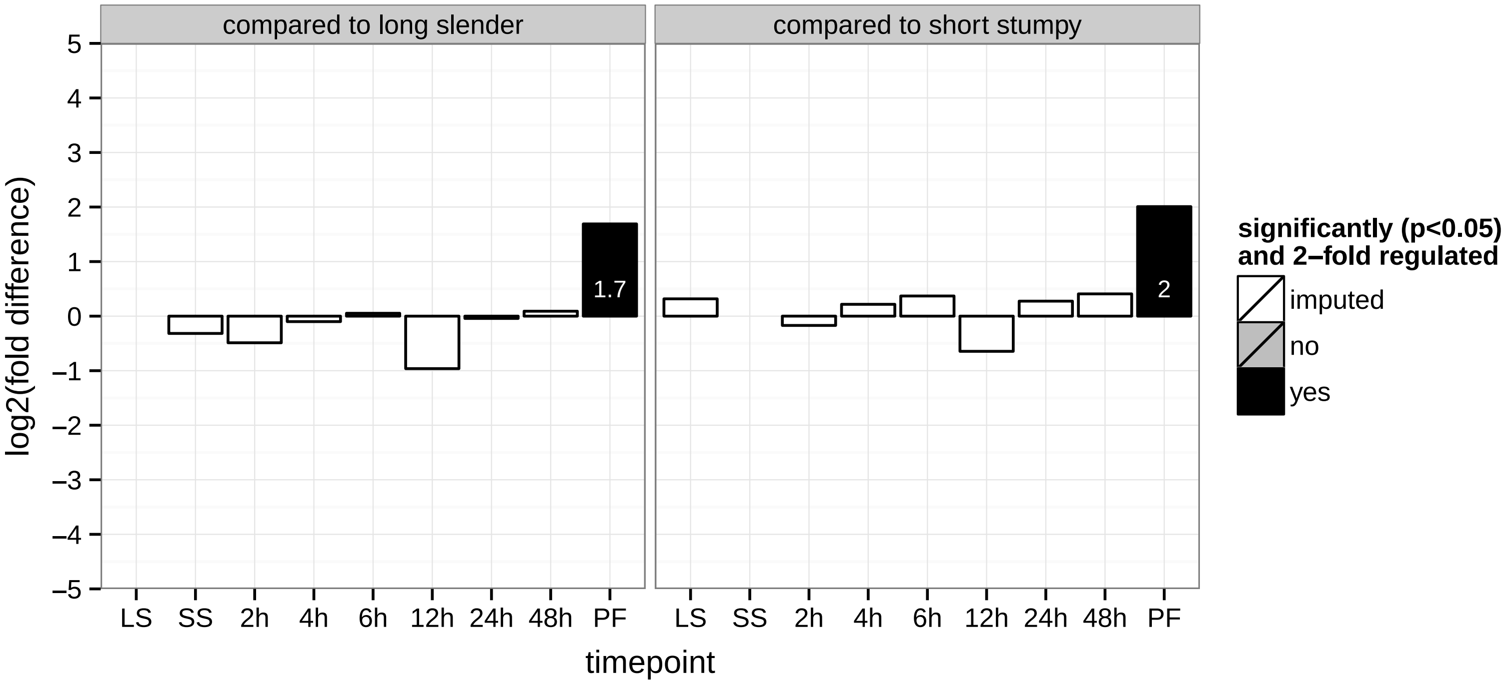
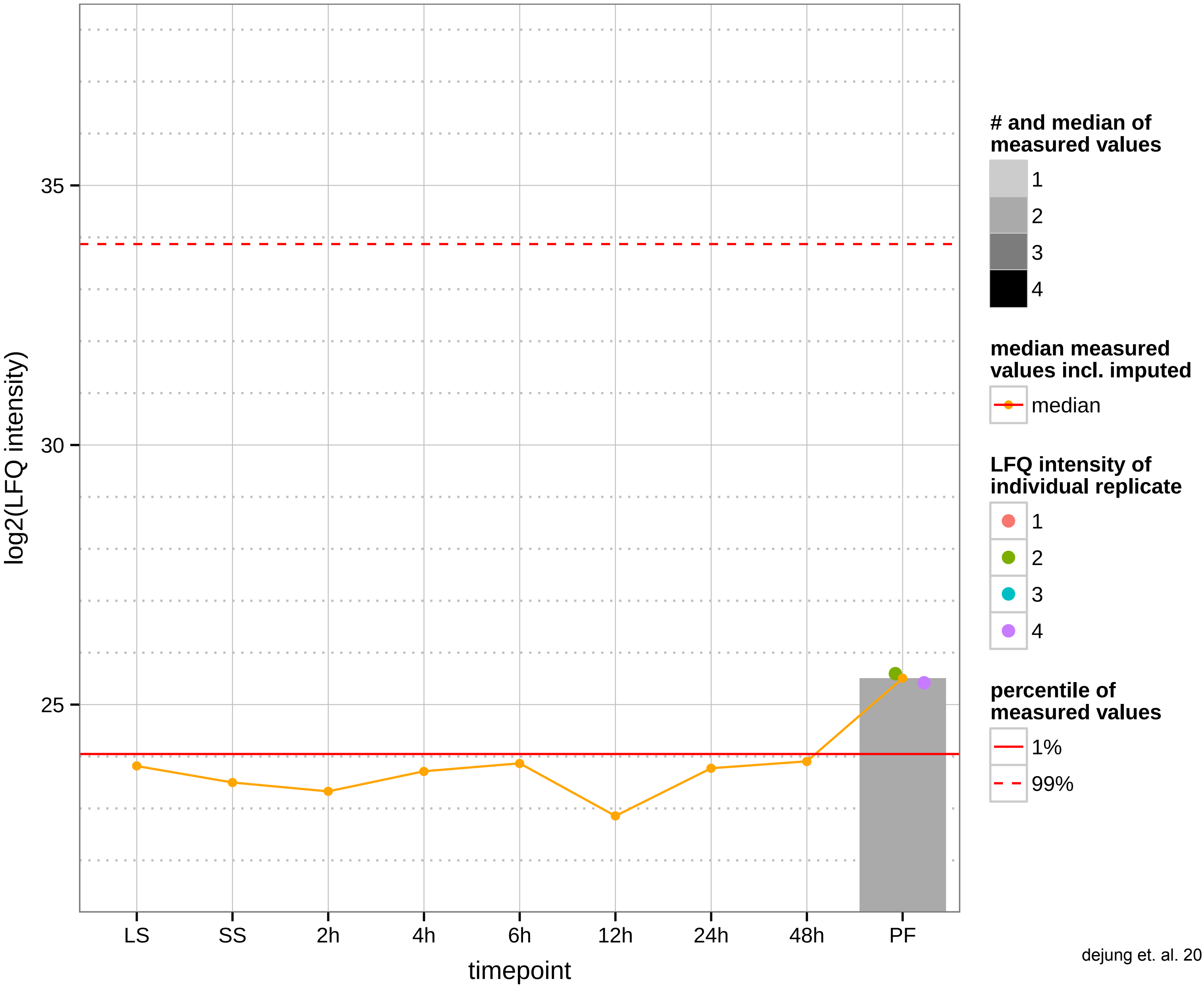
kinetoplastid kinetochore protein 2, serine/threonine−protein kinase, putative, putative (kkt2)
Tb927.11.10520
AGOF: ATP binding, protein serine/threonine kinase activity
AGOC: kinetochore
AGOP: chromosome segregation, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus−containing groups
PGOC: null
PGOP: protein phosphorylation





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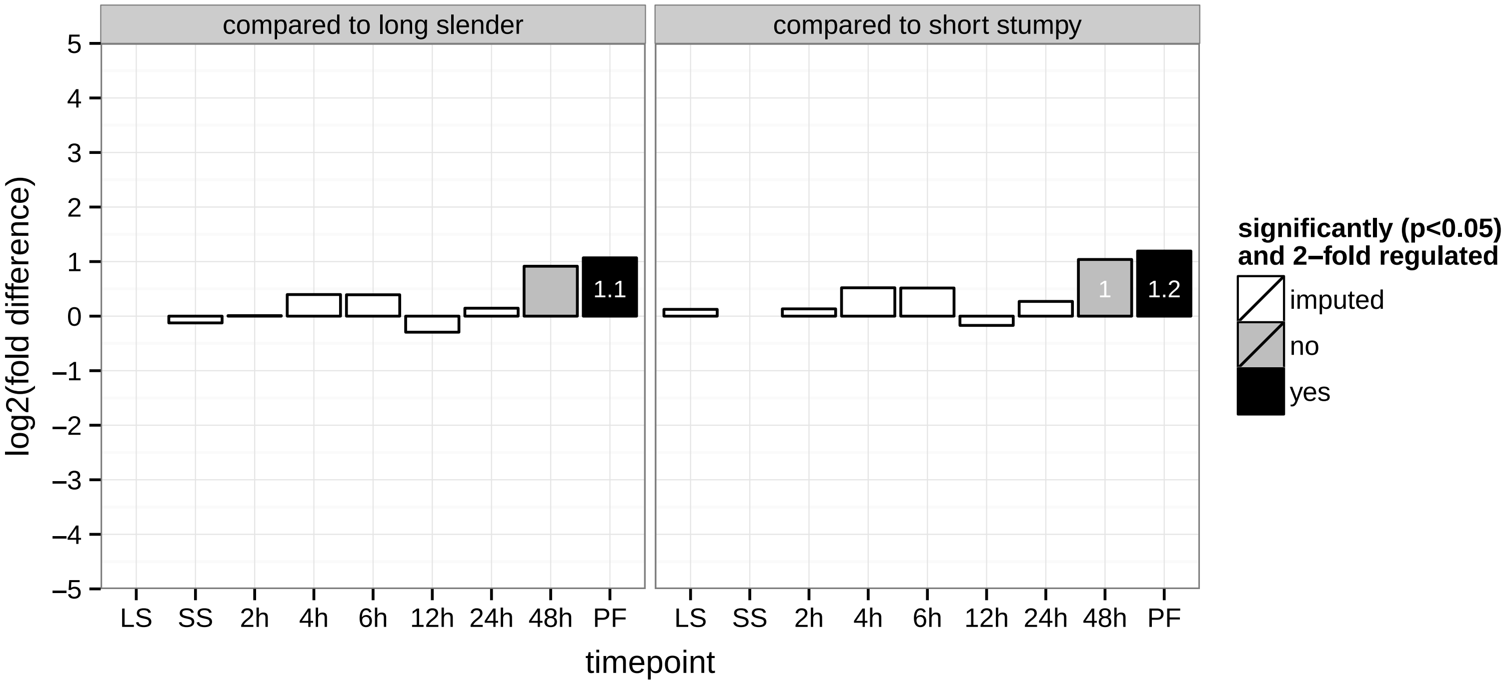
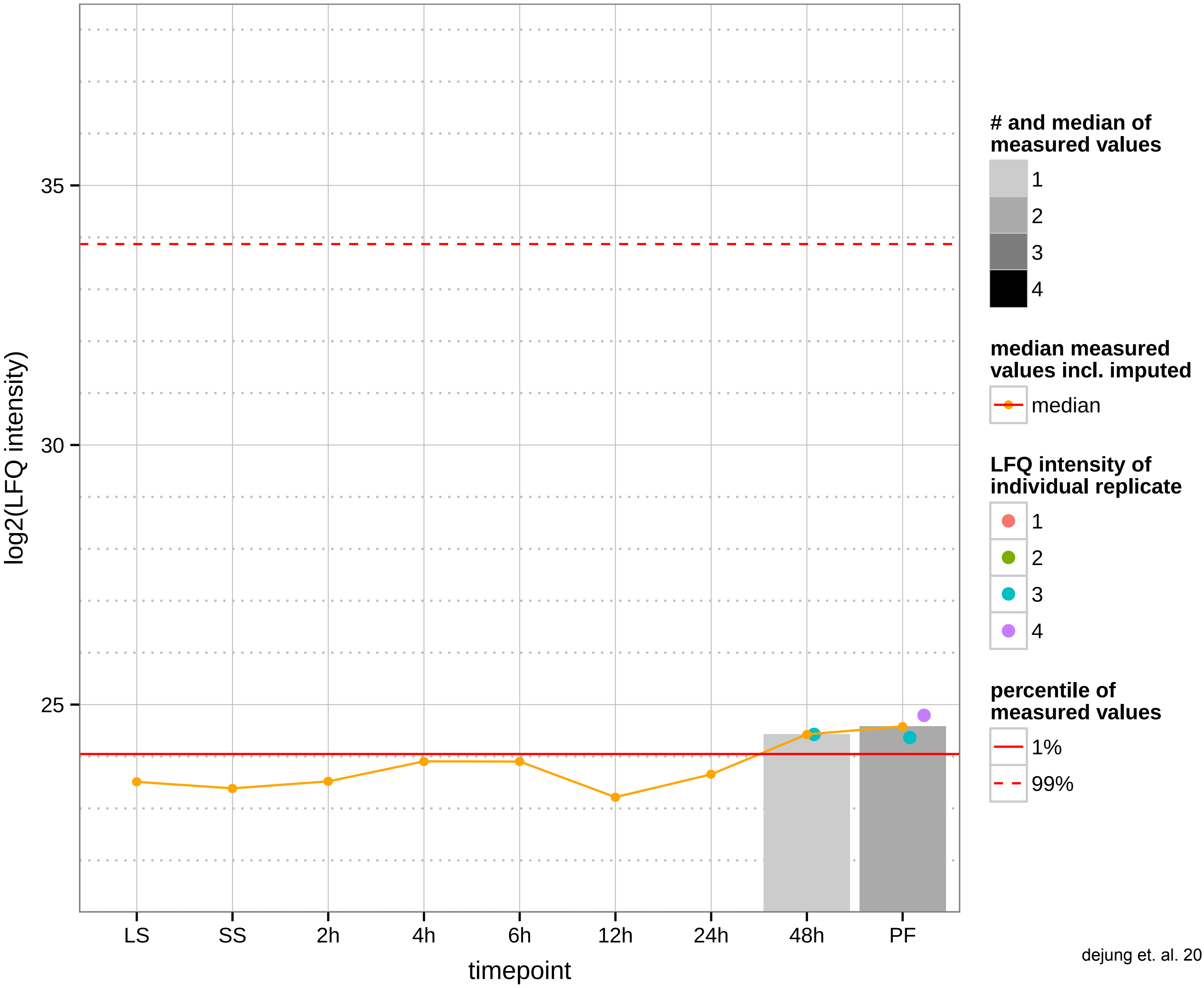
hypothetical protein, conserved
Tb927.11.10590
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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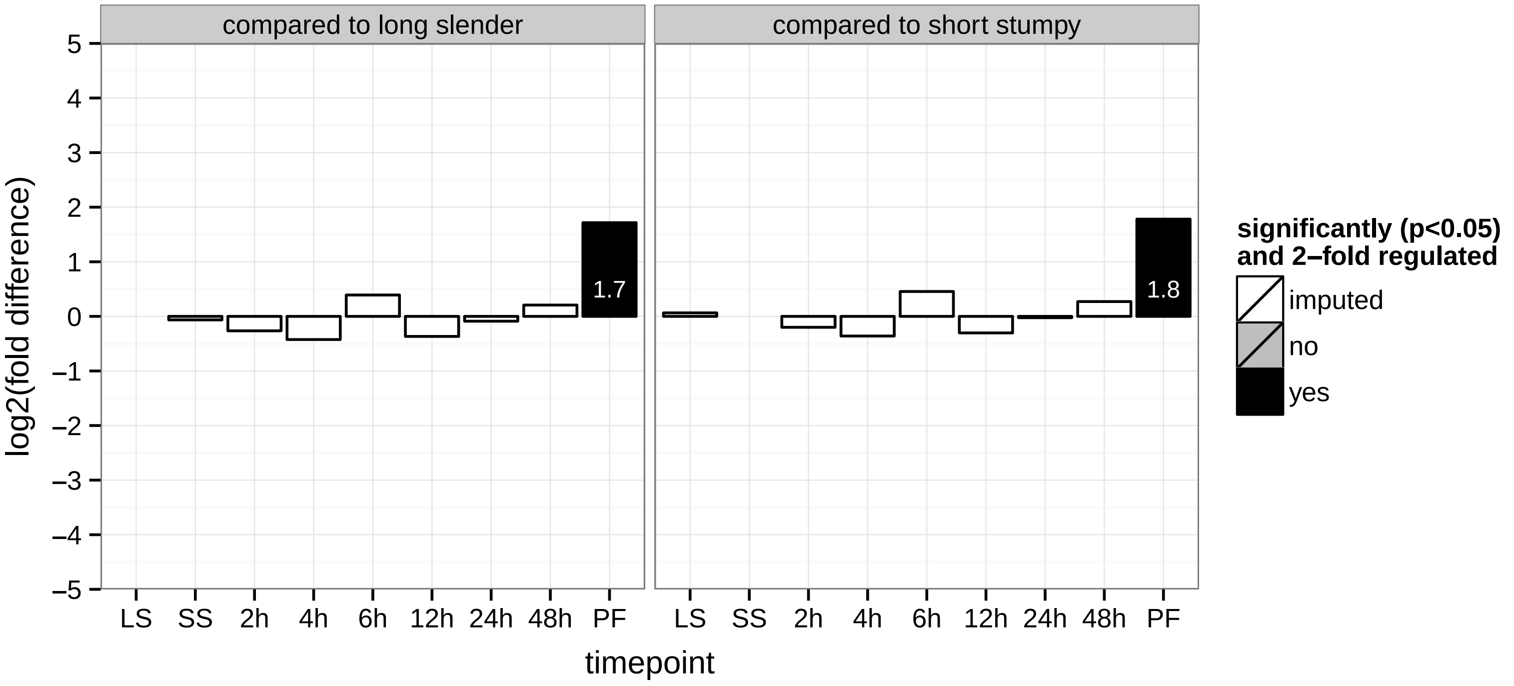
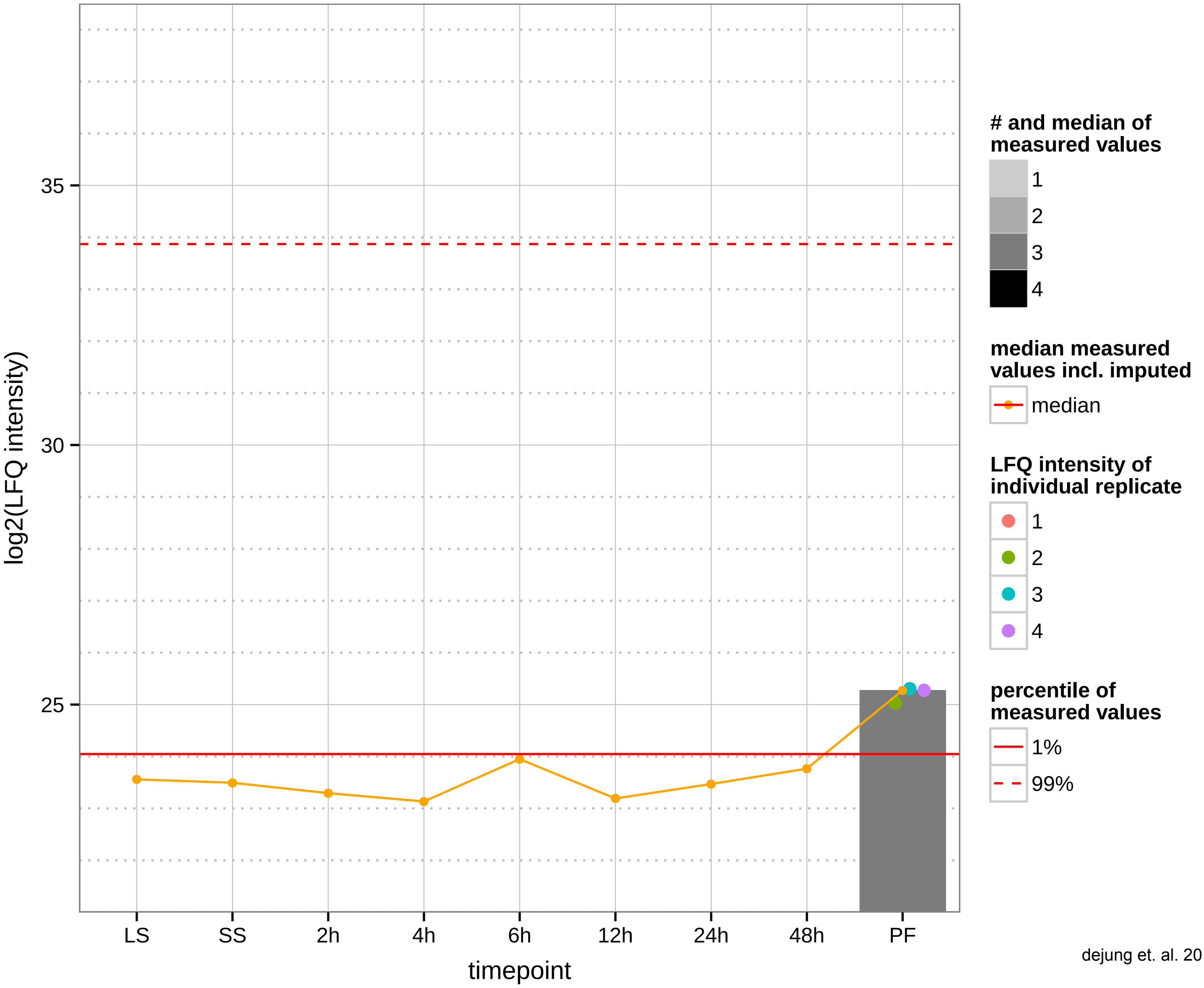
hypothetical protein, conserved
Tb927.11.10660;Tb11.v5.0377;Tb11.v5.0762;Tb11.v5.0378
AGOF: null
AGOC: null
AGOP: null, protein metabolic process
PGOF: null
PGOC: null
PGOP: null





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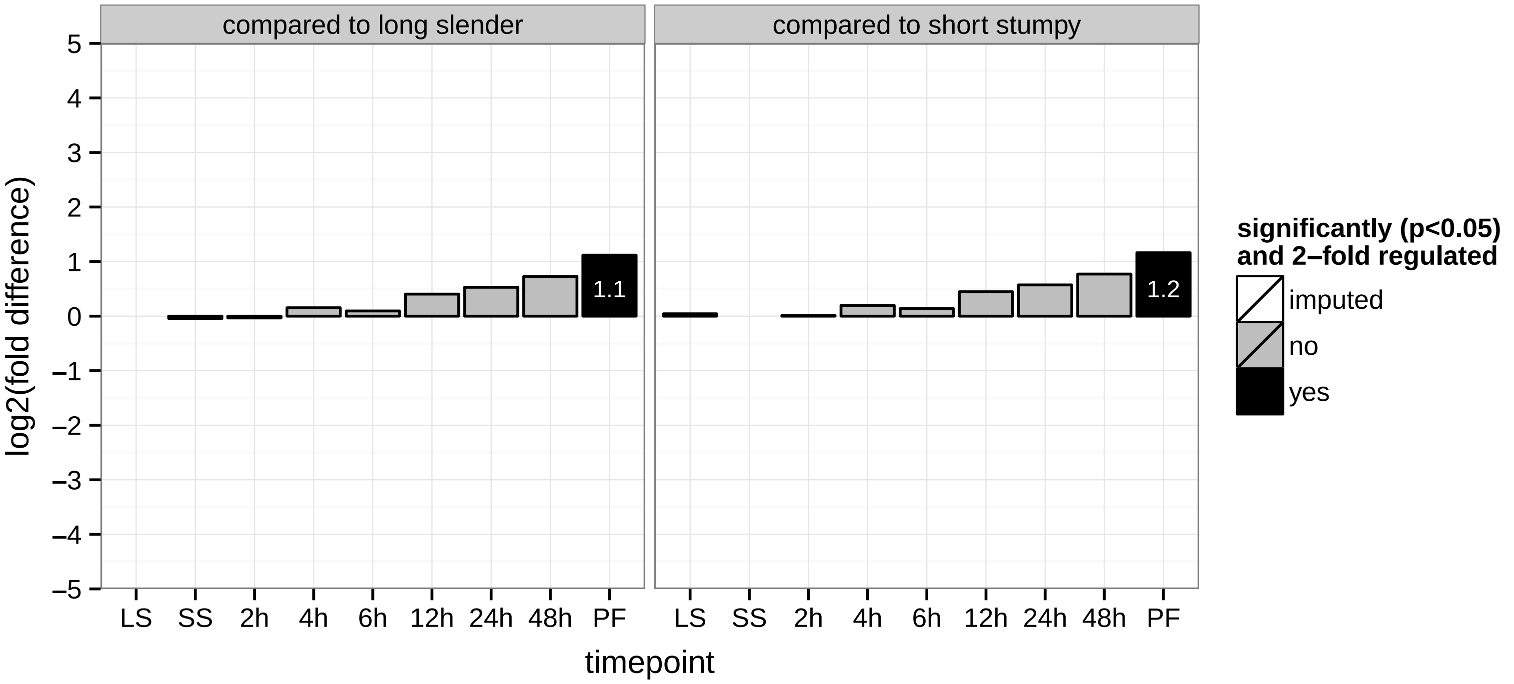
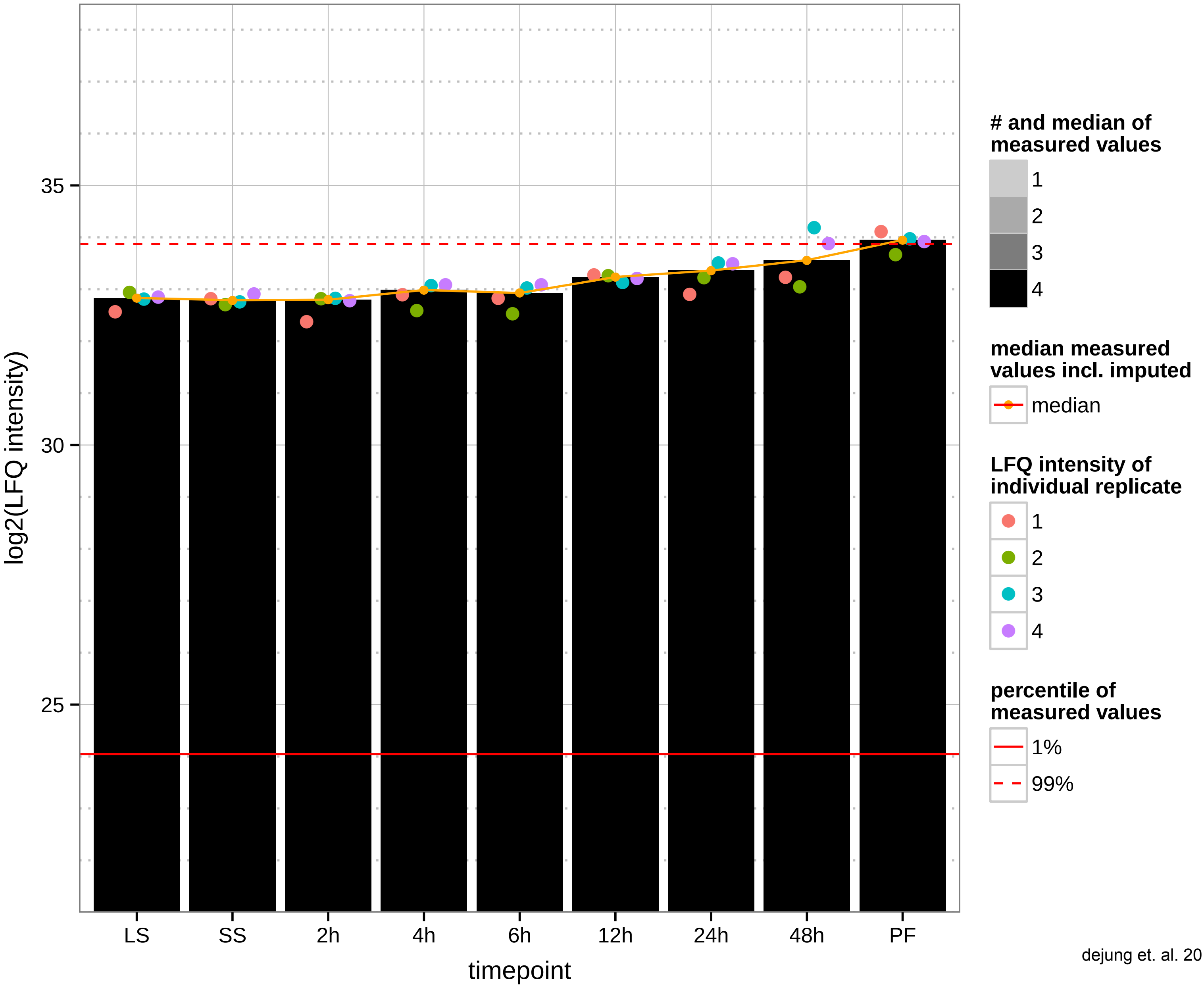
receptor for activated C kinase 1 (RACK1)
Tb927.11.11370;Tb927.11.11360
AGOF: protein kinase C binding
AGOC: ribosome
AGOP: apoptotic process, regulation of cytokinesis
PGOF: null, protein binding
PGOC: null
PGOP: null





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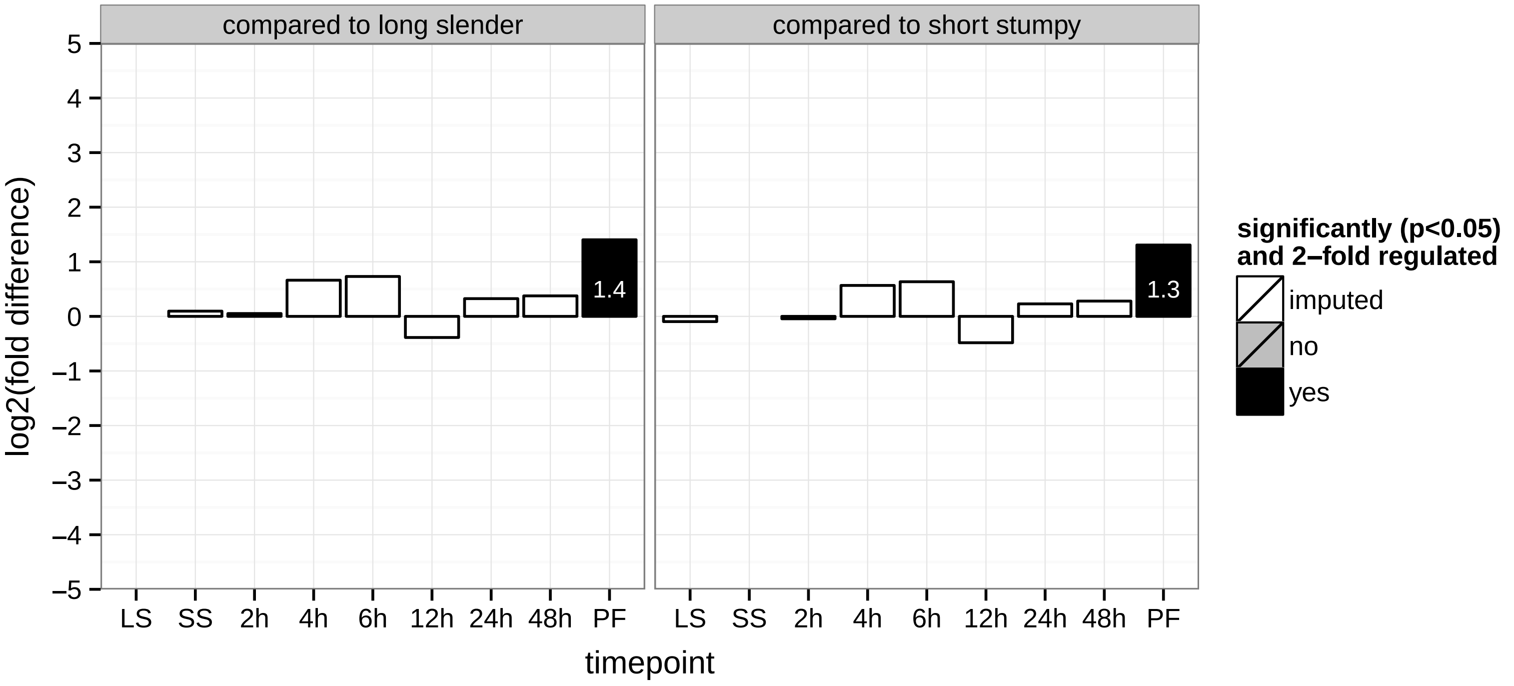
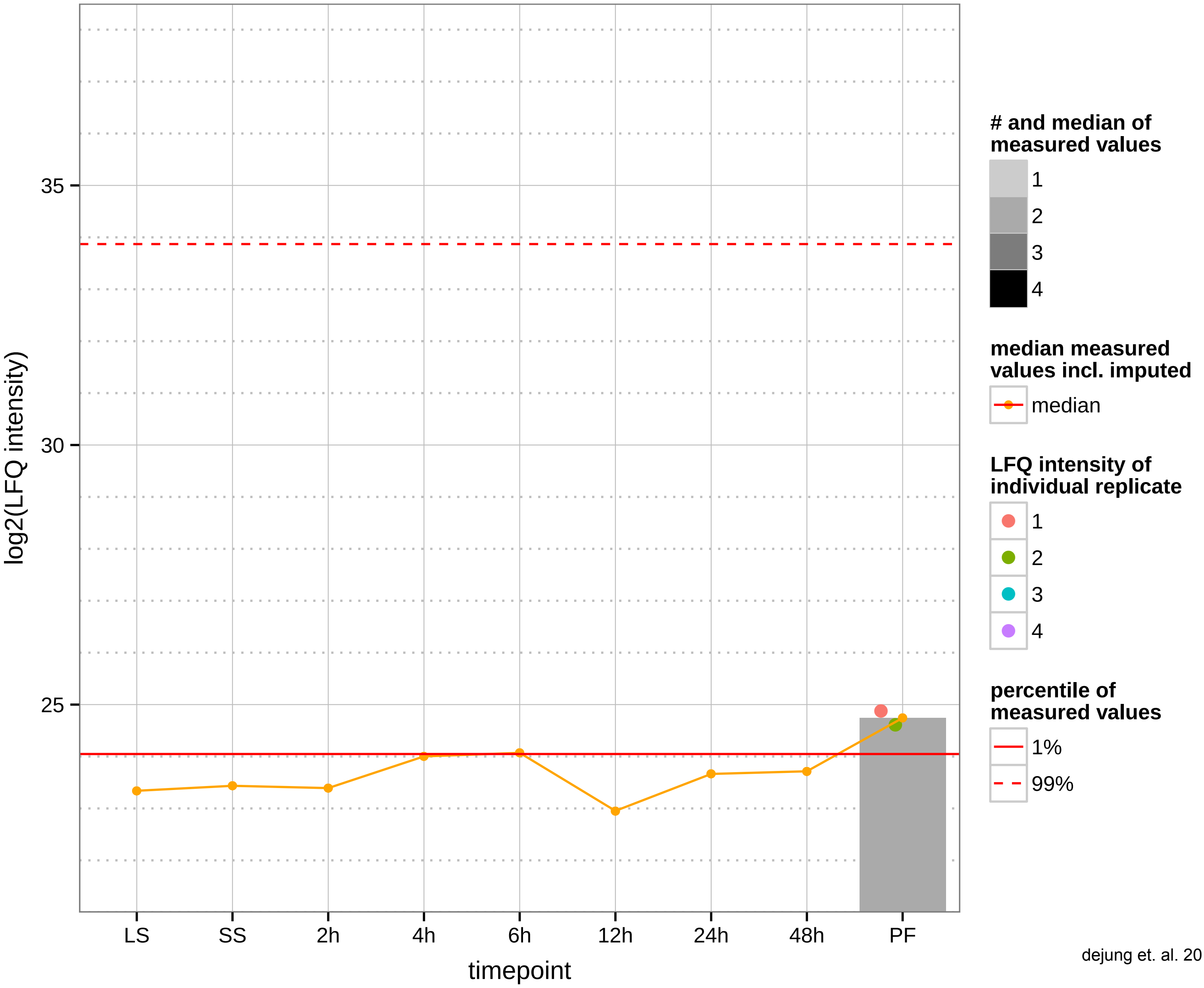
DNA replication licensing factor MCM6, putative
Tb927.11.11640
AGOF: ATP binding, DNA binding
AGOC: nucleus
AGOP: DNA replication, DNA–dependent DNA replication initiation
PGOF: ATP binding, DNA binding
PGOC: null
PGOP: DNA replication





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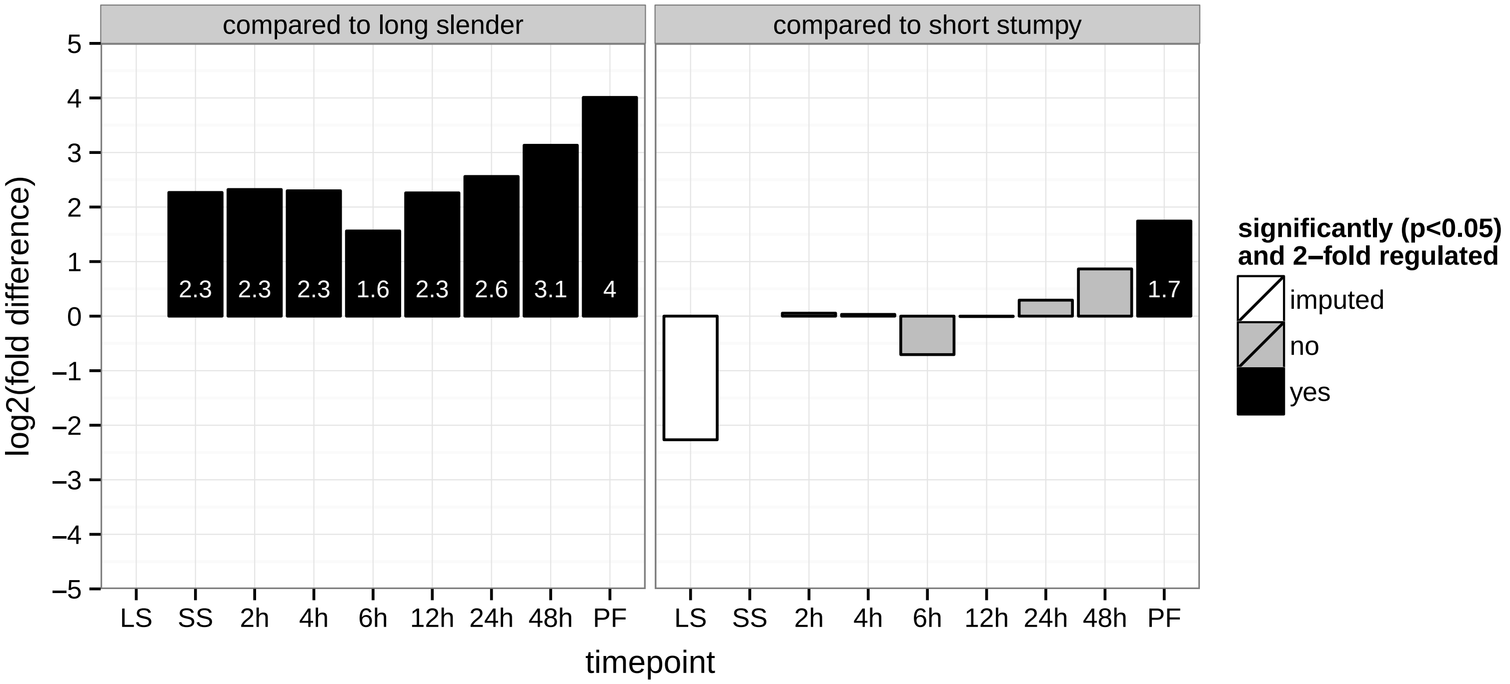
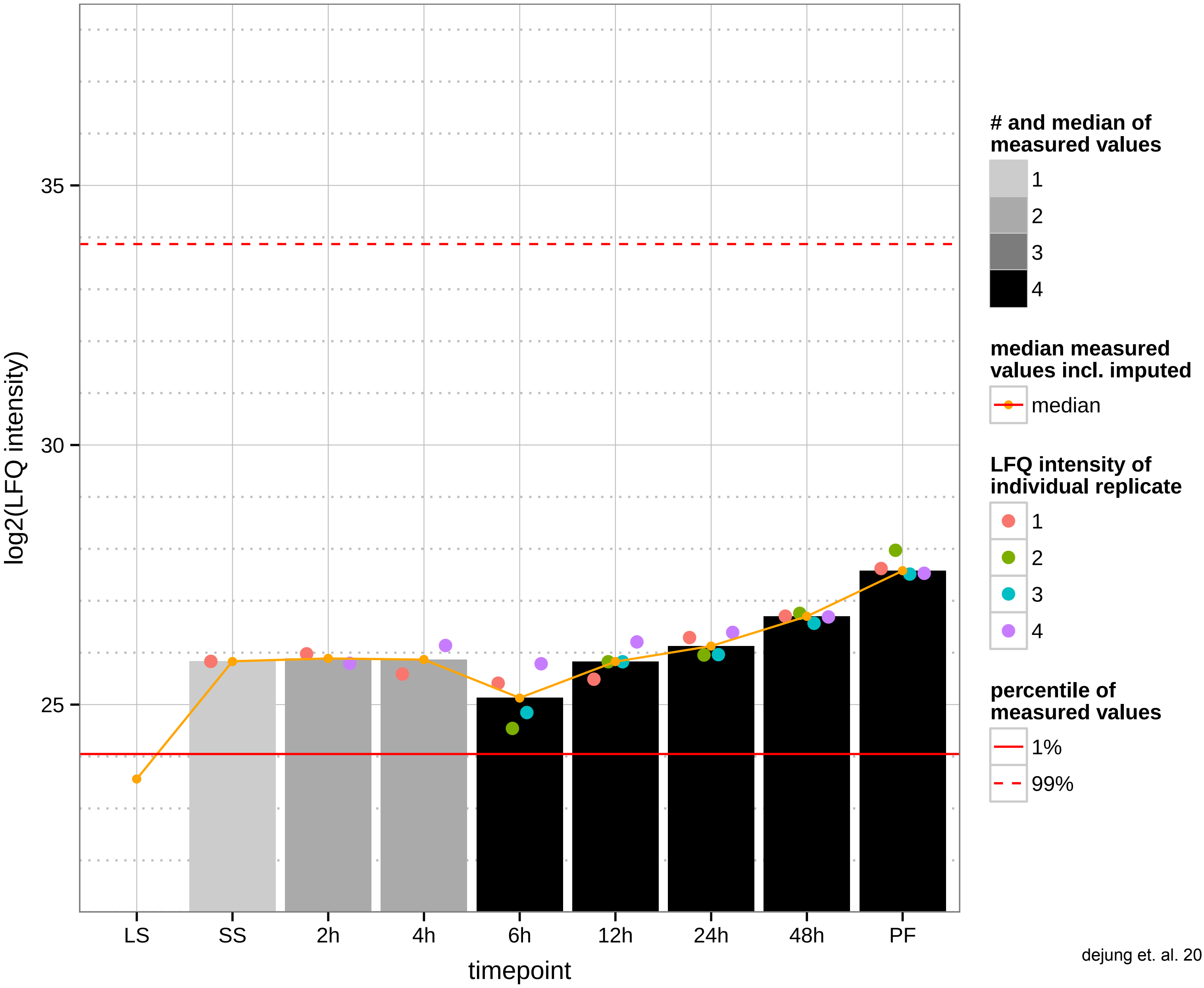
acyl–CoA dehydrogenase, putative
Tb927.11.11780
AGOF: oxidoreductase activity, oxidoreductase activity, acting on the CH–CH group of donors
AGOC: null
AGOP: metabolic process, oxidation–reduction process
PGOF: oxidoreductase activity, acting on the CH–CH group of donors
PGOC: null
PGOP: metabolic process, oxidation–reduction process





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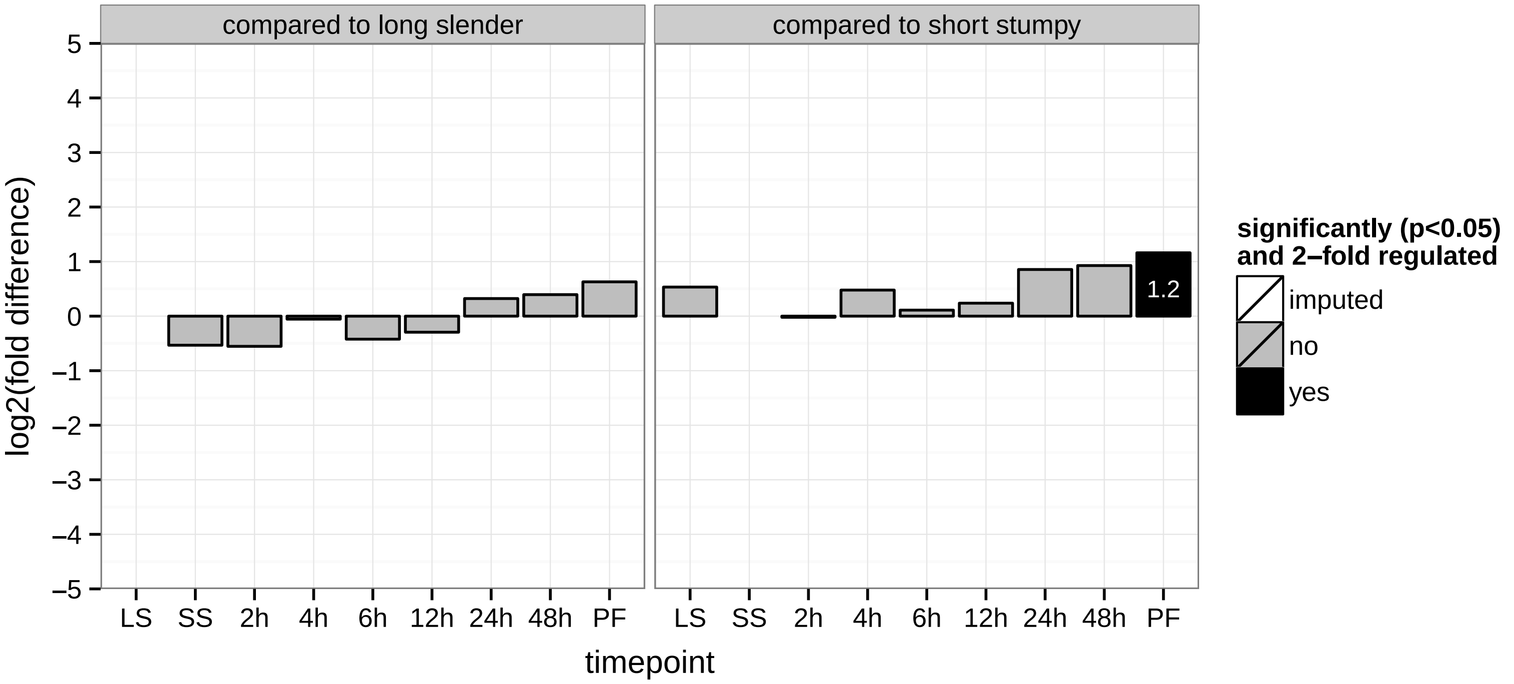
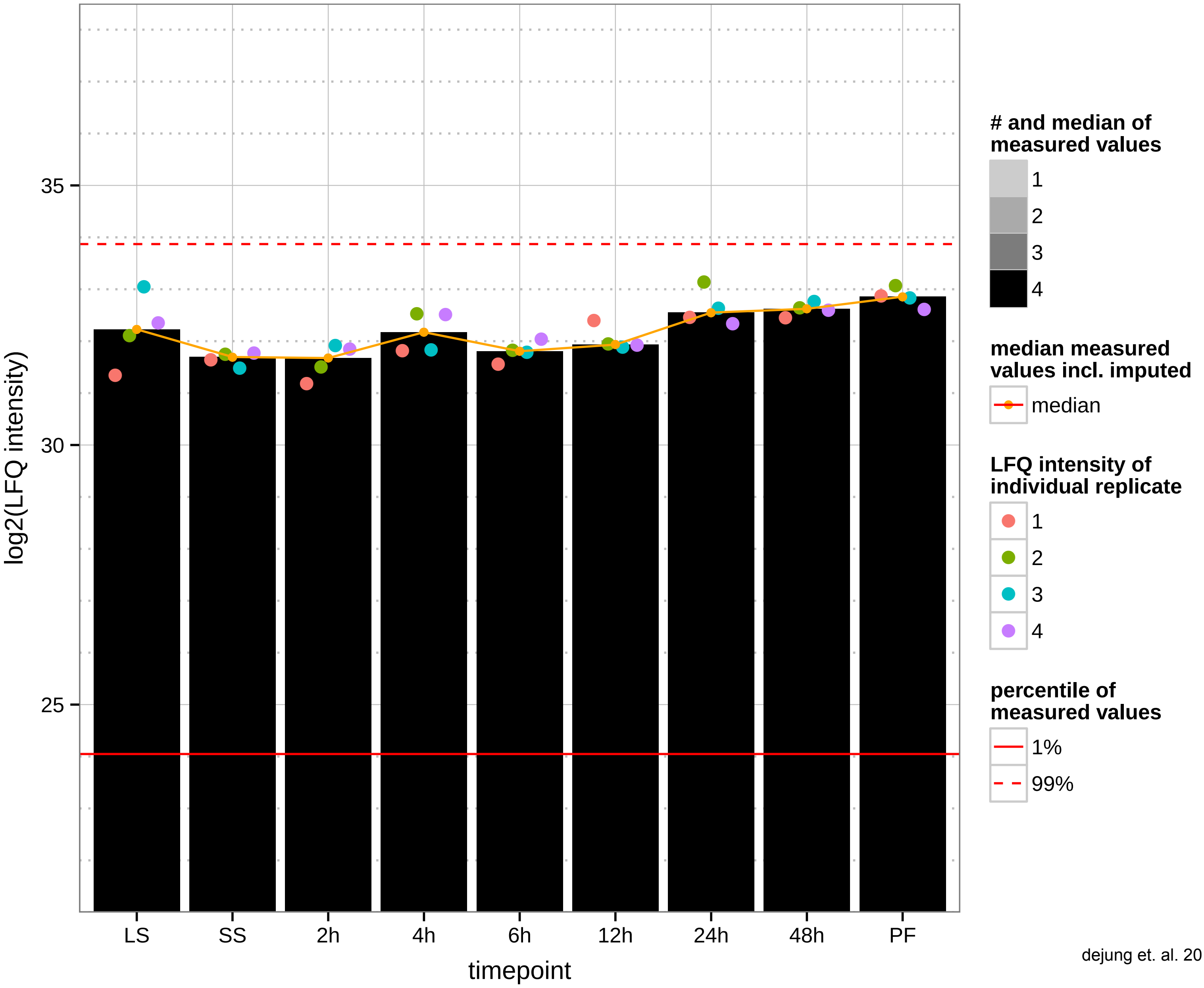
40S ribosomal protein S17, putative
Tb927.11.11830;Tb927.11.11820
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome, null
PGOC: intracellular, ribosome, null
PGOP: translation, null





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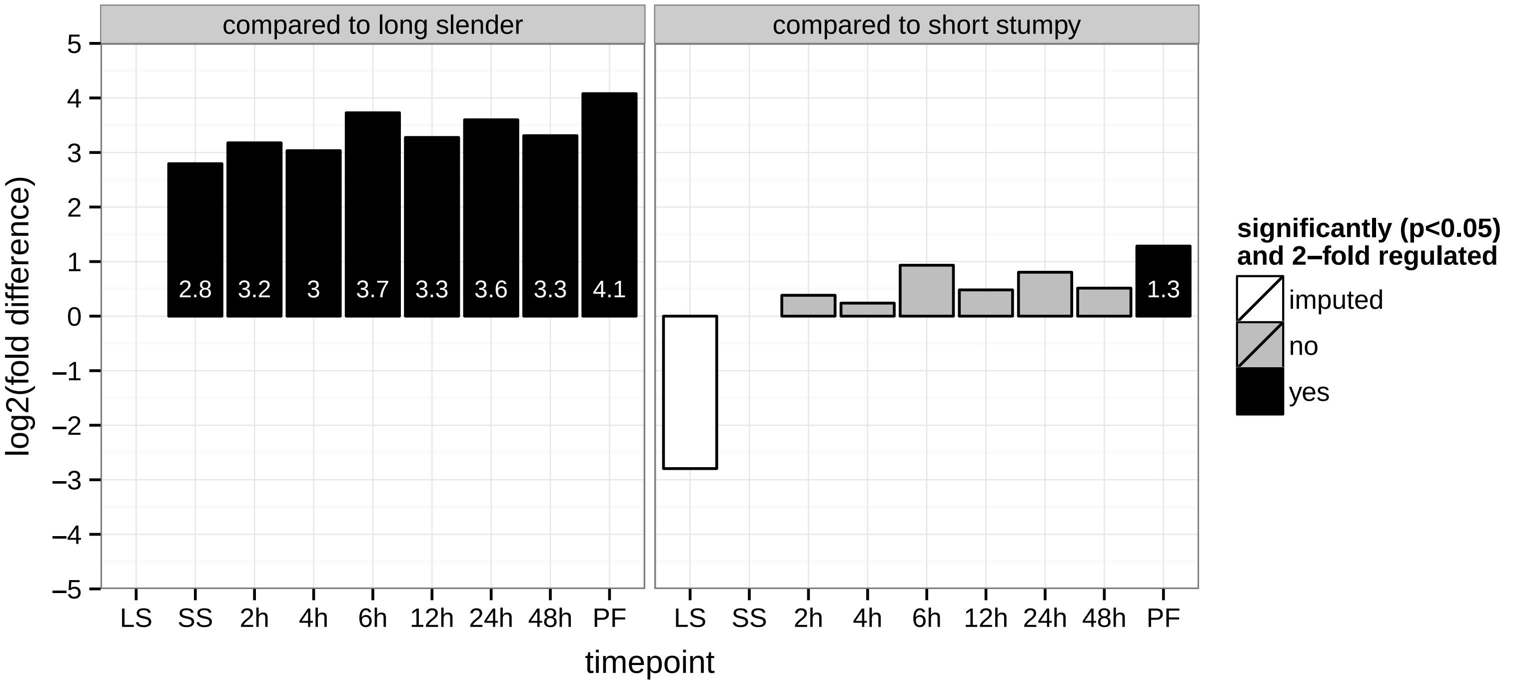
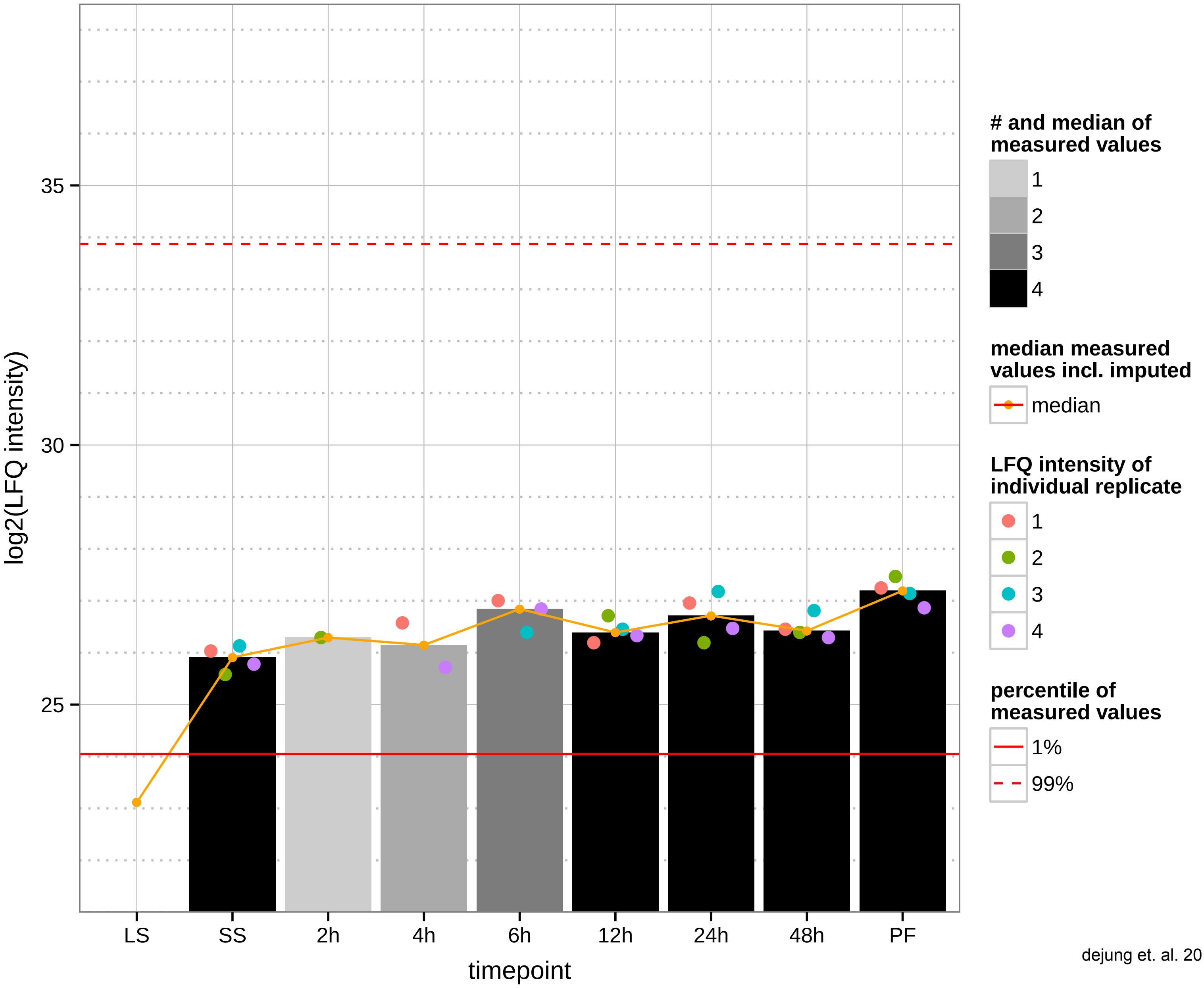
hypothetical protein, conserved
Tb927.11.12030
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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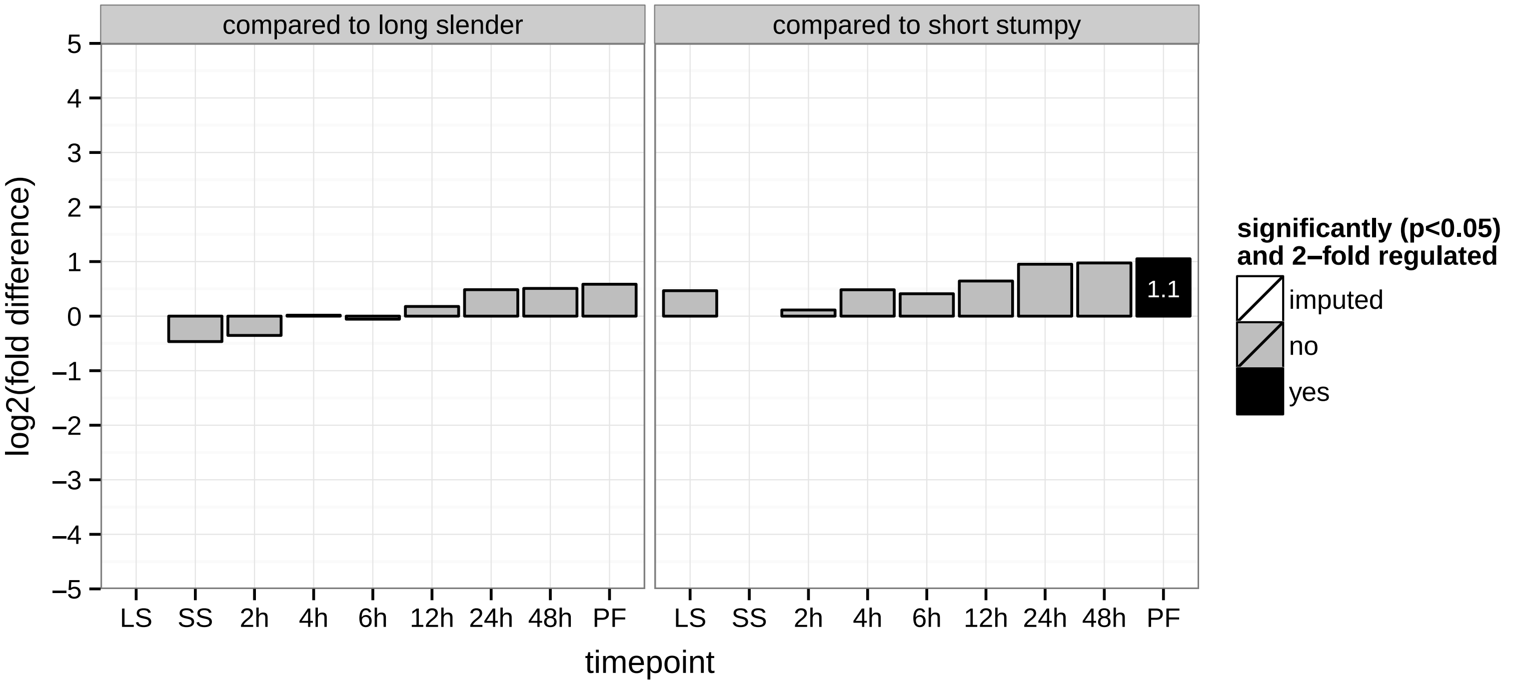
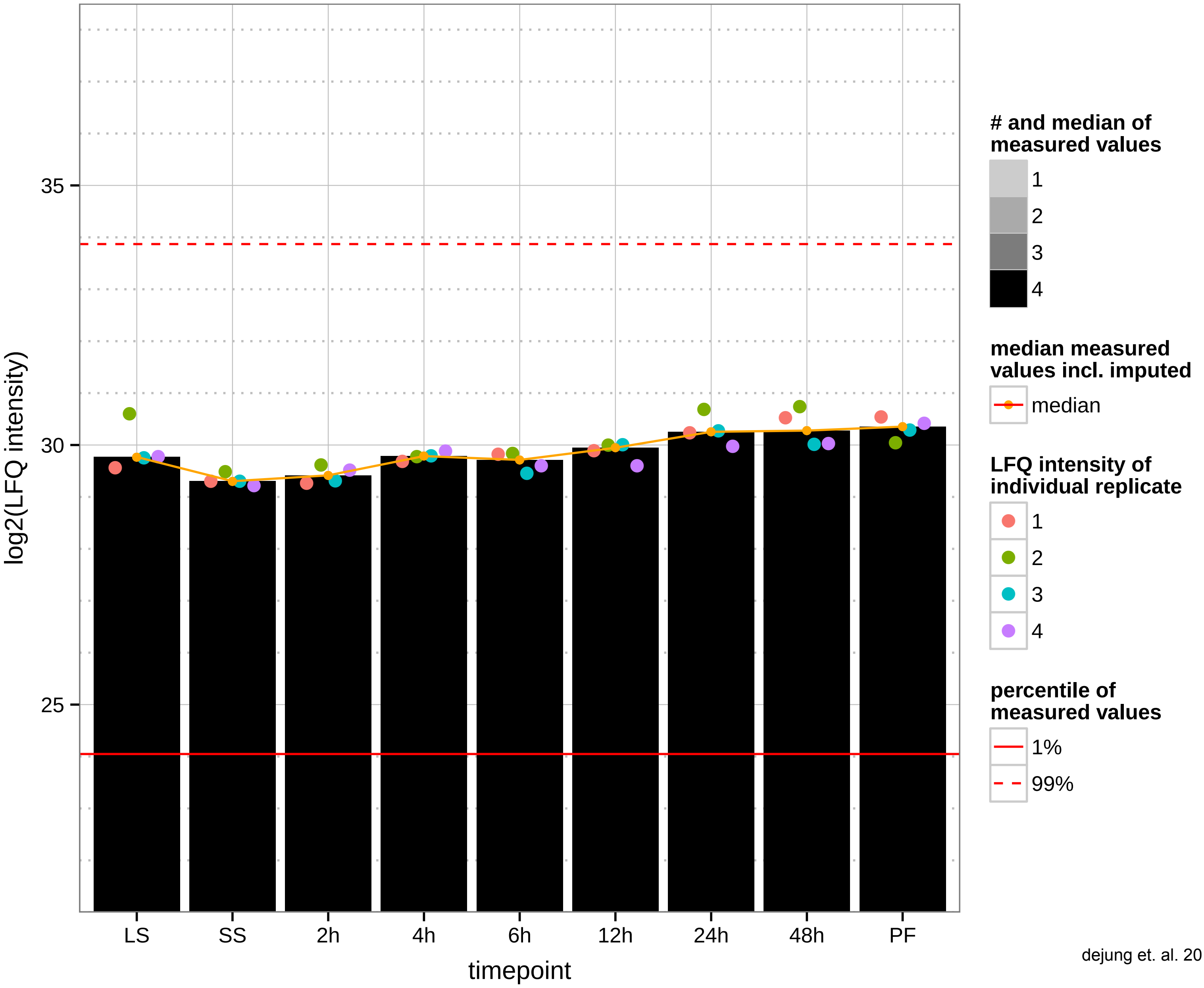
flagellar protein essential for flagellar pocket biogenesis (BILBO1)
Tb927.11.12150
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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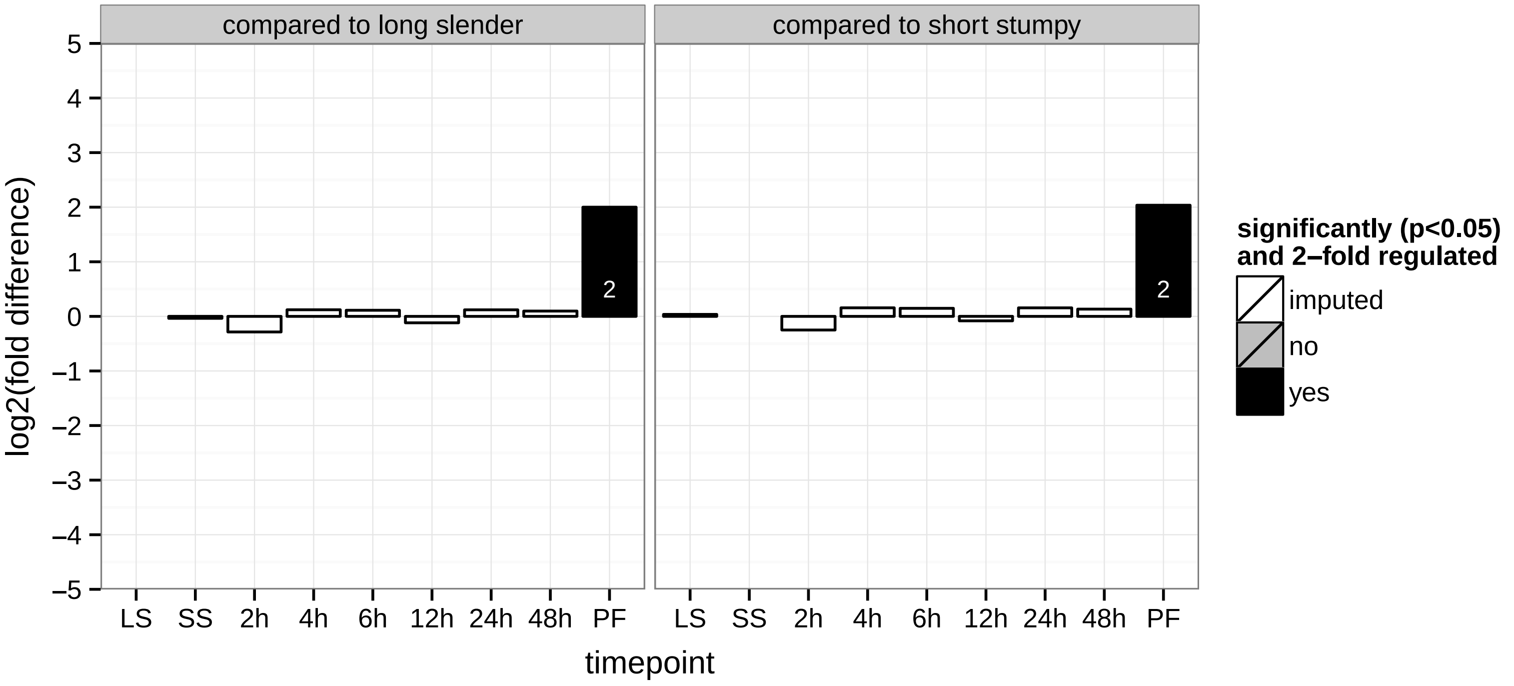
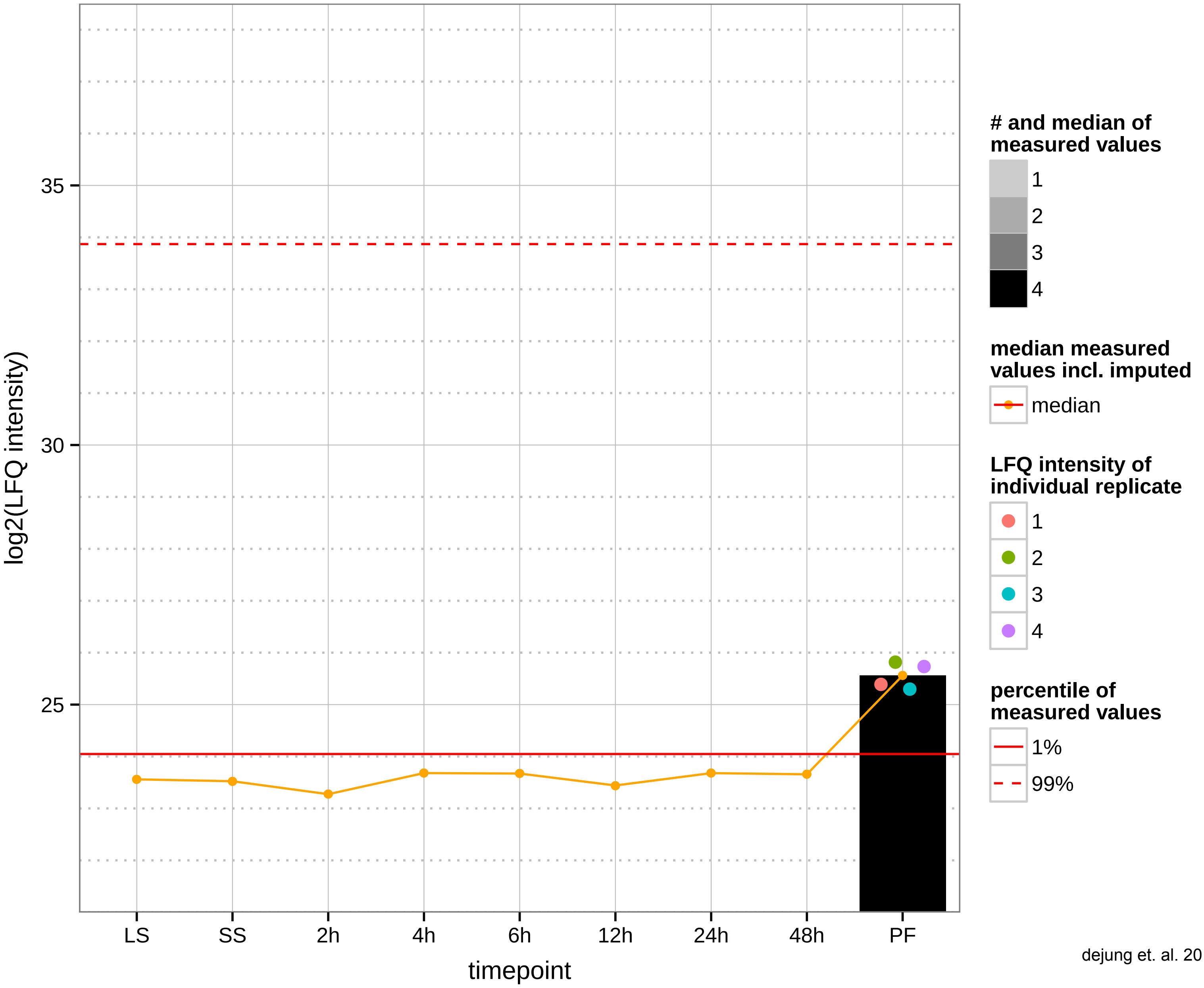
hypothetical protein, conserved
Tb927.11.12160
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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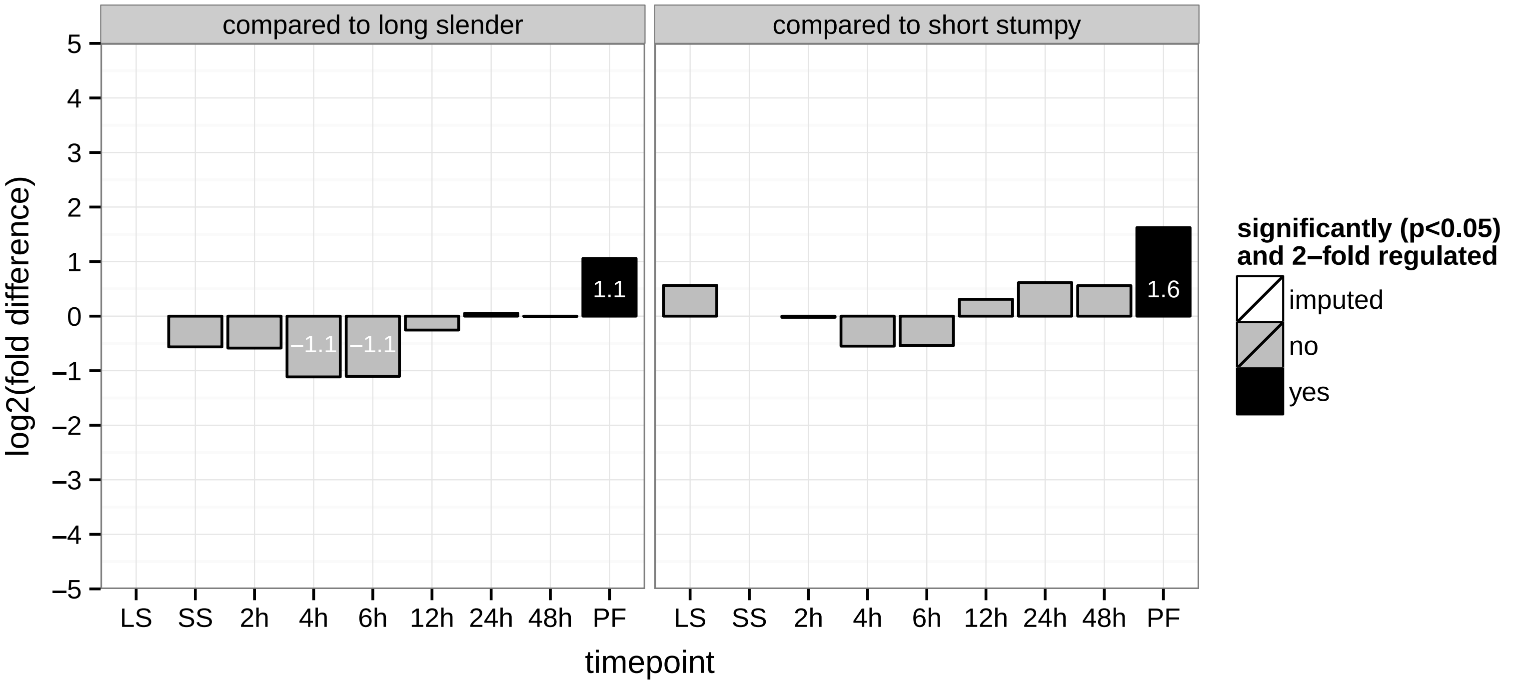
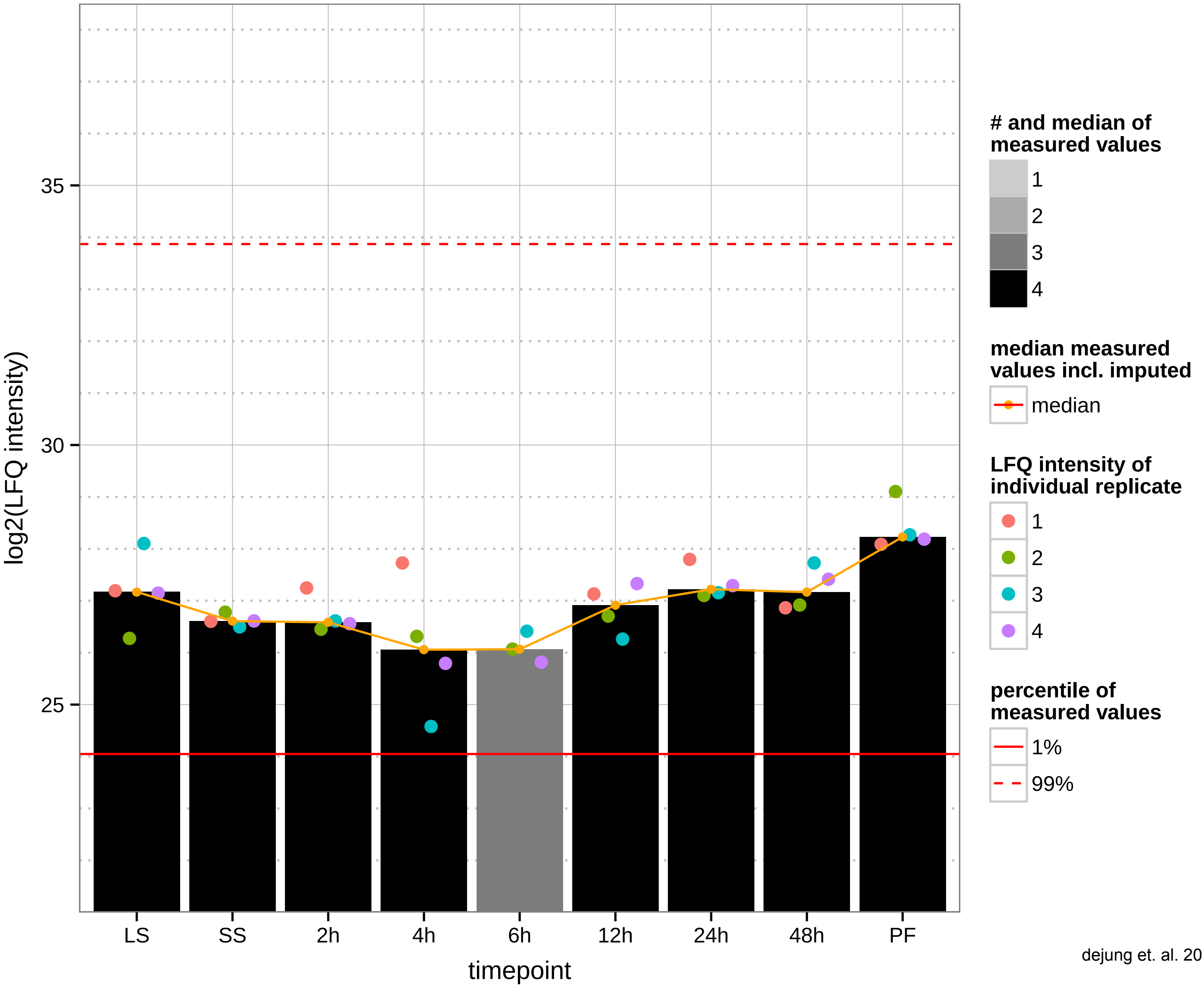
kinetoplastid kinetochore protein 10 (kkt10)
Tb927.11.12410
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: cell proliferation, mitotic cell cycle, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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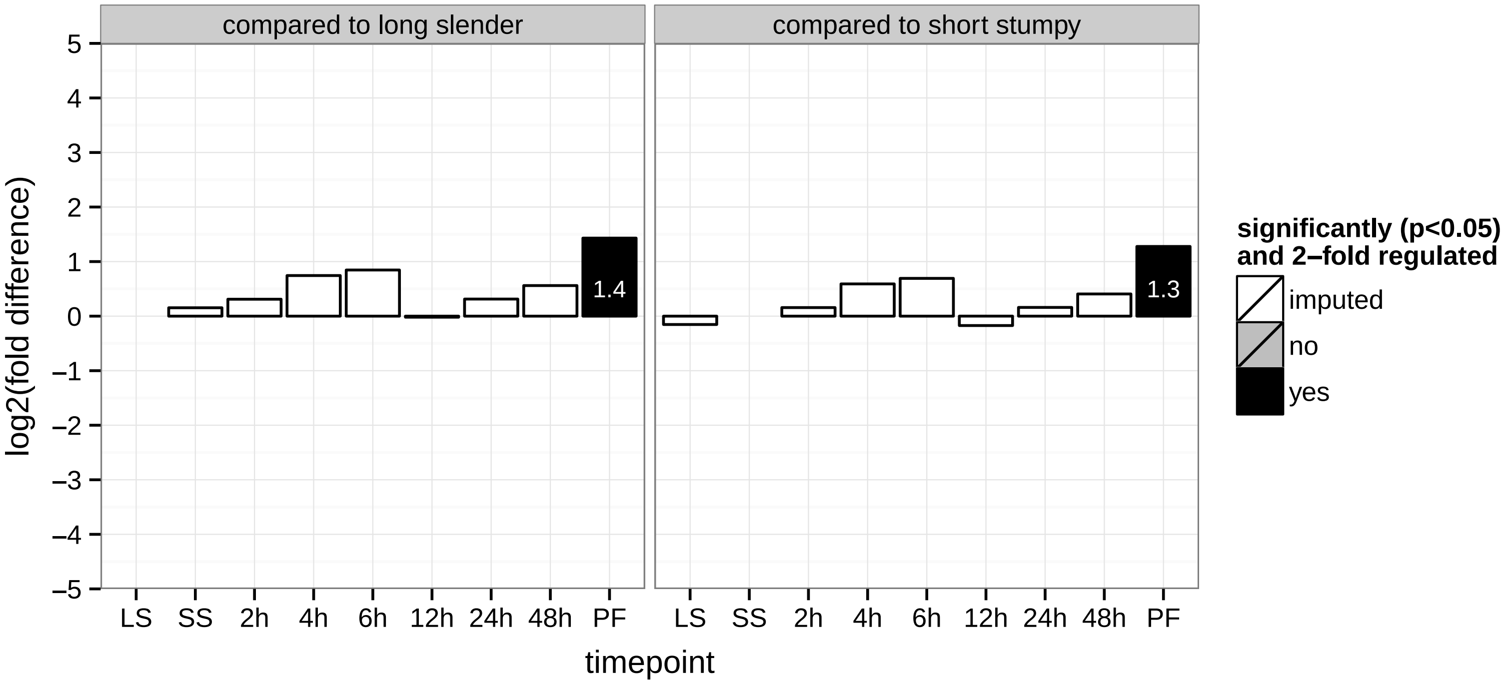
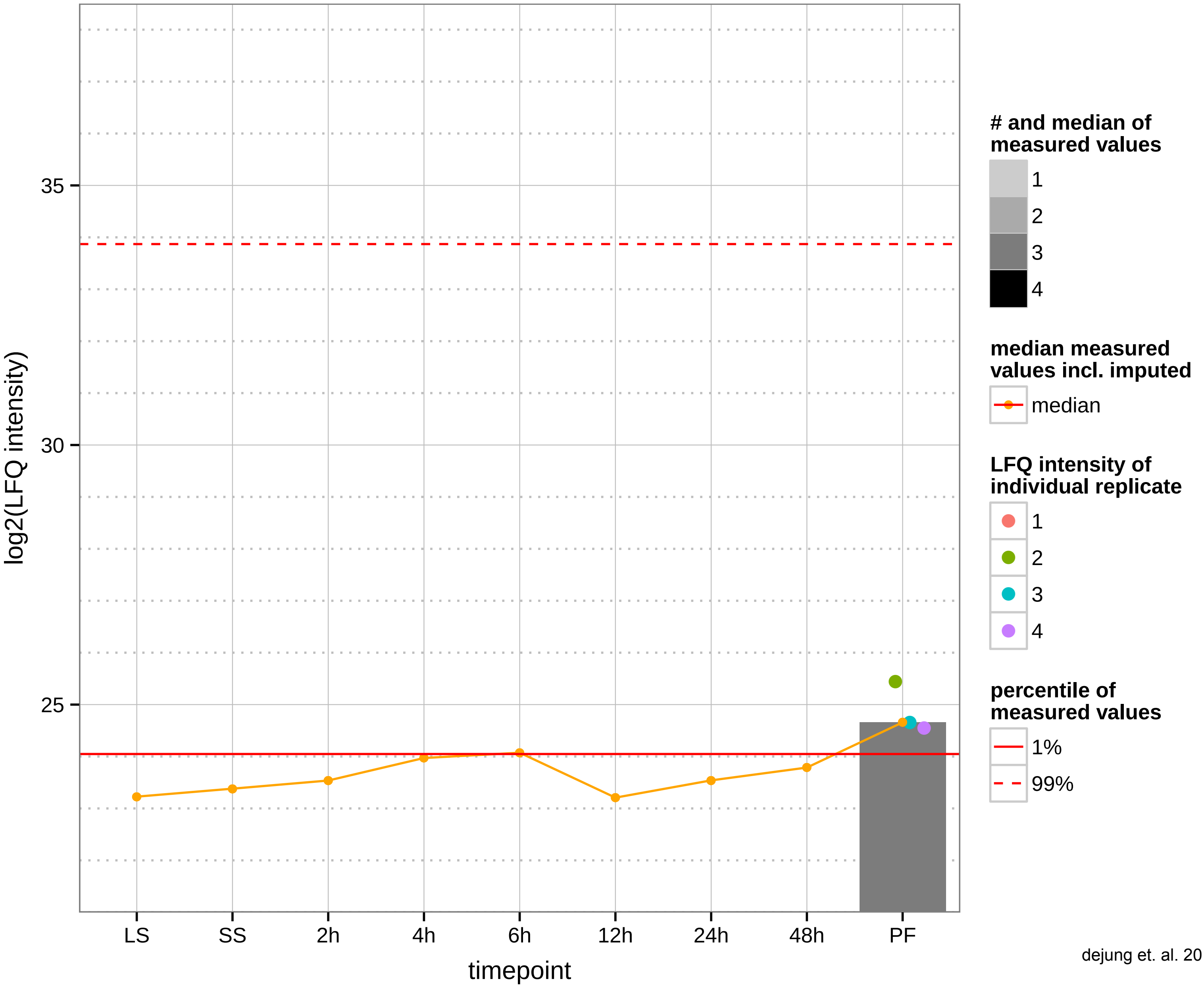
hypothetical protein
Tb927.11.12560
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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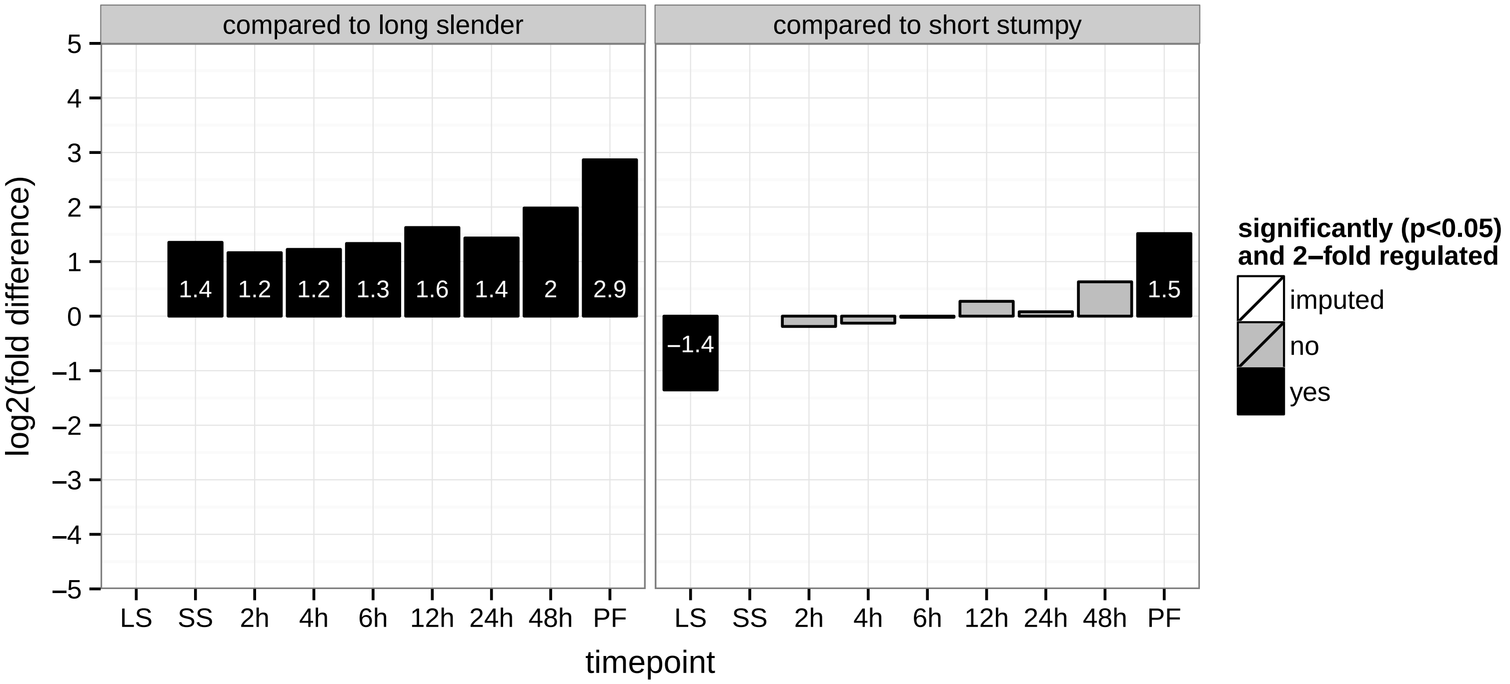
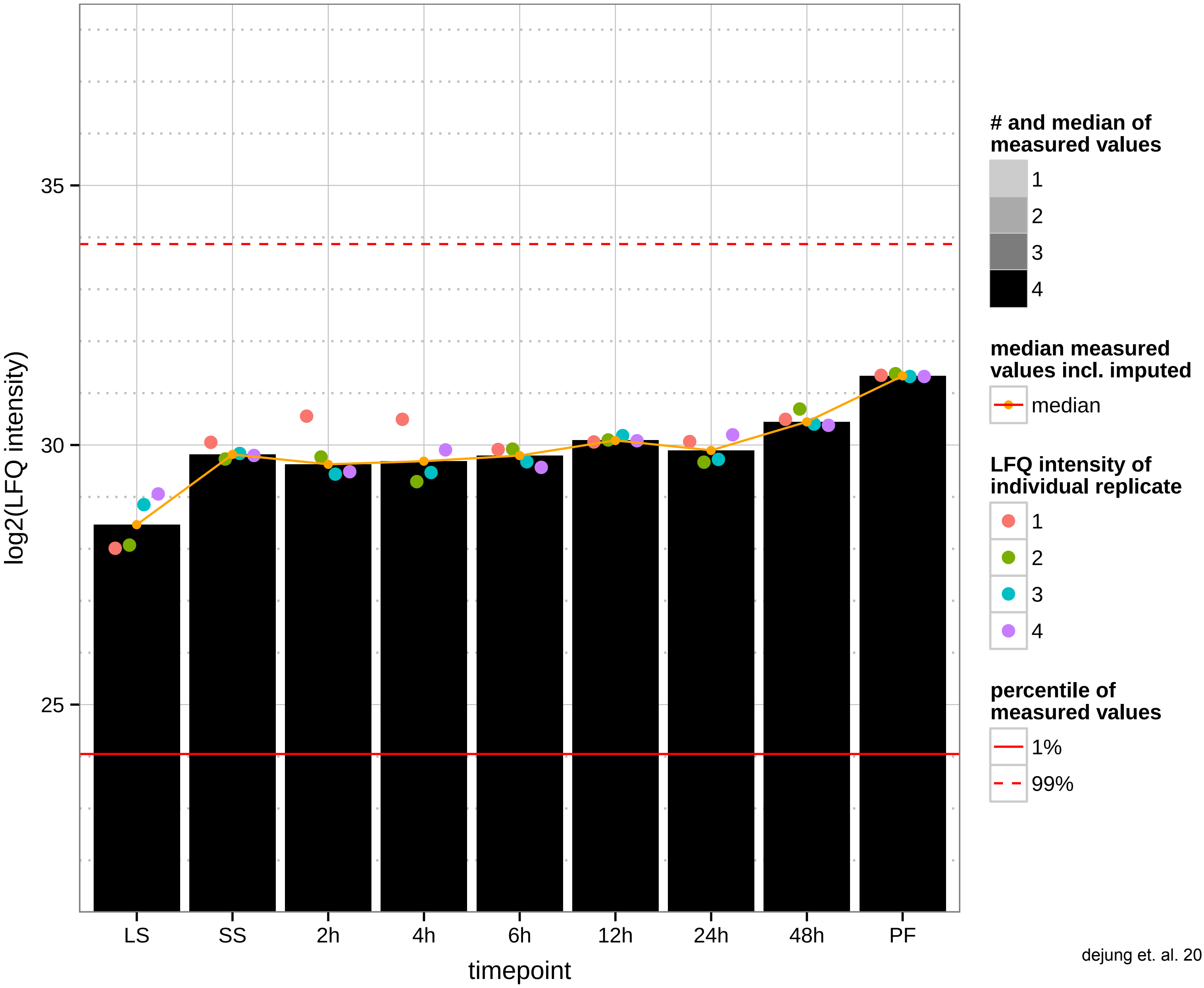
oligopeptidase b, serine peptidase, clan SC, family S9A–like protein (OPB)
Tb927.11.12850
AGOF: serine–type endopeptidase activity, serine–type peptidase activity
AGOC: null
AGOP: proteolysis
PGOF: serine–type endopeptidase activity, serine–type peptidase activity
PGOC: null
PGOP: proteolysis





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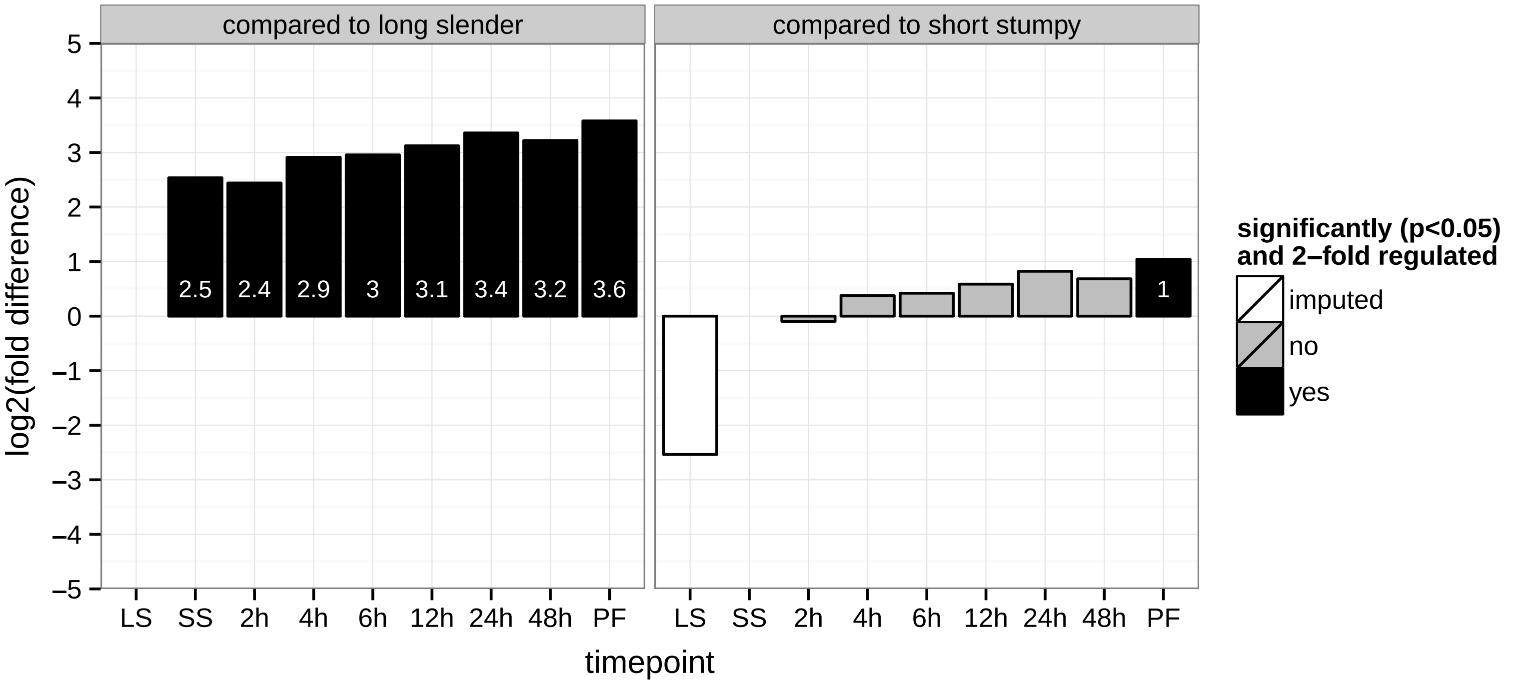
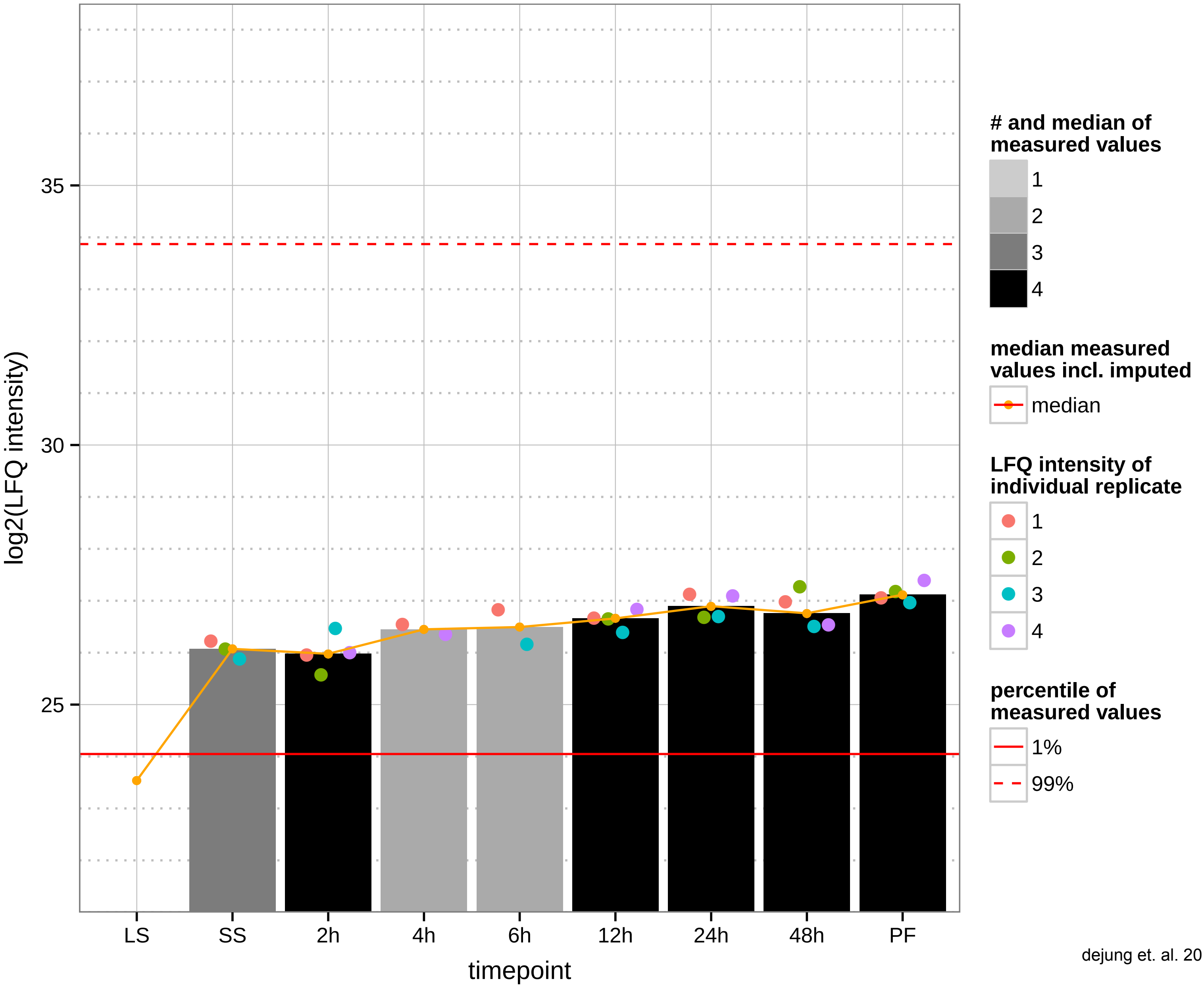
translation–associated element 2, putative
Tb927.11.13060
AGOF: null
AGOC: cytoplasm
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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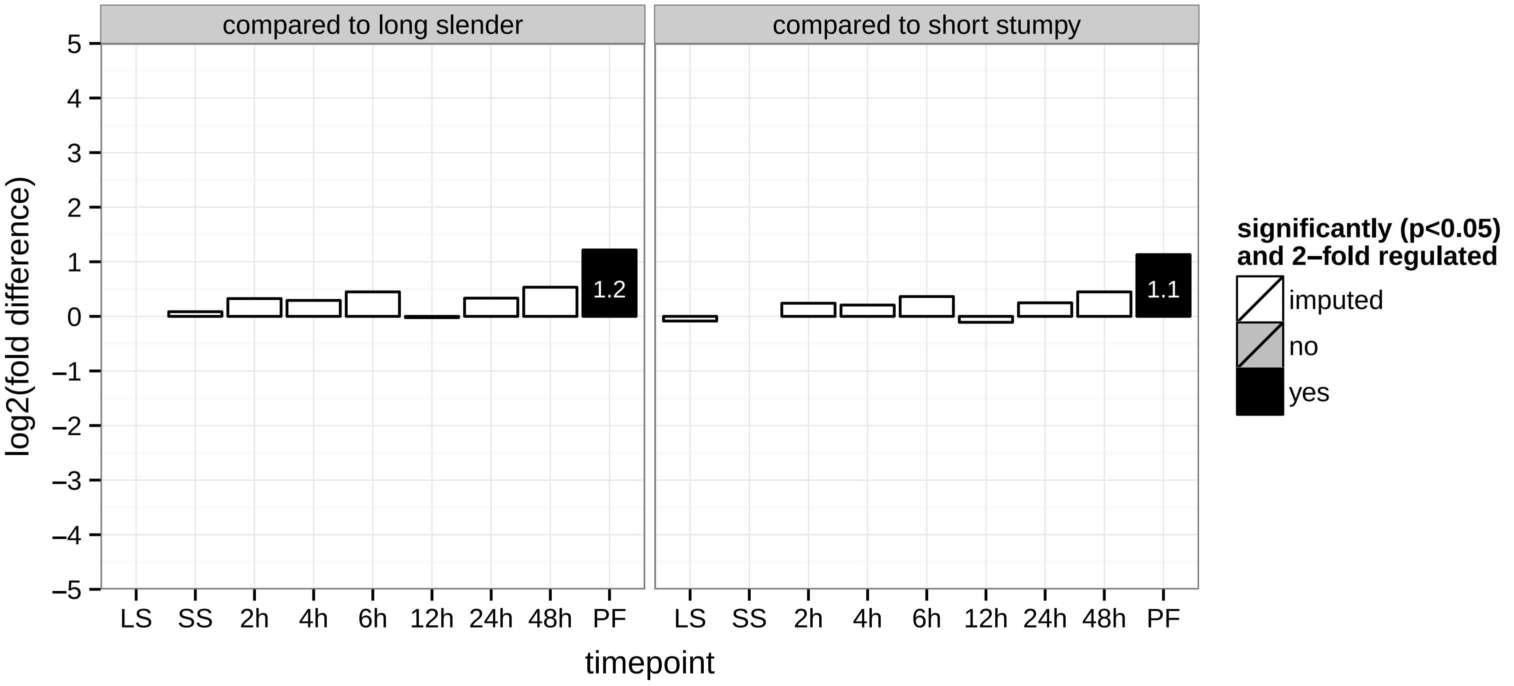
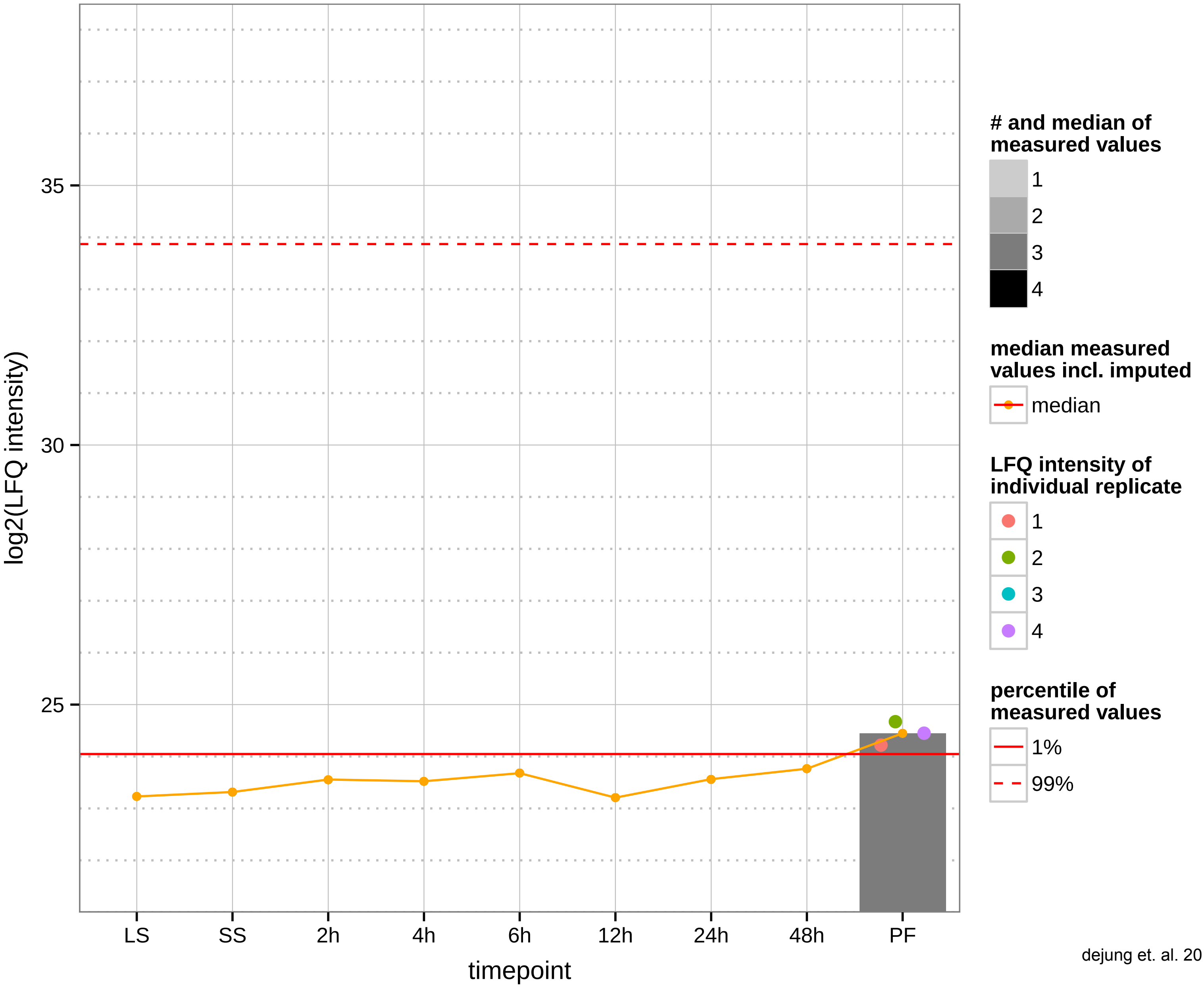
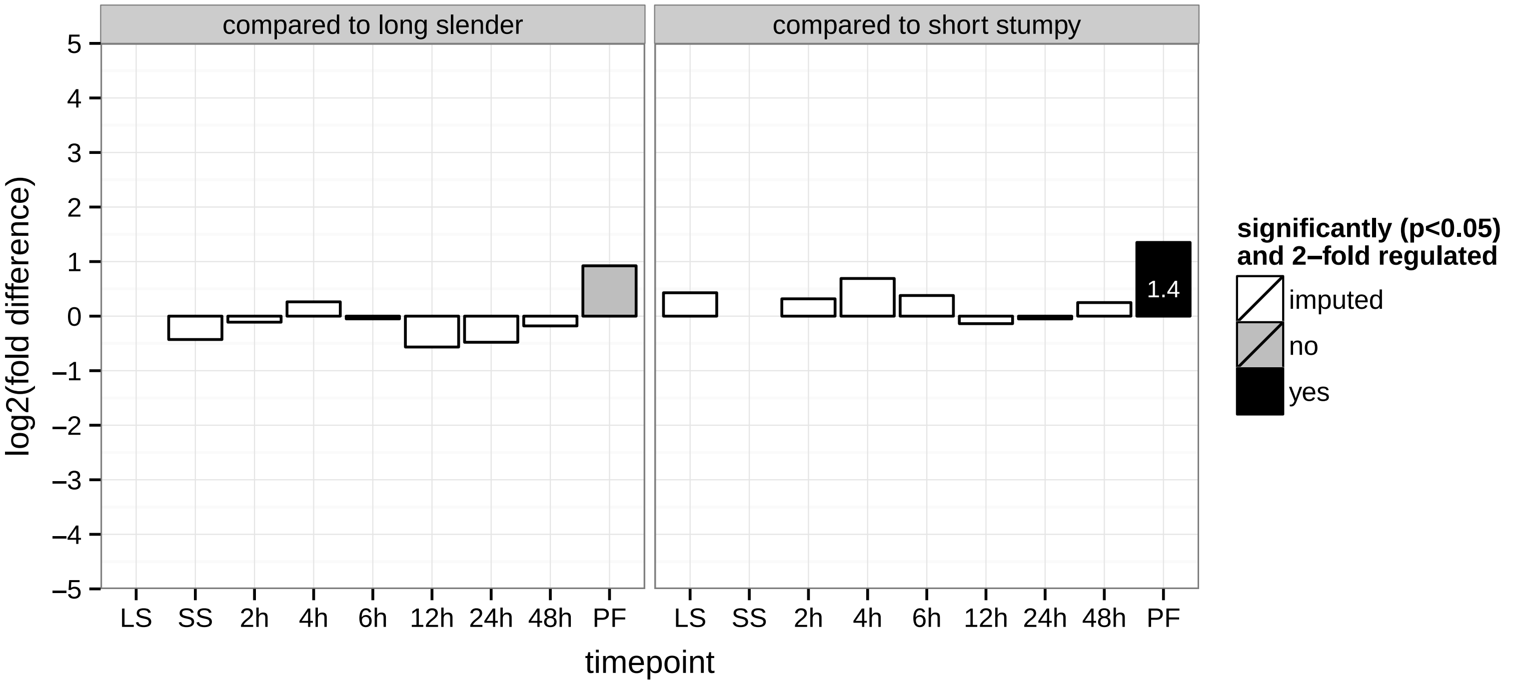
NADH–cytochrome b5 reductase, putative (B5R)
Tb927.11.1310
AGOF: cytochrome–b5 reductase activity, electron carrier activity
AGOC: mitochondrion
AGOP: oxidation–reduction process
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process

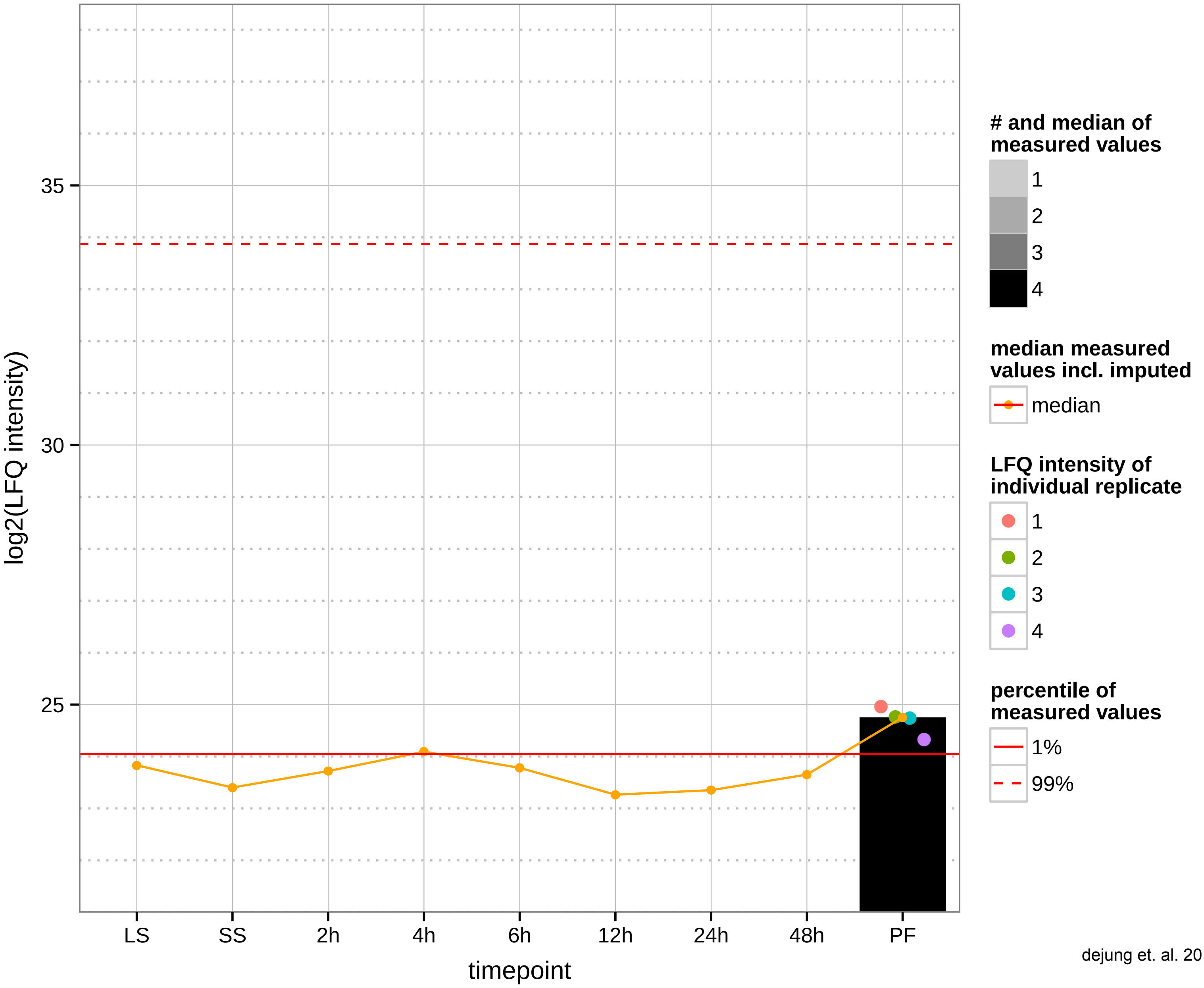




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.13200
AGOF: null
AGOC: membrane
AGOP: null
PGOF: null
PGOC: membrane
PGOP: null





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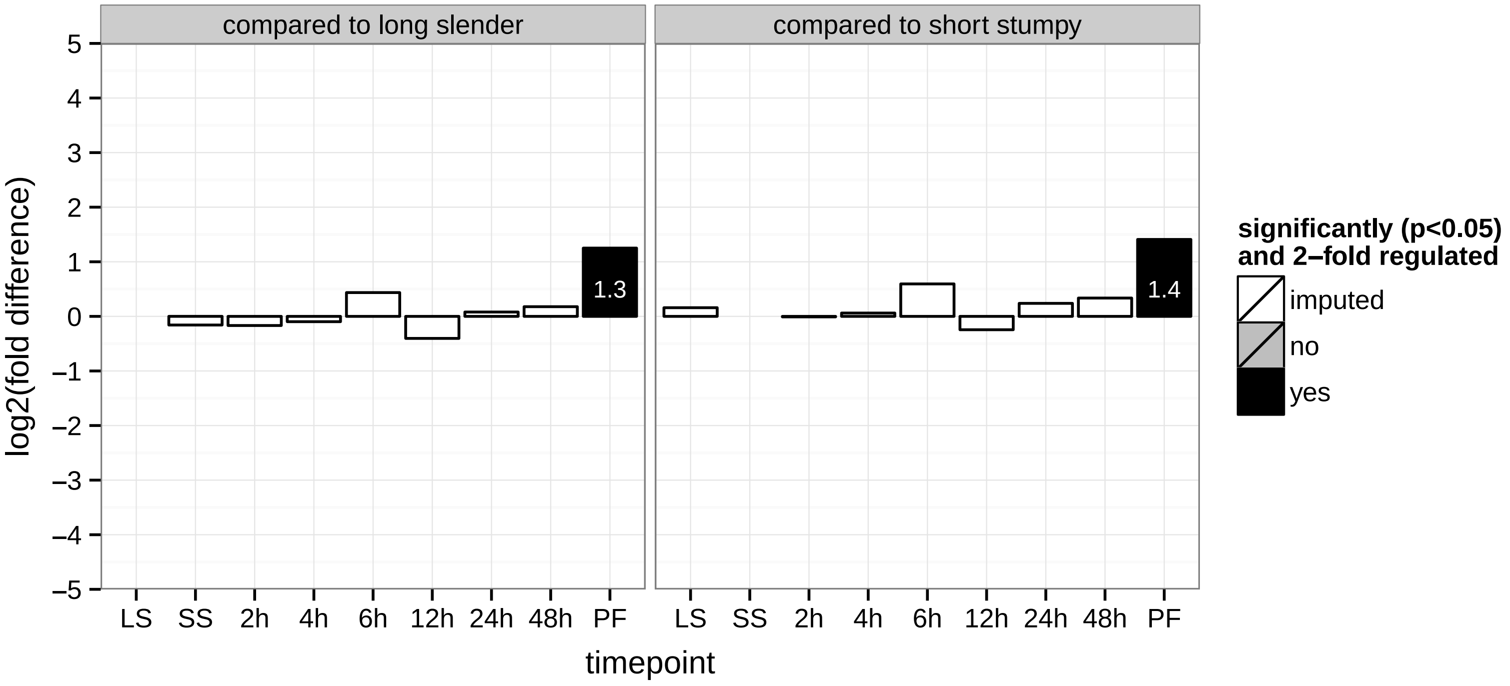
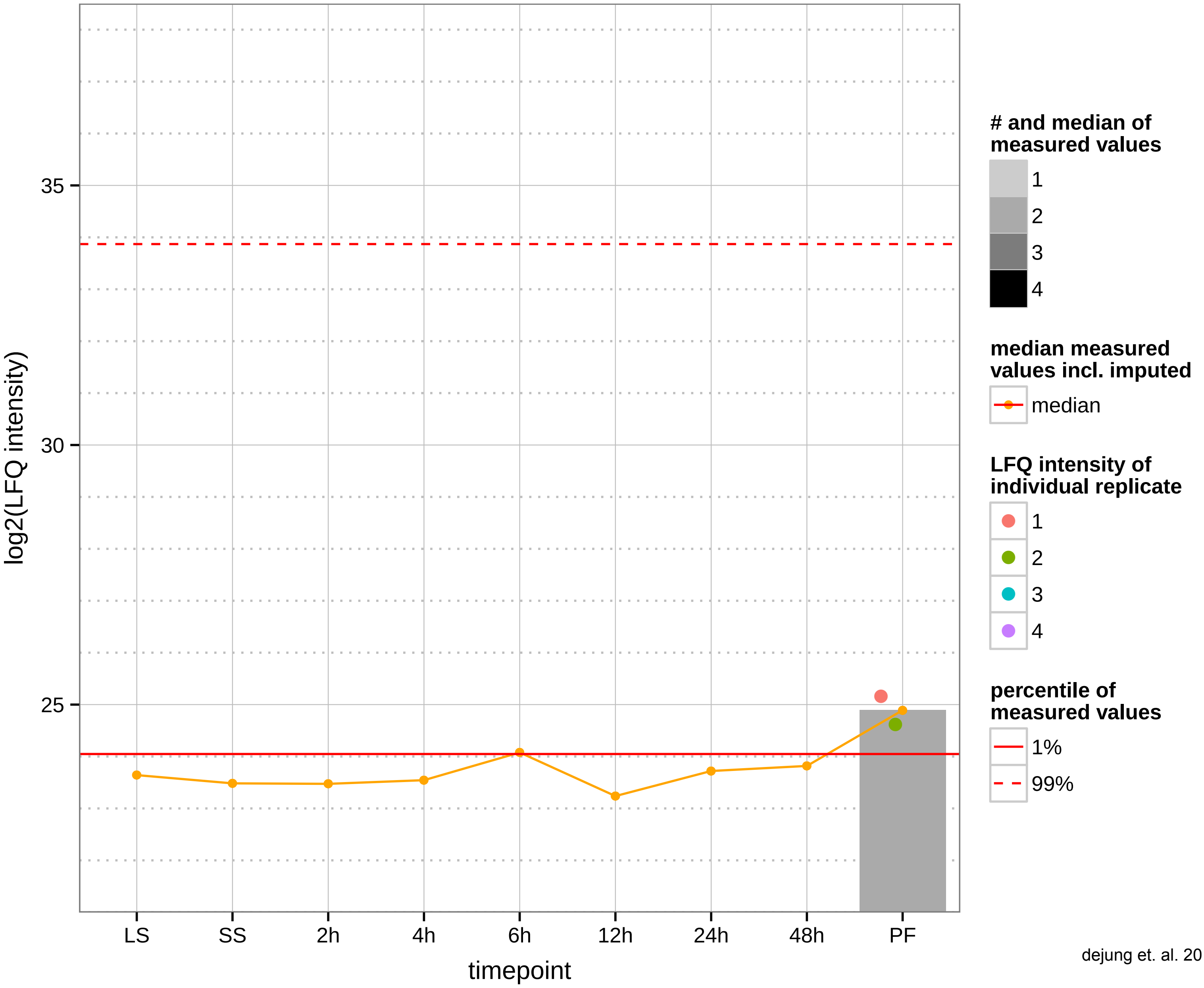
hypothetical protein, conserved
Tb927.11.13310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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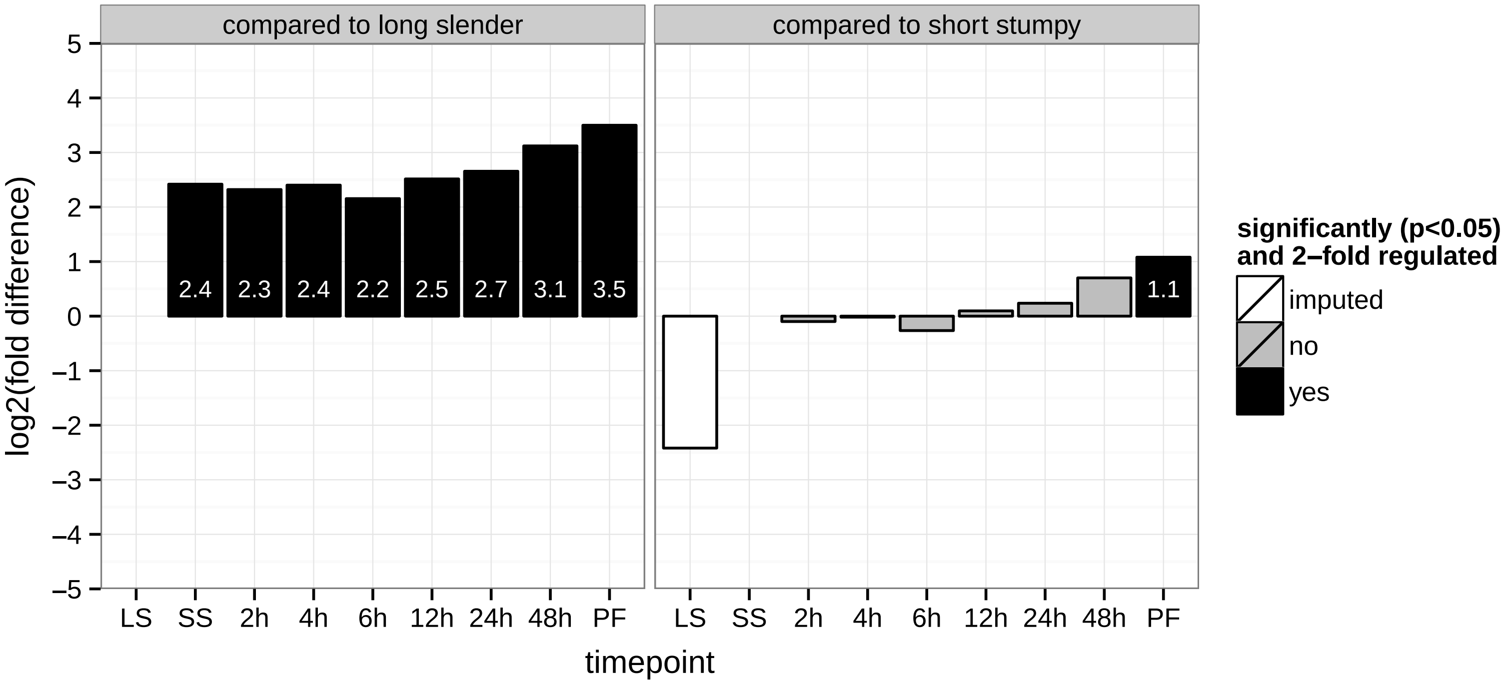
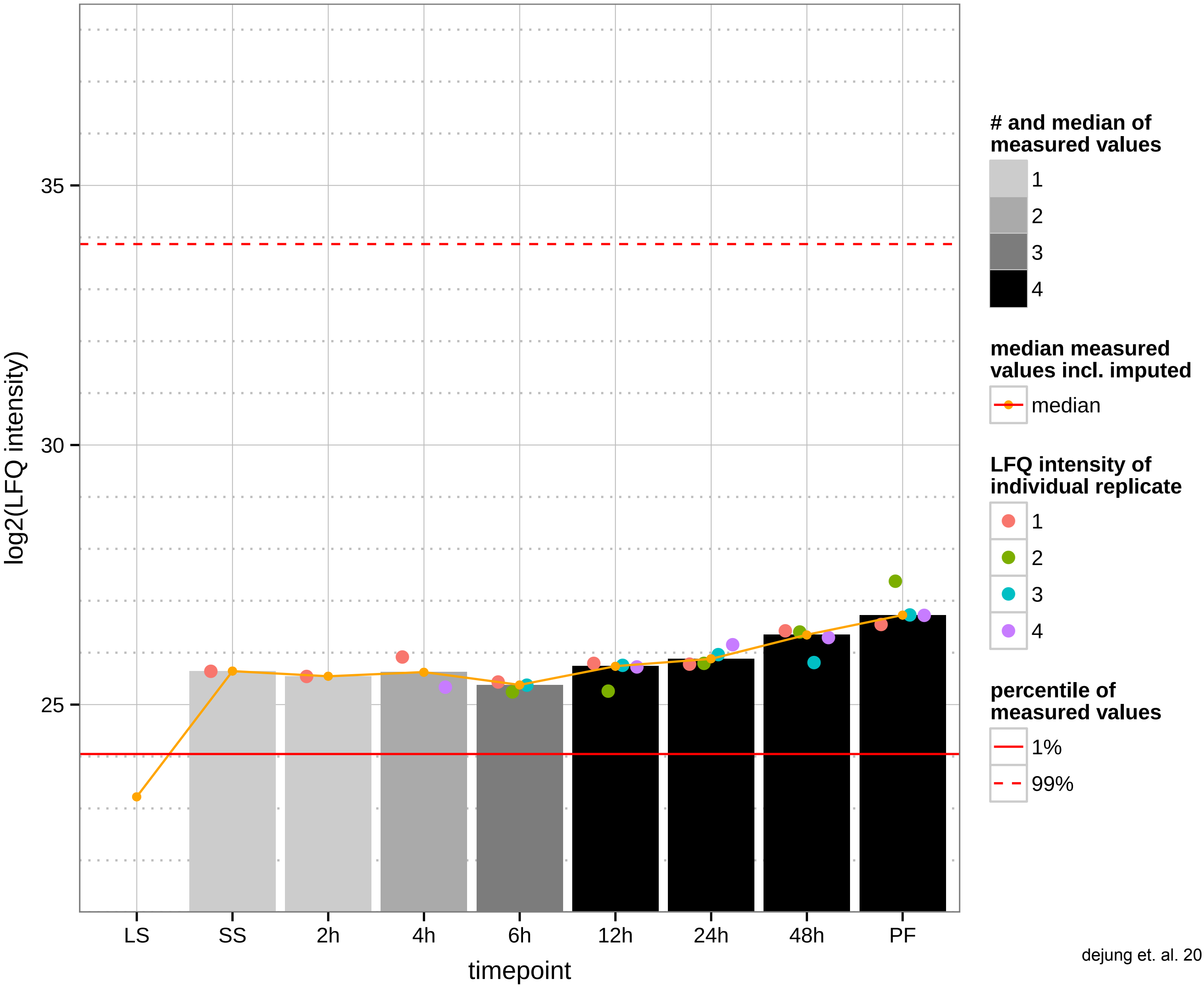
ATP–dependent helicase, putative
Tb927.11.13380
AGOF: nucleoside–triphosphatase activity, nucleotide binding
AGOC: null
AGOP: null
PGOF: nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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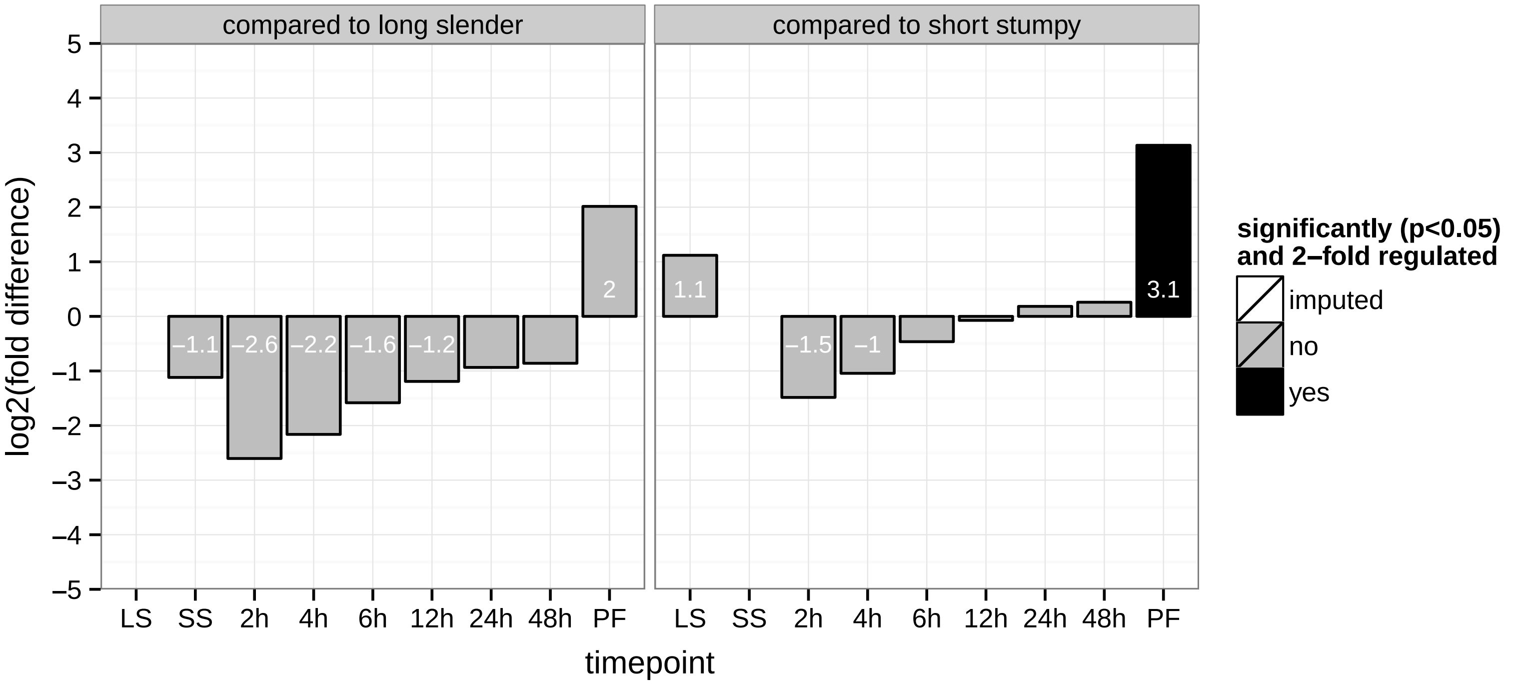
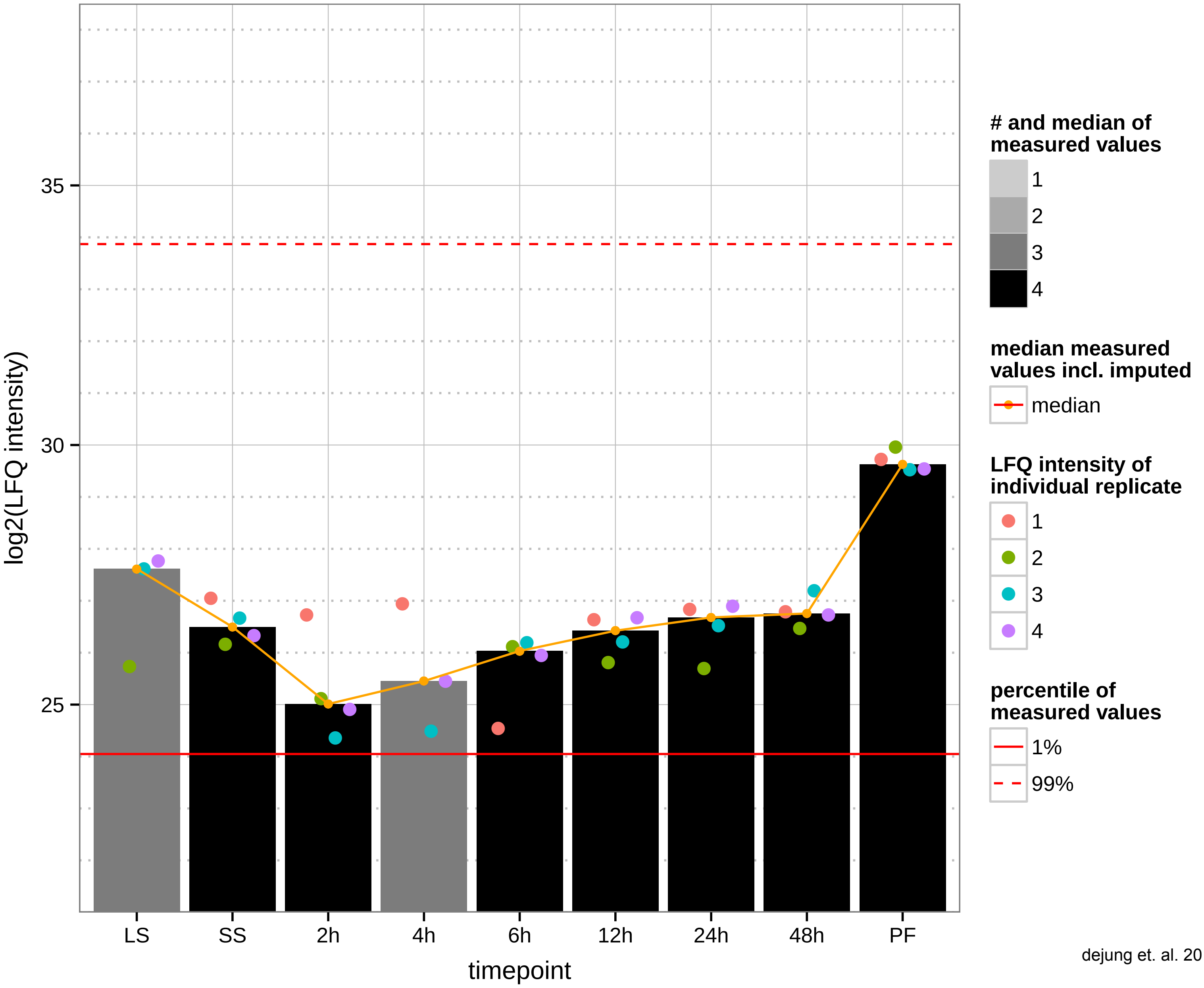
hypothetical protein, conserved
Tb927.11.13520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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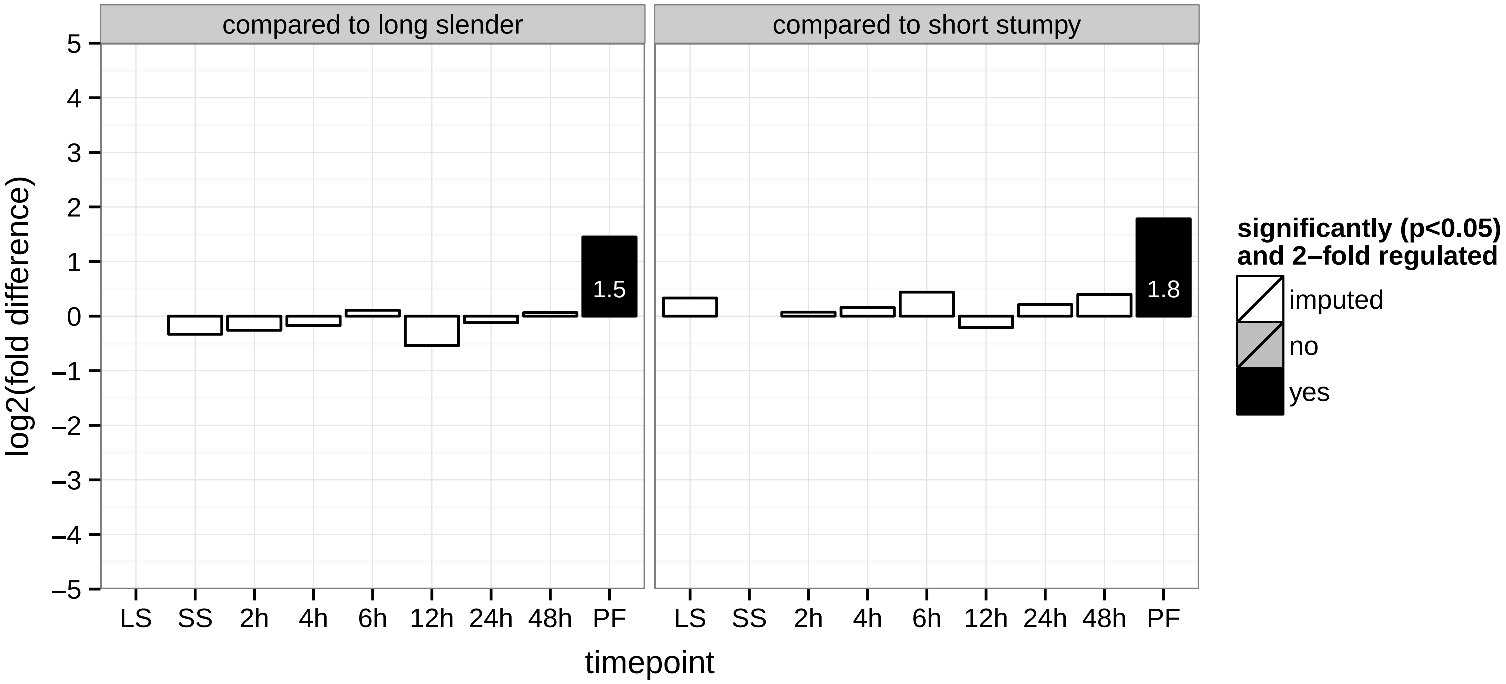
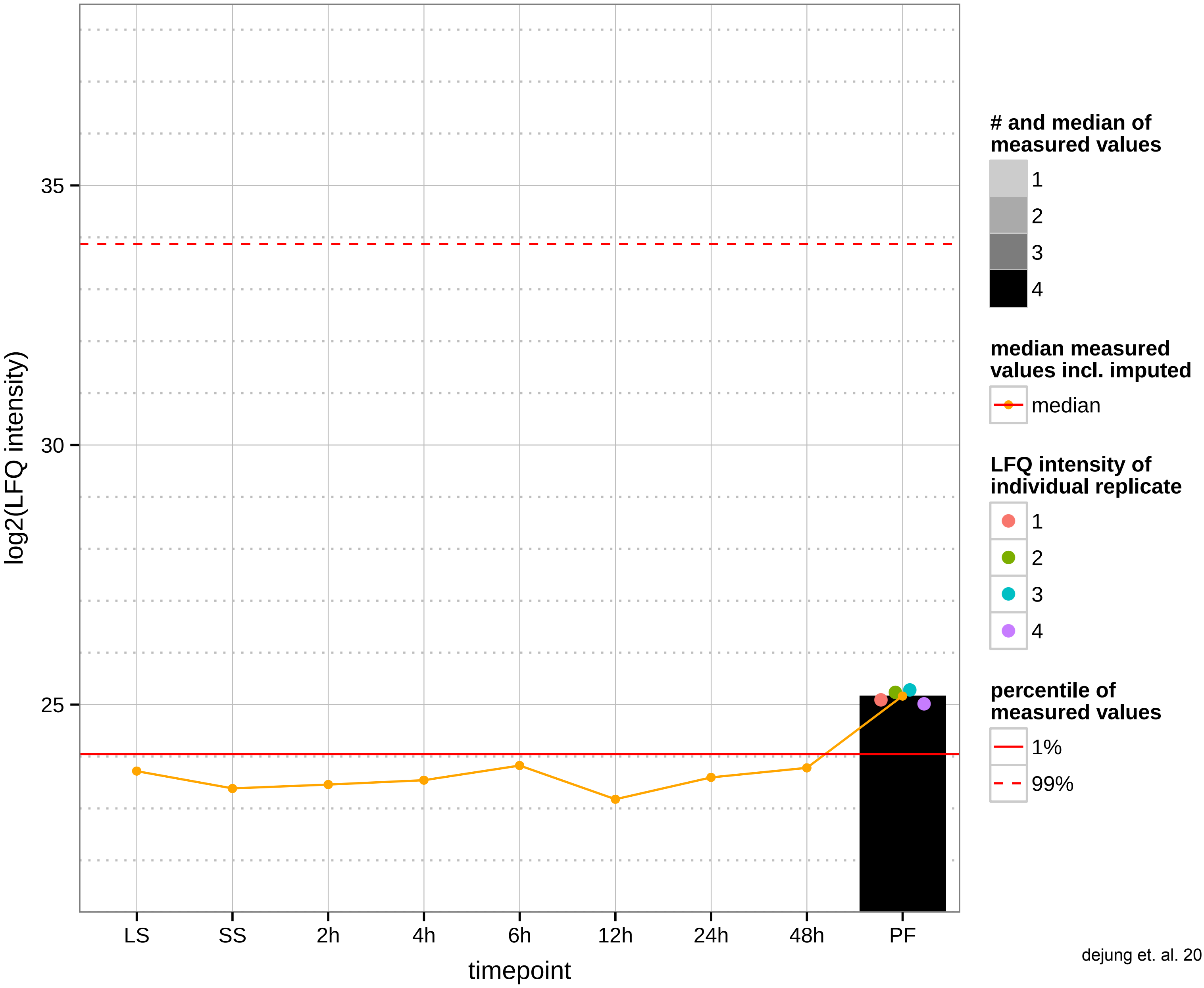
hypothetical protein, conserved
Tb927.11.13680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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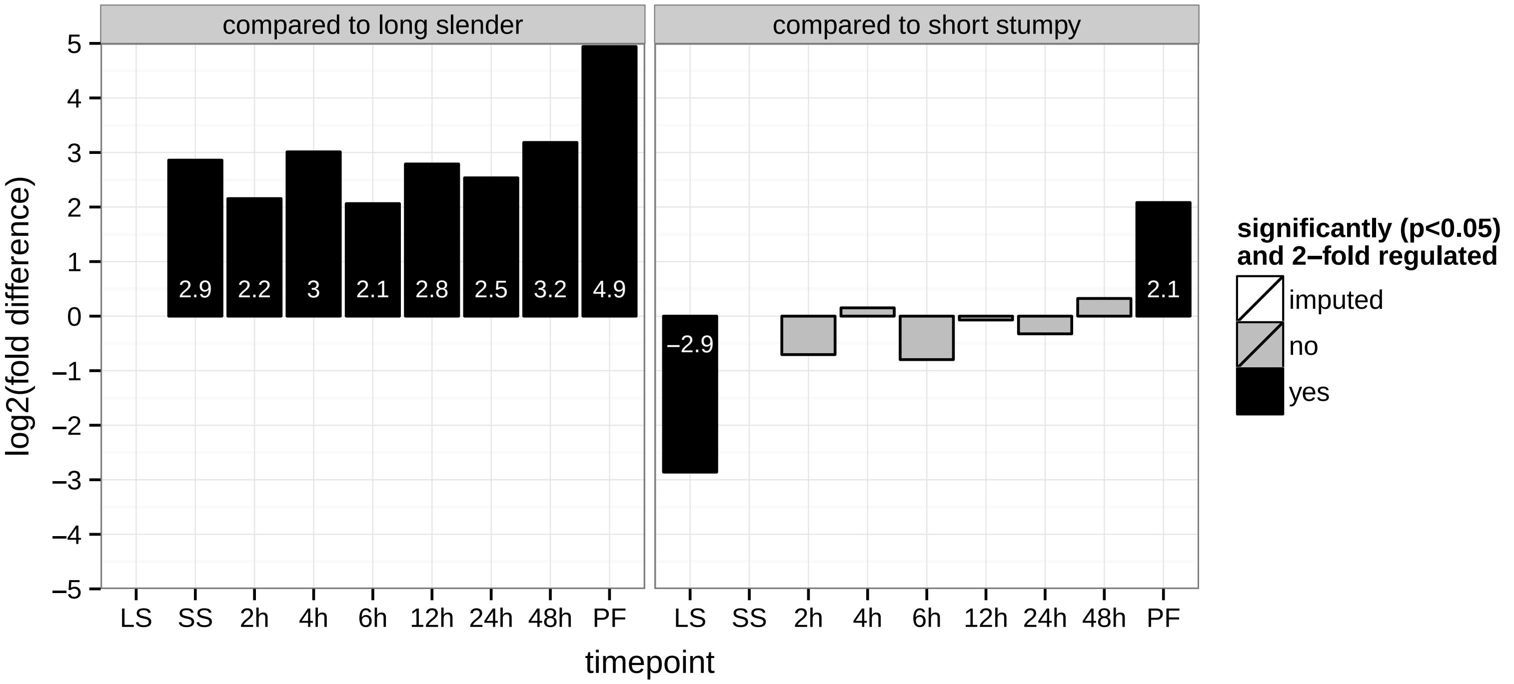
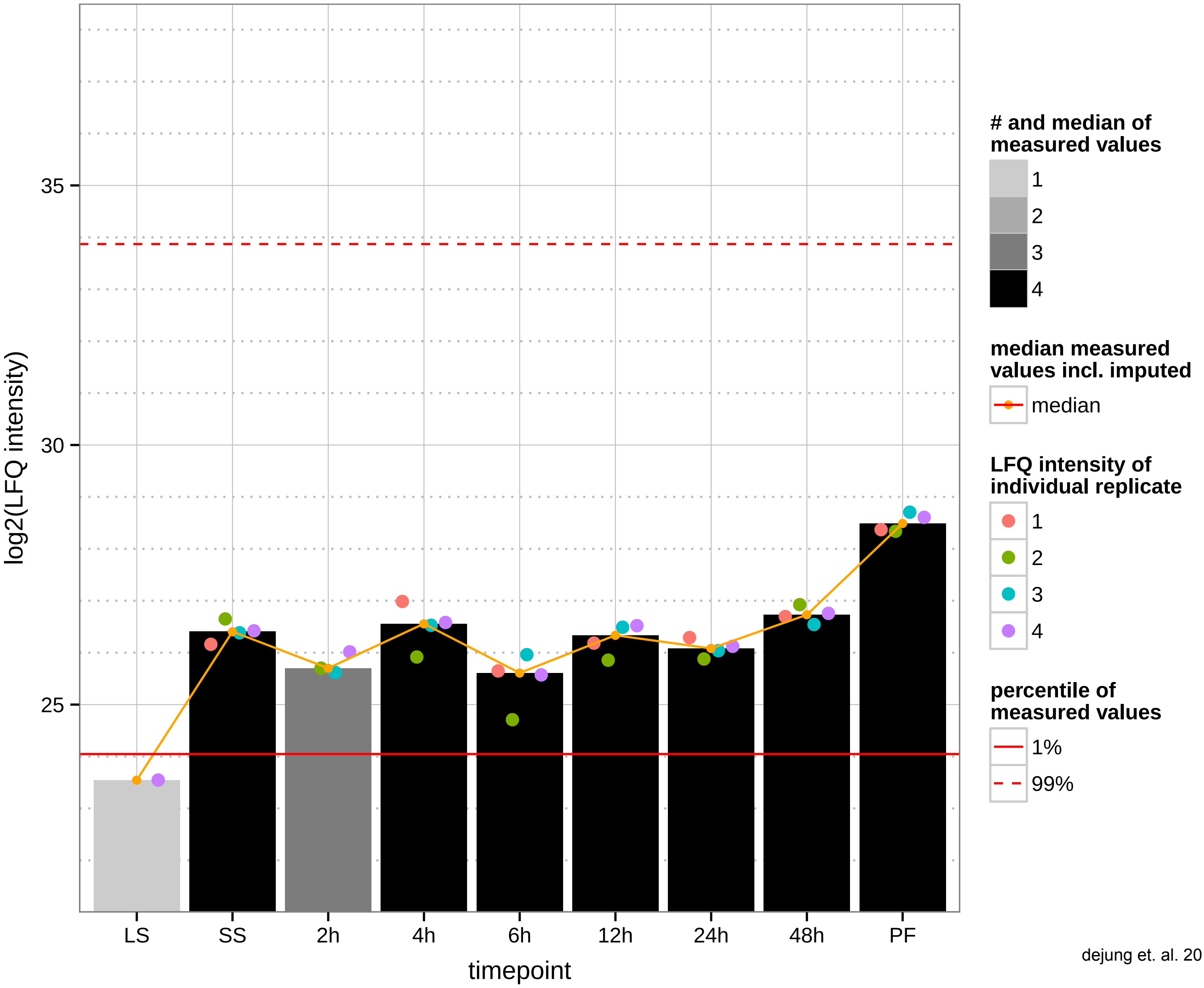
hypothetical protein, conserved
Tb927.11.13870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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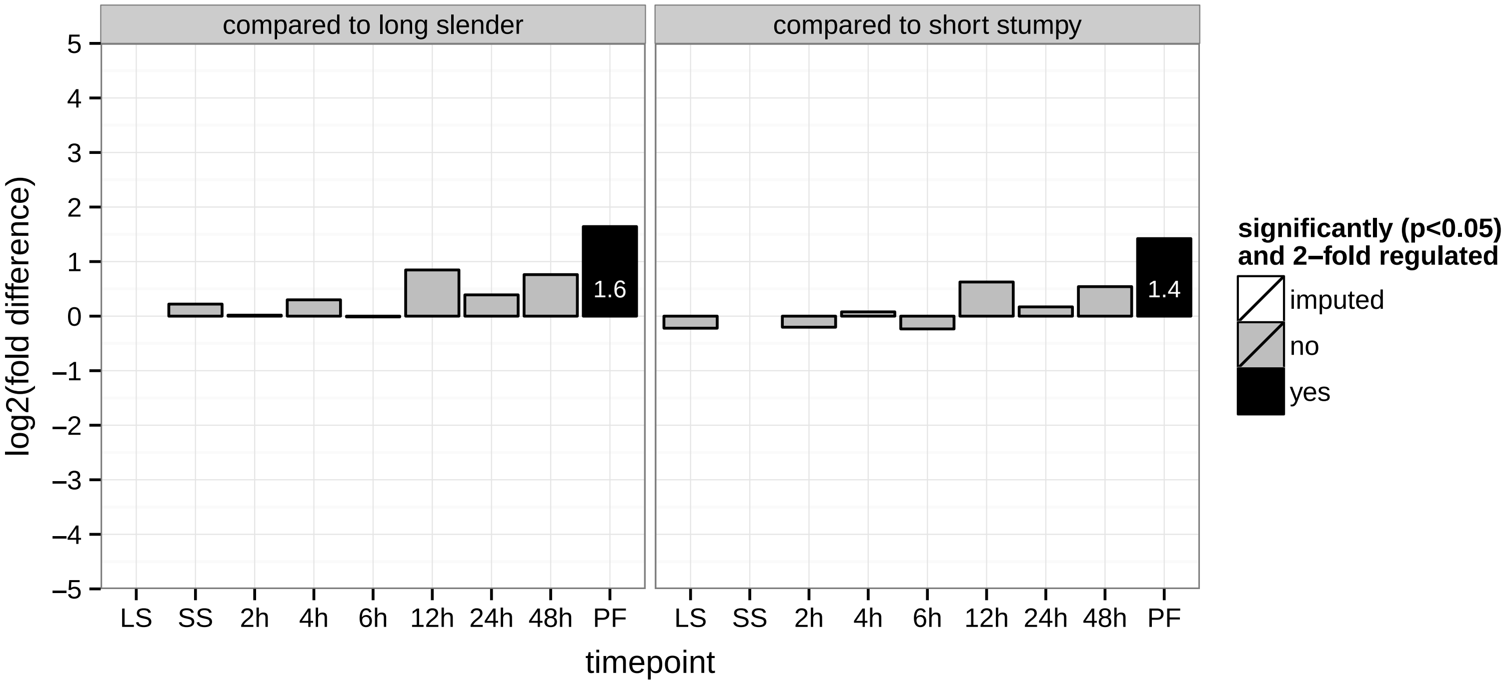
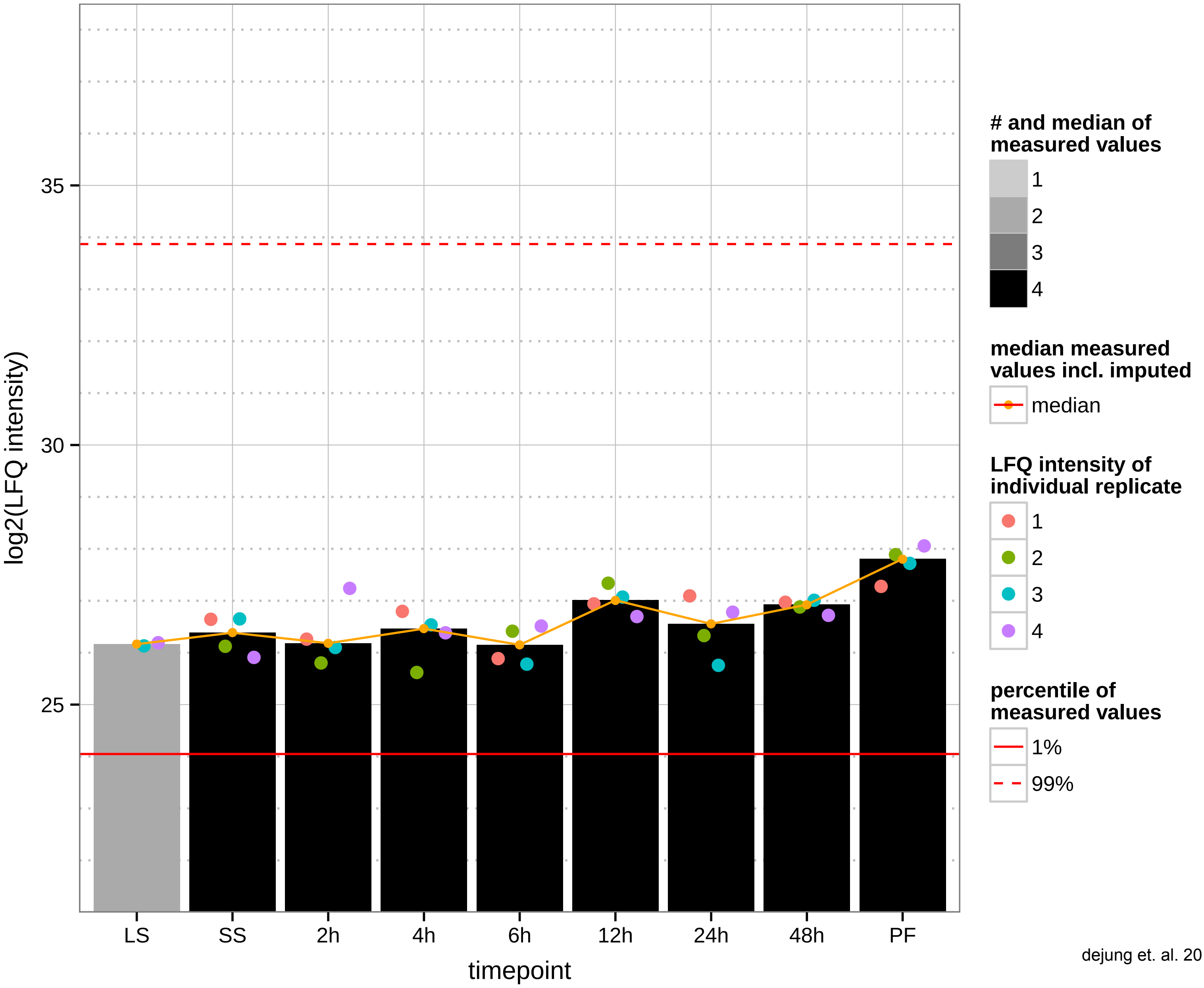
Pab1p−dependent poly(A) ribonuclease subunit, putative, PAN3
Tb927.11.13970
AGOF: null
AGOC: null
AGOP: null
PGOF: transferase activity, transferring phosphorus−containing groups
PGOC: null
PGOP: null





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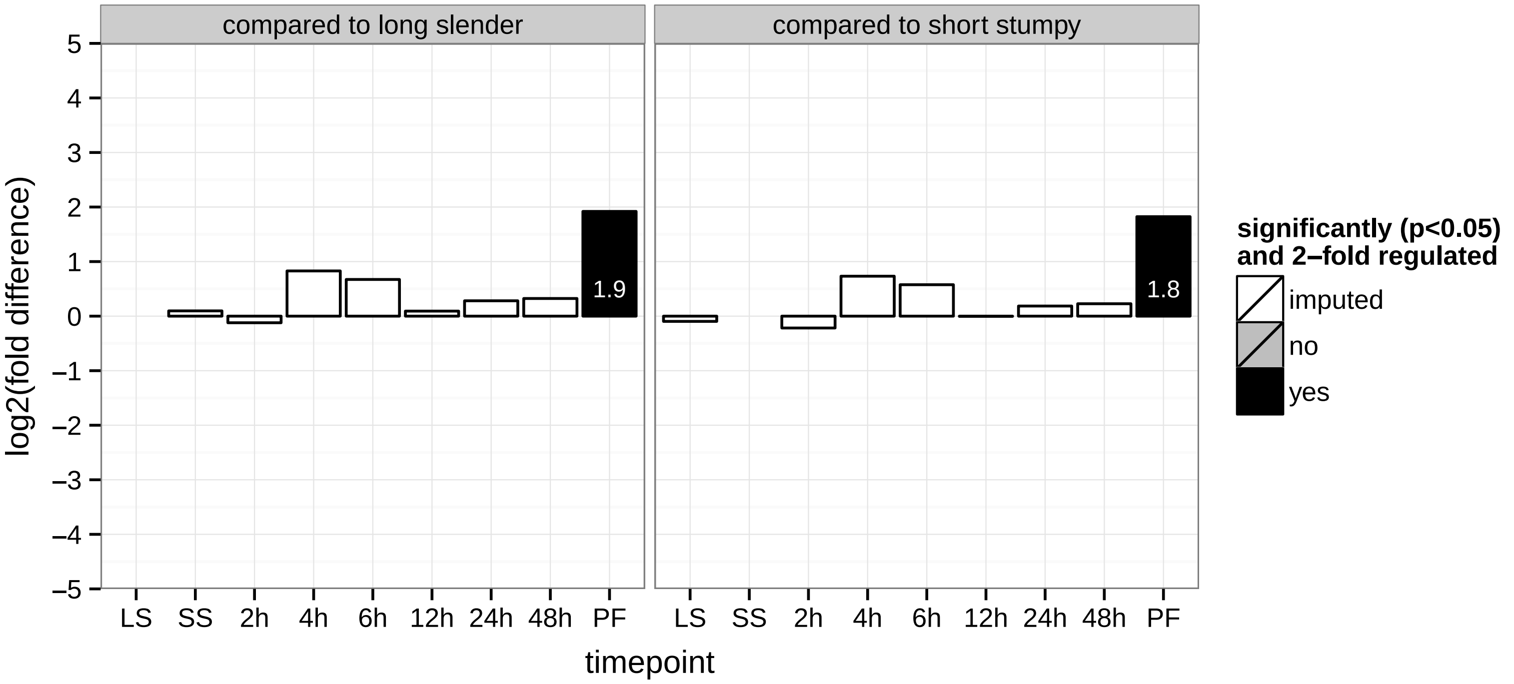
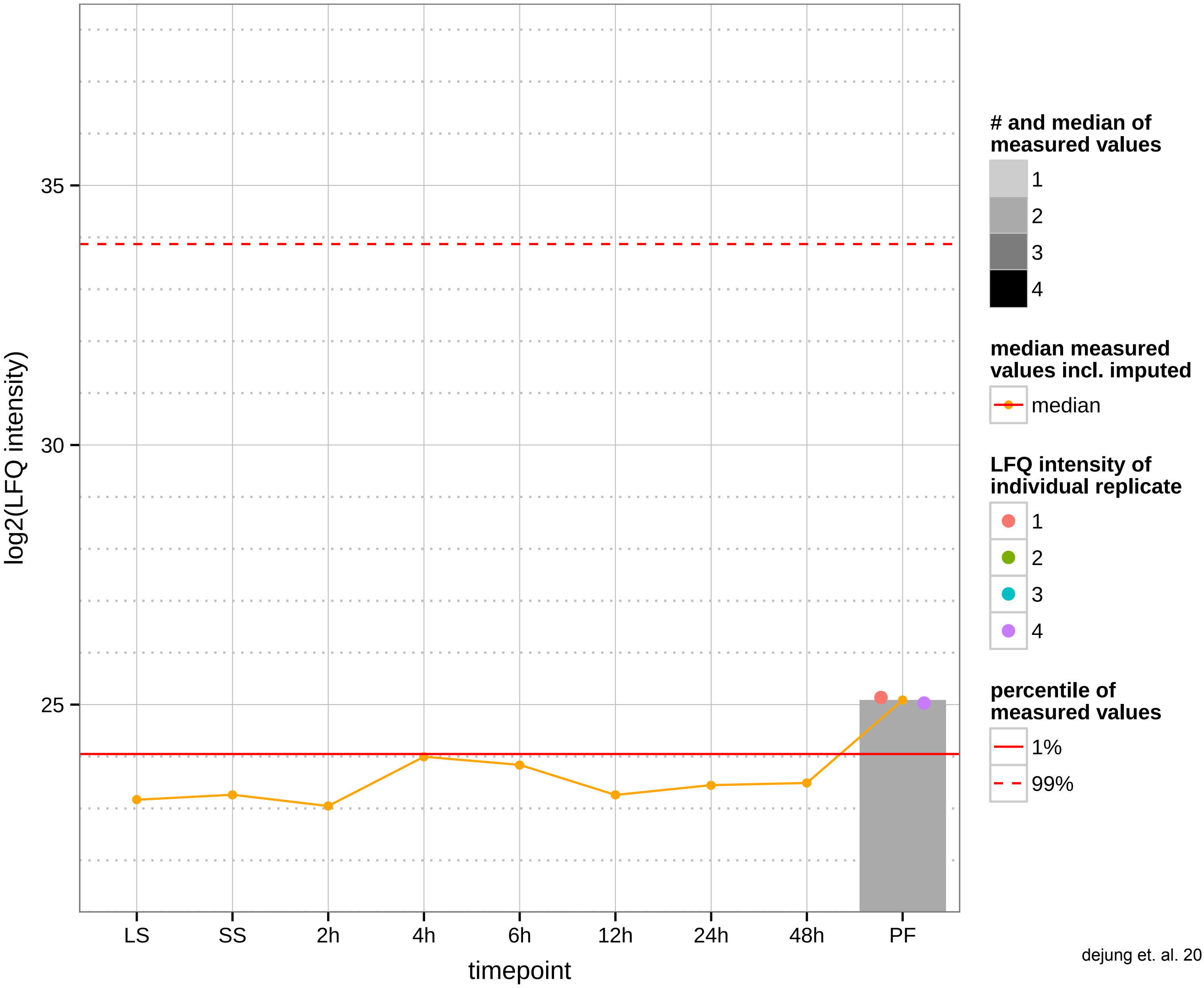
Repressor of differentiation kinase 1 (RDK1)
Tb927.11.14070
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: cilium, integral to membrane, plasma membrane
AGOP: growth, modulation of development of symbiont involved in interaction with host, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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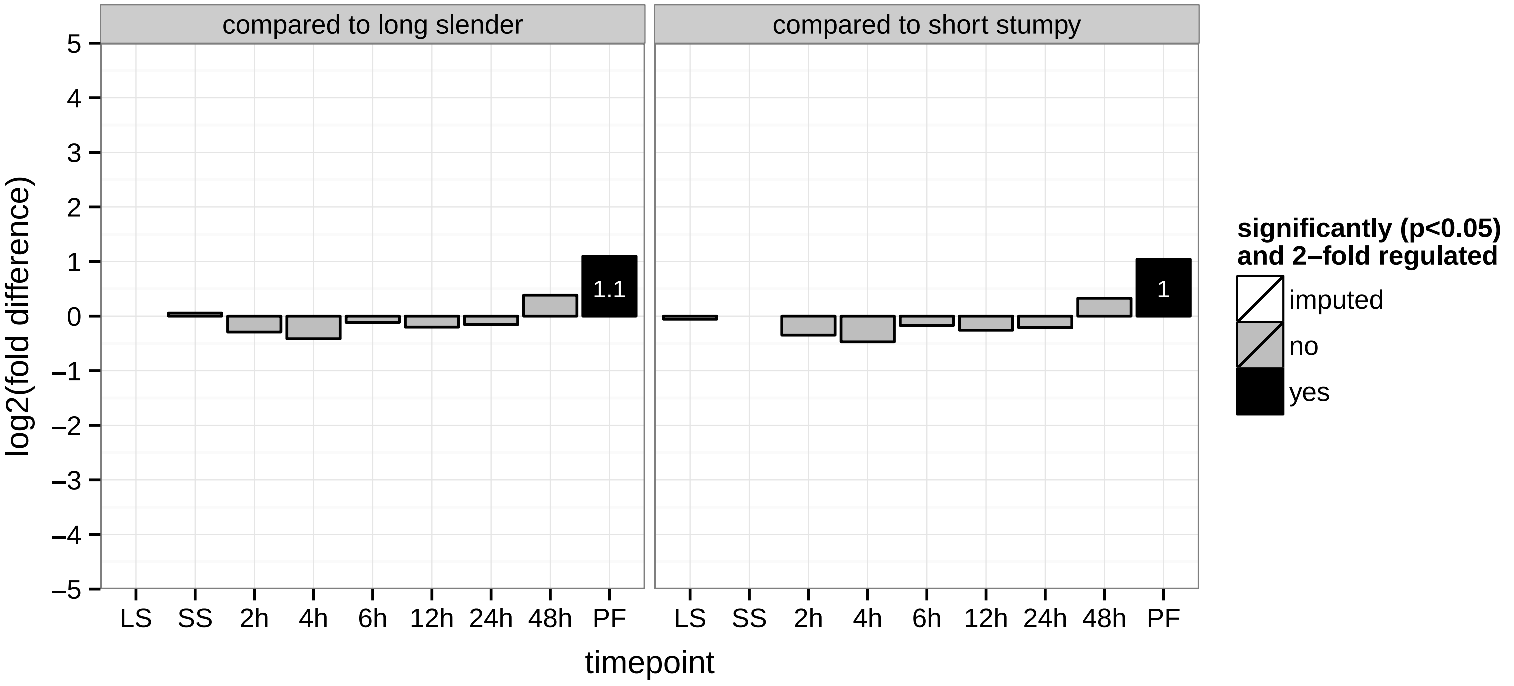
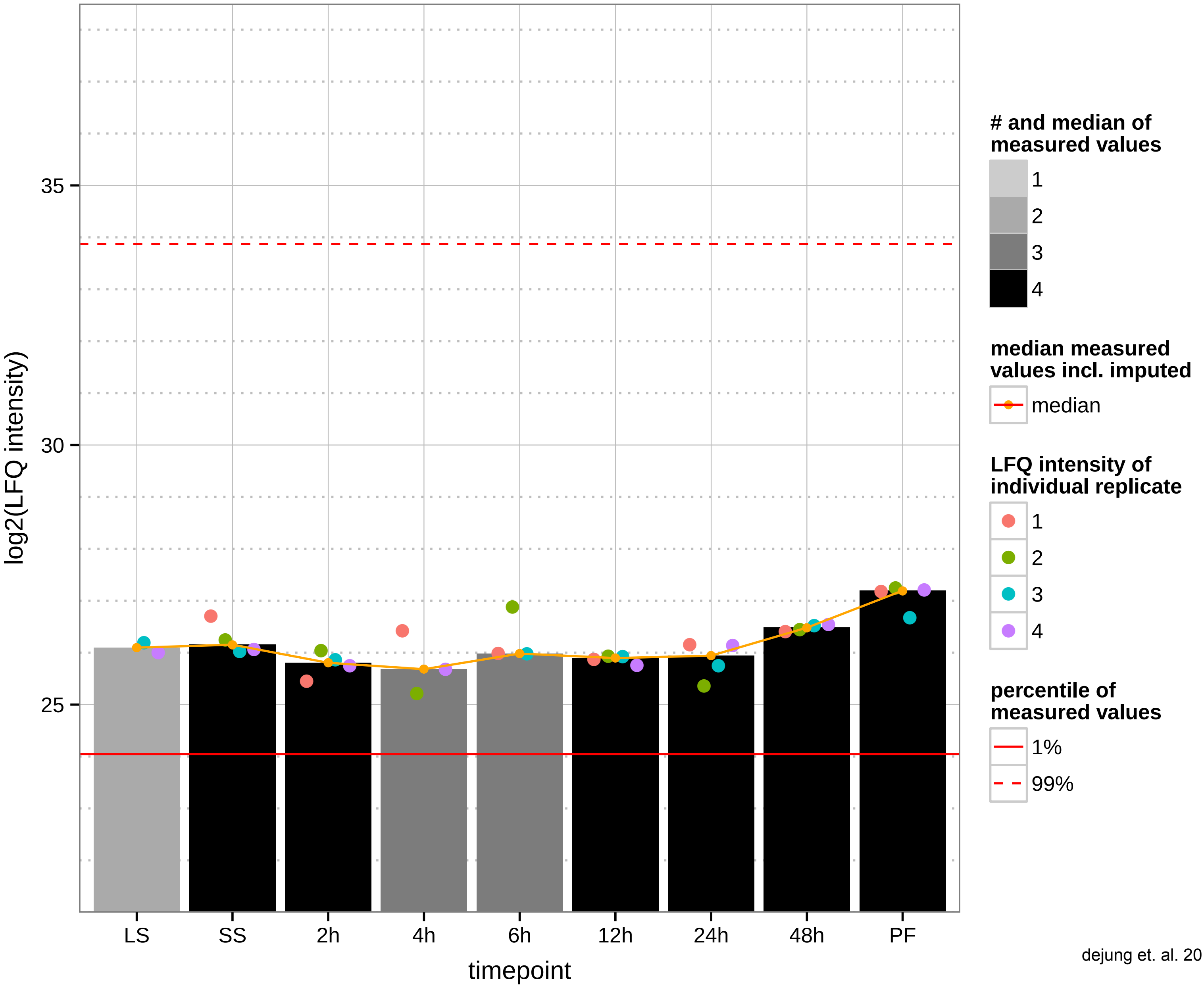
conserved protein
Tb927.11.14210
AGOF: calcium−dependent cysteine−type endopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: calcium−dependent cysteine−type endopeptidase activity
PGOC: intracellular
PGOP: proteolysis





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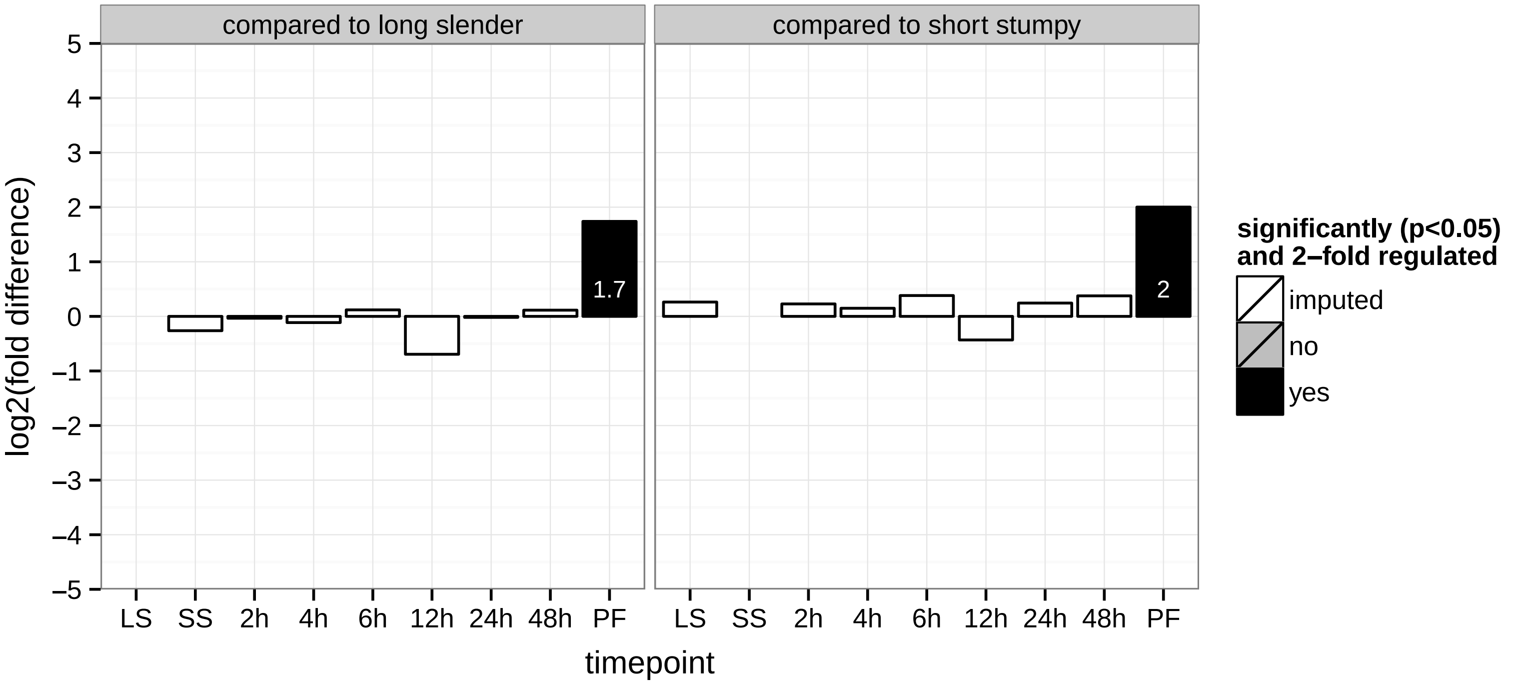
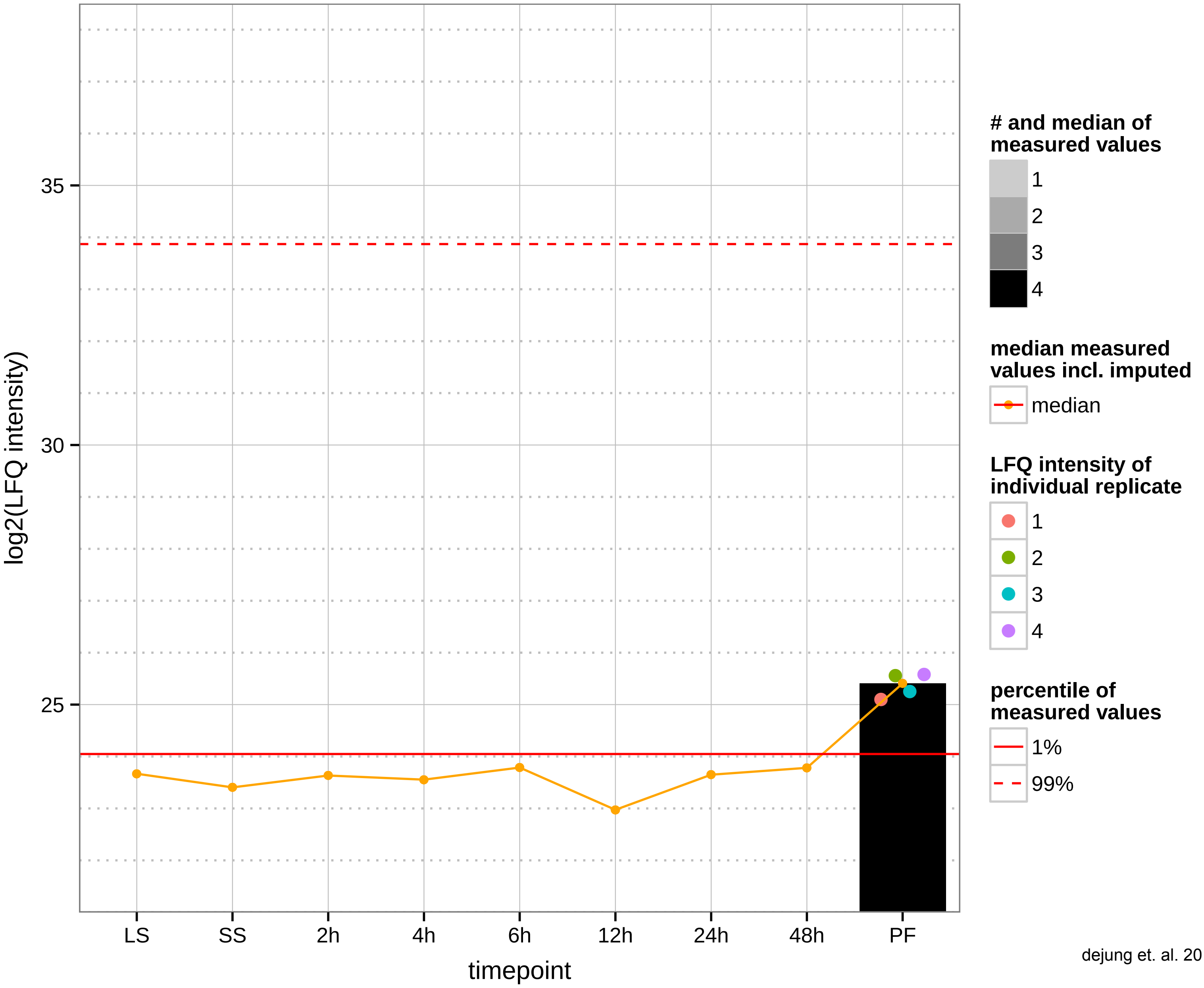
RNA guanylyltransferase
Tb927.11.14580
AGOF: mRNA guanylyltransferase activity
AGOC: nucleus
AGOP: 7−methylguanosine mRNA capping
PGOF: mRNA guanylyltransferase activity
PGOC: null
PGOP: 7−methylguanosine mRNA capping, mRNA processing





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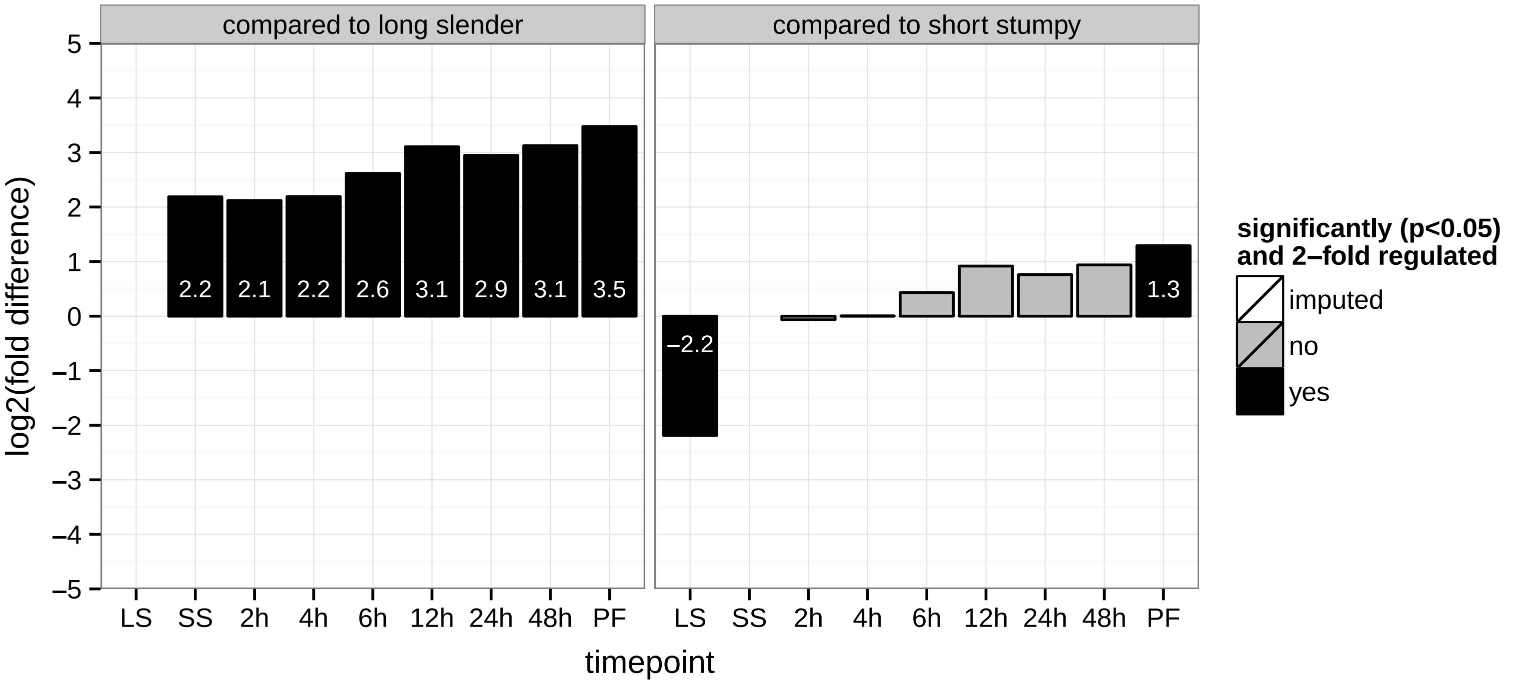
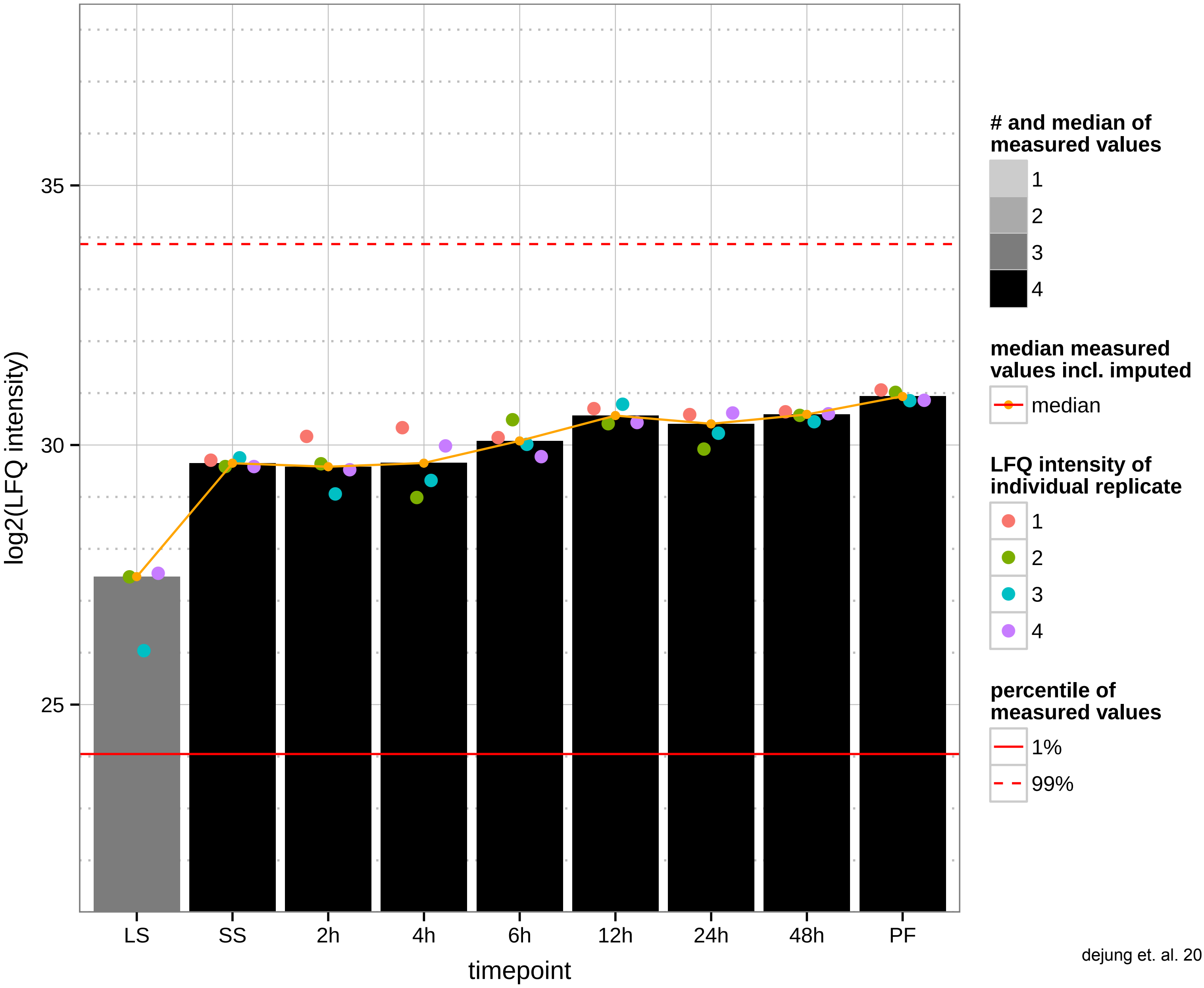
pumilio/PUF RNA binding protein 7, putative (PUF7)
Tb927.11.14960
AGOF: RNA binding, protein binding
AGOC: nucleolus
AGOP: mRNA metabolic process, rRNA processing
PGOF: RNA binding, binding
PGOC: null
PGOP: null





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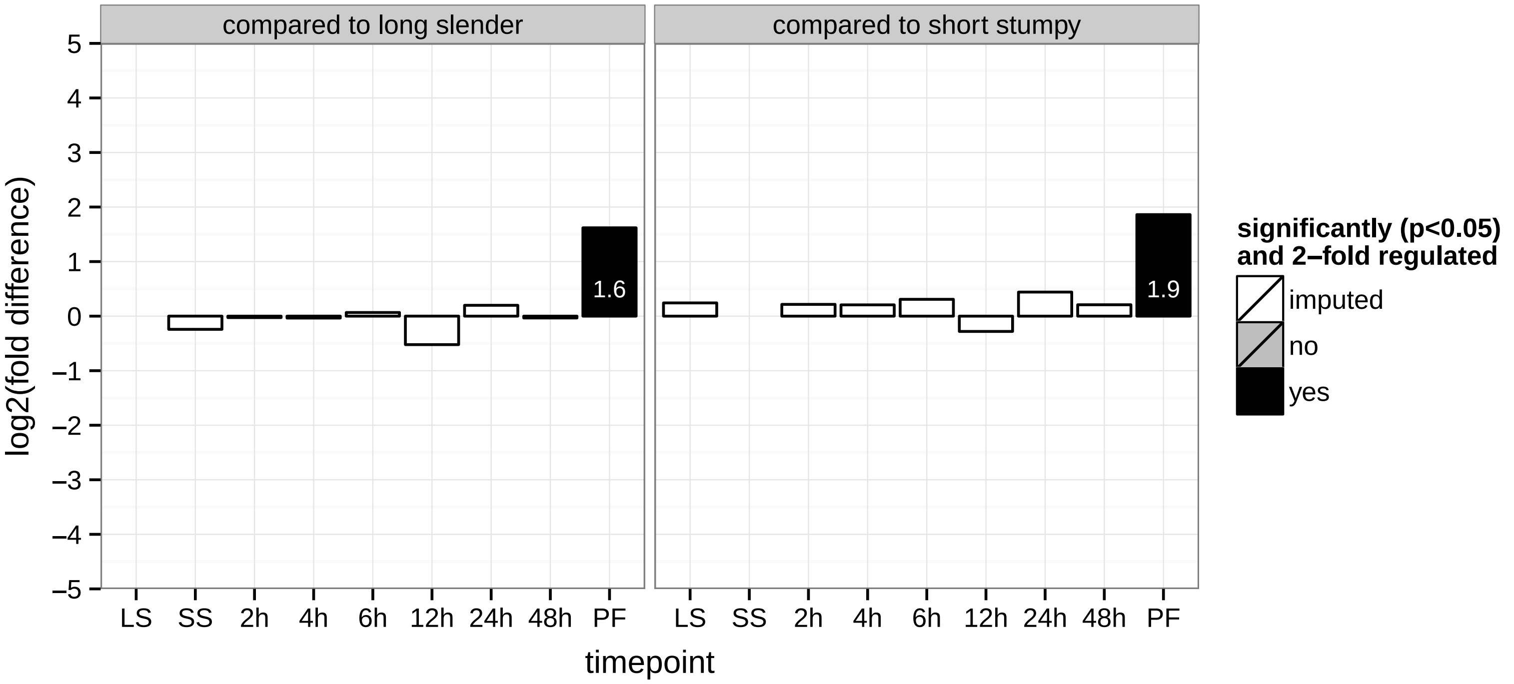
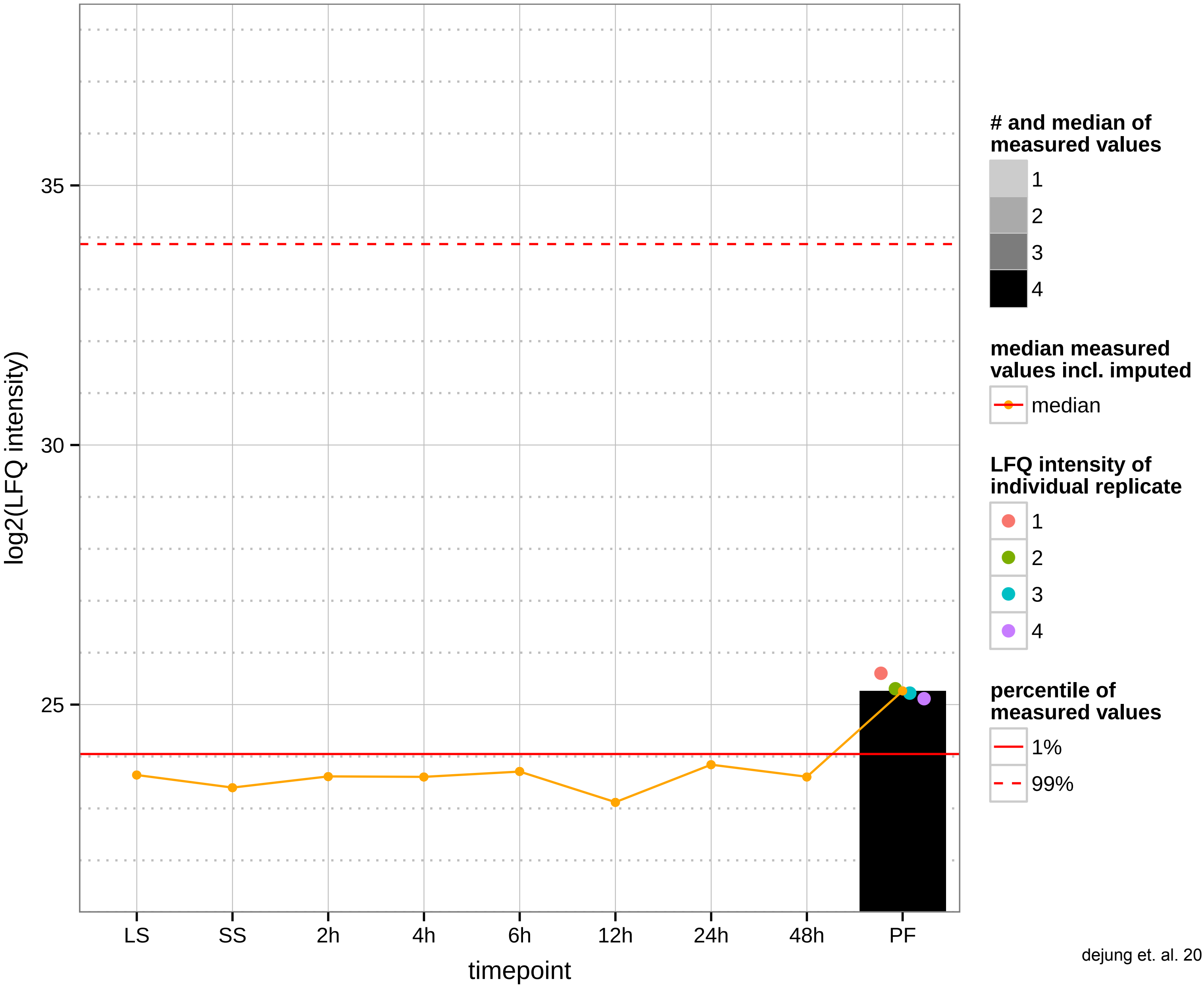
hypothetical protein, conserved
Tb927.11.15050
AGOF: null
AGOC: null
AGOP: null
PGOF: cation transmembrane transporter activity
PGOC: integral to membrane
PGOP: cation transport, transmembrane transport





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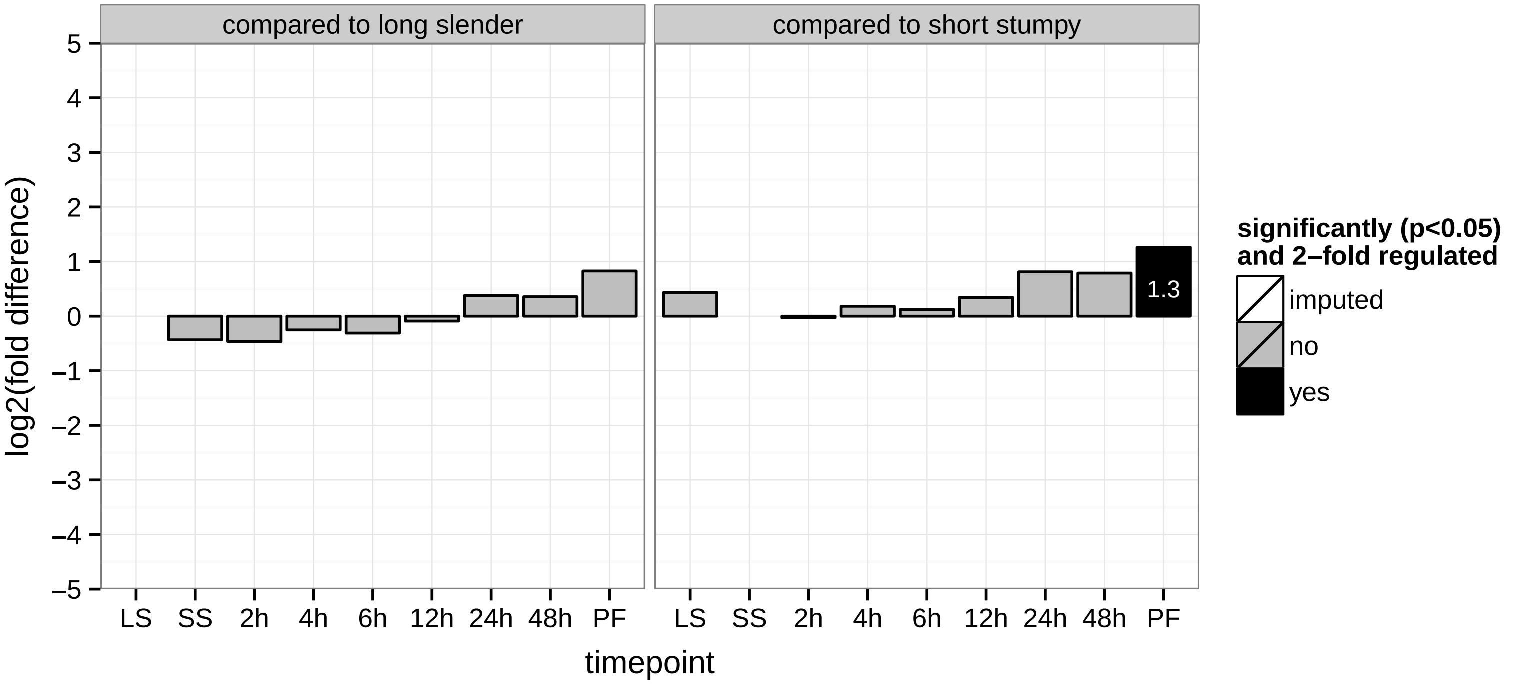
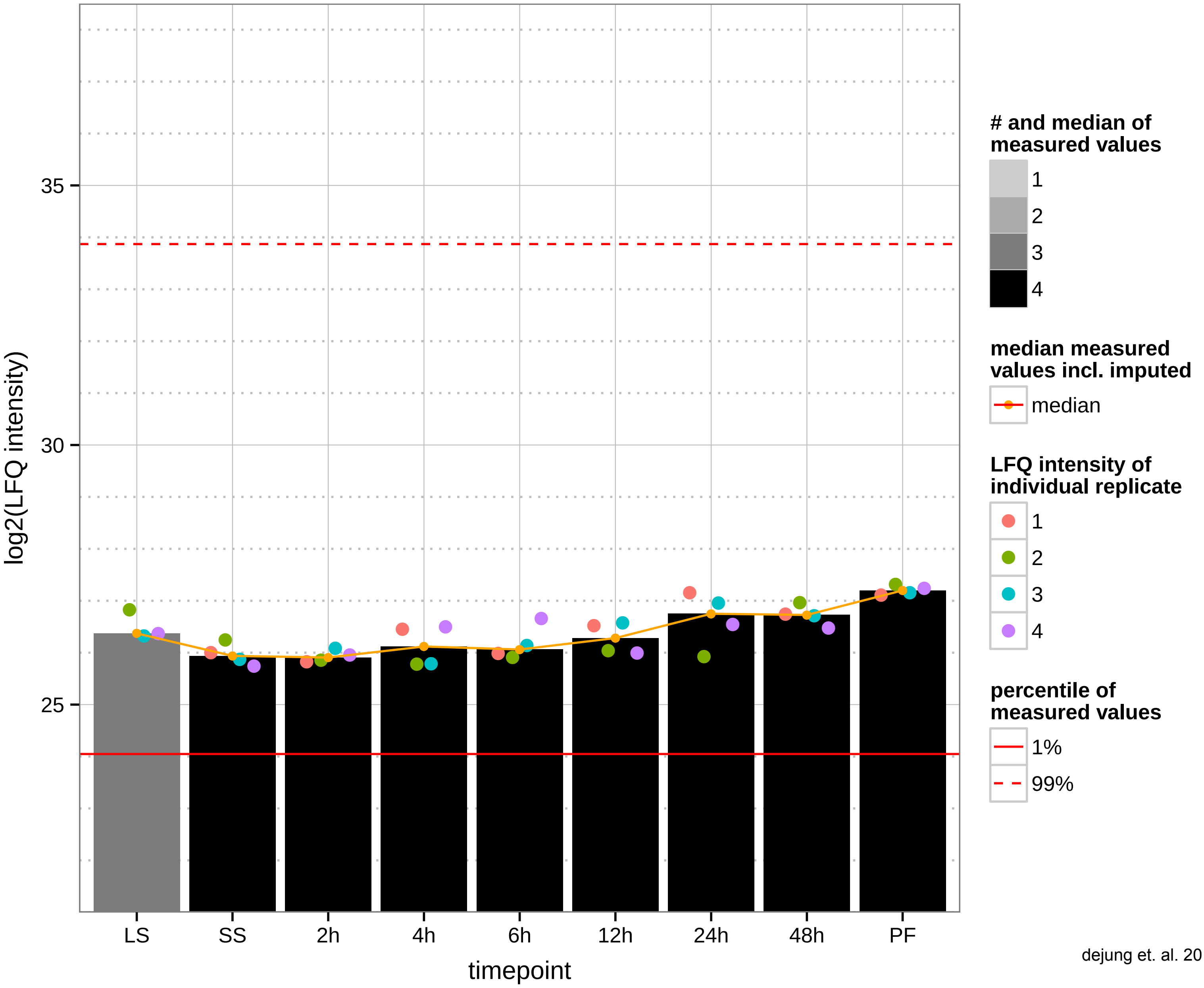
hypothetical protein, conserved
Tb927.11.15220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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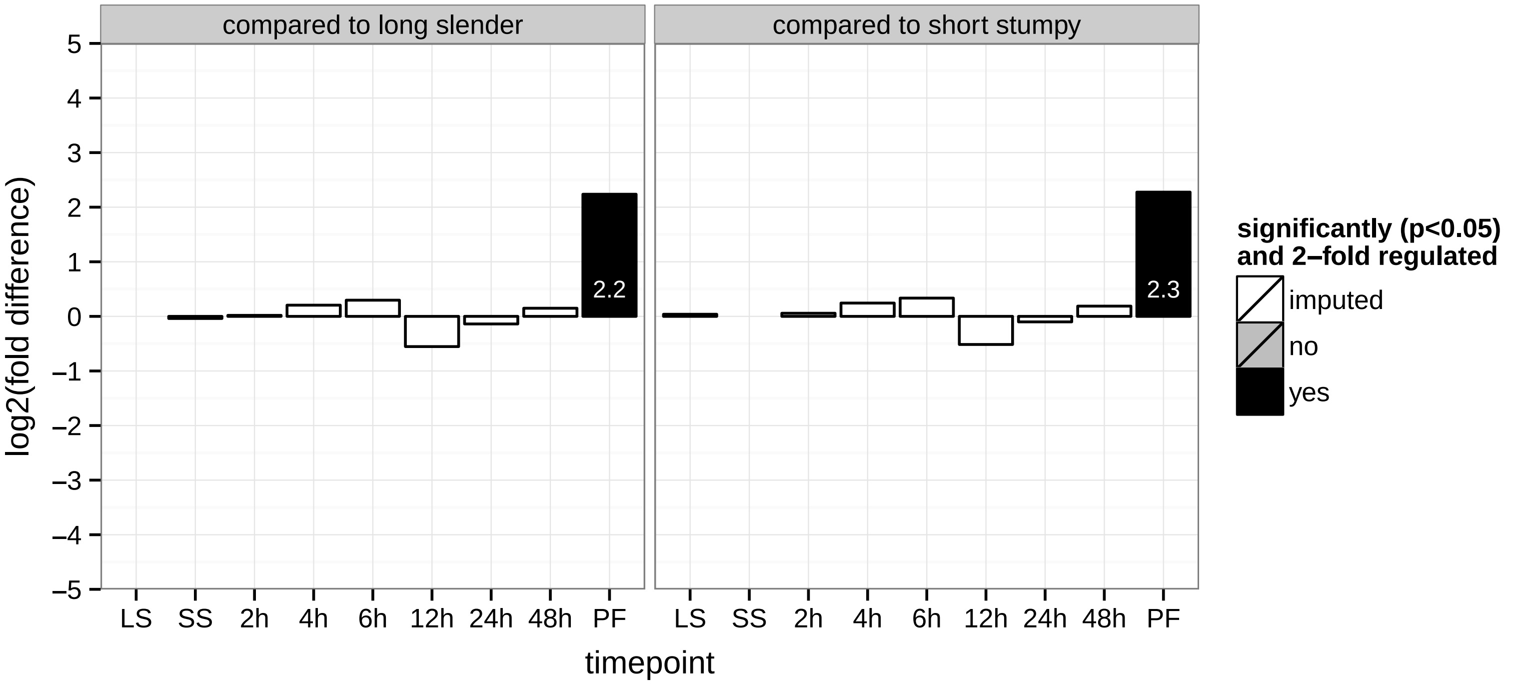
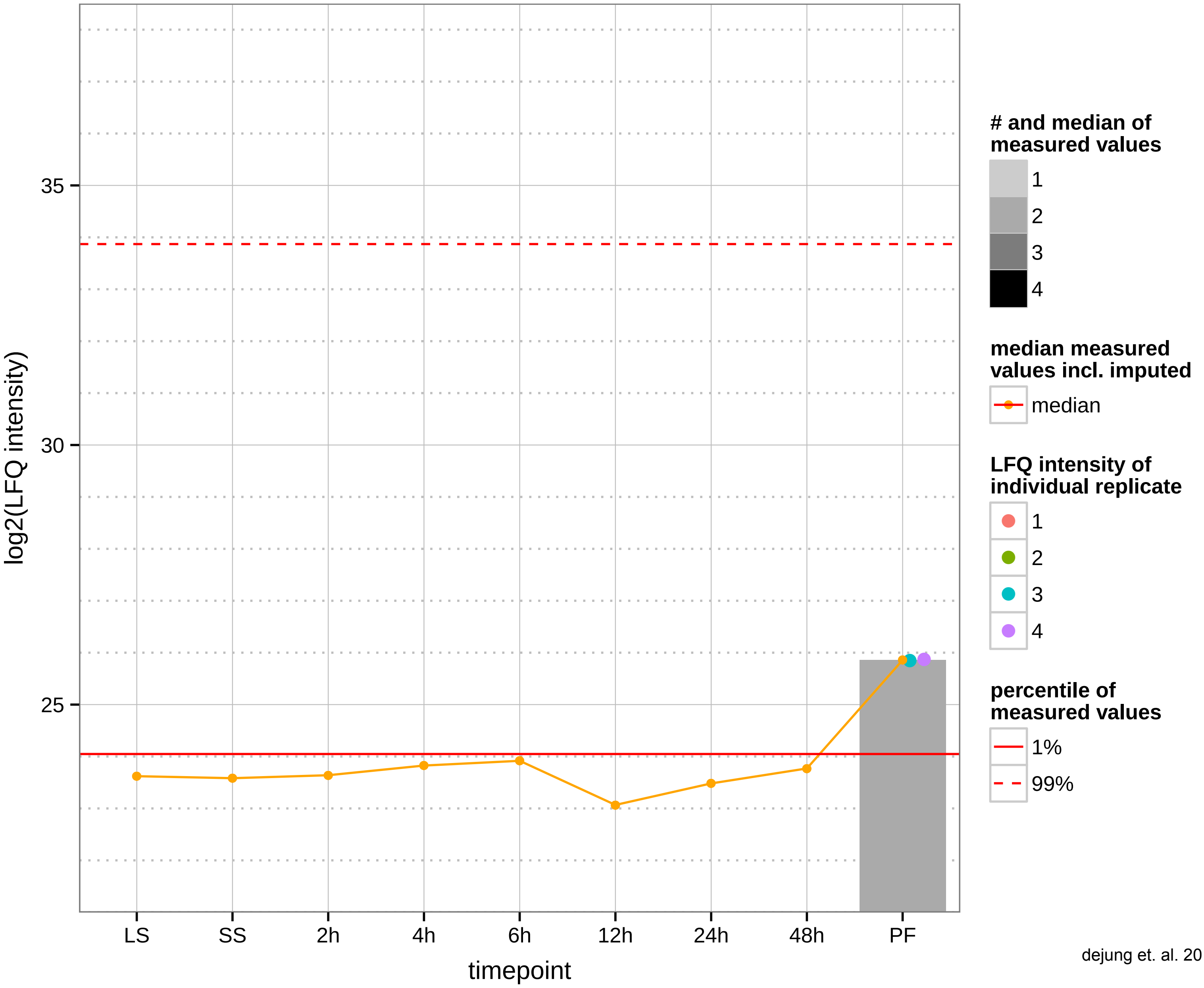
eRF1 methyltransferase catalytic subunit, putative
Tb927.11.15290
AGOF: protein methyltransferase activity
AGOC: cytoplasm
AGOP: regulation of translation
PGOF: null
PGOC: null
PGOP: null





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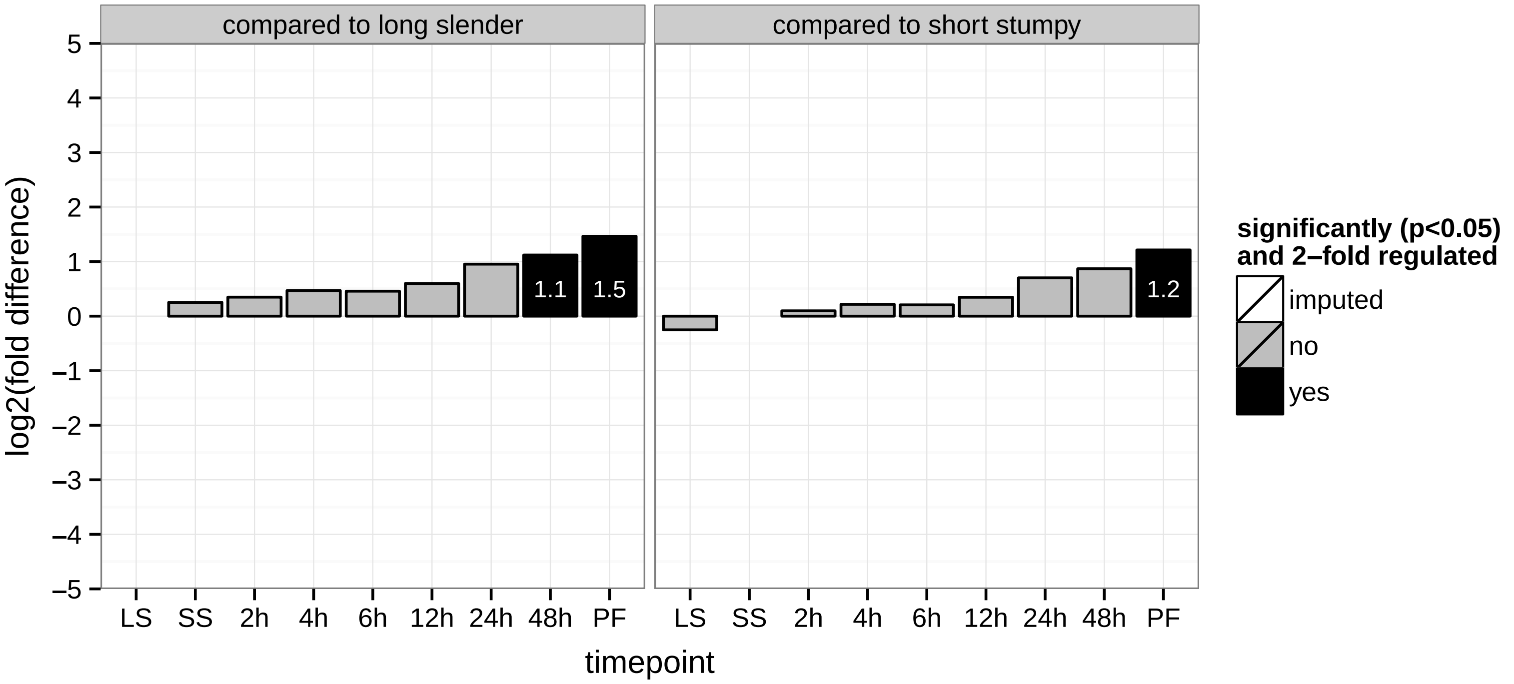
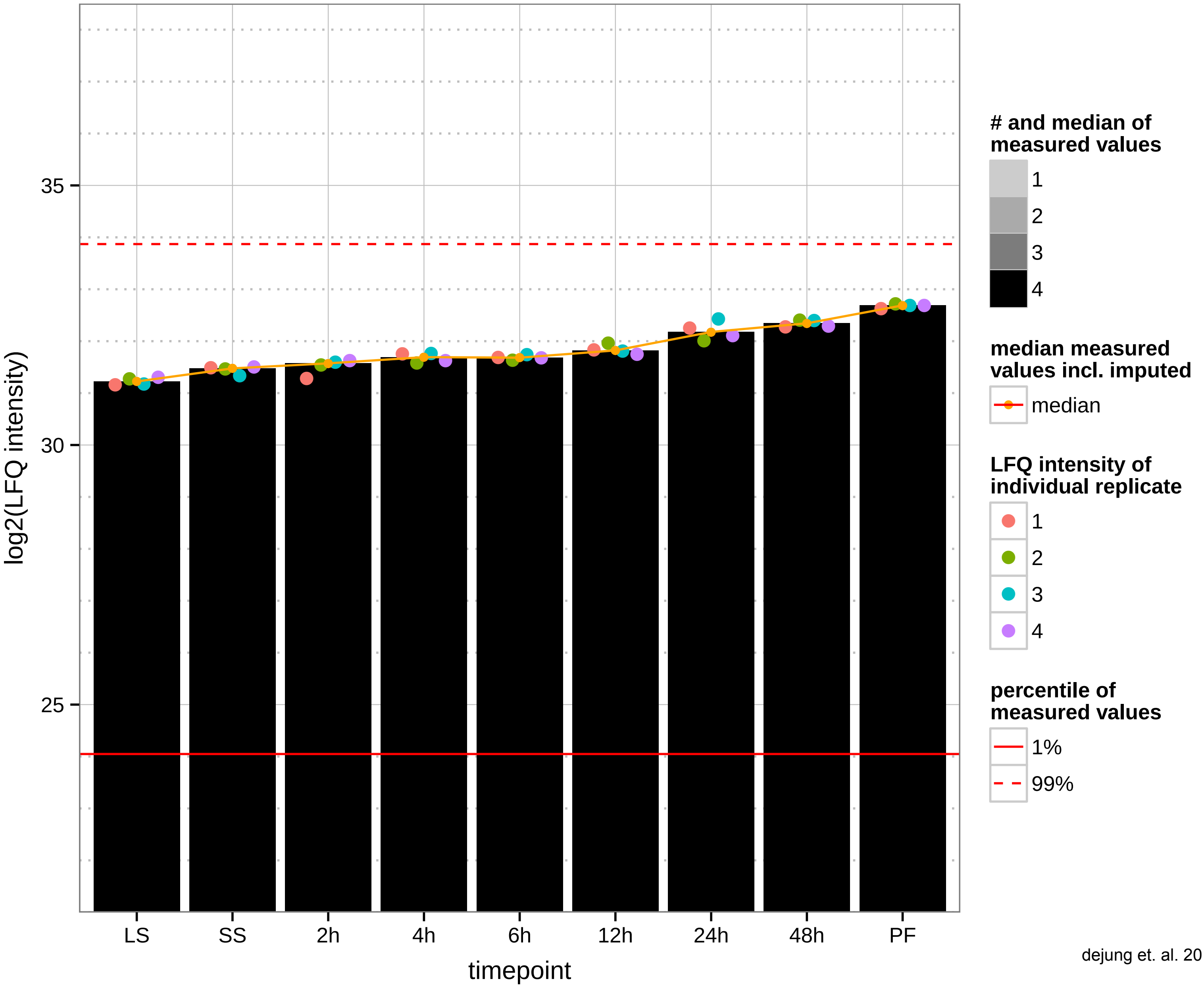
hypothetical protein, conserved (TbKap123)
Tb927.11.15370
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: membrane coat
PGOP: intracellular protein transport, vesicle–mediated transport





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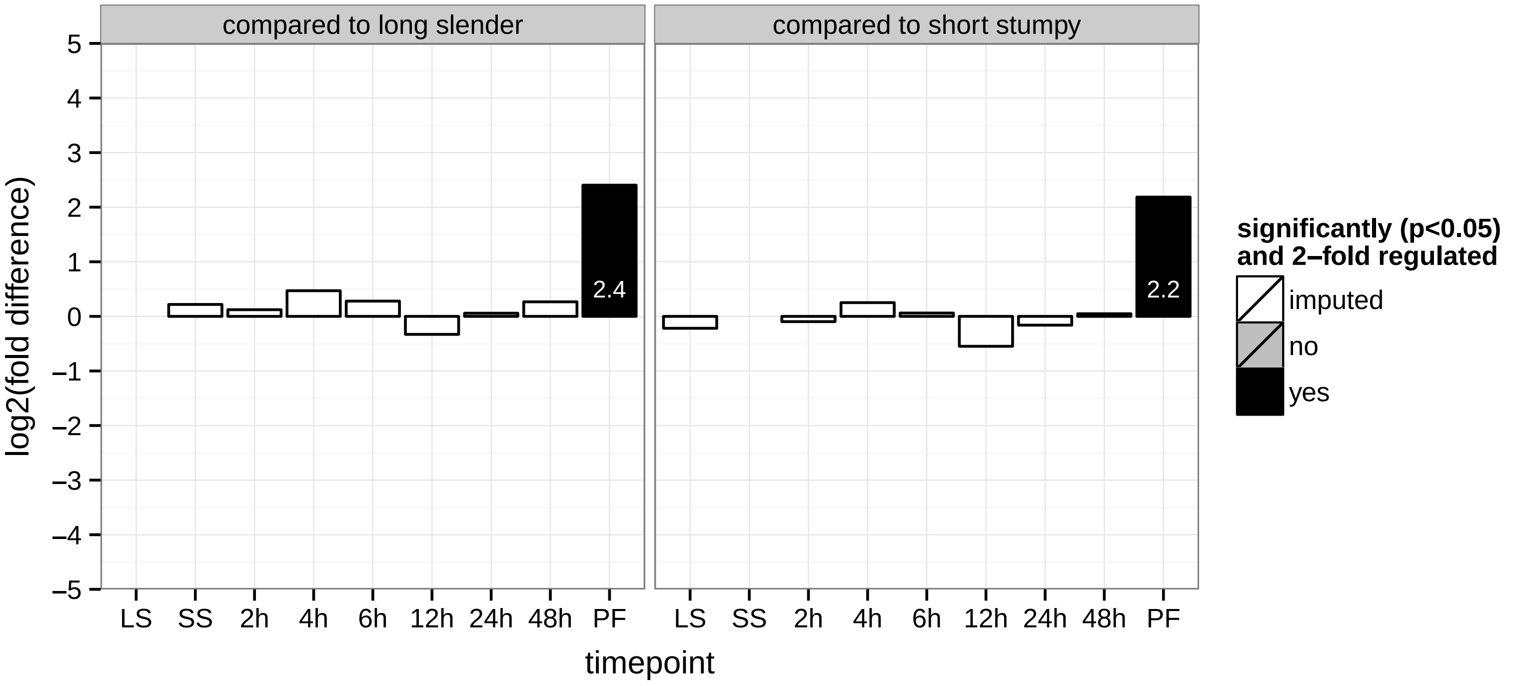
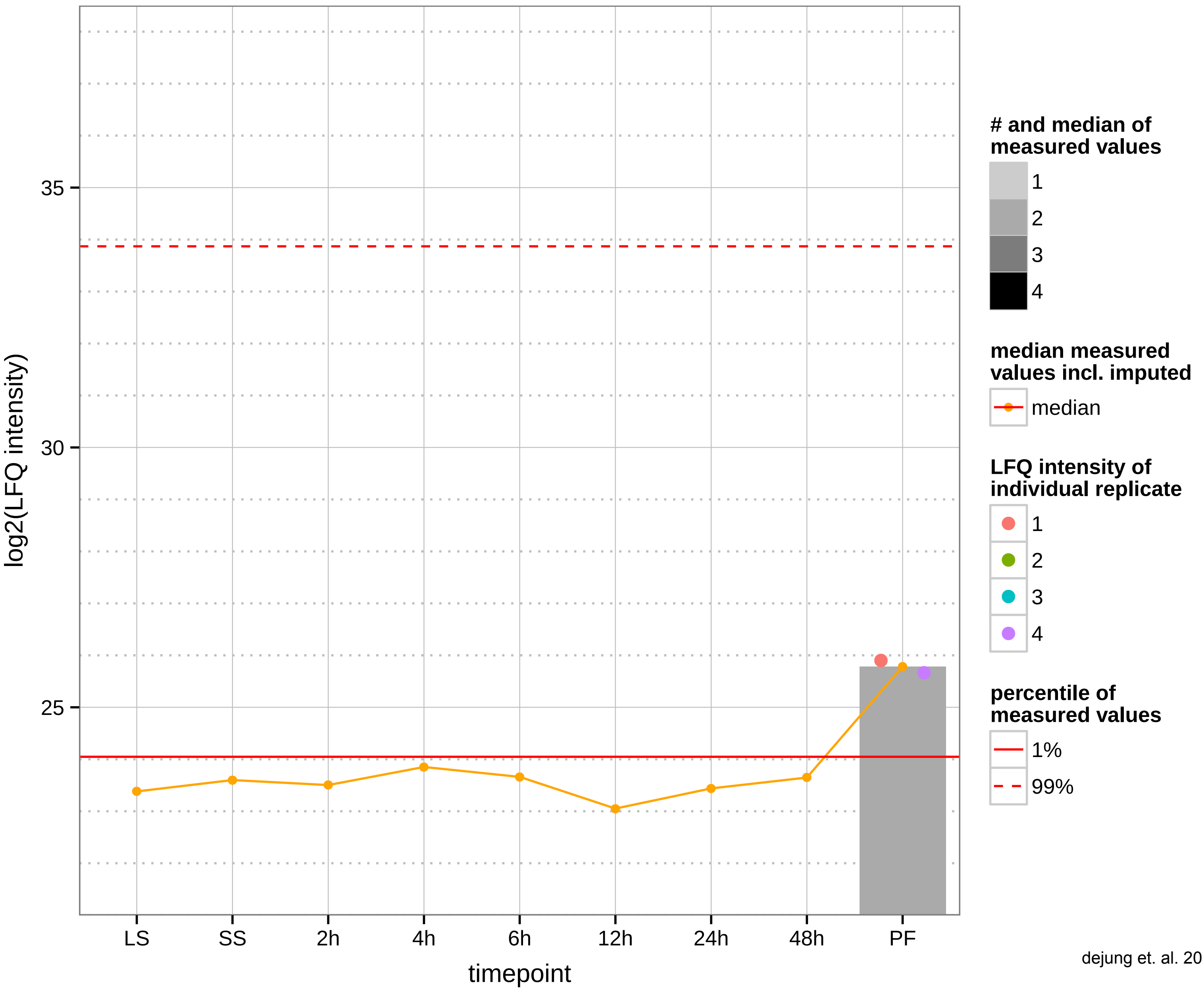
poly(A) polymerase, putative
Tb927.11.15650;Tb11.v5.0667
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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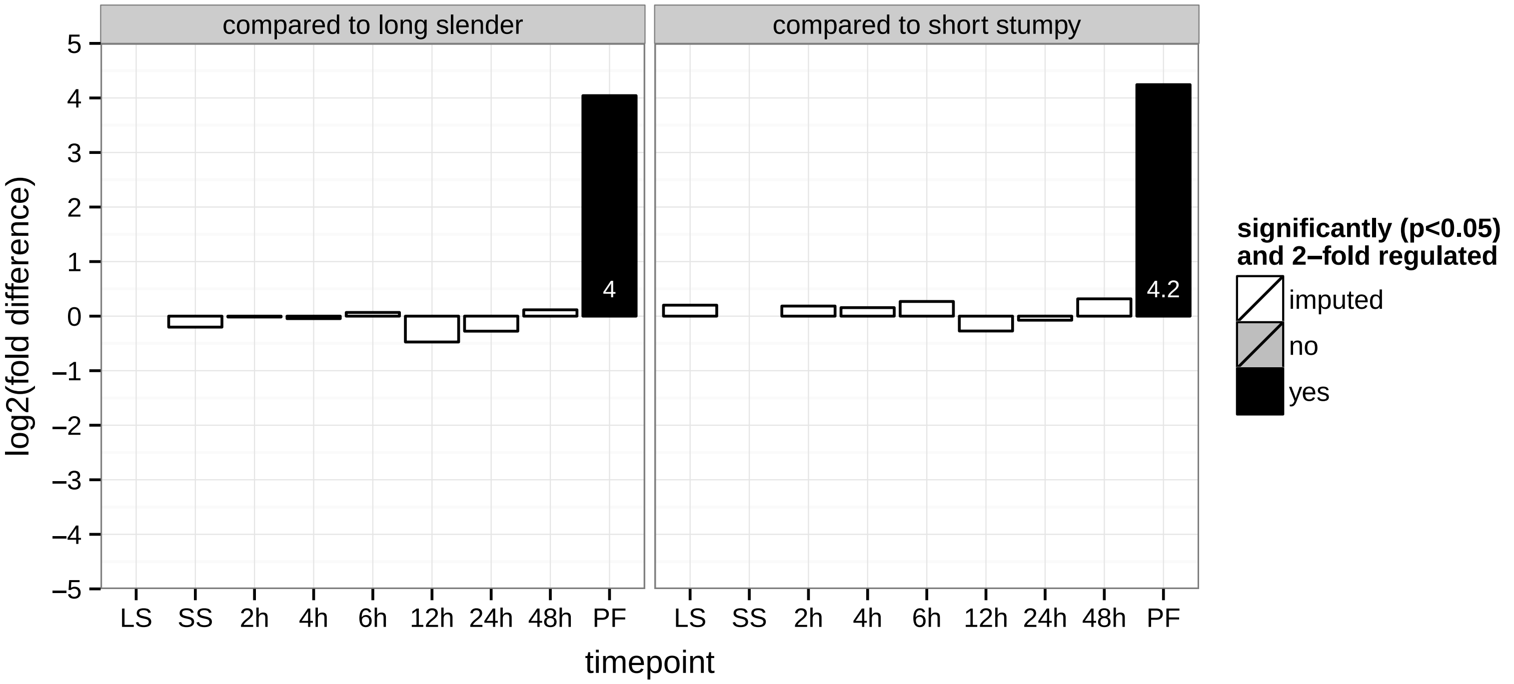
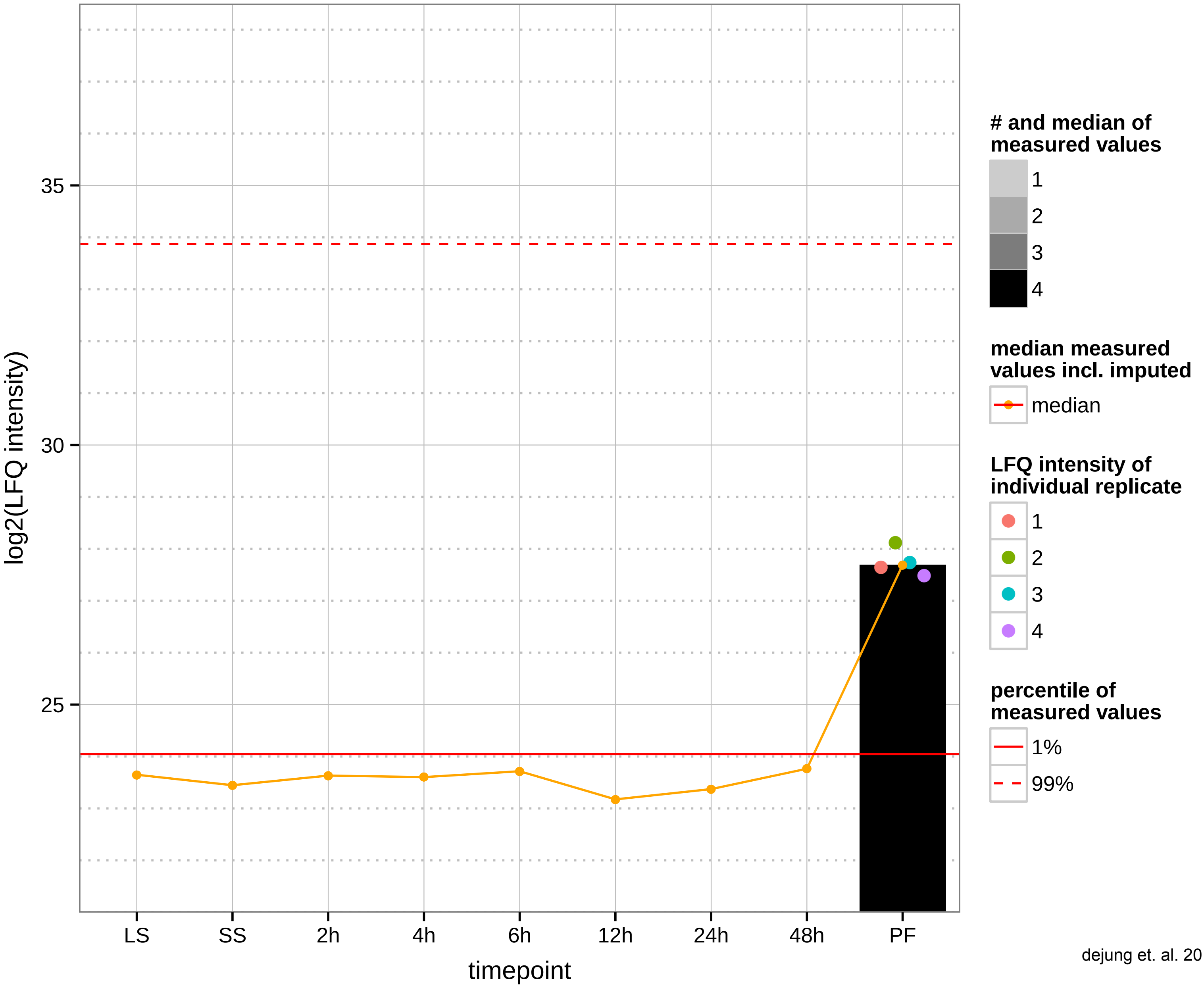
microtubule–associated protein, corset–associated protein 17 (CAP17)
Tb927.11.16200
AGOF: null
AGOC: microtubule cytoskeleton
AGOP: cytoskeleton organization
PGOF: null
PGOC: null
PGOP: null





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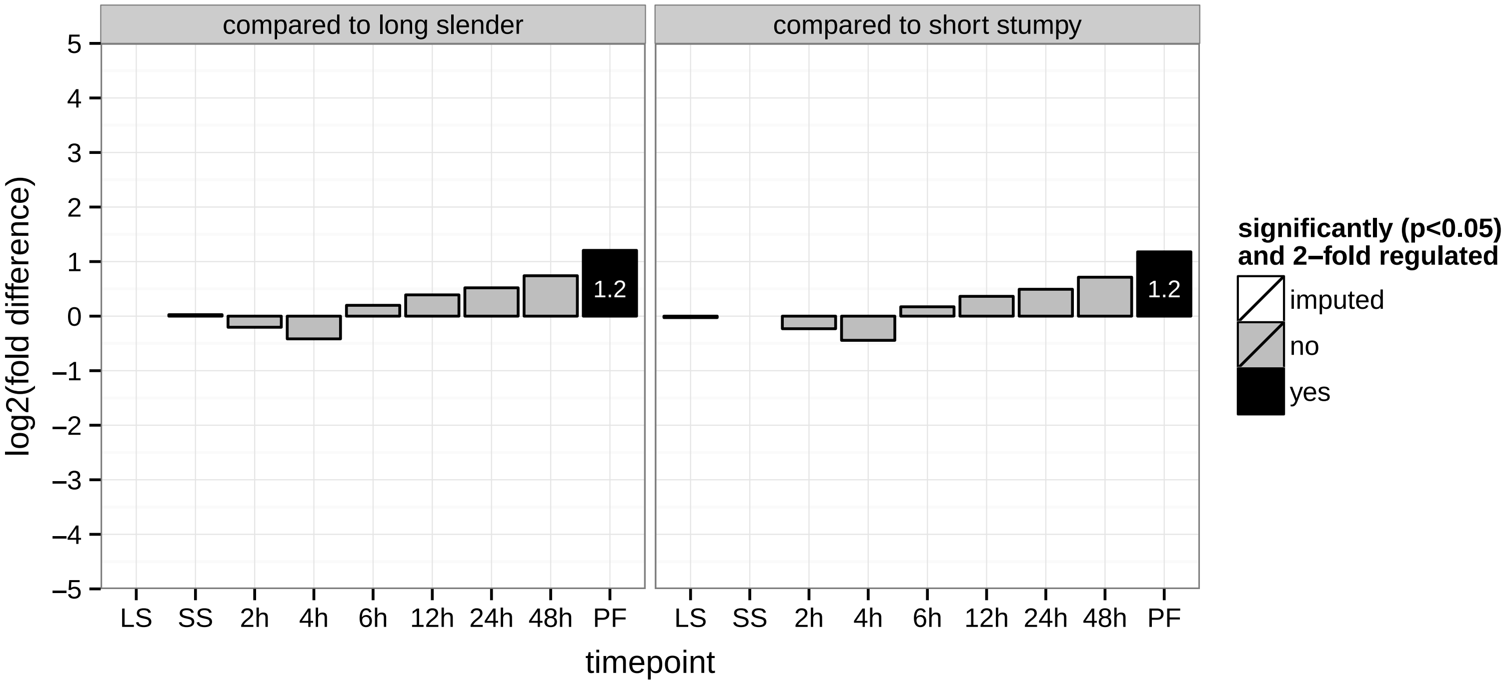
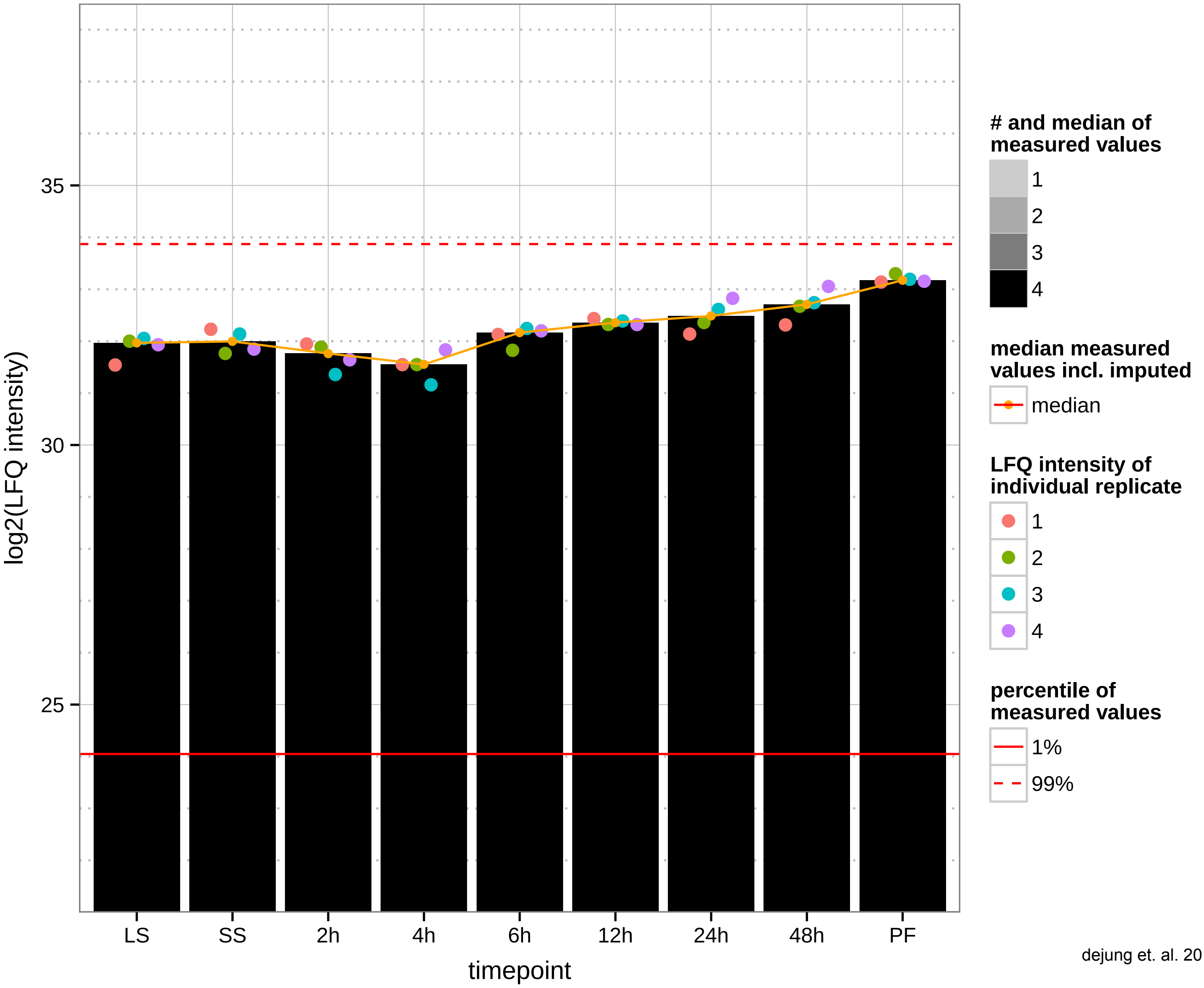
60S ribosomal protein L2, putative, 60S ribosomal protein L8
Tb927.5.1110;Tb927.11.16280
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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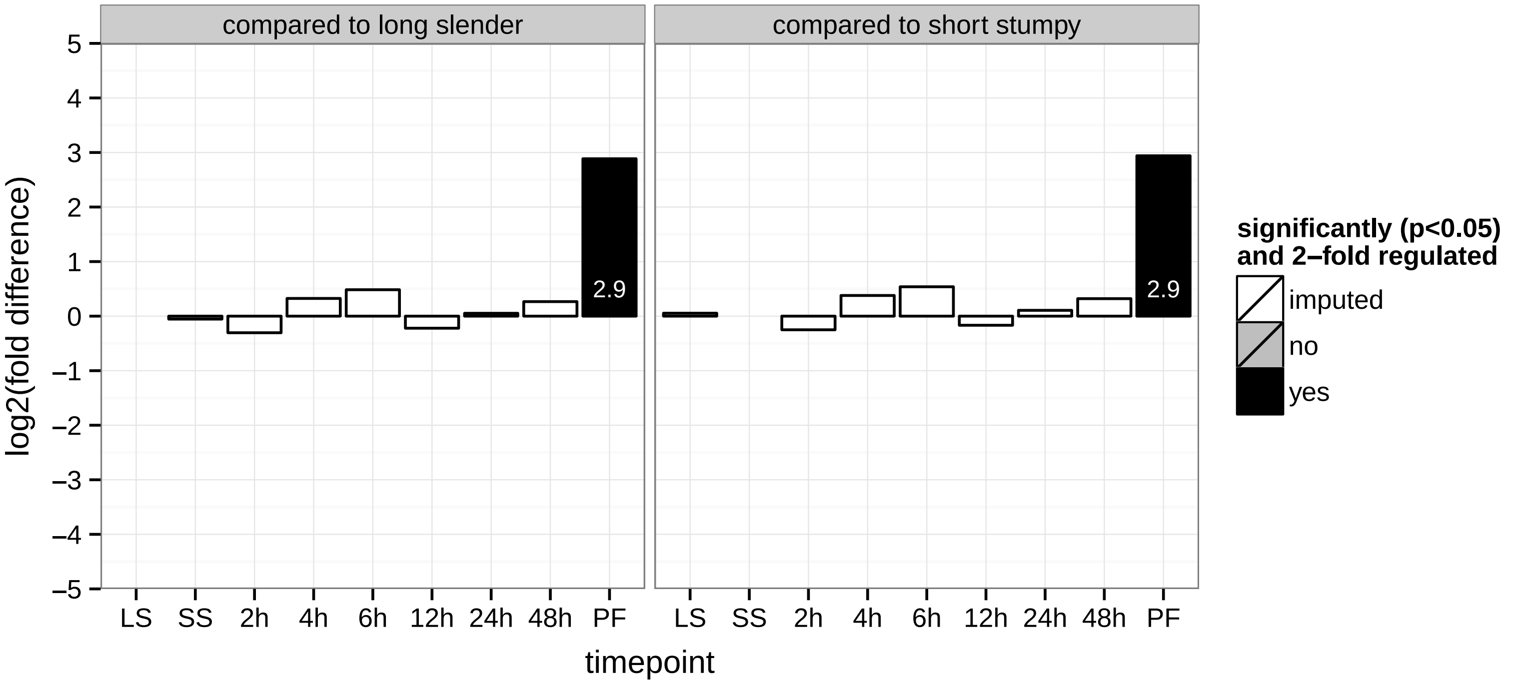
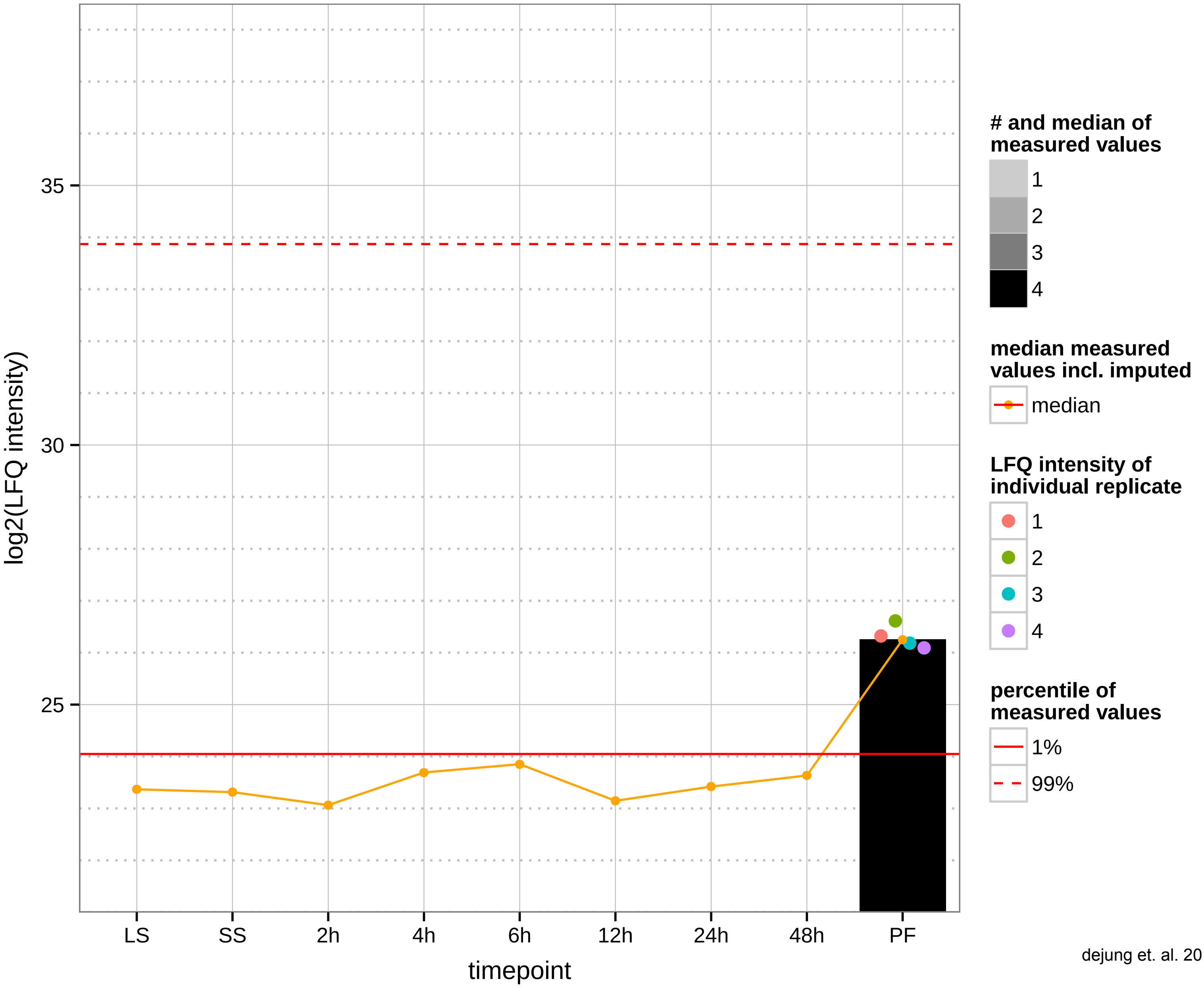
hypothetical protein, conserved
Tb927.11.16530
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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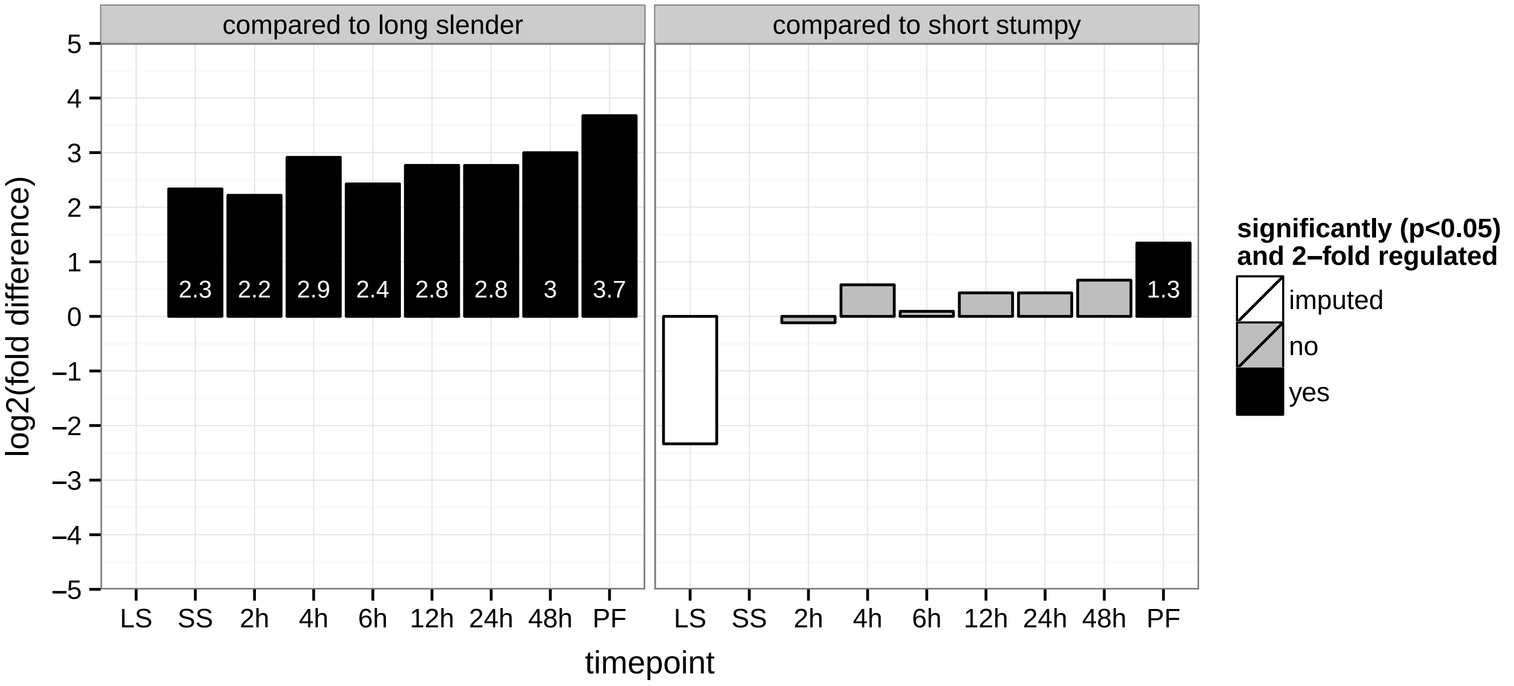
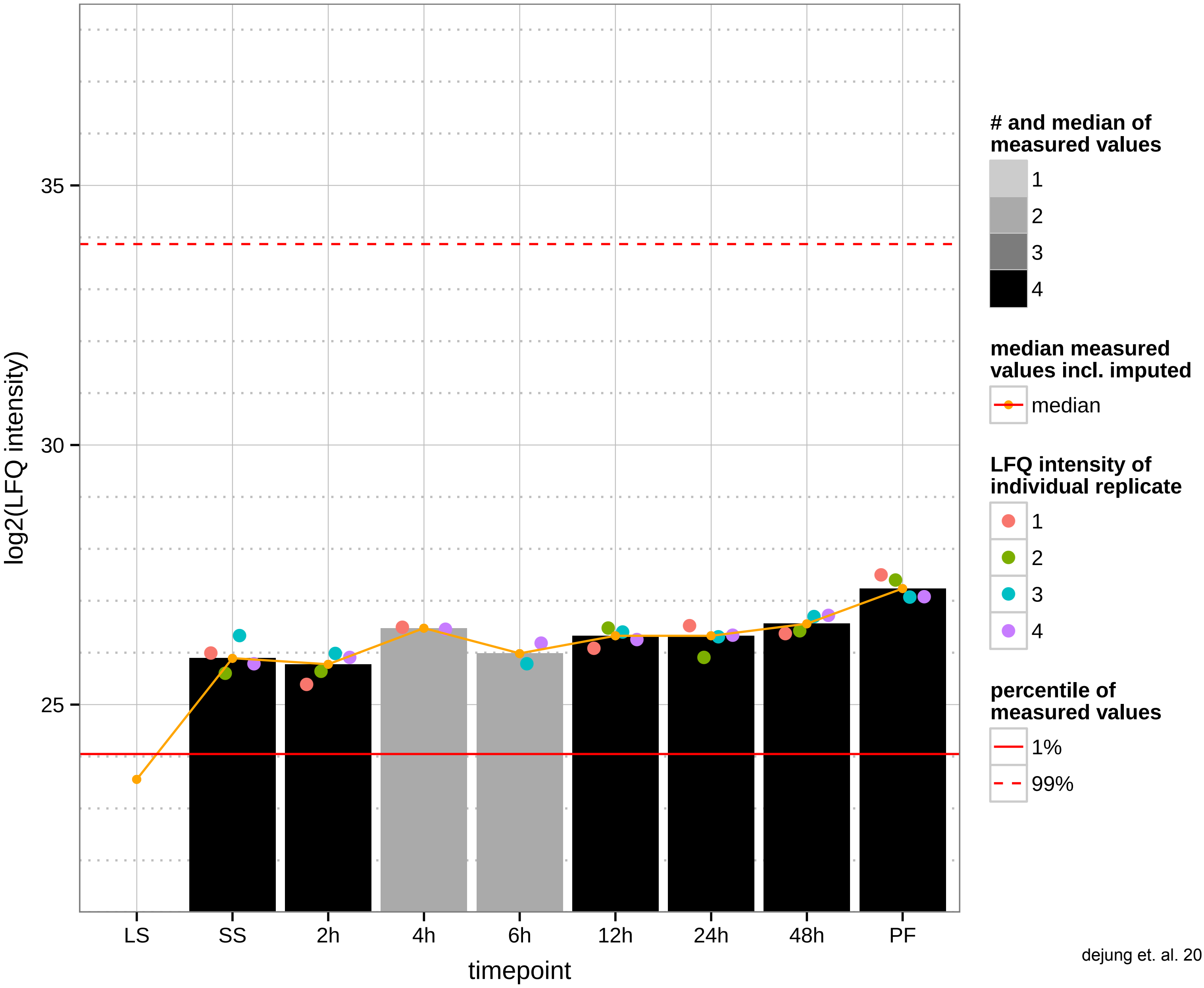
hypothetical protein, conserved
Tb927.11.16670
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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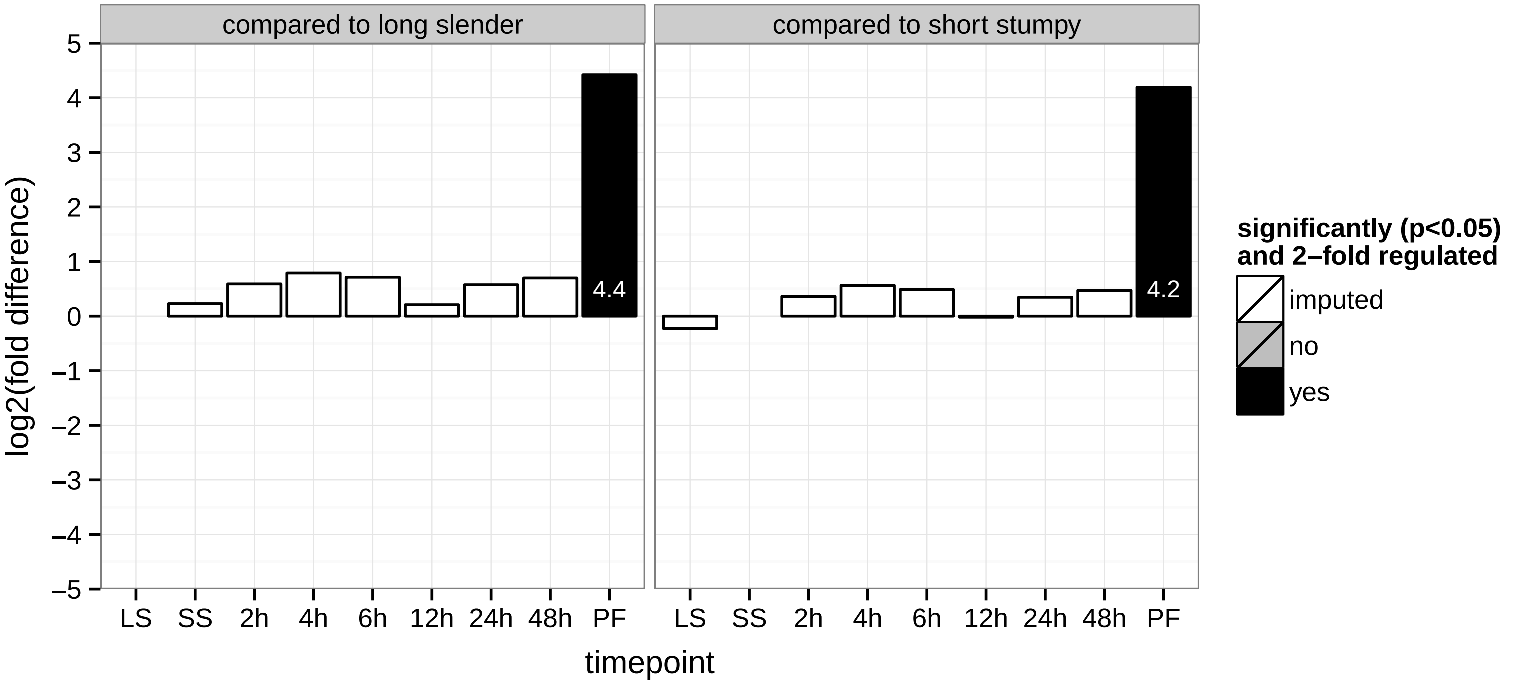
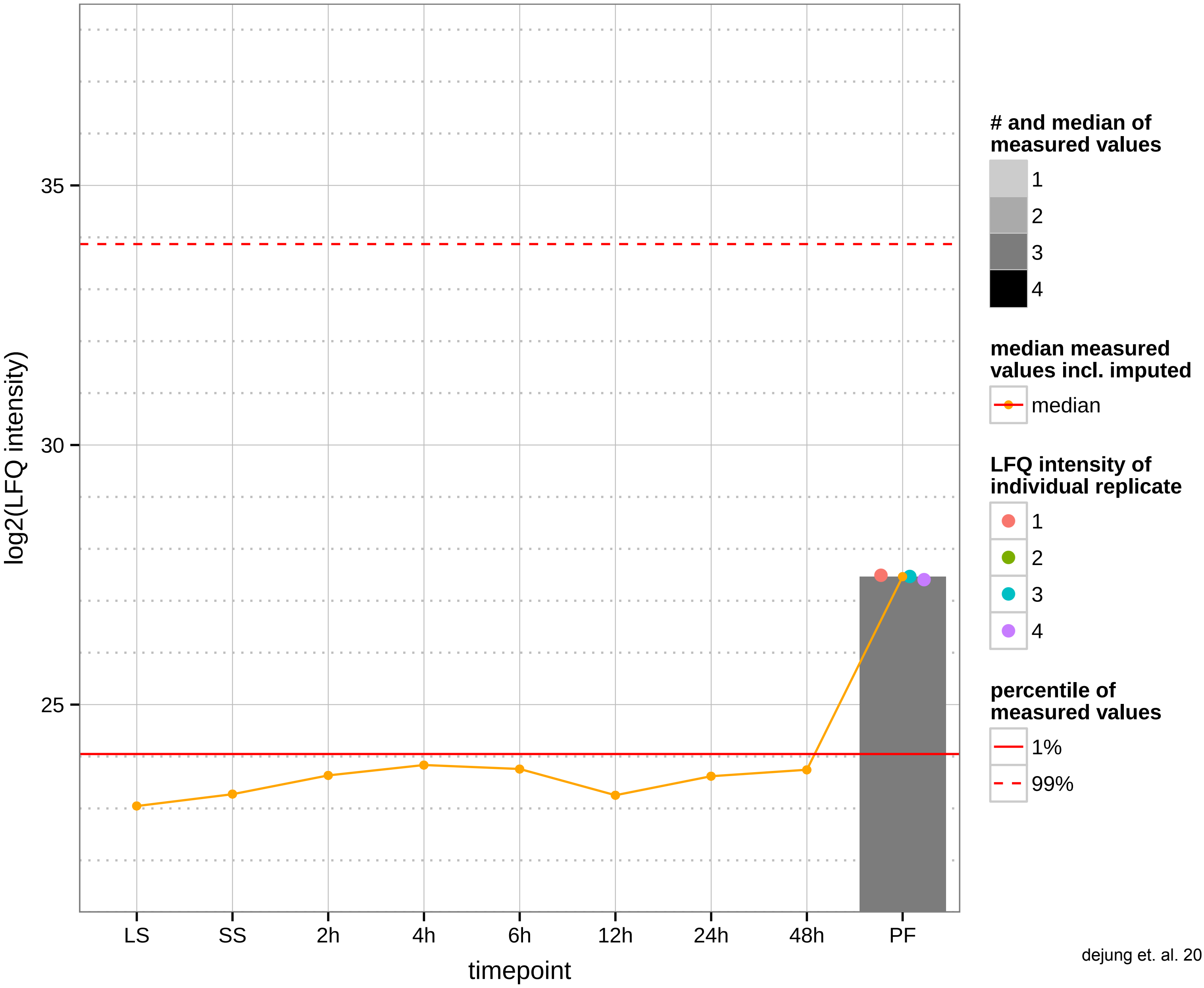
mitotic cyclin 6, cyclin 6 (CYC6)
Tb927.11.16720
AGOF: protein binding
AGOC: nuclear cyclin–dependent protein kinase holoenzyme complex, nucleus
AGOP: cytokinesis, regulation of cell cycle
PGOF: protein kinase binding
PGOC: nucleus
PGOP: regulation of cell cycle, regulation of cyclin–dependent protein kinase activity





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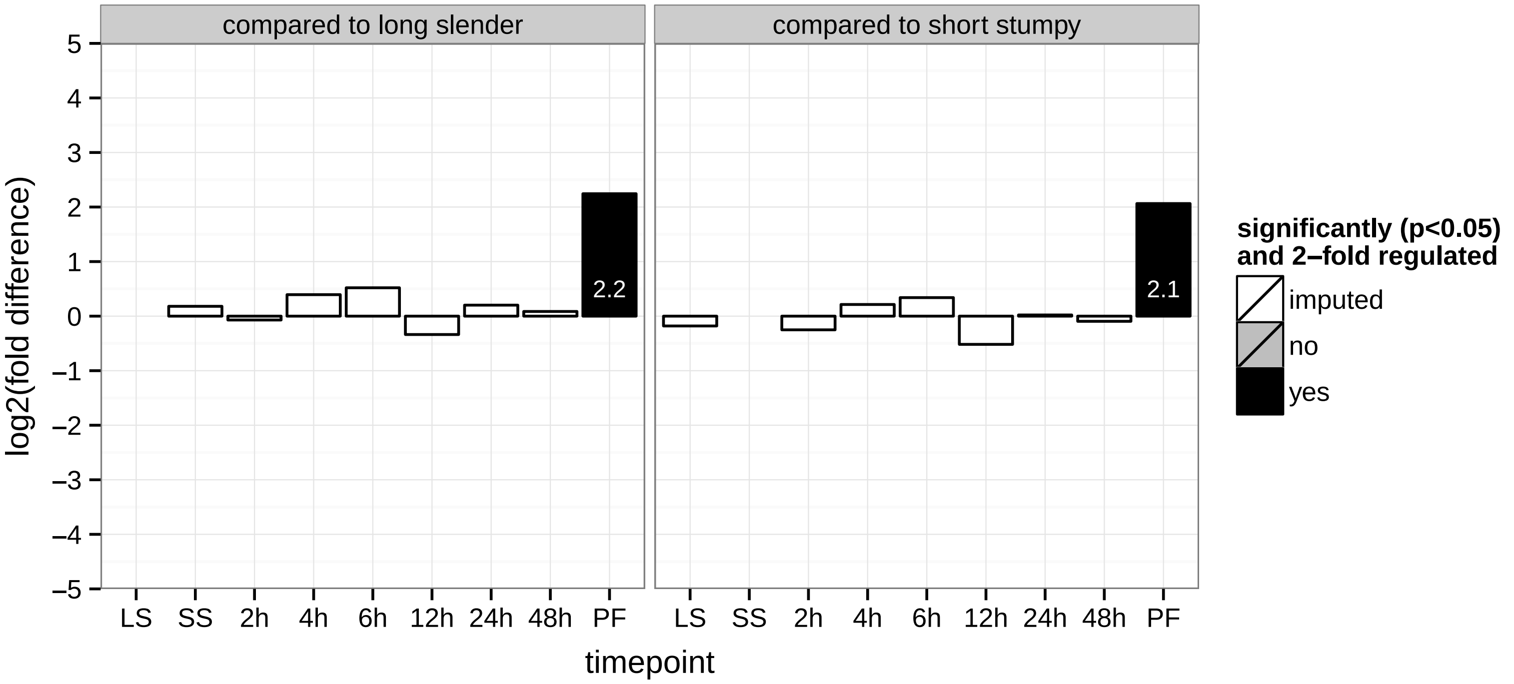
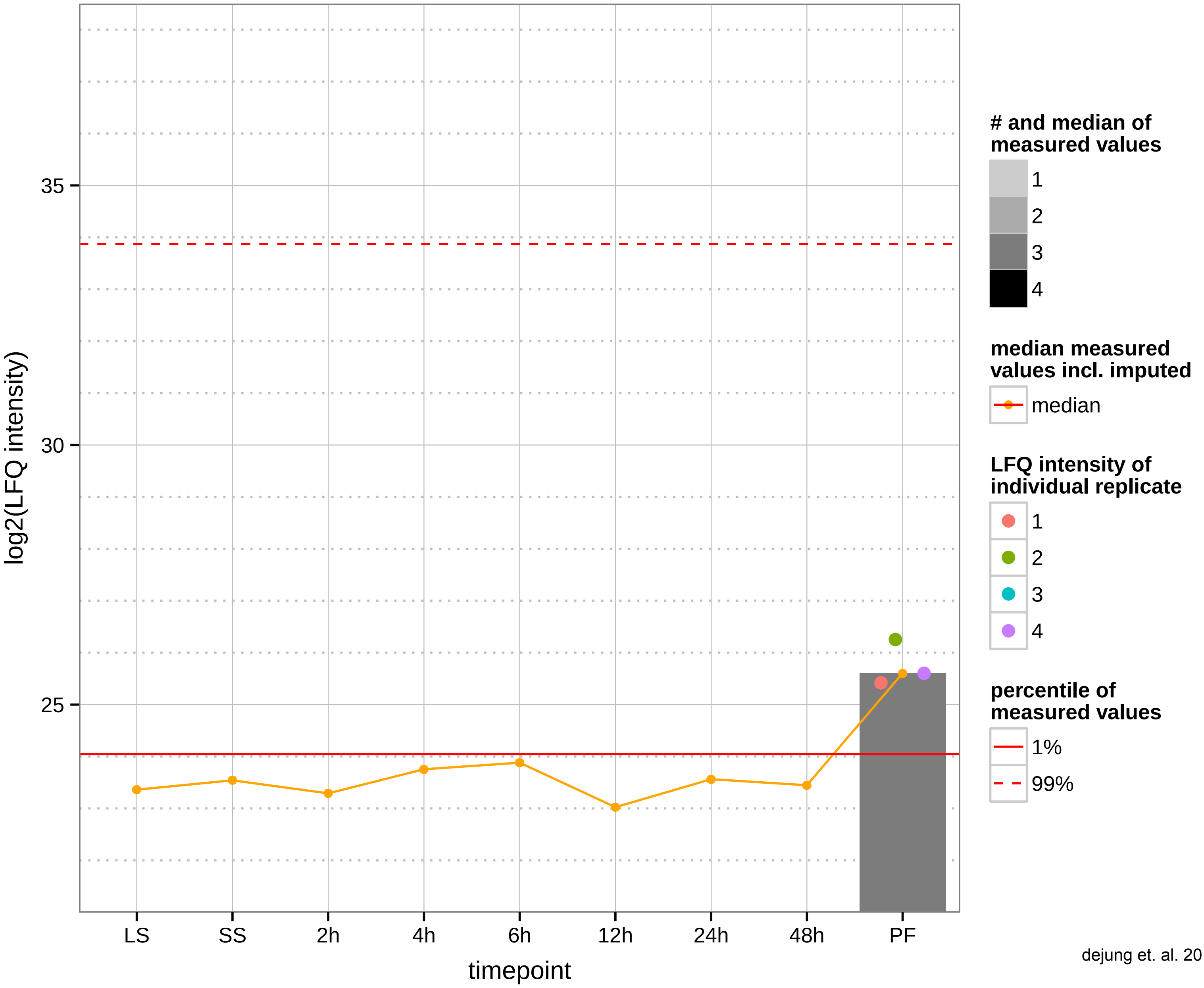
hypothetical protein, conserved
Tb927.11.16840.1;Tb927.11.16840.2
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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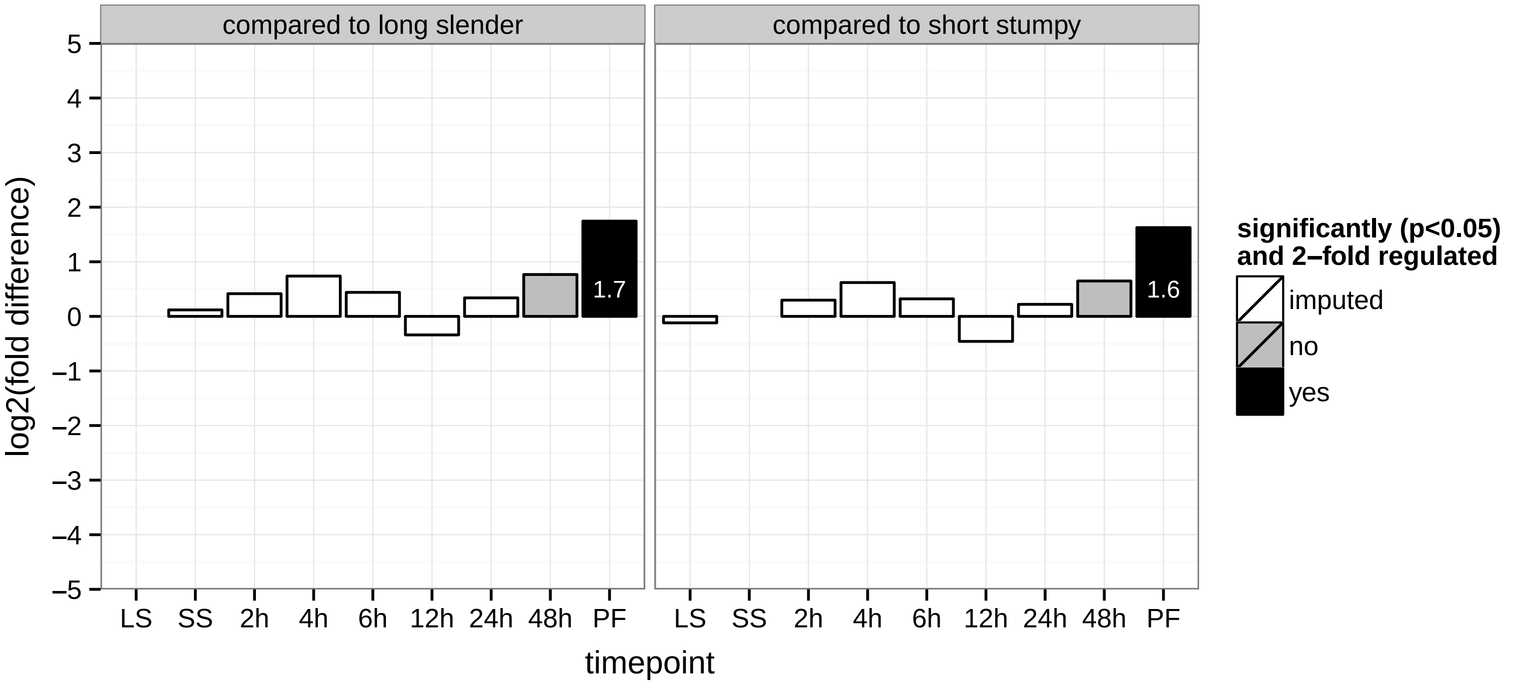
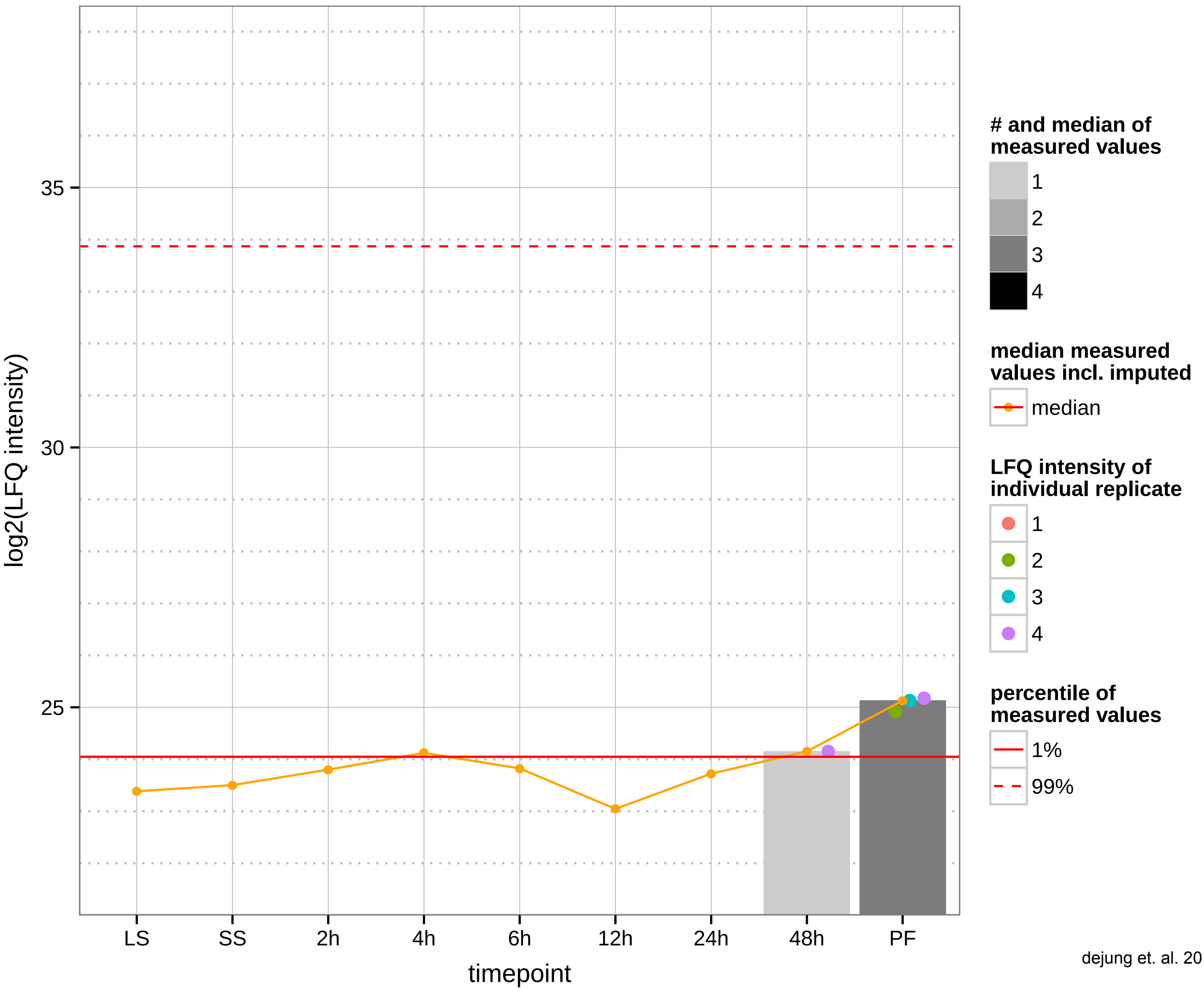
hypothetical protein
Tb927.11.1730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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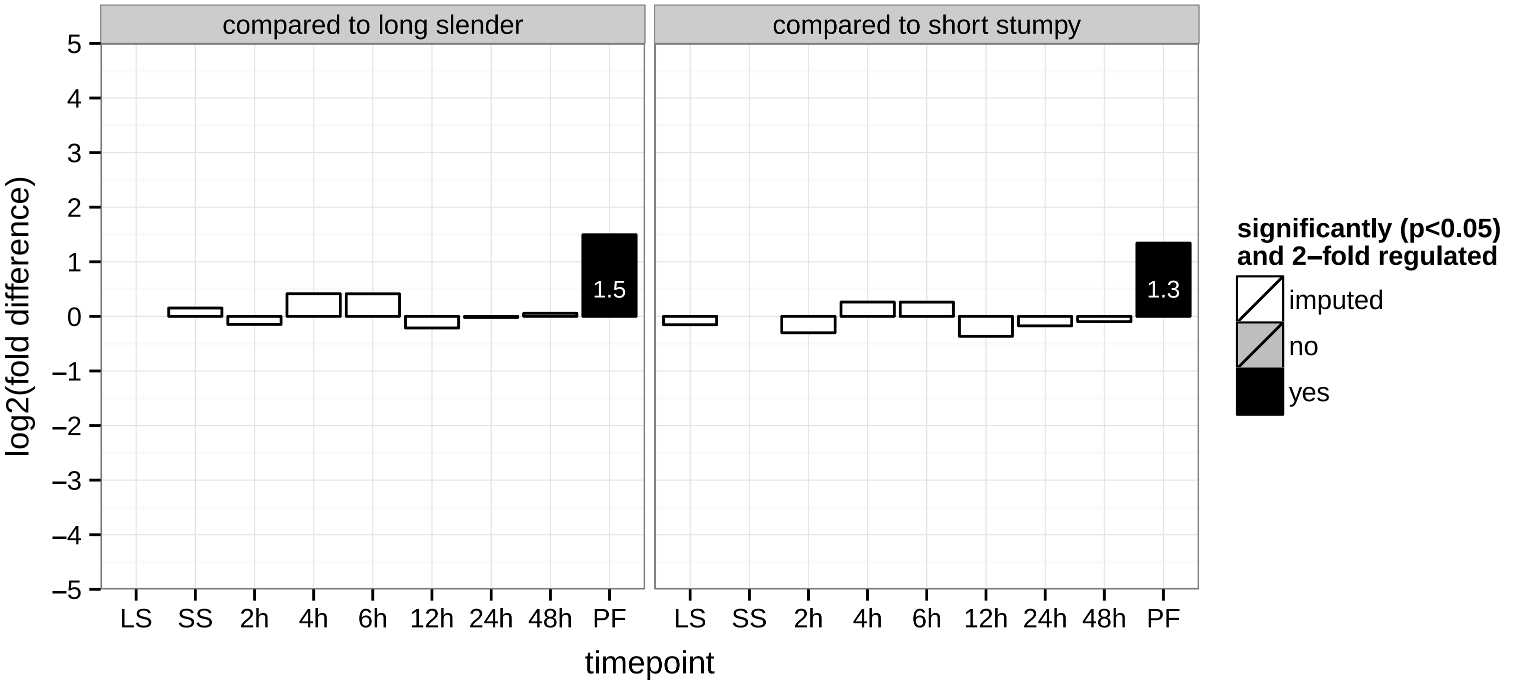
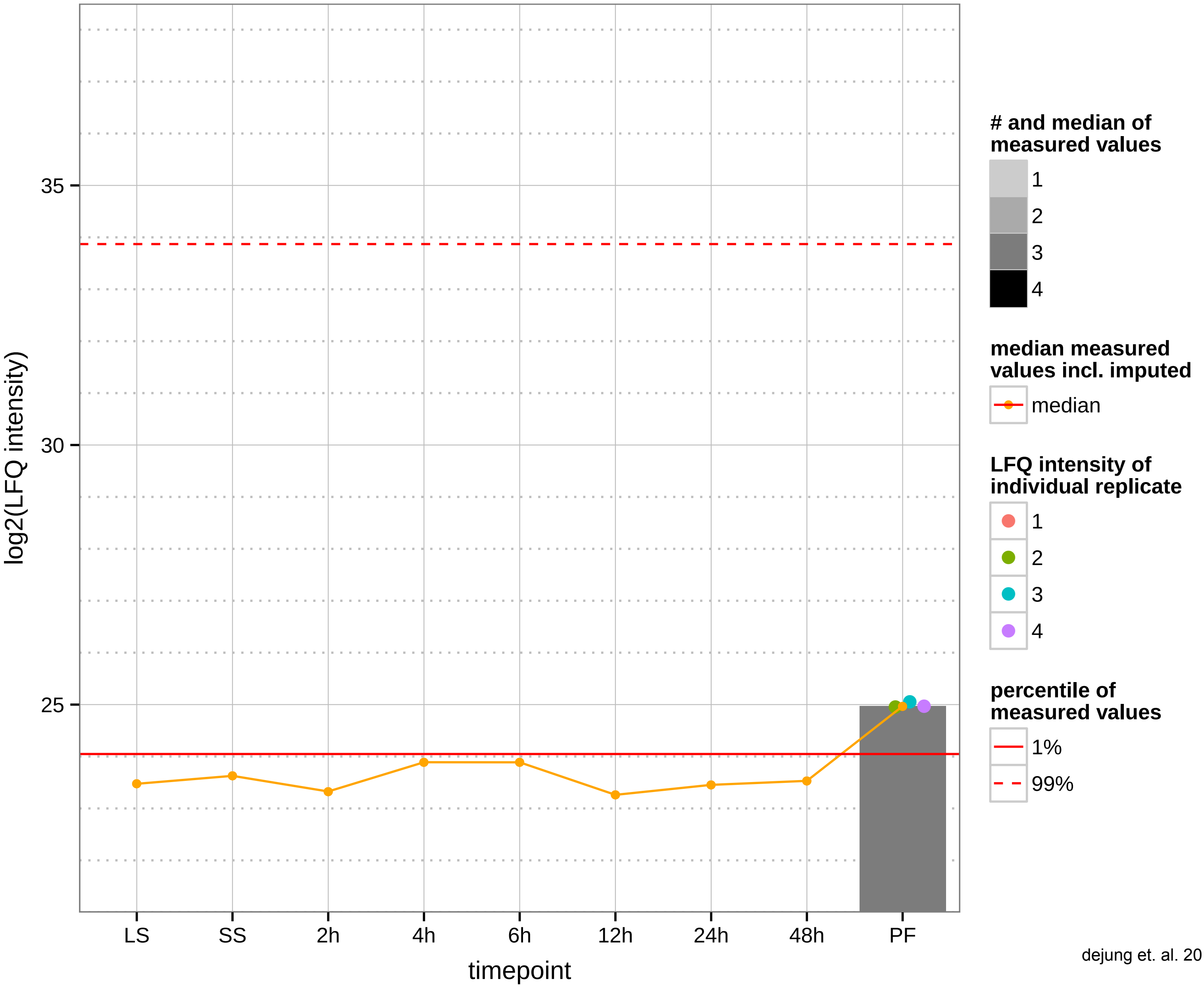
hypothetical protein, conserved
Tb927.11.2000
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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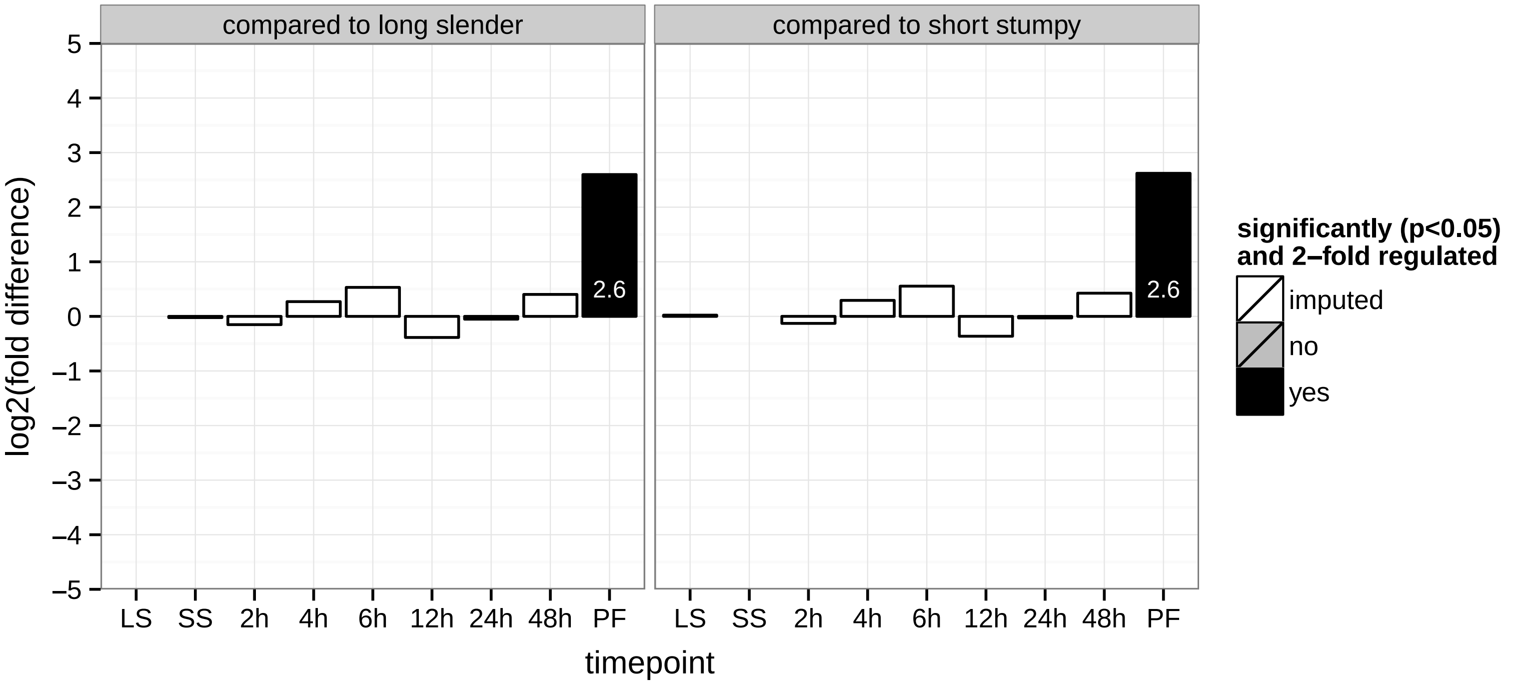
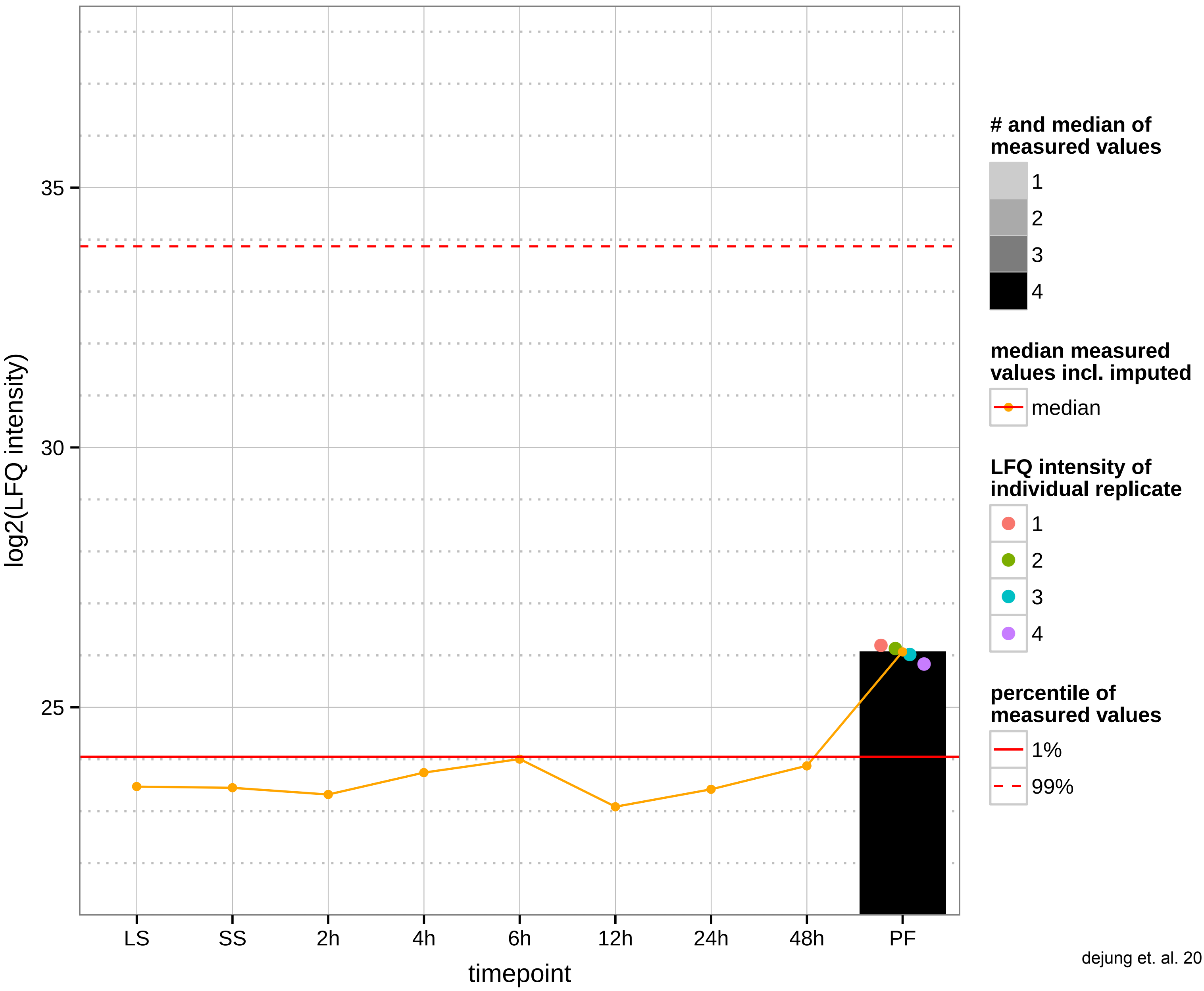
carnitine O–acetyltransferase, putative (CAT)
Tb927.11.2230
AGOF: carnitine O–acetyltransferase activity
AGOC: integral to membrane
AGOP: generation of precursor metabolites and energy
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: null





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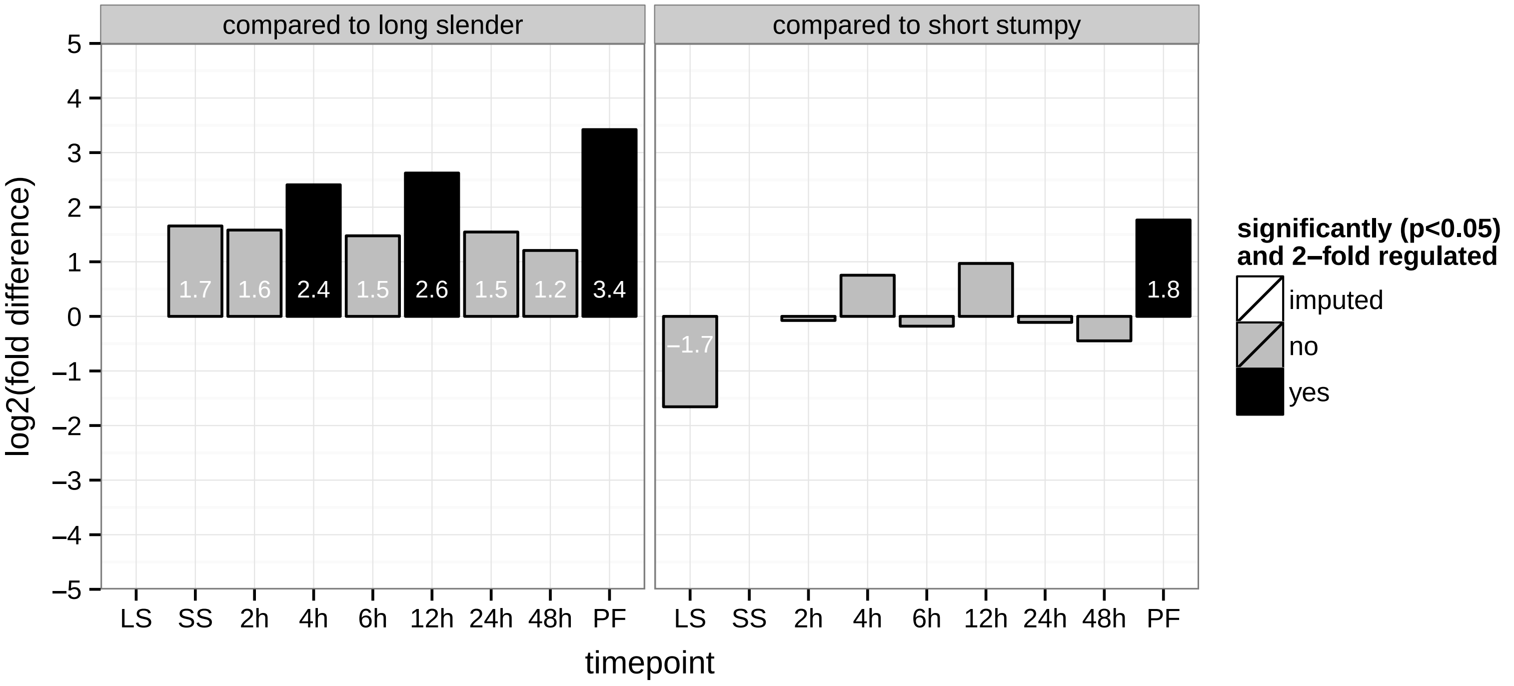
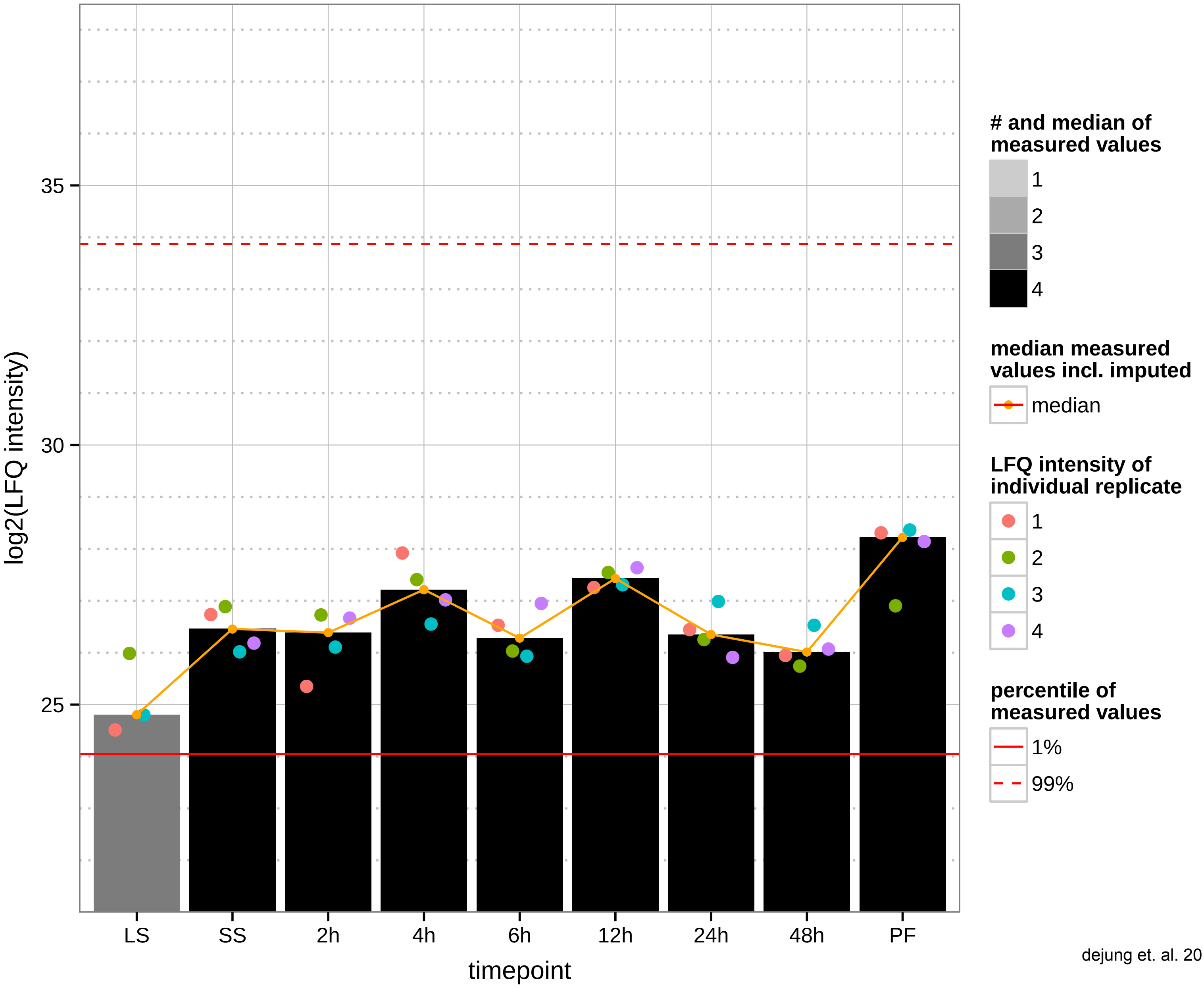
hypothetical protein, conserved
Tb927.11.2250
AGOF: null
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, quorum sensing involved in interaction with ho
PGOF: null
PGOC: null
PGOP: null





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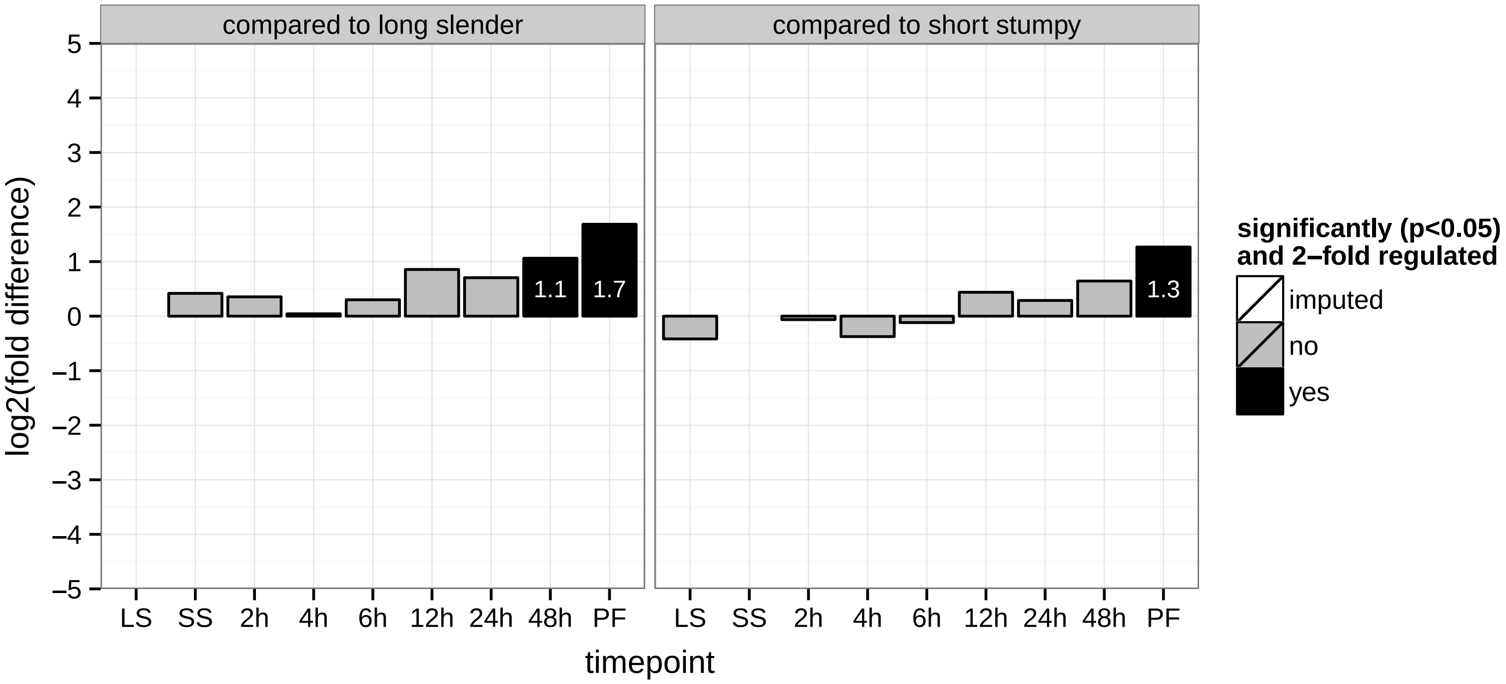
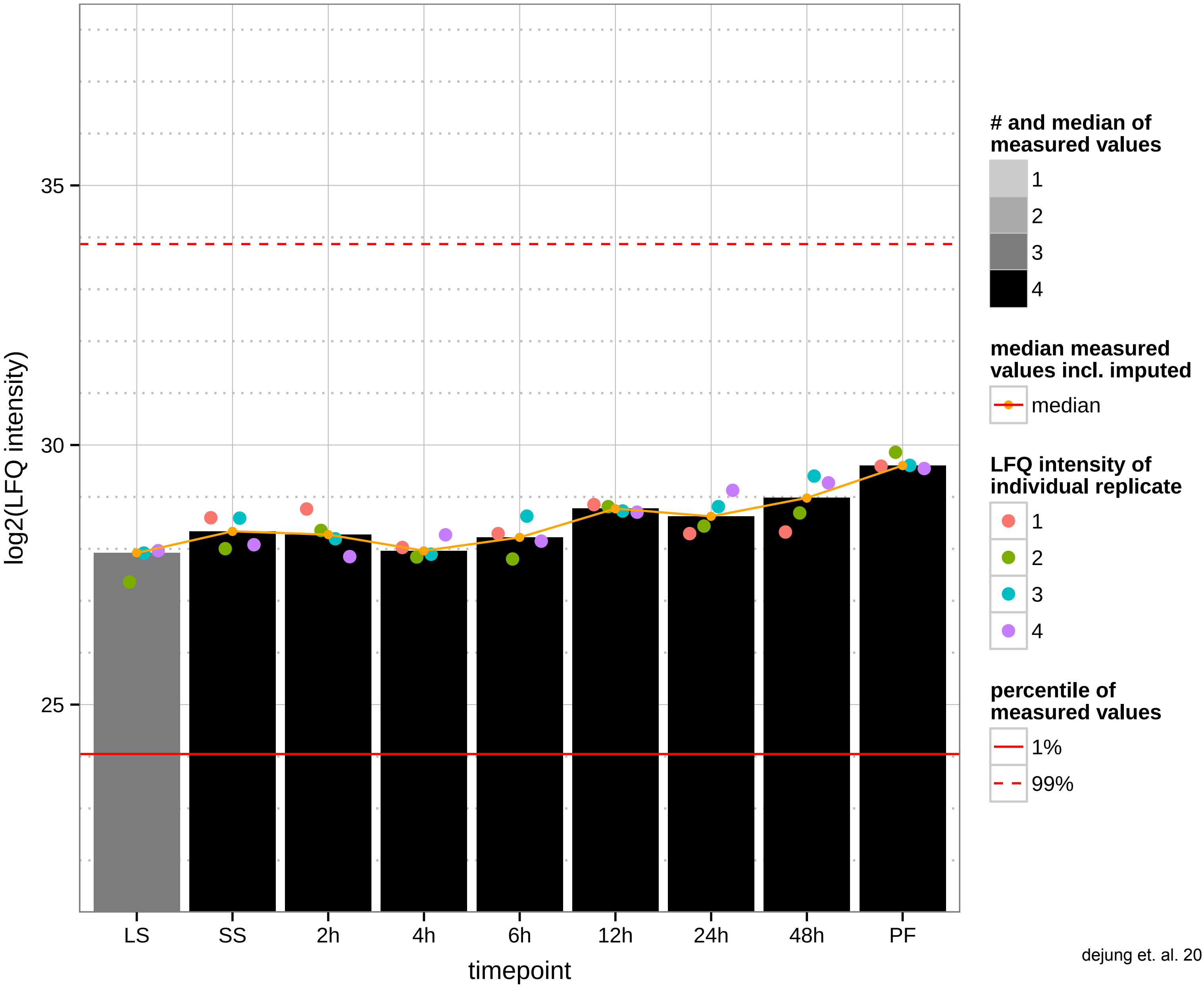
aminopeptidase, putative, metallo–peptidase, Clan MF, Family M17
Tb927.11.2470
AGOF: aminopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: aminopeptidase activity
PGOC: intracellular
PGOP: proteolysis





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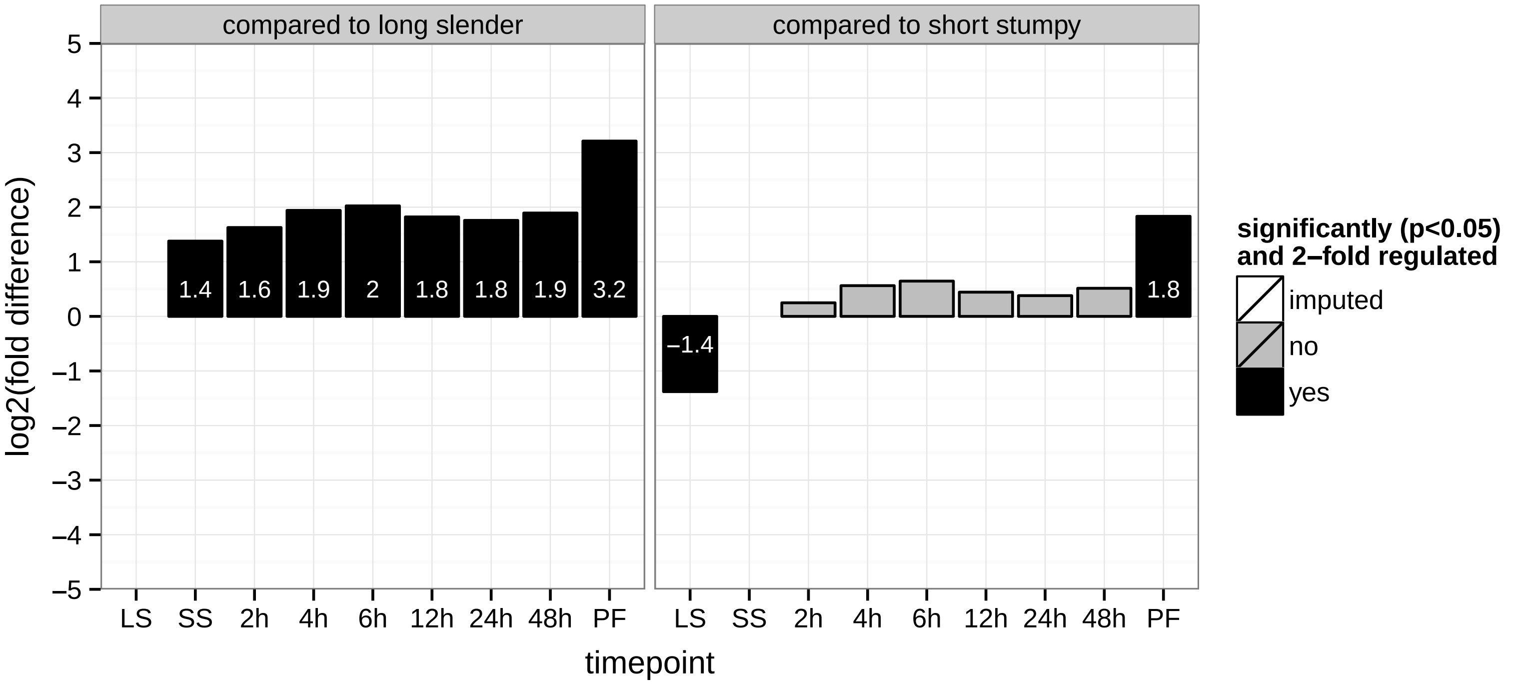
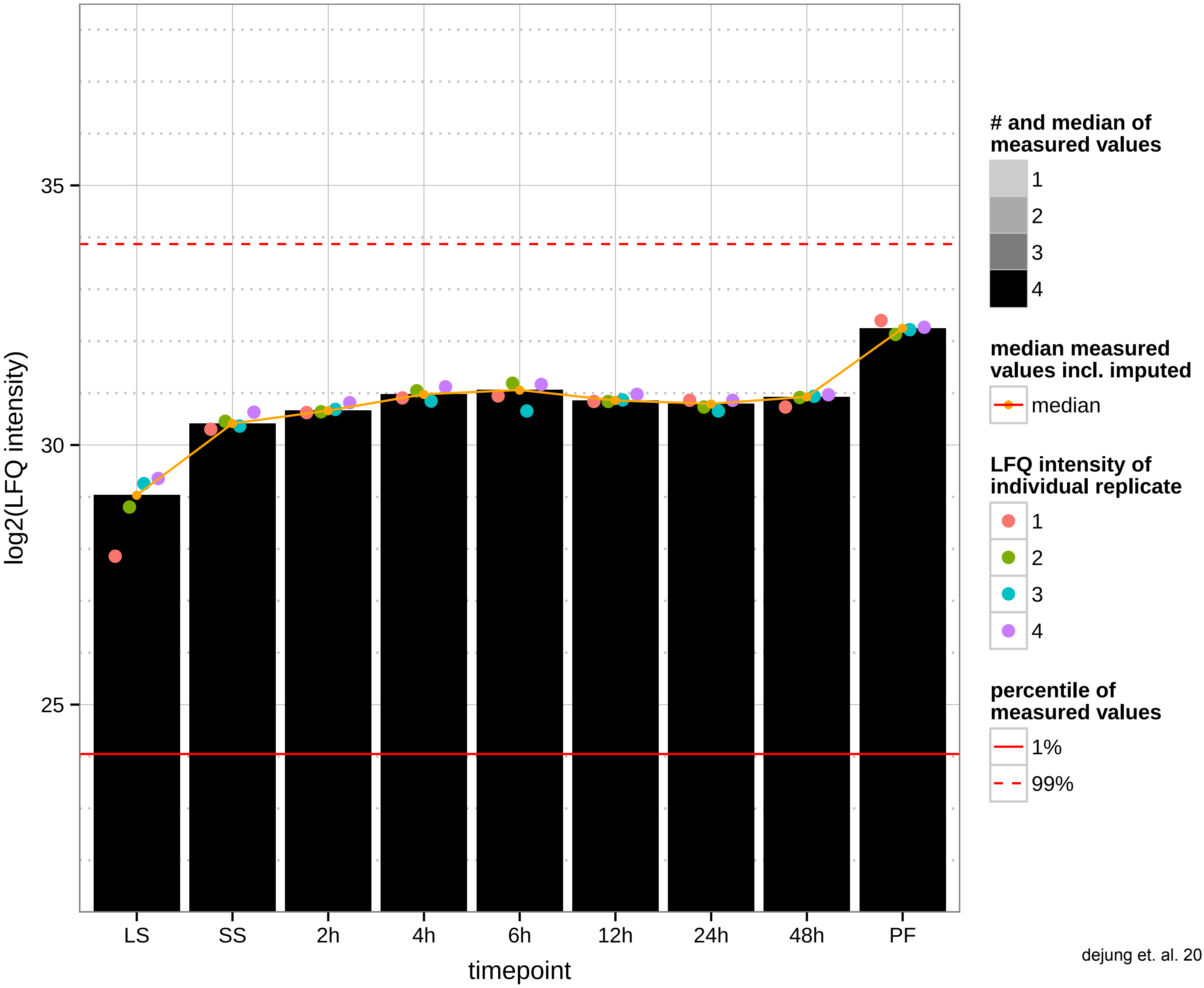
carboxypeptidase, putative, metallo–peptidase, Clan MA(E) Family M32
Tb927.11.2500
AGOF: metallocarboxypeptidase activity
AGOC: cytosol
AGOP: peptide metabolic process, proteolysis
PGOF: metallocarboxypeptidase activity
PGOC: null
PGOP: proteolysis





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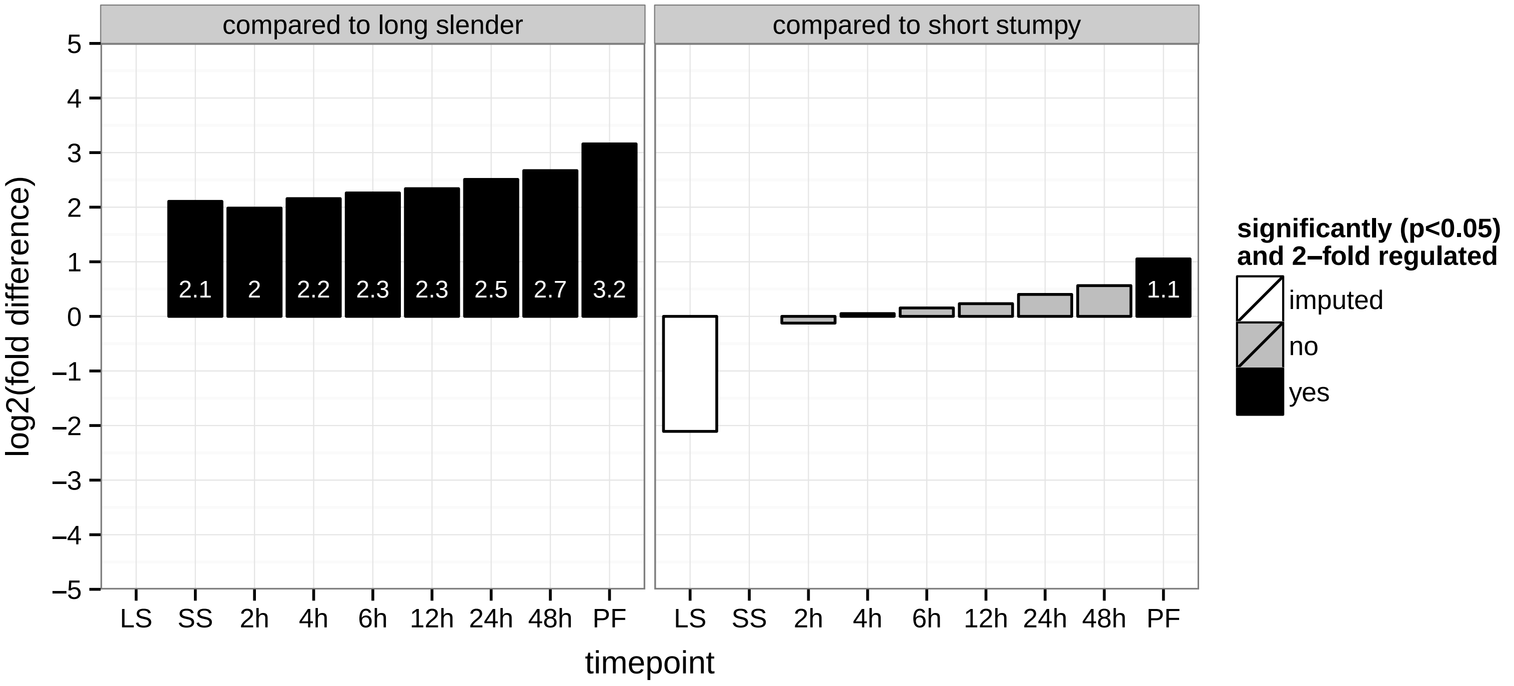
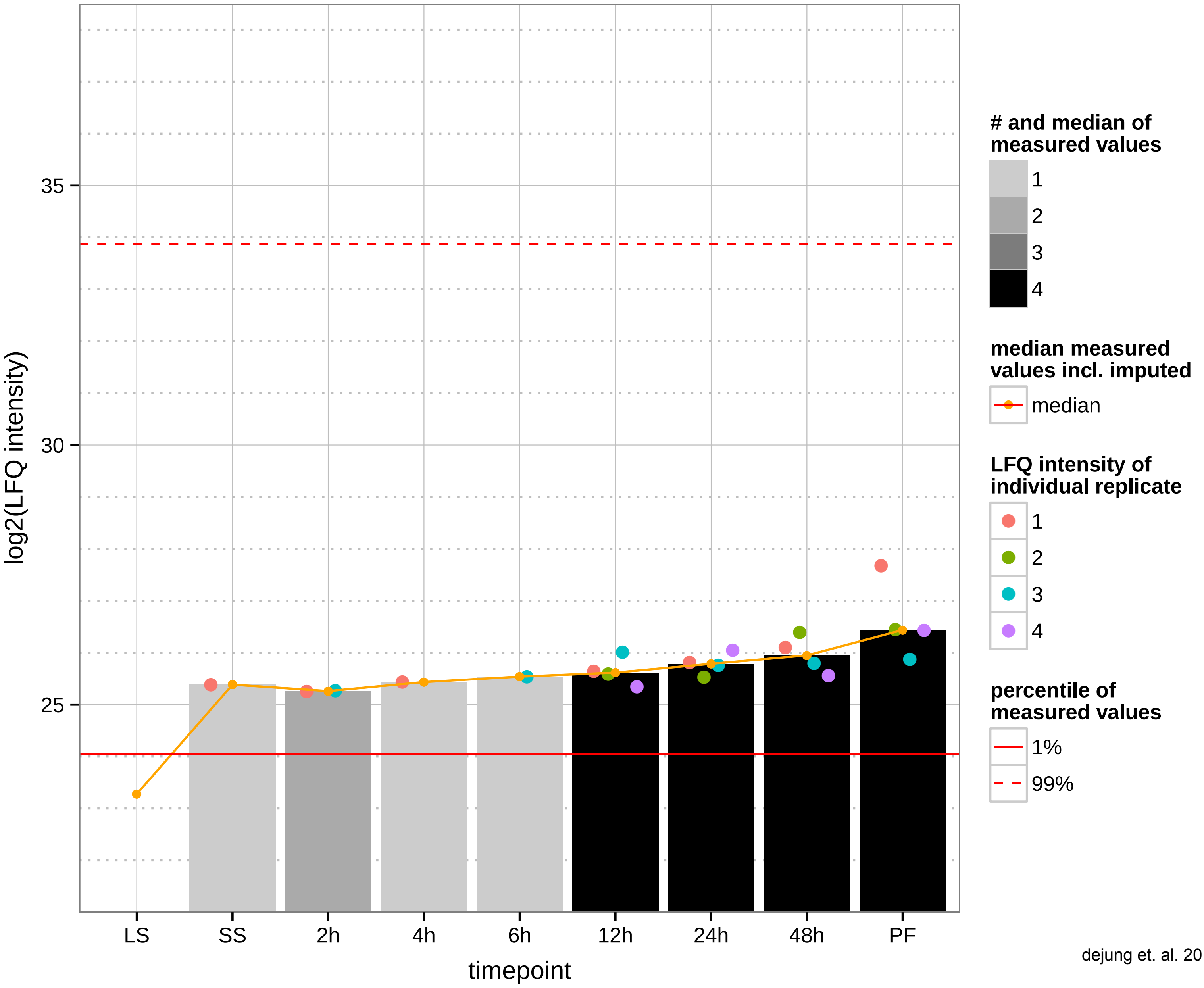
mitochondrial carrier protein (MCP10)
Tb927.11.270
AGOF: transporter activity
AGOC: mitochondrial inner membrane, mitochondrial part
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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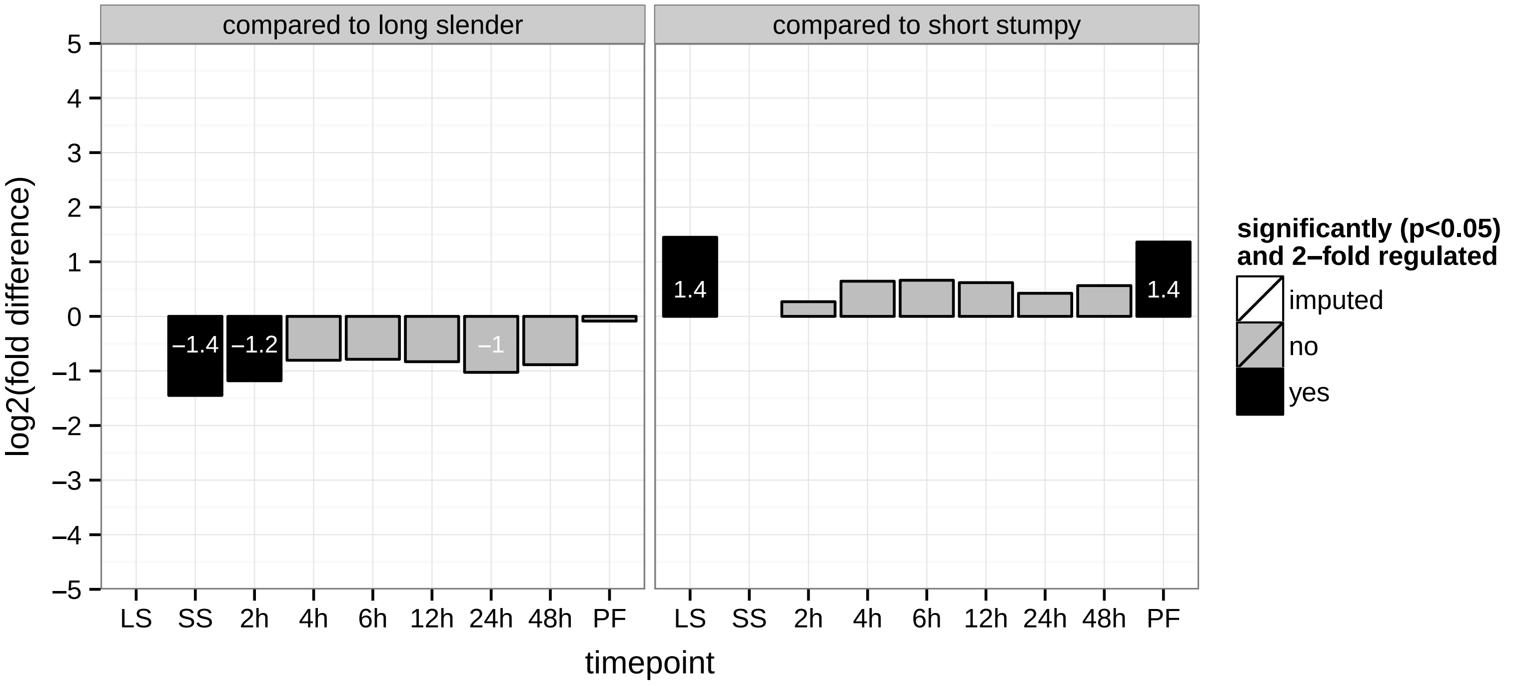
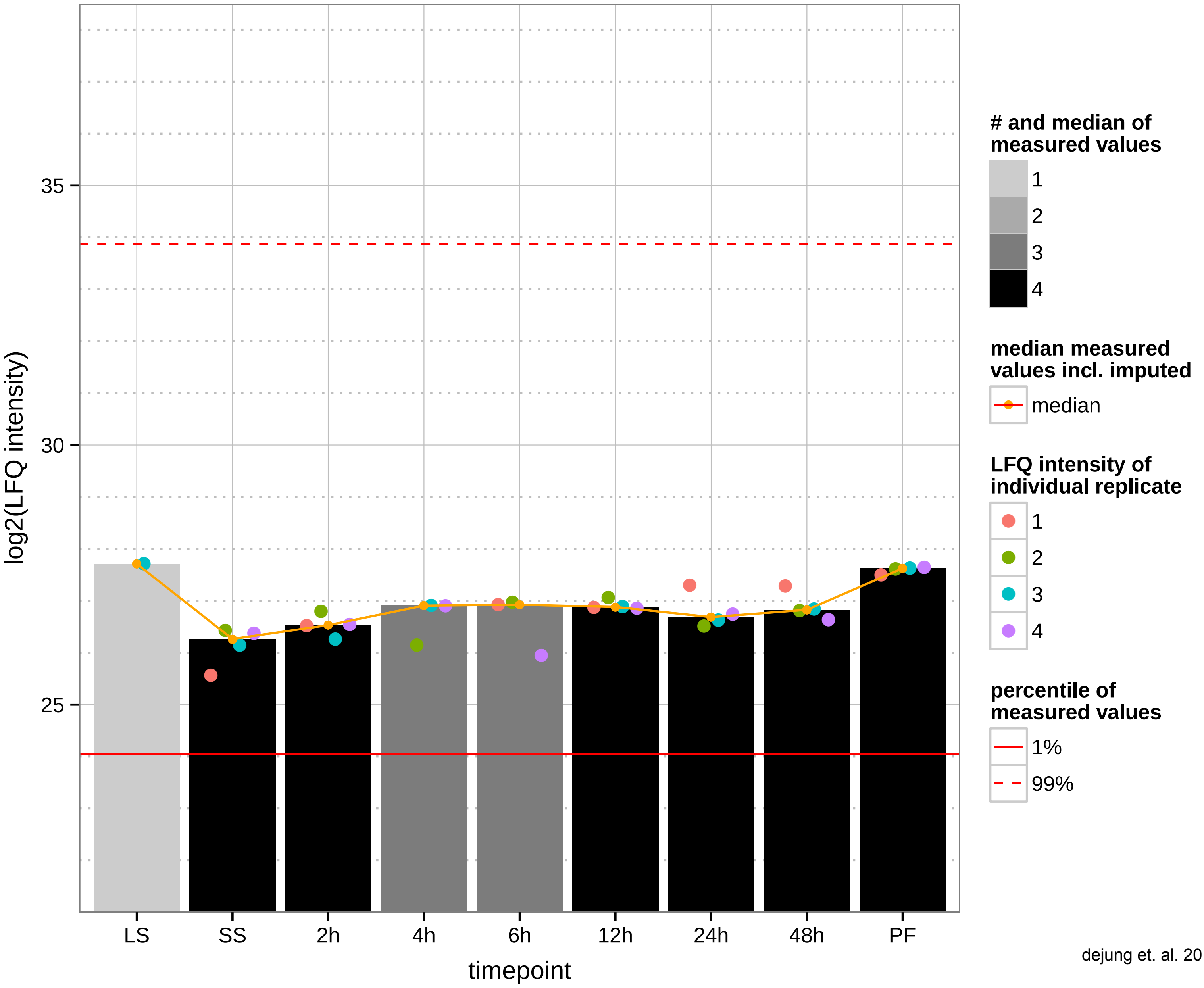
hypothetical protein, conserved
Tb927.11.2940
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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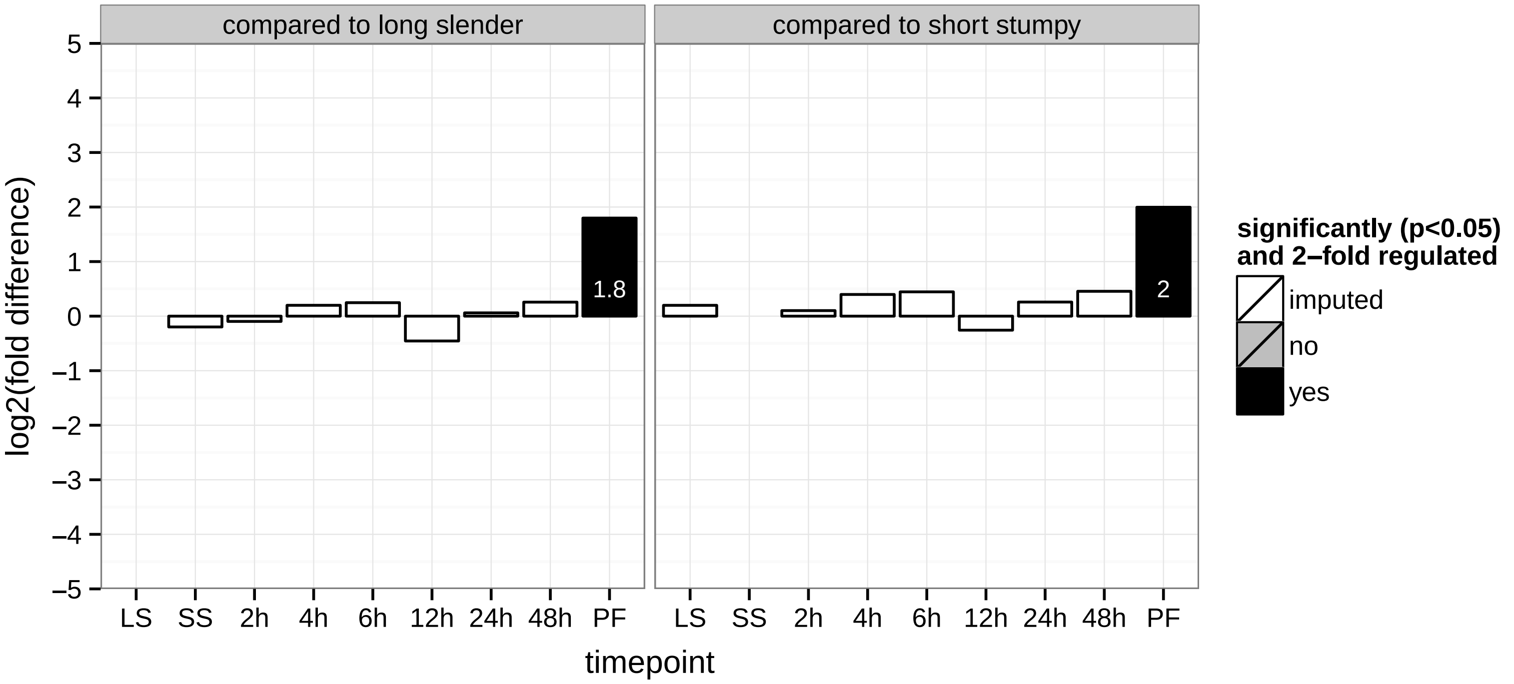
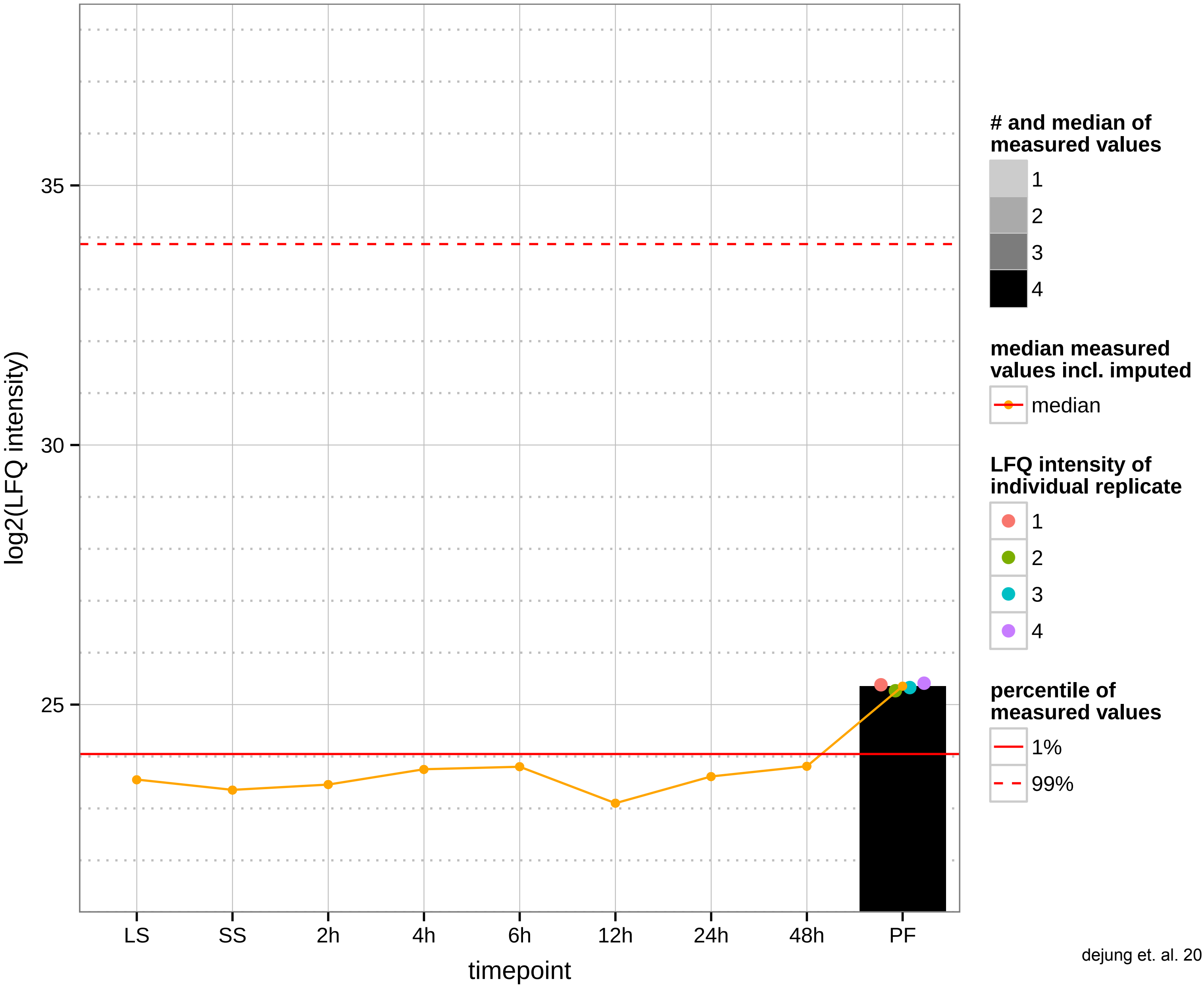
hypothetical protein, conserved
Tb927.11.3060
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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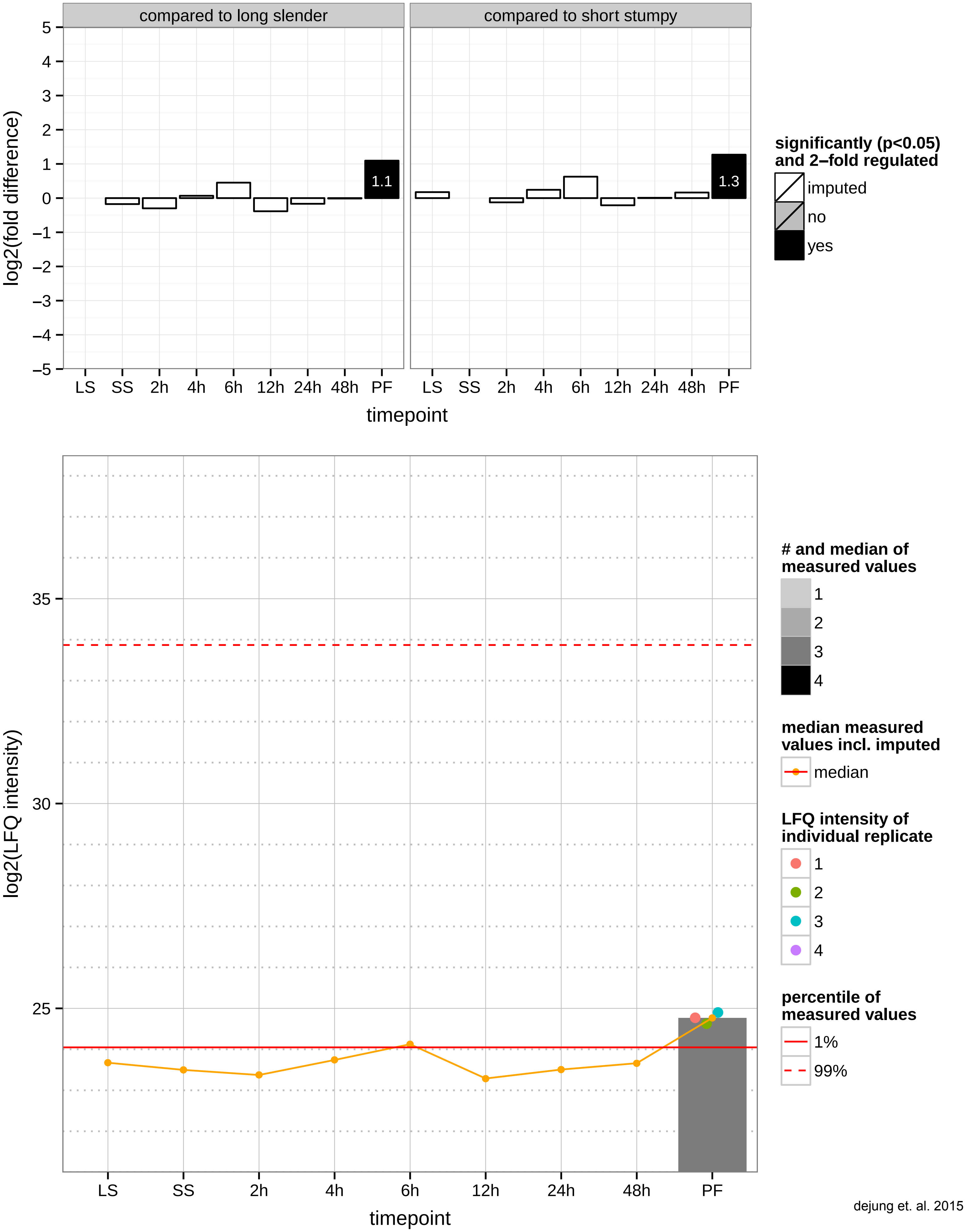
hypothetical protein, conserved
Tb927.11.3110
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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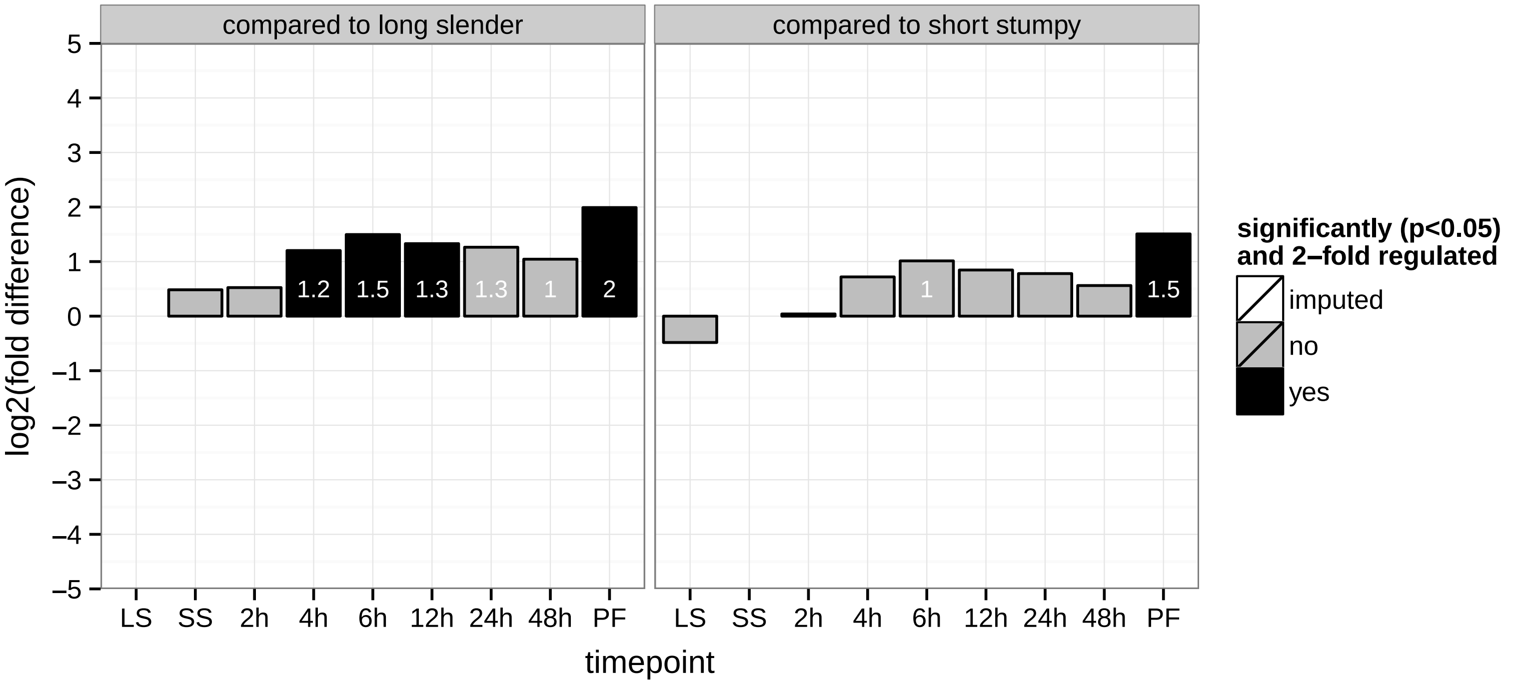
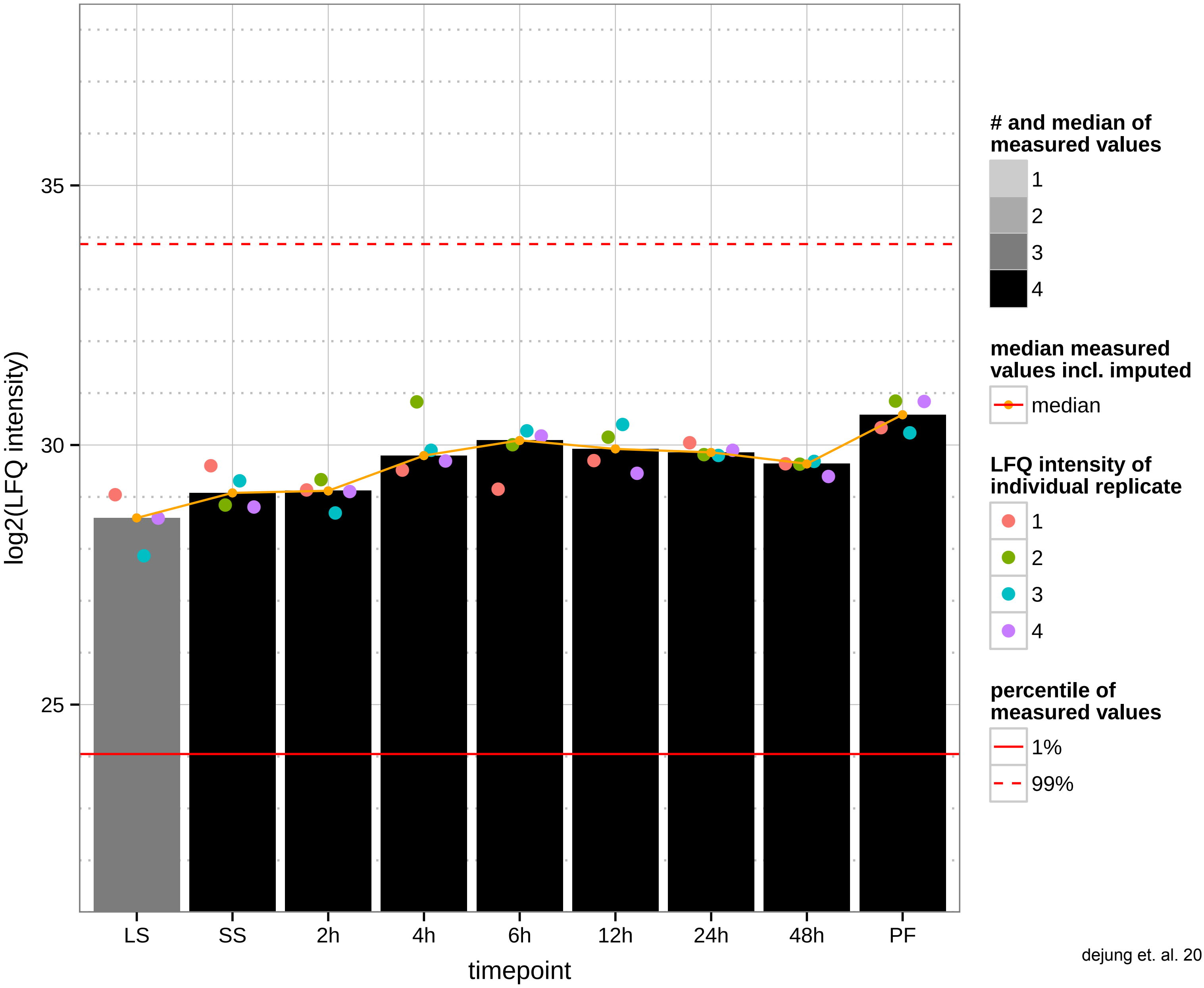
Nucleoporin, Myosin–like protein (TbMlp–1)
Tb927.11.330
AGOF: null
AGOC: nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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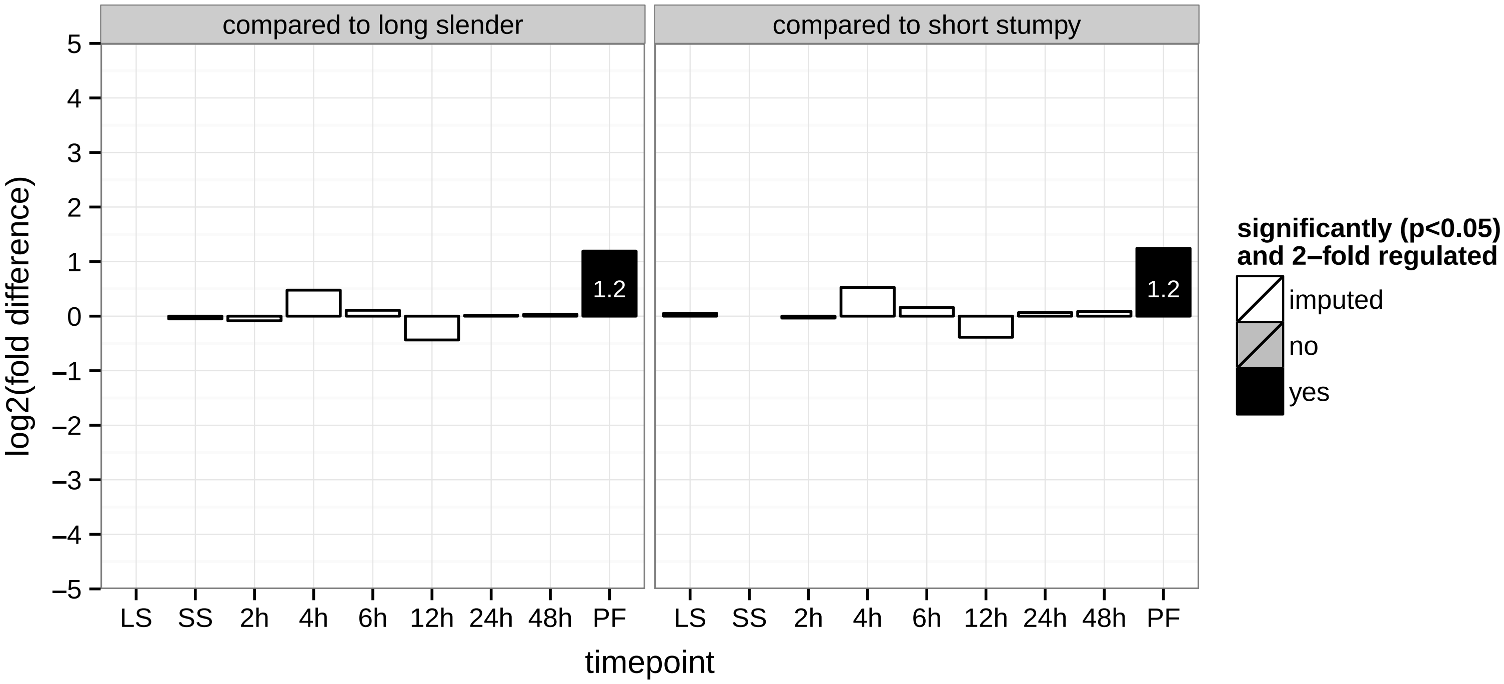
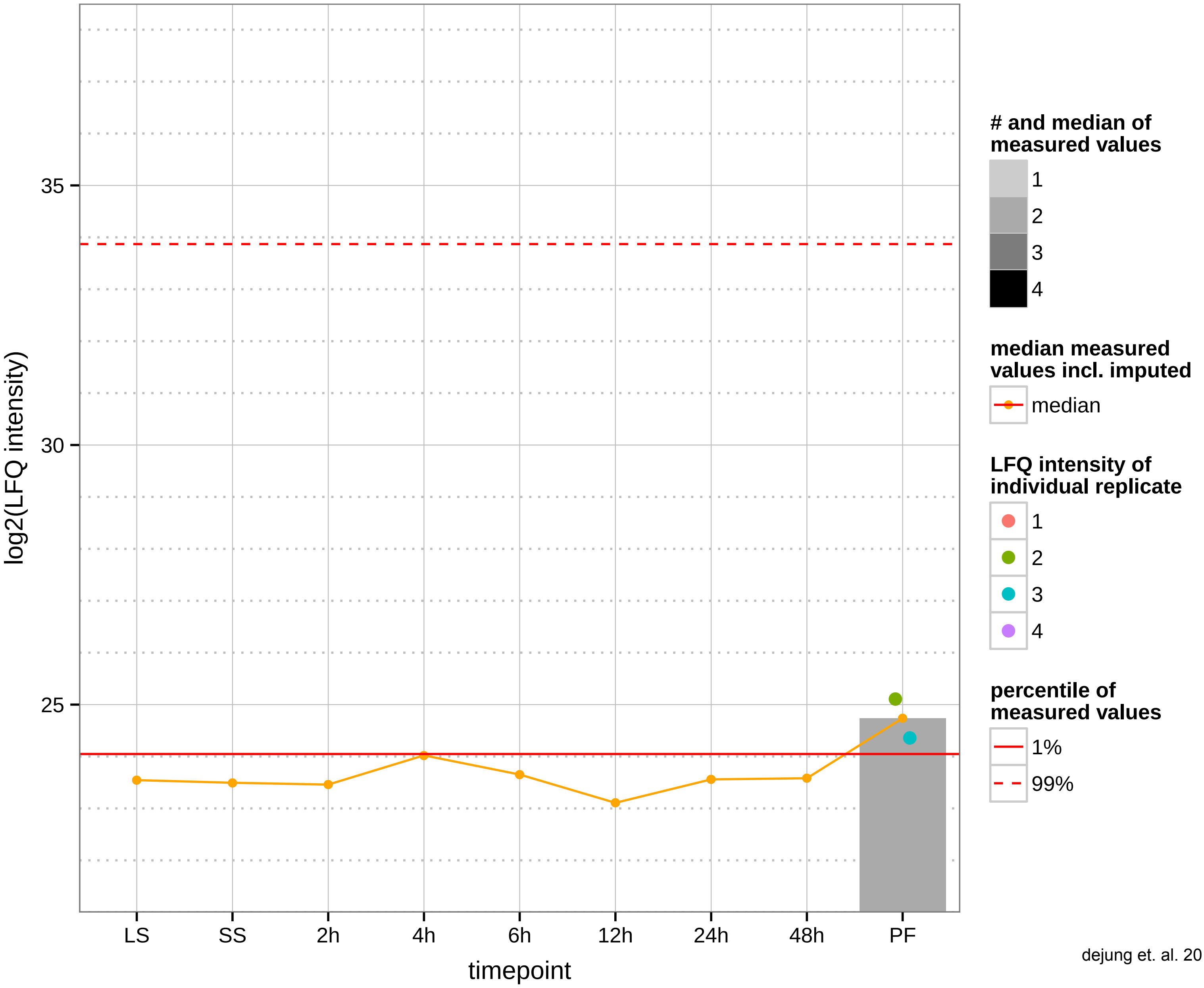
hypothetical protein, conserved
Tb927.11.3460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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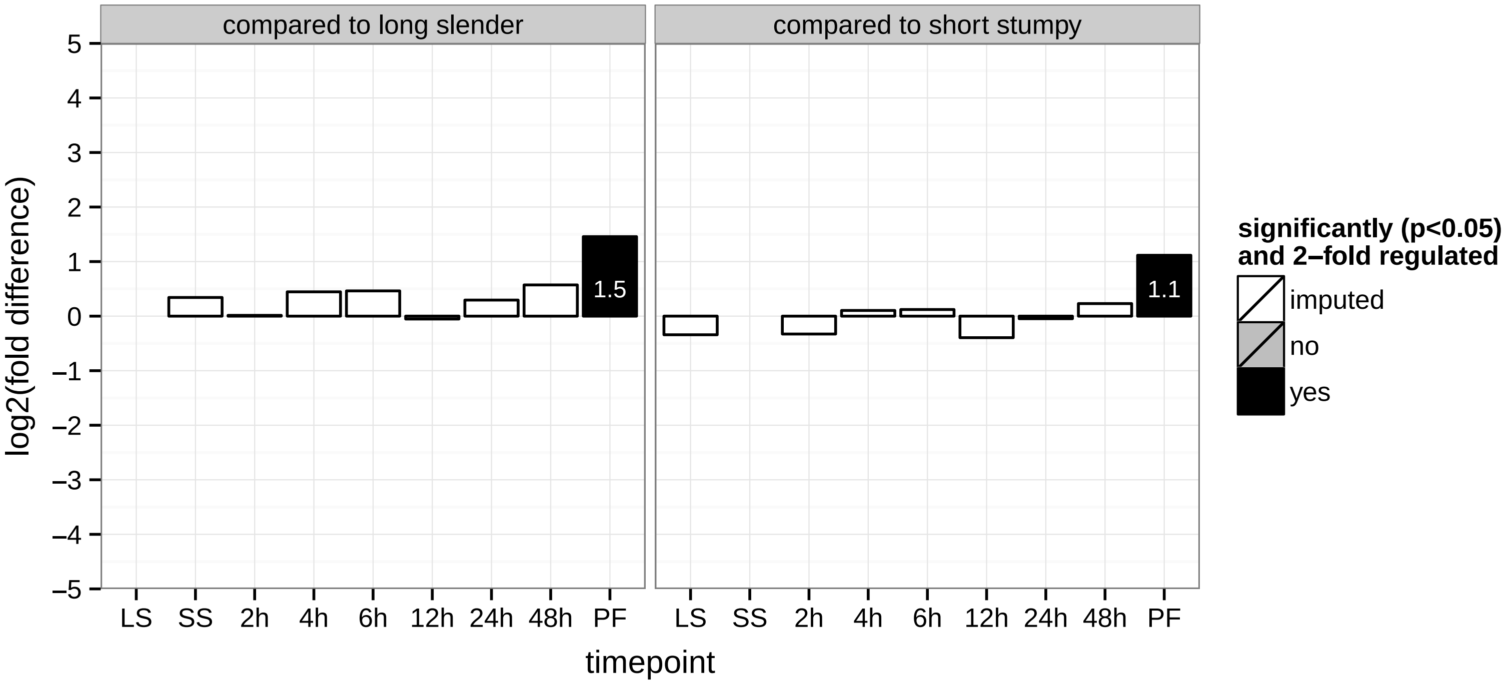
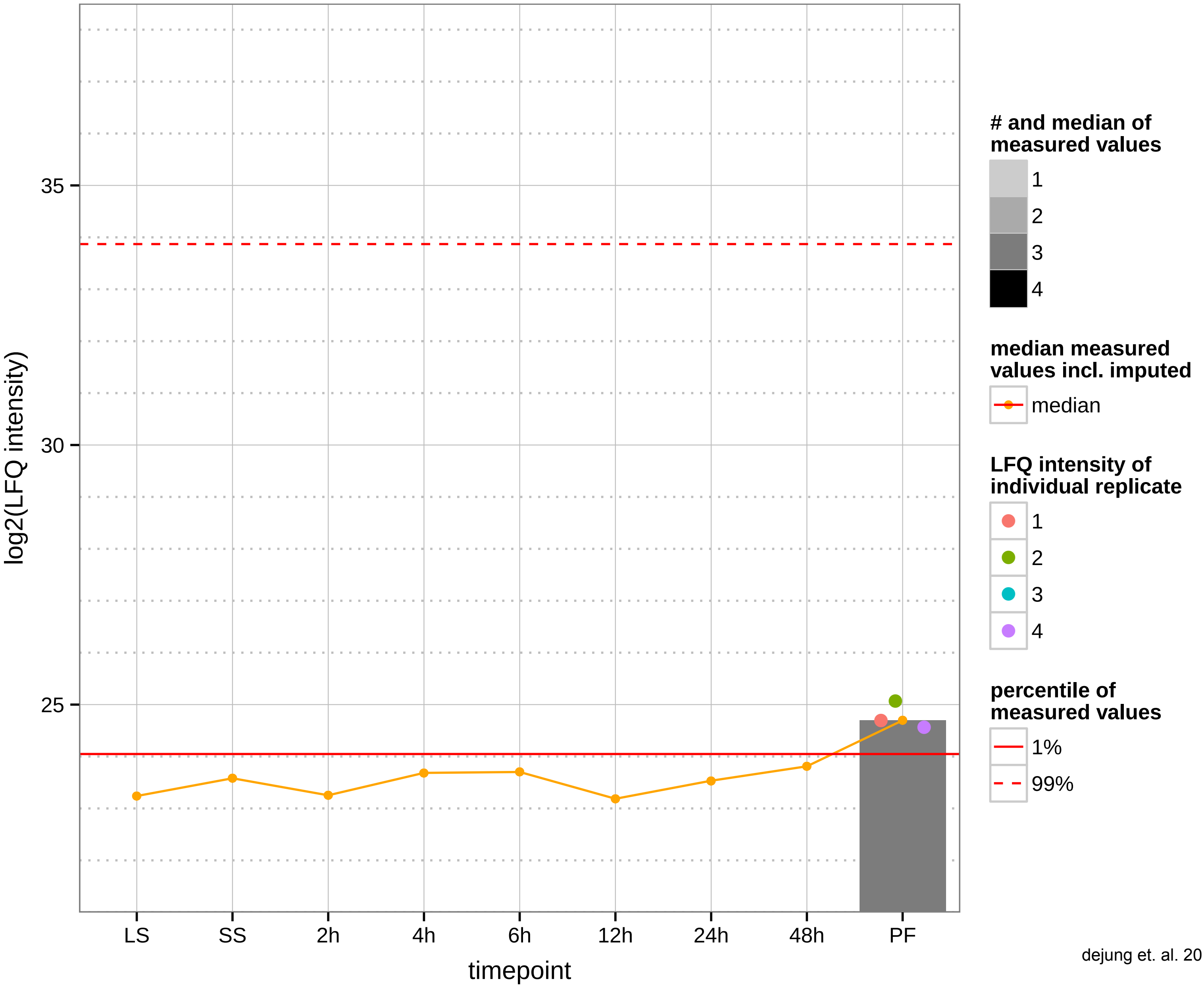
predicted C2 domain protein
Tb927.11.4160
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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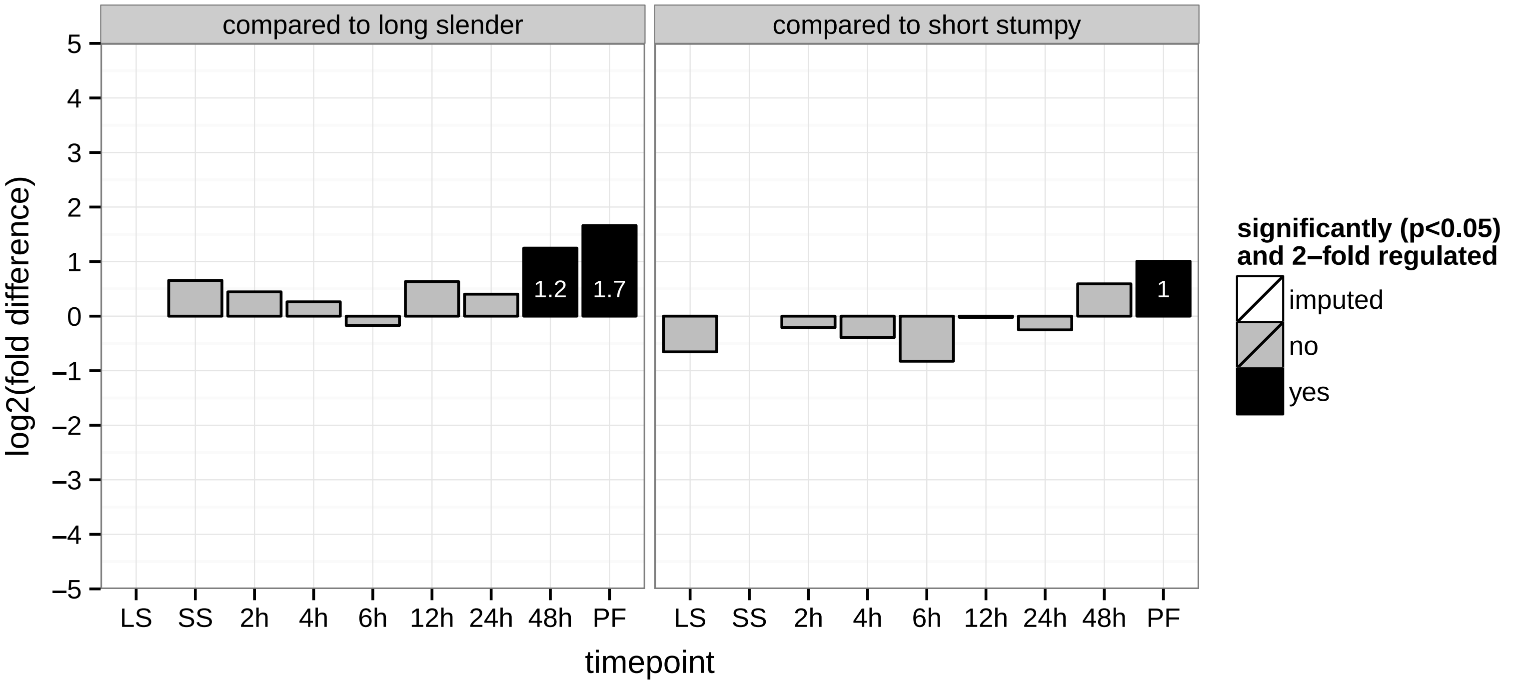
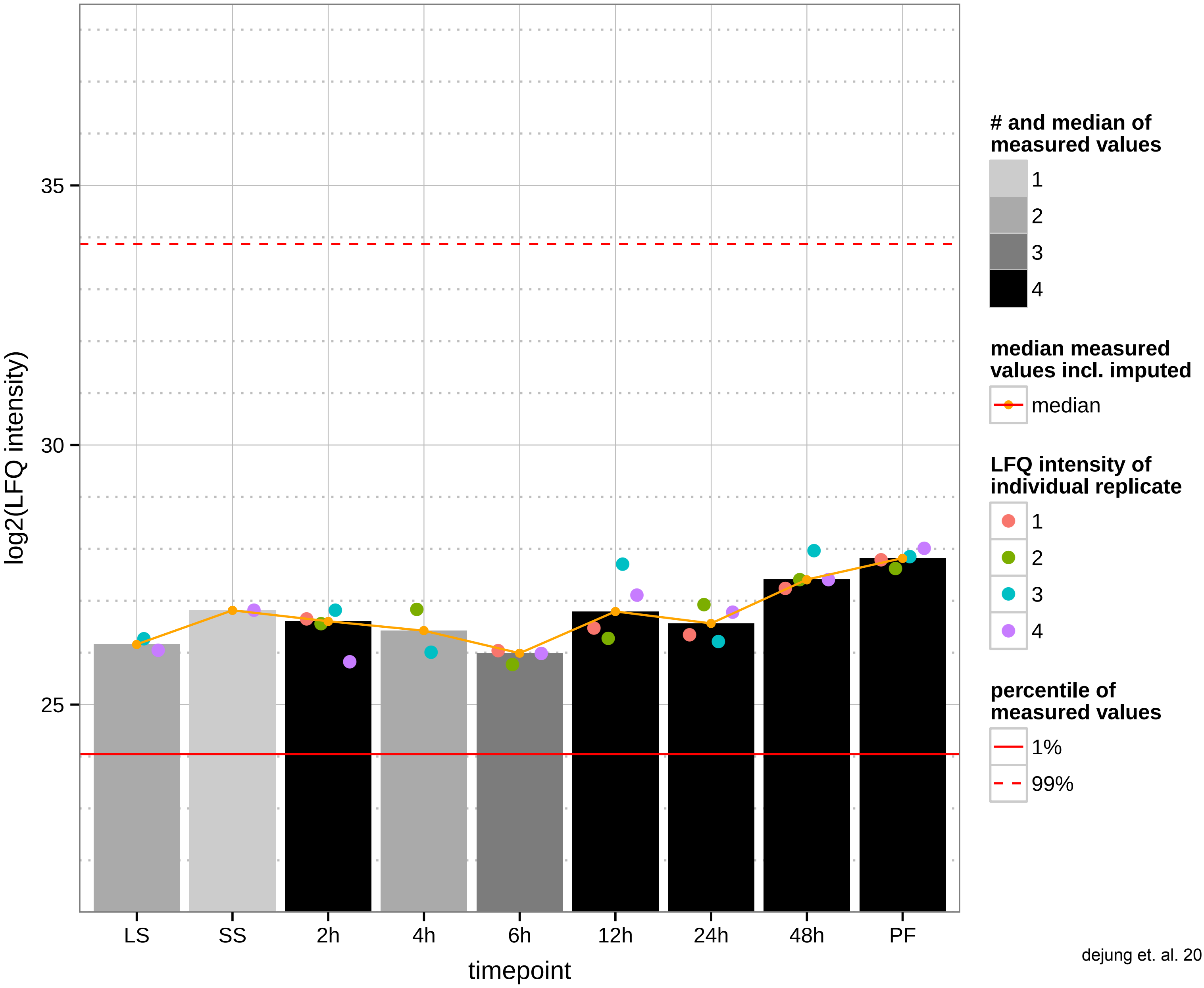
conserved protein
Tb927.11.440
AGOF: translation initiation factor activity
AGOC: integral to membrane
AGOP: translational initiation
PGOF: translation initiation factor activity
PGOC: null
PGOP: translational initiation





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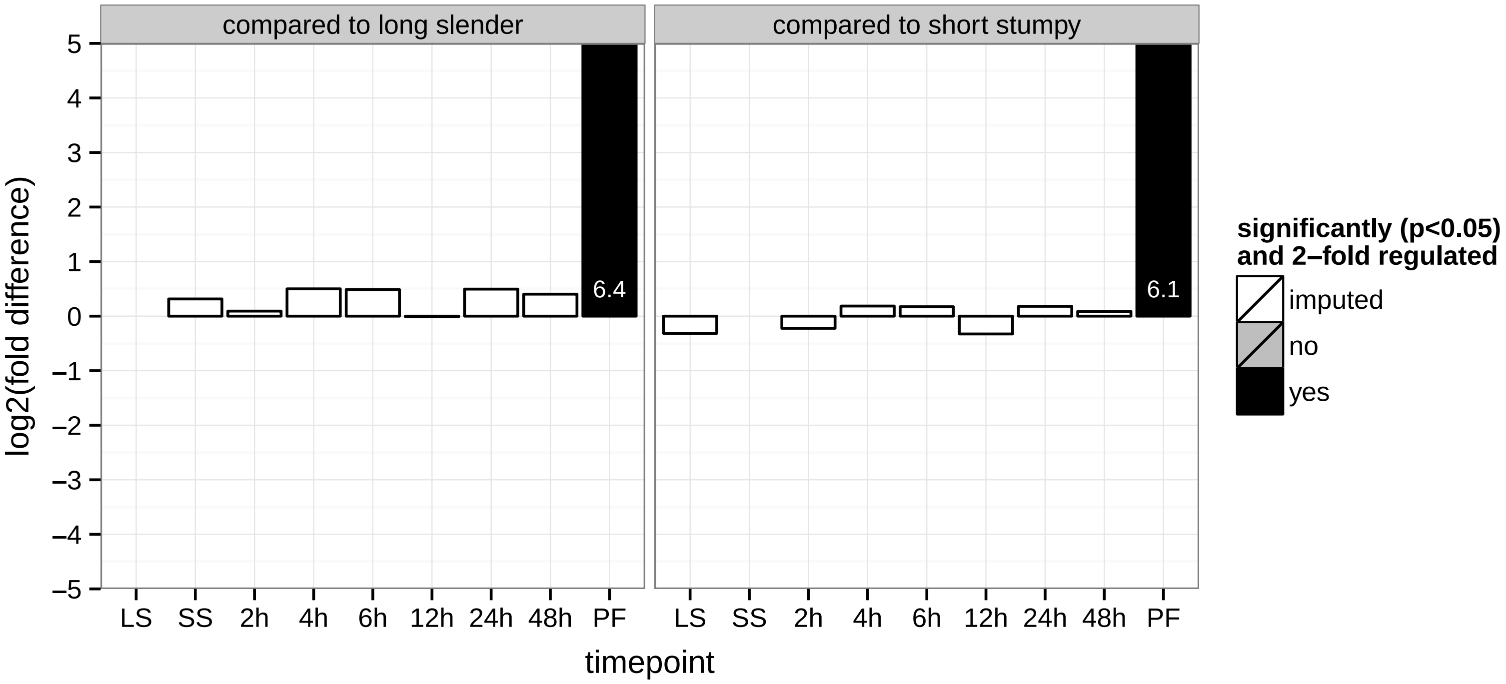
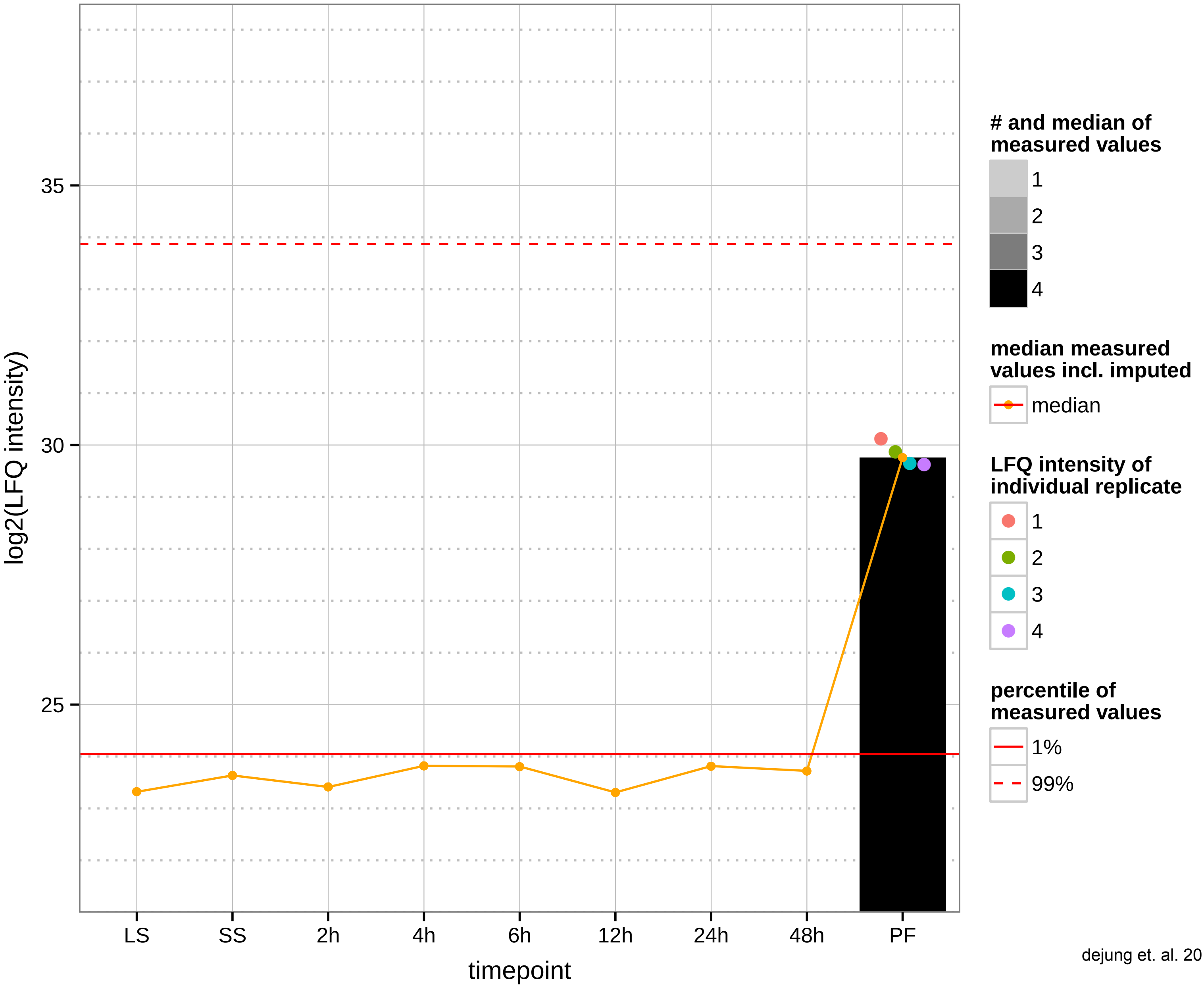
hypothetical protein, conserved
Tb927.11.4500
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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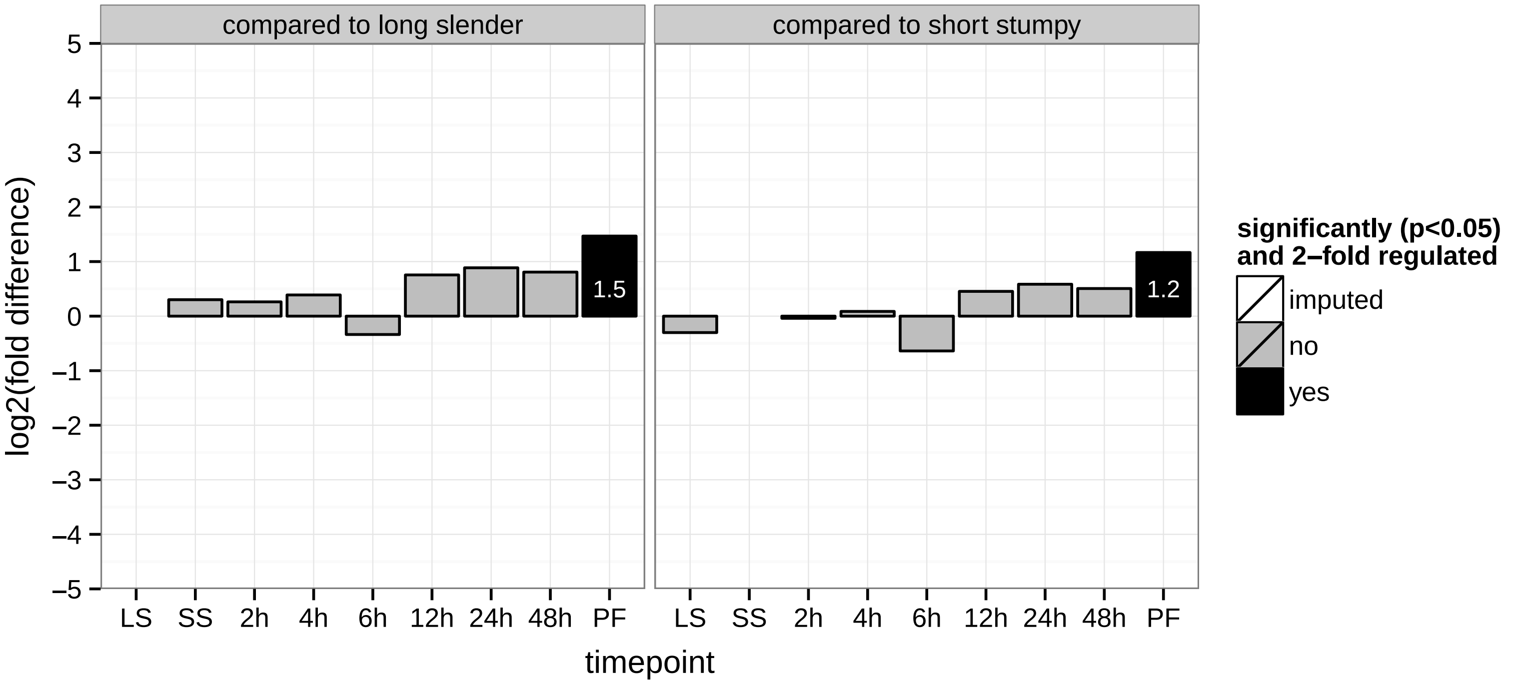
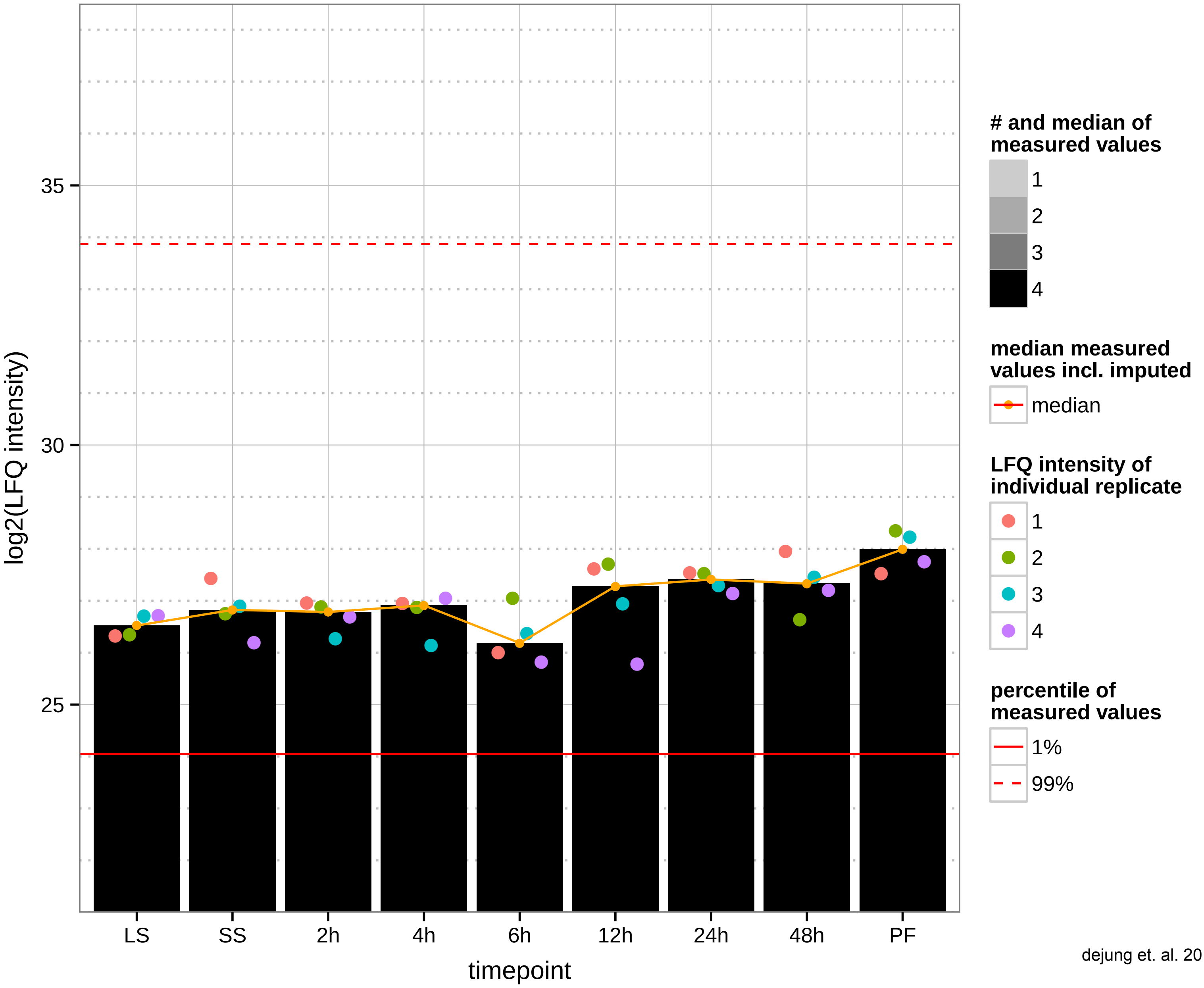
N–acetyltransferase subunit ARD1 (ARD1)
Tb927.11.4530
AGOF: N–acetyltransferase activity, catalytic activity
AGOC: null
AGOP: N–terminal protein amino acid acetylation, cell growth
PGOF: N–acetyltransferase activity
PGOC: null
PGOP: null





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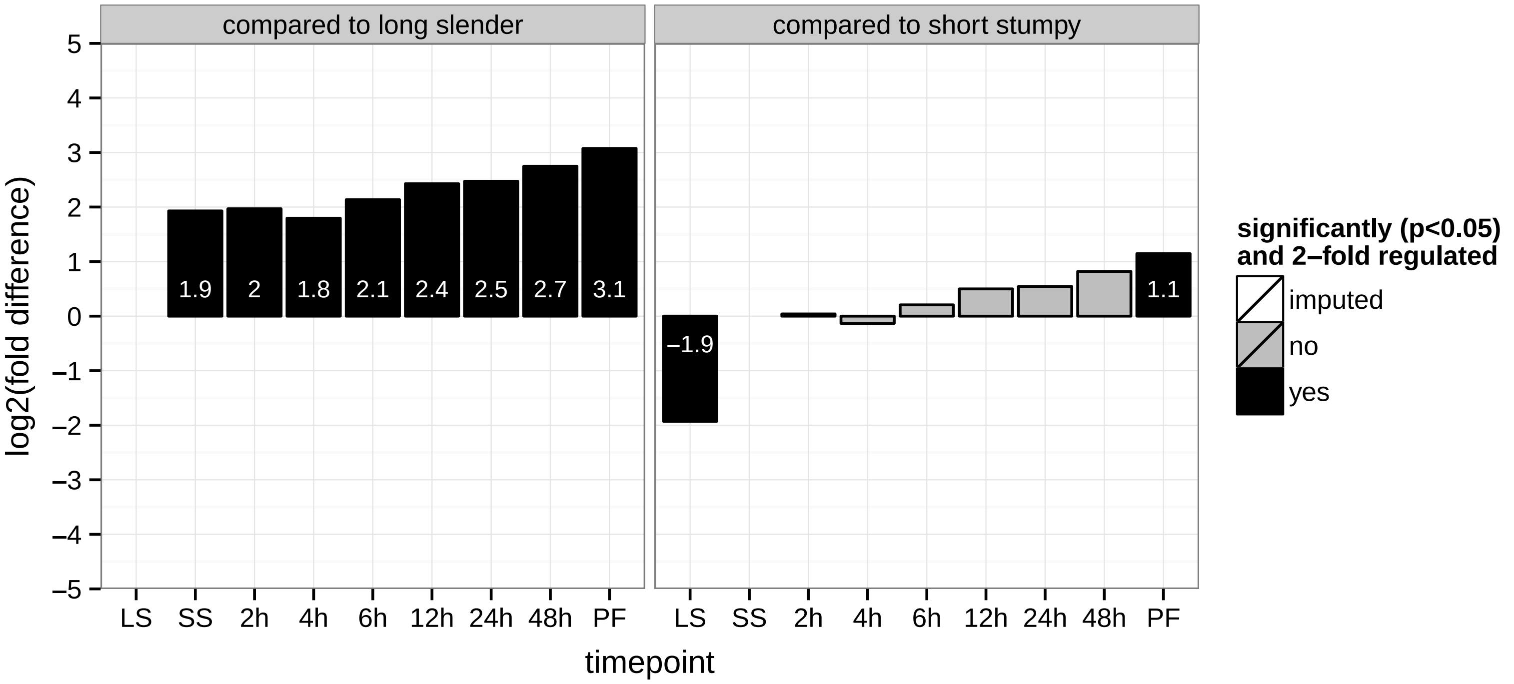
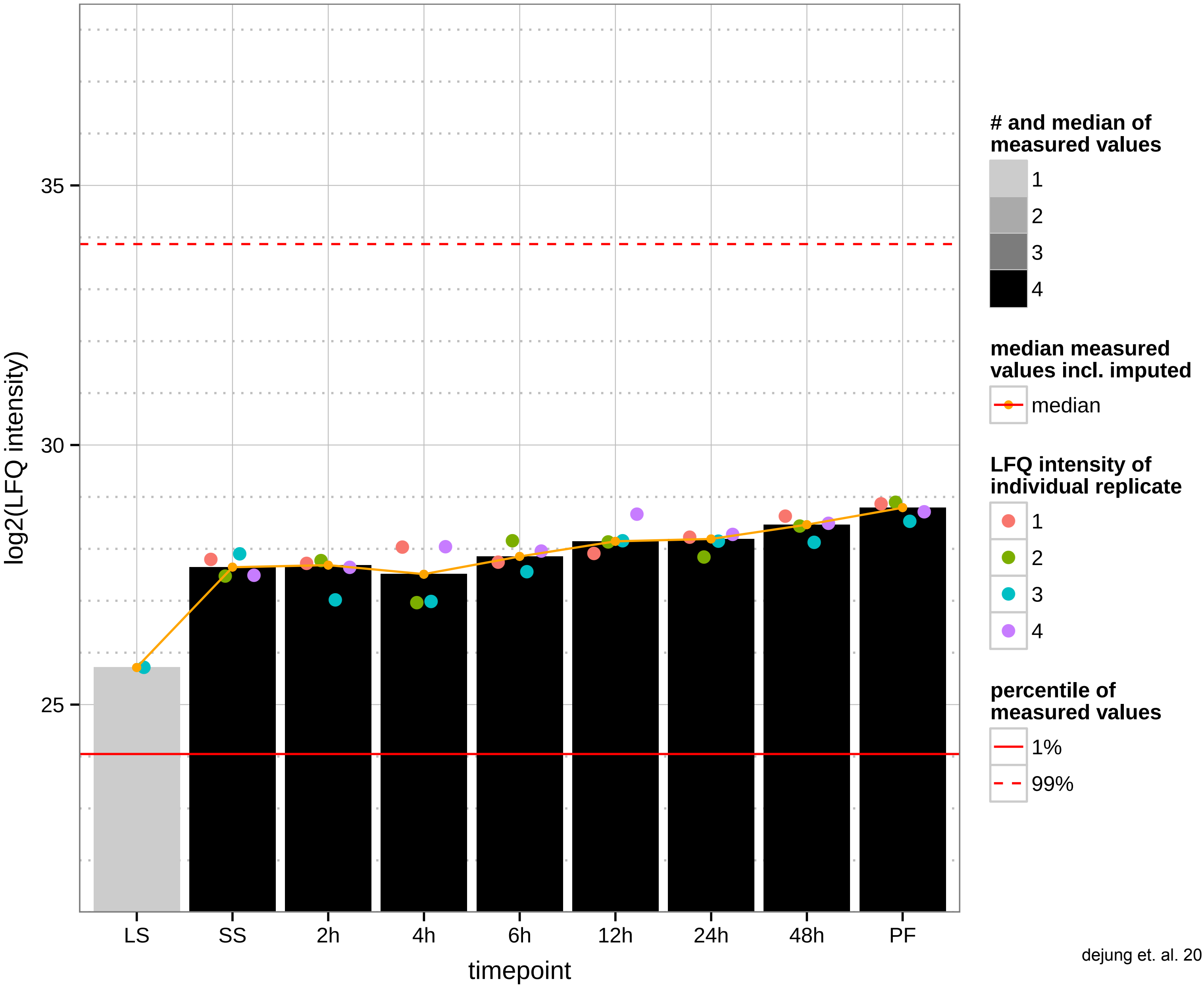
hypothetical protein, conserved, predicted WD40 repeat protein
Tb927.11.460;Tb11.v5.0726
AGOF: null
AGOC: null, small−subunit processome
AGOP: null, rRNA processing
PGOF: protein binding
PGOC: small−subunit processome
PGOP: rRNA processing





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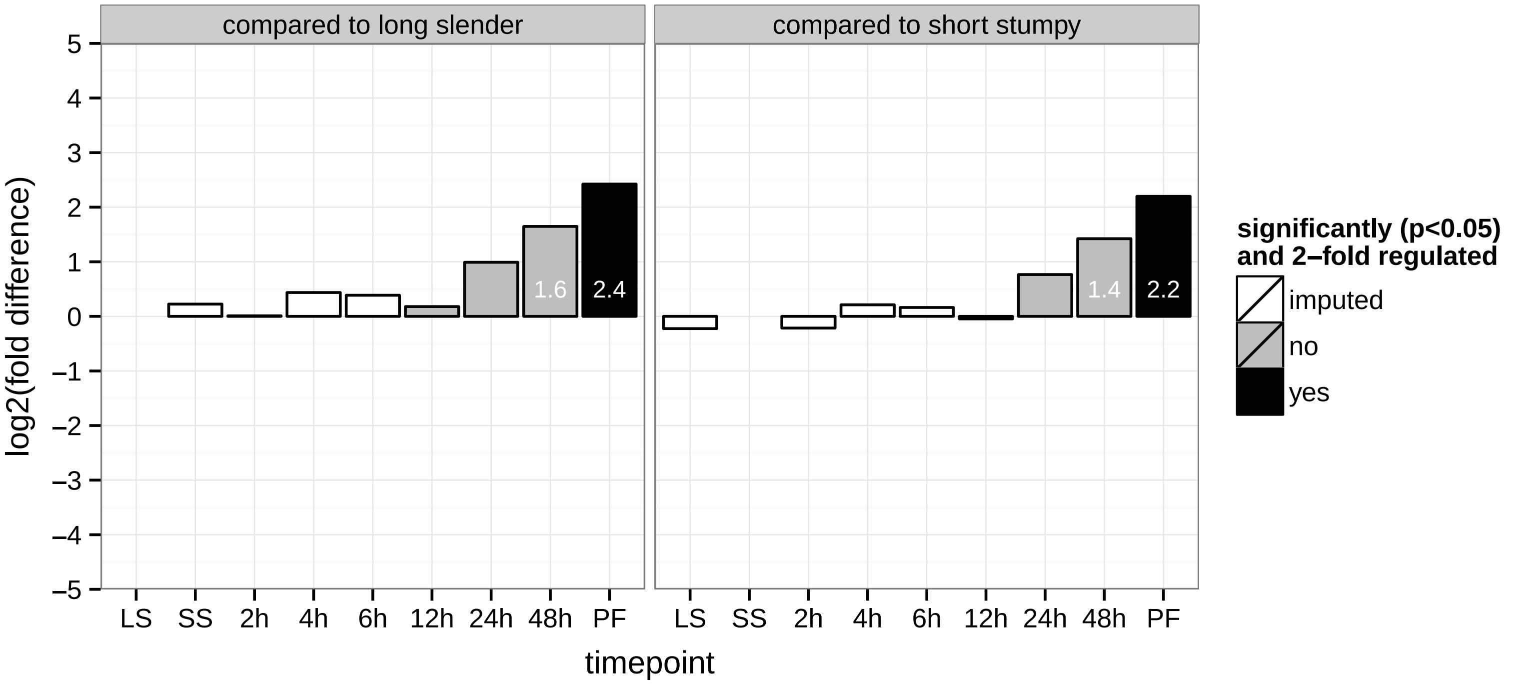
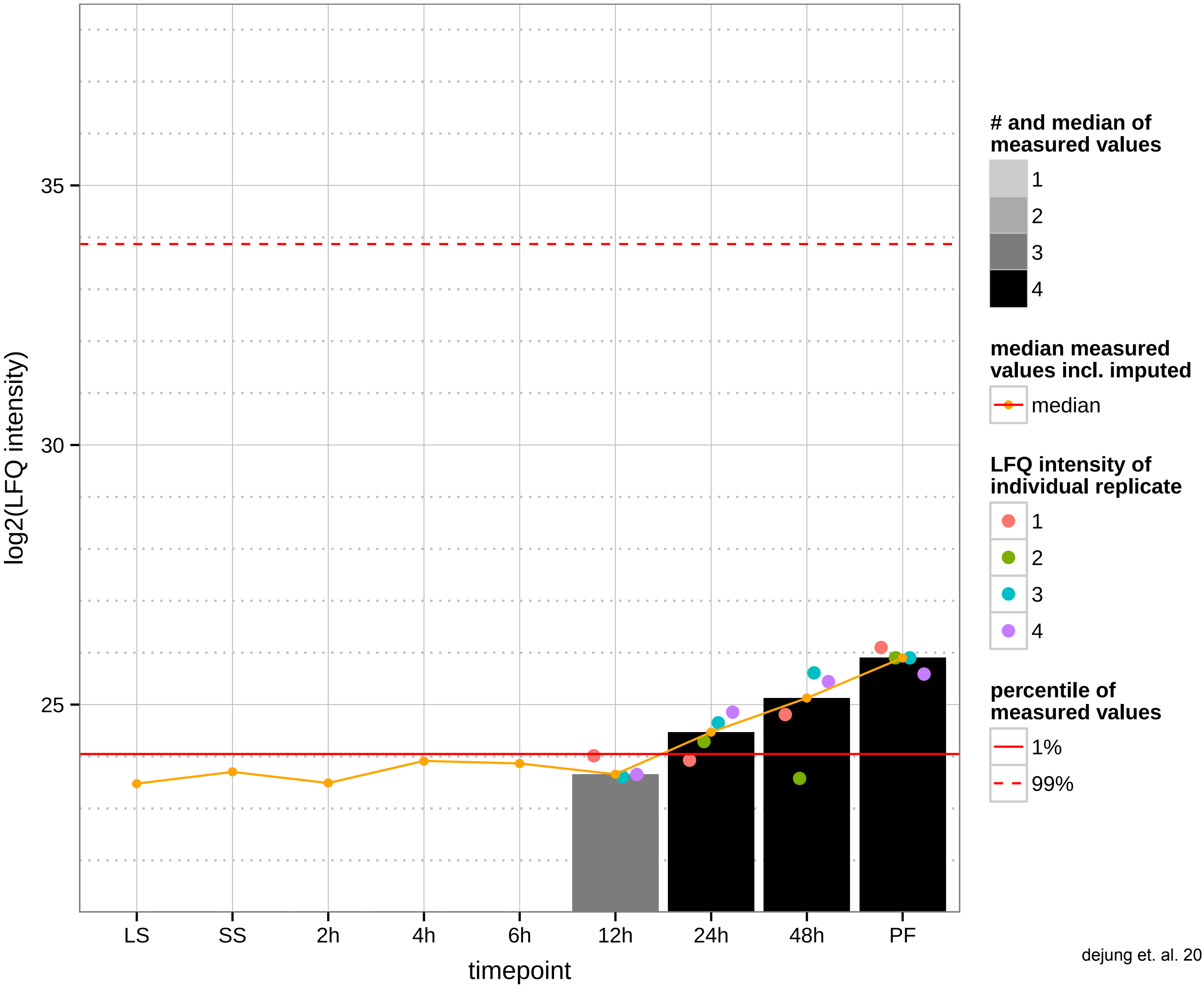
hypothetical protein, conserved
Tb927.11.4870
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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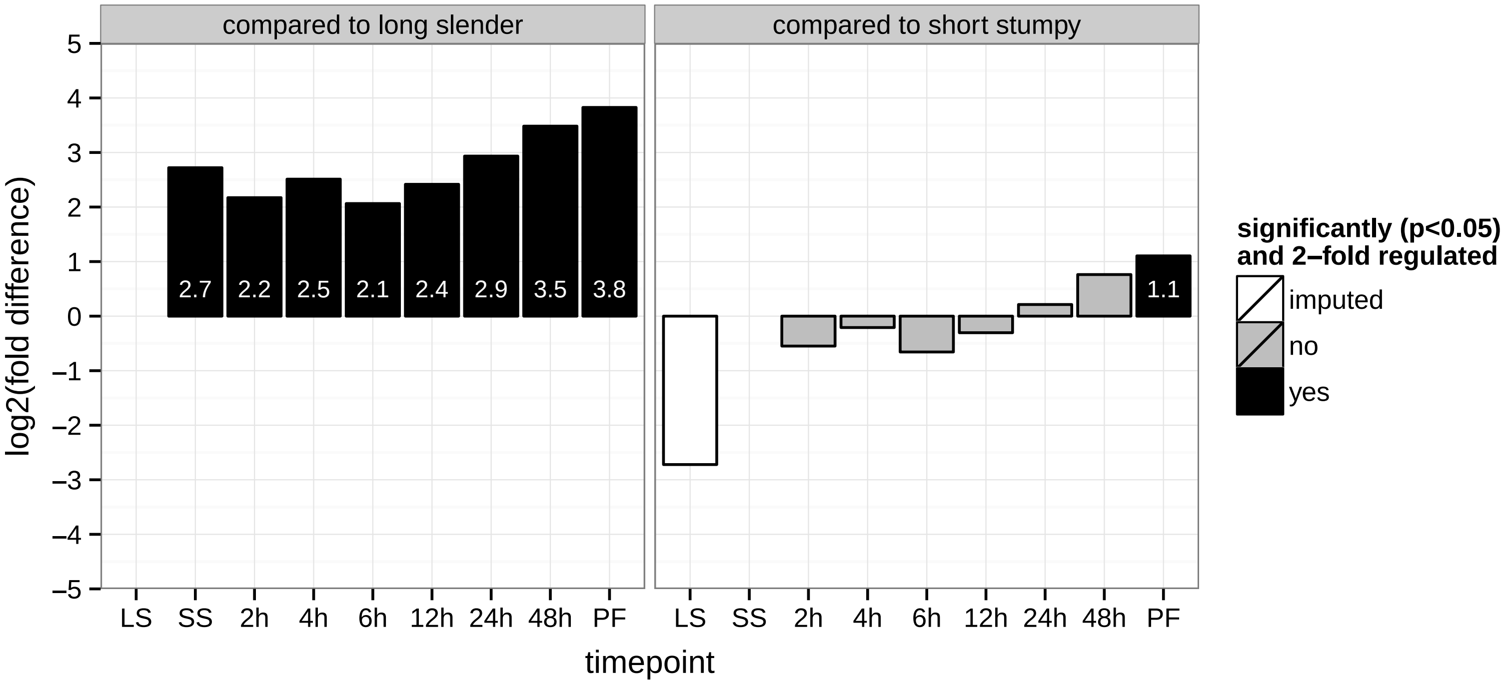
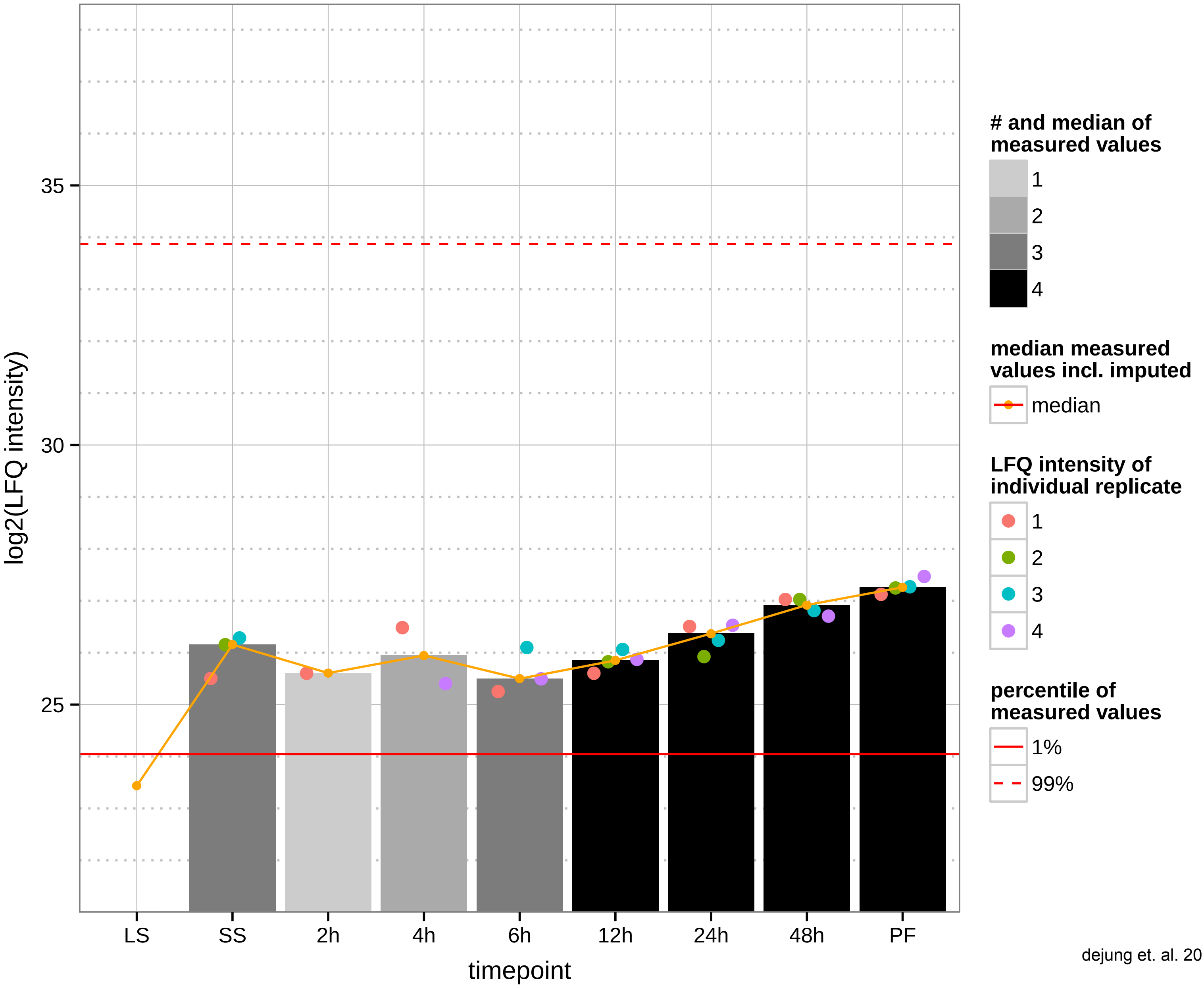
hypothetical protein, conserved
Tb927.11.5020
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: binding, protein binding, zinc ion binding
PGOC: null
PGOP: null





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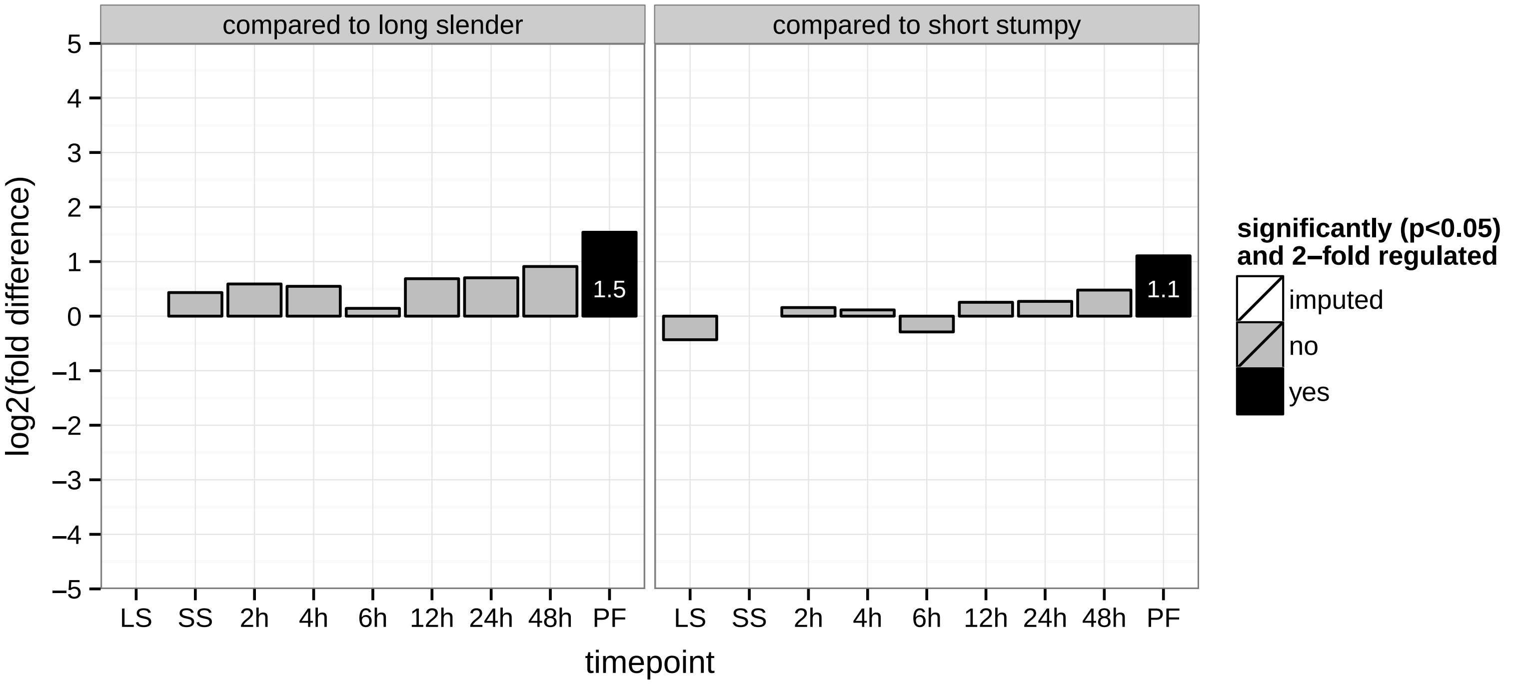
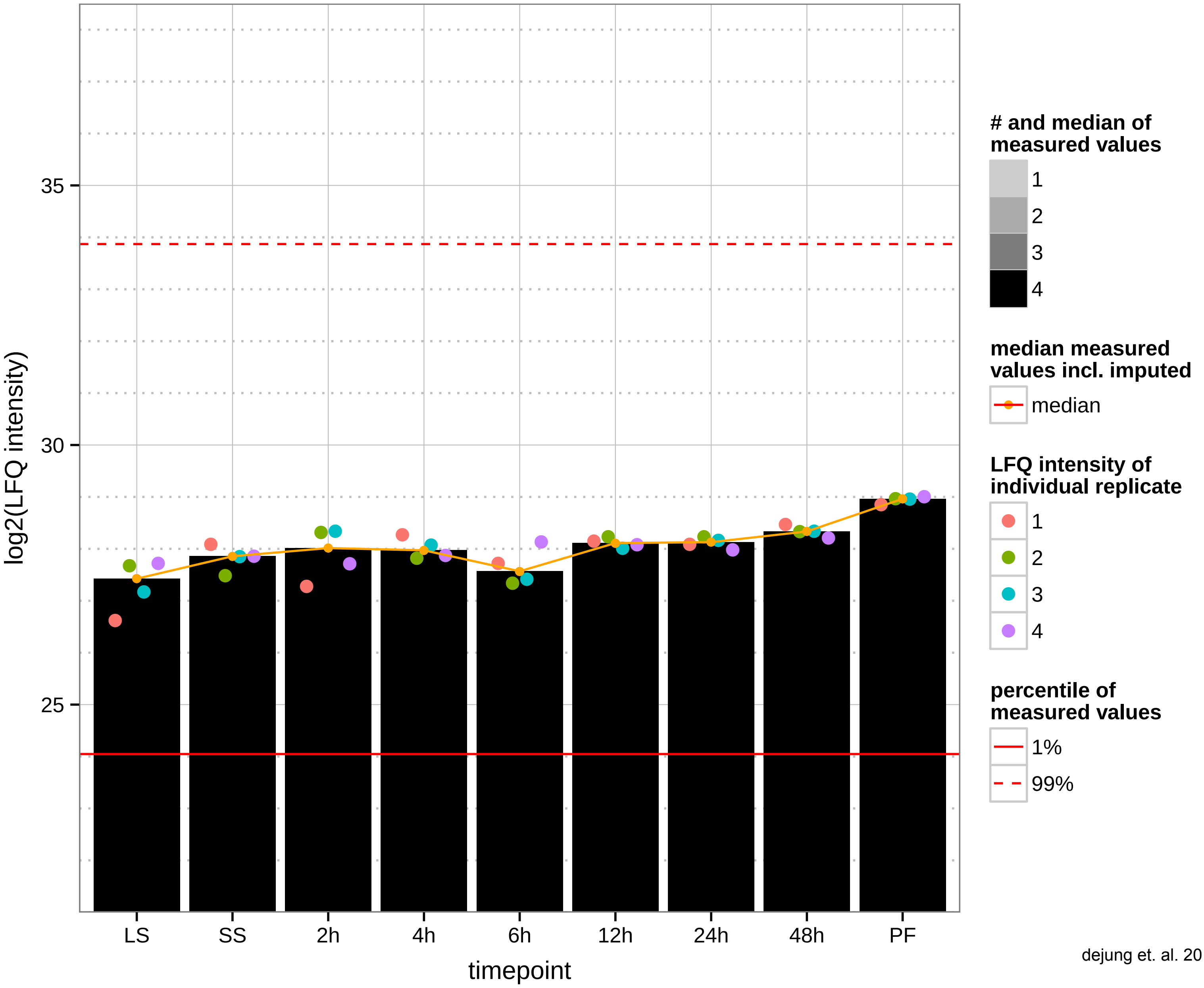
ubiquitin carboxyl–terminal hydrolase, putative, cysteine peptidase, Clan CA, family C12
Tb927.11.5140
AGOF: ubiquitin thiolesterase activity
AGOC: cytoplasm, intracellular, proteasome regulatory particle
AGOP: ubiquitin–dependent protein catabolic process
PGOF: omega peptidase activity, ubiquitin thiolesterase activity
PGOC: intracellular
PGOP: ubiquitin–dependent protein catabolic process





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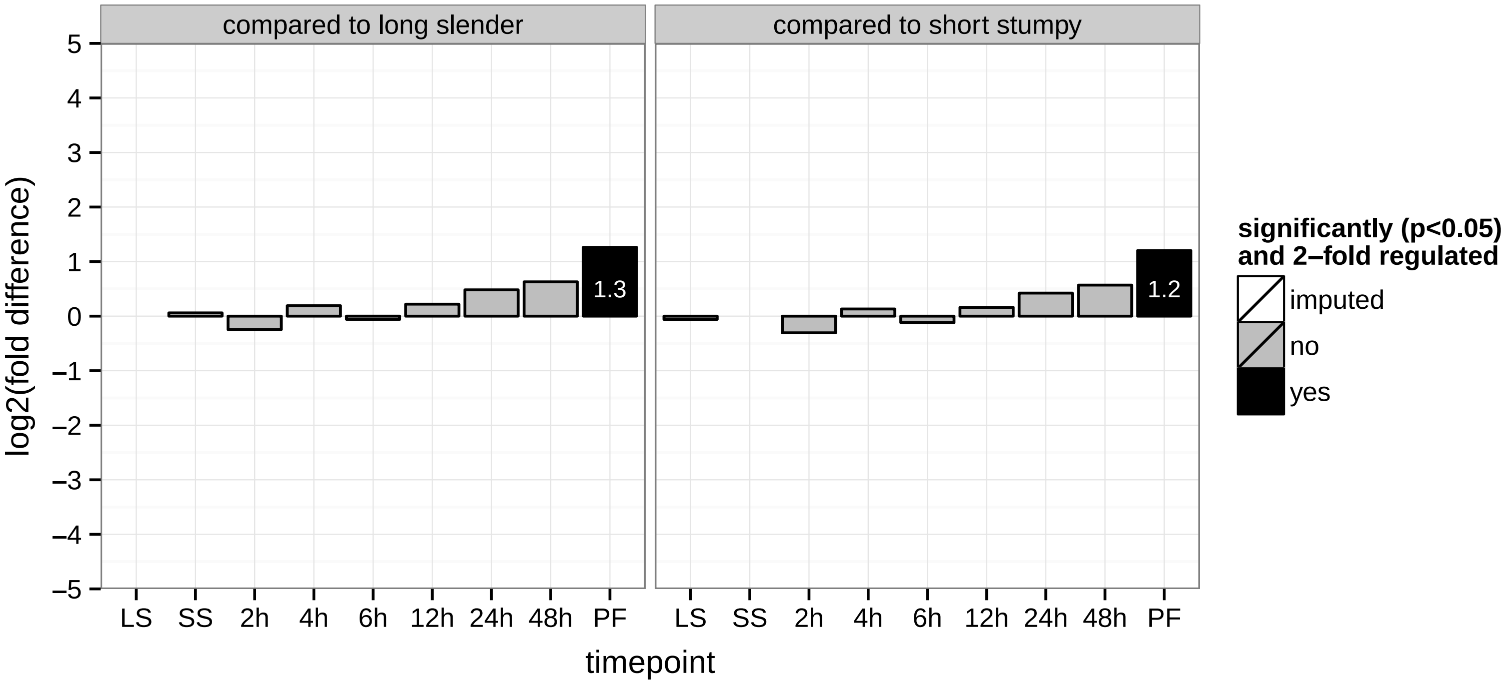
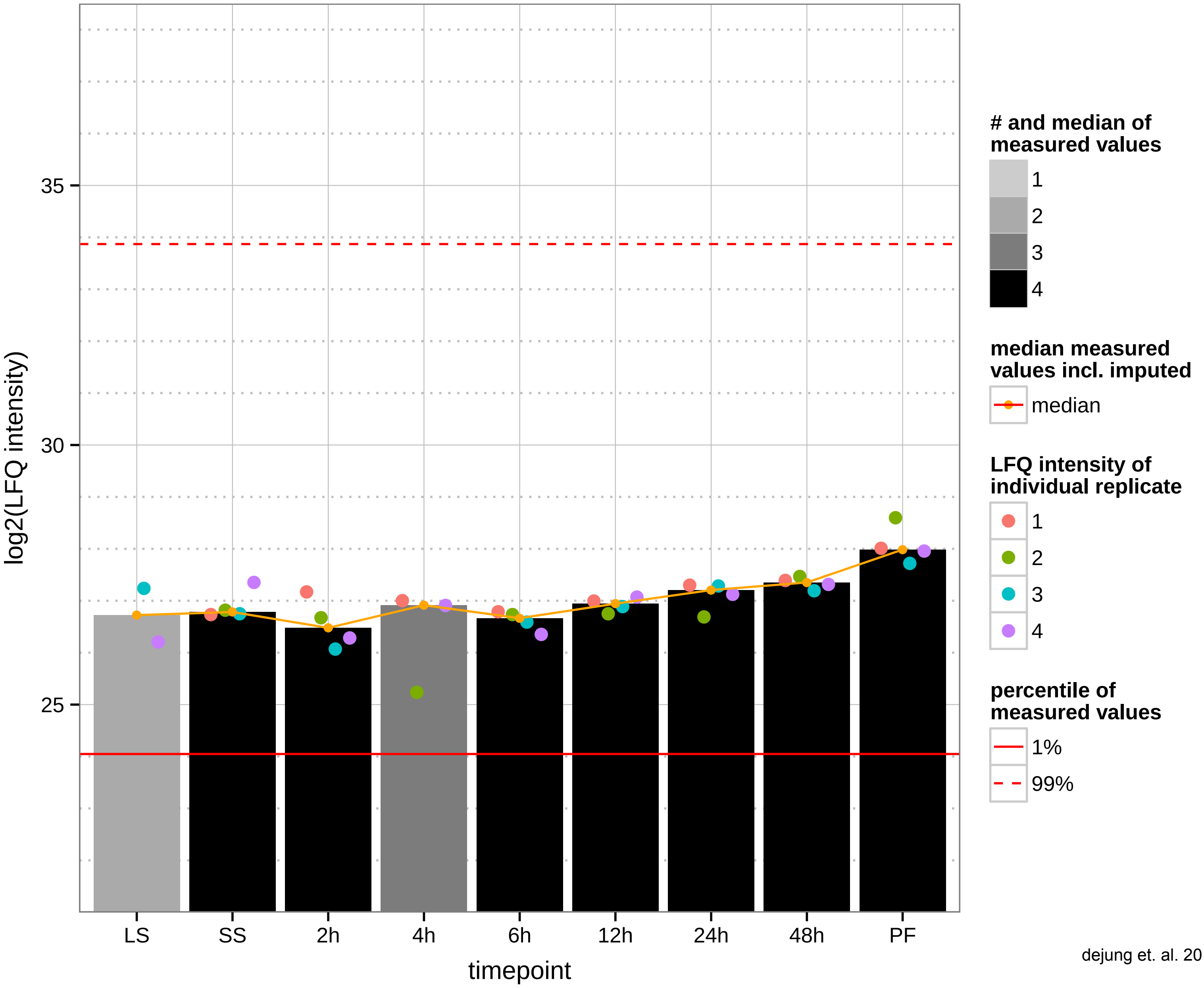
hypothetical protein, conserved
Tb927.11.5250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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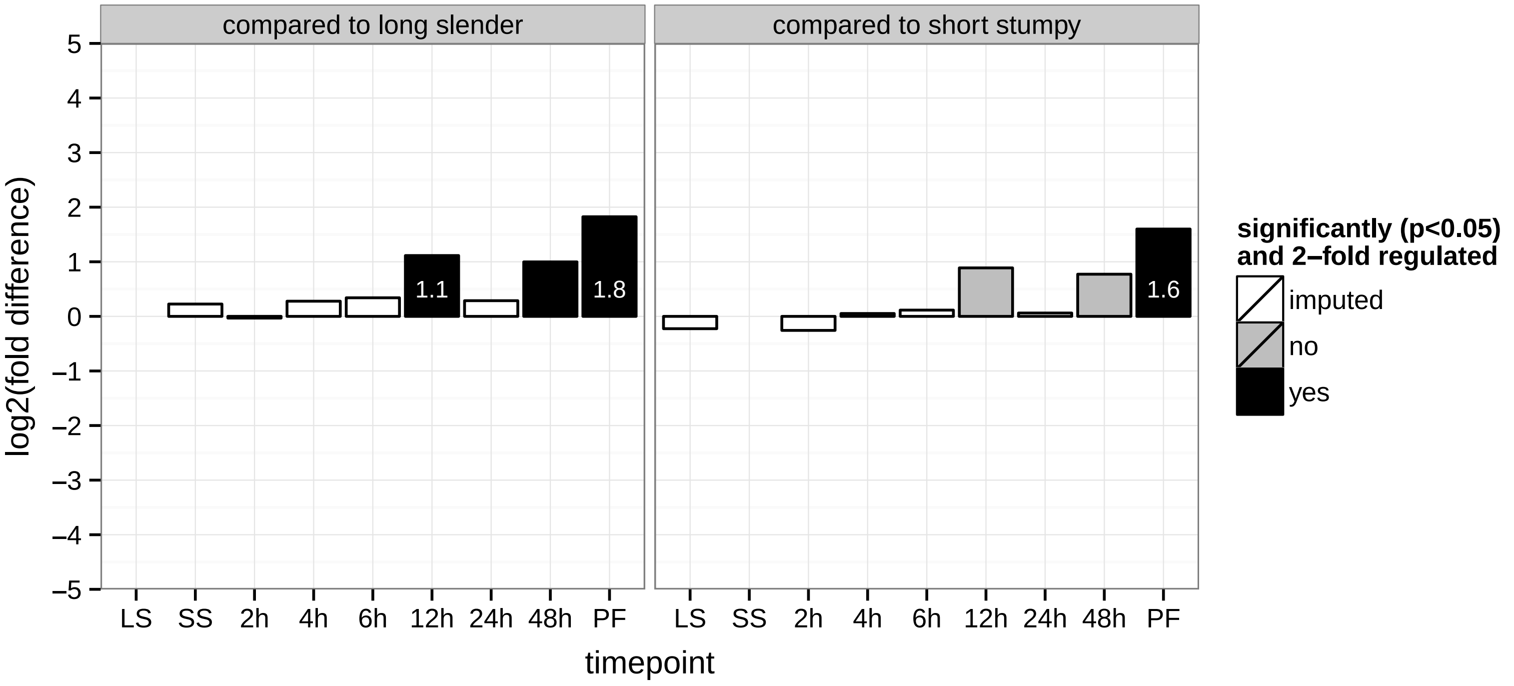
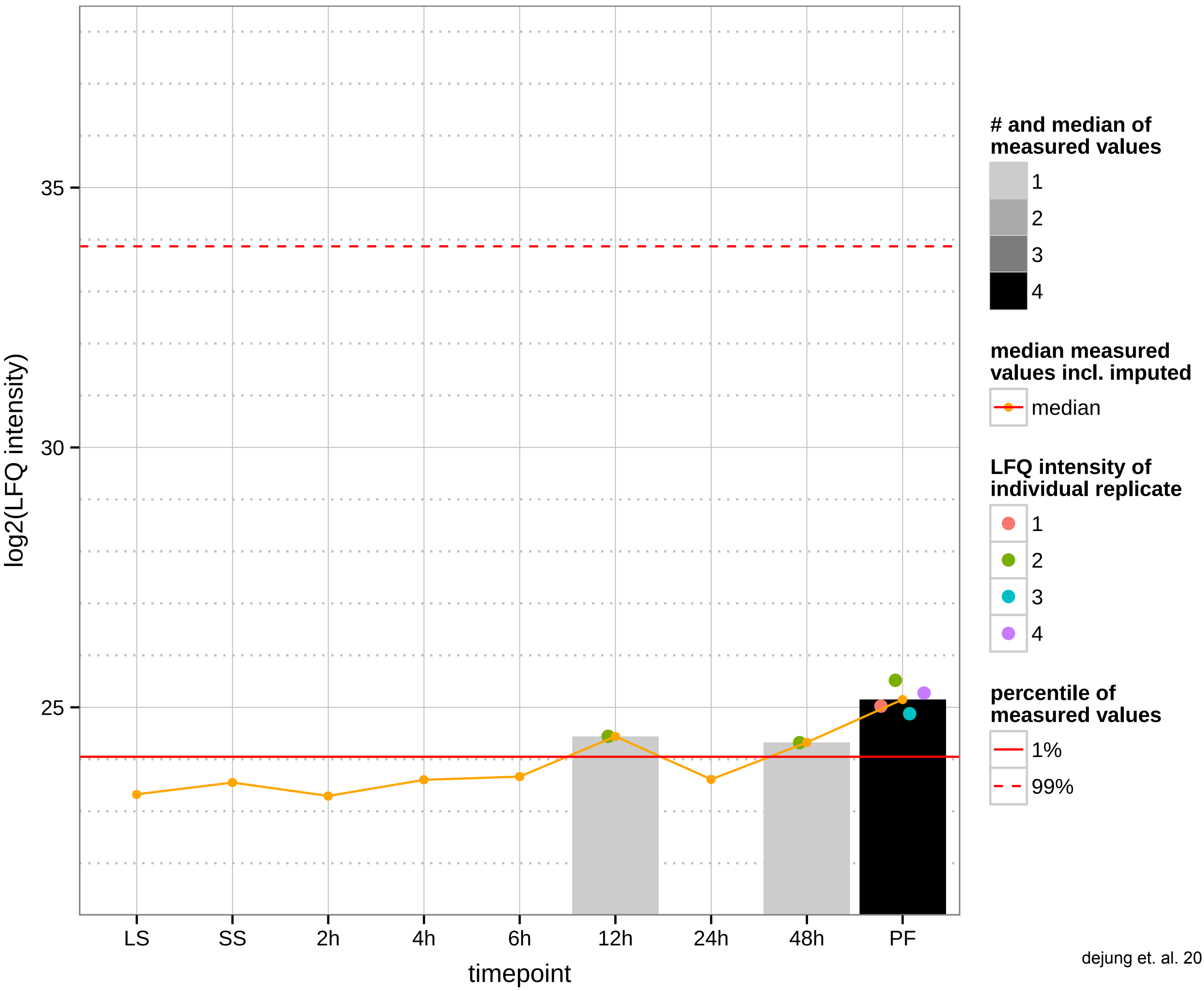
hypothetical protein, conserved
Tb927.11.560
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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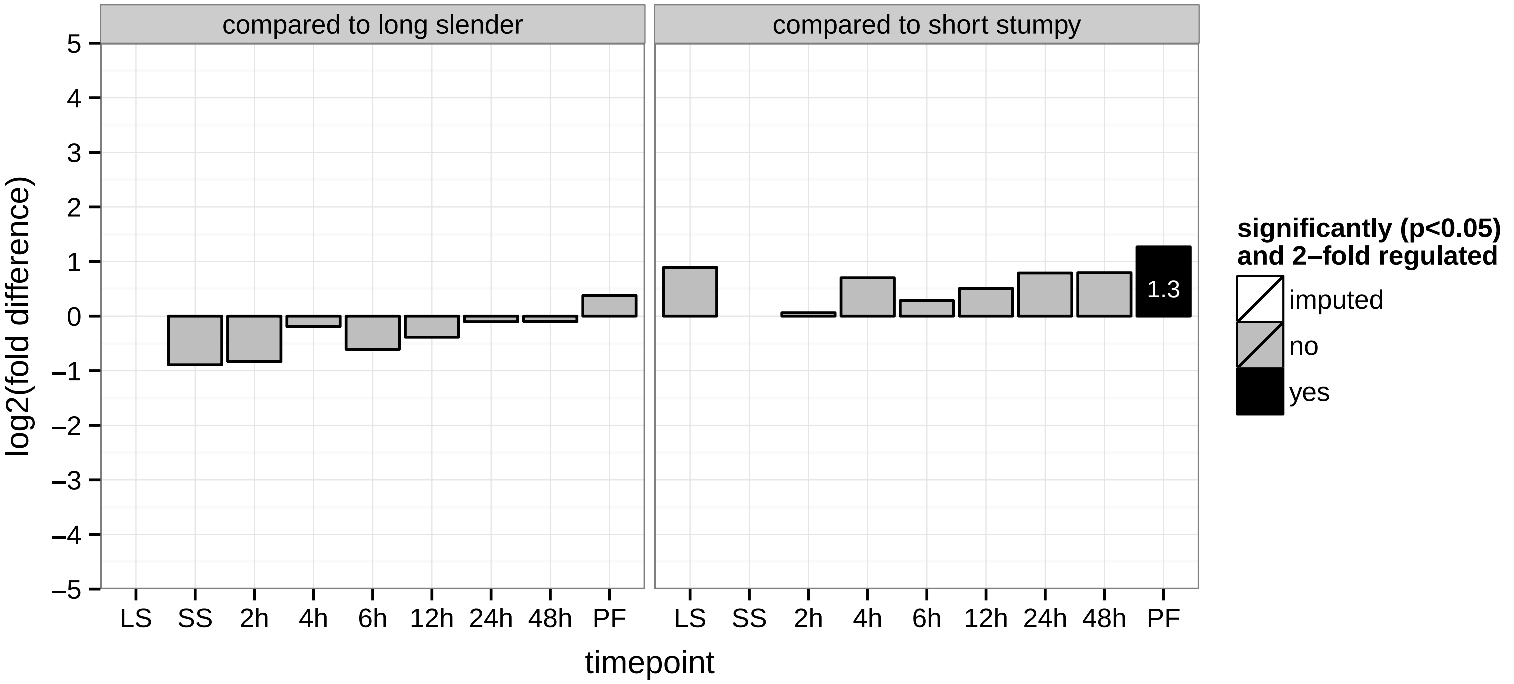
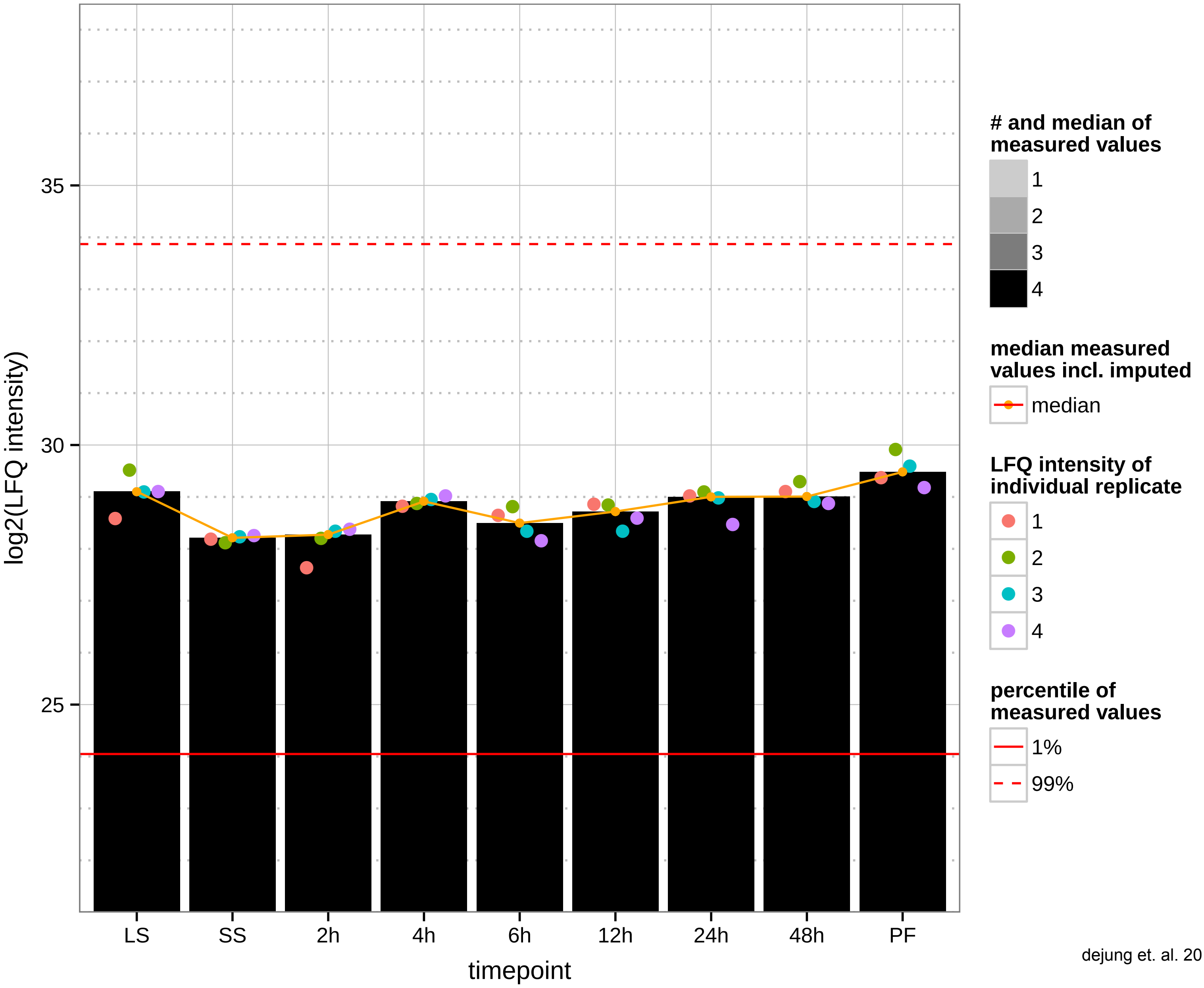
dynein light chain, putative
Tb927.11.5680
AGOF: motor activity
AGOC: dynein complex
AGOP: microtubule–based movement
PGOF: protein binding
PGOC: null
PGOP: null





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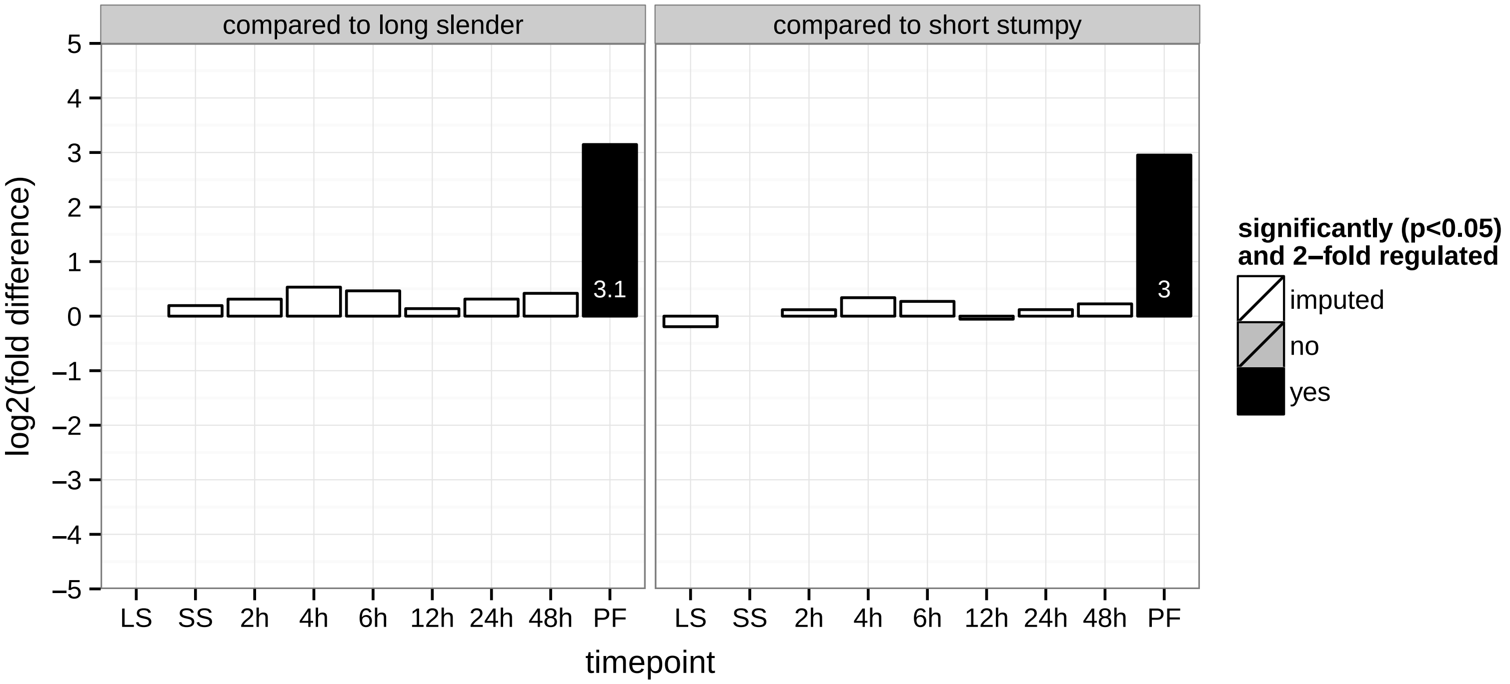
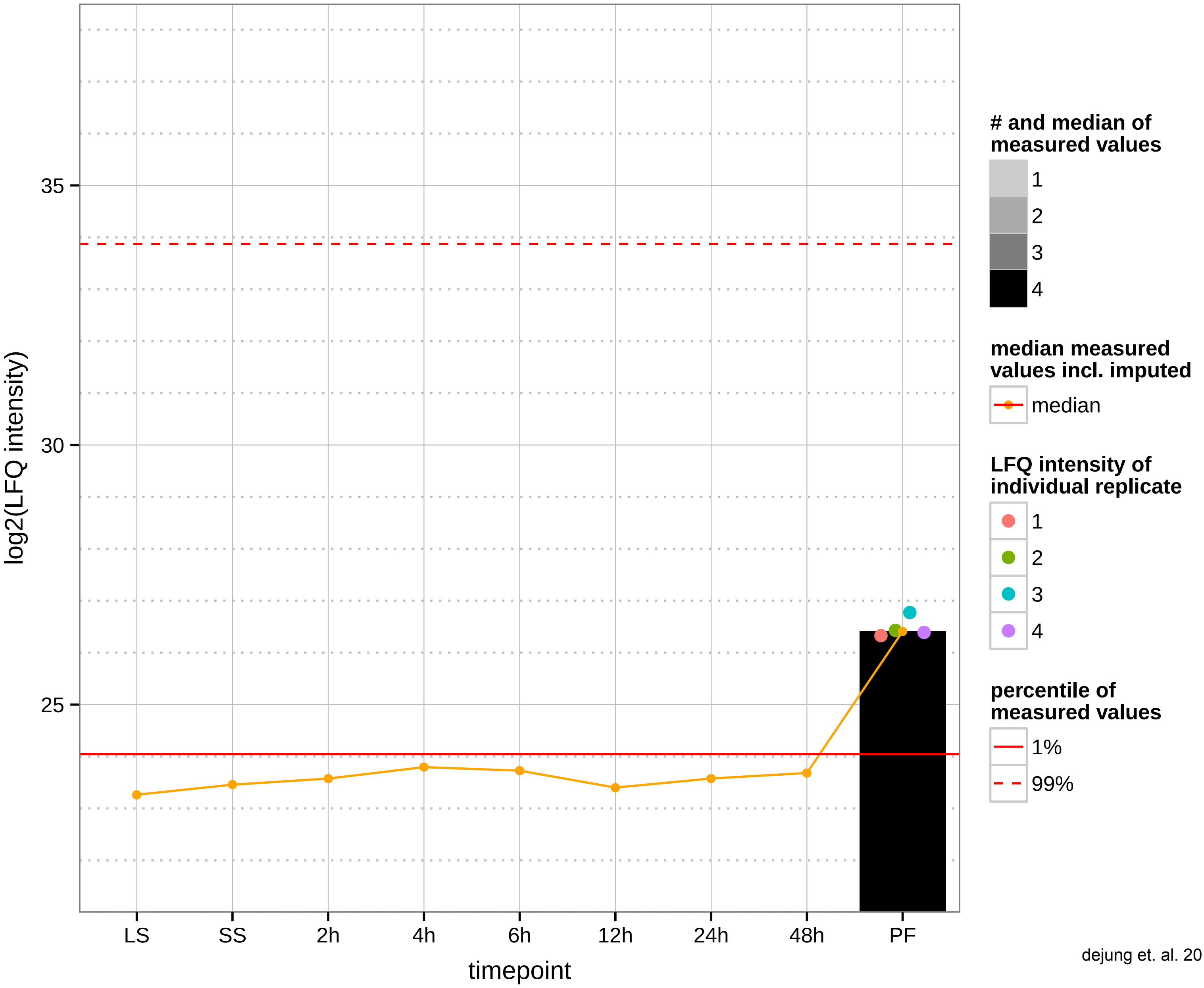
hypothetical protein, conserved
Tb927.11.5900
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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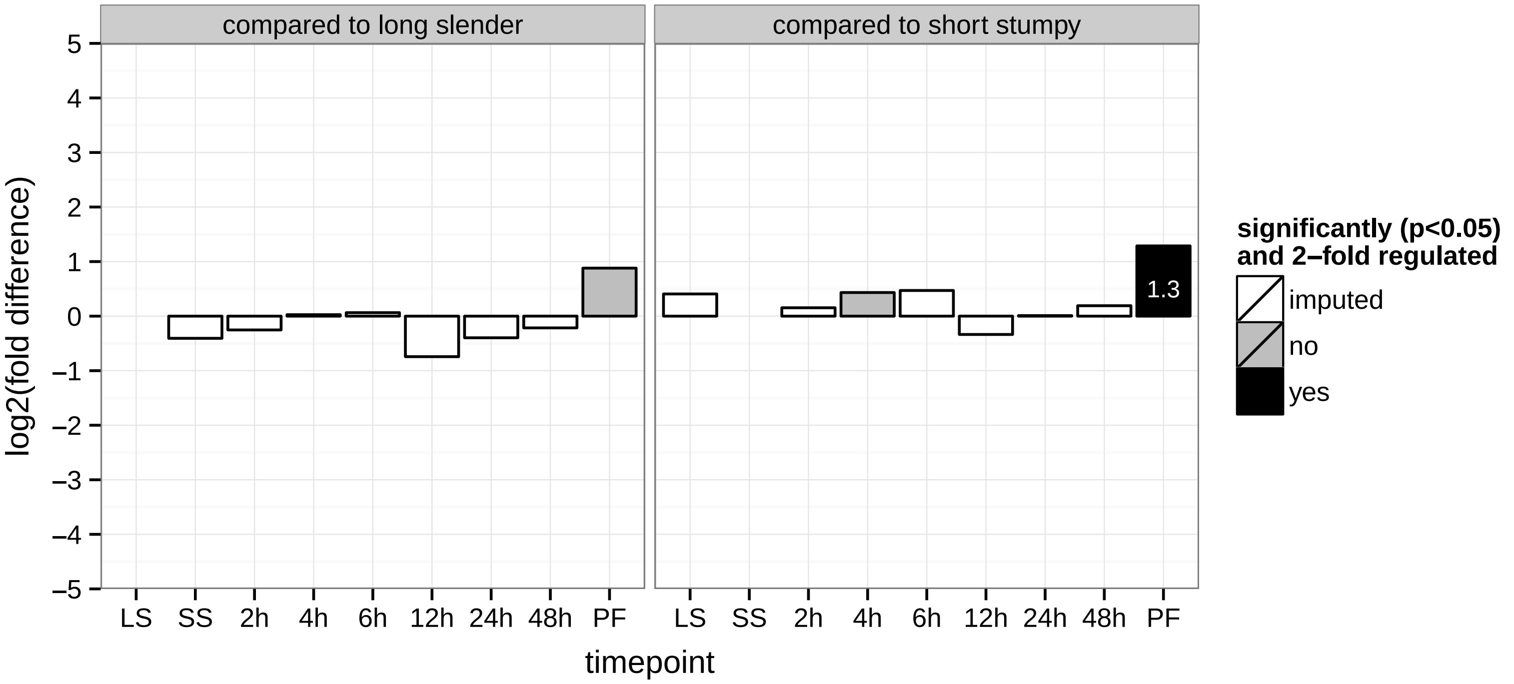
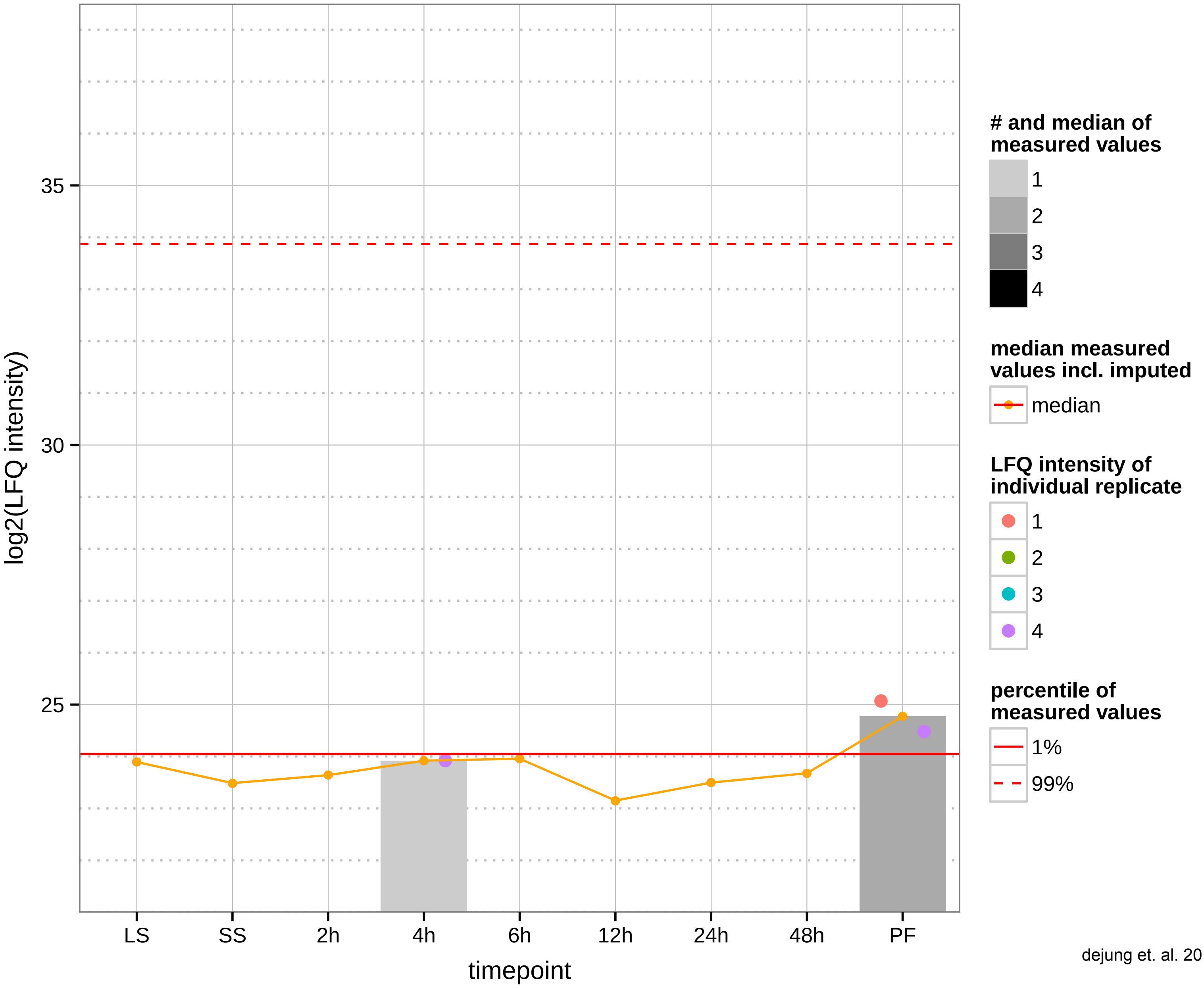
hypothetical protein, conserved
Tb927.11.5990
AGOF: RNA binding, pseudouridine synthase activity
AGOC: mitochondrion
AGOP: pseudouridine synthesis
PGOF: RNA binding, pseudouridine synthase activity
PGOC: null
PGOP: RNA modification, pseudouridine synthesis





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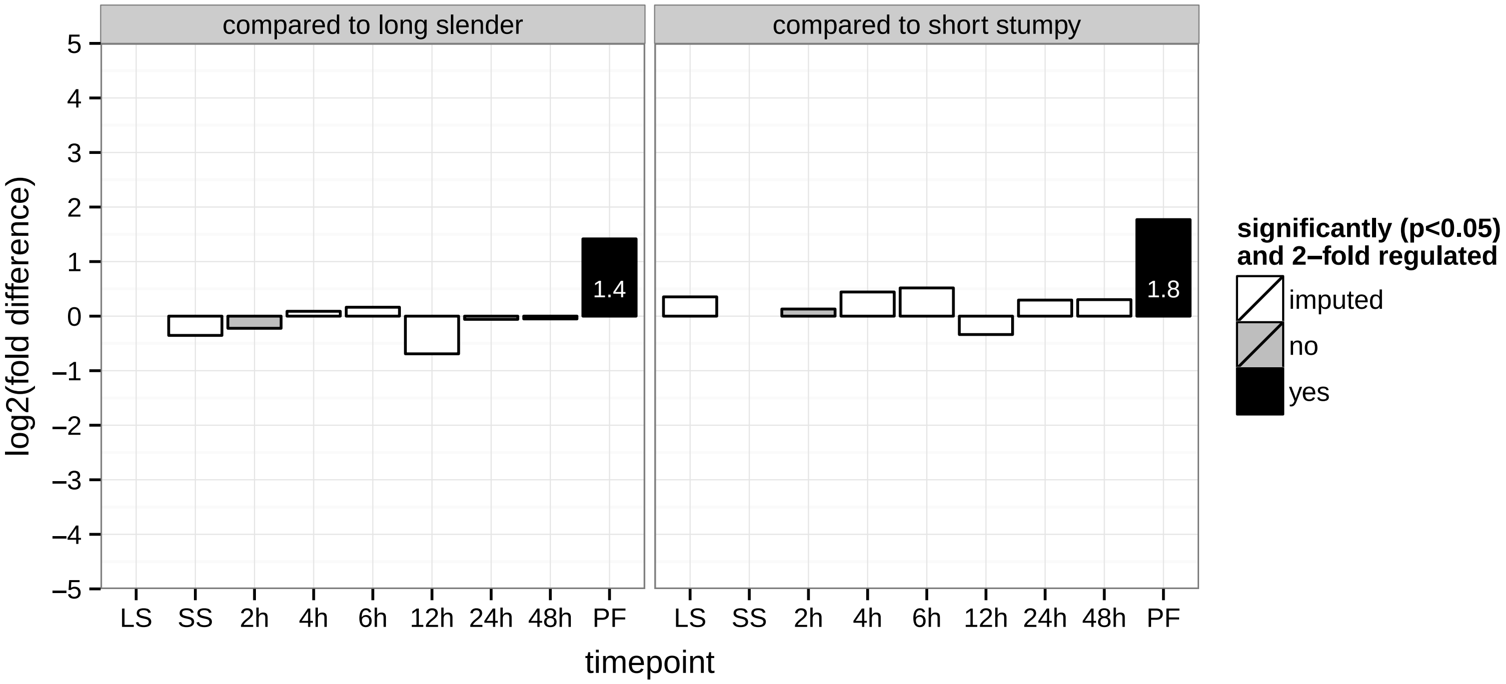
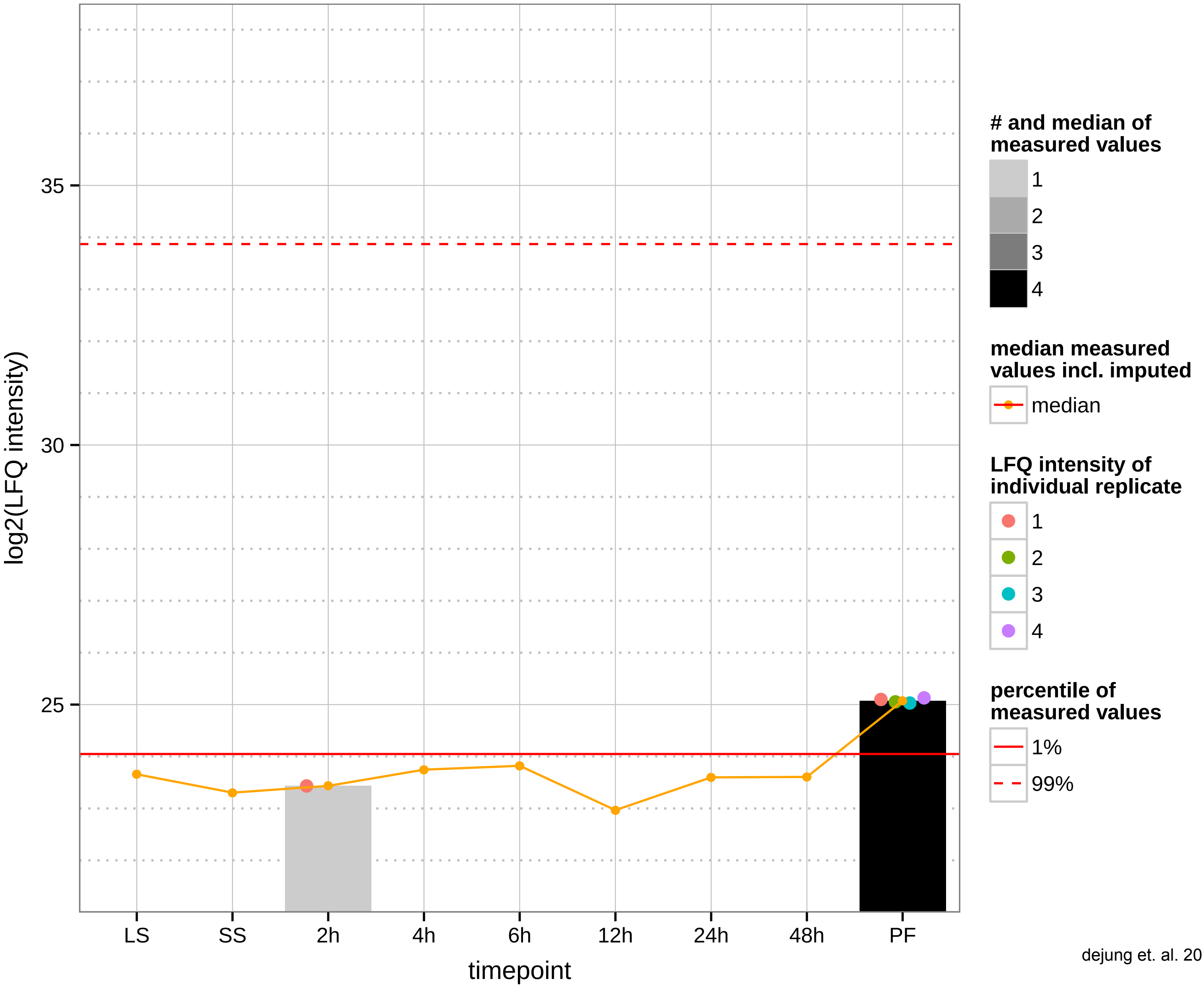
hypothetical protein, conserved
Tb927.11.6150
AGOF: null
AGOC: integral to membrane, mitochondrion
AGOP: protein insertion into membrane
PGOF: null
PGOC: integral to membrane
PGOP: protein insertion into membrane





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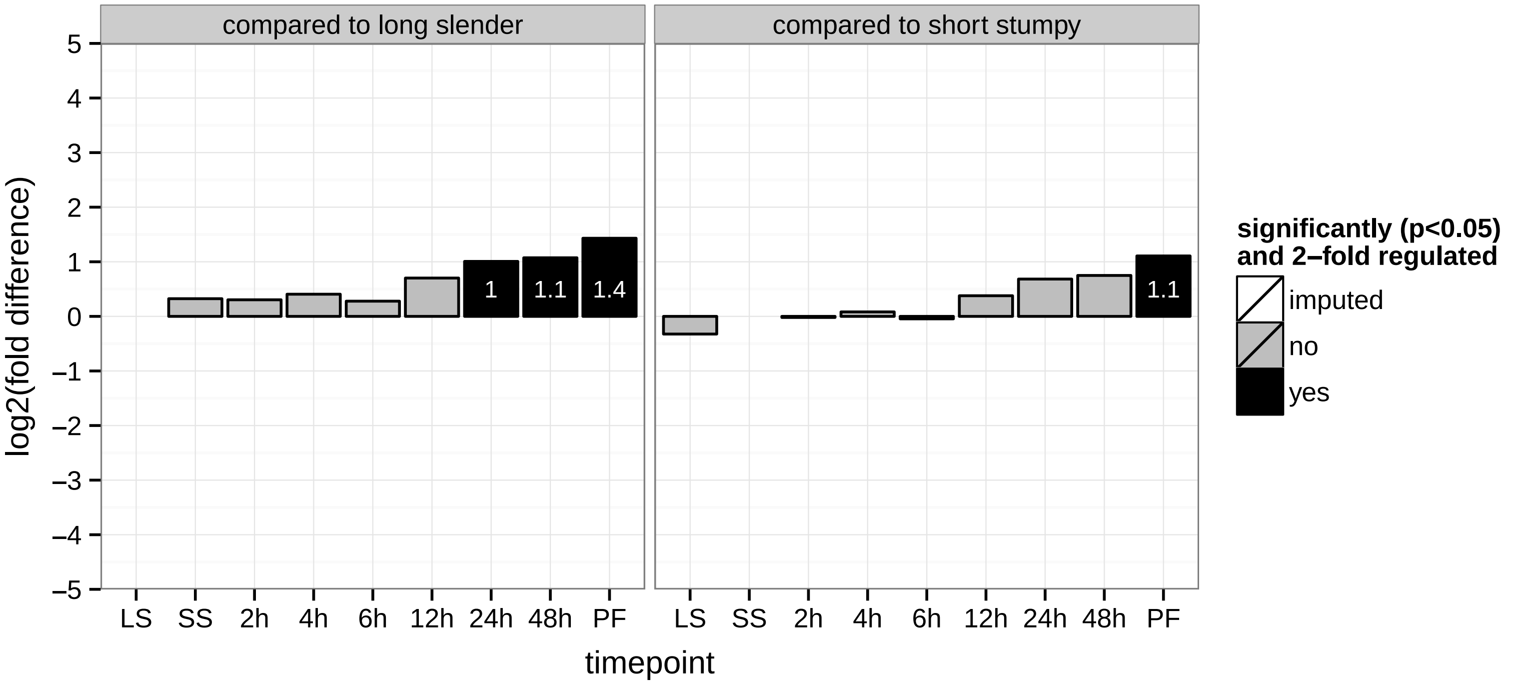
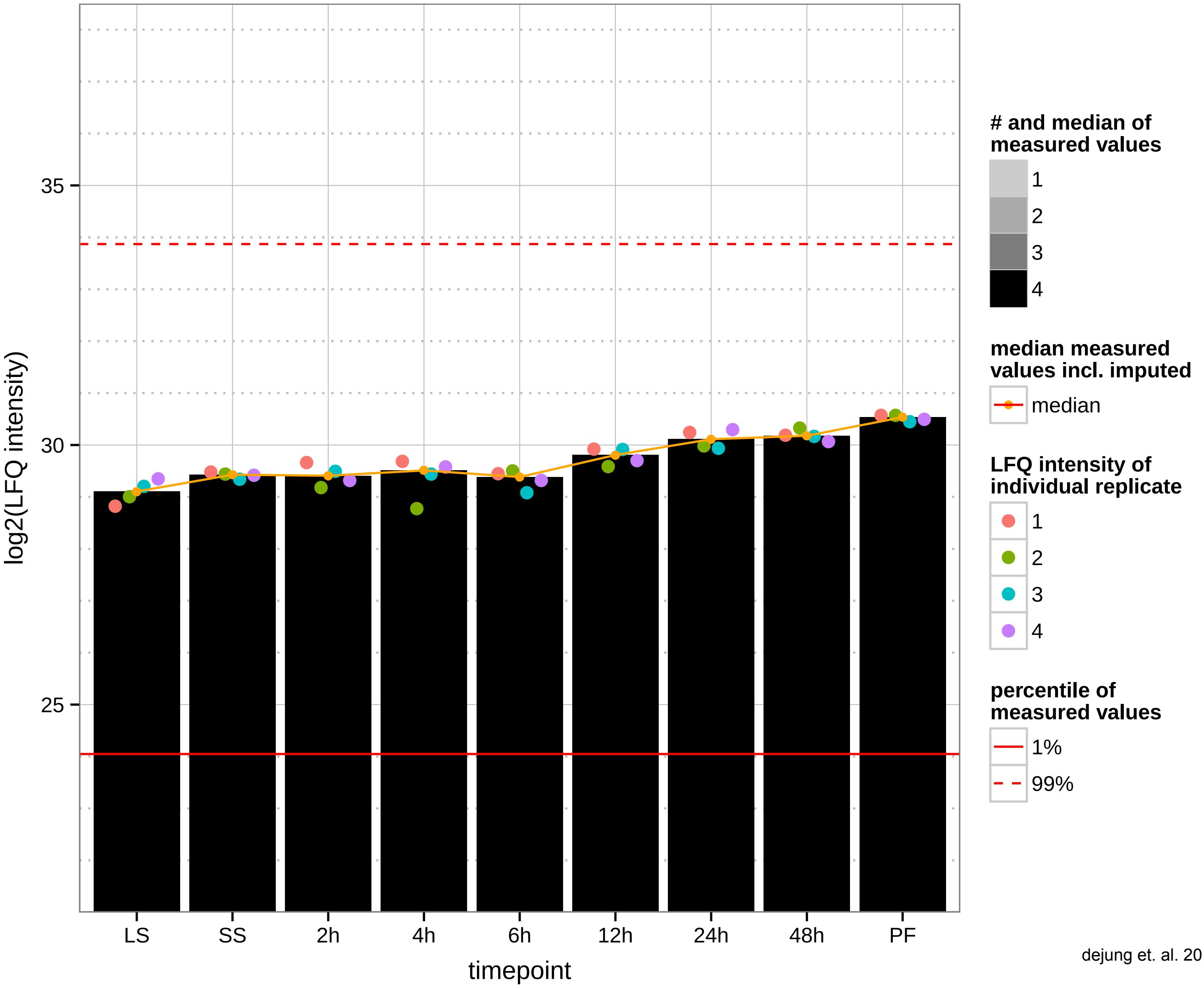
eukaryotic release factor 3, putative (ERF3)
Tb927.11.6160
AGOF: GTP binding, GTPase activity, translation elongation factor activity
AGOC: null
AGOP: translation, translational elongation
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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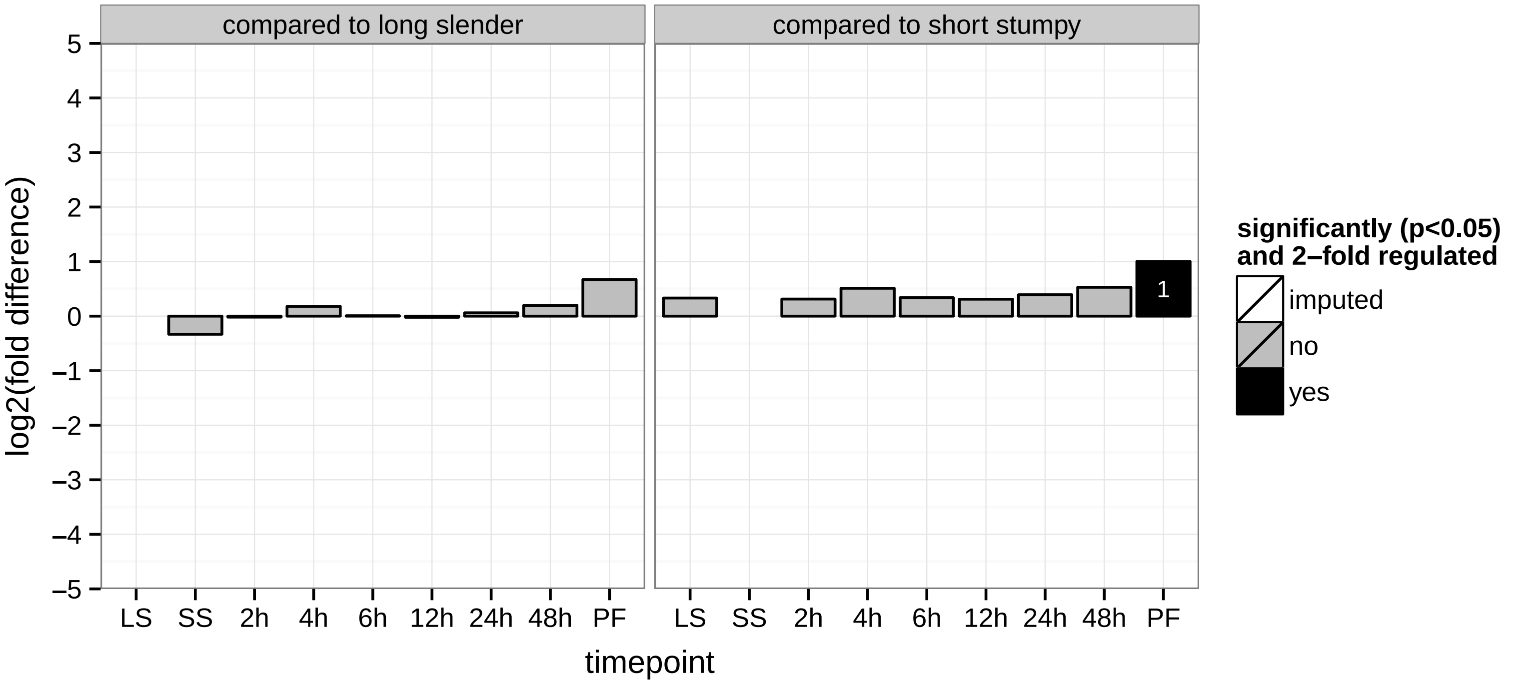
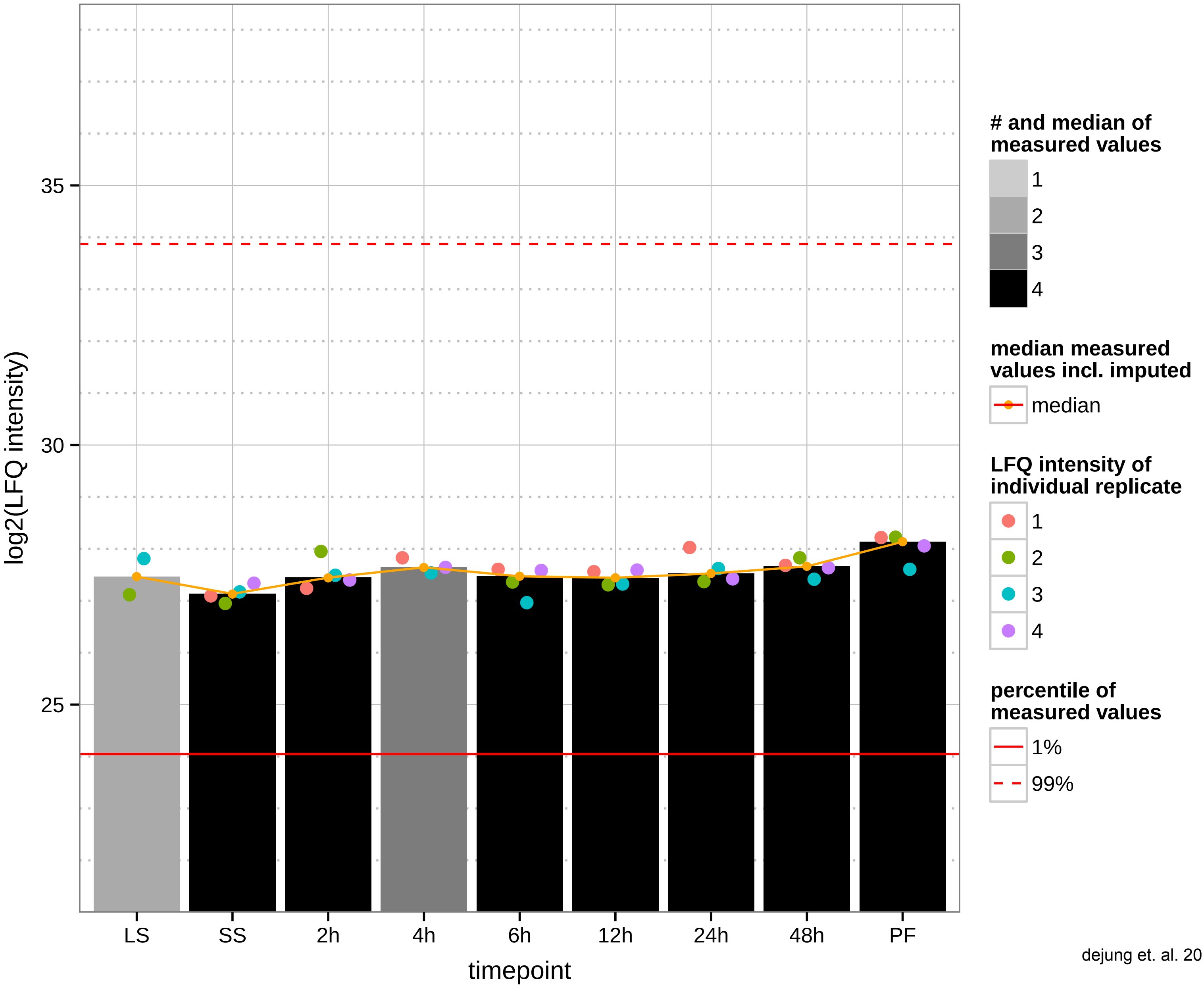
inositol–1, 4, 5–trisphosphate (IP3) 5–phosphatase, putative
Tb927.11.6270
AGOF: inositol–polyphosphate 5–phosphatase activity
AGOC: null
AGOP: intracellular signal transduction
PGOF: null
PGOC: null
PGOP: phosphatidylinositol phosphorylation





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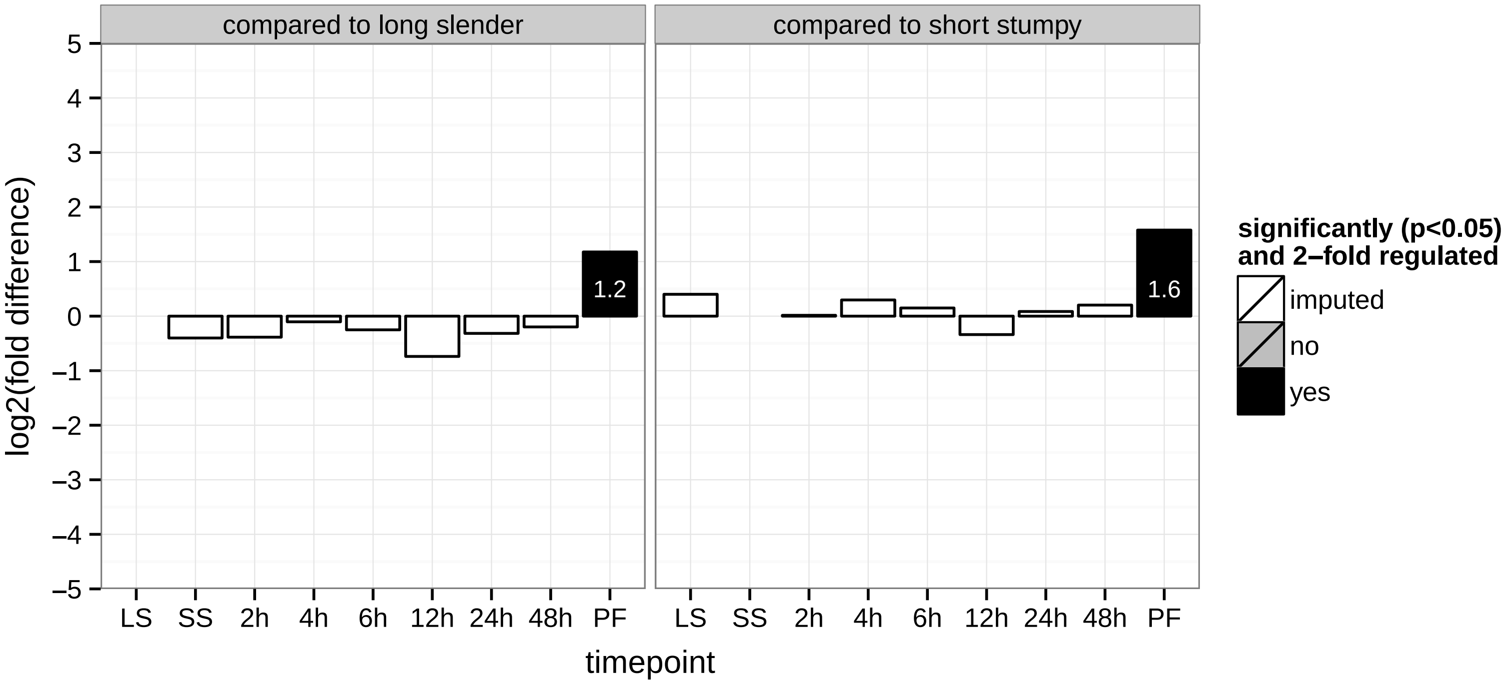
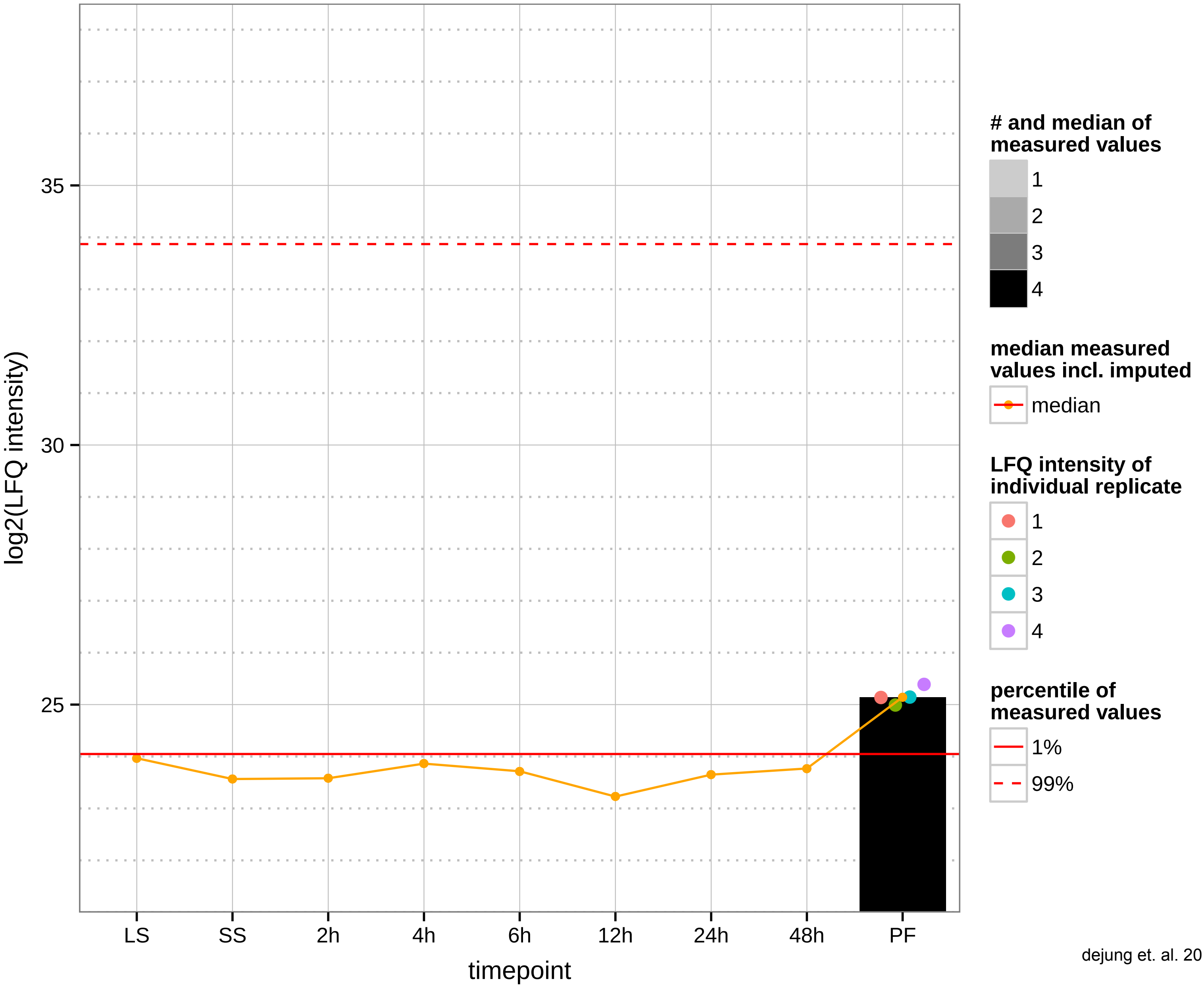
hypothetical protein, conserved
Tb927.11.6490
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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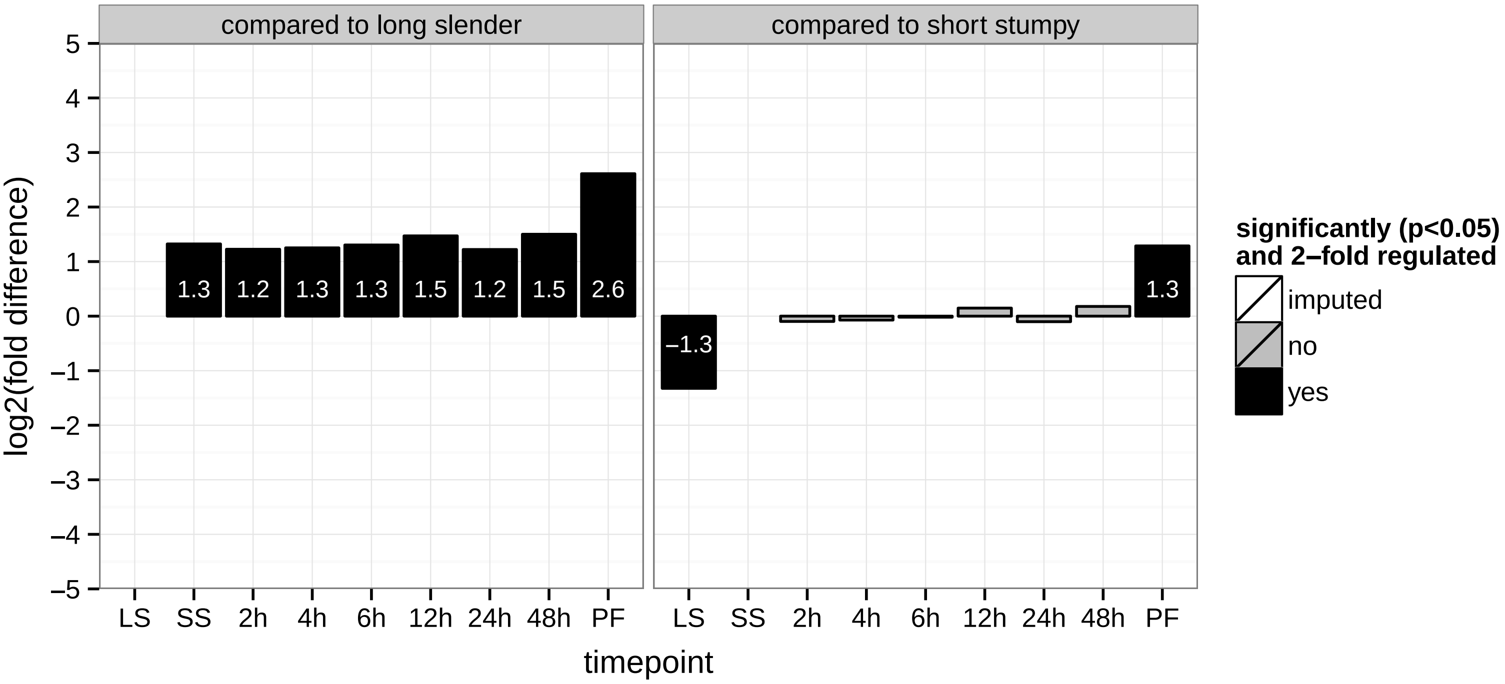
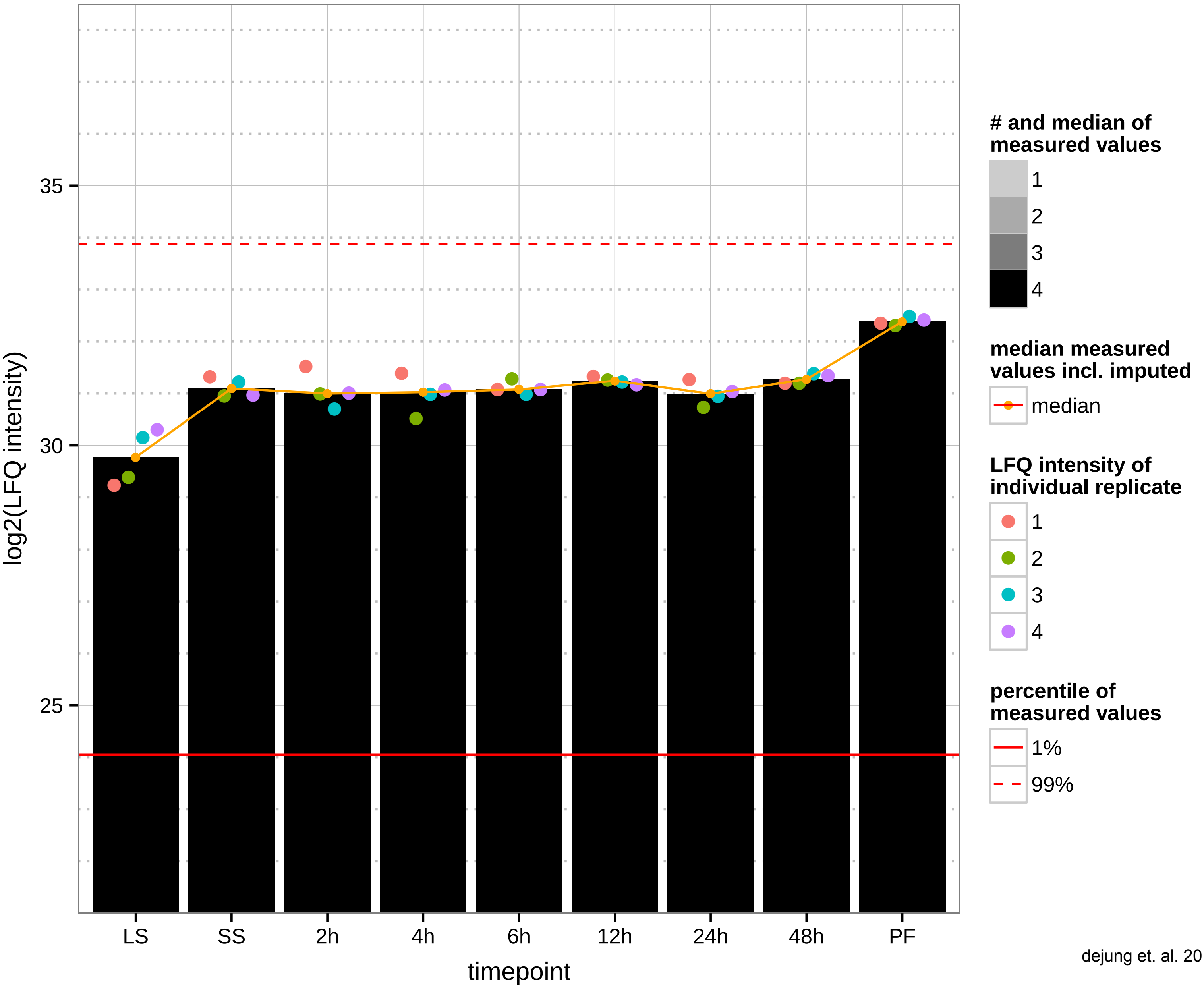
aminopeptidase, putative, metallo–peptidase, Clan MF, Family M17
Tb927.11.6590
AGOF: null, aminopeptidase activity
AGOC: null, intracellular
AGOP: null, proteolysis
PGOF: aminopeptidase activity
PGOC: intracellular
PGOP: proteolysis





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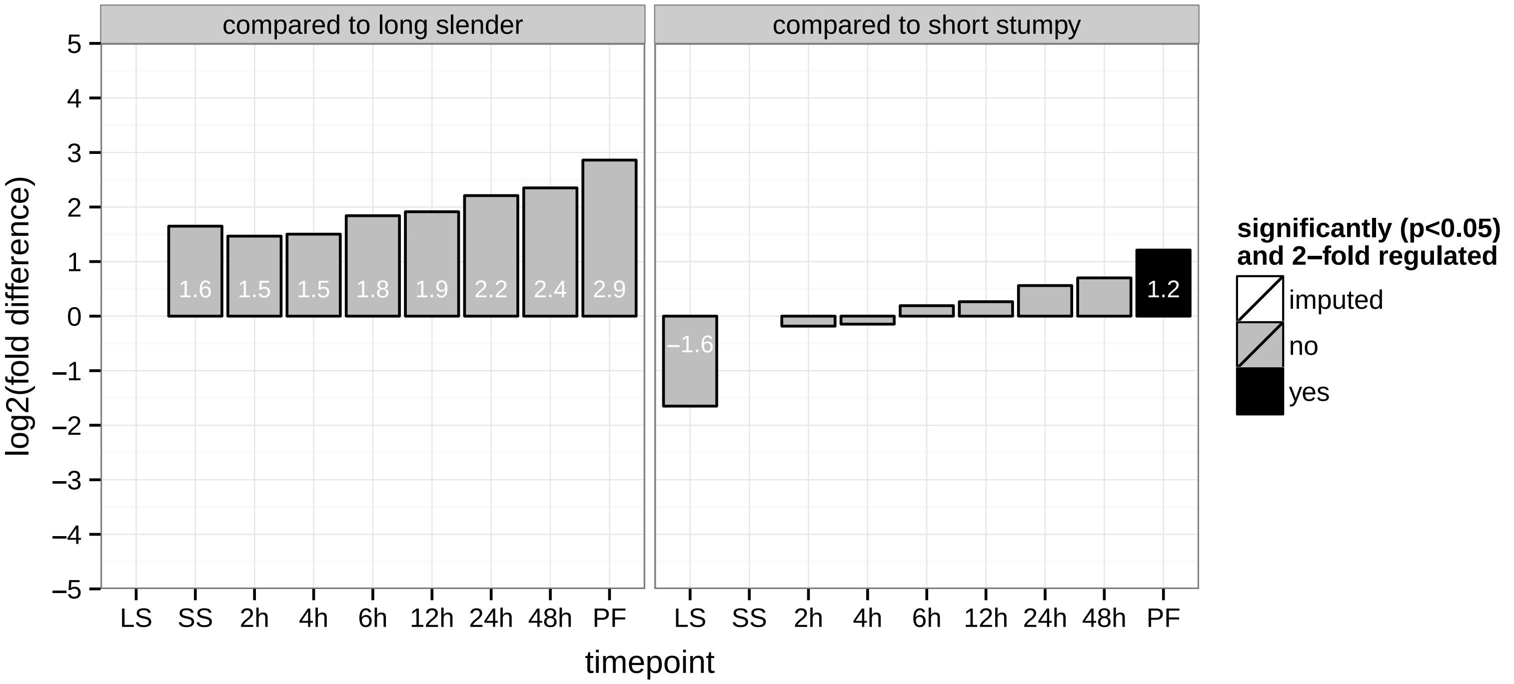
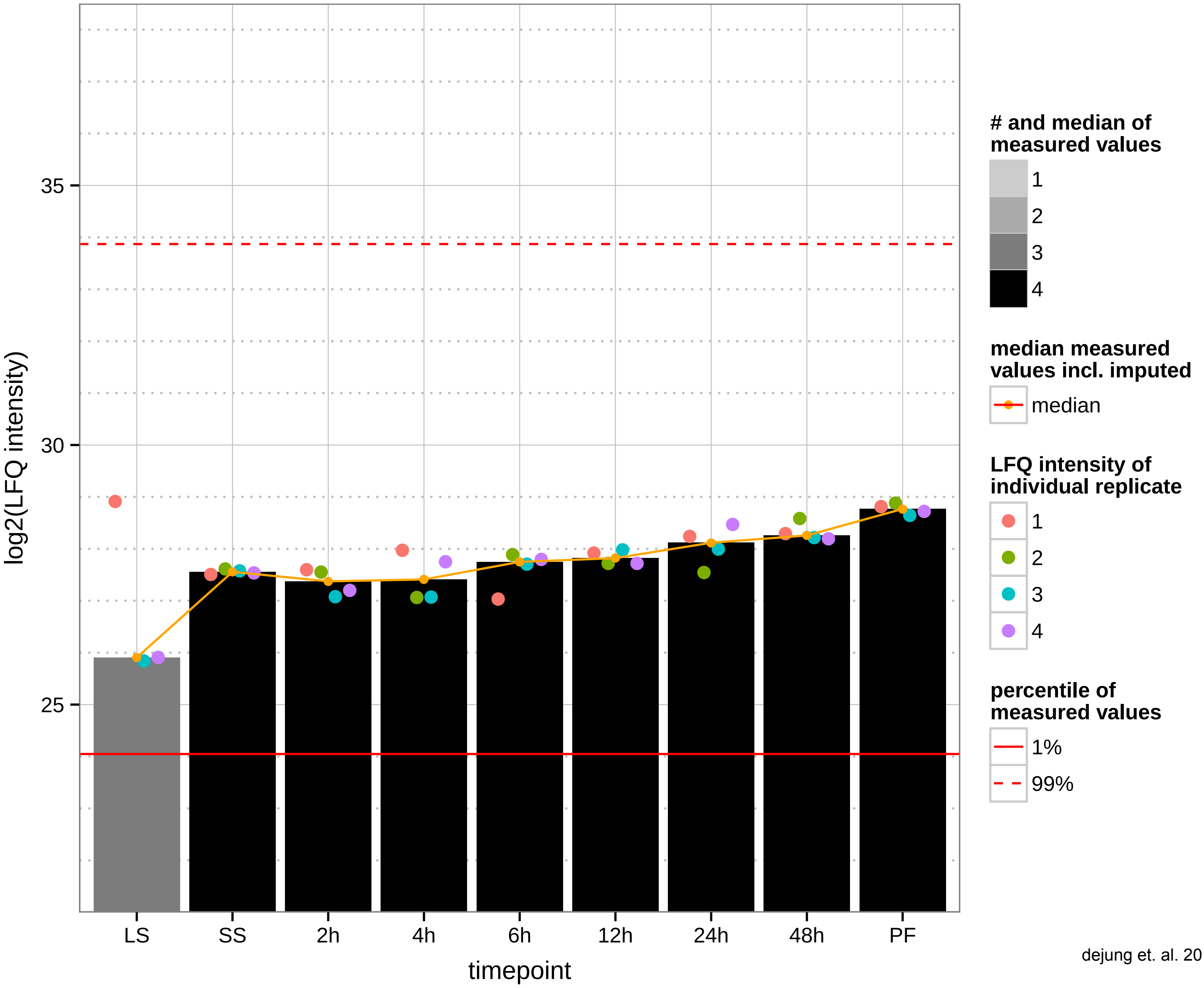
hypothetical protein, conserved
Tb927.11.6980
AGOF: phosphoenolpyruvate carboxykinase activity, purine nucleotide binding
AGOC: mitochondrion
AGOP: gluconeogenesis
PGOF: phosphoenolpyruvate carboxykinase activity, purine nucleotide binding
PGOC: null
PGOP: gluconeogenesis





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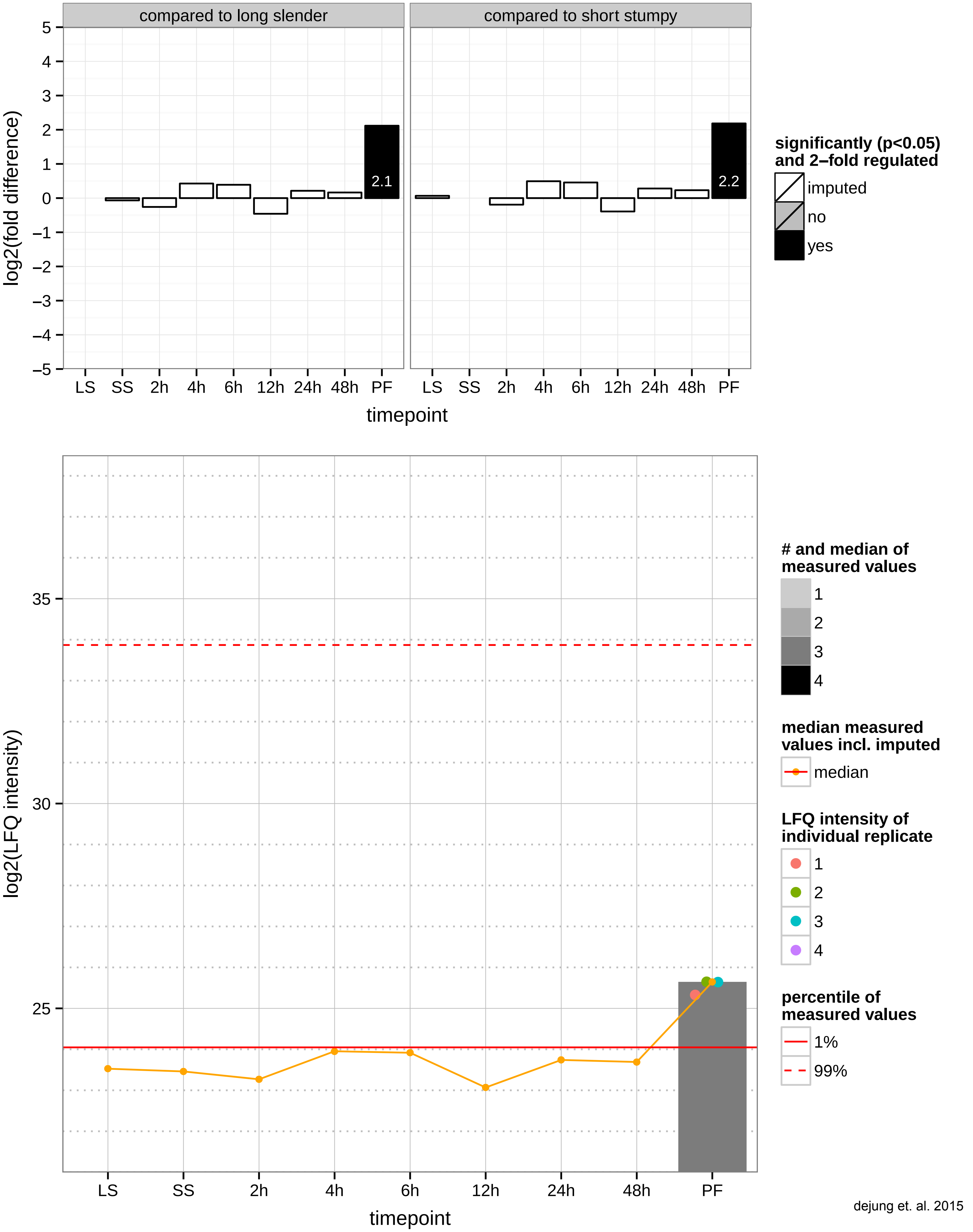
hypothetical protein, conserved
Tb927.11.7050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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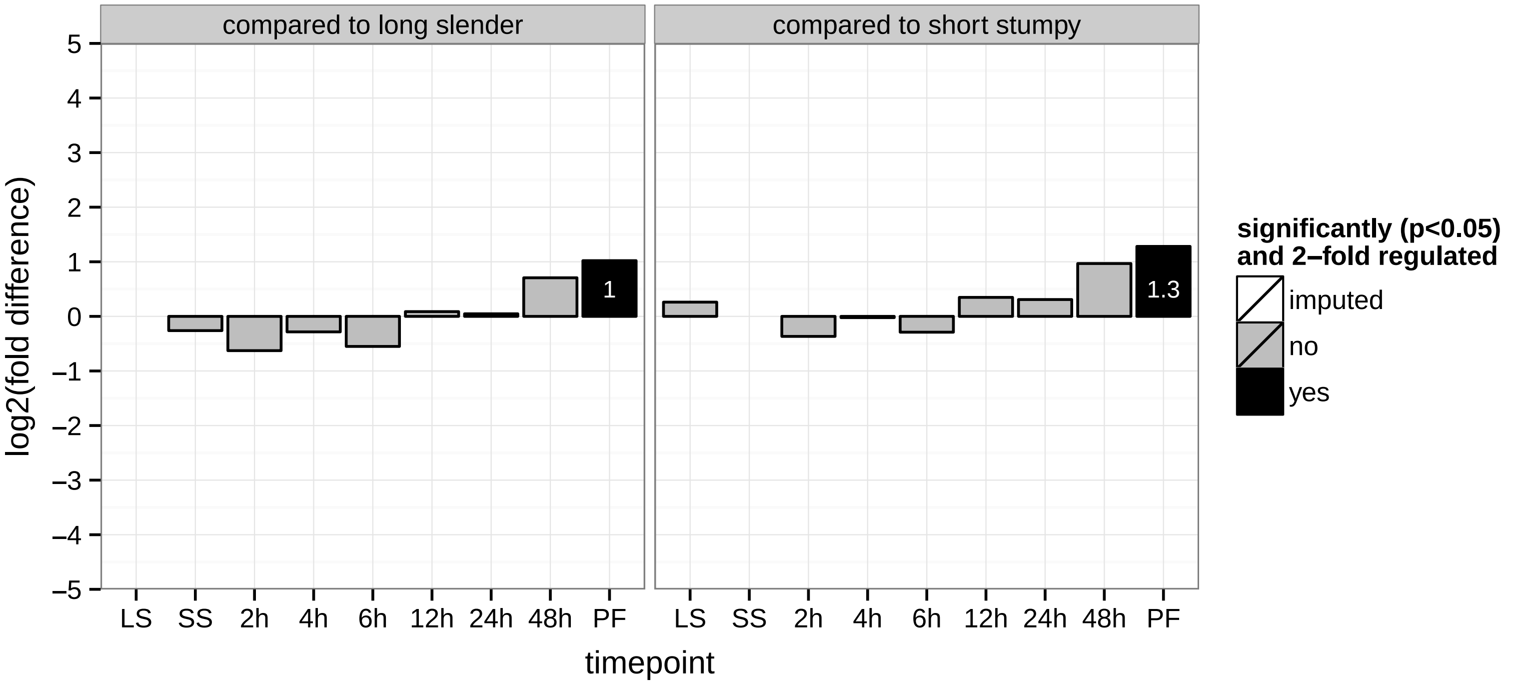
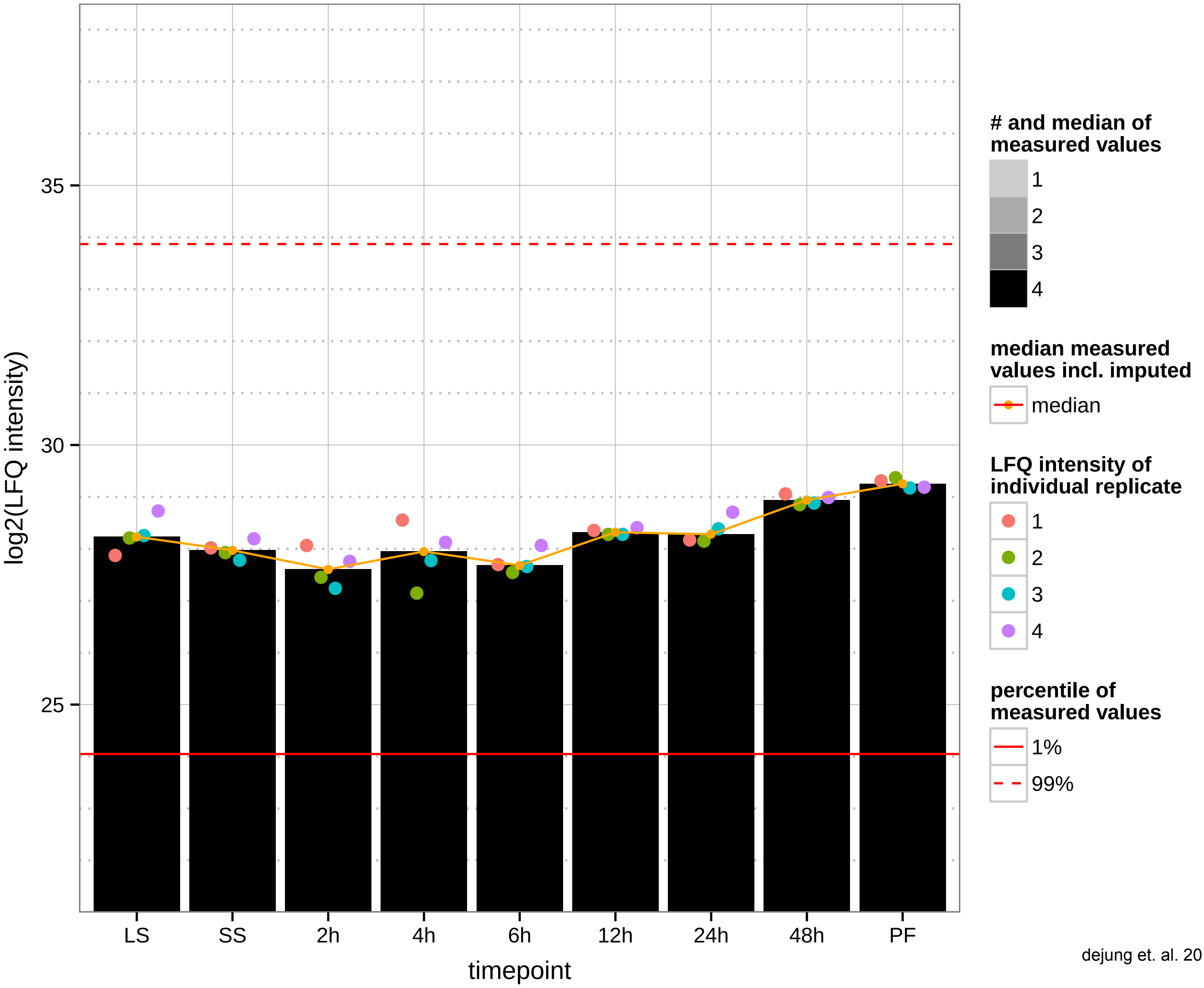
protein phosphatase 1, putative
Tb927.11.8090
AGOF: hydrolase activity, protein serine/threonine phosphatase activity
AGOC: null
AGOP: cellular process
PGOF: hydrolase activity
PGOC: null
PGOP: null





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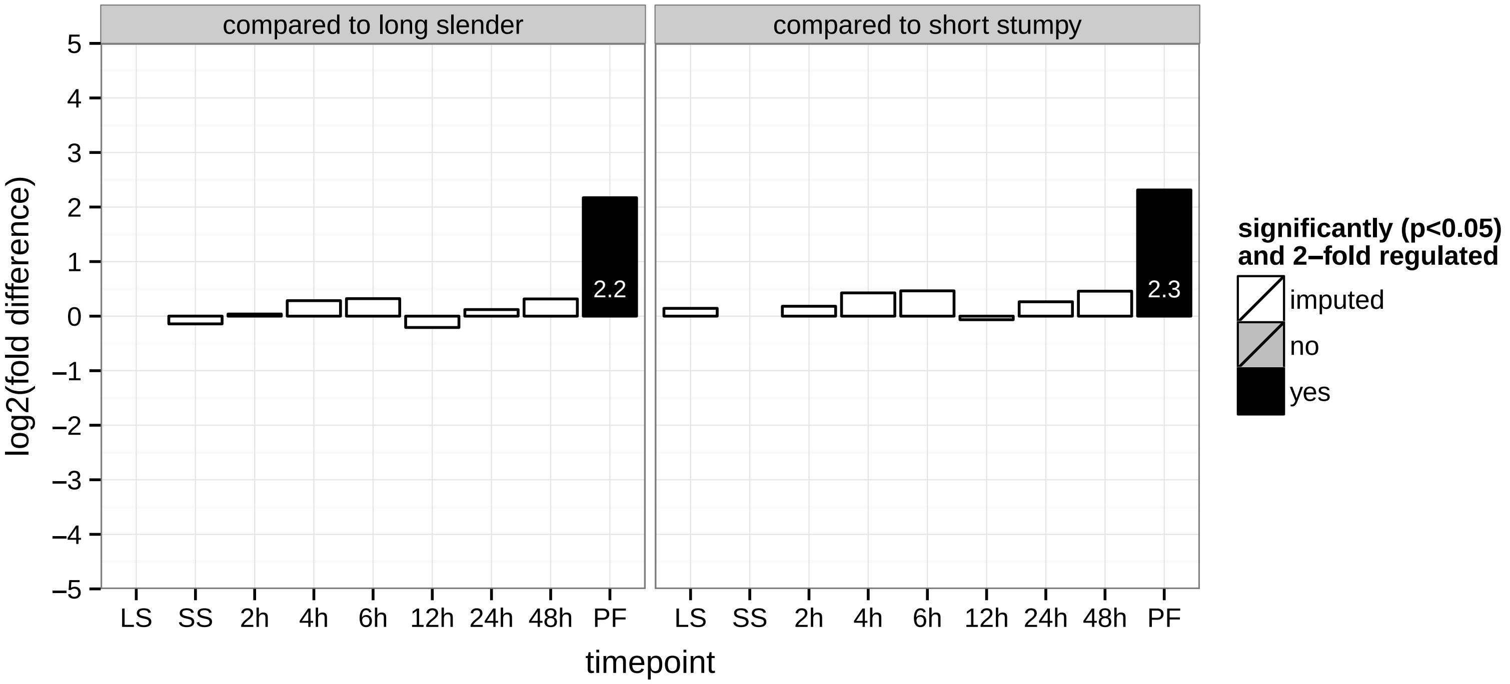
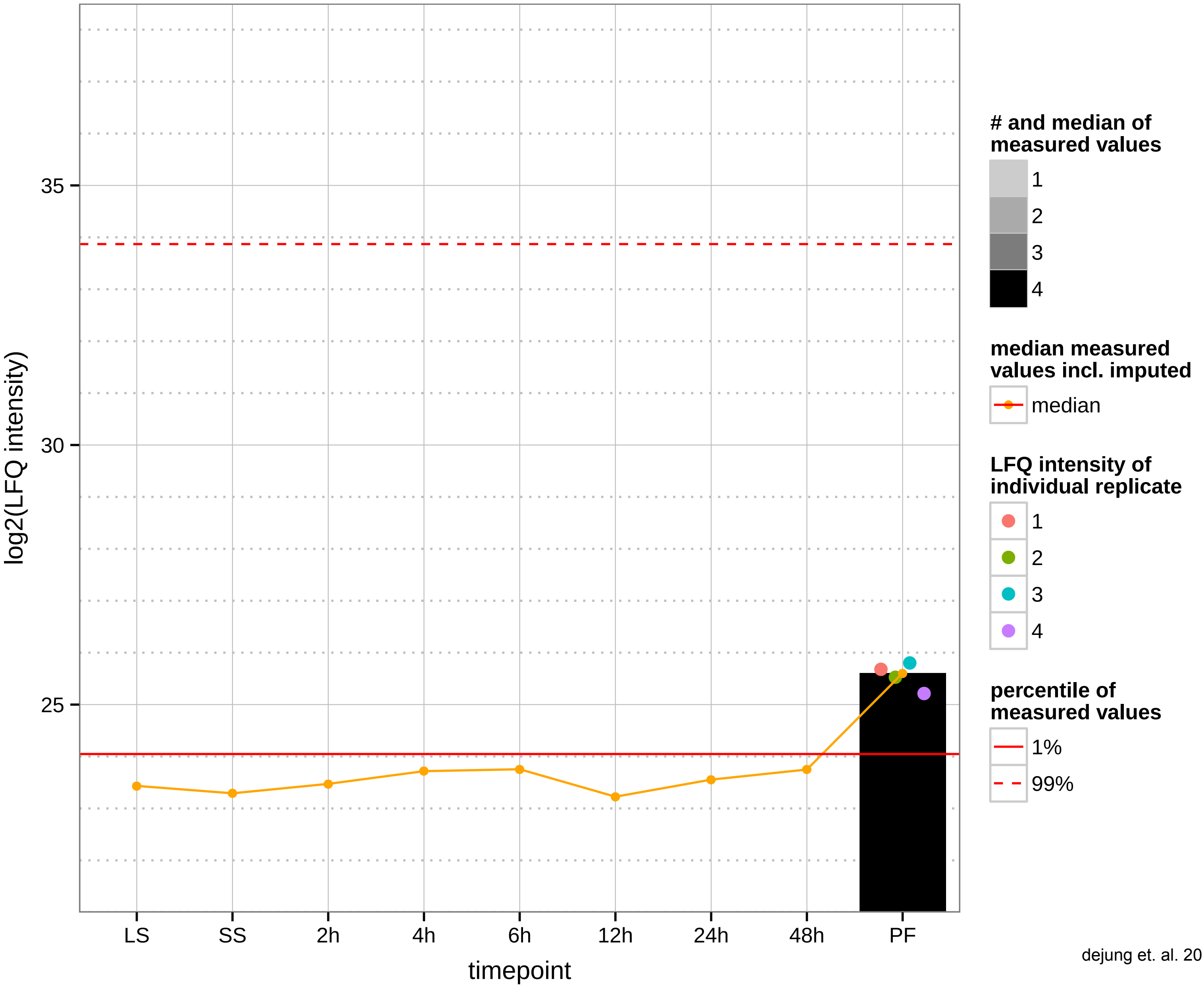
DNA repair protein RAD51 (RAD51)
Tb927.11.8190
AGOF: ATP binding, ATPase activity, damaged DNA binding, double−stranded DNA binding, double−stranded DNA−depende
AGOC: nucleus, site of double−strand break
AGOP: DNA recombination, double−strand break repair via homologous recombination, evasion or tolerance of host immune
PGOF: ATP binding, DNA binding, DNA−dependent ATPase activity, damaged DNA binding, nucleoside−triphosphatase activi
PGOC: null
PGOP: DNA metabolic process, DNA repair





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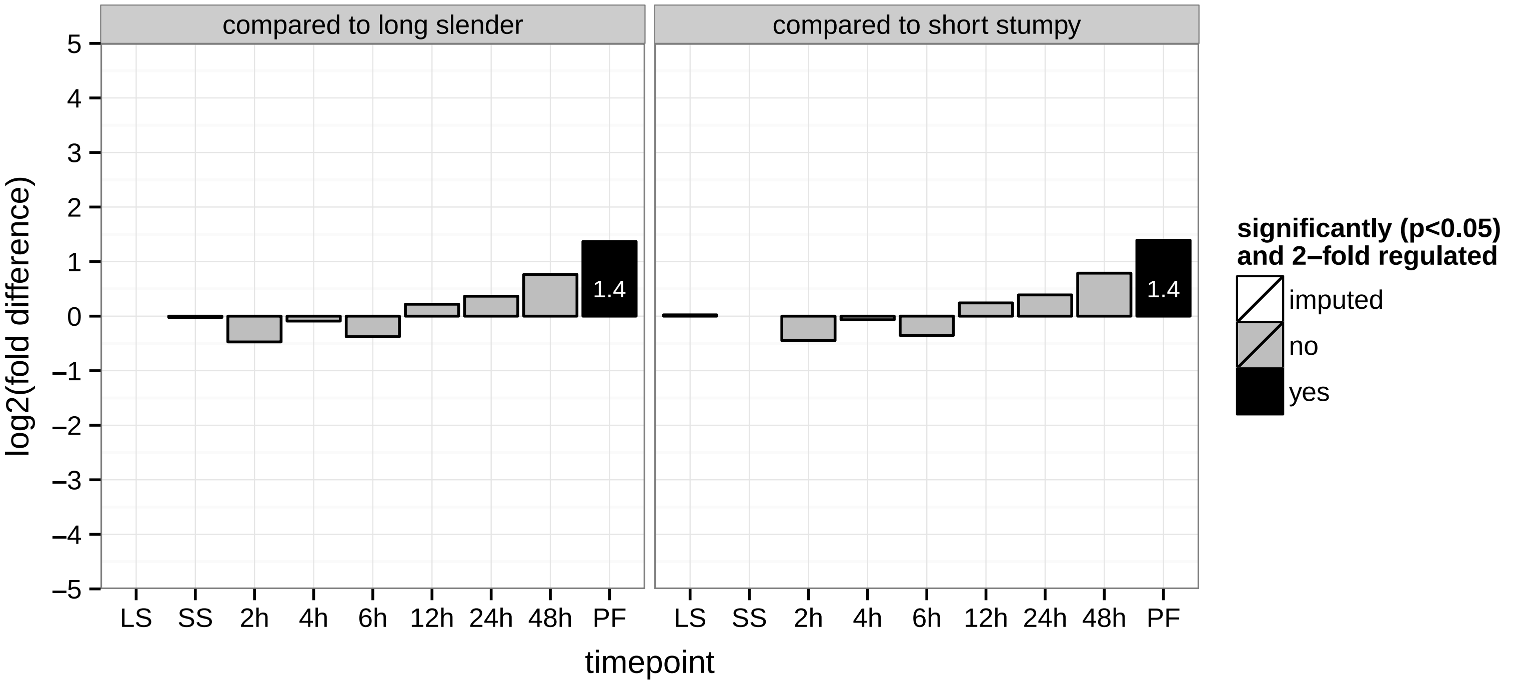
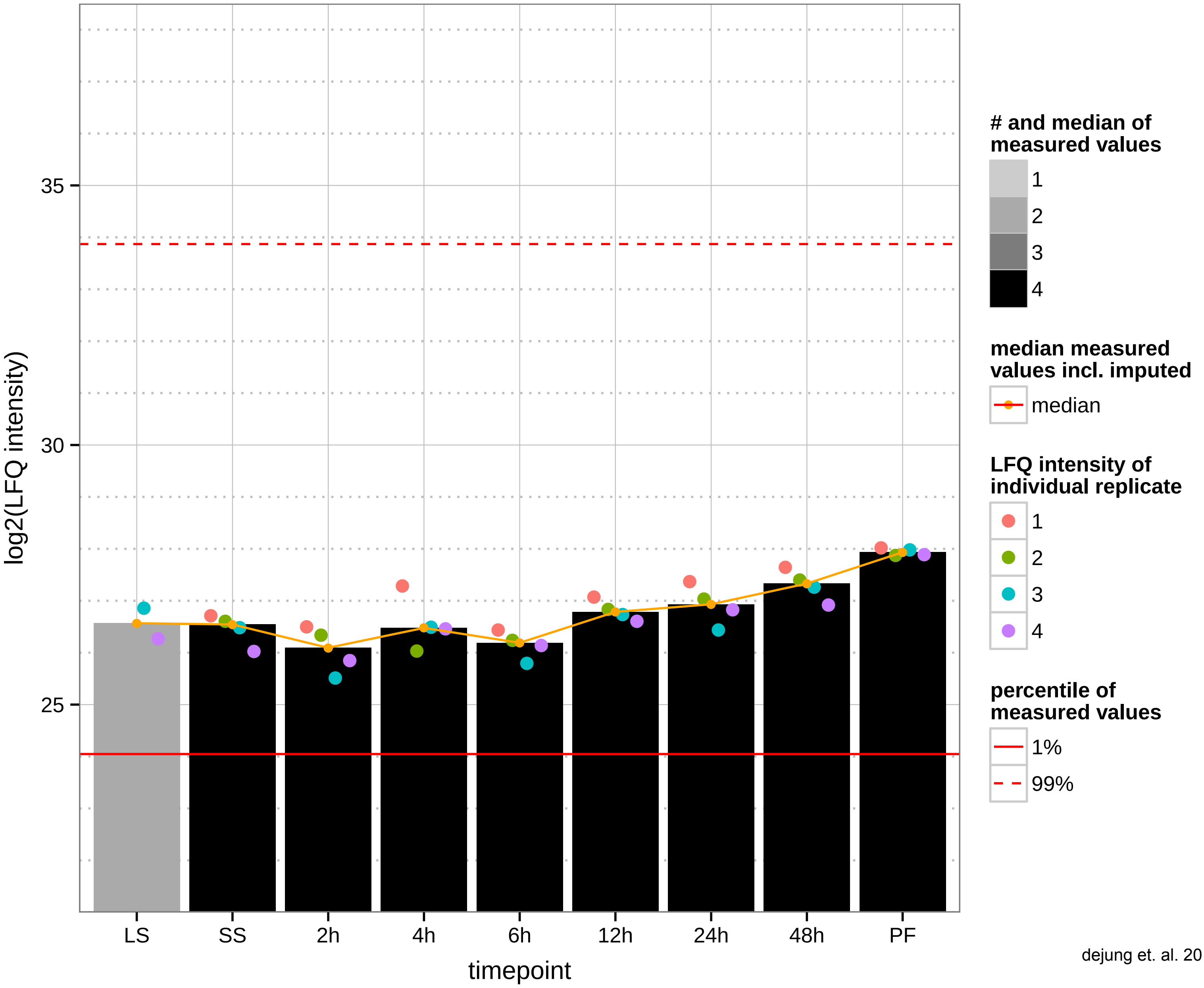
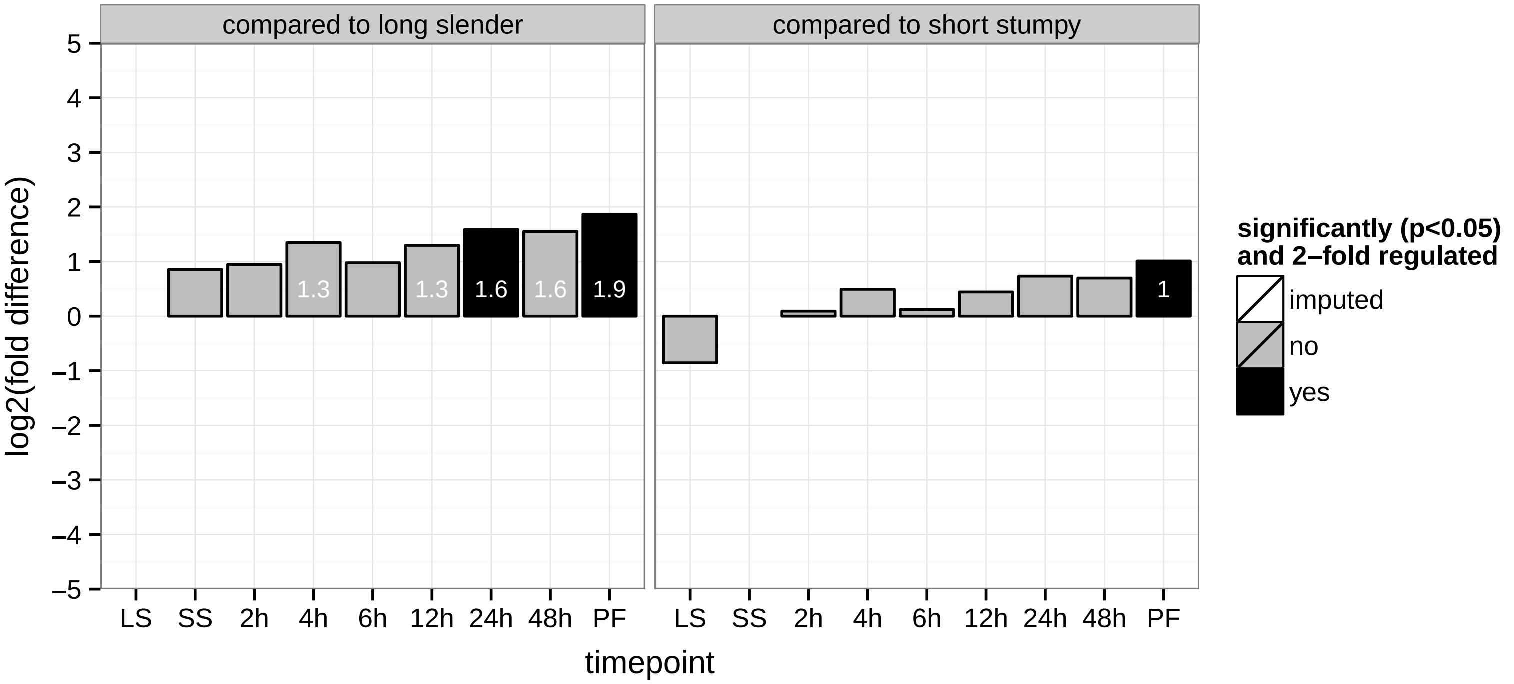
hypothetical protein, conserved
Tb927.11.8230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

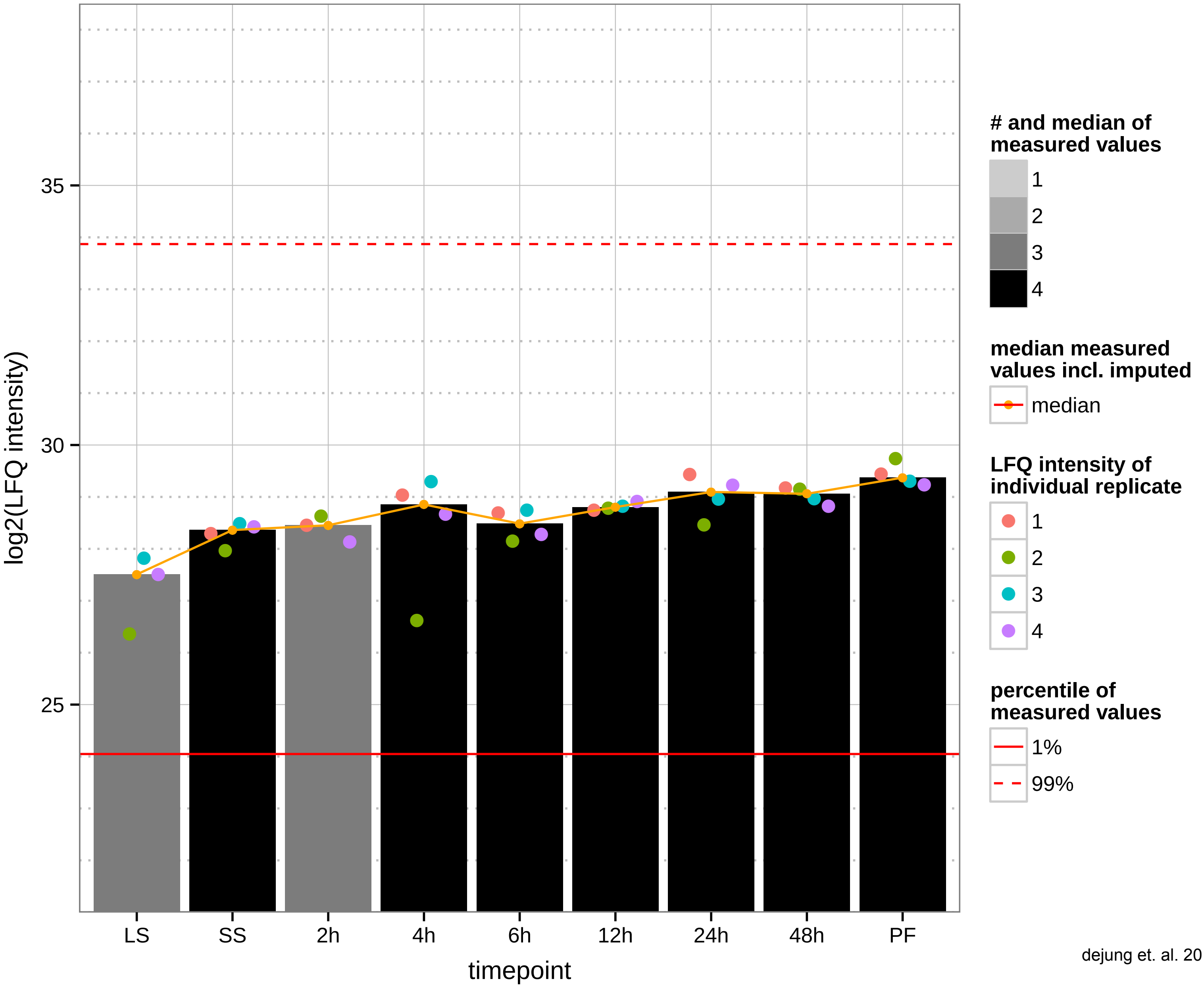




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.8270
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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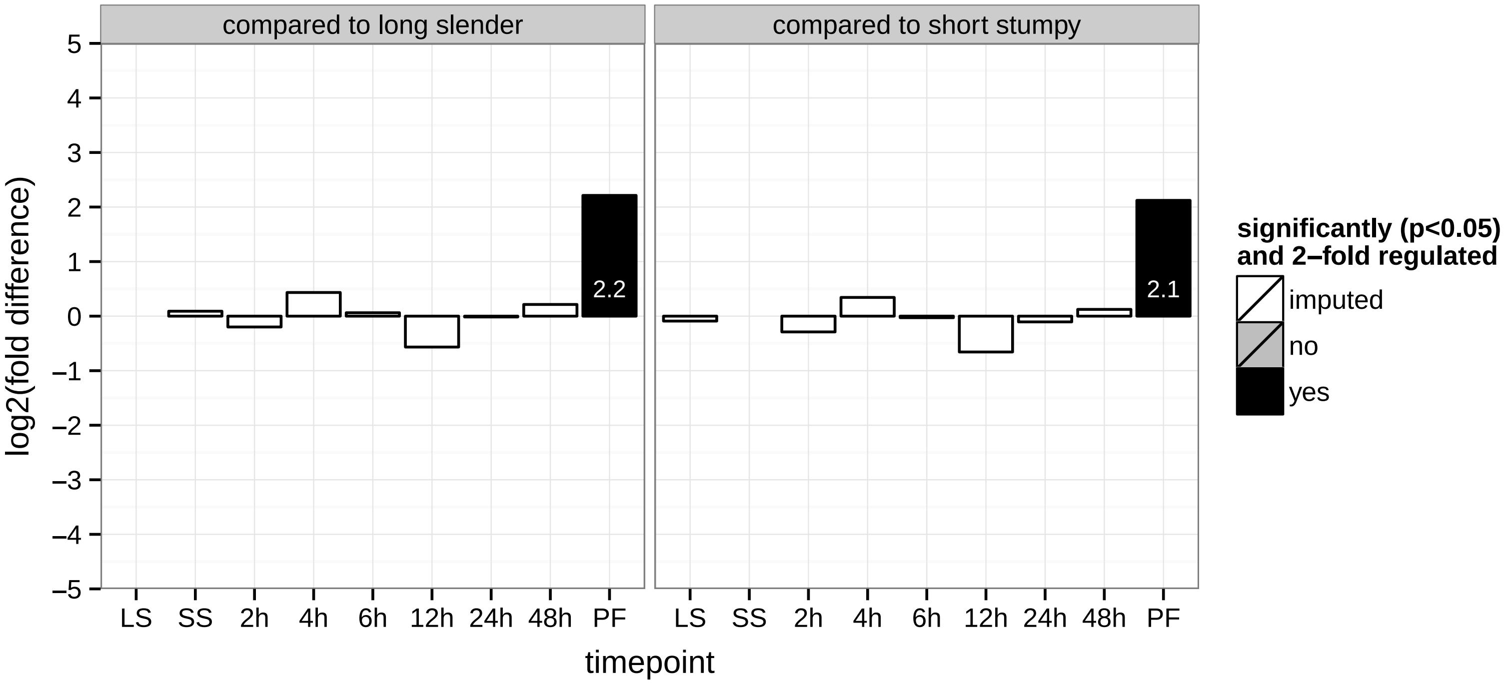
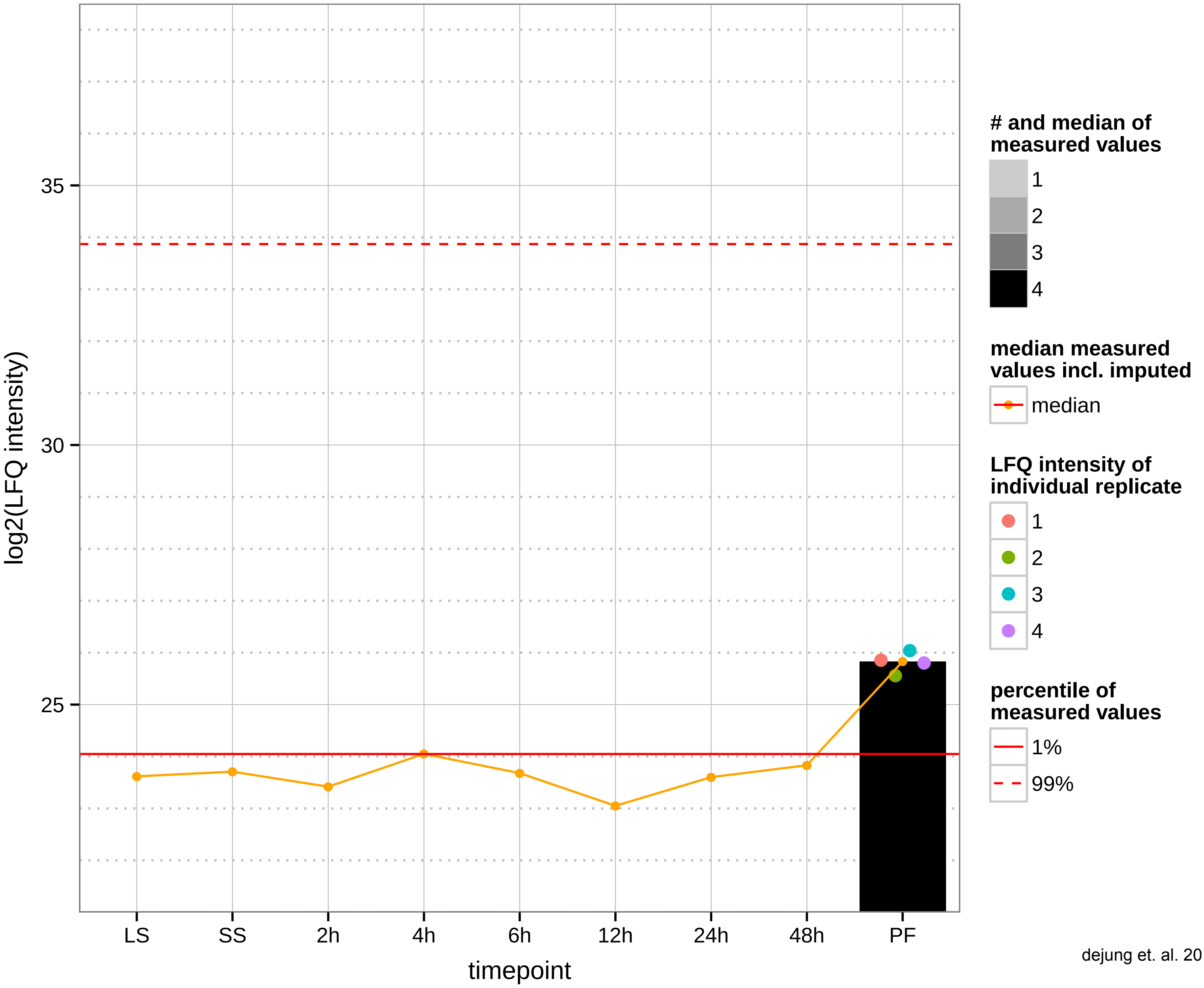
hypothetical protein, conserved
Tb927.11.9120
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: ATP binding, DNA binding, protein binding, zinc ion binding
PGOC: null
PGOP: null





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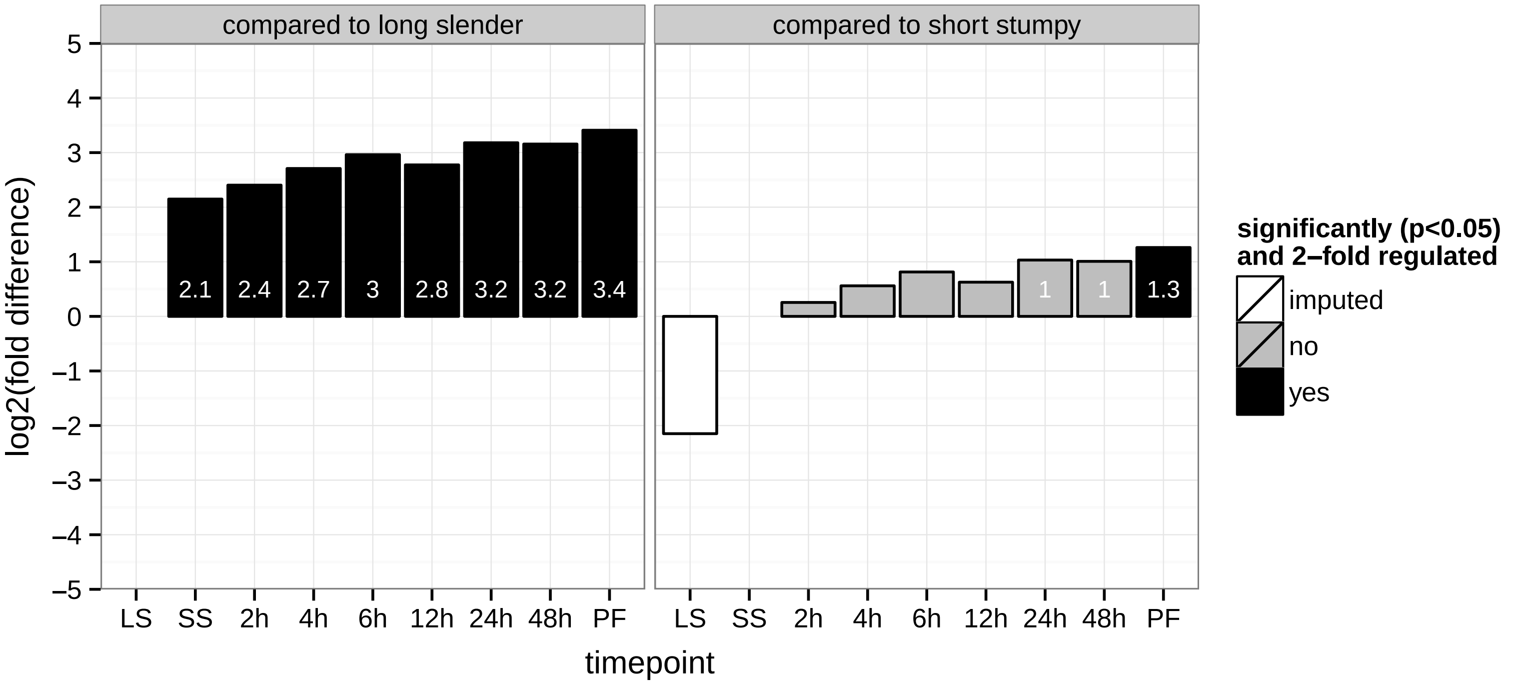
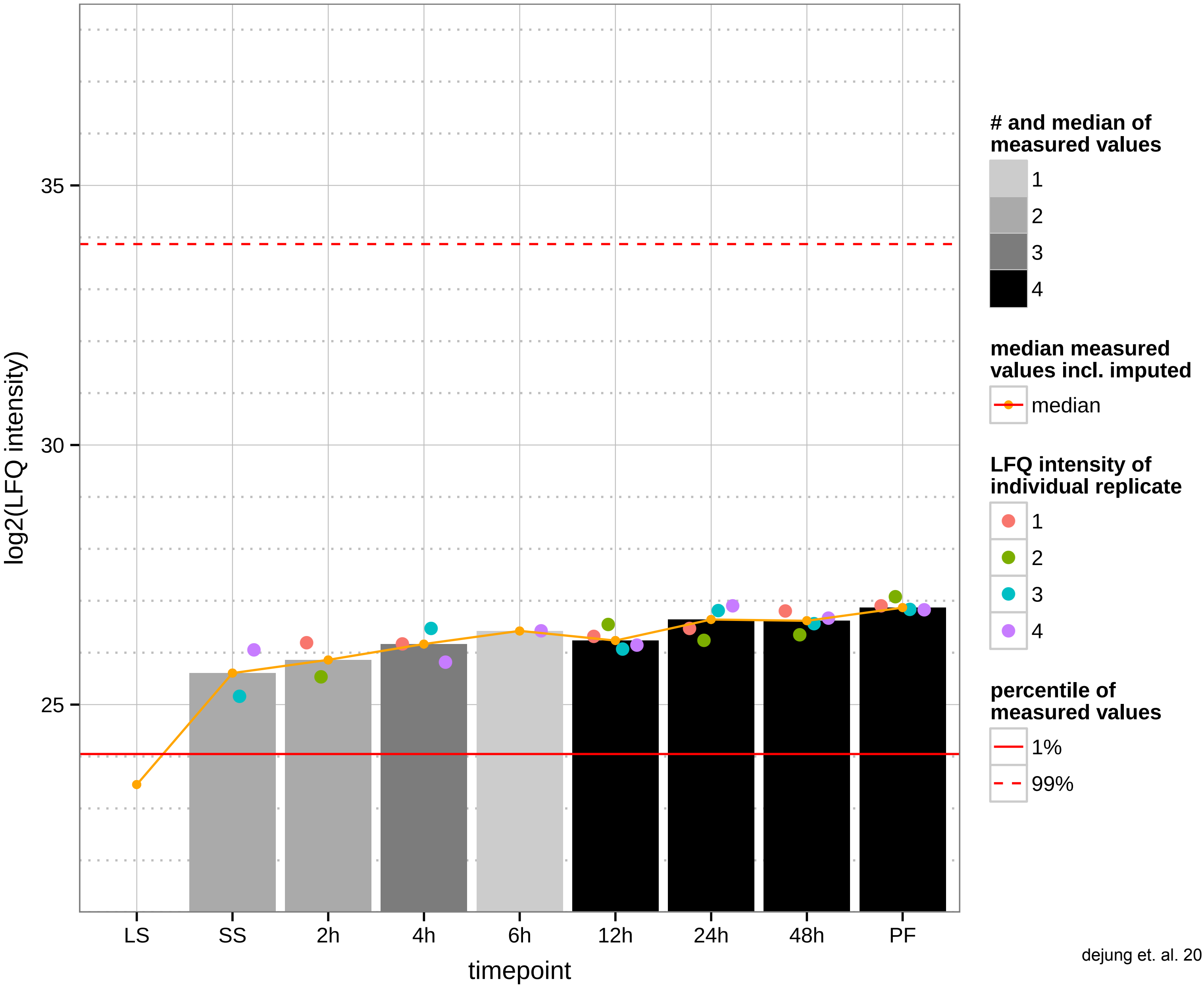
cyclophilin type peptidyl–prolyl cis–trans isomerase, putative (PPIase)
Tb927.11.9450
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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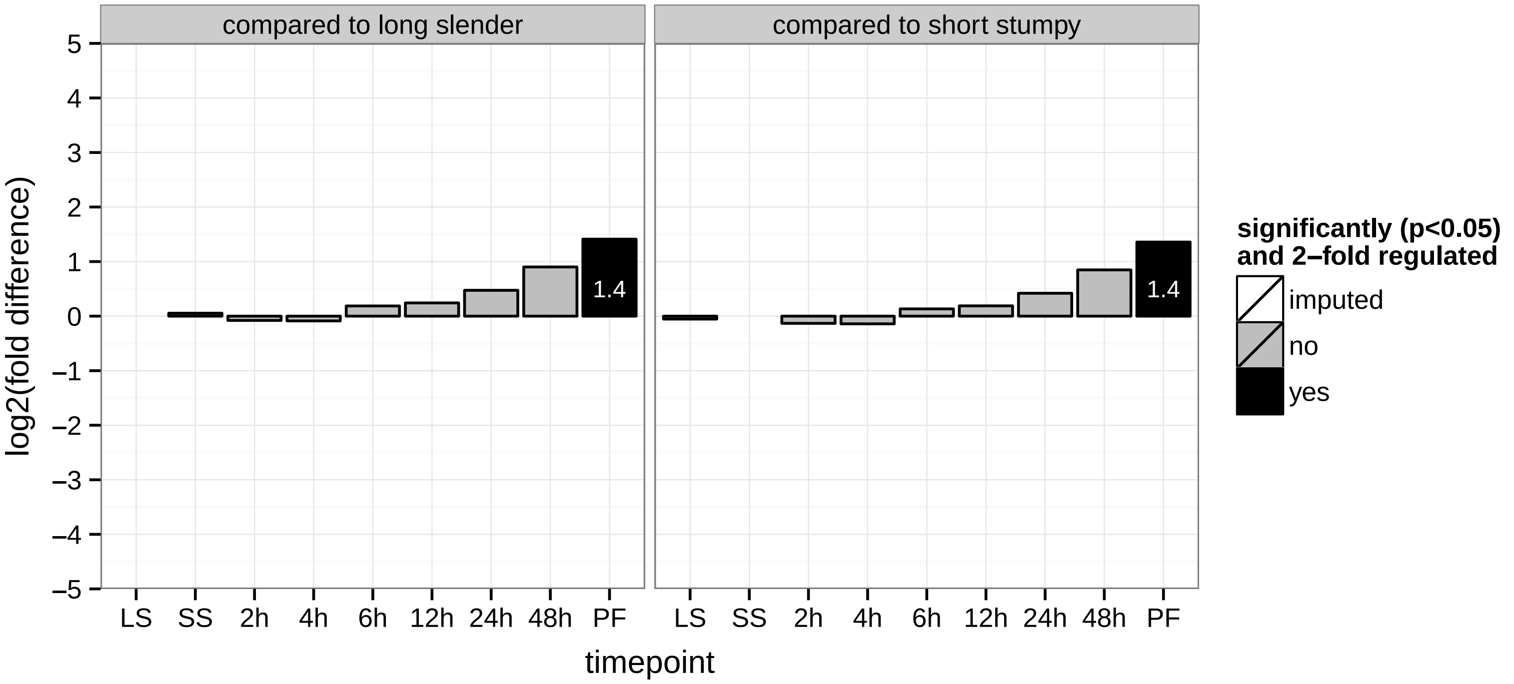
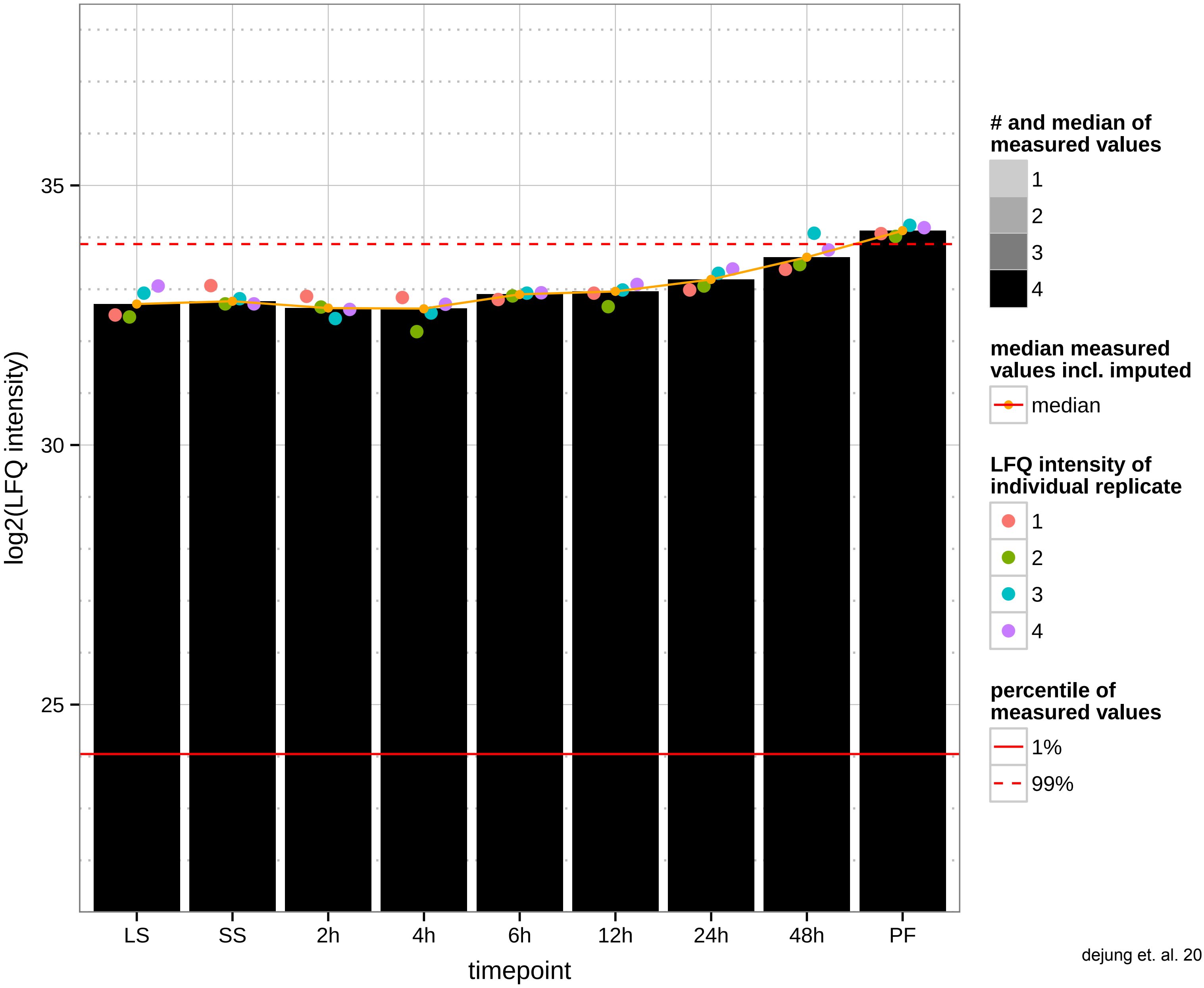
S–adenosylhomocysteine hydrolase, putative
Tb927.11.9590
AGOF: adenosylhomocysteinase activity
AGOC: null
AGOP: one–carbon metabolic process
PGOF: adenosylhomocysteinase activity
PGOC: null
PGOP: one–carbon metabolic process





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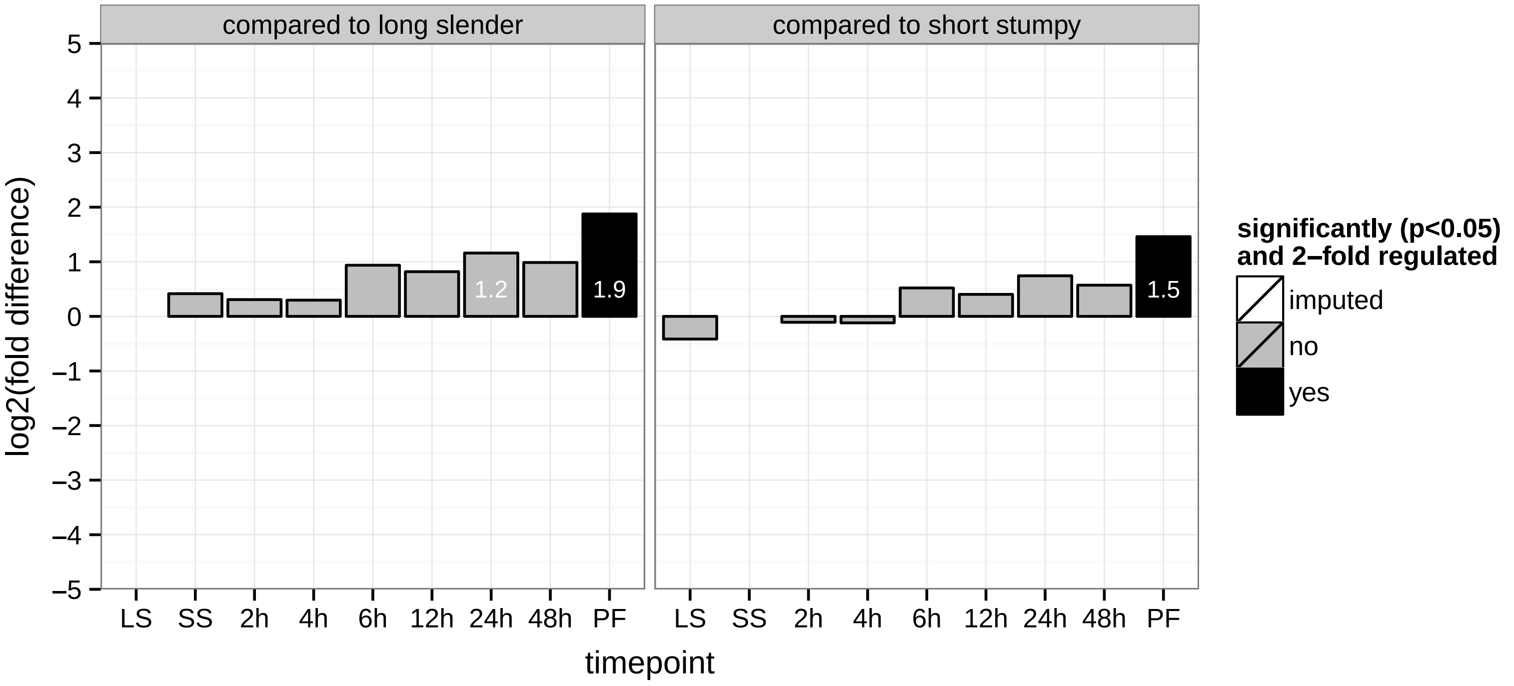
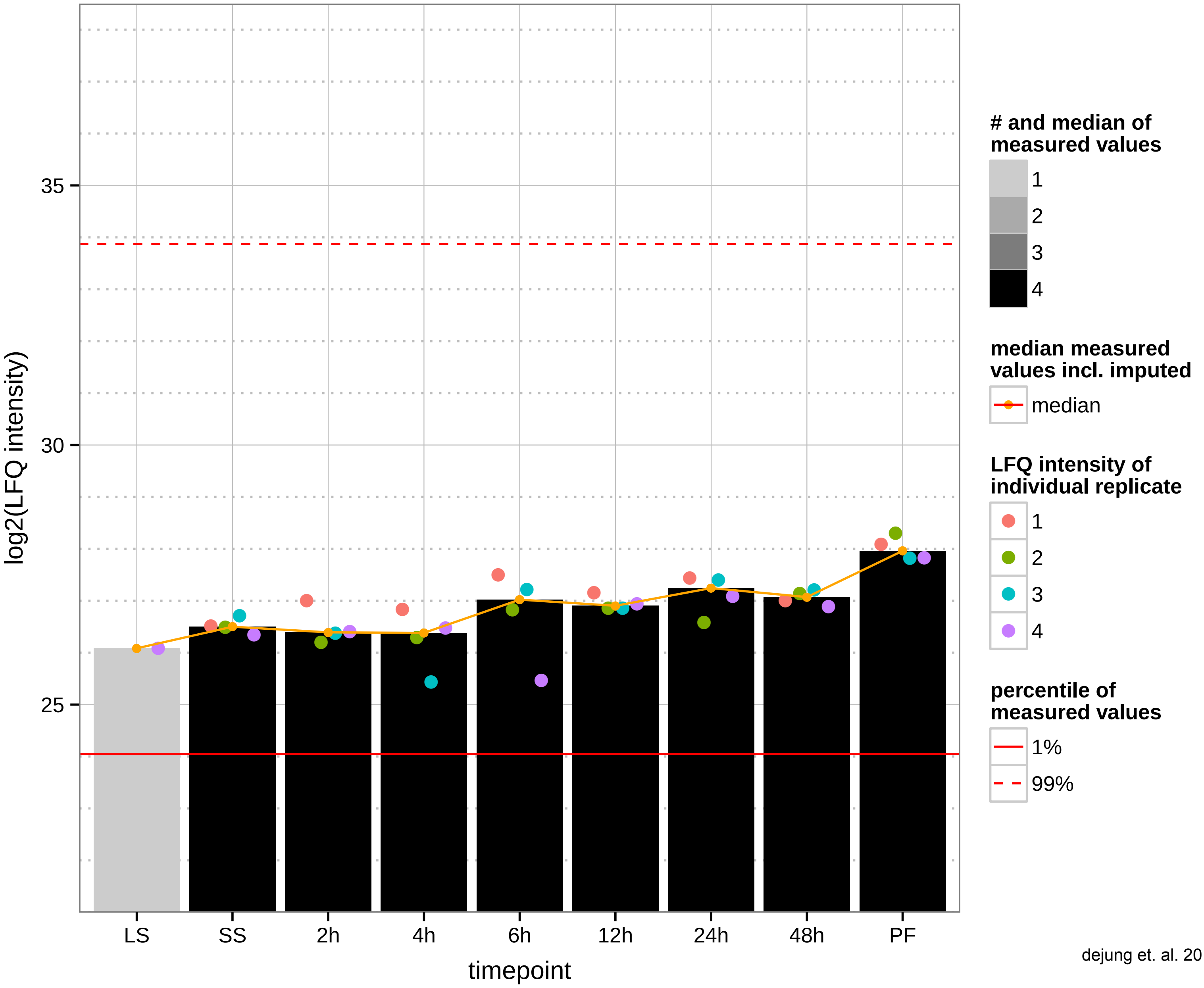
conserved protein
Tb927.11.9780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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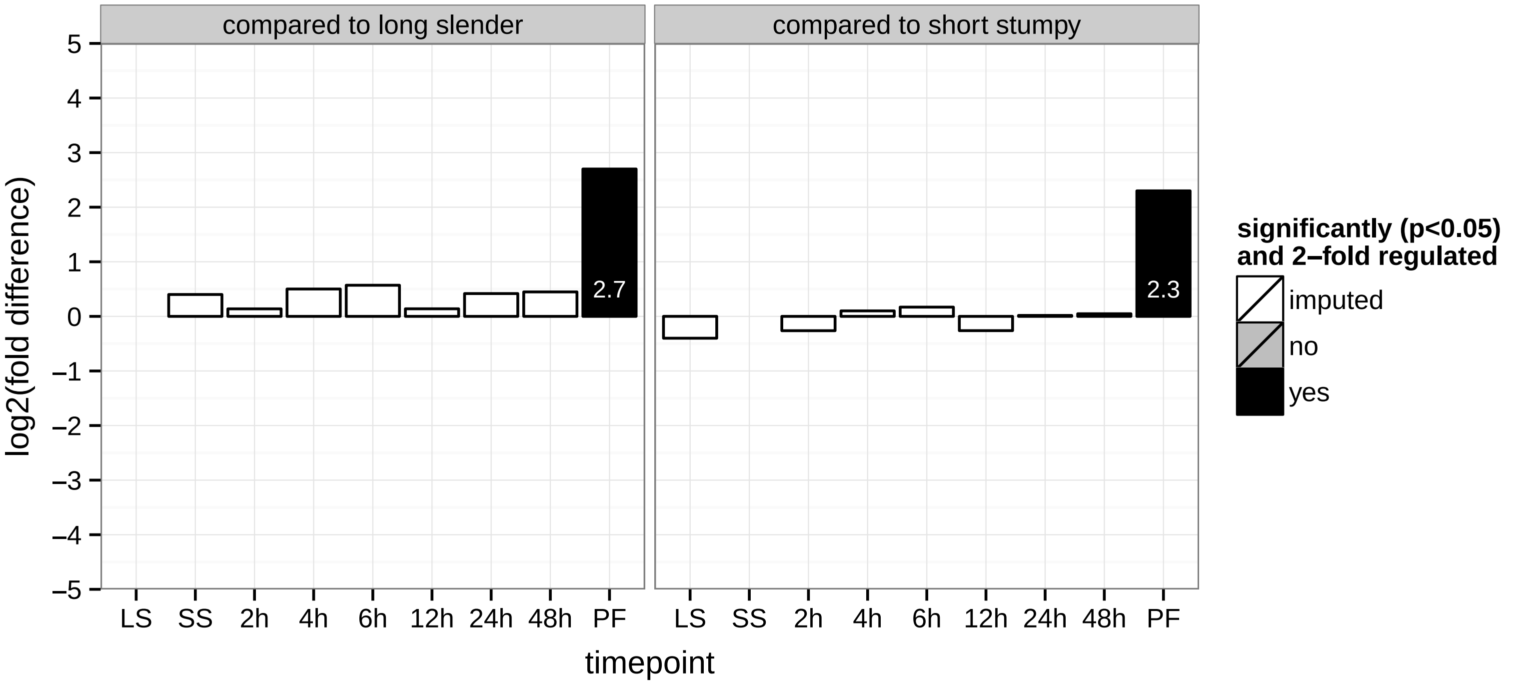
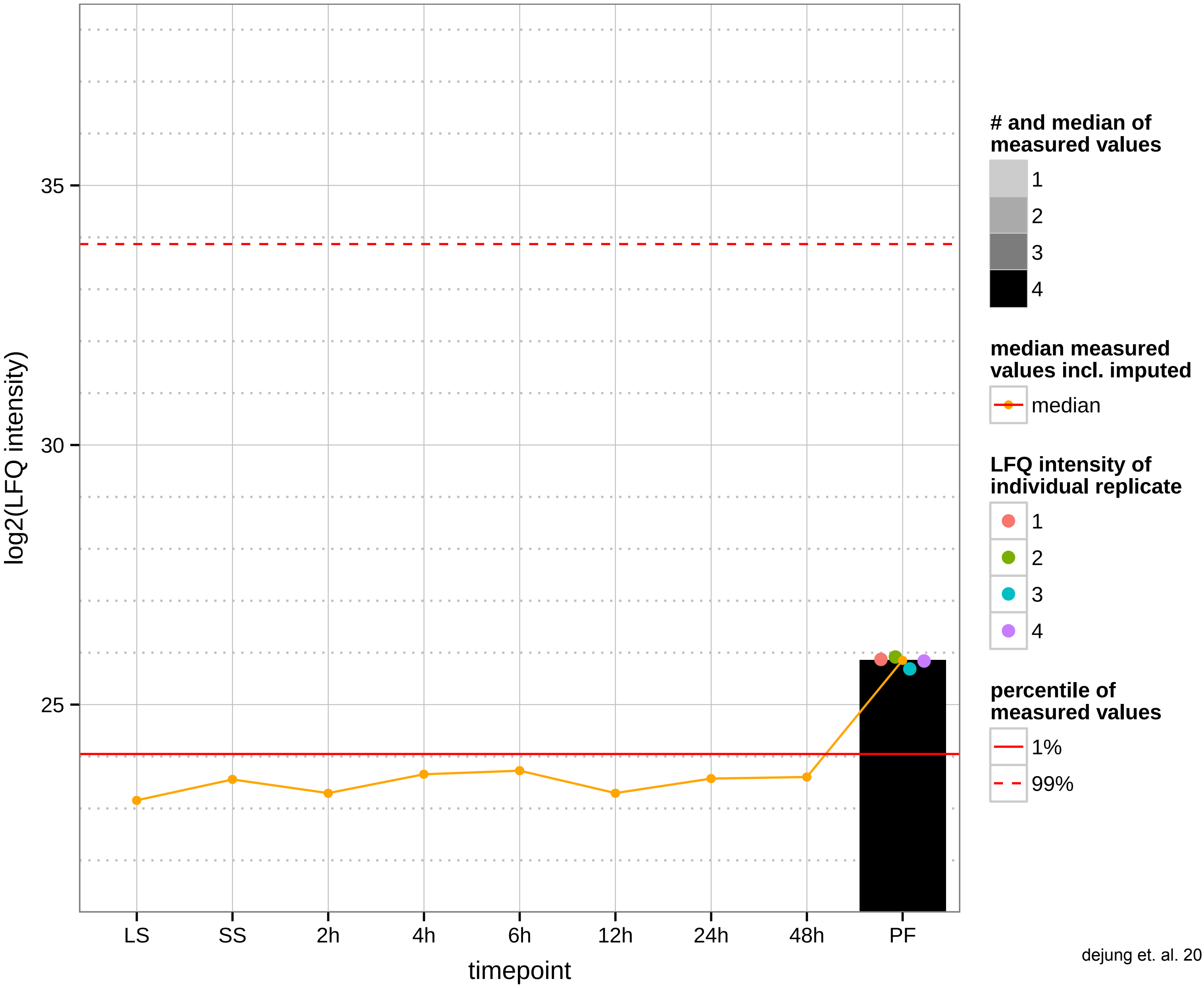
hypothetical protein, conserved
Tb927.11.9870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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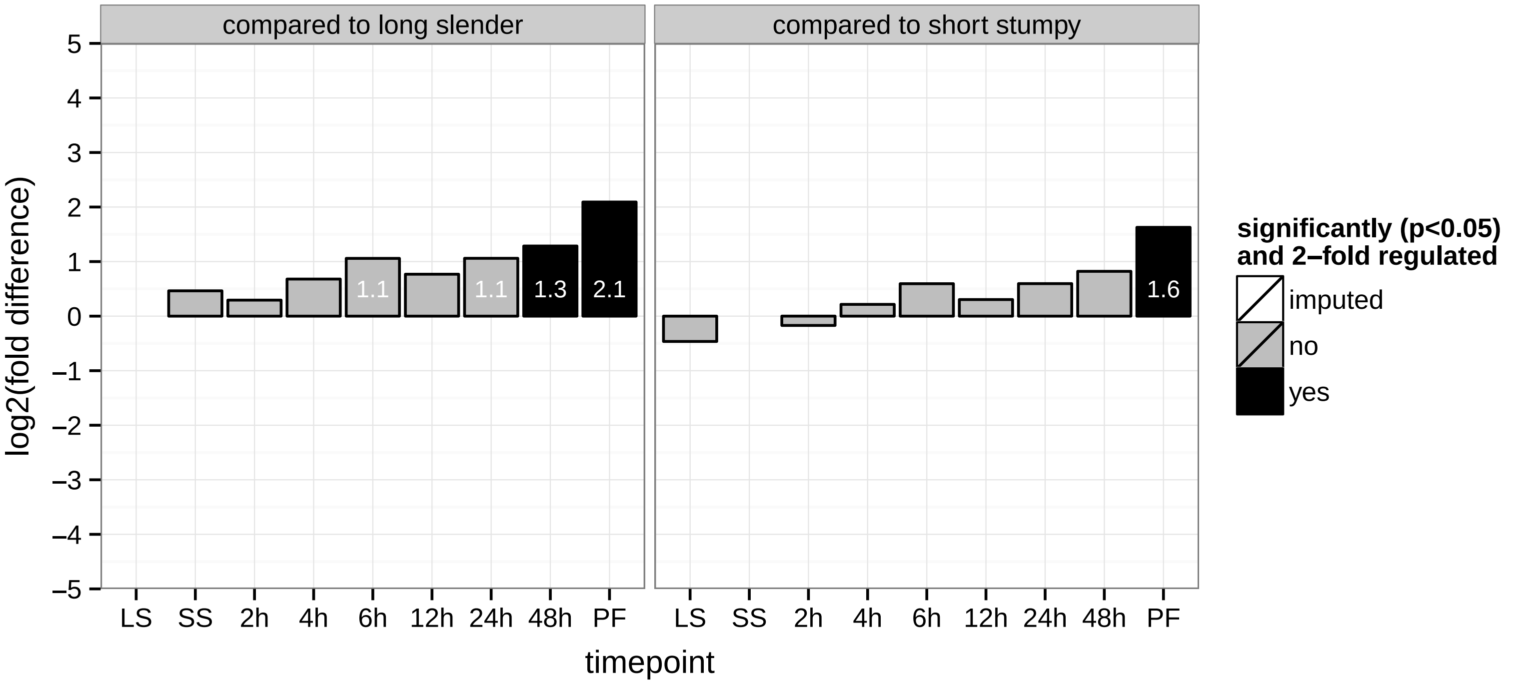
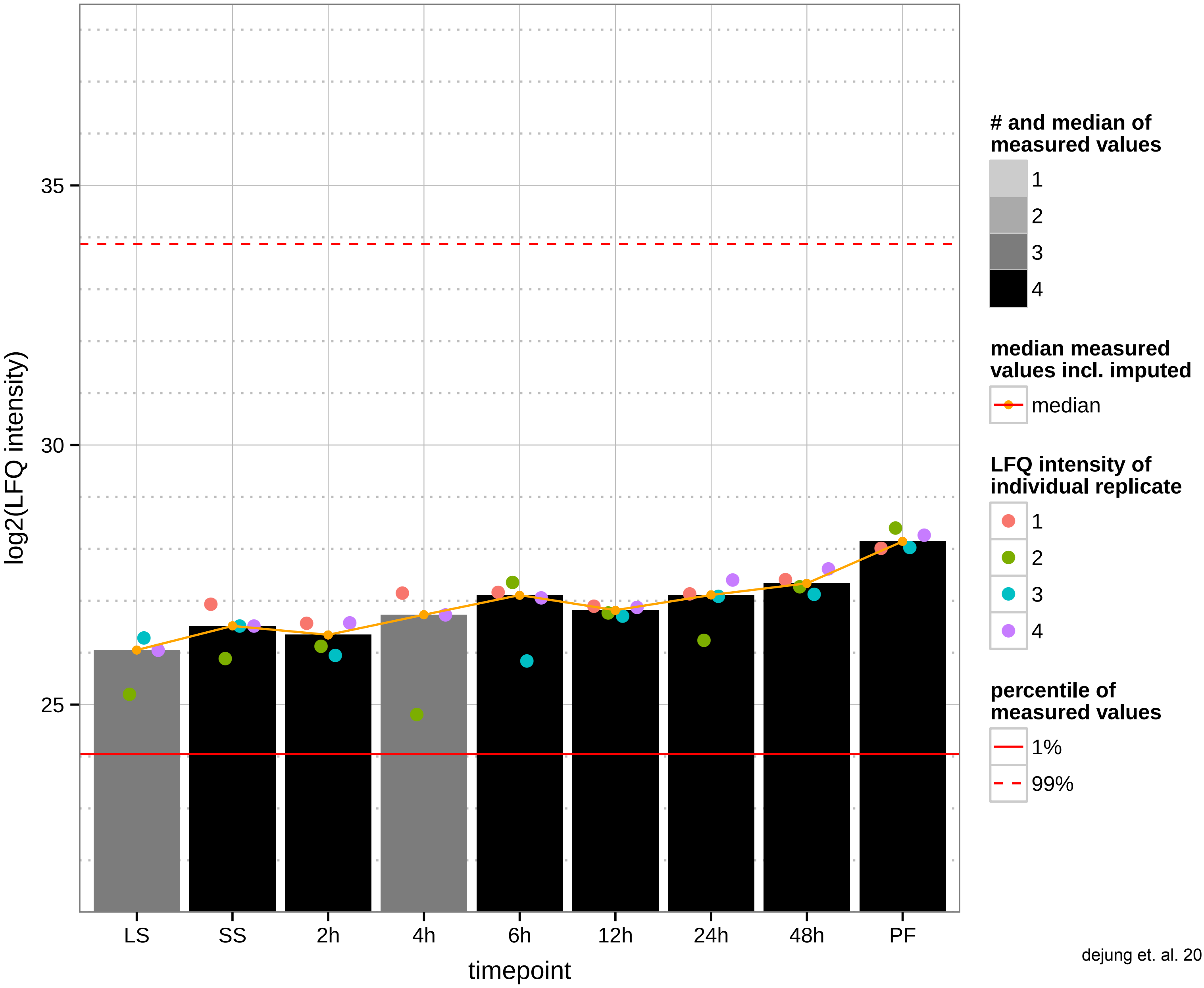
signal recognition particle receptor alpha subunit, putative
Tb927.11.9890
AGOF: GTP binding, nucleoside–triphosphatase activity, signal recognition particle binding
AGOC: signal recognition particle receptor complex
AGOP: SRP–dependent cotranslational protein targeting to membrane, cotranslational protein targeting to membrane
PGOF: GTP binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: SRP–dependent cotranslational protein targeting to membrane, transport





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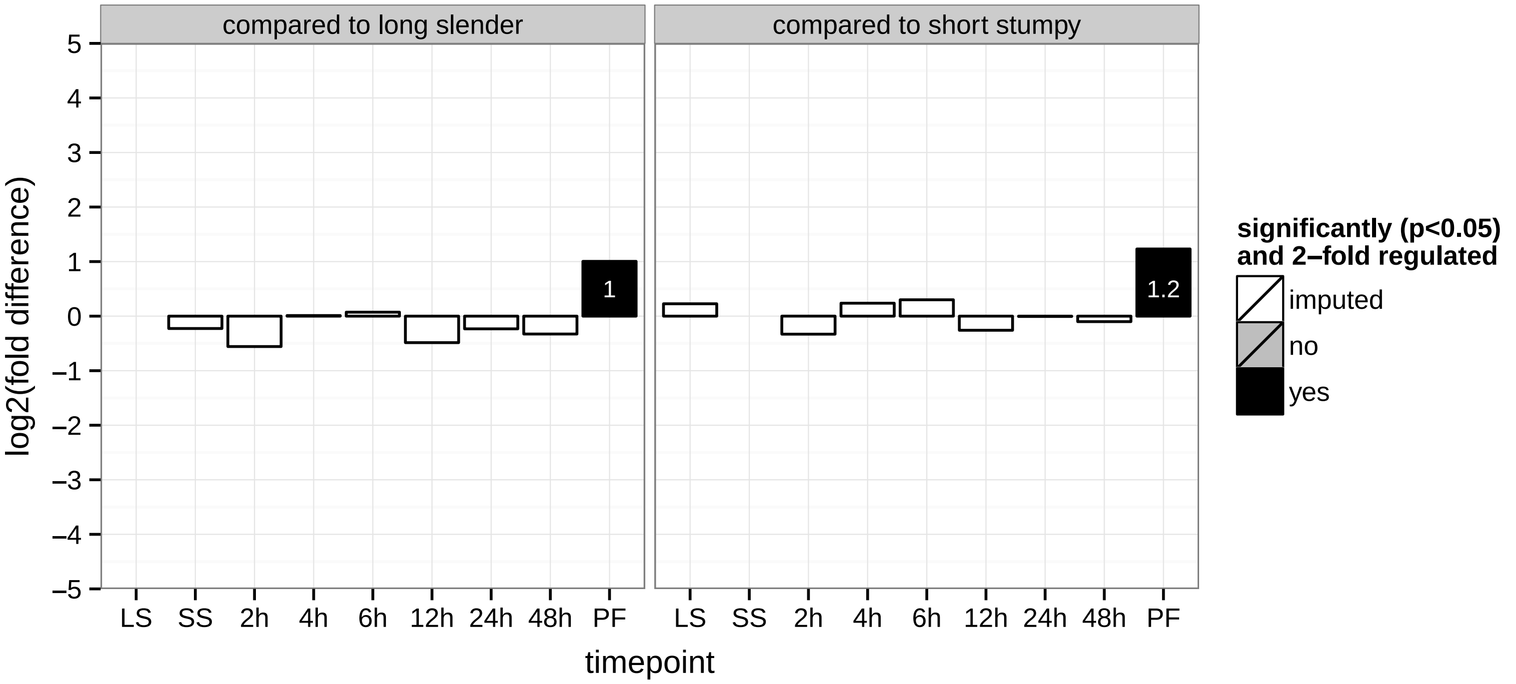
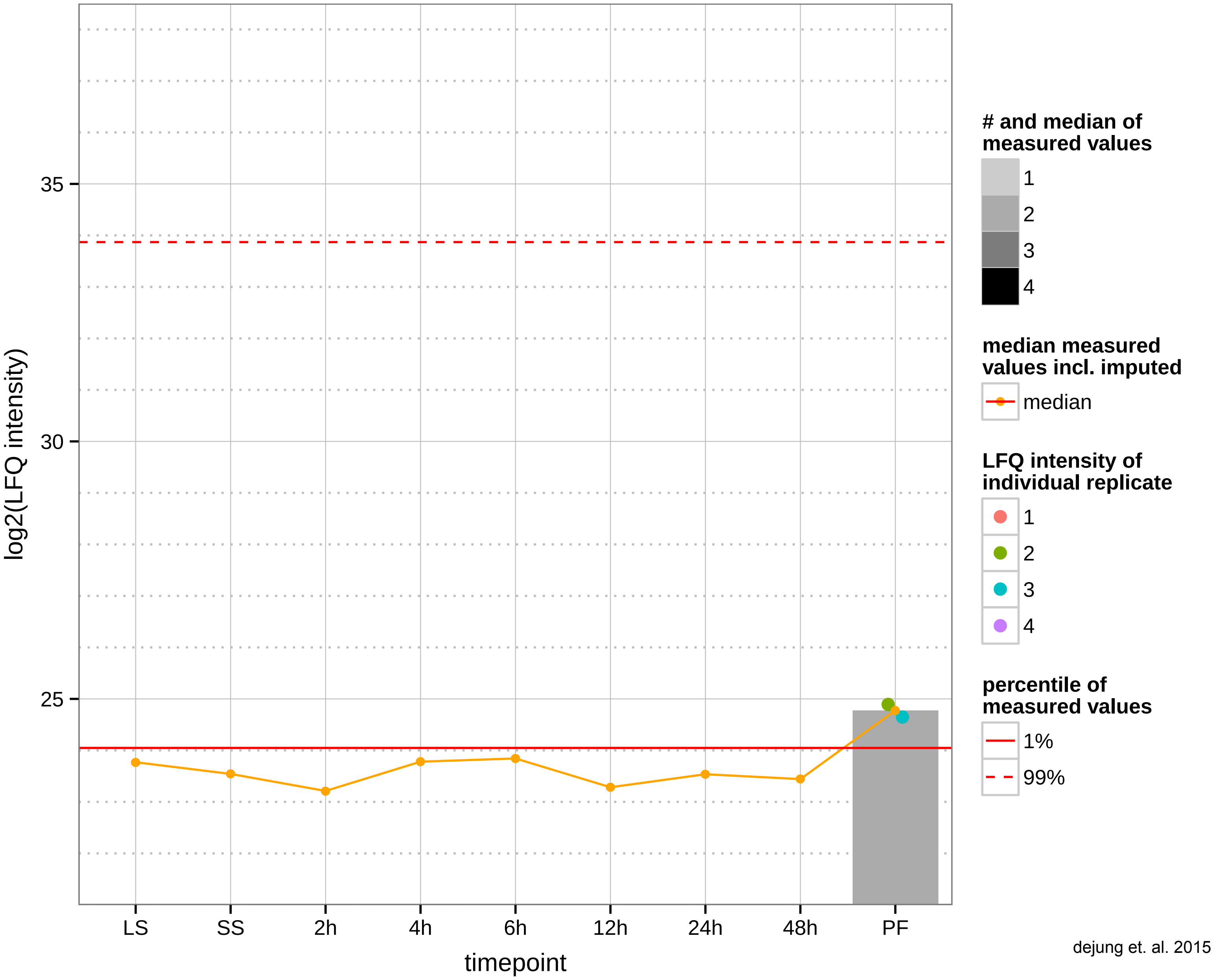
hypothetical protein, conserved
Tb927.2.1760
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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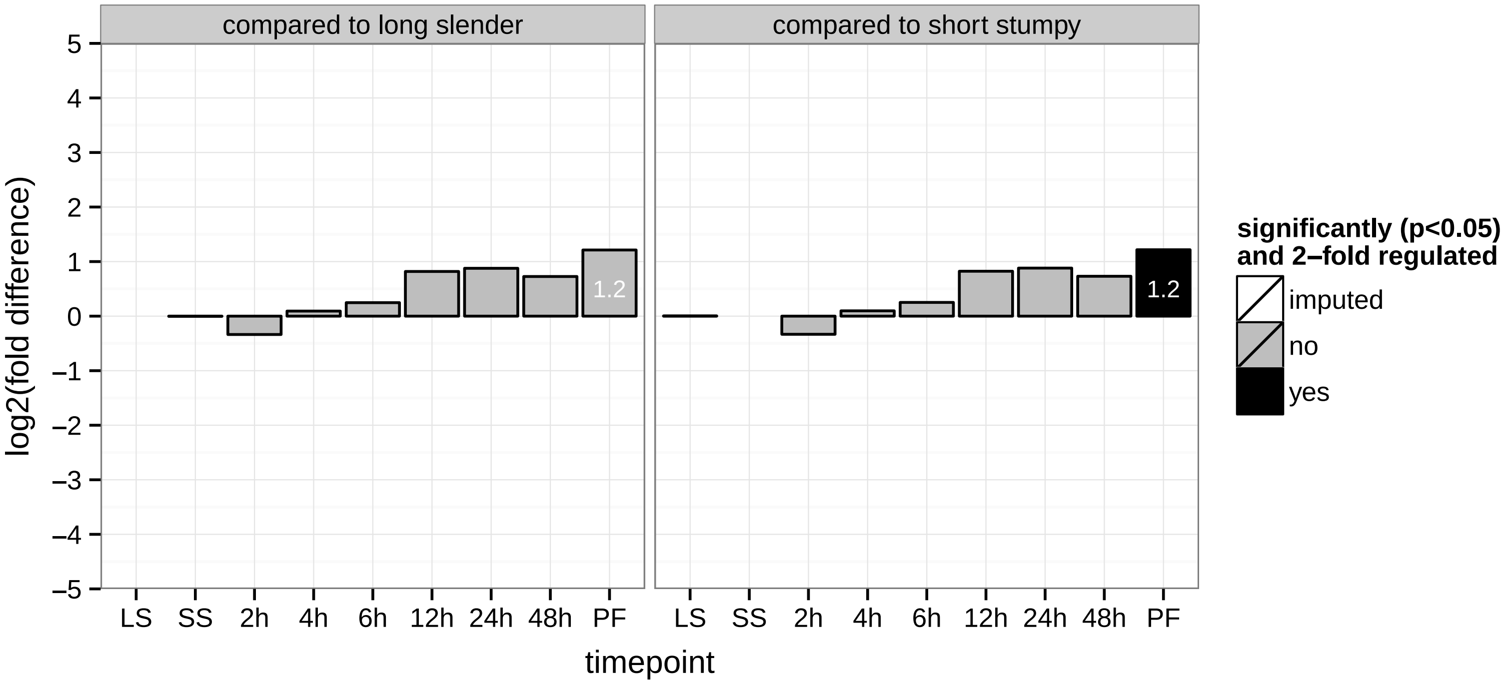
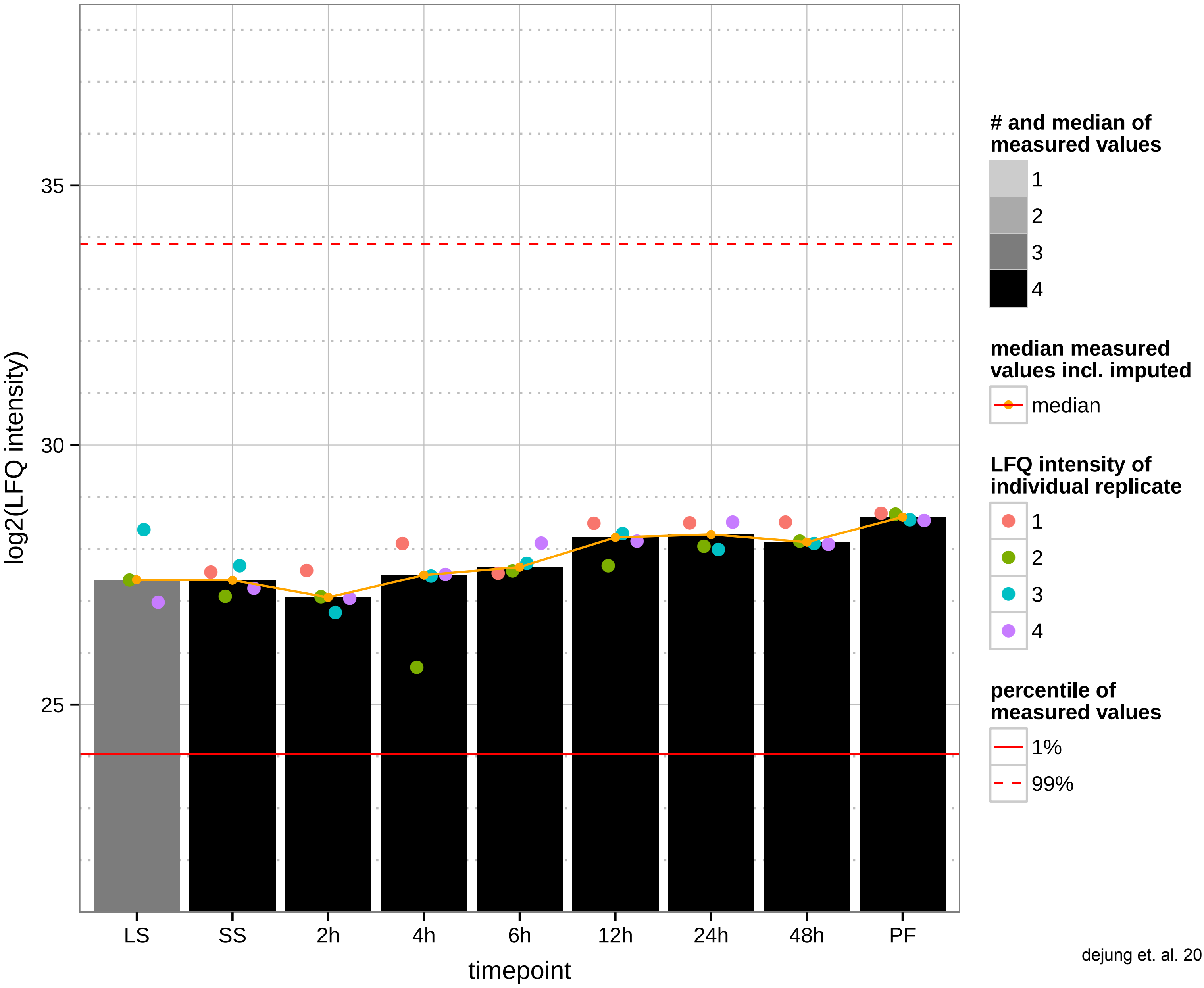
hypothetical protein, conserved
Tb927.2.2950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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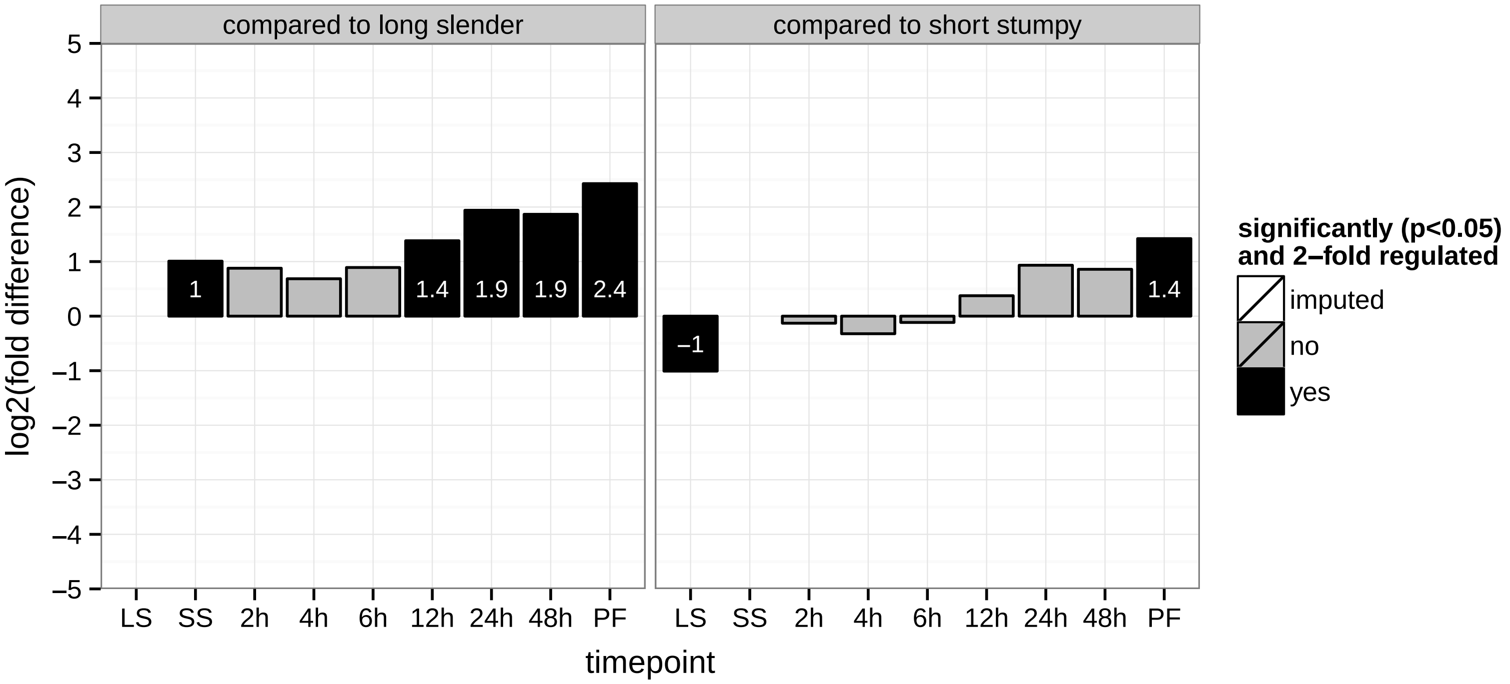
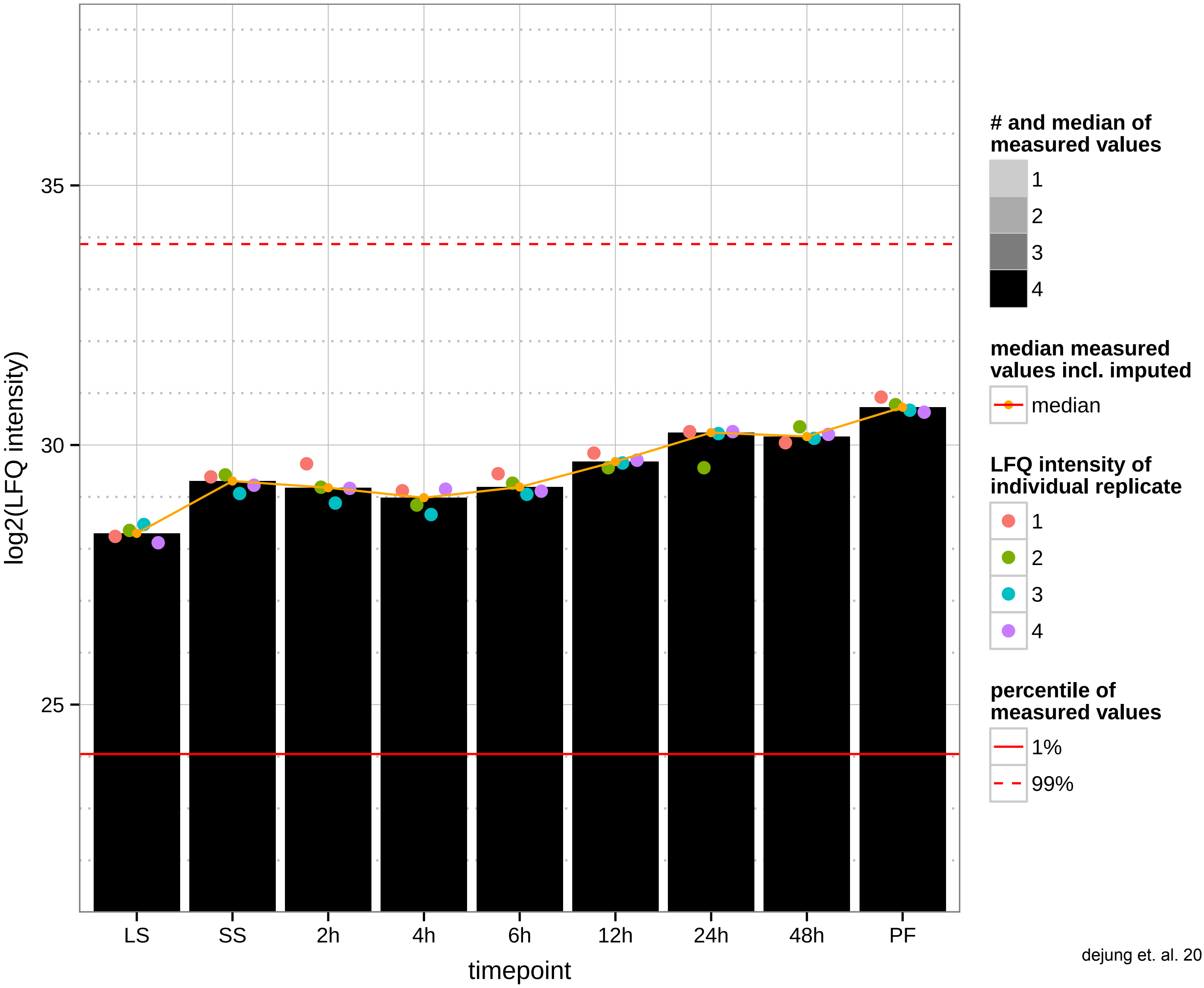
translation initiation factor IF–2, putative
Tb927.2.3780
AGOF: GTP binding, GTPase activity, translation initiation factor activity
AGOC: null
AGOP: translation
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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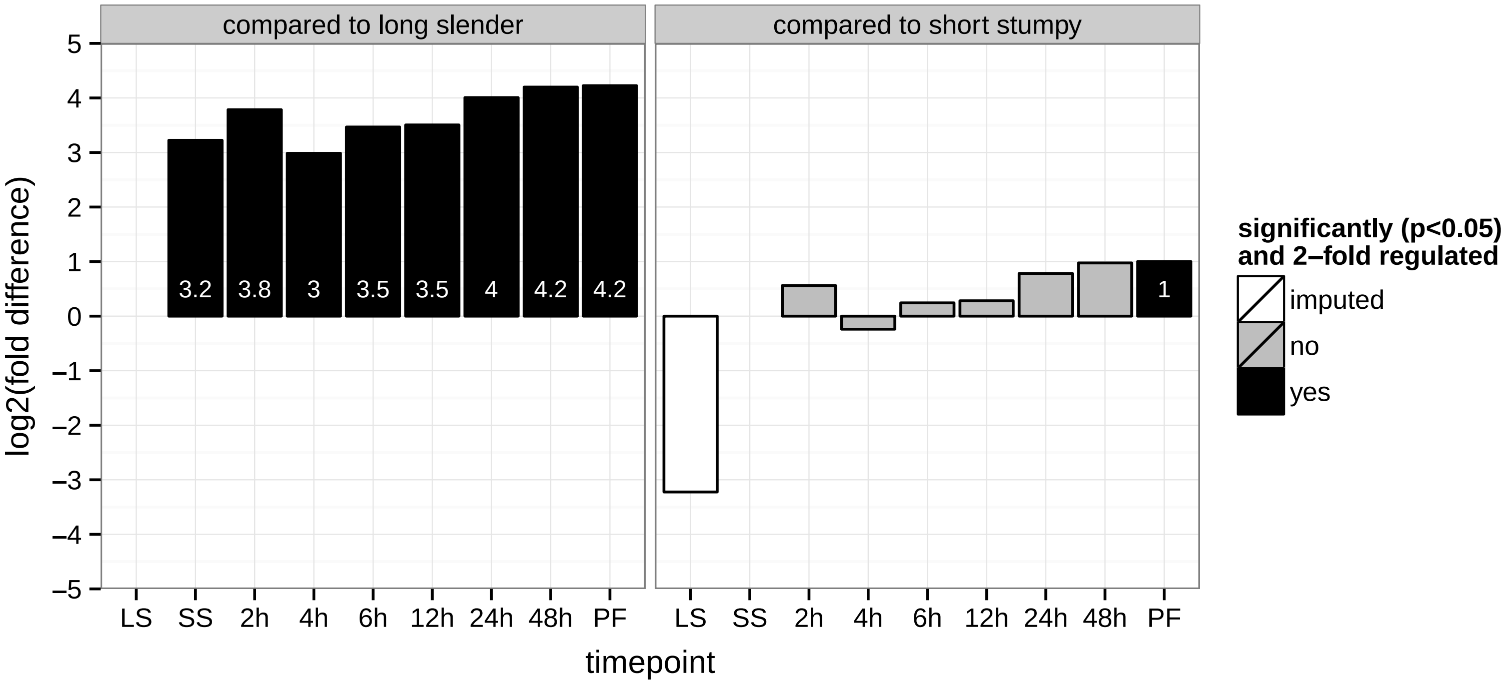
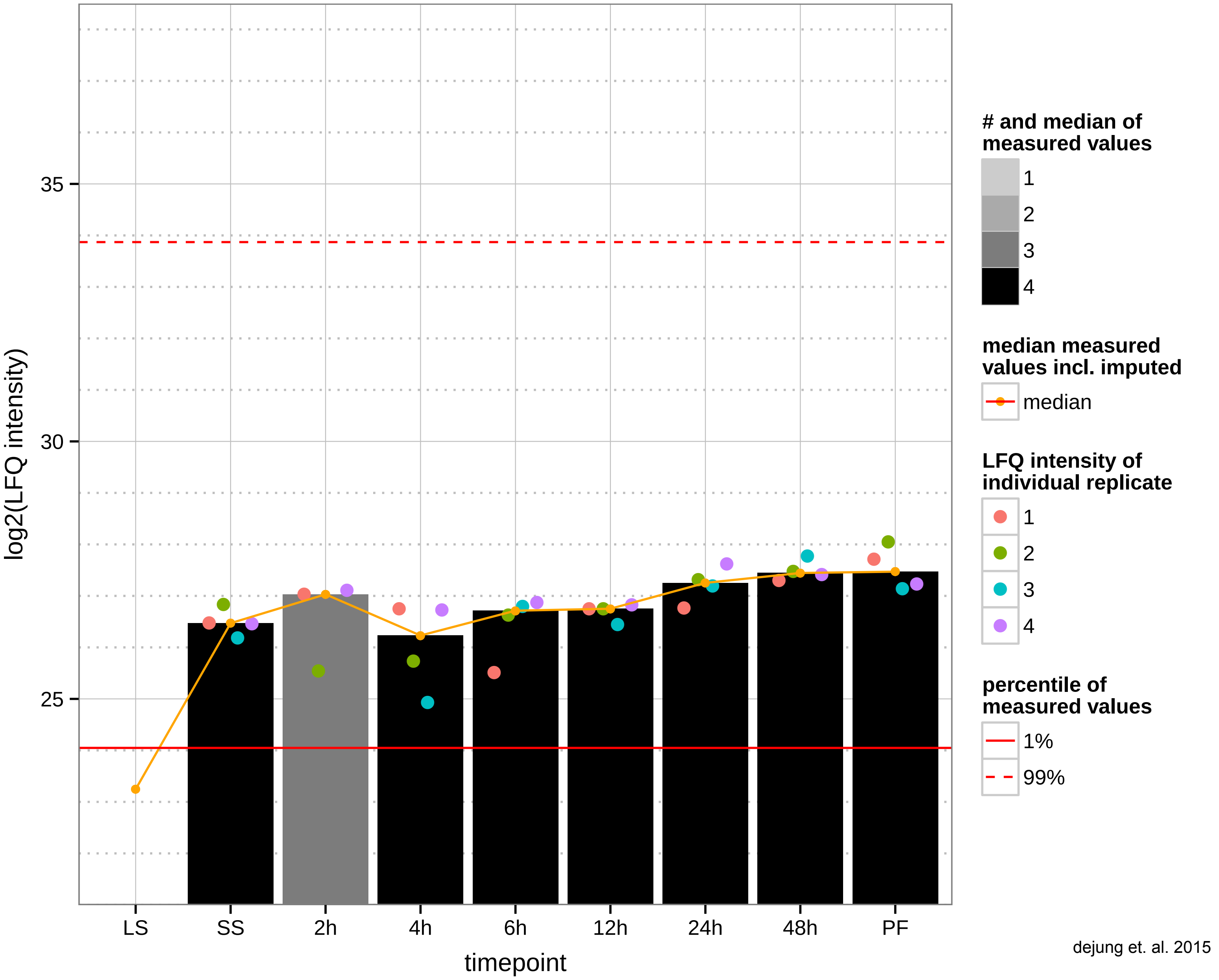
TFIIF−stimulated CTD phosphatase, putative
Tb927.2.4830
AGOF: null
AGOC: integral to membrane, mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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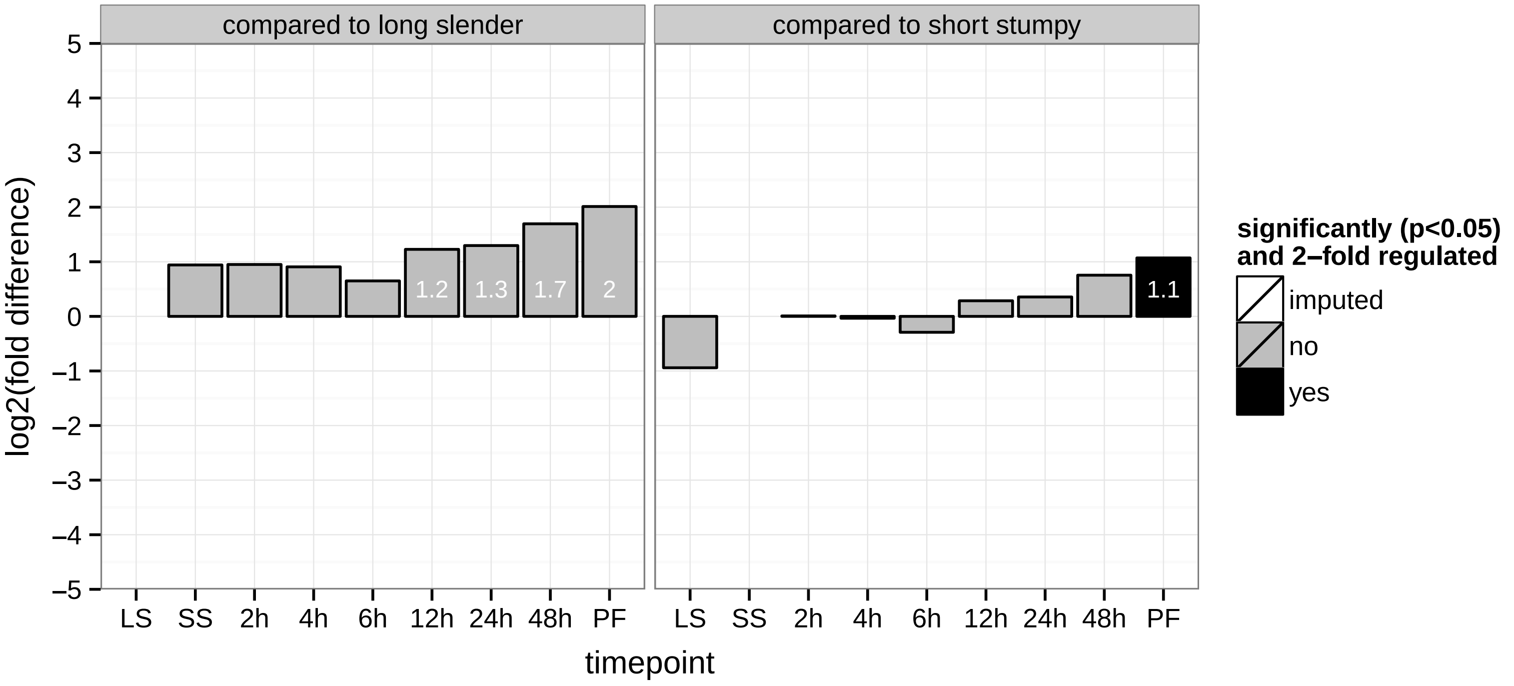
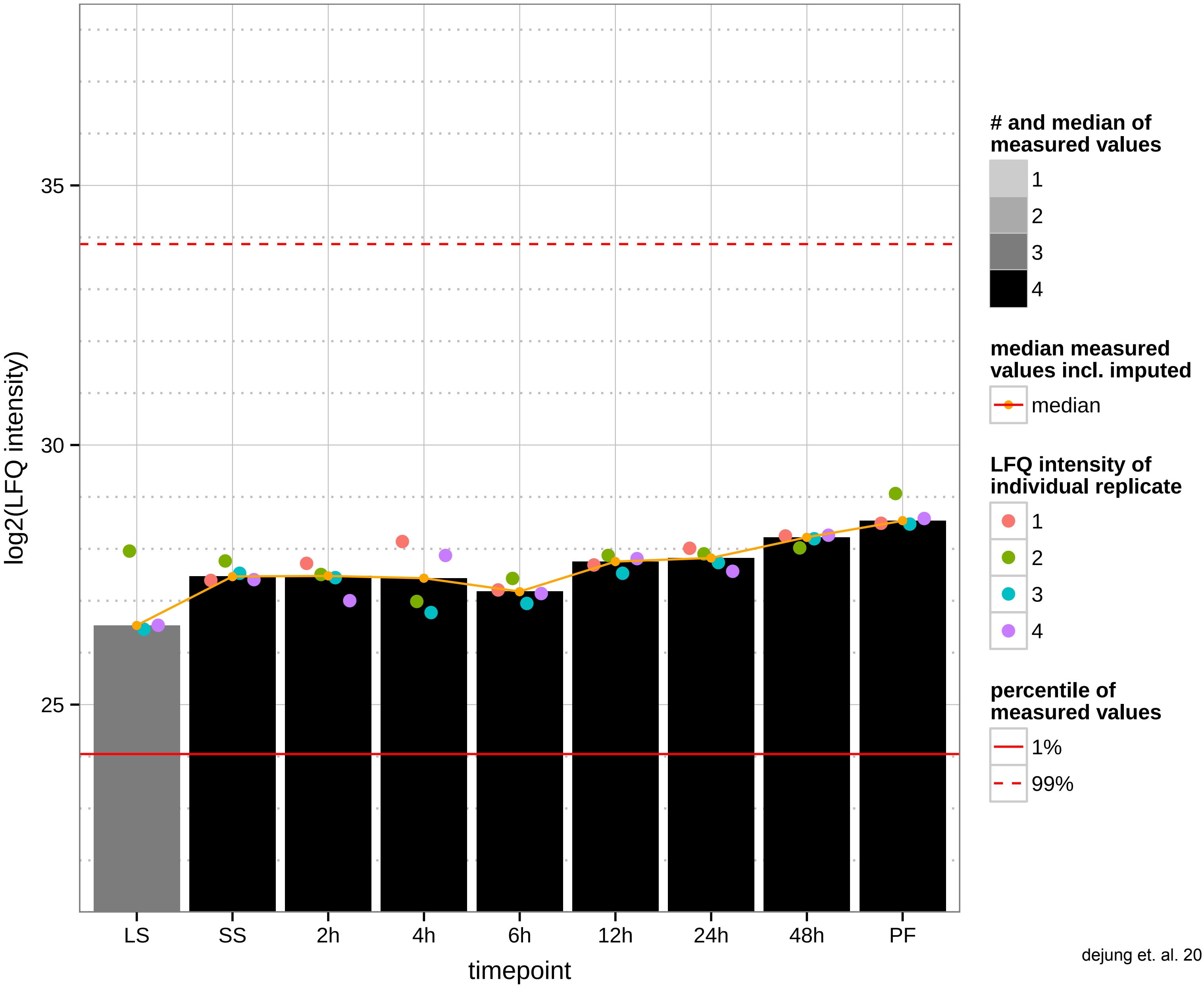
hypothetical protein, conserved
Tb927.2.5130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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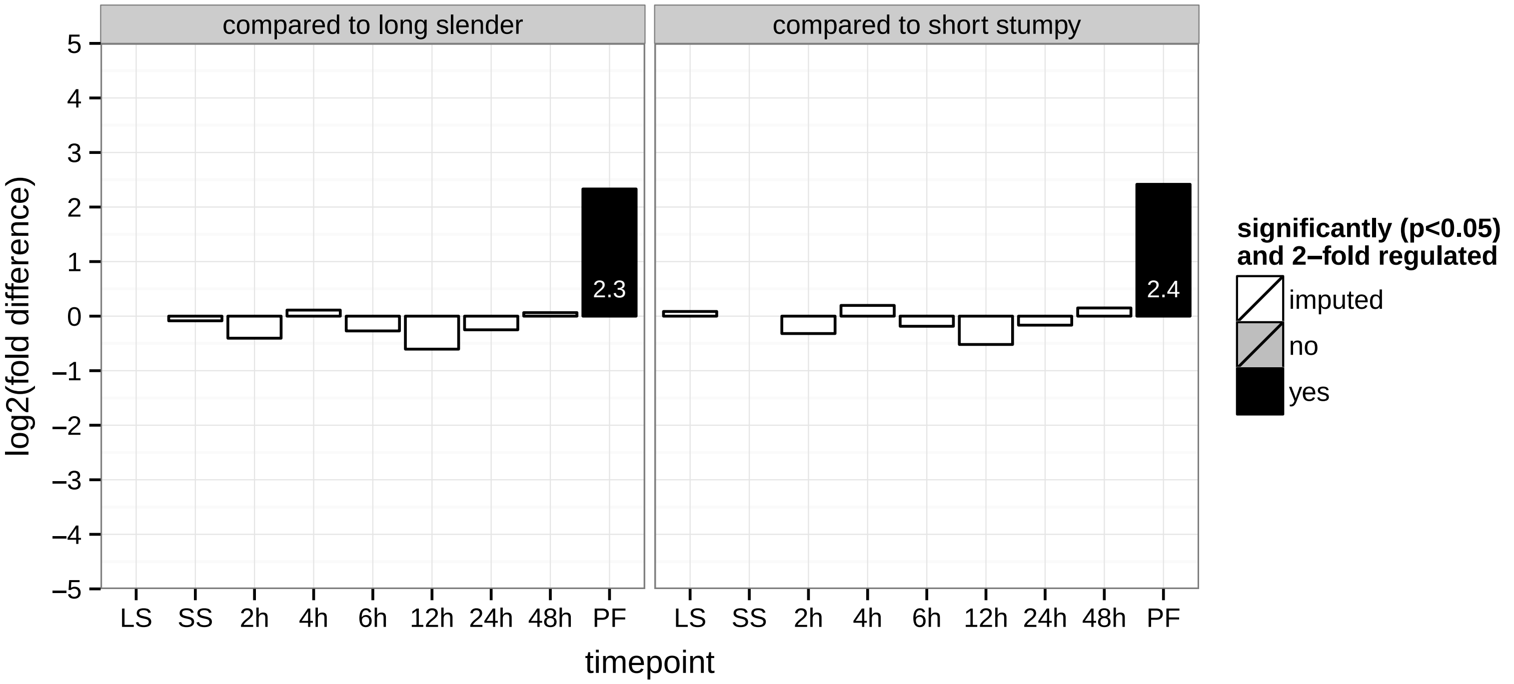
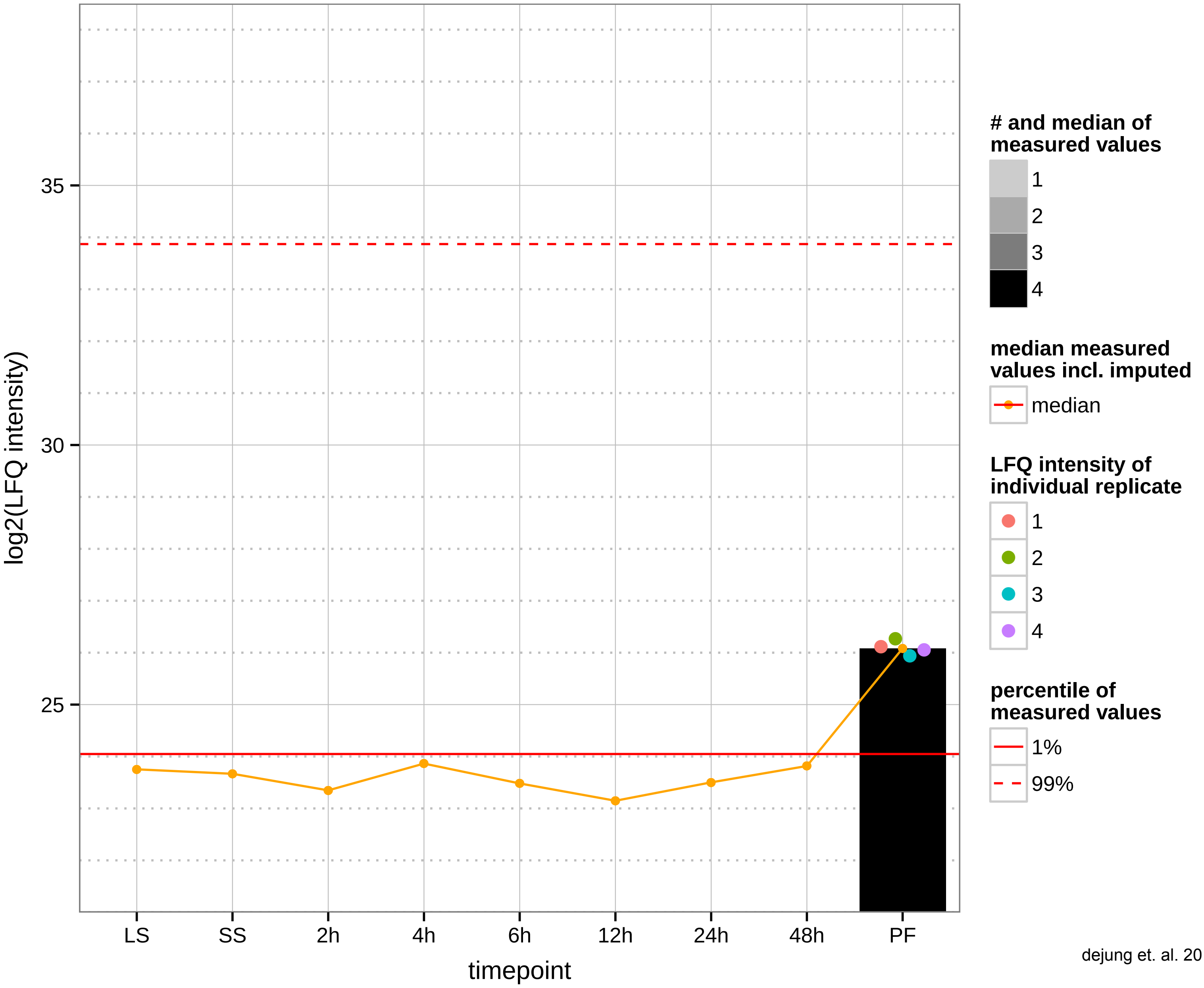
trans–sialidase, putative
Tb927.2.5280
AGOF: exo–alpha–sialidase activity
AGOC: null
AGOP: pathogenesis
PGOF: null
PGOC: null
PGOP: null





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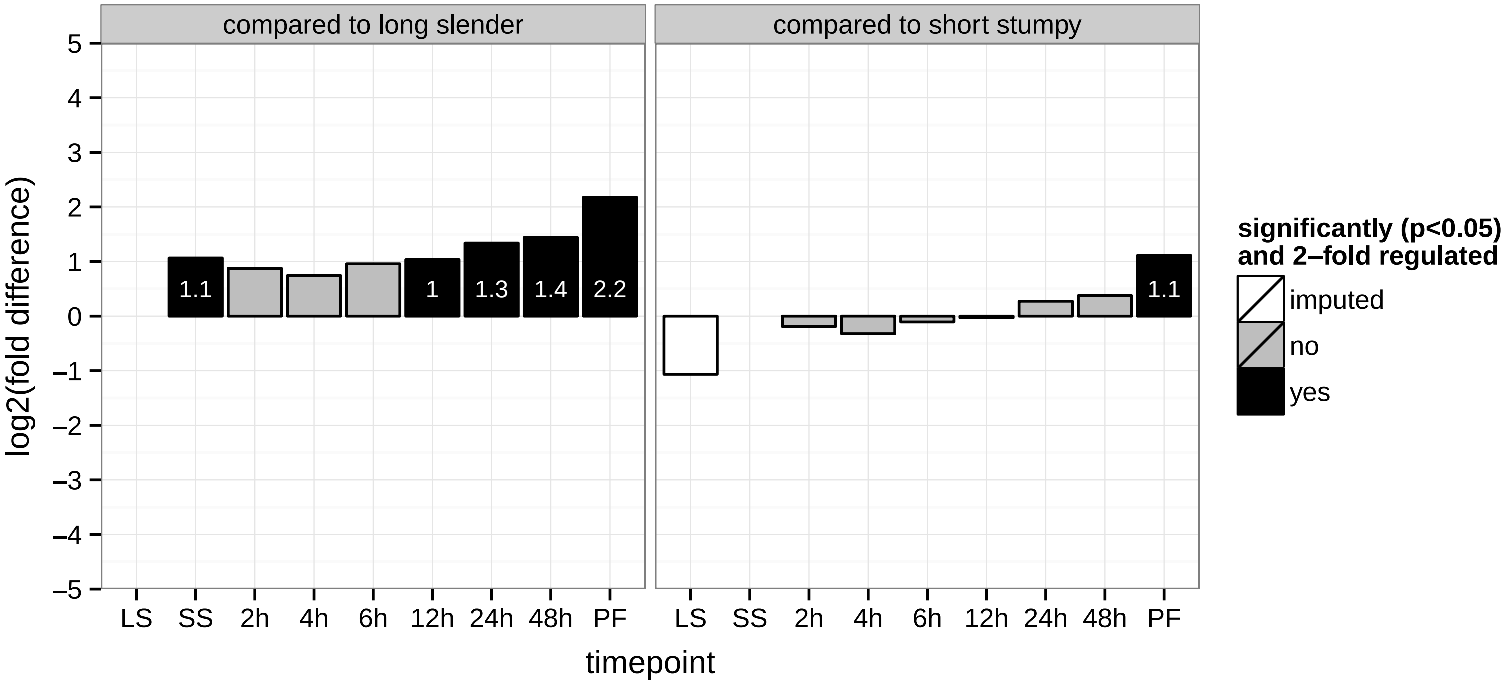
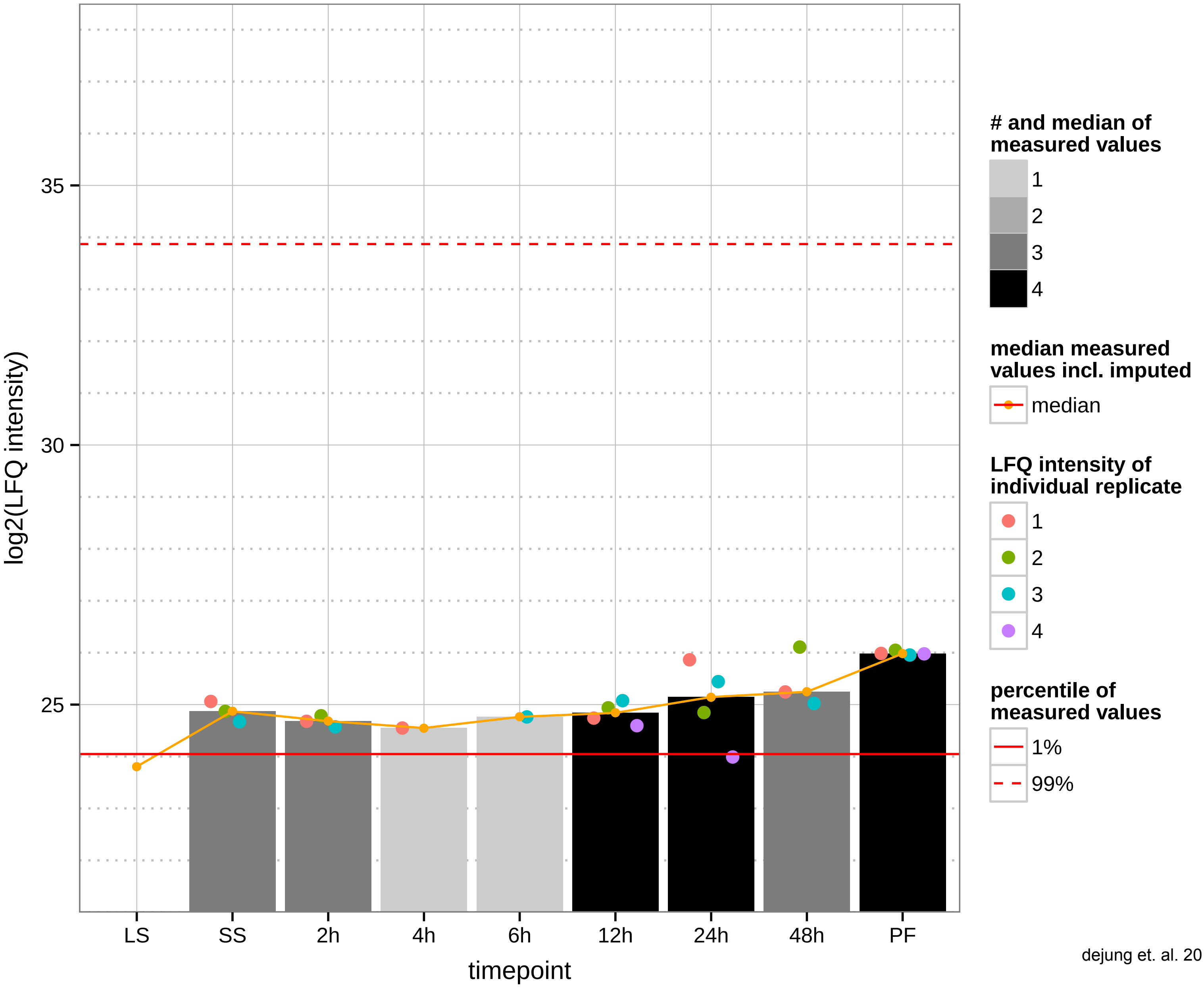
hypothetical protein, conserved
Tb927.3.1020
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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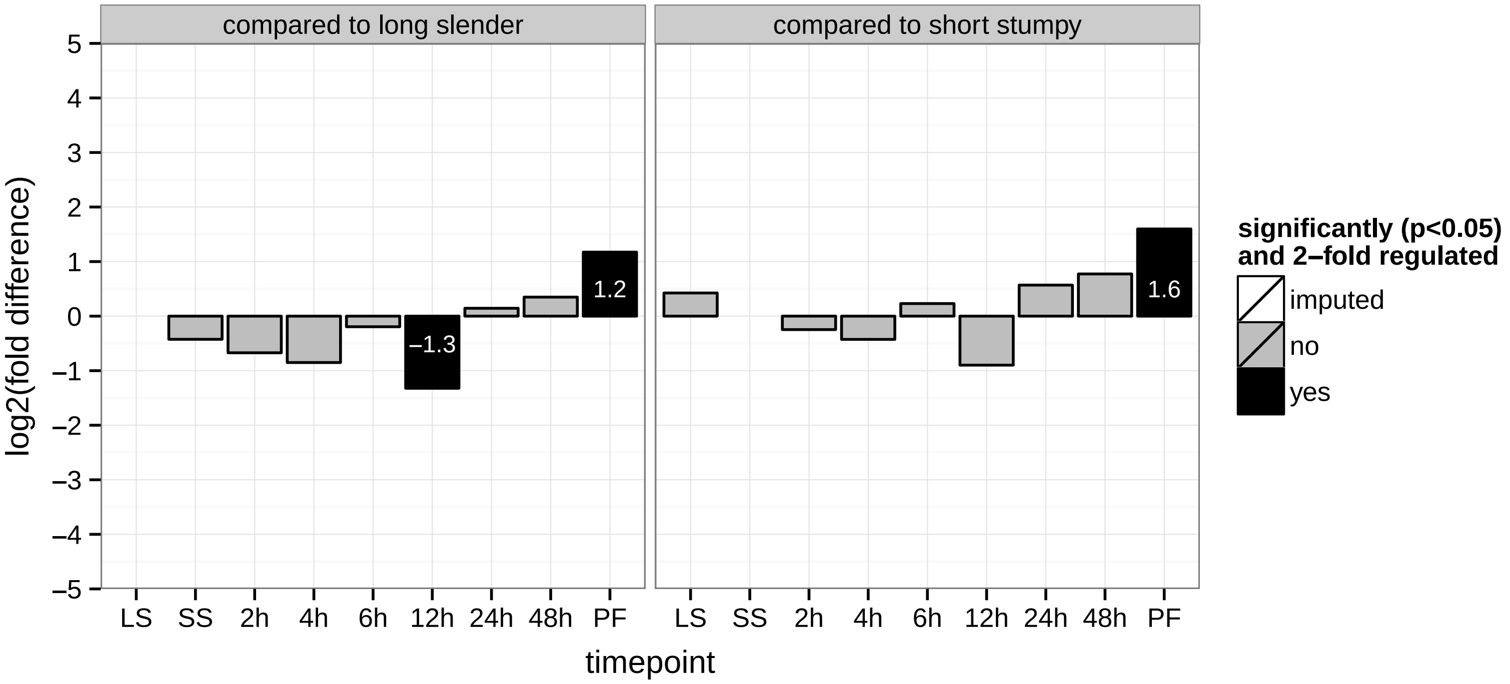
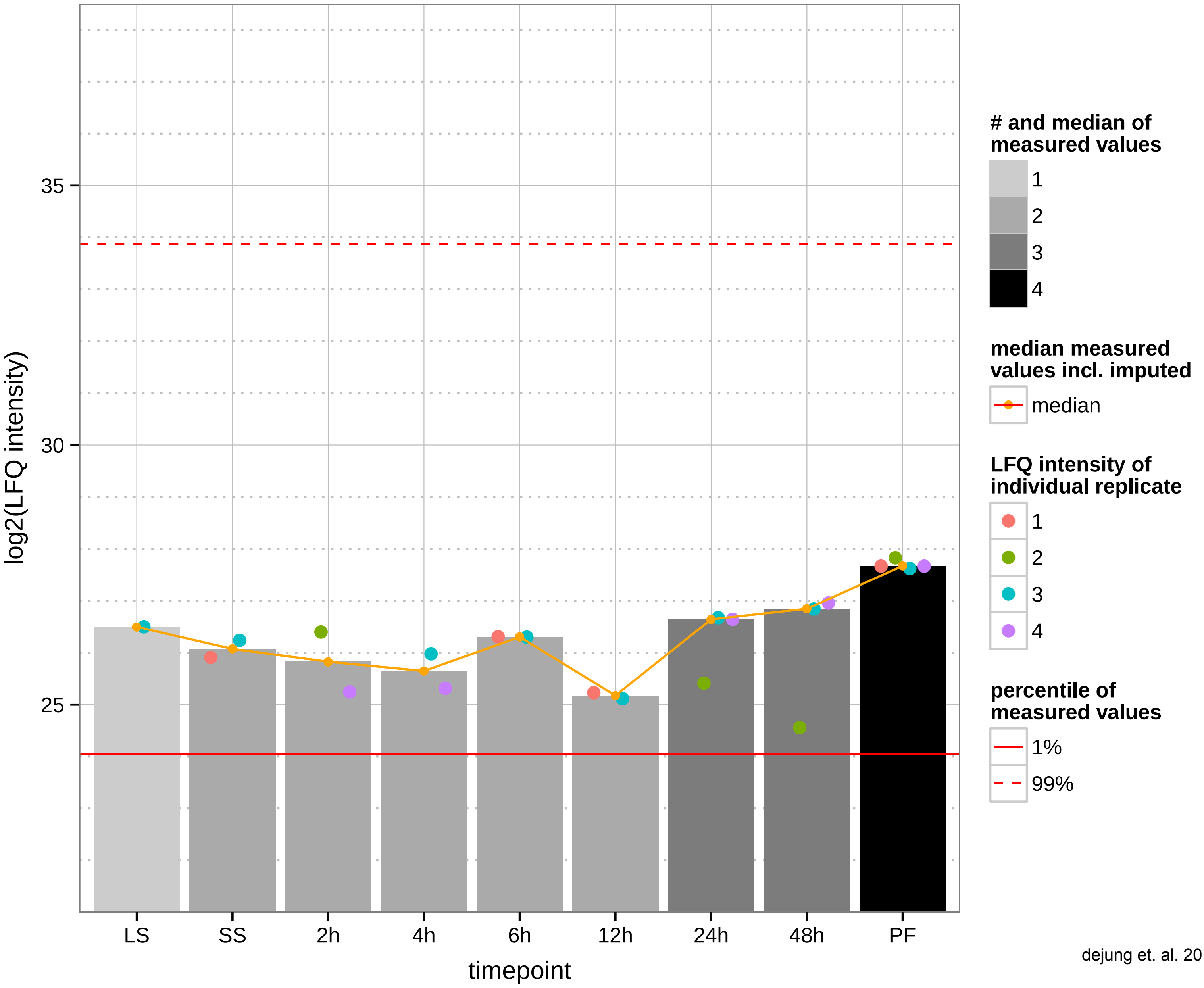
protein phosphatase 2A, putative
Tb927.3.1240
AGOF: hydrolase activity, protein serine/threonine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: hydrolase activity
PGOC: null
PGOP: null





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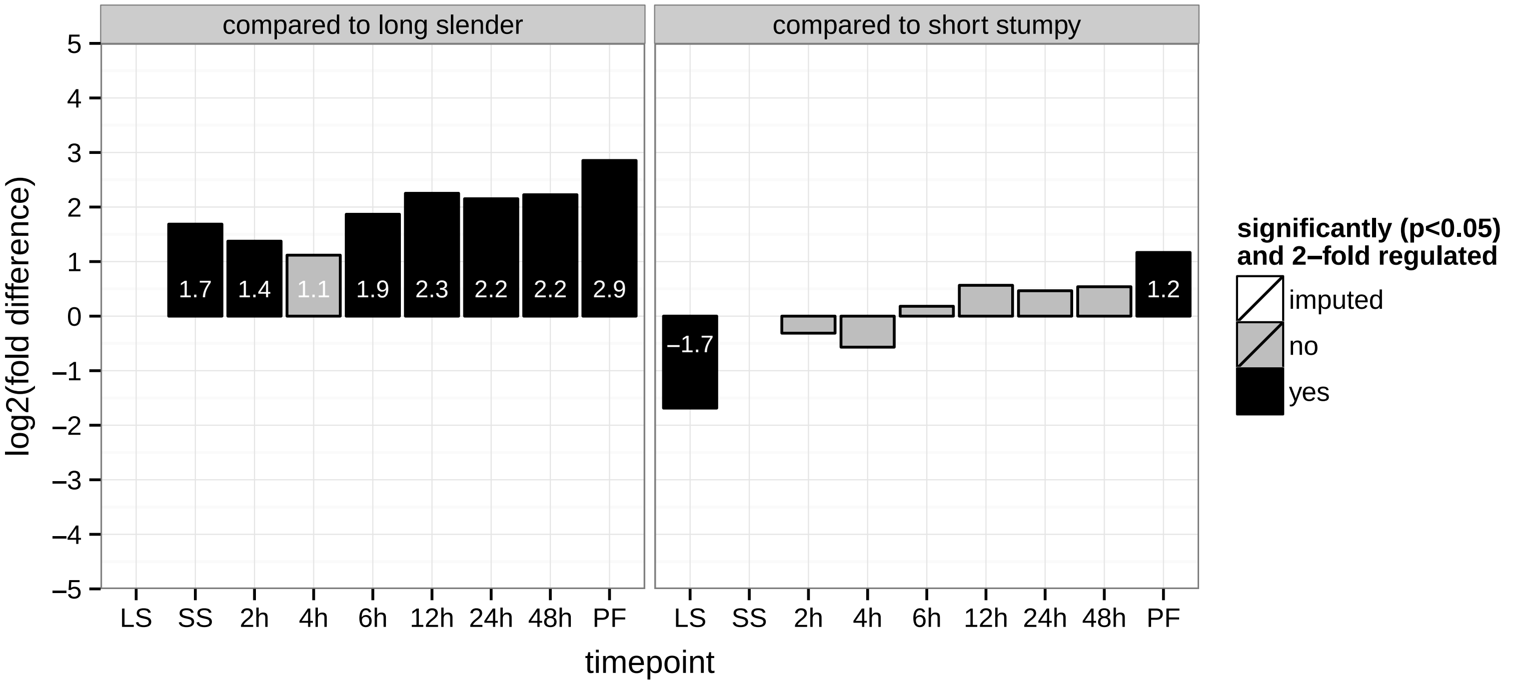
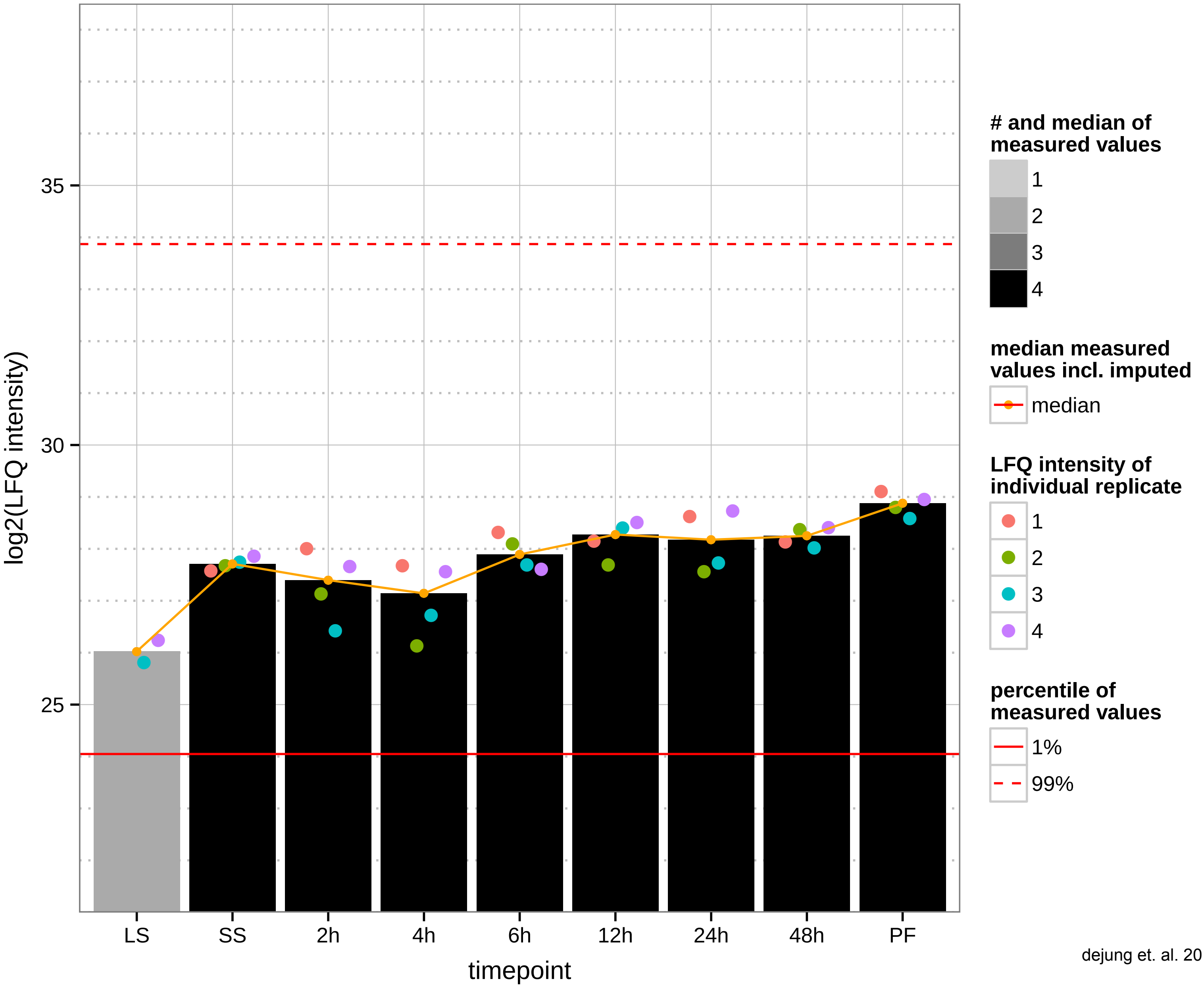
hypothetical protein, conserved
Tb927.3.1350
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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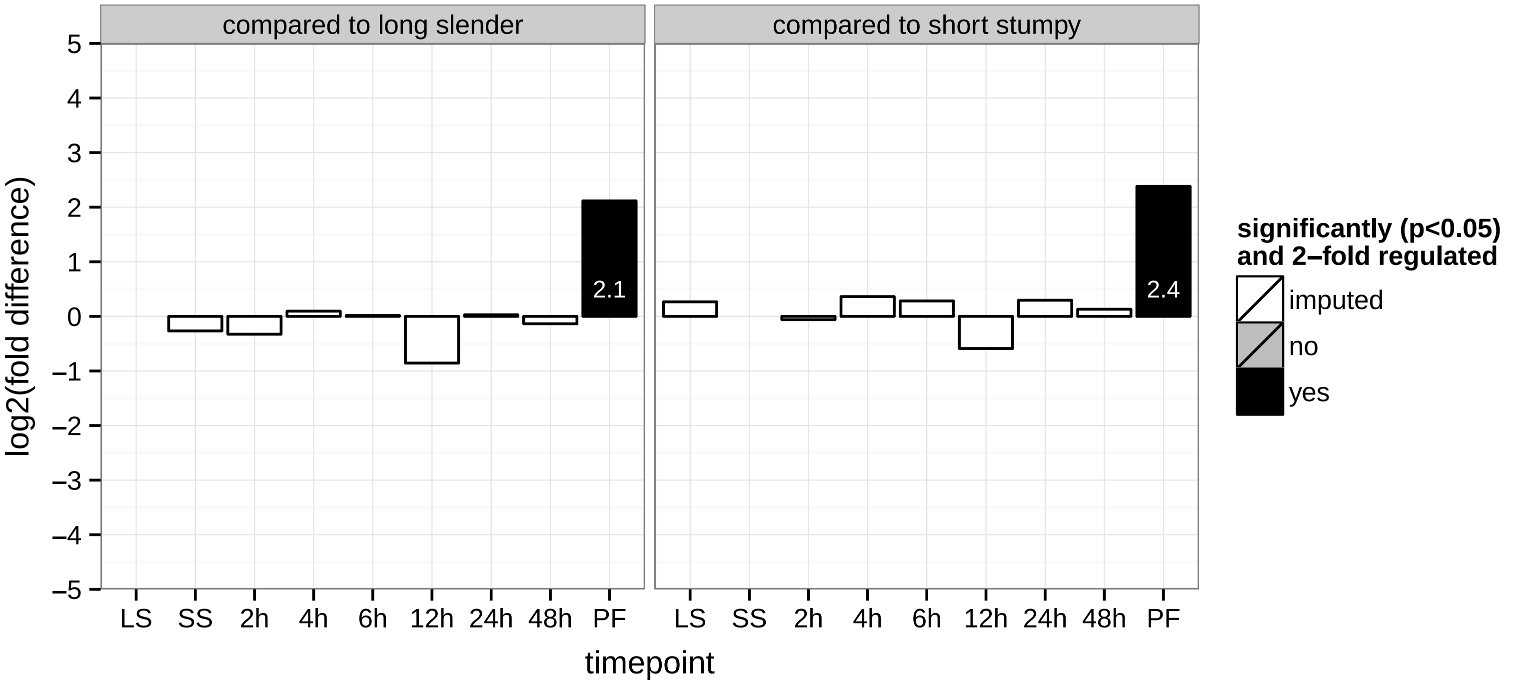
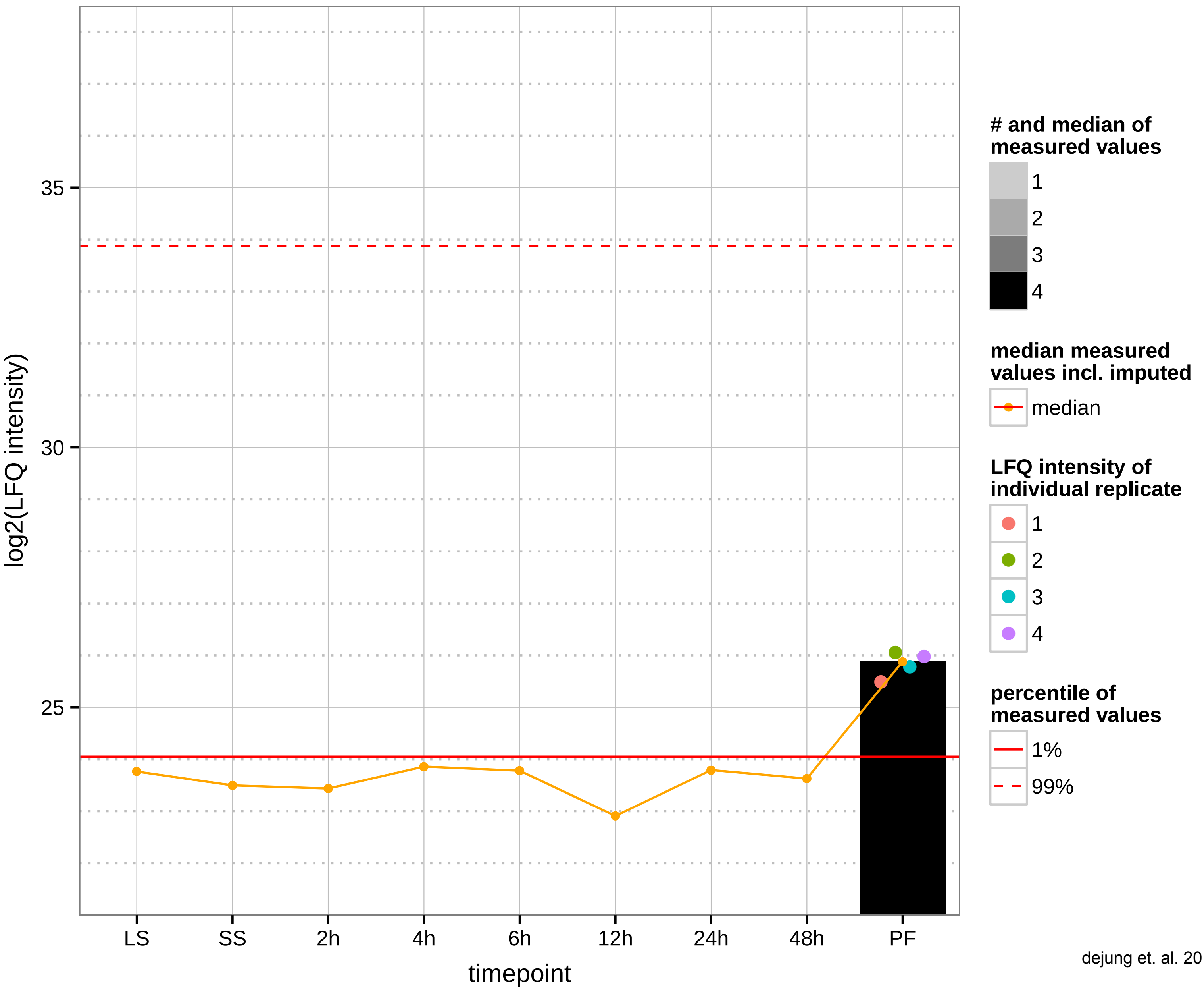
hypothetical protein, conserved
Tb927.3.1550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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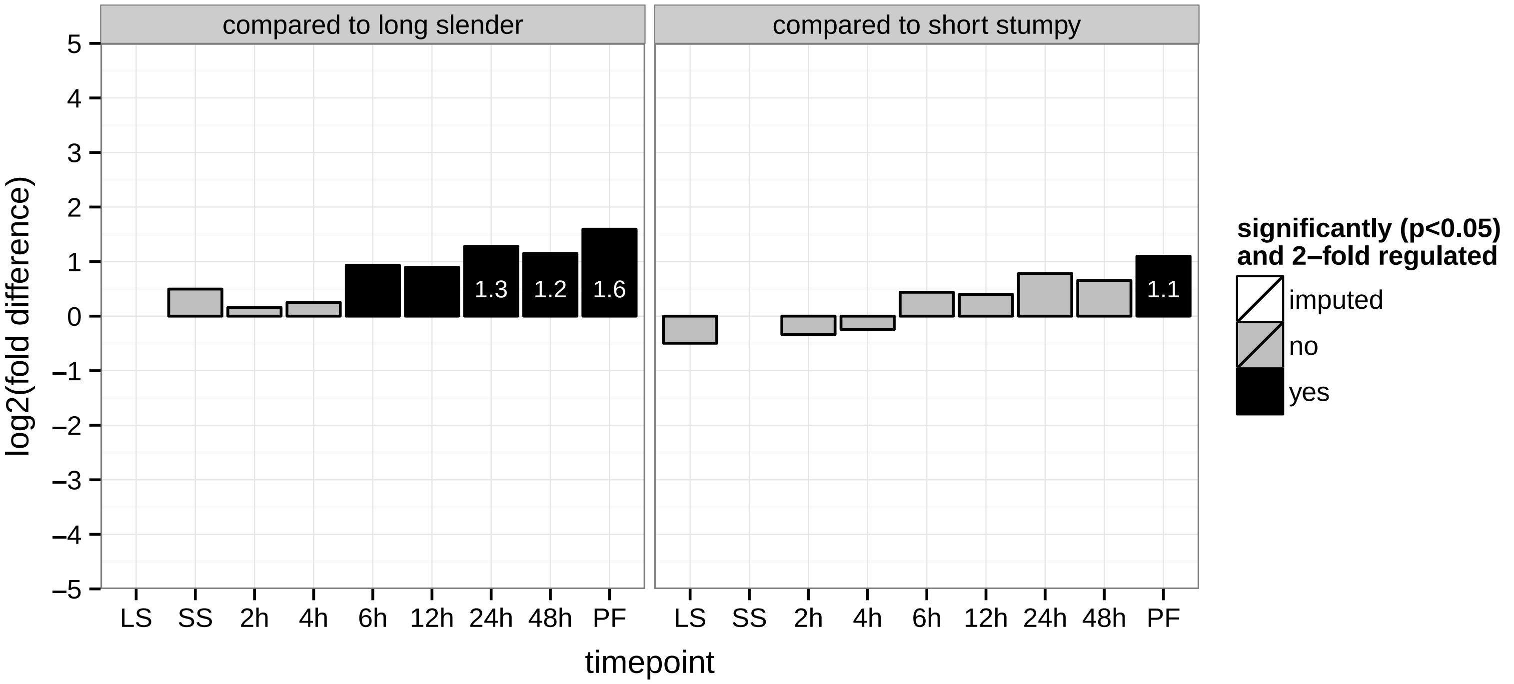
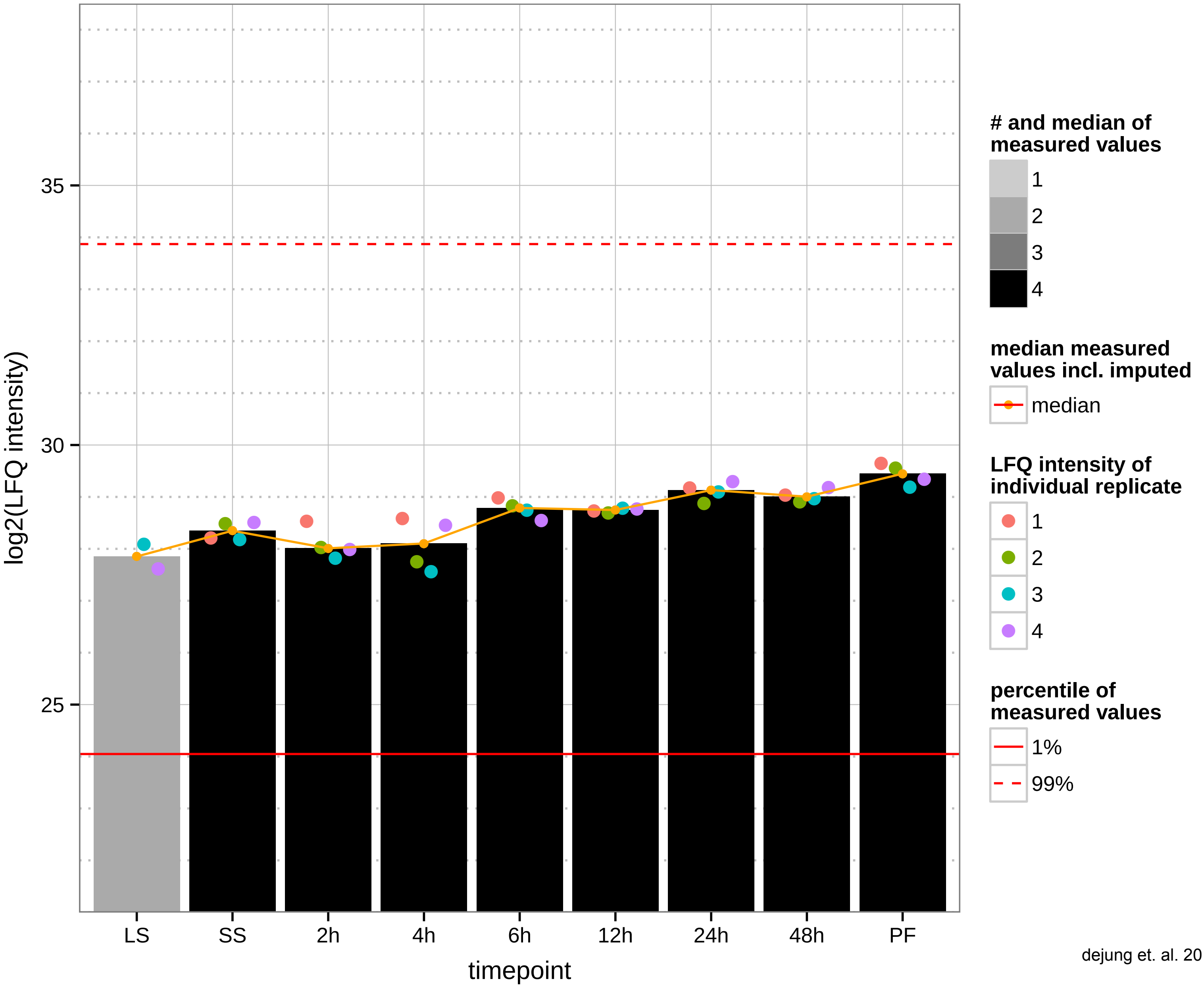
pumilio RNA binding protein, putative (PUF8)
Tb927.3.2470
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: RNA binding, binding
PGOC: null
PGOP: null





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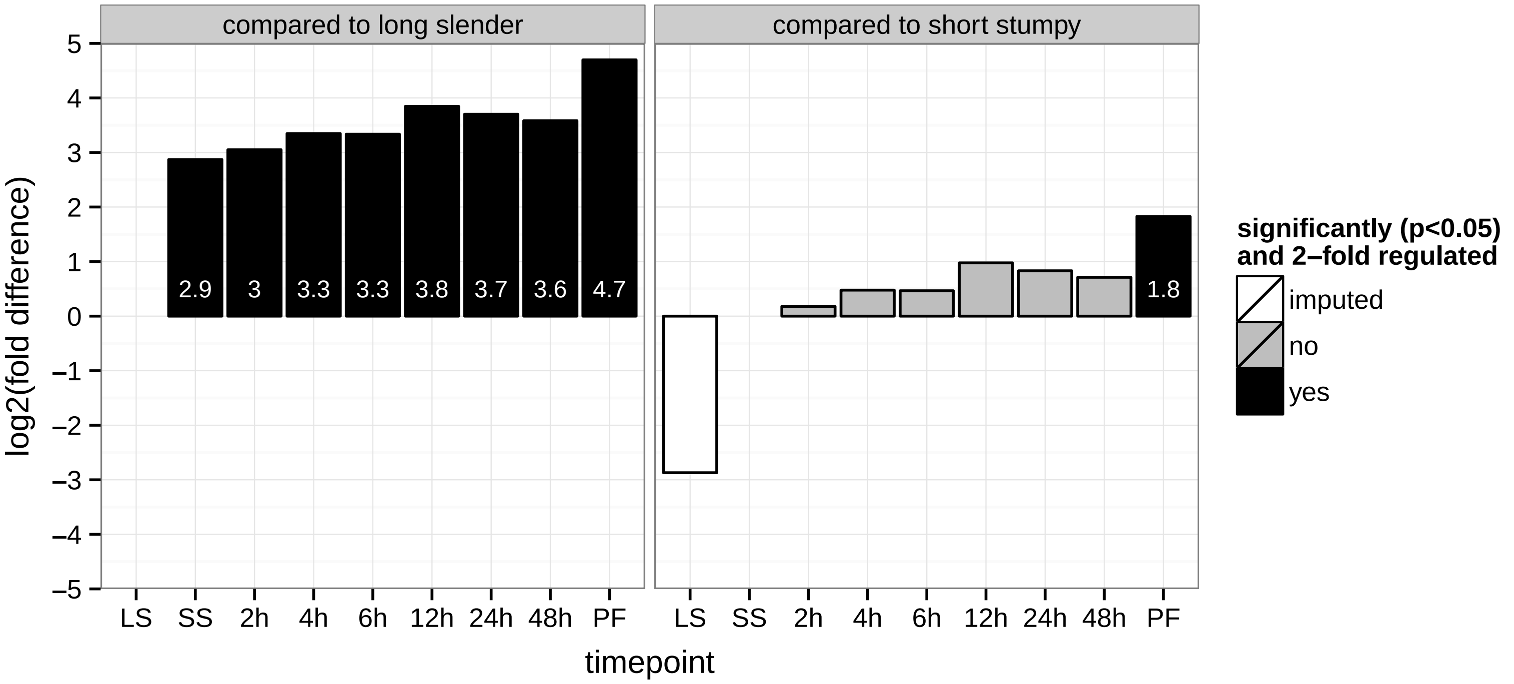
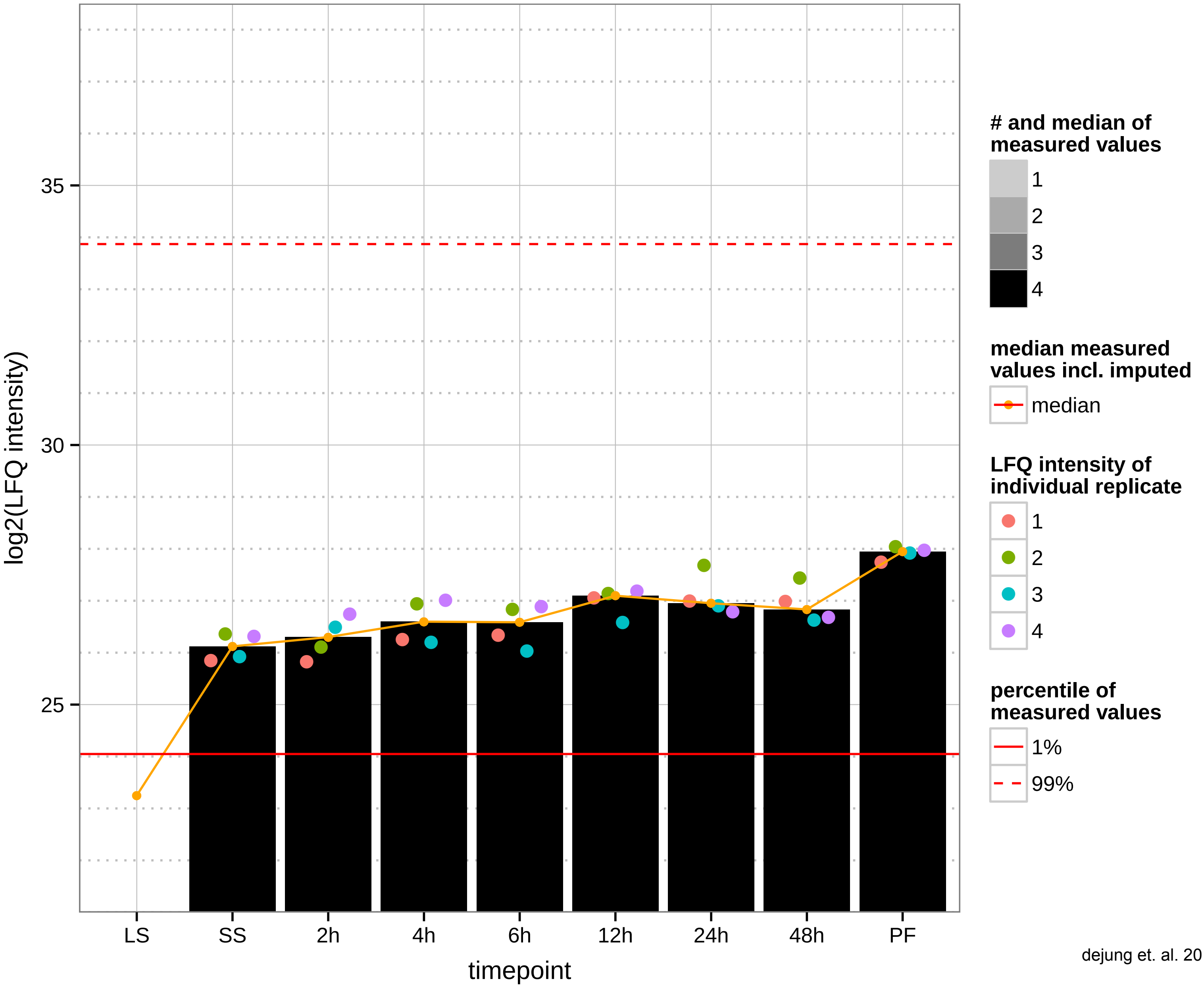
hypothetical protein, conserved
Tb927.3.2670
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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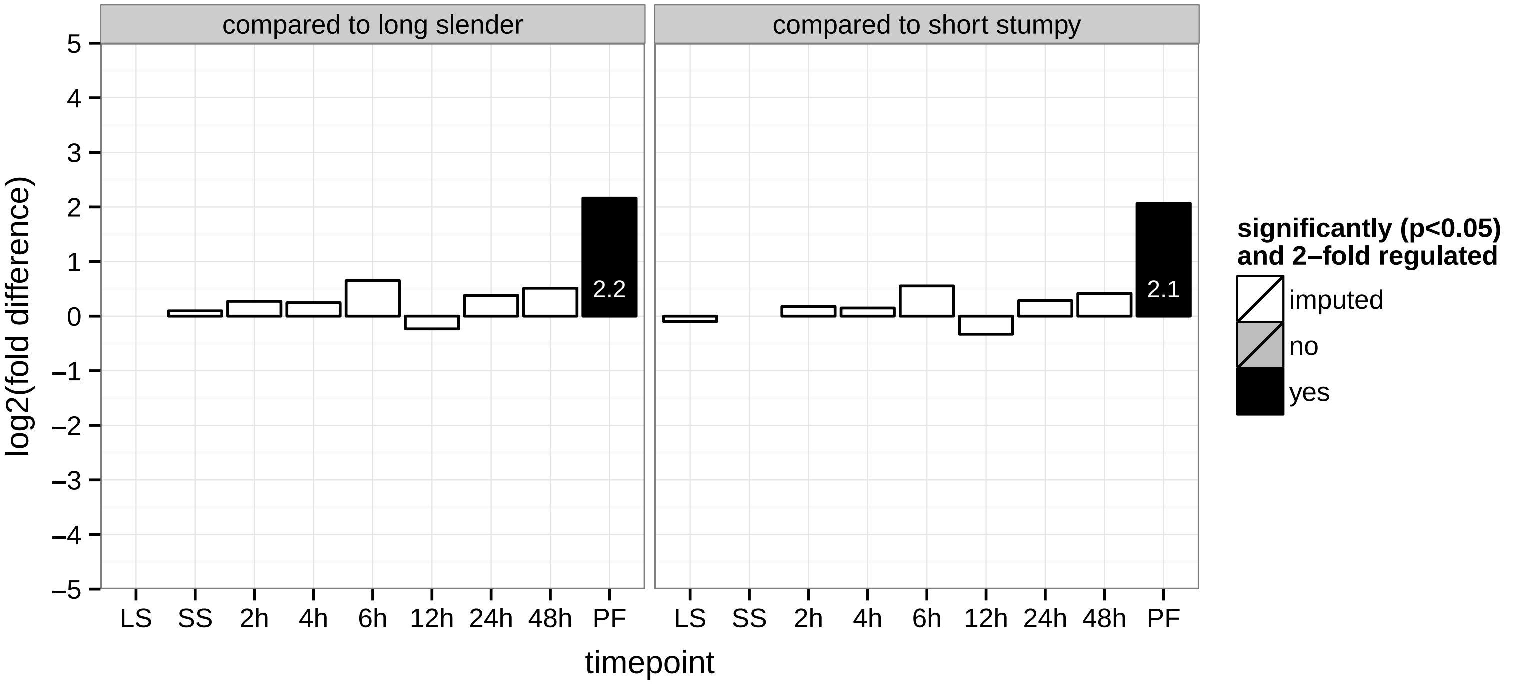
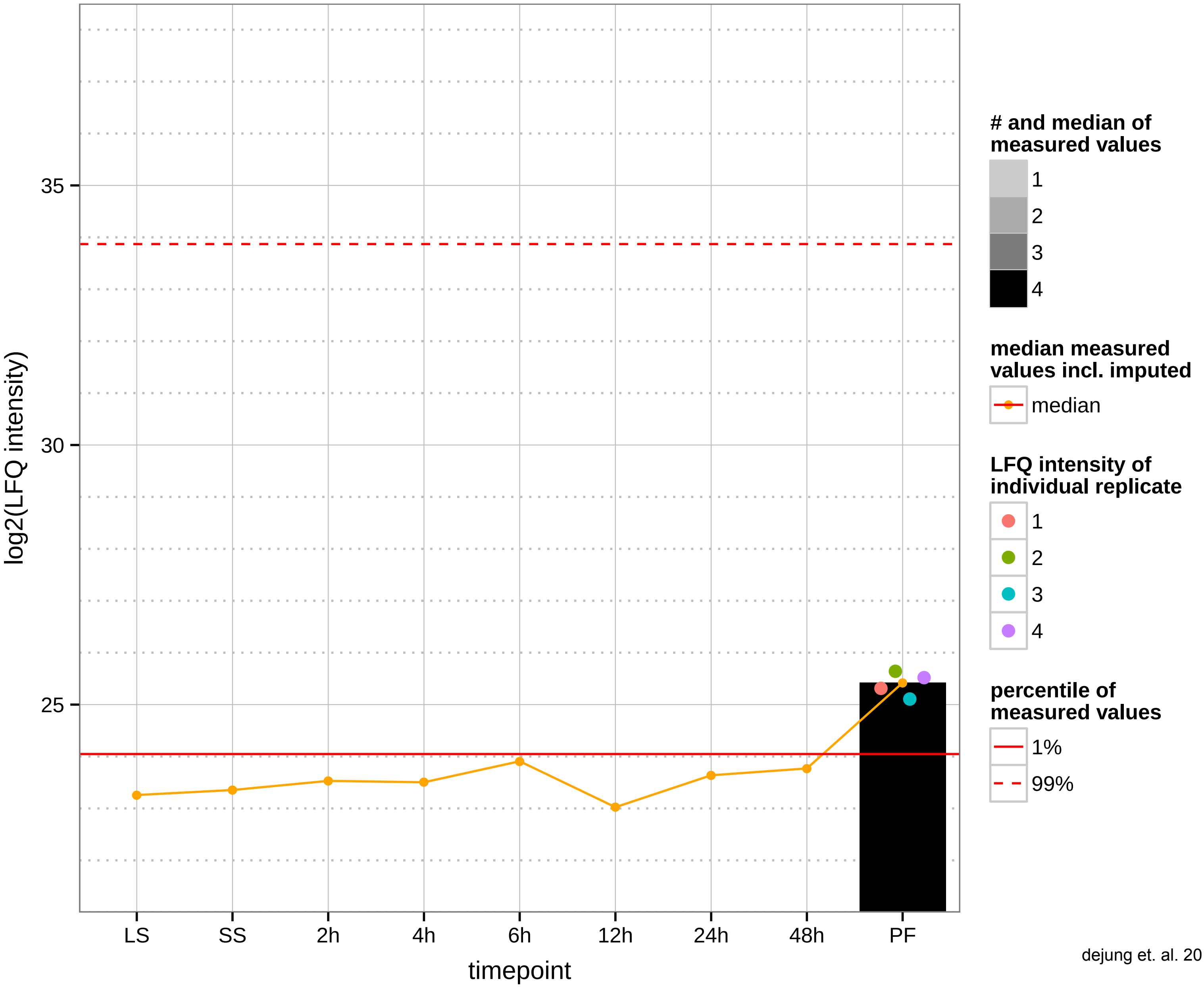
hypothetical protein, conserved
Tb927.3.3370
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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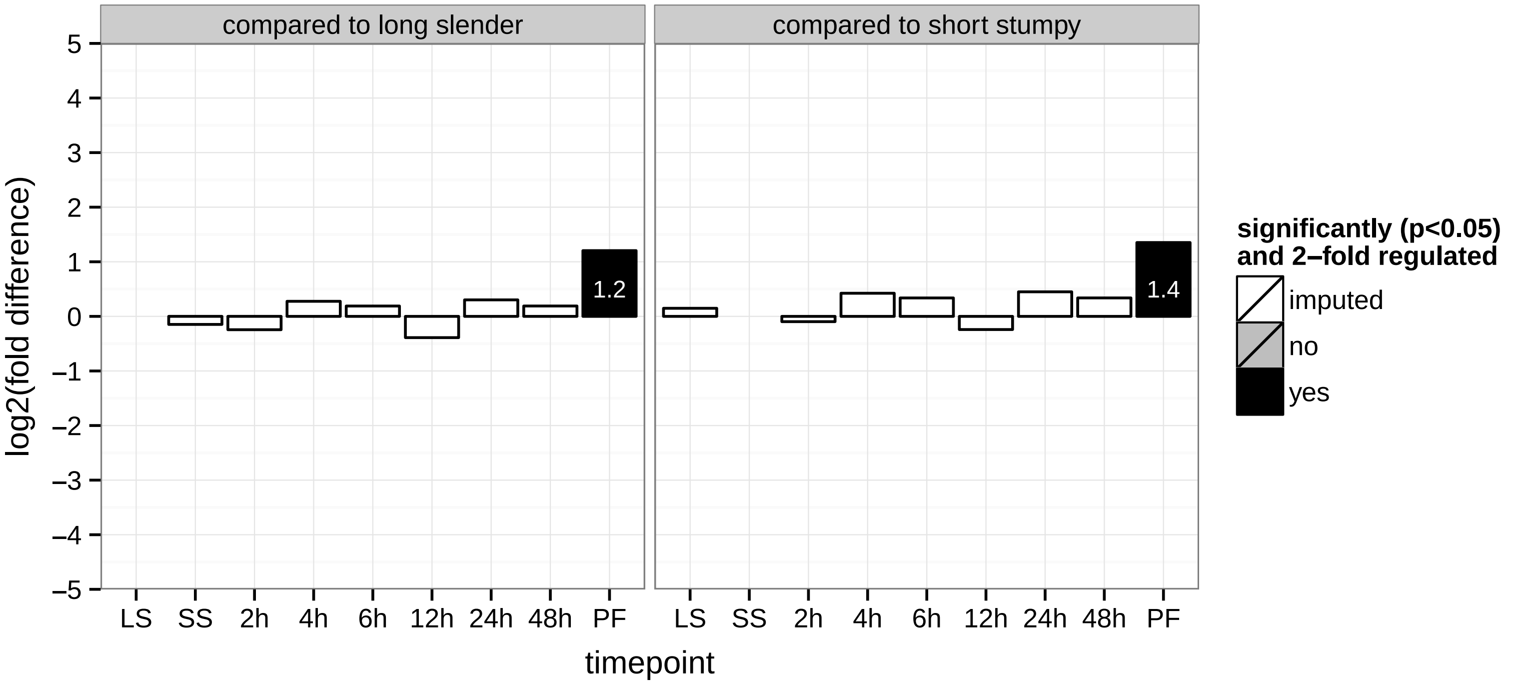
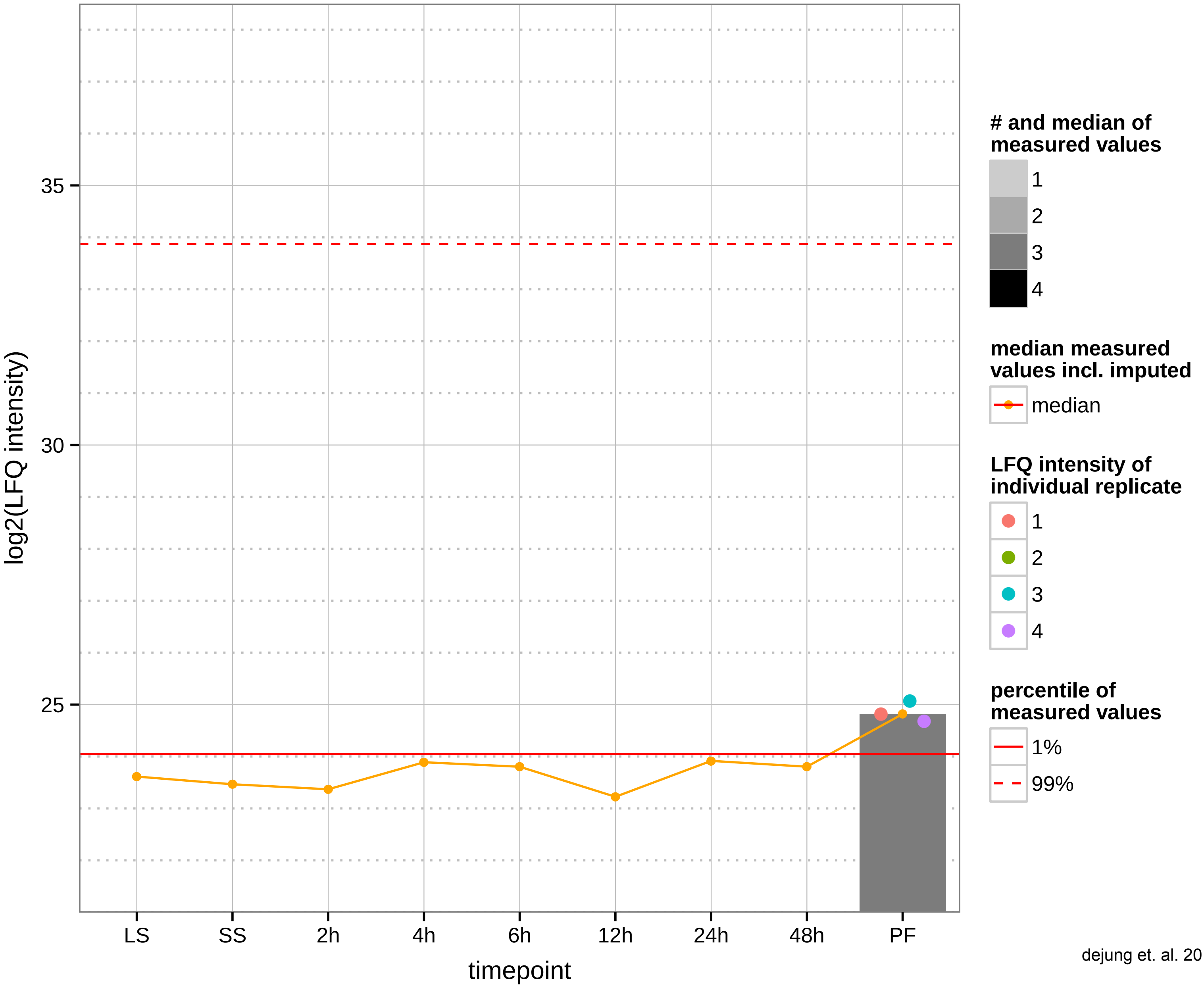
hypothetical protein, conserved
Tb927.3.3510
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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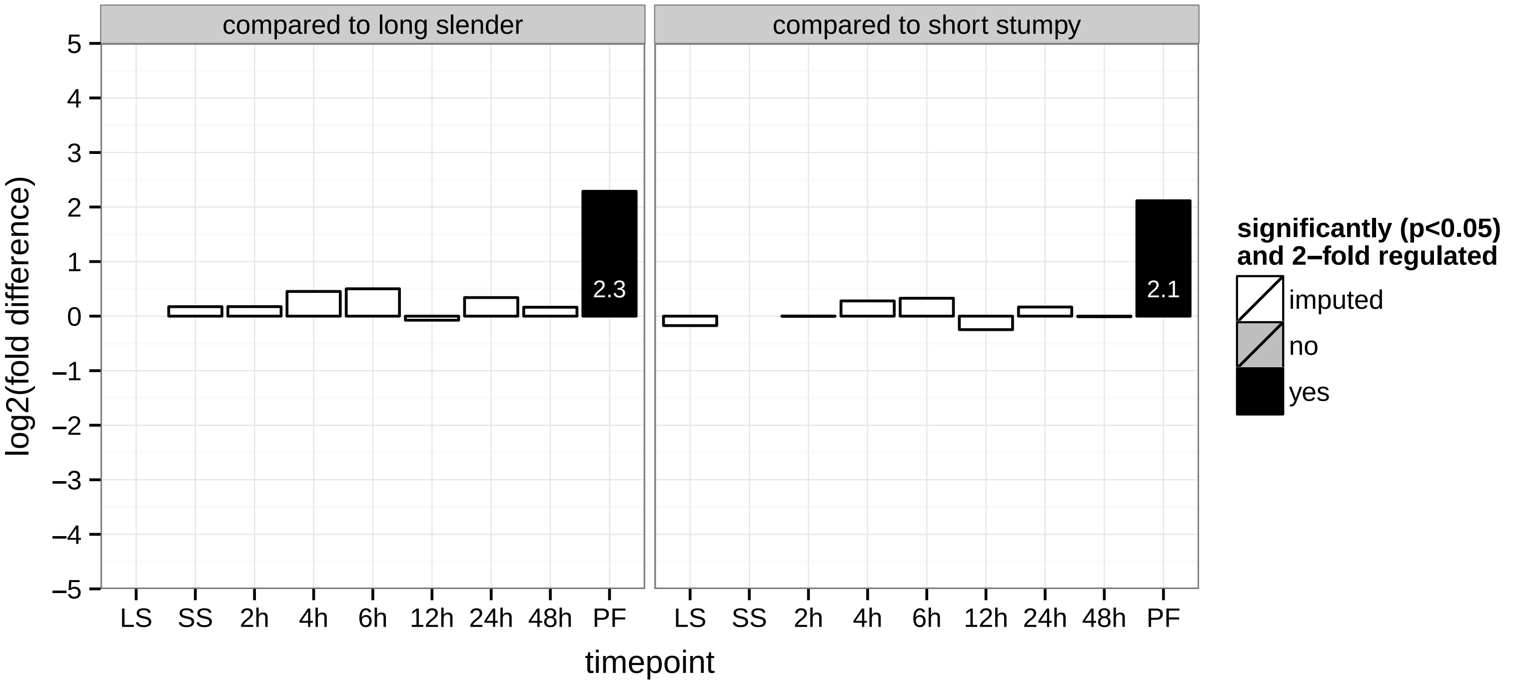
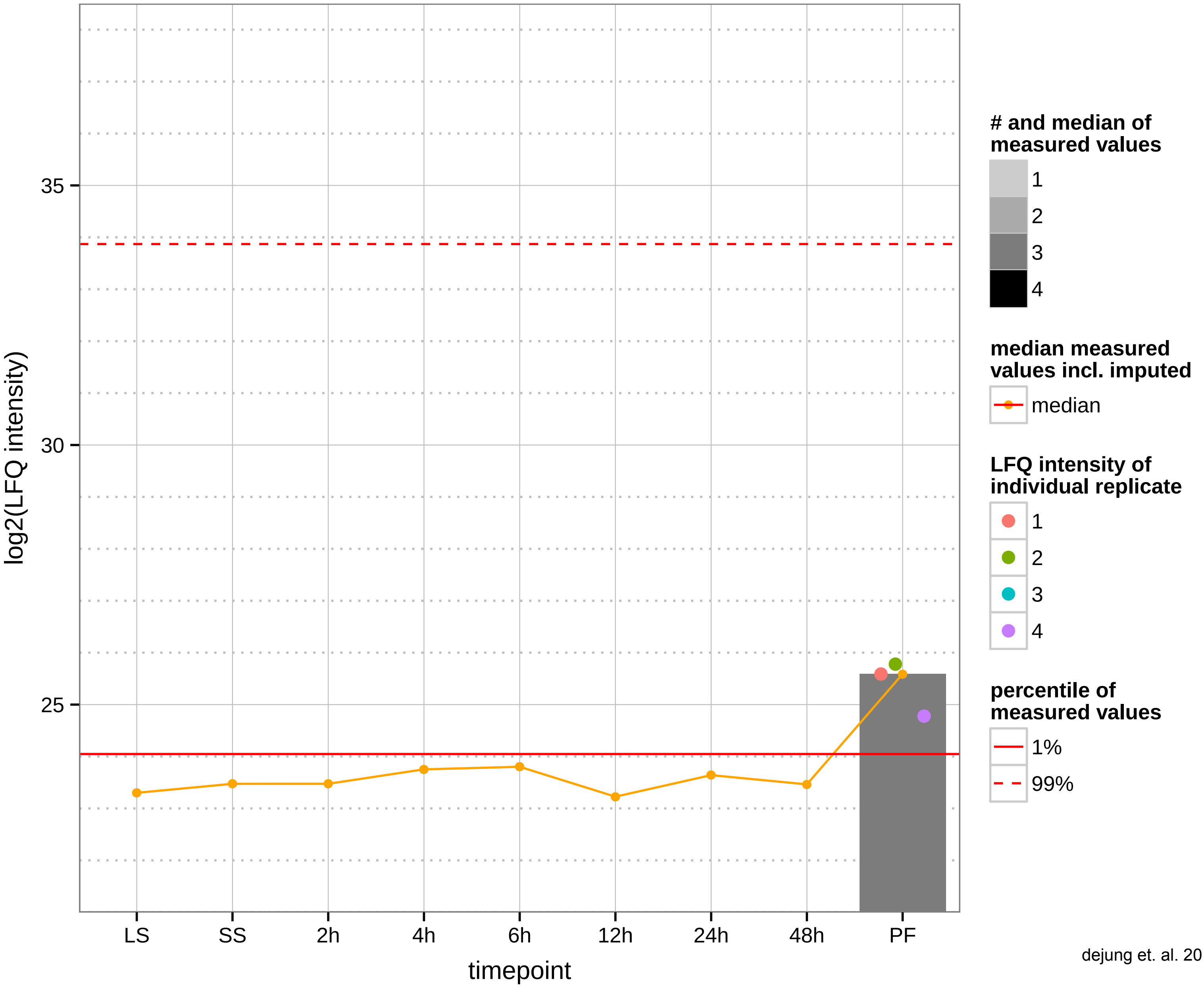
hypothetical protein, conserved
Tb927.3.3710
AGOF: catalytic activity
AGOC: null
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null





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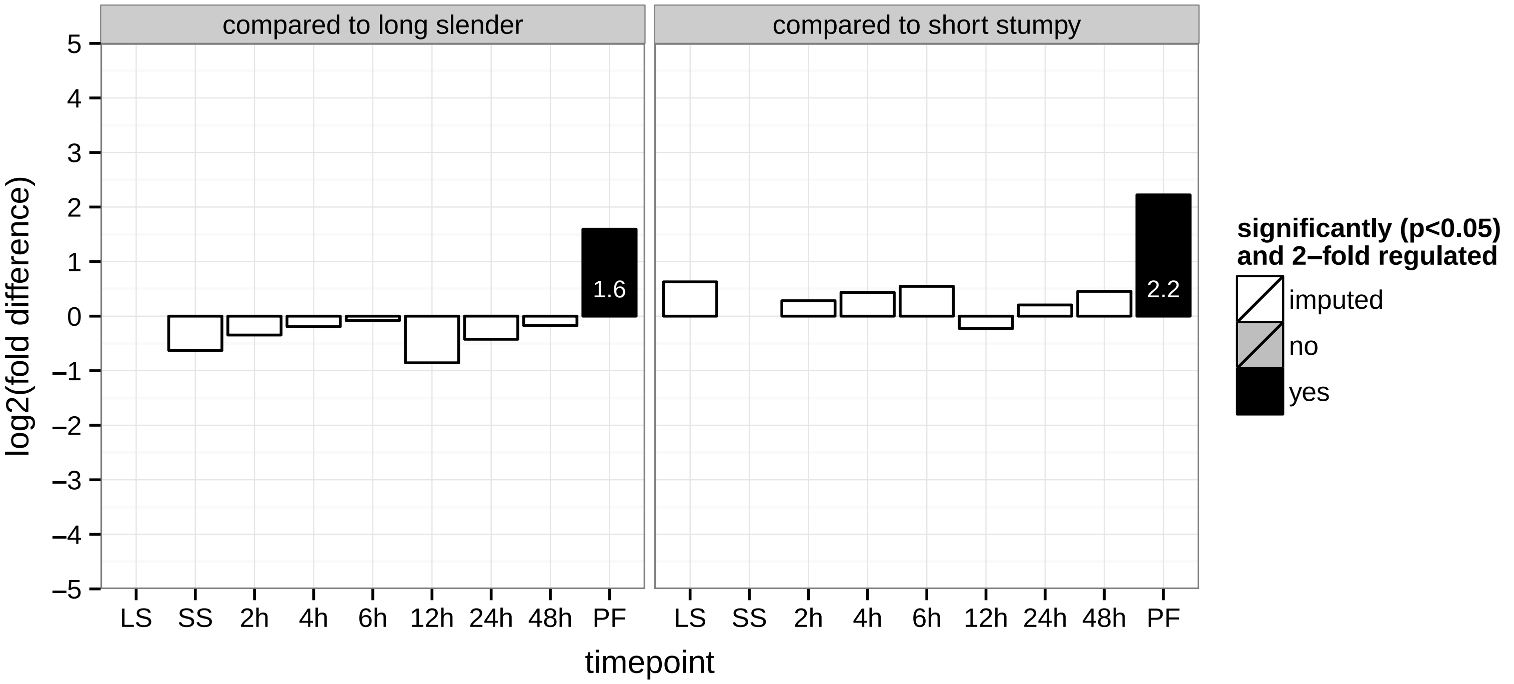
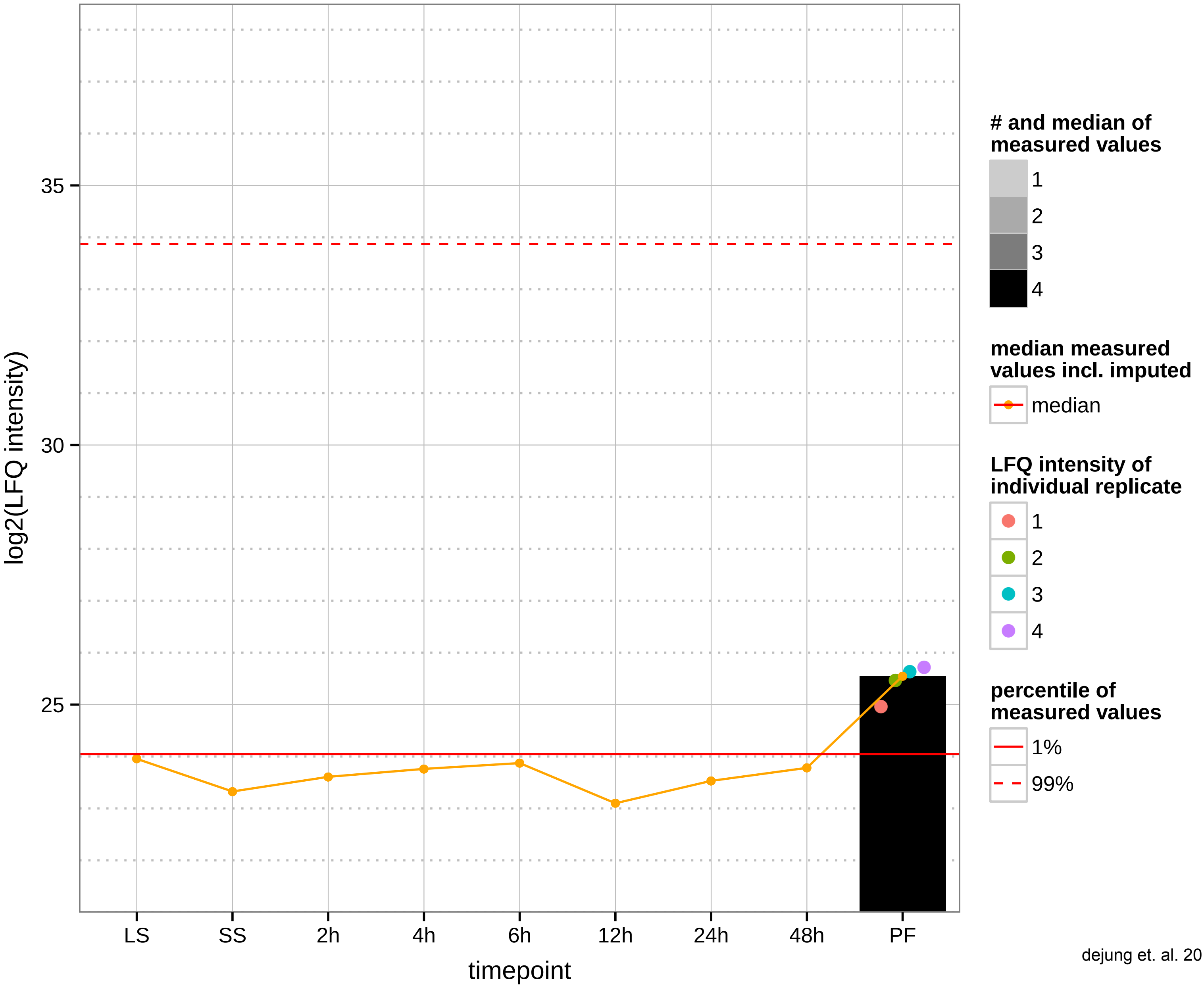
hypothetical protein, conserved
Tb927.3.3880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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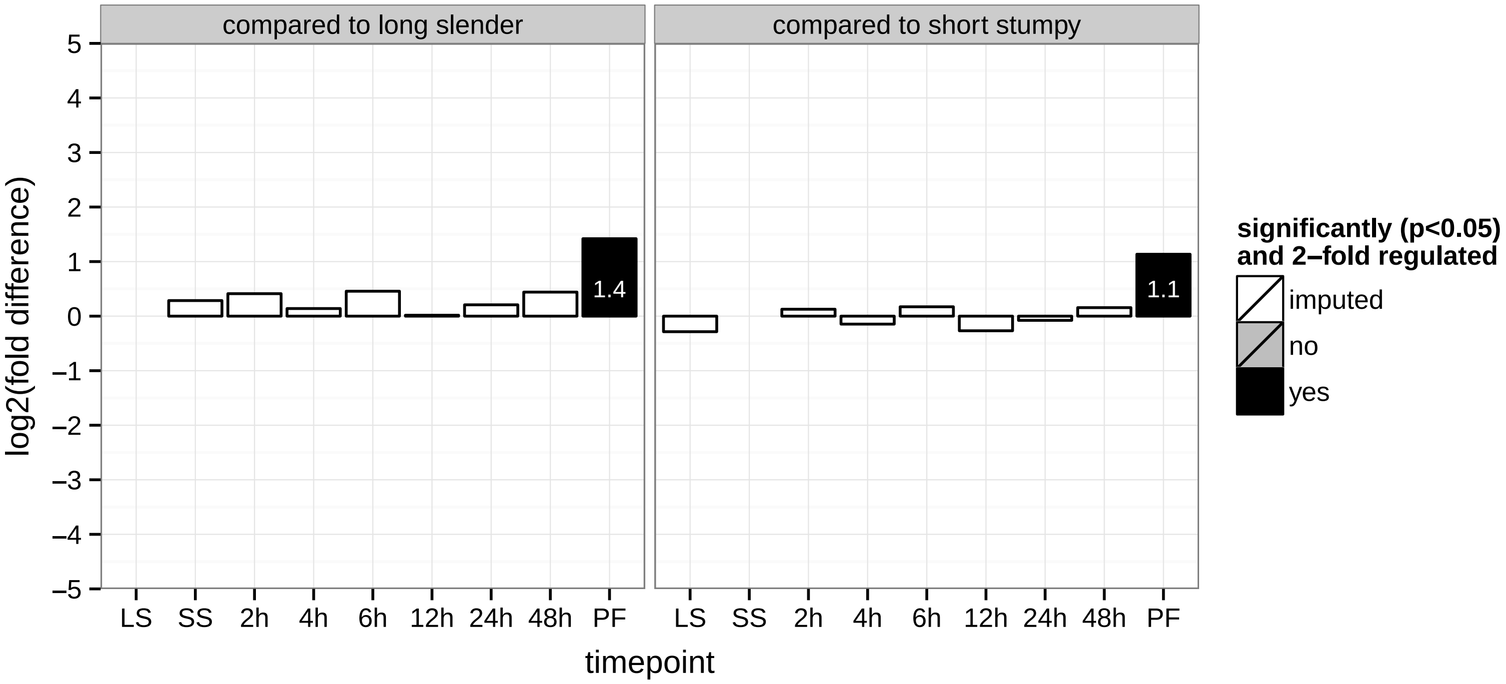
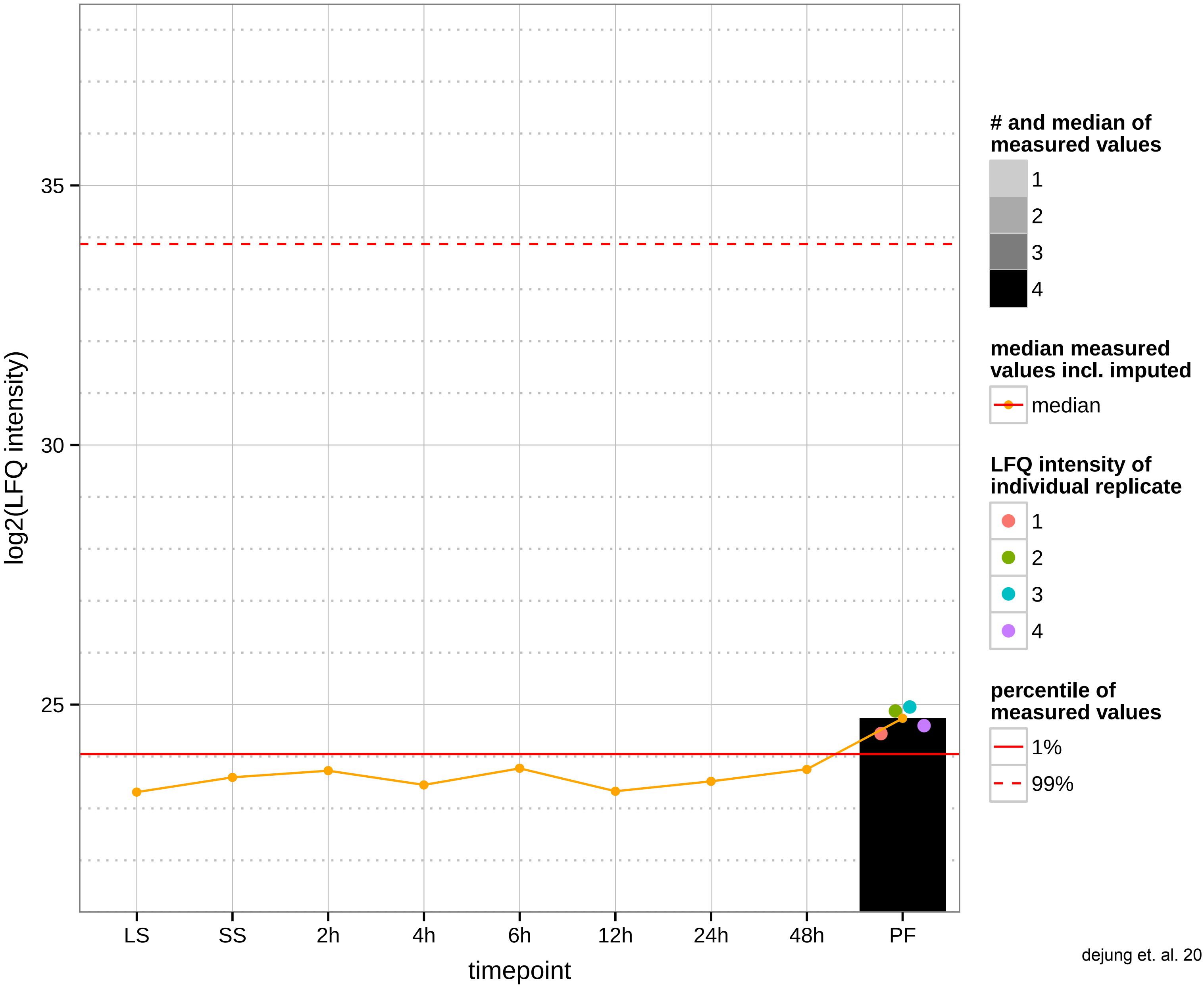
protein farnesyltransferase alpha subunit, putative
Tb927.3.4490
AGOF: protein farnesyltransferase activity
AGOC: null
AGOP: protein prenylation
PGOF: protein prenyltransferase activity
PGOC: null
PGOP: protein prenylation





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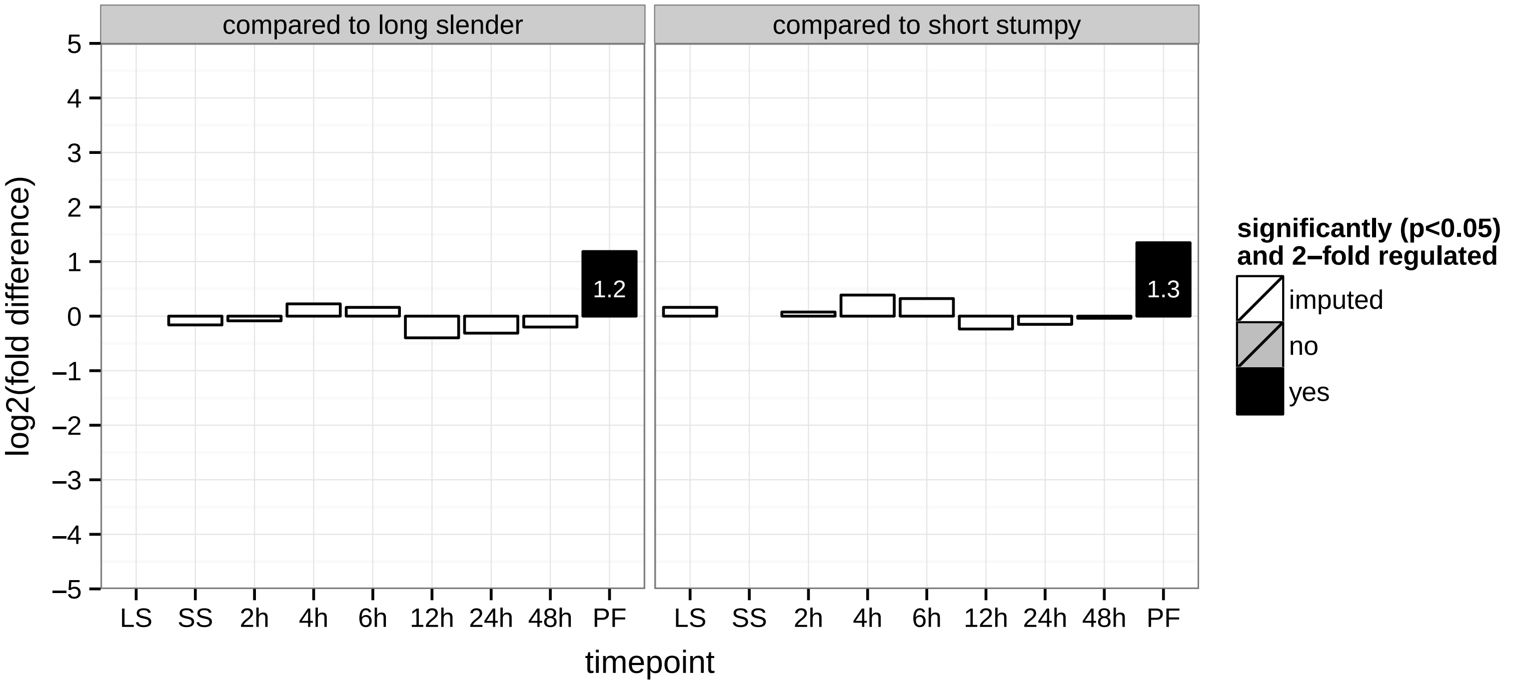
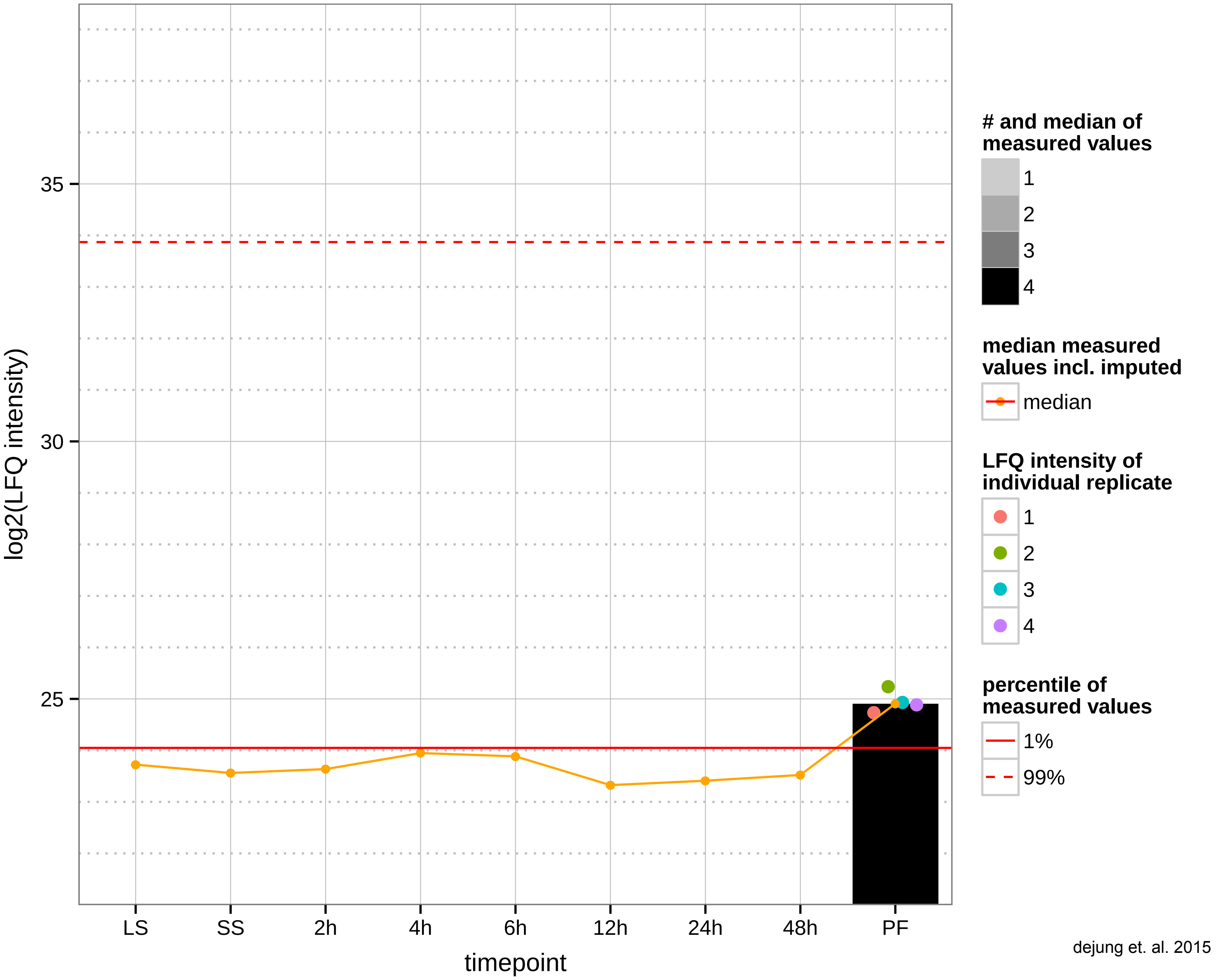
hypothetical protein, conserved
Tb927.3.4950
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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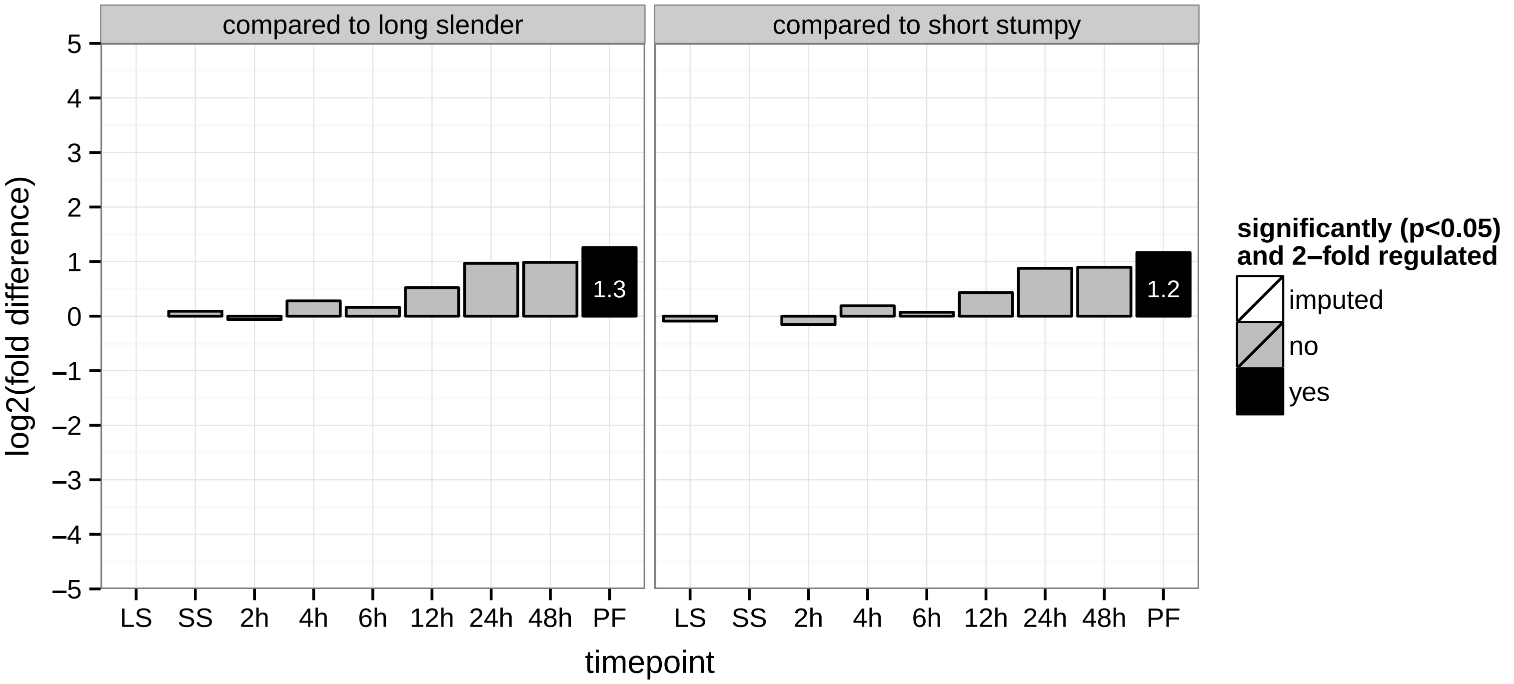
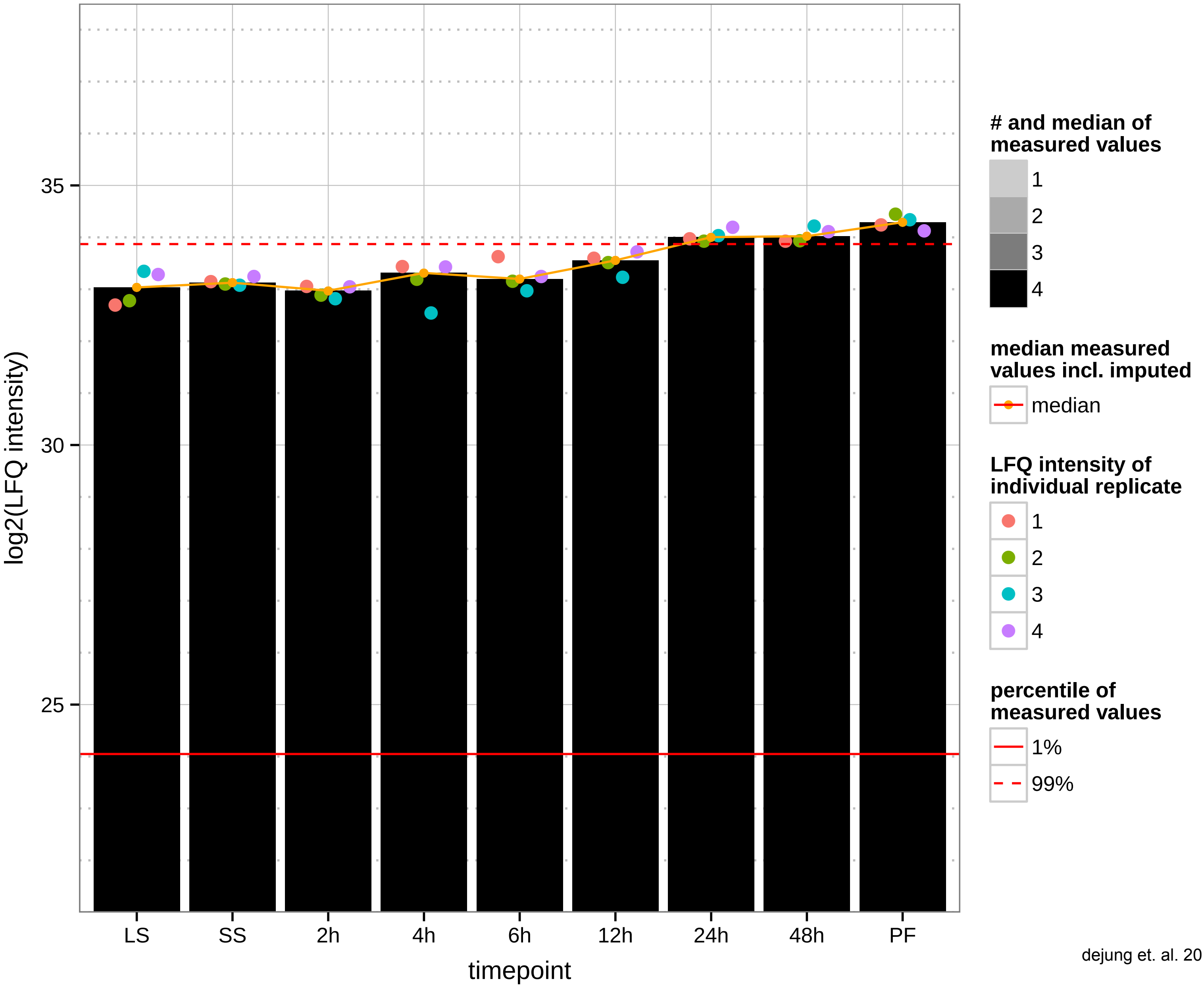
60S ribosomal protein L4
Tb927.3.5050
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: ribosome
PGOP: translation





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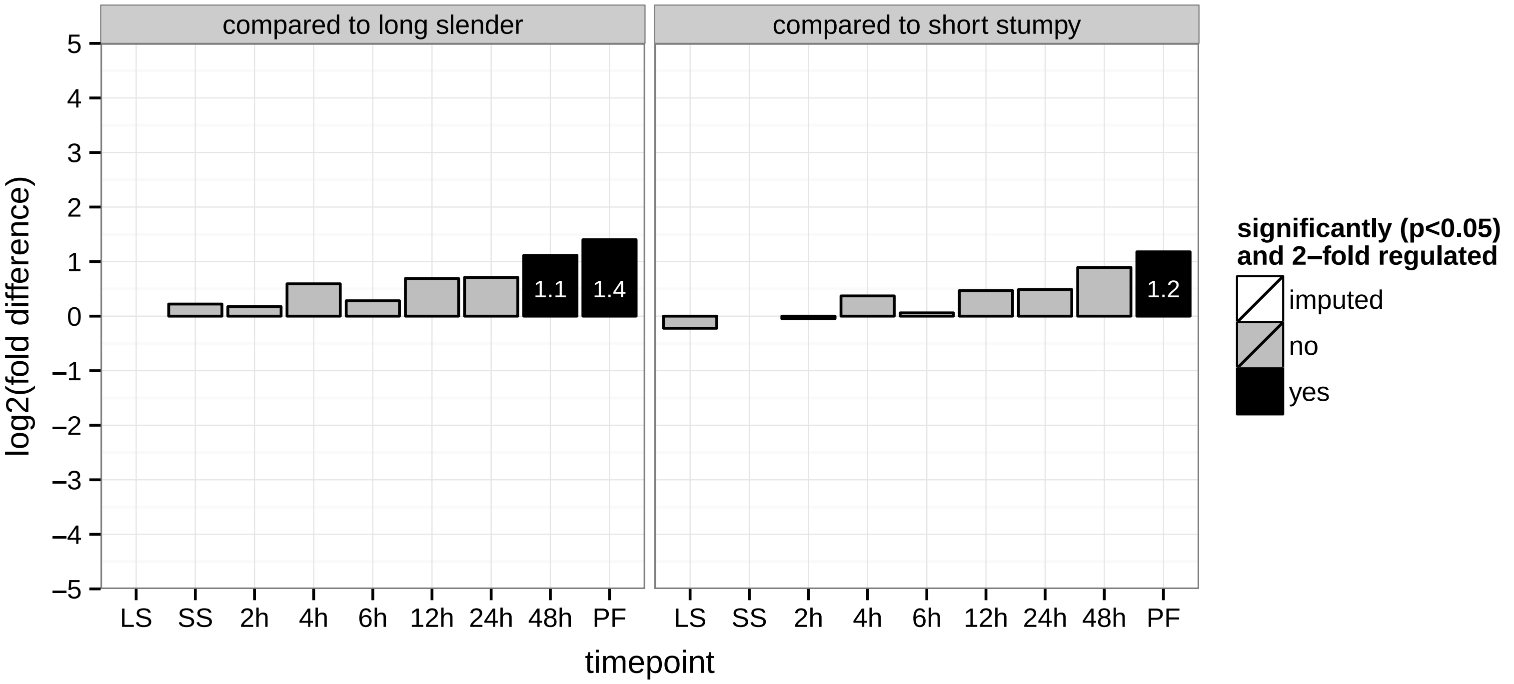
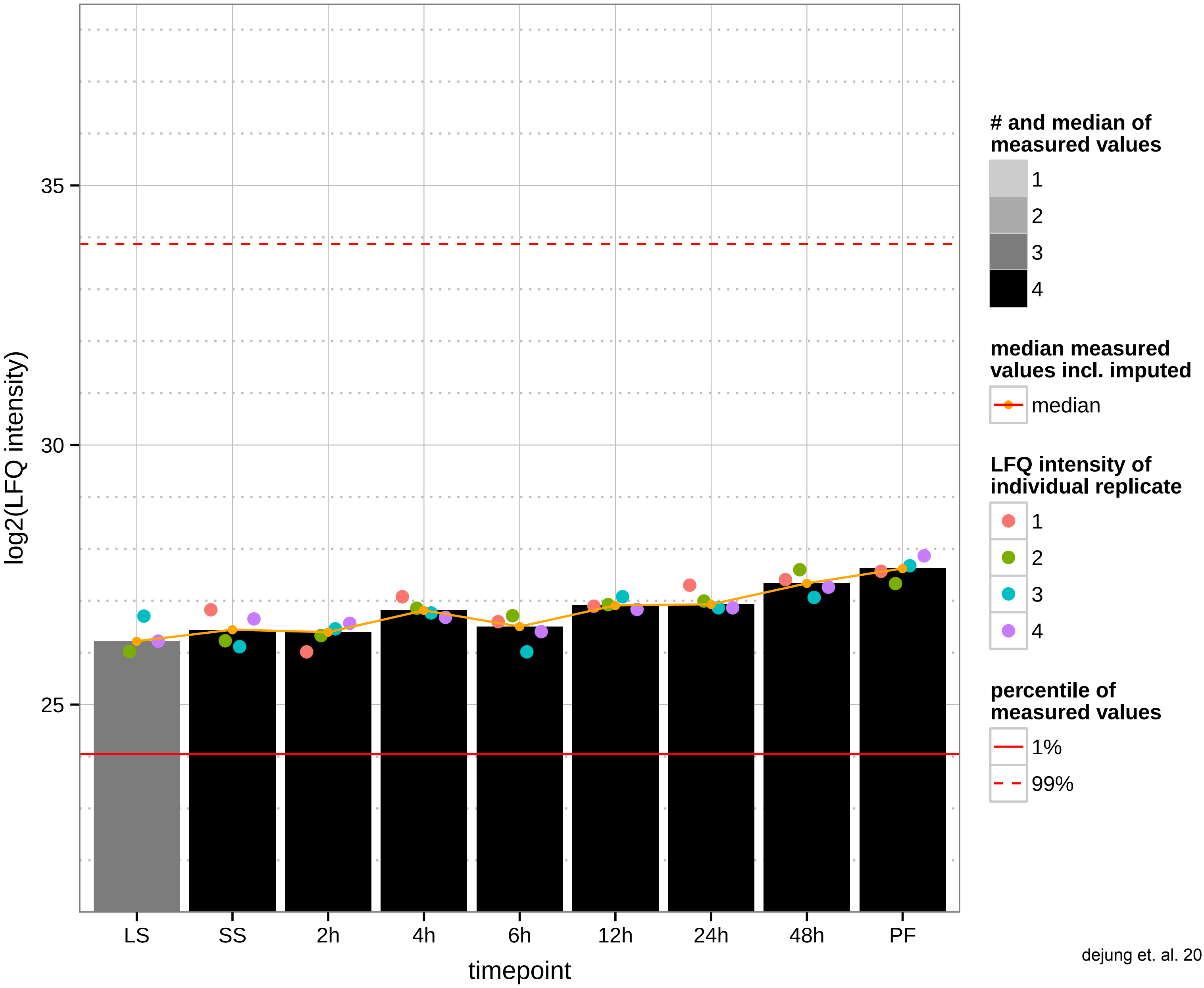
UBX domain–containing protein
Tb927.3.5320
AGOF: ubiquitin binding, ubiquitin protein ligase binding
AGOC: cytoplasm, nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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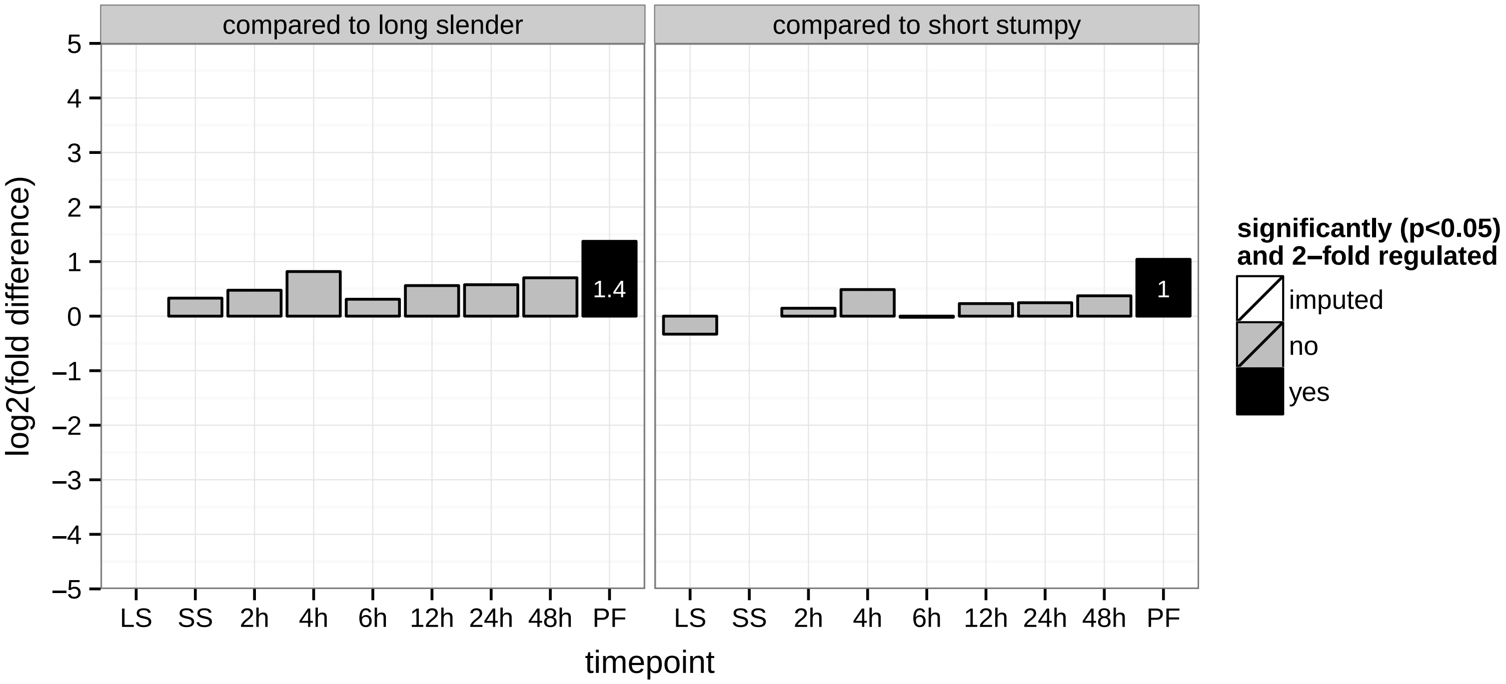
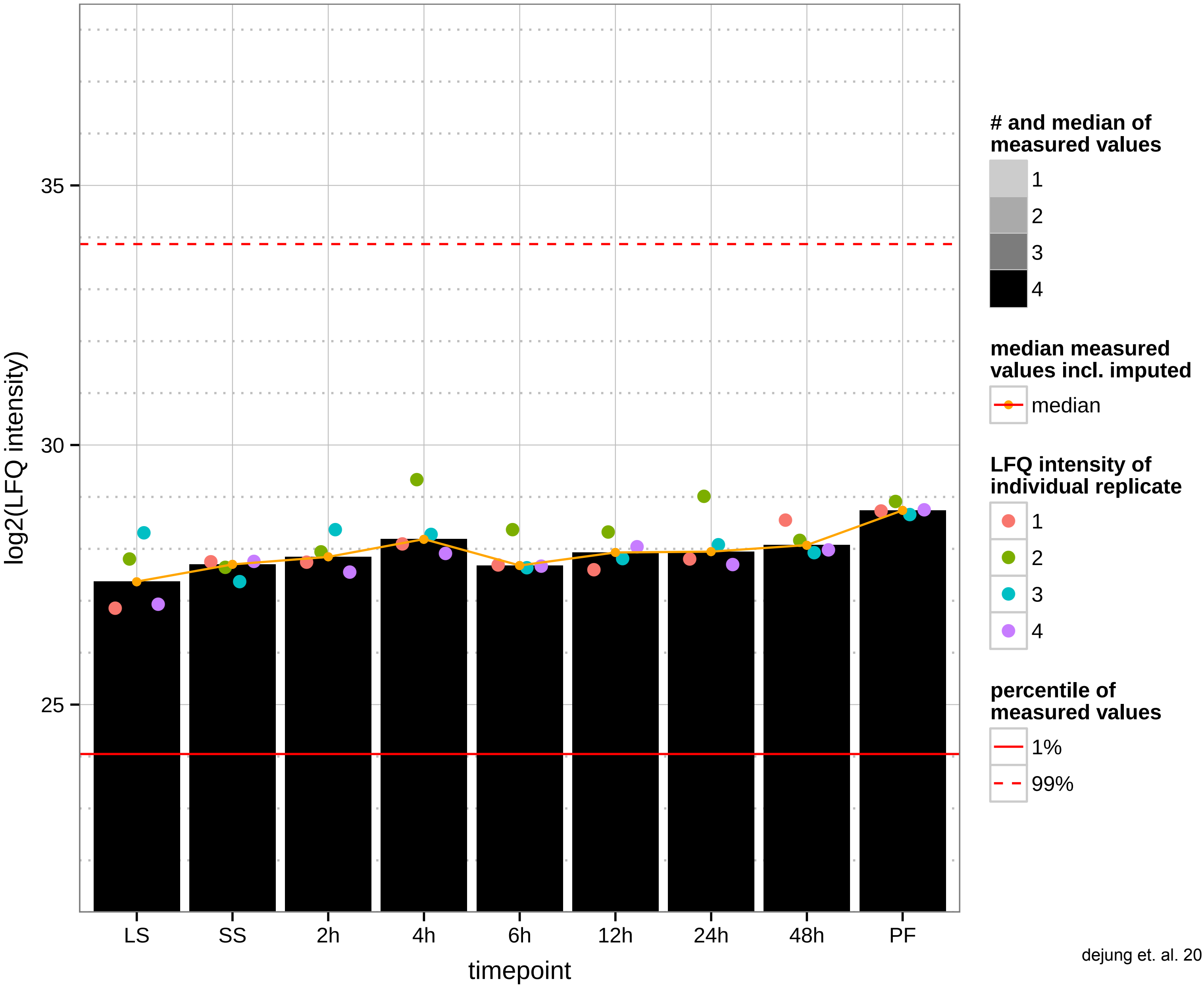
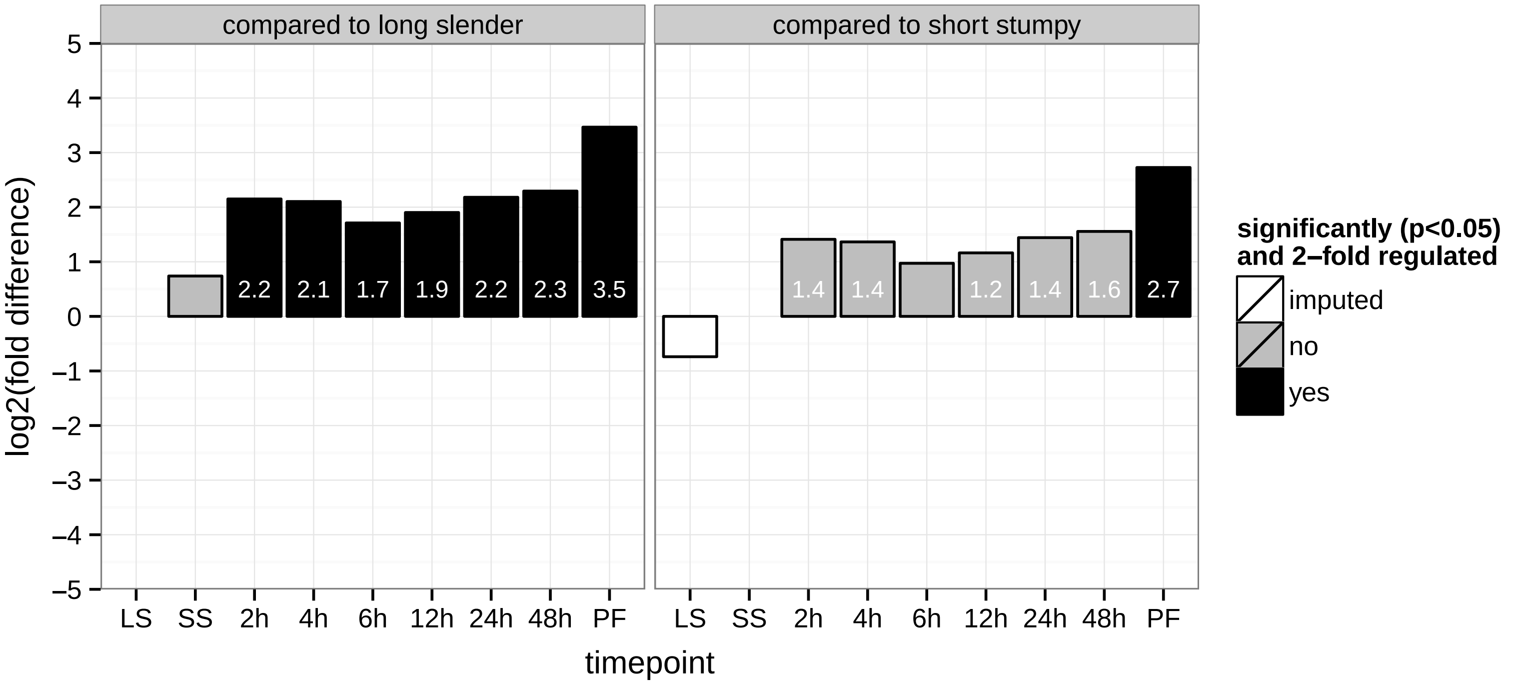
hypothetical protein, conserved
Tb927.3.5430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

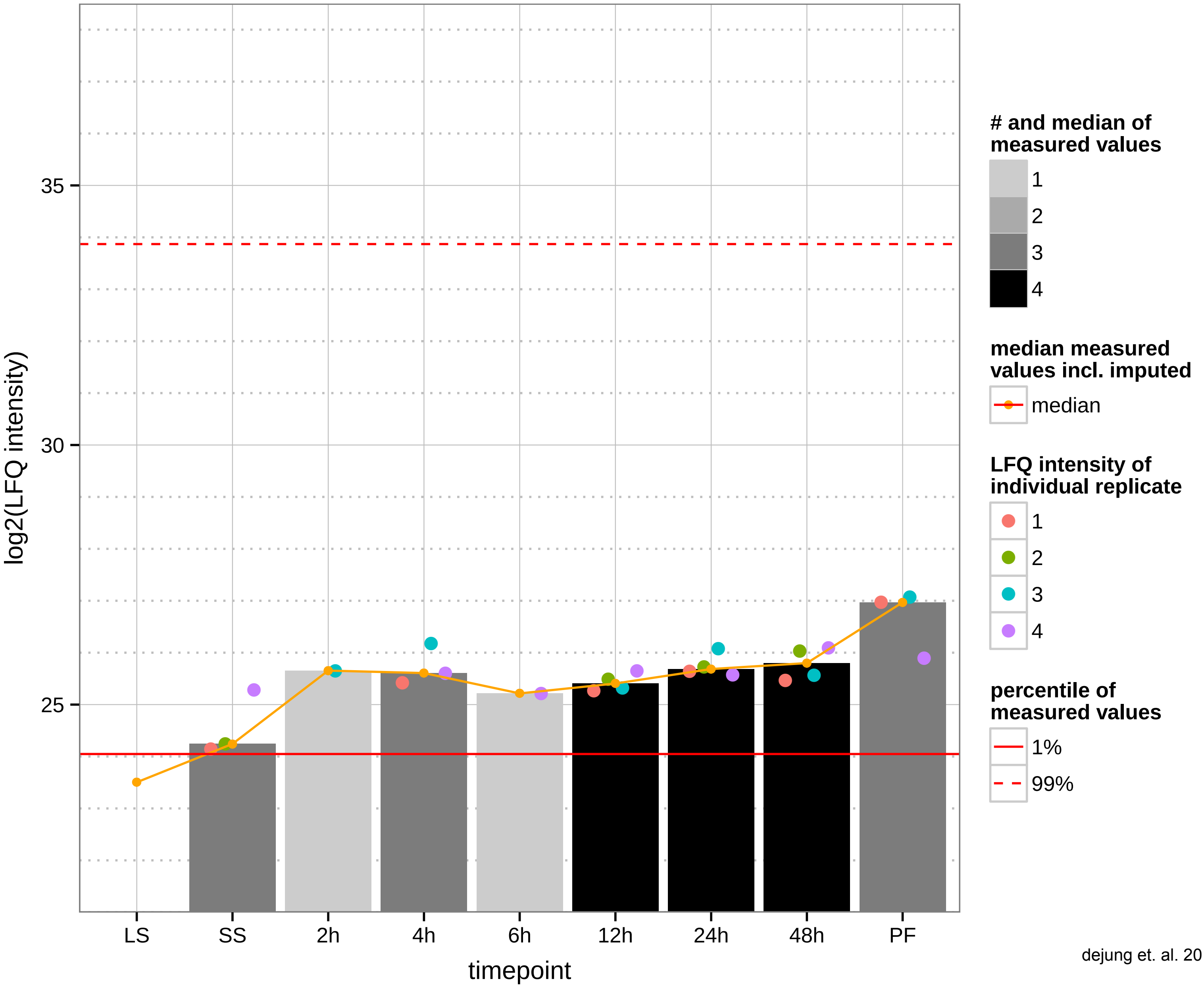




dejung et. al. 2015

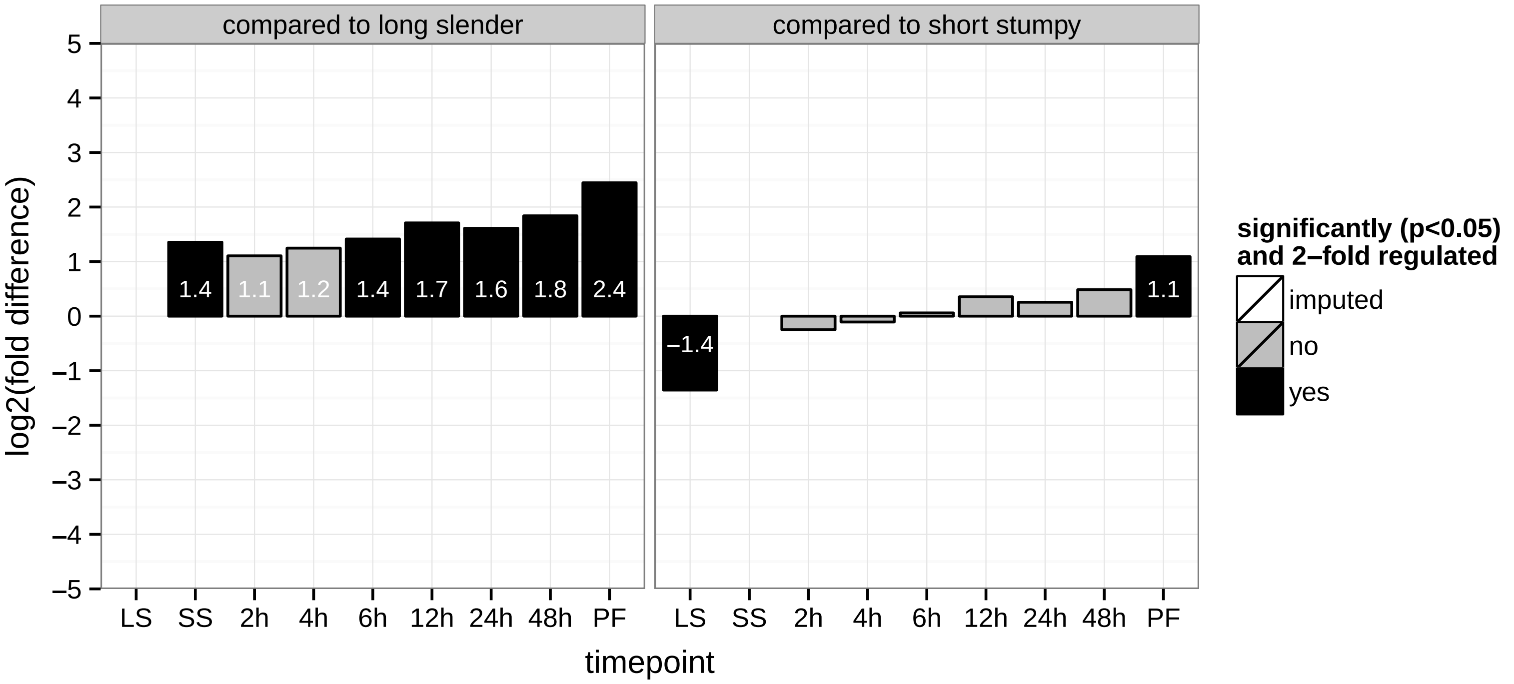
hypothetical protein, conserved
Tb927.3.5600
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

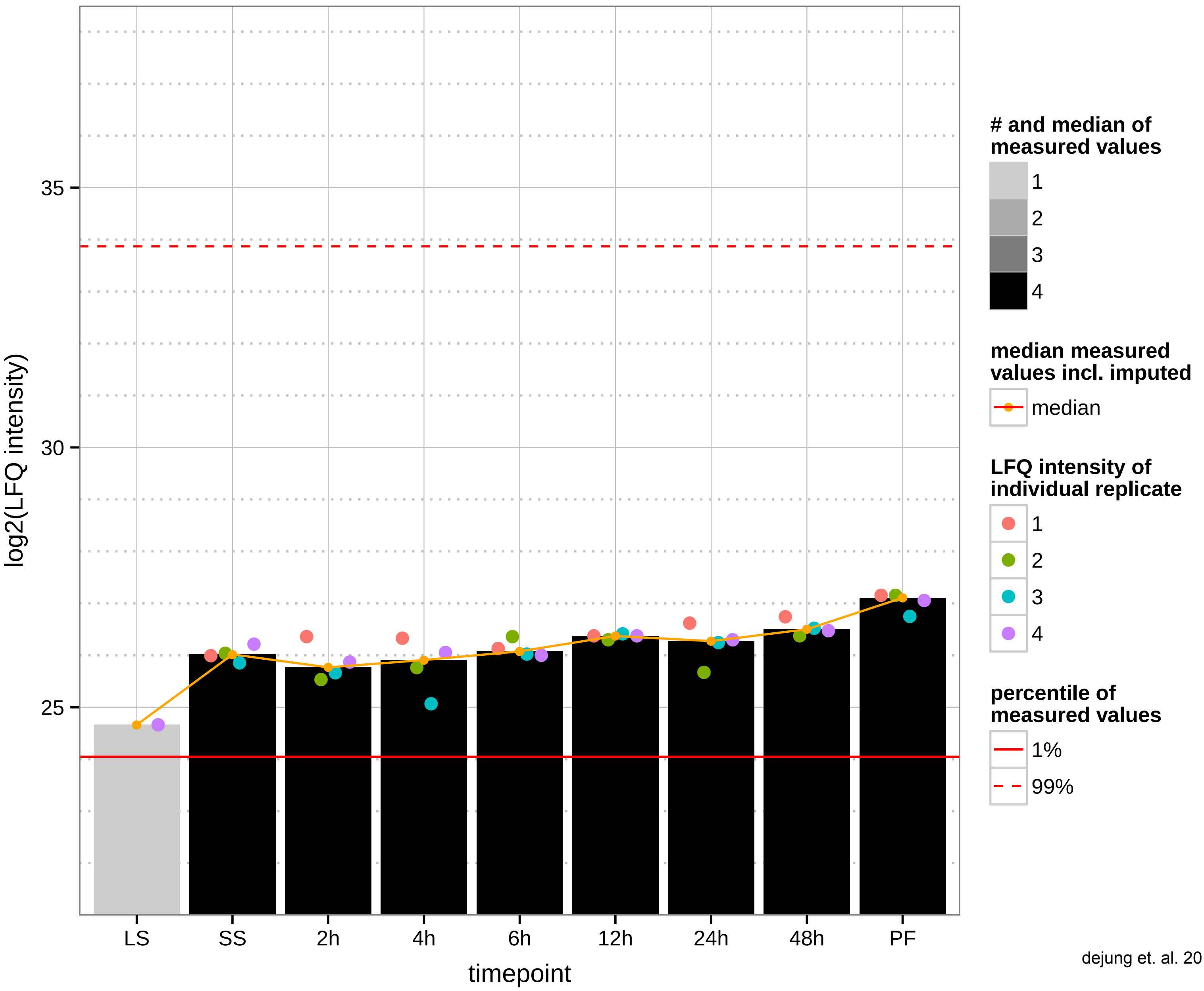




dejung et. al. 2015

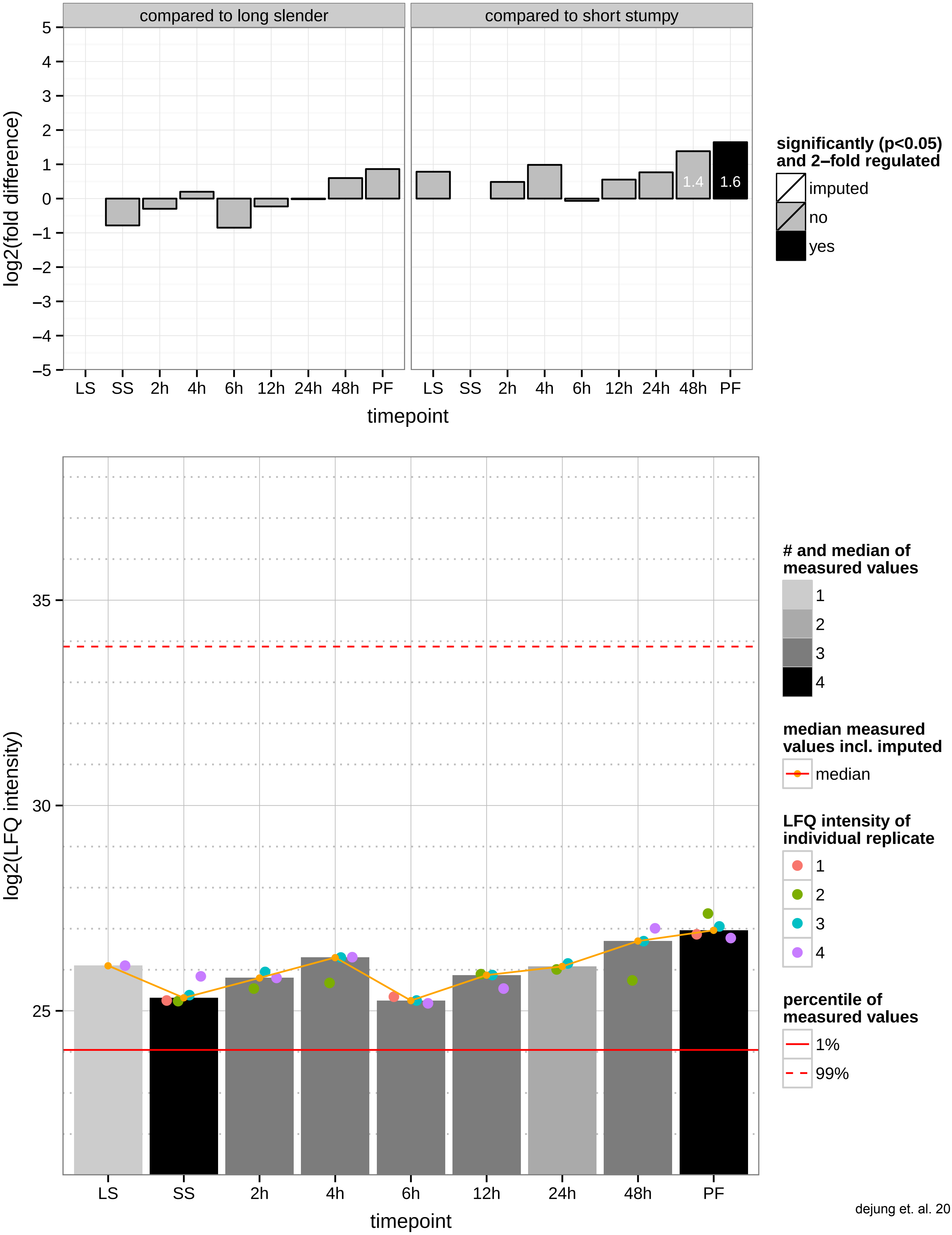
ATP−dependent DEAD/H RNA helicase, putative
Tb927.3.620
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





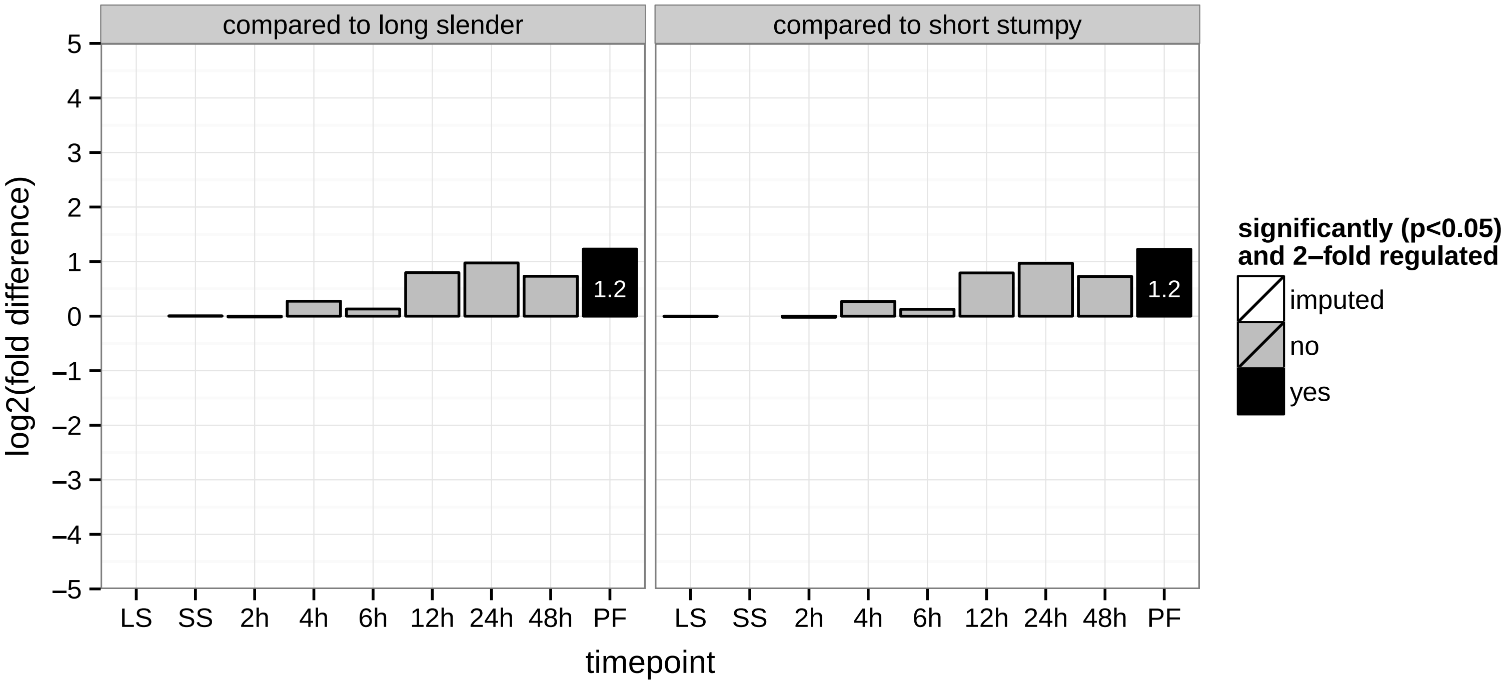
dejung et. al. 2015

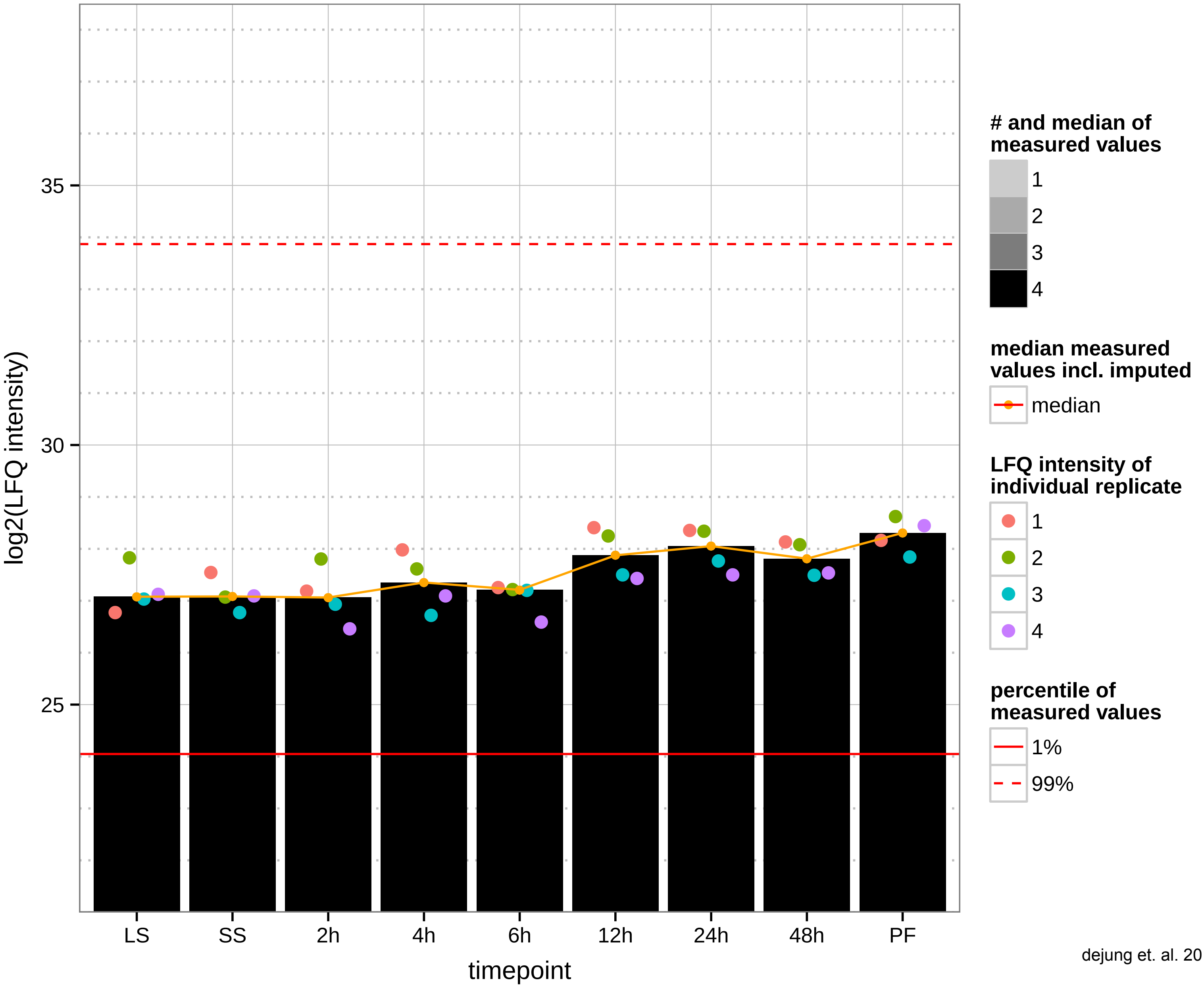
ZFP family member, putative (ZC3H5)
Tb927.3.740
AGOF: RNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null



dejung et. al. 2015

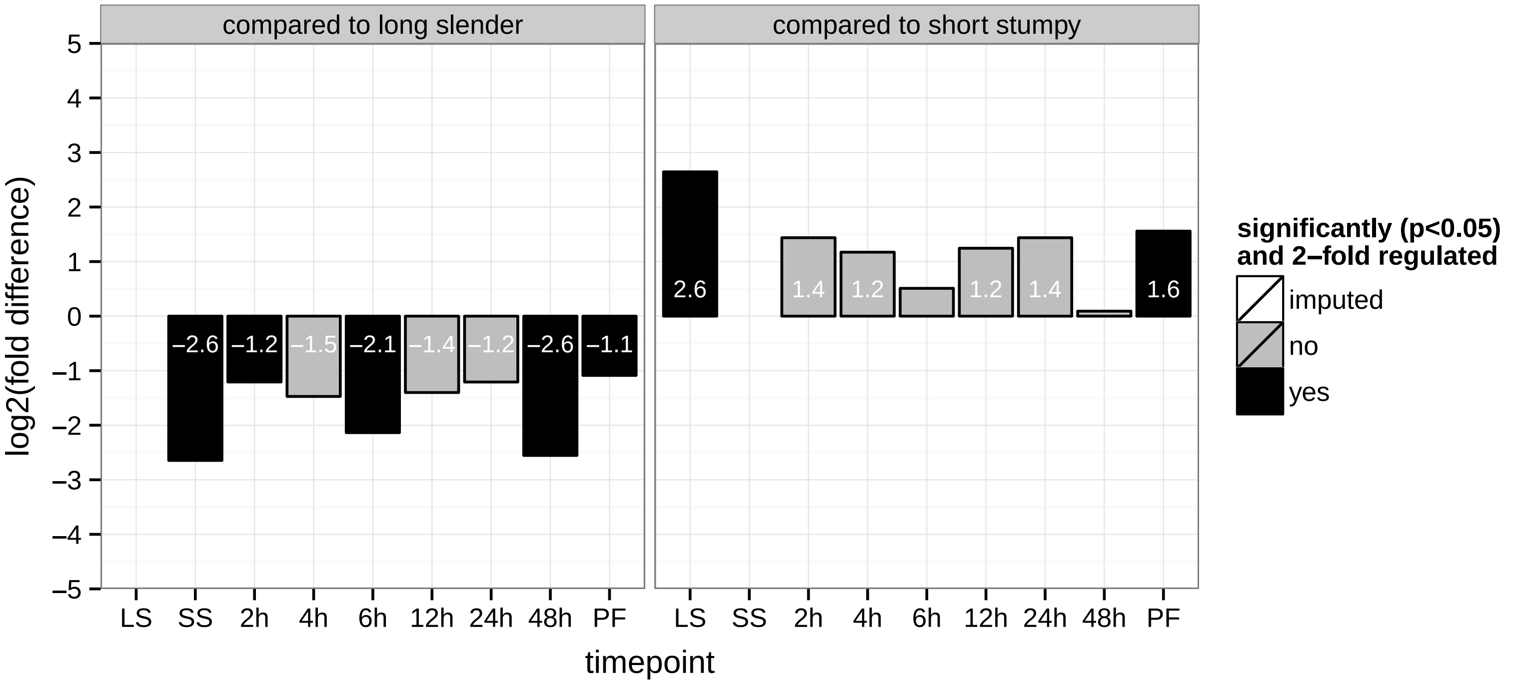
flap endonuclease−1 (FEN−1), putative
Tb927.3.830
AGOF: DNA binding, nuclease activity
AGOC: null
AGOP: DNA repair
PGOF: DNA binding, catalytic activity, nuclease activity
PGOC: null
PGOP: DNA repair

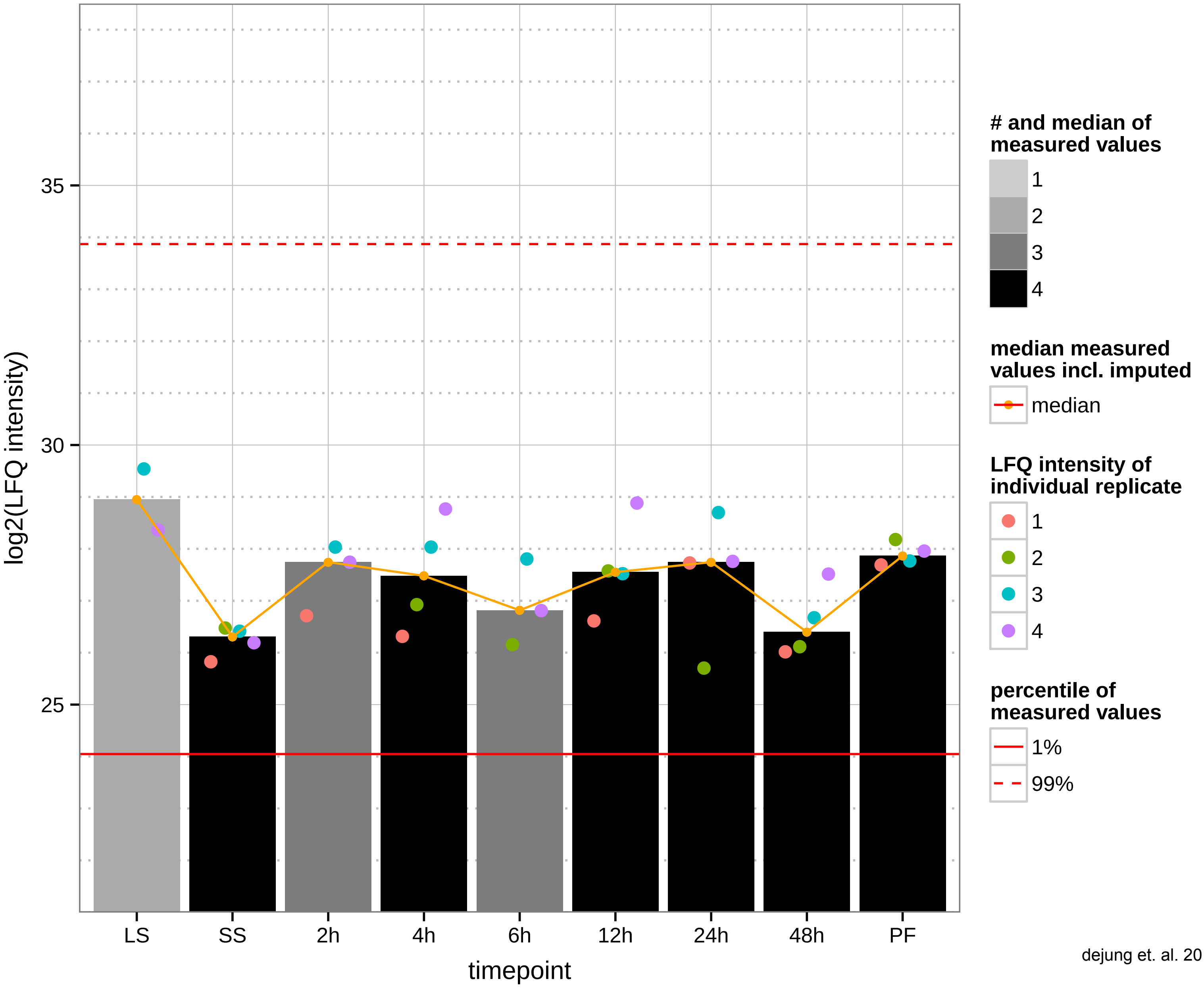




dejung et. al. 2015

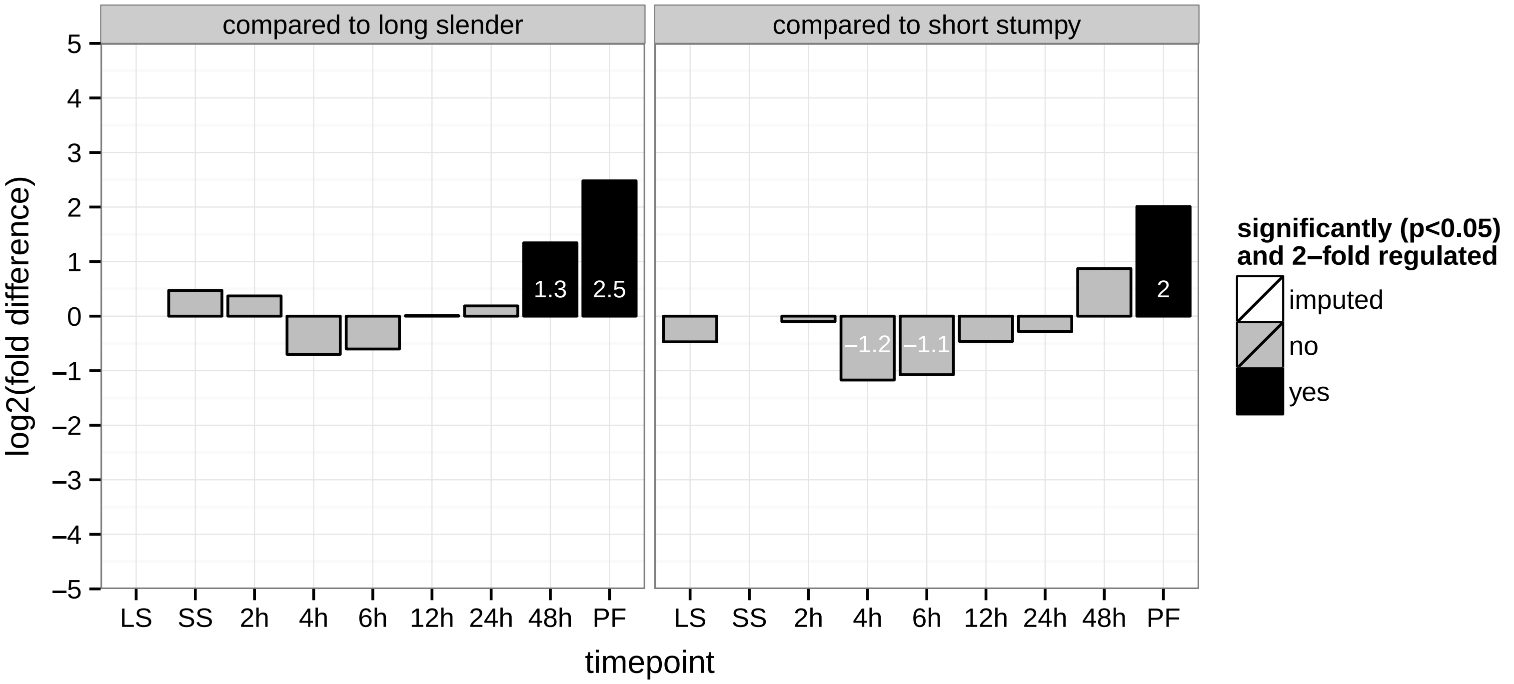
protein transport protein Sec61 gamma subunit, putative
Tb927.3.960
AGOF: P–P–bond–hydrolysis–driven protein transmembrane transporter activity
AGOC: membrane
AGOP: protein targeting
PGOF: P–P–bond–hydrolysis–driven protein transmembrane transporter activity
PGOC: membrane
PGOP: intracellular protein transport, protein targeting, protein transport

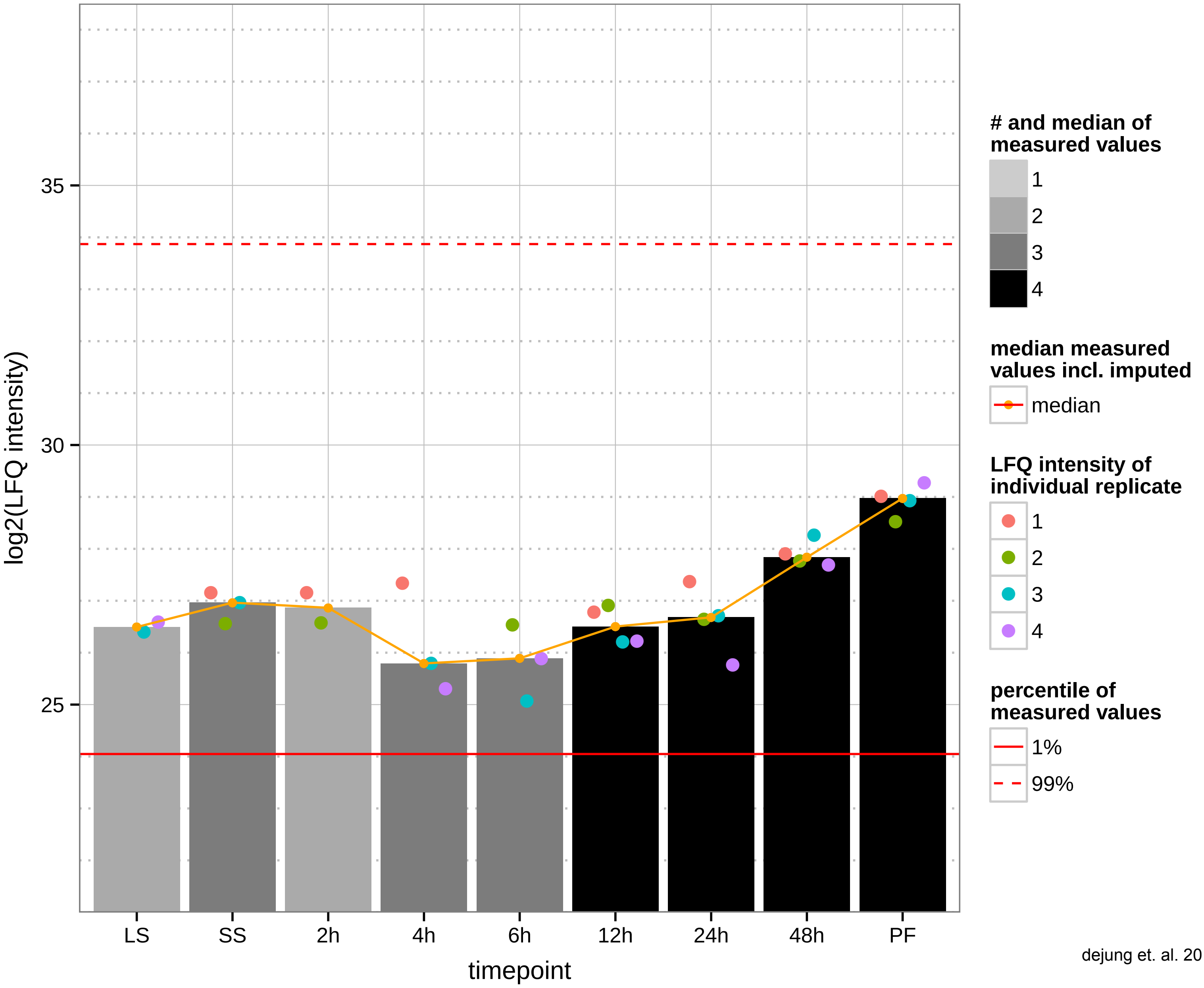




dejung et. al. 2015

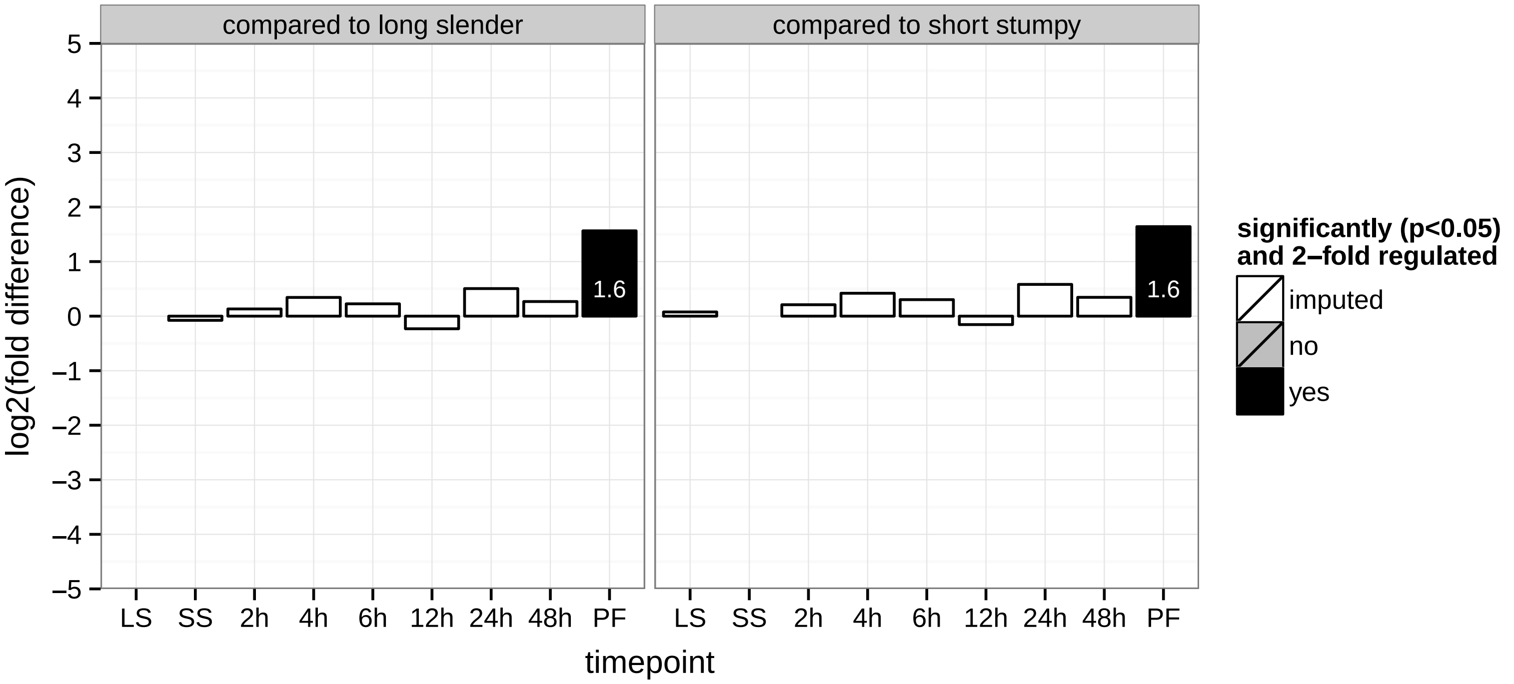
serine–palmitoyl–CoA transferase, putative
Tb927.4.1020
AGOF: pyridoxal phosphate binding, transferase activity, transferring nitrogenous groups
AGOC: endoplasmic reticulum
AGOP: biosynthetic process, membrane lipid metabolic process
PGOF: pyridoxal phosphate binding, transferase activity
PGOC: null
PGOP: biosynthetic process

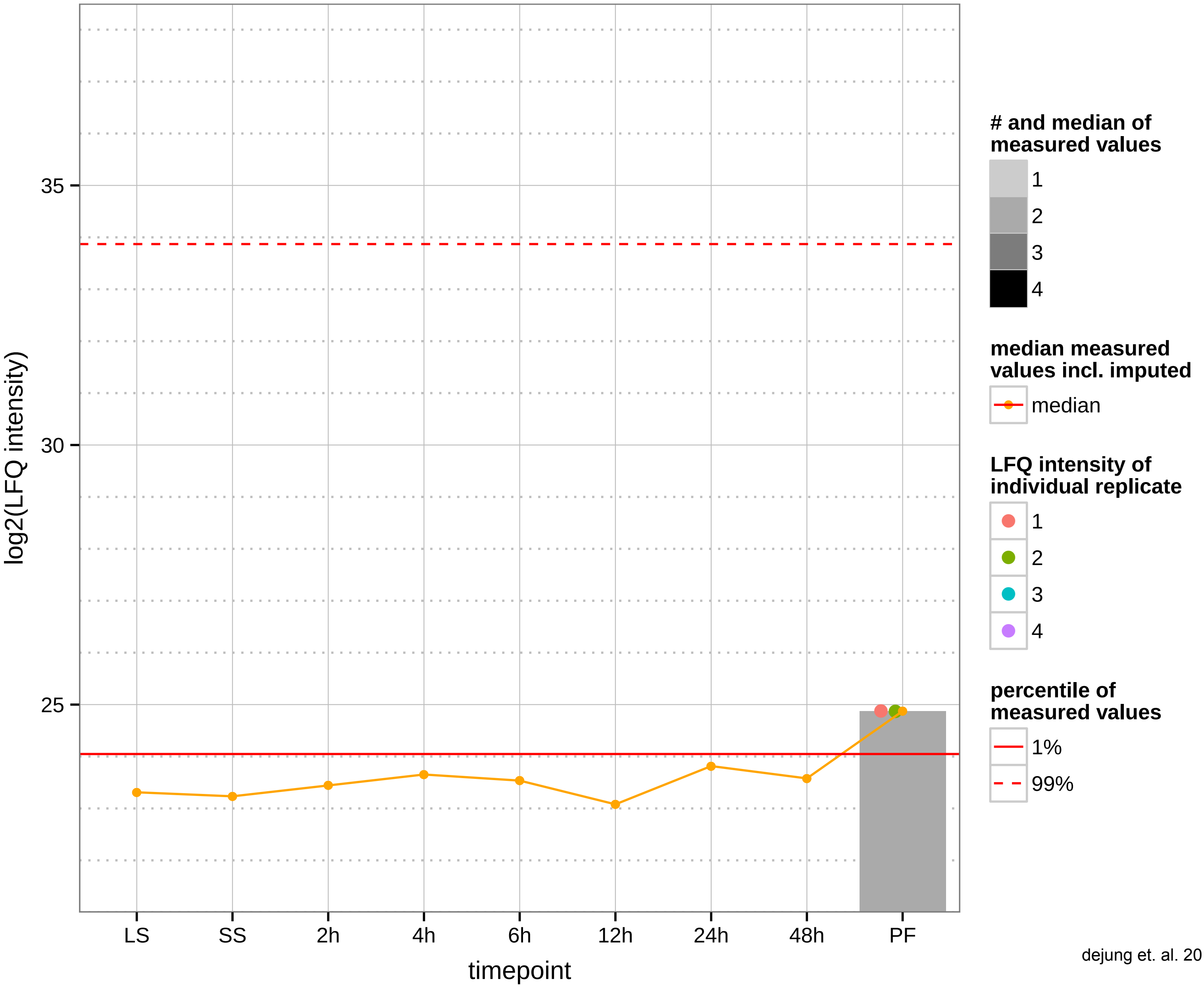




dejung et. al. 2015

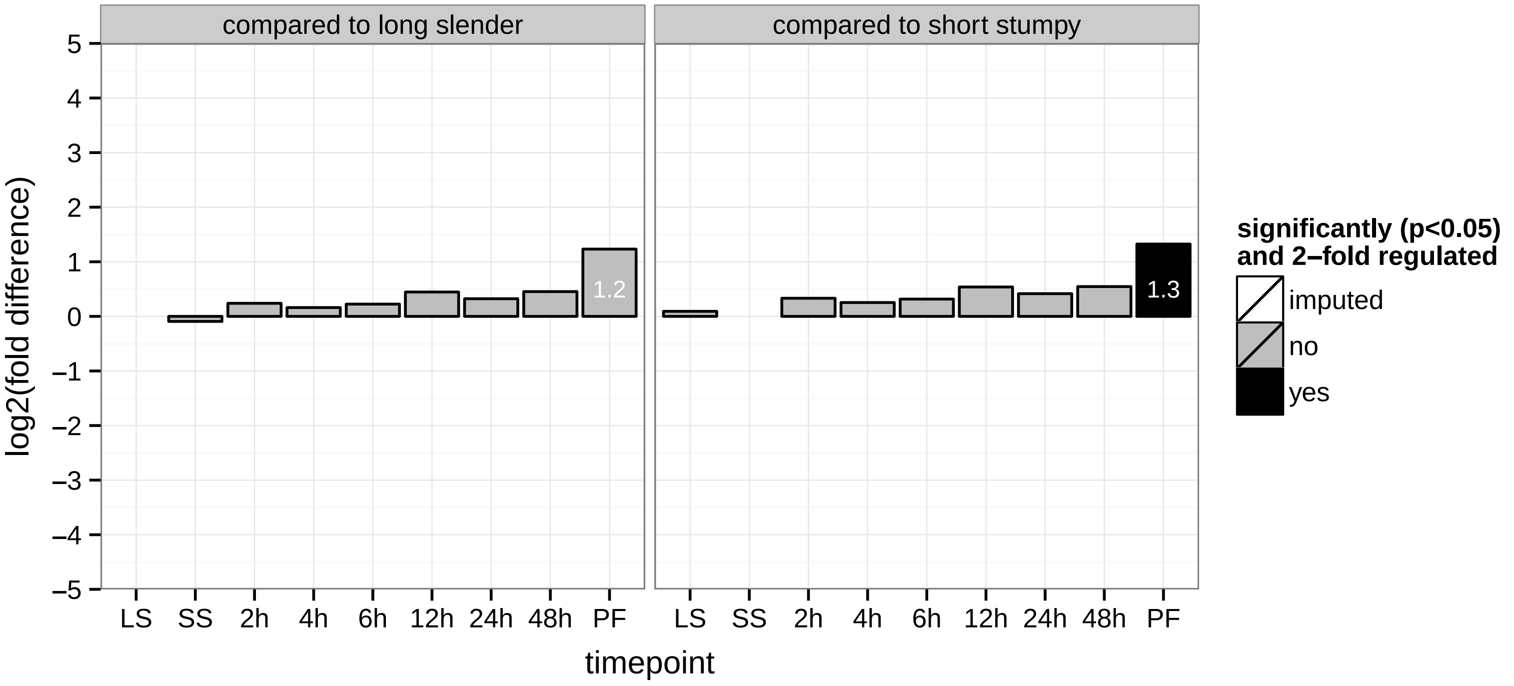
endosomal integral membrane protein, putative
Tb927.4.1090
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: integral to membrane
PGOP: null

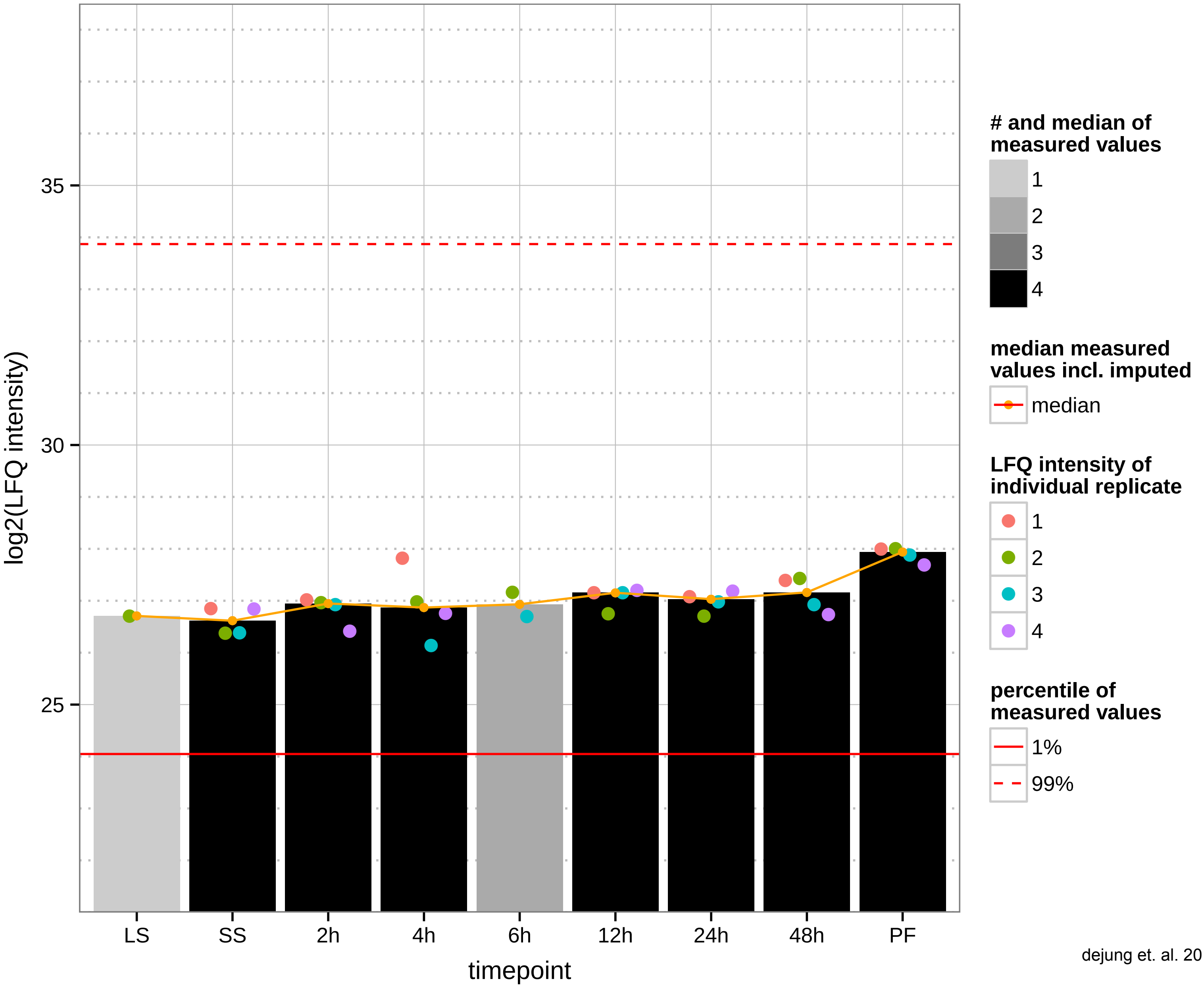




dejung et. al. 2015

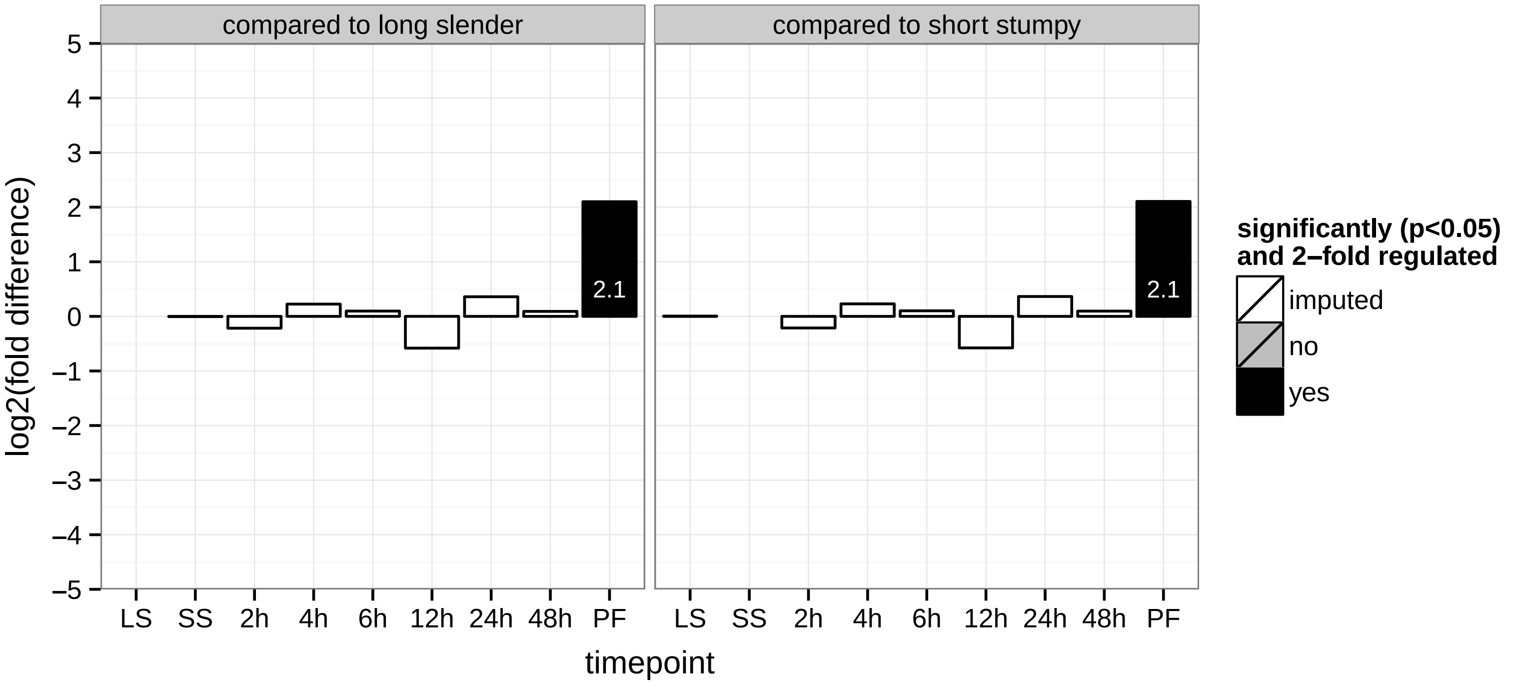
ZFP family member, putative (ZC3H9)
Tb927.4.1310
AGOF: RNA binding, zinc ion binding
AGOC: intracellular
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: intracellular
PGOP: null

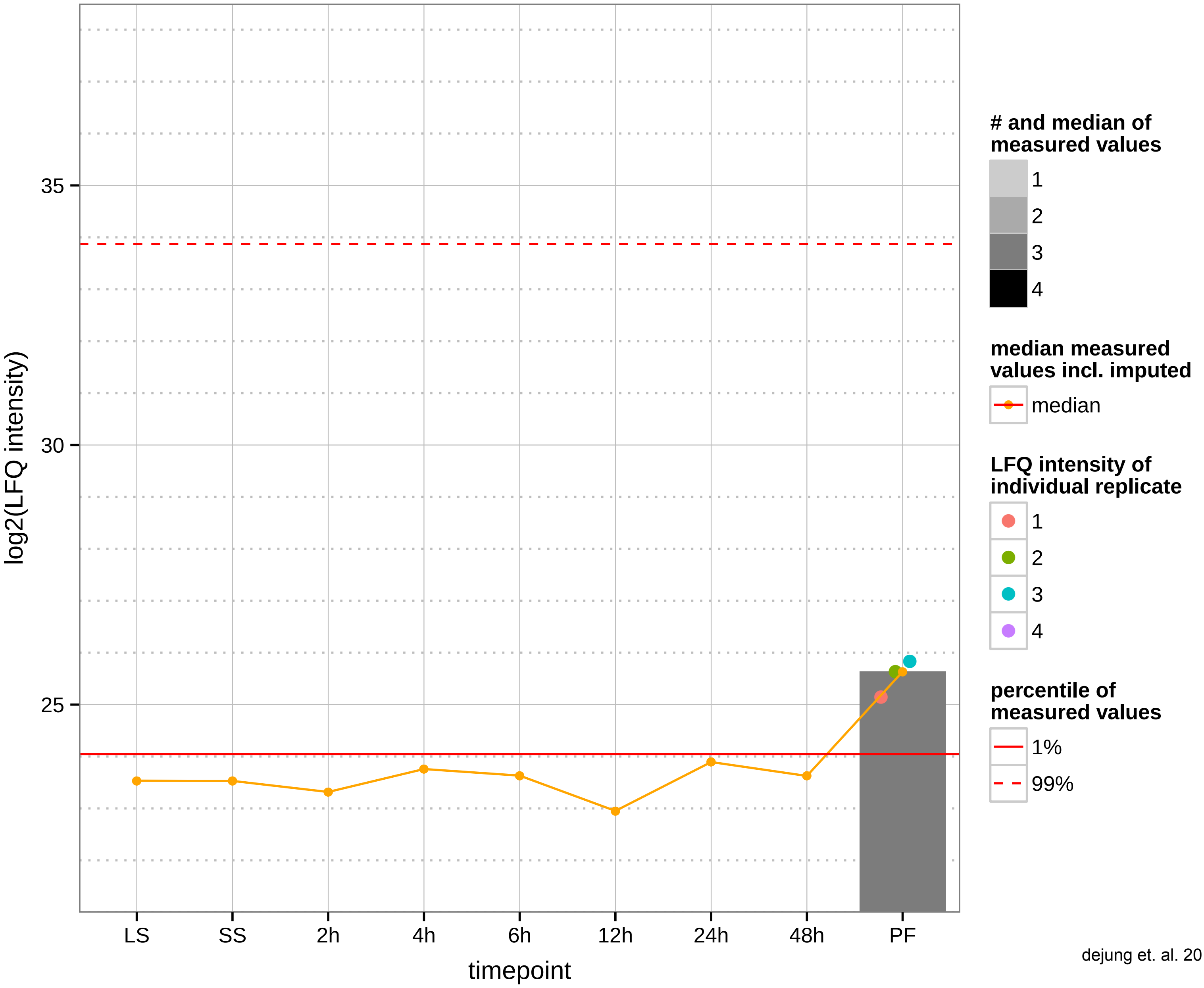




dejung et. al. 2015

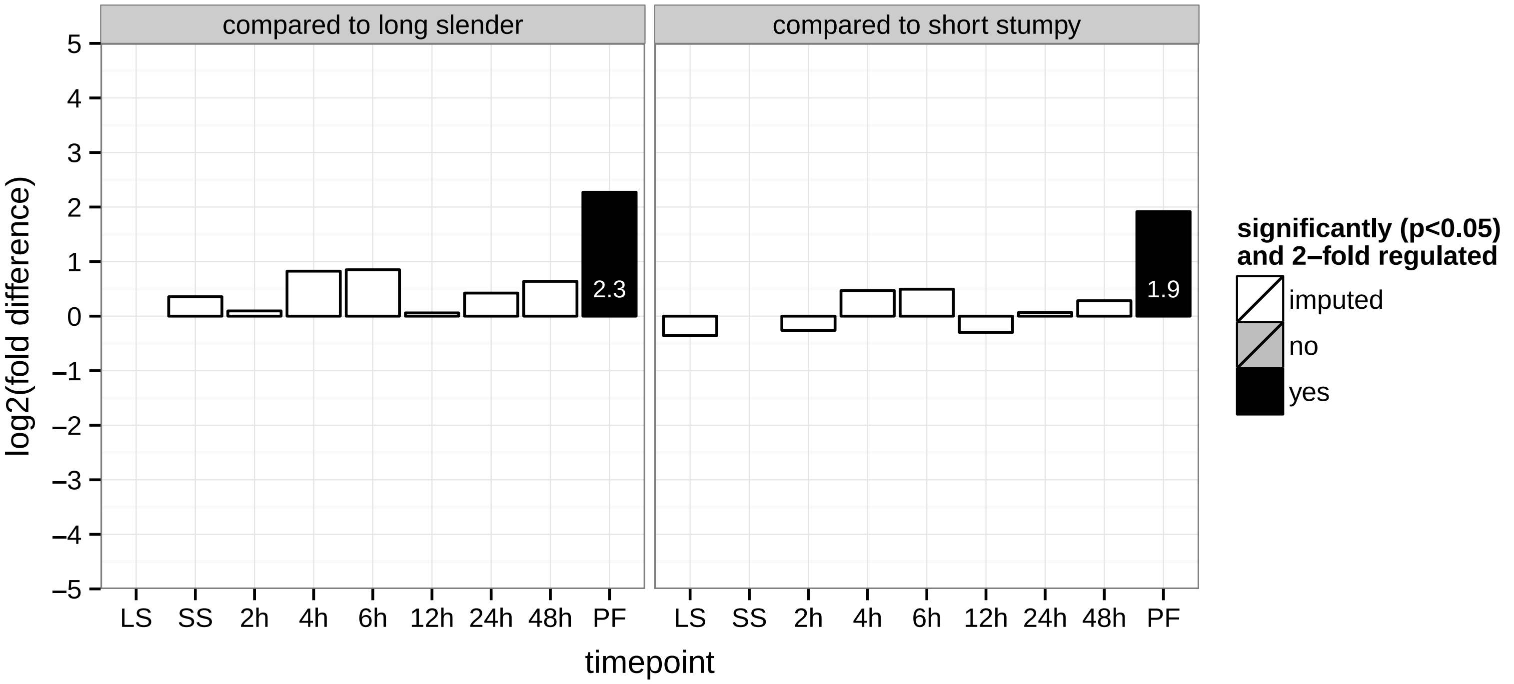
hypothetical protein, conserved
Tb927.4.1380
AGOF: hydrolase activity, acting on ester bonds
AGOC: cytoplasm
AGOP: D–amino acid catabolic process
PGOF: hydrolase activity, acting on ester bonds
PGOC: cytoplasm
PGOP: D–amino acid catabolic process

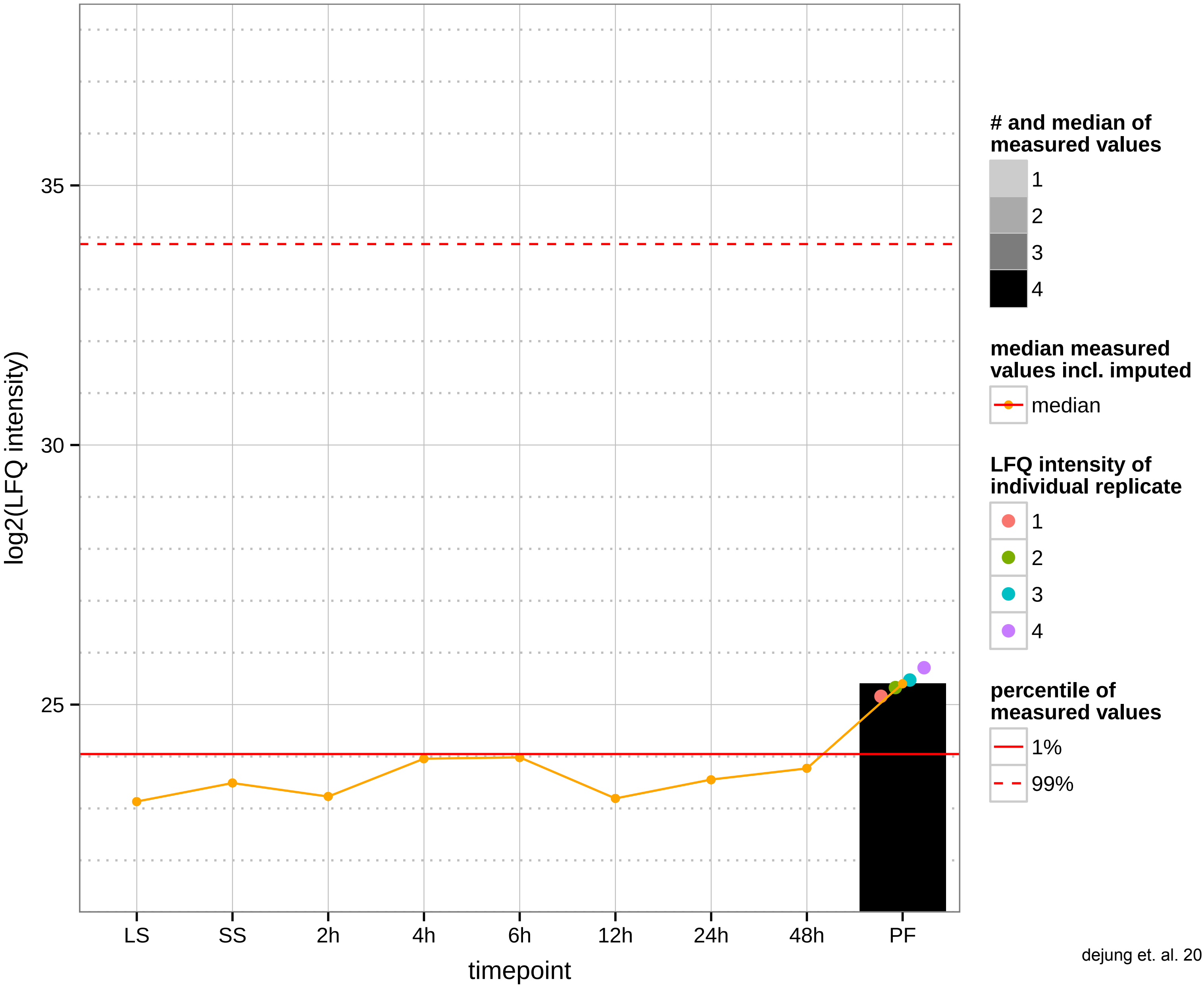




dejung et. al. 2015

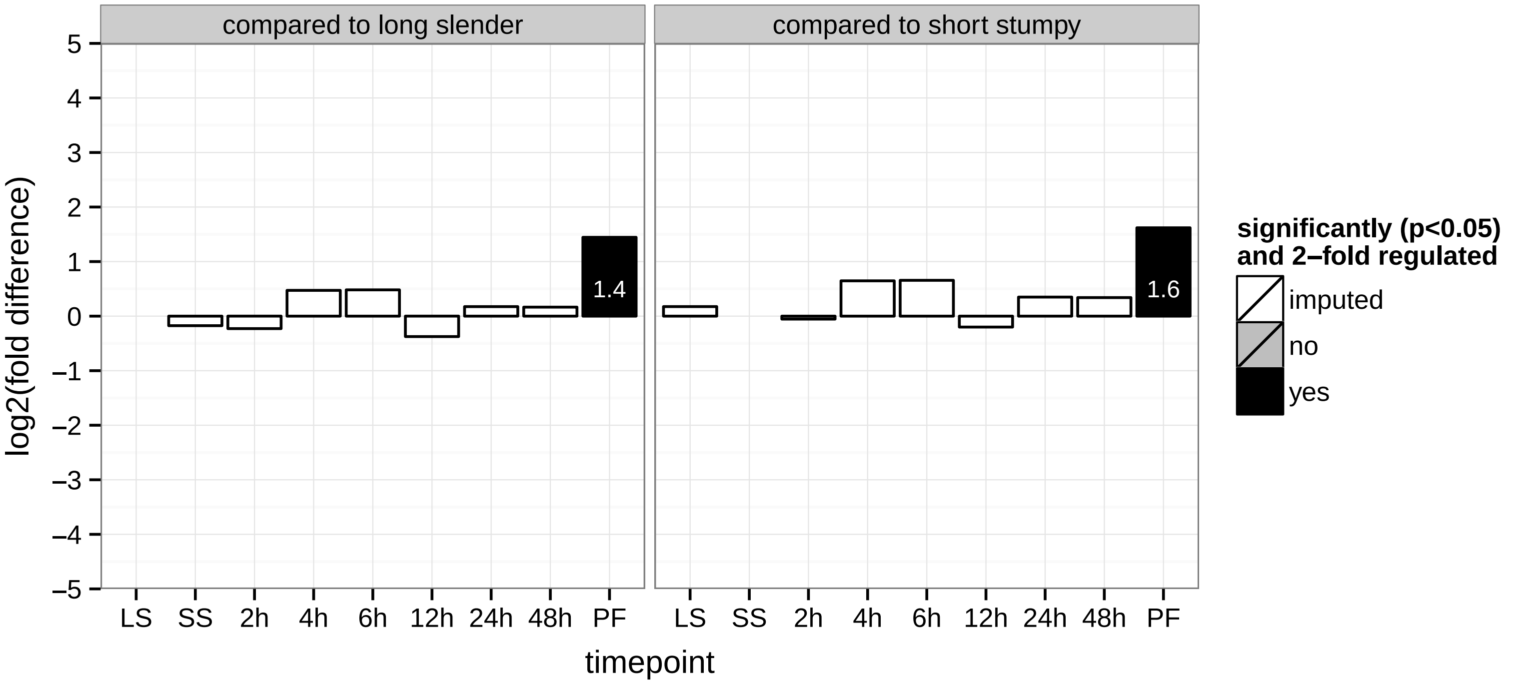
hypothetical protein, conserved
Tb927.4.1440
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: metal ion binding
PGOC: null
PGOP: null

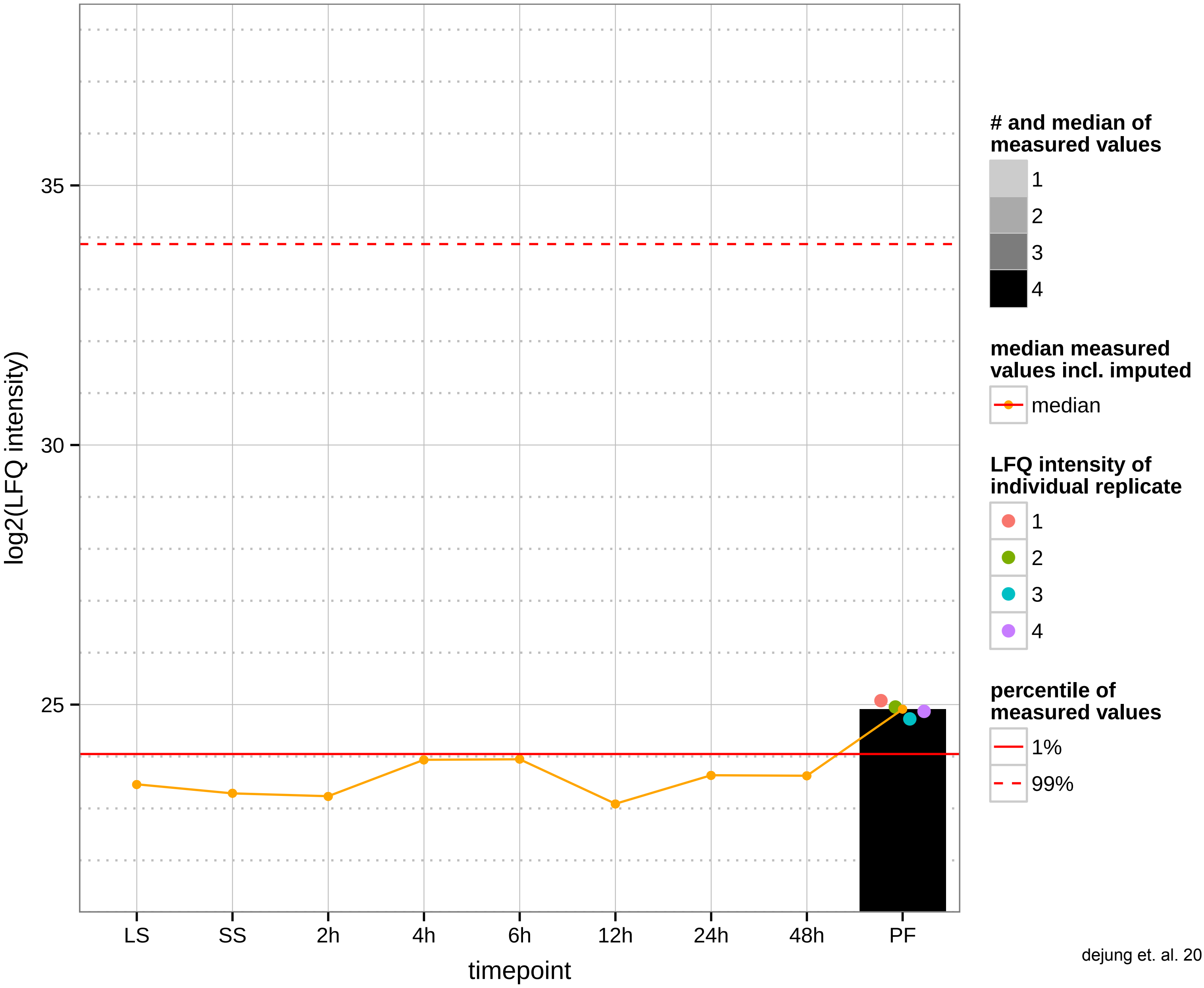




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.1590.1;Tb927.4.1590.2
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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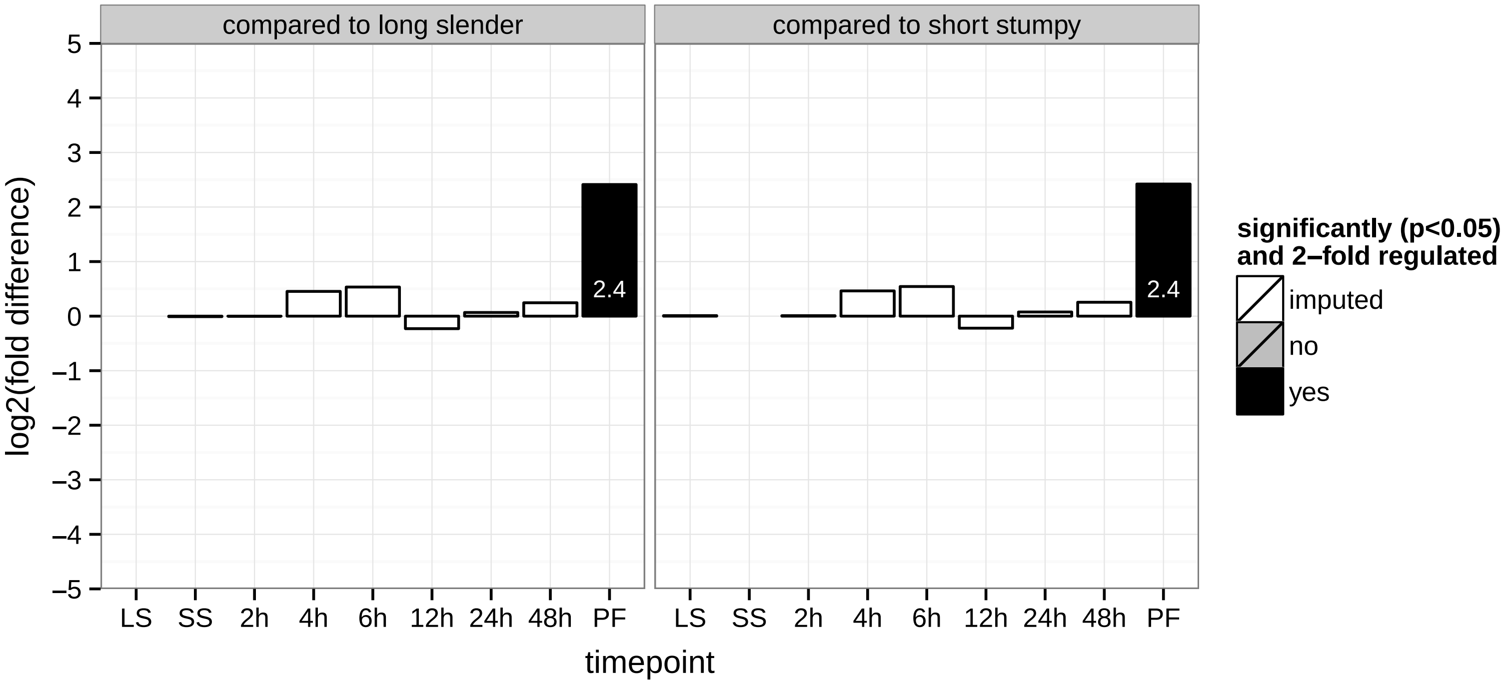
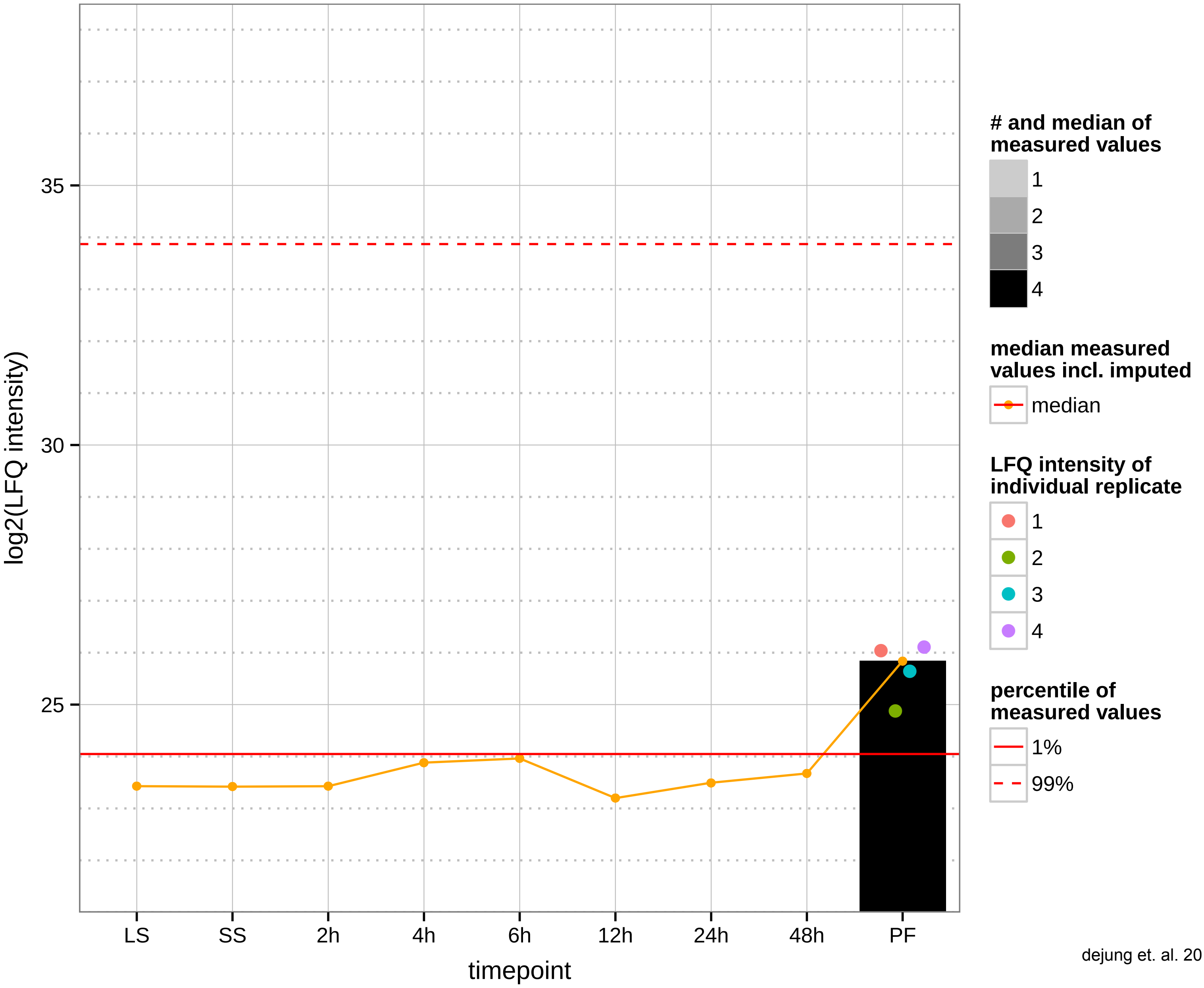
hypothetical protein, conserved
Tb927.4.1690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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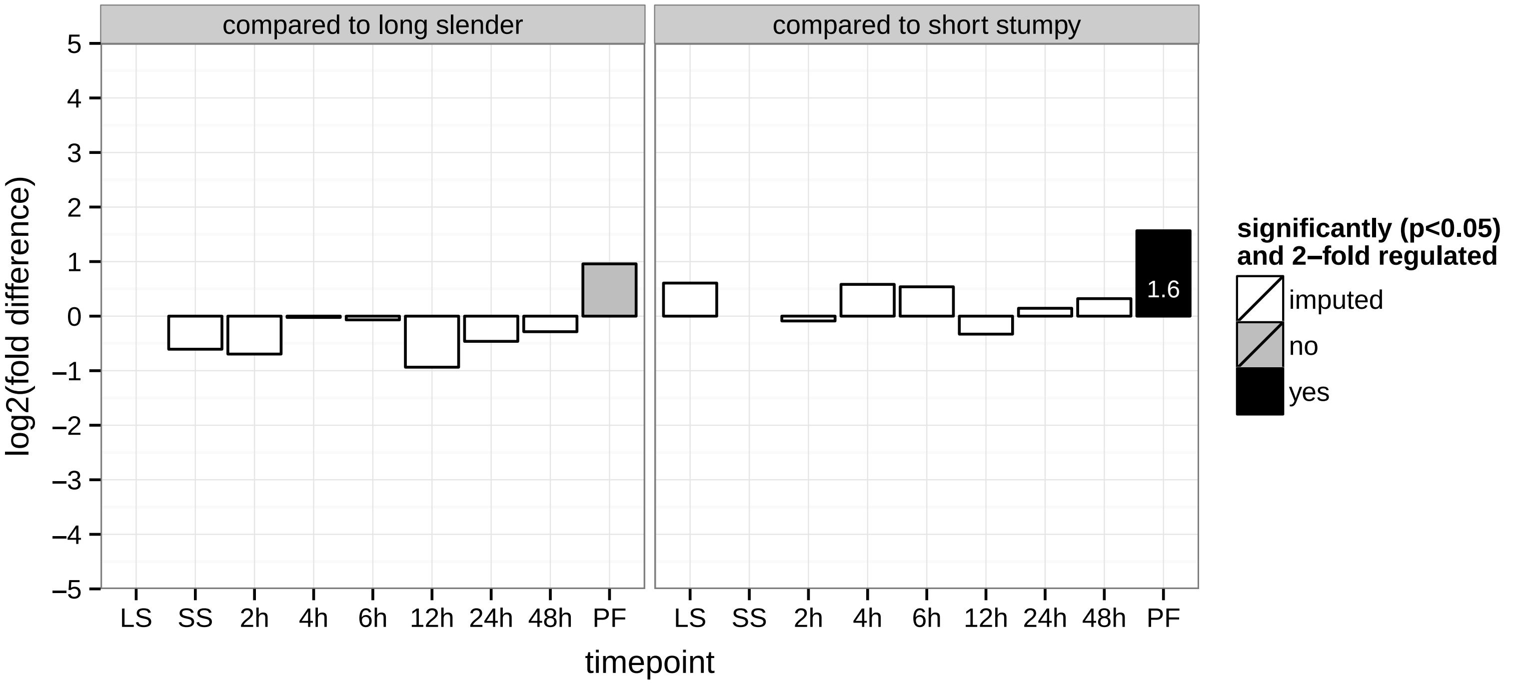
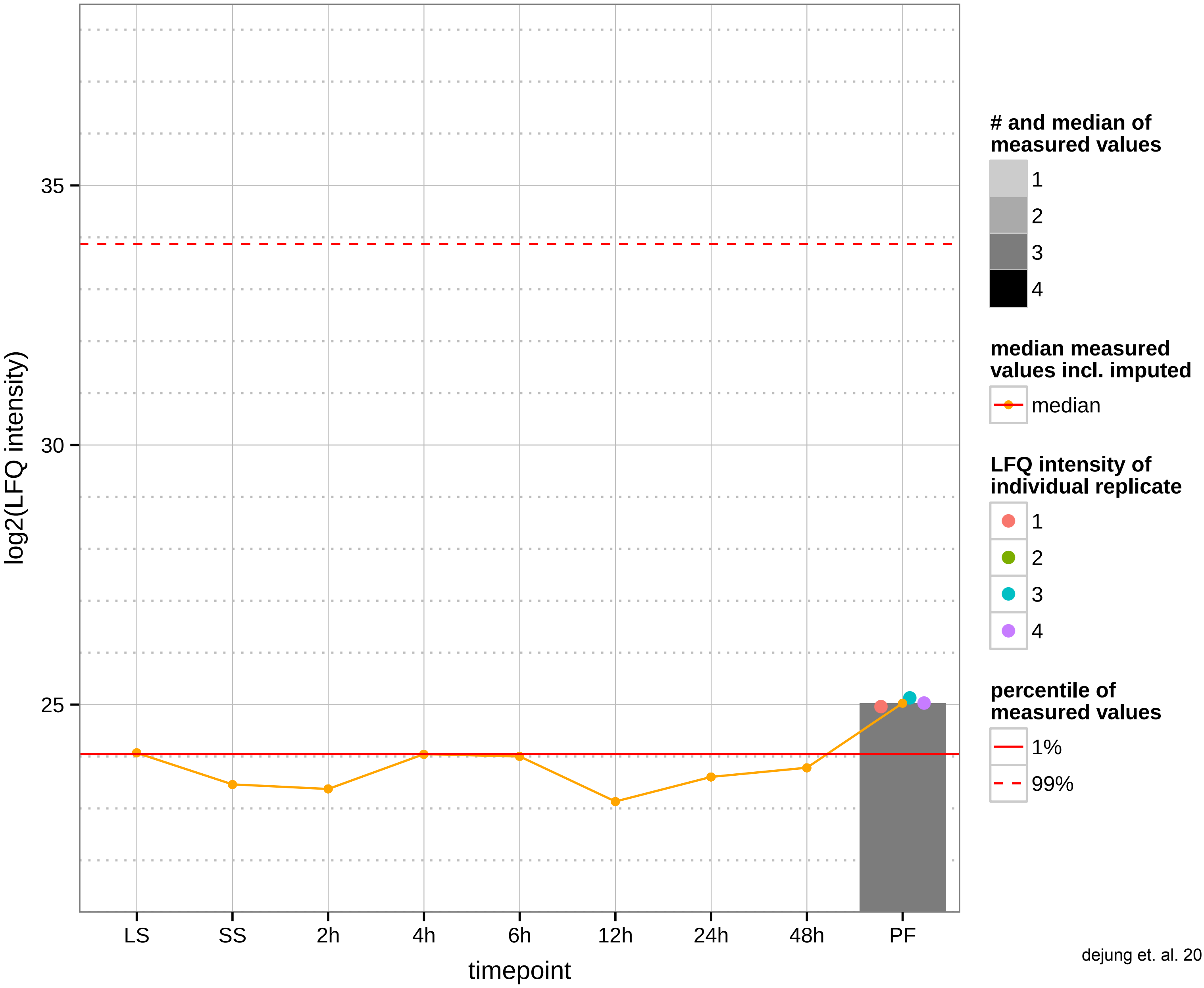
hypothetical protein, conserved
Tb927.4.1710
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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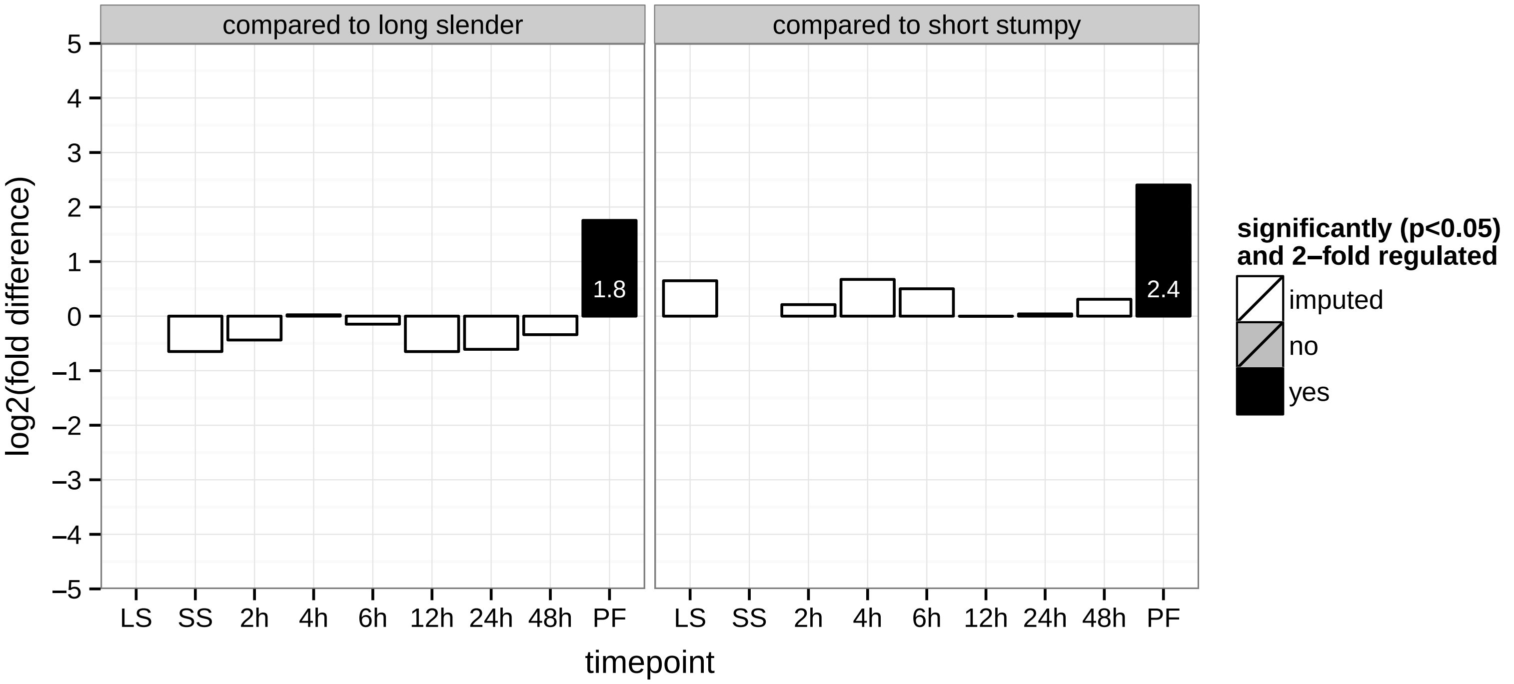
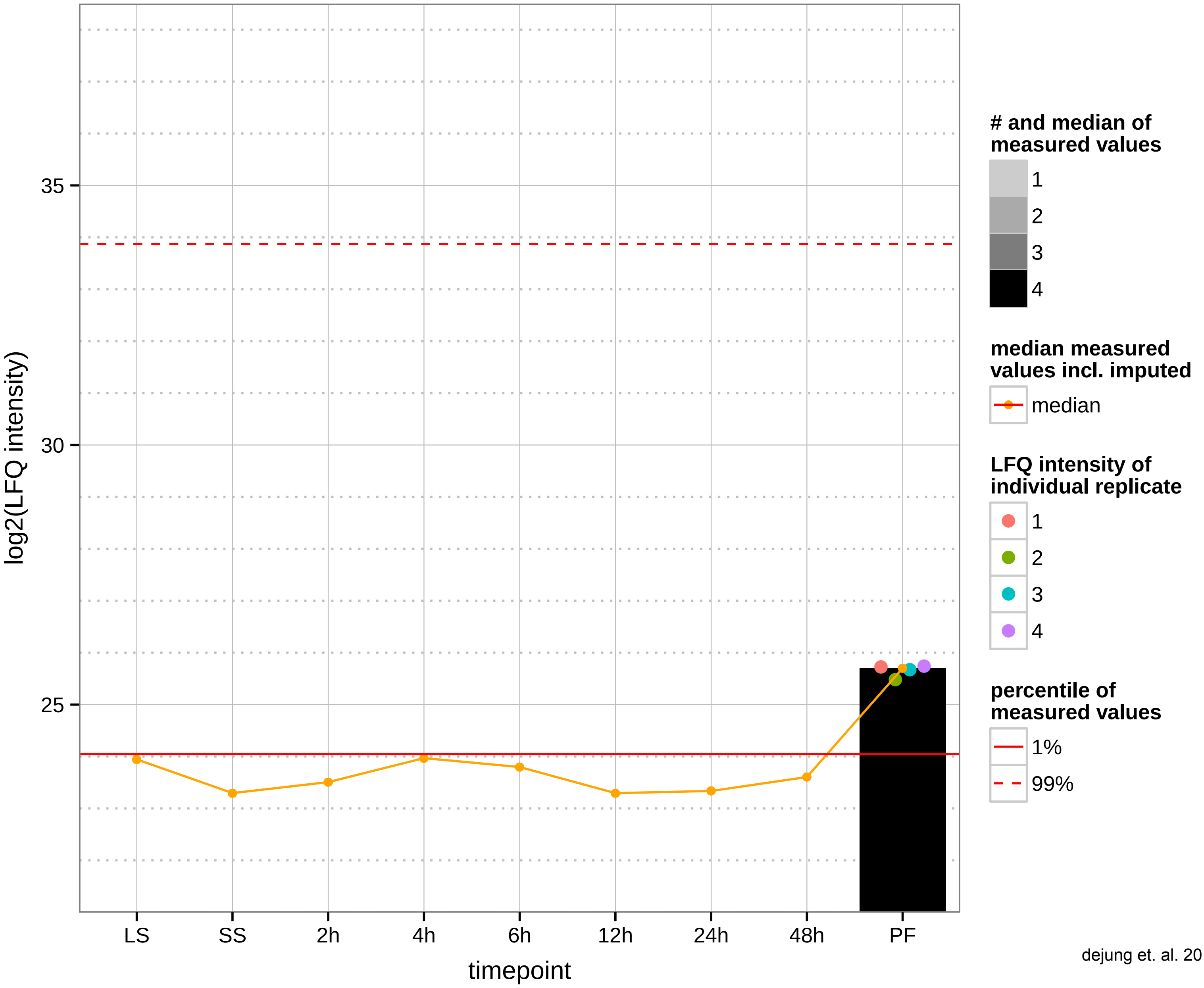
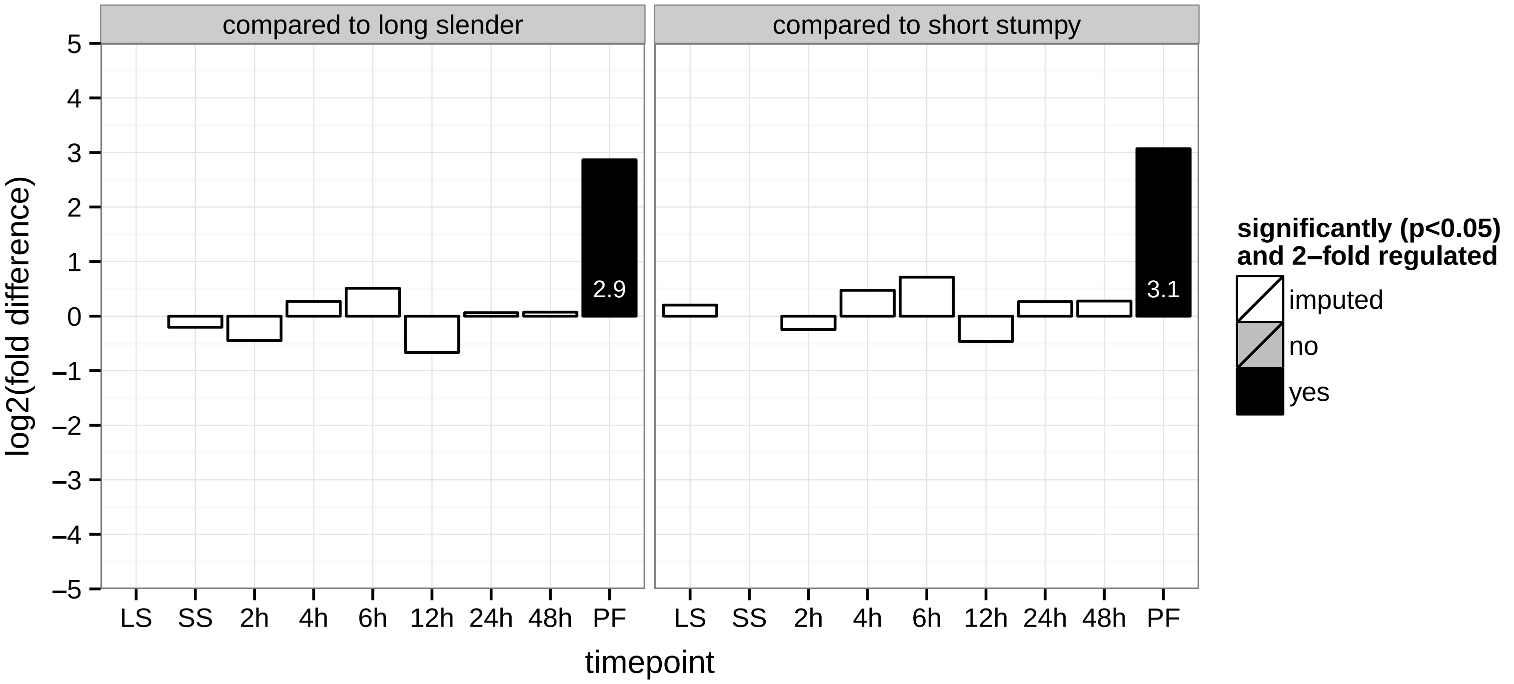
retrotransposon hot spot protein 1 (RHS1), putative
Tb927.4.200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

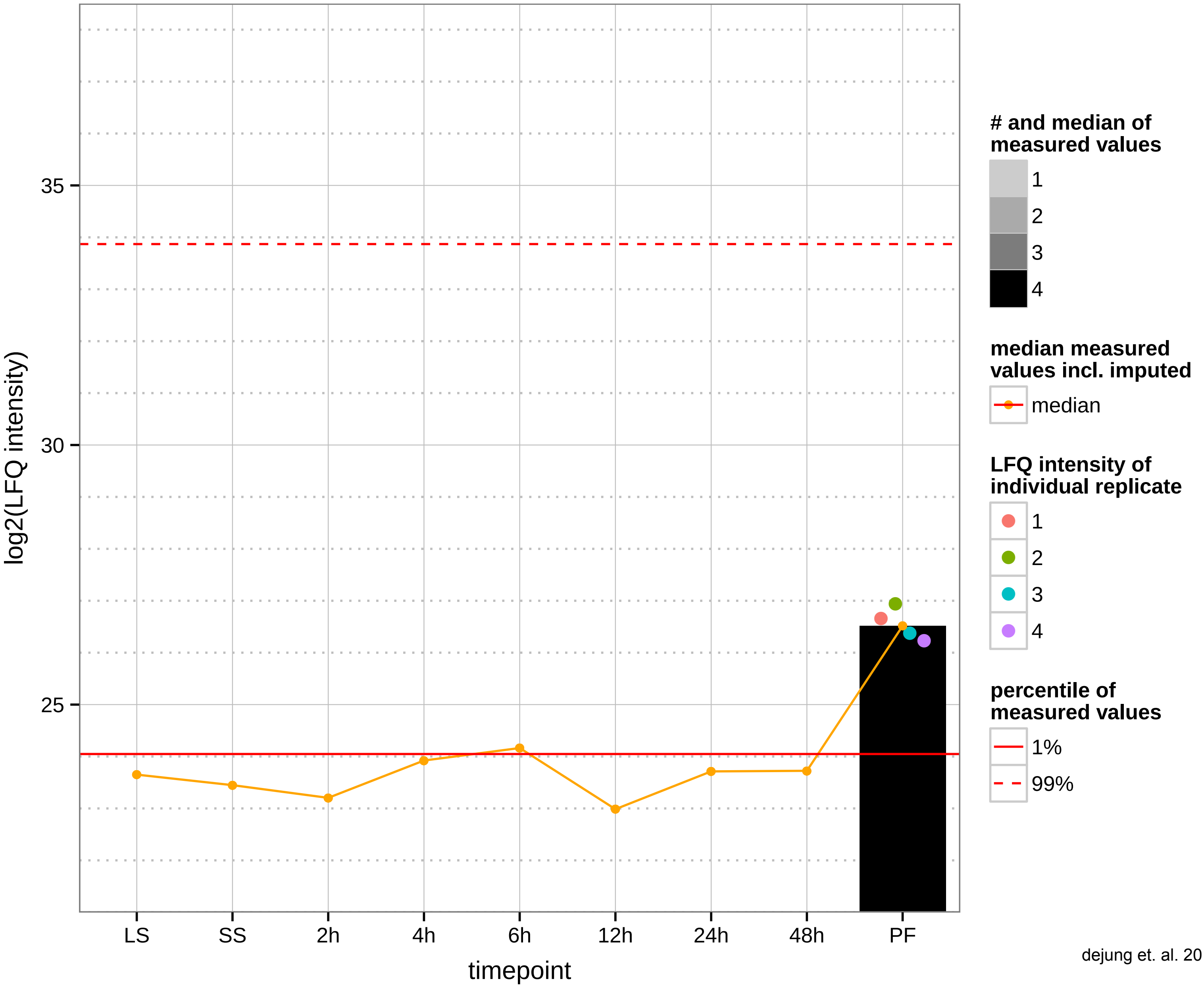




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.2410
AGOF: catalytic activity
AGOC: null
AGOP: carbohydrate metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: carbohydrate metabolic process





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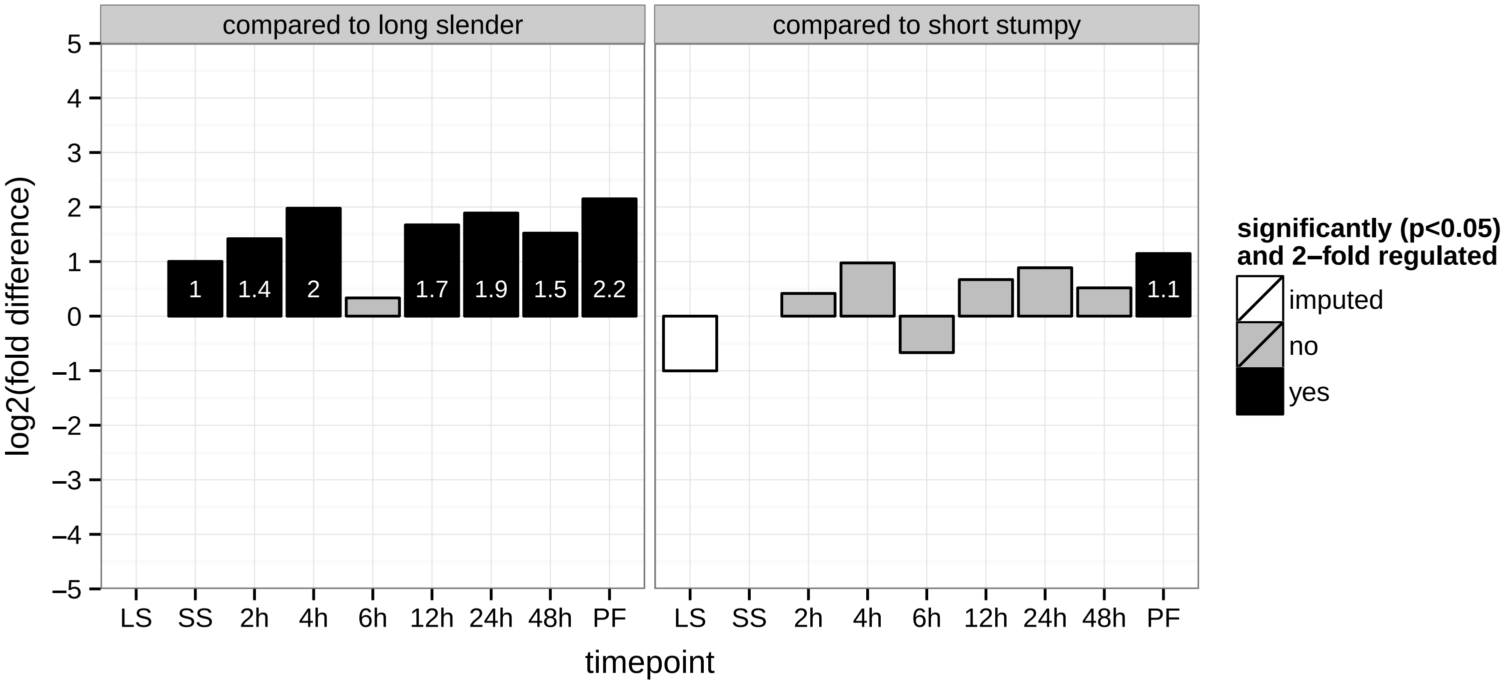
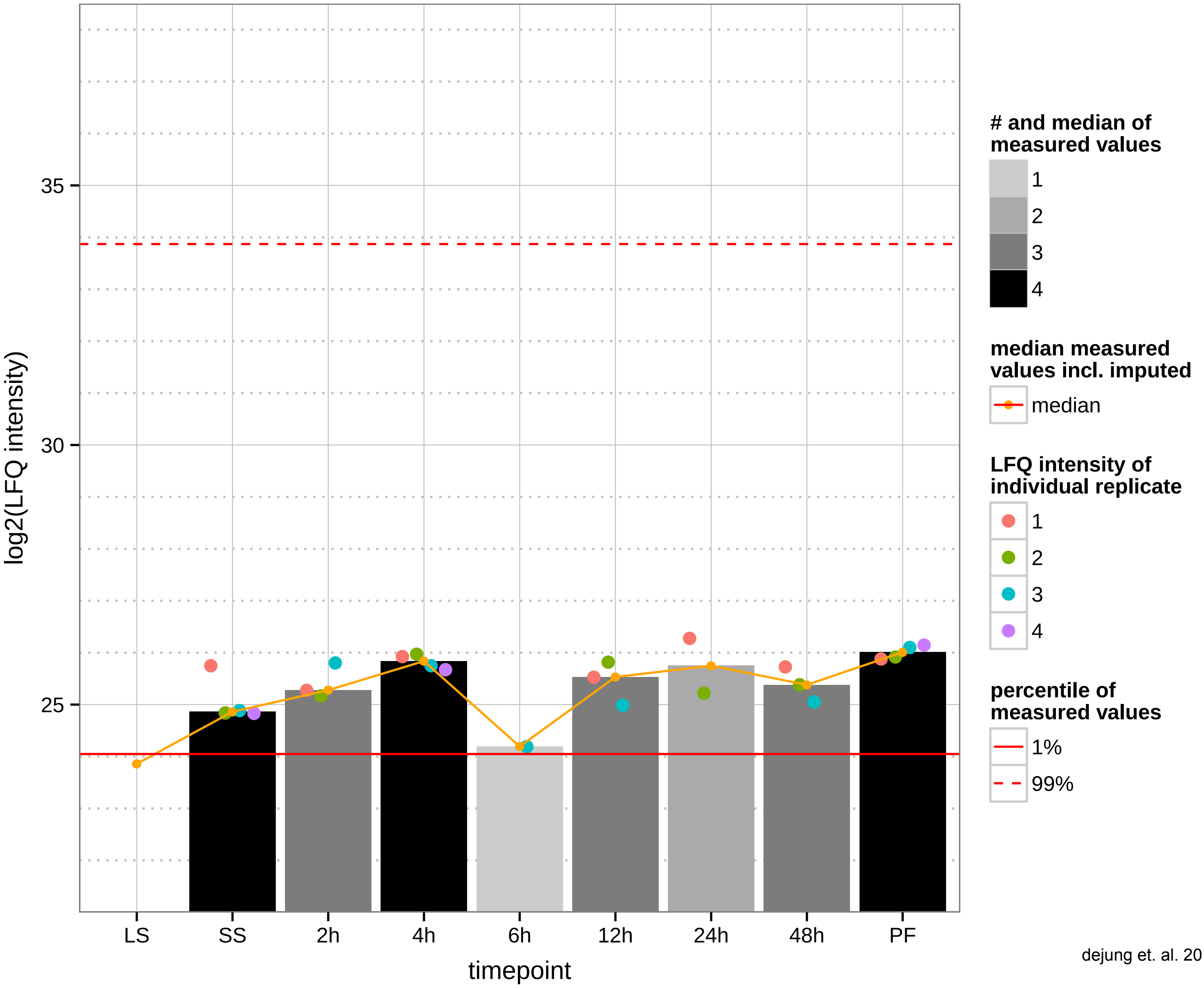
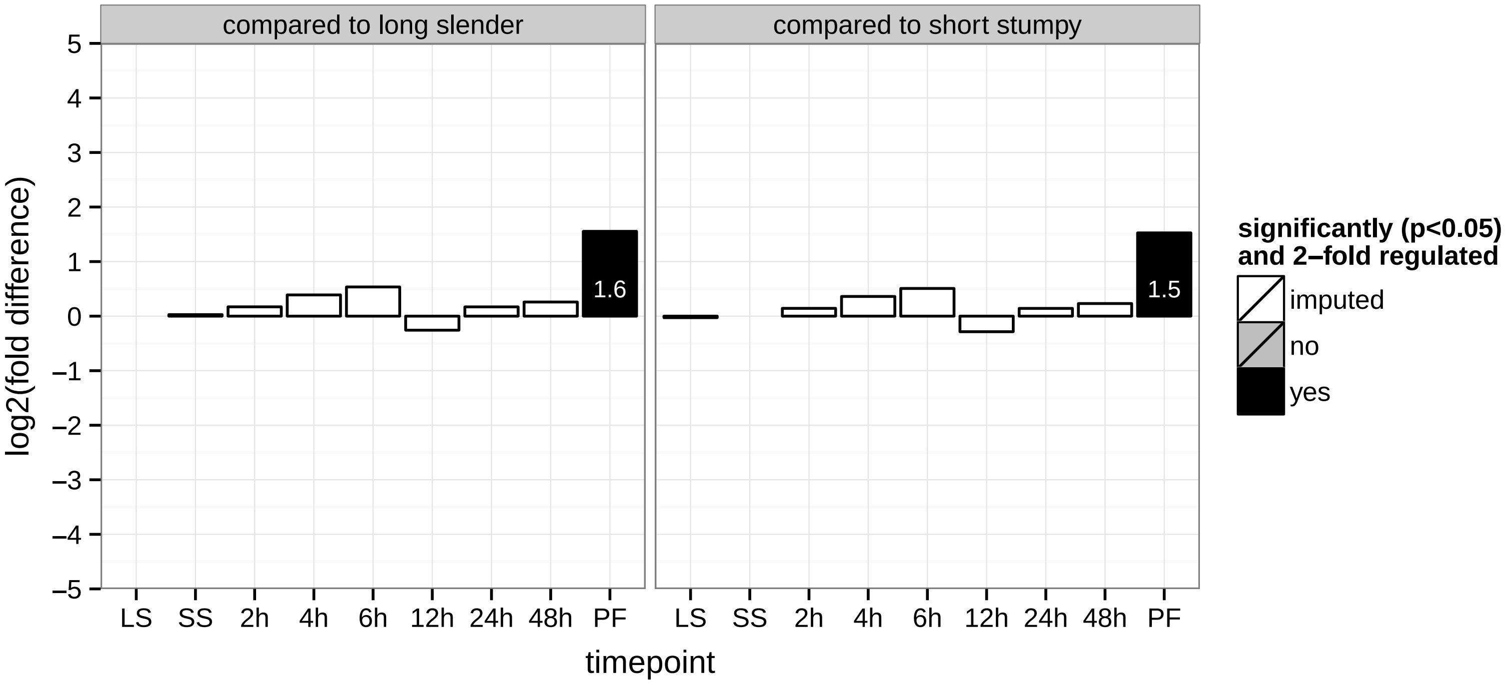
pyroglutamyl–peptidase I (PGP), putative, cysteine peptidase, Clan CF, family C15
Tb927.4.2670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: proteolysis

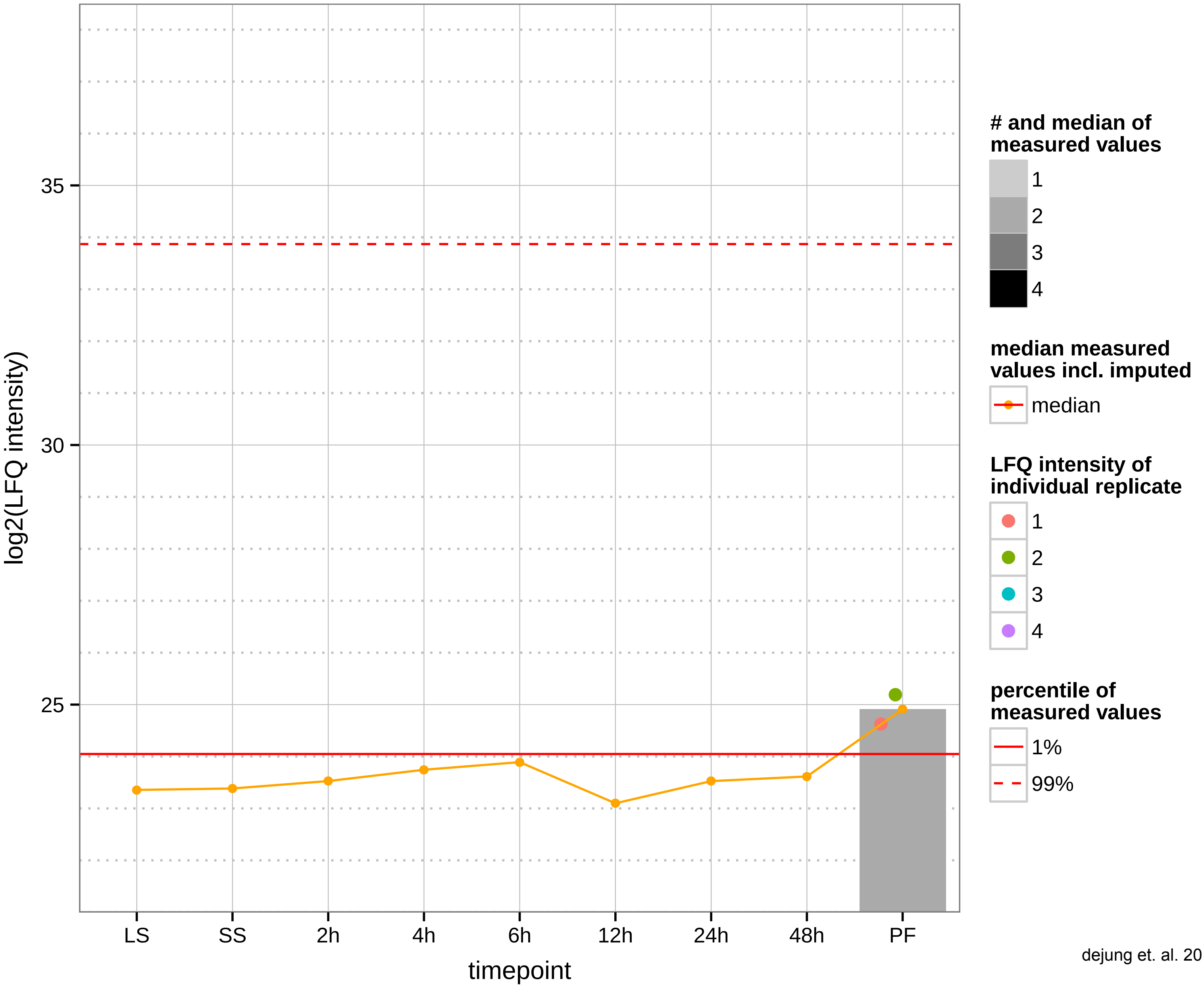




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.2790
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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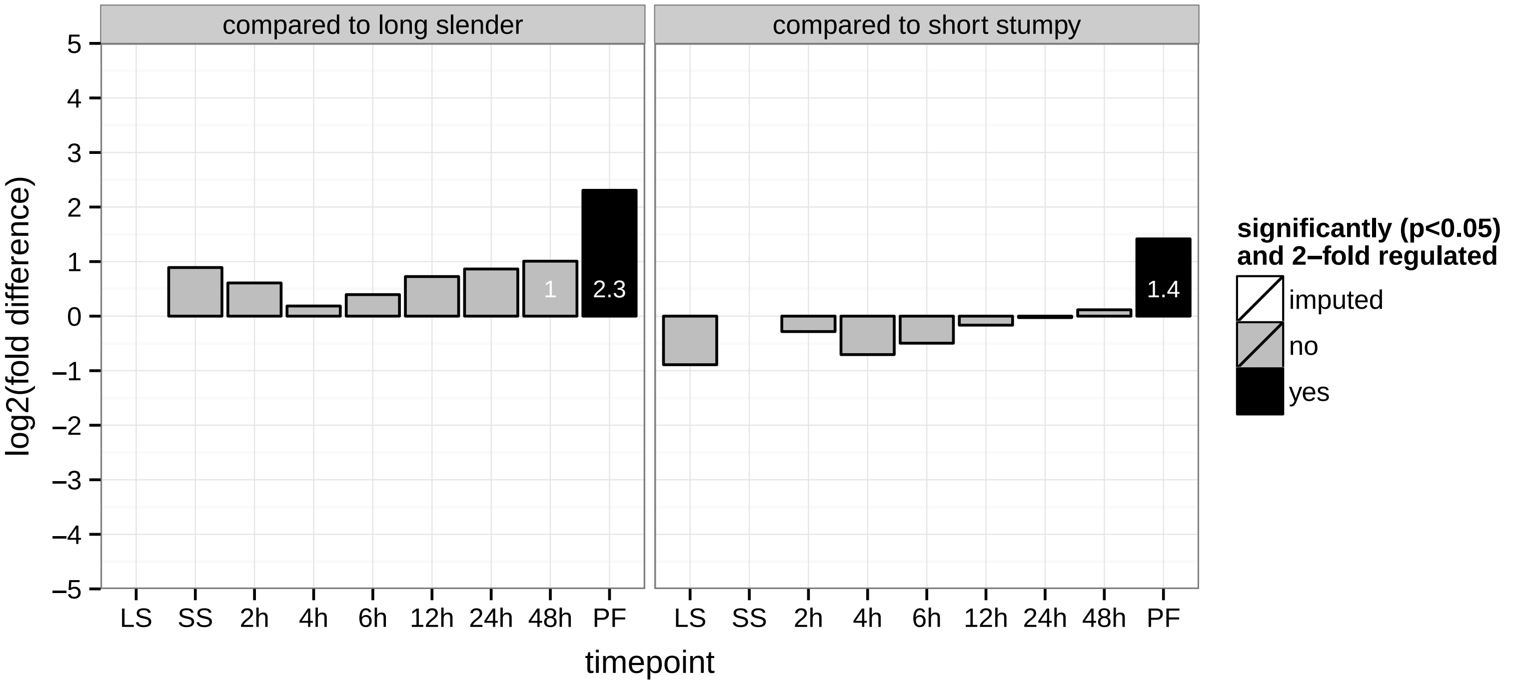
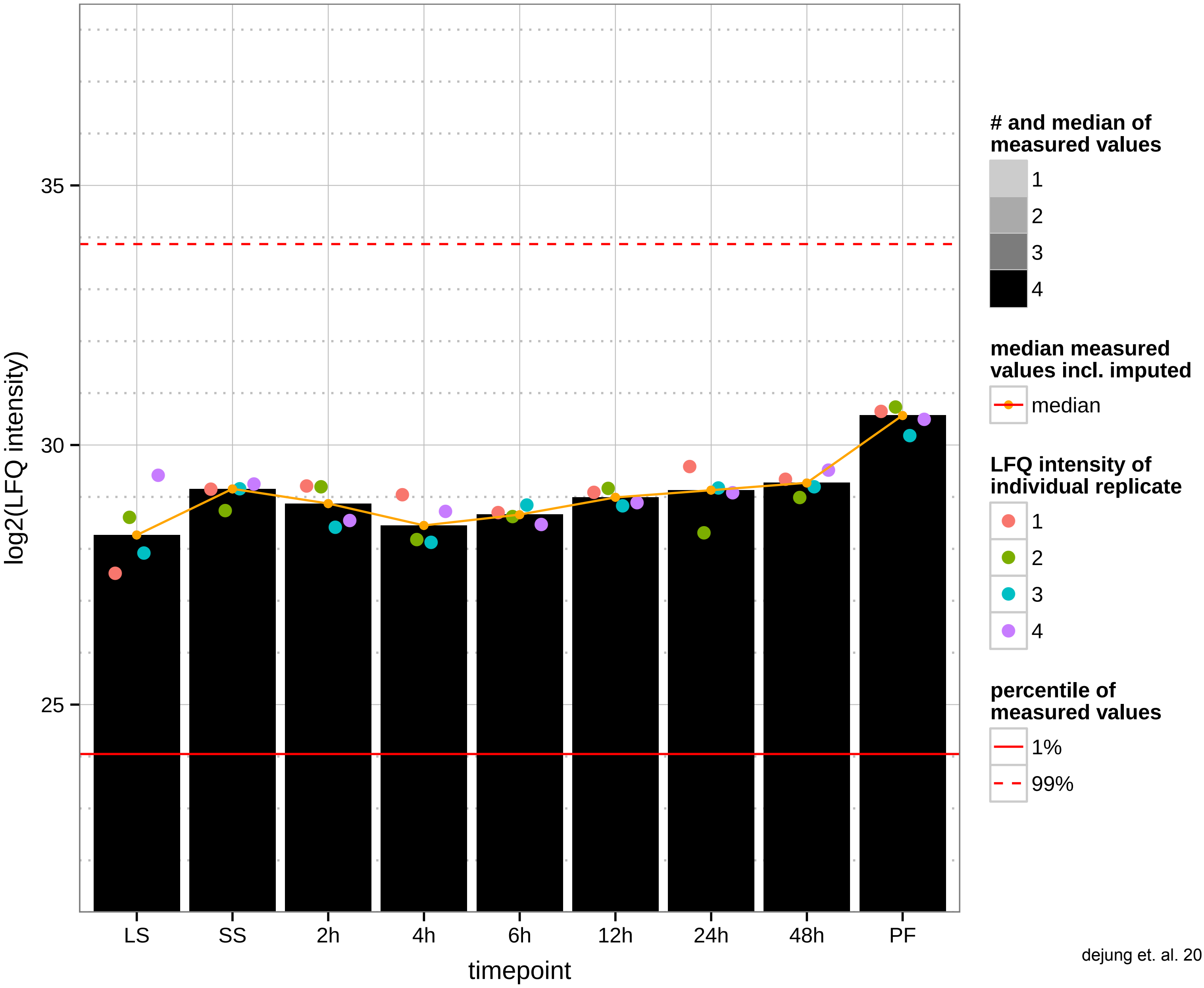
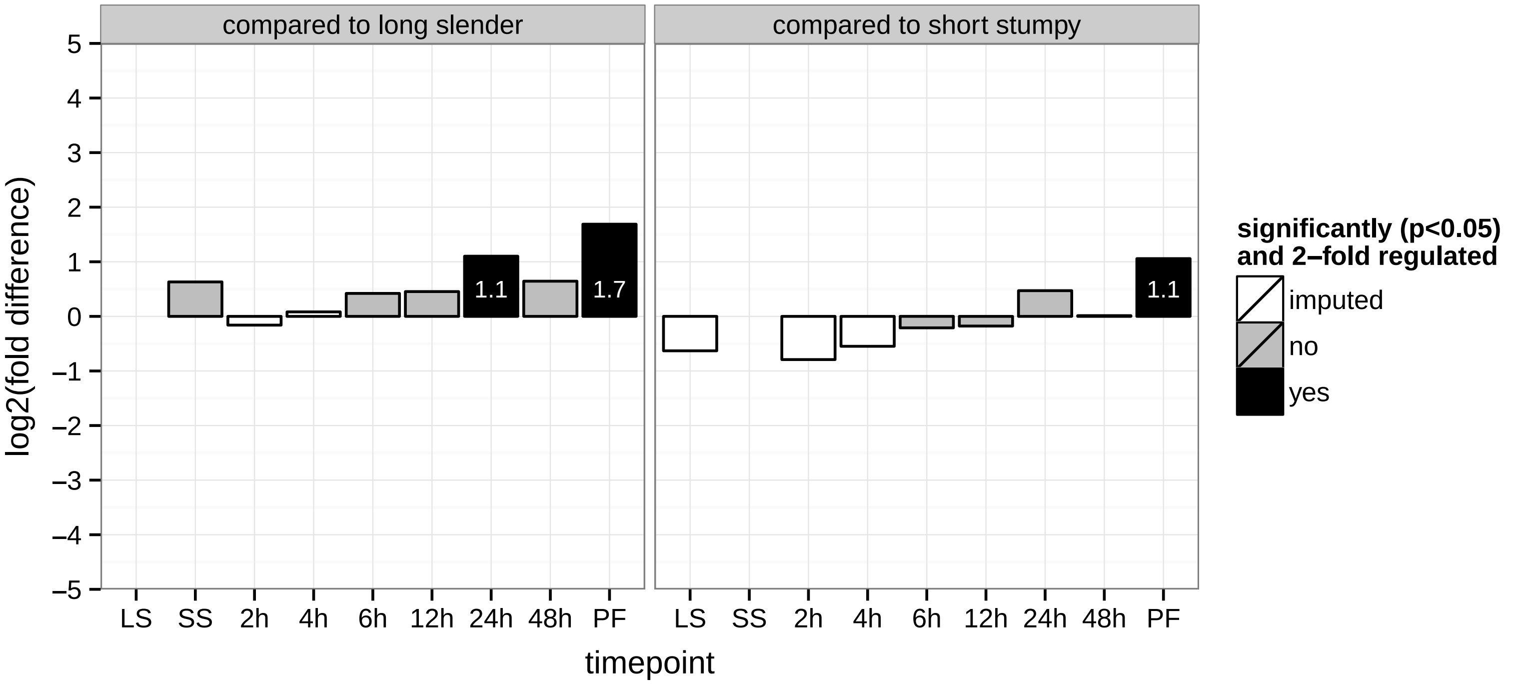
Nucleoporin (TbNup225)
Tb927.4.2880
AGOF: null
AGOC: nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null

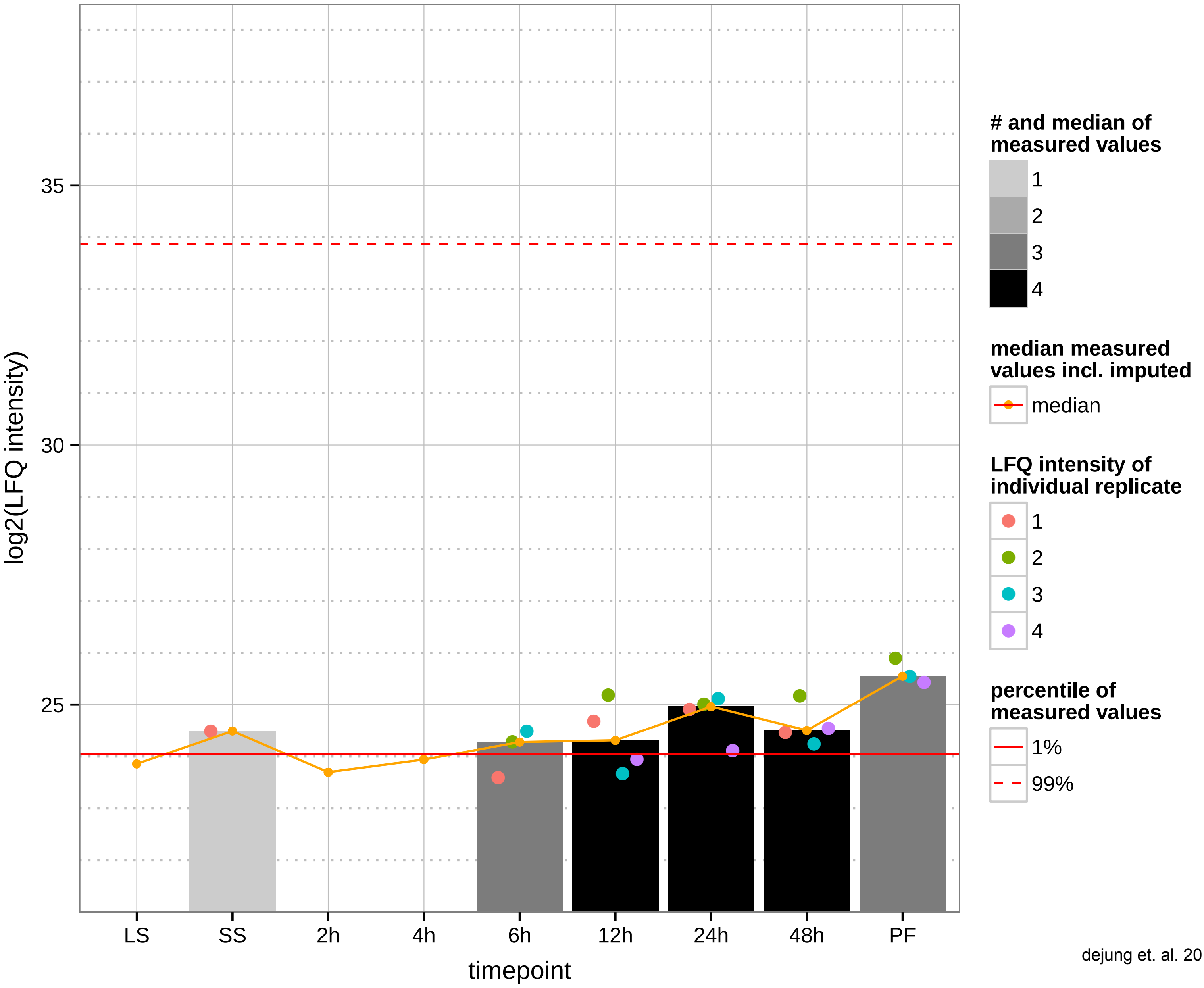




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.3330
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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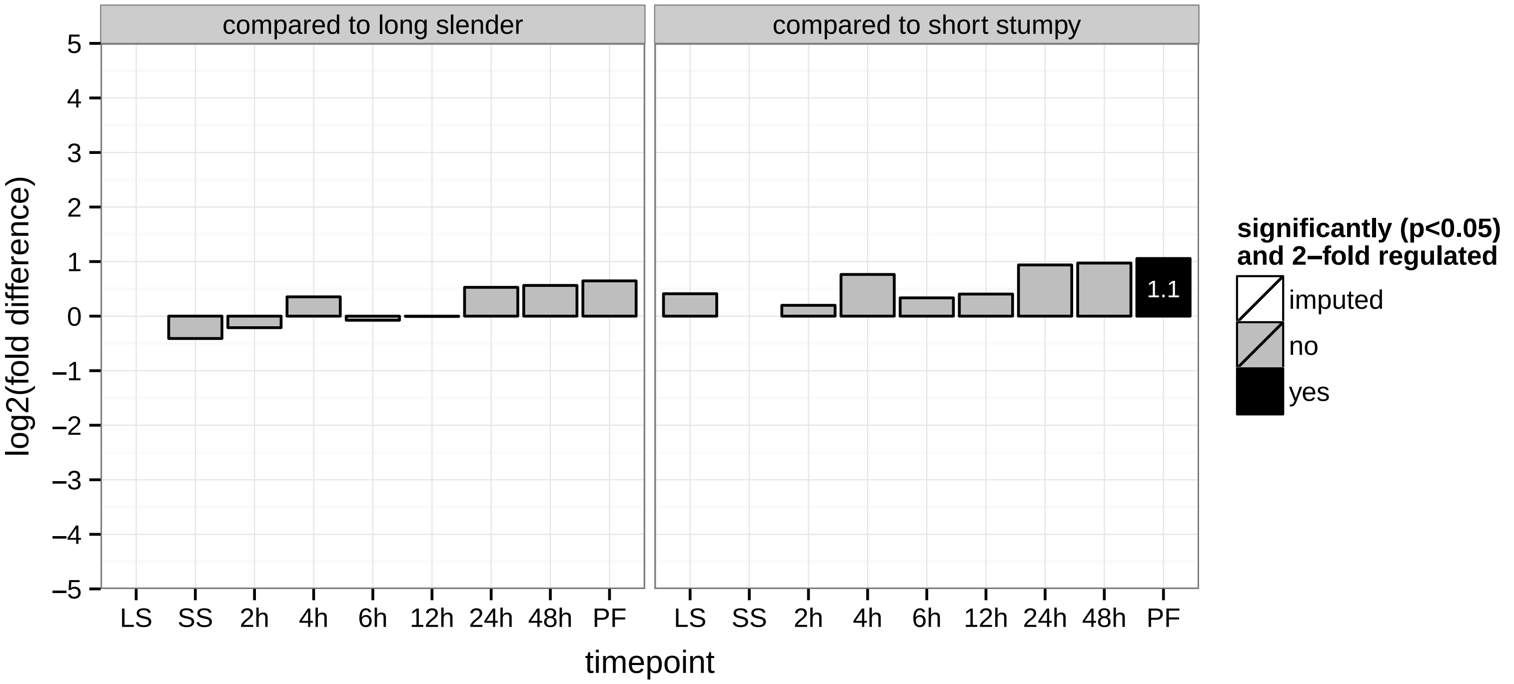
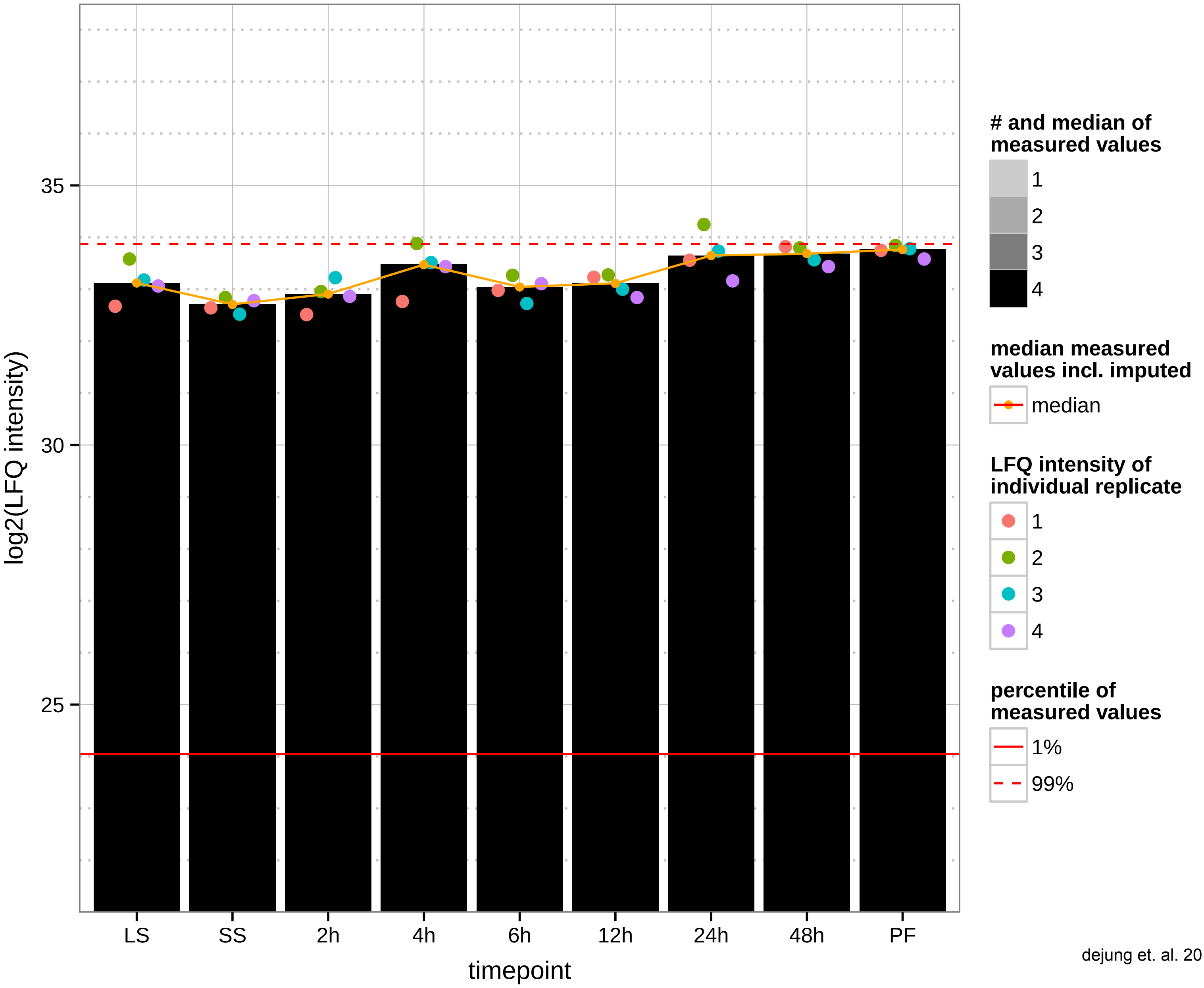
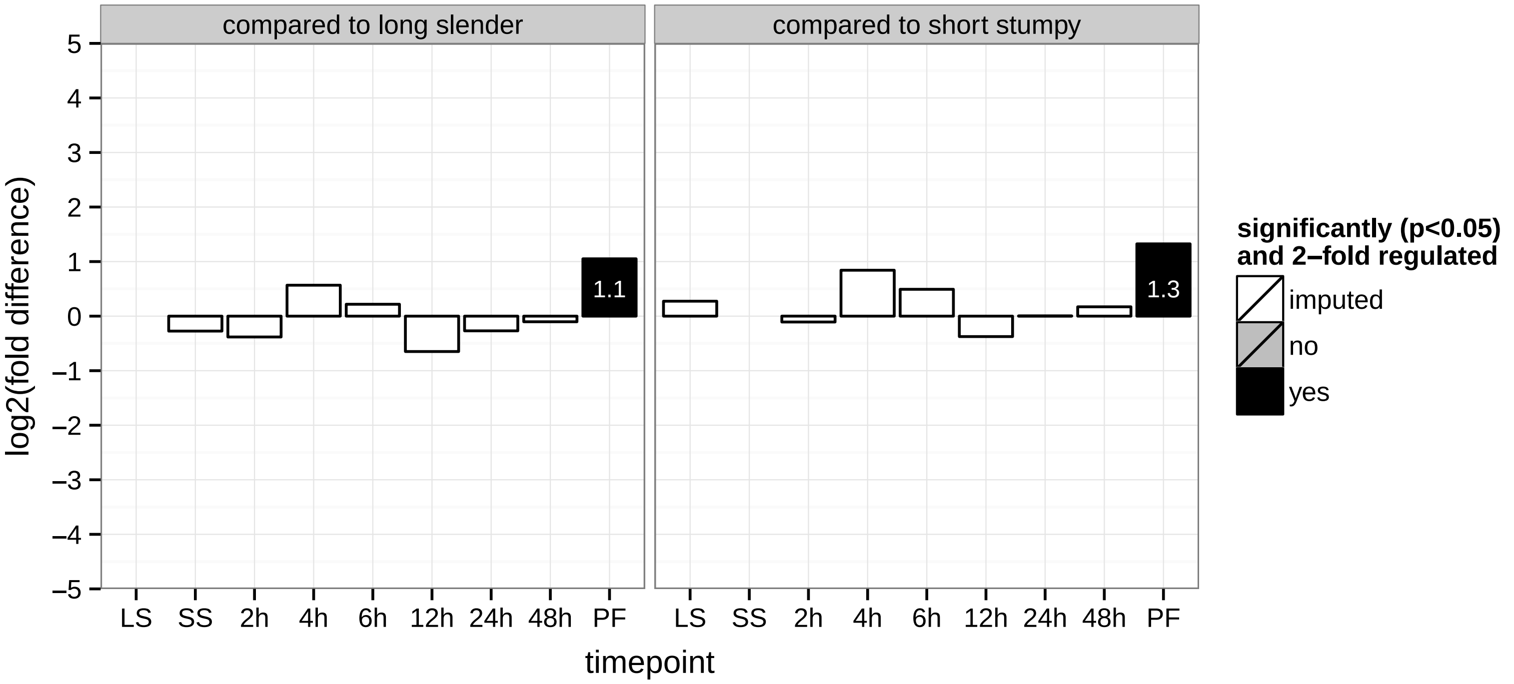
translation elongation factor 1−beta, putative
Tb927.4.3590;Tb927.4.3570
AGOF: translation elongation factor activity
AGOC: eukaryotic translation elongation factor 1 complex
AGOP: translational elongation
PGOF: translation elongation factor activity
PGOC: eukaryotic translation elongation factor 1 complex
PGOP: translational elongation

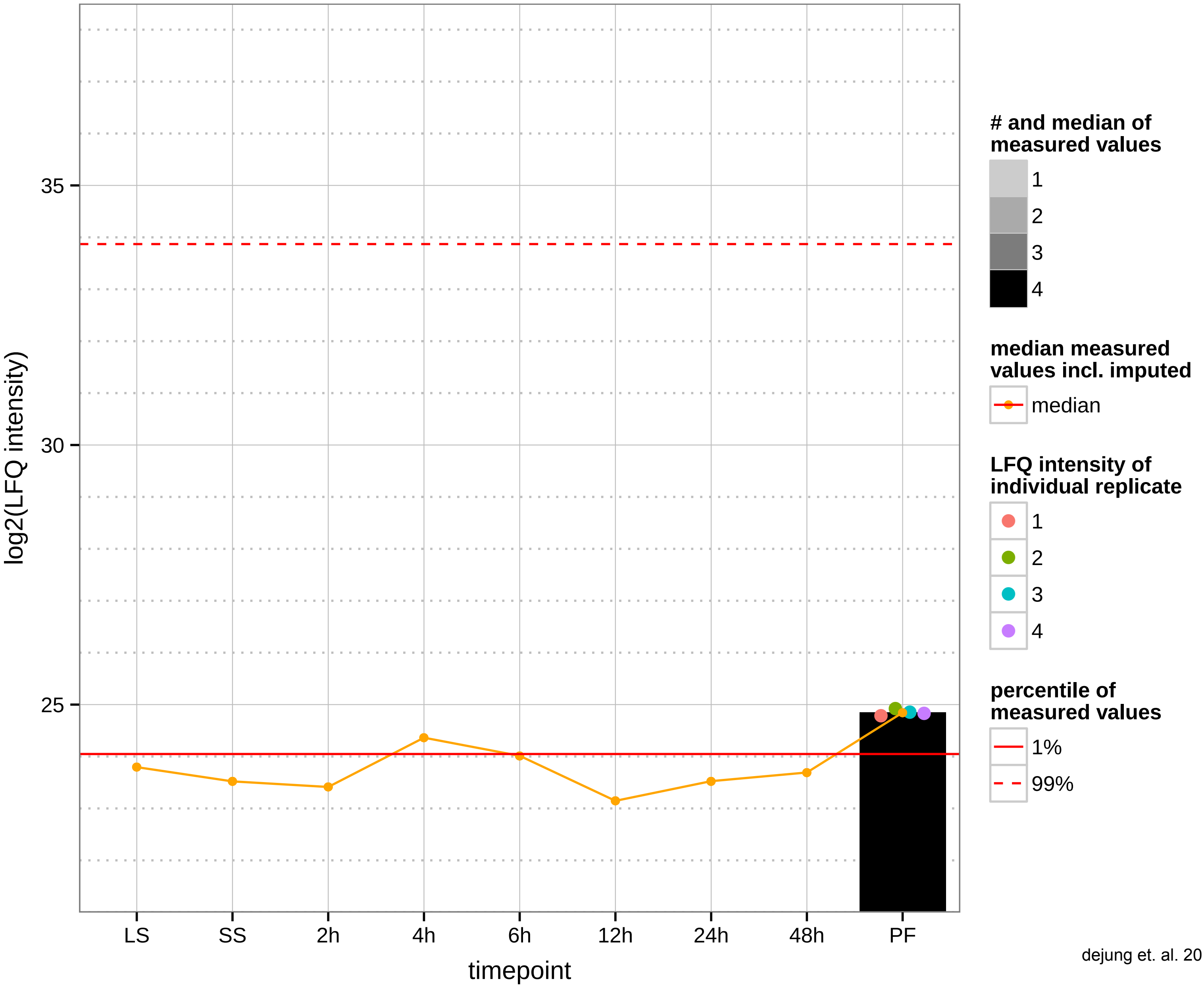




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.3690
AGOF: metal ion binding, superoxide dismutase activity
AGOC: mitochondrion
AGOP: oxidation–reduction process, superoxide metabolic process
PGOF: metal ion binding, superoxide dismutase activity
PGOC: null
PGOP: oxidation–reduction process, superoxide metabolic process





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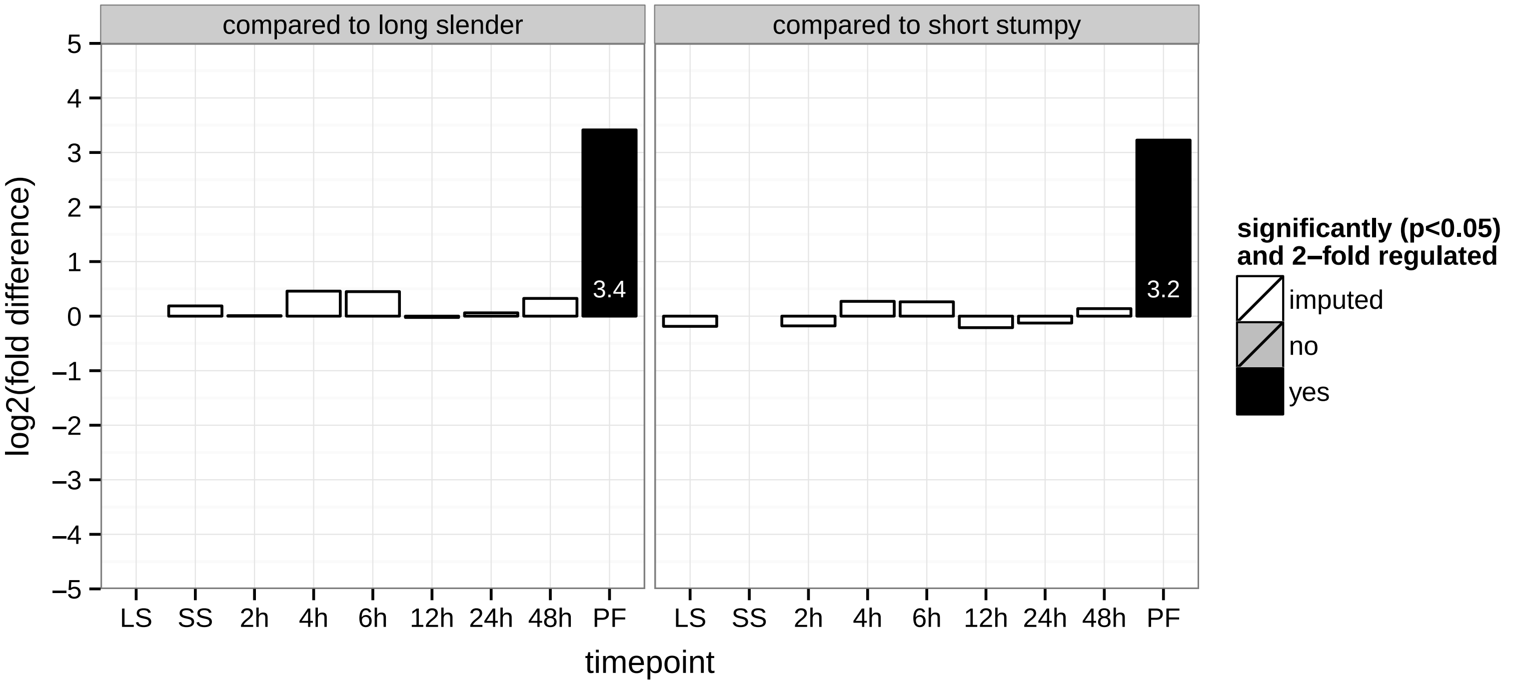
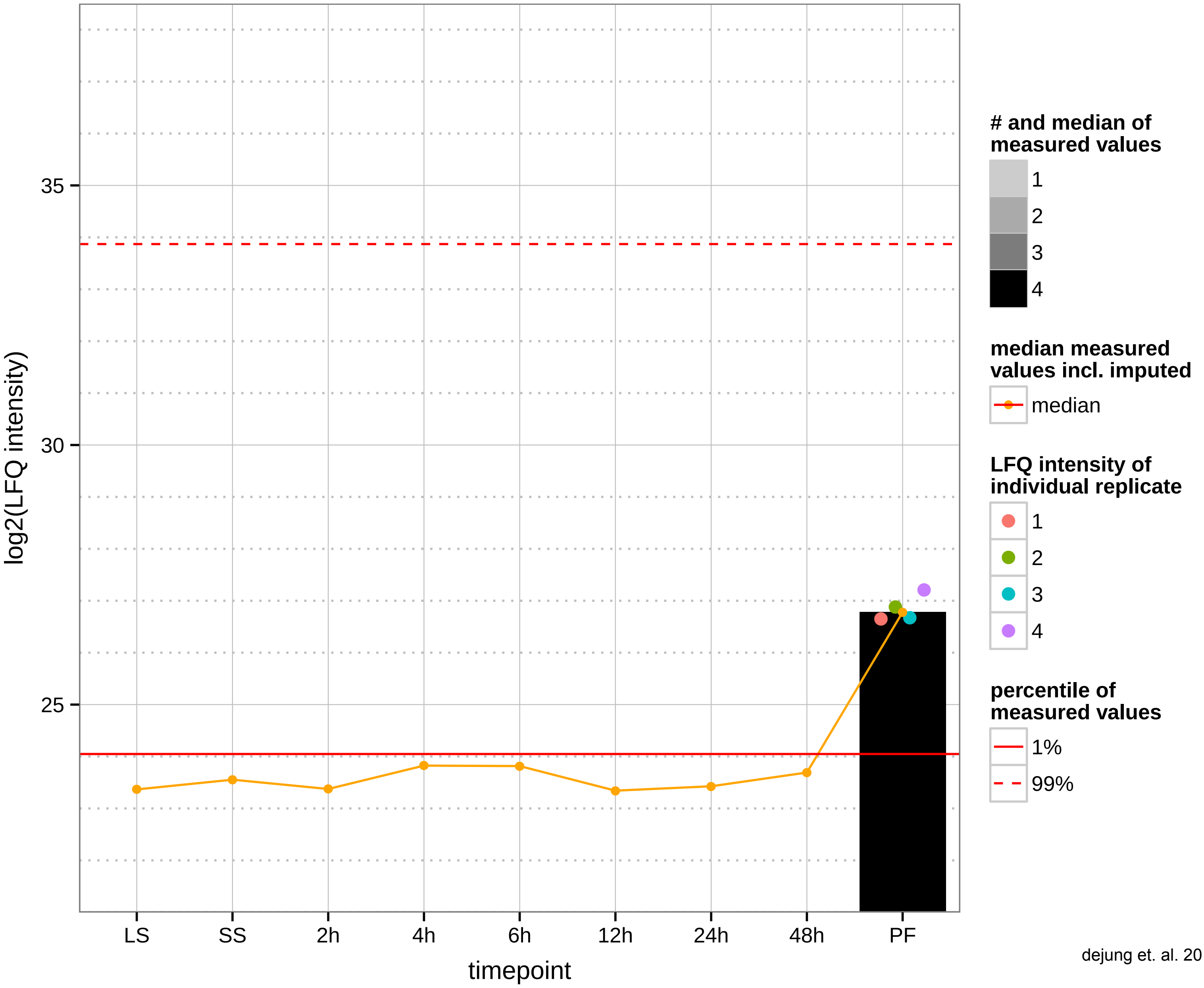
protein kinase, putative
Tb927.4.3770
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity, zinc ion bin
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups, zinc ion binding
PGOC: null
PGOP: protein phosphorylation





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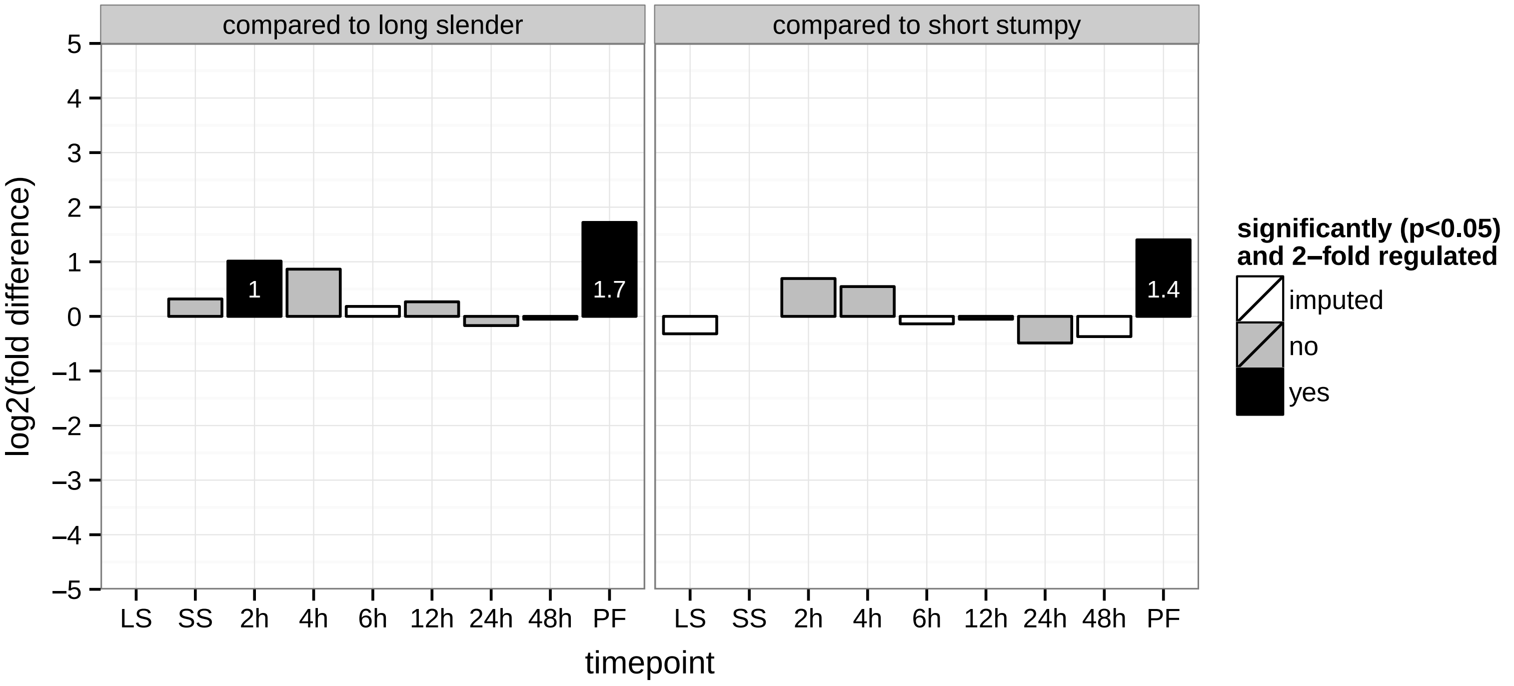
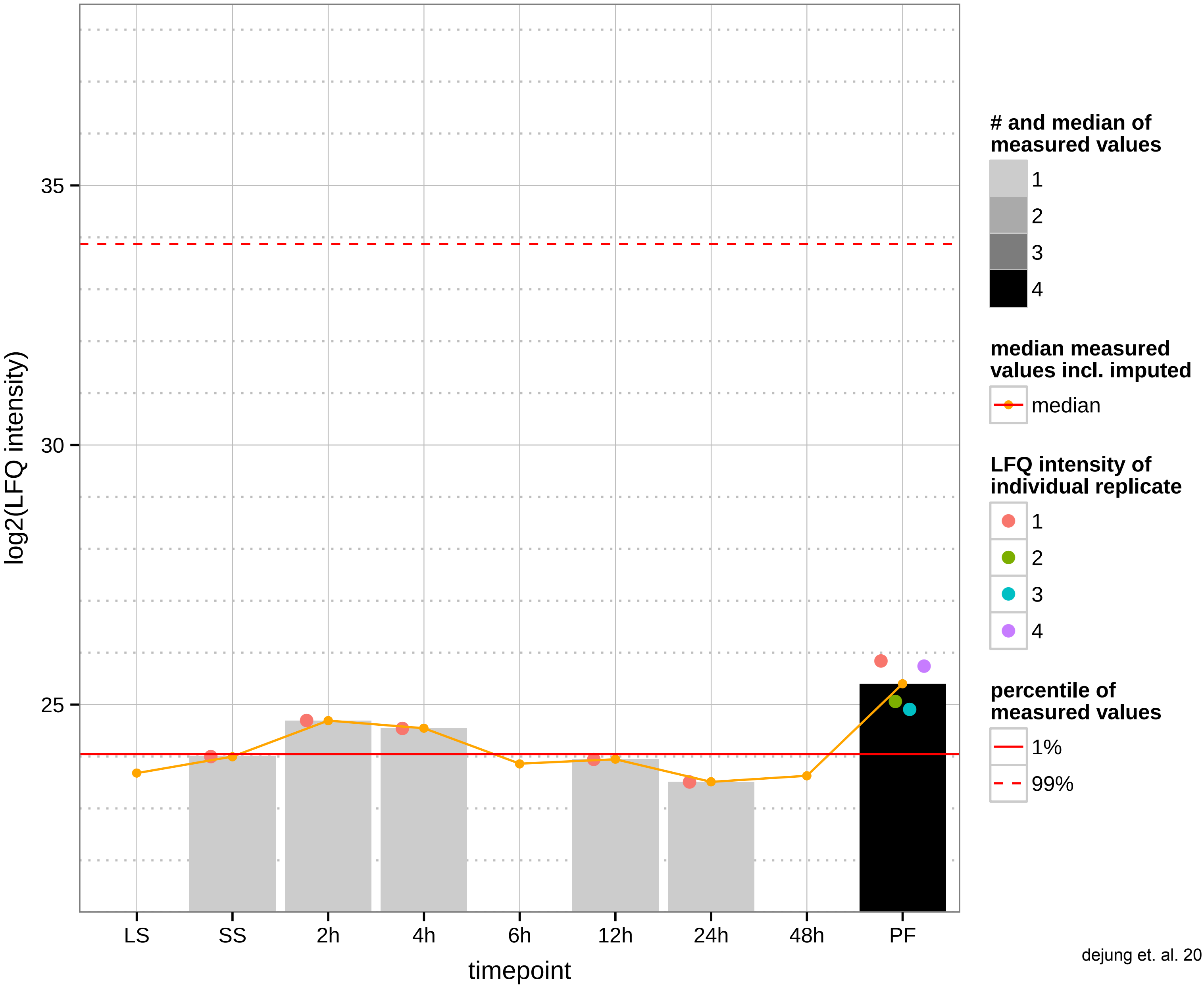
calpain–like cysteine peptidase, putative, cysteine peptidase, Clan CA, family C2, putative (TbCALP2)
Tb927.4.3940
AGOF: calcium–dependent cysteine–type endopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: calcium–dependent cysteine–type endopeptidase activity
PGOC: intracellular
PGOP: proteolysis





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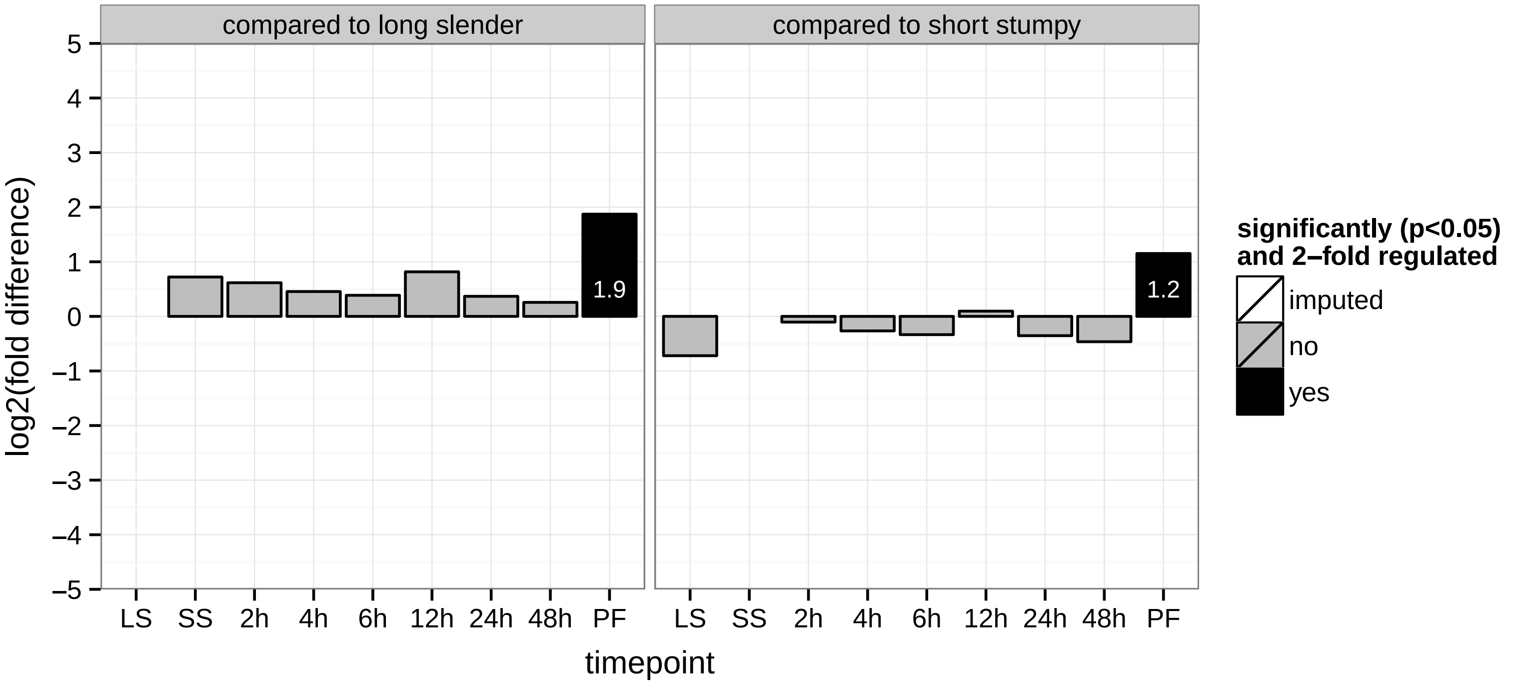
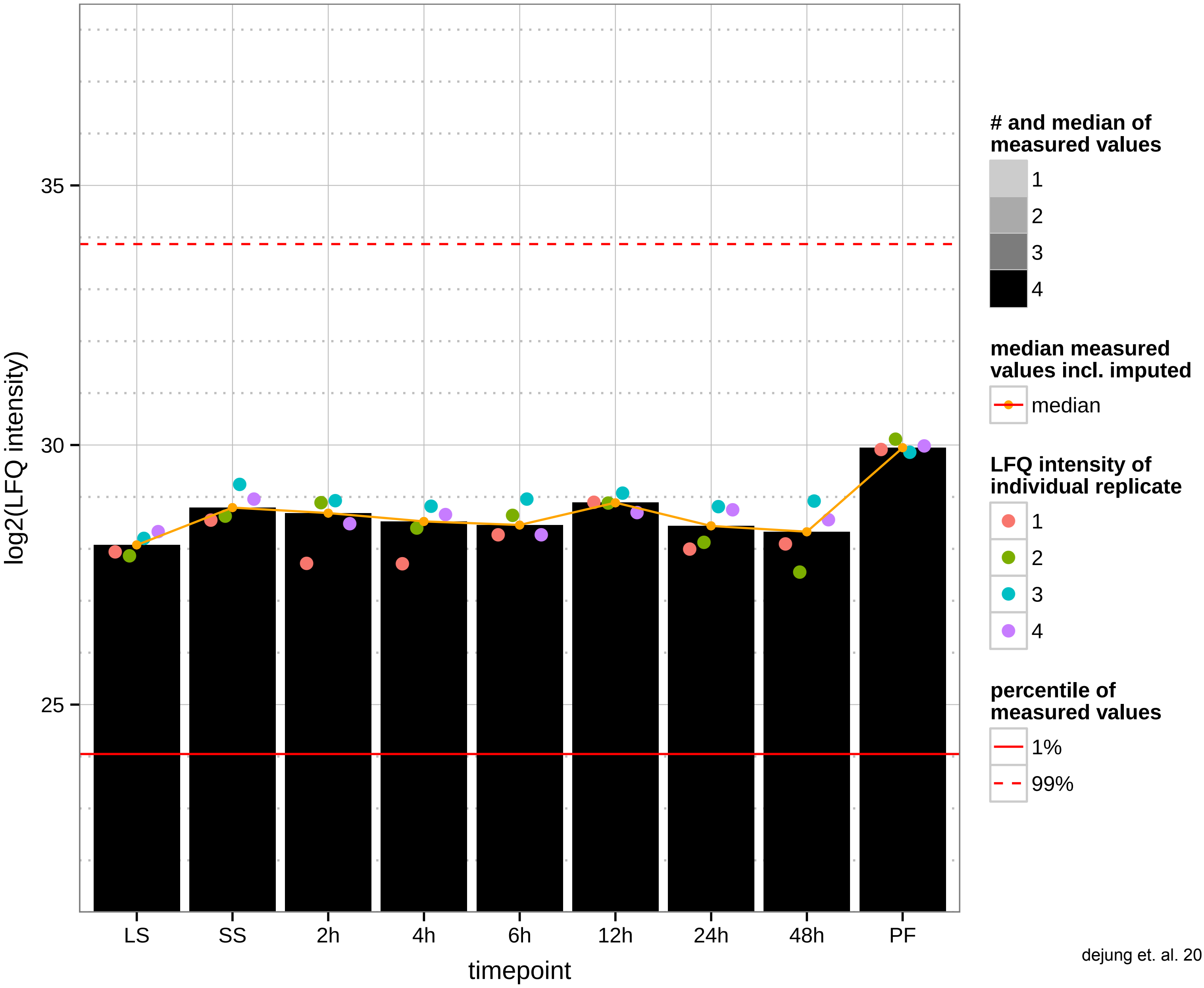
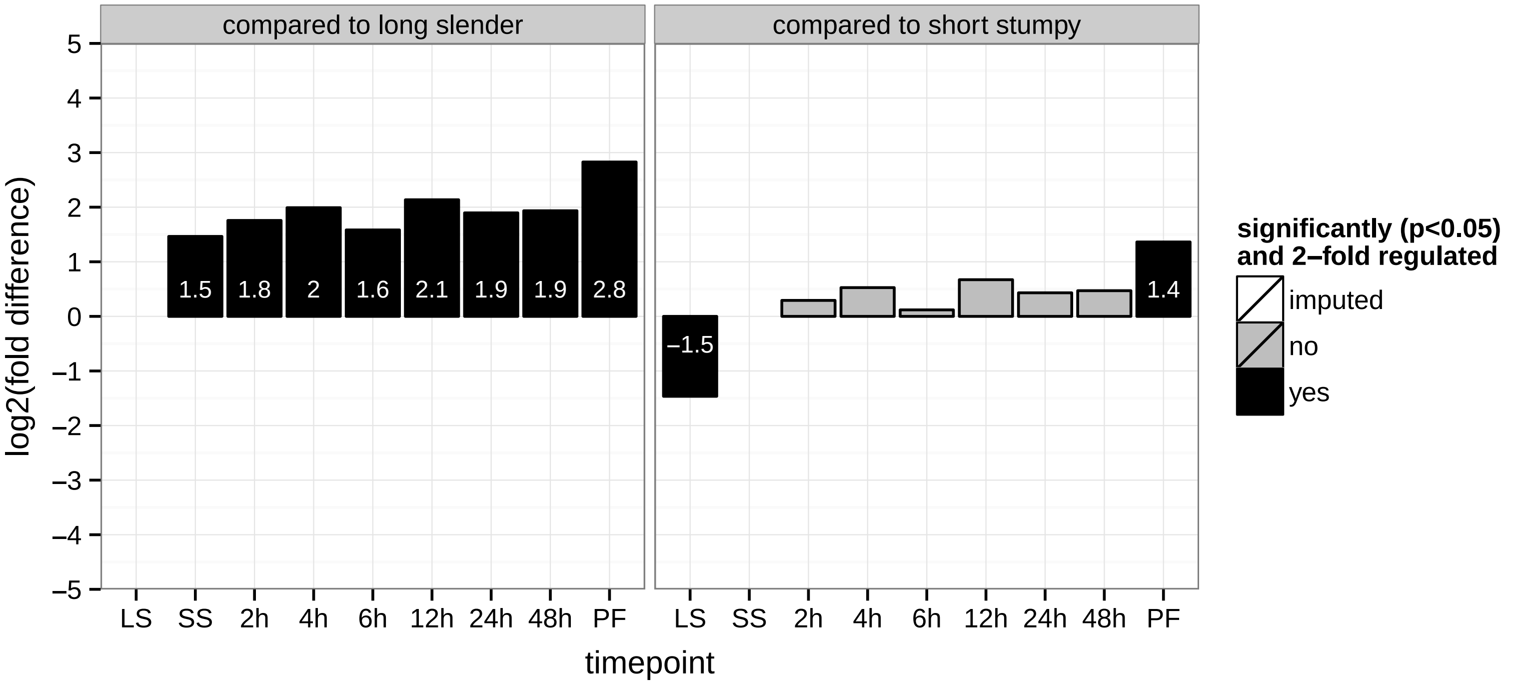
proteasome beta 7 subunit
Tb927.4.430
AGOF: endopeptidase activity, threonine−type endopeptidase activity
AGOC: proteasome core complex, proteasome core complex, beta−subunit complex
AGOP: protein metabolic process, proteolysis involved in cellular protein catabolic process
PGOF: threonine−type endopeptidase activity
PGOC: proteasome core complex
PGOP: proteolysis involved in cellular protein catabolic process

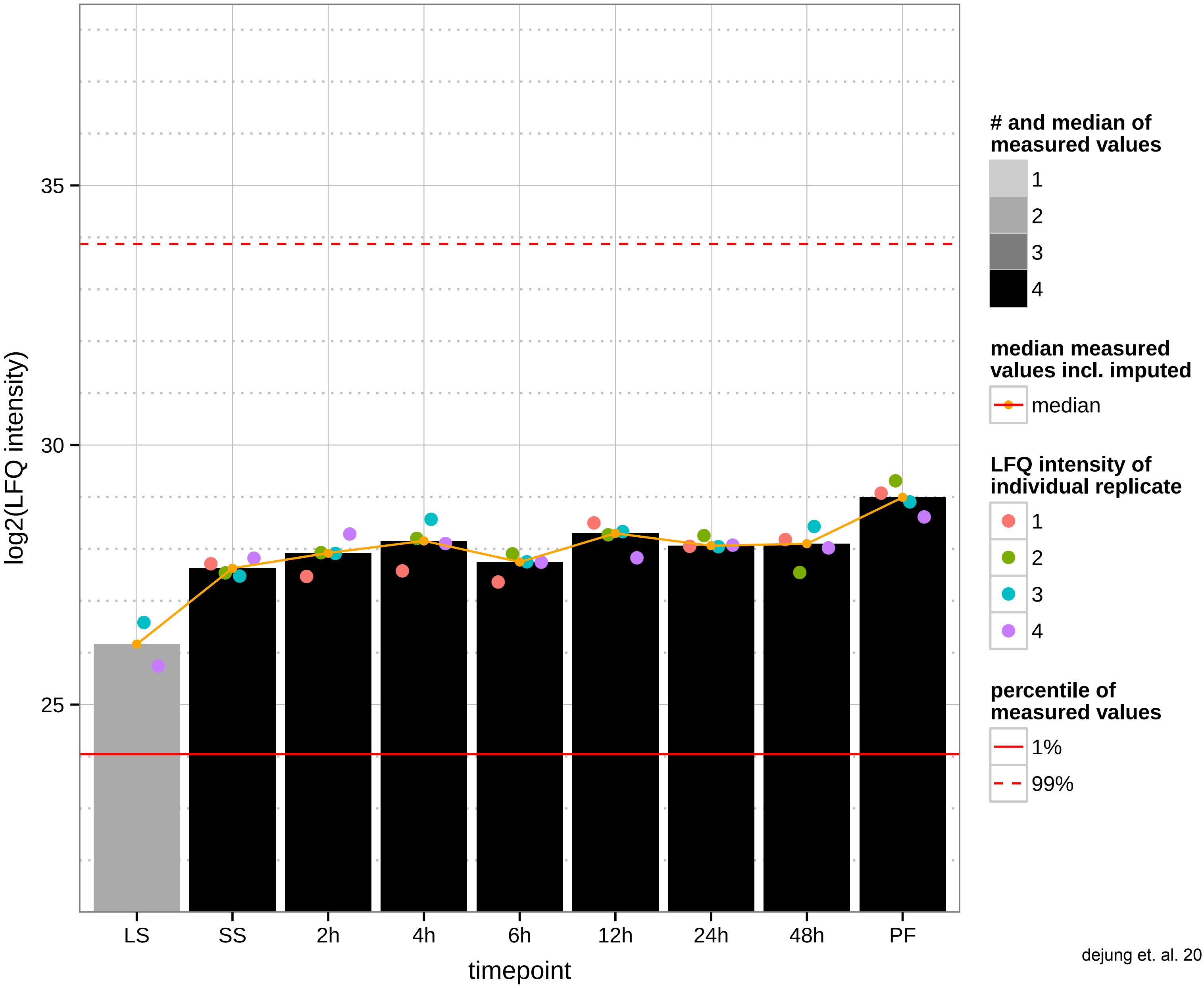




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.4350
AGOF: null
AGOC: integral to membrane
AGOP: transport
PGOF: null
PGOC: integral to membrane
PGOP: transport





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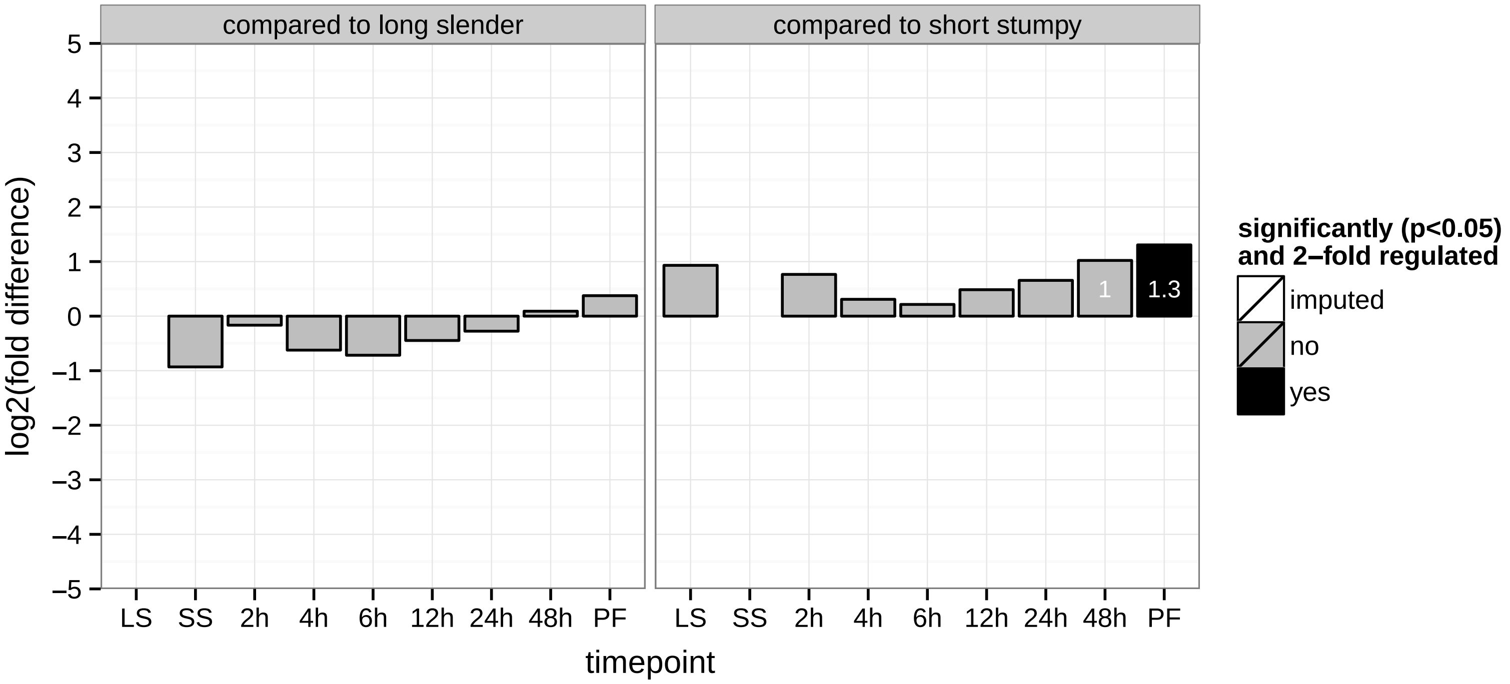
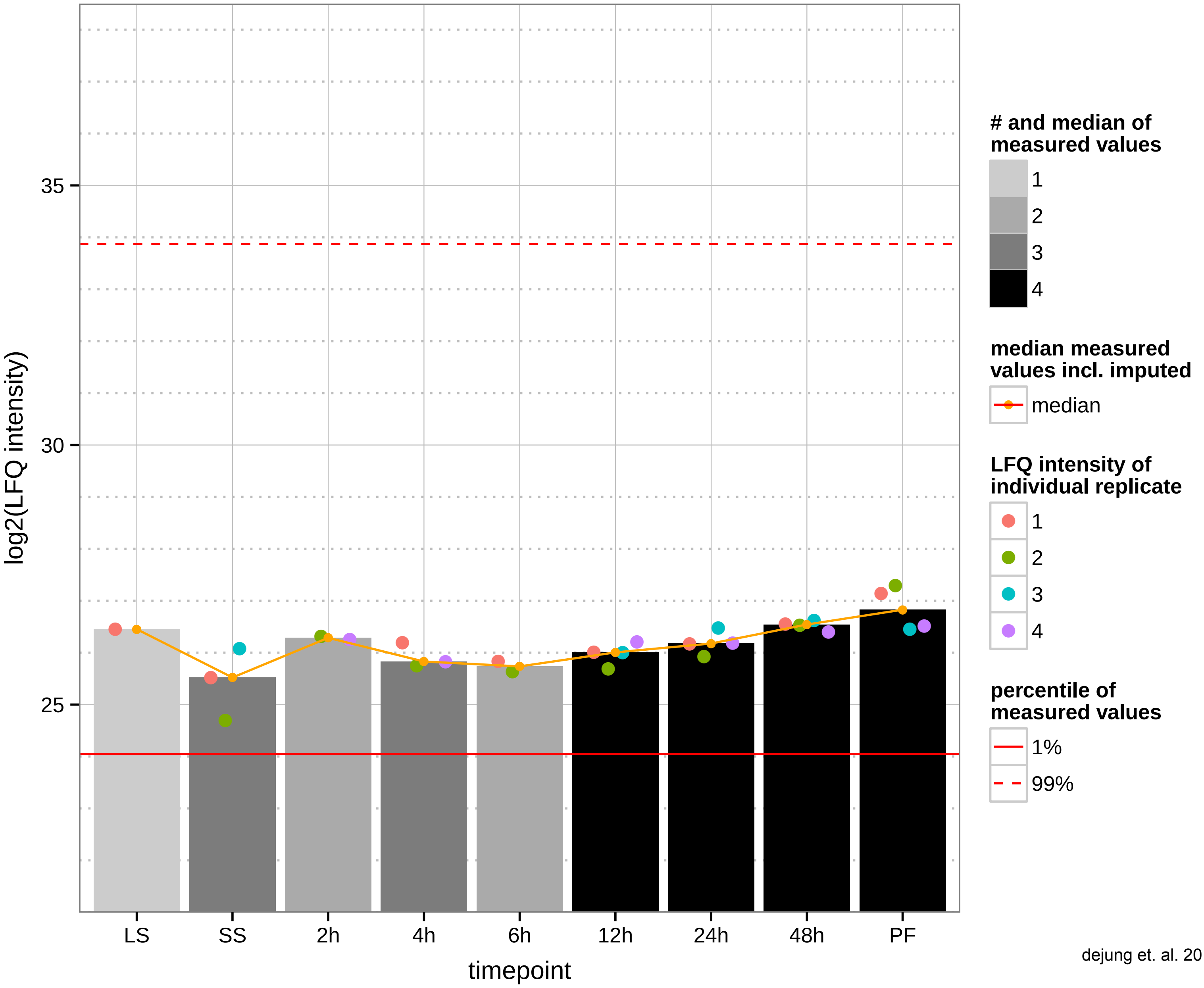
hypothetical protein, conserved
Tb927.4.4600
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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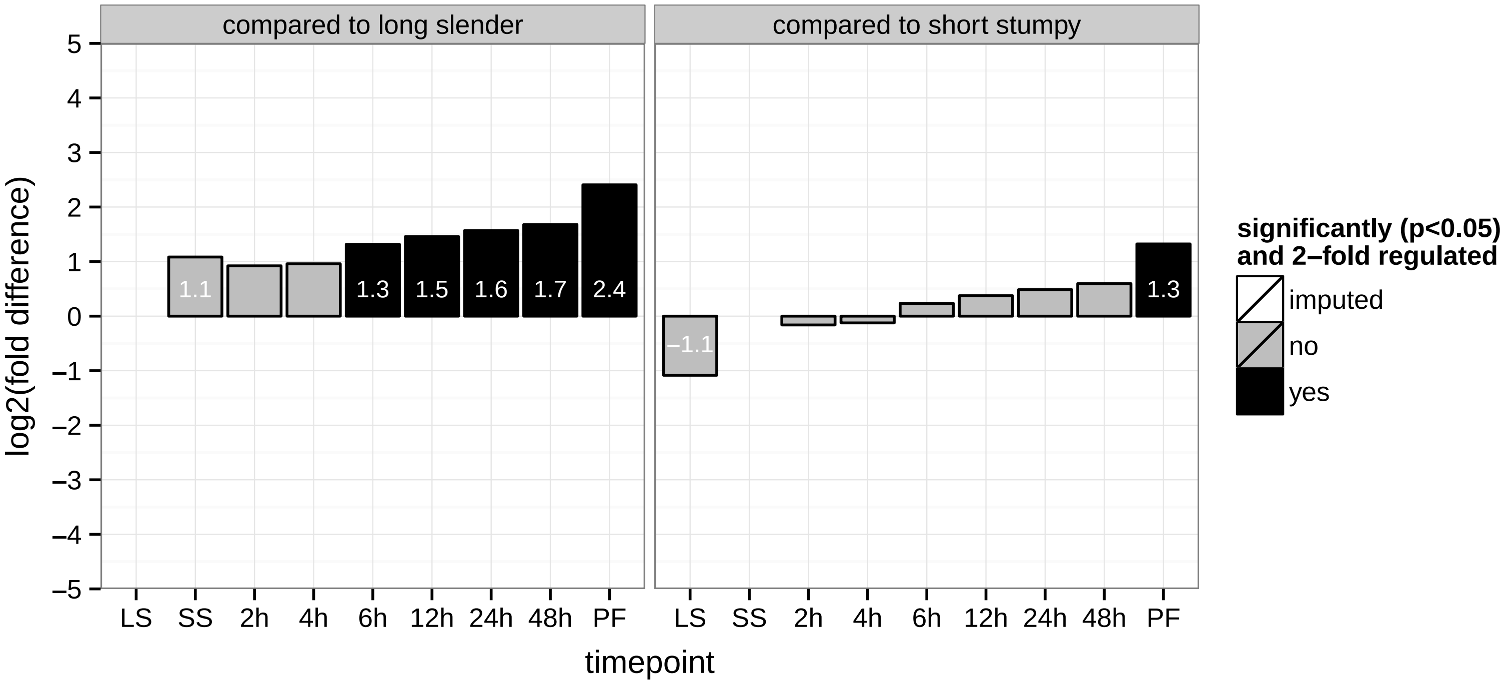
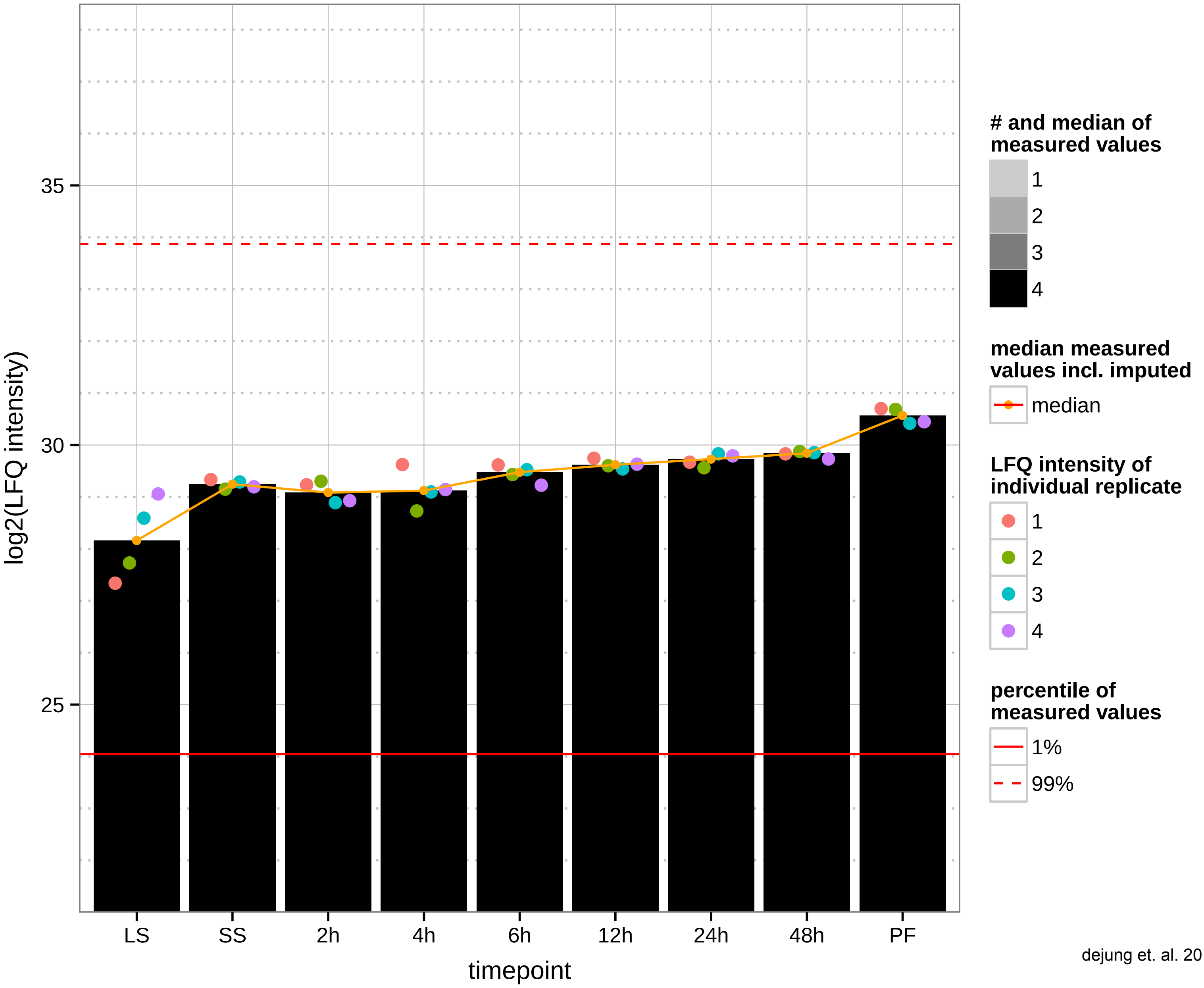
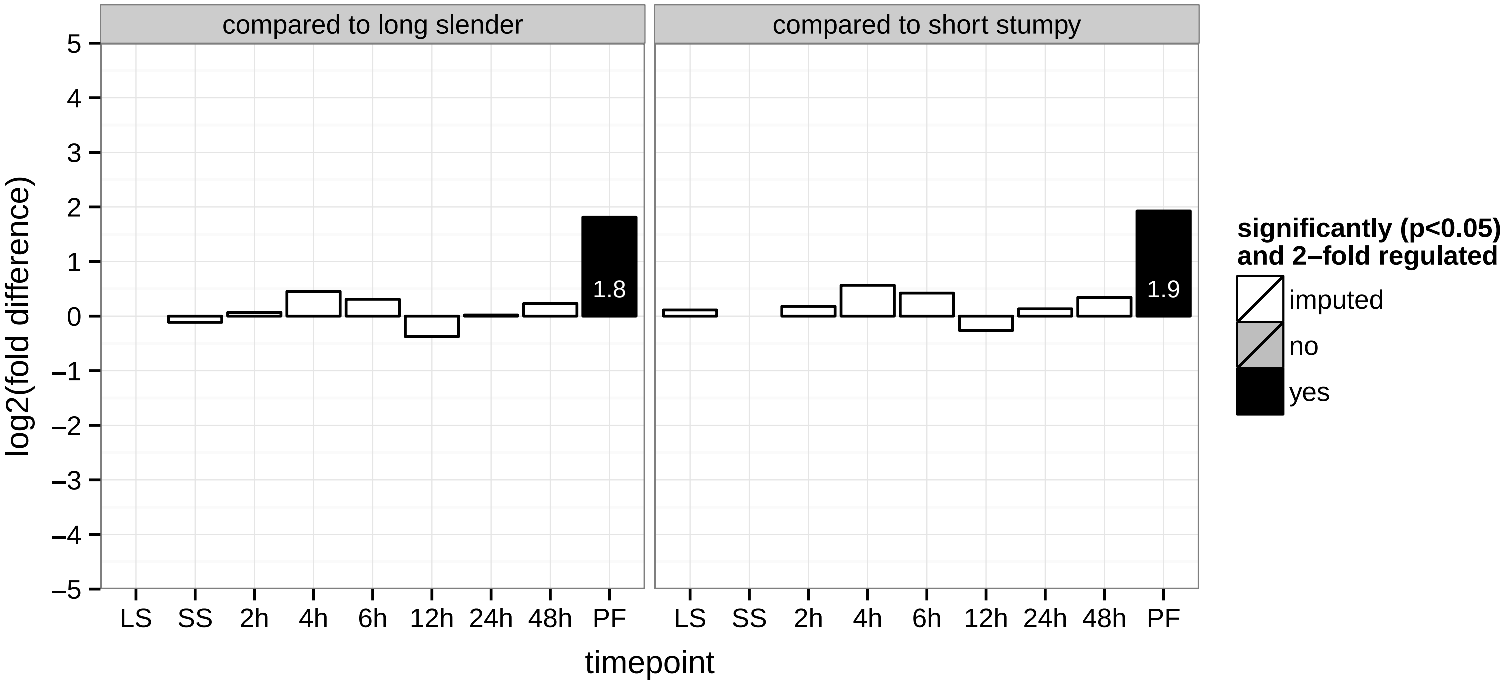
hypothetical protein, conserved
Tb927.4.590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

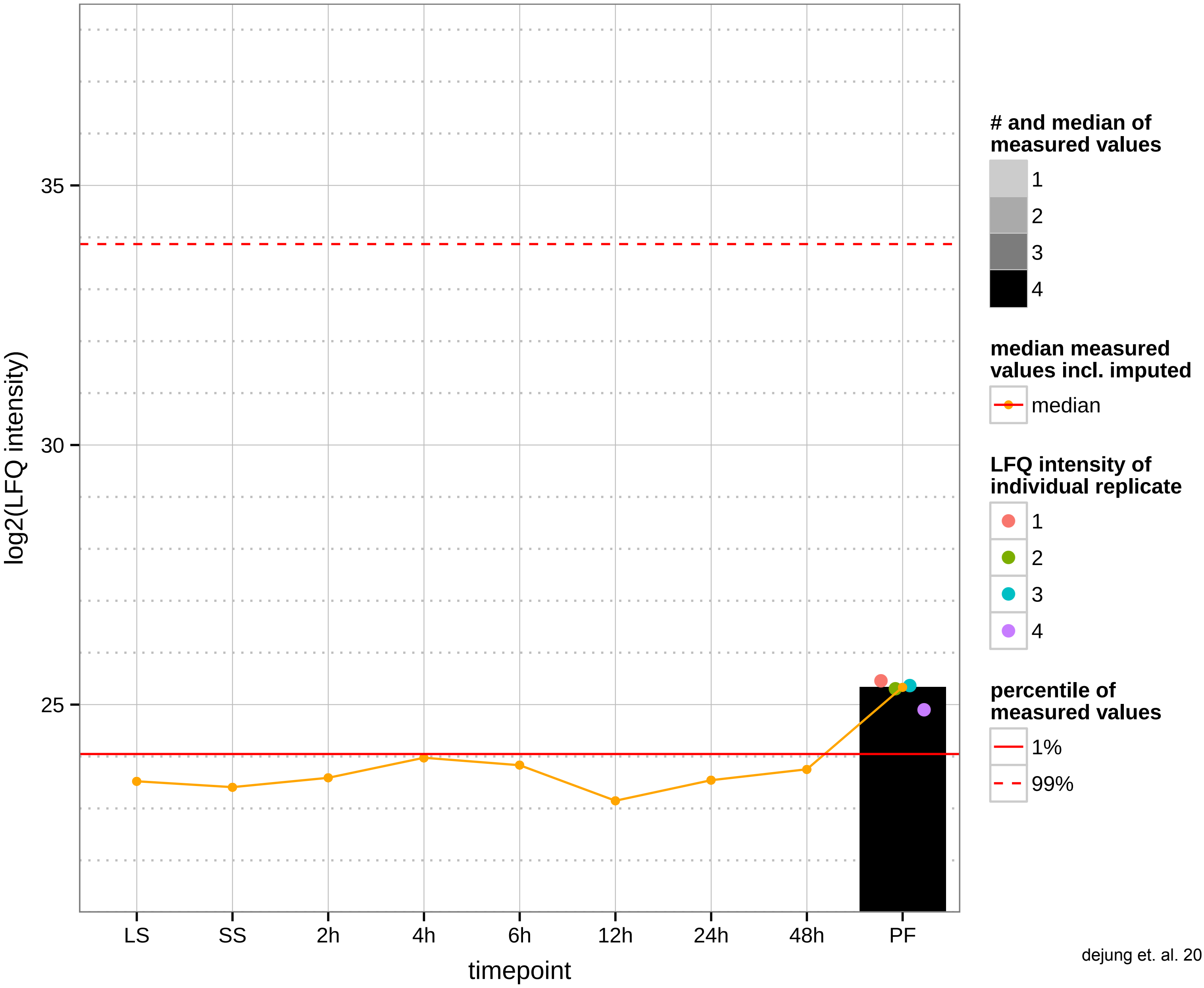




dejung et. al. 2015

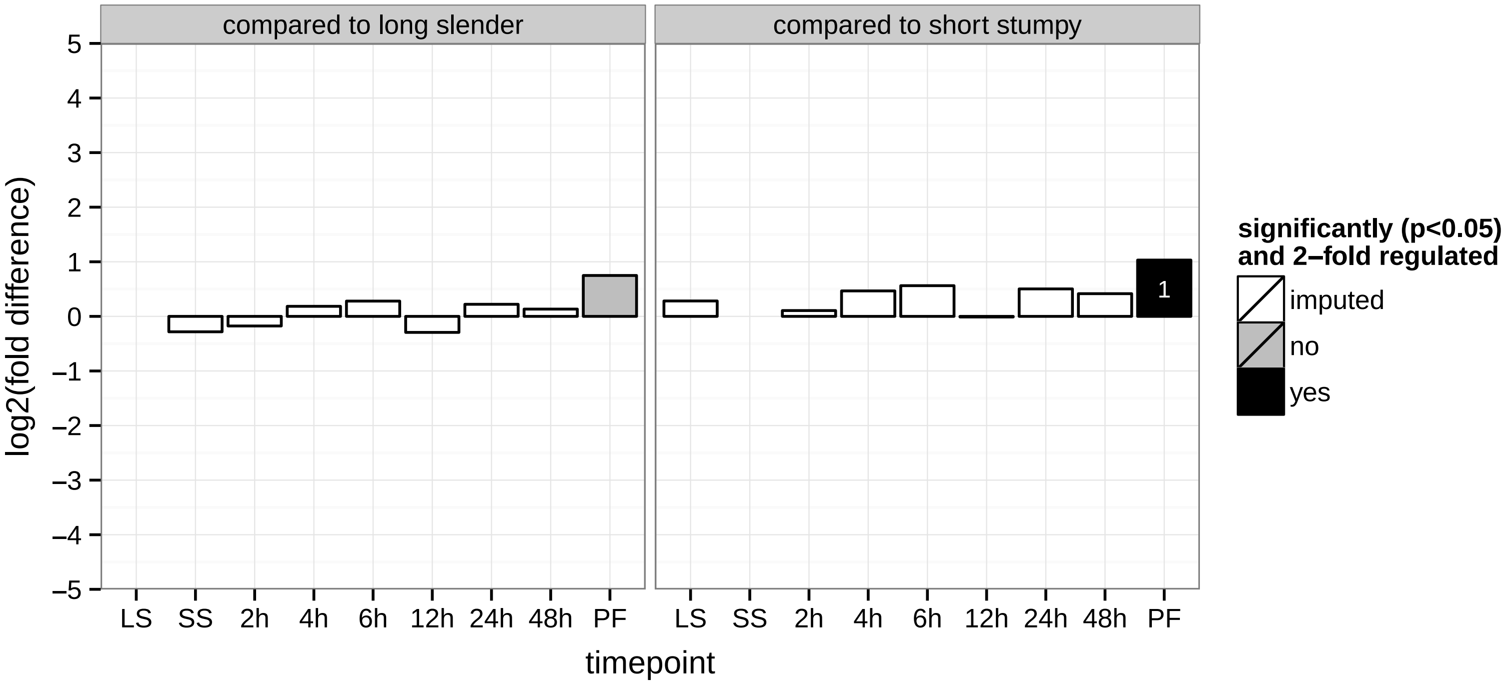
hypothetical protein, conserved
Tb927.4.790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

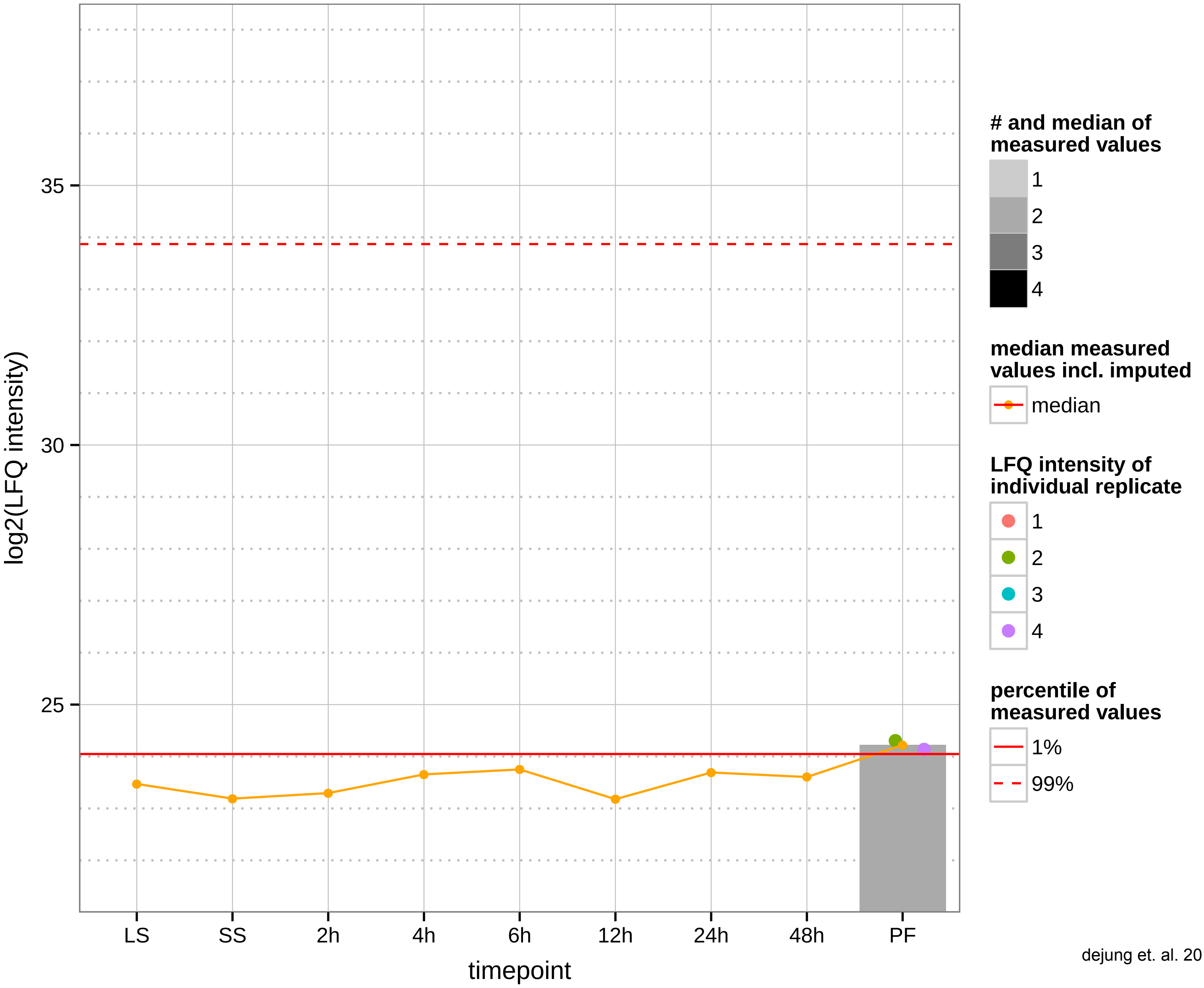




dejung et. al. 2015

actin, putative
Tb927.4.980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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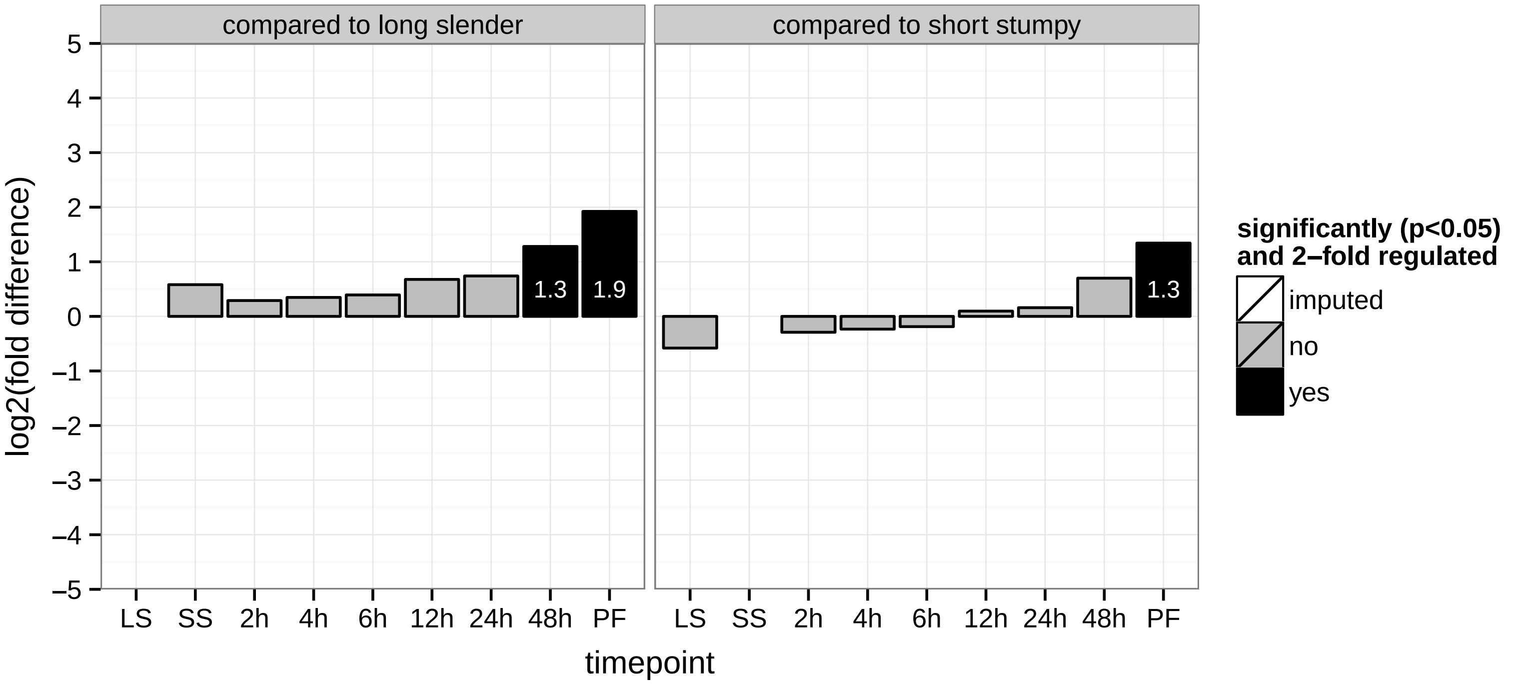
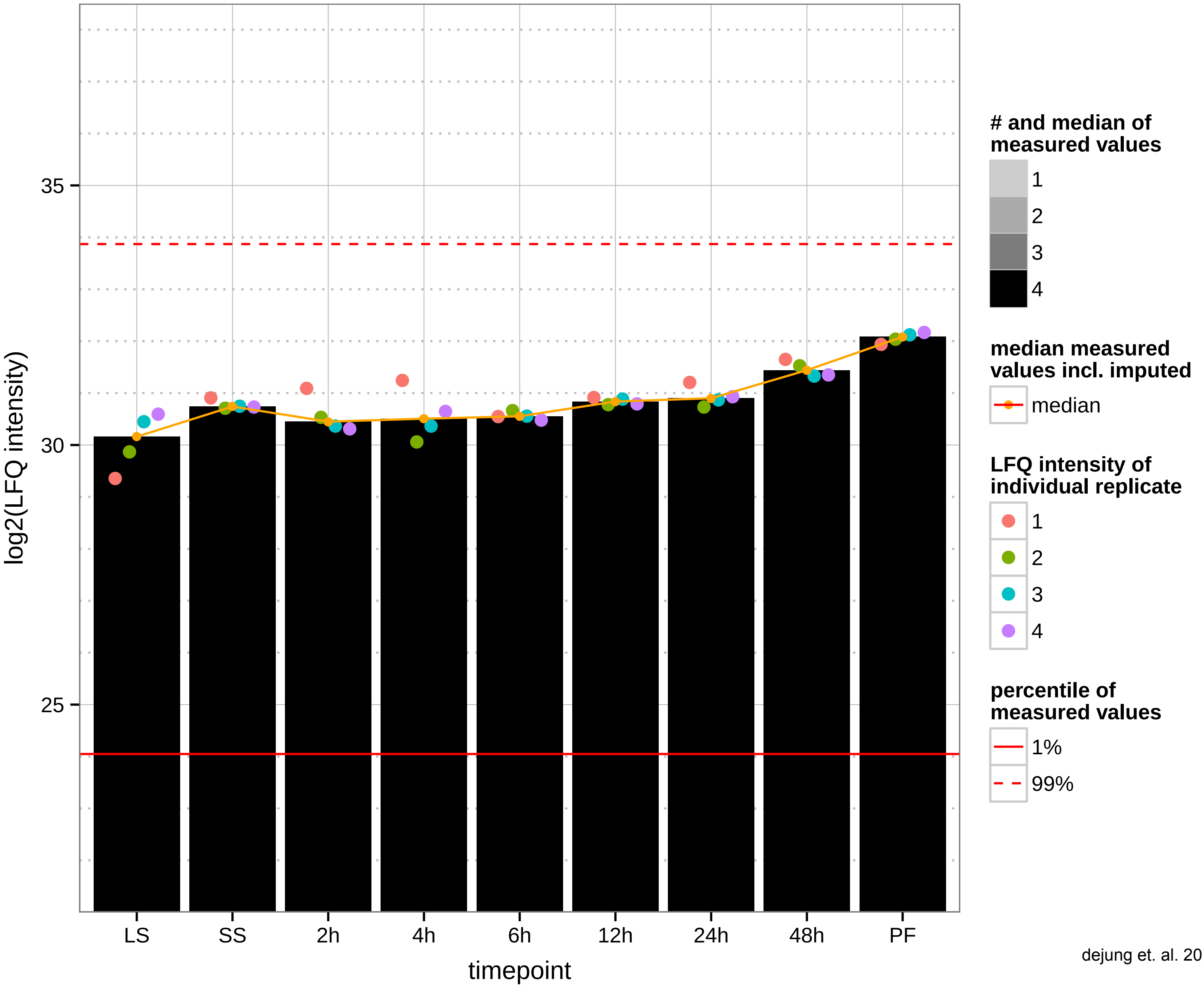
threonyl–tRNA synthetase, putative
Tb927.5.1090
AGOF: ATP binding, aminoacyl–tRNA ligase activity, threonine–tRNA ligase activity
AGOC: null
AGOP: threonyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, ligase activity, forming aminoacyl–tRNA and related compounds, nucleot
PGOC: cytoplasm
PGOP: tRNA aminoacylation, tRNA aminoacylation for protein translation, threonyl–tRNA aminoacylation





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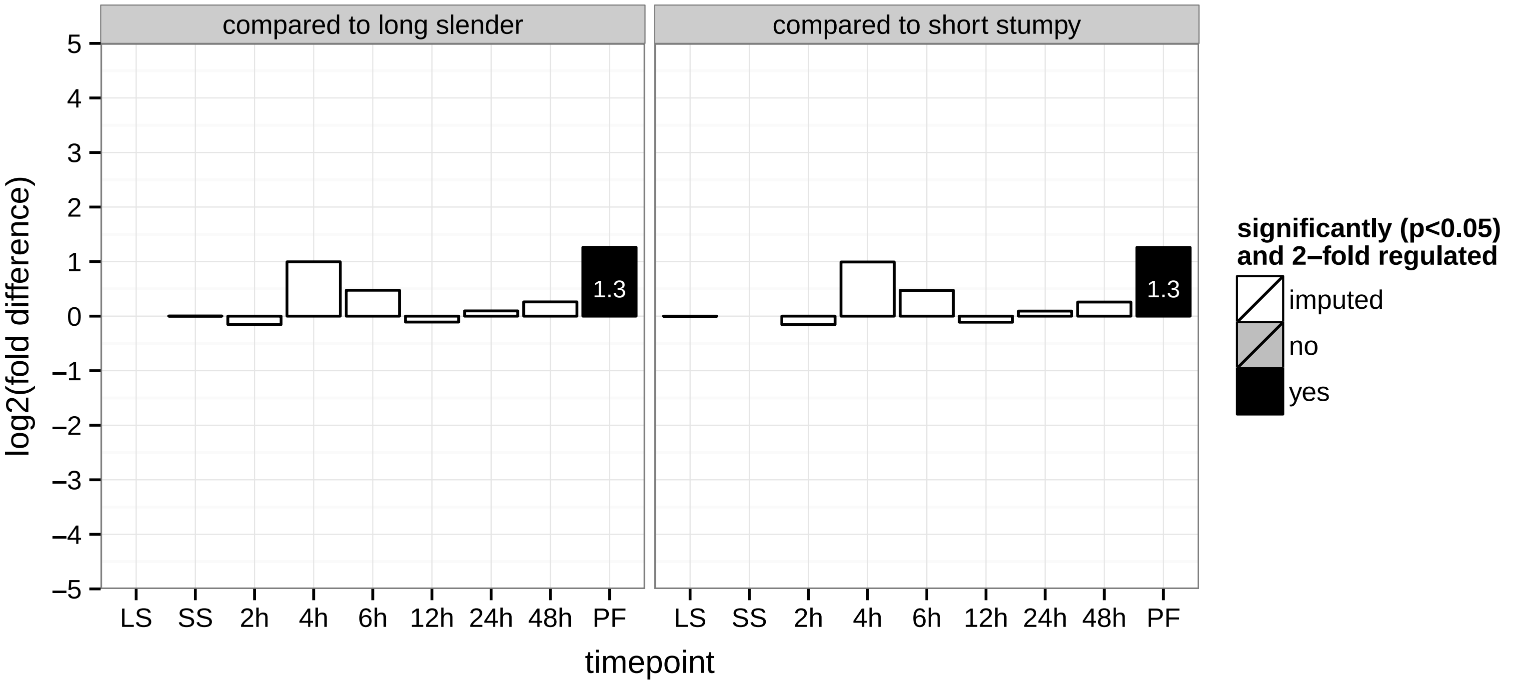
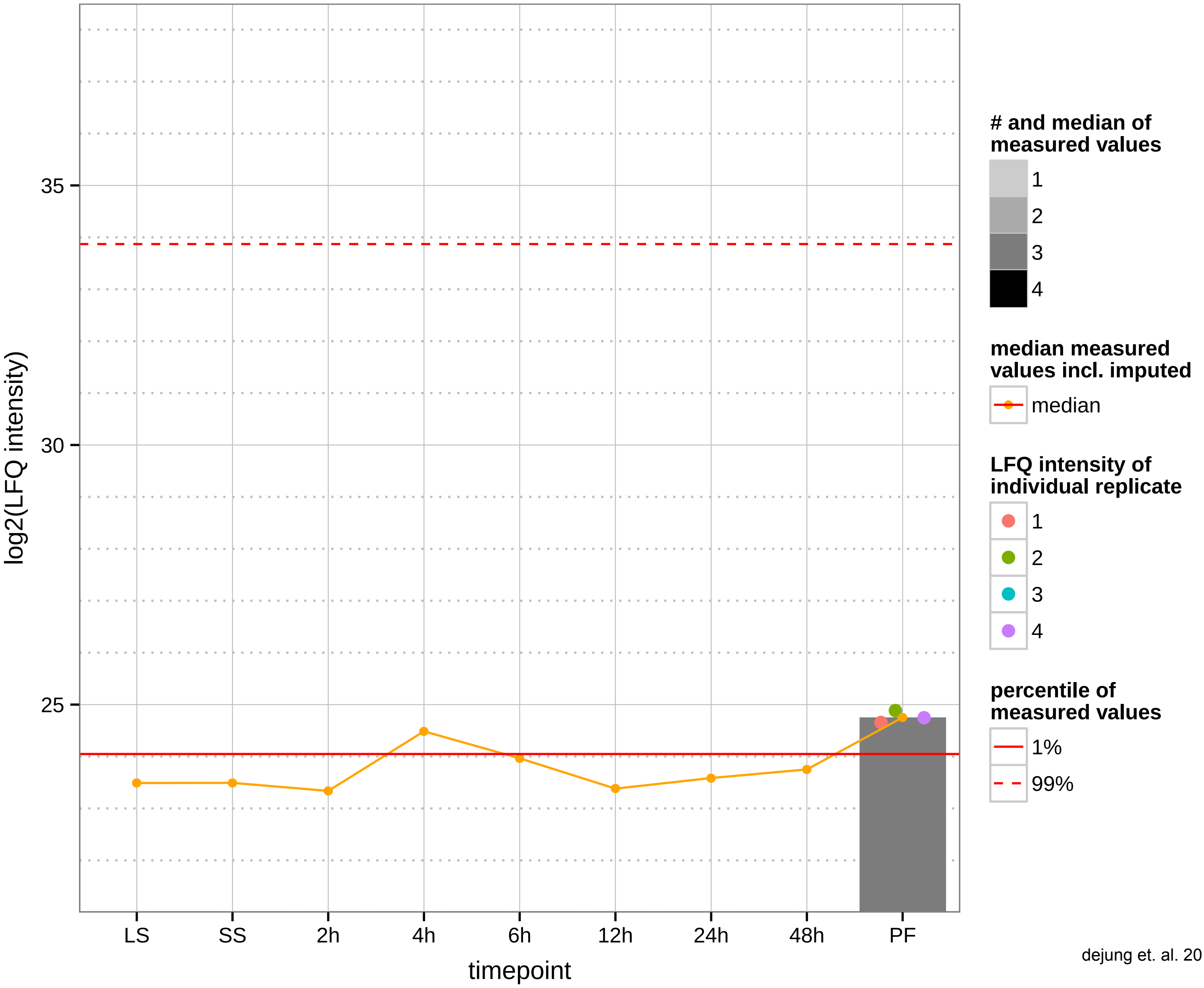
hypothetical protein, conserved
Tb927.5.1240
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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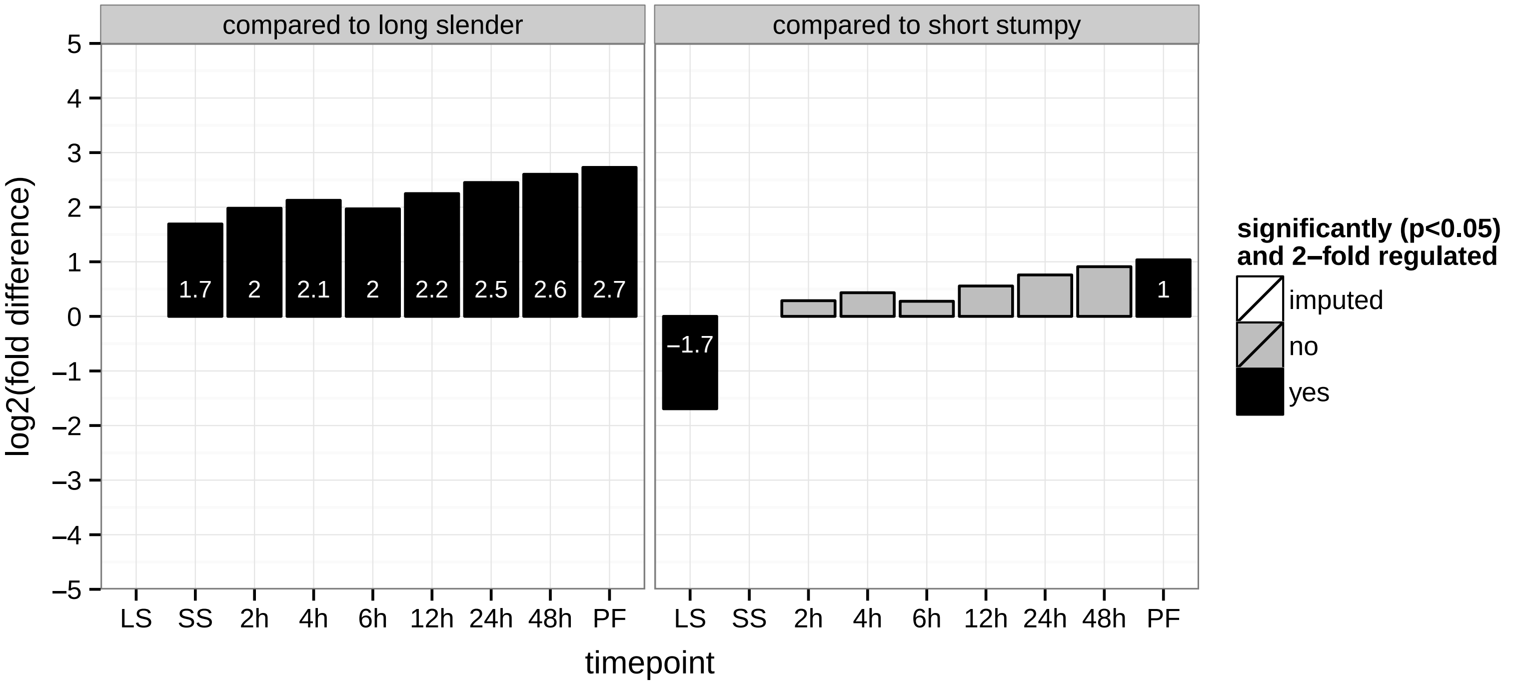
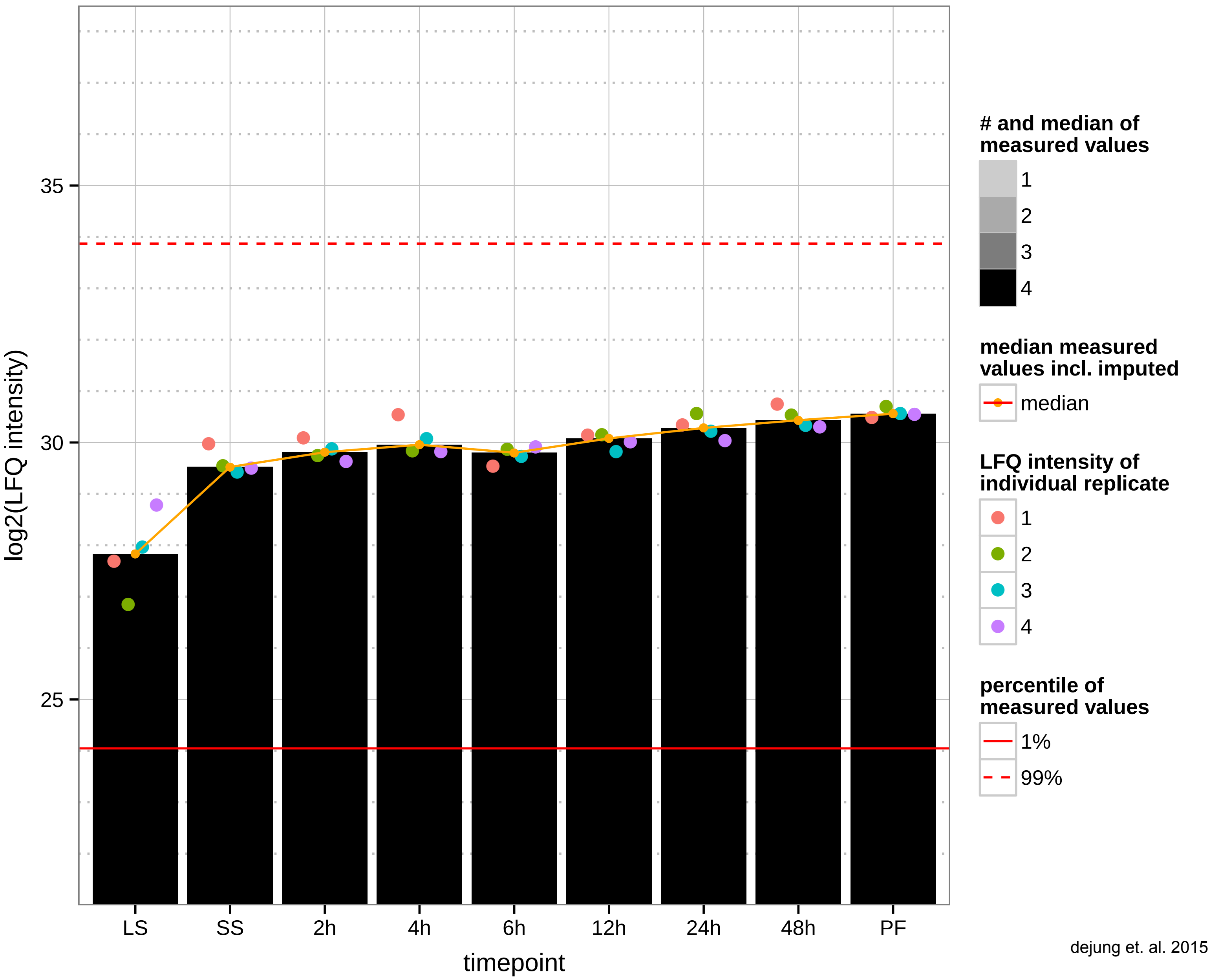
heat shock protein HslVU, ATPase subunit HslU, putative
Tb927.5.1520
AGOF: ATP binding, ATPase activity, peptidase activity, acting on L−amino acid peptides
AGOC: HslUV protease complex, cytoplasm, mitochondrion
AGOP: rolling circle DNA replication
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding, peptidase activity, acting on L−am
PGOC: HslUV protease complex, cytoplasm
PGOP: null





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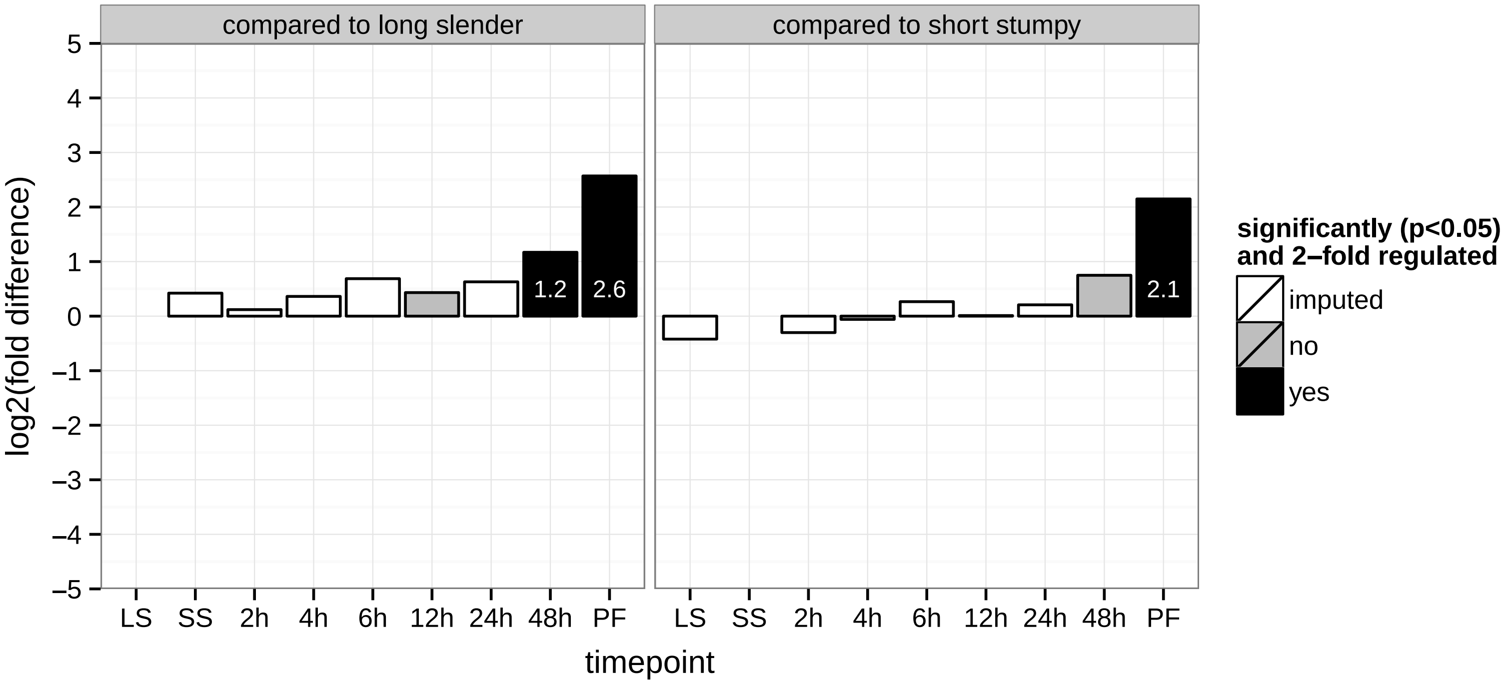
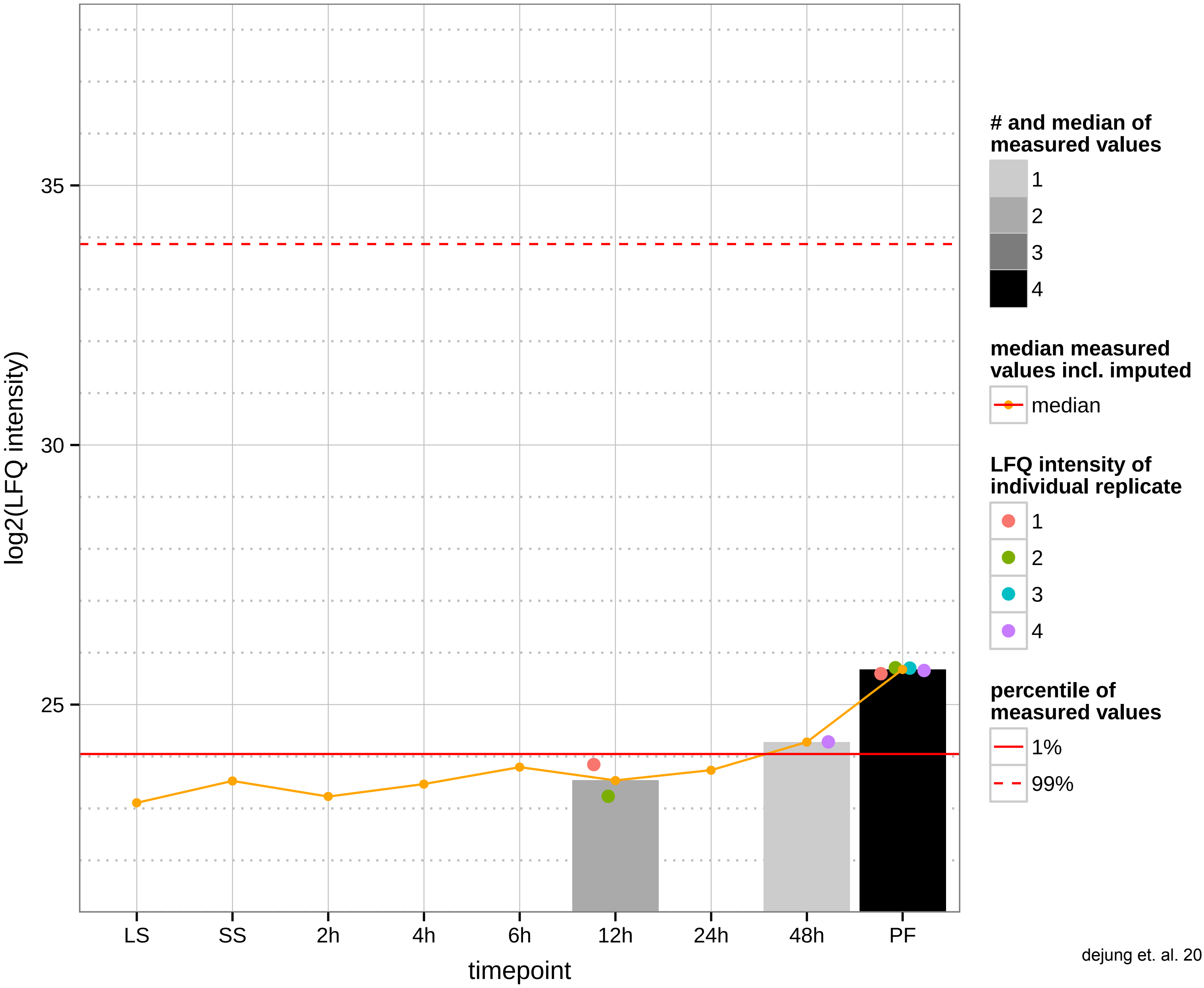
hypothetical protein, conserved
Tb927.5.1670
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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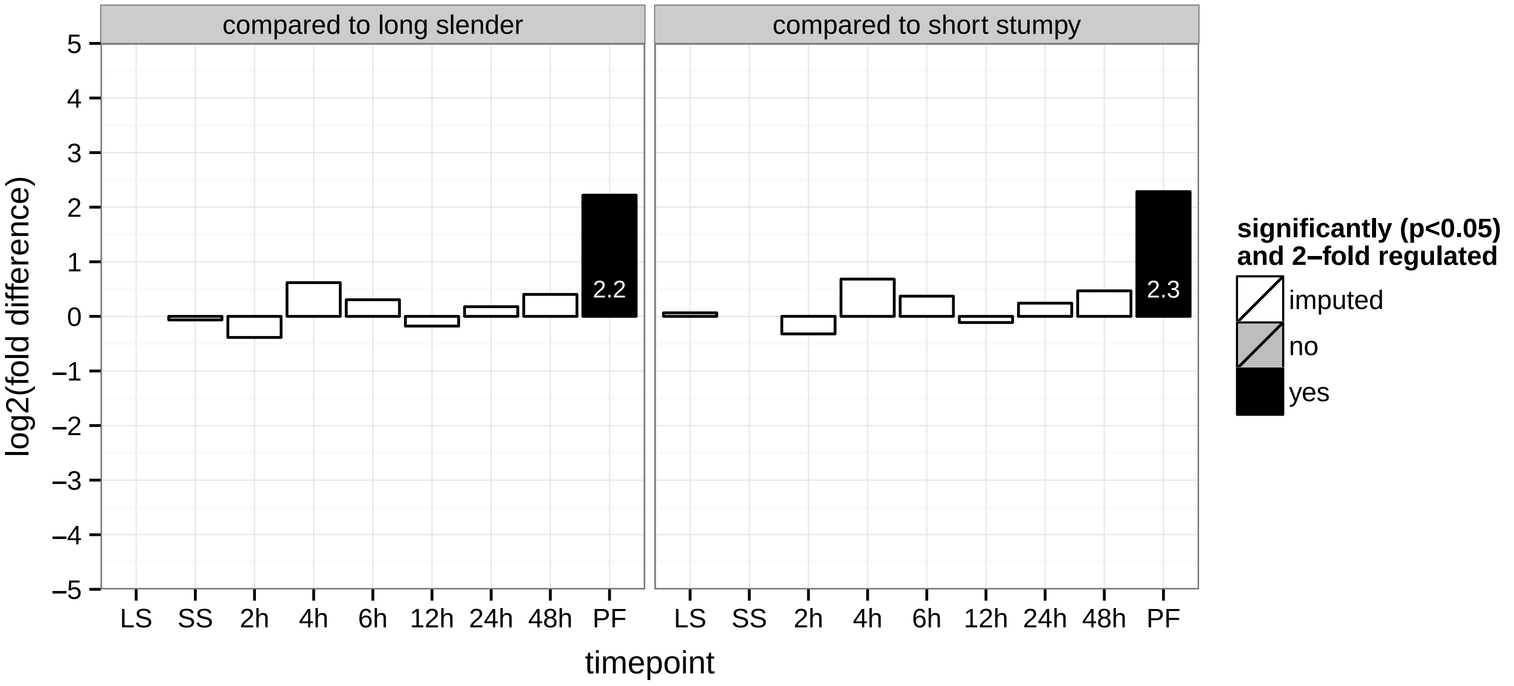
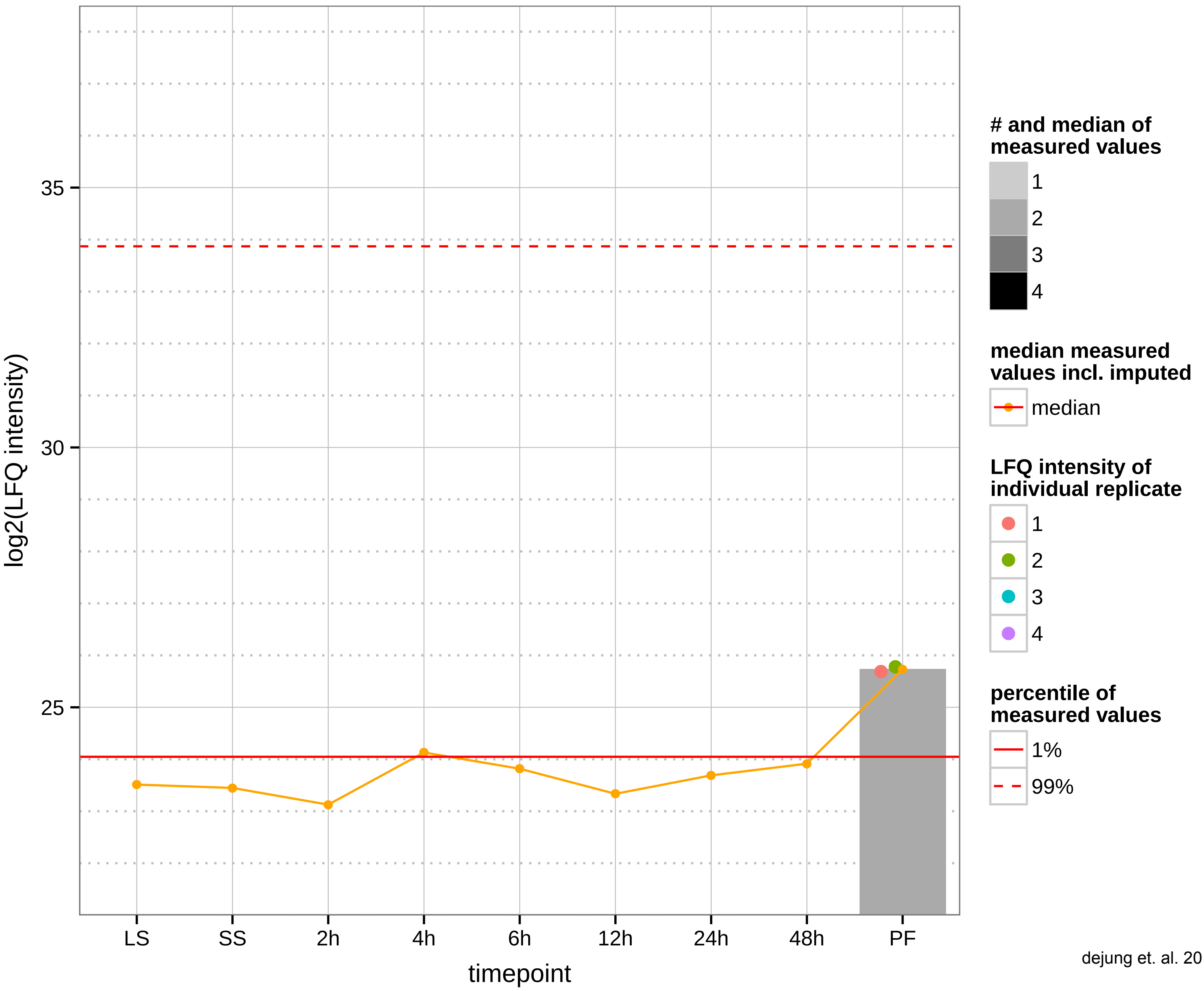
hypothetical protein, conserved
Tb927.5.1720
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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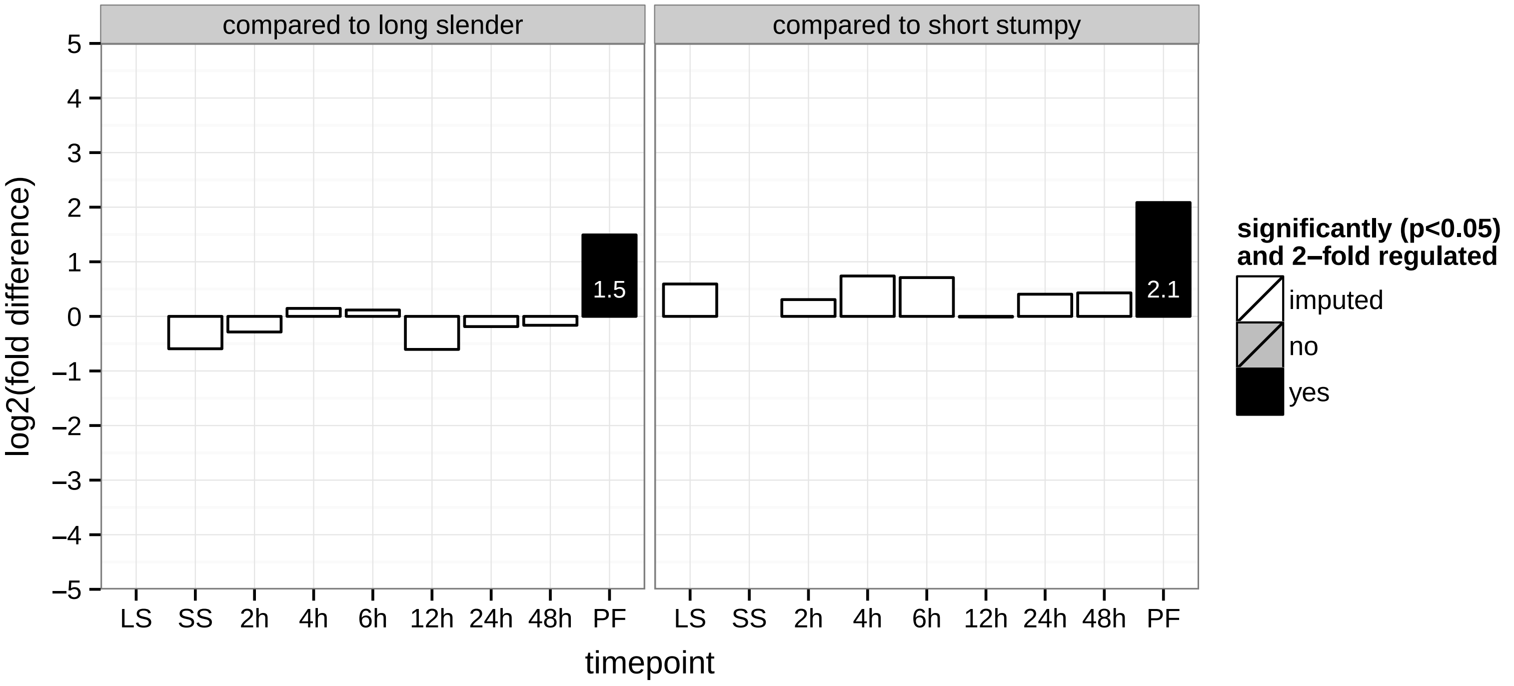
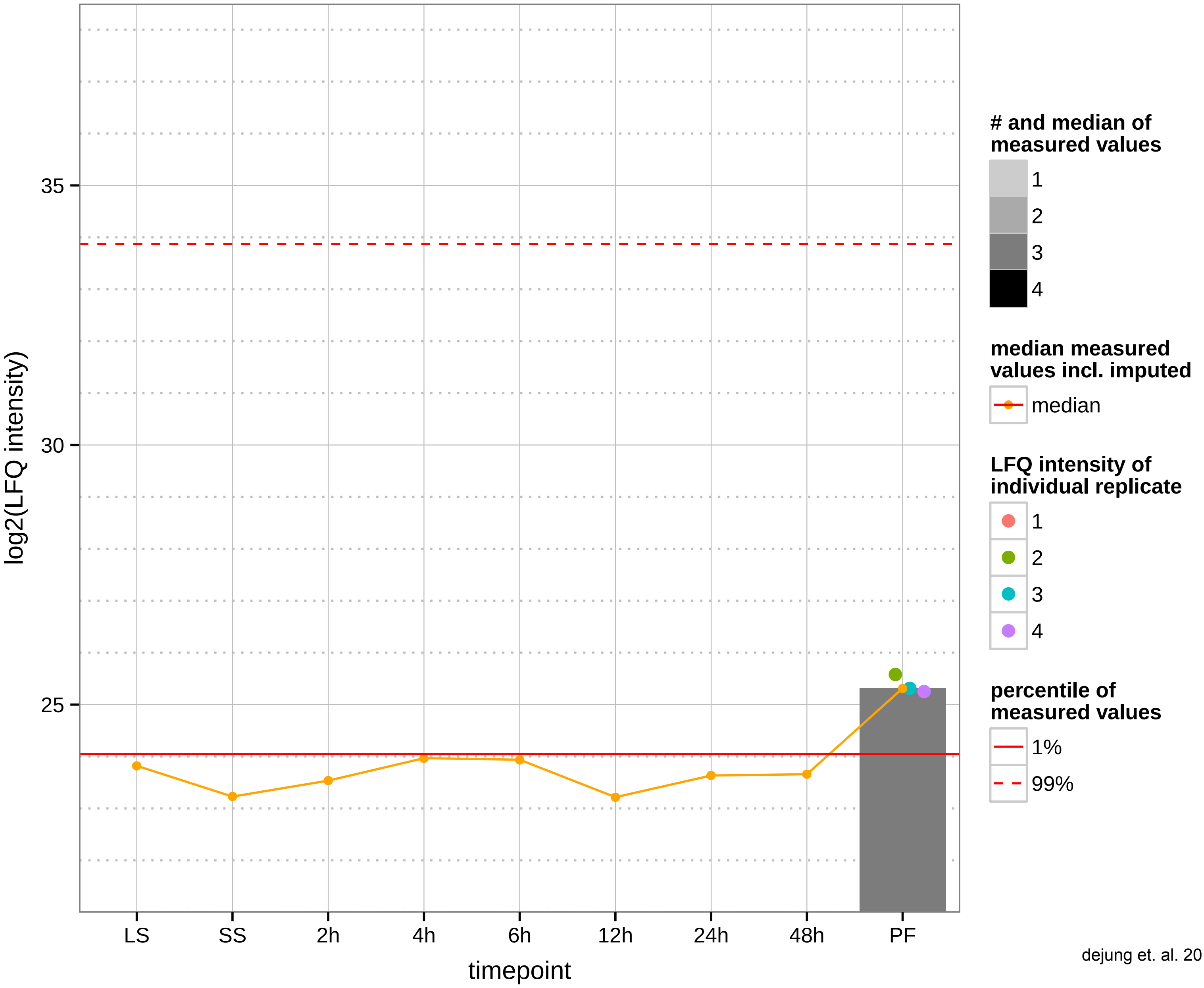
hypothetical protein, conserved
Tb927.5.2130
AGOF: hydrolase activity
AGOC: null
AGOP: null
PGOF: hydrolase activity, acting on ester bonds
PGOC: null
PGOP: mRNA processing





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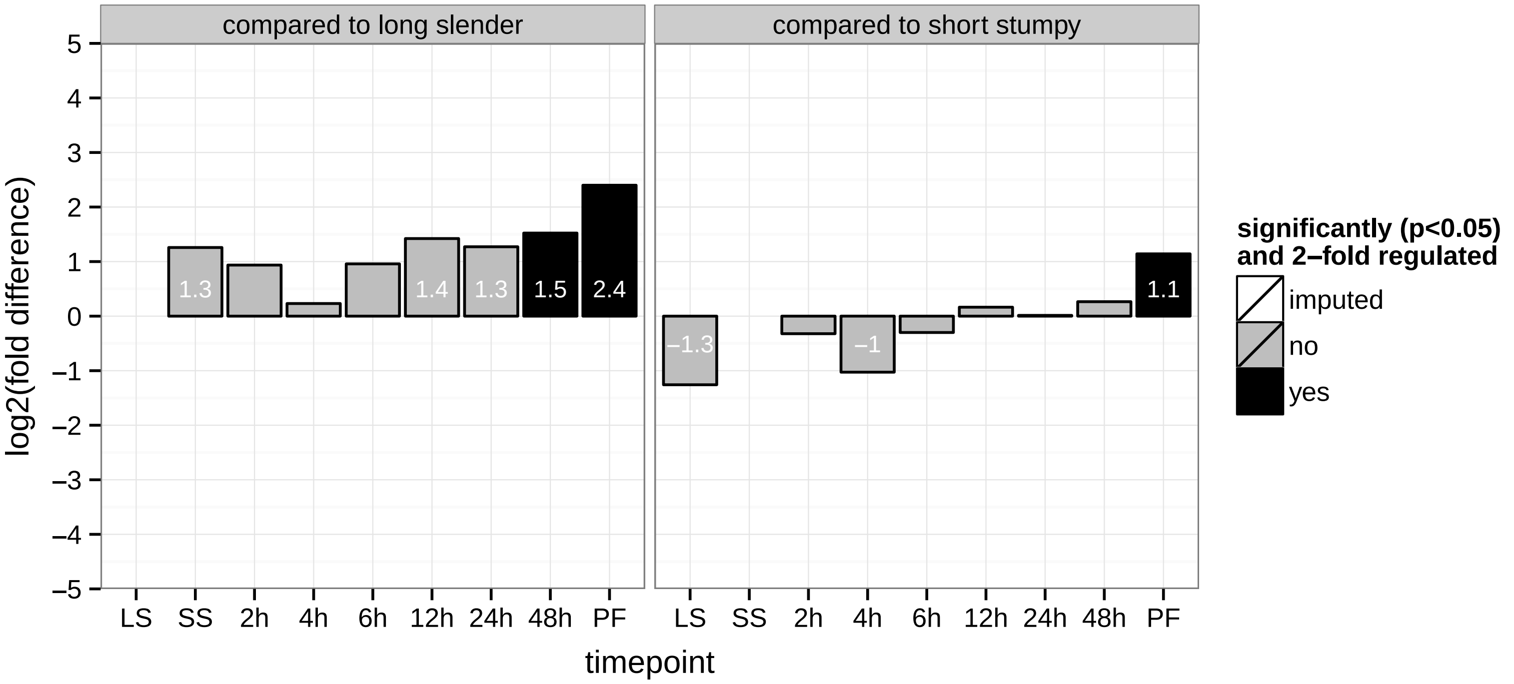
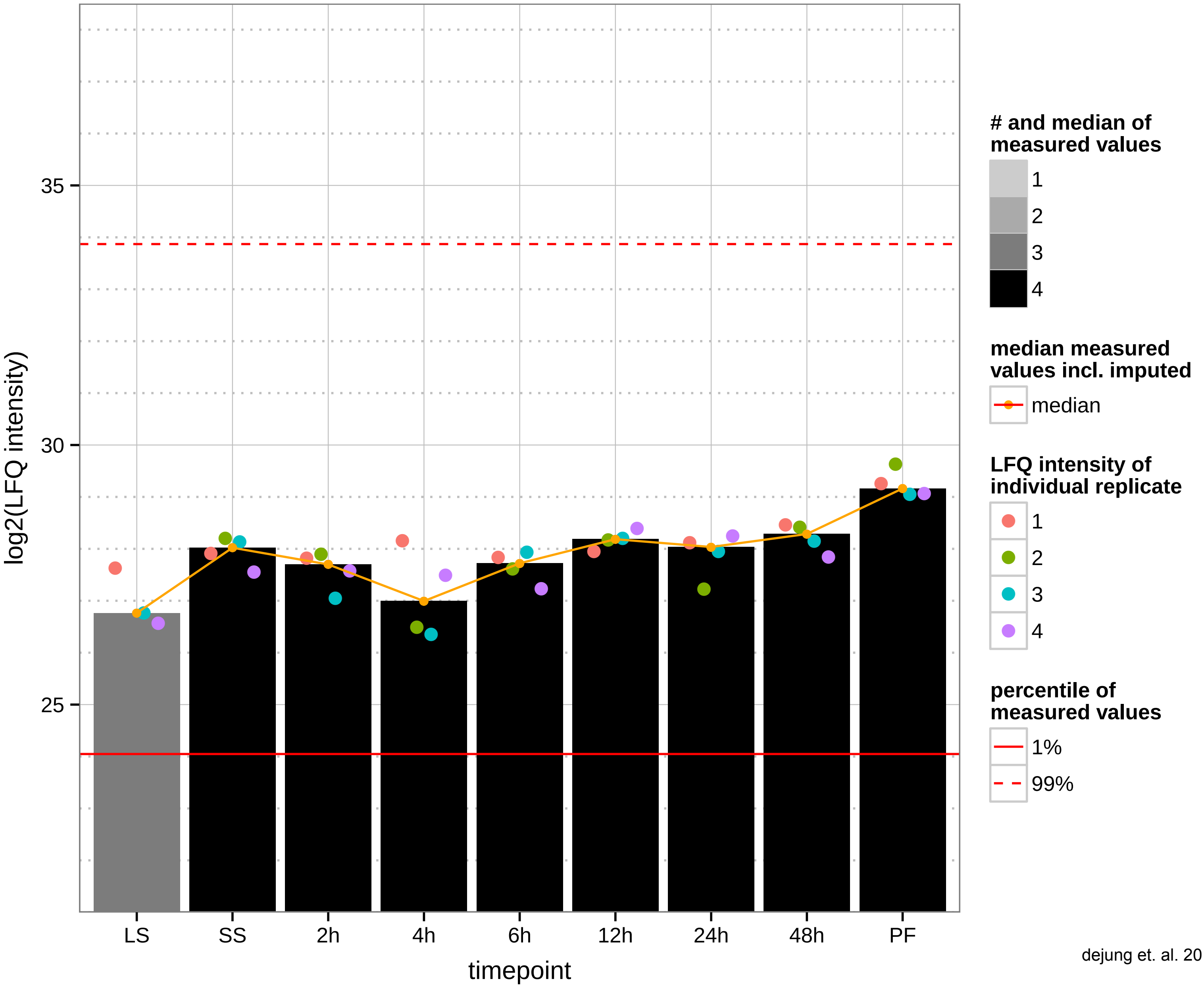
ATP–dependent RNA helicase, putative
Tb927.5.2290
AGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: null
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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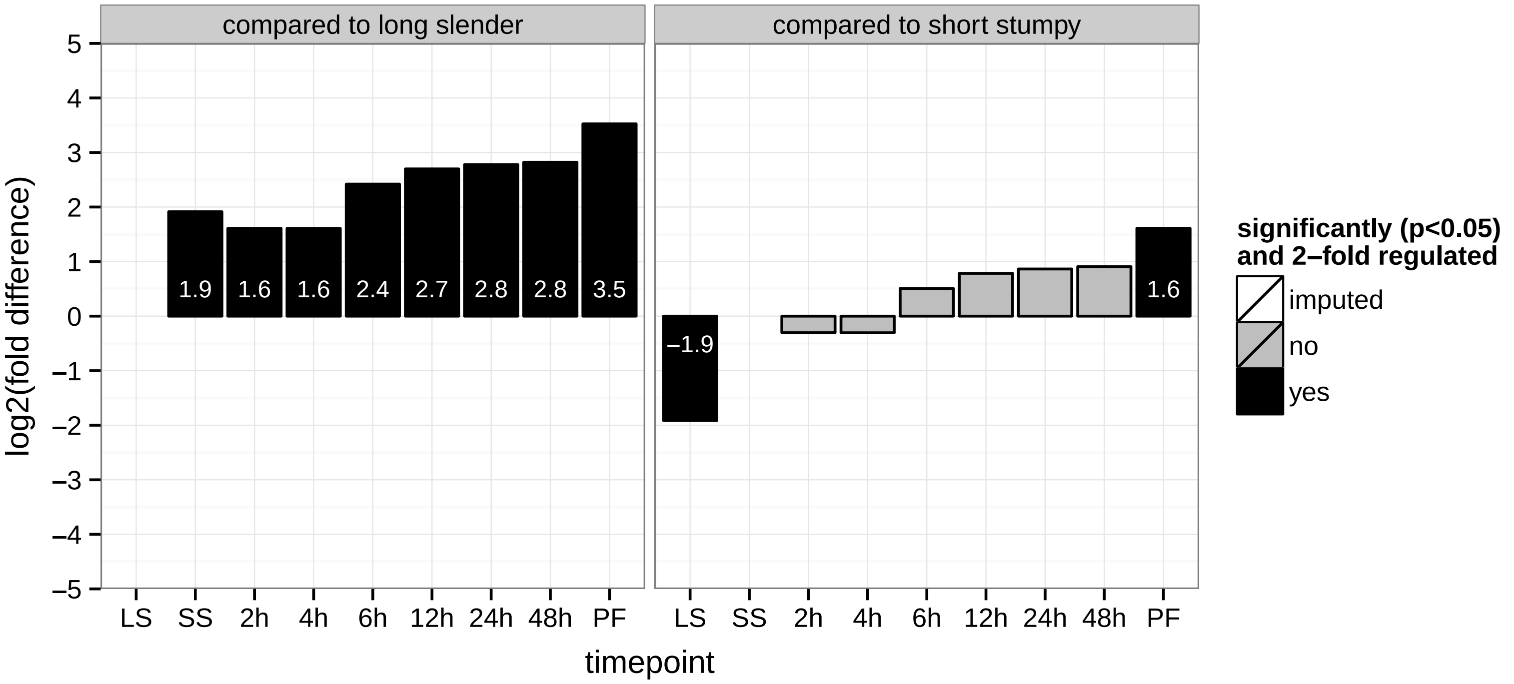
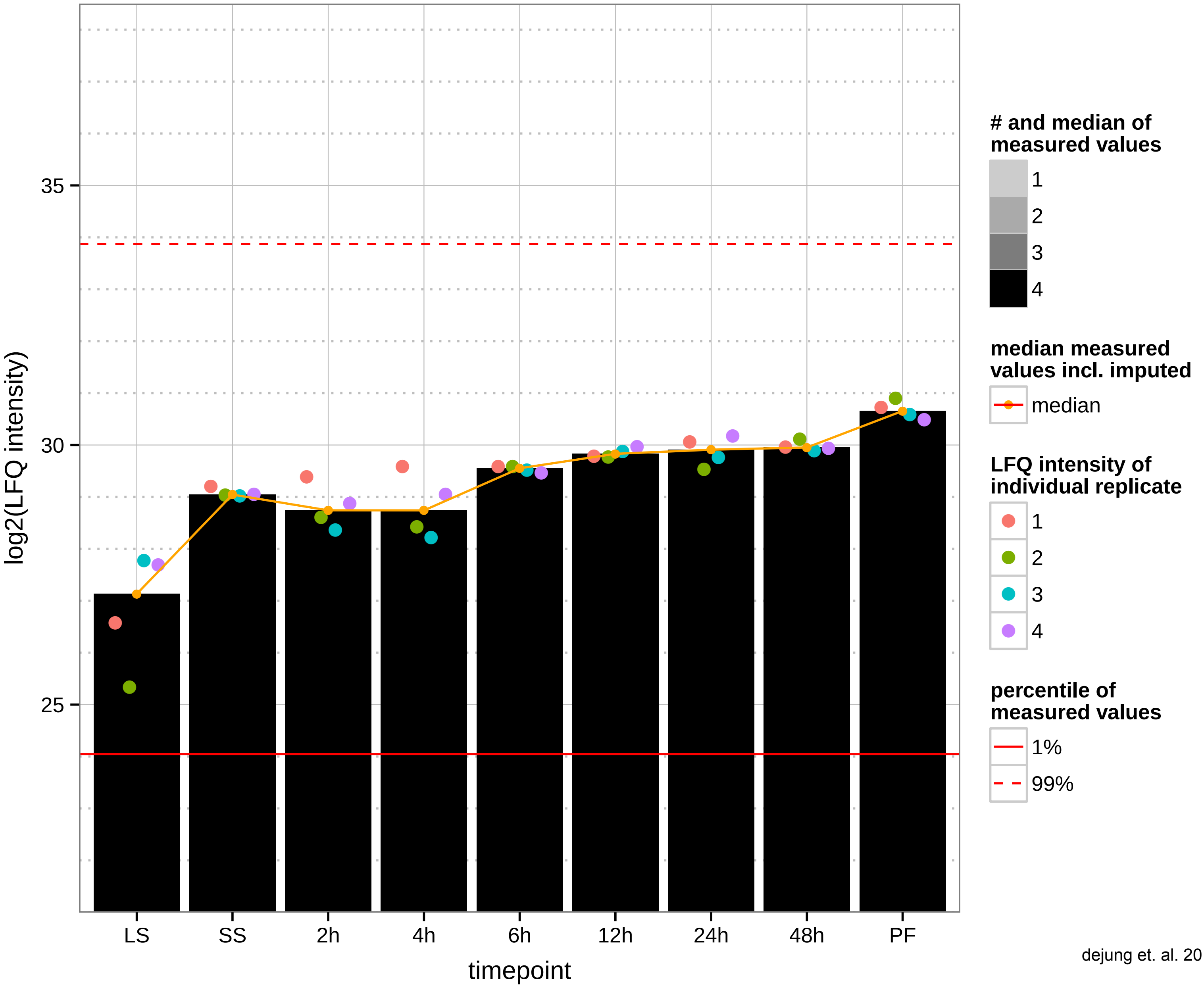
hypothetical protein, conserved
Tb927.5.2530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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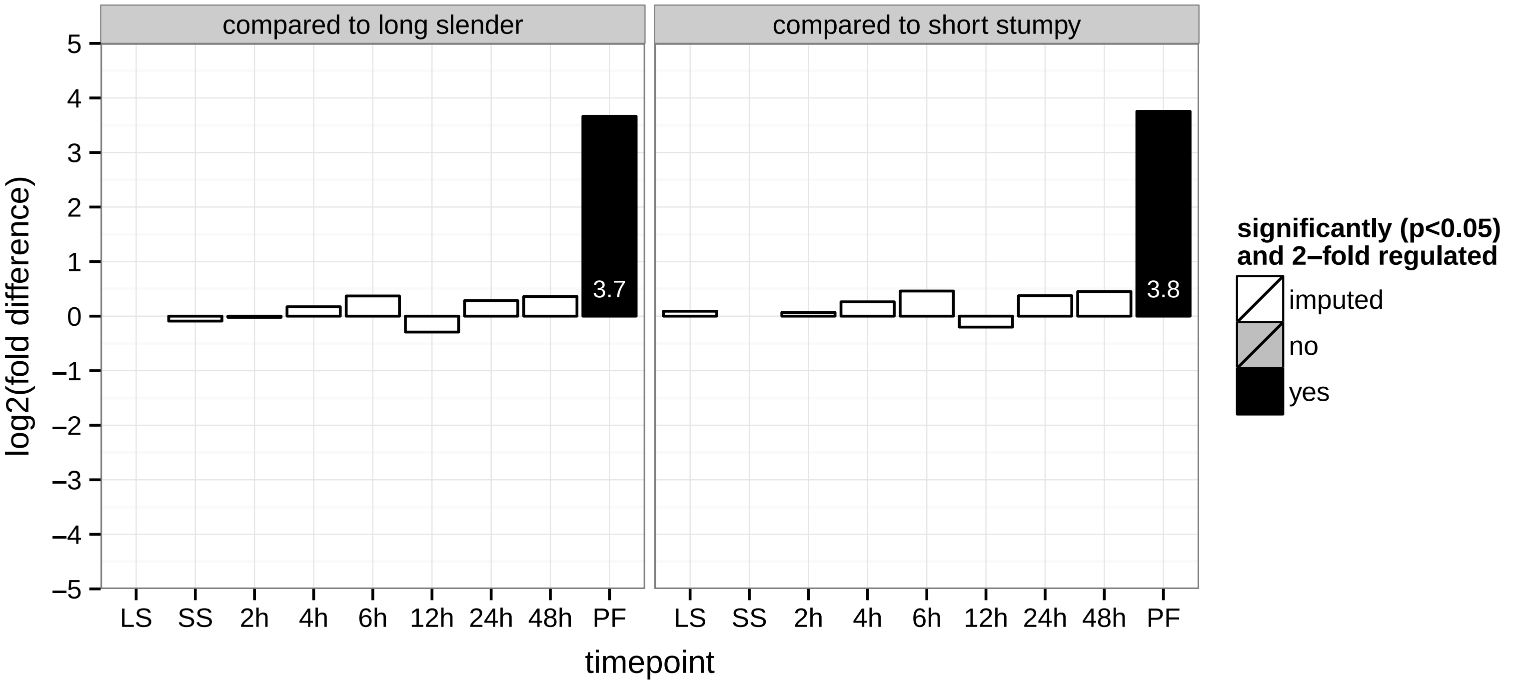
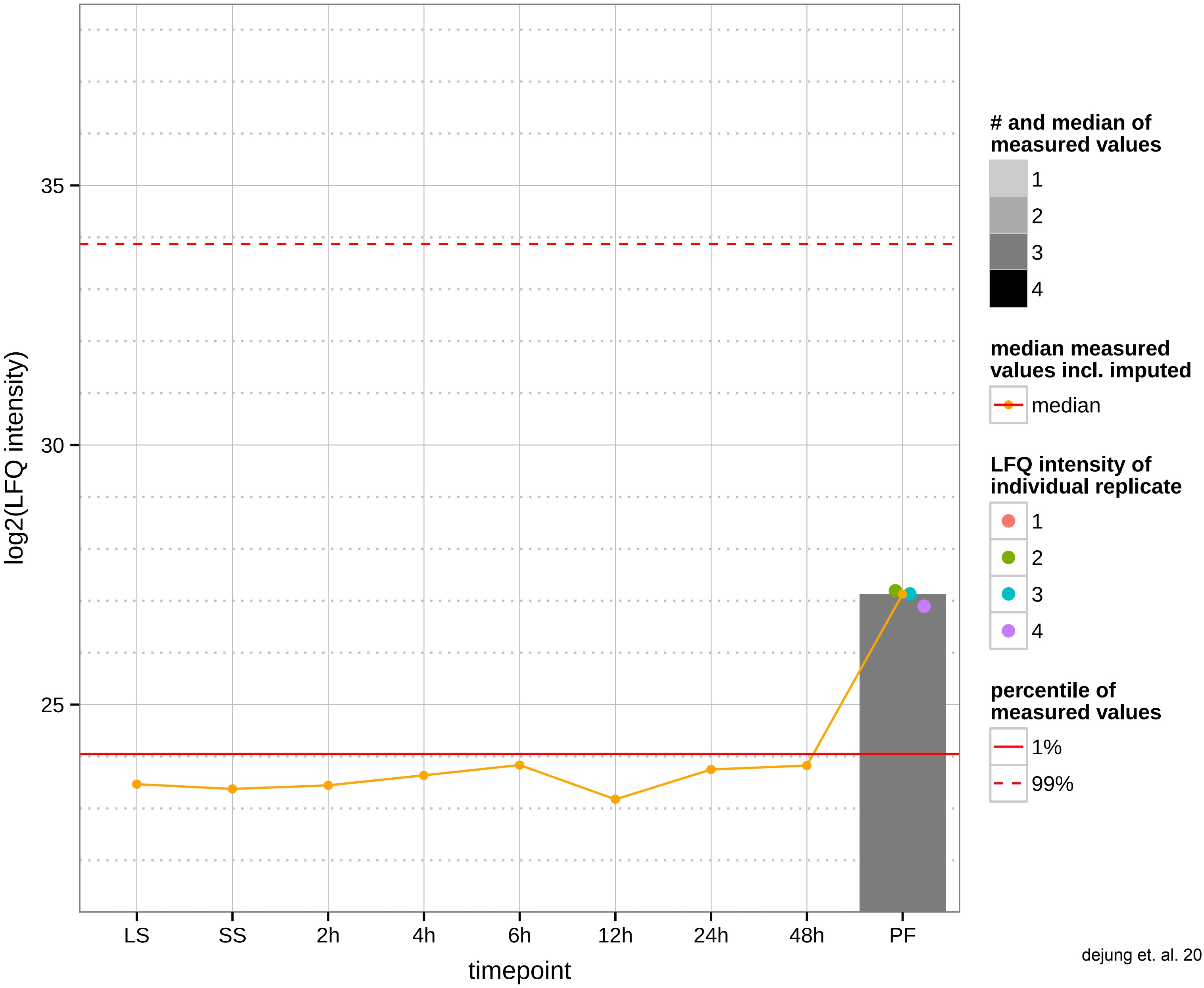
hypothetical protein, conserved
Tb927.5.2550
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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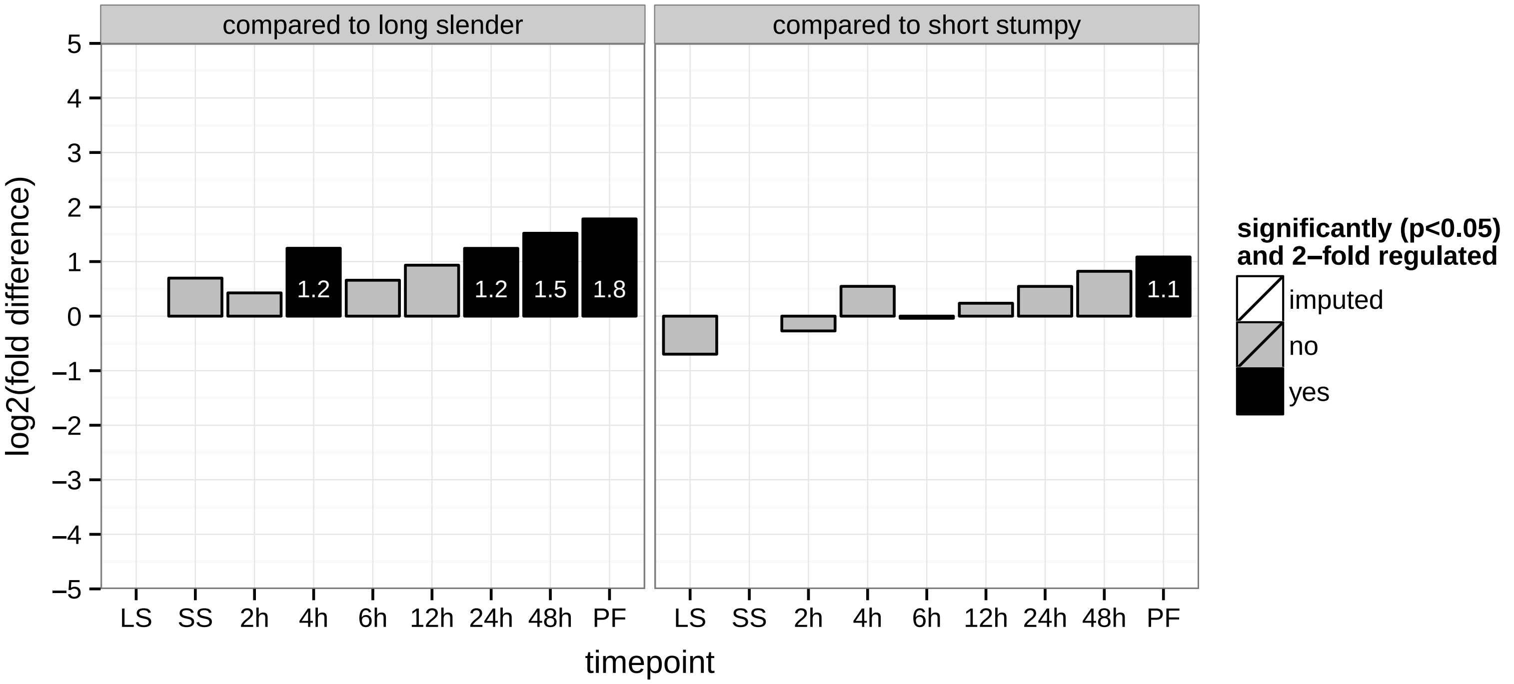
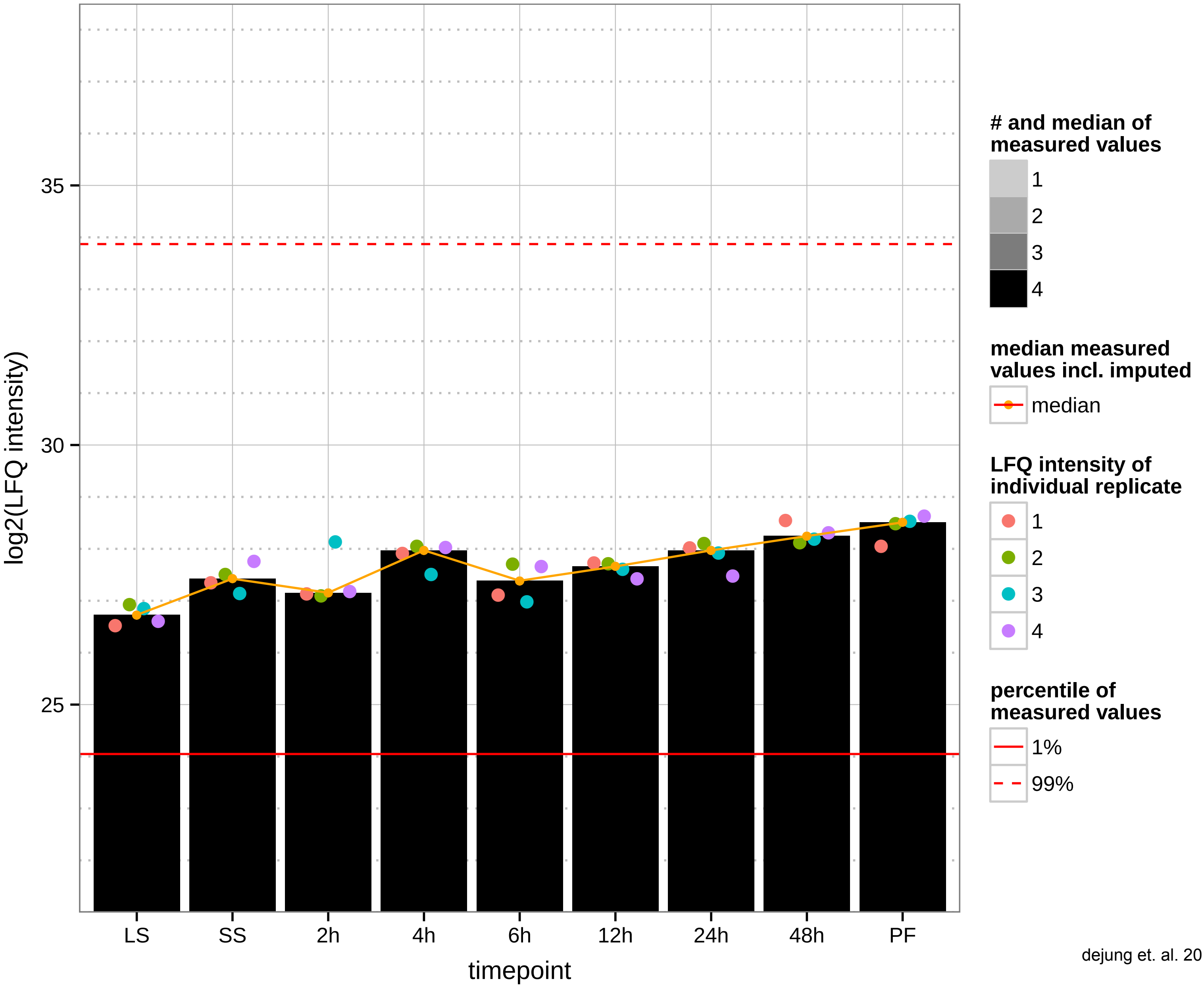
zinc–finger protein ZPR1, putative
Tb927.5.2720
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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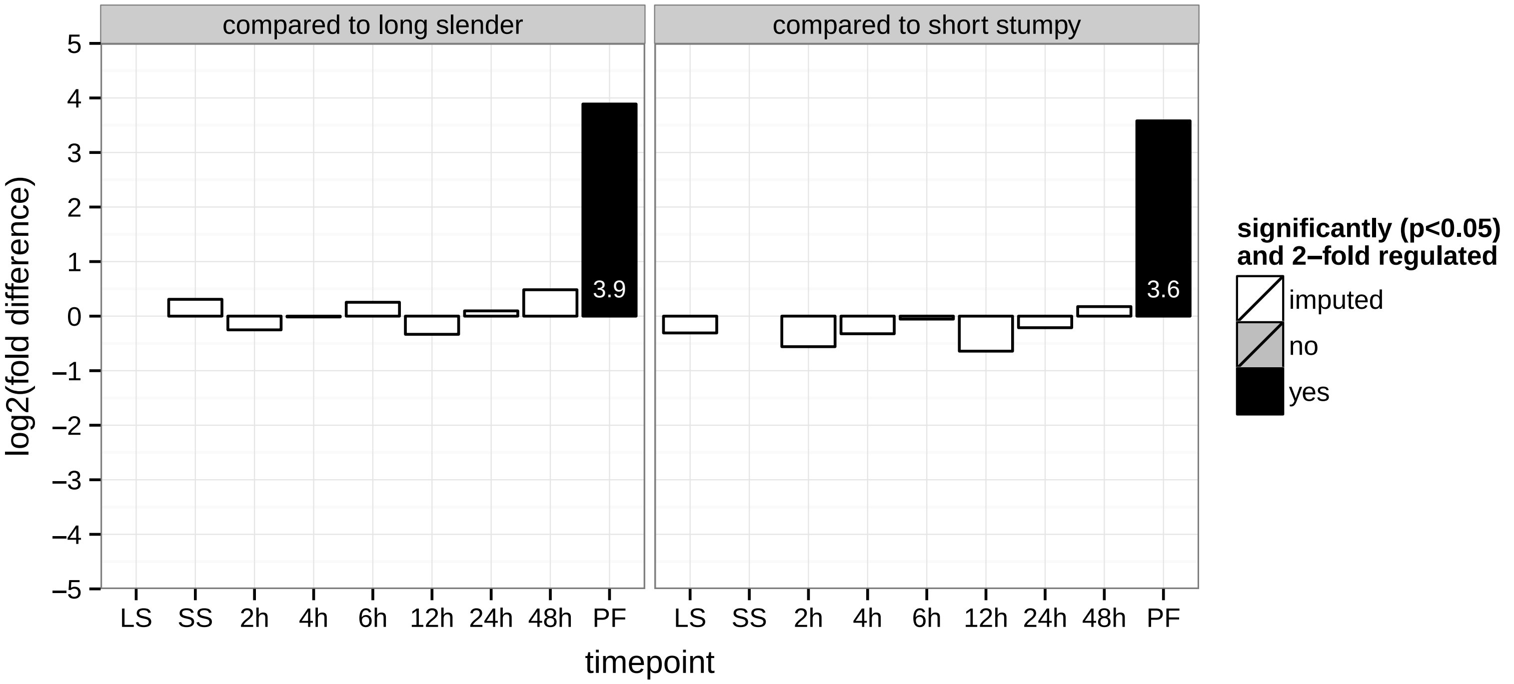
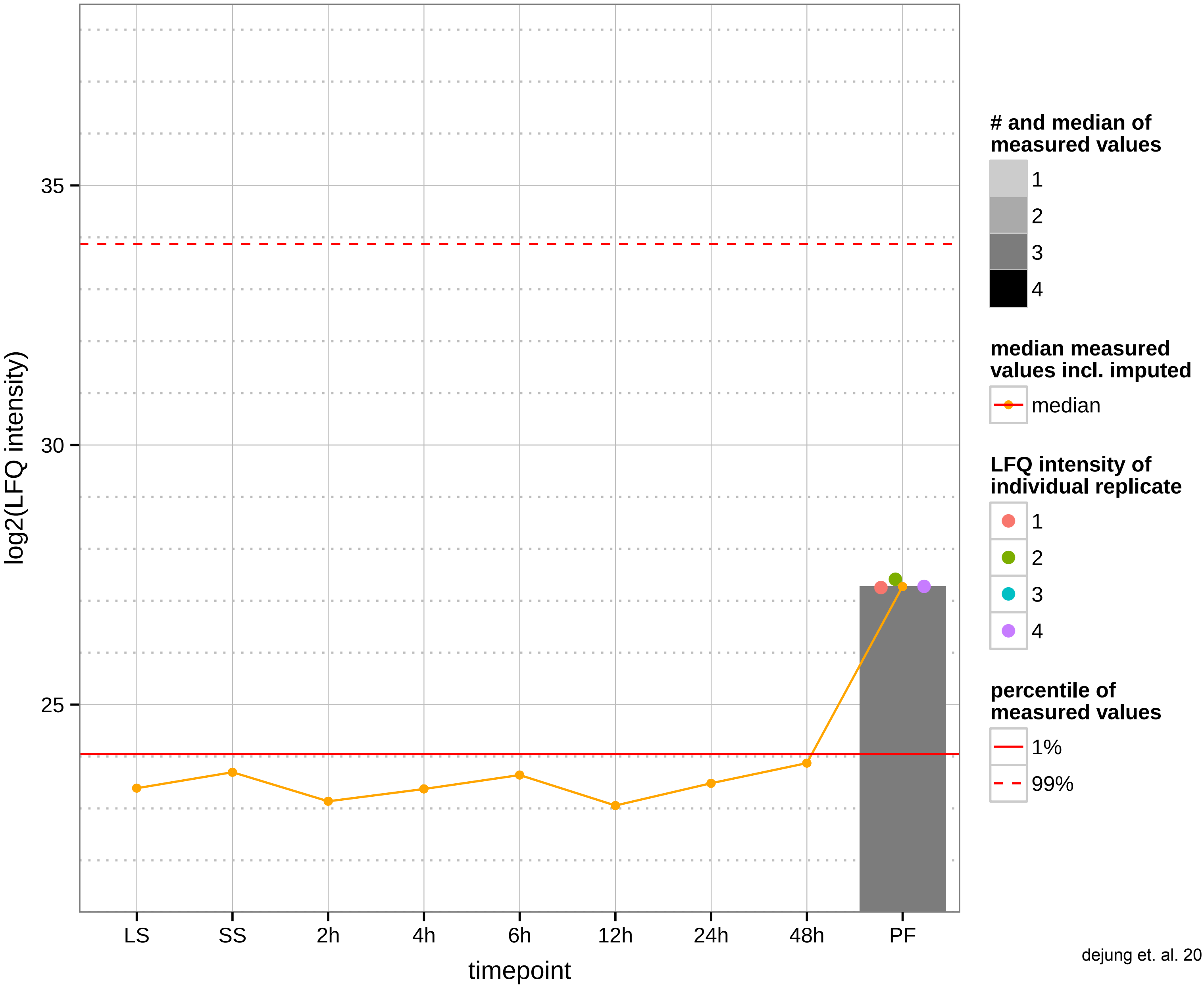
hypothetical protein, conserved
Tb927.5.2890
AGOF: ATP binding, ATPase activity
AGOC: null
AGOP: null
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding, protein binding
PGOC: null
PGOP: null





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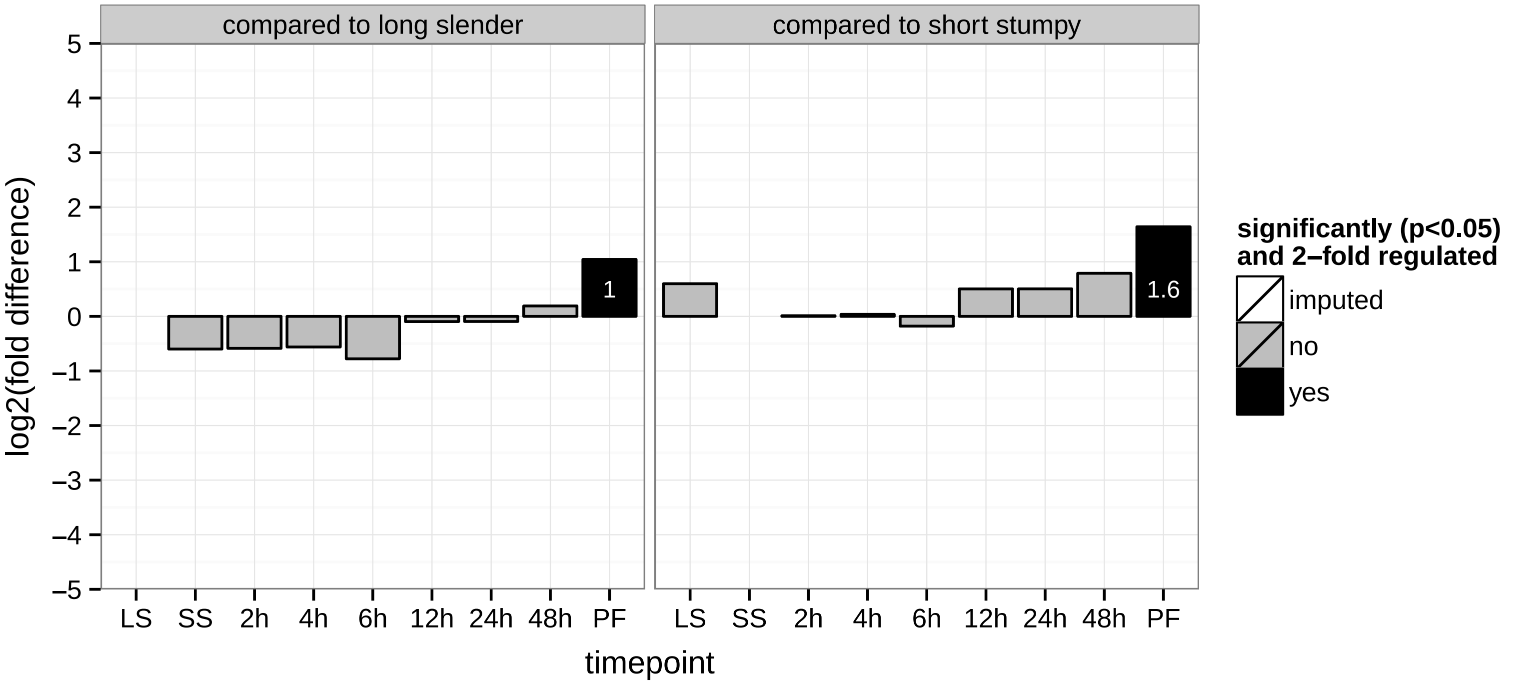
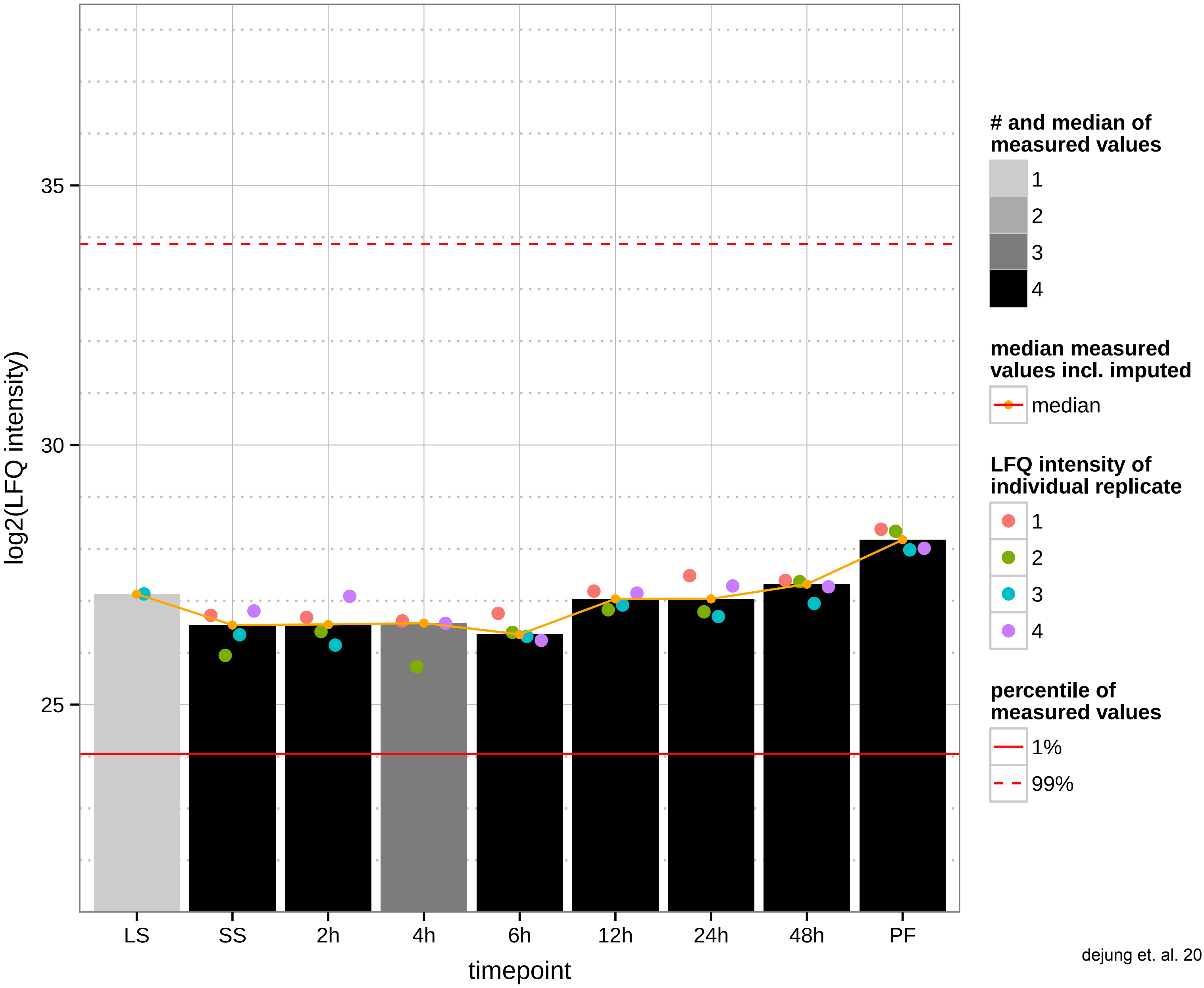
hypothetical protein, conserved
Tb927.5.3230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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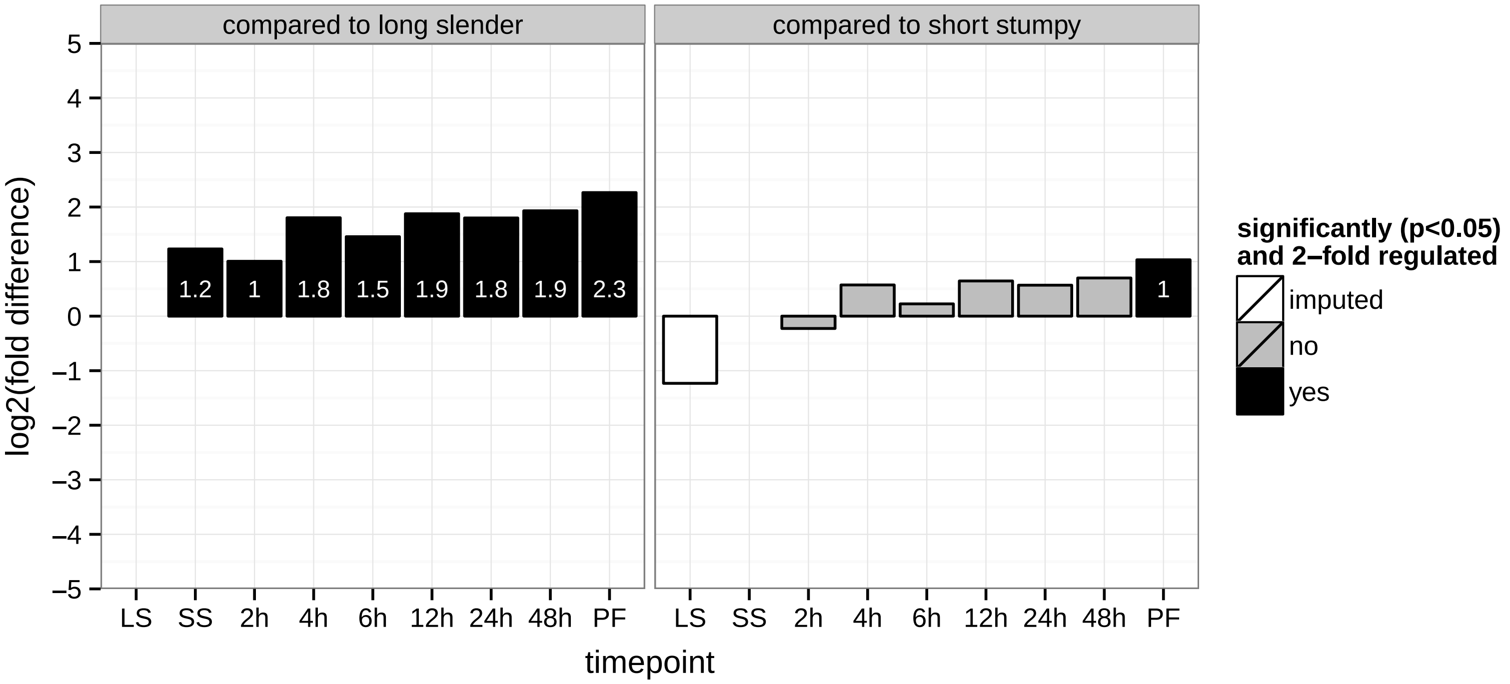
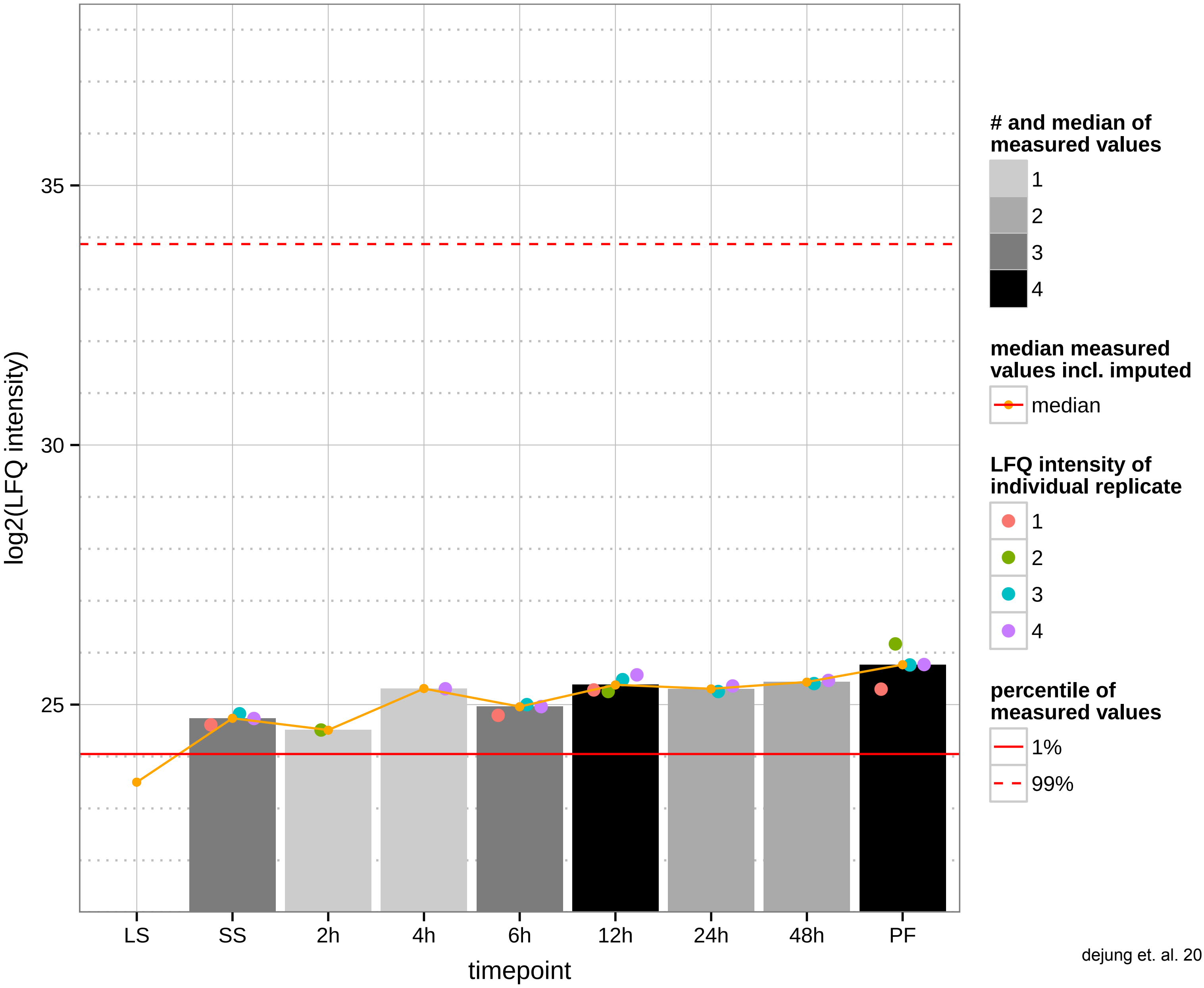
queuine tRNA–ribosyltransferase, putative
Tb927.5.3520
AGOF: queuine tRNA–ribosyltransferase activity
AGOC: null
AGOP: queuosine biosynthetic process
PGOF: queuine tRNA–ribosyltransferase activity
PGOC: null
PGOP: queuosine biosynthetic process, tRNA modification





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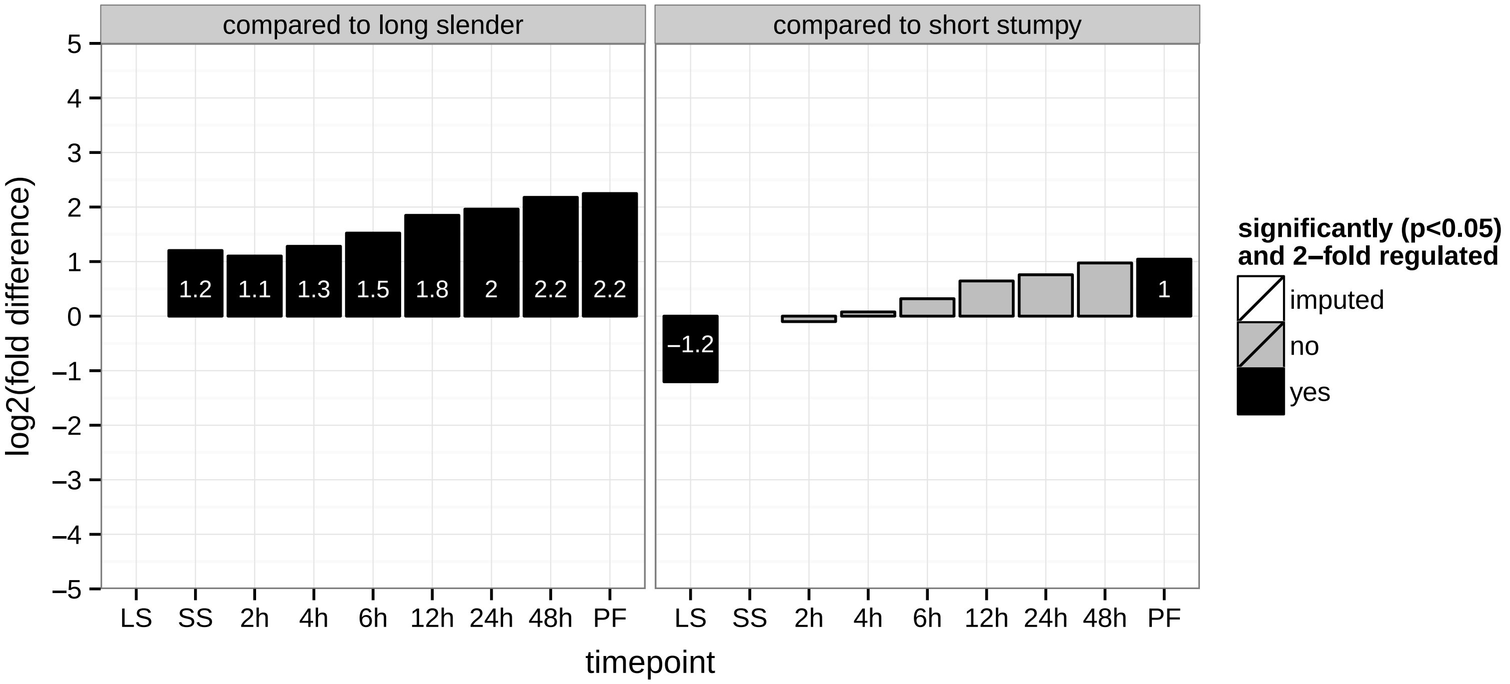
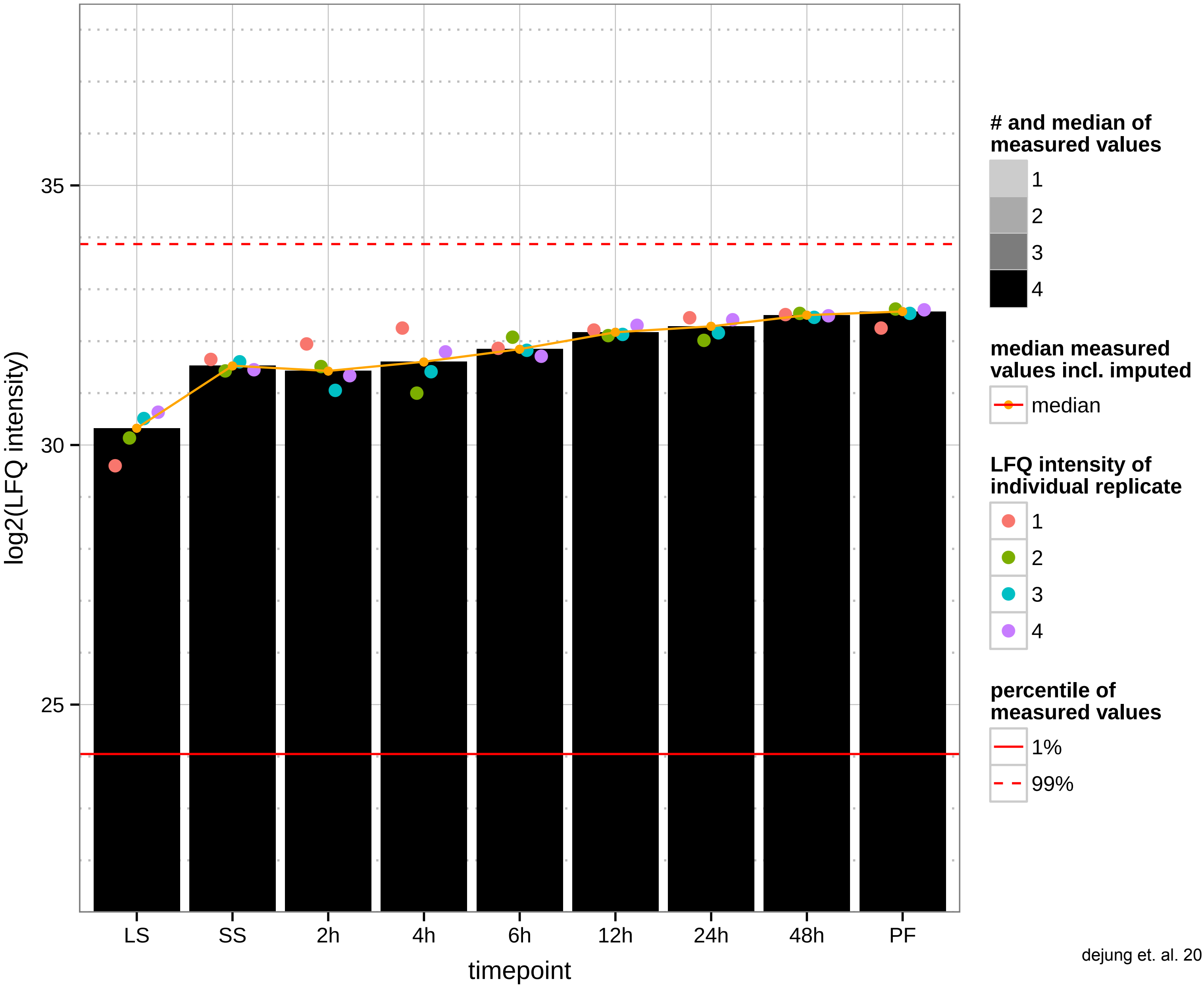
glutamine hydrolysing (not ammonia–dependent) carbomoyl phosphate synthase, putative
Tb927.5.3800
AGOF: ATP binding, argininosuccinate synthase activity
AGOC: null
AGOP: arginine biosynthetic process, glutamine metabolic process, nitrogen compound metabolic process
PGOF: ATP binding, argininosuccinate synthase activity, catalytic activity, metal ion binding
PGOC: null
PGOP: arginine biosynthetic process, carbamoyl phosphate biosynthetic process, glutamine catabolic process, metabolic proc





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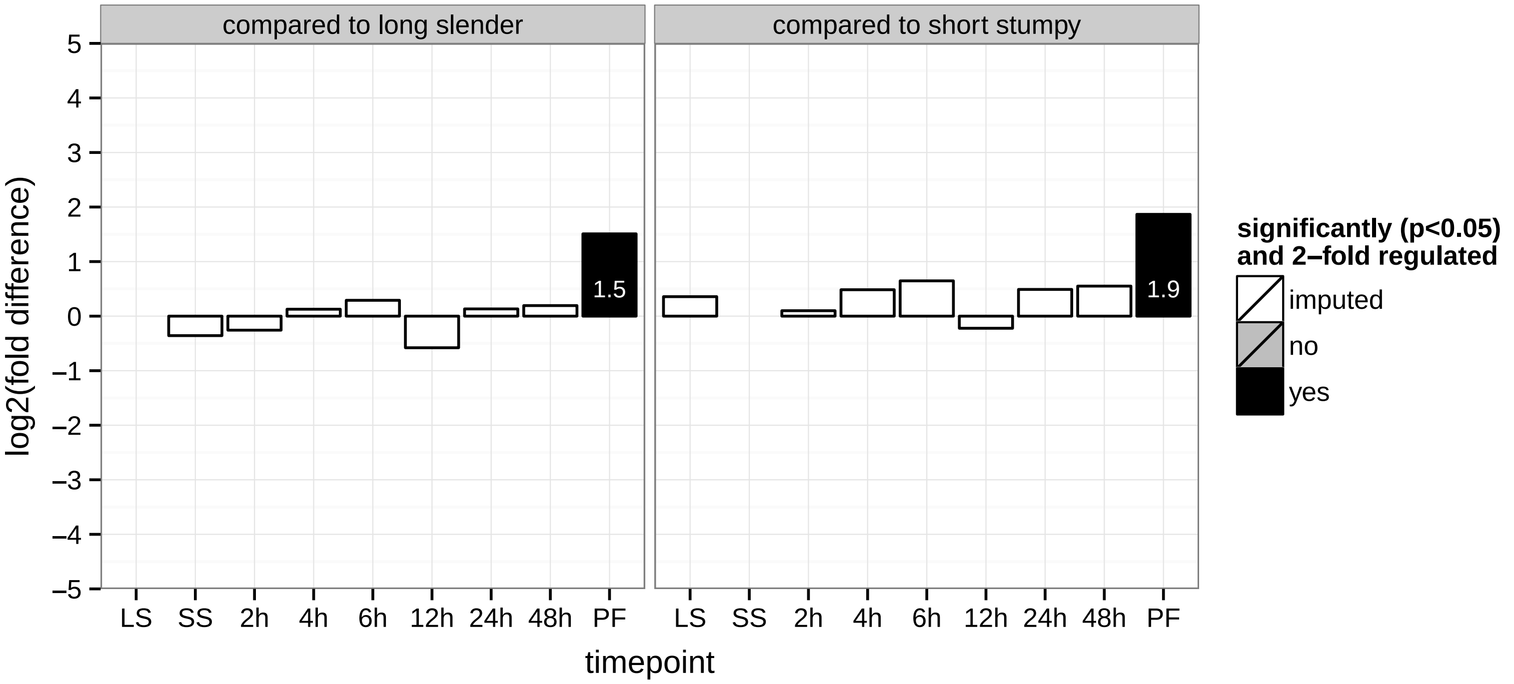
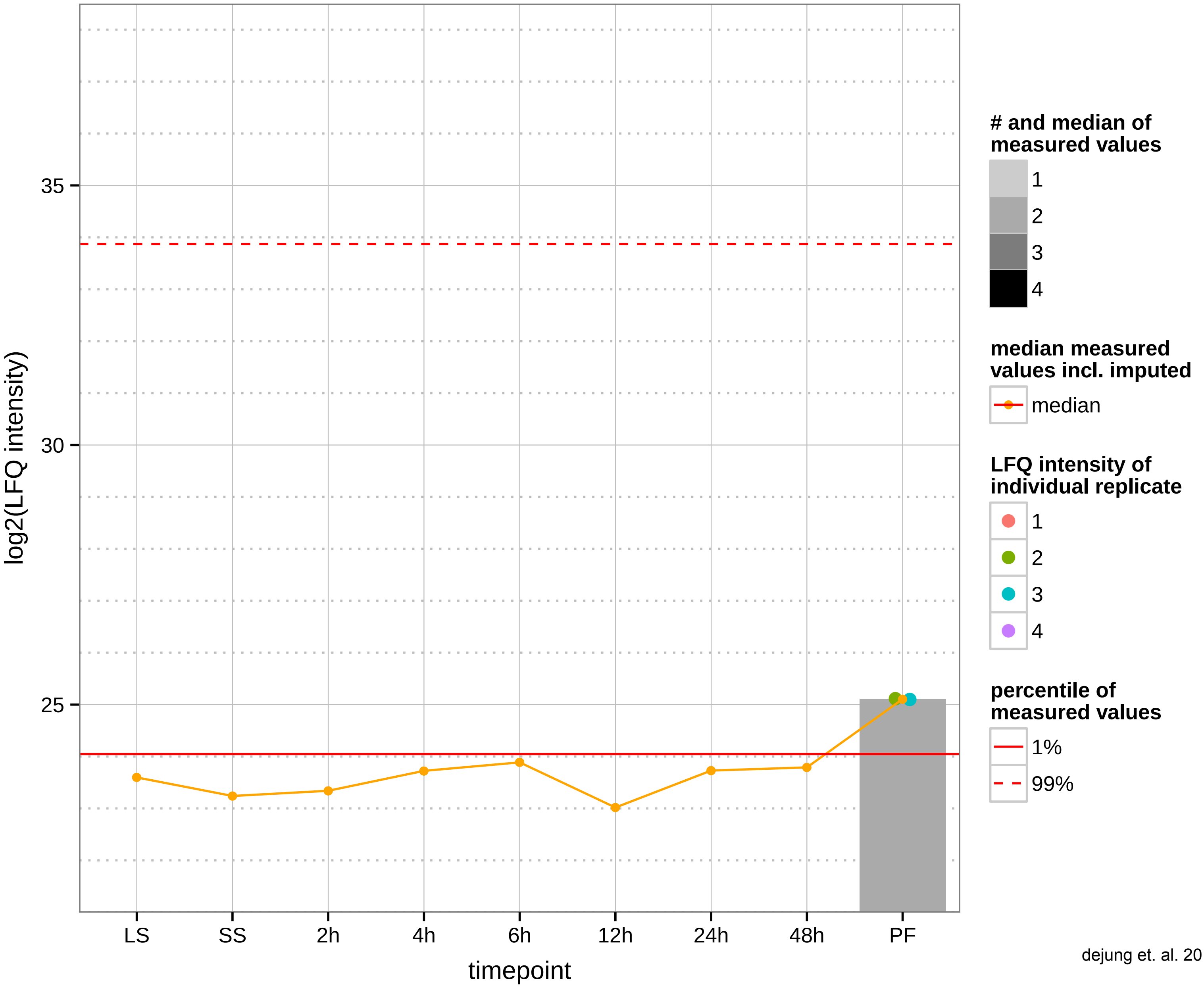
tubulin tyrosine ligase, putative
Tb927.5.3860
AGOF: tubulin−tyrosine ligase activity
AGOC: null
AGOP: cellular protein modification process
PGOF: tubulin−tyrosine ligase activity
PGOC: null
PGOP: cellular protein modification process





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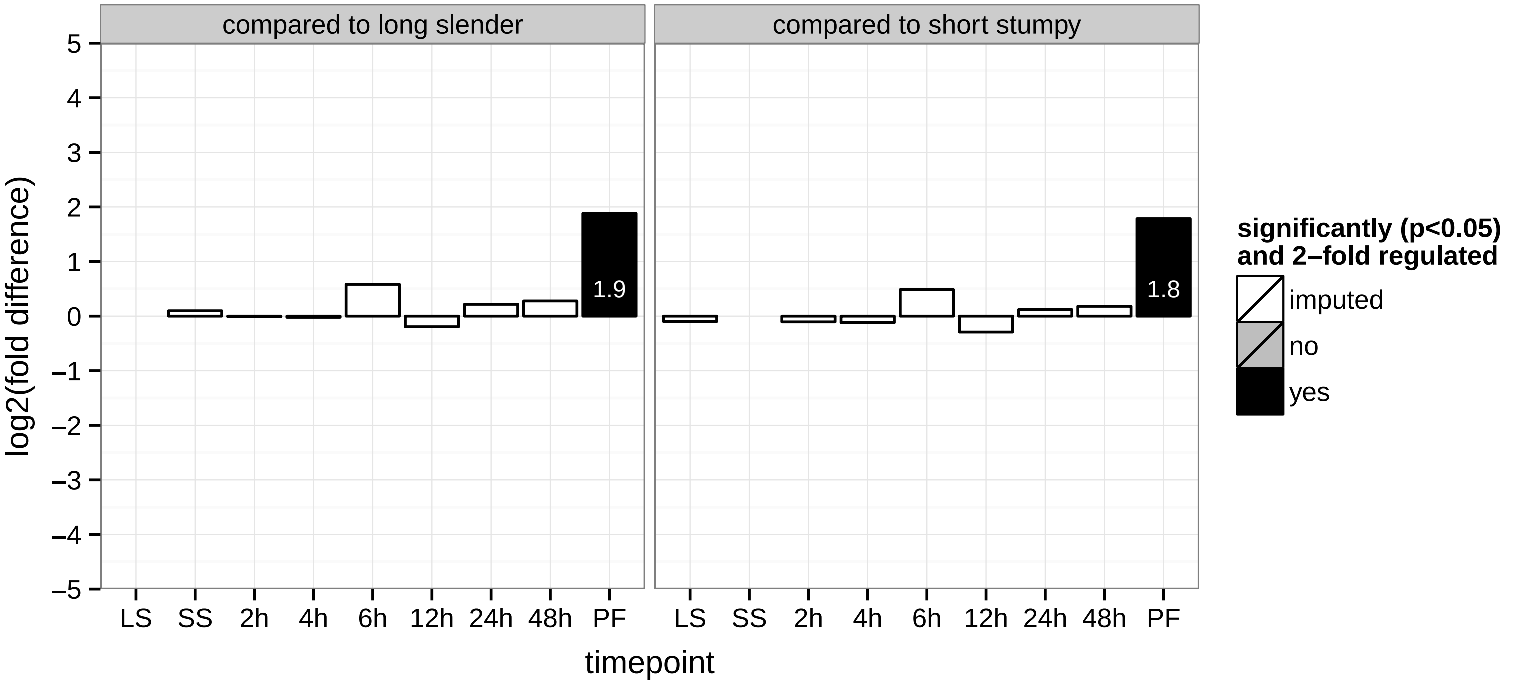
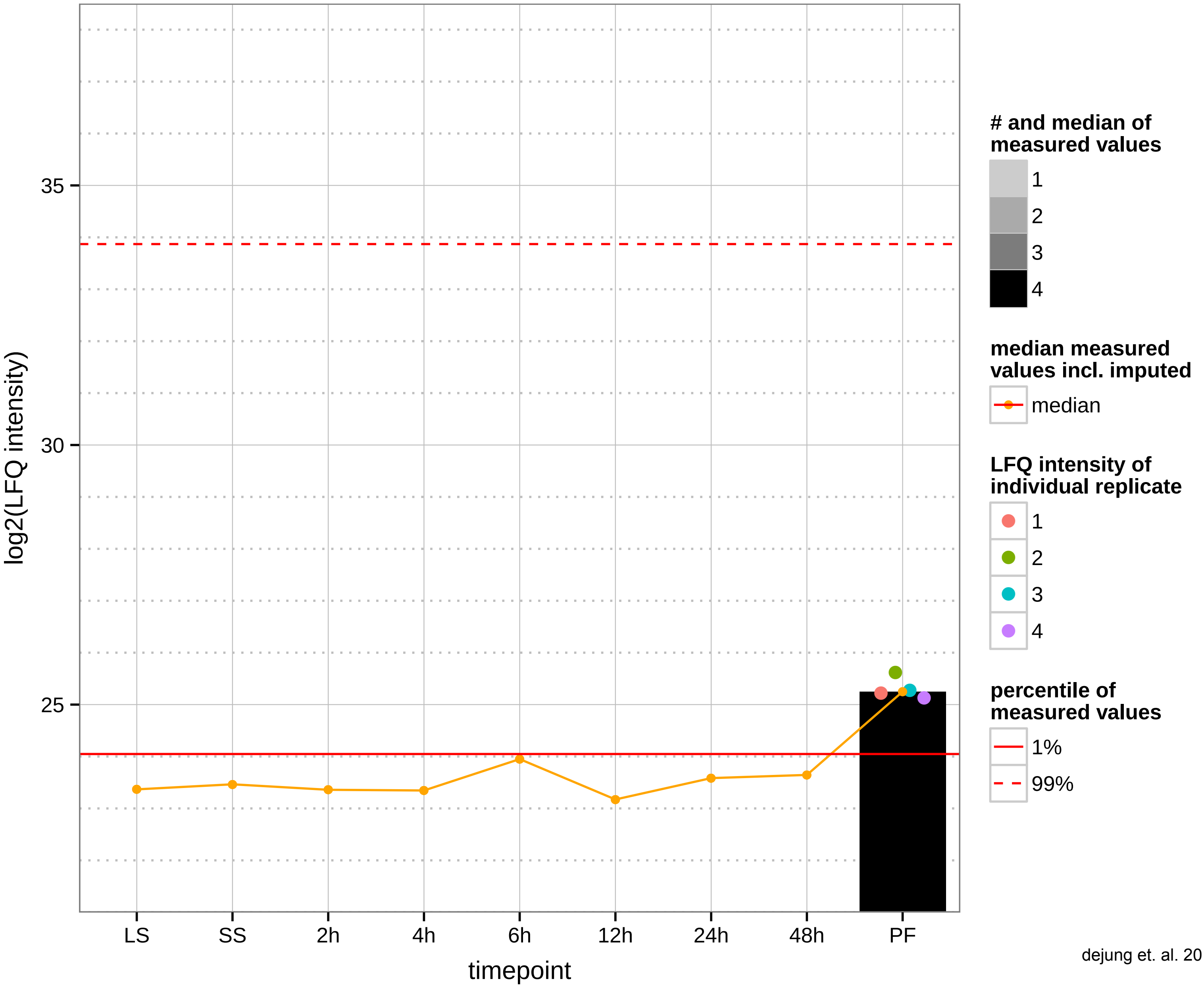
hypothetical protein, conserved
Tb927.5.4060
AGOF: null
AGOC: integral to membrane
AGOP: protein processing
PGOF: null
PGOC: integral to membrane
PGOP: protein processing





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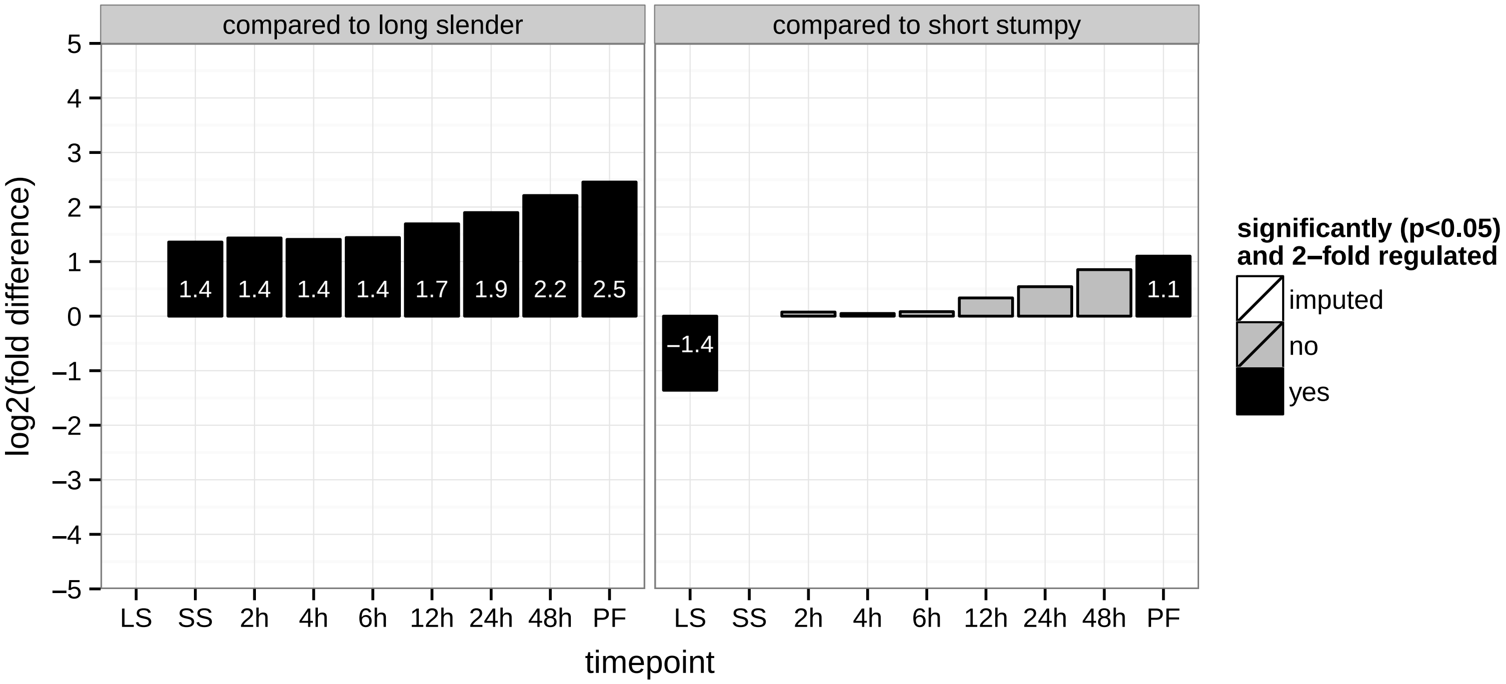
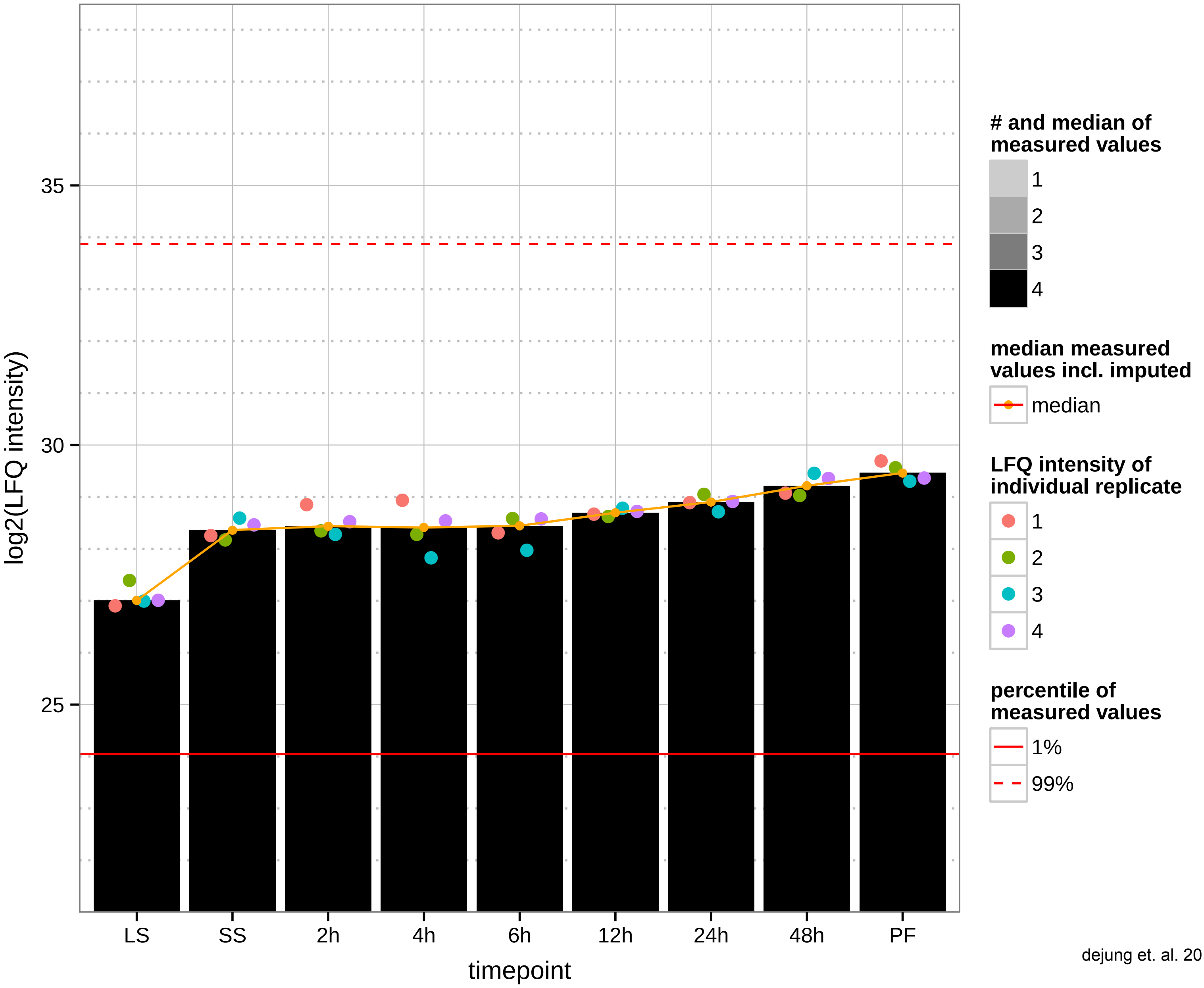
stomatin–like protein, putative
Tb927.5.520
AGOF: null
AGOC: integral to membrane, membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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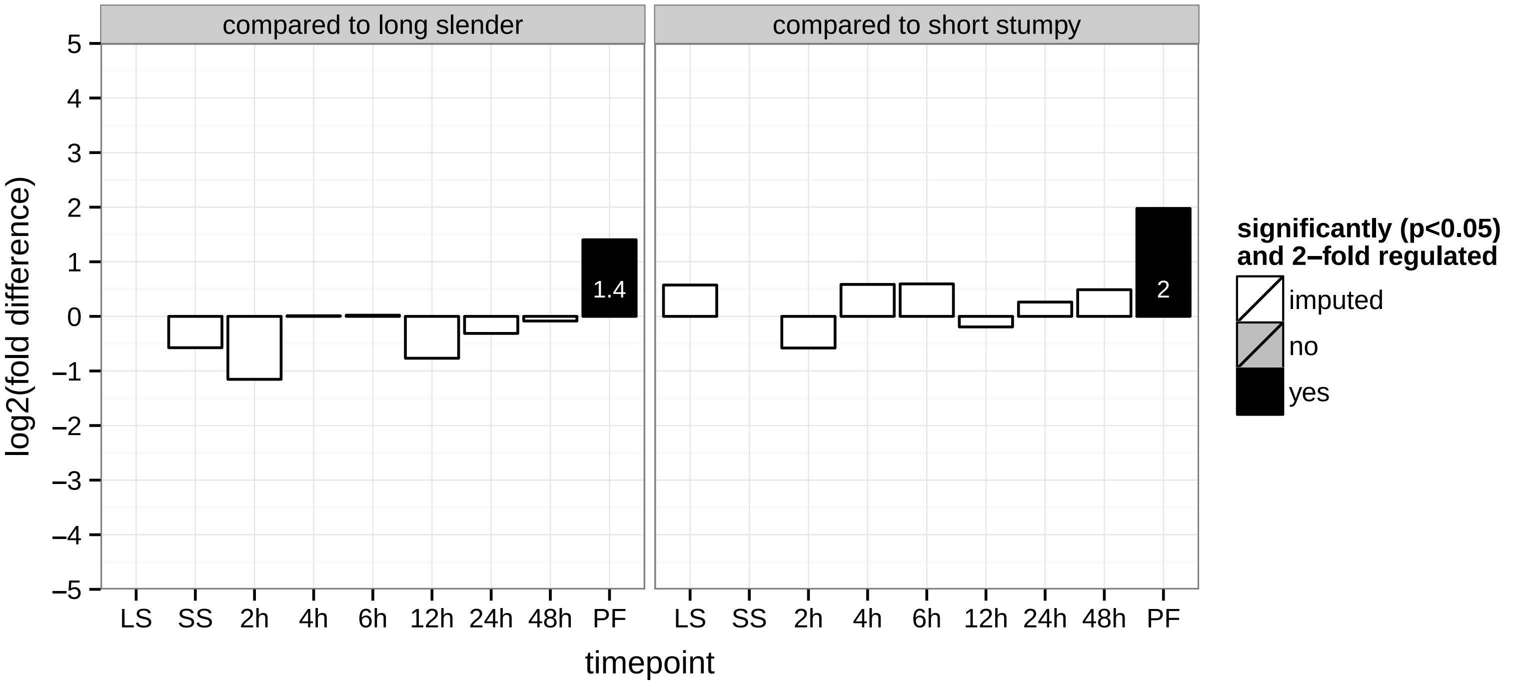
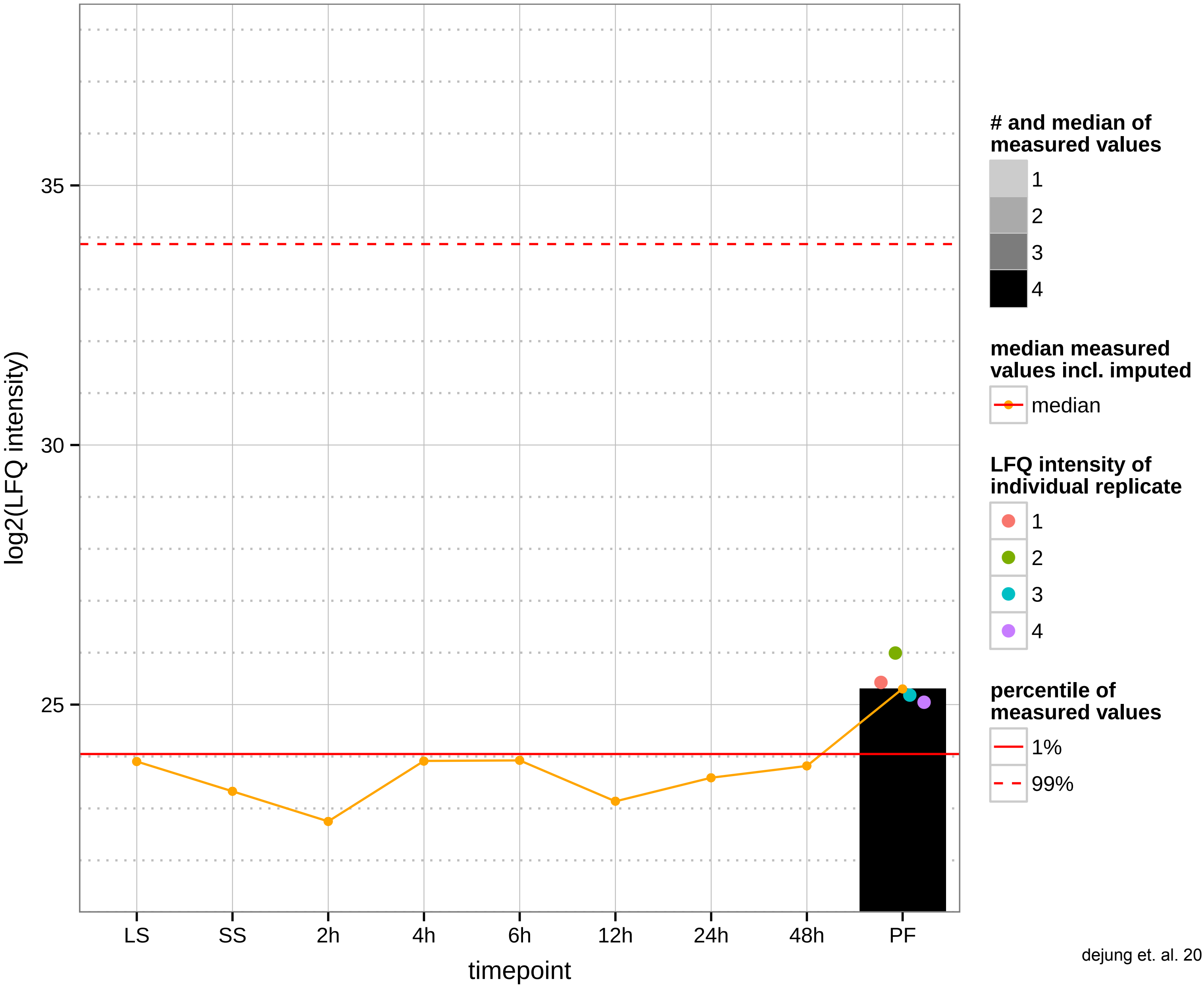
hypothetical protein, conserved
Tb927.5.600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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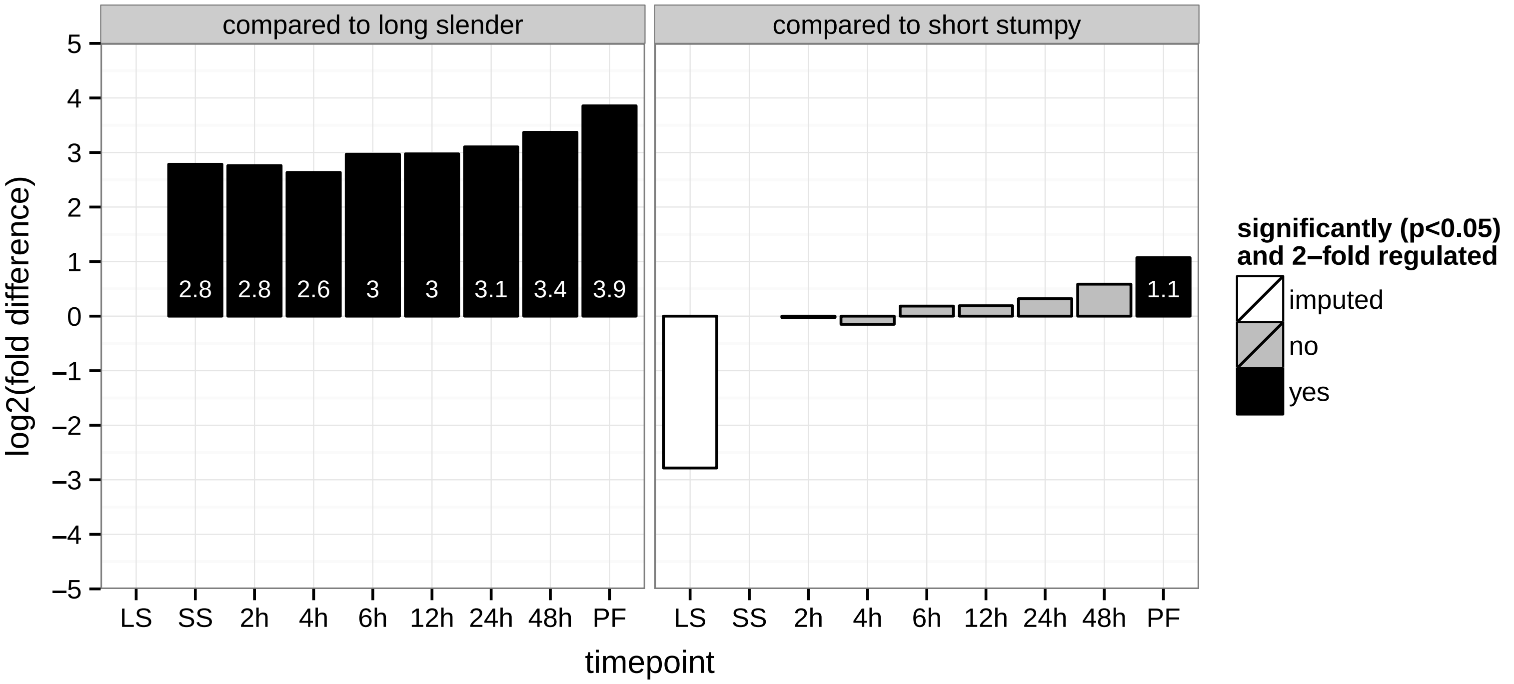
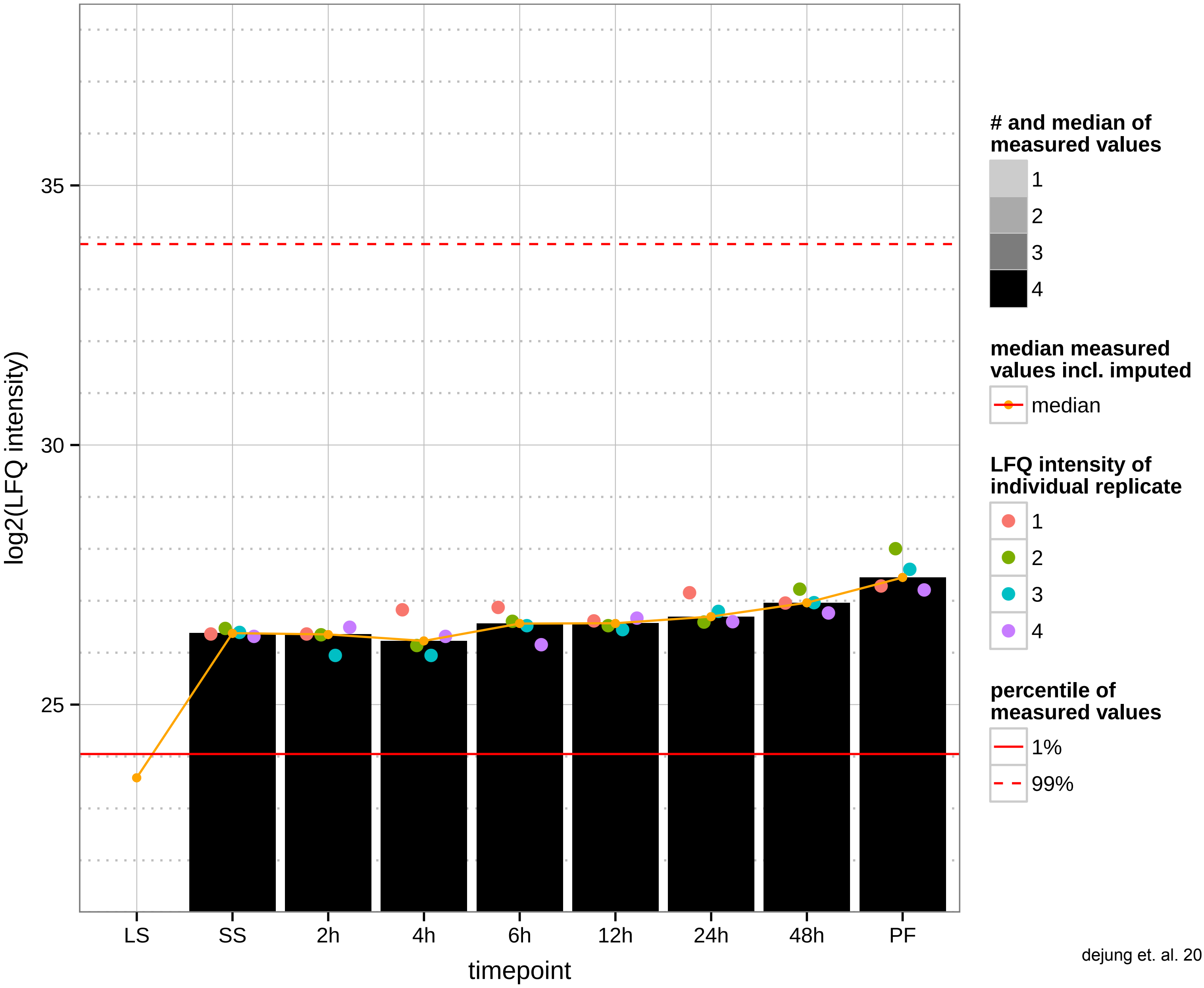
hypothetical protein, conserved
Tb927.6.1200
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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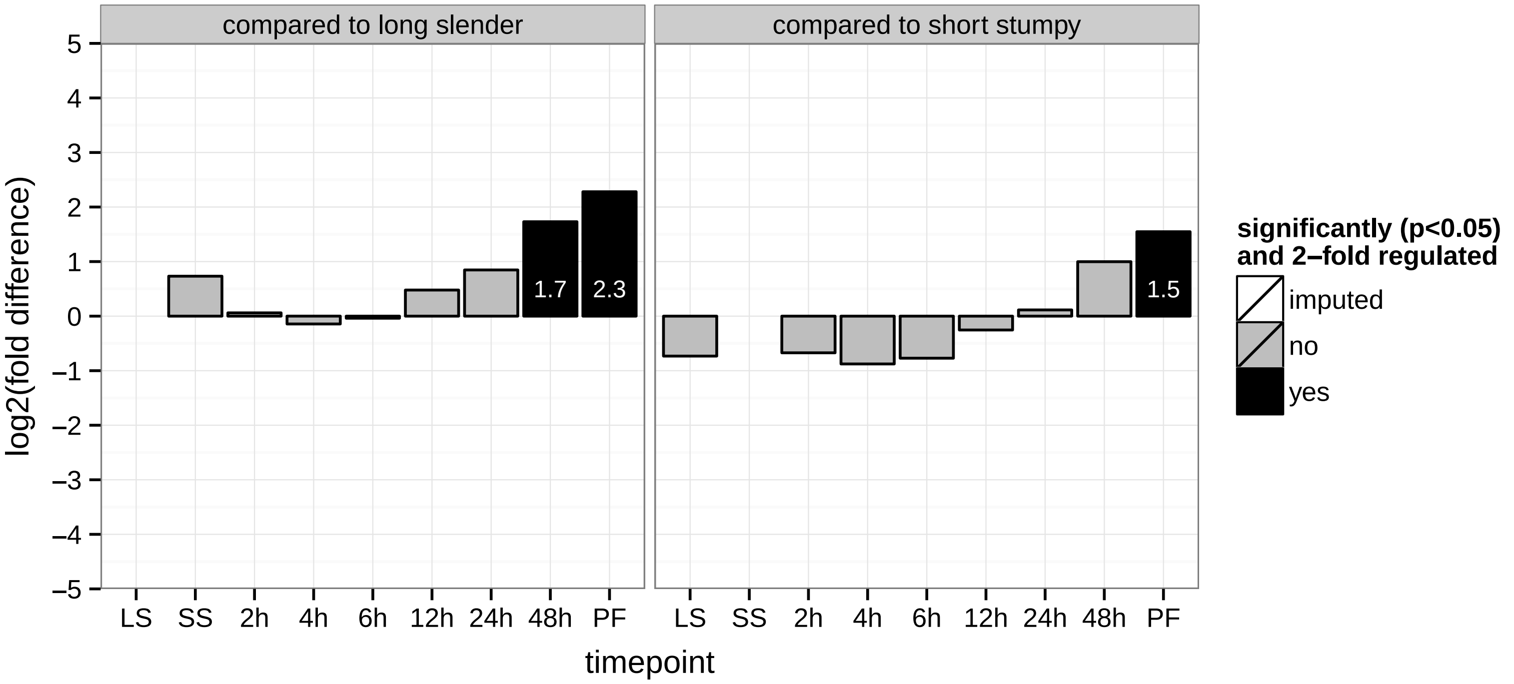
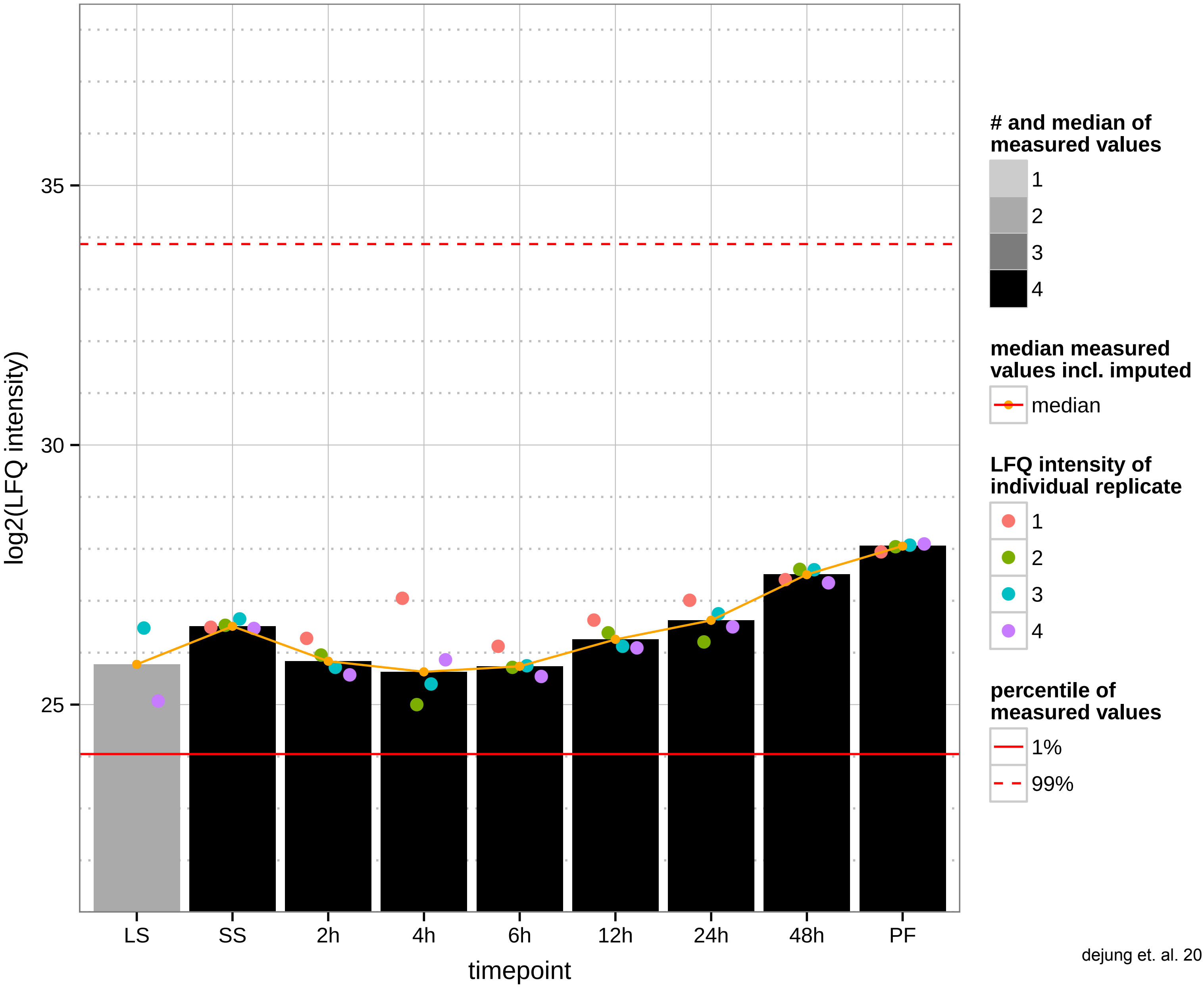
hypothetical protein, conserved
Tb927.6.1290
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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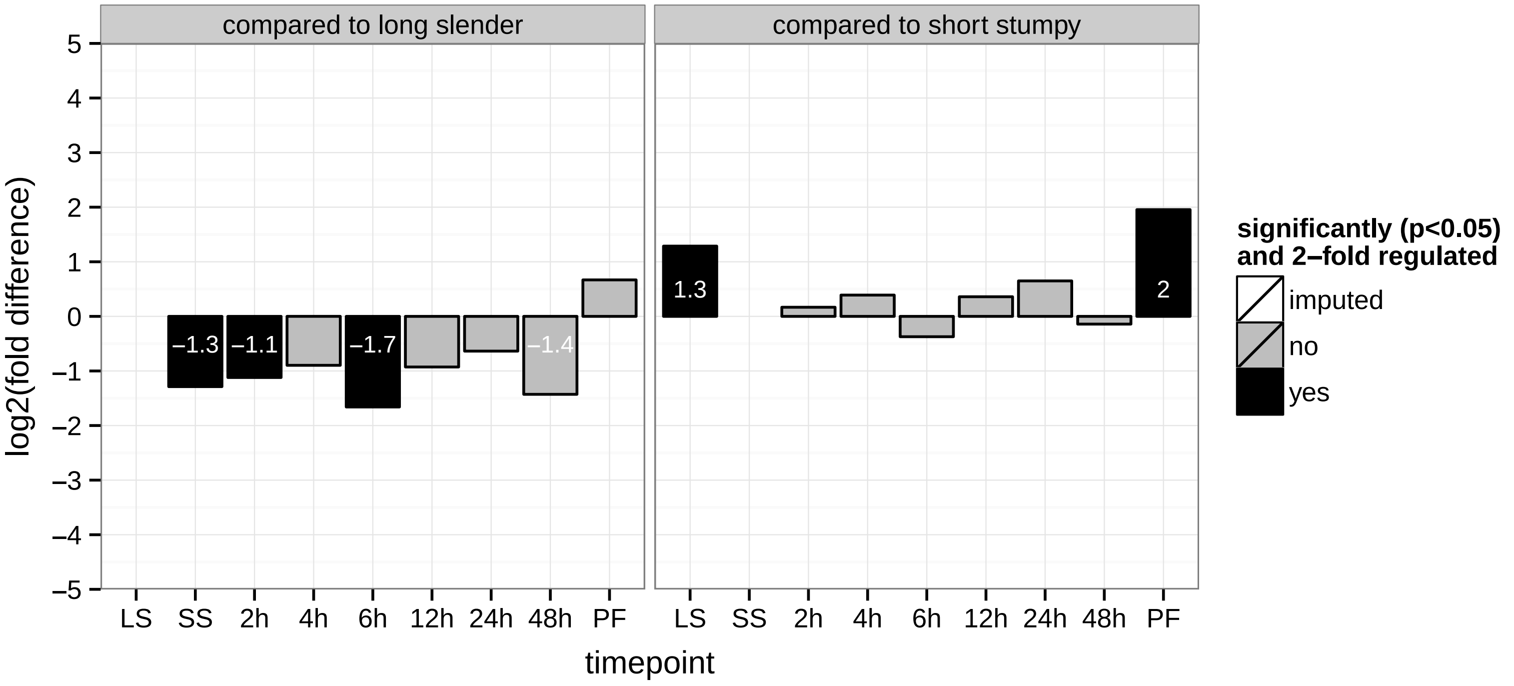
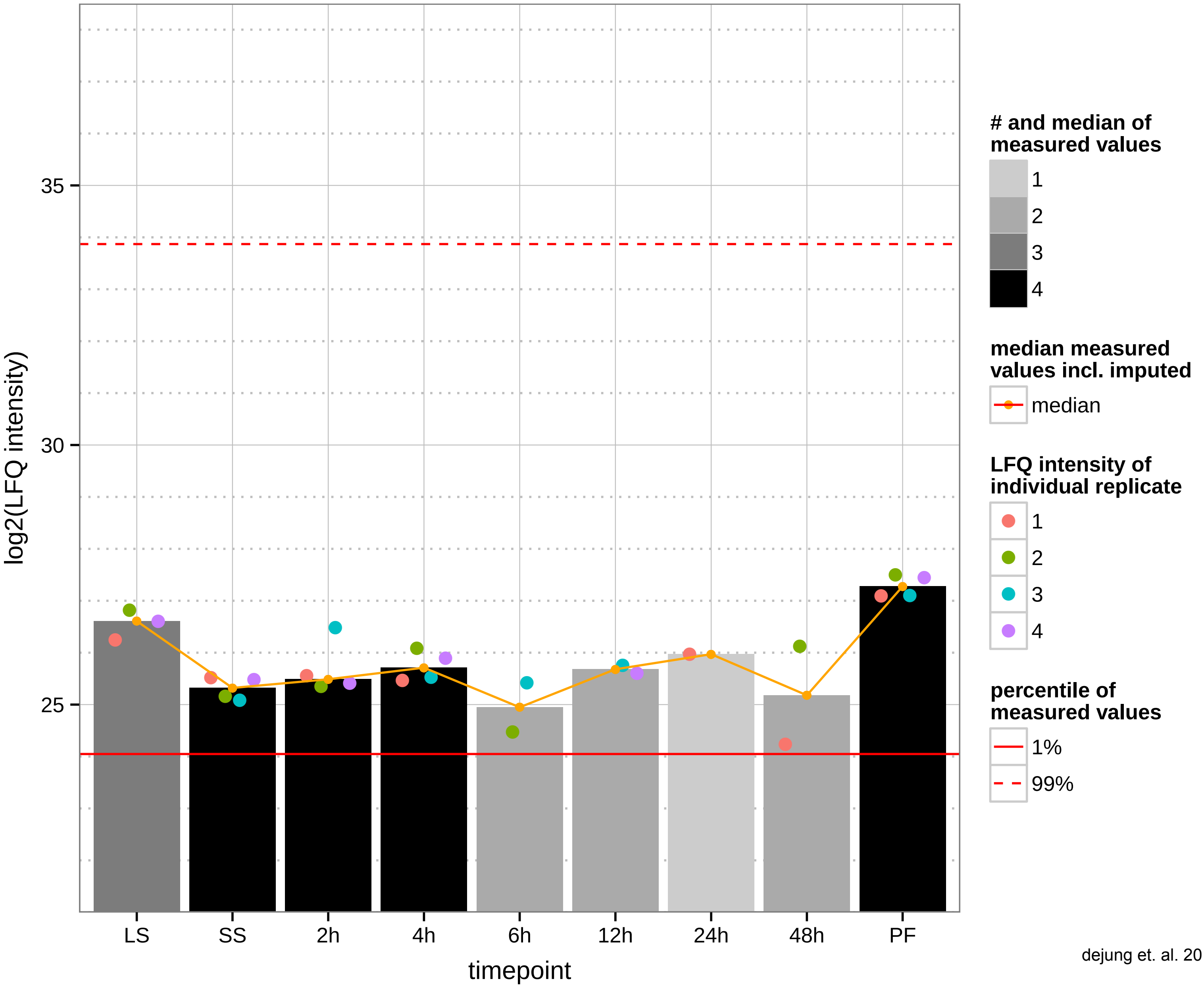
cyclophilin–type peptidyl–prolyl cis–trans isomerase, putative (PPIase)
Tb927.6.1400;Tb927.6.1380;Tb927.6.1360;Tb927.6.1320;Tb927.6.1340
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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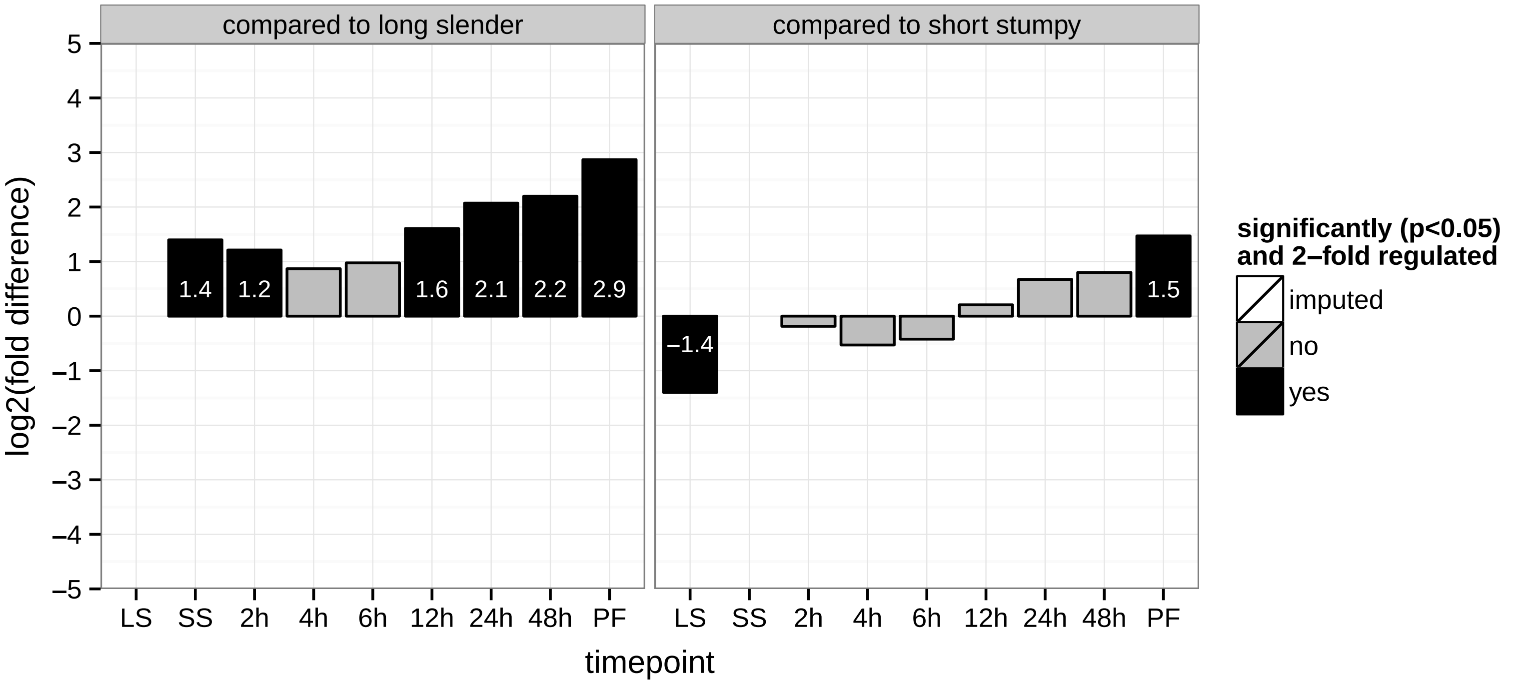
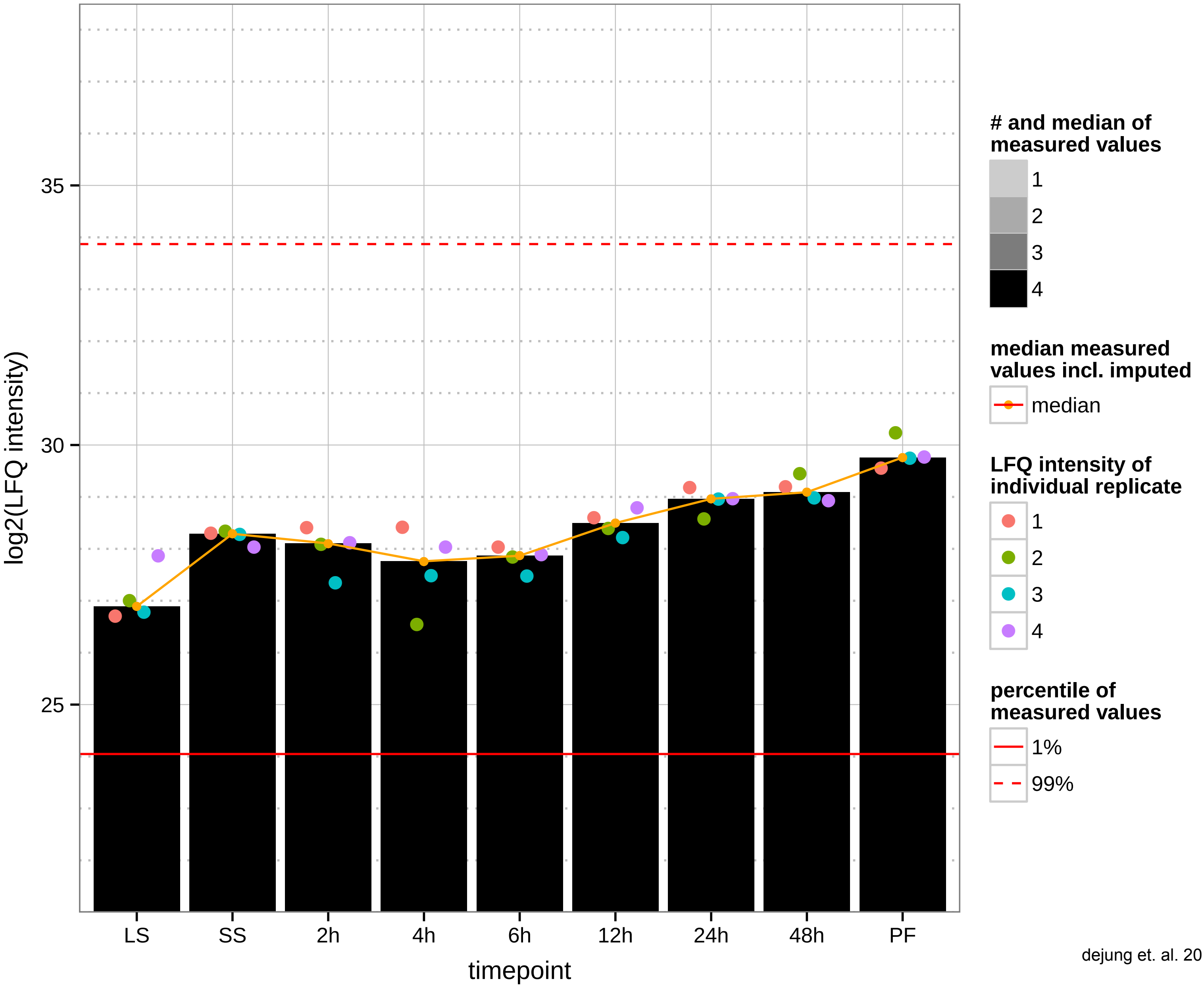
alkyl–dihydroxyacetone phosphate synthase, alkylglycerone–phosphate synthase, alkyl–DHAP synthase (DHAP)
Tb927.6.1500
AGOF: alkylglycerone–phosphate synthase activity, flavin adenine dinucleotide binding, oxidoreductase activity
AGOC: glycosome
AGOP: ether lipid biosynthetic process
PGOF: UDP–N–acetylmuramate dehydrogenase activity, catalytic activity, flavin adenine dinucleotide binding, oxidoreductase
PGOC: null
PGOP: oxidation–reduction process





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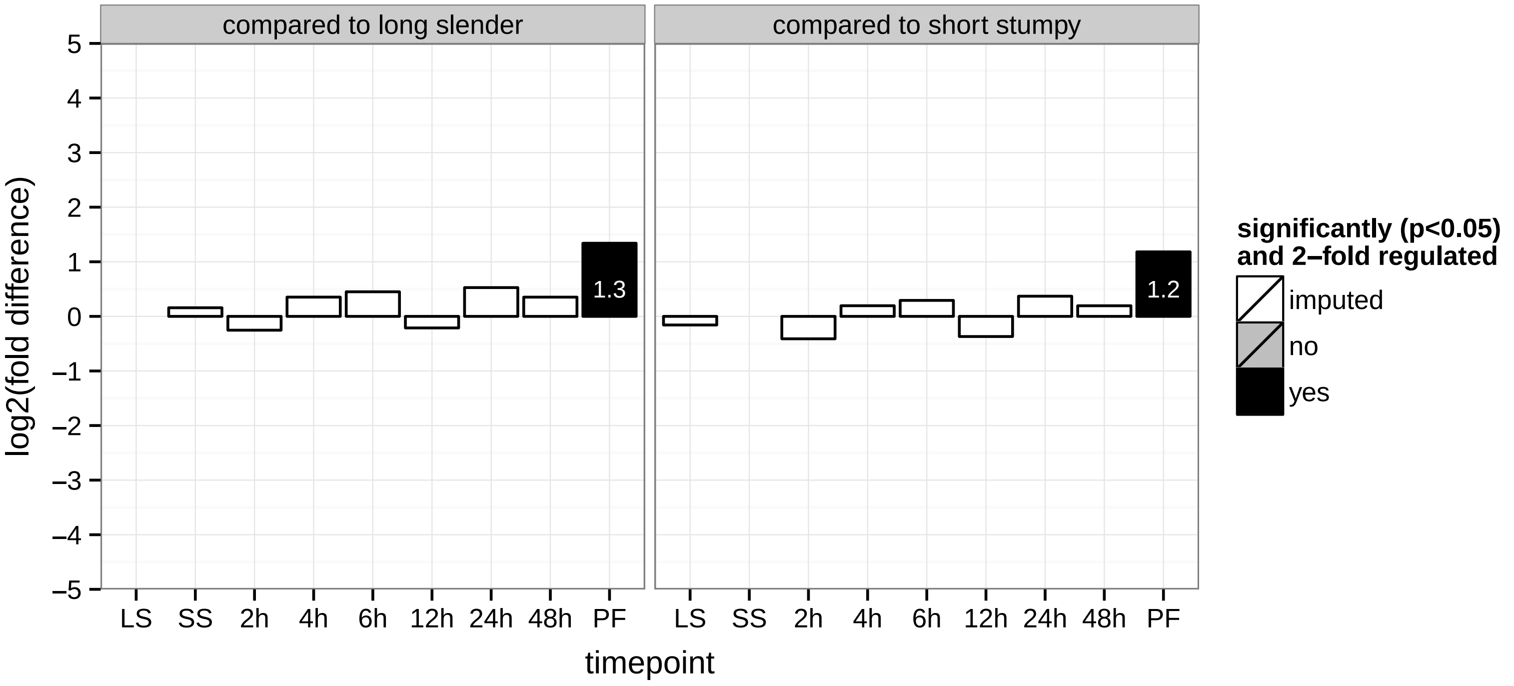
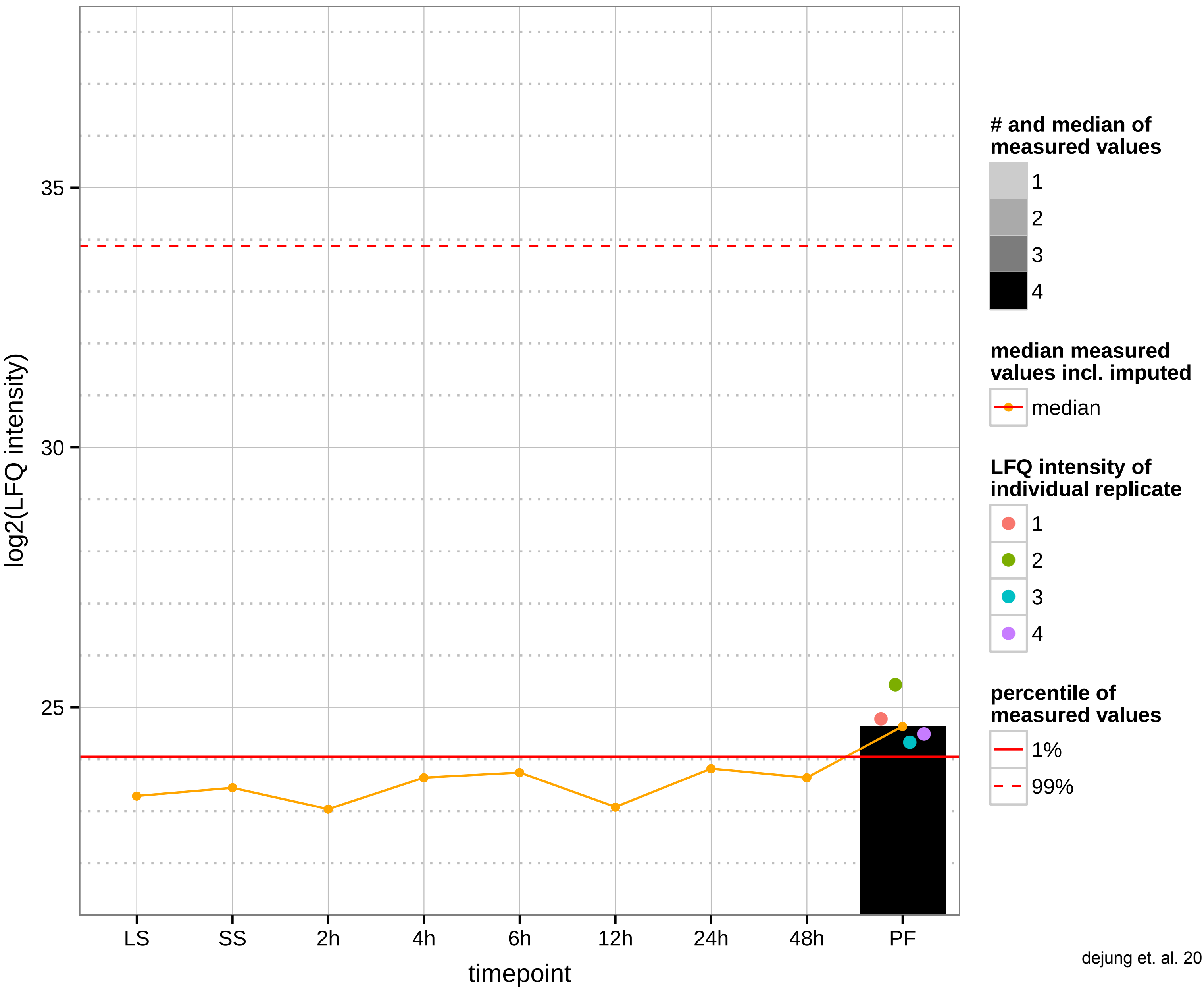
hypothetical protein, conserved
Tb927.6.1700
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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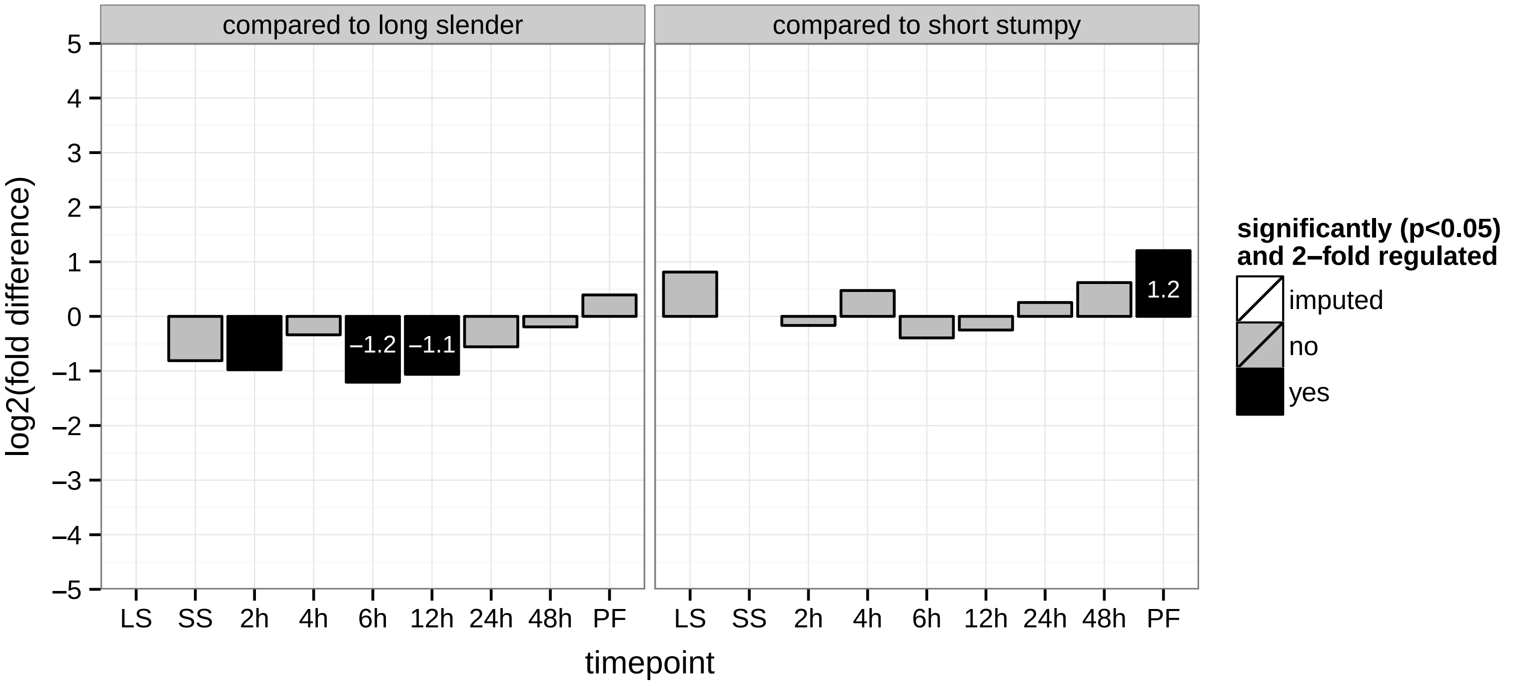
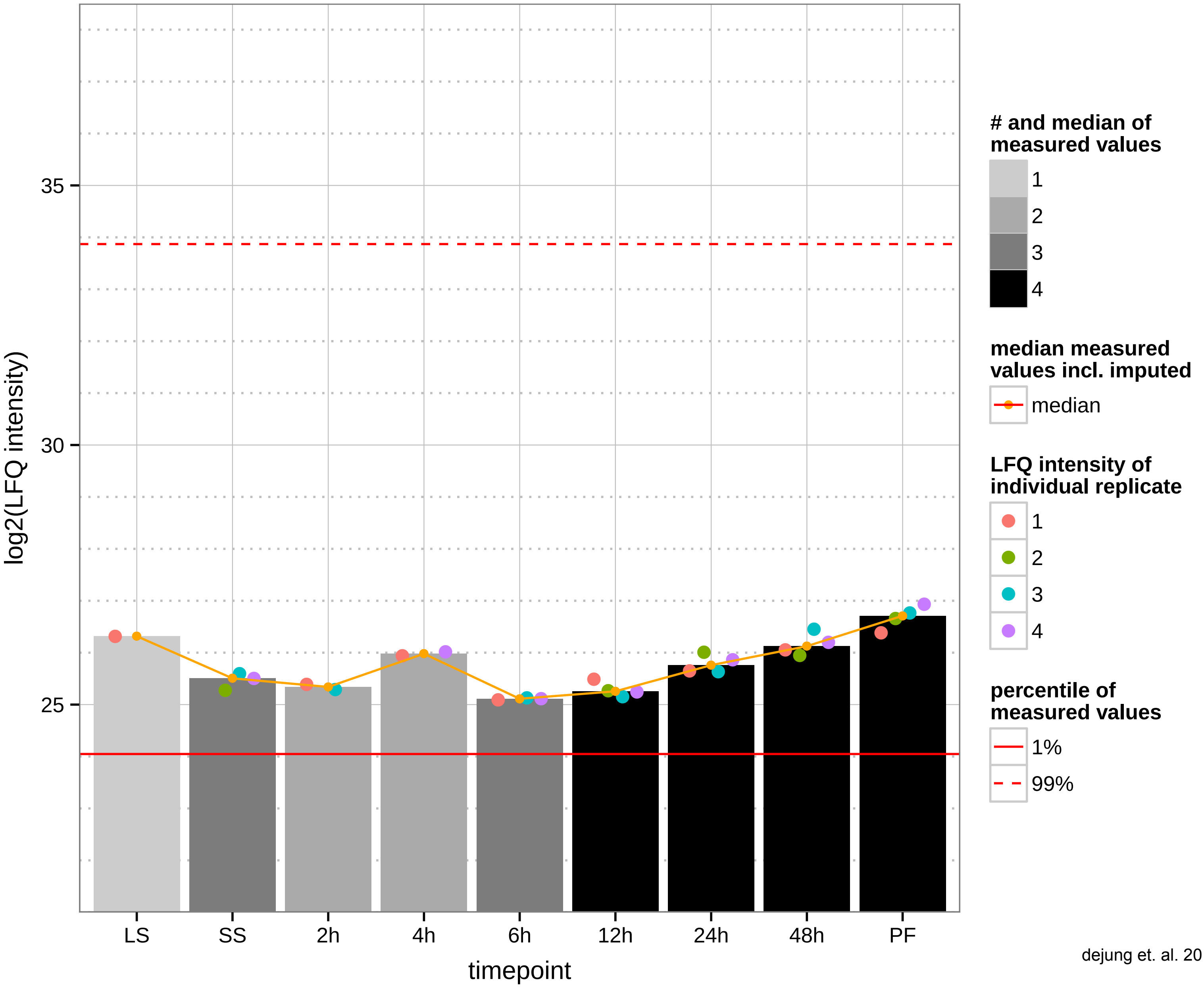
hypothetical protein, conserved
Tb927.6.1810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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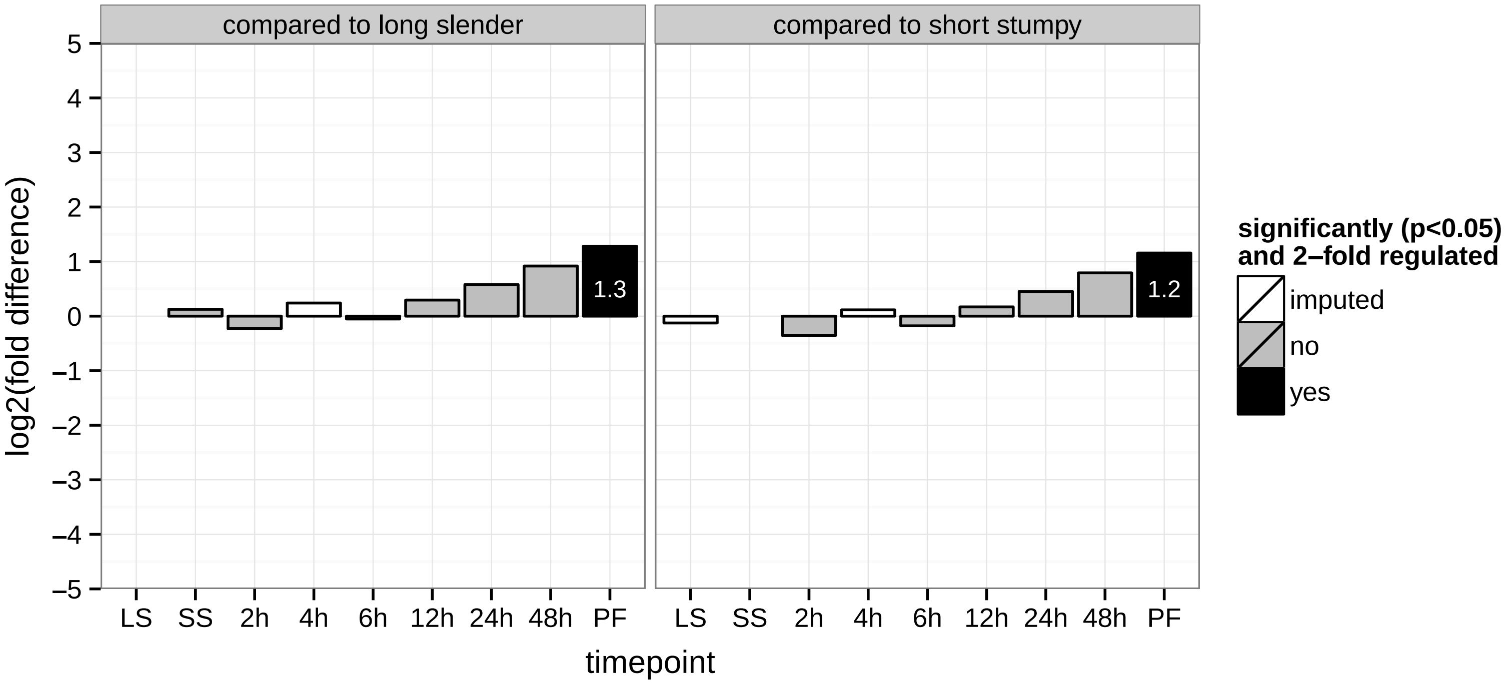
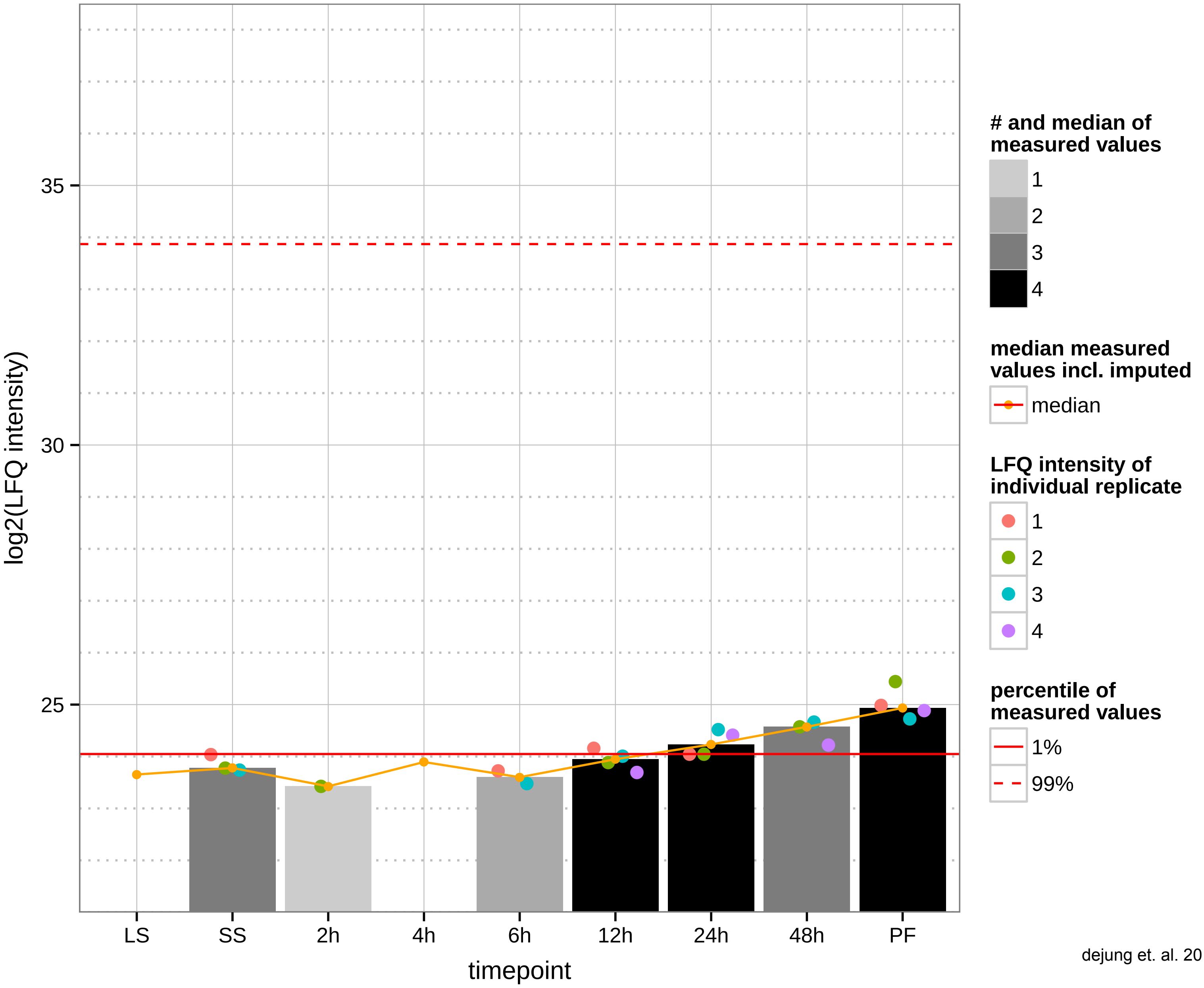
quiescin sulfhydryl oxidase (QSOX)
Tb927.6.1850
AGOF: flavin–linked sulfhydryl oxidase activity, thiol oxidase activity
AGOC: null
AGOP: cell redox homeostasis, oxidation–reduction process, protein folding
PGOF: thiol oxidase activity
PGOC: null
PGOP: cell redox homeostasis, oxidation–reduction process





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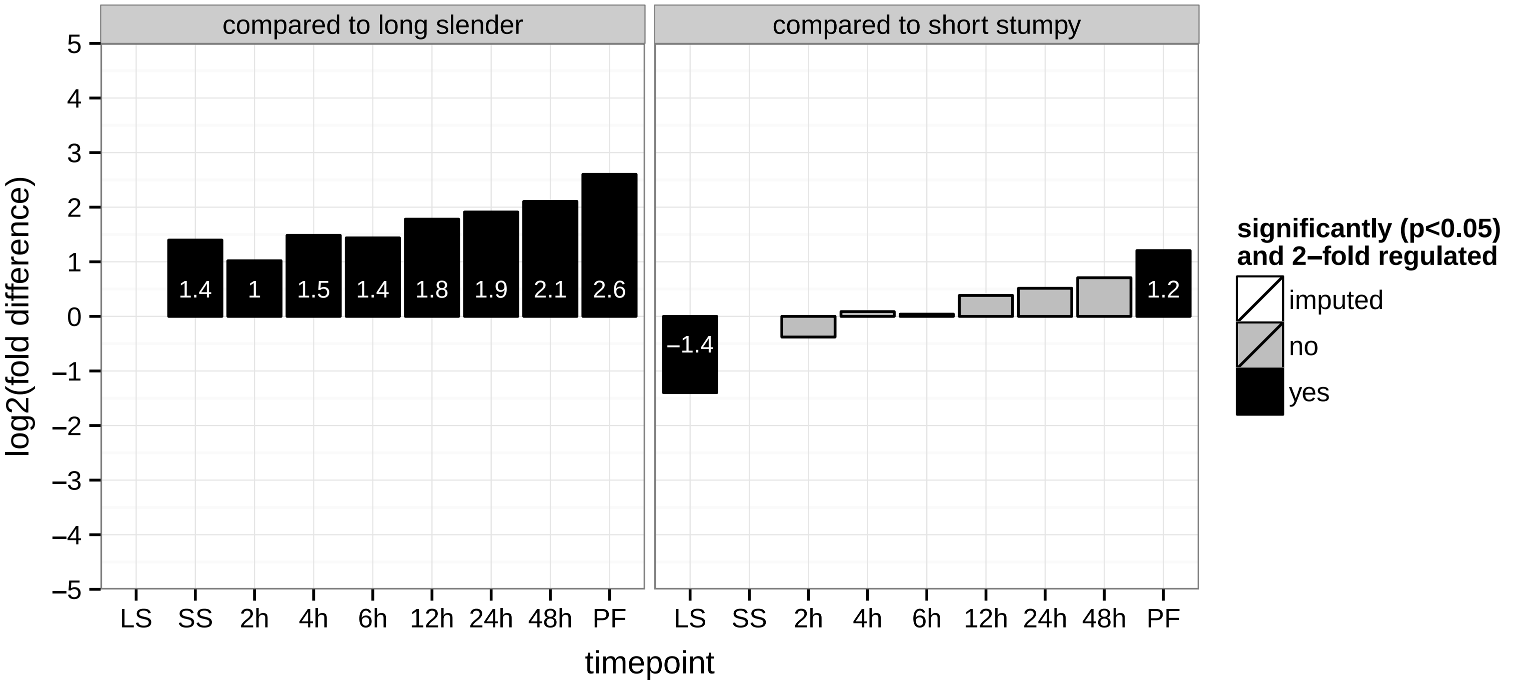
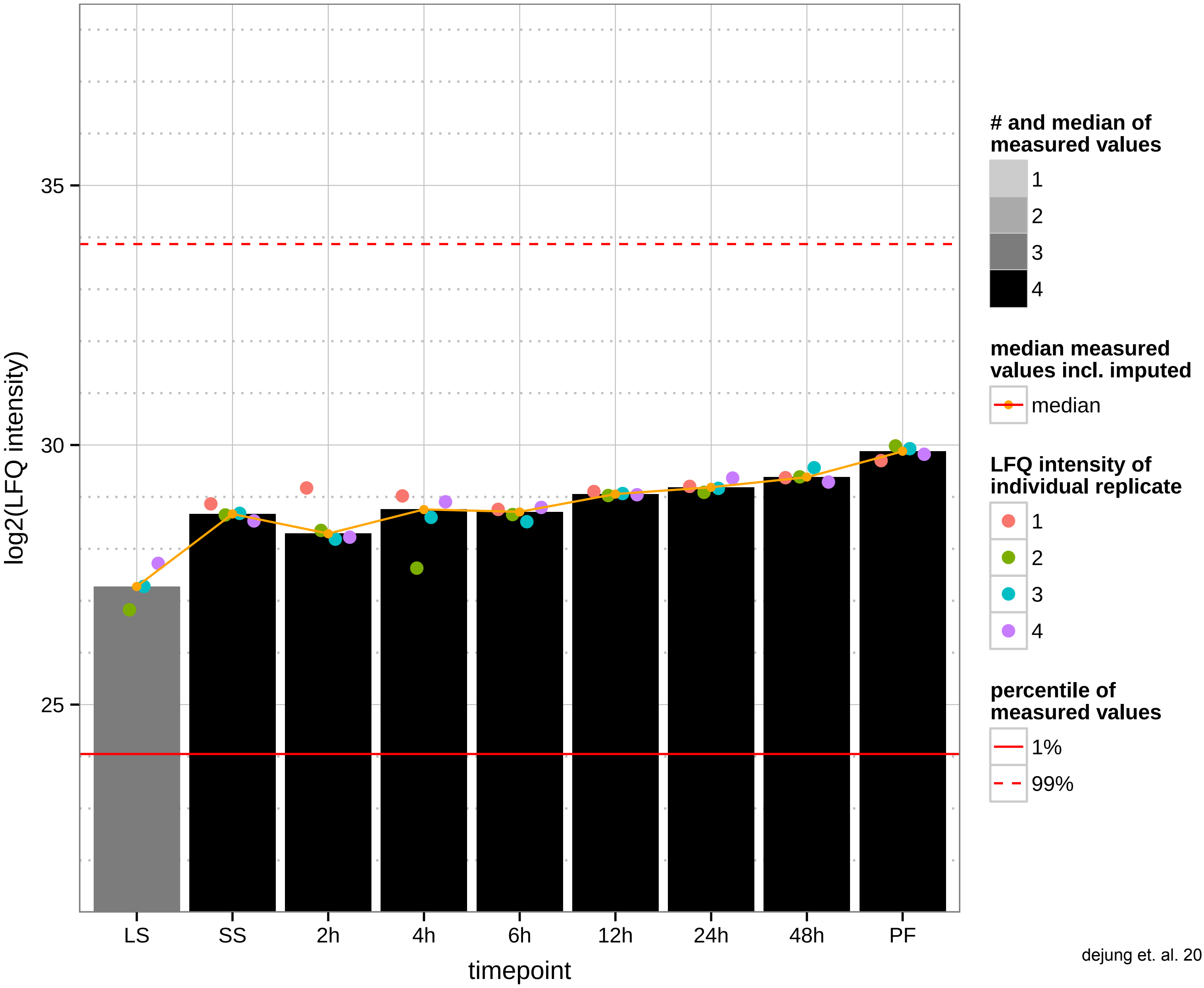
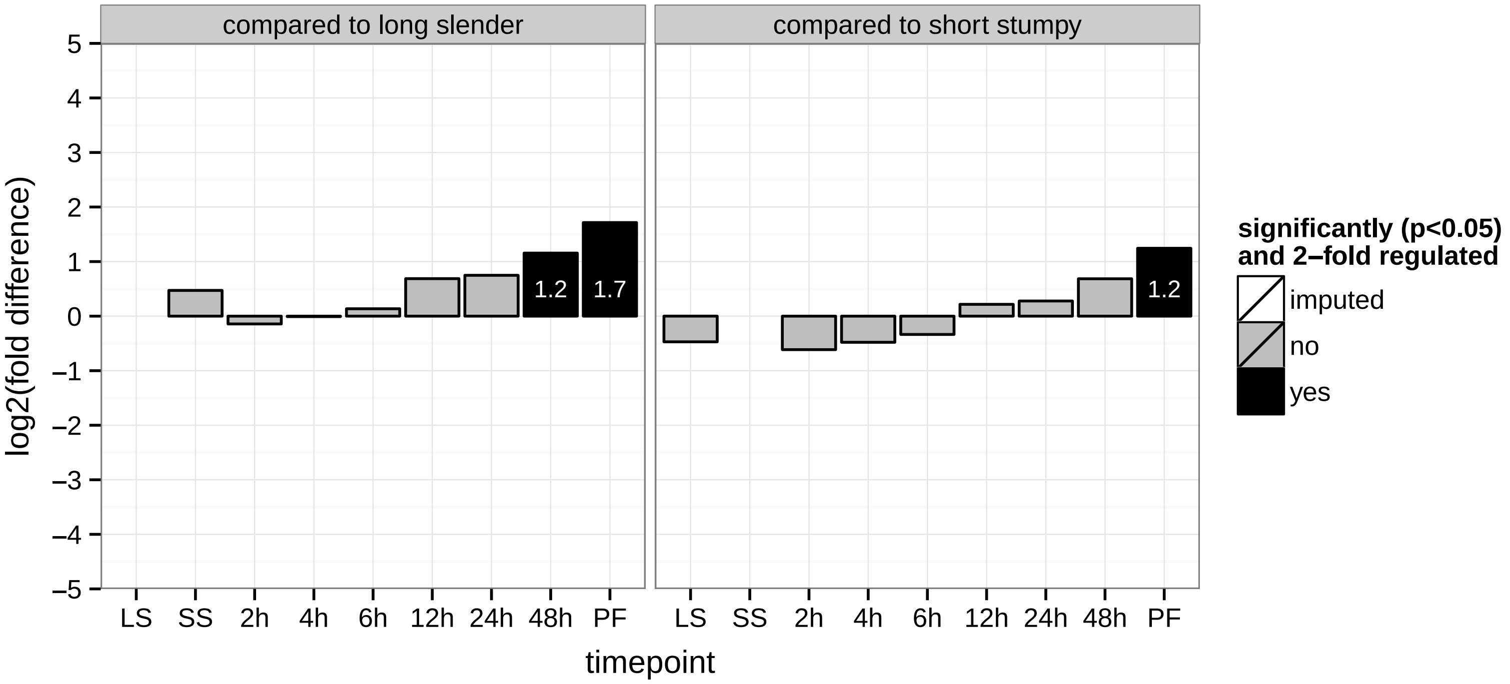
eukaryotic translation initiation factor 4e, putative
Tb927.6.1870
AGOF: RNA cap binding, translation initiation factor activity
AGOC: cytoplasm
AGOP: translational initiation
PGOF: RNA binding, translation initiation factor activity
PGOC: cytoplasm
PGOP: translational initiation

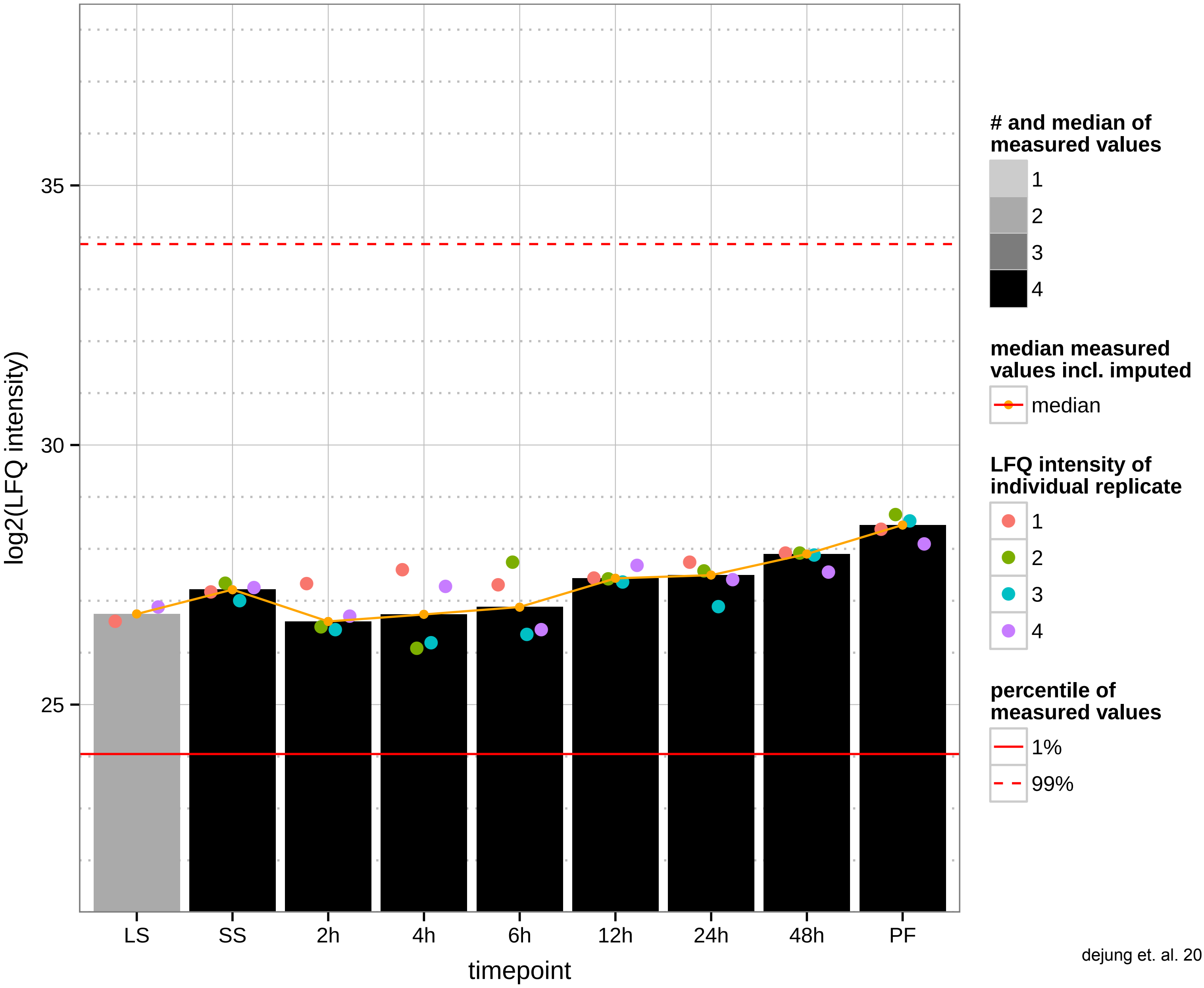




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.2140
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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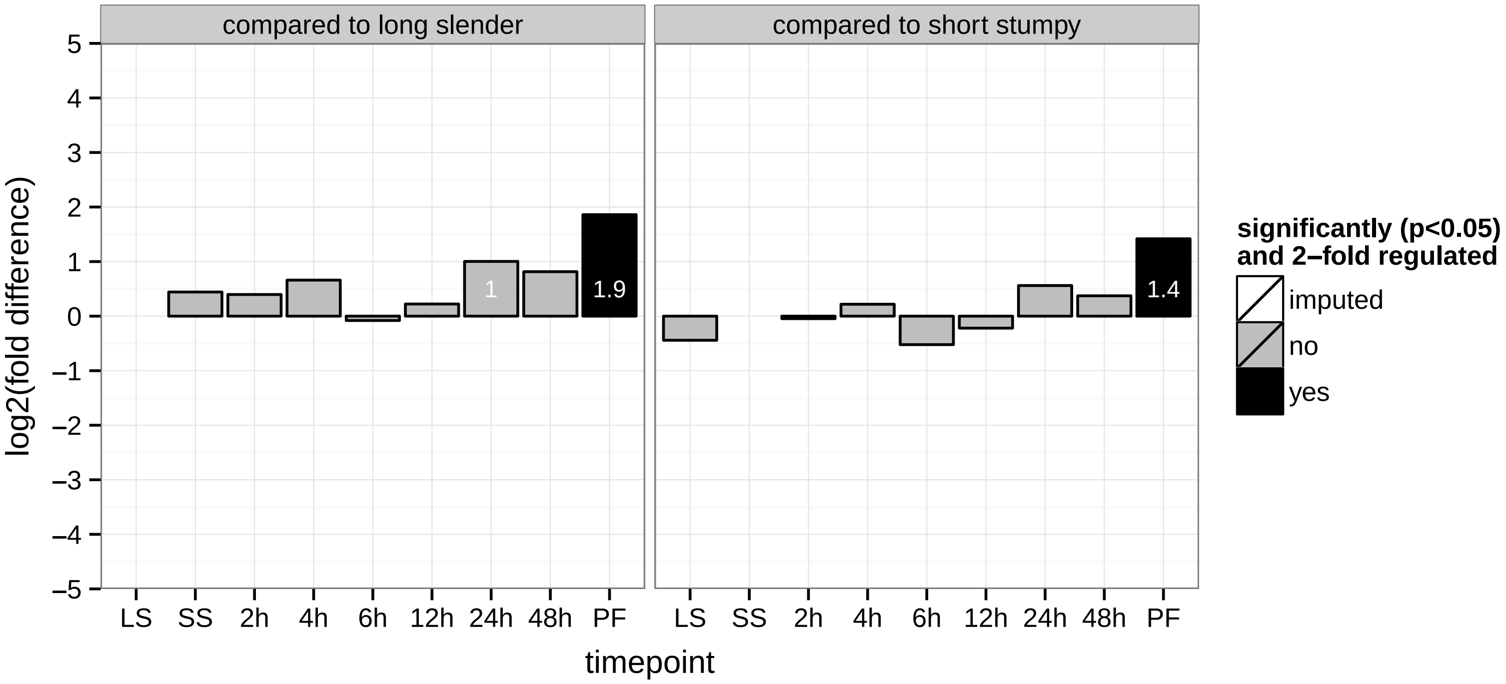
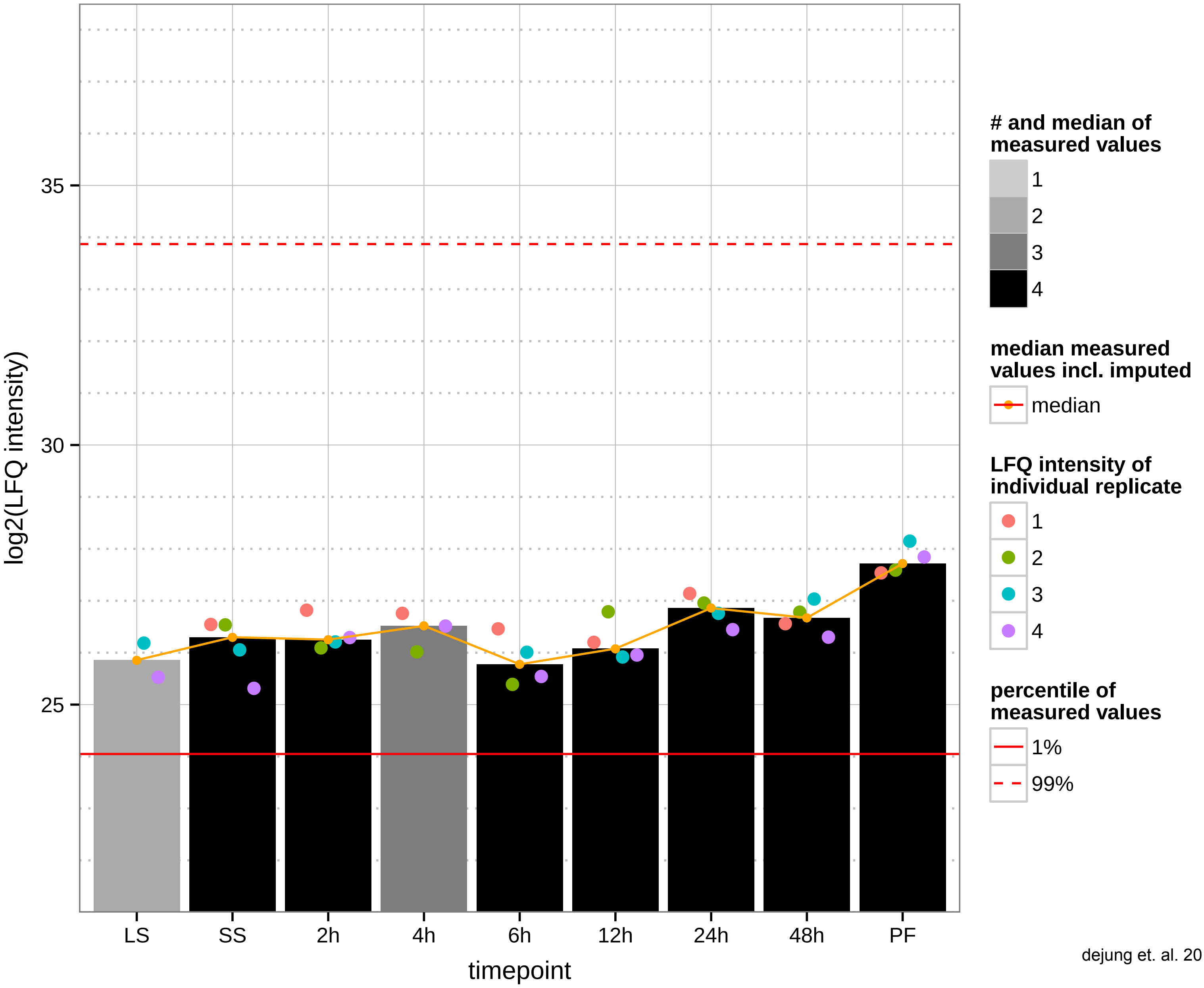
hypothetical protein, conserved, RGG protein (RGG1)
Tb927.6.2330;Tb927.6.2270
AGOF: methyltransferase activity, protein binding
AGOC: null
AGOP: null
PGOF: methyltransferase activity
PGOC: null
PGOP: null





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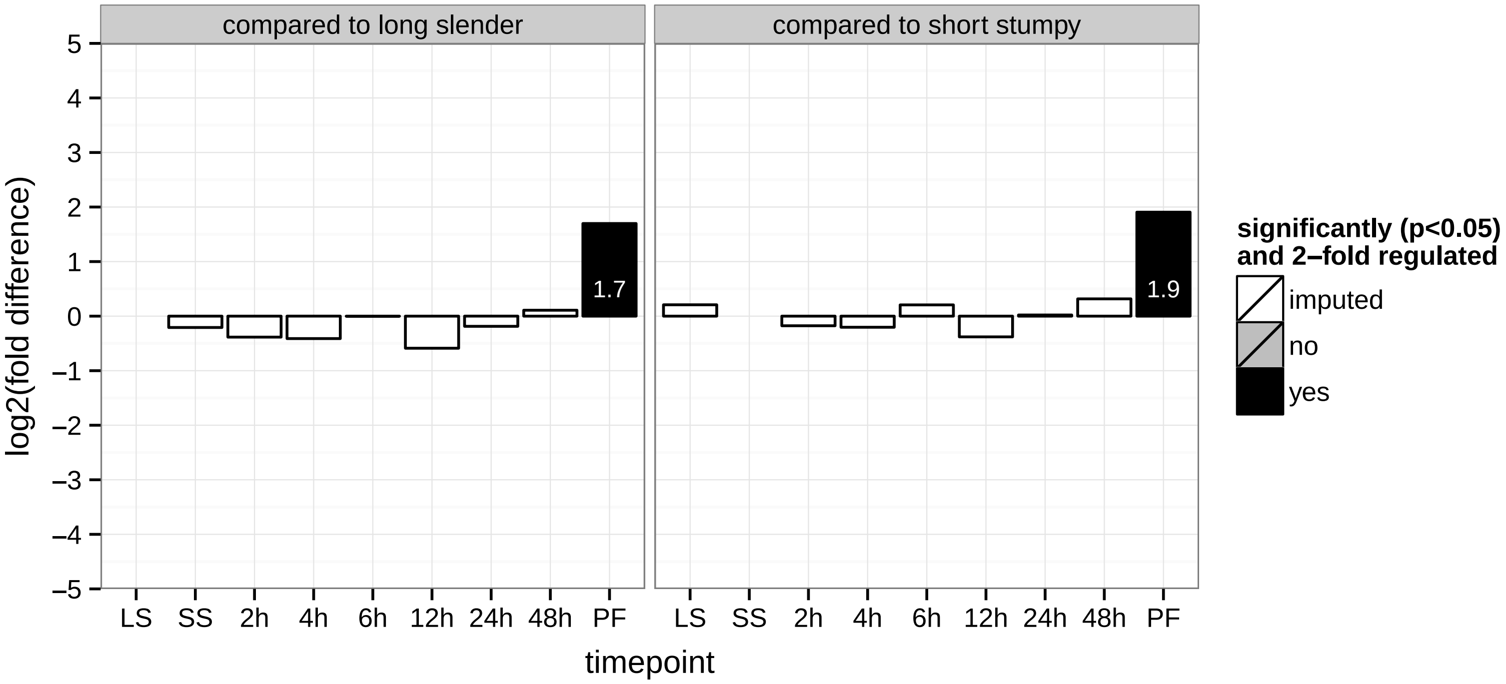
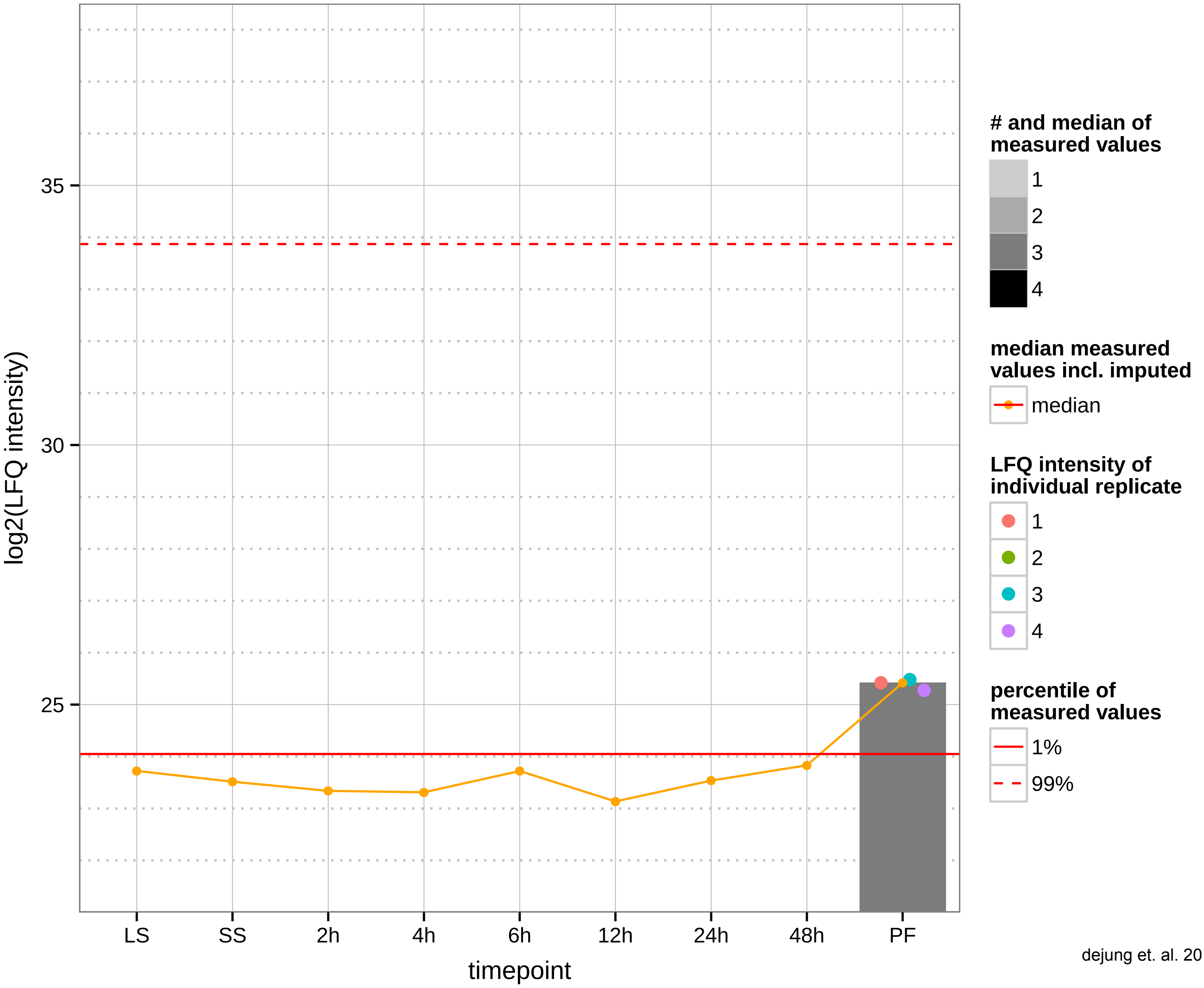
DREV methyltransferase, putative
Tb927.6.2540
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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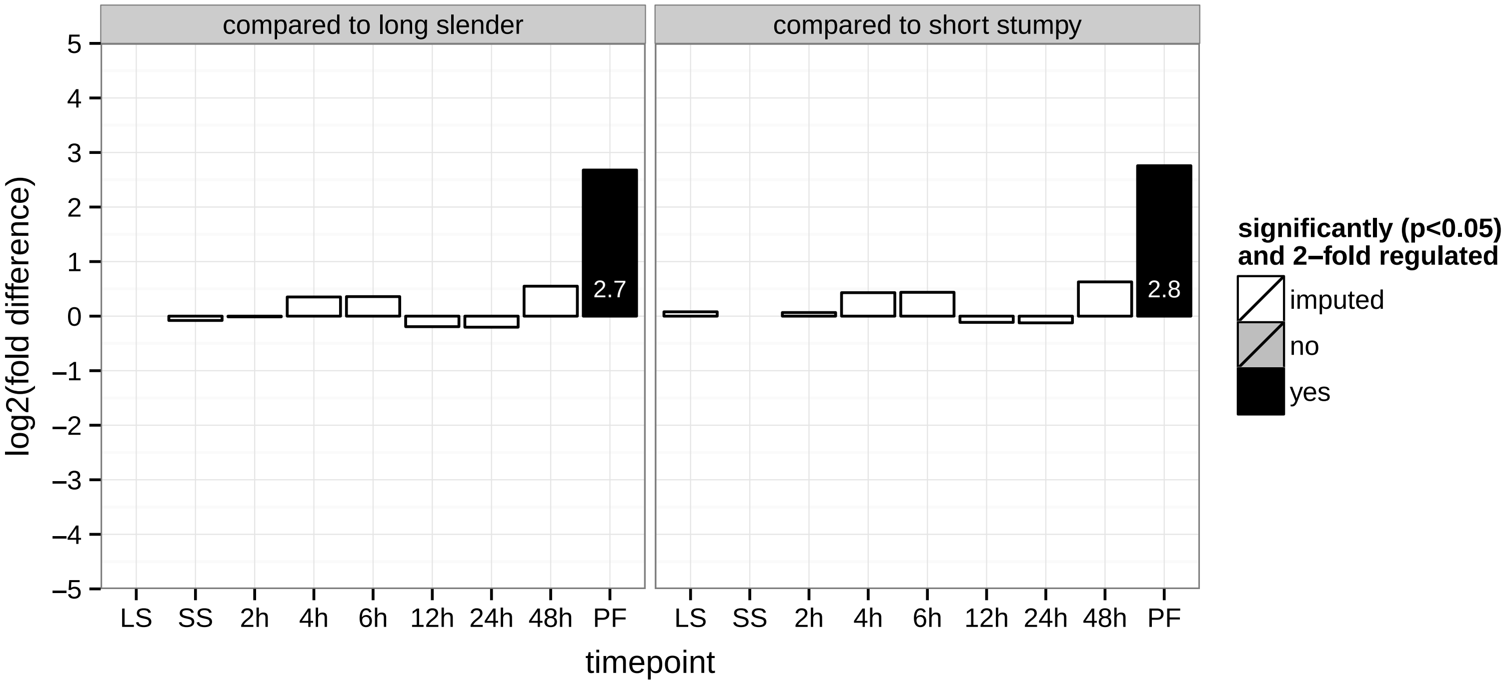
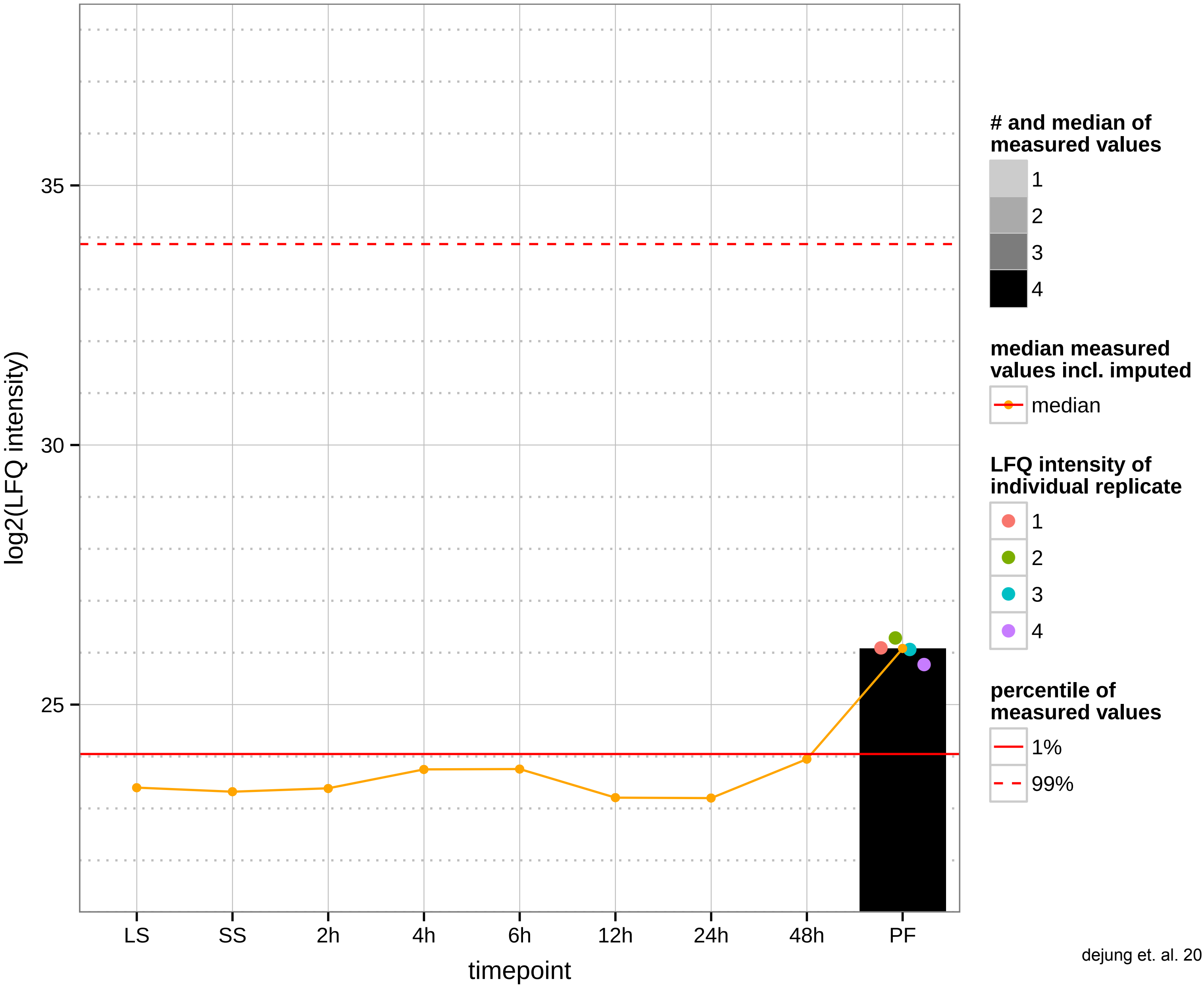
dendritic cell−derived IFNG−induced protein, SAM domain and HD domain−containing protein 1
Tb927.6.2900
AGOF: catalytic activity
AGOC: null
AGOP: null
PGOF: catalytic activity, metal ion binding, phosphoric diester hydrolase activity
PGOC: null
PGOP: null





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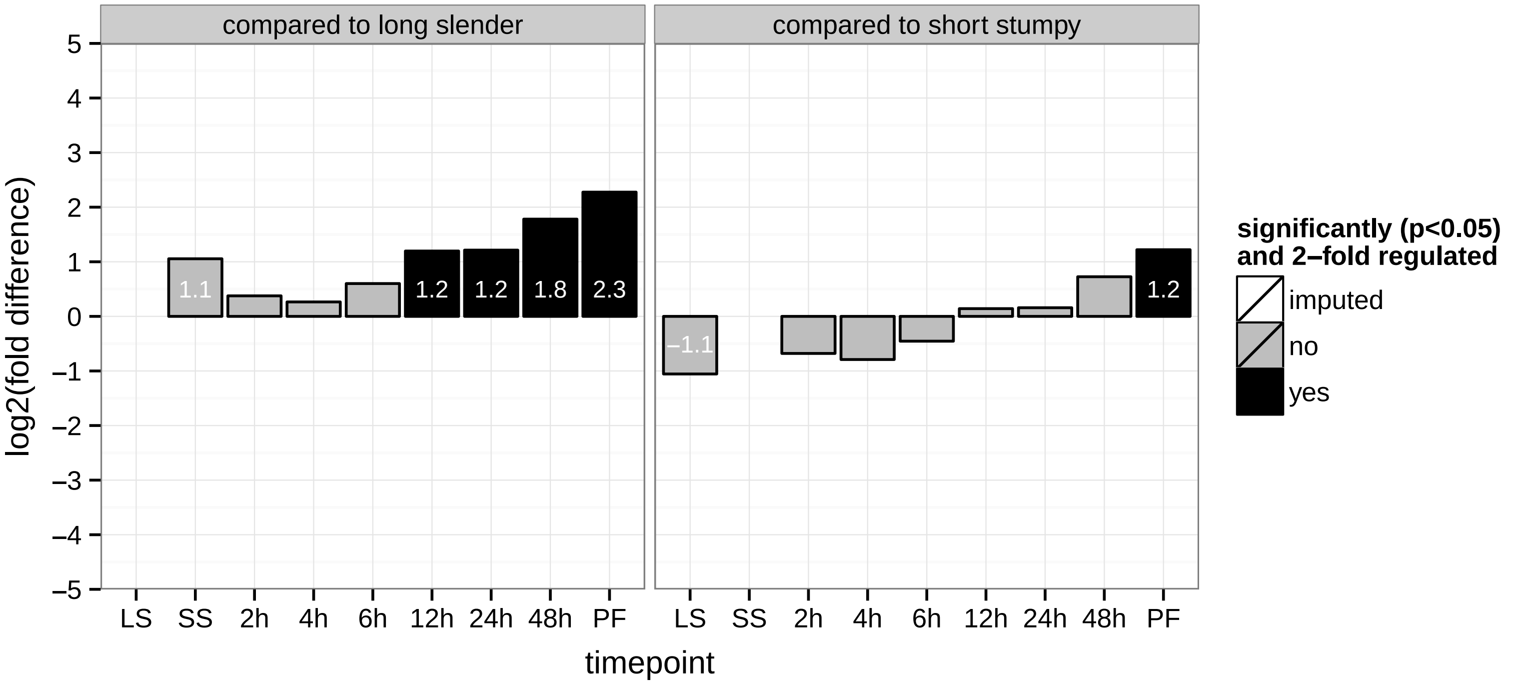
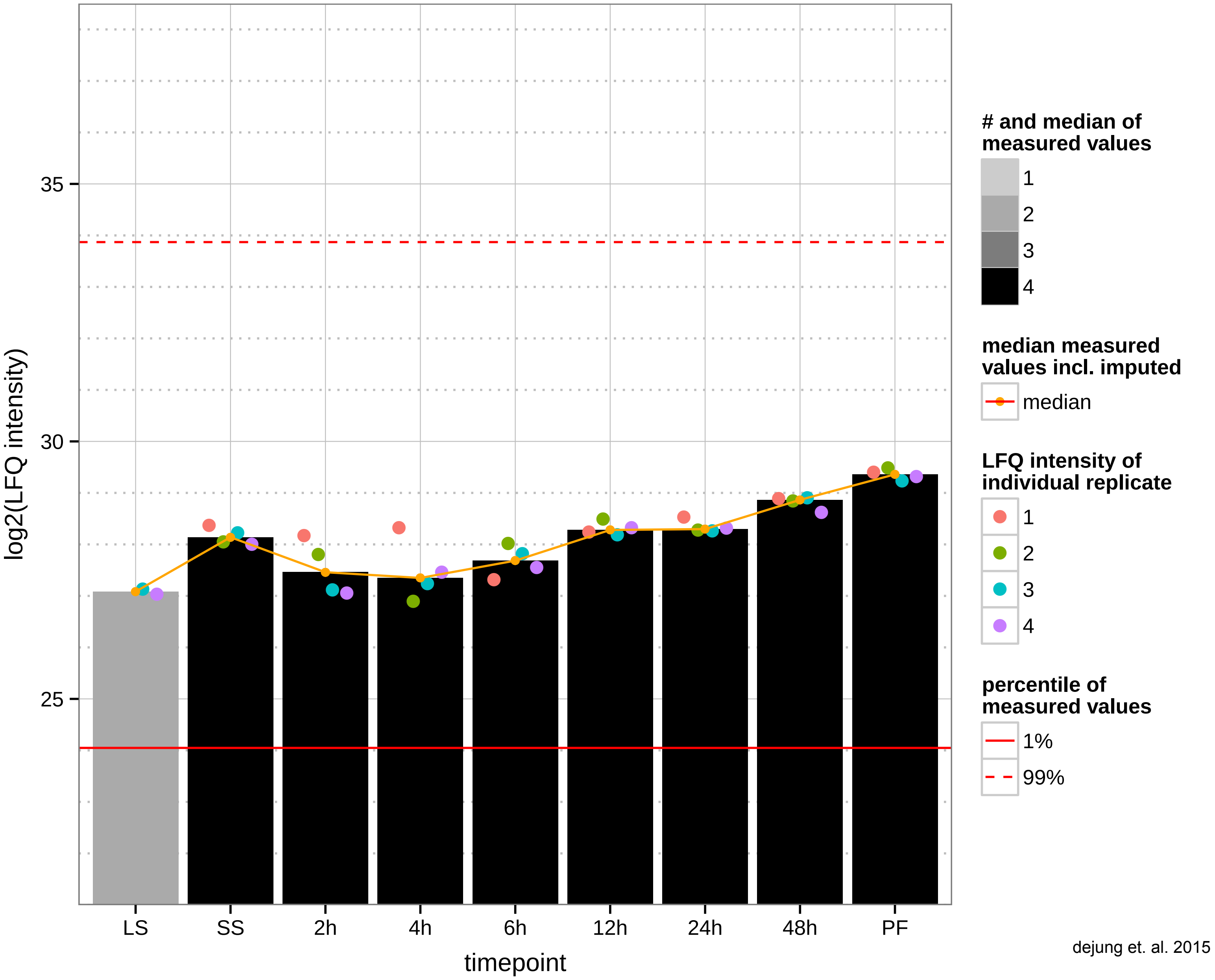
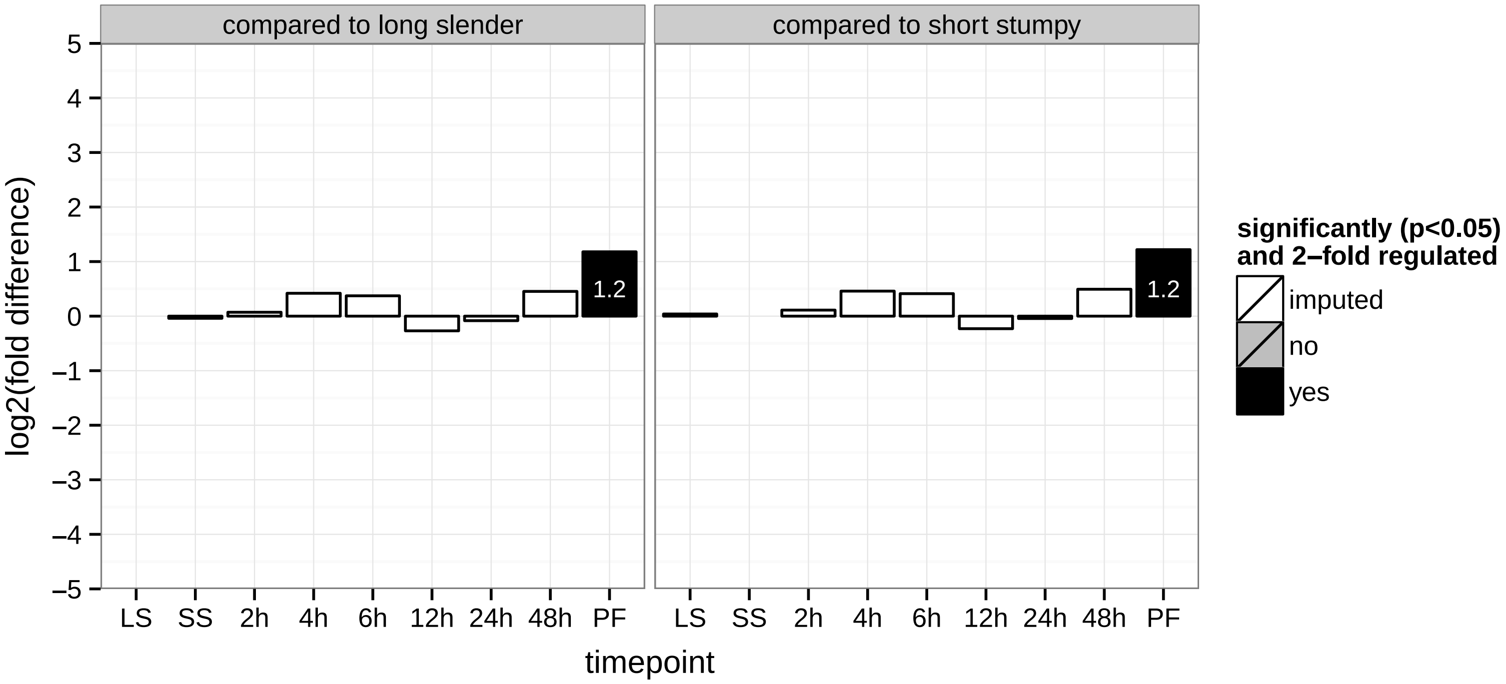
sphingosine 1−phosphate lyase, putative, sphingosine phosphate lyase−like protein, putative (SPL)
Tb927.6.3630
AGOF: carboxy−lyase activity, pyridoxal phosphate binding, sphinganine−1−phosphate aldolase activity
AGOC: null
AGOP: carboxylic acid metabolic process, ethanolamine biosynthetic process
PGOF: carboxy−lyase activity, pyridoxal phosphate binding
PGOC: null
PGOP: carboxylic acid metabolic process

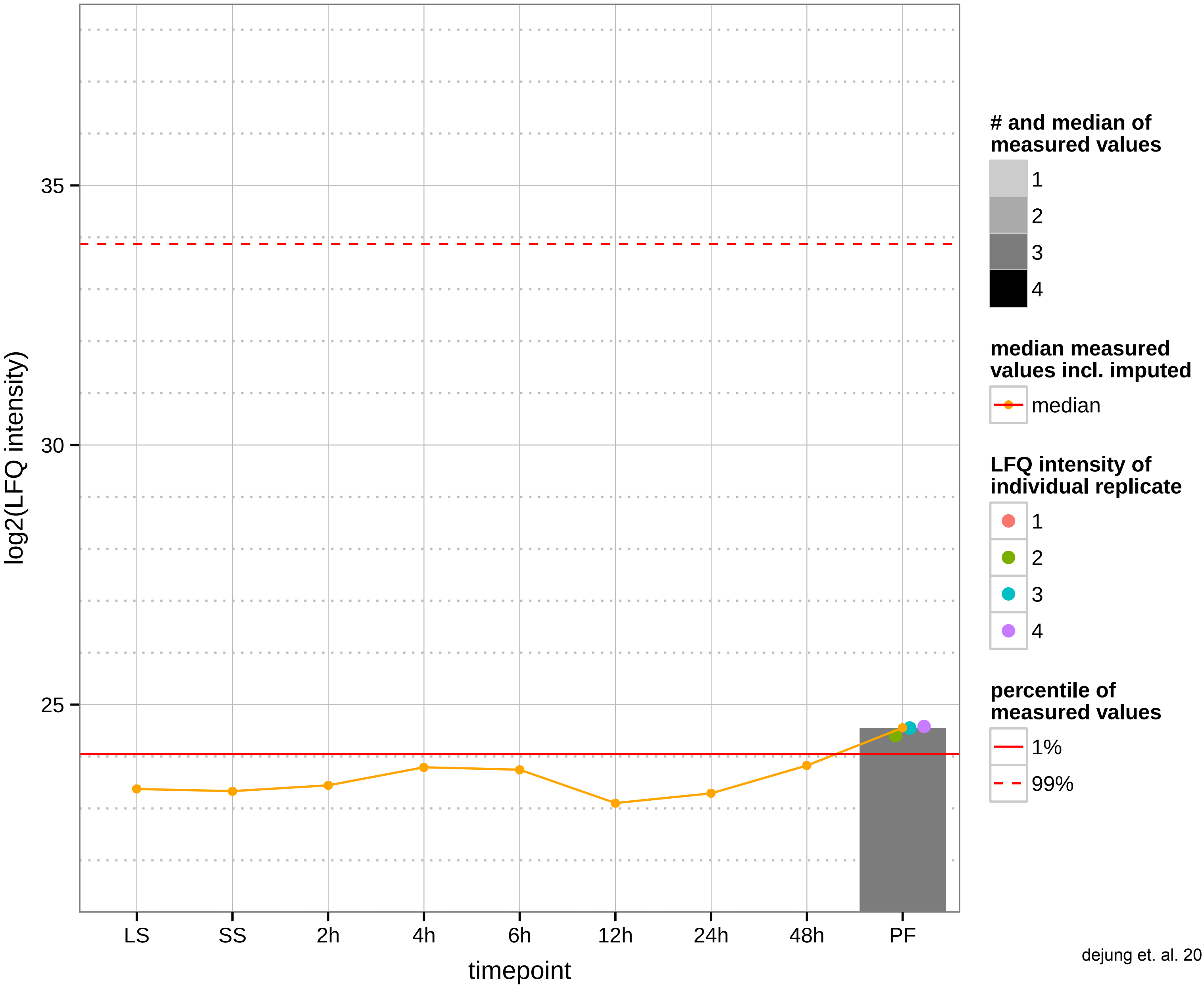




dejung et. al. 2015

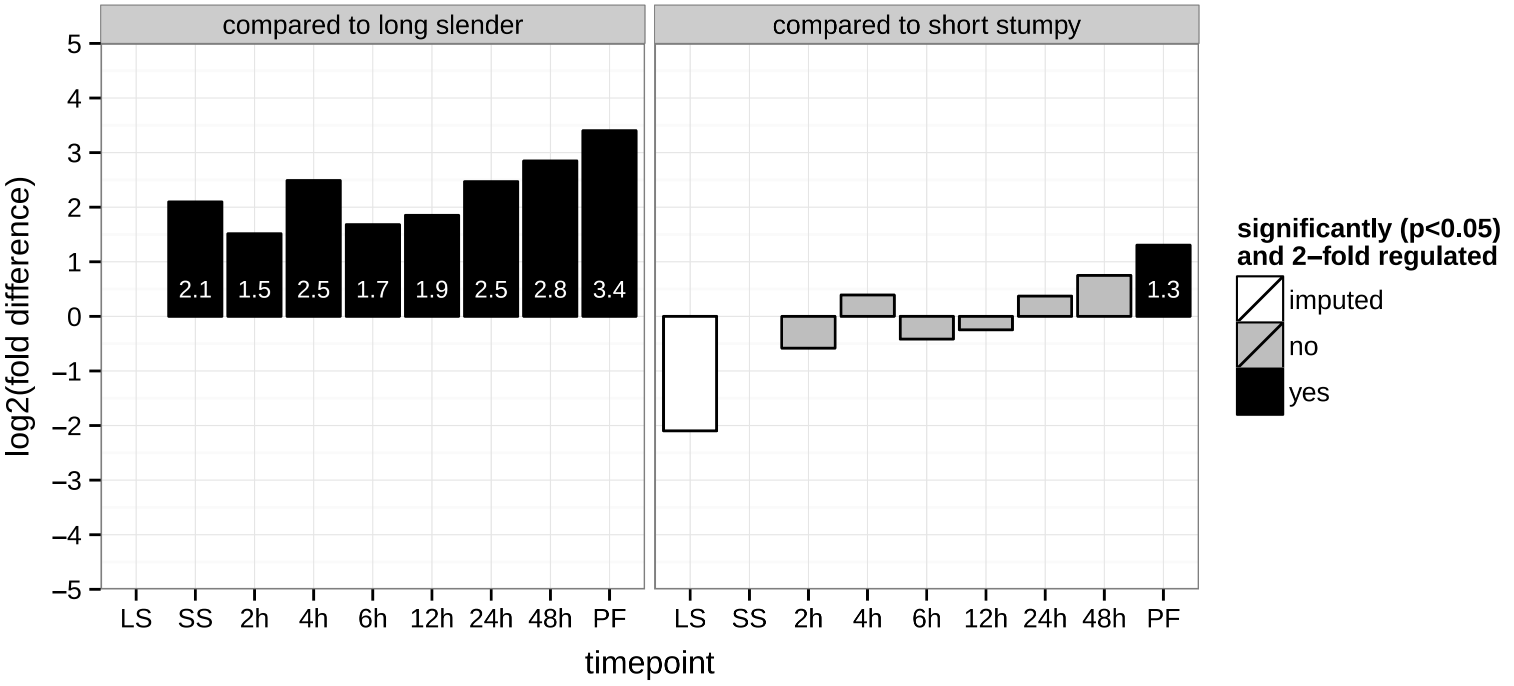
hypothetical protein, conserved
Tb927.6.4360
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

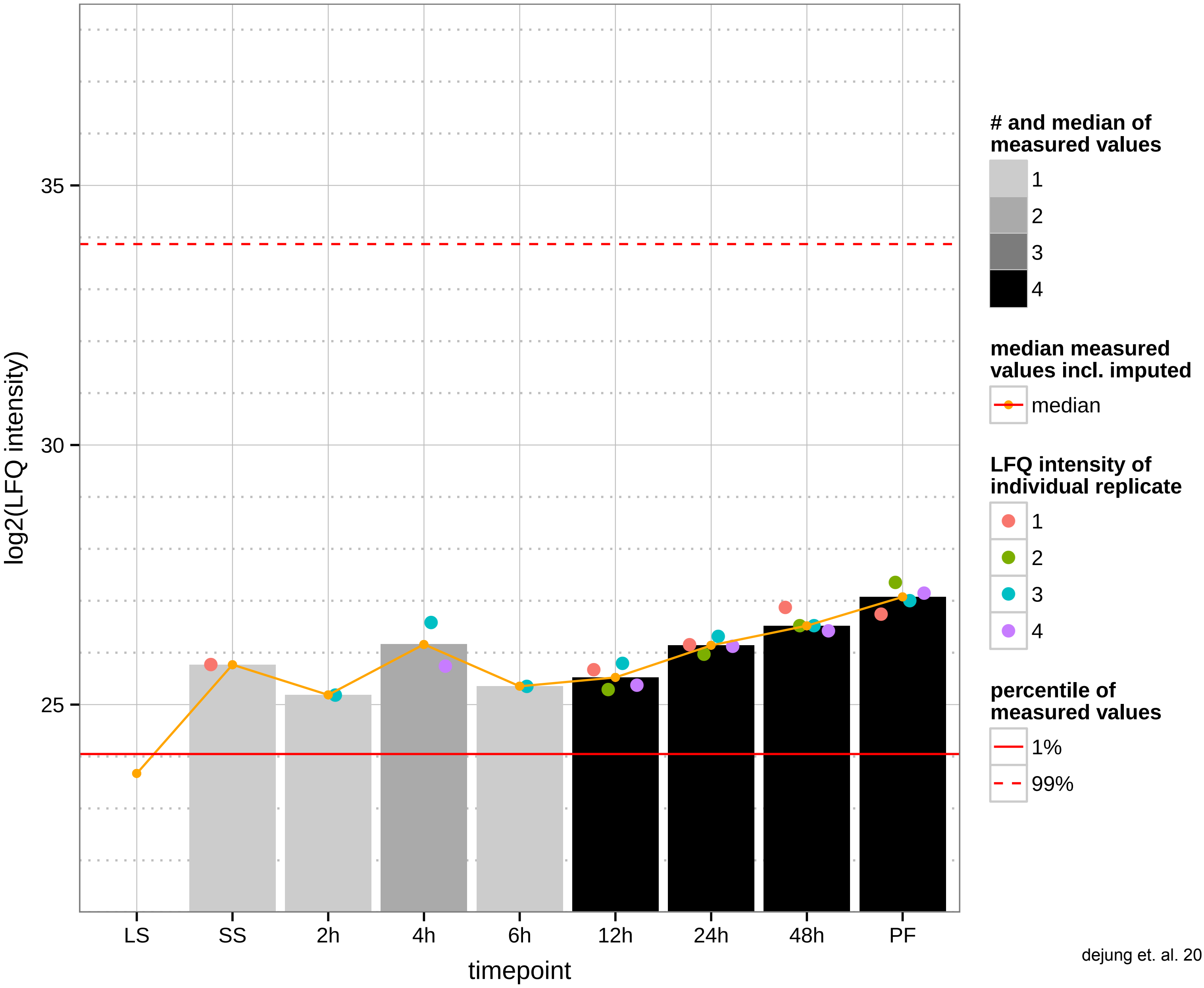




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.4380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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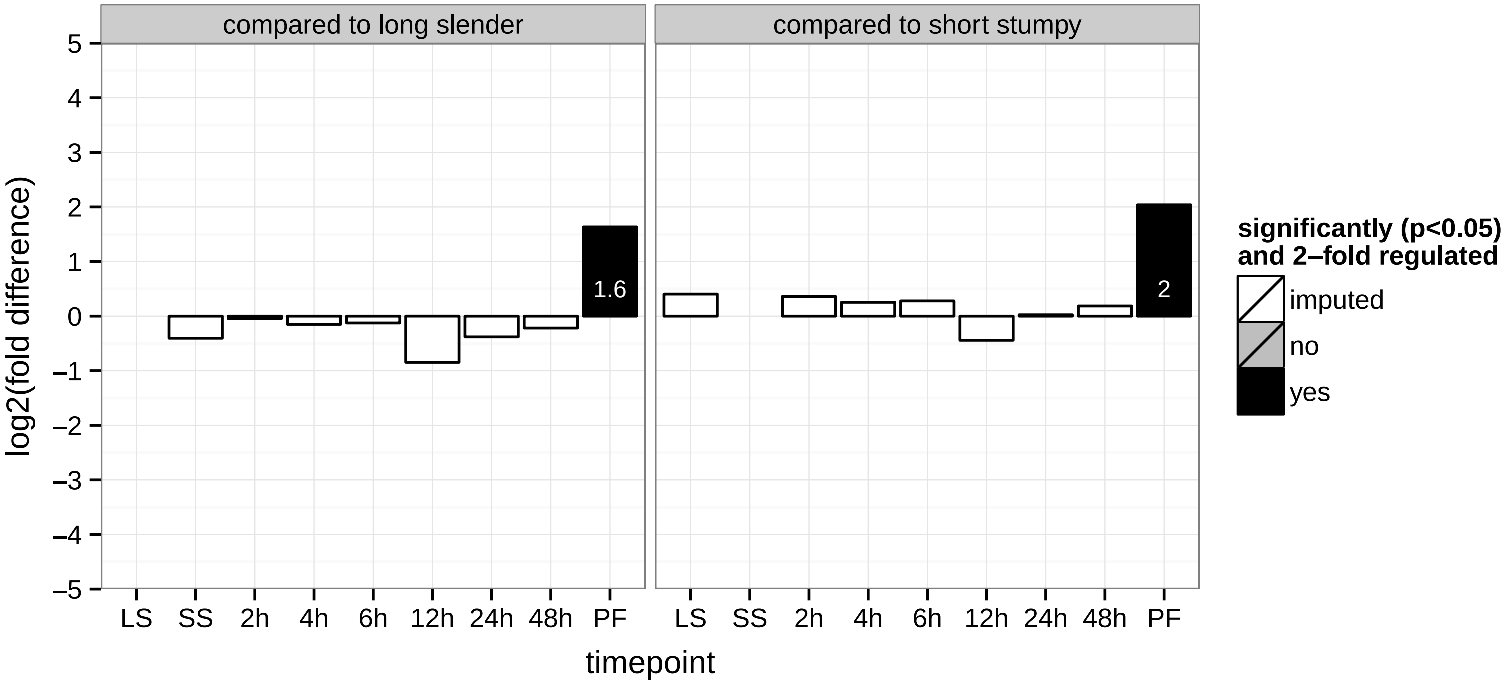
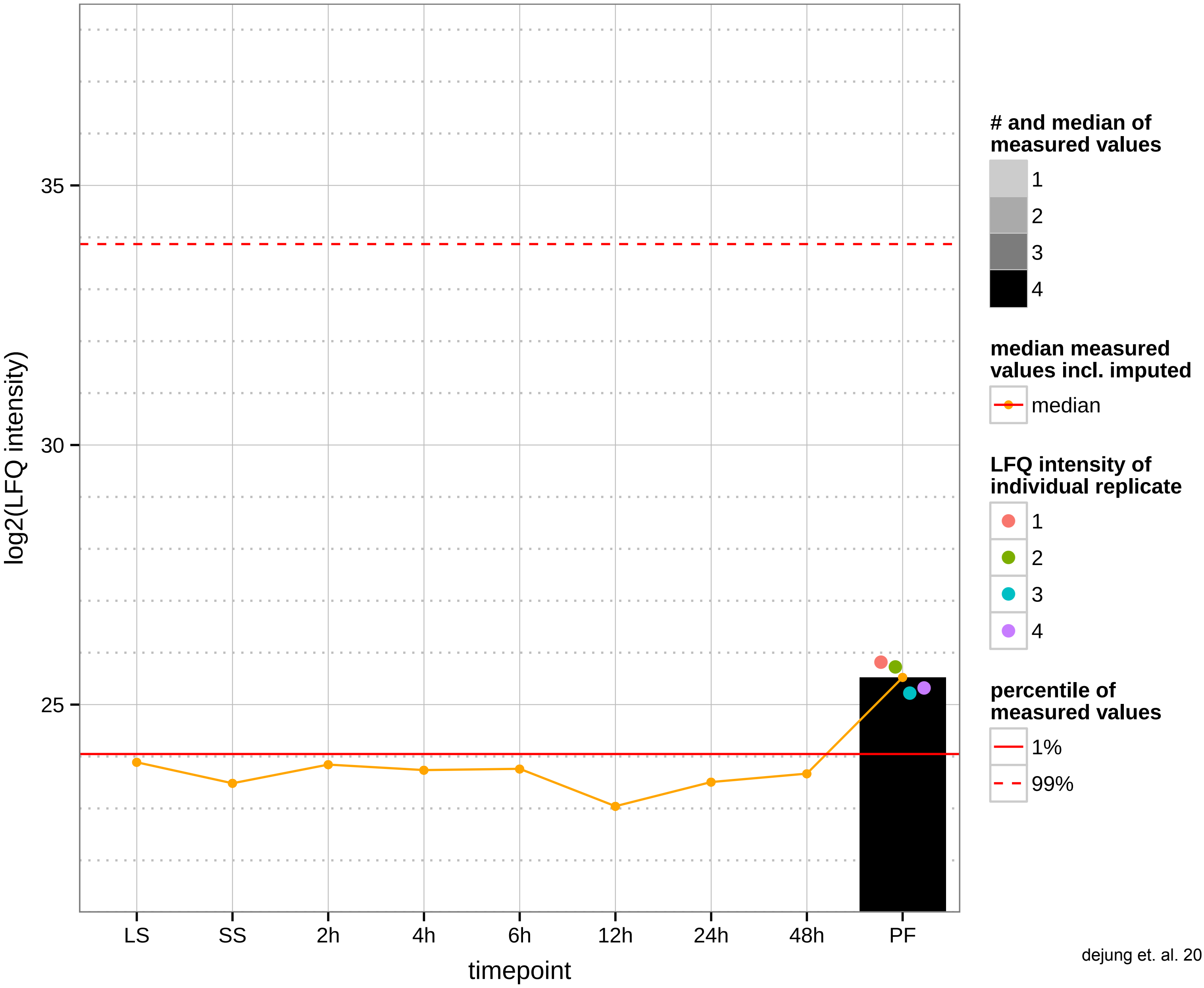
hypothetical protein, conserved
Tb927.6.4510
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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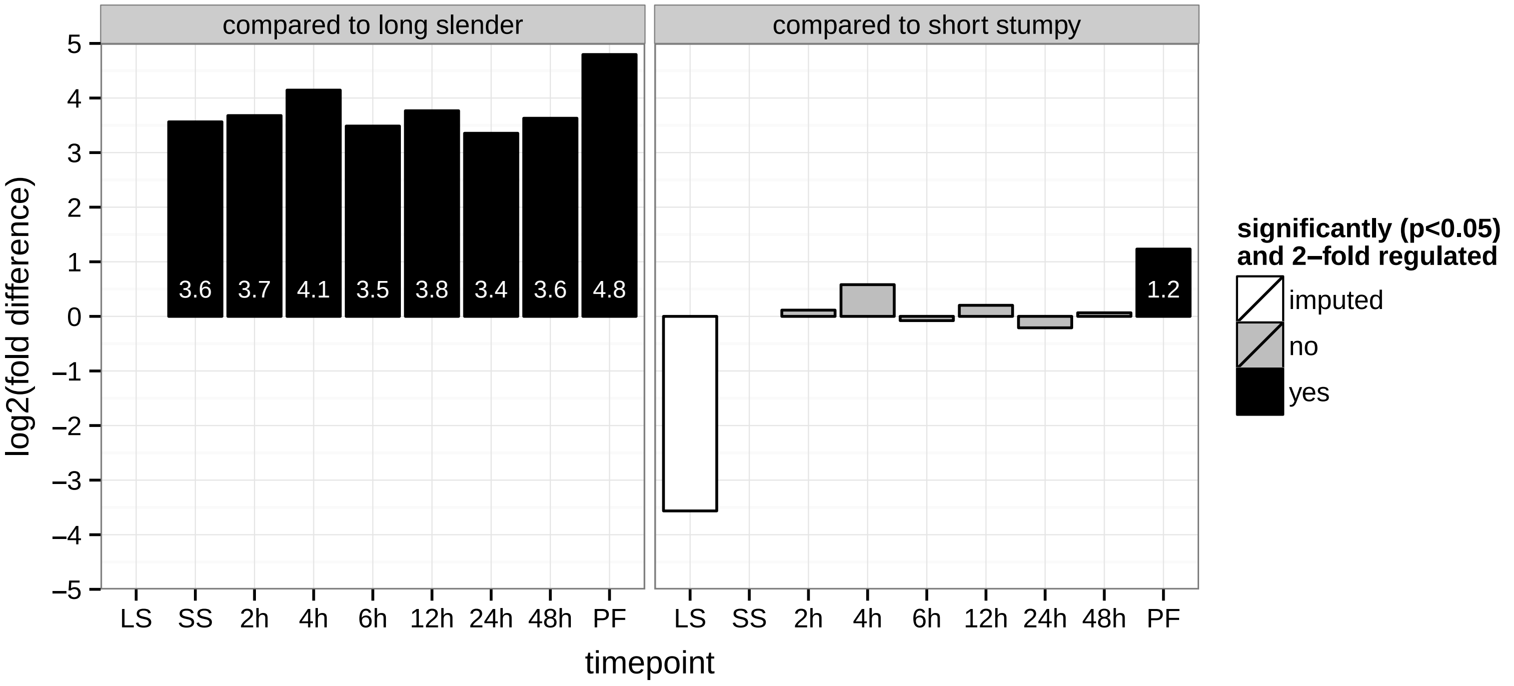
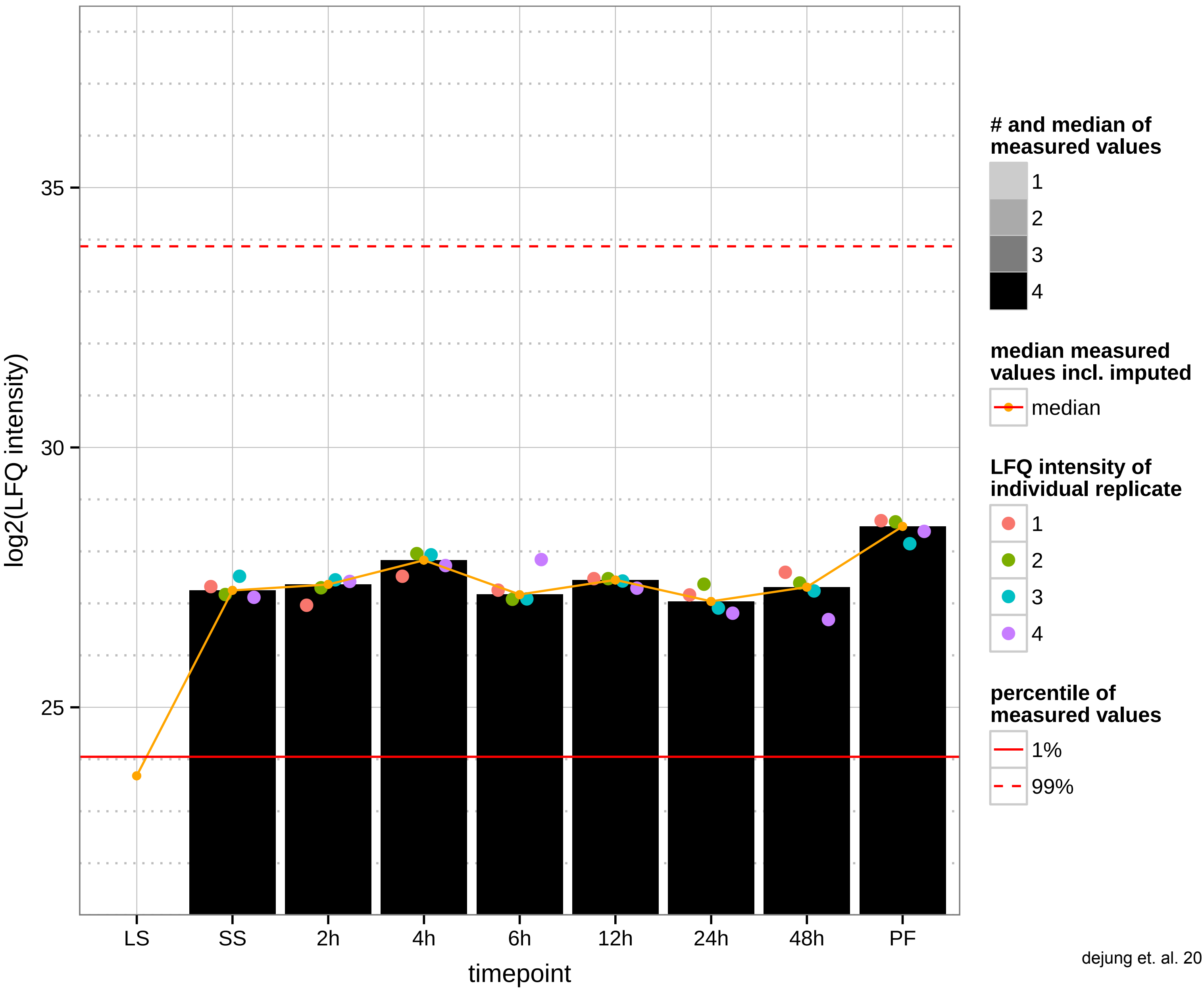
kinetoplastid–specific phospho–protein phosphatase, putative
Tb927.6.4630
AGOF: hydrolase activity, protein serine/threonine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: hydrolase activity
PGOC: null
PGOP: null





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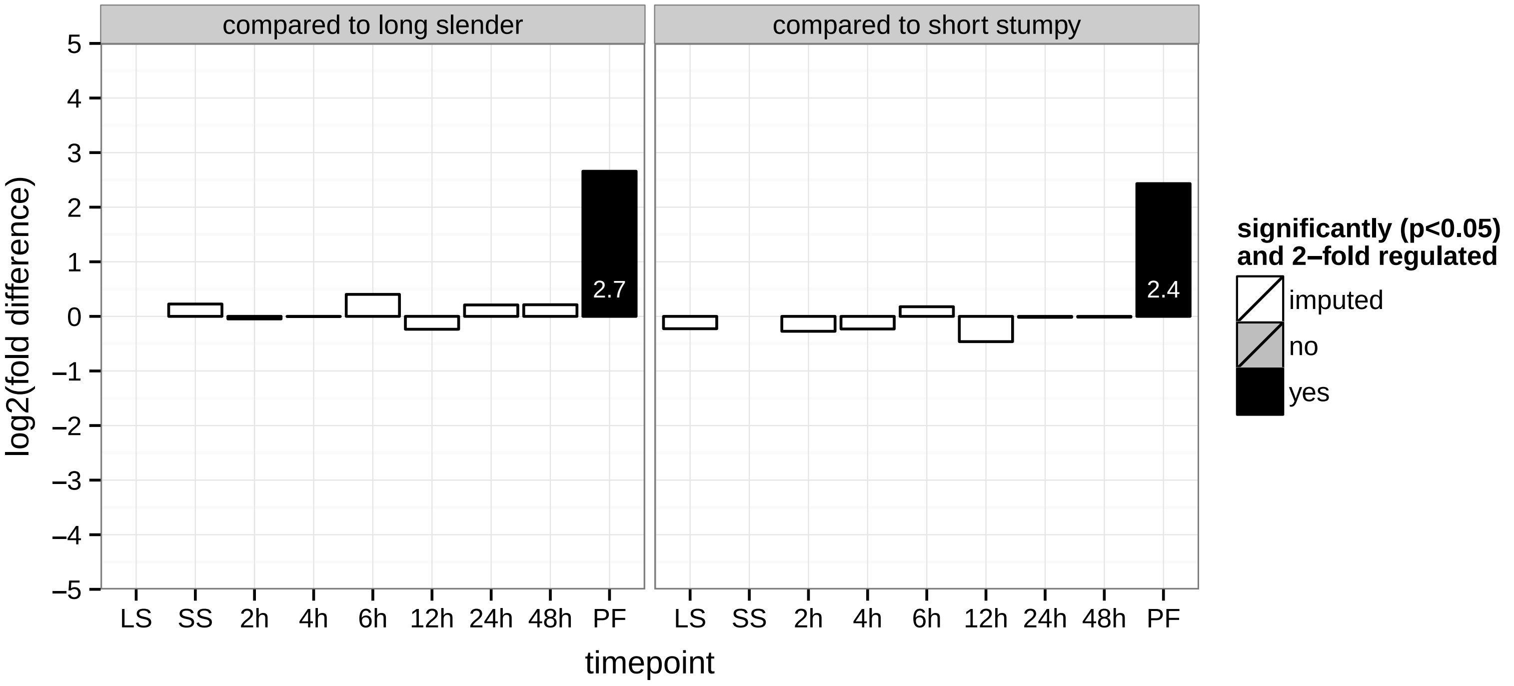
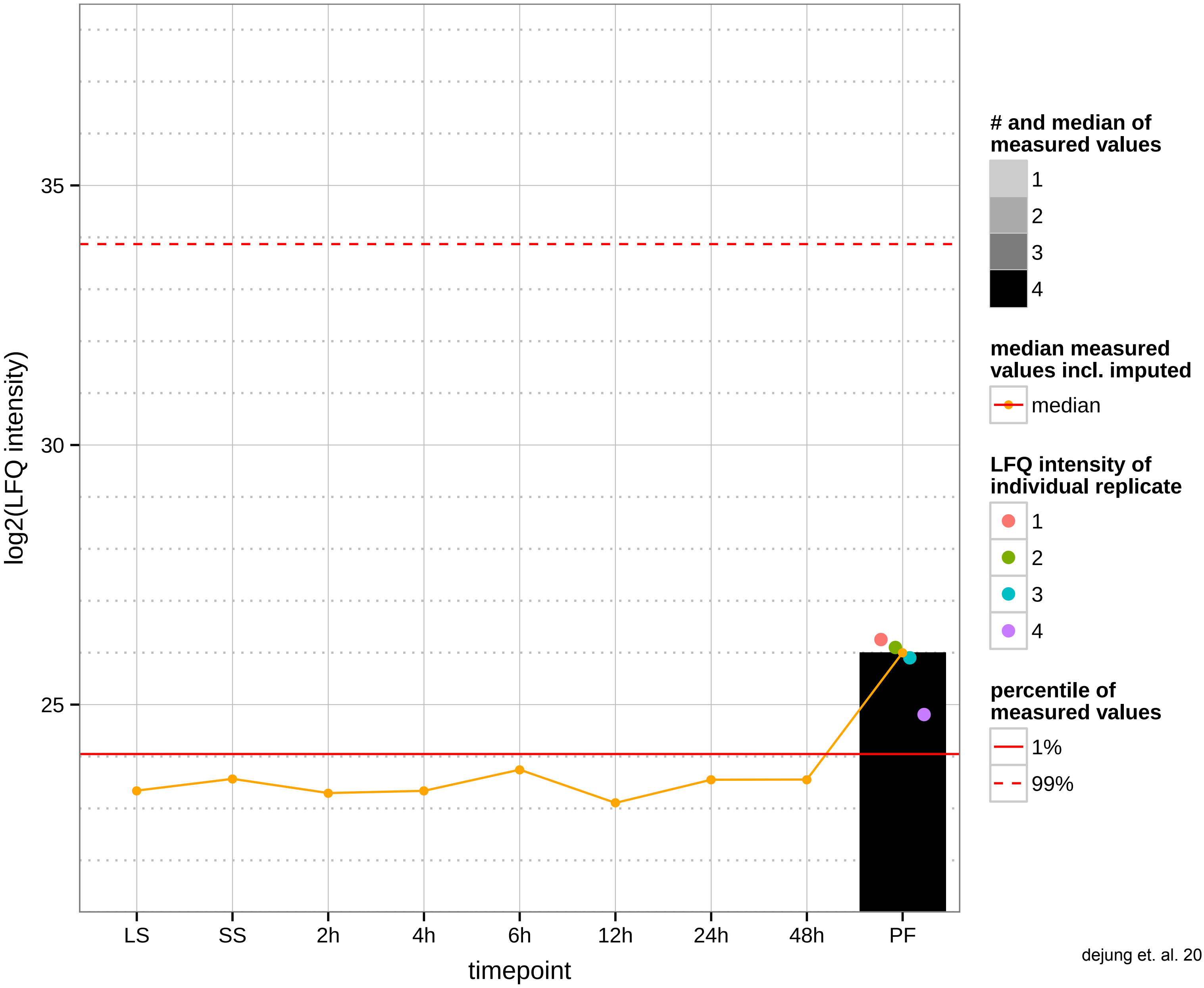
hypothetical protein, conserved
Tb927.6.4700
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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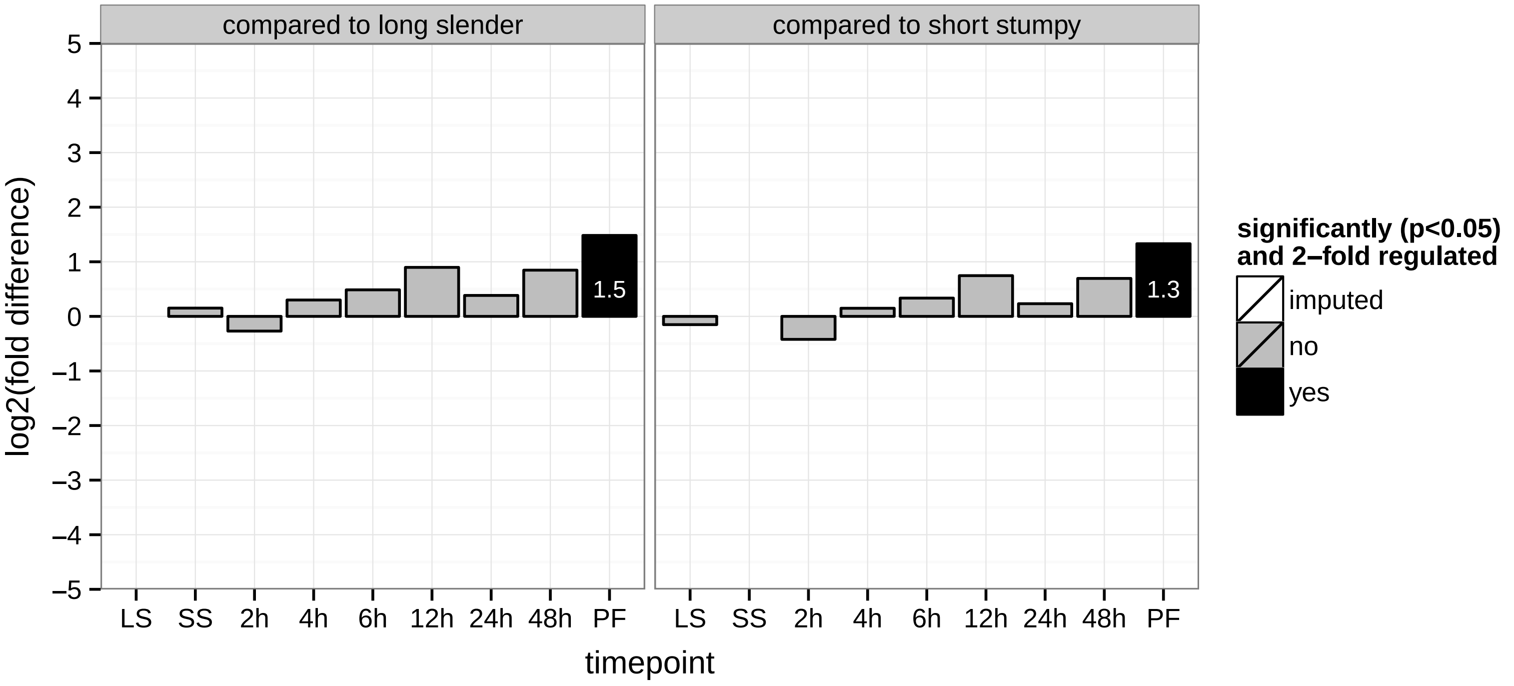
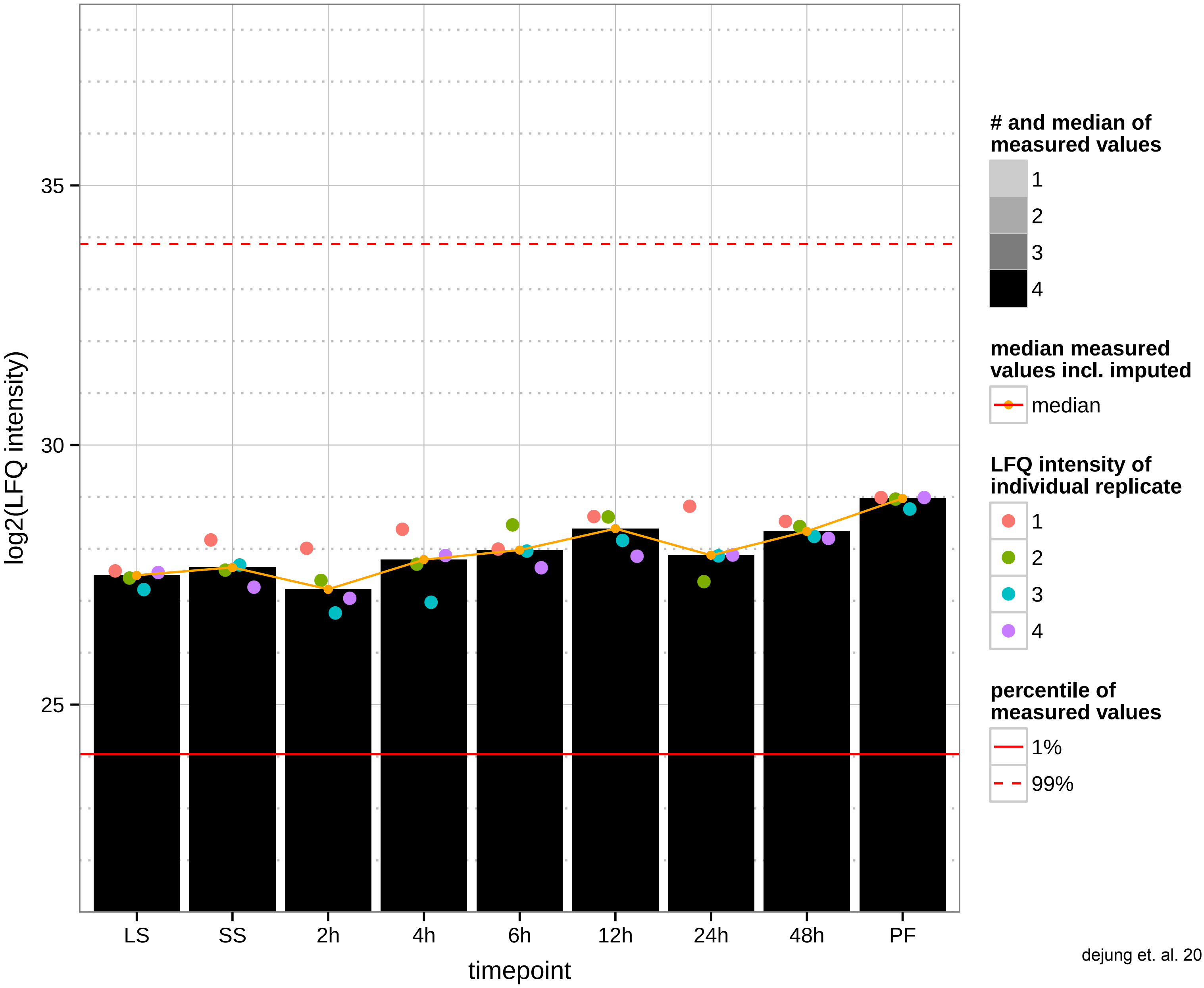
CCR4 associated factor, putative, CAF1 family ribonuclease, putative (CAF1)
Tb927.6.600
AGOF: poly(A) RNA binding
AGOC: cytoplasm, nucleus
AGOP: mRNA catabolic process
PGOF: nucleic acid binding
PGOC: nucleus
PGOP: null





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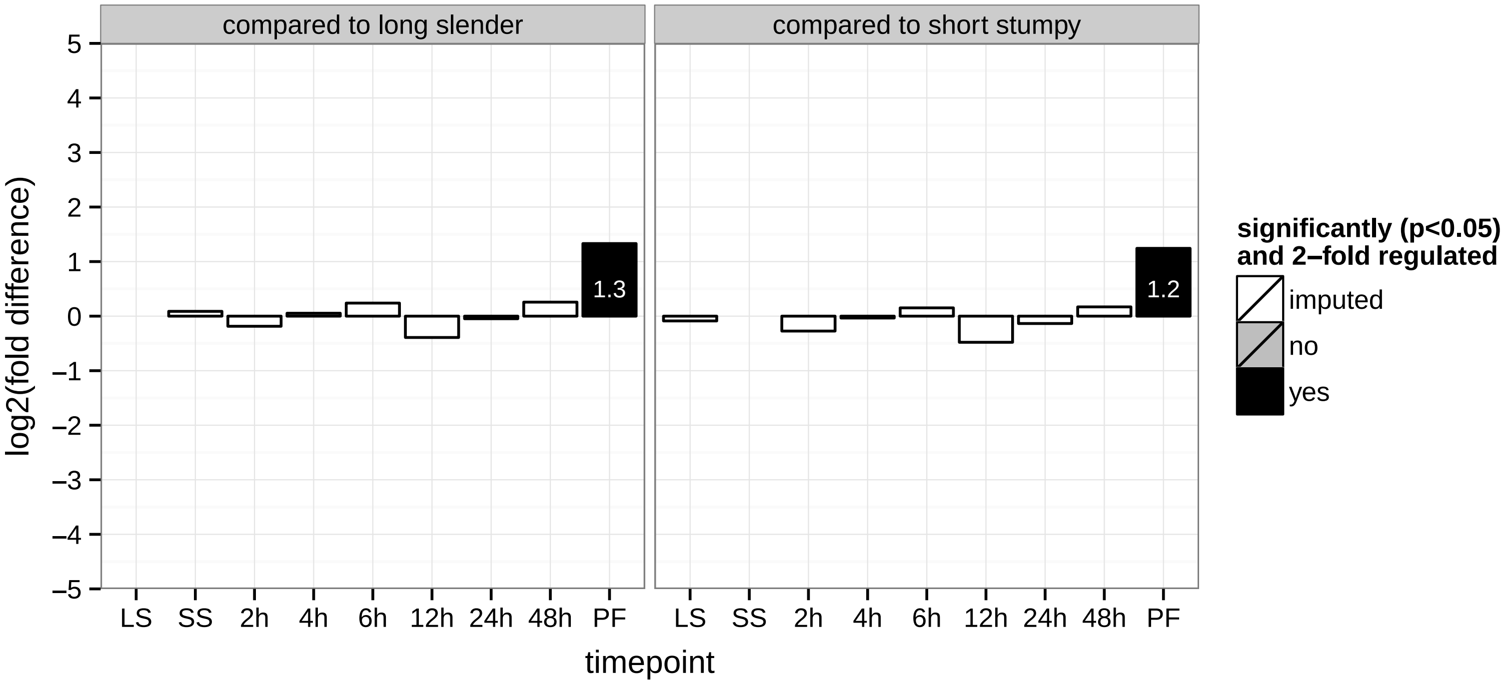
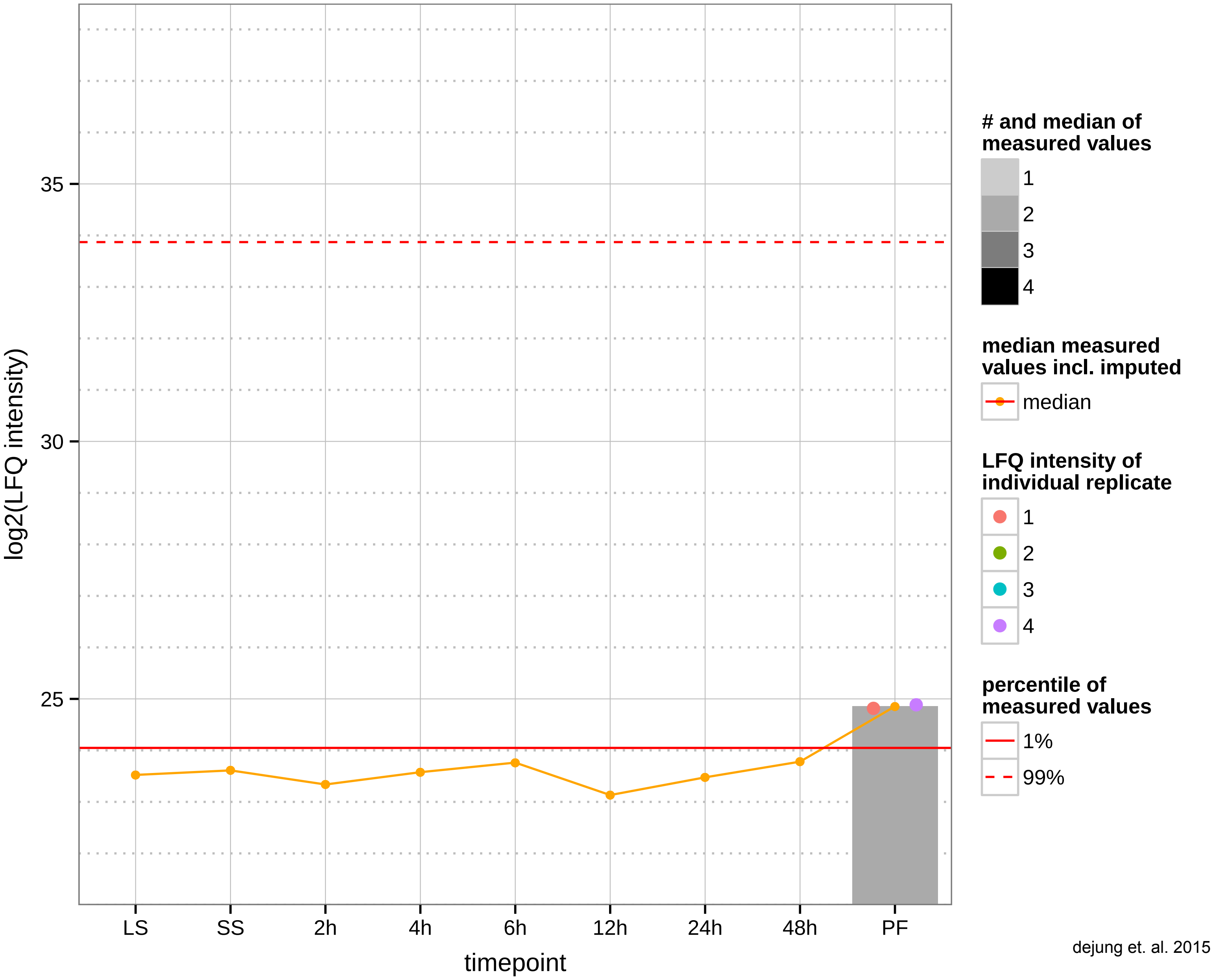
hypothetical protein, conserved
Tb927.6.890
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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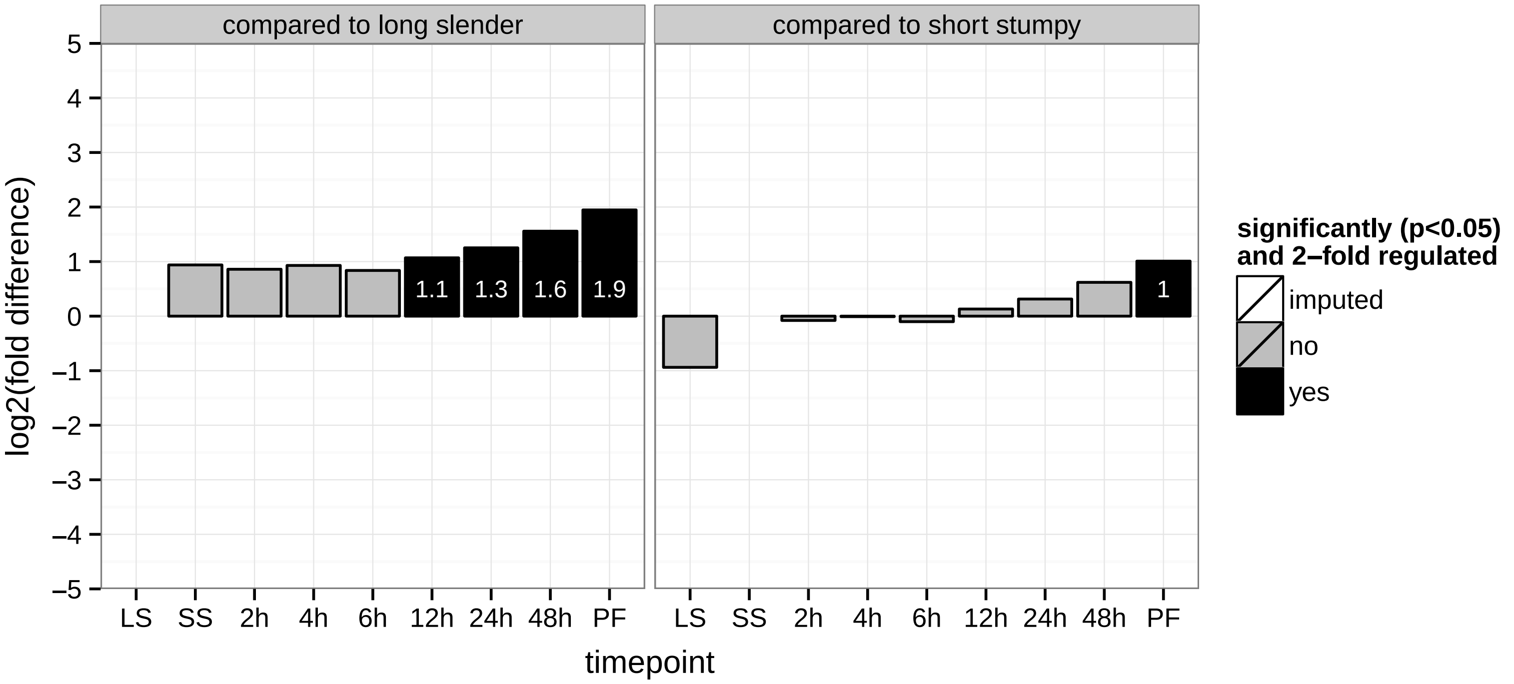
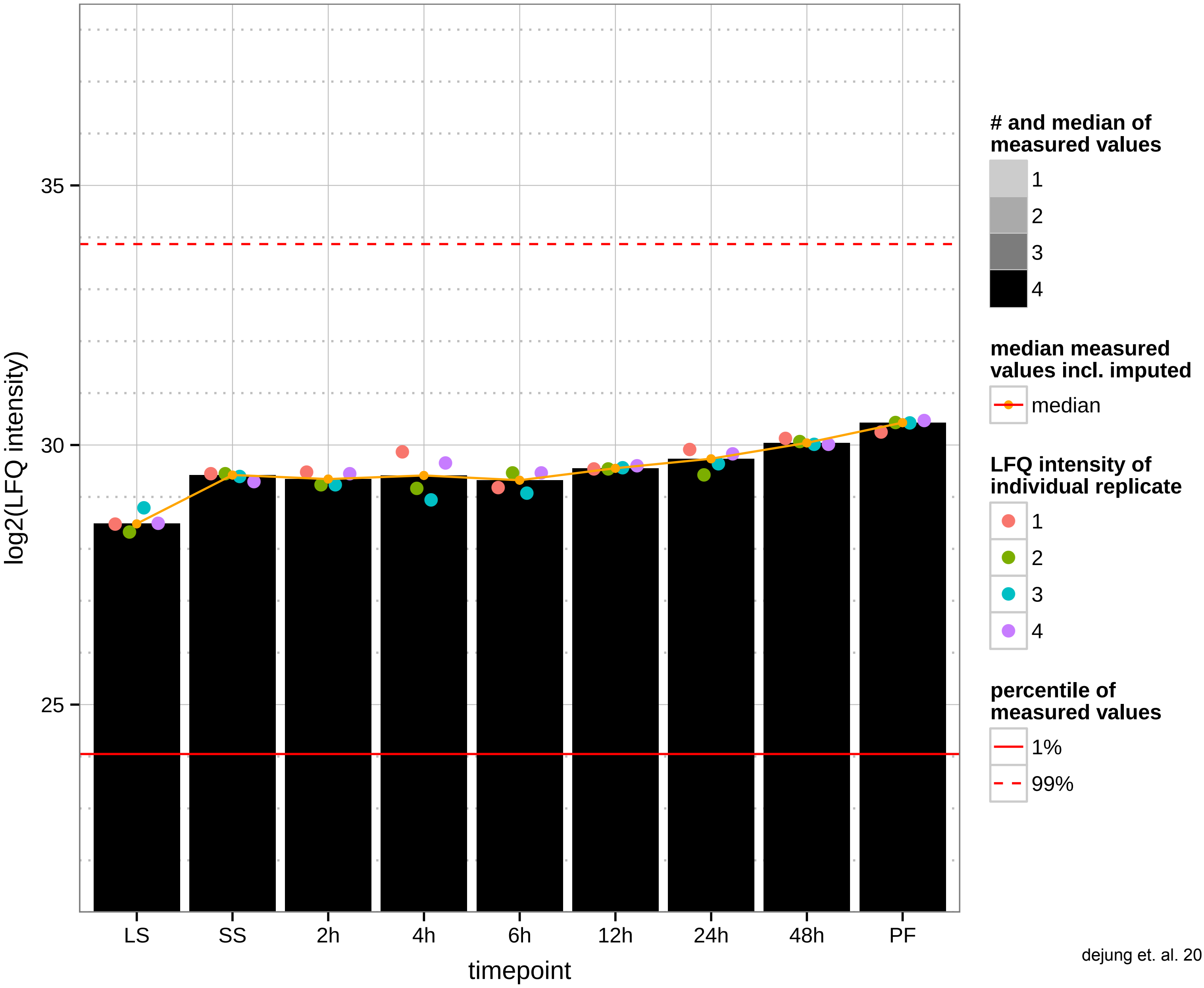
cysteinyl–tRNA synthetase, putative
Tb927.6.950
AGOF: ATP binding, cysteine–tRNA ligase activity
AGOC: cytoplasm
AGOP: cysteinyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, cysteine–tRNA ligase activity, nucleotide binding
PGOC: cytoplasm
PGOP: cysteinyl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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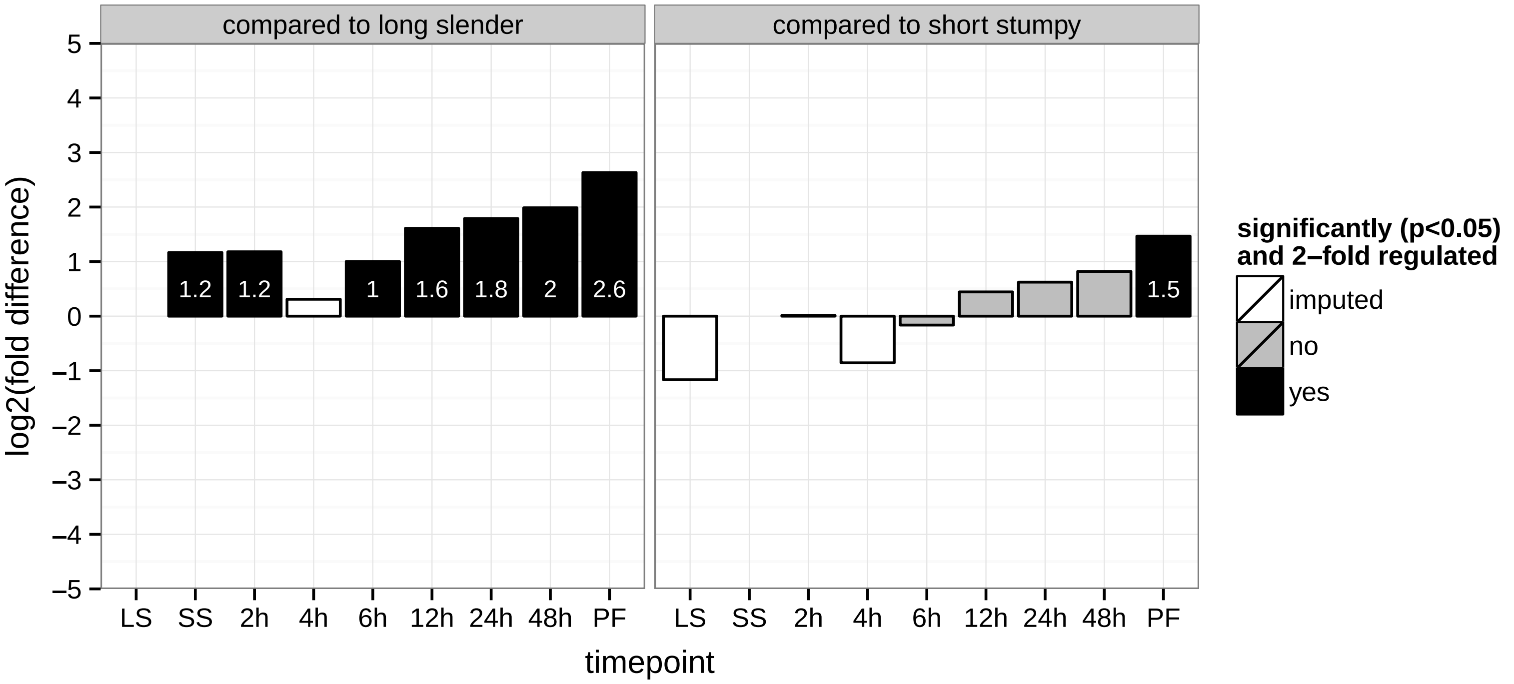
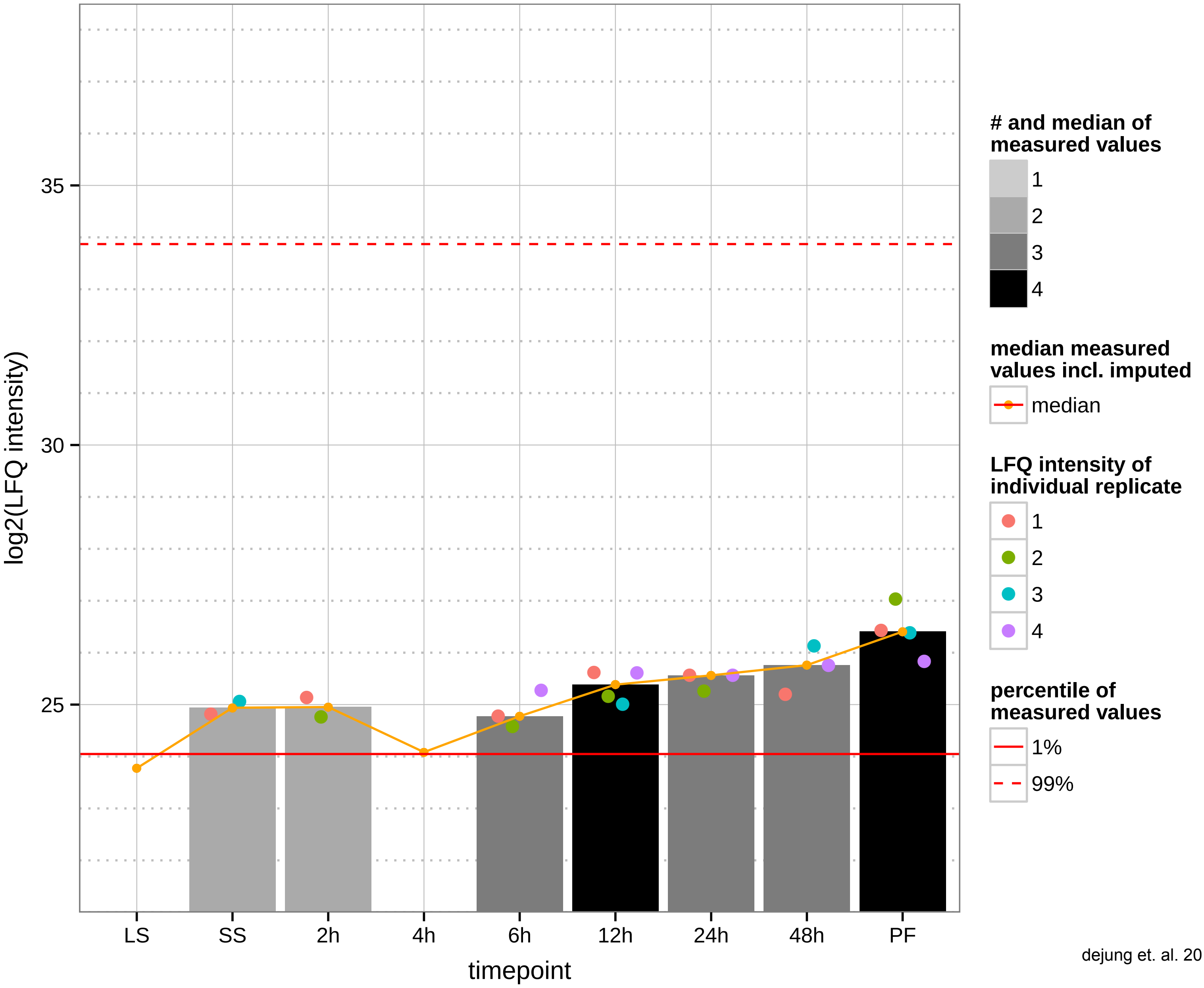
hypothetical protein, conserved
Tb927.7.1220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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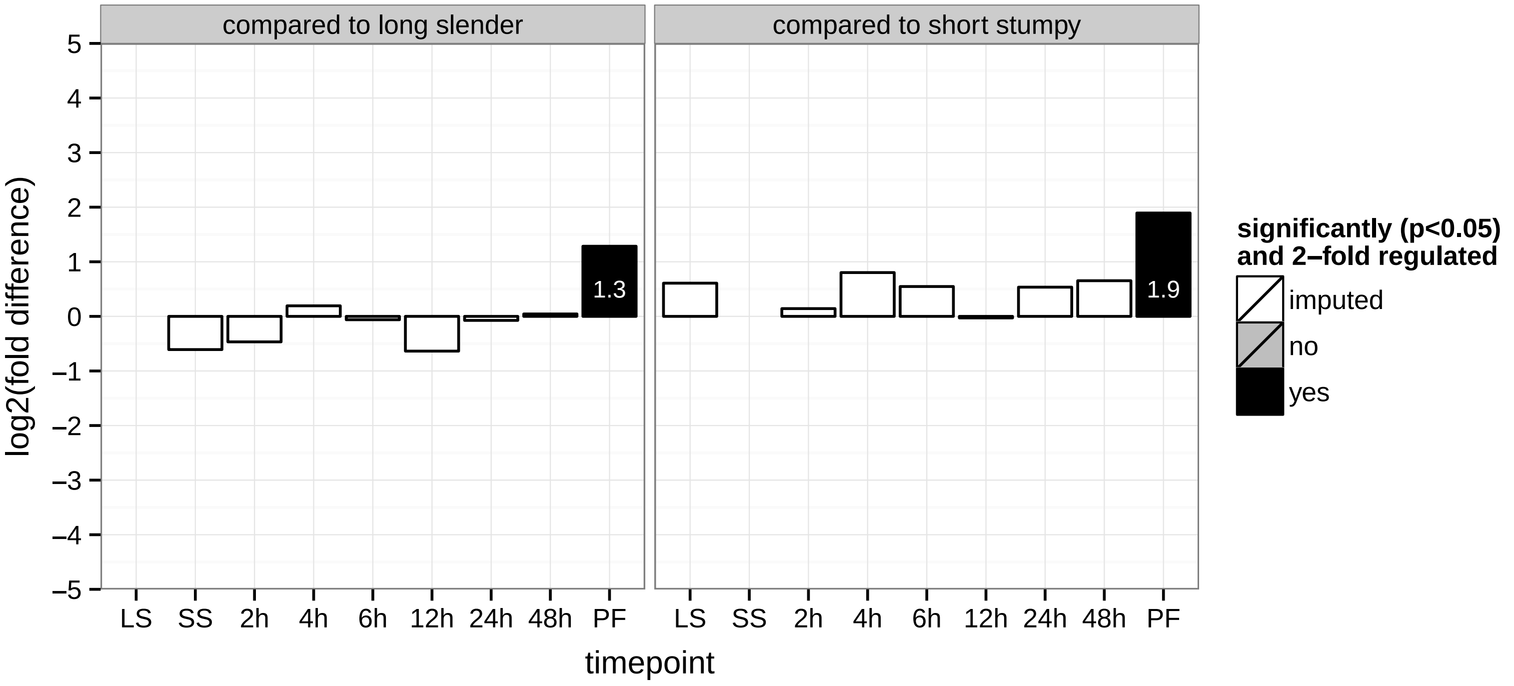
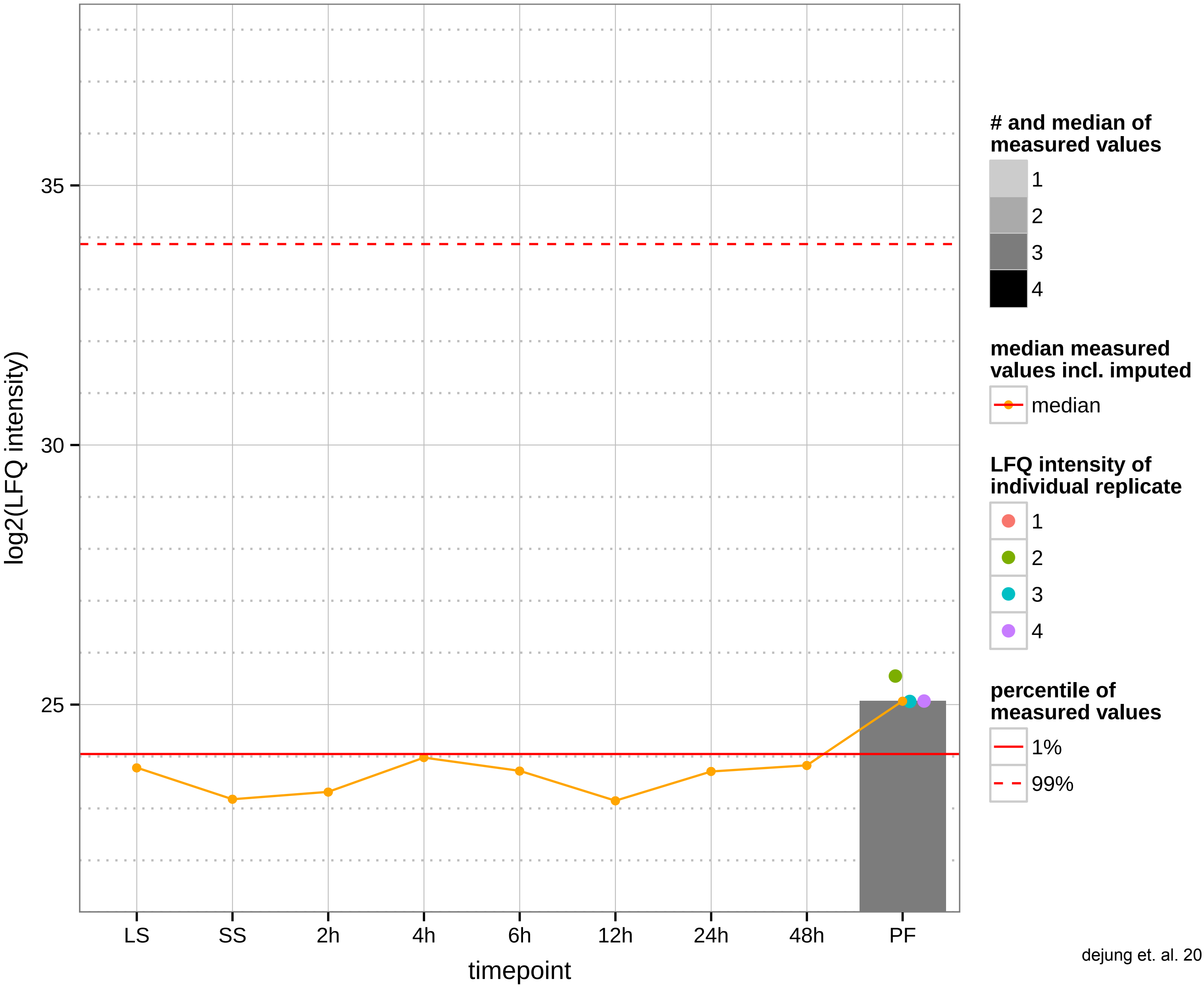
hypothetical protein, conserved
Tb927.7.1460
AGOF: protein transporter activity
AGOC: cytoplasm, nuclear pore, nucleus
AGOP: intracellular protein transport, protein import into nucleus, docking
PGOF: binding, protein transporter activity
PGOC: null
PGOP: intracellular protein transport





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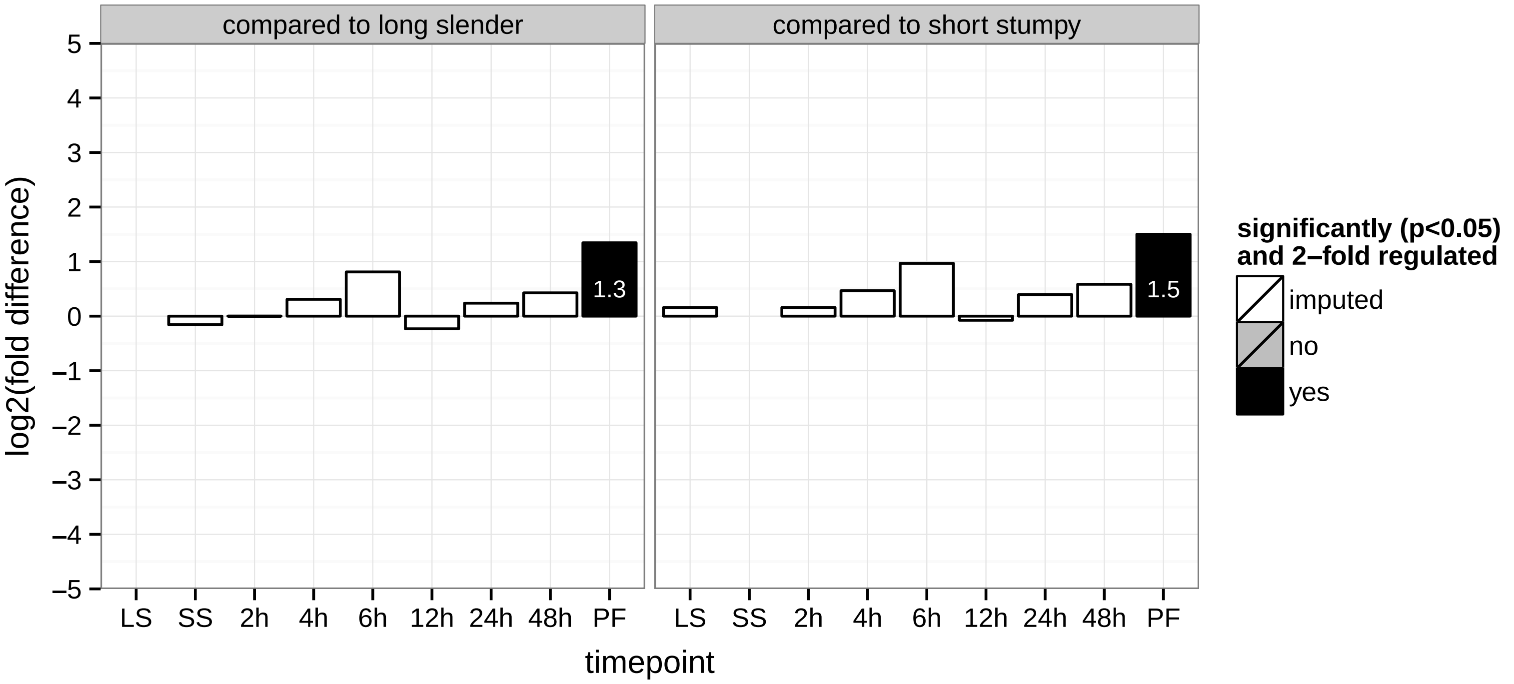
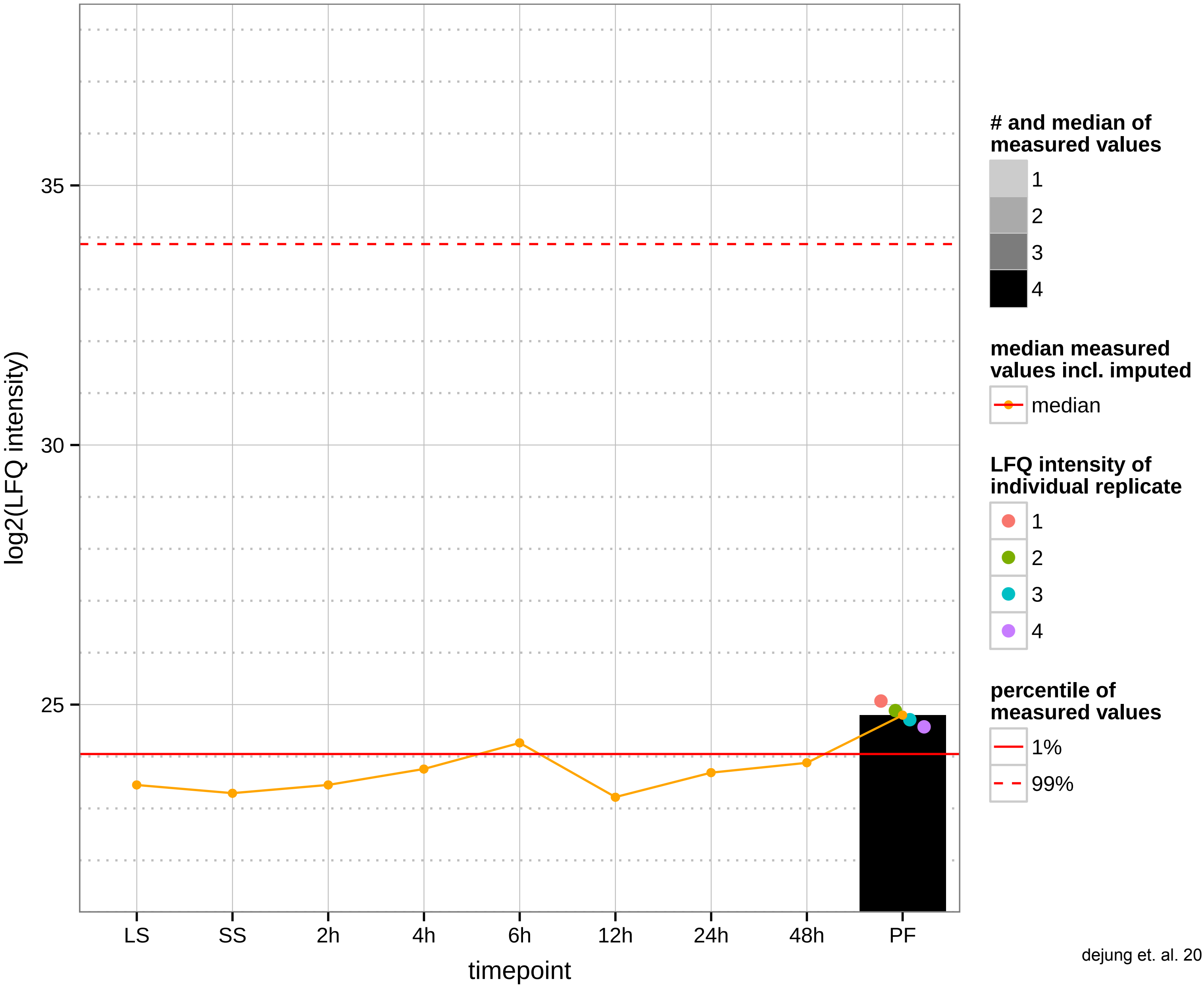
KRET2, RNA–editing 3' terminal uridylyl transferase 2, RNA–editing complex protein (KRET2)
Tb927.7.1550
AGOF: null
AGOC: mitochondrial mRNA editing complex, mitochondrion
AGOP: null
PGOF: nucleotidyltransferase activity
PGOC: null
PGOP: null





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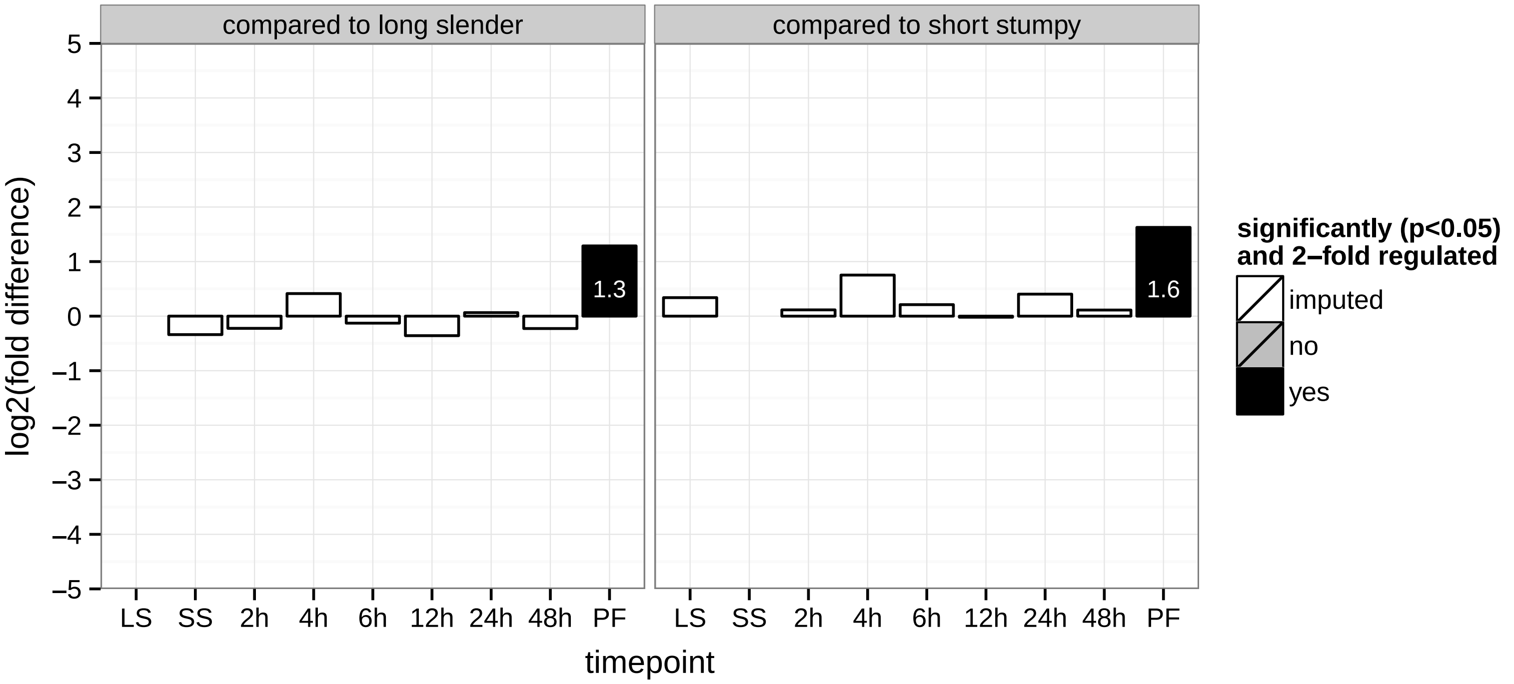
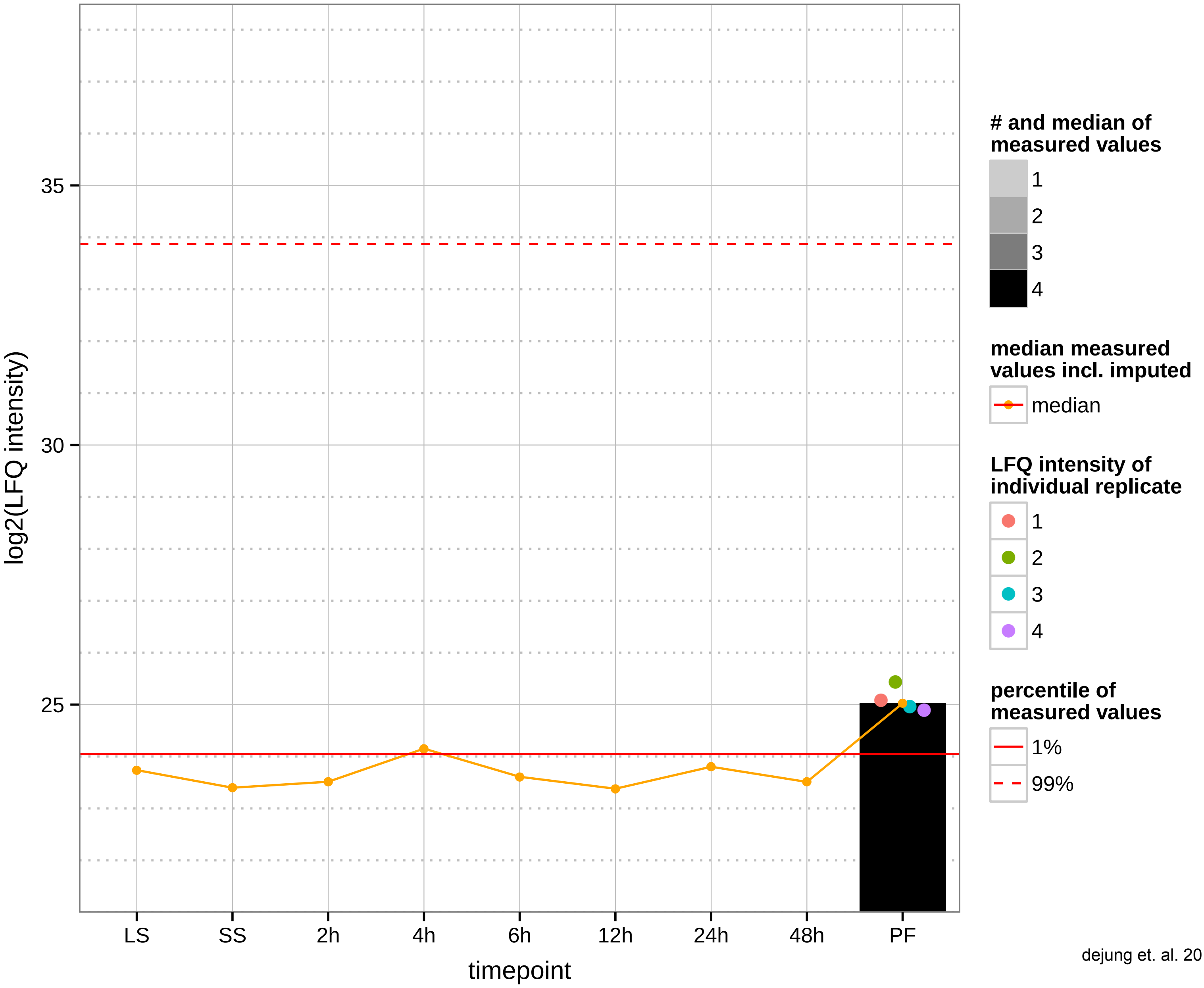
hypothetical protein, conserved
Tb927.7.1700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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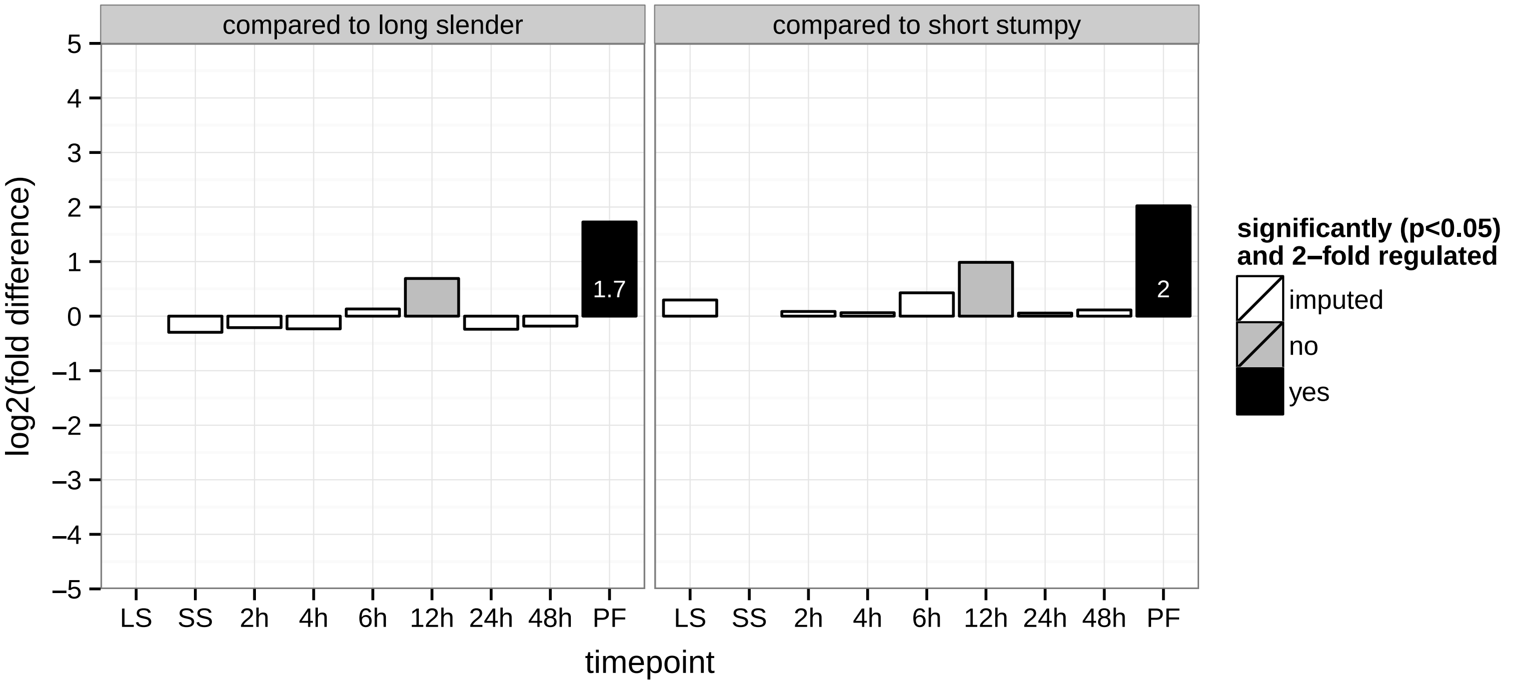
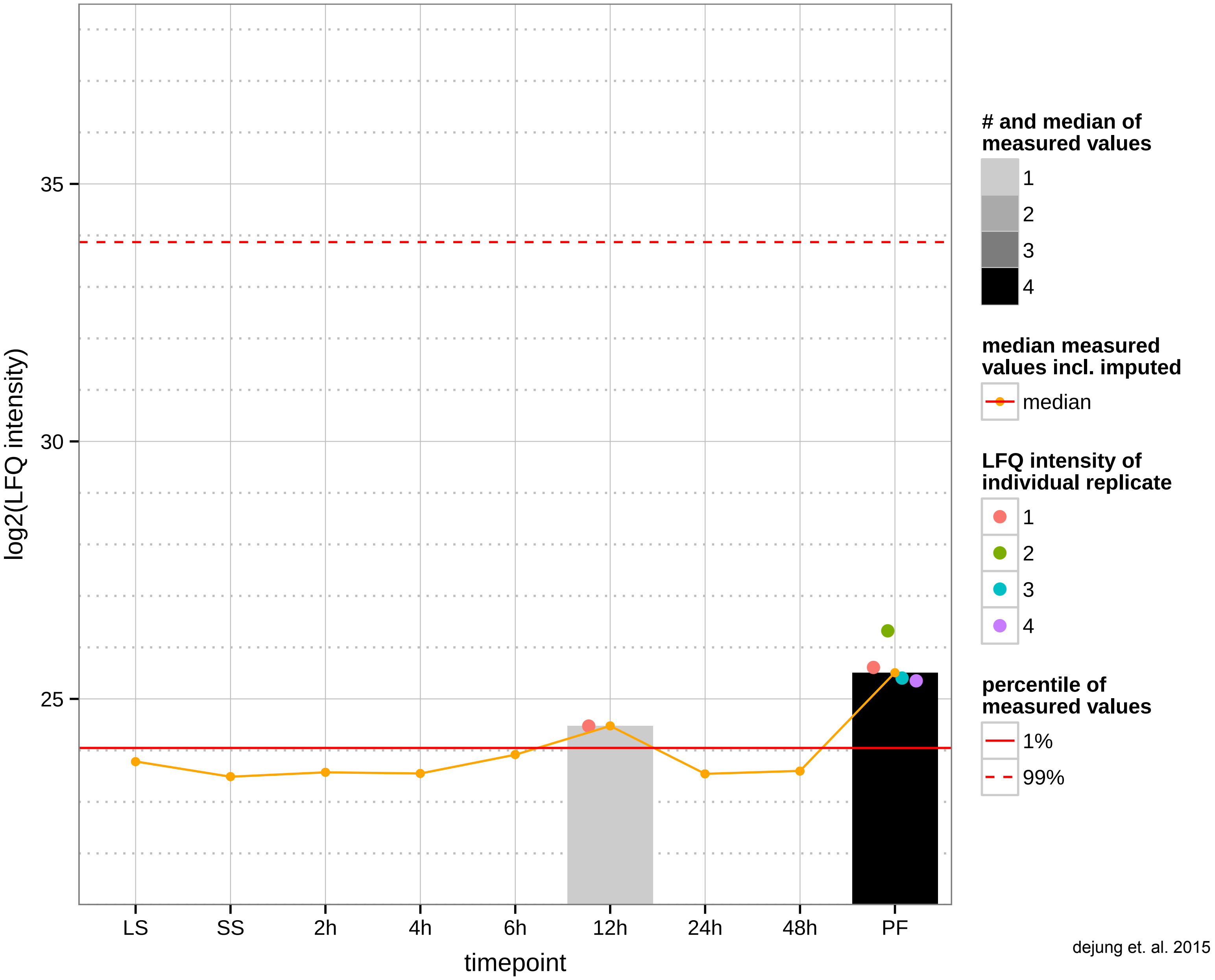
hypothetical protein, conserved
Tb927.7.1860;Tb927.7.1820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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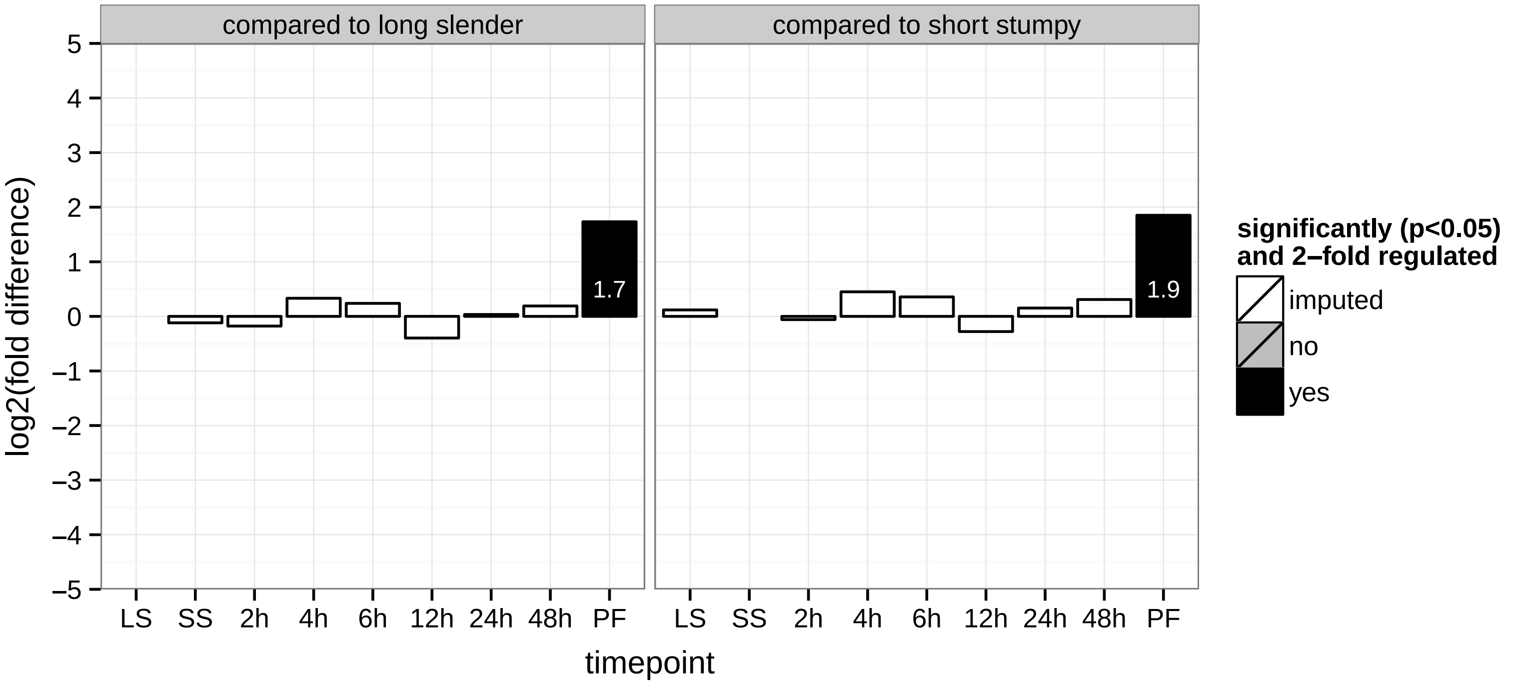
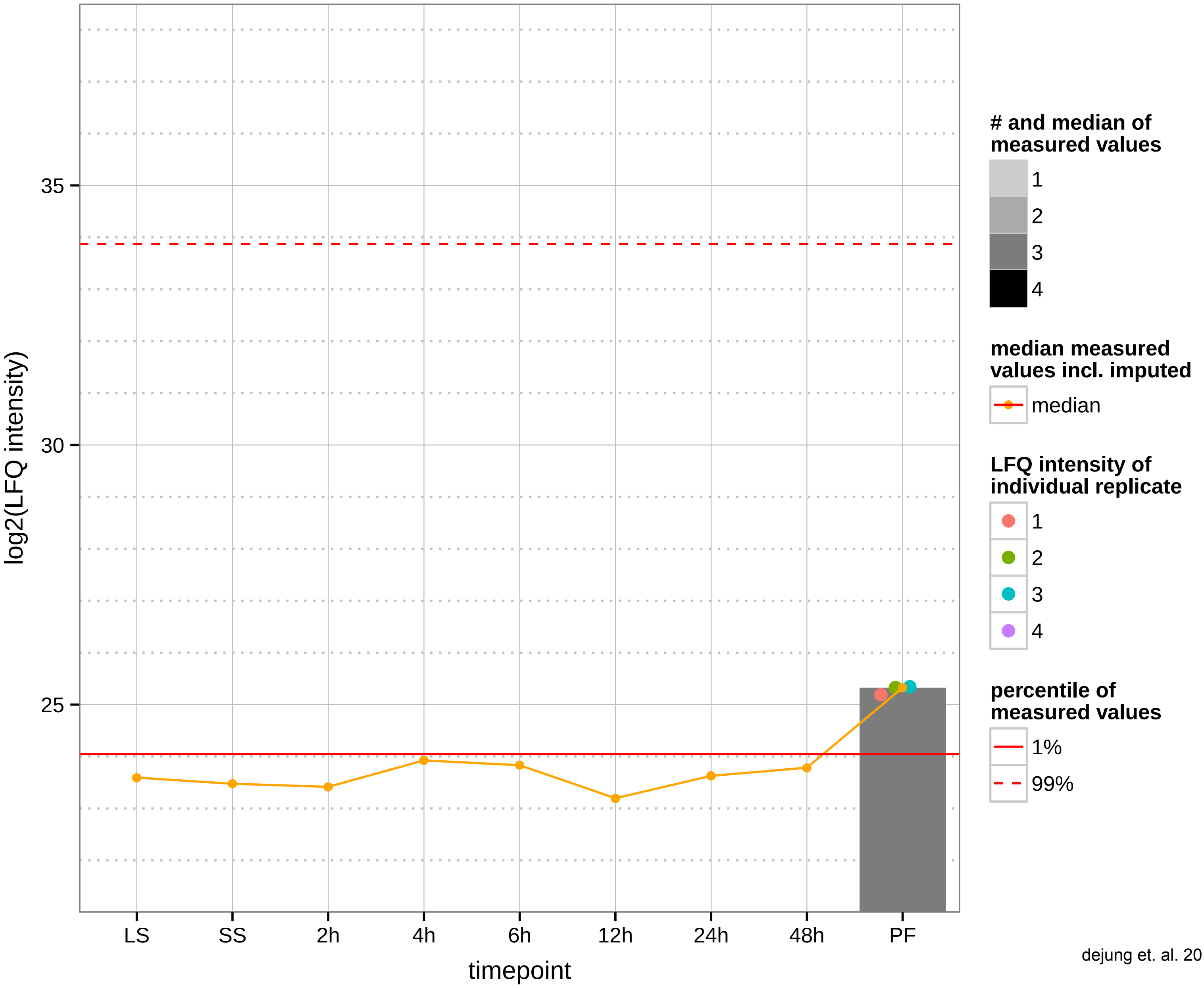
hypothetical protein, conserved
Tb927.7.1870;Tb927.7.1830
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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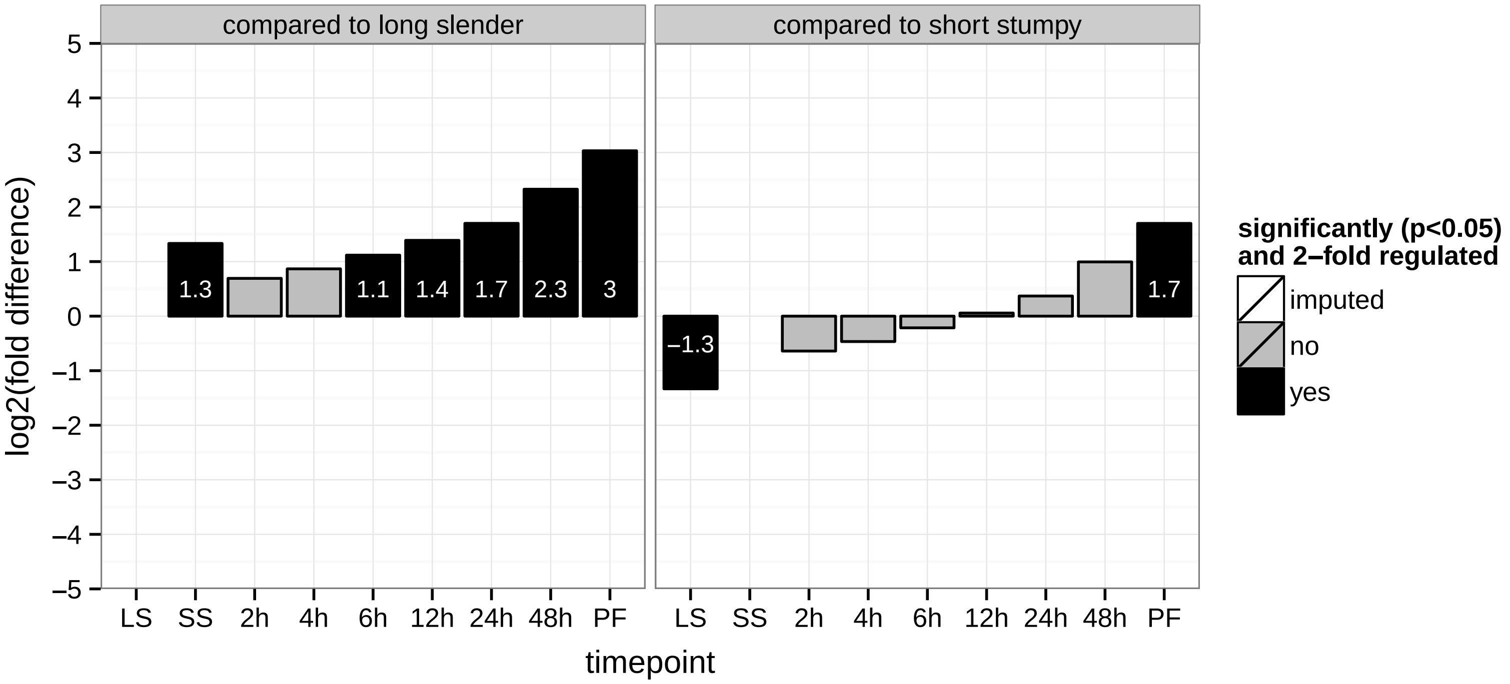
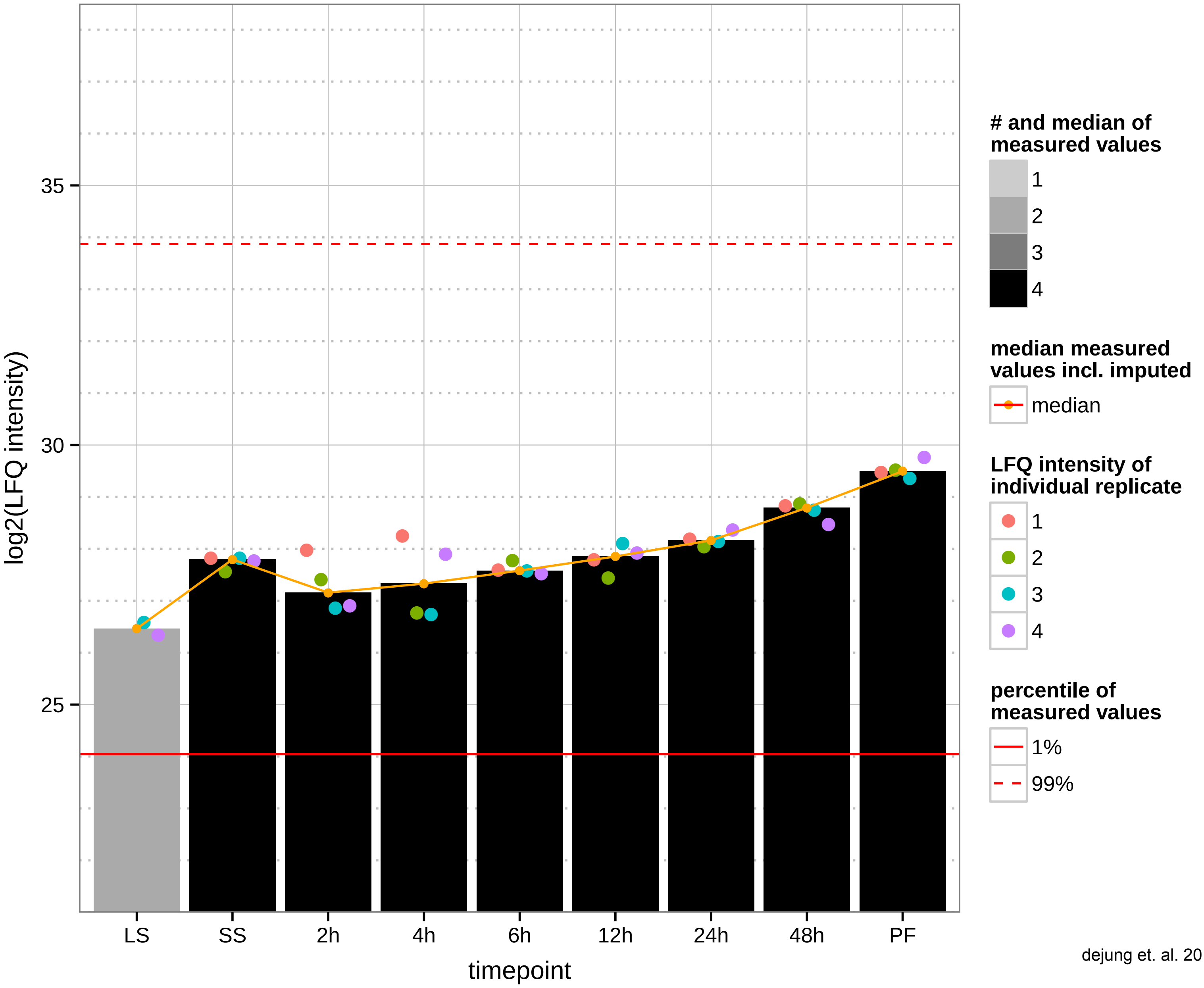
pyridoxal phosphate containing glycine decarboxylase, putative, glycine dehydrogenase, putative (GCVP)
Tb927.7.1910
AGOF: glycine dehydrogenase (decarboxylating) activity
AGOC: mitochondrion
AGOP: glycine decarboxylation via glycine cleavage system, oxidation–reduction process
PGOF: glycine dehydrogenase (decarboxylating) activity, lyase activity
PGOC: null
PGOP: cellular amino acid metabolic process, glycine metabolic process, oxidation–reduction process





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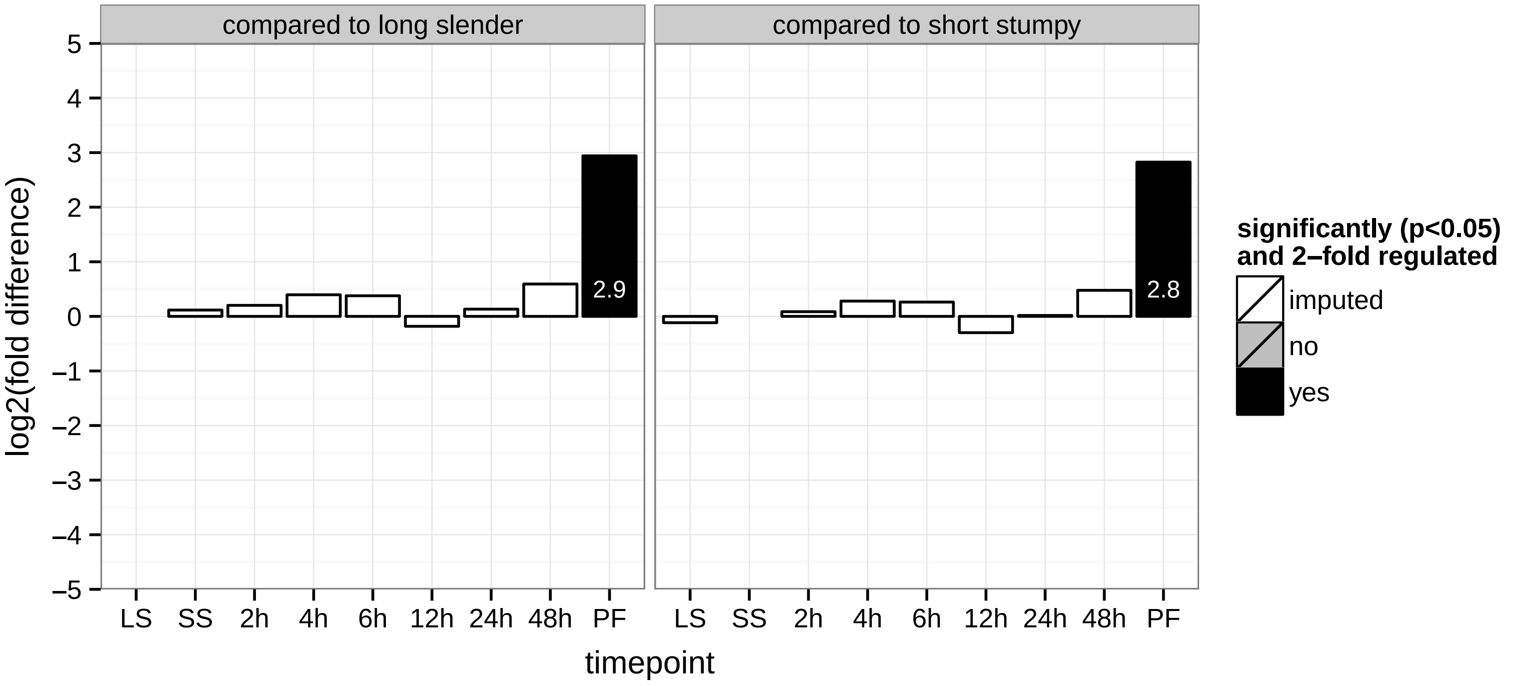
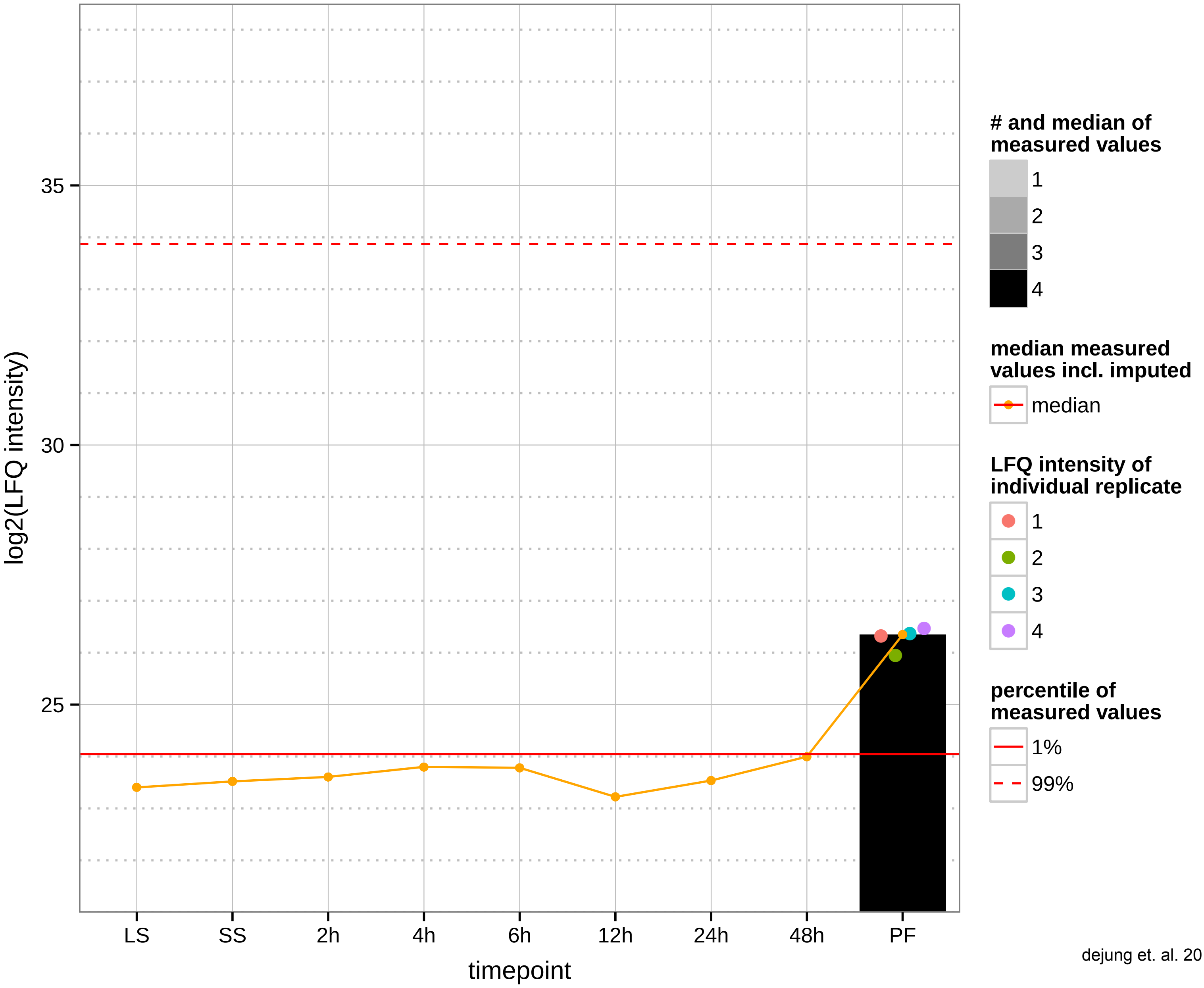
retrotransposon hot spot protein 7 (RHS7), putative, retrotransposon hot spot protein (RHS, pseudogene), point mutation
Tb927.7.1970;Tb927.7.1950;Tb927.7.1990;Tb927.7.1980;Tb927.7.1960
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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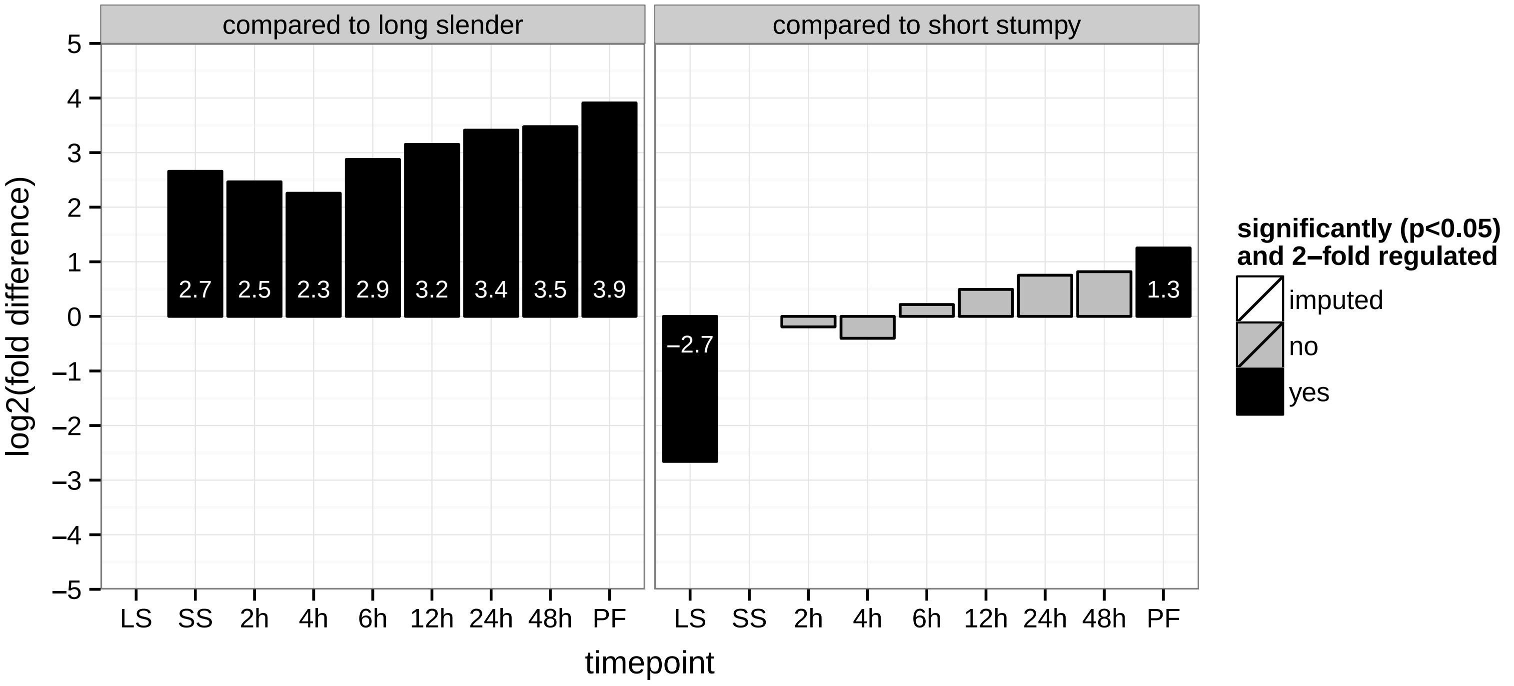
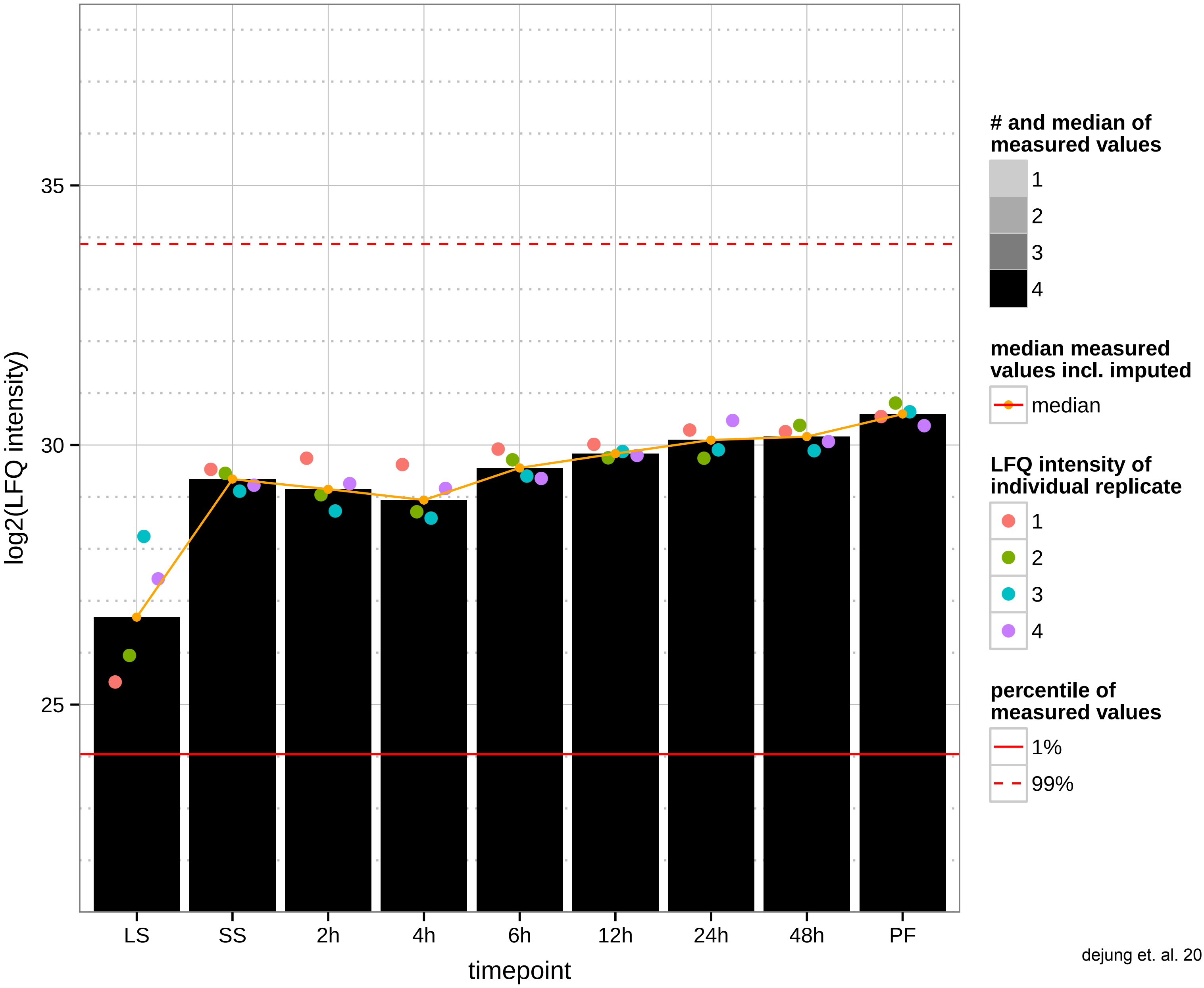
hypothetical protein, conserved
Tb927.7.2170
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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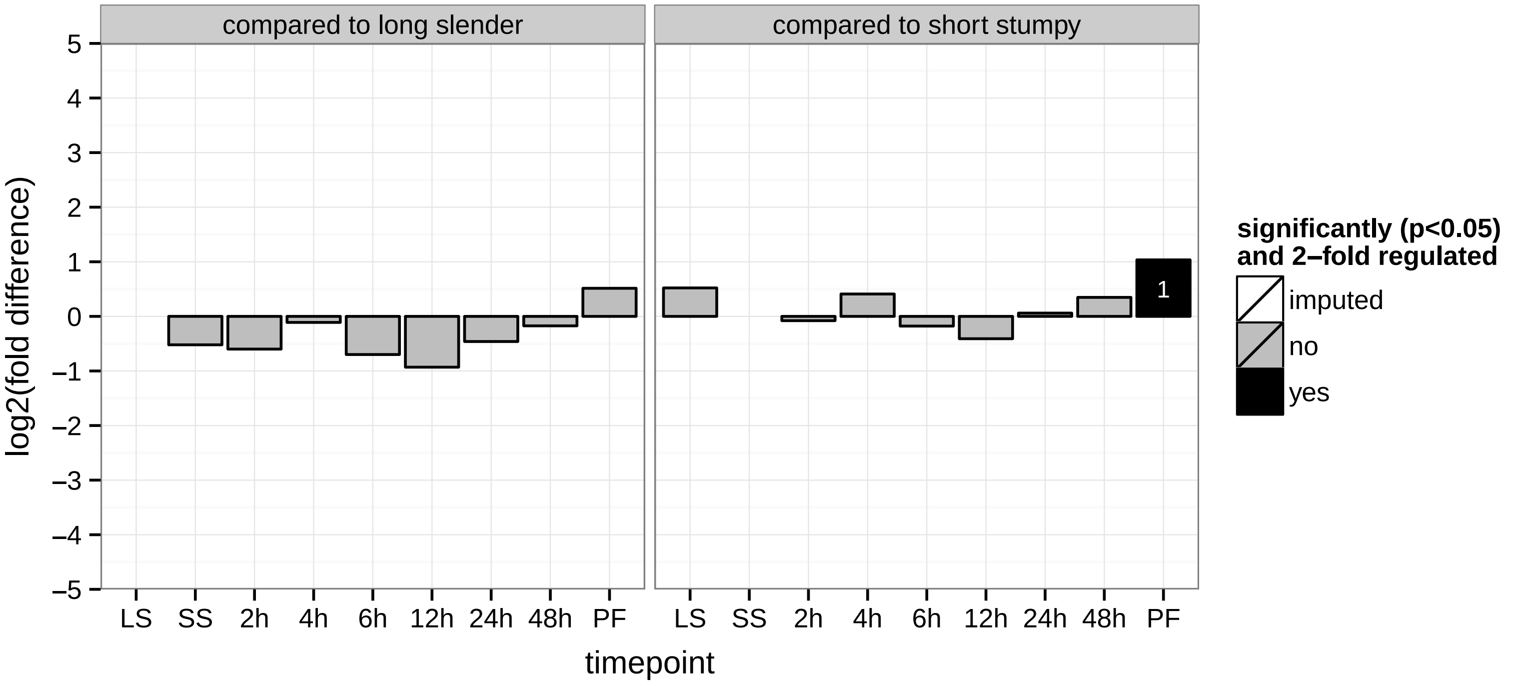
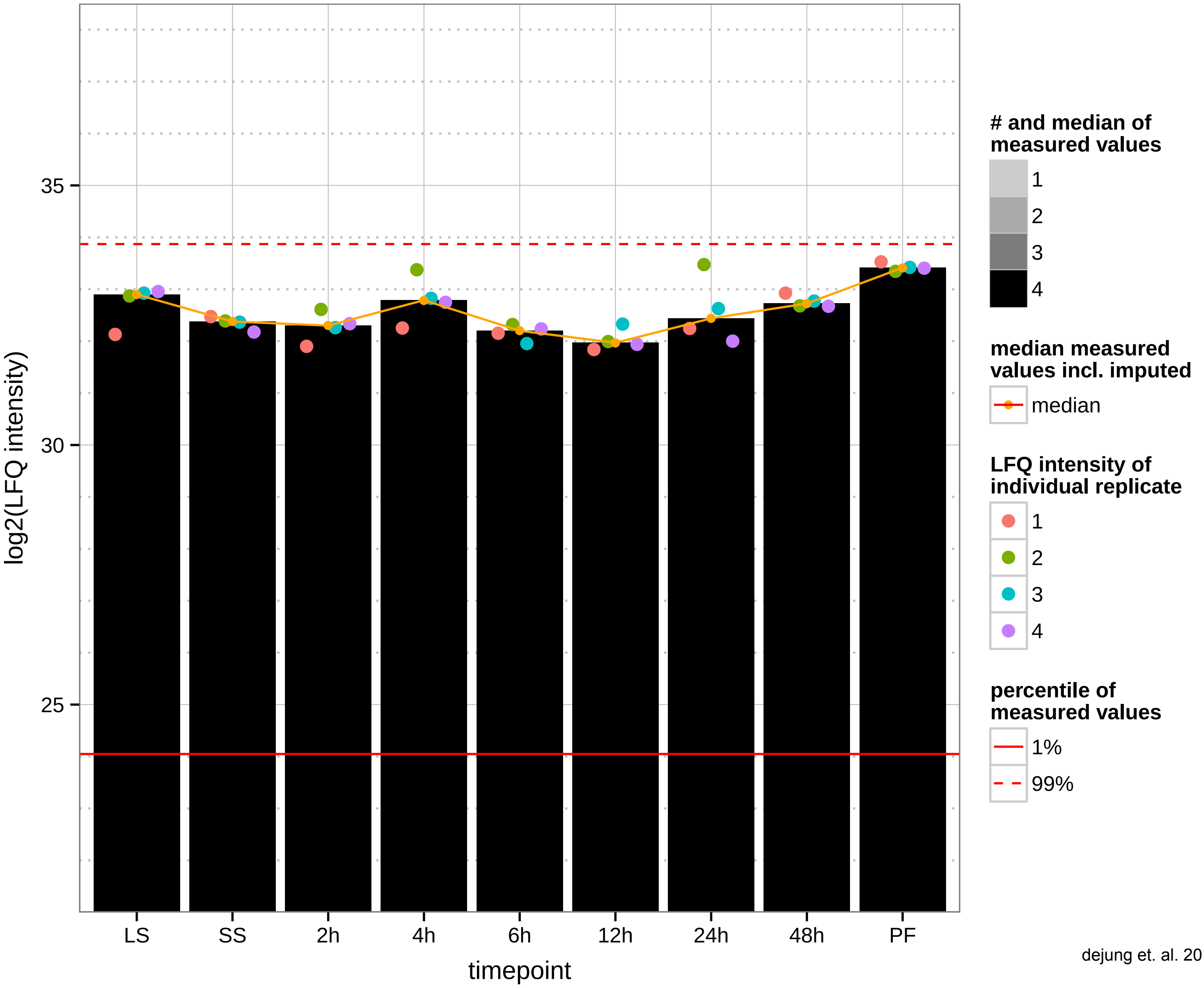
40S ribosomal protein S15, putative
Tb927.7.2340;Tb927.7.2370
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome, small ribosomal subunit
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: ribosome, small ribosomal subunit
PGOP: translation





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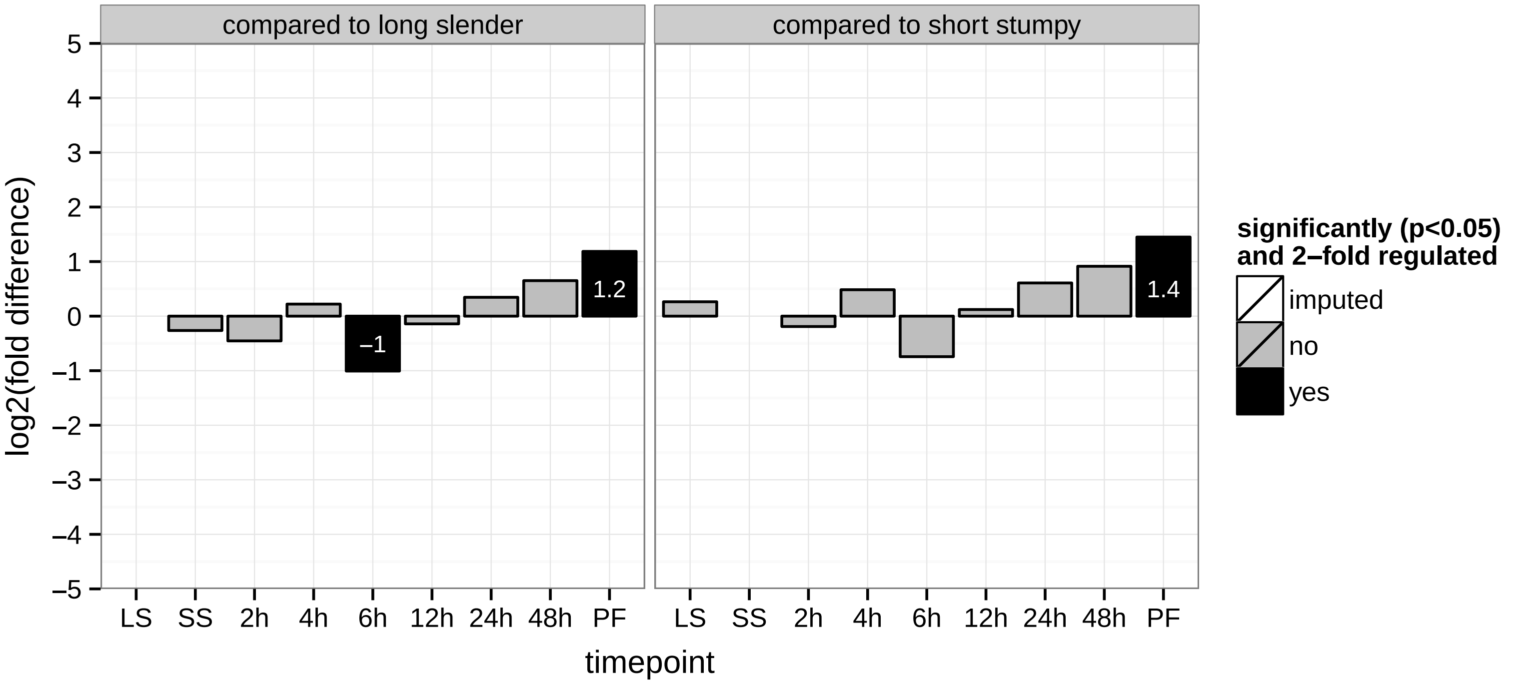
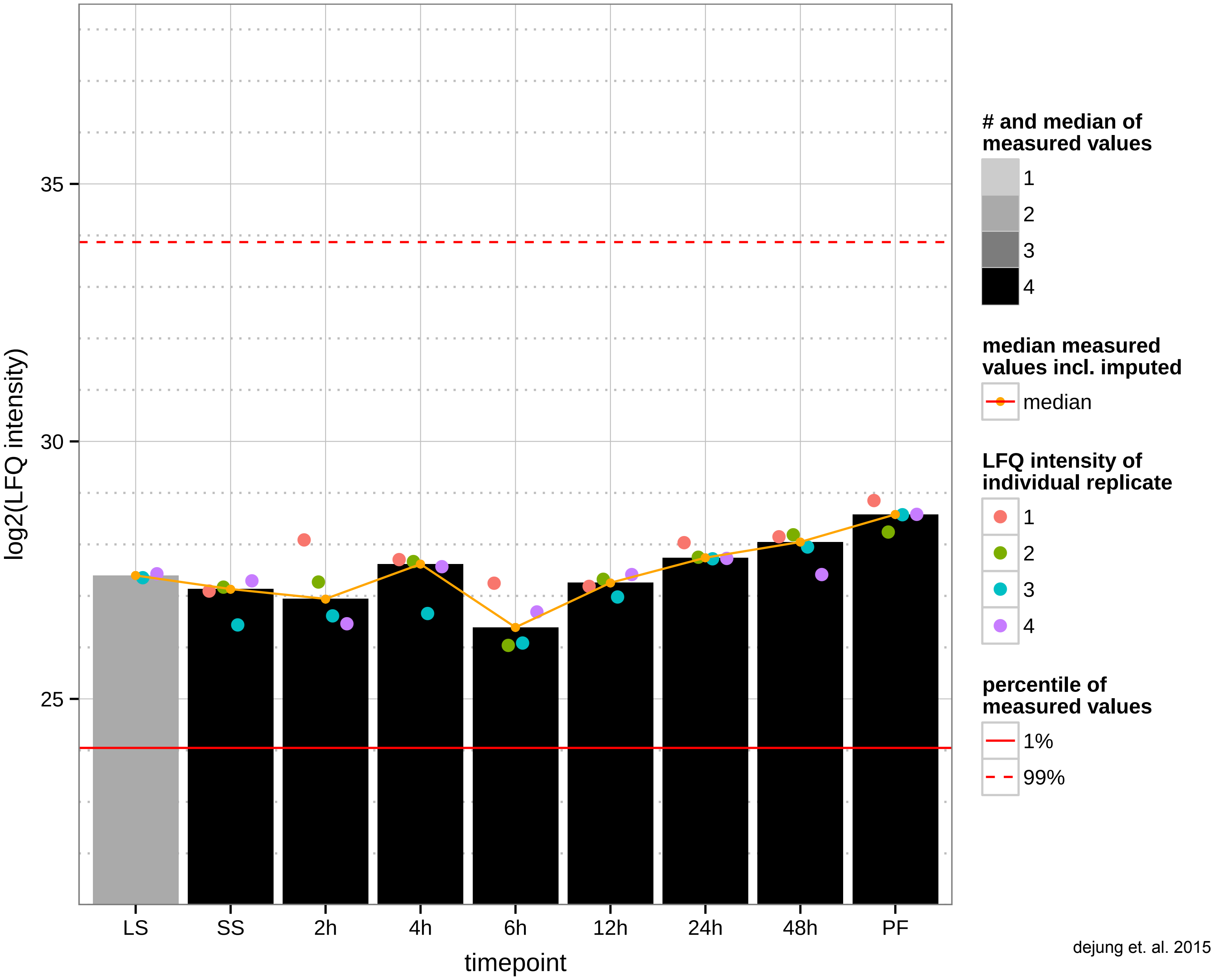
hypothetical protein, conserved
Tb927.7.3050
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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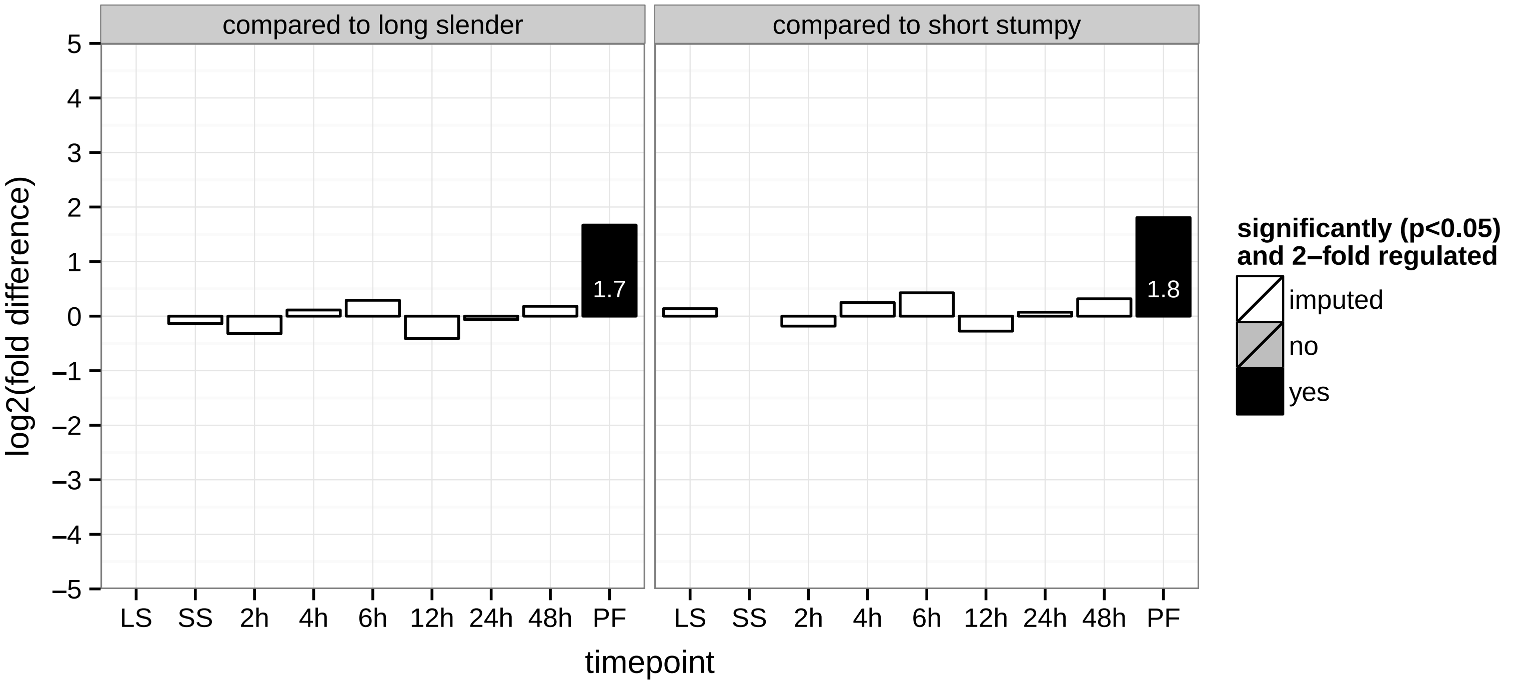
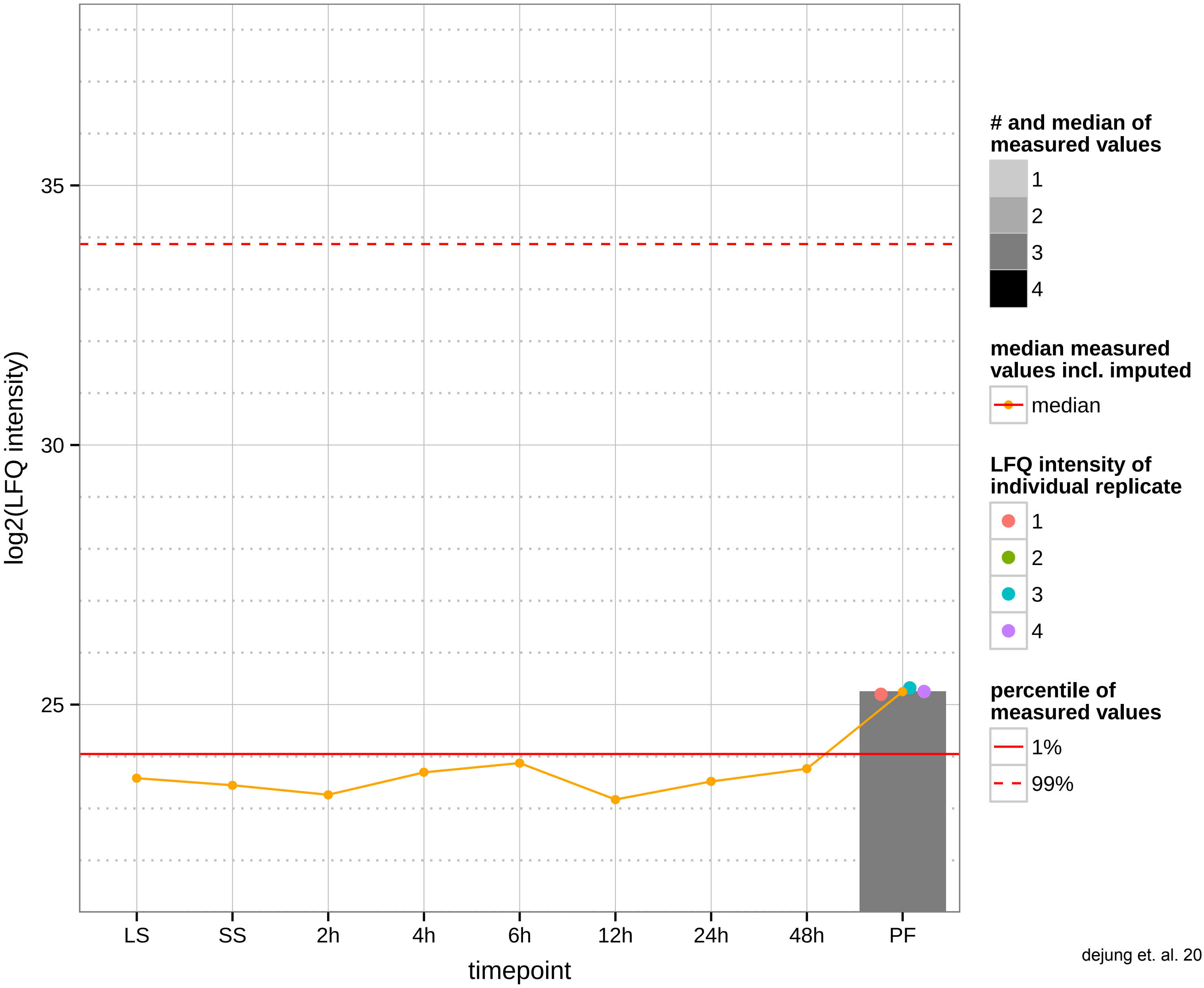
hypothetical protein, conserved
Tb927.7.3220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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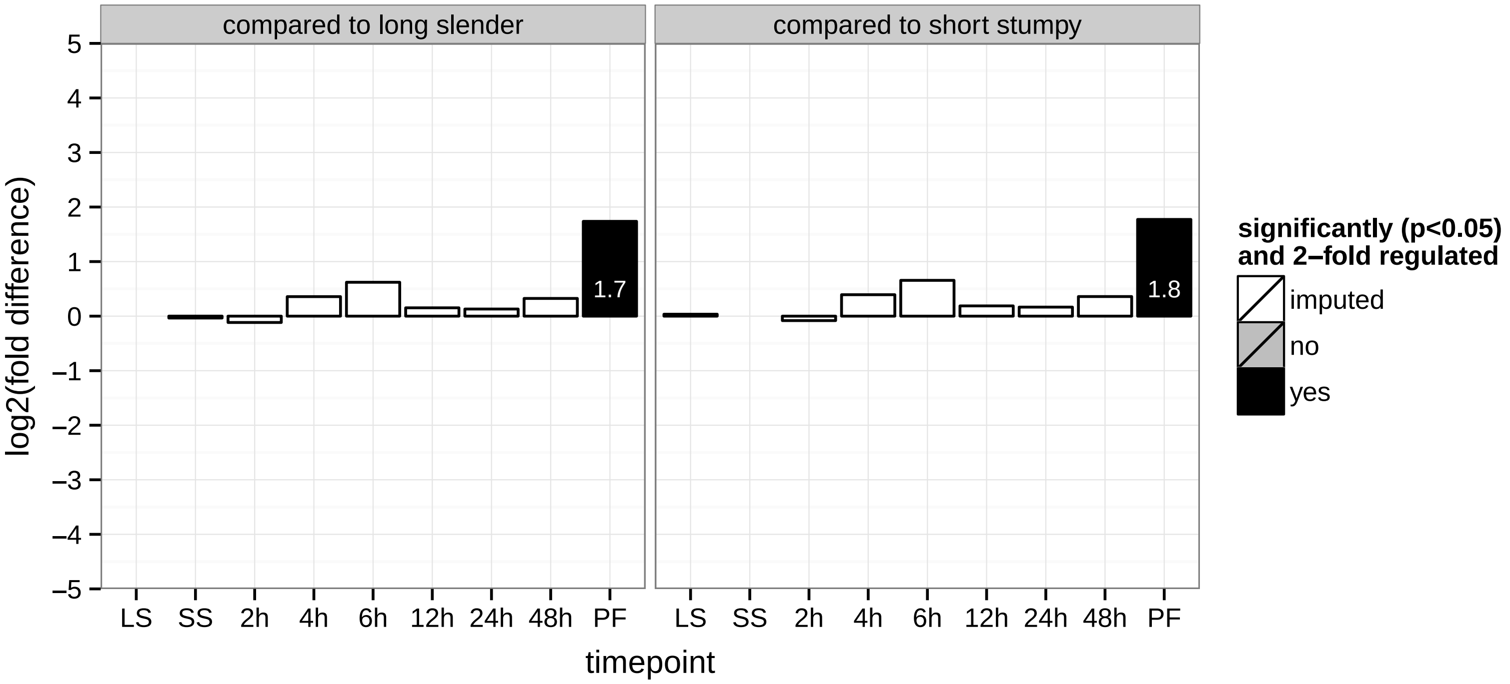
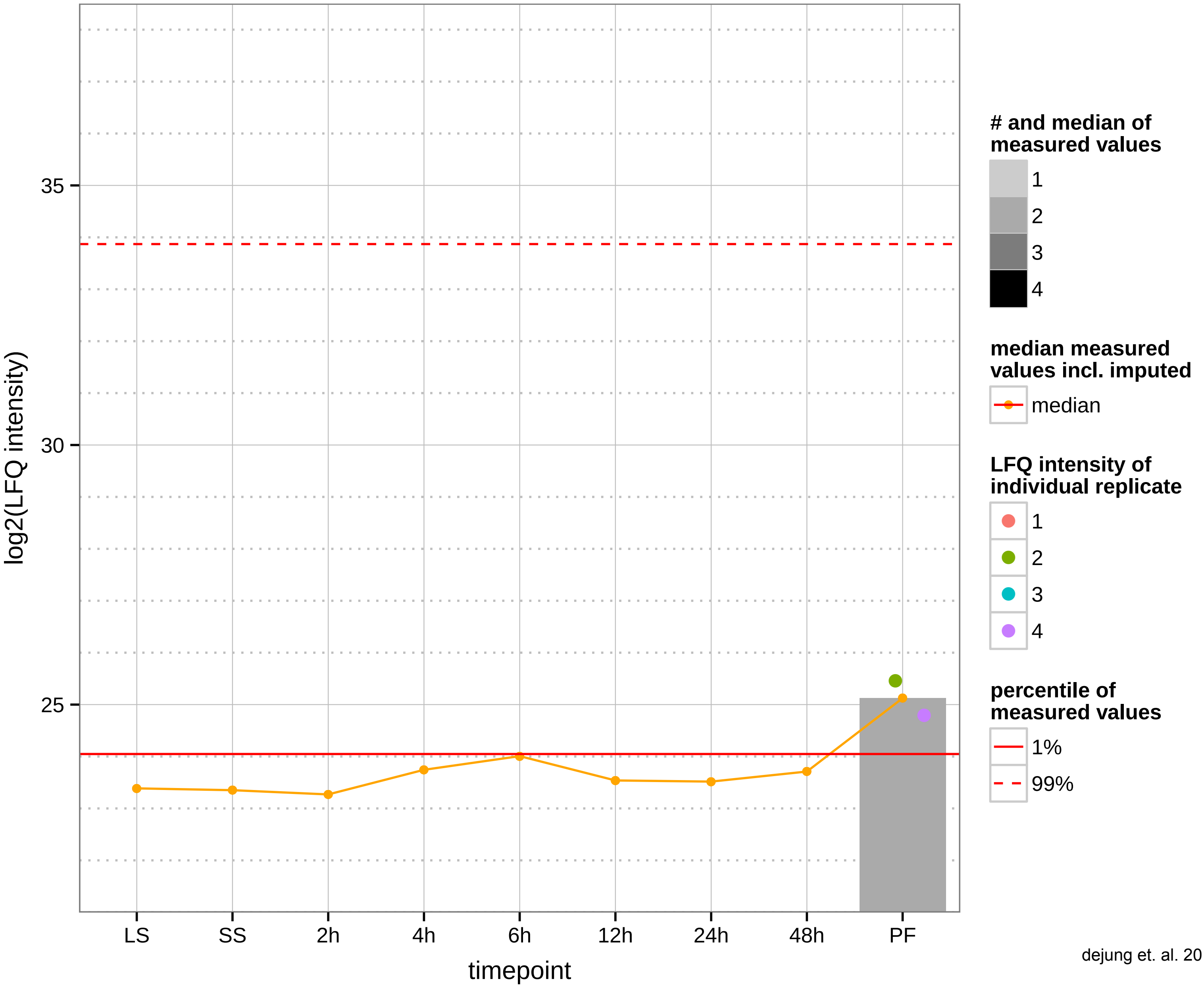
hypothetical protein, conserved
Tb927.7.3240
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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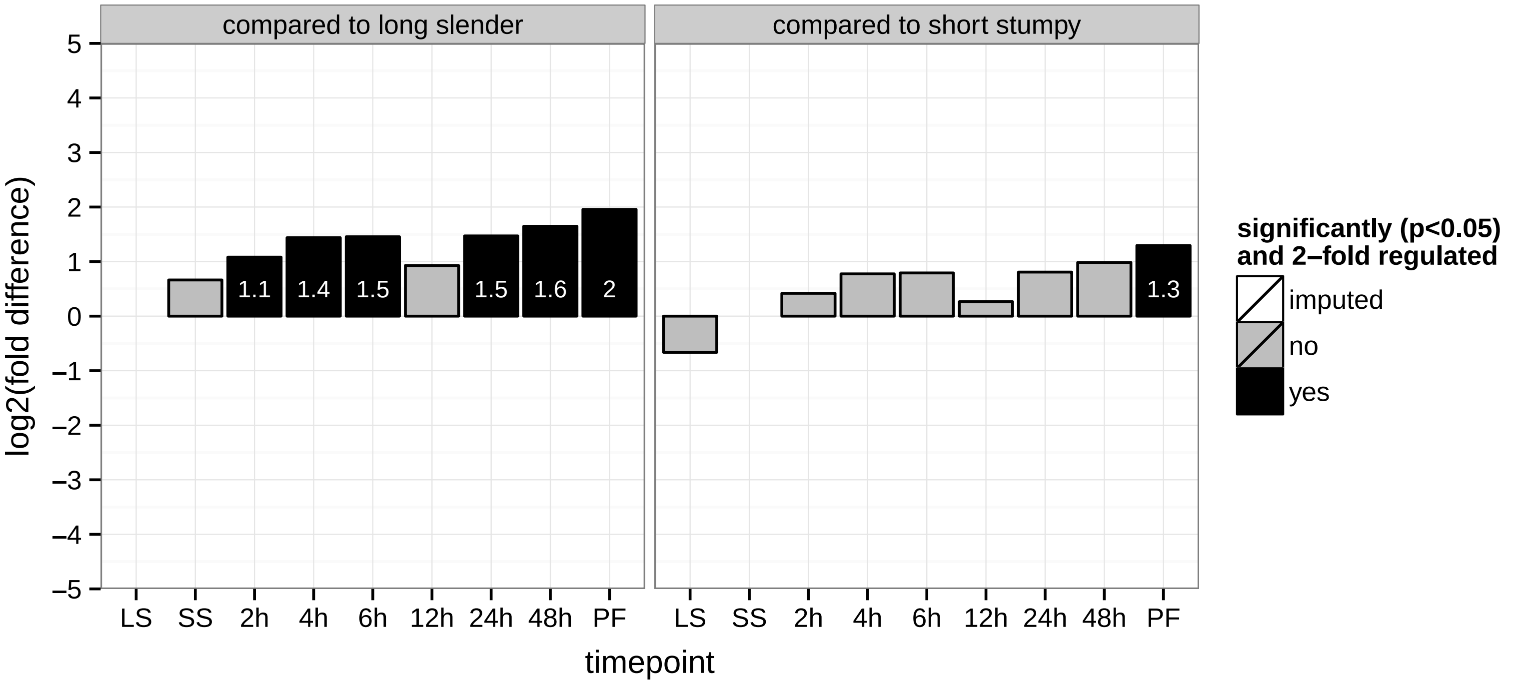
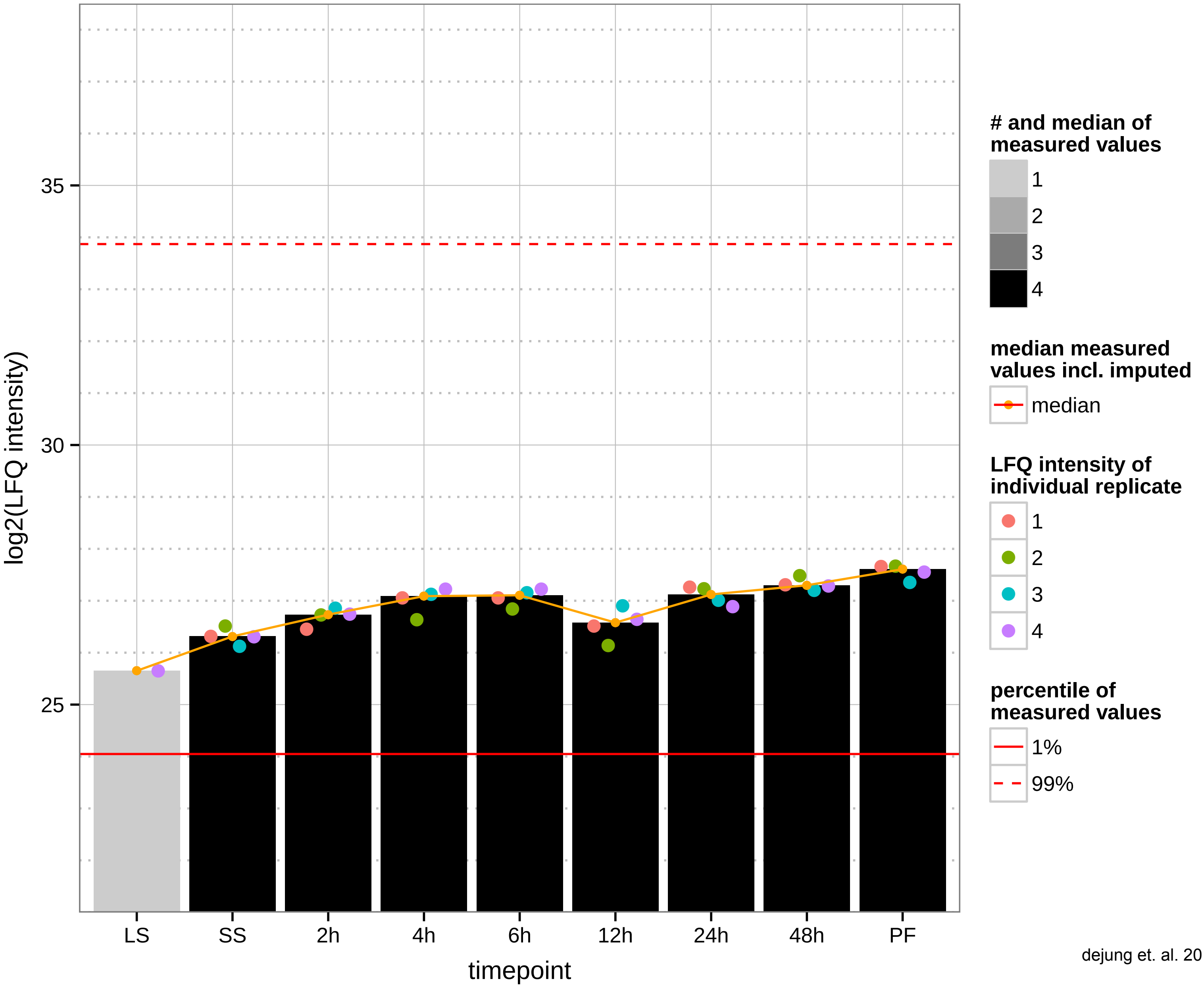
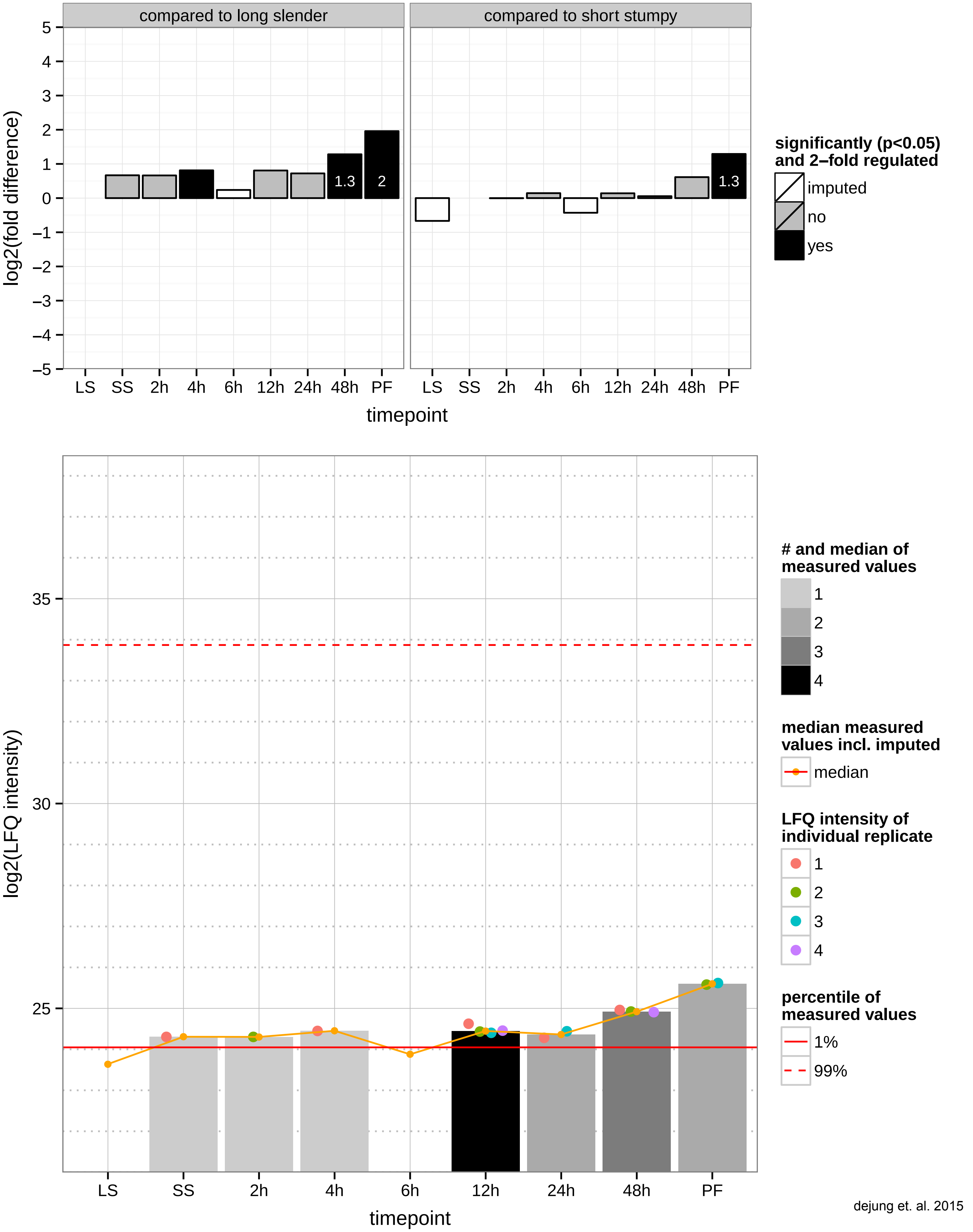
cyclophilin–type peptidyl–prolyl cis–trans isomerase, putative (PPIase)
Tb927.7.3430
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





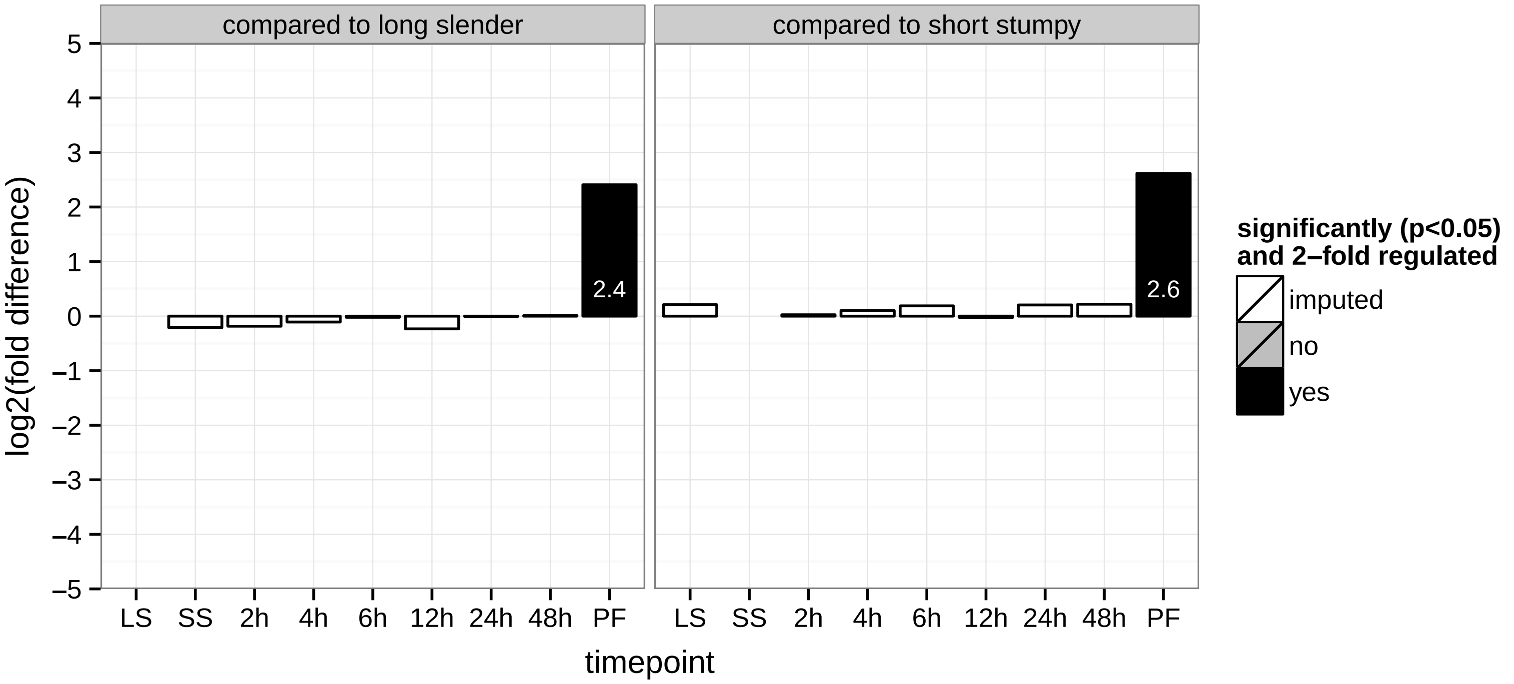
dejung et. al. 2015

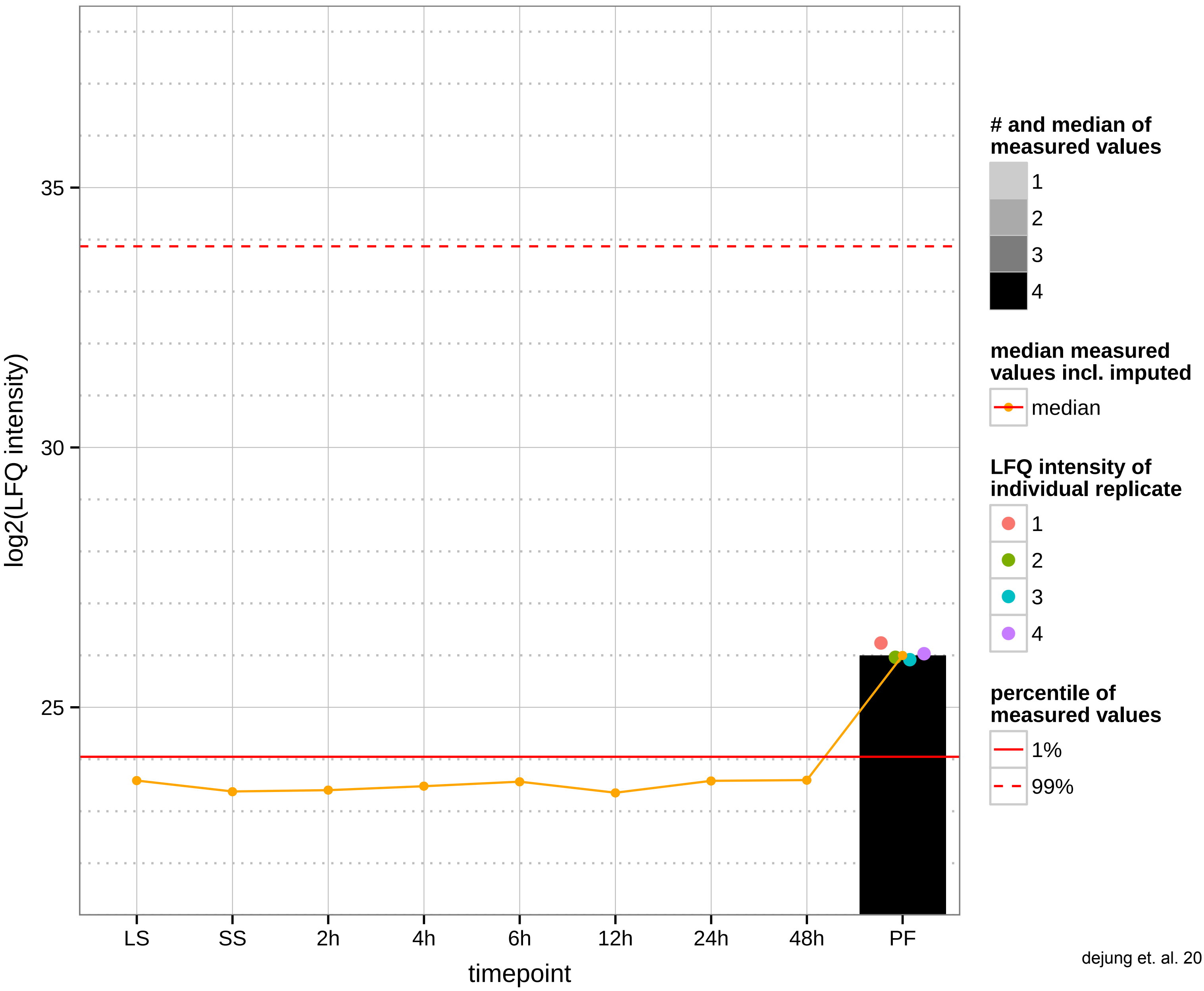
hypothetical protein, conserved
Tb927.7.3460
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015

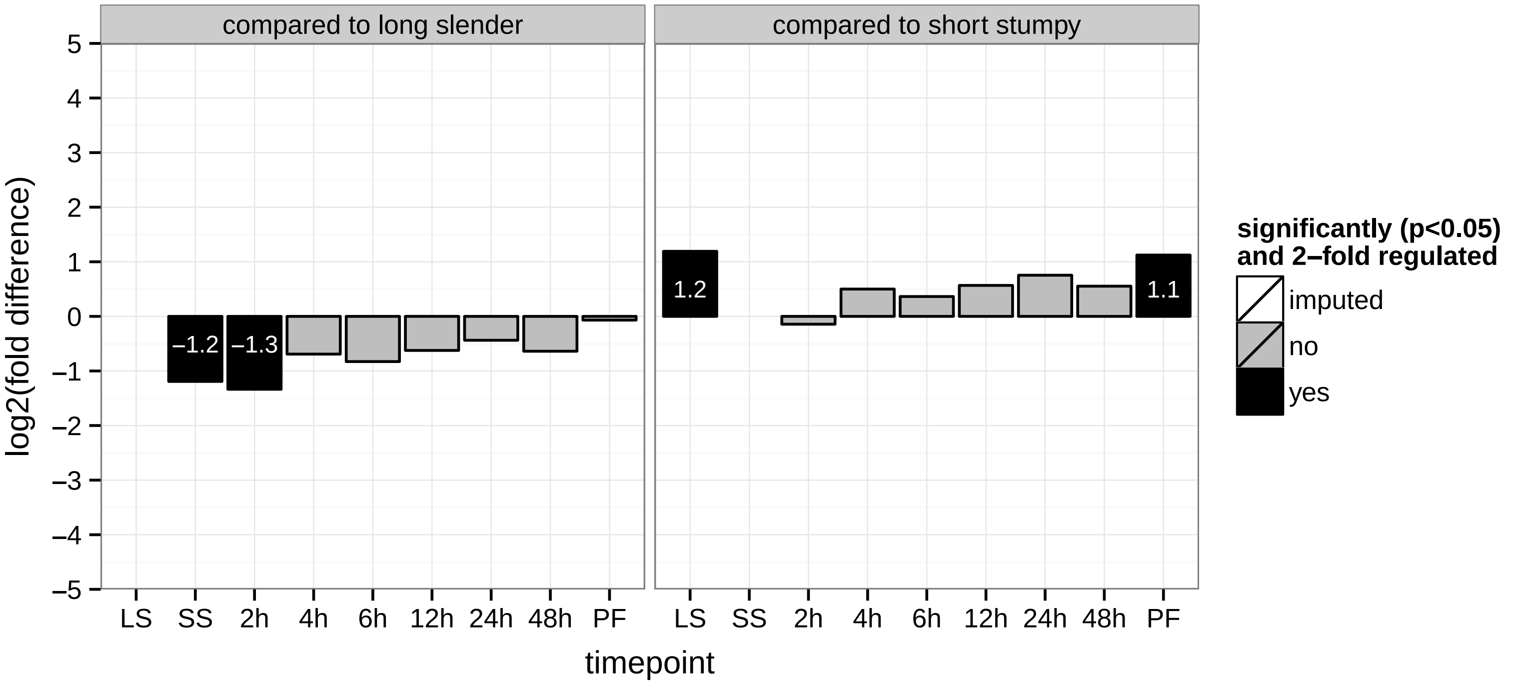
poly(A) polymerase, putative
Tb927.7.3780
AGOF: RNA binding, nucleotidyltransferase activity, polynucleotide adenylyltransferase activity
AGOC: nucleus
AGOP: RNA polyadenylation, transcription, DNA–dependent
PGOF: RNA binding, nucleotidyltransferase activity, polynucleotide adenylyltransferase activity
PGOC: nucleus
PGOP: RNA 3'–end processing, RNA polyadenylation, transcription, DNA–dependent

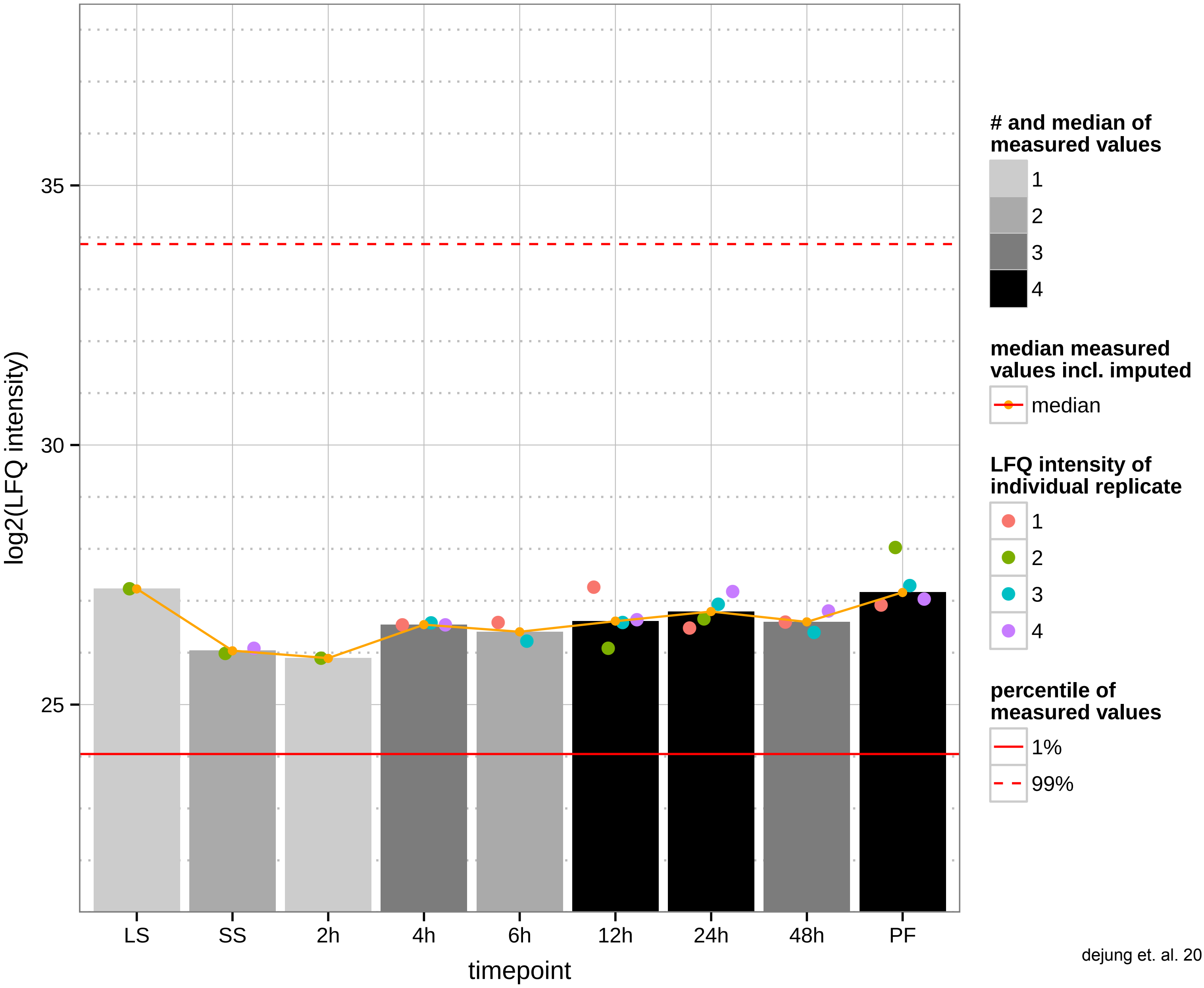




dejung et. al. 2015

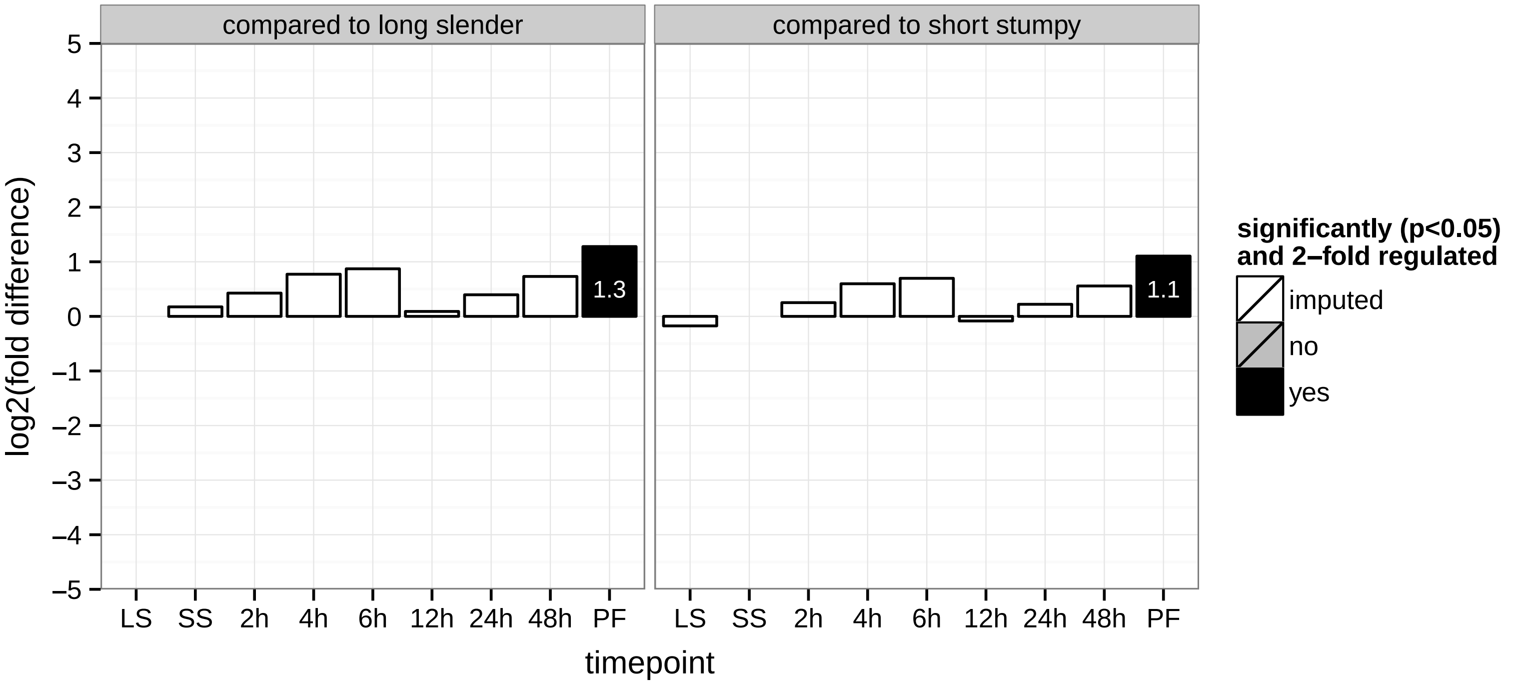
hypothetical protein, conserved
Tb927.7.4120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

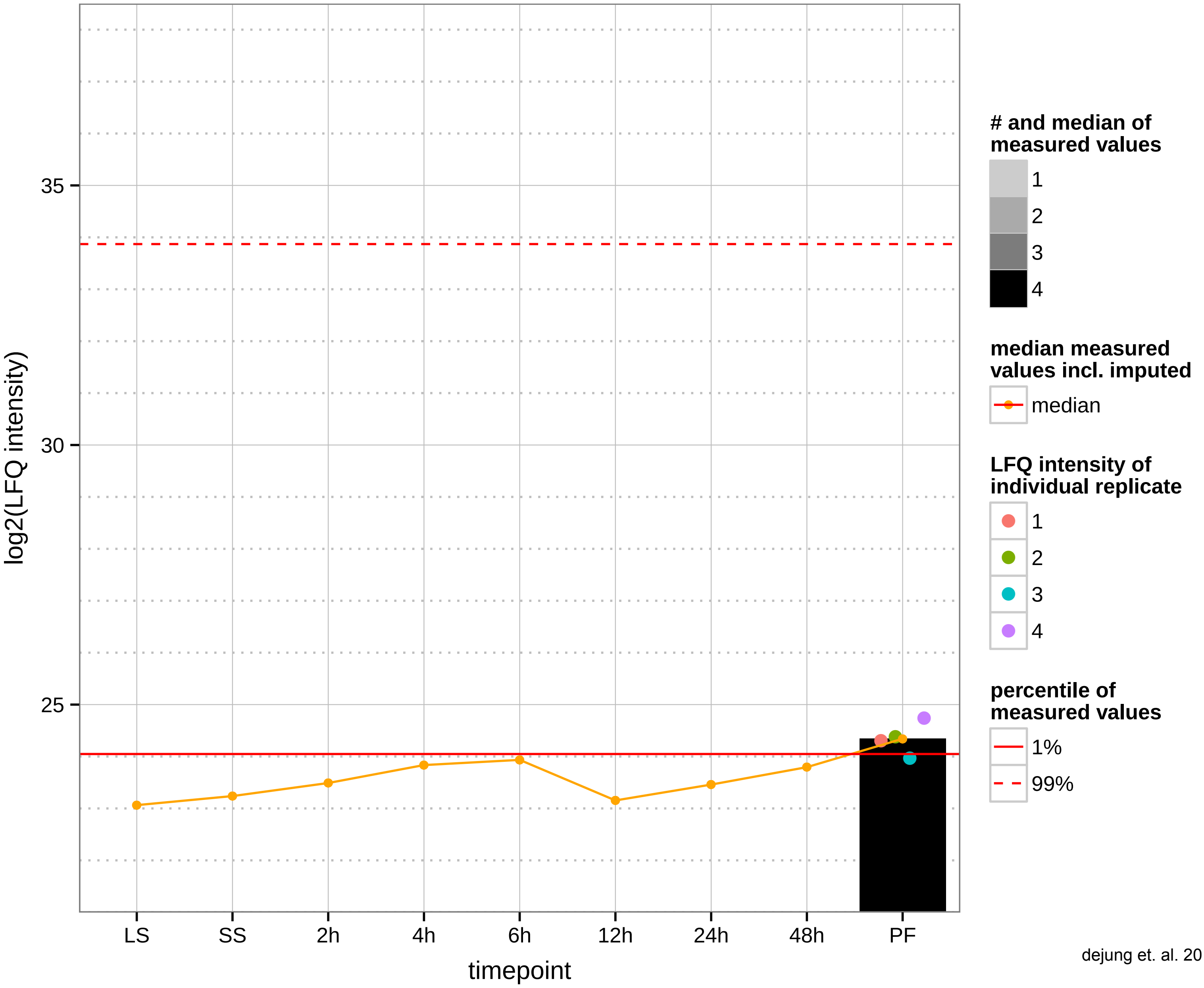




dejung et. al. 2015

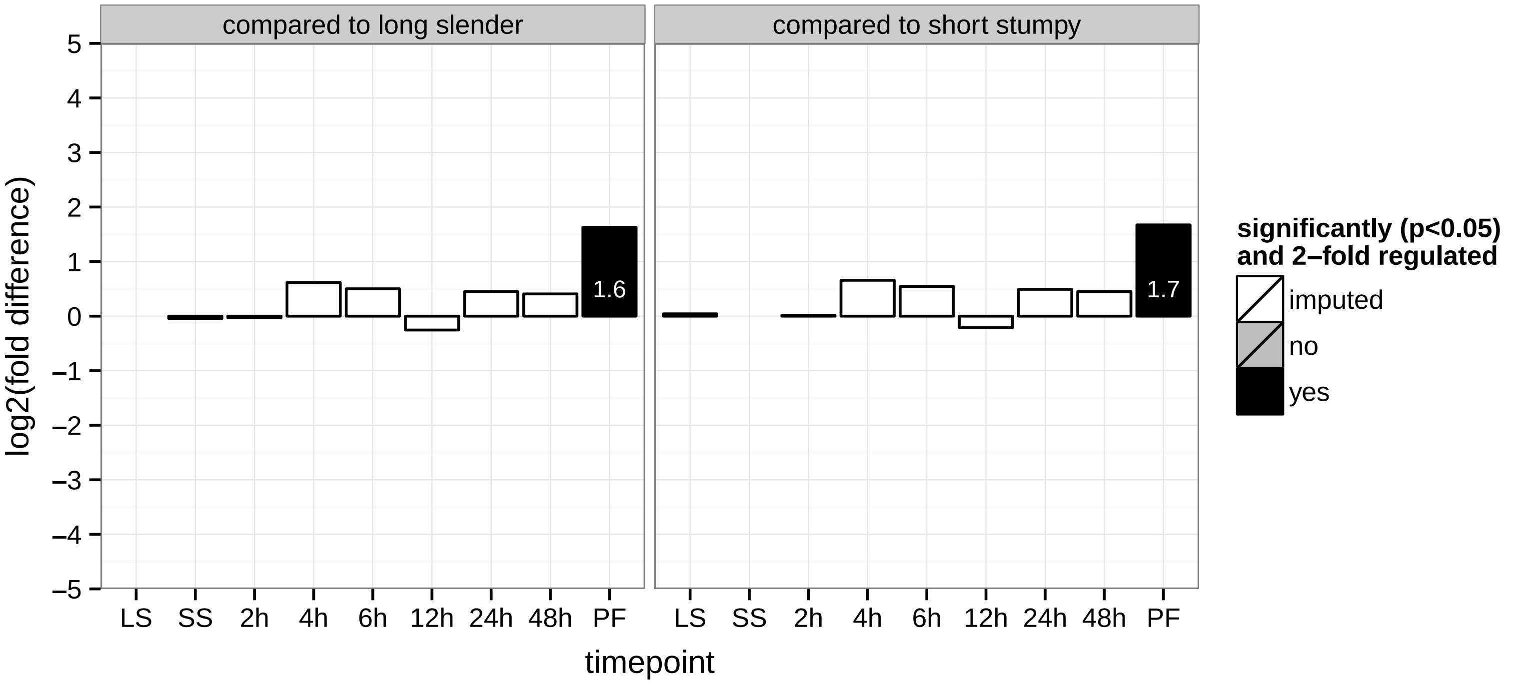
hypothetical protein, conserved
Tb927.7.5090;Tb11.v5.0189
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

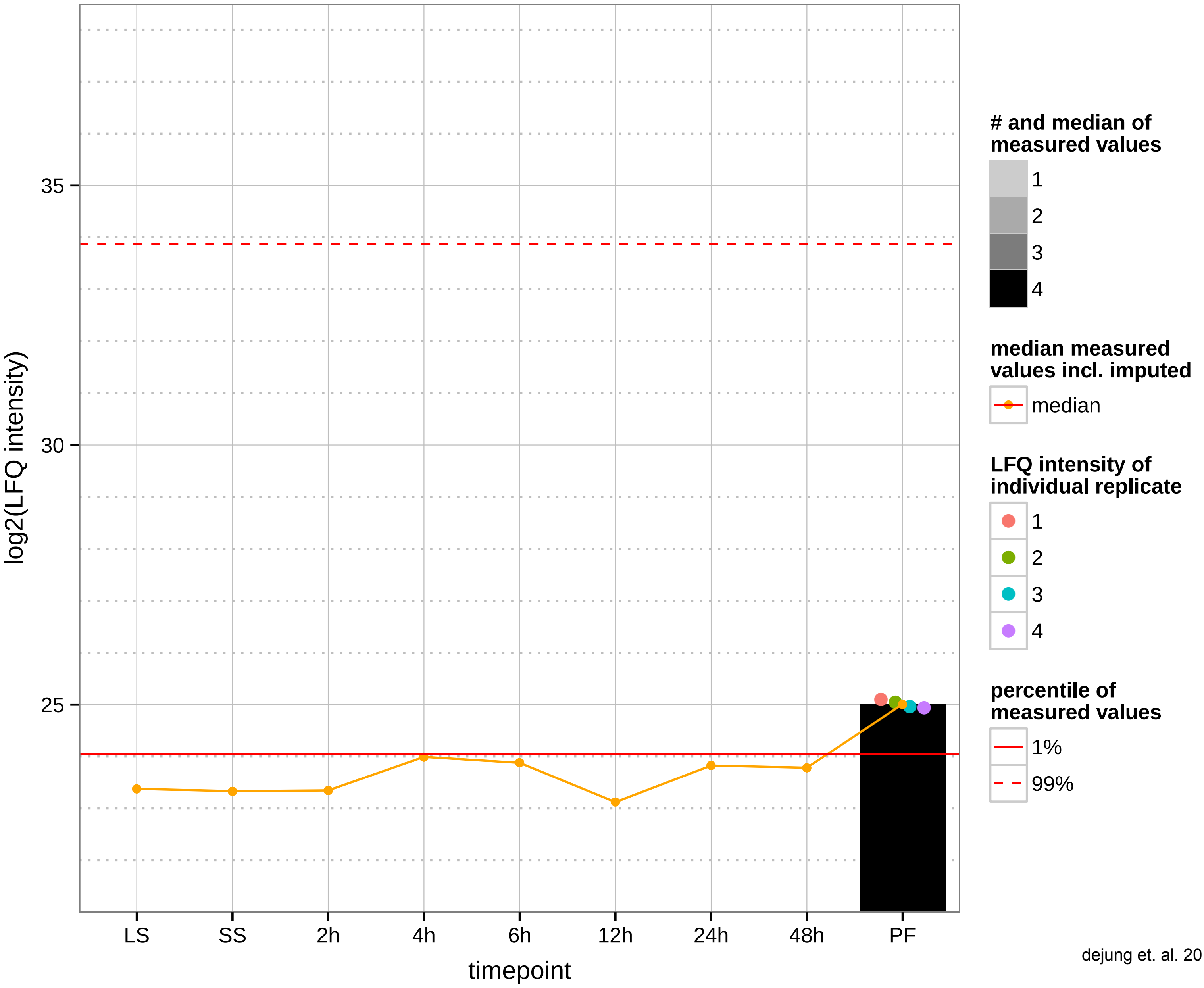




dejung et. al. 2015

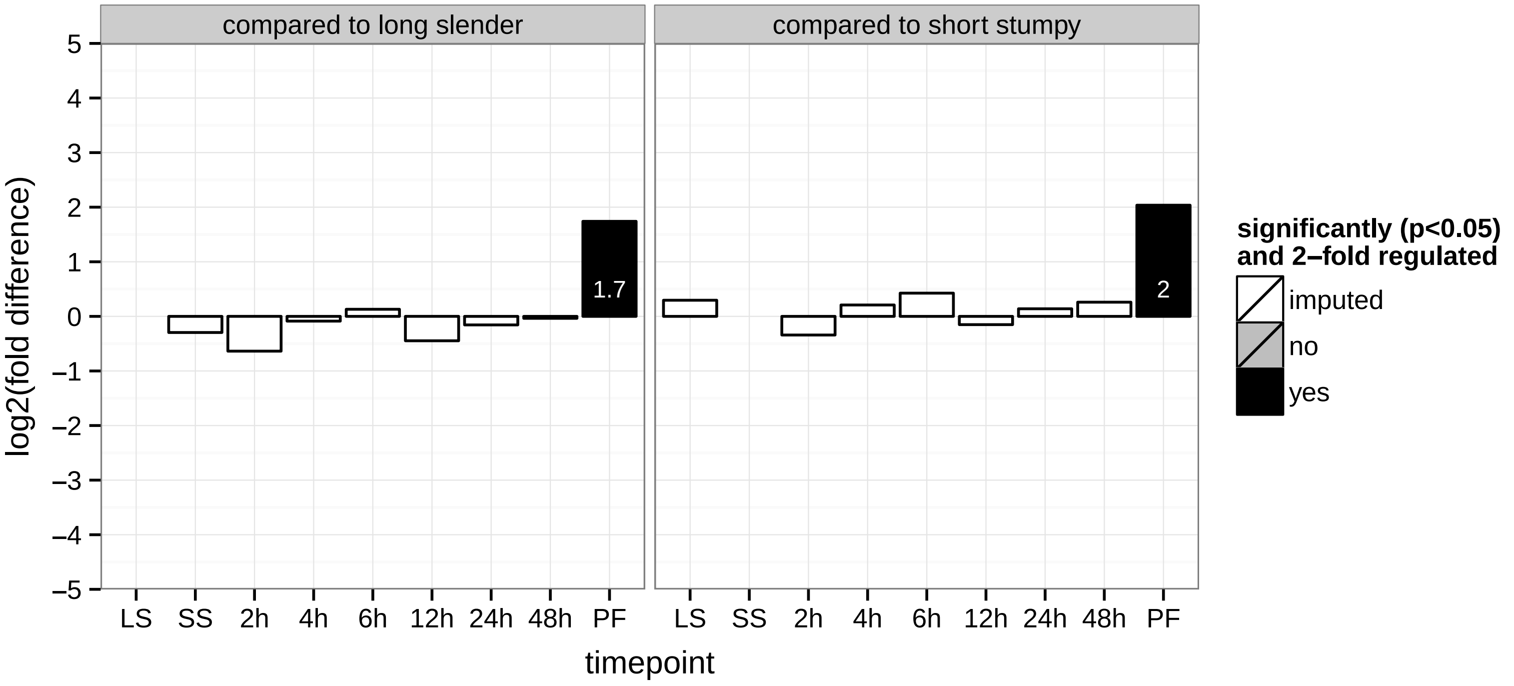
hypothetical protein, conserved
Tb927.7.5130
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

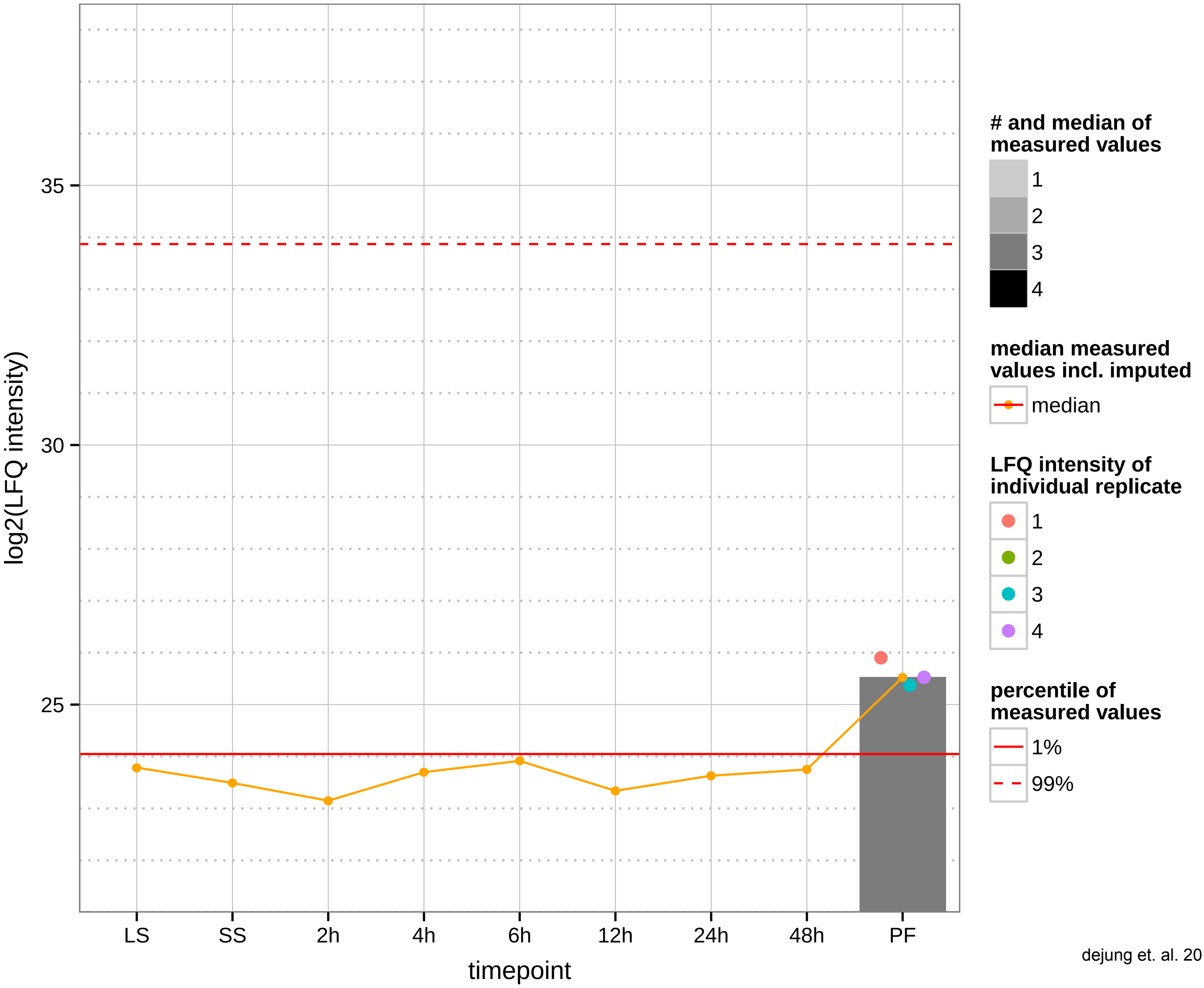




dejung et. al. 2015

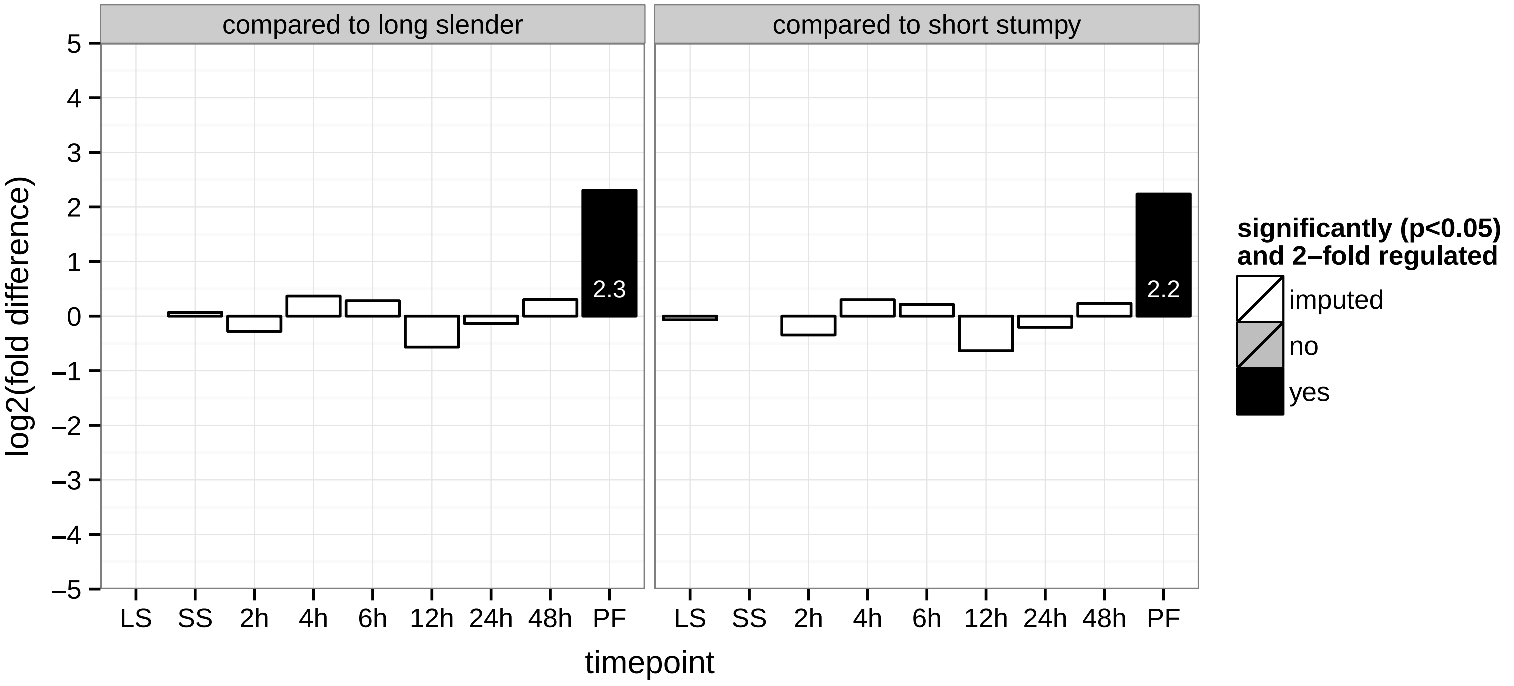
hypothetical protein, conserved
Tb927.7.5260
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

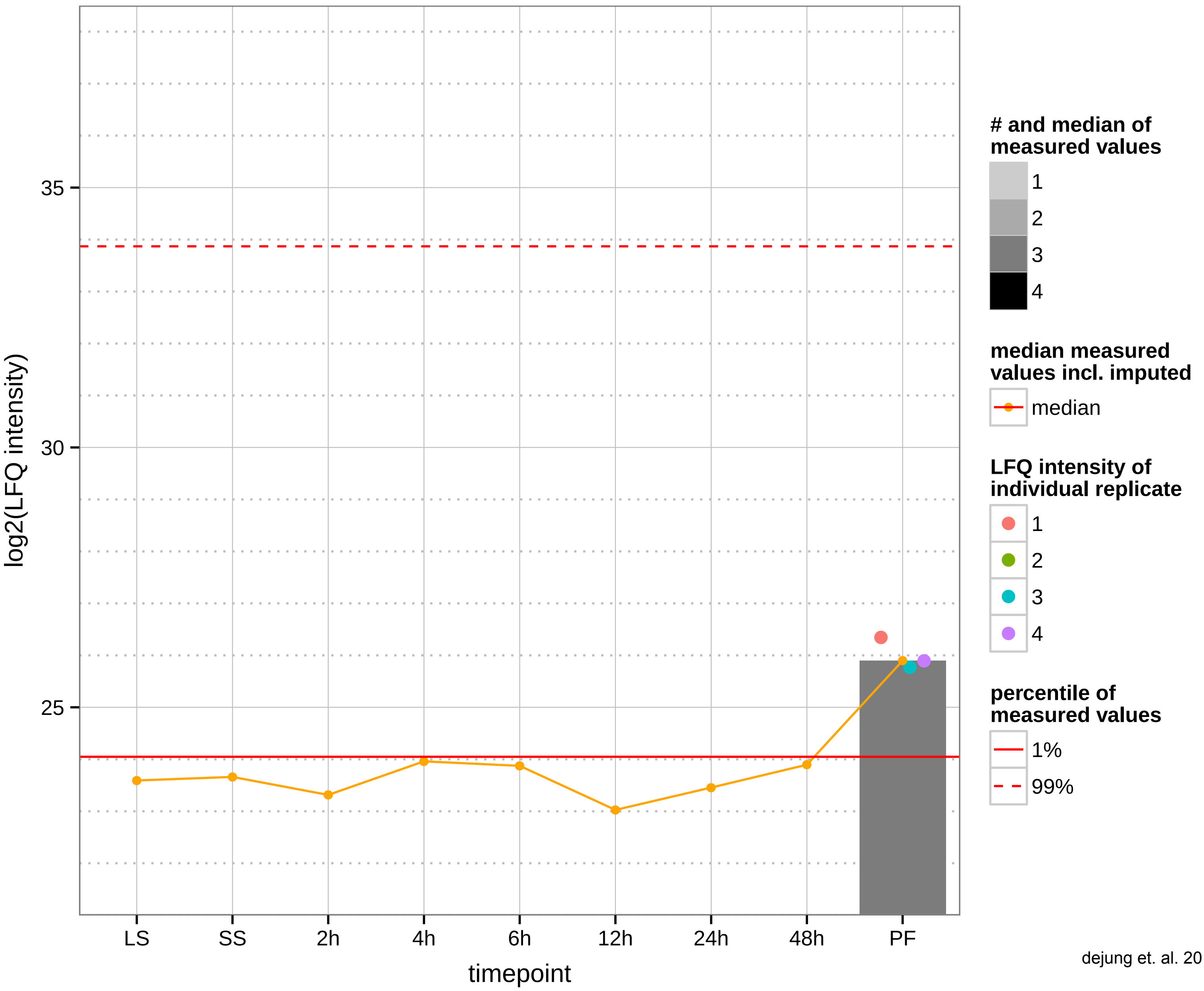




dejung et. al. 2015

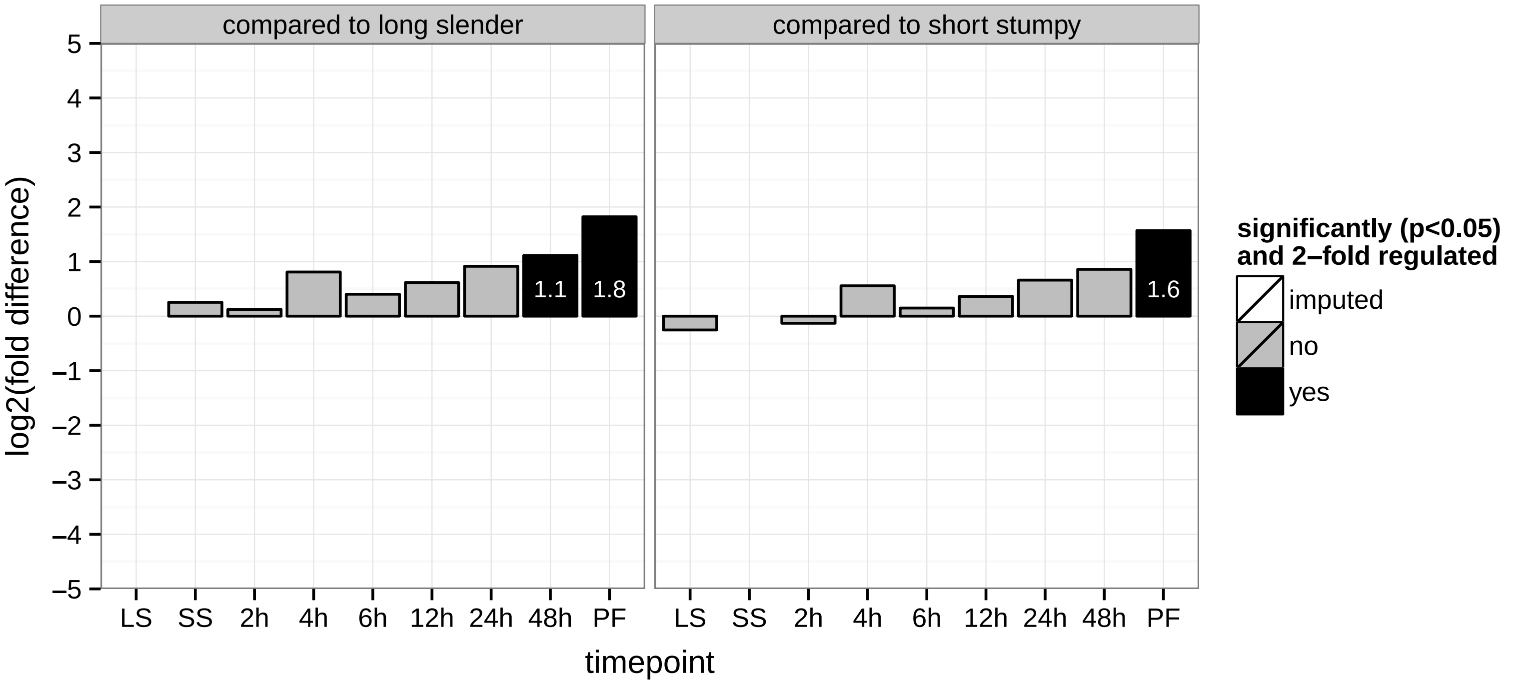
hypothetical protein, conserved
Tb927.7.5300
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

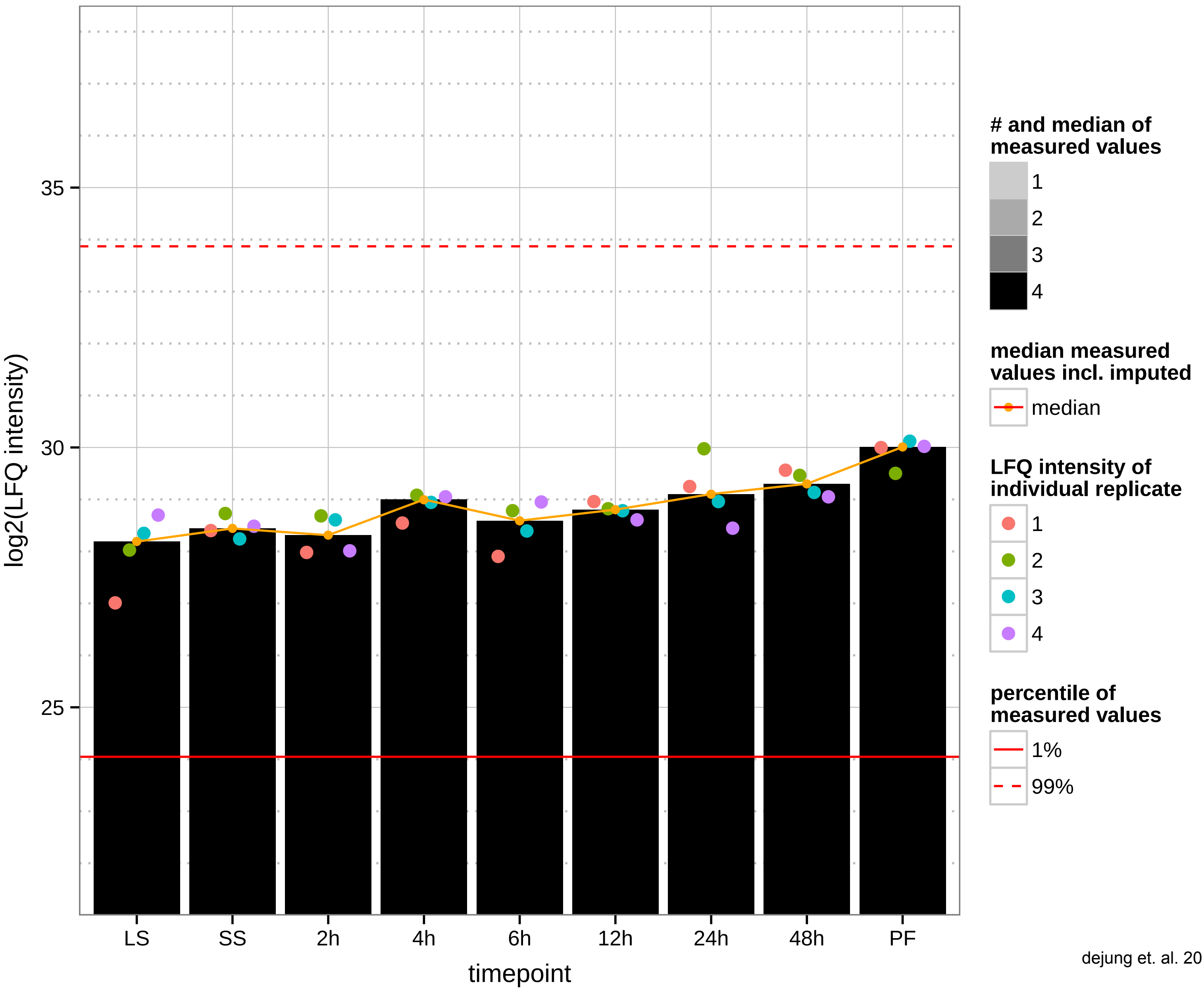




dejung et. al. 2015

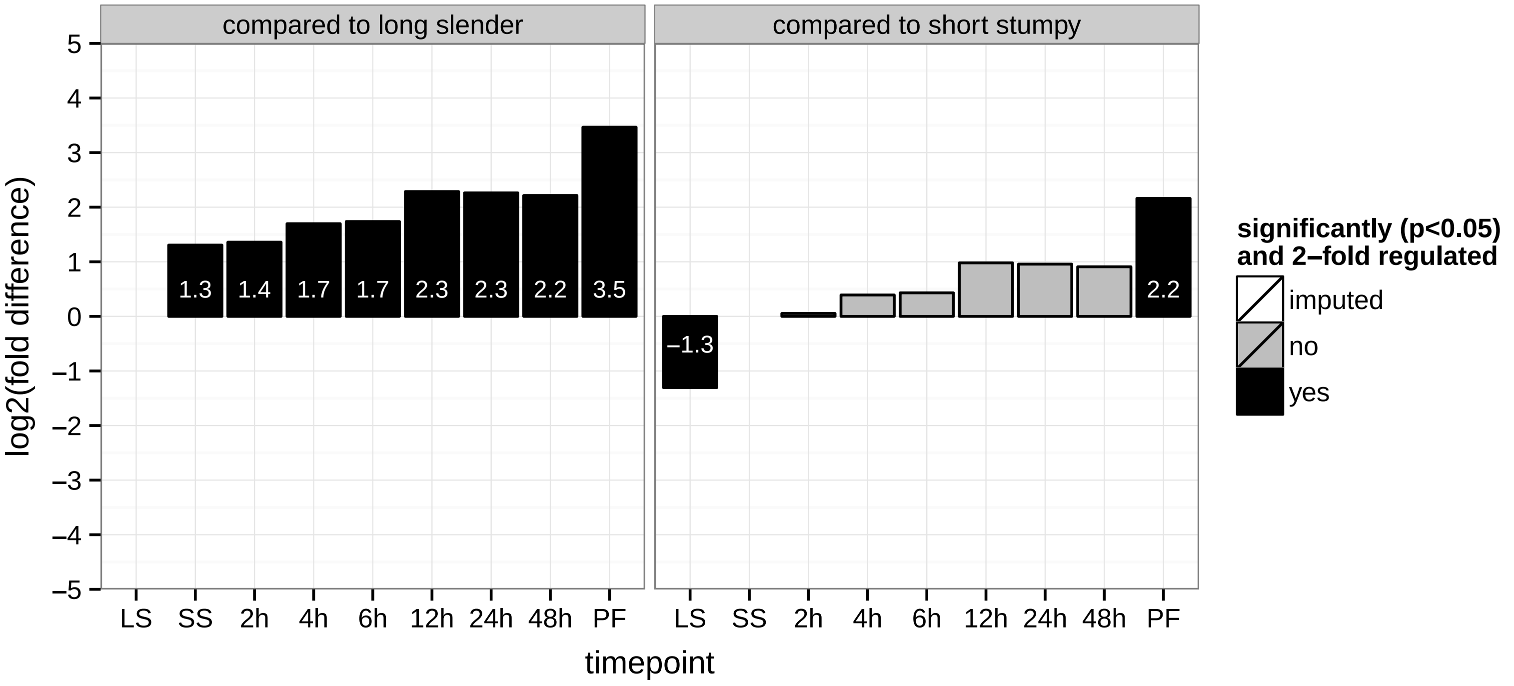
prefoldin, putative
Tb927.7.570
AGOF: unfolded protein binding
AGOC: prefoldin complex
AGOP: protein folding
PGOF: unfolded protein binding
PGOC: prefoldin complex
PGOP: protein folding

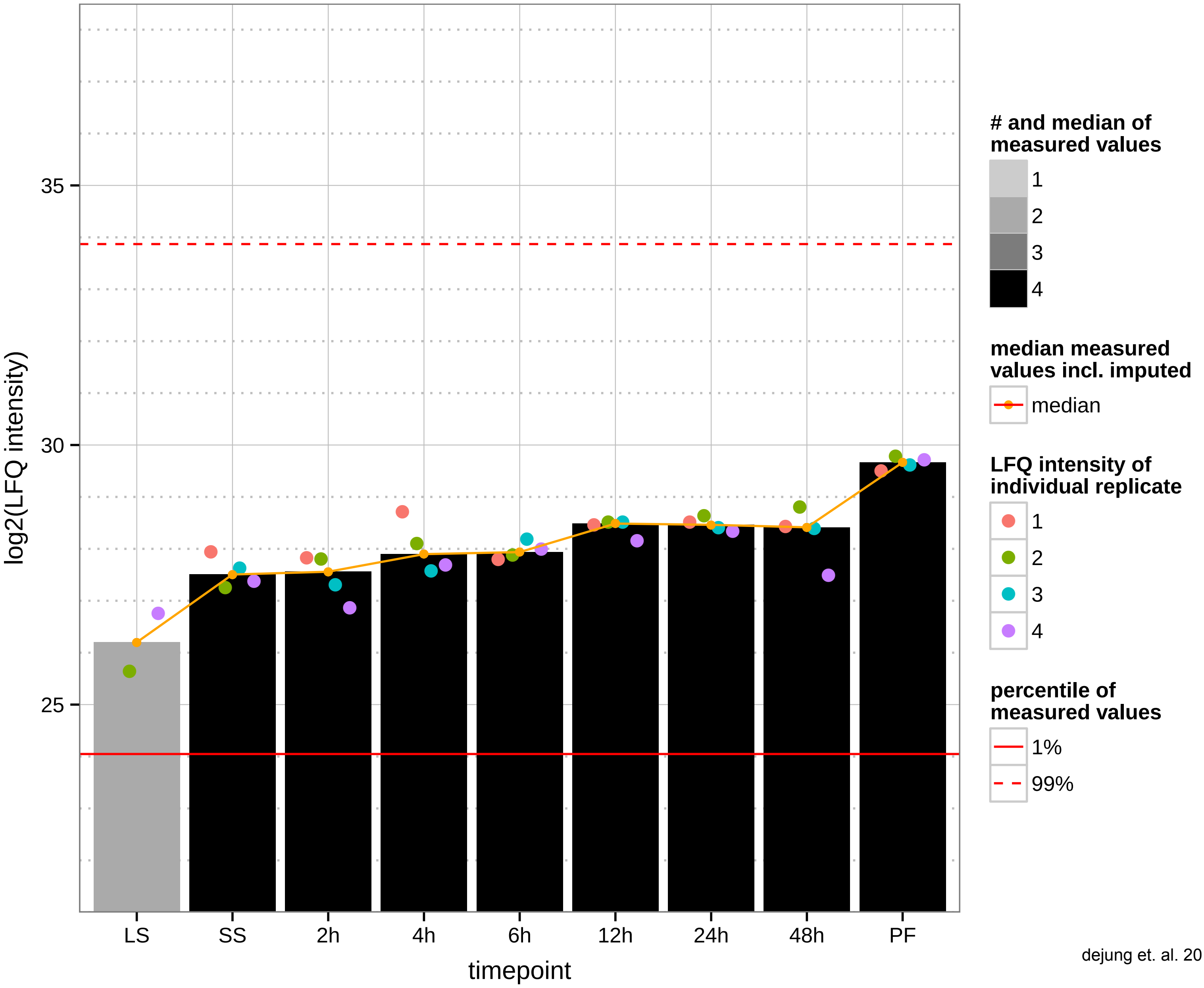




dejung et. al. 2015

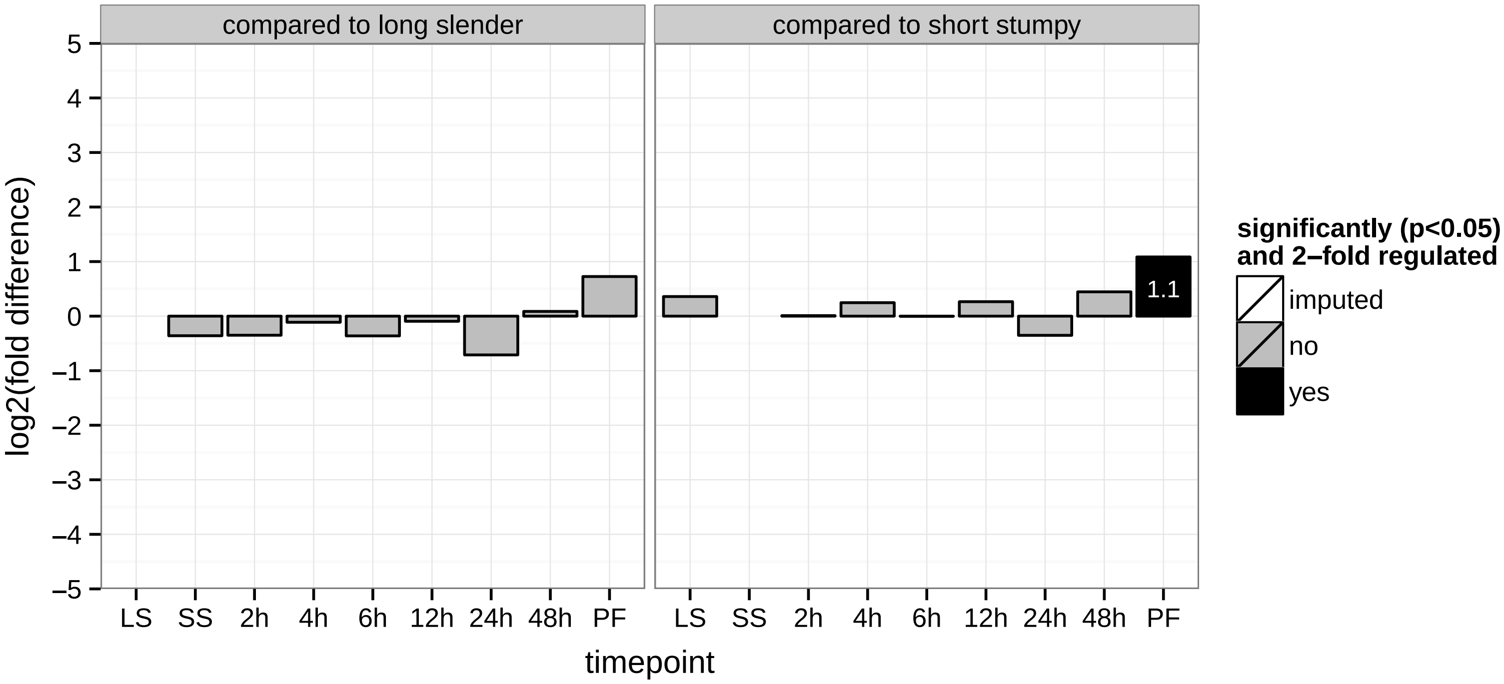
hypothetical protein, conserved
Tb927.7.6260
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

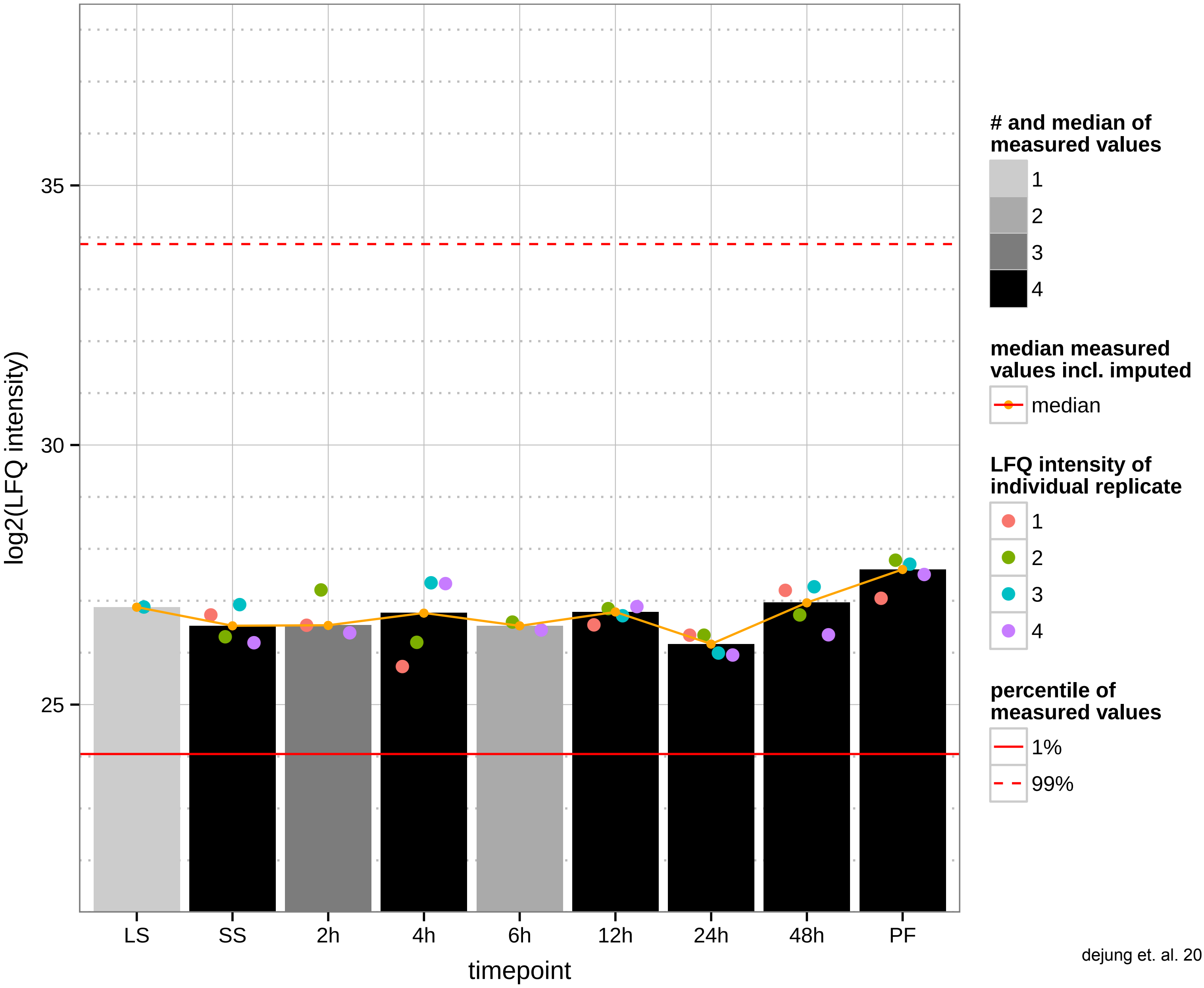




dejung et. al. 2015

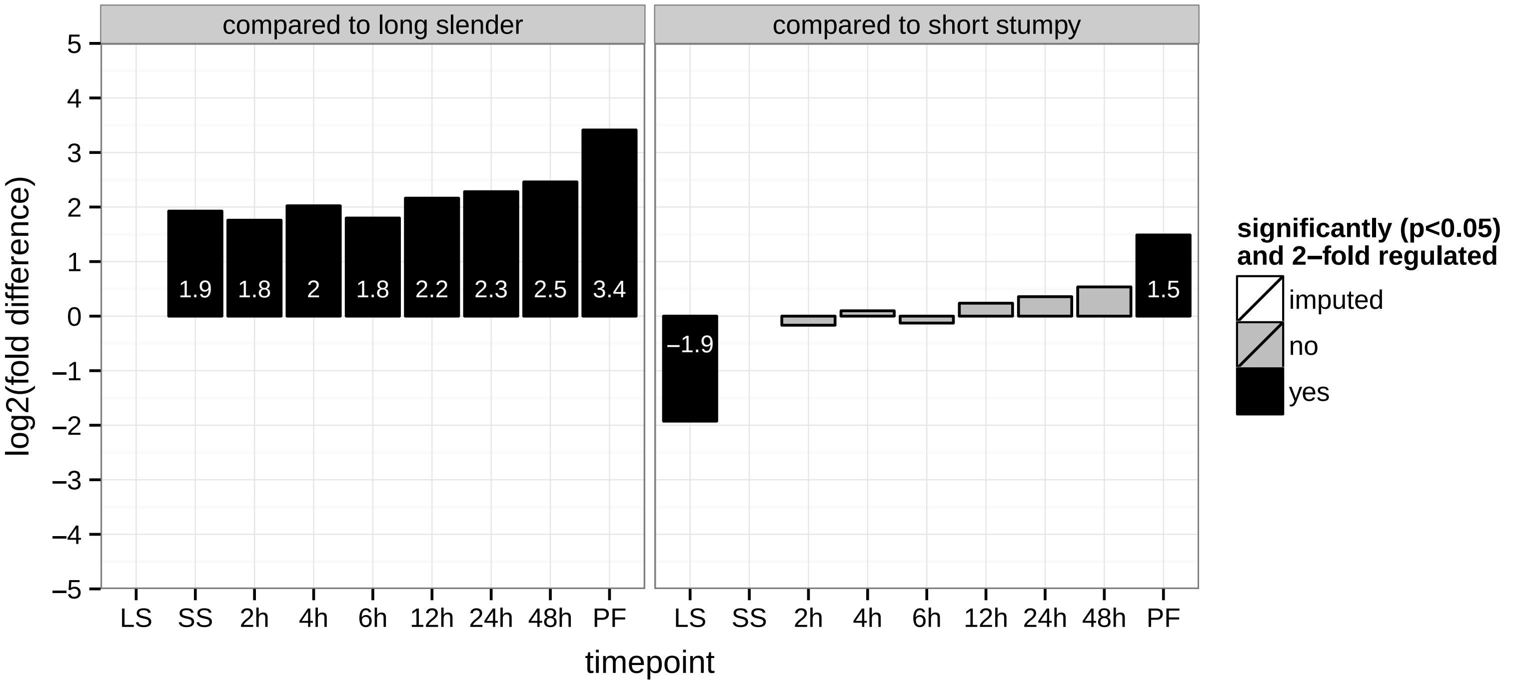
FG−GAP repeat protein, putative, intergrin alpha chain protein
Tb927.7.6460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

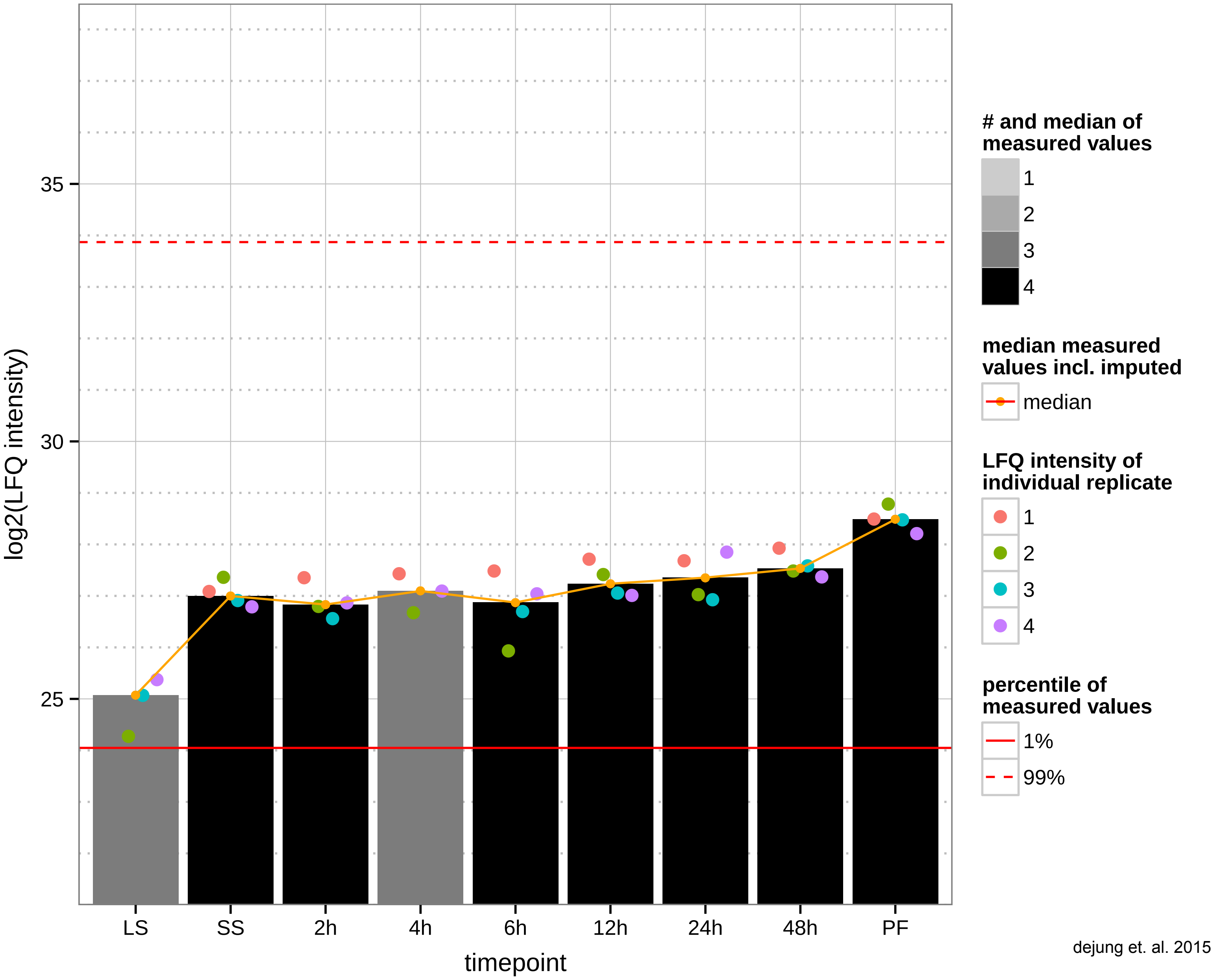




dejung et. al. 2015

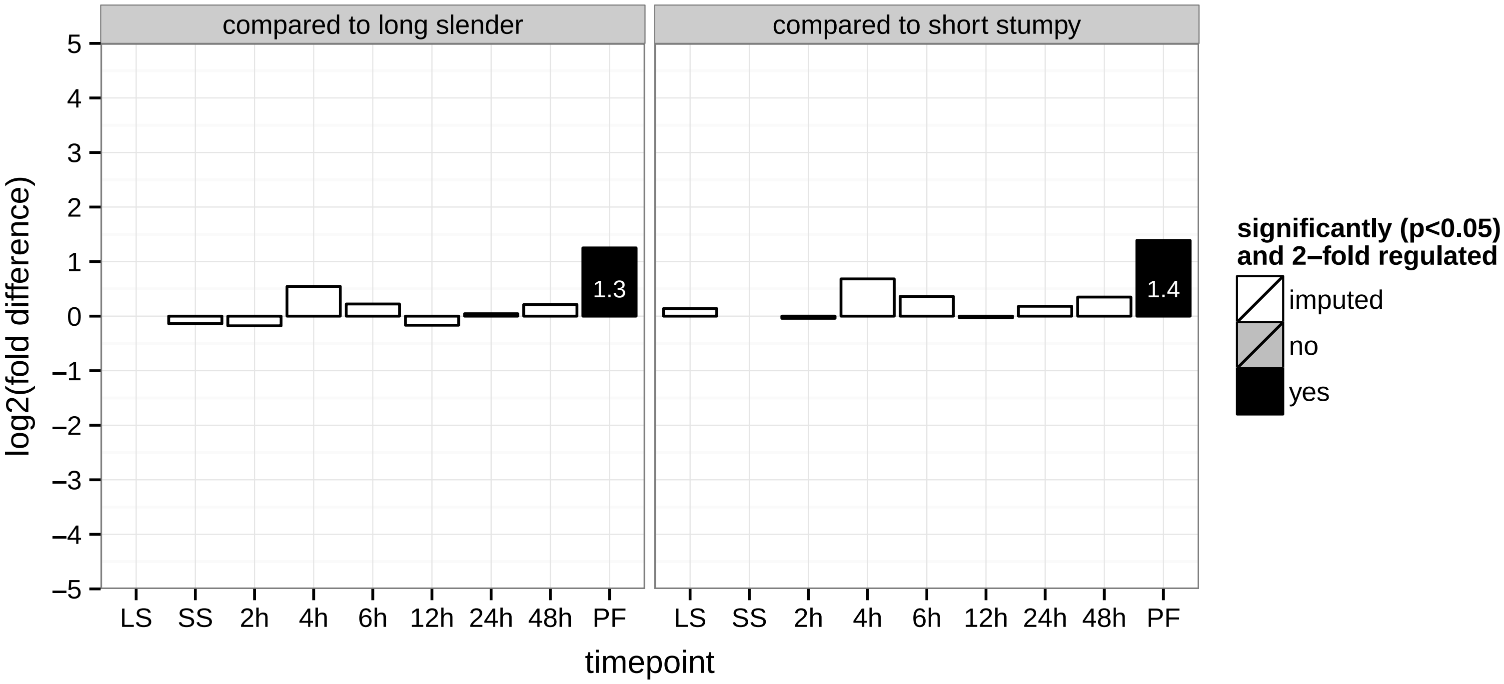
hypothetical protein, conserved
Tb927.7.650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

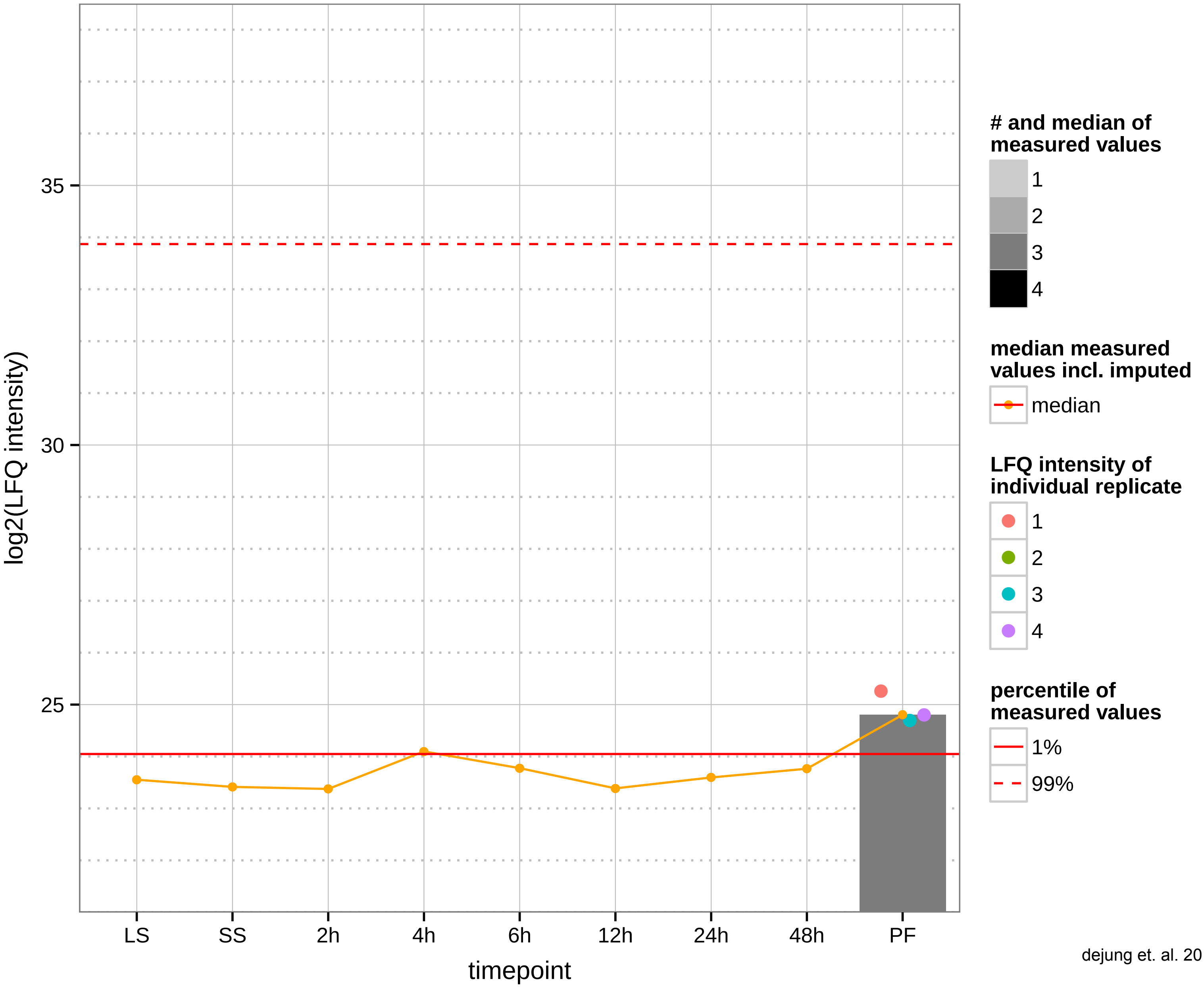




dejung et. al. 2015

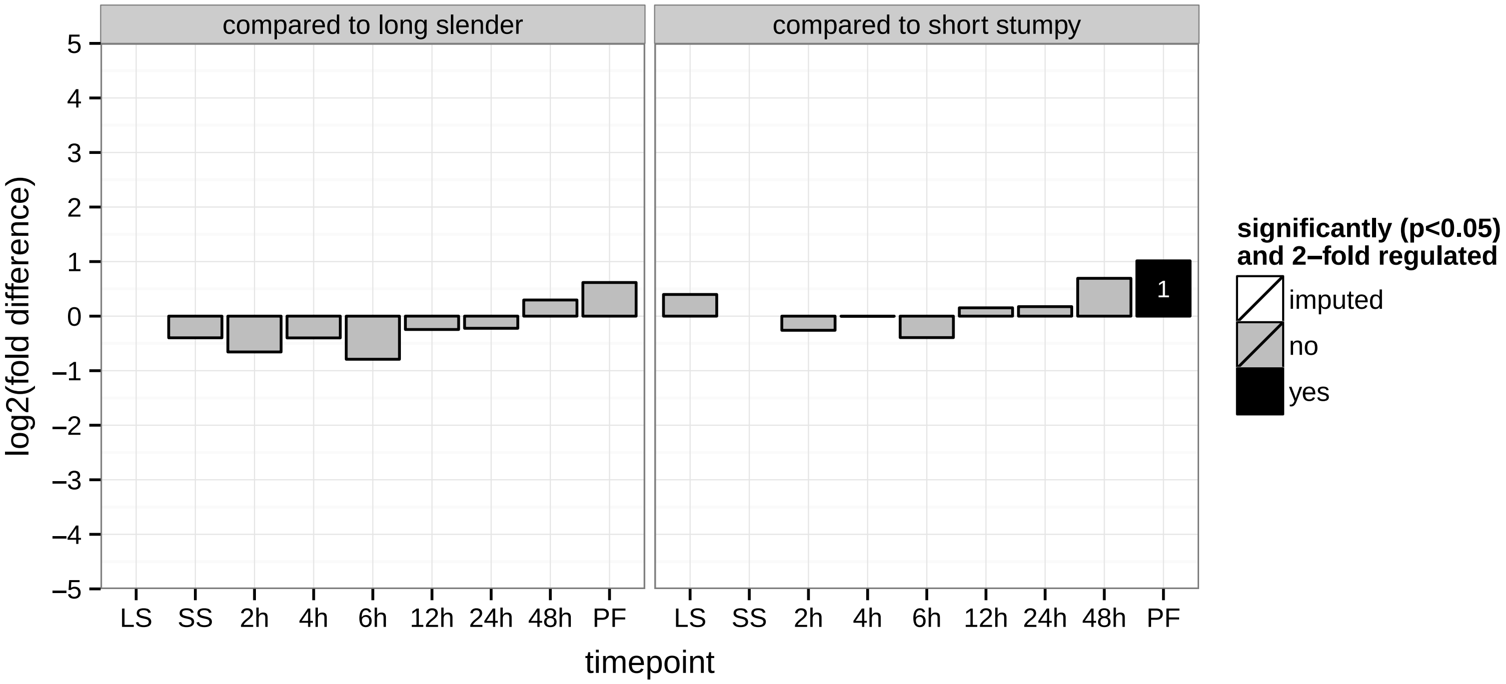
trans−sialidase, putative
Tb927.7.6830
AGOF: exo−alpha−sialidase activity
AGOC: null
AGOP: pathogenesis
PGOF: null
PGOC: null
PGOP: null

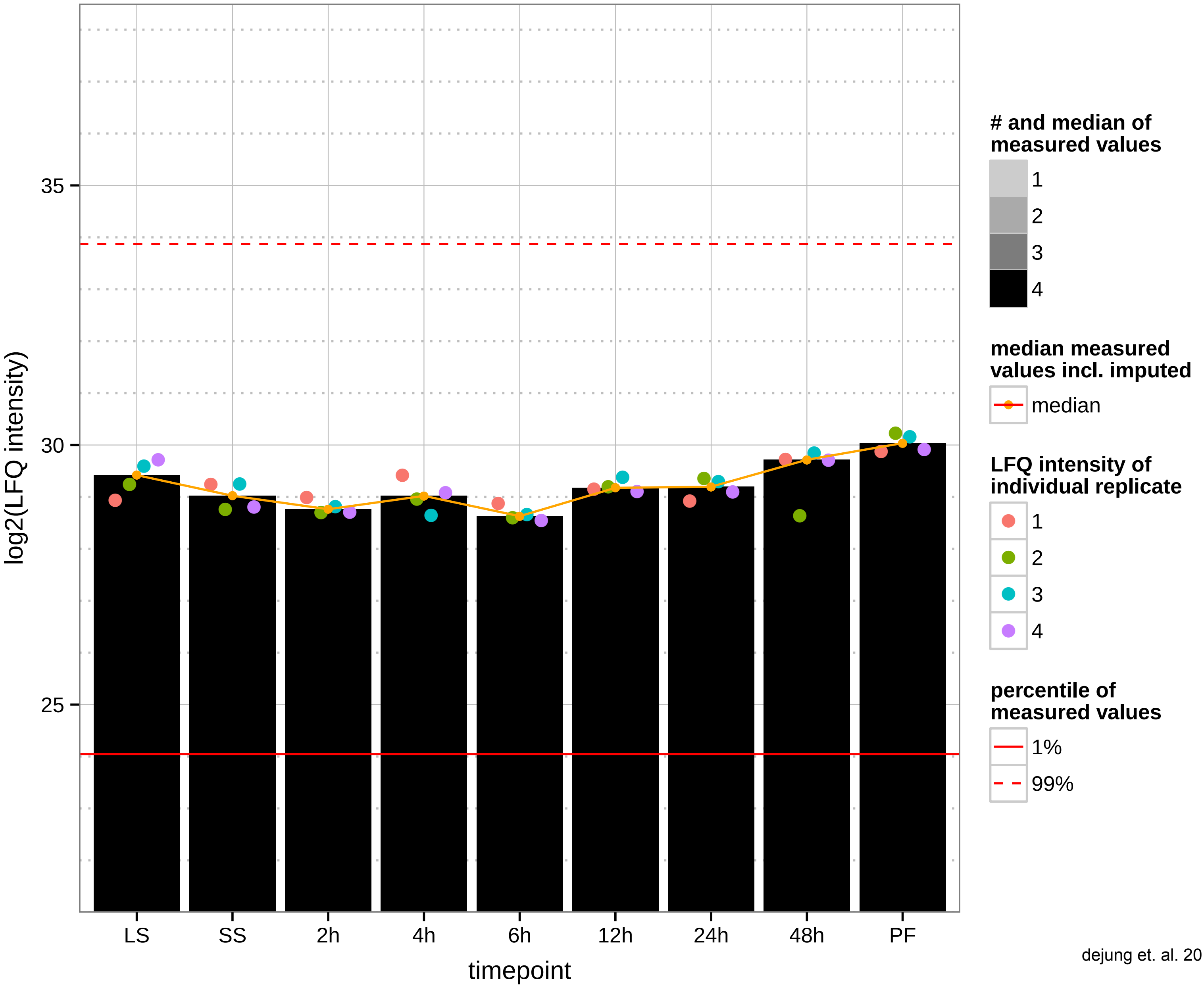




dejung et. al. 2015

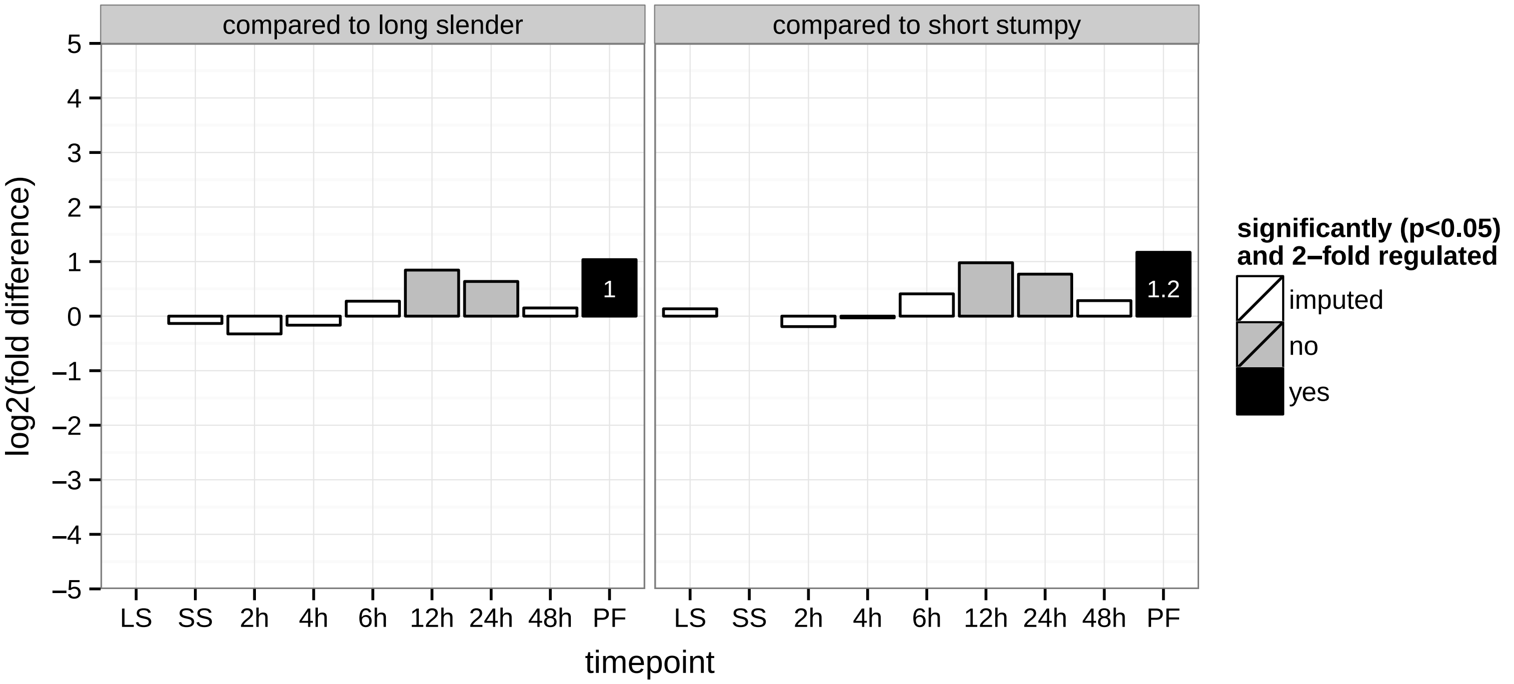
hypothetical protein, conserved
Tb927.7.6890
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

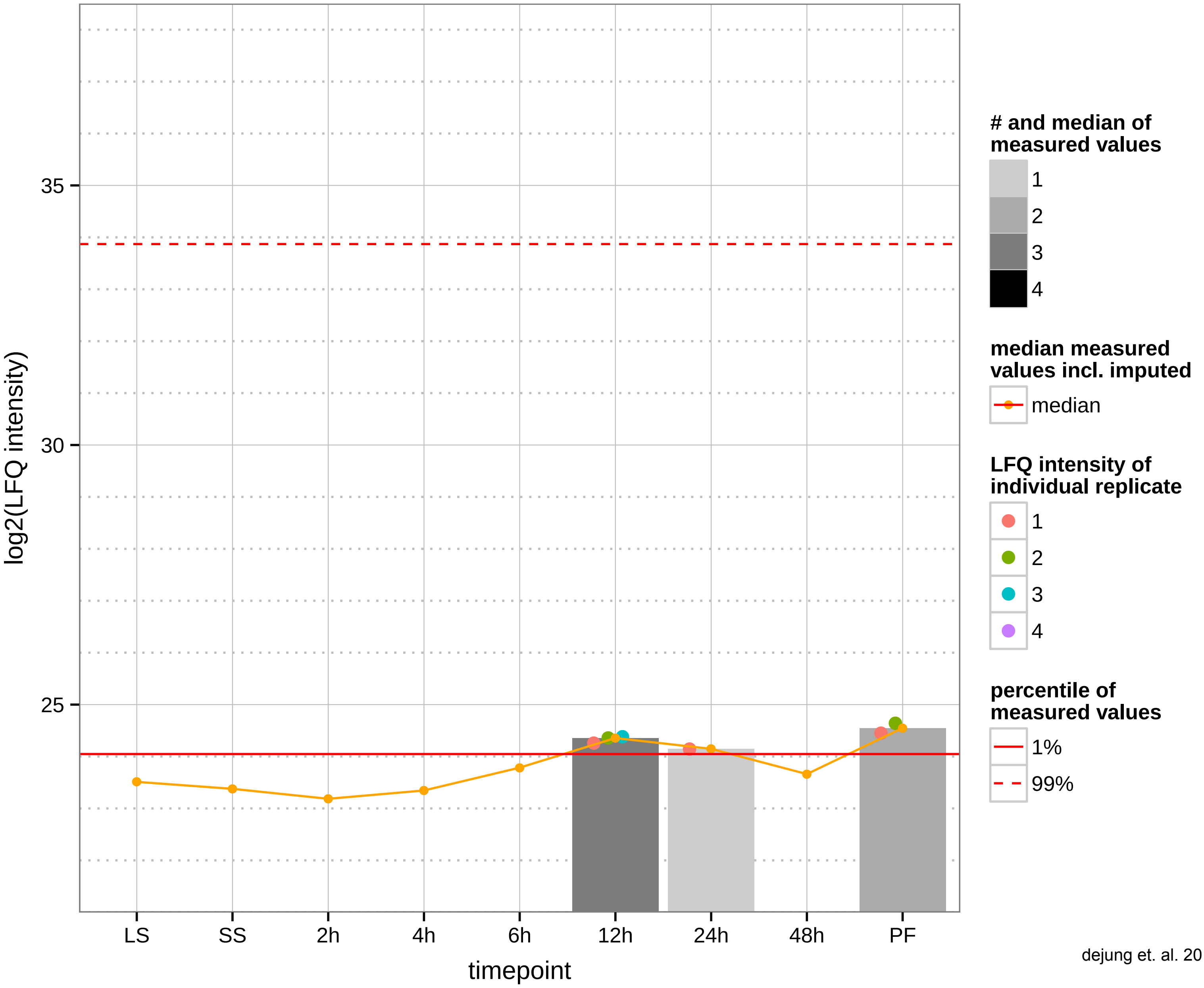




dejung et. al. 2015

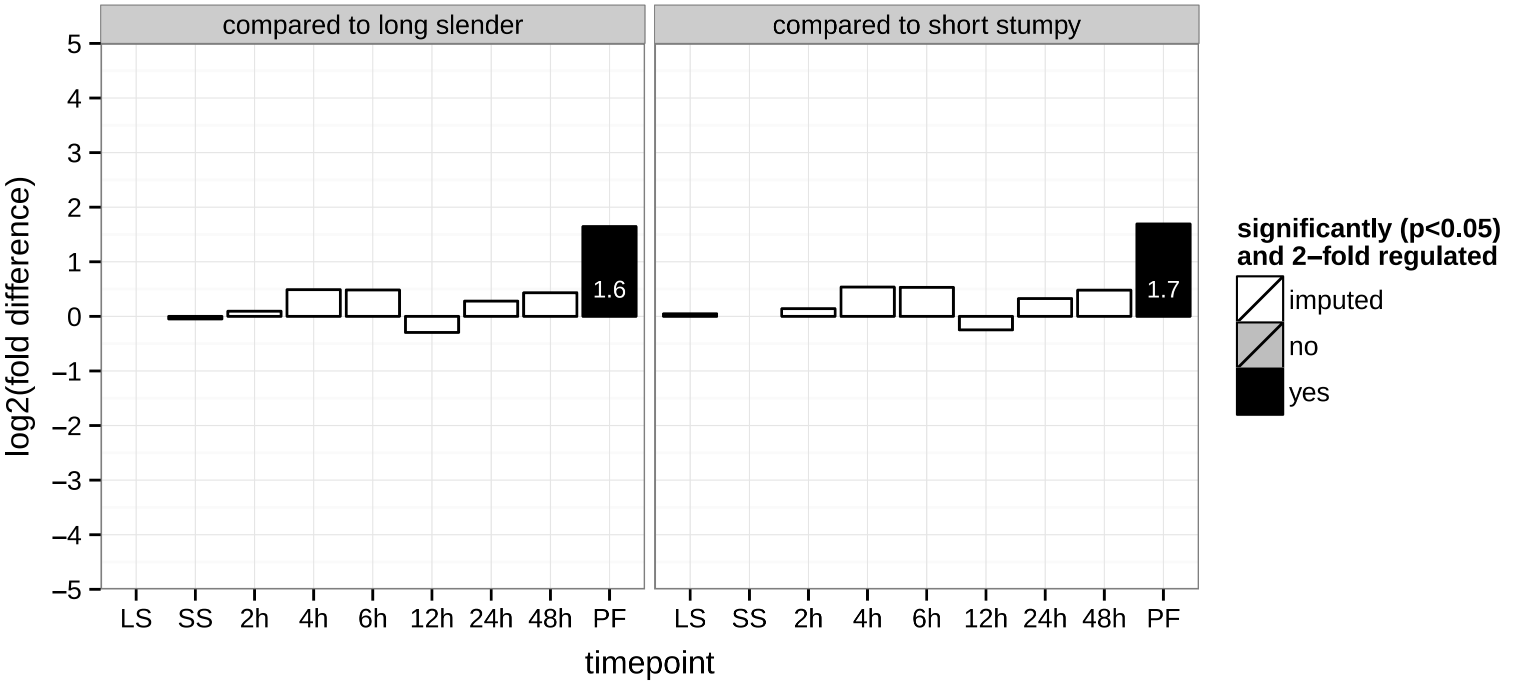
RNA–binding protein, putative
Tb927.7.7280
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: RNA binding
PGOC: null
PGOP: RNA processing

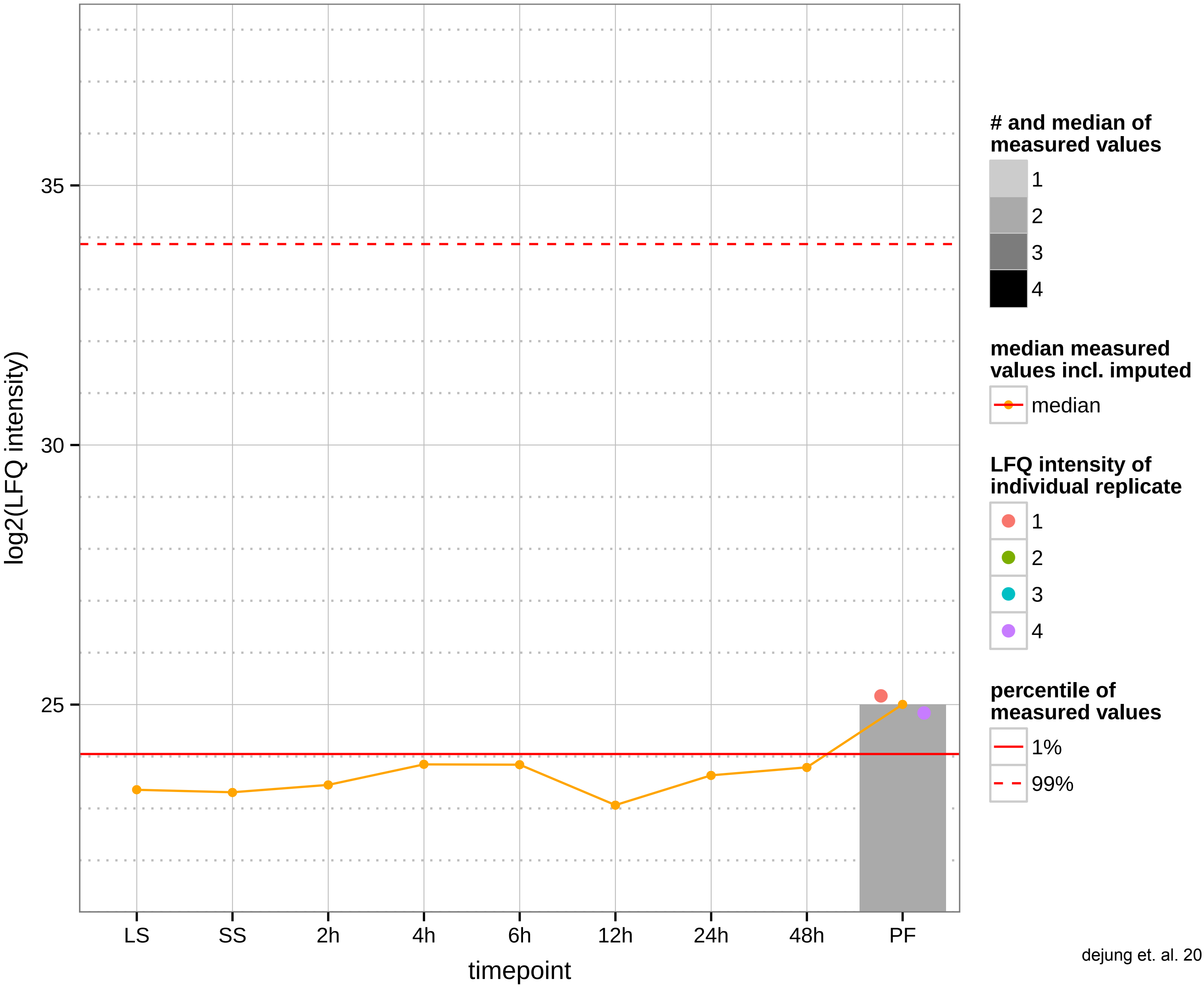




dejung et. al. 2015

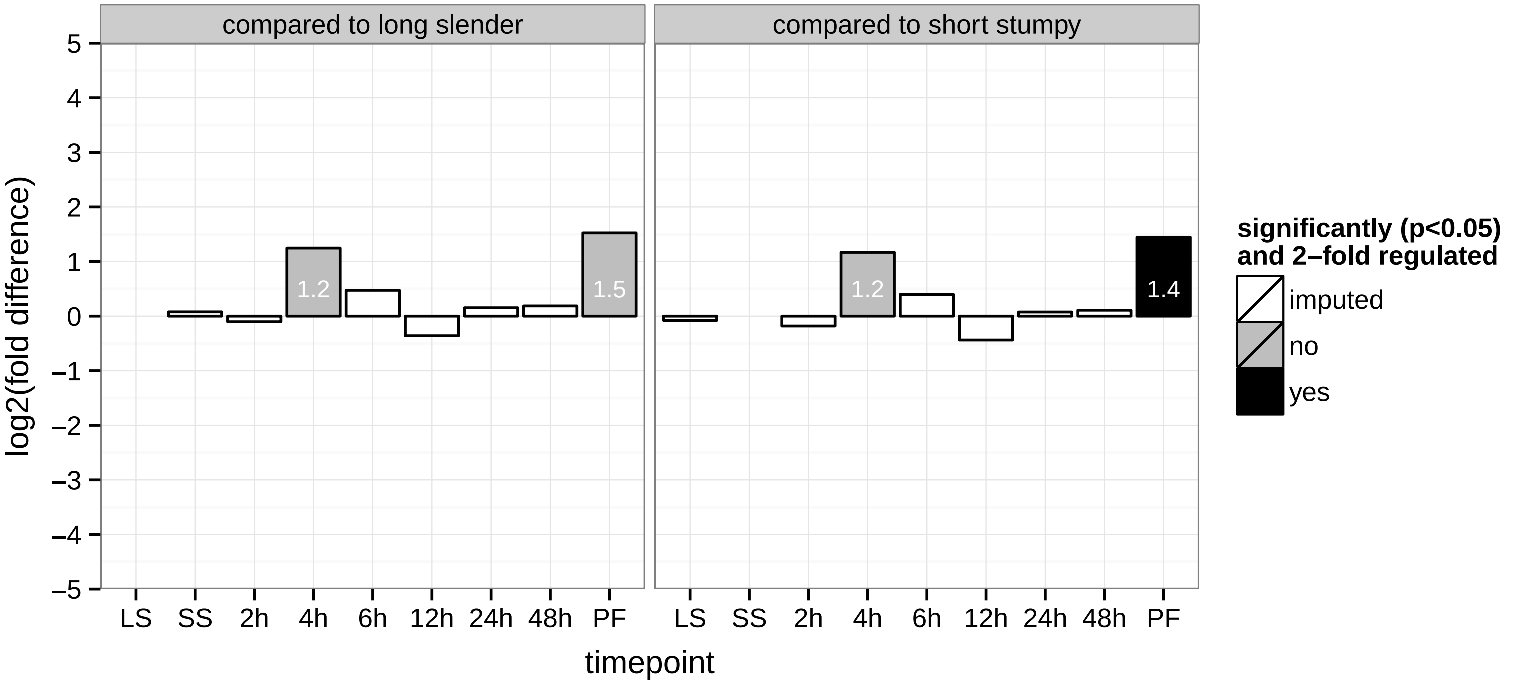
cdc2–related kinase 2, cell division control protein 2 homolog 2 (CRK2)
Tb927.7.7360
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: mitochondrion
AGOP: cell cycle, growth, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

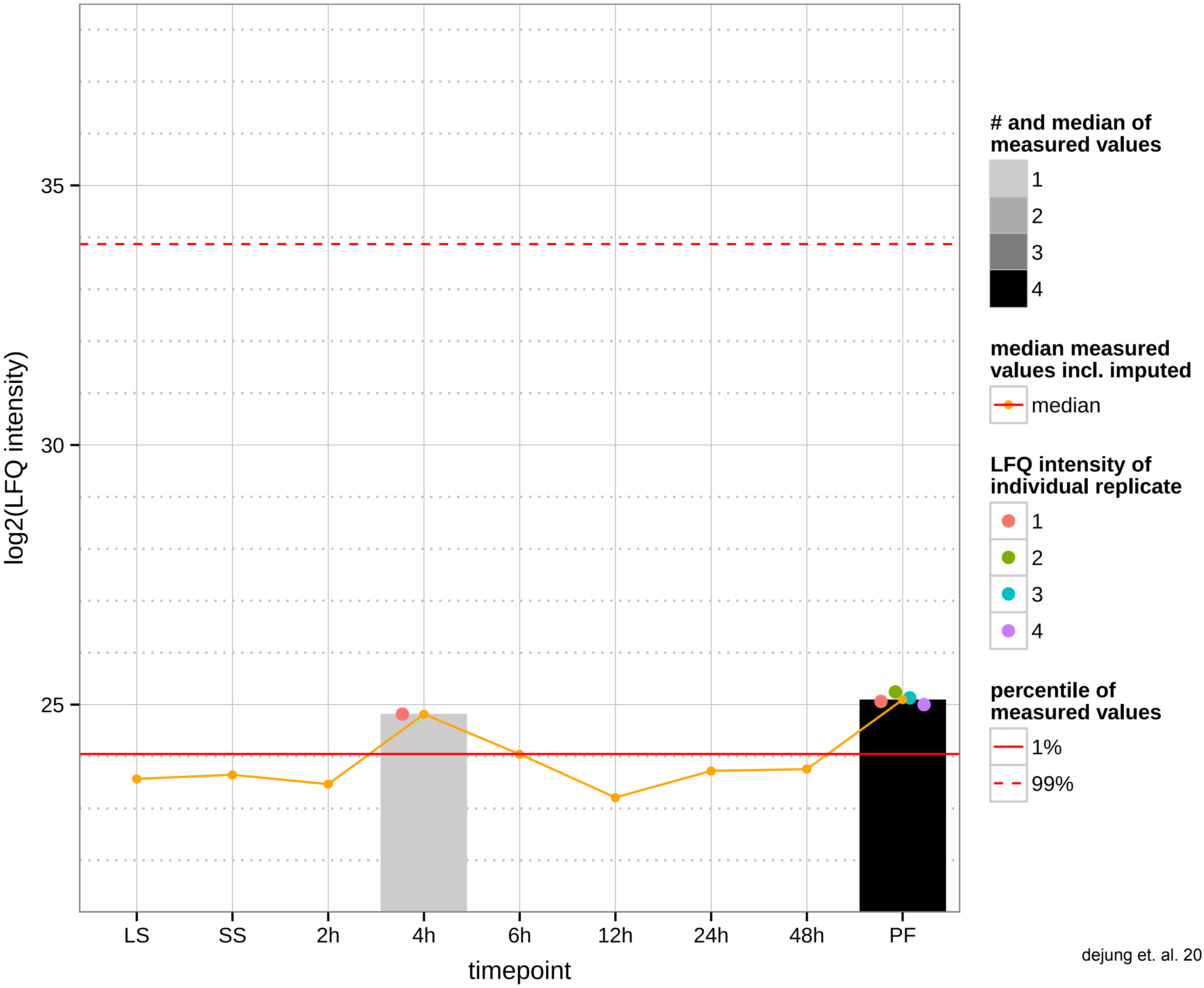




dejung et. al. 2015

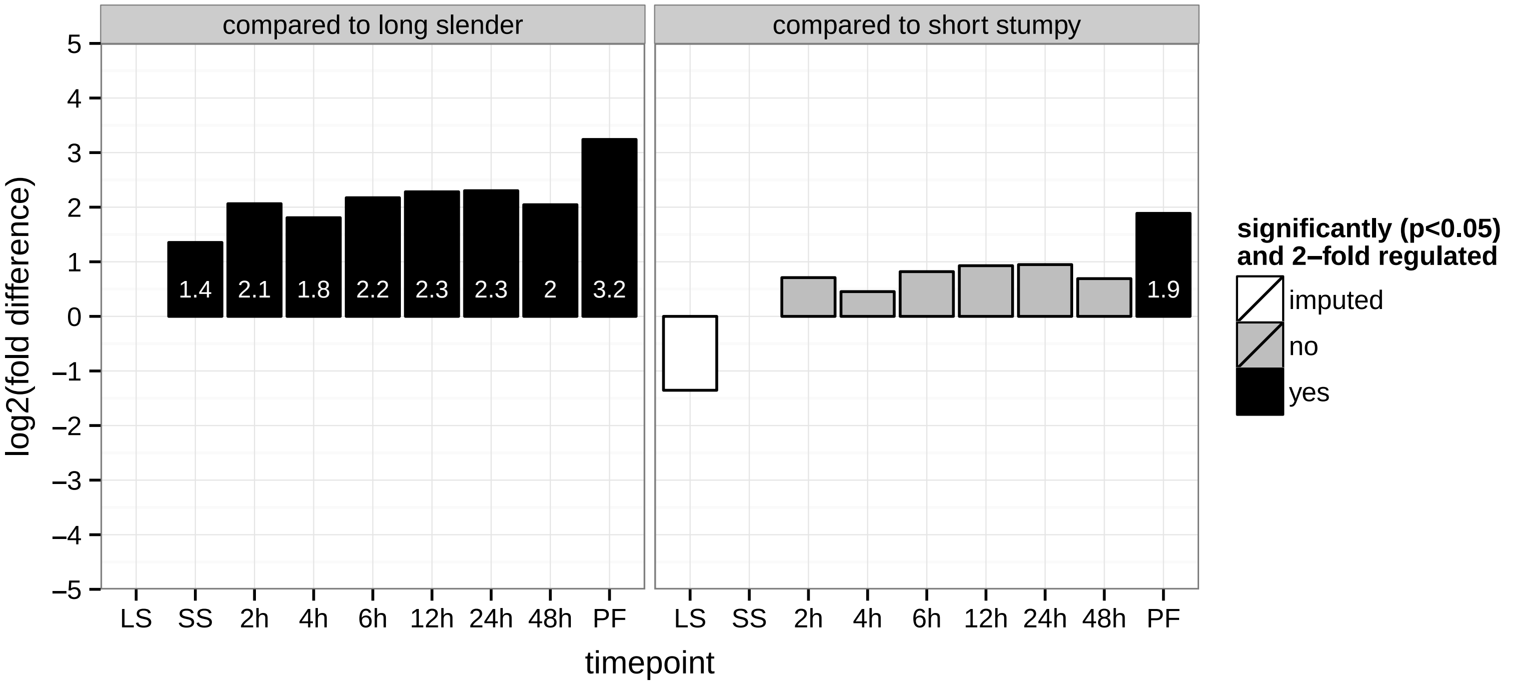
mitochondrial RNA binding complex 1 subunit (MRB800)
Tb927.7.800
AGOF: RNA binding
AGOC: mitochondrion
AGOP: cytidine to uridine editing, mRNA stabilization
PGOF: null
PGOC: null
PGOP: null

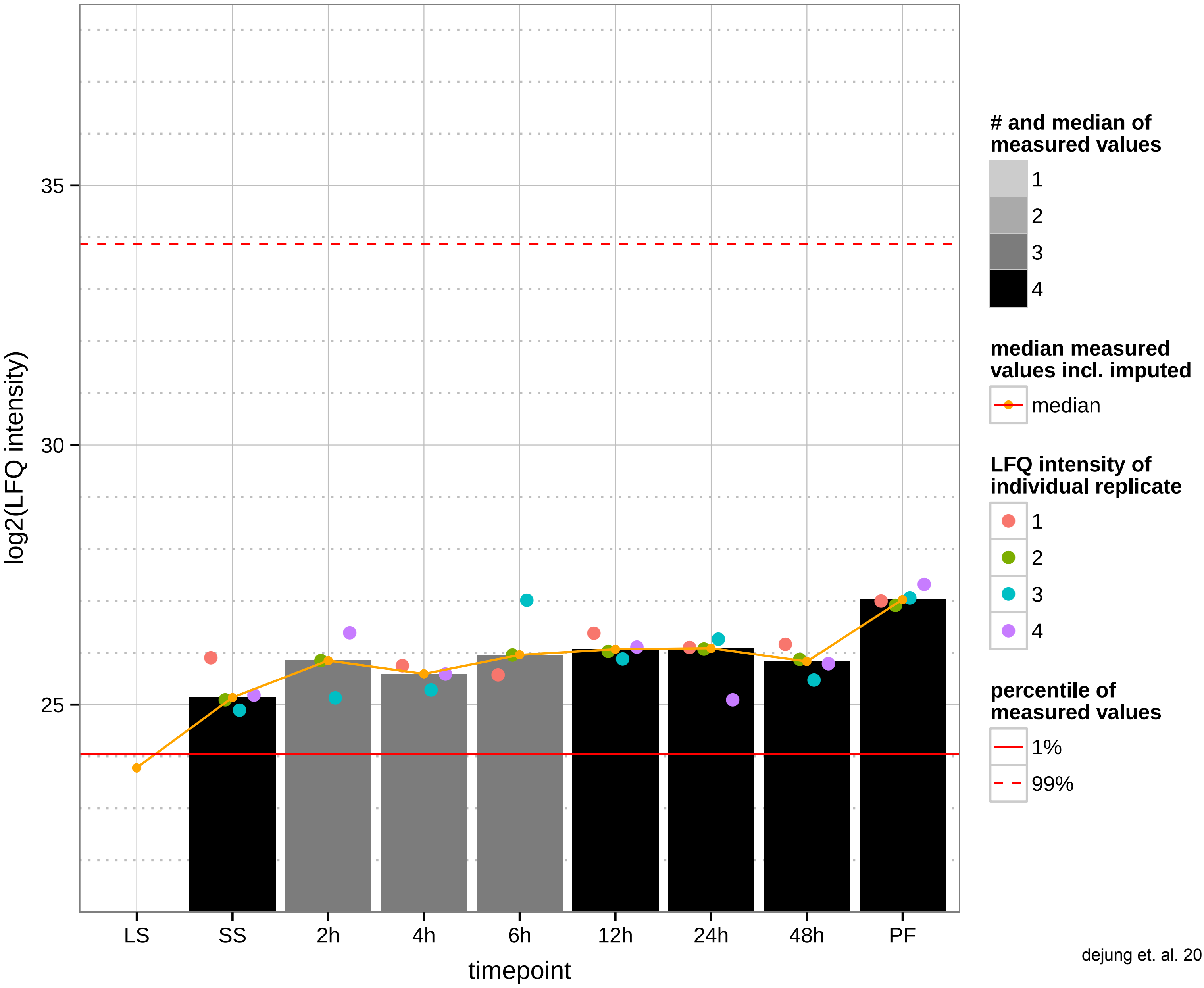




dejung et. al. 2015

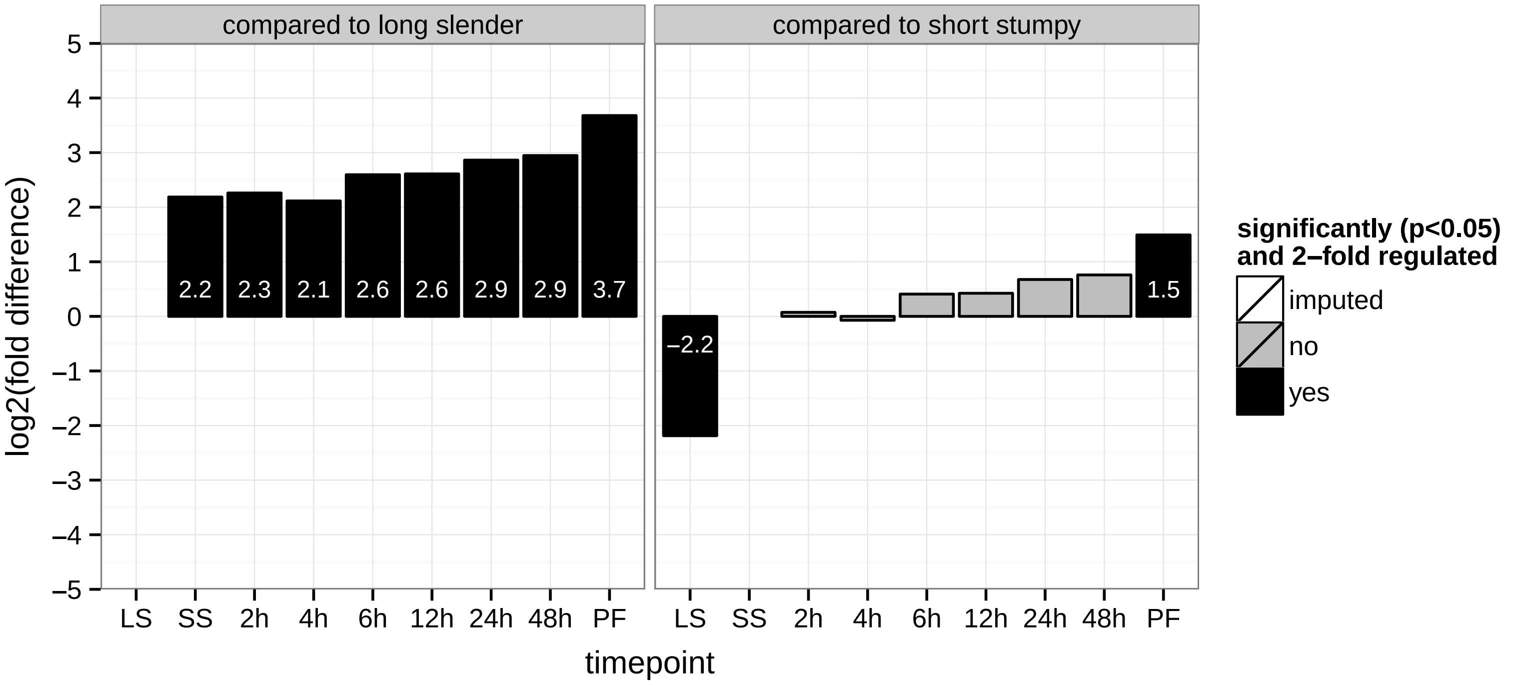
hypothetical protein, conserved
Tb927.7.910;Tb11.v5.0841
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

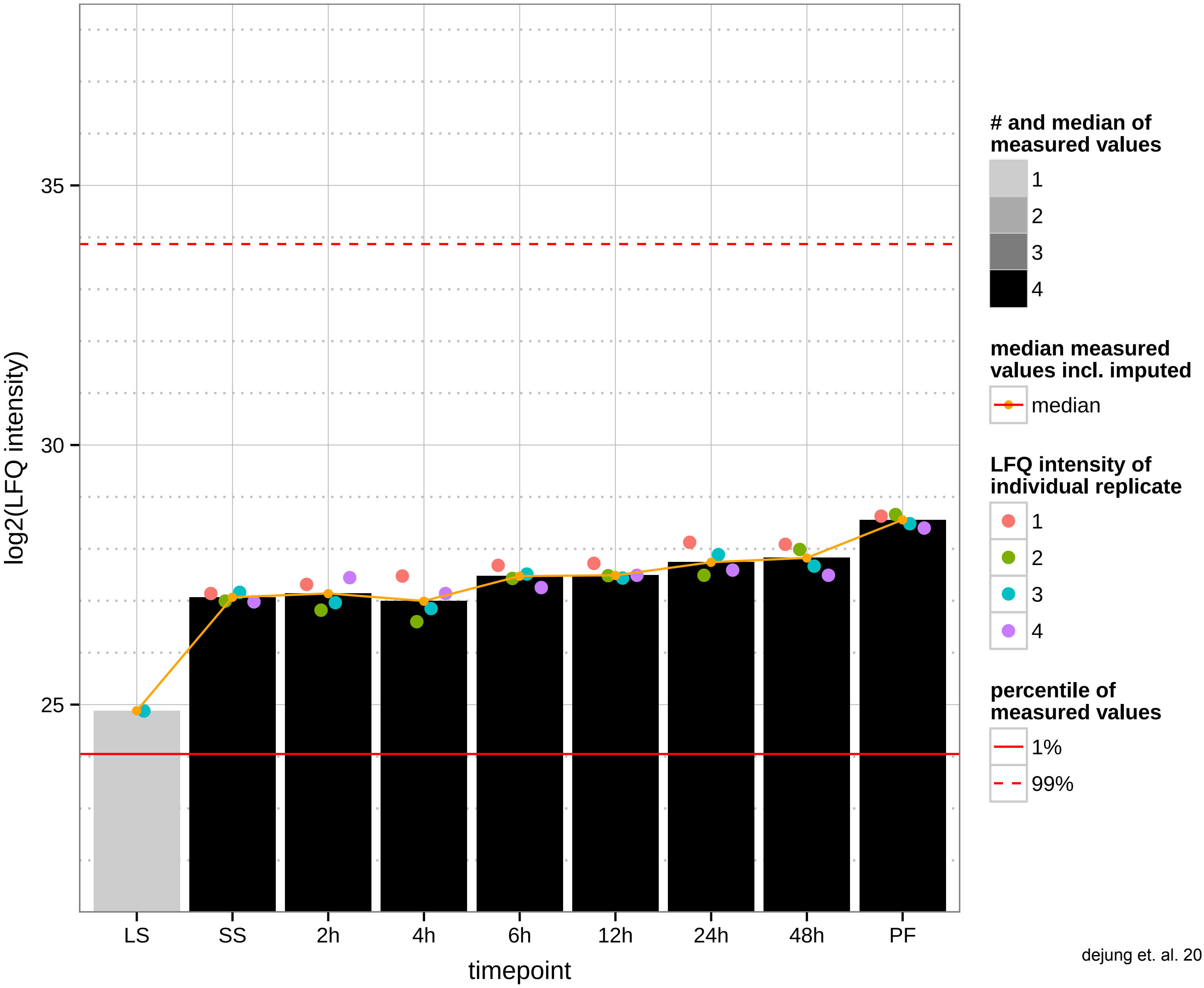




dejung et. al. 2015

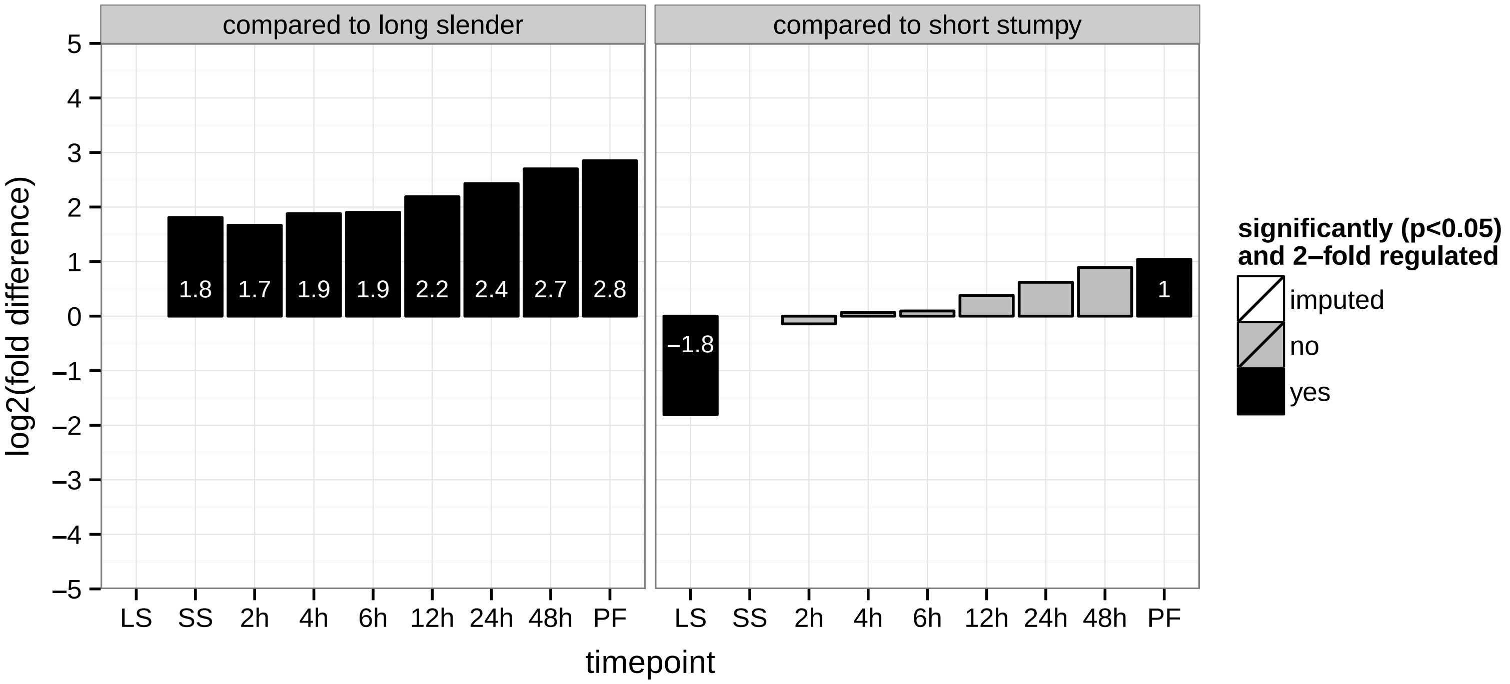
hypothetical protein, conserved
Tb927.7.970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

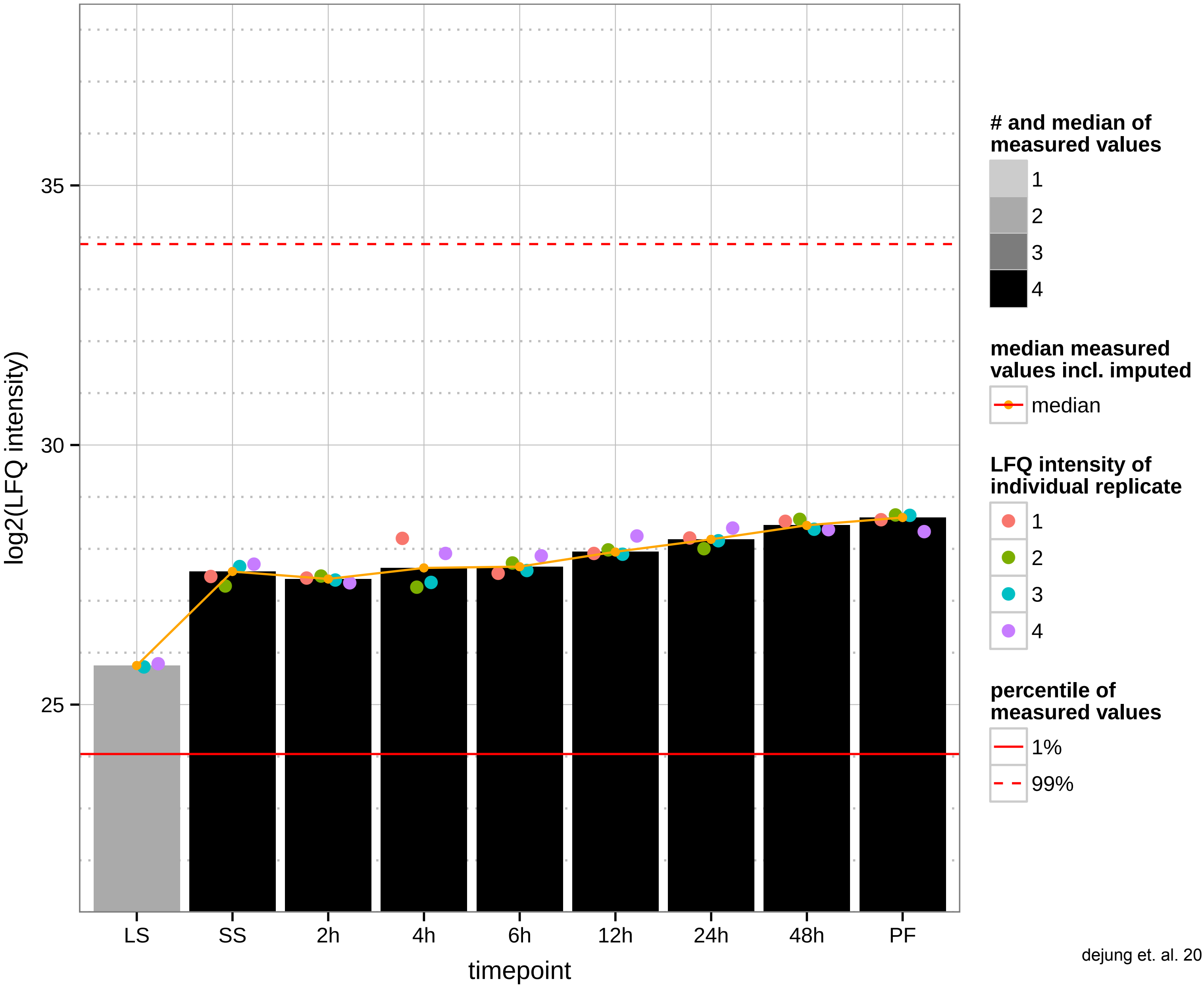




dejung et. al. 2015

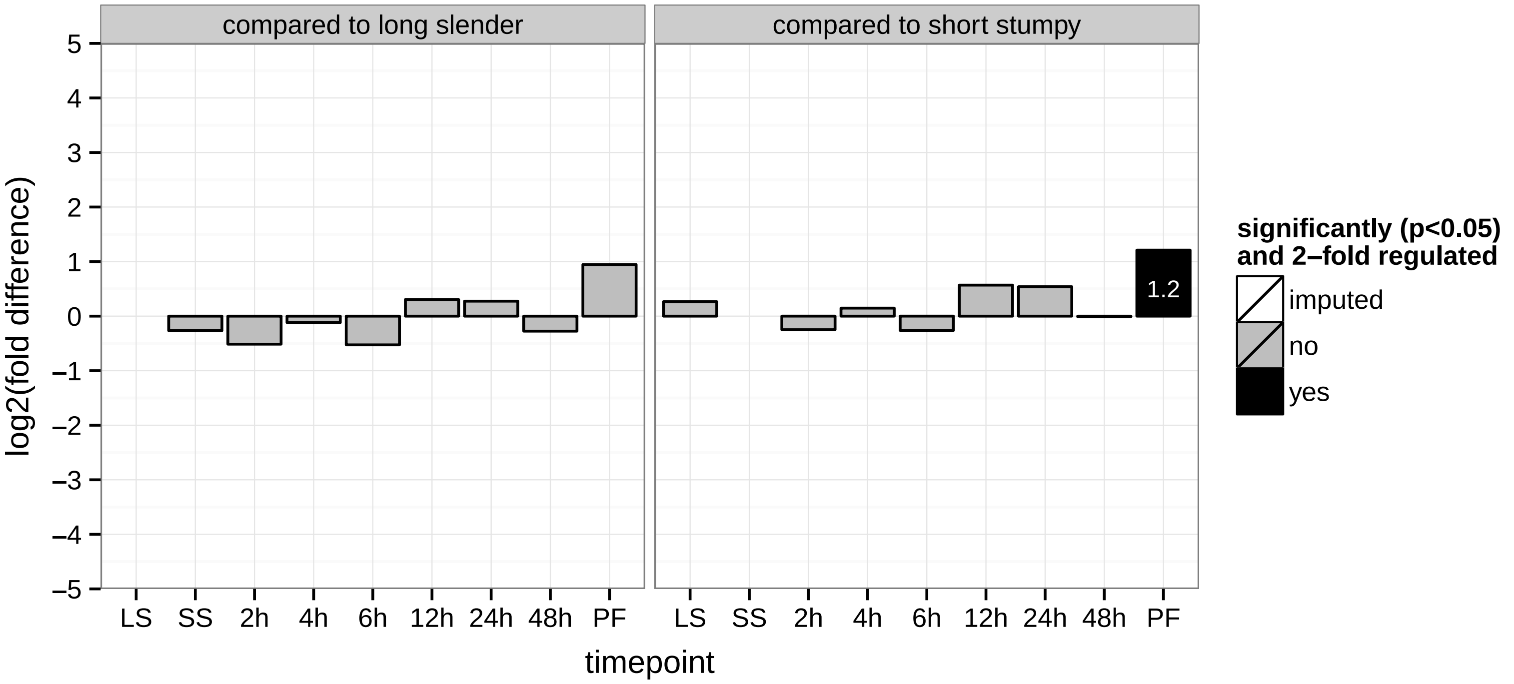
chaperone protein DNAj, putative
Tb927.7.990
AGOF: heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: null
PGOF: heat shock protein binding
PGOC: null
PGOP: null

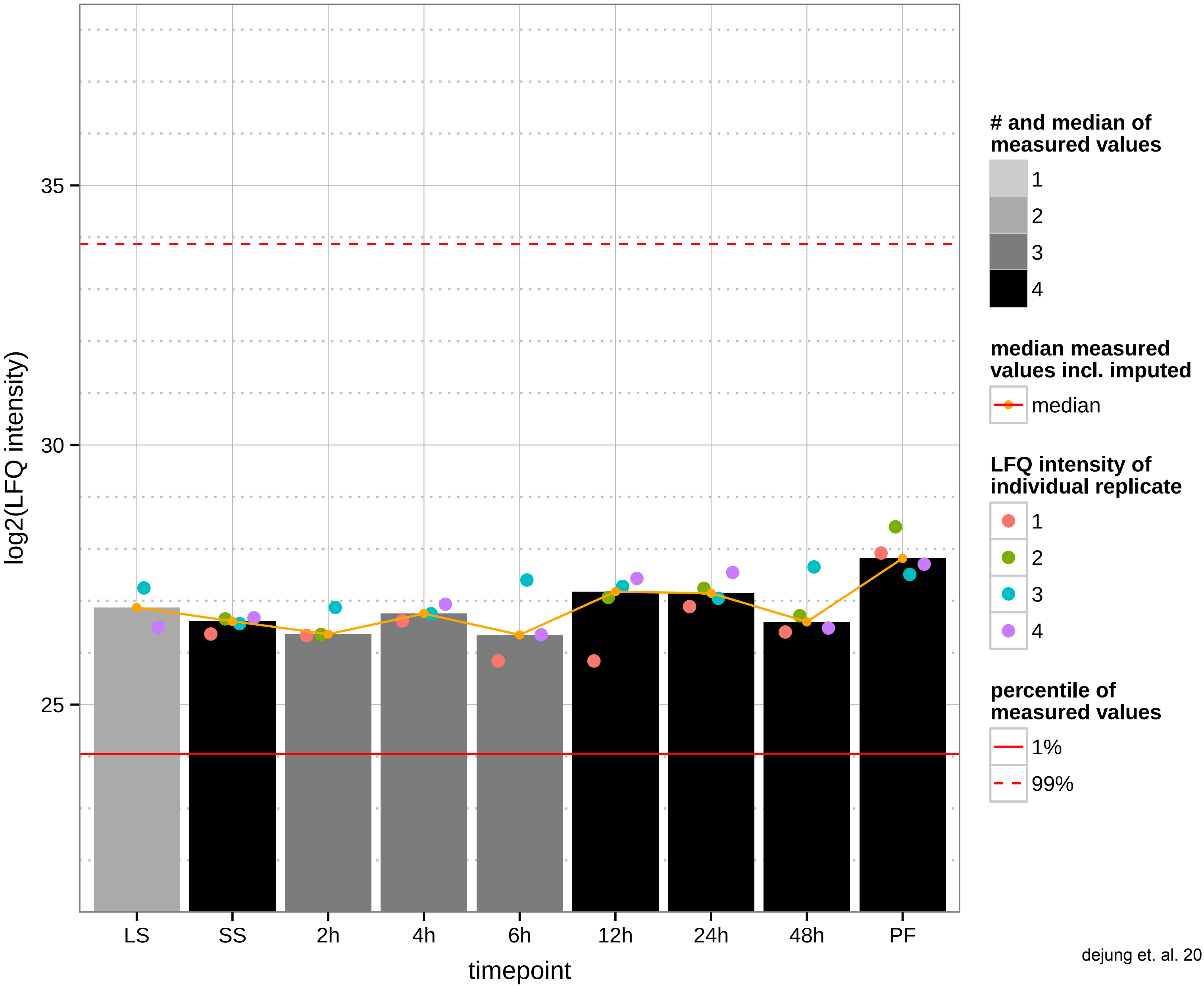




dejung et. al. 2015

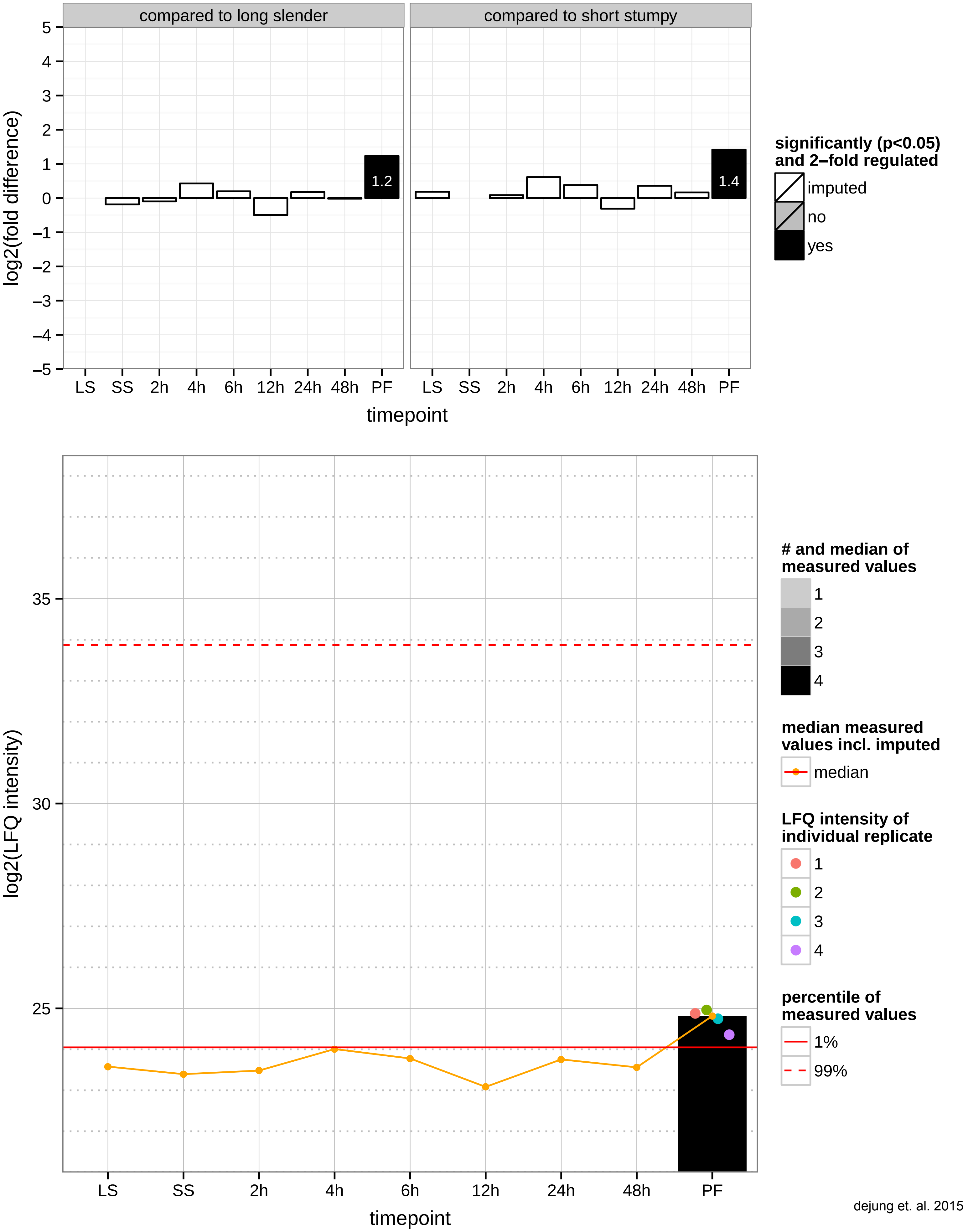
hypothetical protein, conserved
Tb927.8.1230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.1430
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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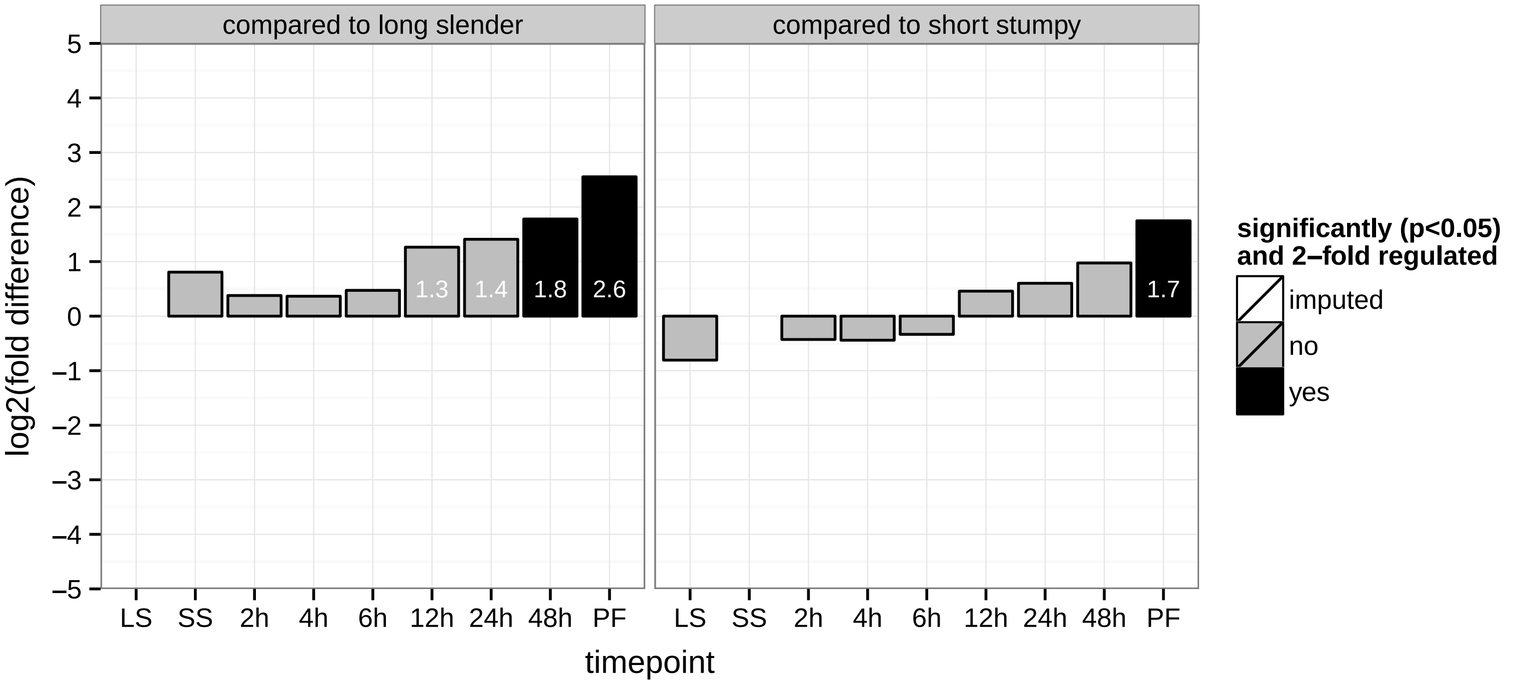
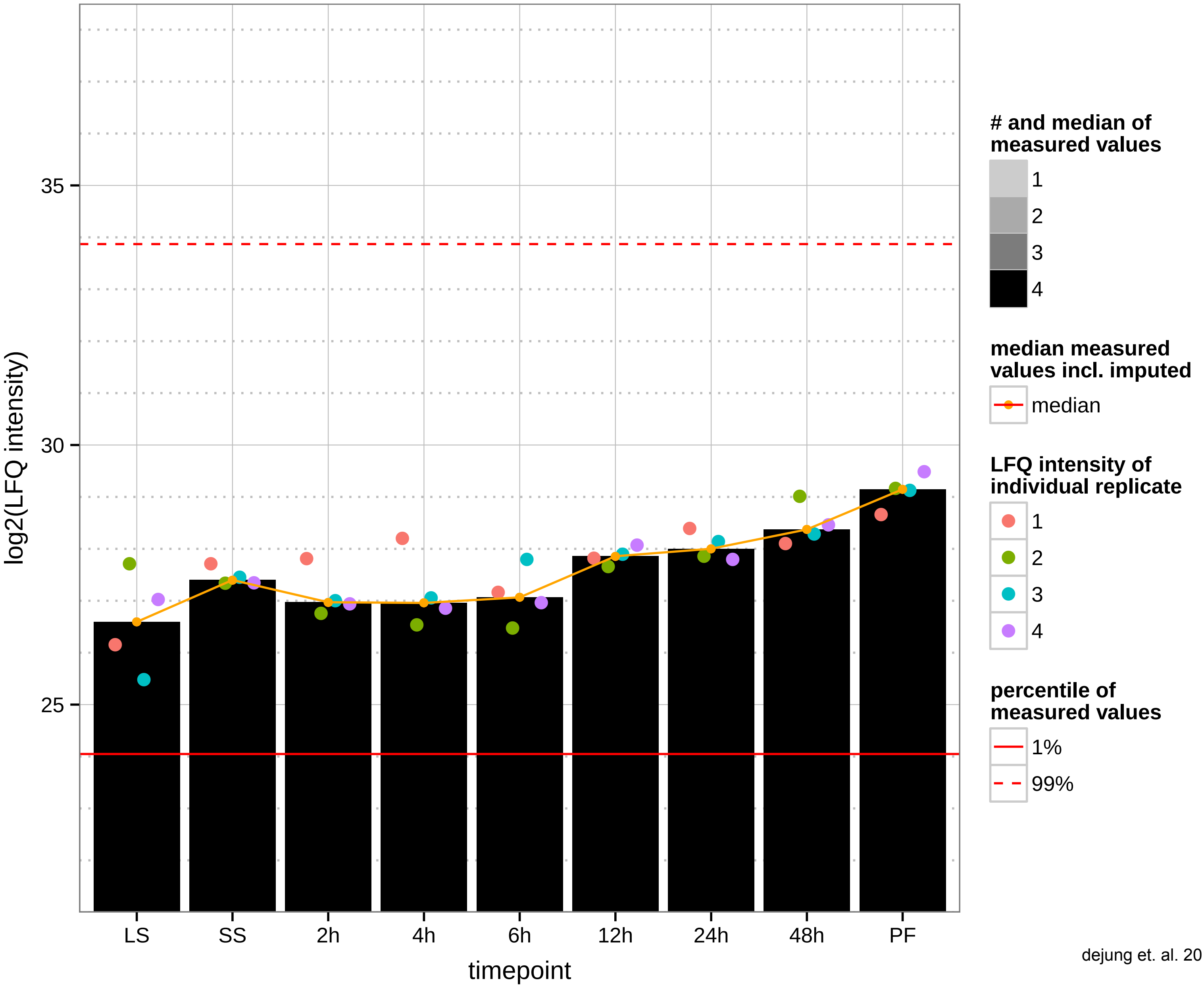
ubiquitin–protein ligase, putative (upl3)
Tb927.8.1590
AGOF: RNA binding, ubiquitin–protein ligase activity, zinc ion binding
AGOC: intracellular, mitochondrion
AGOP: cellular protein modification process
PGOF: acid–amino acid ligase activity
PGOC: intracellular
PGOP: cellular protein modification process





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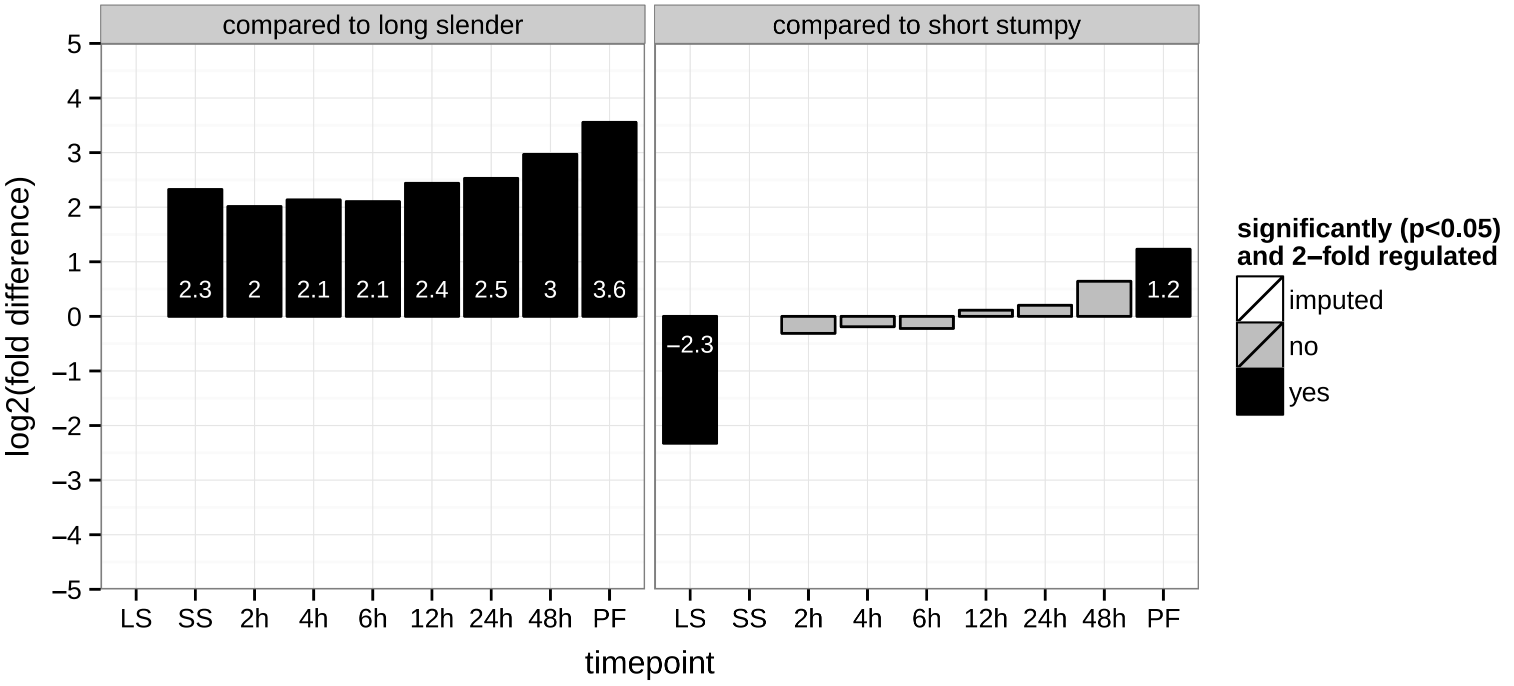
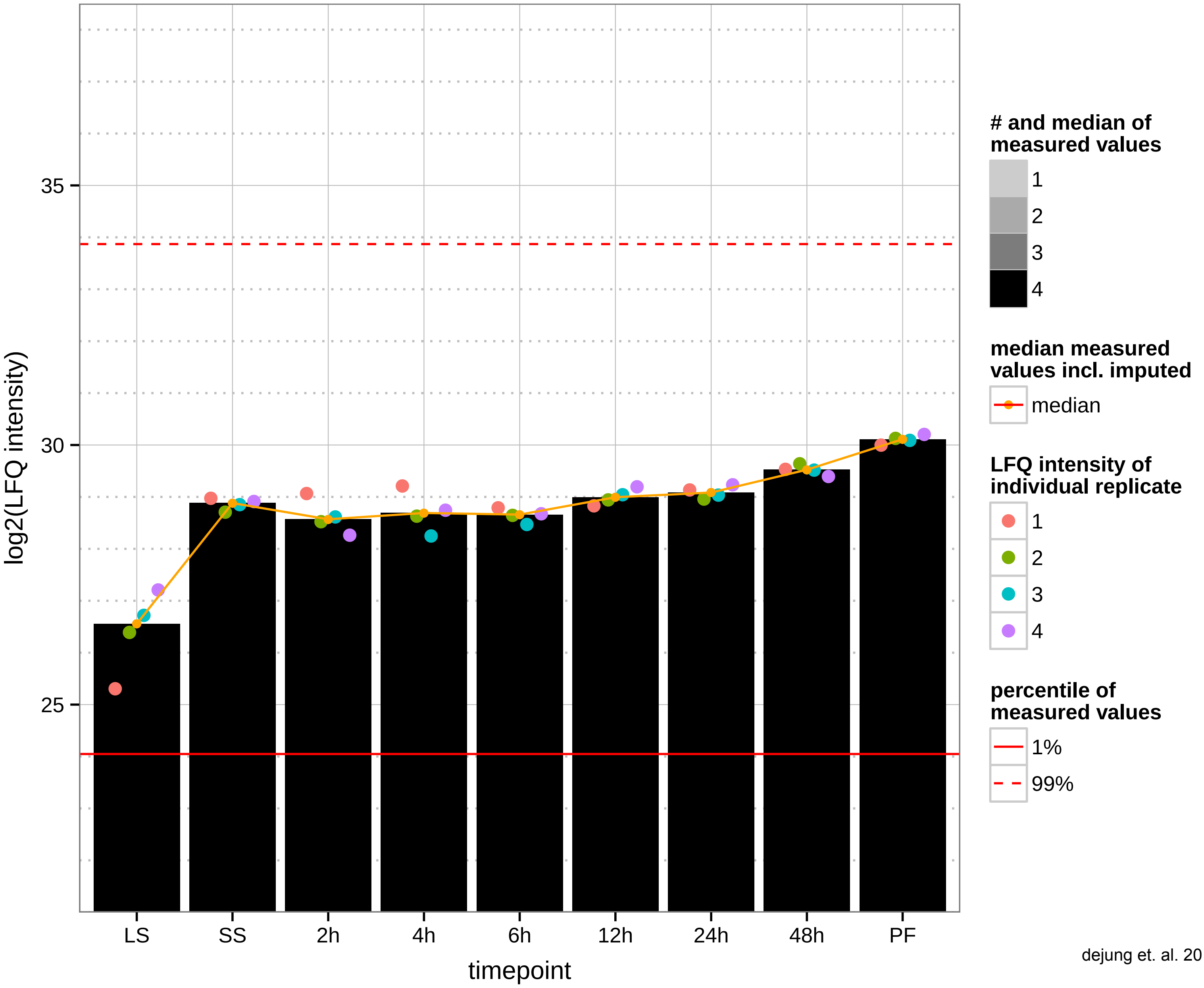
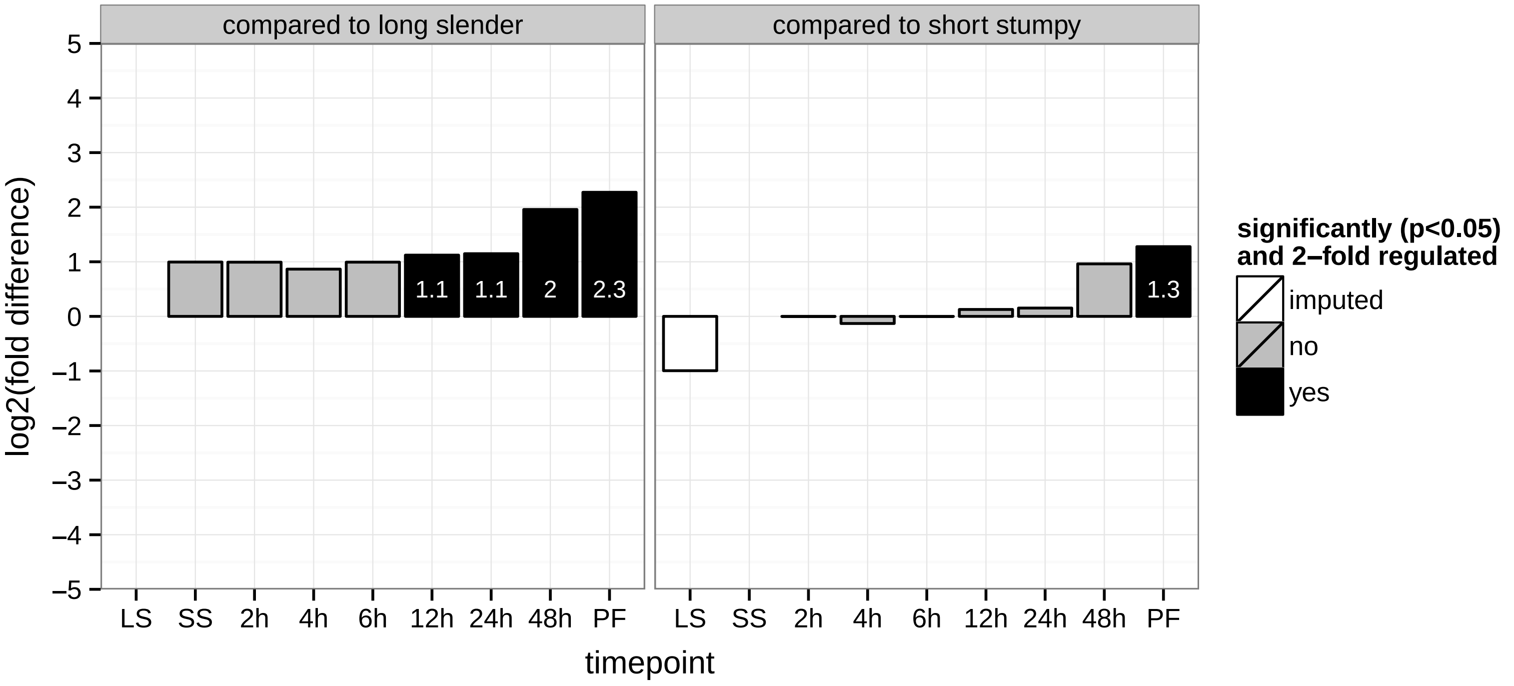
pitrilysin–like metalloprotease, metallo–peptidase, Clan ME, Family M16C
Tb927.8.1860
AGOF: catalytic activity, metalloendopeptidase activity, zinc ion binding
AGOC: mitochondrion
AGOP: proteolysis
PGOF: catalytic activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, zinc ion binding
PGOC: null
PGOP: proteolysis

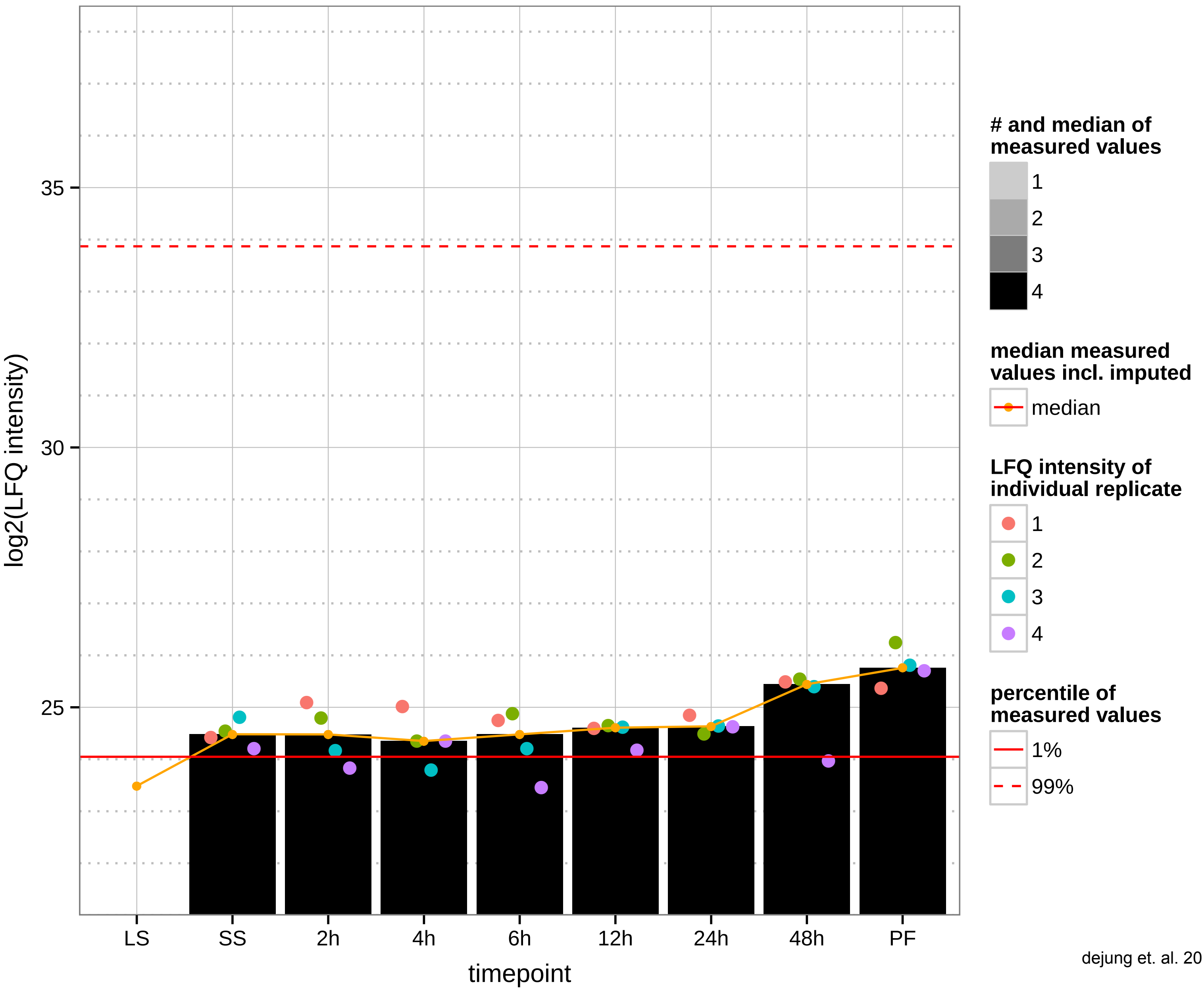




dejung et. al. 2015

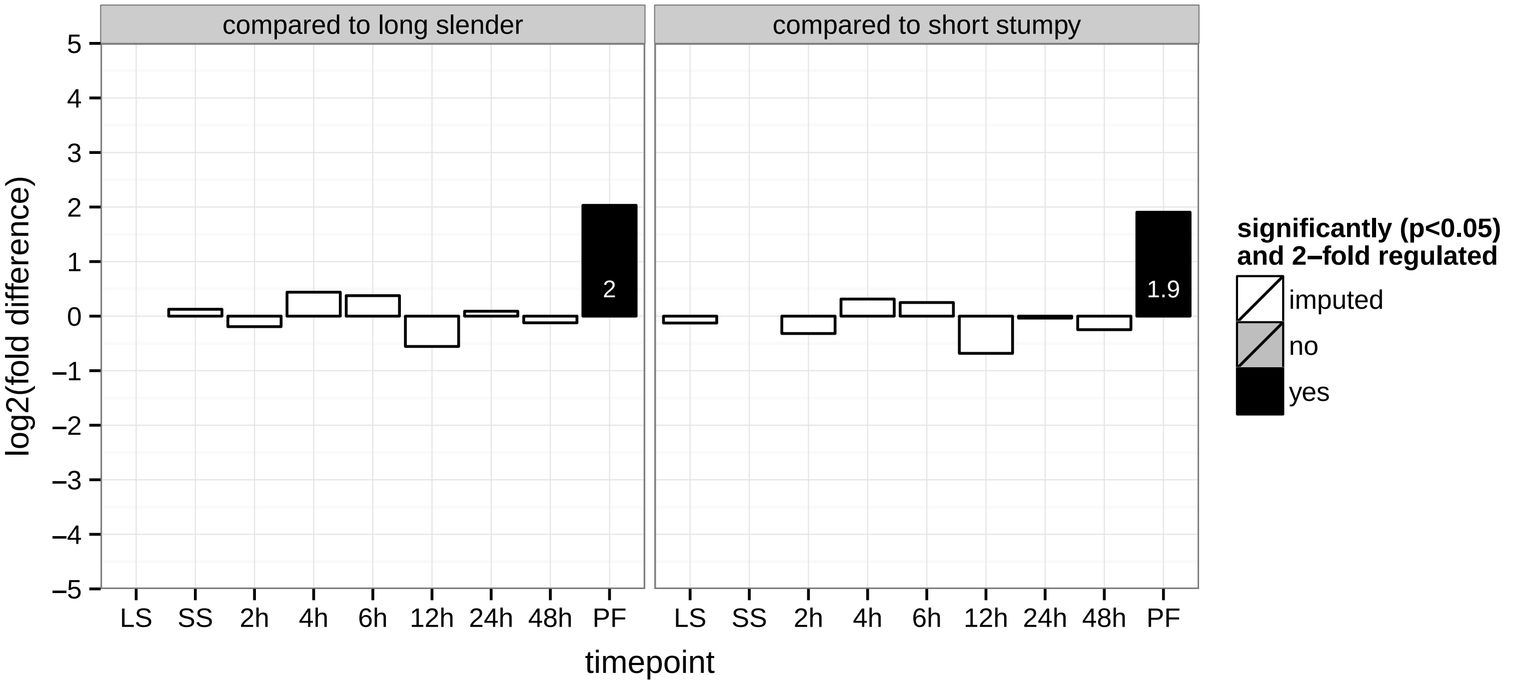
hypothetical protein, conserved
Tb927.8.2130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

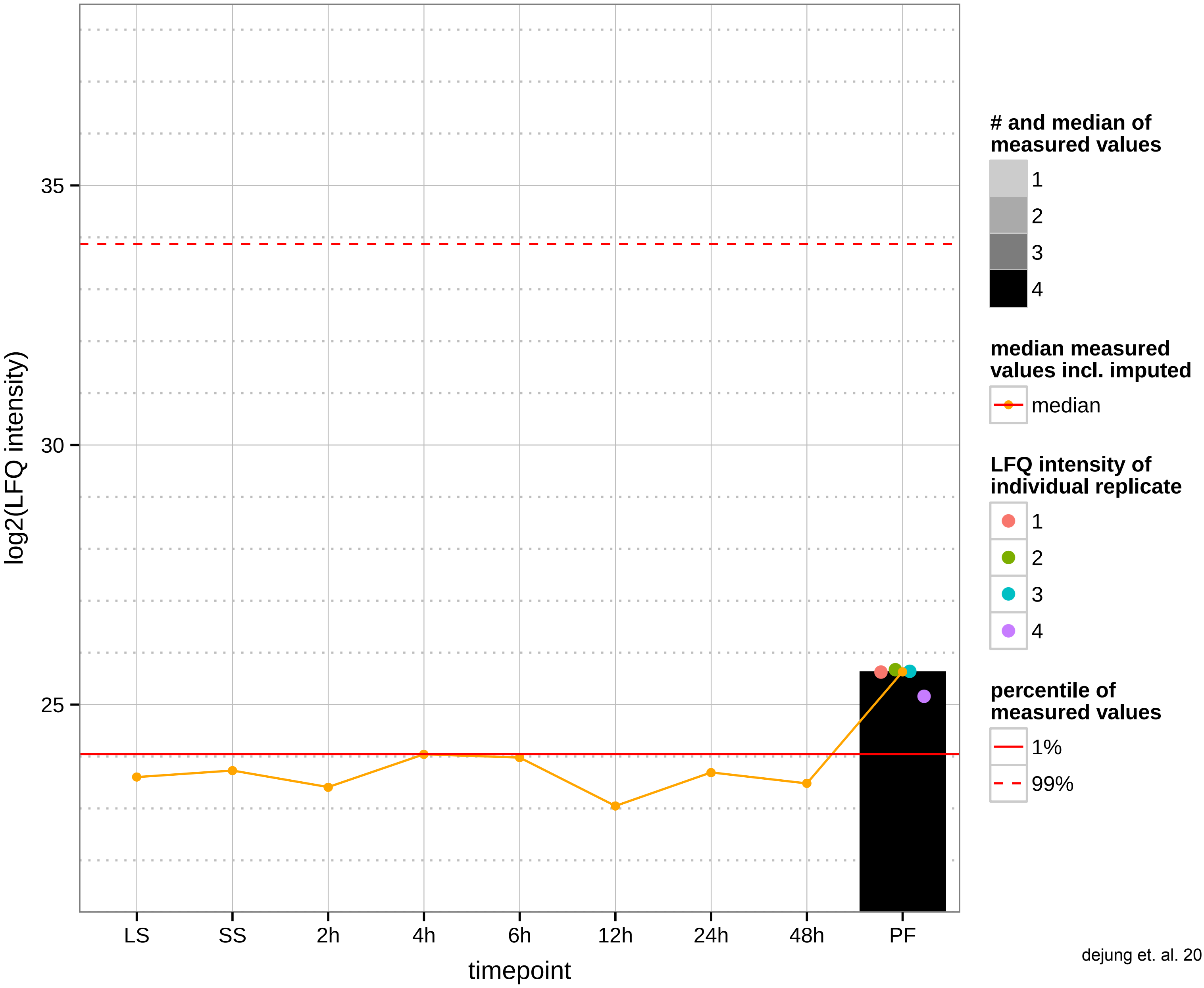




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.2300
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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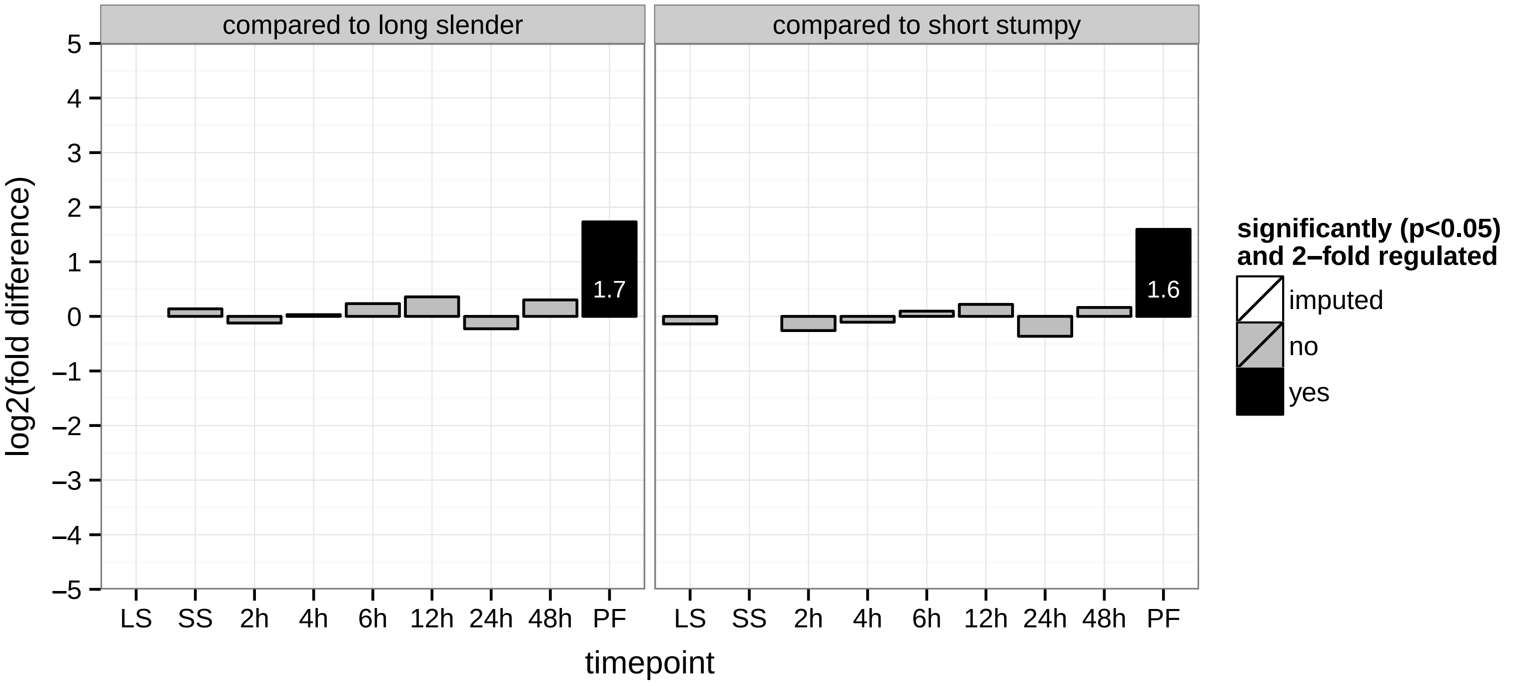
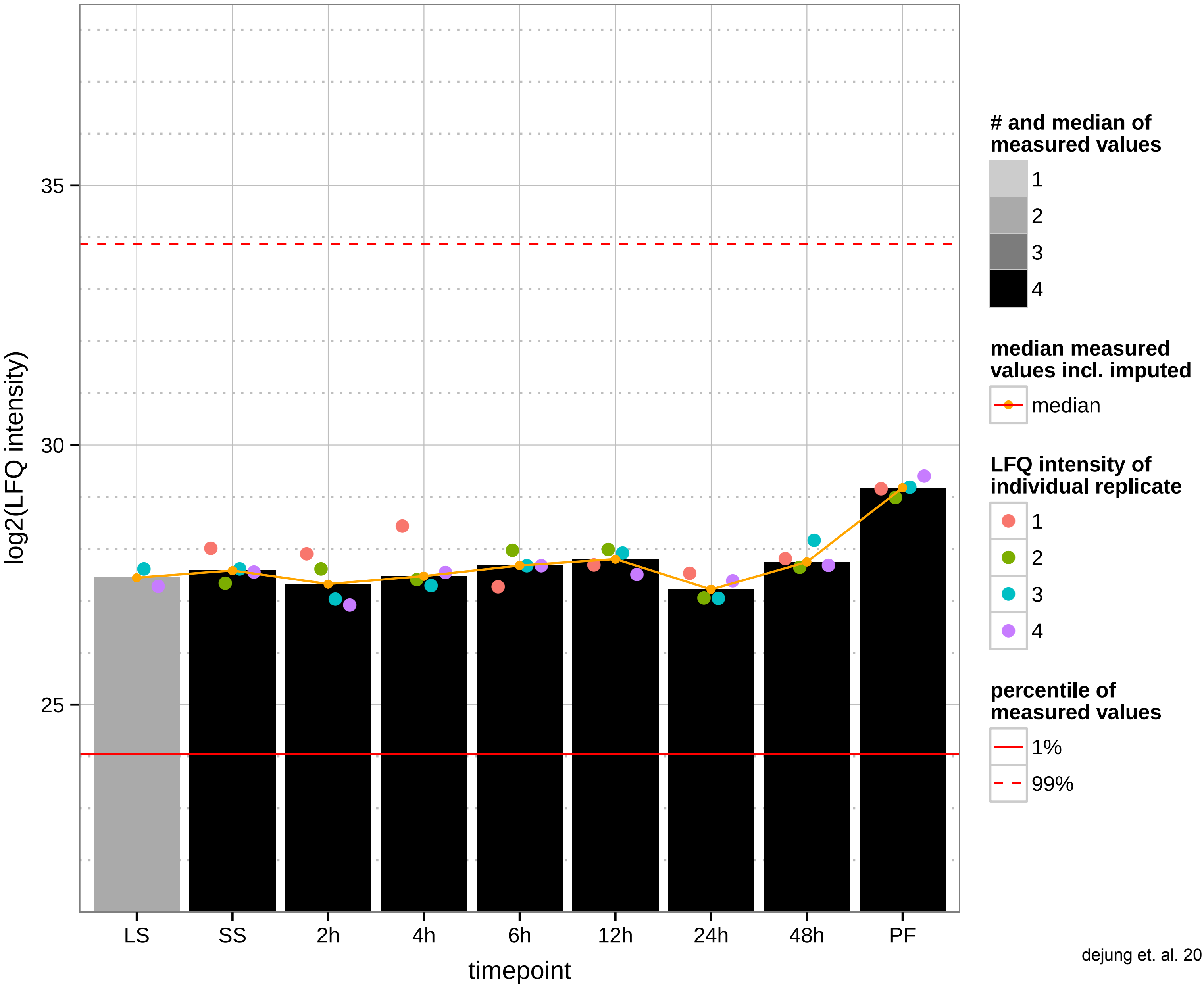
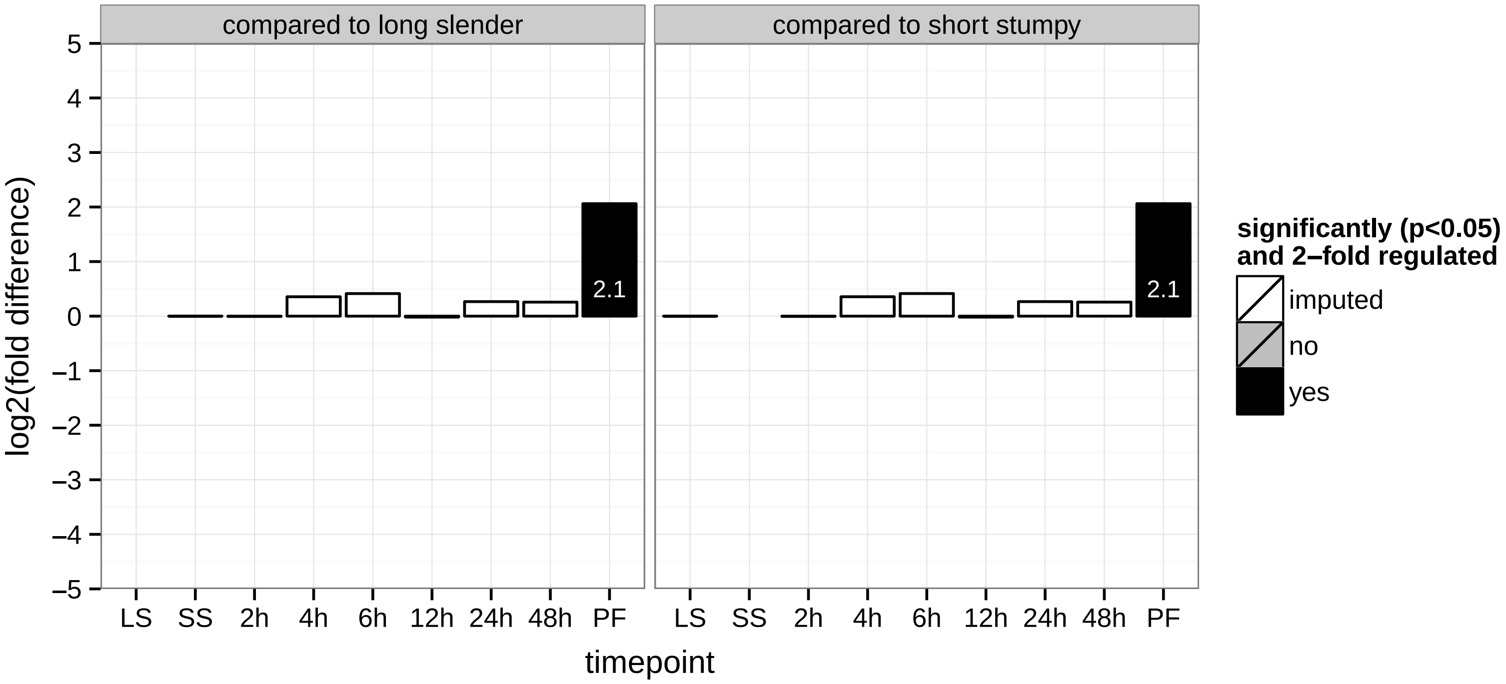
acetyl–CoA synthetase, putative, acetyl–CoA synthetase (pseudogene), truncated
Tb927.8.2520
AGOF: AMP binding, acetate–CoA ligase activity, catalytic activity, catalytic activity
AGOC: integral to membrane, null
AGOP: metabolic process
PGOF: AMP binding, acetate–CoA ligase activity, catalytic activity, catalytic activity
PGOC: null
PGOP: metabolic process

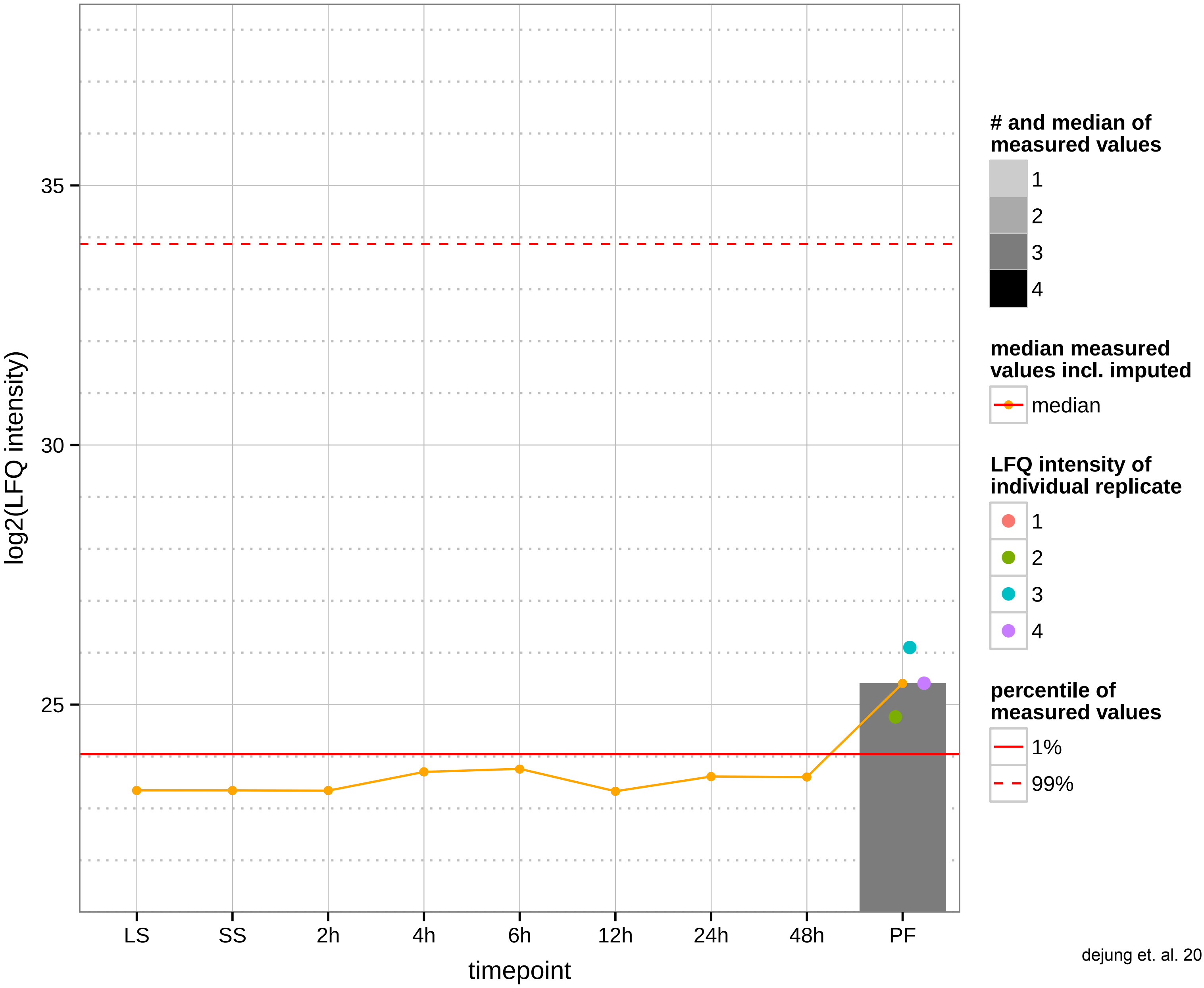




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.2750
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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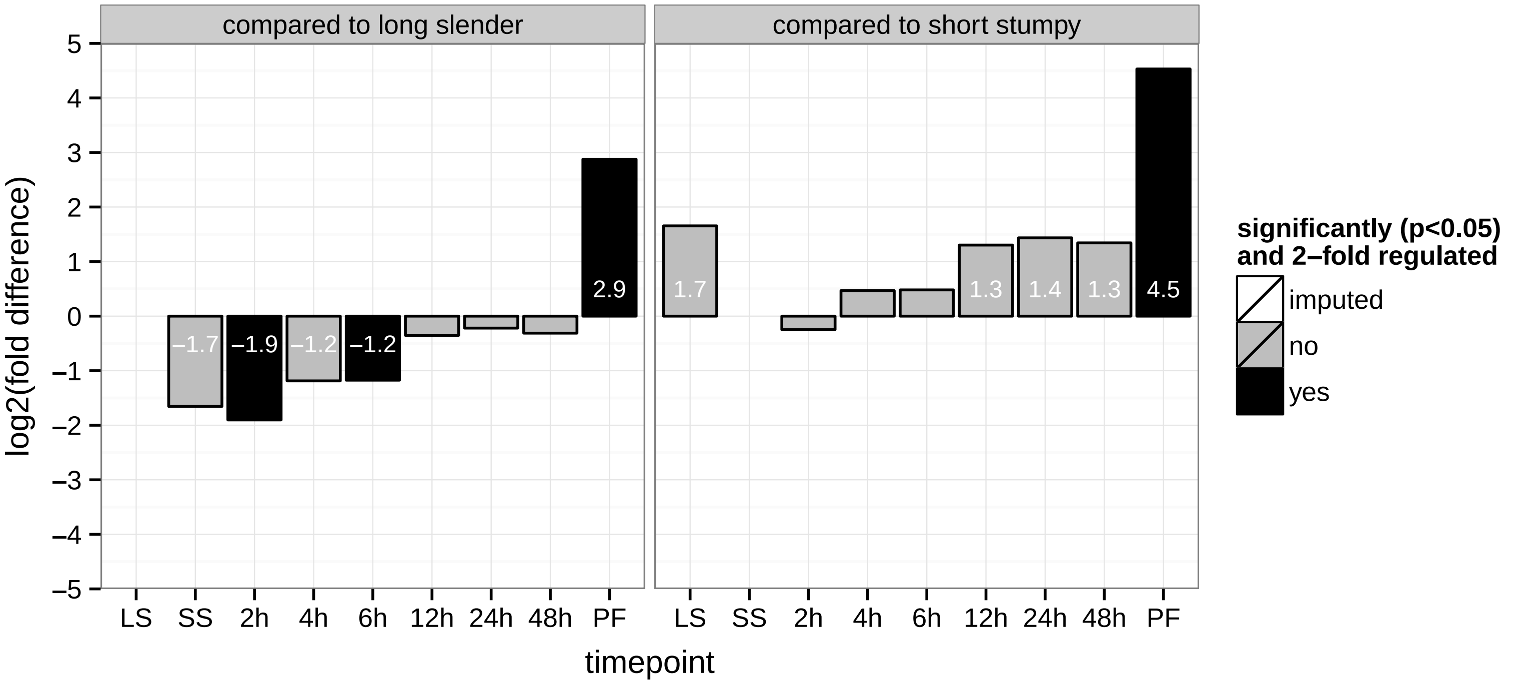
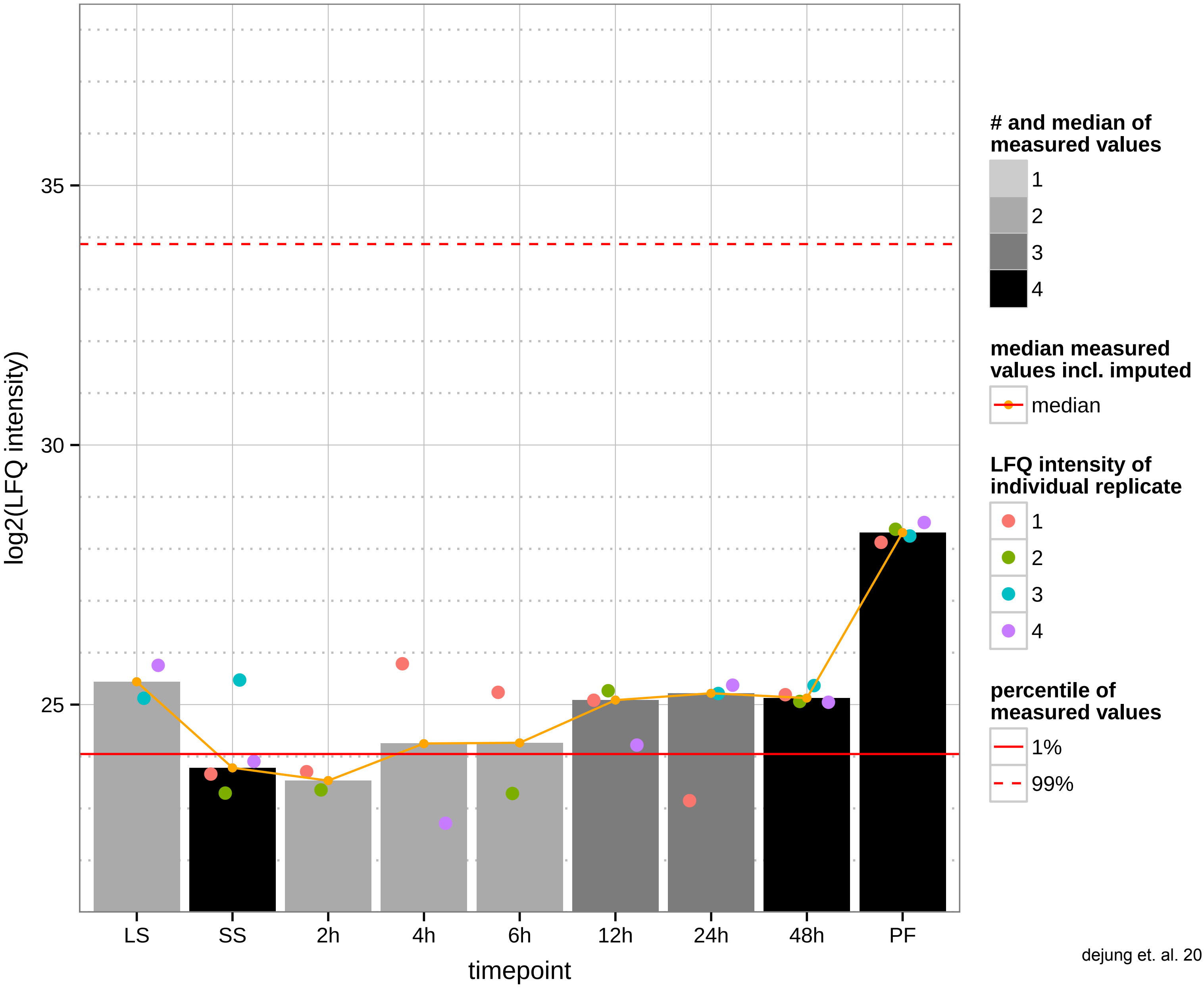
mannosyl–oligosaccharide 1, 2–alpha–mannosidase IB, putative
Tb927.8.2920;Tb927.8.2930;Tb927.8.2940
AGOF: calcium ion binding, mannosyl–oligosaccharide 1, 2–alpha–mannosidase activity
AGOC: endoplasmic reticulum, membrane
AGOP: protein N–linked glycosylation
PGOF: calcium ion binding, mannosyl–oligosaccharide 1, 2–alpha–mannosidase activity
PGOC: membrane
PGOP: null





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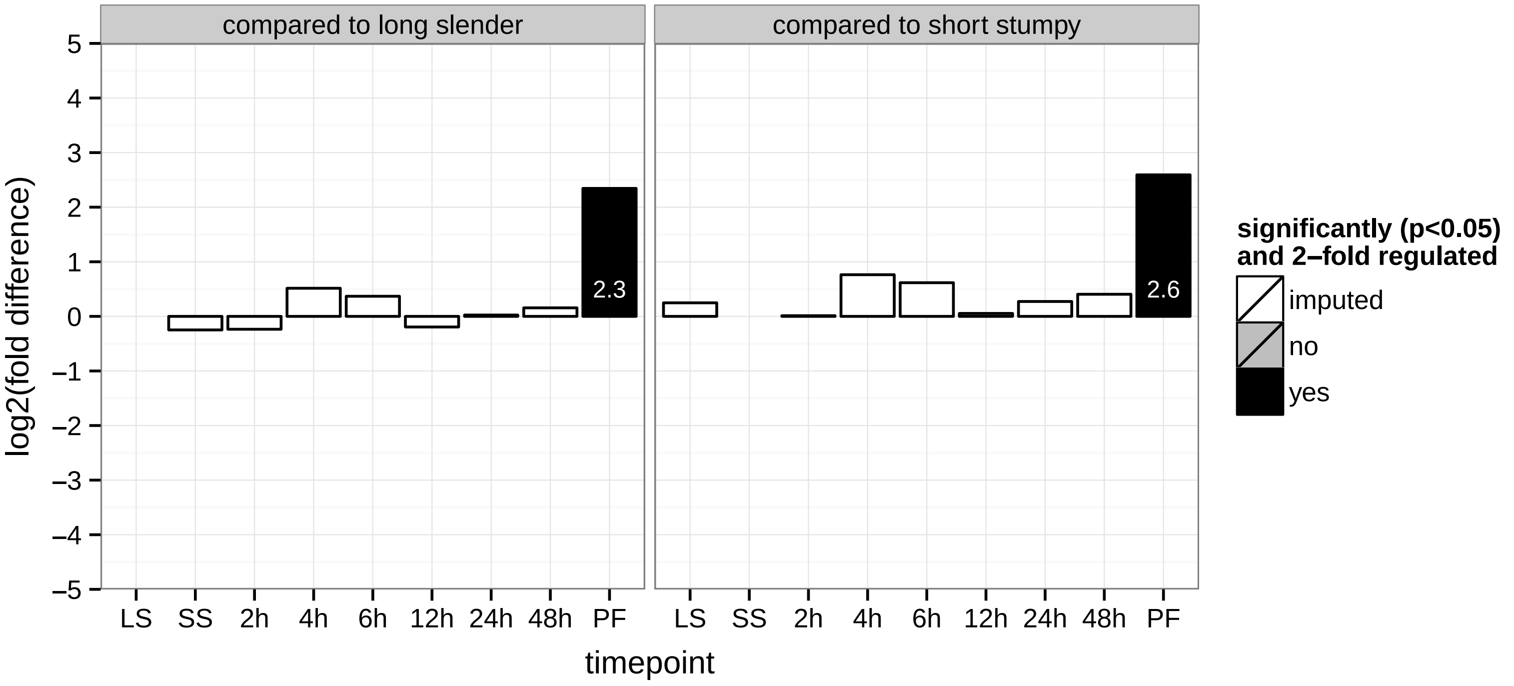
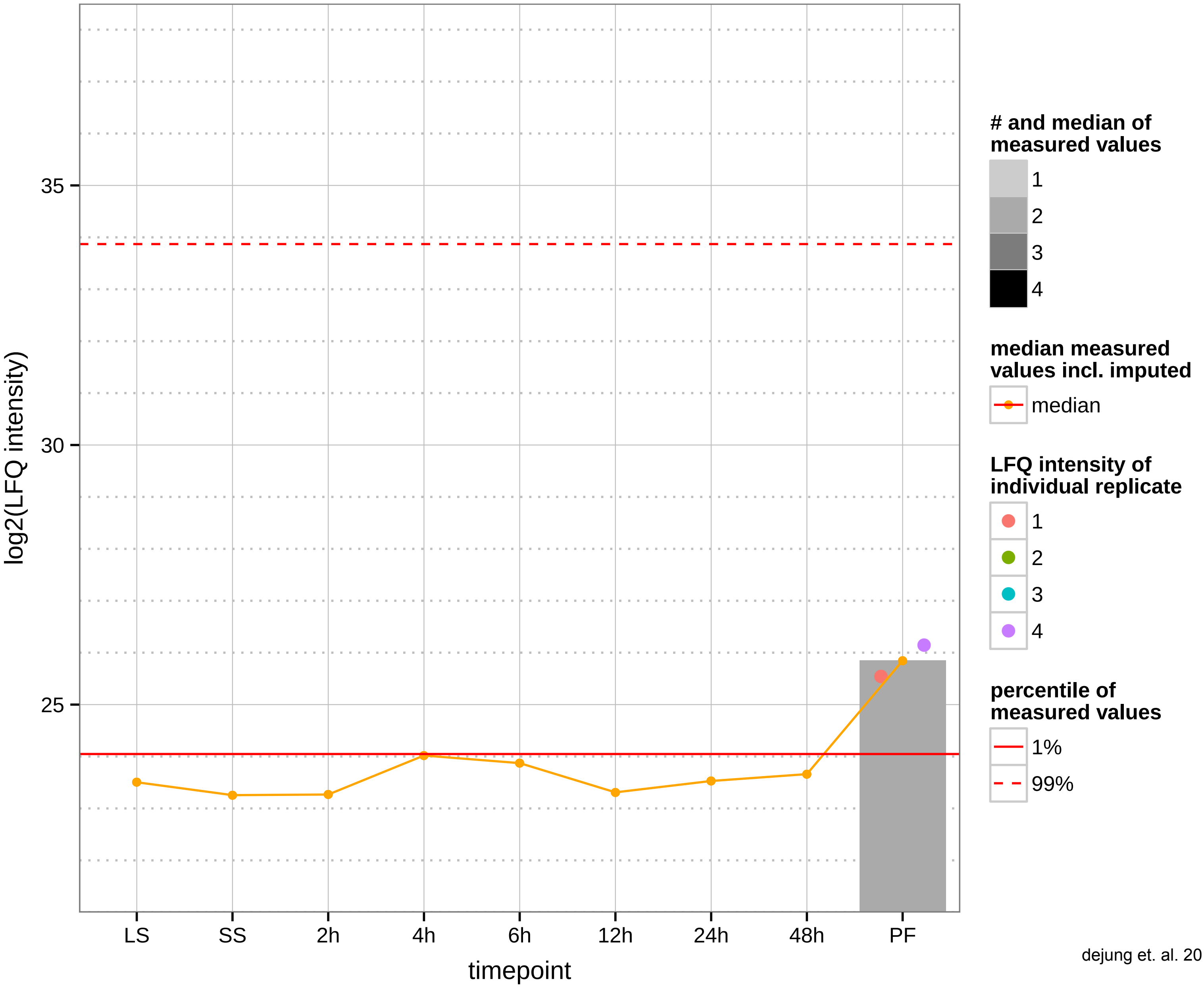
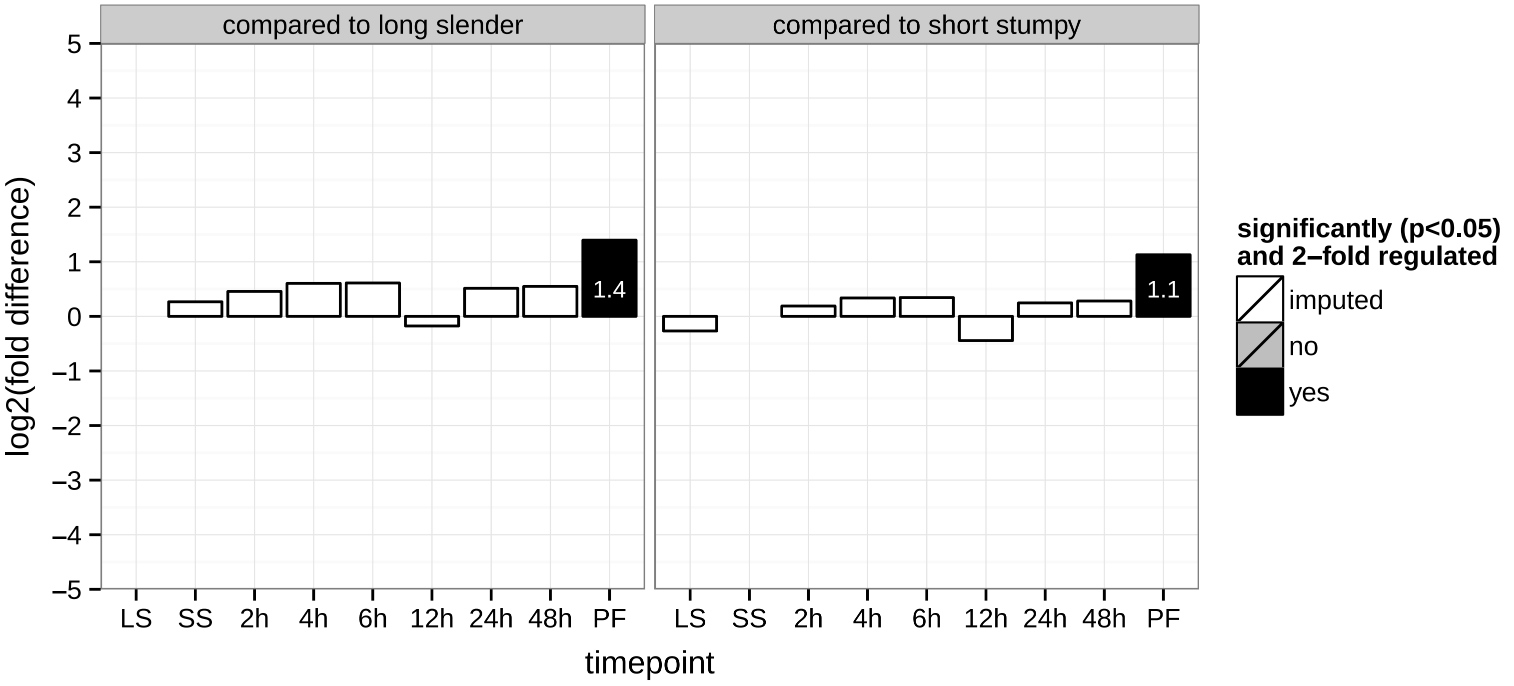
hypothetical protein, conserved
Tb927.8.2950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

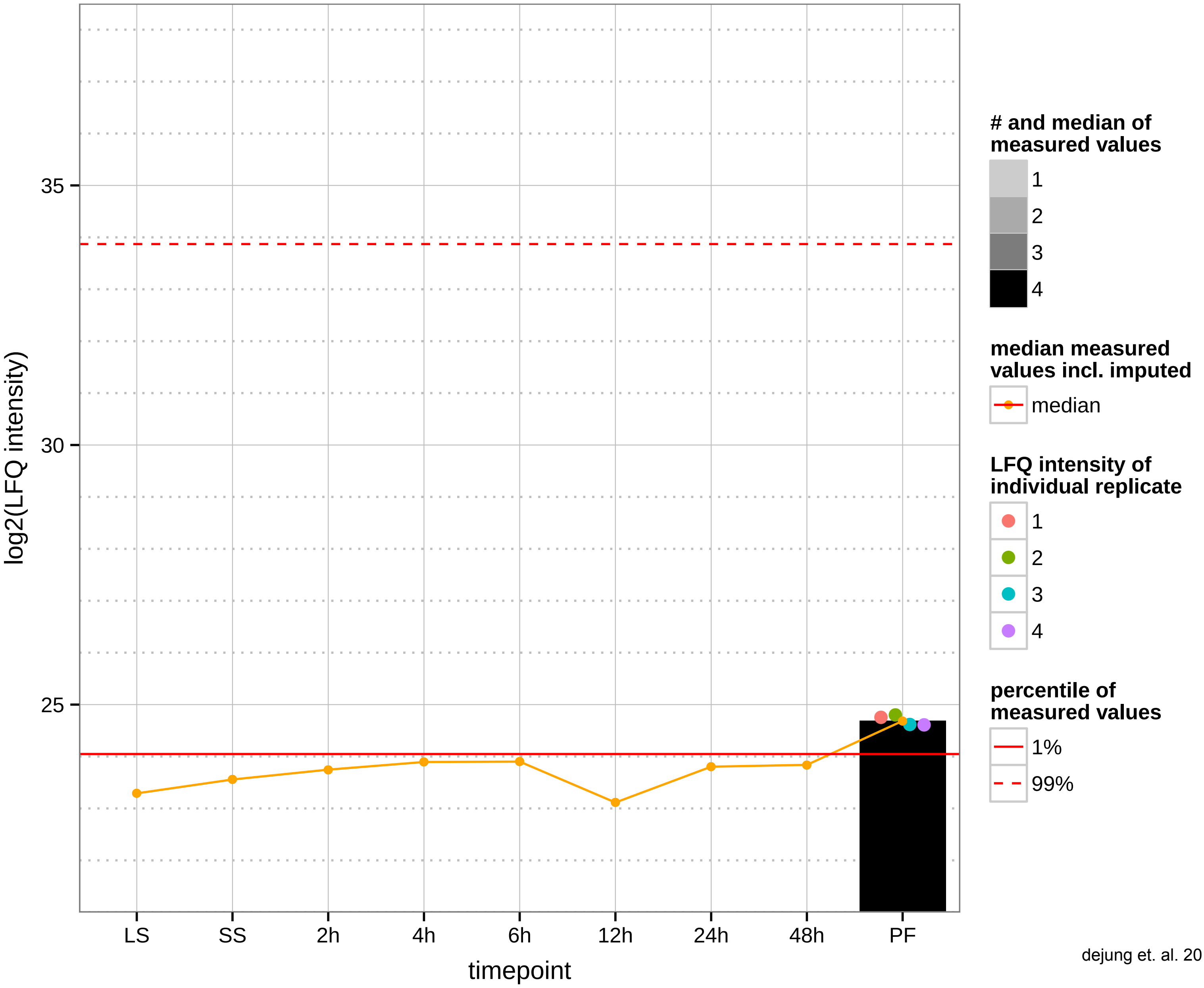




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.3090
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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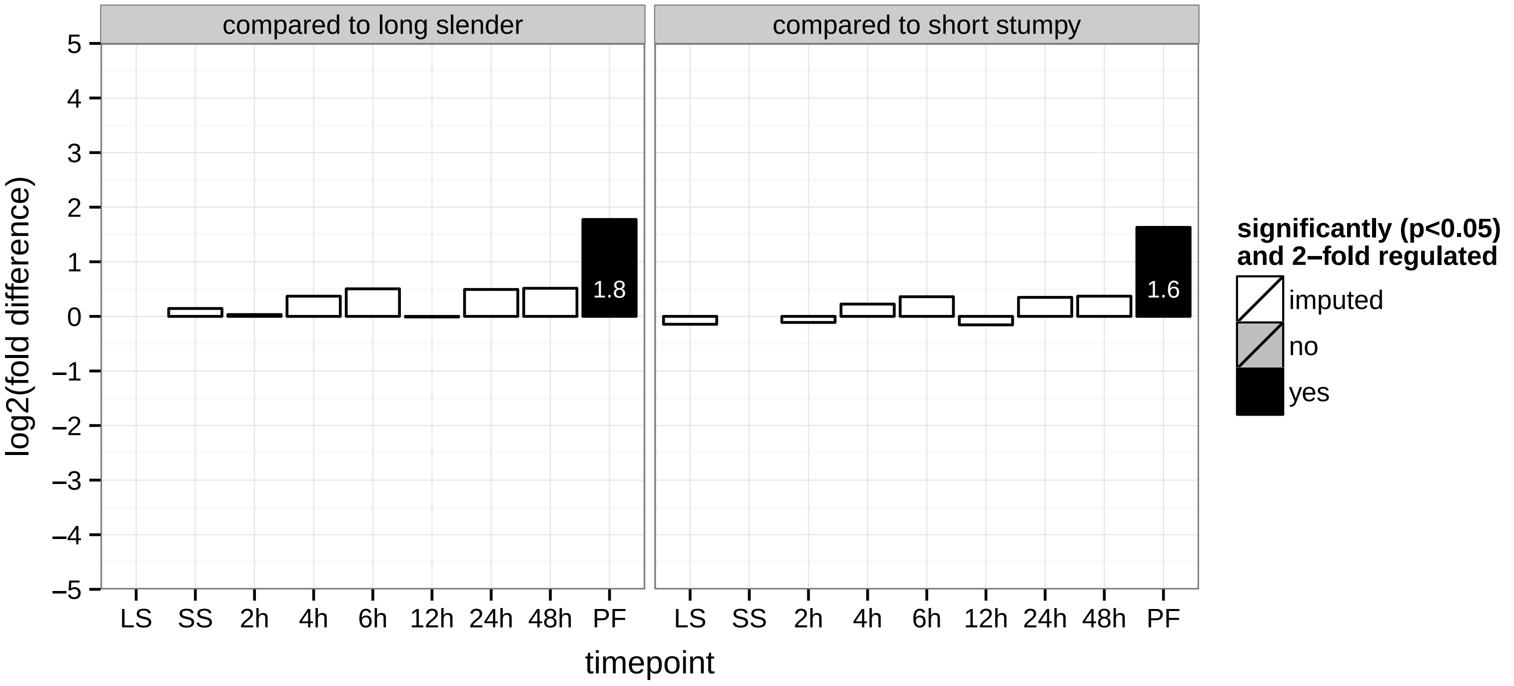
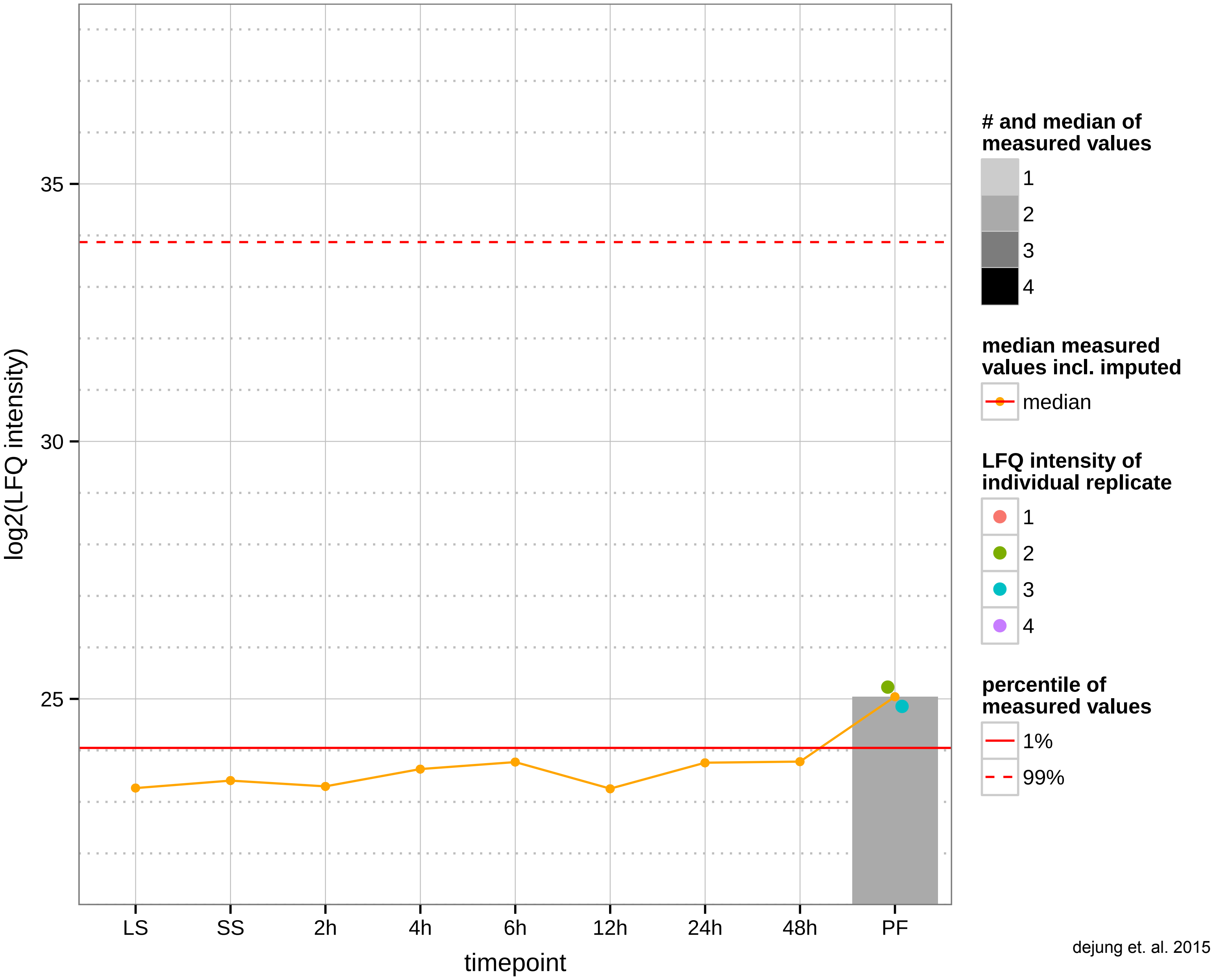
lathosterol oxidase, putative
Tb927.8.3240
AGOF: C–5 sterol desaturase activity, iron ion binding, oxidoreductase activity
AGOC: endoplasmic reticulum, integral to membrane
AGOP: fatty acid biosynthetic process, lipid metabolic process, oxidation–reduction process
PGOF: iron ion binding, oxidoreductase activity
PGOC: null
PGOP: fatty acid biosynthetic process, oxidation–reduction process





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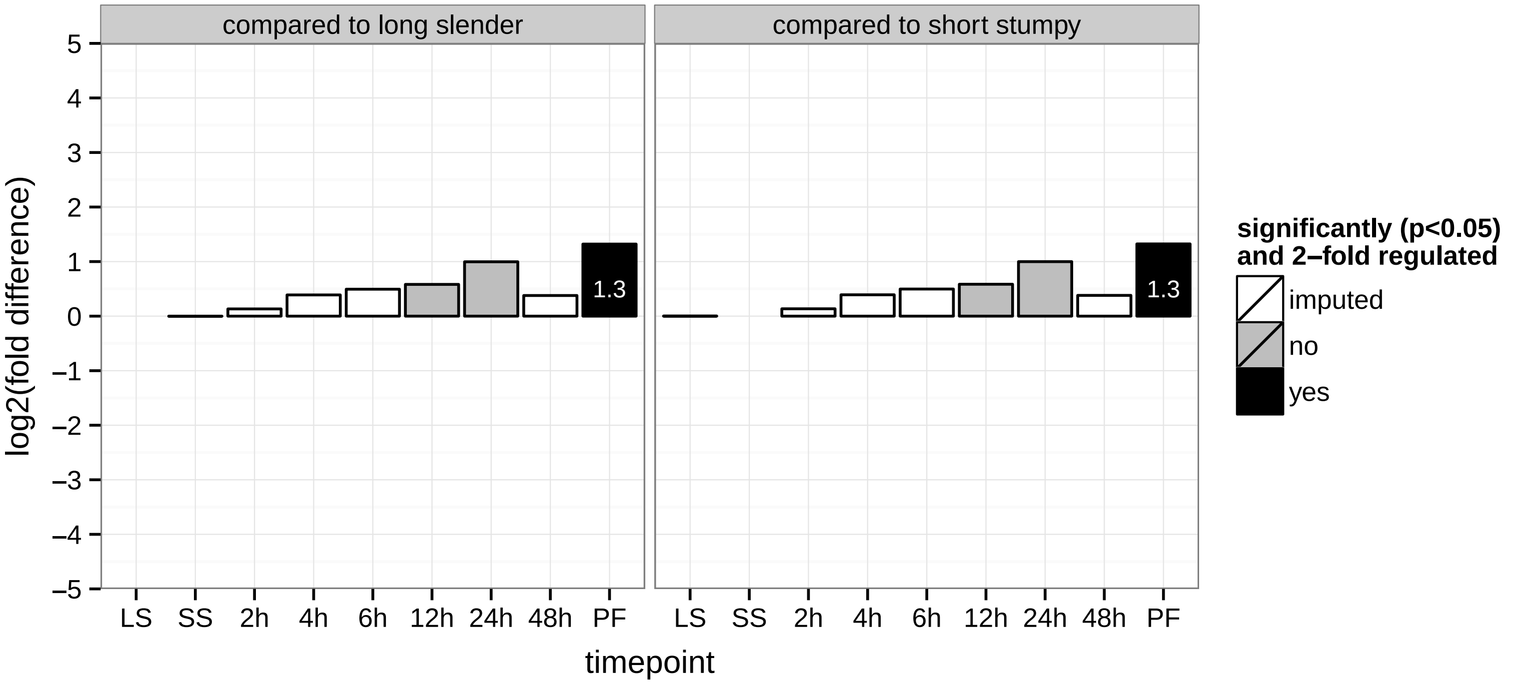
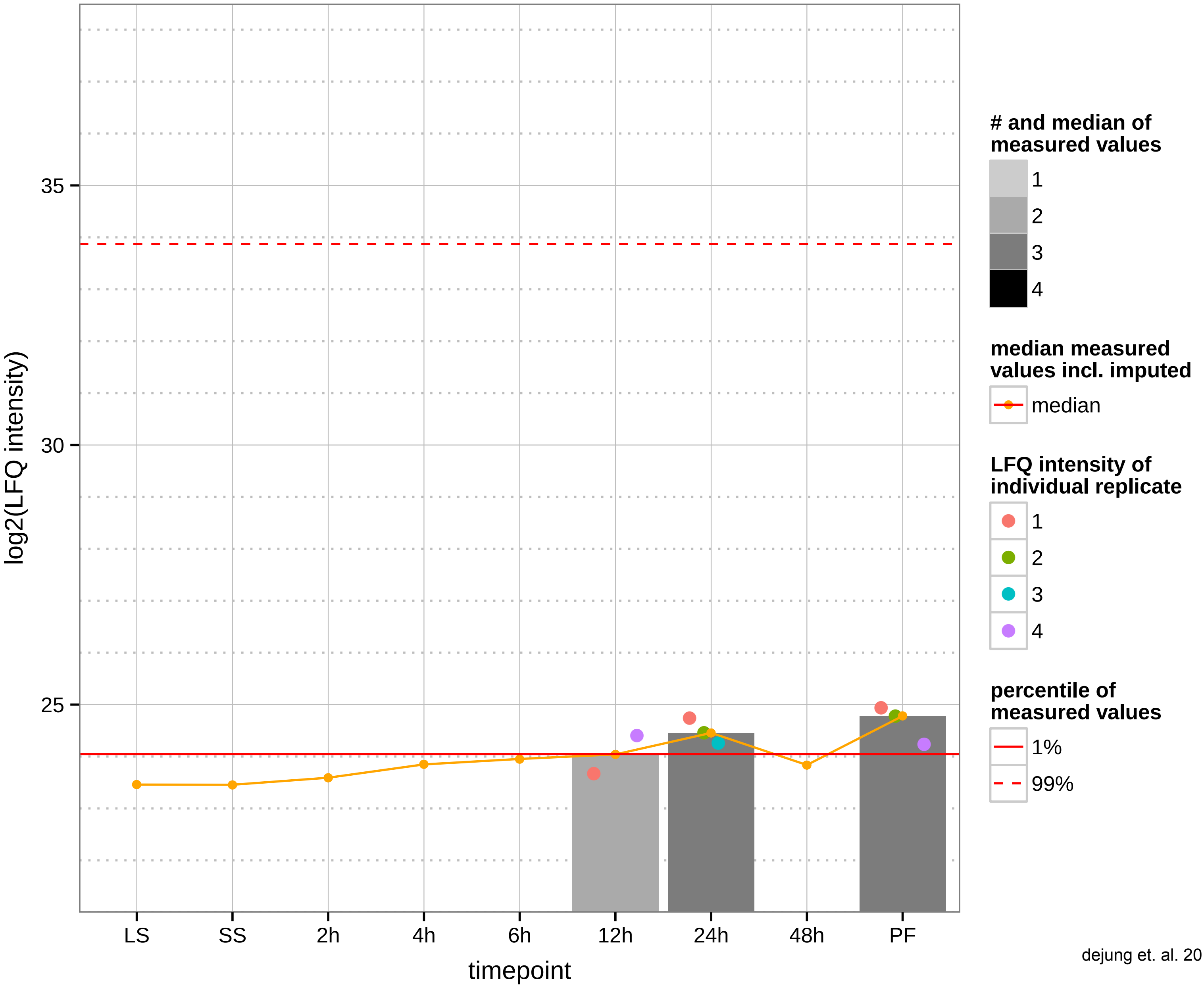
hypothetical protein, conserved
Tb927.8.3490
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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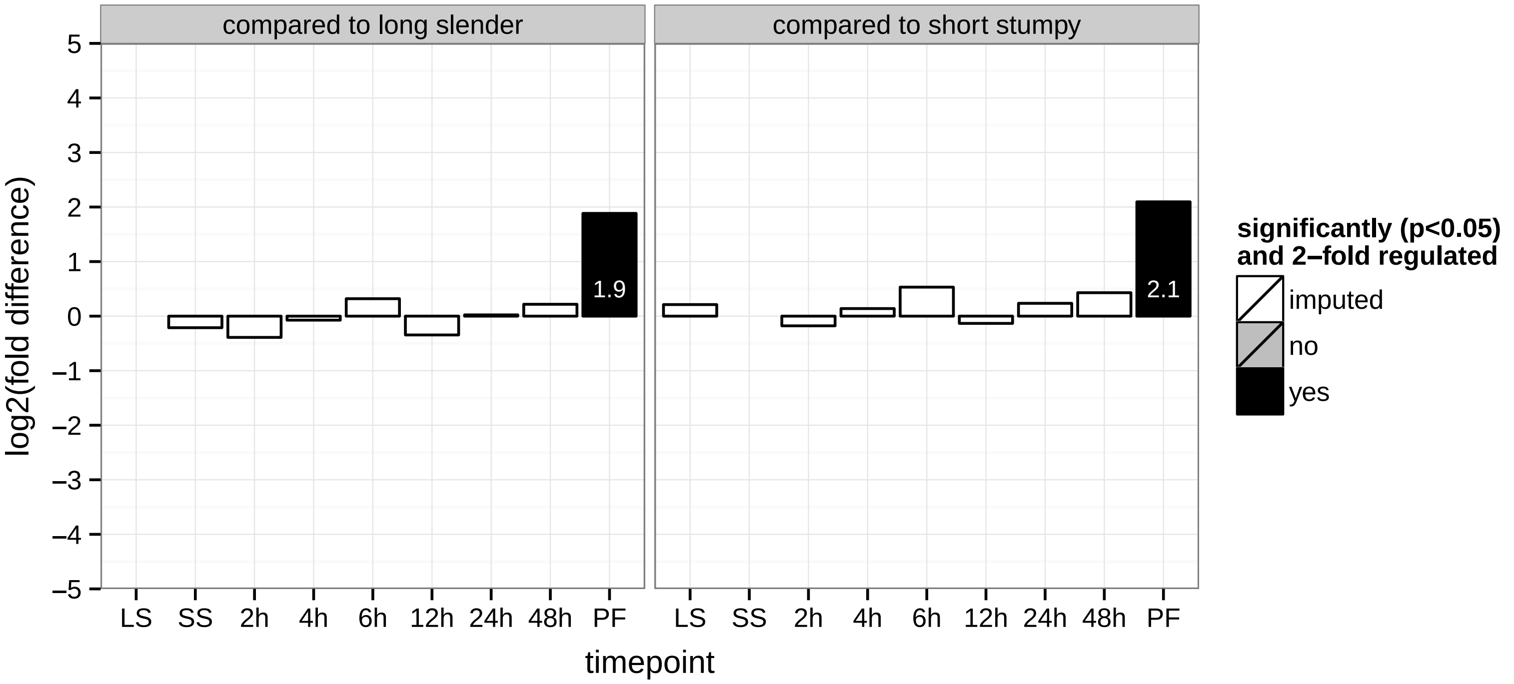
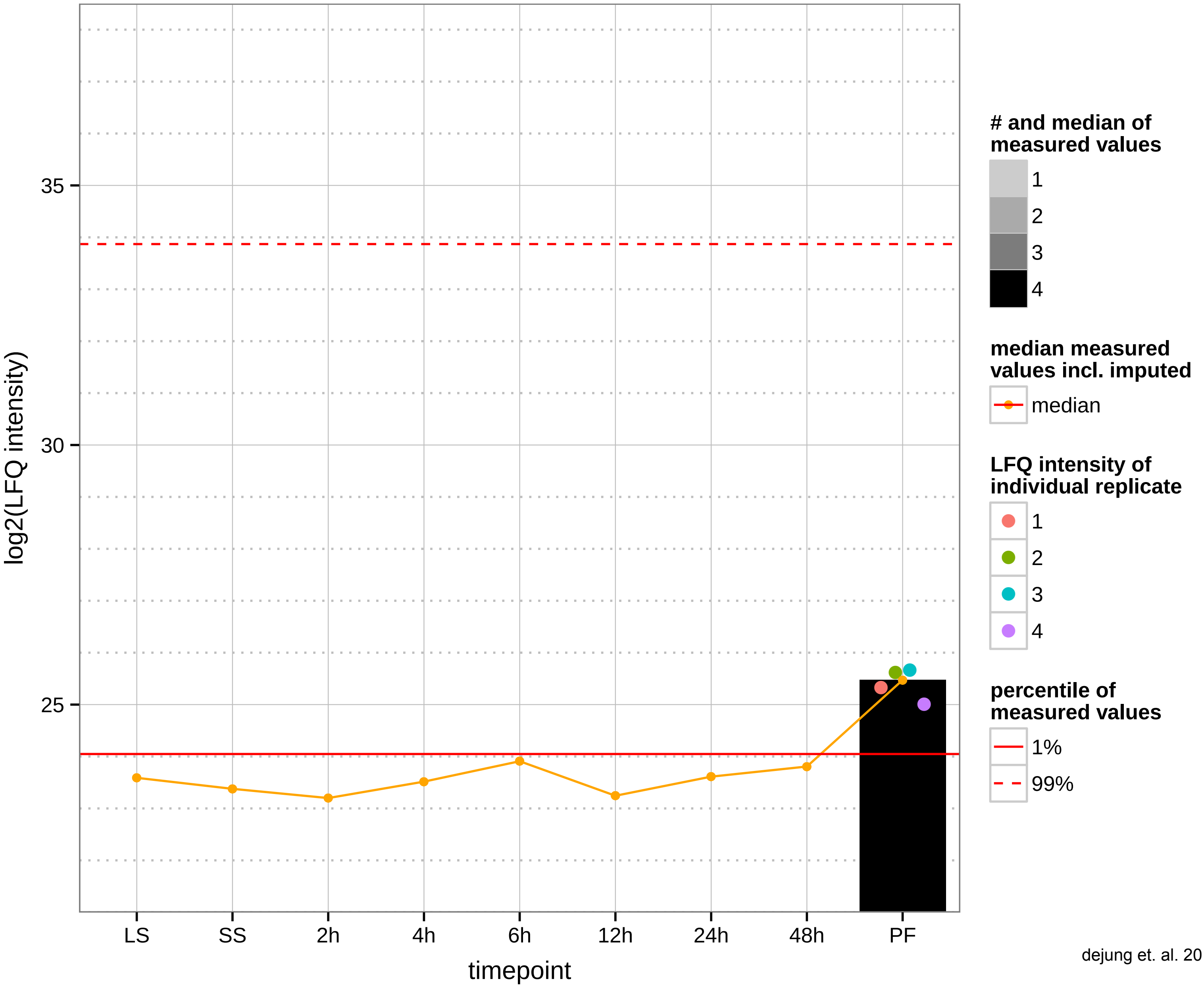
hypothetical protein, conserved
Tb927.8.3590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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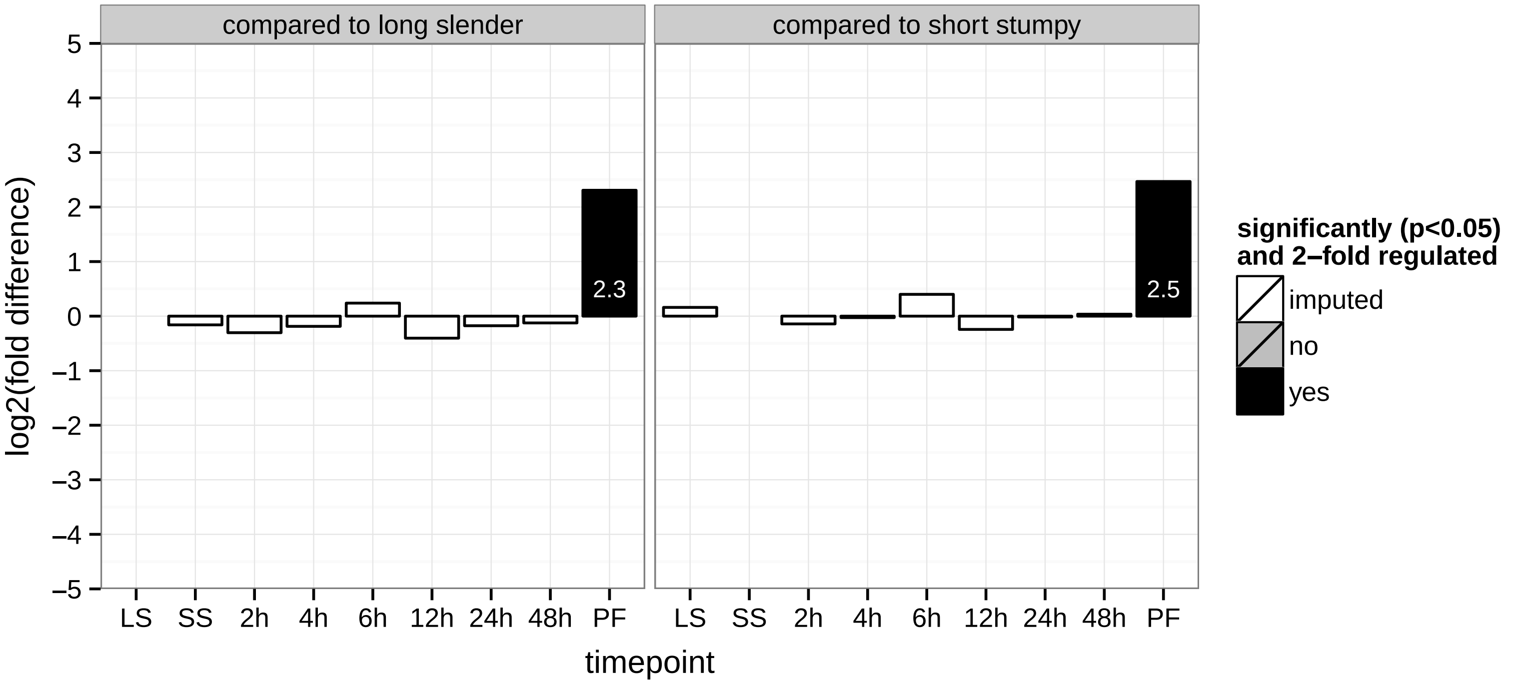
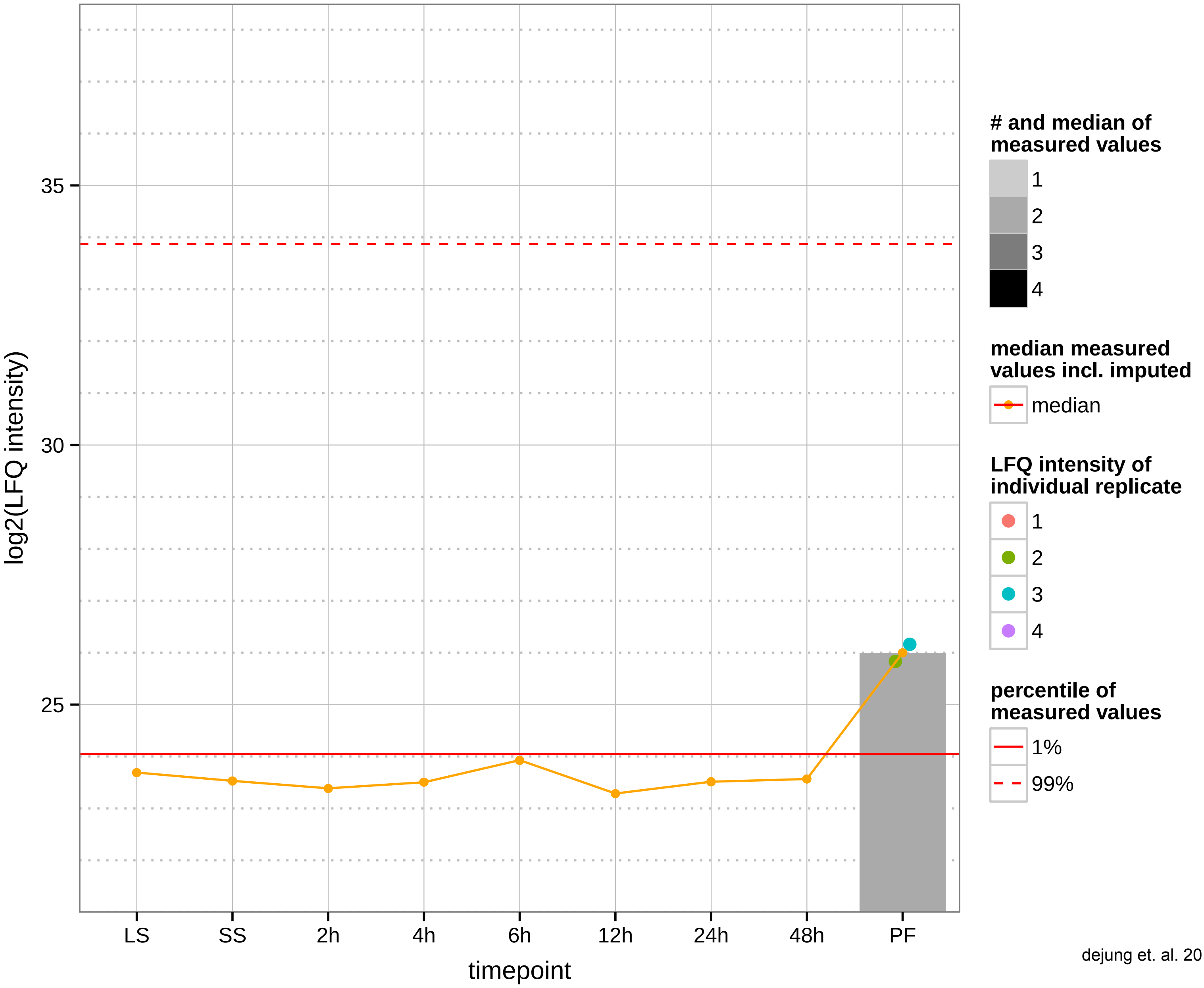
hypothetical protein, conserved
Tb927.8.3820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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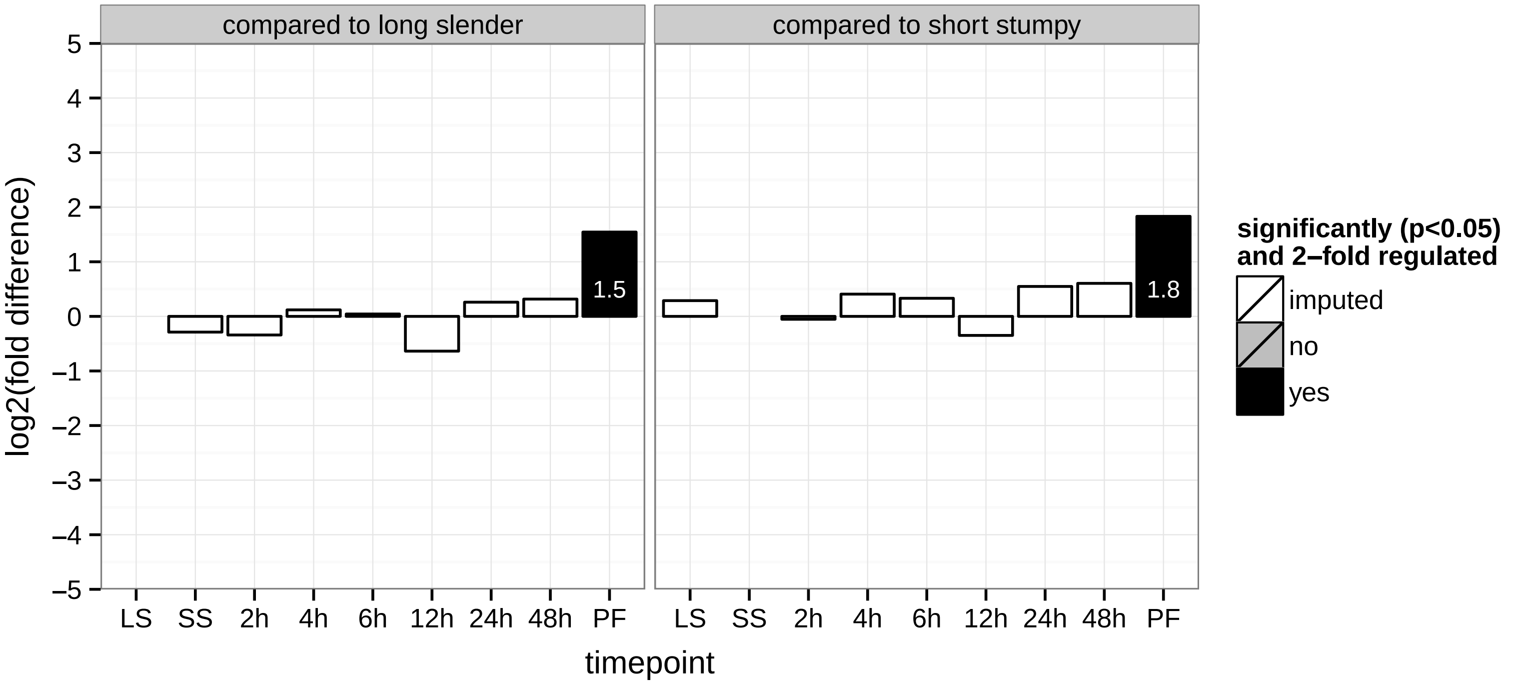
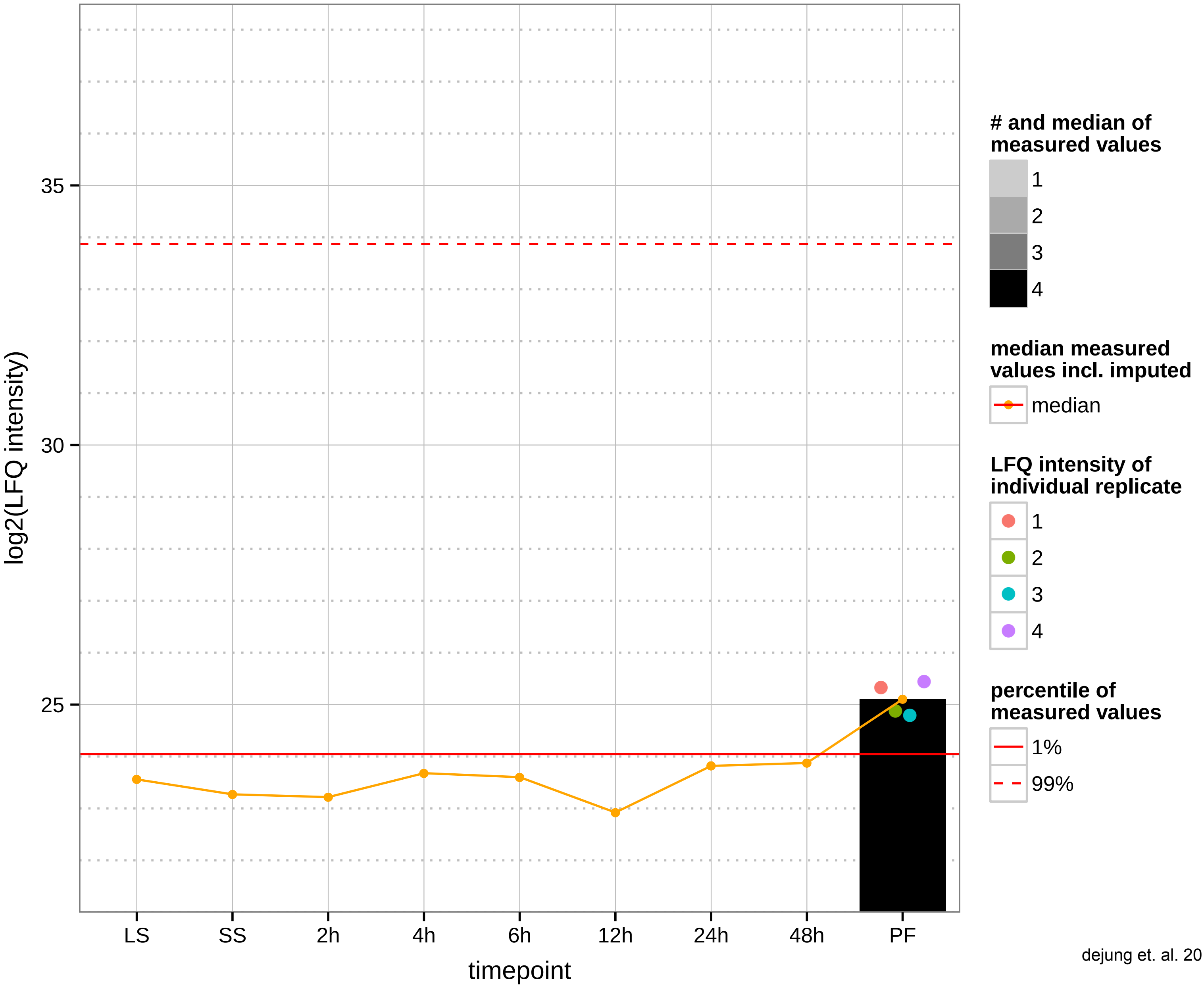
hypothetical protein, conserved
Tb927.8.4240
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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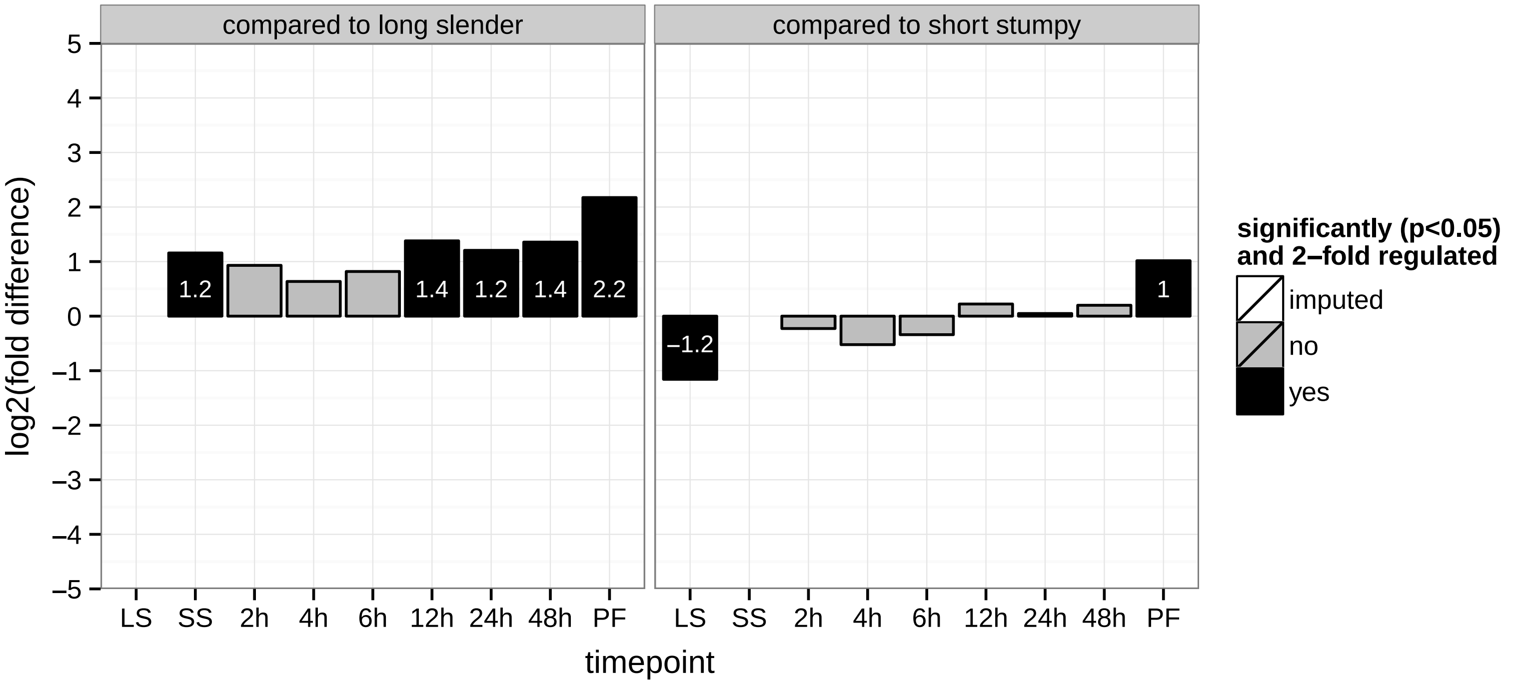
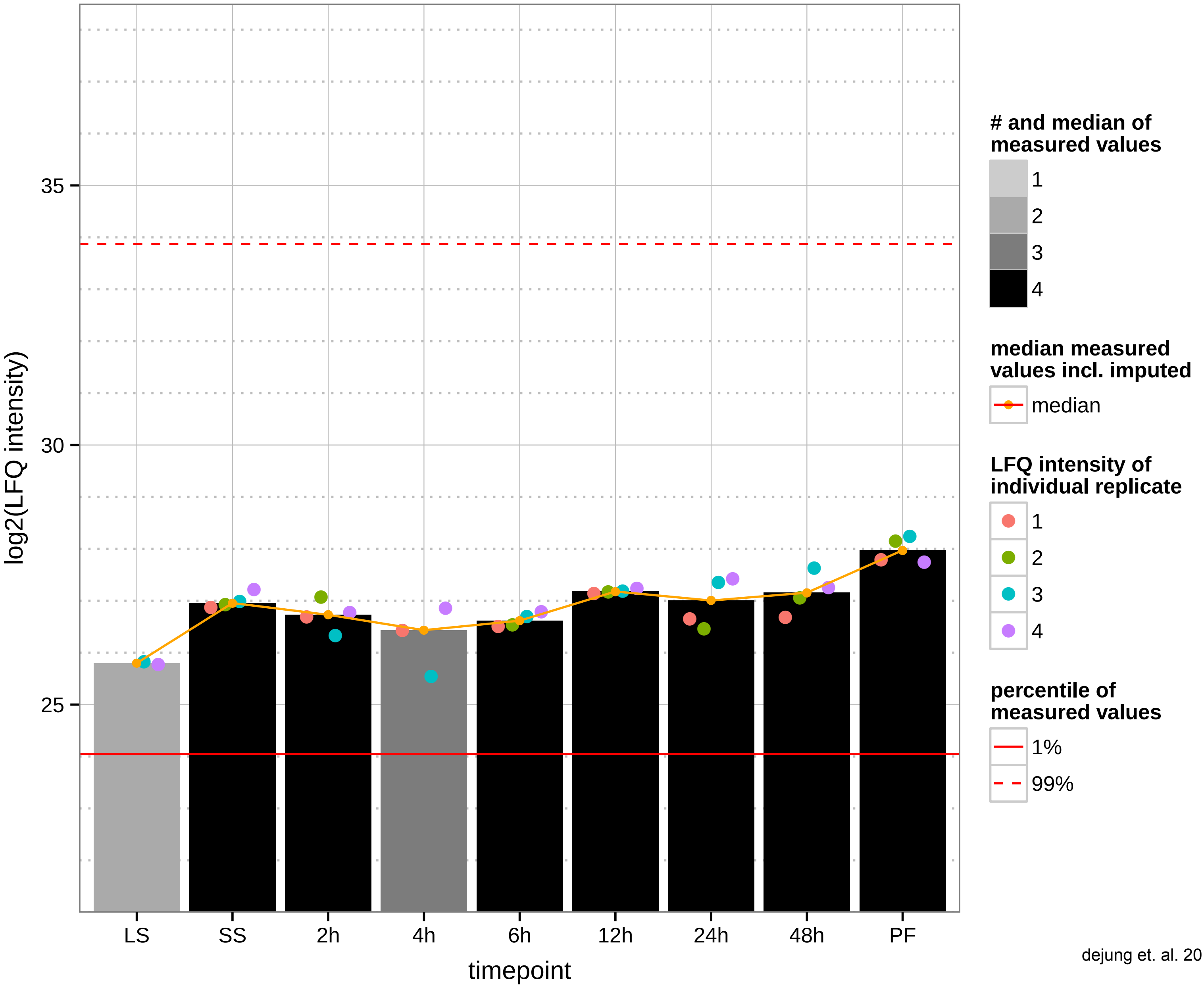
Translation initiation factor eIF−2B subunit beta, putative (EIF2BB)
Tb927.8.4390
AGOF: GTP binding, translation initiation factor activity
AGOC: eukaryotic translation initiation factor 2B complex
AGOP: cellular metabolic process, translational initiation
PGOF: null
PGOC: null
PGOP: cellular metabolic process





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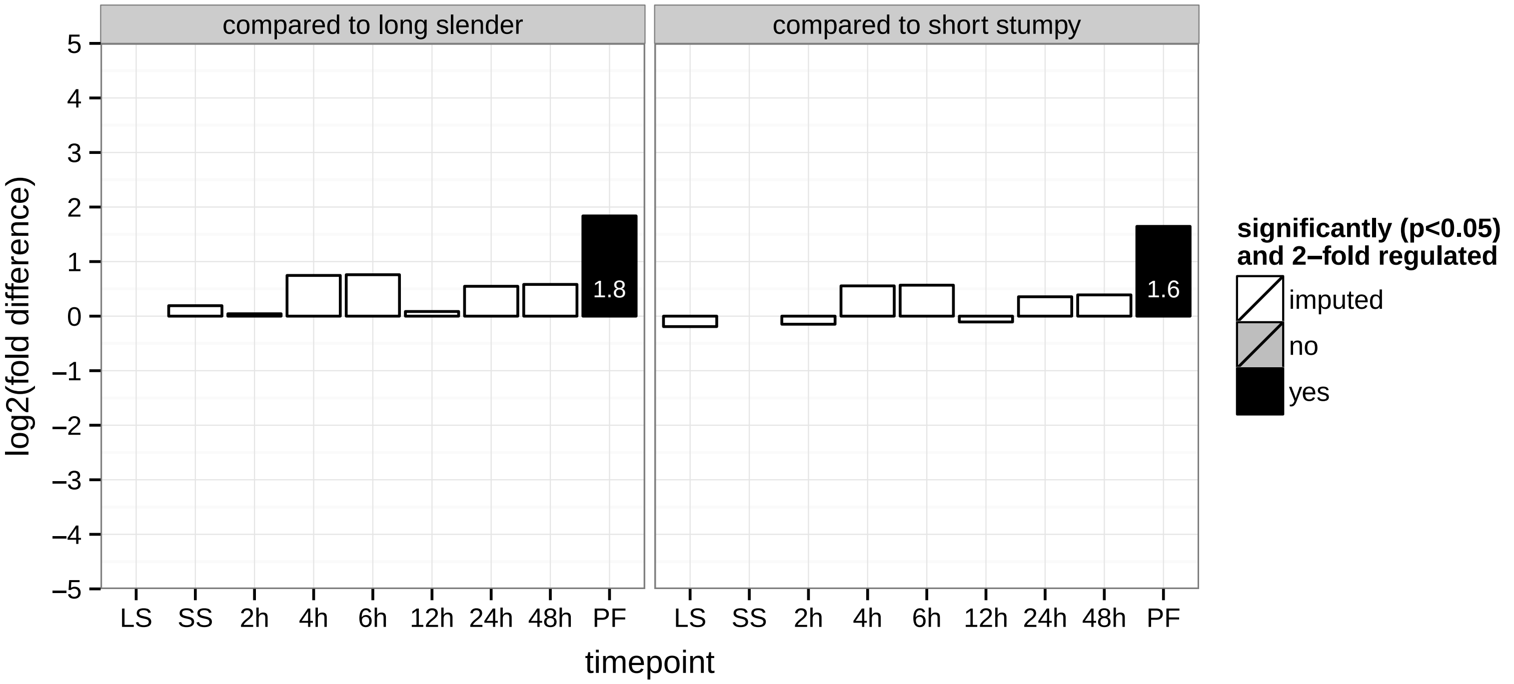
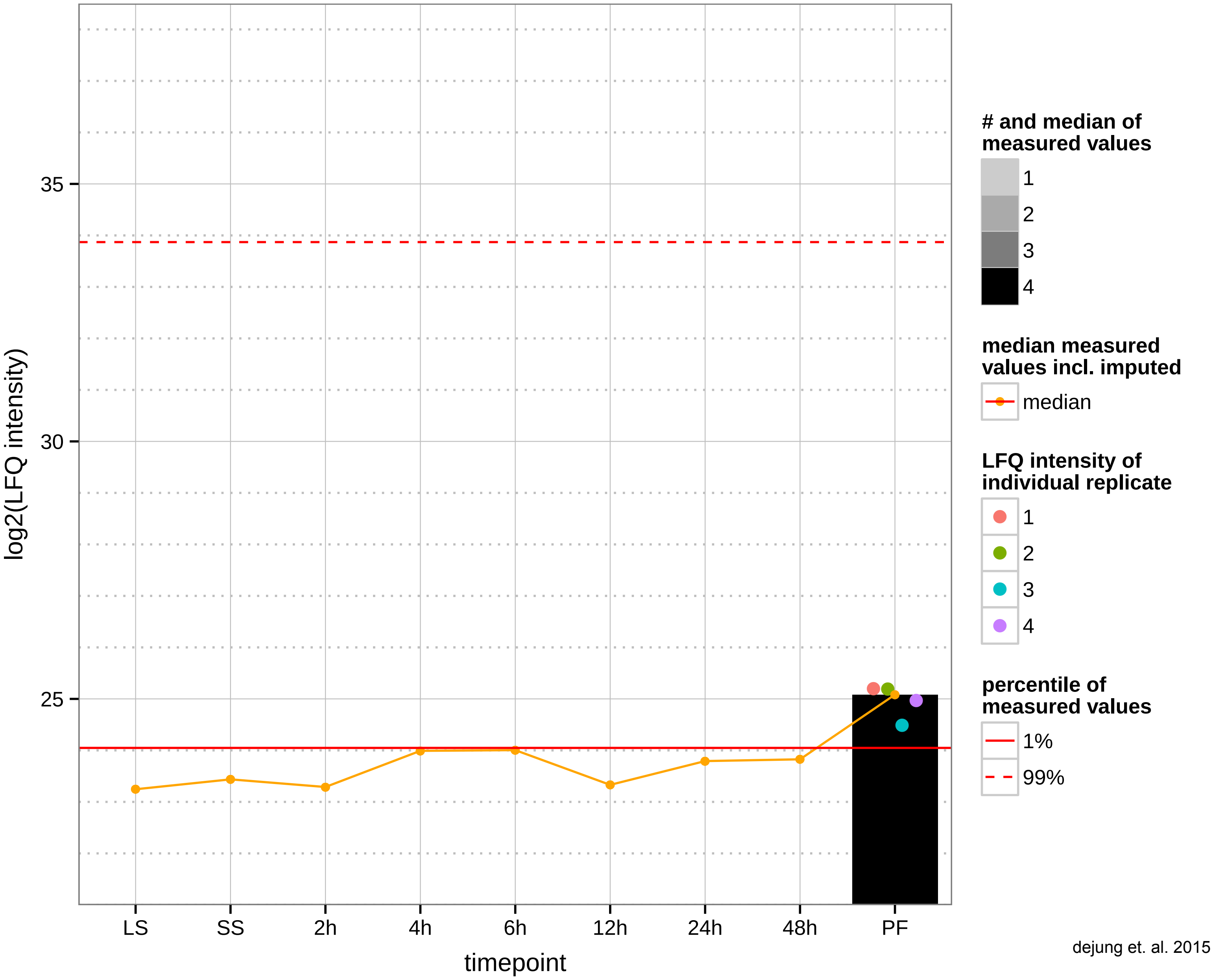
hypothetical protein, conserved
Tb927.8.4800
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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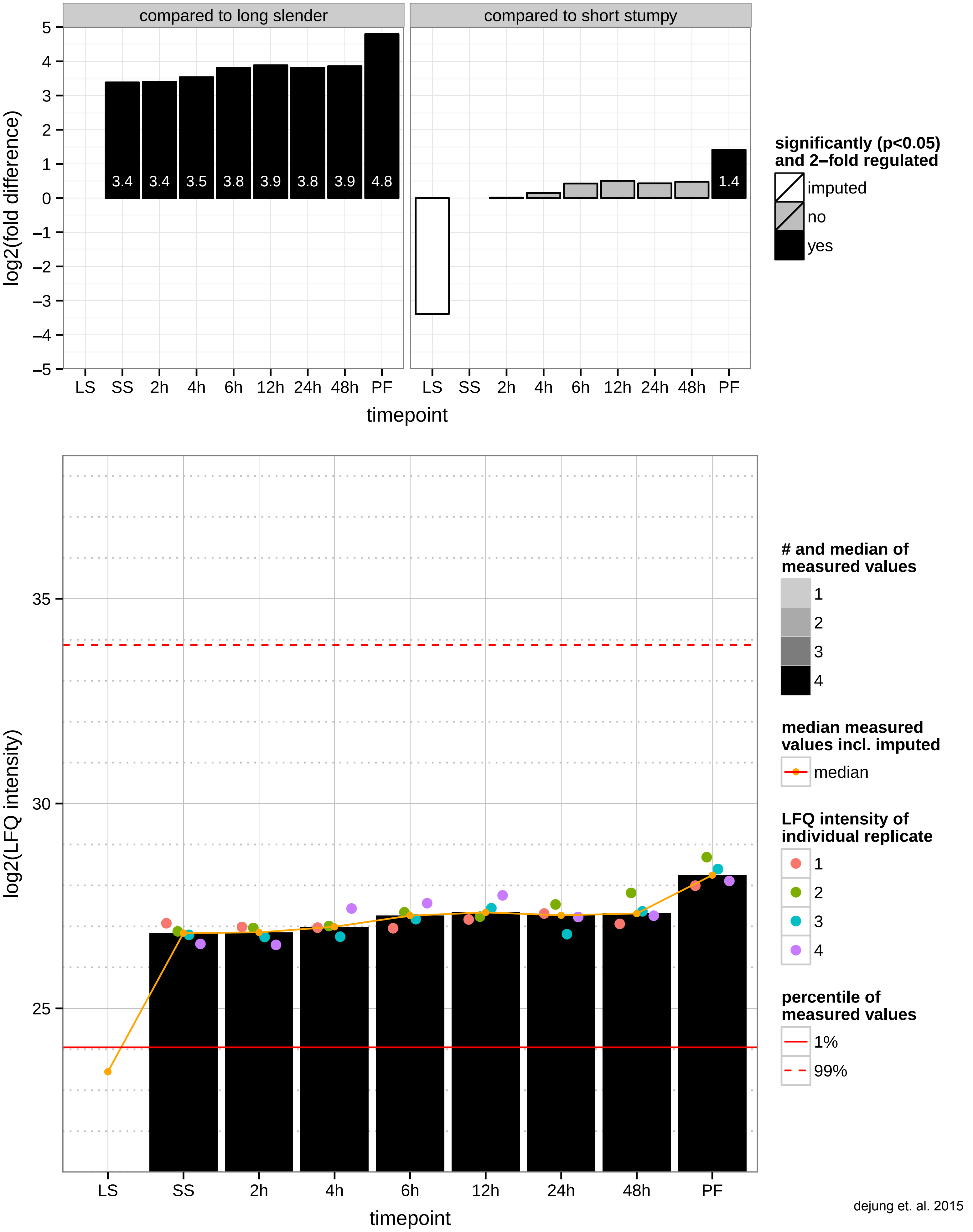
hypothetical protein, conserved
Tb927.8.4930
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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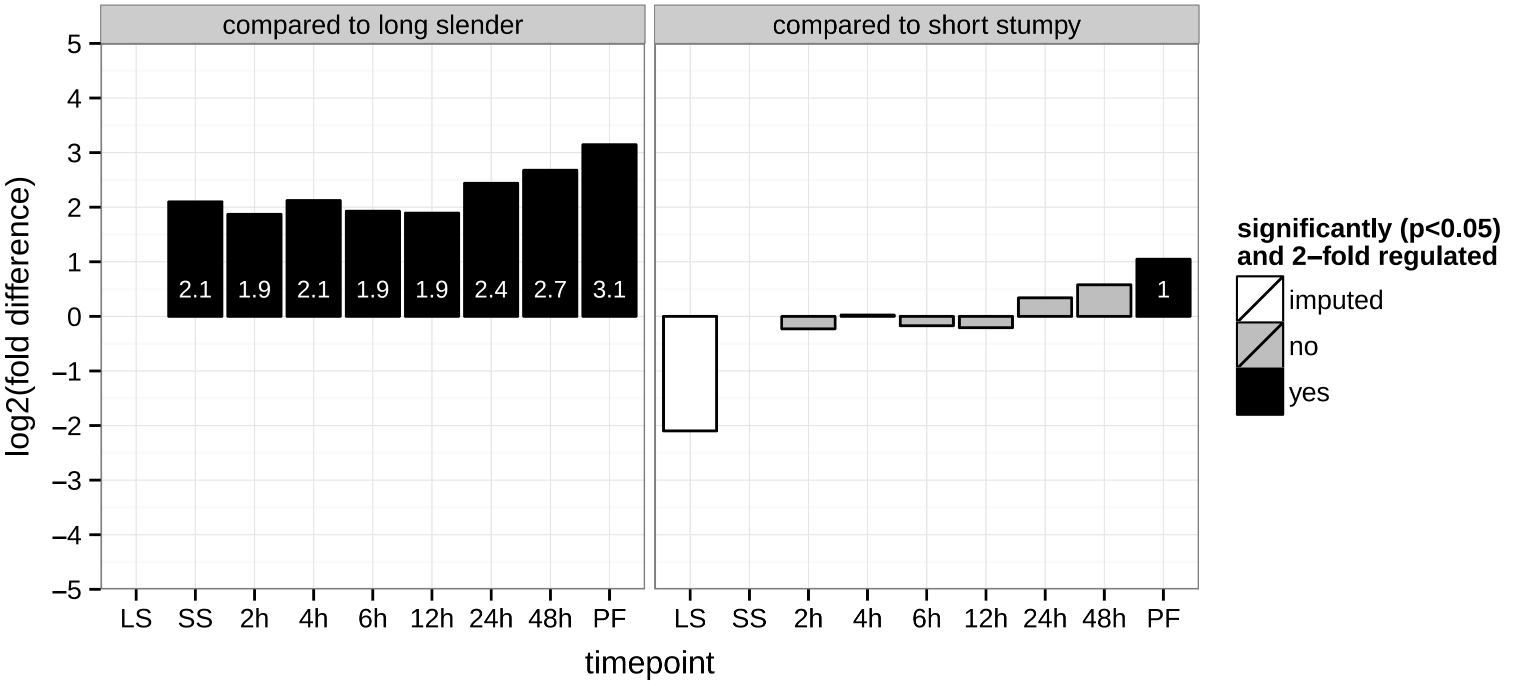
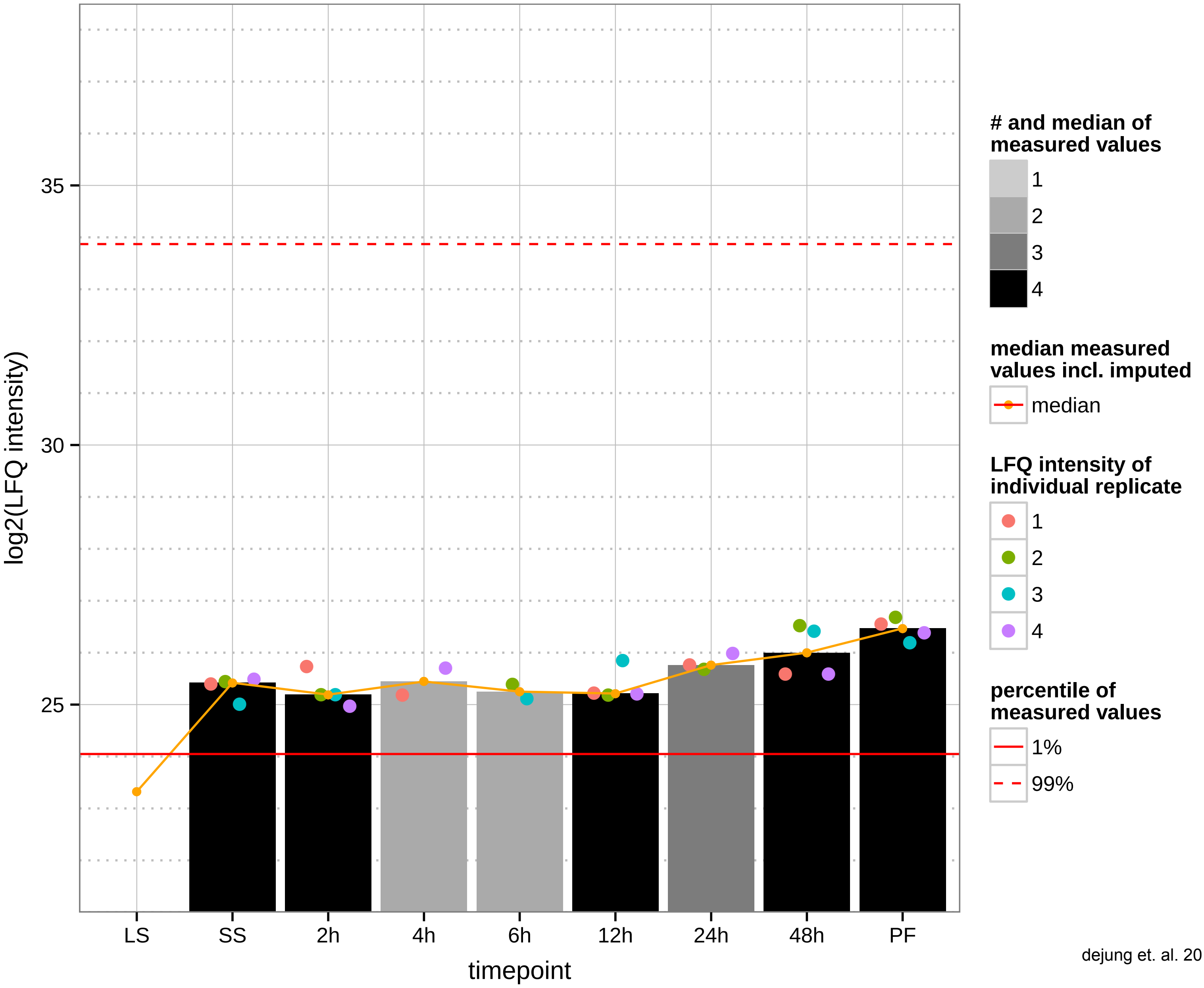
hypothetical protein, conserved
Tb927.8.5040
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: methyltransferase activity
PGOC: null
PGOP: null





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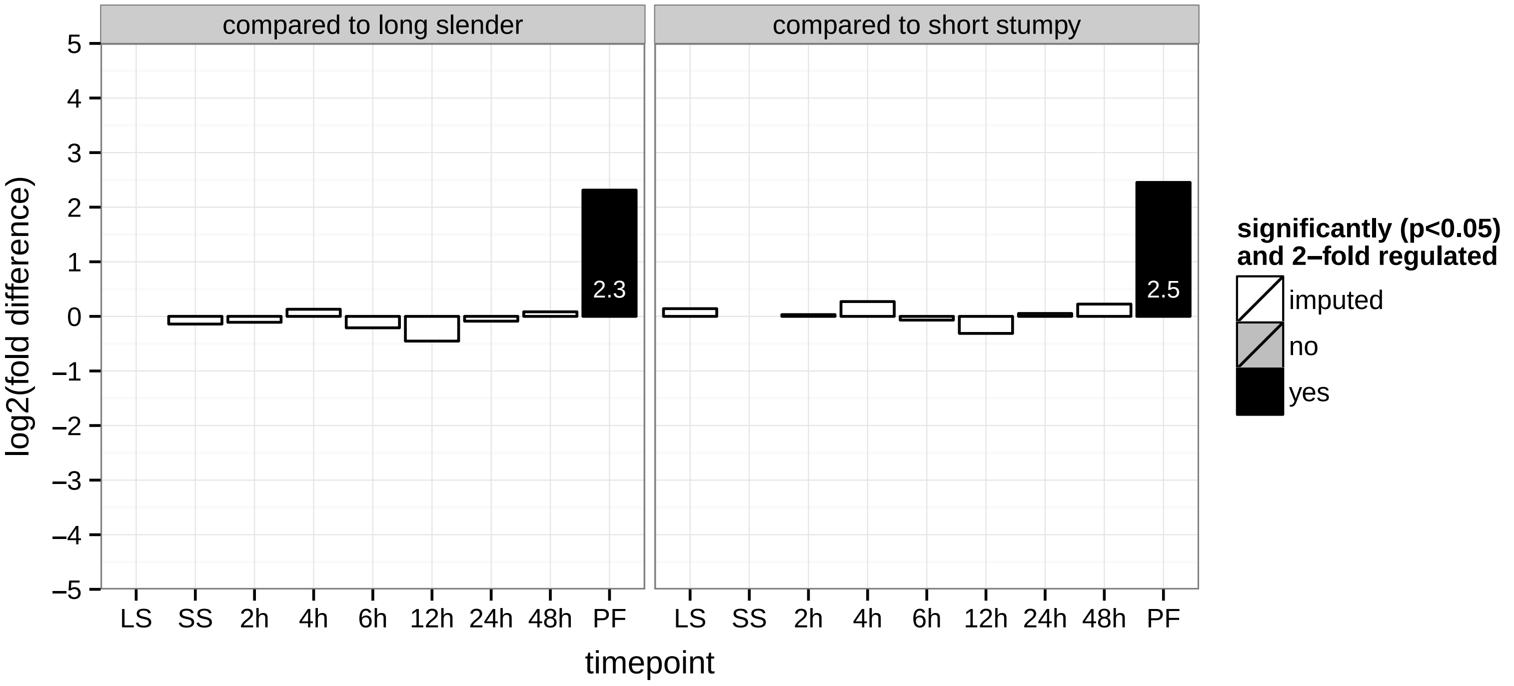
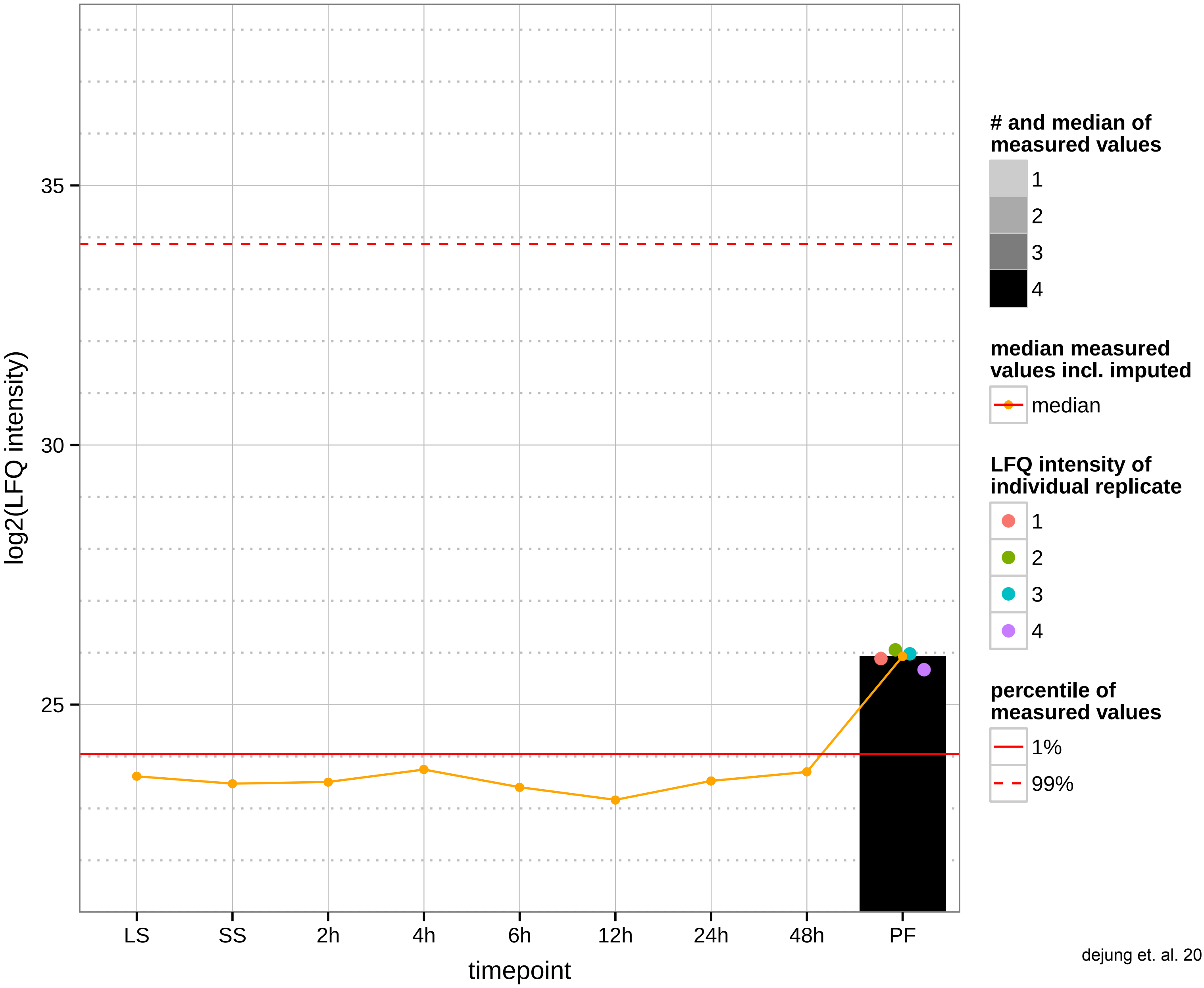
hypothetical protein, conserved
Tb927.8.5100
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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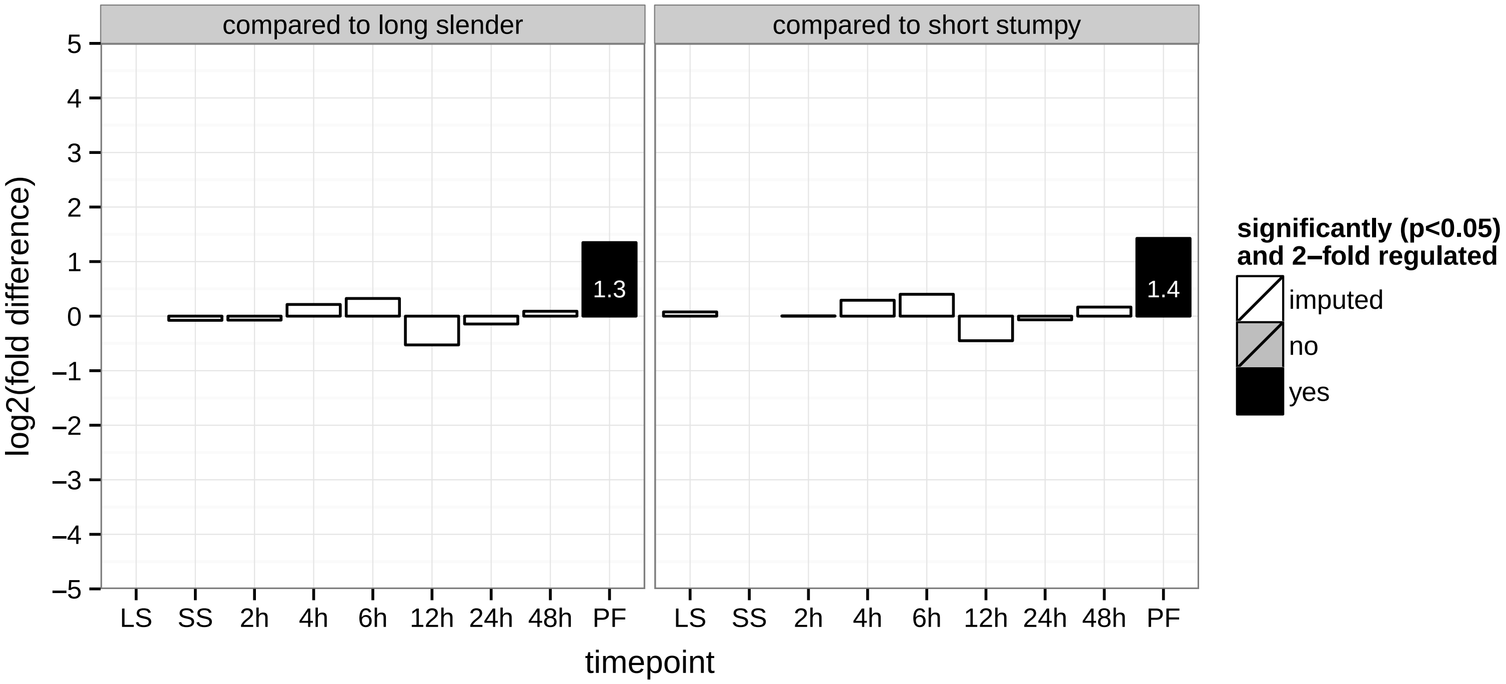
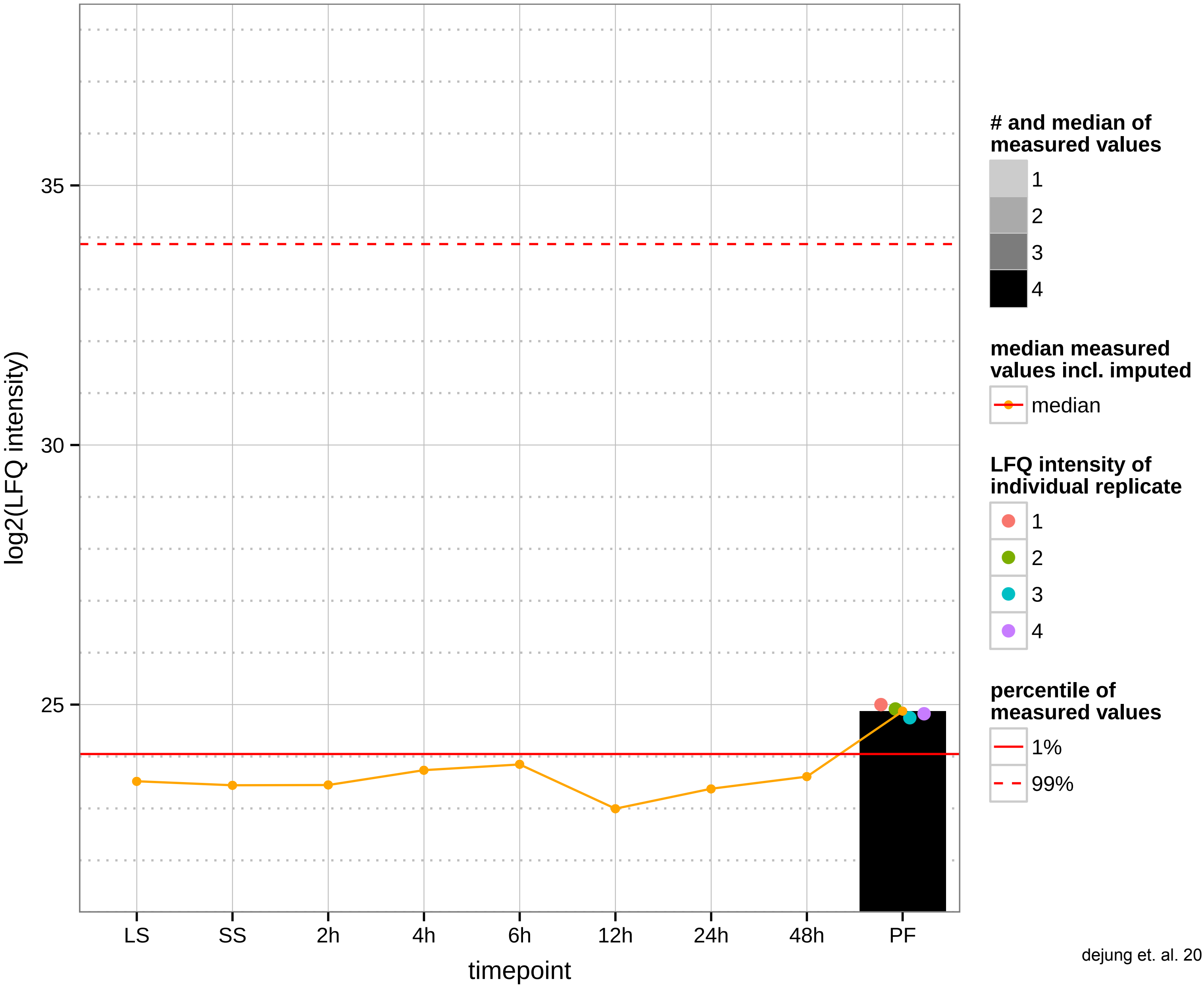
hypothetical protein, conserved
Tb927.8.5320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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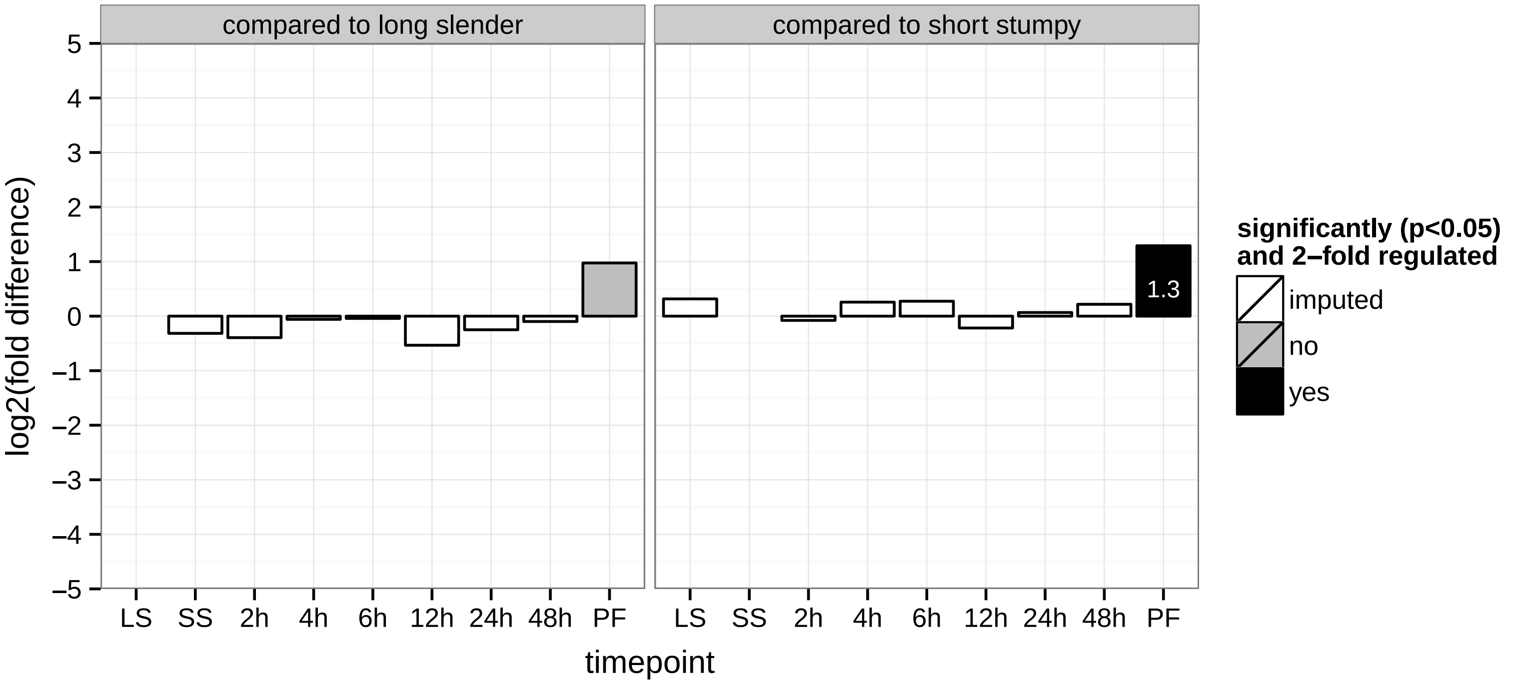
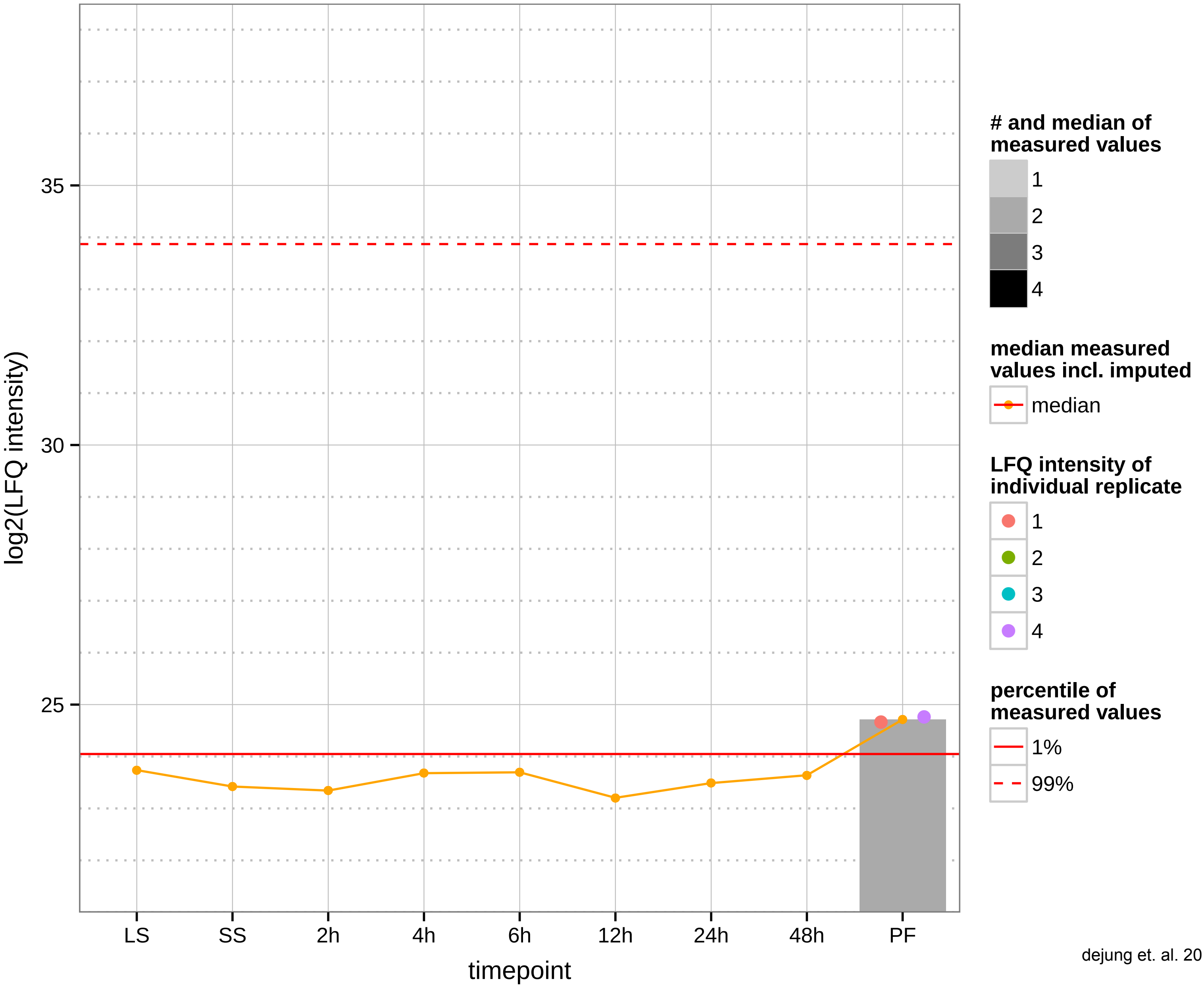
amino acid permease 24 (AAT6)
Tb927.8.5450
AGOF: L–proline transmembrane transporter activity, alanine transmembrane transporter activity, drug transmembrane transp
AGOC: integral to membrane, plasma membrane
AGOP: amino acid homeostasis, drug transport, hypotonic response, proline transmembrane transport, regulation of L–glutam
PGOF: null
PGOC: null
PGOP: null





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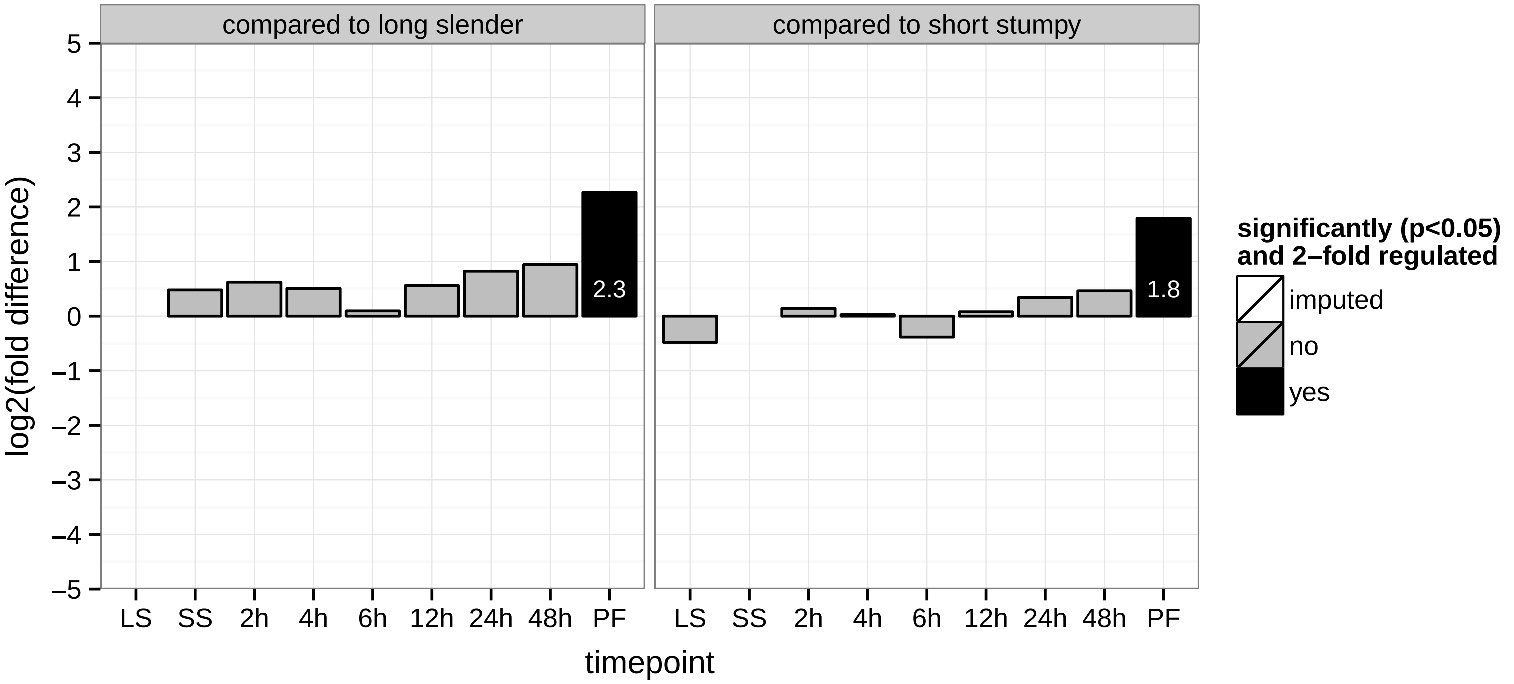
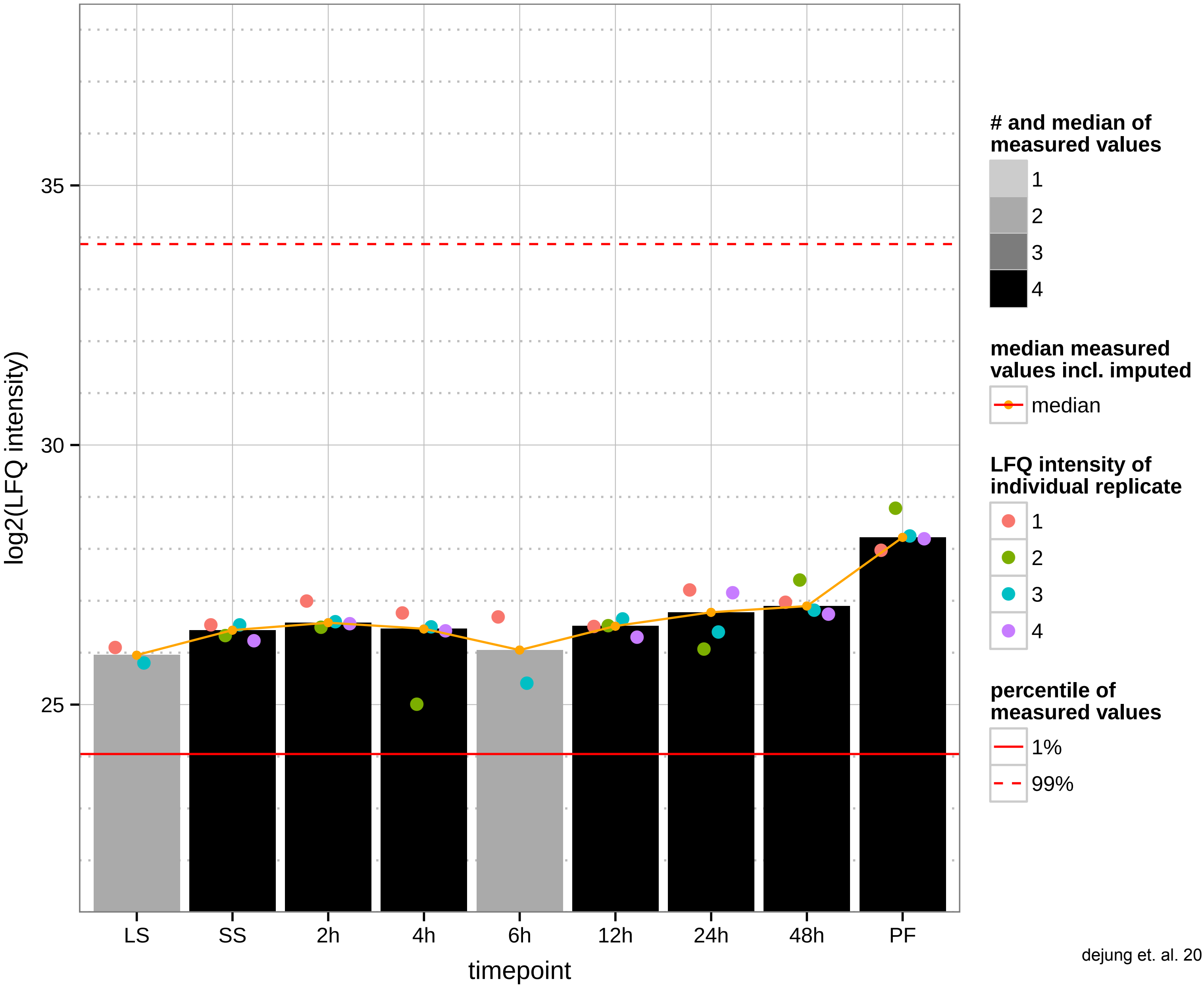
hypothetical protein, conserved
Tb927.8.560
AGOF: calcium ion binding
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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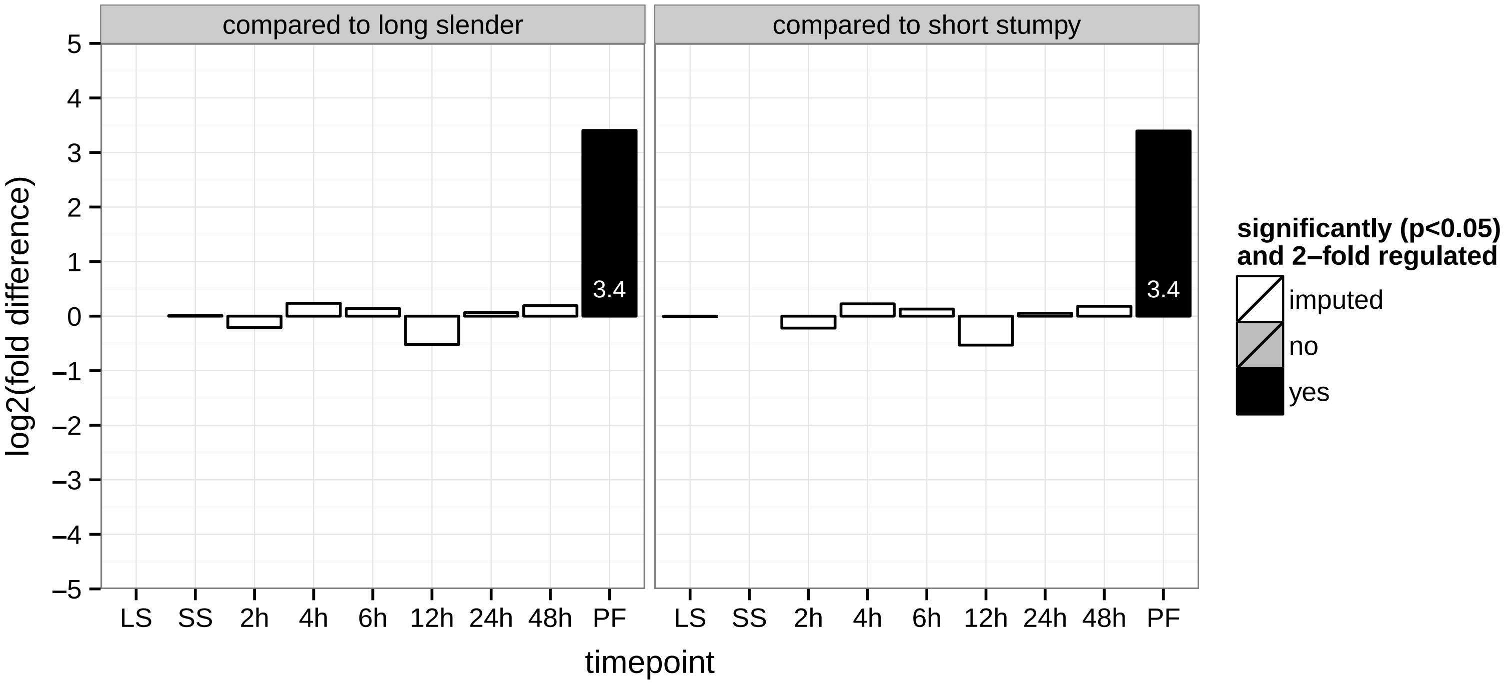
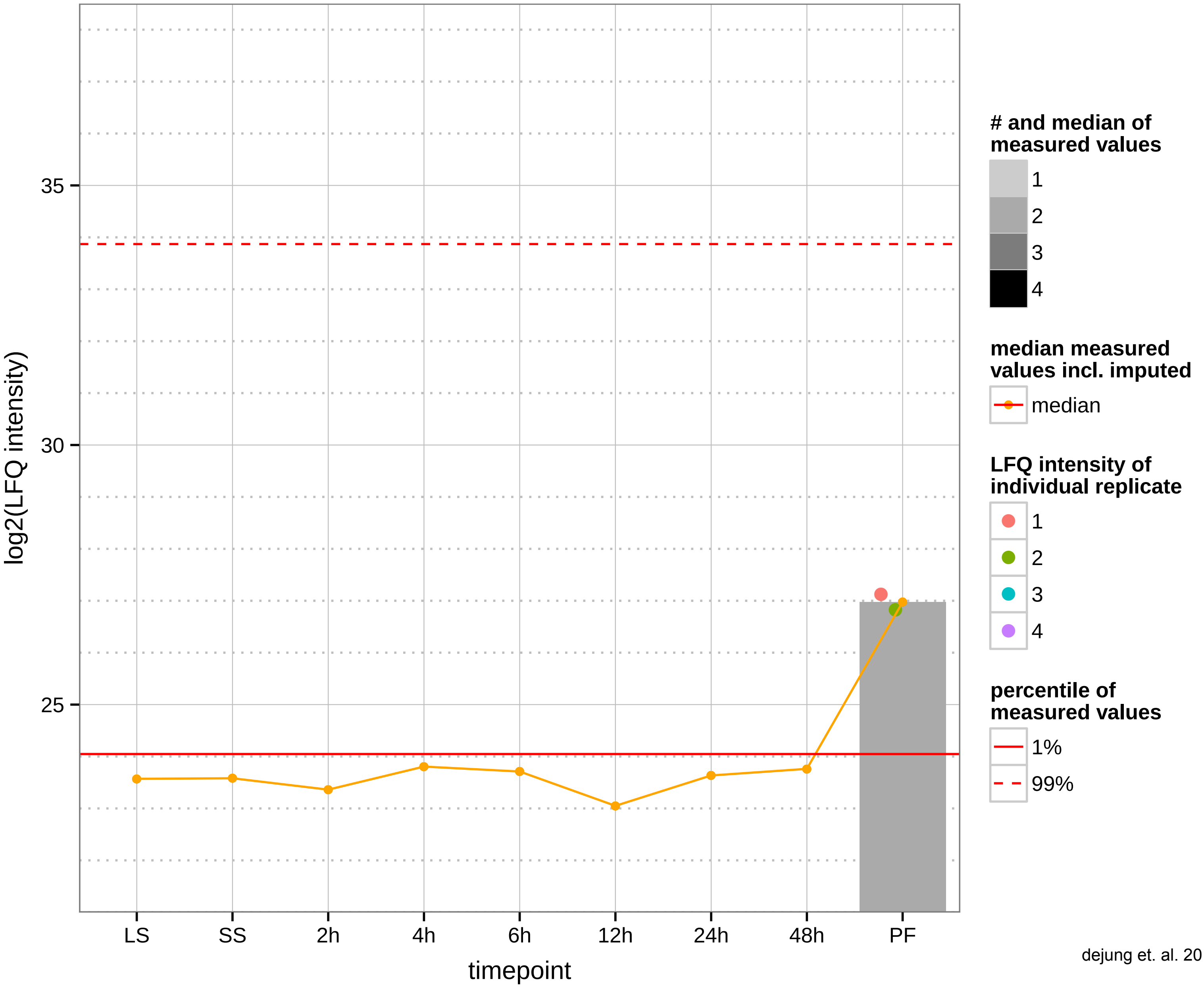
ubiquitin carboxyl–terminal hydrolase, putative
Tb927.8.5620
AGOF: cysteine–type endopeptidase activity, ubiquitin thiolesterase activity, zinc ion binding
AGOC: intracellular
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ubiquitin thiolesterase activity, zinc ion binding
PGOC: intracellular
PGOP: ubiquitin–dependent protein catabolic process





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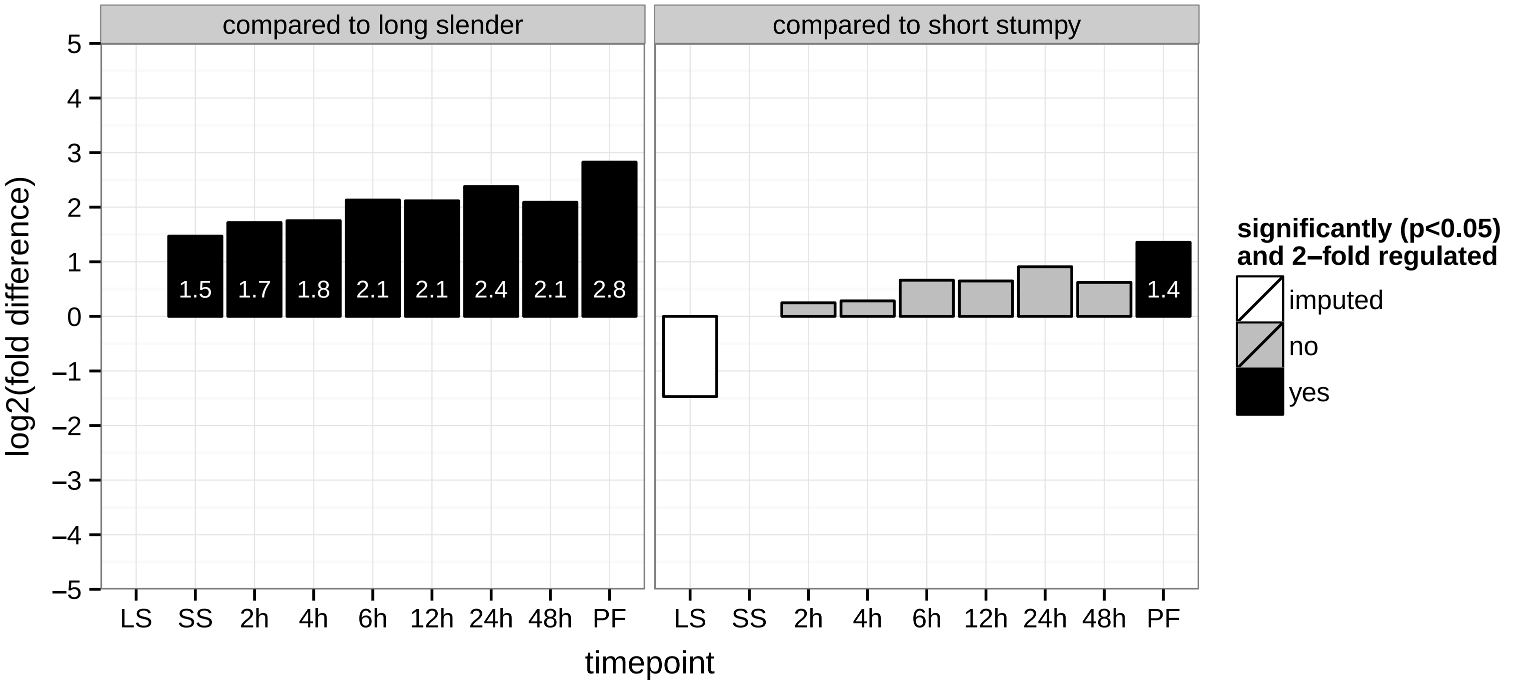
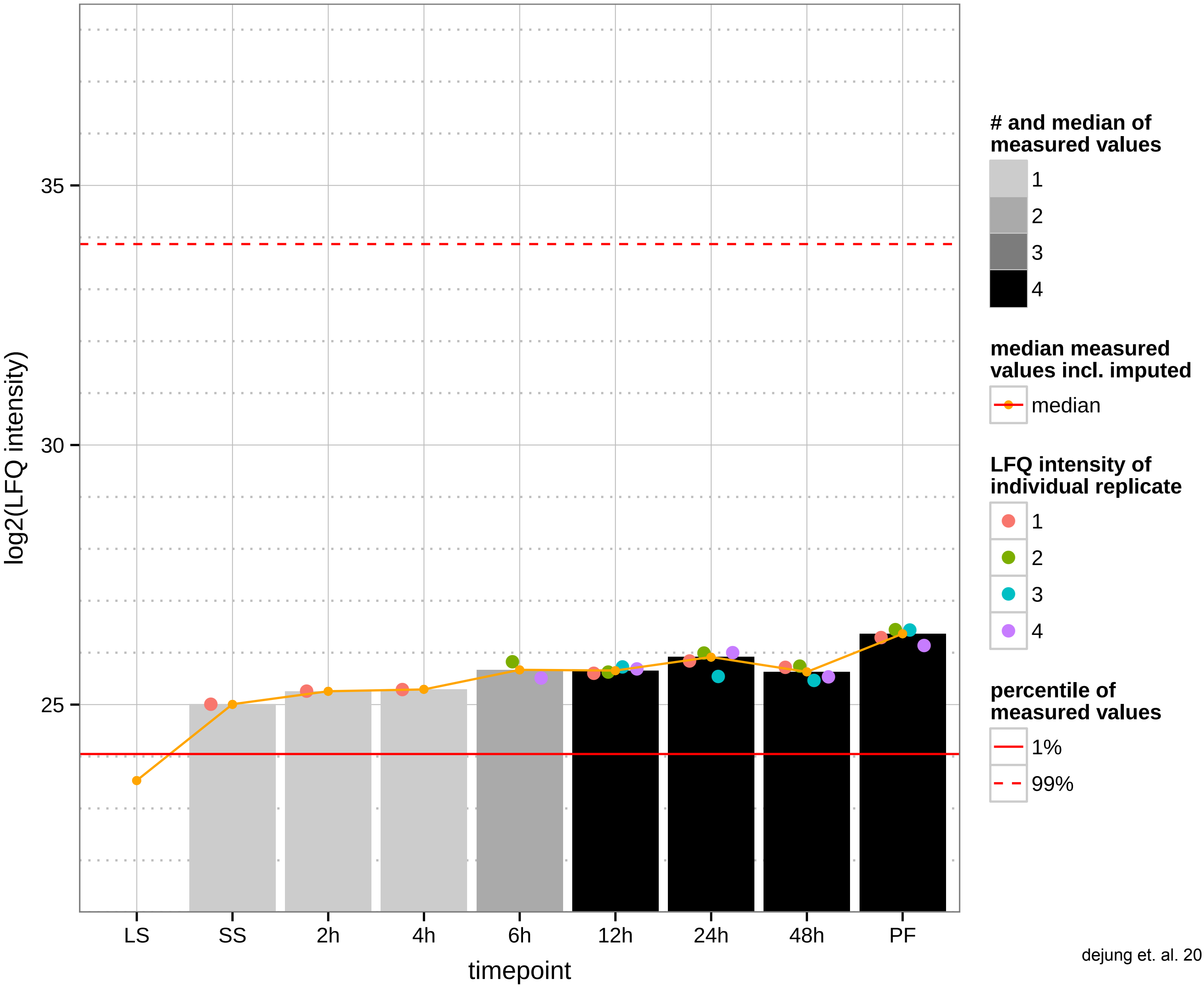
hypothetical protein, conserved
Tb927.8.580
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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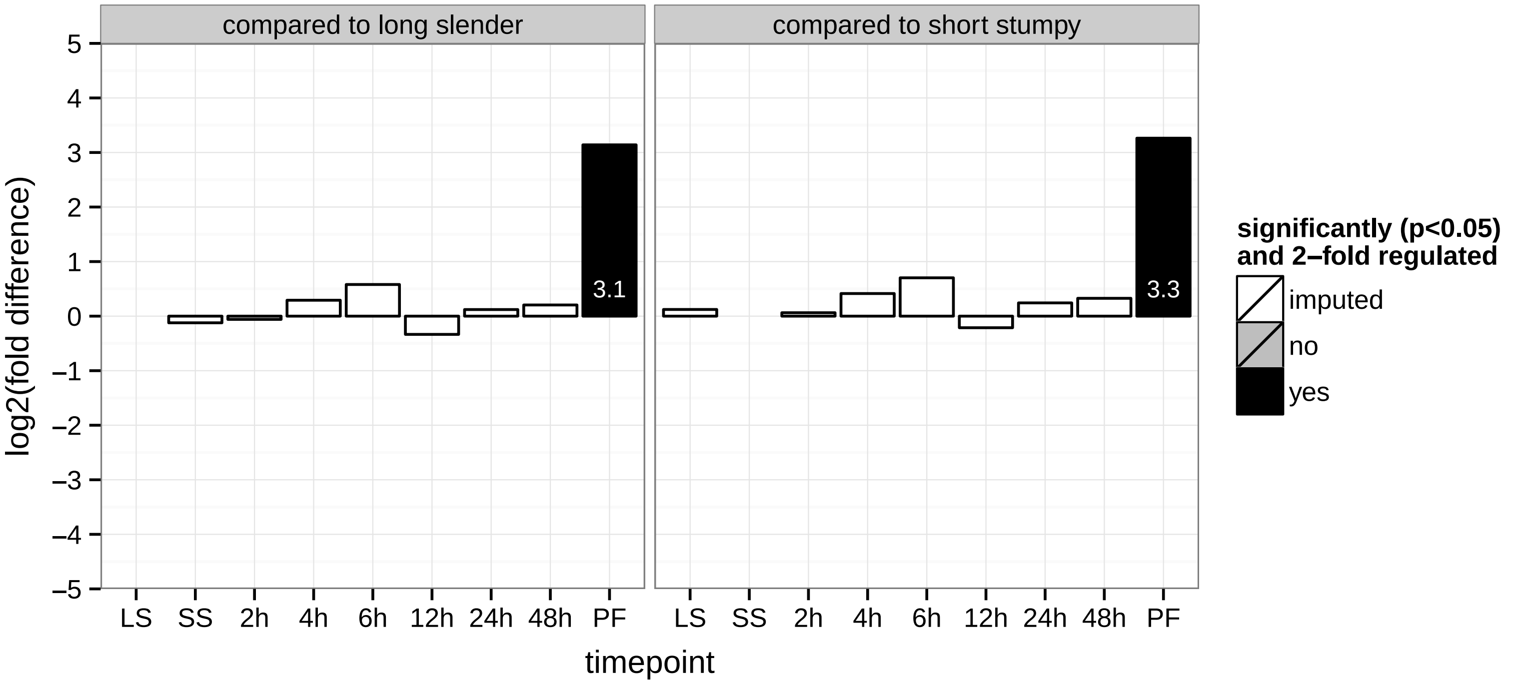
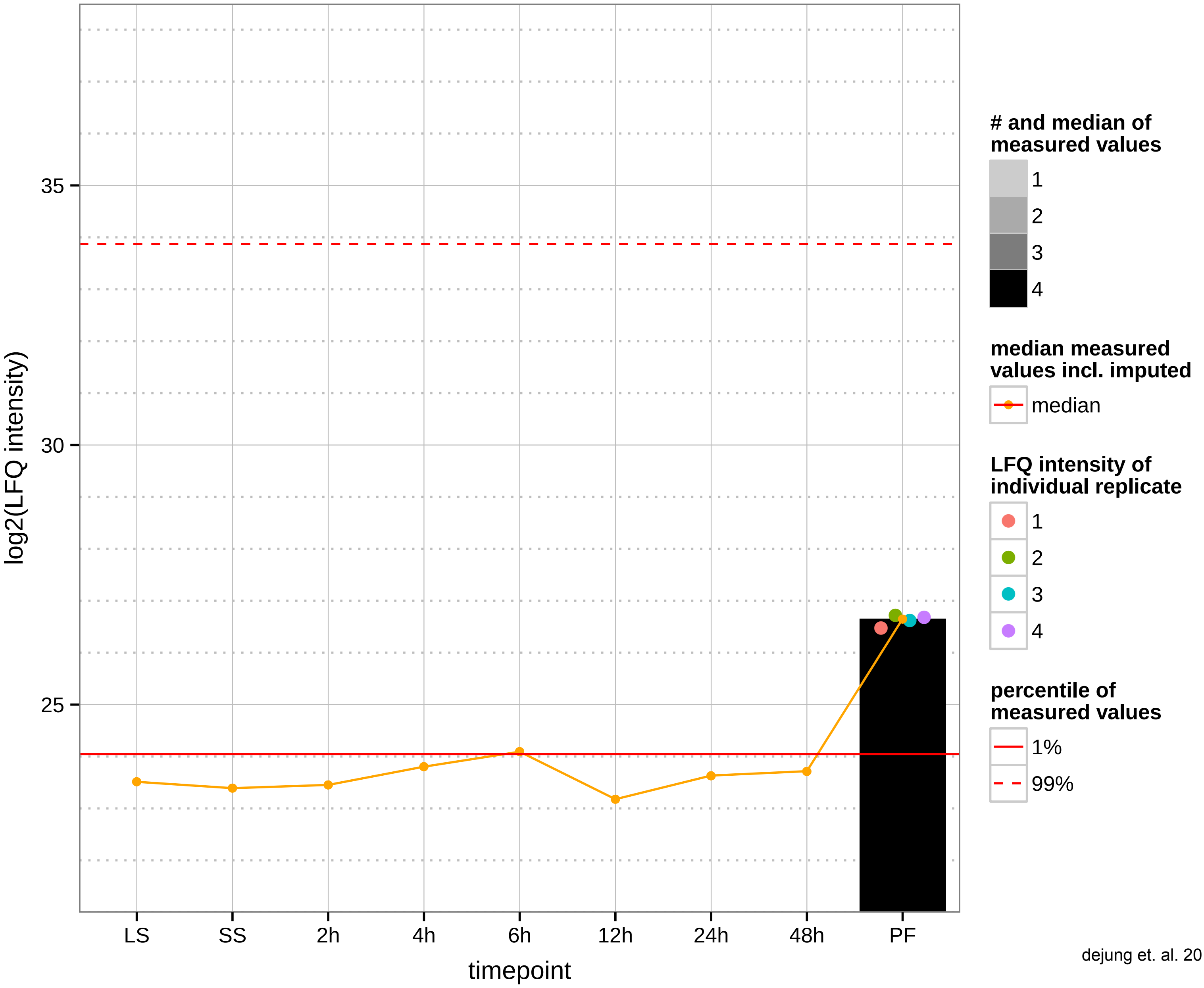
hypothetical protein, conserved
Tb927.8.5800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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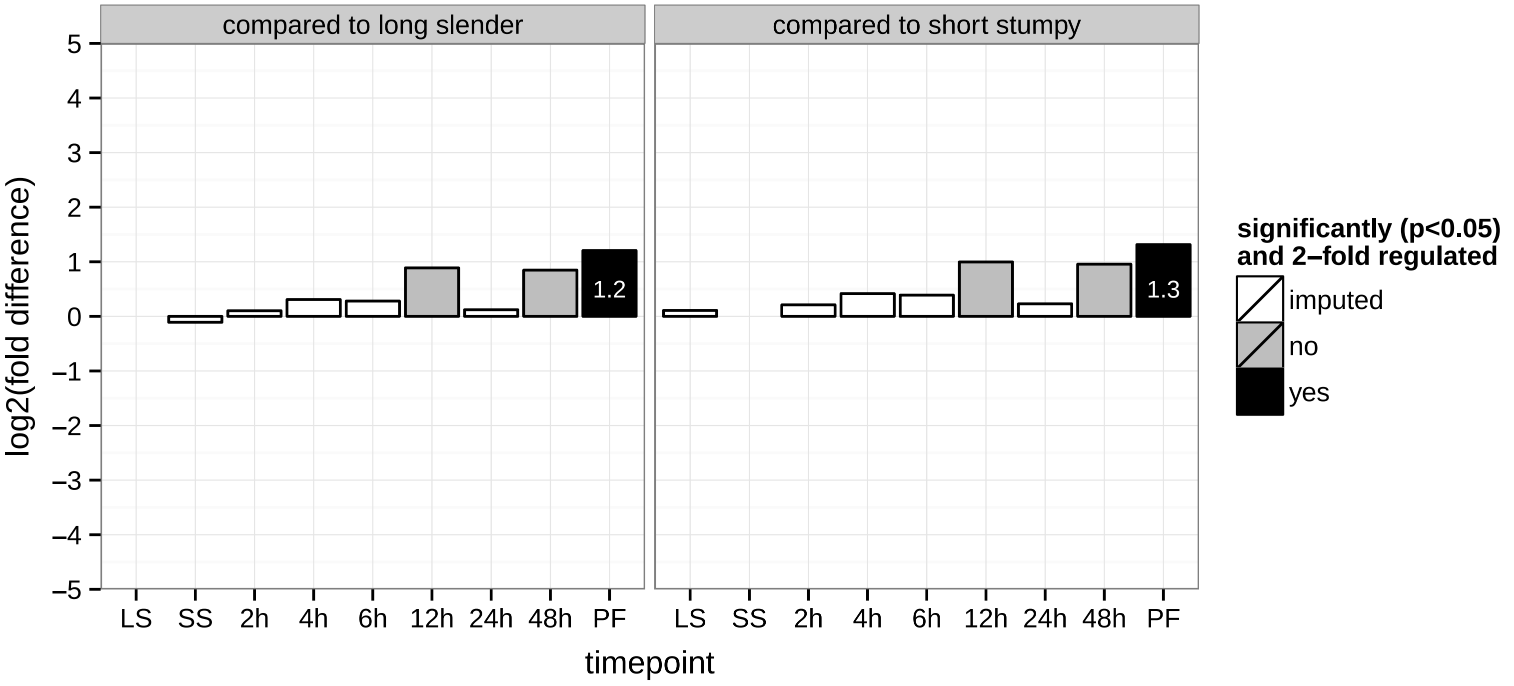
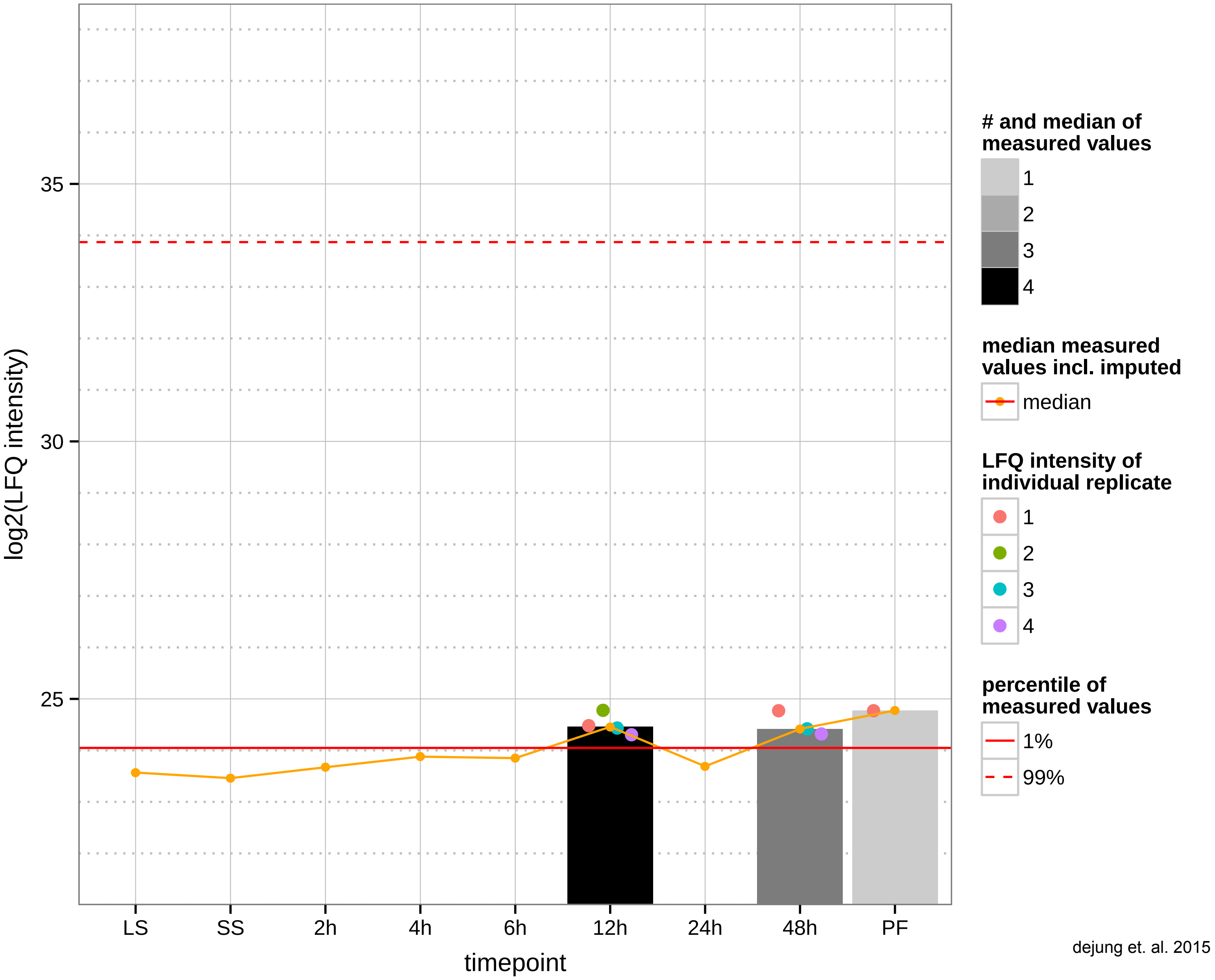
protein kinase, putative
Tb927.8.5950
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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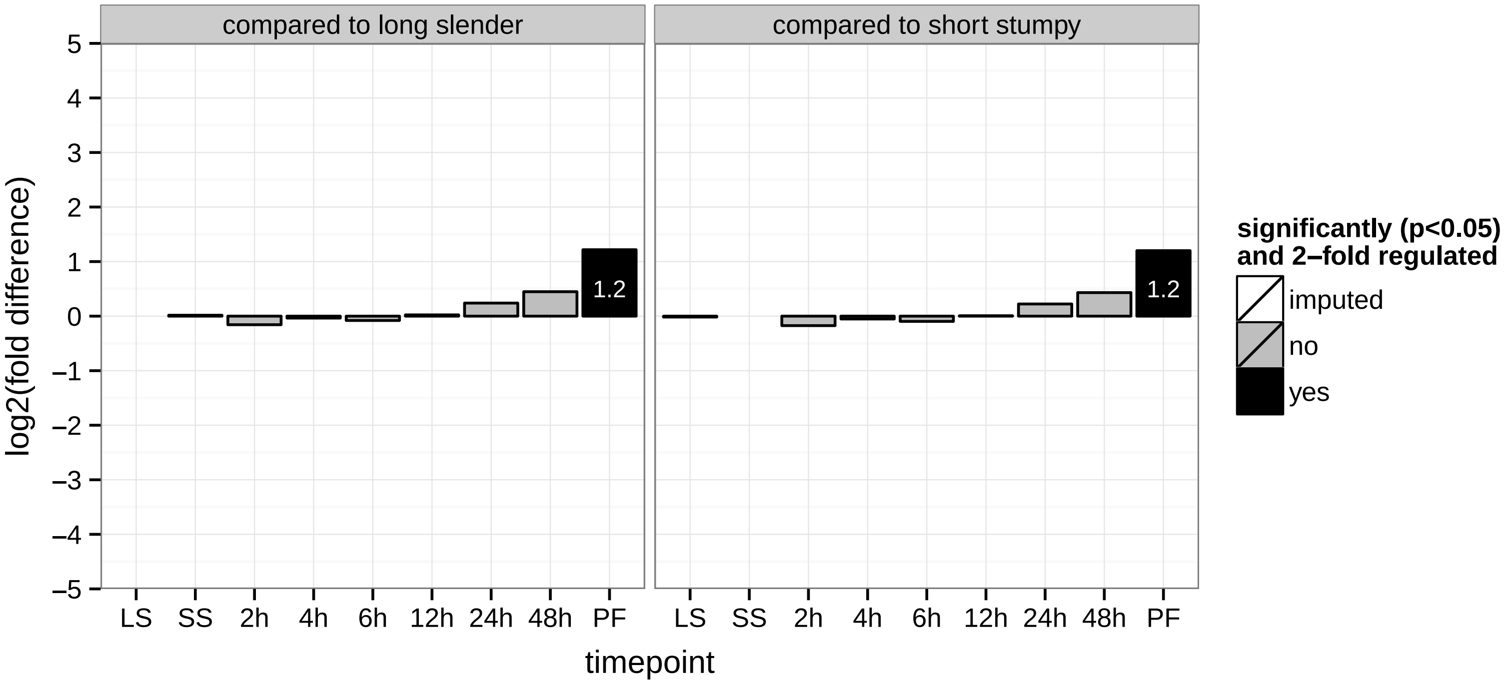
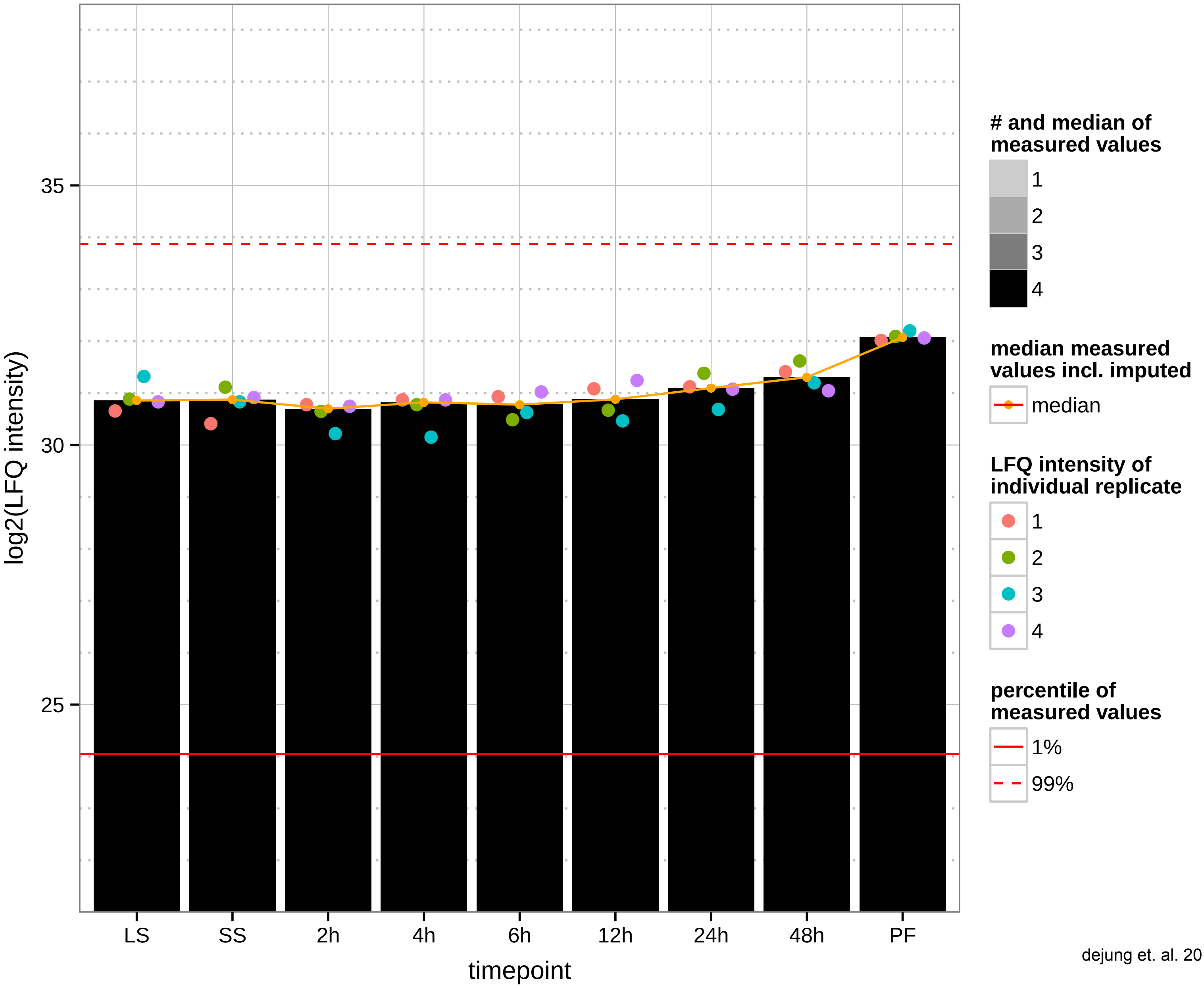
60S ribosomal protein L26, putative
Tb927.9.14370;Tb927.8.6180
AGOF: structural constituent of ribosome
AGOC: large ribosomal subunit, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: large ribosomal subunit
PGOP: translation





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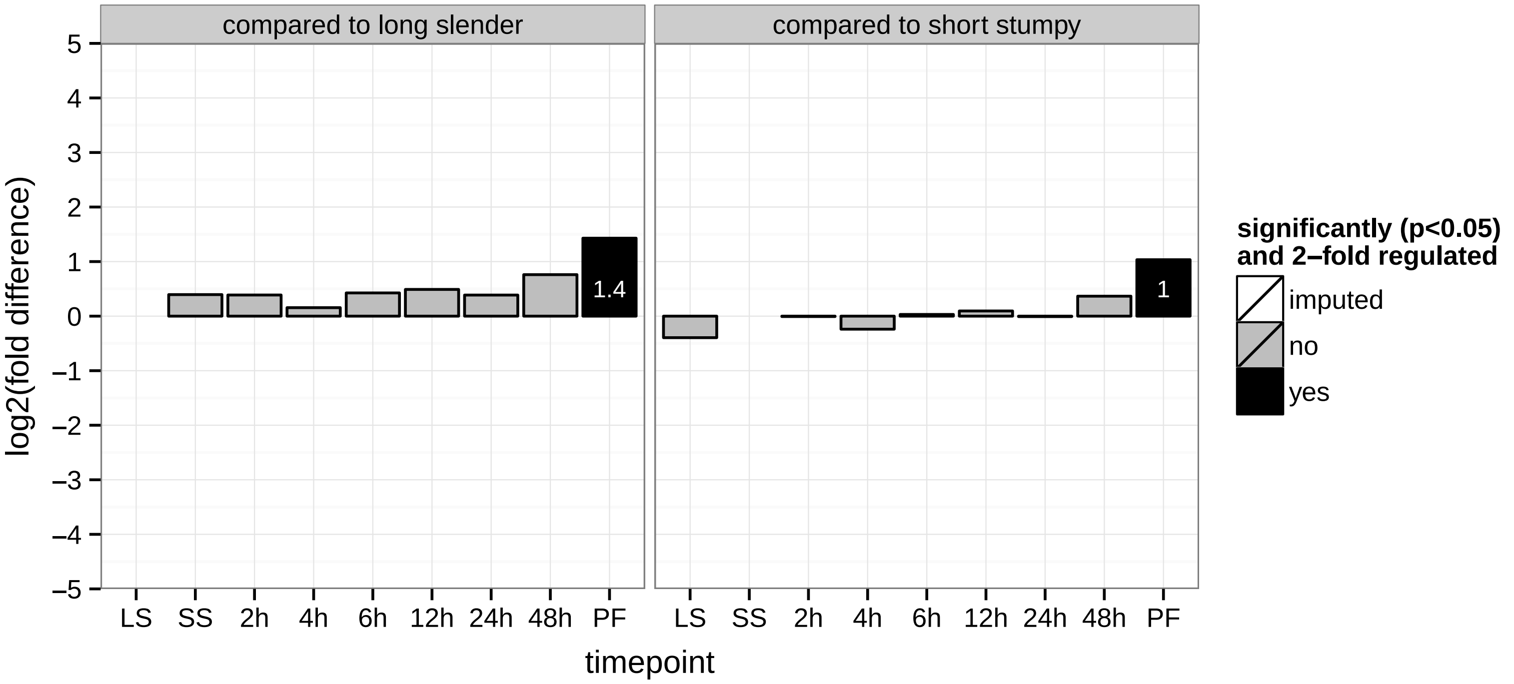
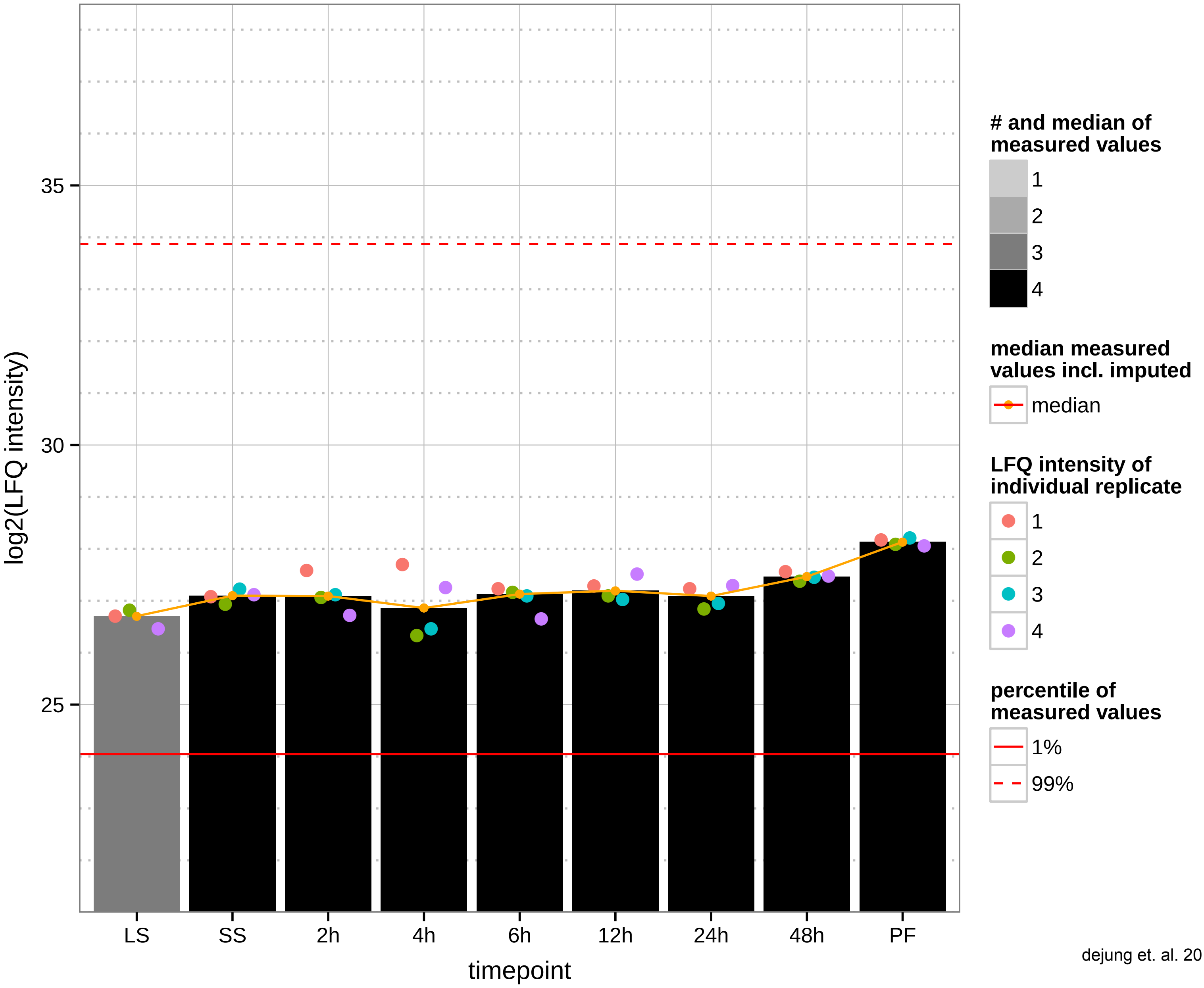
tubulin folding cofactor D, putative
Tb927.8.6200
AGOF: microtubule binding
AGOC: null
AGOP: protein folding
PGOF: binding
PGOC: null
PGOP: null





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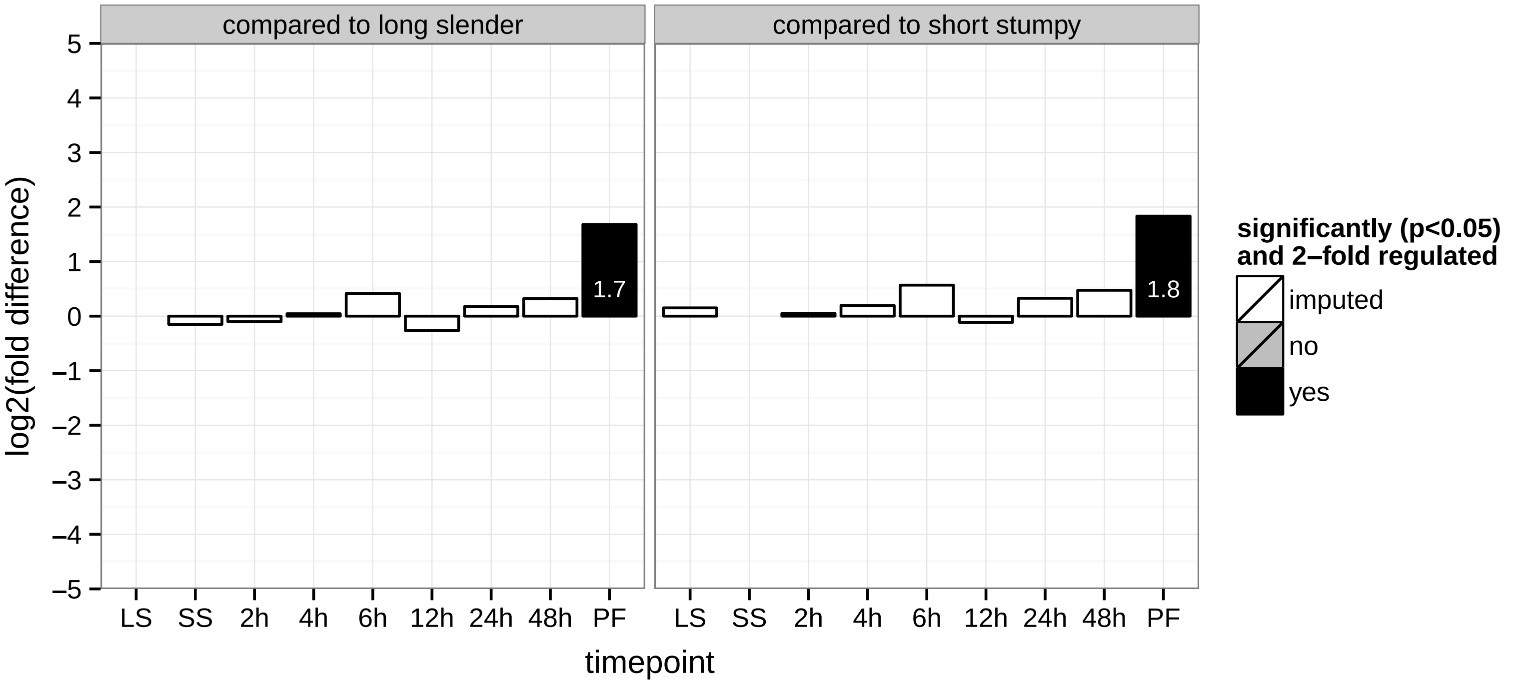
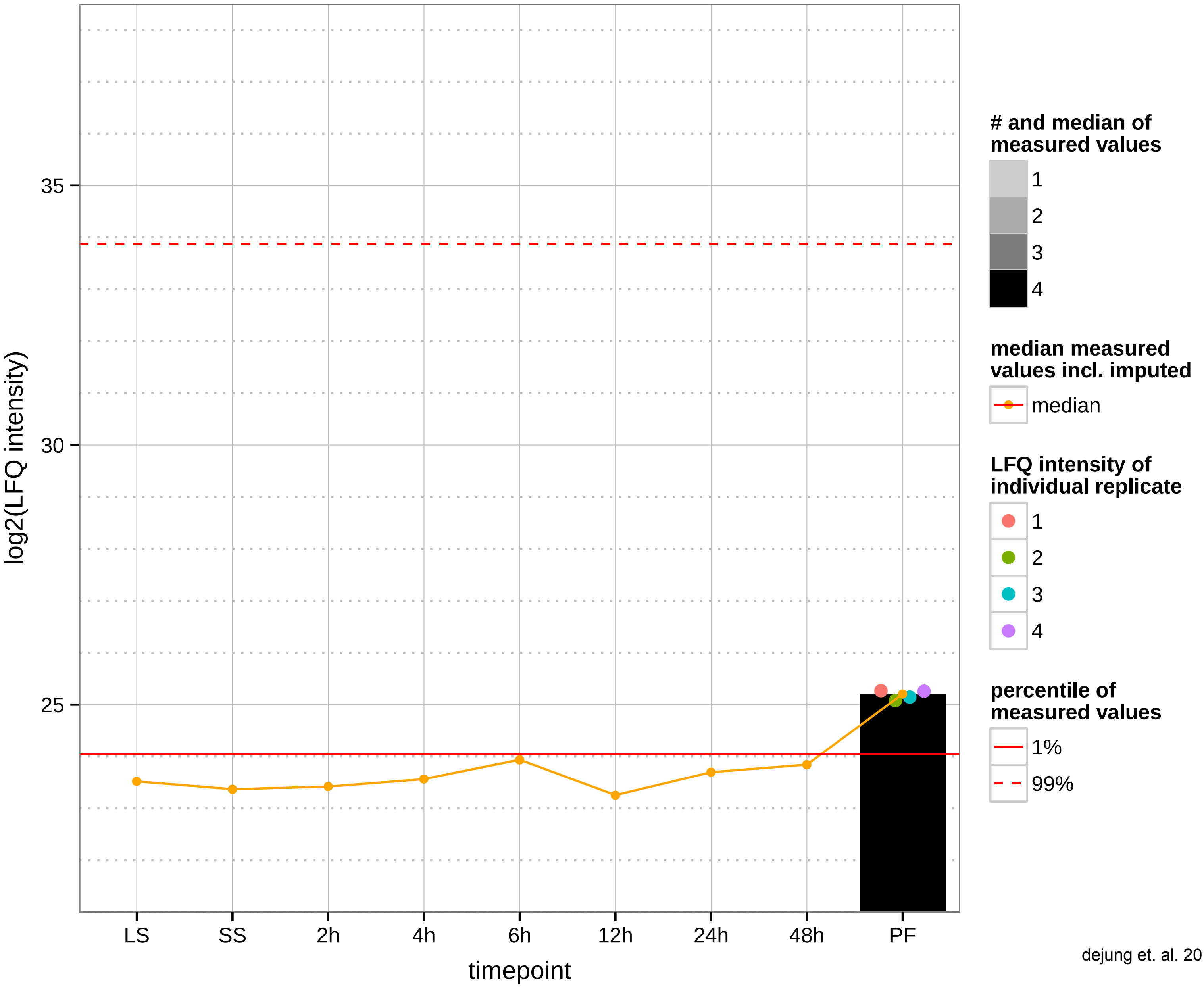
hypothetical protein, conserved
Tb927.8.6220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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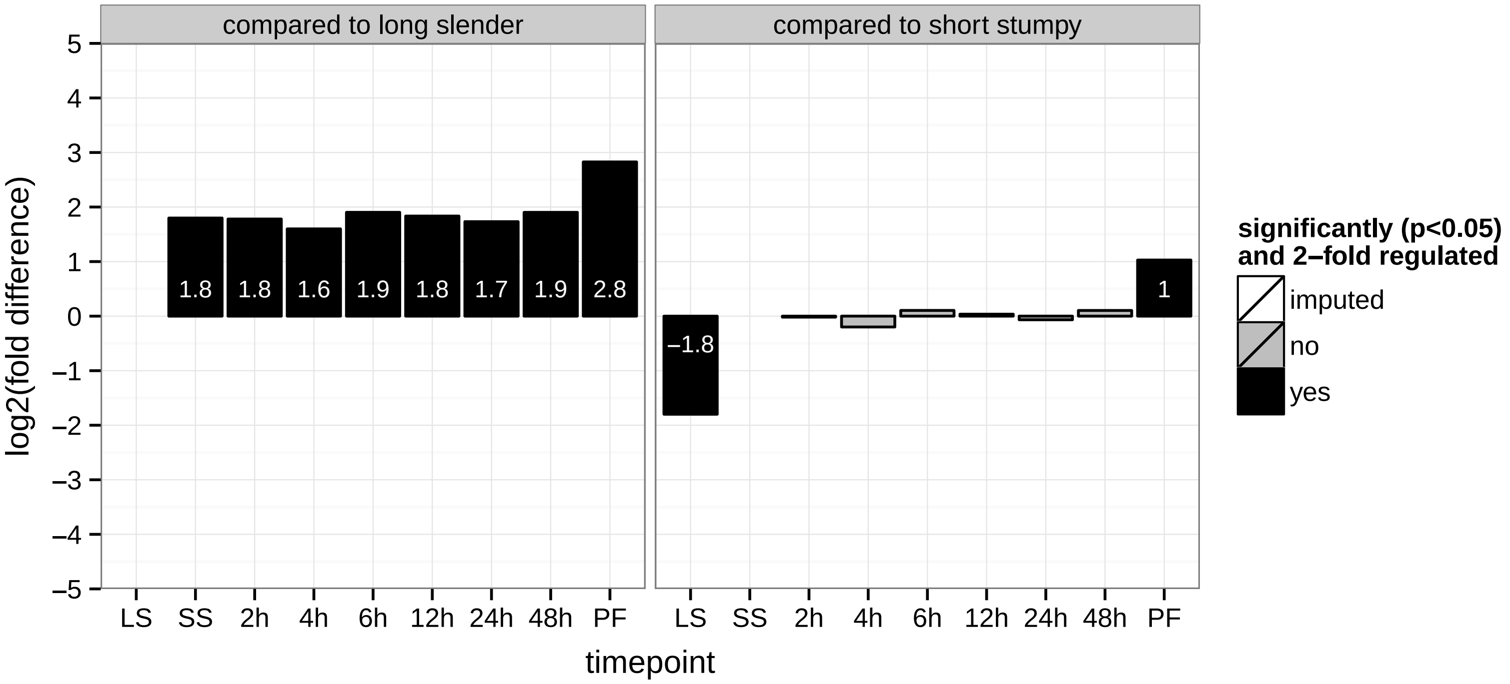
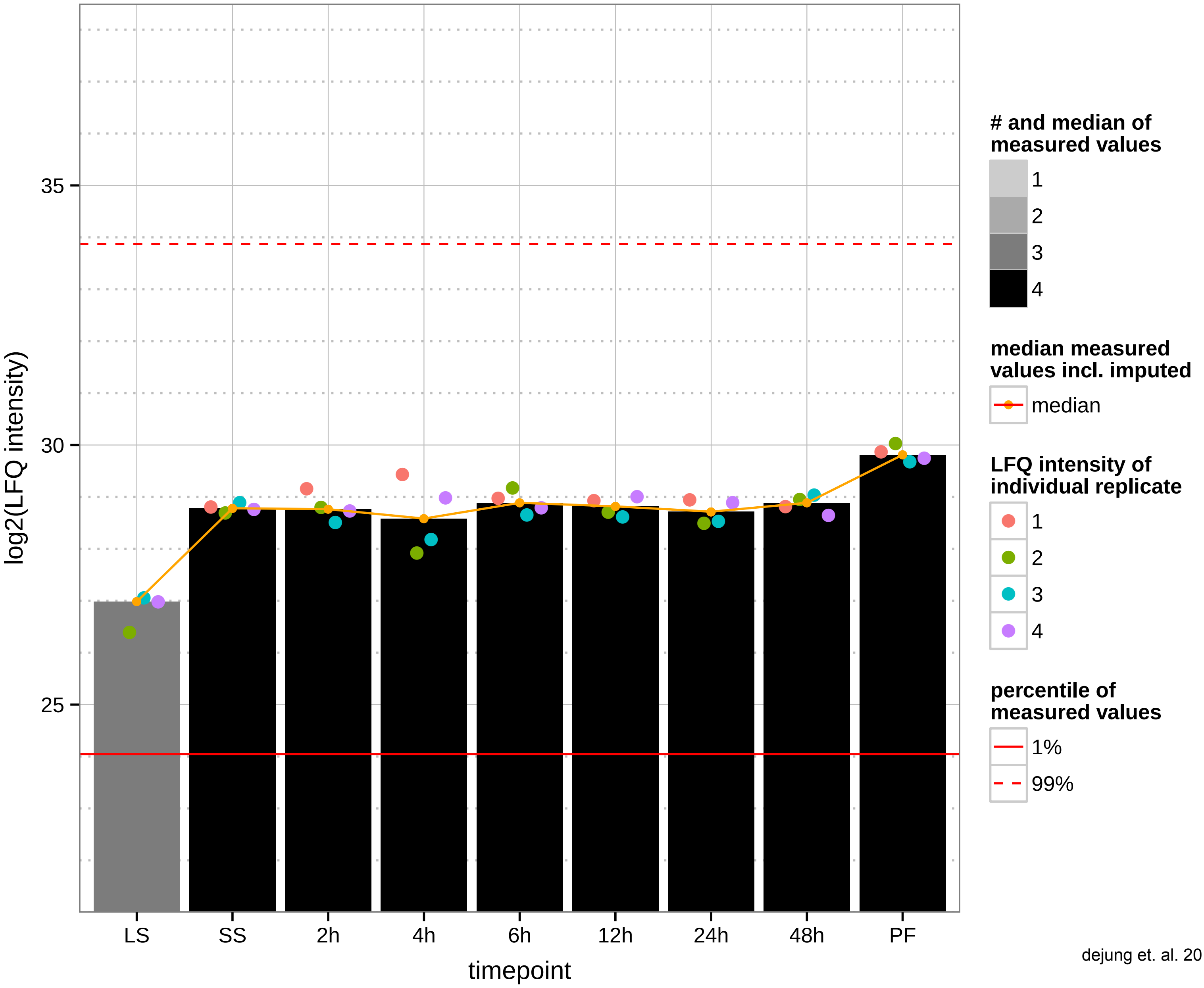
cation−transporting ATPase, putative
Tb927.8.650
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, hydrolase ac
AGOC: integral to membrane, membrane
AGOP: ATP biosynthetic process, cation transport, metabolic process
PGOF: ATPase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, me
PGOC: integral to membrane
PGOP: cation transport





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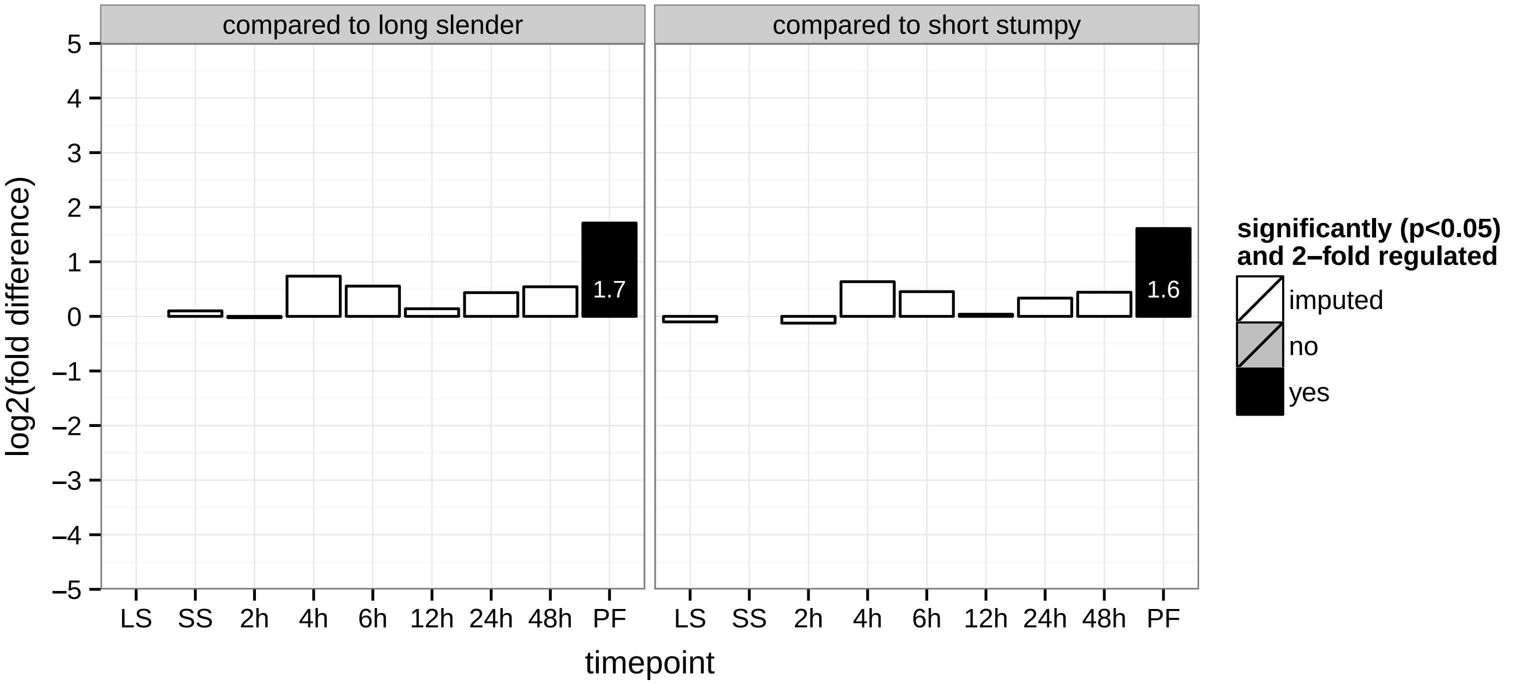
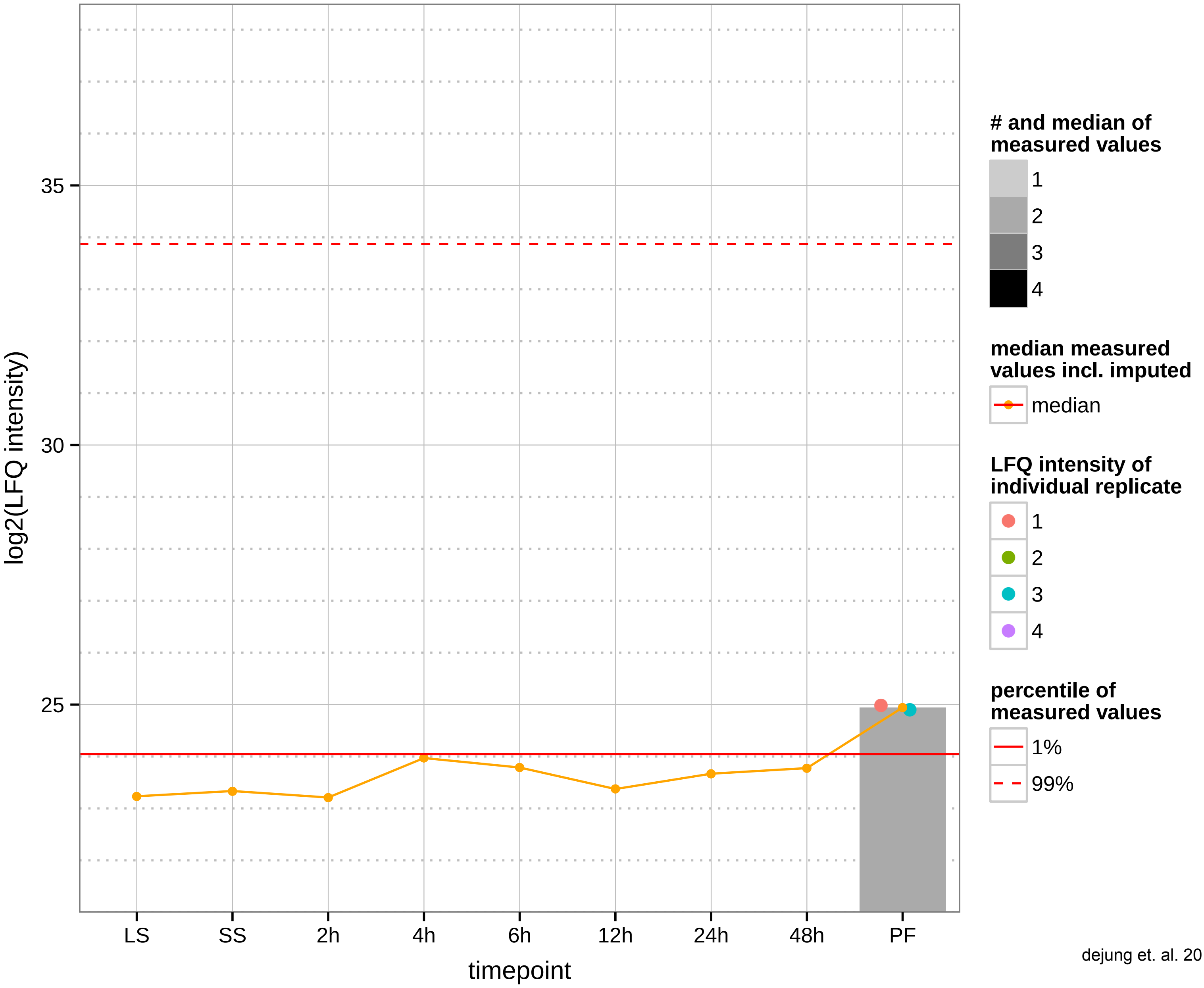
hypothetical protein, conserved
Tb927.8.6820
AGOF: carbon−carbon lyase activity
AGOC: mitochondrion
AGOP: cellular aromatic compound metabolic process
PGOF: carbon−carbon lyase activity, catalytic activity
PGOC: null
PGOP: cellular aromatic compound metabolic process





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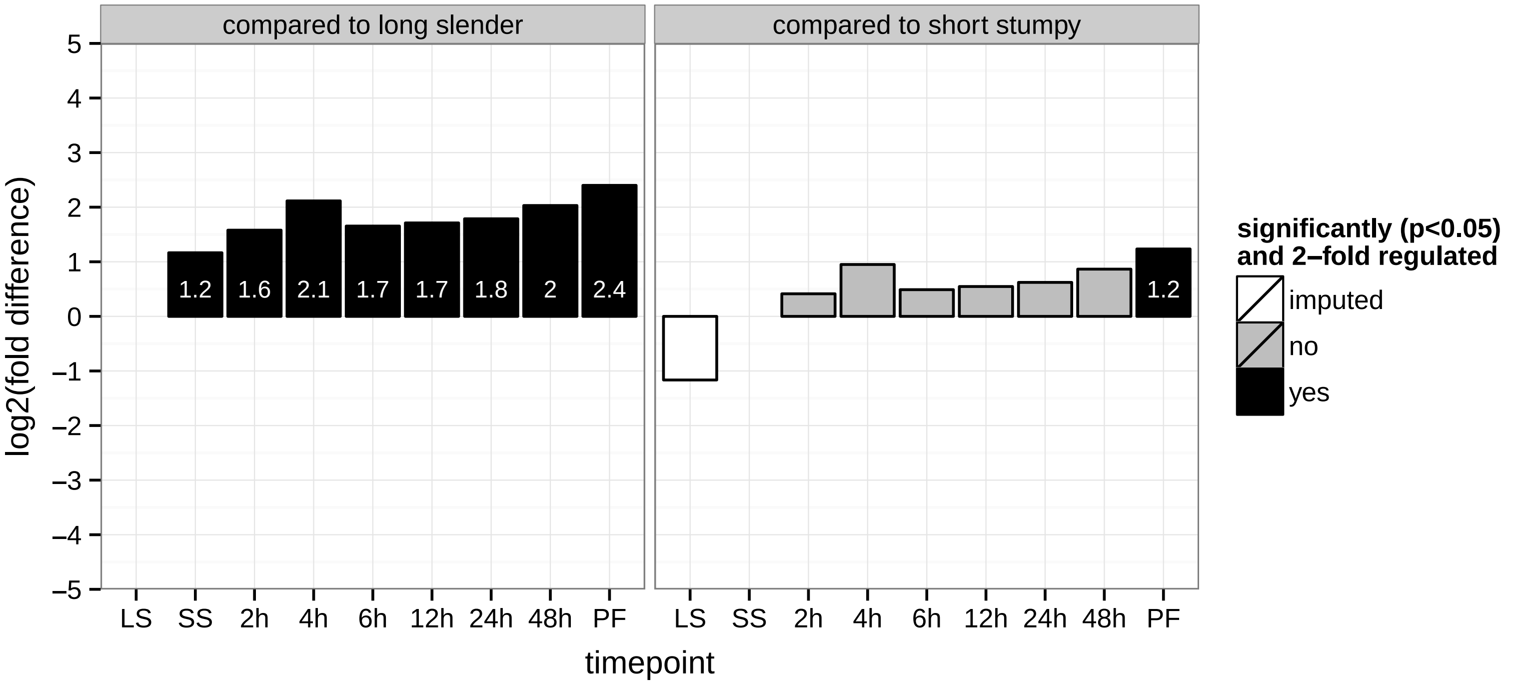
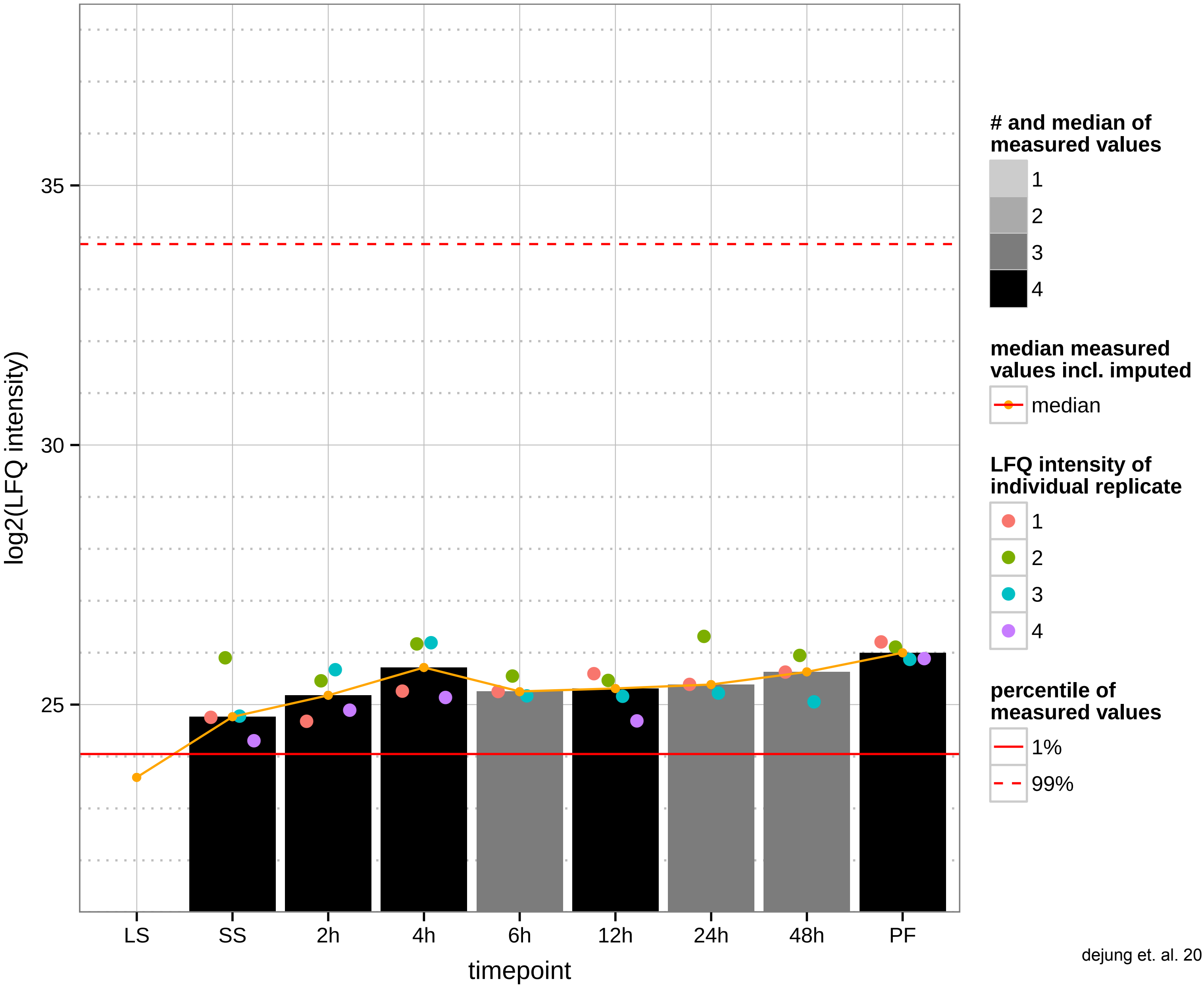
chaperone protein DNAj, putative
Tb927.8.7010
AGOF: heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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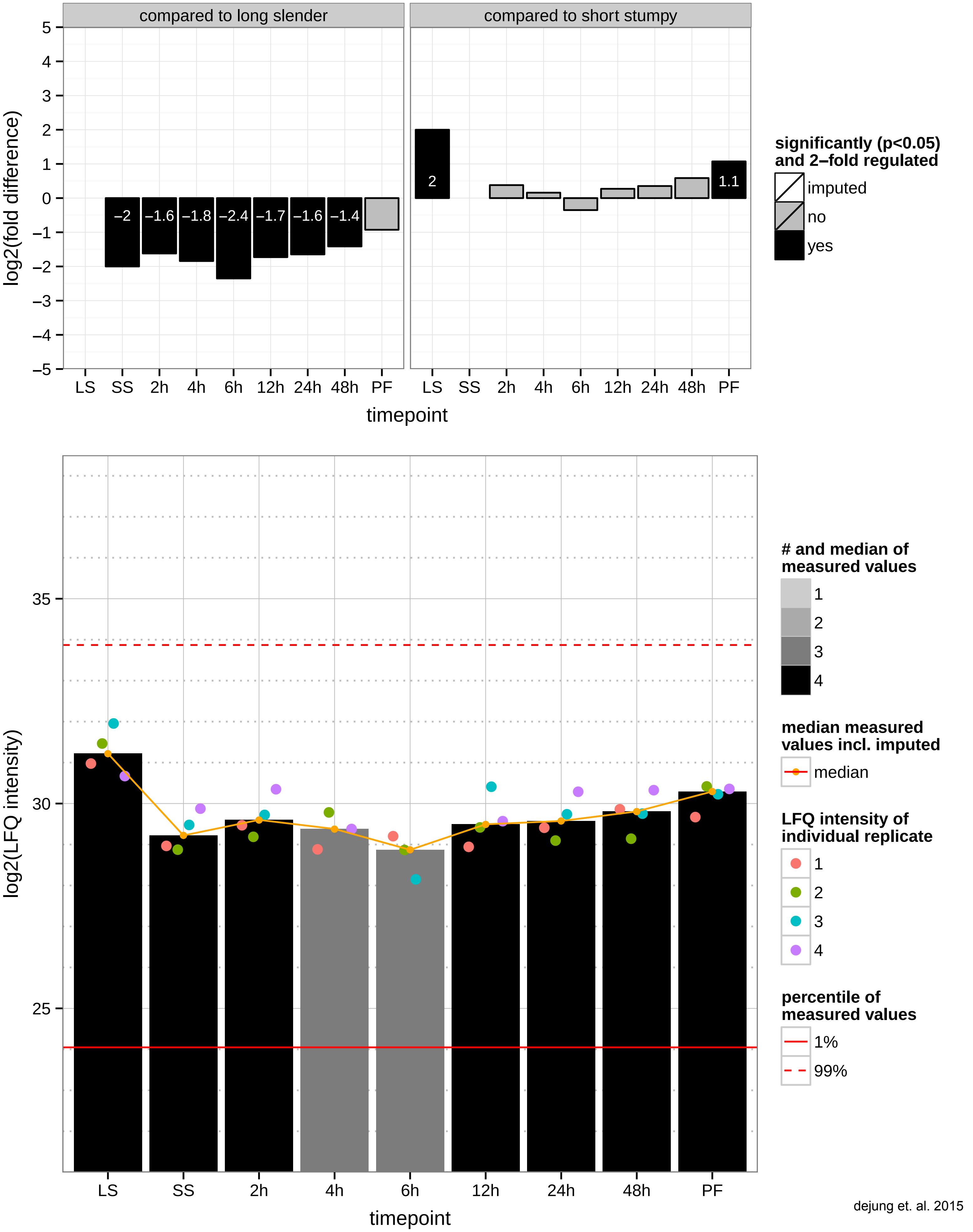
hypothetical protein, conserved
Tb927.8.7090
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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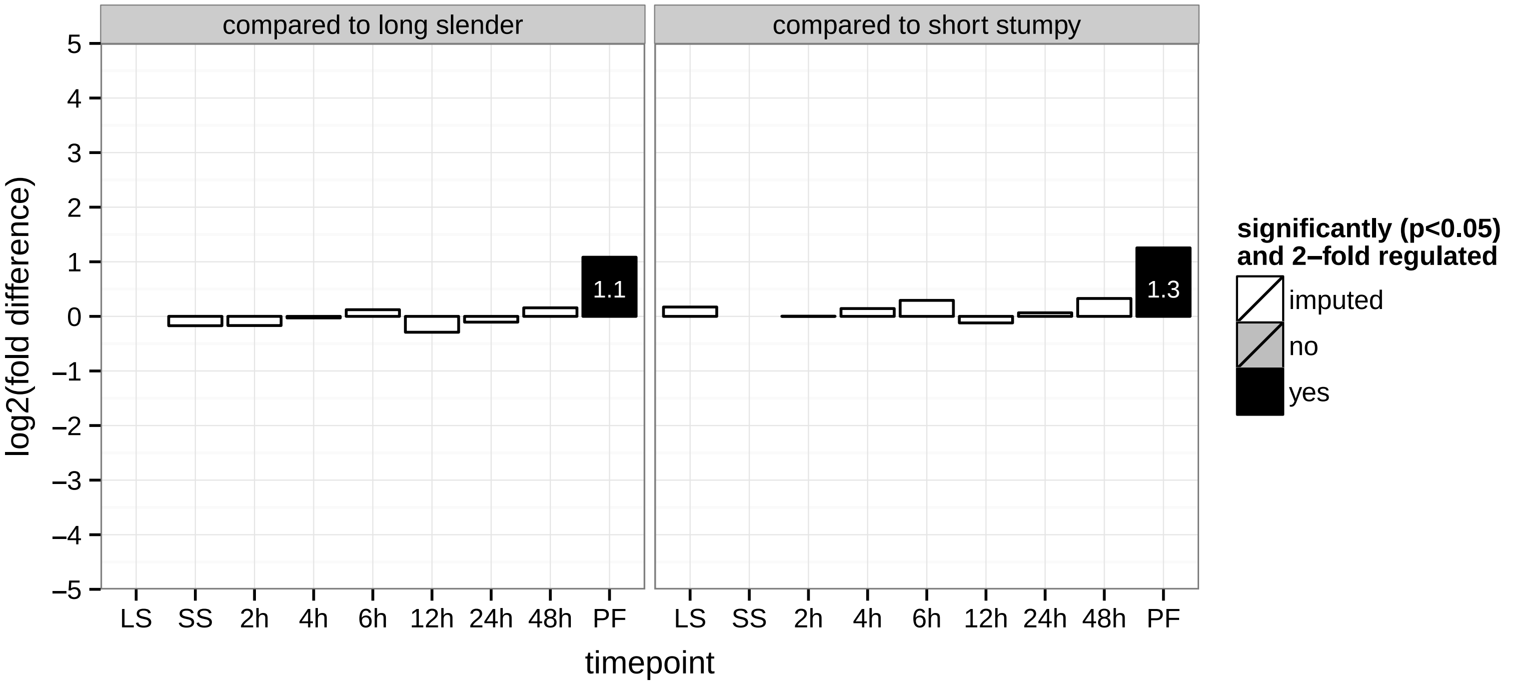
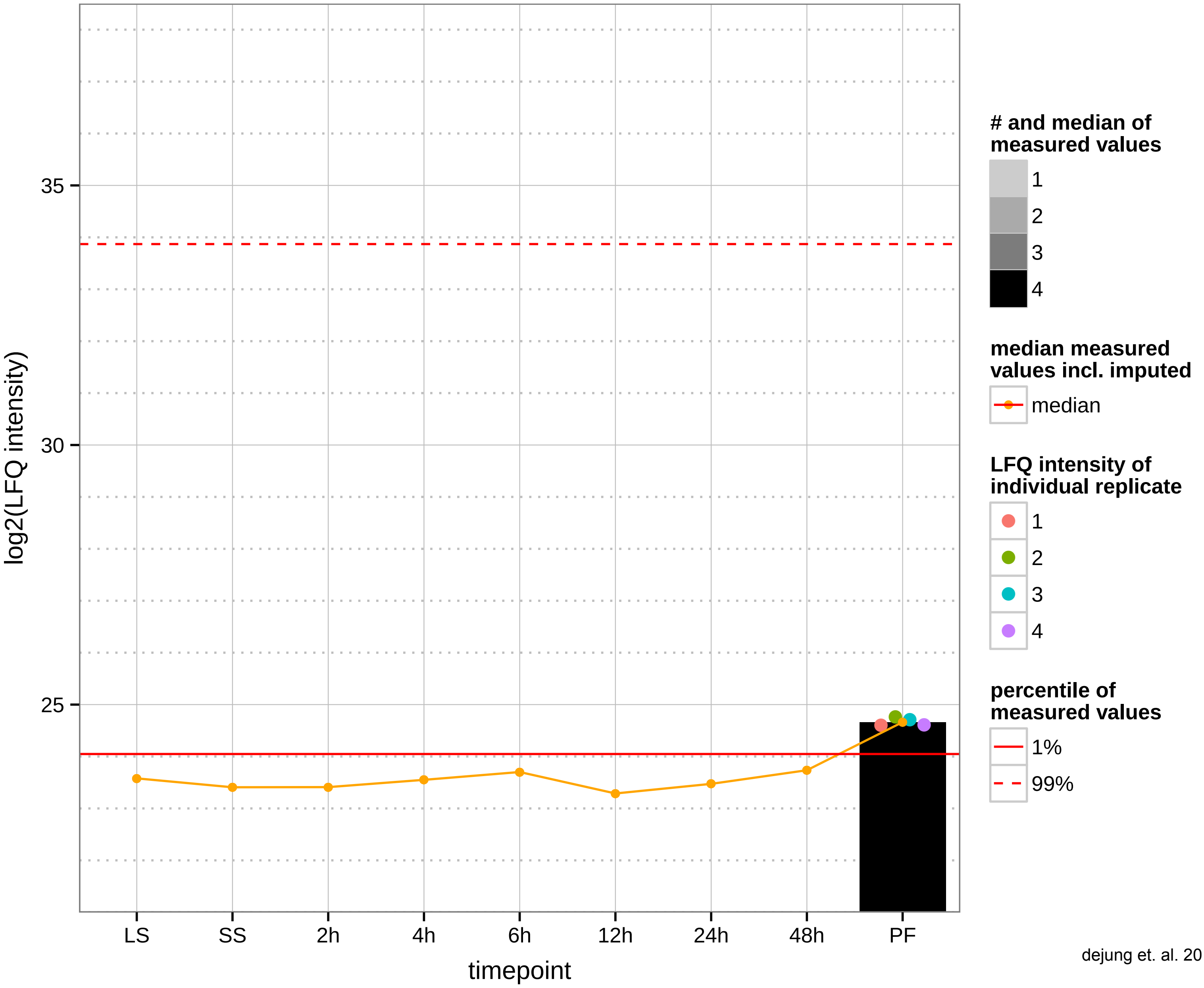
RNA–binding protein, putative (DRBD17)
Tb927.8.710
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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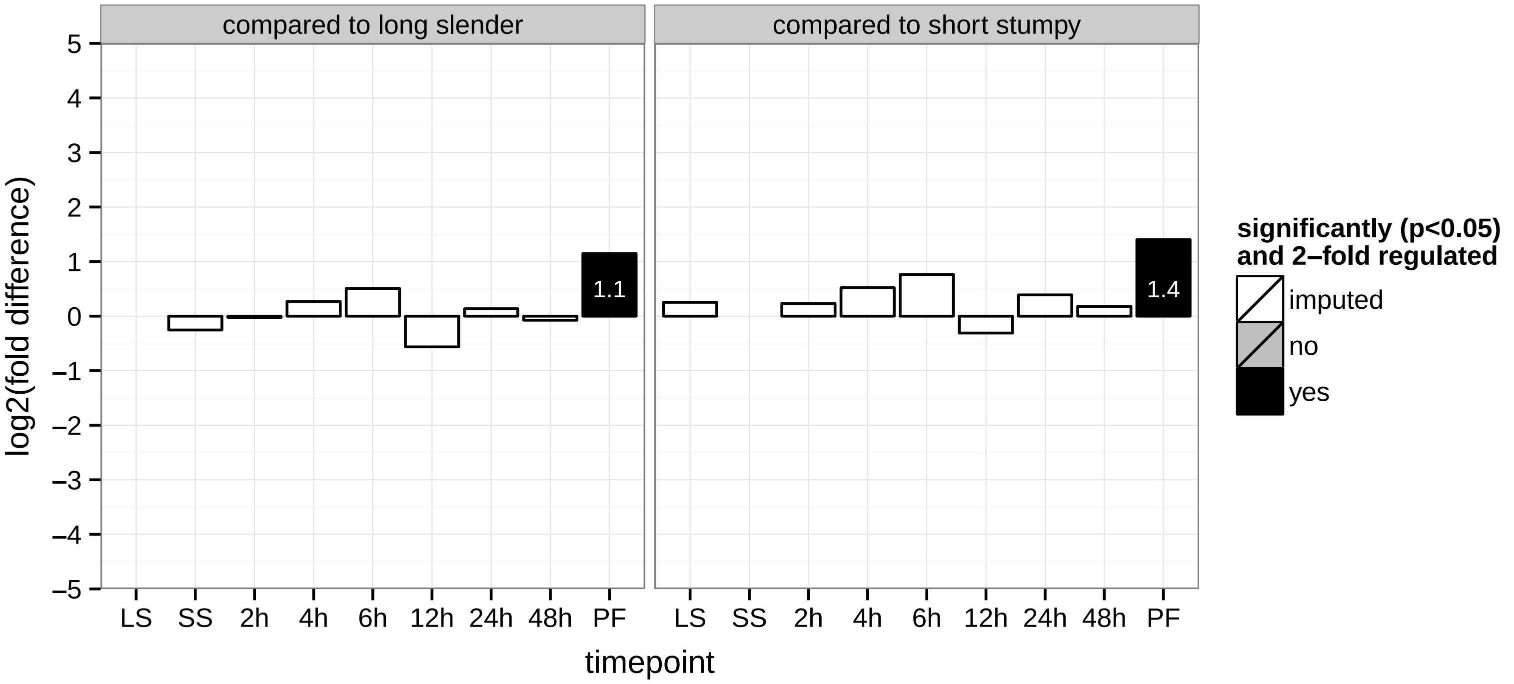
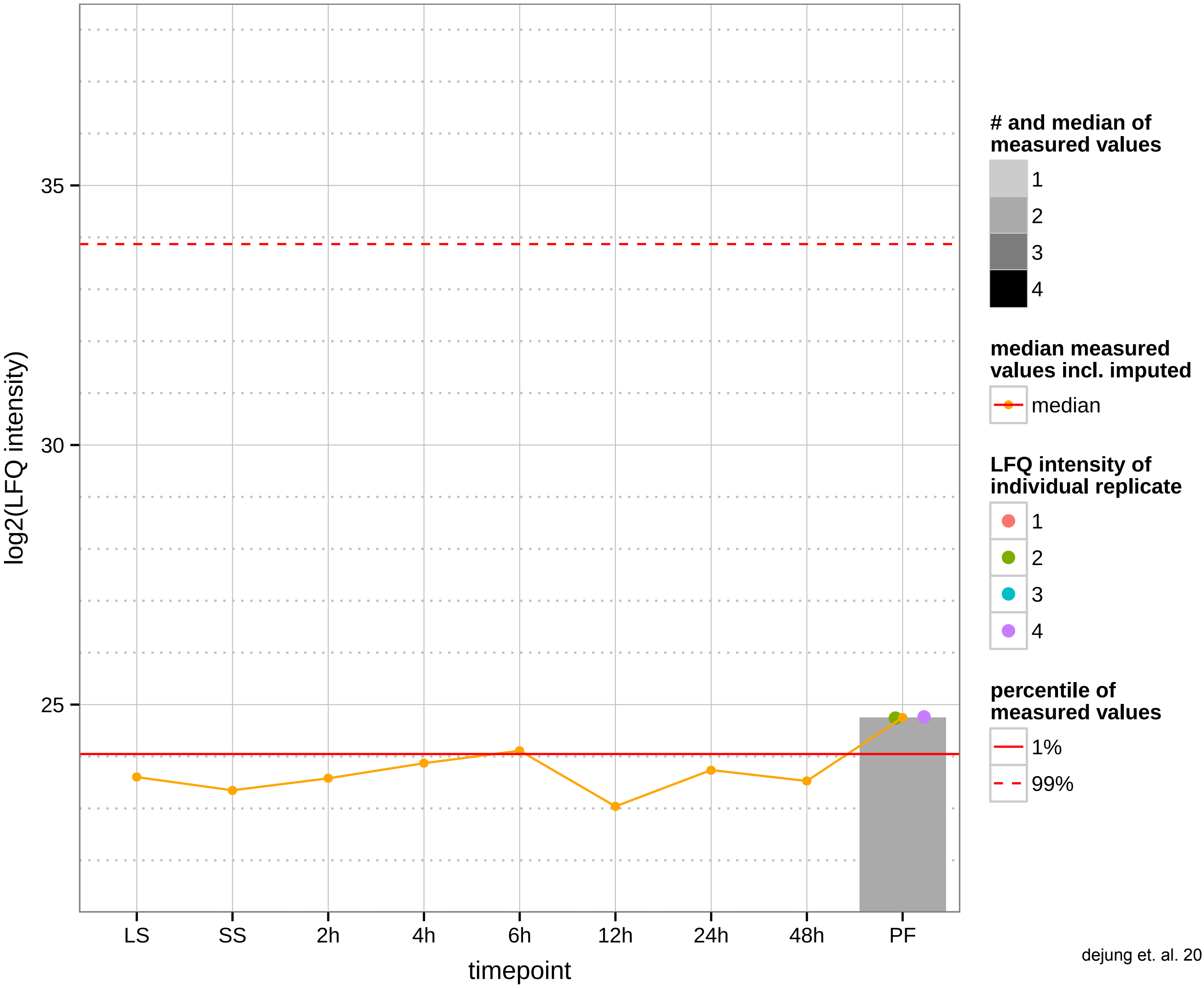
hypothetical protein
Tb927.8.7370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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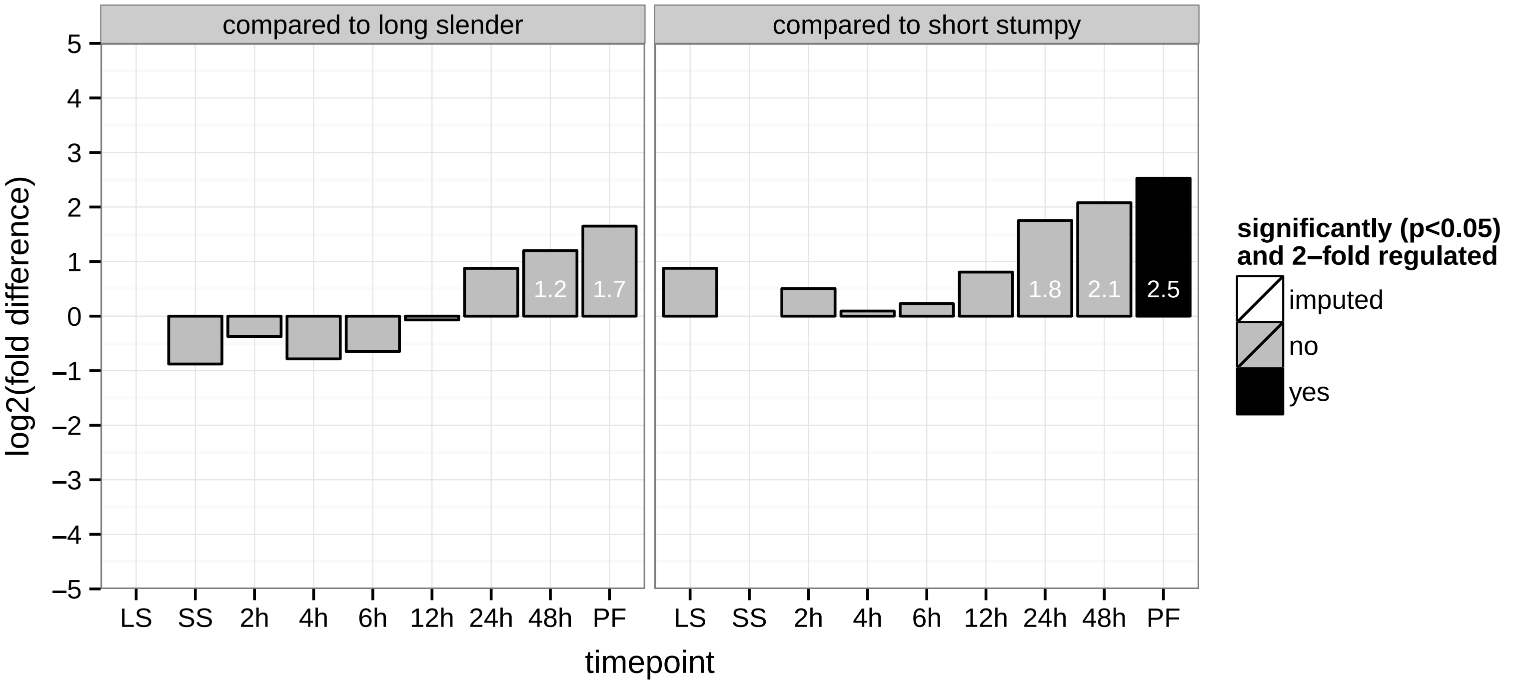
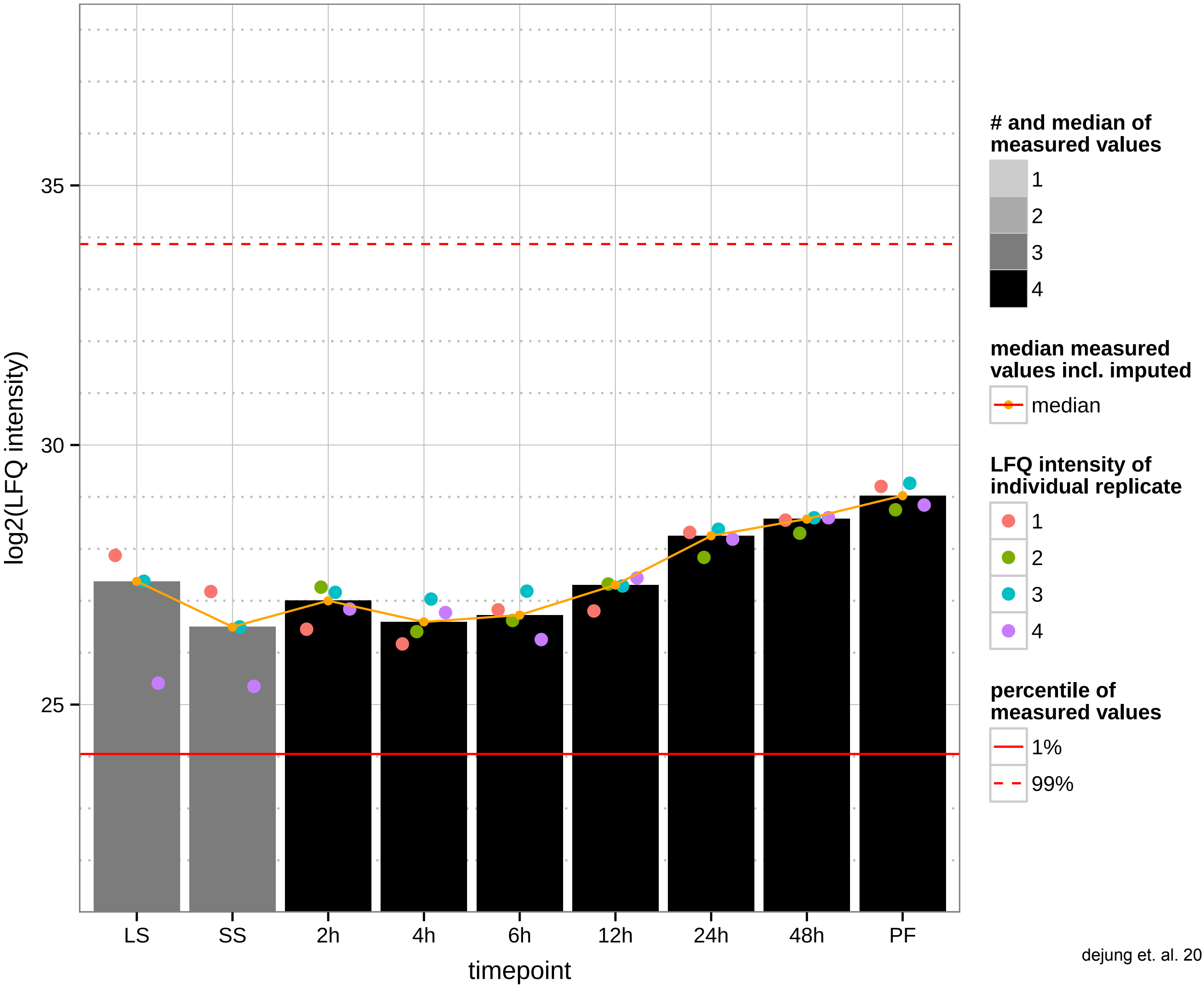
amino acid transporter 1, putative (AATP1)
Tb927.8.7640;Tb927.8.7610
AGOF: amine transmembrane transporter activity
AGOC: membrane, null
AGOP: amino acid transport
PGOF: null
PGOC: null
PGOP: null





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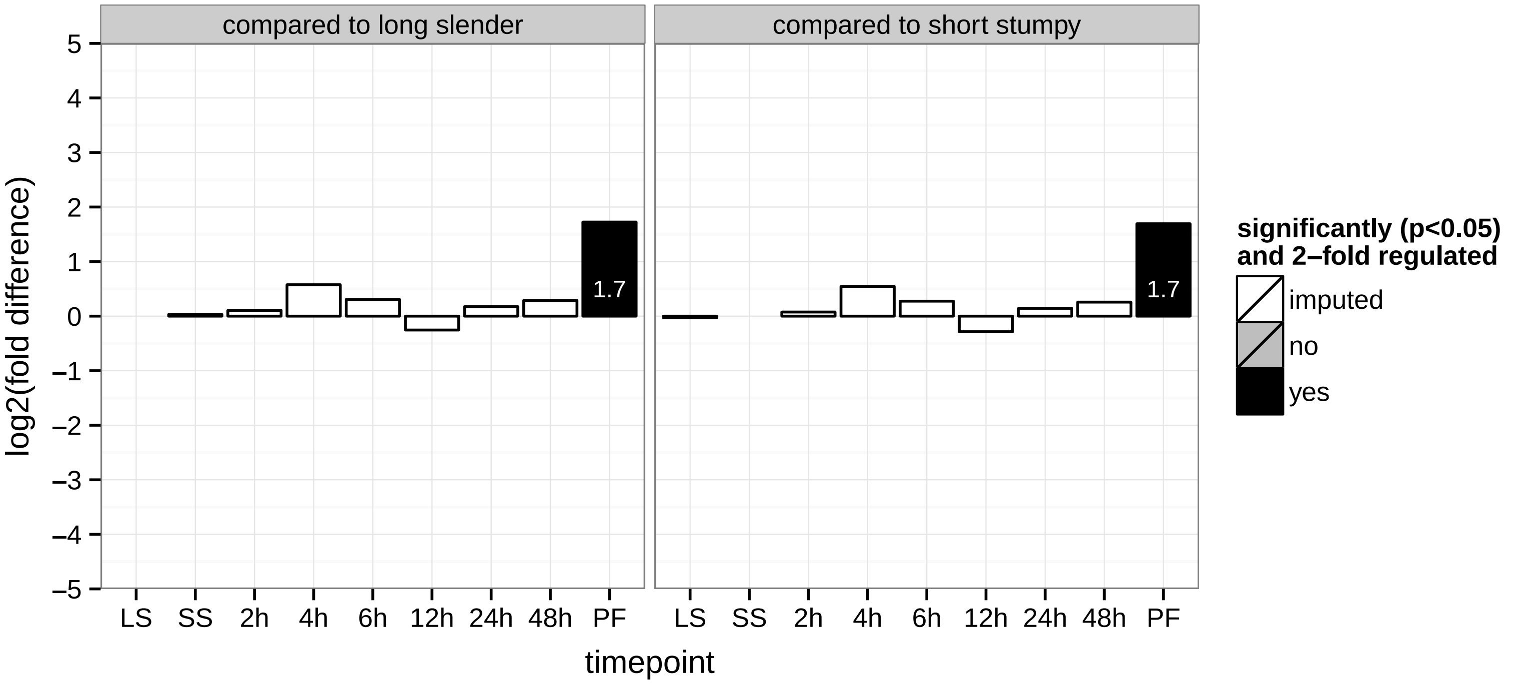
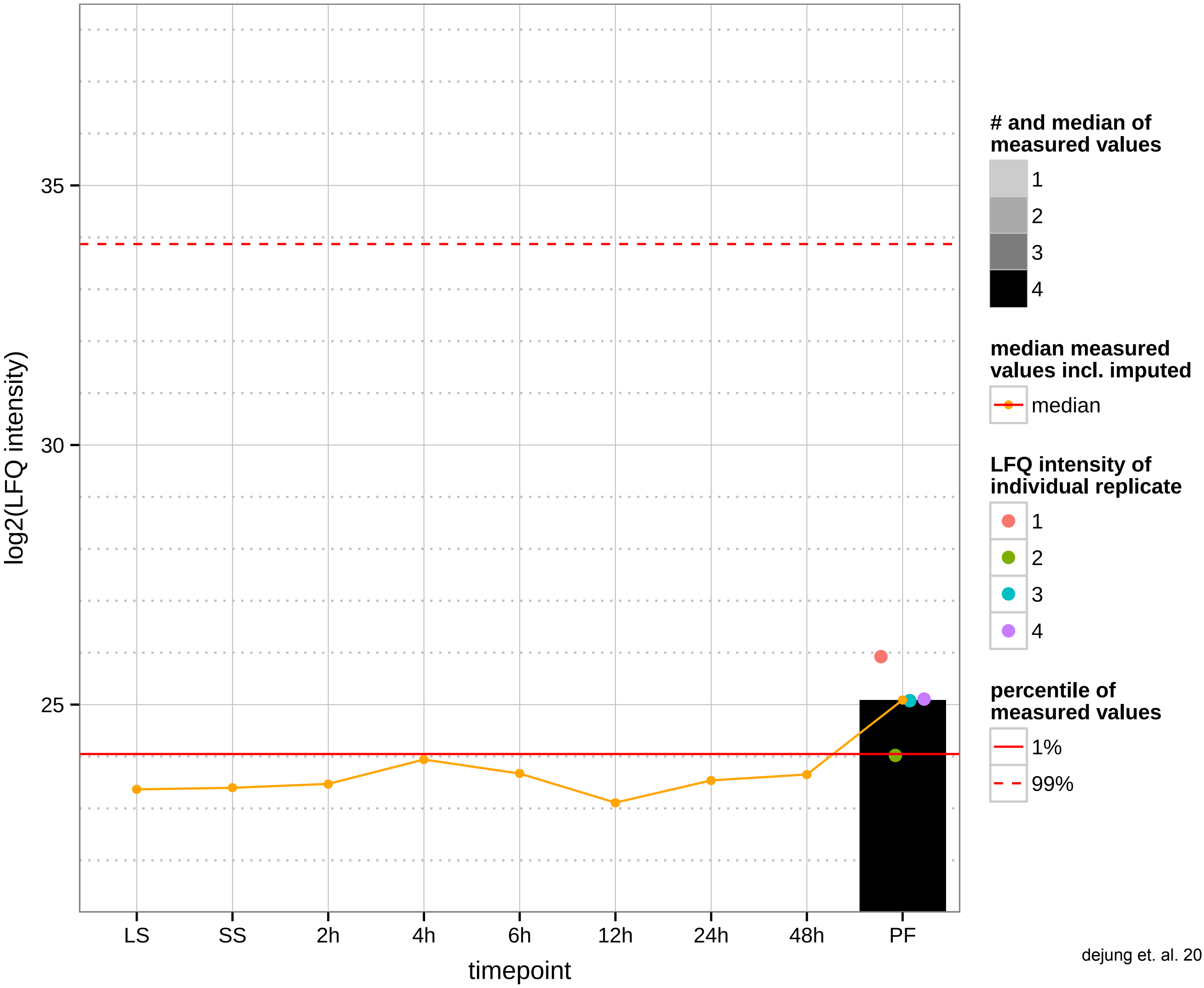
amino acid transporter, putative, amino acid transporter (pseudogene)
Tb927.8.7670;Tb927.8.7650
AGOF: amine transmembrane transporter activity, null
AGOC: membrane, null
AGOP: null, amino acid transport
PGOF: null
PGOC: null
PGOP: null





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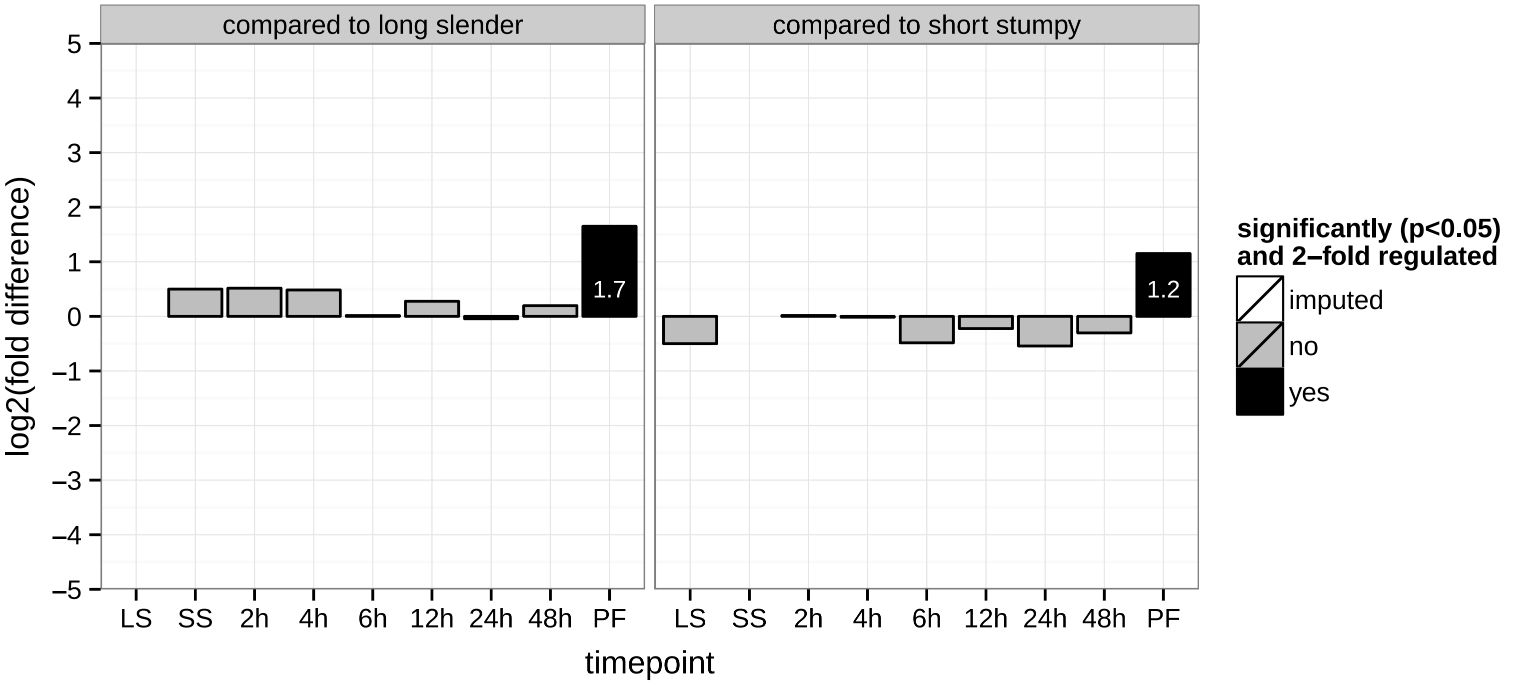
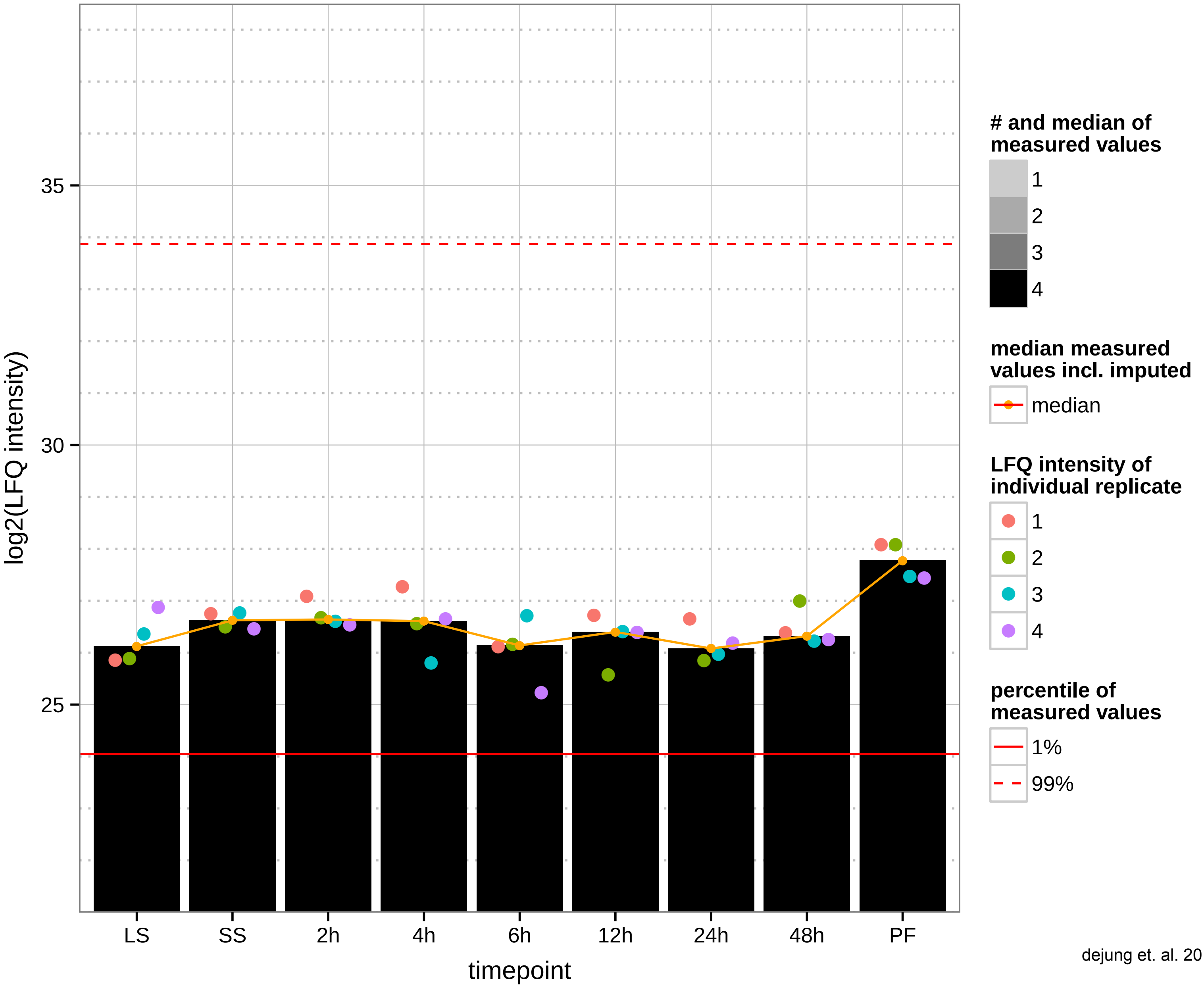
hypothetical protein, conserved
Tb927.8.820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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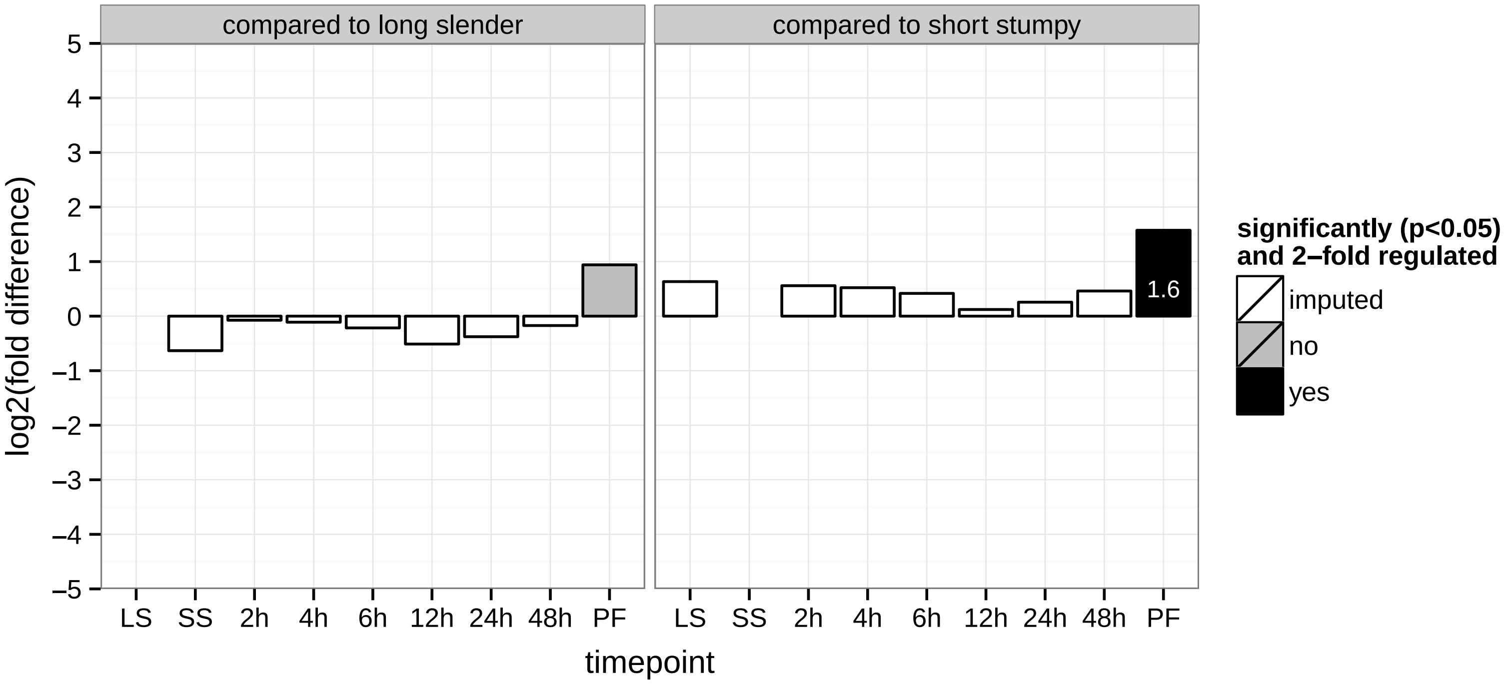
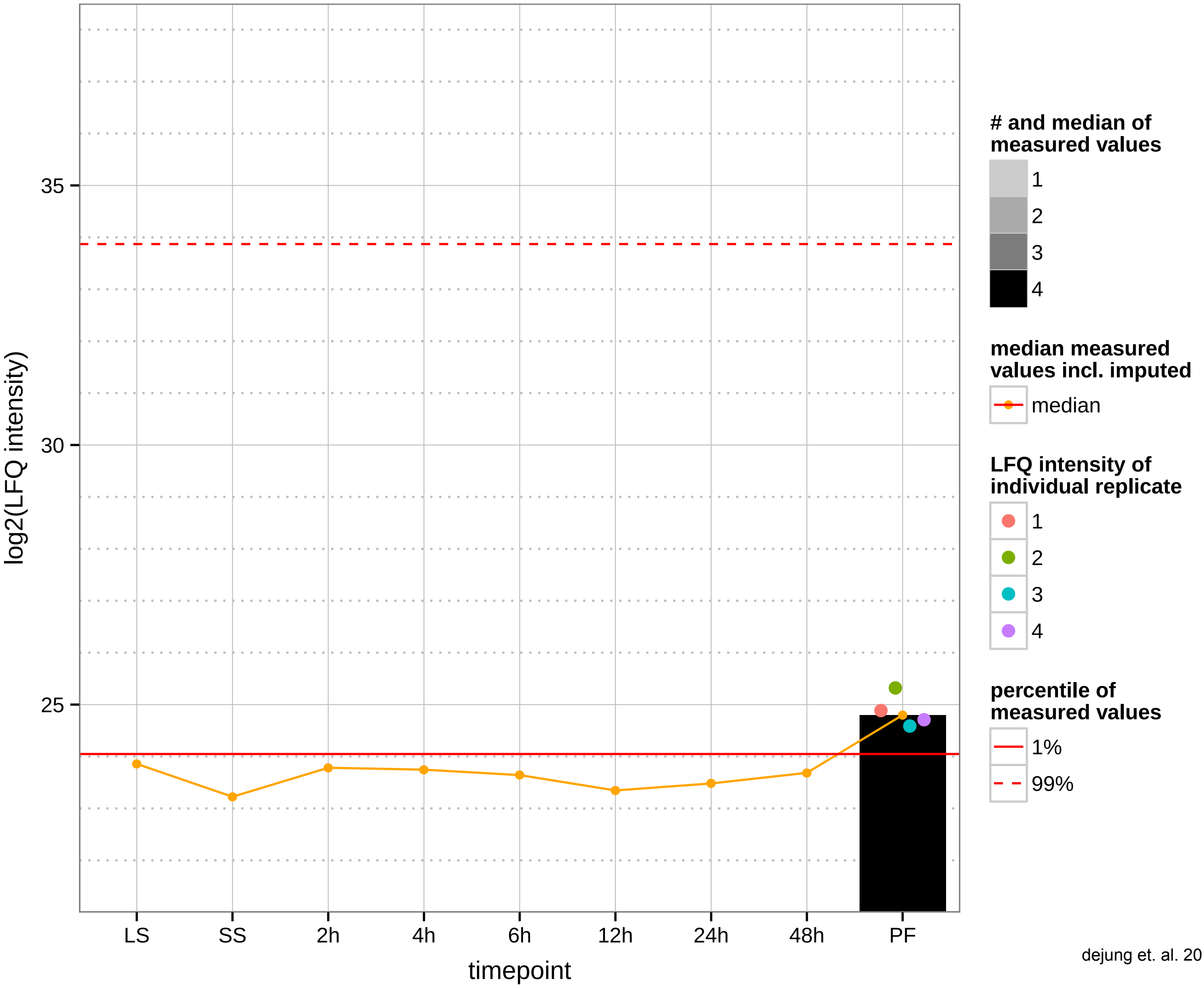
hypothetical protein, conserved
Tb927.9.10050
AGOF: null
AGOC: integral to membrane
AGOP: protein insertion into membrane
PGOF: null
PGOC: integral to membrane
PGOP: protein insertion into membrane





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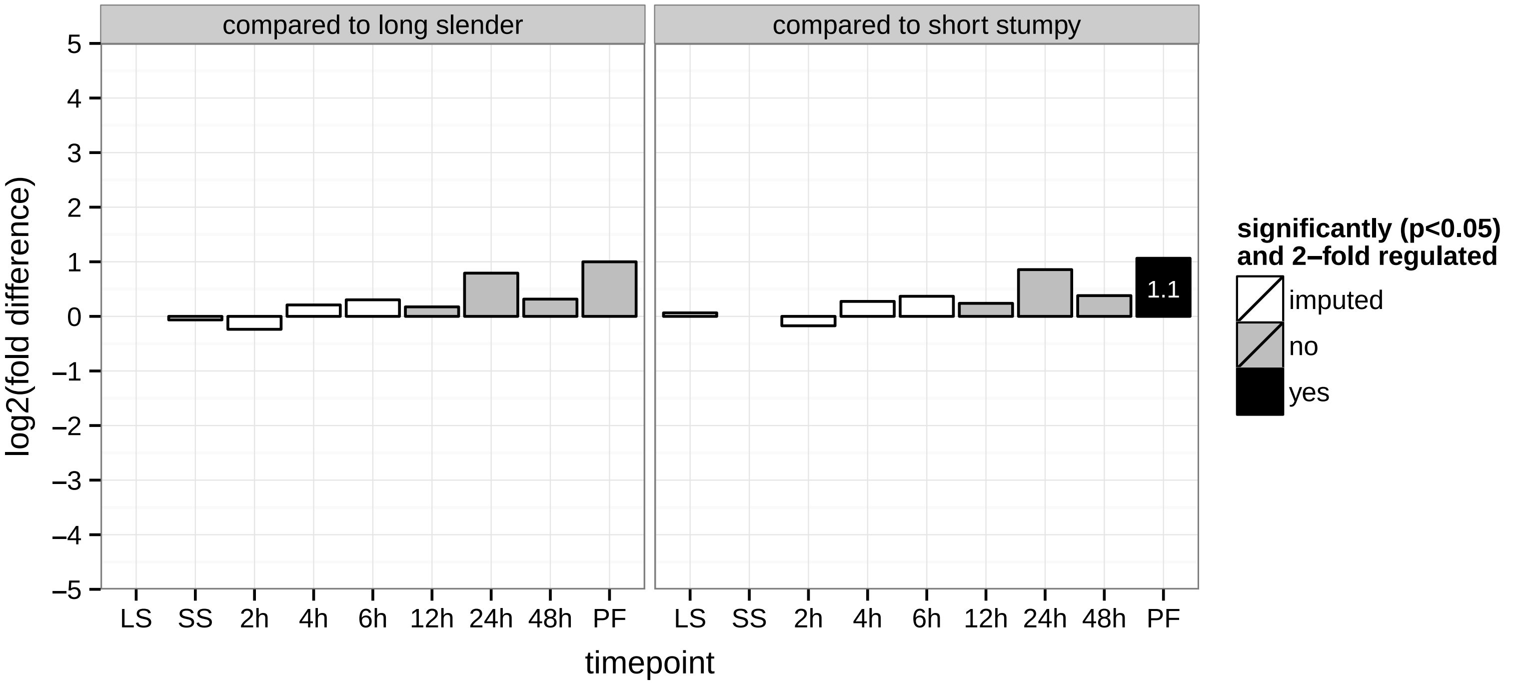
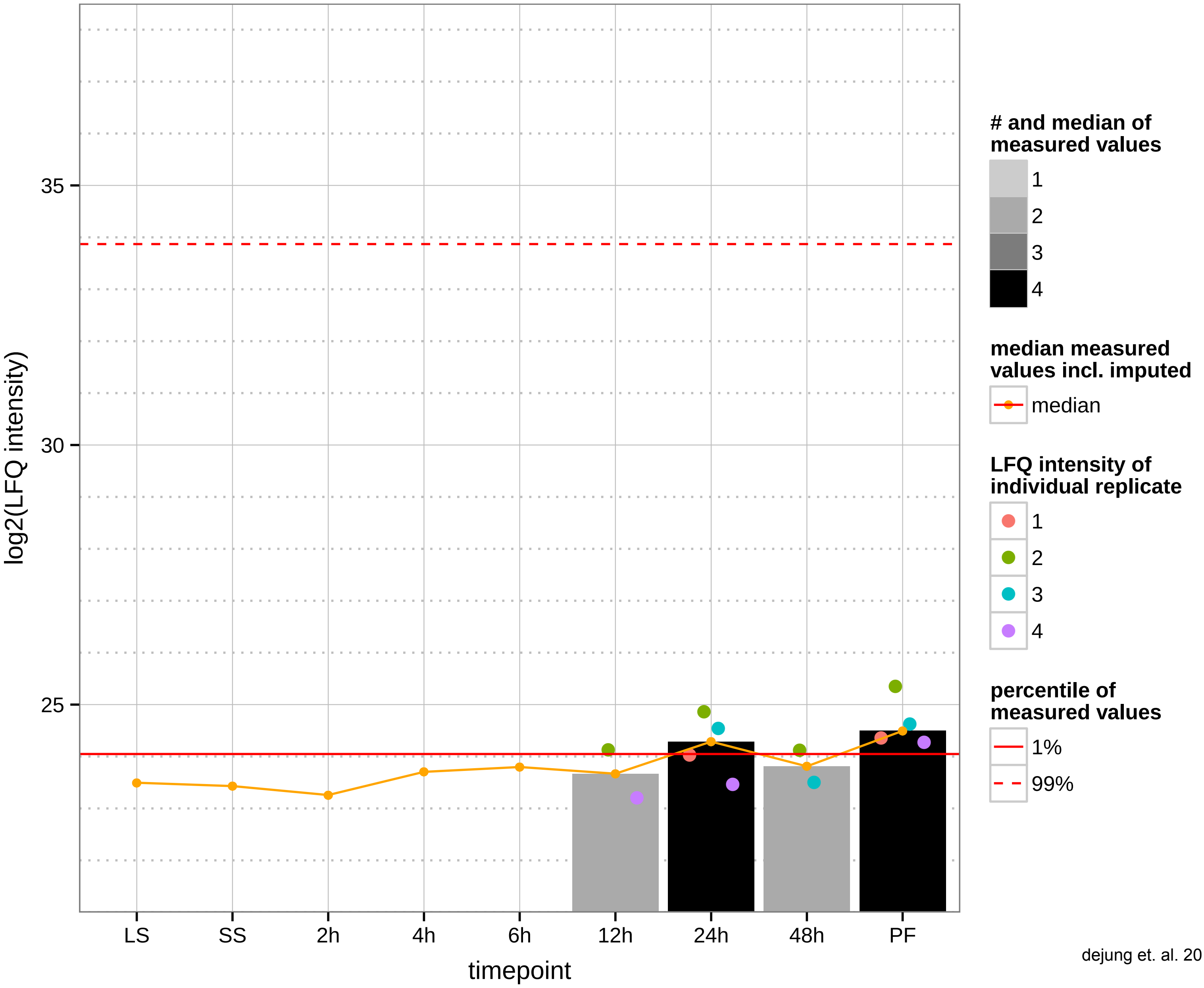
hypothetical protein, conserved
Tb927.9.10200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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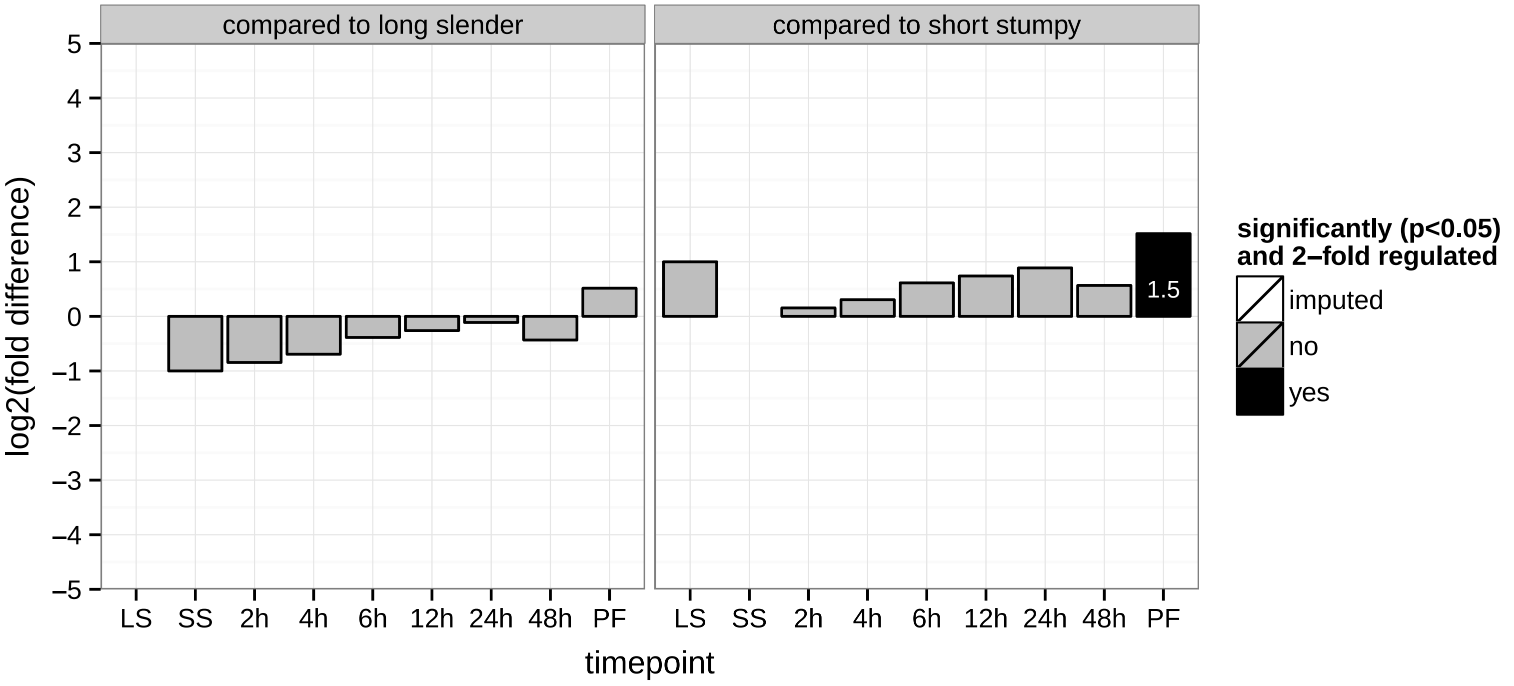
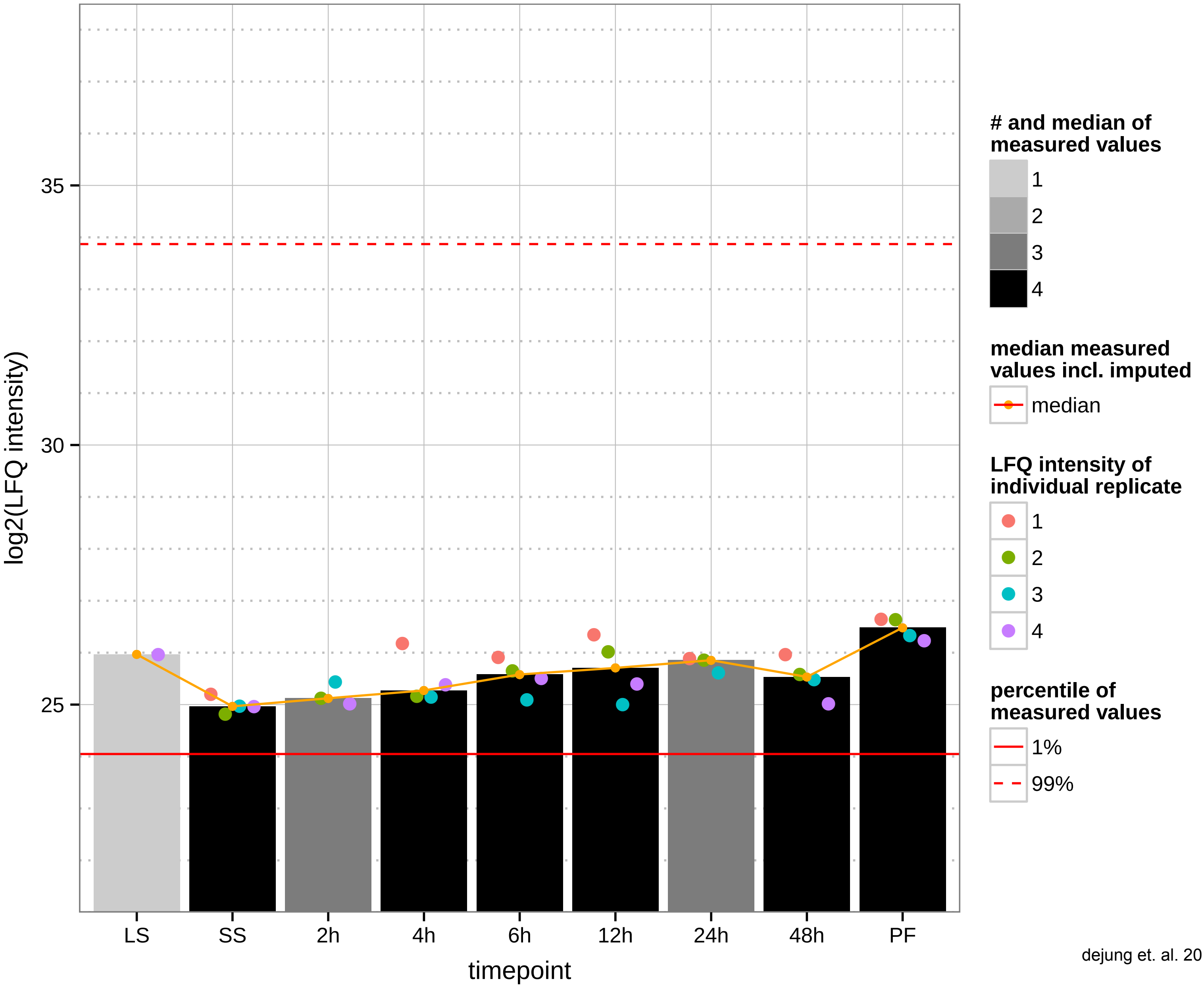
TAX−1
Tb927.9.10370
AGOF: null
AGOC: cilium part
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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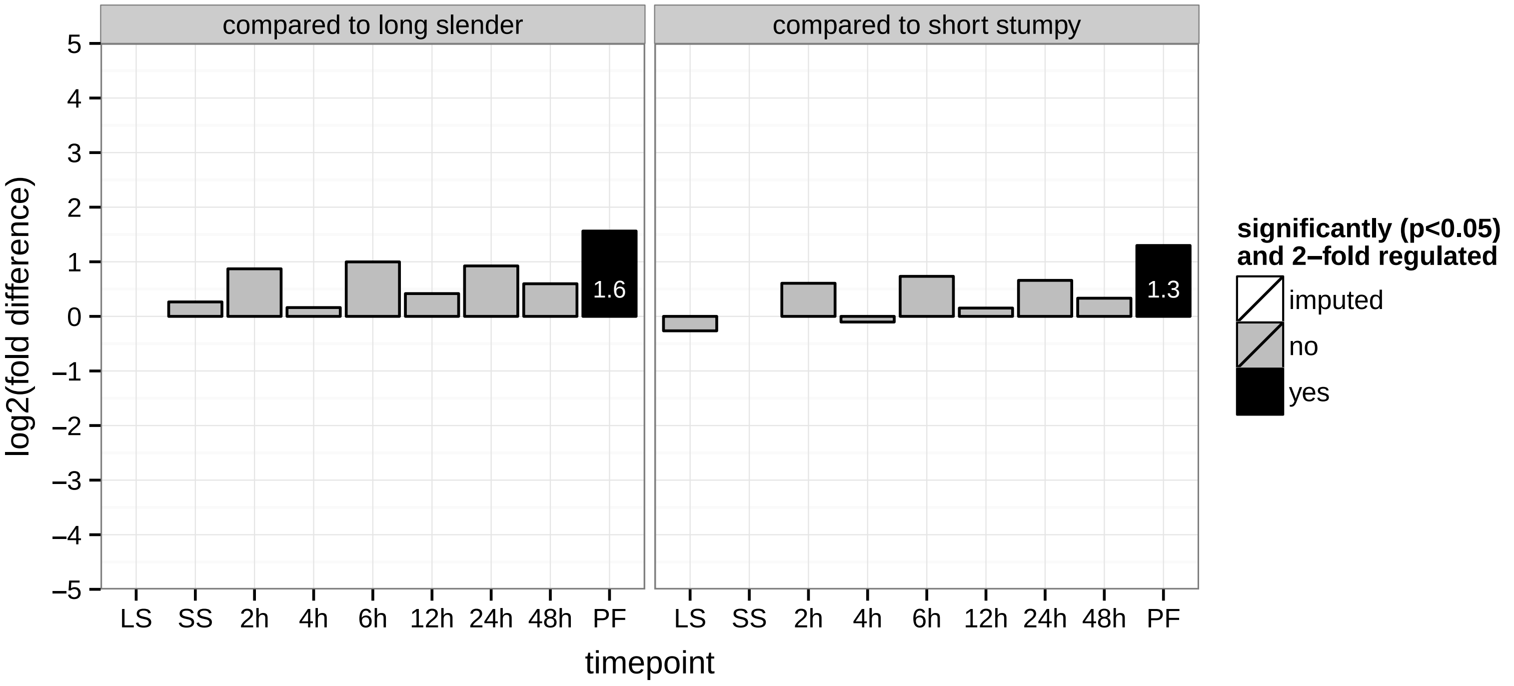
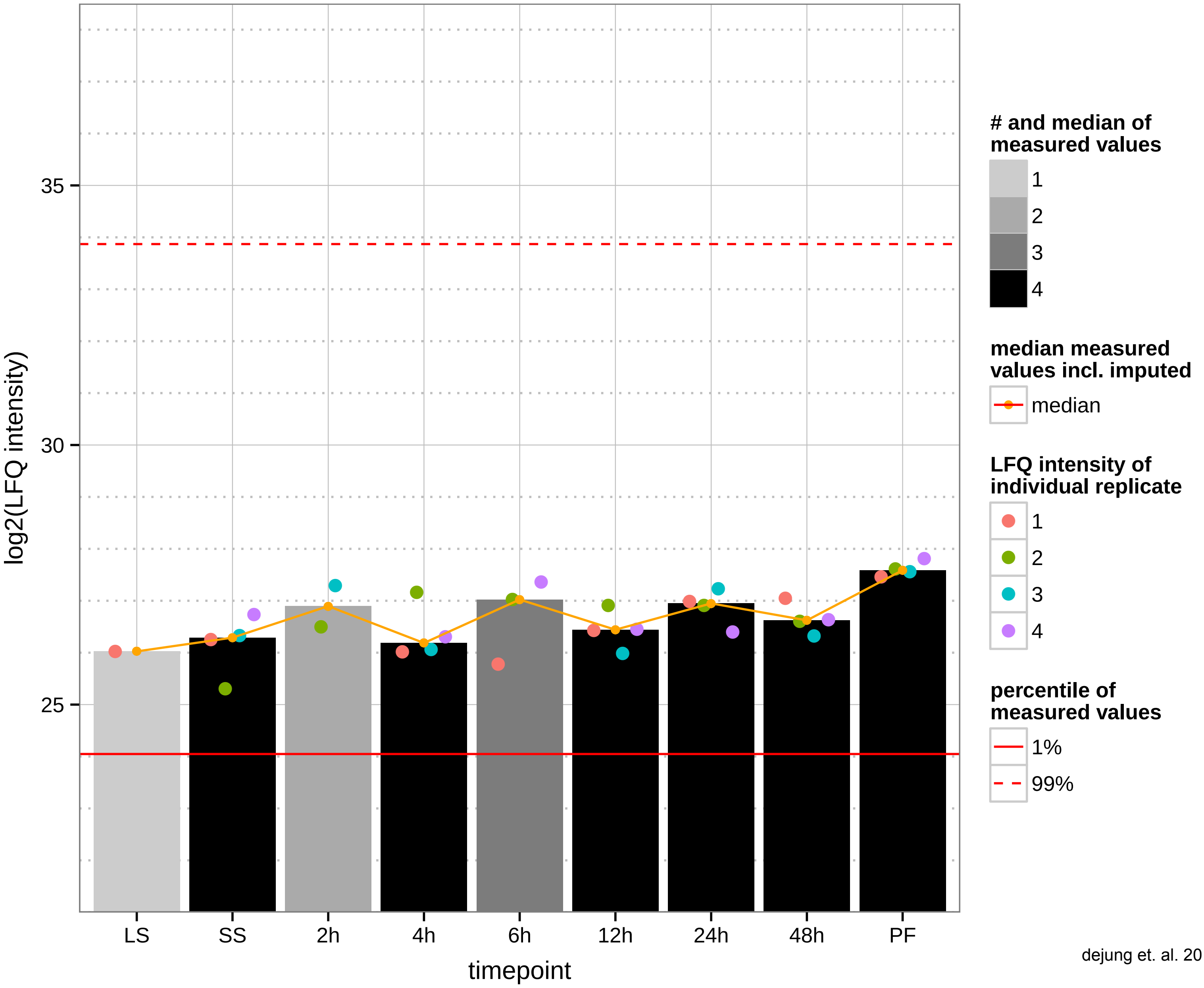
hypothetical protein, conserved
Tb927.9.10830
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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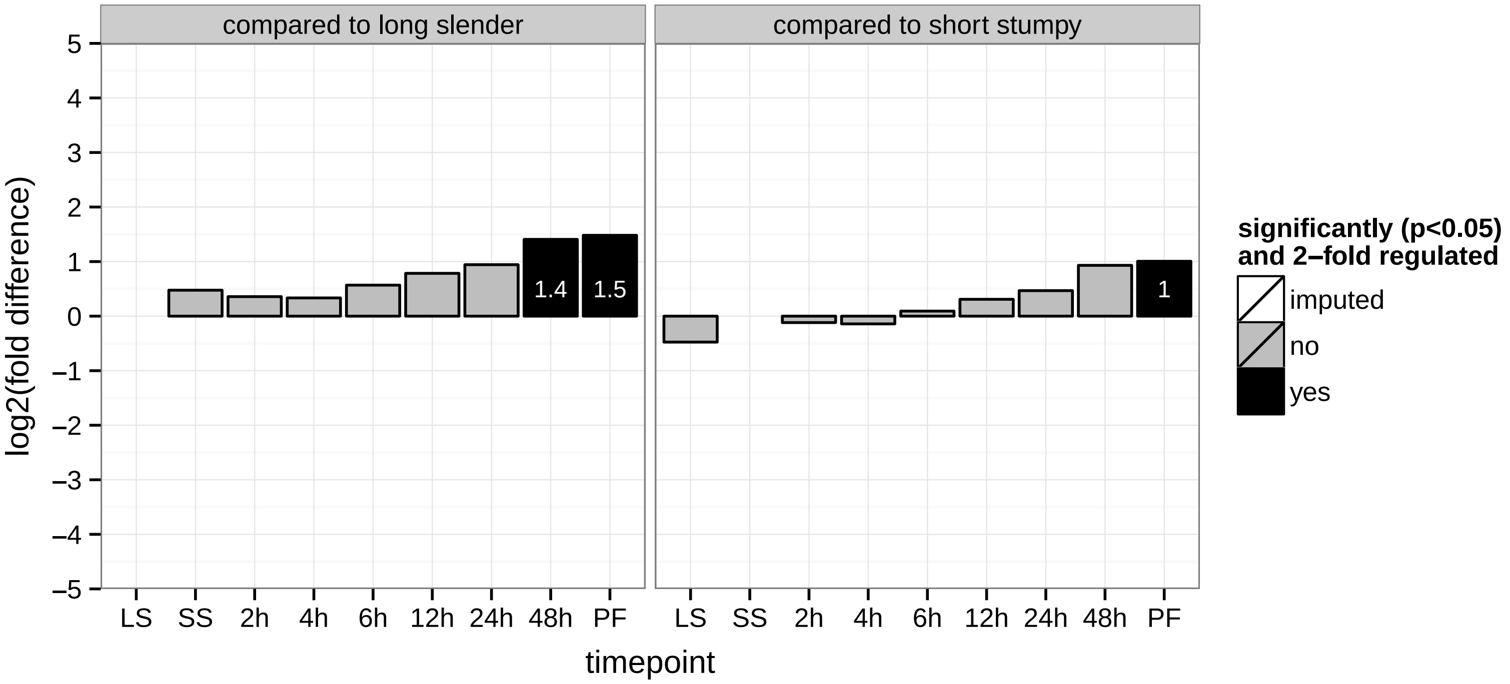
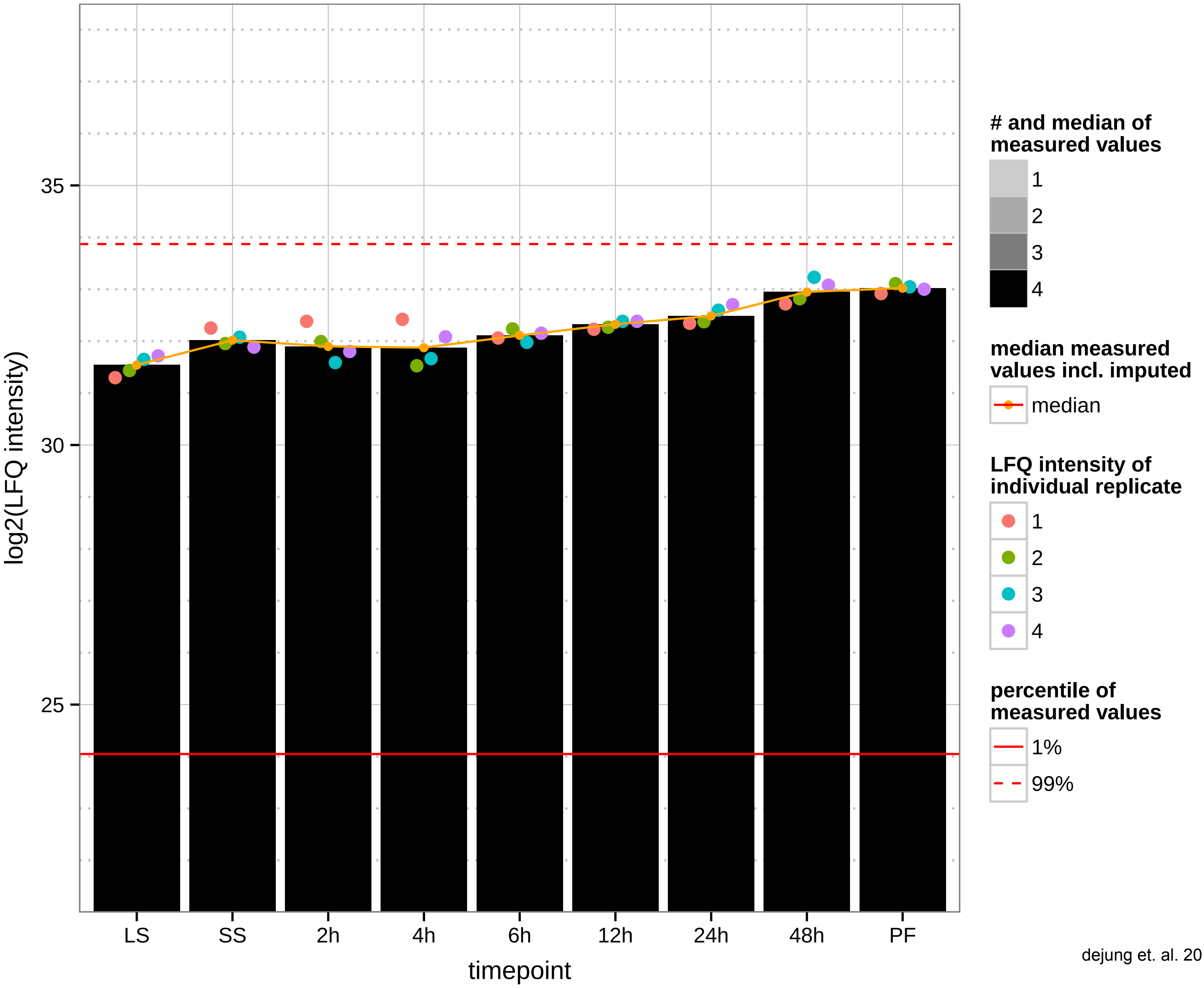
T−complex protein 1, eta subunit, putative, t− complex protein 1 (eta subunit), putative (TCP−1−eta)
Tb927.9.11270
AGOF: ATP binding, unfolded protein binding
AGOC: chaperonin−containing T−complex
AGOP: protein folding, regulation of cell cycle
PGOF: ATP binding, unfolded protein binding
PGOC: null
PGOP: cellular protein metabolic process, protein folding





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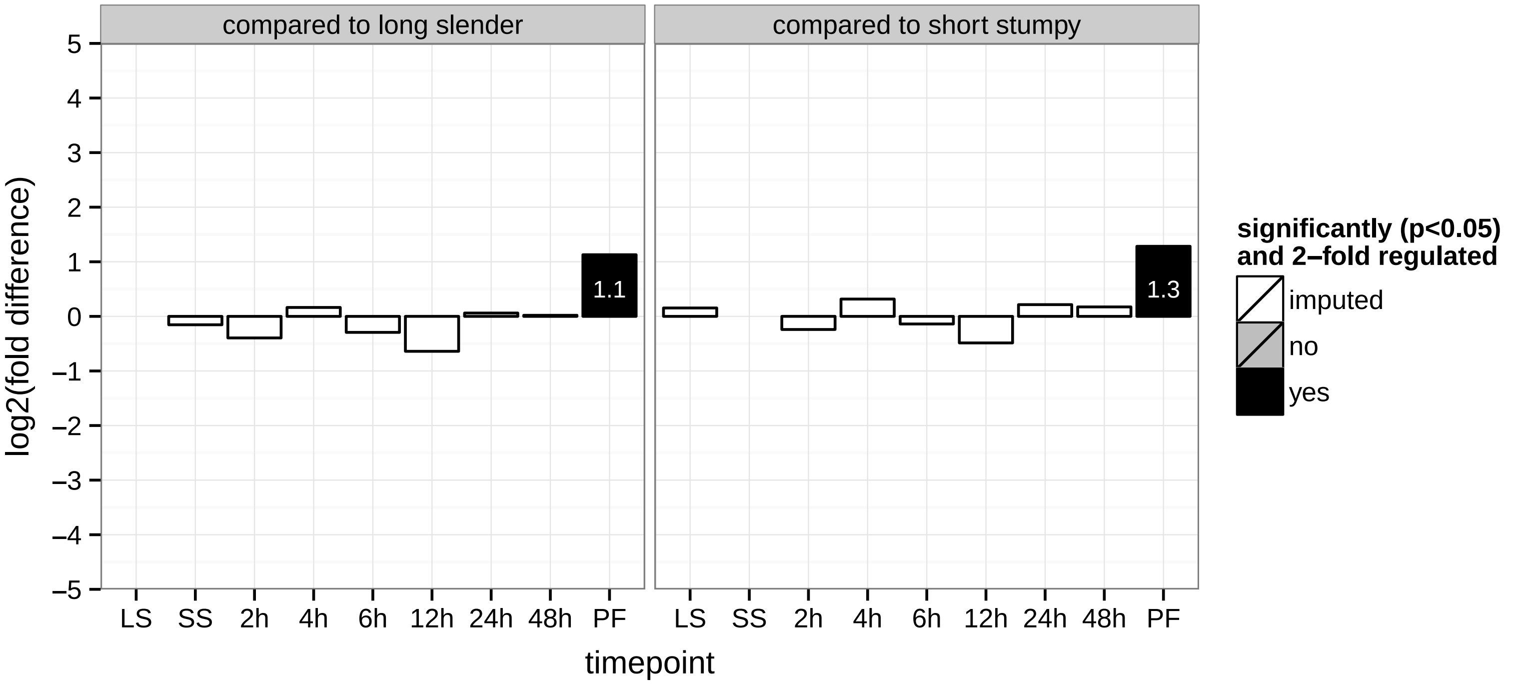
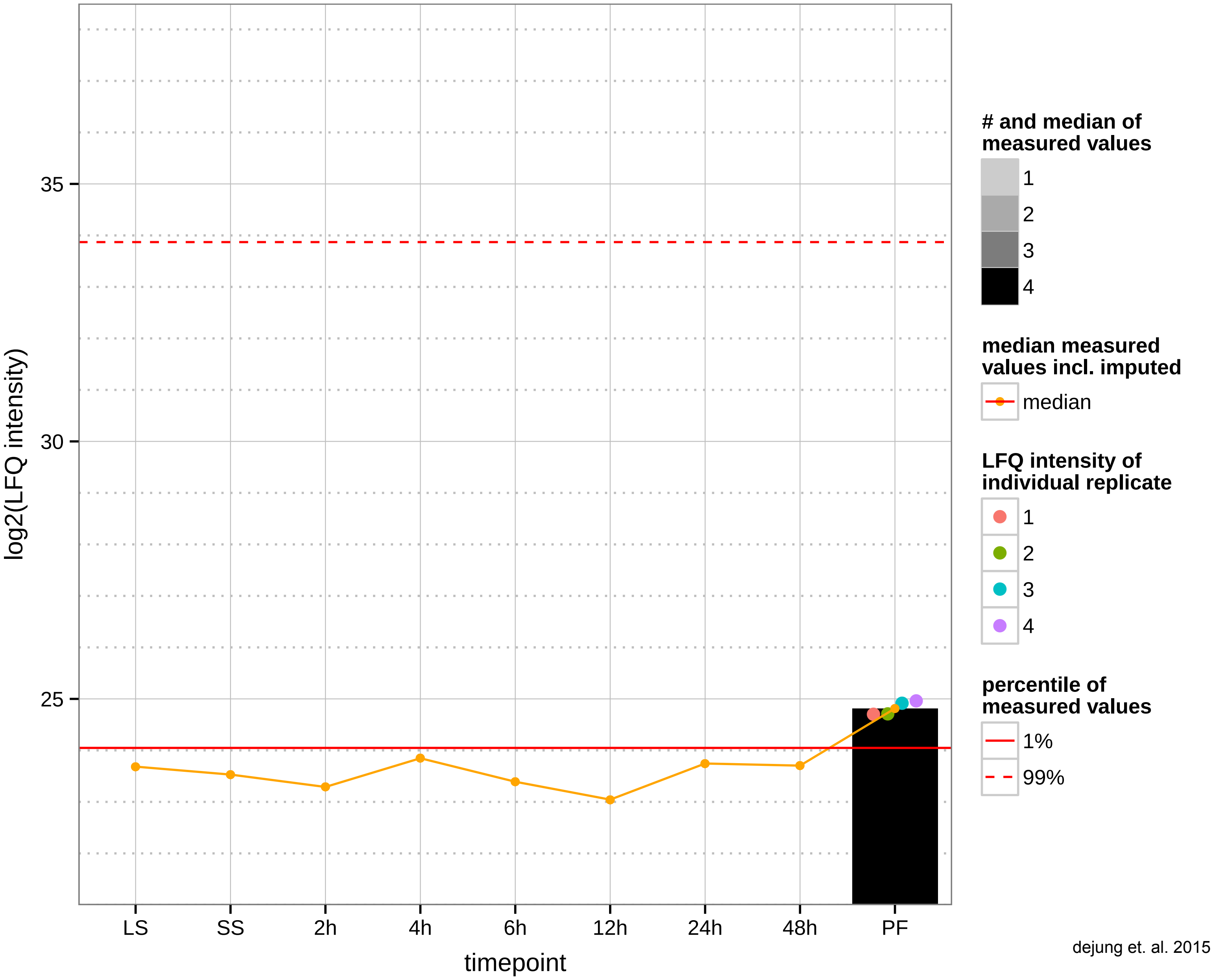
hypothetical protein, conserved
Tb927.9.11500
AGOF: ubiquitin protein ligase binding
AGOC: cullin−RING ubiquitin ligase complex
AGOP: ubiquitin−dependent protein catabolic process
PGOF: ubiquitin protein ligase binding
PGOC: cullin−RING ubiquitin ligase complex
PGOP: ubiquitin−dependent protein catabolic process





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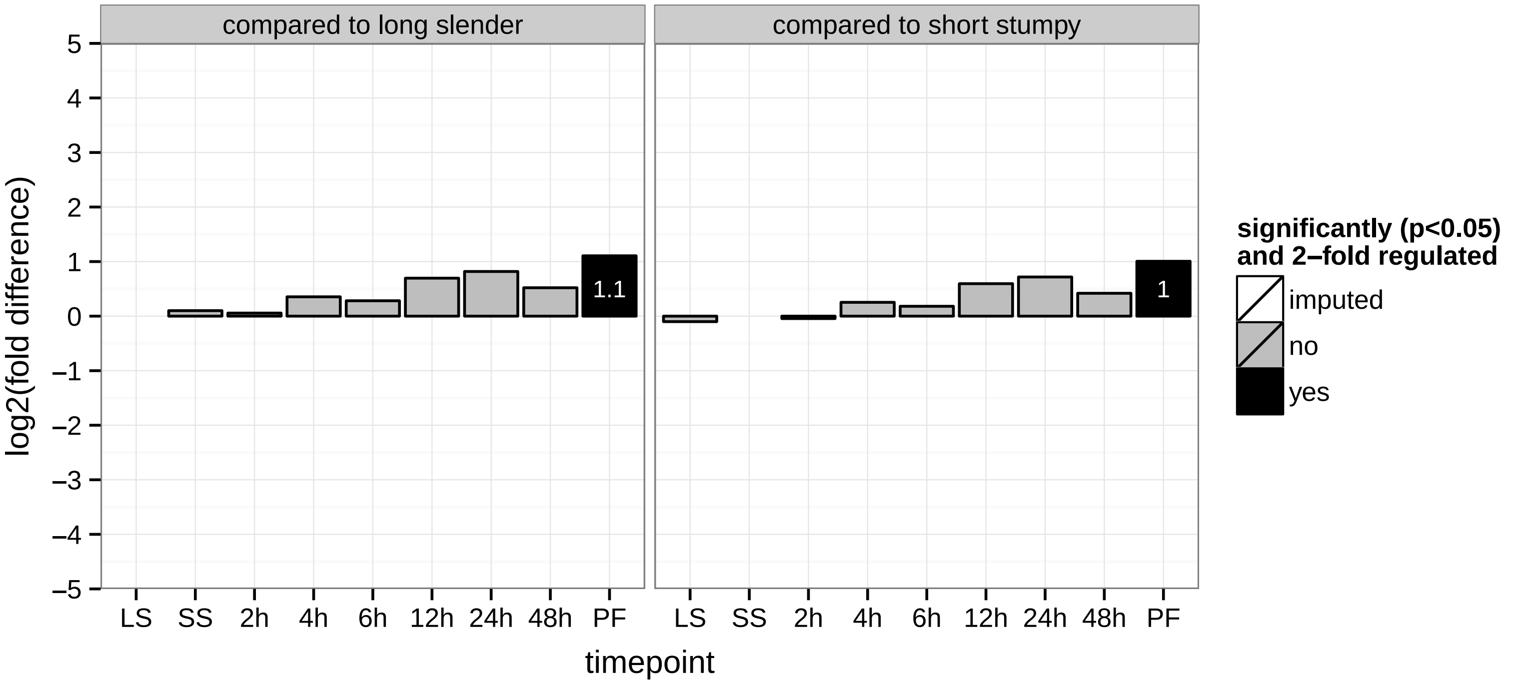
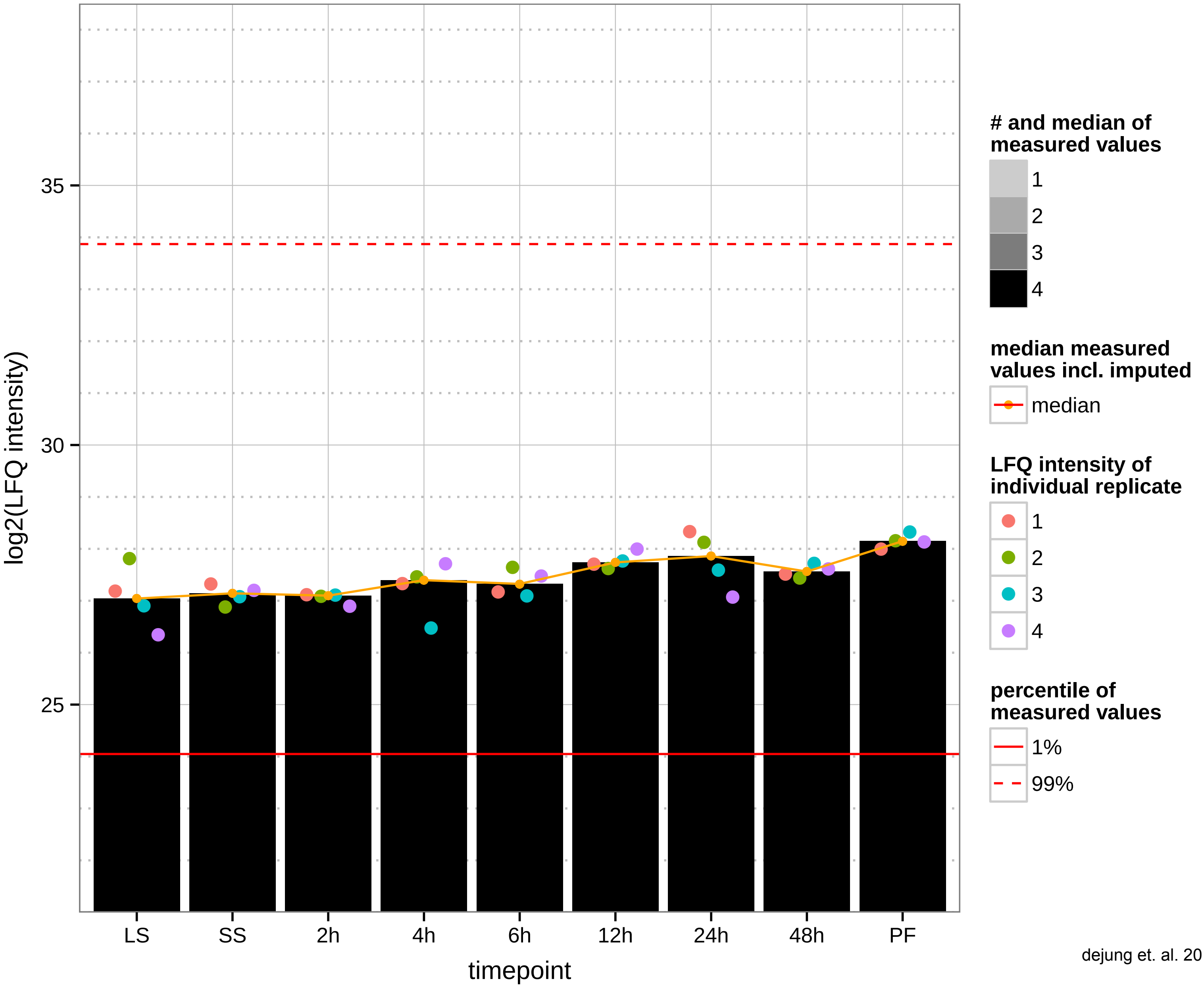
Pre–rRNA–processing protein PNO1, putative (PNO1)
Tb927.9.11840
AGOF: RNA binding
AGOC: nucleolus
AGOP: null
PGOF: RNA binding
PGOC: null
PGOP: null





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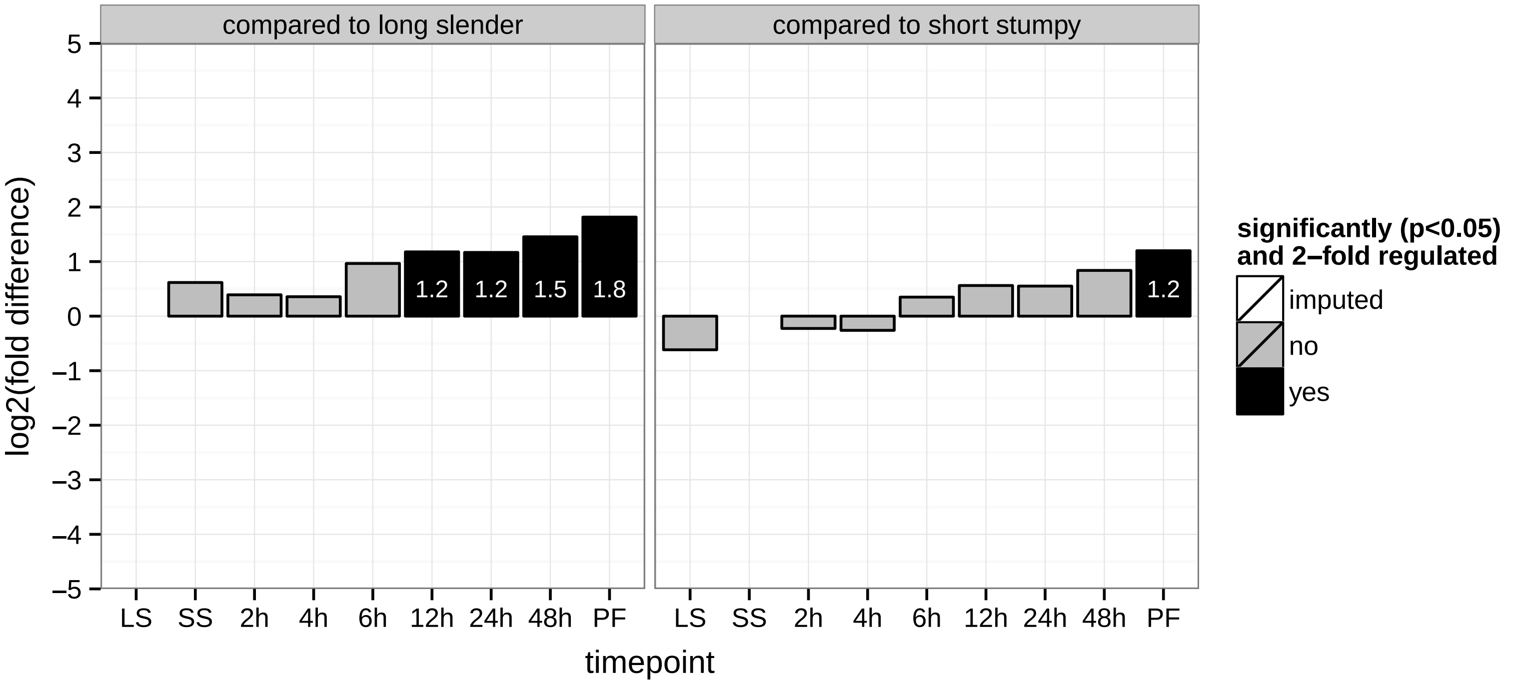
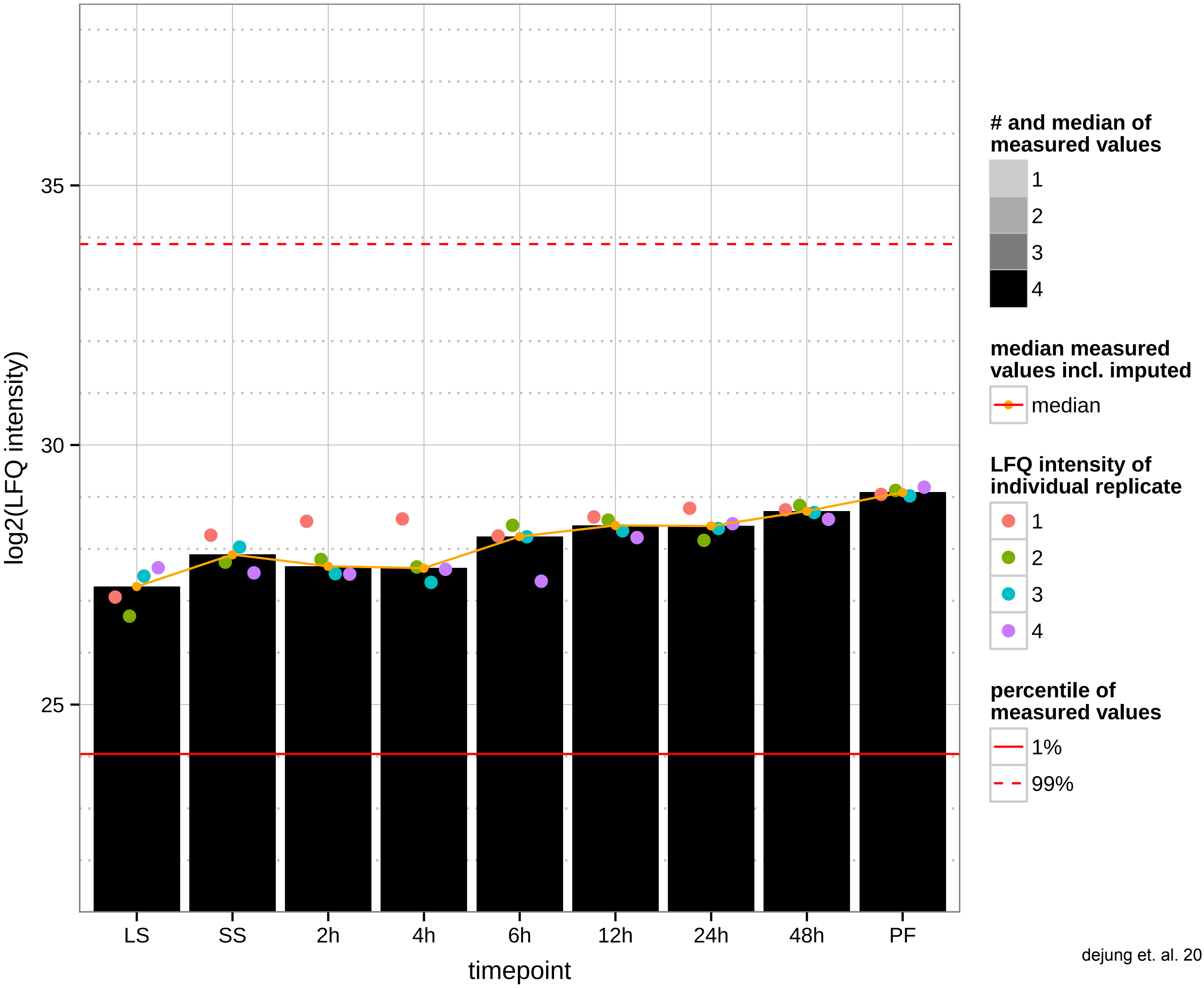
hypothetical protein, conserved
Tb927.9.12070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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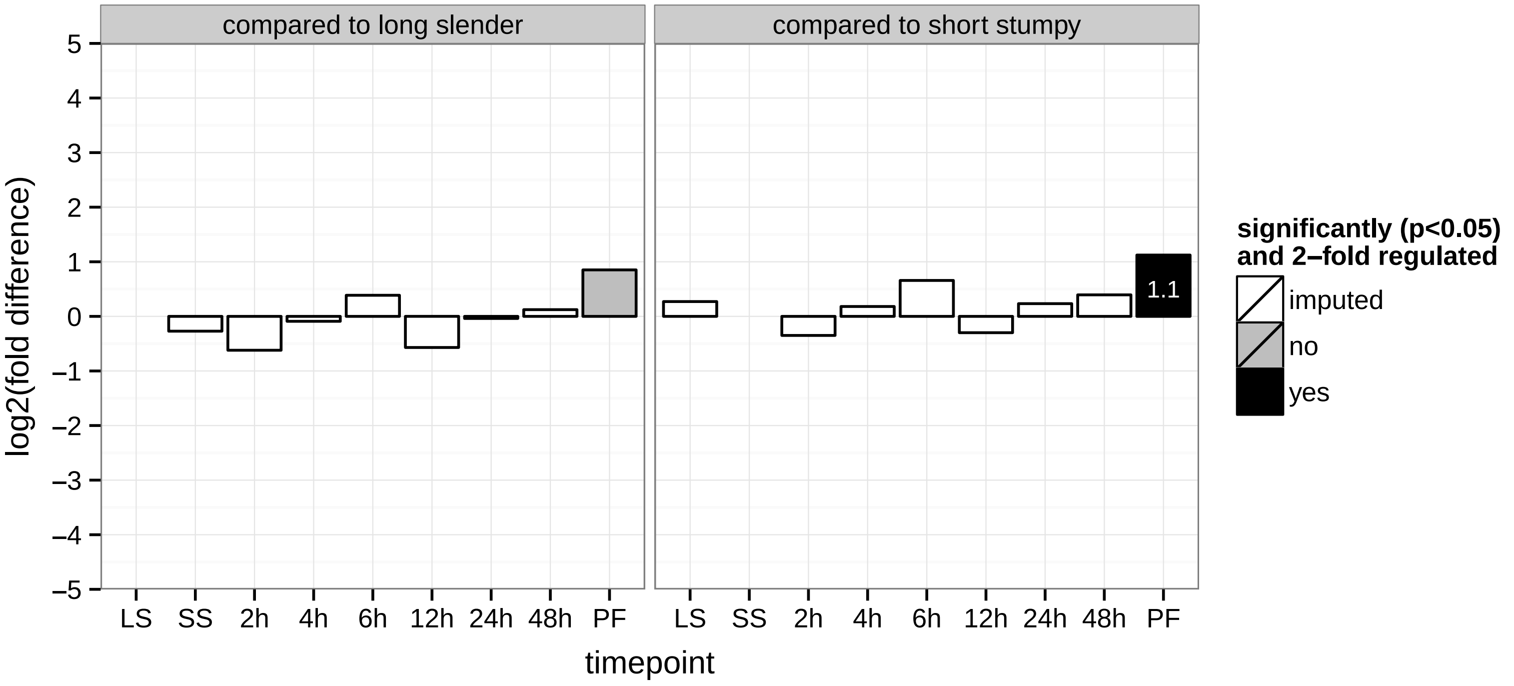
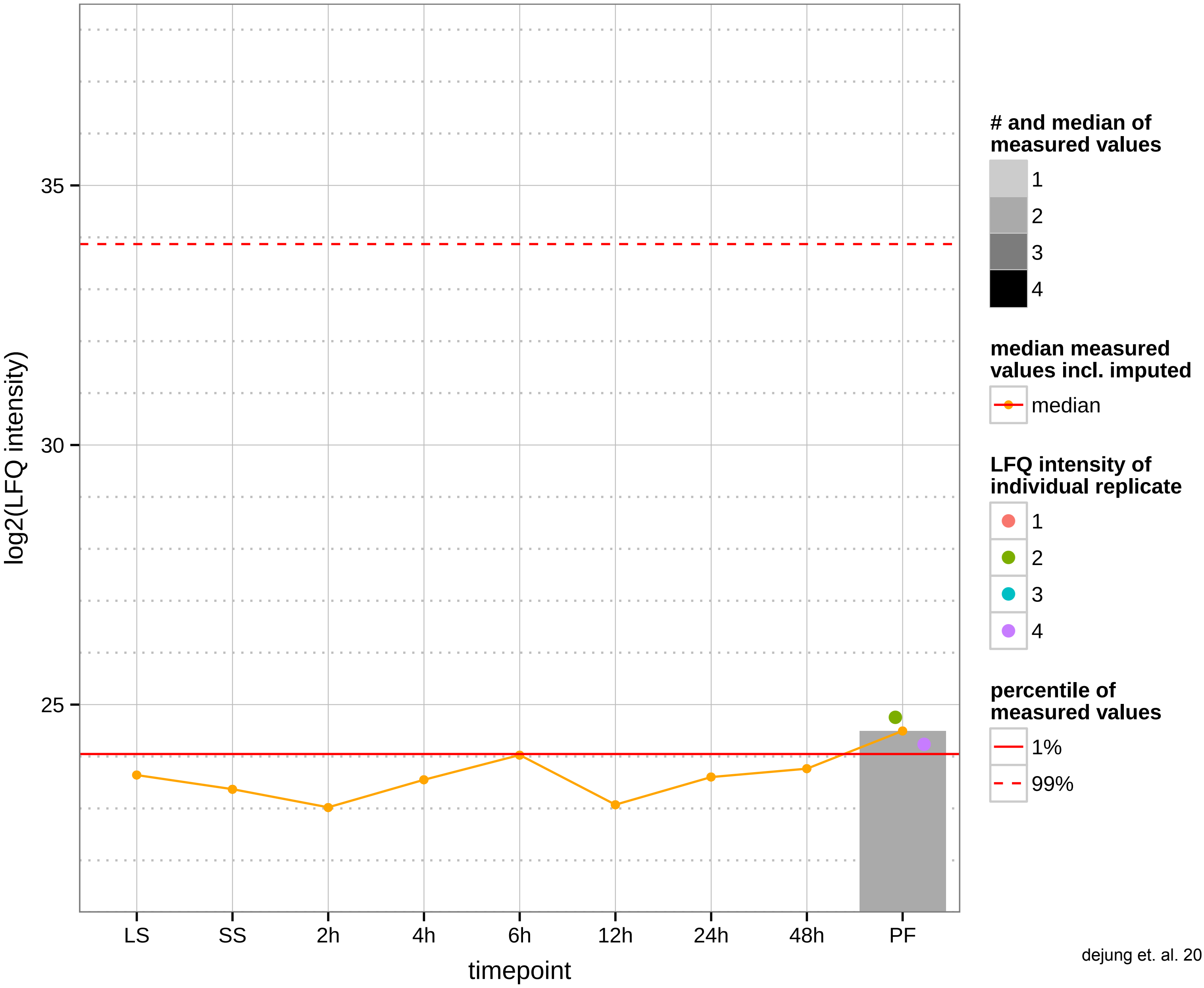
class I transcription factor A, subunit 2 (CITFA−2)
Tb927.9.12450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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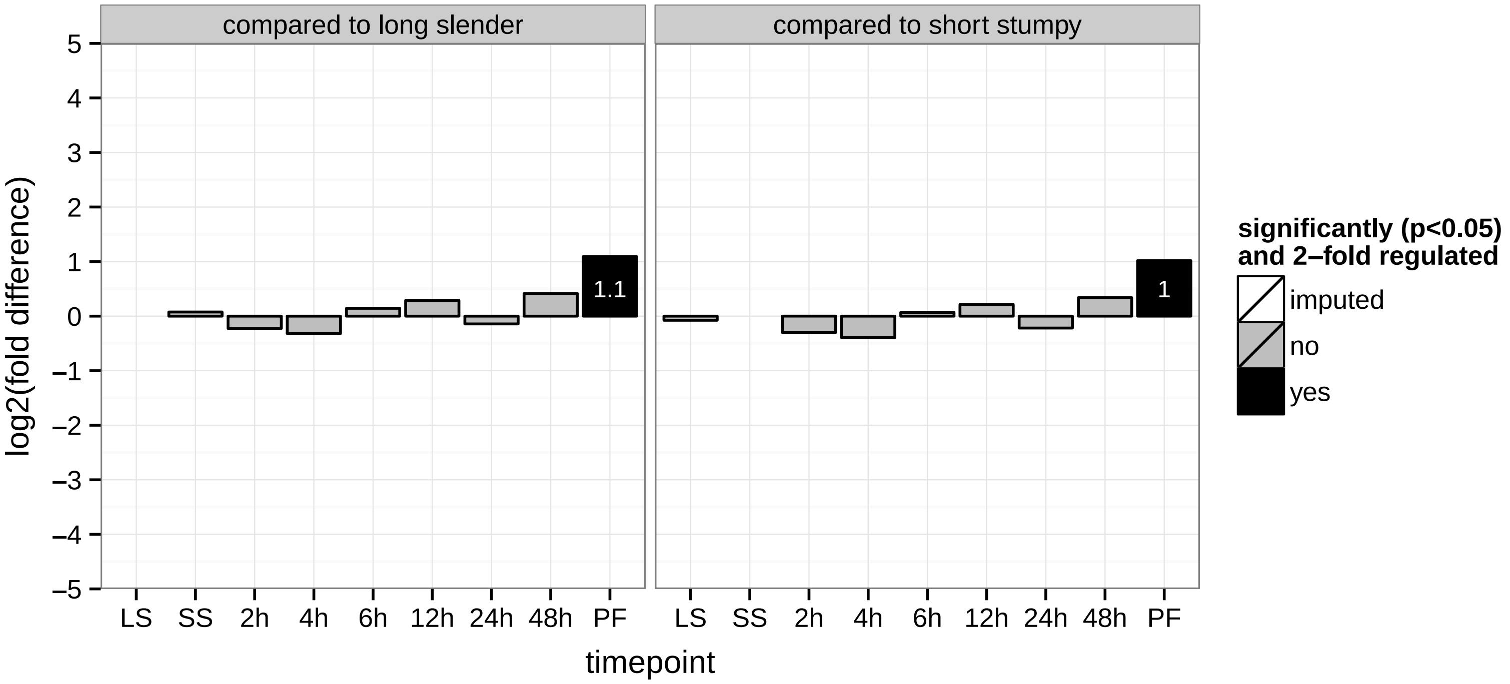
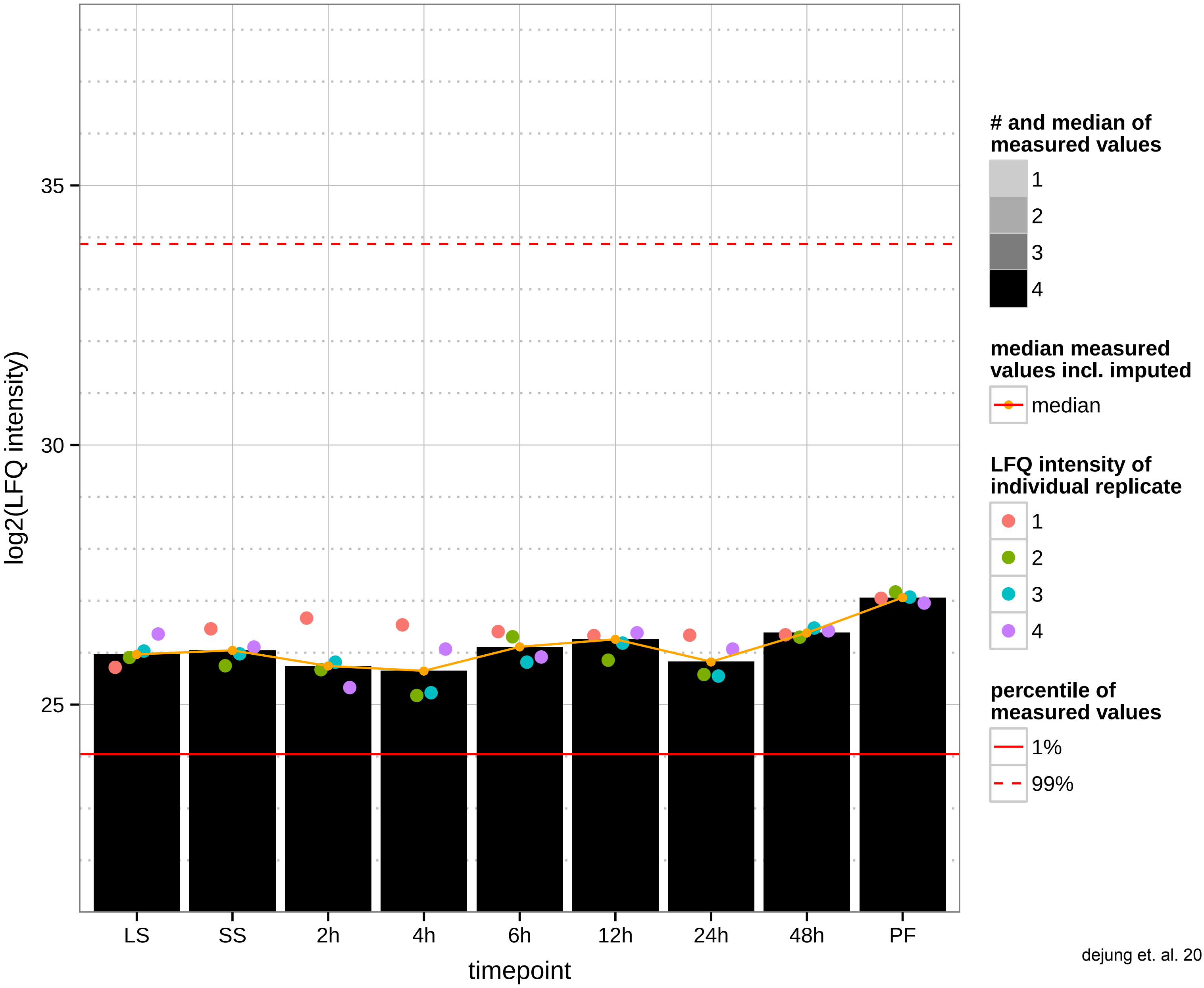
hypothetical protein, conserved
Tb927.9.12830
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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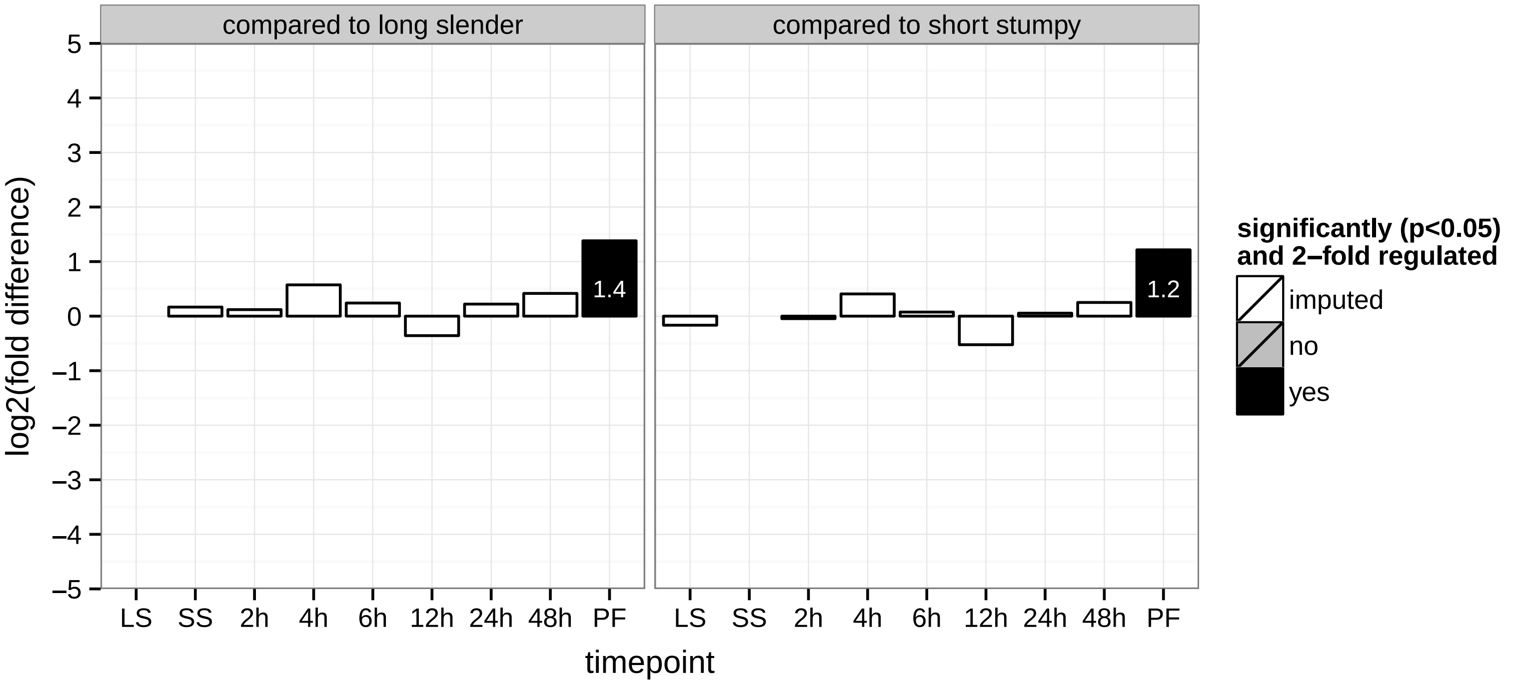
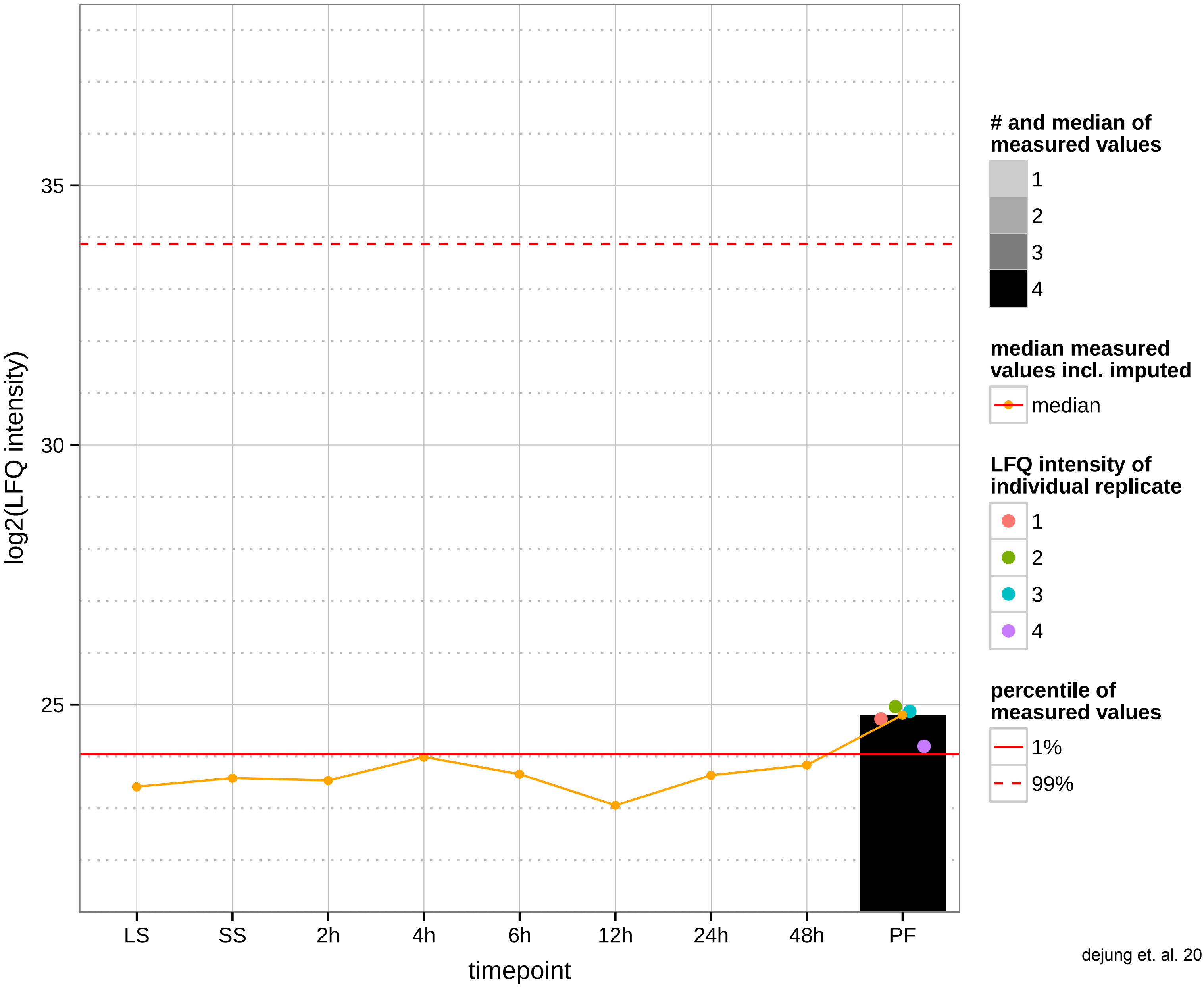
hypothetical protein, conserved
Tb927.9.12980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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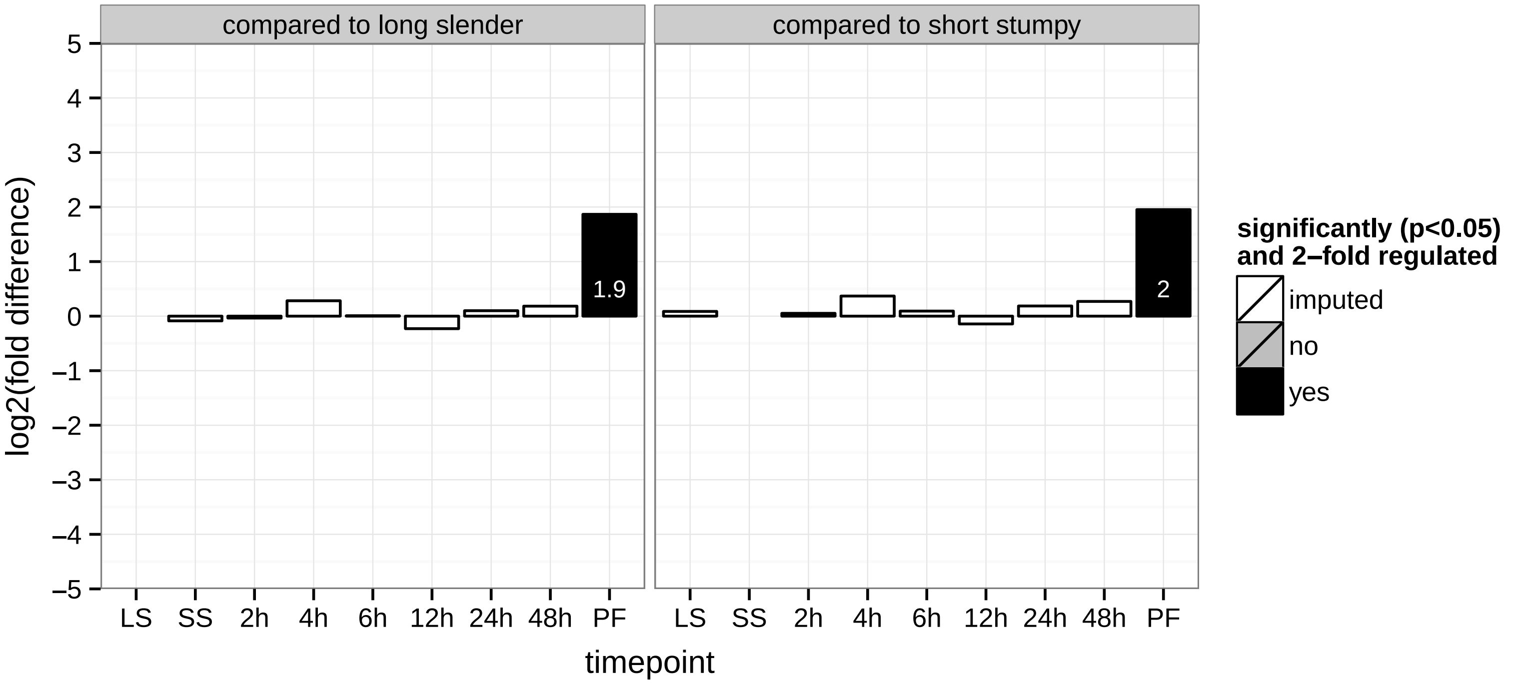
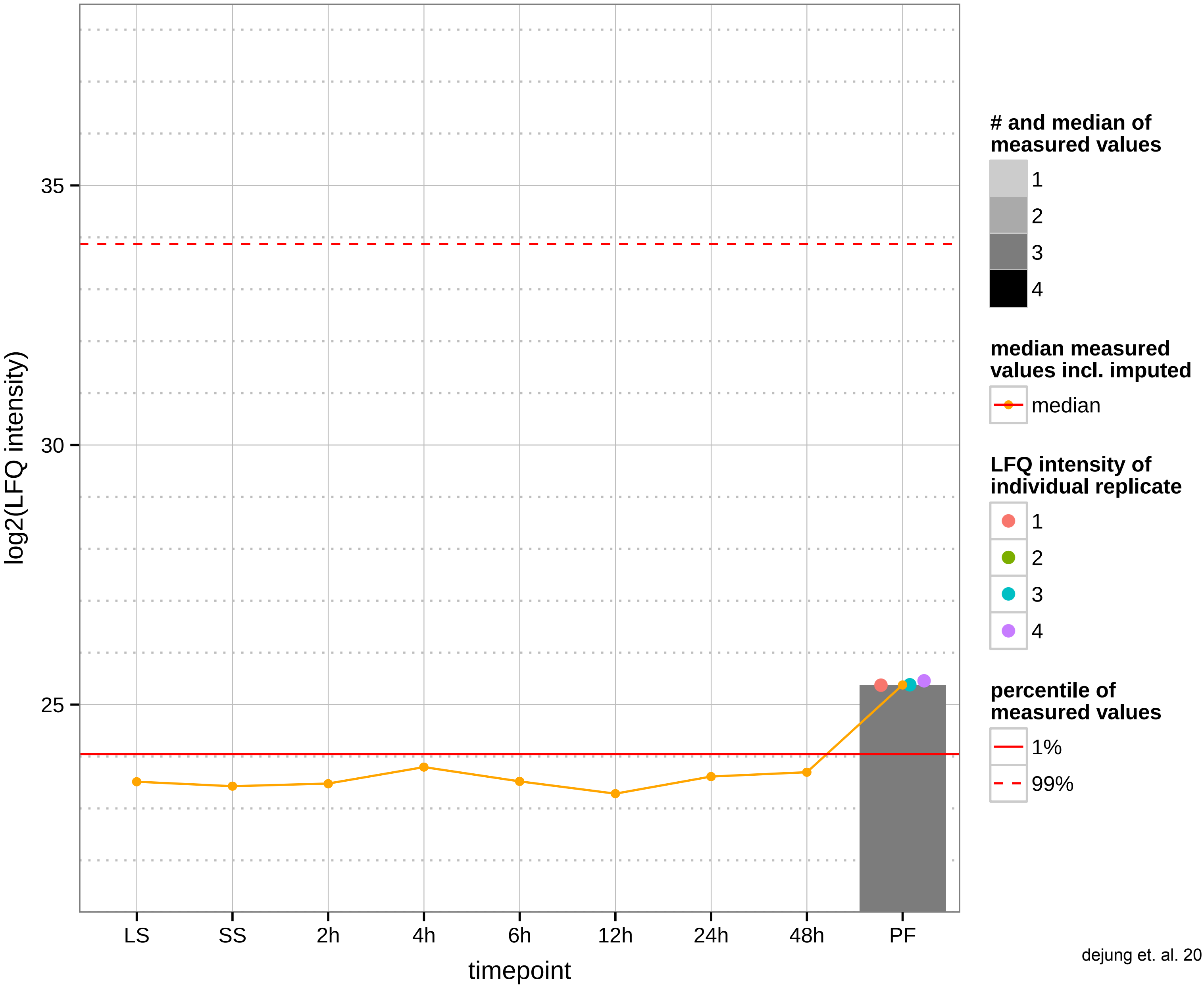
hypothetical protein, conserved
Tb927.9.13350
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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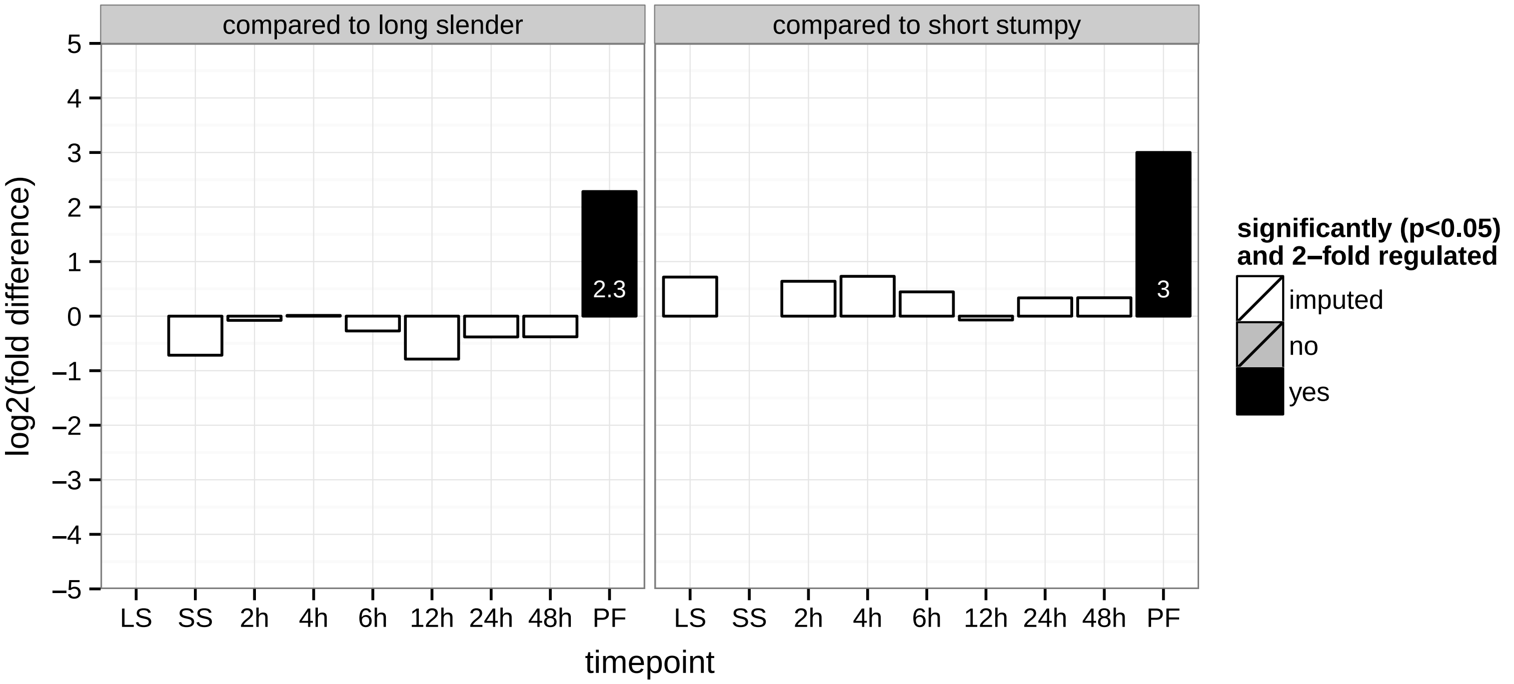
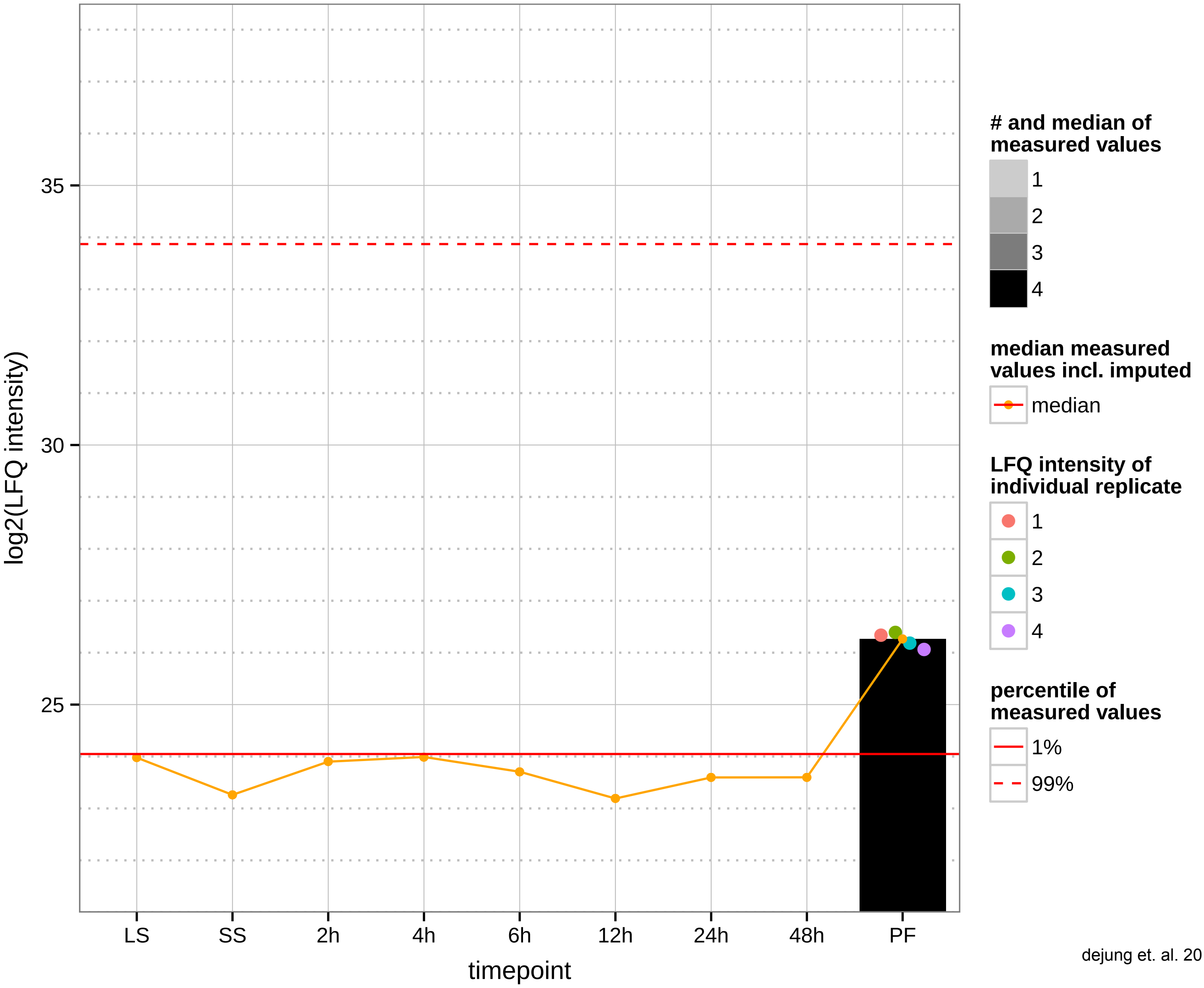
Myosin–like protein, Nucleoporin (TbMlp–2)
Tb927.9.1340
AGOF: null
AGOC: intracellular, nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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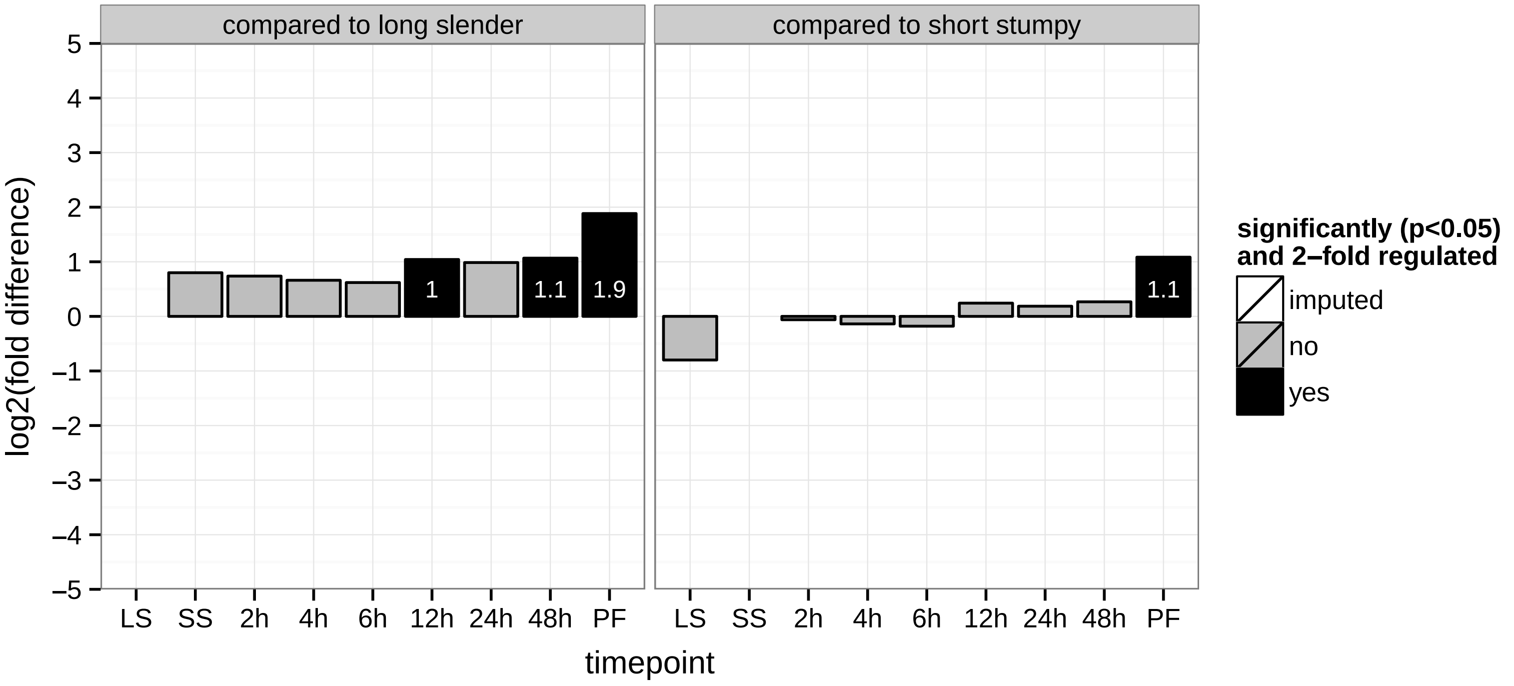
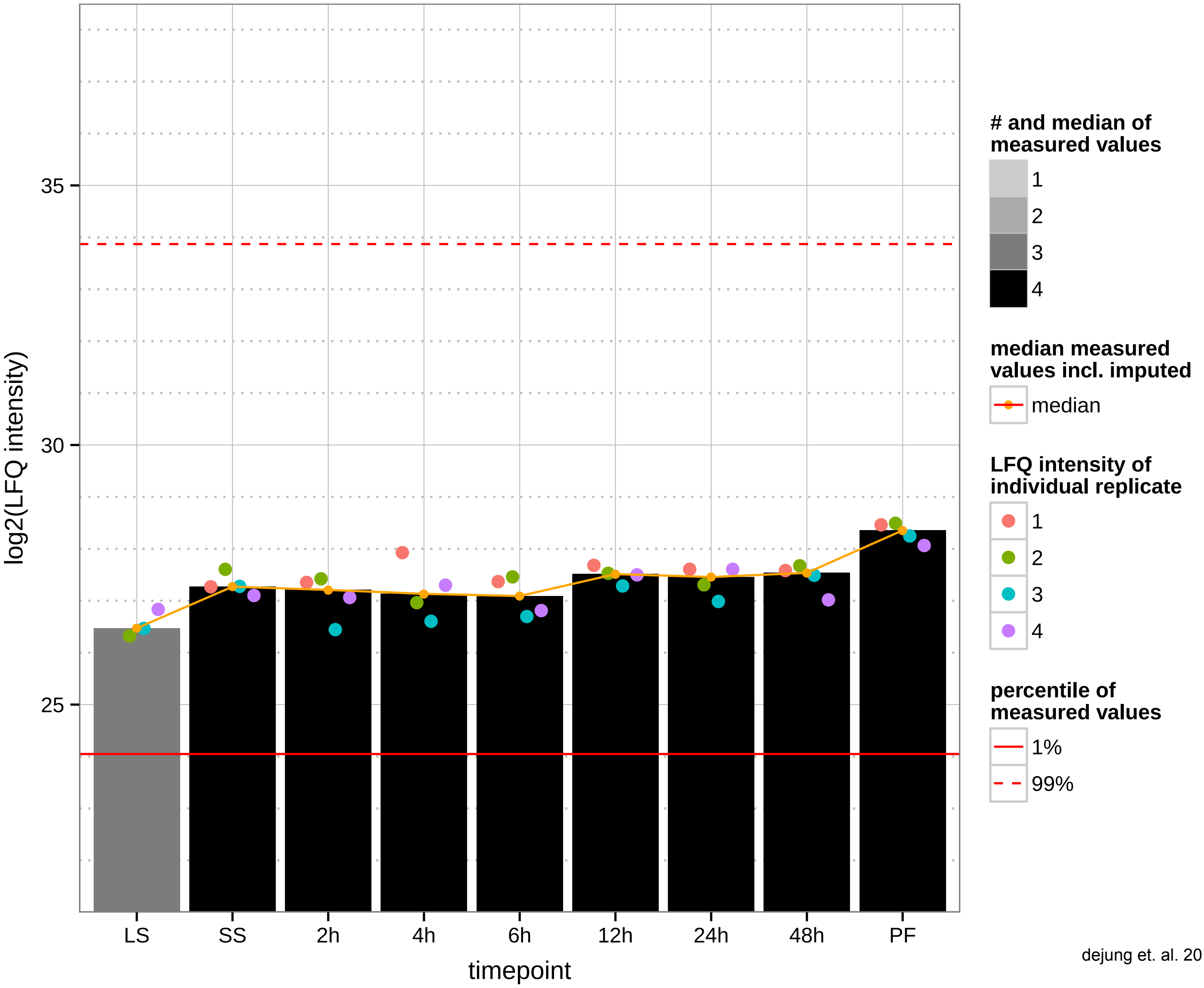
hypothetical protein, conserved
Tb927.9.13970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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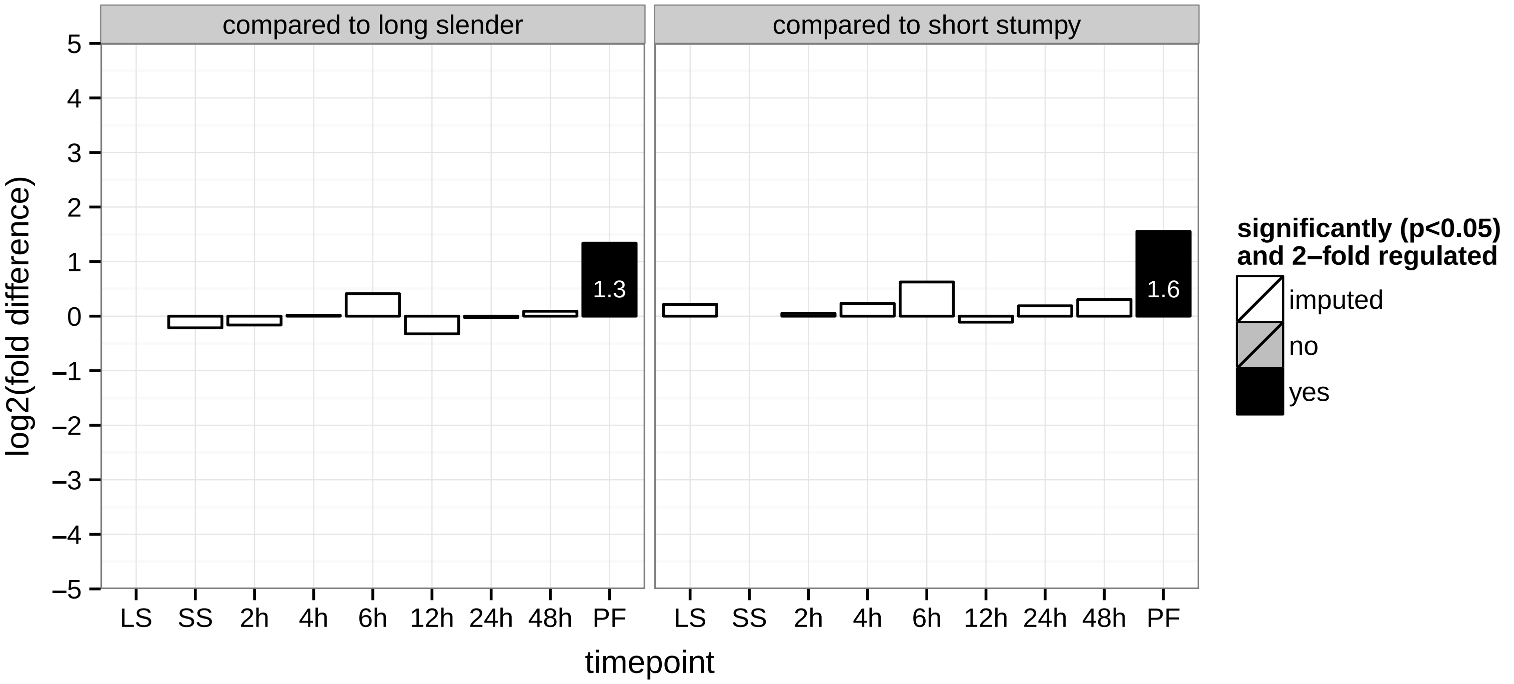
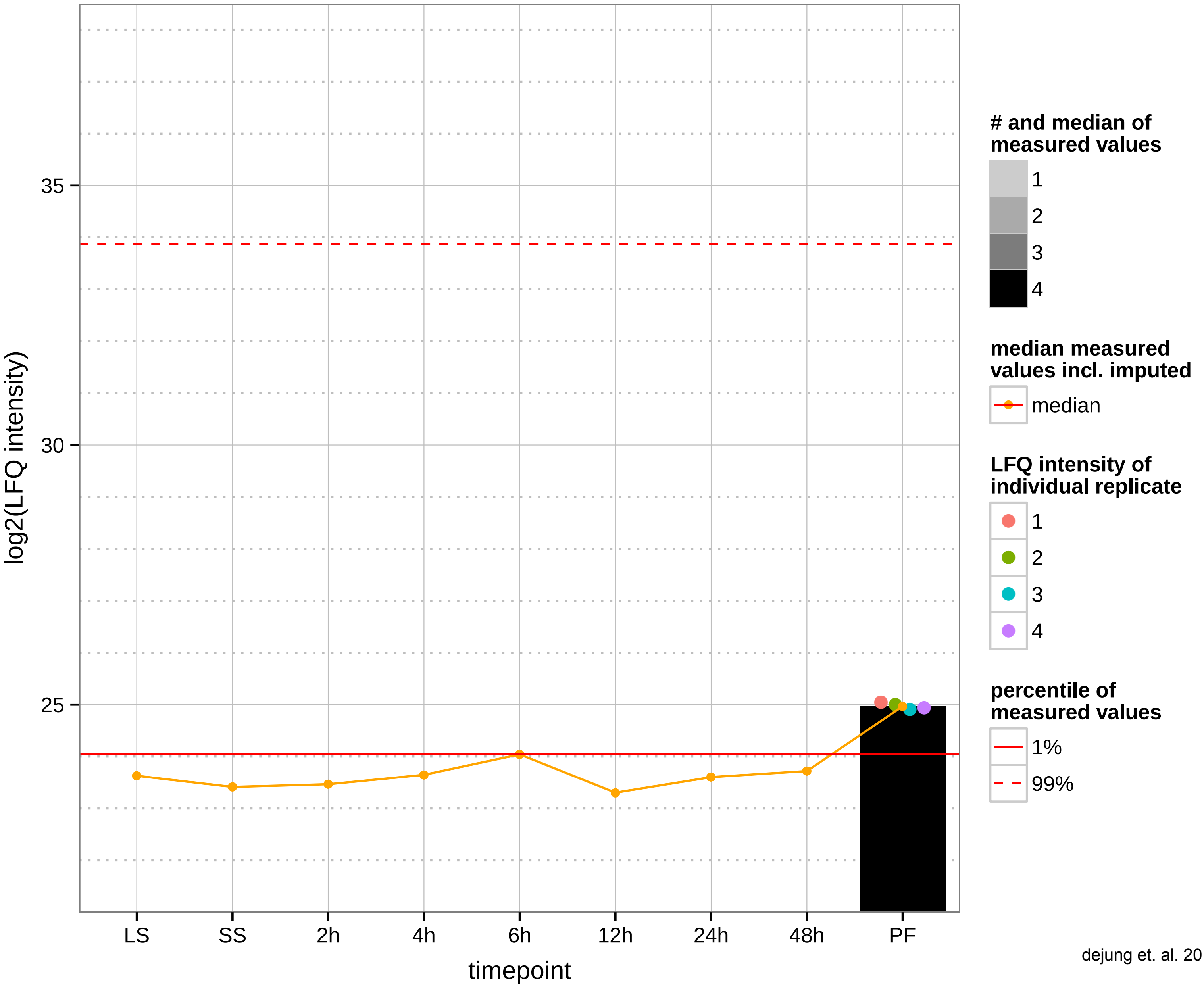
hypothetical protein, conserved
Tb927.9.1410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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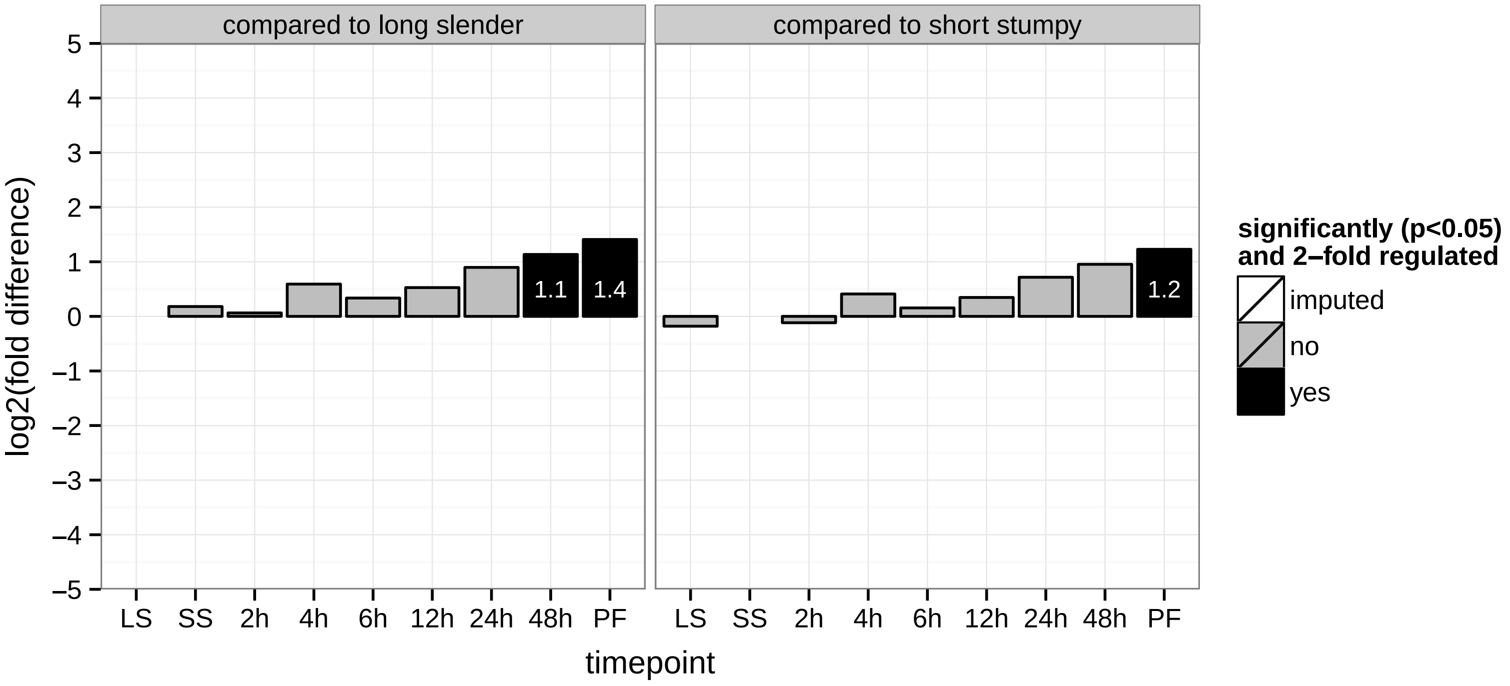
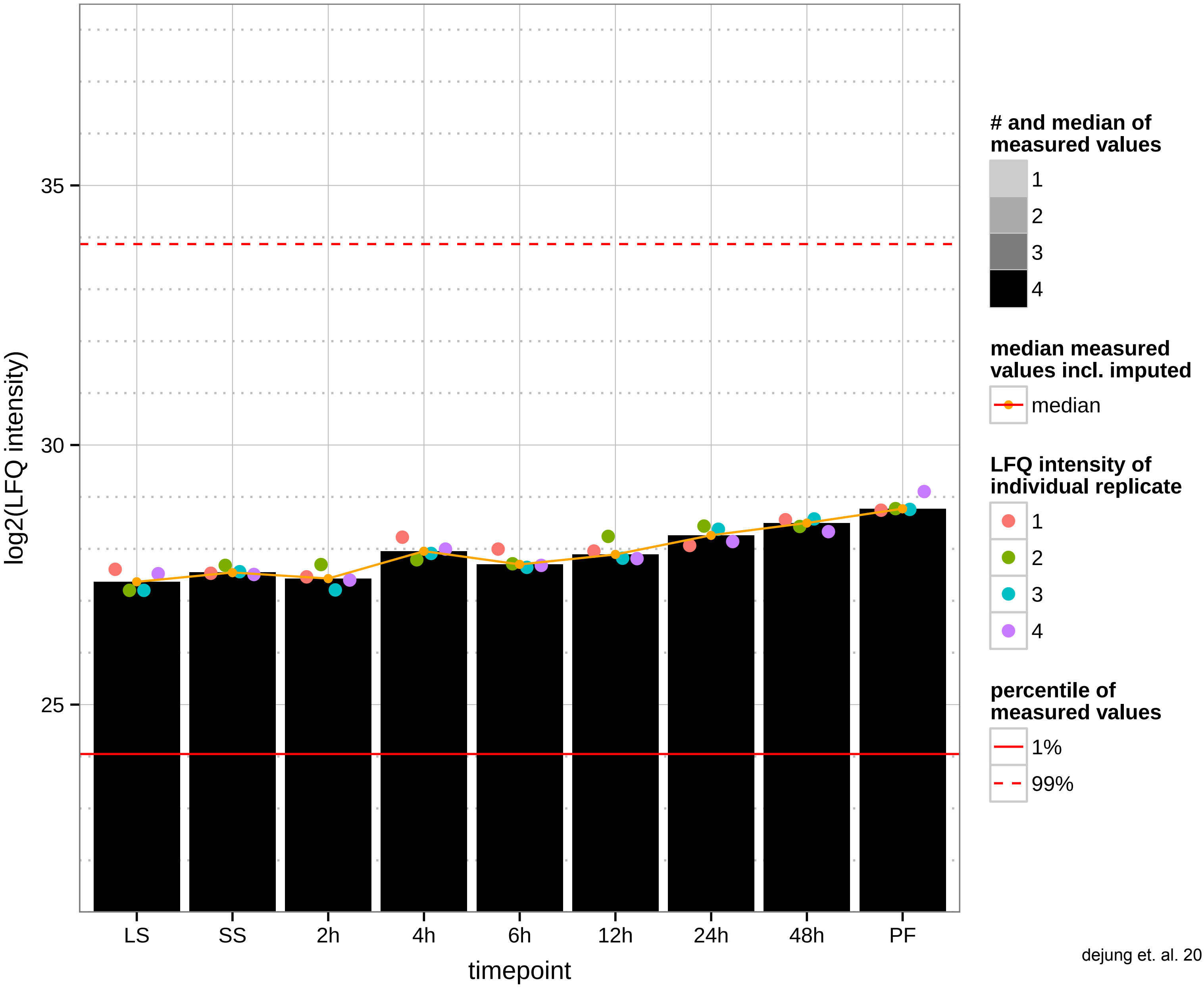
hypothetical protein, conserved
Tb927.9.15000
AGOF: null
AGOC: cytoplasm, nucleus
AGOP: null
PGOF: null
PGOC: cytoplasm, nucleus
PGOP: null





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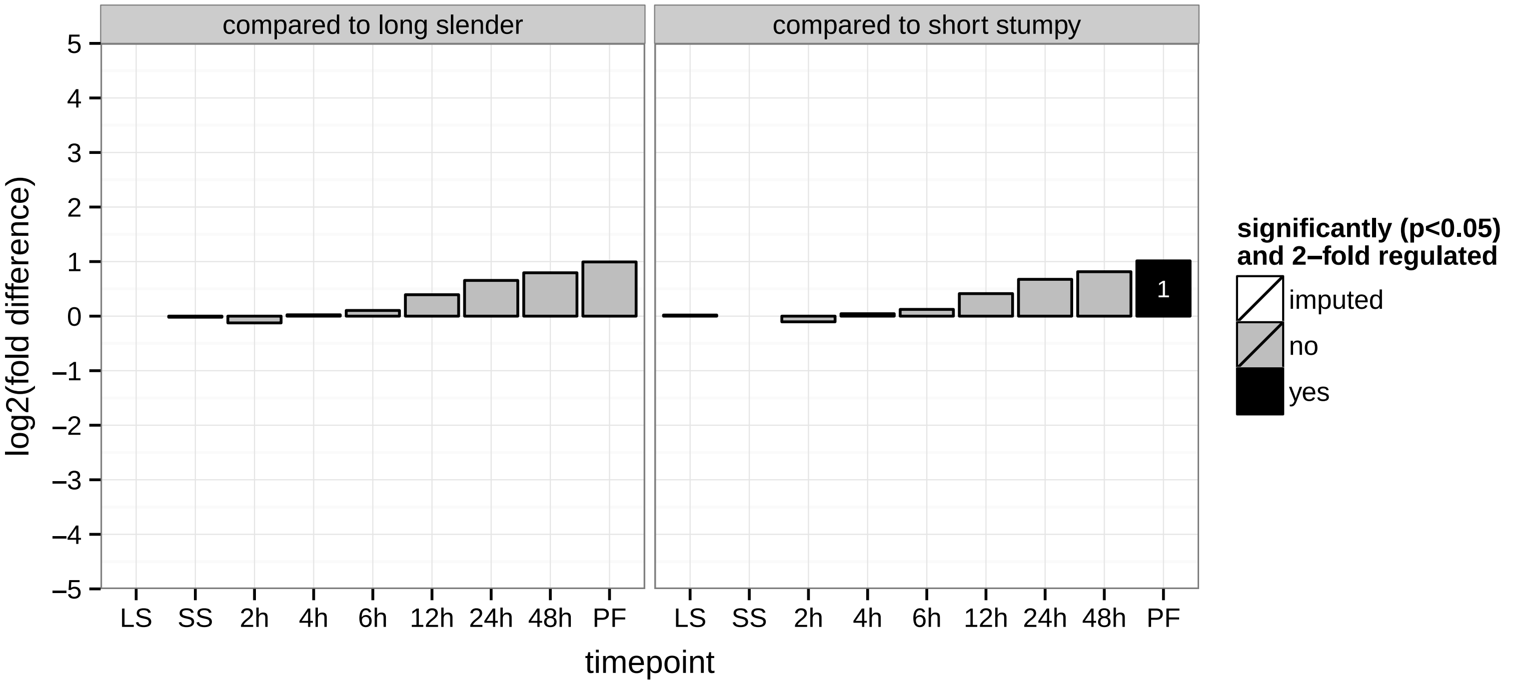
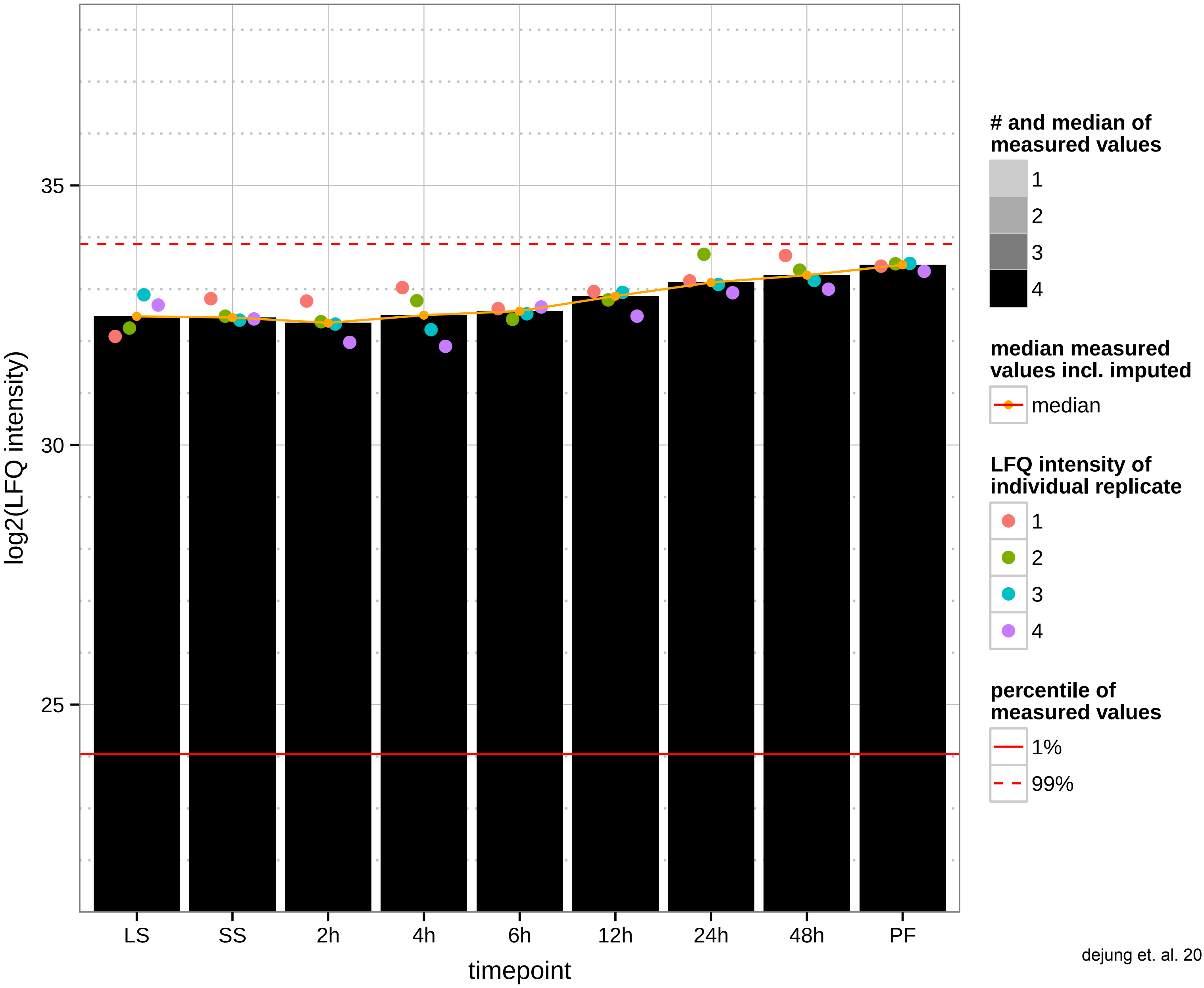
unspecified product
Tb927.9.15150;Tb927.9.15110
AGOF: 5S rRNA binding, structural constituent of ribosome, null
AGOC: intracellular, ribosome, null
AGOP: ribosome assembly, translation, null
PGOF: null, structural constituent of ribosome
PGOC: null, intracellular, ribosome
PGOP: null, translation





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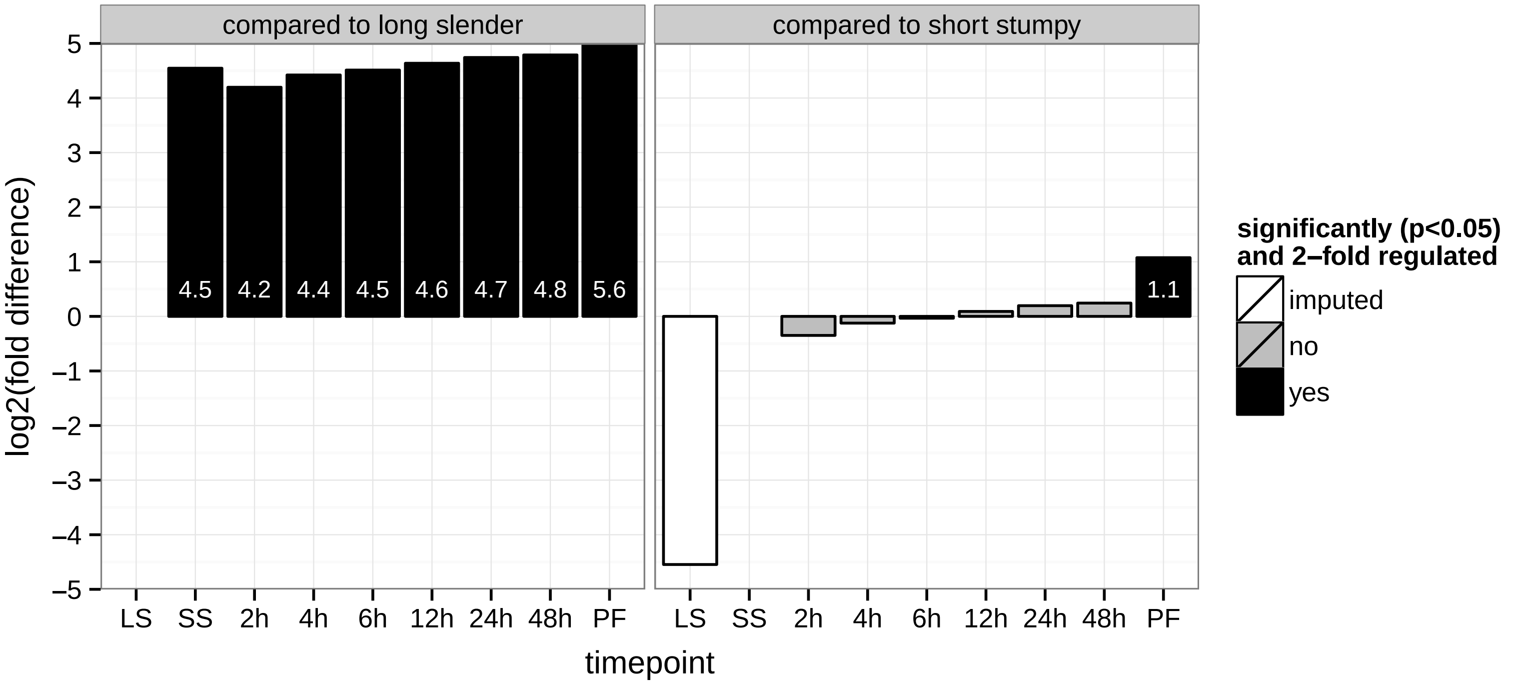
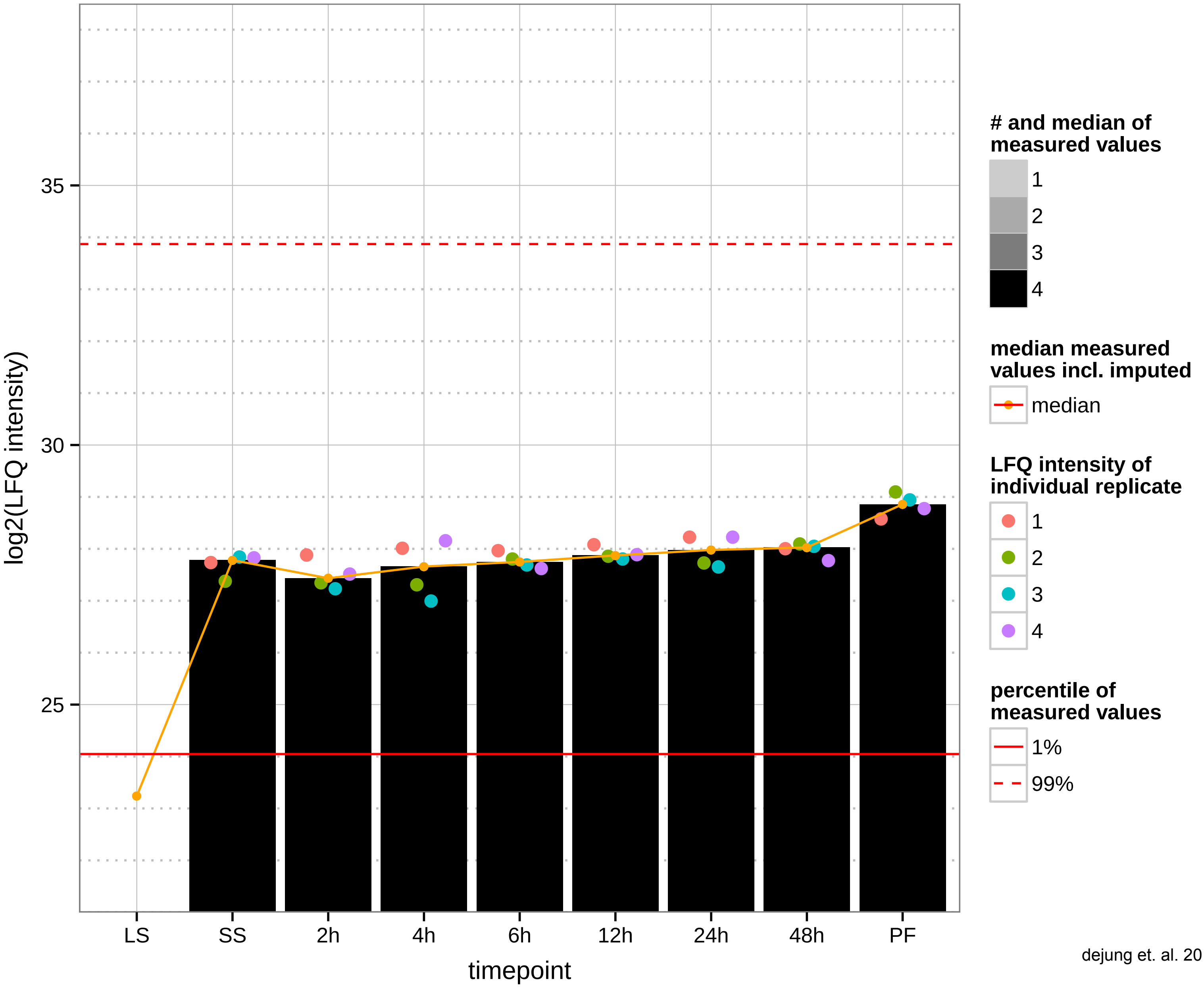
nitrilase, putative
Tb927.9.1960
AGOF: hydrolase activity, acting on carbon–nitrogen (but not peptide) bonds
AGOC: null
AGOP: nitrogen compound metabolic process
PGOF: hydrolase activity, acting on carbon–nitrogen (but not peptide) bonds
PGOC: null
PGOP: nitrogen compound metabolic process





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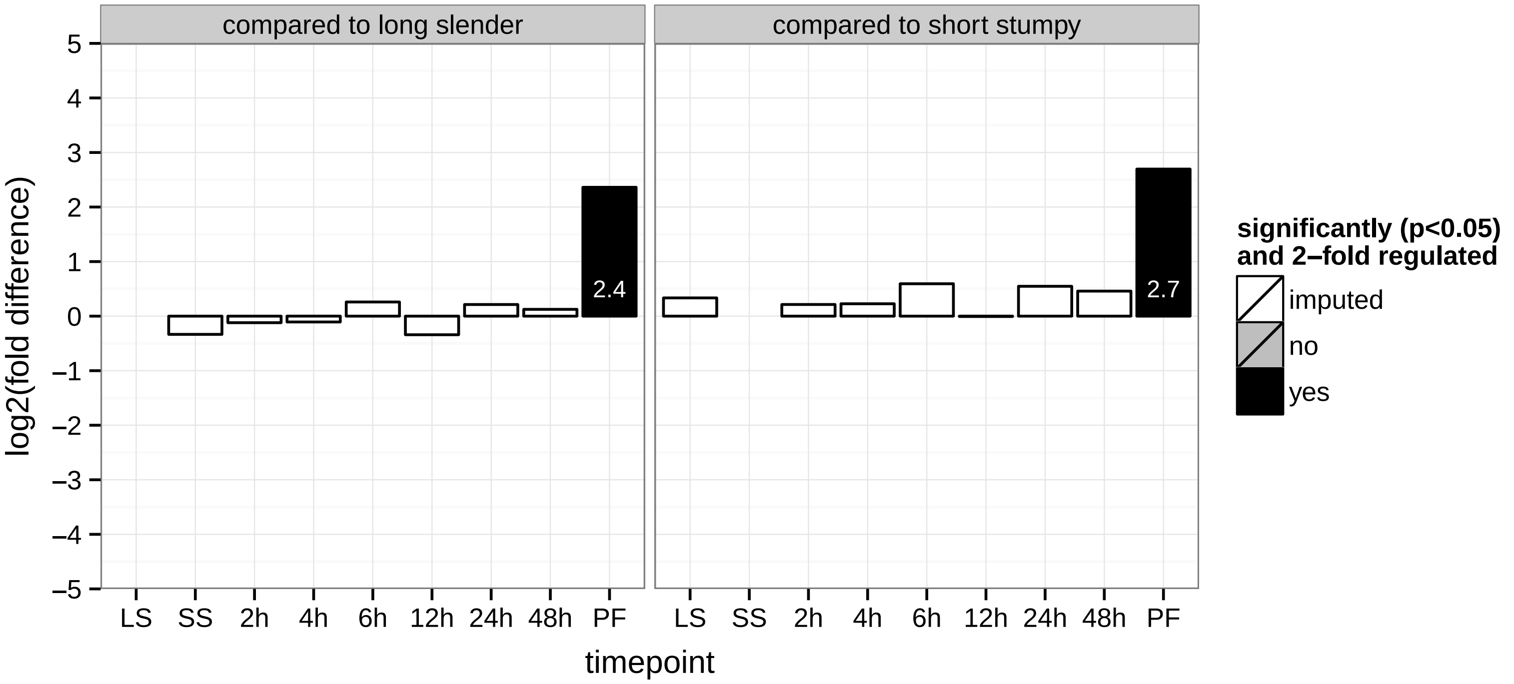
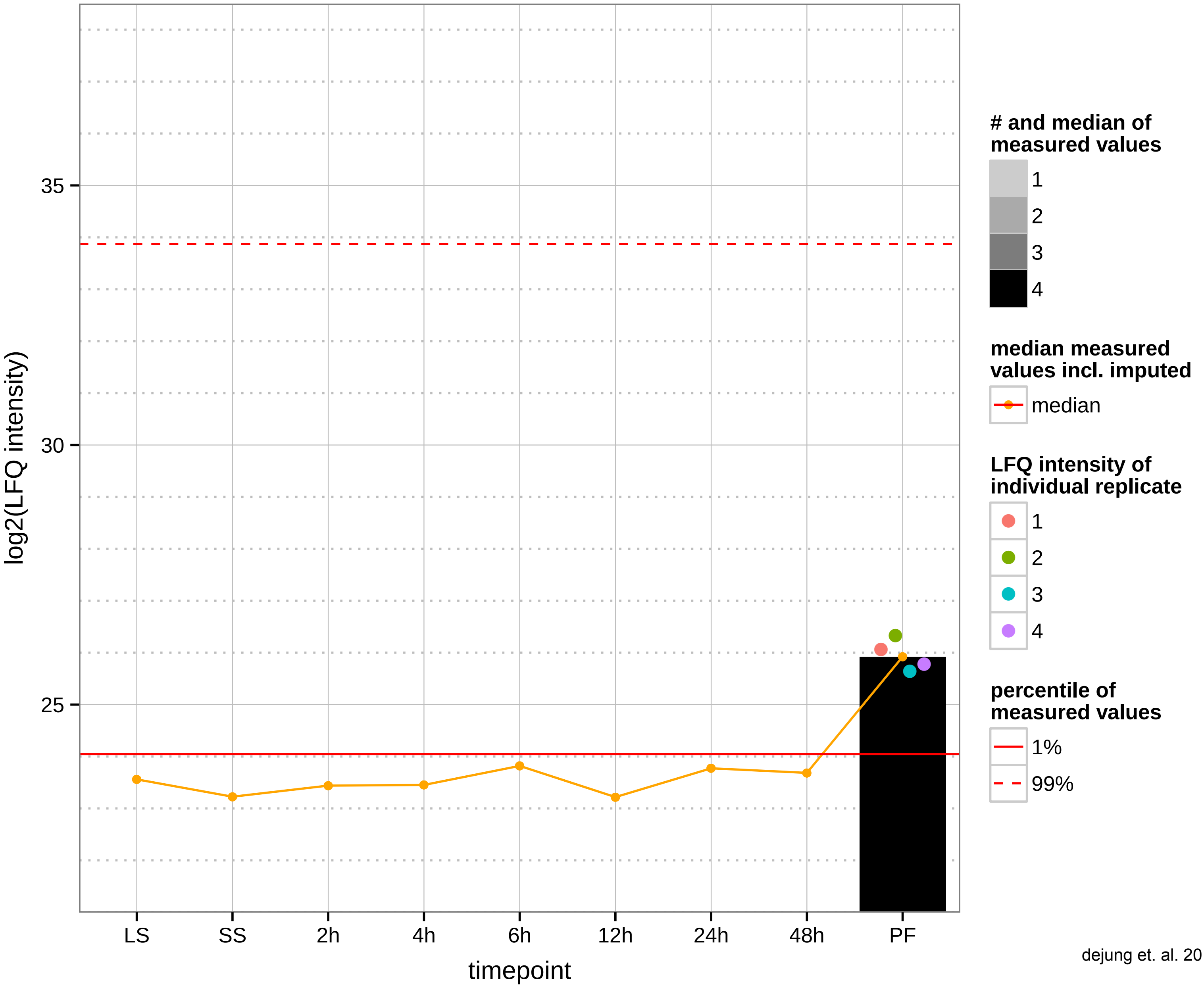
membrane protein YIP1, putative
Tb927.9.2050
AGOF: null
AGOC: Golgi apparatus, integral to membrane
AGOP: vesicle–mediated transport
PGOF: null
PGOC: null
PGOP: null





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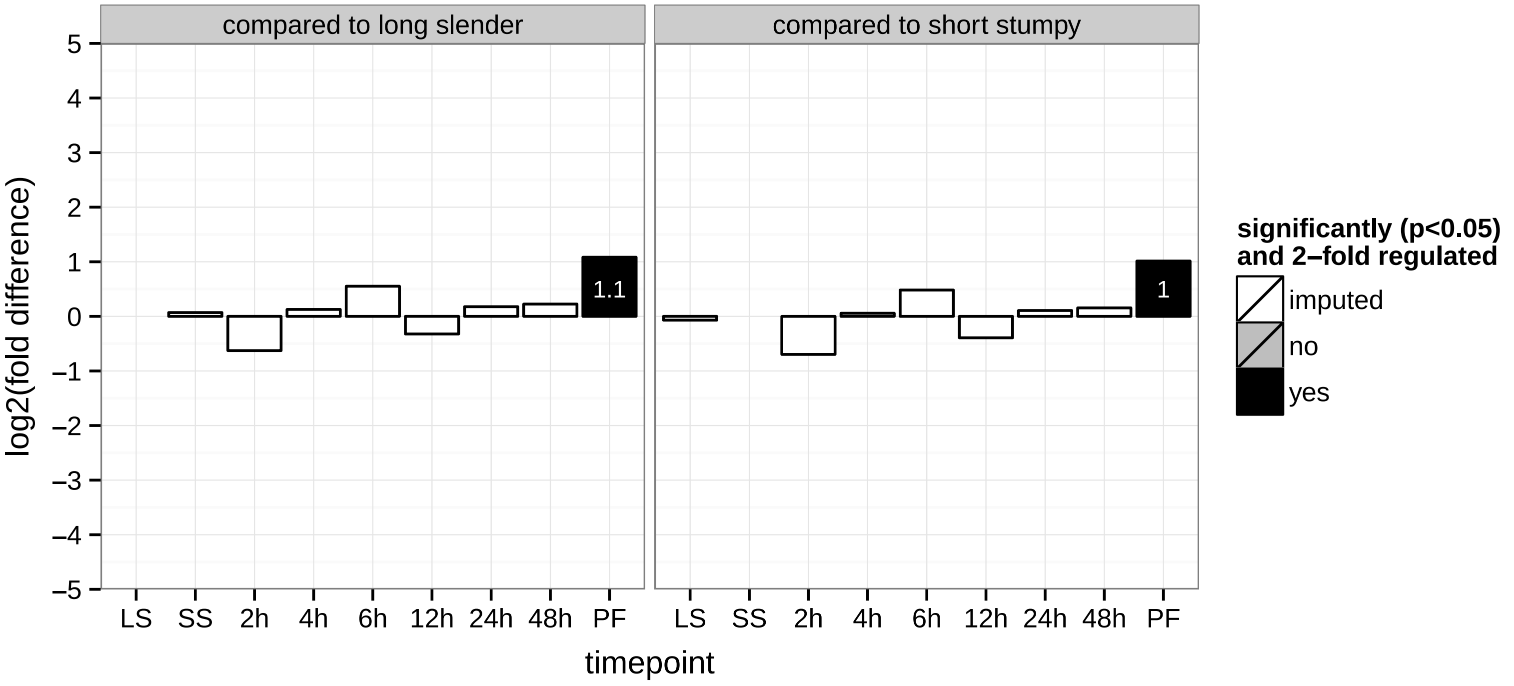
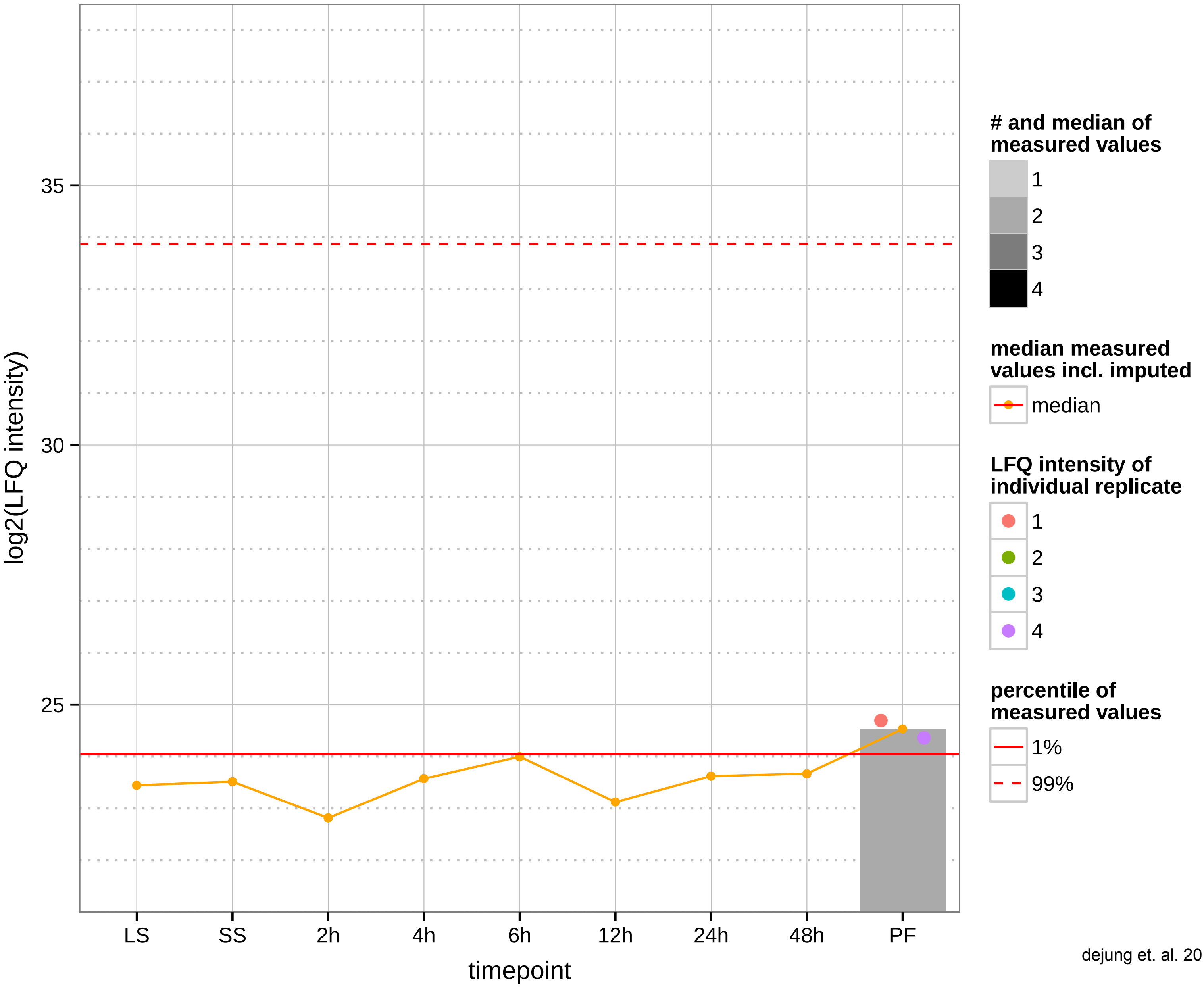
hypothetical protein, conserved
Tb927.9.3580
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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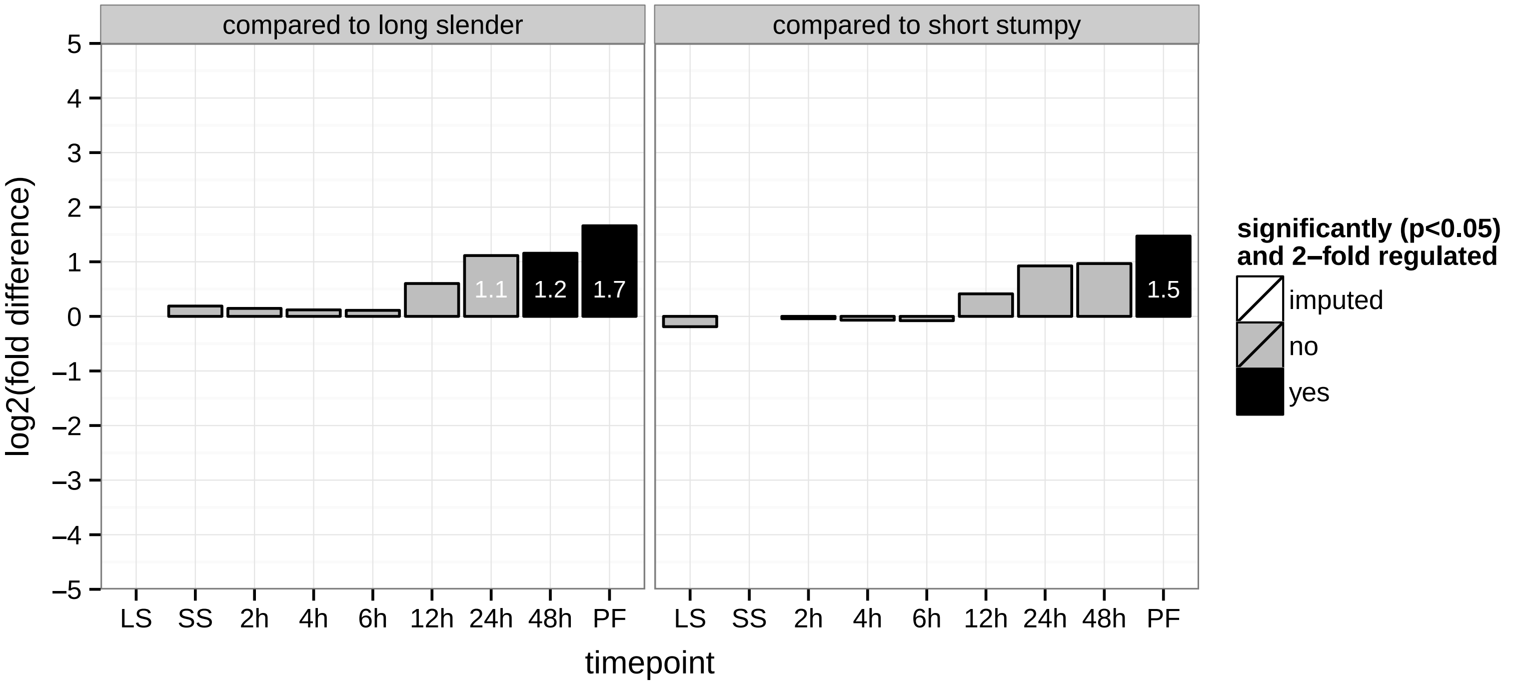
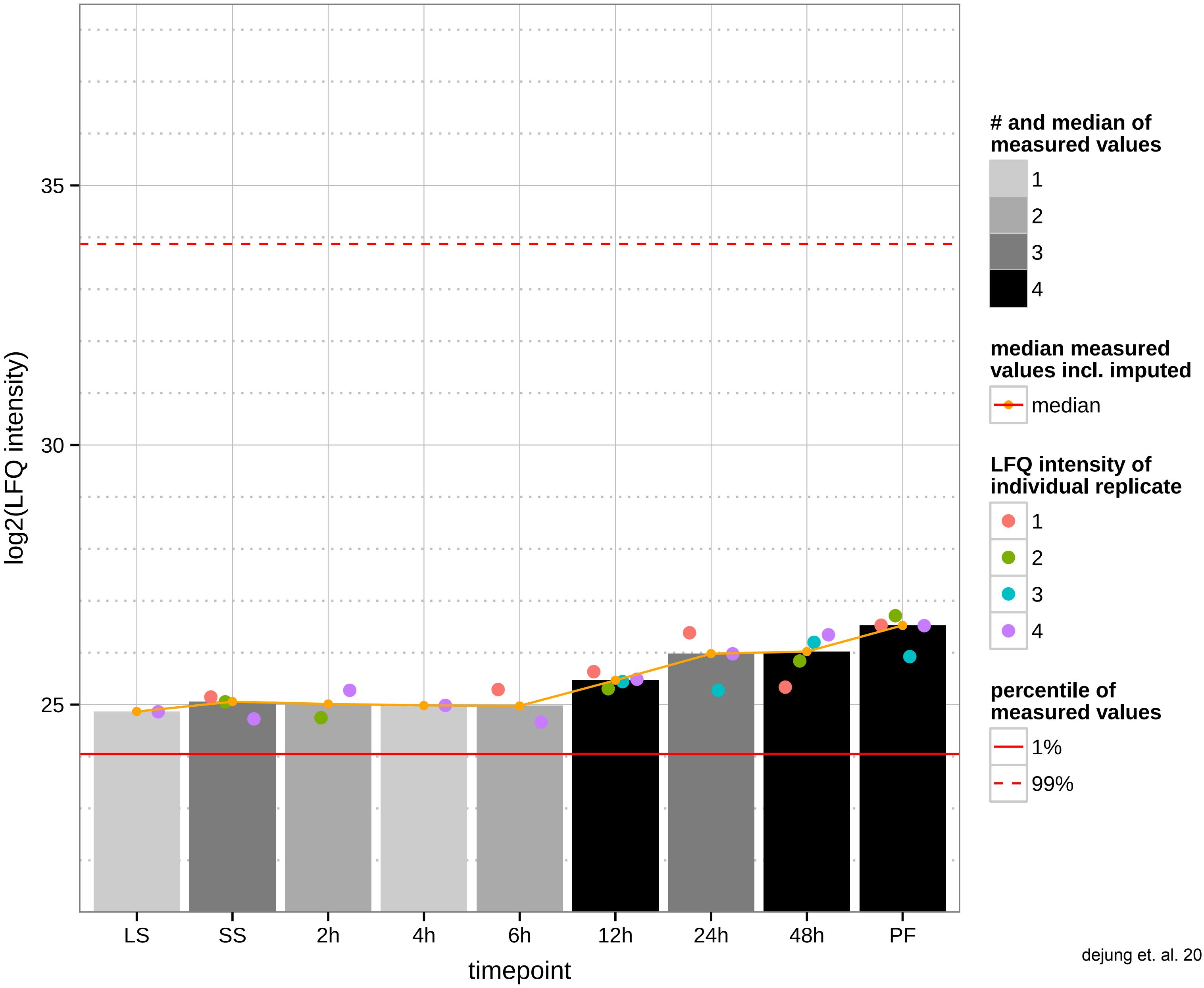
hypothetical protein, conserved
Tb927.9.4290
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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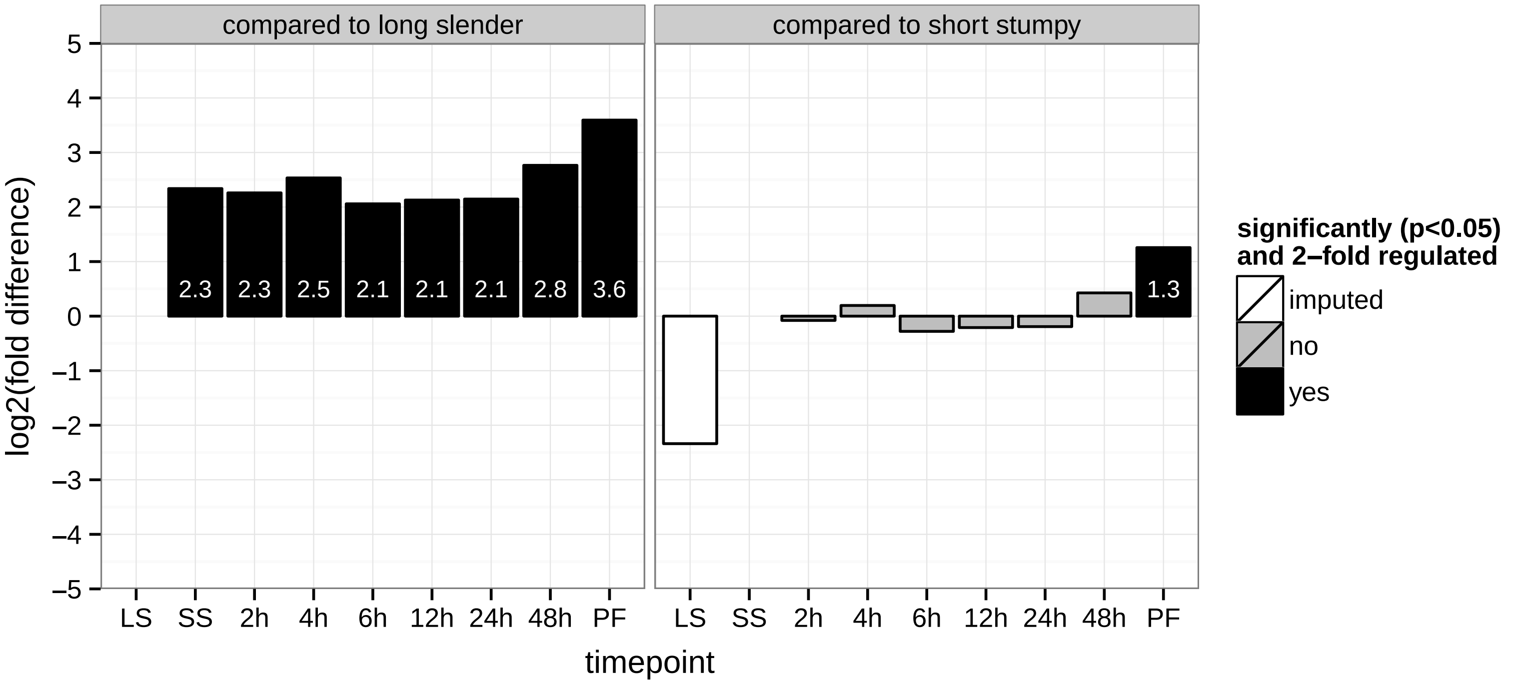
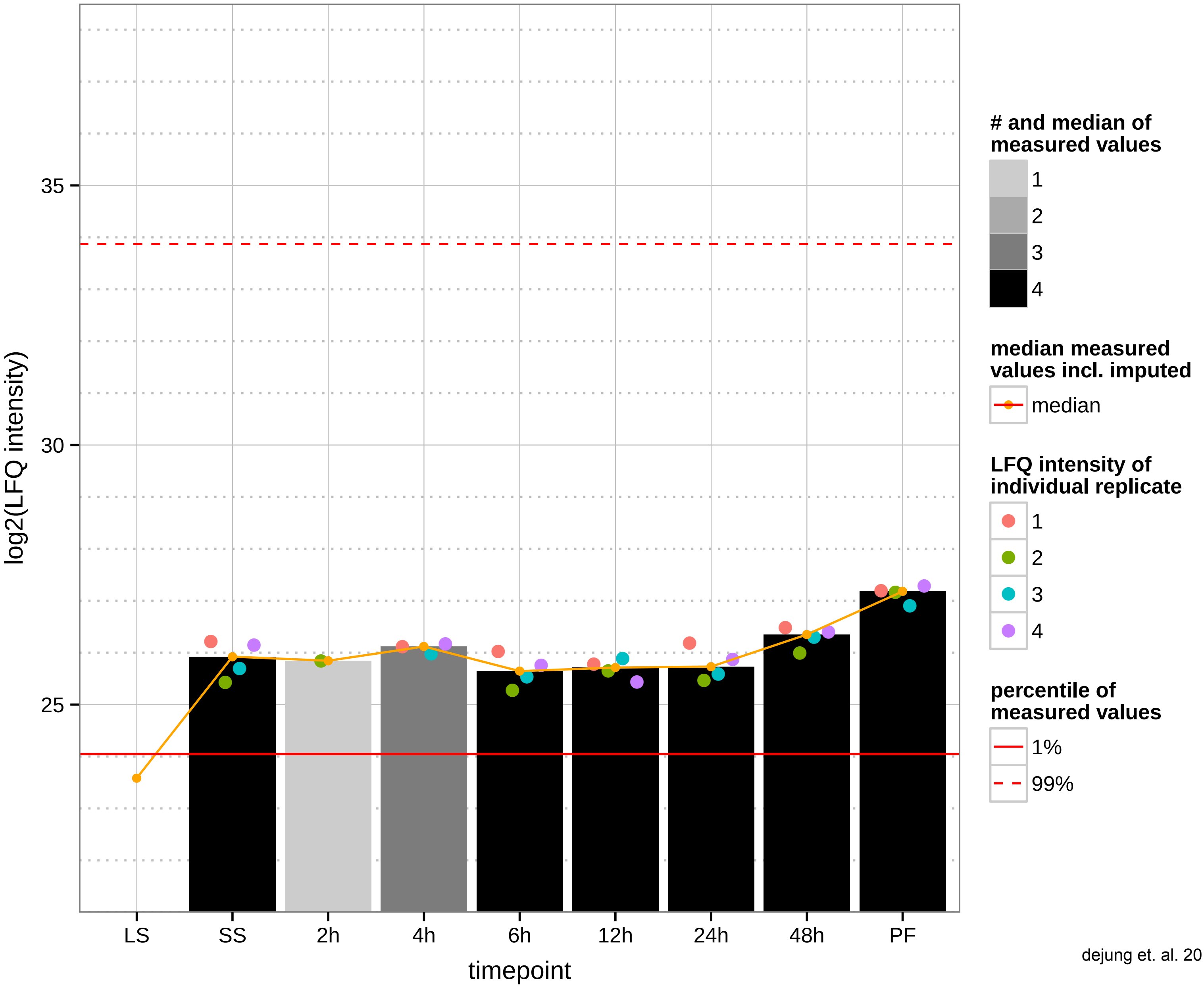
KREL1, RNA editing ligase, RNA–editing complex protein, mitochondrial RNA editing ligase 1 (KREL1)
Tb927.9.4360
AGOF: ATP binding, RNA ligase (ATP) activity
AGOC: mitochondrial mRNA editing complex, mitochondrion
AGOP: RNA modification
PGOF: ATP binding, RNA ligase (ATP) activity, ligase activity
PGOC: null
PGOP: null





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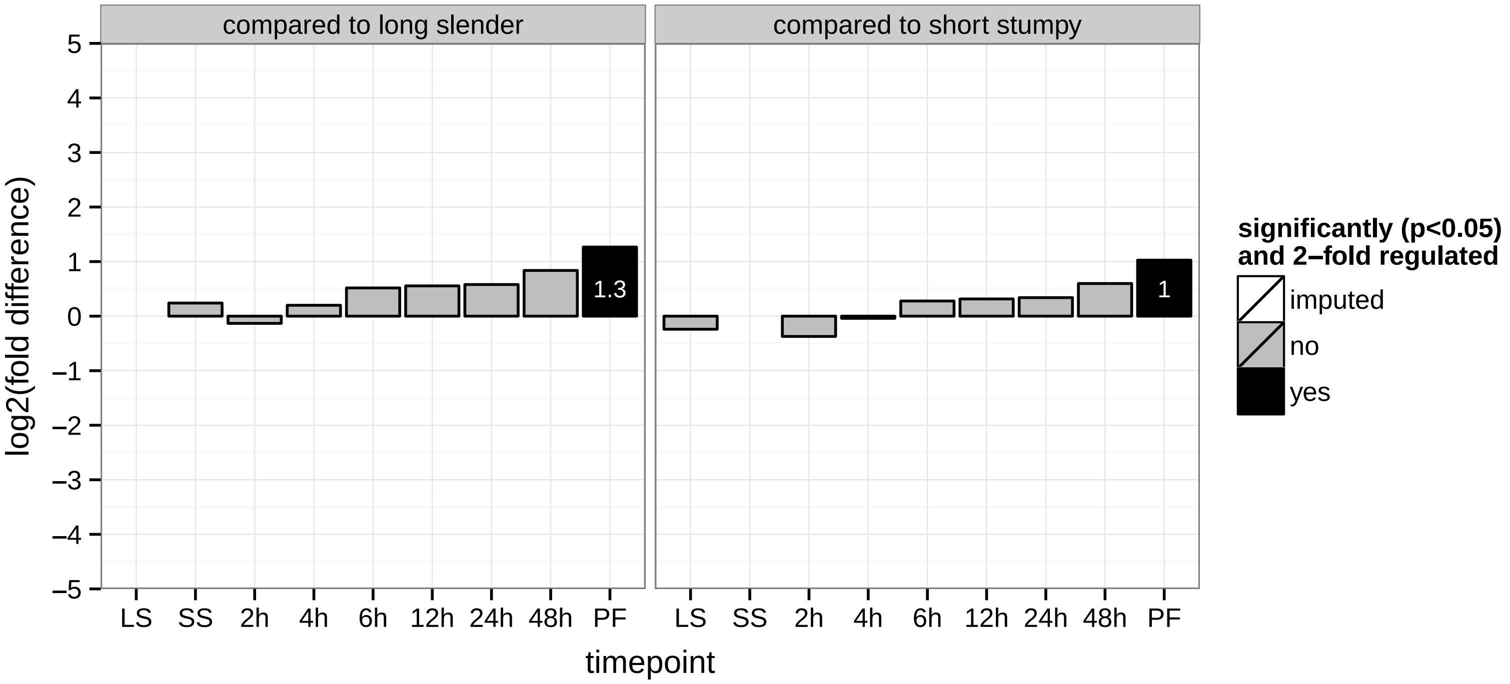
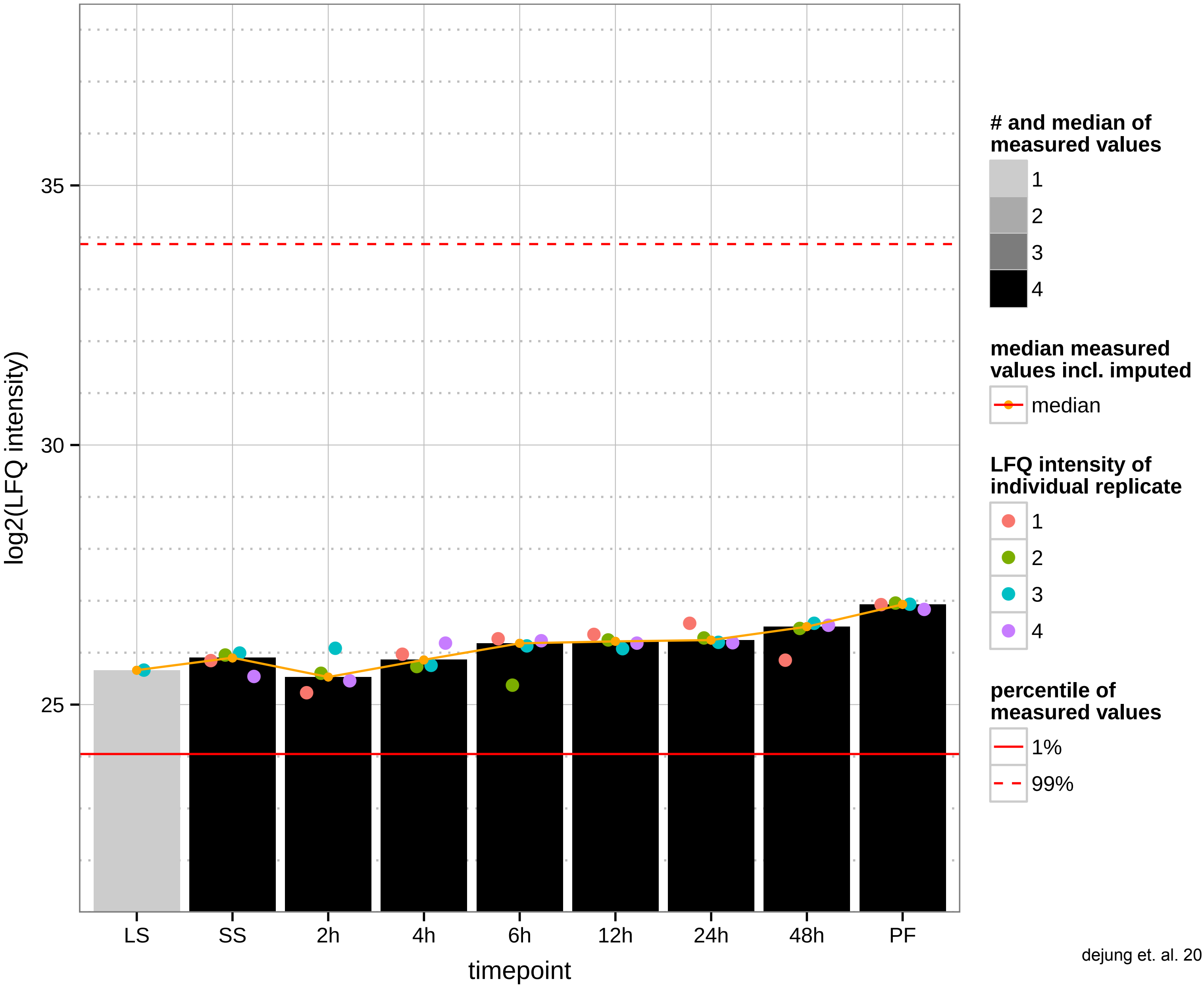
leucine–rich repeat protein (LRRP), putative
Tb927.9.4850
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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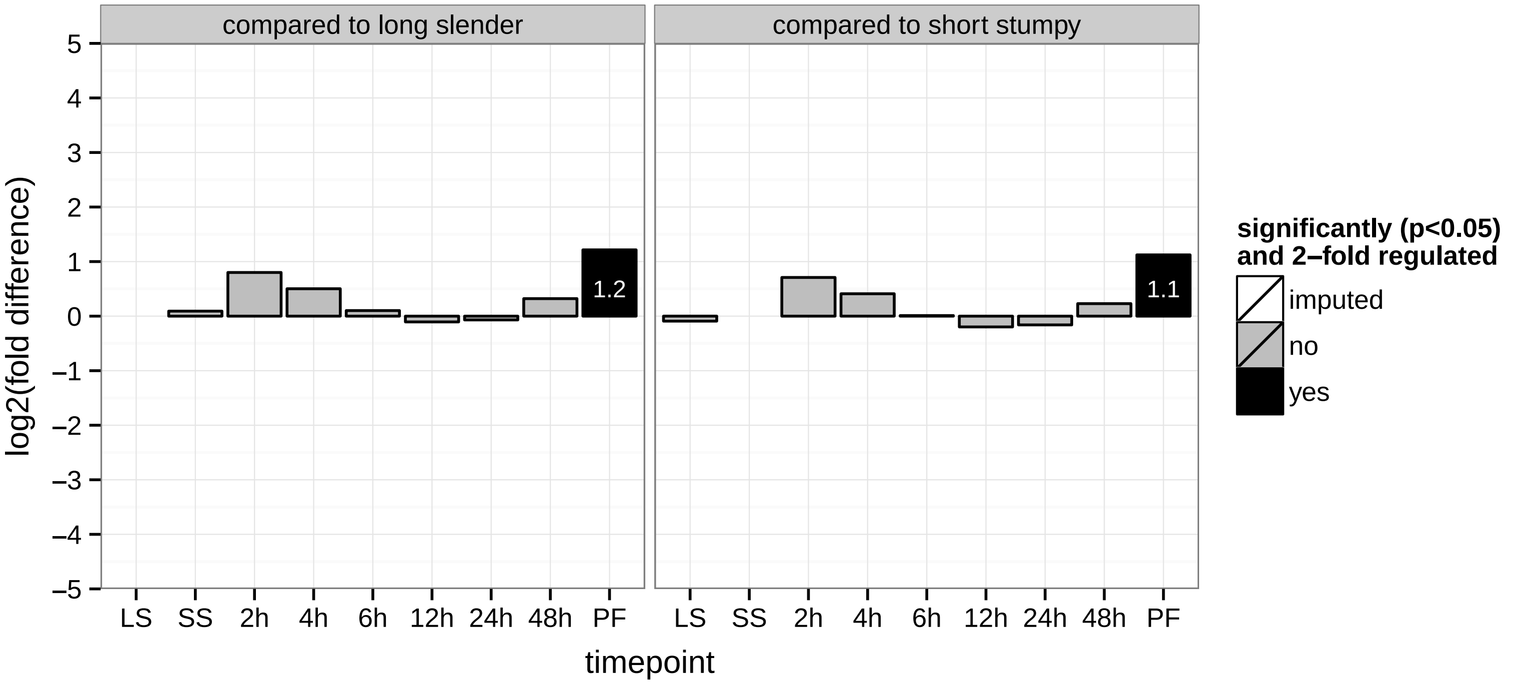
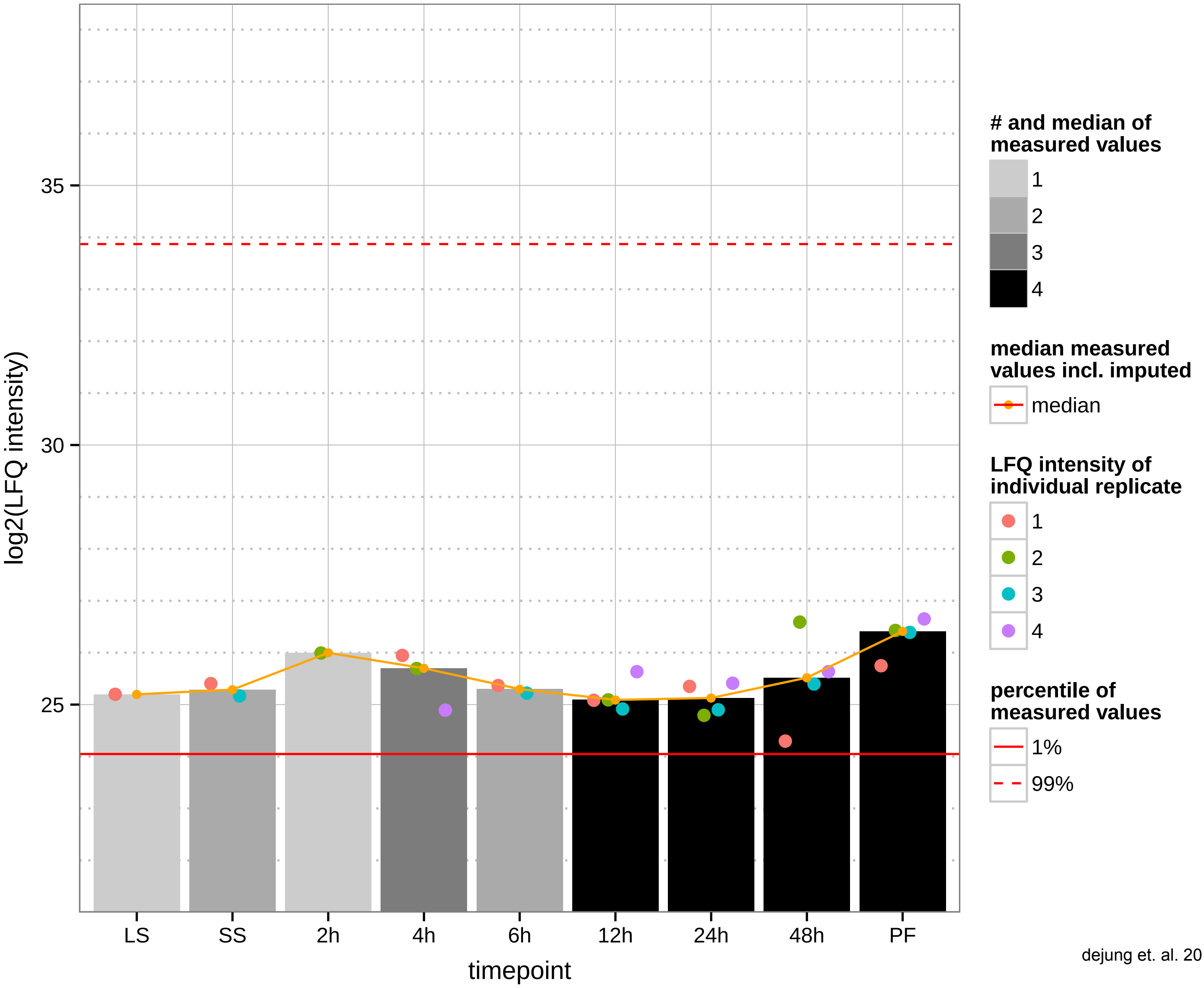
protein kinase, putative
Tb927.9.4910
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity, zinc ion binding
AGOC: null
AGOP: growth, protein phosphorylation
PGOF: ATP binding, metal ion binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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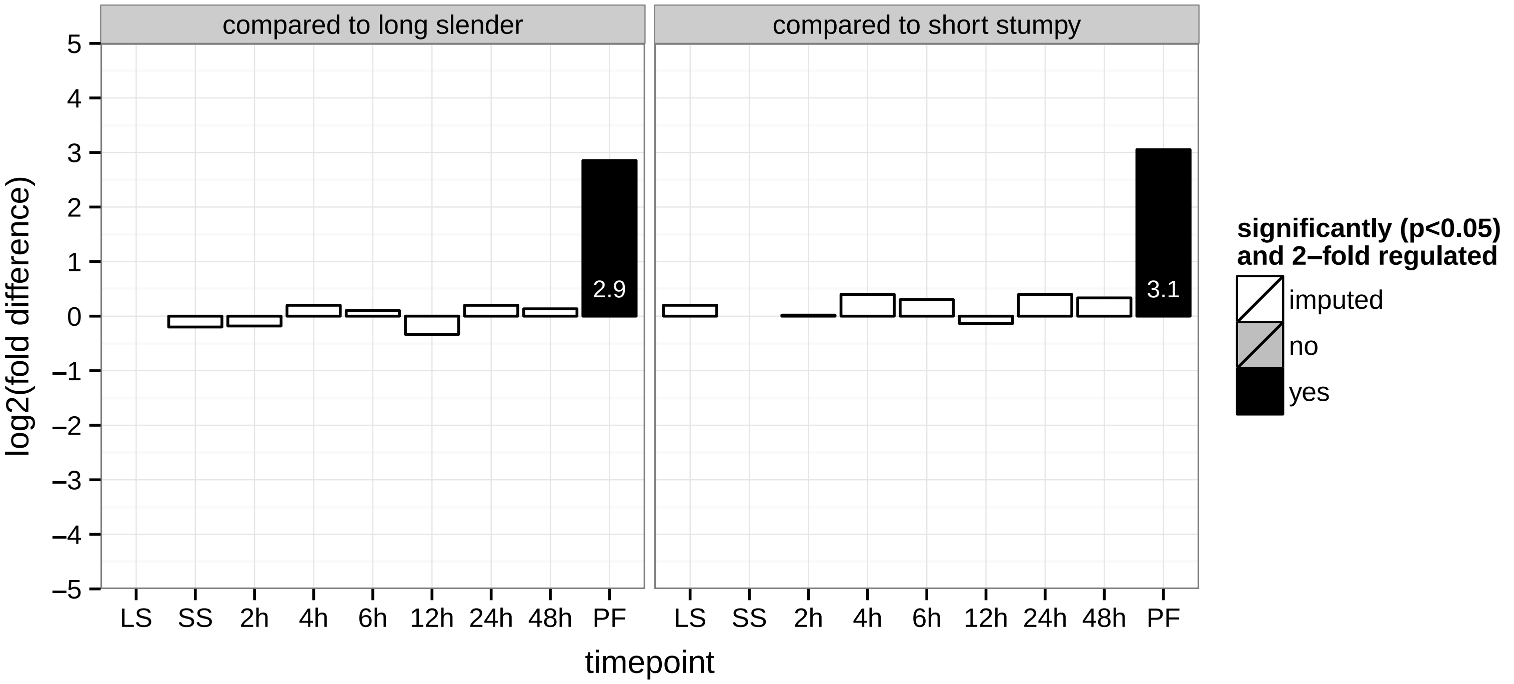
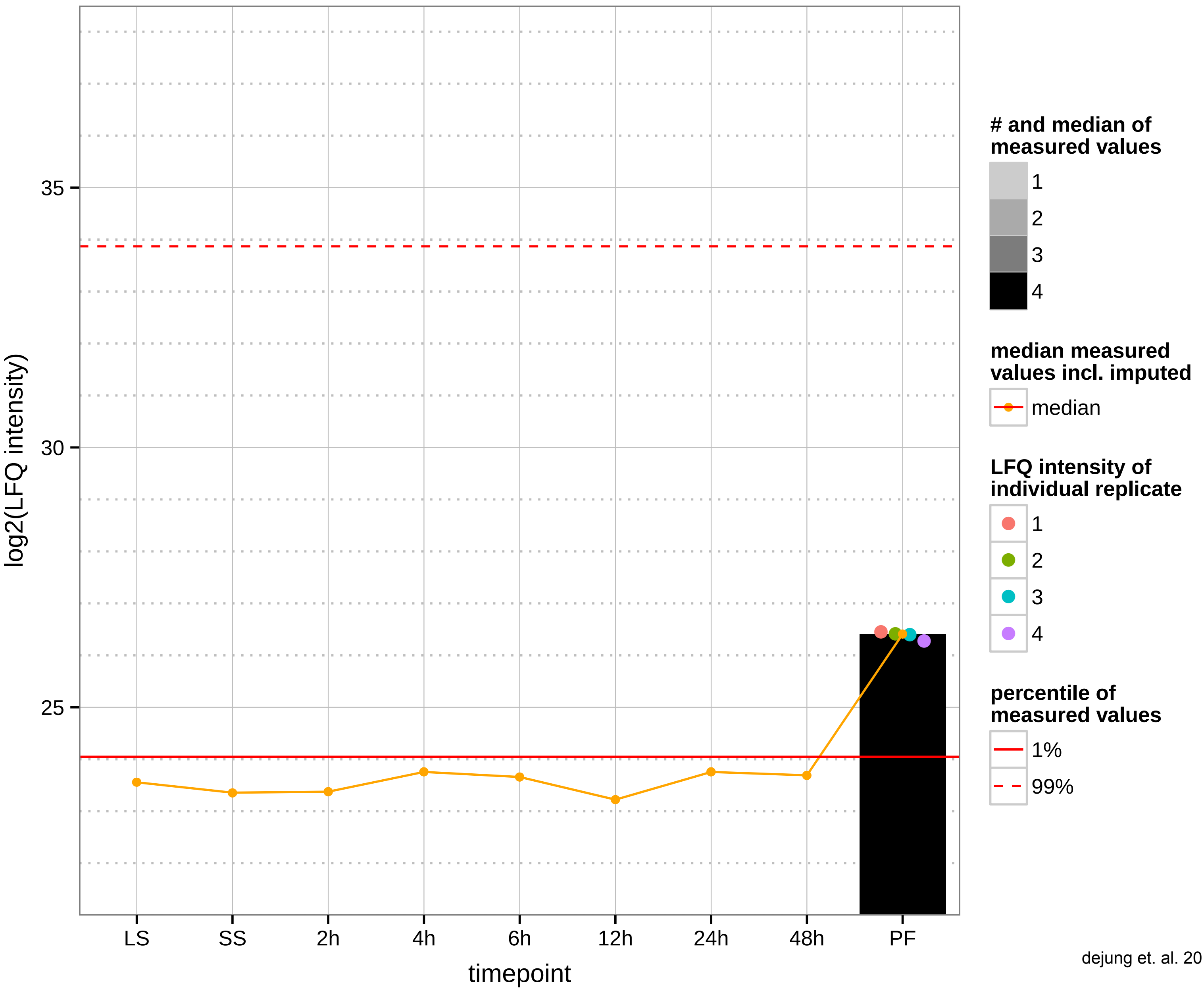
unspecified product
Tb927.9.5280
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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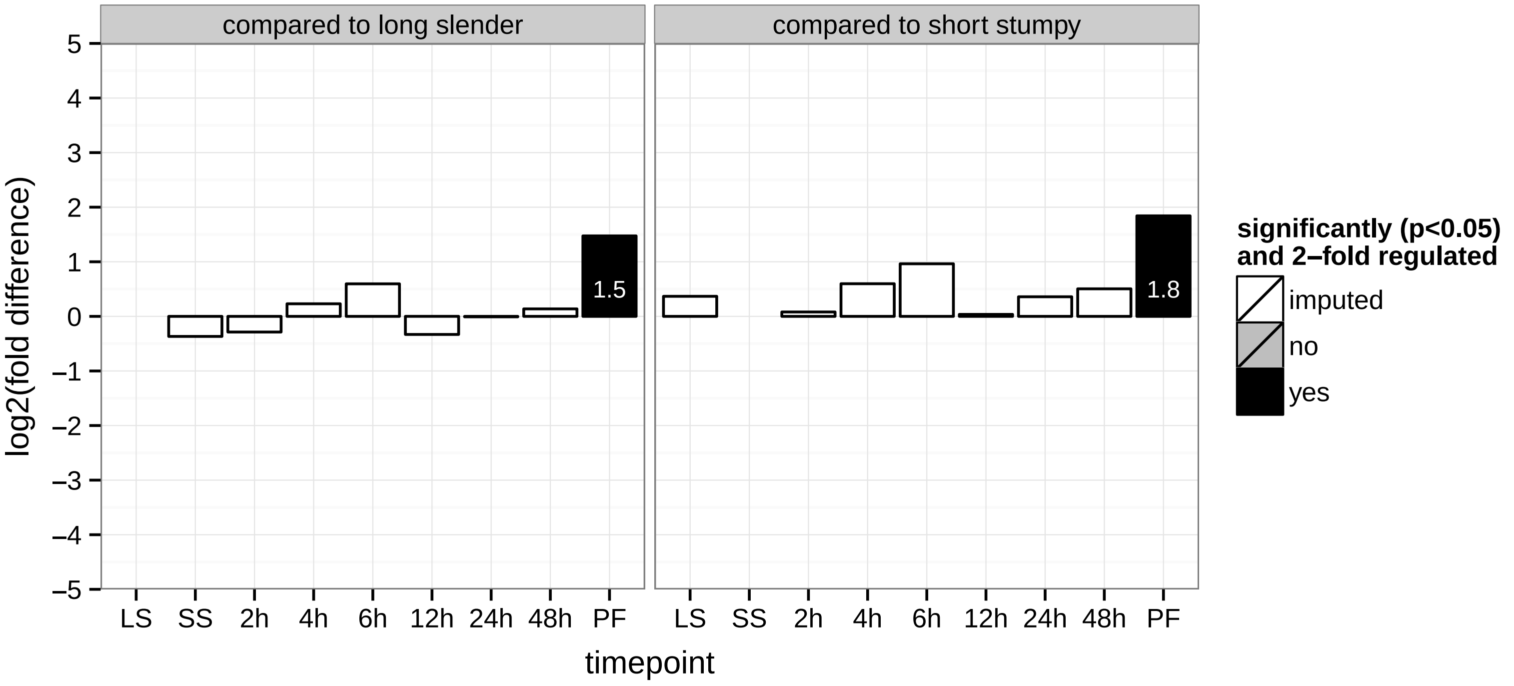
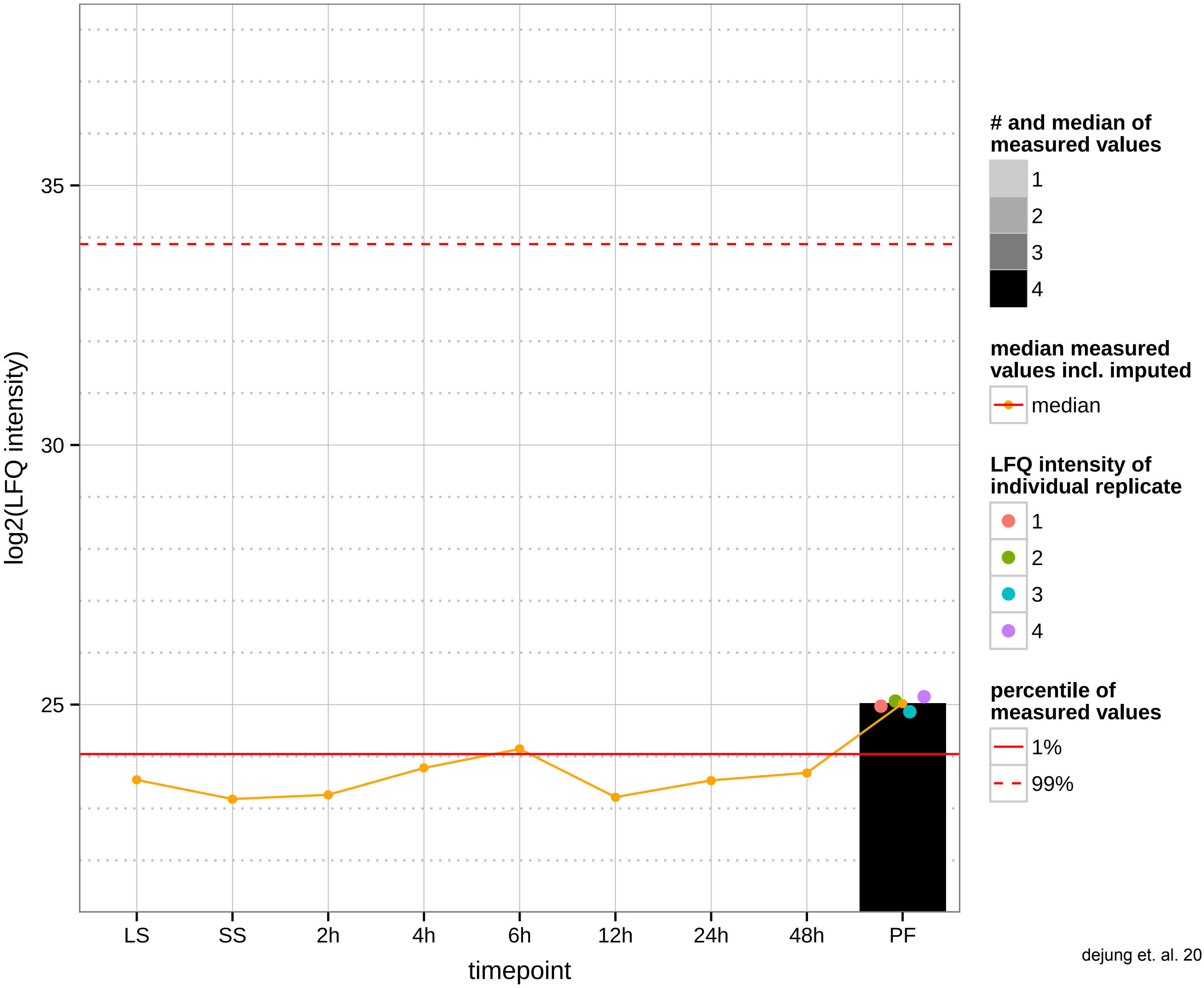
hypothetical protein, conserved
Tb927.9.5380
AGOF: Rab GTPase activator activity
AGOC: intracellular
AGOP: regulation of Rab GTPase activity
PGOF: Rab GTPase activator activity
PGOC: intracellular
PGOP: regulation of Rab GTPase activity





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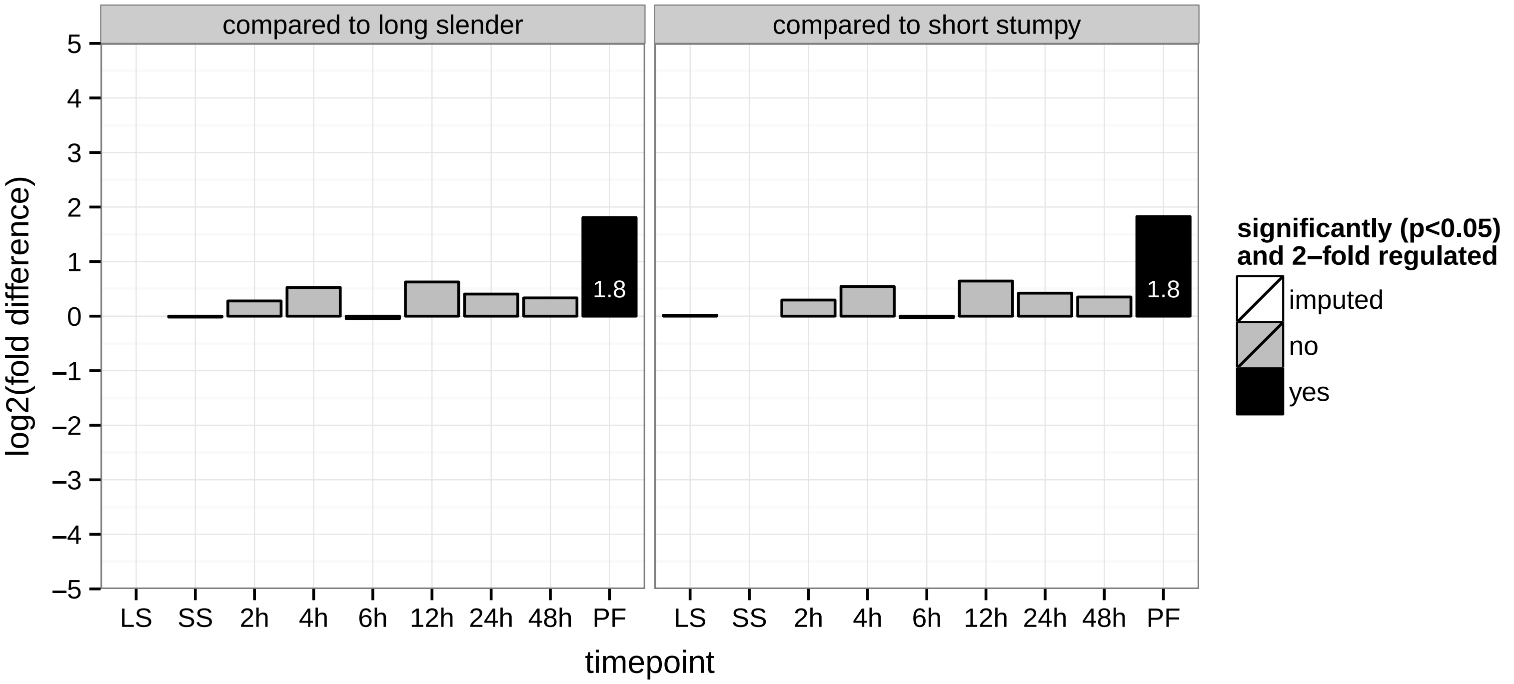
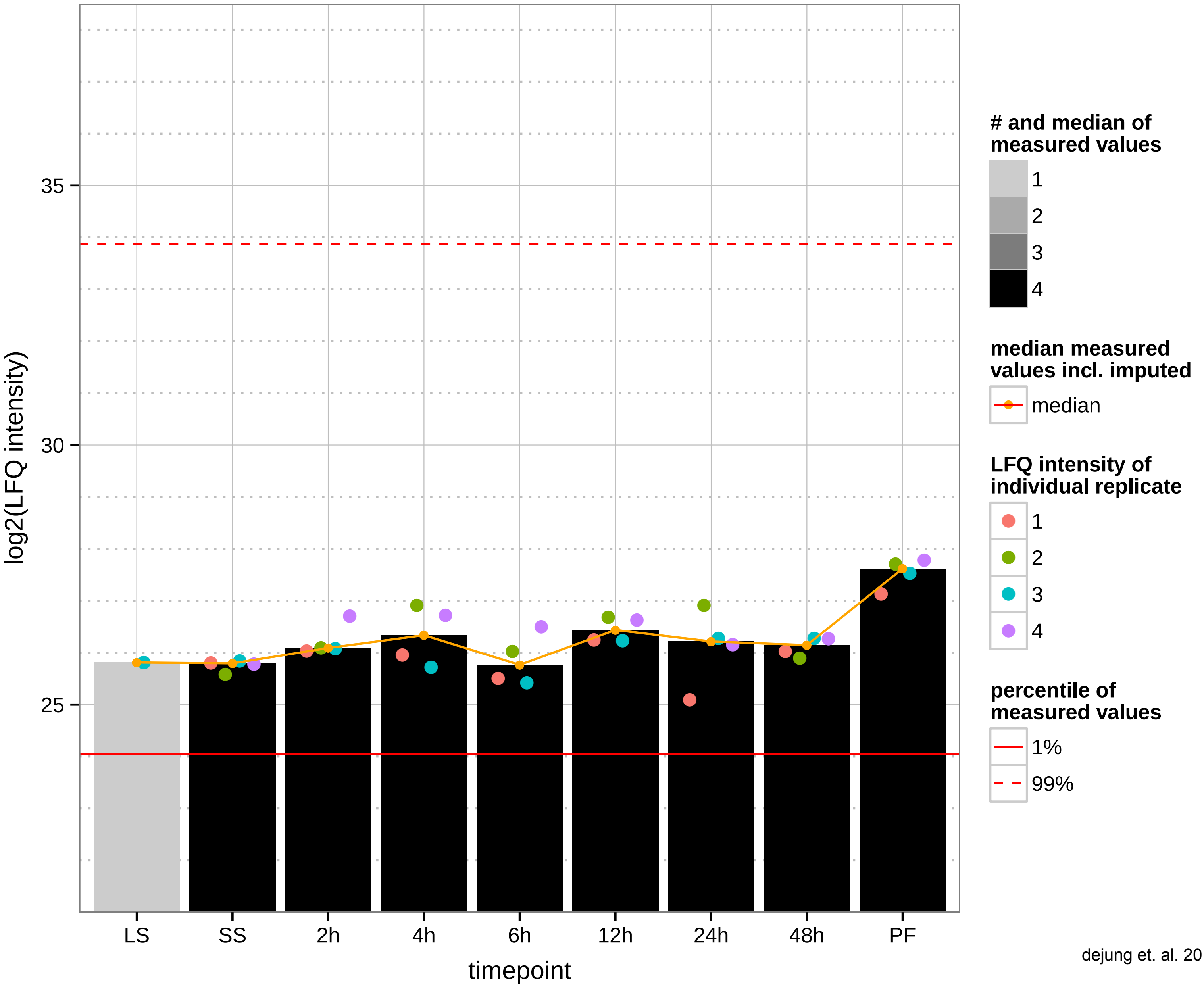
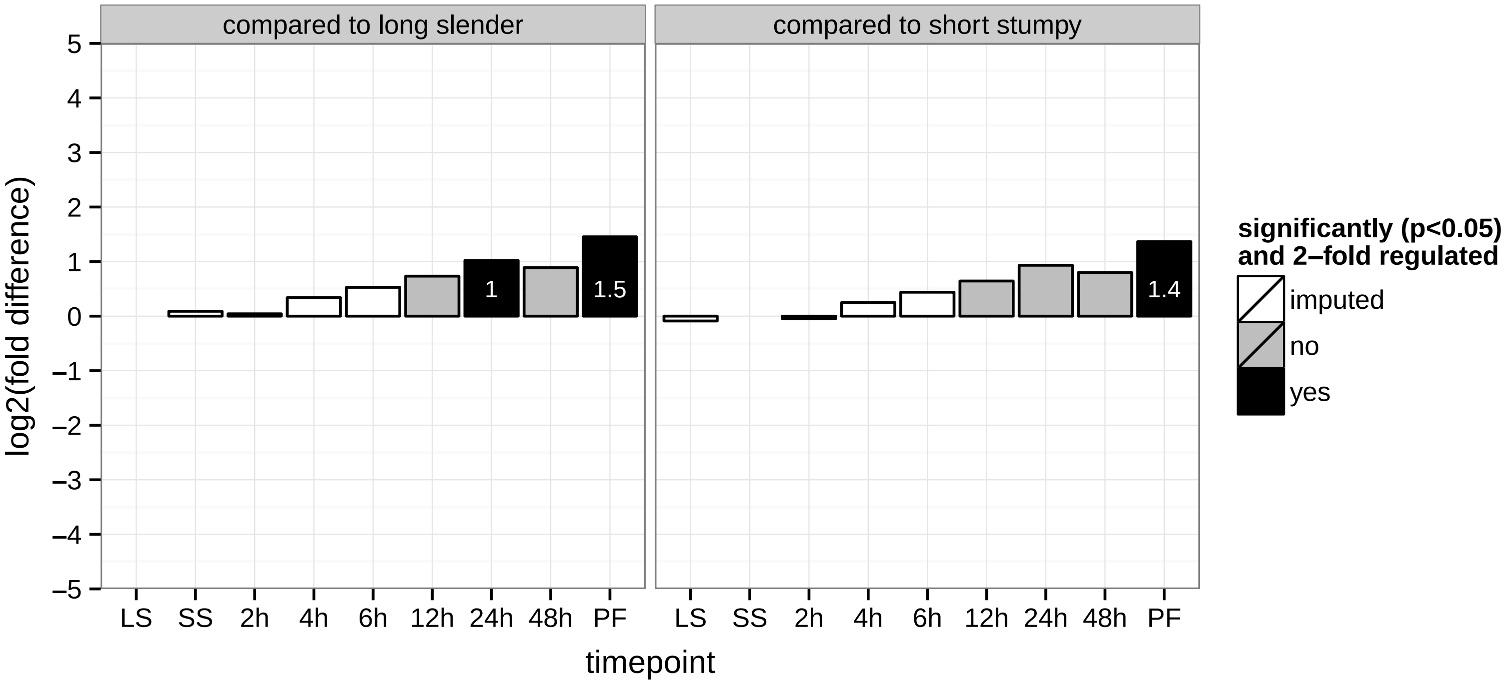
E2–like ubiquitin–conjugation enzyme, putative (UFC1)
Tb927.9.5650
AGOF: small conjugating protein binding
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

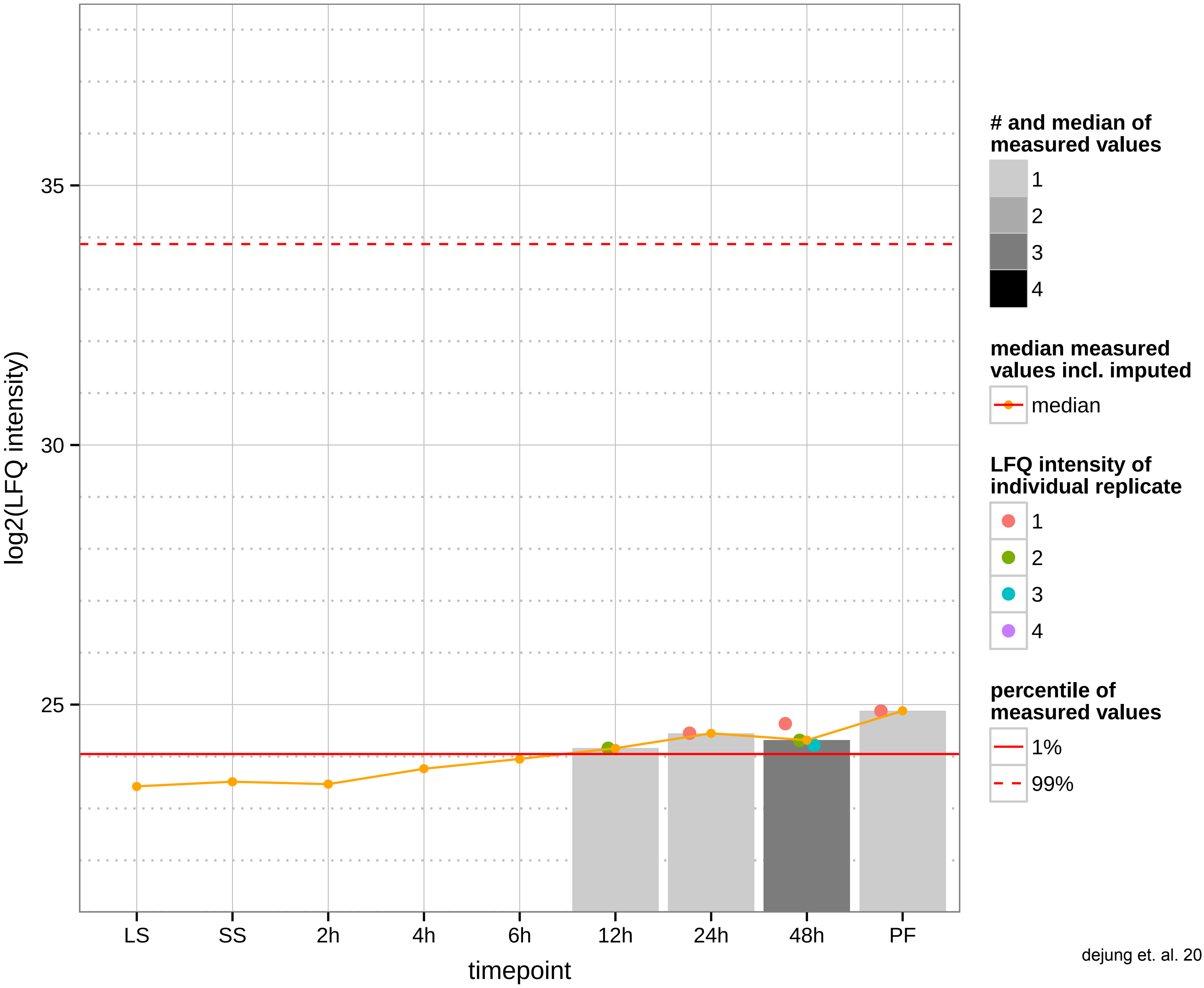




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.6270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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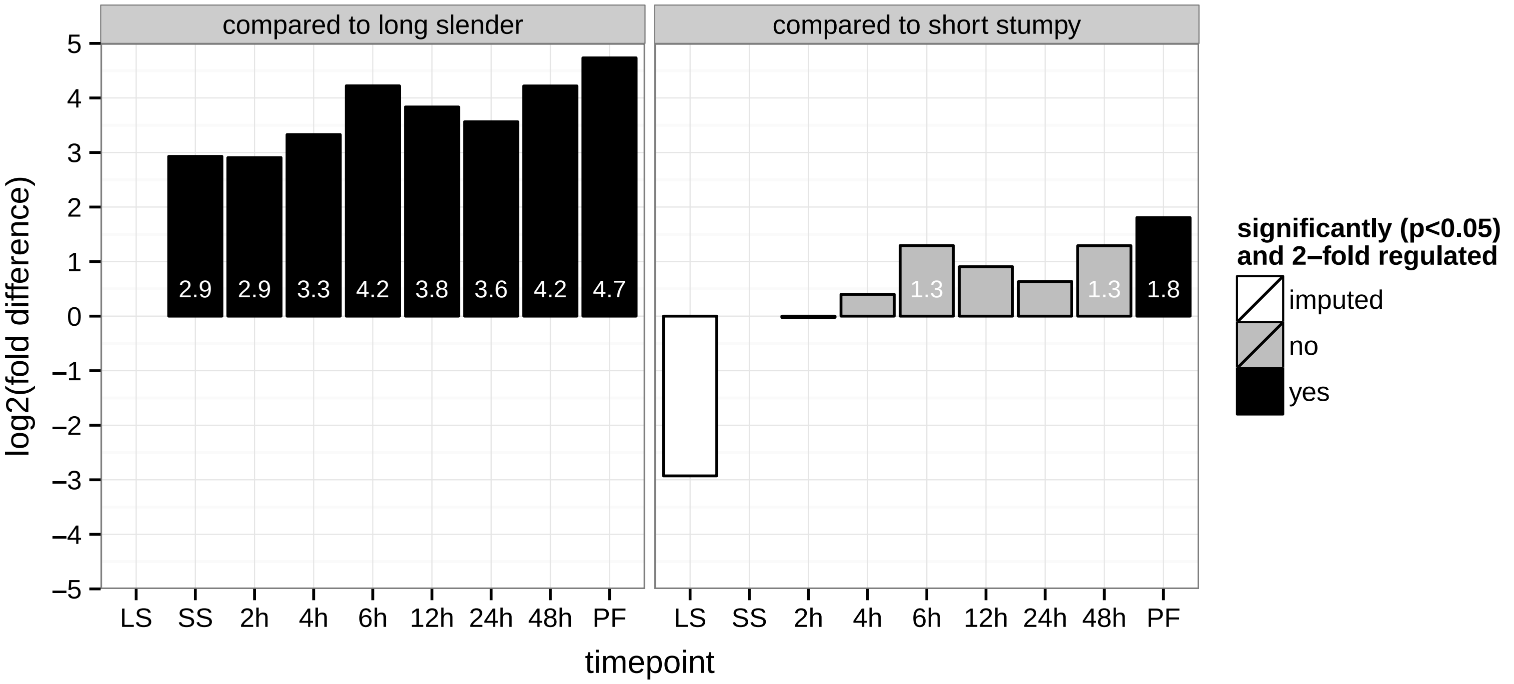
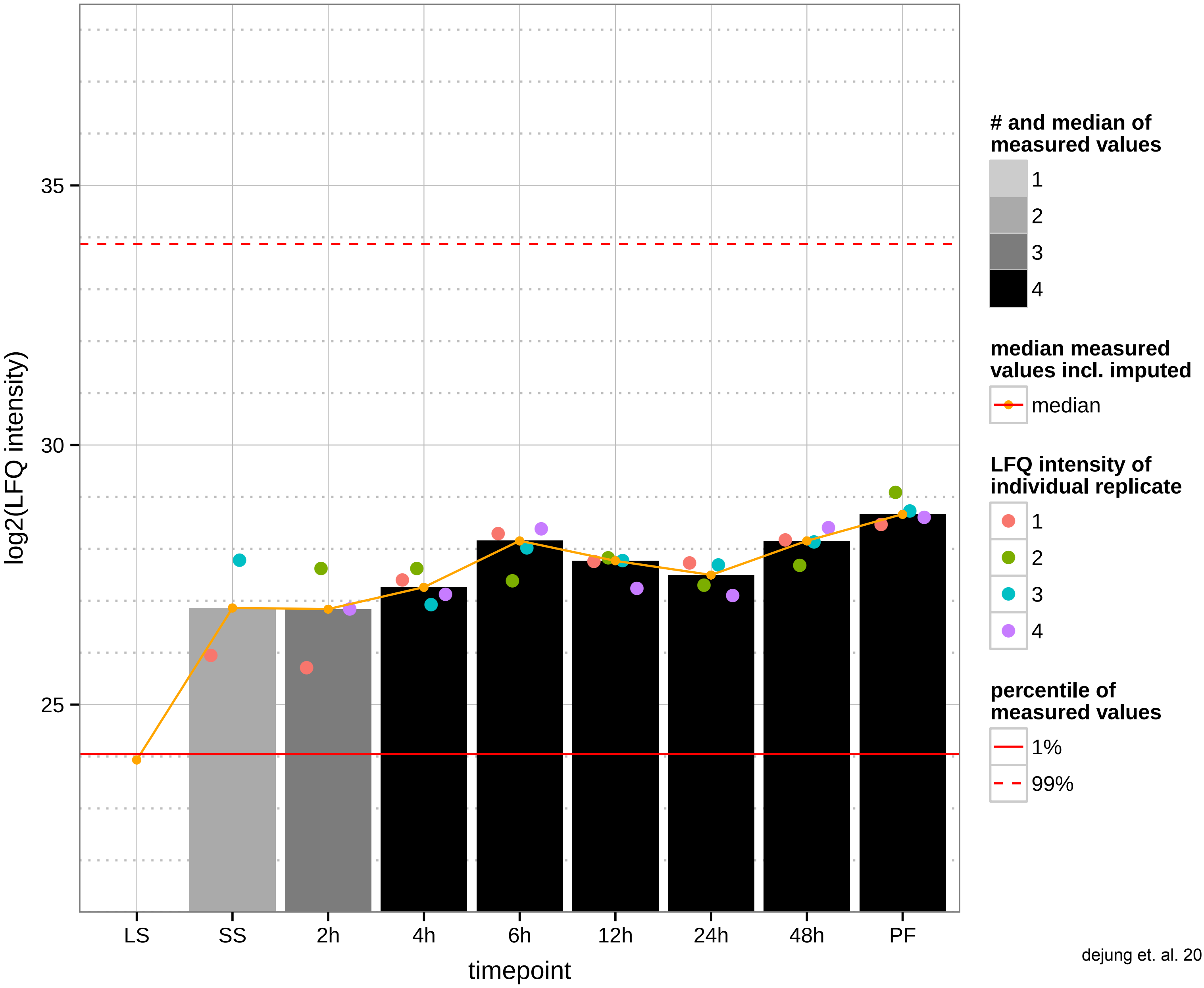
RNA–binding protein, putative (RBSR1)
Tb927.9.6870
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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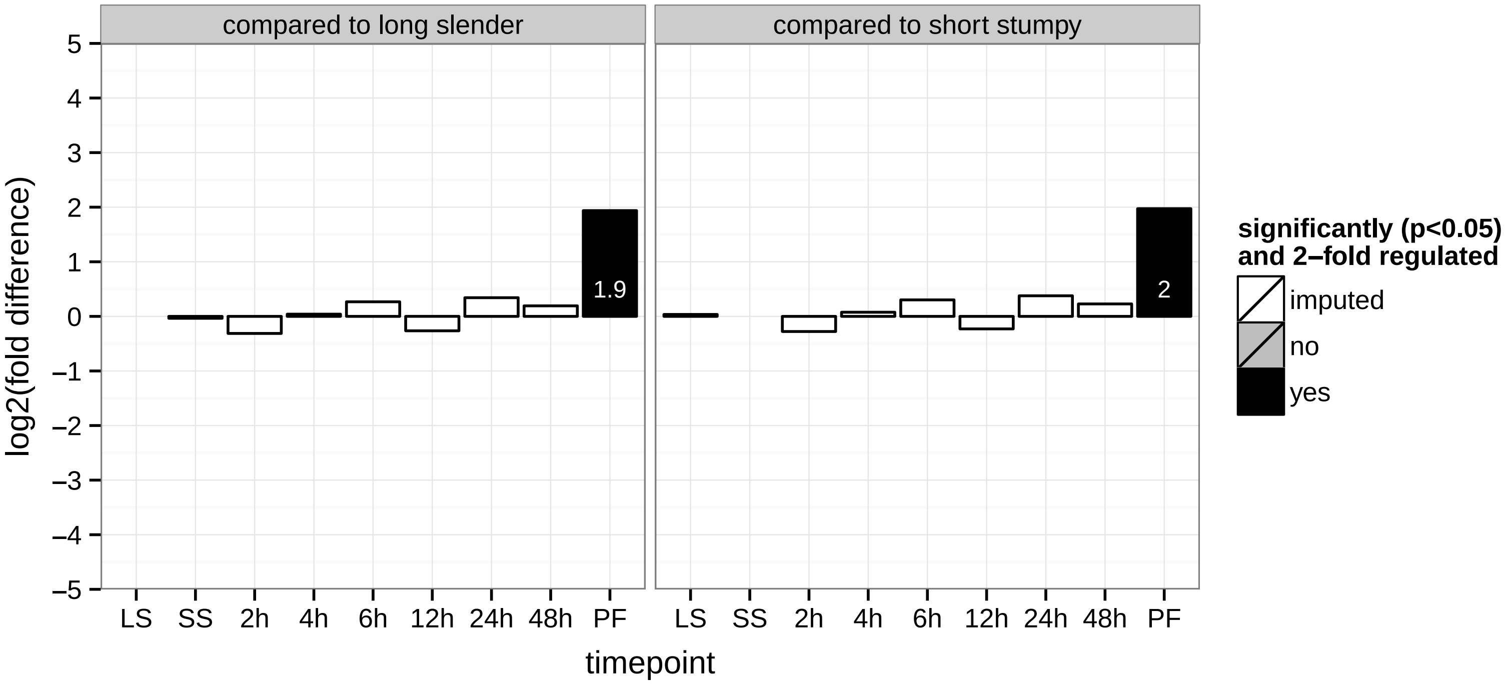
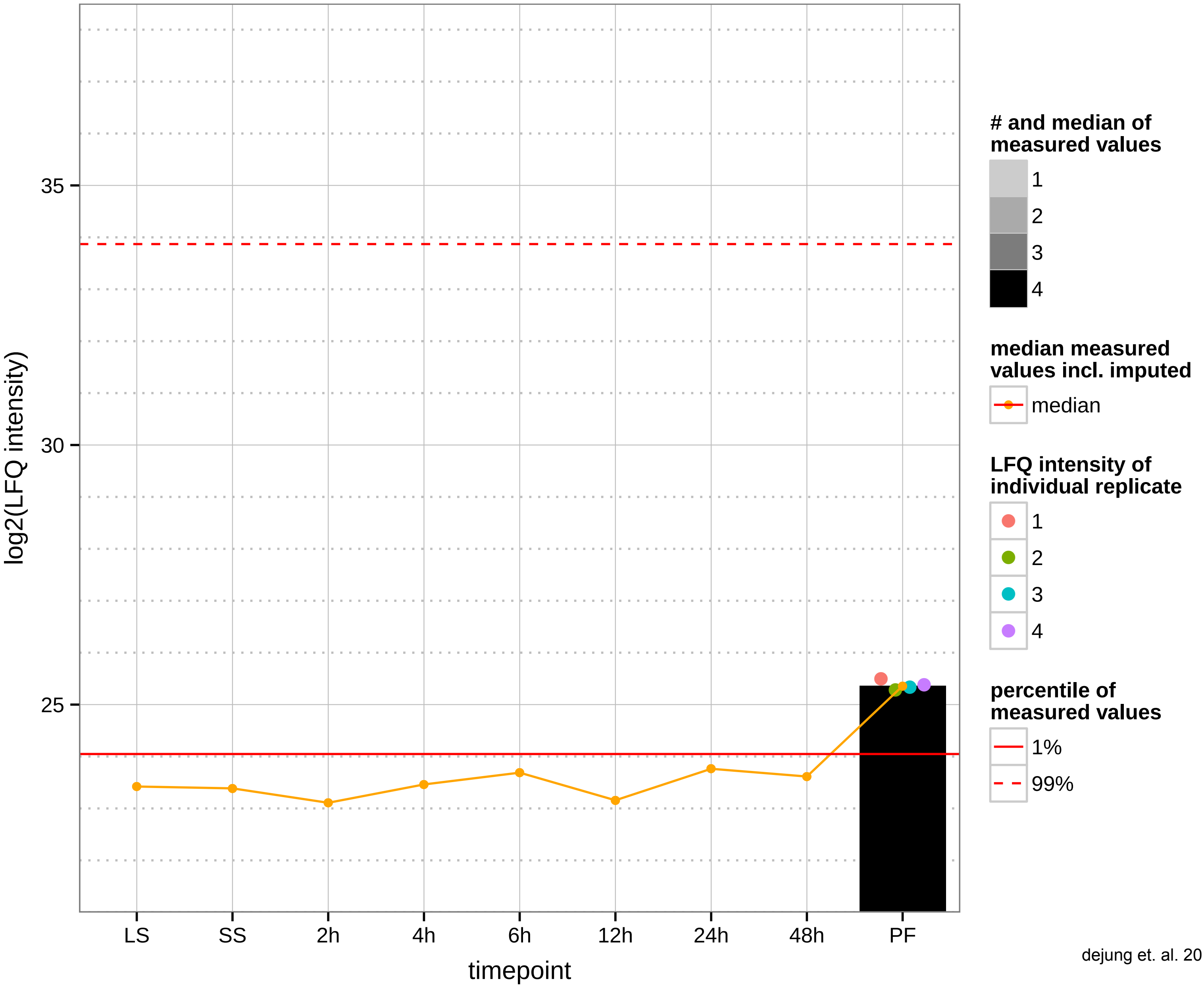
hypothetical protein, conserved
Tb927.9.7200
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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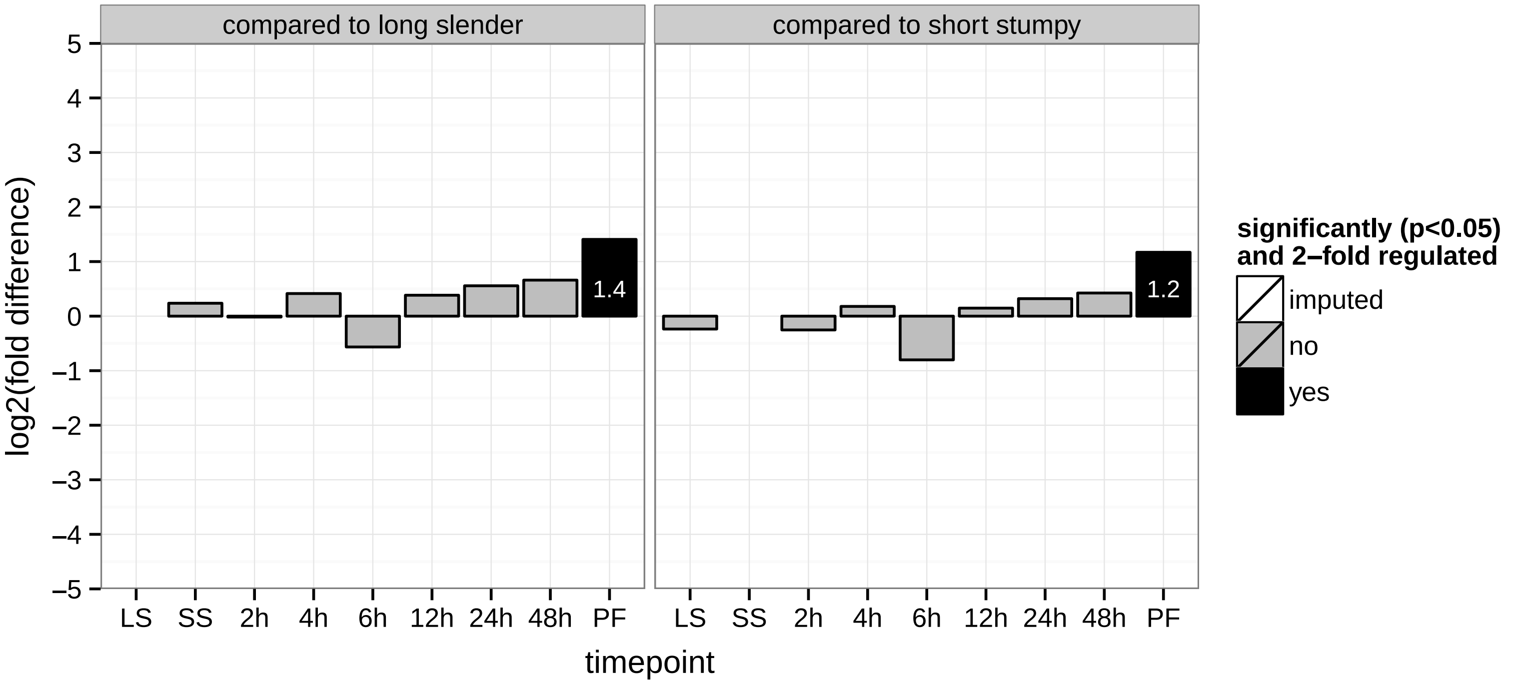
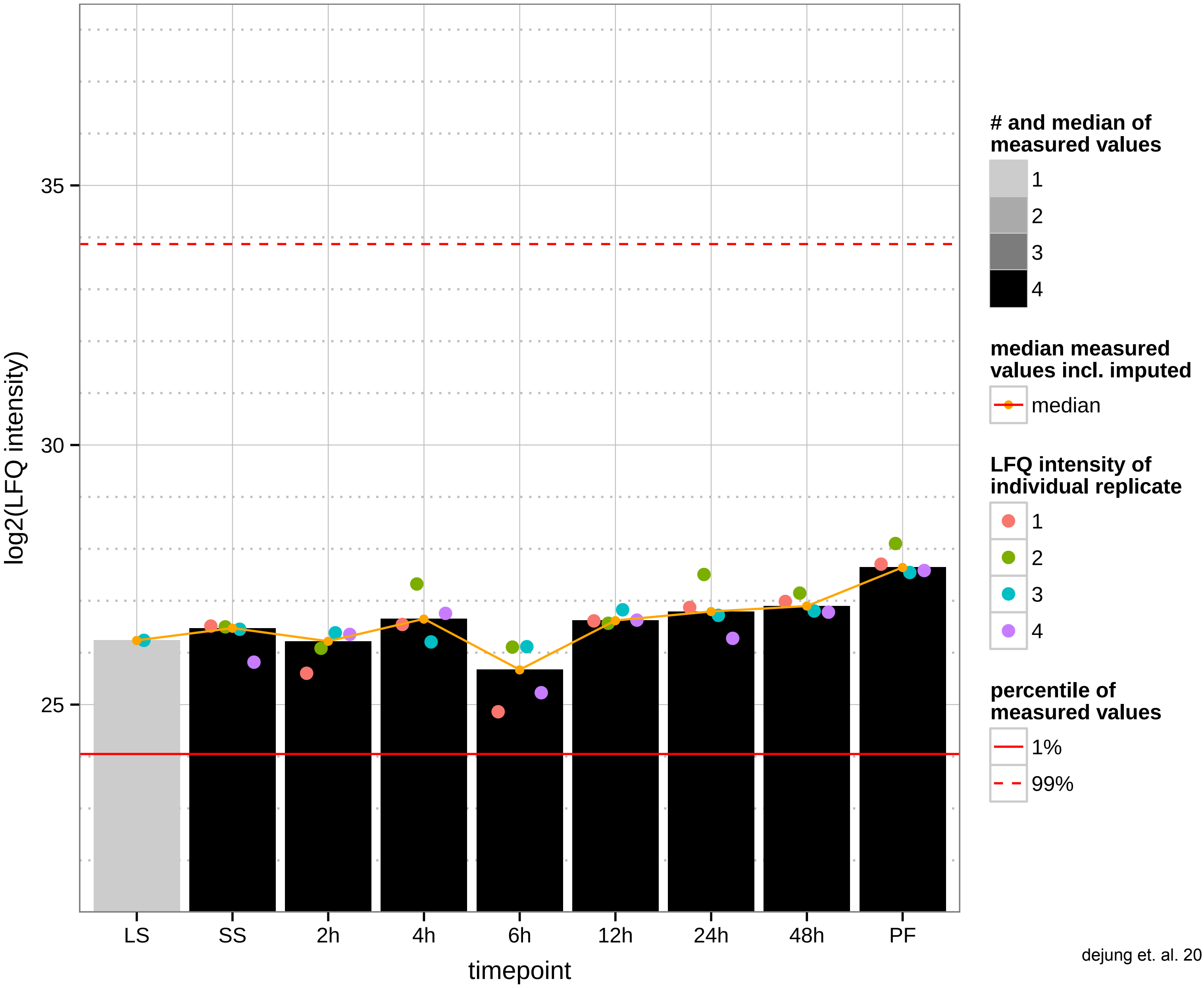
hypothetical protein, conserved
Tb927.9.7250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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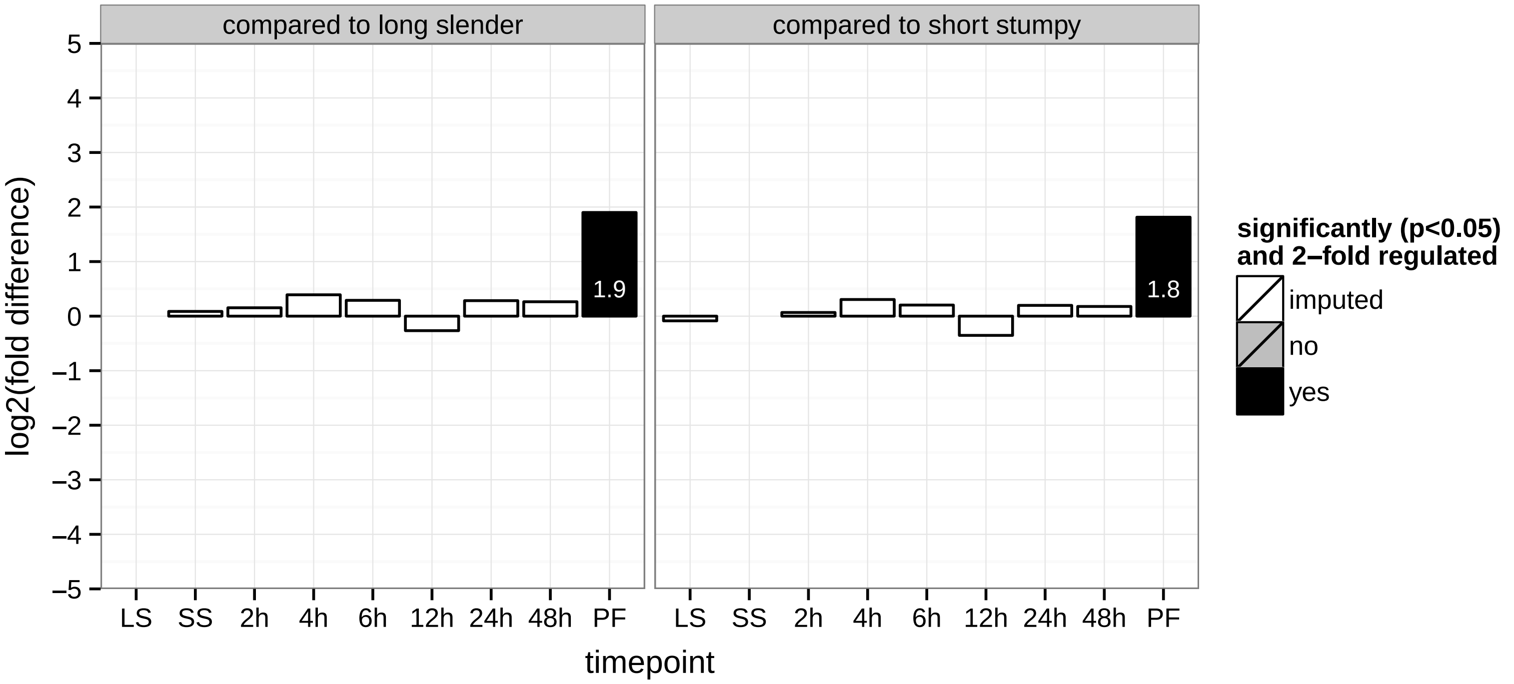
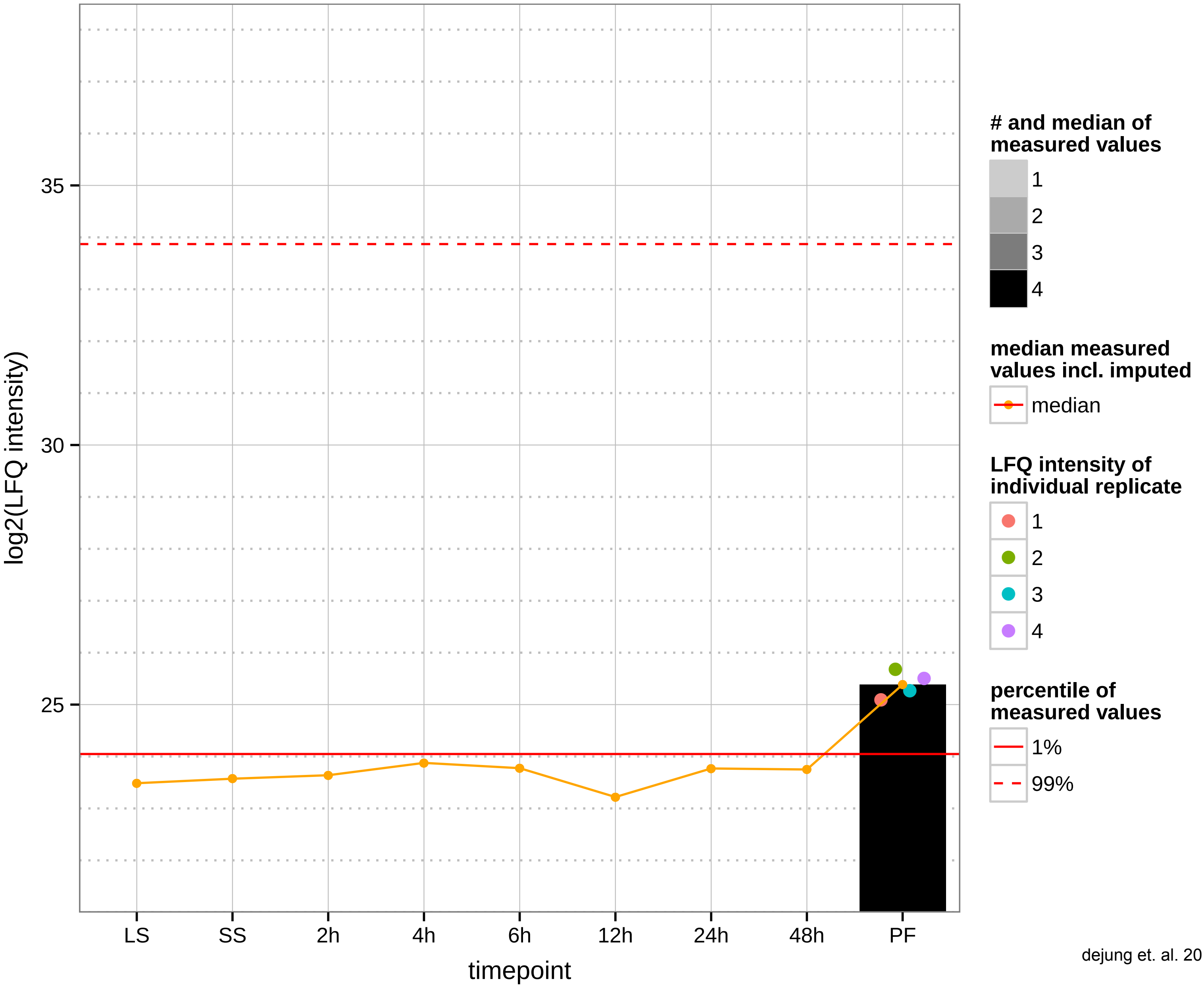
hypothetical protein, conserved
Tb927.9.7260
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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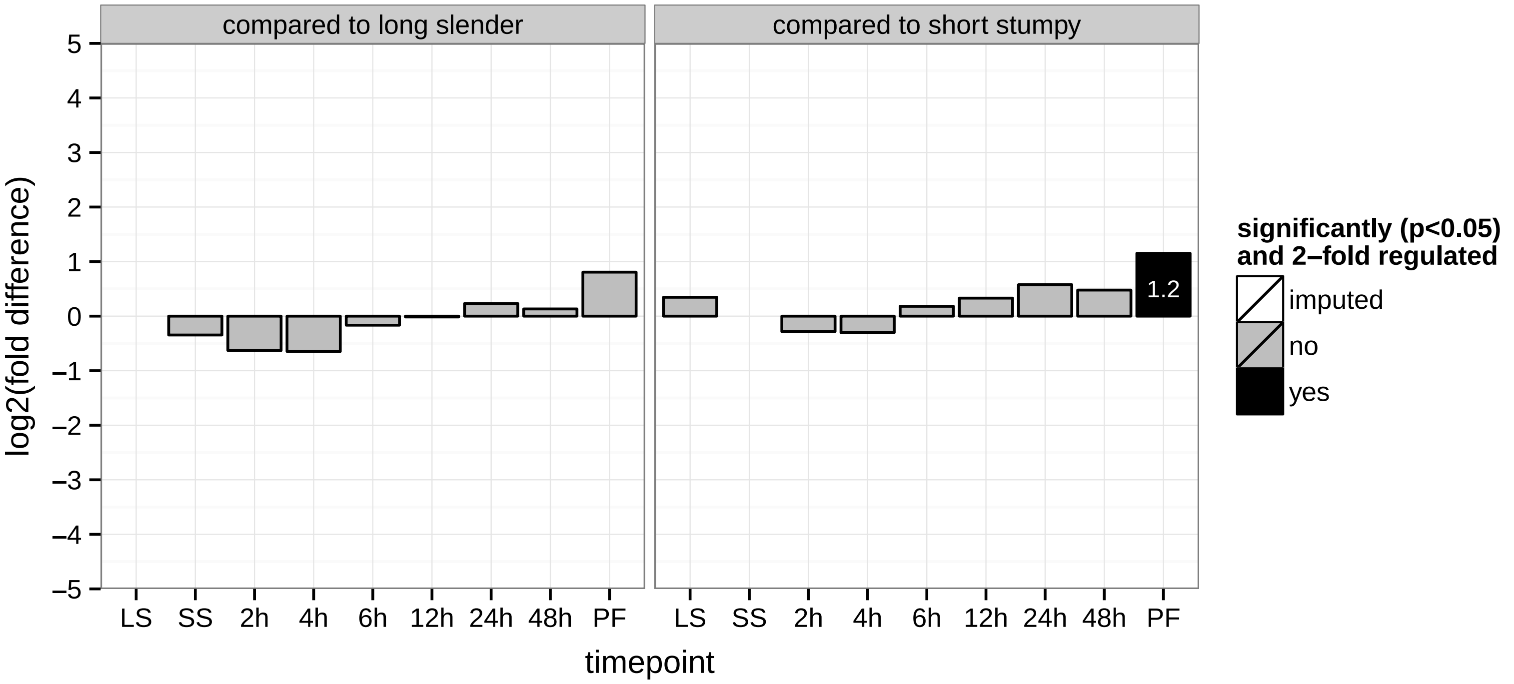
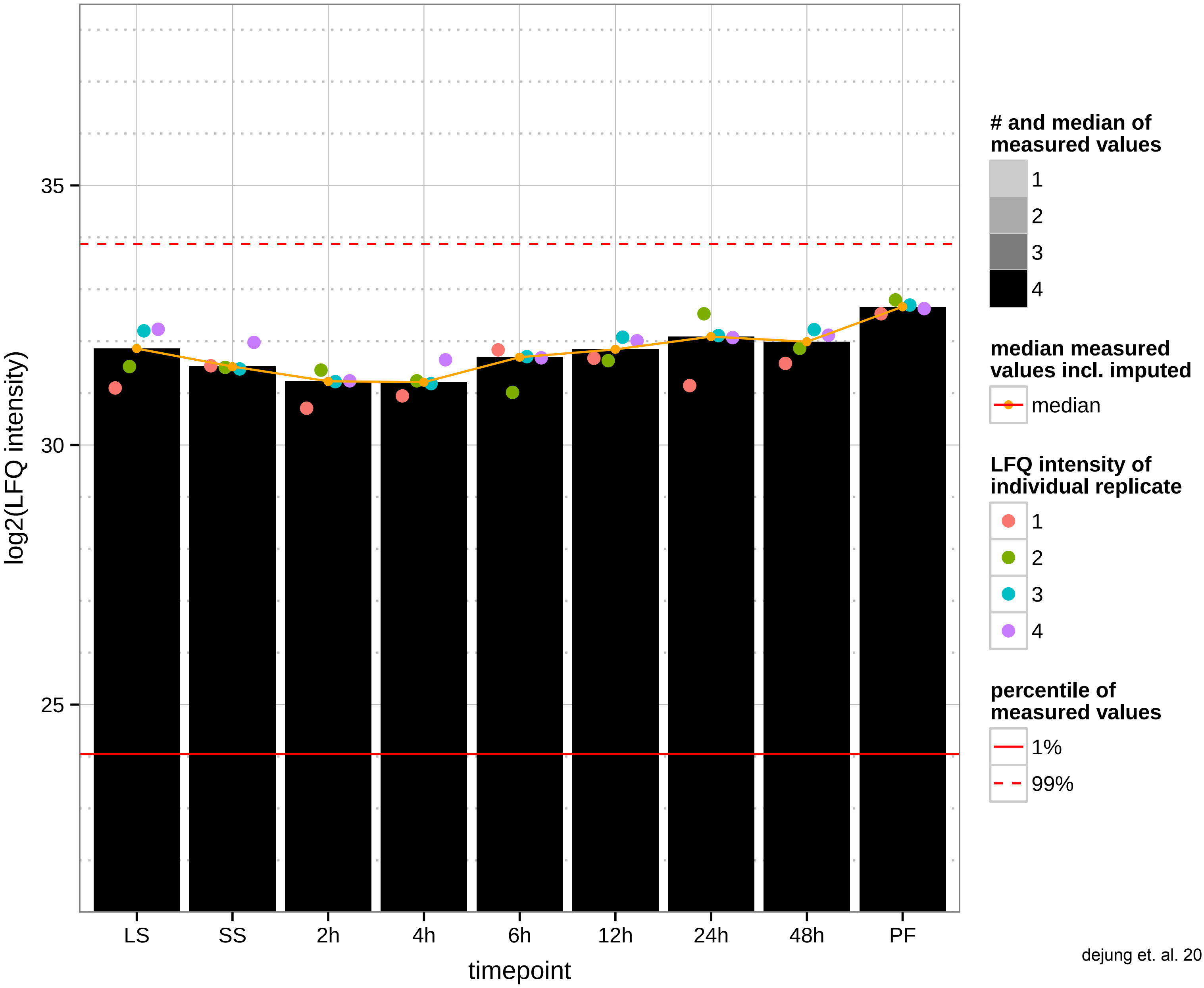
60S ribosomal protein L11, putative
Tb927.9.7620;Tb927.9.7590
AGOF: structural constituent of ribosome
AGOC: intracellular, organellar large ribosomal subunit, ribosome
AGOP: translation
PGOF: null, structural constituent of ribosome
PGOC: null, intracellular, ribosome
PGOP: null, translation





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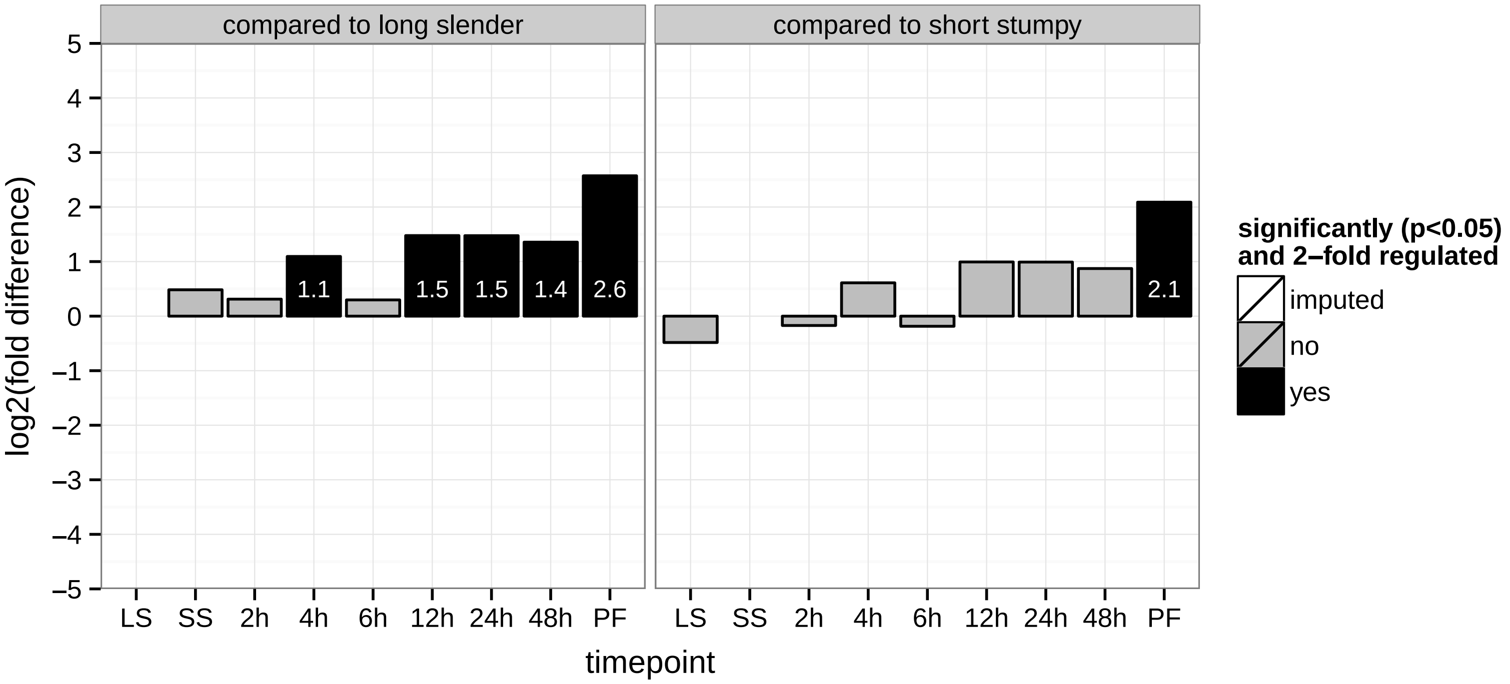
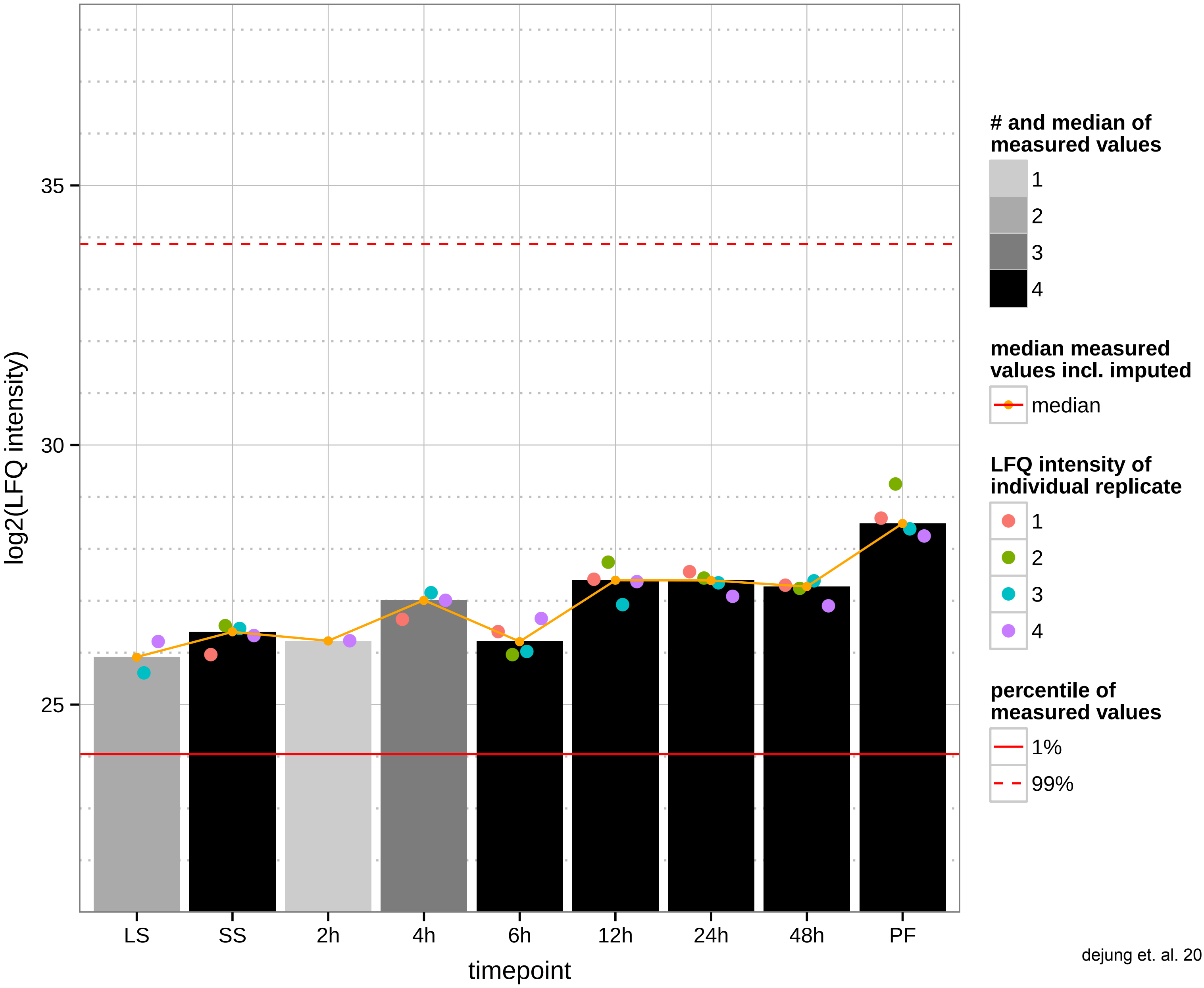
rhomboid–like protein, serine peptidase, Clan S–, family S54, putative
Tb927.9.8260
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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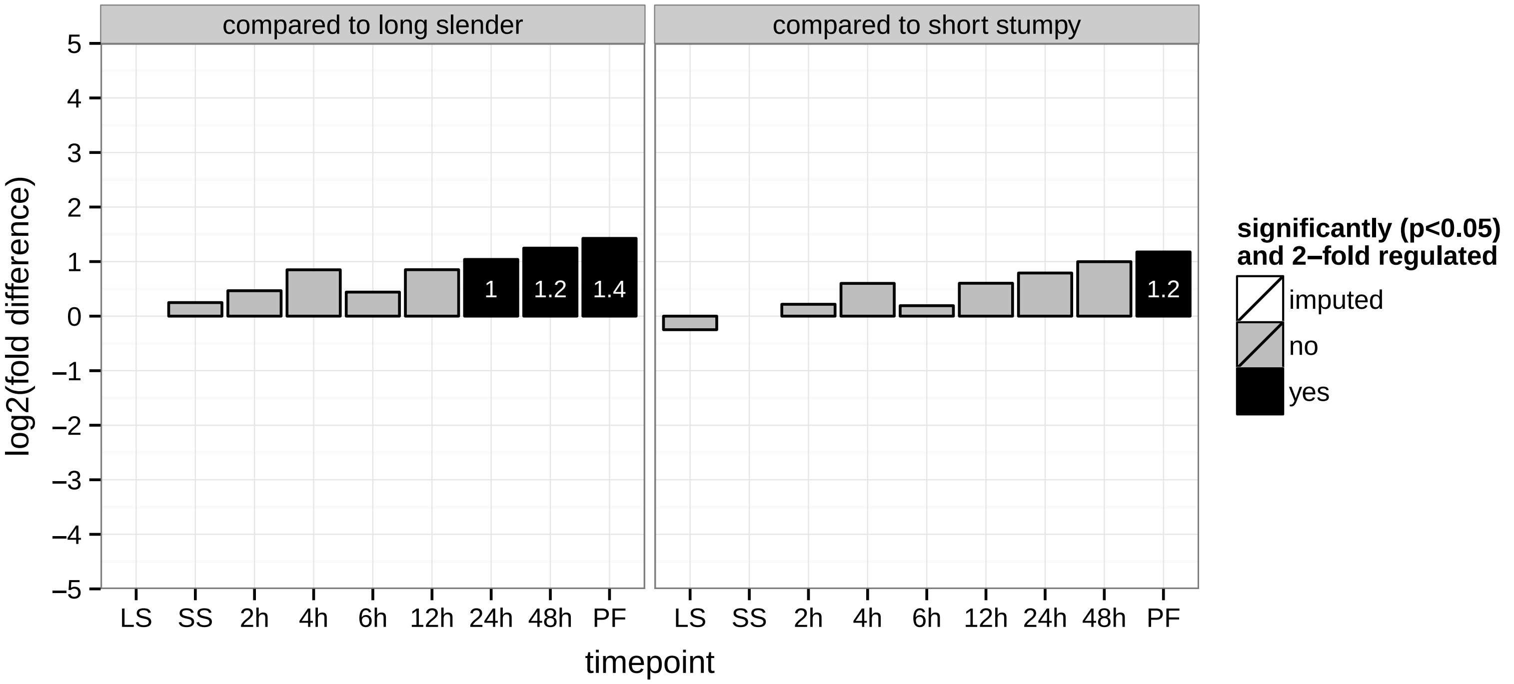
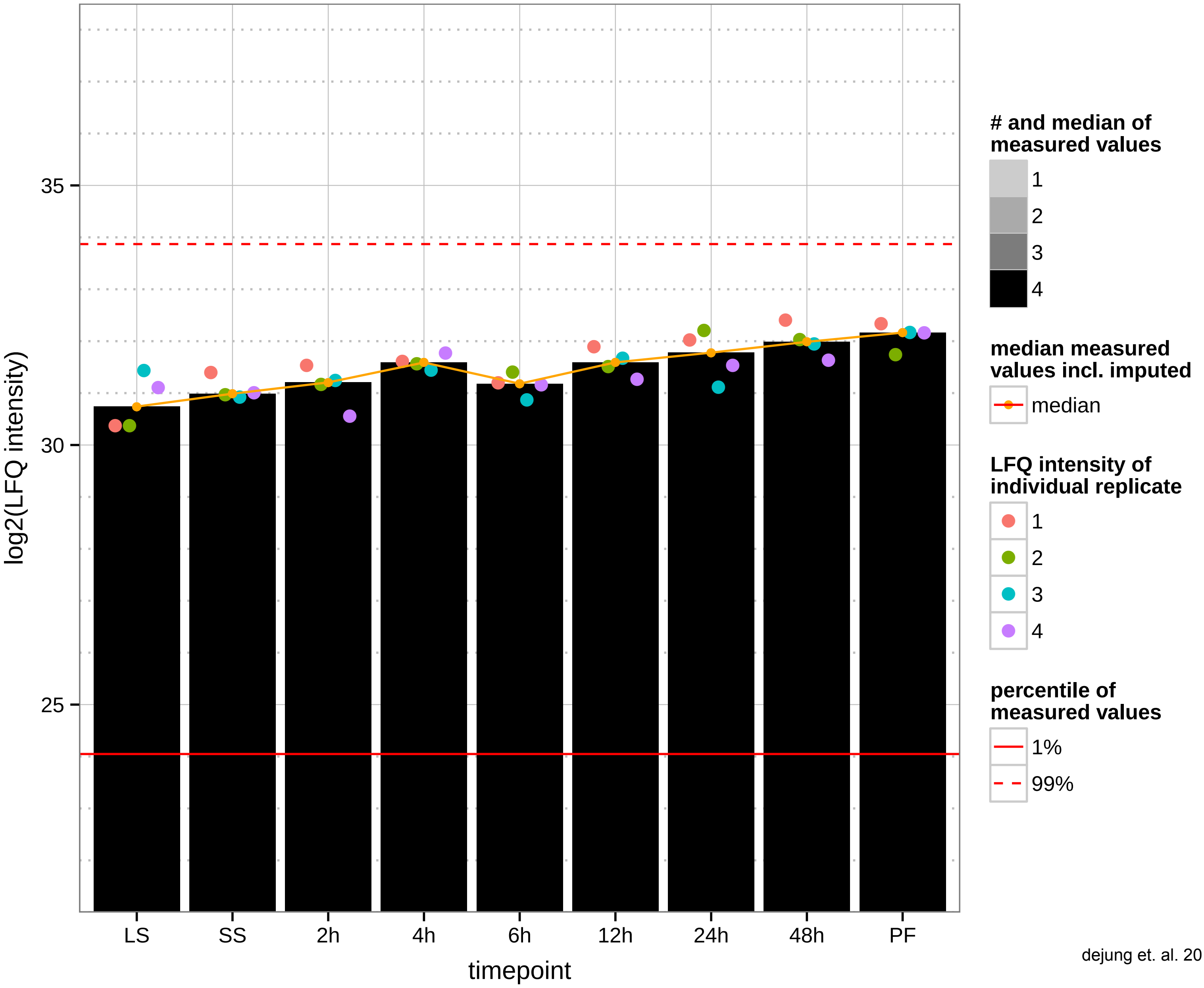
RNA–binding protein (DRBD3)
Tb927.9.8740
AGOF: mRNA 3'–UTR binding, mRNA binding
AGOC: cytosol, nucleus, ribonucleoprotein complex
AGOP: RNA processing, mRNA stabilization
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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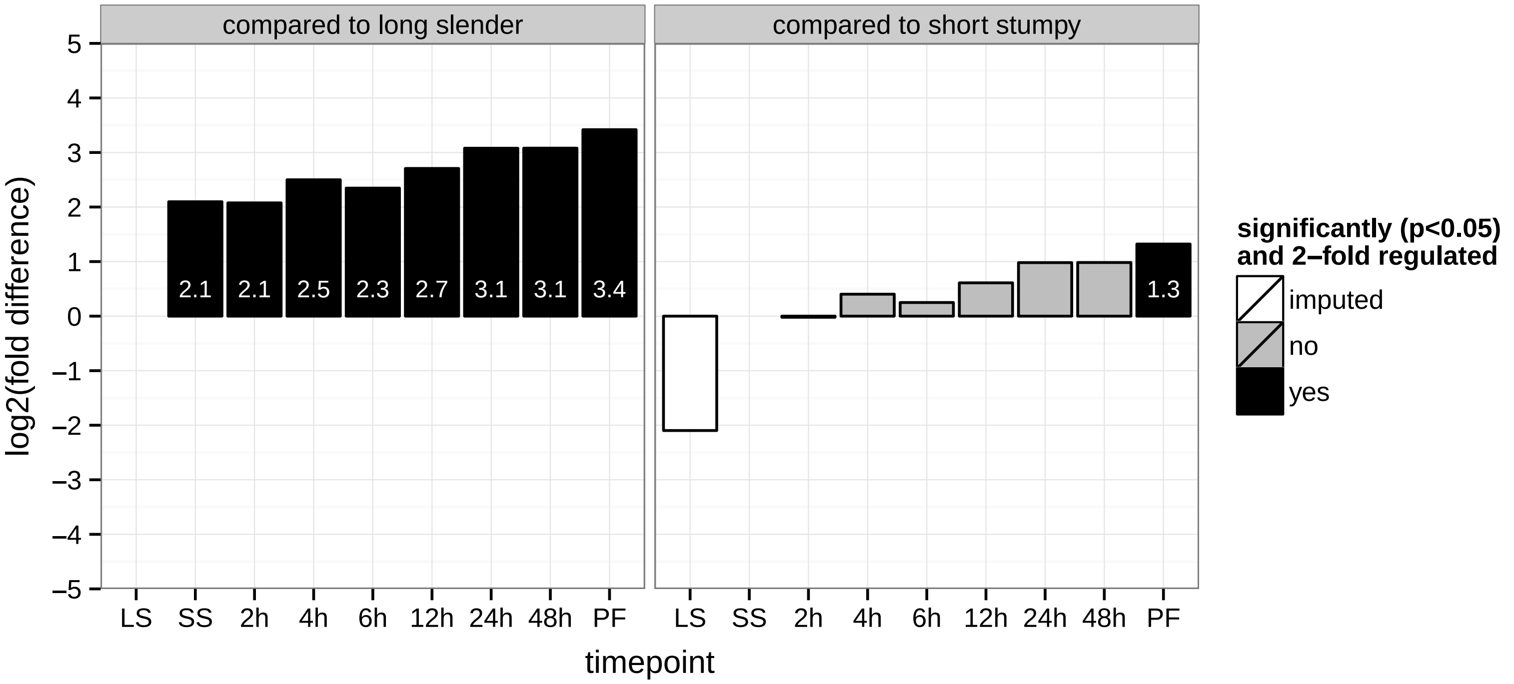
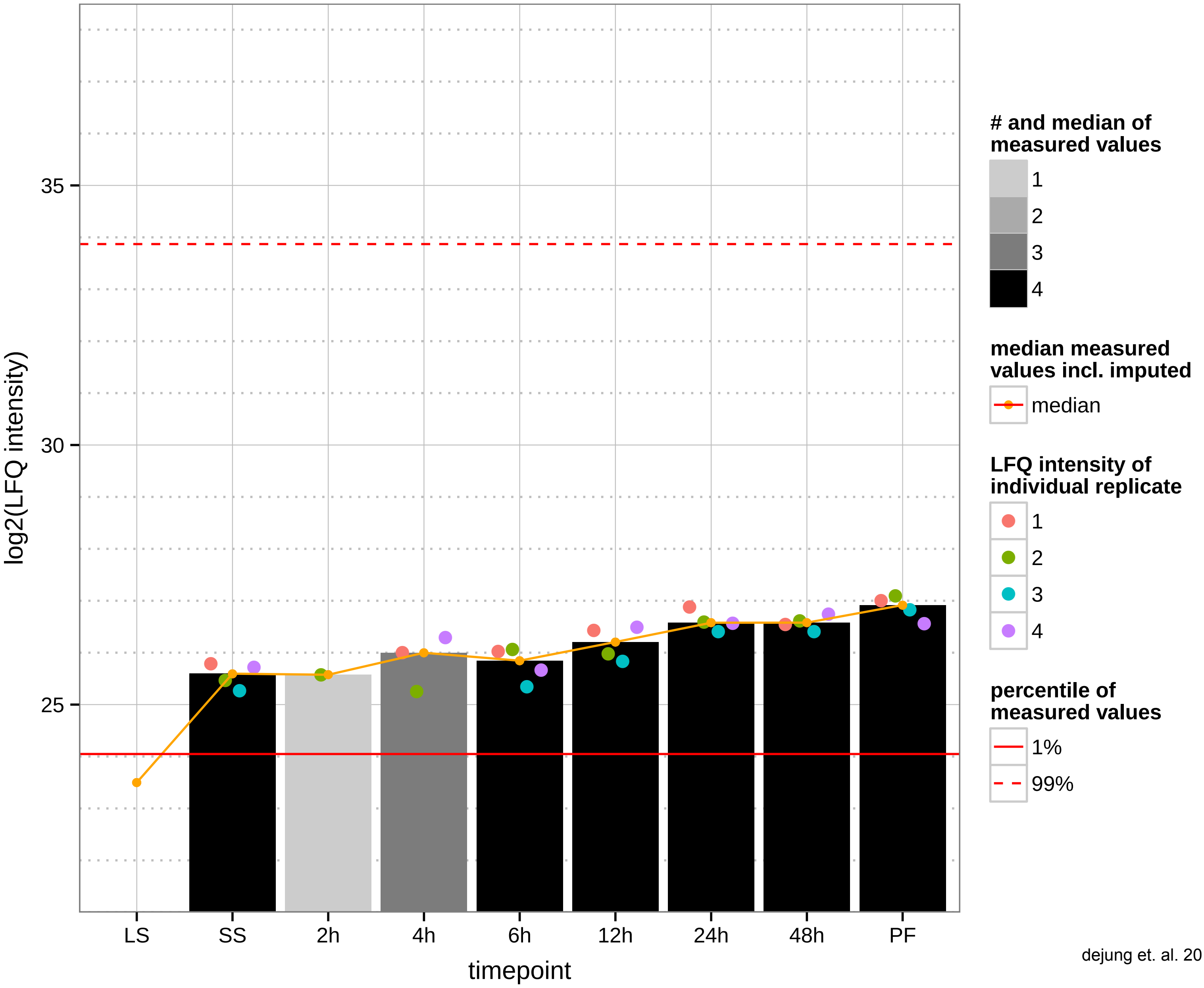
hypothetical protein, conserved
Tb927.9.9080
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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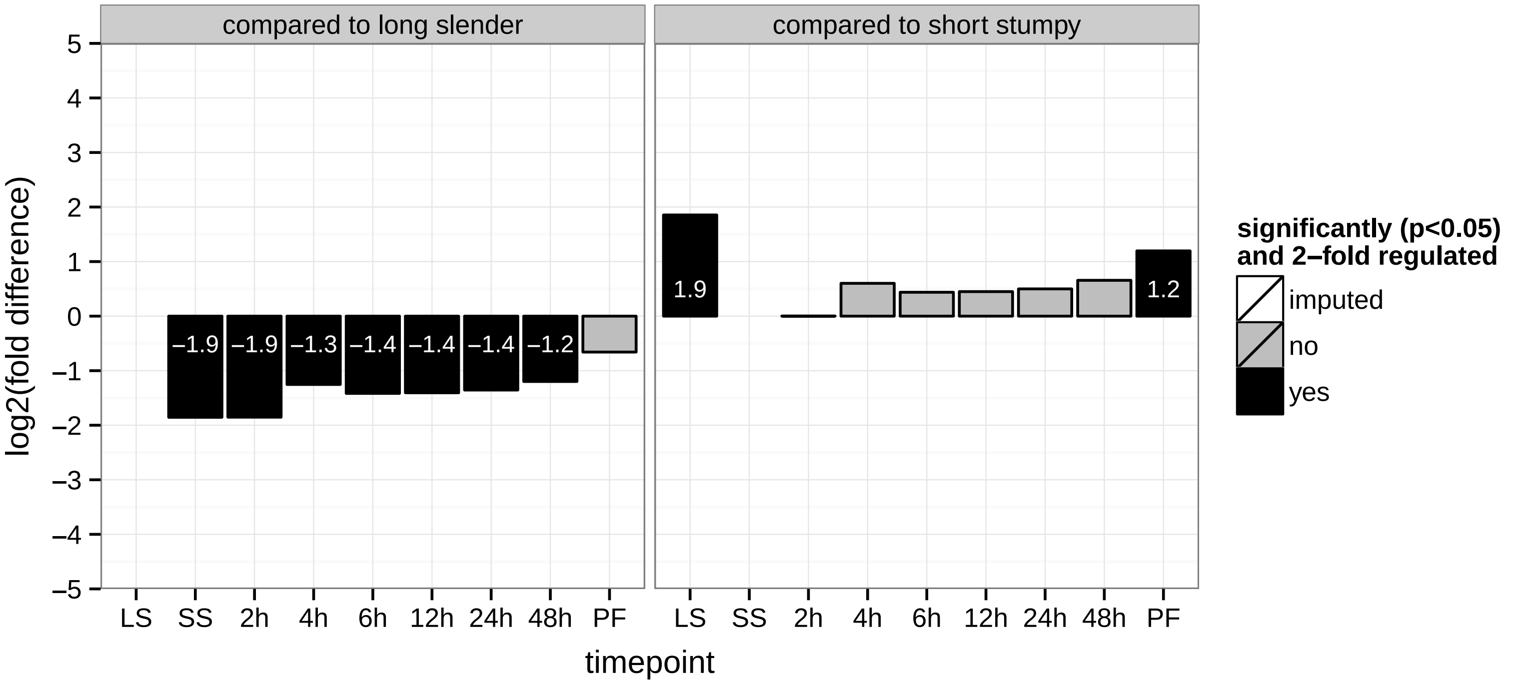
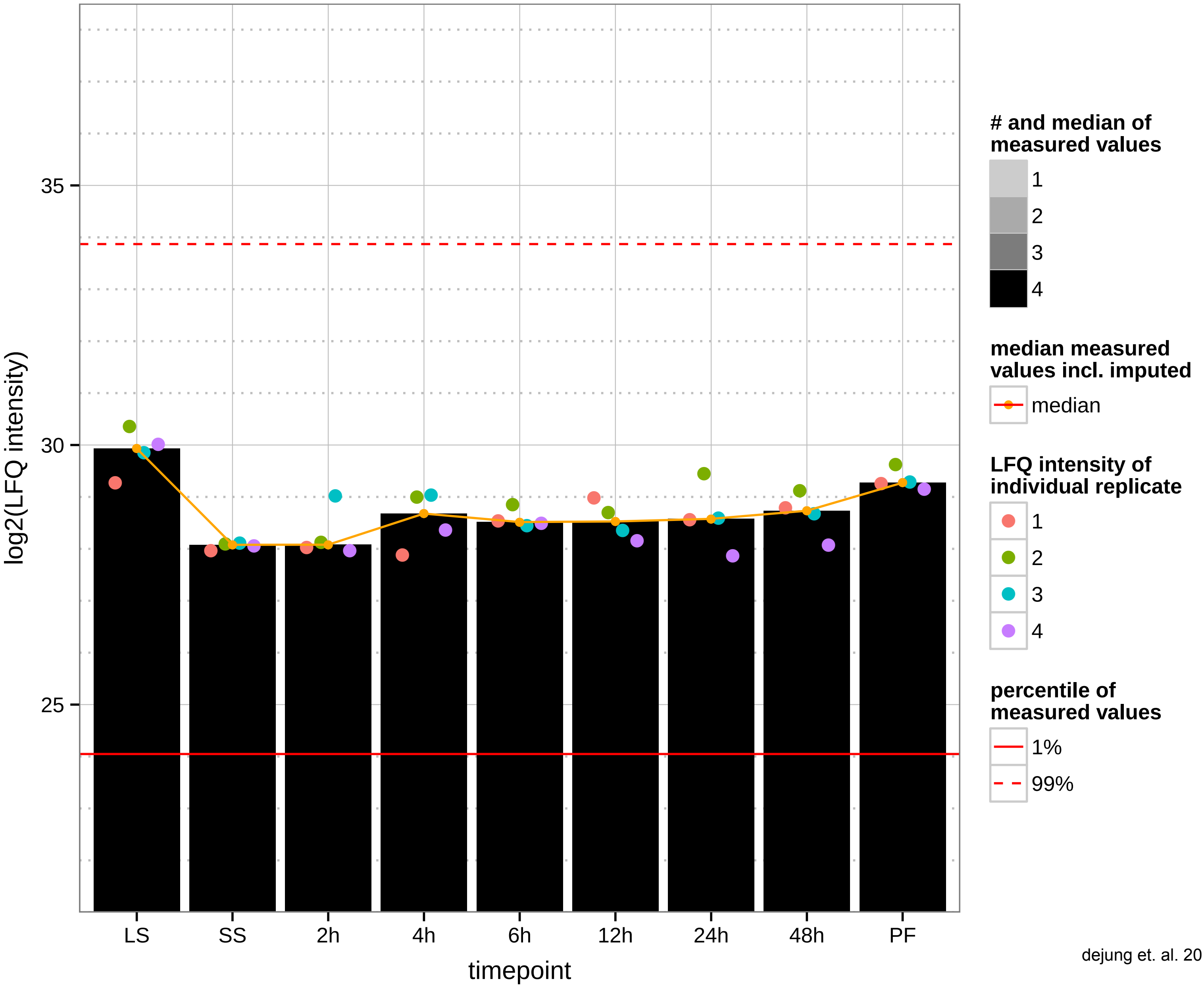
hypothetical protein, conserved
Tb927.9.9550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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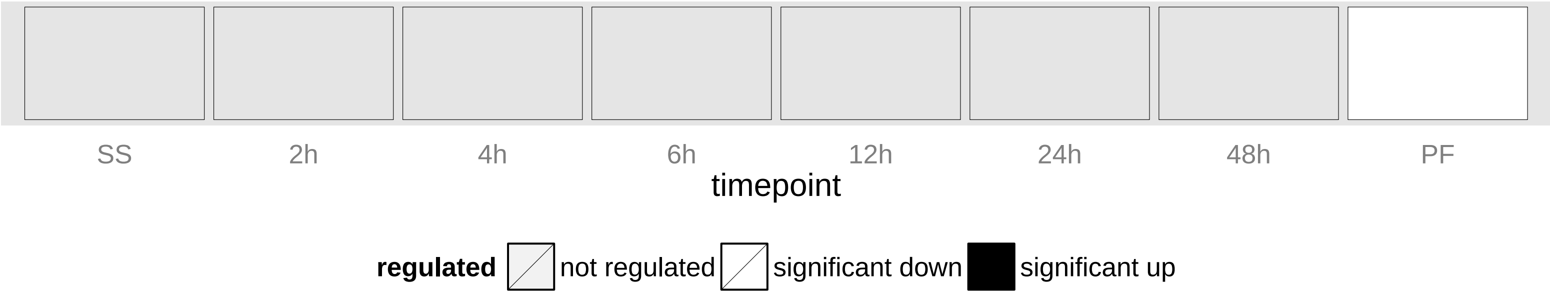

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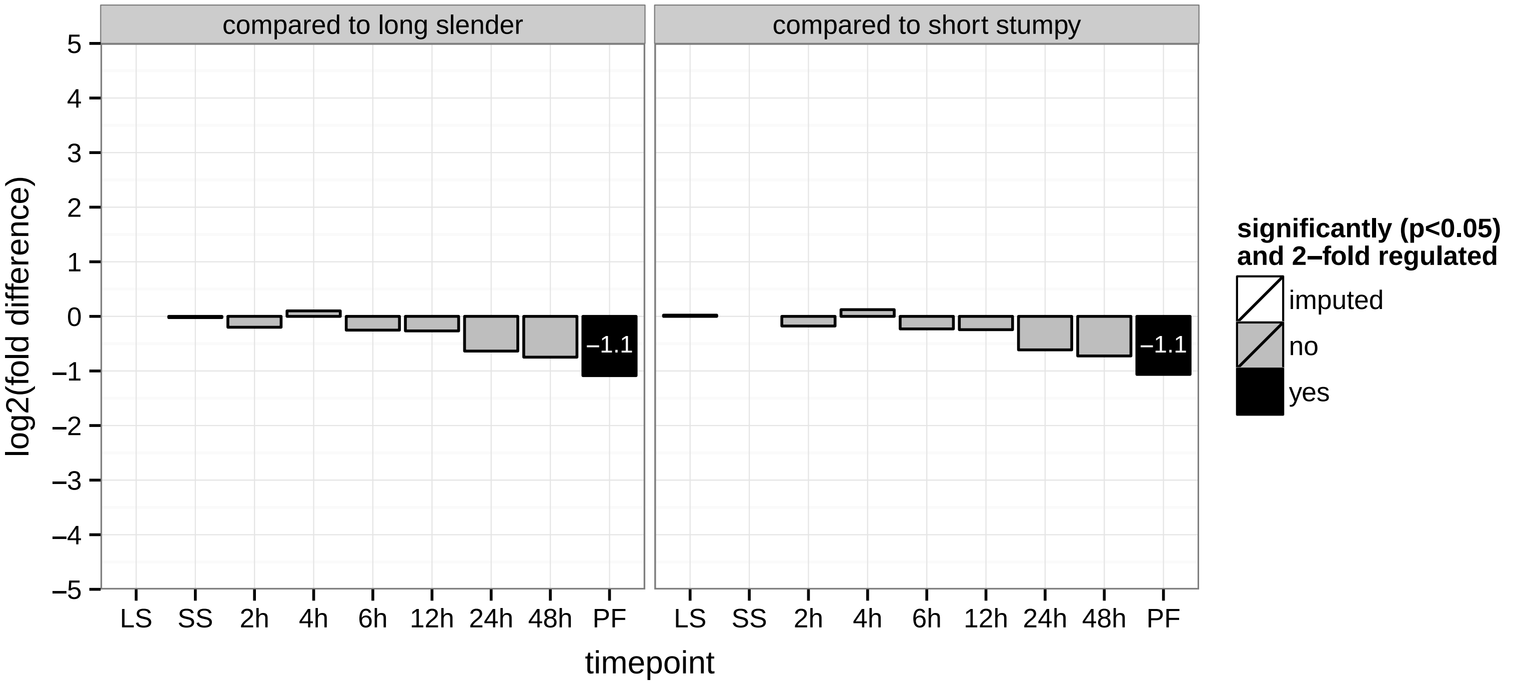
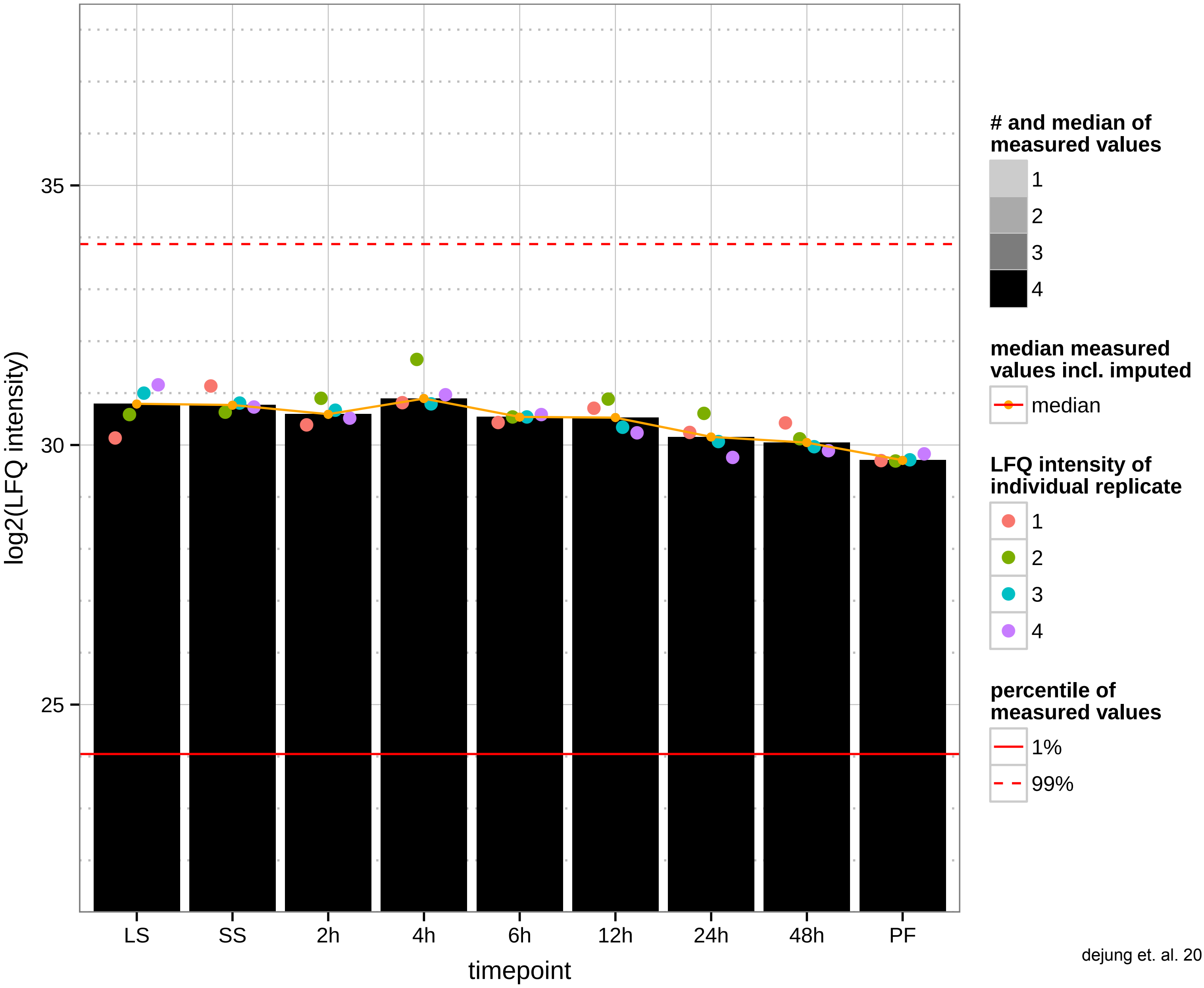
small GTP–binding protein, putative, BAC from homologous region on chr5, ras–like small GTPase, putative (TbSAR1)
Tb927.5.4500;Tb05.5K5.150
AGOF: GTP binding
AGOC: intracellular
AGOP: intracellular protein transport, small GTPase mediated signal transduction
PGOF: GTP binding
PGOC: intracellular
PGOP: intracellular protein transport, small GTPase mediated signal transduction





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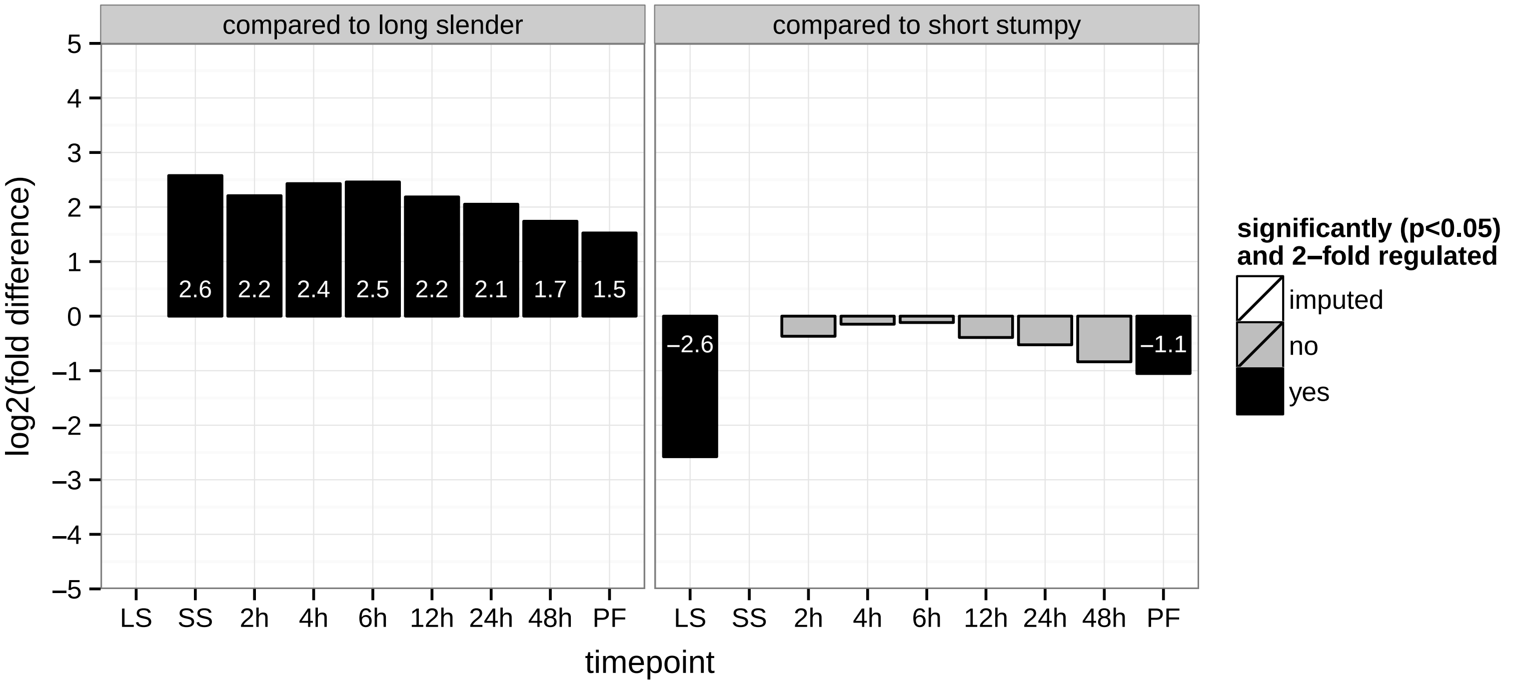
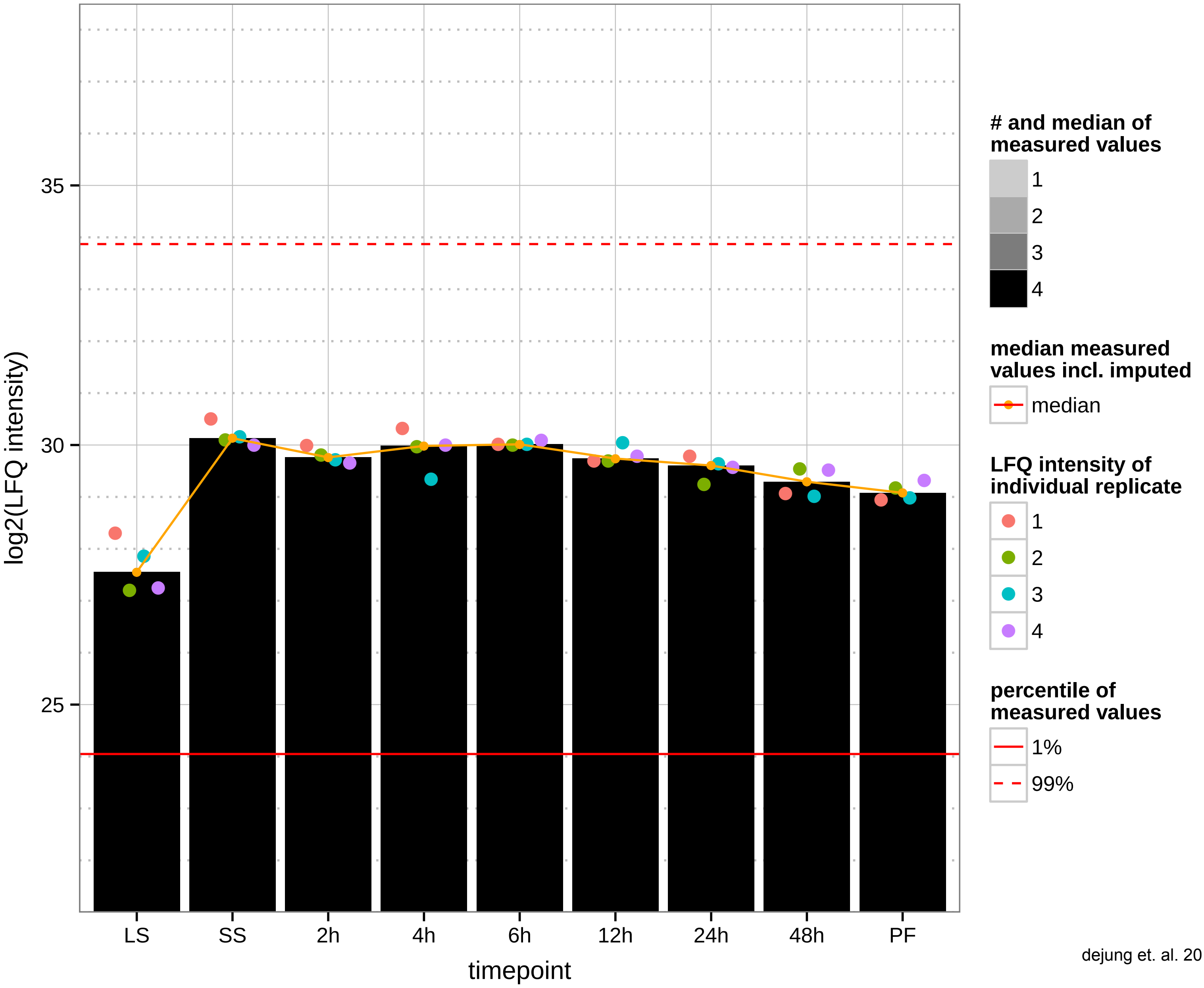
pumillo RNA binding protein PUF1, chrX additional, unordered contigs (PUF1), variant surface glycoprotein, fragment, putative
Tb927.10.4430;Tb10.v4.0033;Tb11.v5.0767
AGOF: RNA binding, null
AGOC: null, cytoplasm
AGOP: null, cell growth, mRNA metabolic process
PGOF: RNA binding, binding, null
PGOC: null
PGOP: null





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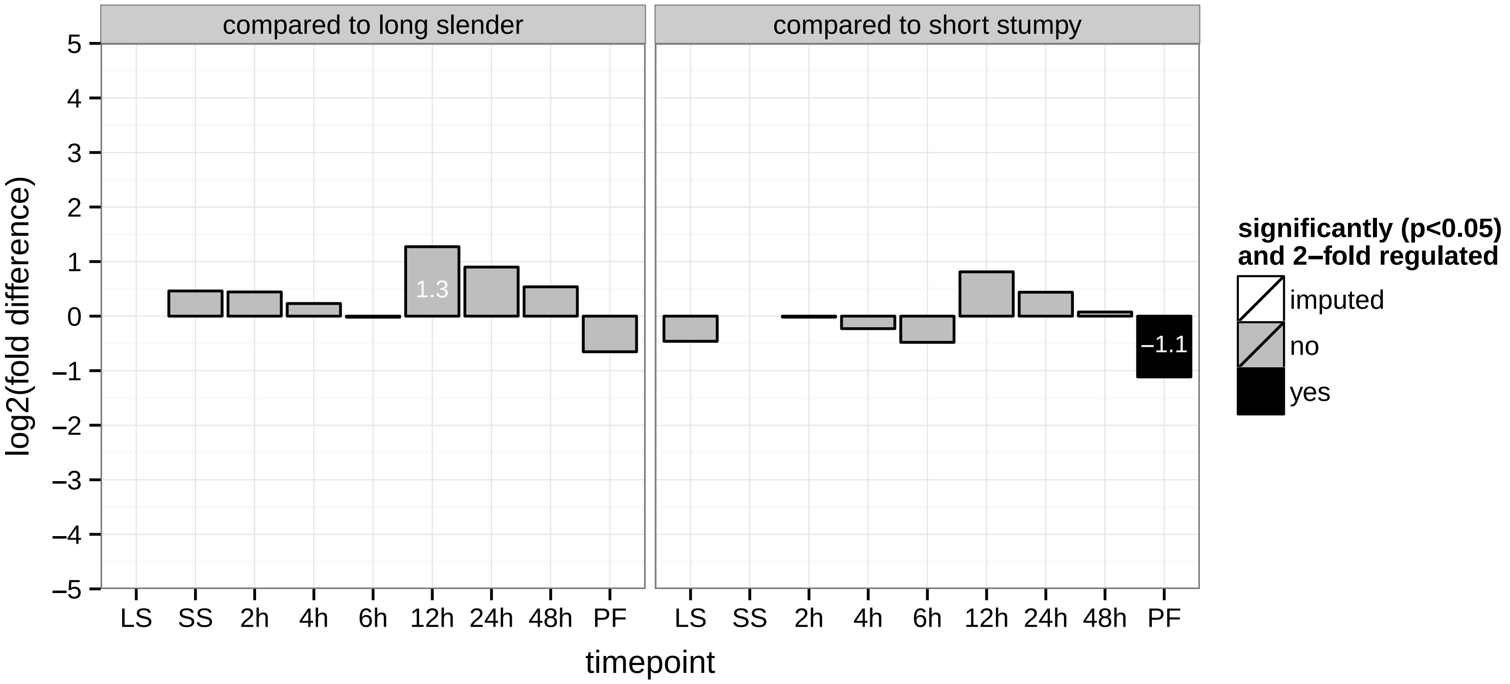
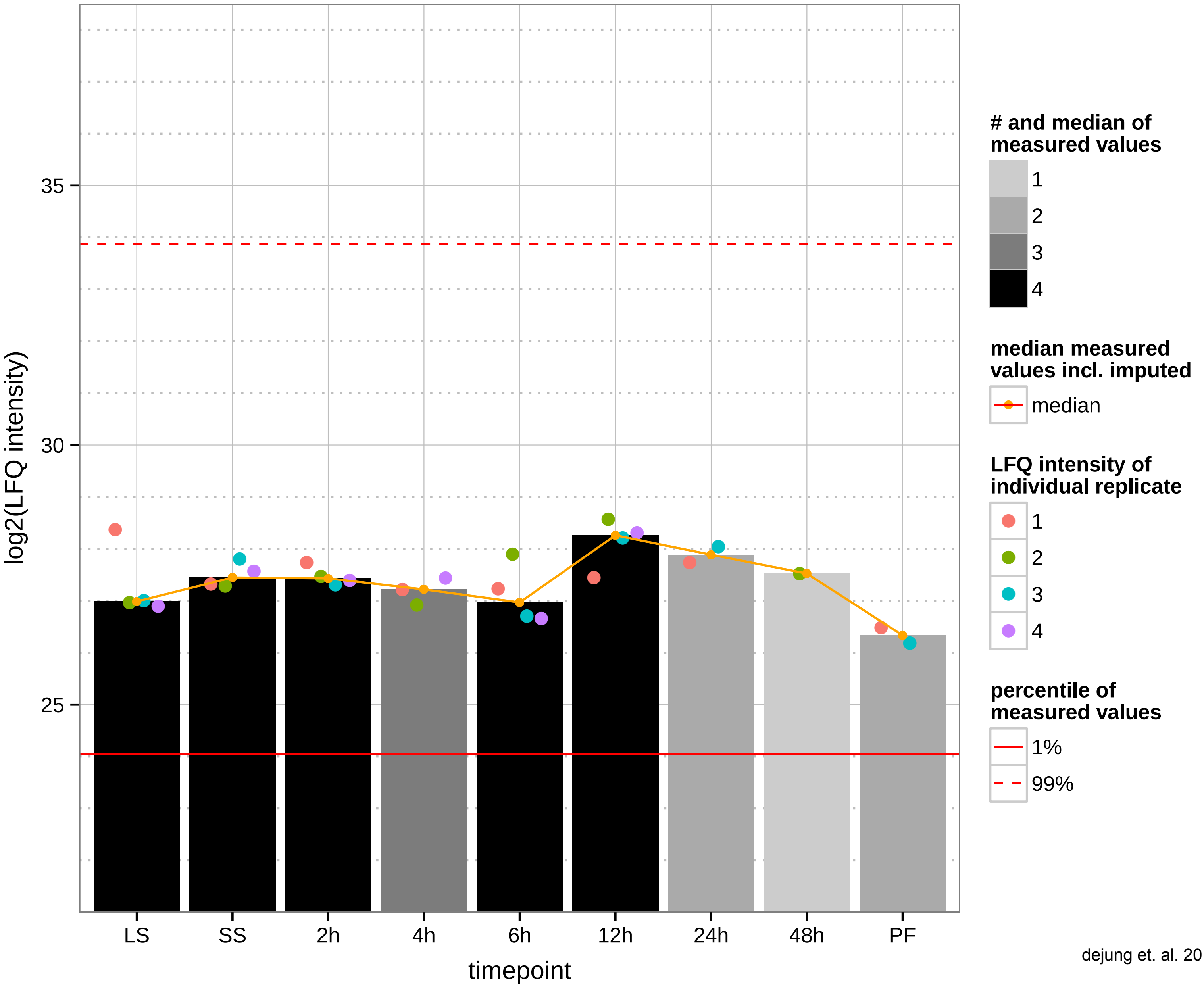
hypothetical protein, conserved
Tb927.11.7213;Tb11.02.5080b
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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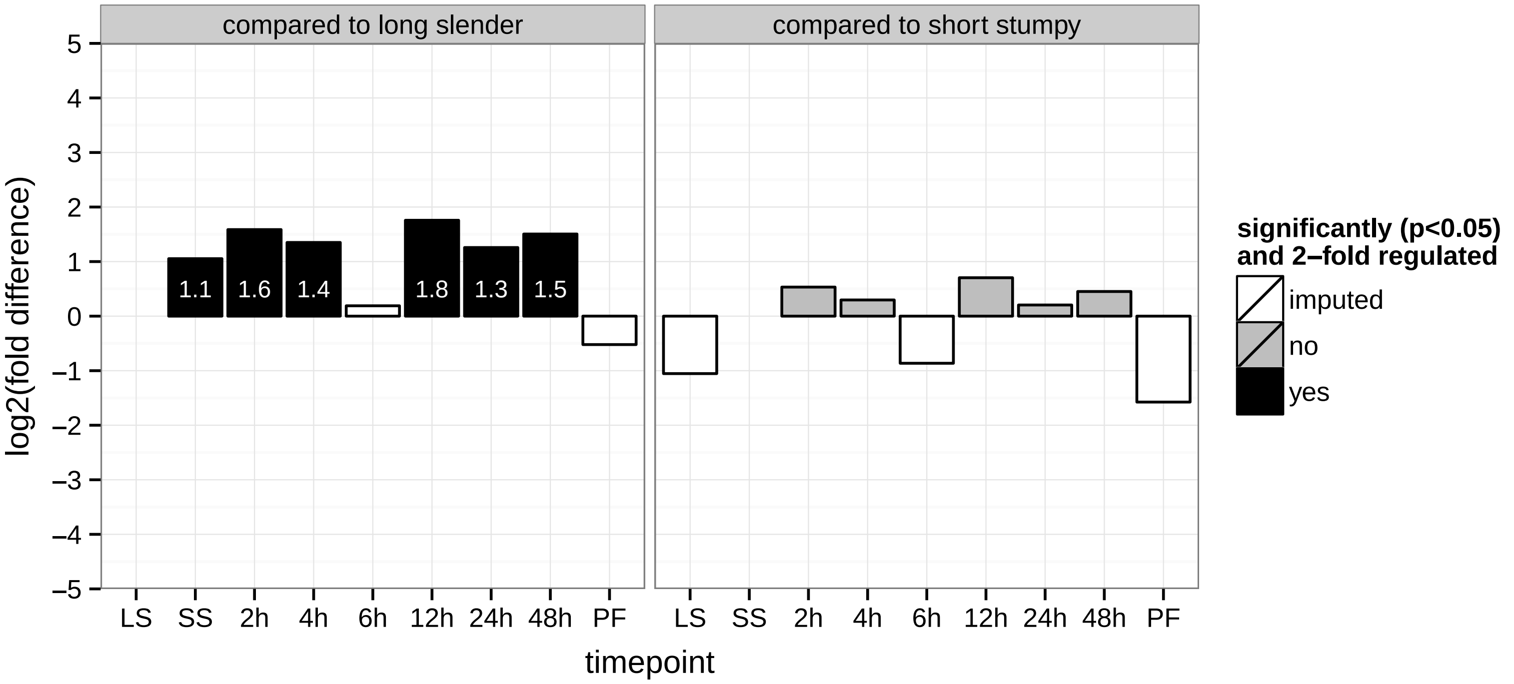
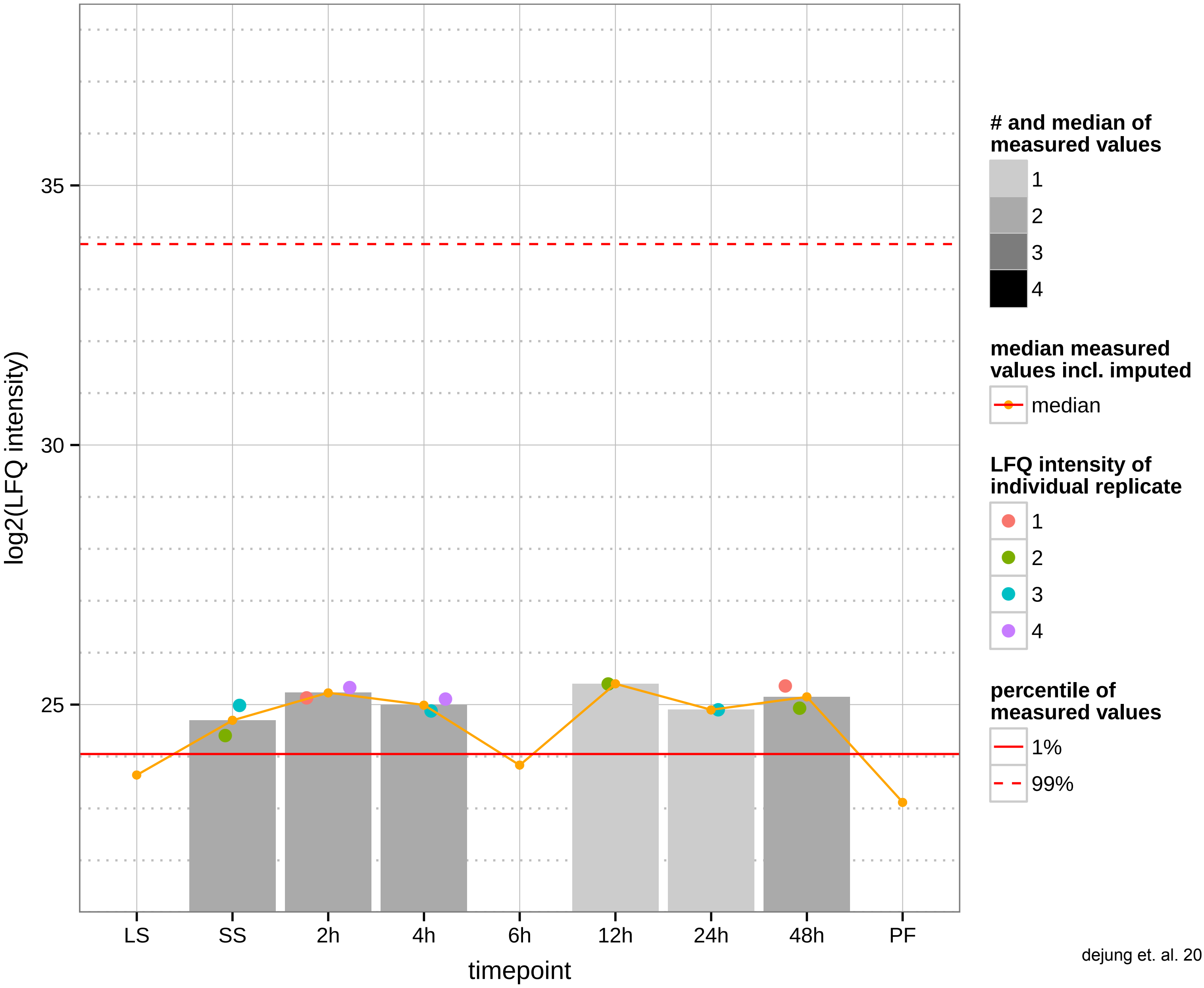
ubiquitin activating enzyme, putative
Tb11.02.5410b;Tb11.02.5410
AGOF: catalytic activity
AGOC: null
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null





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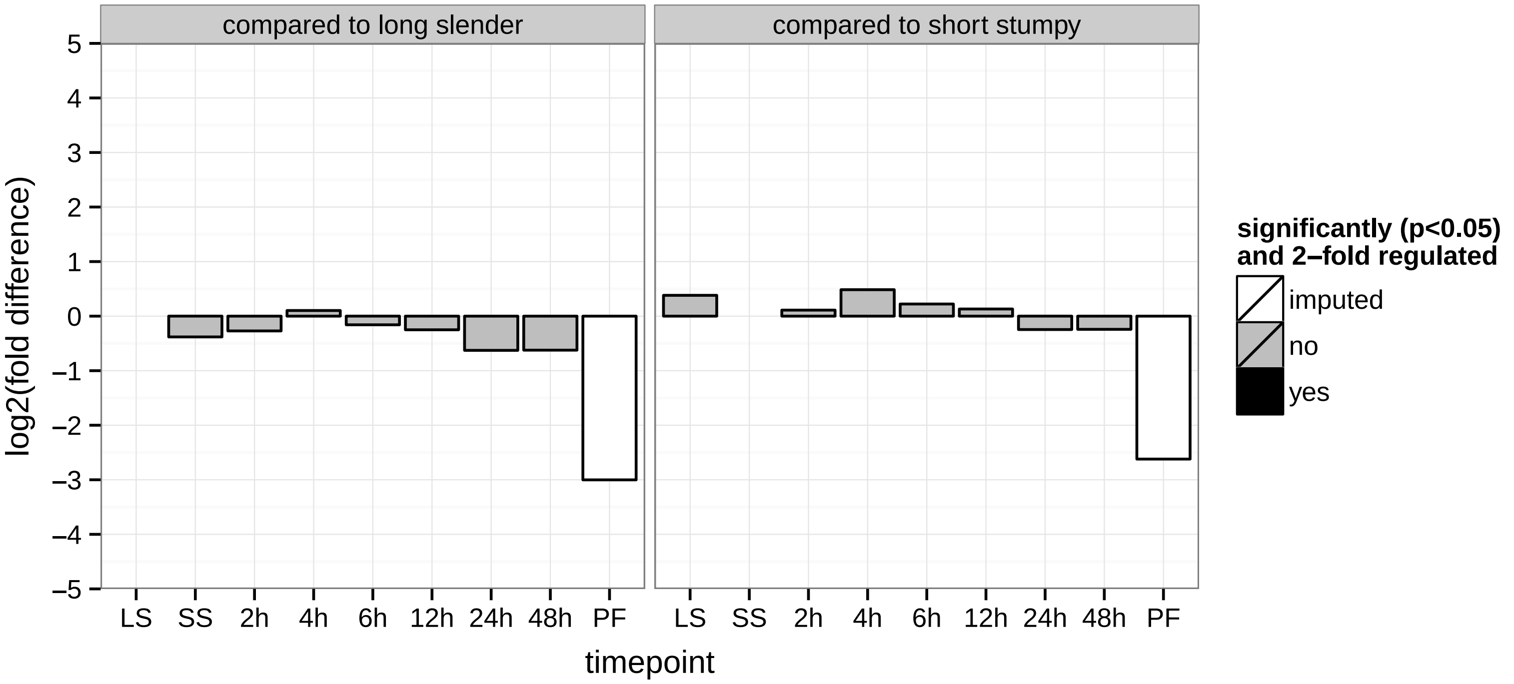
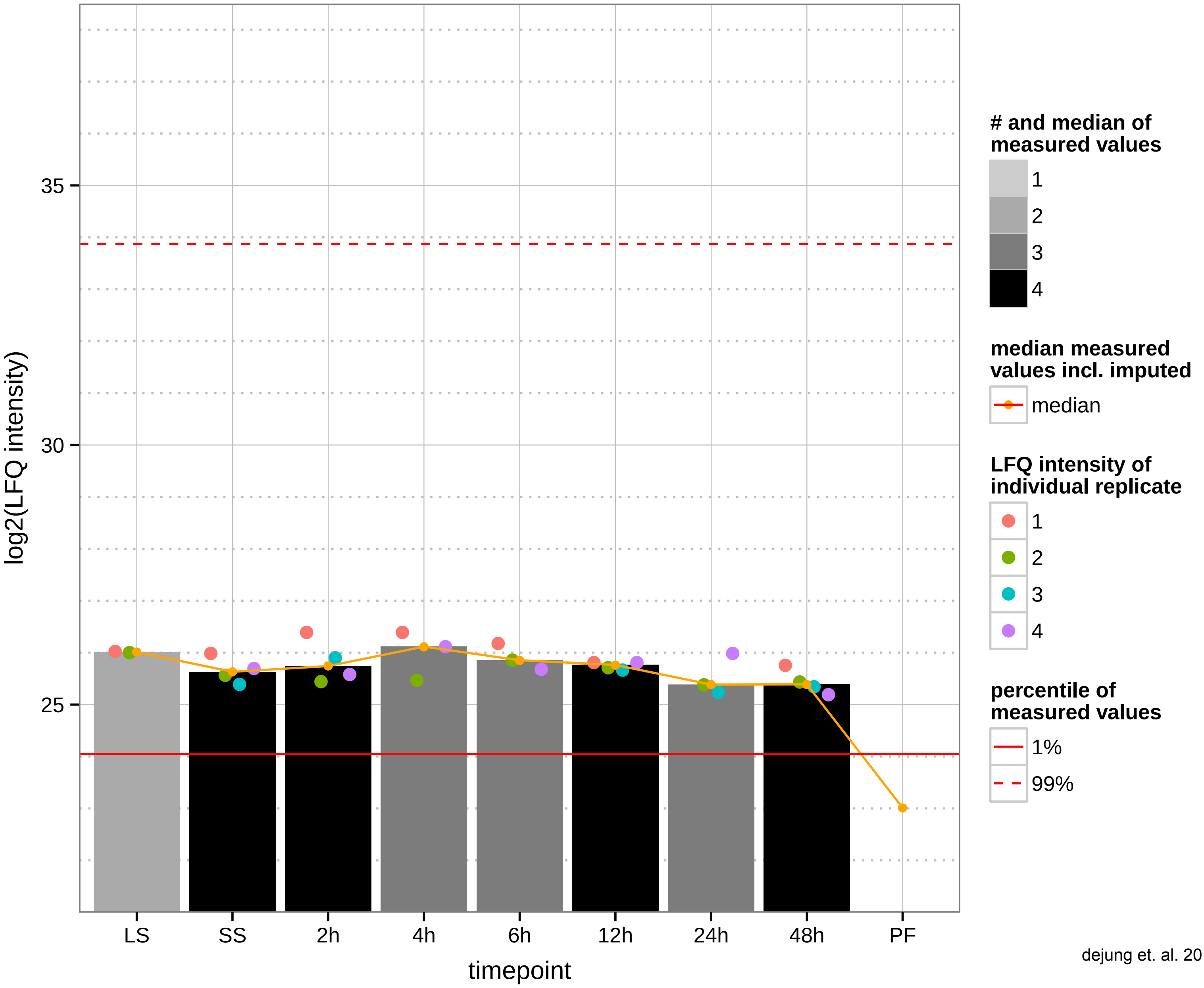
hypothetical protein, chrXI additional, unordered contigs, conserved
Tb11.0850;Tb927.11.710
AGOF: null
AGOC: integral to membrane
AGOP: protein transport
PGOF: null
PGOC: integral to membrane
PGOP: protein transport





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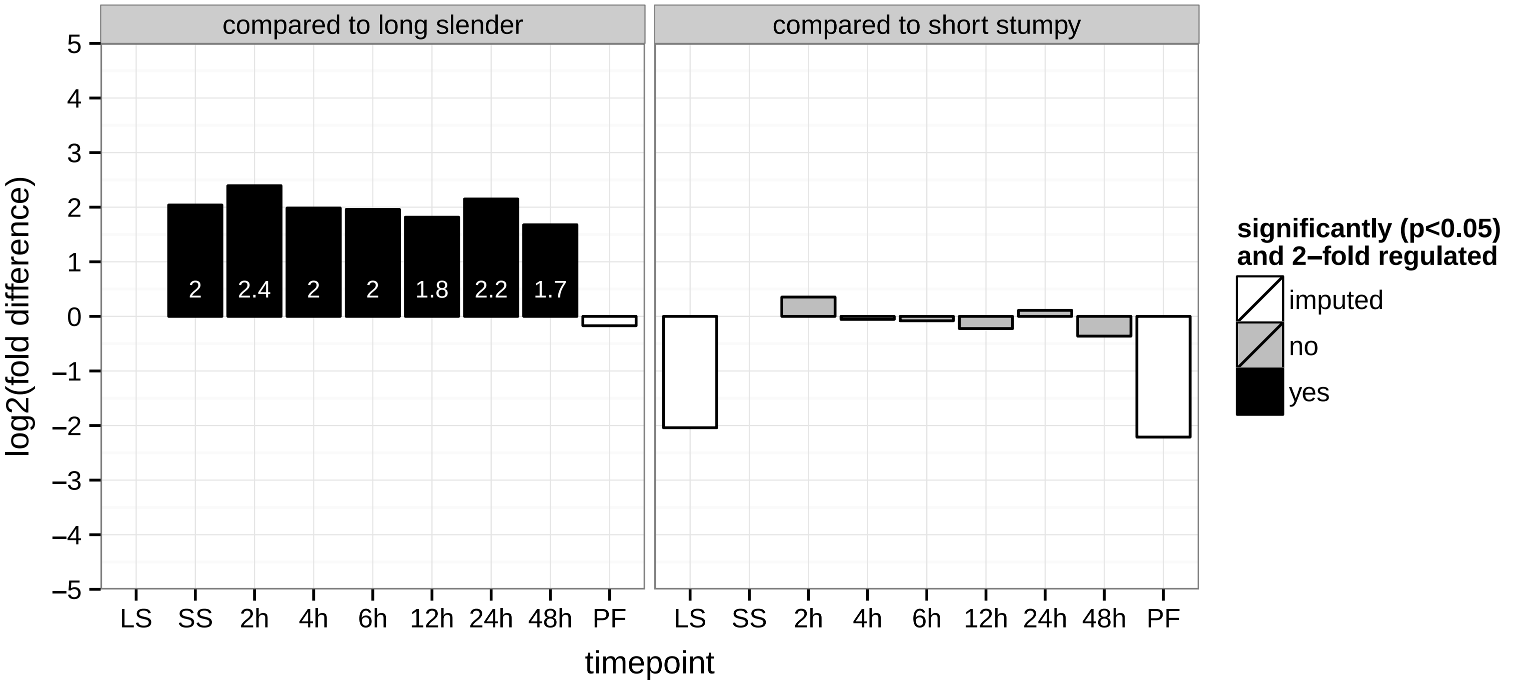
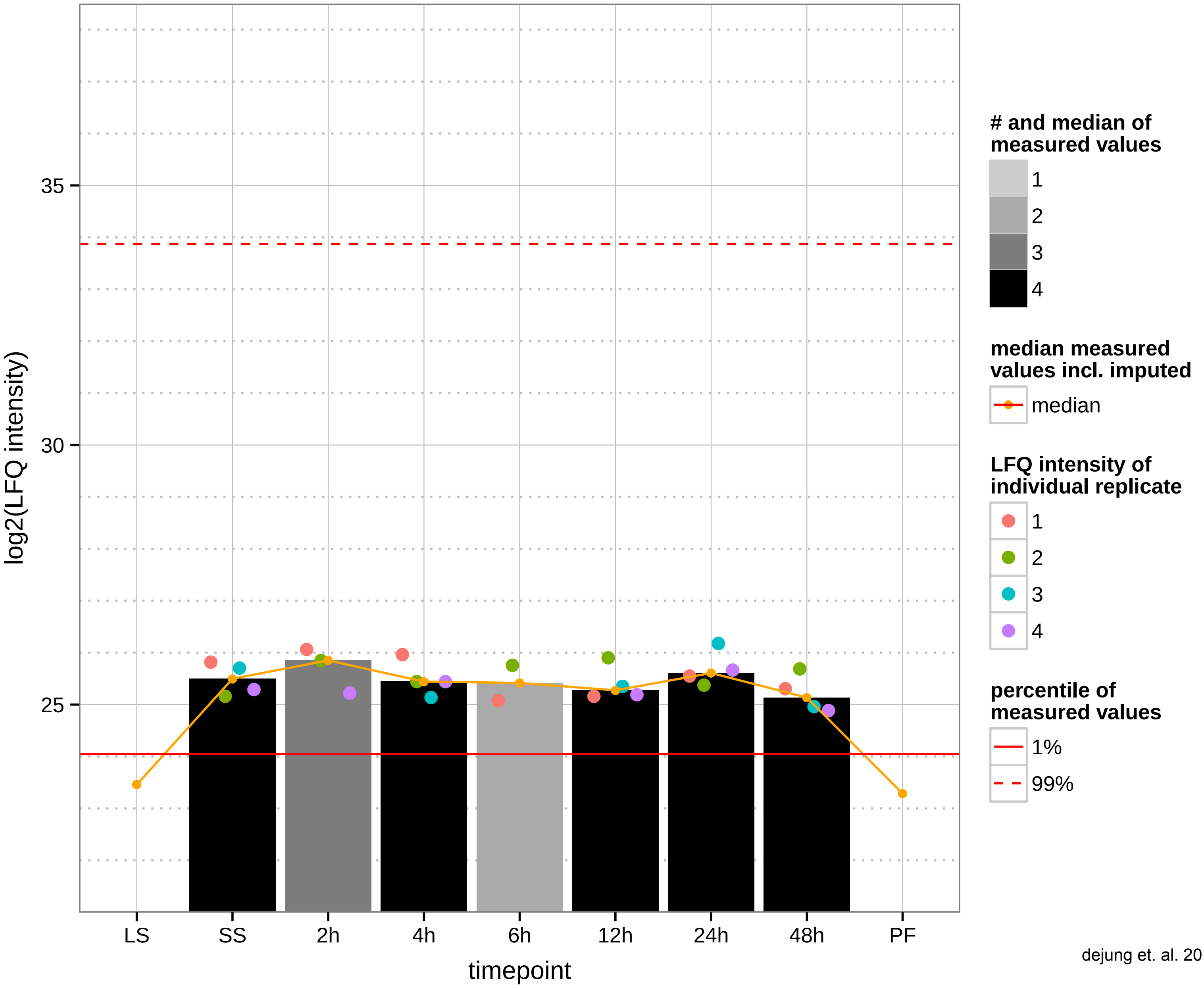
hypothetical protein, conserved
Tb927.7.4810;Tb11.v5.0163
AGOF: null, catalytic activity
AGOC: null
AGOP: null
PGOF: catalytic activity, metal ion binding, phosphoric diester hydrolase activity
PGOC: null
PGOP: null





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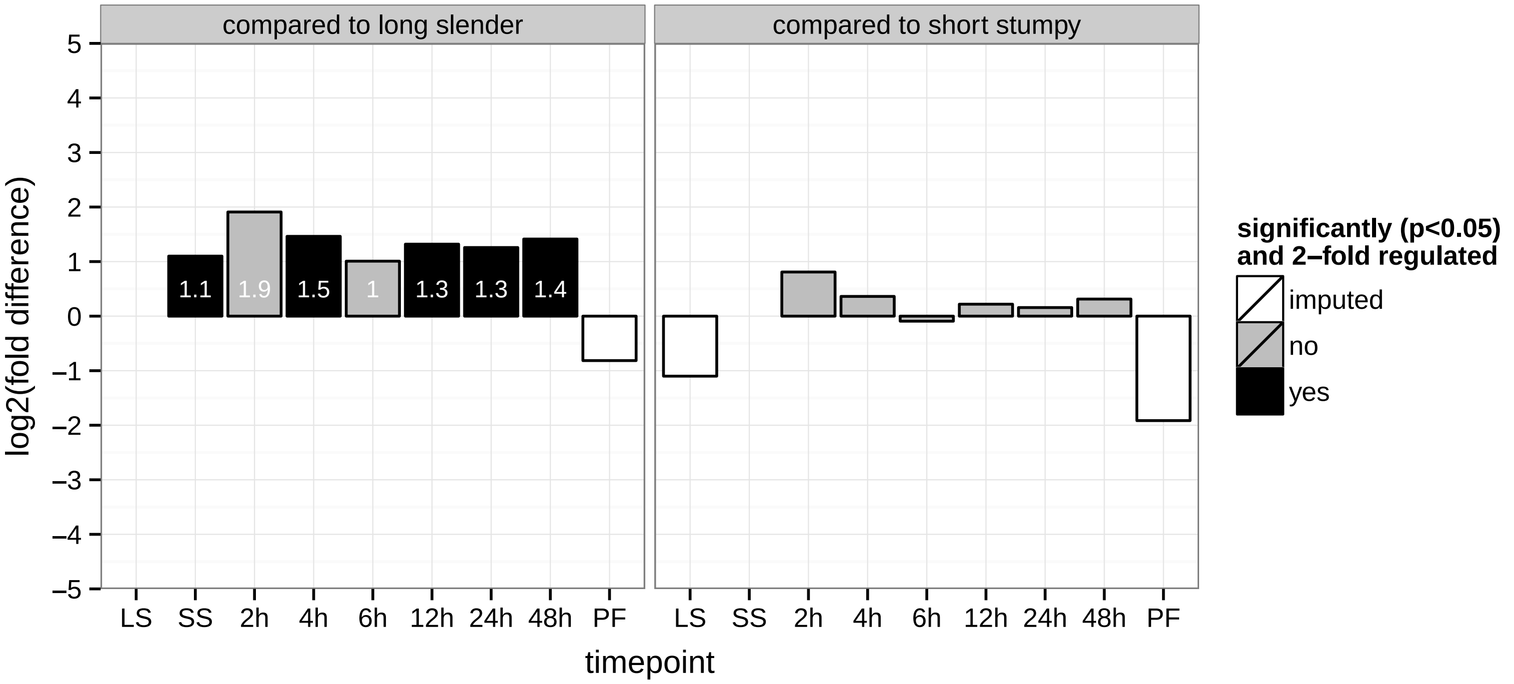
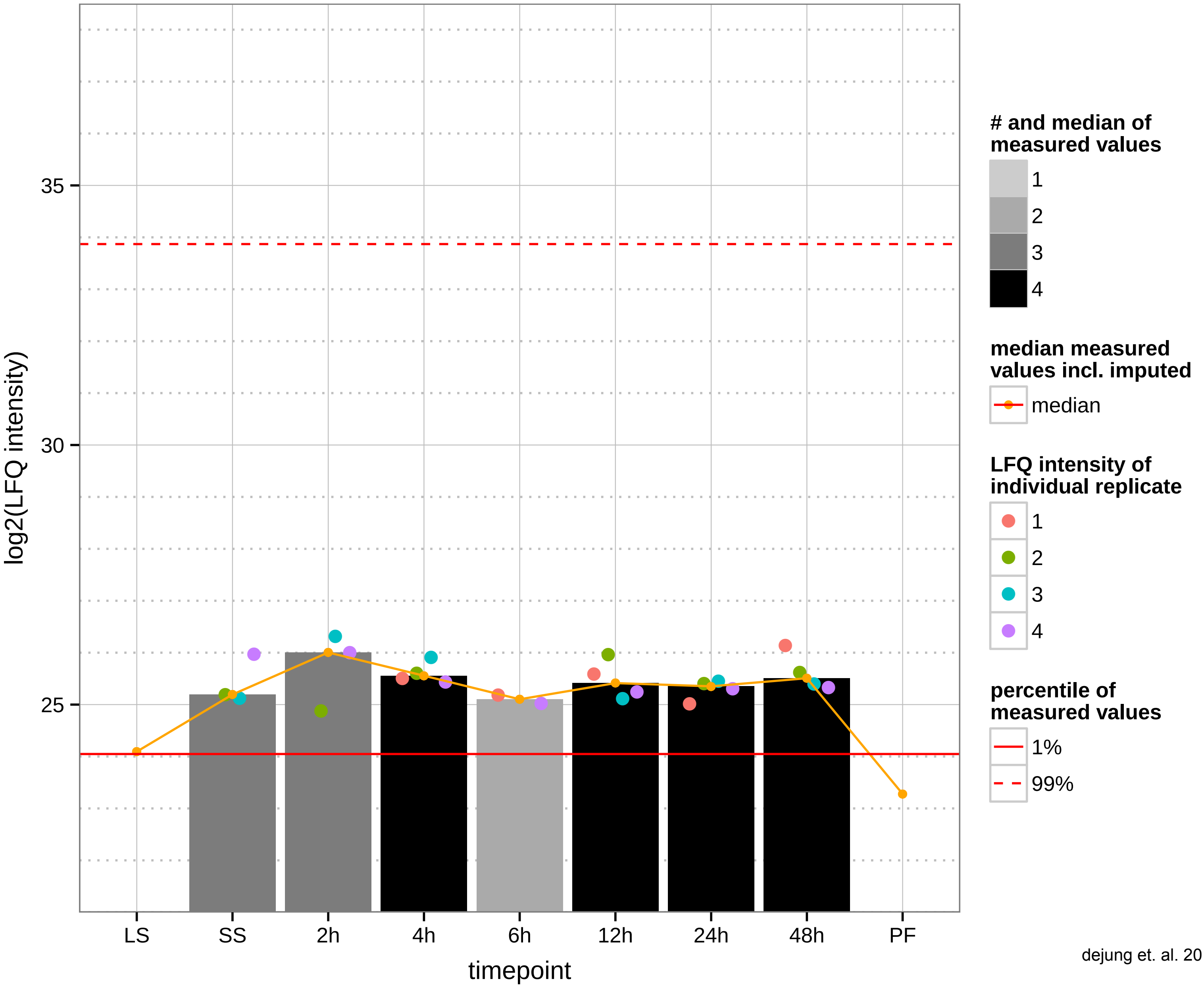
hypothetical protein, conserved
Tb927.10.5990;Tb11.v5.0193
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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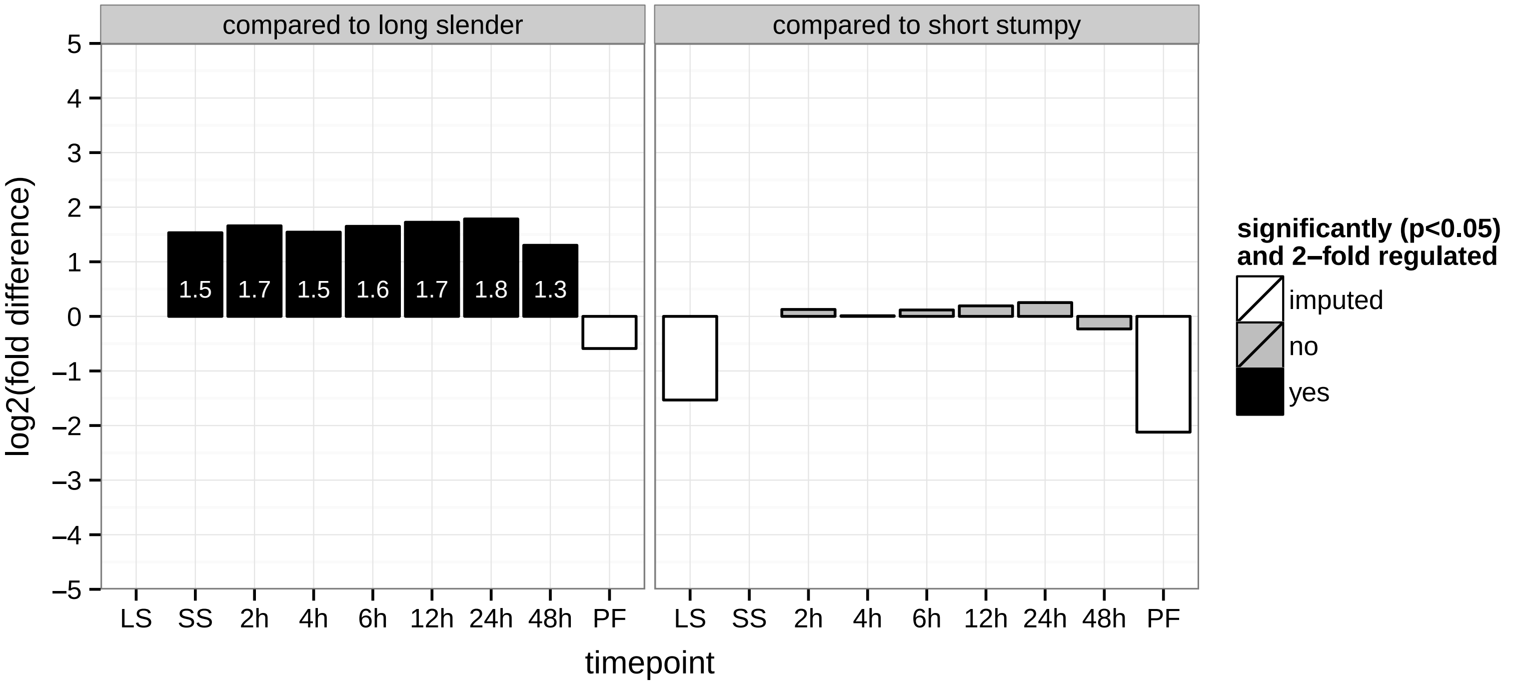
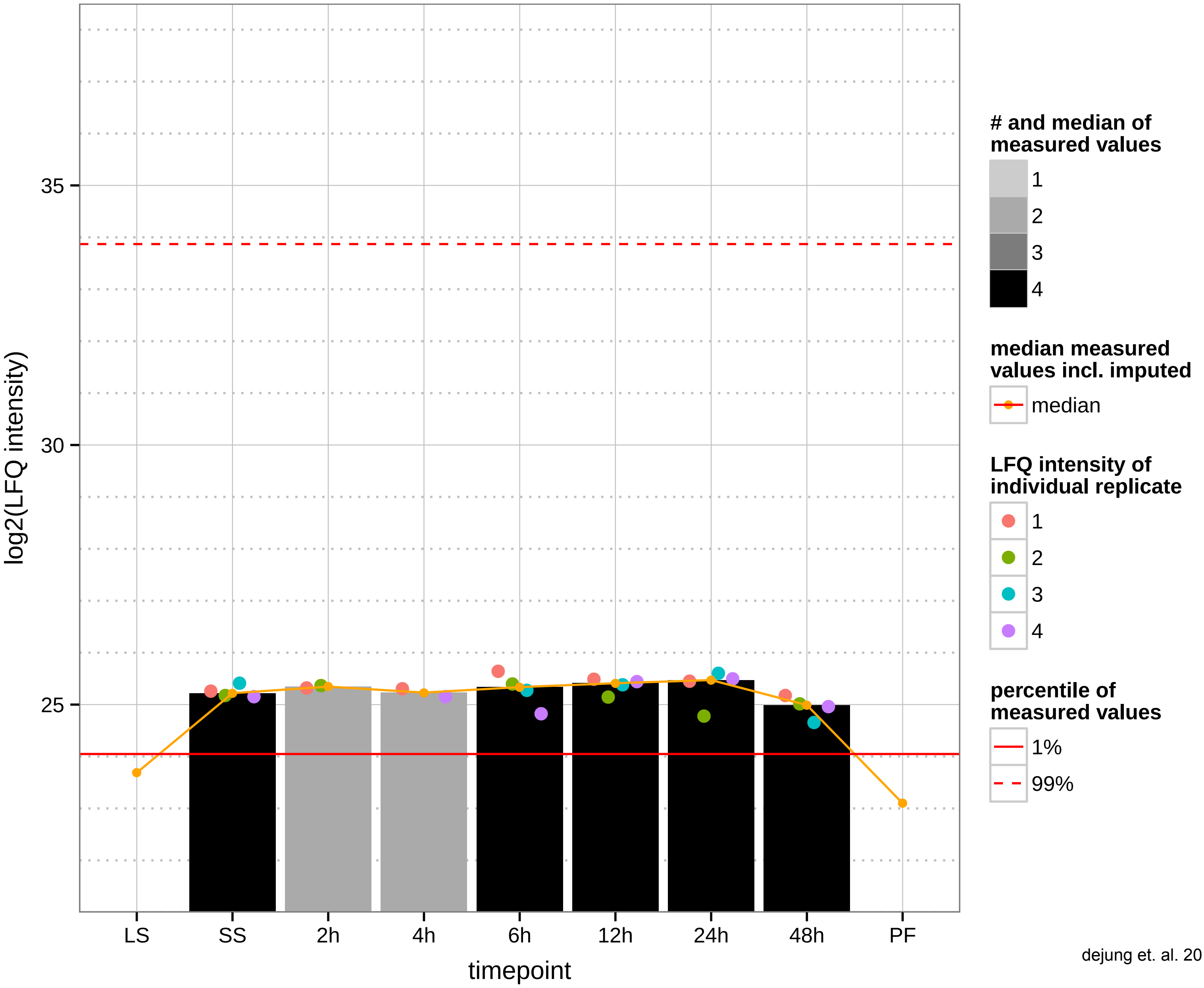
pre–mRNA splicing factor ATP–dependent RNA helicase, putative, DEAH–box RNA helicase
Tb927.10.5280;Tb11.v5.0248
AGOF: null, ATP binding, ATP–dependent RNA helicase activity, nucleic acid binding
AGOC: null, spliceosomal complex
AGOP: null, RNA splicing, RNA splicing, via transesterification reactions
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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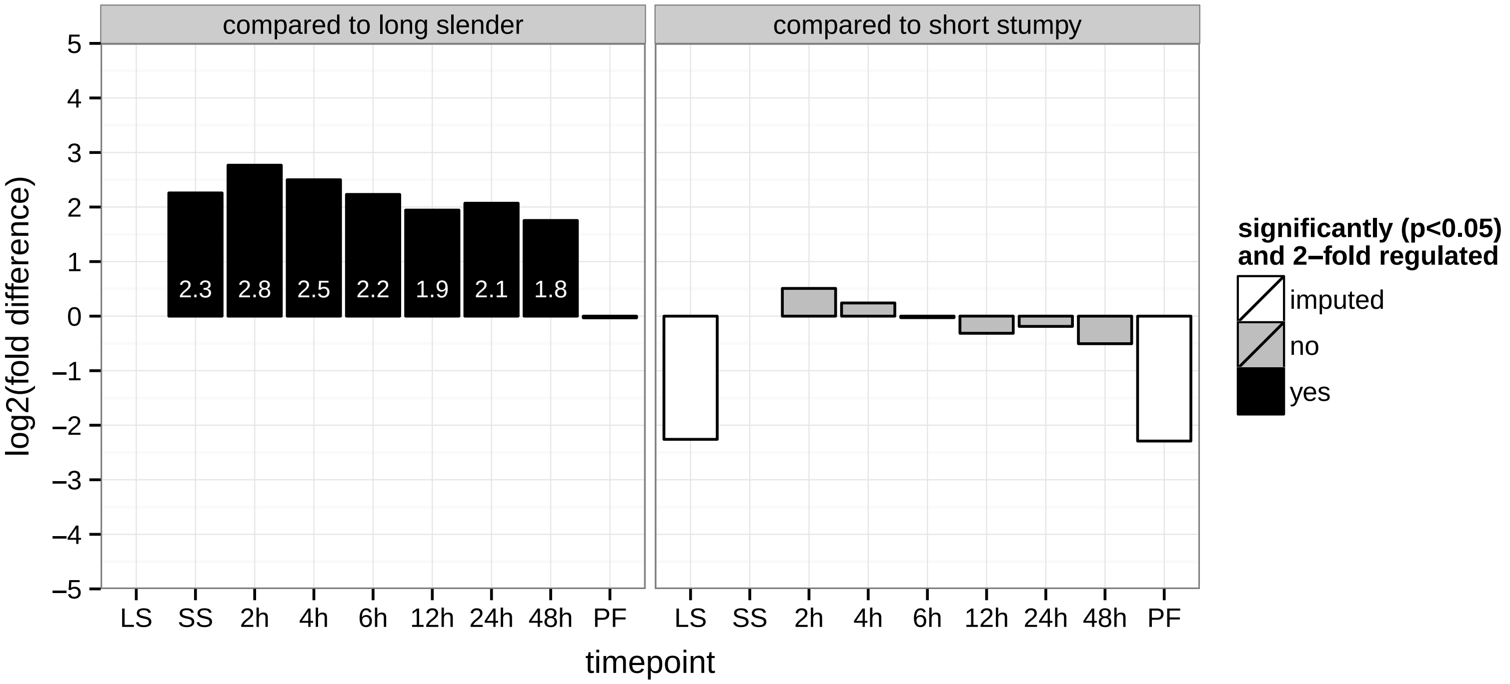
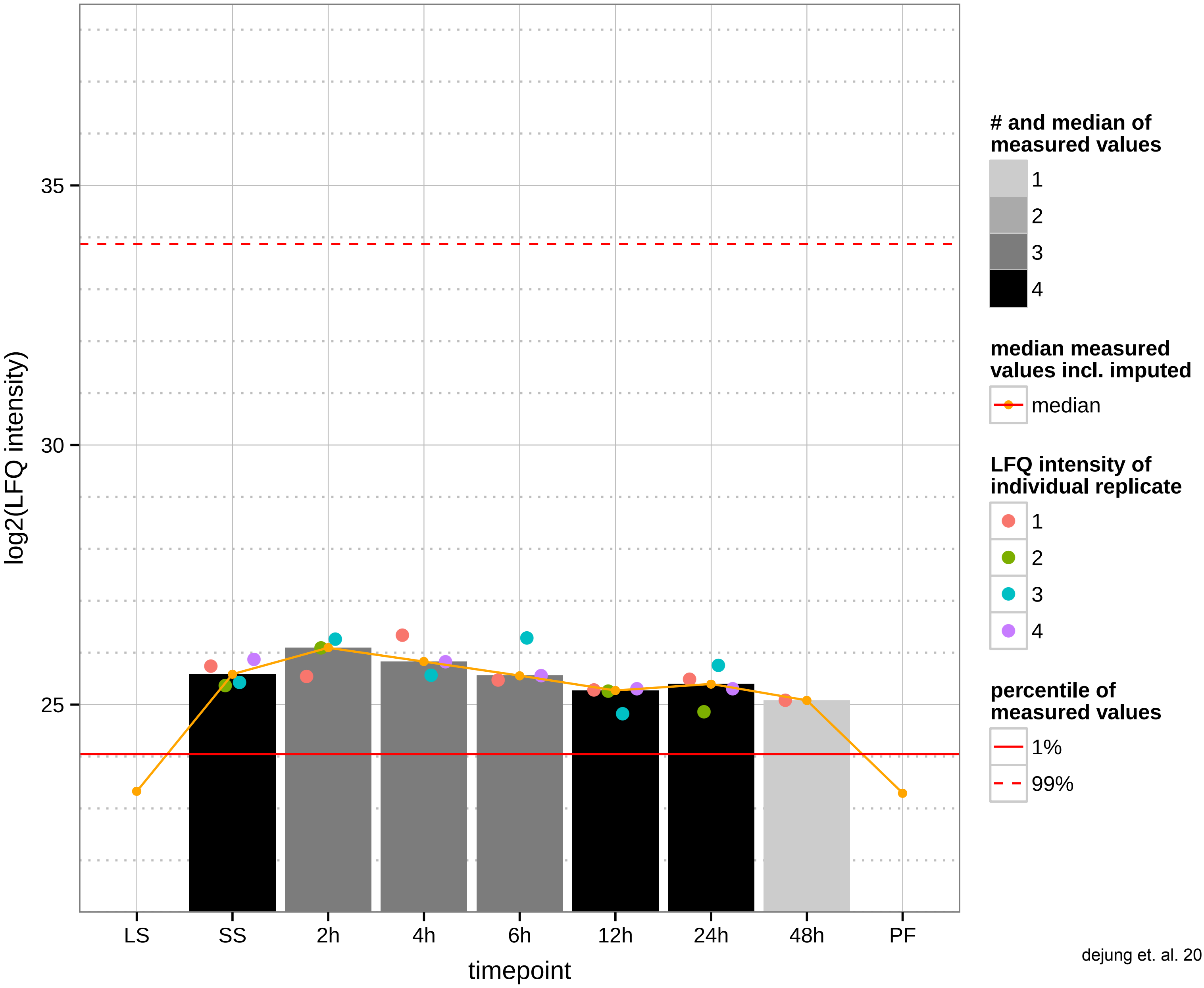
hypothetical protein, conserved
Tb927.11.7300;Tb11.v5.0253
AGOF: null, transporter activity
AGOC: null, integral to membrane
AGOP: null, transport
PGOF: null
PGOC: integral to membrane
PGOP: transmembrane transport





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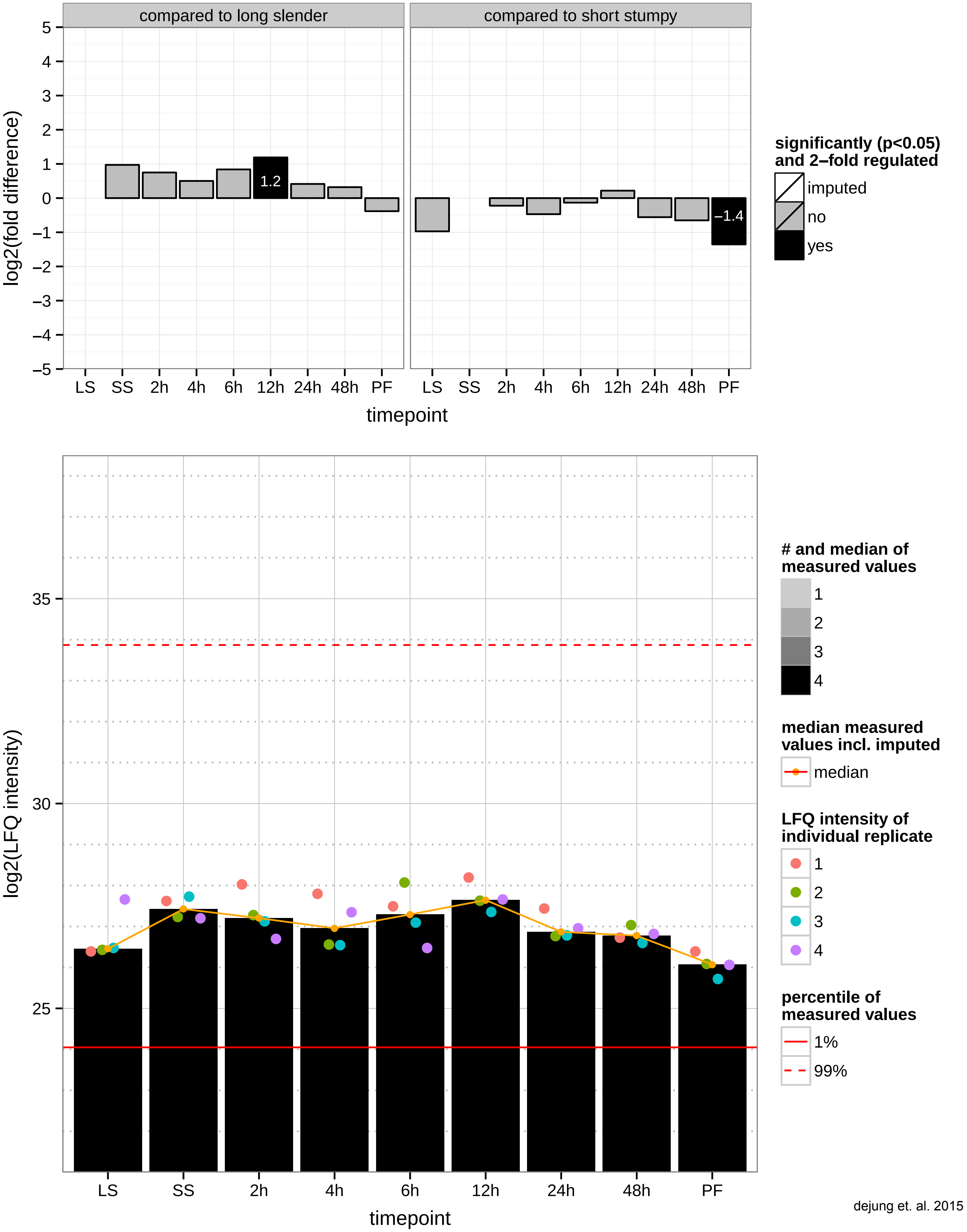
hypothetical protein, conserved, GPI transamidase component Tta2 (TTA2)
Tb927.10.5080;Tb11.v5.0339
AGOF: null, GPI–anchor transamidase activity
AGOC: null, GPI–anchor transamidase complex
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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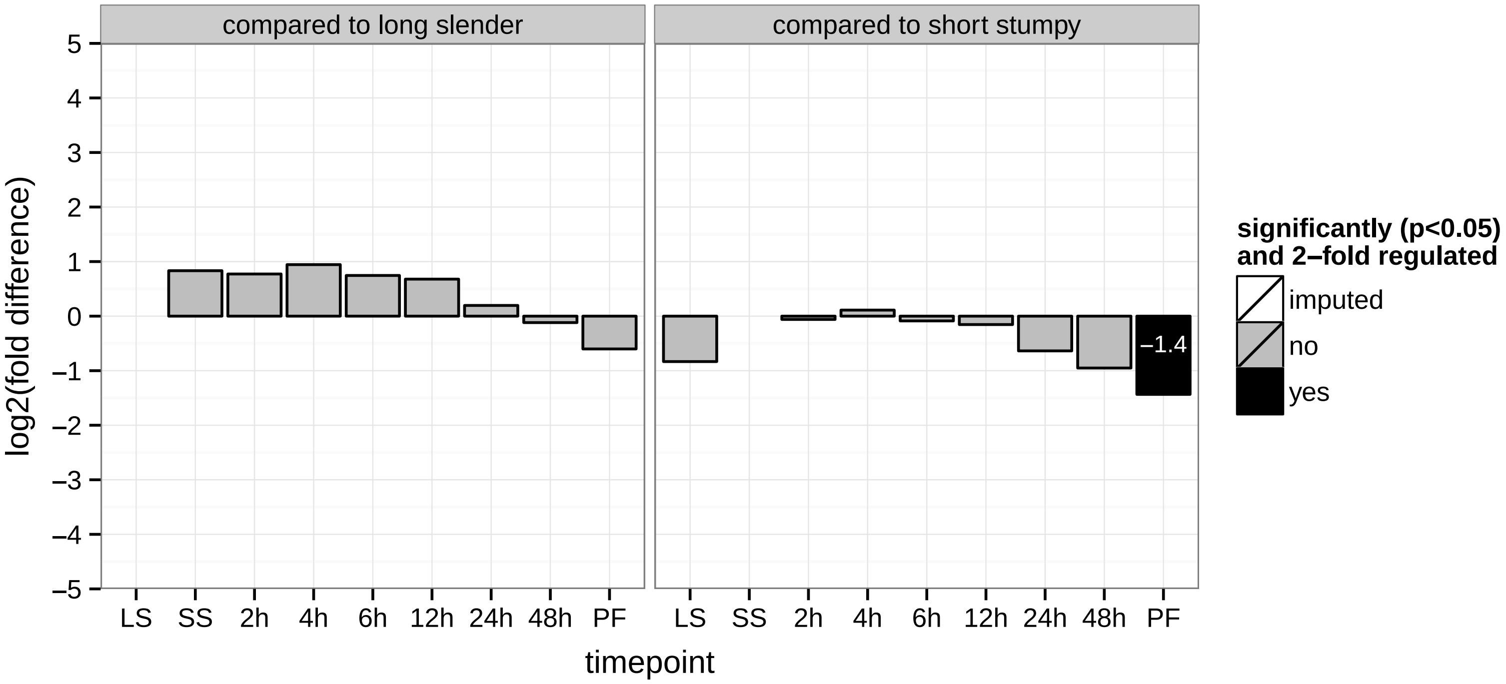
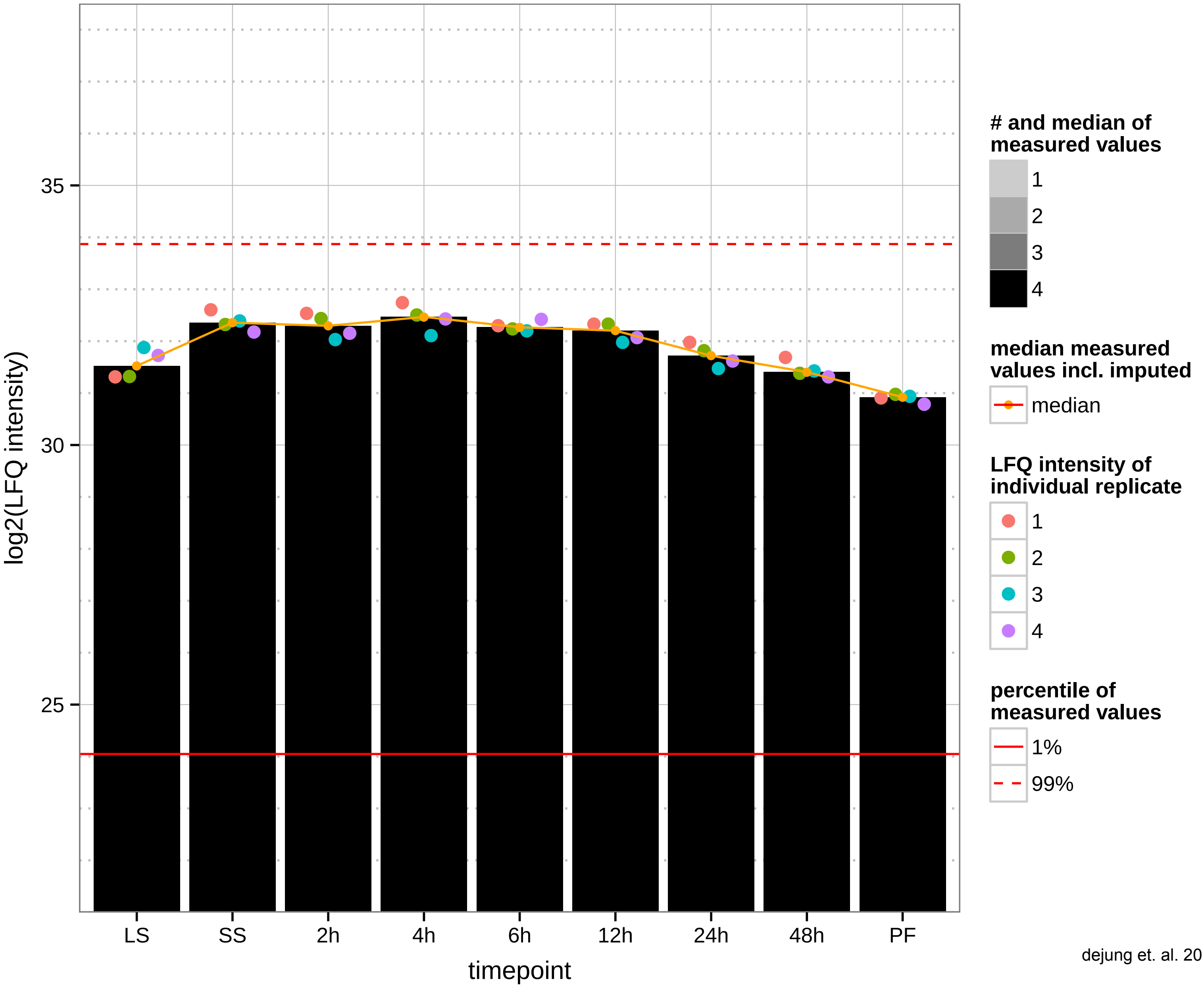
glyceraldehyde 3−phosphate dehydrogenase, cytosolic, putative, cytosolic (GAP)
Tb927.10.6880;Tb11.v5.0516
AGOF: null, glyceraldehyde−3−phosphate dehydrogenase (NAD+) (phosphorylating) activity
AGOC: null, cytosol
AGOP: null, glycolysis
PGOF: NAD binding, NADP binding, oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as
PGOC: null
PGOP: glucose metabolic process, oxidation−reduction process





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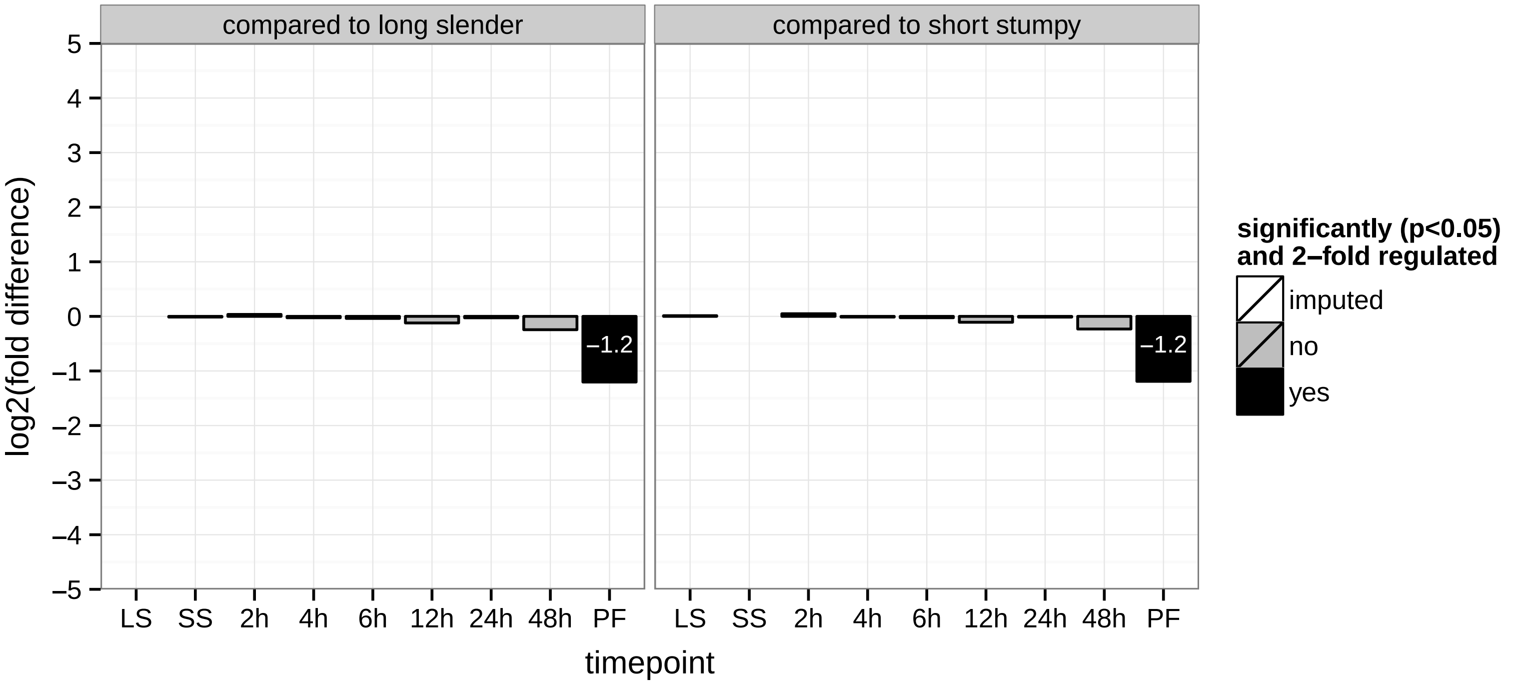
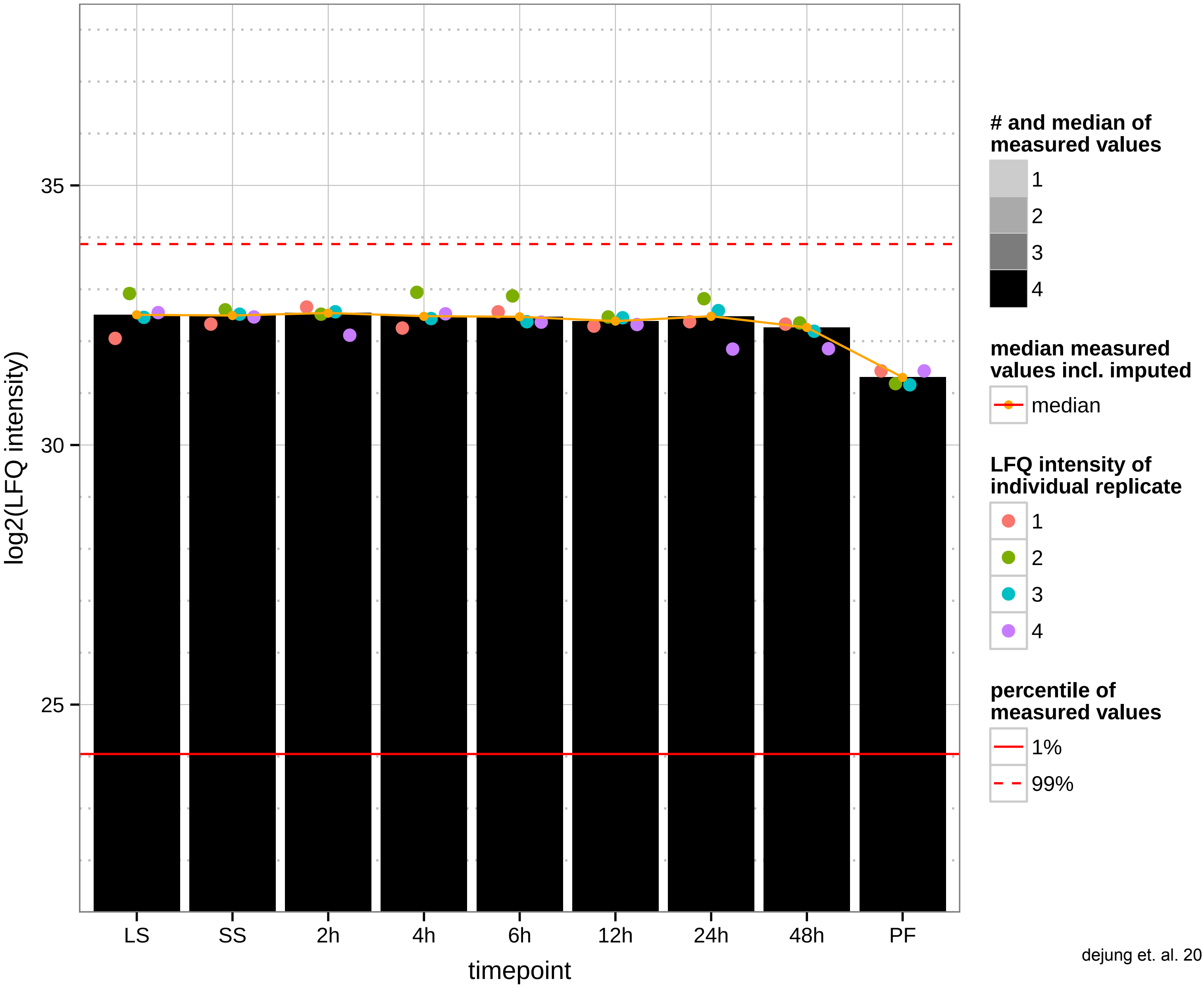
polyubiquitin, putative
Tb11.v5.0537;Tb927.11.9920;Tb11.01.1680.v5
AGOF: null
AGOC: null
AGOP: null, cellular protein modification process
PGOF: protein binding
PGOC: null
PGOP: null





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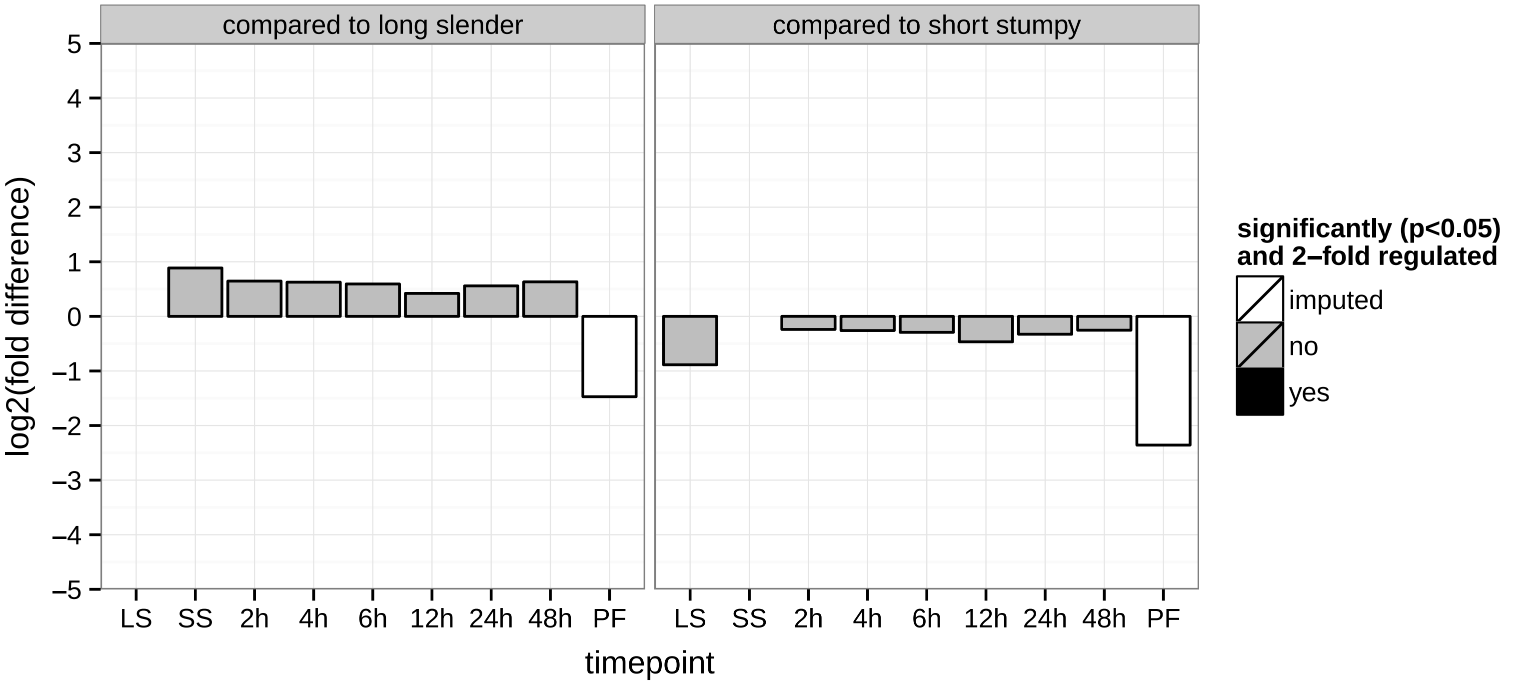
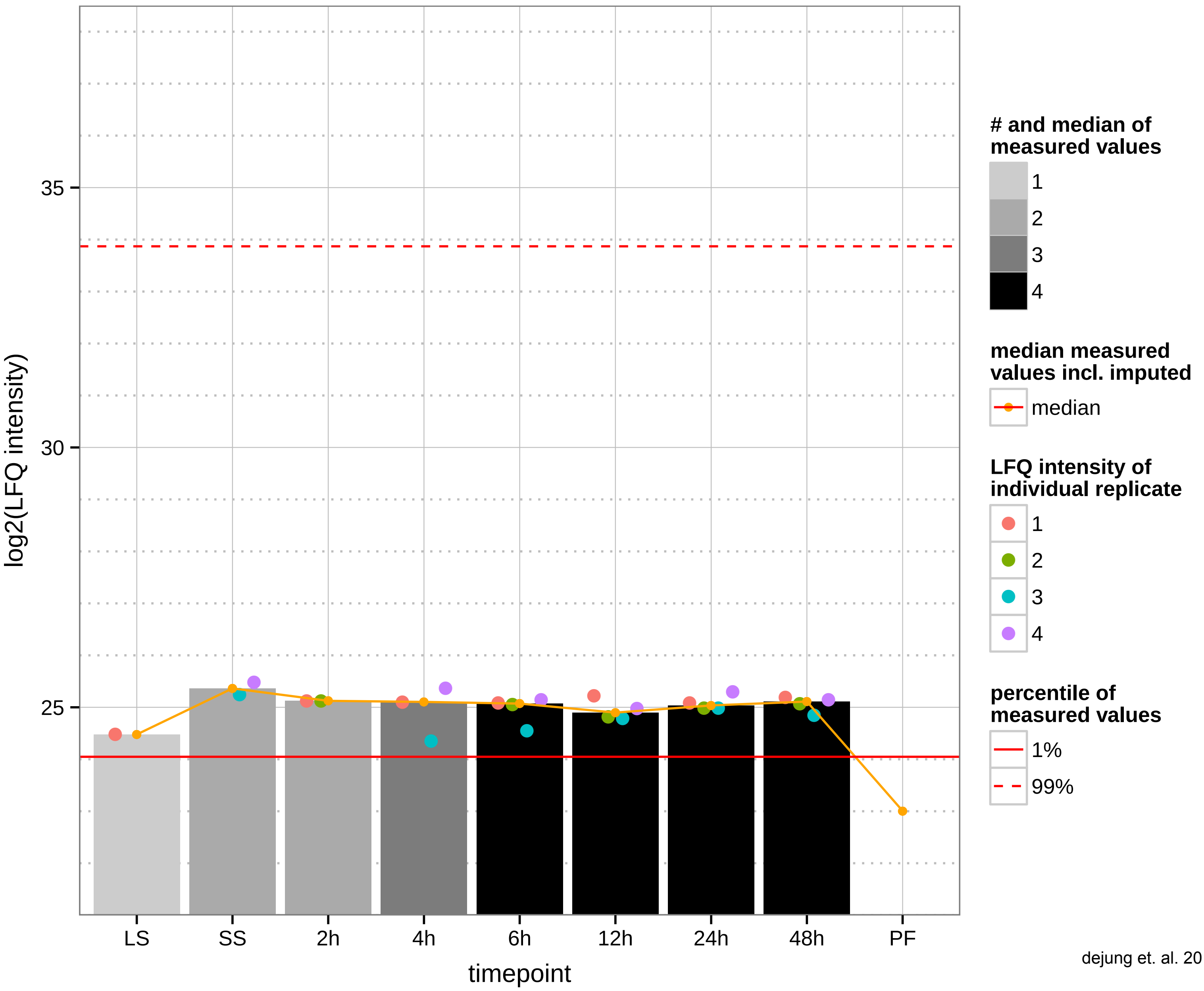
hypothetical protein, conserved, U4/U6−specific protein PRP4
Tb927.10.960;Tb11.v5.0631
AGOF: null, pre−mRNA 5'−splice site binding
AGOC: null, cytoplasm, nucleus
AGOP: null, RNA splicing
PGOF: protein binding
PGOC: null
PGOP: RNA splicing





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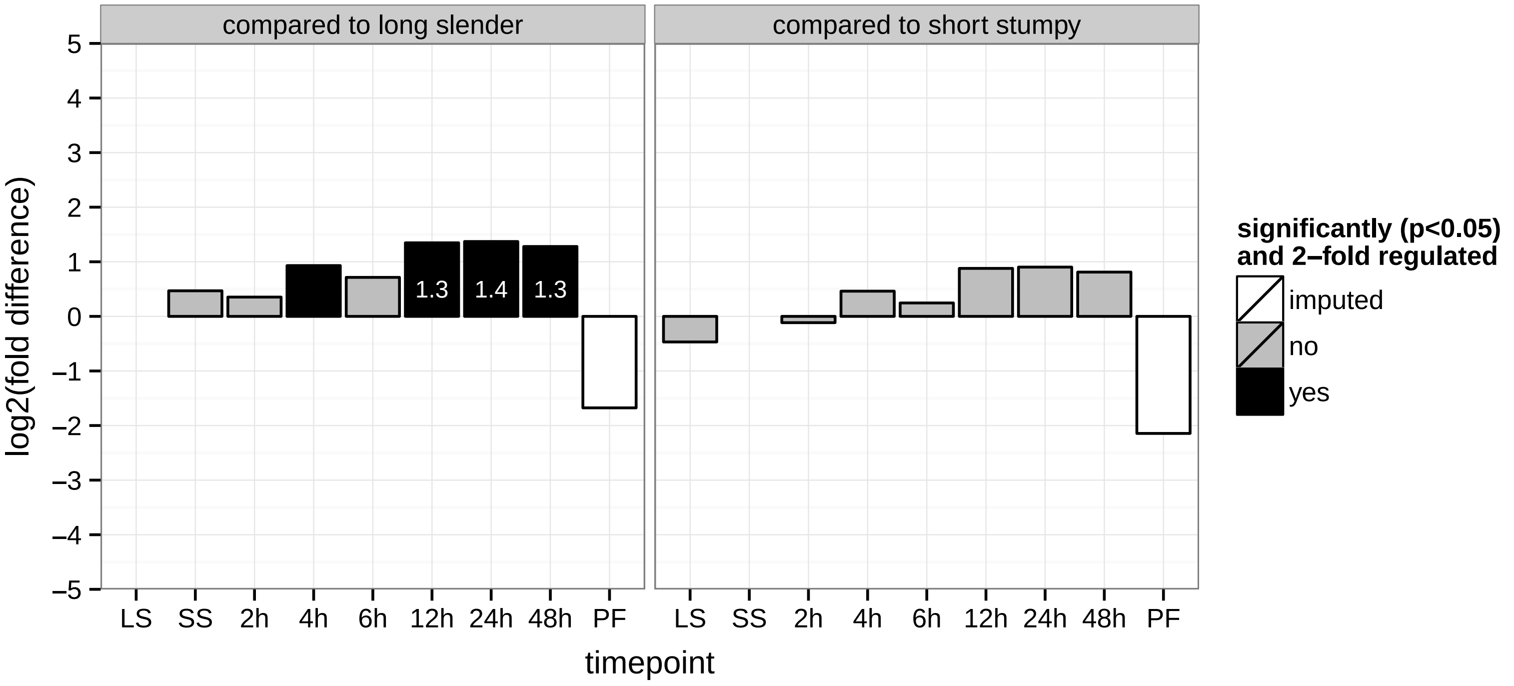
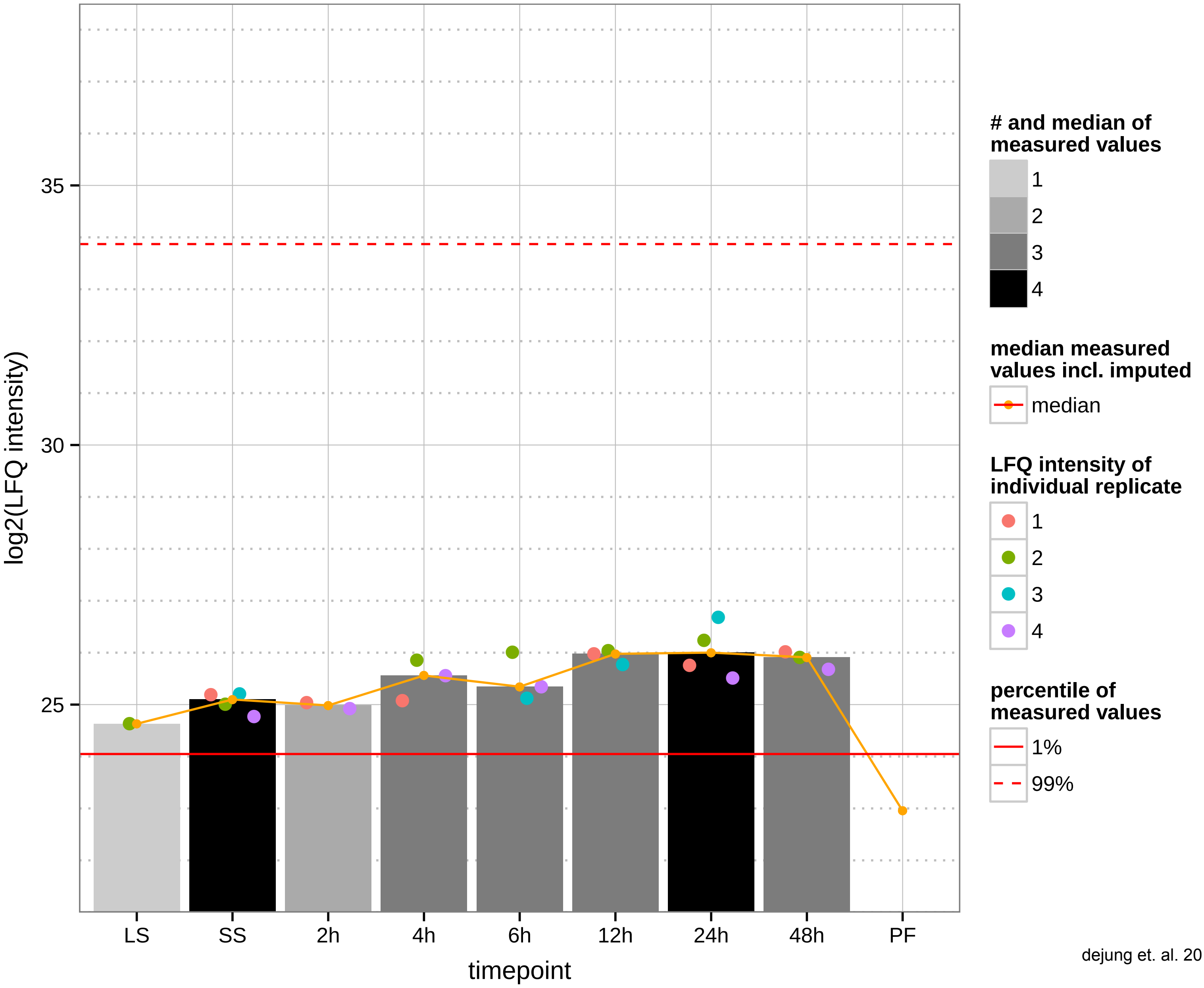
glutaredoxin–like protein, putative, monothiol glutaredoxin
Tb927.9.3590;Tb11.v5.0904
AGOF: null, electron carrier activity, glutathione–disulfide reductase activity, protein disulfide oxidoreductase activity
AGOC: null, mitochondrion
AGOP: null, cell redox homeostasis, oxidation–reduction process
PGOF: electron carrier activity, protein disulfide oxidoreductase activity
PGOC: null
PGOP: cell redox homeostasis





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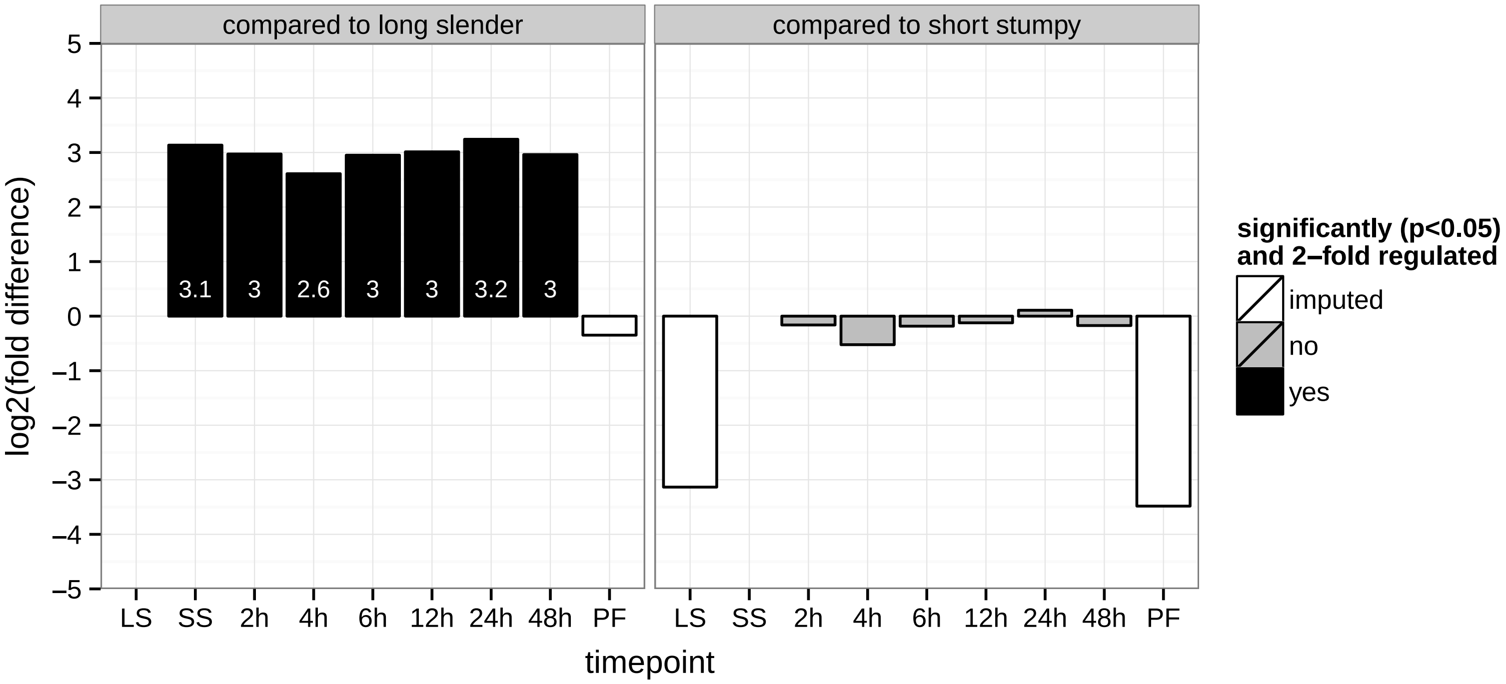
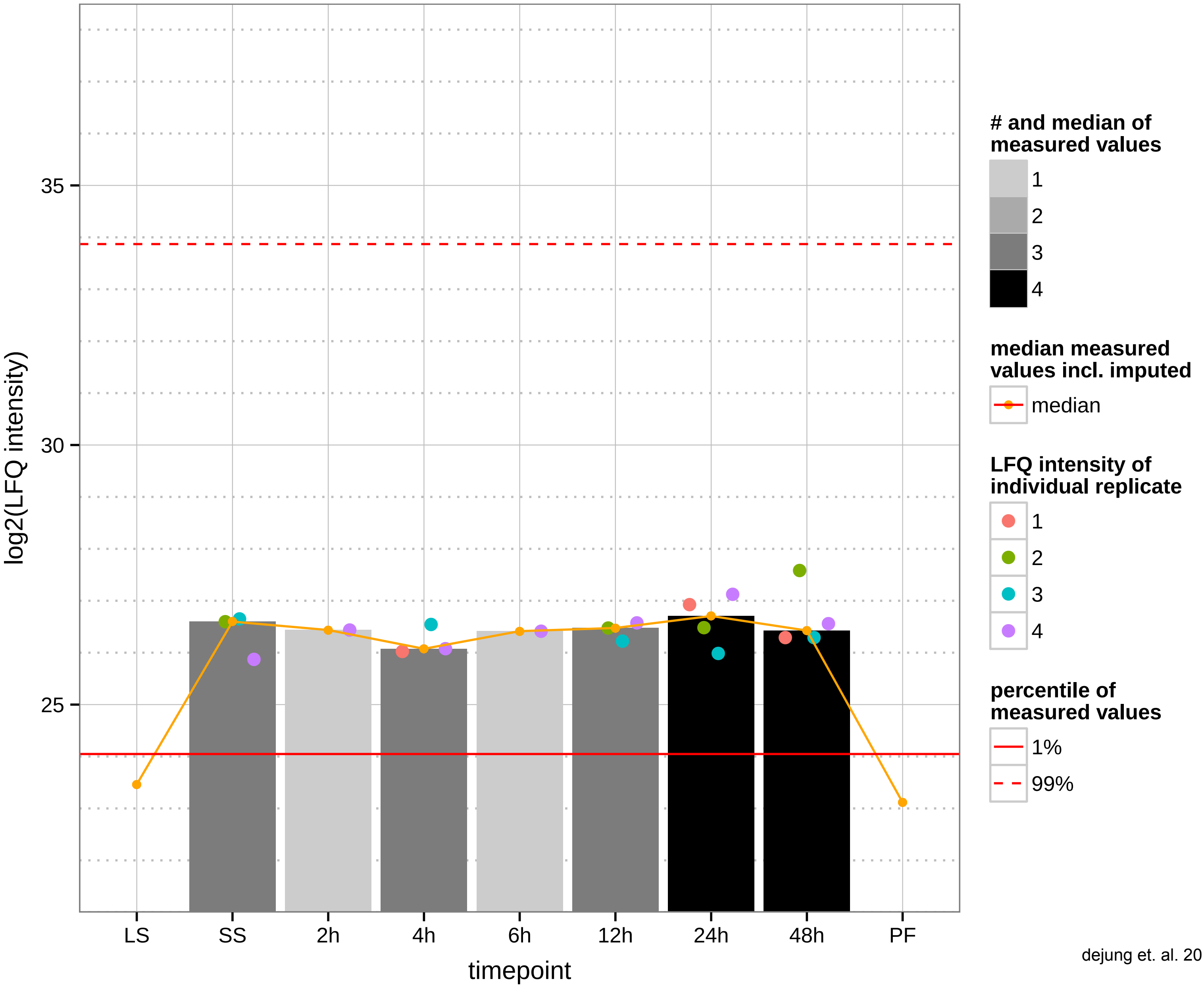
FG−GAP repeat protein, putative, intergrin alpha chain protein
Tb927.1.1340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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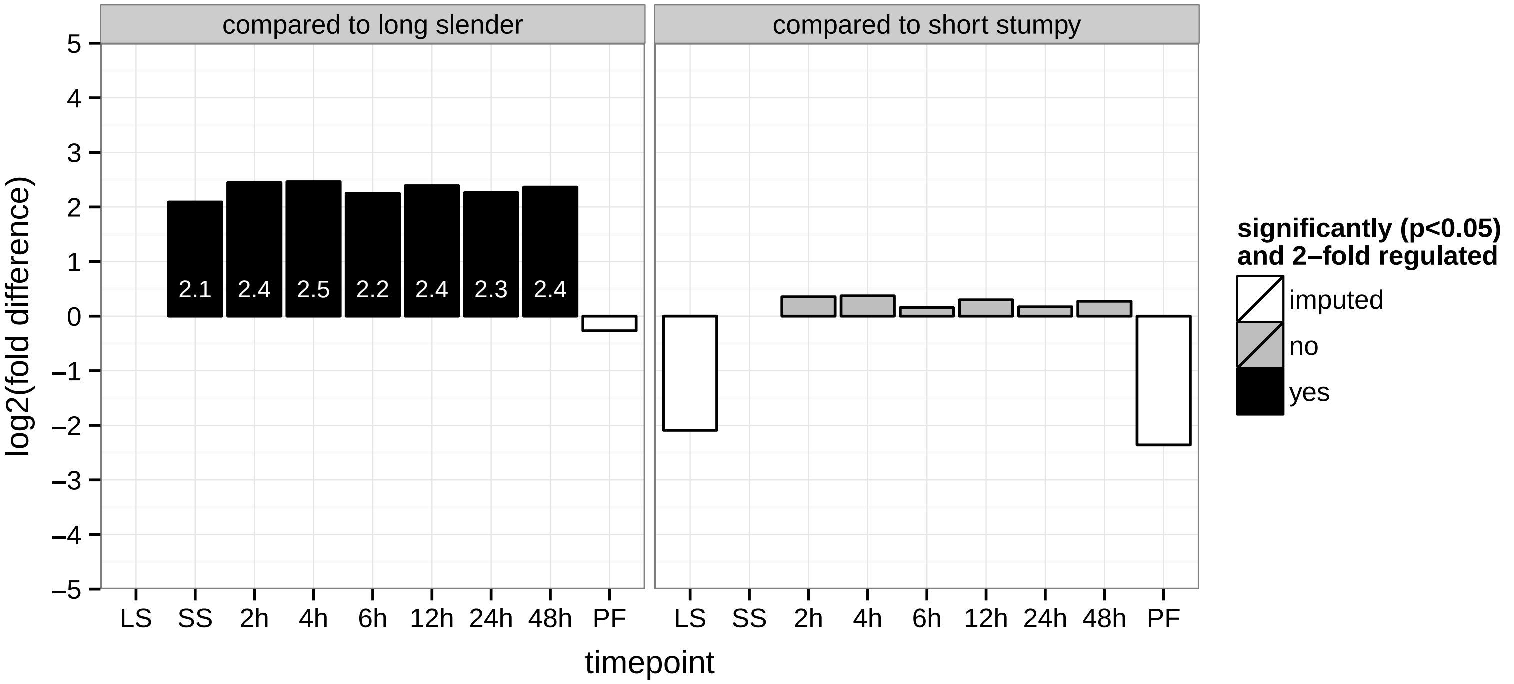
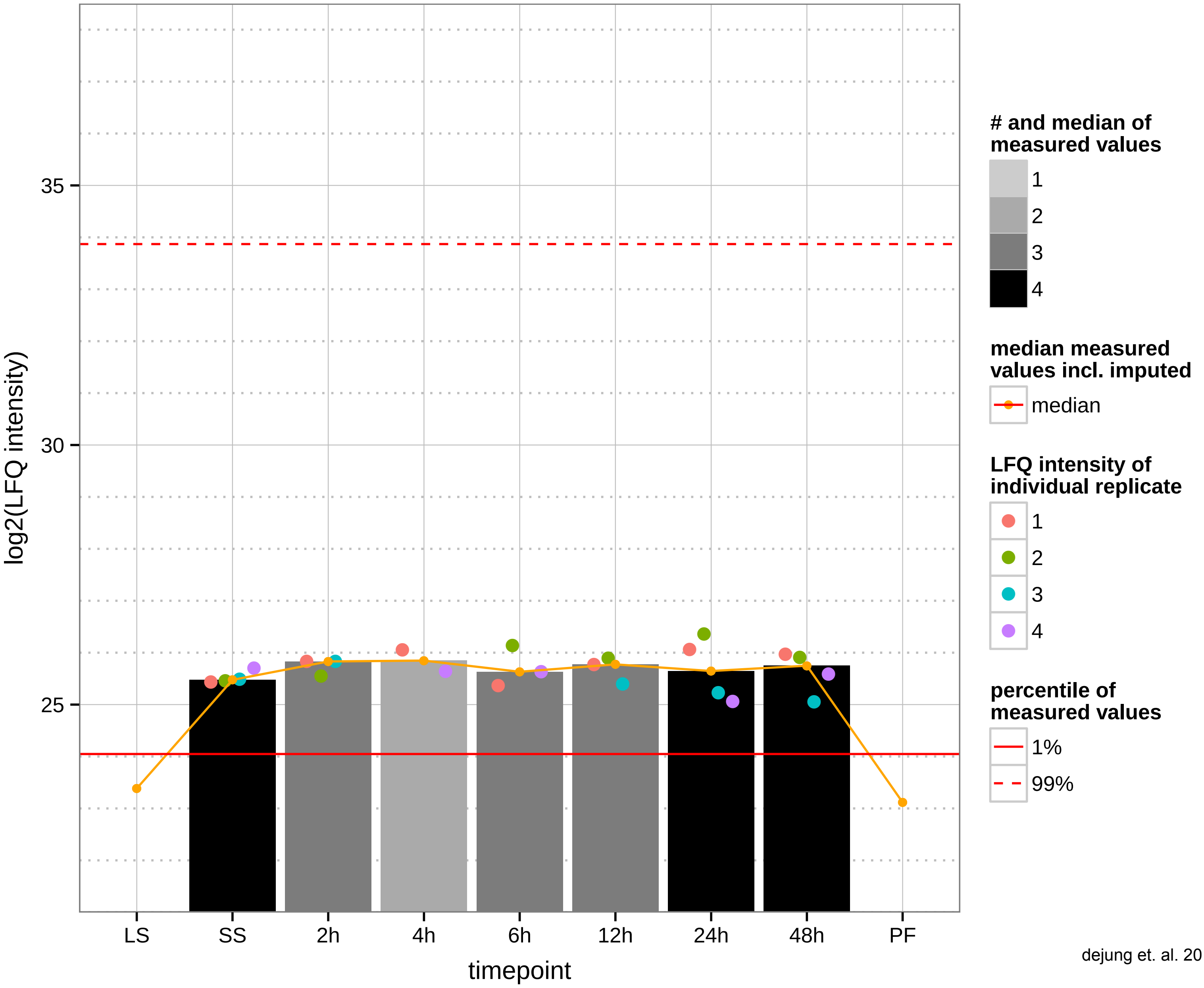
Overproducer of inositol protein 10 homolog, putative
Tb927.1.1400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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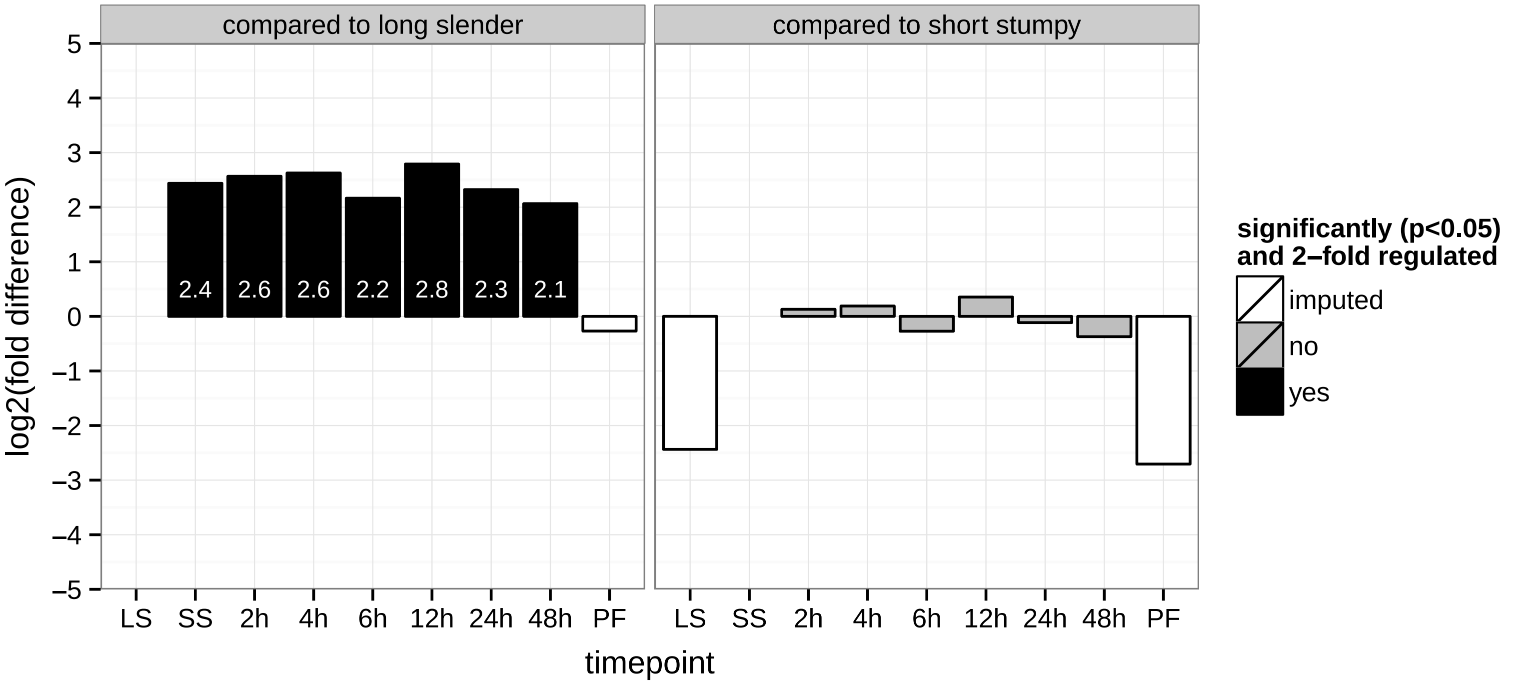
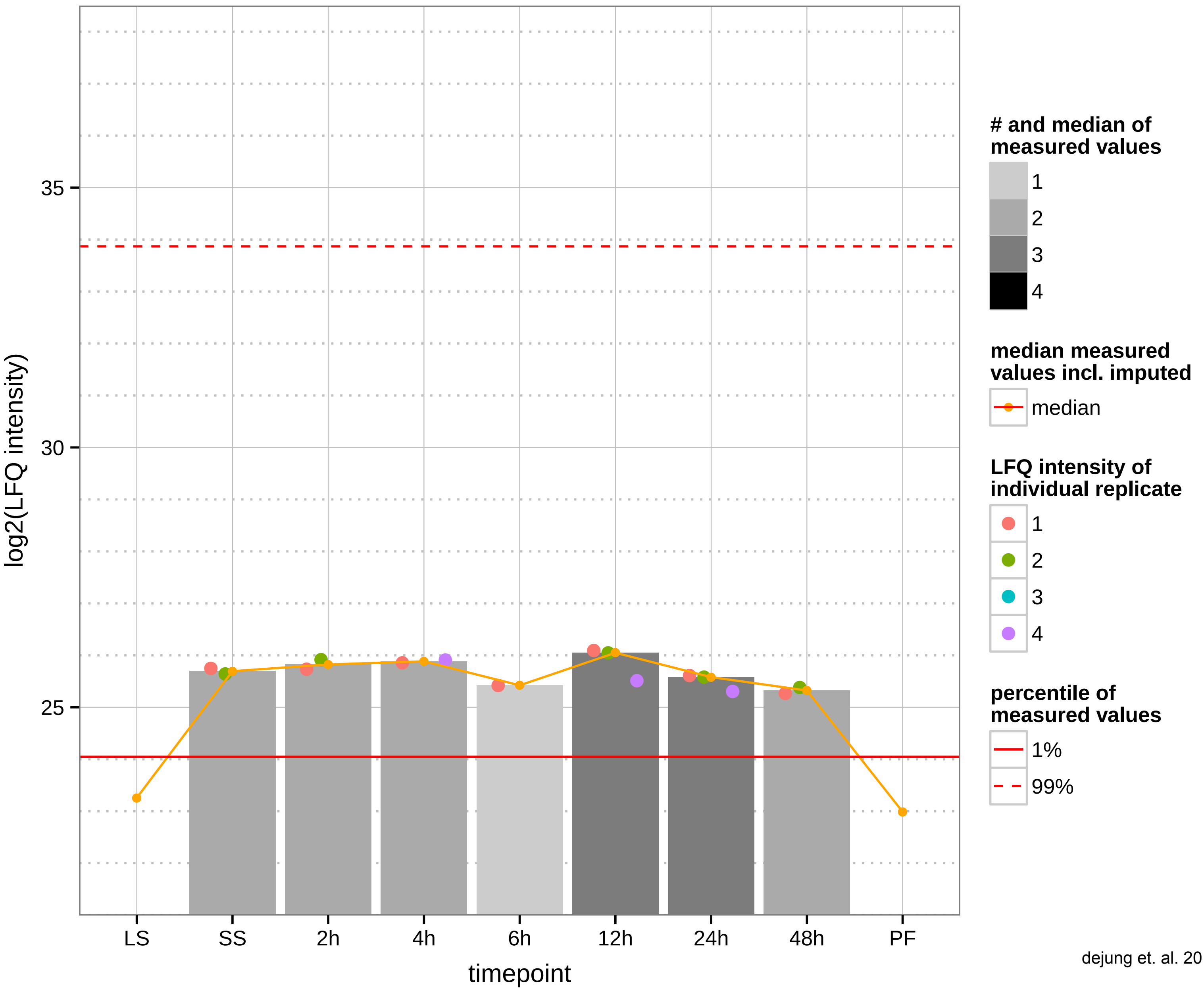
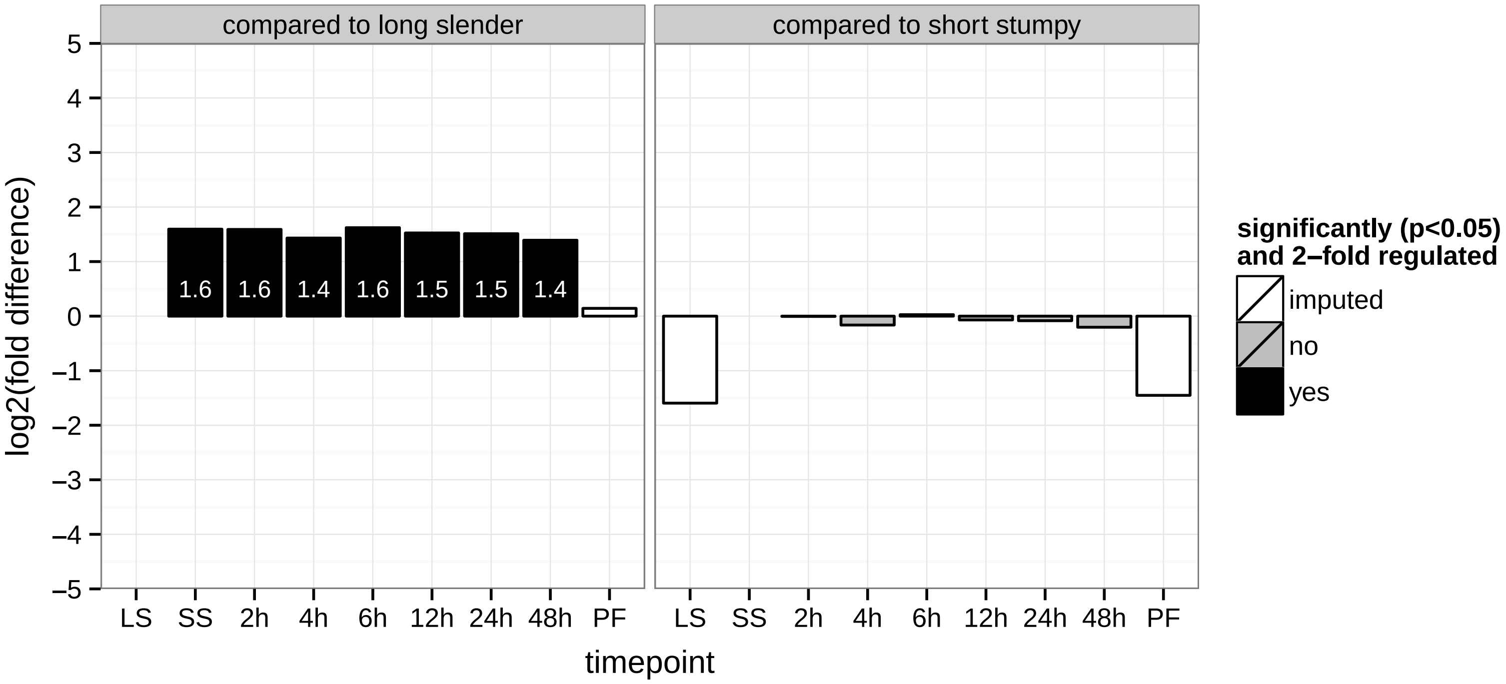
hypothetical protein, conserved
Tb927.1.3390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

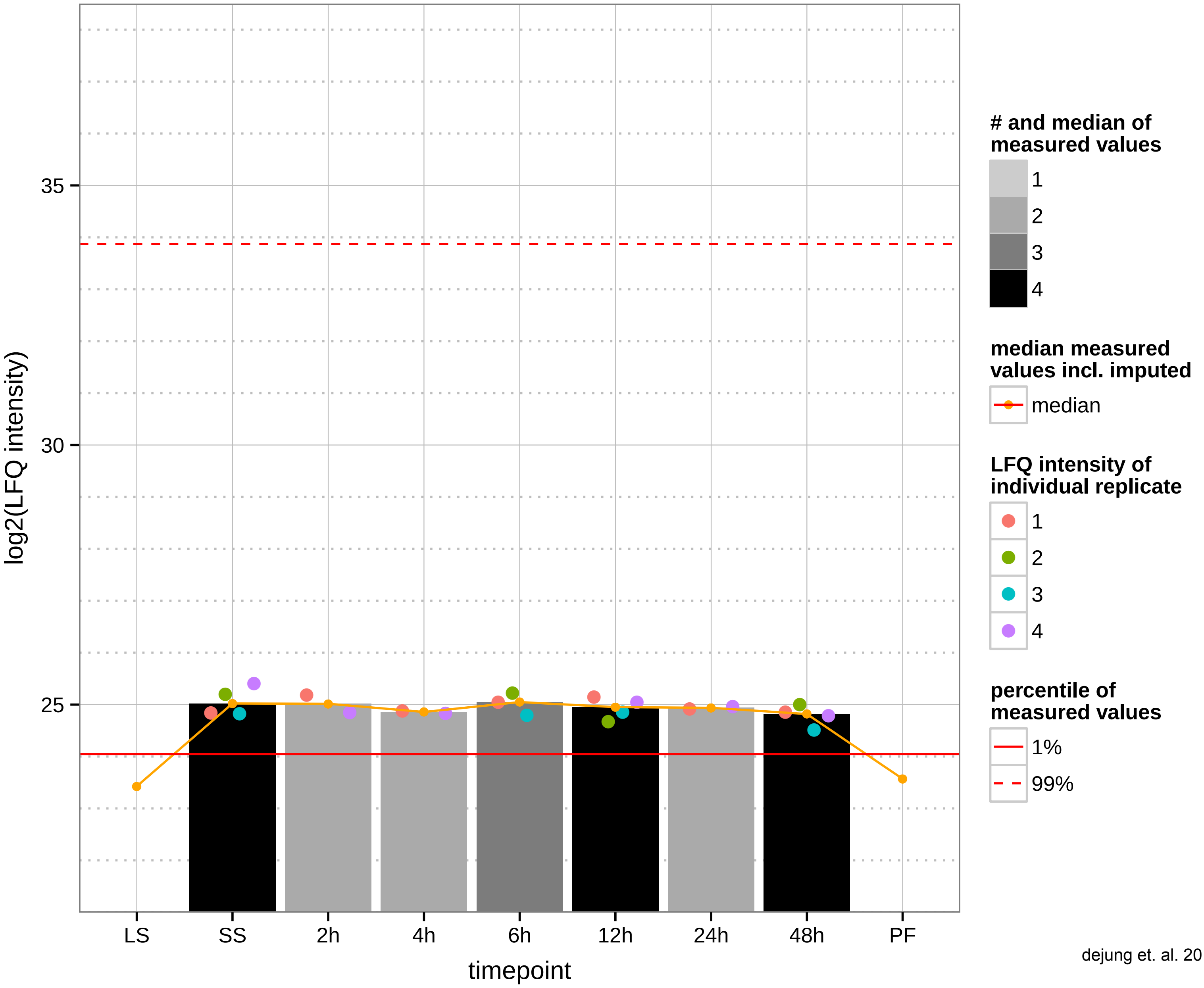




dejung et. al. 2015

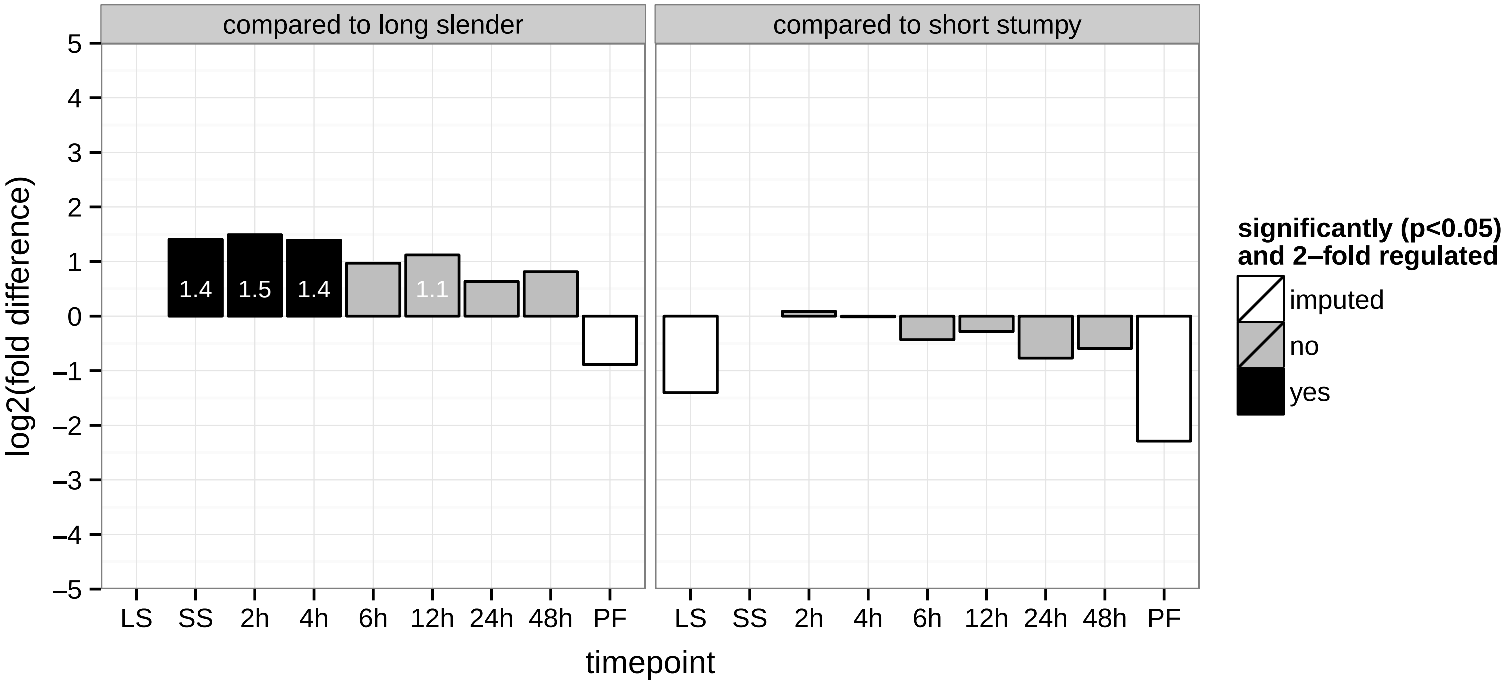
hypothetical protein, conserved
Tb927.1.3410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

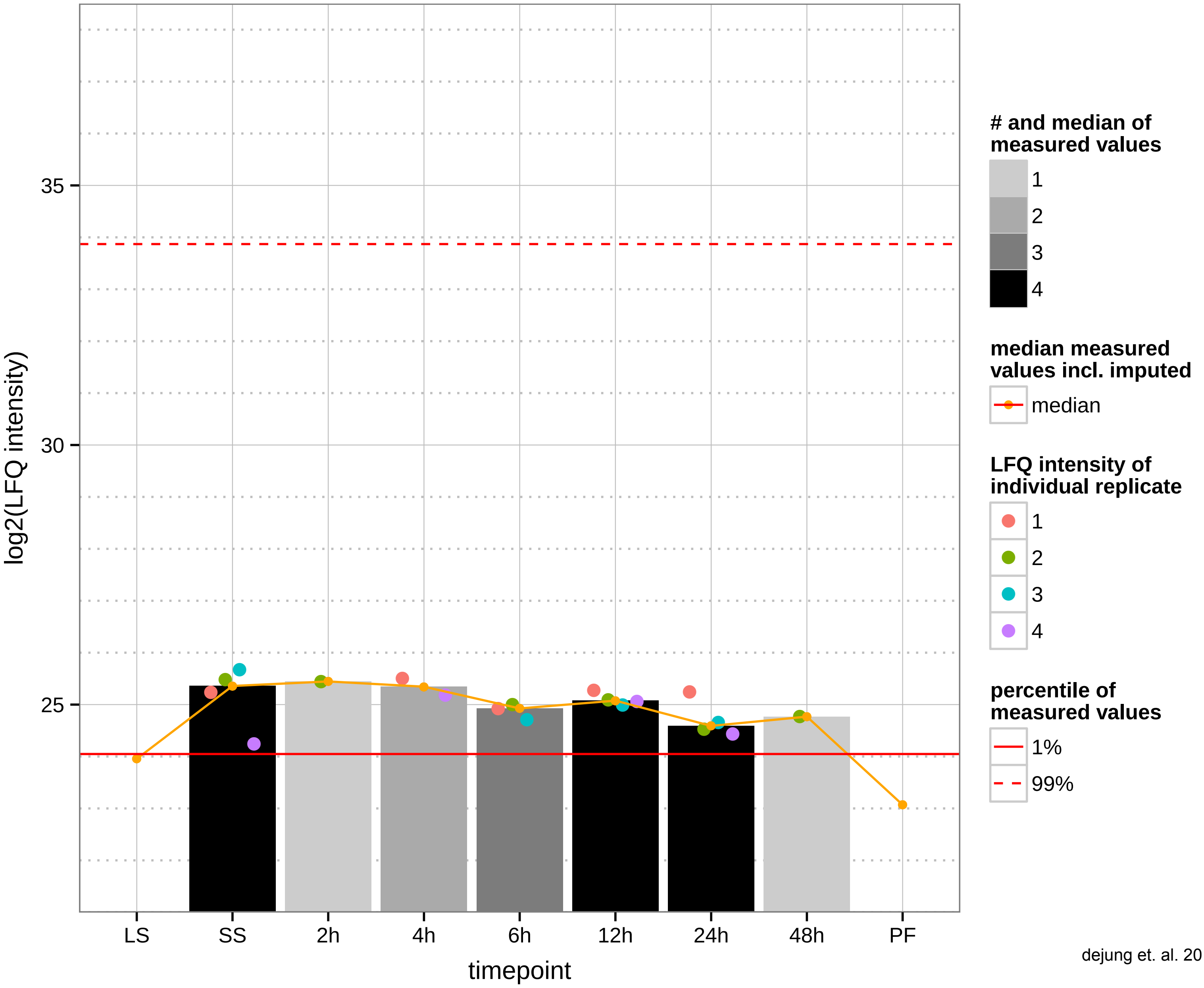




dejung et. al. 2015

hypothetical protein, conserved
Tb927.1.3880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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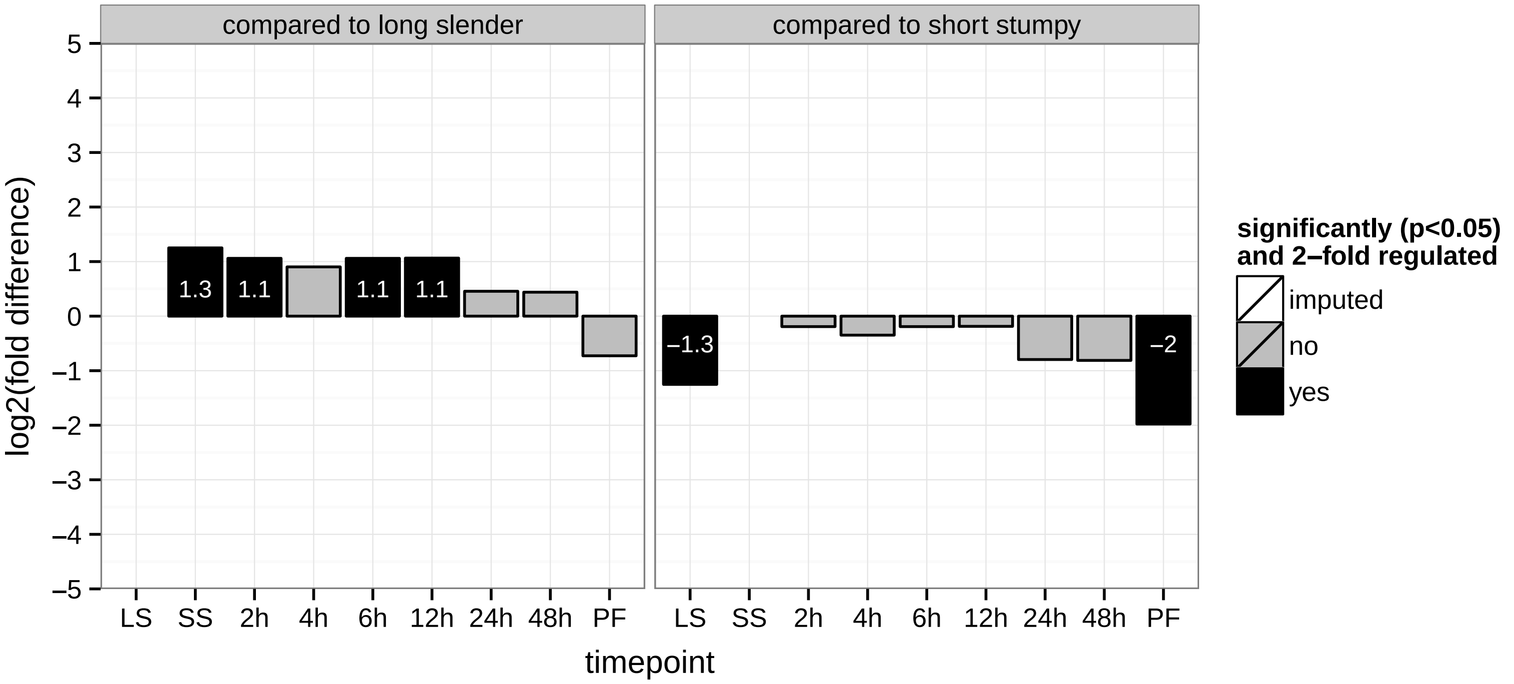
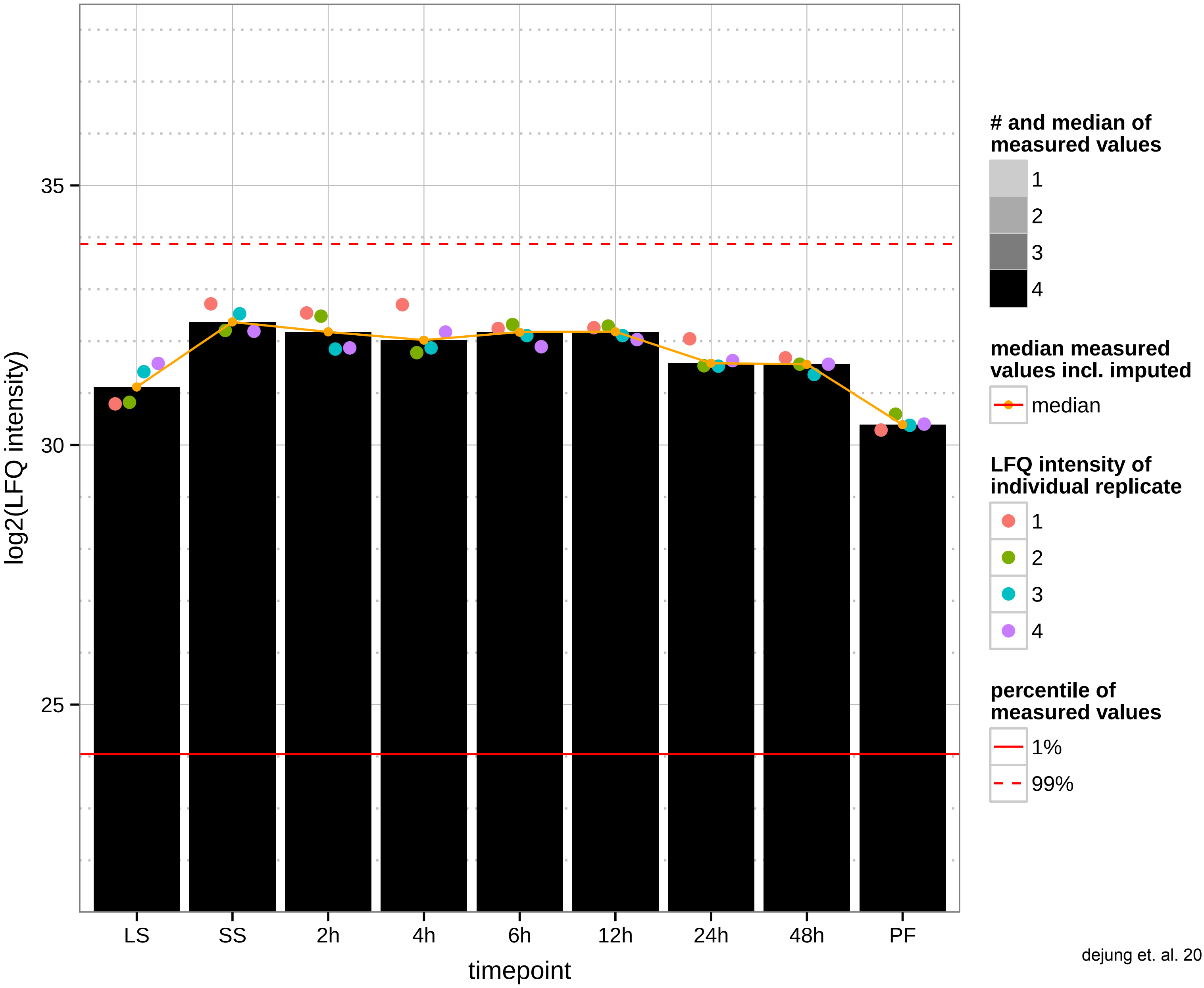
alanine aminotransferase (ALAT)
Tb927.1.3950
AGOF: 1−aminocyclopropane−1−carboxylate synthase activity, L−alanine:2−oxoglutarate aminotransferase activity, pyridoxal
AGOC: cytosol
AGOP: alanine catabolic process, biosynthetic process, proline metabolic process
PGOF: pyridoxal phosphate binding, transferase activity
PGOC: null
PGOP: biosynthetic process





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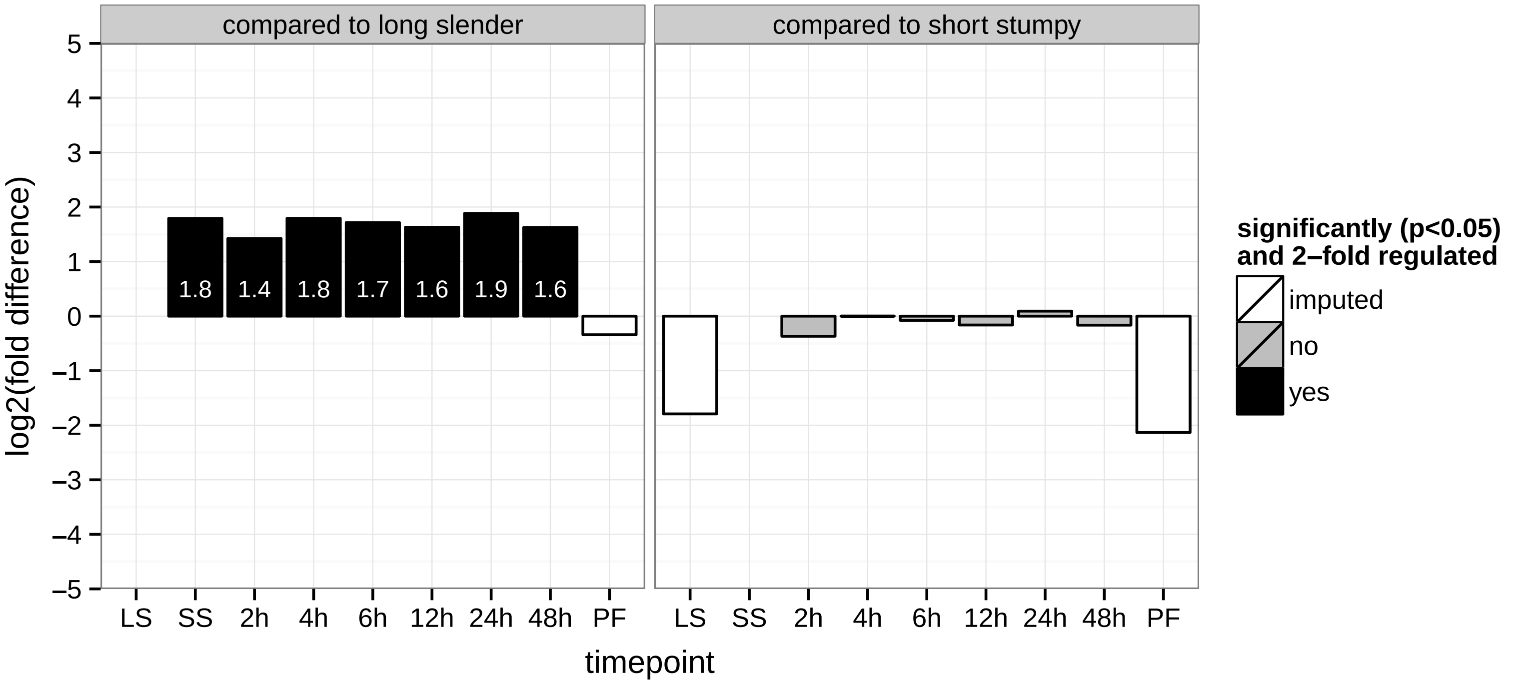
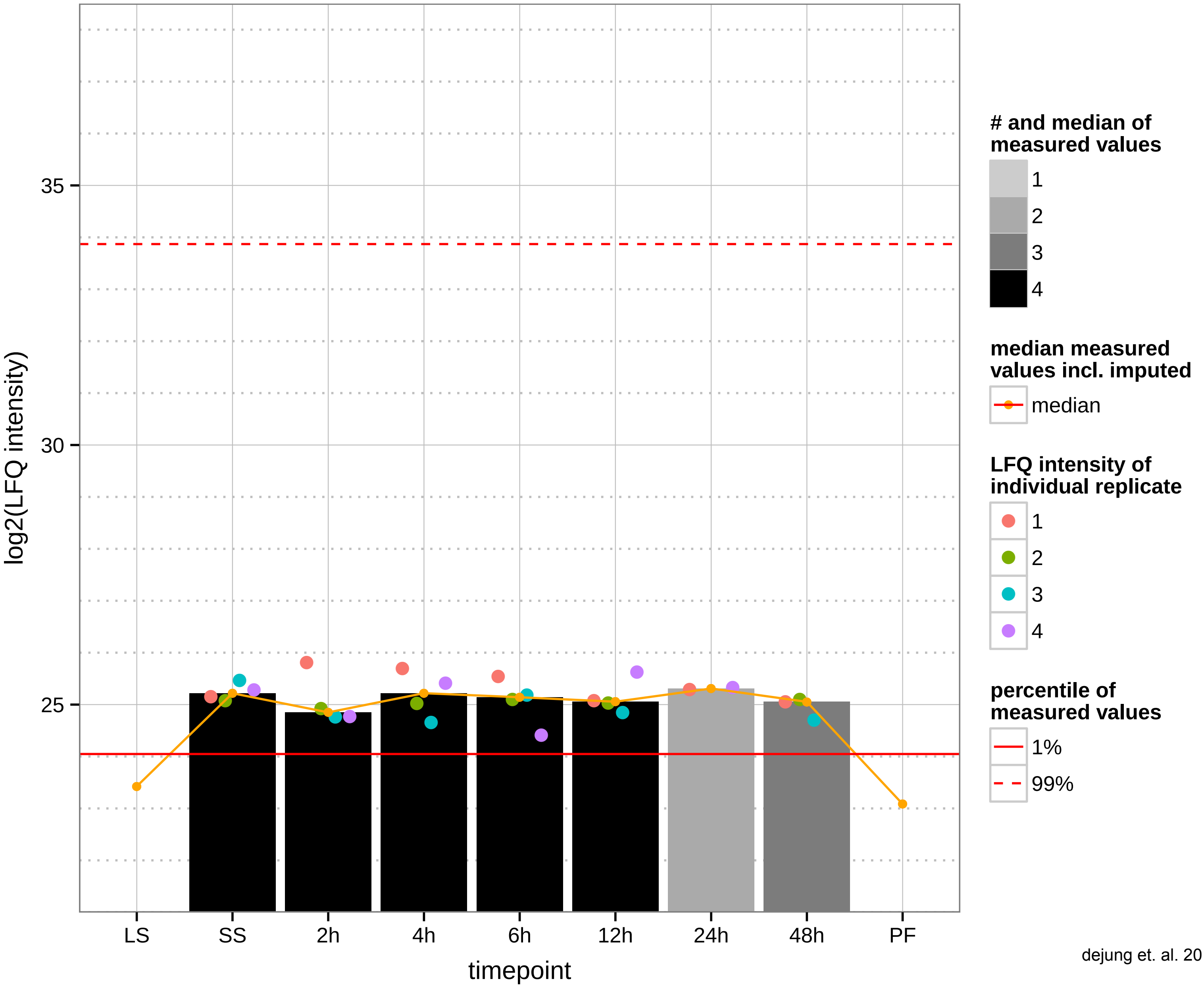
hypothetical protein, conserved
Tb927.1.4760
AGOF: null
AGOC: null
AGOP: null
PGOF: small GTPase regulator activity
PGOC: null
PGOP: null





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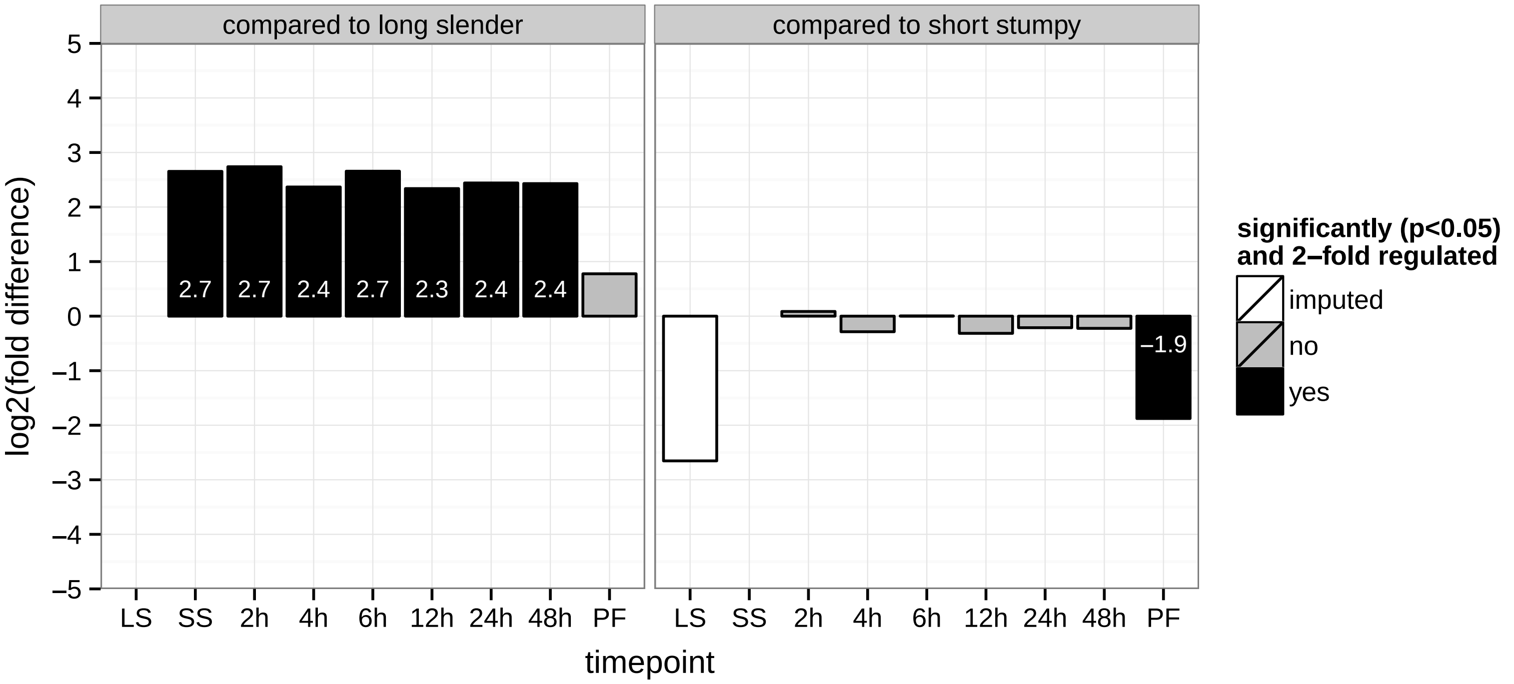
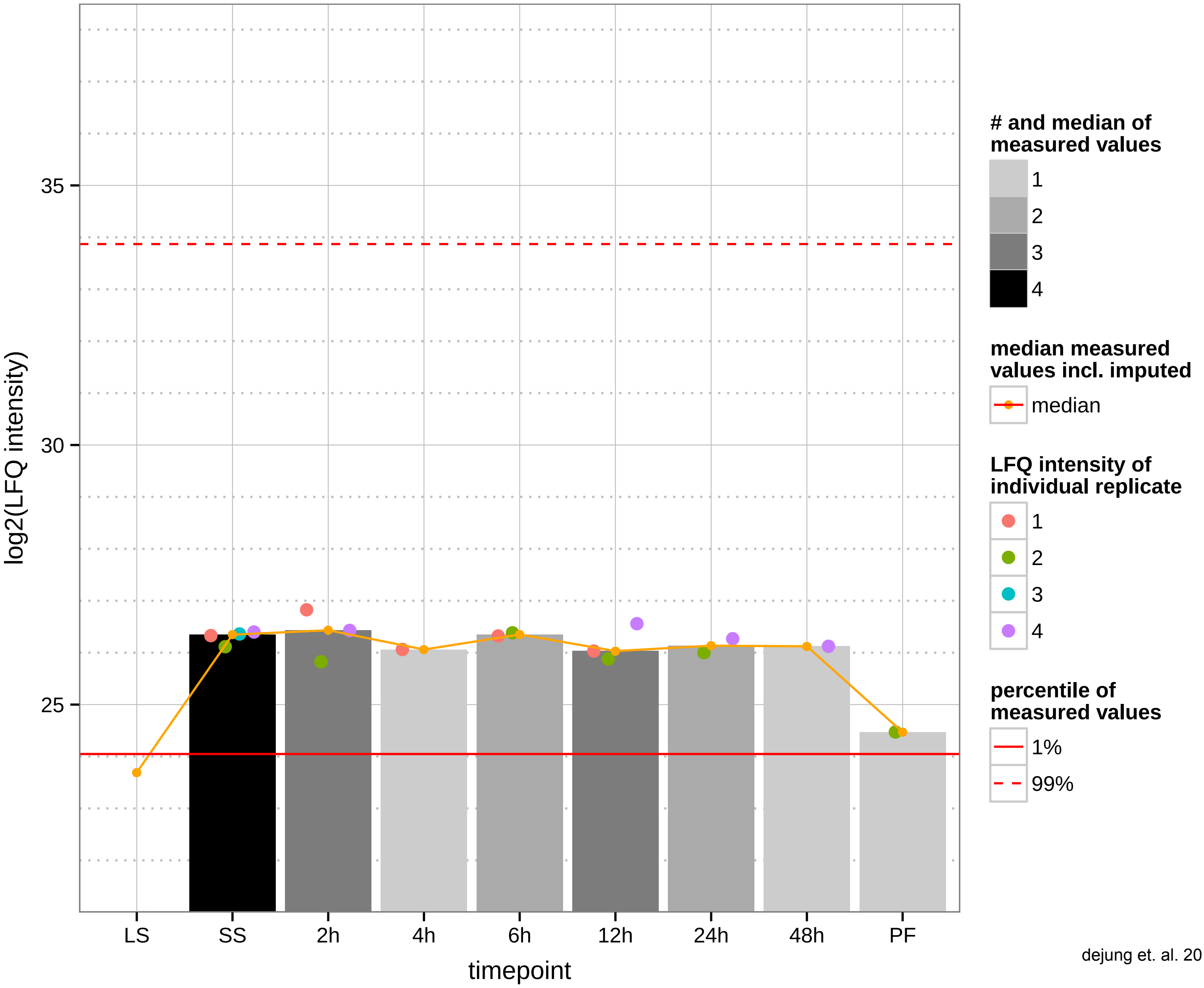
serine peptidase, putative, Clan SC, Family S9D
Tb927.1.4780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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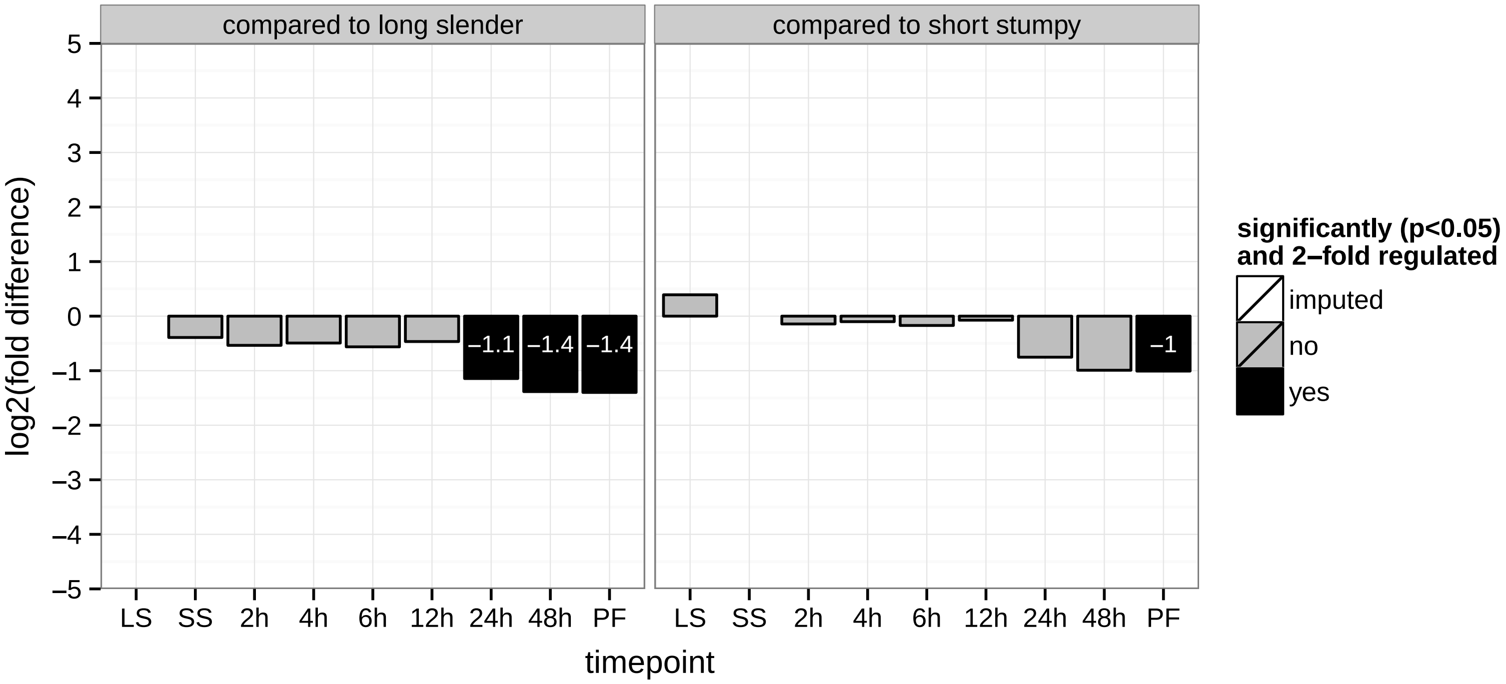
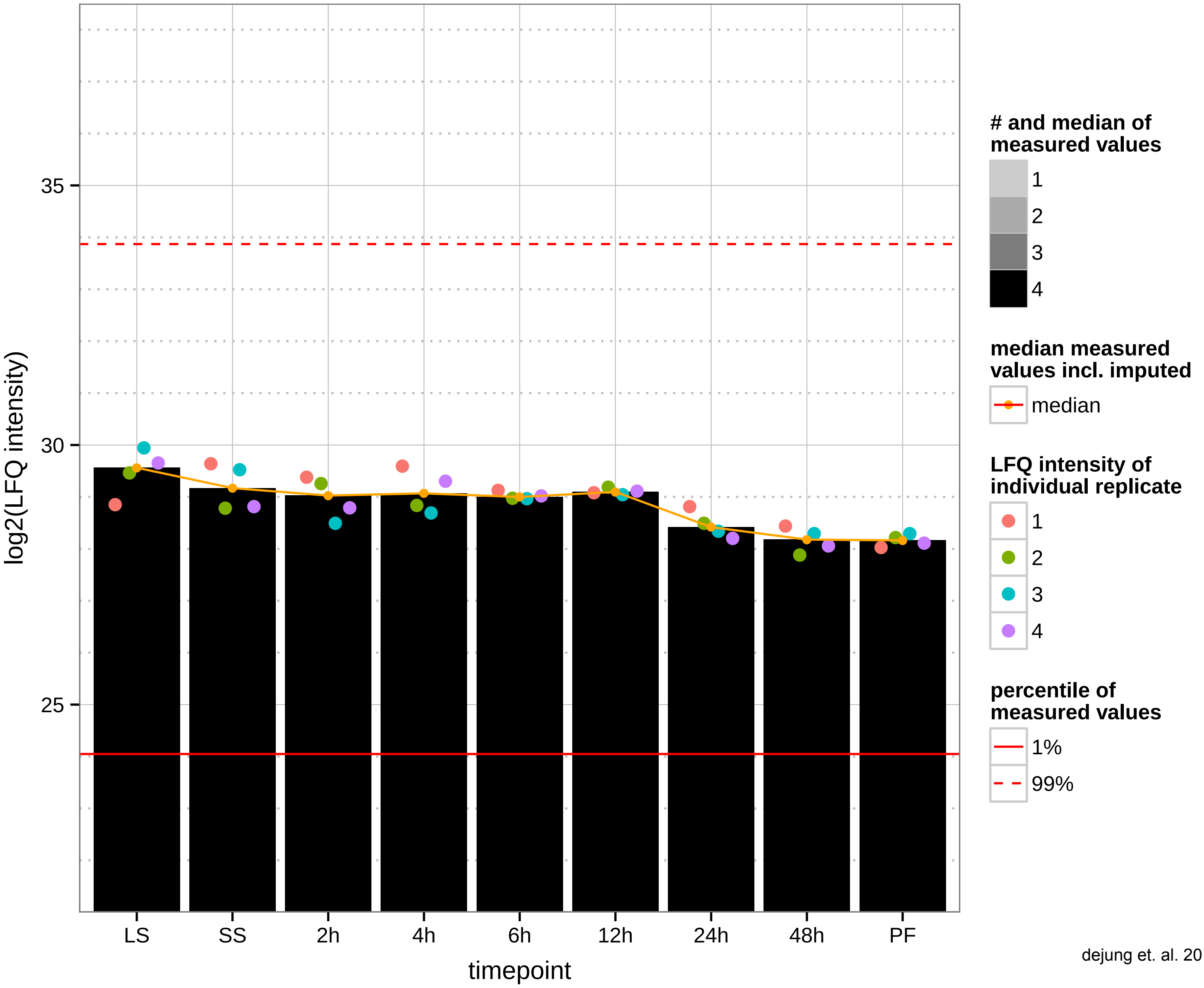
phospholipase A1 (PLA1)
Tb927.1.4830
AGOF: phosphatidylcholine 1−acylhydrolase activity
AGOC: null
AGOP: CDP−choline pathway
PGOF: null
PGOC: null
PGOP: null





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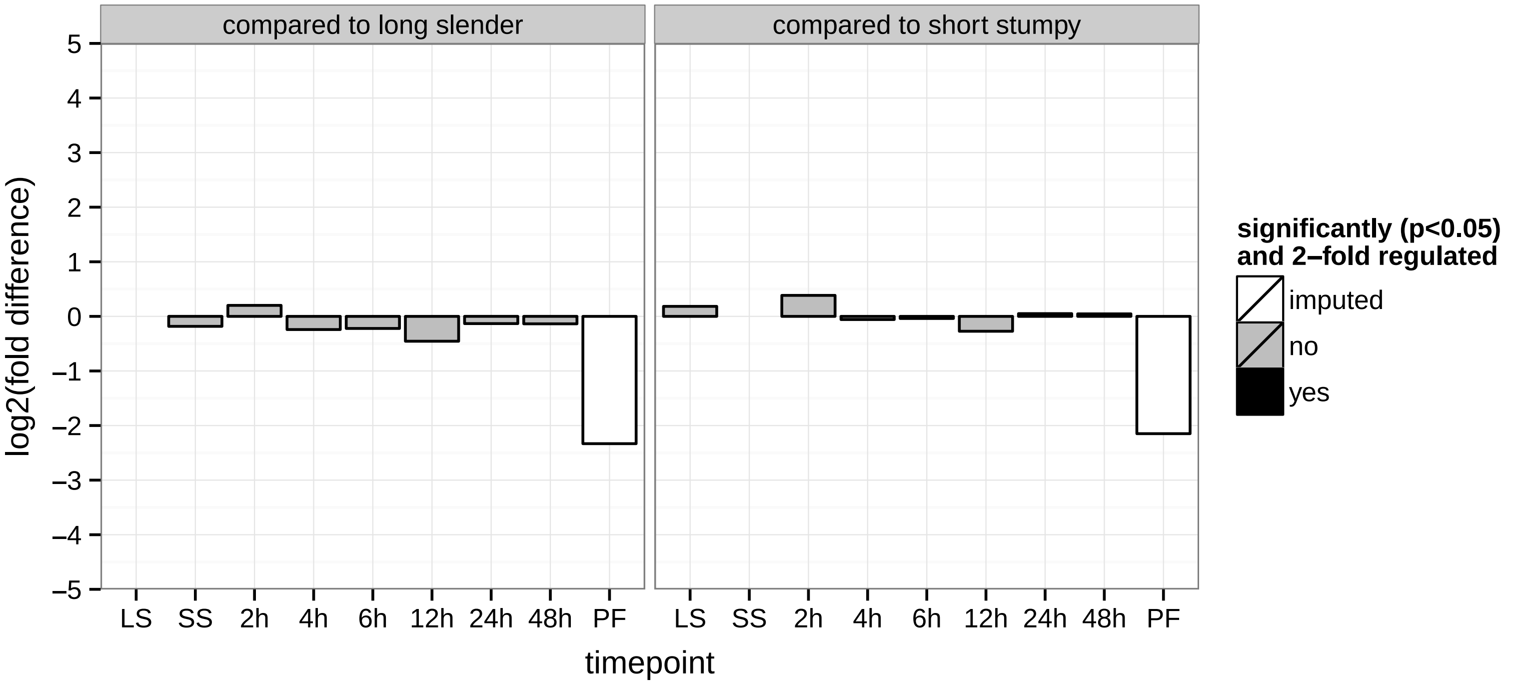
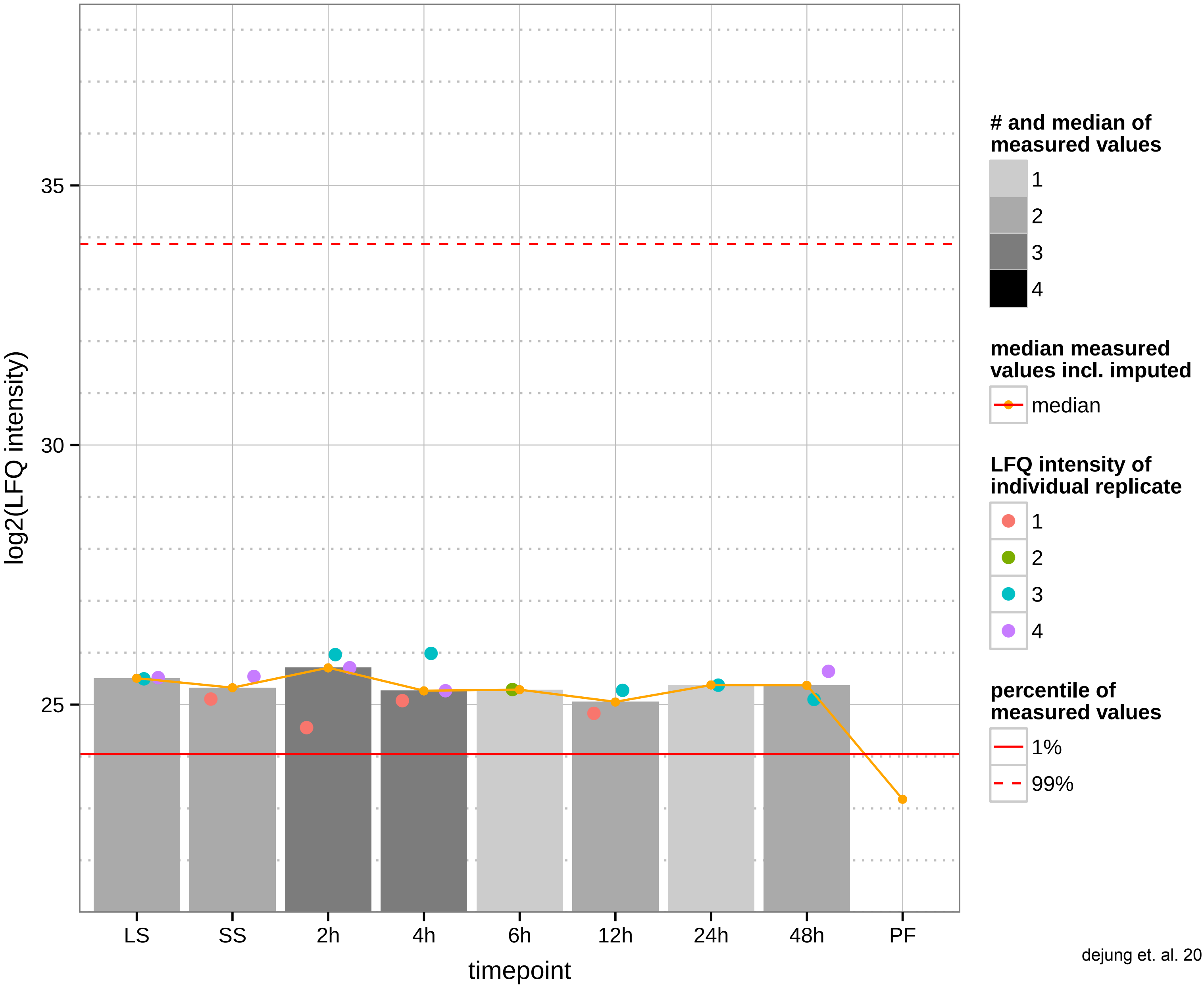
hypothetical protein, conserved
Tb927.1.690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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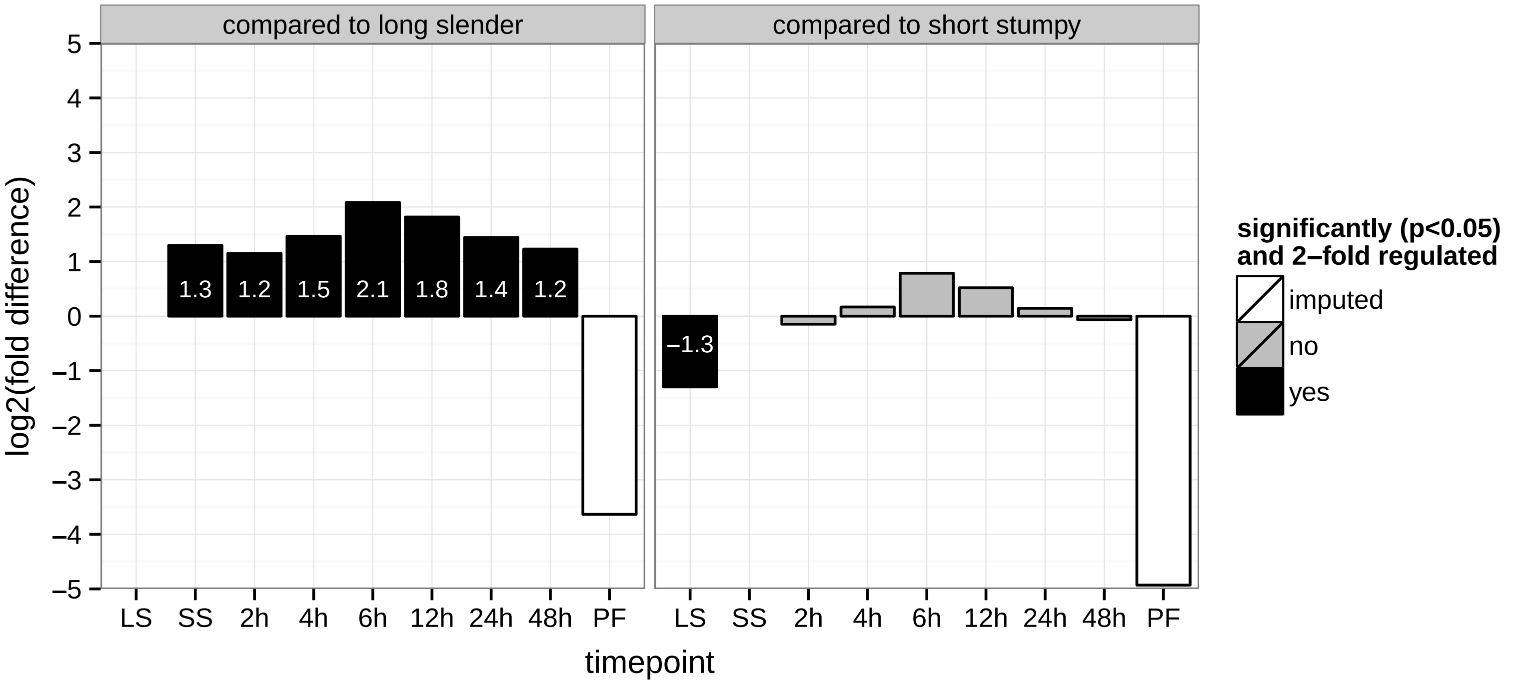
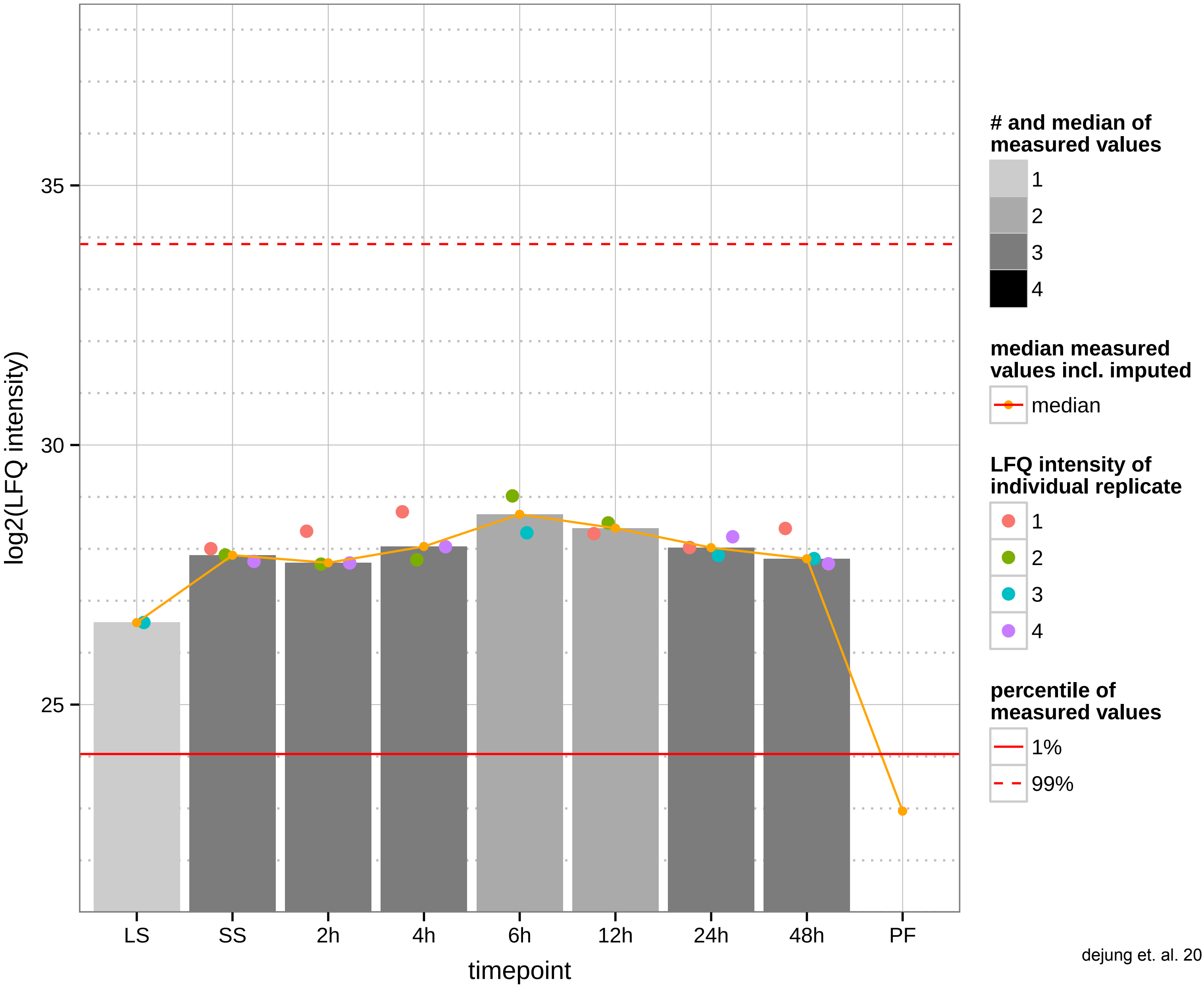
retrotransposon hot spot protein (RHS, pseudogene), putative
Tb927.1.90
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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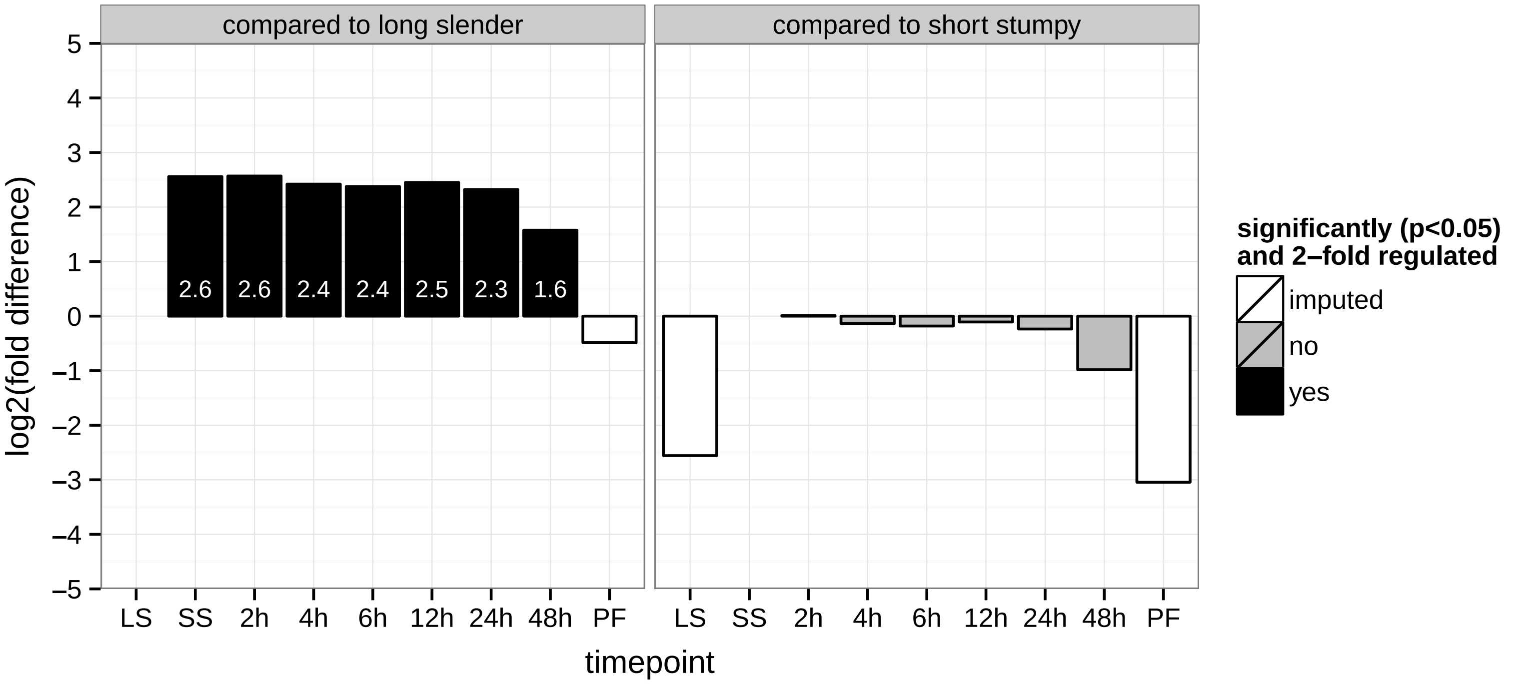
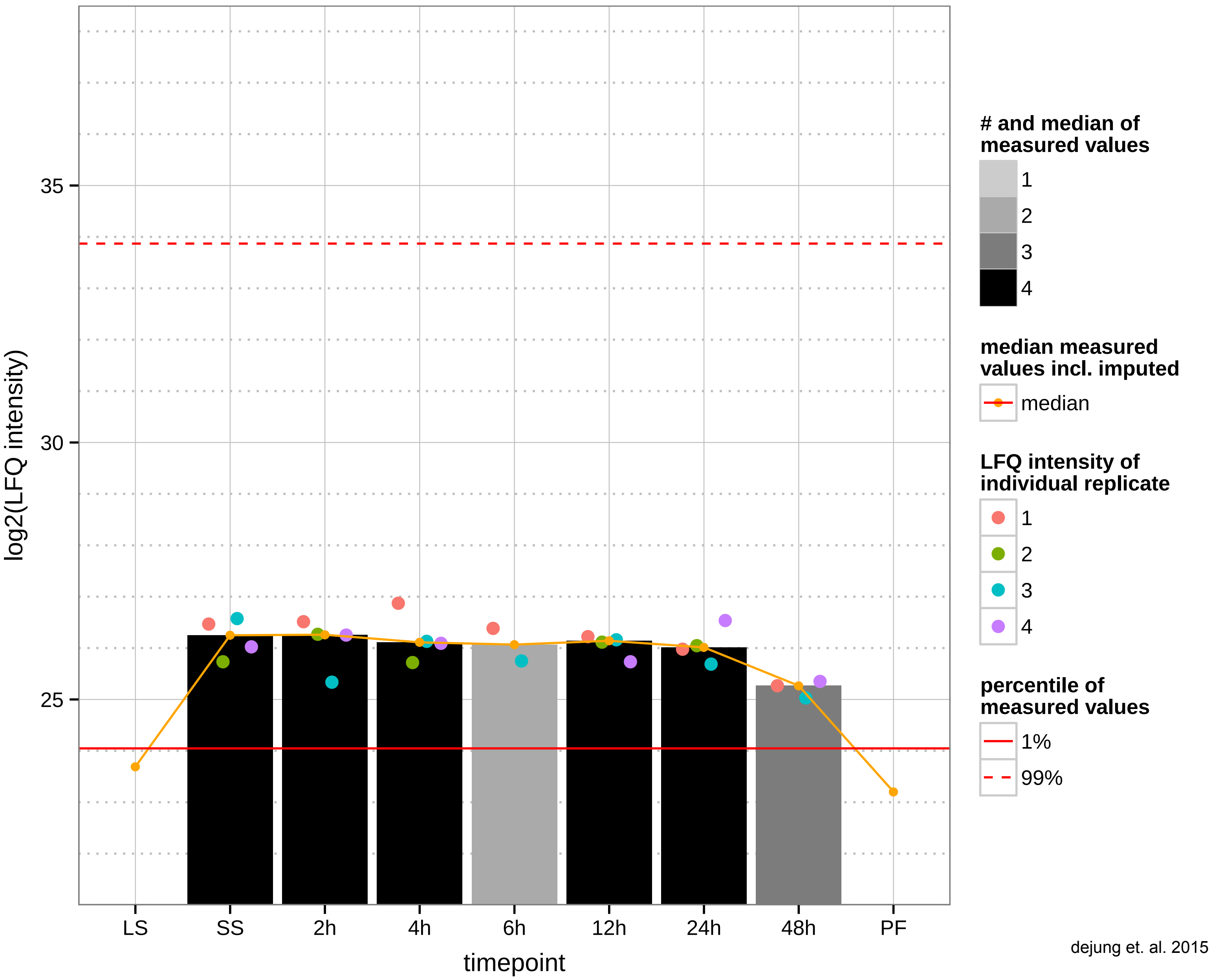
hypothetical protein, conserved
Tb927.10.10020;Tb11.v5.0853
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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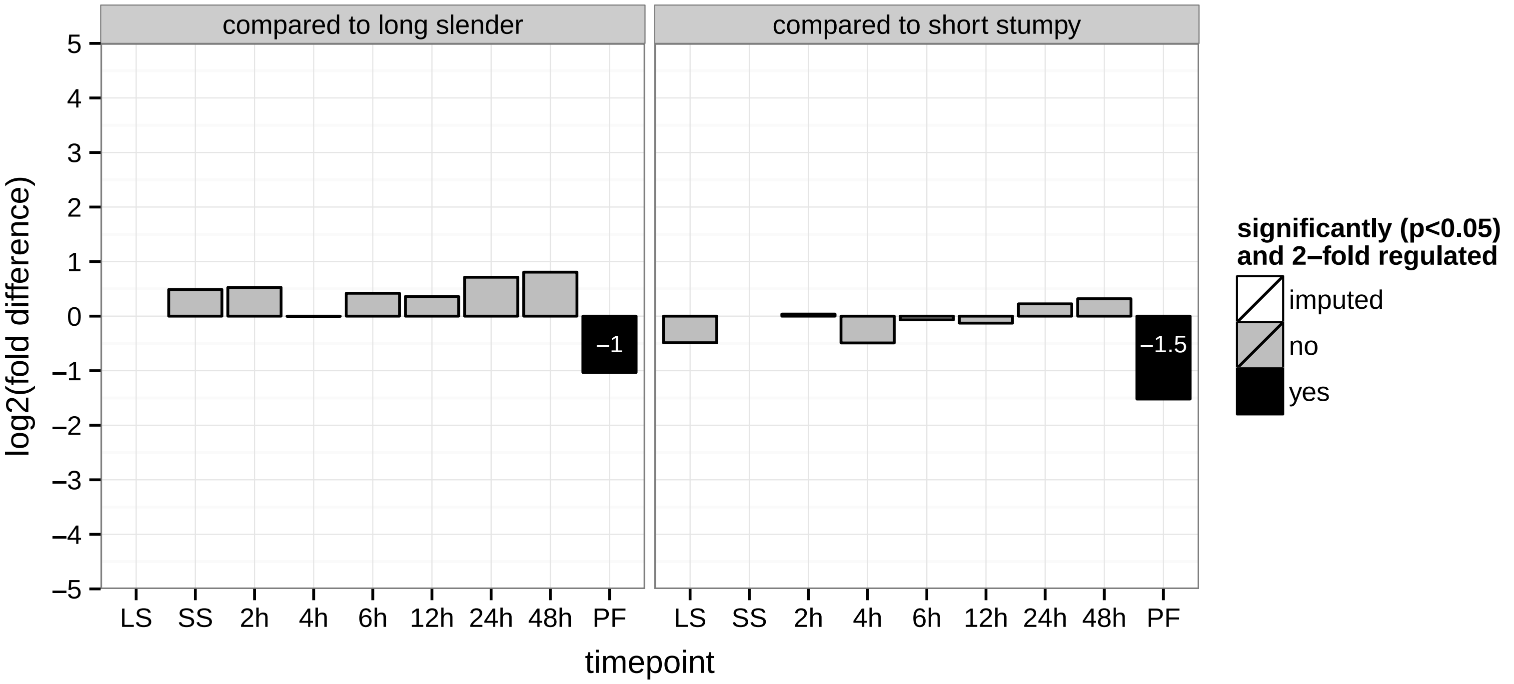
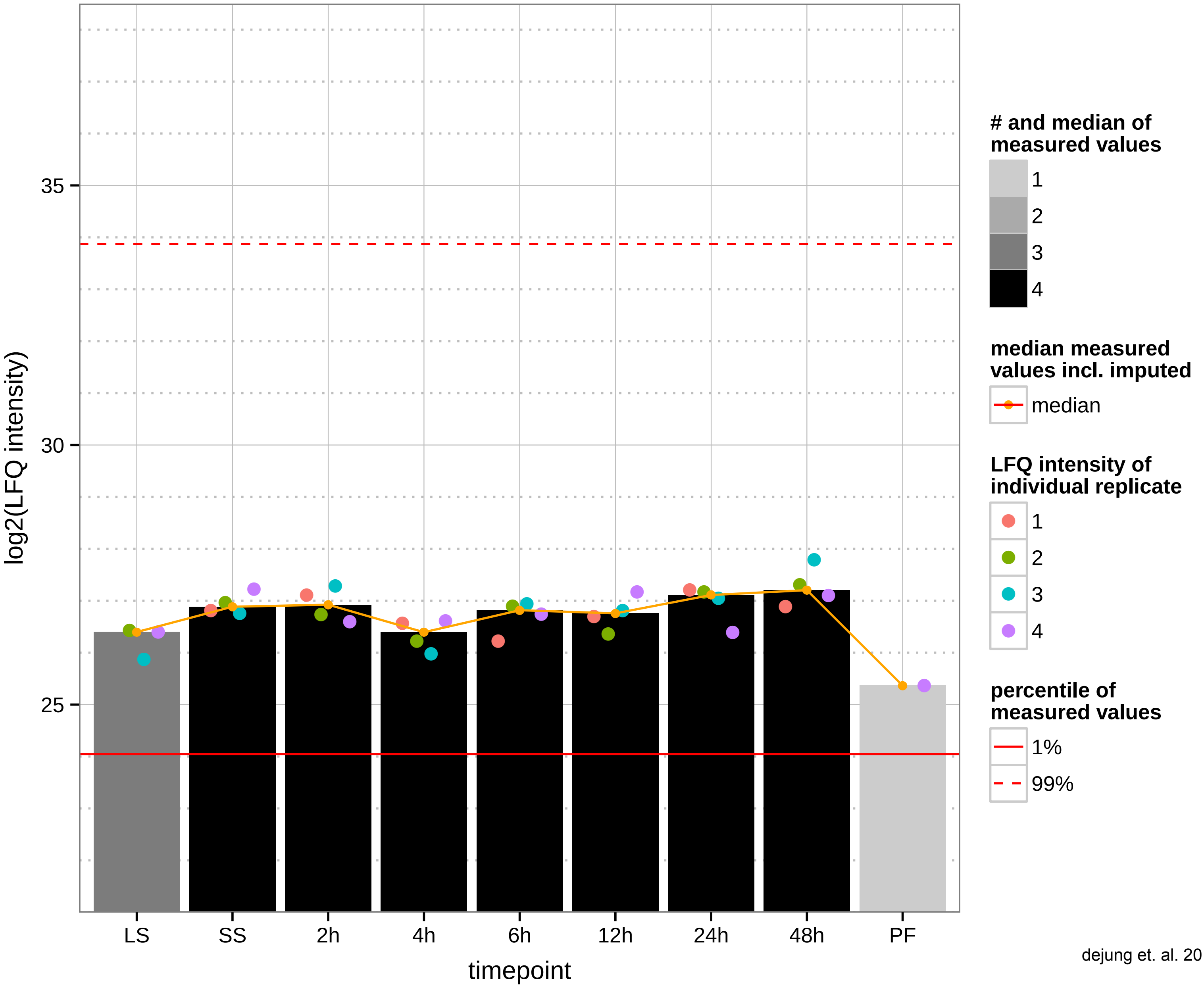
microtubule–associated protein, putative
Tb927.10.10280
AGOF: microtubule binding
AGOC: cytoplasm
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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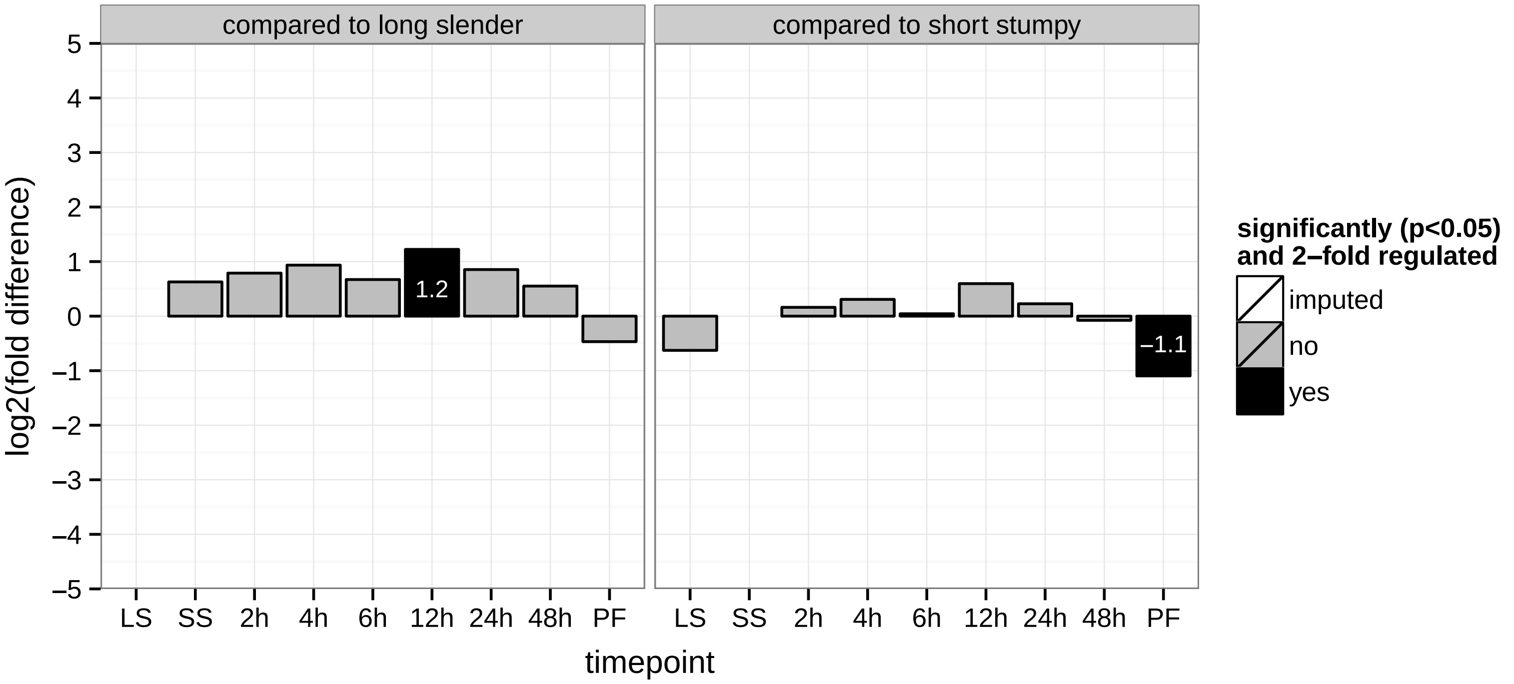
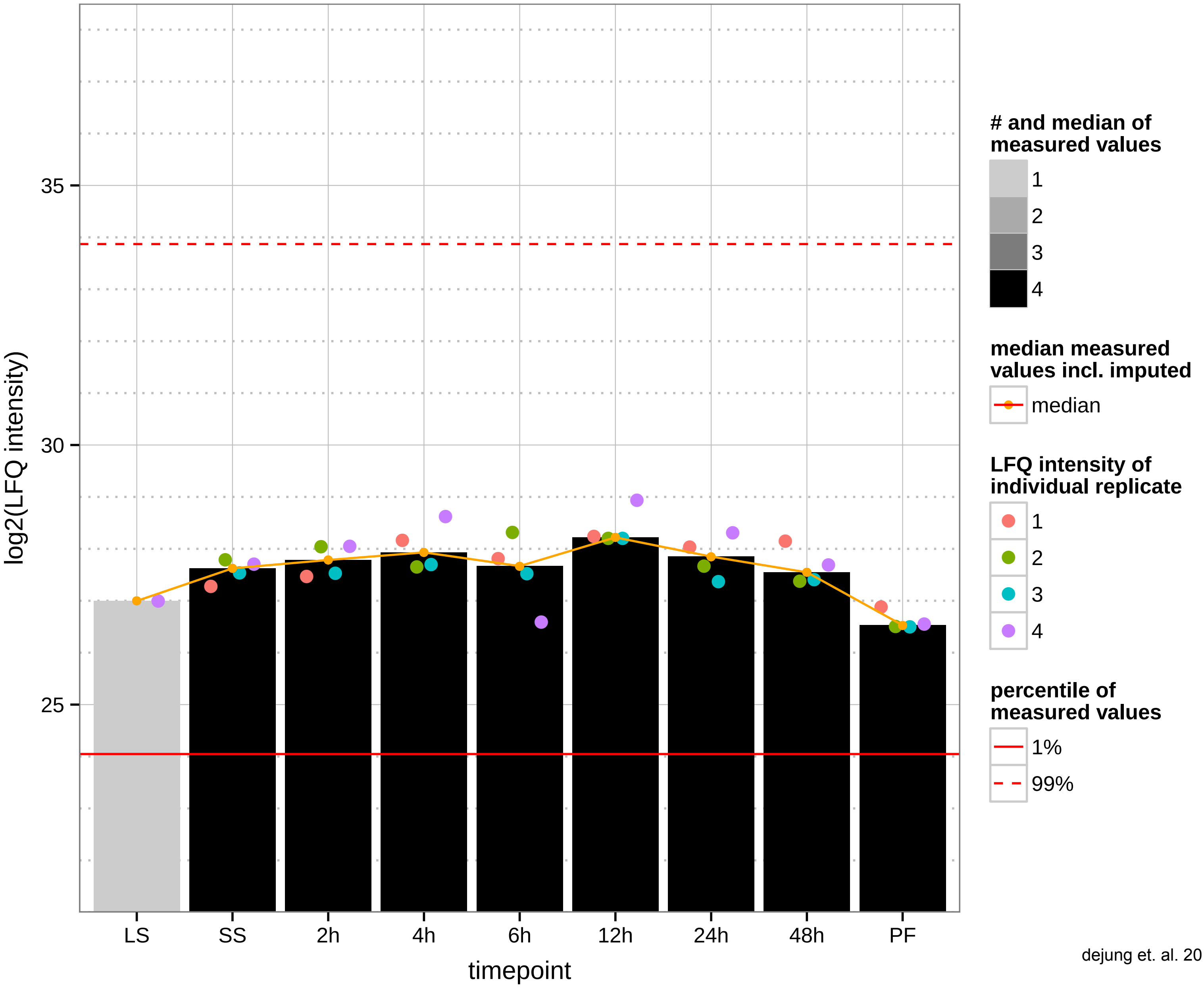
hypothetical protein, conserved
Tb927.10.12030
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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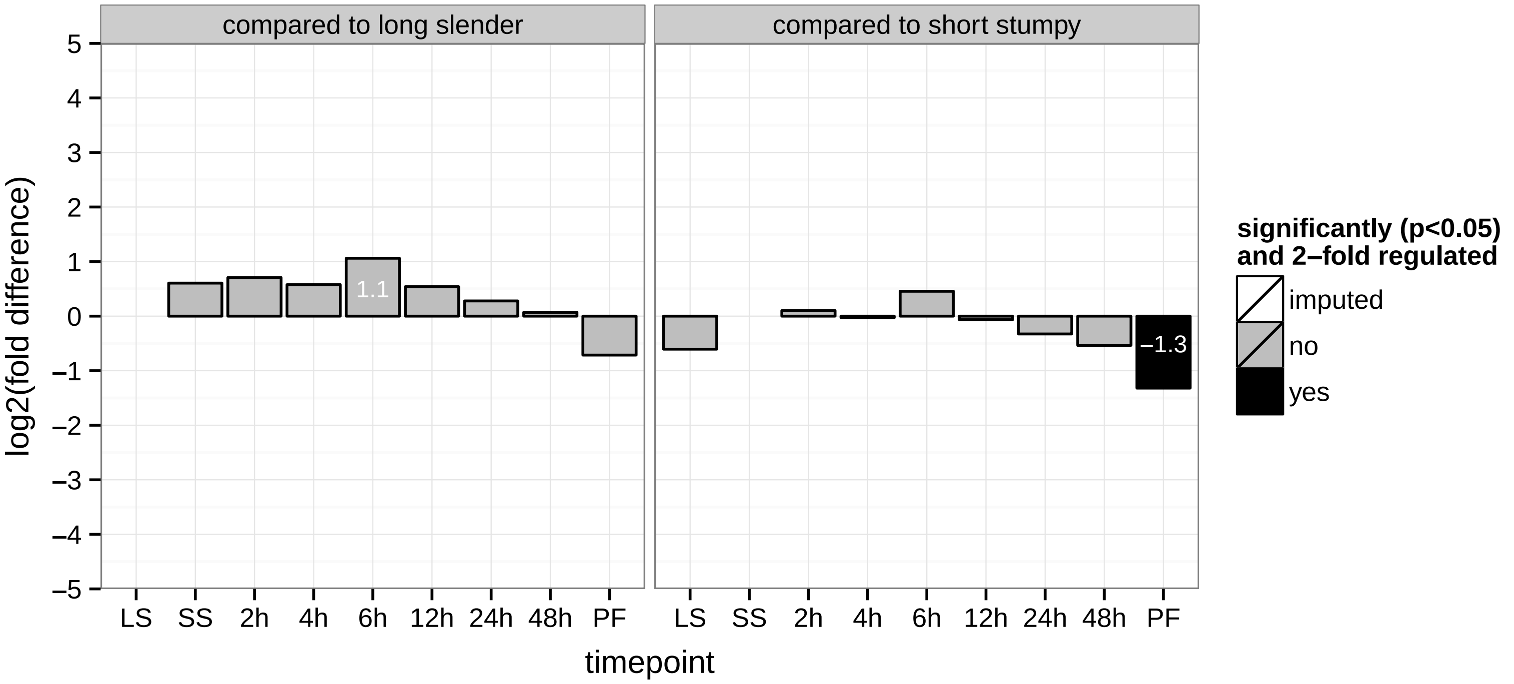
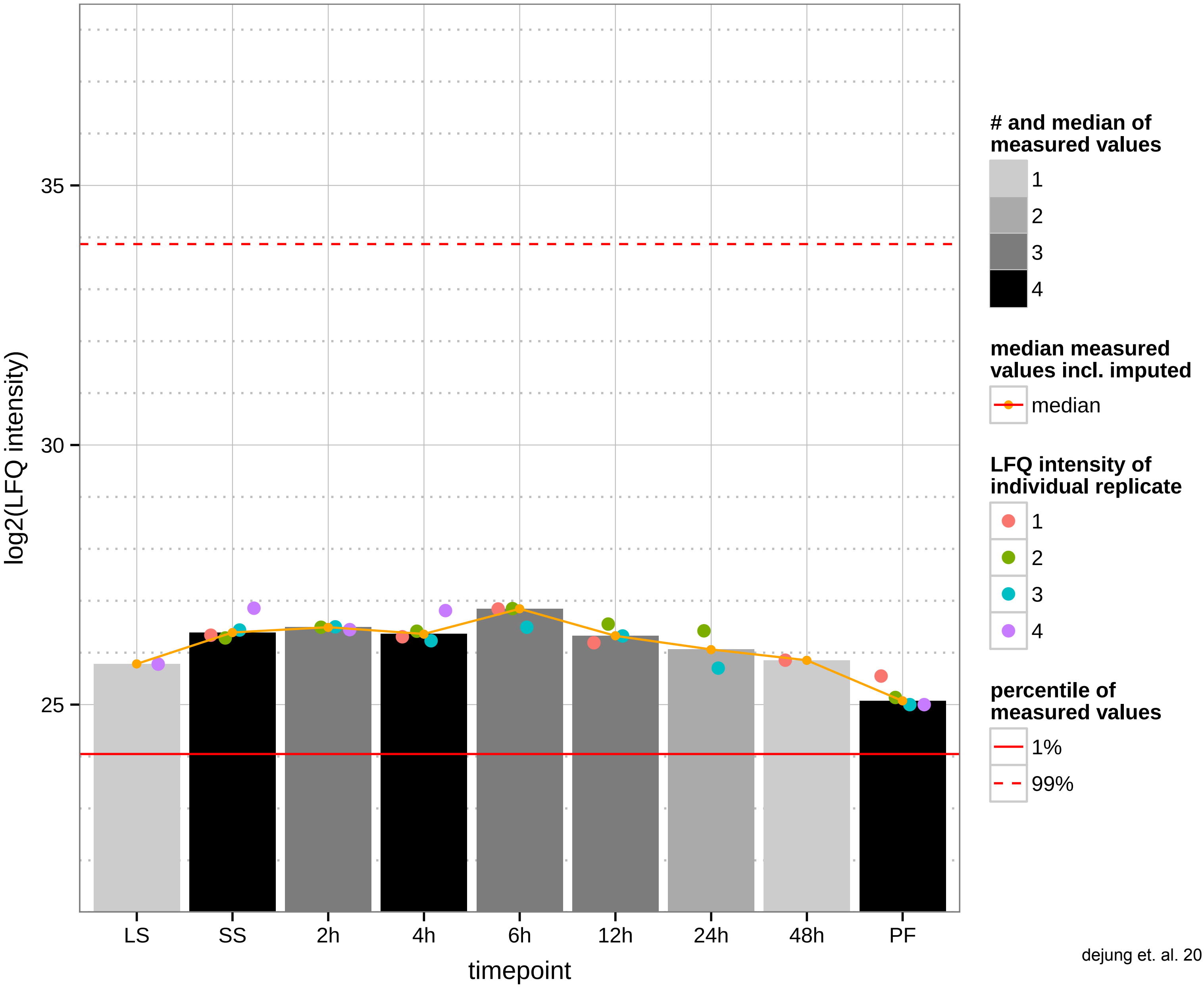
SNARE domain−containing protein, putative
Tb927.10.12450
AGOF: null
AGOC: contractile vacuole, integral to membrane
AGOP: vesicle−mediated transport
PGOF: null
PGOC: null
PGOP: transport





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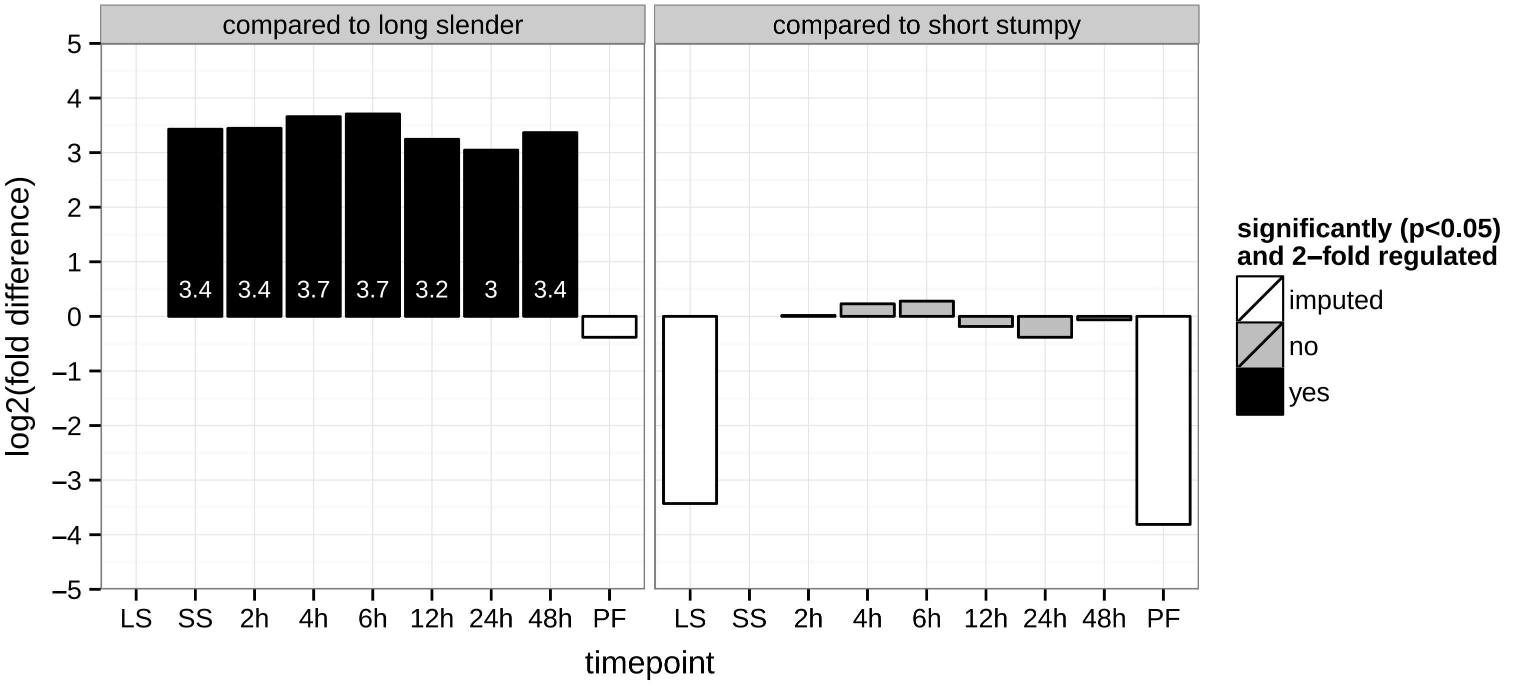
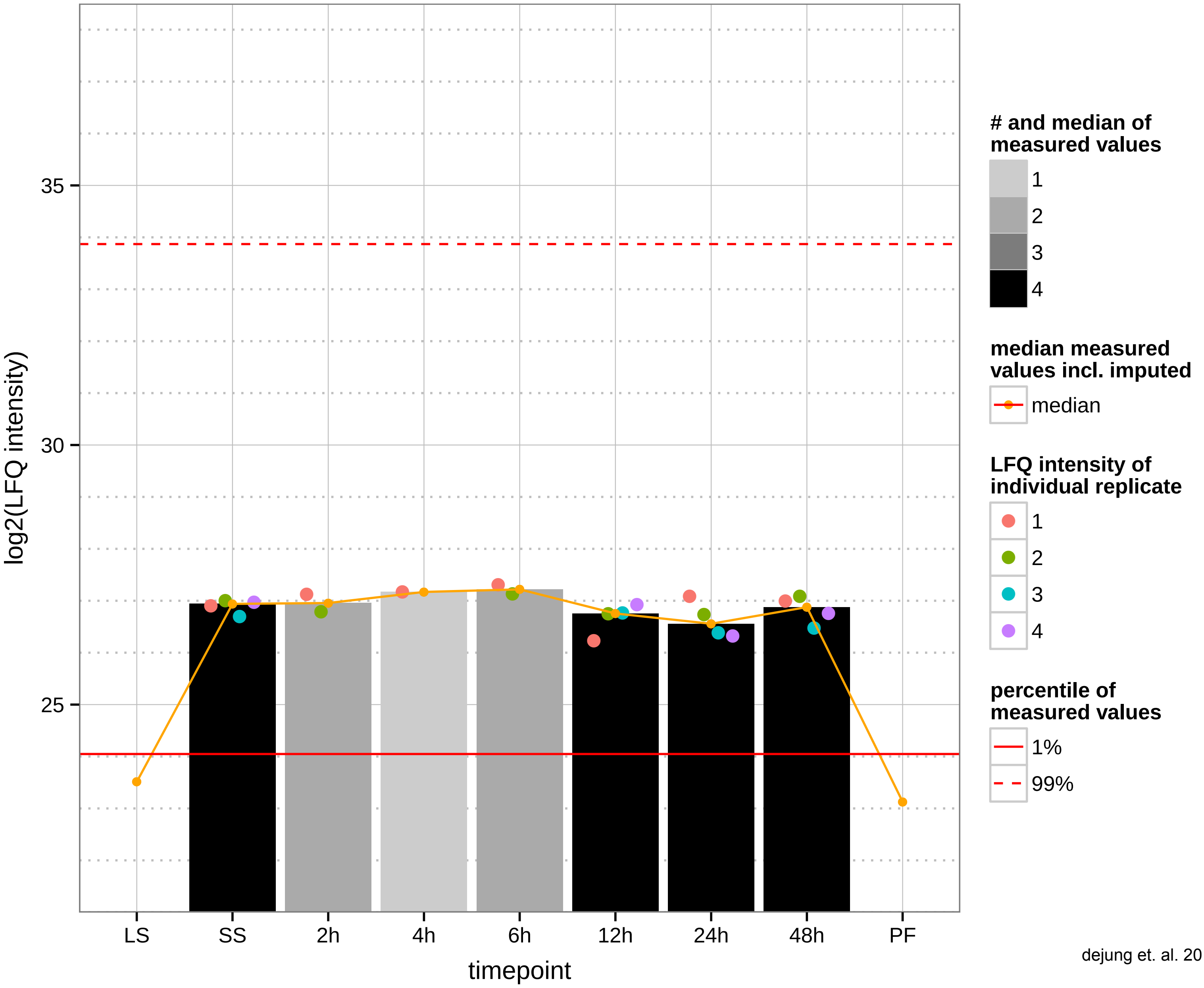
hypothetical protein, conserved
Tb927.10.12720
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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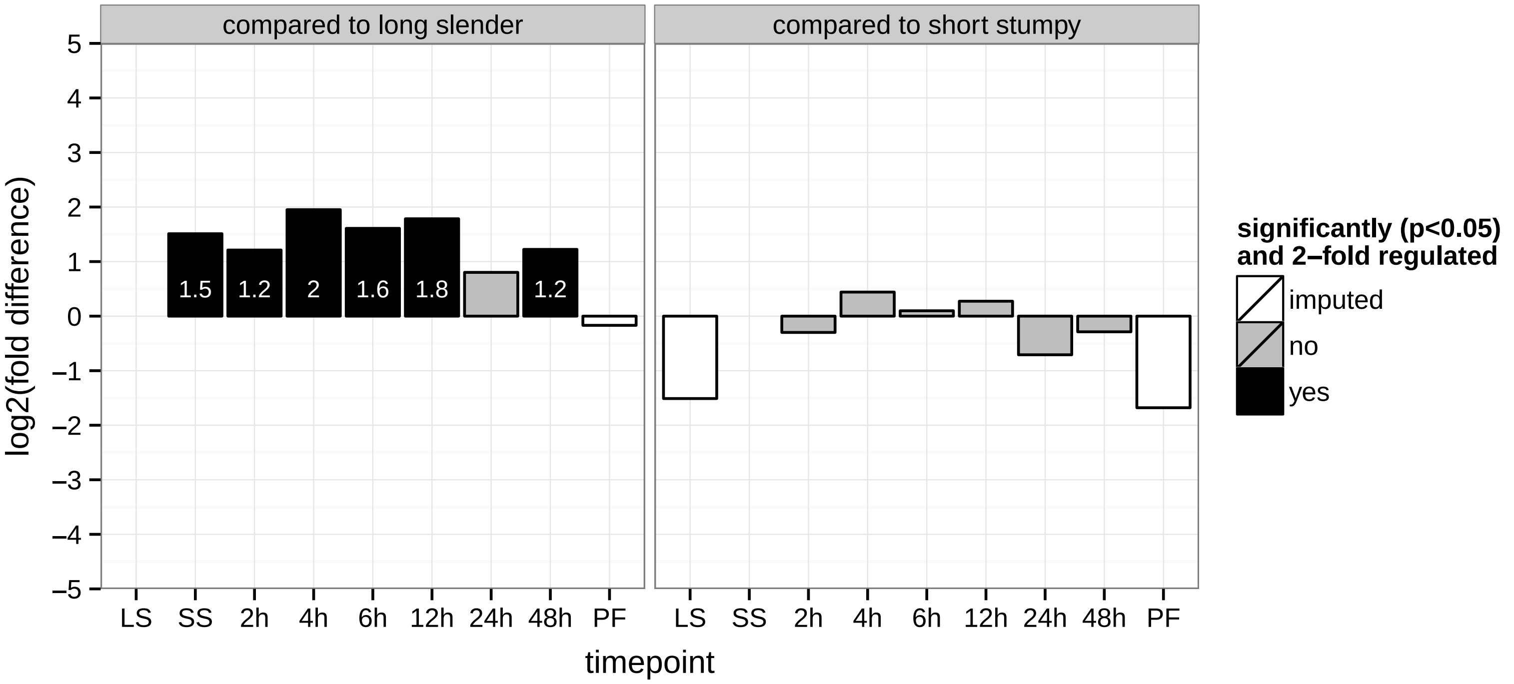
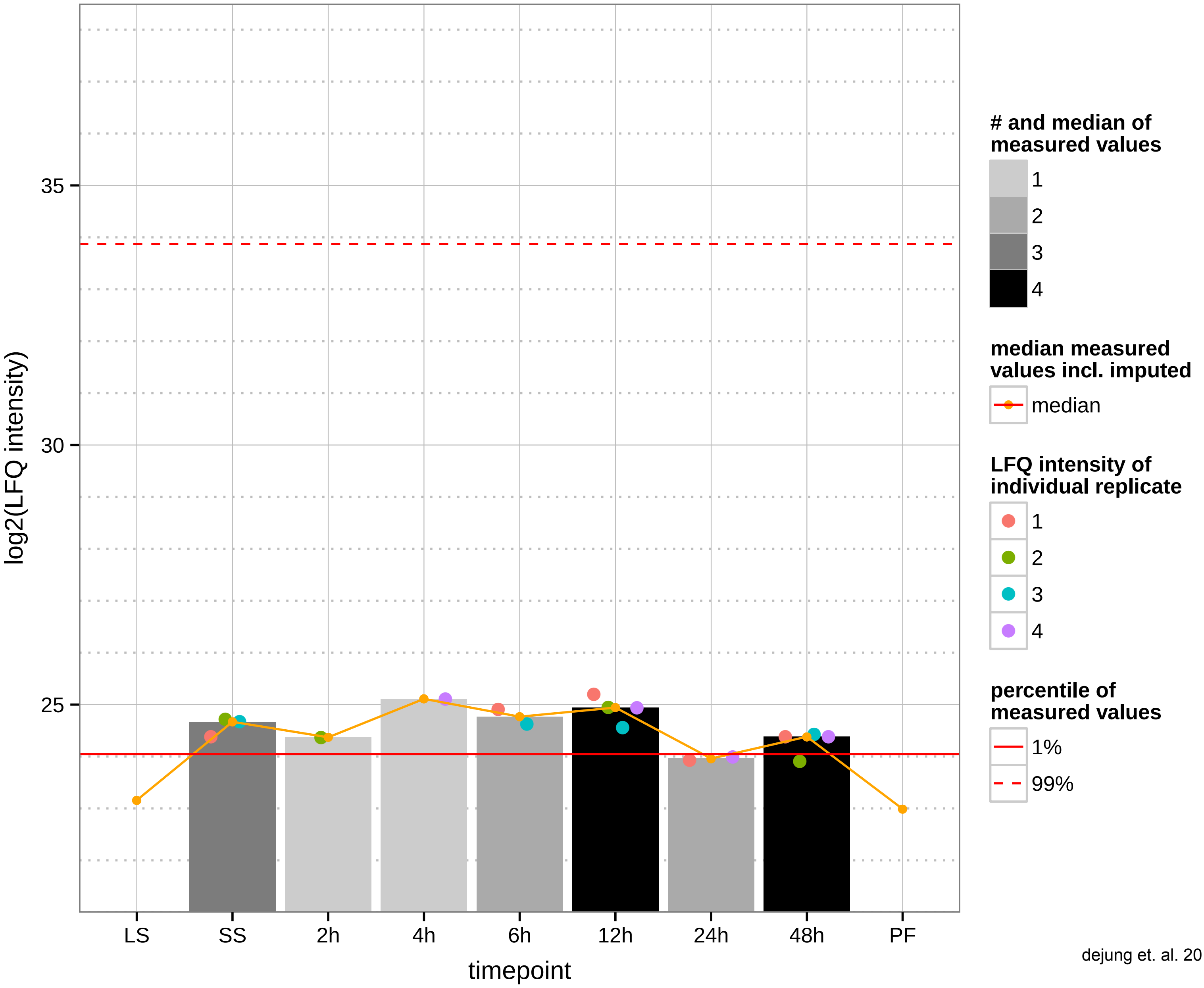
hypothetical protein, conserved
Tb927.10.12970
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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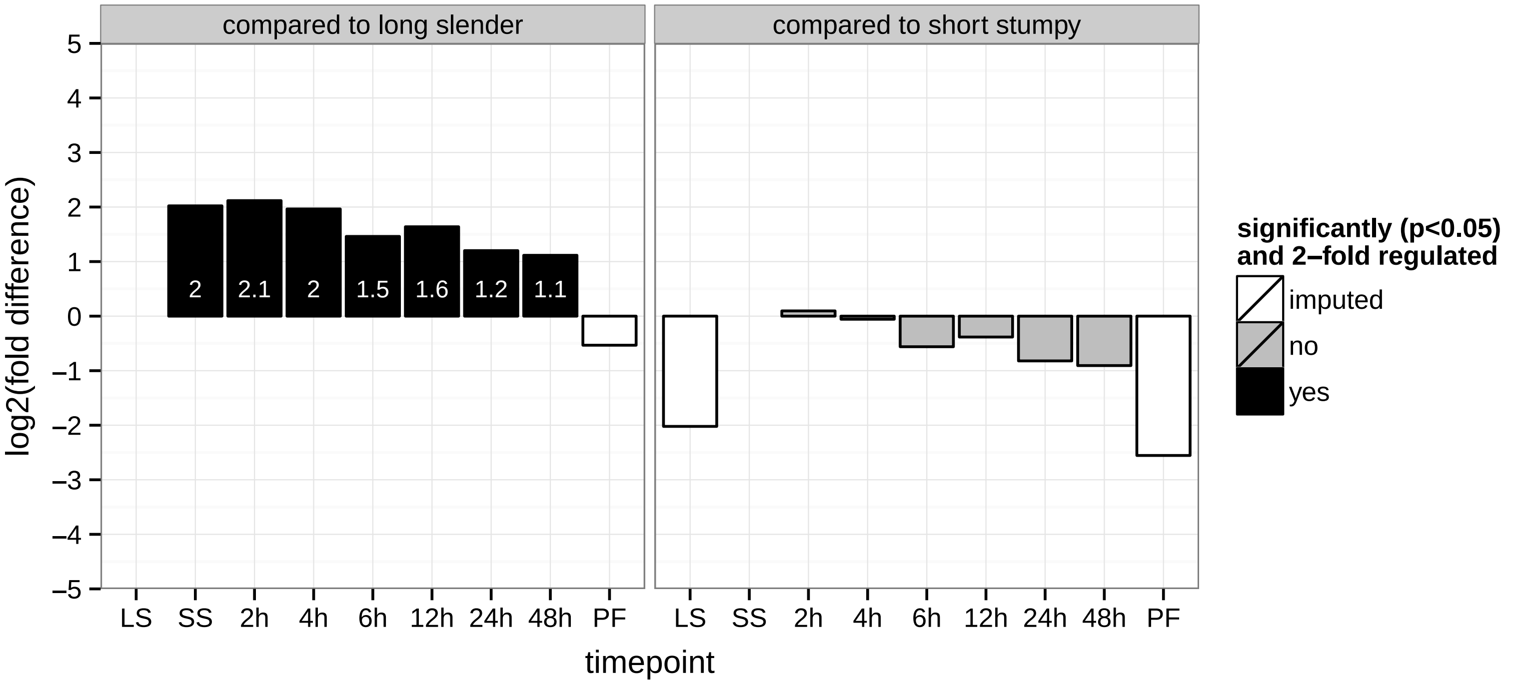
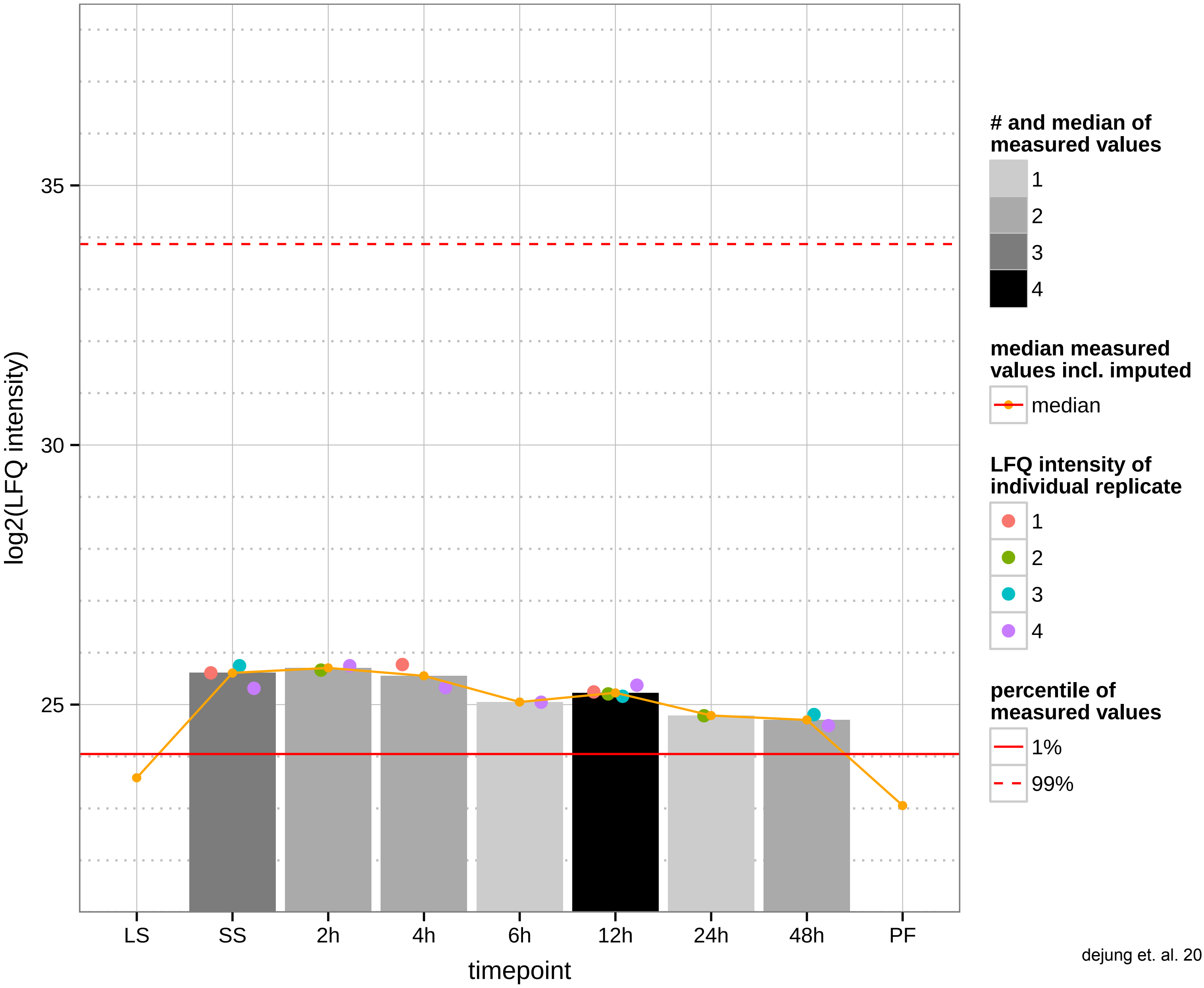
Vacuolar protein sorting–associated protein 16 homolog, putative
Tb927.10.13020
AGOF: null
AGOC: cytoplasm
AGOP: intracellular protein transport
PGOF: null
PGOC: cytoplasm
PGOP: intracellular protein transport





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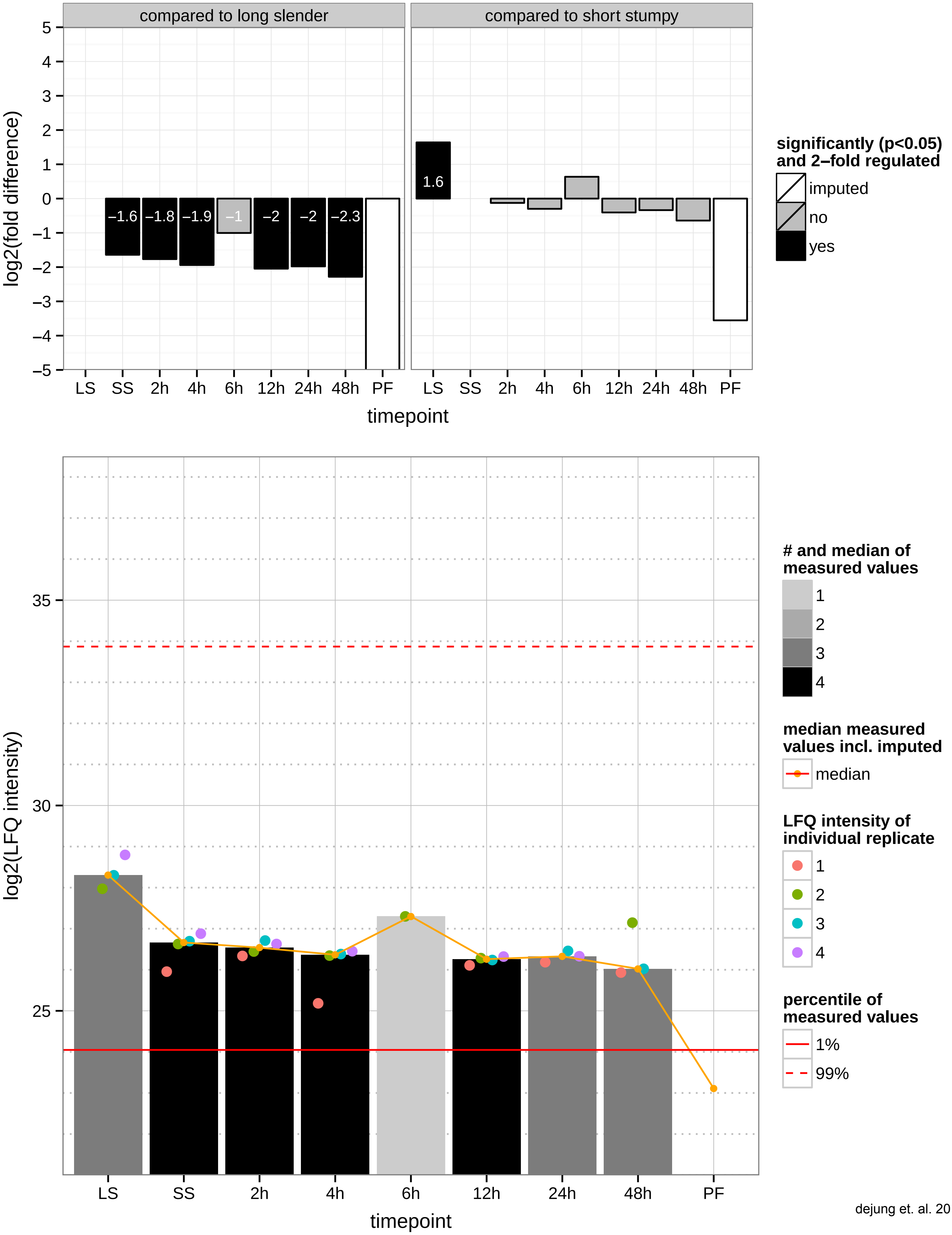
cysteine peptidase, Clan CA, family C2, putative, calpain–like cysteine peptidase
Tb927.10.13030
AGOF: calcium–dependent cysteine–type endopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: calcium–dependent cysteine–type endopeptidase activity
PGOC: intracellular
PGOP: proteolysis



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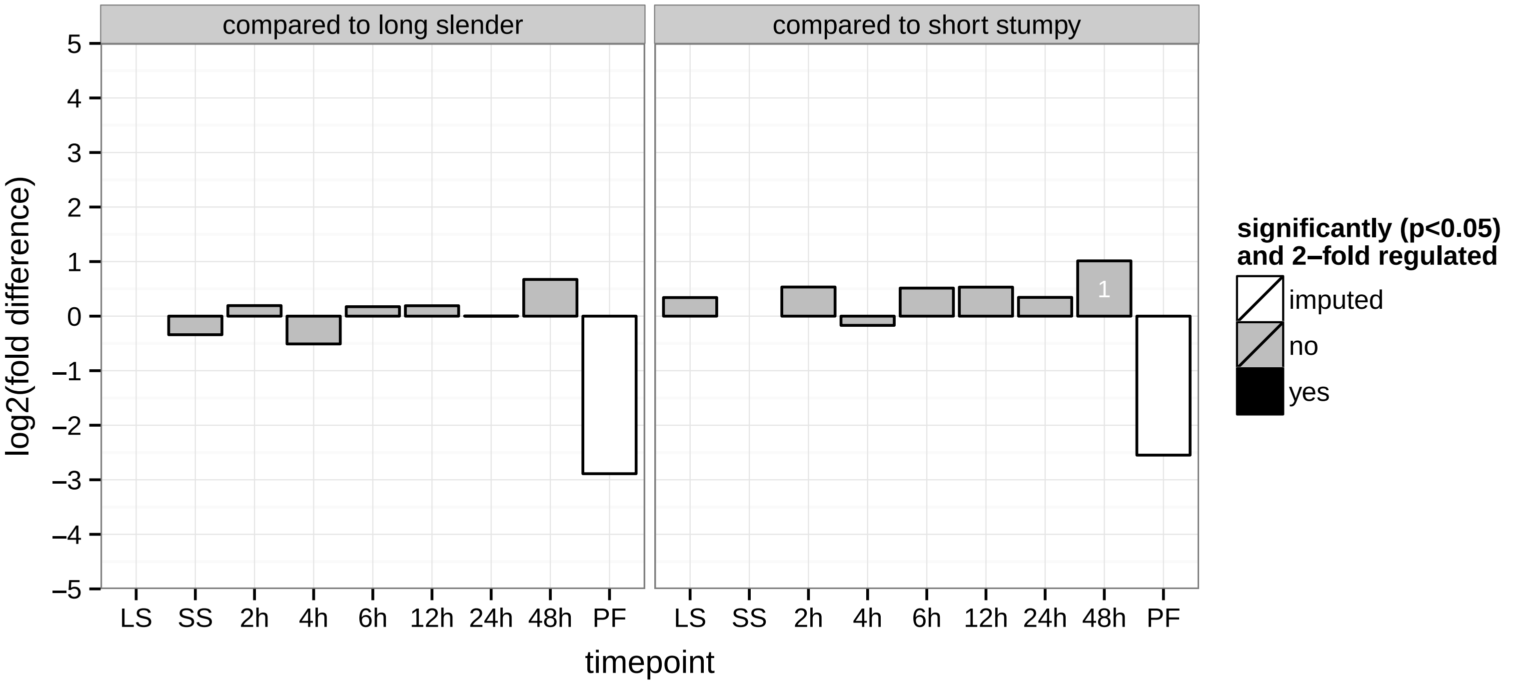
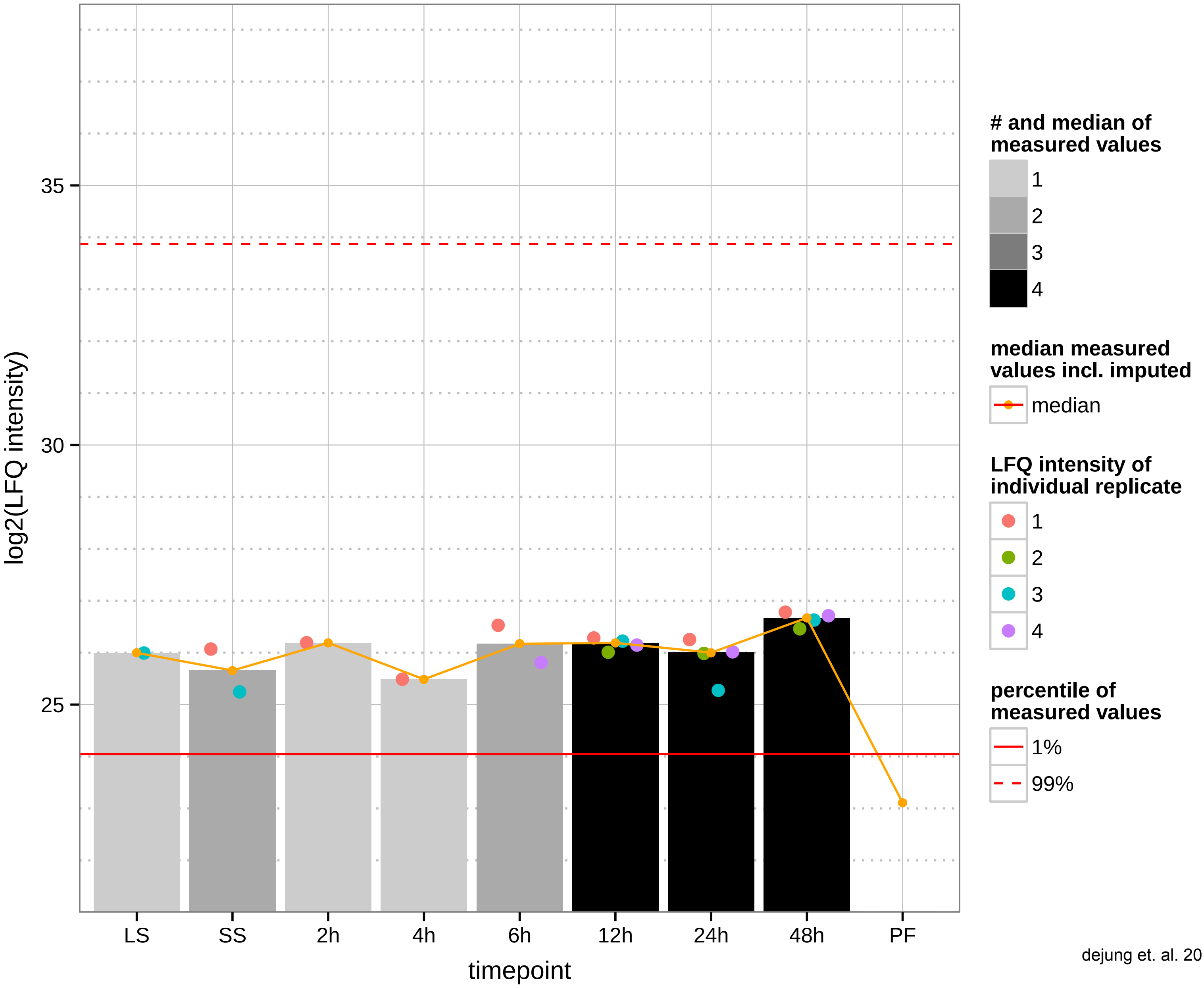
flagellar protein PF20
Tb927.10.13960
AGOF: null
AGOC: axoneme
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null





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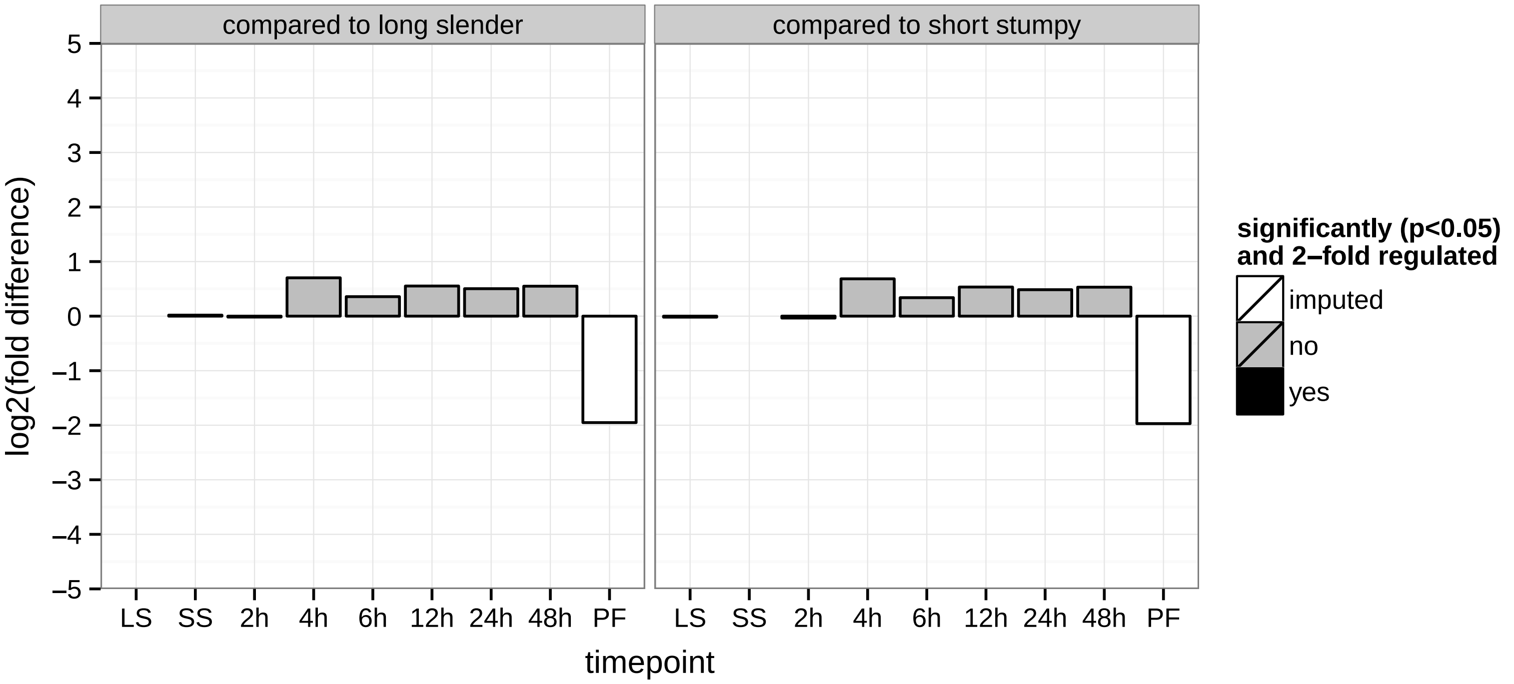
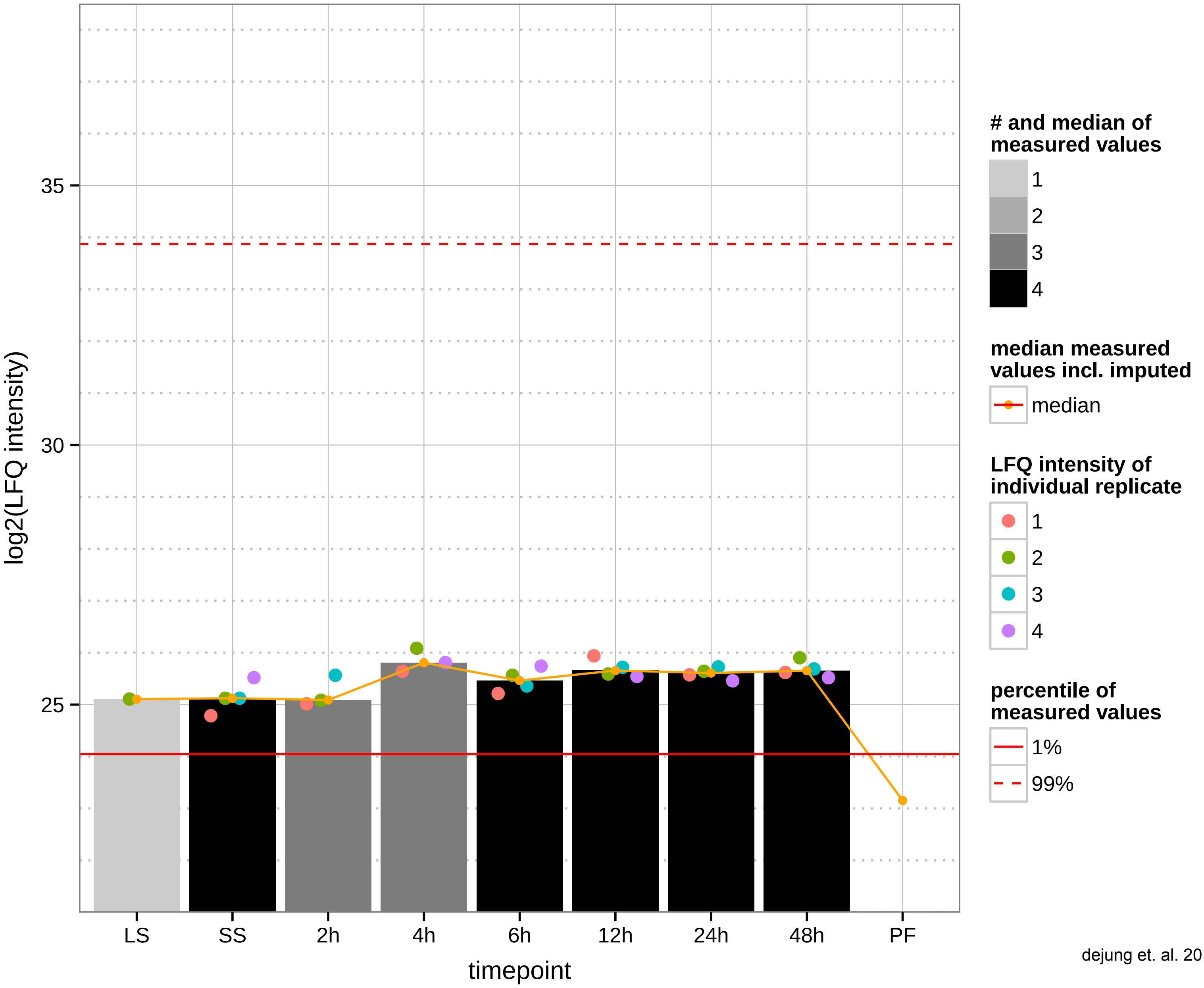
hypothetical protein, conserved
Tb927.10.13990
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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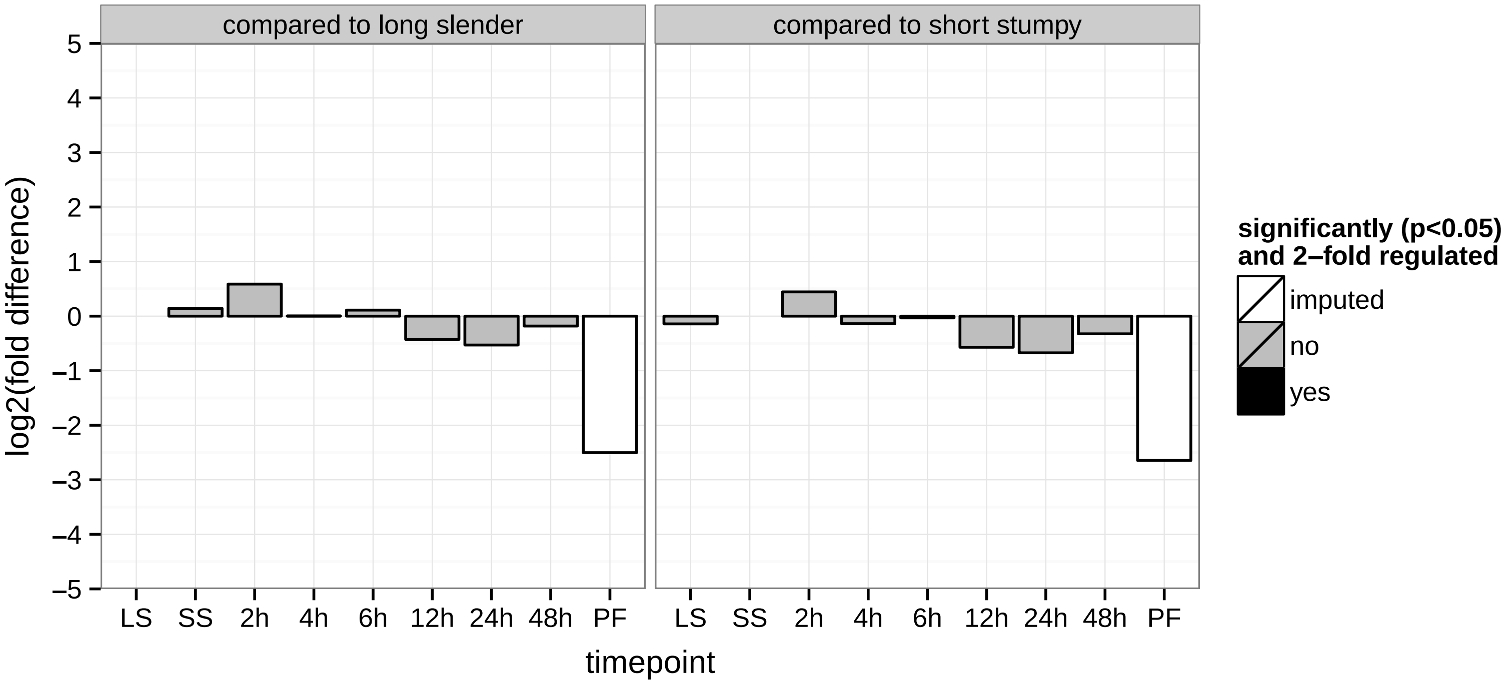
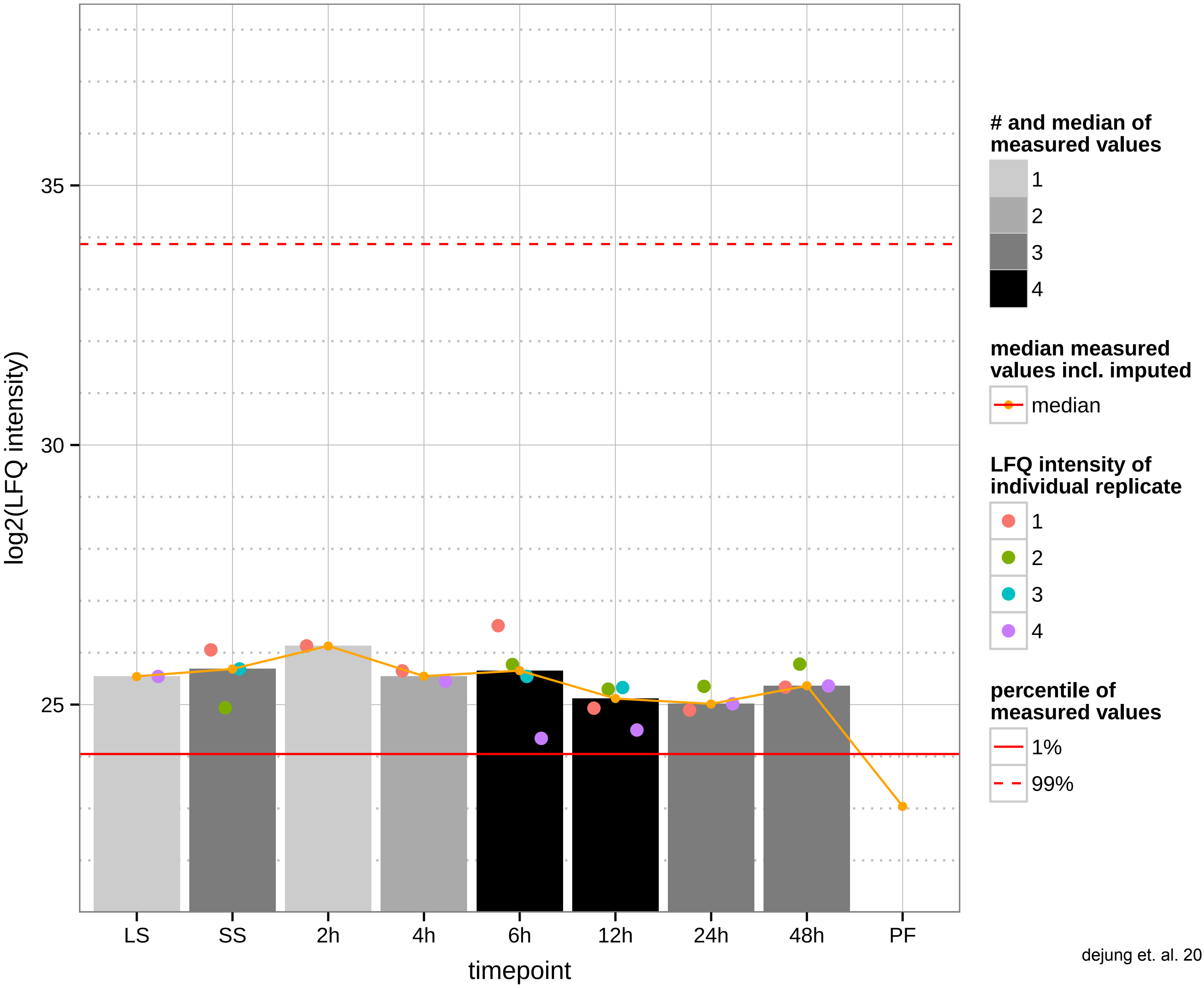
hypothetical protein, conserved
Tb927.10.14220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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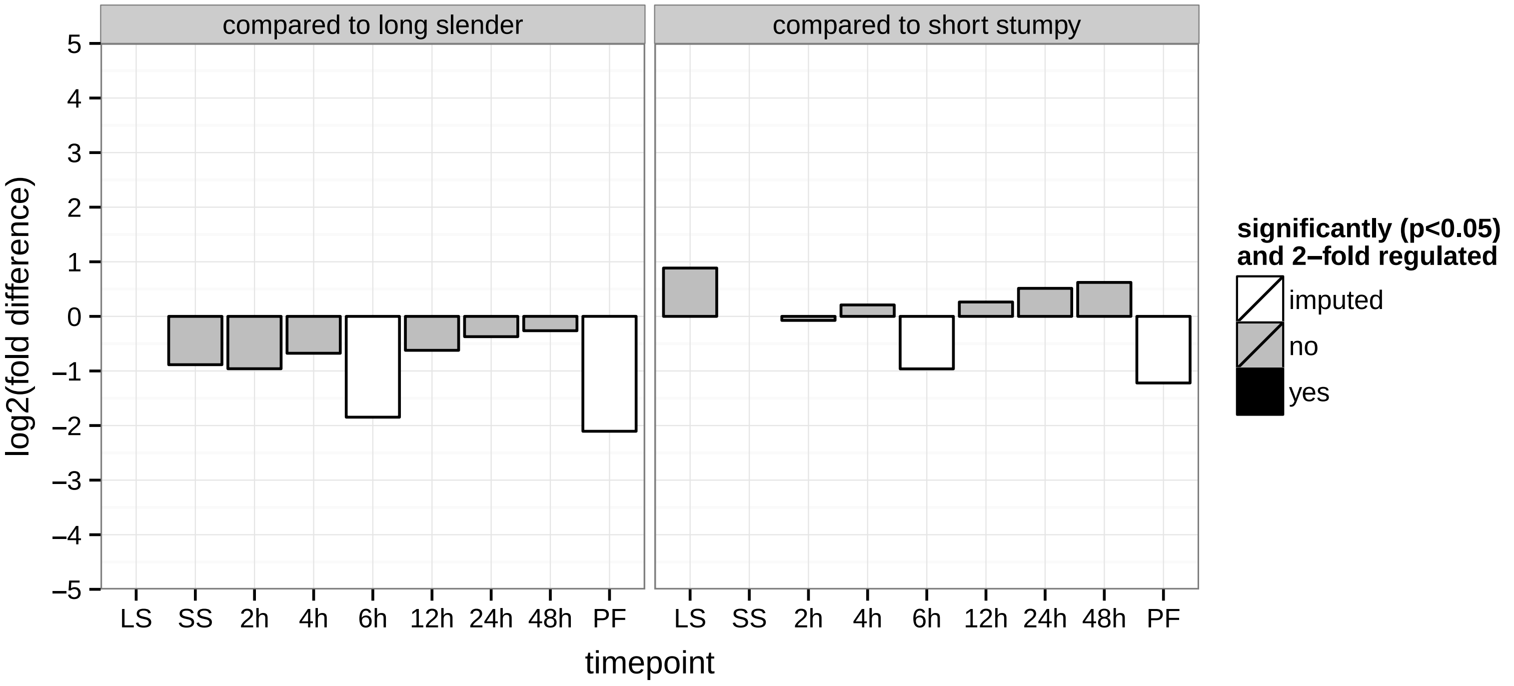
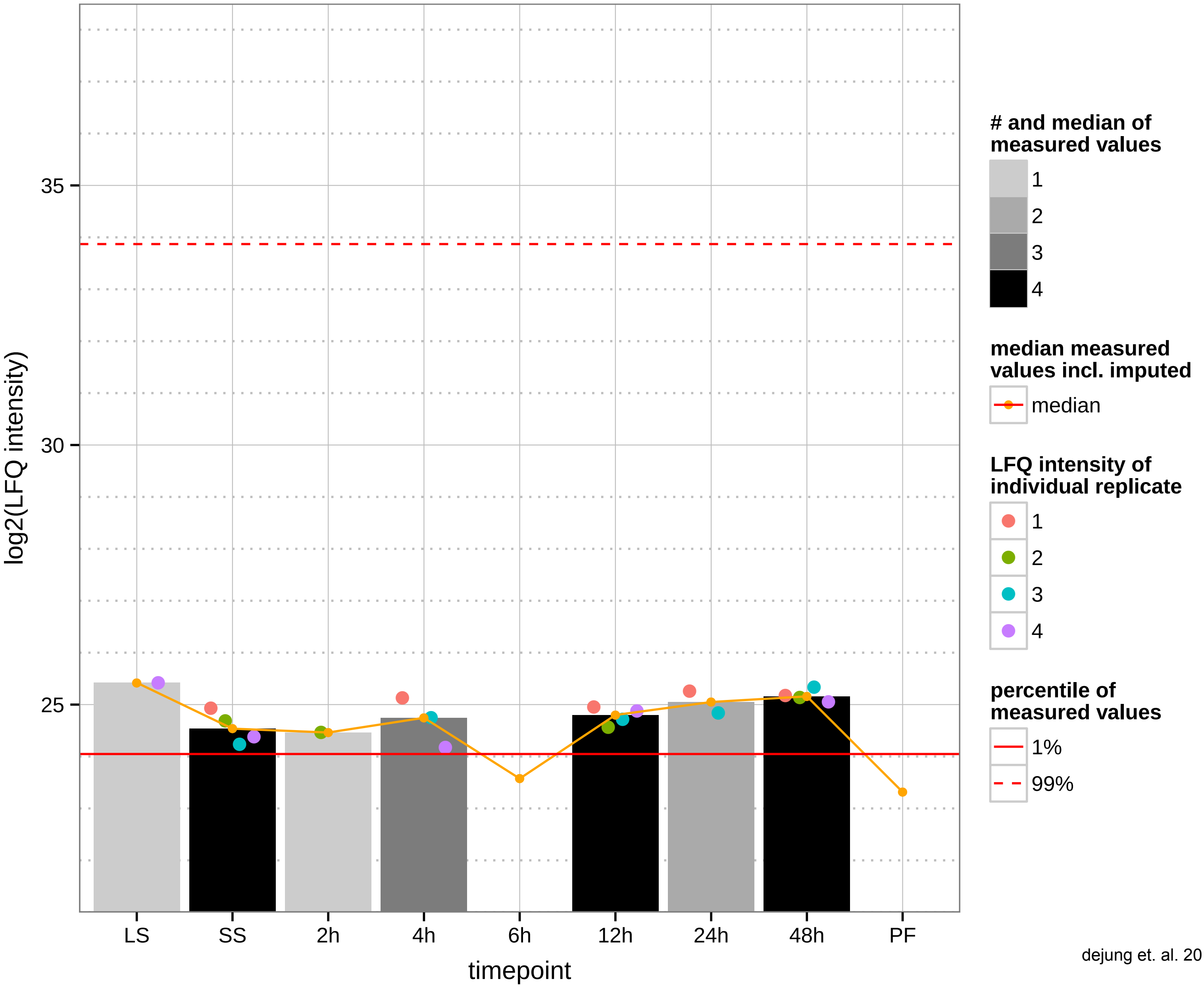
hypothetical protein, conserved
Tb927.10.14340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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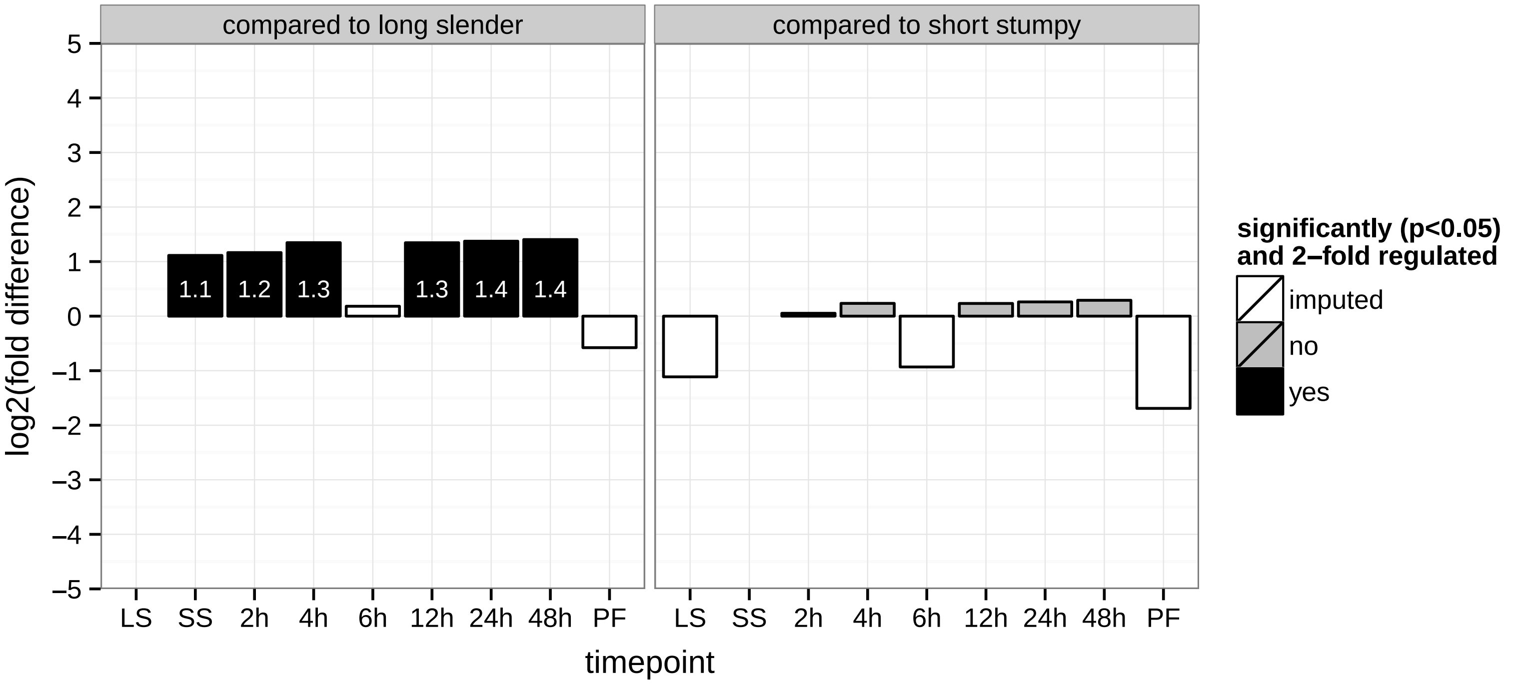
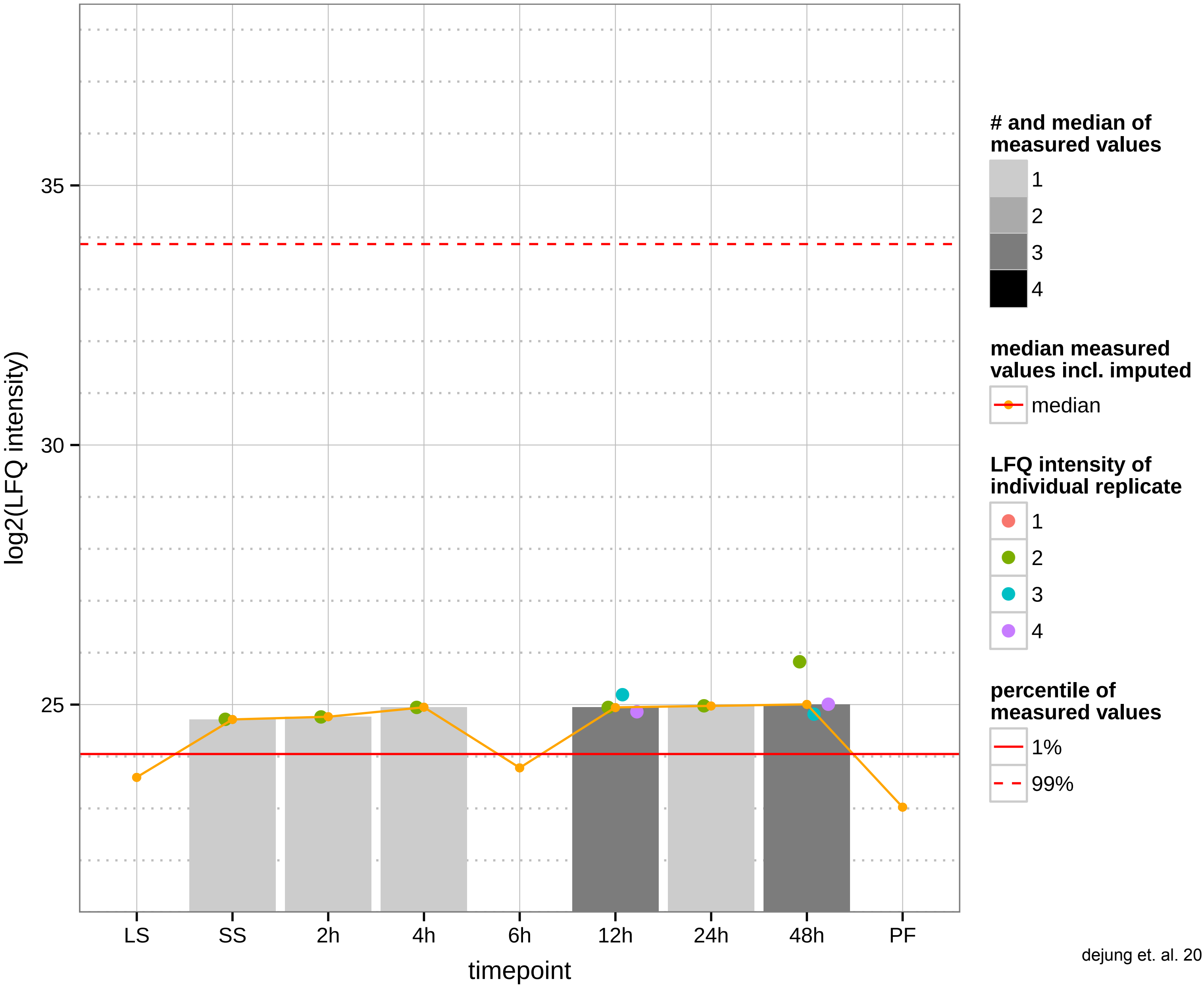
hypothetical protein, conserved
Tb927.10.14640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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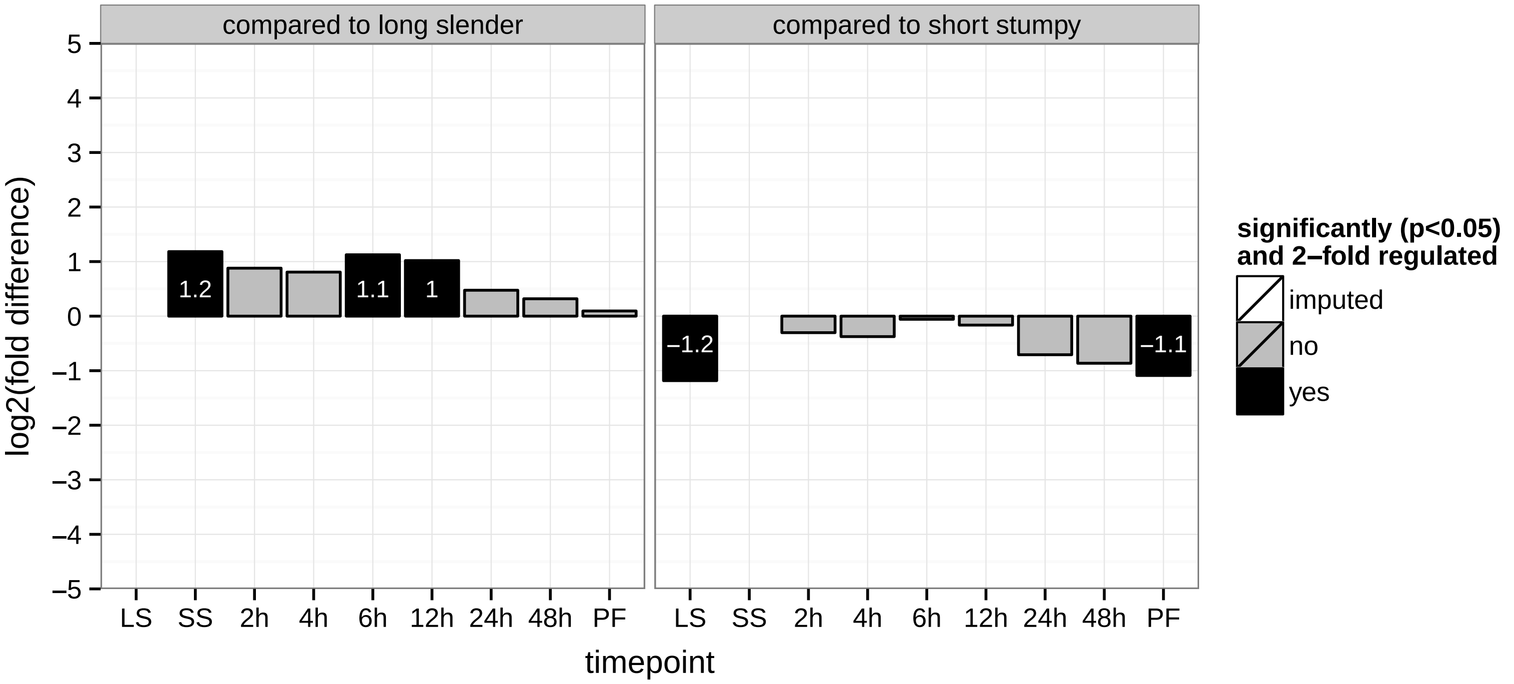
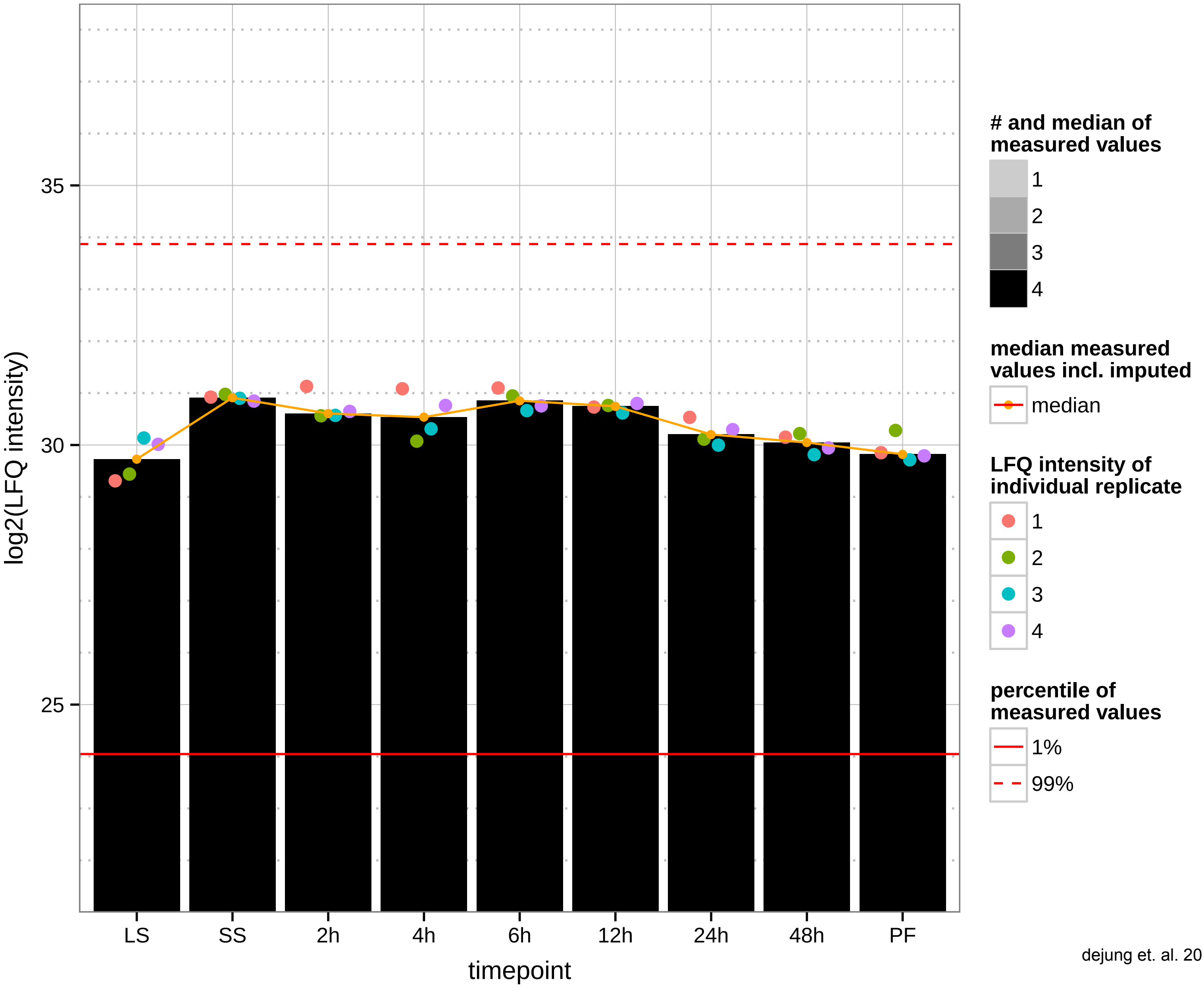
intraflagellar transport protein IFT80/CHE2, putative (IFT80)
Tb927.10.14990
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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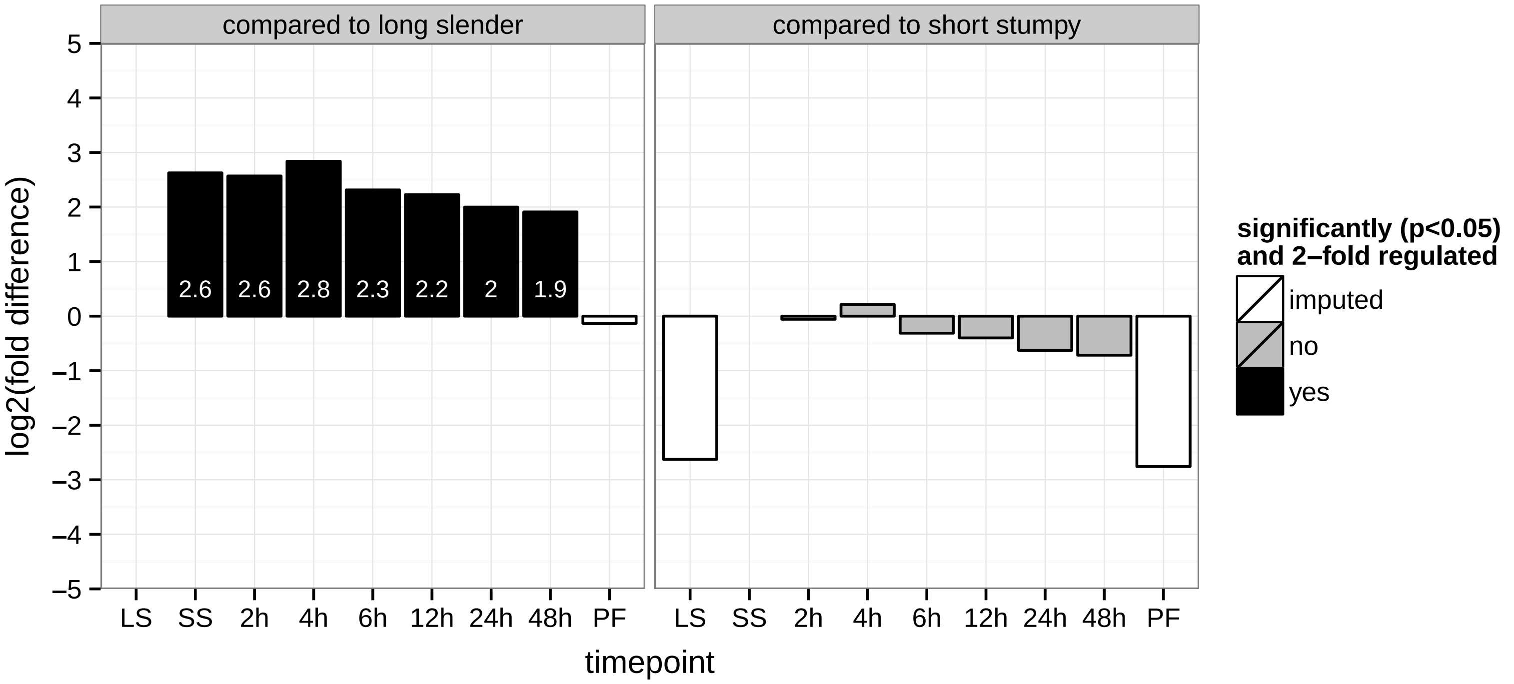
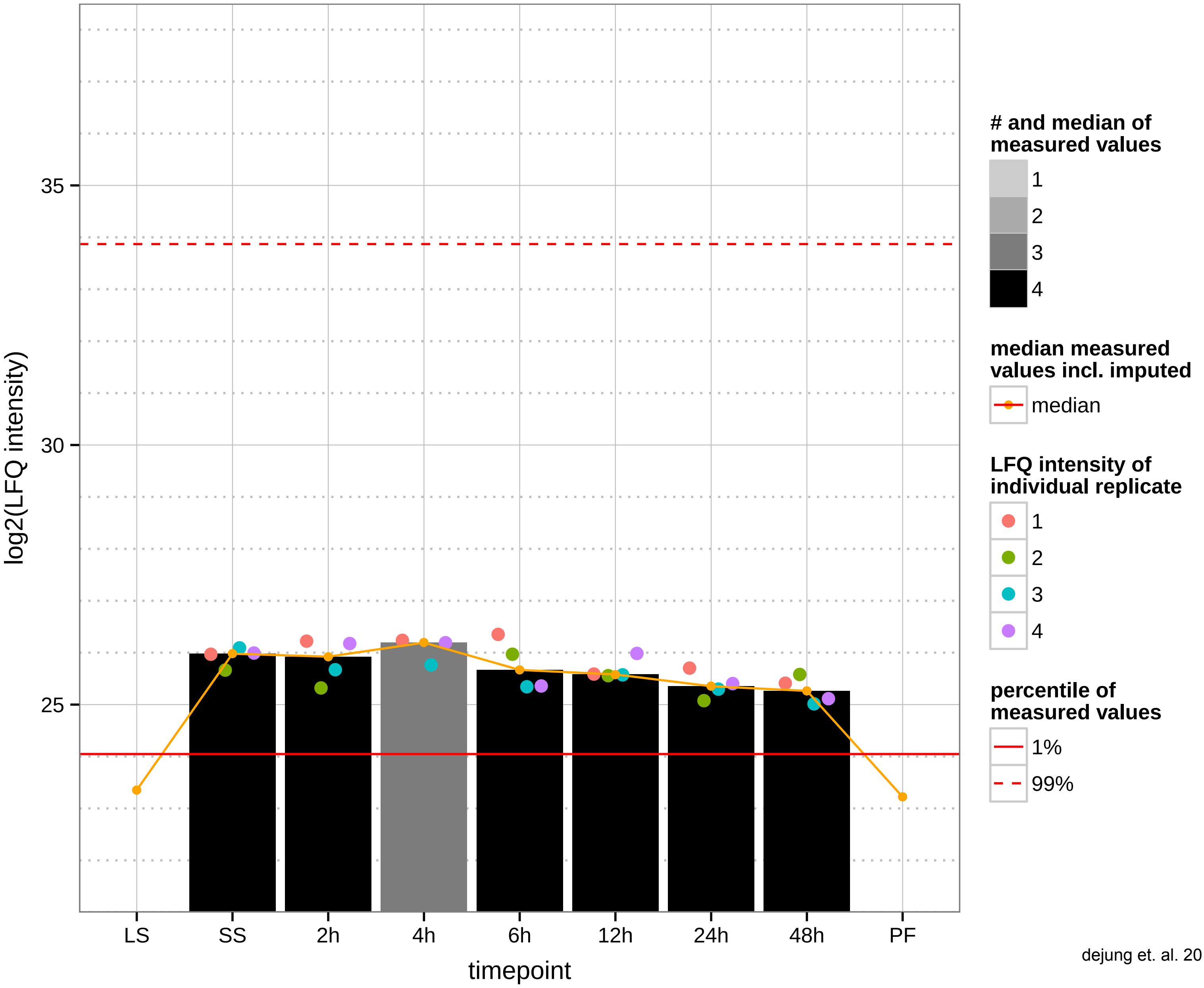
hypothetical protein, conserved, predicted VPS53–like domain protein
Tb927.10.15540;Tb11.v5.0651
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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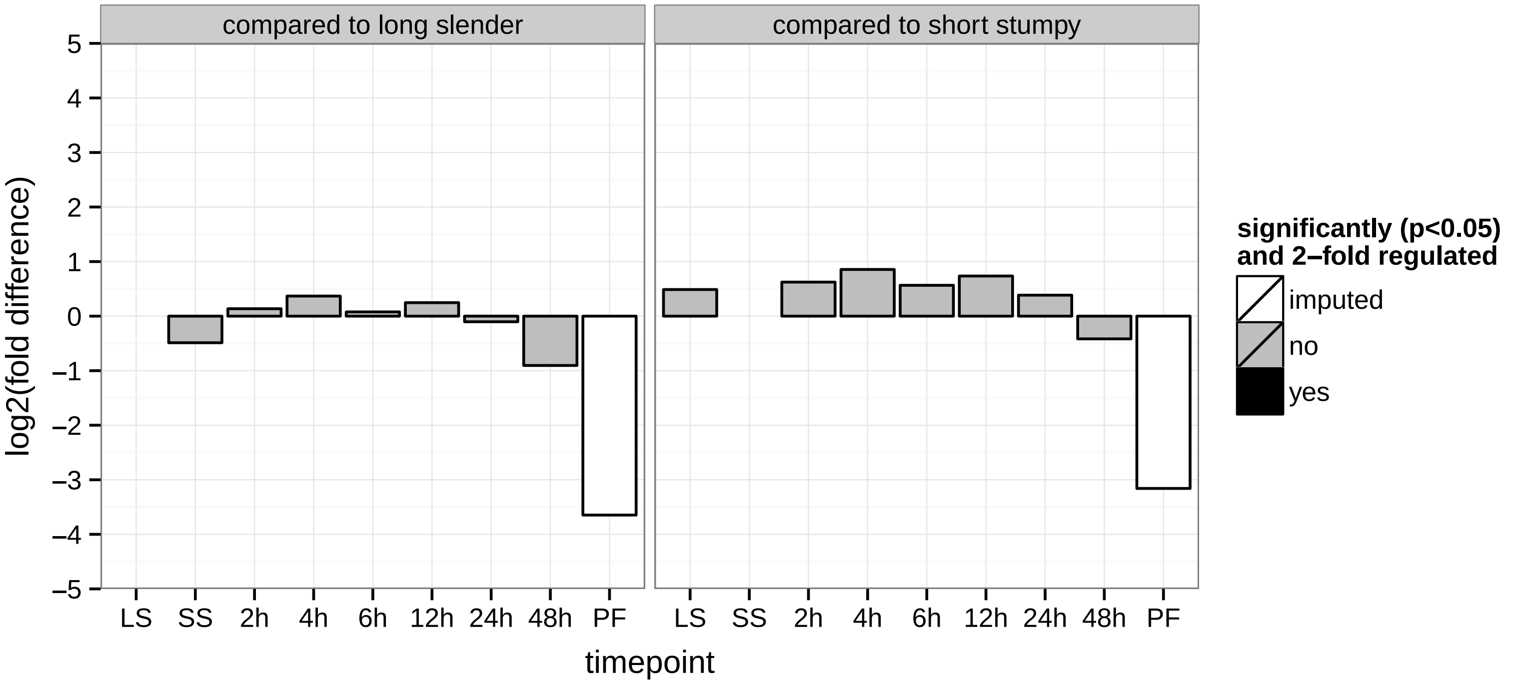
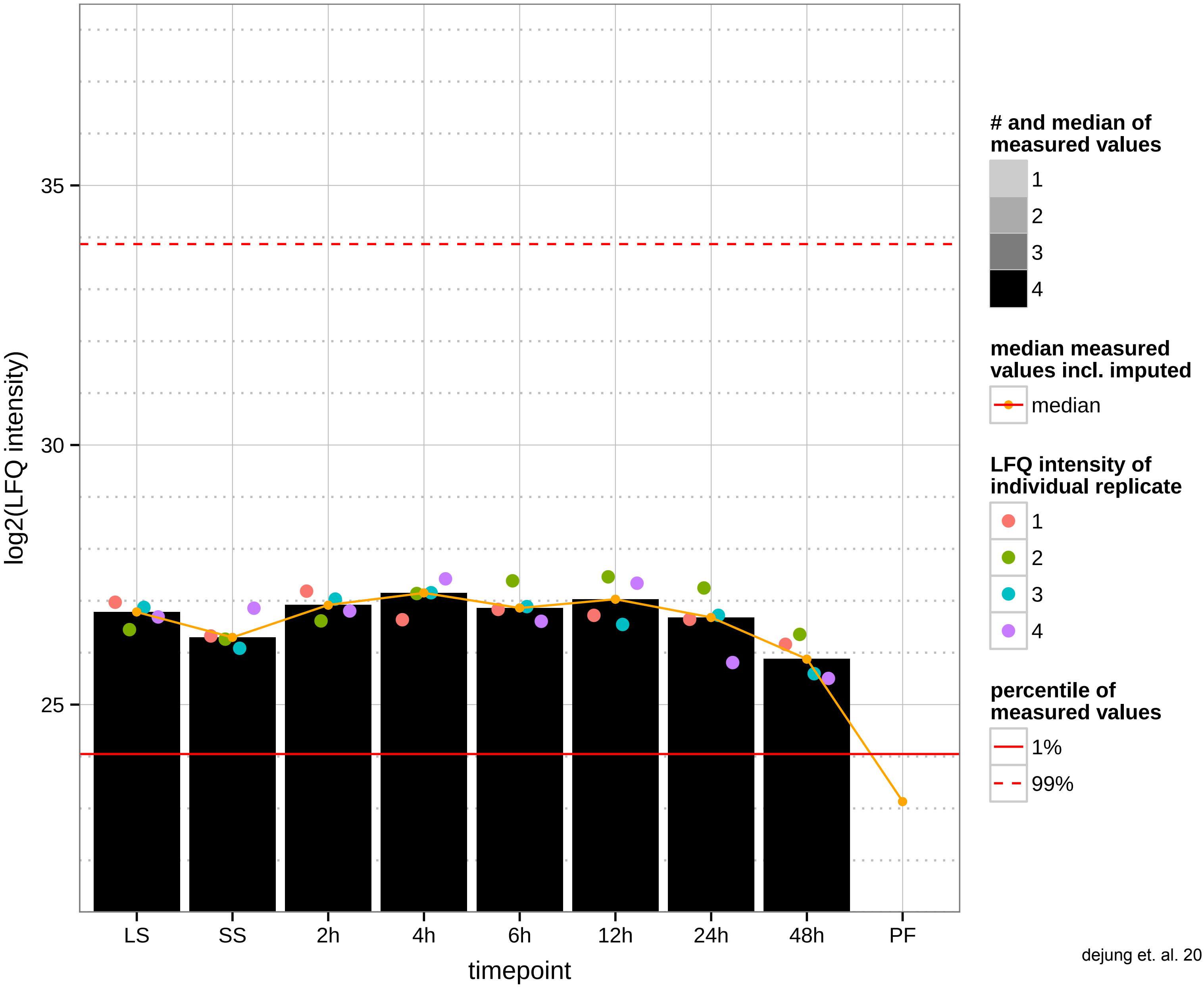
macrophage infectivity potentiator, precursor, putative, FKBP−type peptidylprolyl cis−trans isomerase, putative (MIP)
Tb927.10.15590
AGOF: FK506 binding, peptidyl−prolyl cis−trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: null
PGOC: null
PGOP: protein folding





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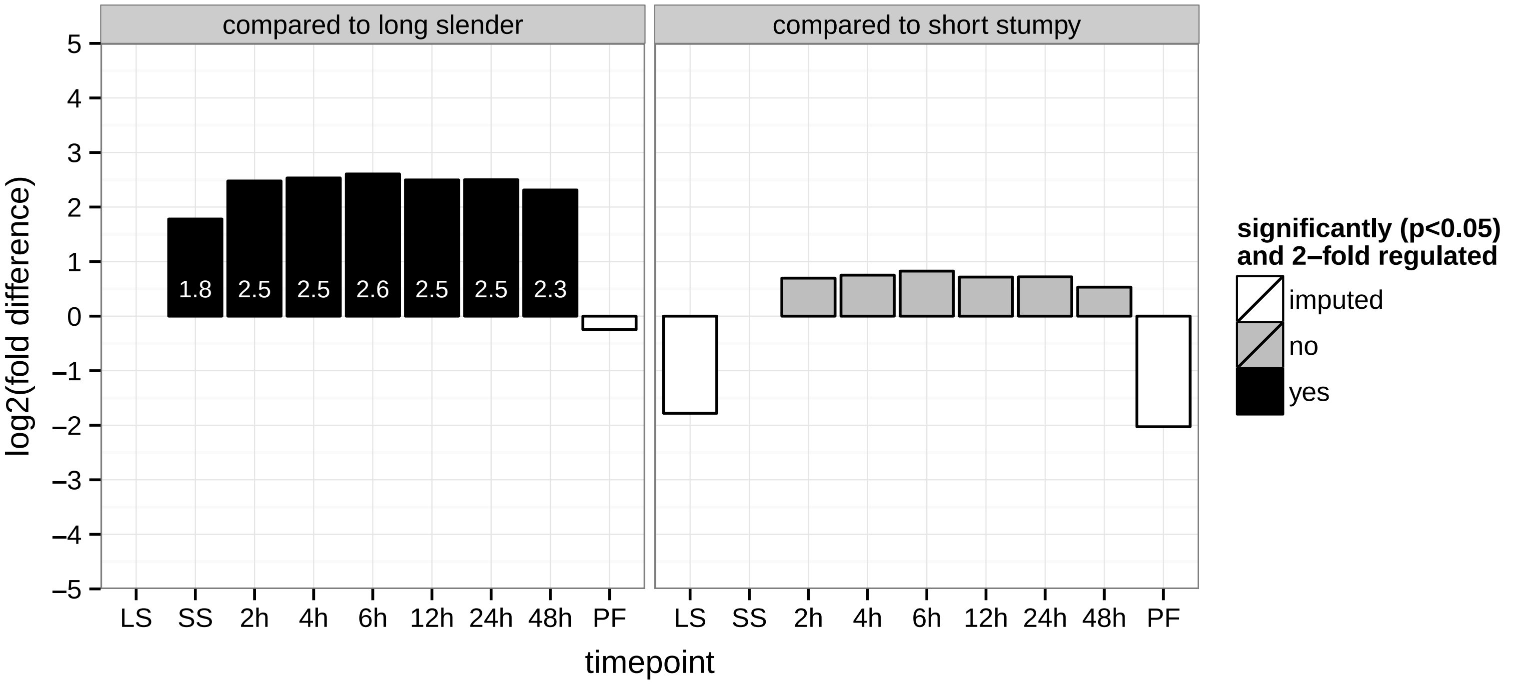
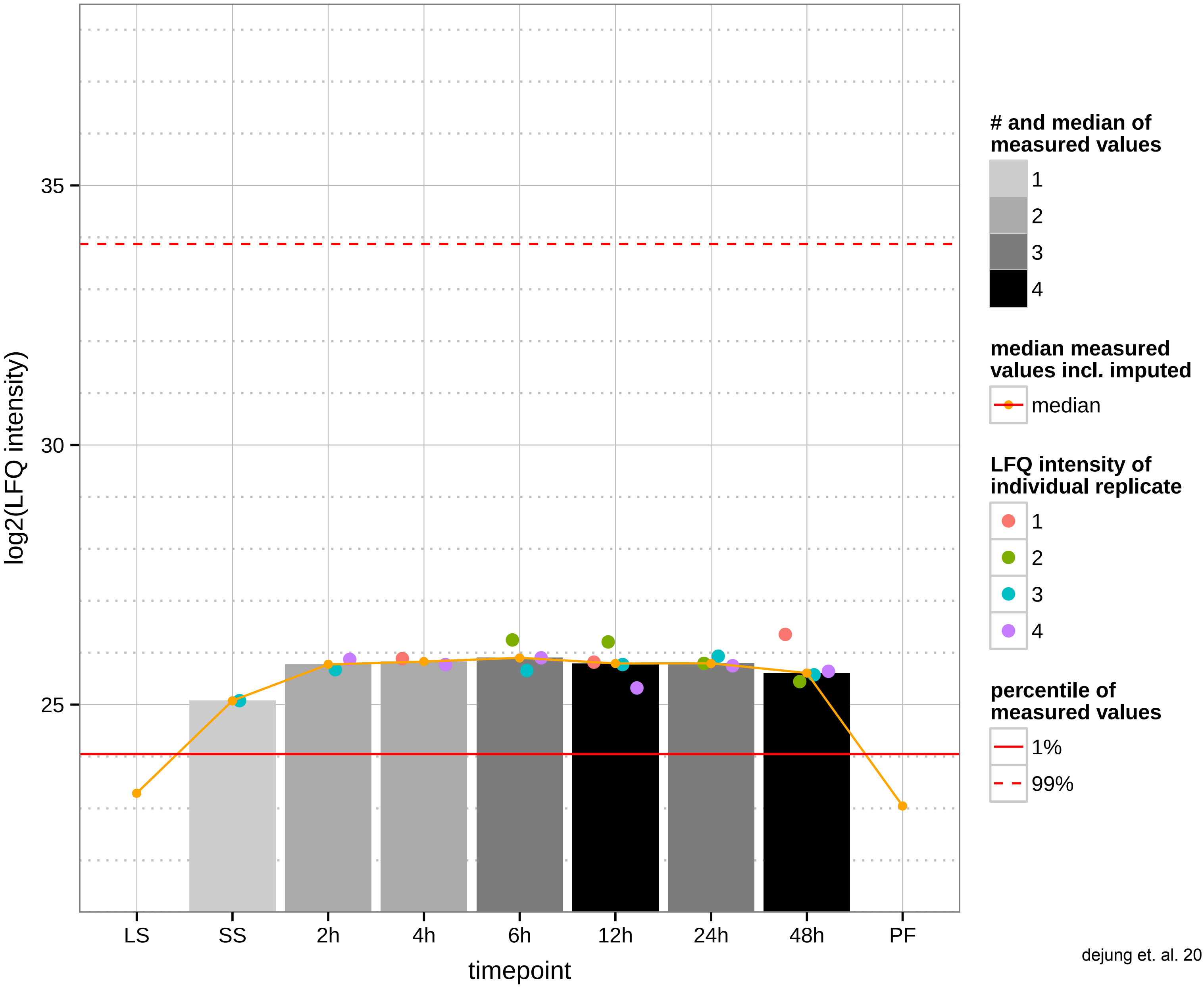
hypothetical protein, conserved
Tb927.10.15640
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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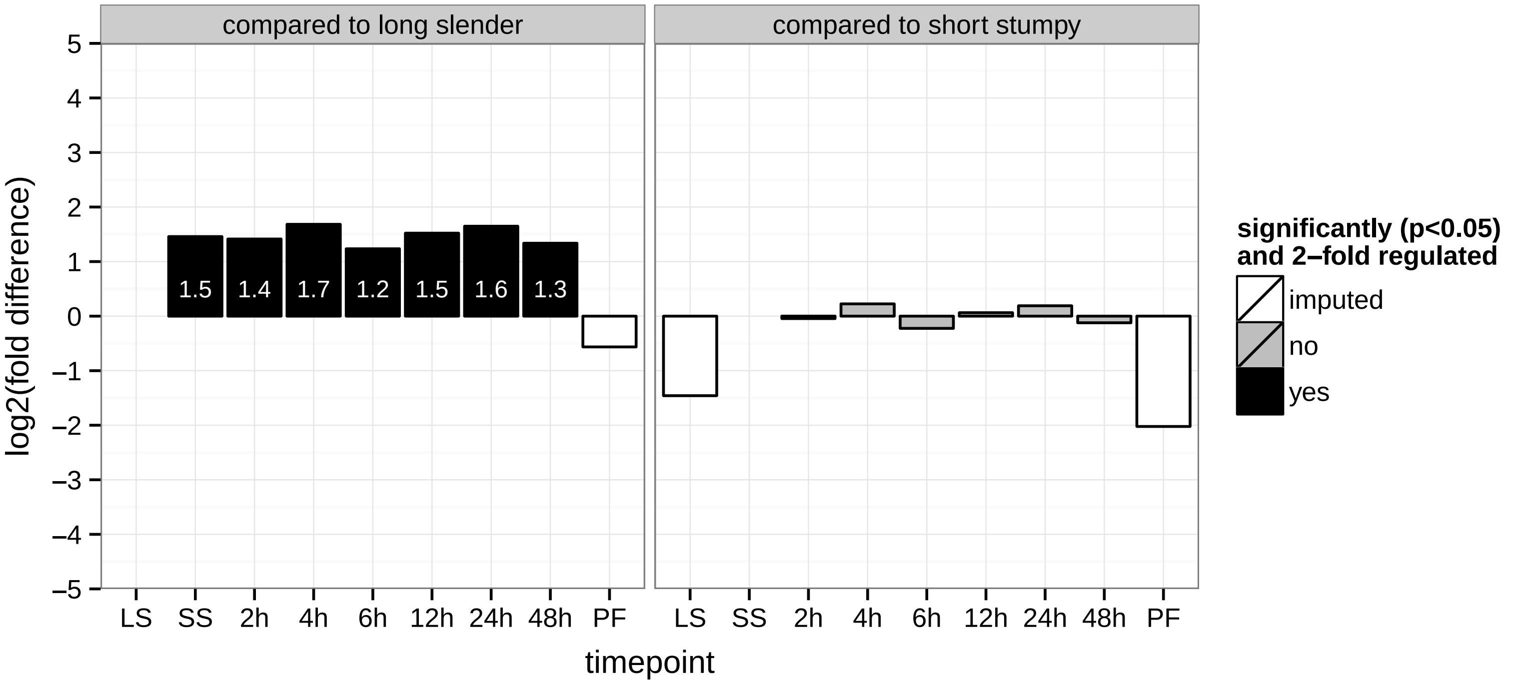
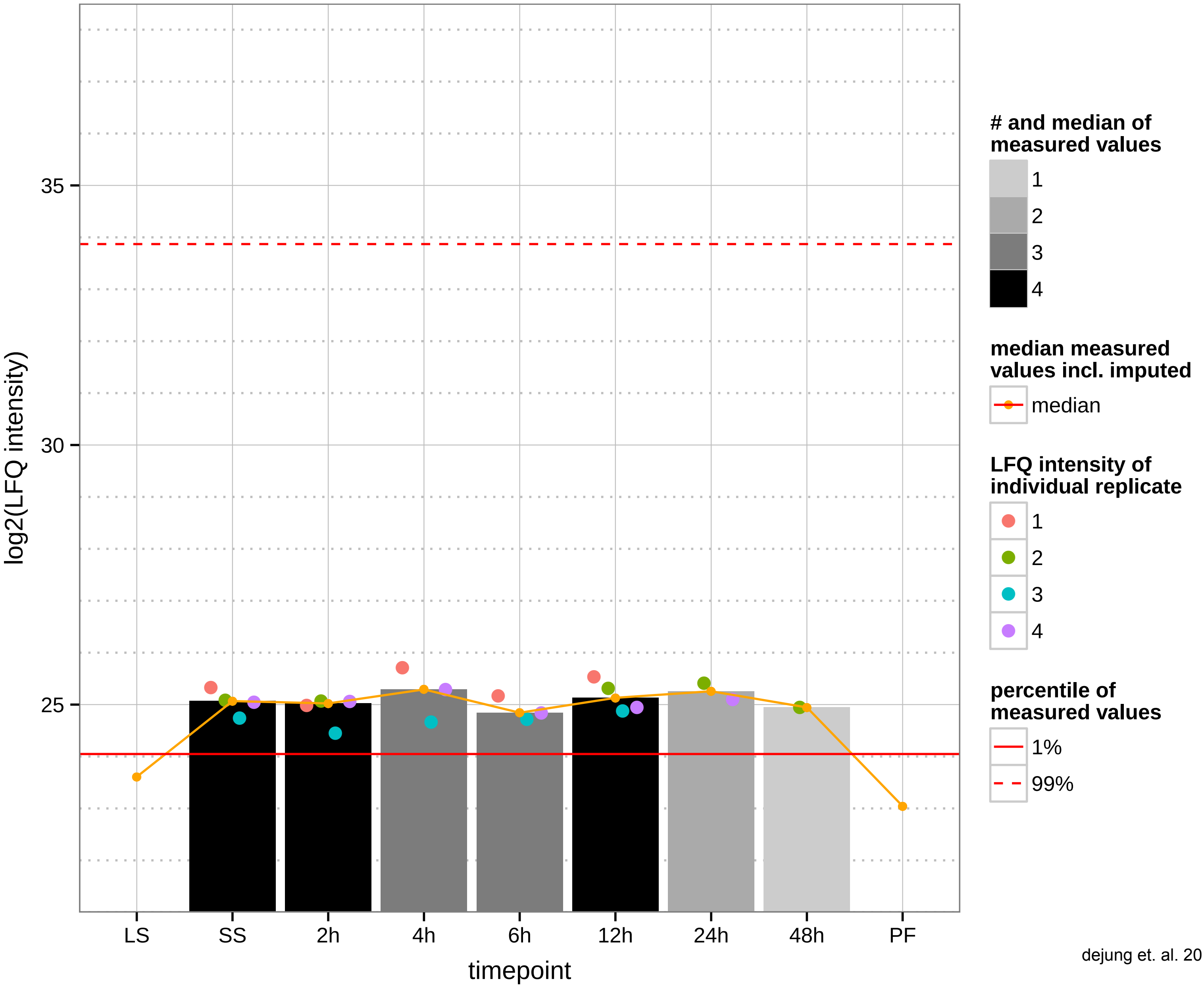
mitogen activated protein kinase 4, putative, map kinase (MAPK2)
Tb927.10.16030
AGOF: ATP binding, MAP kinase activity, kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activit
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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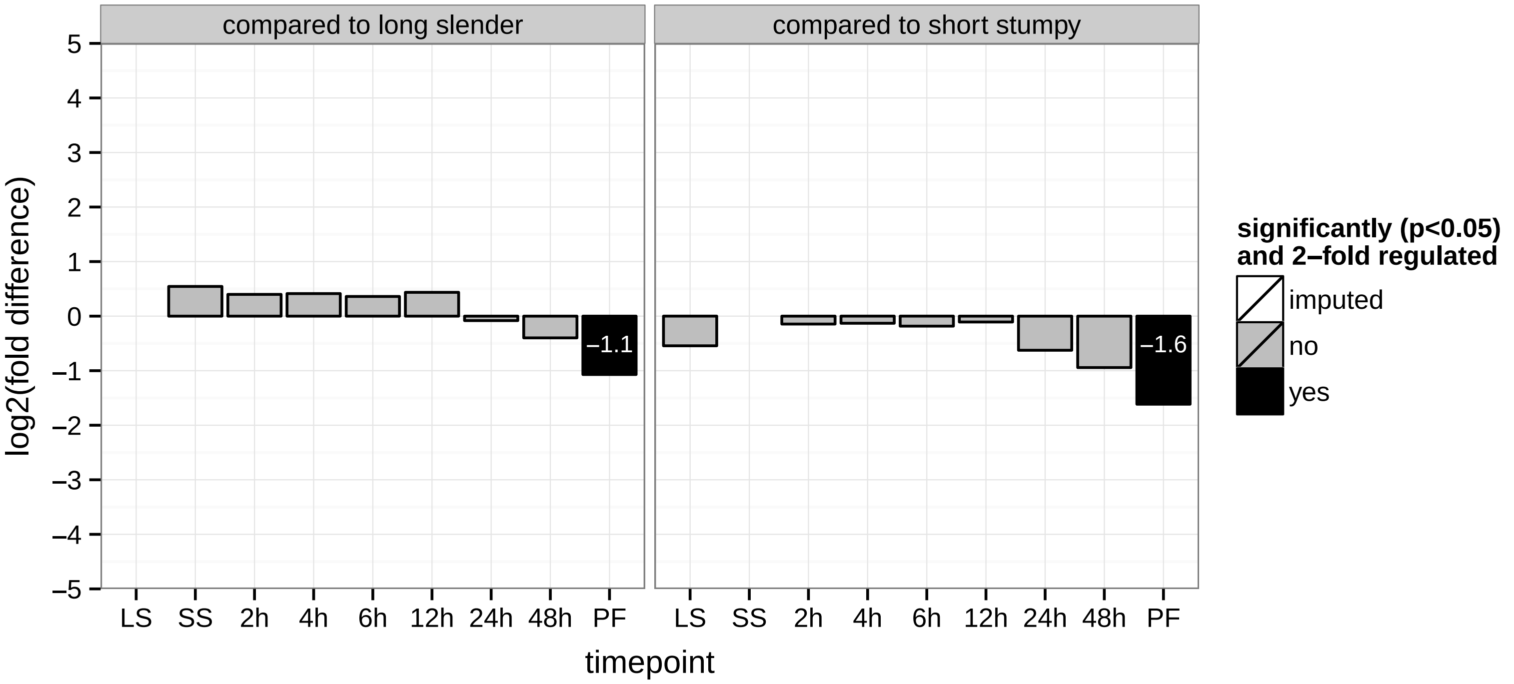
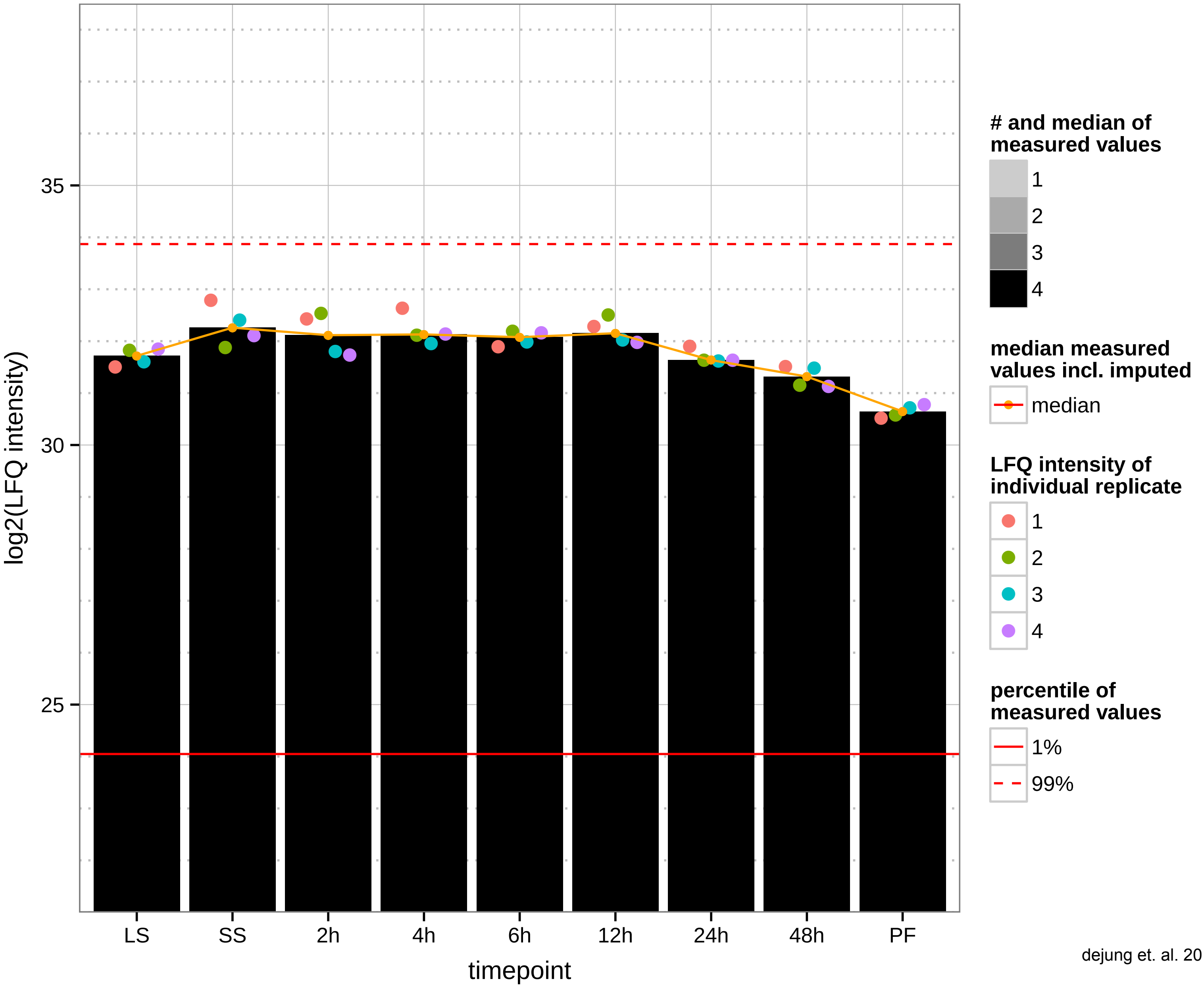
peptidylprolyl isomerase–like protein, putative, FK506–binding protein (FKBP)–type peptidyl–prolyl isomerase
Tb927.10.16100;Tb11.v5.0411
AGOF: null, heat shock protein binding, peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: null, protein folding
PGOF: protein binding
PGOC: null
PGOP: protein folding





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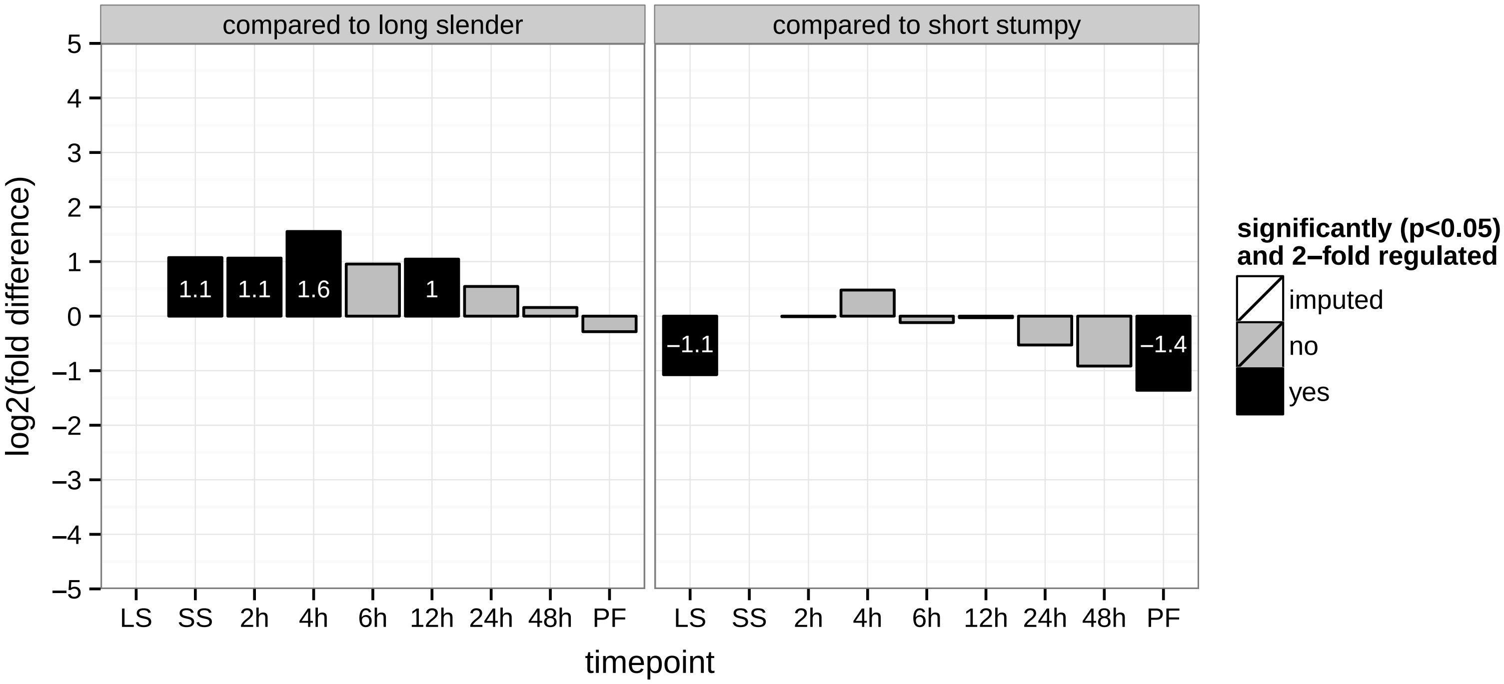
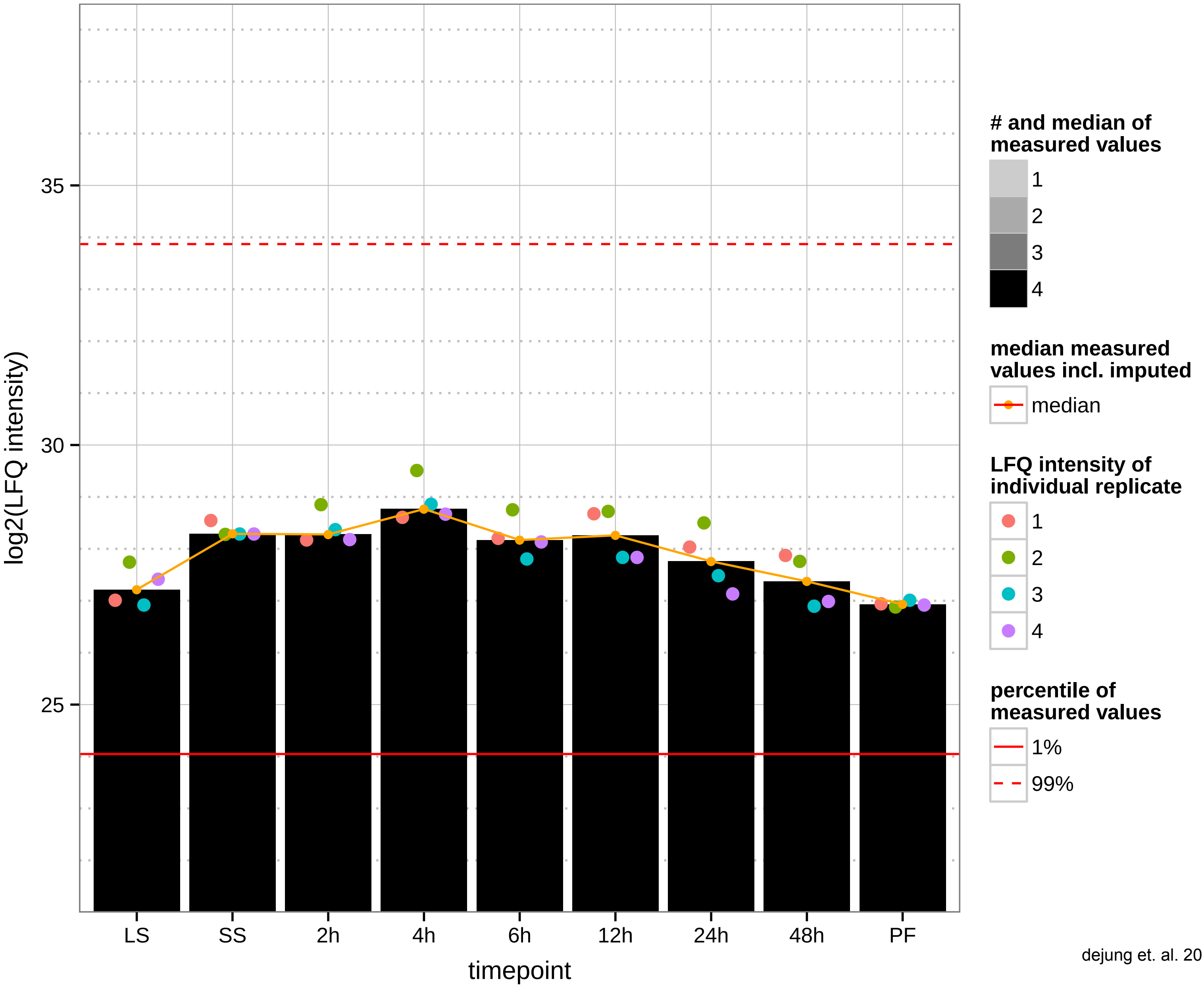
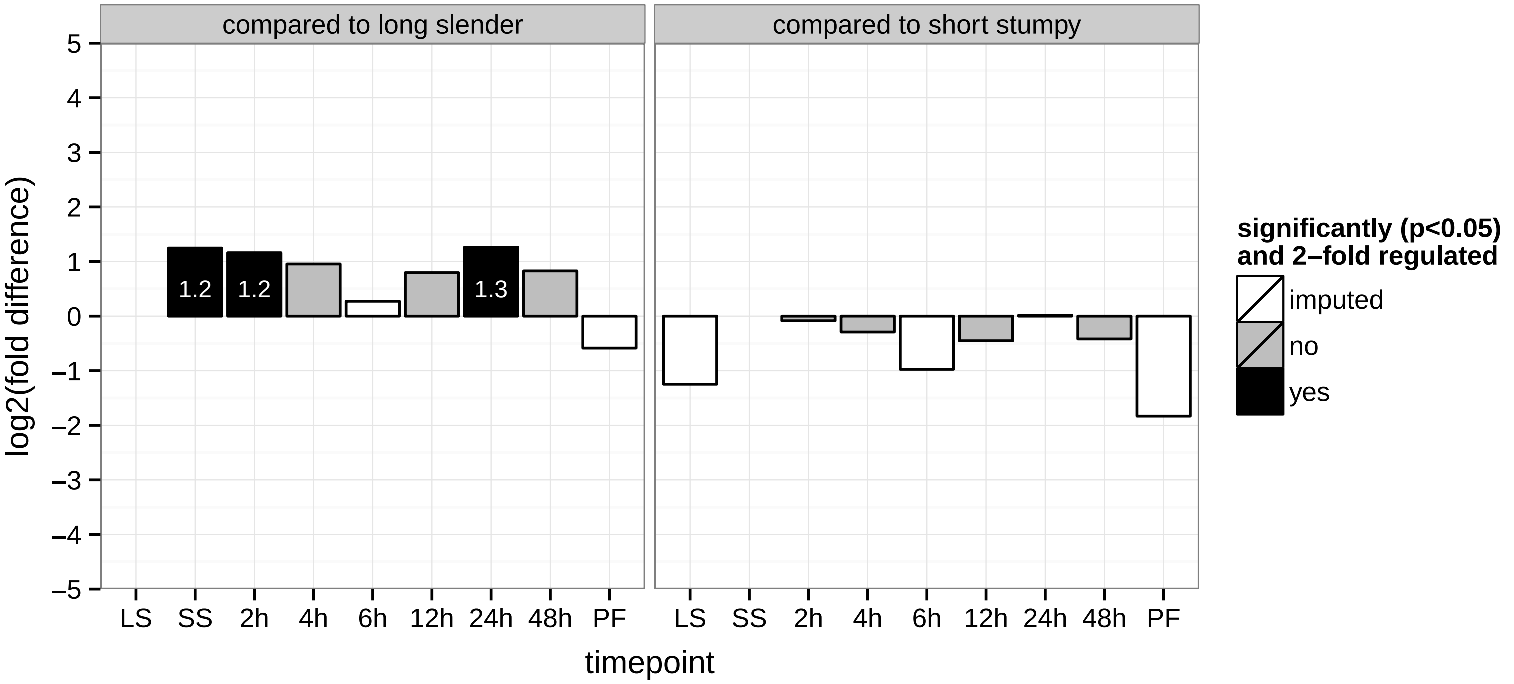
syntaxin, putative
Tb927.10.1830
AGOF: transporter activity
AGOC: membrane
AGOP: vesicle−mediated transport
PGOF: protein binding
PGOC: null
PGOP: null

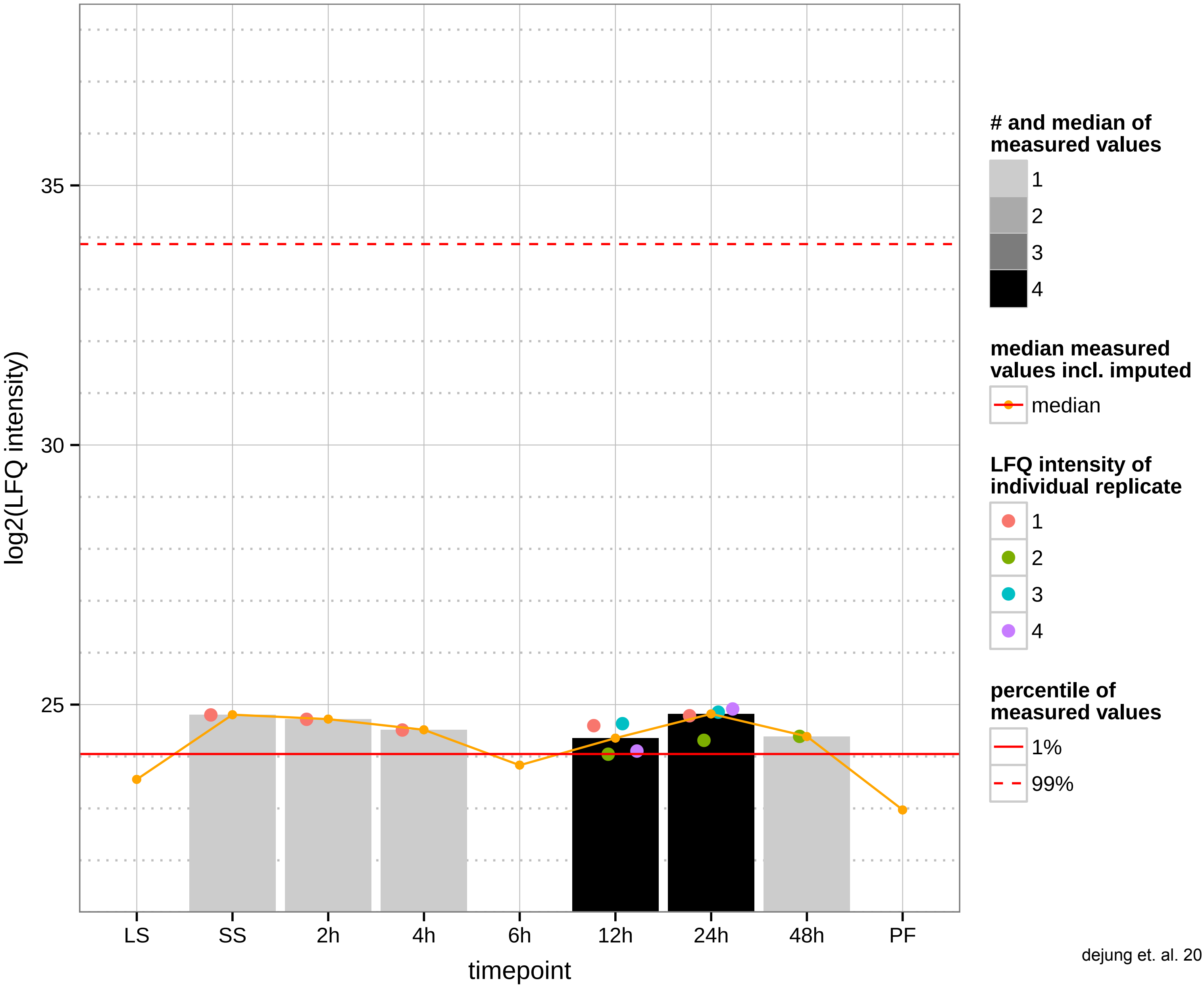




dejung et. al. 2015

leucine–rich repeat protein (LRRP), putative
Tb927.10.1950
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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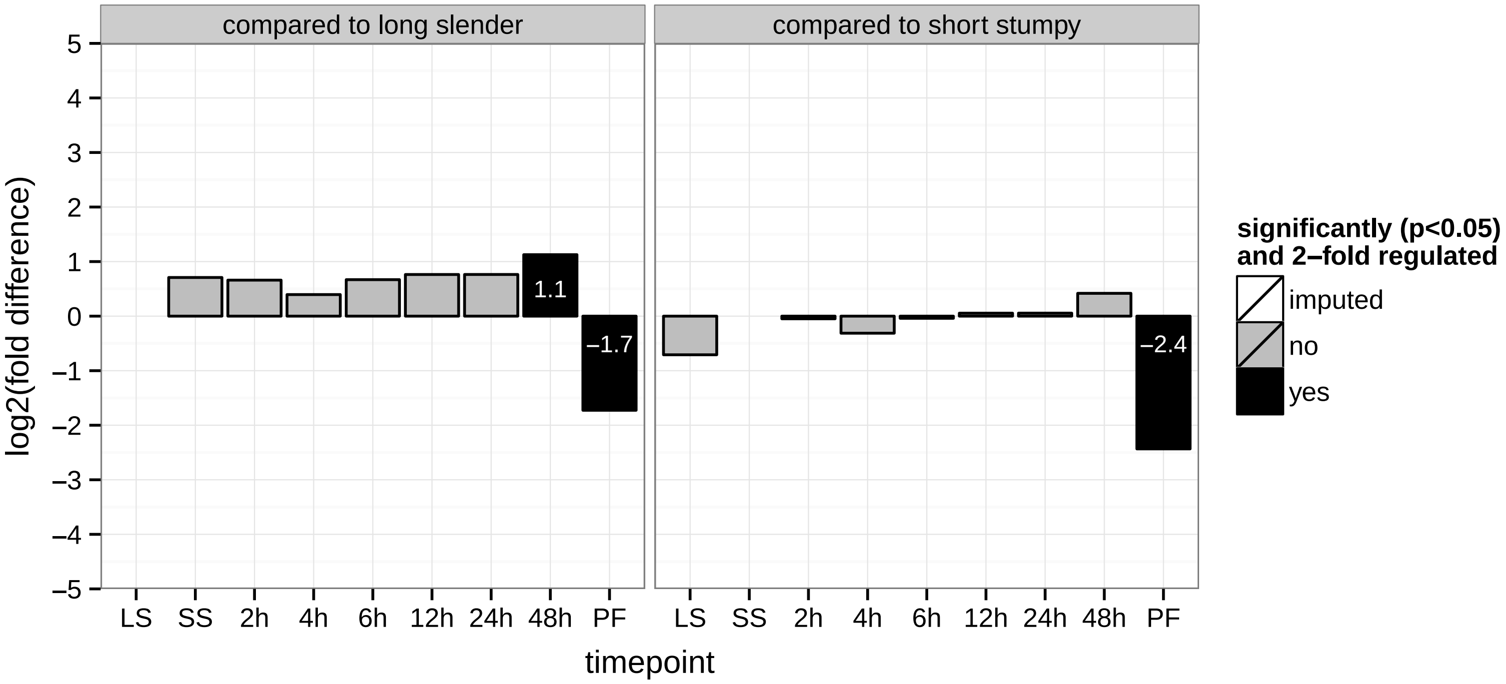
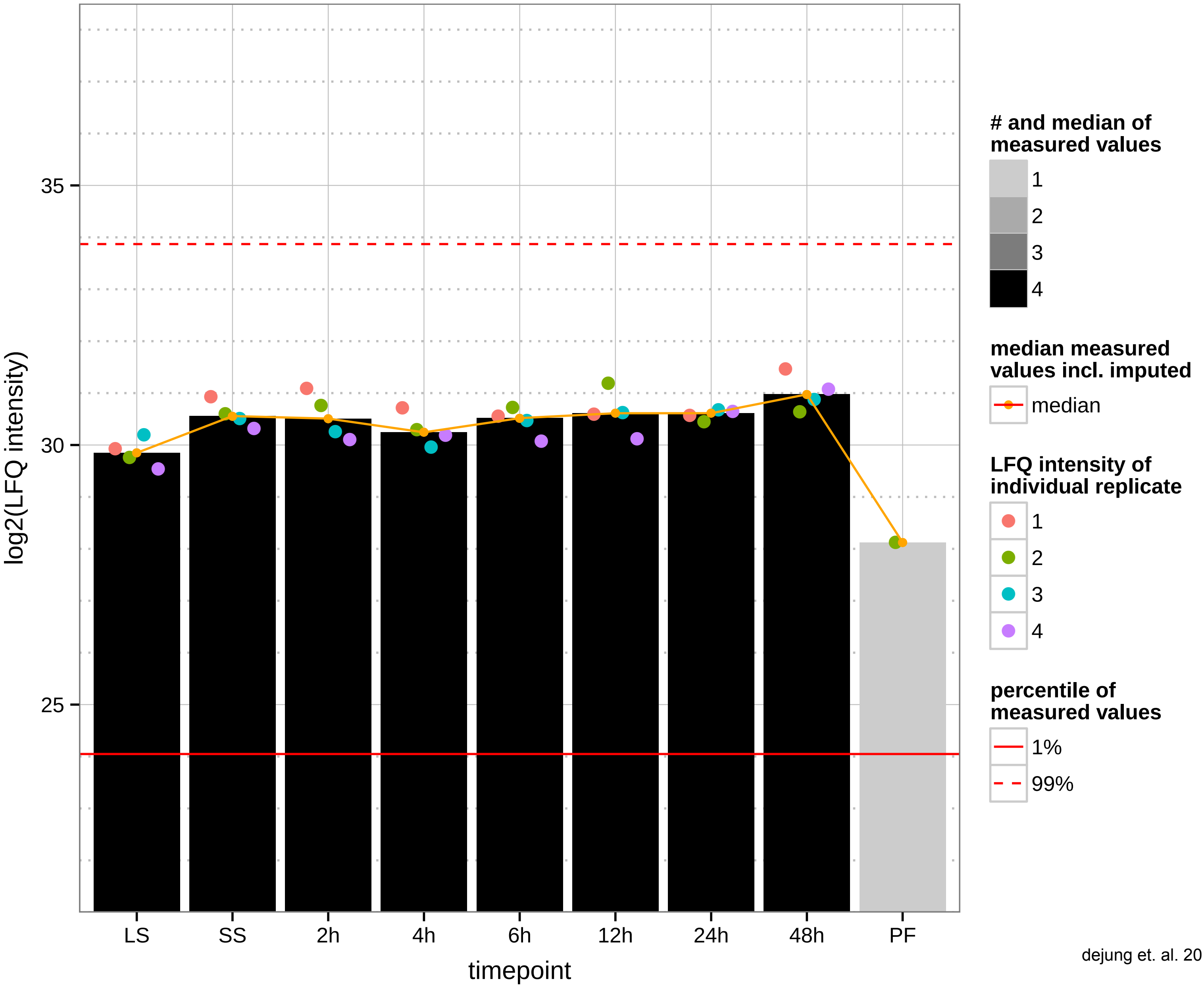
hexokinase (HK1)
Tb927.10.2010
AGOF: ATP binding, hexokinase activity
AGOC: glycosome
AGOP: carbohydrate metabolic process, glycolysis, protein hexamerization
PGOF: ATP binding, phosphotransferase activity, alcohol group as acceptor
PGOC: null
PGOP: carbohydrate metabolic process





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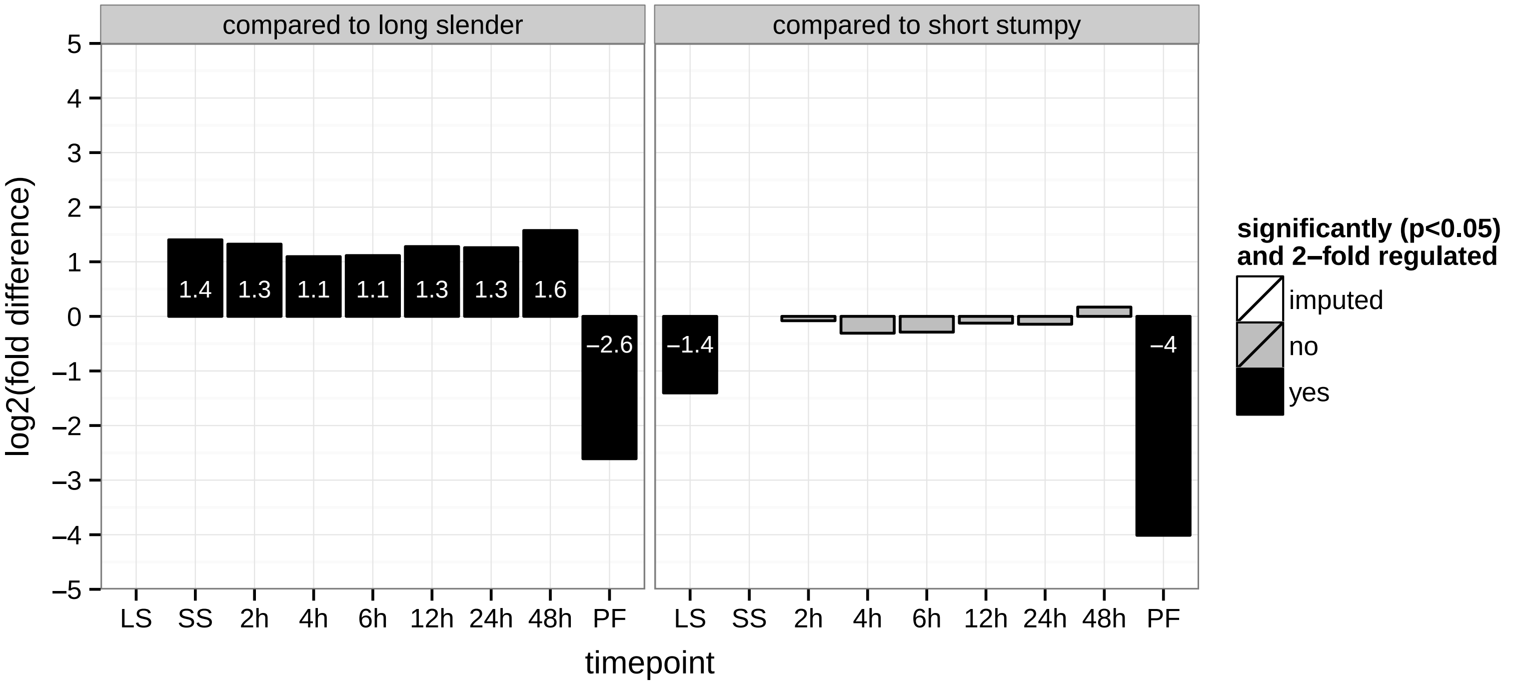
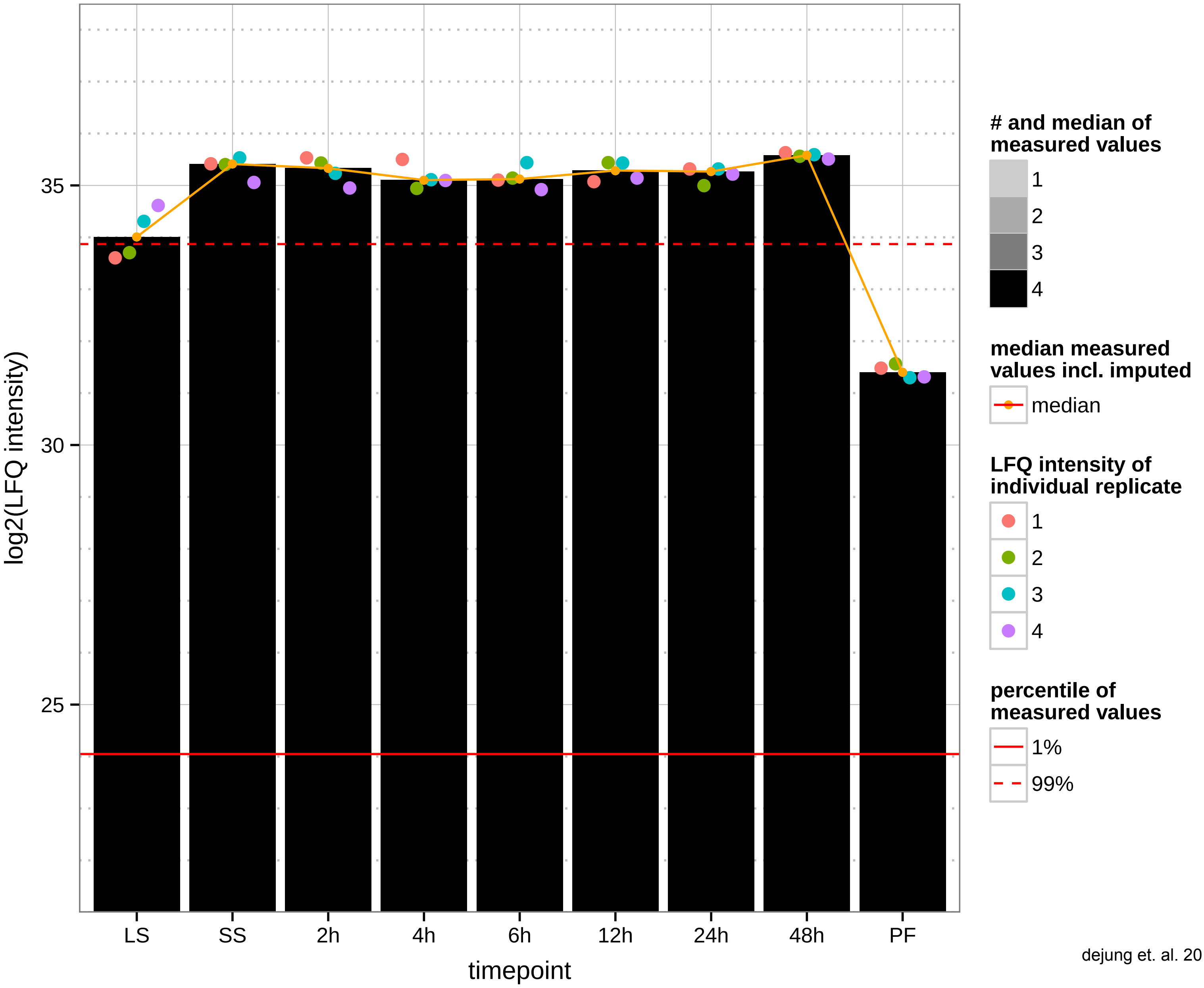
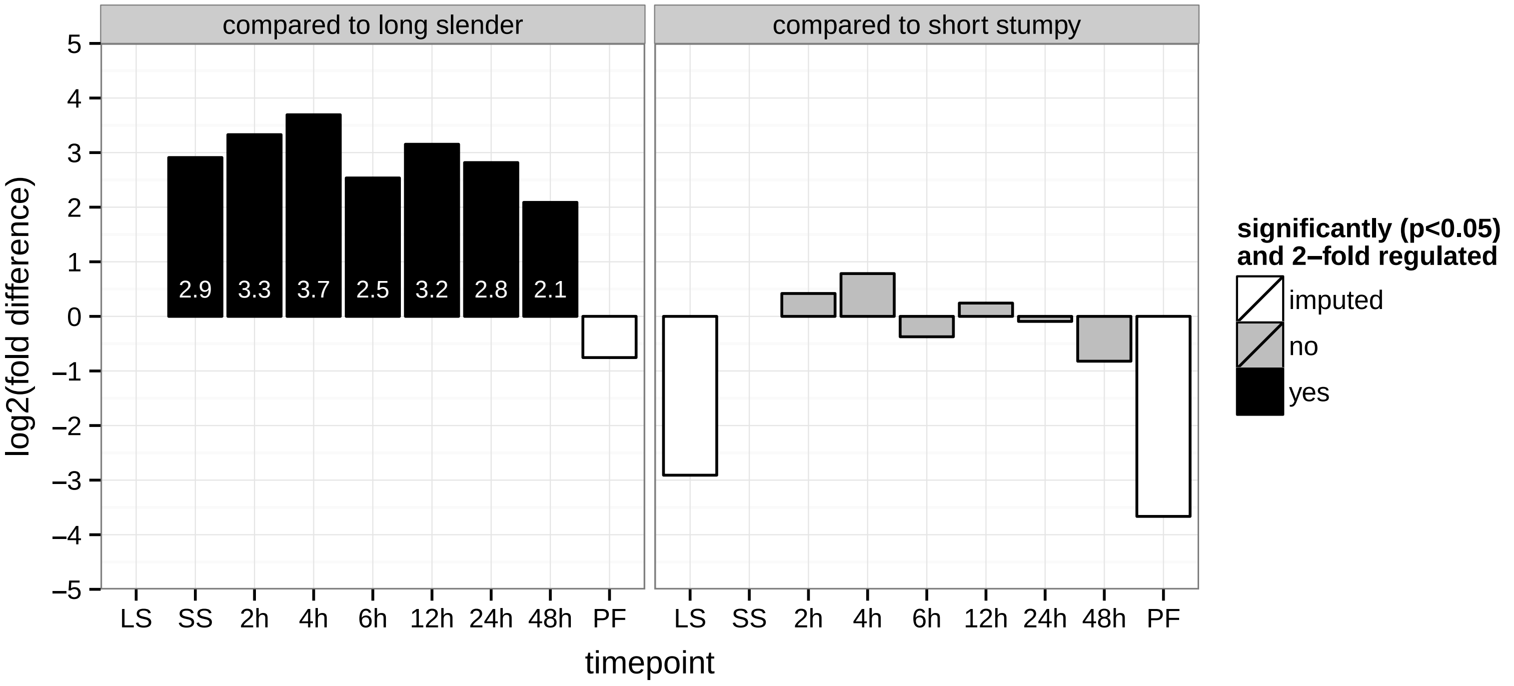
hexokinase (HK2)
Tb927.10.2020
AGOF: ATP binding, hexokinase activity
AGOC: glycosome
AGOP: carbohydrate metabolic process, glycolysis
PGOF: ATP binding, phosphotransferase activity, alcohol group as acceptor
PGOC: null
PGOP: carbohydrate metabolic process

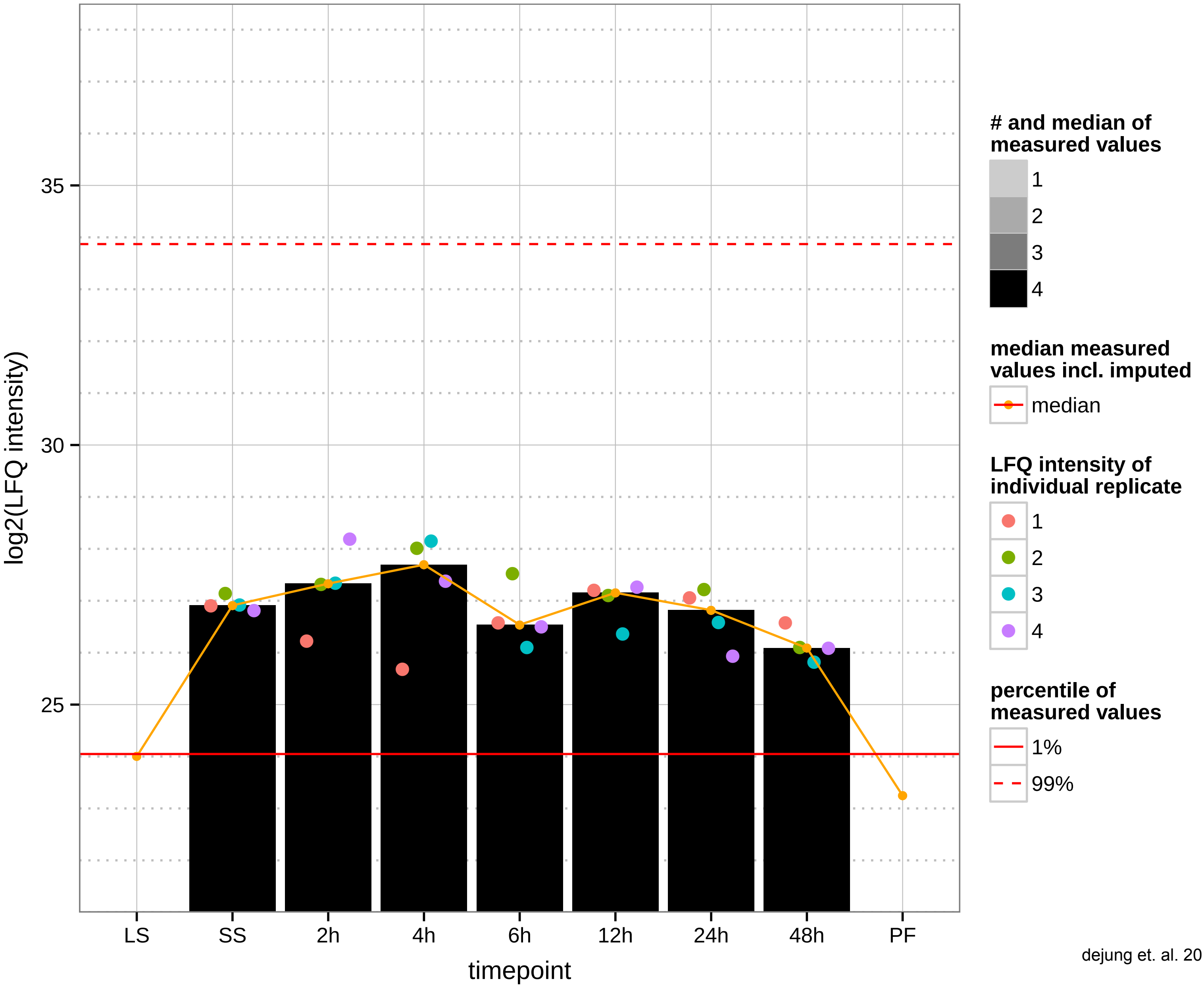




dejung et. al. 2015

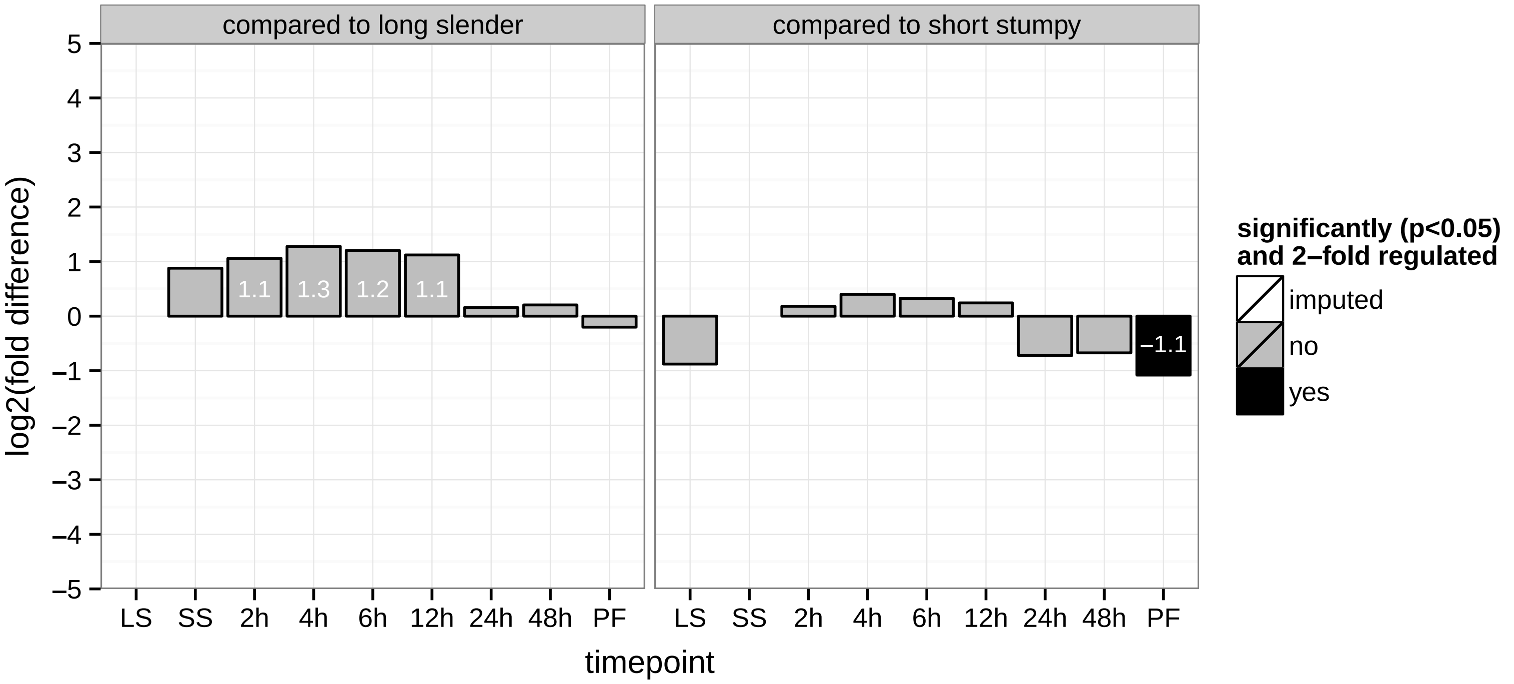
hypothetical protein, conserved
Tb927.10.260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

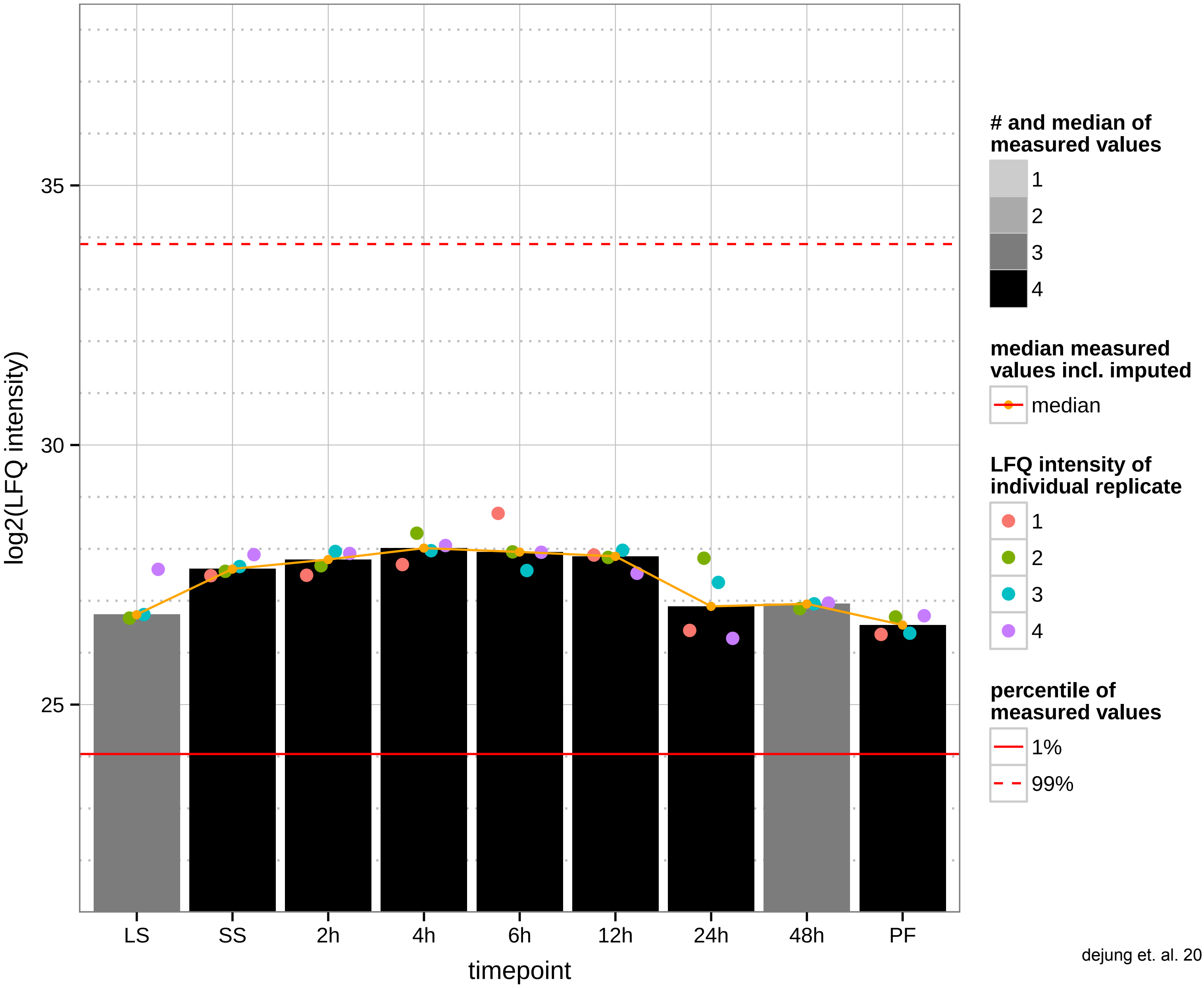




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.2940
AGOF: null
AGOC: Golgi apparatus, endoplasmic reticulum
AGOP: intracellular protein transport
PGOF: null
PGOC: null
PGOP: null





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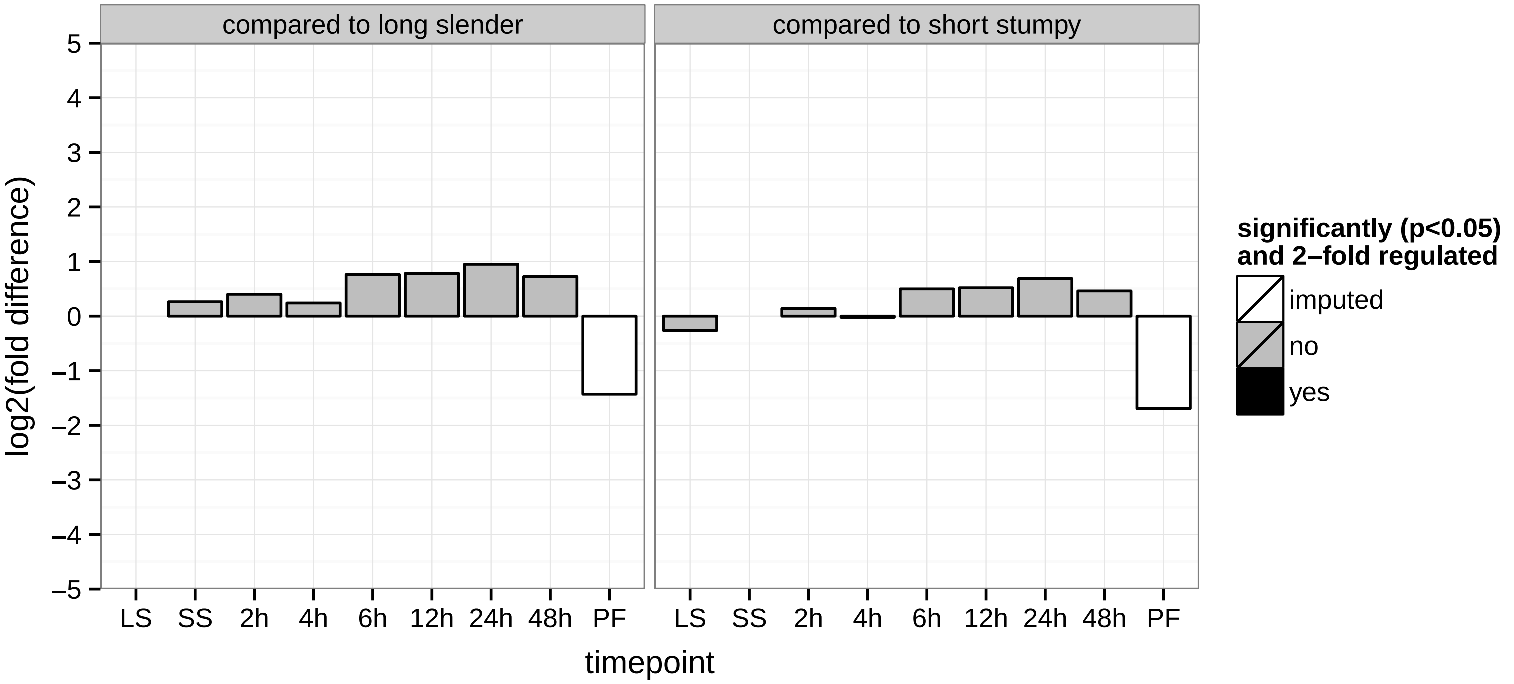
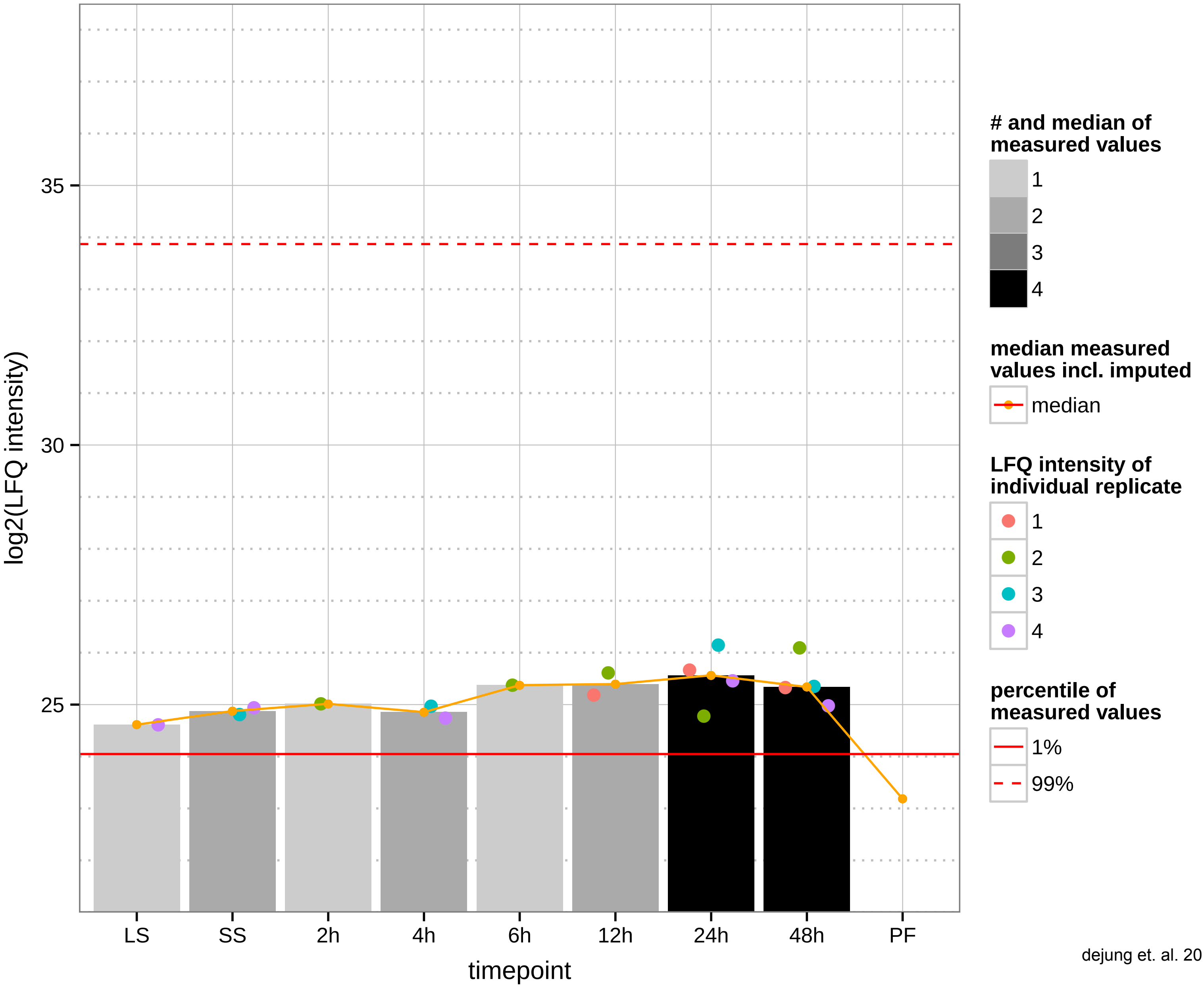
glycerol–3–phosphate acyltransferase, putative
Tb927.10.3100
AGOF: acyl–phosphate glycerol–3–phosphate acyltransferase activity
AGOC: null
AGOP: metabolic process, phospholipid biosynthetic process
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: metabolic process





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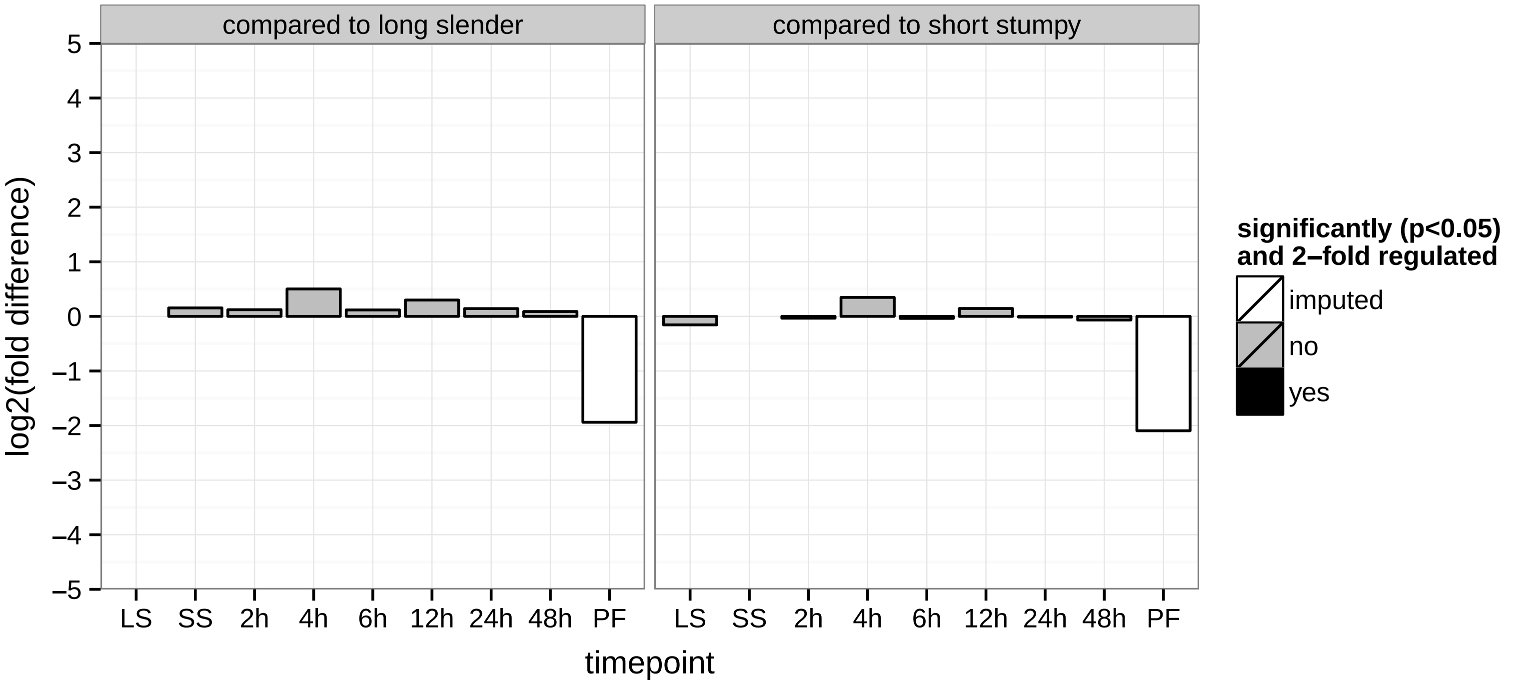
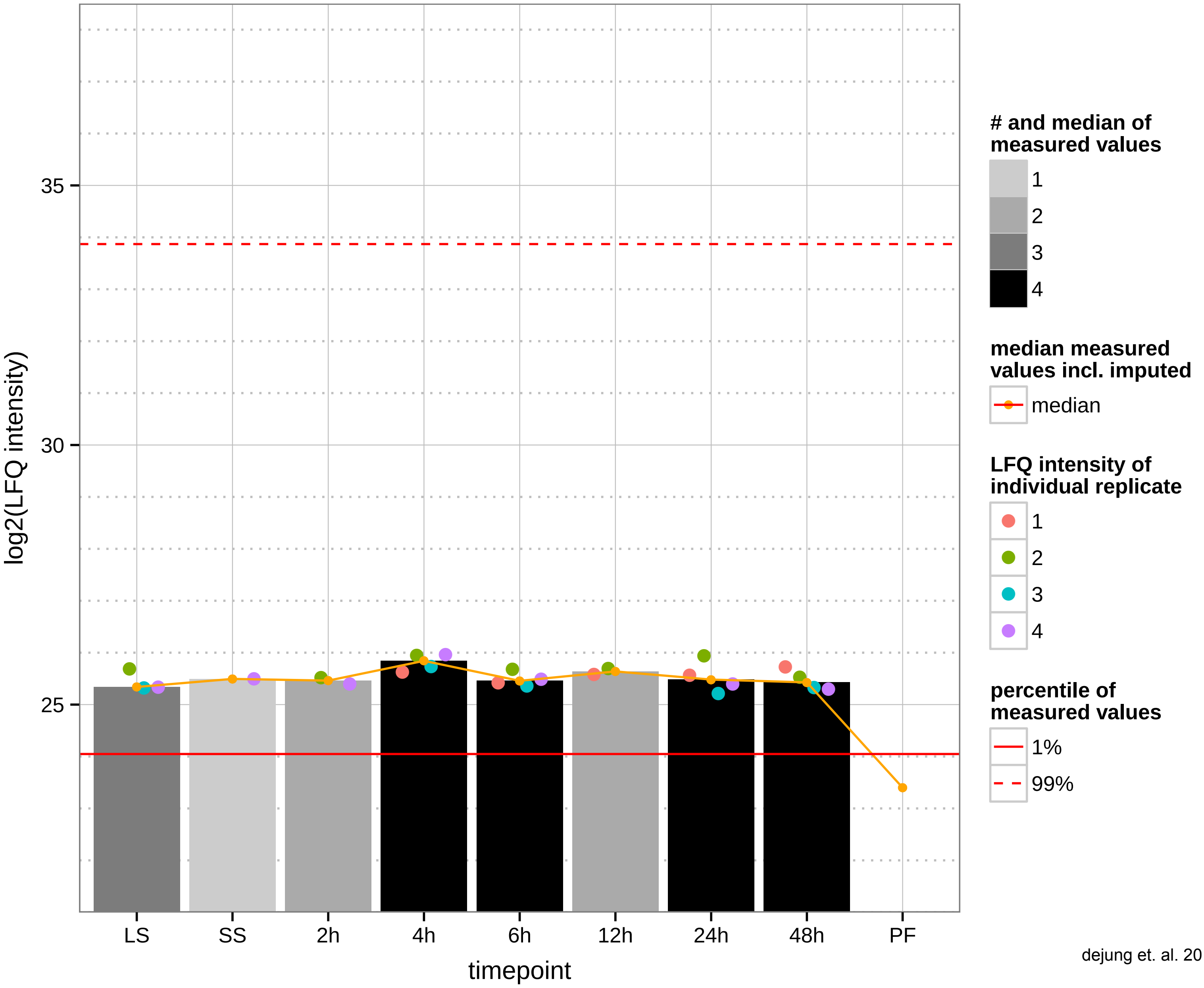
hypothetical protein, conserved
Tb927.10.3330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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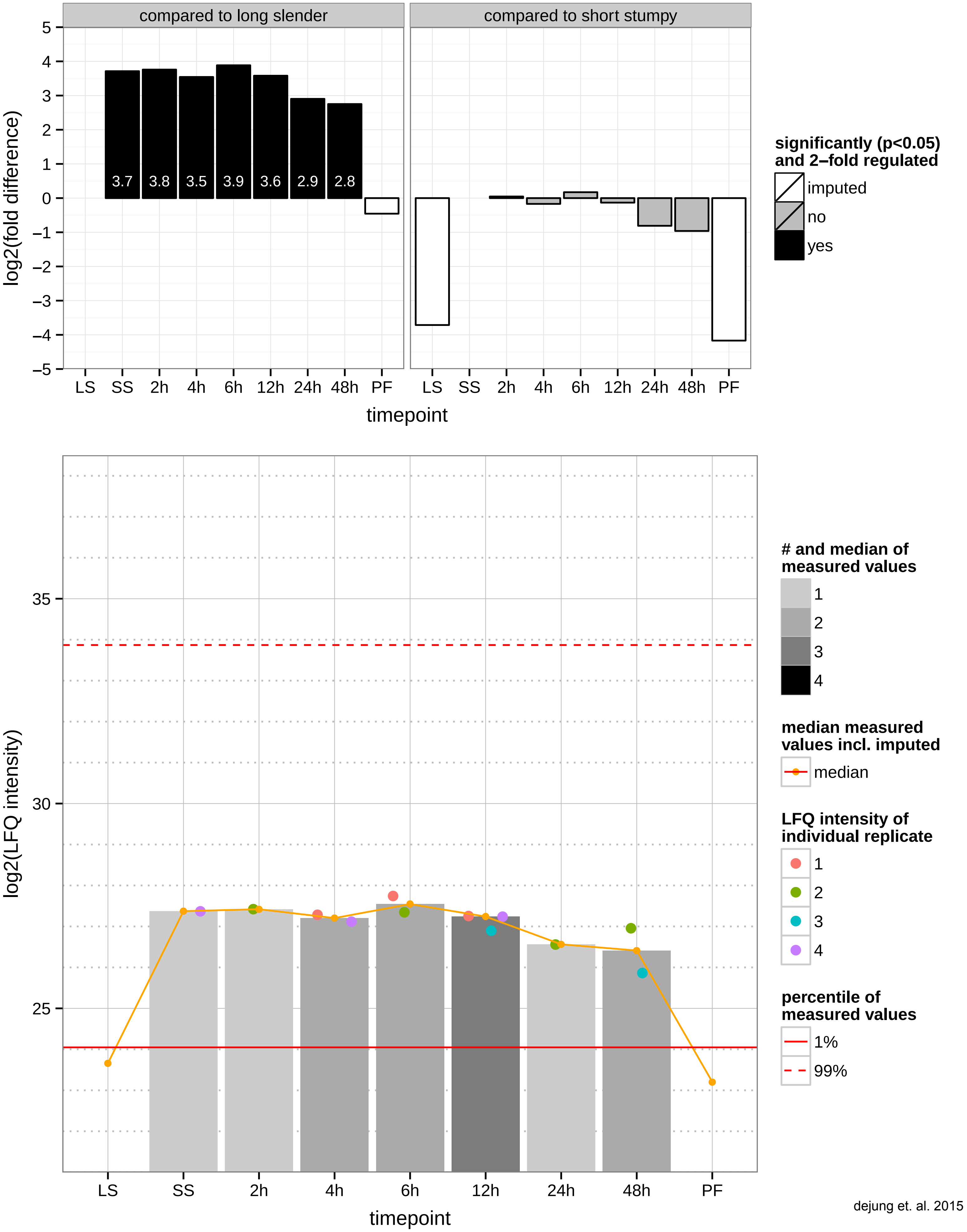
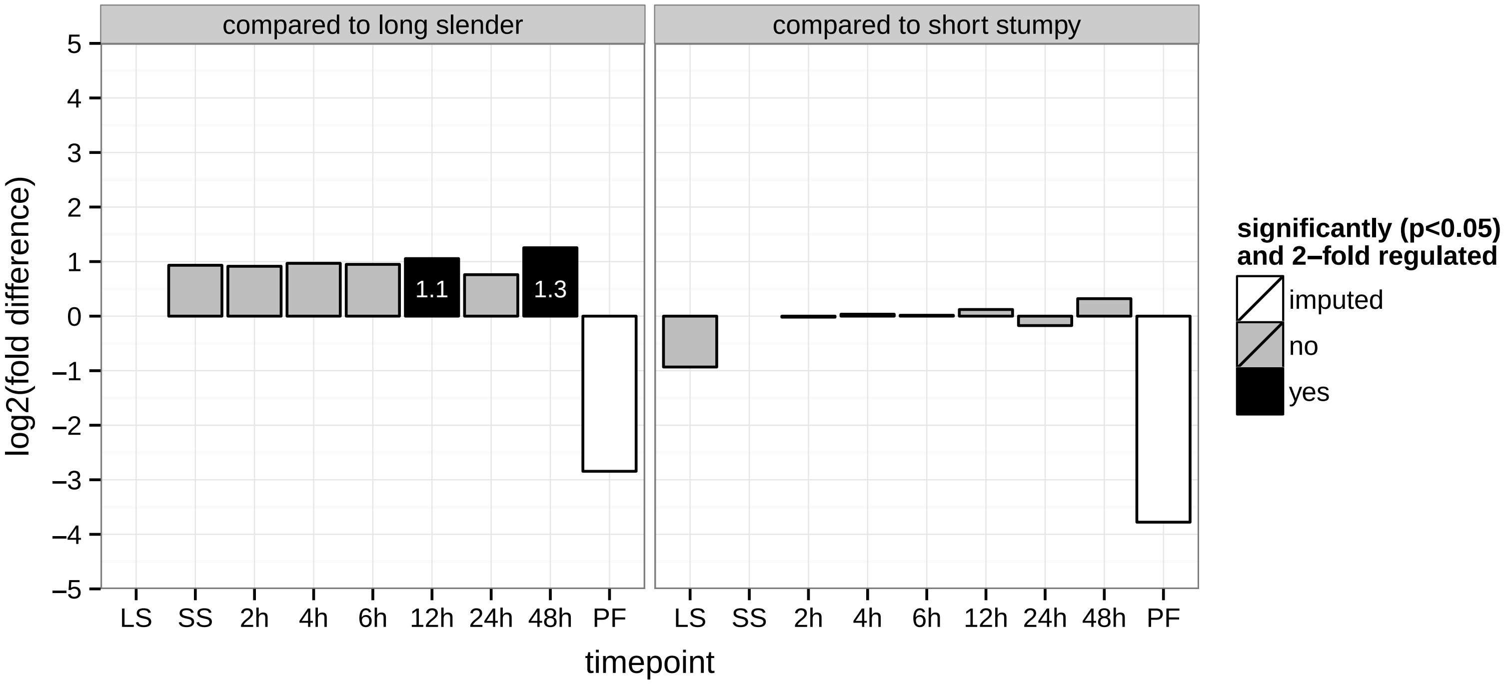
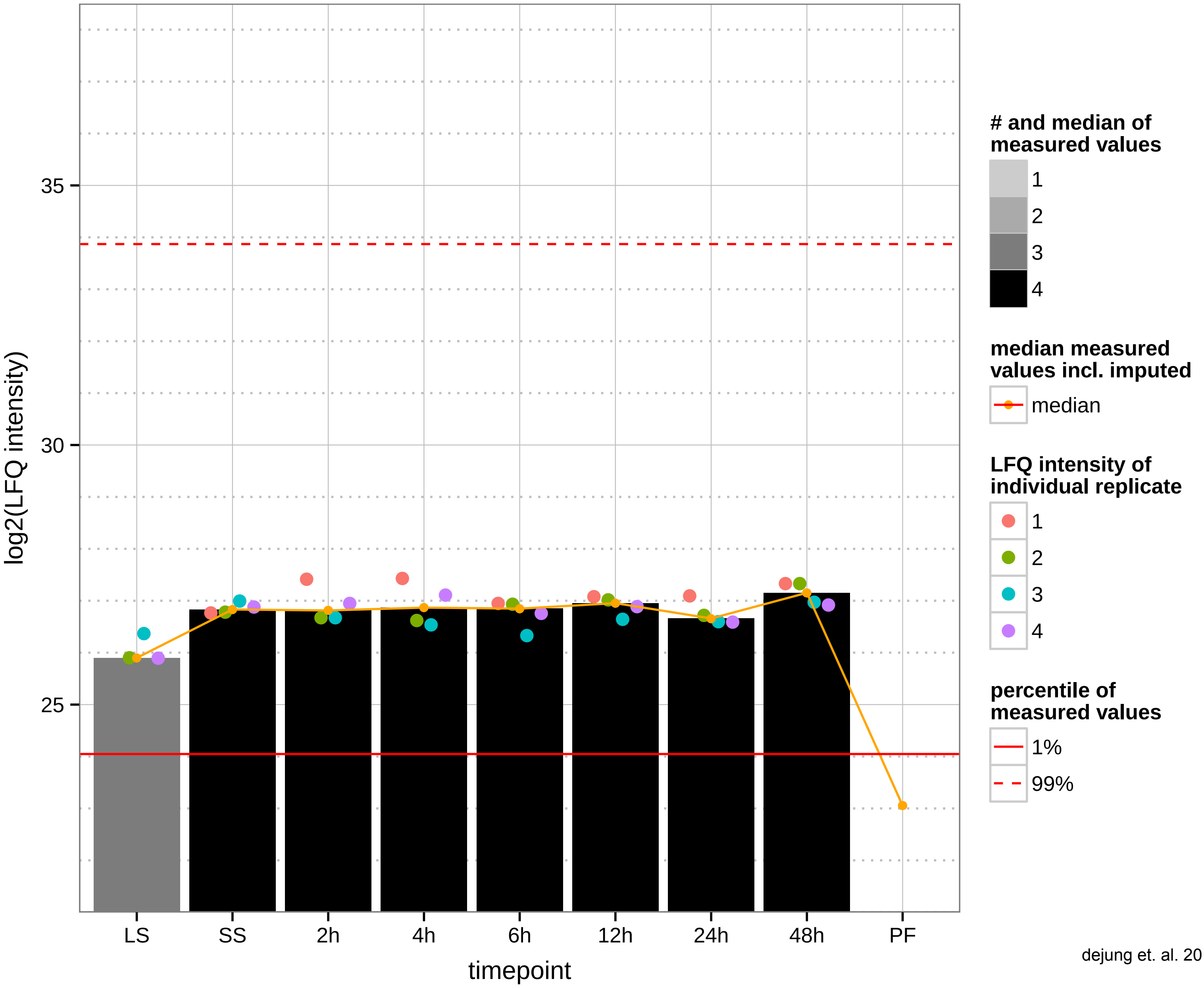
hypothetical protein, conserved
Tb927.10.3880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



protein kinase, putative
Tb927.10.3900
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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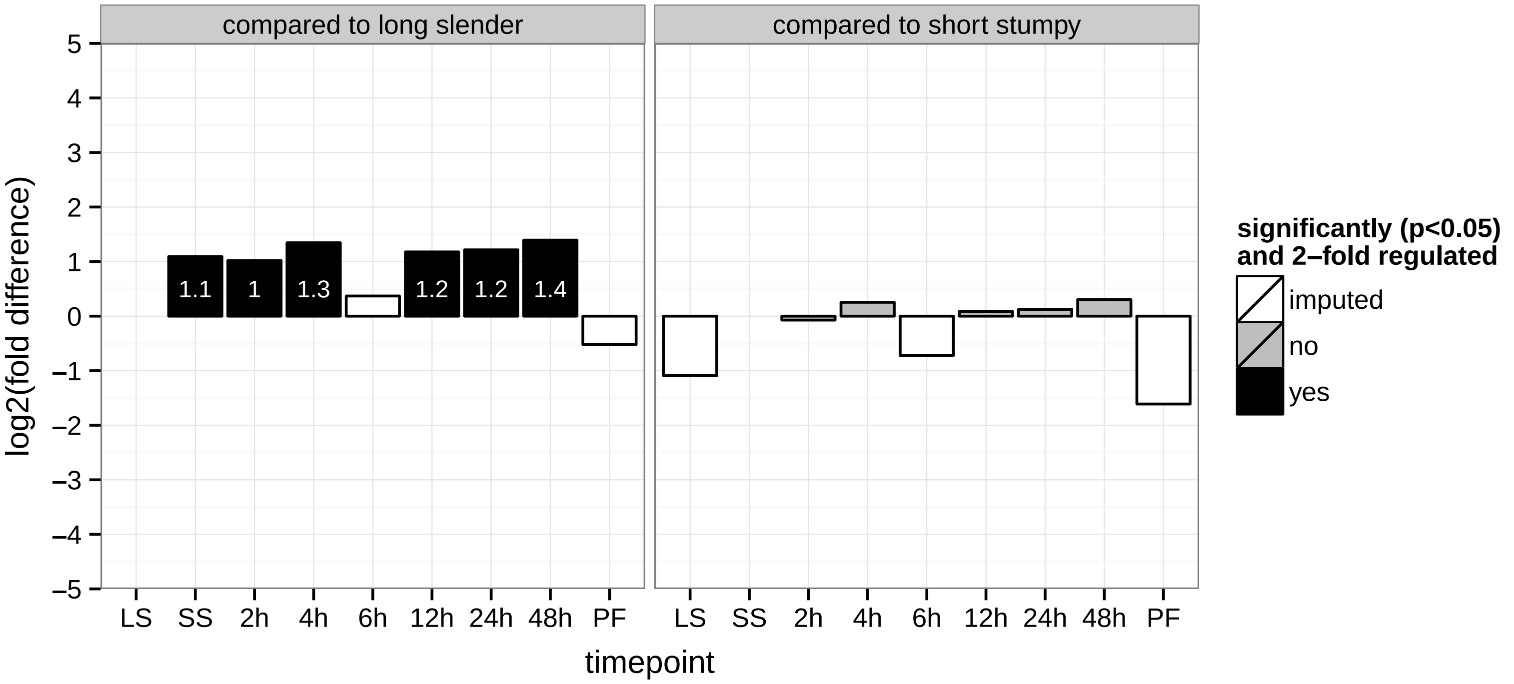
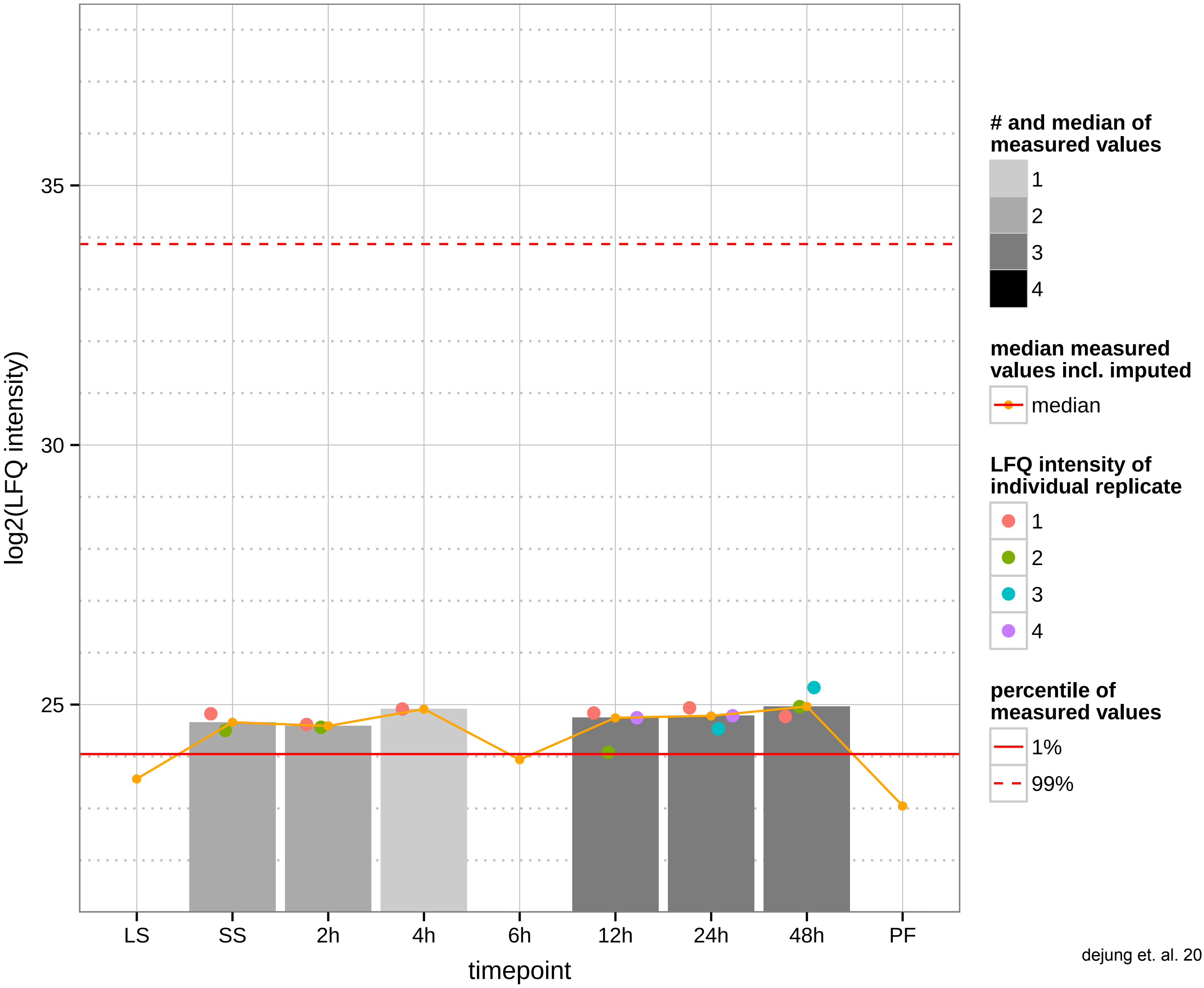
hypothetical protein, conserved
Tb927.10.4100
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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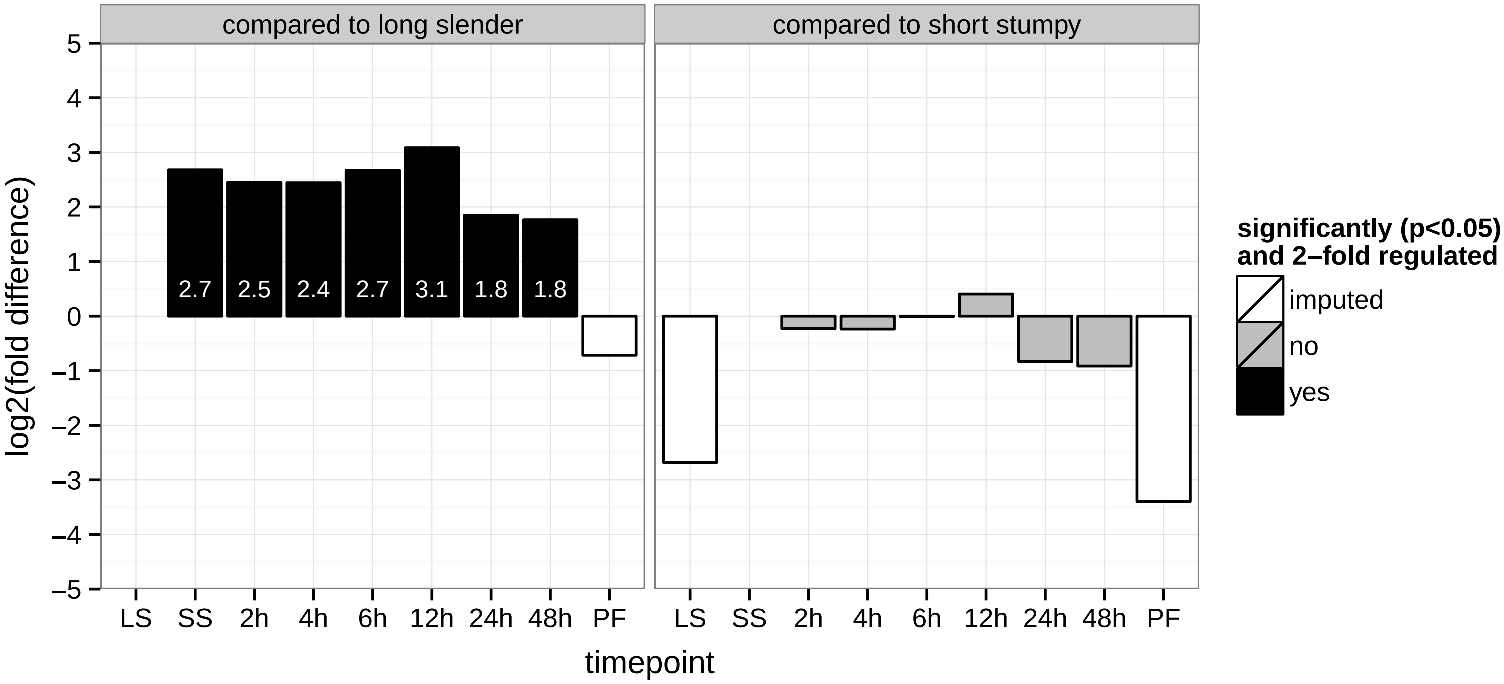
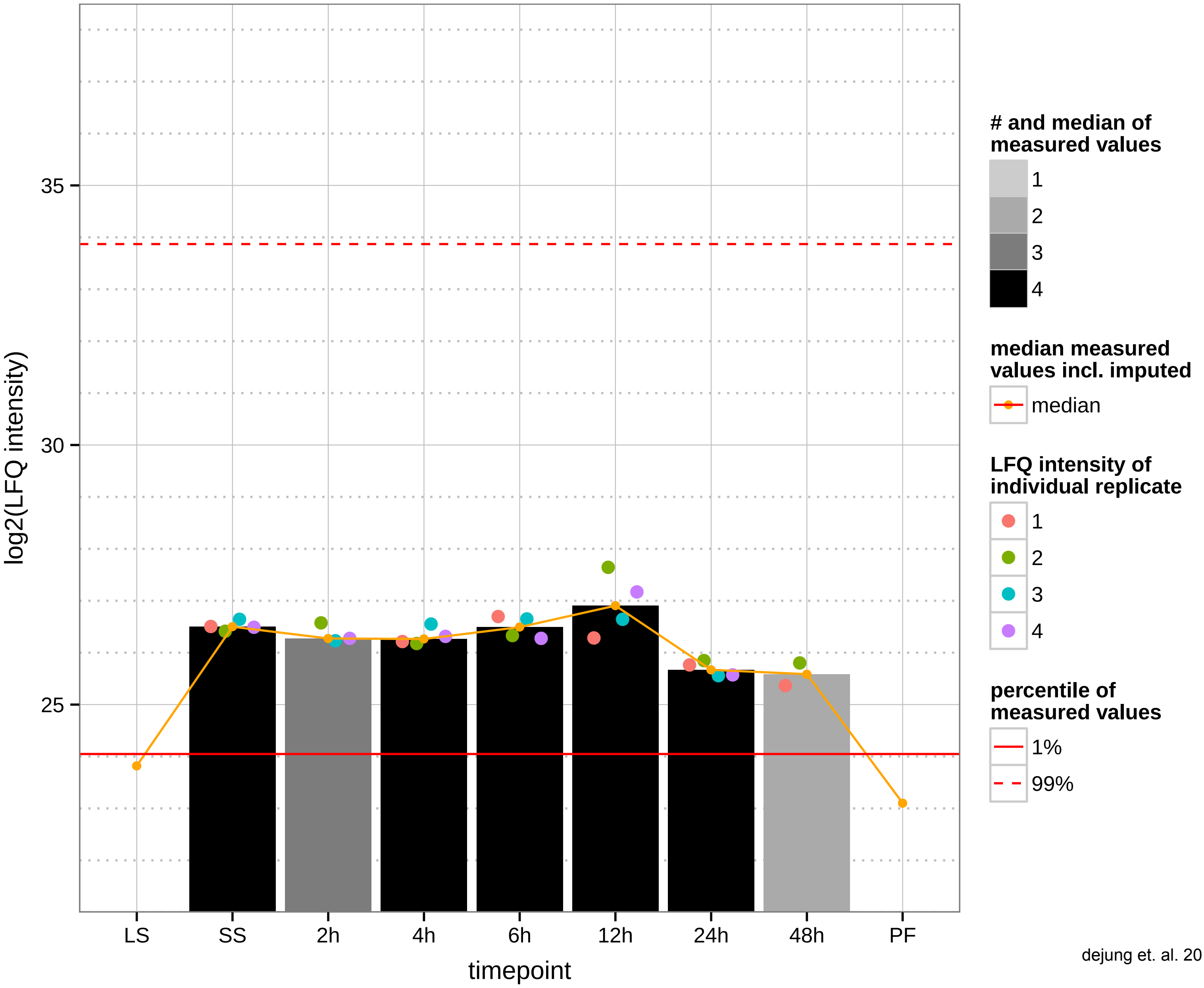
hypothetical protein, conserved
Tb927.10.4260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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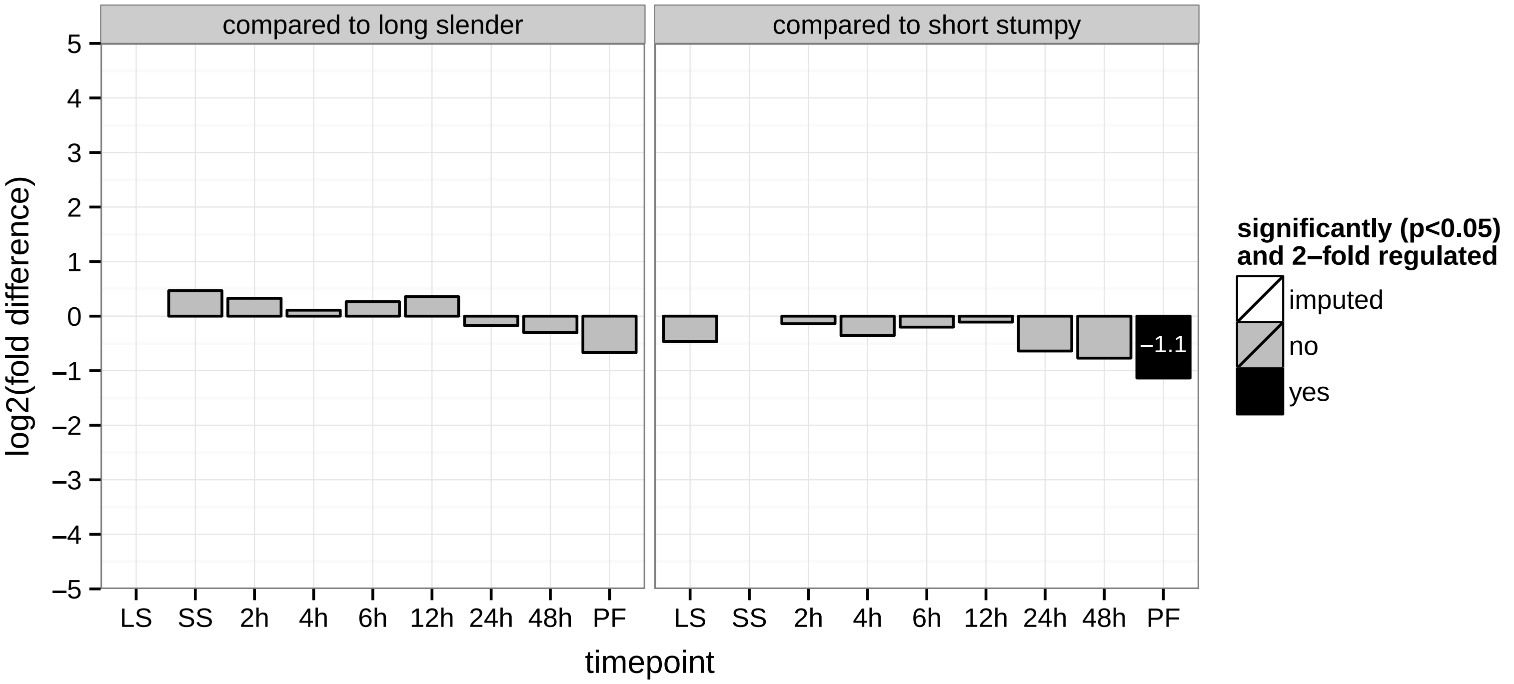
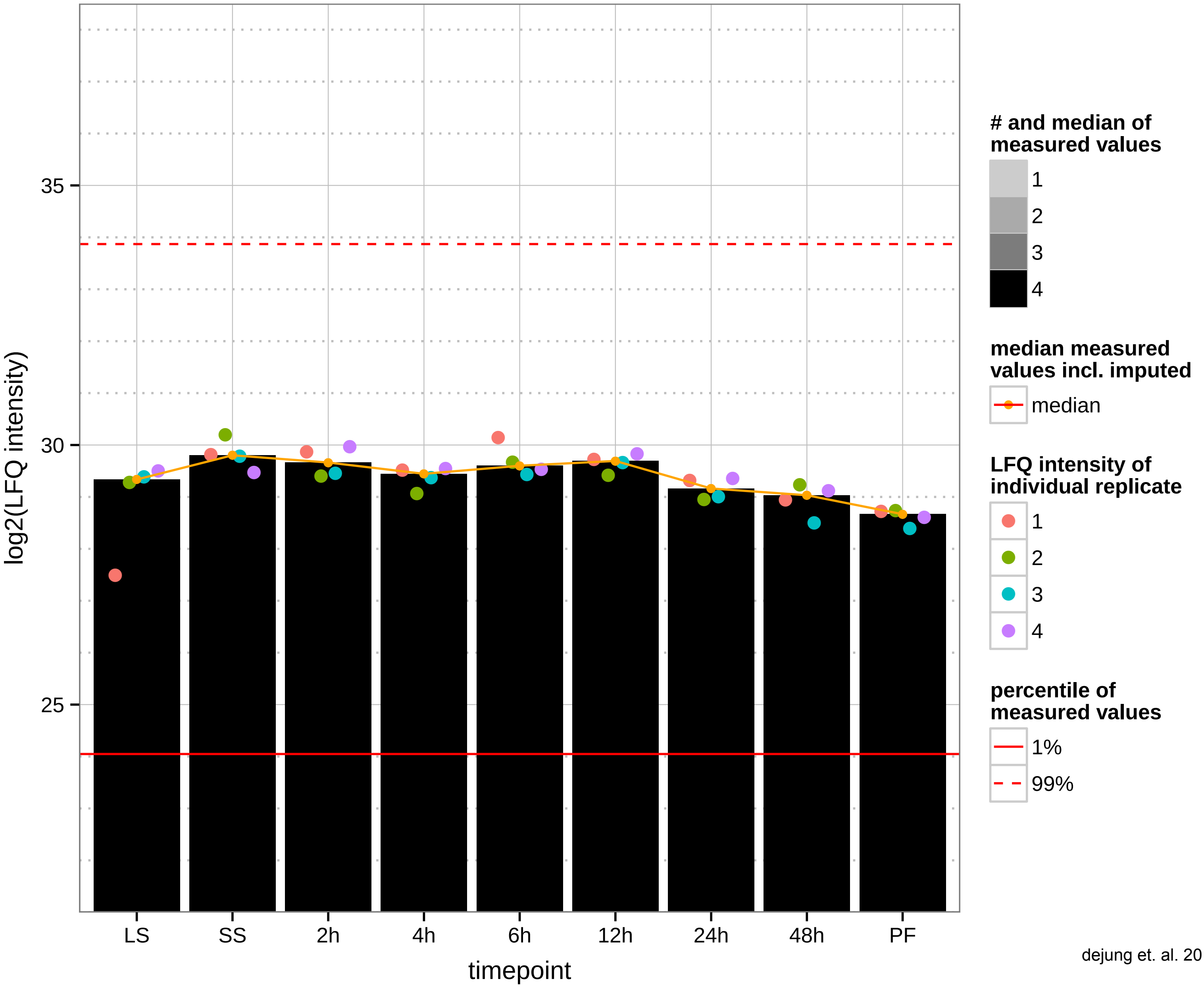
hypothetical protein, conserved
Tb927.10.450
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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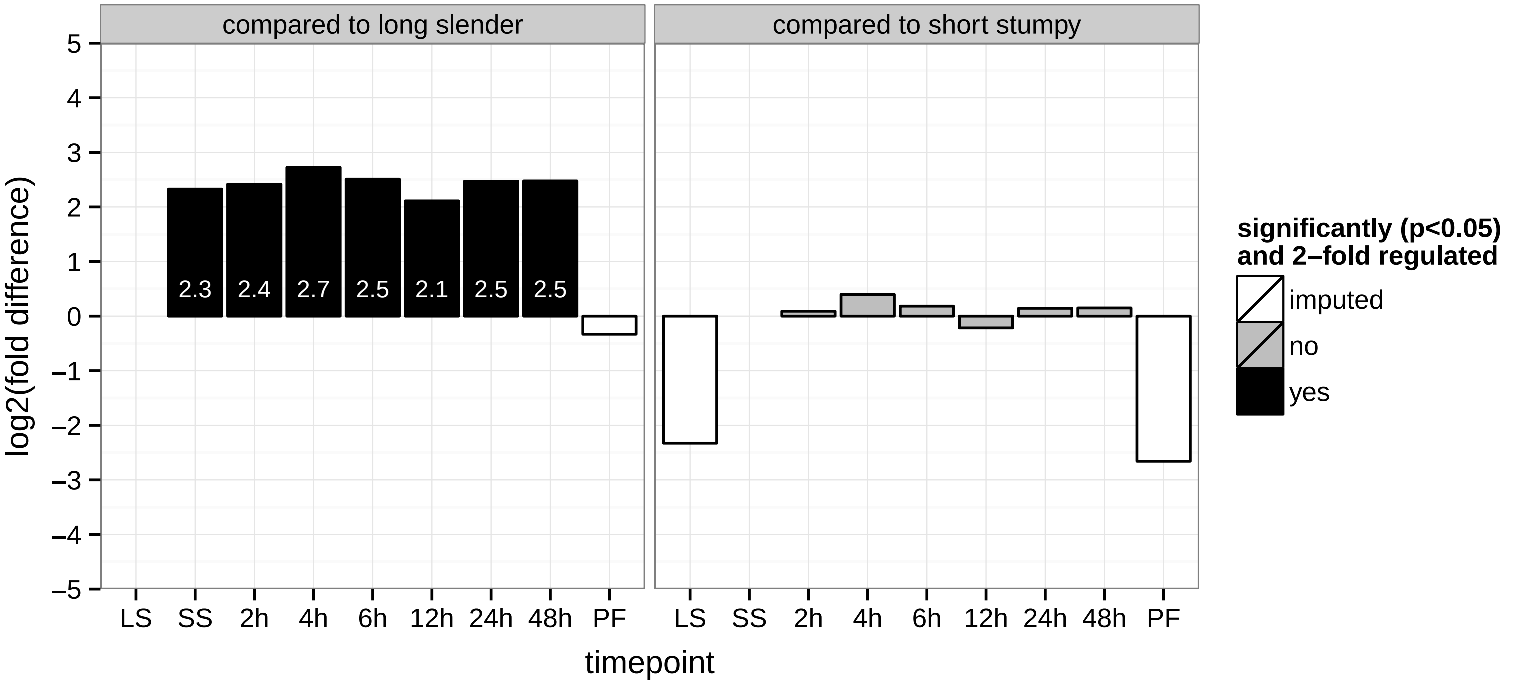
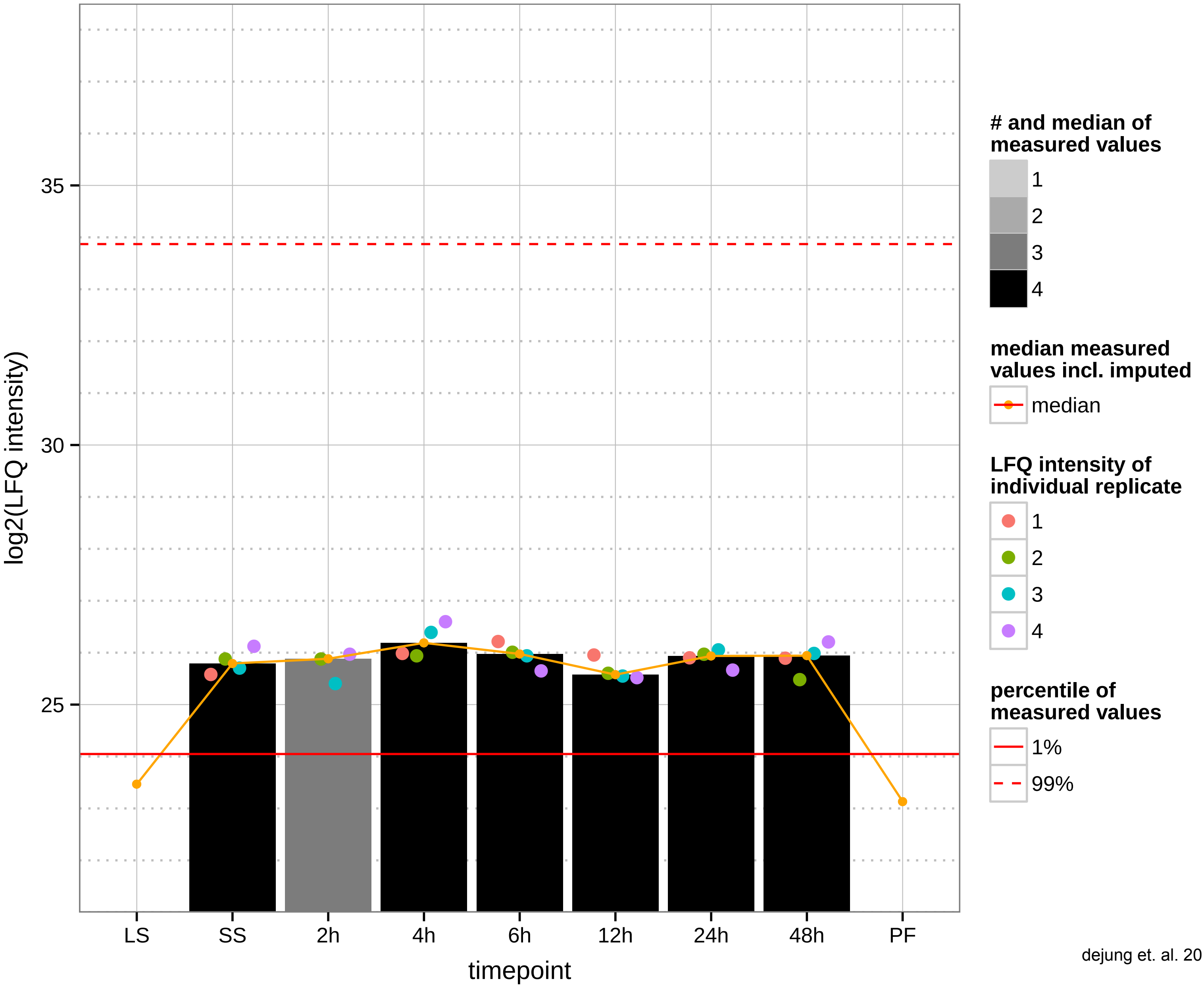
U2 small nuclear ribonucleoprotein 16.5K
Tb927.10.4950
AGOF: RNA binding
AGOC: U2 snRNP, nucleus
AGOP: alternative nuclear mRNA splicing, via spliceosome
PGOF: null
PGOC: null
PGOP: null





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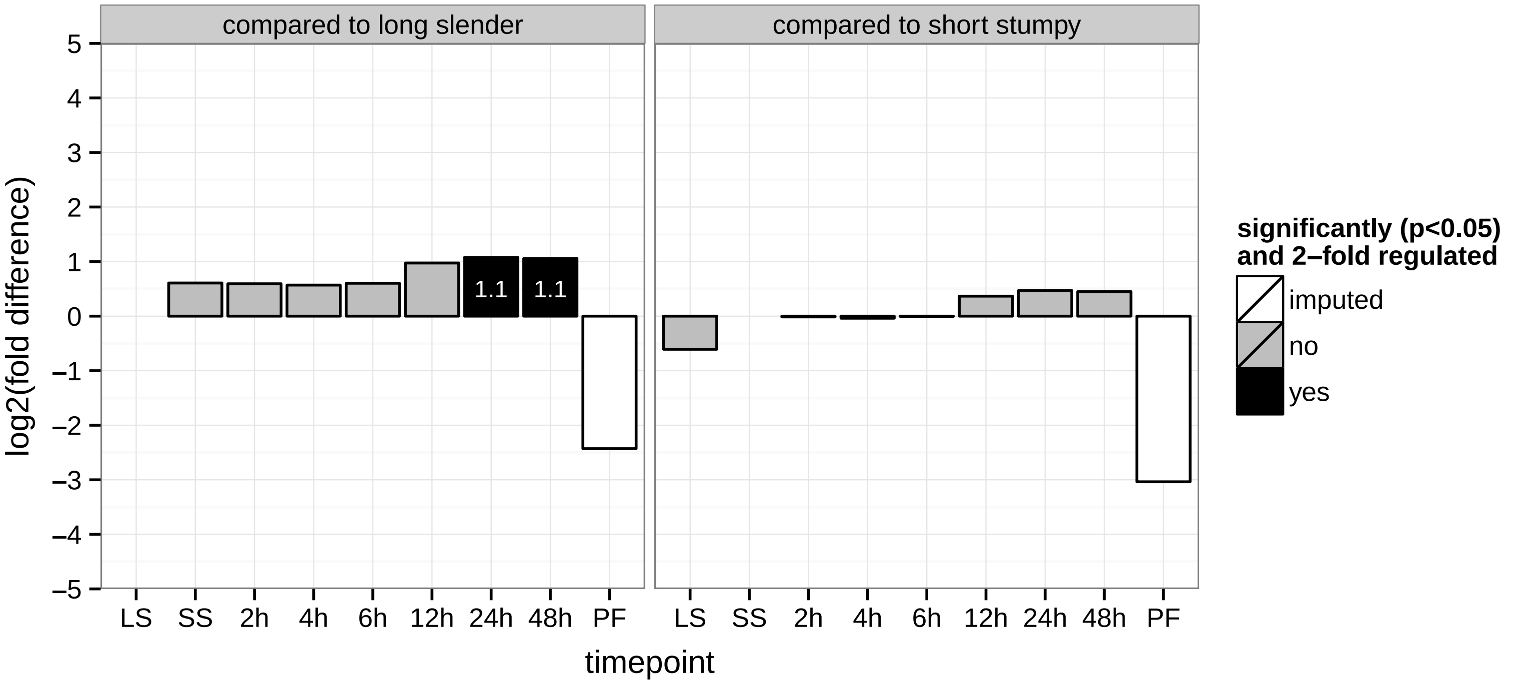
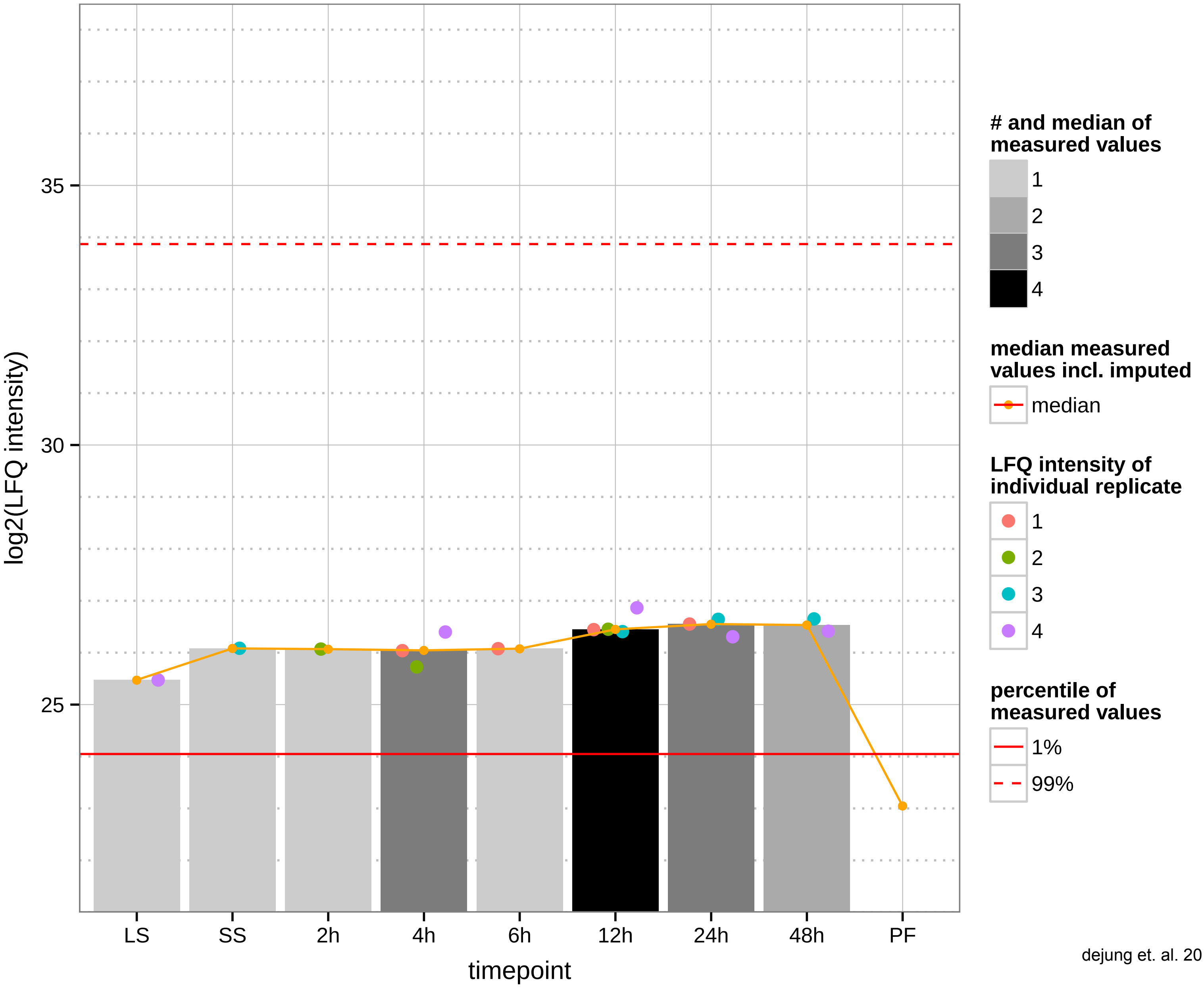
KREPA6, RNA–editing complex protein (KREPA6)
Tb927.10.5120
AGOF: RNA binding, endonuclease activity
AGOC: mitochondrial mRNA editing complex, mitochondrion
AGOP: RNA modification
PGOF: single–stranded DNA binding
PGOC: null
PGOP: null





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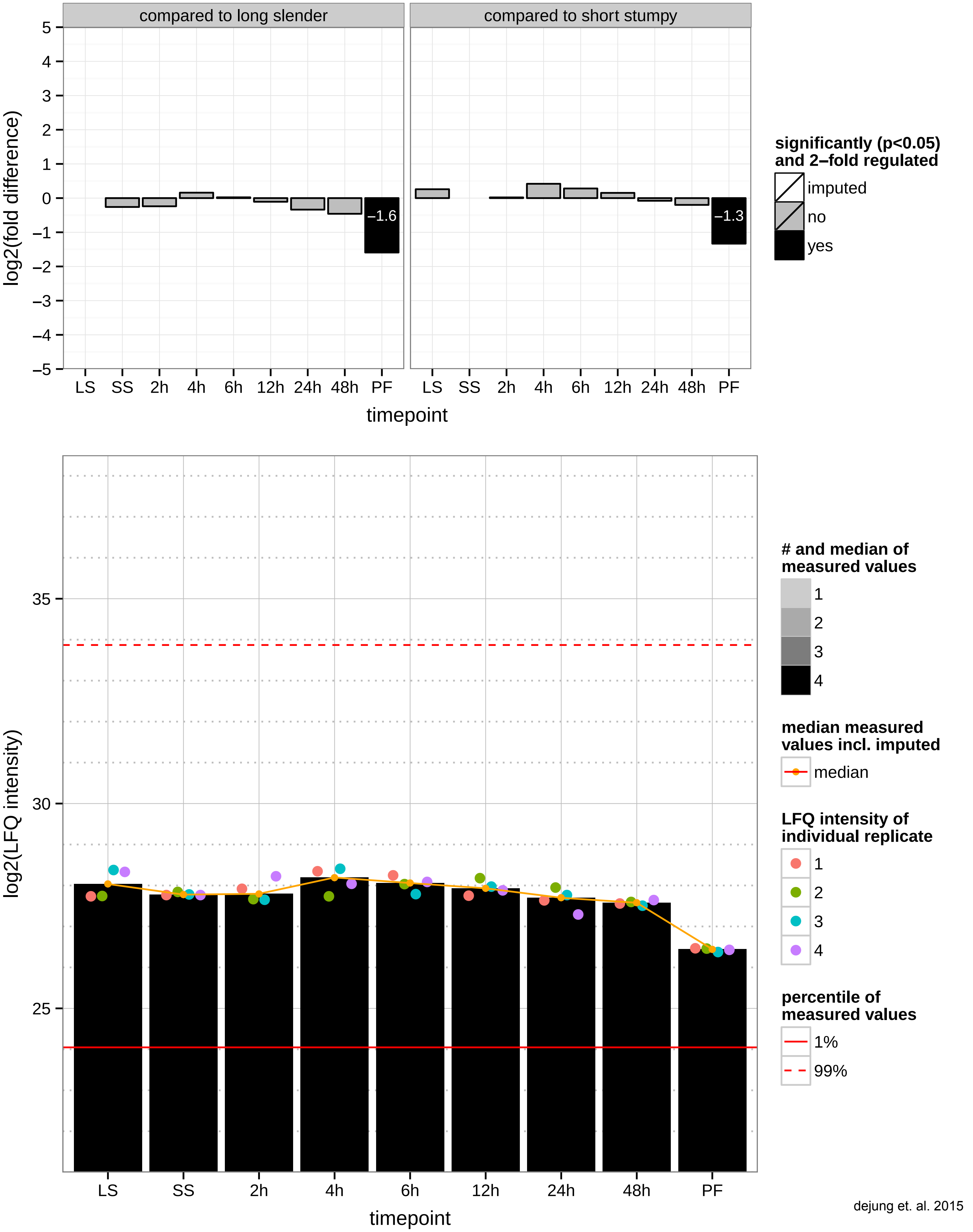
hypothetical protein, conserved
Tb927.10.5400
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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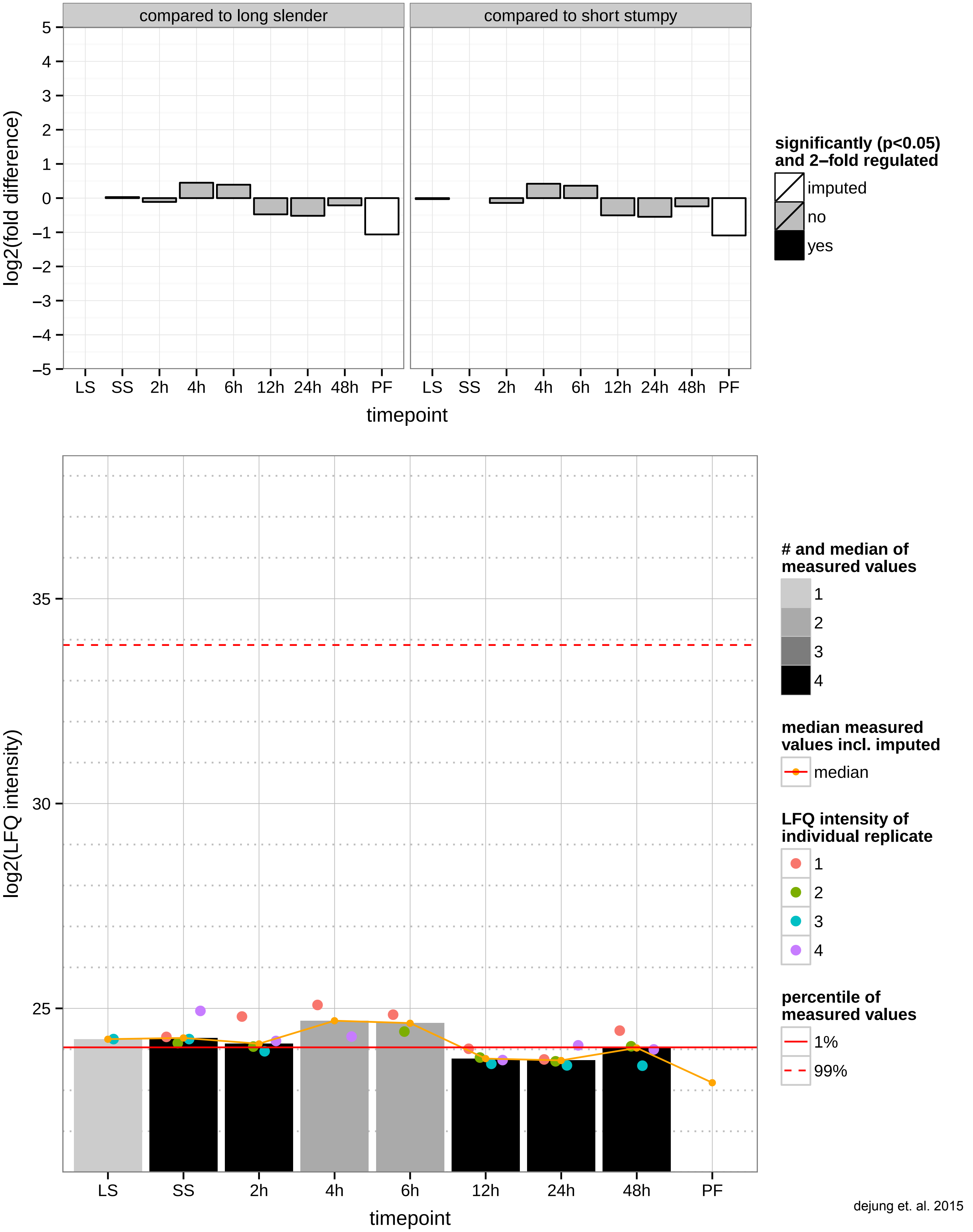
neurobeachin/beige protein, putative
Tb927.10.6150;Tb11.v5.0207
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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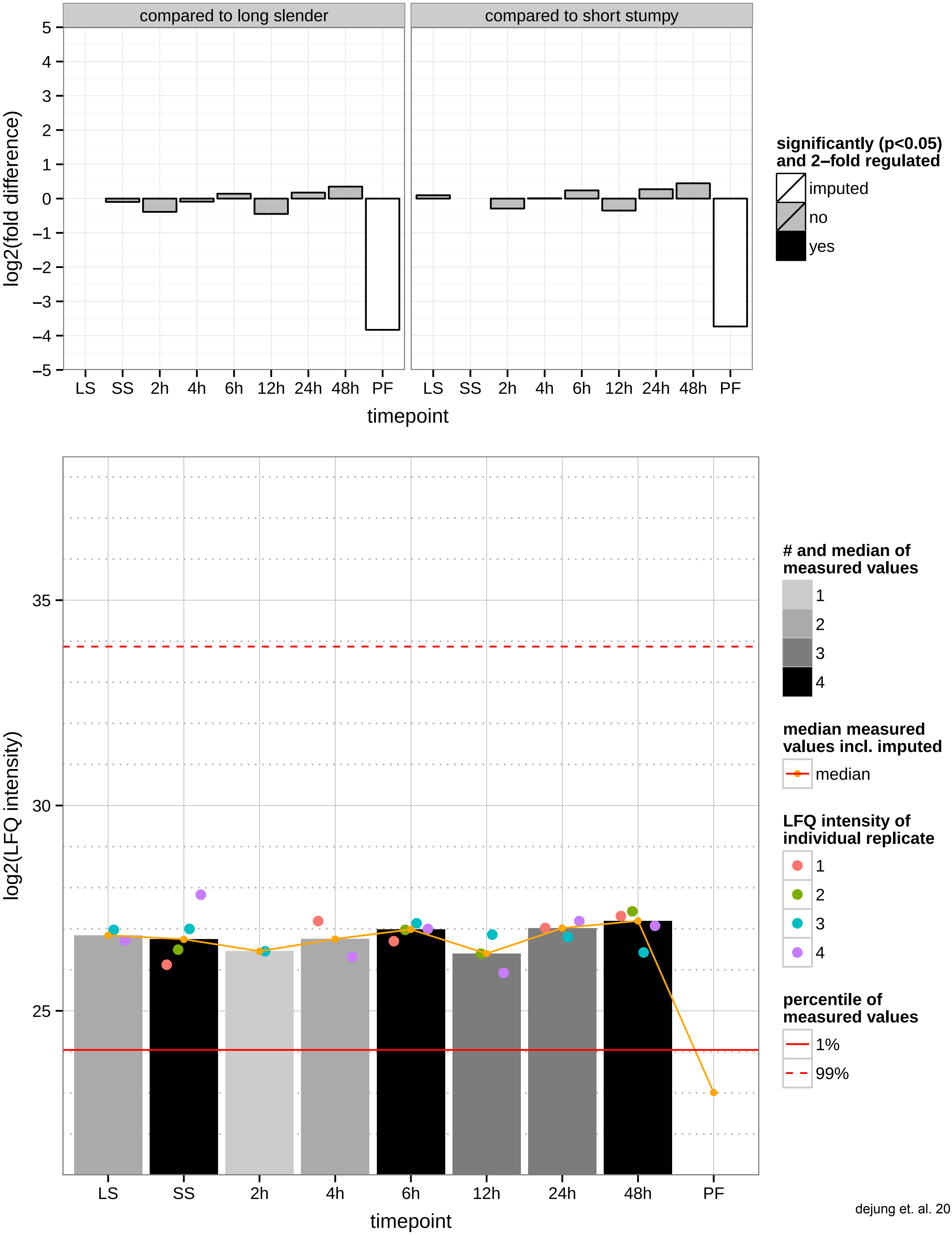
MORN repeat containing protein
Tb927.10.6230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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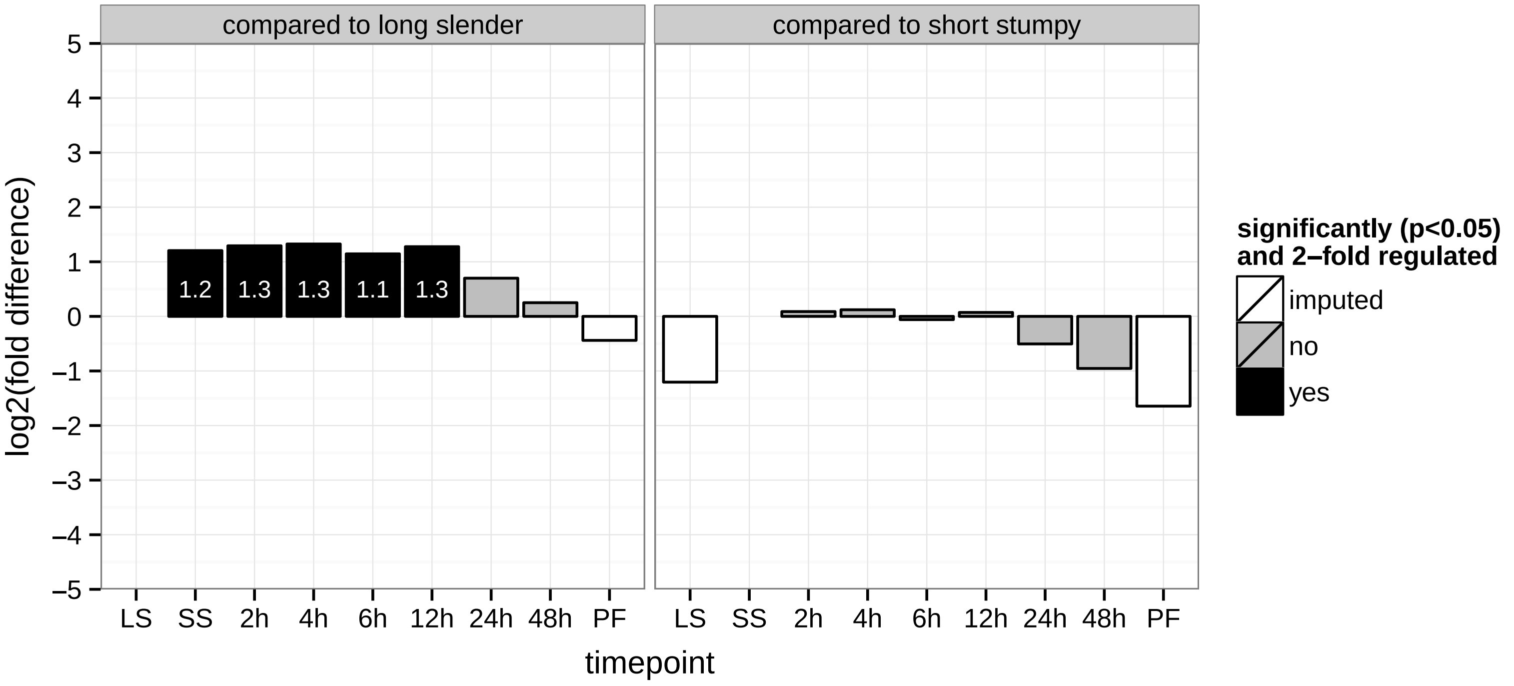
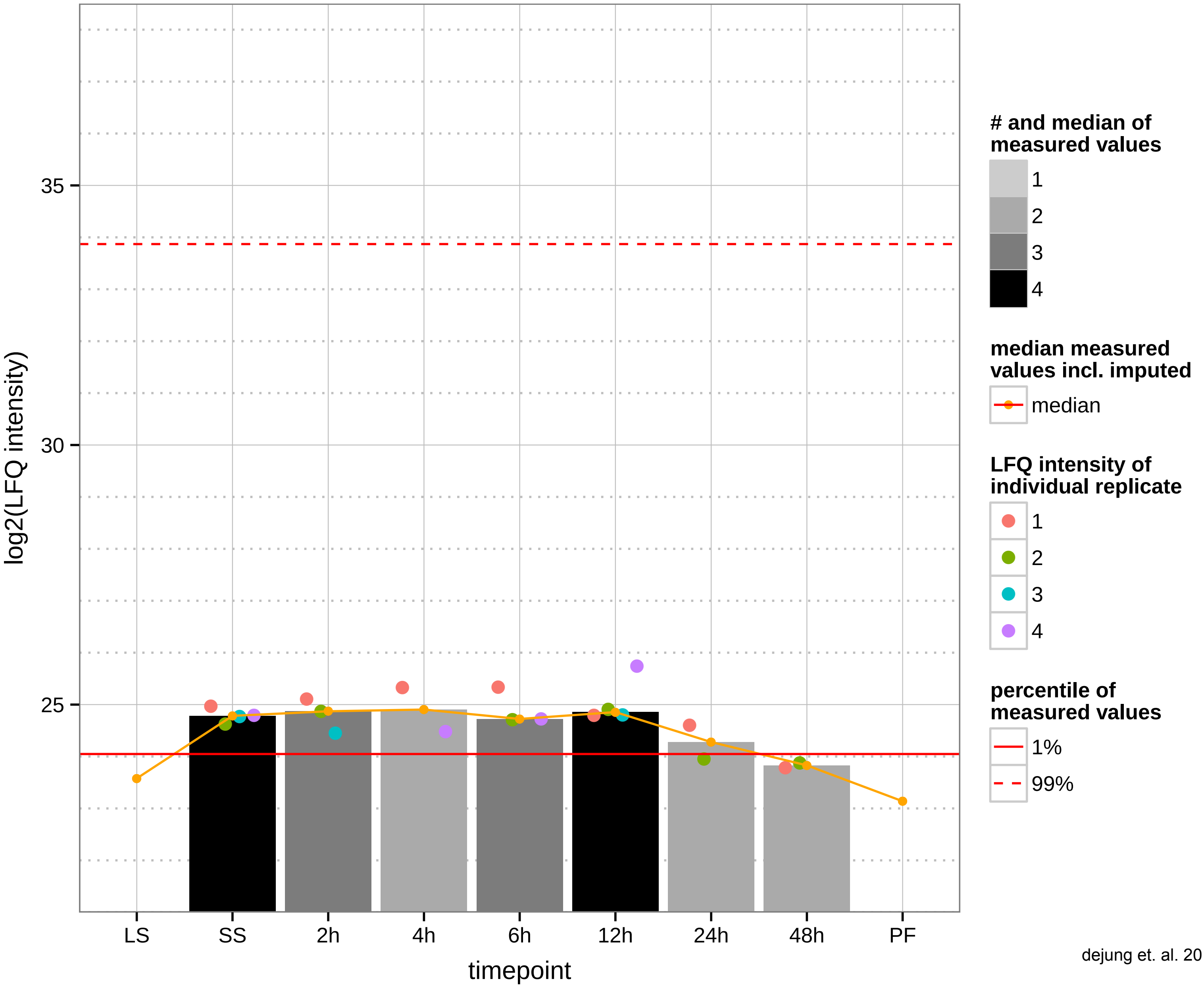
hypothetical protein, conserved
Tb927.10.6590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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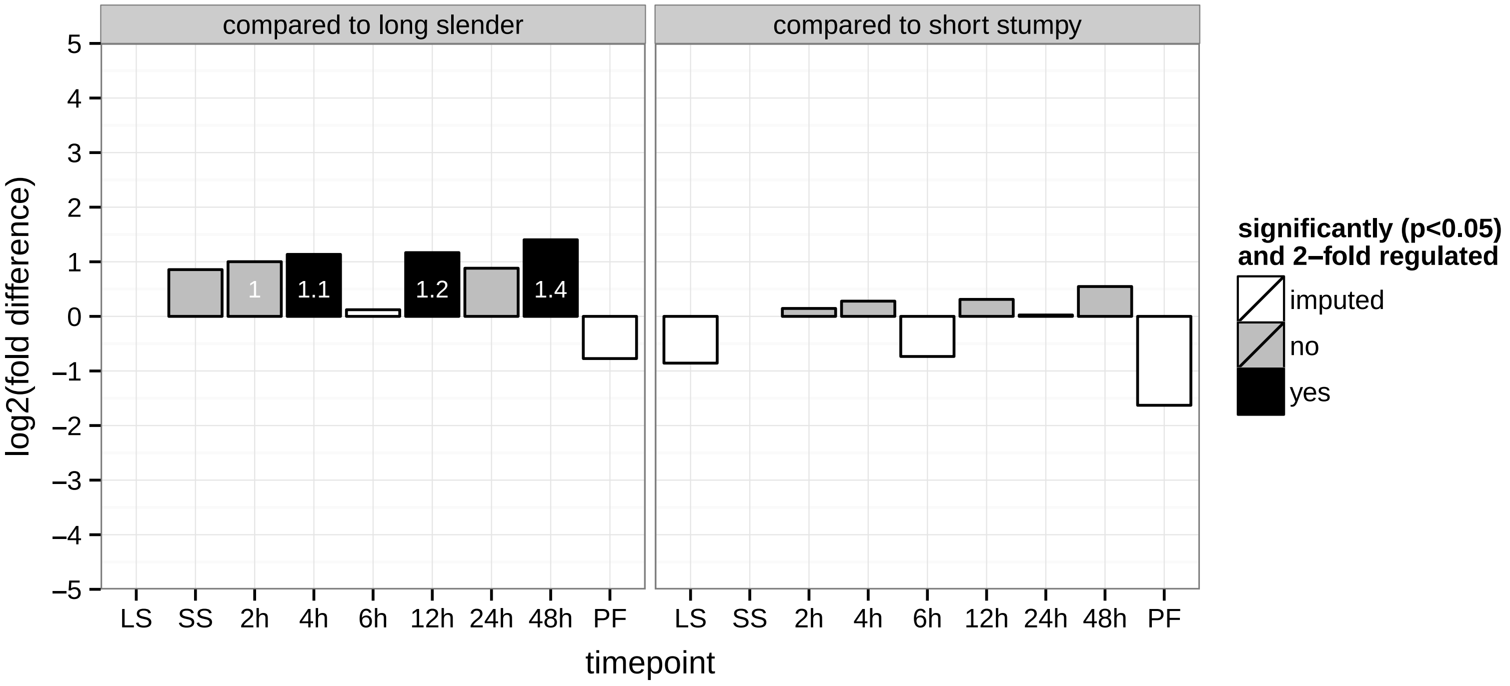
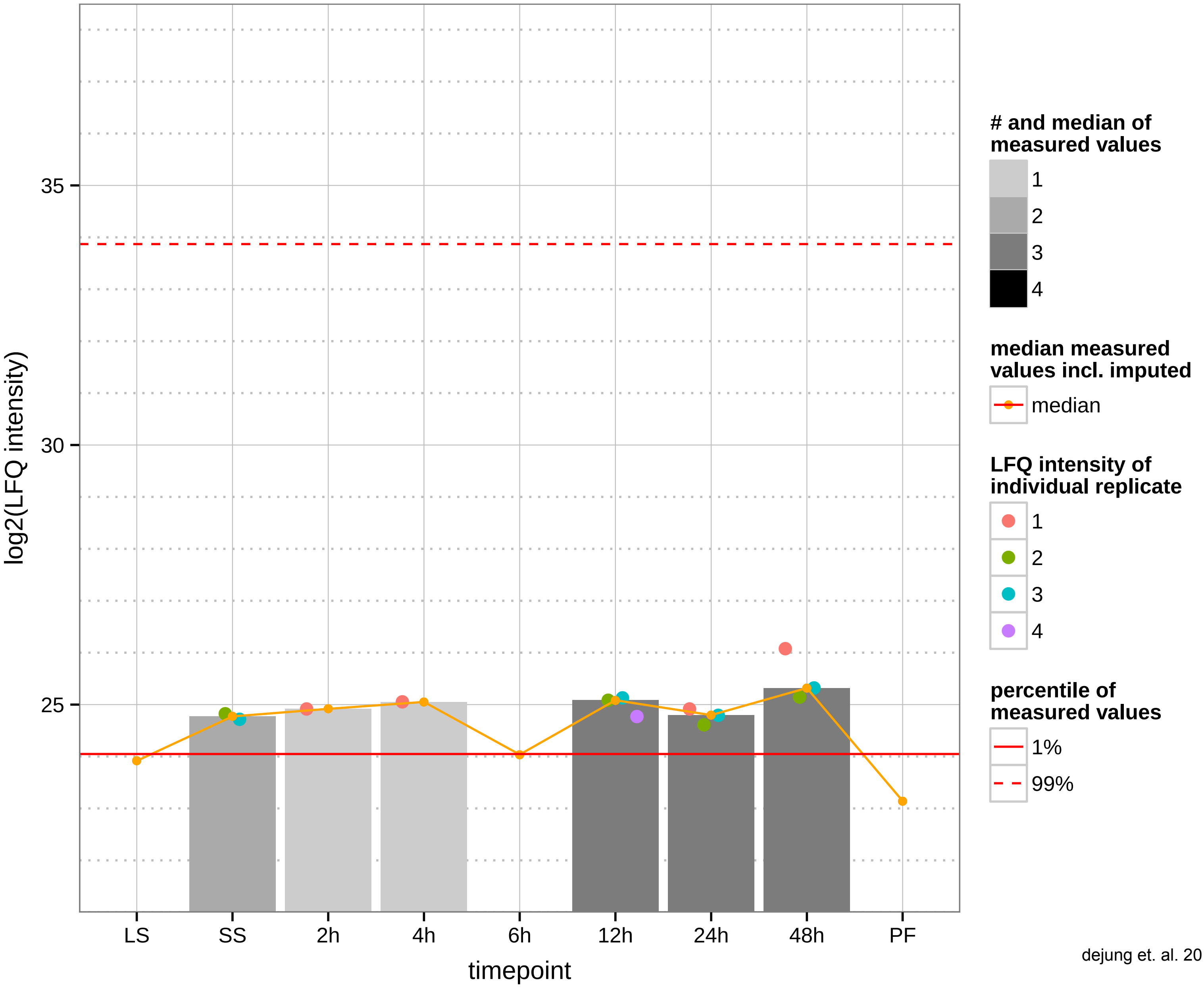
protein tyrosine phosphatase, putative (TbPTP1)
Tb927.10.6690
AGOF: protein tyrosine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: phosphatase activity, protein tyrosine phosphatase activity
PGOC: null
PGOP: dephosphorylation, protein dephosphorylation





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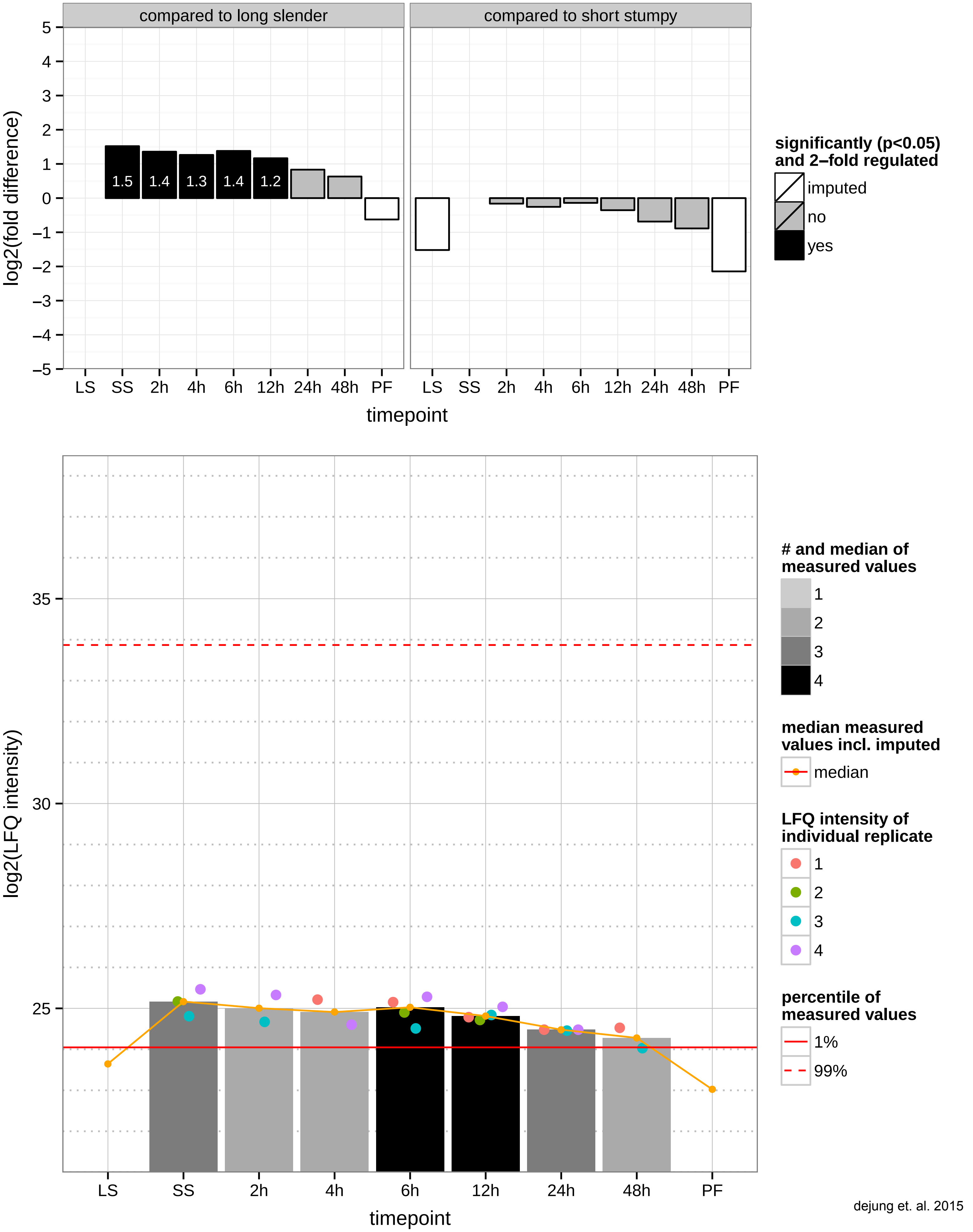
hypothetical protein, conserved
Tb927.10.6700;Tb11.v5.0902
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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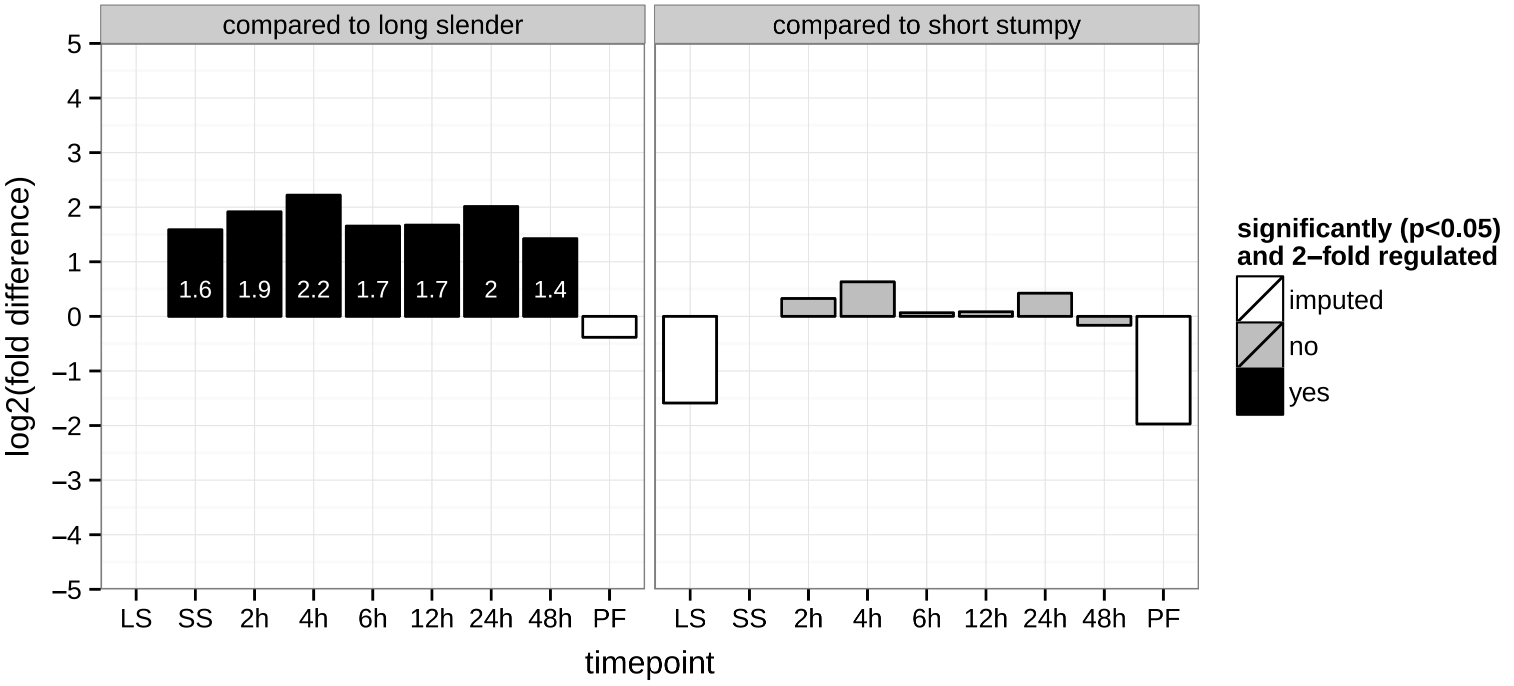
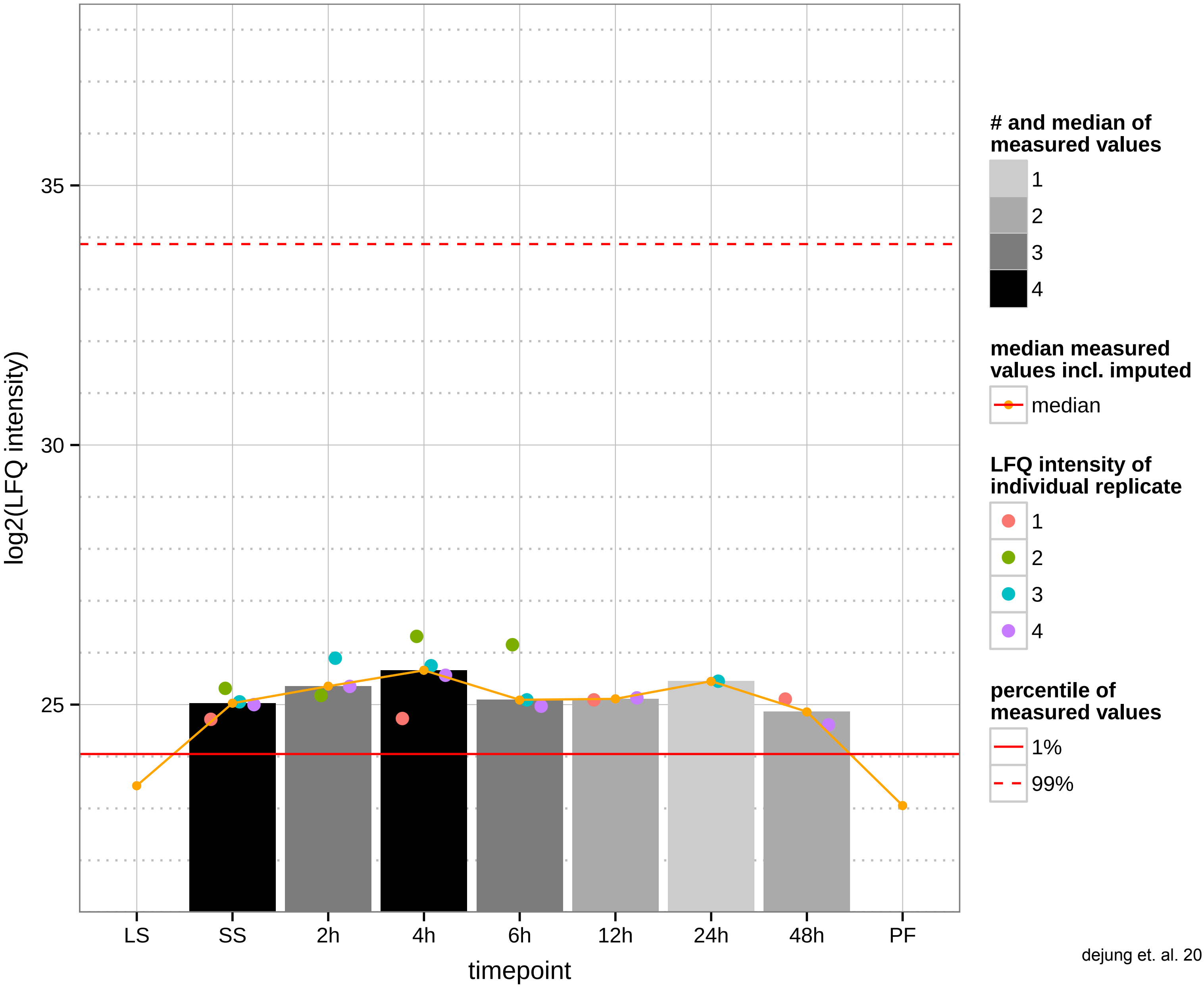
hypothetical protein, conserved
Tb927.10.6990
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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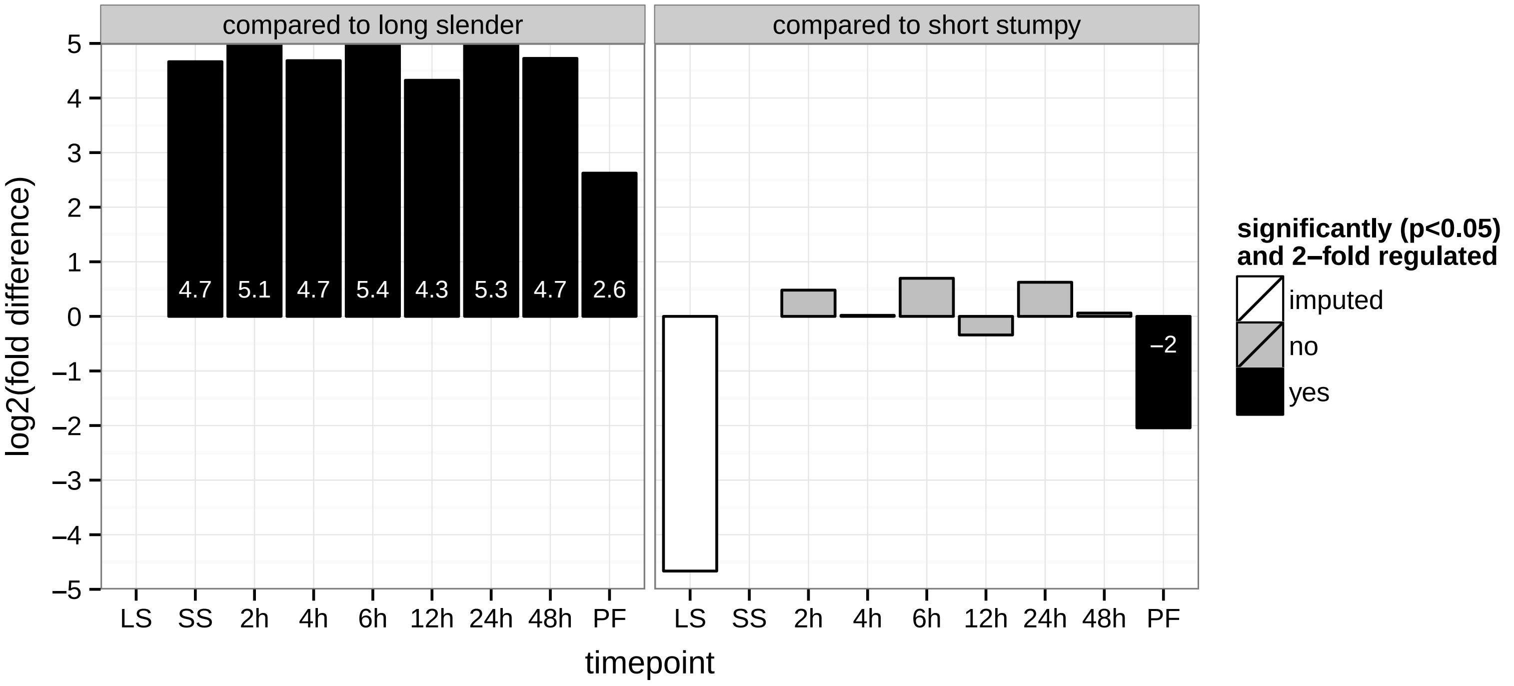
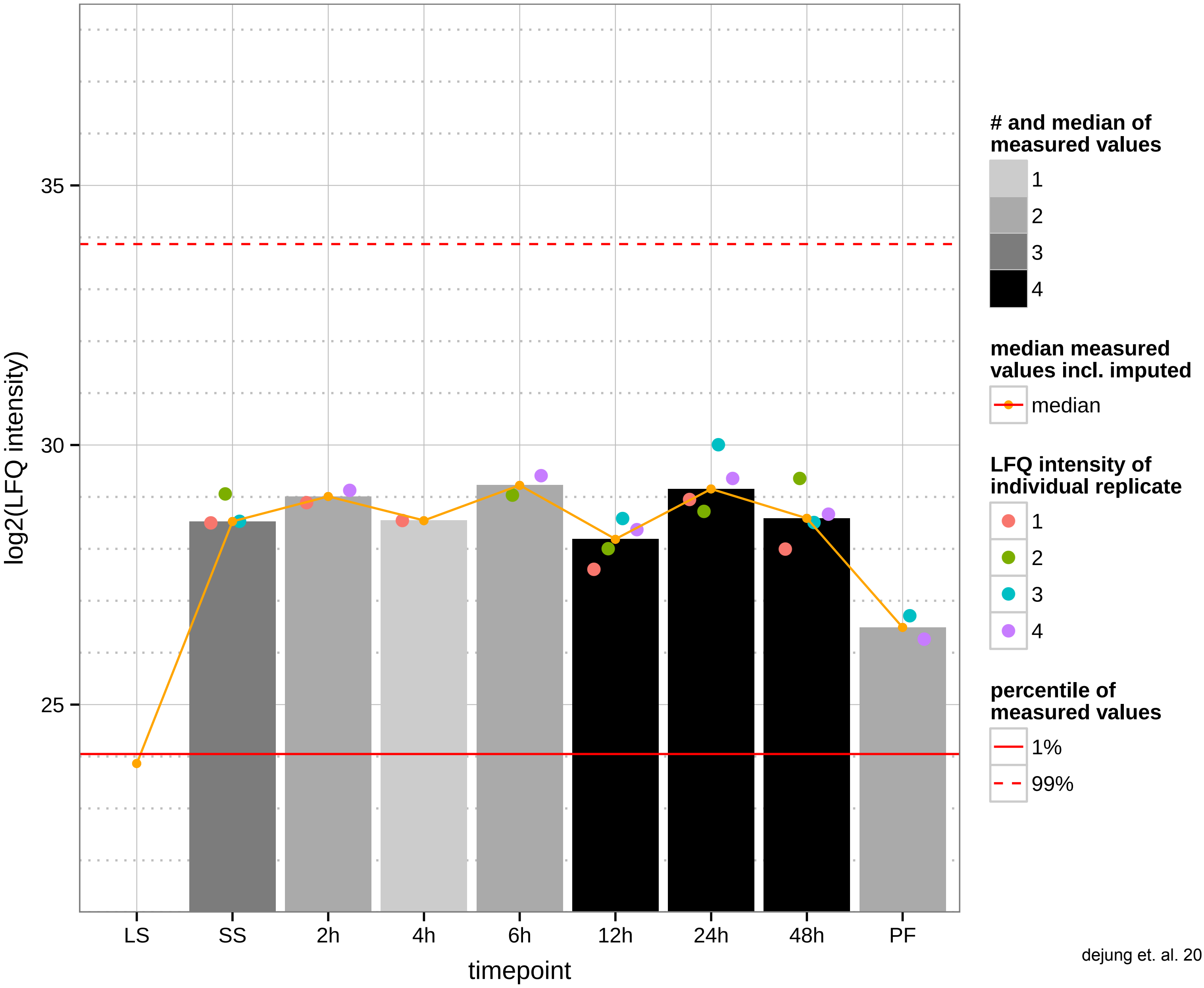
hypothetical protein, conserved
Tb927.10.720
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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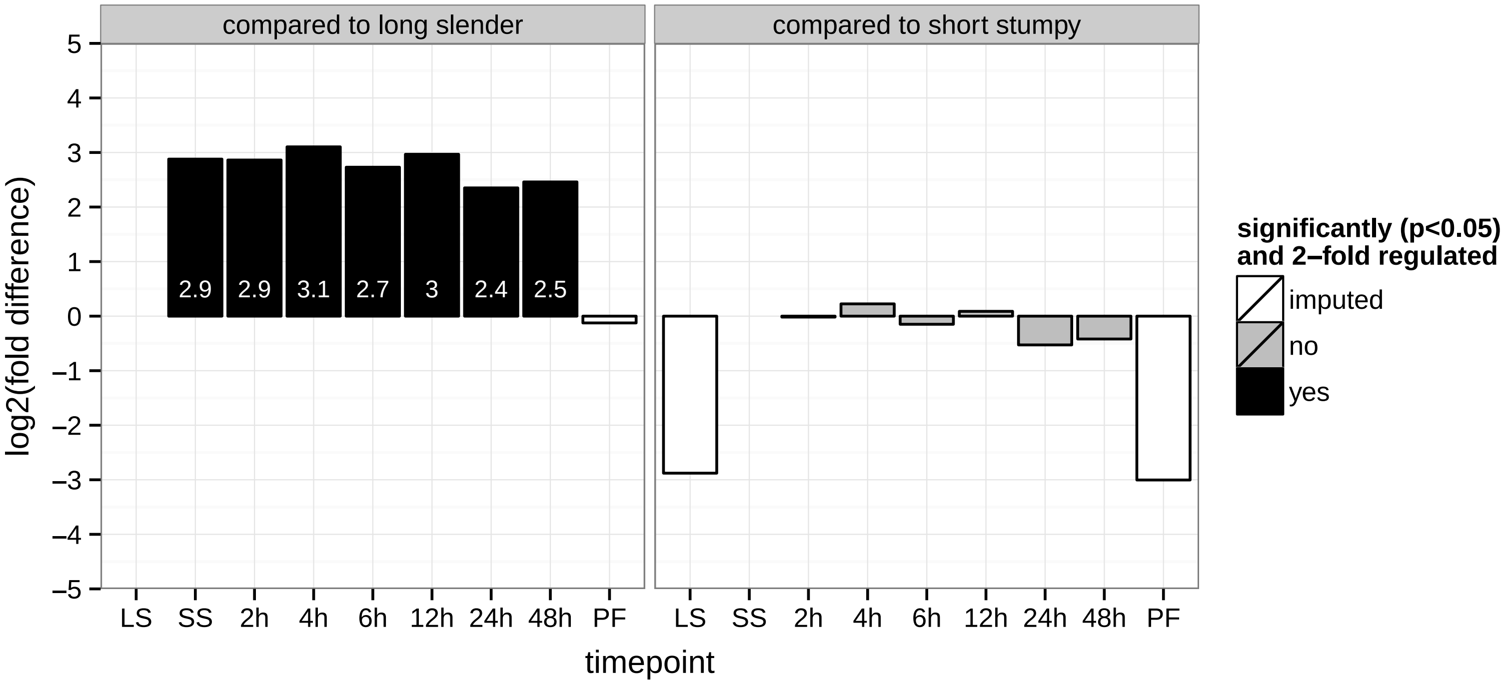
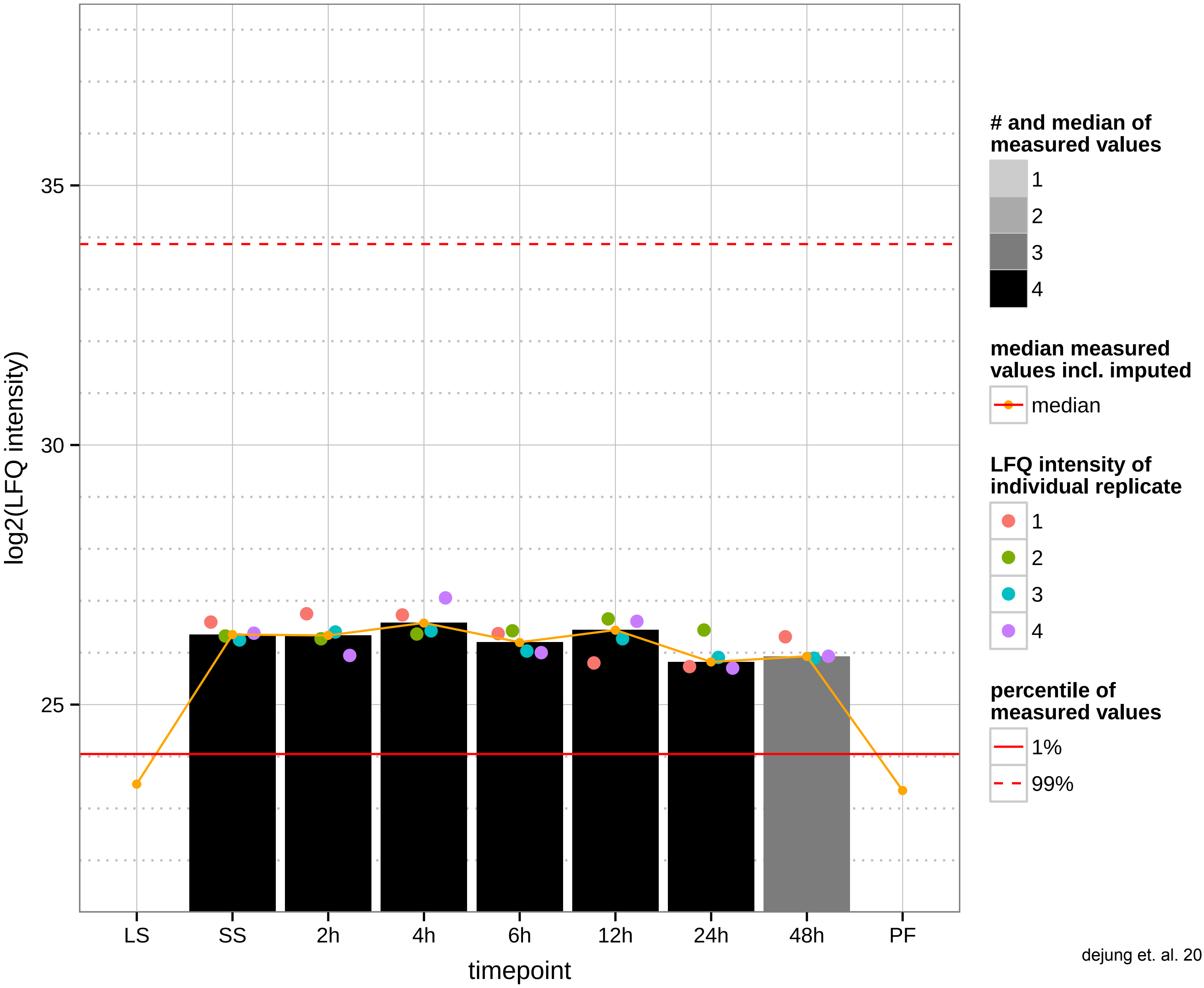
hypothetical protein, conserved
Tb927.10.8140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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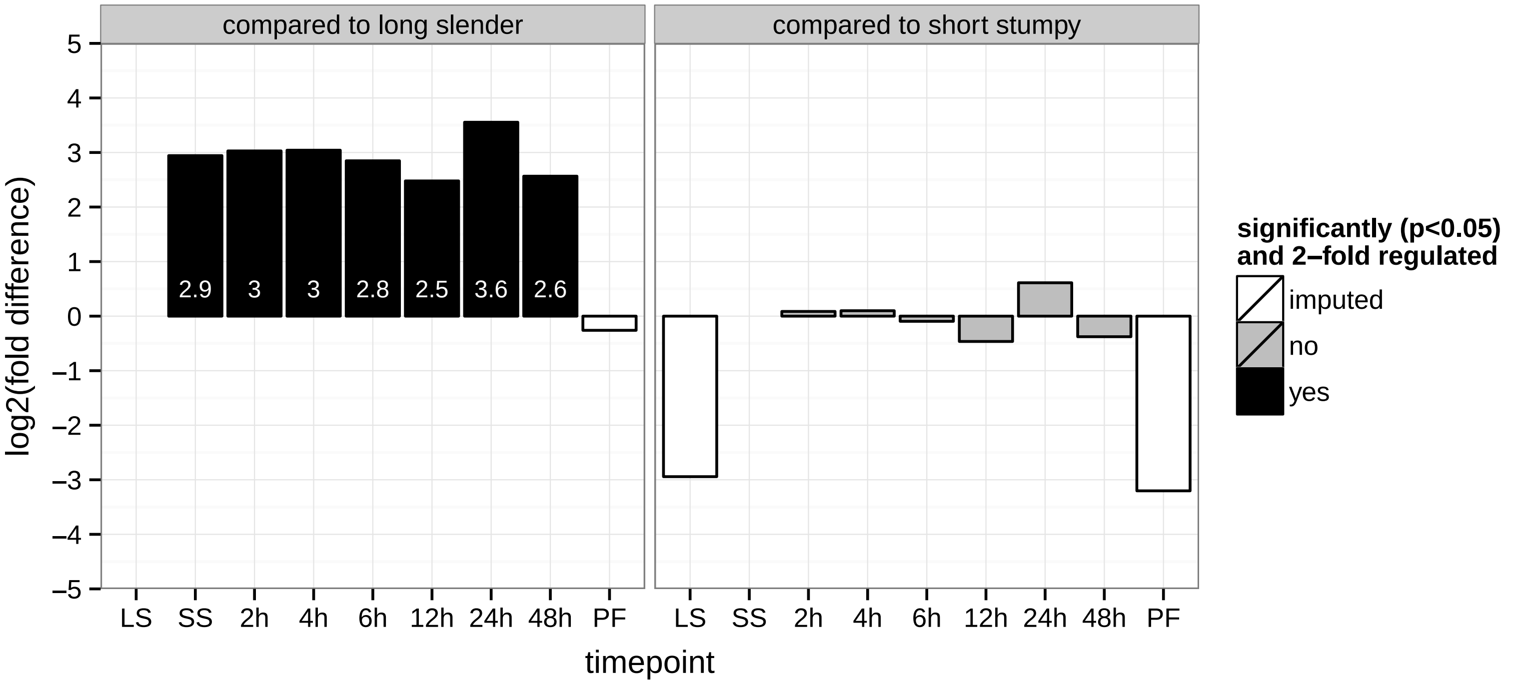
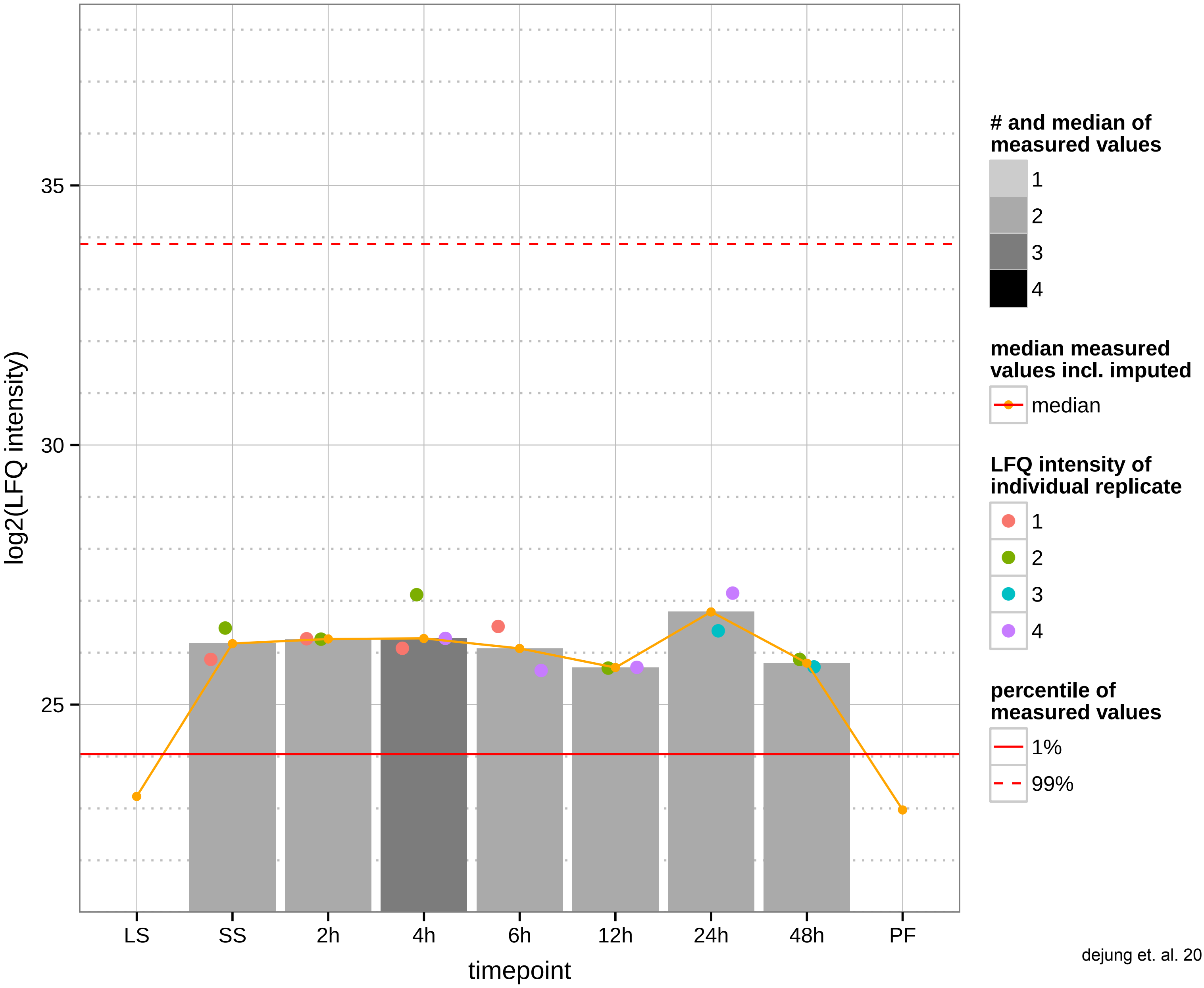
hypothetical protein, conserved
Tb927.10.8160
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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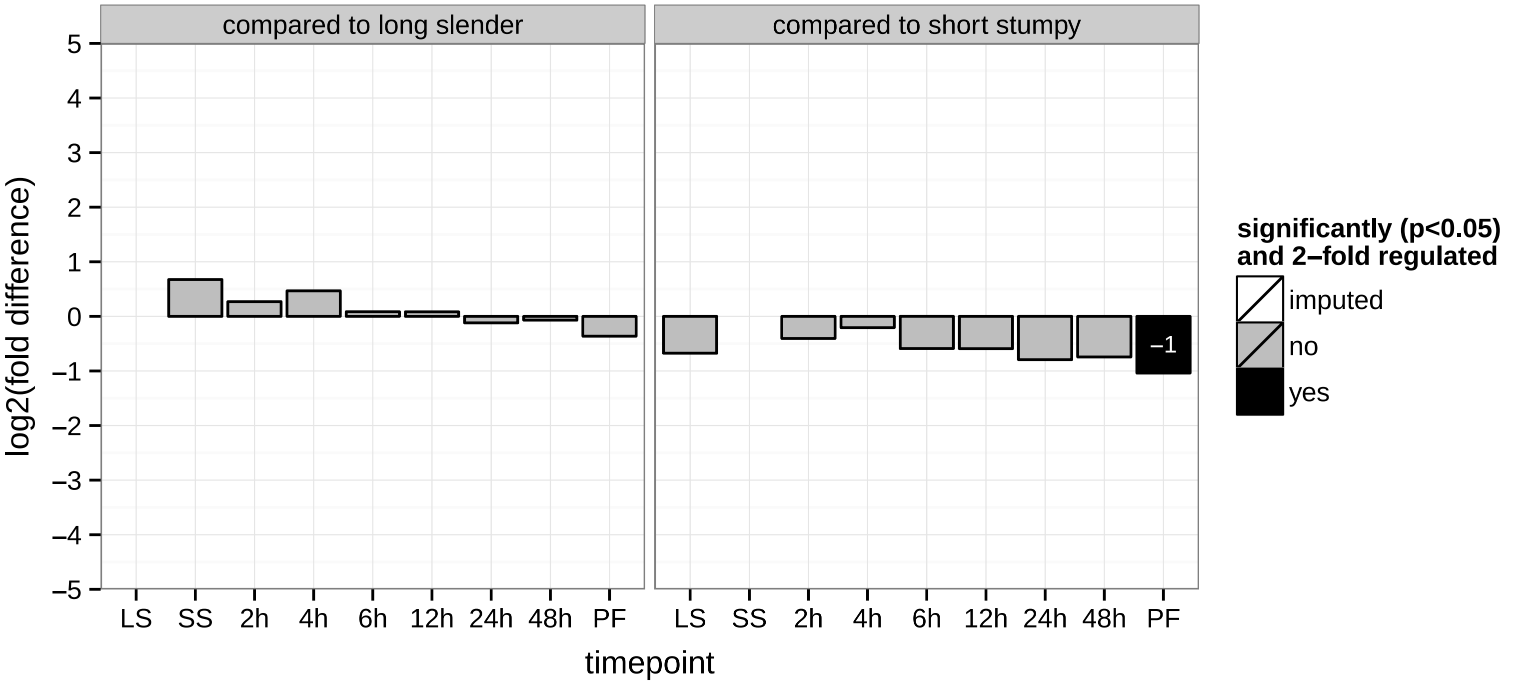
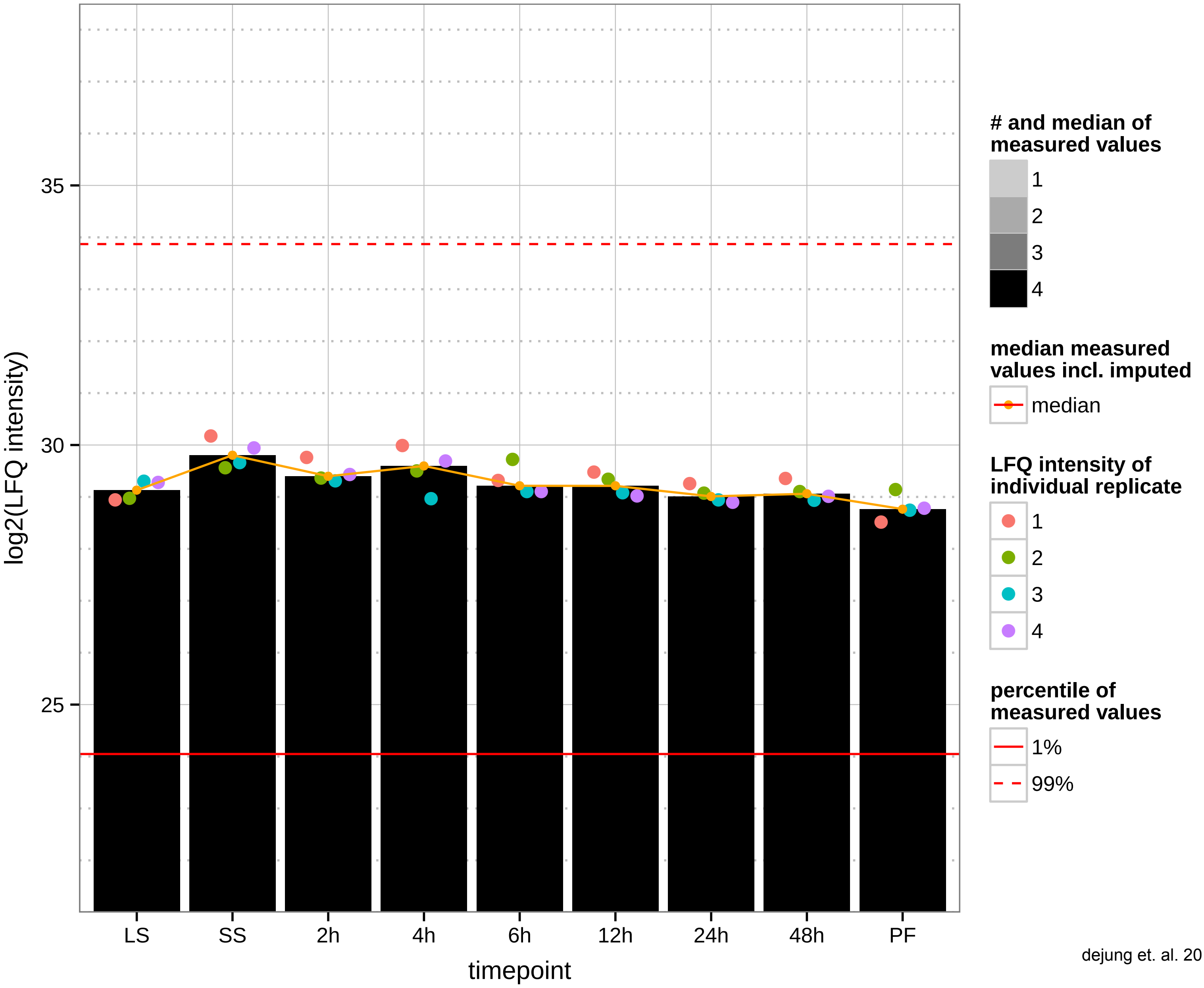
chaperone protein DNAj, putative
Tb927.10.8540
AGOF: heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding, protein refolding, response to unfolded protein
PGOF: heat shock protein binding, unfolded protein binding
PGOC: null
PGOP: protein folding





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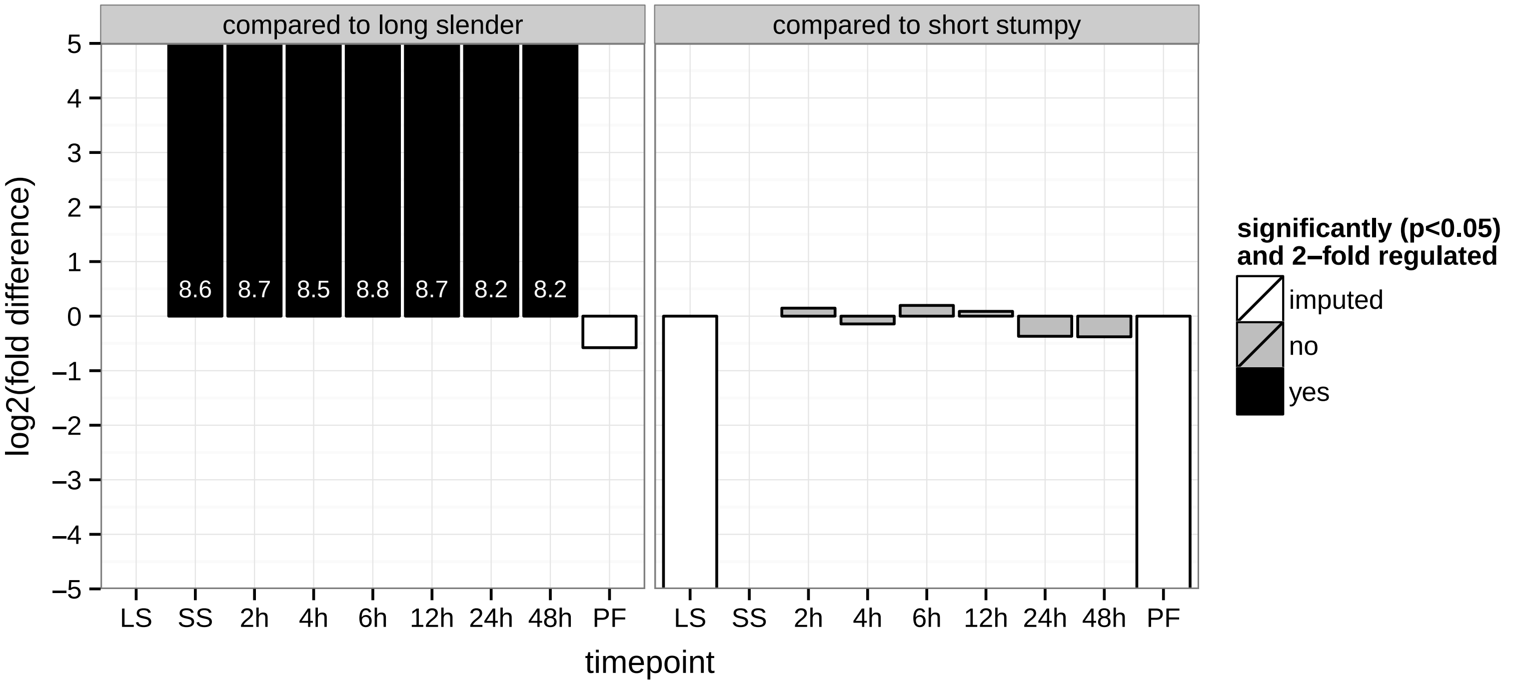
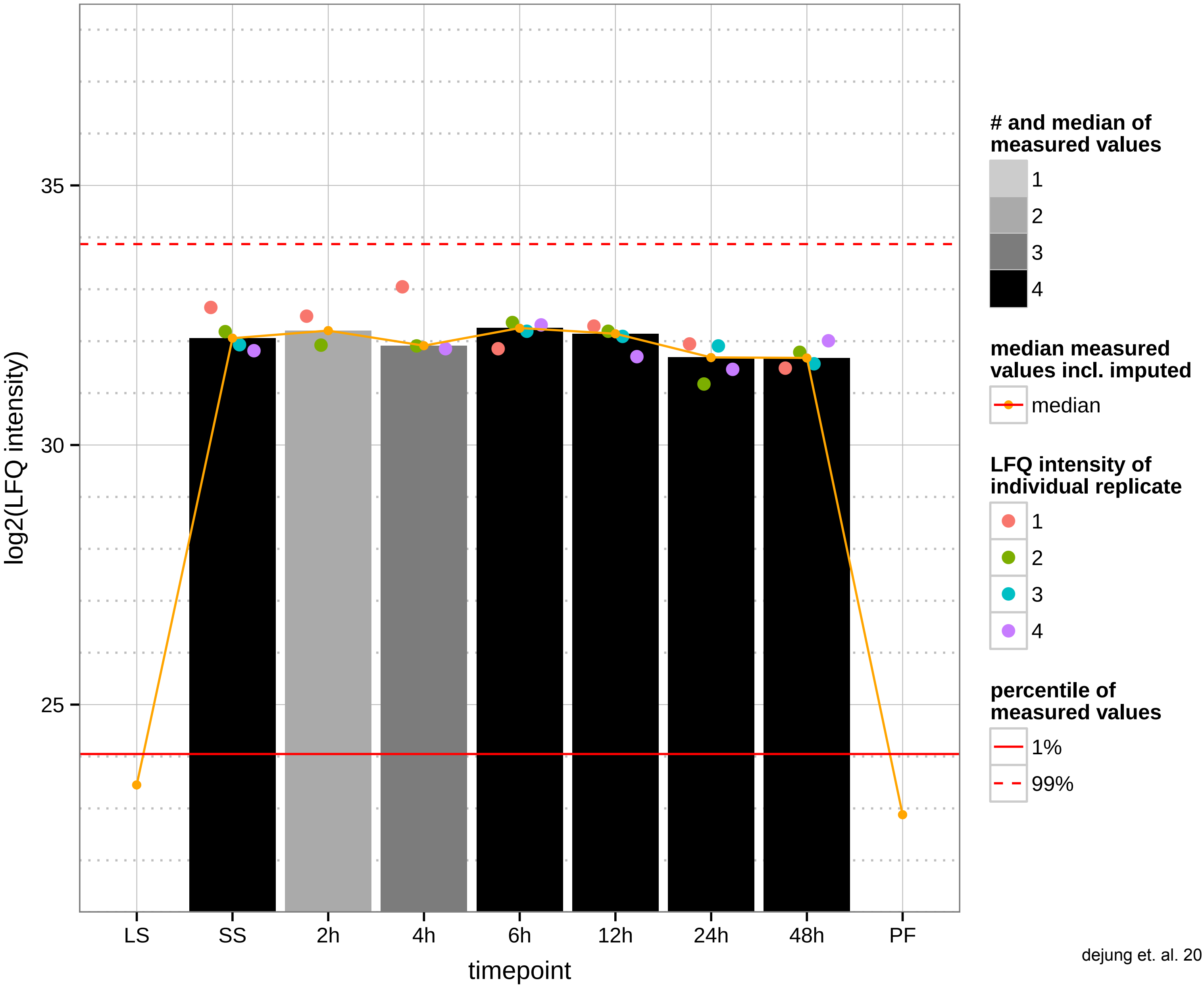
hypothetical protein, conserved
Tb927.10.8600
AGOF: null
AGOC: null
AGOP: retrograde transport, endosome to Golgi
PGOF: null
PGOC: null
PGOP: retrograde transport, endosome to Golgi





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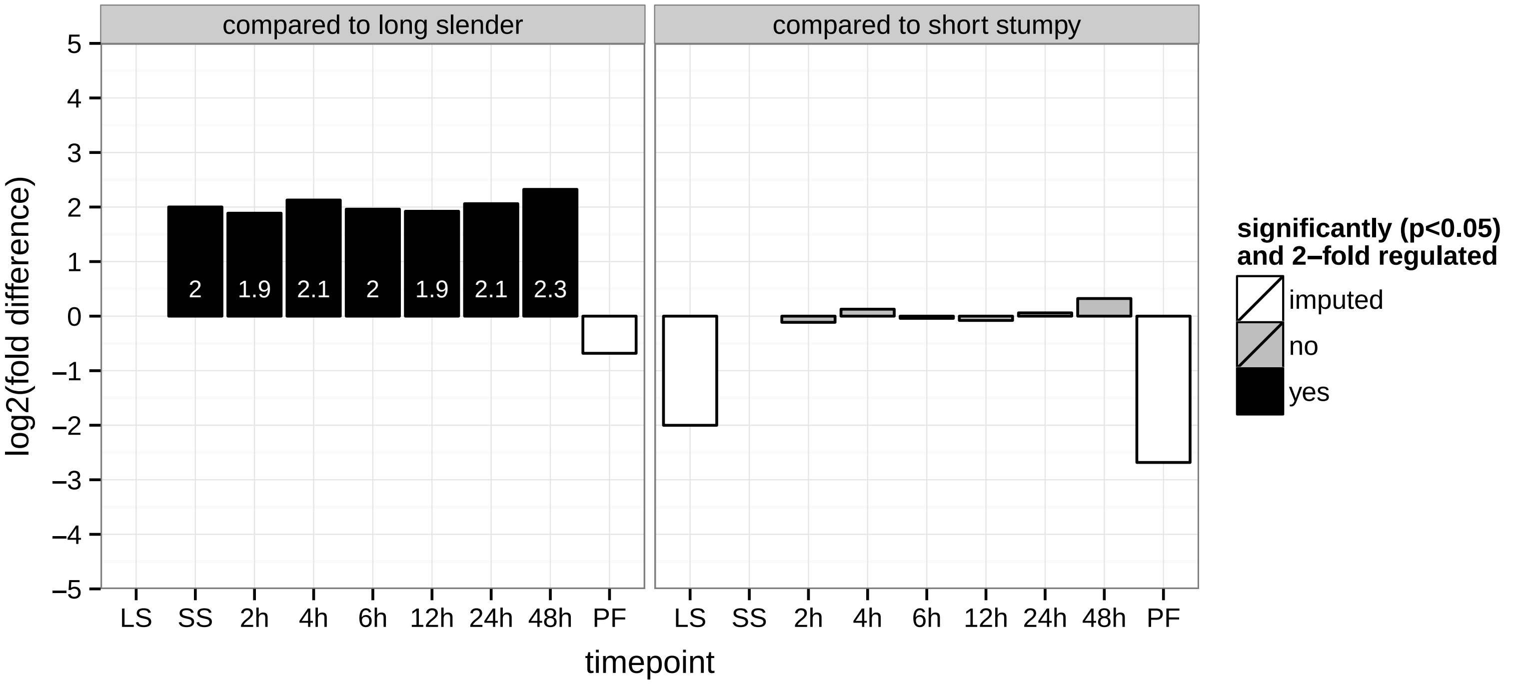
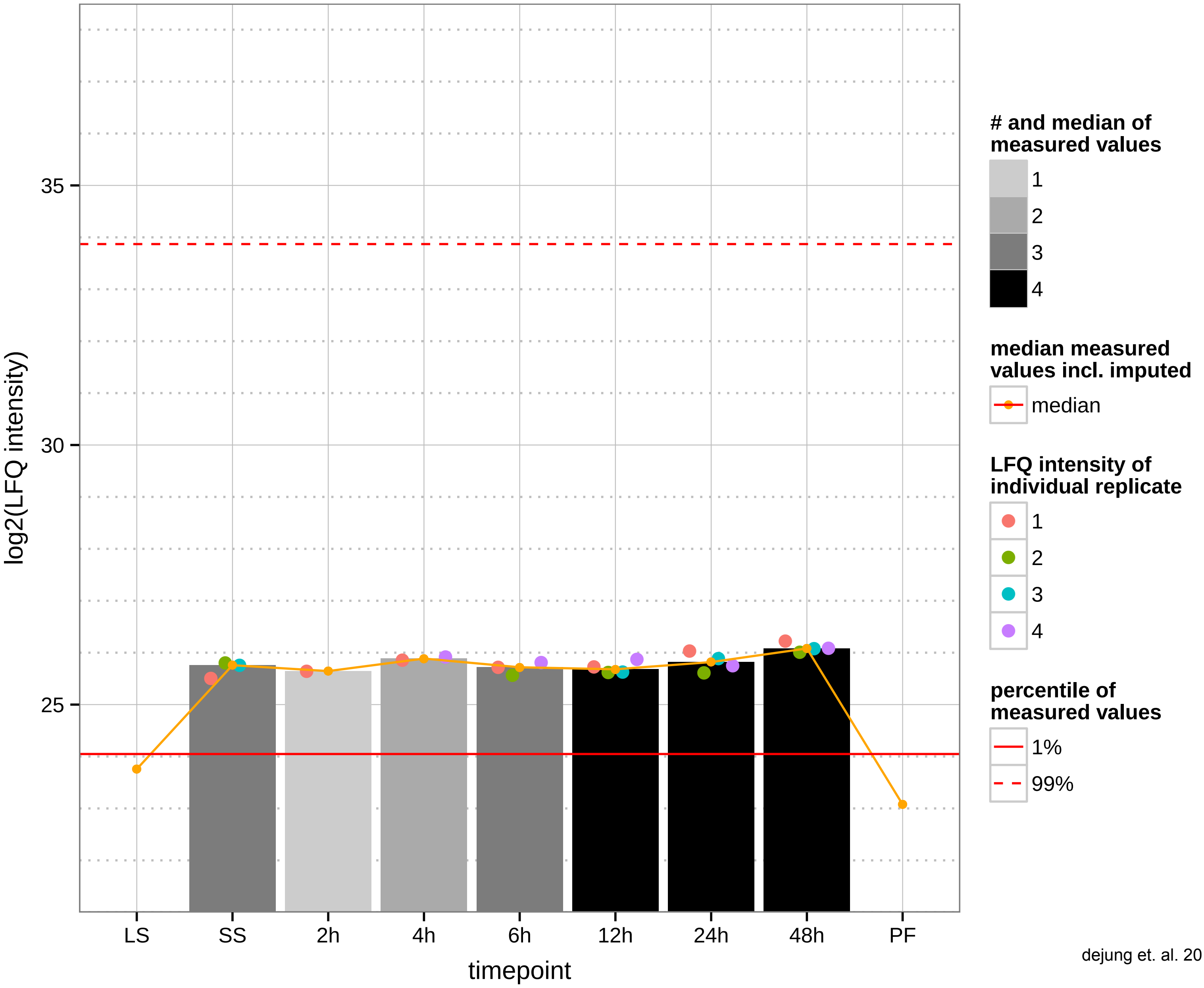
RNA polymerase–associated protein CDC73, putative
Tb927.11.10230
AGOF: RNA polymerase II core binding
AGOC: Cdc73/Paf1 complex
AGOP: positive regulation of transcription elongation from RNA polymerase II promoter
PGOF: null
PGOC: null
PGOP: null





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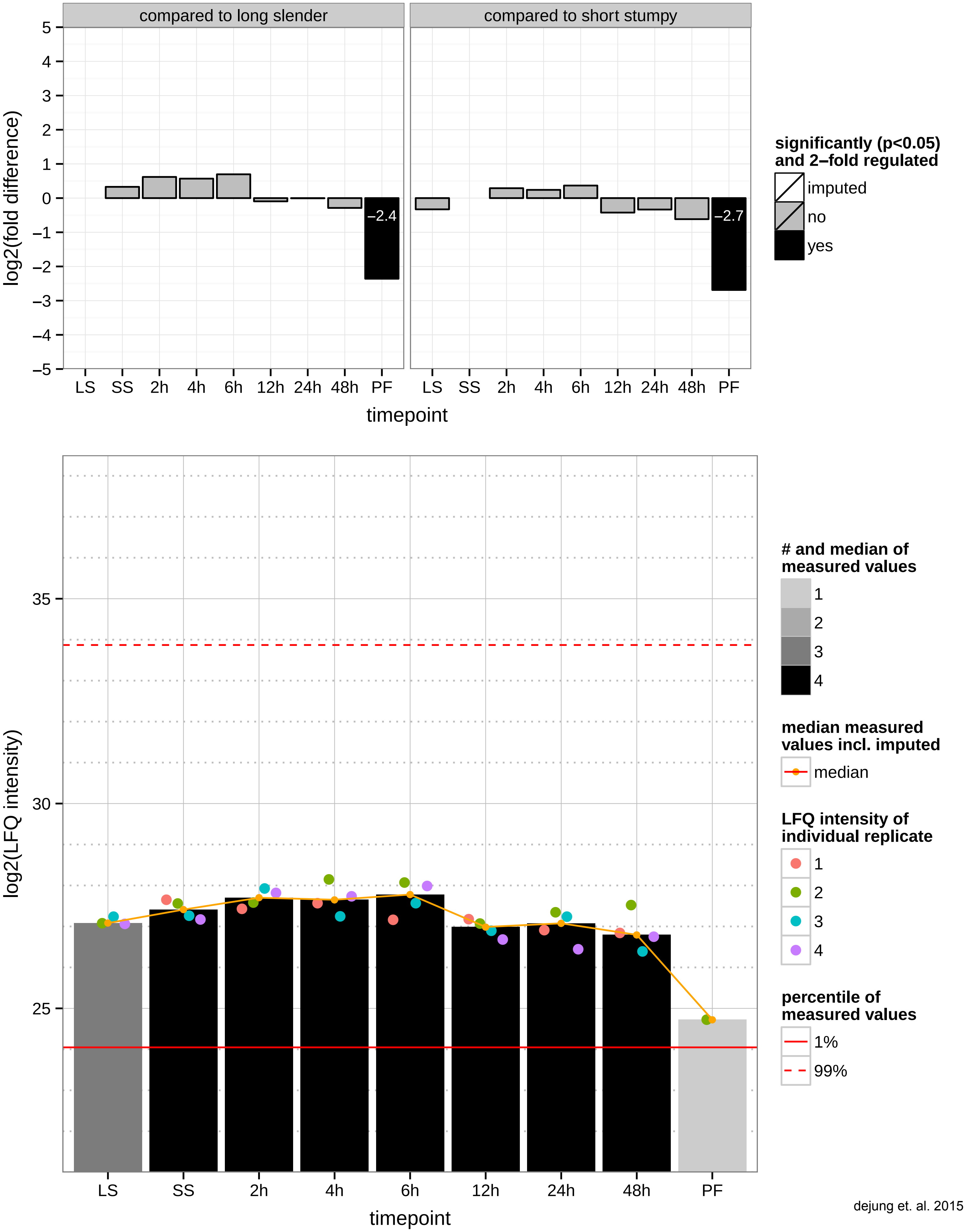
golgi SNARE protein–like, GOLGI SNAP receptor complex member, putative
Tb927.11.10270
AGOF: null
AGOC: membrane
AGOP: intracellular protein transport
PGOF: null
PGOC: null
PGOP: null



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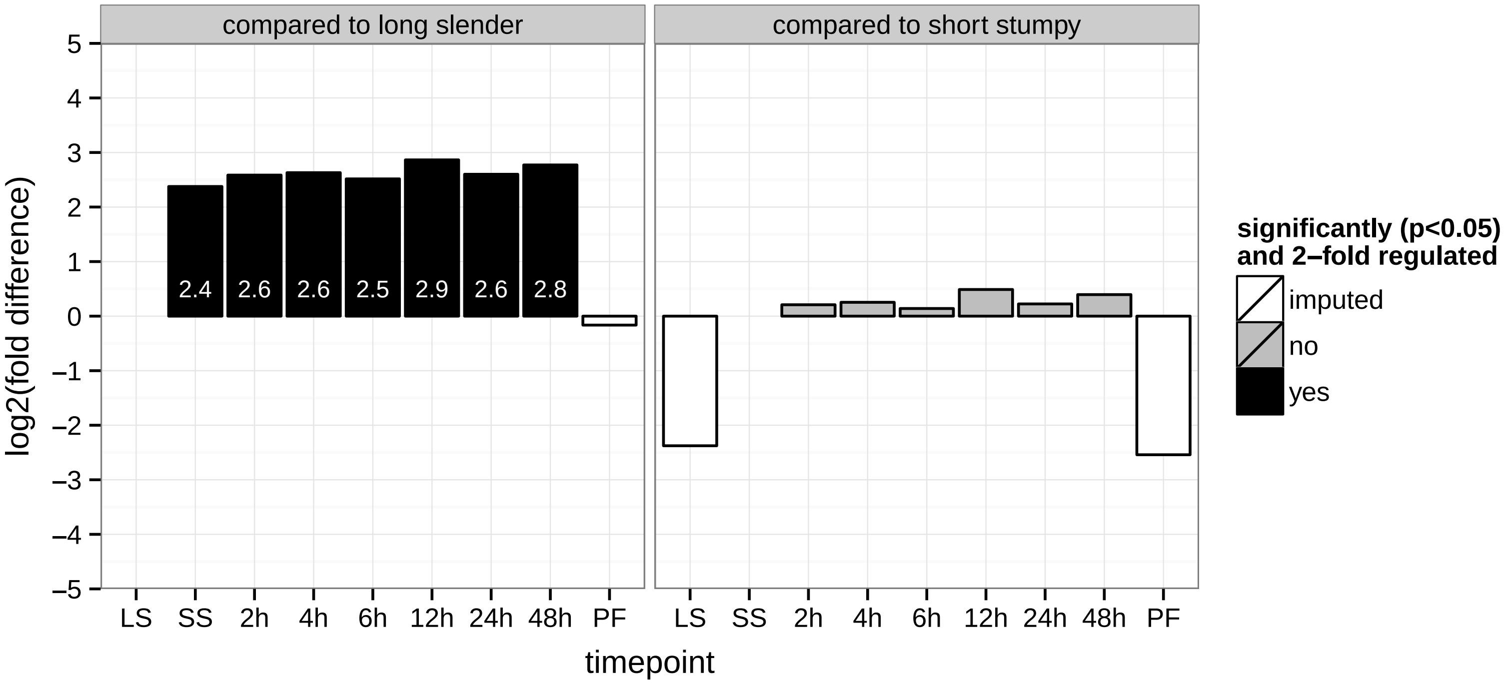
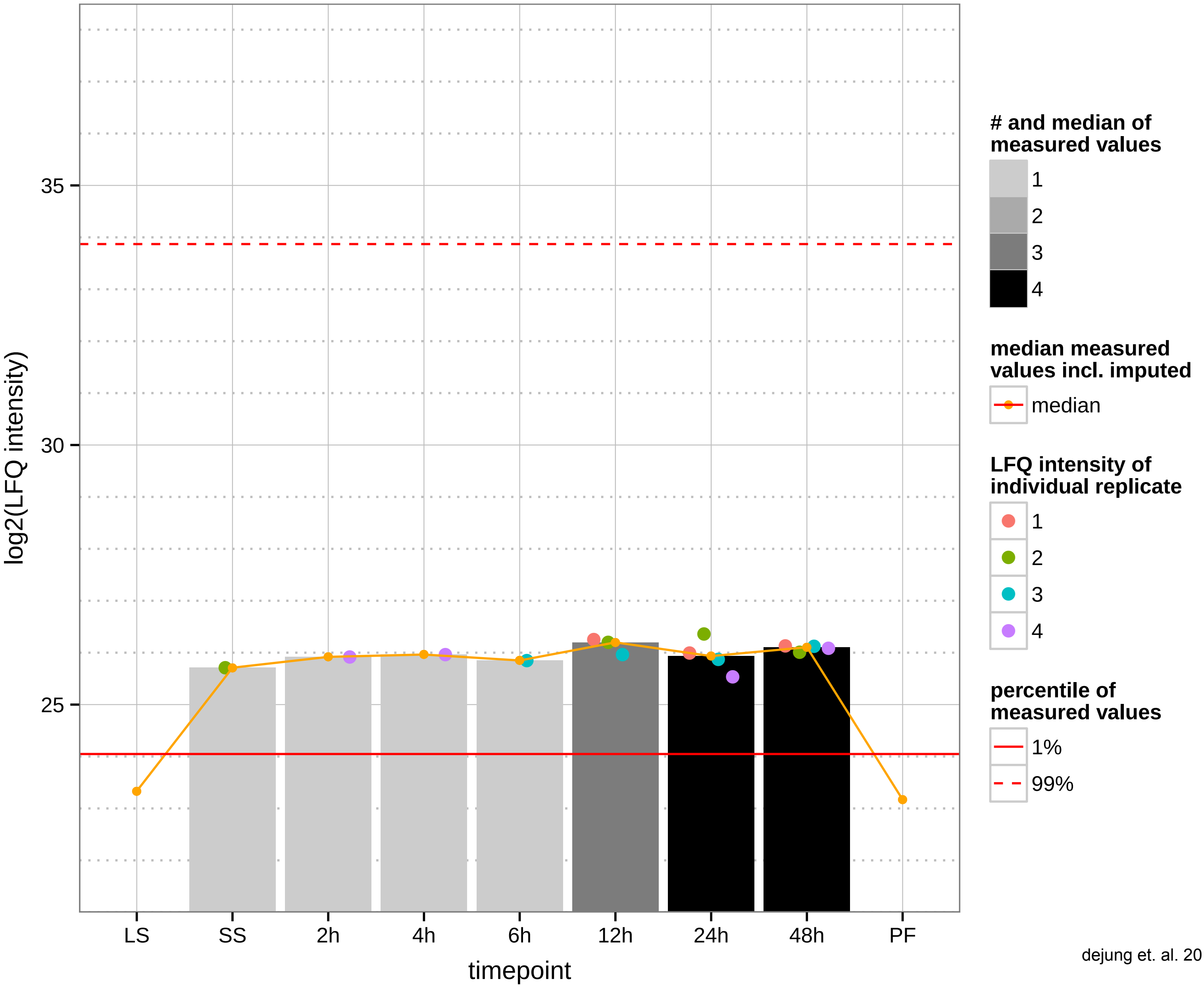
hypothetical protein, conserved
Tb927.11.10620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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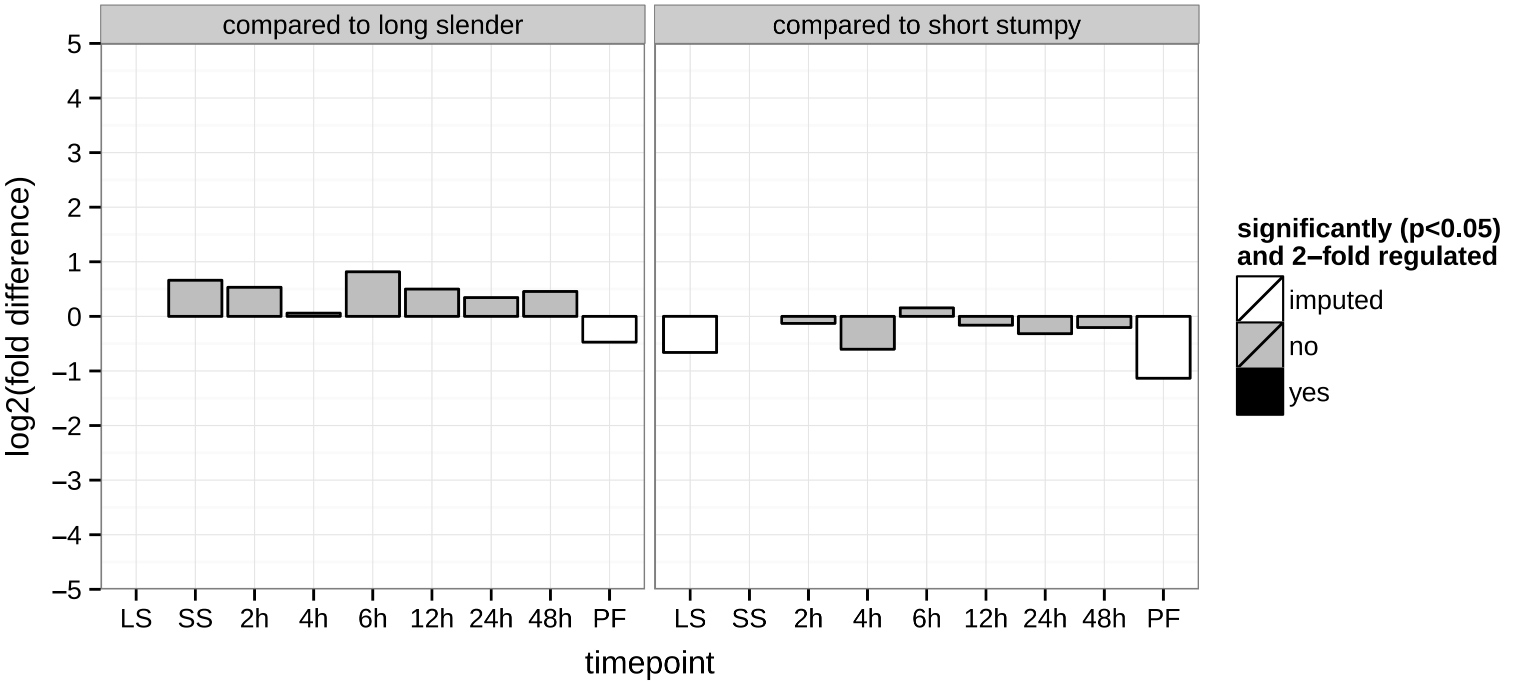
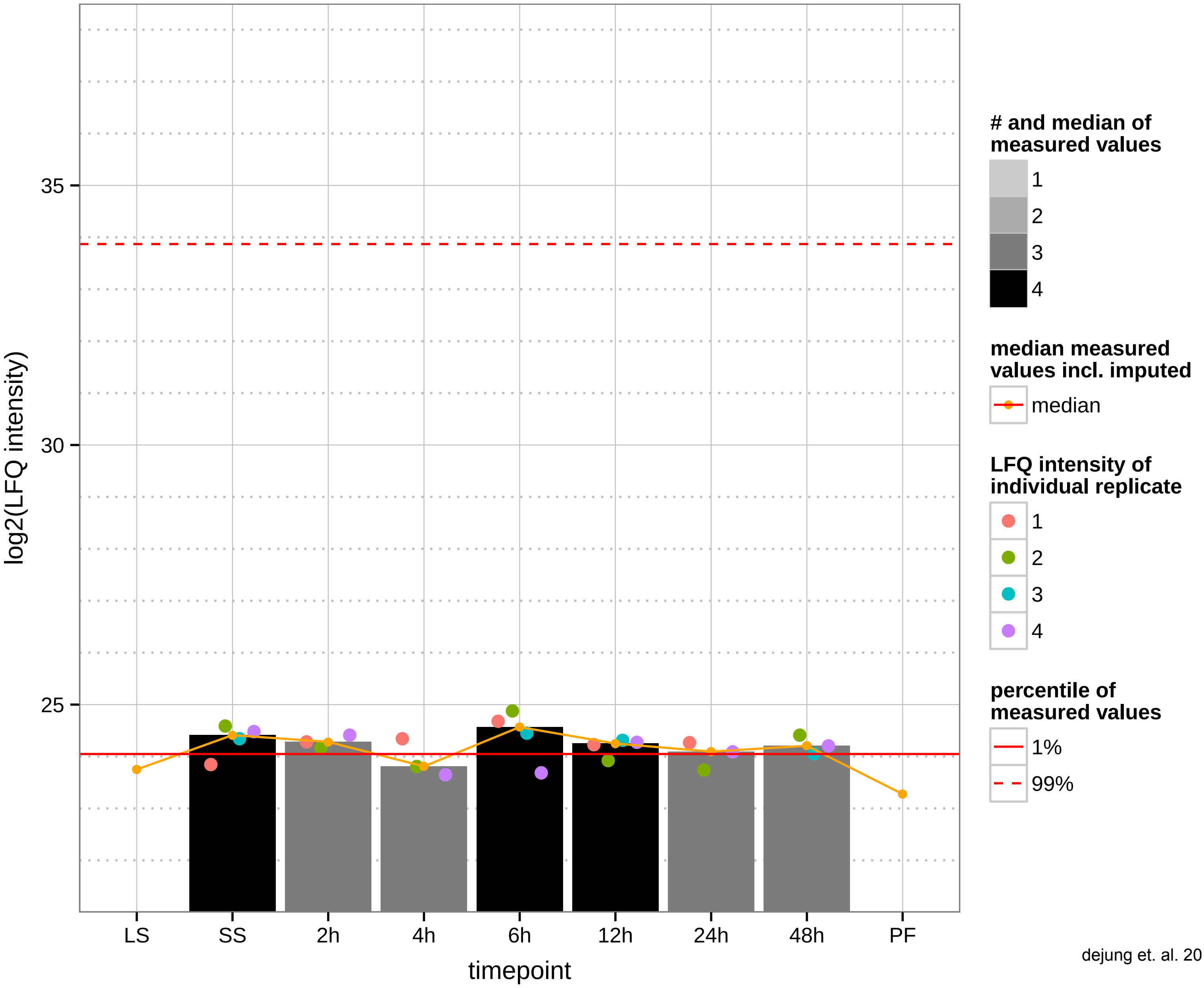
SNF2 DNA repair protein, putative, ATP–dependent helicase, SNF2 family helicase
Tb927.11.10730
AGOF: ATP binding, ATPase activity, DNA binding, helicase activity
AGOC: null
AGOP: chromatin remodeling, meiosis
PGOF: ATP binding, DNA binding, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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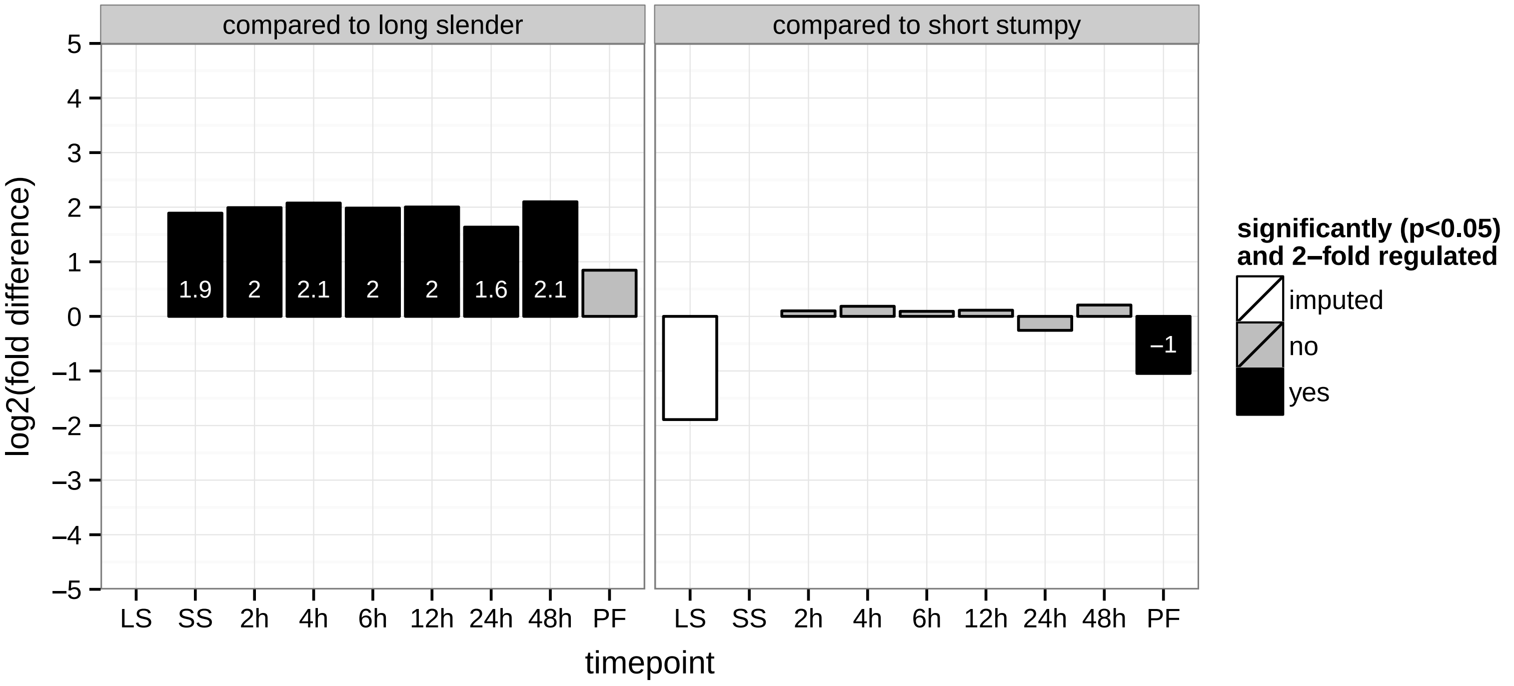
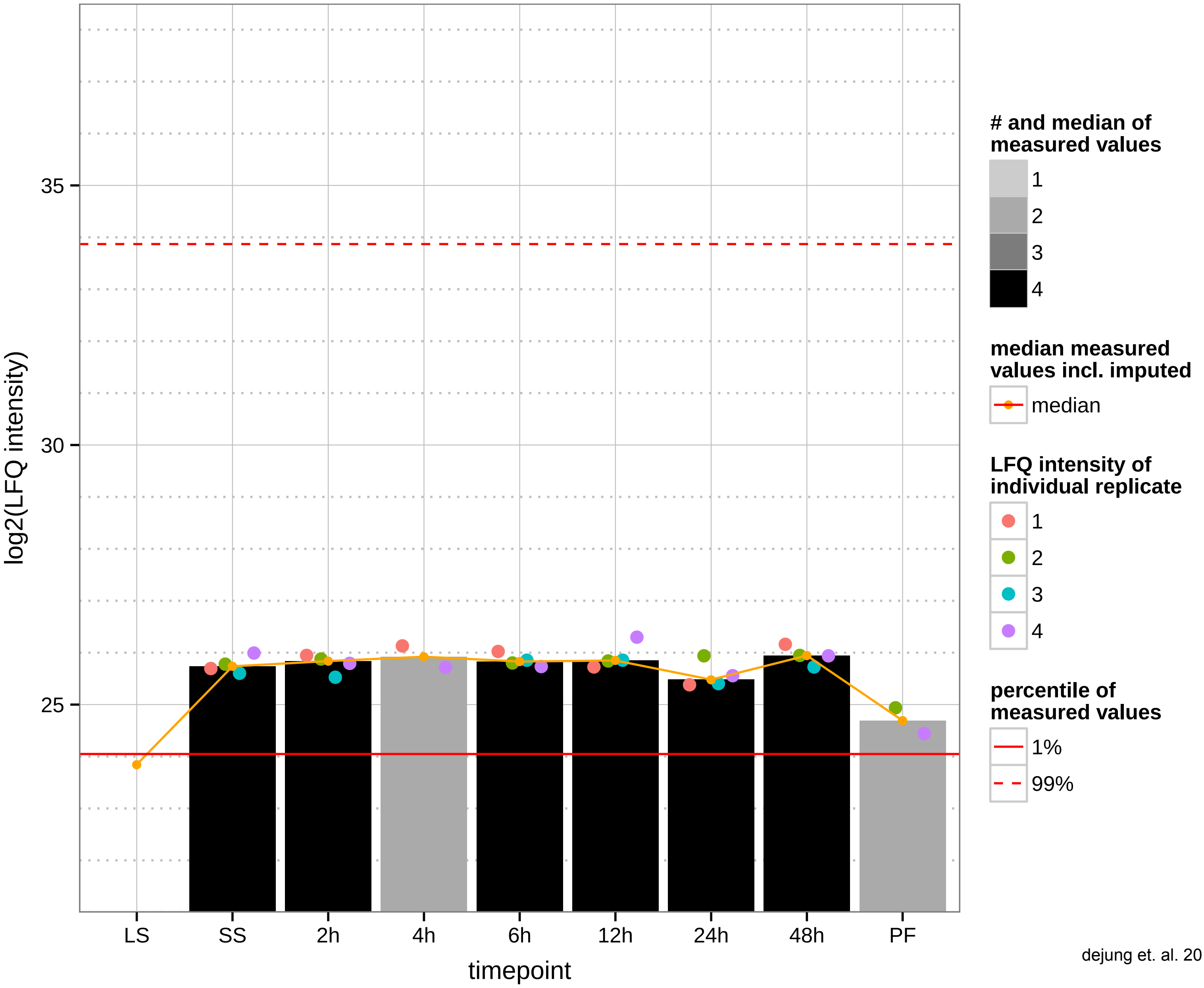
MENG
Tb927.11.10900
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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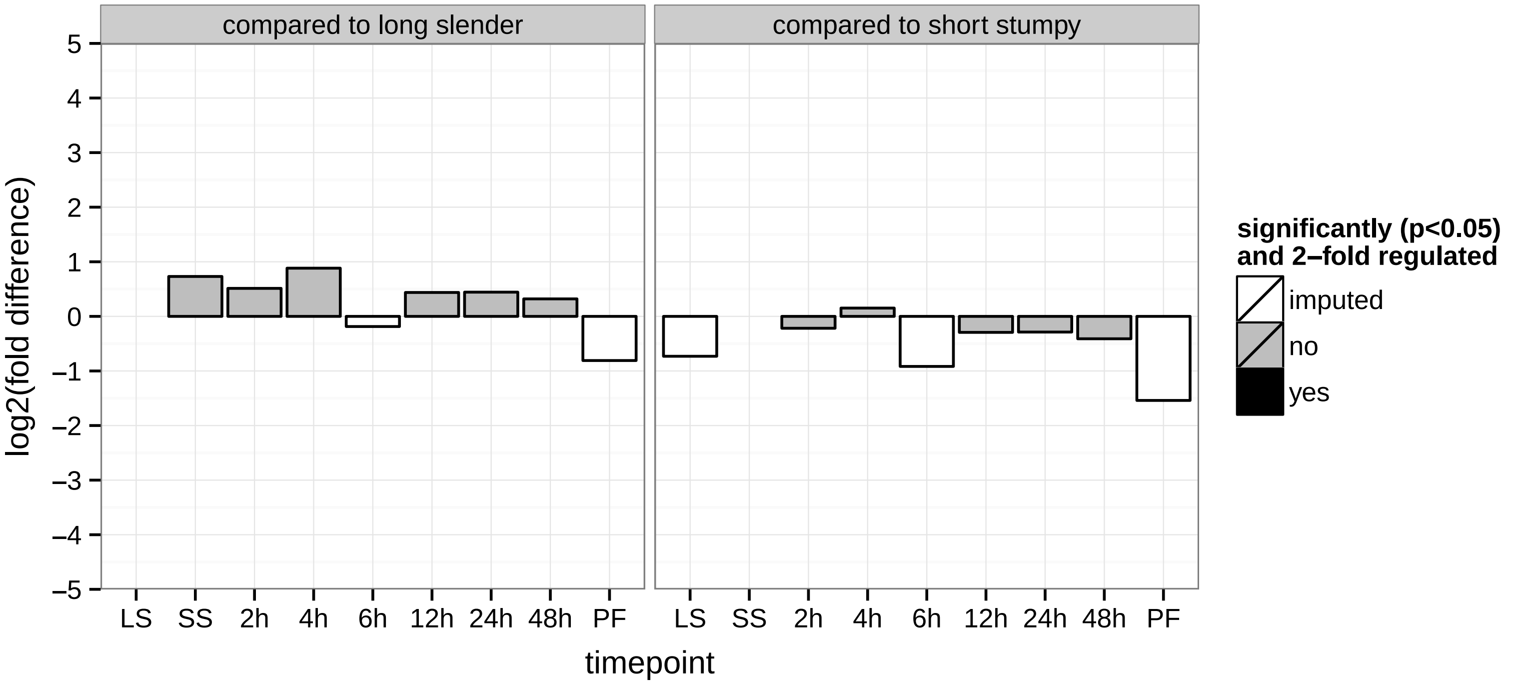
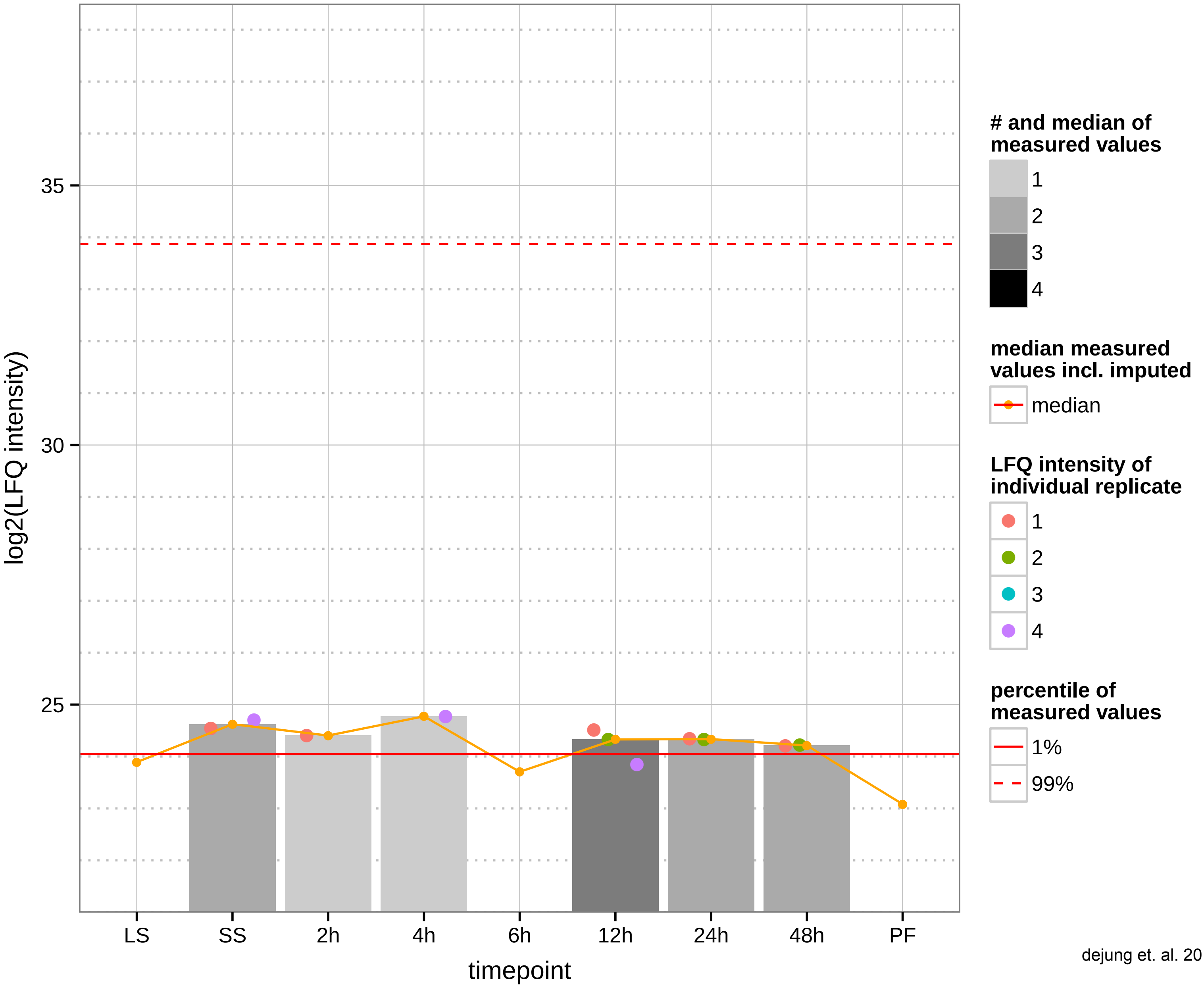
hypothetical protein, conserved
Tb927.11.10970
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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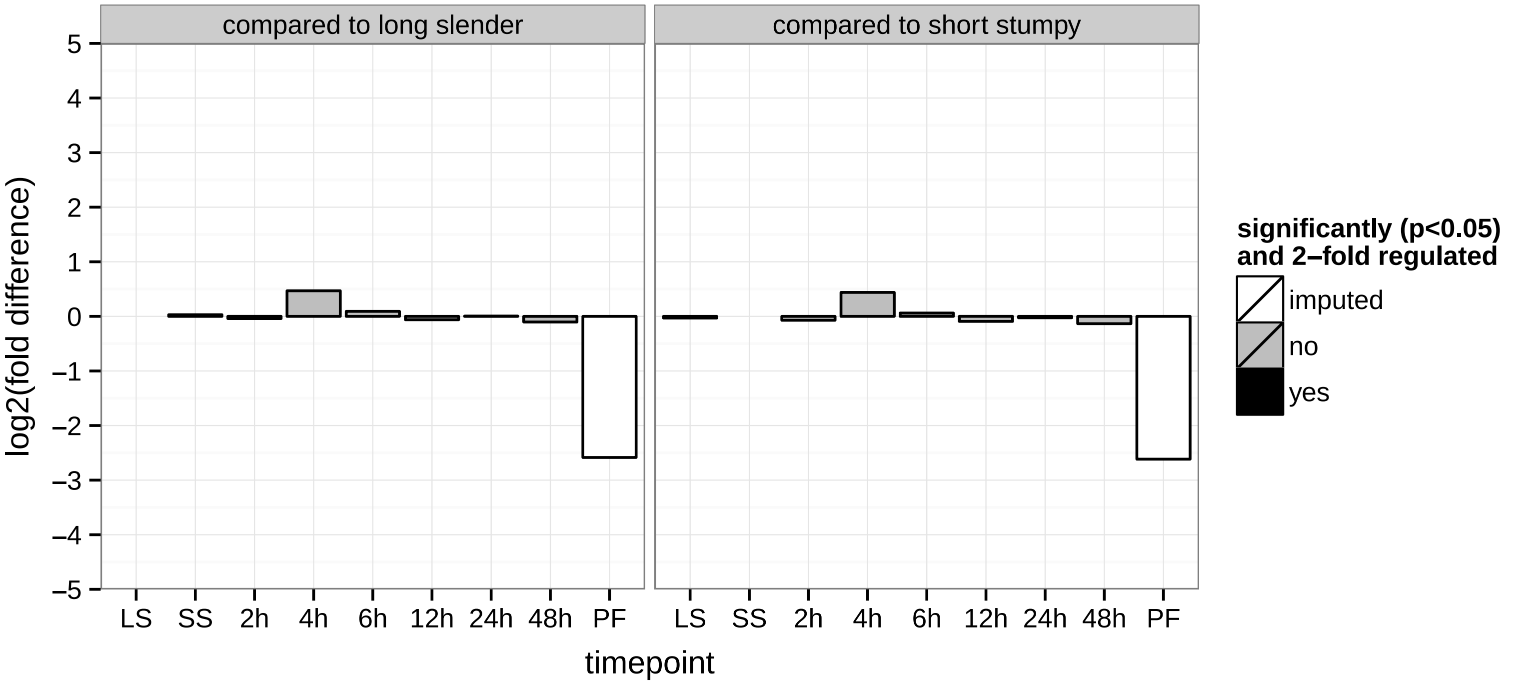
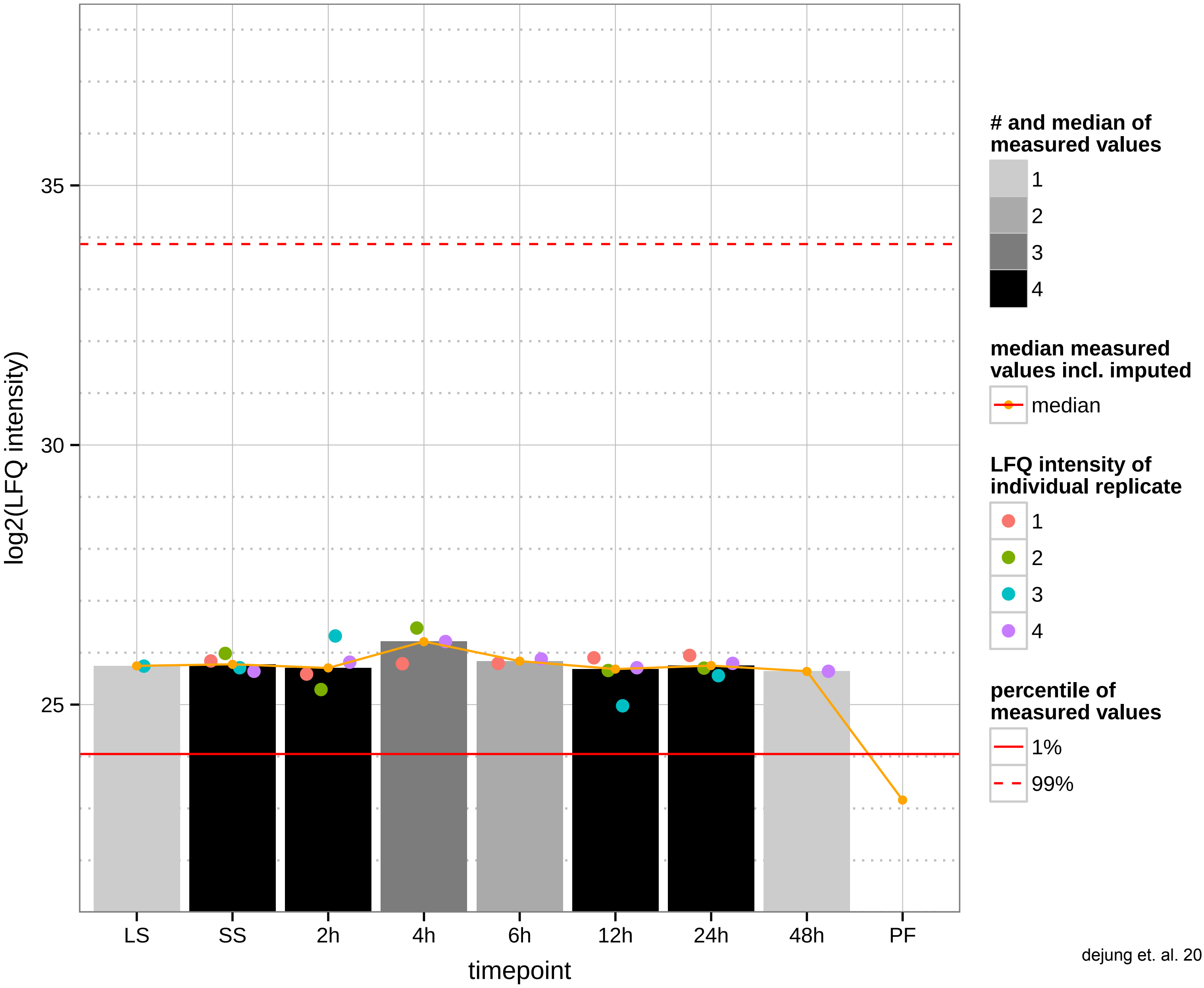
glucosamine 6−phosphate n−acetyltransferase (GNA1)
Tb927.11.11100
AGOF: glucosamine 6−phosphate N−acetyltransferase activity
AGOC: glycosome
AGOP: N−acetylglucosamine metabolic process, metabolic process
PGOF: N−acetyltransferase activity
PGOC: null
PGOP: null





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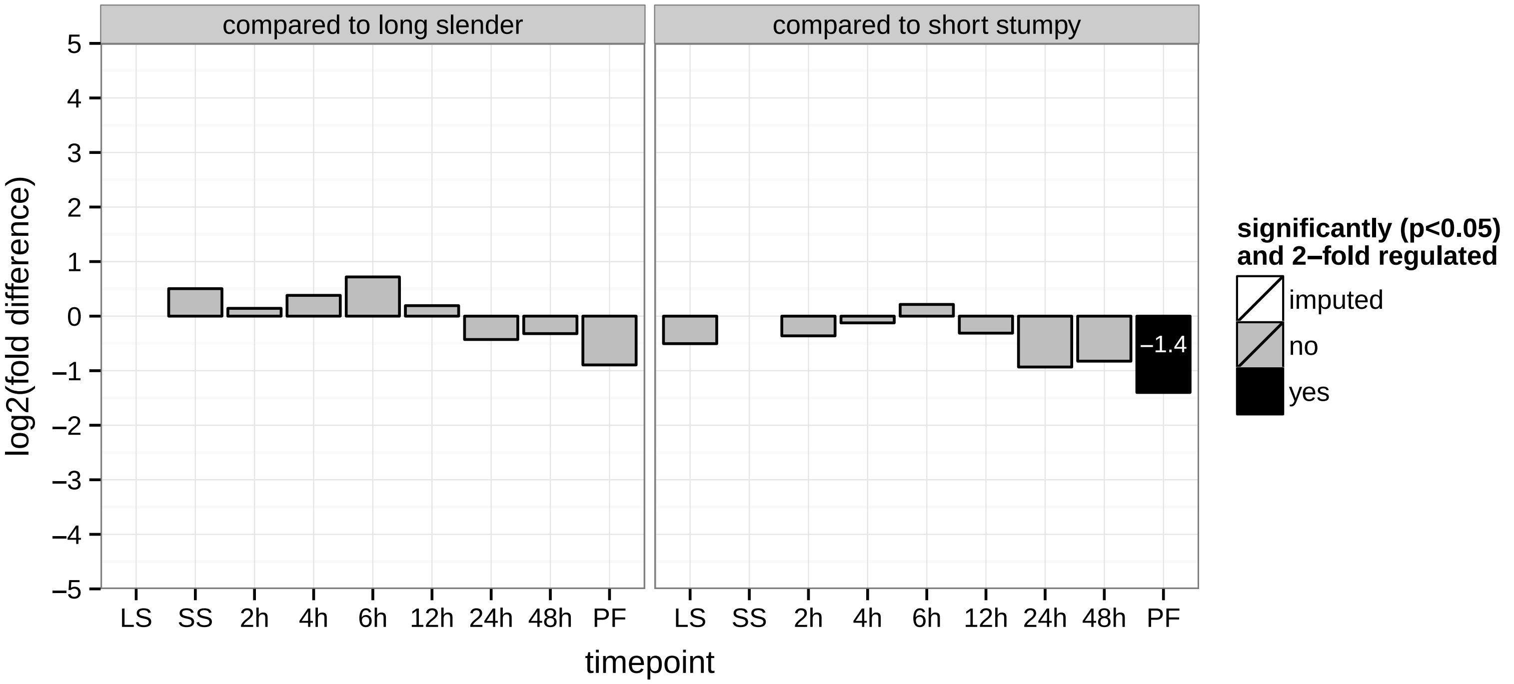
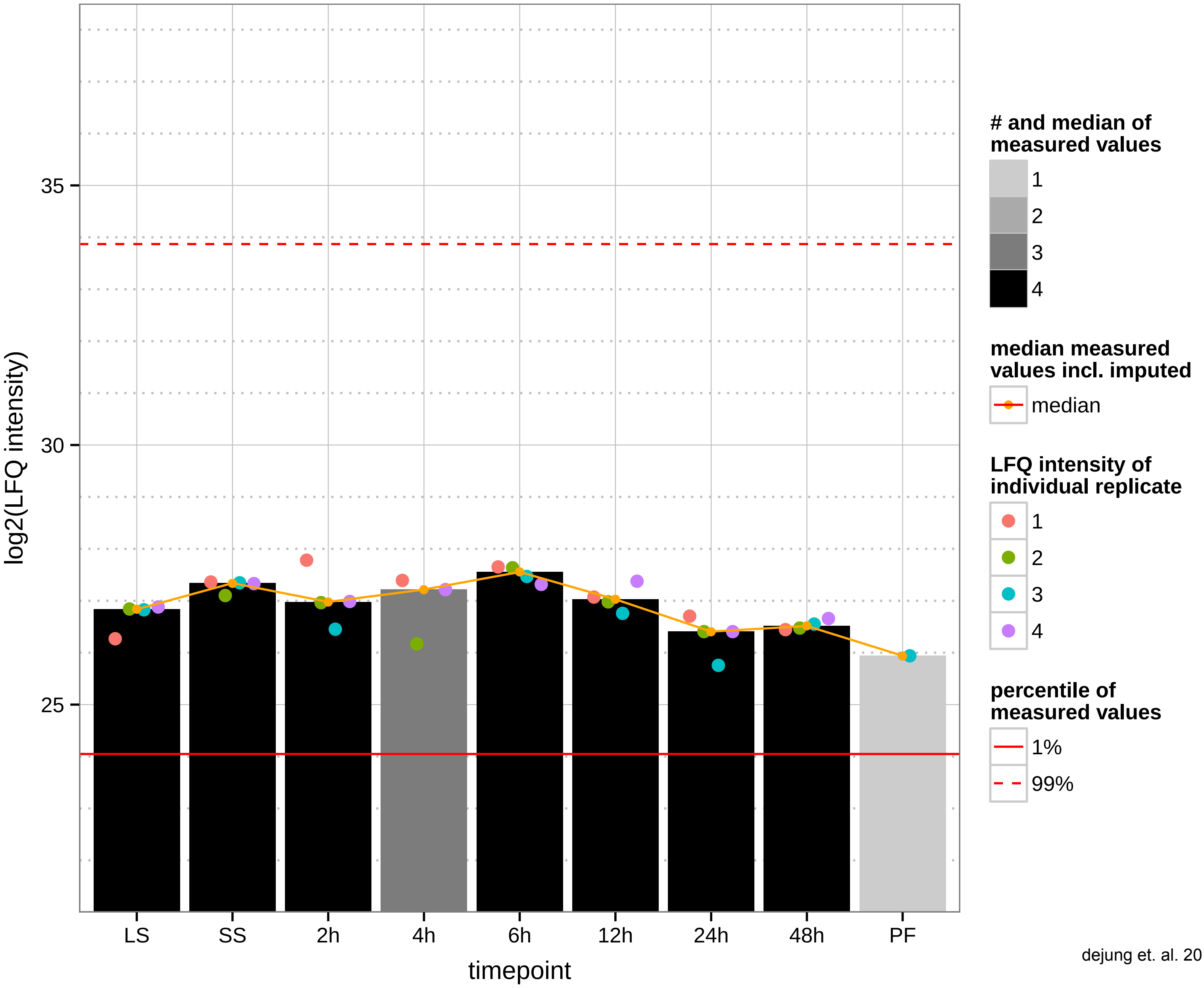
hypothetical protein
Tb927.11.11140
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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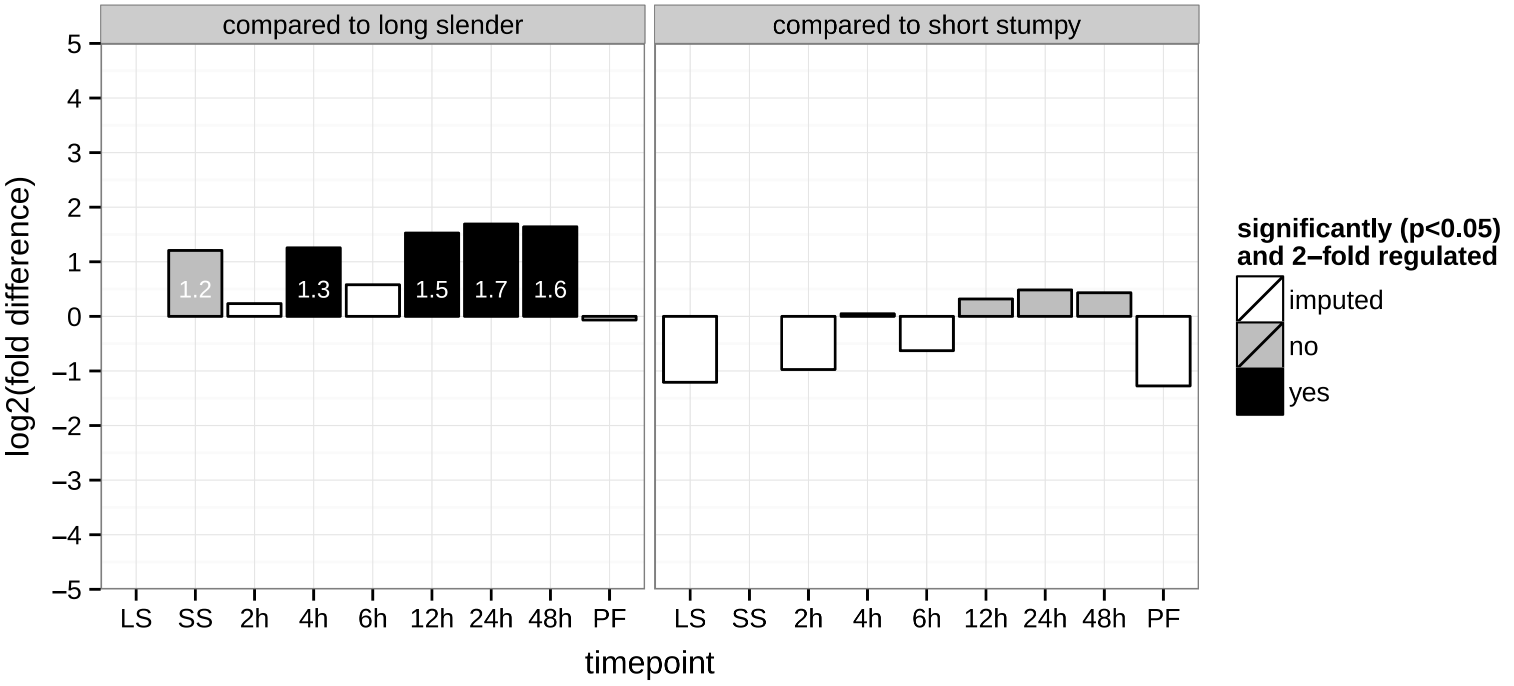
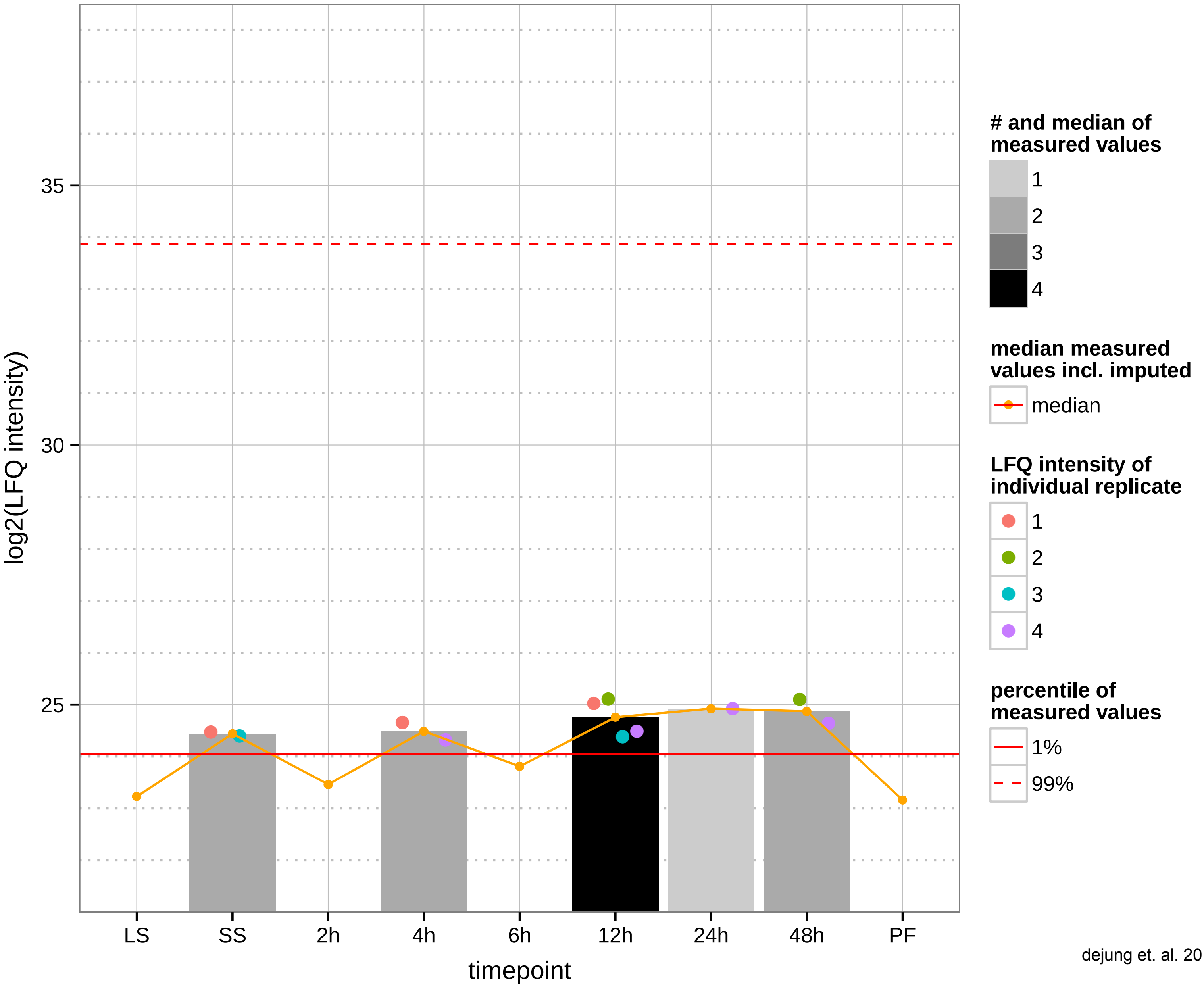
hypothetical protein, conserved
Tb927.11.11610
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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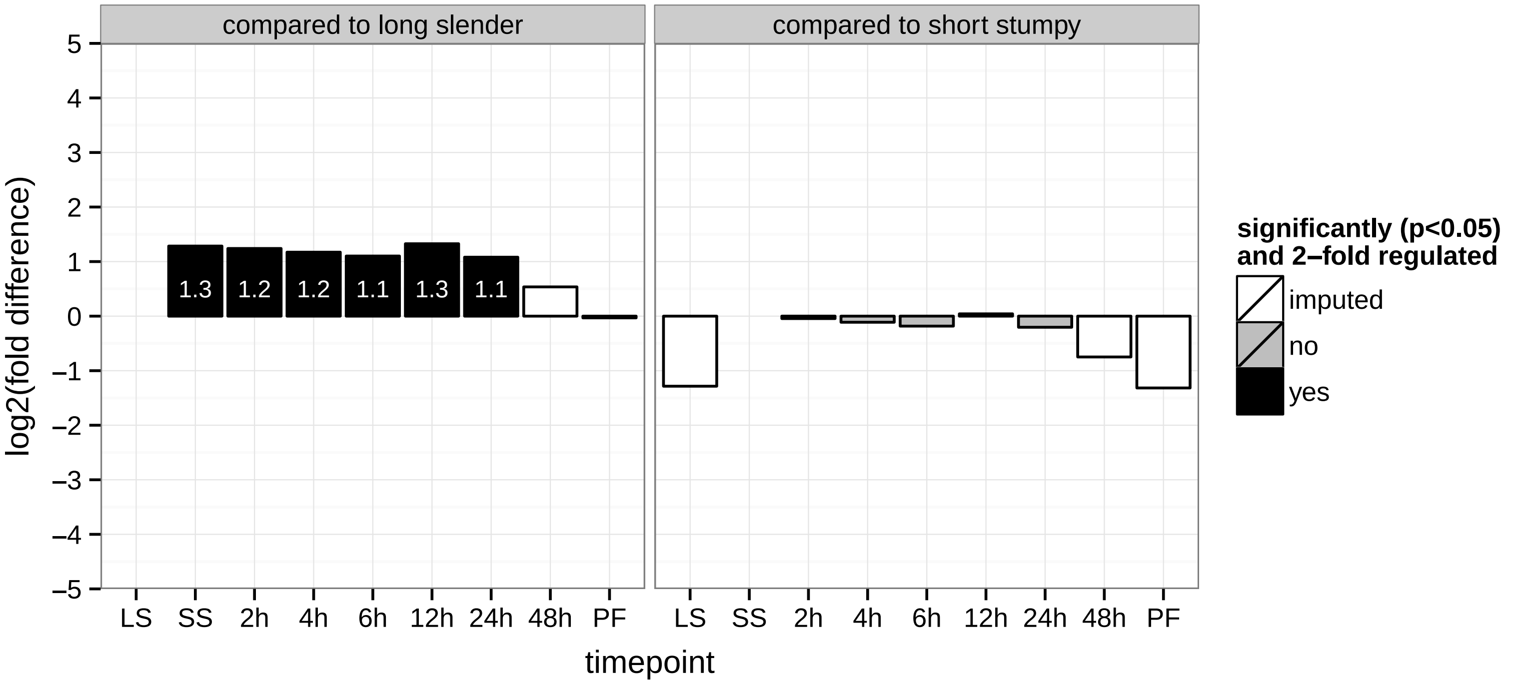
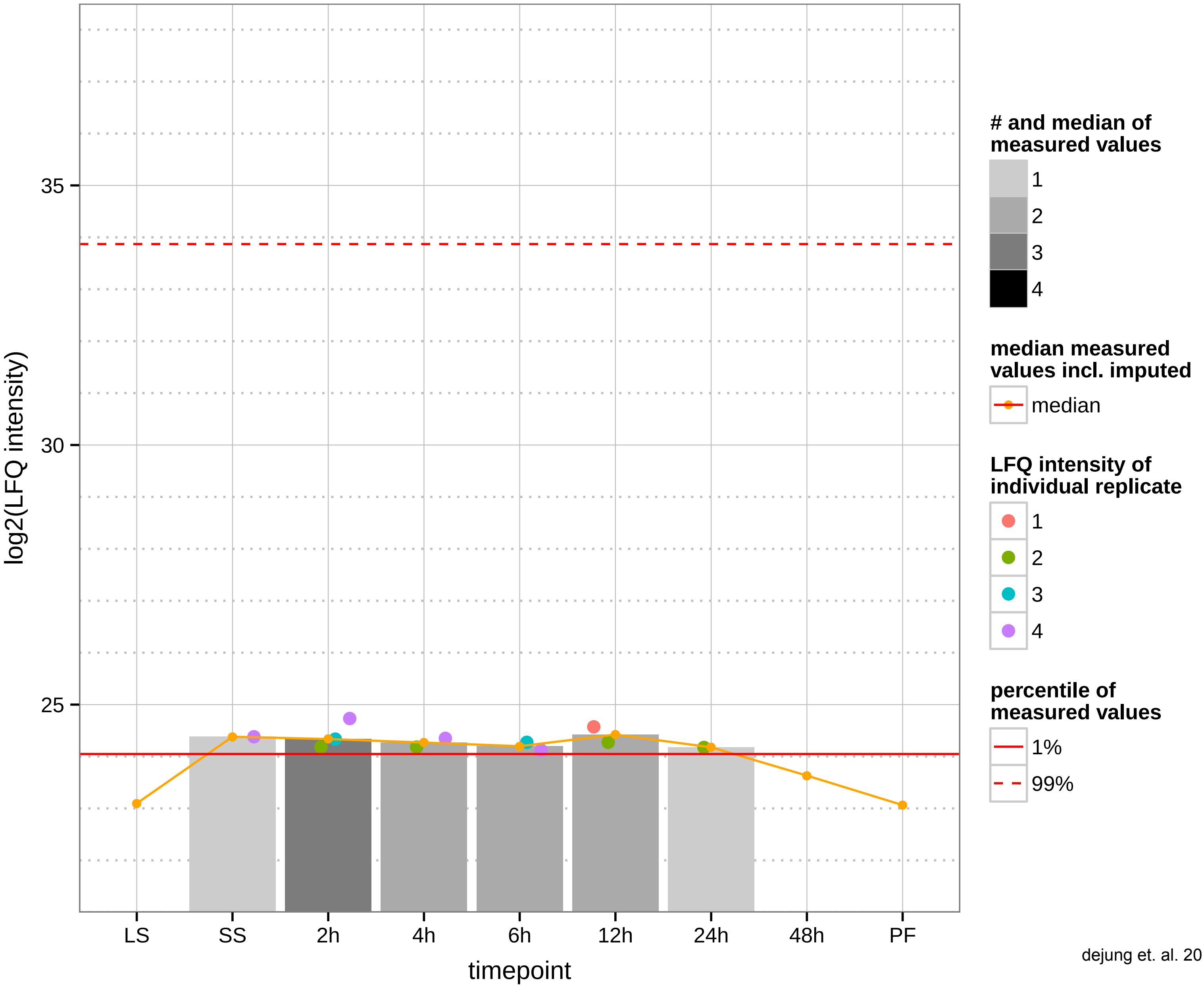
leucine–rich repeat protein (LRRP), putative
Tb927.11.11860
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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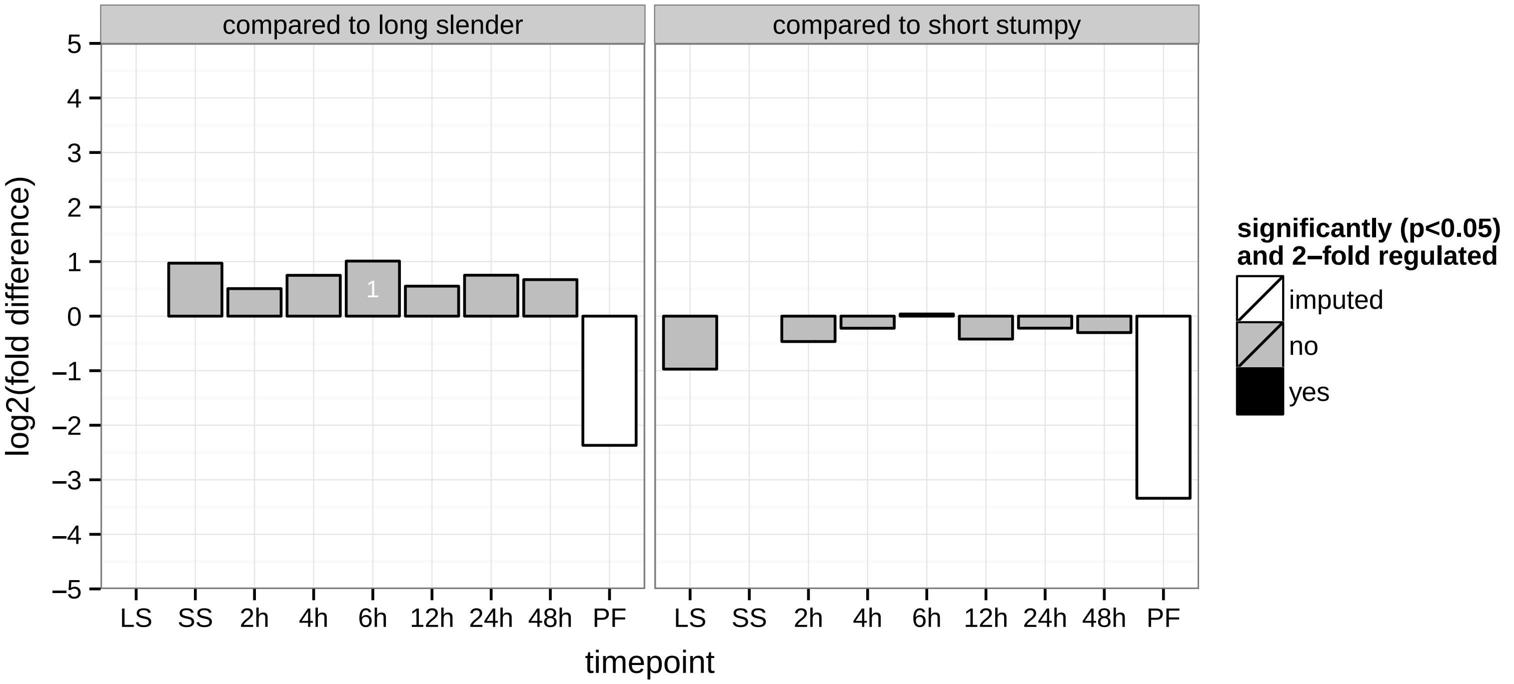
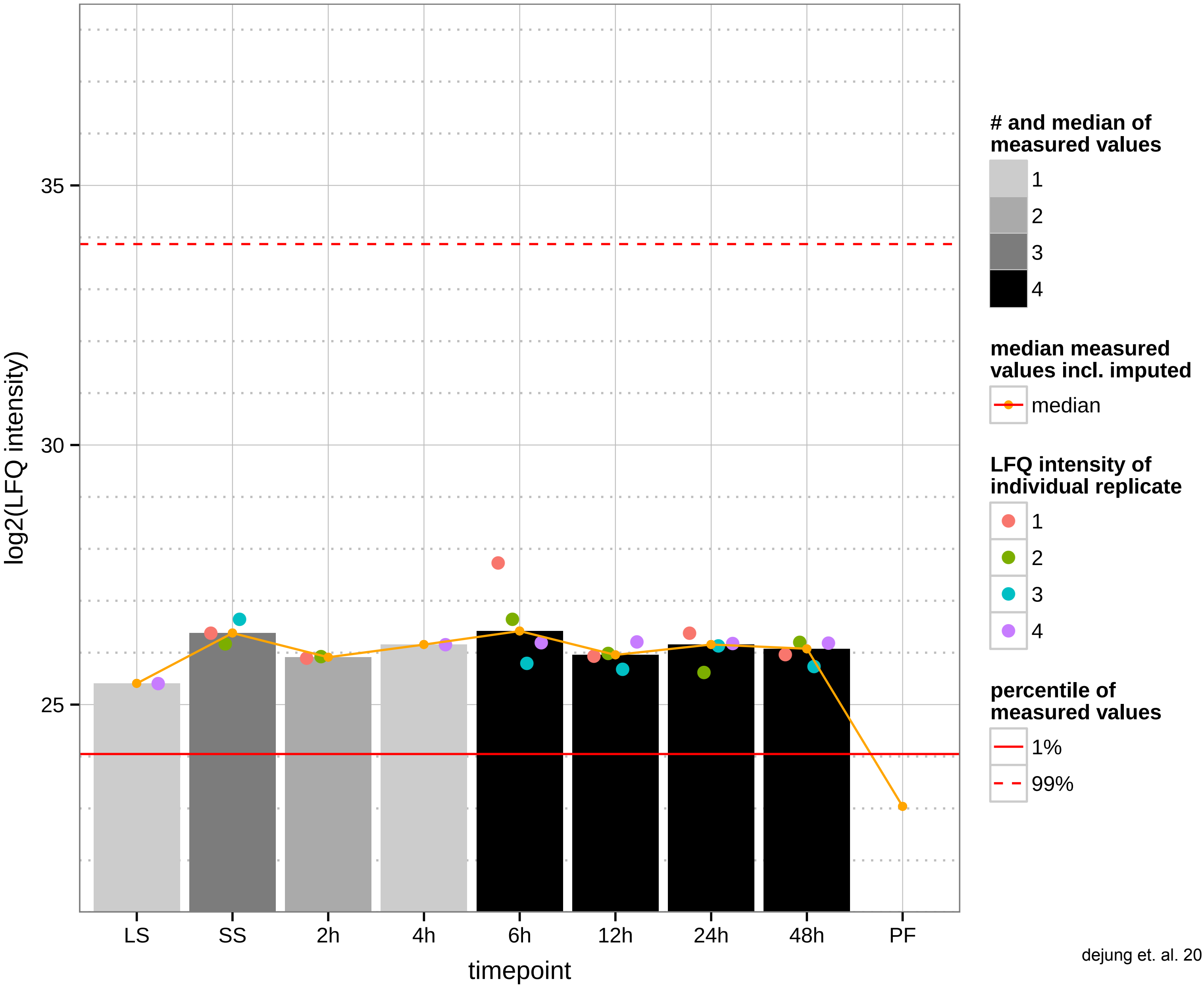
copper–transporting ATPase–like protein, putative
Tb927.11.1260
AGOF: ATP binding, copper ion transmembrane transporter activity, copper–exporting ATPase activity, metal ion binding
AGOC: integral to membrane, membrane
AGOP: ATP biosynthetic process, copper ion transport, metabolic process
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, catalytic acti
PGOC: integral to membrane, membrane
PGOP: ATP biosynthetic process, cation transport, metabolic process, metal ion transport





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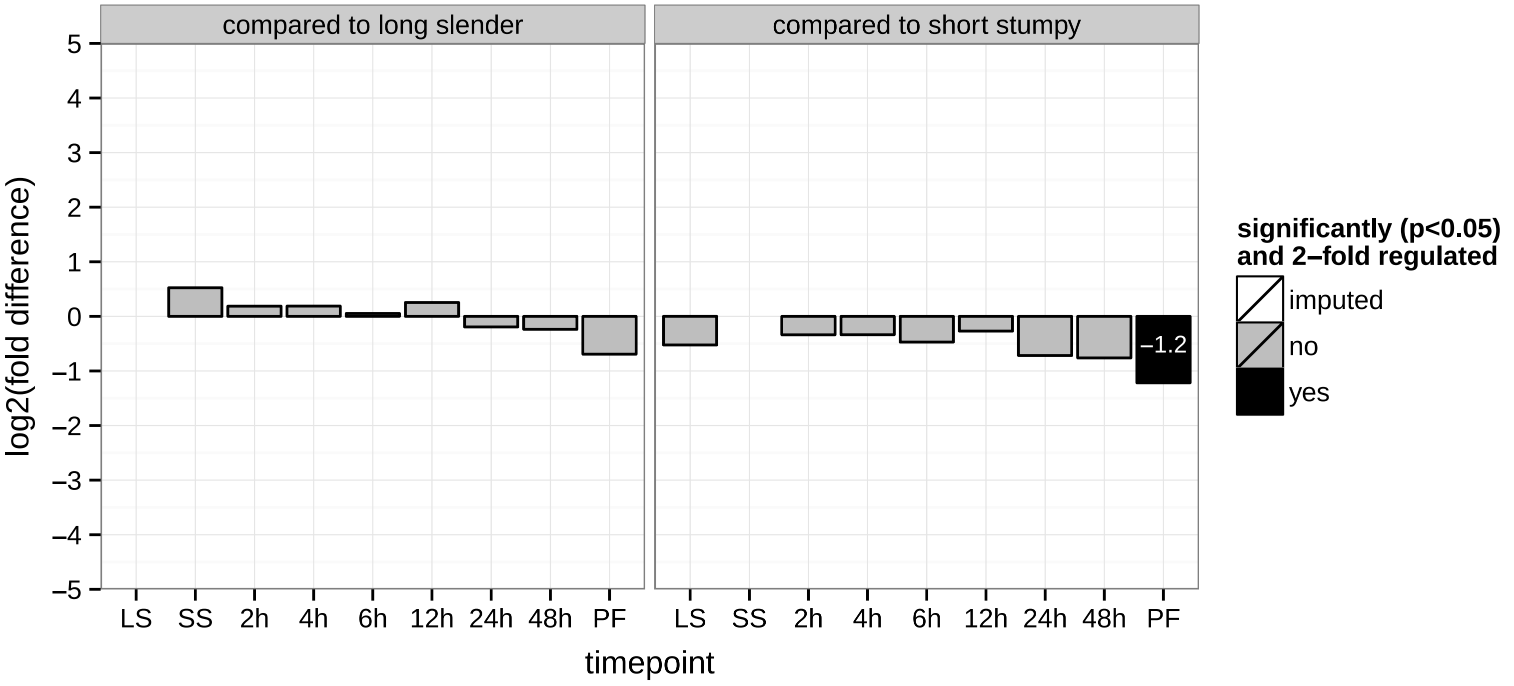
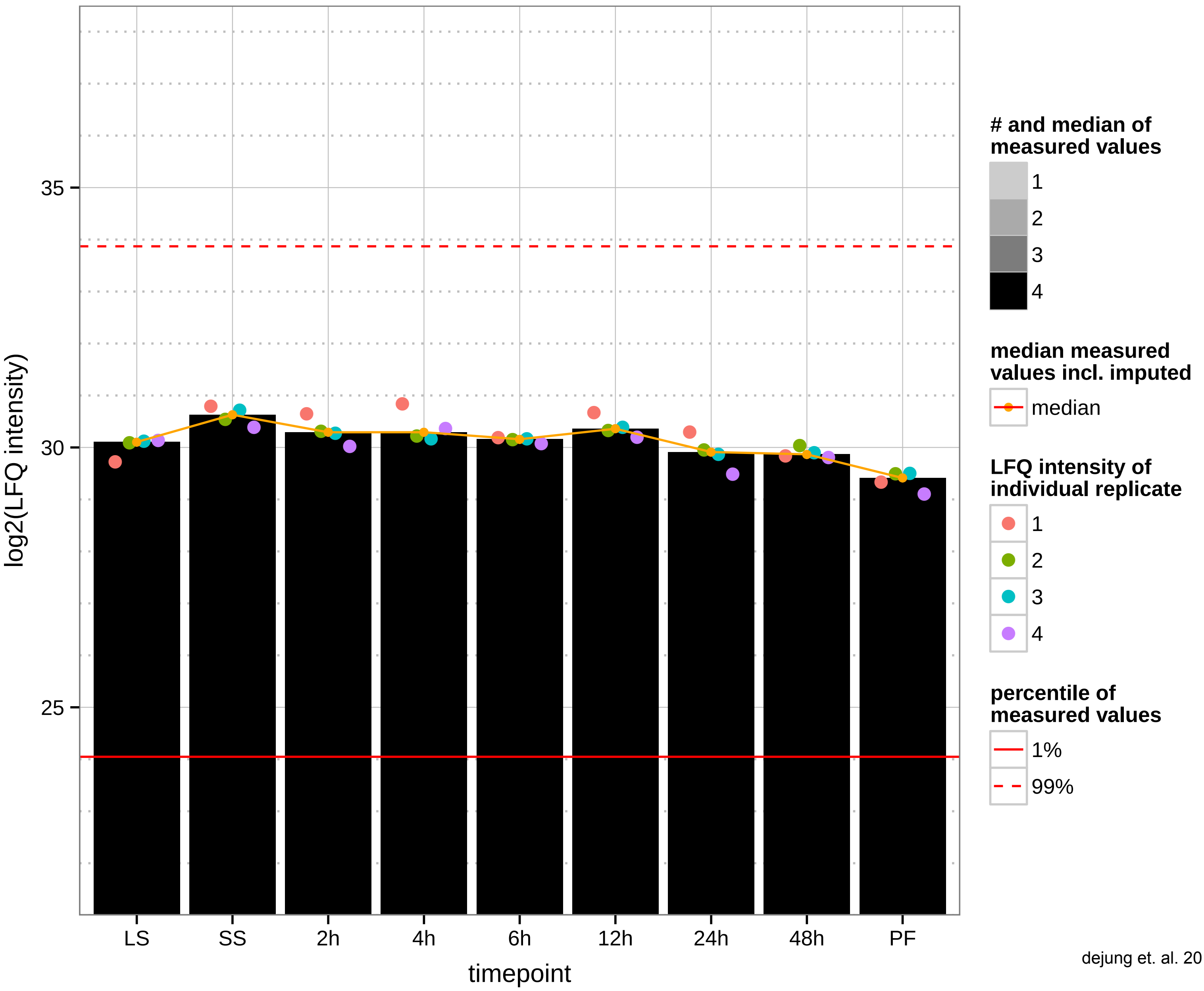
hypothetical protein, conserved
Tb927.11.13230
AGOF: structural molecule activity
AGOC: null
AGOP: null
PGOF: structural molecule activity
PGOC: null
PGOP: null





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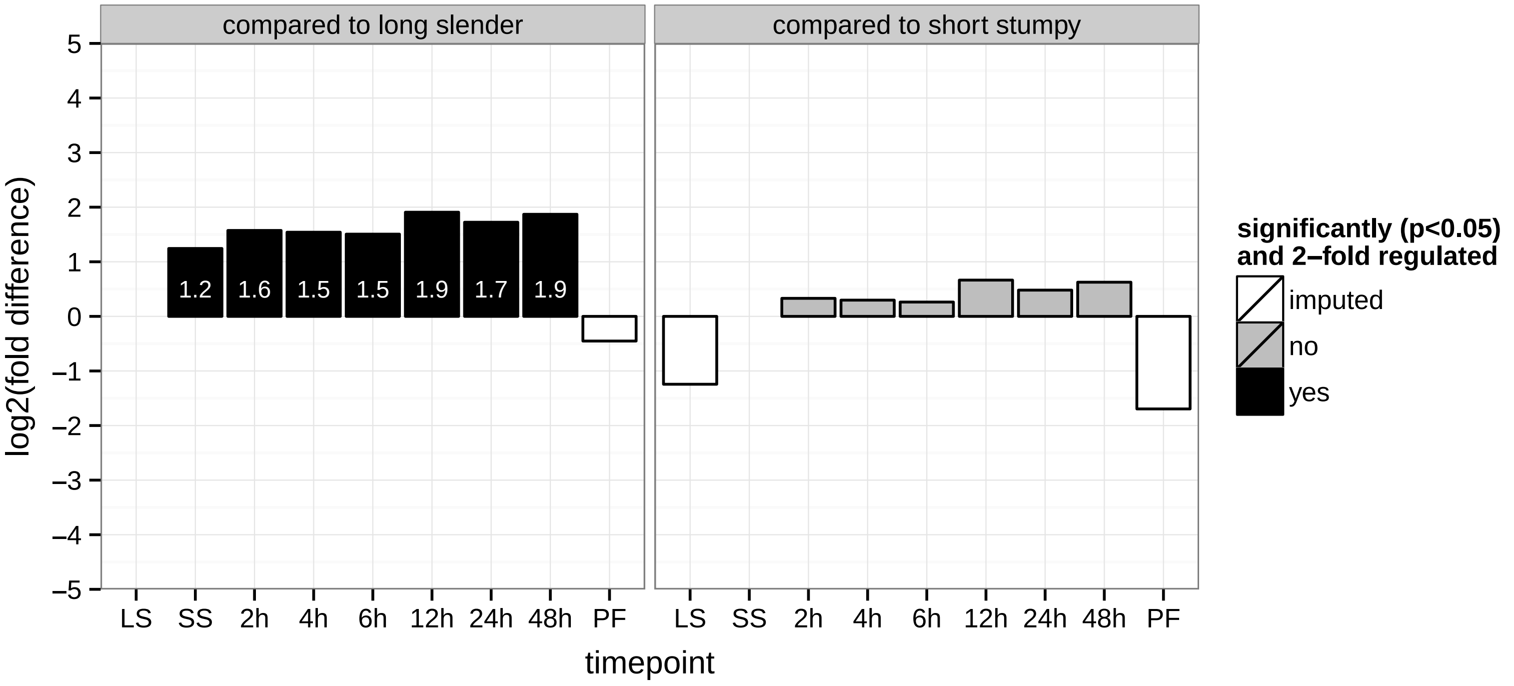
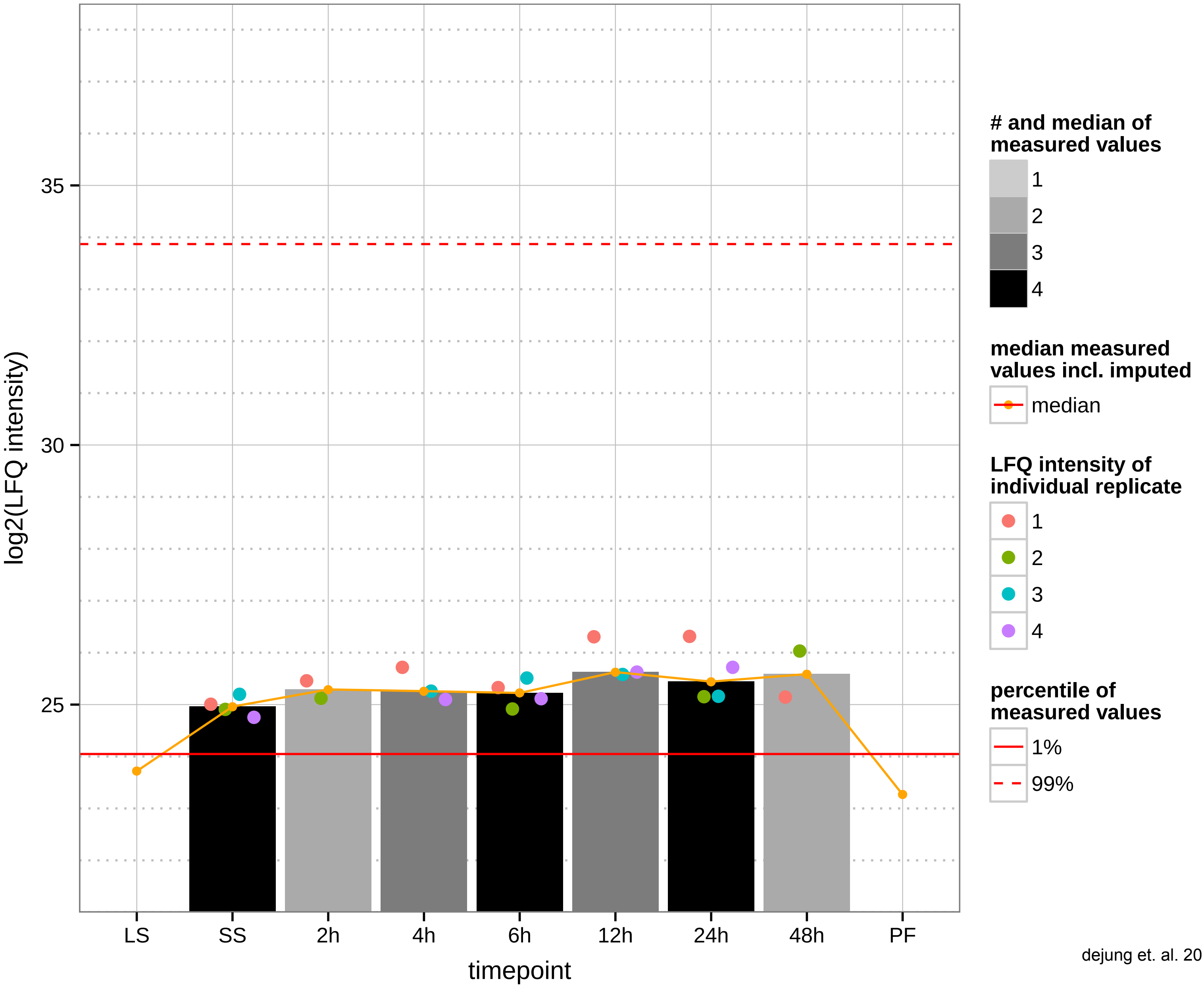
hypothetical protein, conserved
Tb927.11.13910
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null





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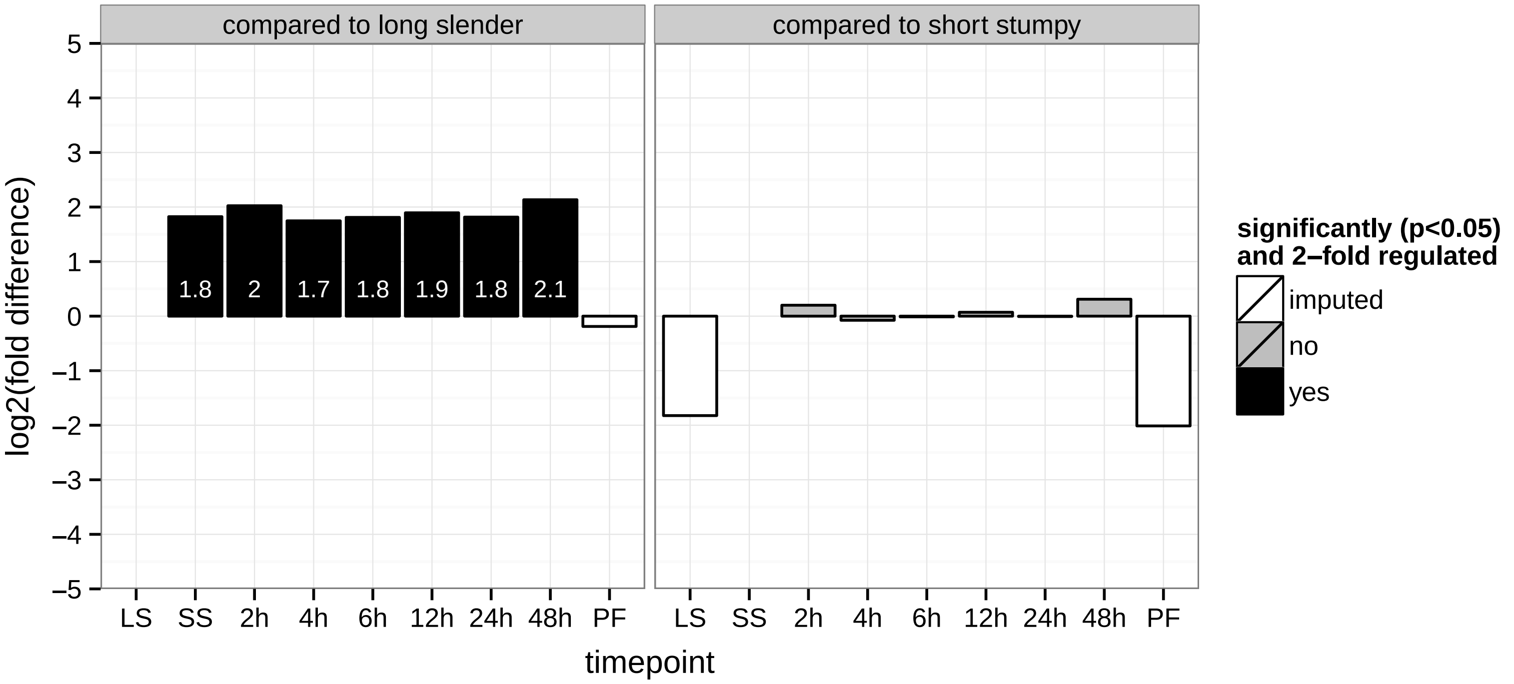
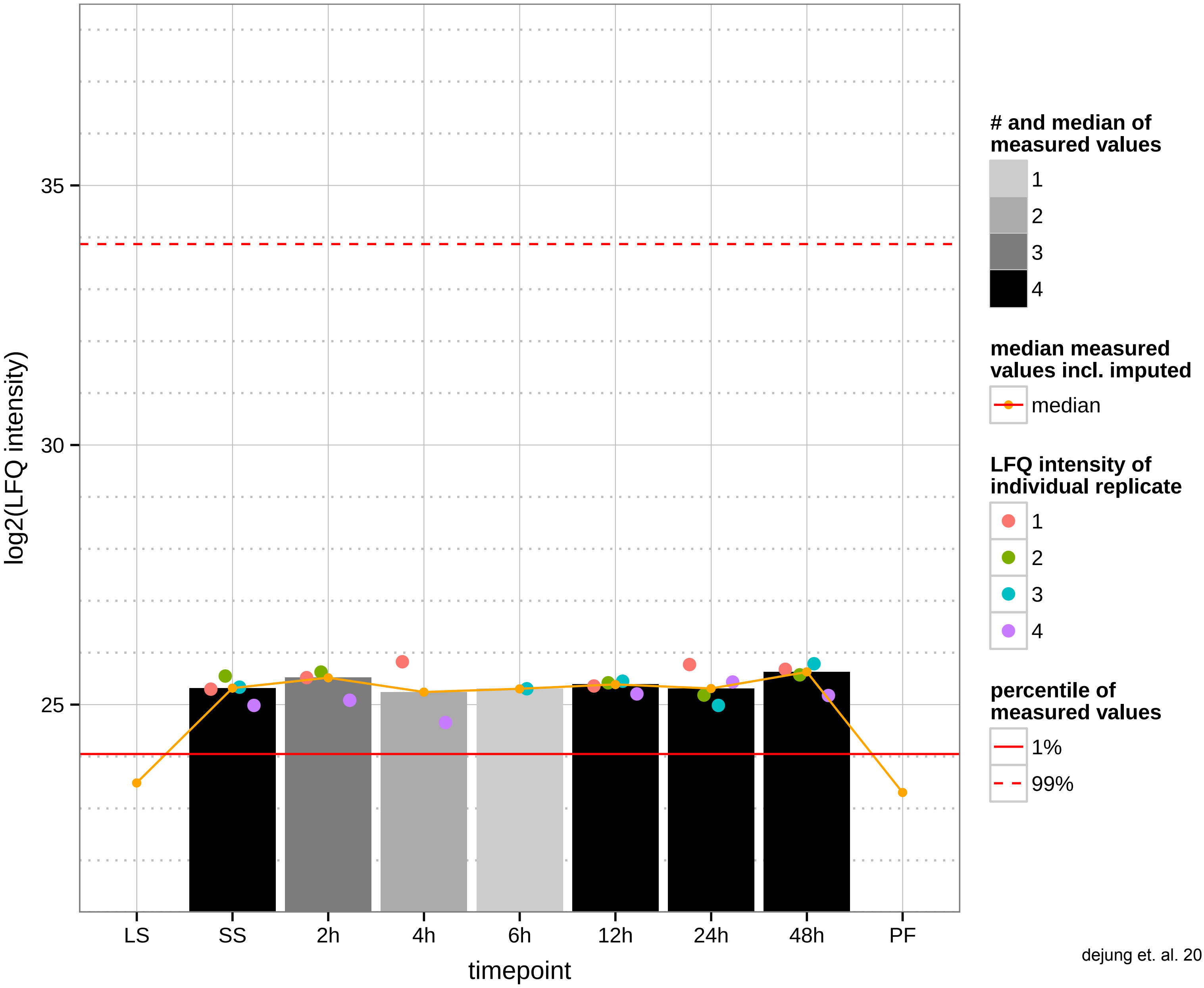
kinetoplast polyadenylation/uridylation factor 2 (KPAF2)
Tb927.11.14380
AGOF: protein binding, ribosome binding
AGOC: mitochondrion
AGOP: mRNA 3'–end processing, mRNA polyadenylation, regulation of mRNA stability
PGOF: null
PGOC: null
PGOP: null





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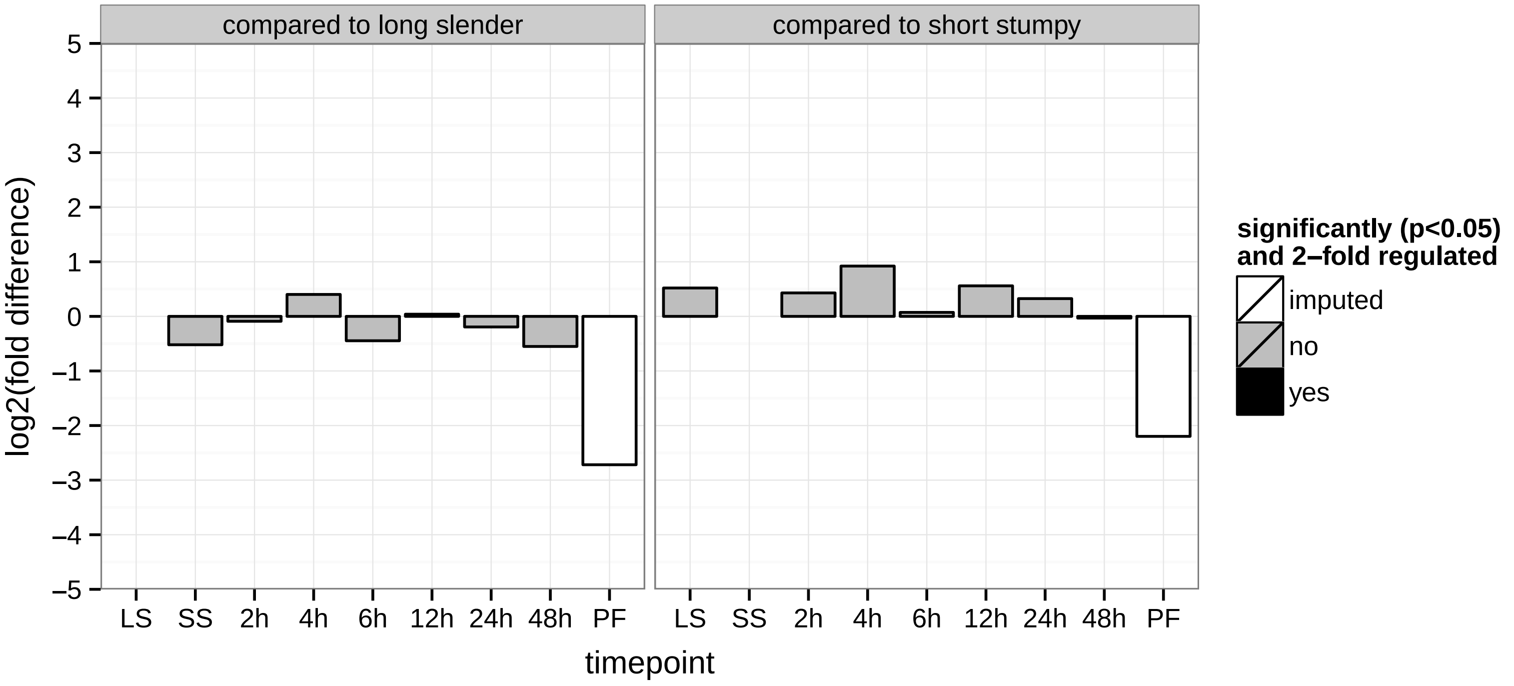
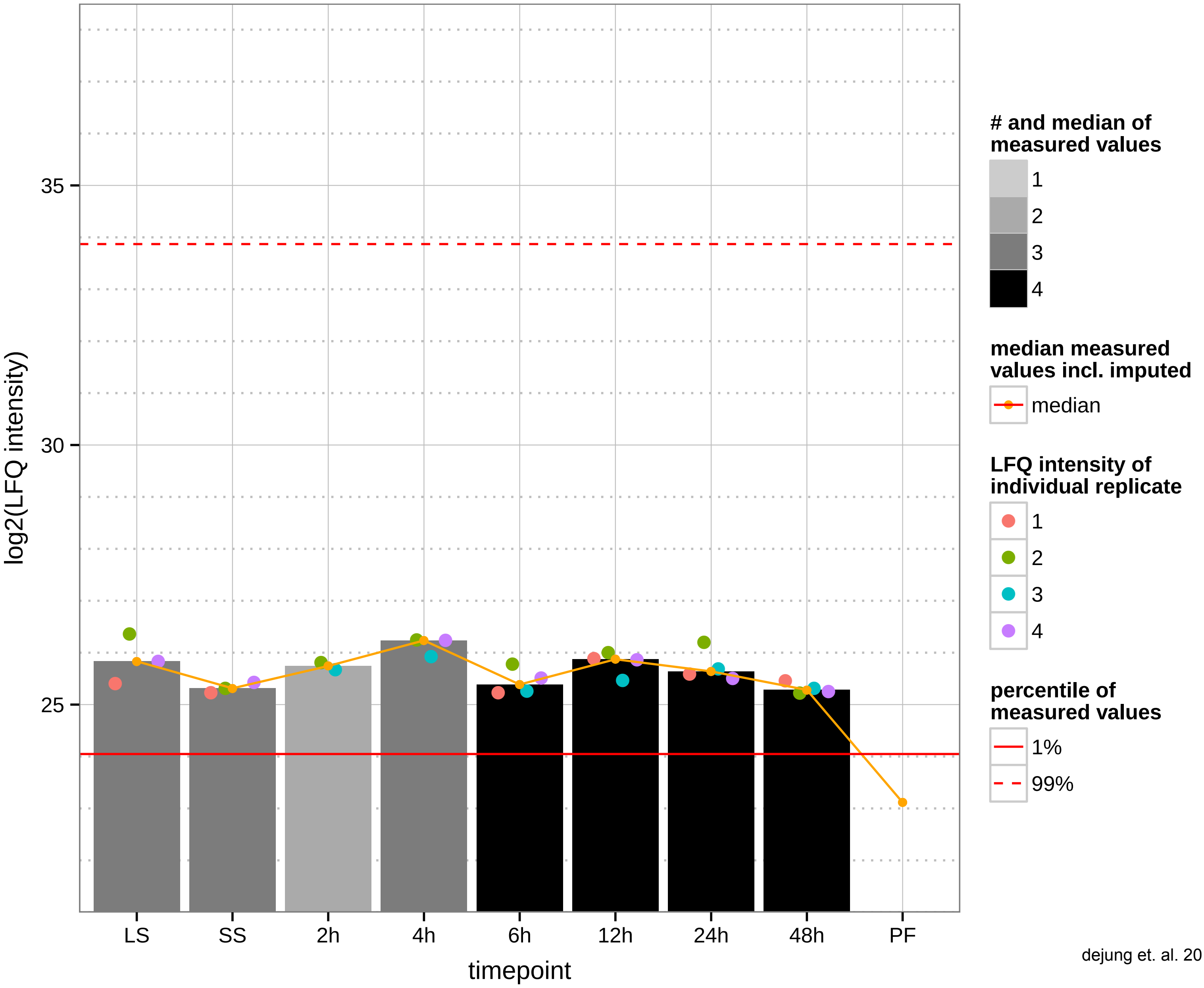
hypothetical protein, conserved
Tb927.11.1440
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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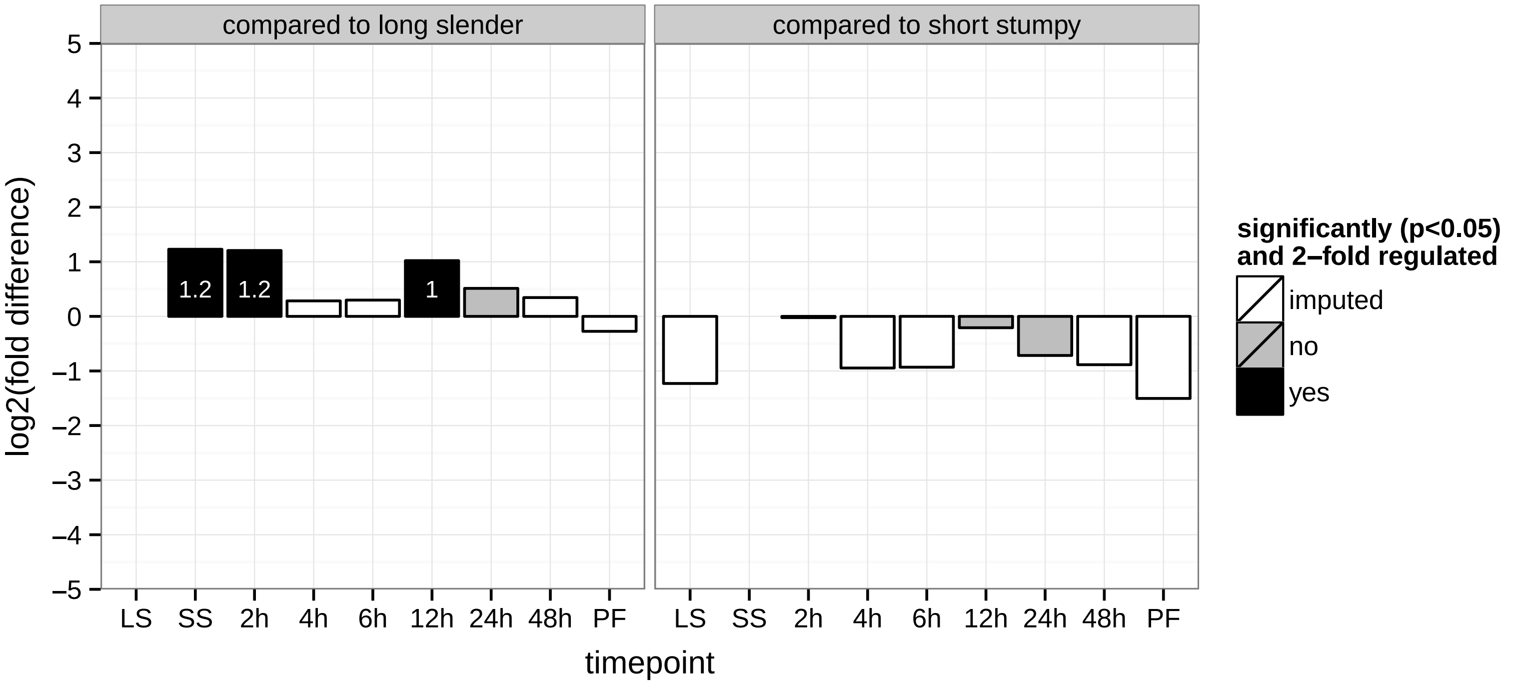
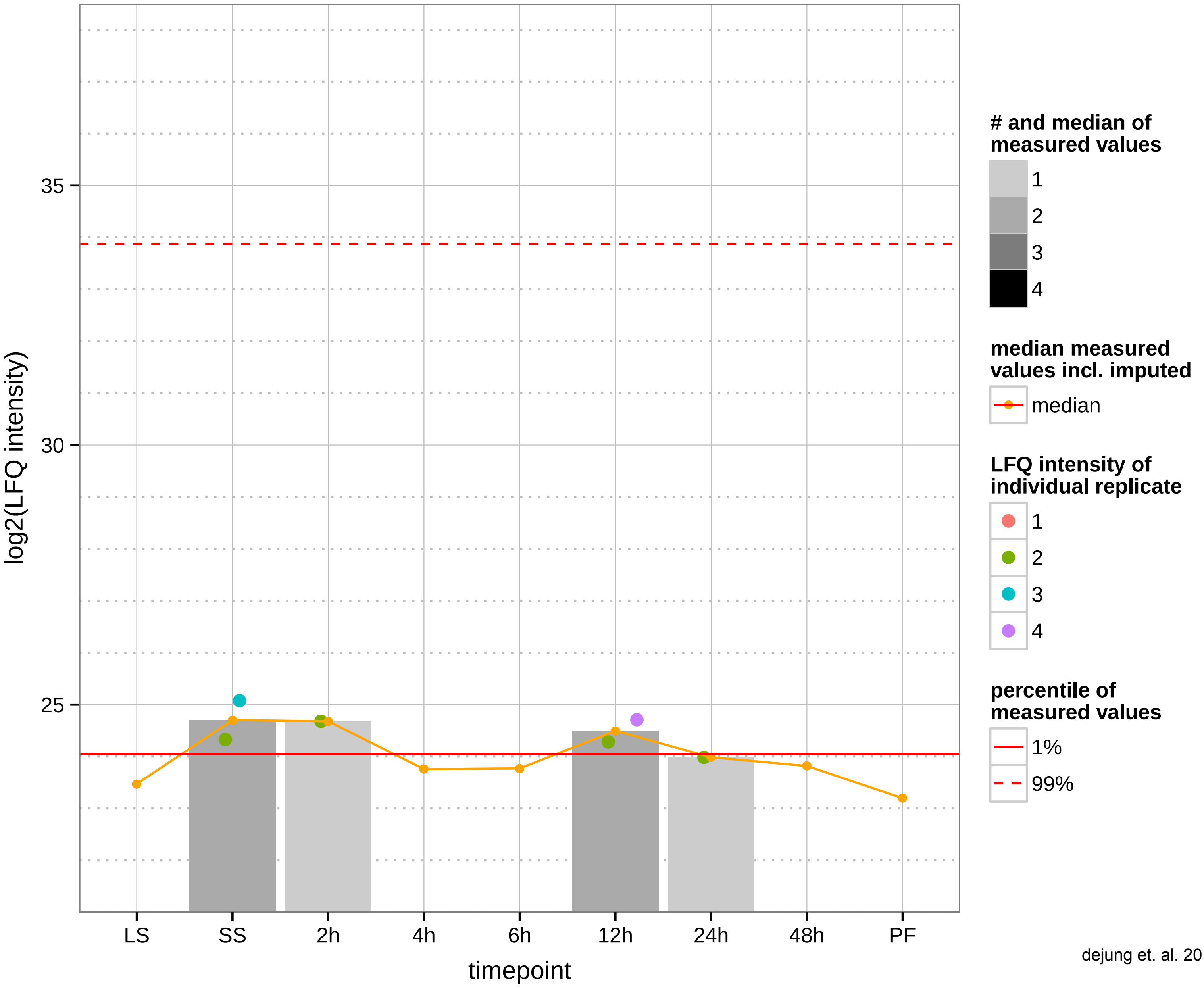
hypothetical protein, conserved
Tb927.11.14570
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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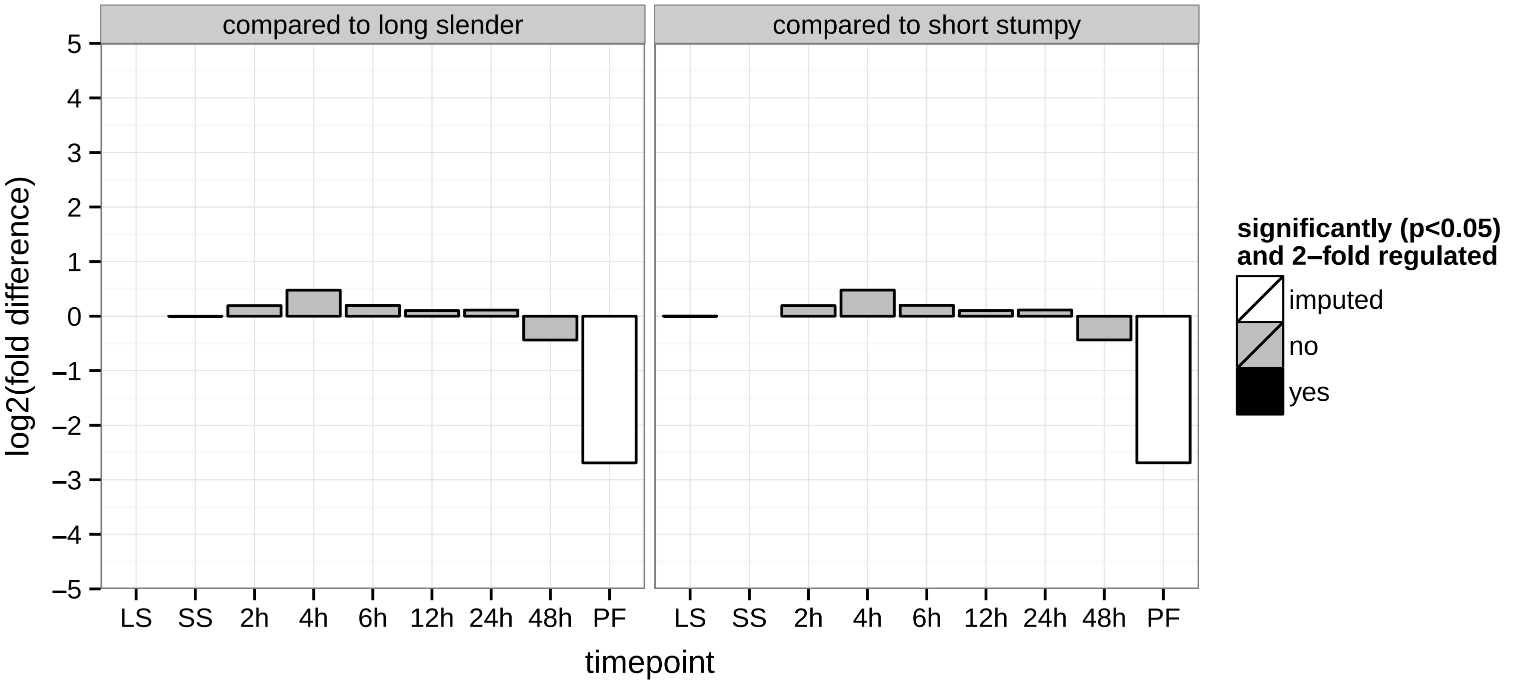
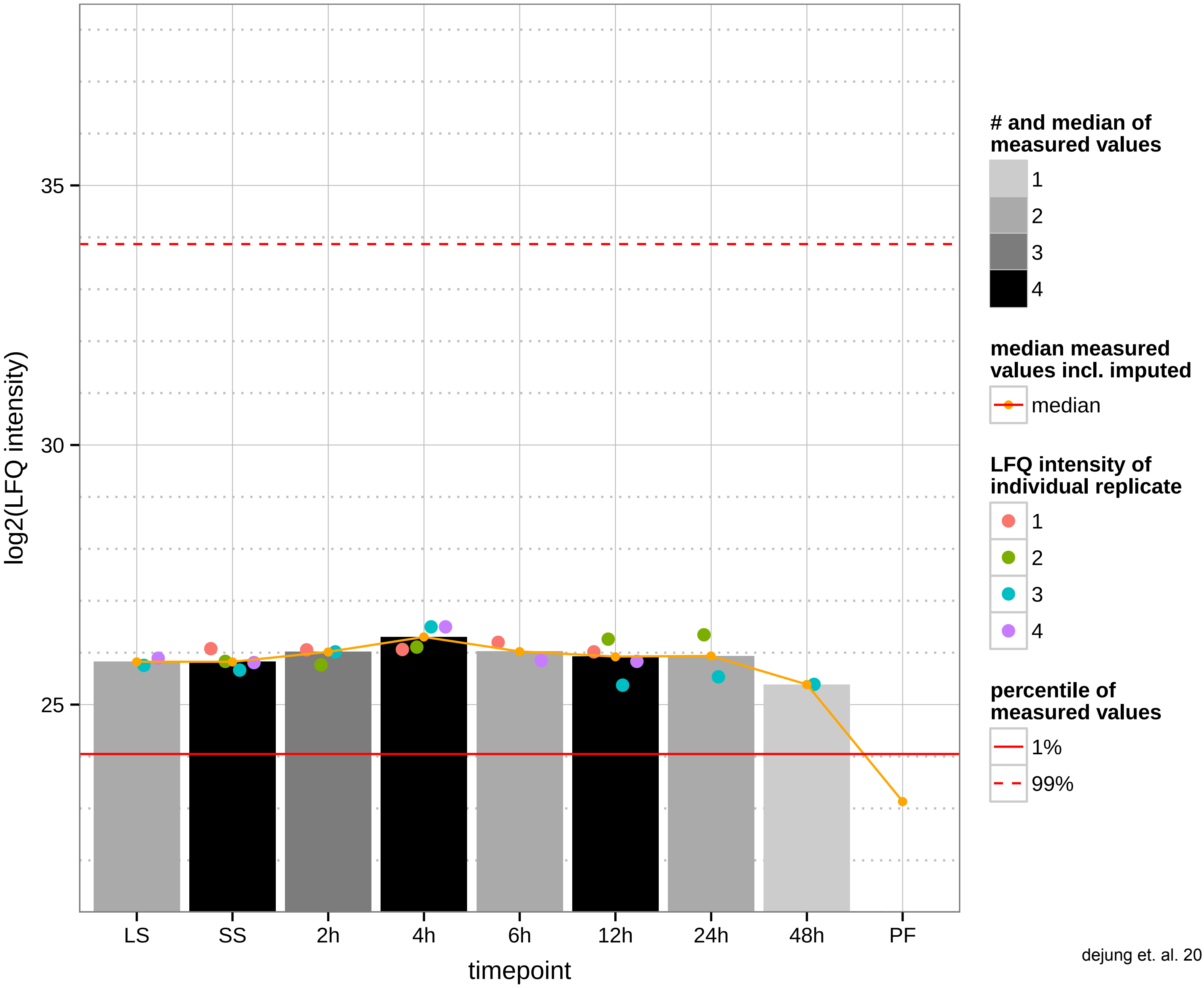
hypothetical protein, conserved
Tb927.11.14690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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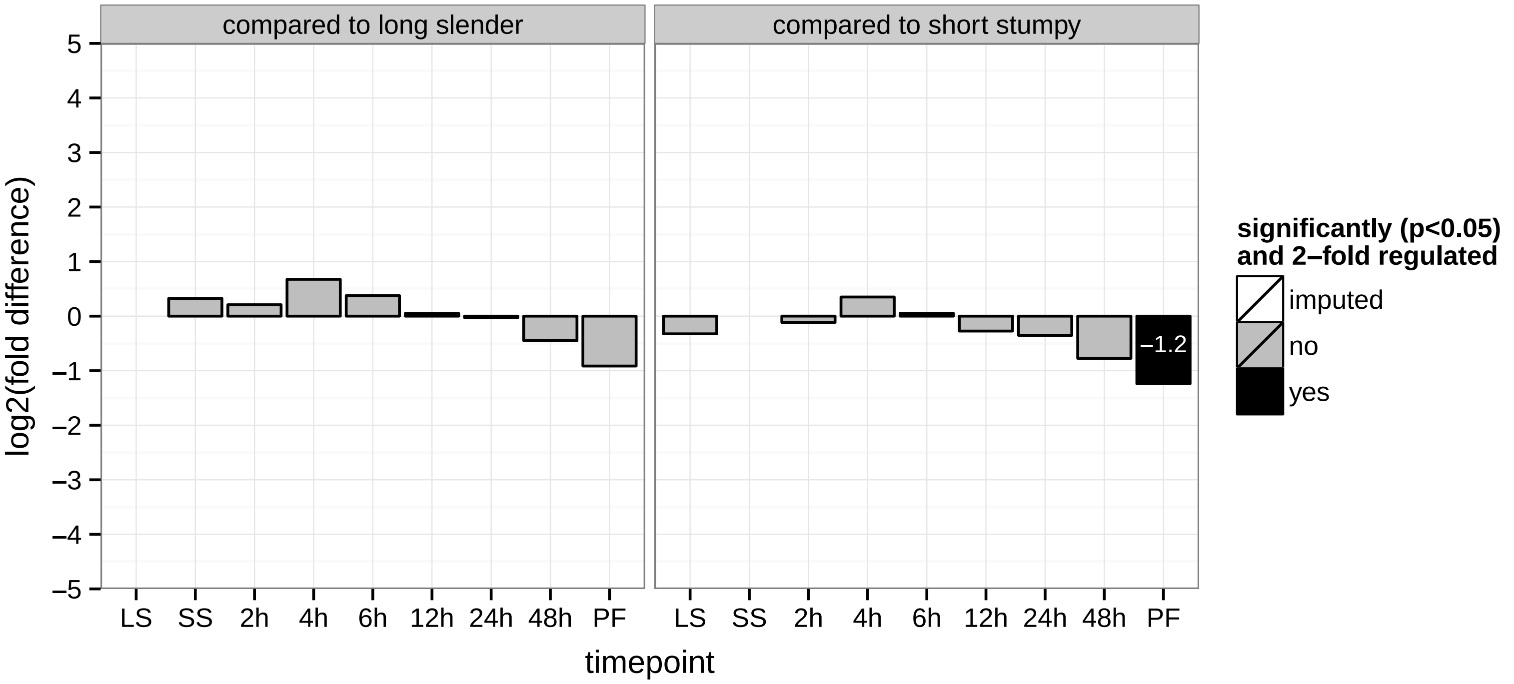
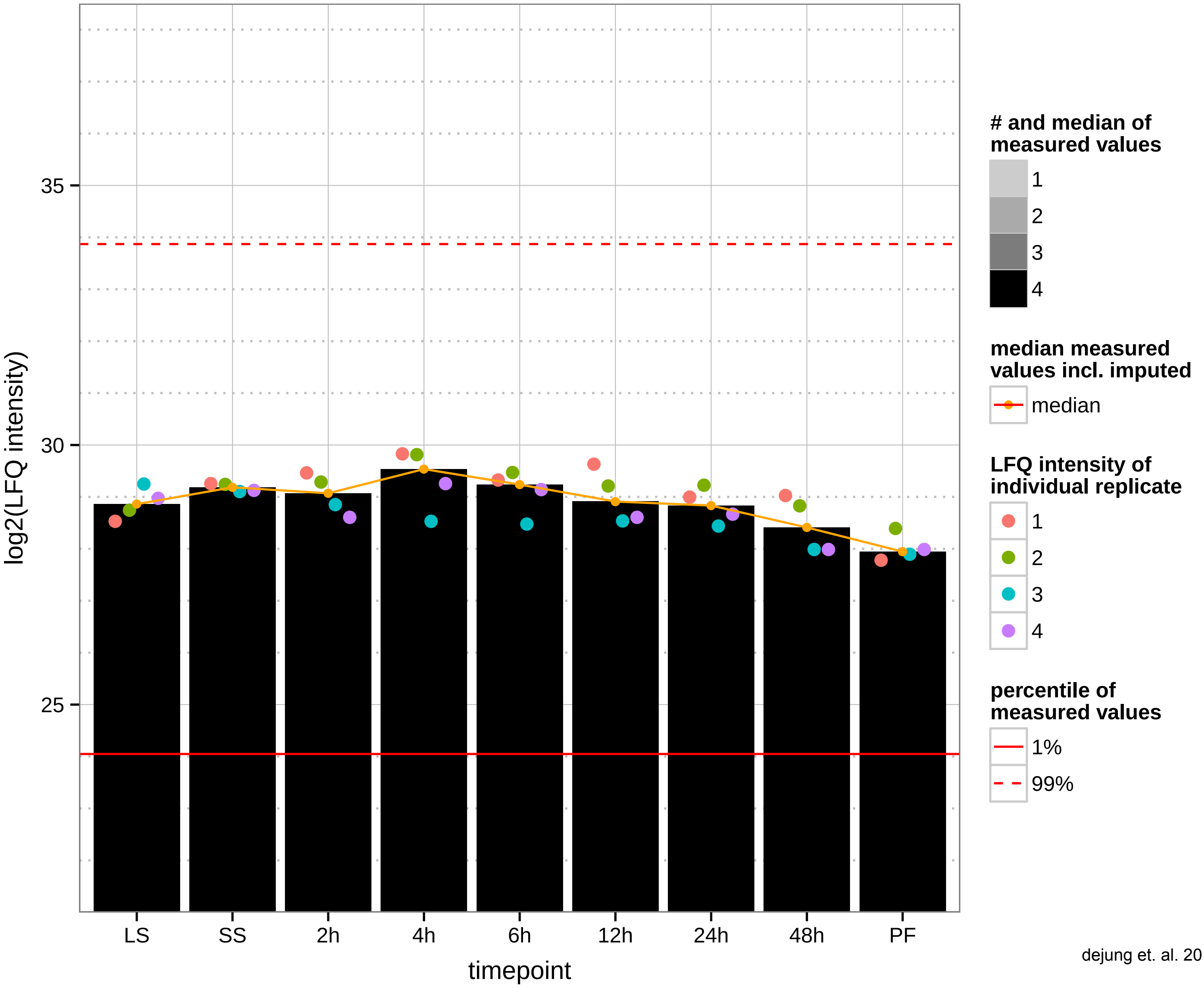
small GTPase (X3)
Tb927.11.15030
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti





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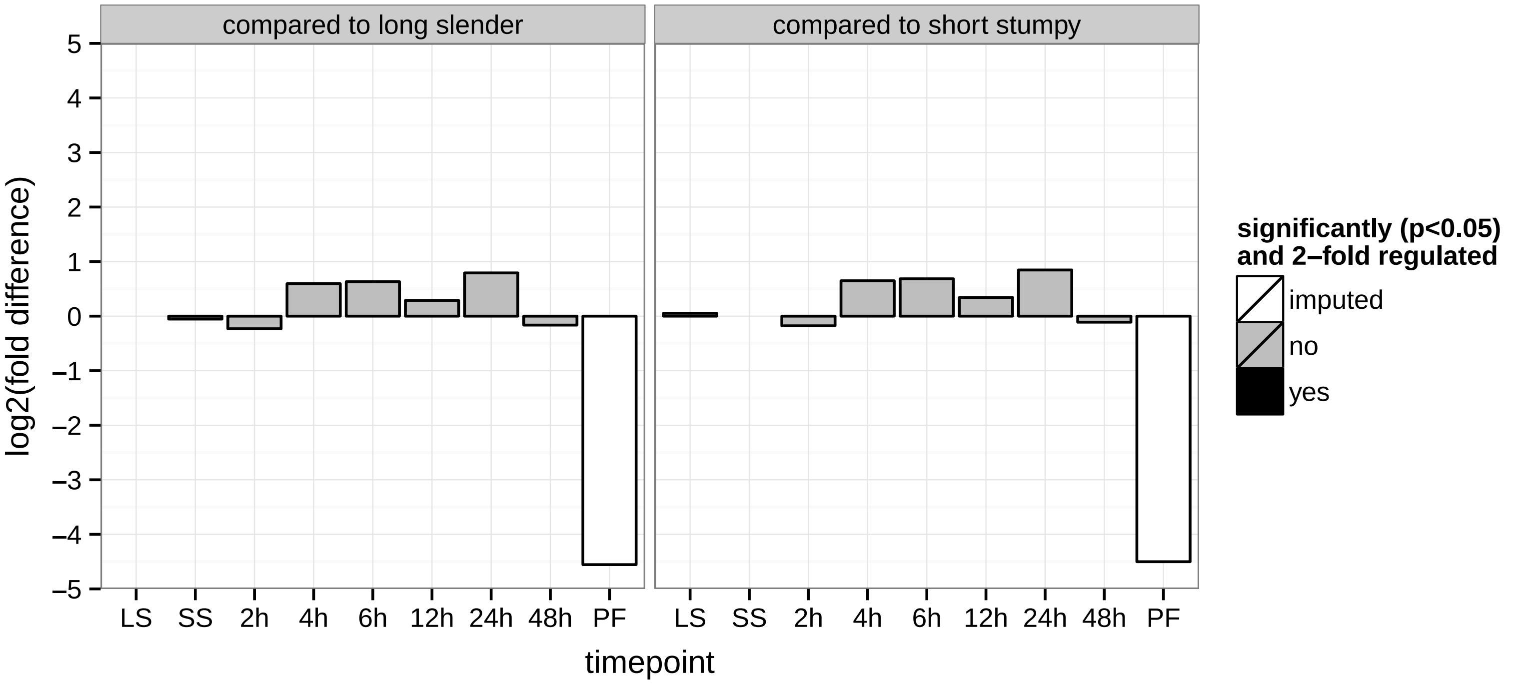
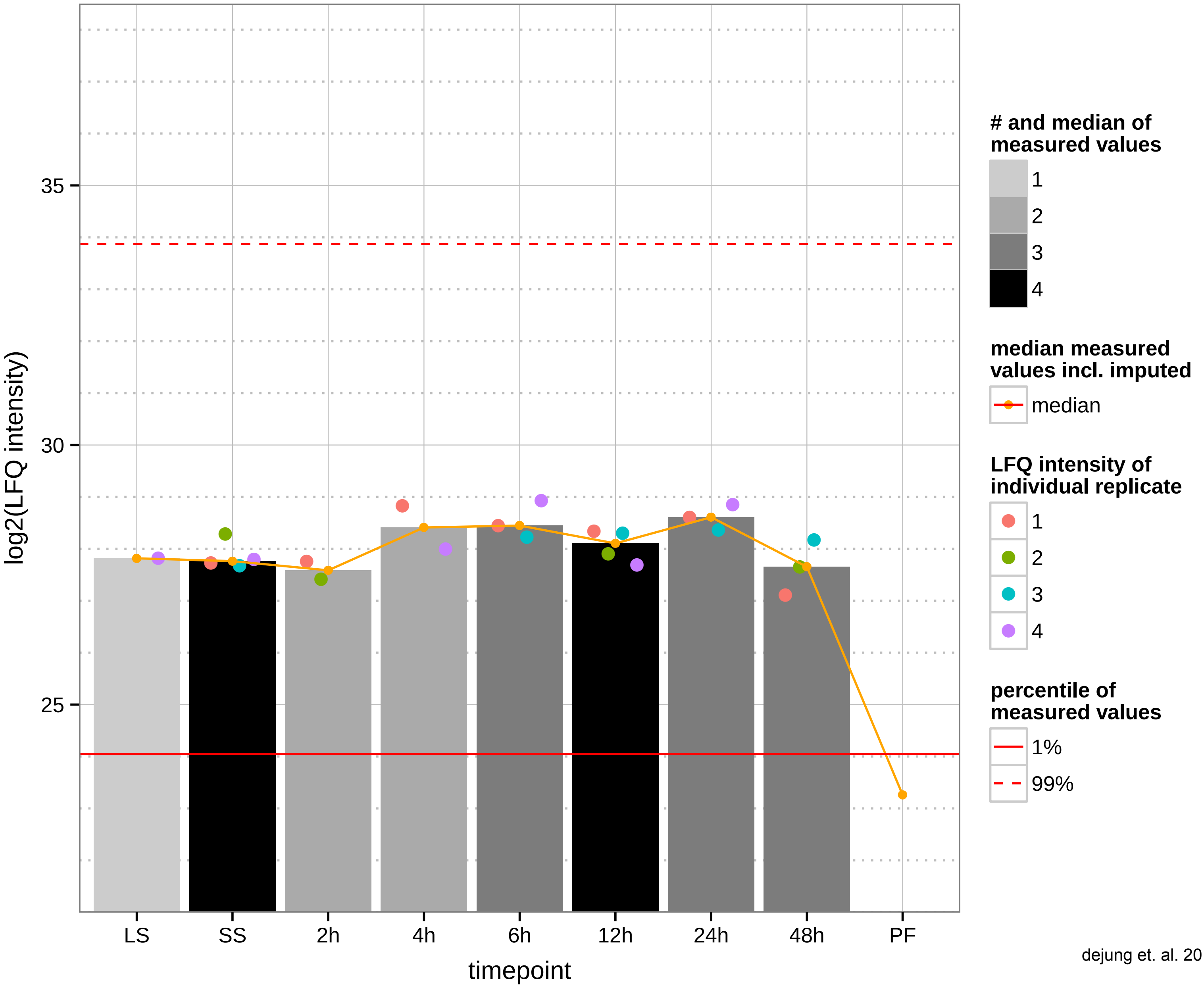
hypothetical protein, conserved
Tb927.11.15120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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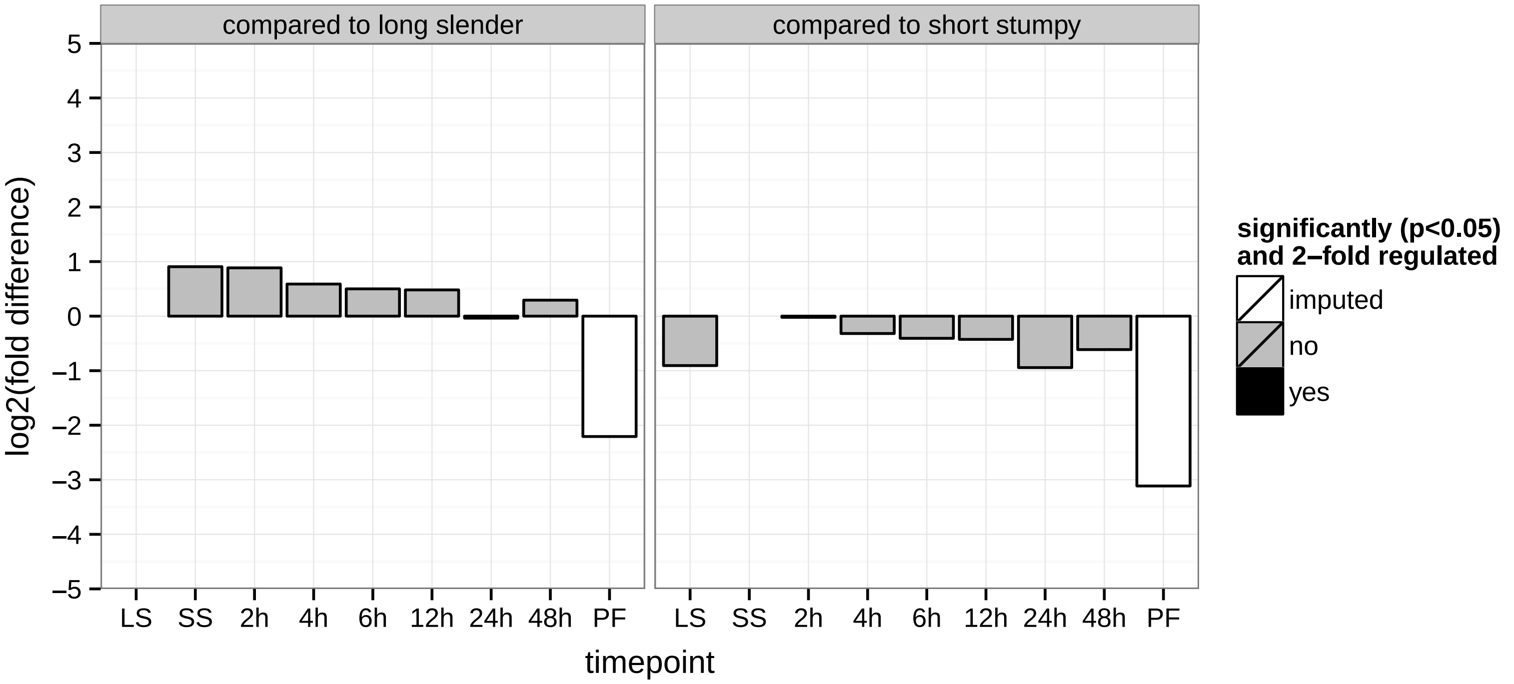
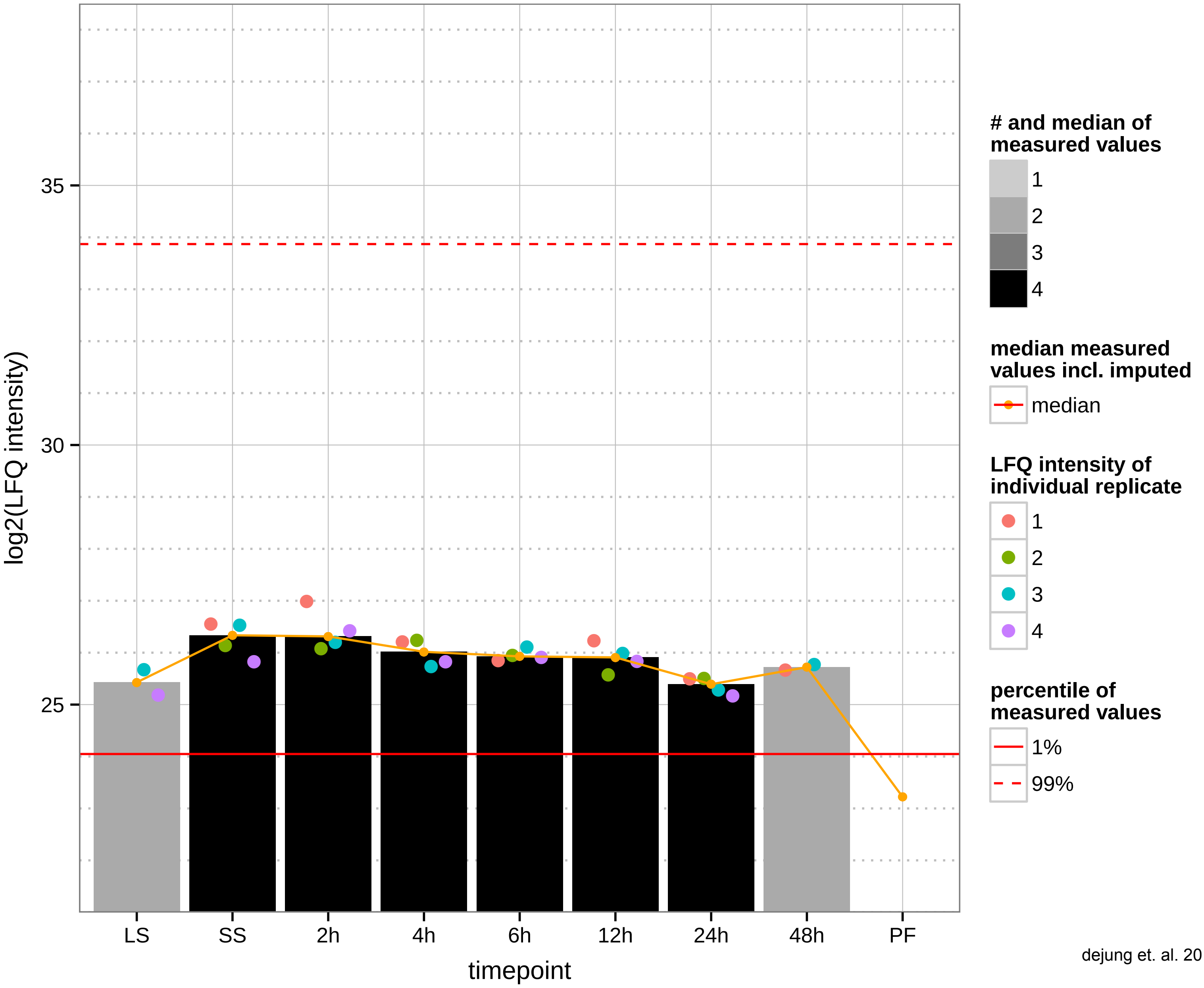
hypothetical protein, conserved
Tb927.11.15400
AGOF: null
AGOC: null, integral to membrane
AGOP: null, vesicle–mediated transport
PGOF: null, protein binding
PGOC: null, integral to membrane
PGOP: null, vesicle–mediated transport





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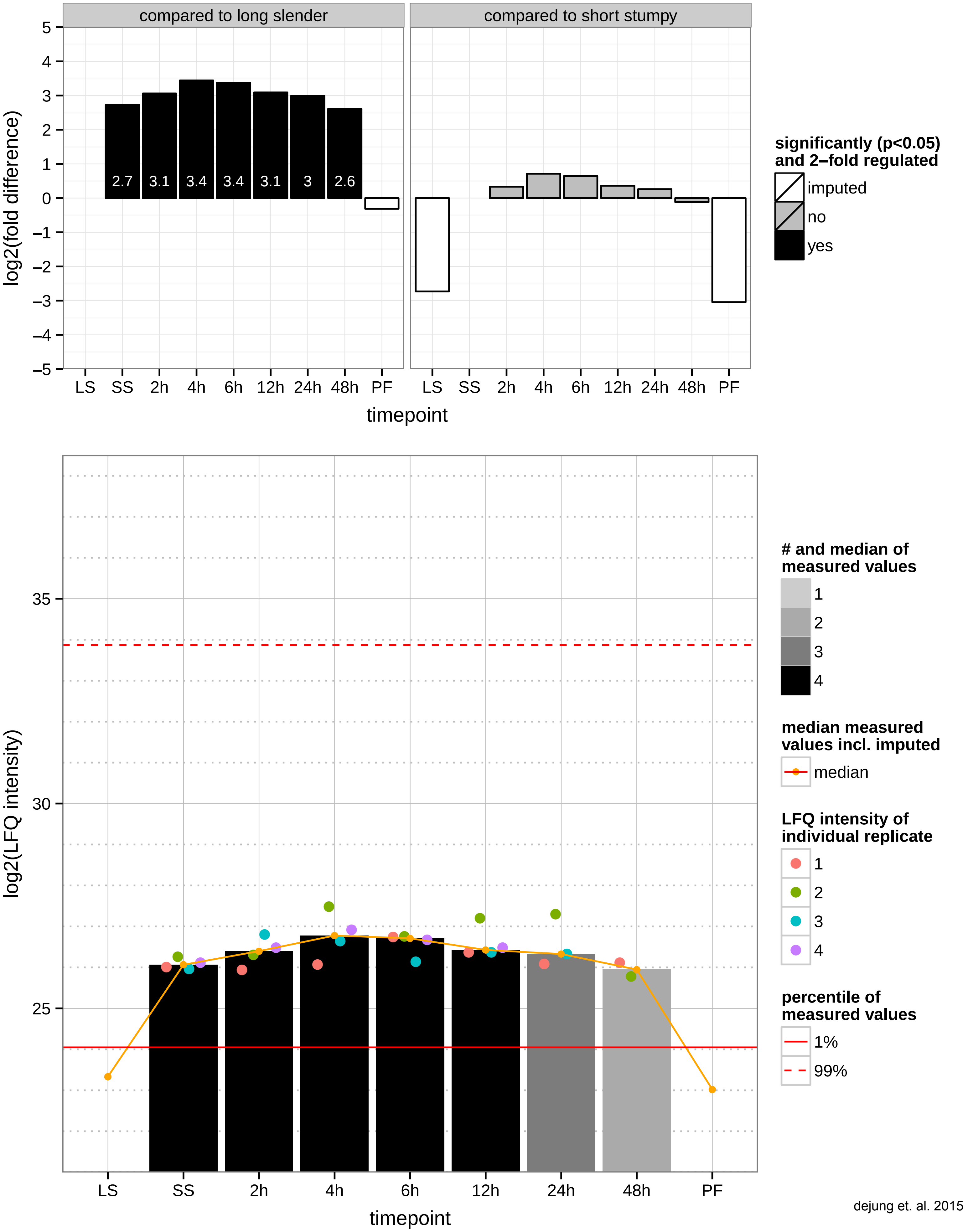
hypothetical protein, conserved
Tb927.11.16320
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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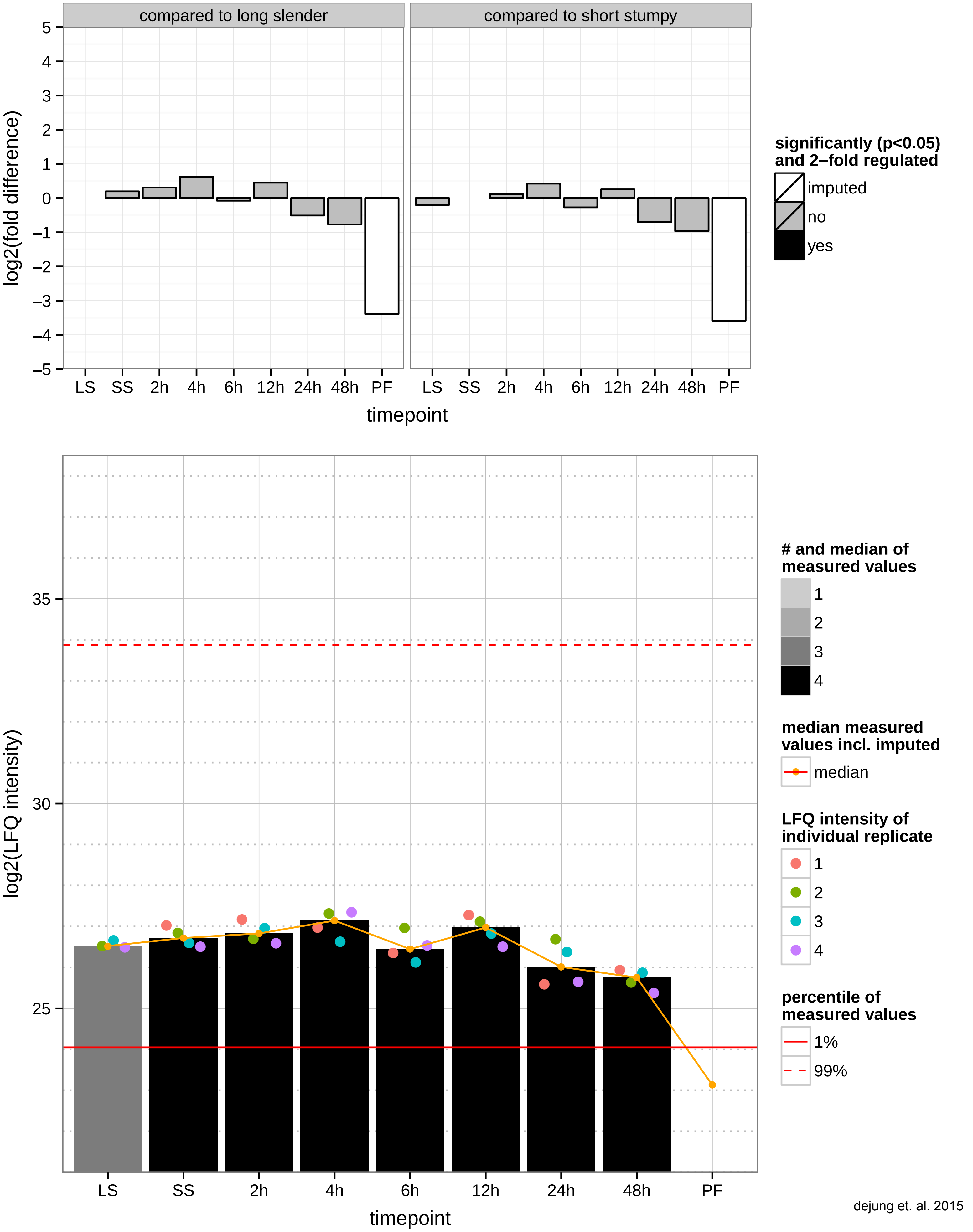
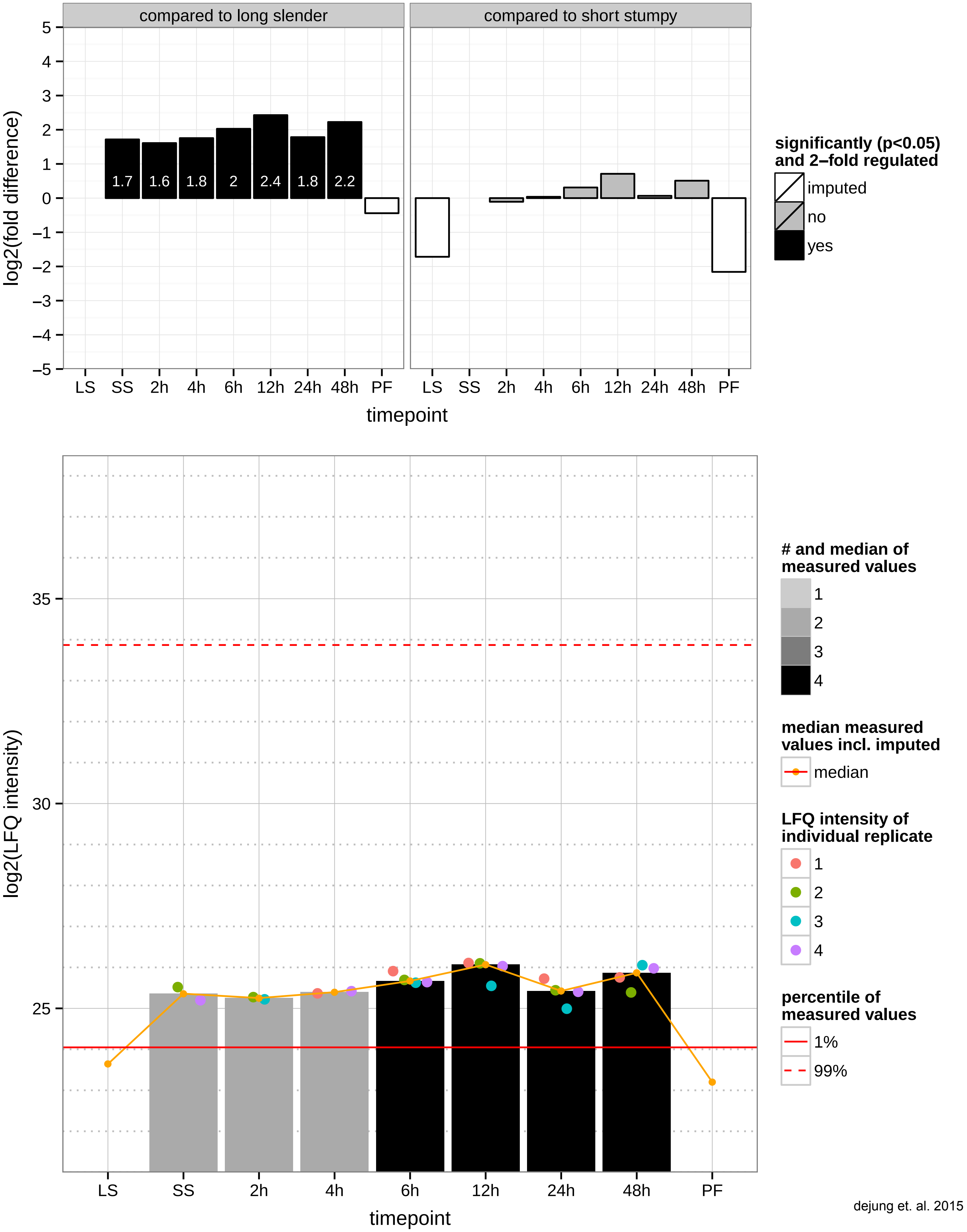
hypothetical protein, conserved
Tb927.11.16540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



hypothetical protein, conserved
Tb927.11.16610
AGOF: null
AGOC: intracellular
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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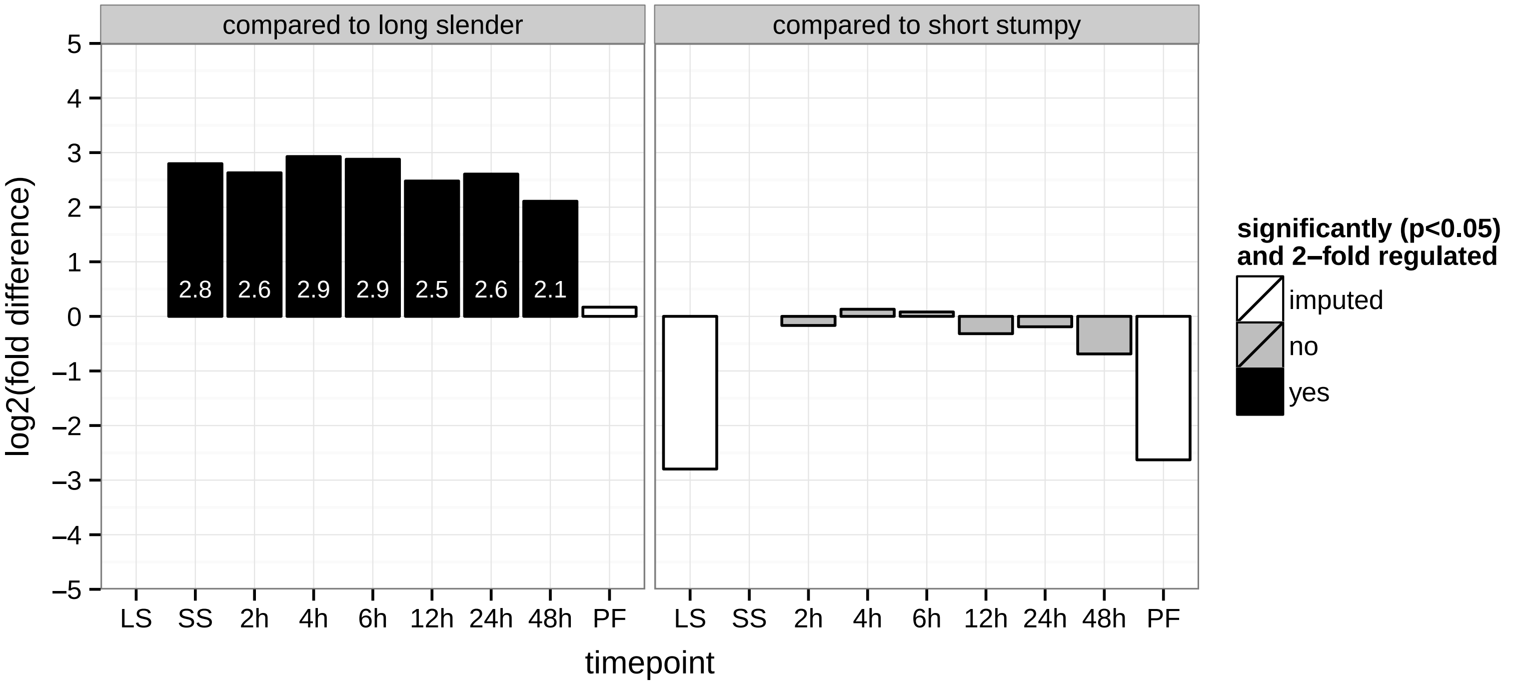
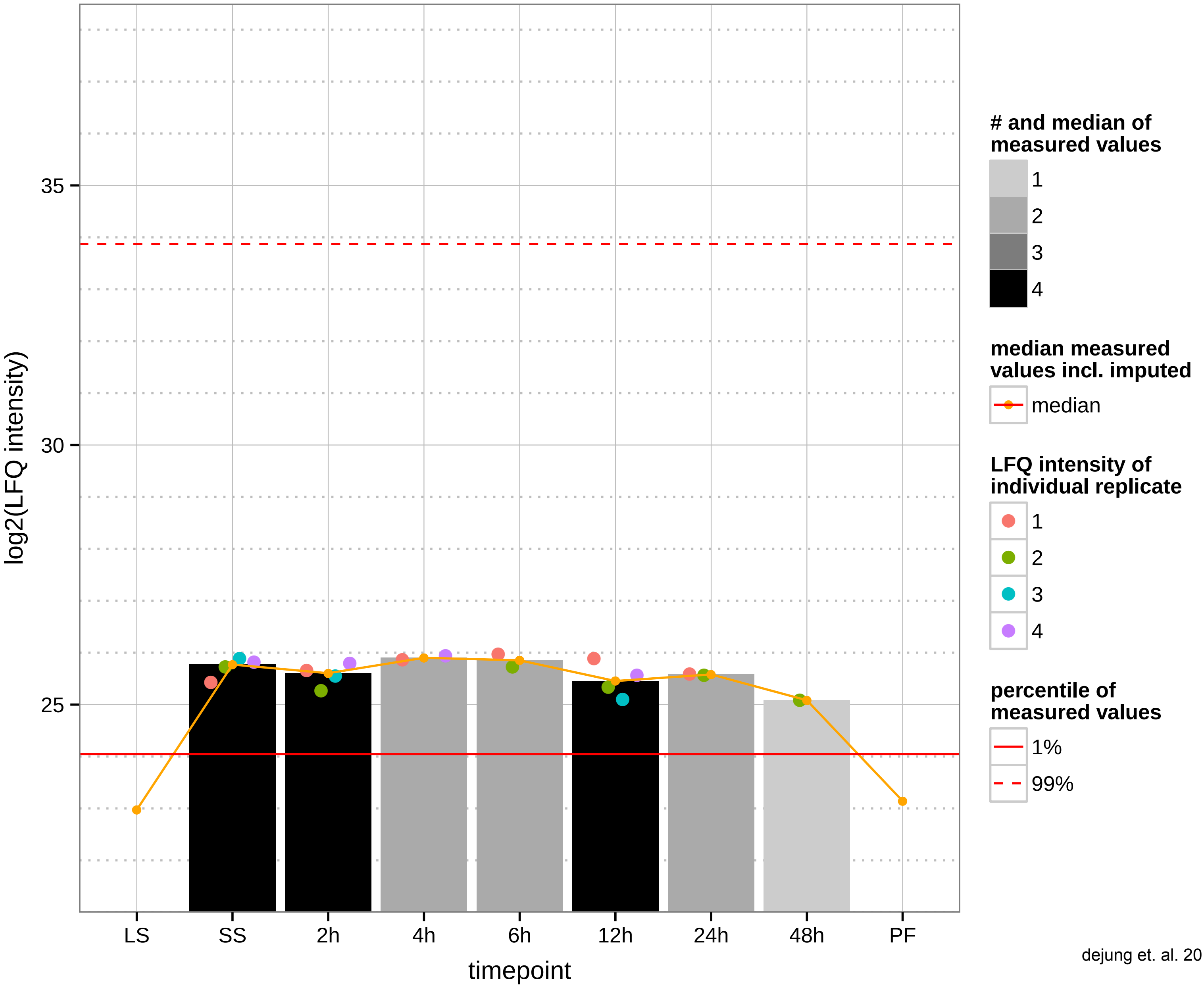
chloride channel protein, putative
Tb927.11.16690
AGOF: voltage–gated chloride channel activity
AGOC: membrane
AGOP: chloride transport
PGOF: ion channel activity, protein binding, voltage–gated chloride channel activity
PGOC: membrane
PGOP: chloride transport, transmembrane transport





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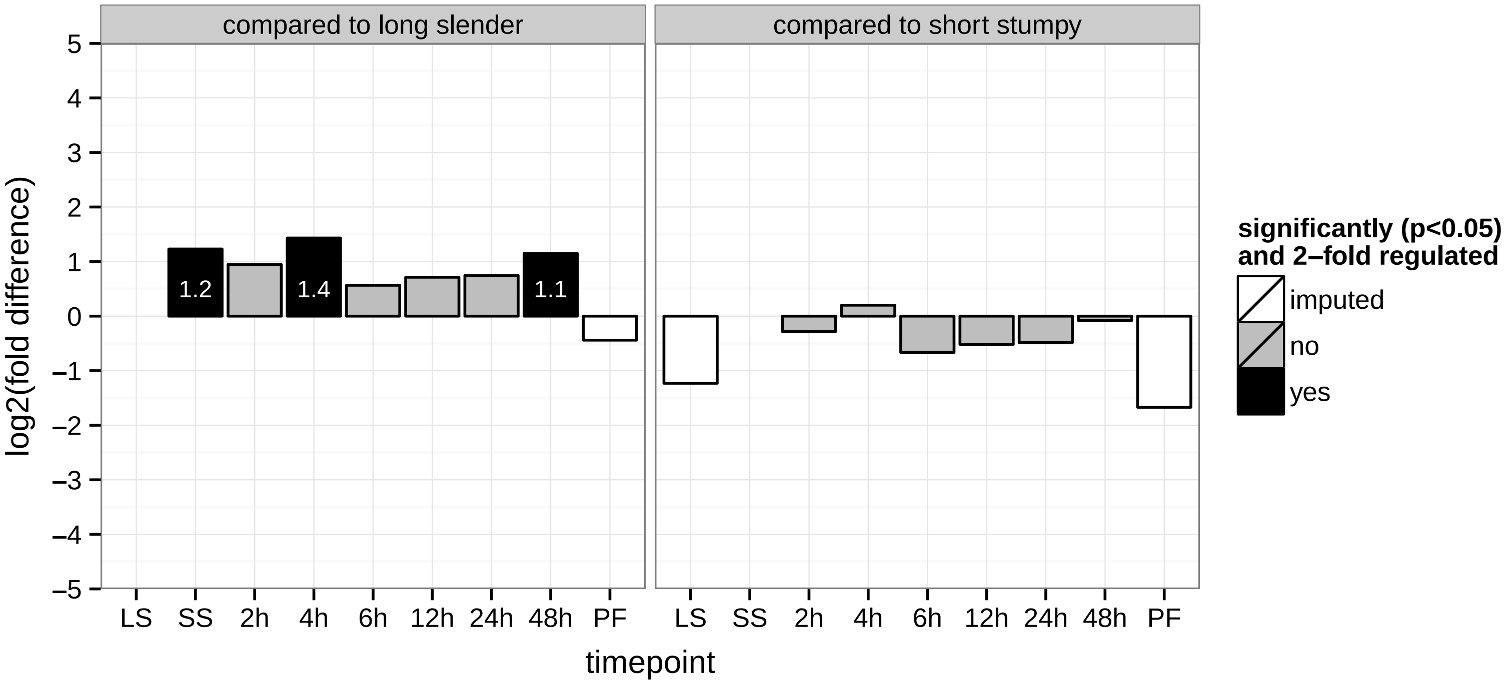
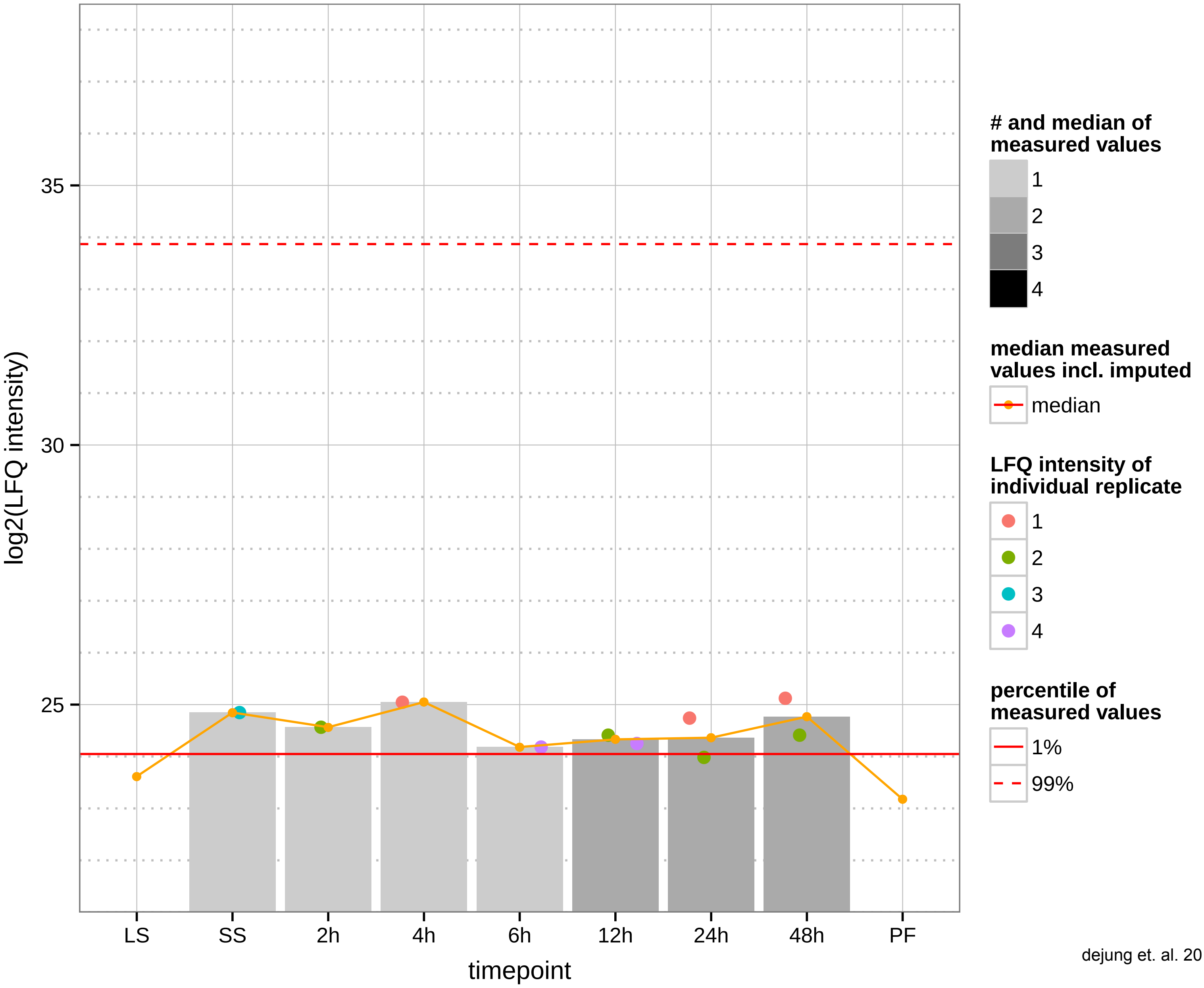
cation transporter protein, putative
Tb927.11.1910
AGOF: cation transmembrane transporter activity, efflux transmembrane transporter activity
AGOC: integral to membrane, membrane
AGOP: cation transport
PGOF: cation transmembrane transporter activity
PGOC: integral to membrane
PGOP: cation transport, transmembrane transport





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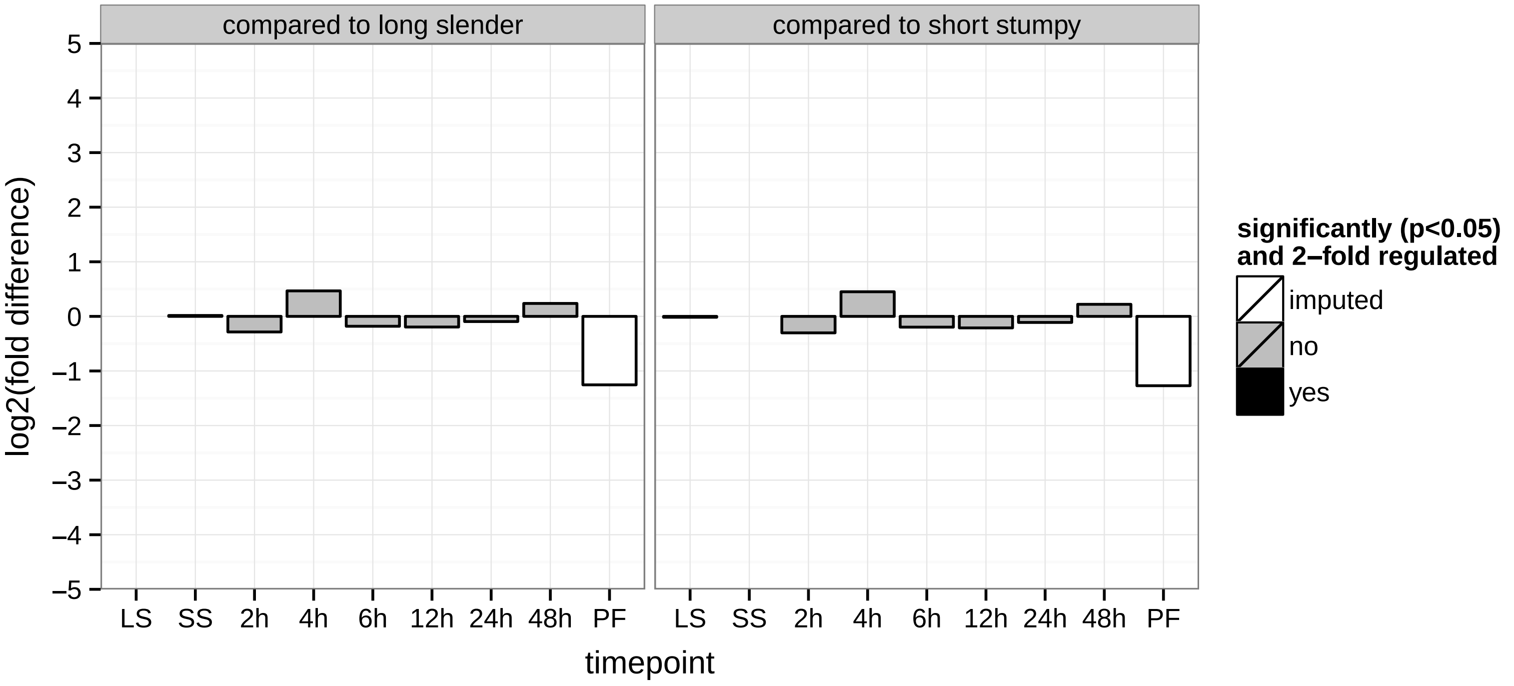
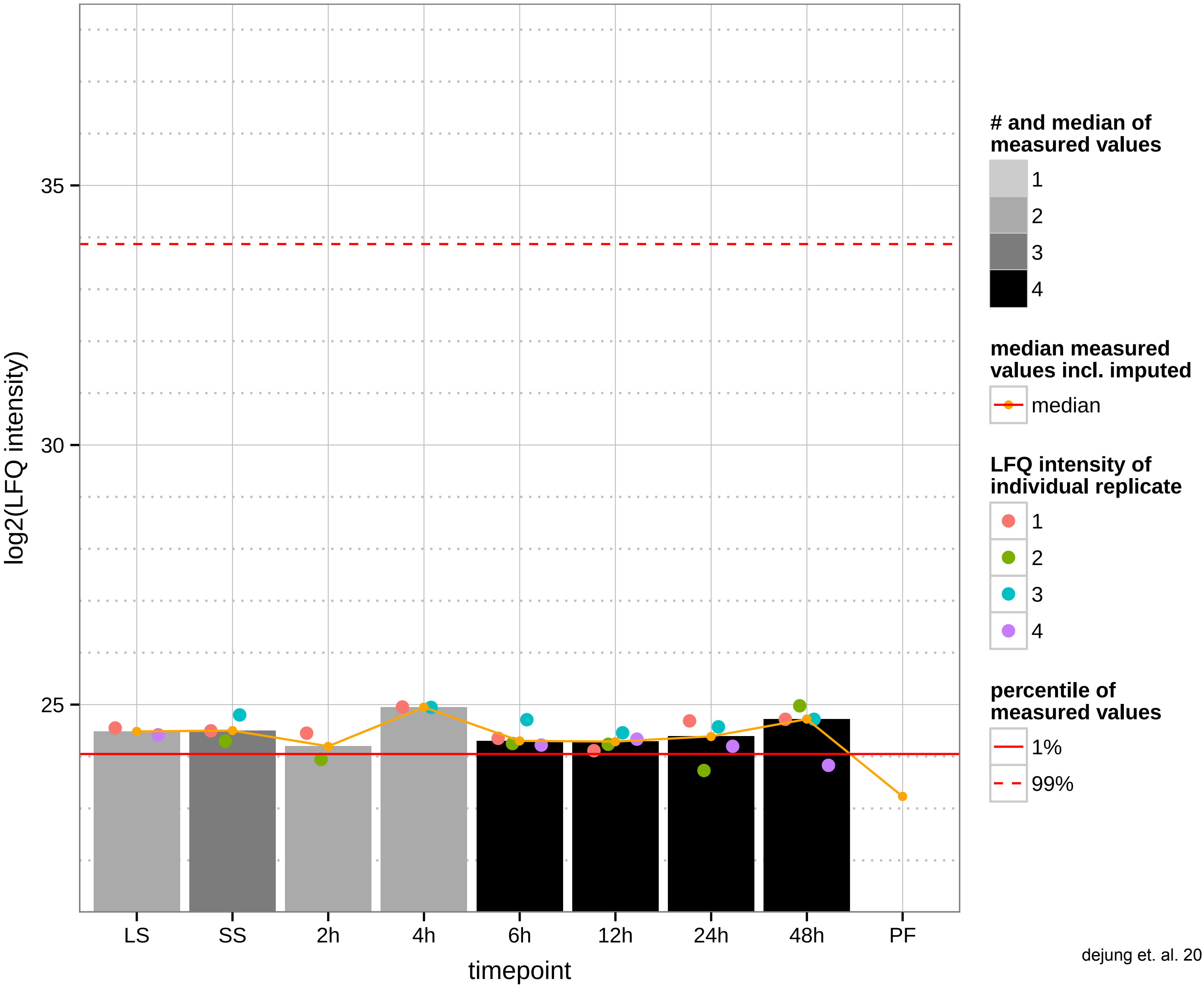
Tubulin cofactor C domain−containing protein 1 (tbccd1)
Tb927.11.2440
AGOF: null
AGOC: Golgi apparatus, apical part of cell, centriole
AGOP: Golgi inheritance, establishment of nucleus localization, mitochondrial DNA inheritance
PGOF: null
PGOC: null
PGOP: null





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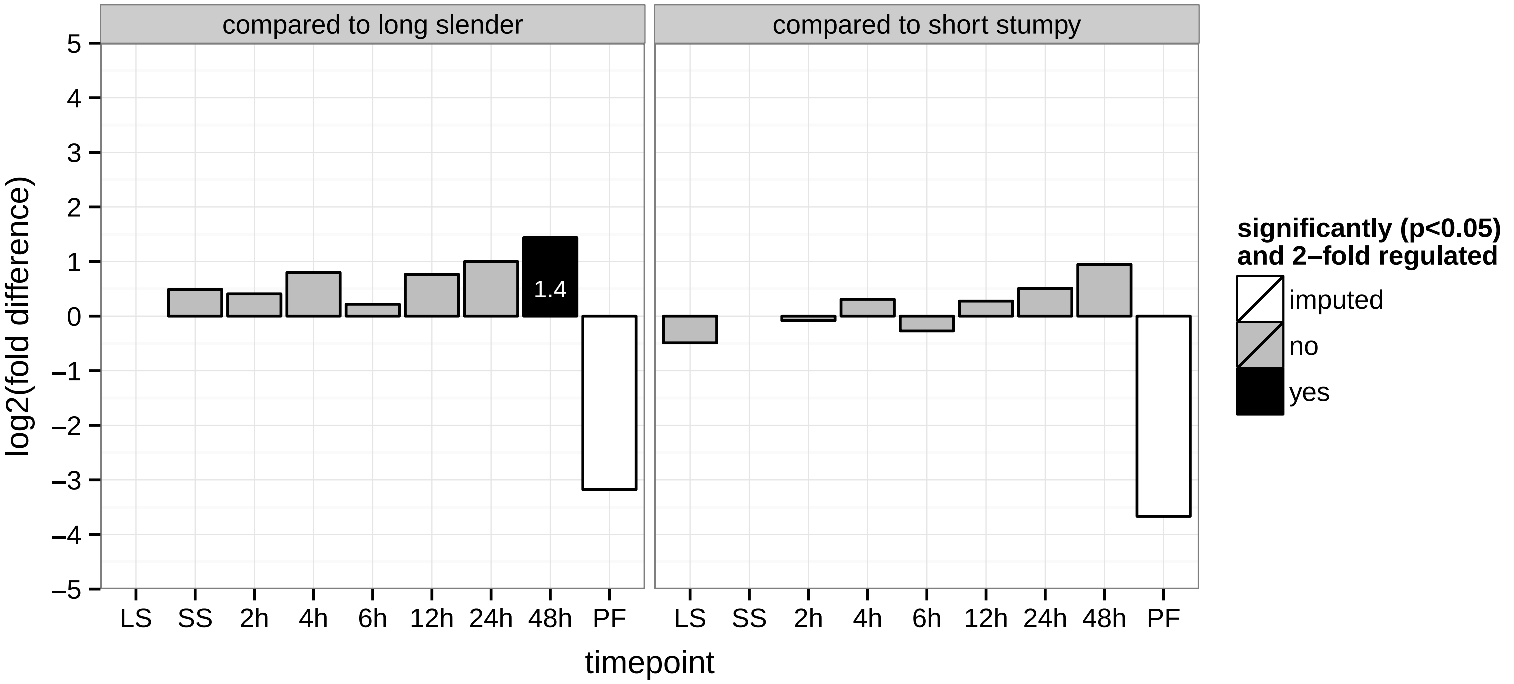
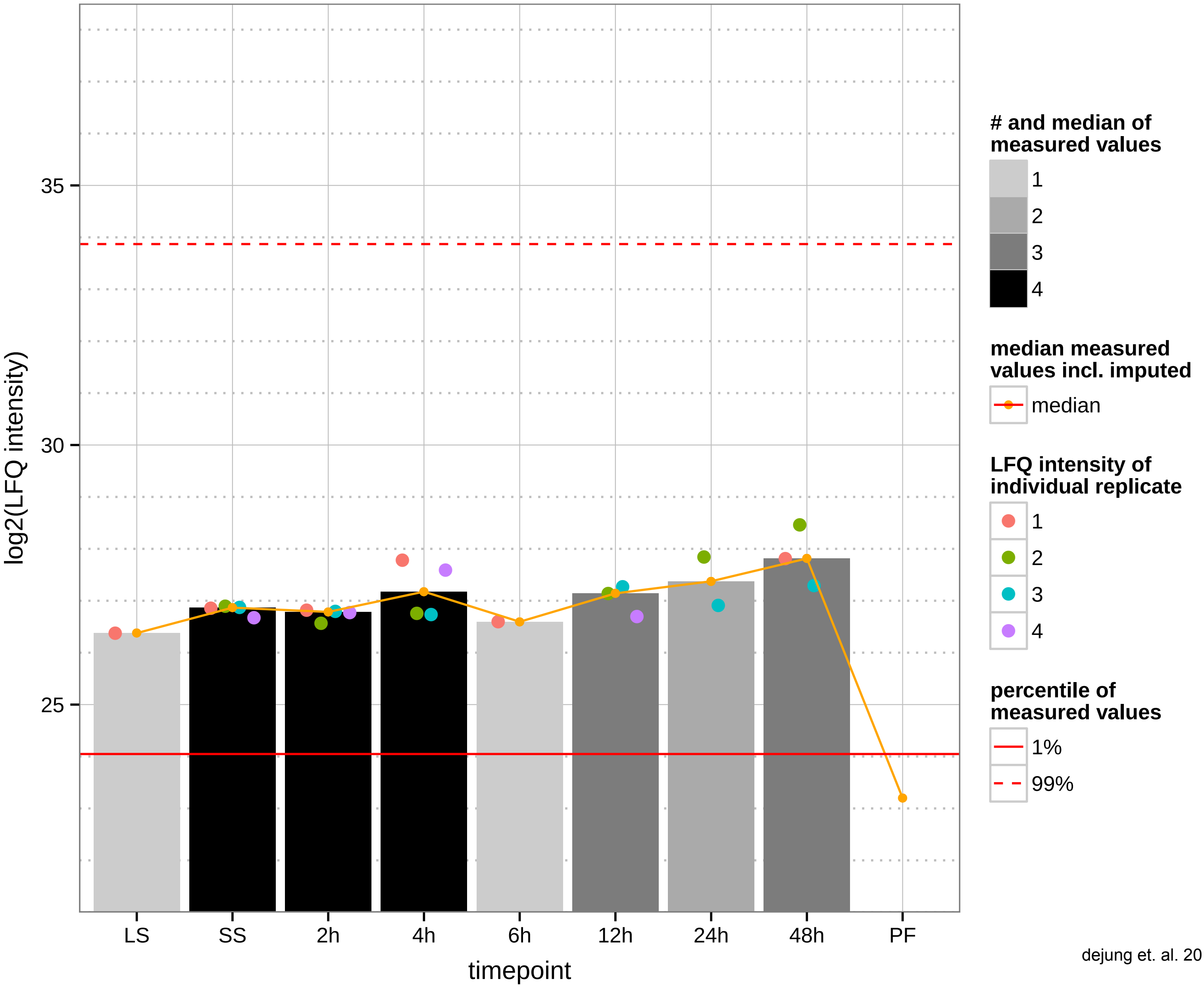
ubiquitin carboxyl–terminal hydrolase, putative, cysteine peptidase, Clan CA, family C12
Tb927.11.250
AGOF: phospholipase C activity, ubiquitin thiolesterase activity
AGOC: cytoplasm, intracellular
AGOP: intracellular signal transduction, lipid metabolic process, ubiquitin–dependent protein catabolic process
PGOF: phospholipase C activity, ubiquitin thiolesterase activity
PGOC: intracellular
PGOP: intracellular signal transduction, lipid metabolic process, ubiquitin–dependent protein catabolic process





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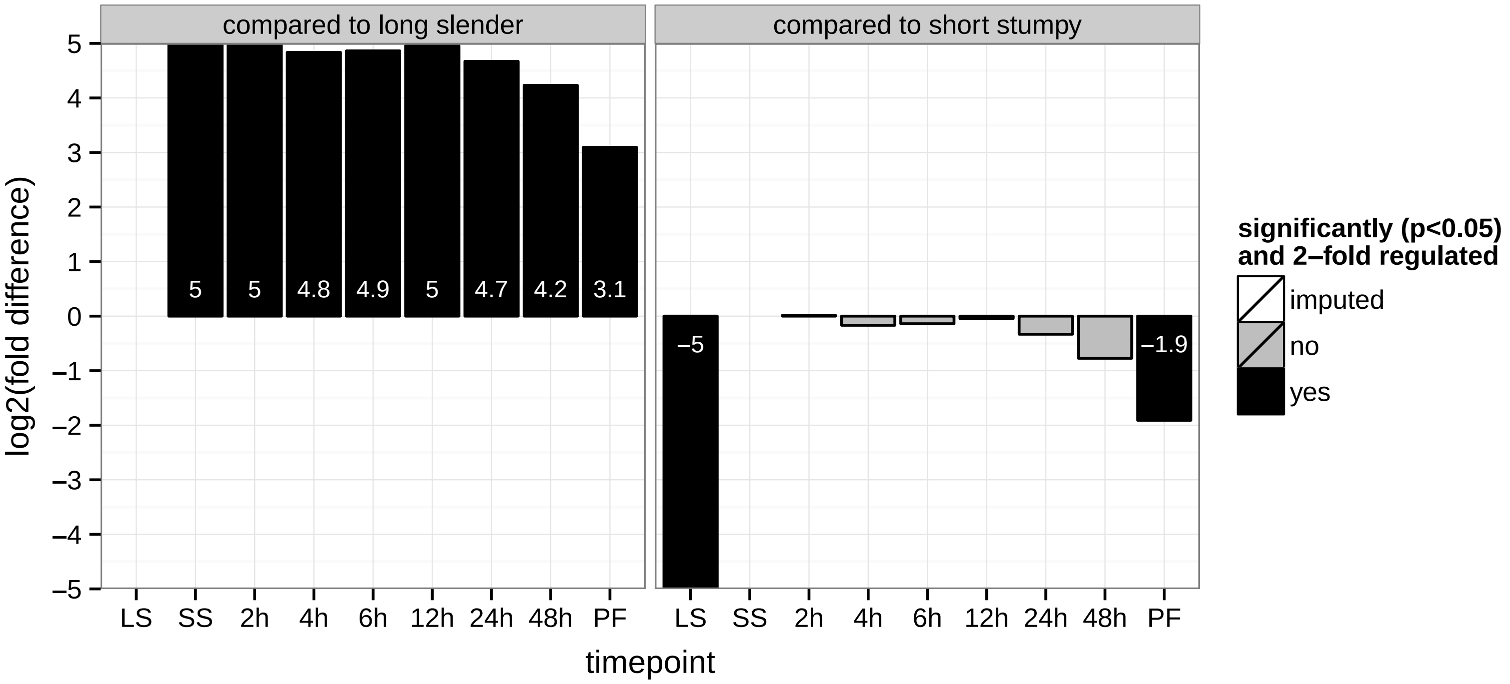
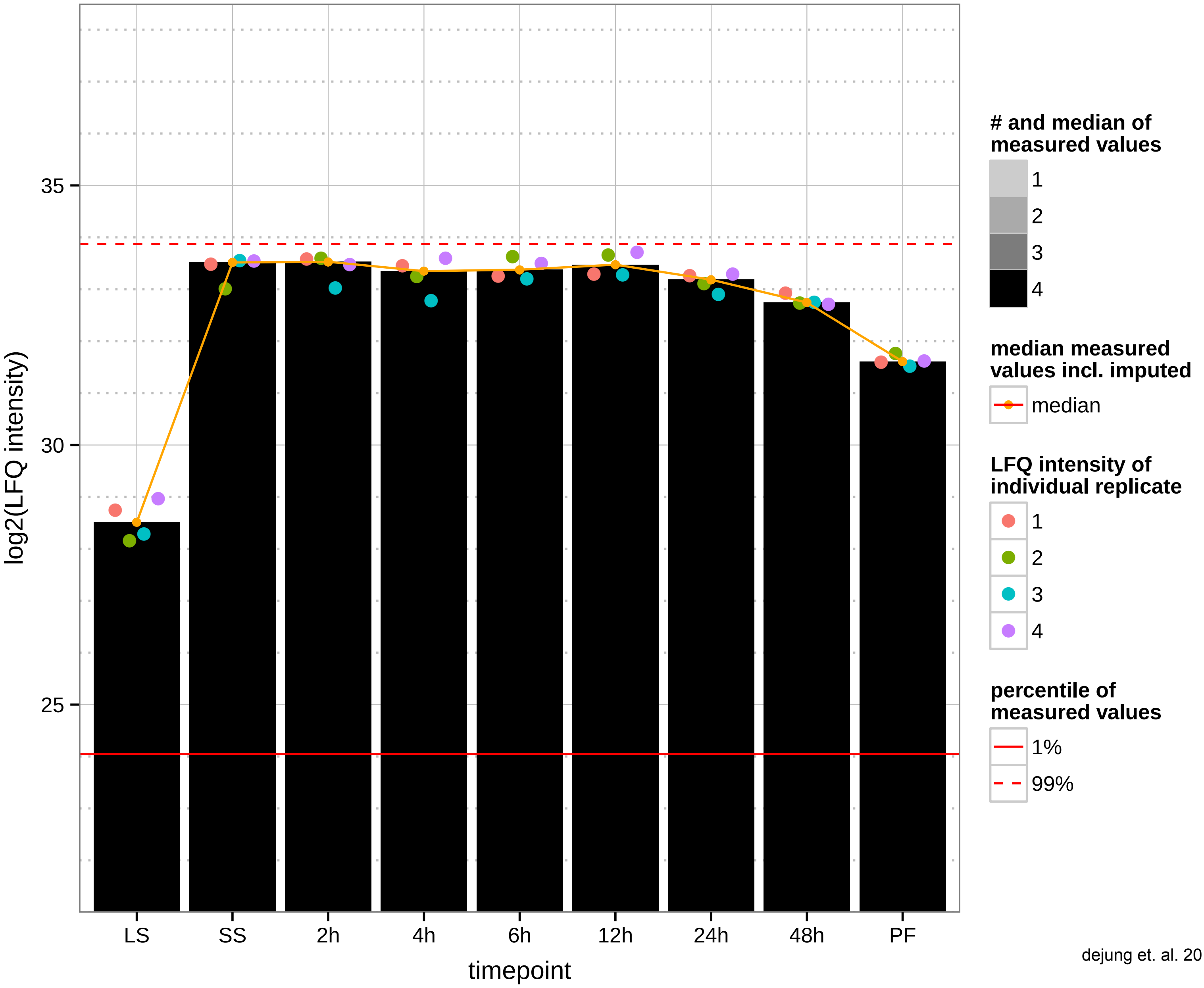
succinyl–coA:3–ketoacid–coenzyme A transferase, mitochondrial precursor, putative
Tb927.11.2690
AGOF: CoA–transferase activity
AGOC: mitochondrion
AGOP: ketone body catabolic process, metabolic process
PGOF: CoA–transferase activity
PGOC: null
PGOP: ketone body catabolic process, metabolic process





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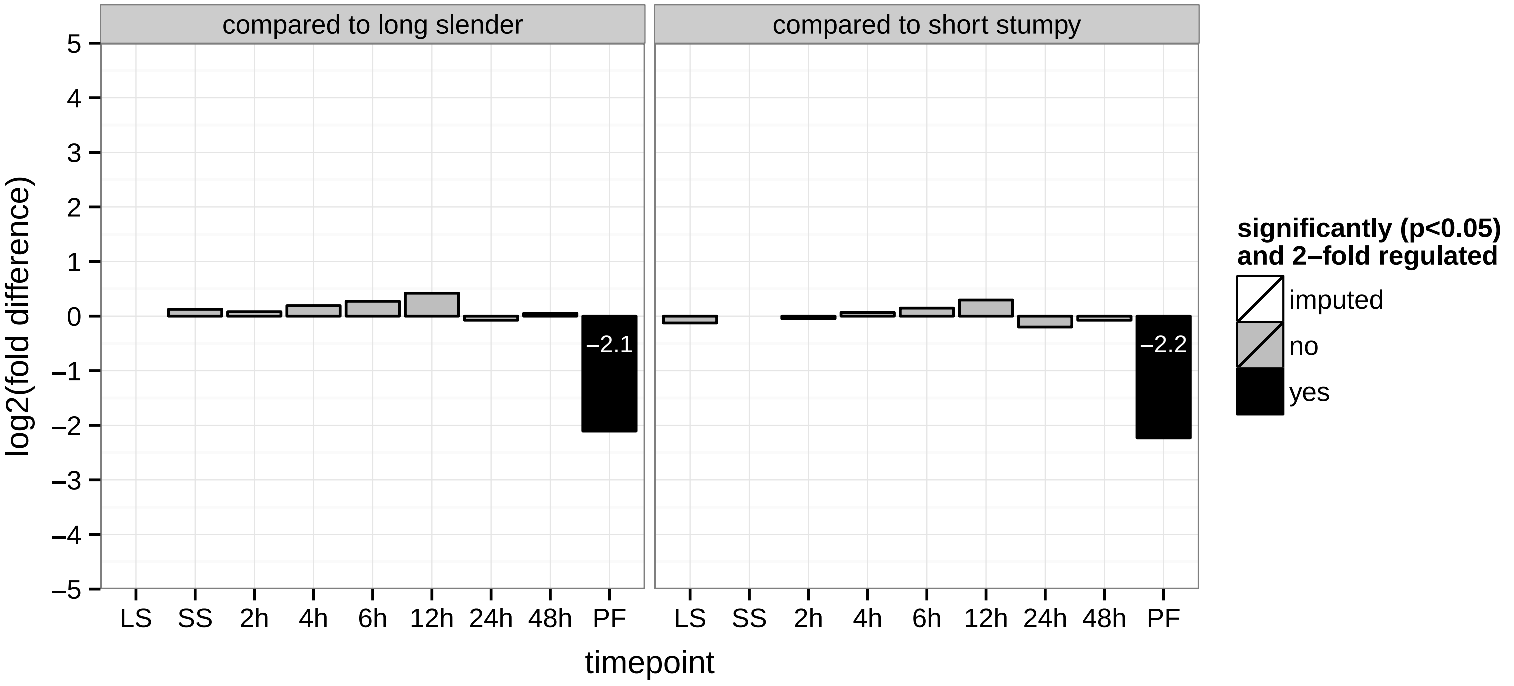
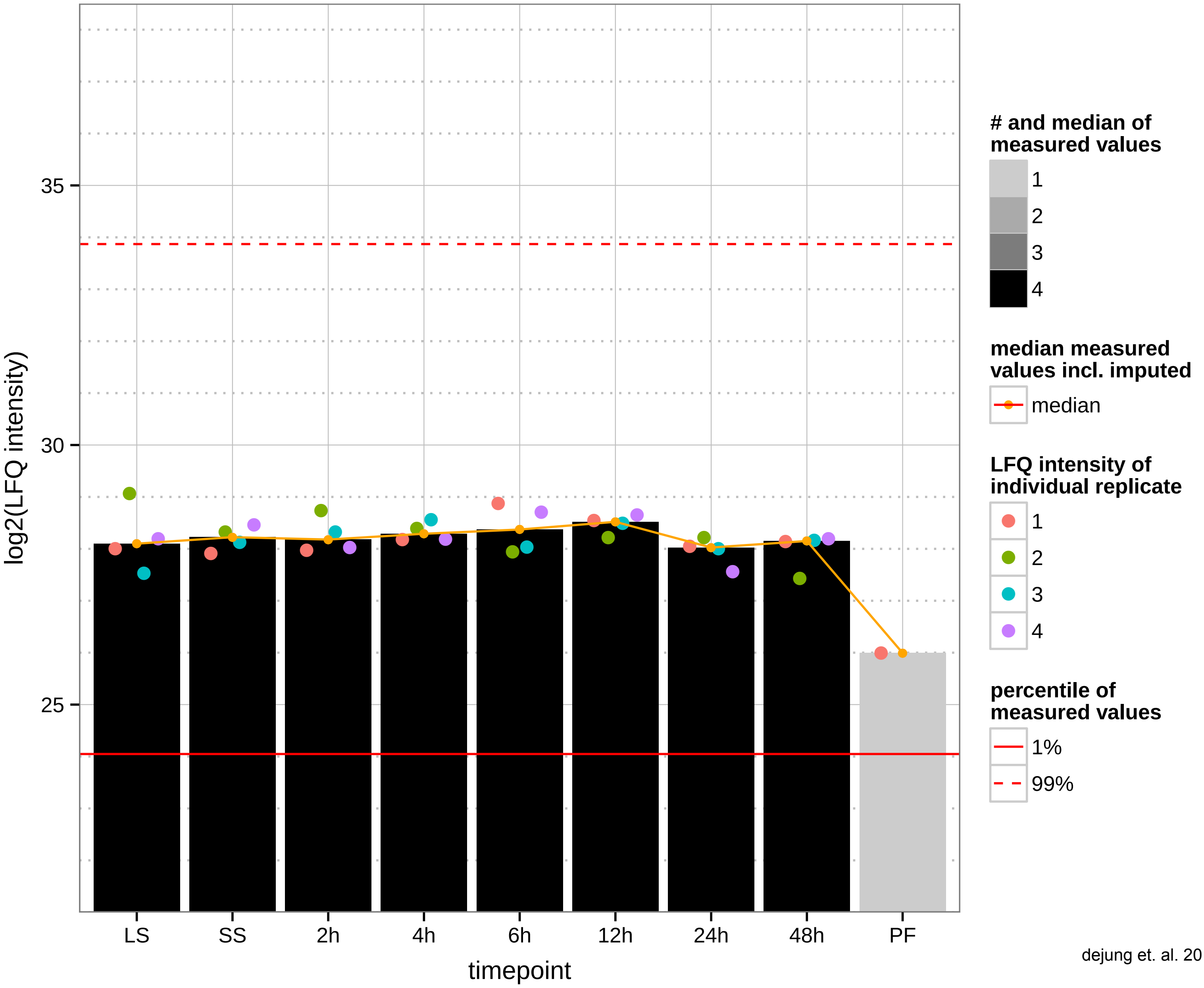
hypothetical protein, conserved
Tb927.11.2750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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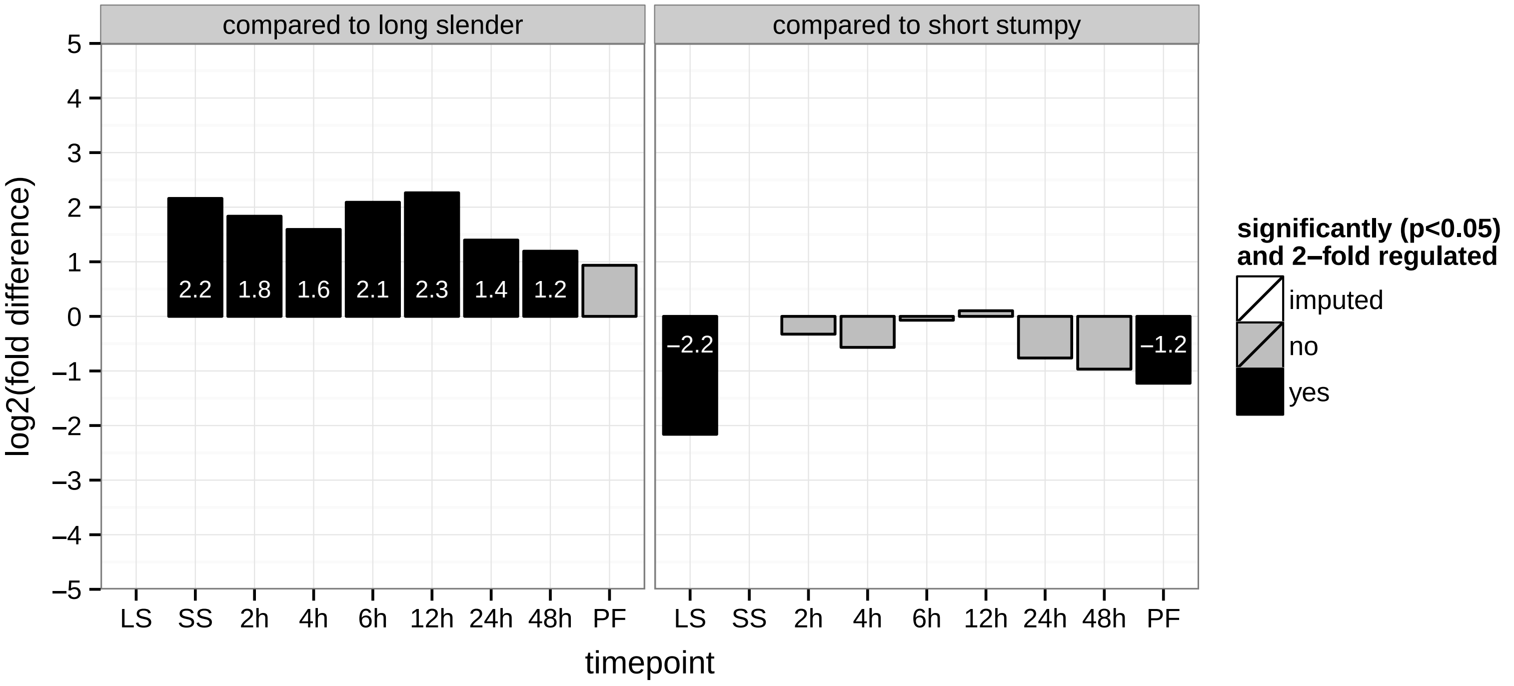
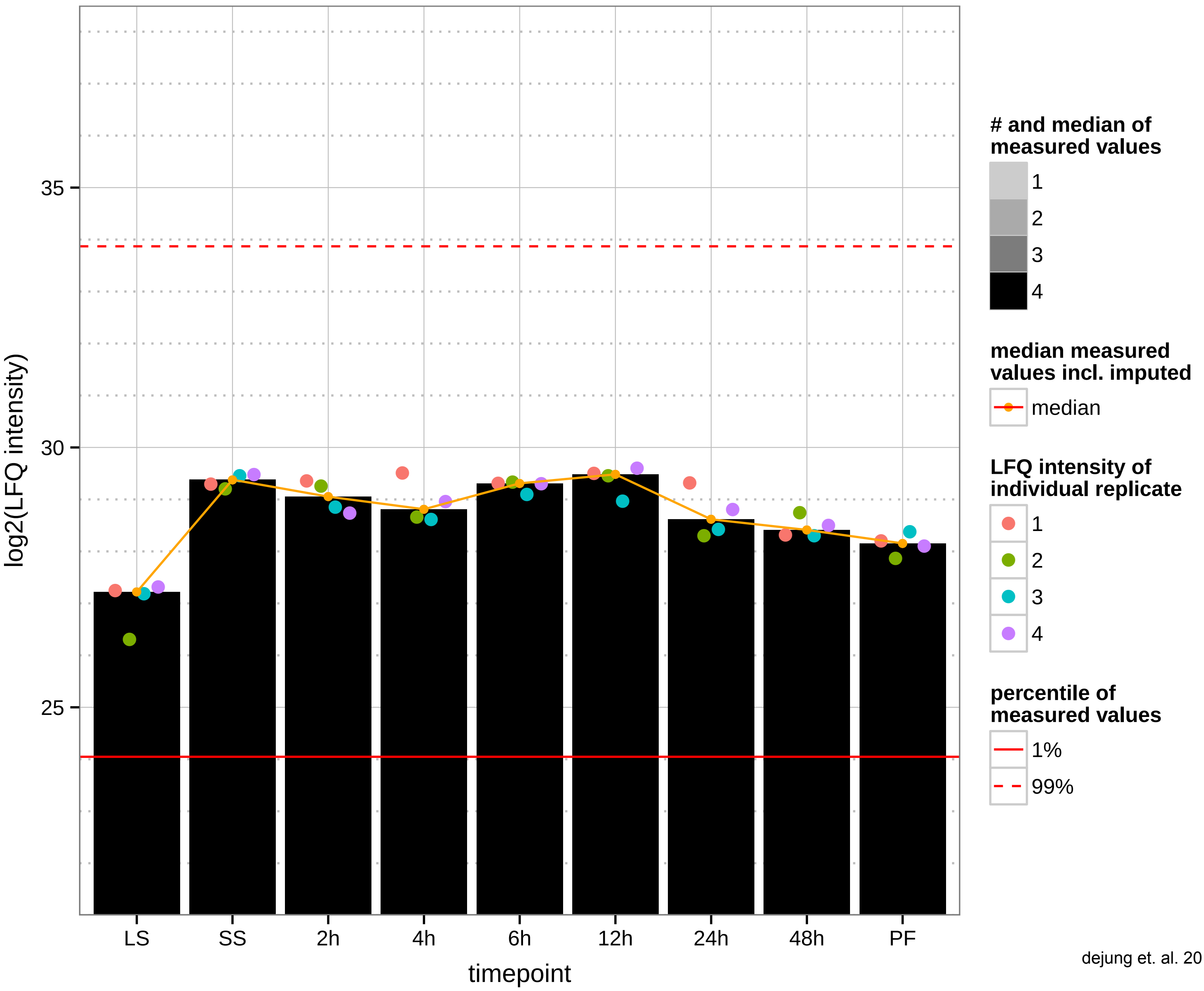
kinesin, putative, MCAK–like kinesin, putative (Kif13–5)
Tb927.11.3280
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: cell, microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity, protein binding
PGOC: null
PGOP: microtubule–based movement





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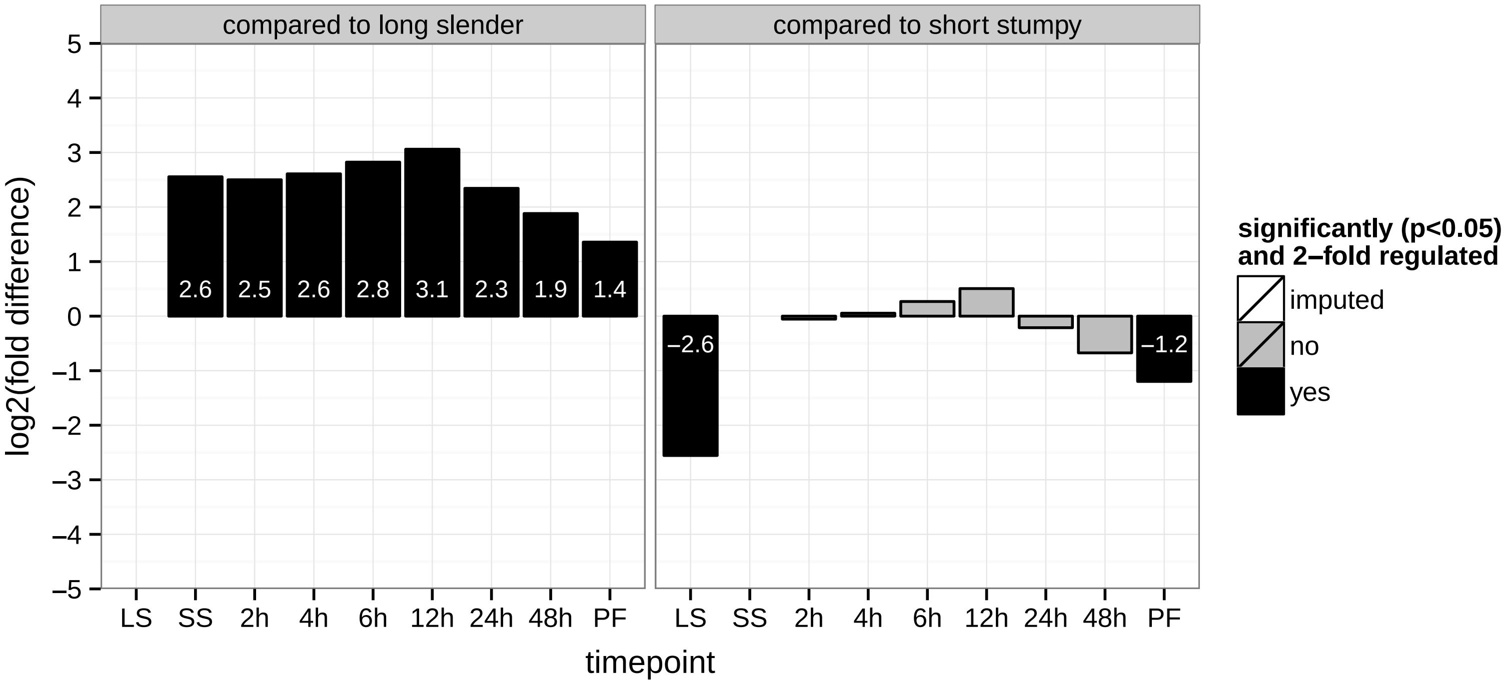
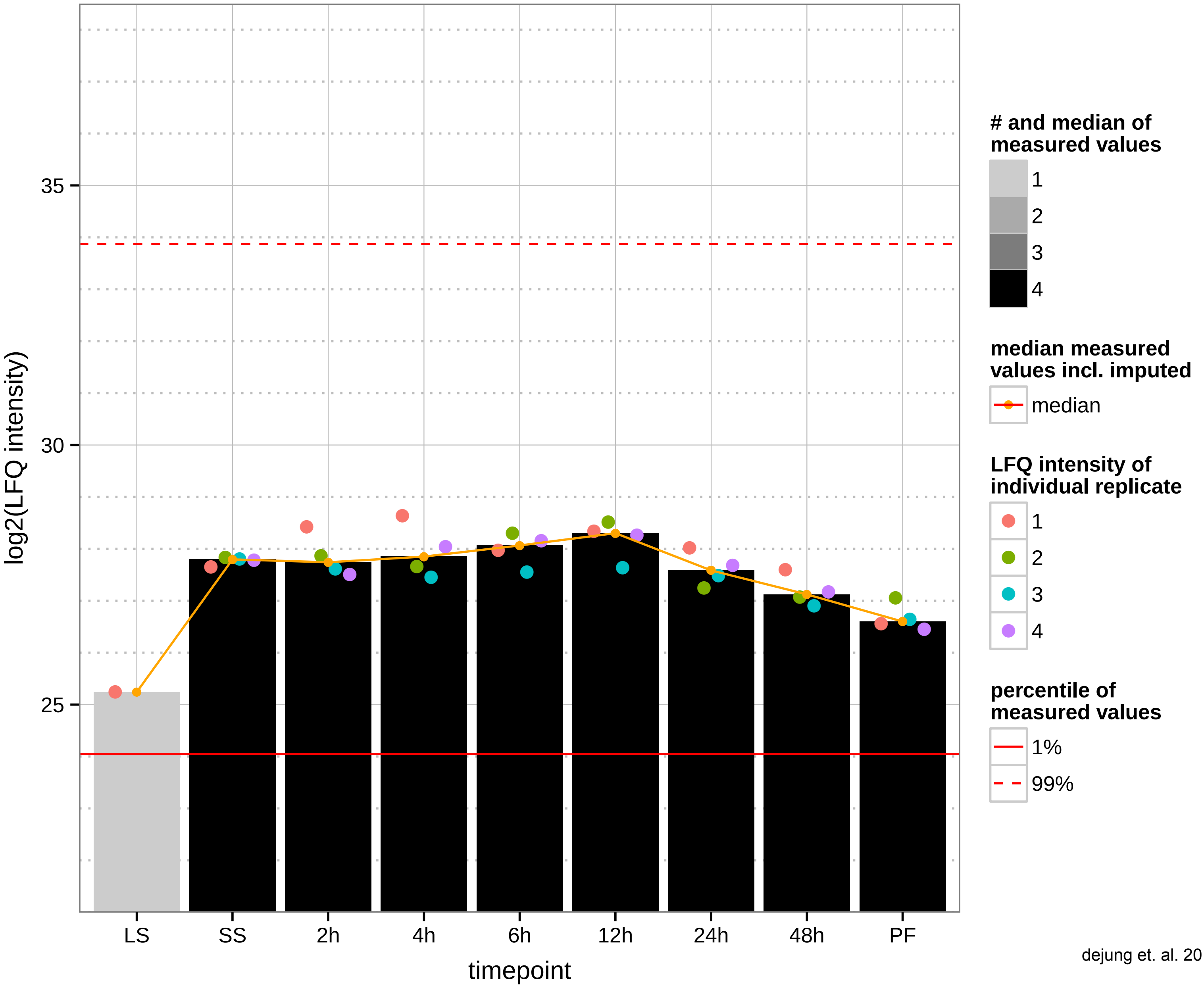
hypothetical protein, conserved
Tb927.11.3690
AGOF: catalytic activity
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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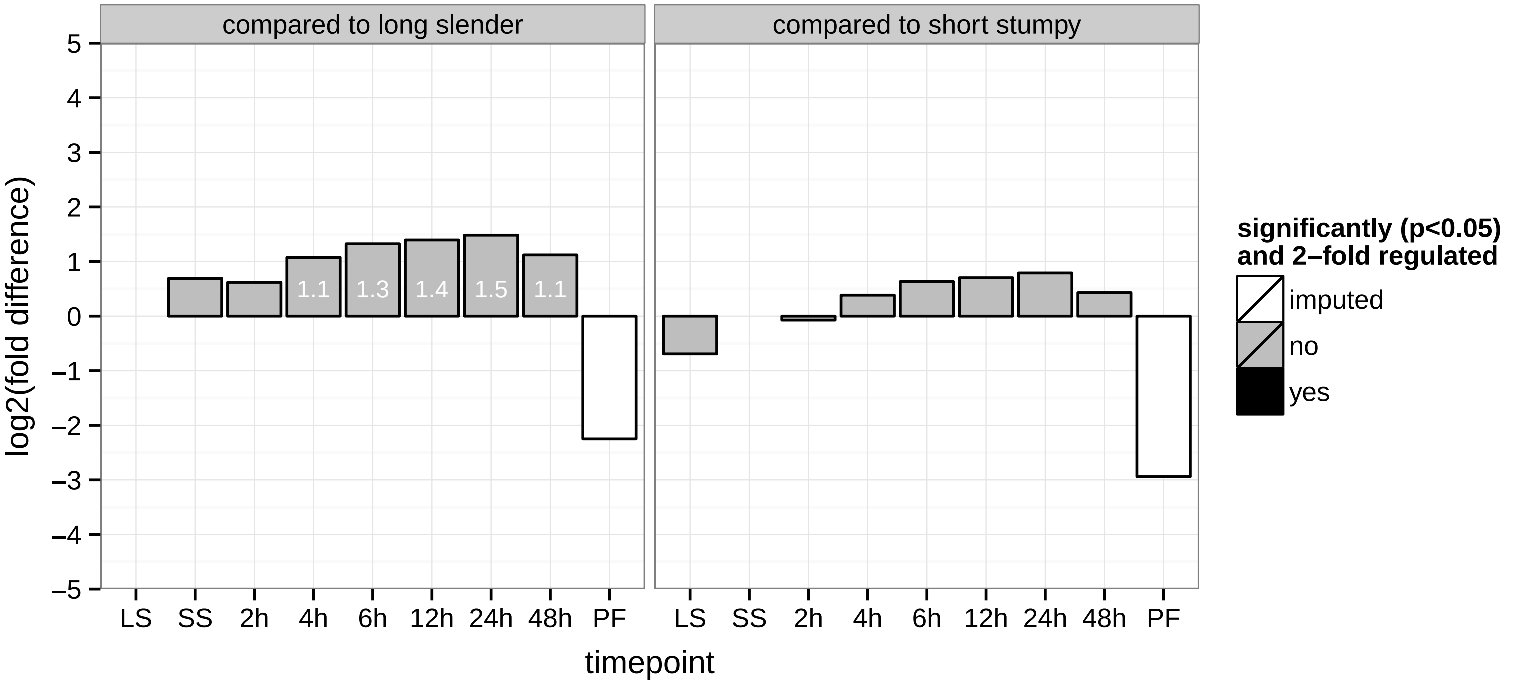
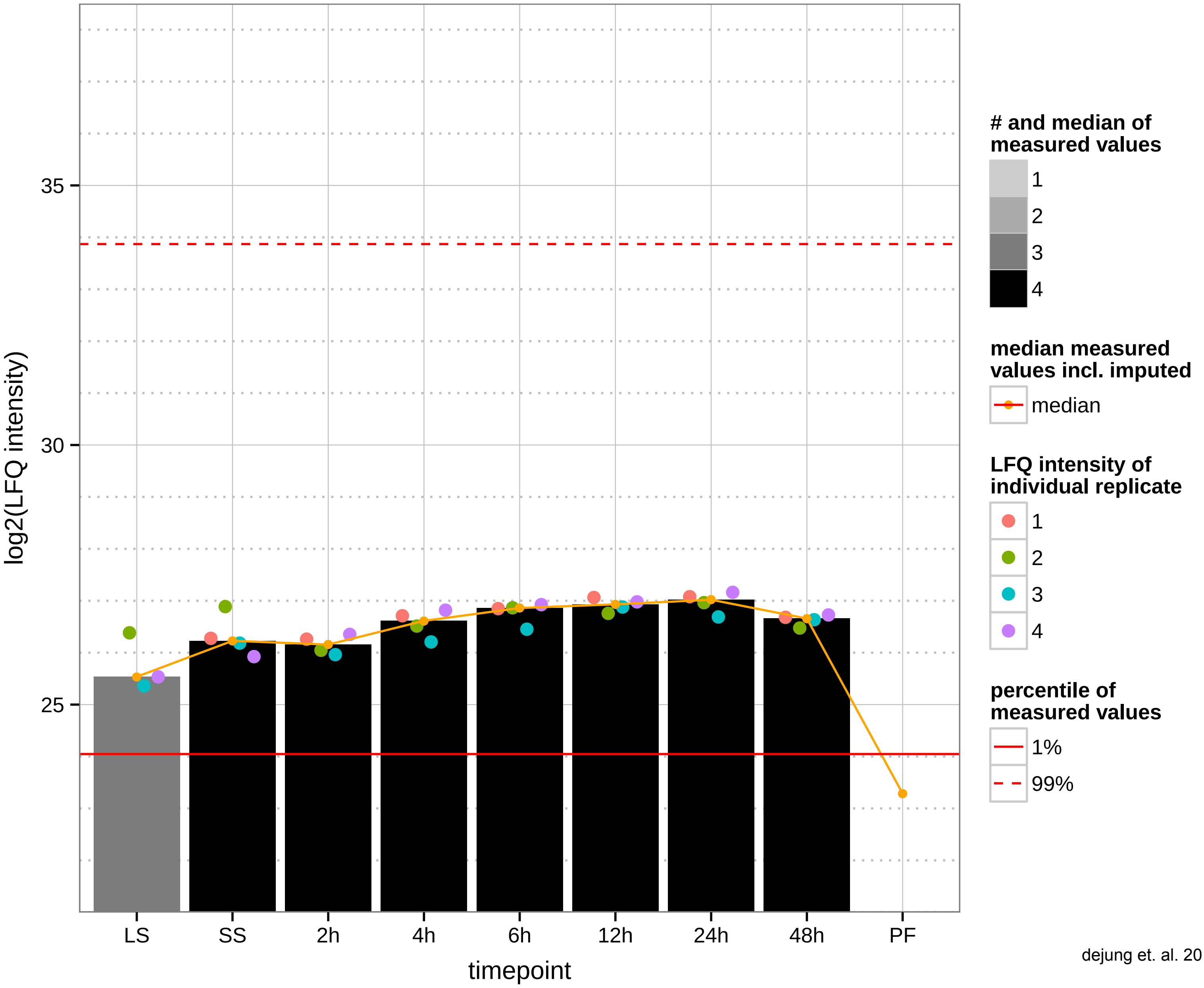
hypothetical protein, conserved
Tb927.11.3840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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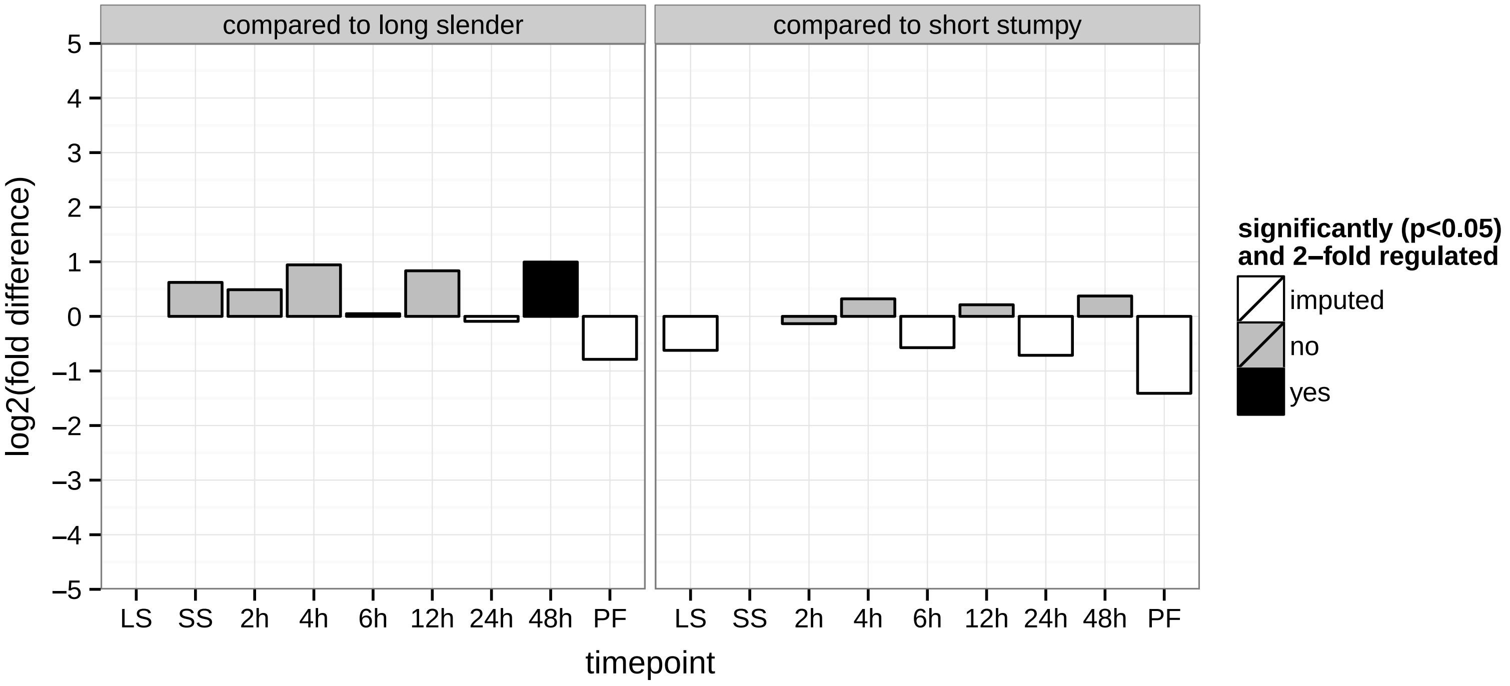
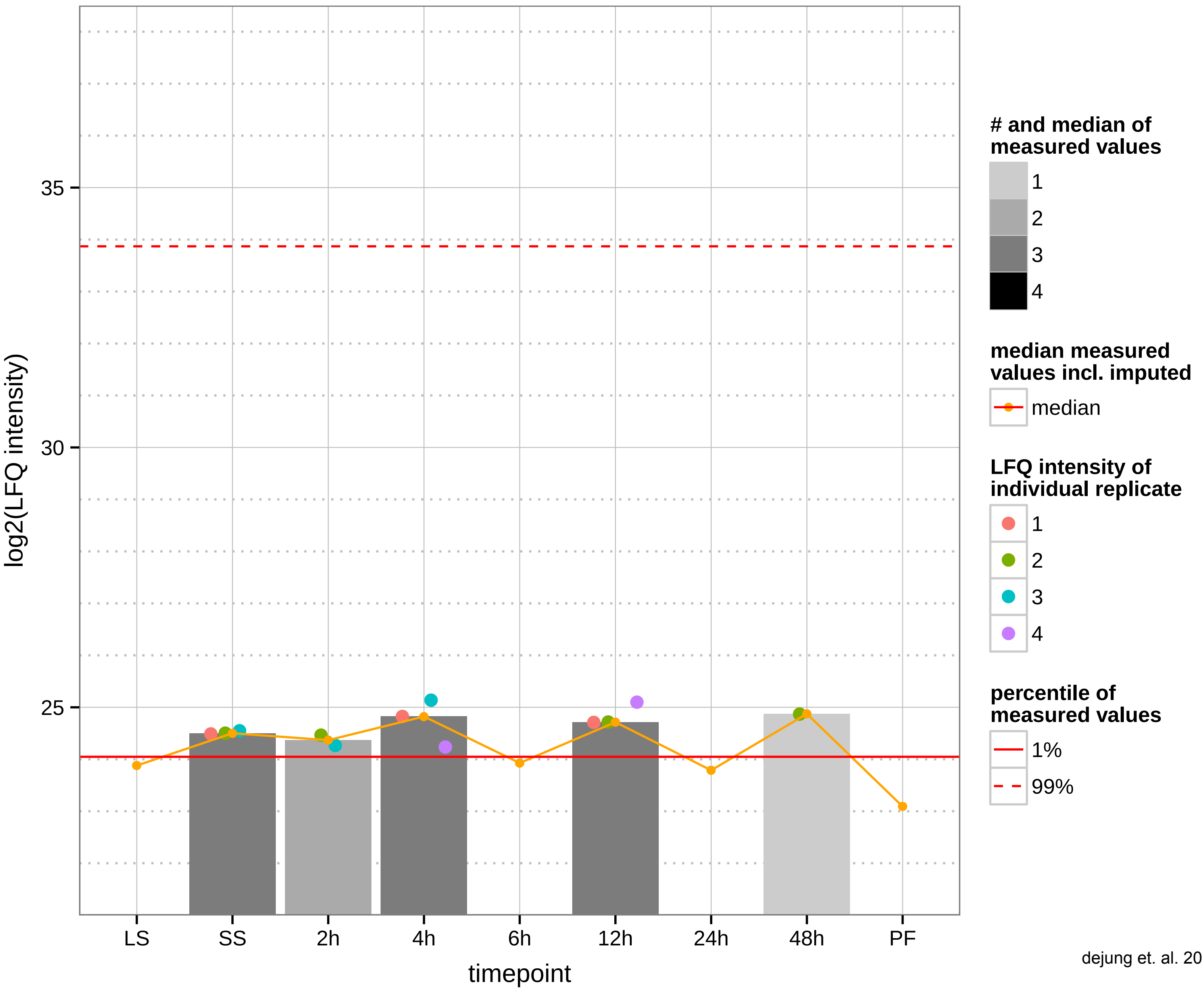
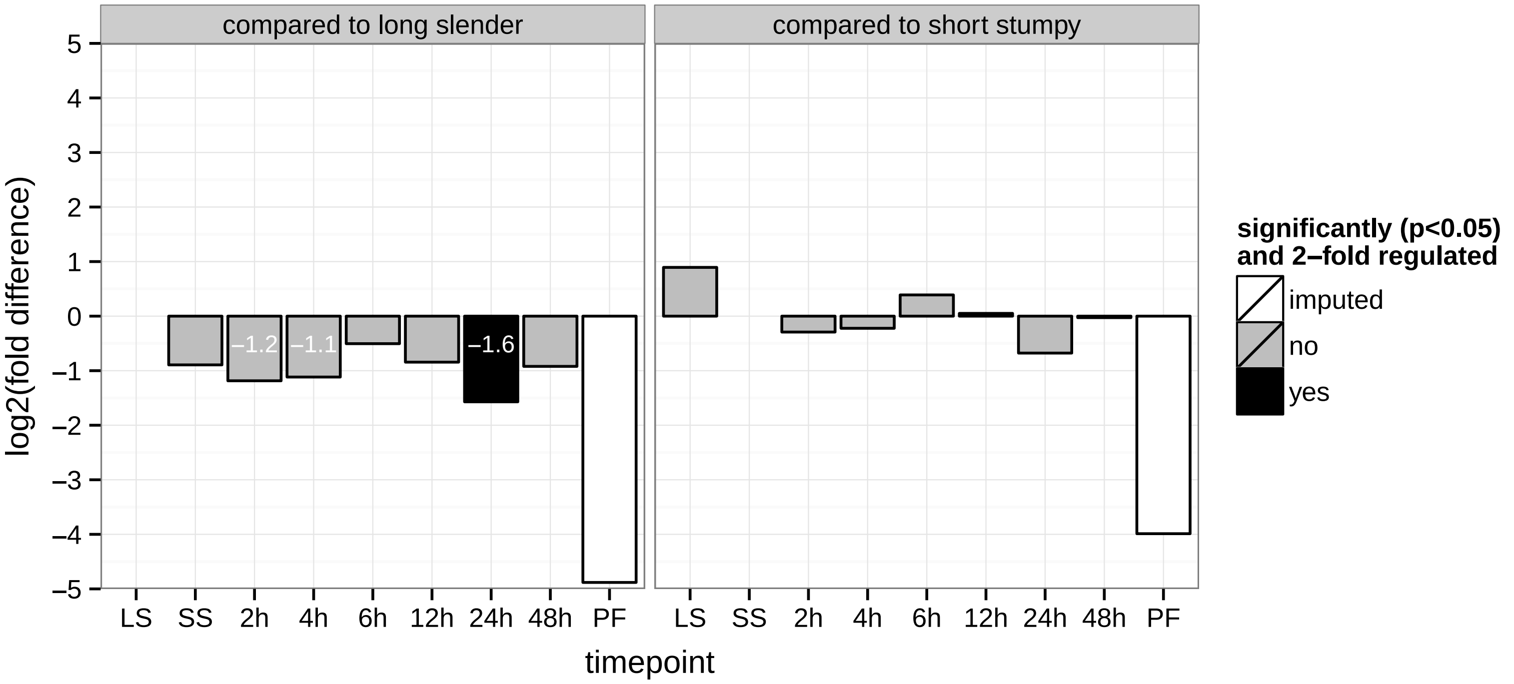
hypothetical protein, conserved
Tb927.11.3920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

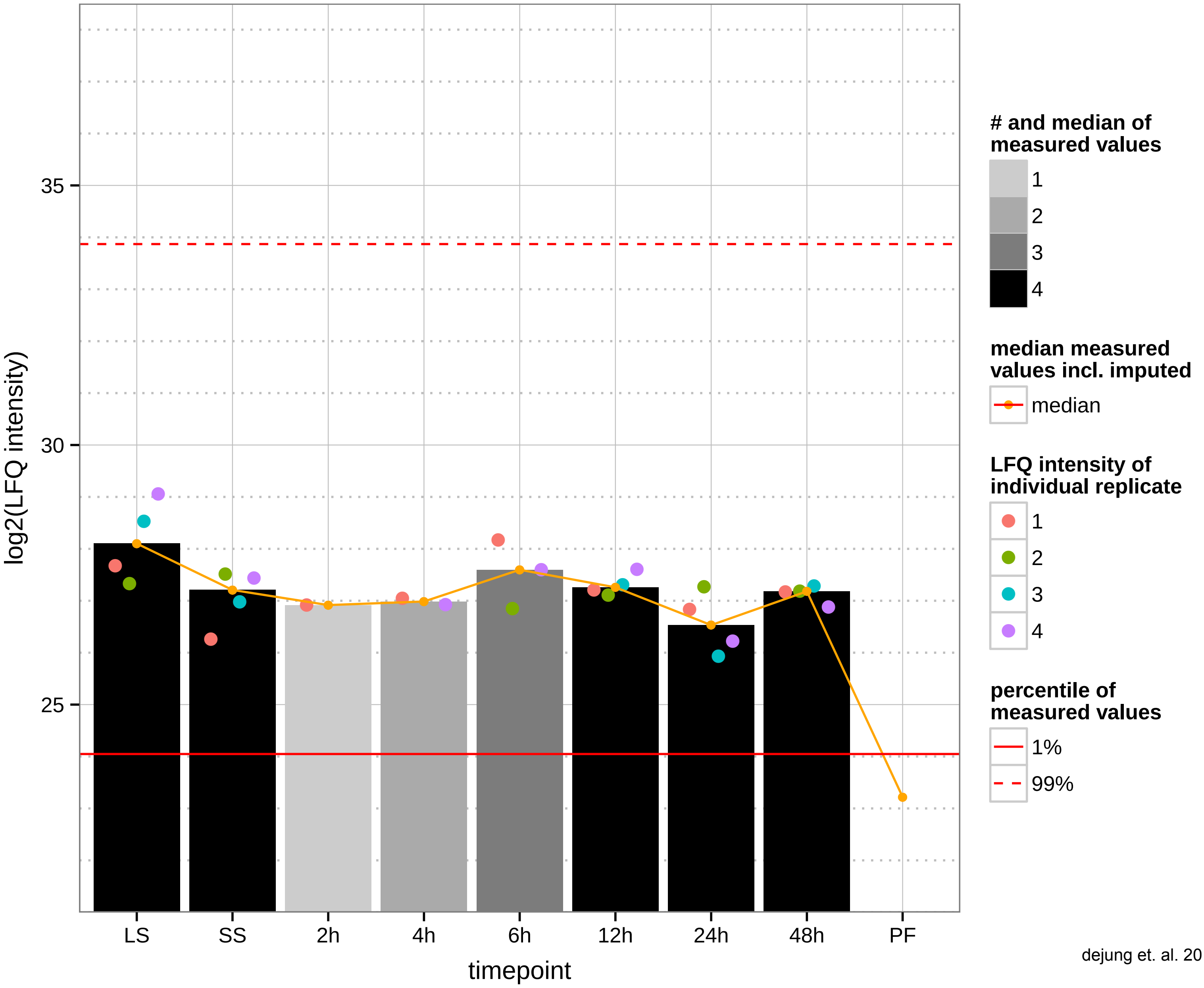




dejung et. al. 2015

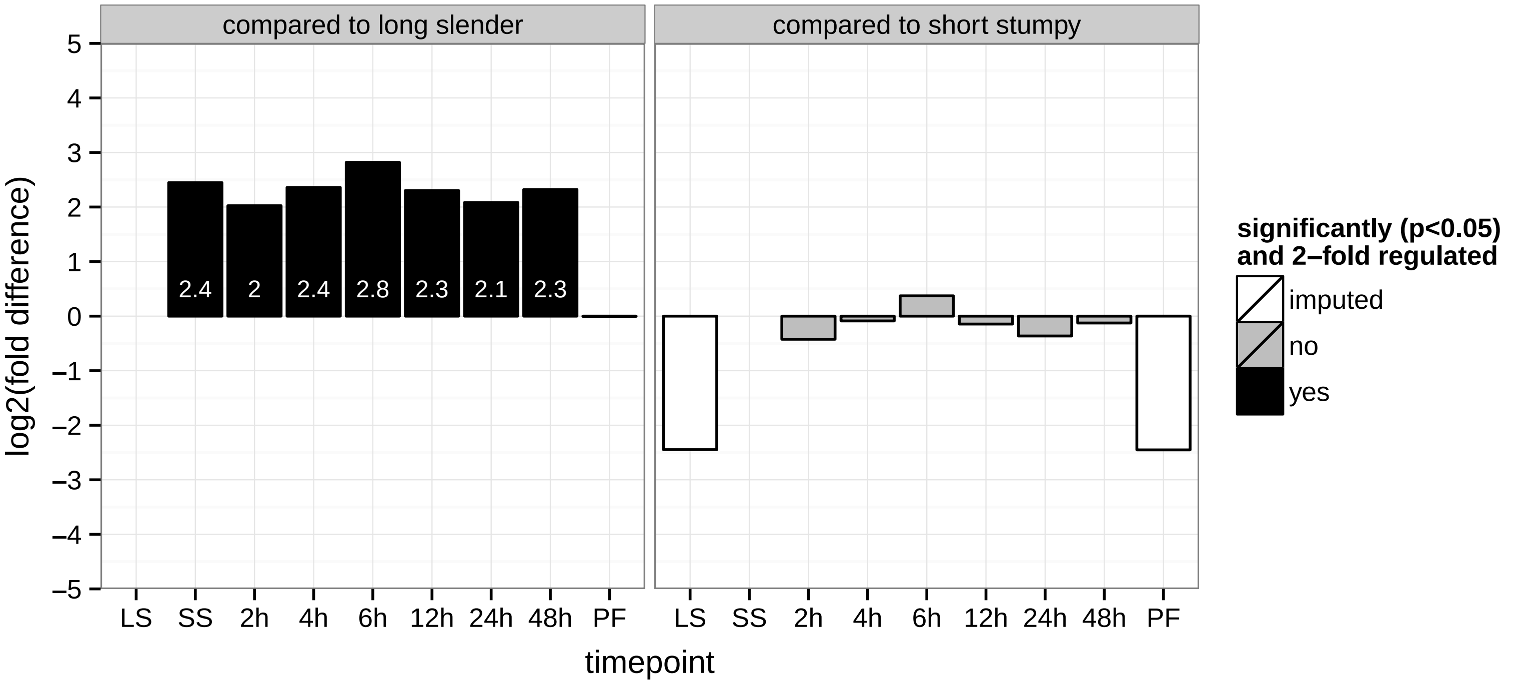
hypothetical protein, conserved
Tb927.11.4030
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

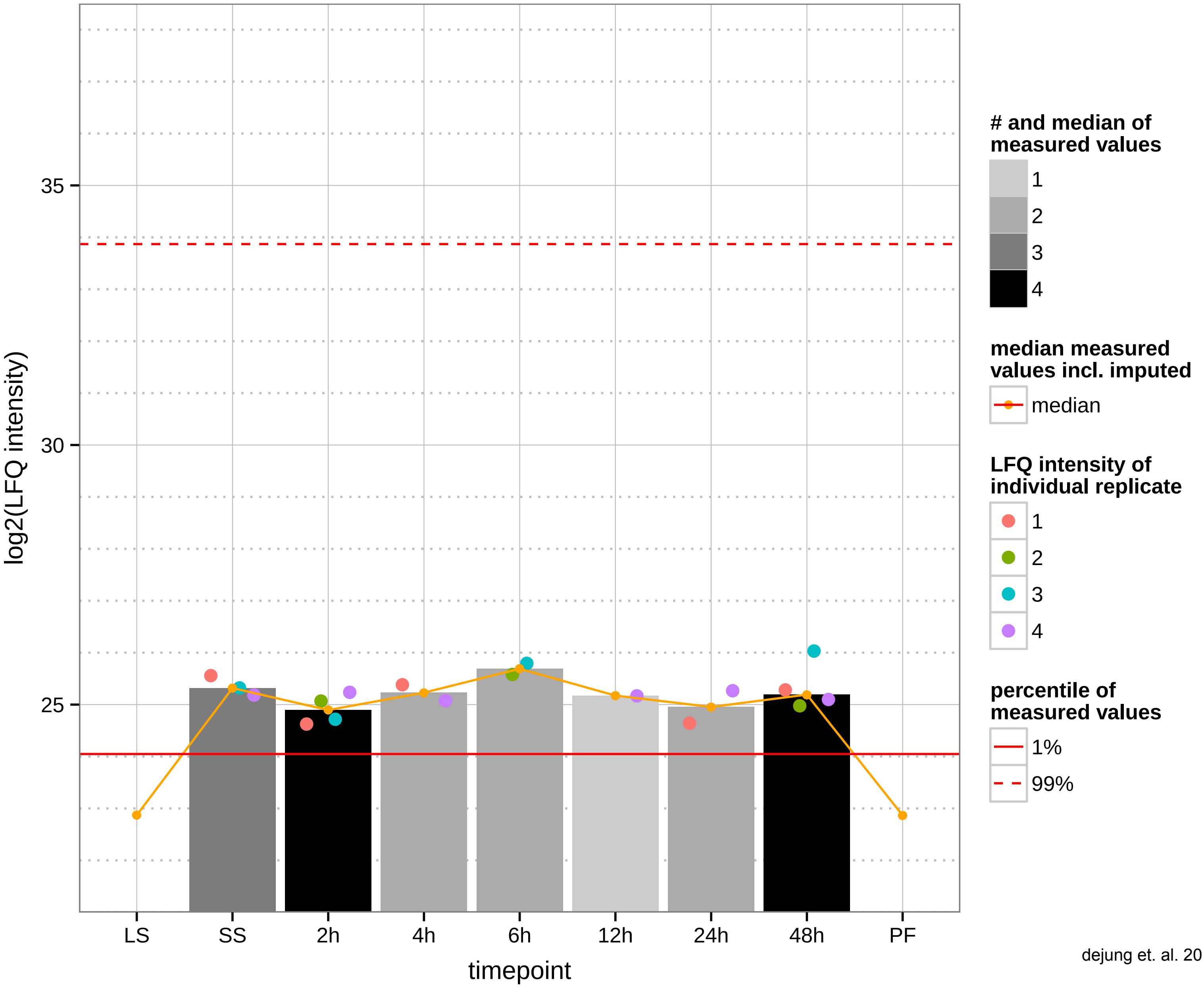




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.5150
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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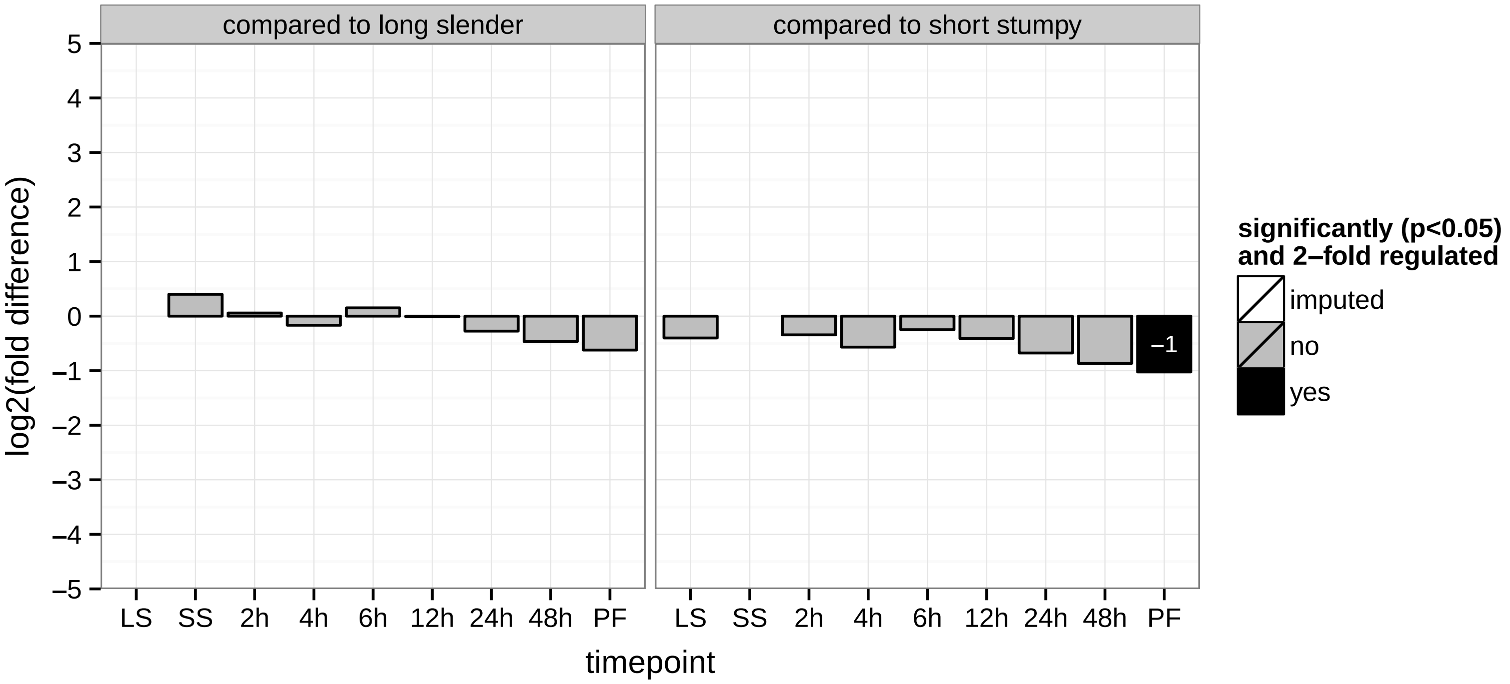
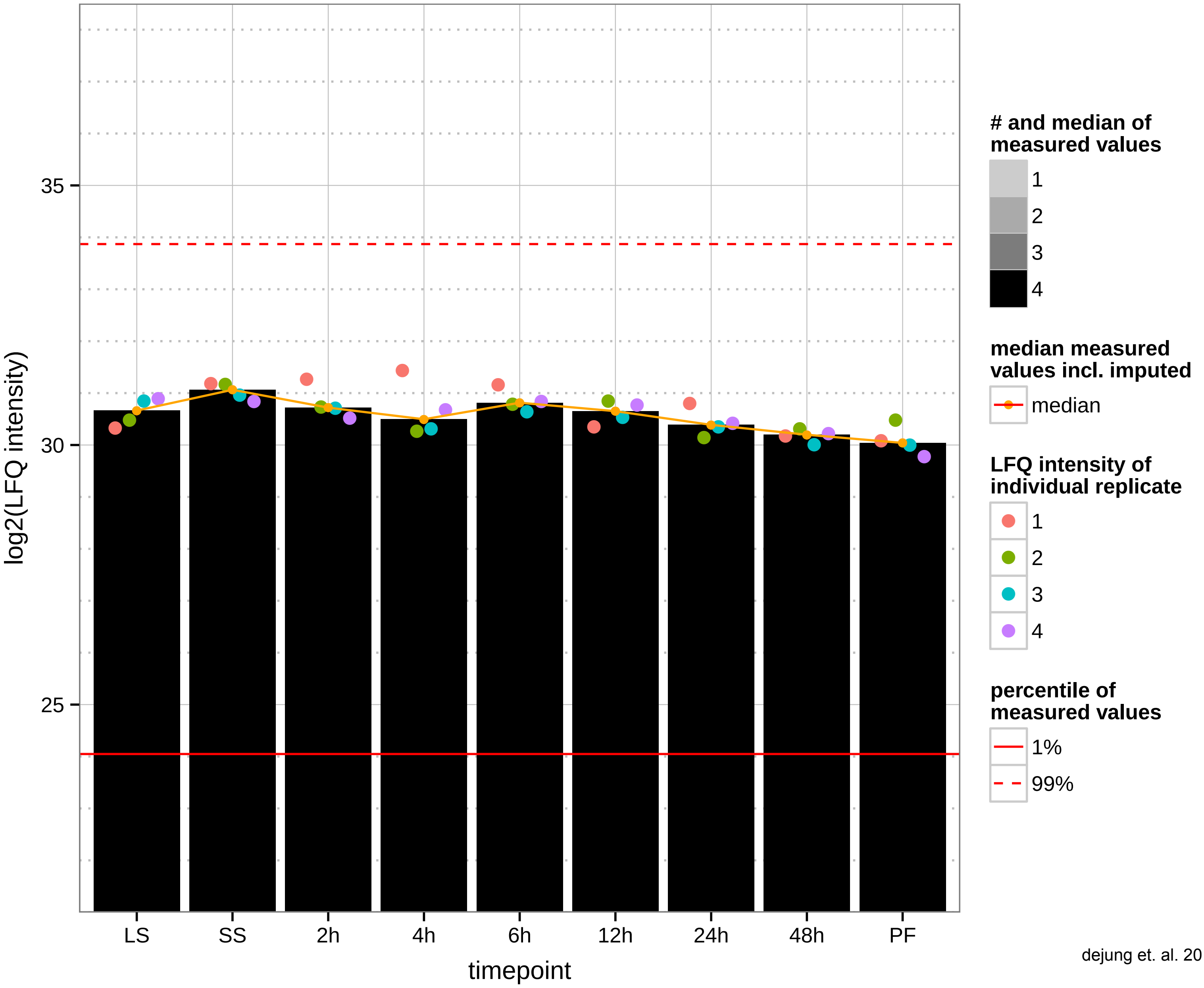
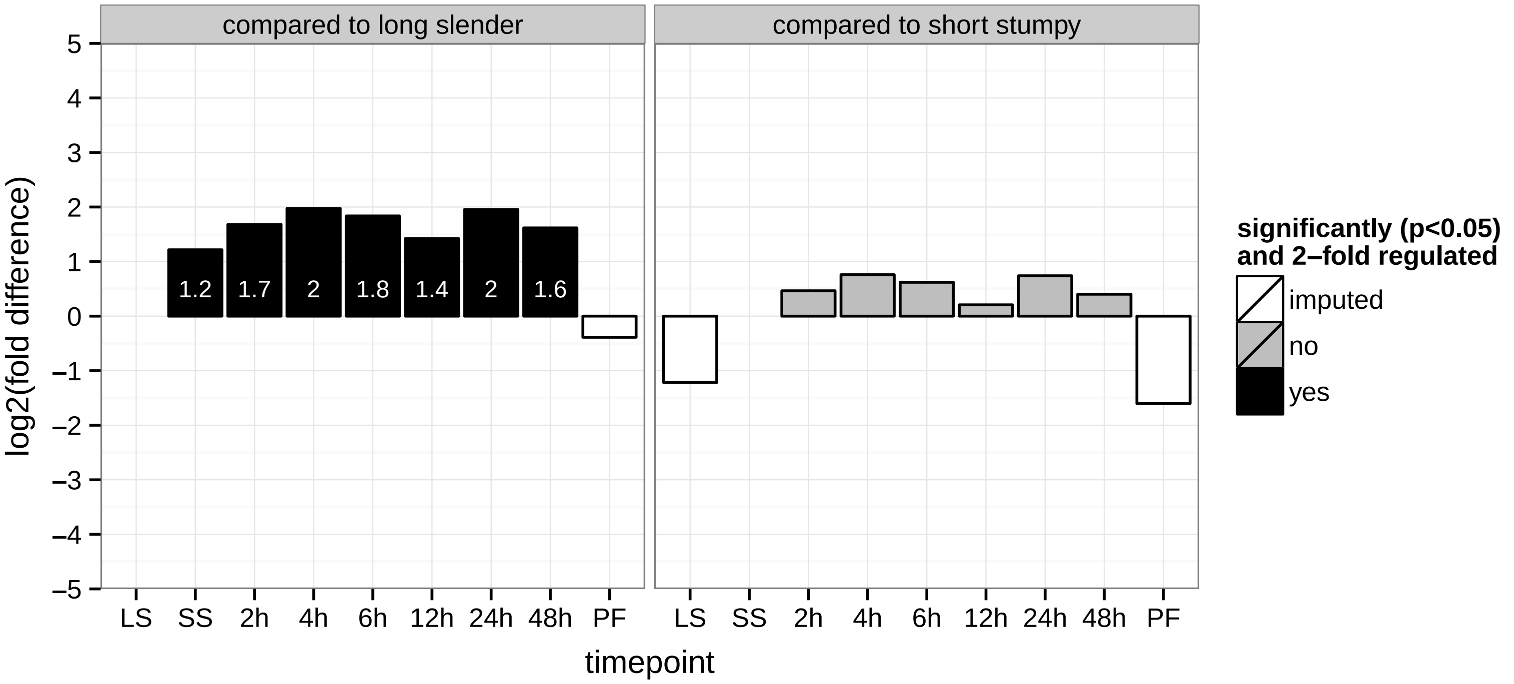
pretranslocation protein, alpha subunit, putative, SEC61–like (pretranslocation process) protein
Tb927.11.6230
AGOF: P–P–bond–hydrolysis–driven protein transmembrane transporter activity
AGOC: endoplasmic reticulum, integral to membrane, membrane
AGOP: protein secretion, protein transport
PGOF: P–P–bond–hydrolysis–driven protein transmembrane transporter activity
PGOC: membrane
PGOP: protein transport

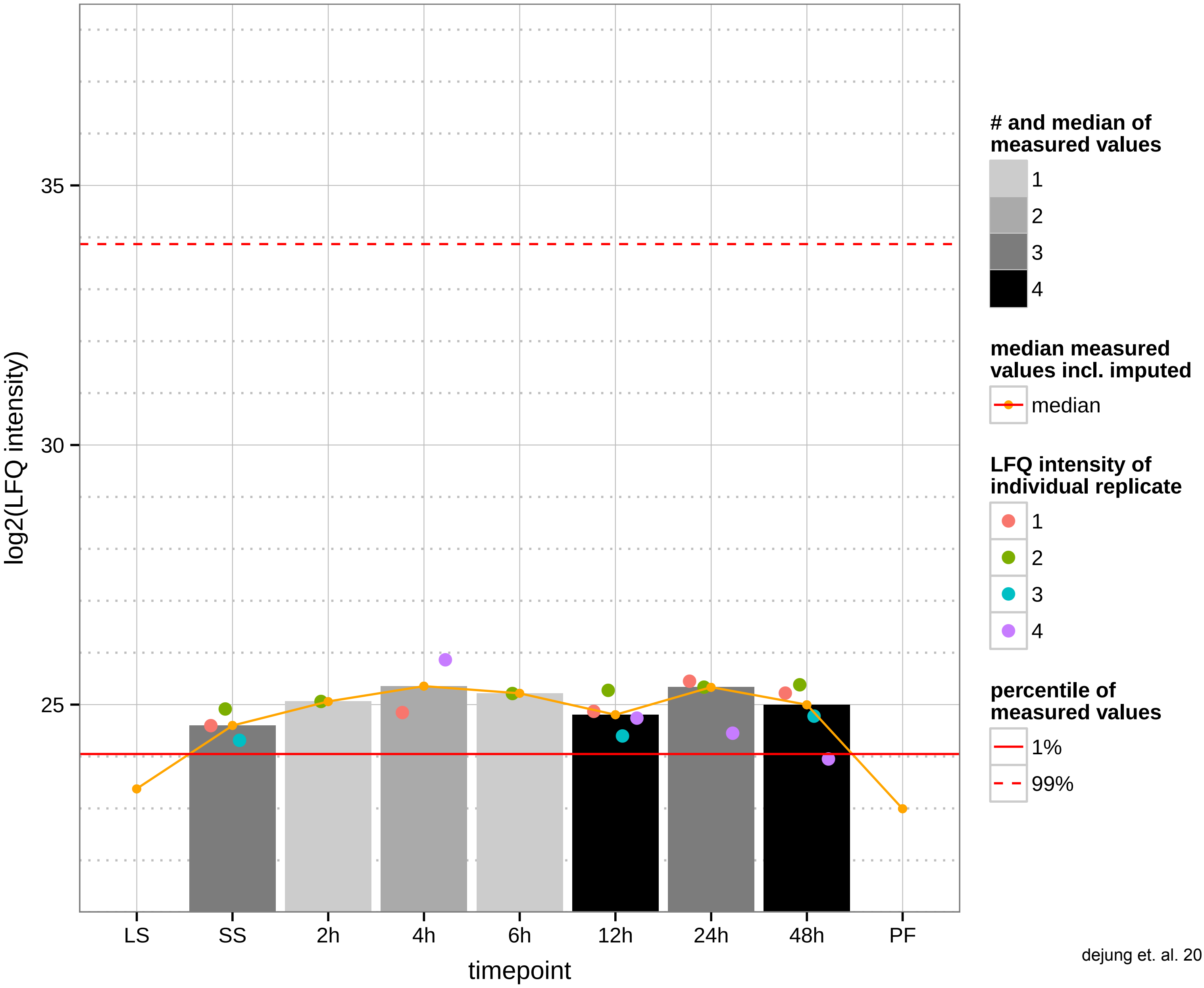




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.6520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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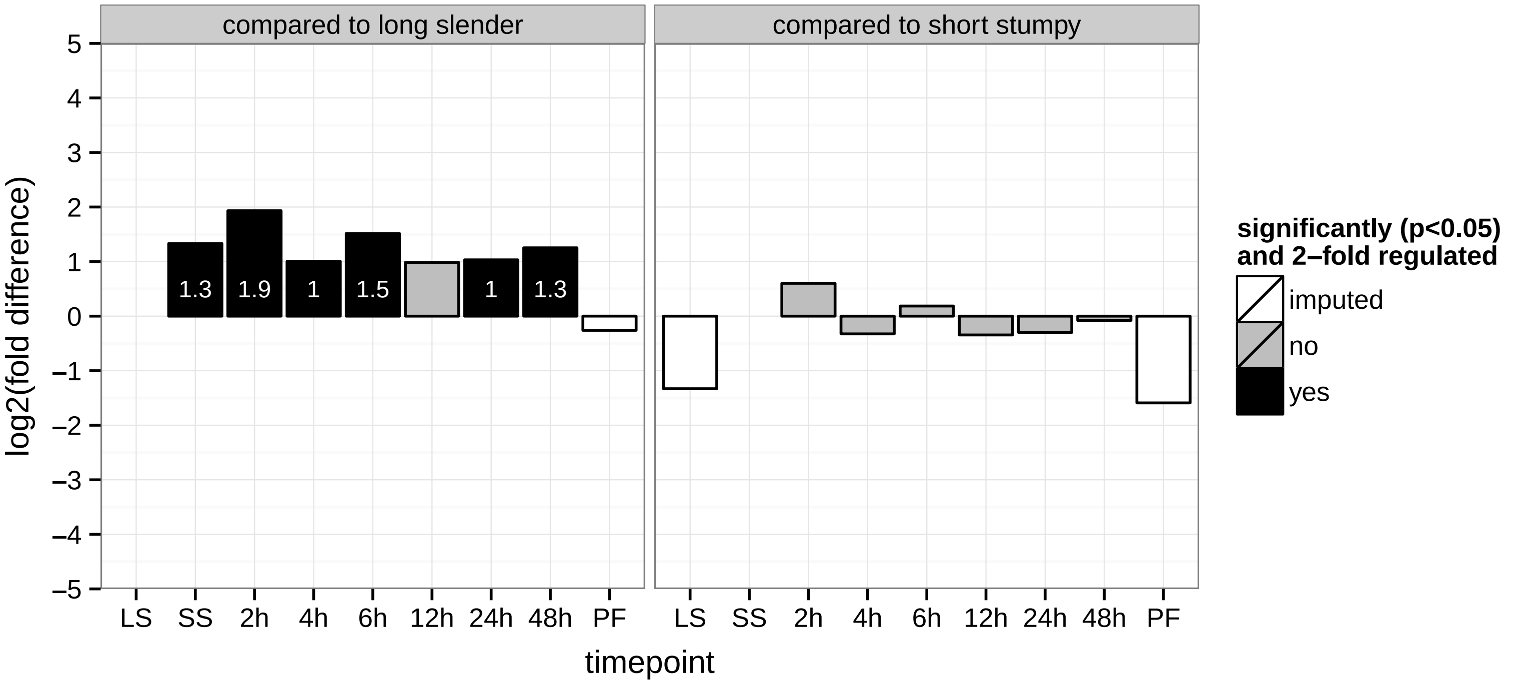
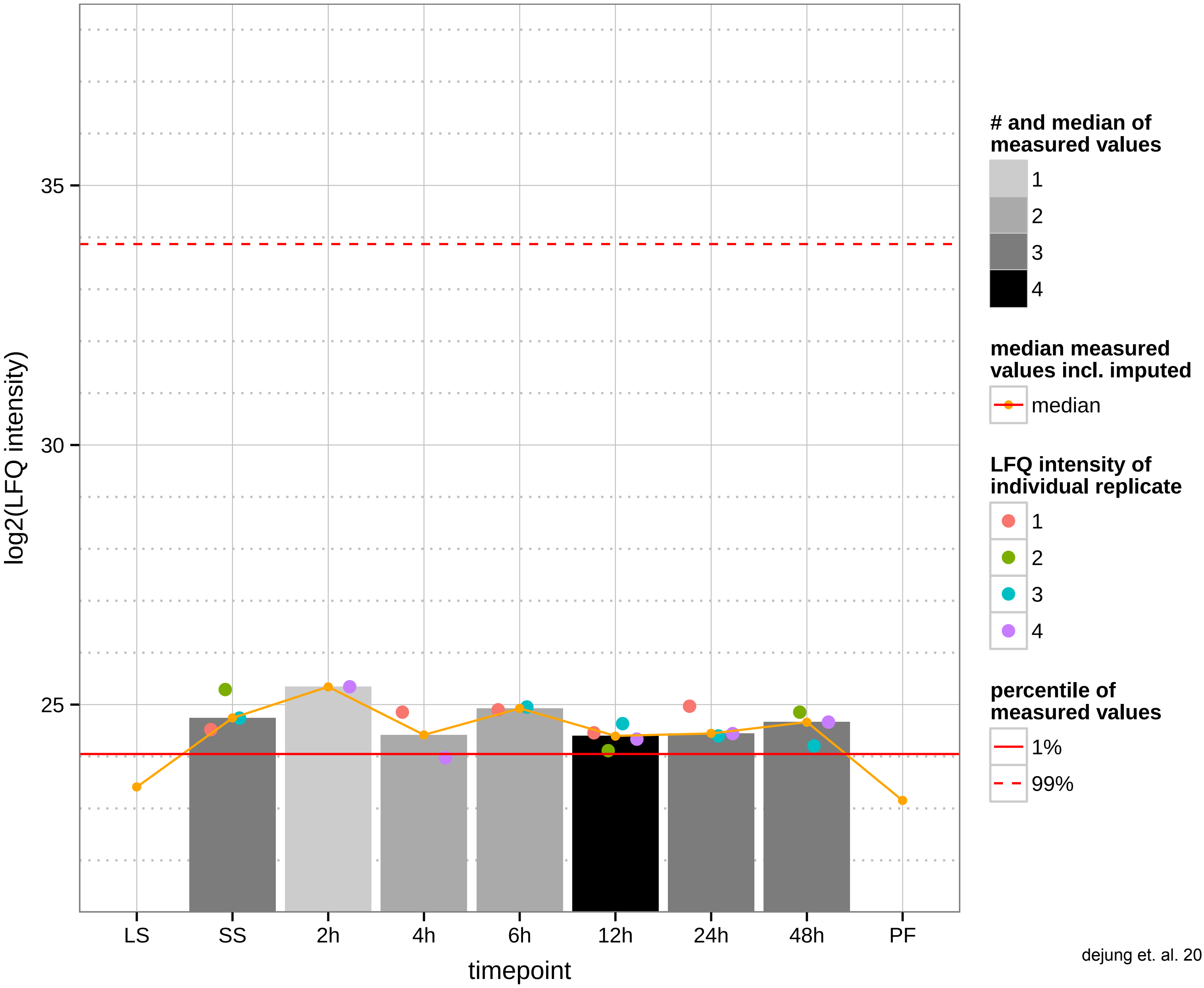
hypothetical protein, conserved
Tb927.11.6920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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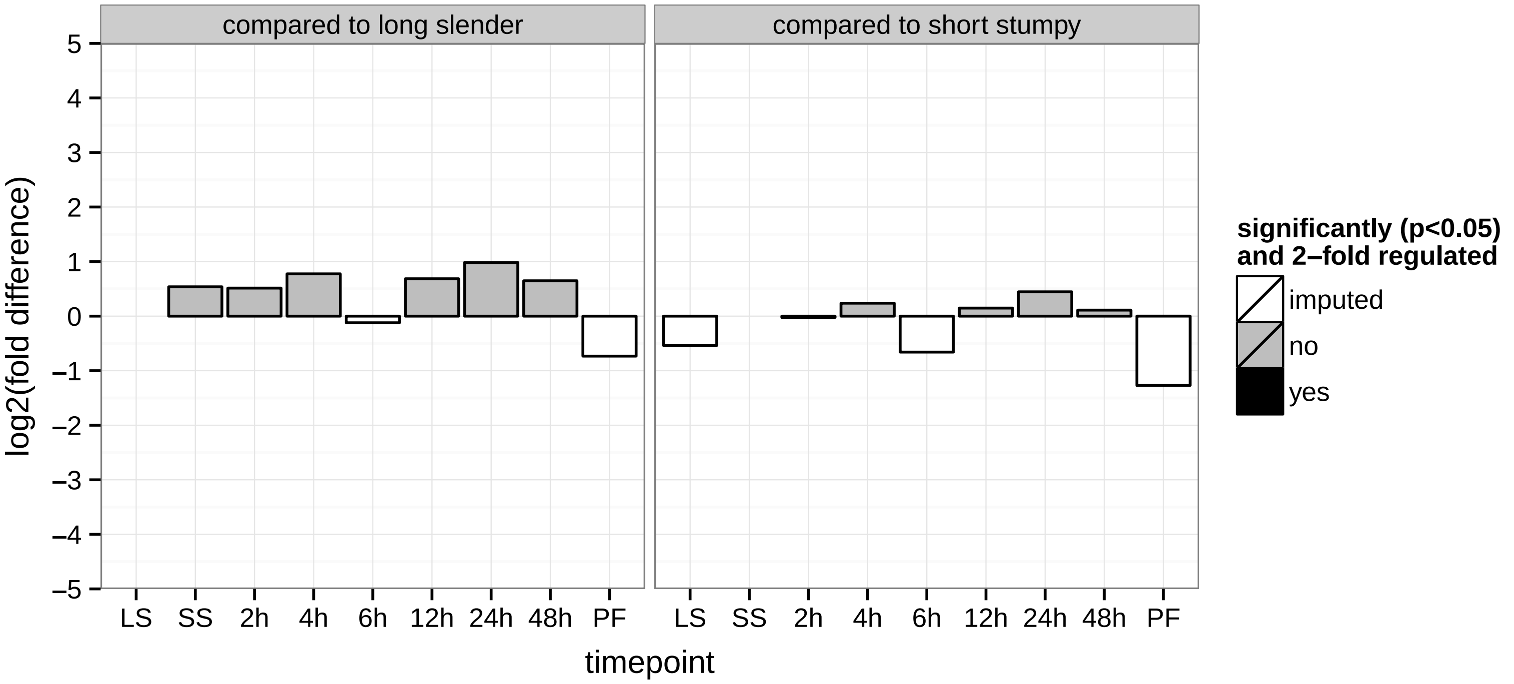
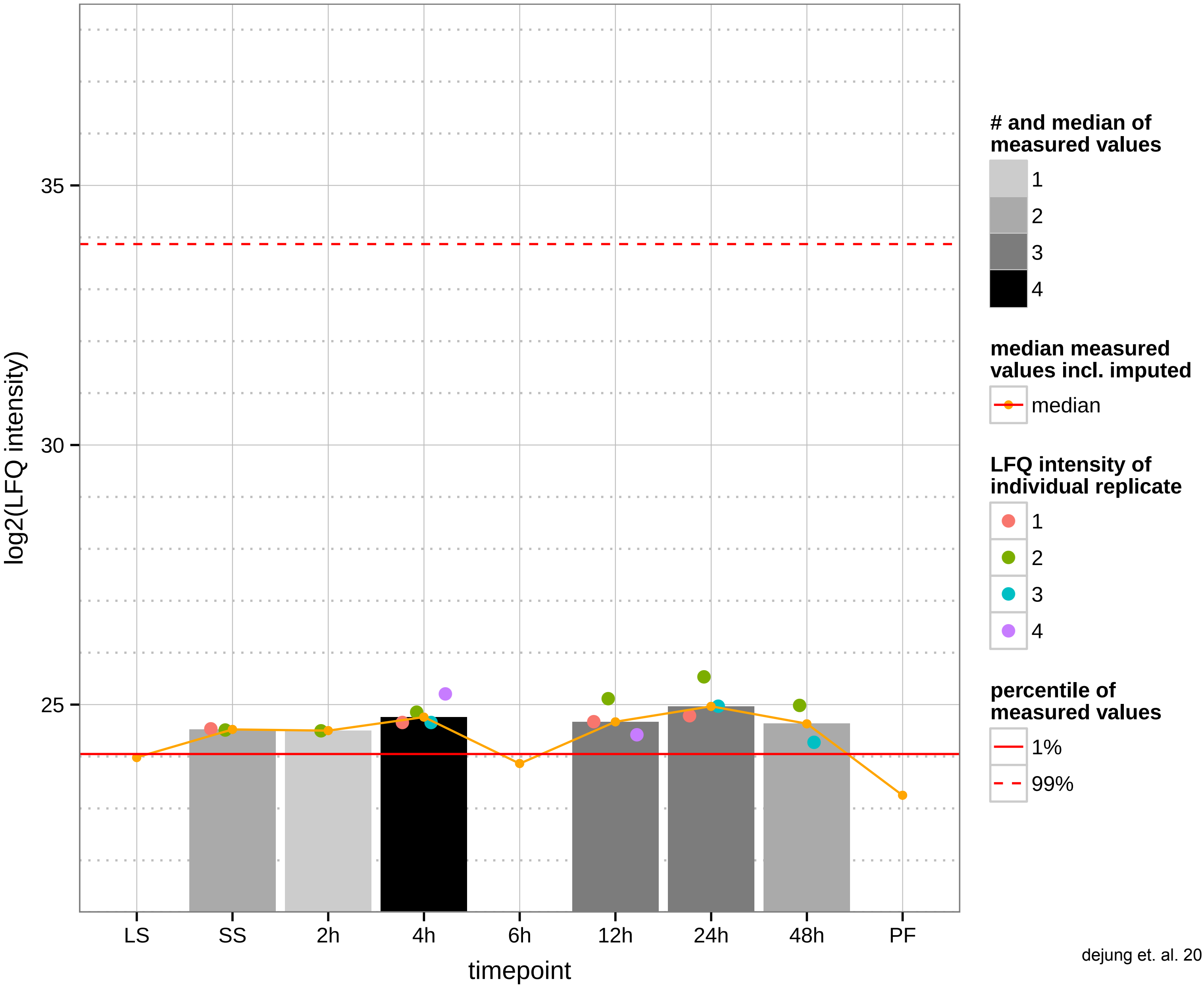
pterin–4–alpha–carbinolamine dehydratase, putative
Tb927.11.7040
AGOF: 4–alpha–hydroxytetrahydrobiopterin dehydratase activity
AGOC: mitochondrion
AGOP: tetrahydrobiopterin biosynthetic process
PGOF: 4–alpha–hydroxytetrahydrobiopterin dehydratase activity
PGOC: null
PGOP: tetrahydrobiopterin biosynthetic process





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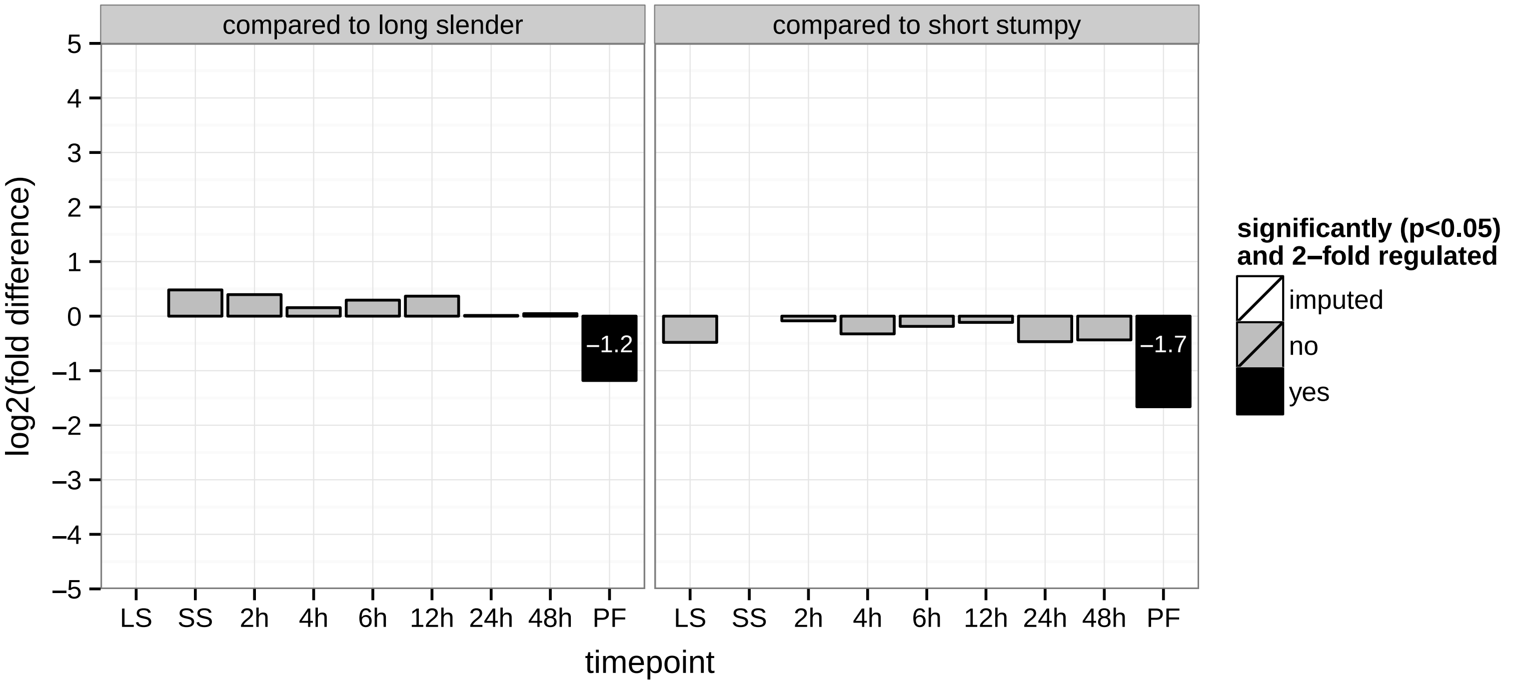
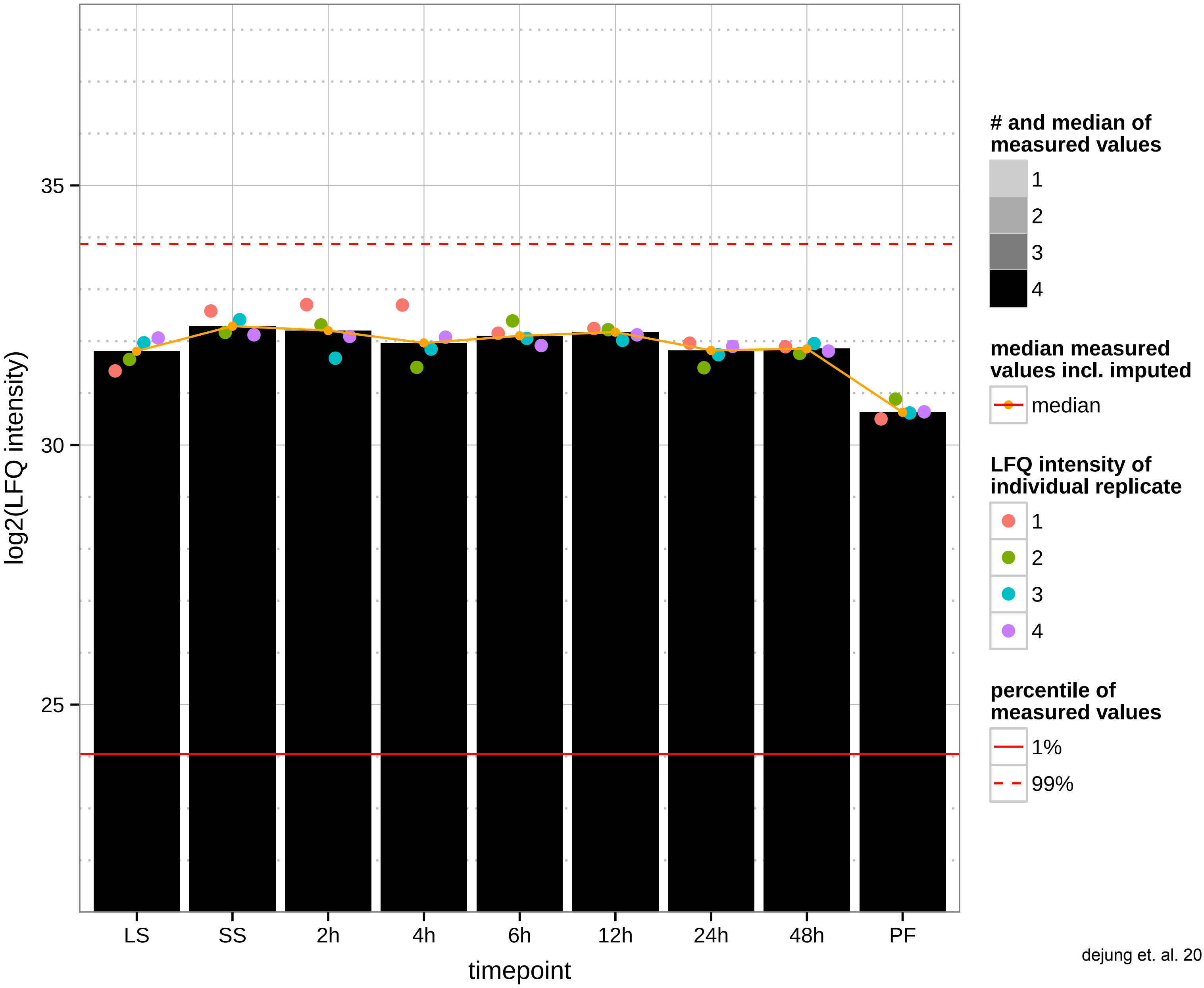
glycerol−3−phosphate dehydrogenase (FAD−dependent), mitochondrial
Tb927.11.7380
AGOF: flavin adenine dinucleotide binding, glycerol−3−phosphate dehydrogenase activity
AGOC: glycerol−3−phosphate dehydrogenase complex, mitochondrion
AGOP: glycerol catabolic process, glycerol−3−phosphate metabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation−reduction process





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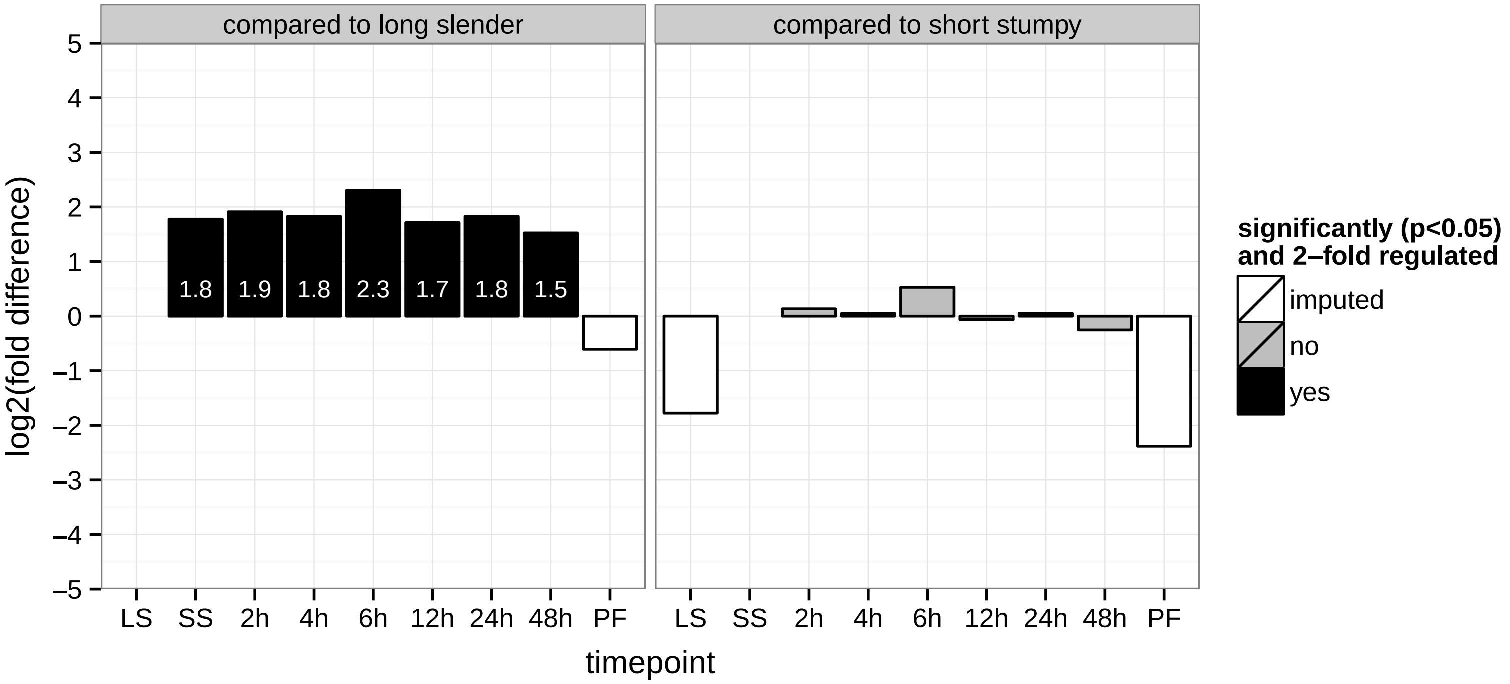
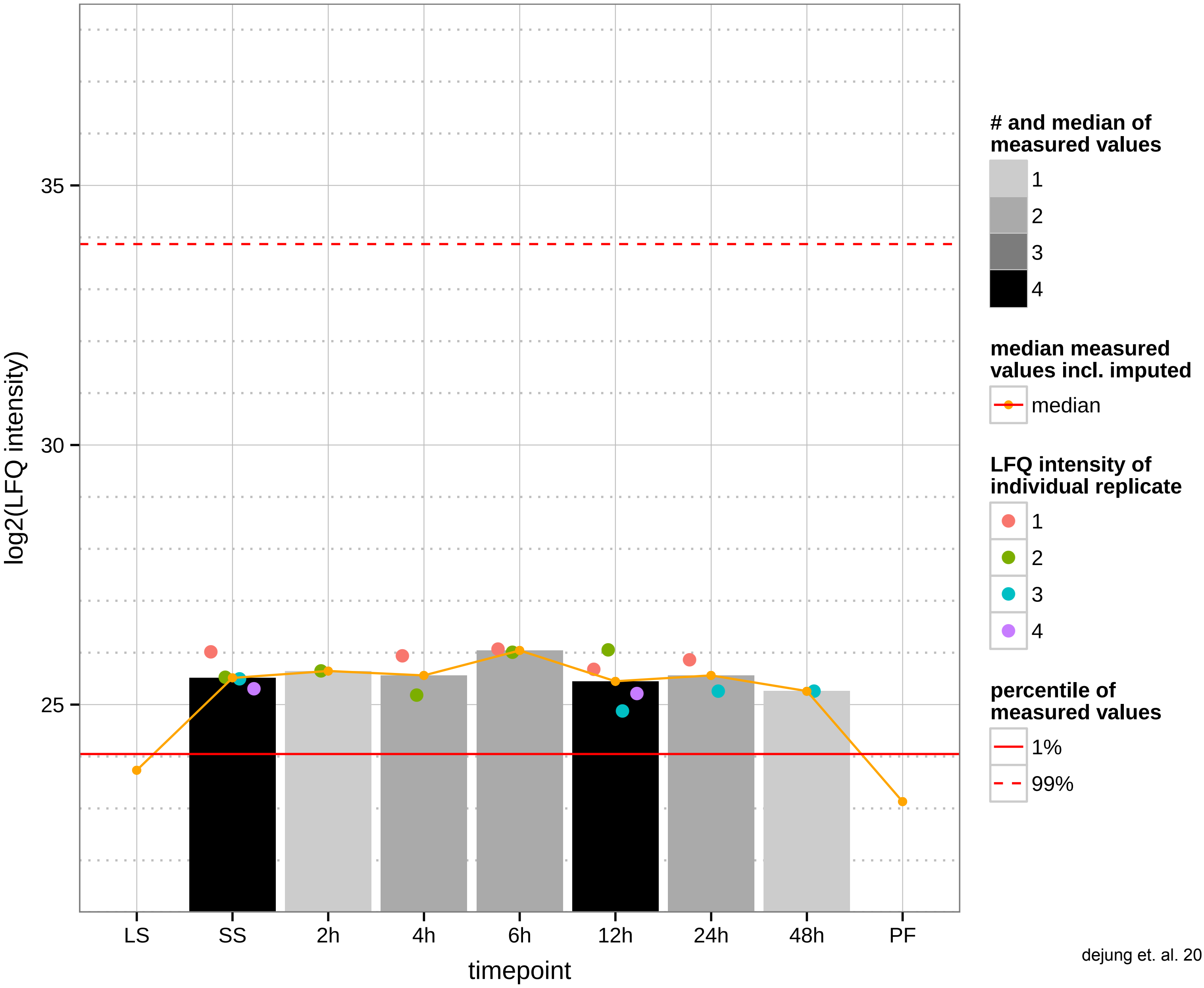
NADPH−−cytochrome p450 reductase, putative (CPR)
Tb927.11.8380
AGOF: FMN binding, electron carrier activity, iron ion binding, oxidoreductase activity
AGOC: integral to membrane
AGOP: oxidation−reduction process
PGOF: FMN binding, oxidoreductase activity
PGOC: null
PGOP: oxidation−reduction process





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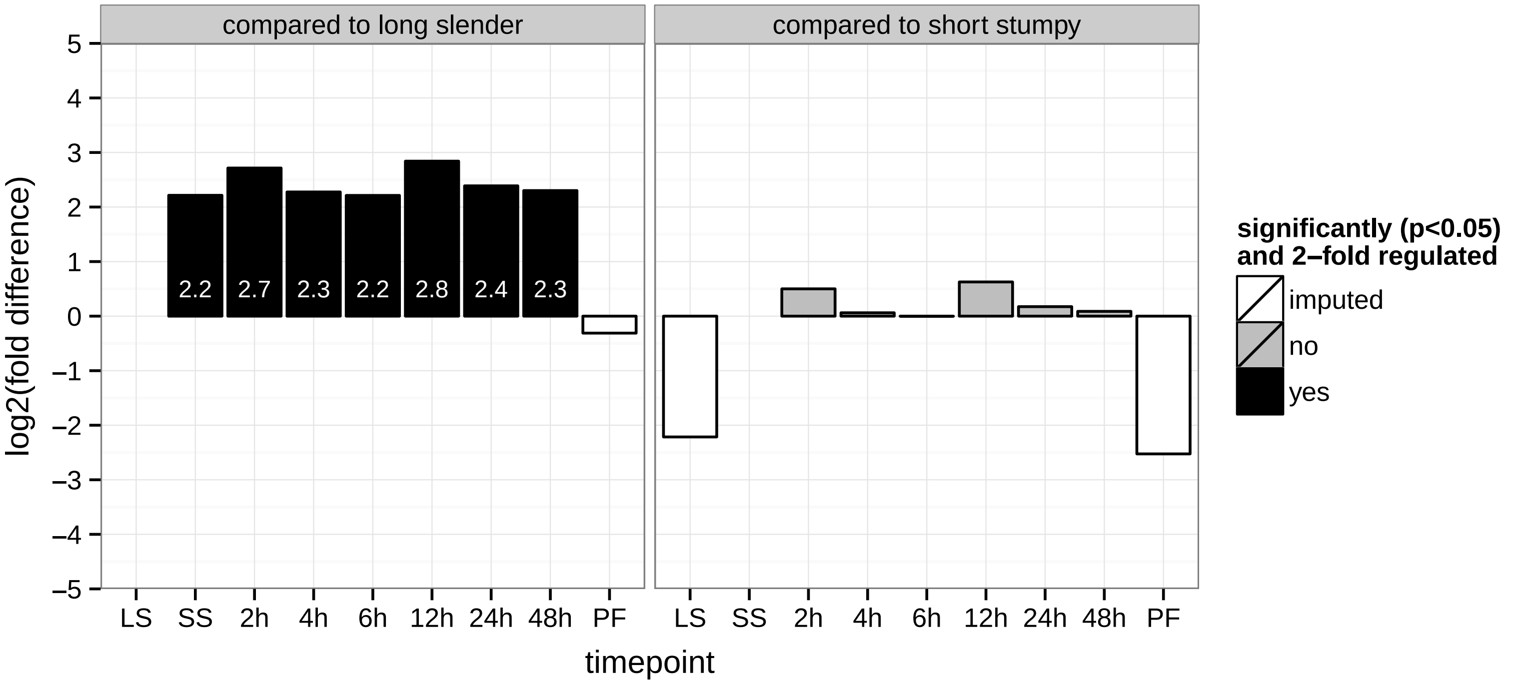
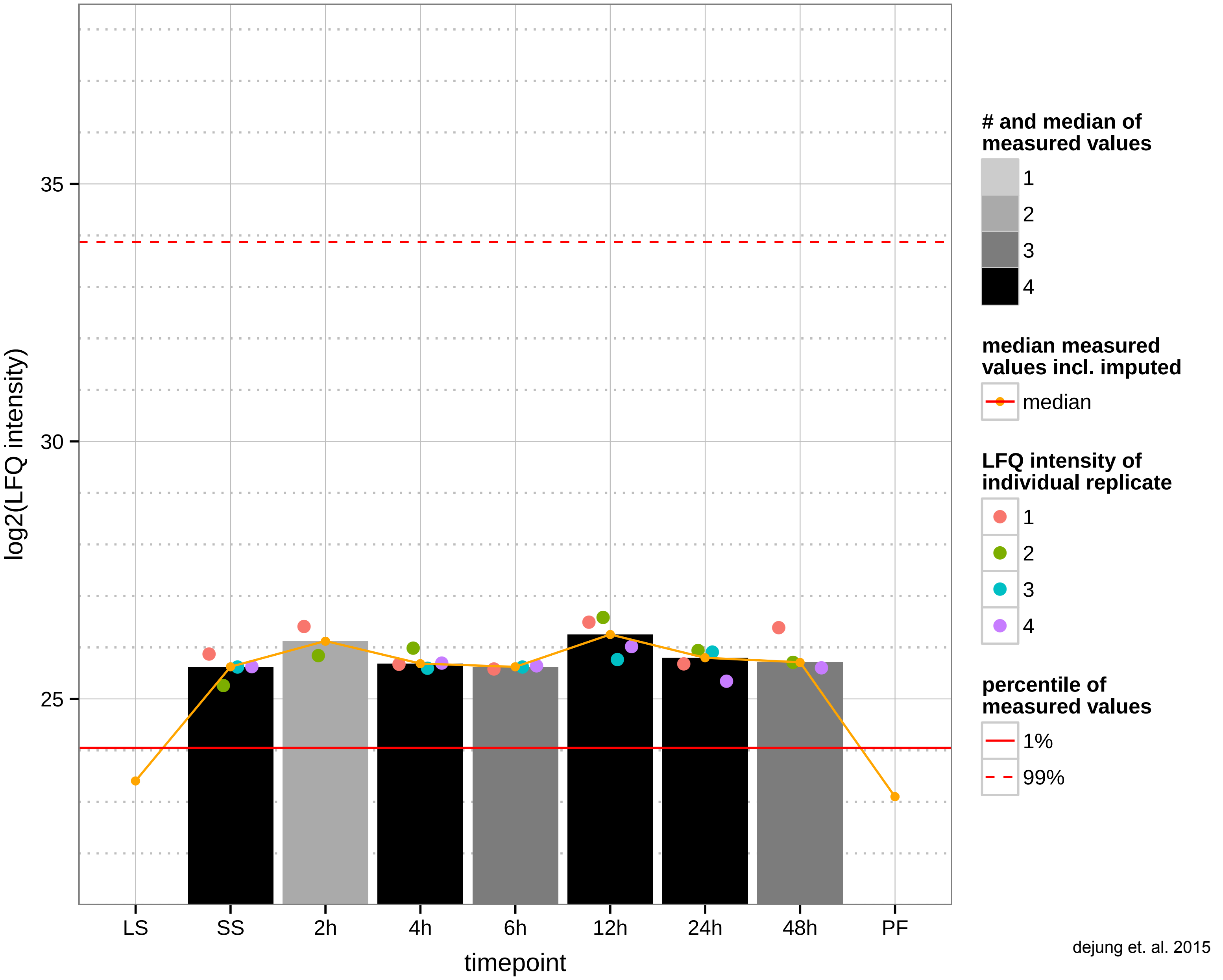
protein kinase, putative
Tb927.11.850
AGOF: ATP binding, protein kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, catalytic activity, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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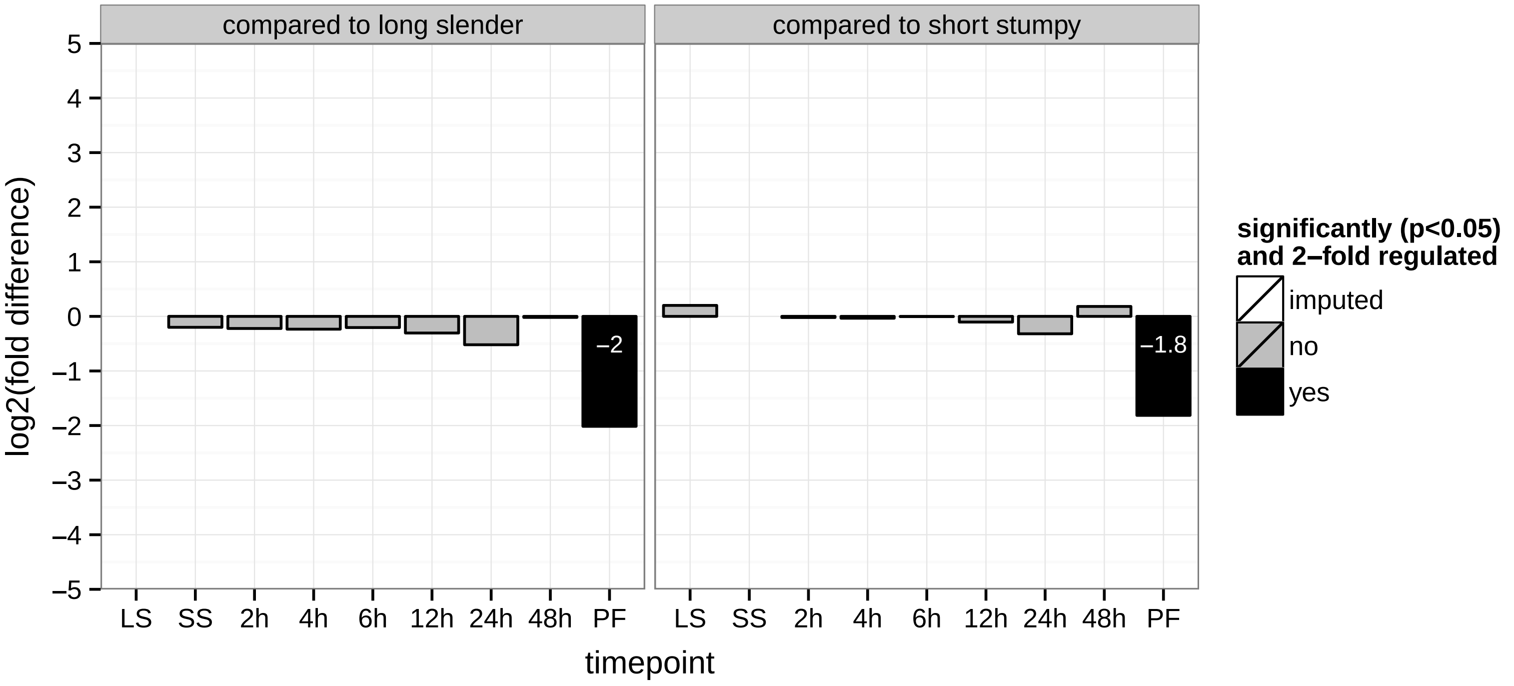
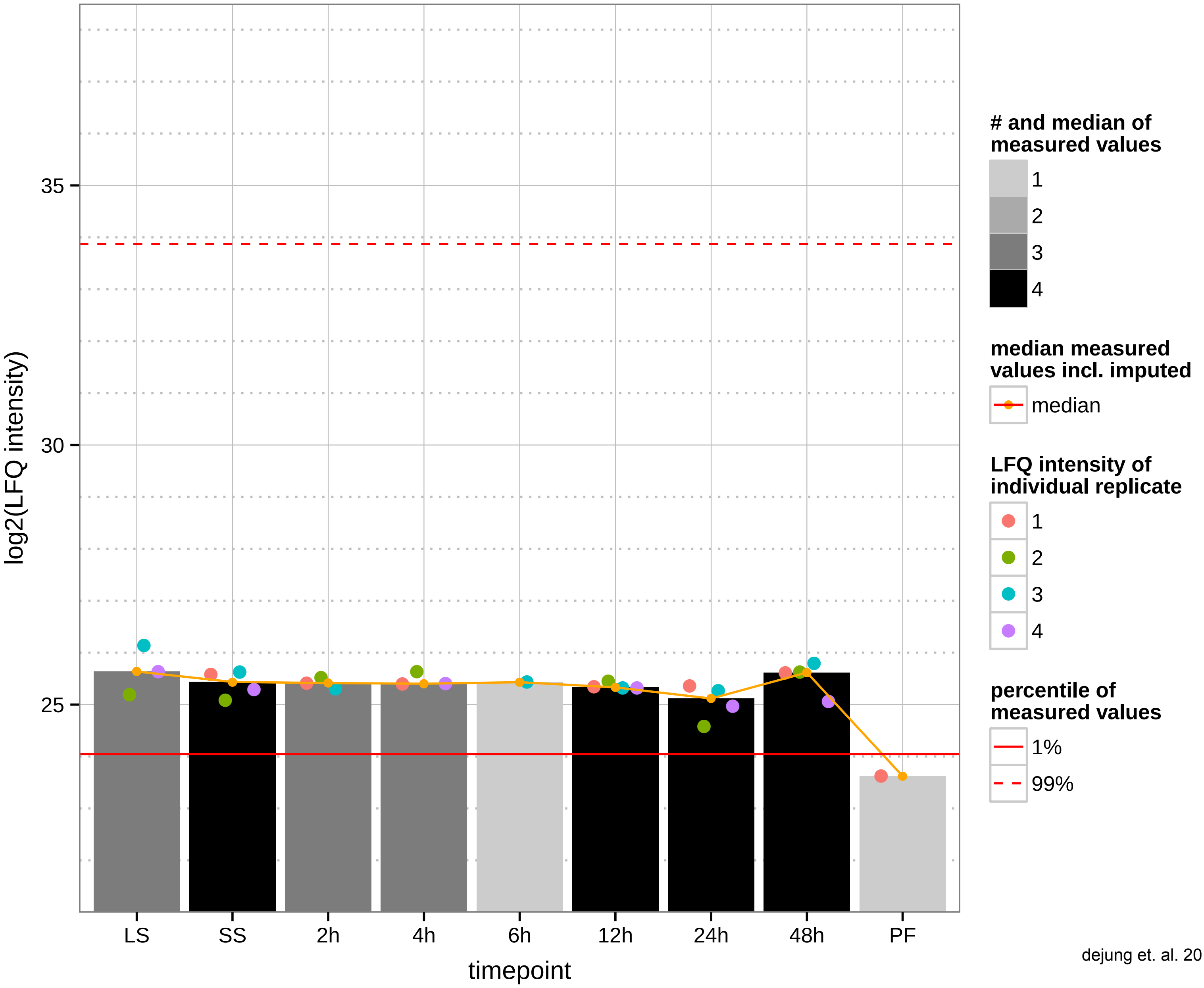
hypothetical protein, conserved
Tb927.11.9100
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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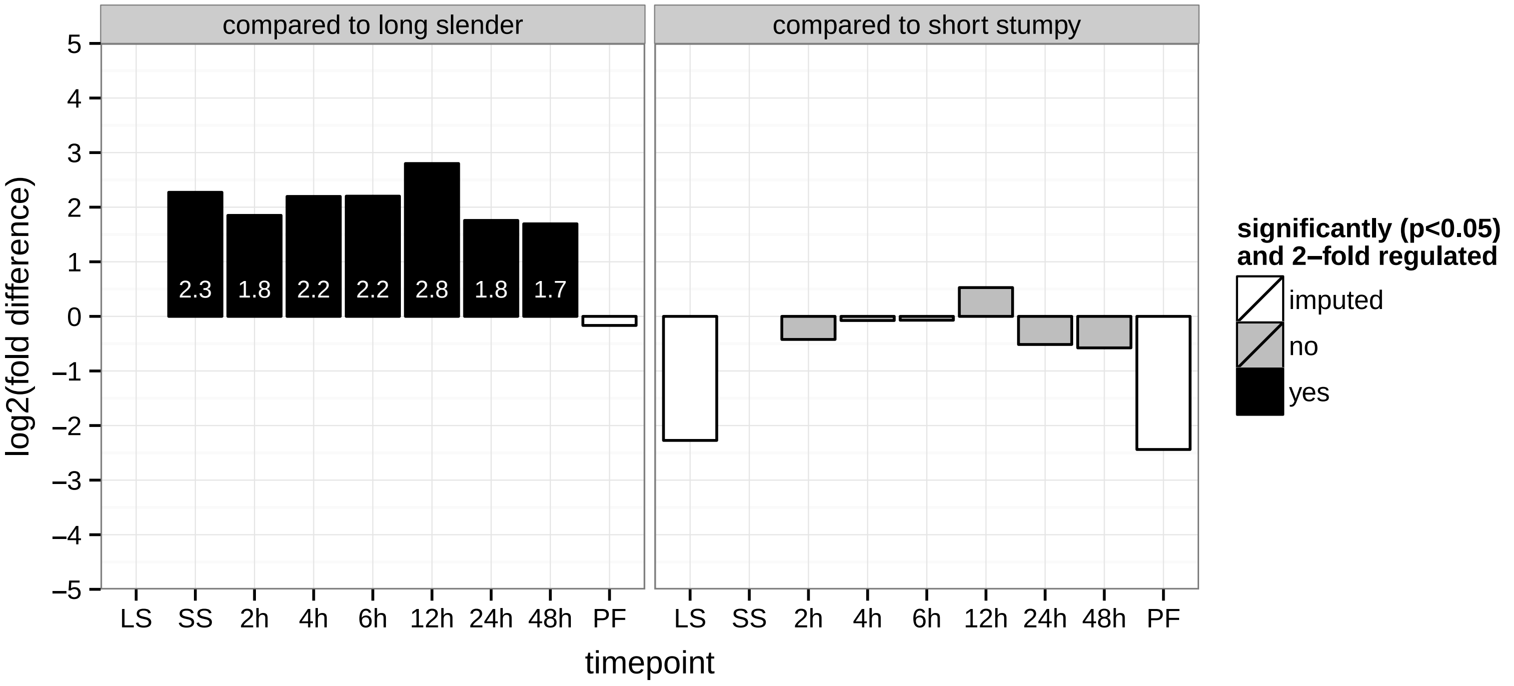
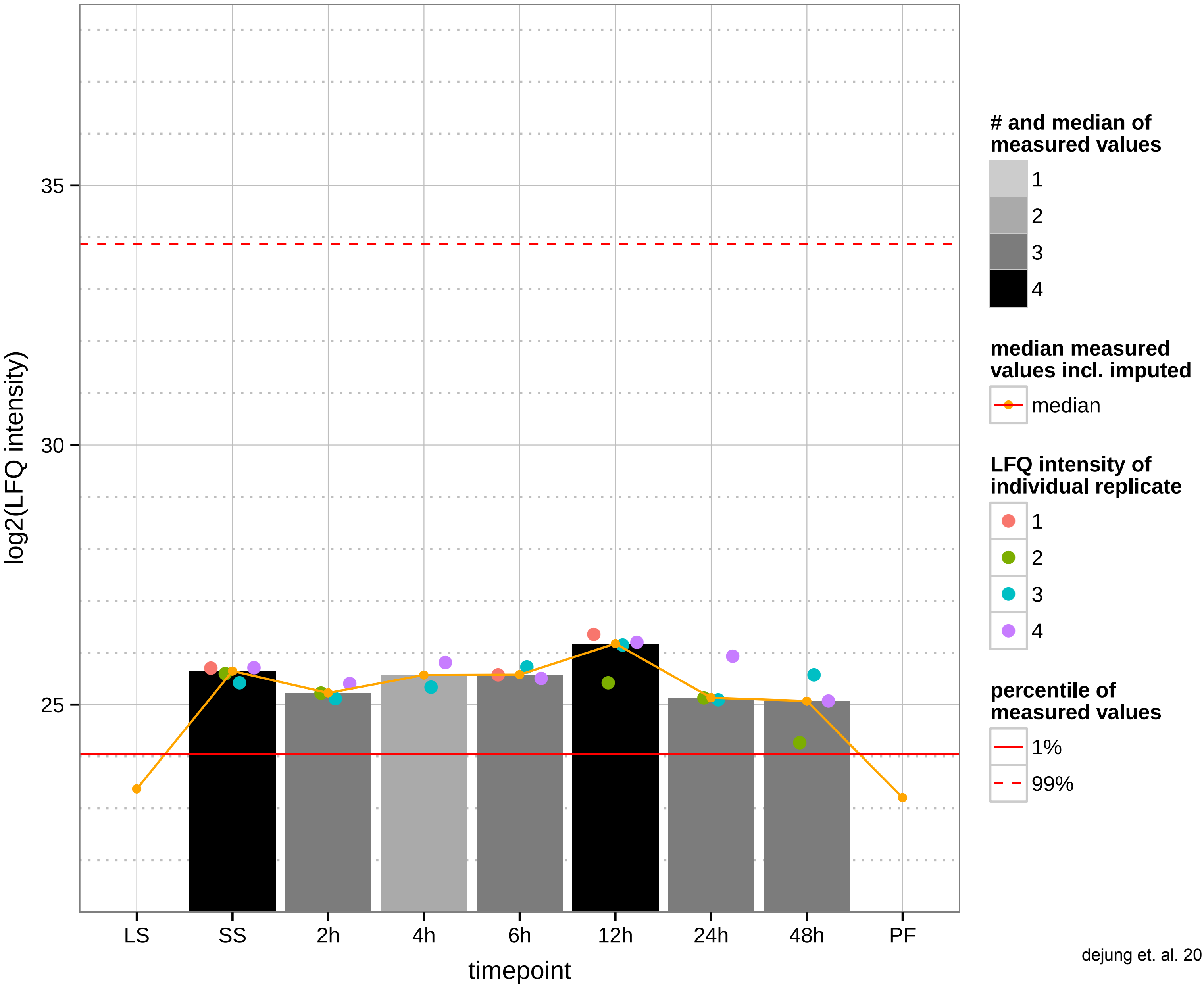
oxidoreductase, putative
Tb927.11.9560
AGOF: flavin adenine dinucleotide binding, oxidoreductase activity, acting on CH–OH group of donors
AGOC: mitochondrion
AGOP: alcohol metabolic process, oxidation–reduction process
PGOF: choline dehydrogenase activity, flavin adenine dinucleotide binding, oxidoreductase activity, acting on CH–OH group o
PGOC: null
PGOP: alcohol metabolic process, oxidation–reduction process





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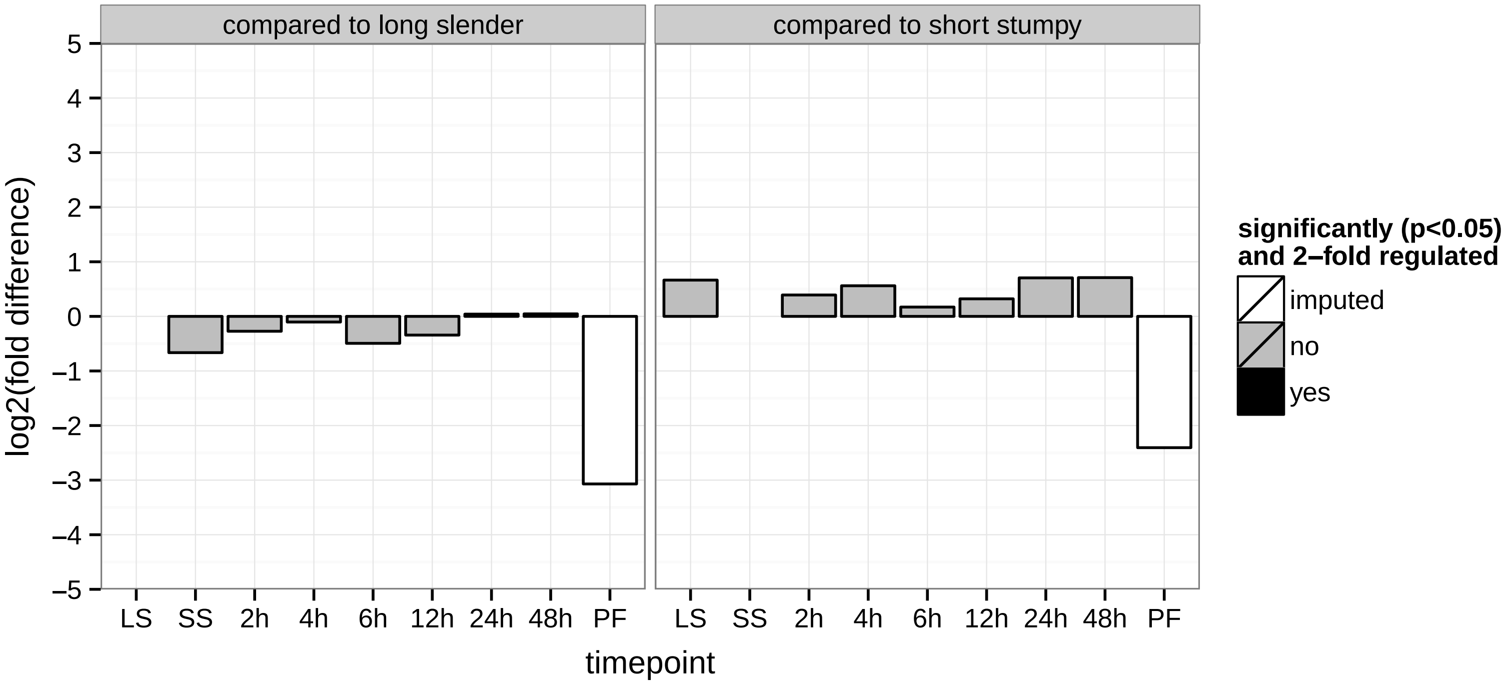
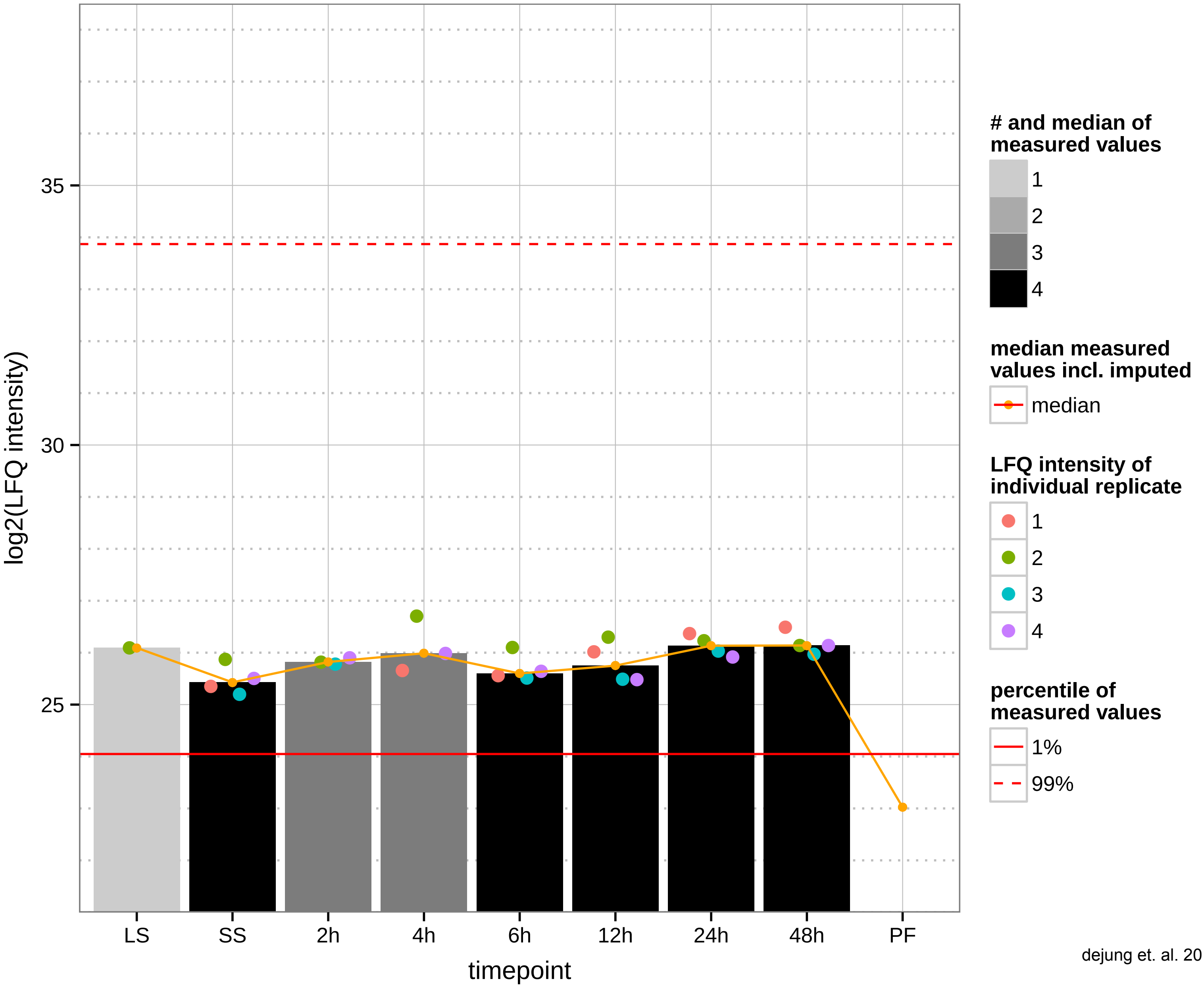
hypothetical protein, conserved
Tb927.11.9960
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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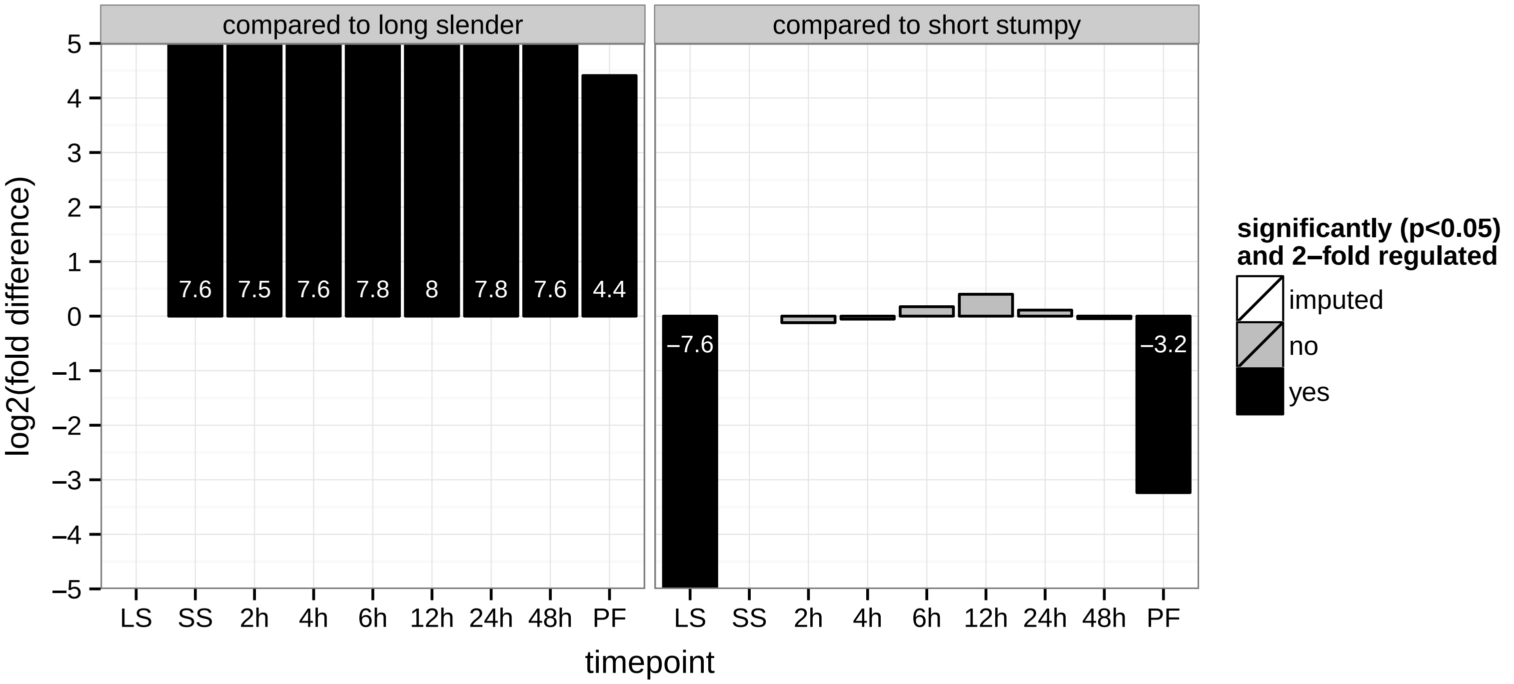
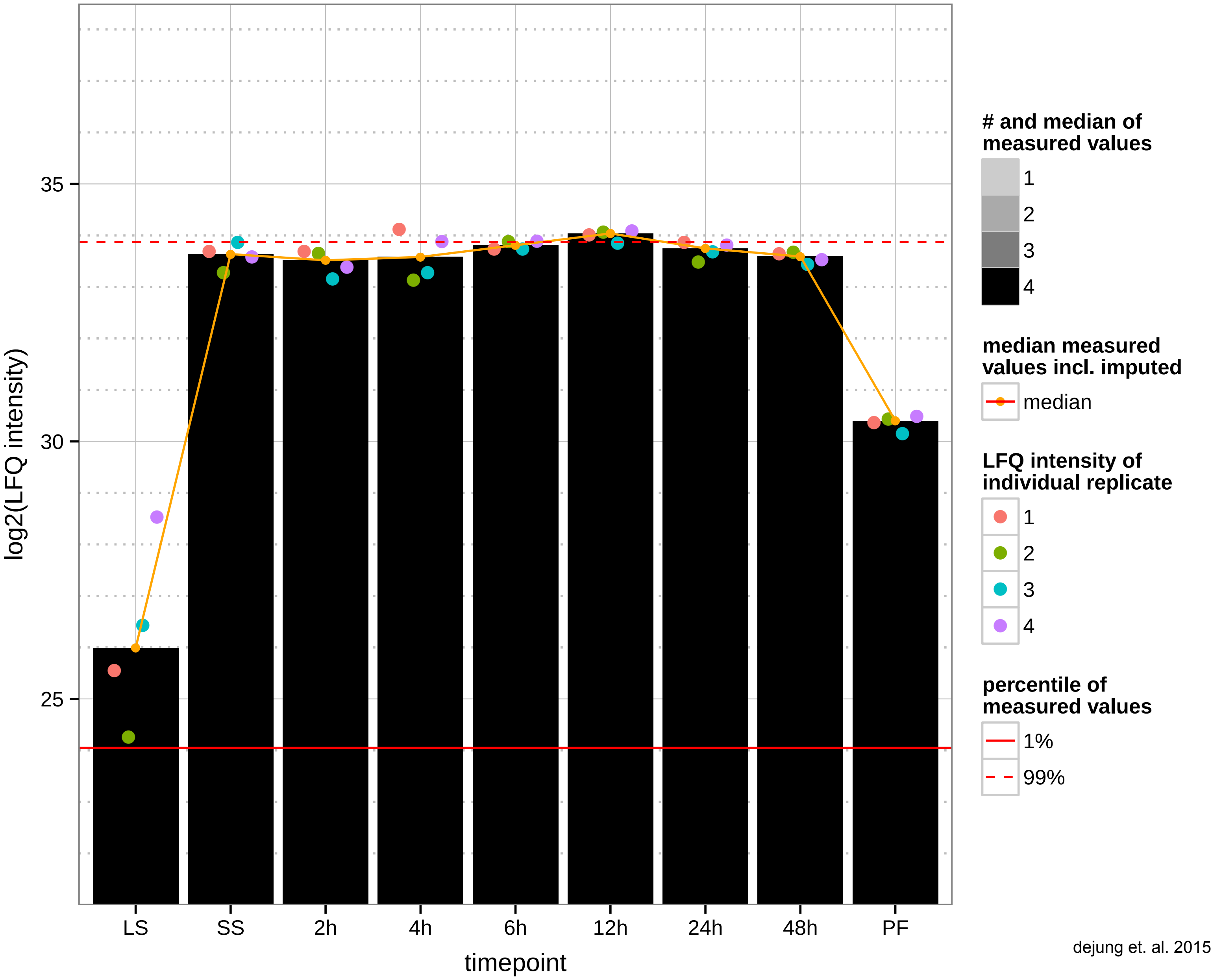
2–oxoglutarate dehydrogenase E1 component, putative
Tb927.11.9980
AGOF: oxoglutarate dehydrogenase (succinyl–transferring) activity, thiamine pyrophosphate binding
AGOC: mitochondrion, oxoglutarate dehydrogenase complex
AGOP: glycolysis, lysine catabolic process, tricarboxylic acid cycle, tryptophan metabolic process
PGOF: oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, oxoglutarate dehydrogen
PGOC: null
PGOP: metabolic process, oxidation–reduction process, tricarboxylic acid cycle





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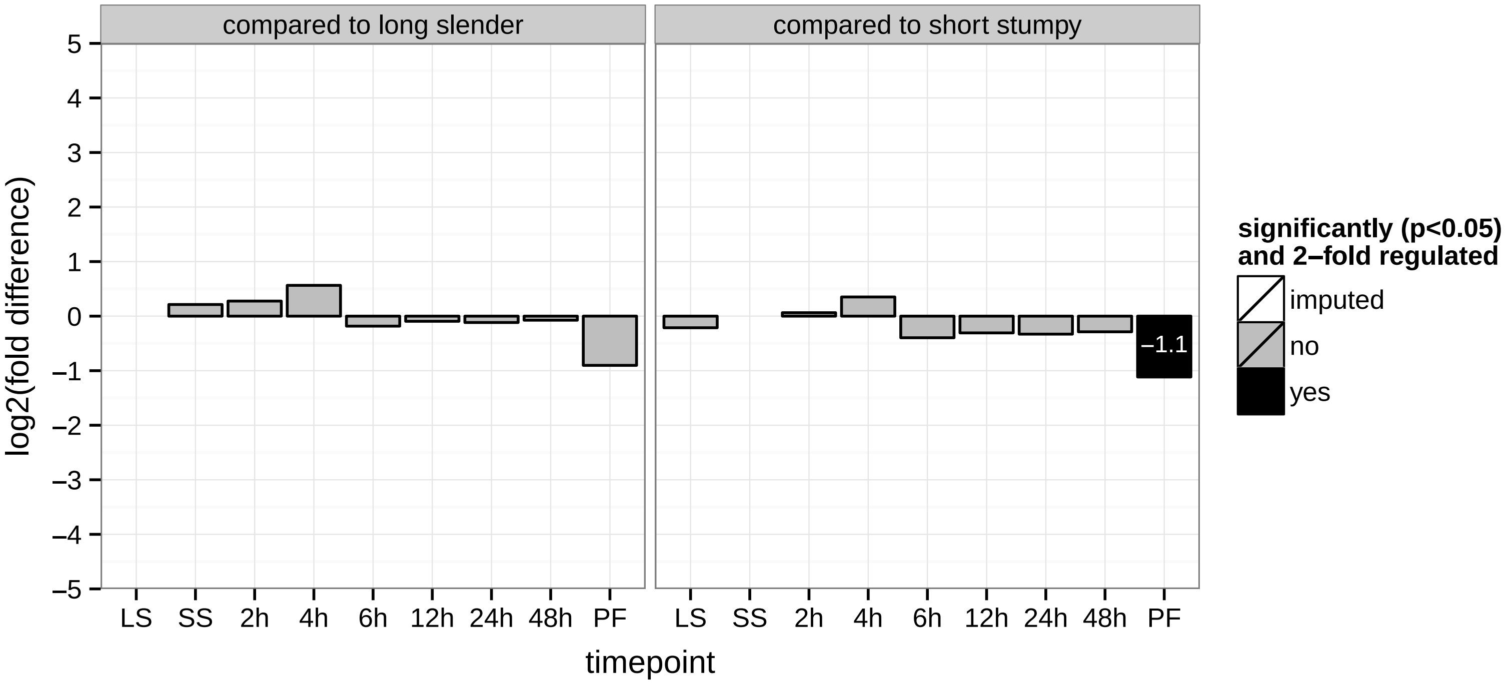
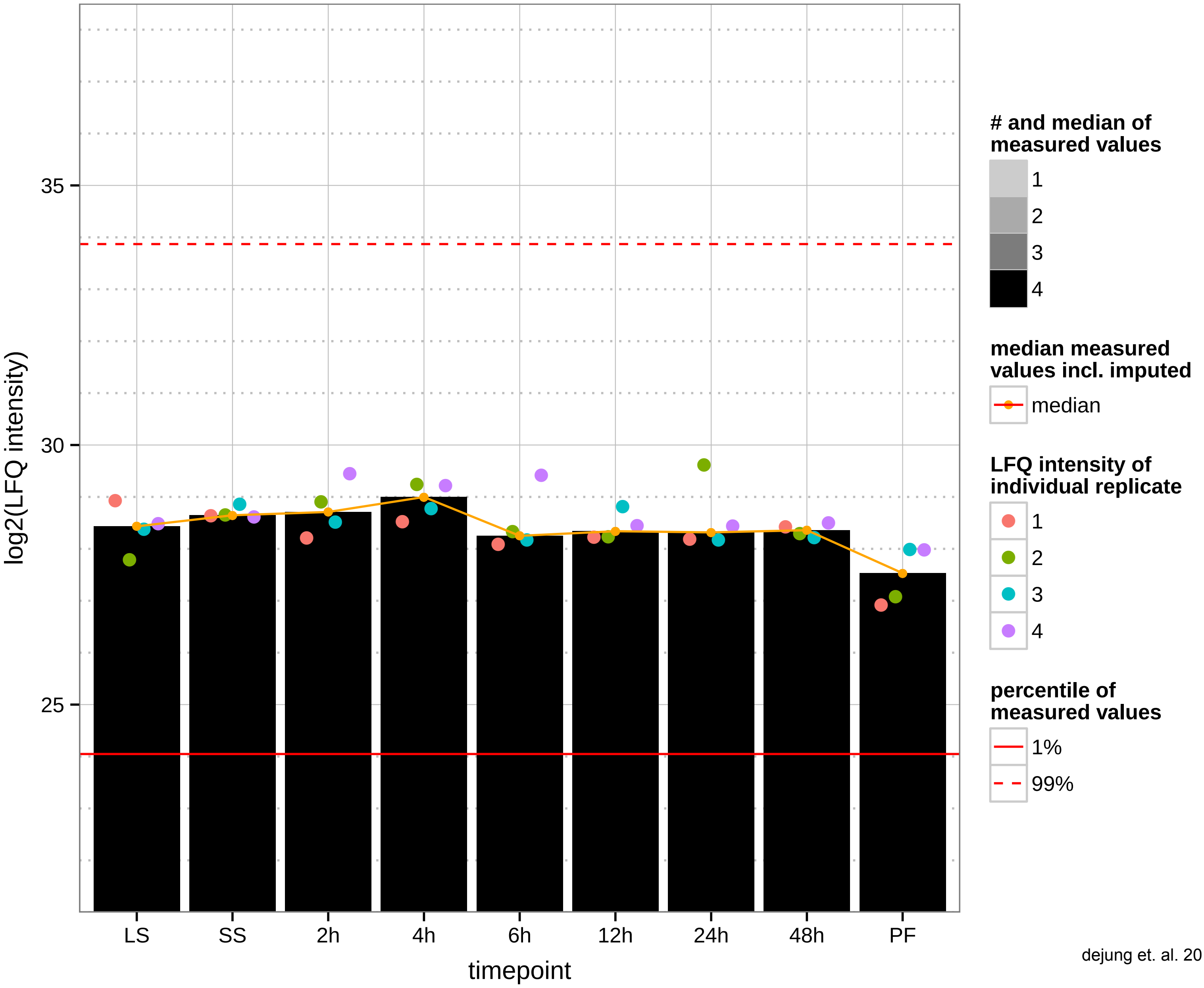
hypothetical protein, conserved
Tb927.2.2390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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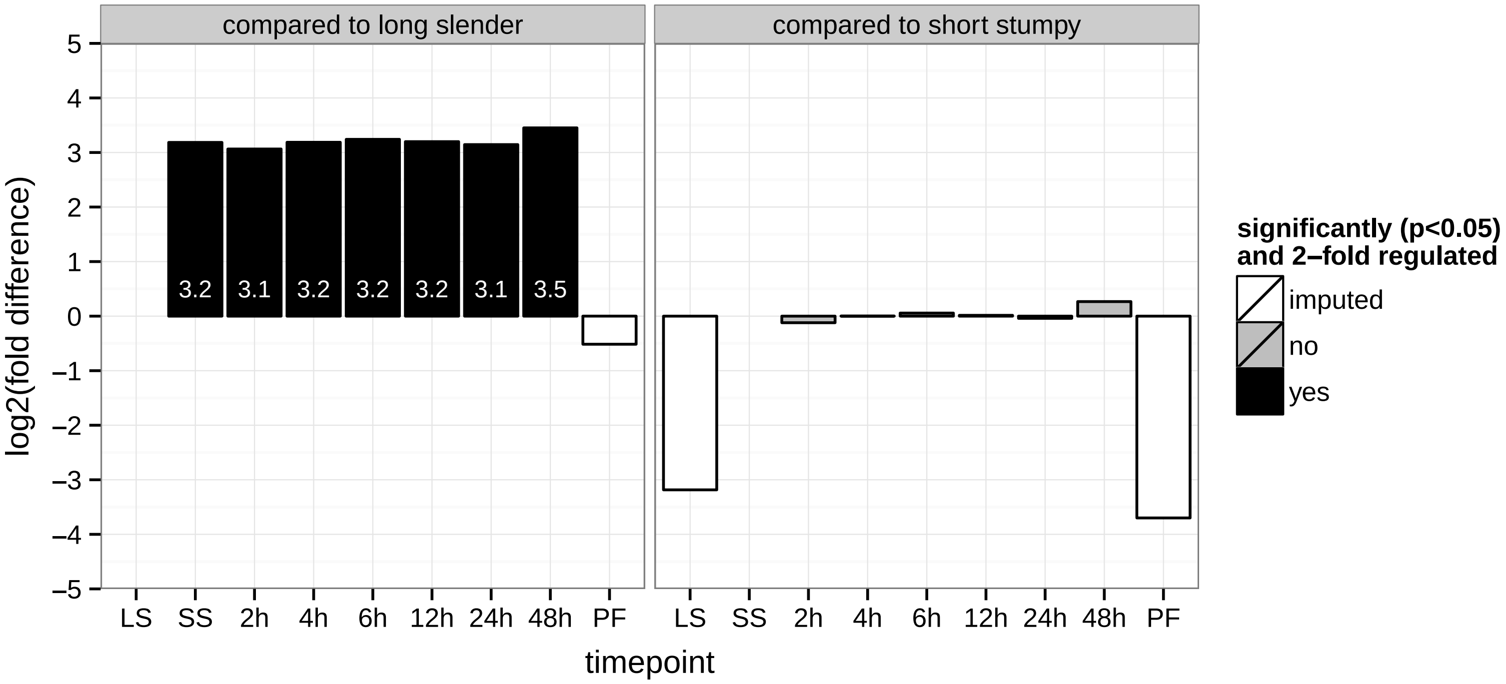
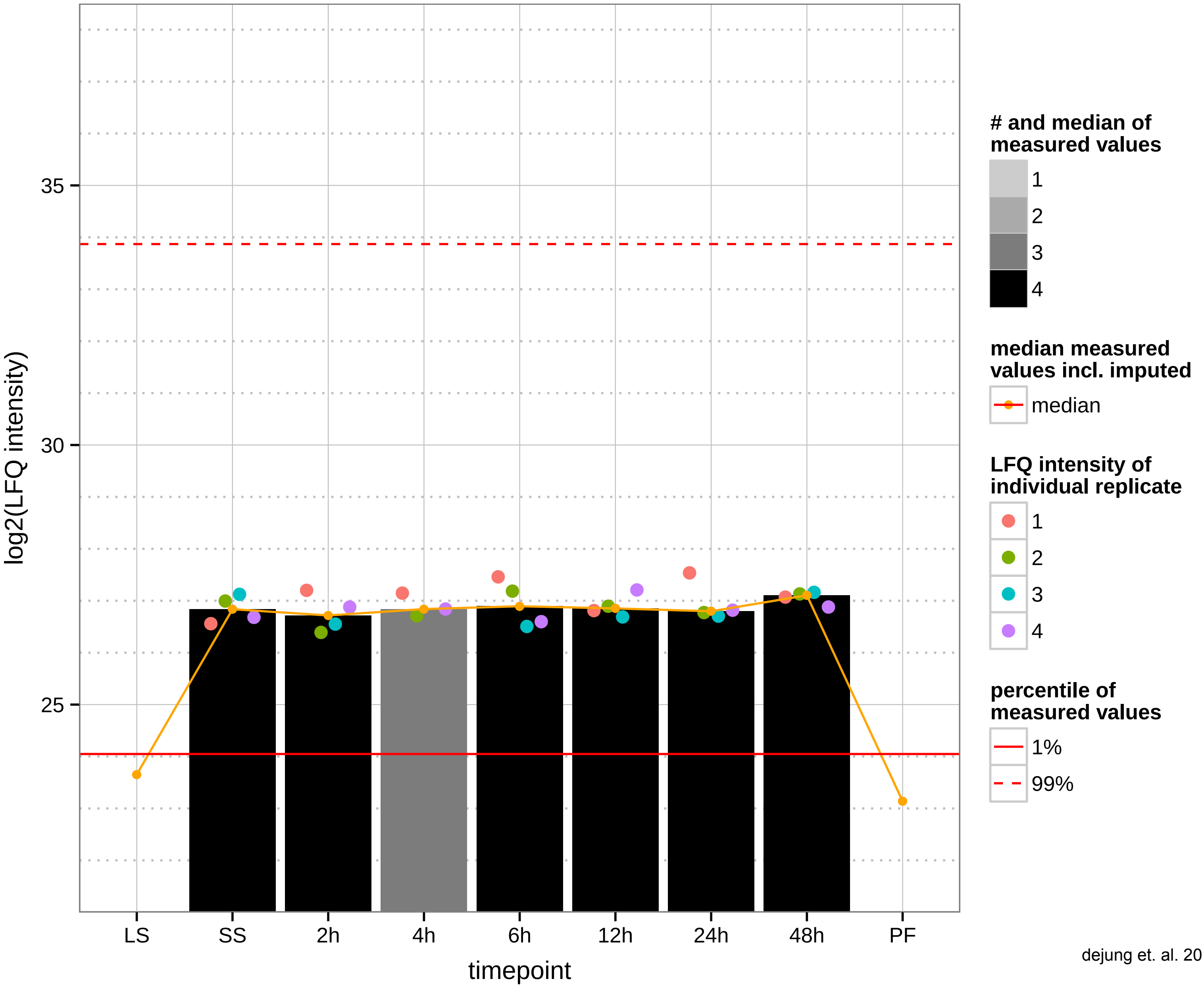
retrotransposon hot spot protein (RHS, pseudogene), putative, retrotransposon hot spot protein 3 (RHS3), frameshift
Tb927.2.270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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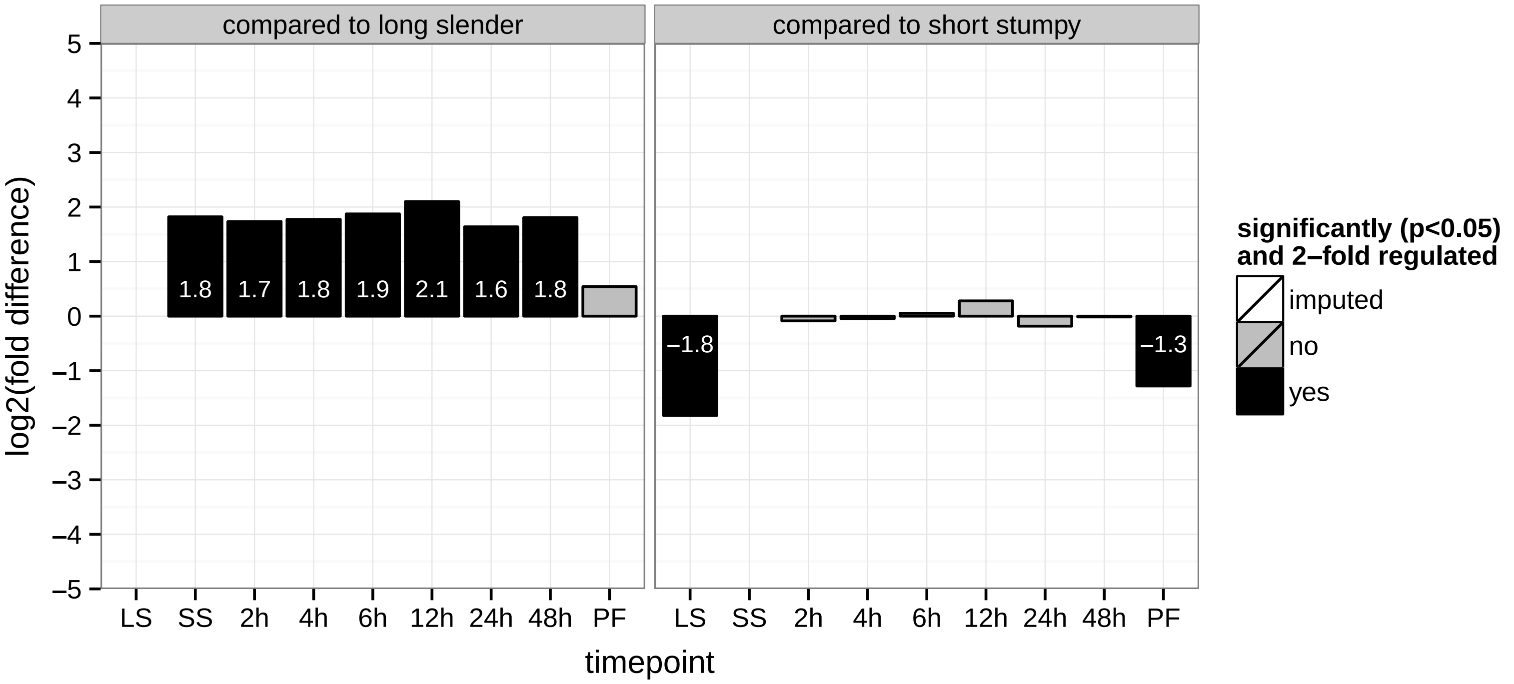
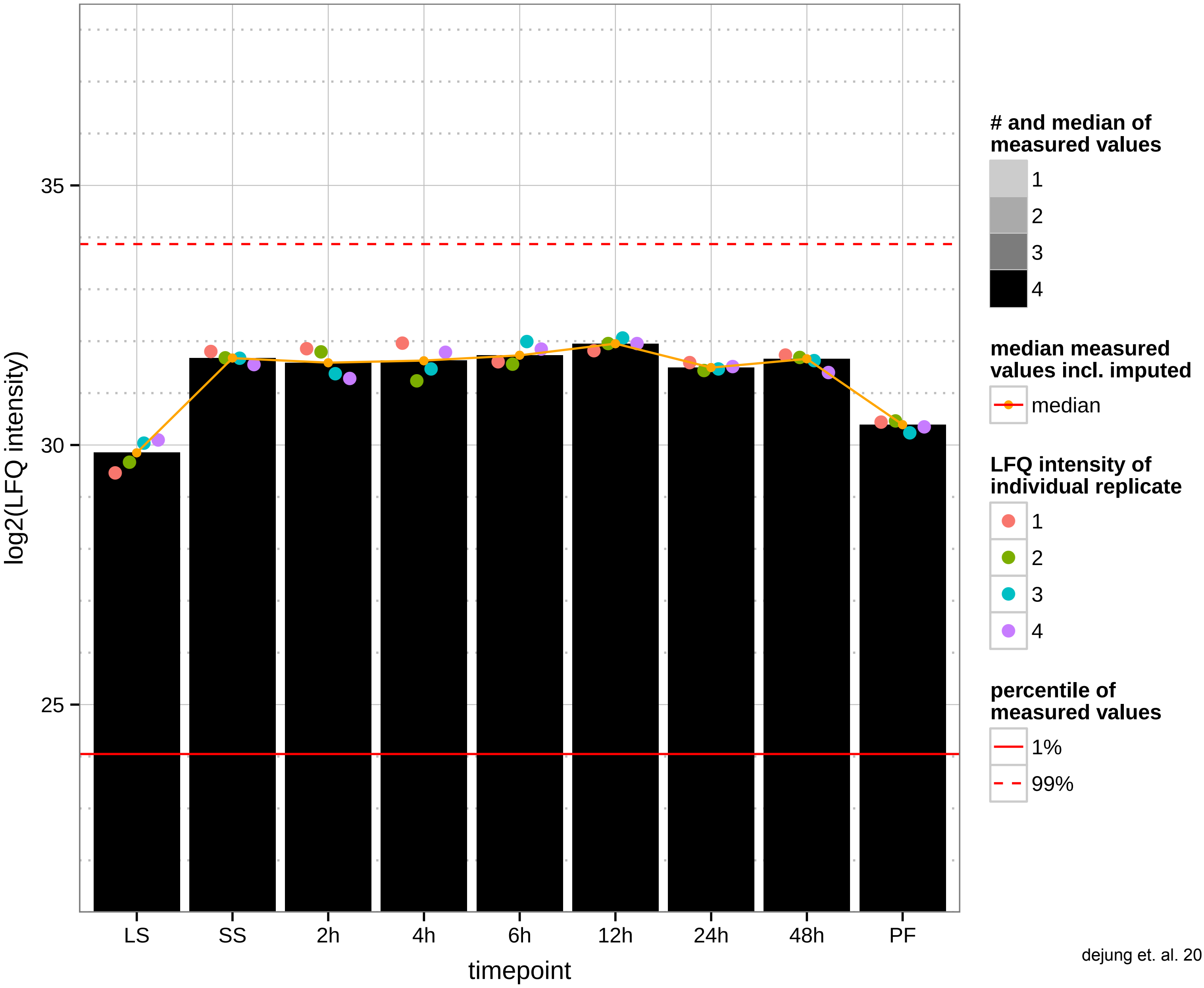
retrotransposon hot spot protein 4 (RHS4), putative
Tb927.2.340
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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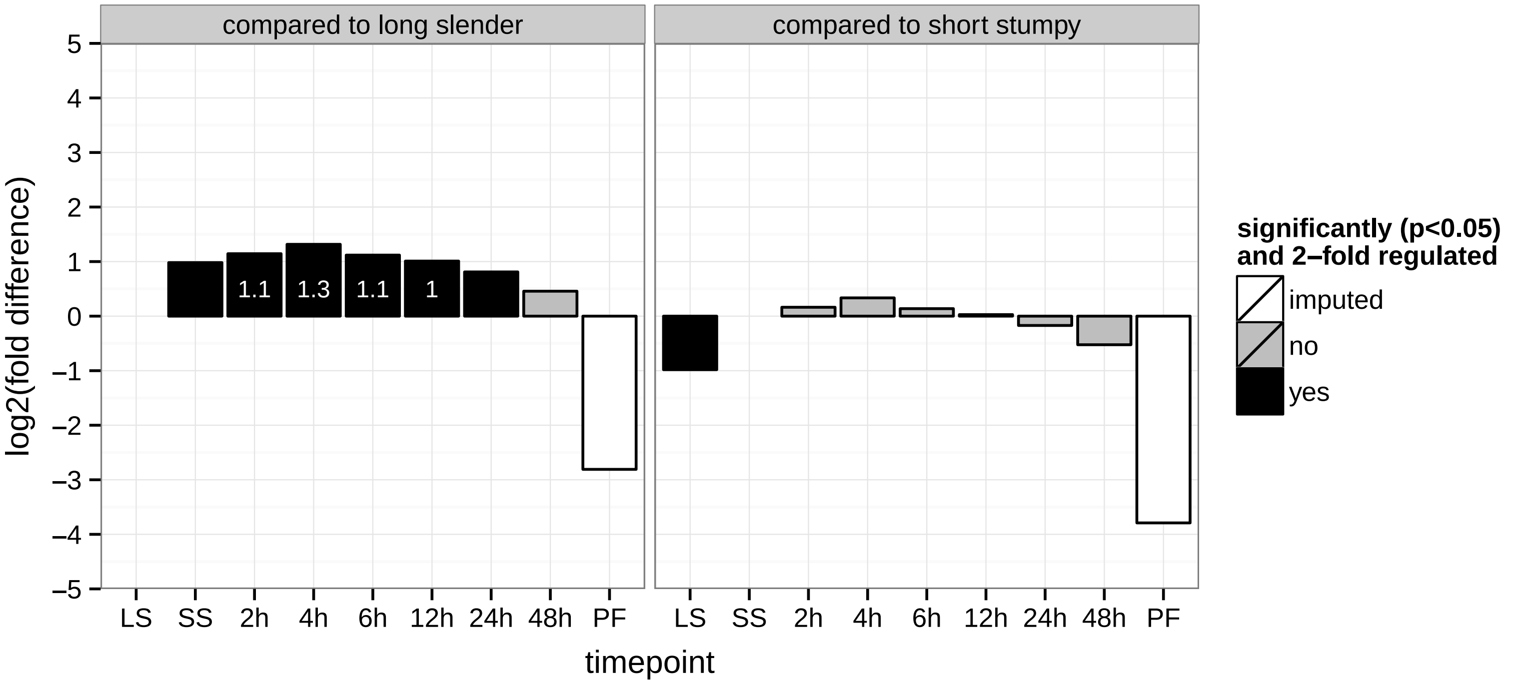
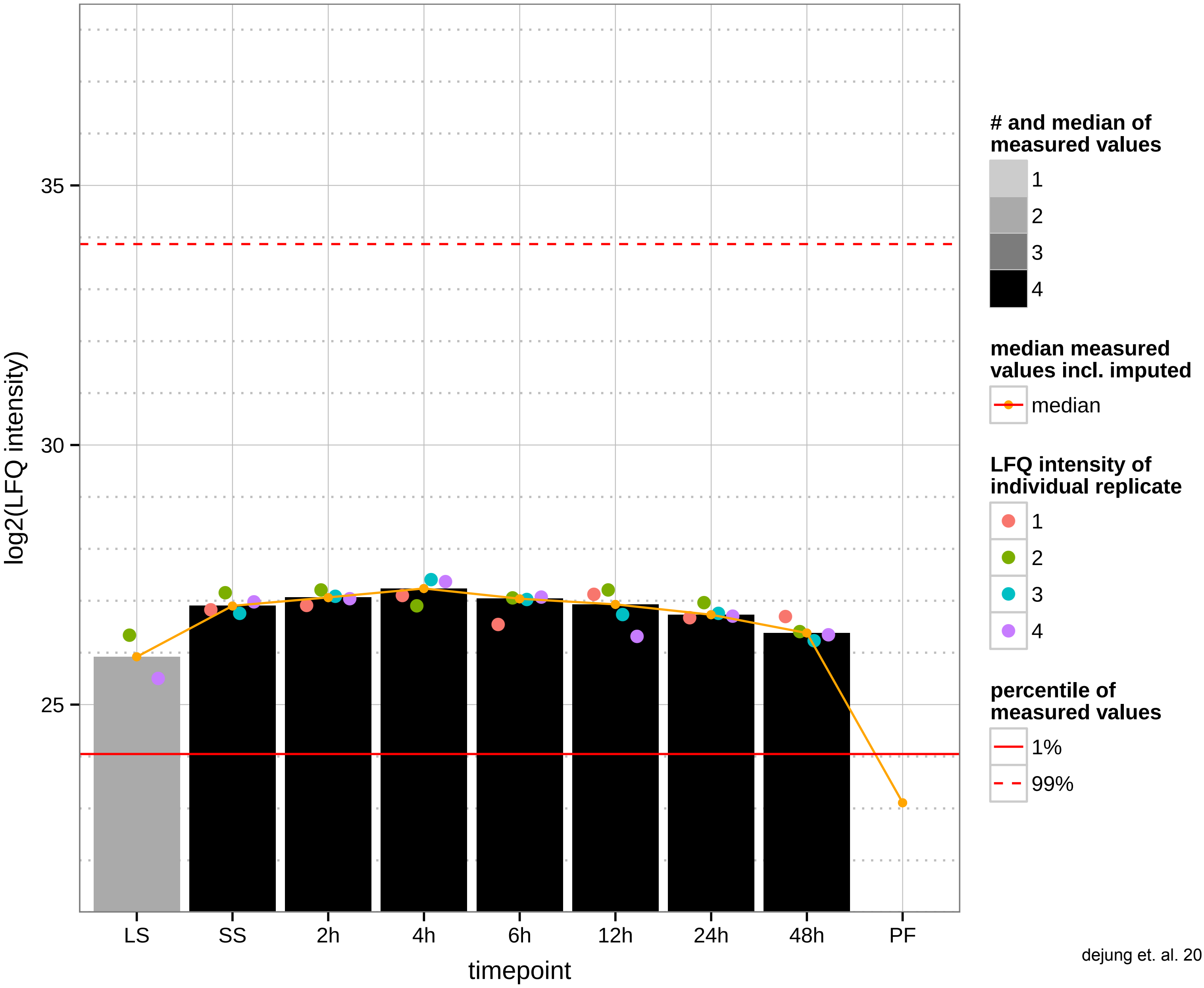
hypothetical protein, conserved
Tb927.2.3990
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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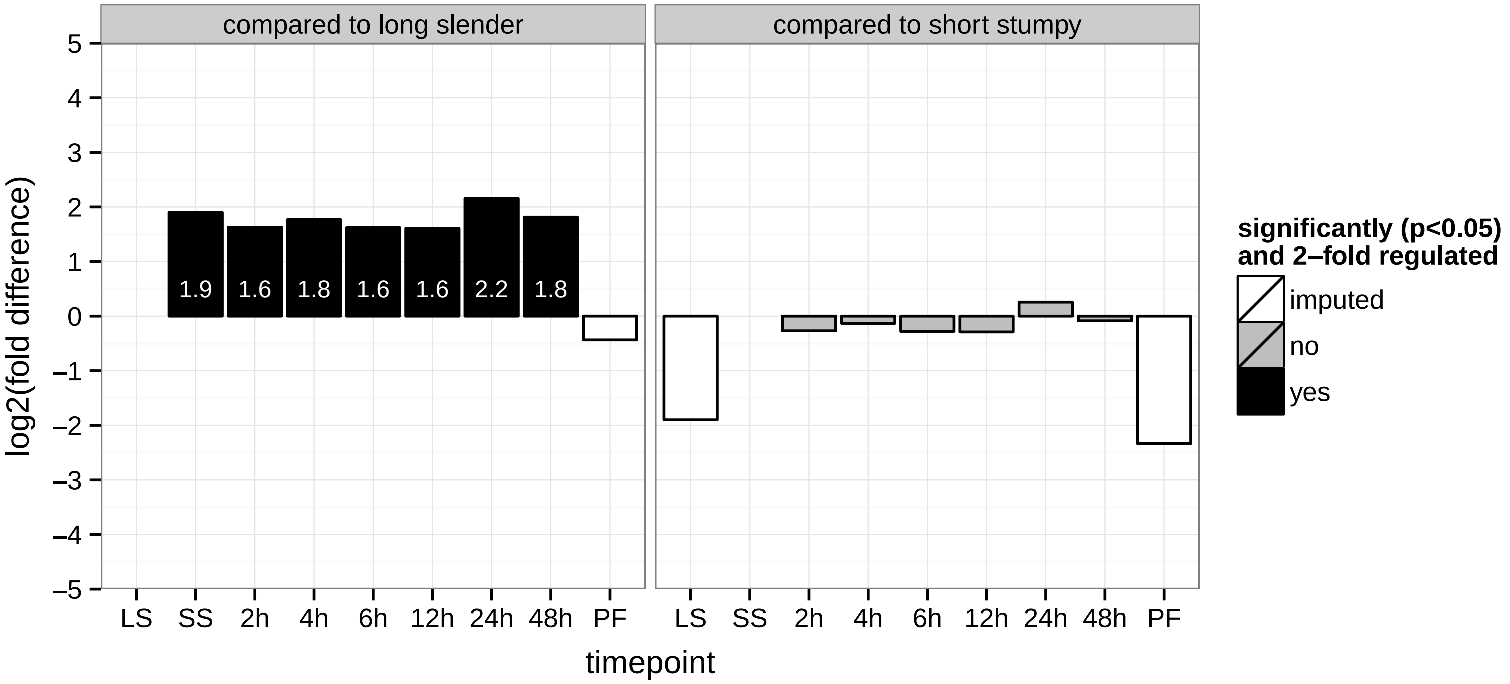
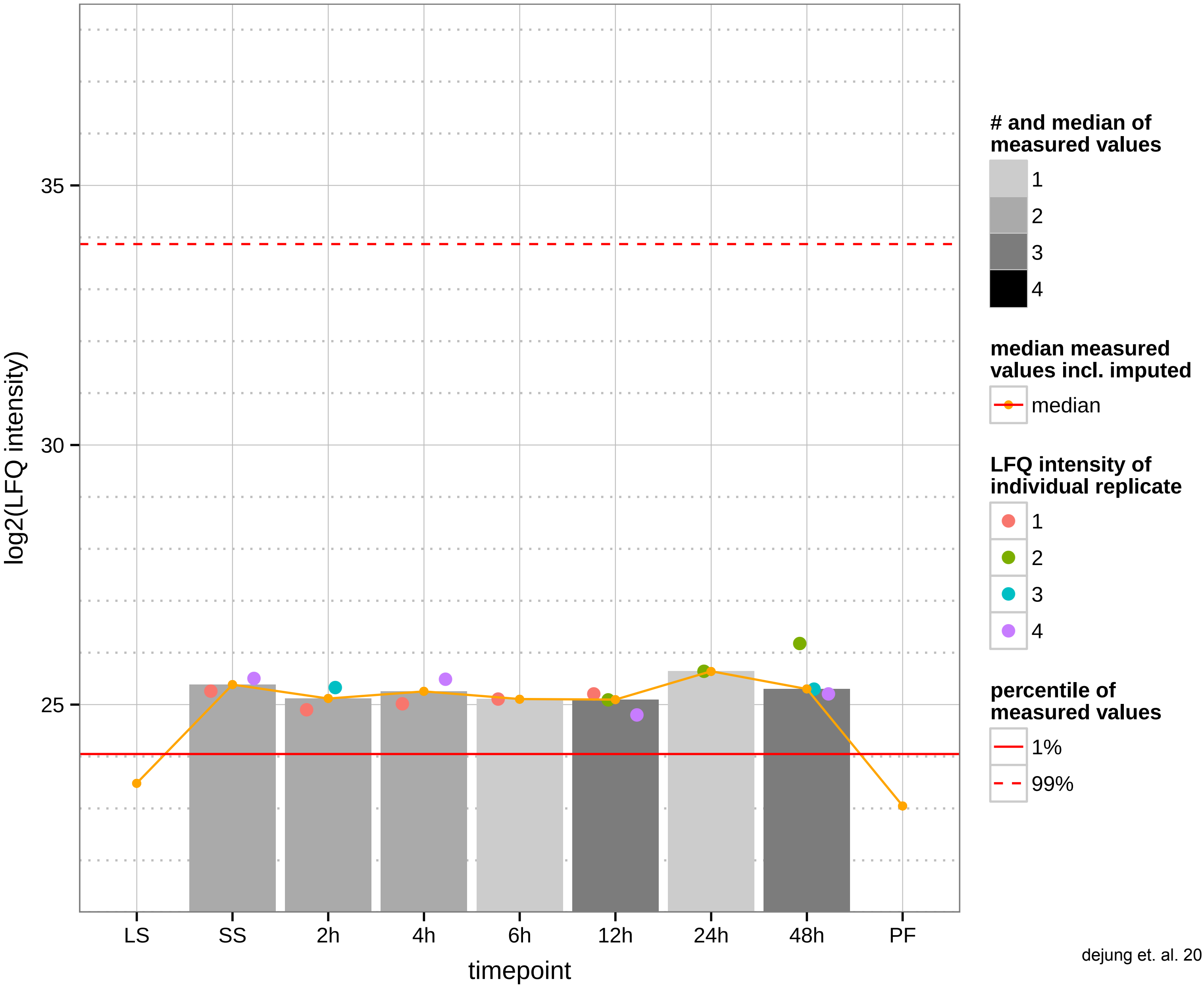
hypothetical protein, conserved
Tb927.2.4380
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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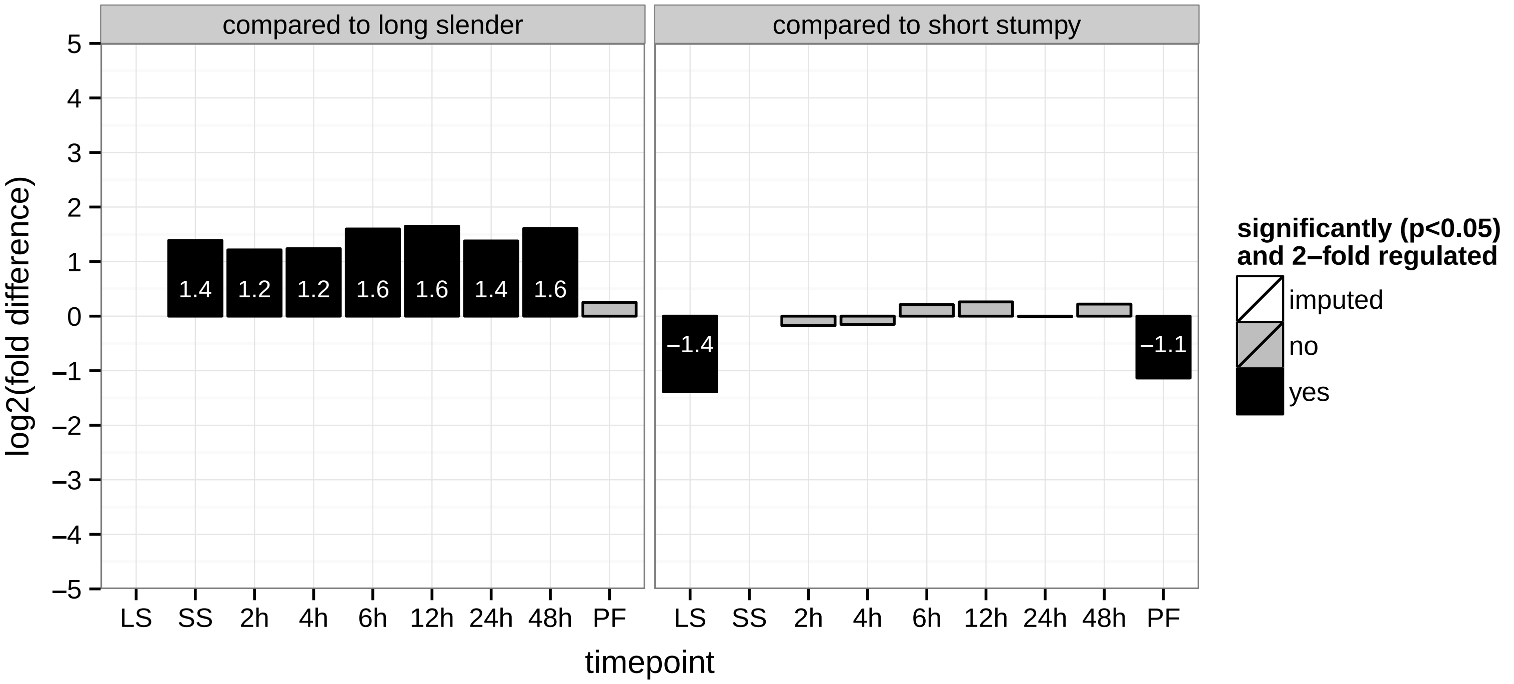
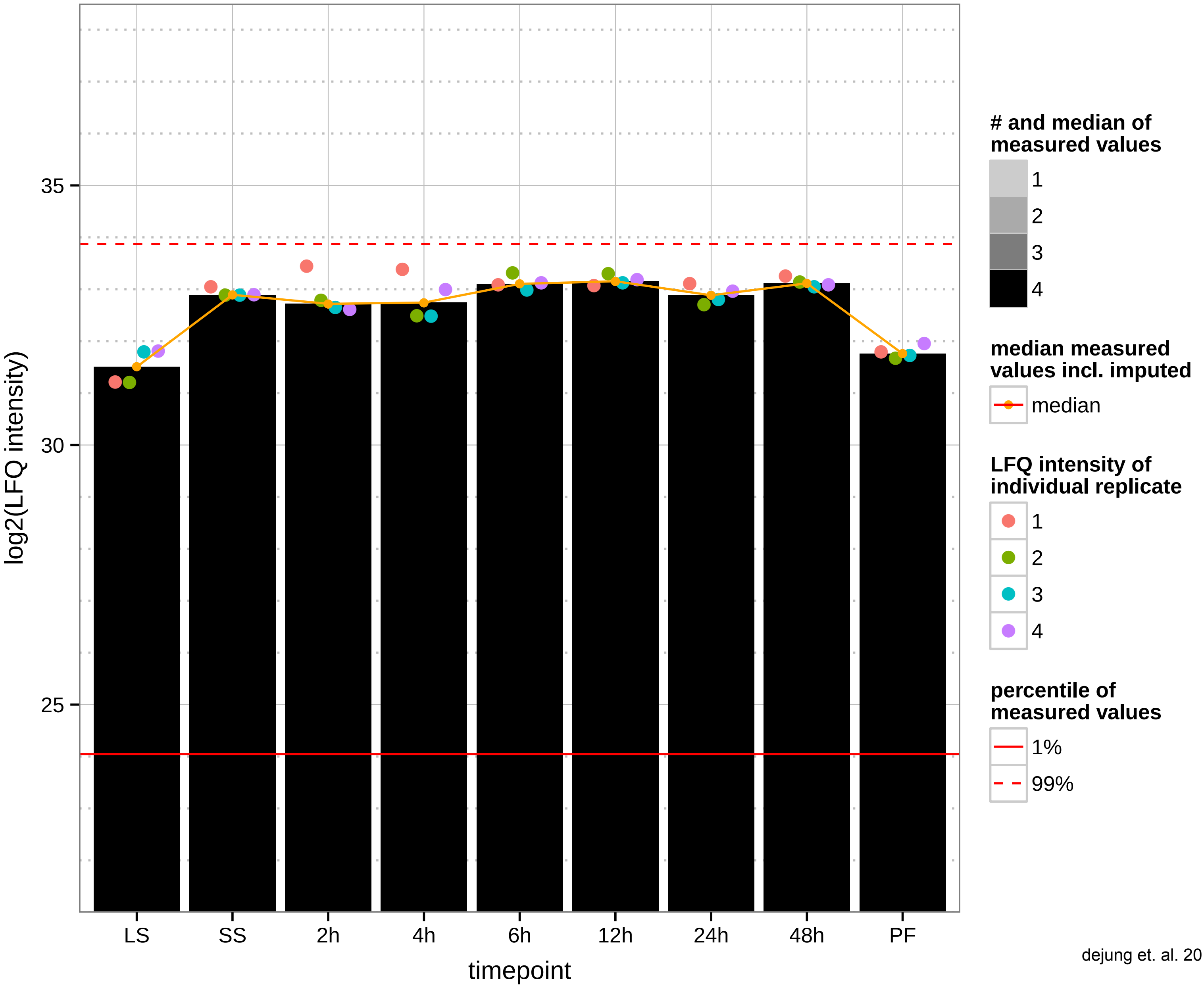
retrotransposon hot spot (RHS), putative, retrotransposon hot spot protein 4 (RHS4), retrotransposon hot spot protein (RHS, p
Tb927.2.470
AGOF: null
AGOC: null, nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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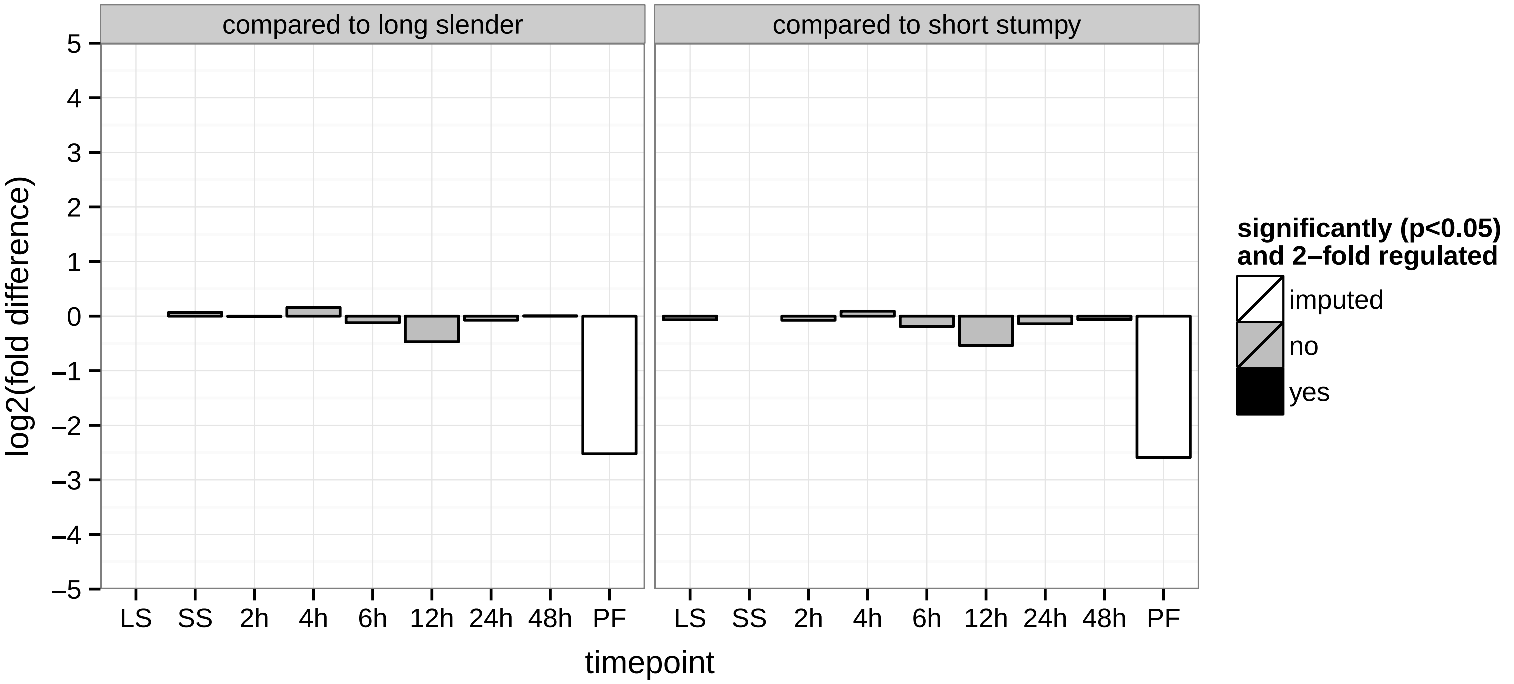
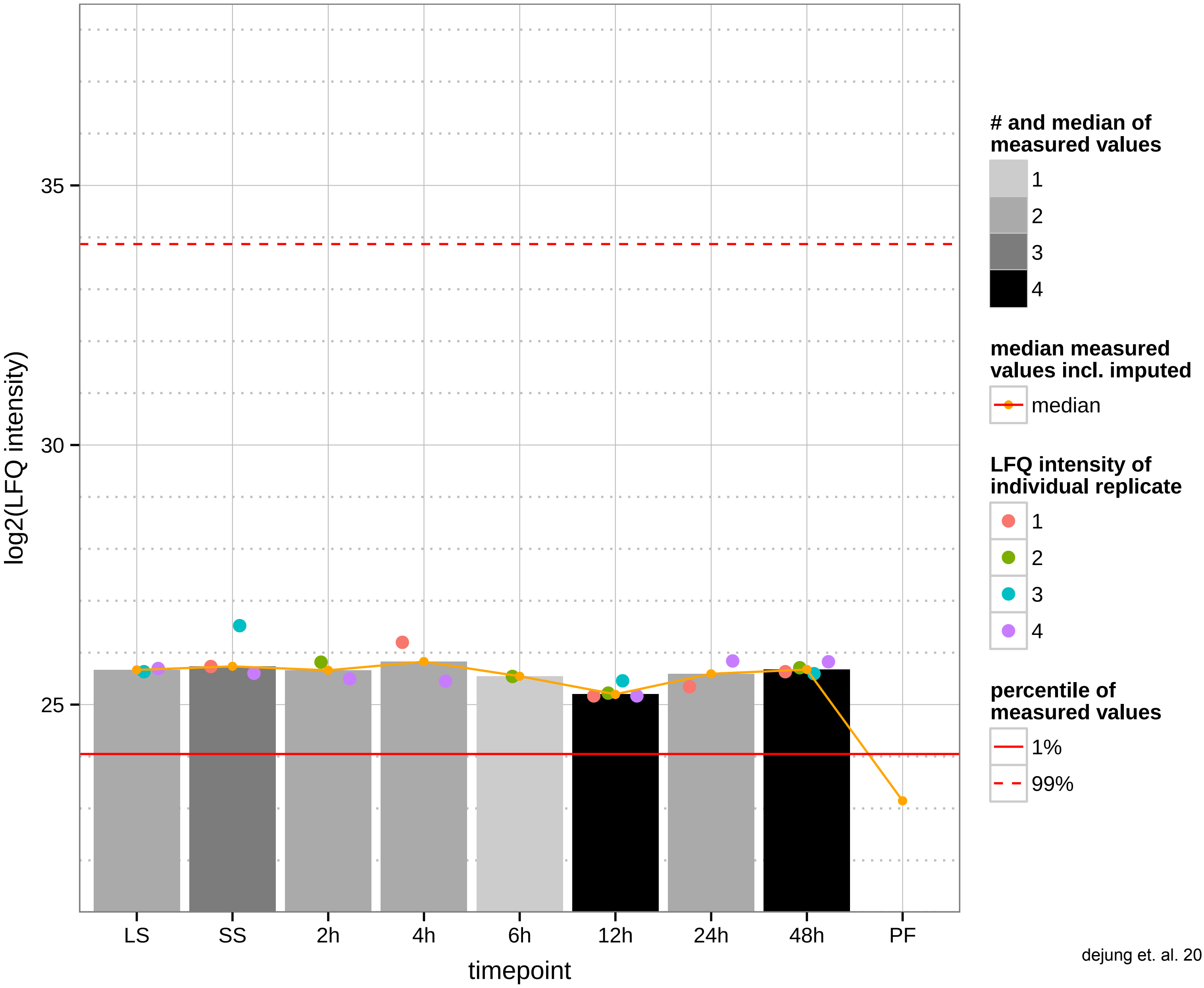
hypothetical protein, conserved
Tb927.2.4780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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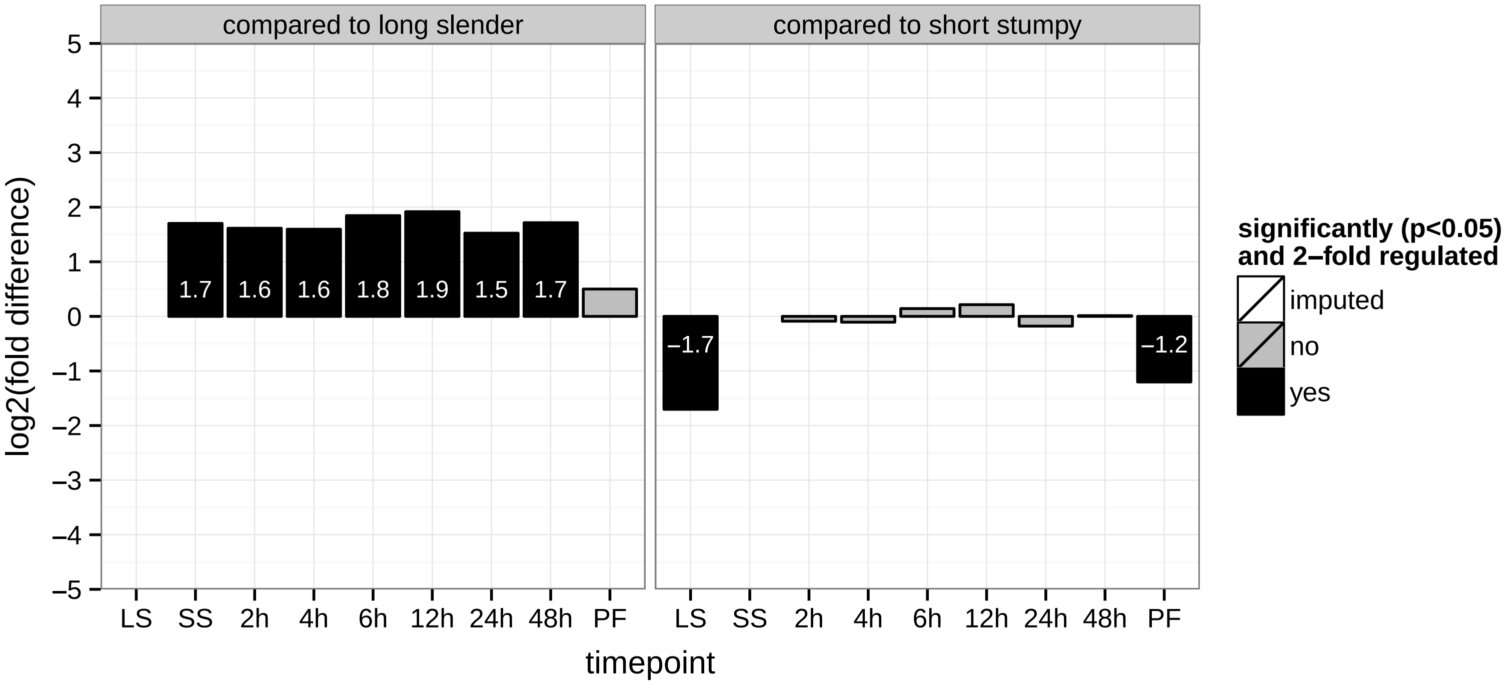
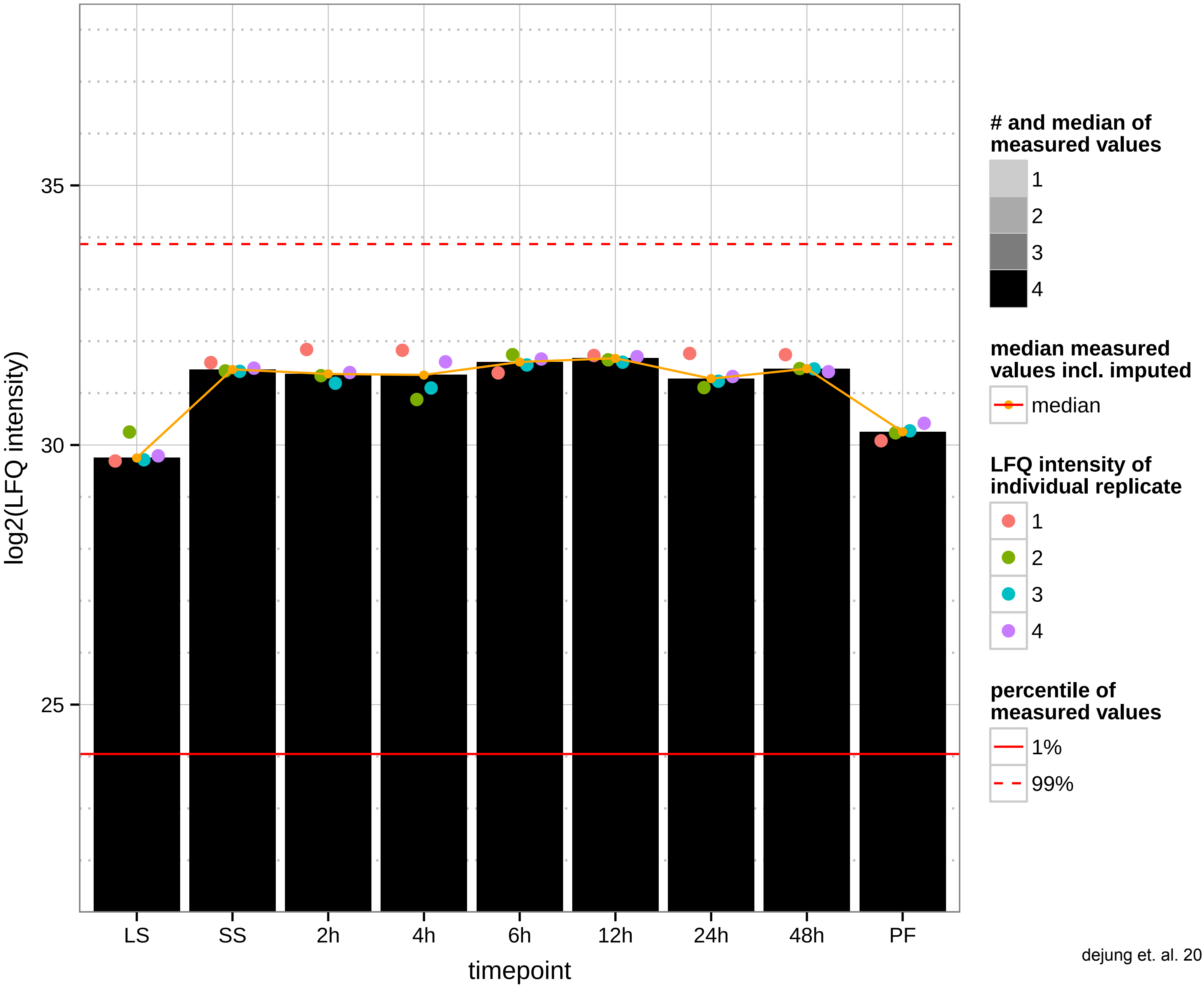
retrotransposon hot spot protein 4 (RHS4), putative, retrotransposon hot spot protein 7 (RHS7)
Tb927.2.560
AGOF: null
AGOC: nucleus, null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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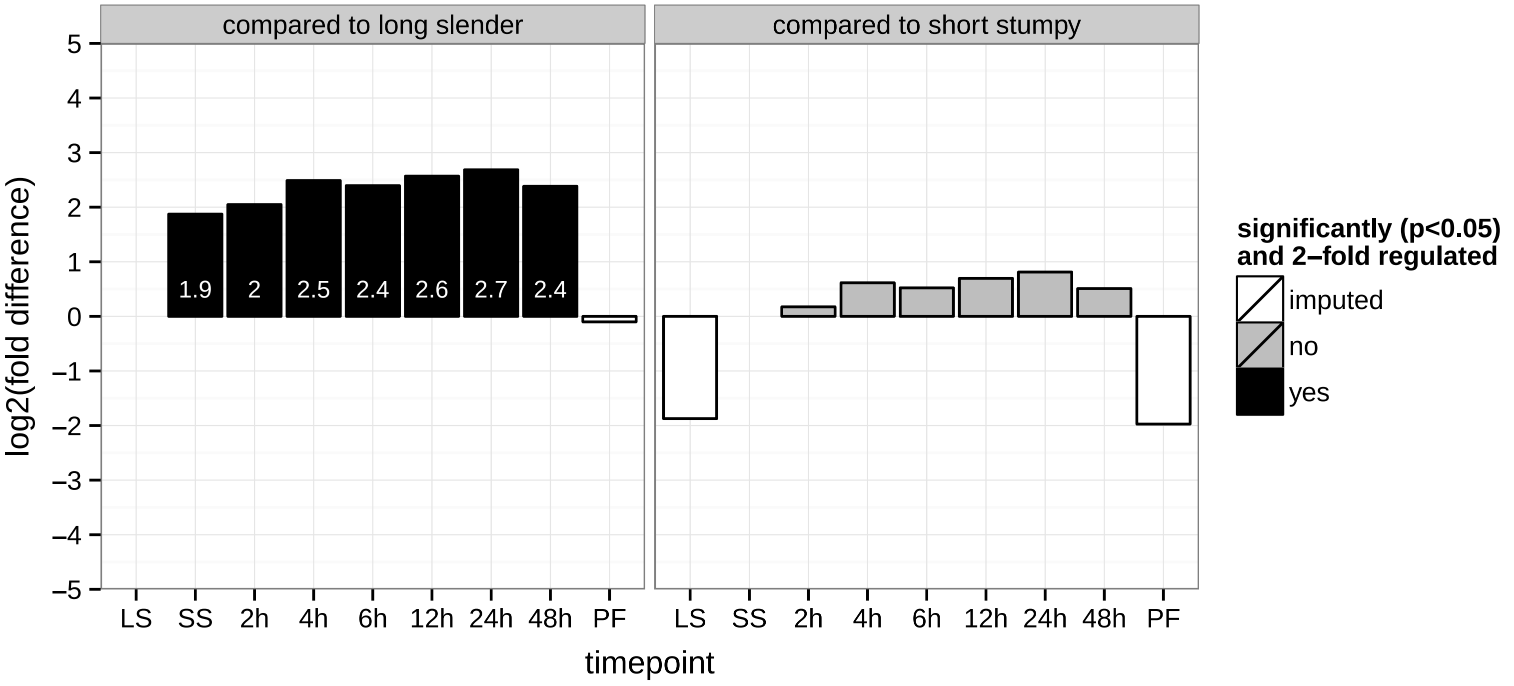
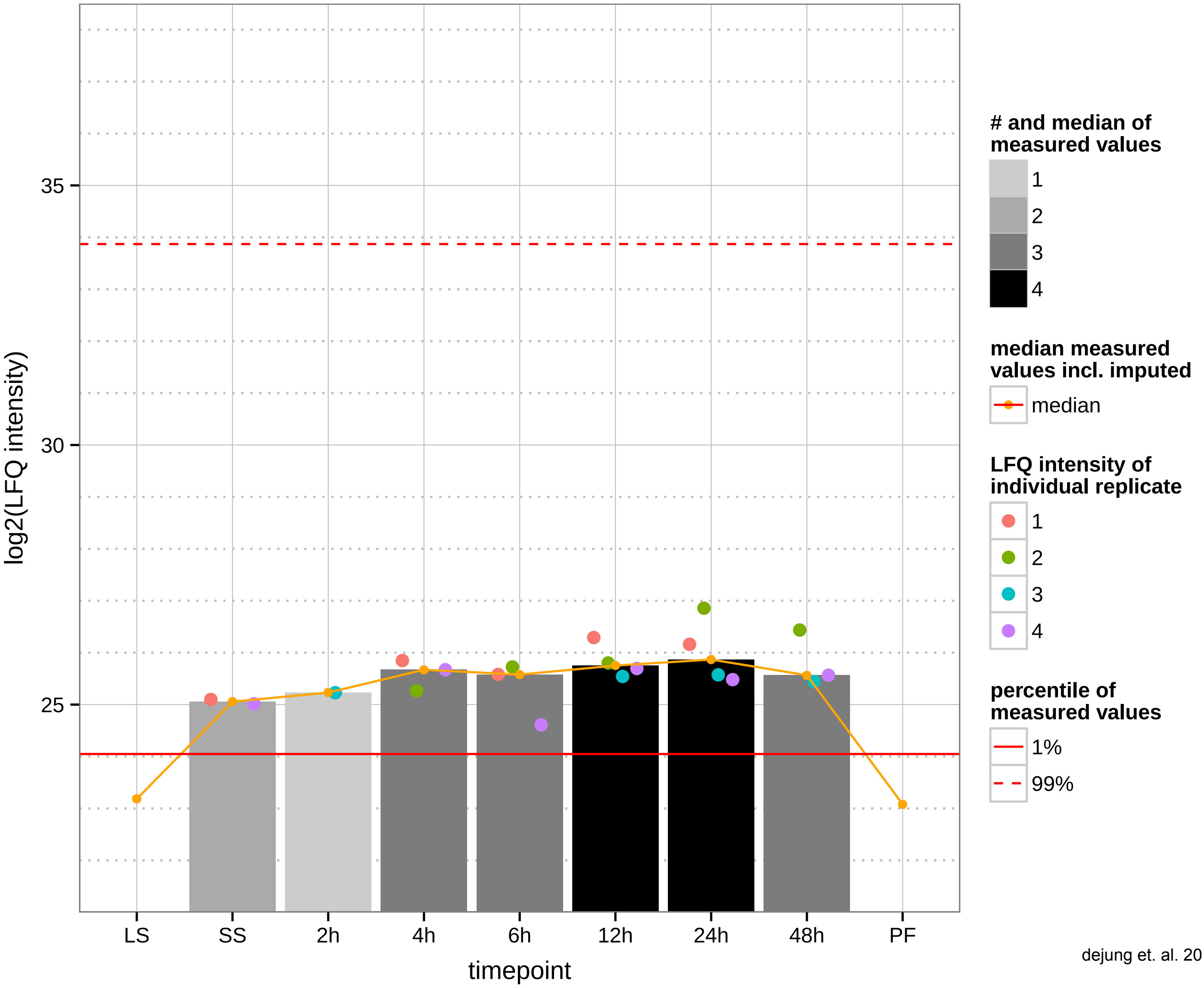
hypothetical protein, conserved
Tb927.3.1140
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: RNA binding
PGOC: null
PGOP: RNA processing





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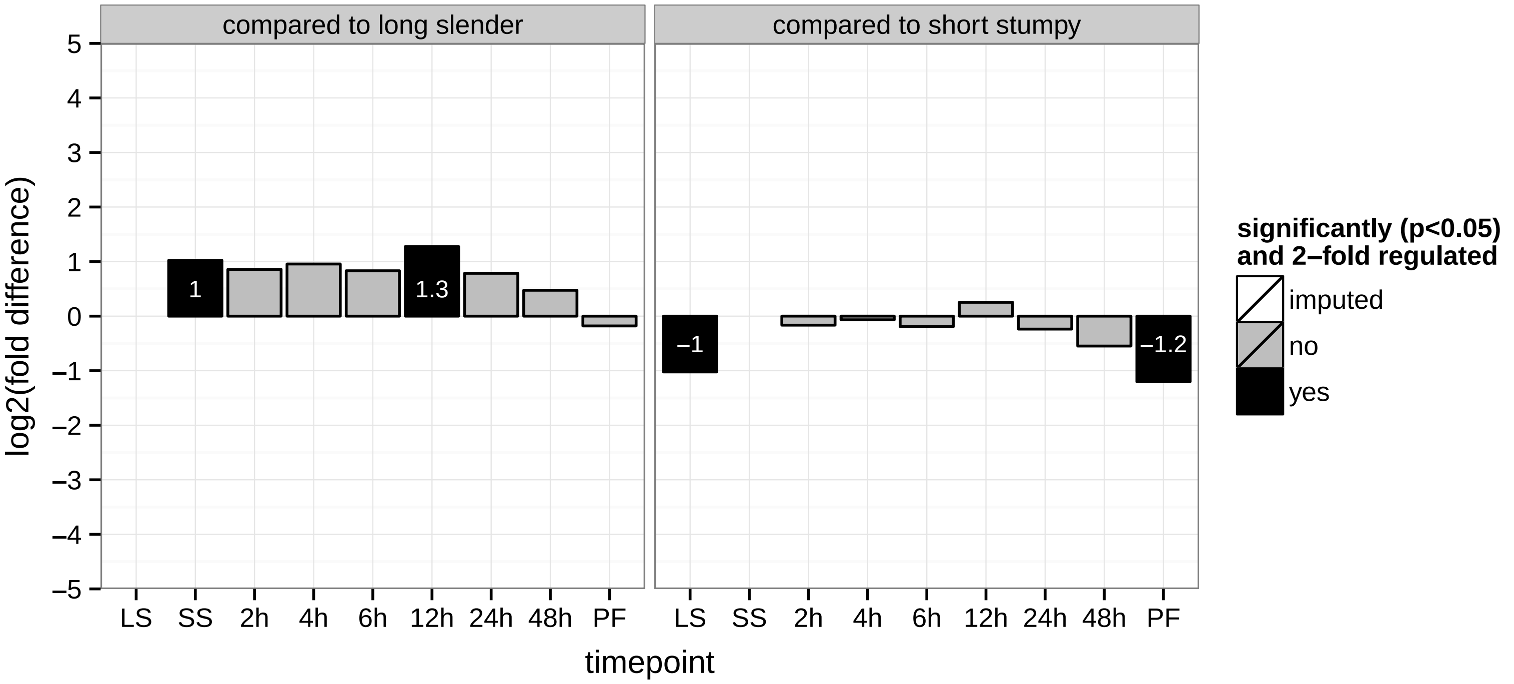
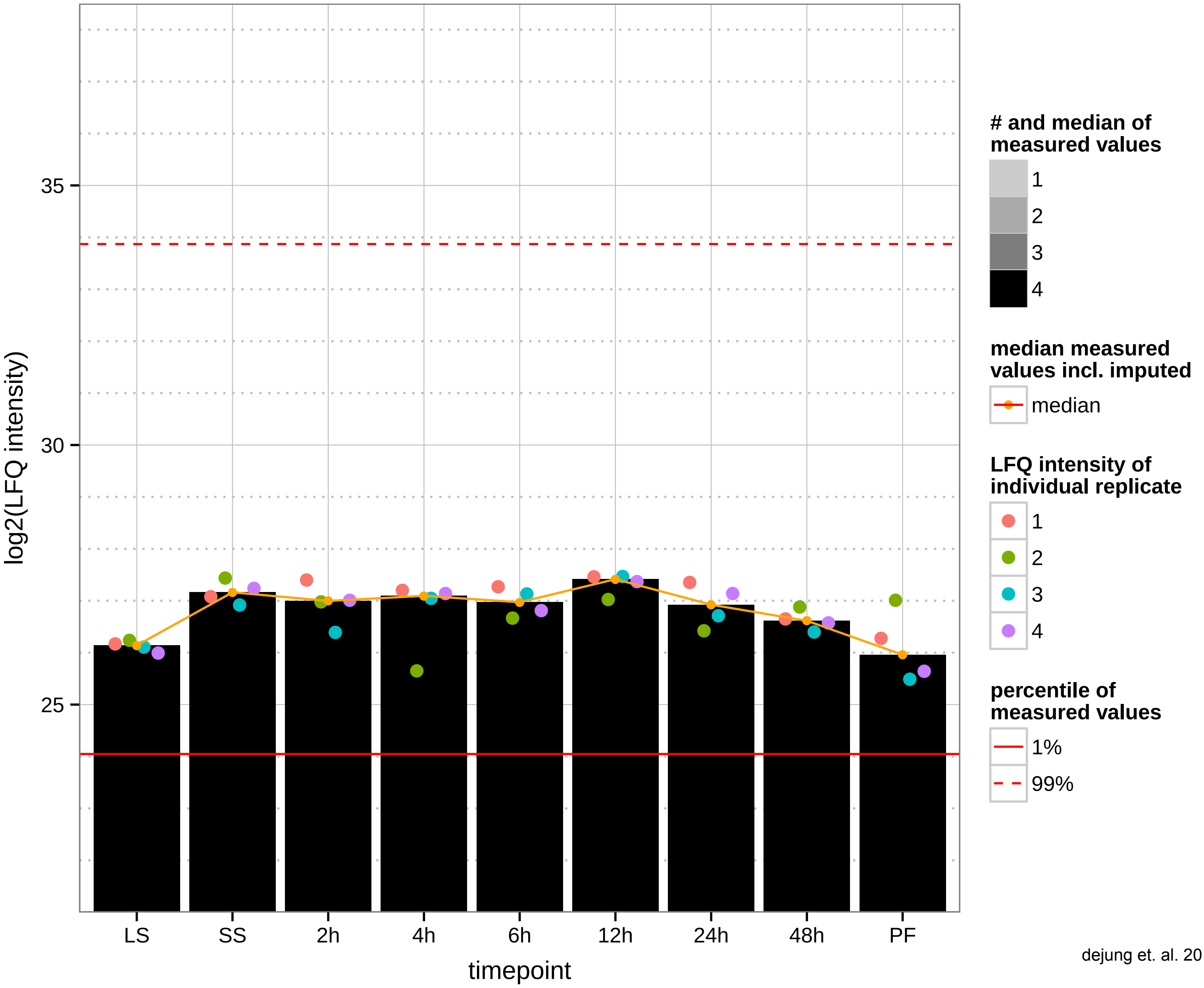
hypothetical protein, conserved
Tb927.3.1800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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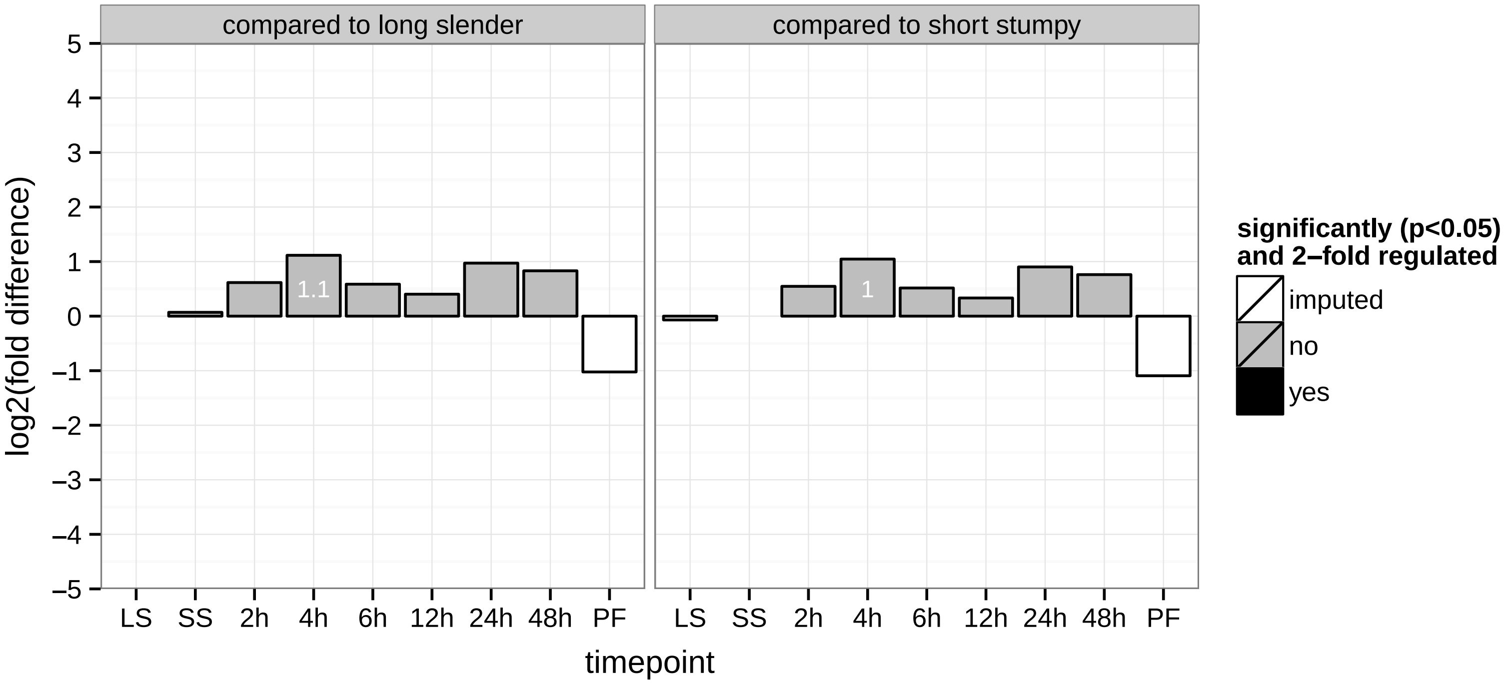
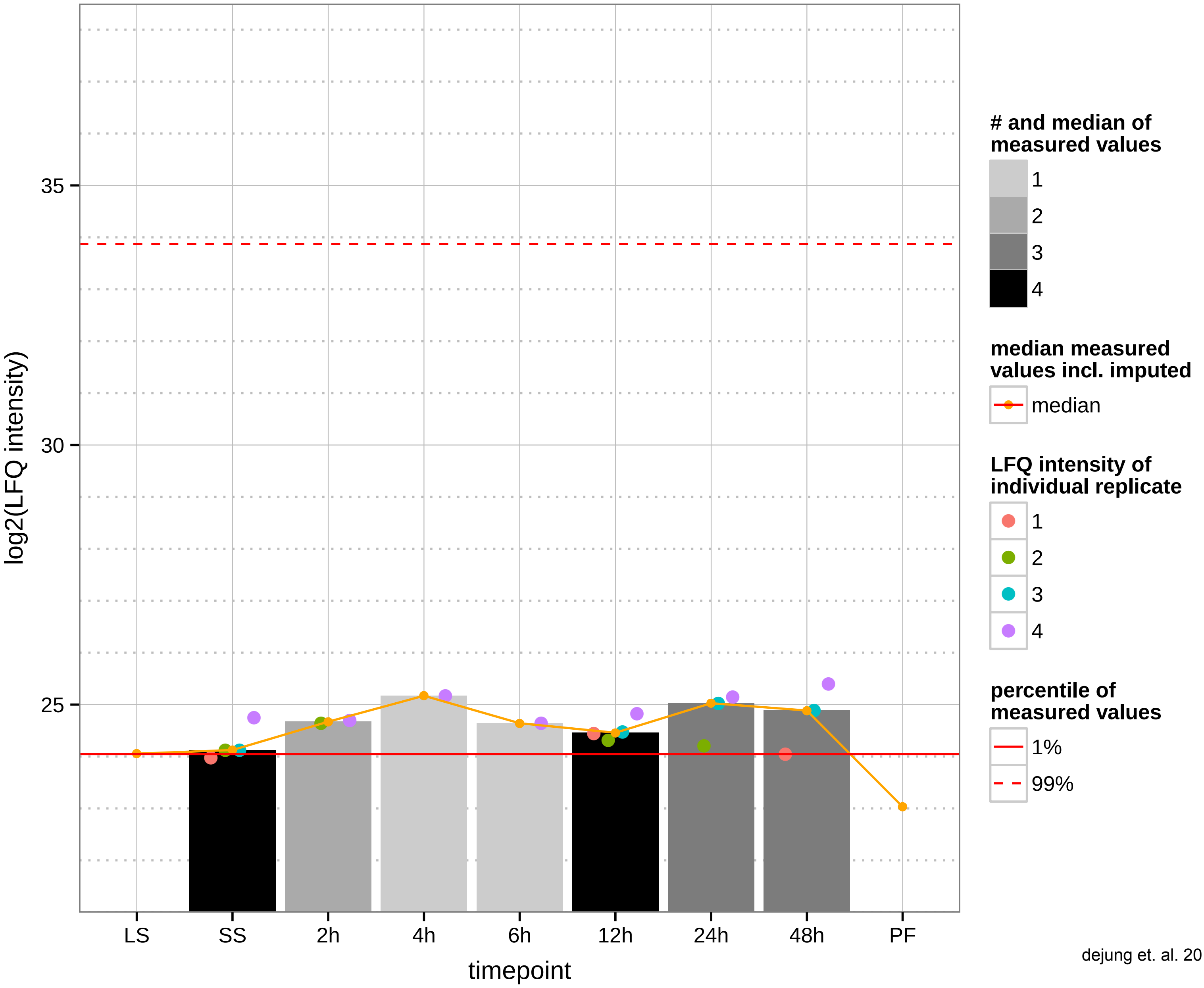
hypothetical protein, conserved
Tb927.3.1980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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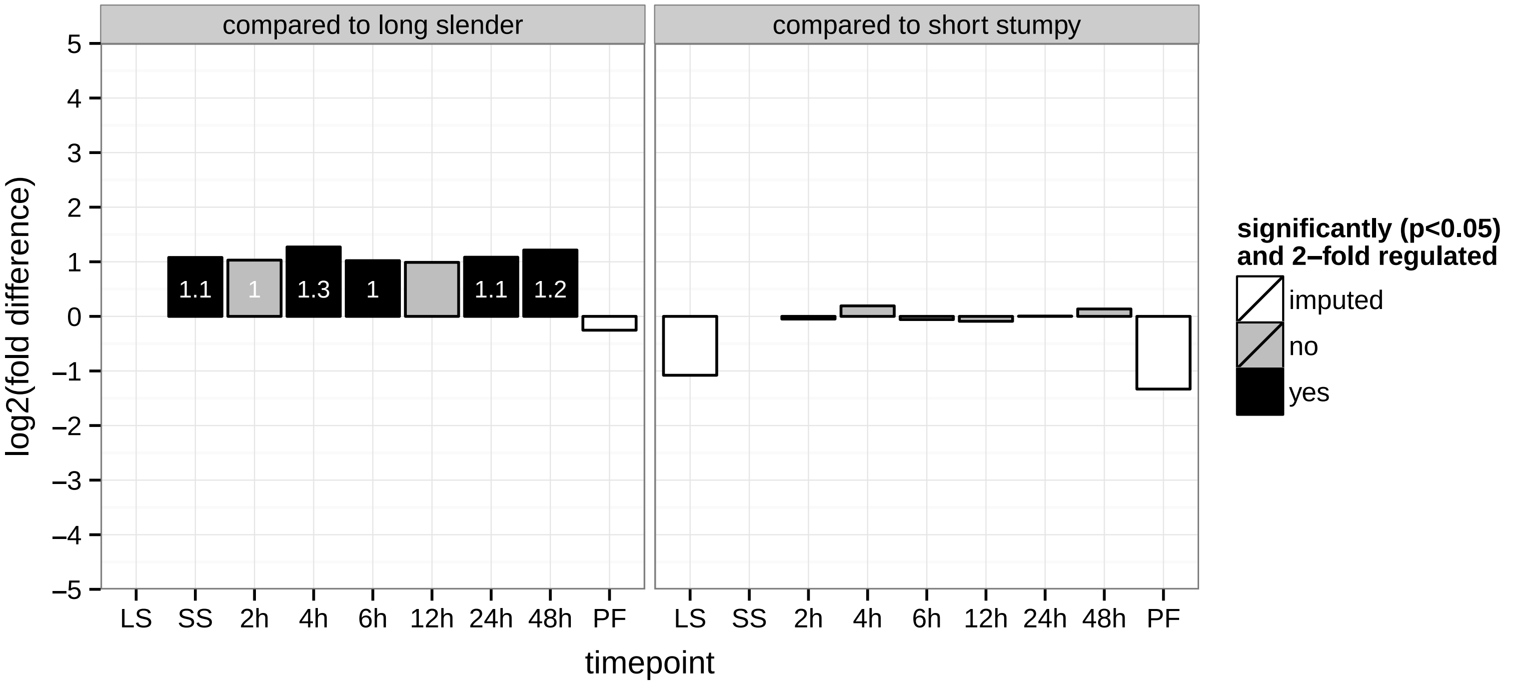
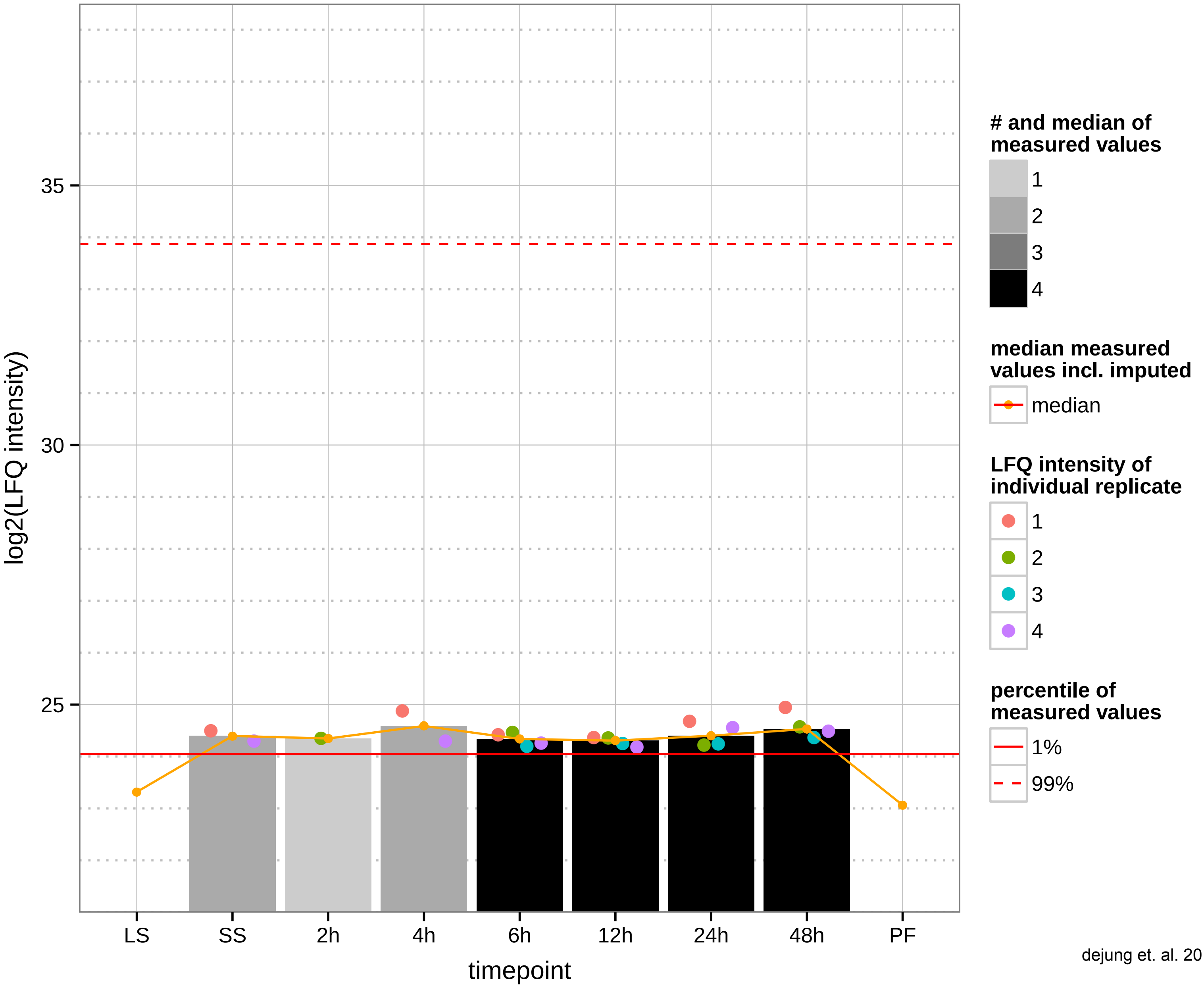
RNA–binding protein, putative (RBP21)
Tb927.3.2000
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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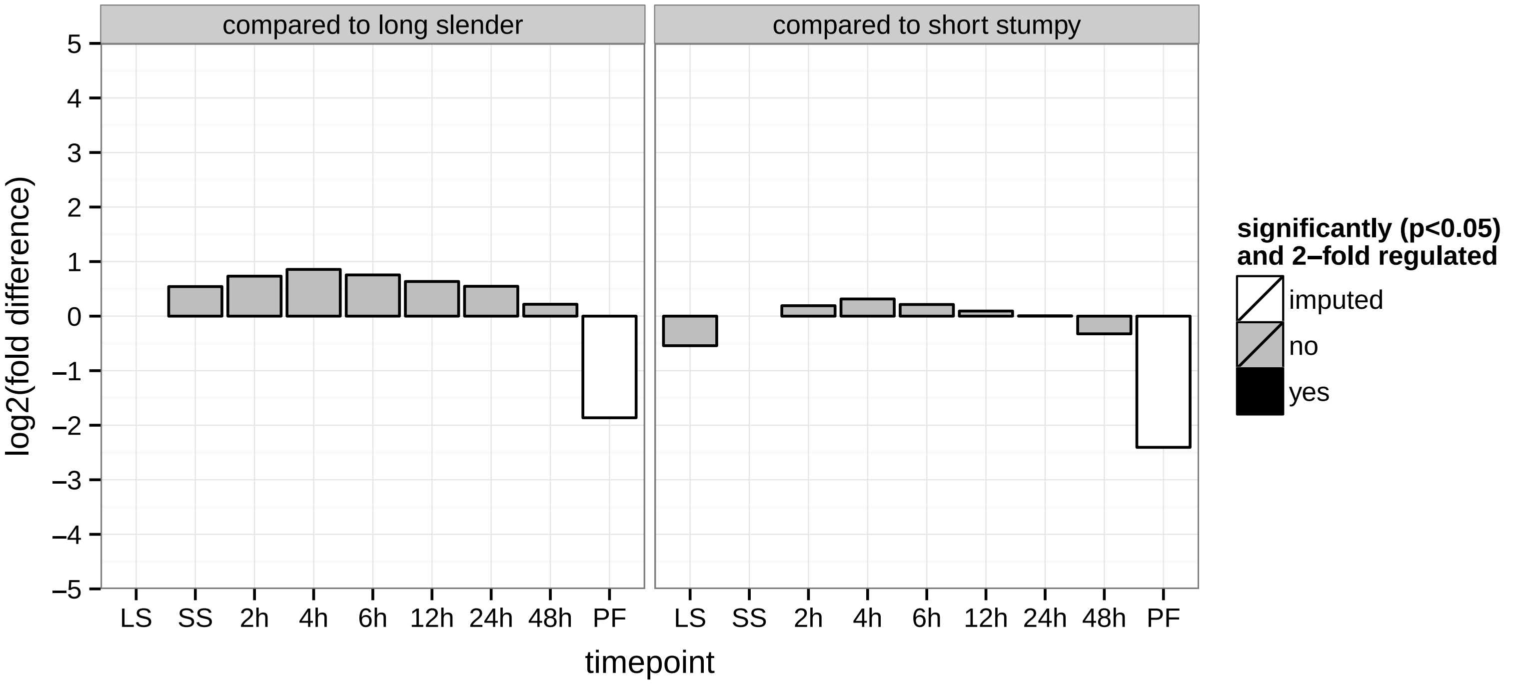
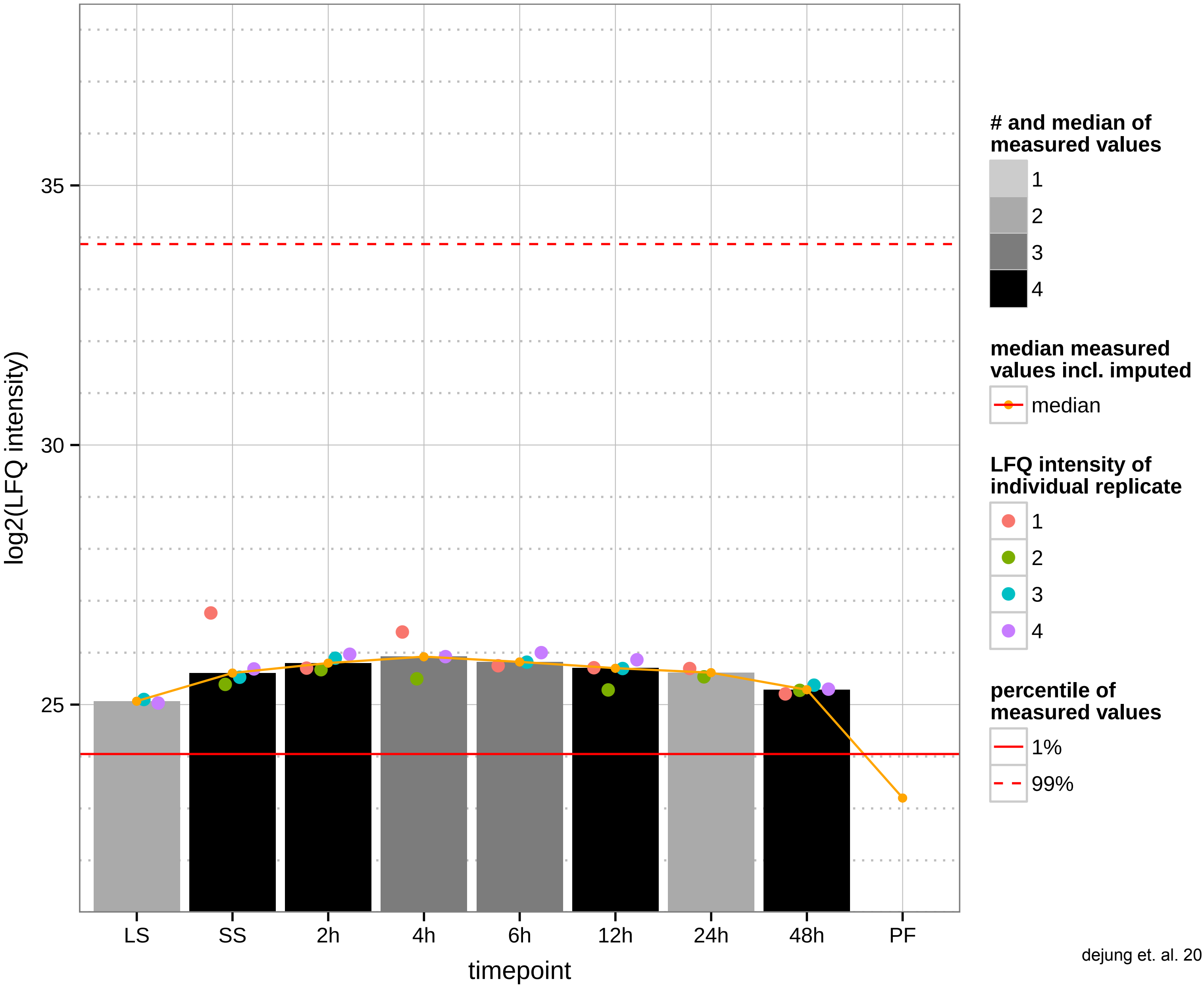
vacuolar sorting protein 33, putative
Tb927.3.2280
AGOF: null
AGOC: null
AGOP: vesicle docking involved in exocytosis, vesicle–mediated transport
PGOF: null
PGOC: null
PGOP: vesicle docking involved in exocytosis, vesicle–mediated transport





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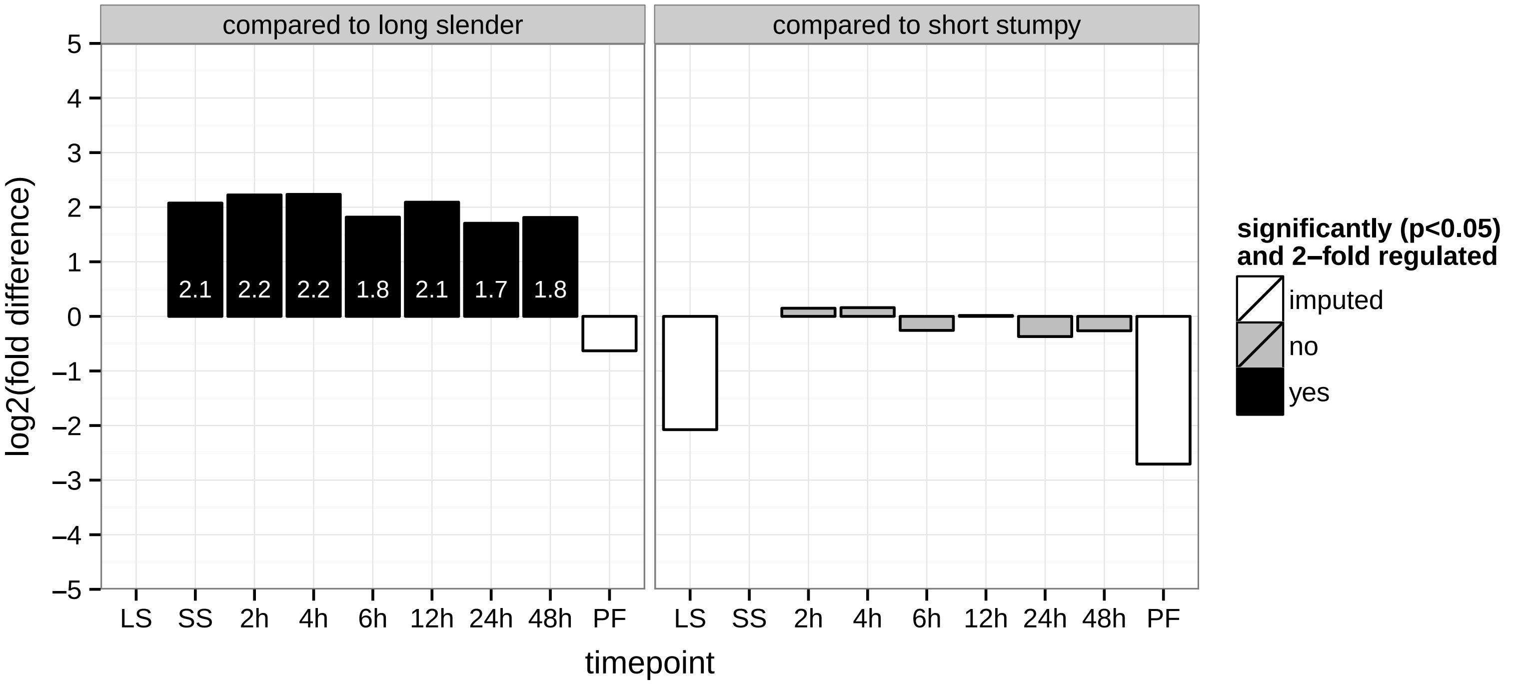
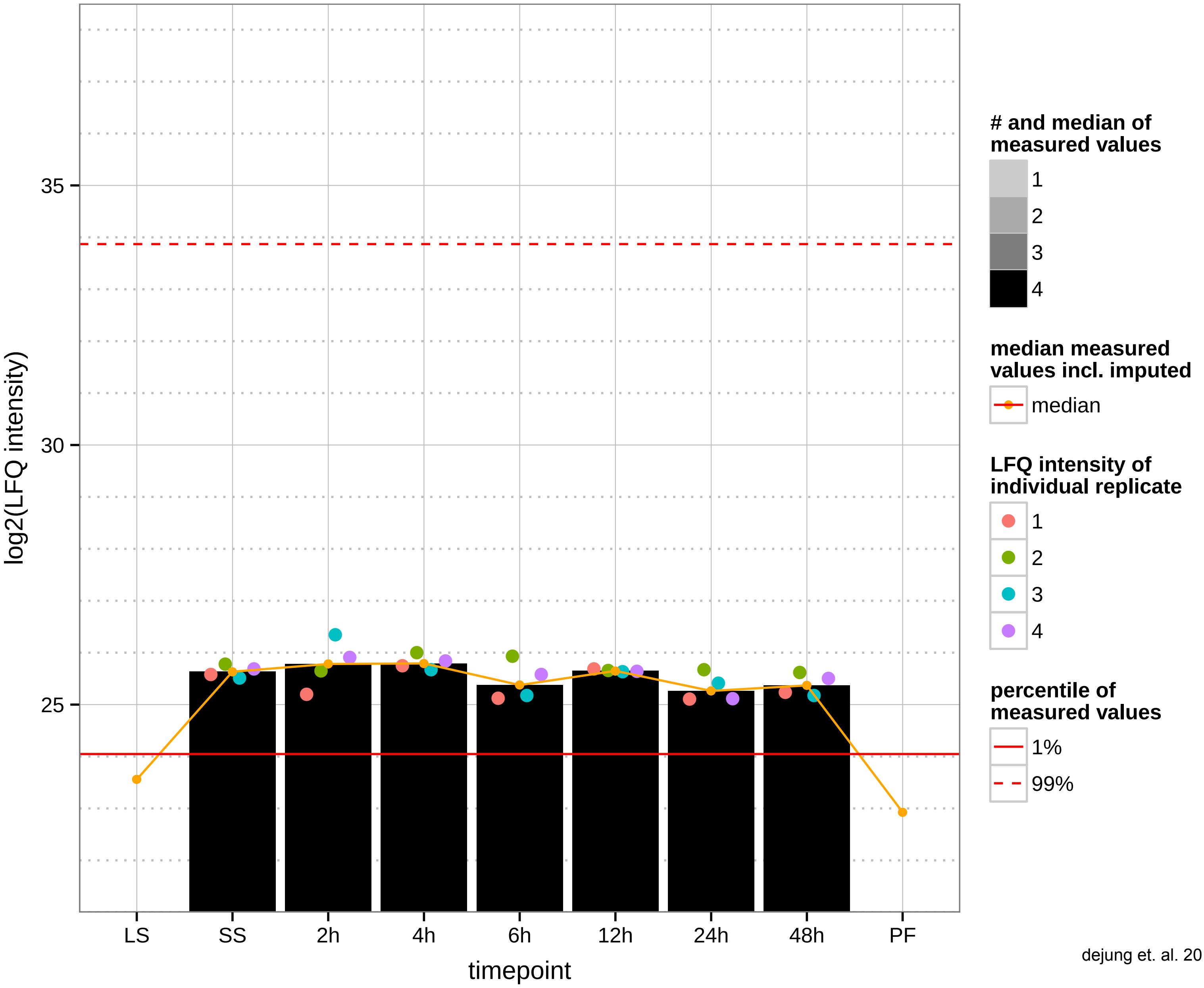
hypothetical protein, conserved
Tb927.3.2870
AGOF: copper ion binding, oxidoreductase activity
AGOC: null
AGOP: null
PGOF: copper ion binding, oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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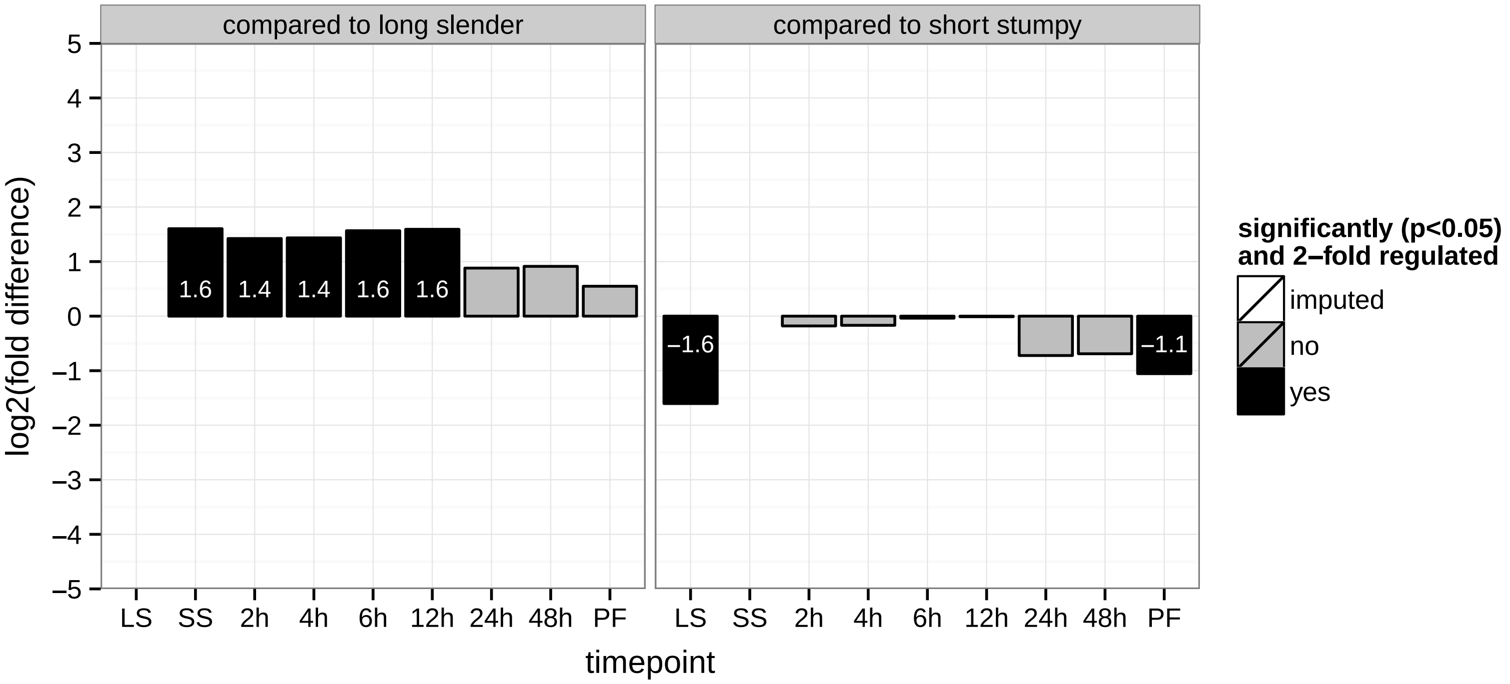
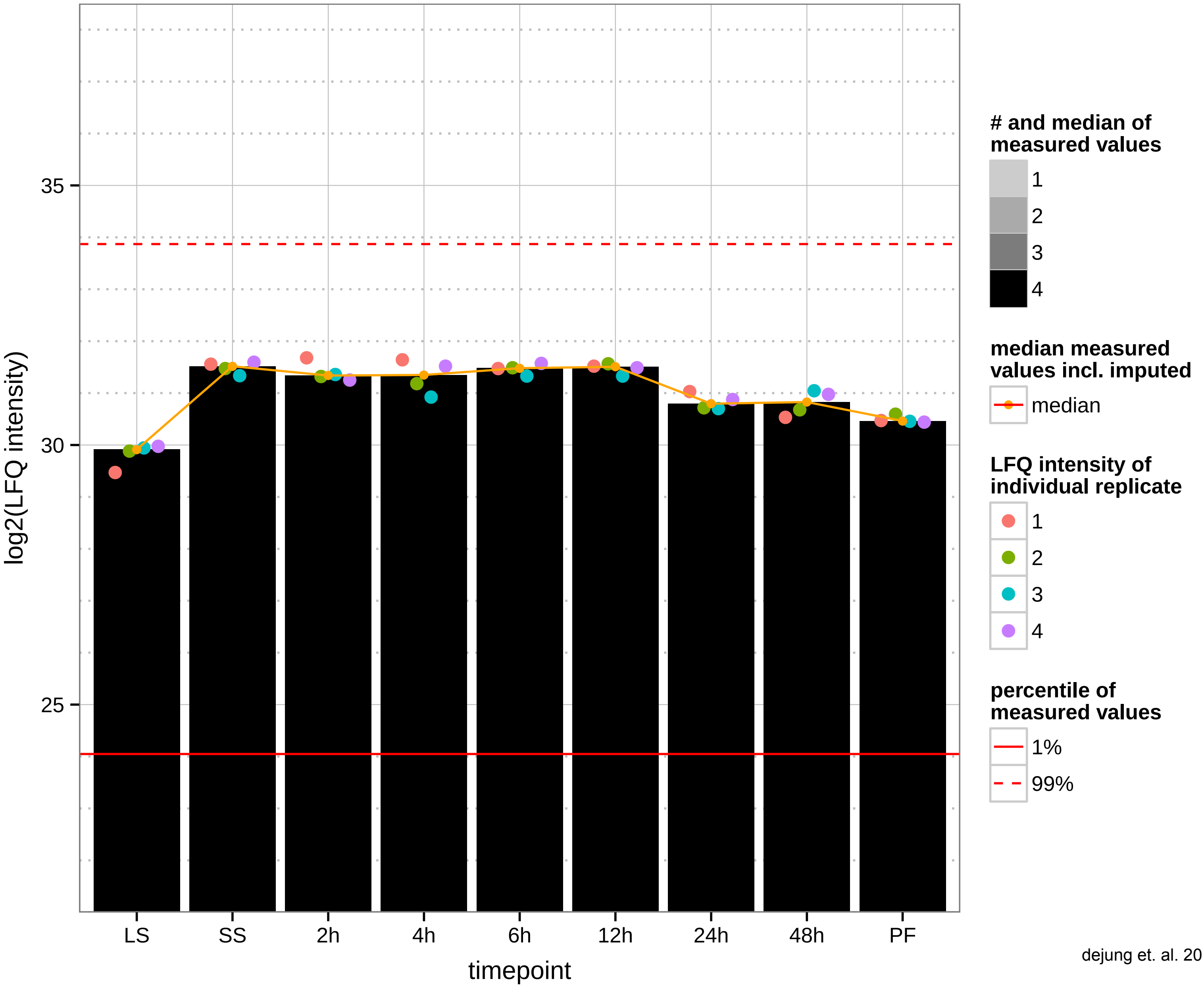
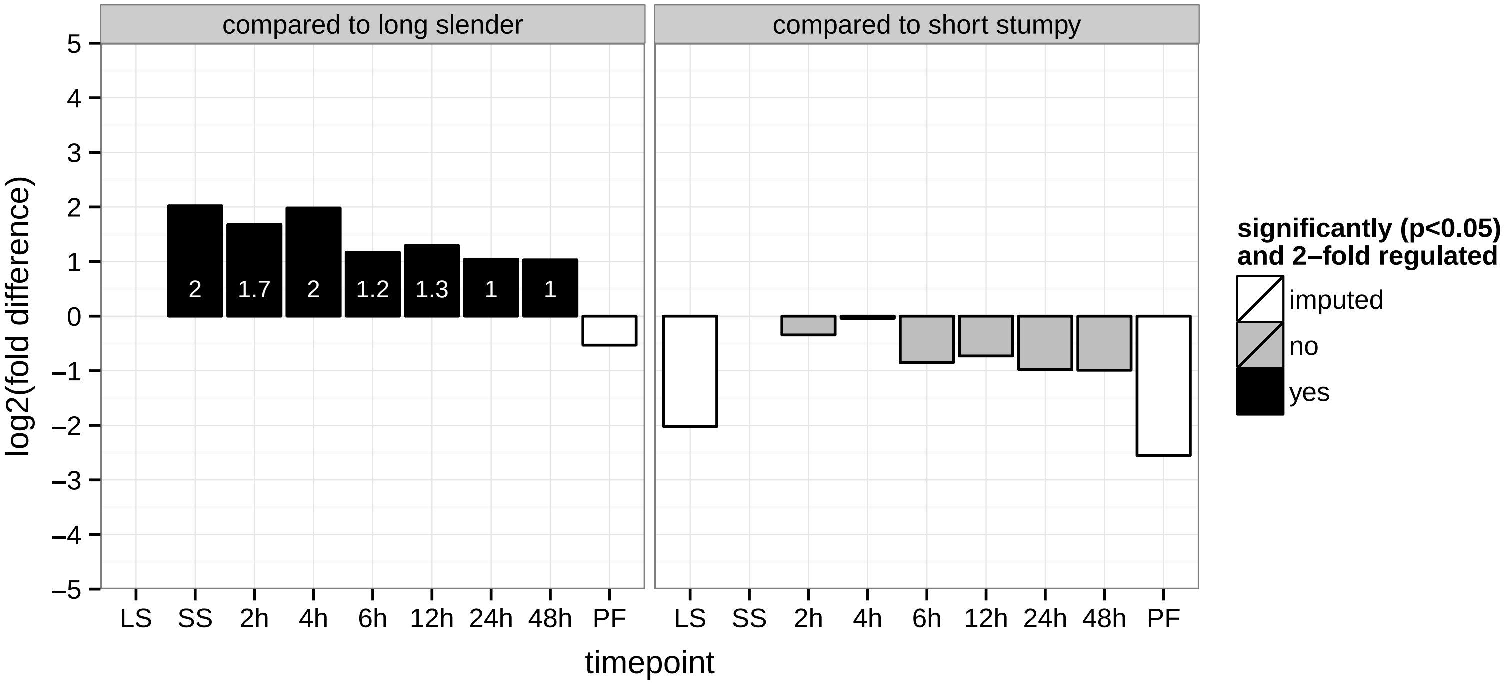
serine/threonine–protein kinase, putative, protein kinase
Tb927.3.3190
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

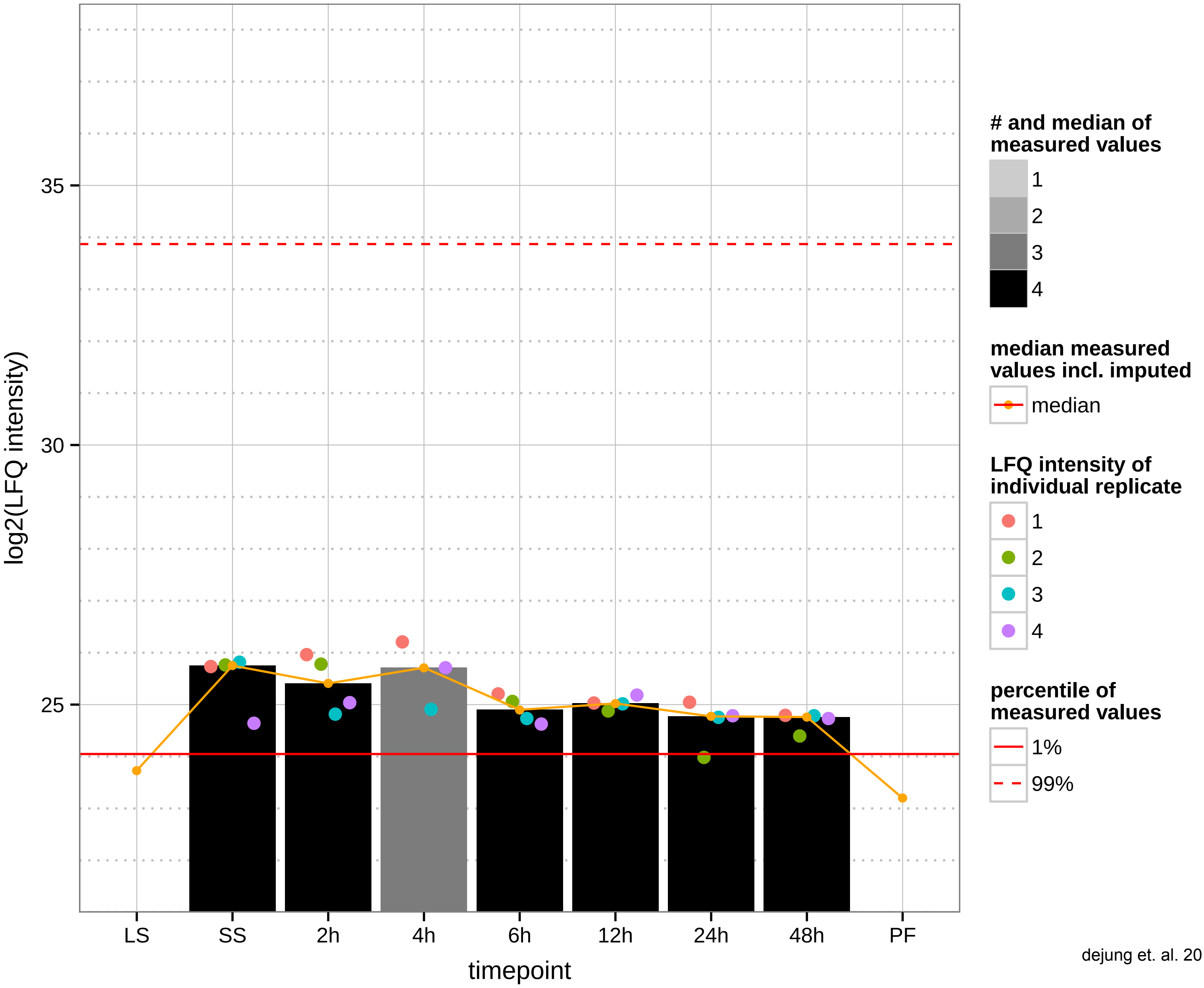




dejung et. al. 2015

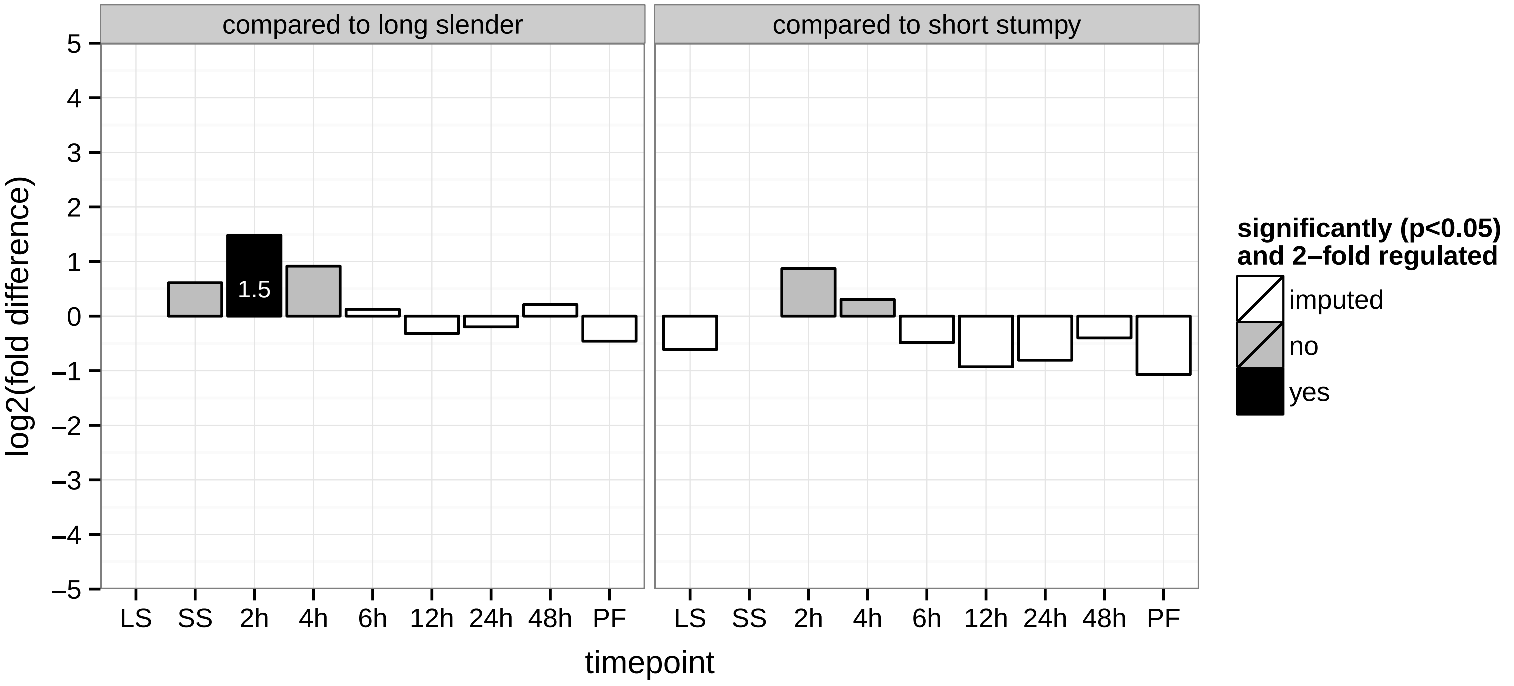
acyltransferase, putative
Tb927.3.3360
AGOF: transferase activity, transferring acyl groups
AGOC: null
AGOP: metabolic process
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: metabolic process

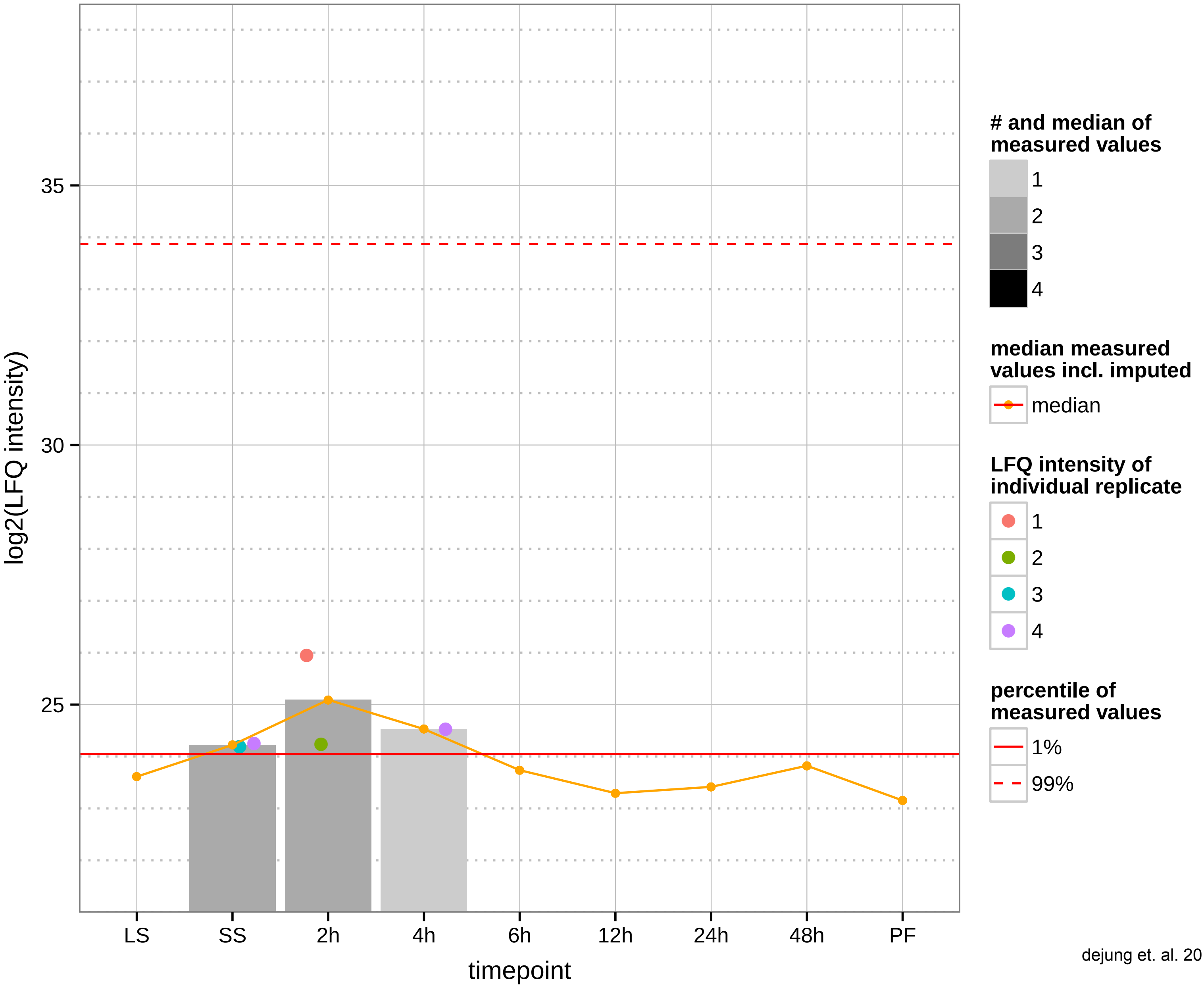




dejung et. al. 2015

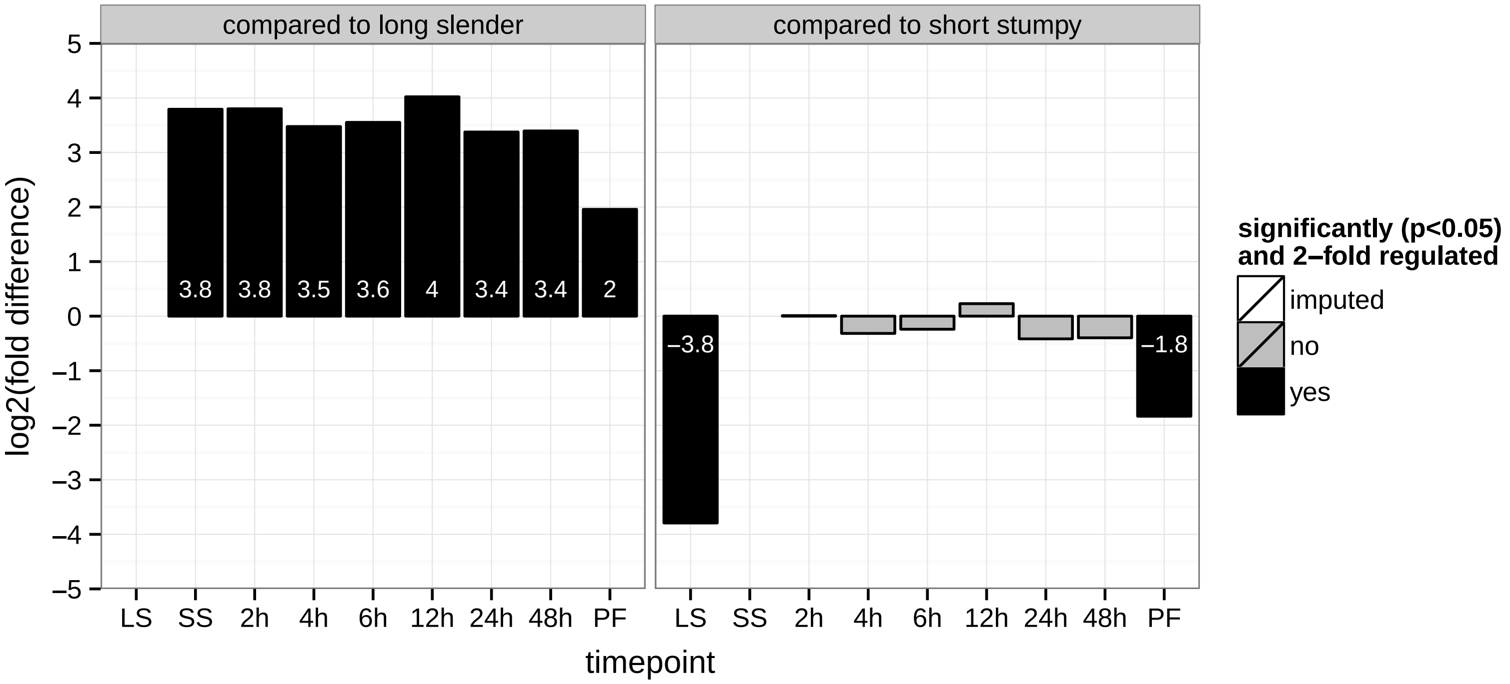
lipase domain protein, putative
Tb927.3.3870
AGOF: triglyceride lipase activity
AGOC: null
AGOP: lipid metabolic process
PGOF: triglyceride lipase activity
PGOC: null
PGOP: lipid metabolic process

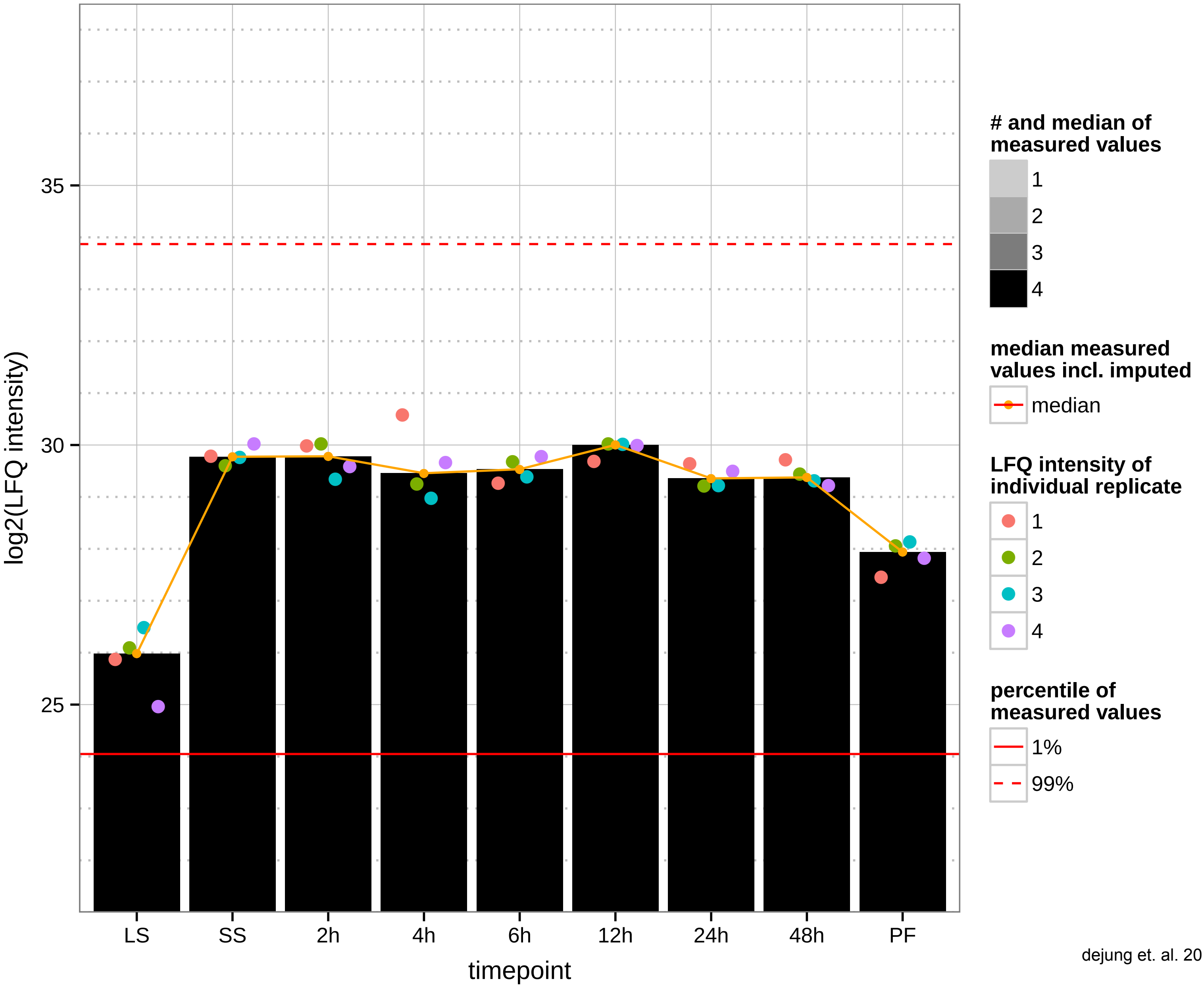




dejung et. al. 2015

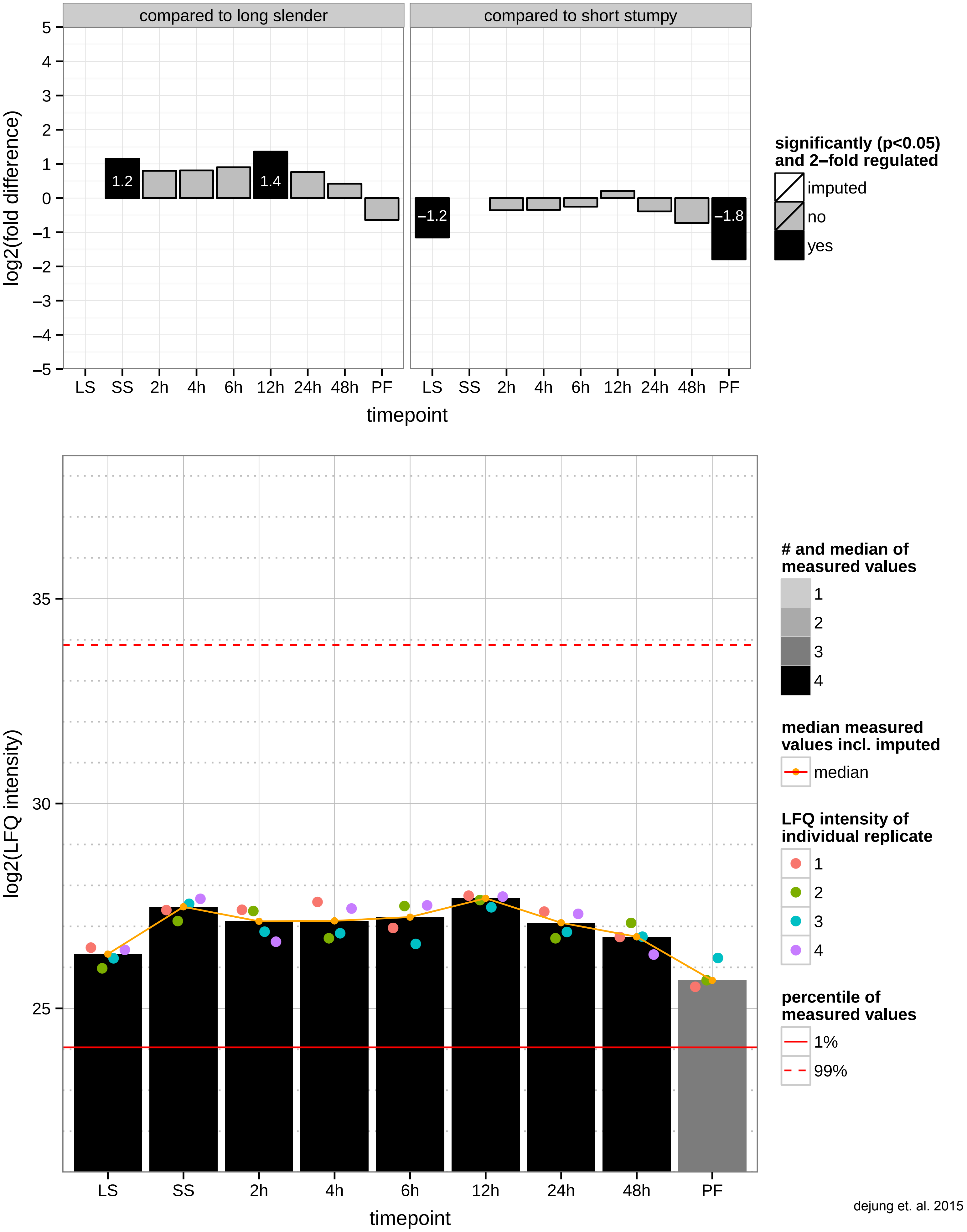
hypothetical protein, conserved
Tb927.3.4260
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.4420
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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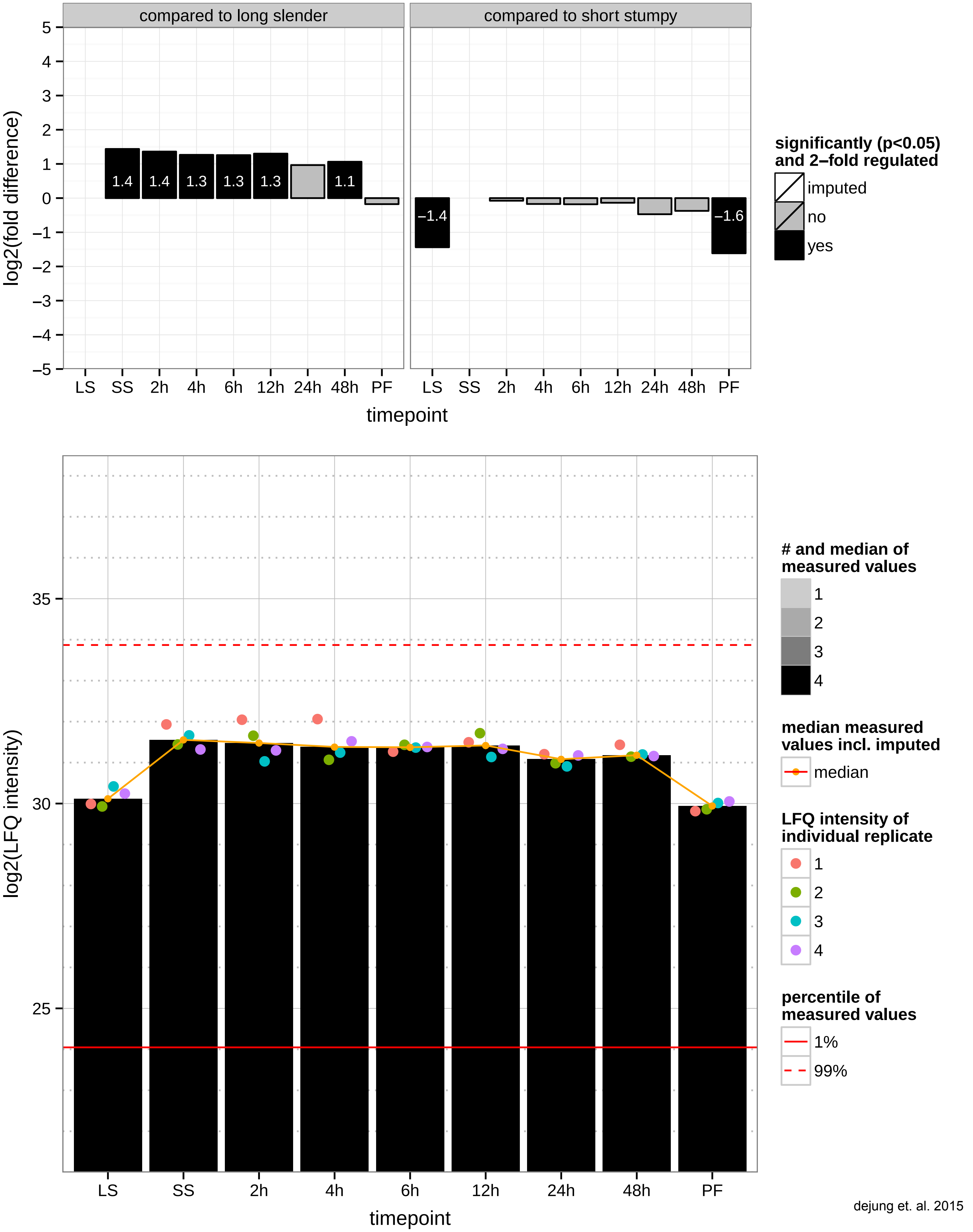
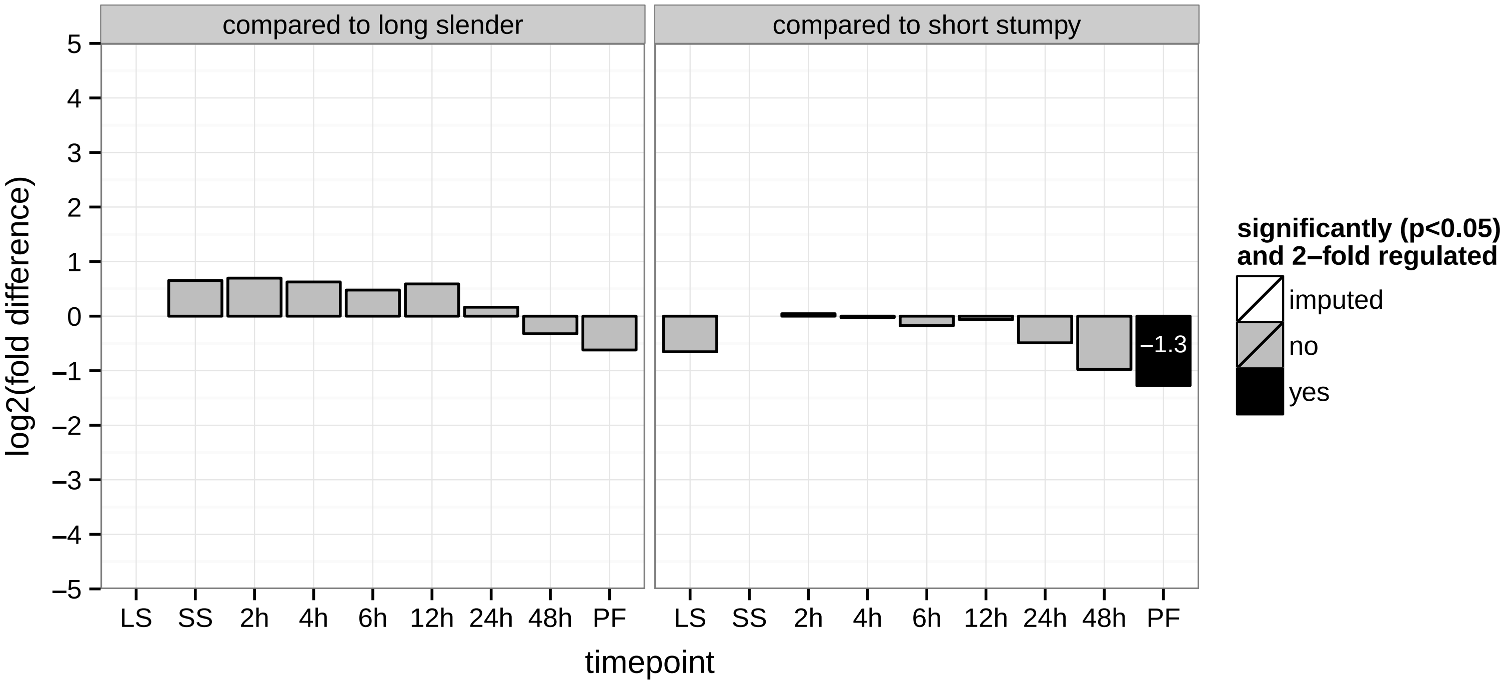
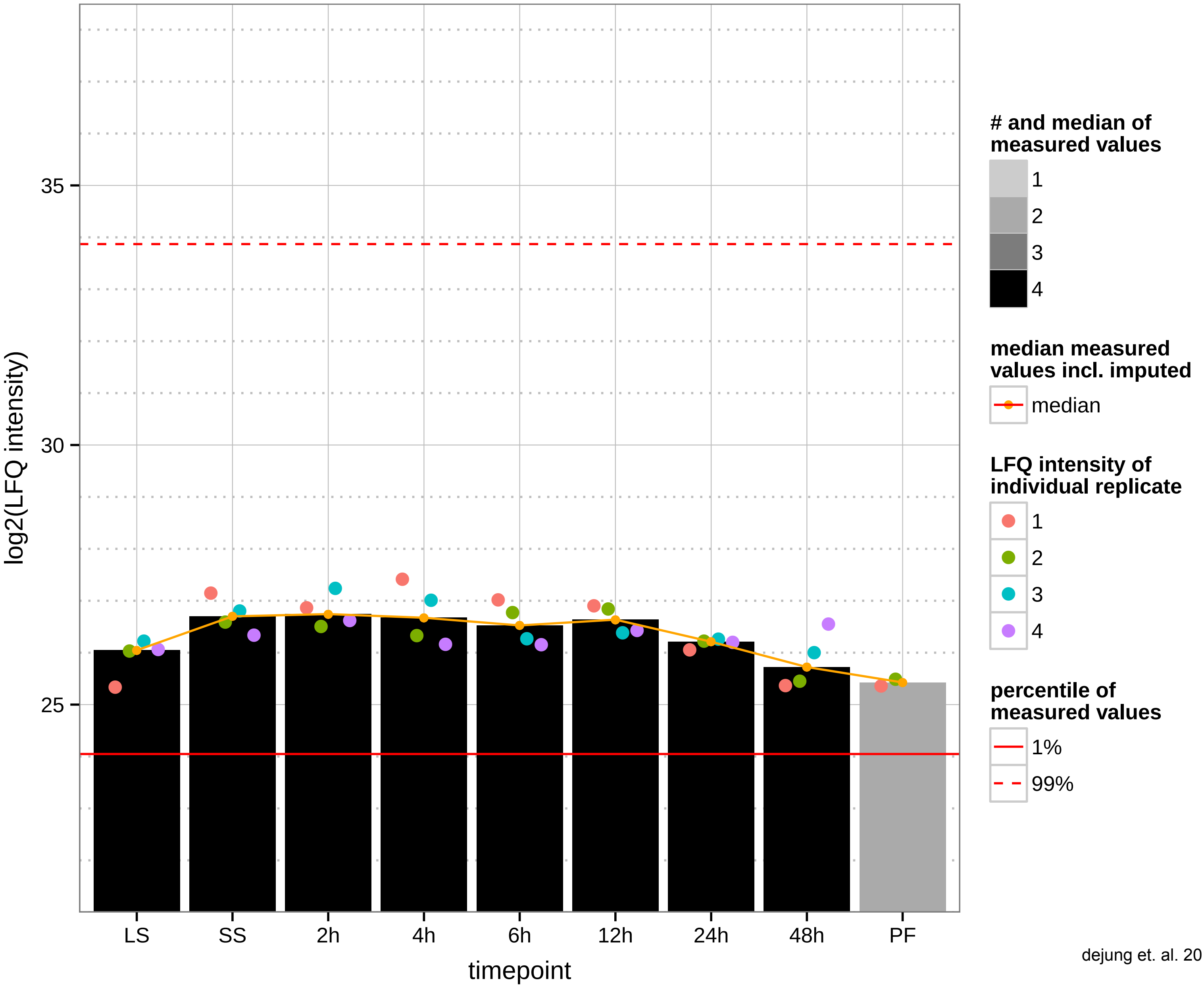
RAB GDP dissociation inhibitor alpha, putative
Tb927.3.4680
AGOF: Rab GDP−dissociation inhibitor activity
AGOC: null
AGOP: protein transport, regulation of GTPase activity
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.4800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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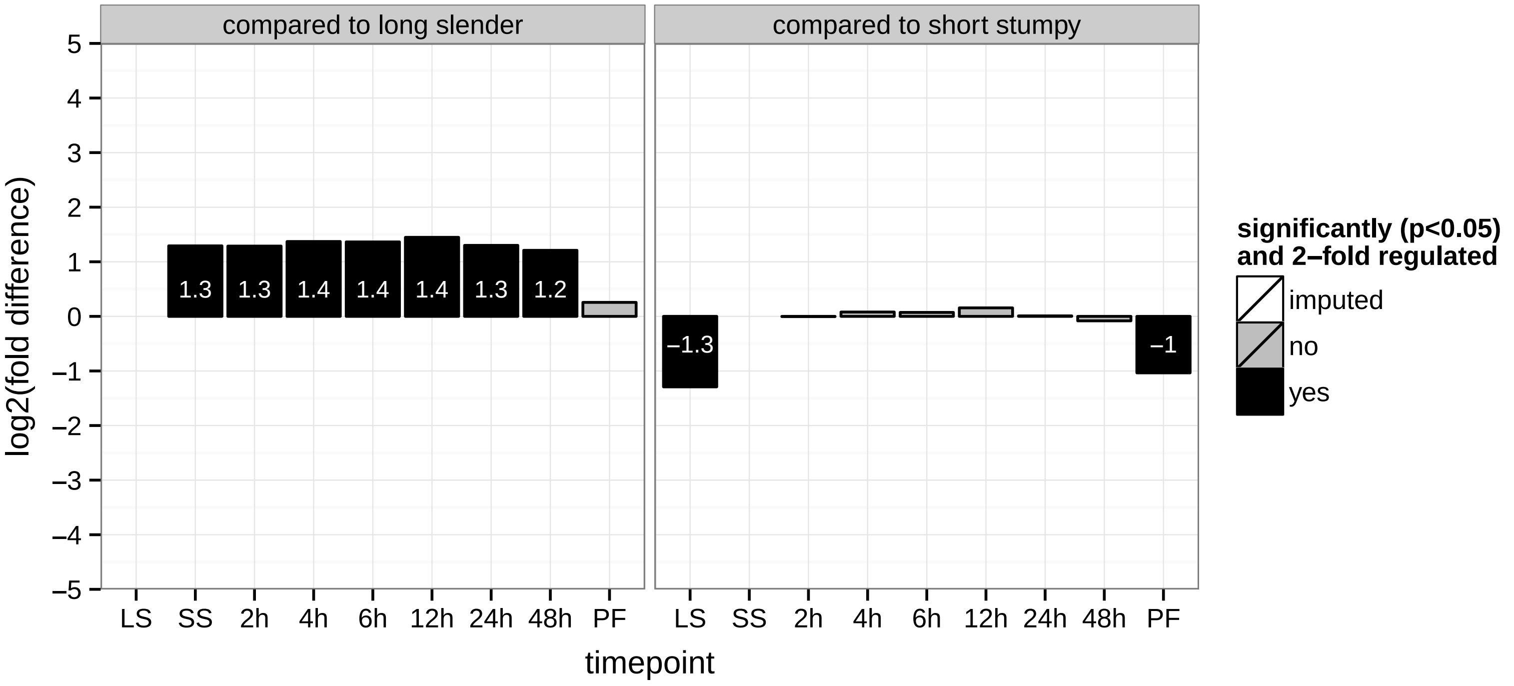
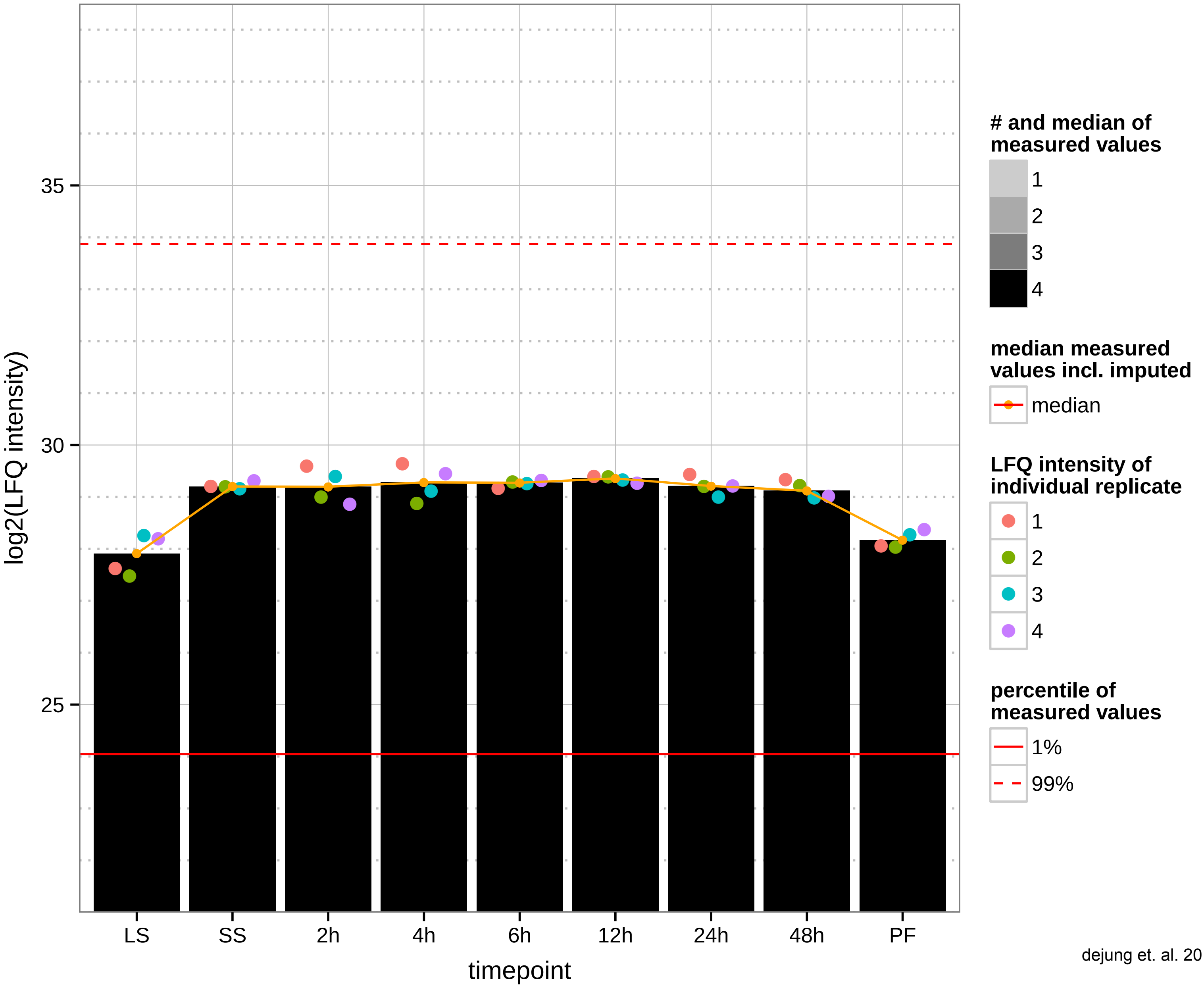
ubiquitin hydrolase, putative, cysteine peptidase, Clan CA, family C19
Tb927.3.4840
AGOF: ubiquitin thiolesterase activity, zinc ion binding
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: omega peptidase activity, protein binding, ubiquitin thiolesterase activity, zinc ion binding
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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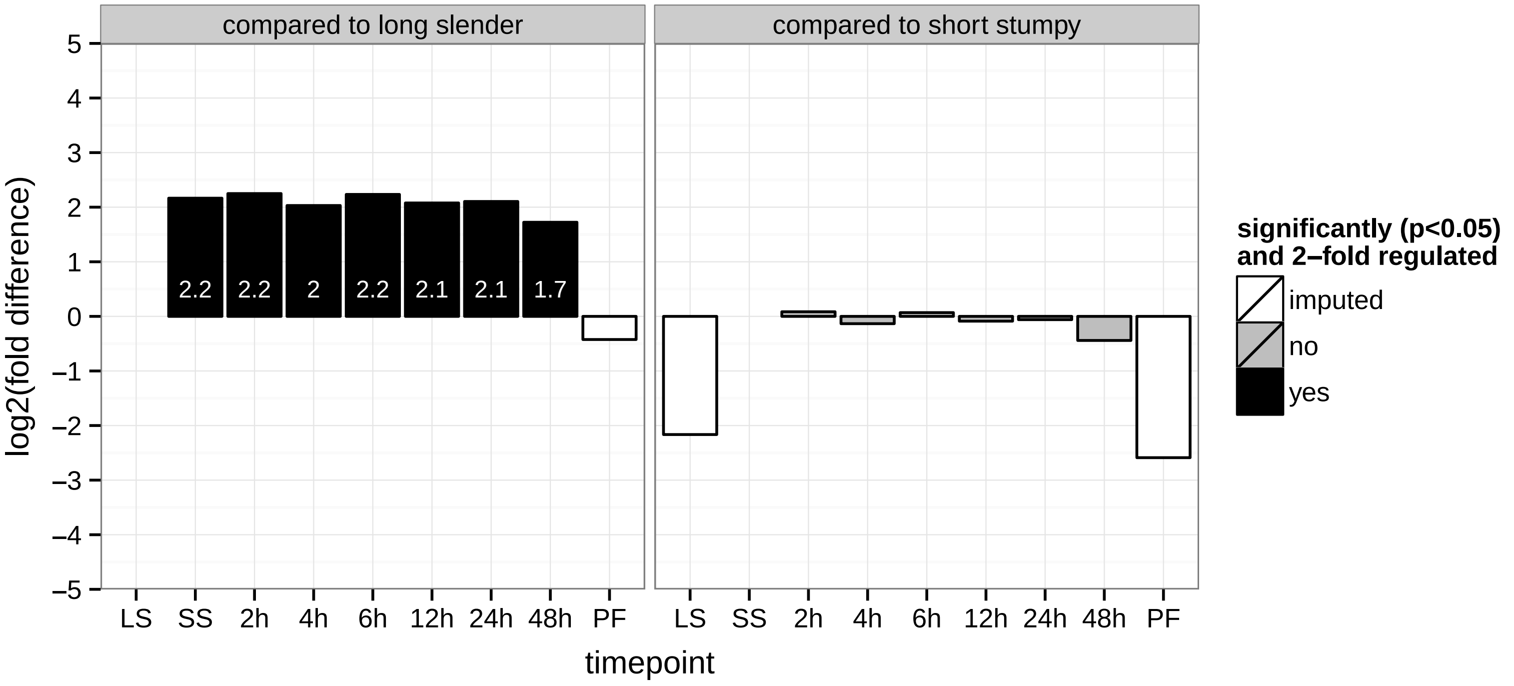
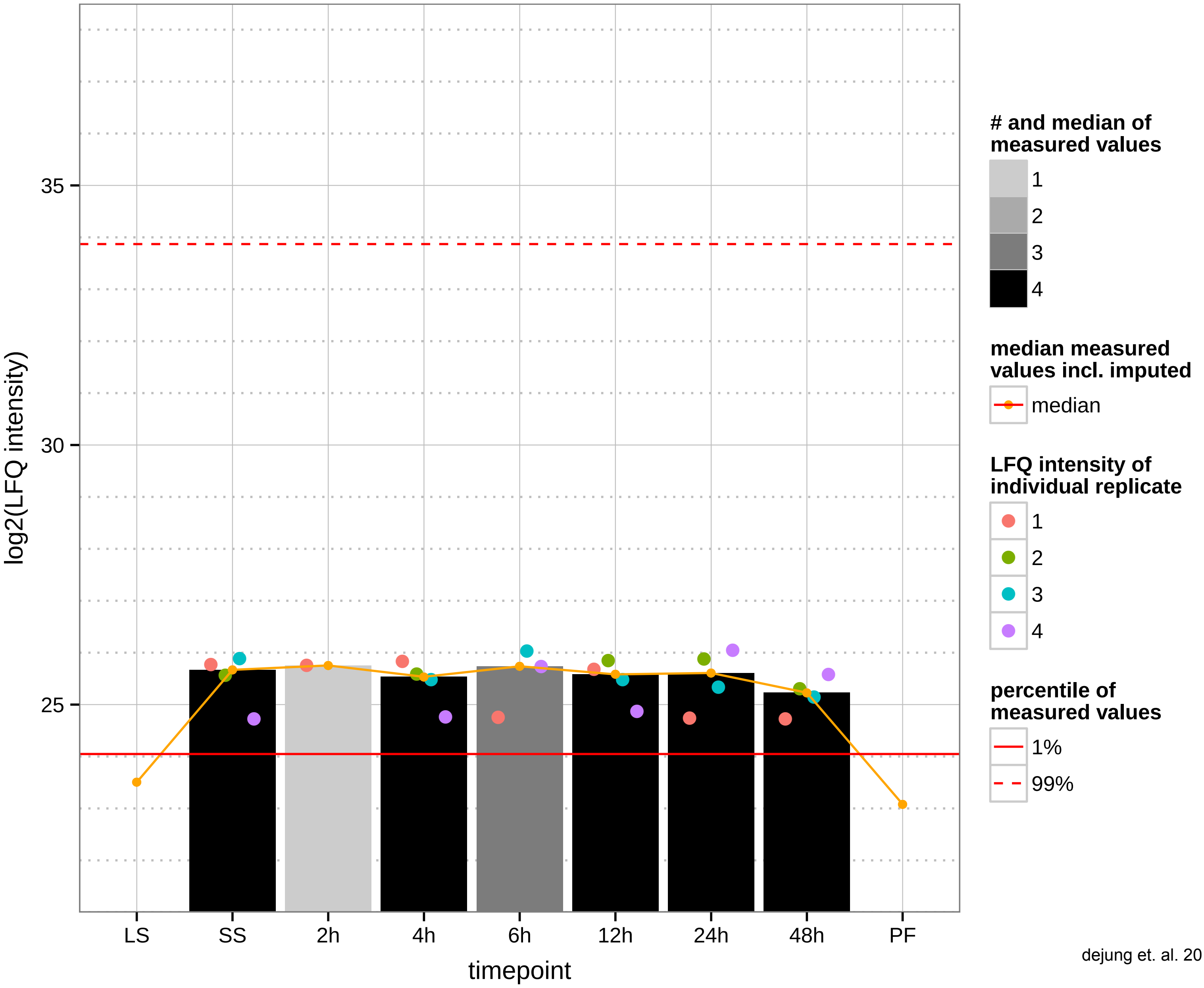
spliceosome–associated protein 49, putative (DRBD1)
Tb927.3.5280
AGOF: nucleic acid binding, protein binding
AGOC: nucleus
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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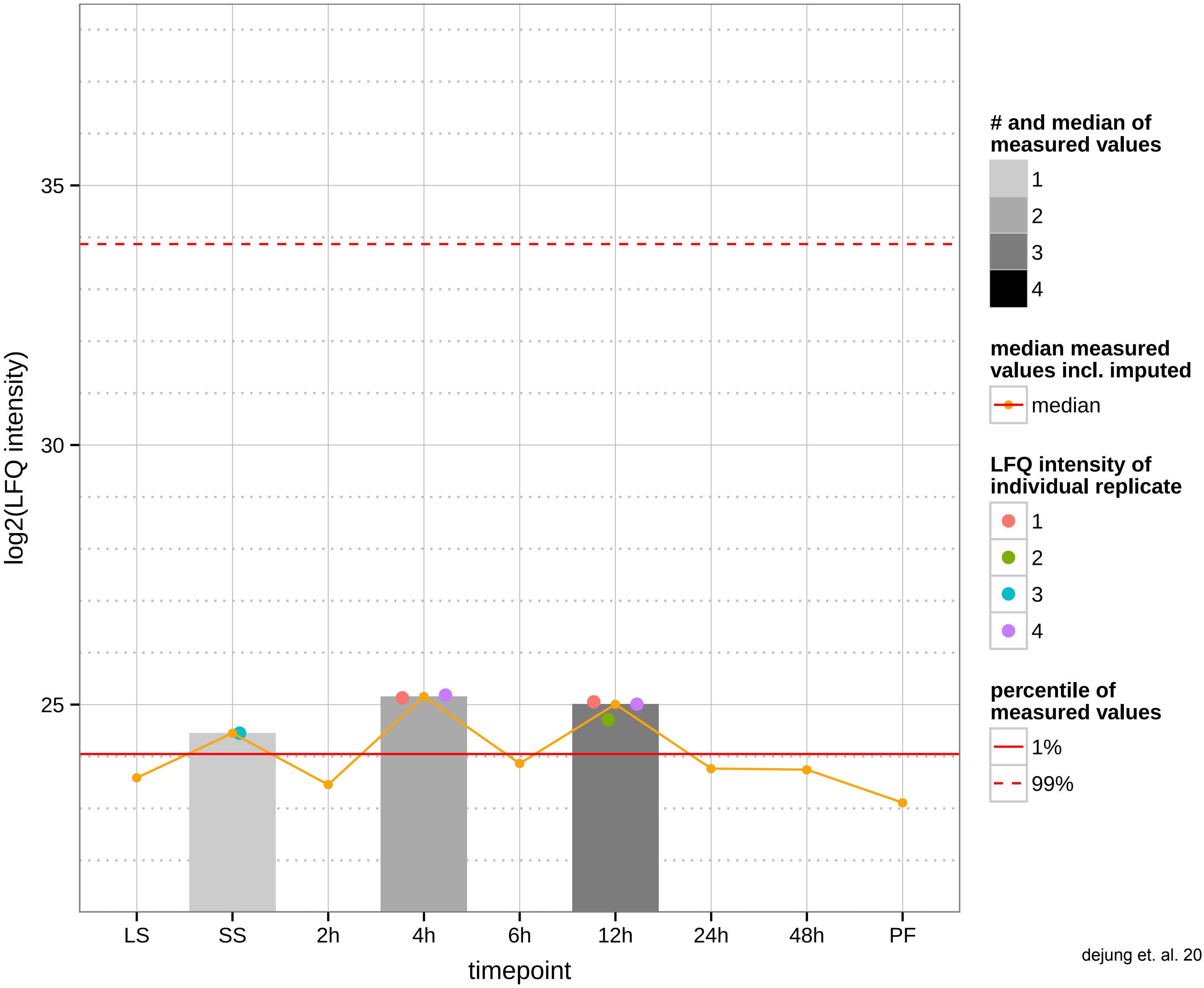
hypothetical protein, conserved
Tb927.3.5360
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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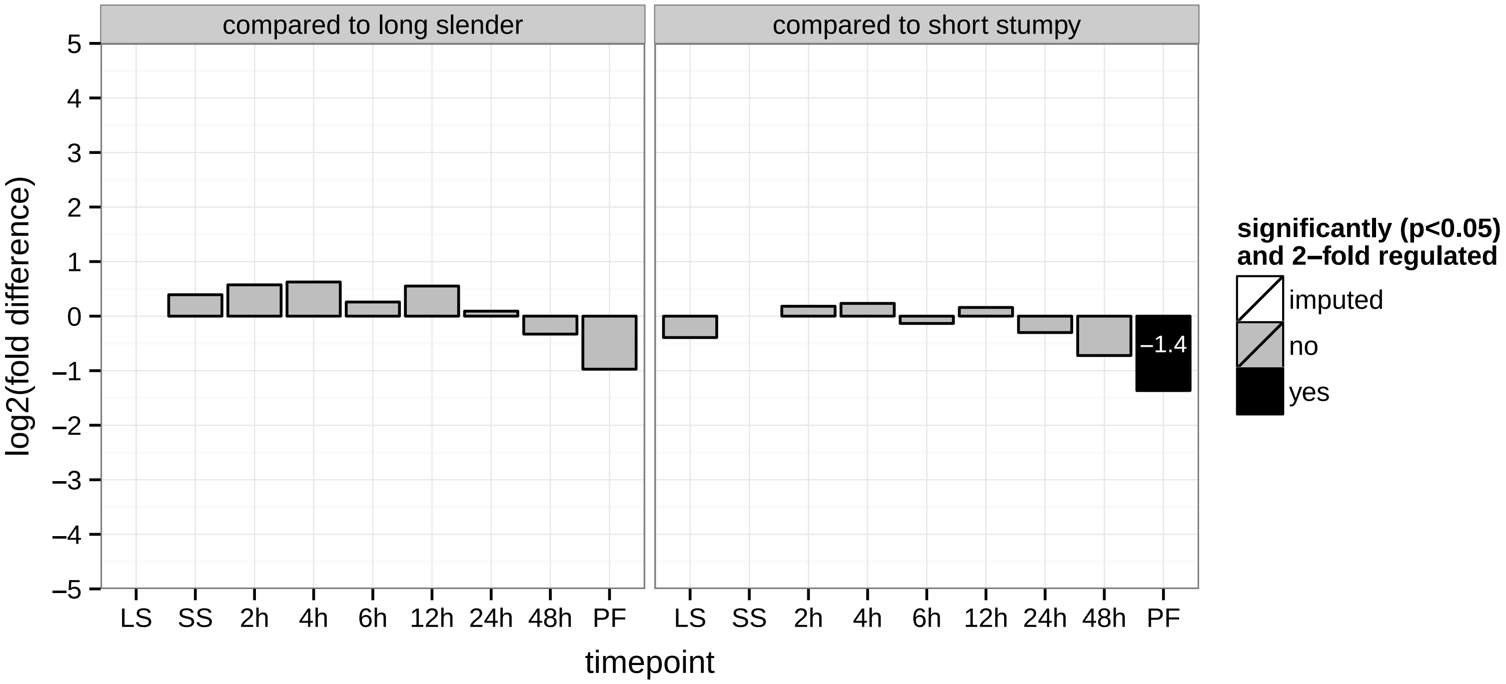
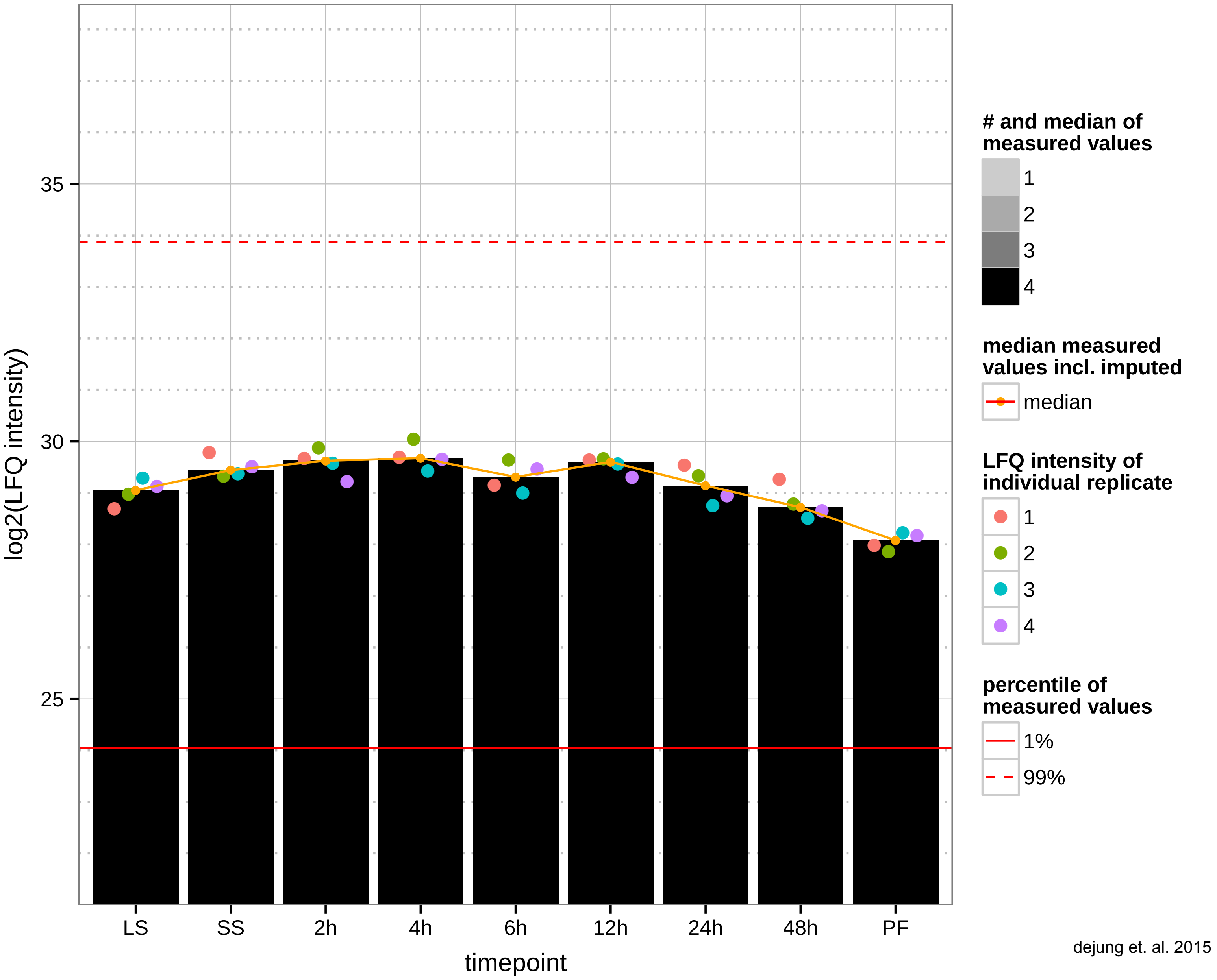
small GTP–binding protein, putative (TbRX1)
Tb927.3.5550
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: protein transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, protein transport, signal transduction, small GTPase mediated signal transduction





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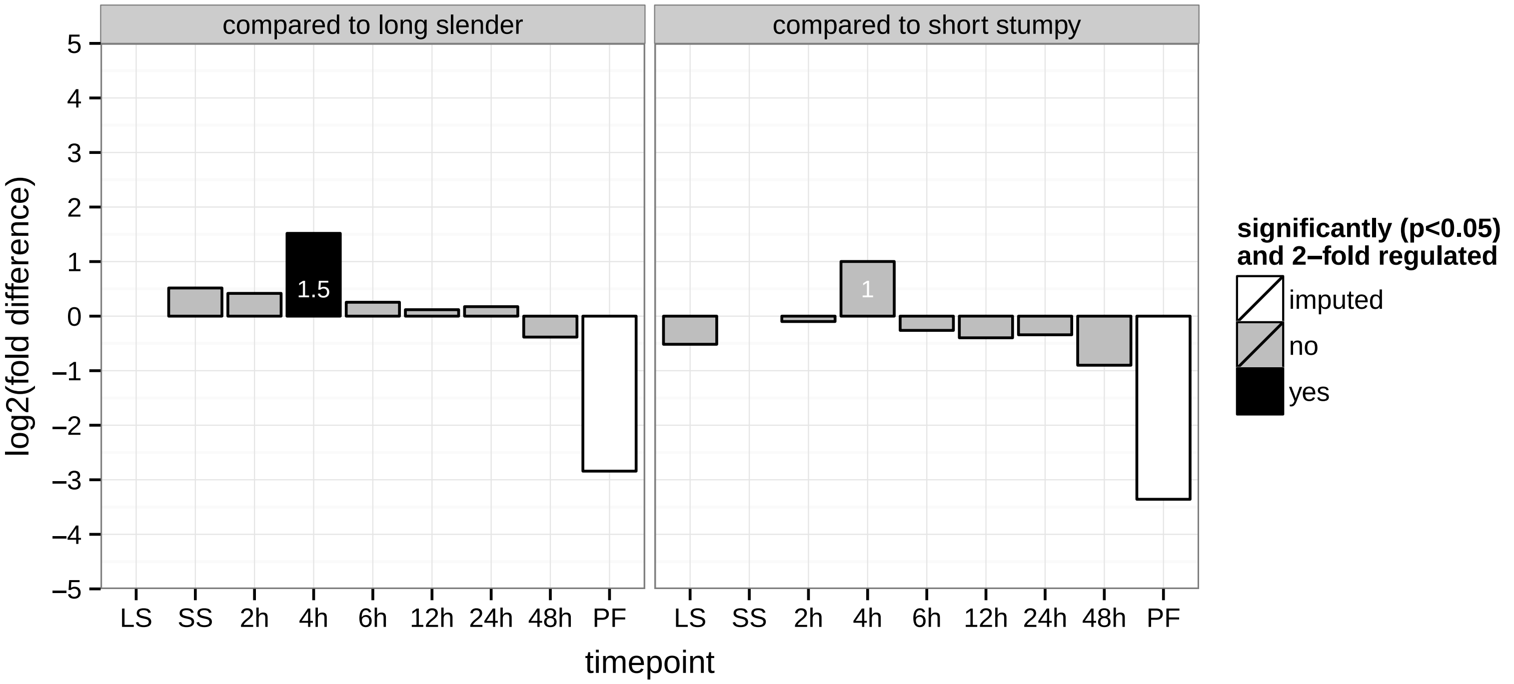
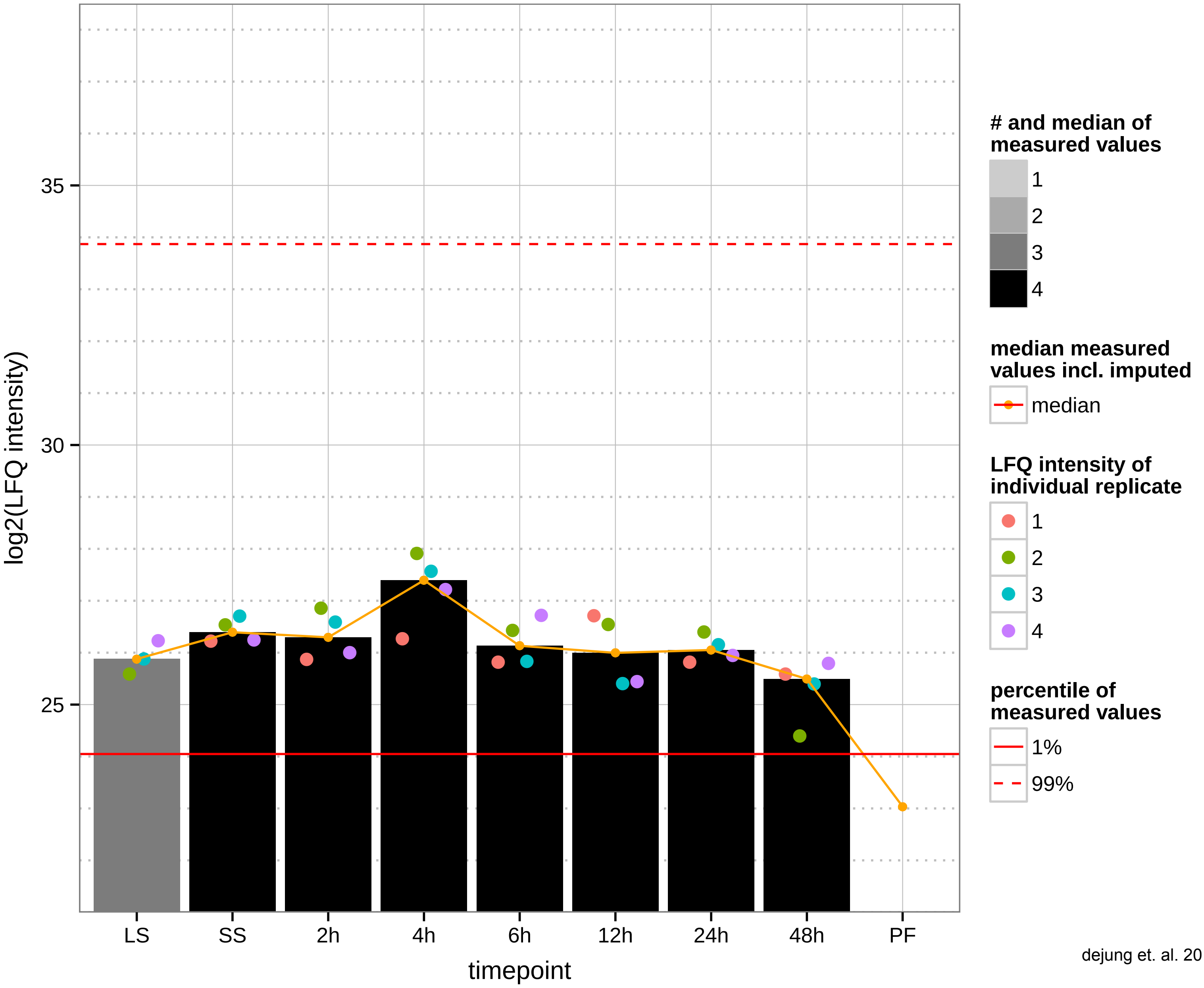
syntaxin, putative
Tb927.3.5570
AGOF: null
AGOC: membrane
AGOP: vesicle–mediated transport
PGOF: protein binding
PGOC: membrane
PGOP: vesicle–mediated transport





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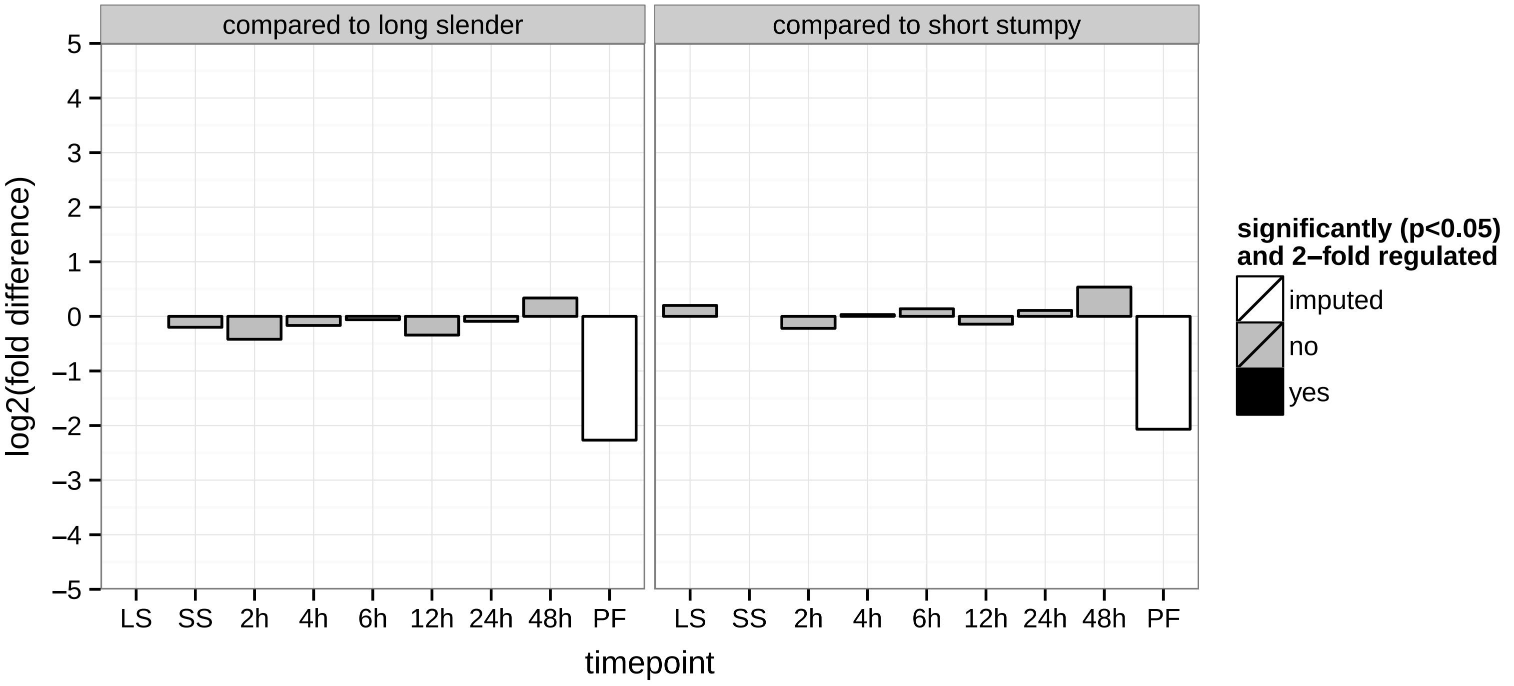
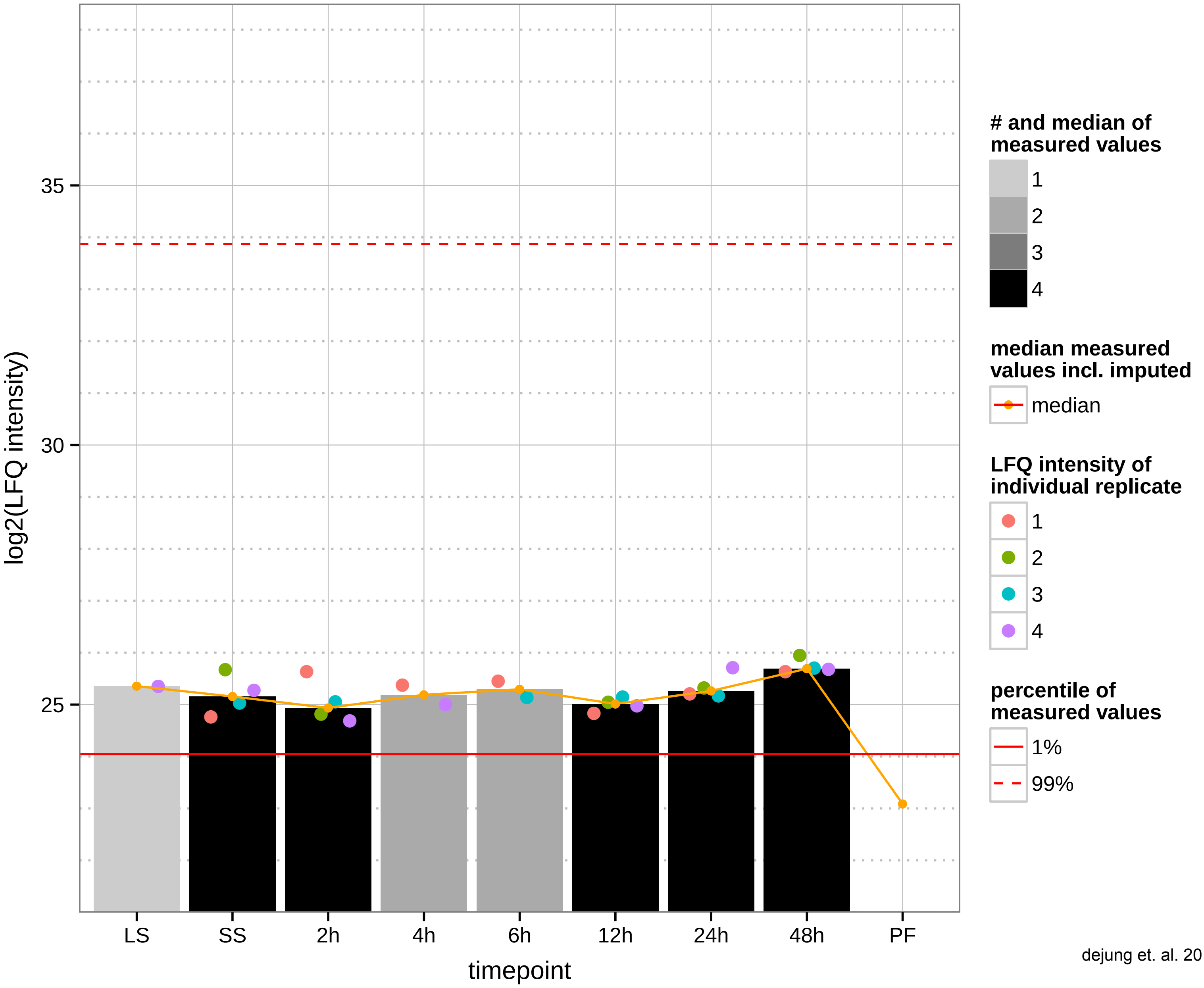
hypothetical protein, conserved
Tb927.3.880
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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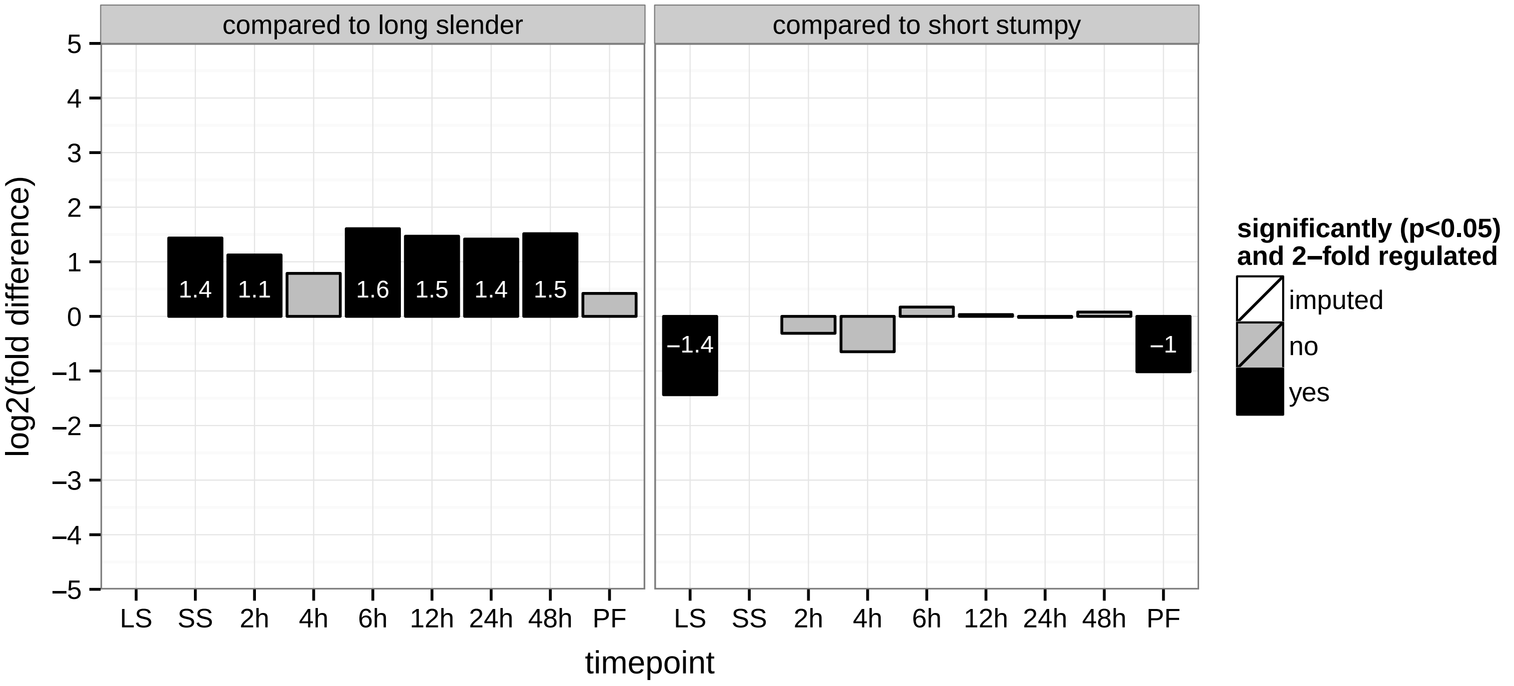
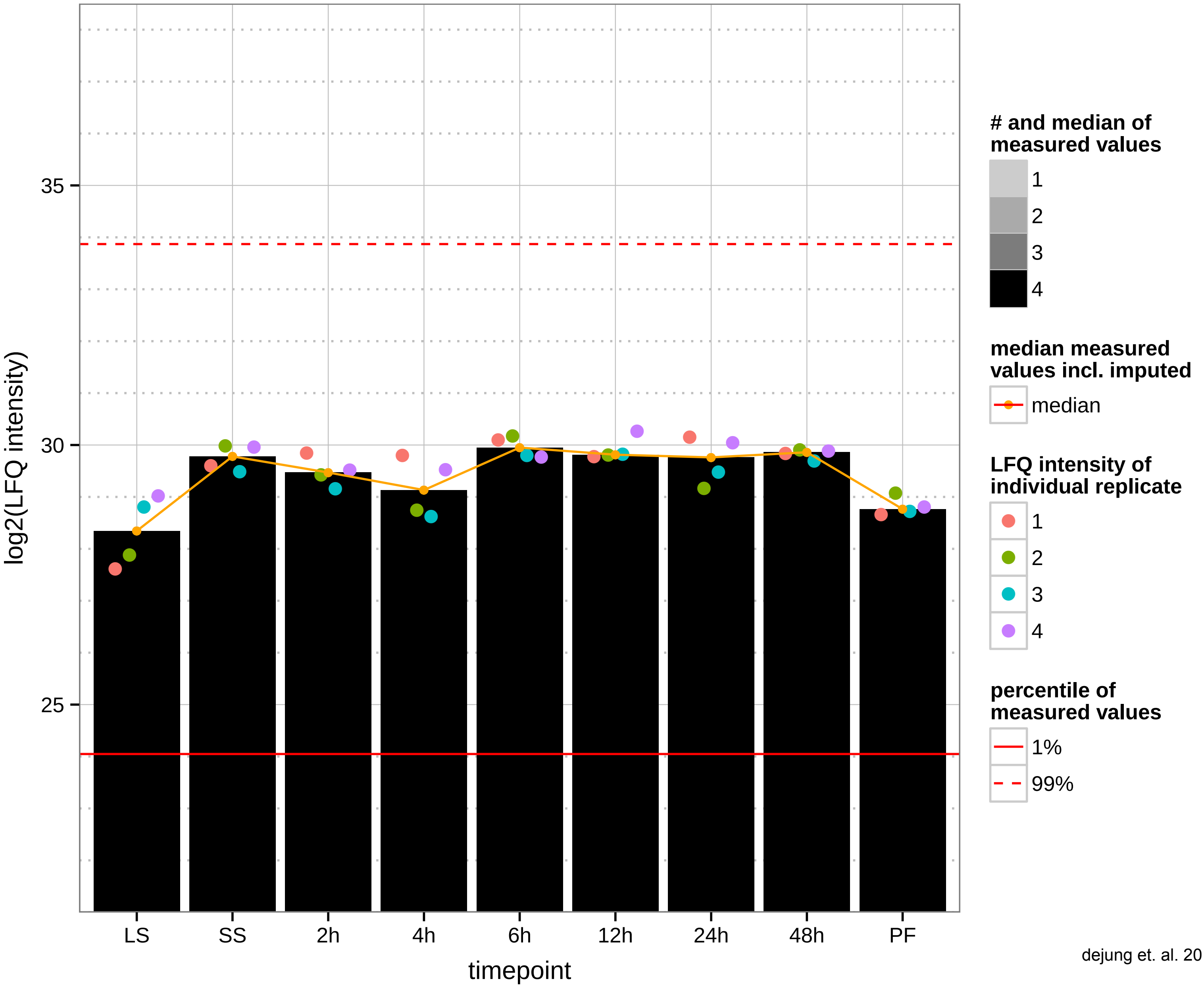
DNA topoisomerase IB, large subunit
Tb927.4.1330
AGOF: DNA topoisomerase (ATP−hydrolyzing) activity, DNA topoisomerase type I activity
AGOC: chromosome, membrane, nucleus
AGOP: DNA topological change, regulation of transcription, DNA−dependent
PGOF: DNA binding, DNA topoisomerase (ATP−hydrolyzing) activity, DNA topoisomerase type I activity
PGOC: chromosome
PGOP: DNA topological change





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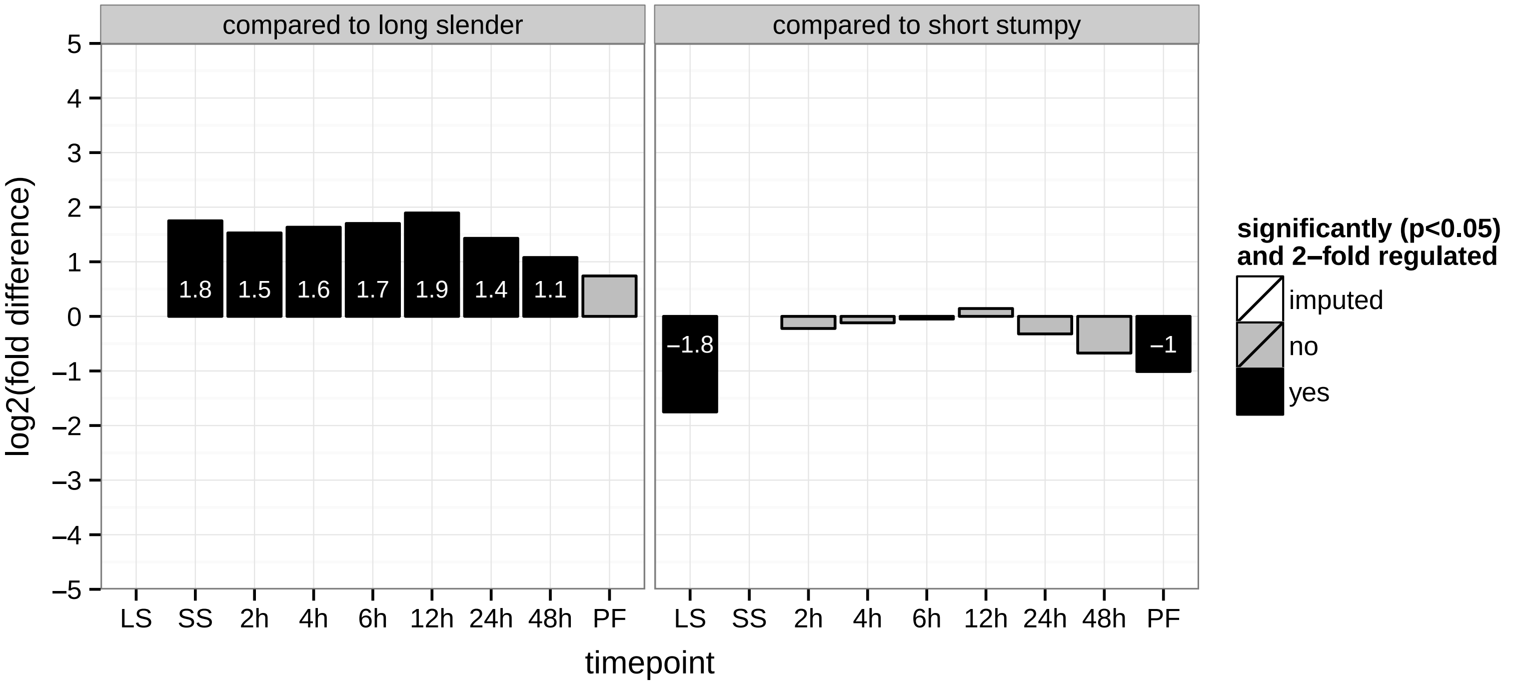
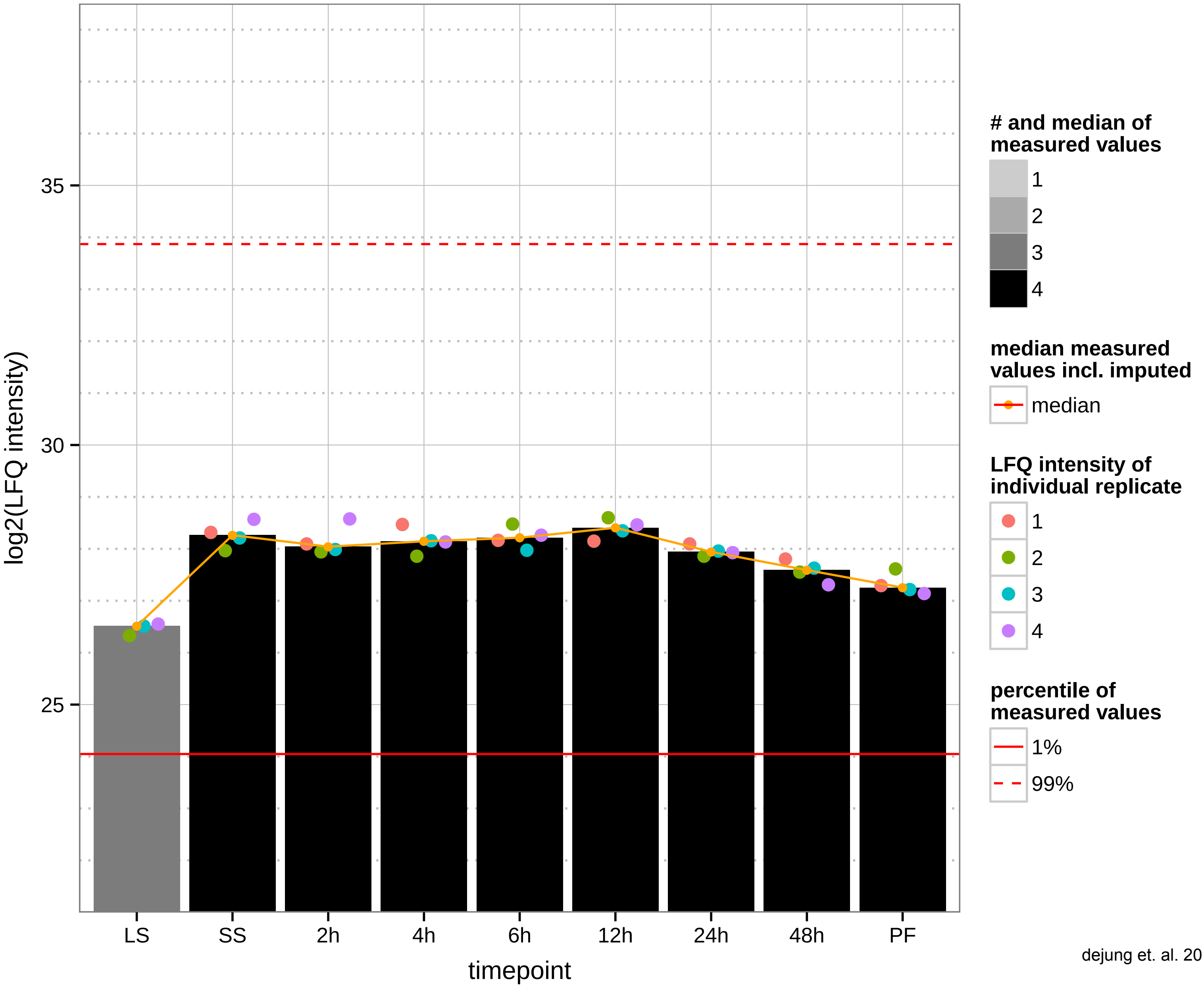
hypothetical protein, conserved
Tb927.4.1610
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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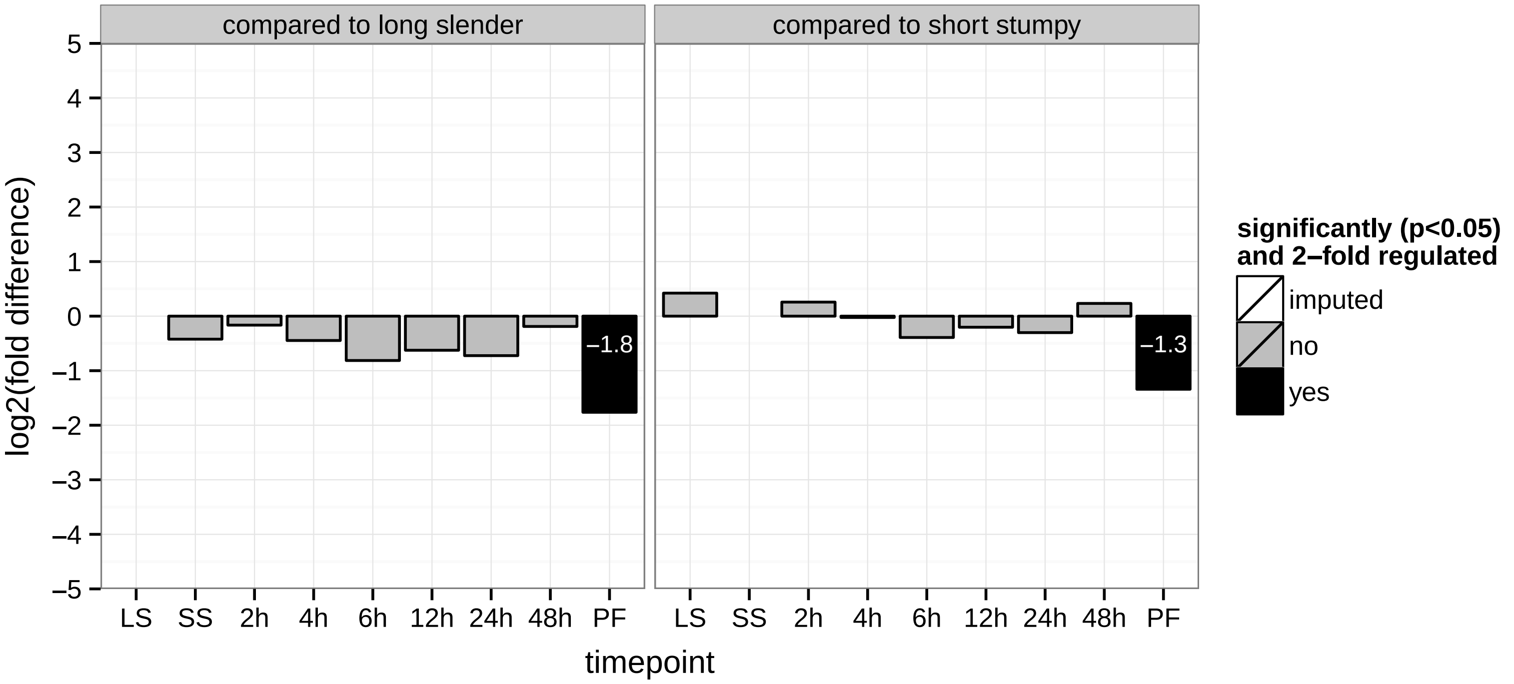
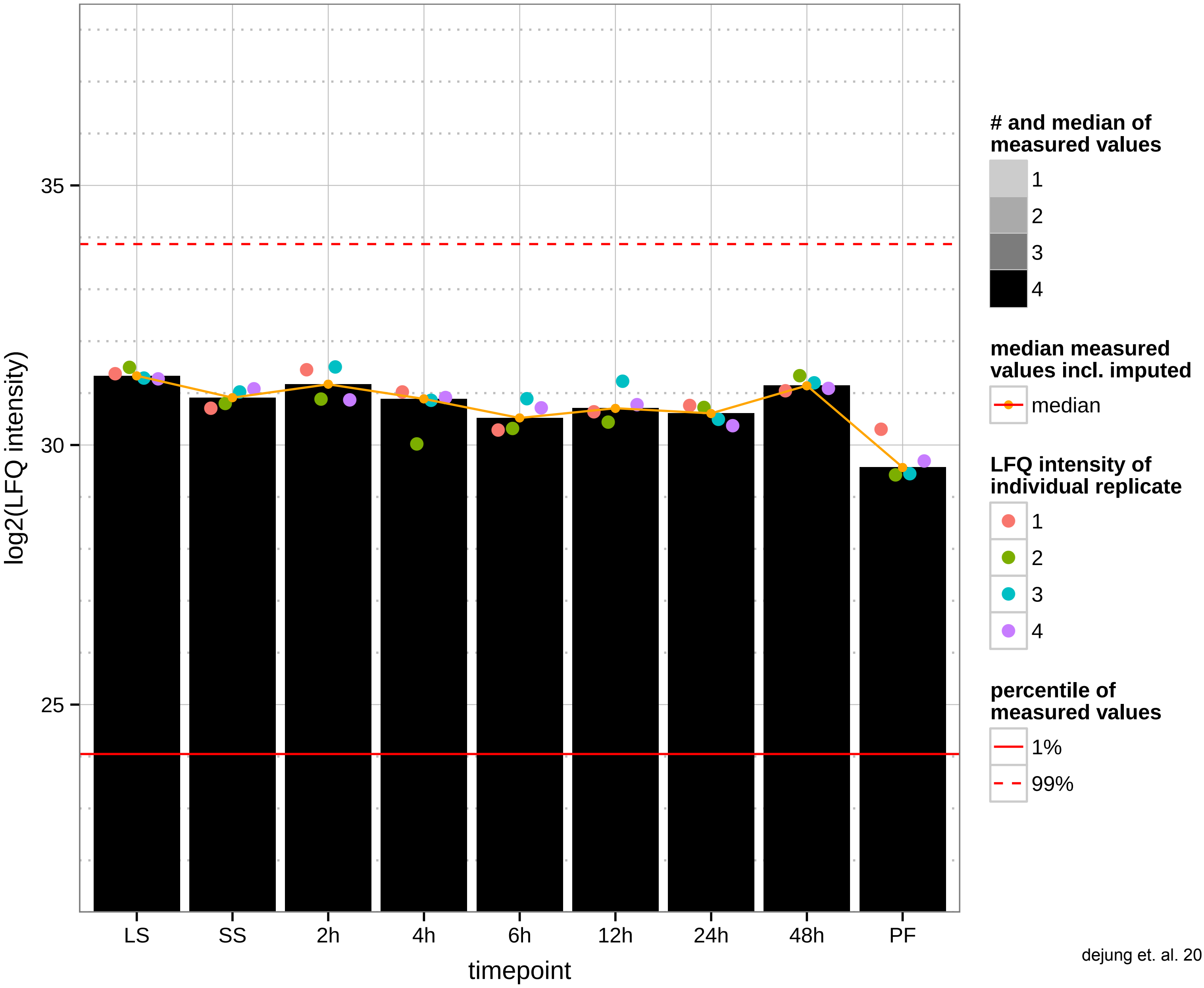
antigenic protein, putative
Tb927.4.2070
AGOF: ATP binding, aminoacyl–tRNA ligase activity
AGOC: cytoplasm
AGOP: tRNA aminoacylation for protein translation, translation
PGOF: null
PGOC: null
PGOP: null





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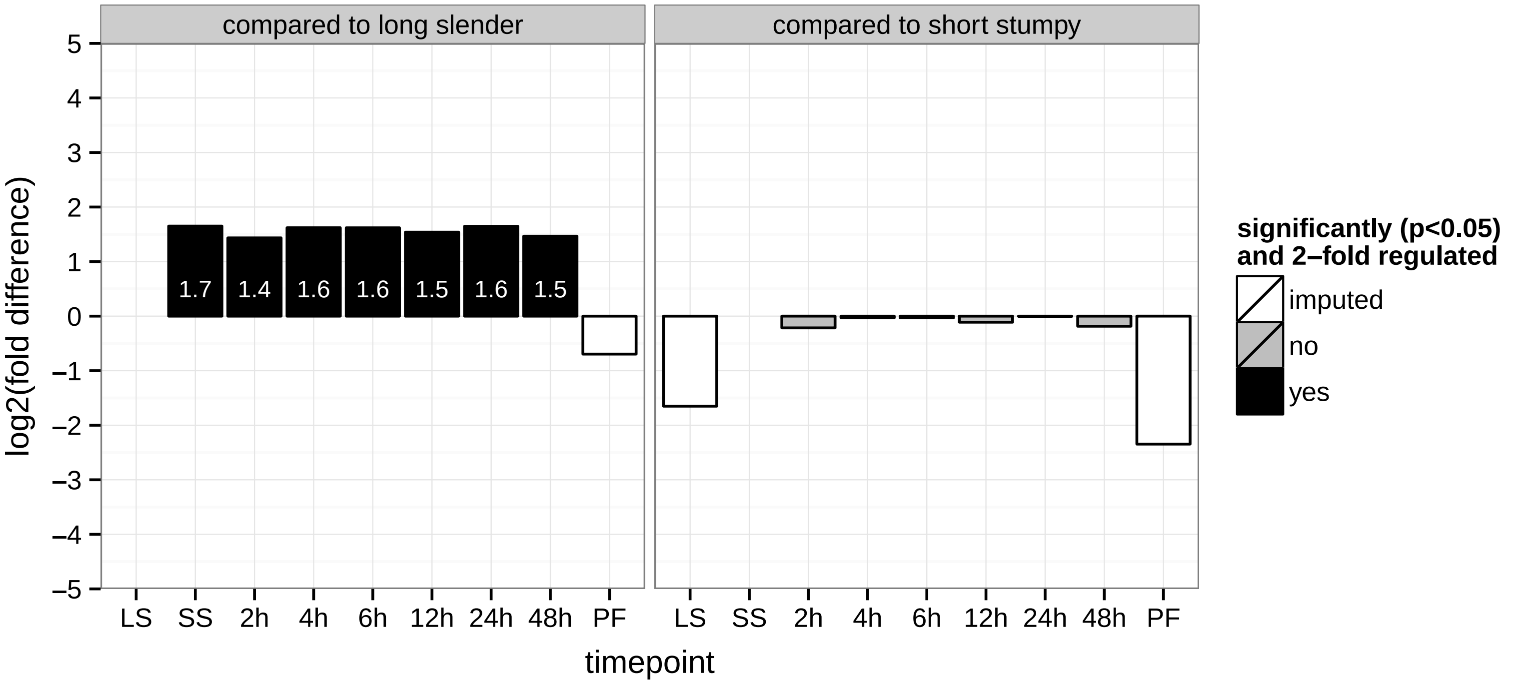
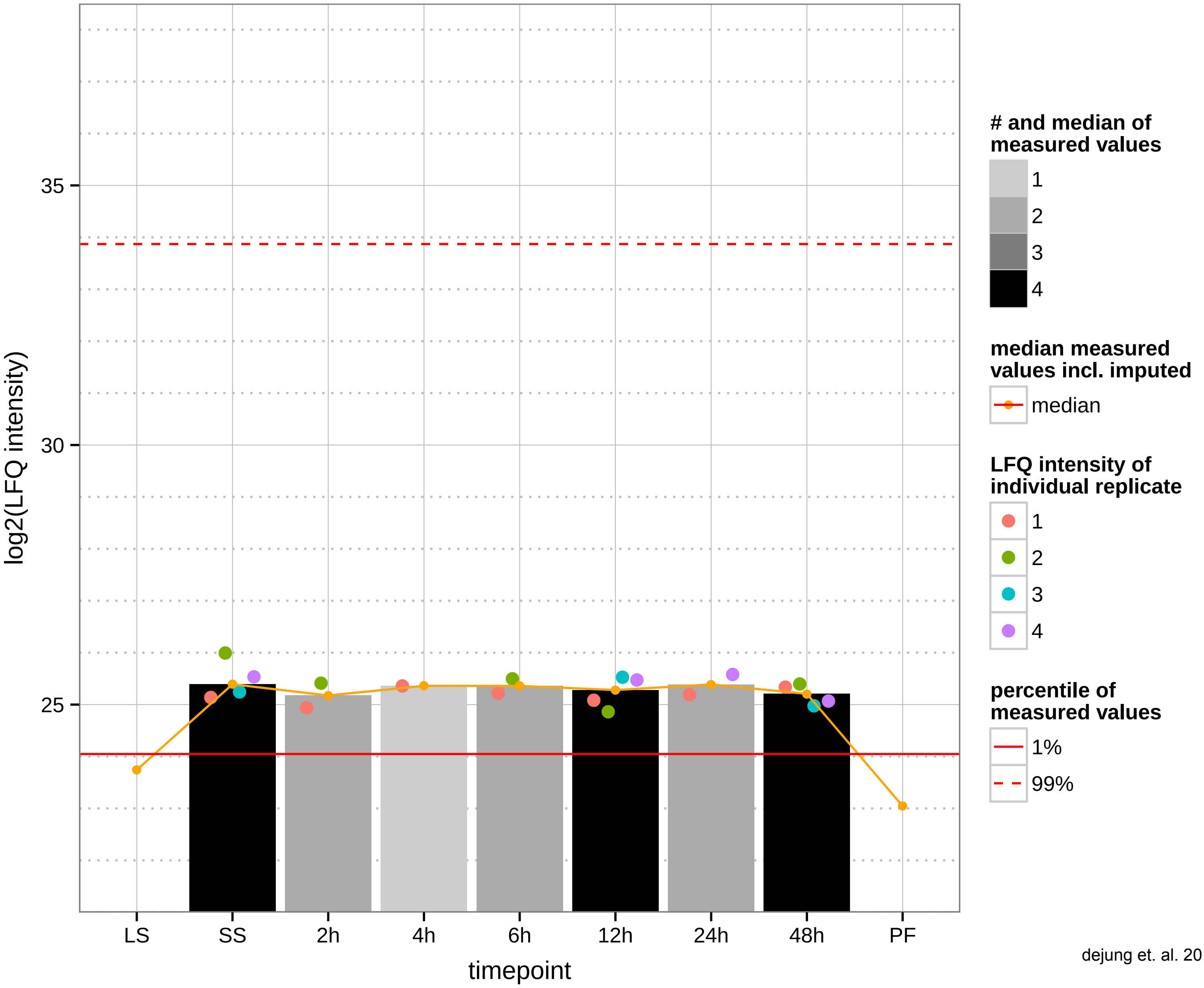
MBO2, flagellar component
Tb927.4.2140
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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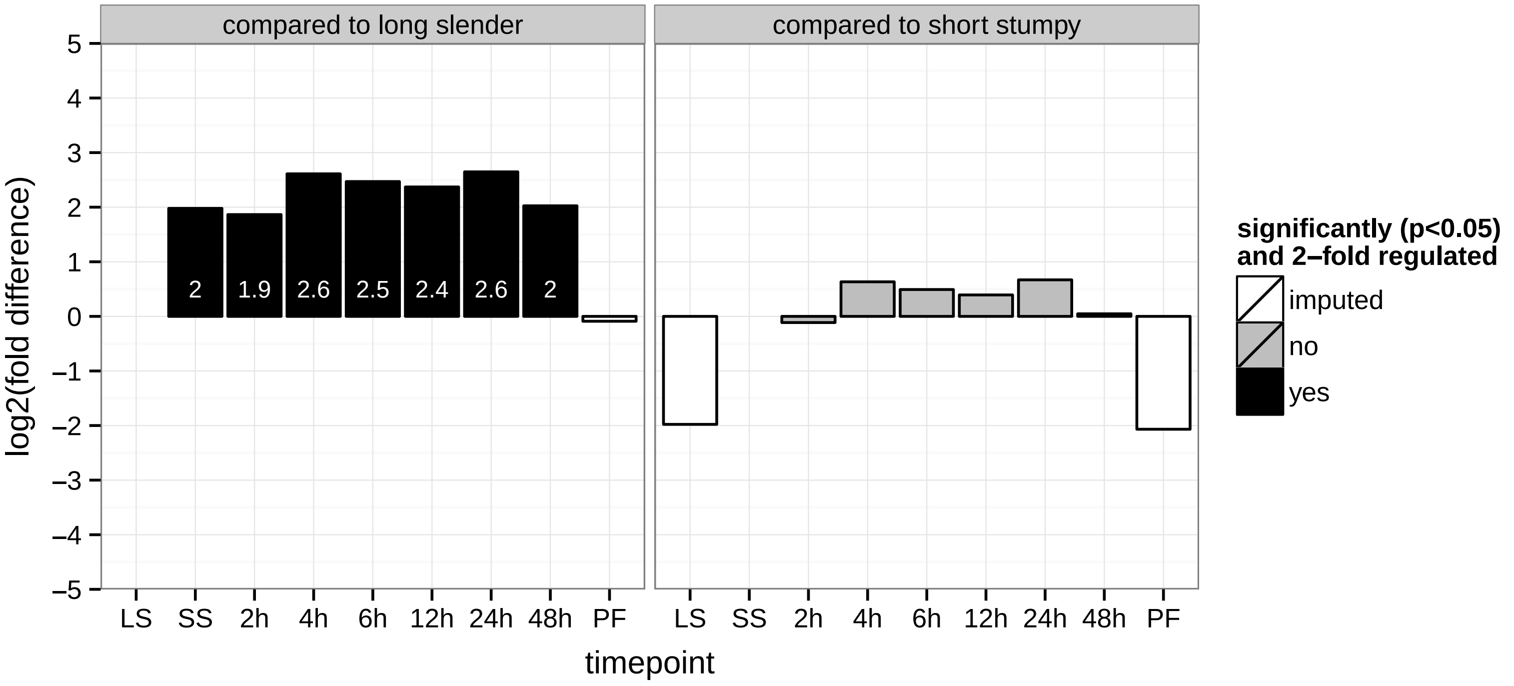
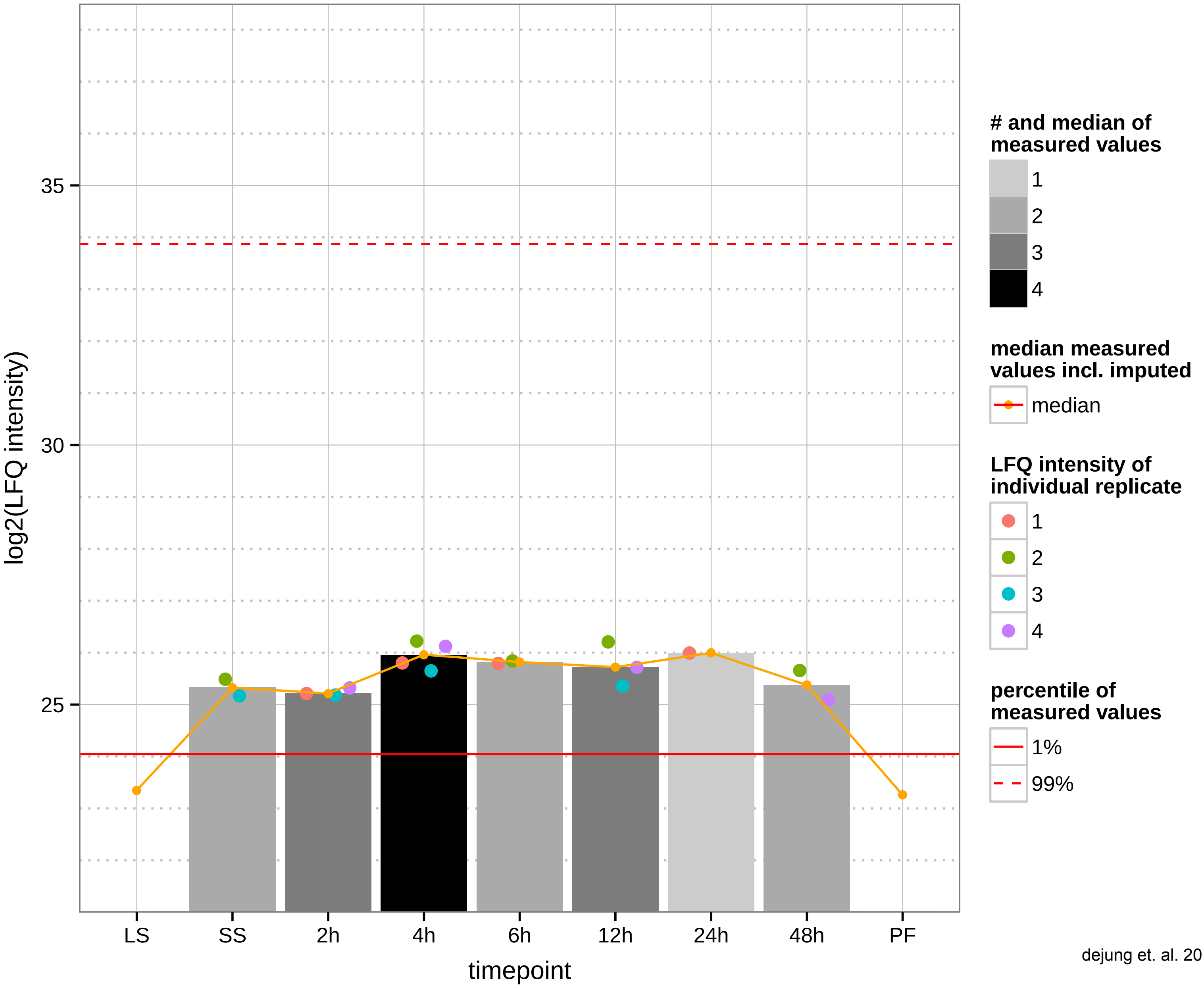
hypothetical protein, conserved
Tb927.4.2930
AGOF: null
AGOC: null
AGOP: response to stress
PGOF: null
PGOC: null
PGOP: response to stress





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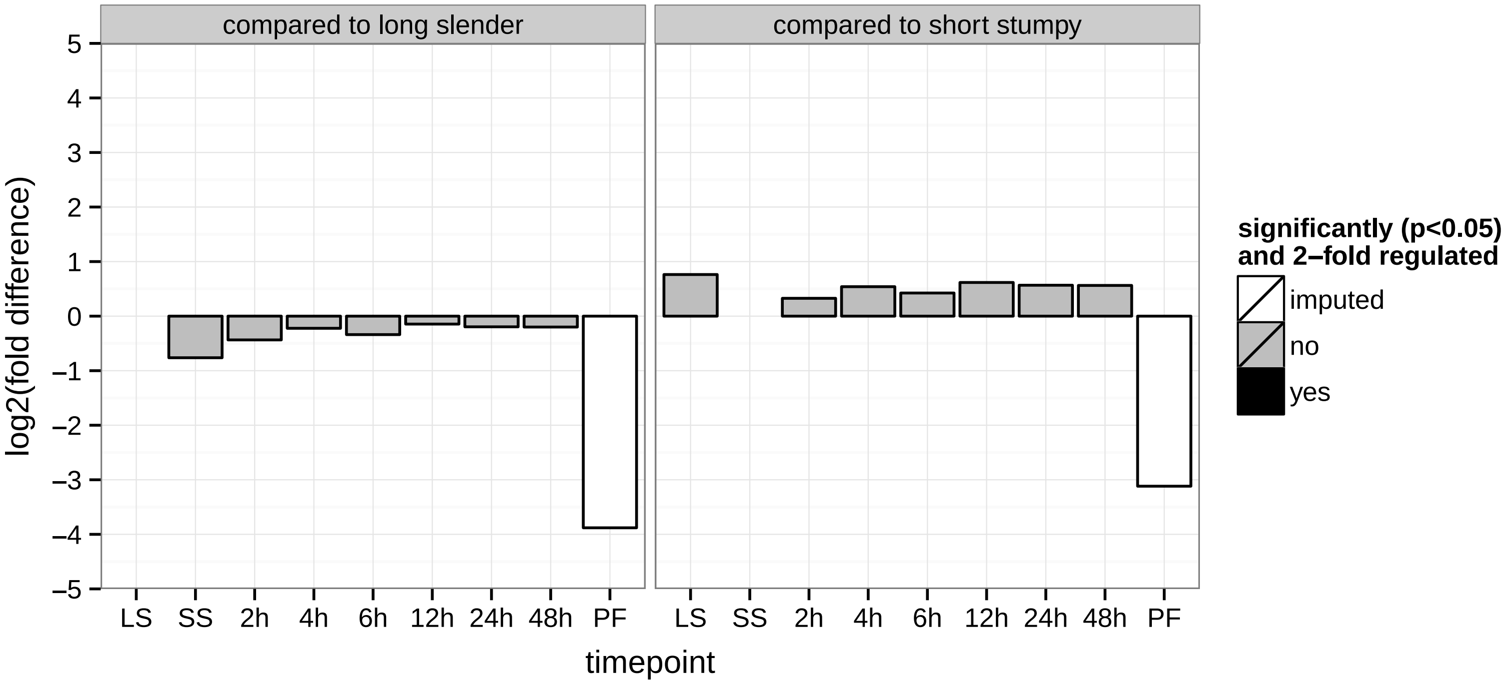
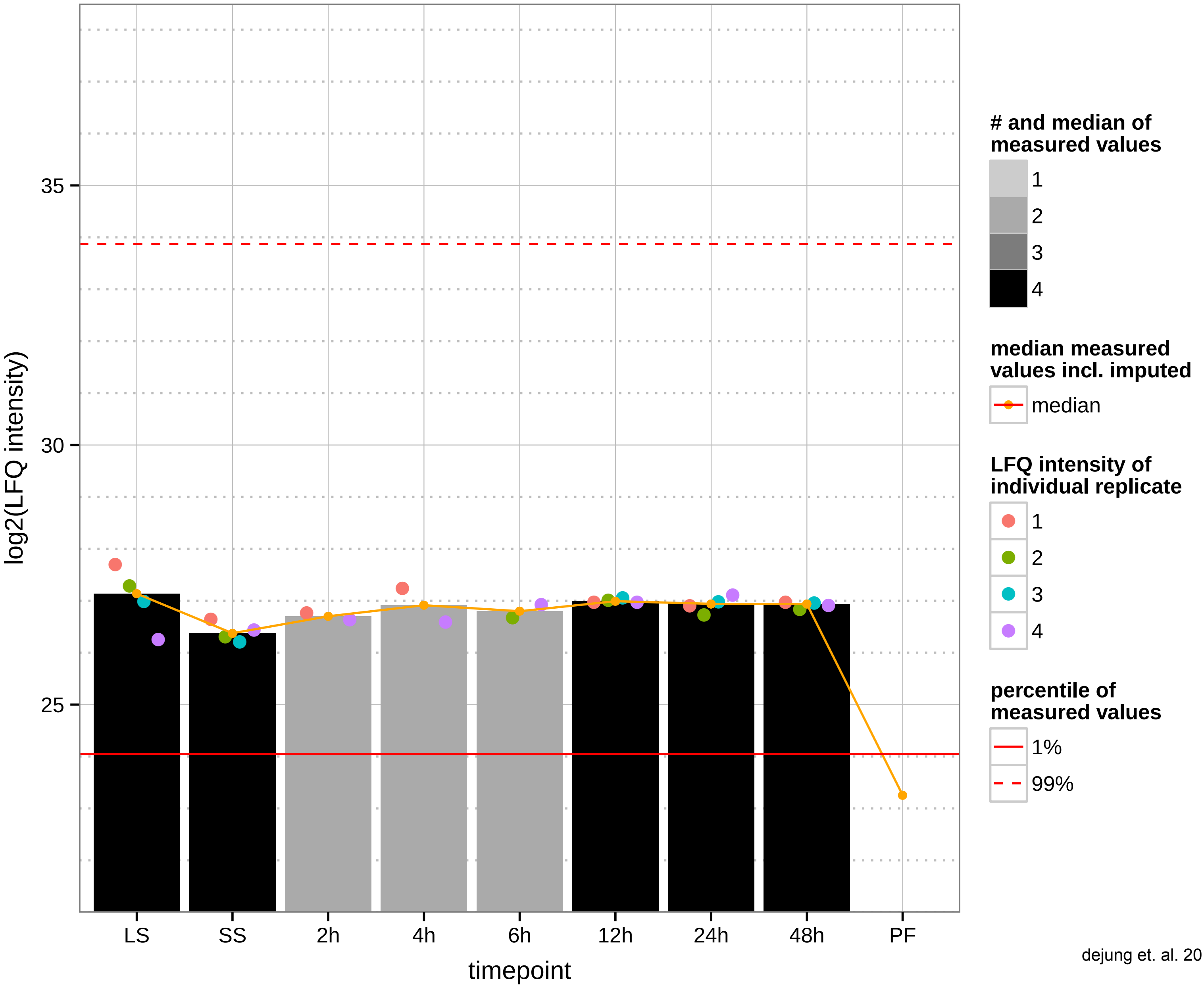
hypothetical protein, conserved
Tb927.4.310
AGOF: acid–amino acid ligase activity
AGOC: intracellular
AGOP: cellular protein modification process
PGOF: acid–amino acid ligase activity, protein binding, transferase activity, transferring phosphorus–containing groups
PGOC: intracellular
PGOP: cellular protein modification process





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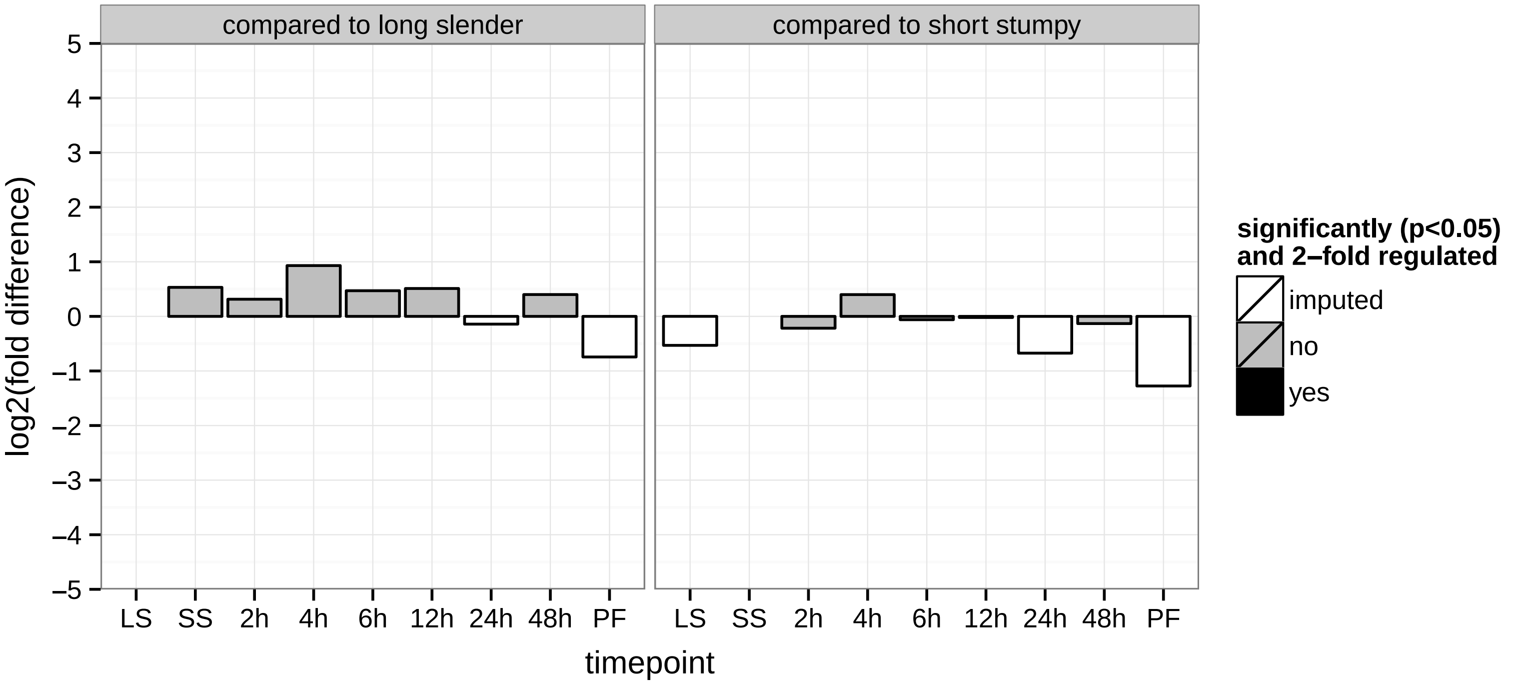
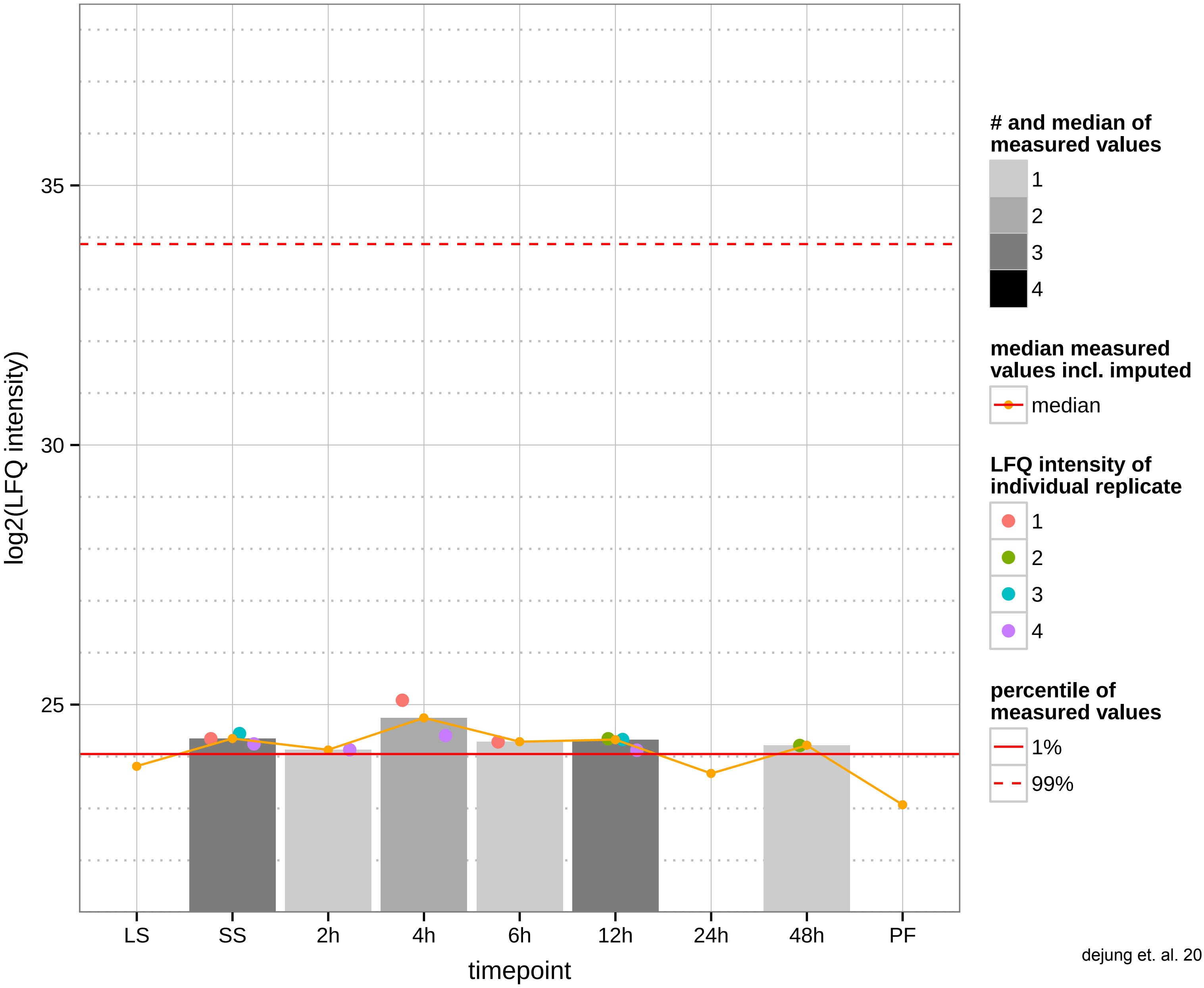
tuzin, putative
Tb927.4.3390
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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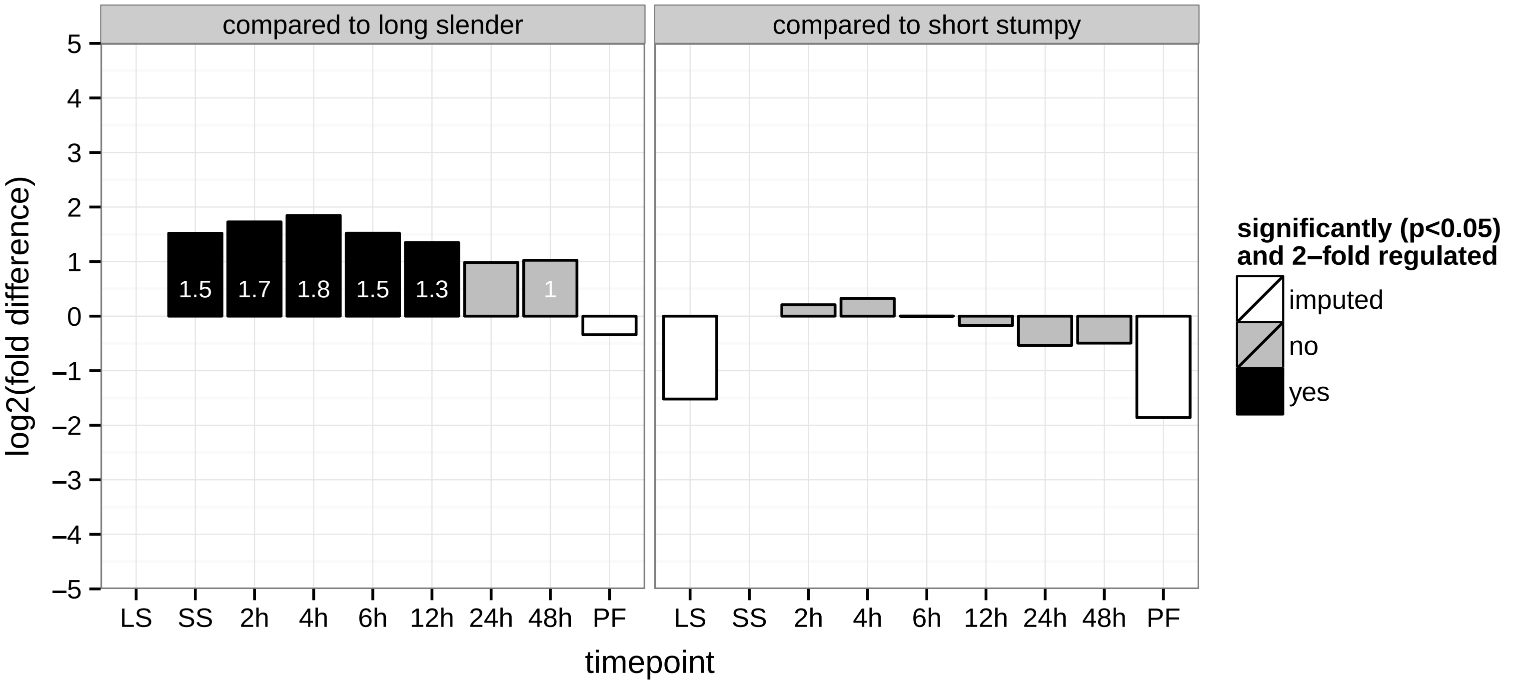
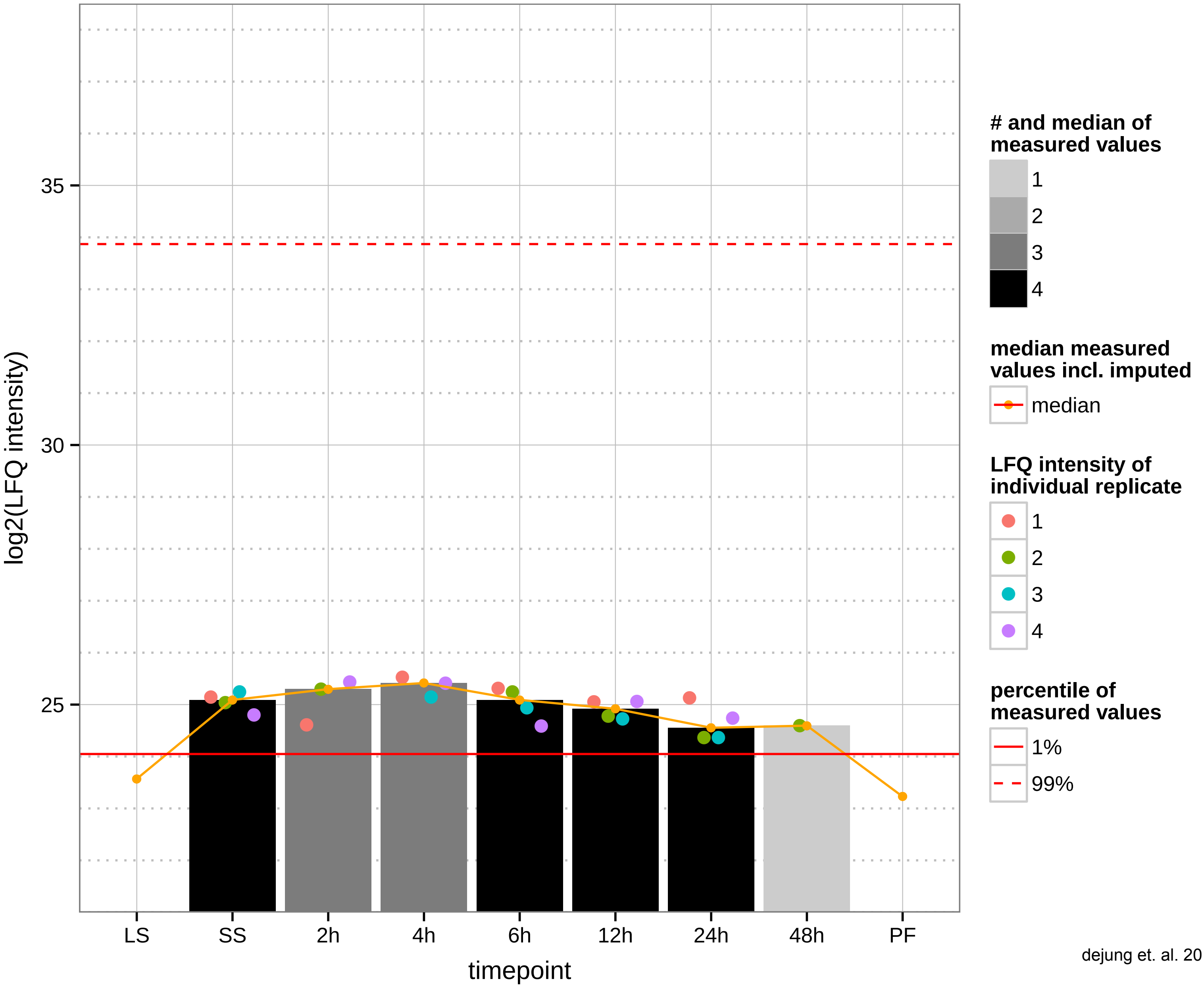
phosphatidylinositol 3−kinase tor, putative, phosphatidylinositol 3−kinase (tor2) (TOR2)
Tb927.4.420
AGOF: null, phosphotransferase activity, alcohol group as acceptor, protein binding
AGOC: null, TORC2 complex, cytosol, endoplasmic reticulum, mitochondrion
AGOP: null, actin cytoskeleton organization
PGOF: phosphotransferase activity, alcohol group as acceptor, transferase activity, transferring phosphorus−containing group
PGOC: null
PGOP: null





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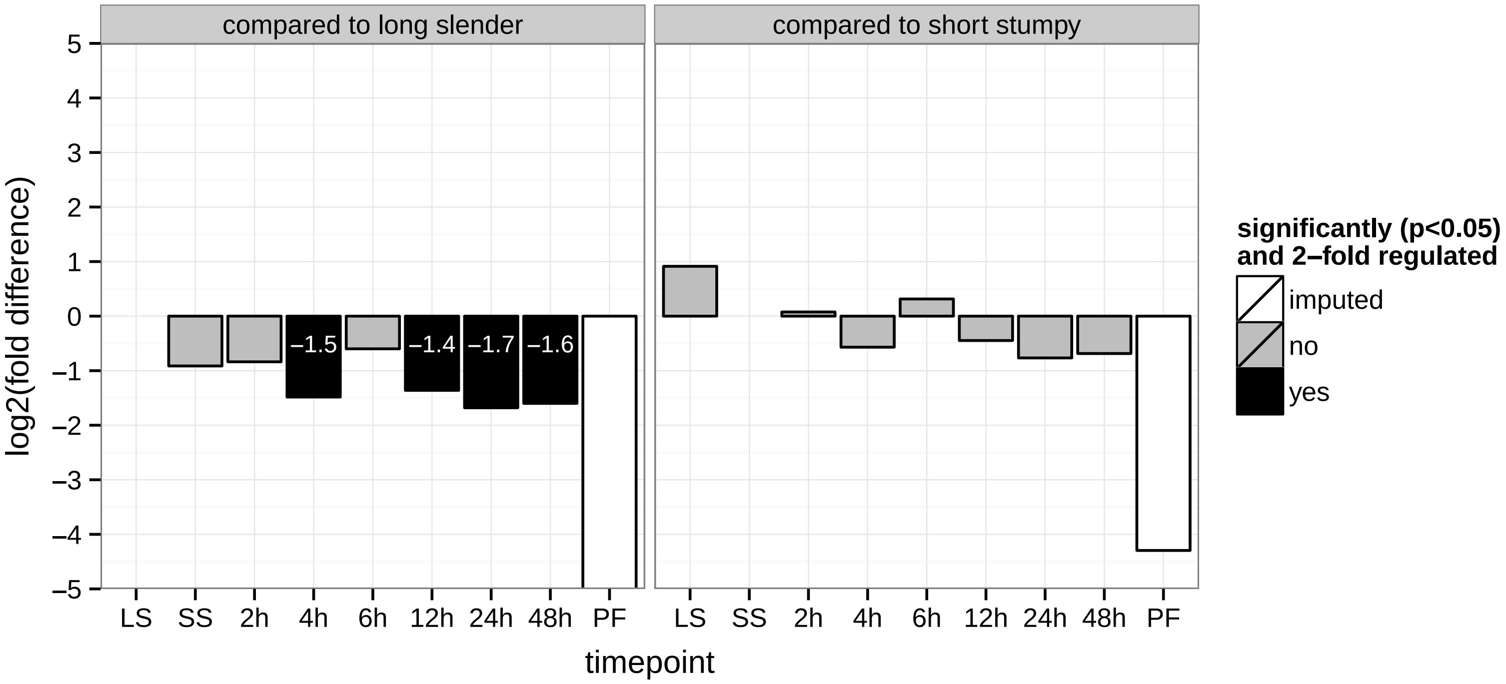
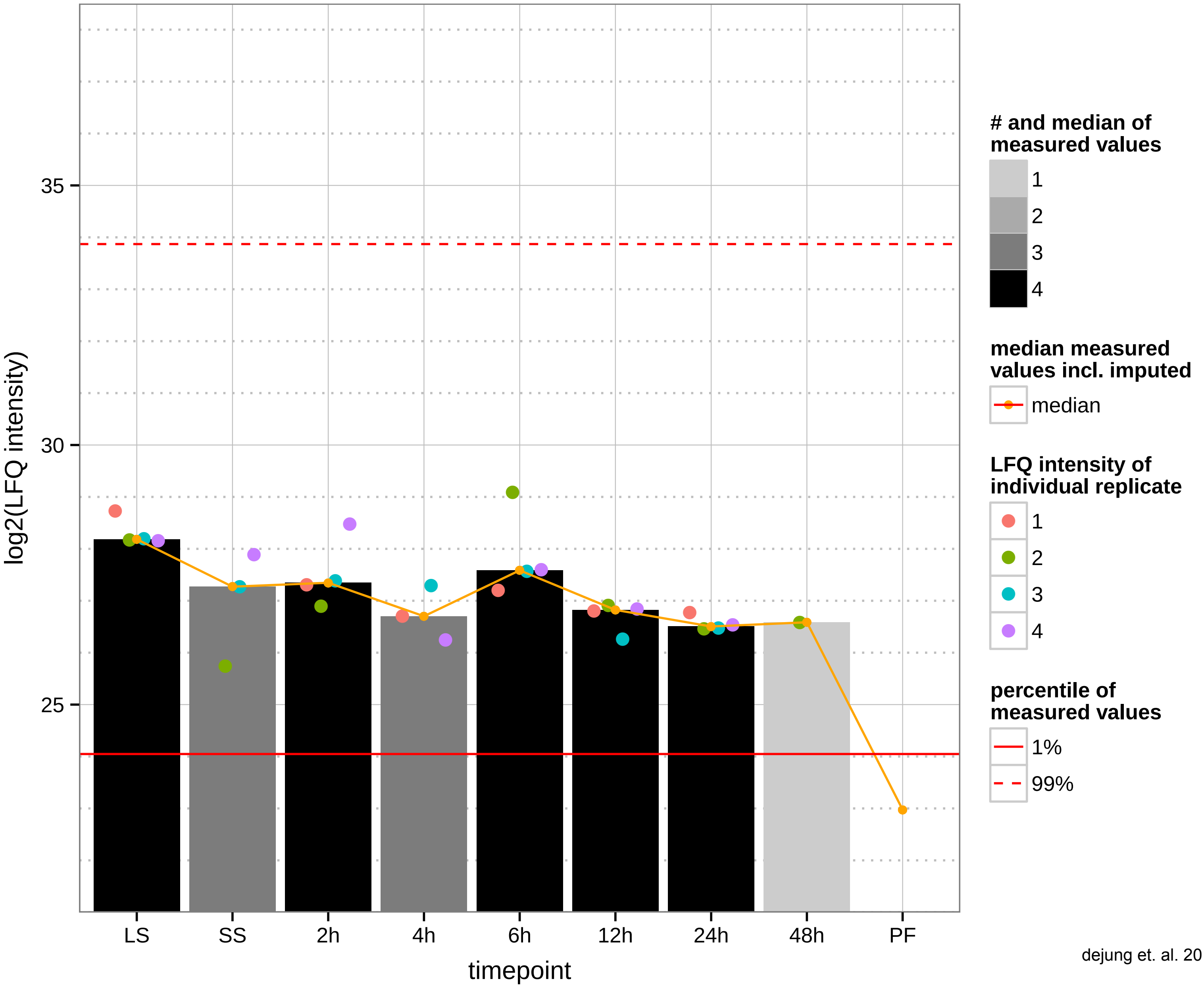
adenylyl cyclase (GRESAG 4.4)
Tb927.4.4430;Tb927.4.4450
AGOF: ATP binding, adenylate cyclase activity
AGOC: integral to membrane
AGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction
PGOF: phosphorus–oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction





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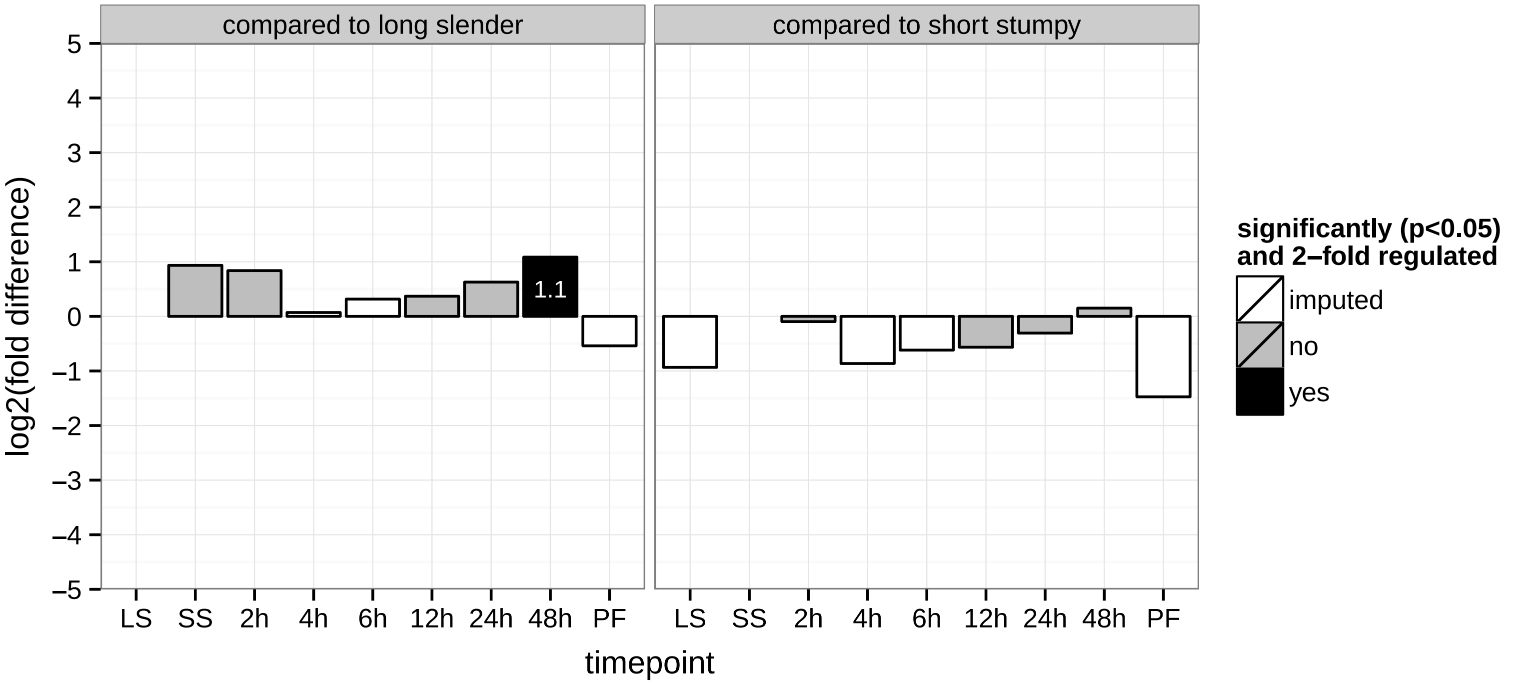
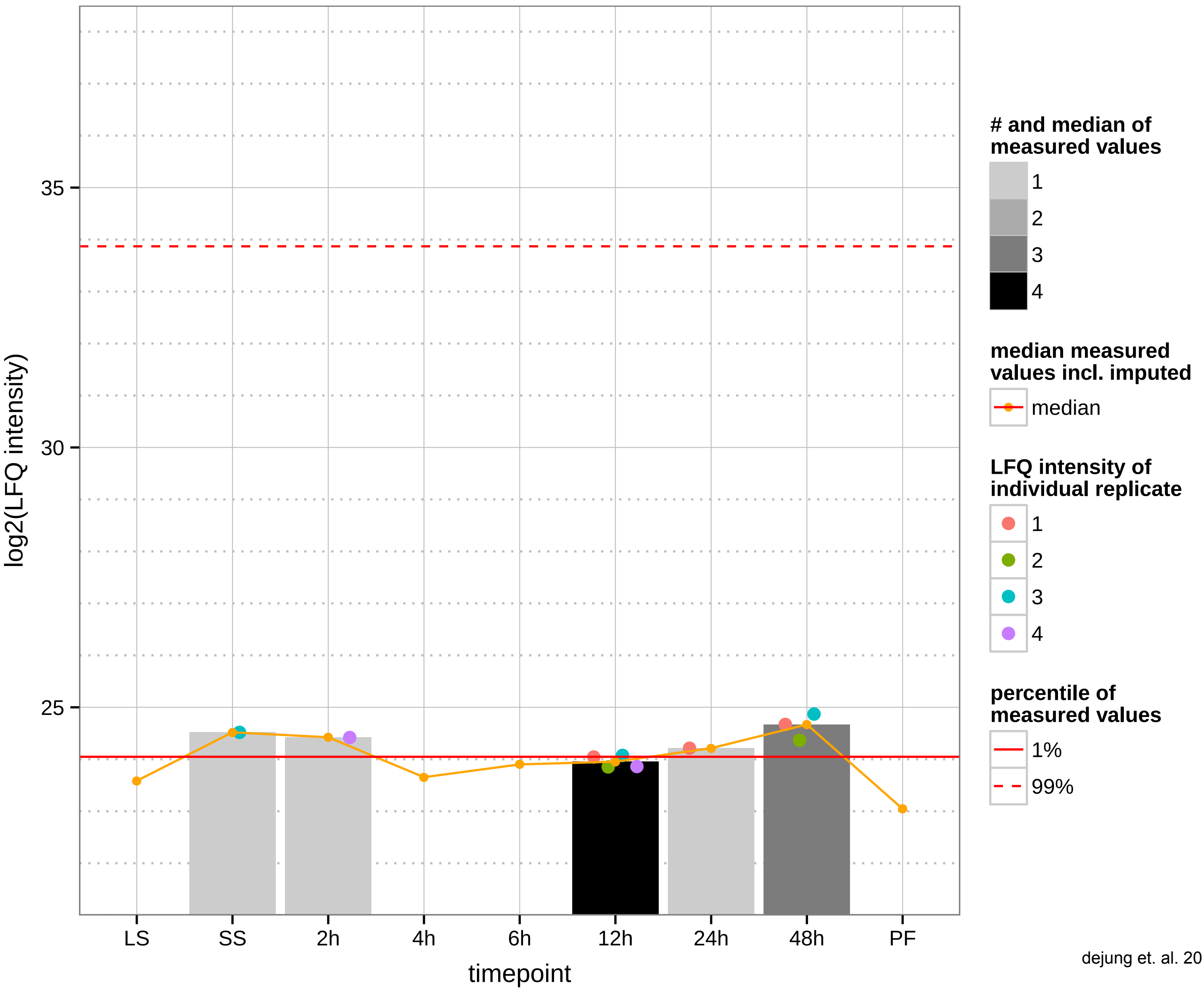
hypothetical protein, conserved
Tb927.4.4750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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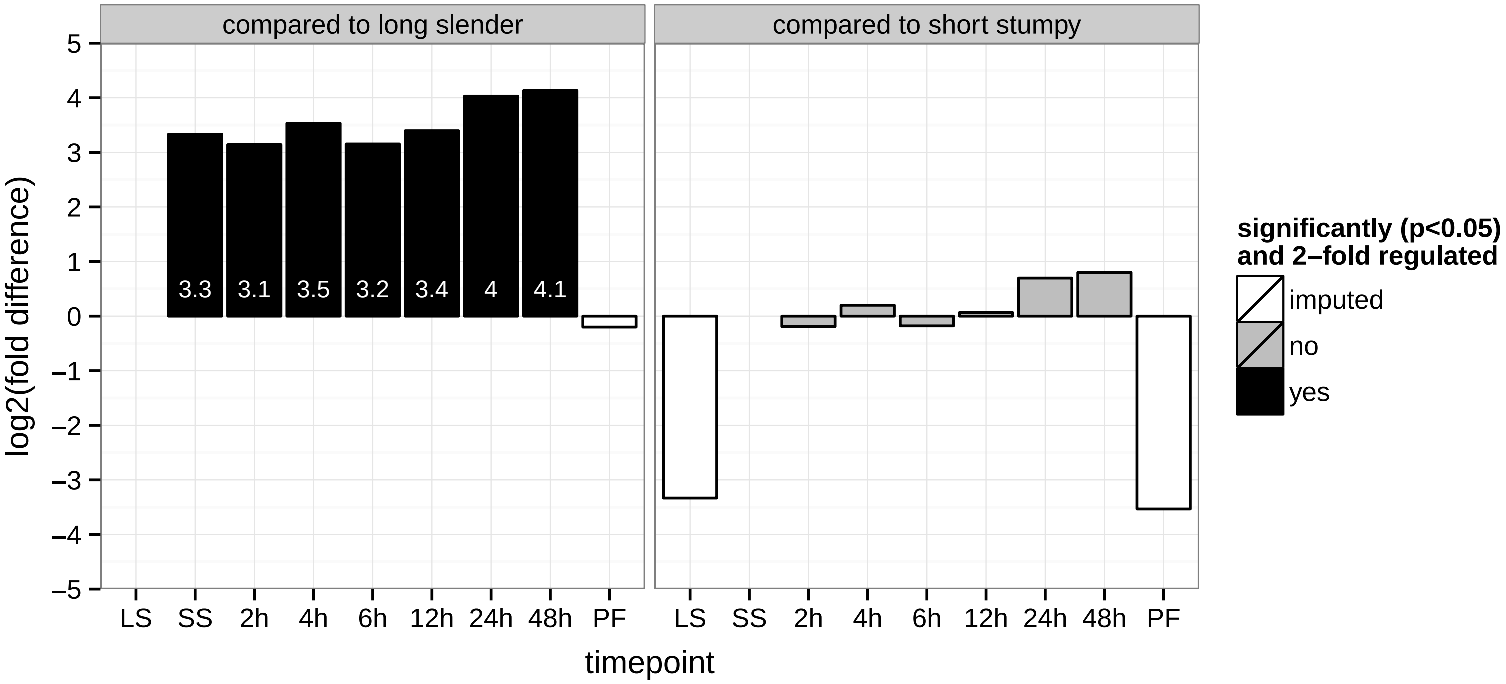
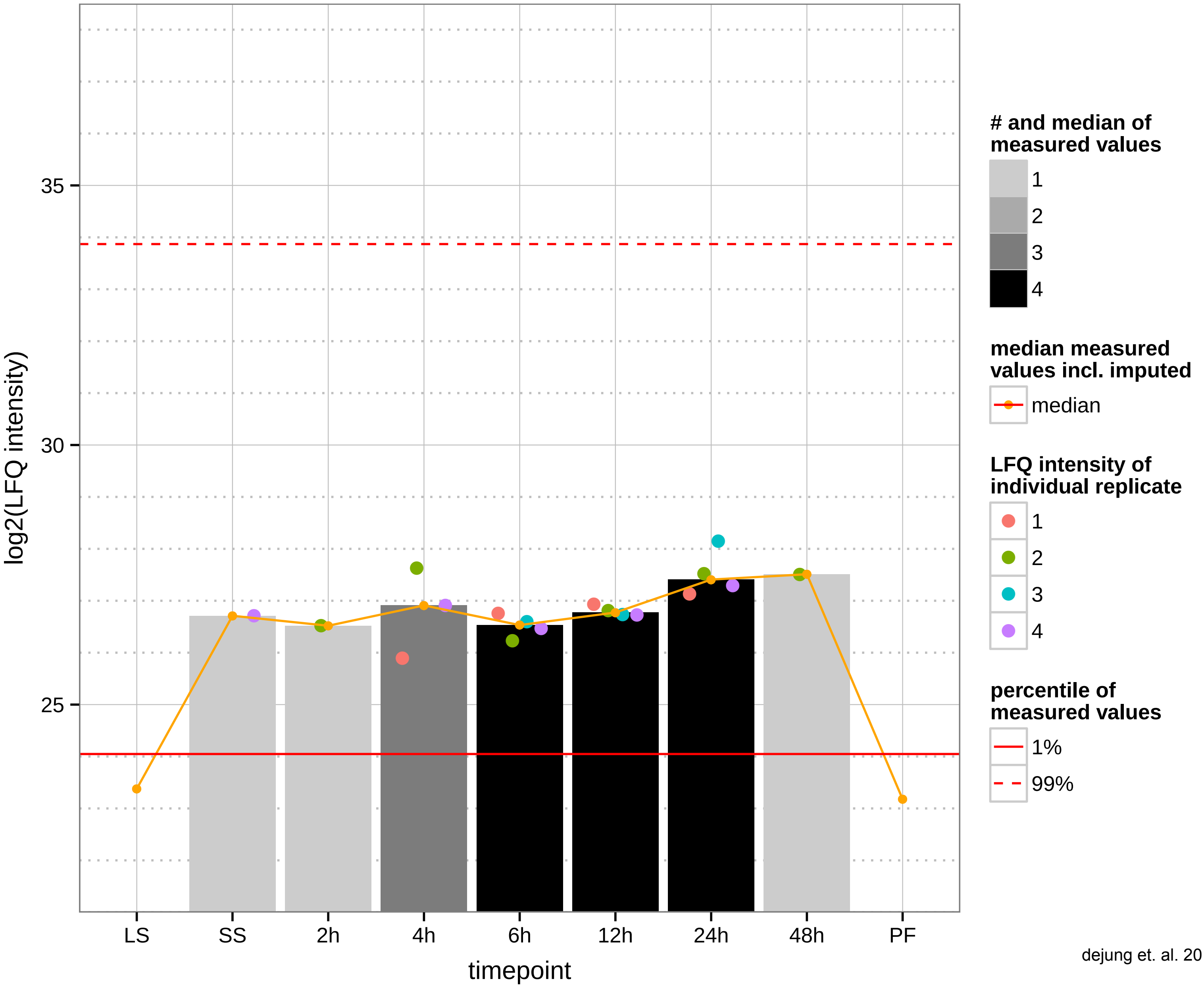
hypothetical protein, conserved
Tb927.4.5080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: endoplasmic reticulum, integral to membrane
PGOP: intracellular protein transport





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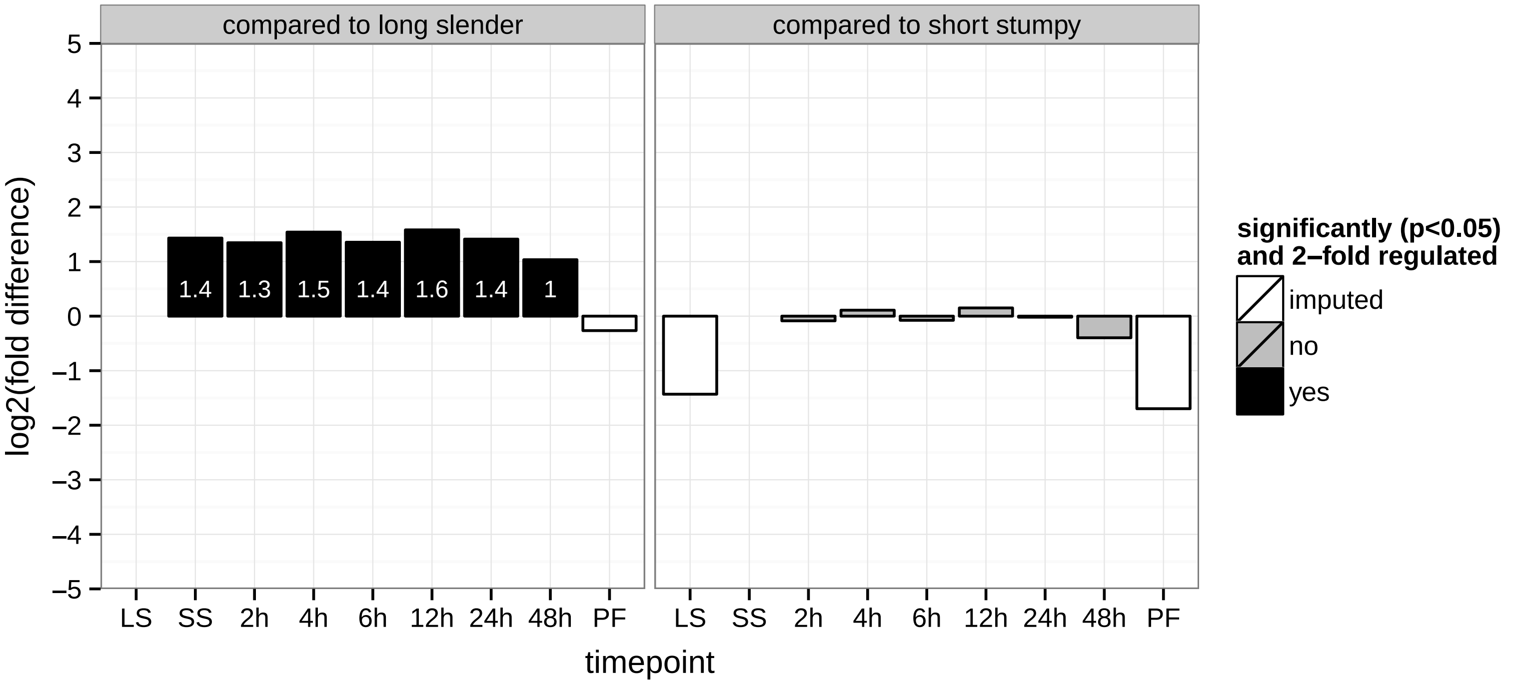
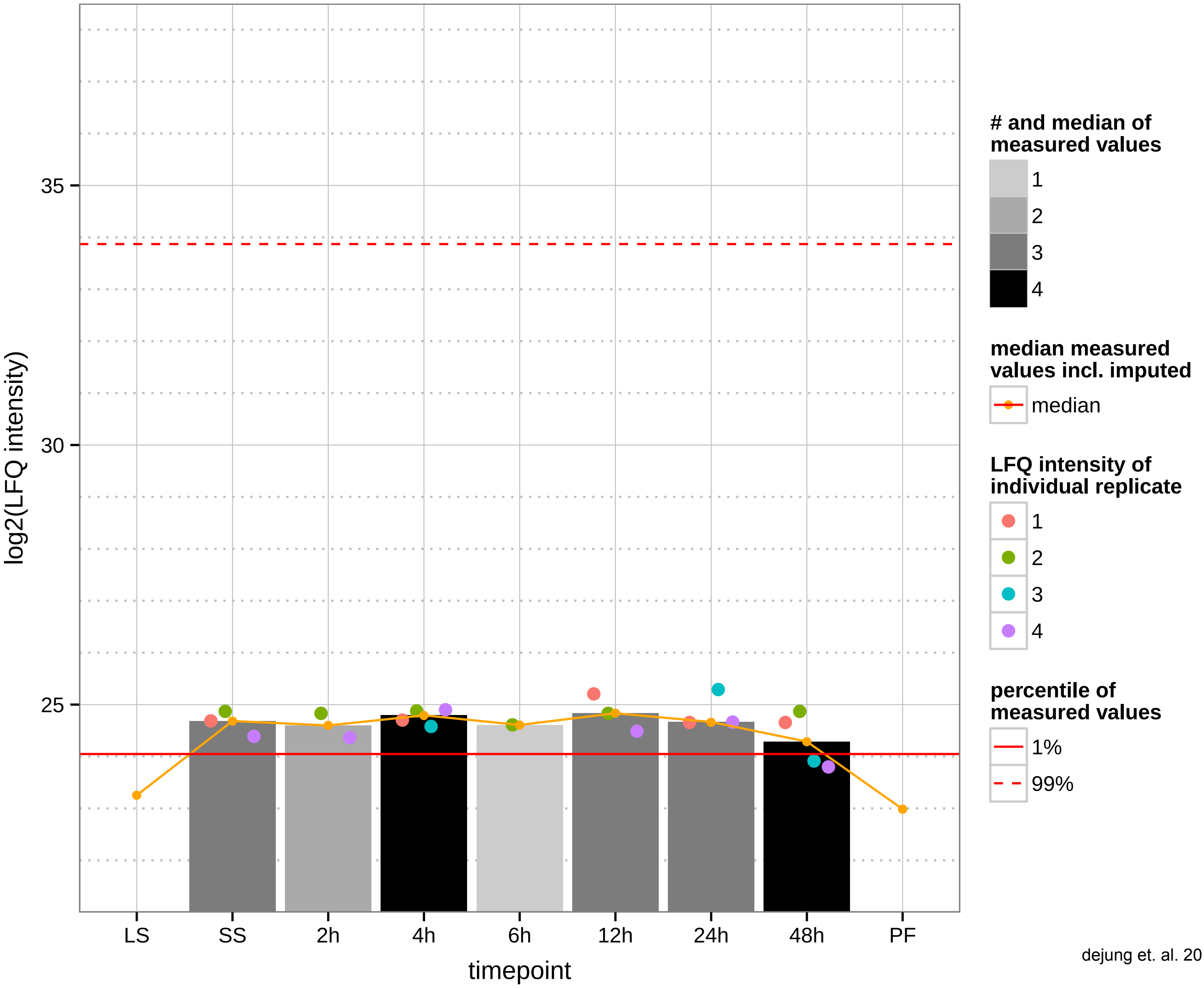
hypothetical protein, conserved
Tb927.4.640
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: protein targeting to Golgi





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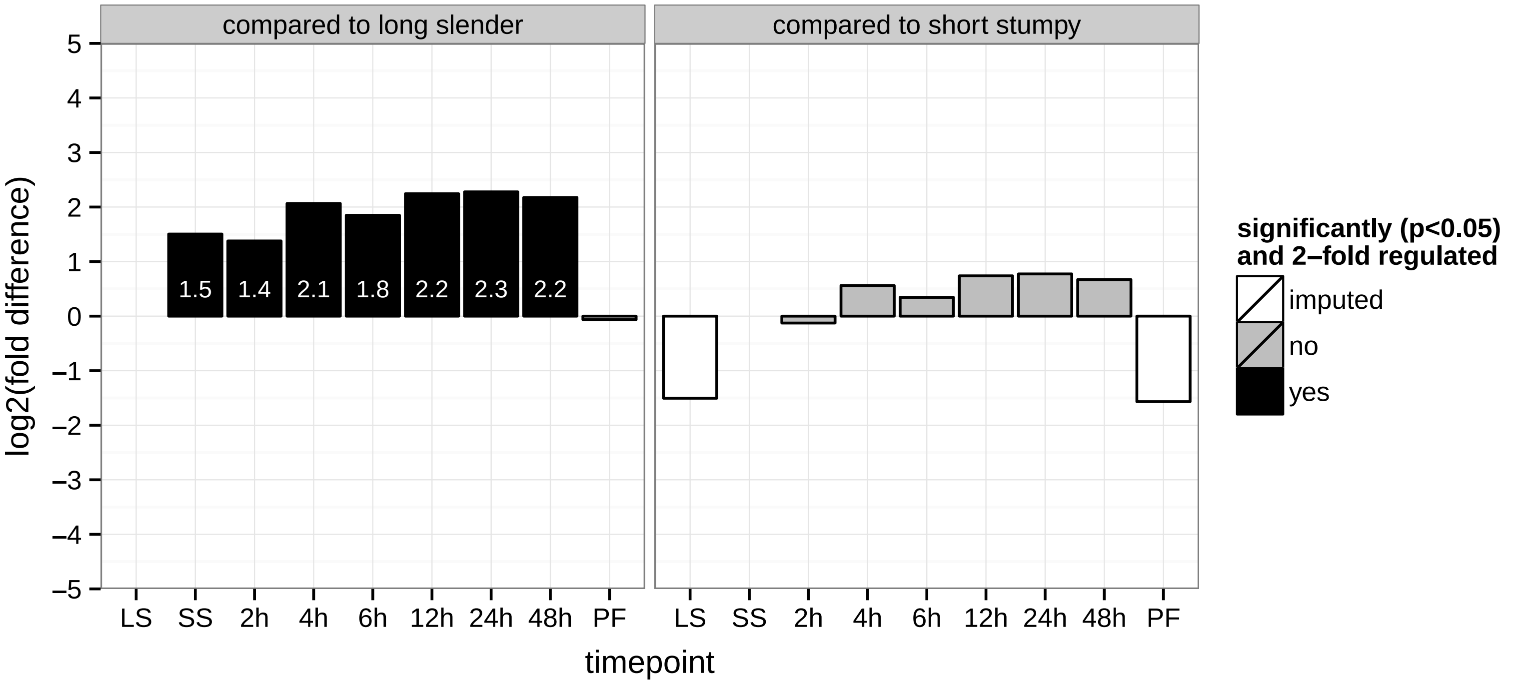
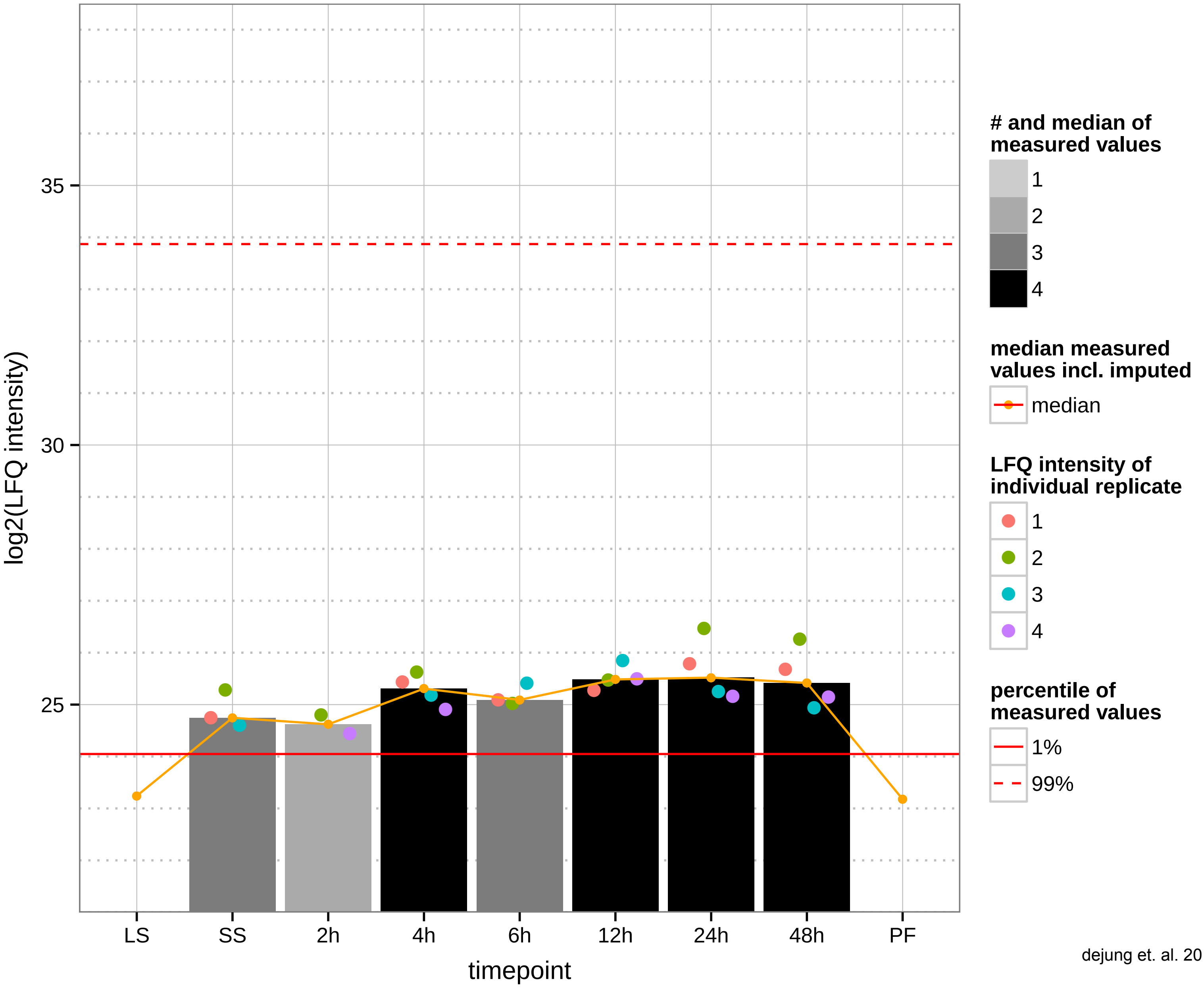
Iron–sulfur assembly protein 2 (Isa2)
Tb927.5.1030
AGOF: null
AGOC: mitochondrion
AGOP: [4Fe–4S] cluster assembly, growth, regulation of reactive oxygen species metabolic process
PGOF: null
PGOC: null
PGOP: null





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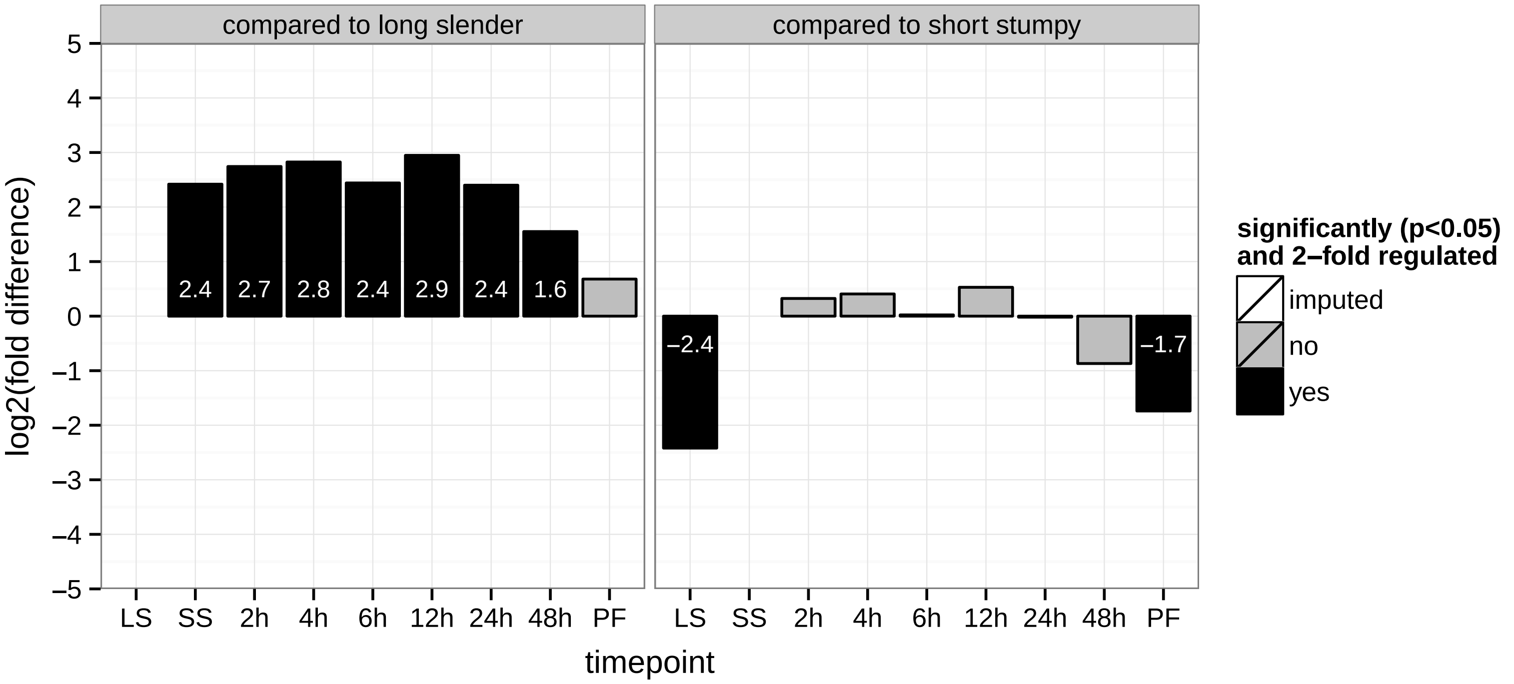
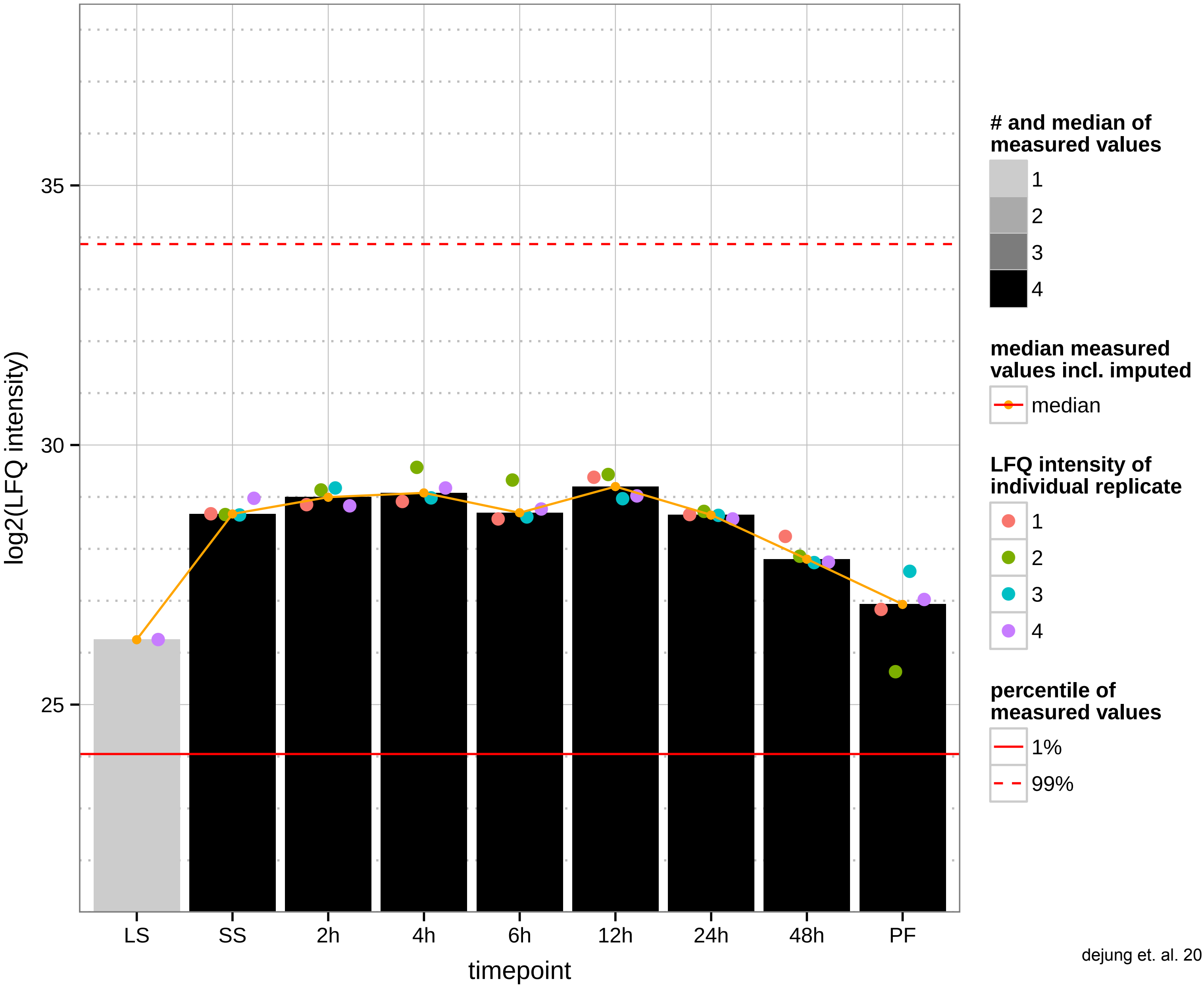
alanine racemase, putative
Tb927.5.1280
AGOF: alanine racemase activity
AGOC: cytosol
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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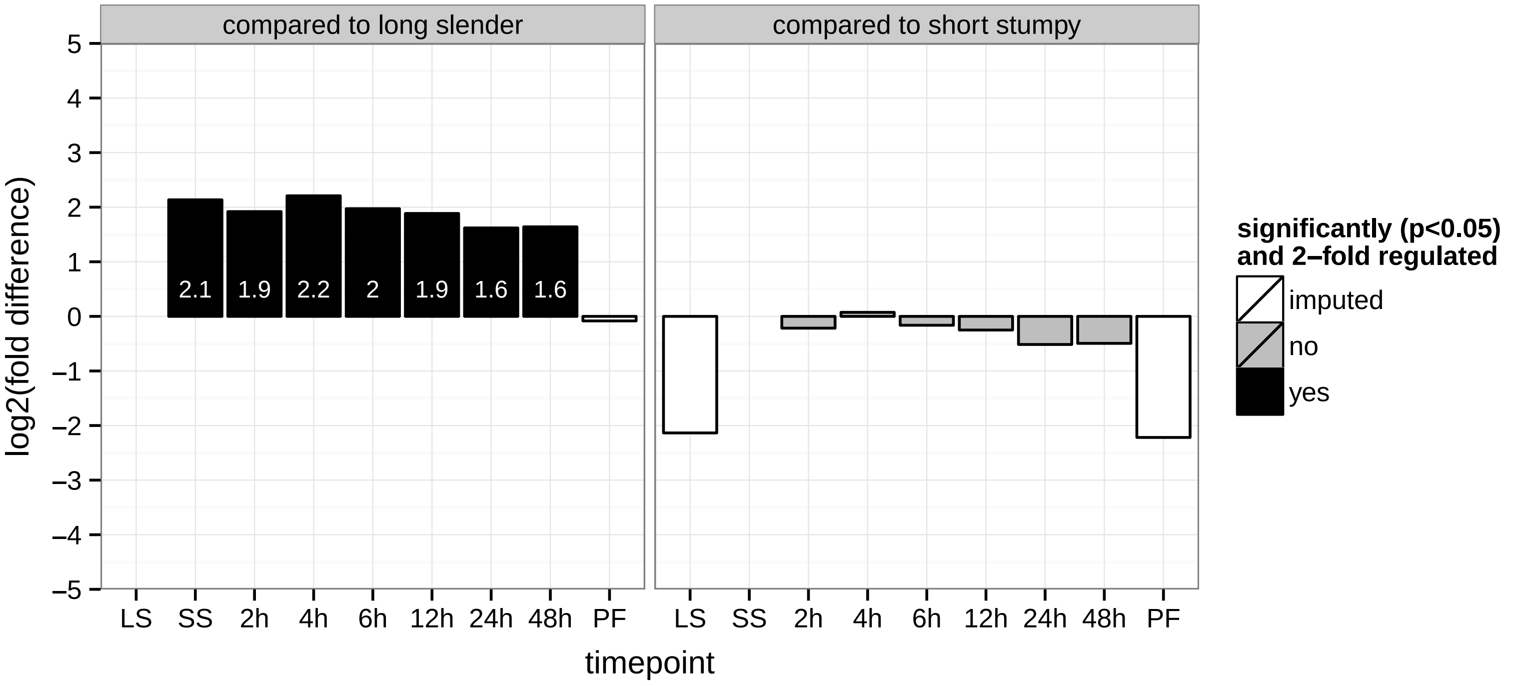
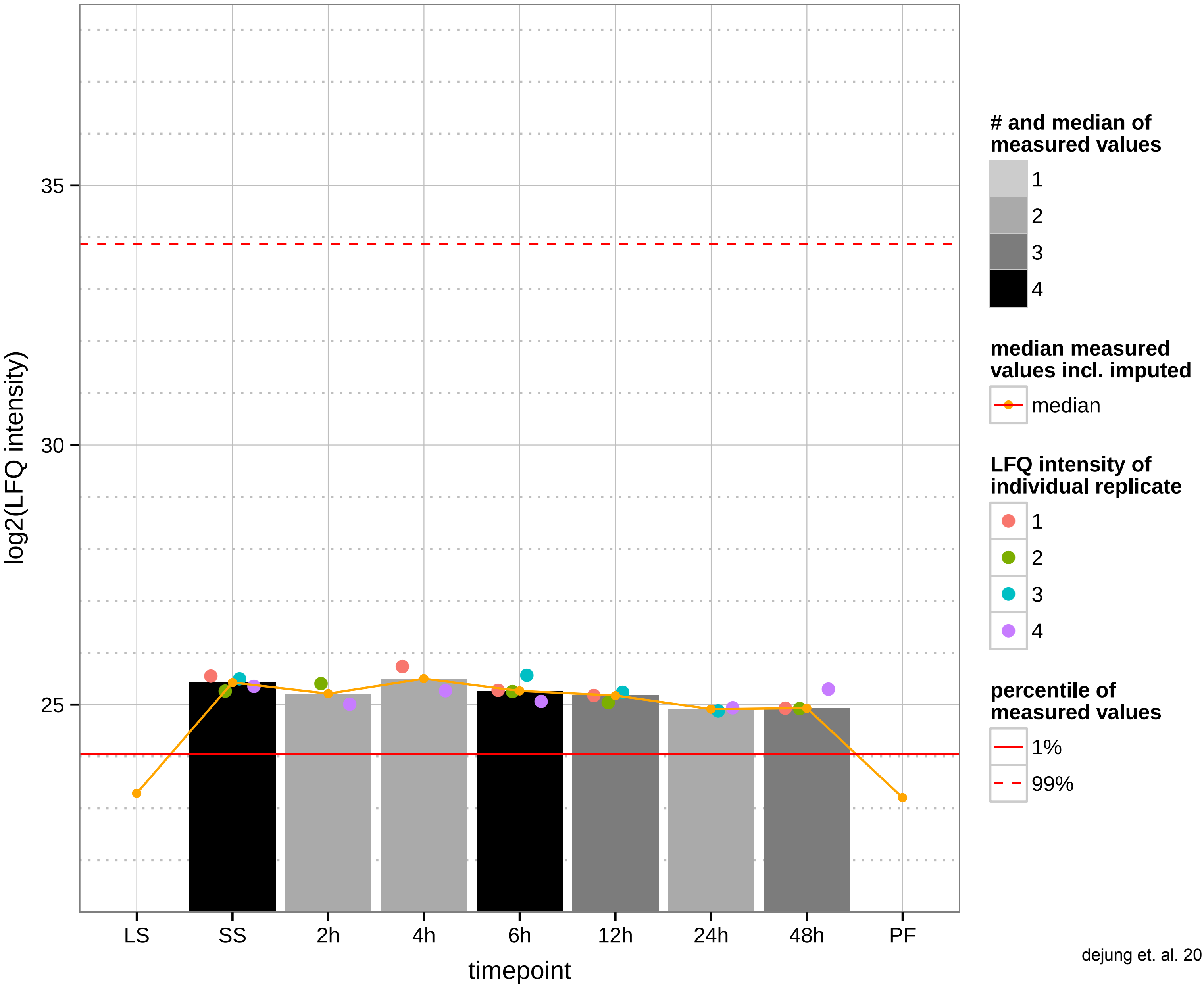
hypothetical protein, conserved
Tb927.5.1320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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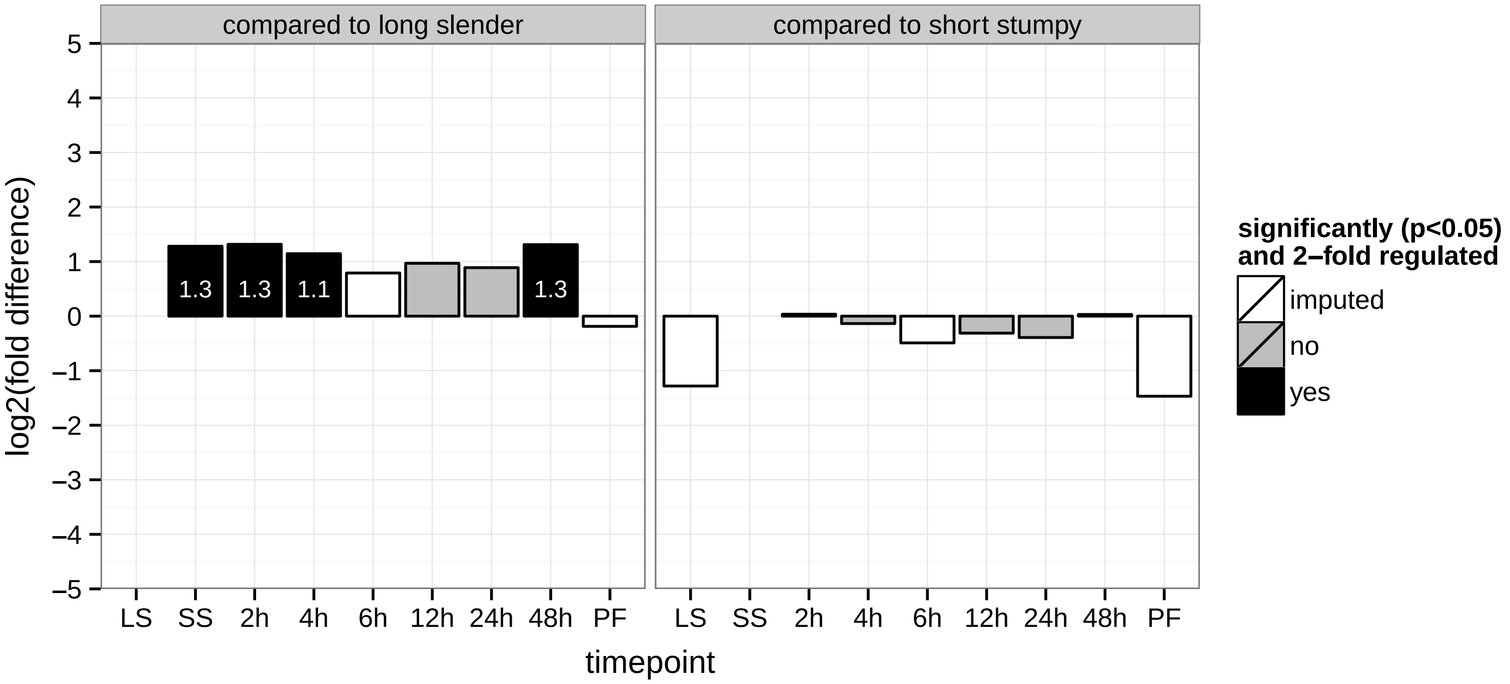
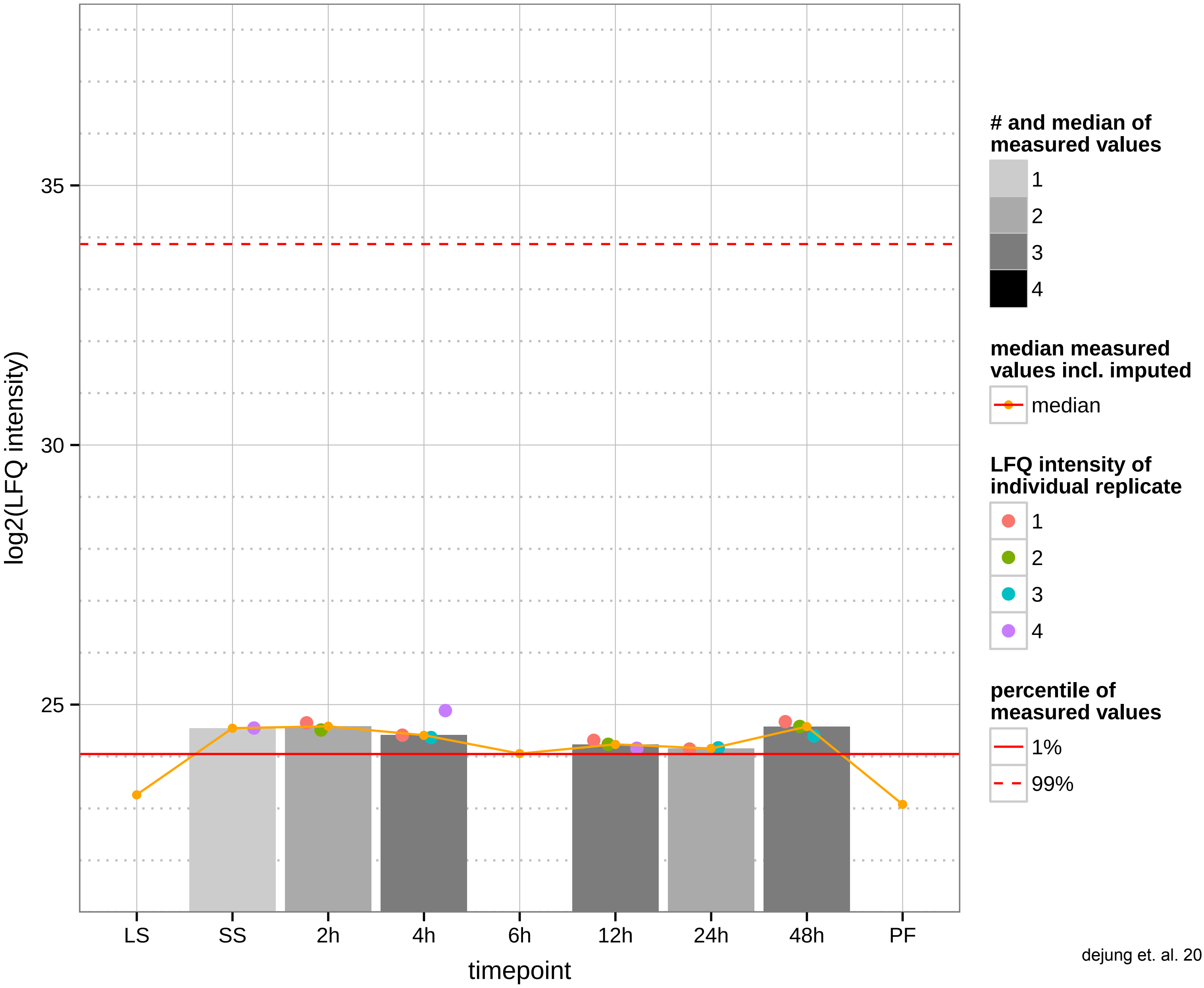
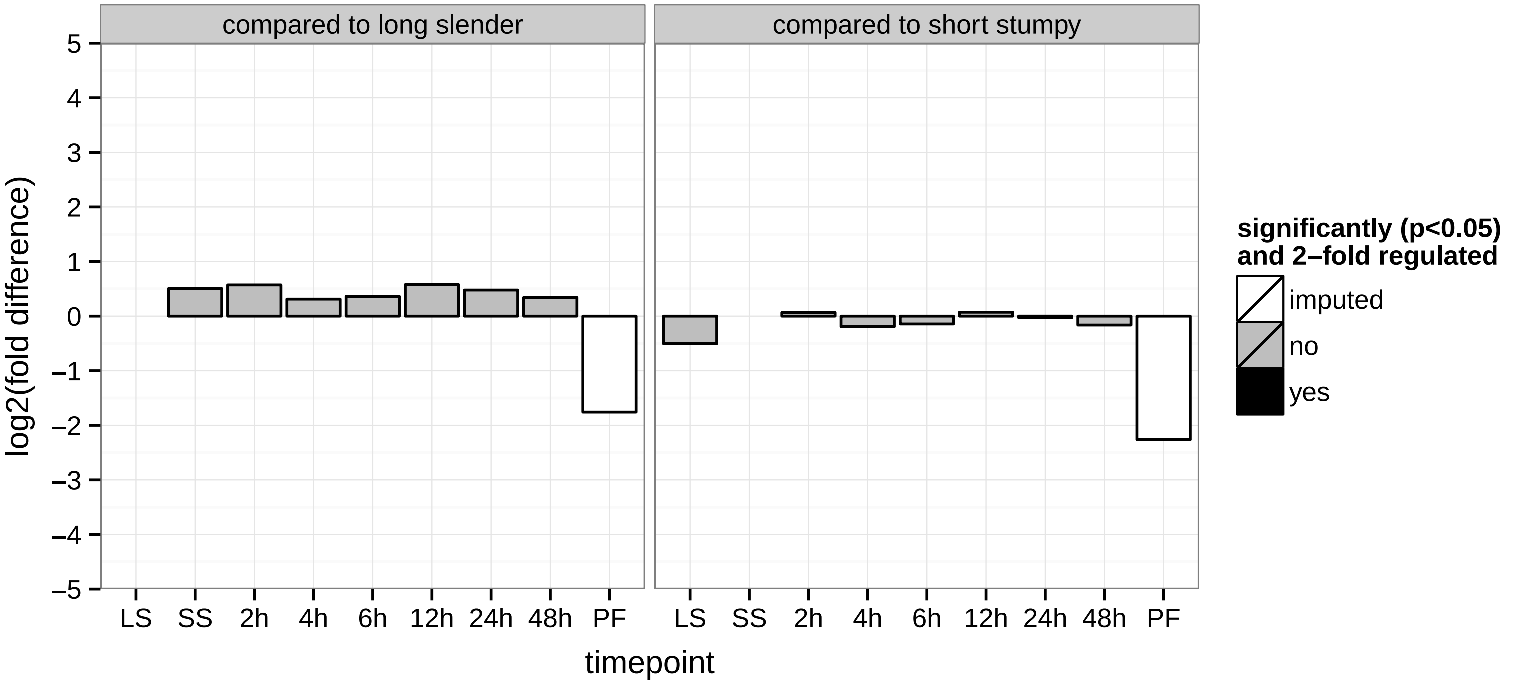
hypothetical protein, conserved
Tb927.5.1540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

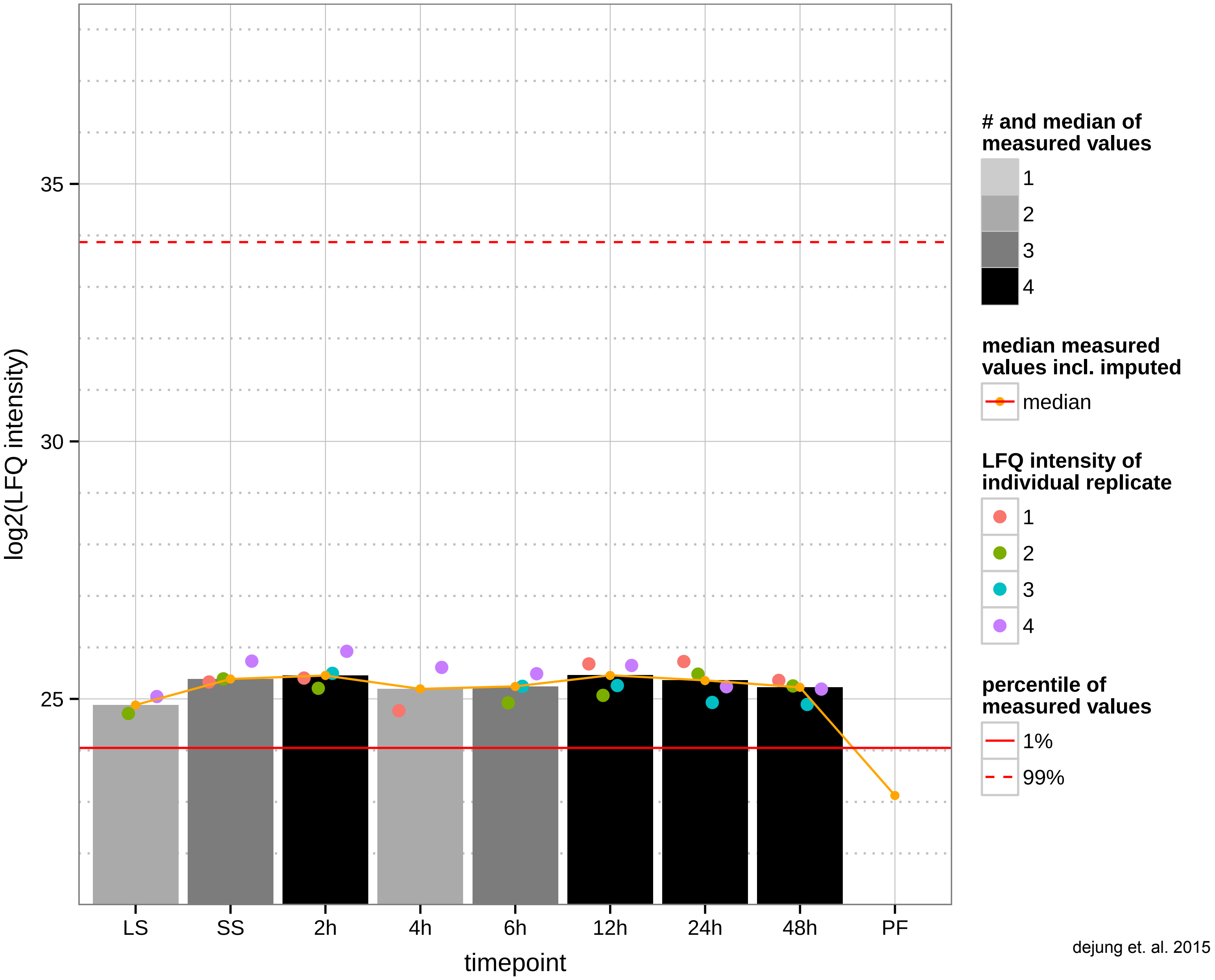




dejung et. al. 2015

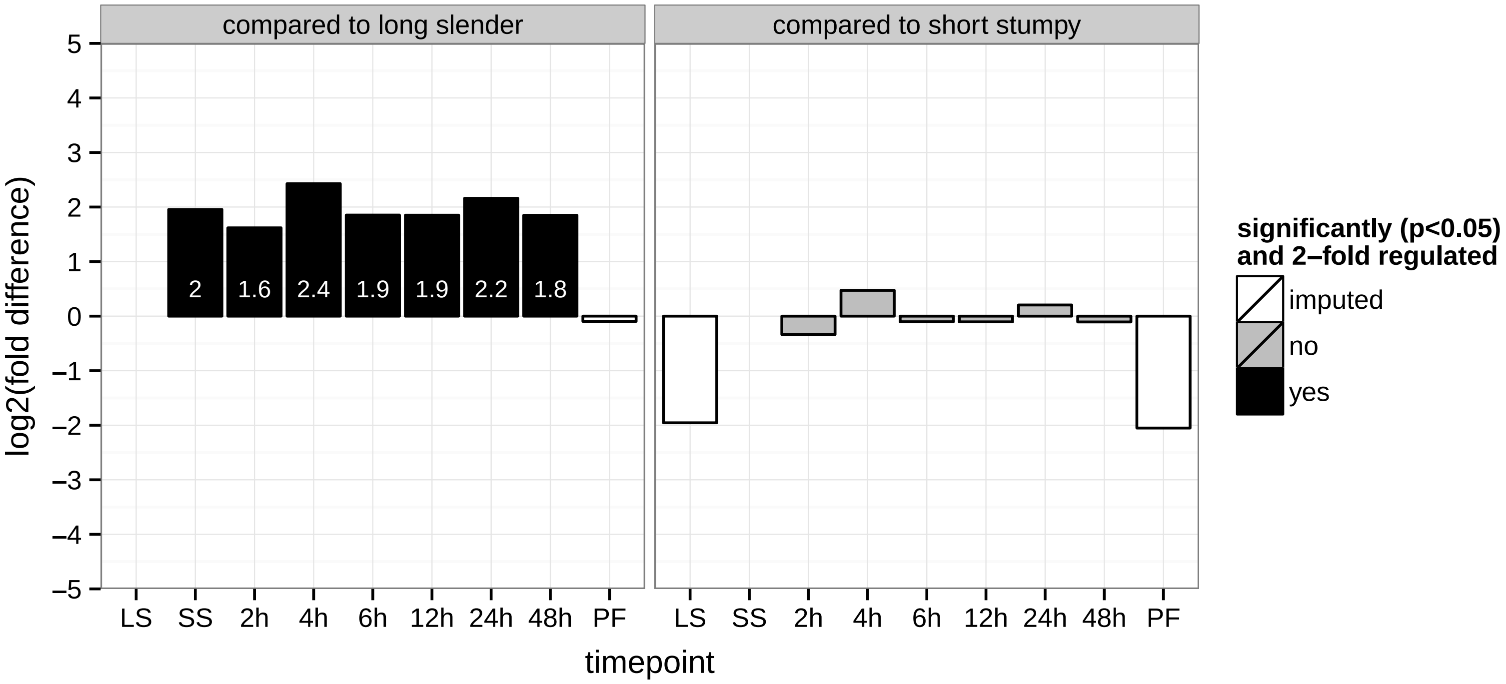
zinc finger CCCH domain containing protein 13 (ZC3H13)
Tb927.5.1580
AGOF: RNA binding, zinc ion binding
AGOC: cytosol
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null

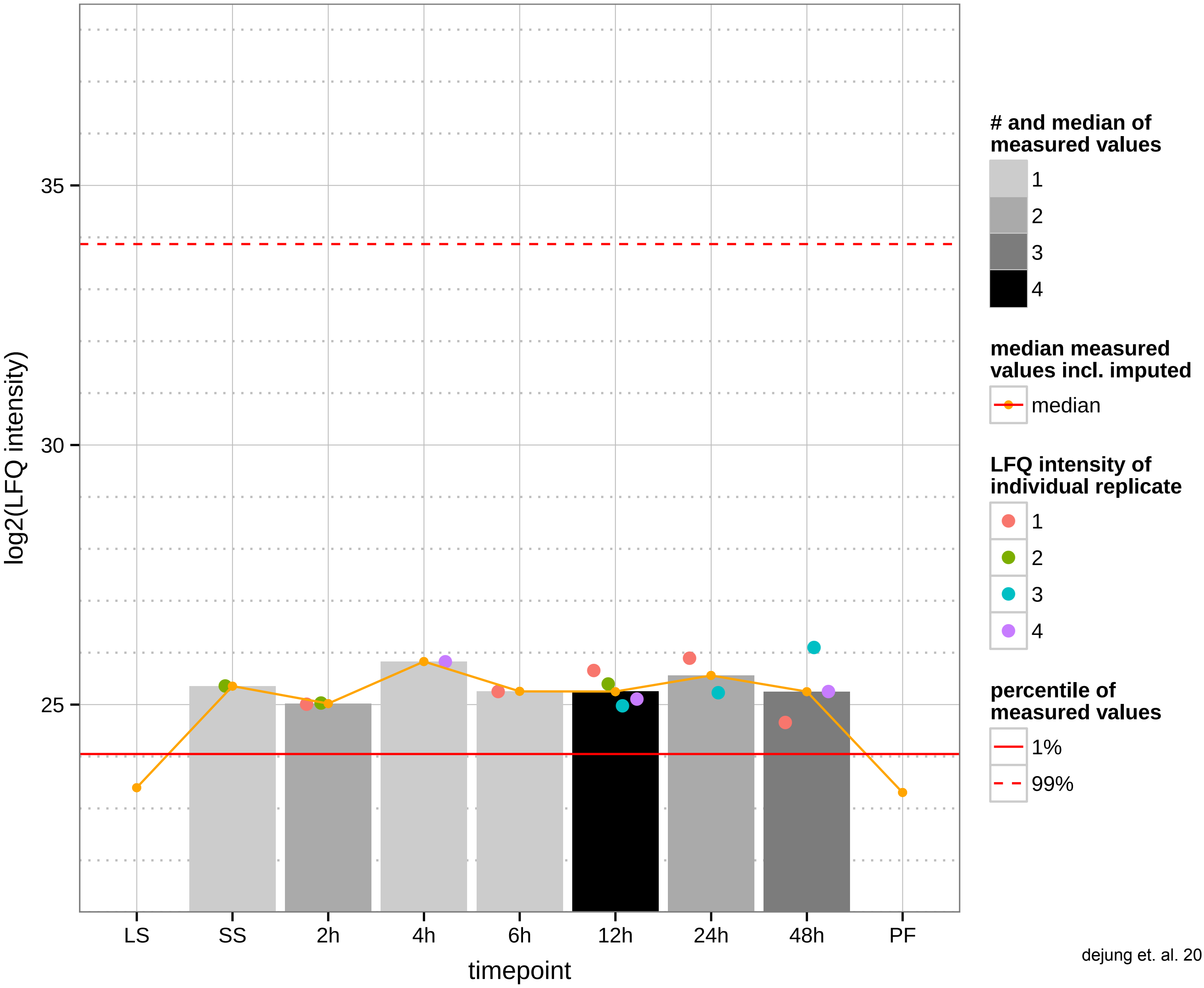




dejung et. al. 2015

hypothetical protein, conserved
Tb927.5.1590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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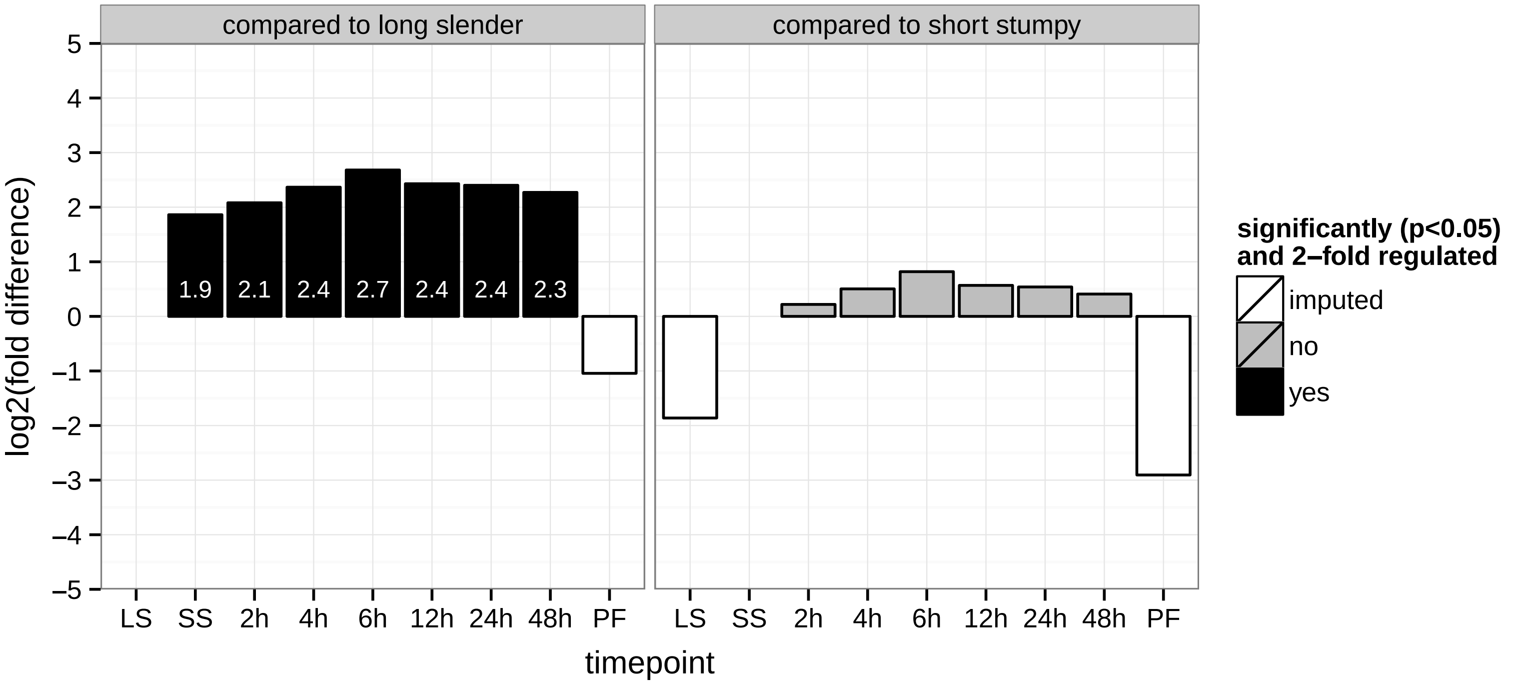
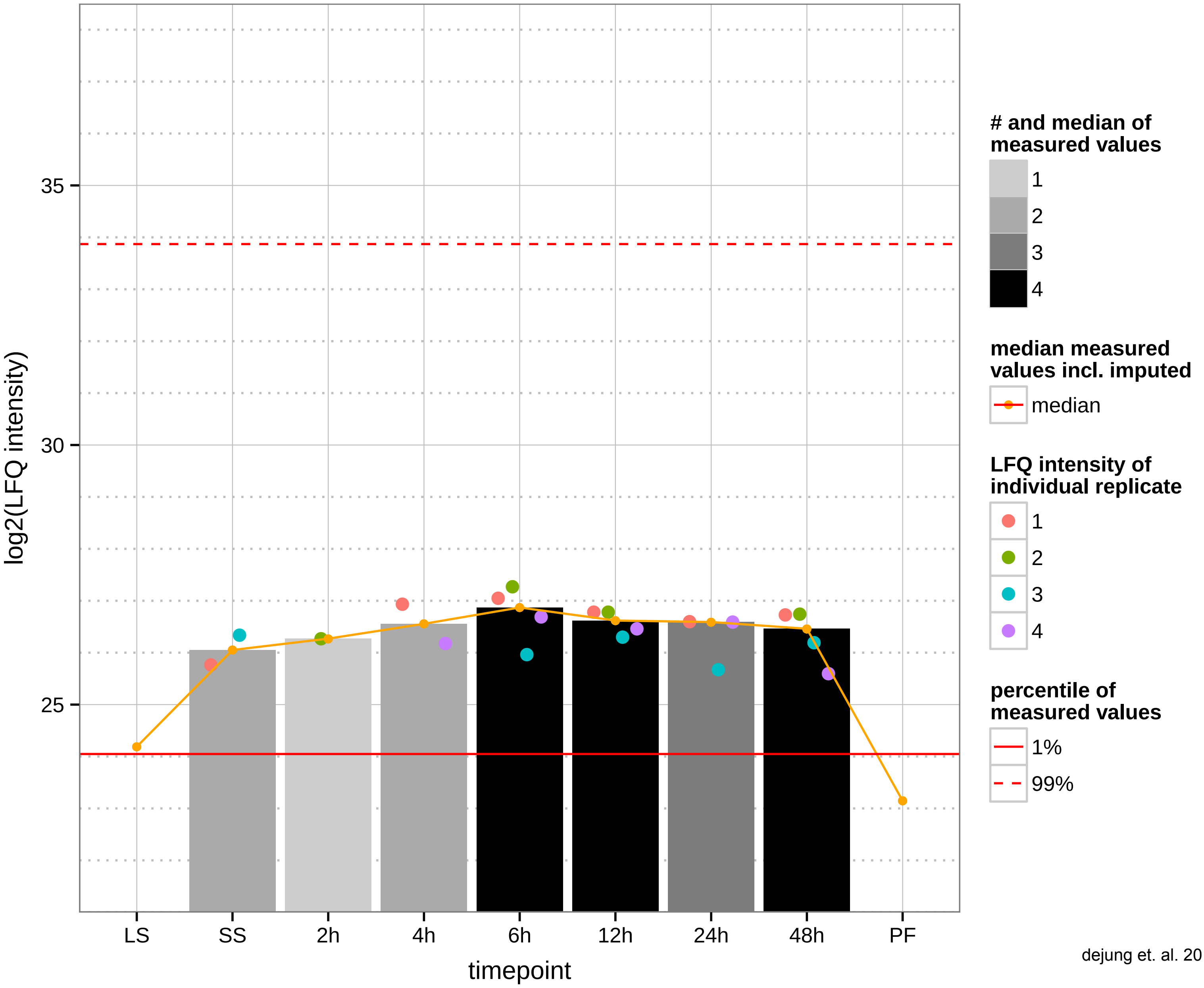
Isoprenylcysteine alpha–carbonyl methylesterase, putative
Tb927.5.1760
AGOF: hydrolase activity
AGOC: null
AGOP: null
PGOF: hydrolase activity
PGOC: null
PGOP: metabolic process





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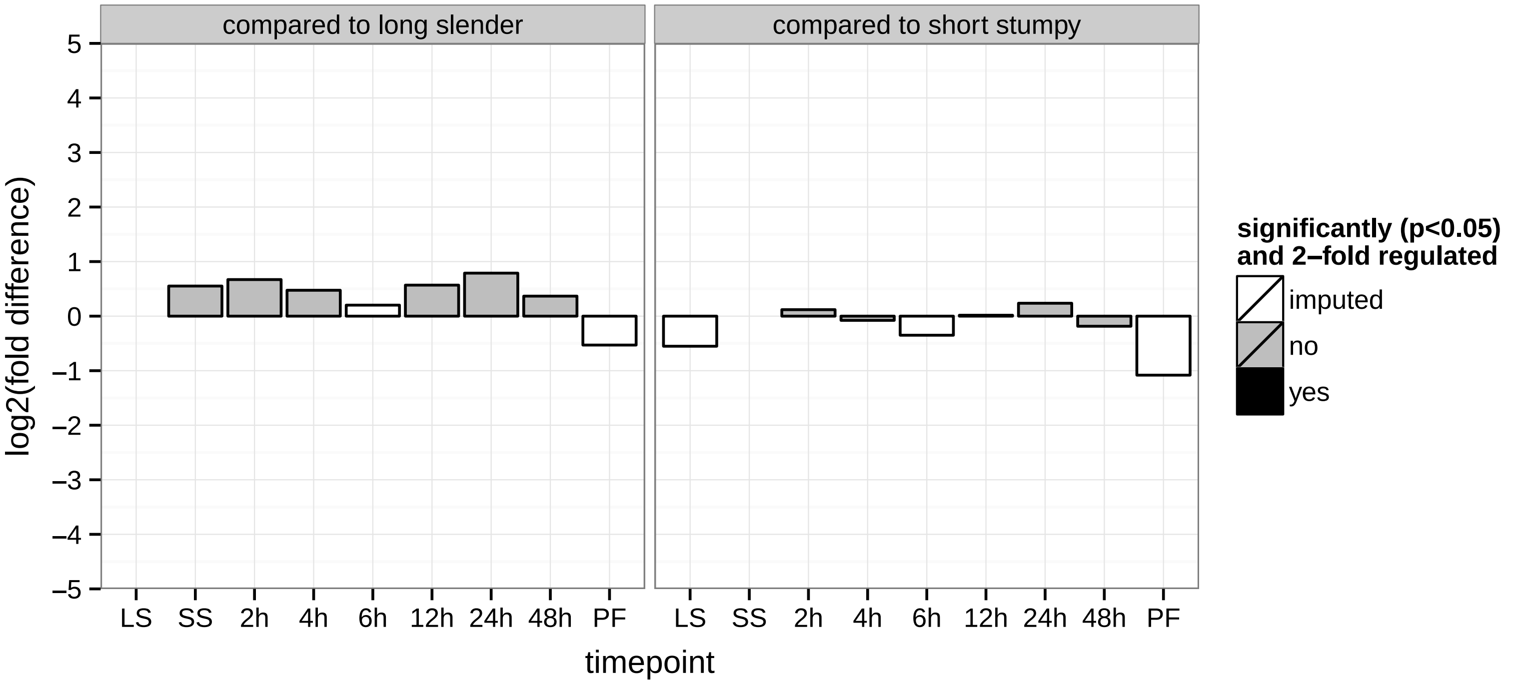
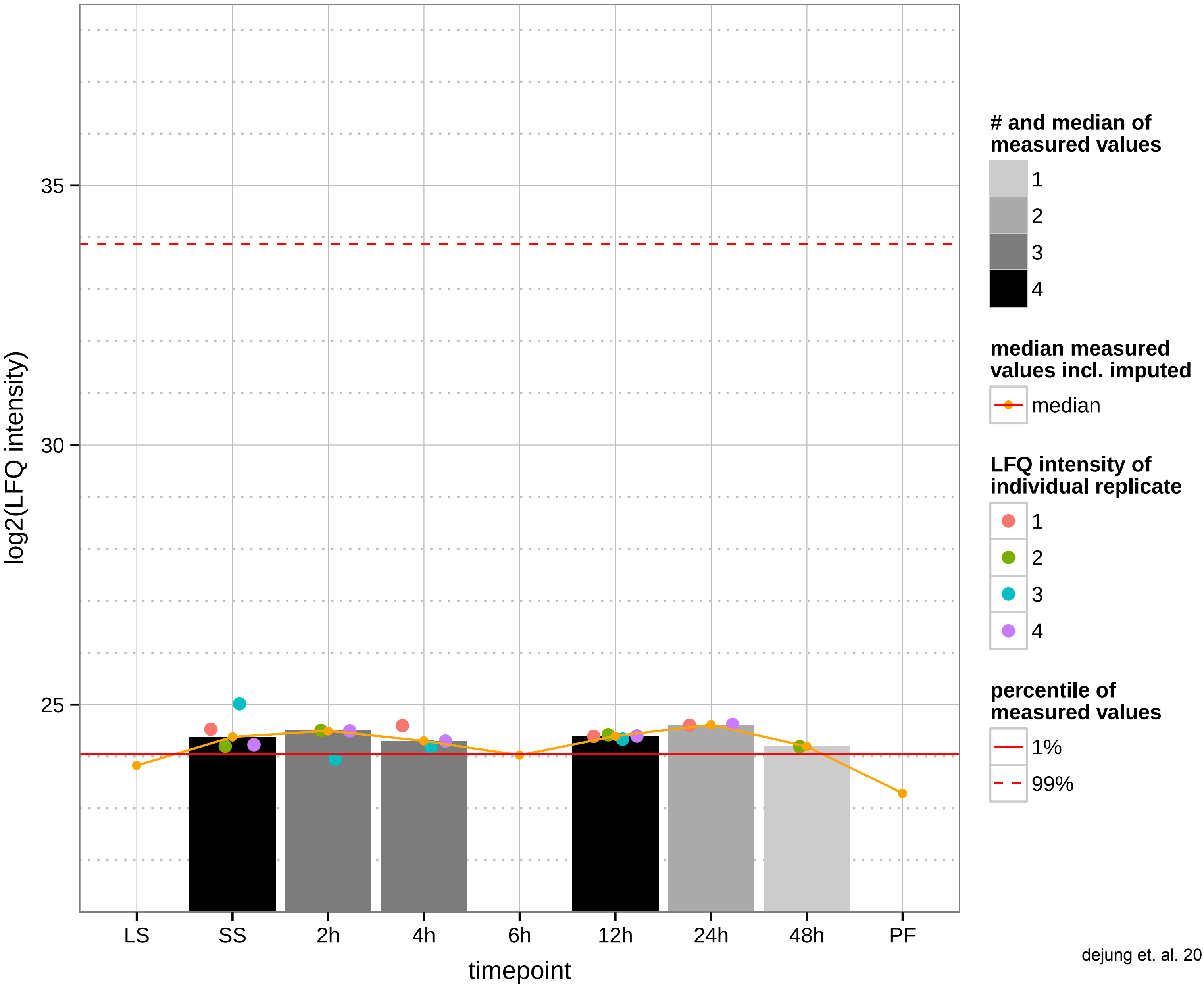
hypothetical protein, conserved
Tb927.5.1910
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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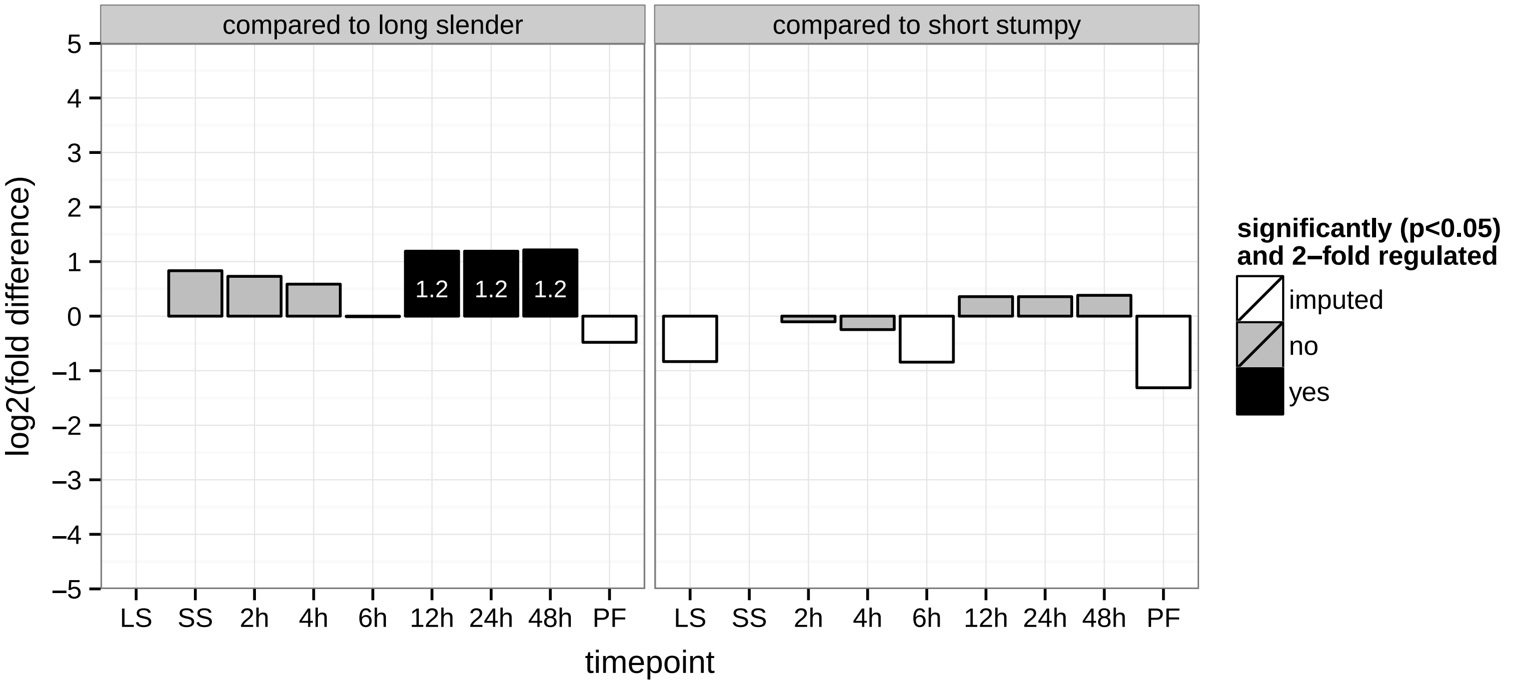
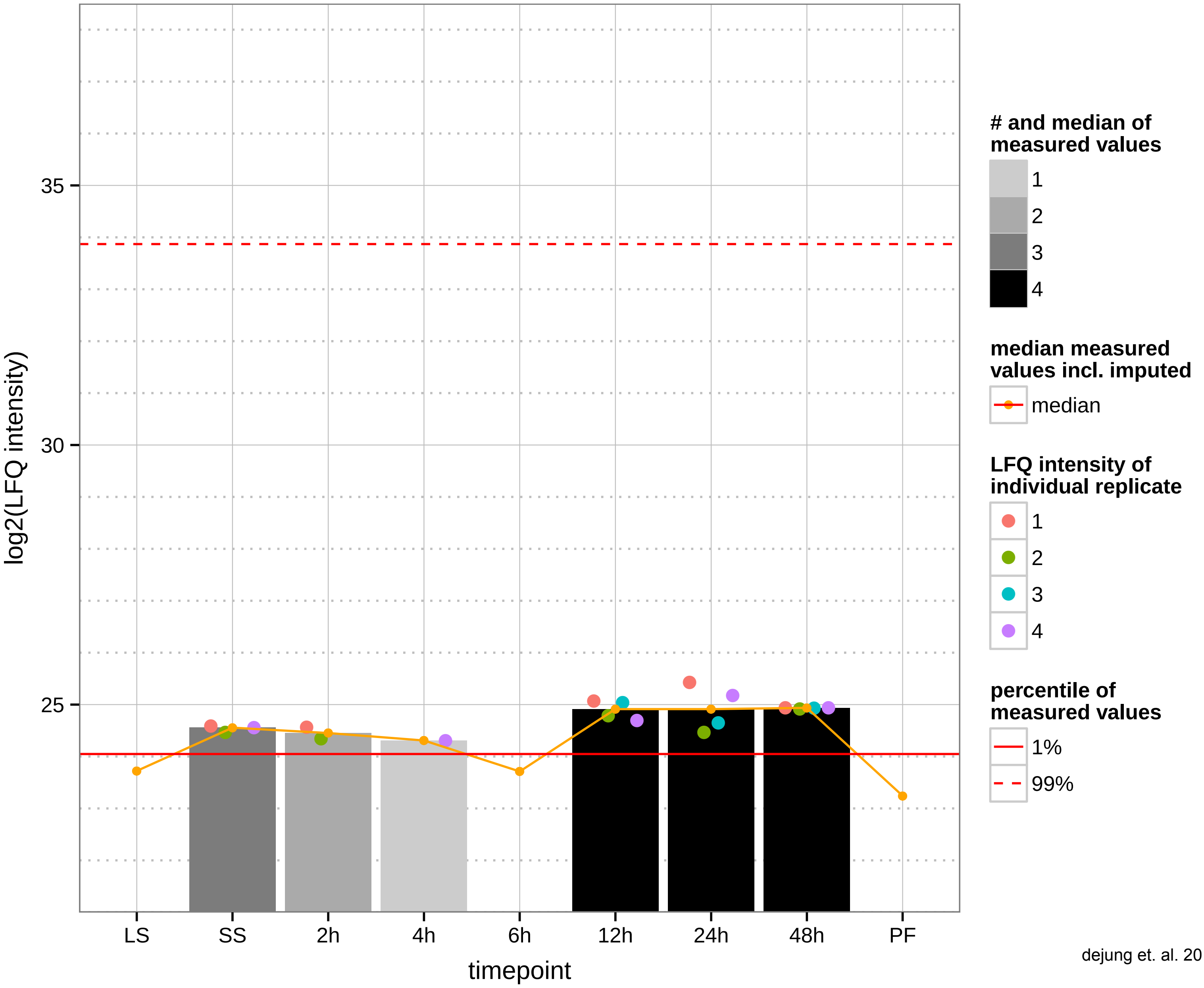
cell division control protein, putative
Tb927.5.2060
AGOF: DNA binding
AGOC: null
AGOP: null
PGOF: DNA binding
PGOC: null
PGOP: null





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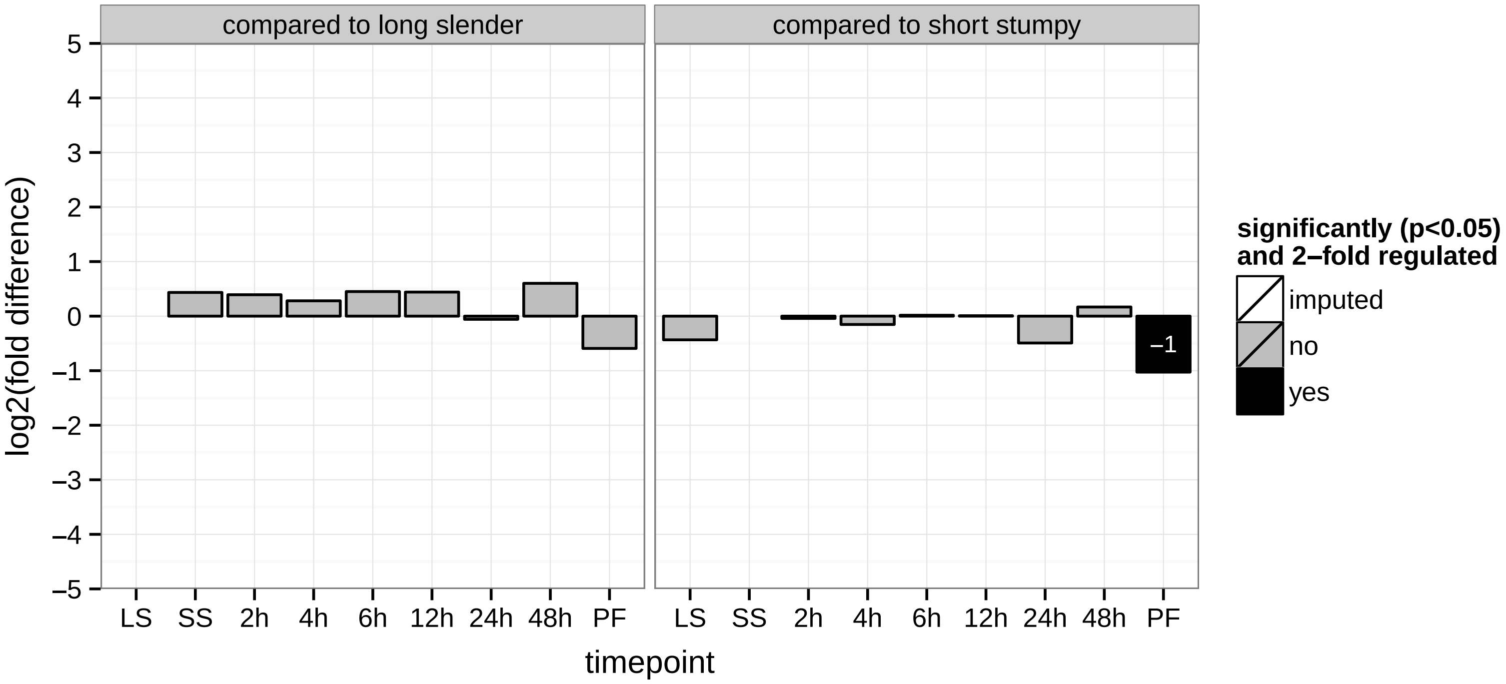
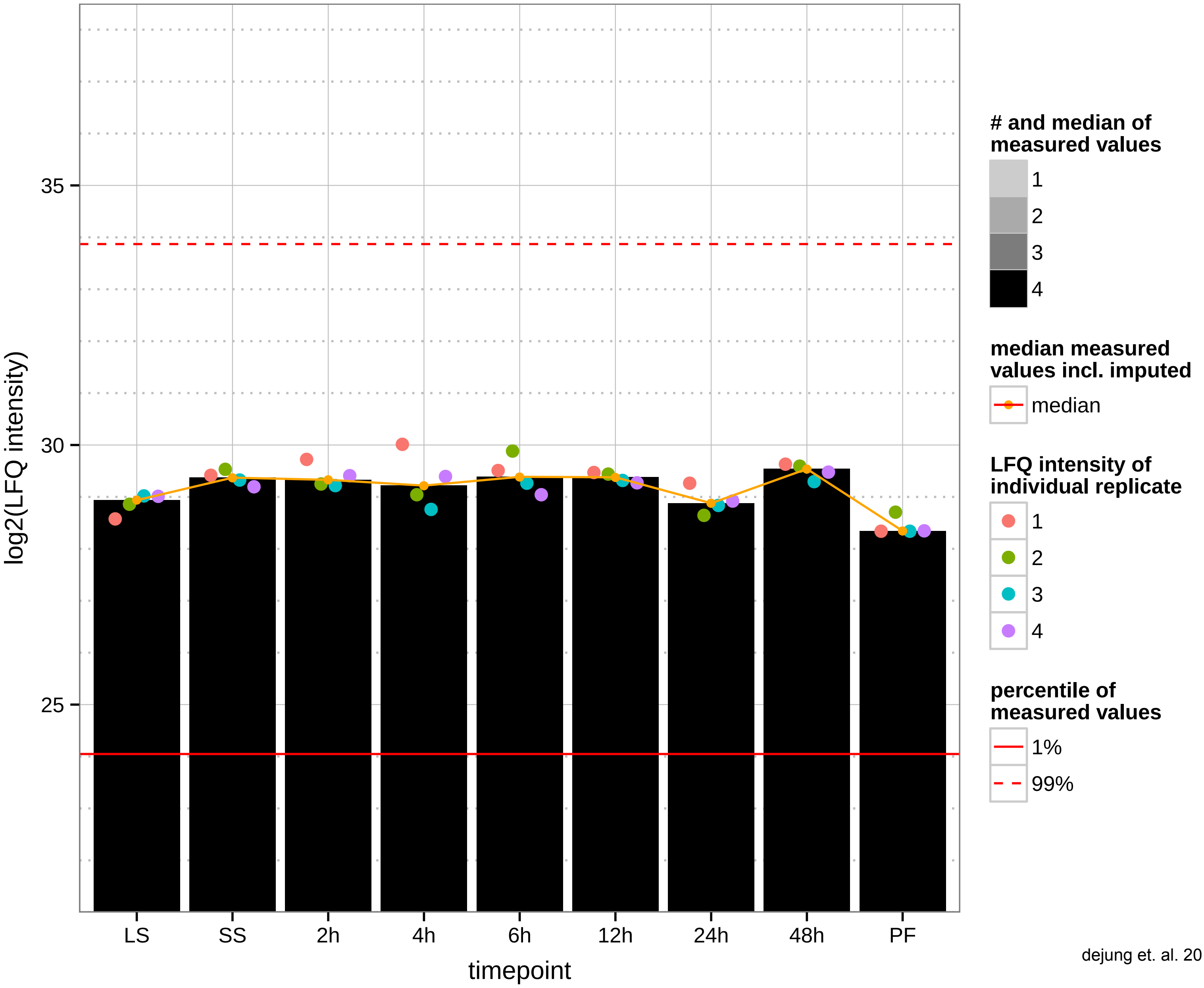
hypothetical protein, conserved
Tb927.5.2250;Tb927.5.2220;Tb927.5.2190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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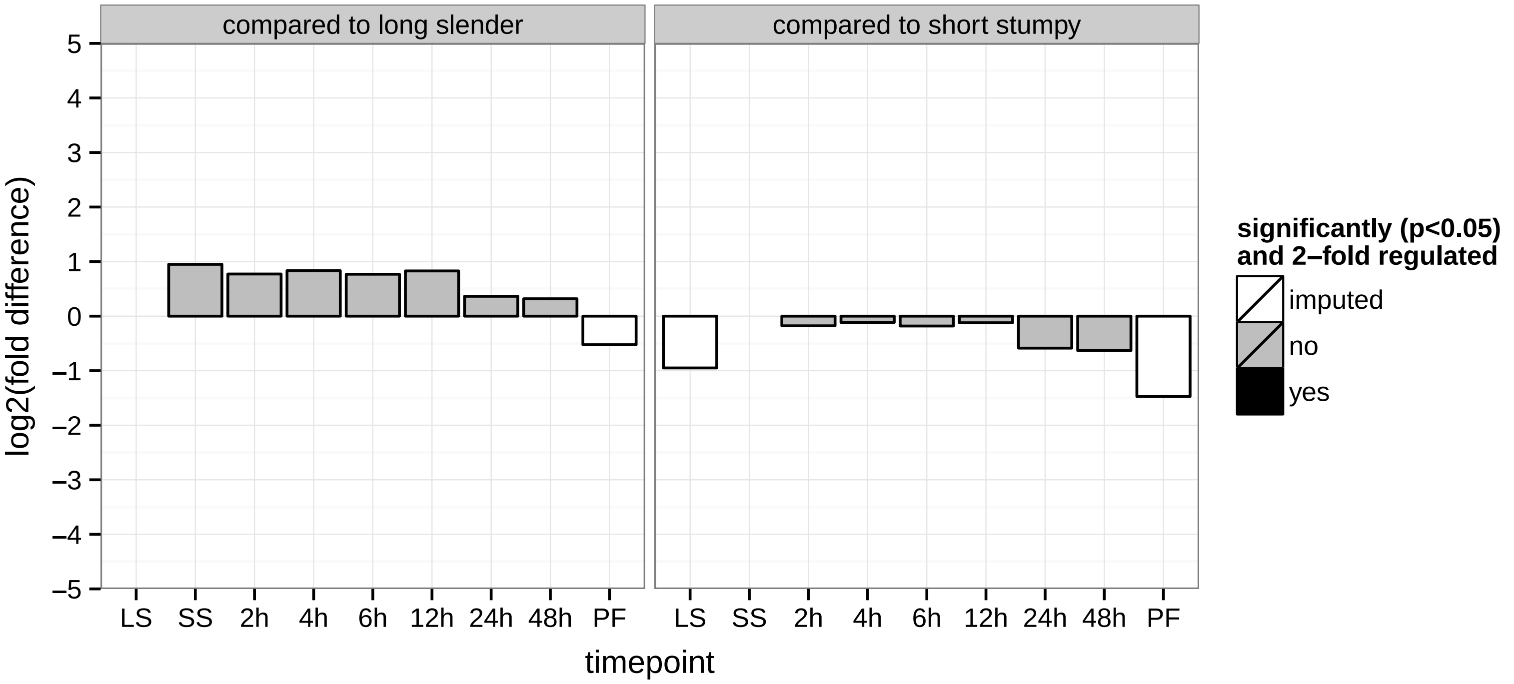
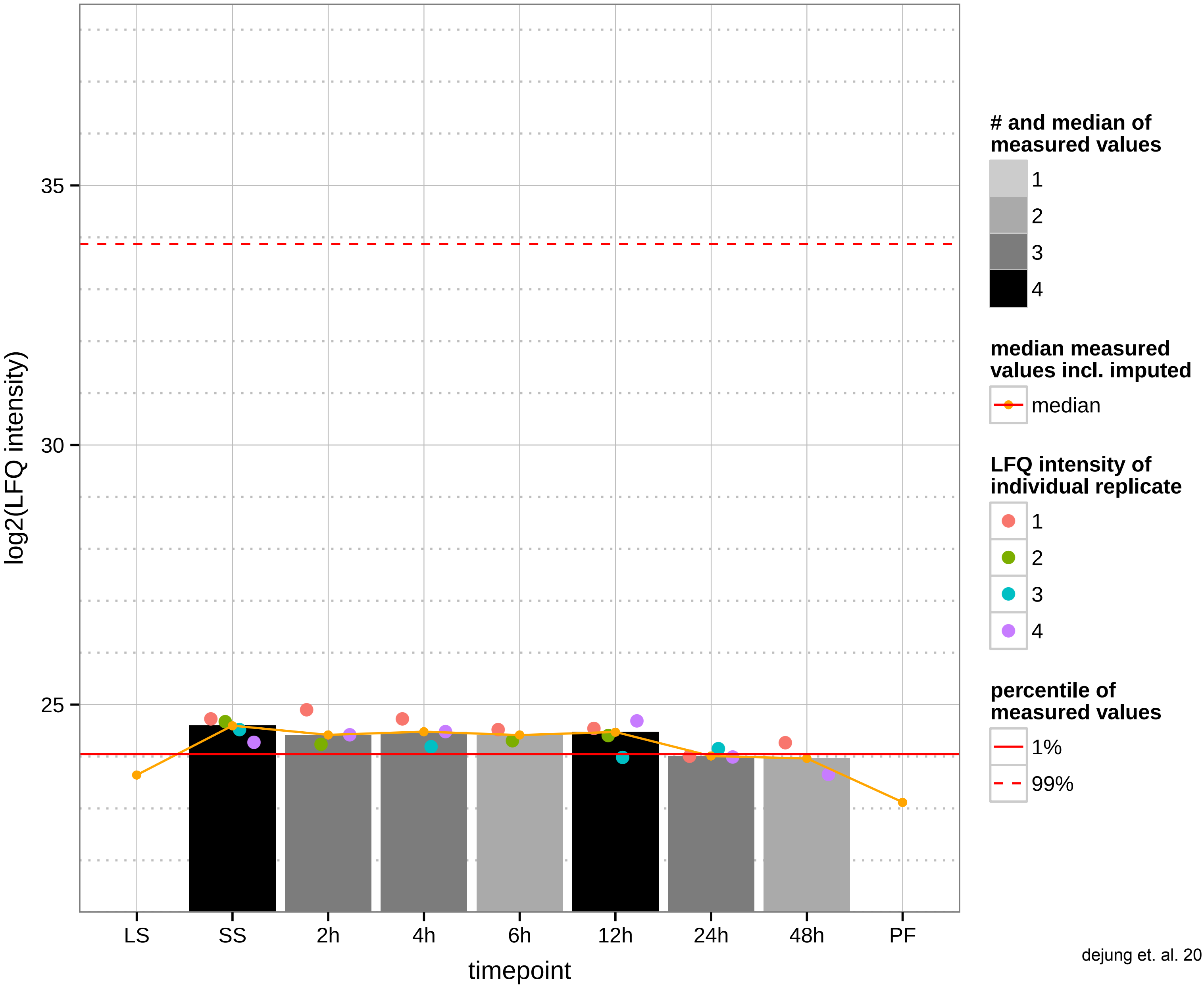
hypothetical protein, conserved
Tb927.5.2980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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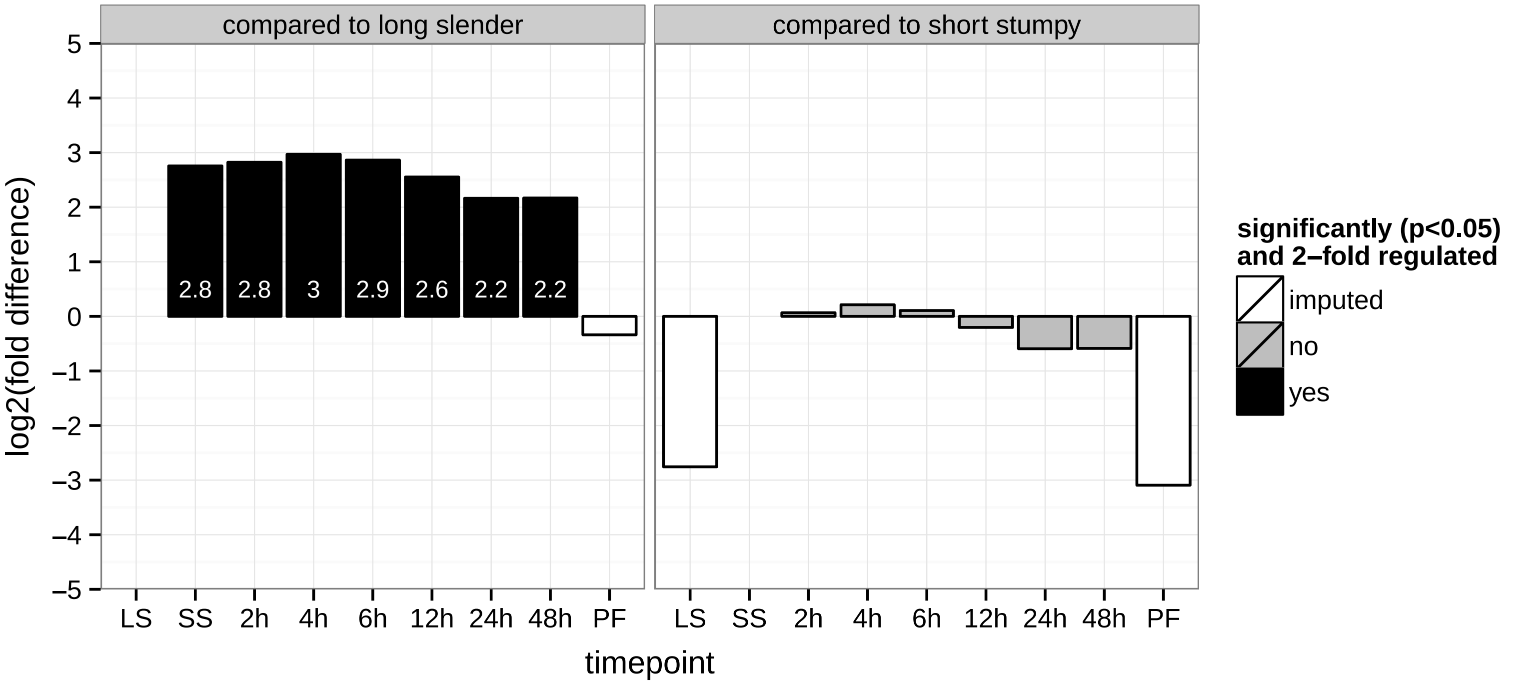
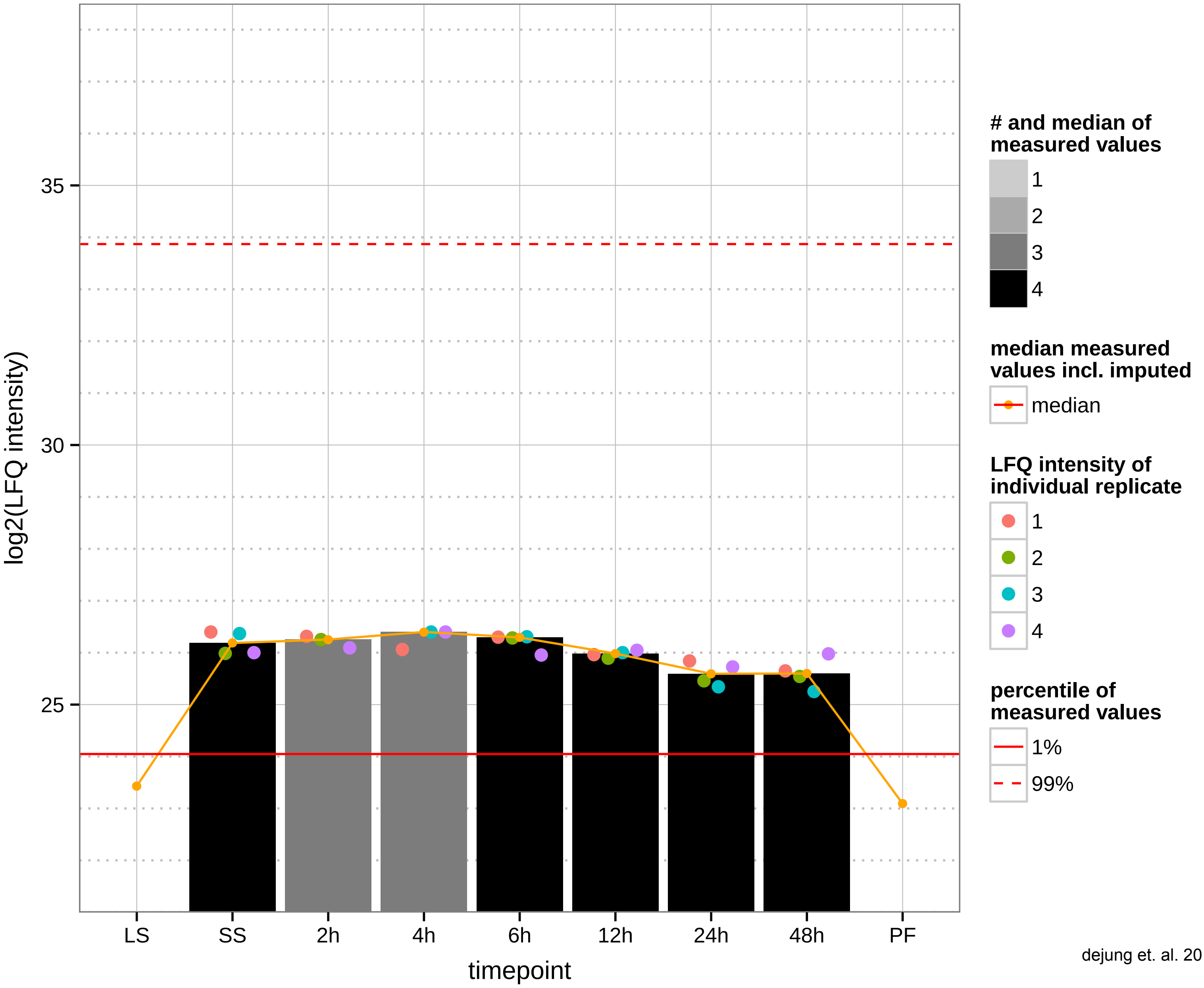
ATP–dependent DEAD/H RNA helicase, putative
Tb927.5.3600
AGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase–containing compound metabolic process
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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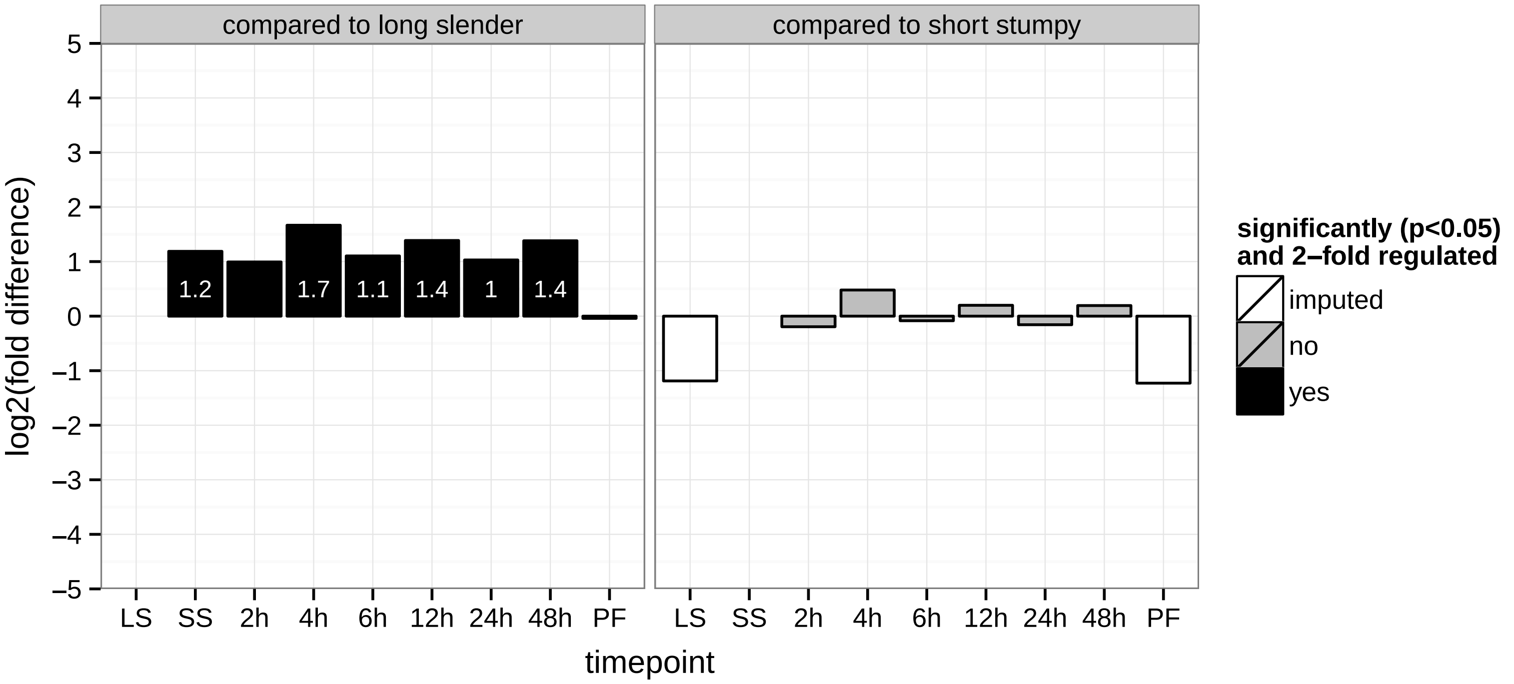
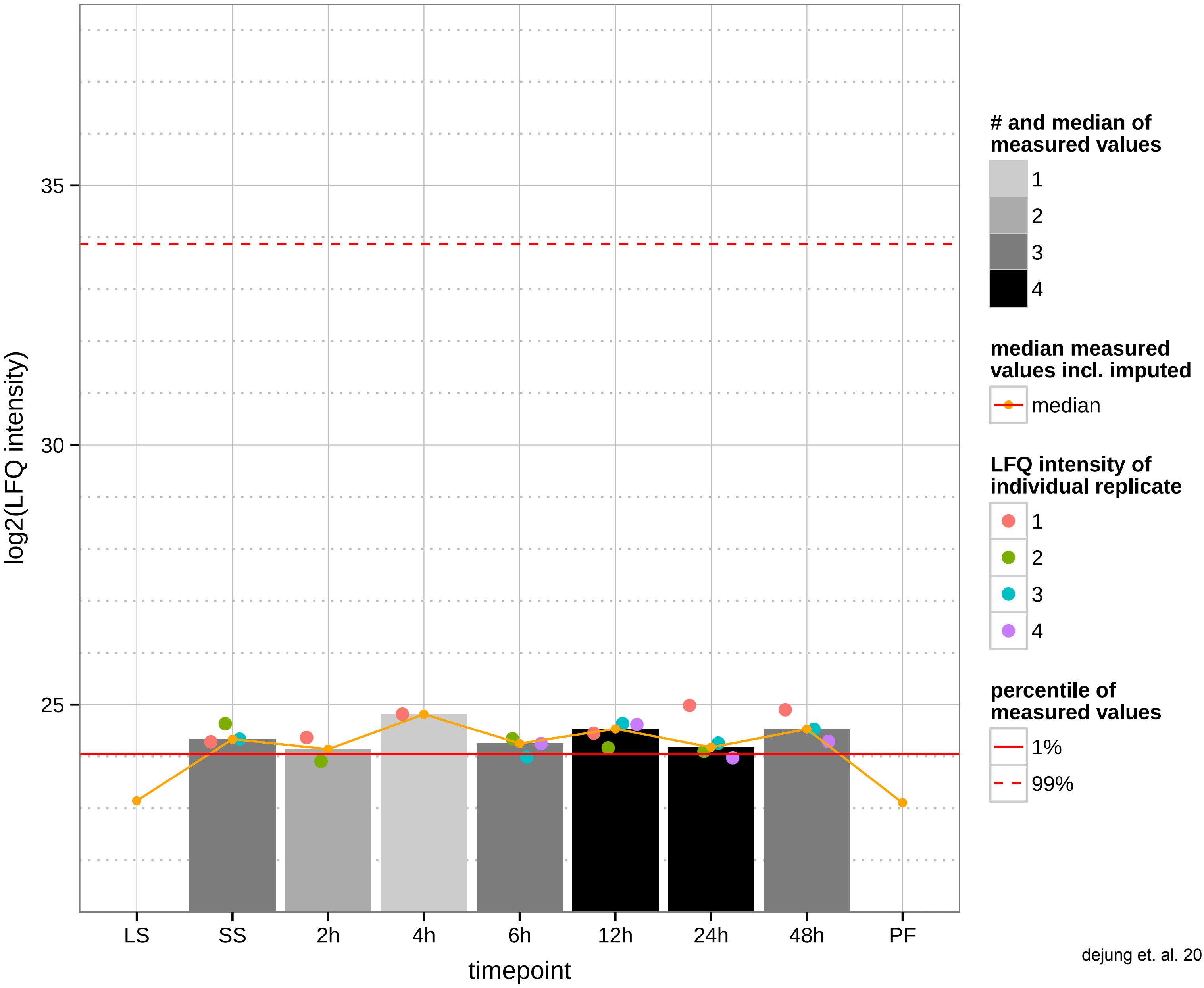
RNA–binding protein, putative (PPCT1)
Tb927.5.3750
AGOF: RNA binding, peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding, peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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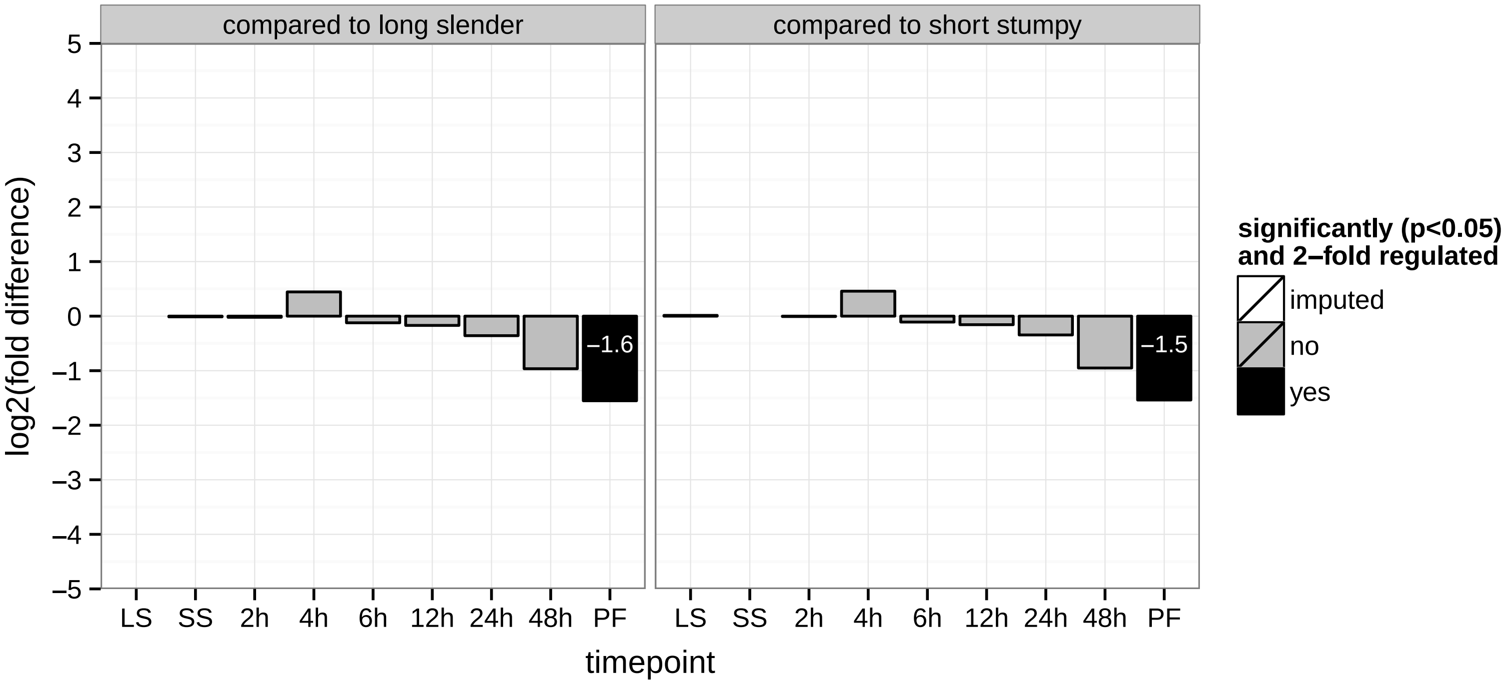
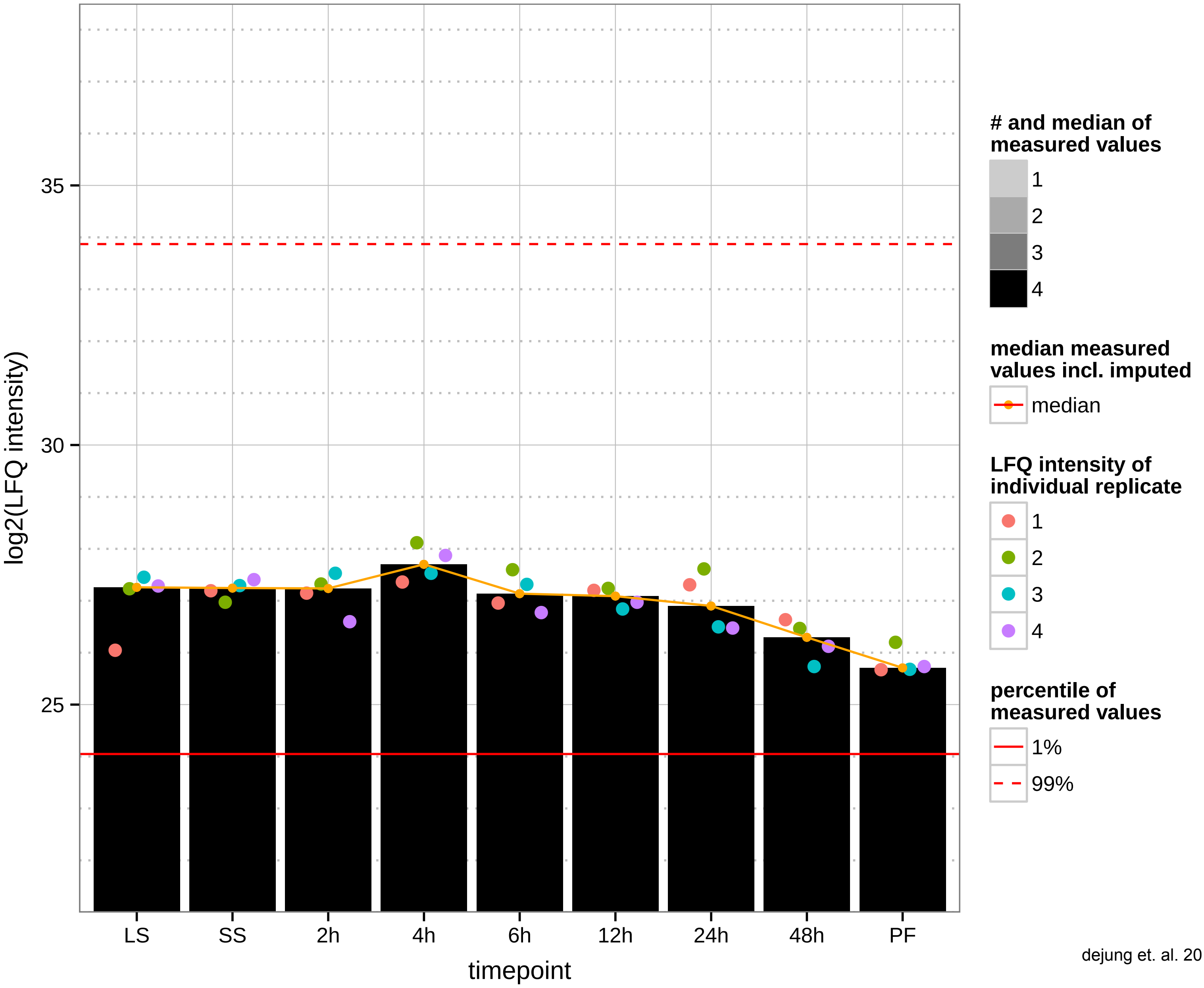
Selenoprotein T, putative (SelT)
Tb927.5.860
AGOF: selenium binding
AGOC: null
AGOP: cell redox homeostasis
PGOF: selenium binding
PGOC: null
PGOP: cell redox homeostasis





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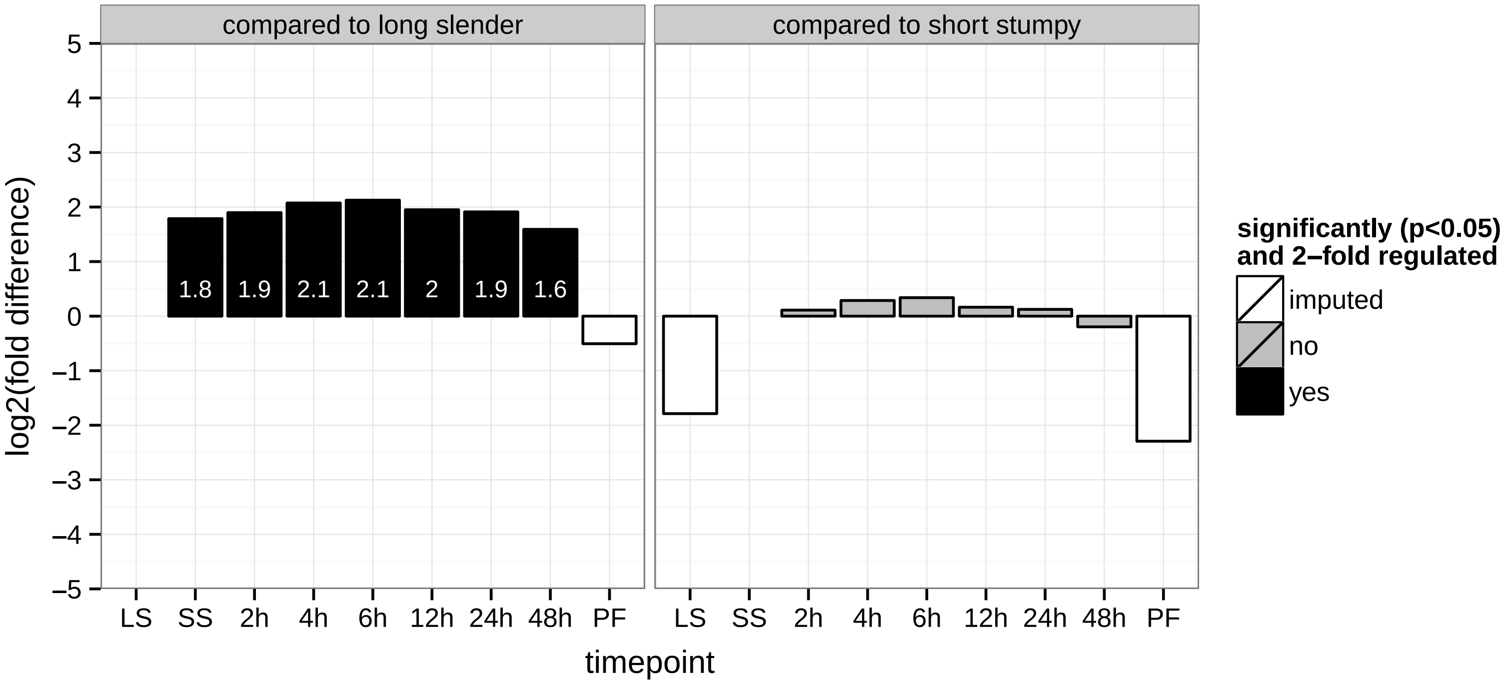
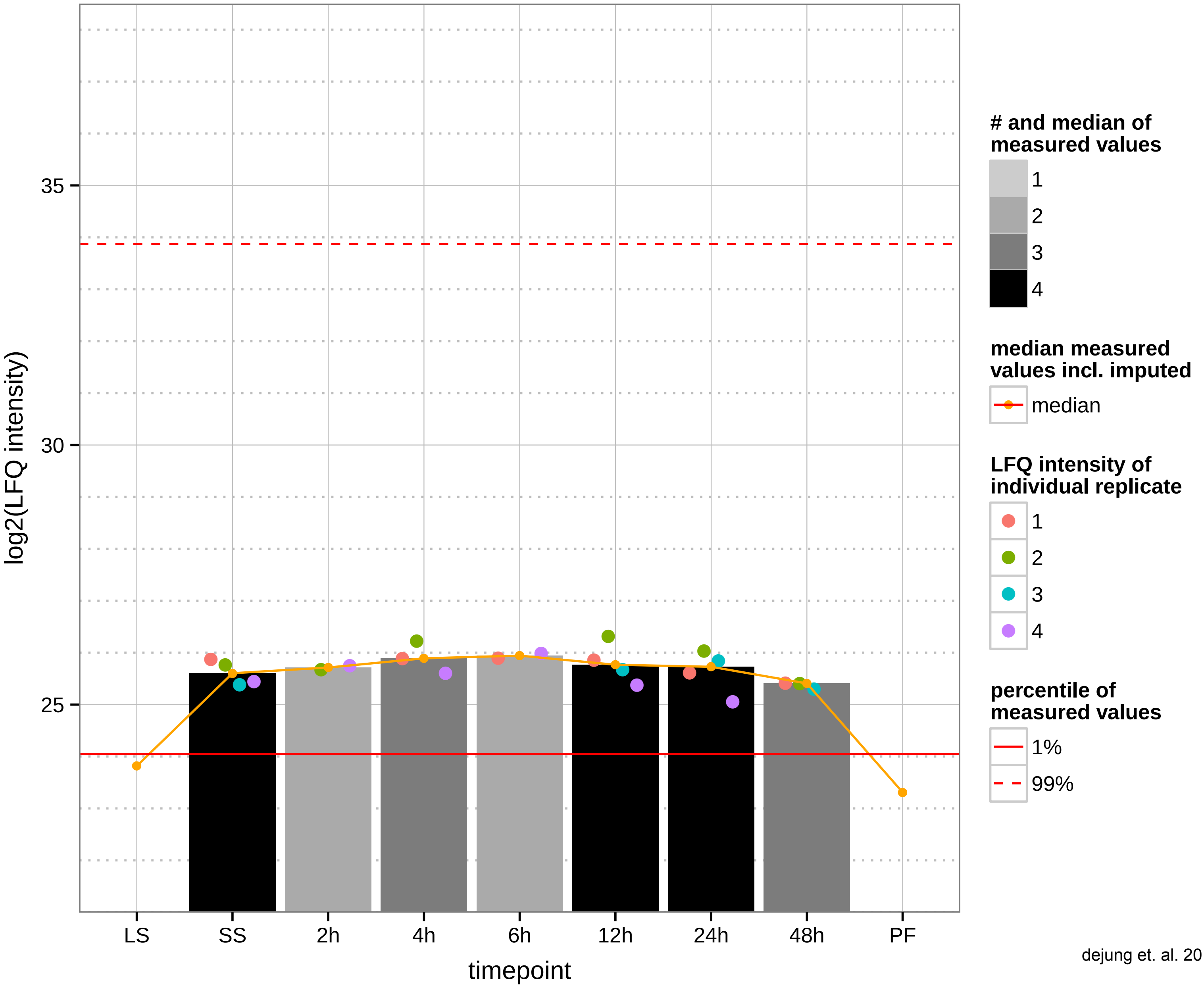
hypothetical protein, conserved
Tb927.5.990
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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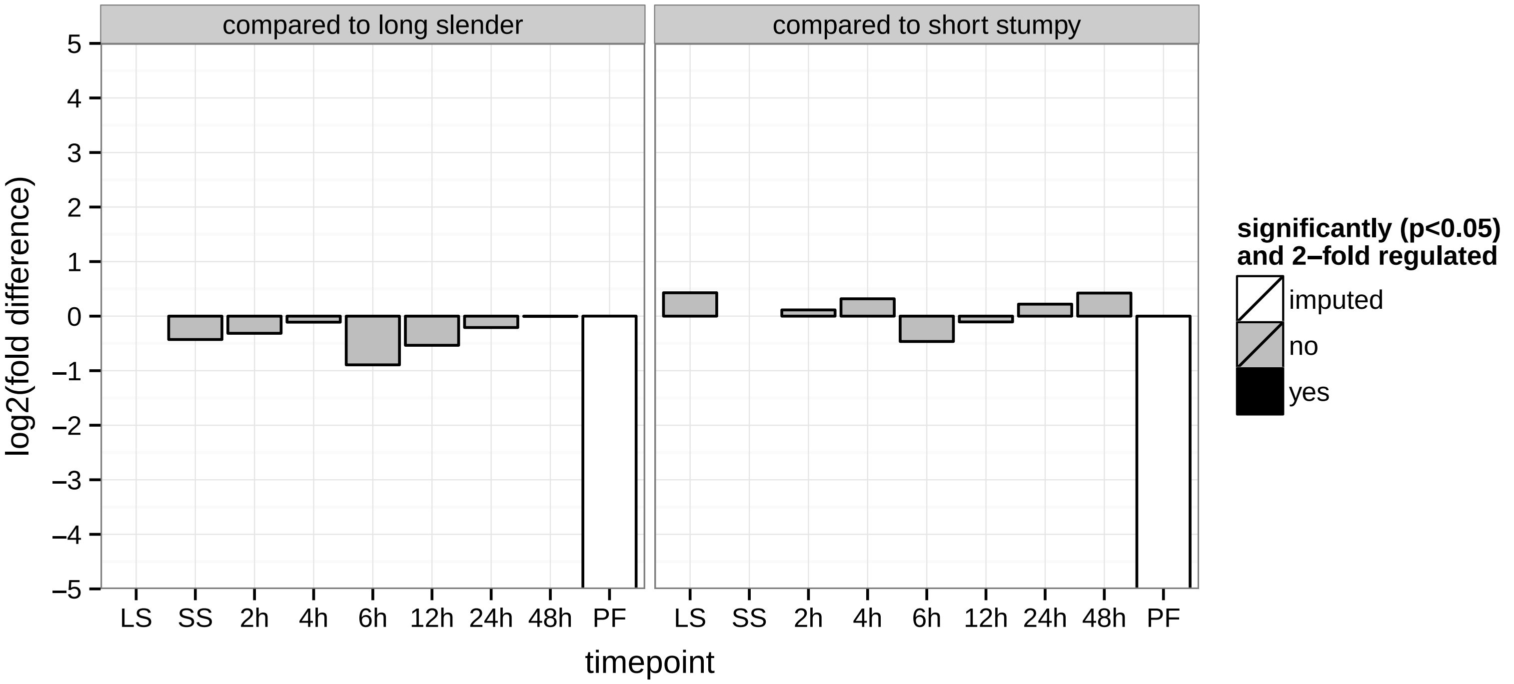
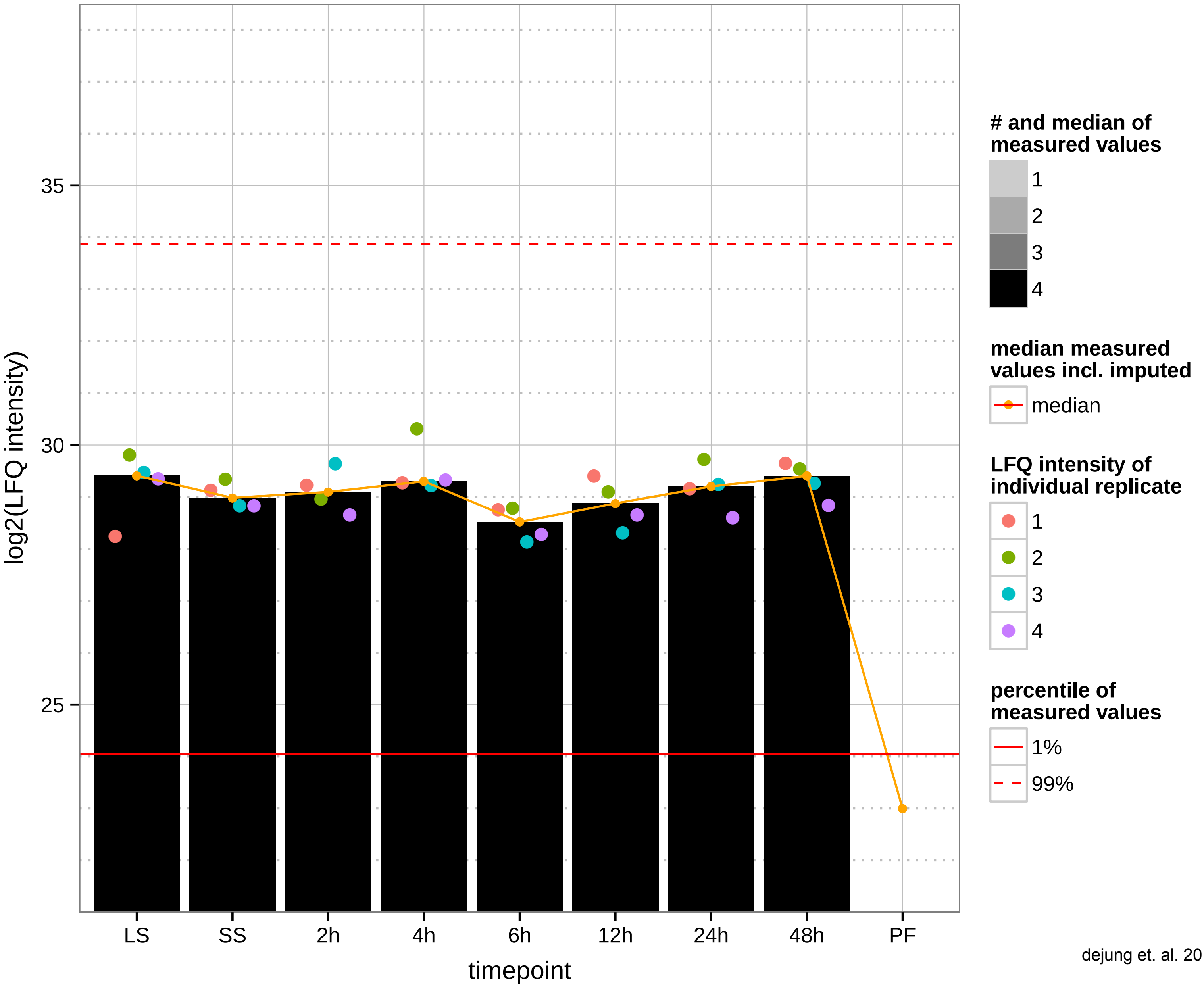
hypothetical protein, conserved
Tb927.6.1470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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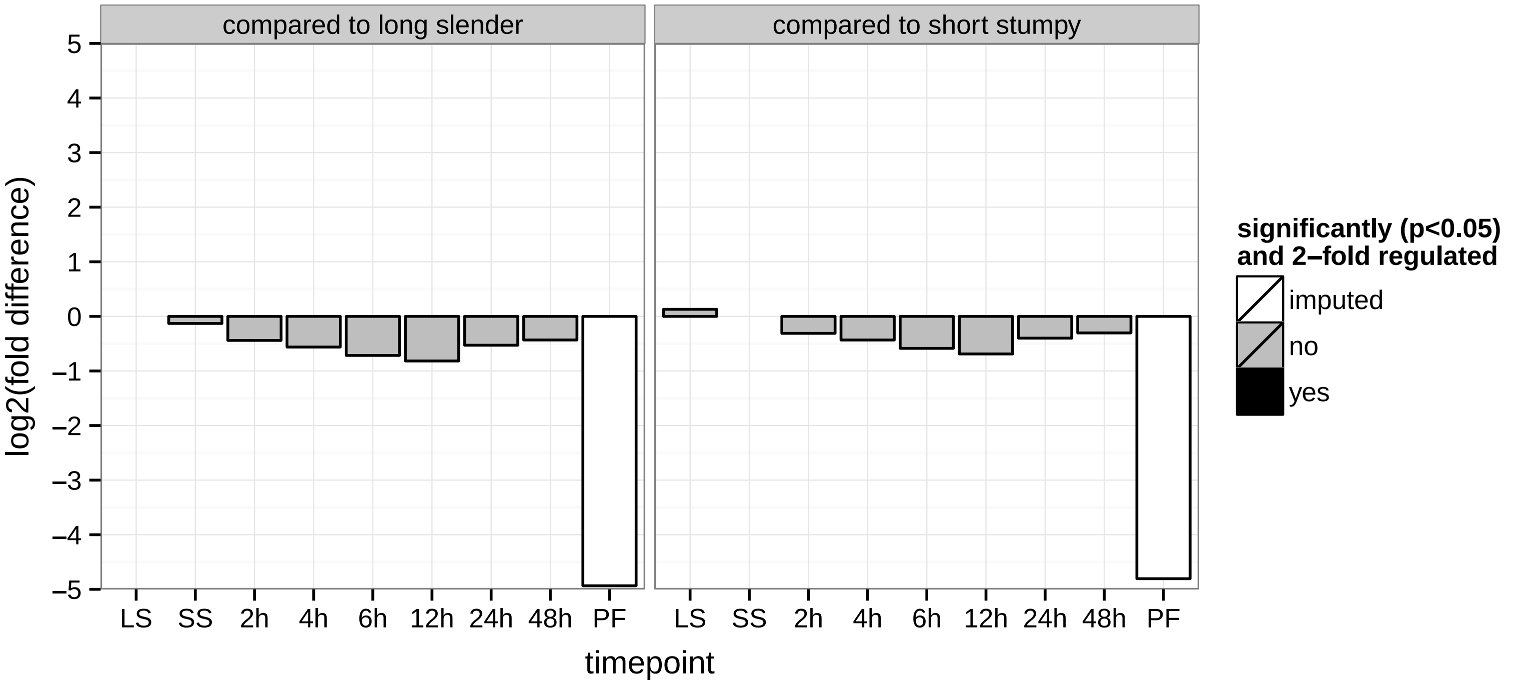
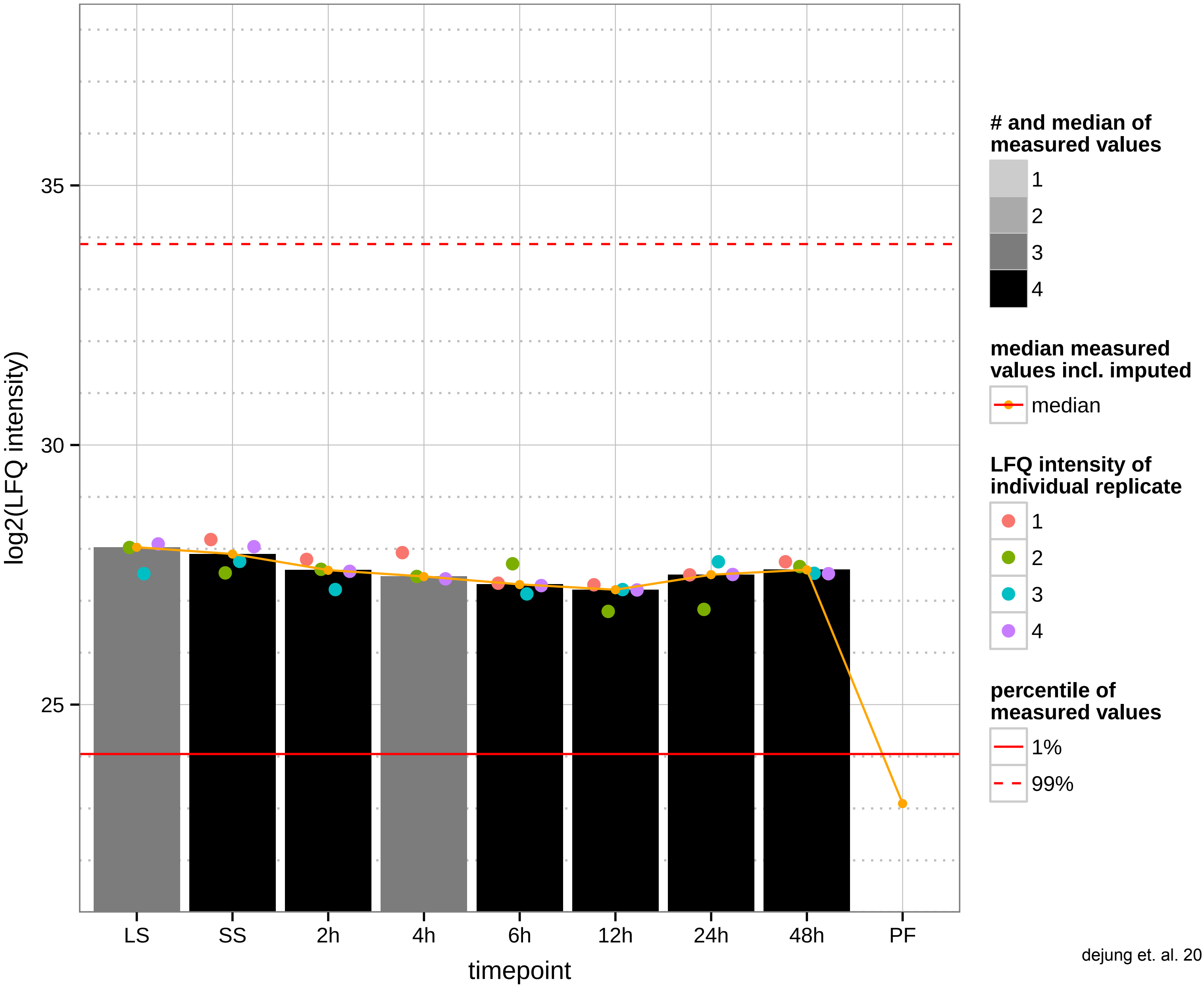
hypothetical protein, conserved
Tb927.6.1480
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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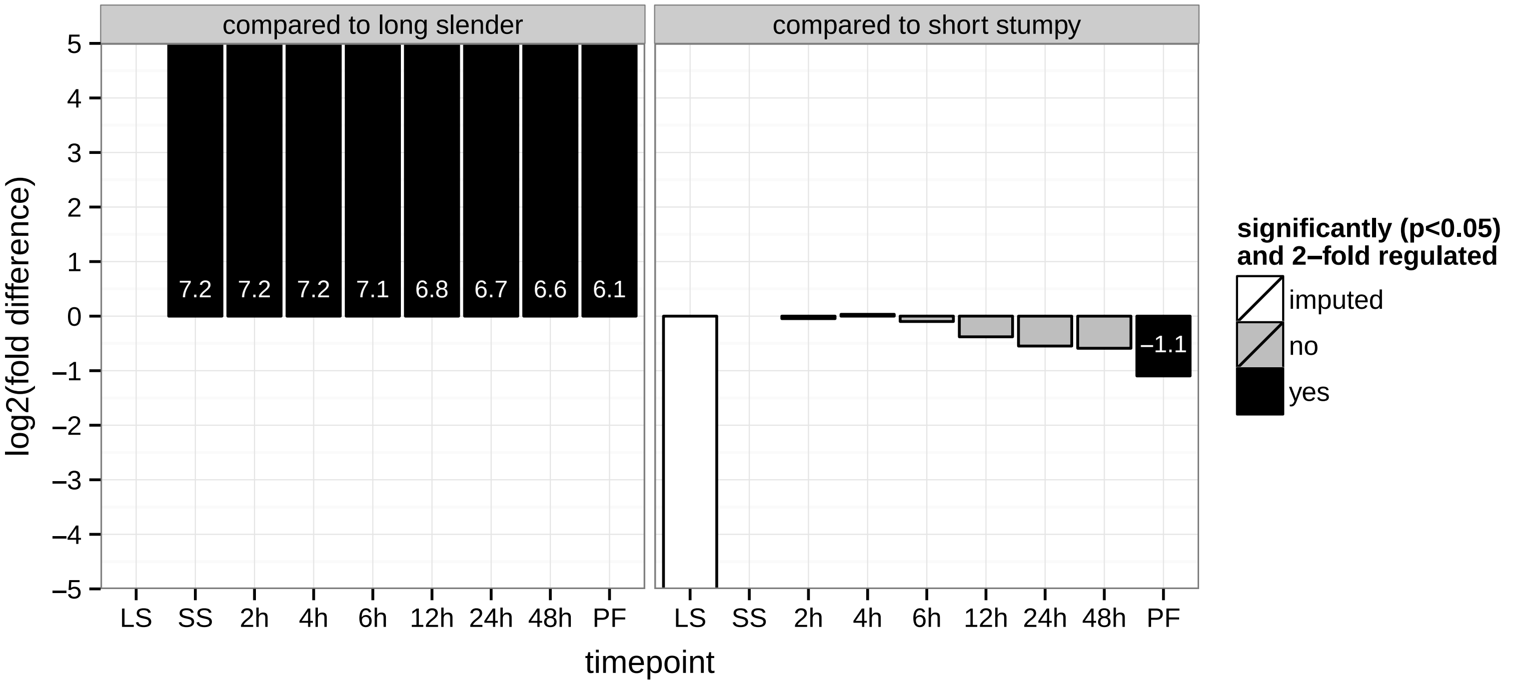
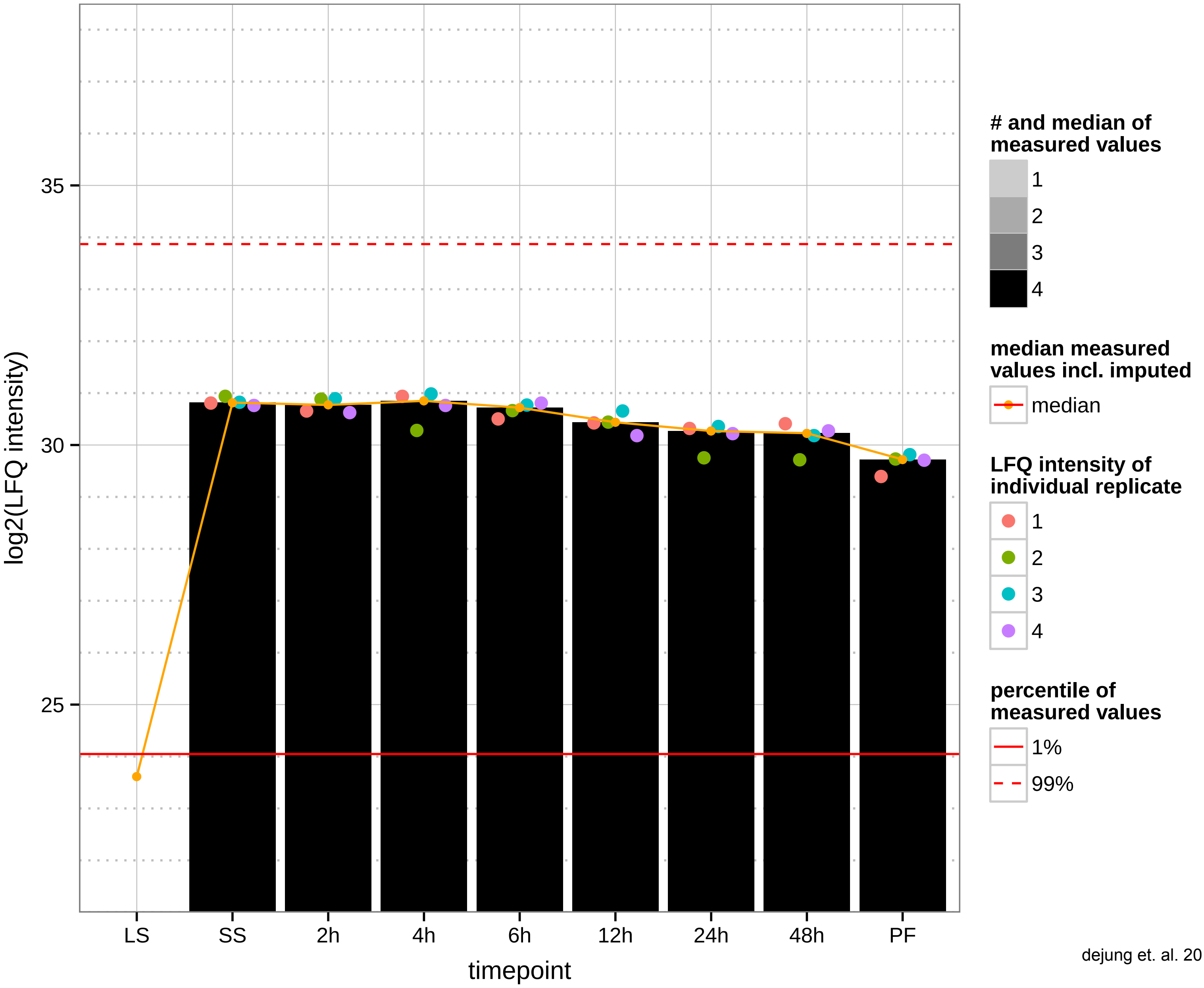
Aquaglyceroporin 1 (AQP1)
Tb927.6.1520
AGOF: drug transmembrane transporter activity, glycerol channel activity, water channel activity
AGOC: membrane
AGOP: detection of osmotic stimulus, drug transmembrane transport, glycerol transport, hypotonic response, response to dru
PGOF: transporter activity
PGOC: integral to membrane, membrane
PGOP: transmembrane transport, transport, water transport





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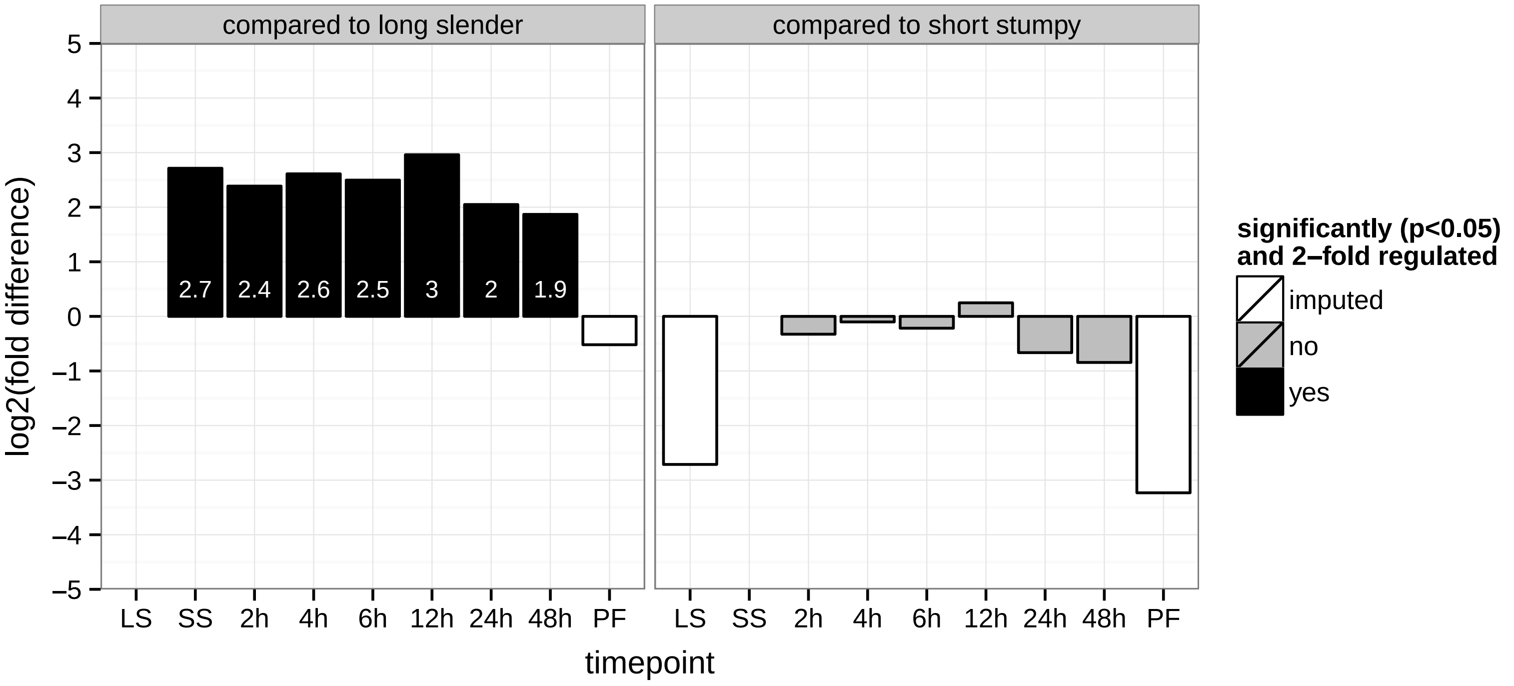
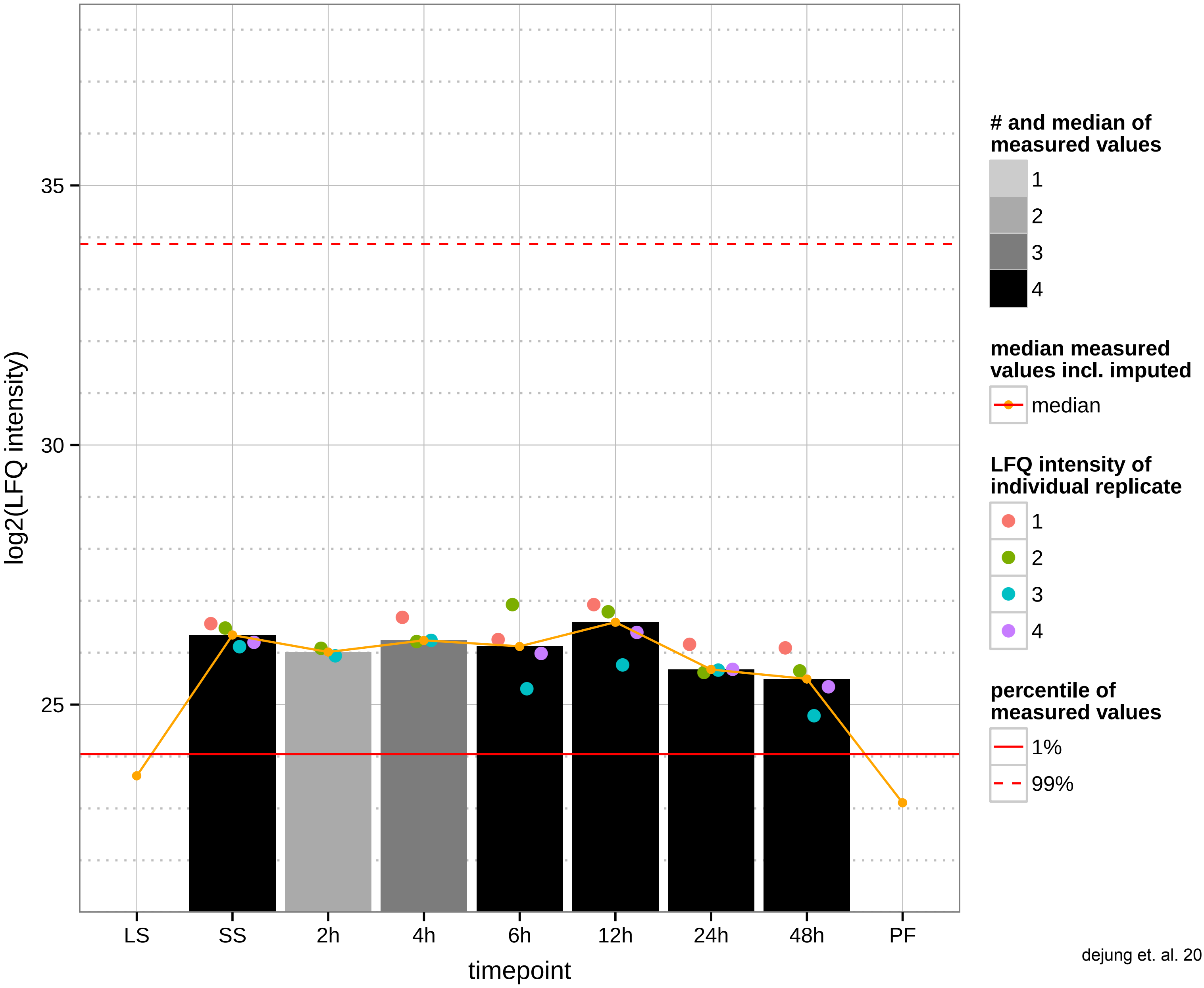
hypothetical protein, conserved
Tb927.6.1540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: membrane
PGOP: null





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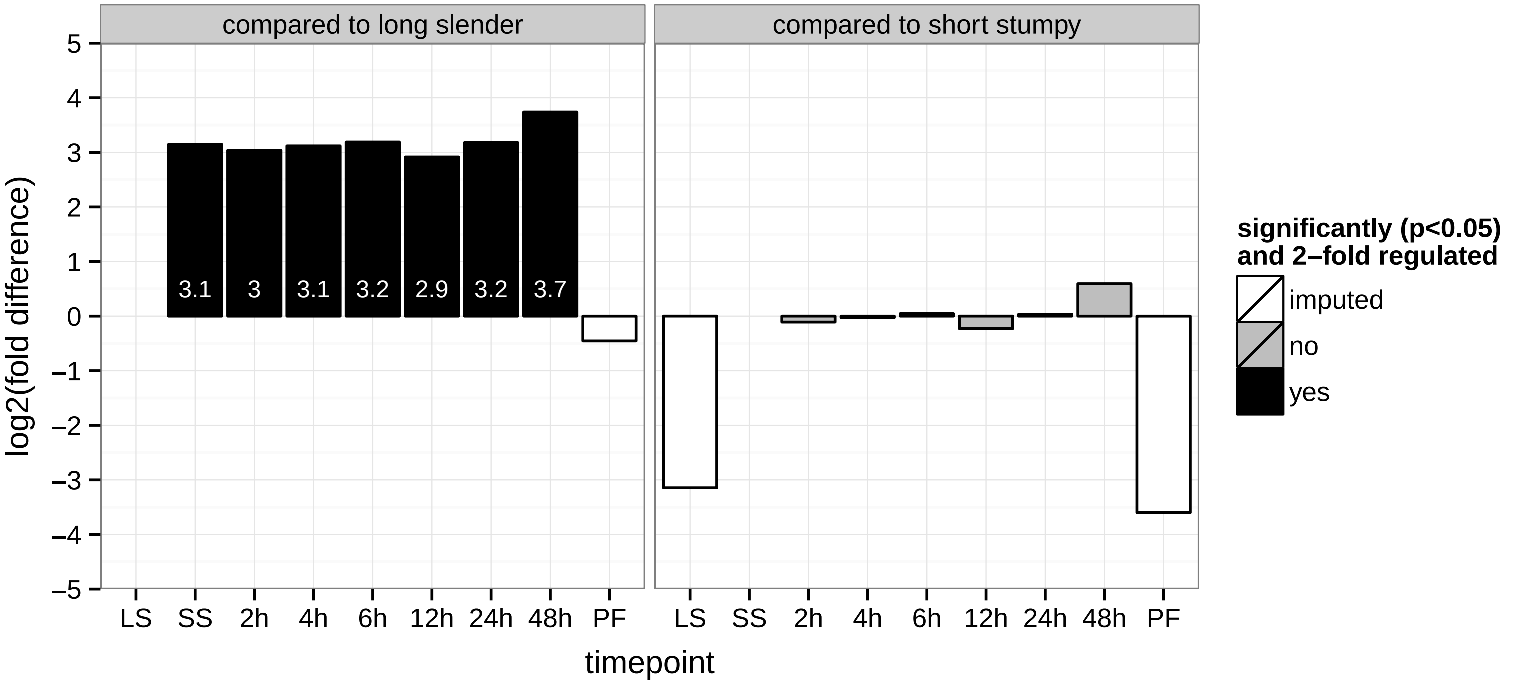
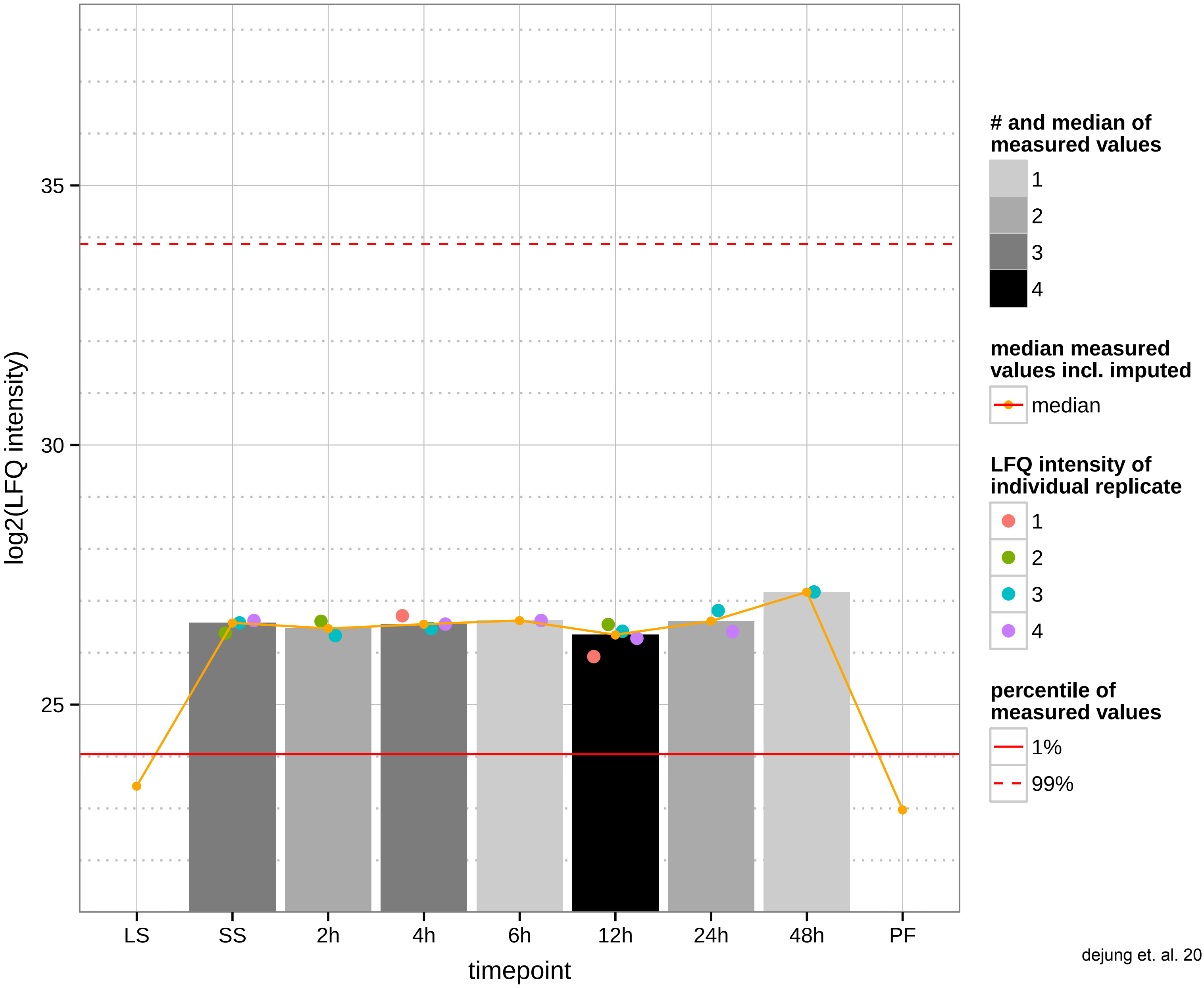
leucine–rich repeat protein (LRRP), putative
Tb927.6.1550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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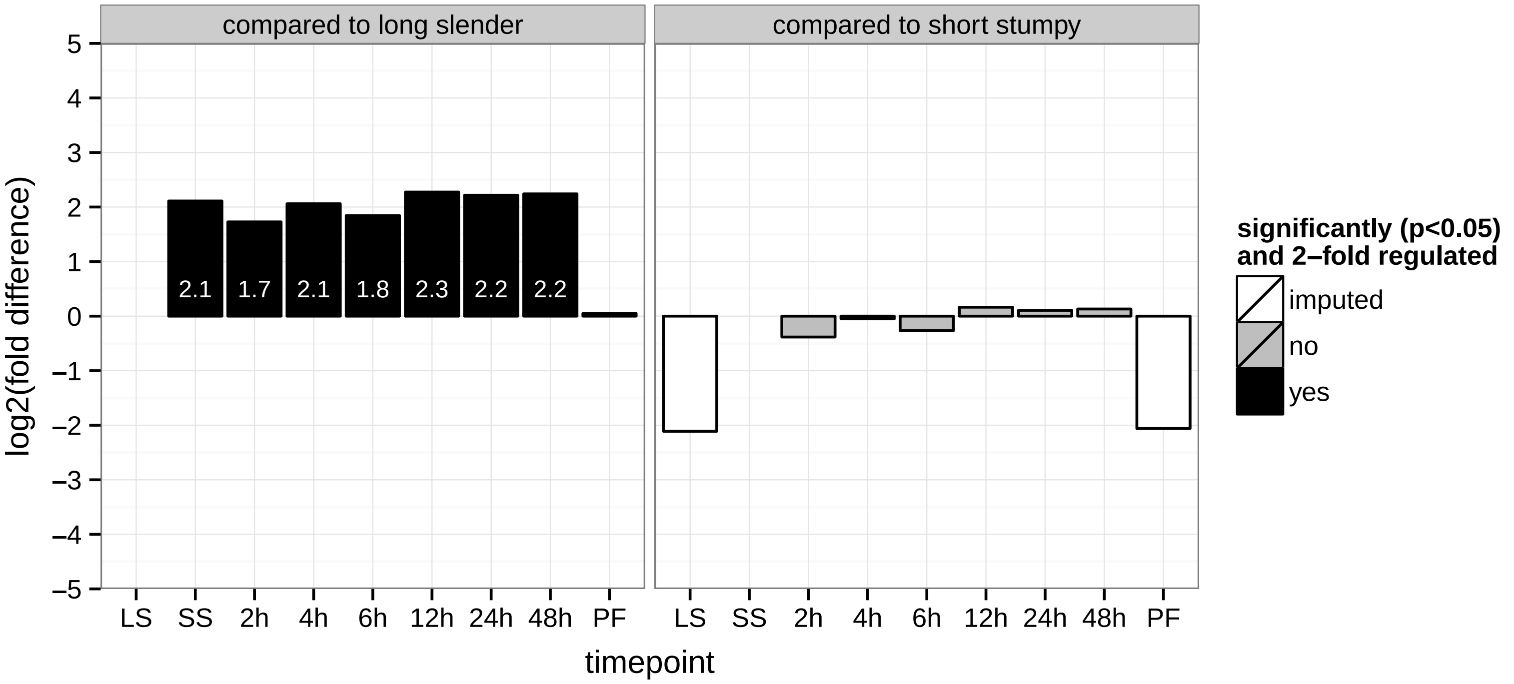
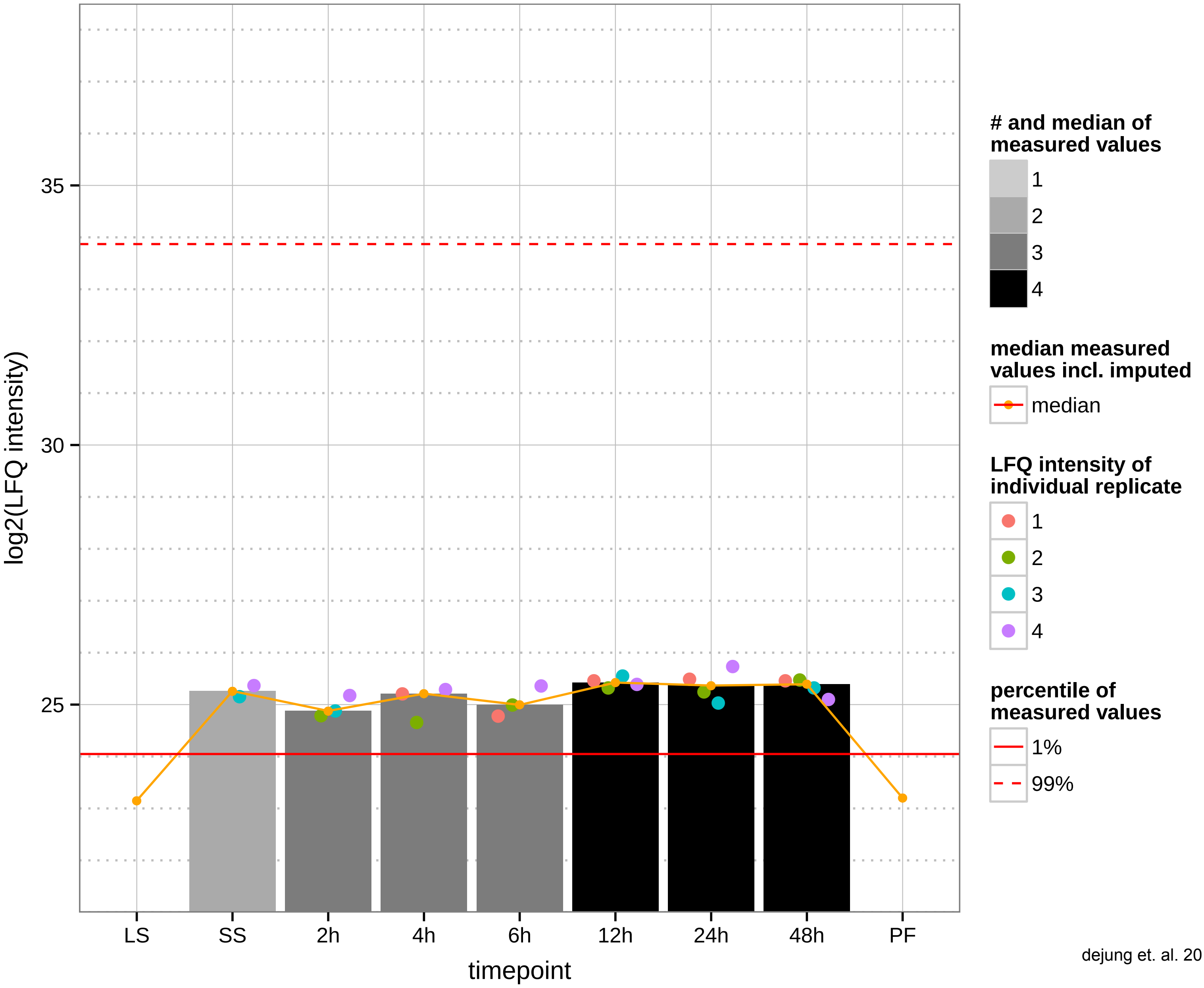
polynucleotide kinase 3'−phosphatase, putative
Tb927.6.1580
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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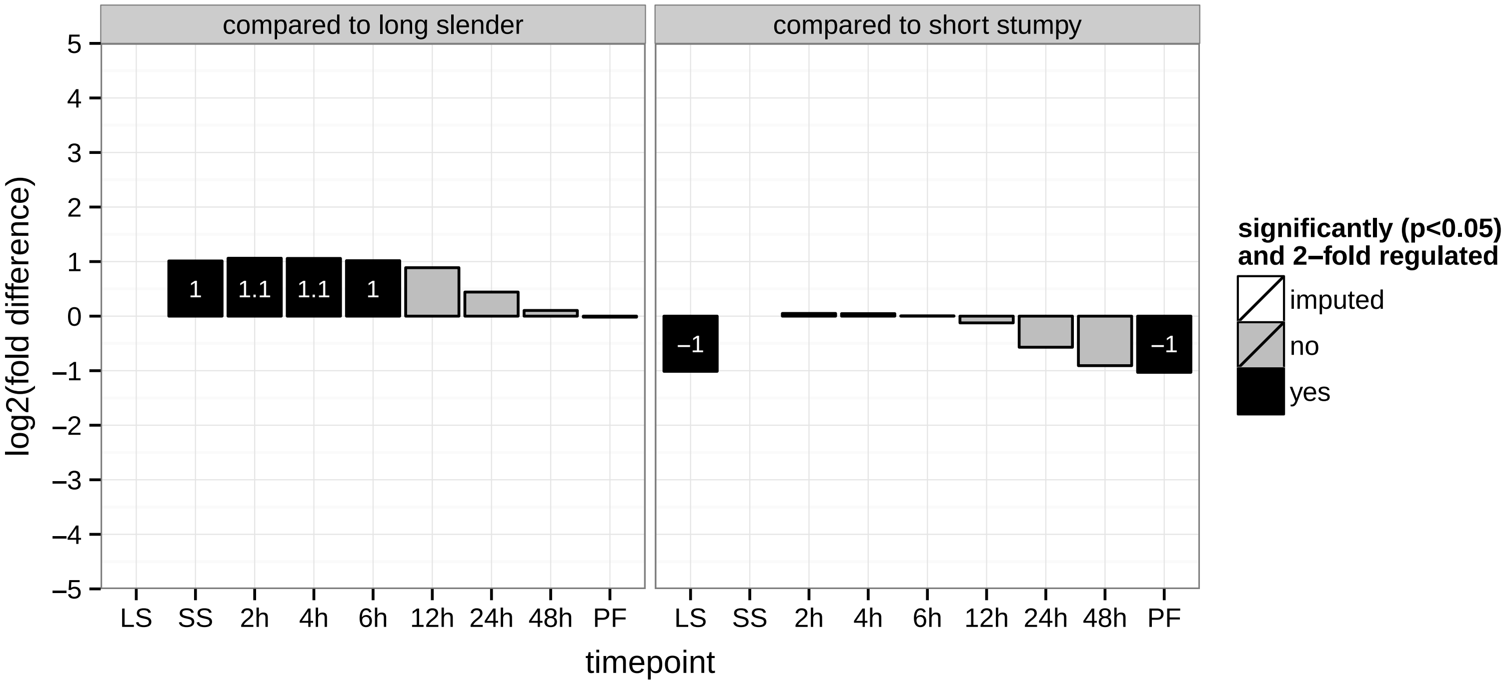
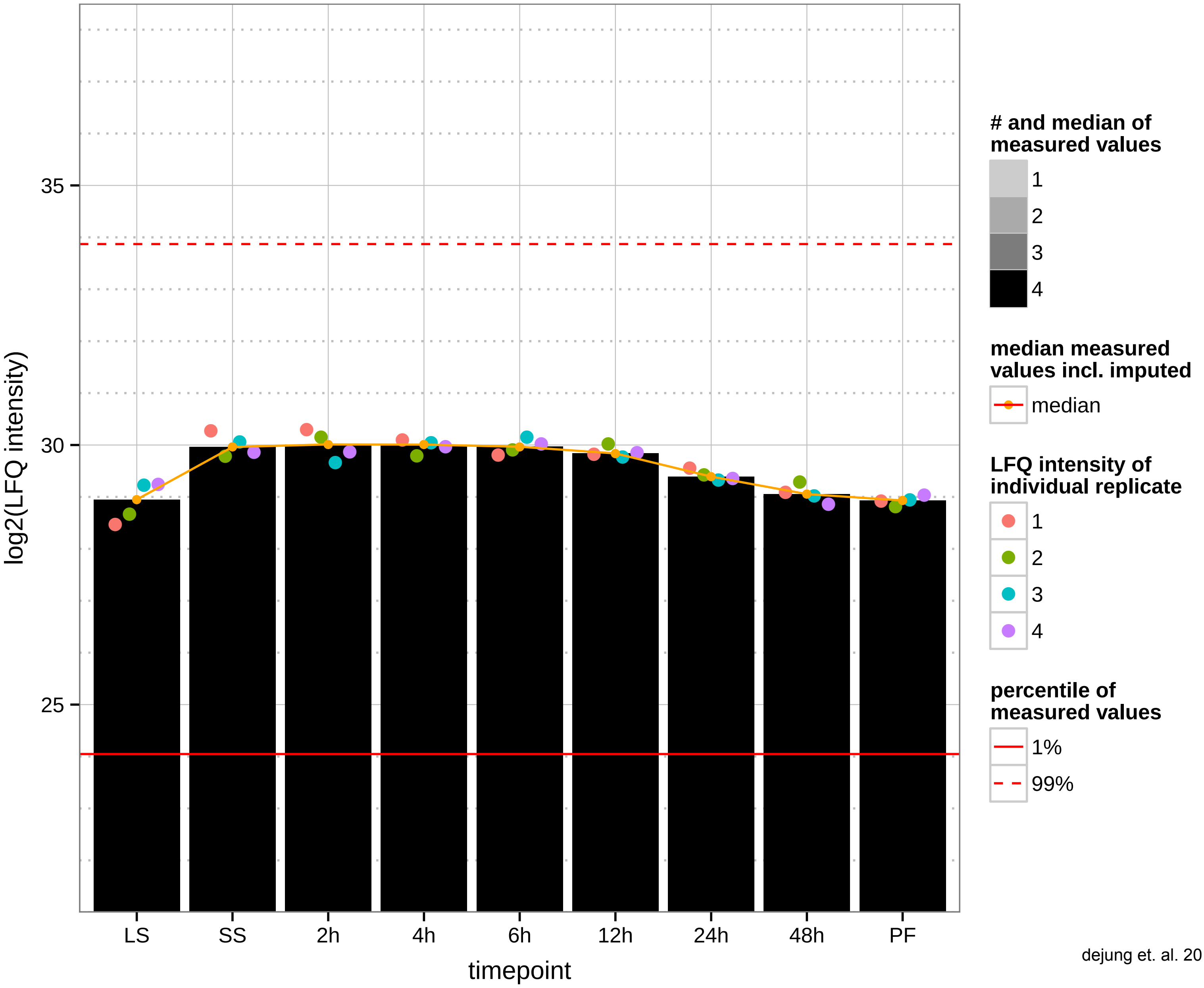
kinesin, putative
Tb927.6.1770
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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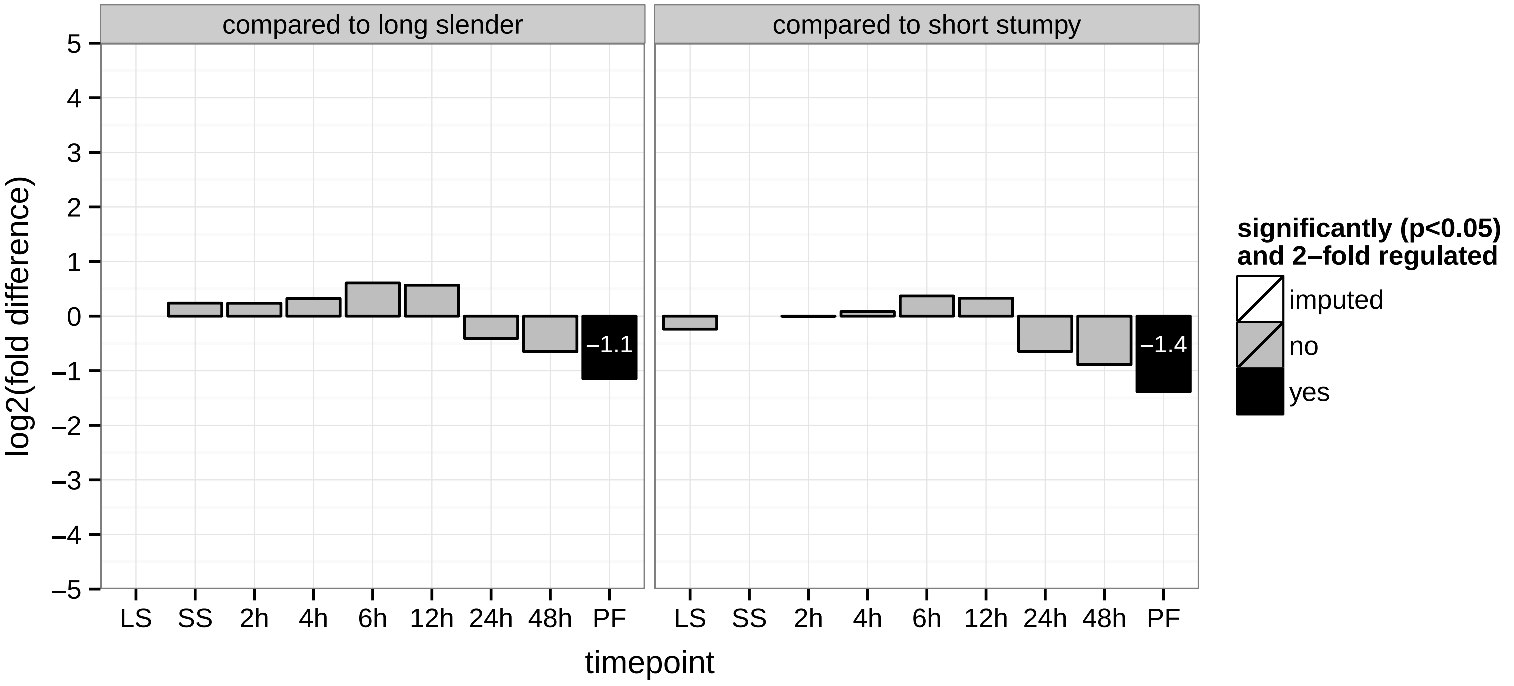
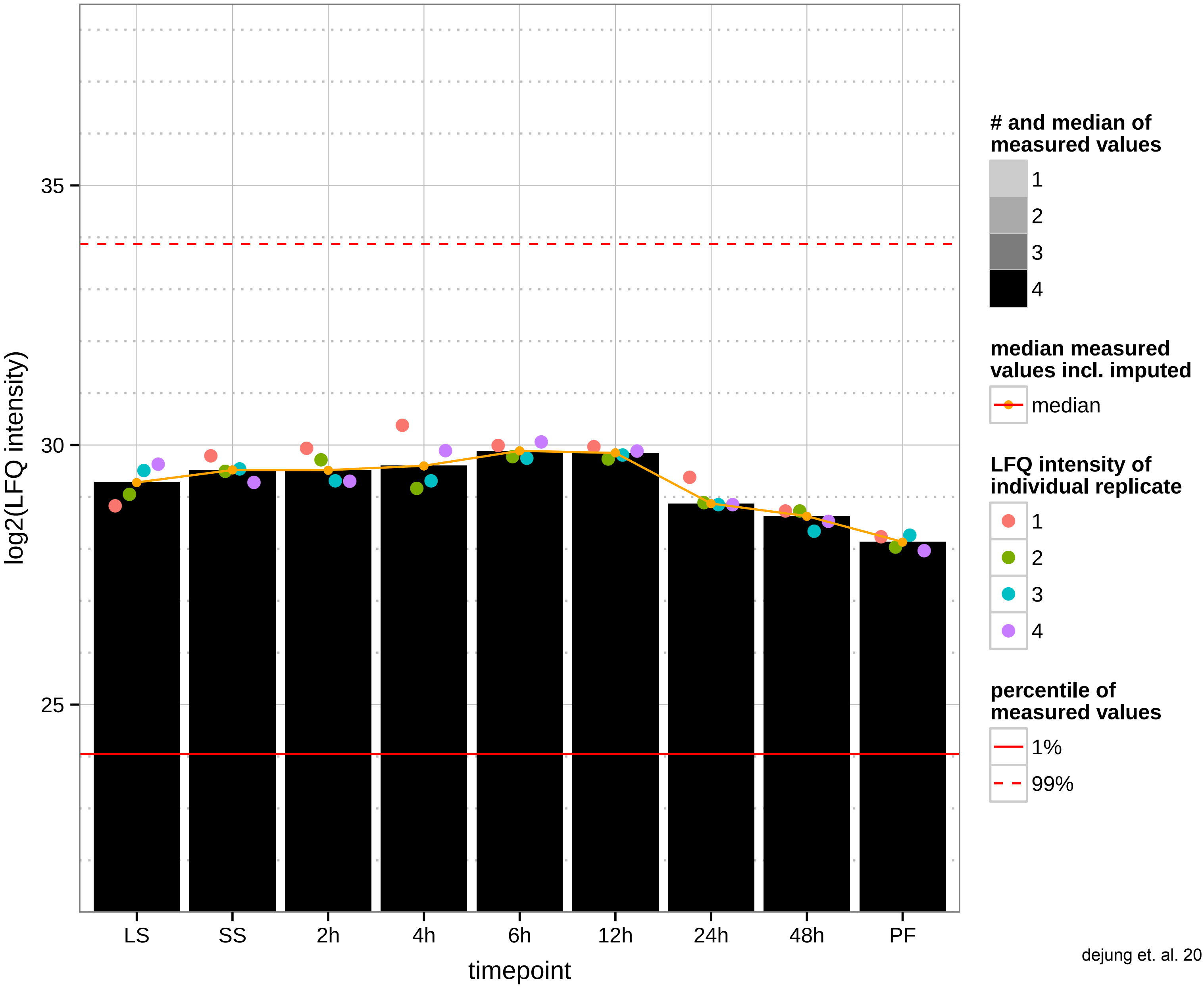
protein phosphatase 2C, putative
Tb927.6.1800
AGOF: phosphatase activity
AGOC: null
AGOP: dephosphorylation
PGOF: catalytic activity
PGOC: null
PGOP: null





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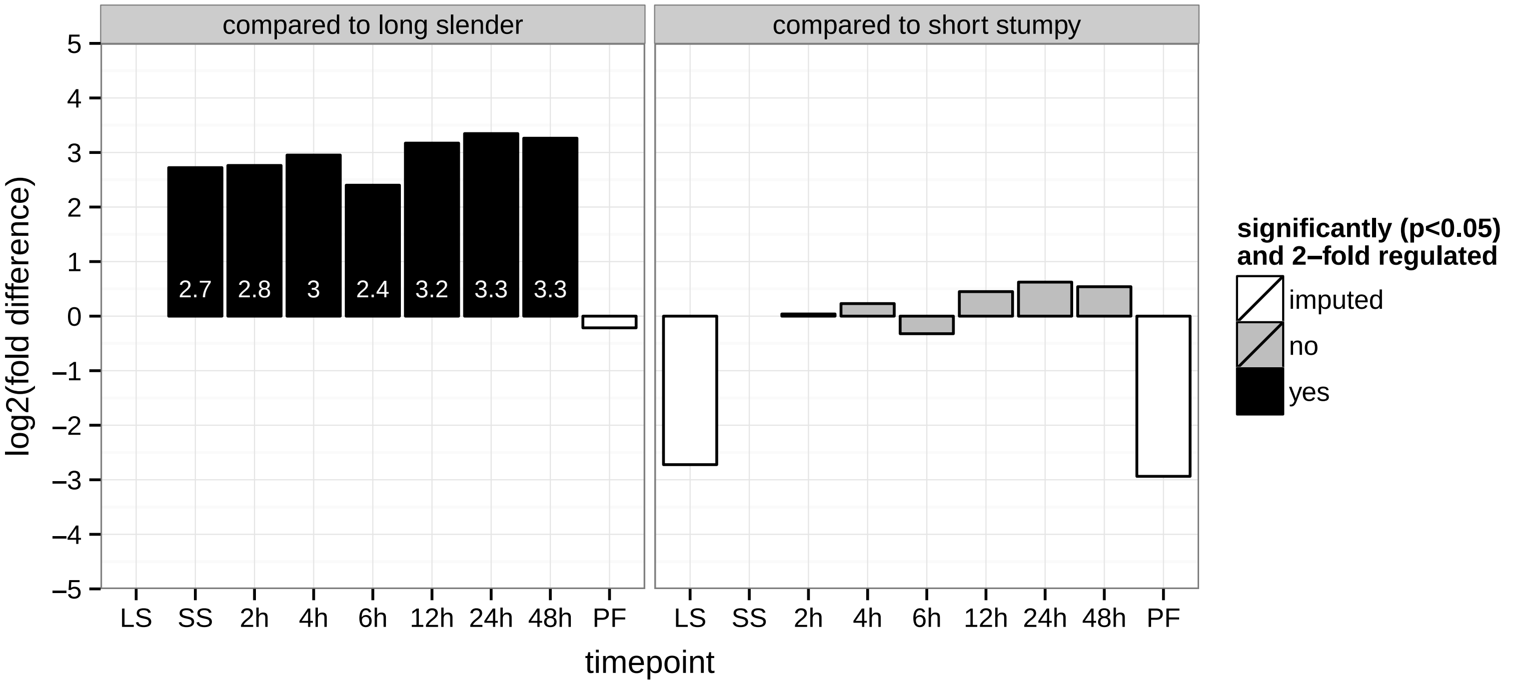
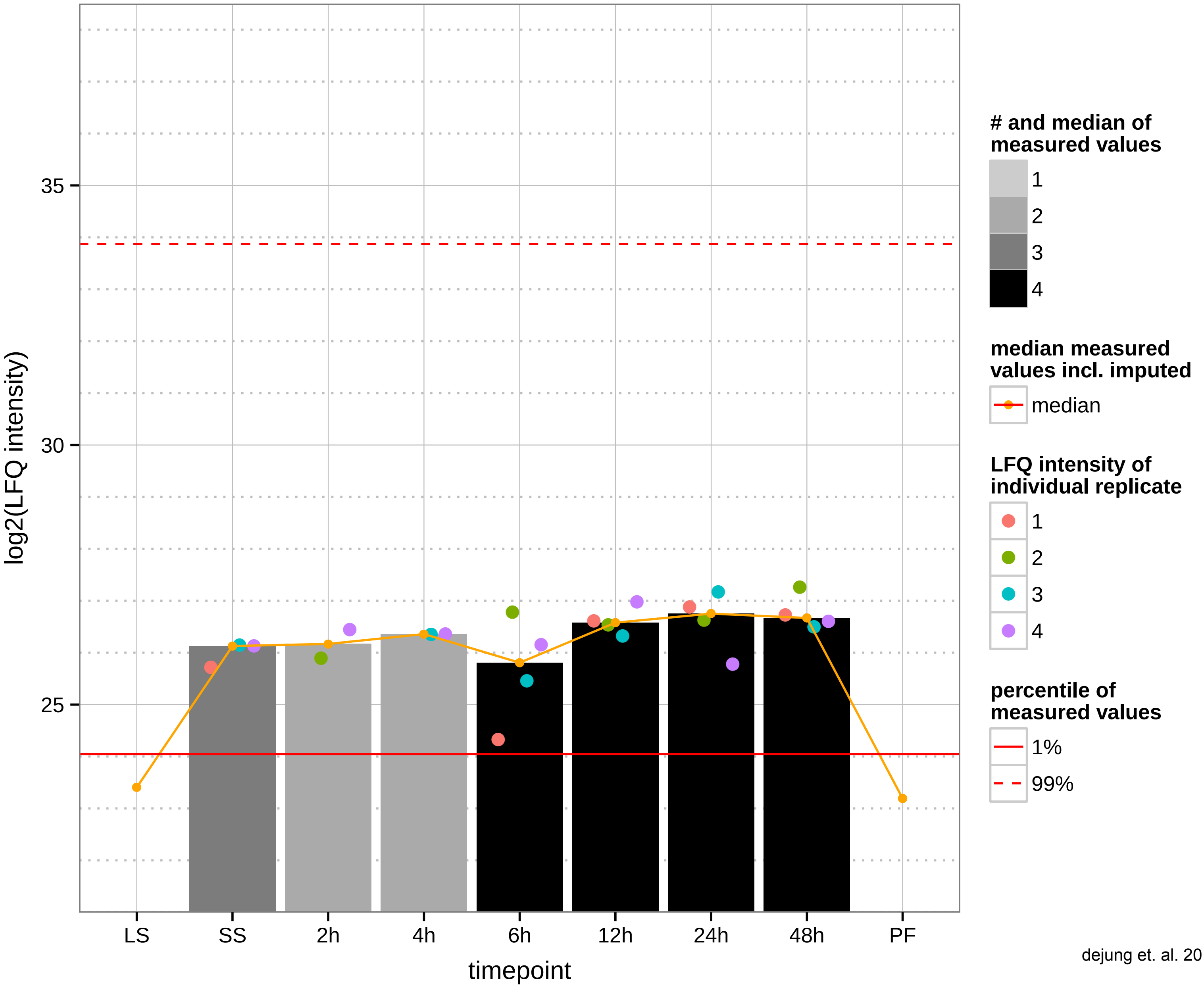
hypothetical protein, conserved
Tb927.6.2510
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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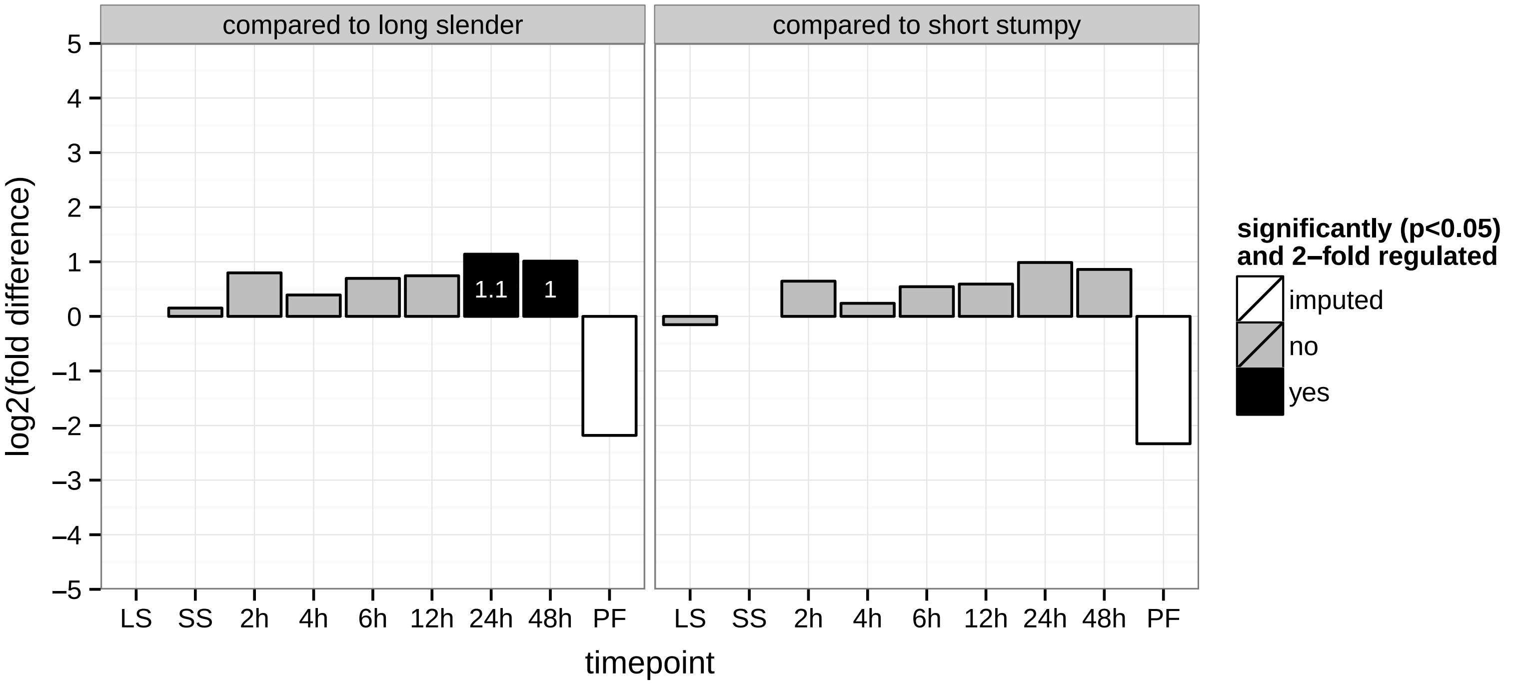
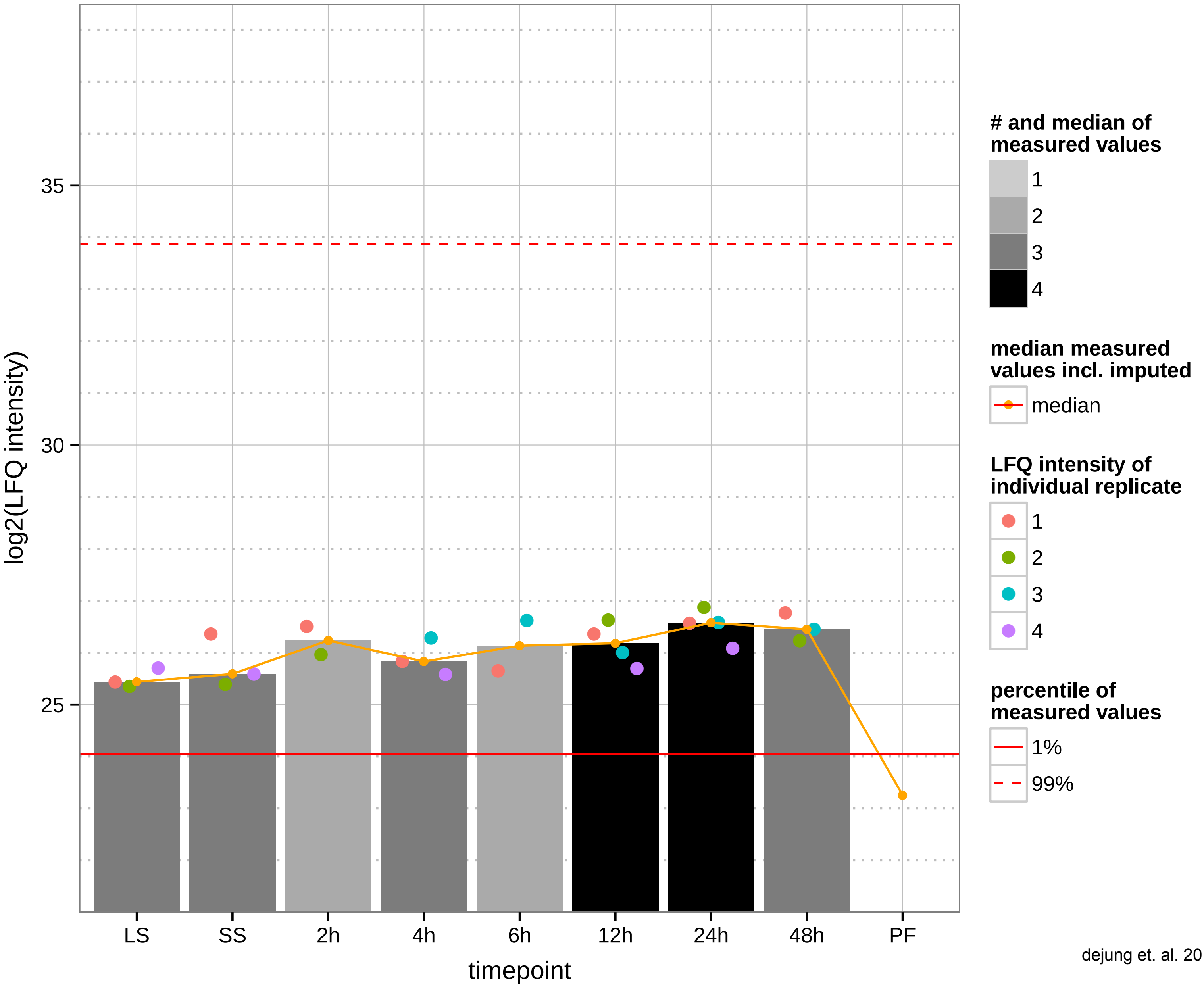
hypothetical protein, conserved
Tb927.6.2600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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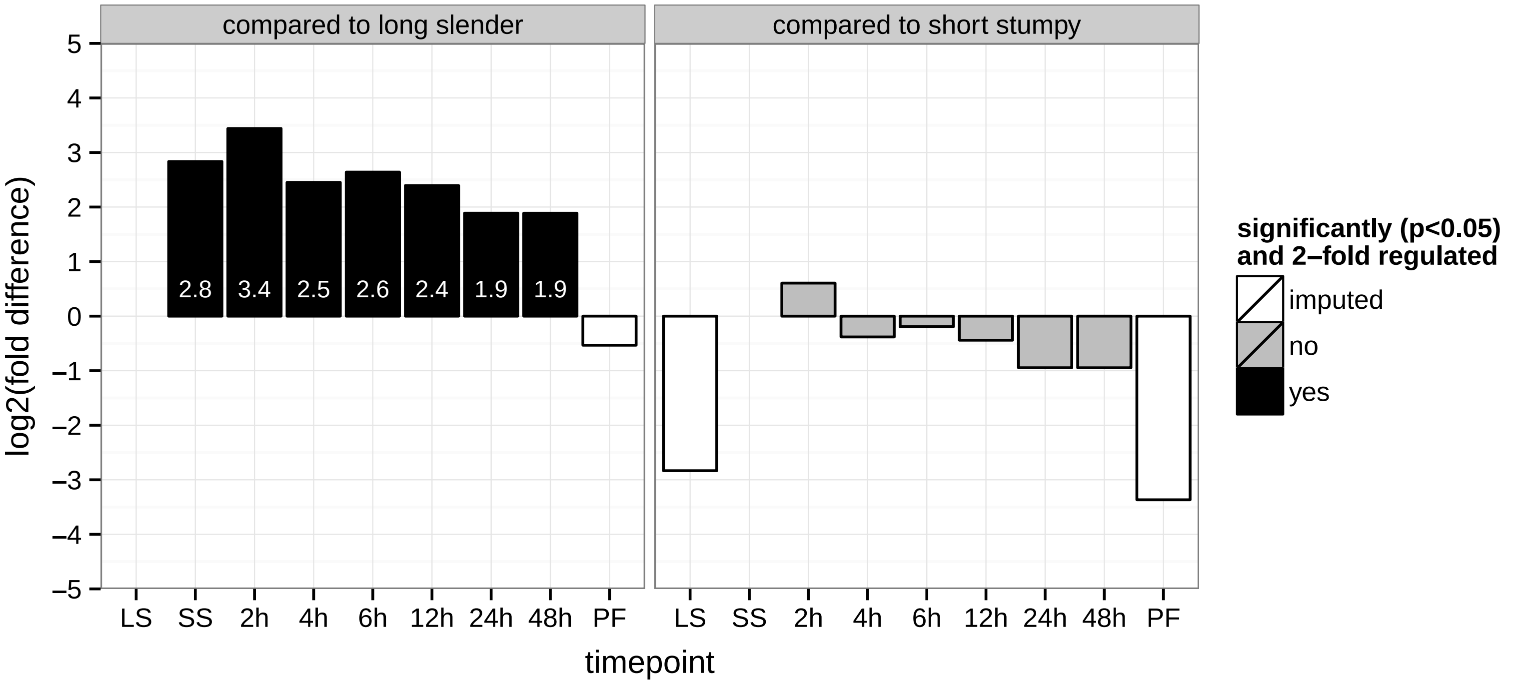
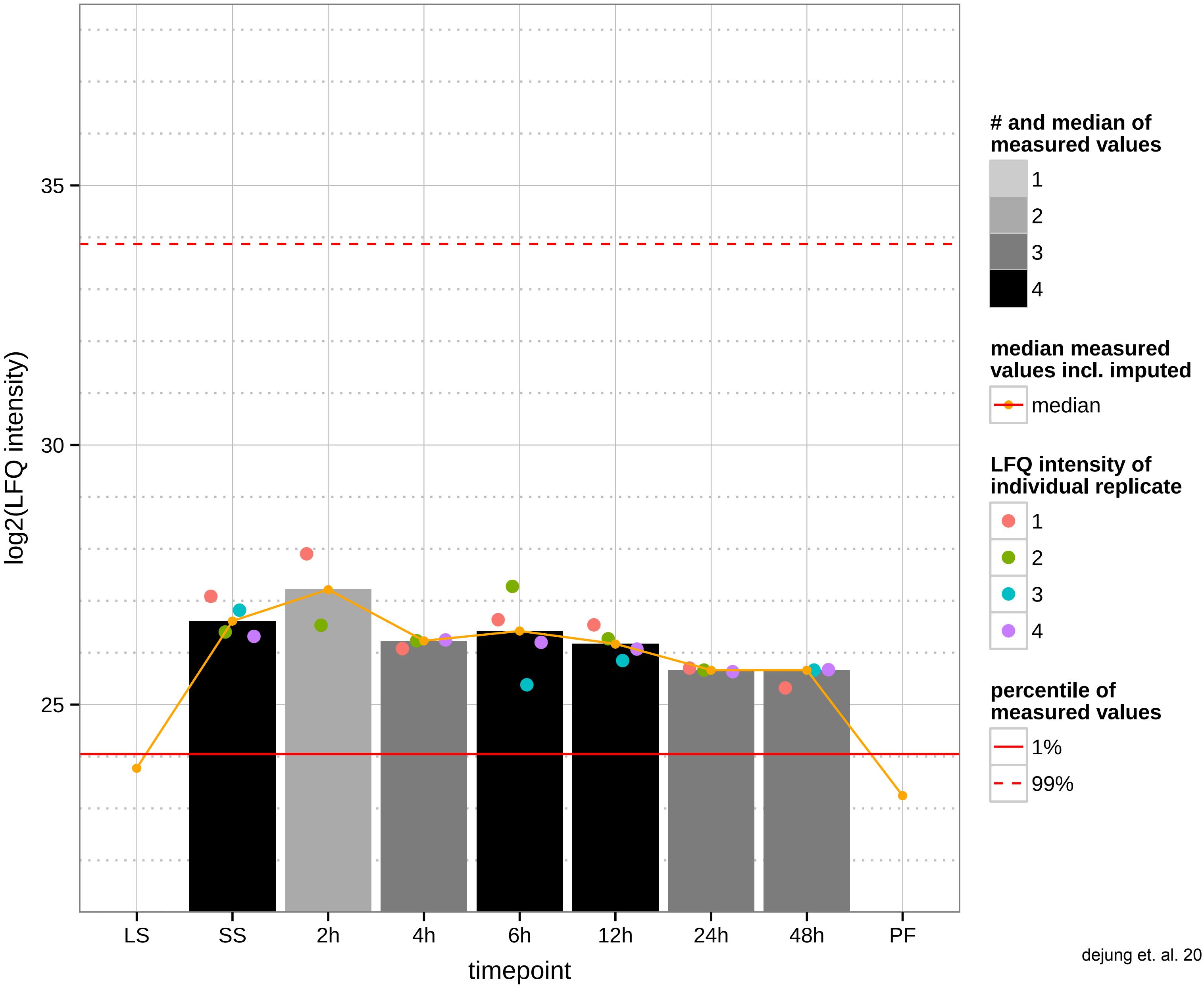
GTPase activating protein, conserved
Tb927.6.2830
AGOF: Rab GTPase activator activity
AGOC: intracellular
AGOP: regulation of Rab GTPase activity
PGOF: Rab GTPase activator activity
PGOC: intracellular
PGOP: regulation of Rab GTPase activity





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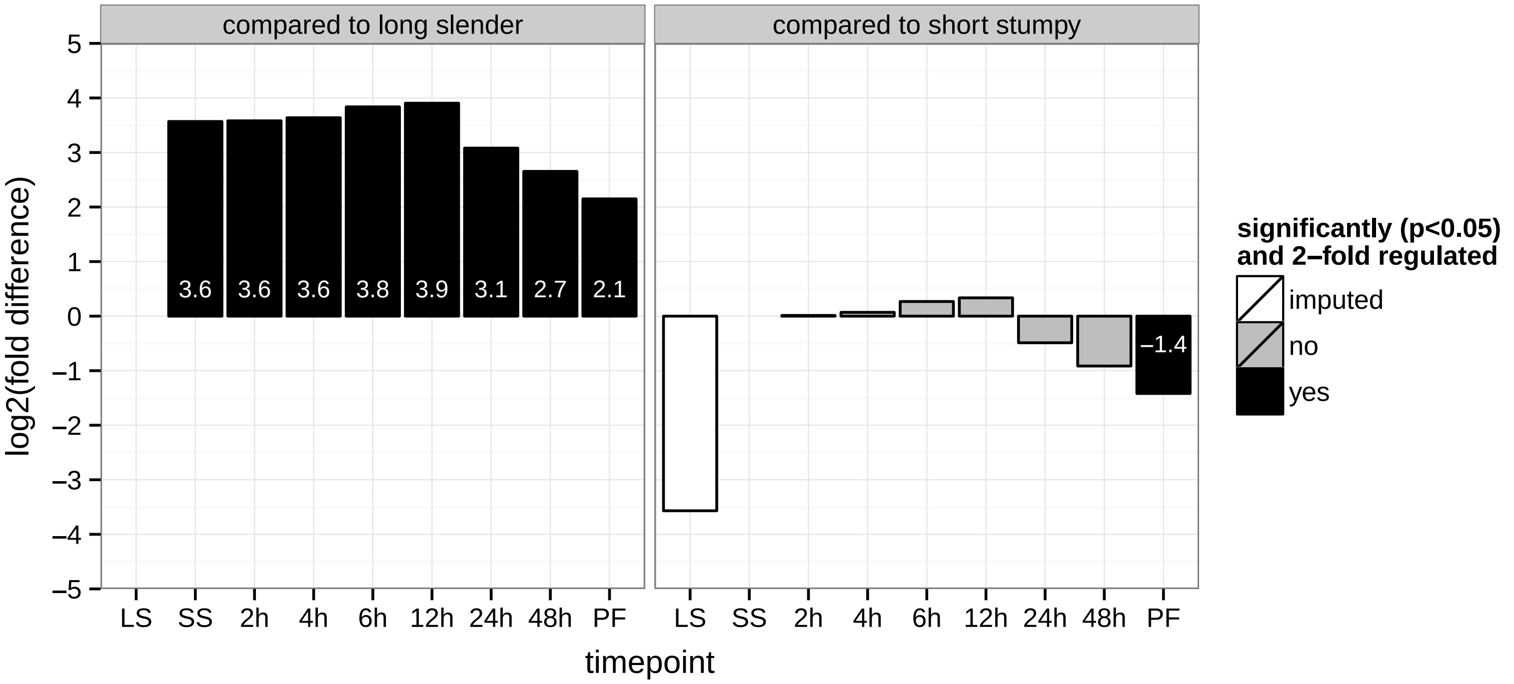
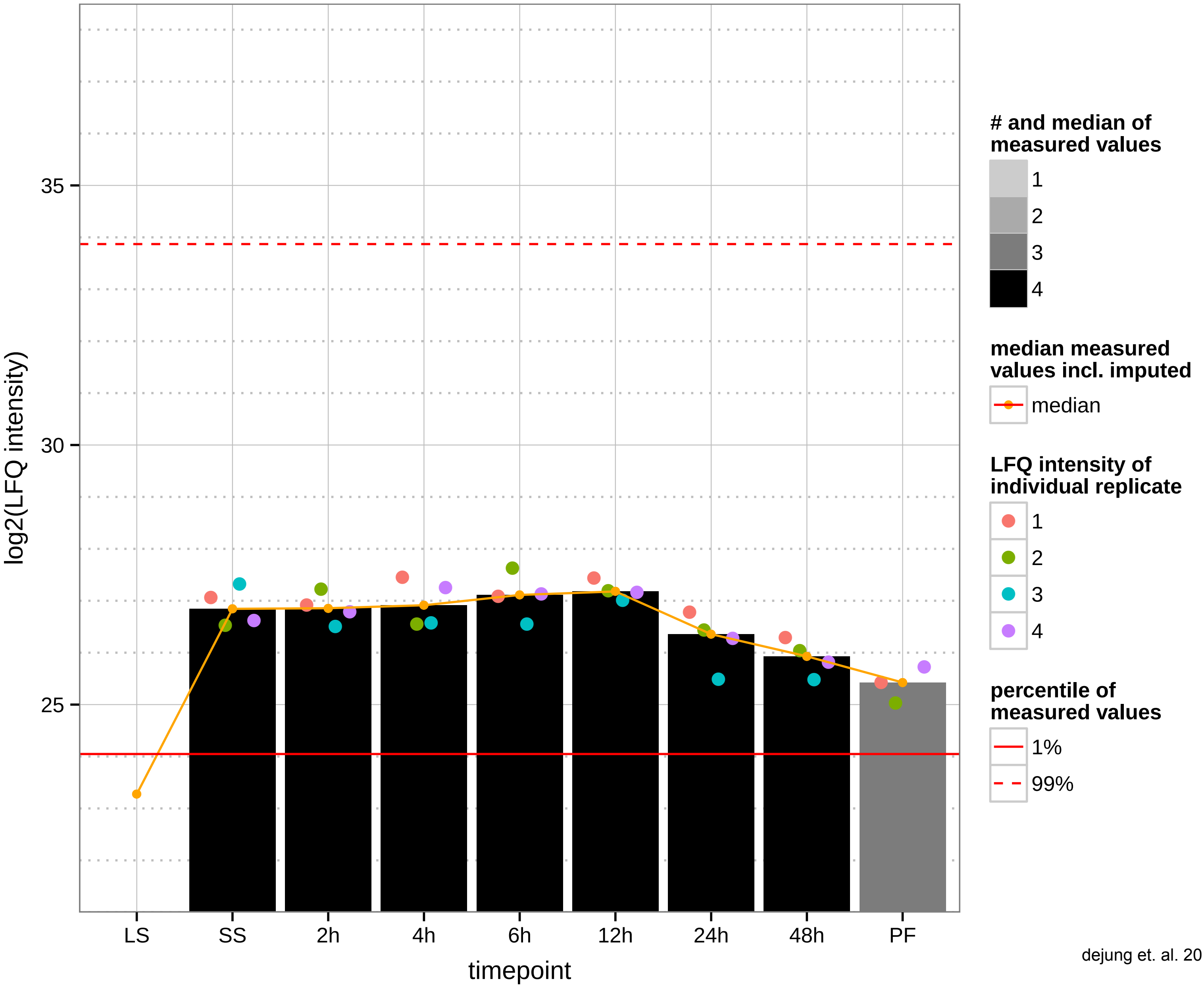
hypothetical protein, conserved
Tb927.6.2930
AGOF: ATP binding, nucleoside−triphosphatase activity
AGOC: null
AGOP: null
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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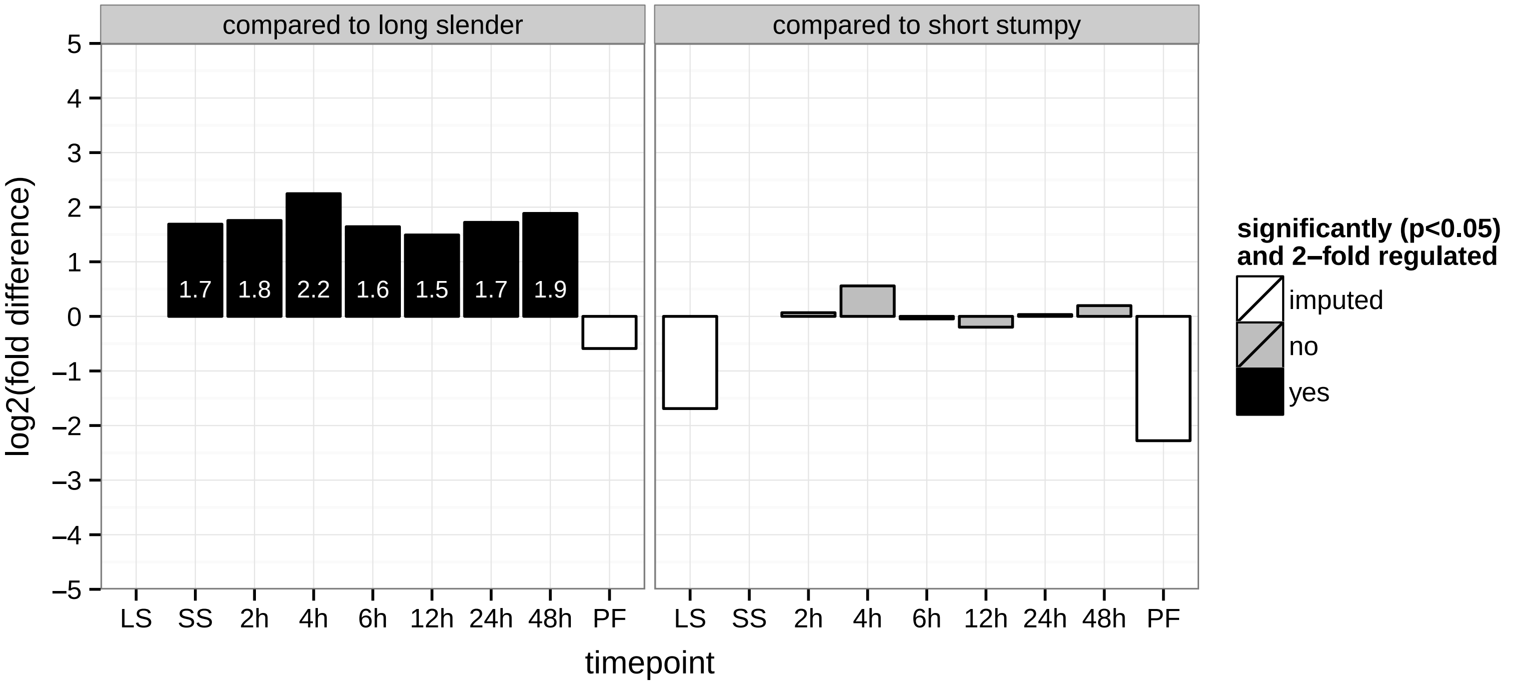
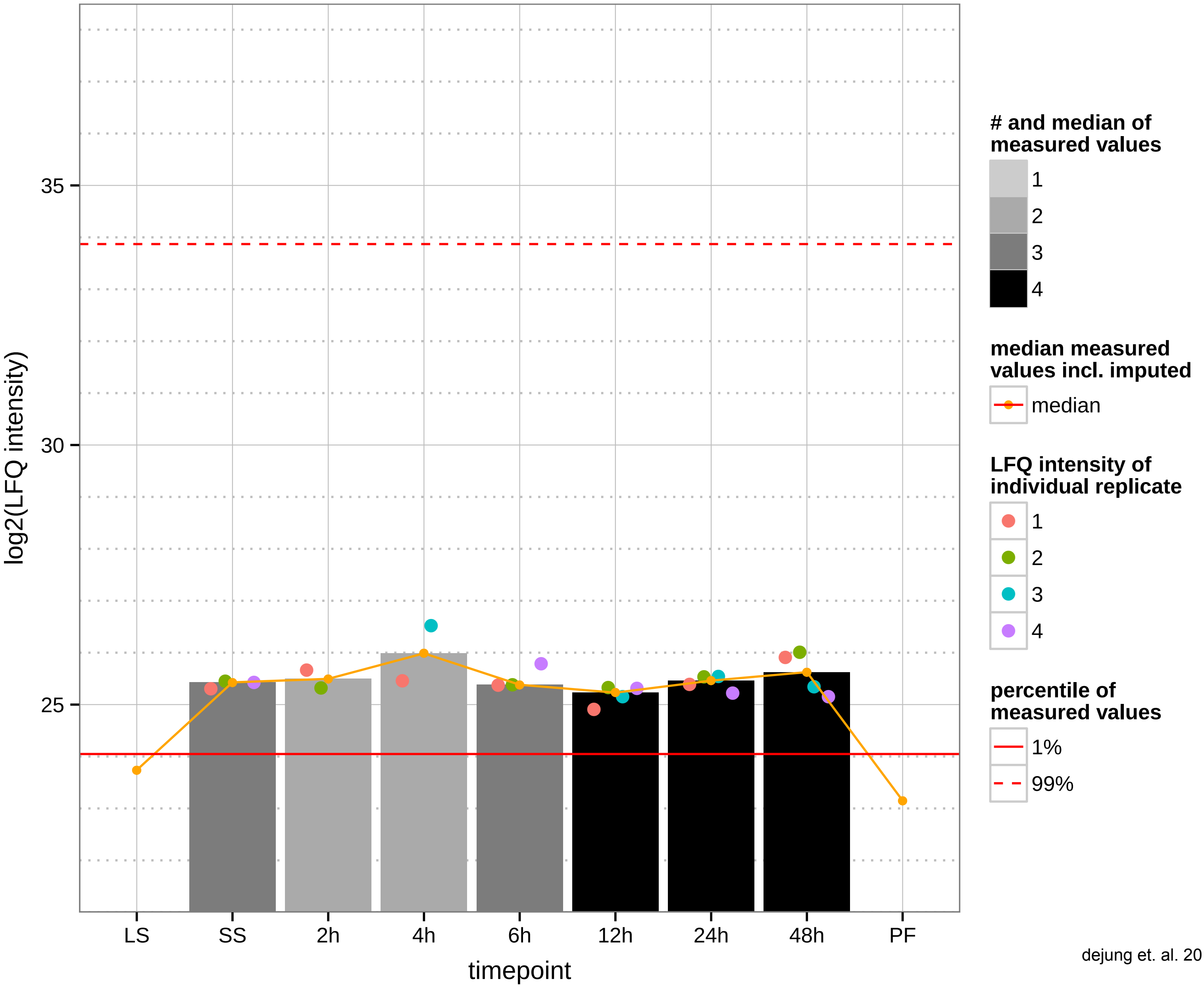
protein kinase, putative, cdc2–related kinase, putative (CRK11)
Tb927.6.3110
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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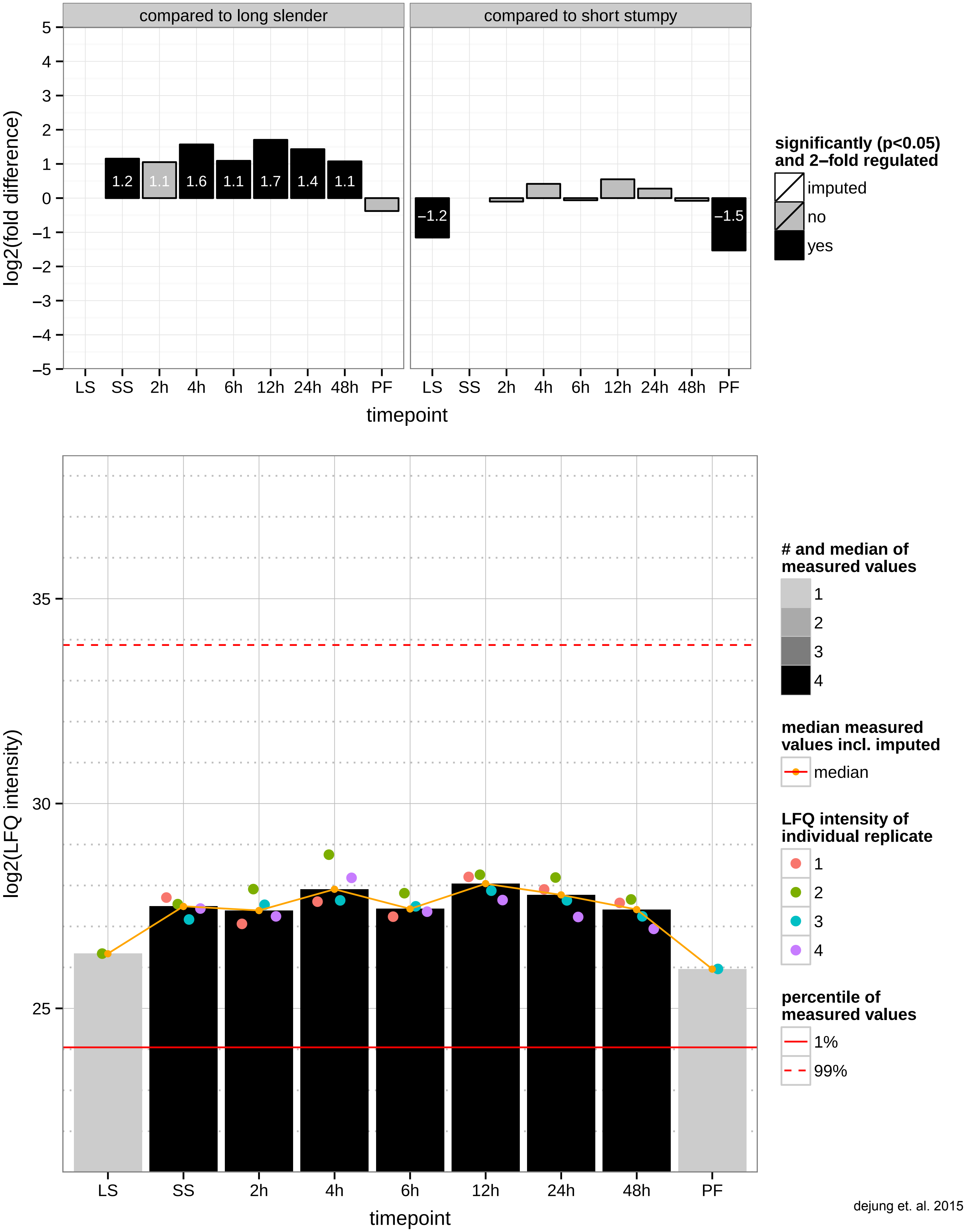
hypothetical protein, conserved
Tb927.6.3140
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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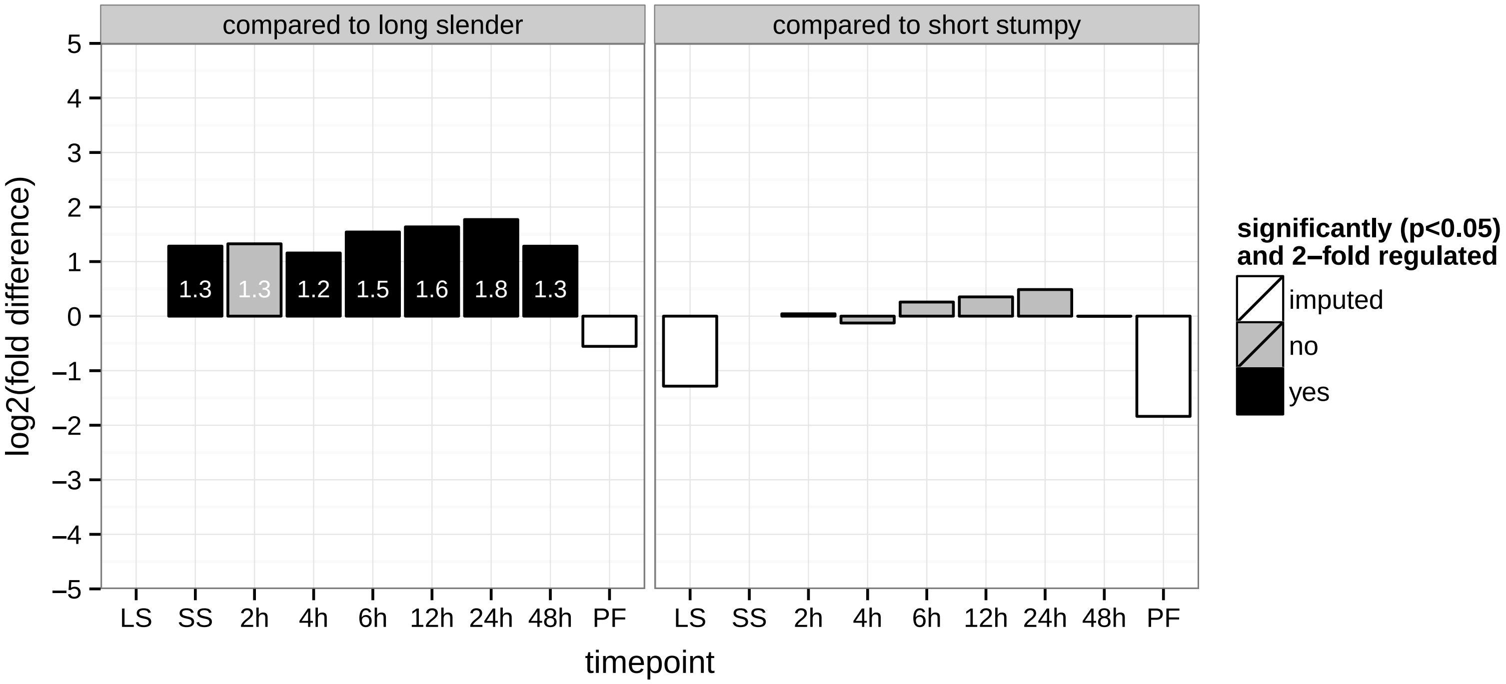
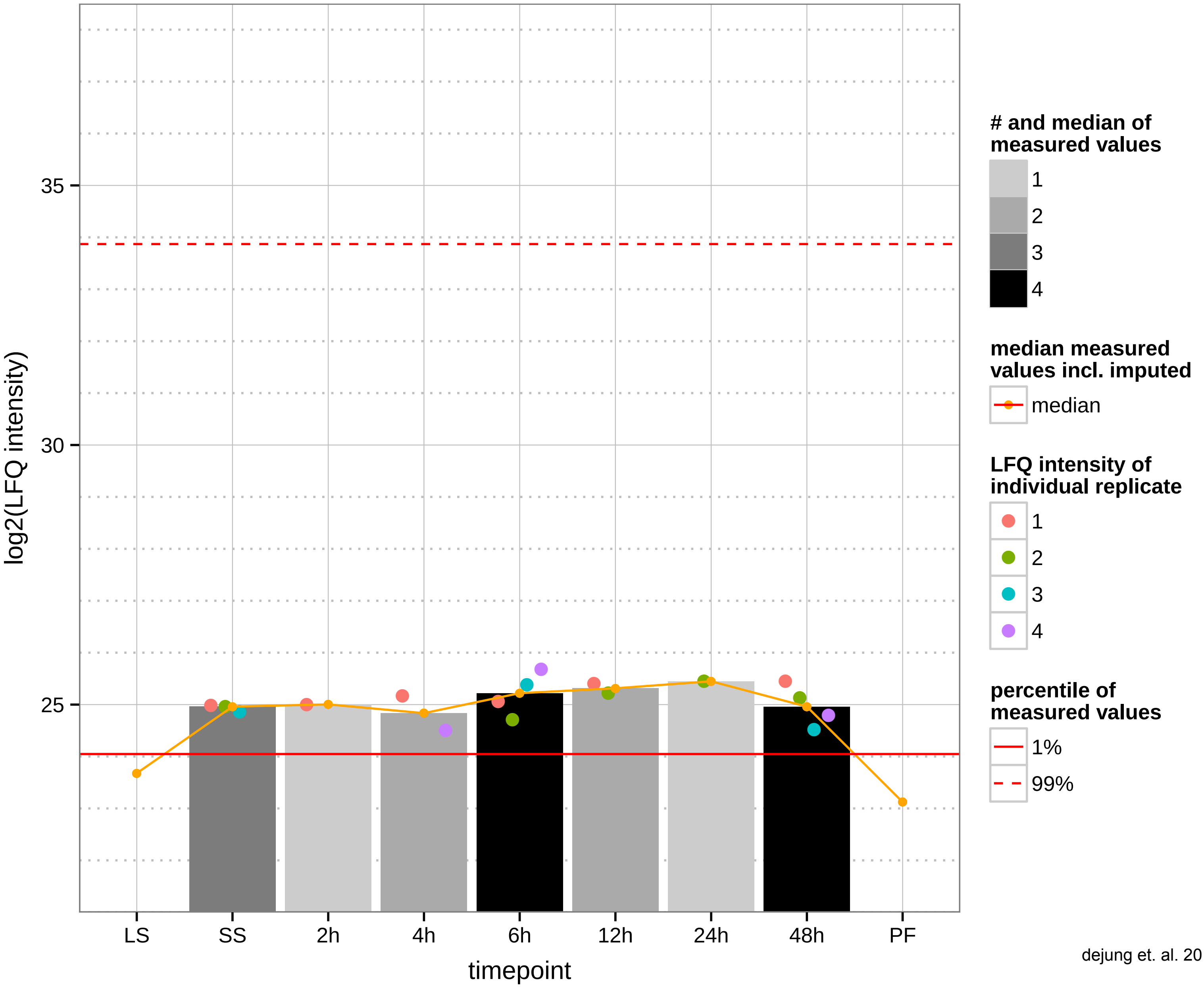
valosin–containing protein homolog, putative, AAA ATPase
Tb927.6.3790
AGOF: ATP binding, nucleoside–triphosphatase activity
AGOC: null
AGOP: null
PGOF: ATP binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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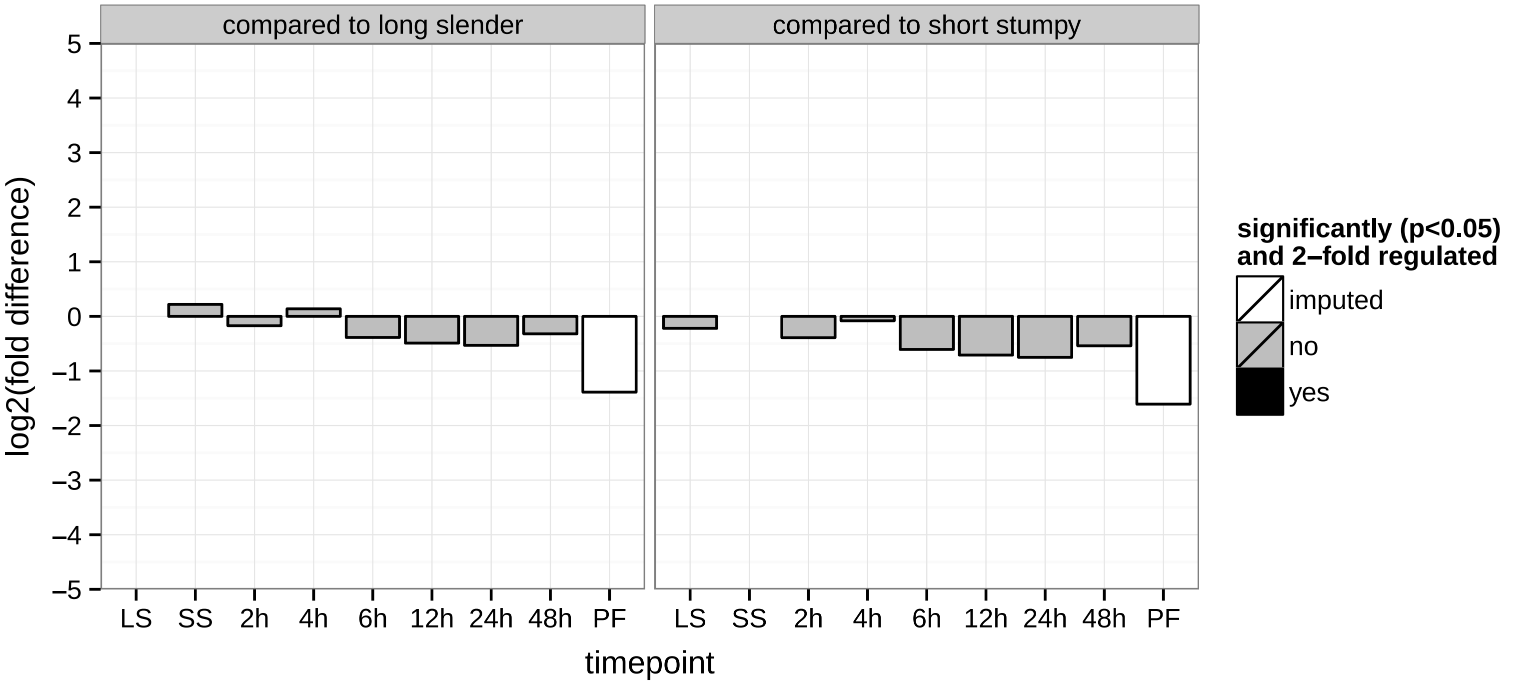
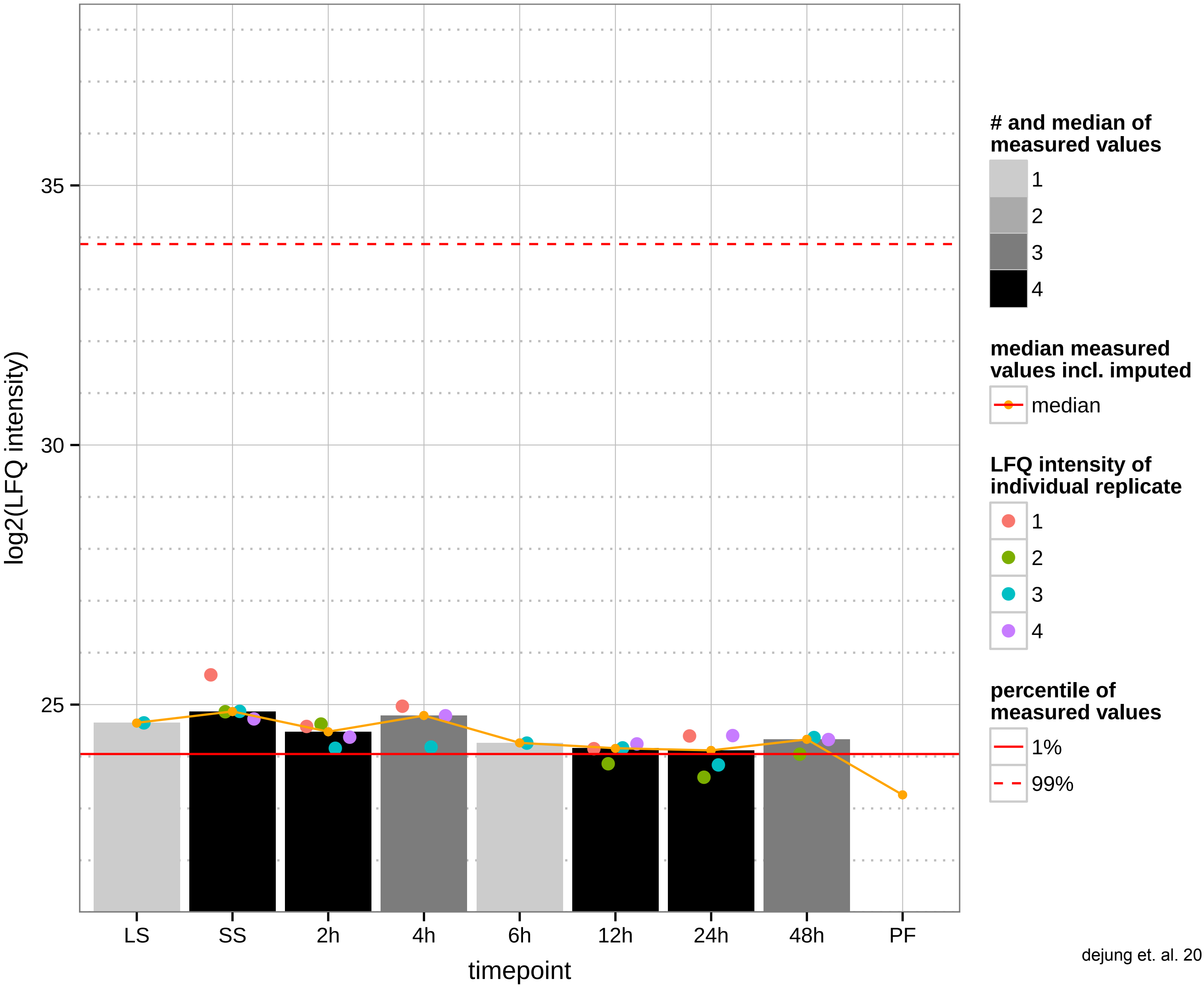
hypothetical protein, conserved
Tb927.6.3820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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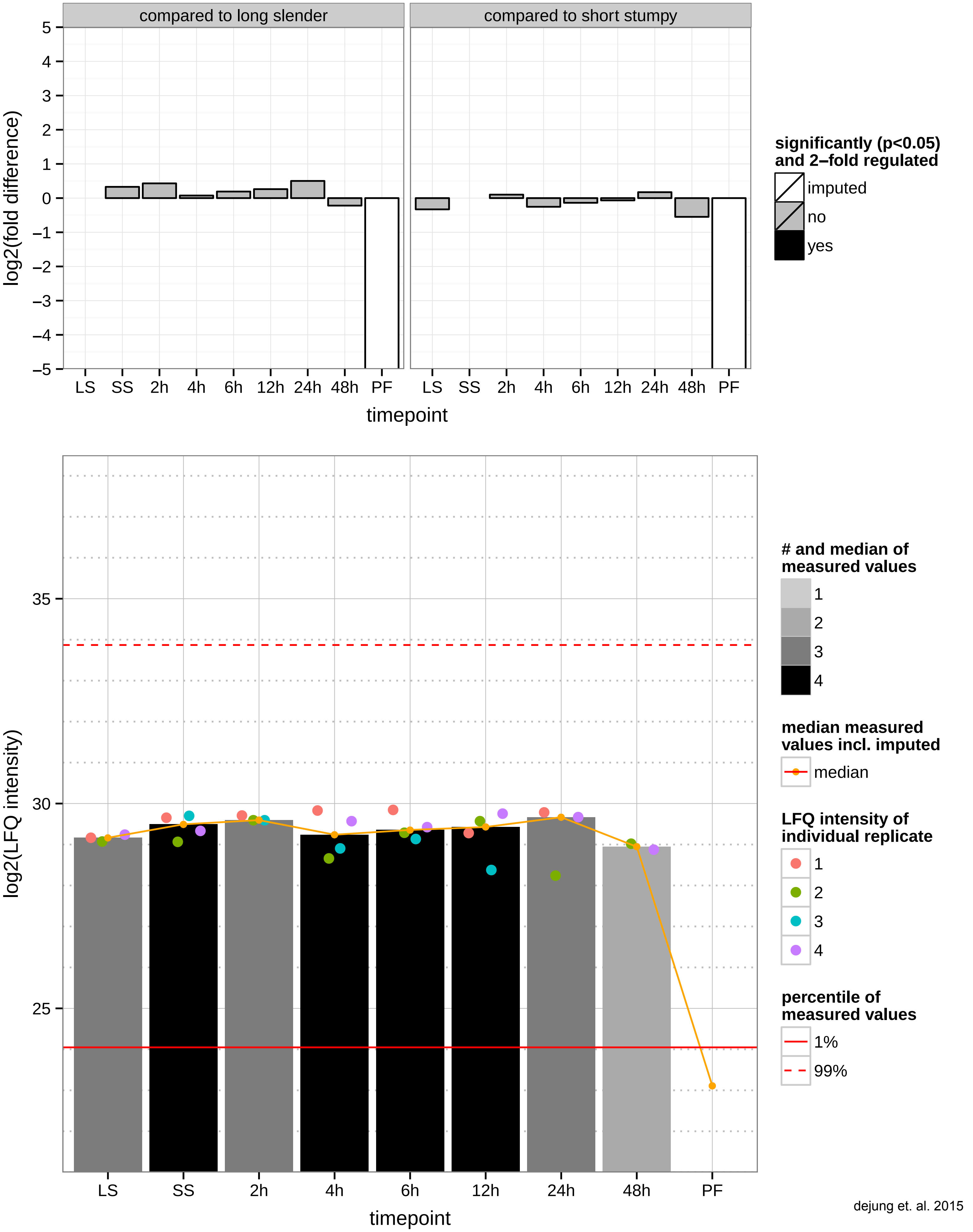
hypothetical protein, conserved
Tb927.6.410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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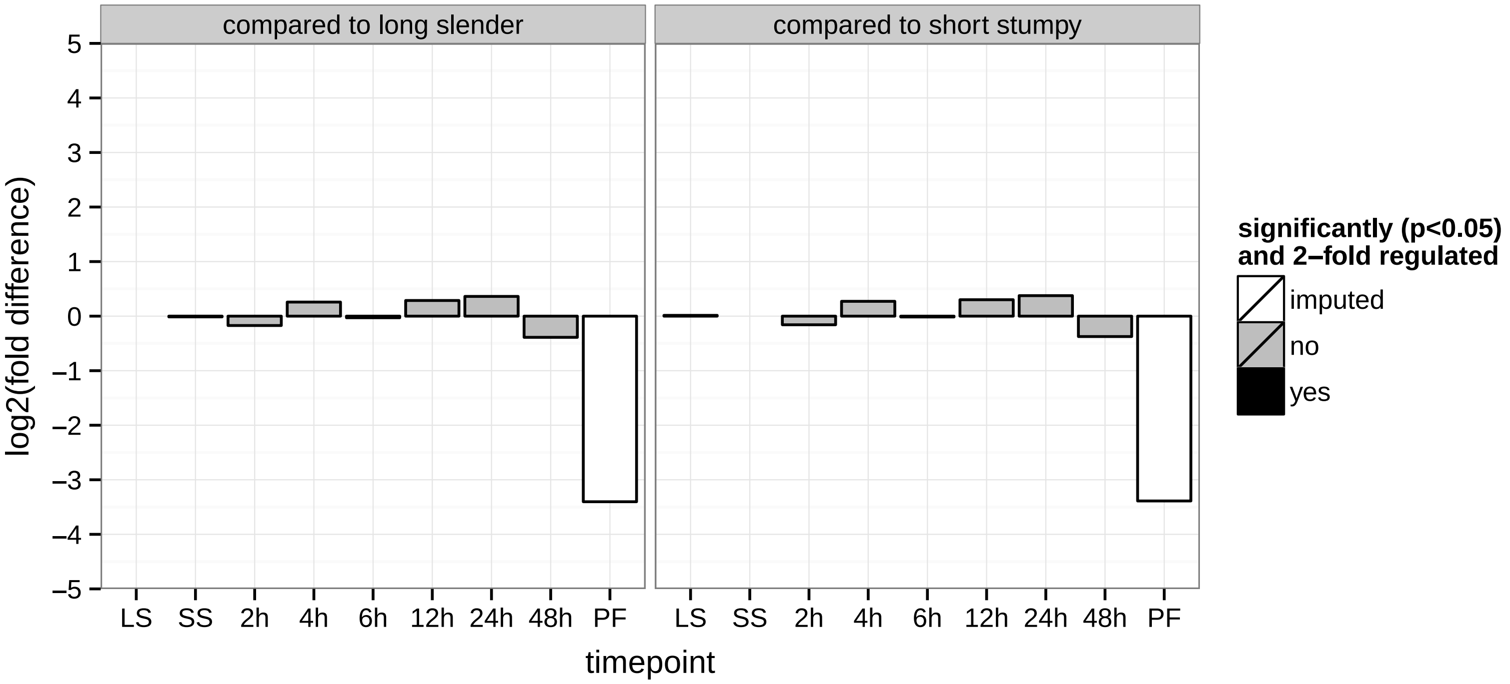
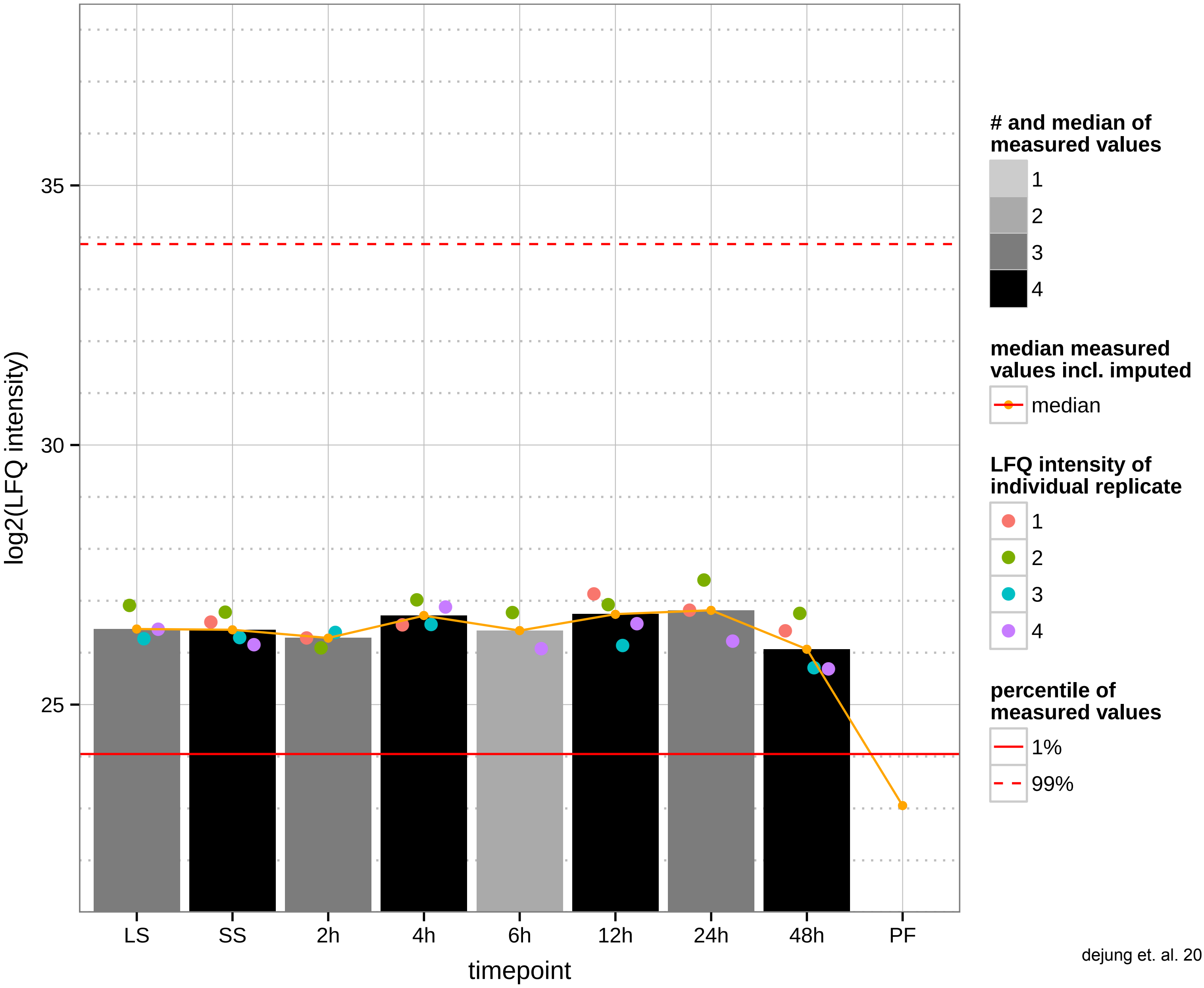
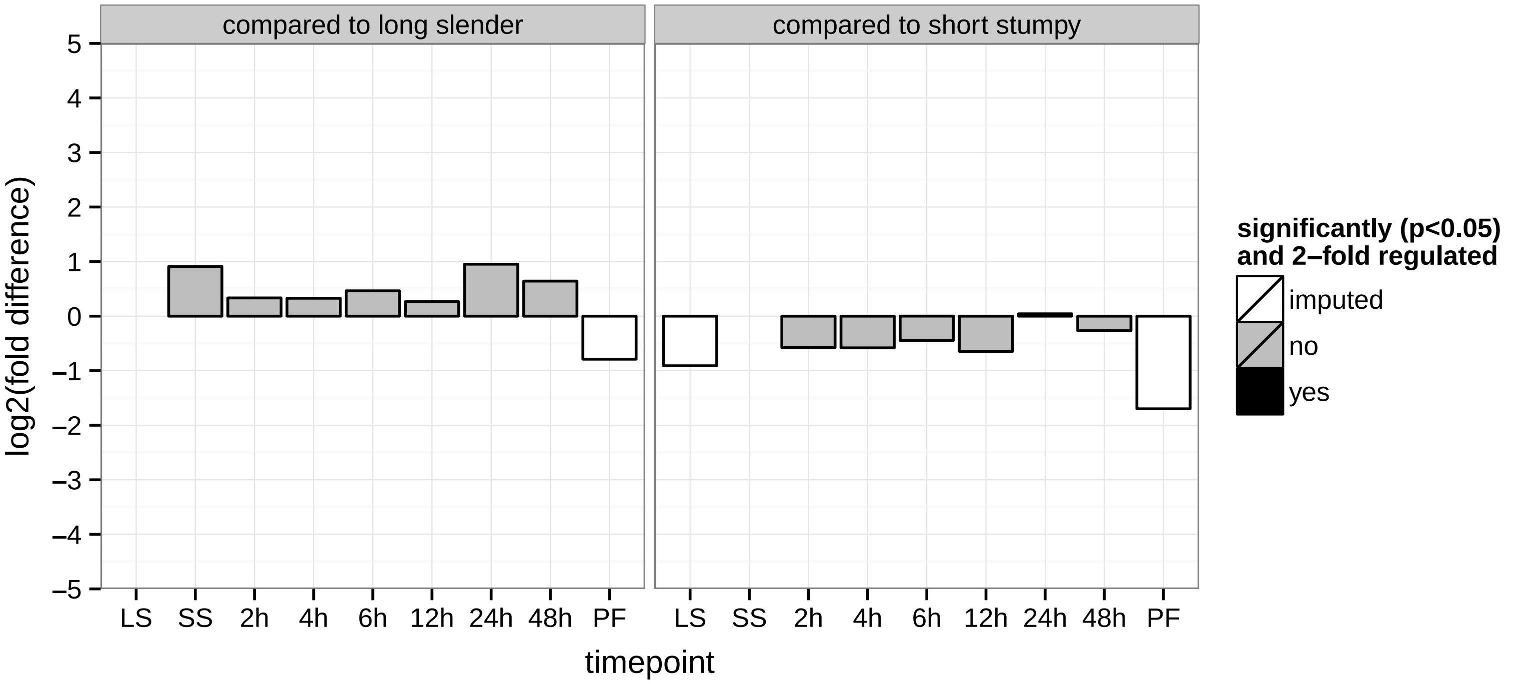
hypothetical protein, conserved
Tb927.6.4180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

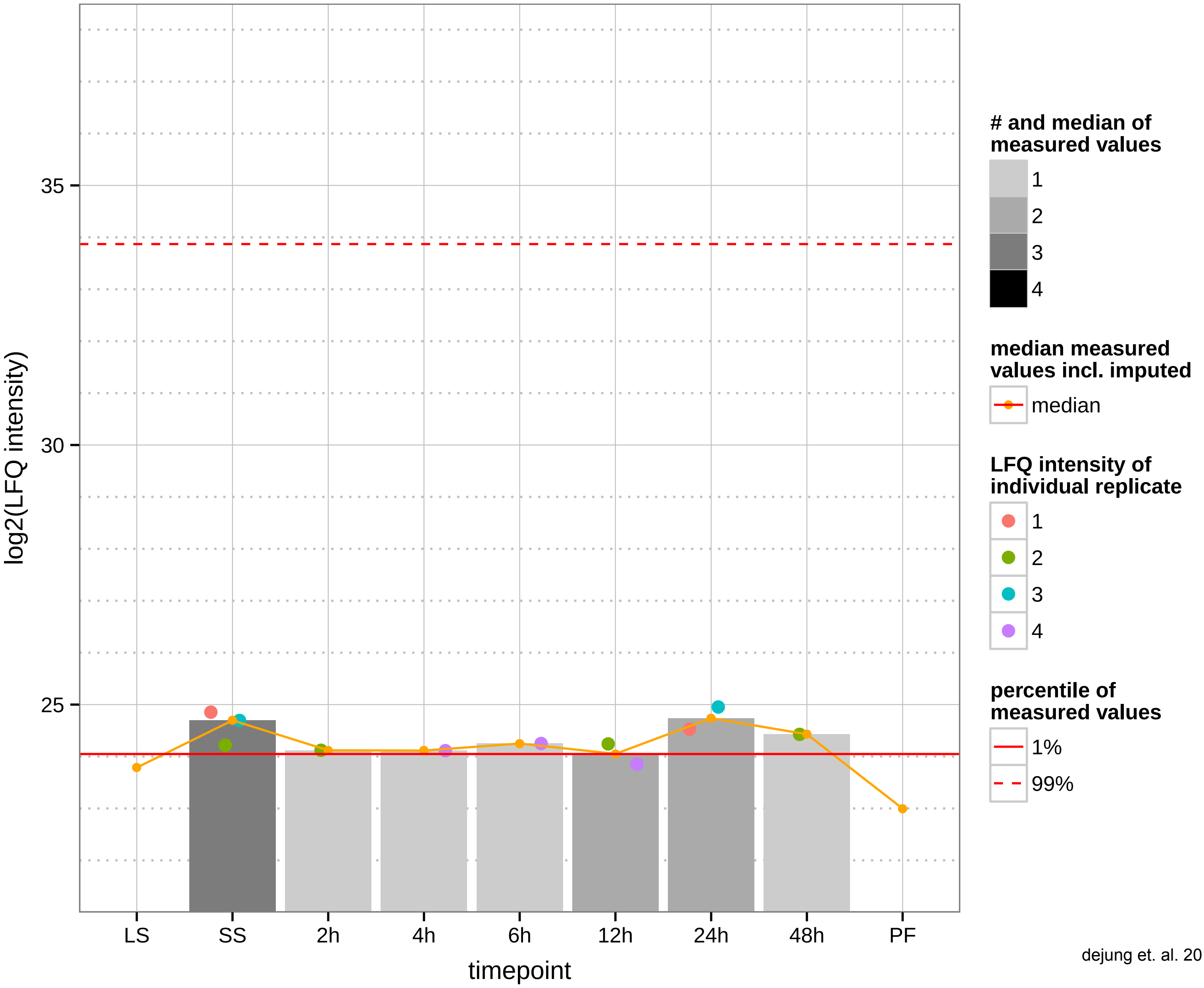




dejung et. al. 2015

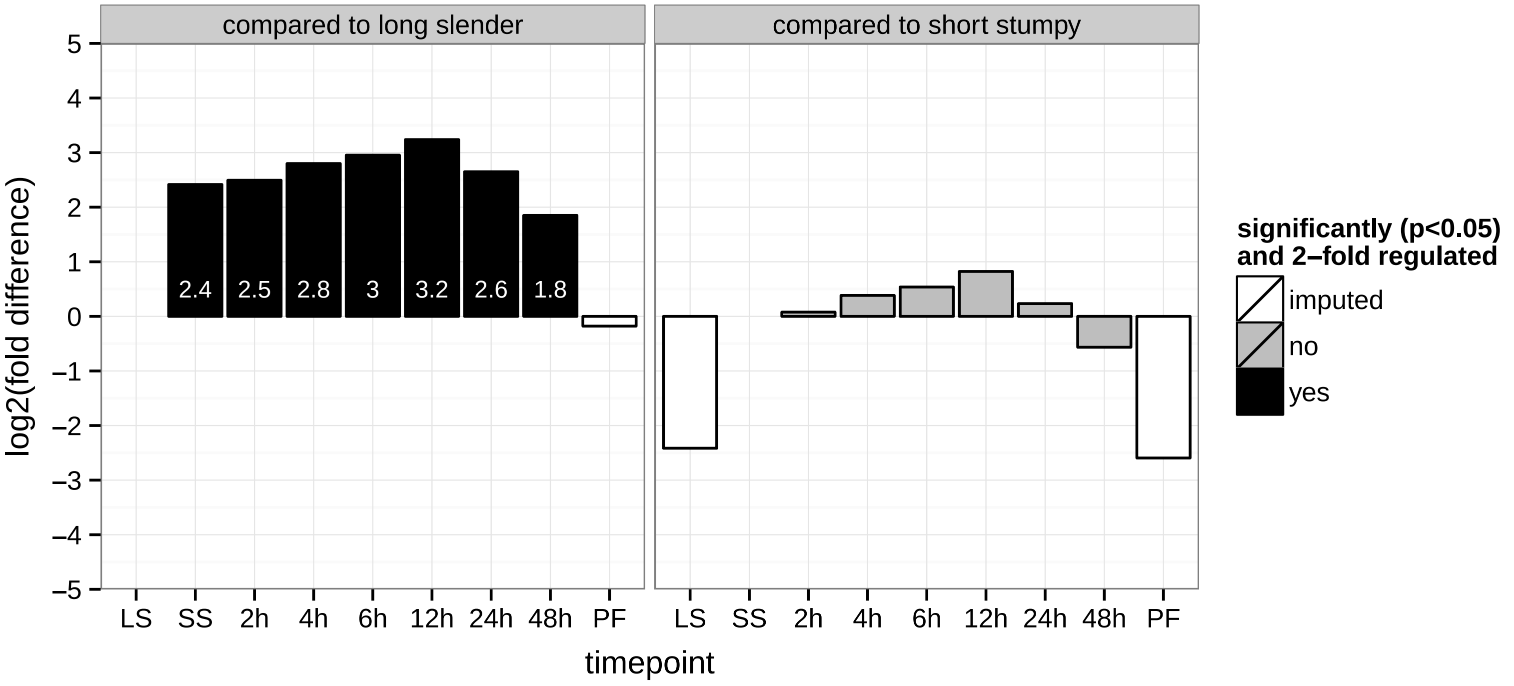
mitogen–activated protein kinase 5 (MAPK5)
Tb927.6.4220
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

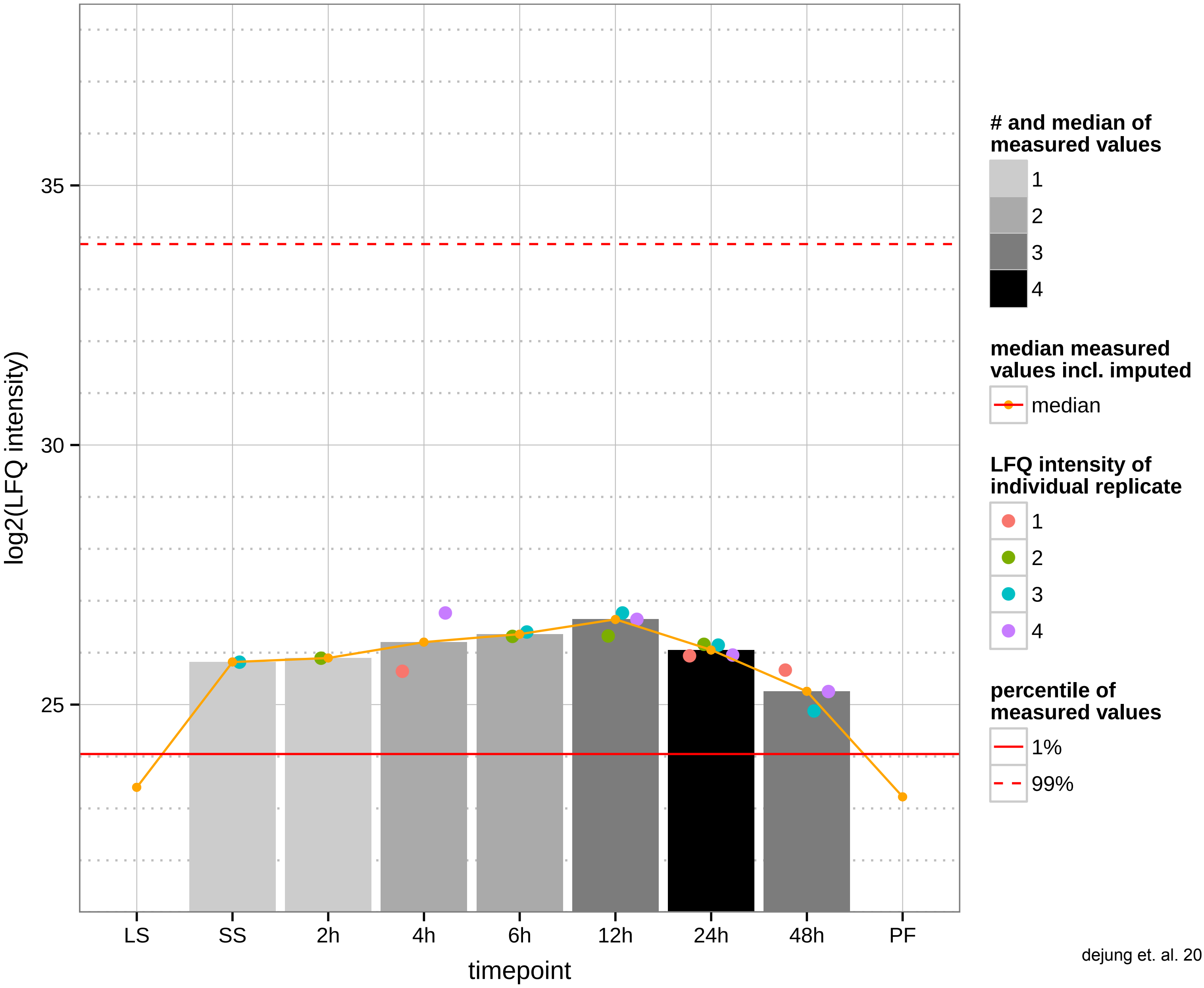




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.4250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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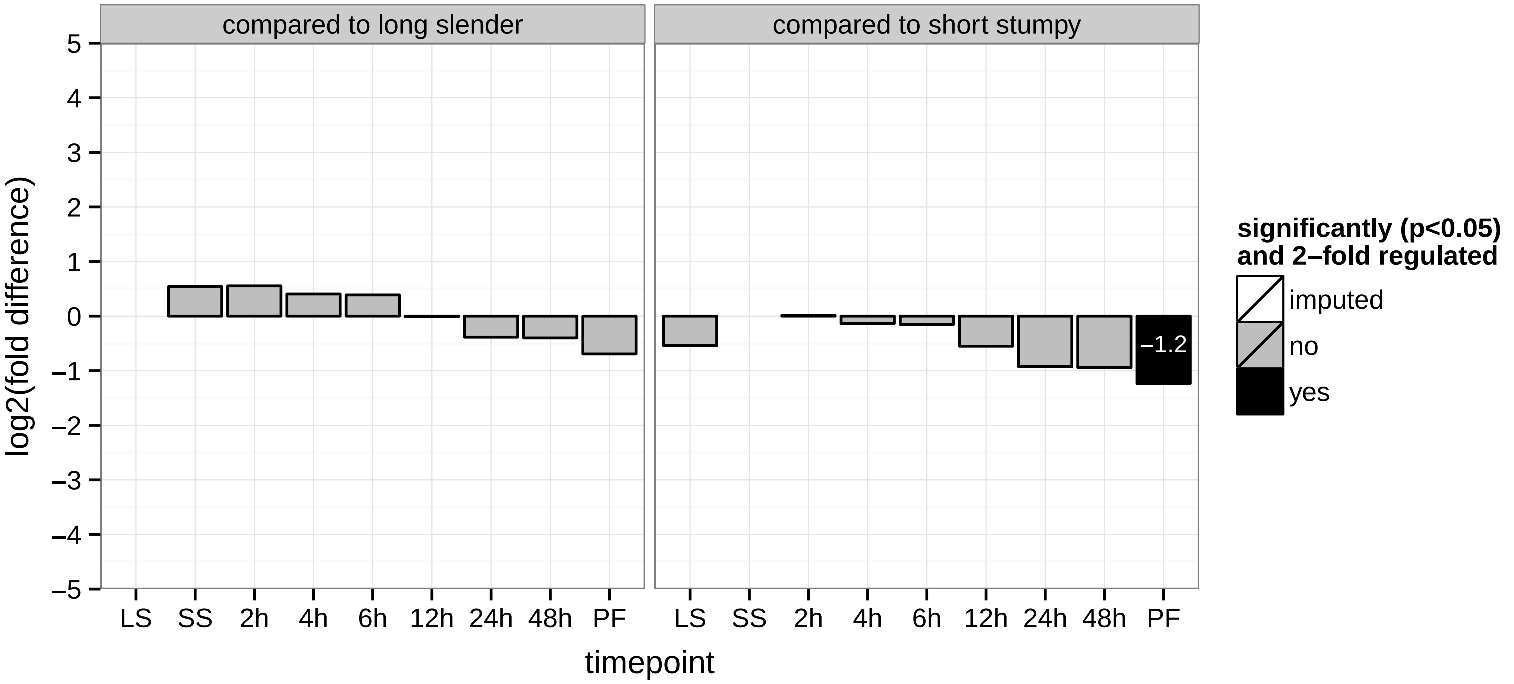
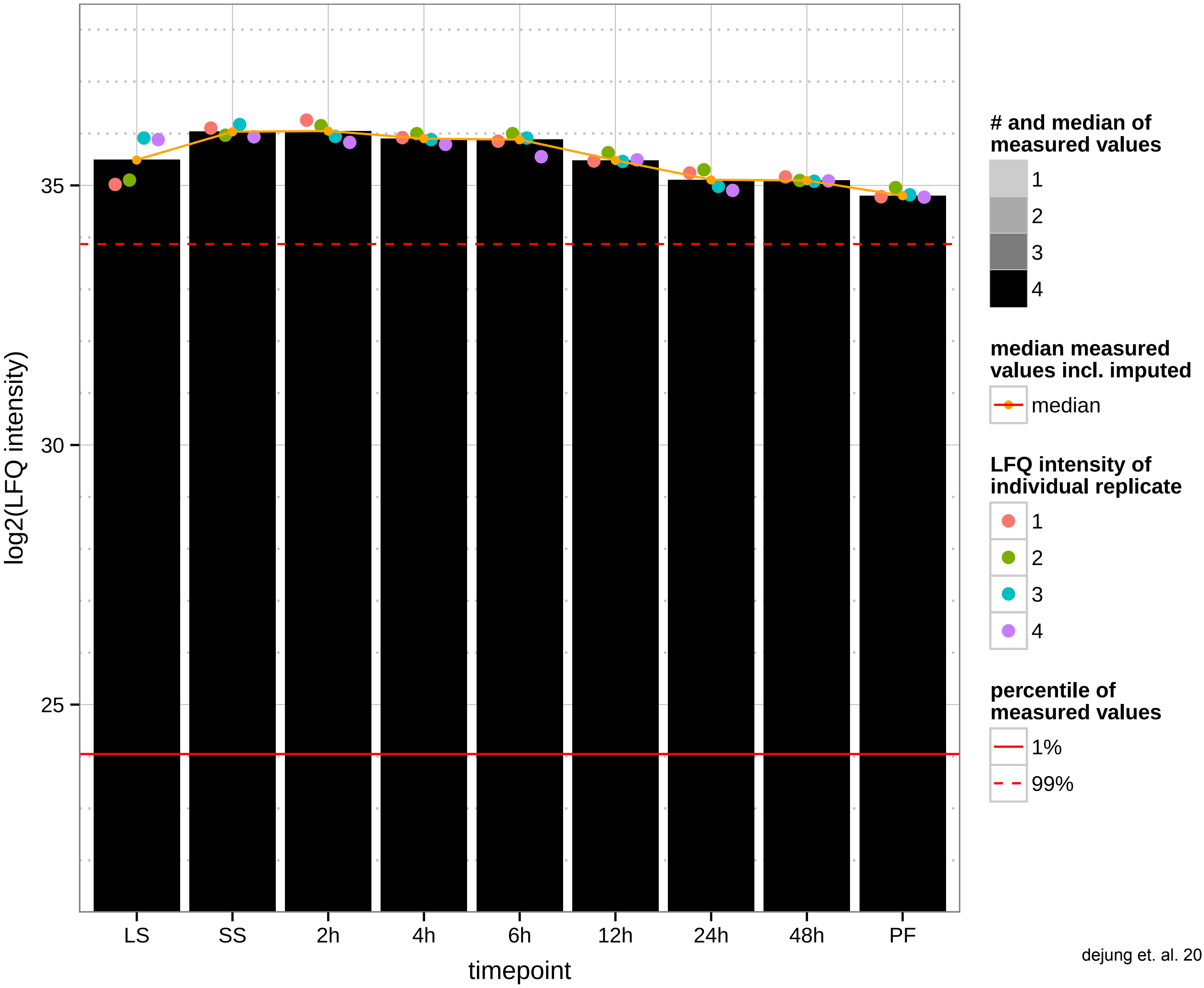
glyceraldehyde 3–phosphate dehydrogenase, glycosomal (GAPDH)
Tb927.6.4300;Tb927.6.4280
AGOF: glyceraldehyde–3–phosphate dehydrogenase (NAD+) (phosphorylating) activity
AGOC: glycosome
AGOP: glycolysis
PGOF: NAD binding, NADP binding, oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as
PGOC: null
PGOP: glucose metabolic process, oxidation–reduction process, null





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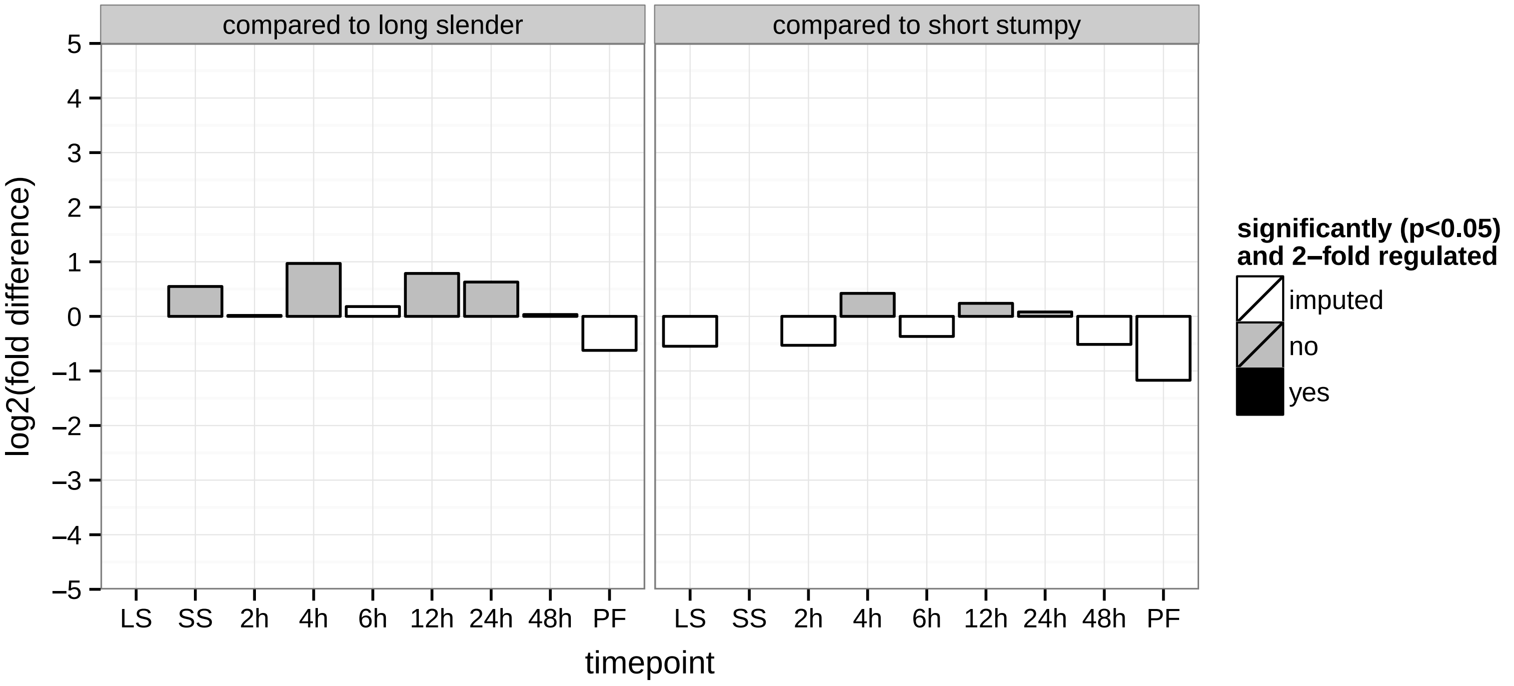
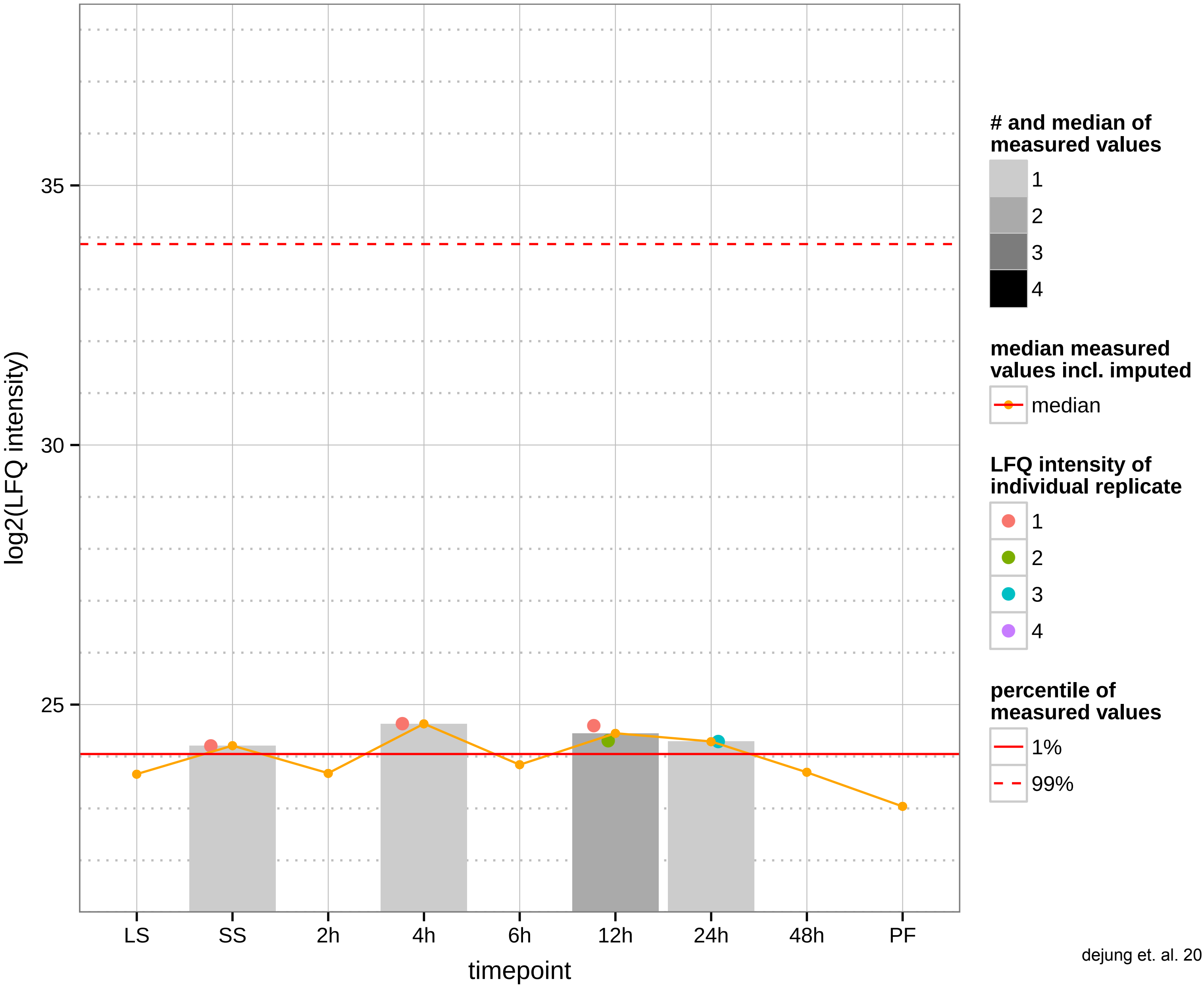
hypothetical protein, conserved
Tb927.6.4330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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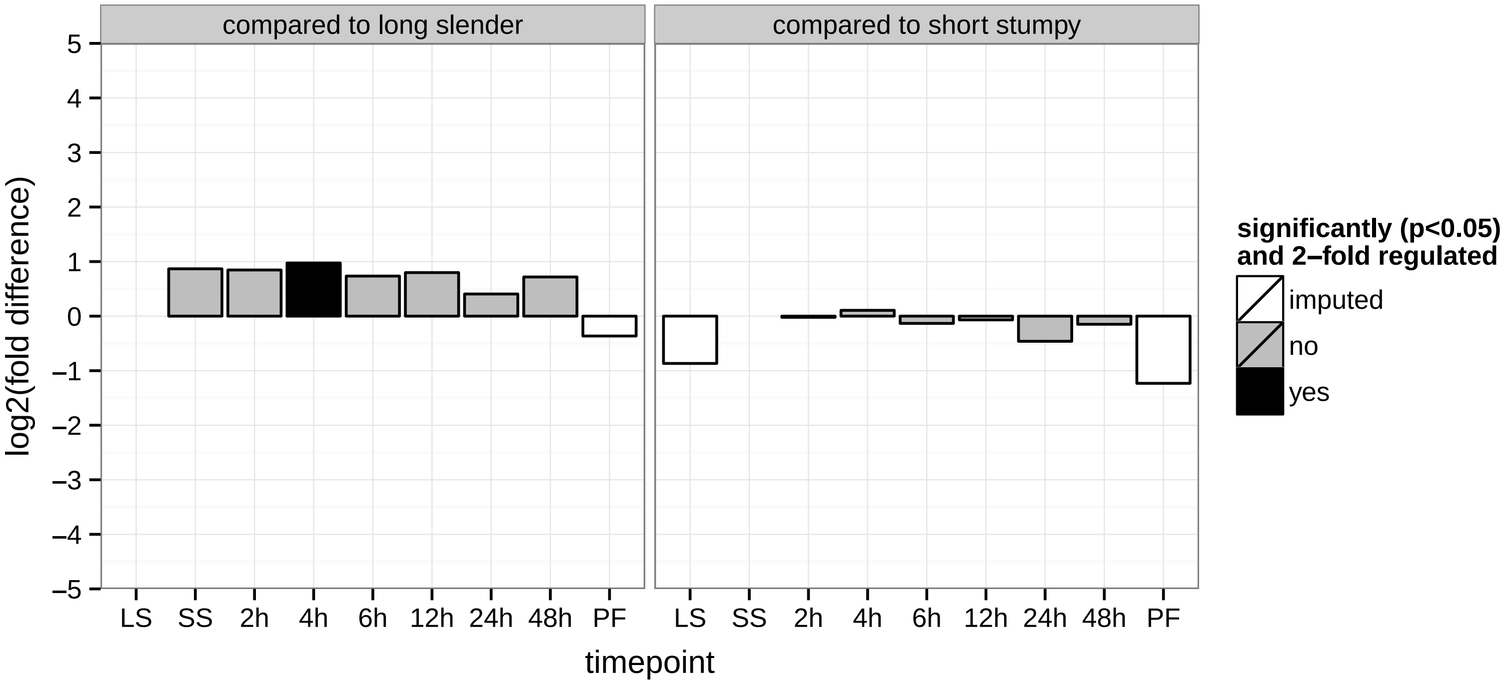
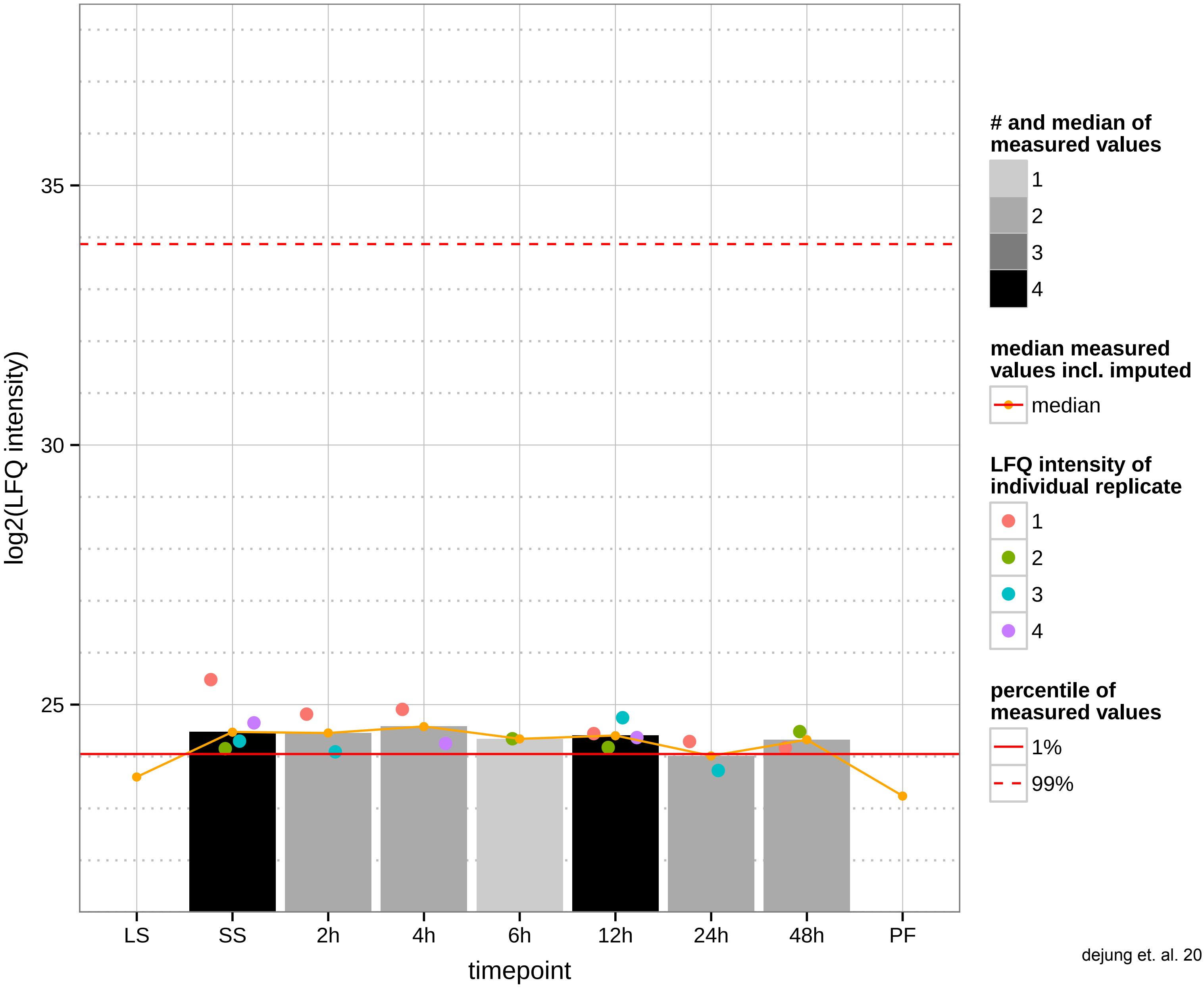
pumillio RNA binding protein 4, putative, pumilio RNA binding protein, putative (PUF4)
Tb927.6.820
AGOF: null, RNA binding
AGOC: null
AGOP: null
PGOF: RNA binding, binding
PGOC: null
PGOP: null





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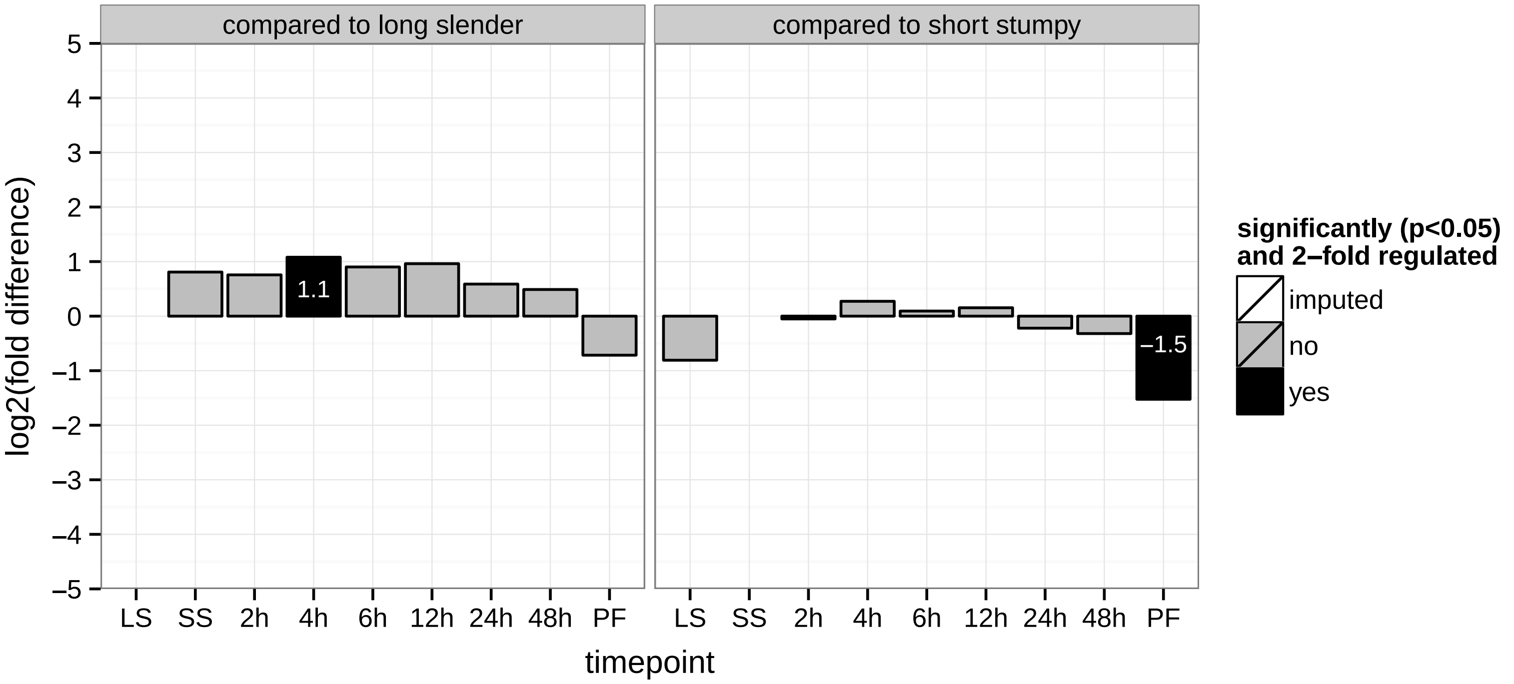
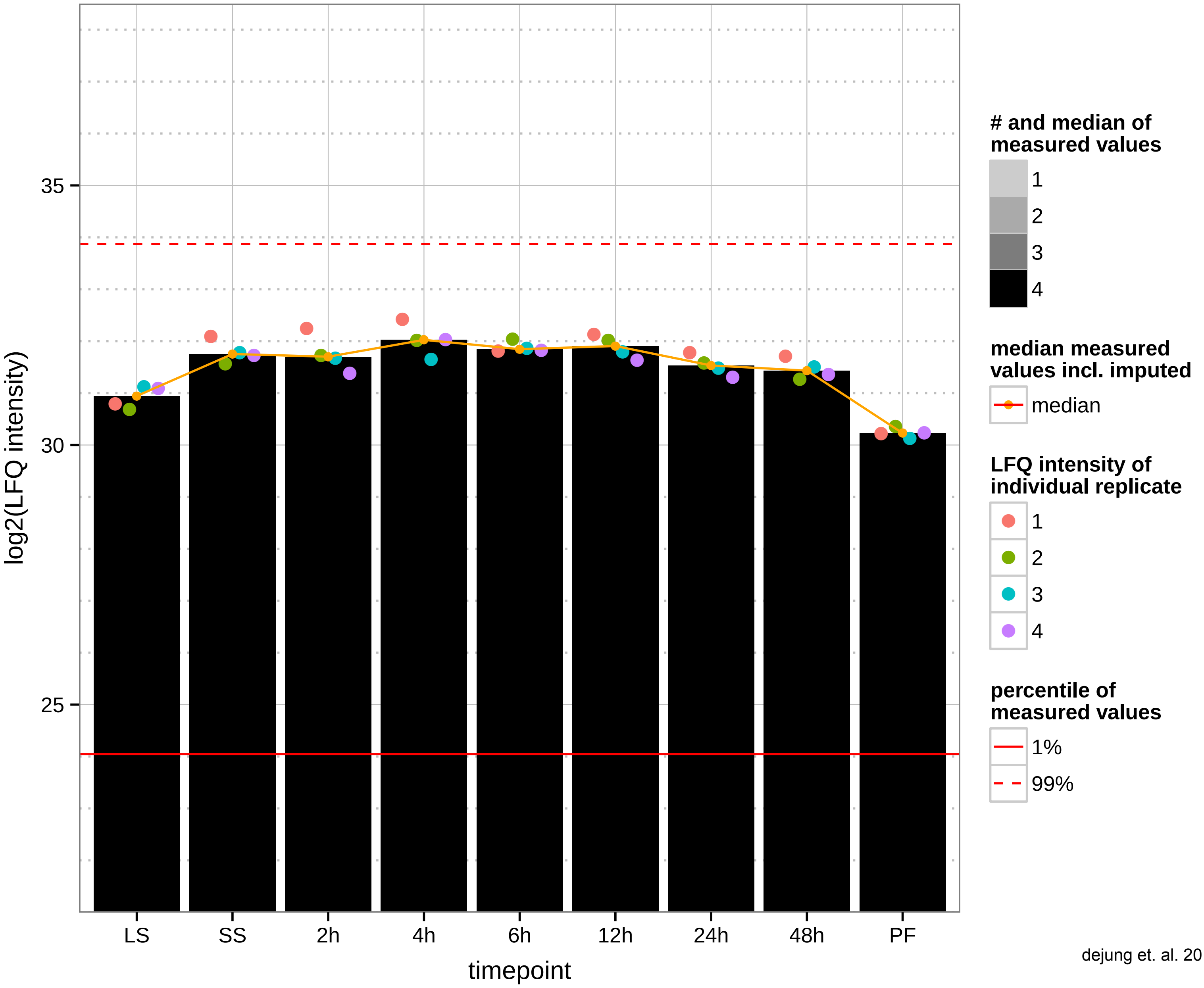
asparagine synthetase a, putative
Tb927.7.1110
AGOF: ATP binding, aminoacyl–tRNA ligase activity, aspartate–ammonia ligase activity
AGOC: cytoplasm
AGOP: asparagine biosynthetic process, tRNA aminoacylation for protein translation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, aspartate–ammonia ligase activity, nucleotide binding
PGOC: cytoplasm
PGOP: asparagine biosynthetic process, tRNA aminoacylation for protein translation





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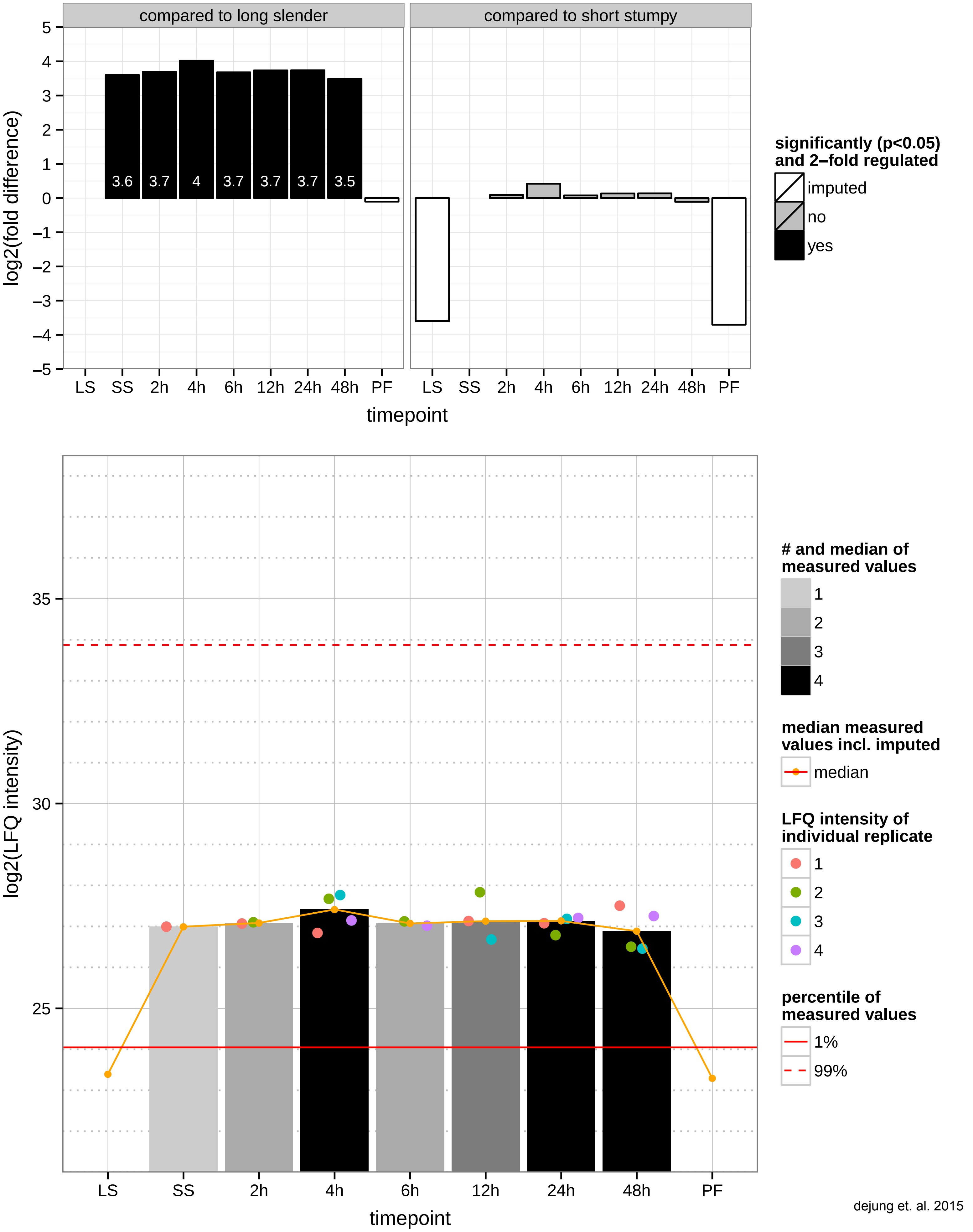
hypothetical protein, conserved
Tb927.7.1280;Tb927.7.1260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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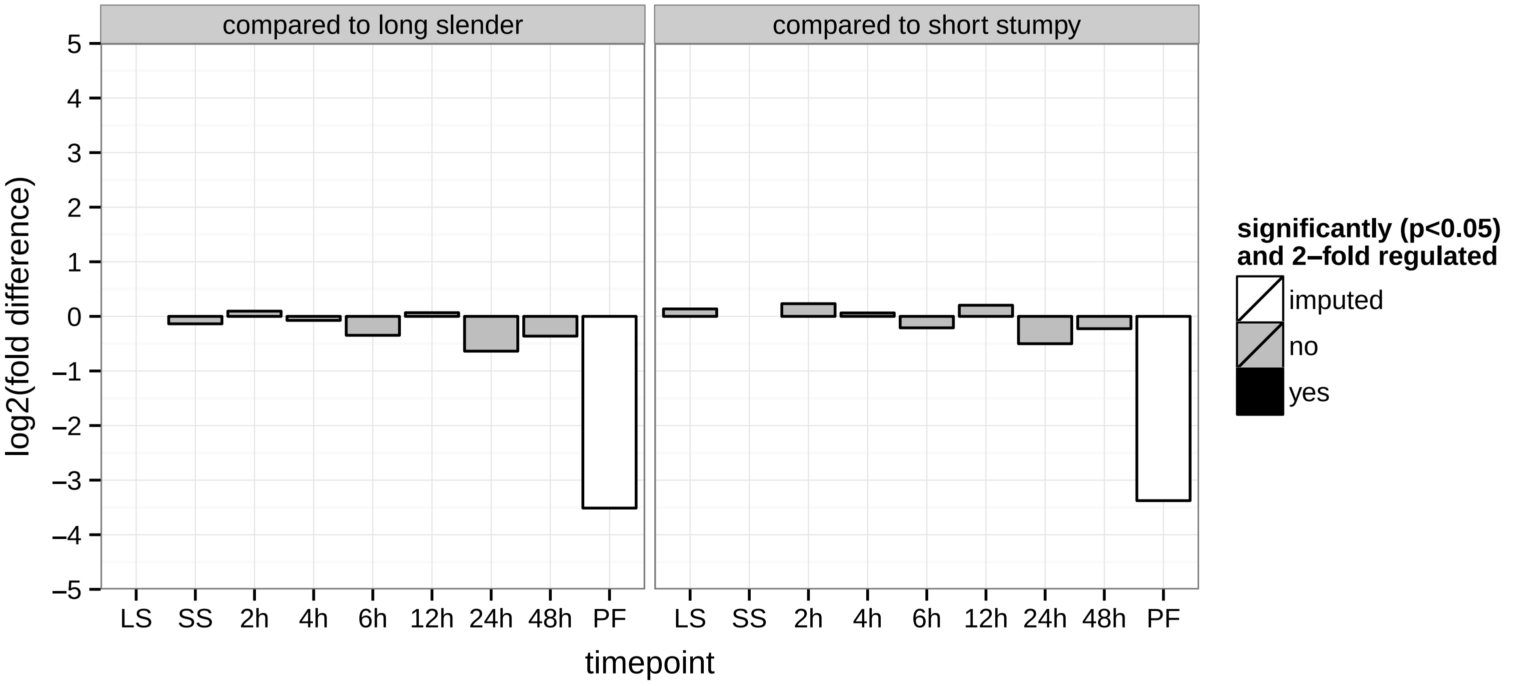
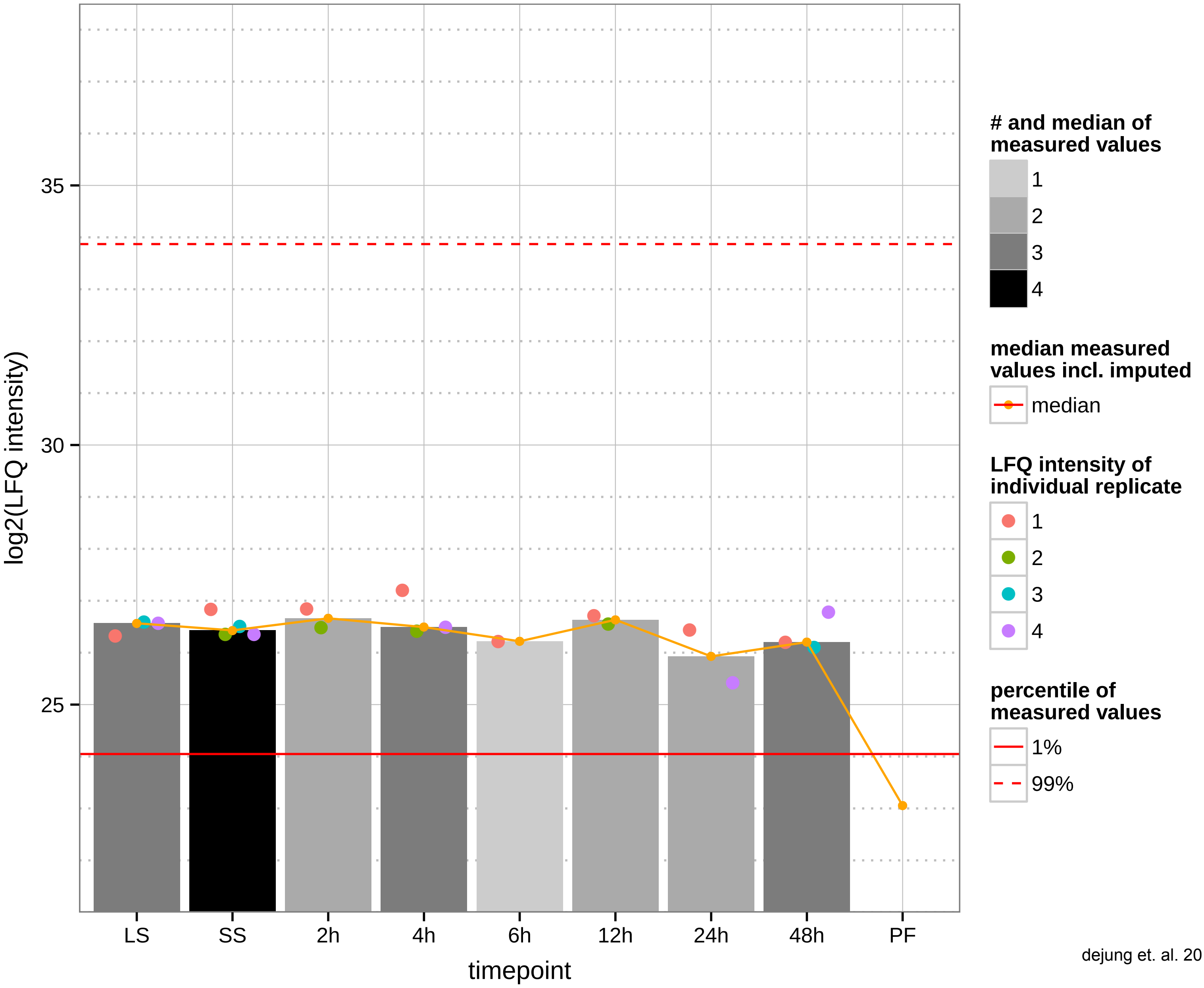
hypothetical protein, conserved
Tb927.7.1330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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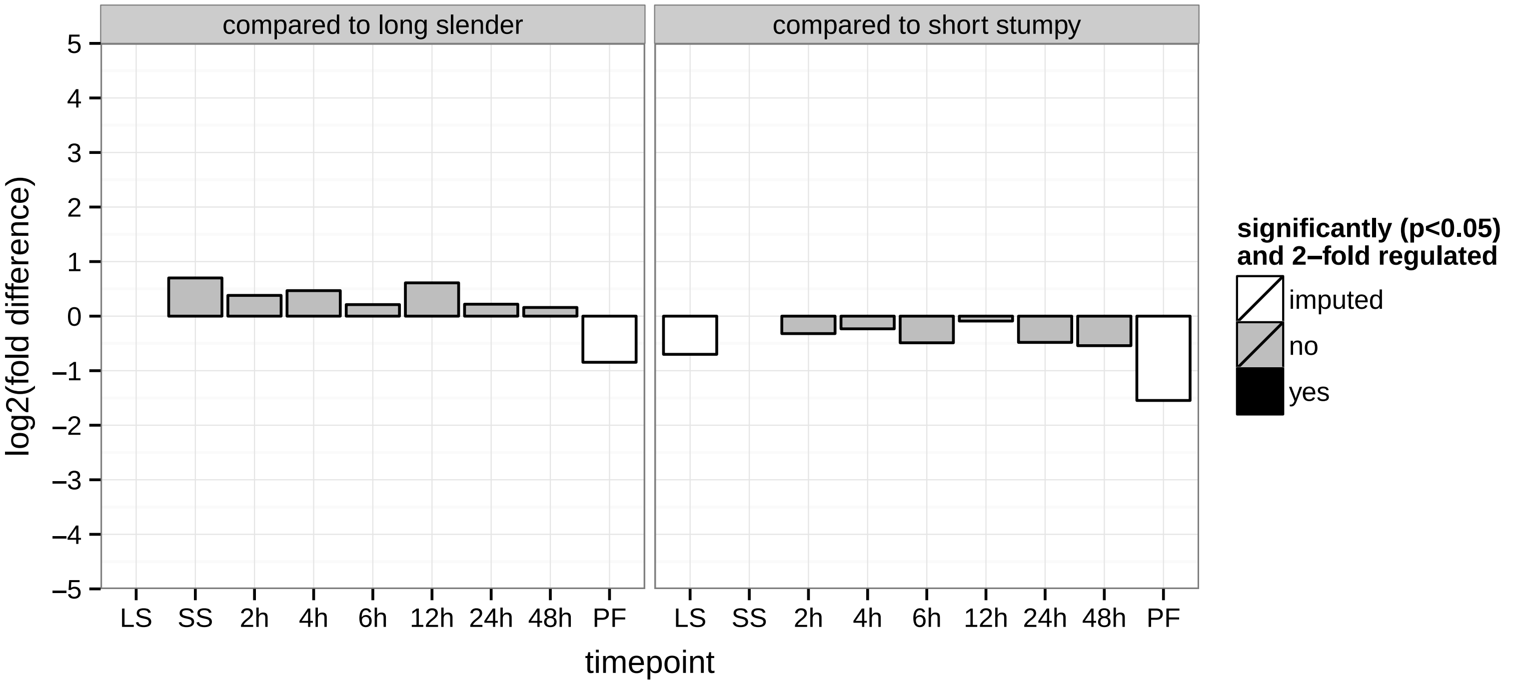
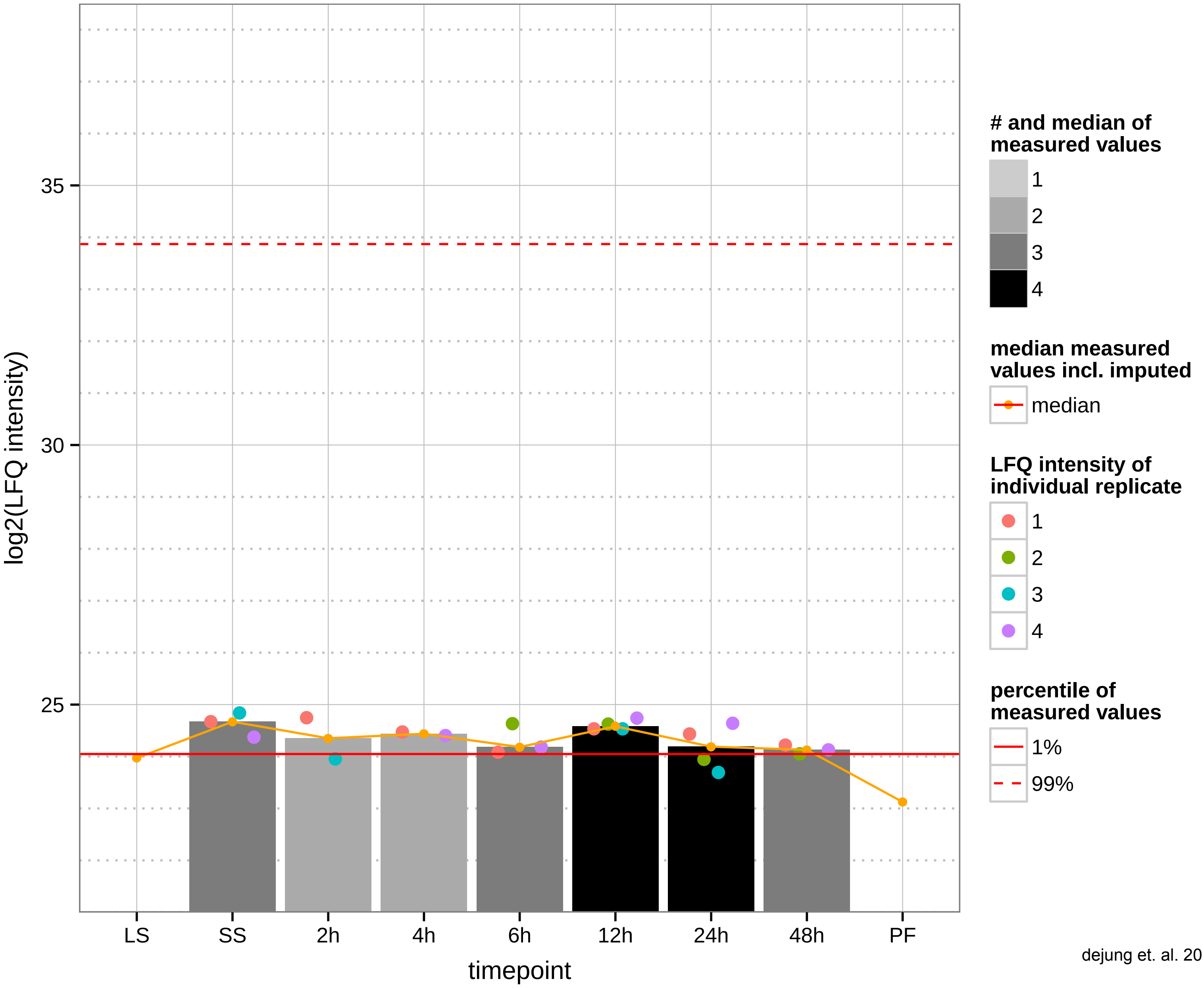
spliced leader RNA PSE–promoter transcription factor, putative (PPB1)
Tb927.7.1370
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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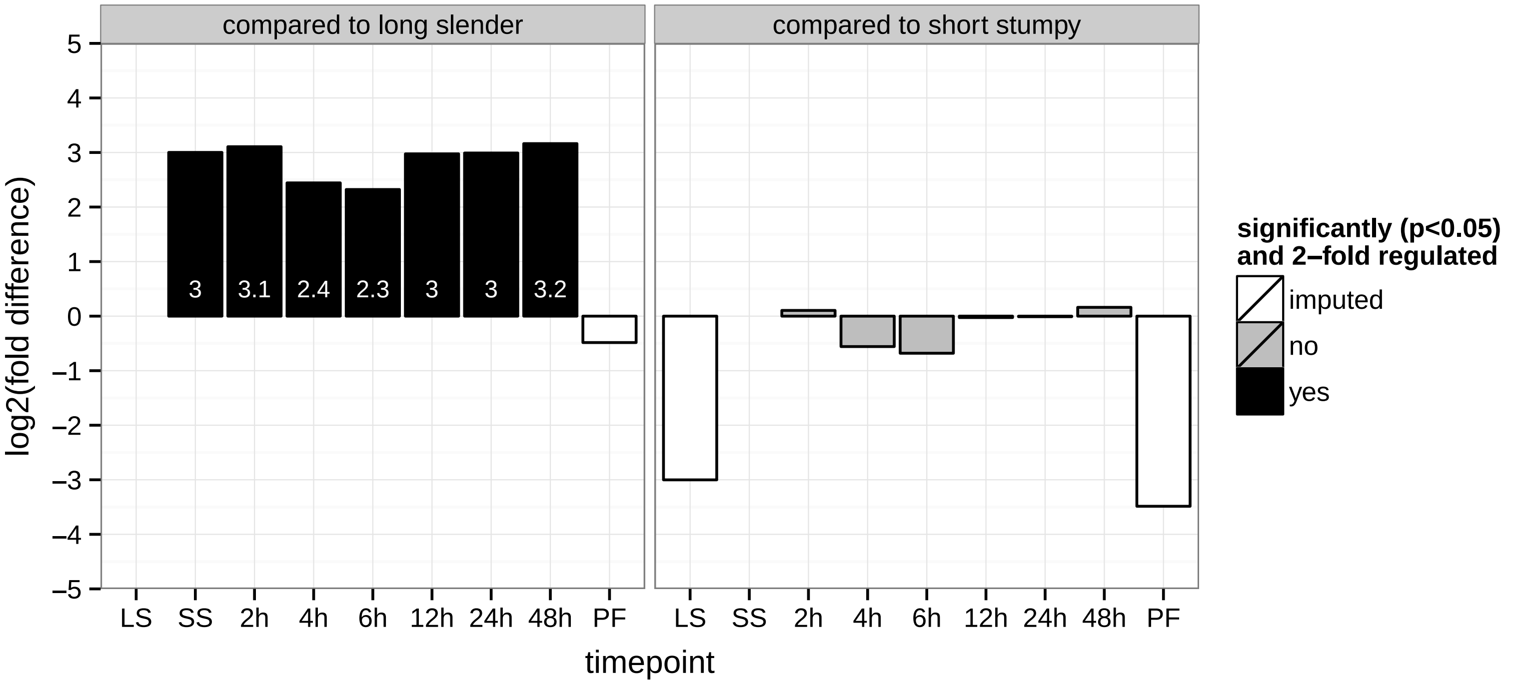
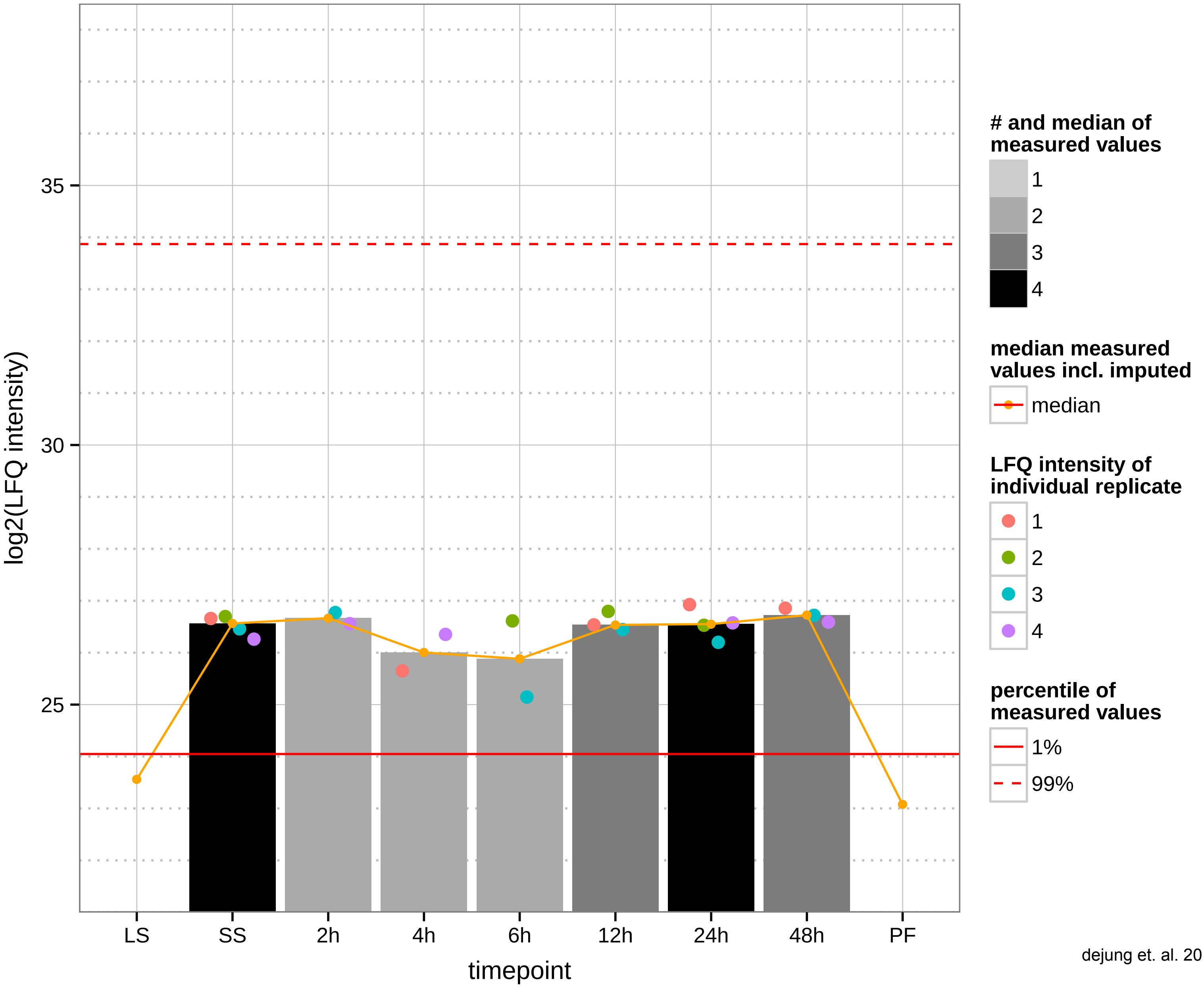
hypothetical protein, conserved
Tb927.7.1400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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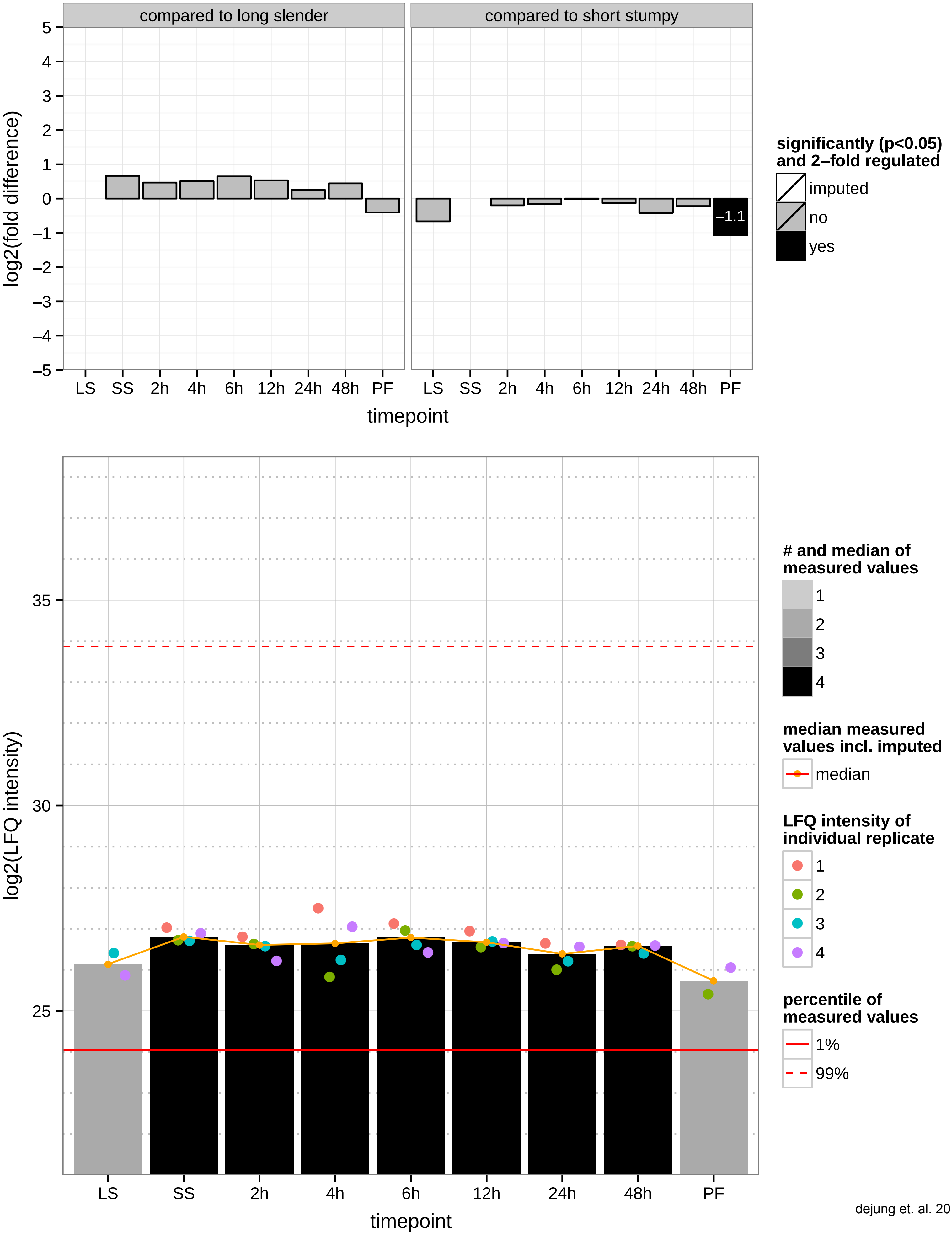
hypothetical protein, conserved
Tb927.7.1580
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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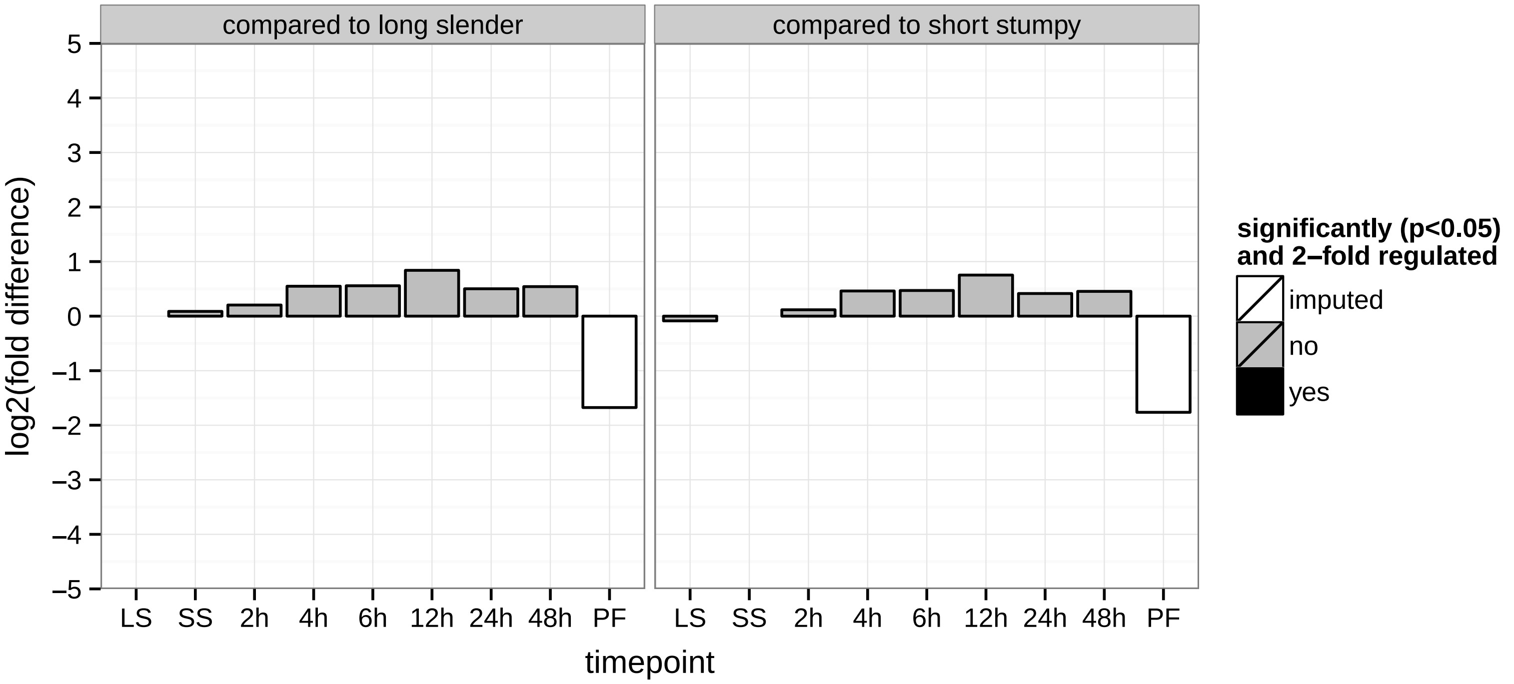
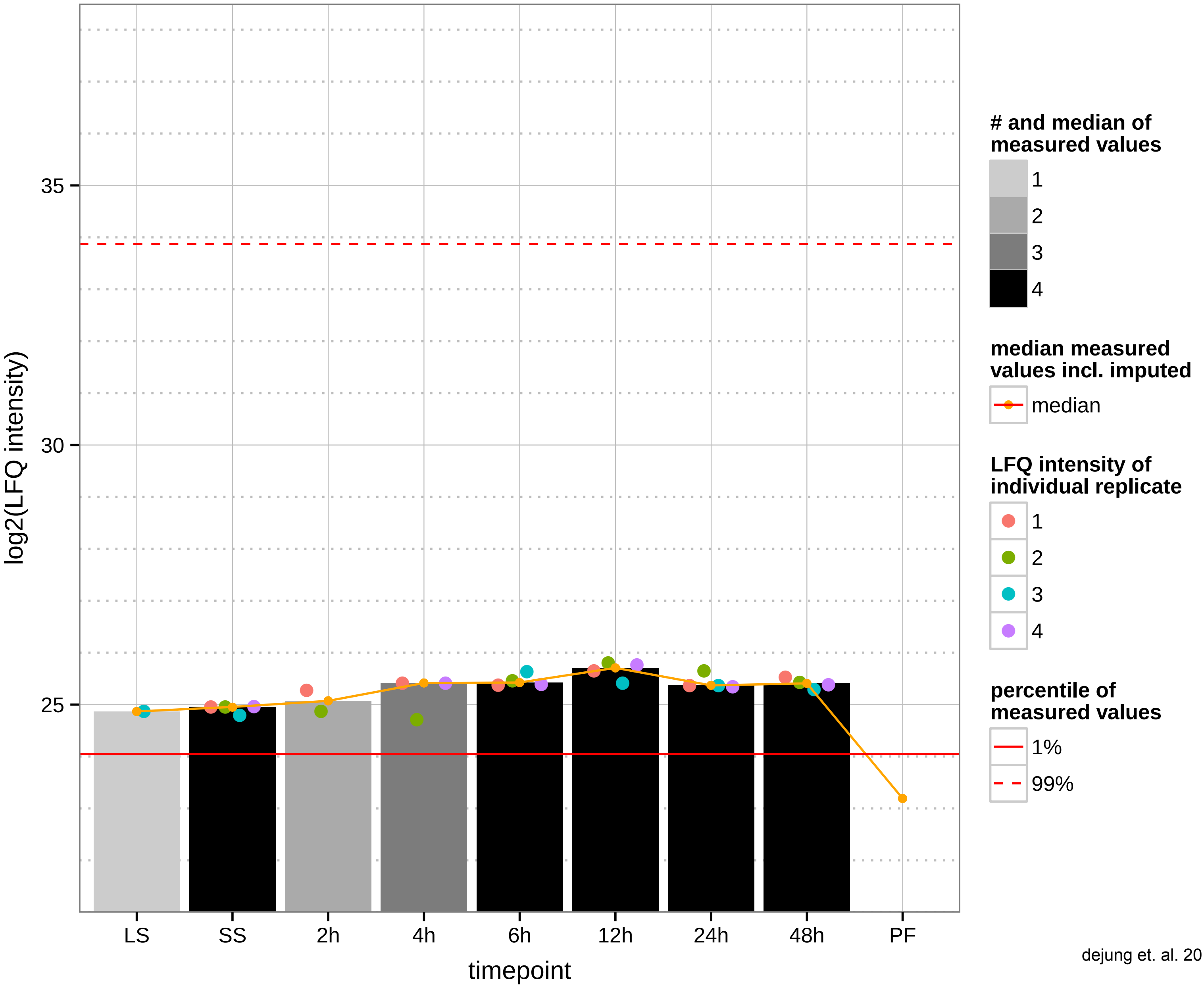
hypothetical protein, conserved
Tb927.7.1620
AGOF: null
AGOC: null
AGOP: null
PGOF: mRNA binding
PGOC: mRNA cleavage factor complex
PGOP: mRNA polyadenylation





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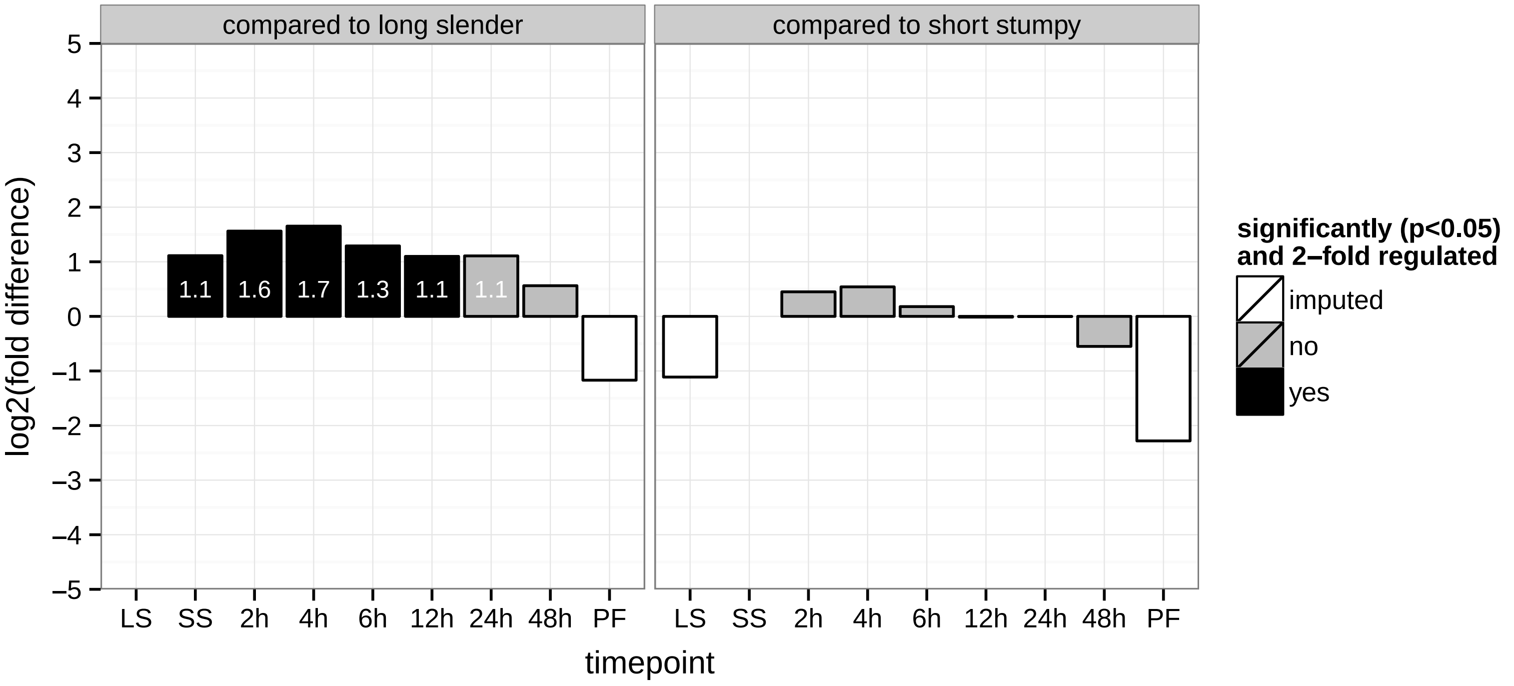
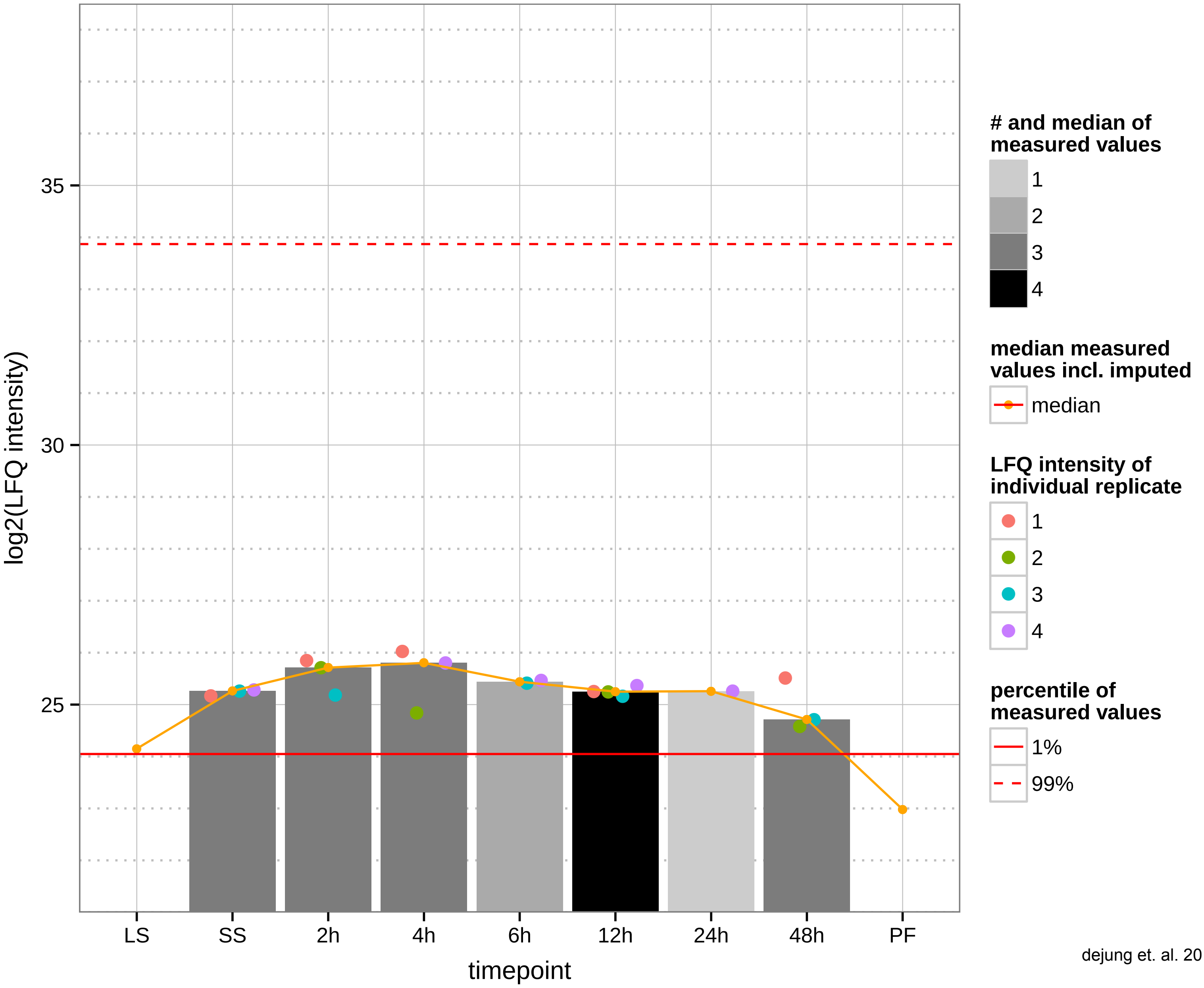
GTPase activating protein, putative
Tb927.7.2470
AGOF: Rab GTPase activator activity
AGOC: intracellular
AGOP: regulation of Rab GTPase activity
PGOF: Rab GTPase activator activity
PGOC: intracellular
PGOP: regulation of Rab GTPase activity





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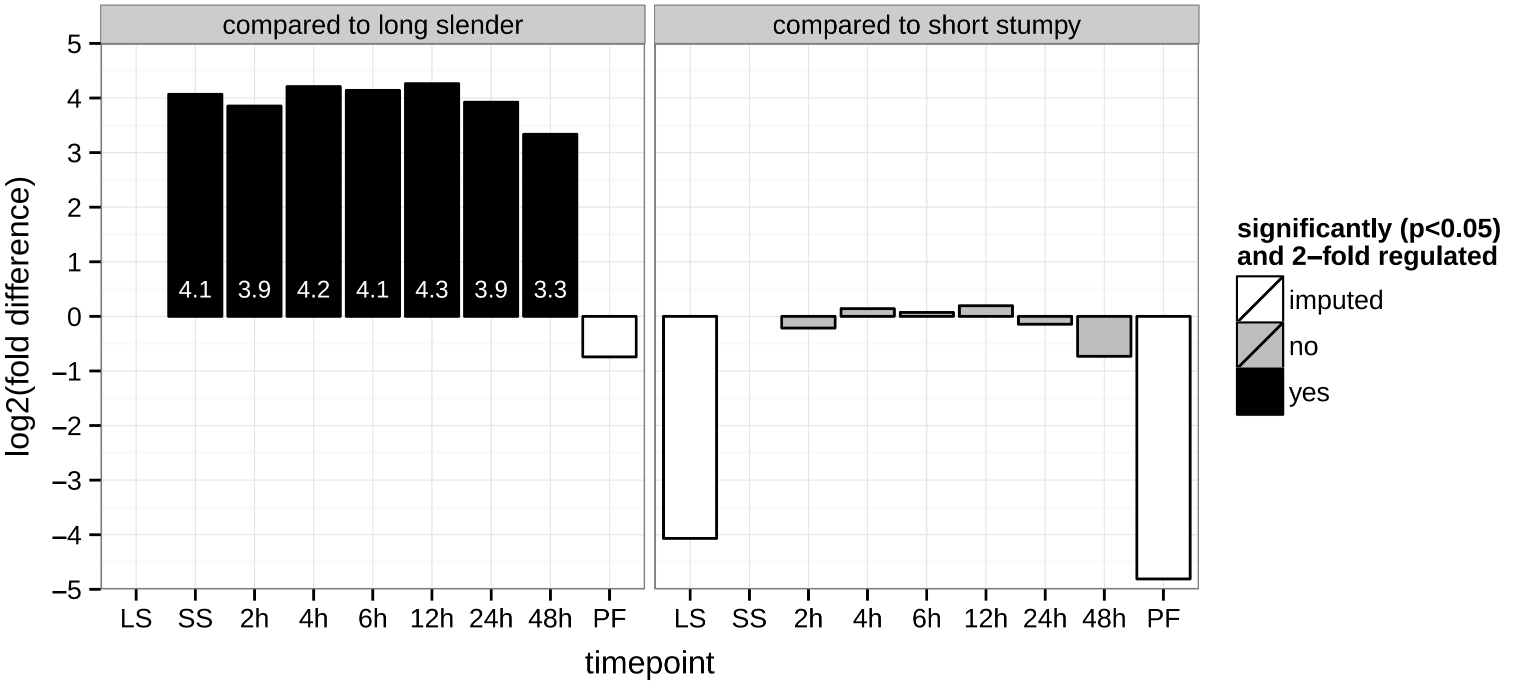
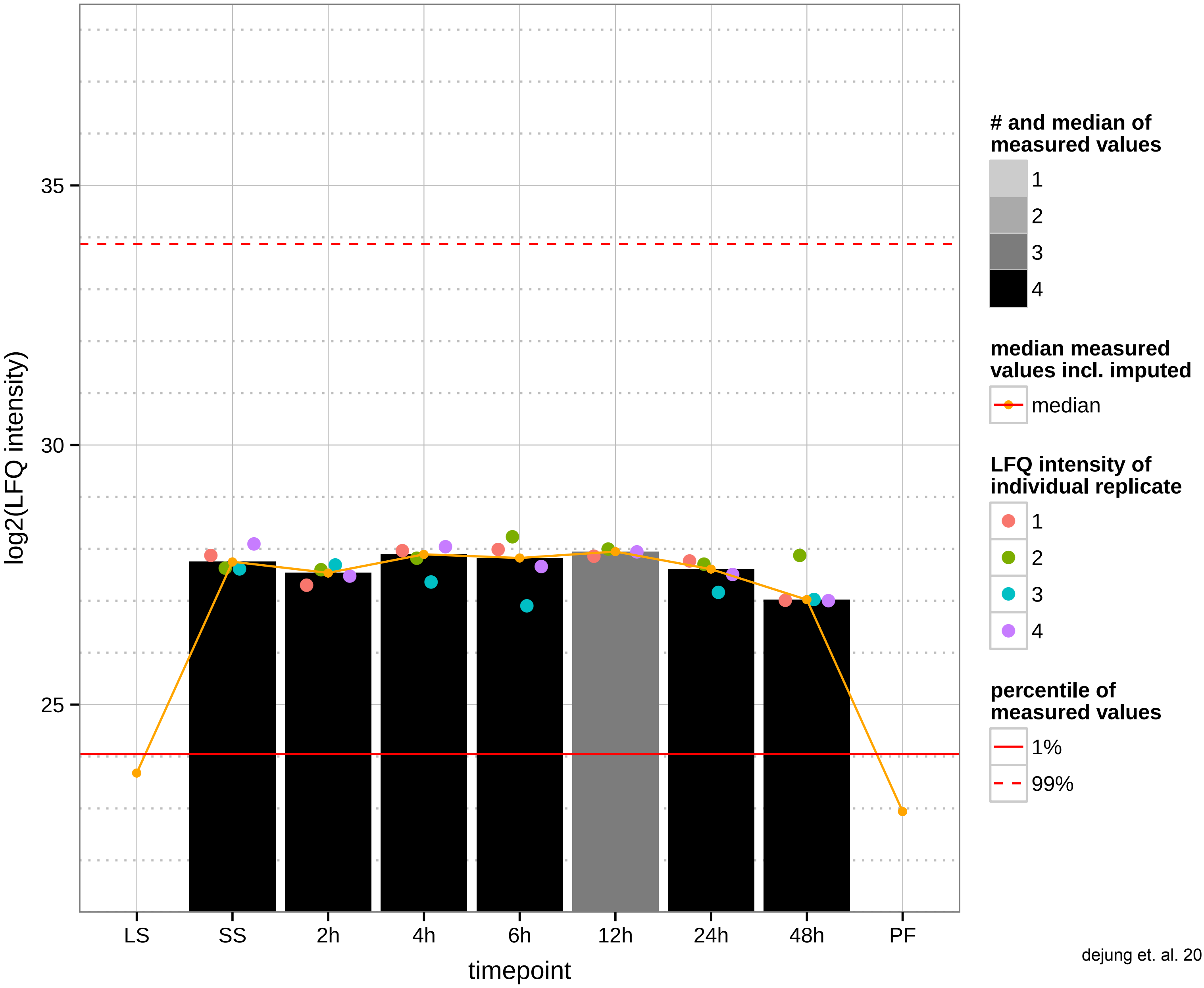
endoplasmatic reticulum retrieval protein, putative
Tb927.7.2510
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: integral to membrane
PGOP: null





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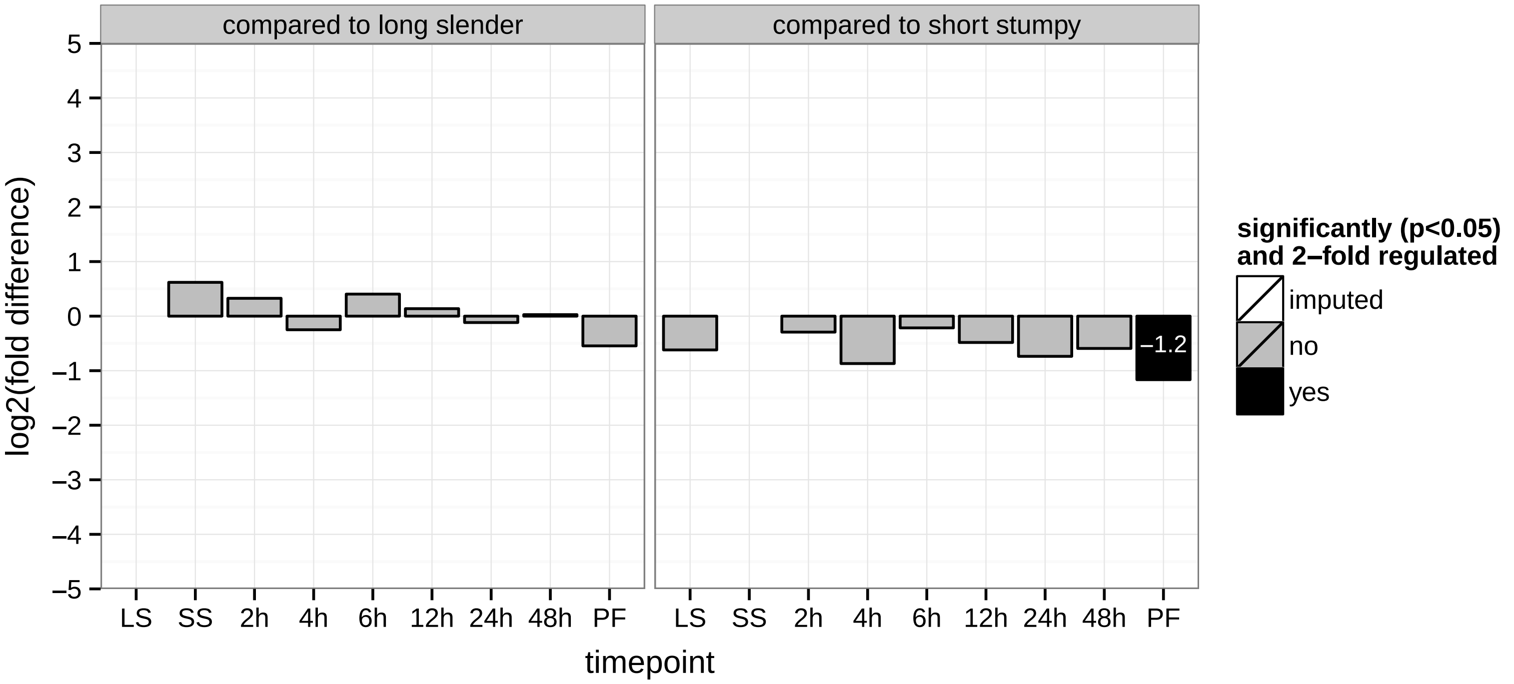
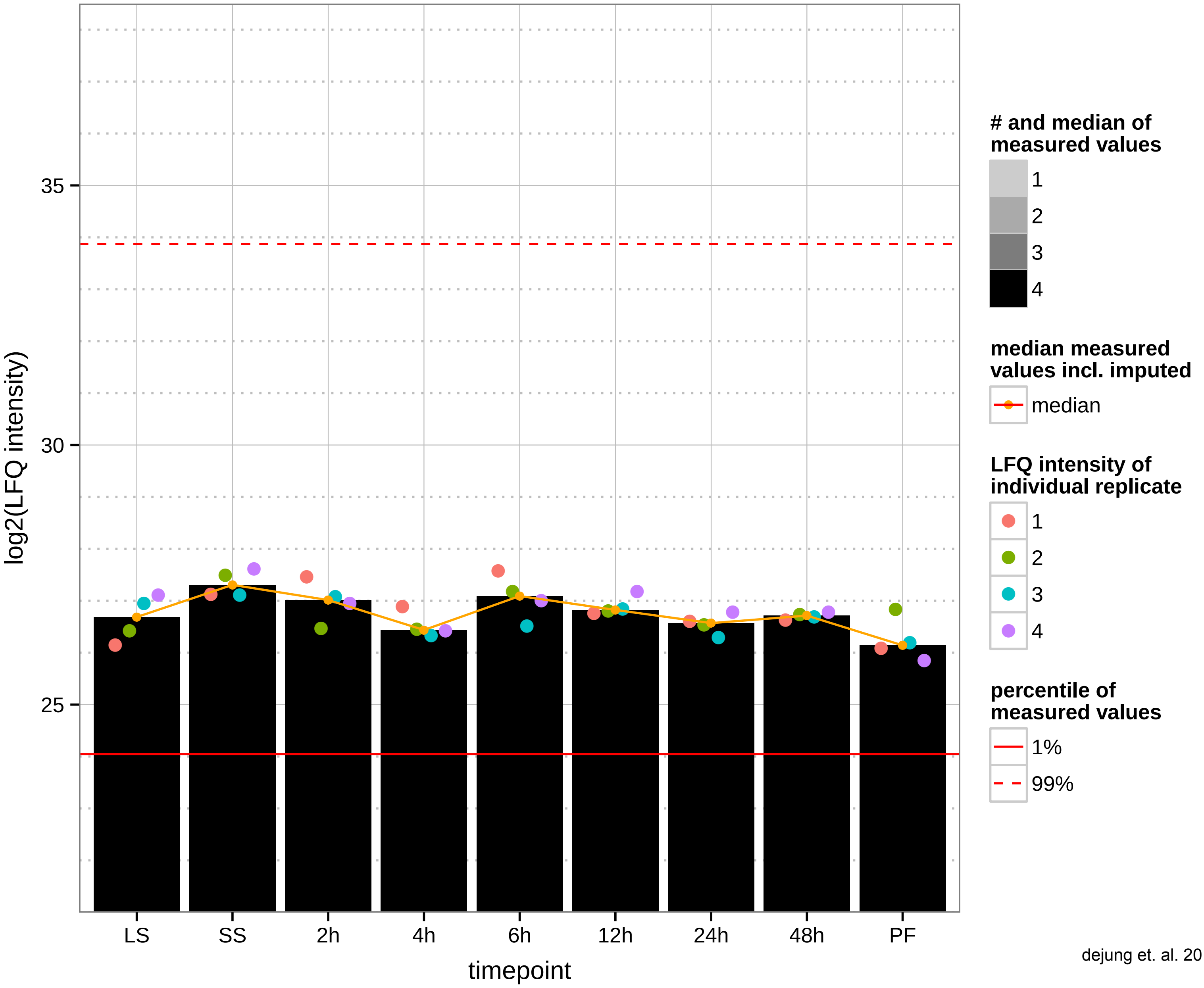
hypothetical protein, conserved
Tb927.7.3070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: transmembrane transport





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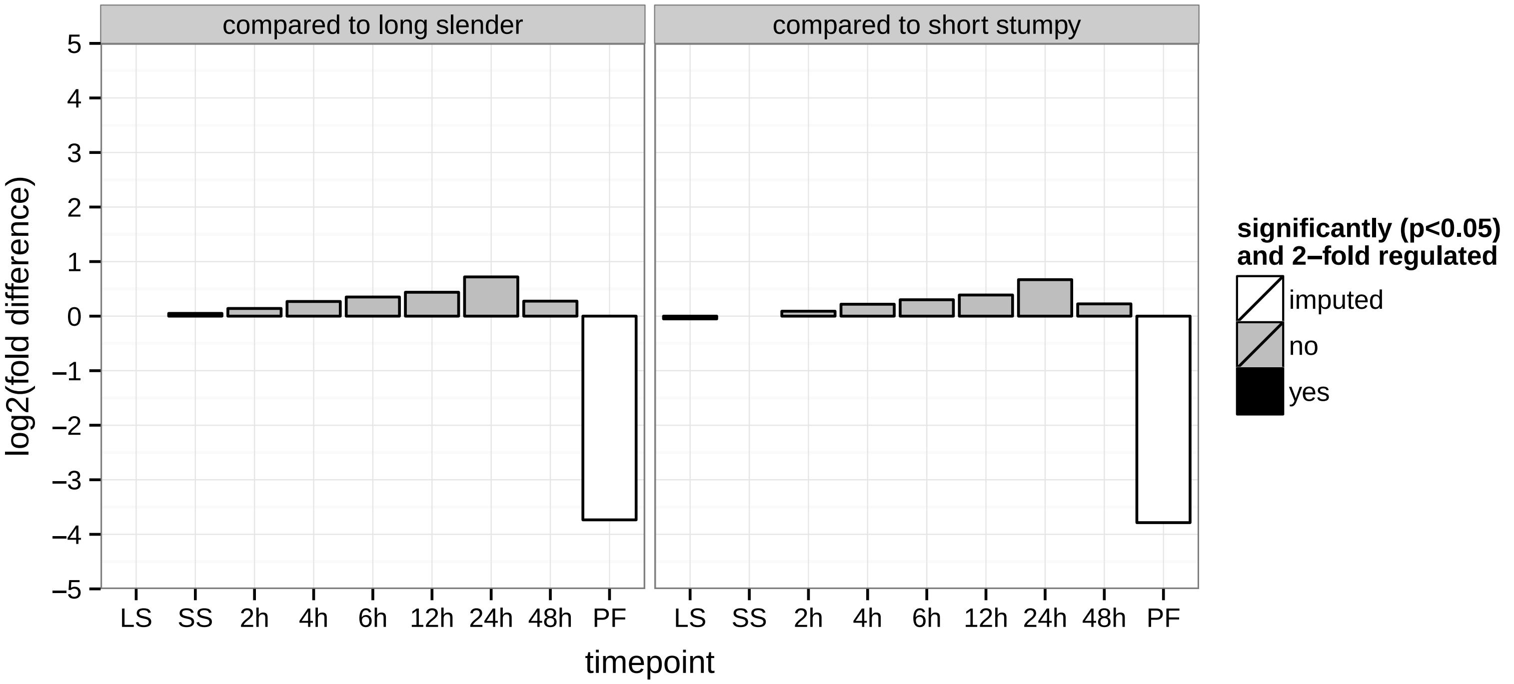
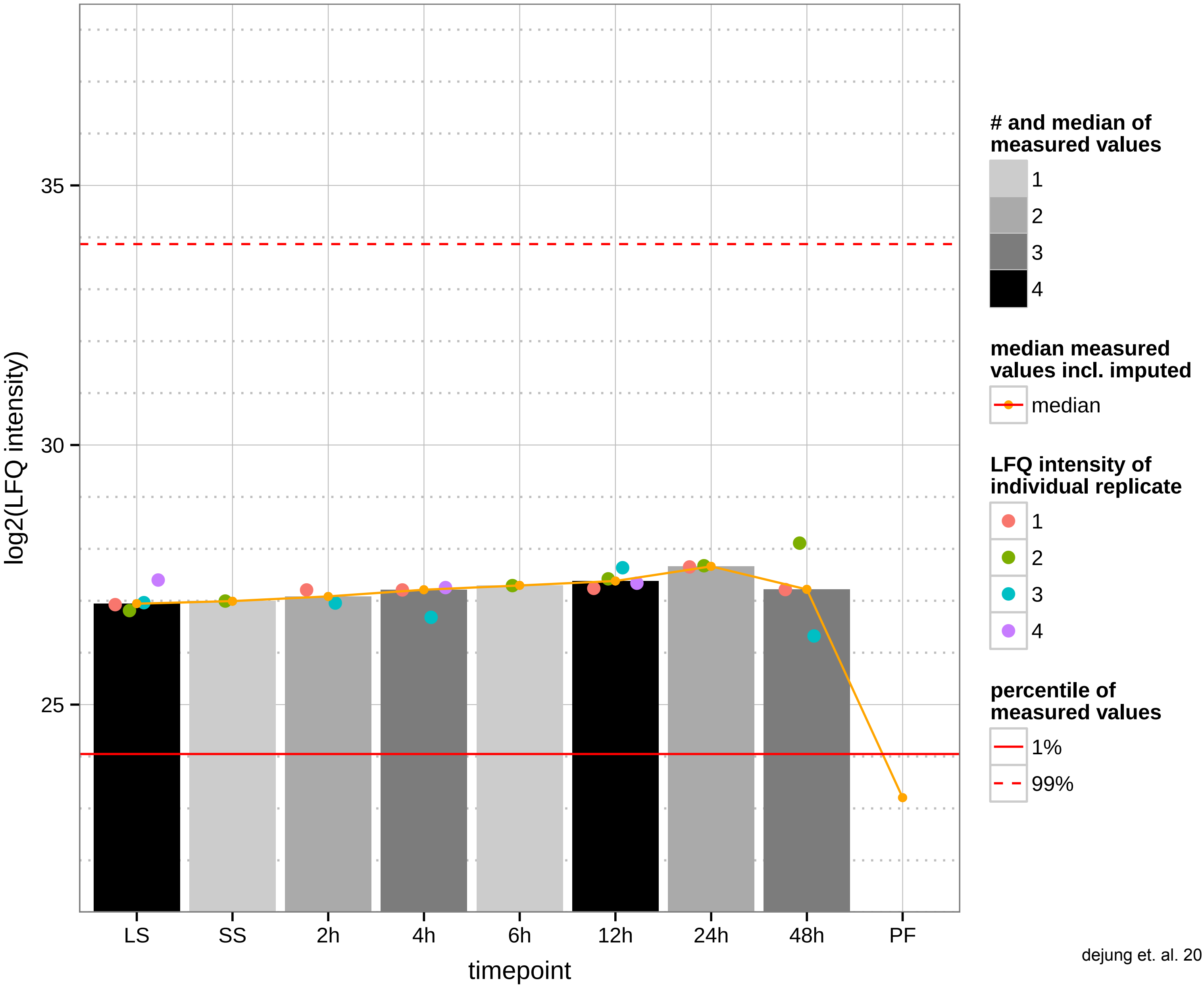
peptidyl–prolyl cis–trans isomerase, putative (PPIase)
Tb927.7.3420
AGOF: null
AGOC: null
AGOP: protein folding
PGOF: null
PGOC: null
PGOP: protein folding





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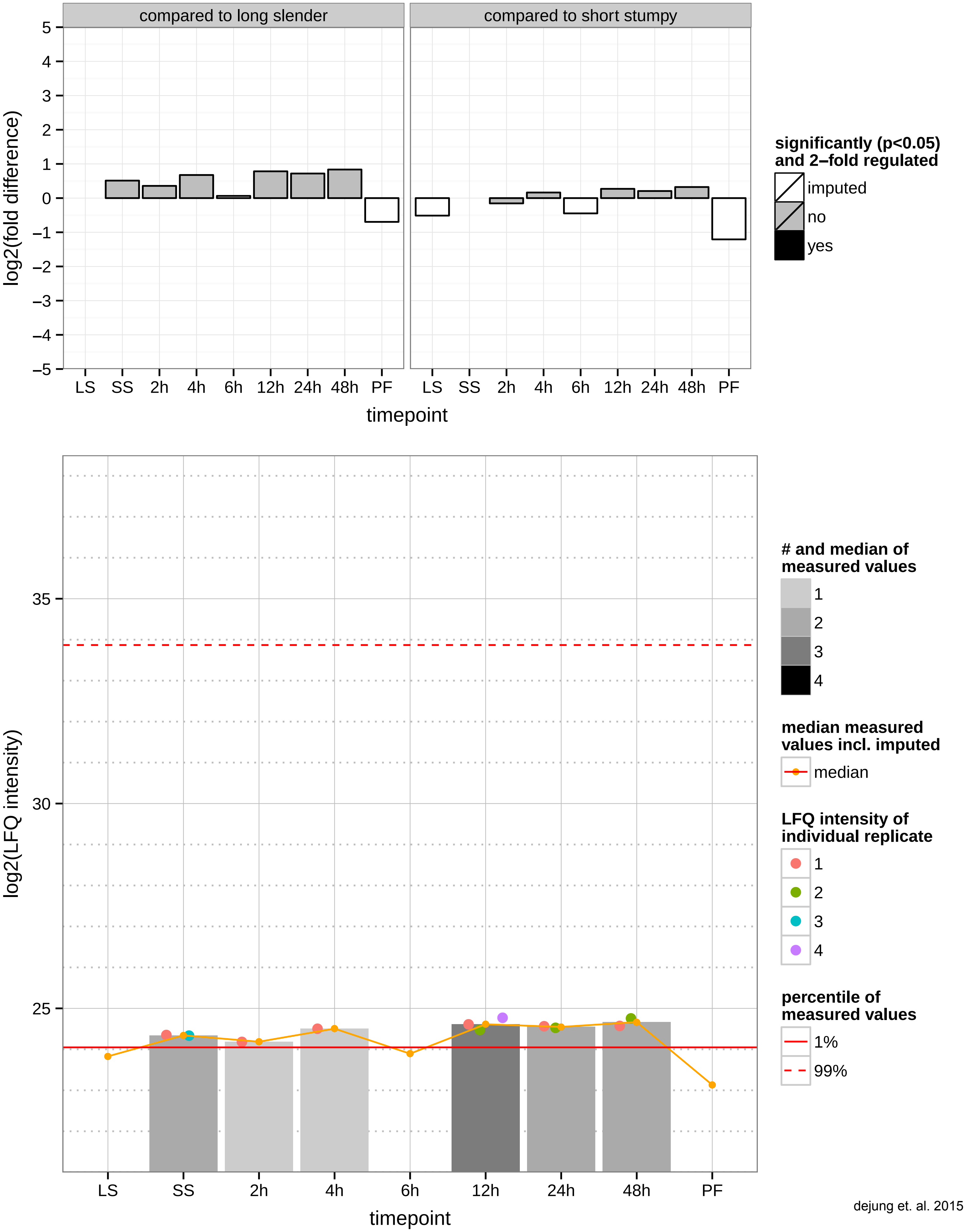
hypothetical protein, conserved
Tb927.7.3510
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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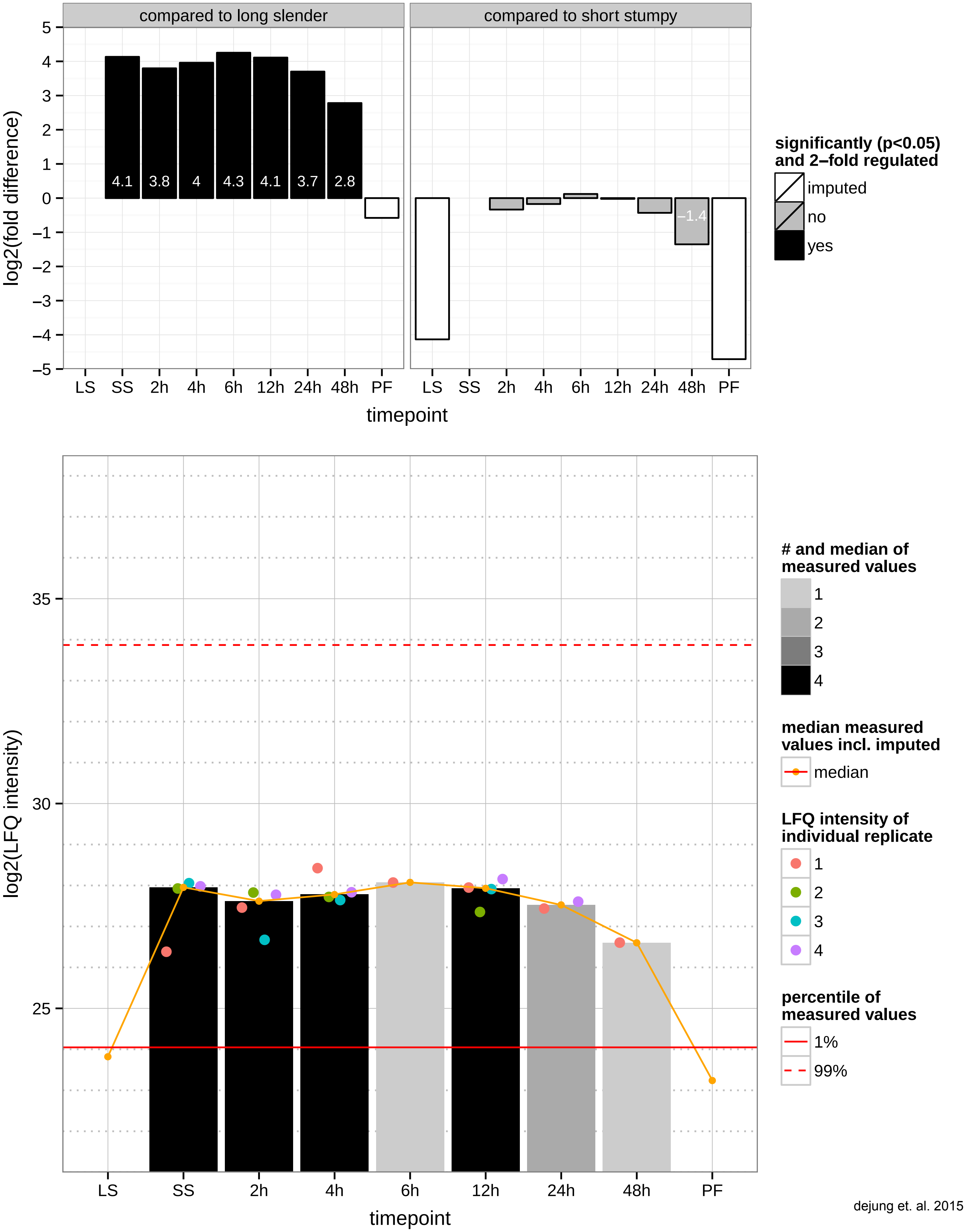
hypothetical protein, conserved
Tb927.7.3530
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null



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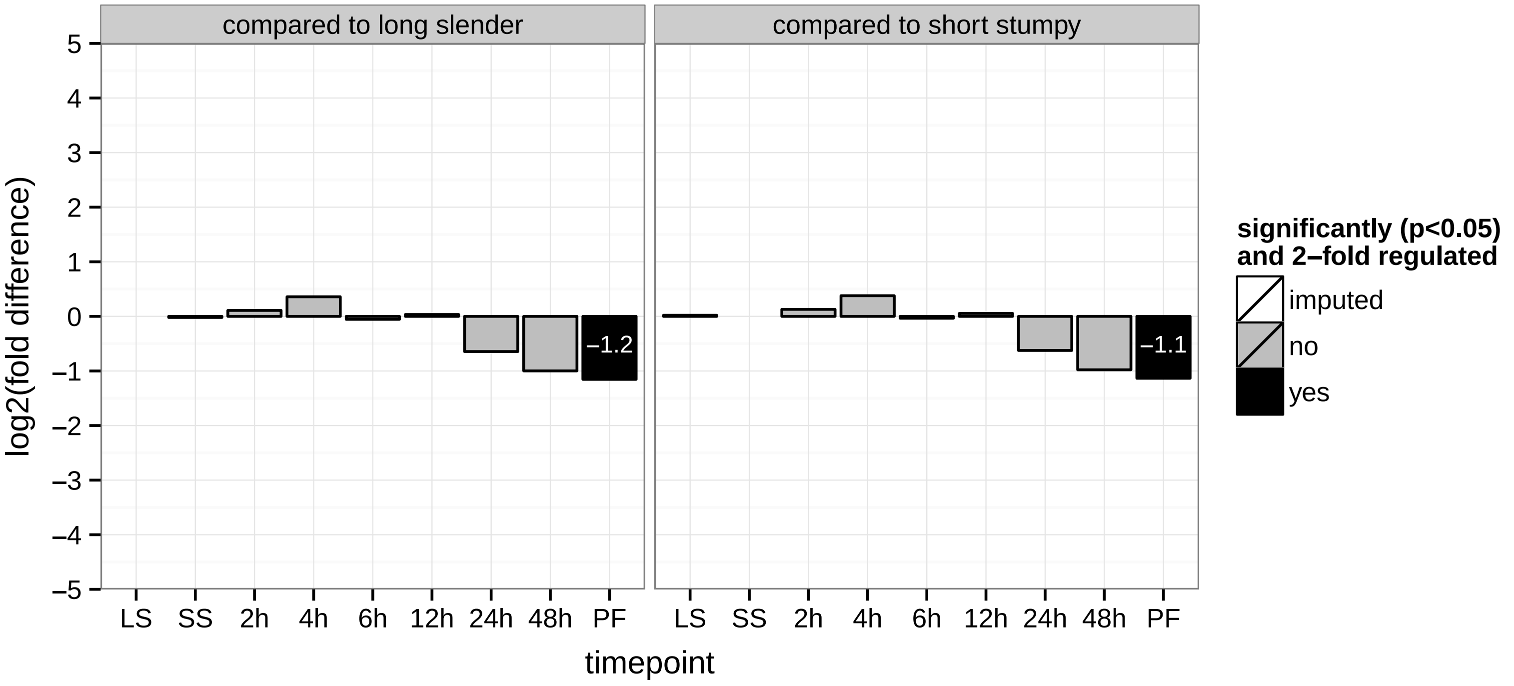
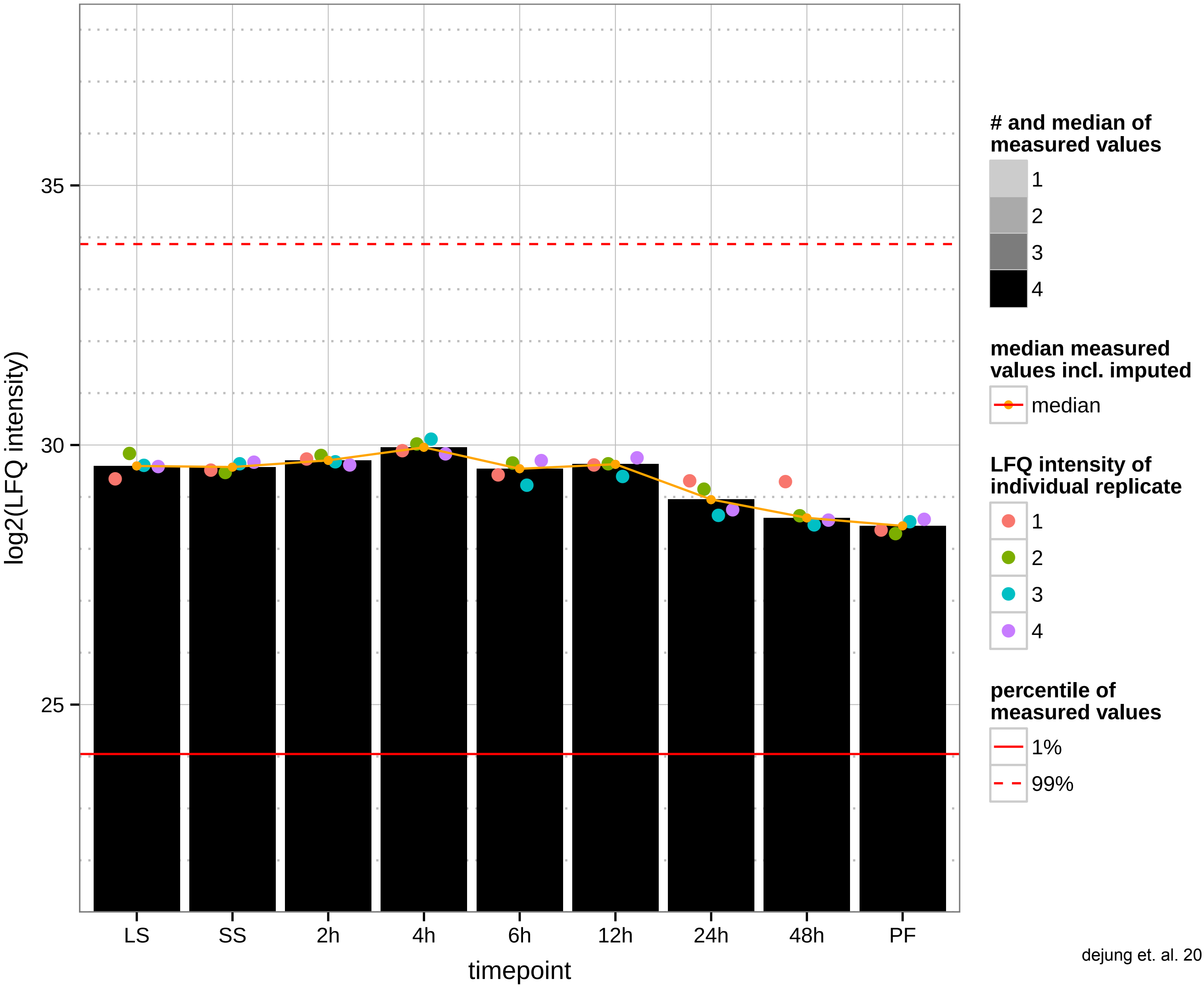
TPR–repeat–containing chaperone protein DNAJ, putative
Tb927.7.3630
AGOF: heat shock protein binding
AGOC: null
AGOP: null
PGOF: heat shock protein binding, protein binding
PGOC: null
PGOP: null





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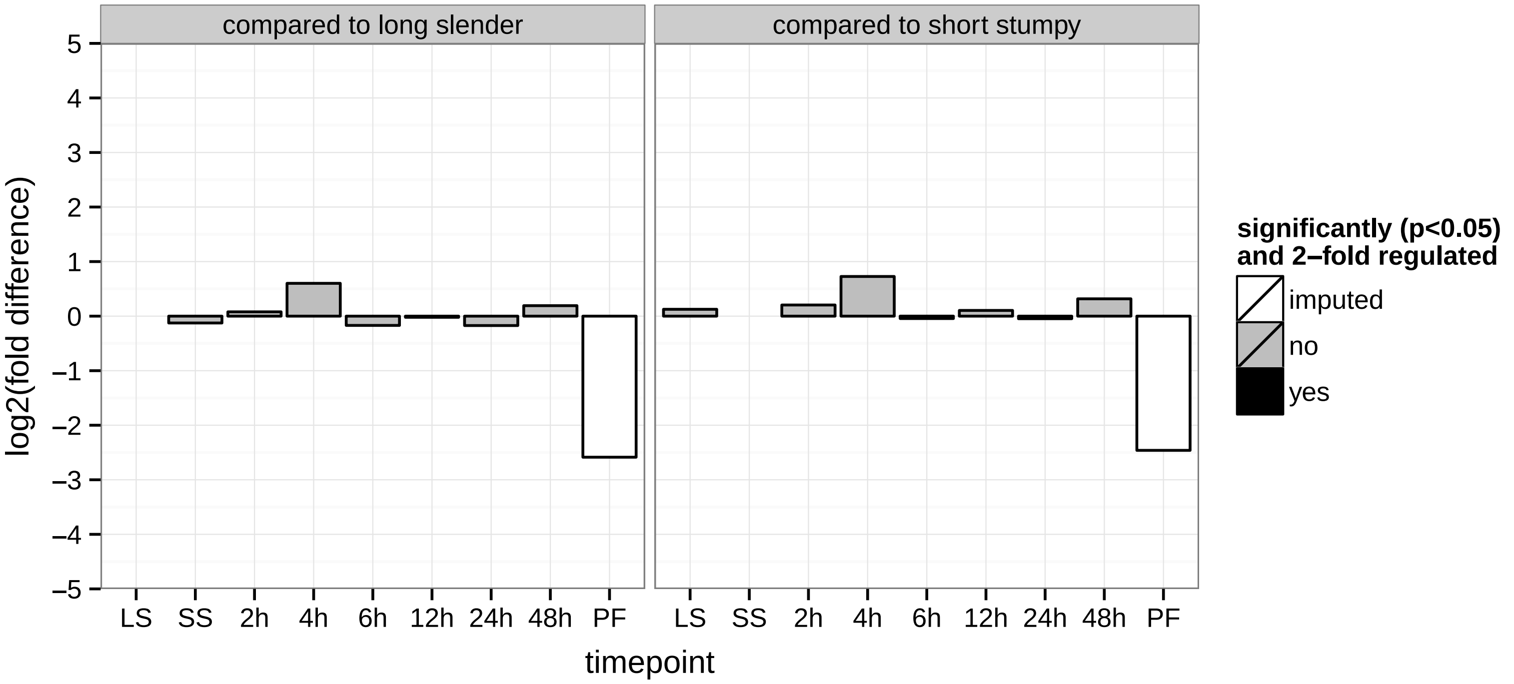
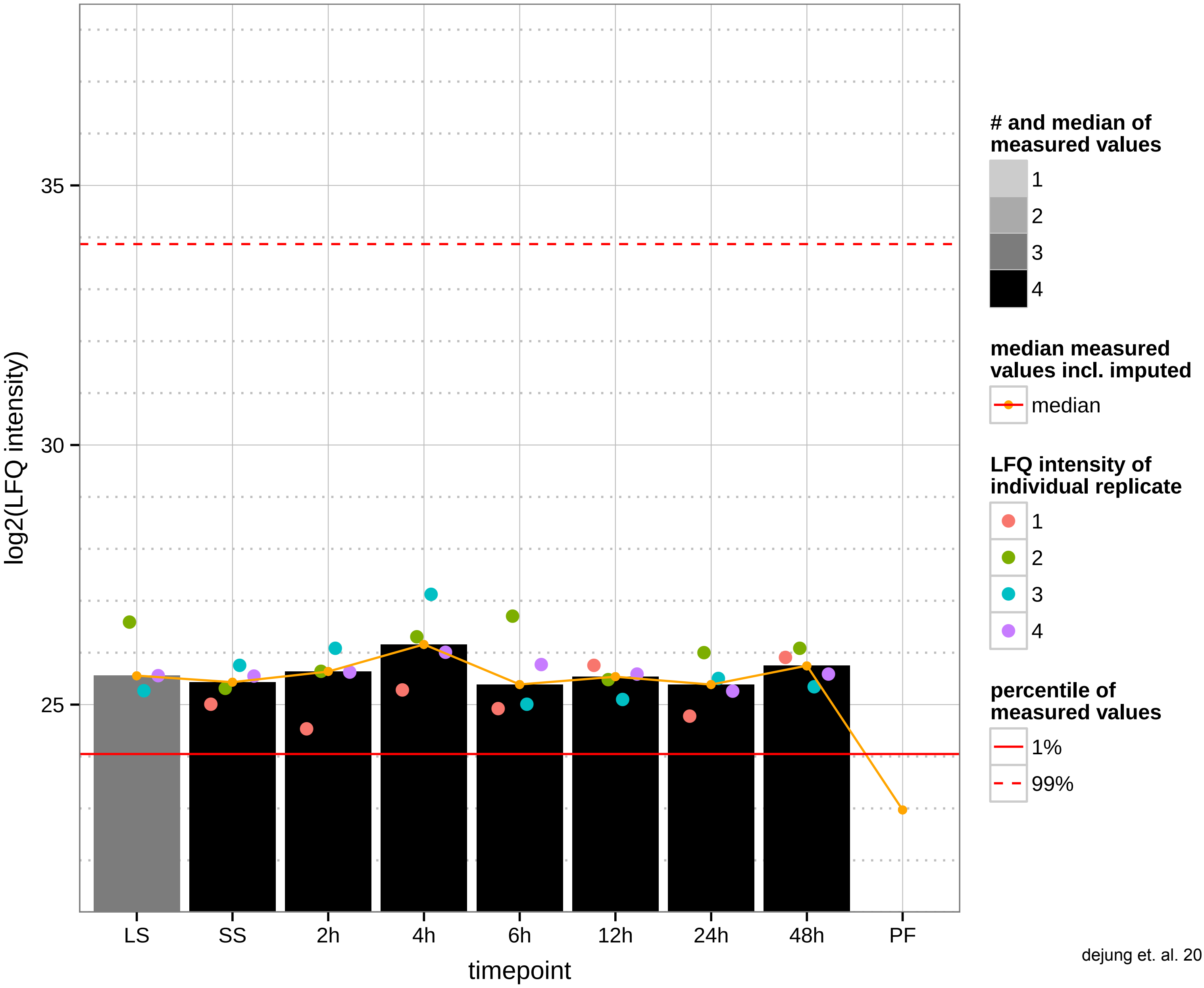
hypothetical protein, conserved
Tb927.7.3870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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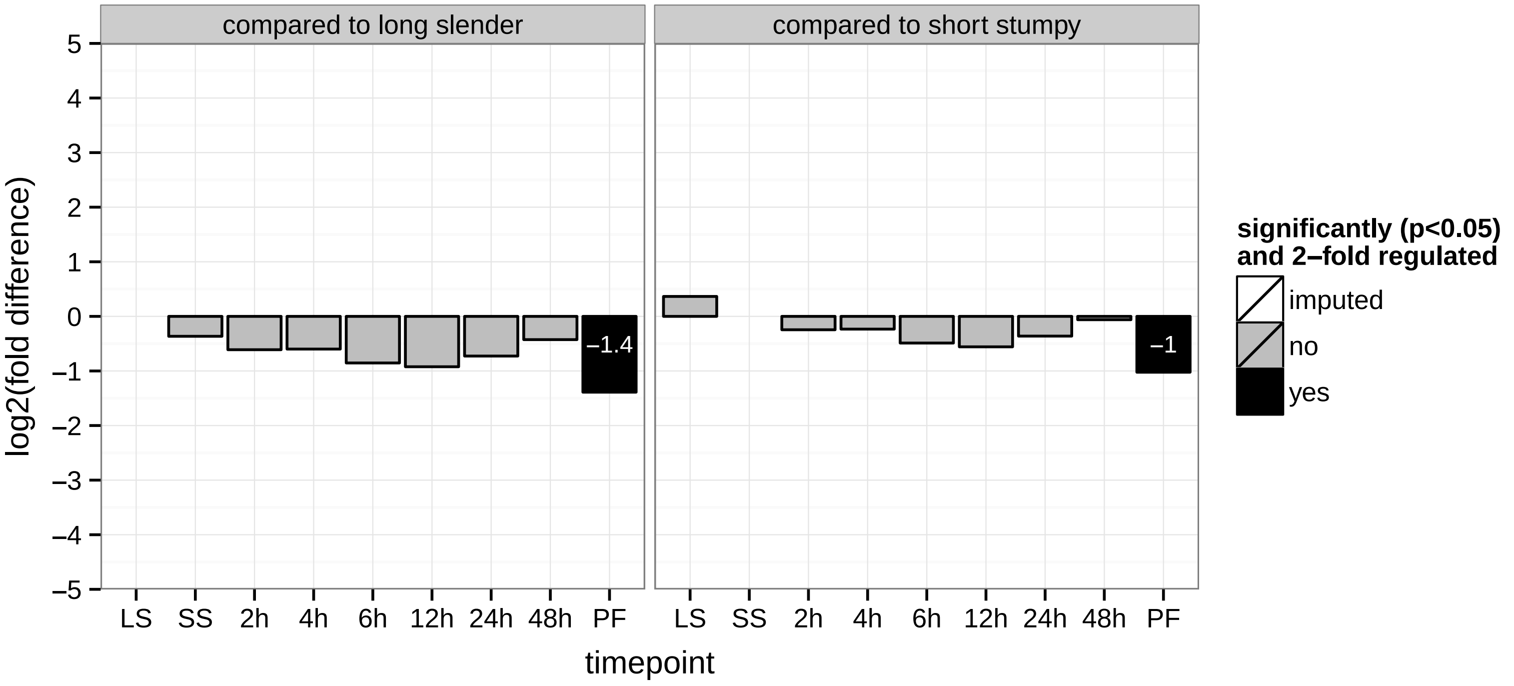
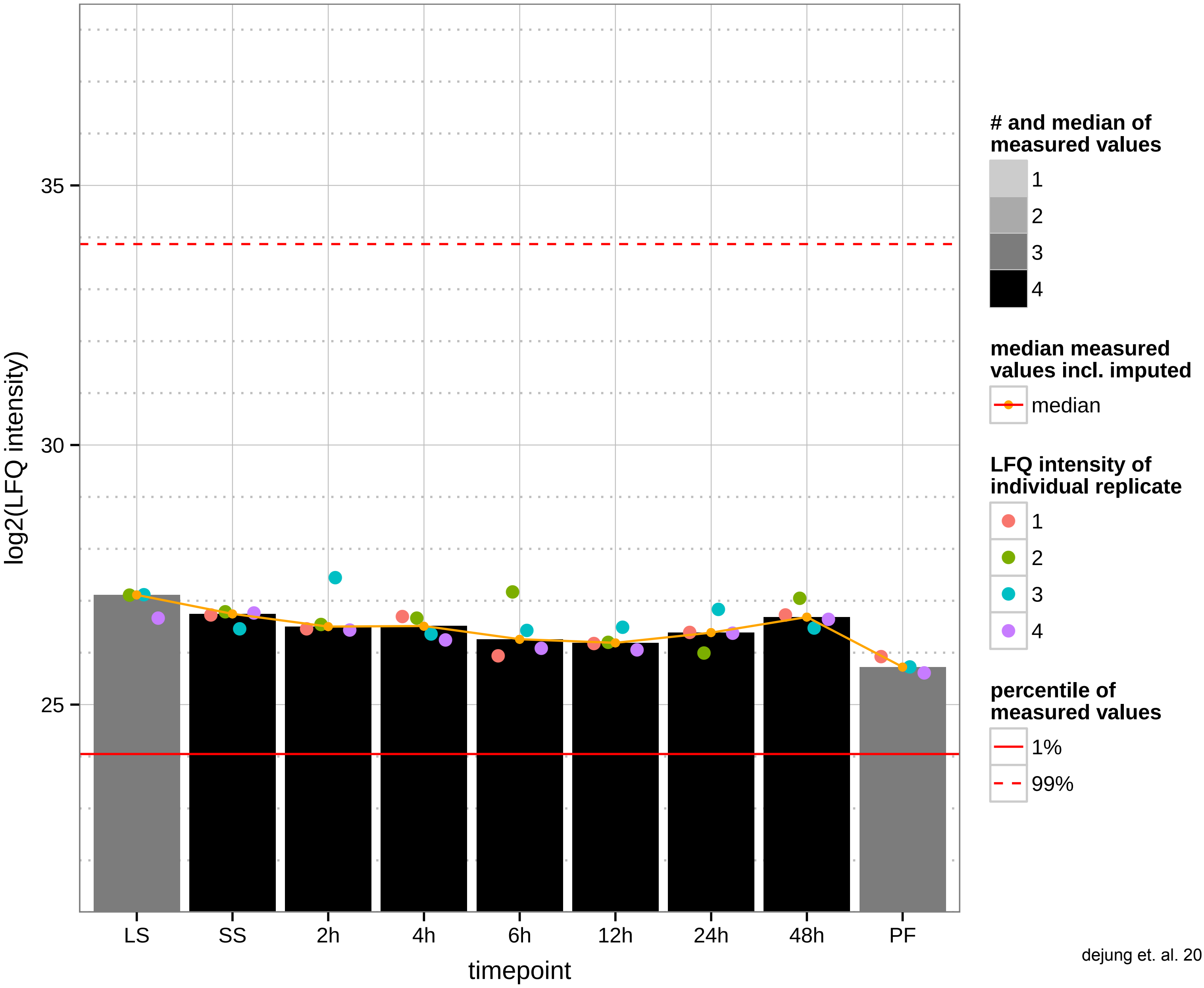
hypothetical protein, conserved
Tb927.7.4100
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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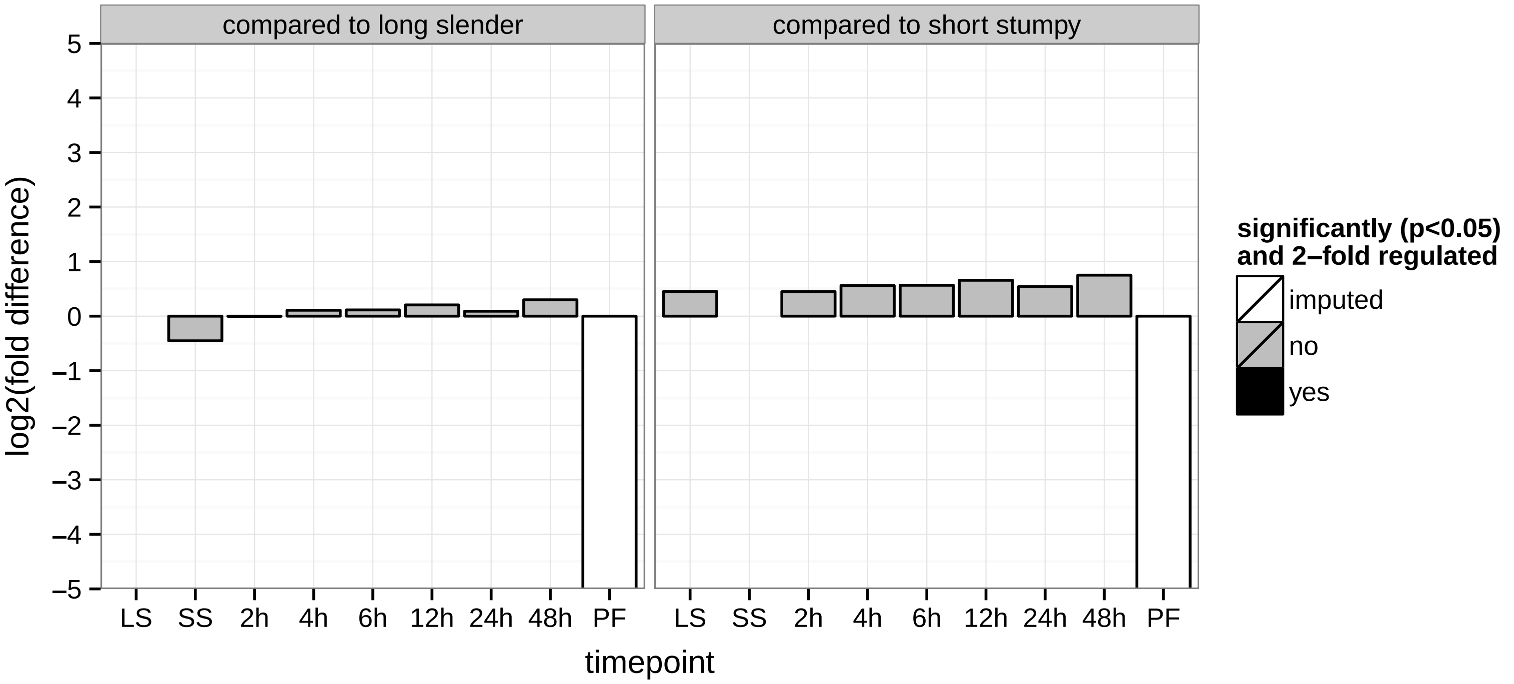
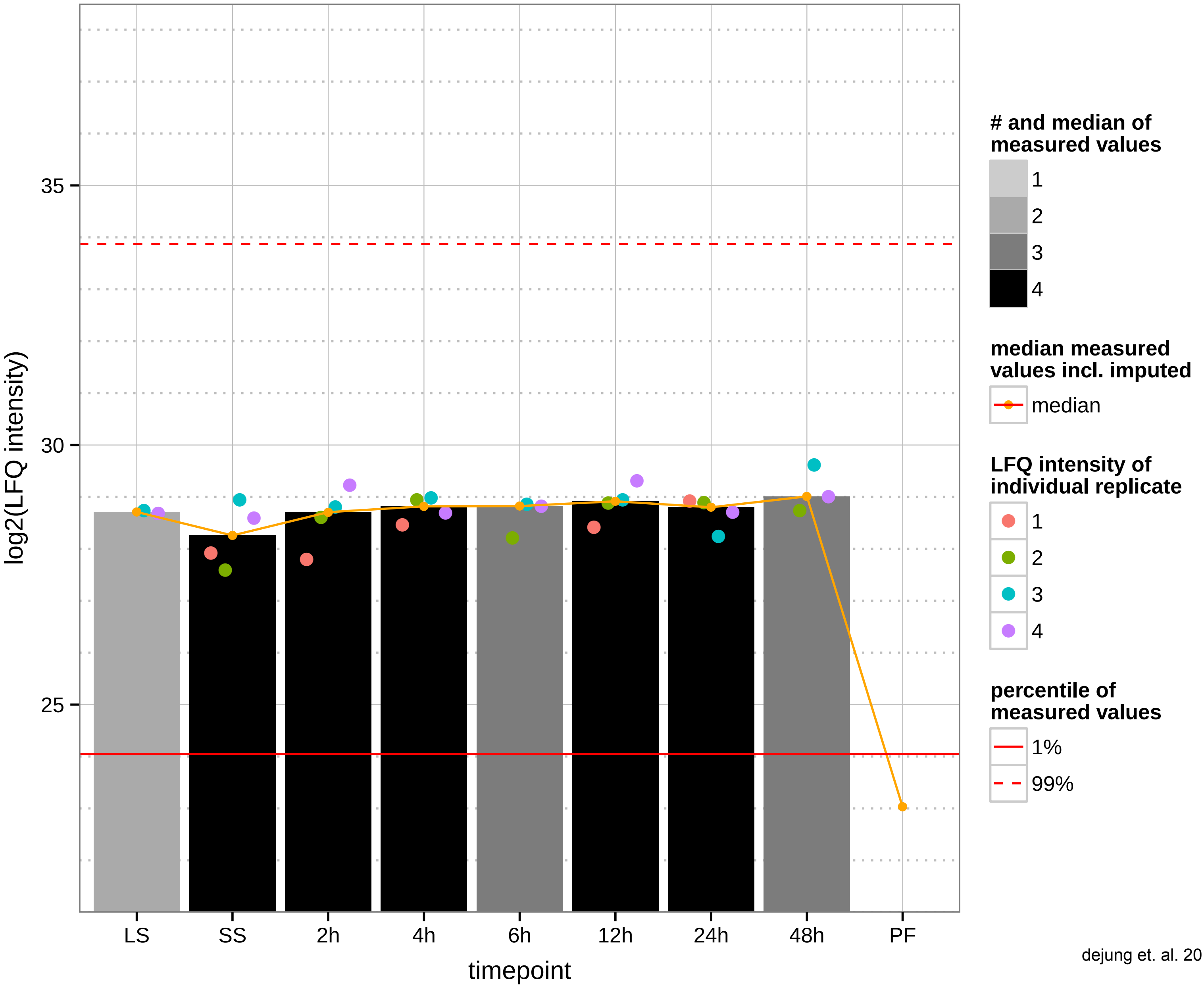
fatty acid elongase, putative
Tb927.7.4170
AGOF: fatty acid elongase activity
AGOC: integral to endoplasmic reticulum membrane
AGOP: long–chain fatty acid biosynthetic process
PGOF: null
PGOC: integral to membrane
PGOP: null





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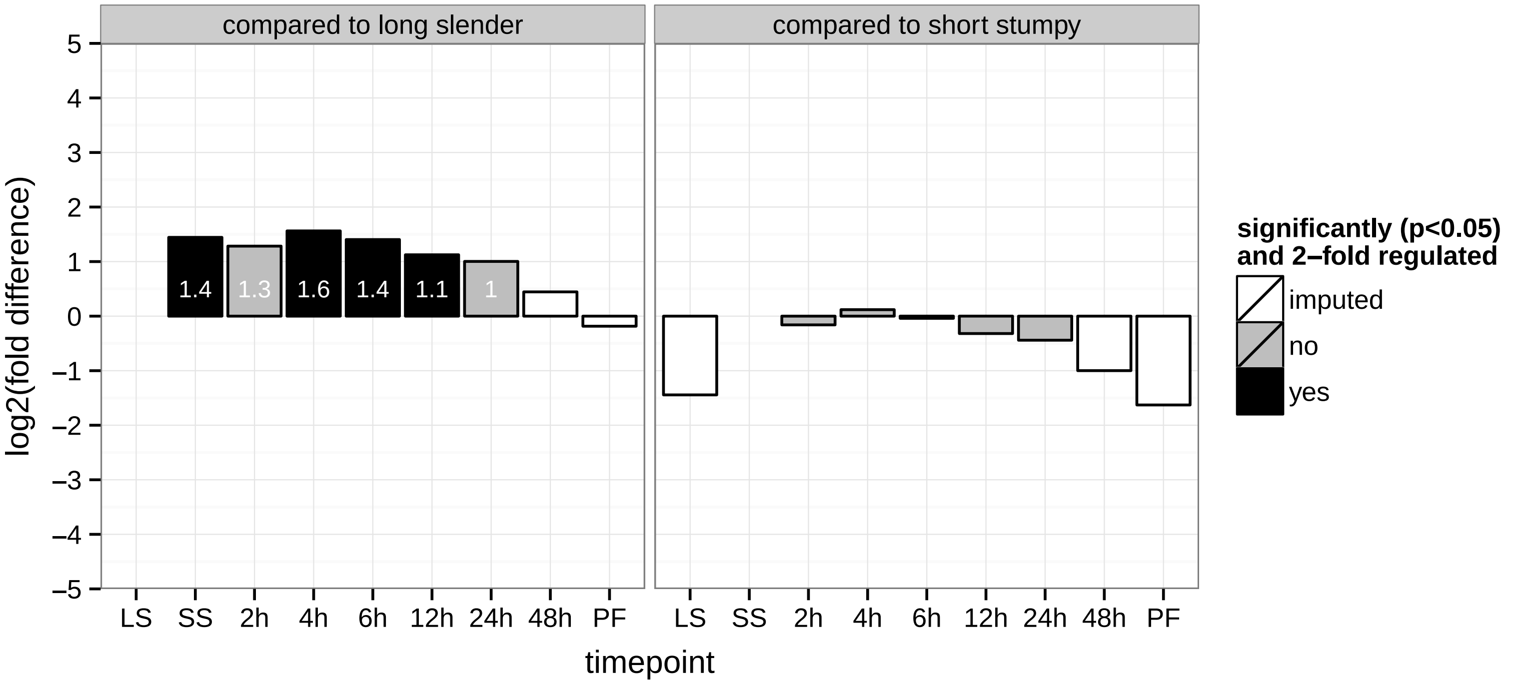
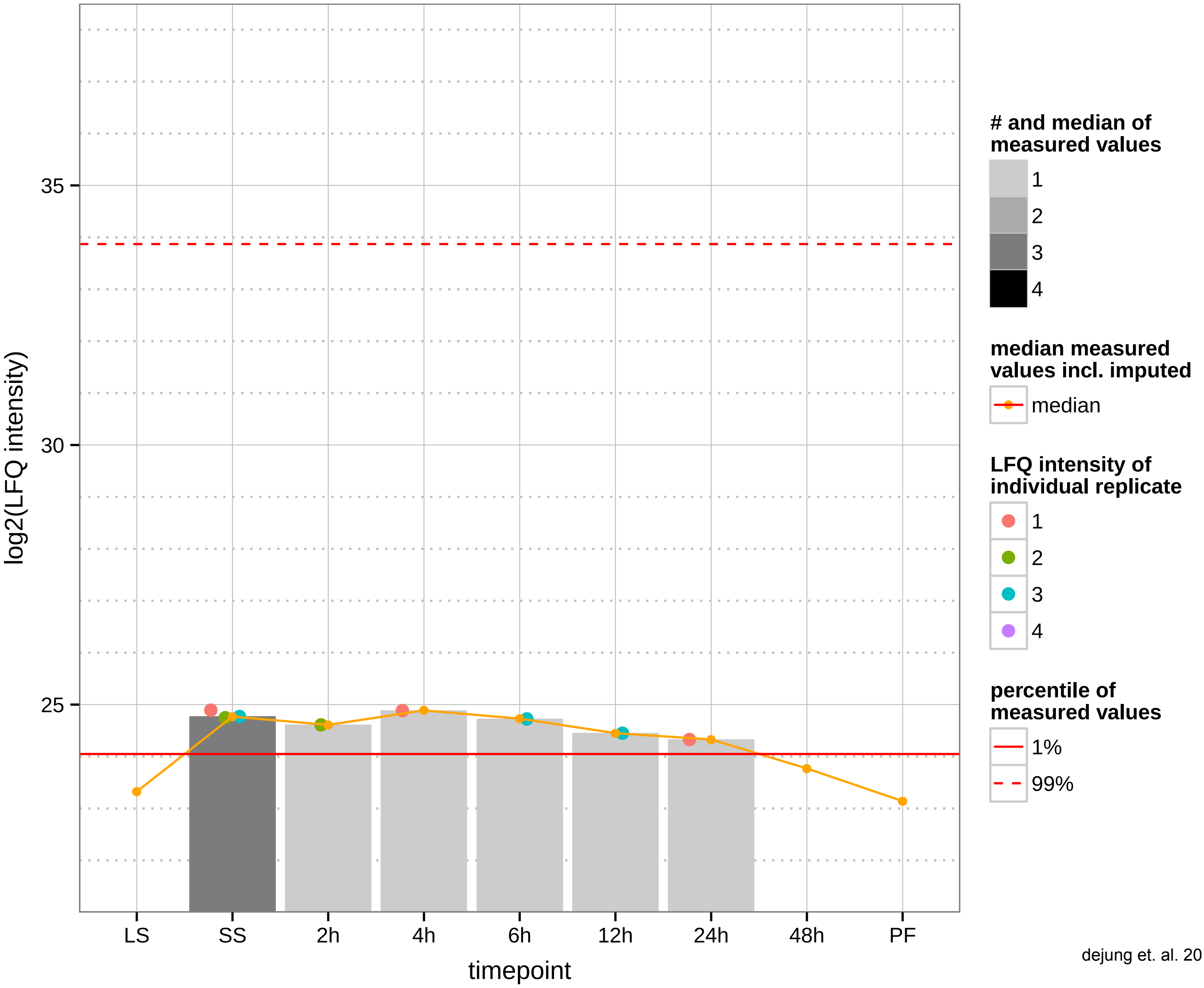
hypothetical protein, conserved
Tb927.7.450;Tb927.7.390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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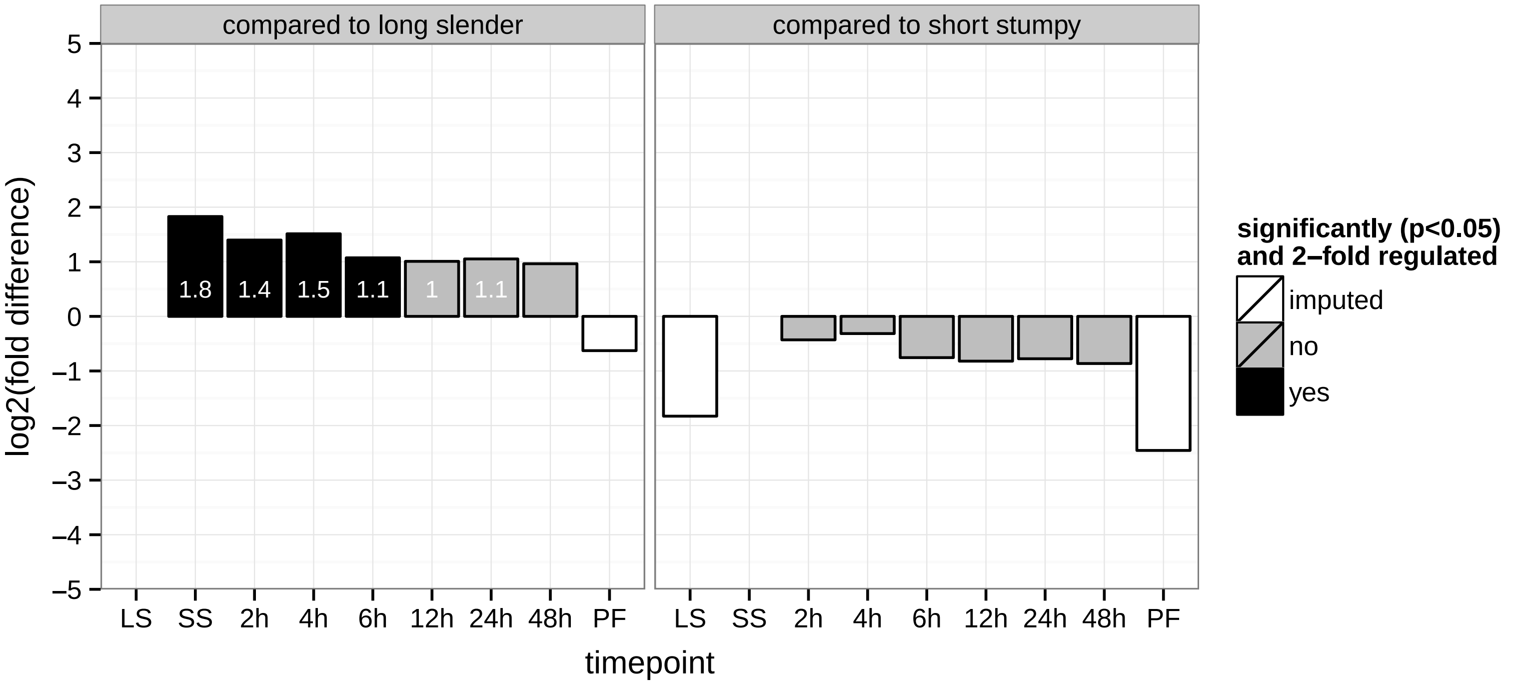
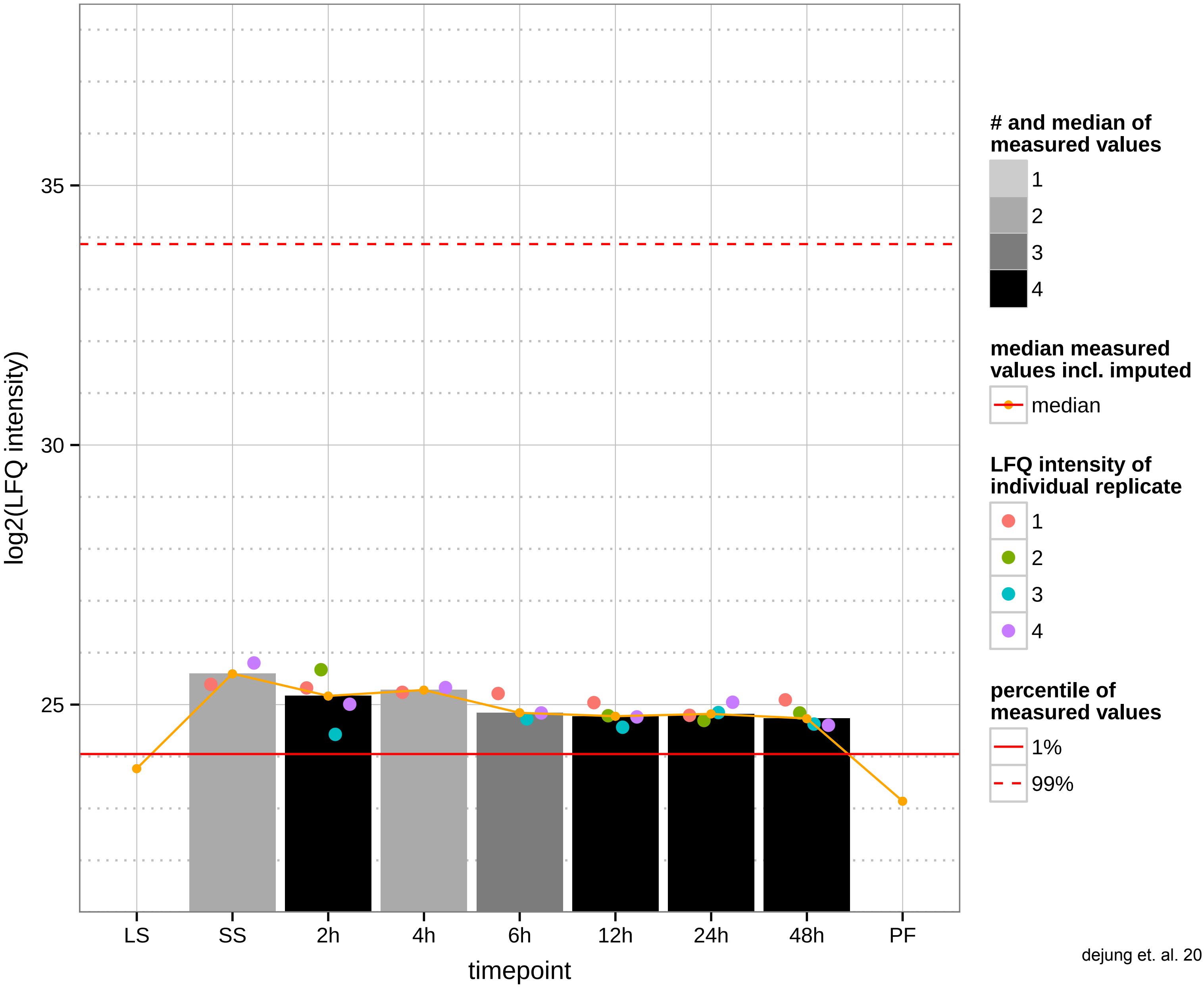
hypothetical protein, conserved
Tb927.7.5310
AGOF: null
AGOC: nucleus
AGOP: regulation of transcription, DNA–dependent
PGOF: null
PGOC: nucleus
PGOP: regulation of transcription, DNA–dependent





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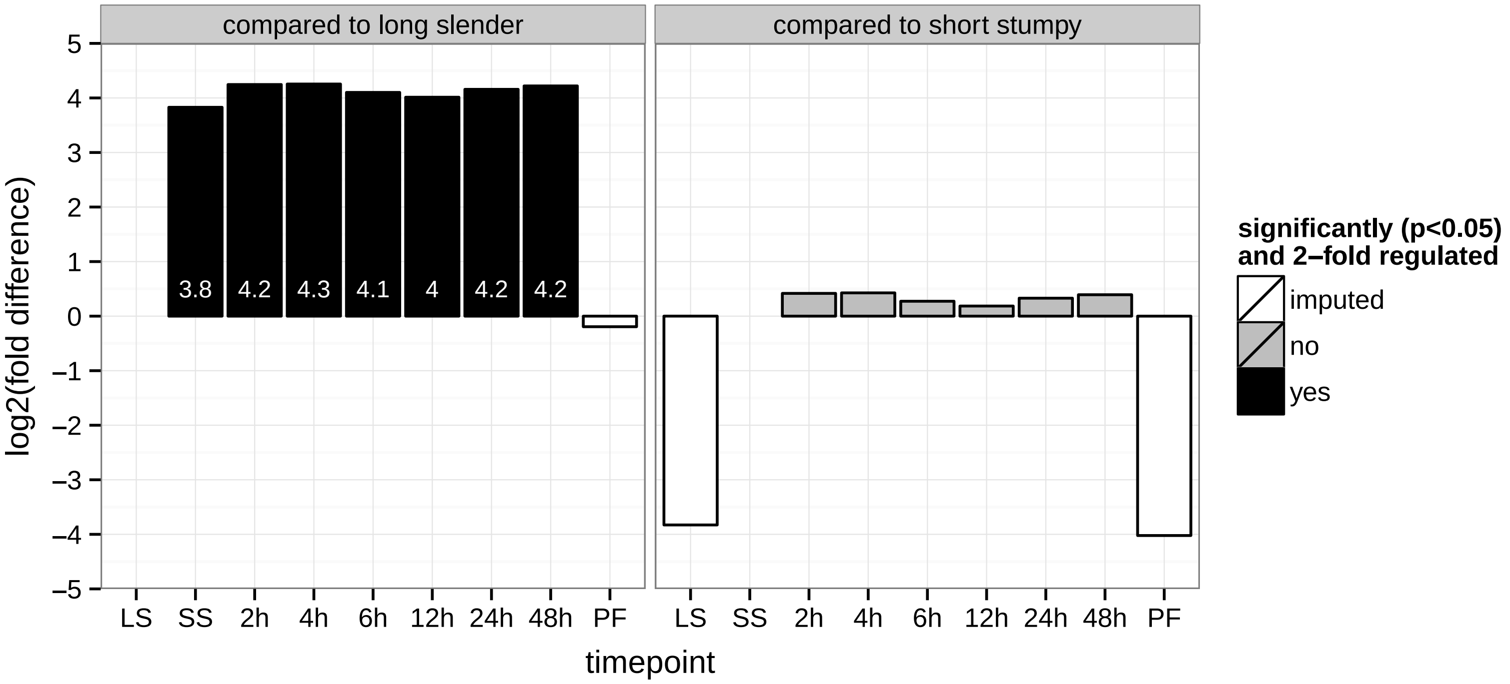
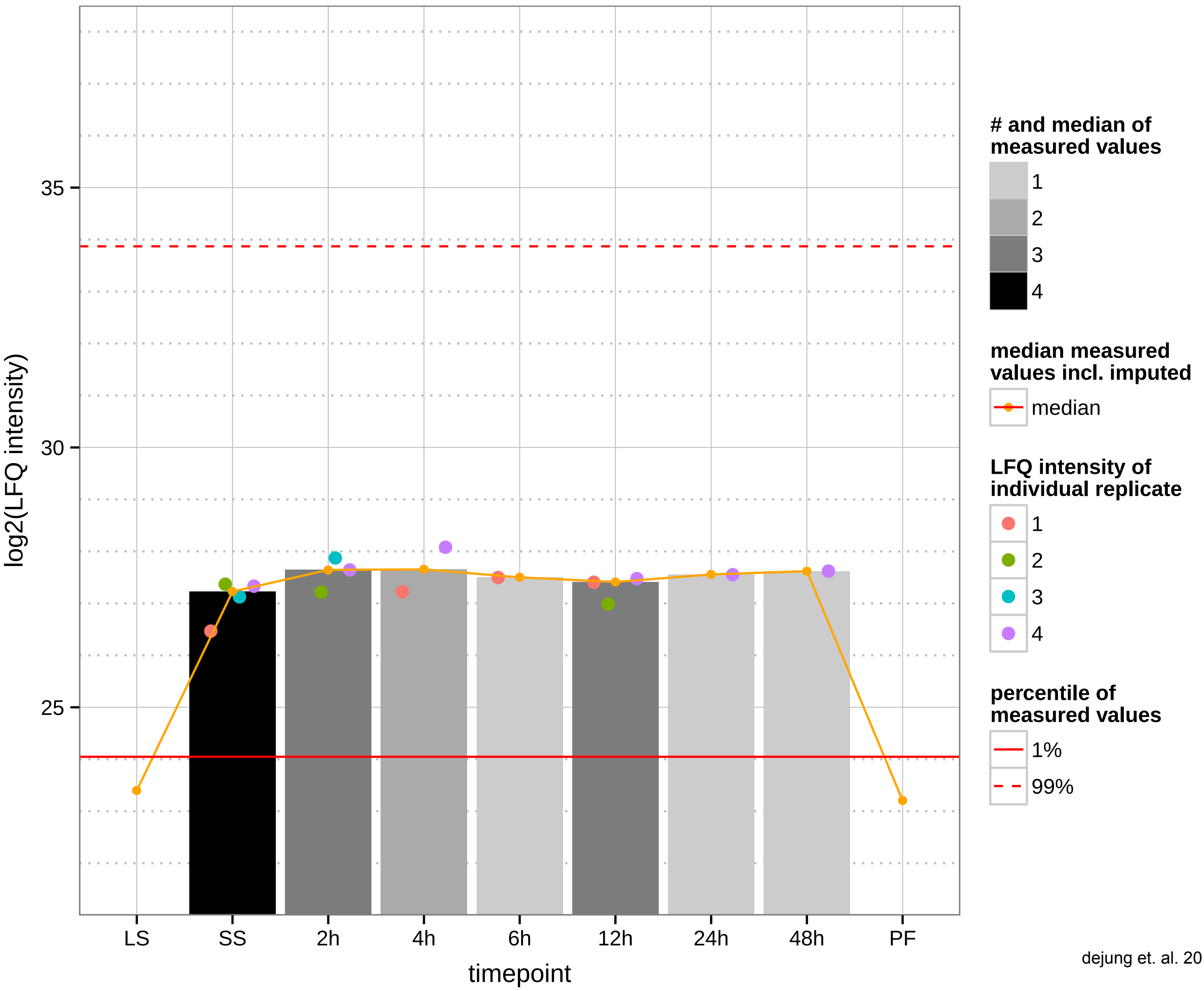
hypothetical protein, conserved
Tb927.7.5330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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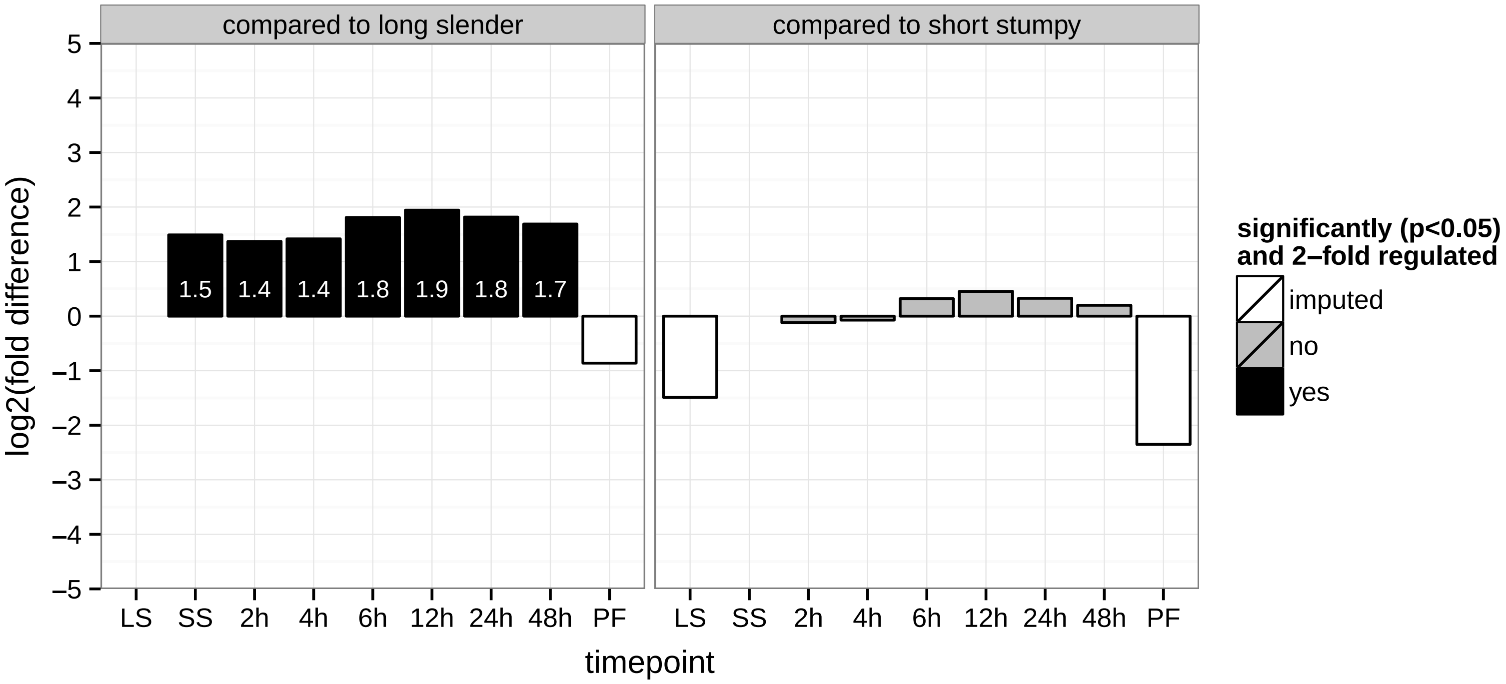
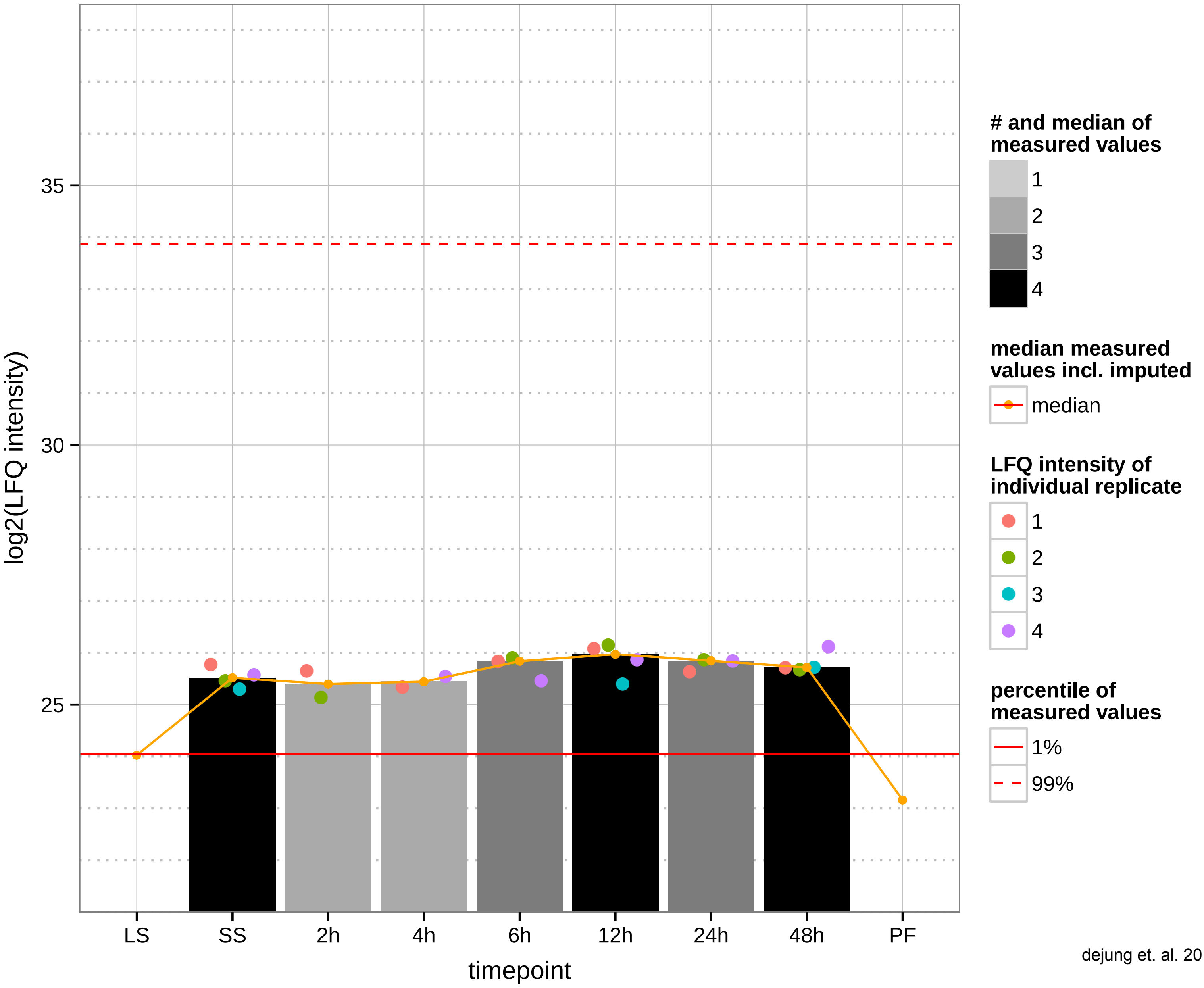
chaperone protein DNAj, putative
Tb927.7.540
AGOF: heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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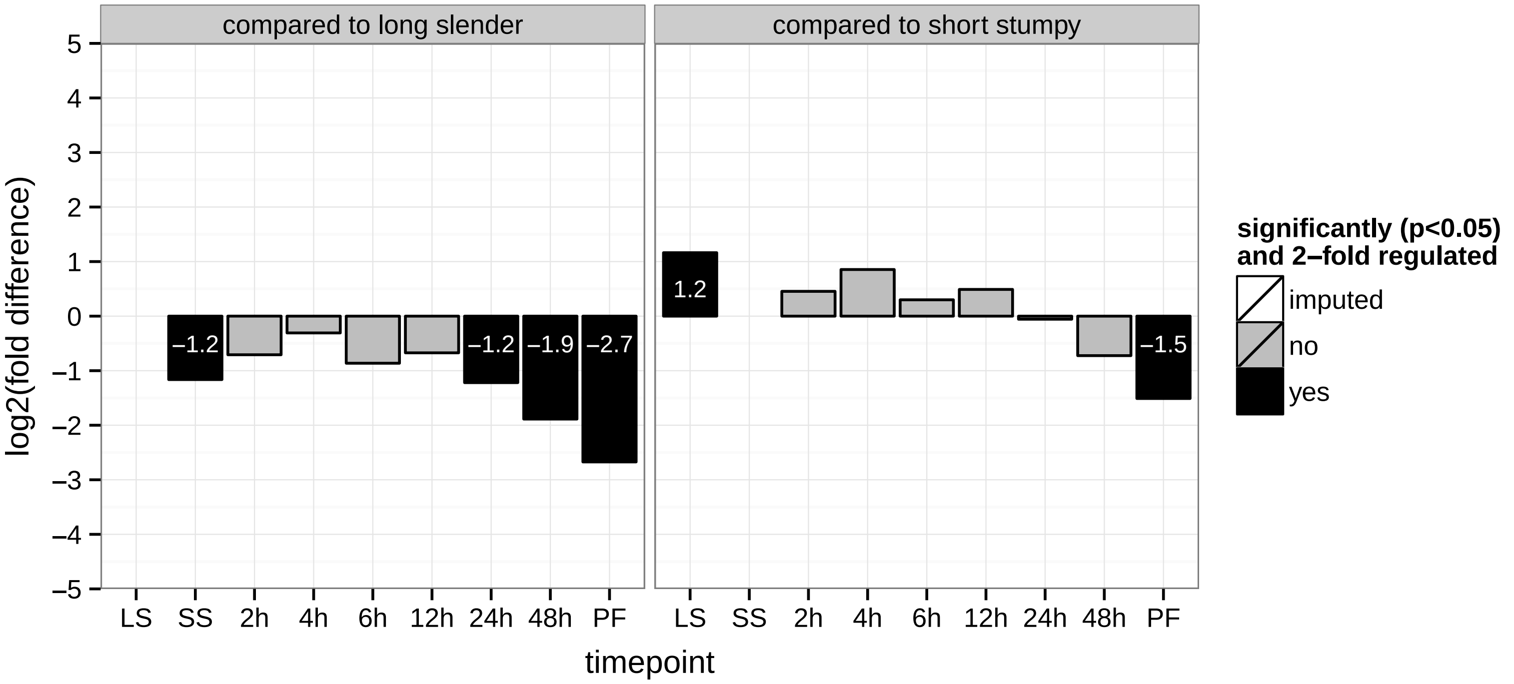
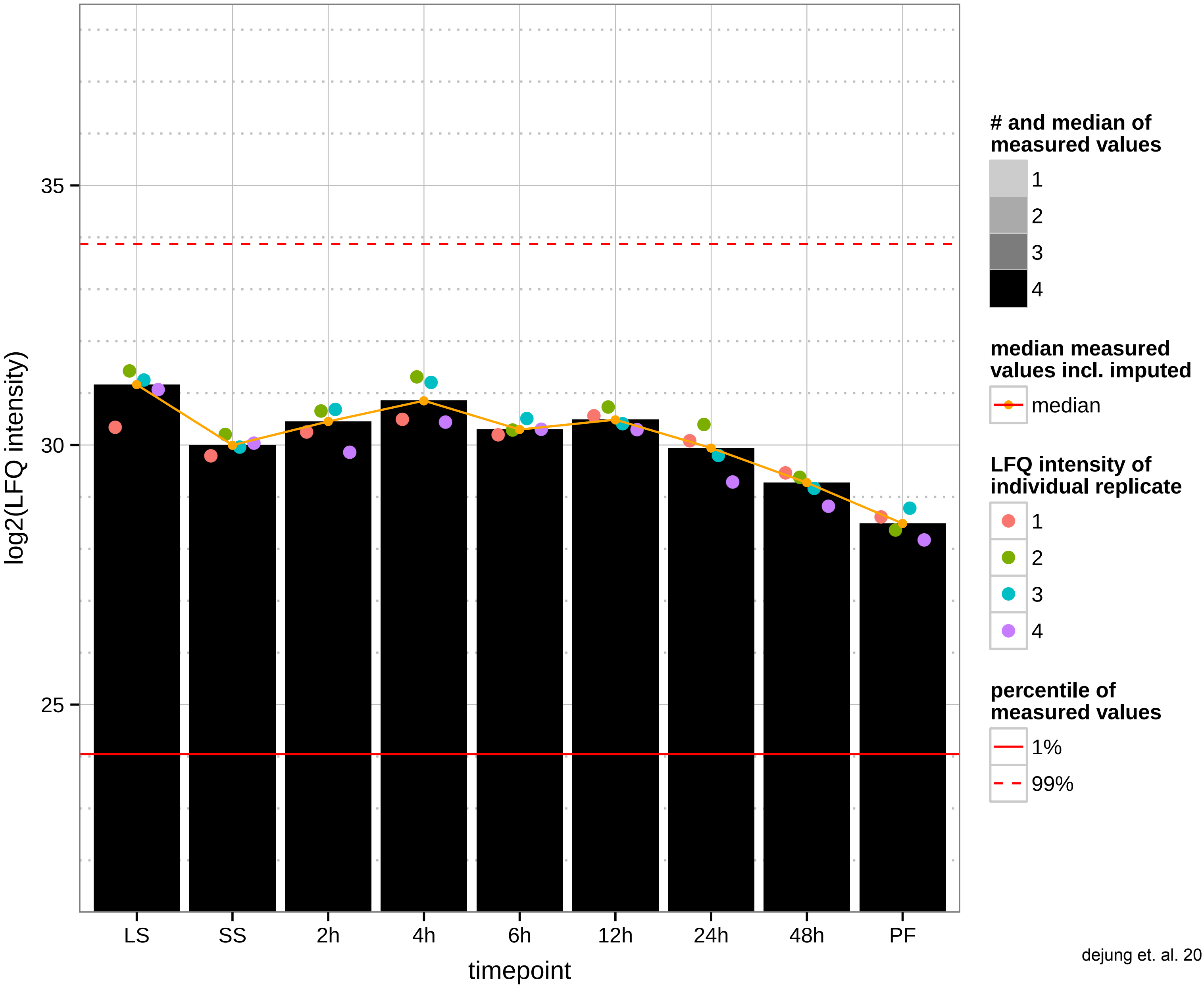
protein disulfide isomerase, putative
Tb927.7.5790
AGOF: null
AGOC: endoplasmic reticulum
AGOP: cell redox homeostasis
PGOF: electron carrier activity, isomerase activity, protein disulfide oxidoreductase activity
PGOC: null
PGOP: cell redox homeostasis, glycerol ether metabolic process





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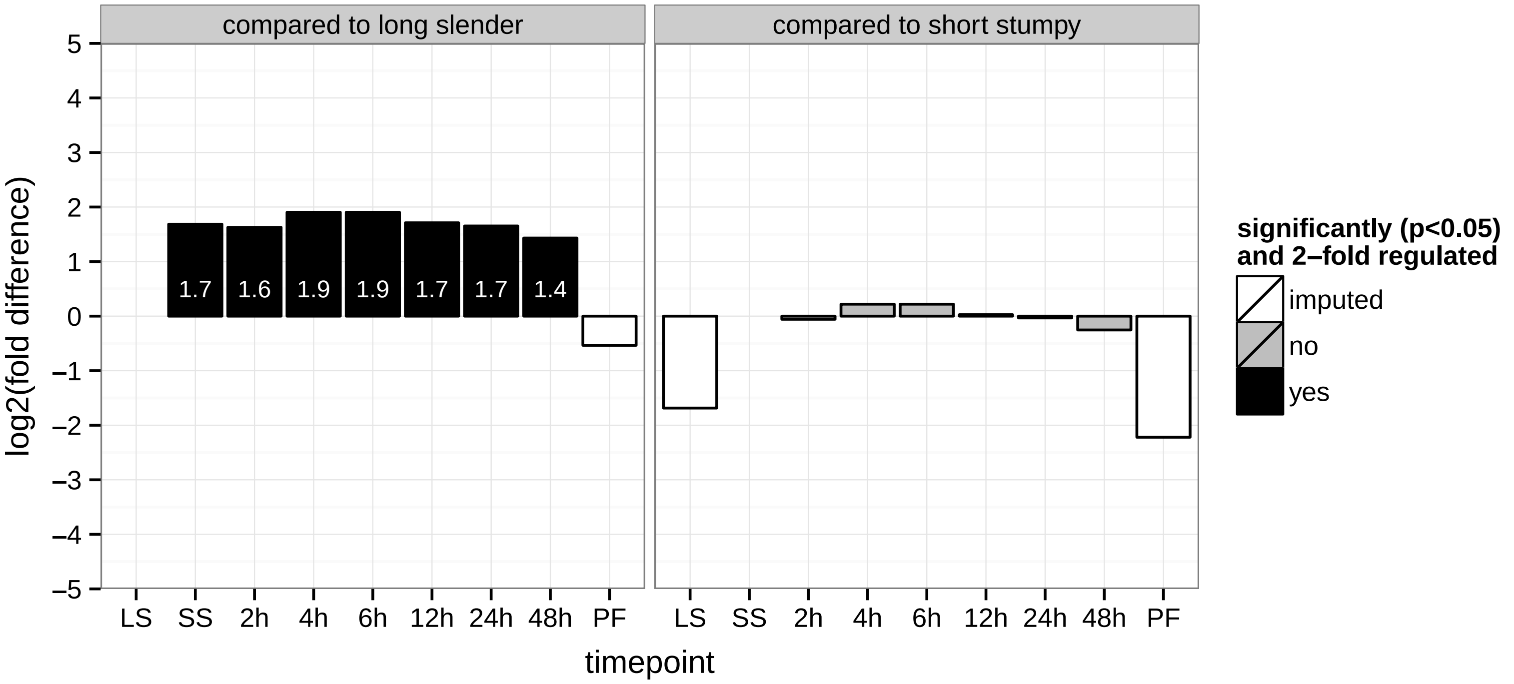
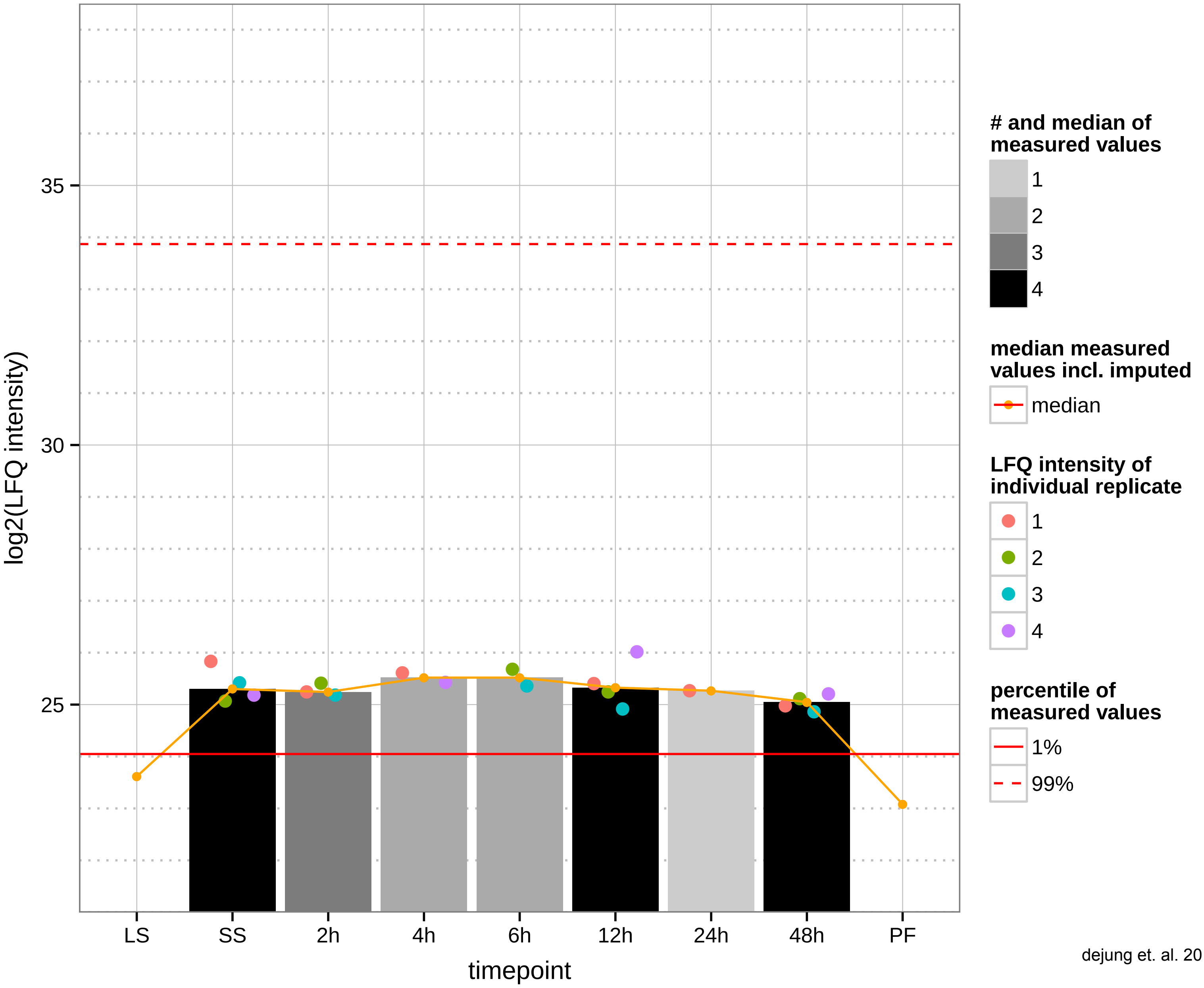
hypothetical protein, conserved
Tb927.7.5850
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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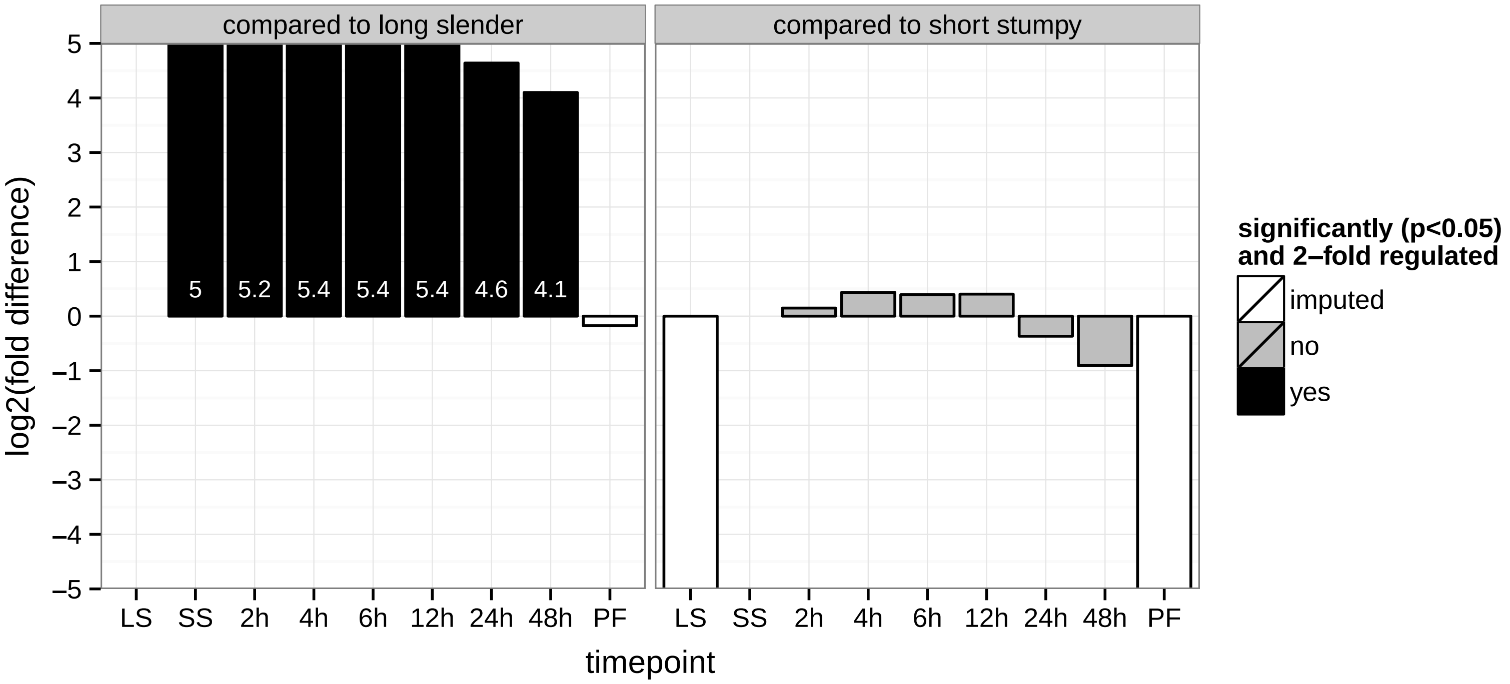
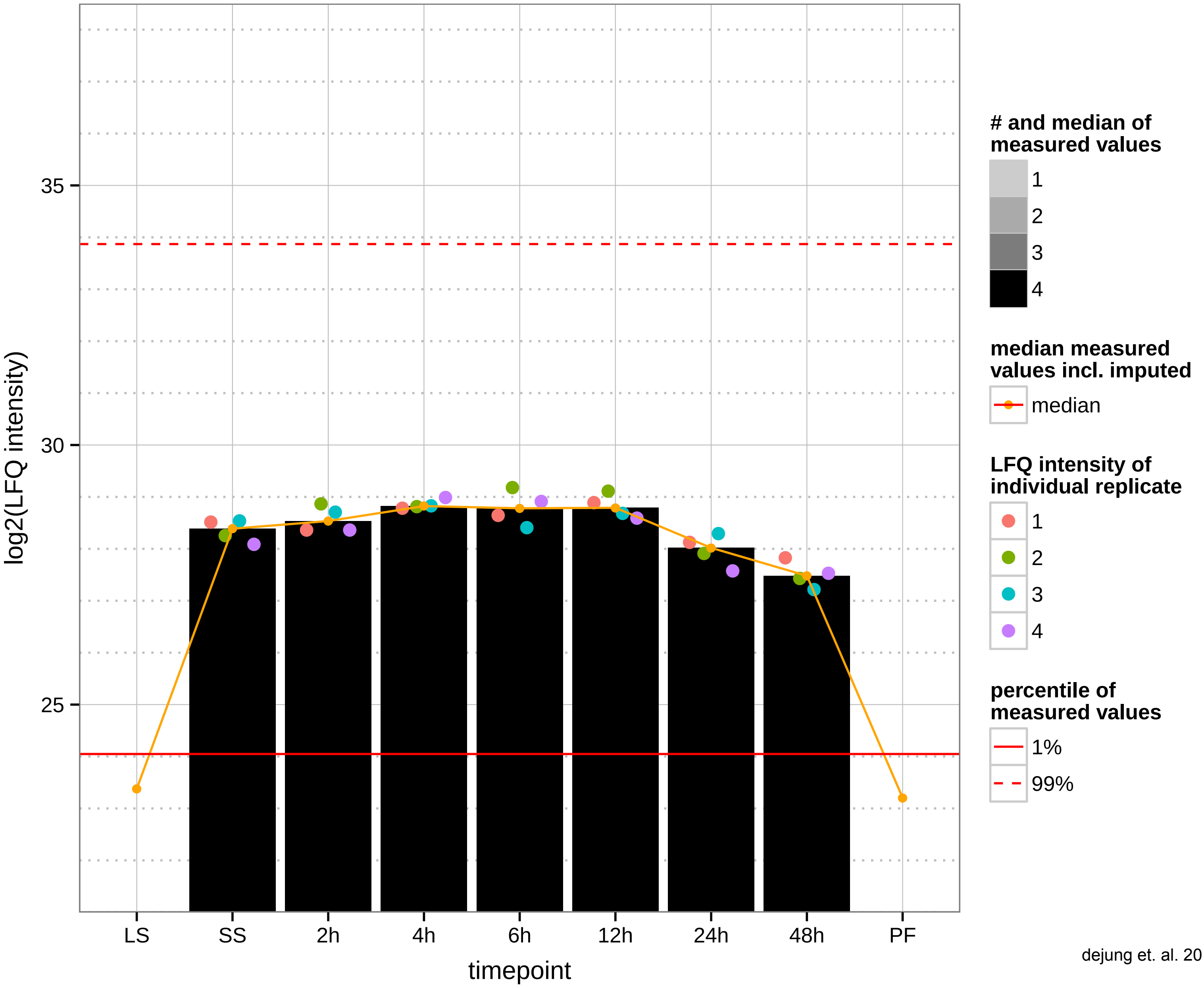
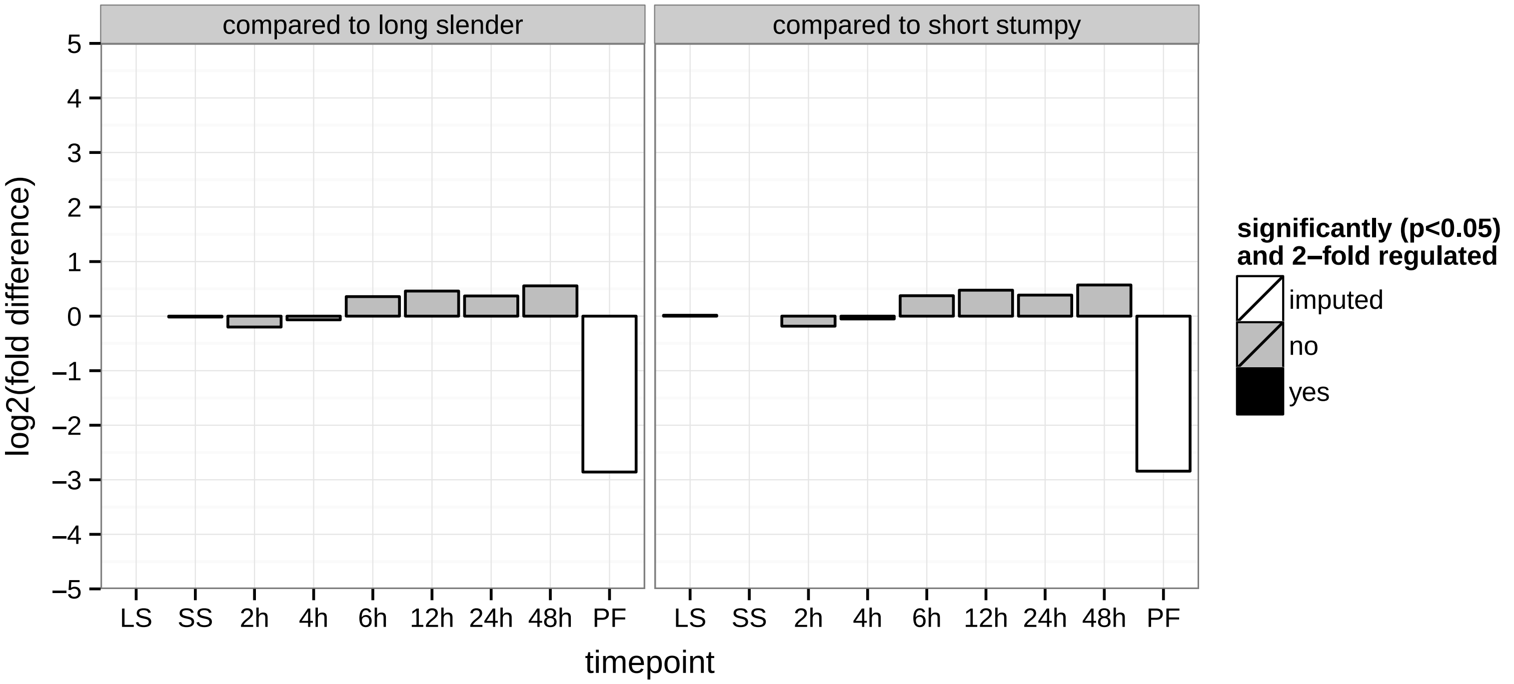
hypothetical protein, conserved
Tb927.7.6340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

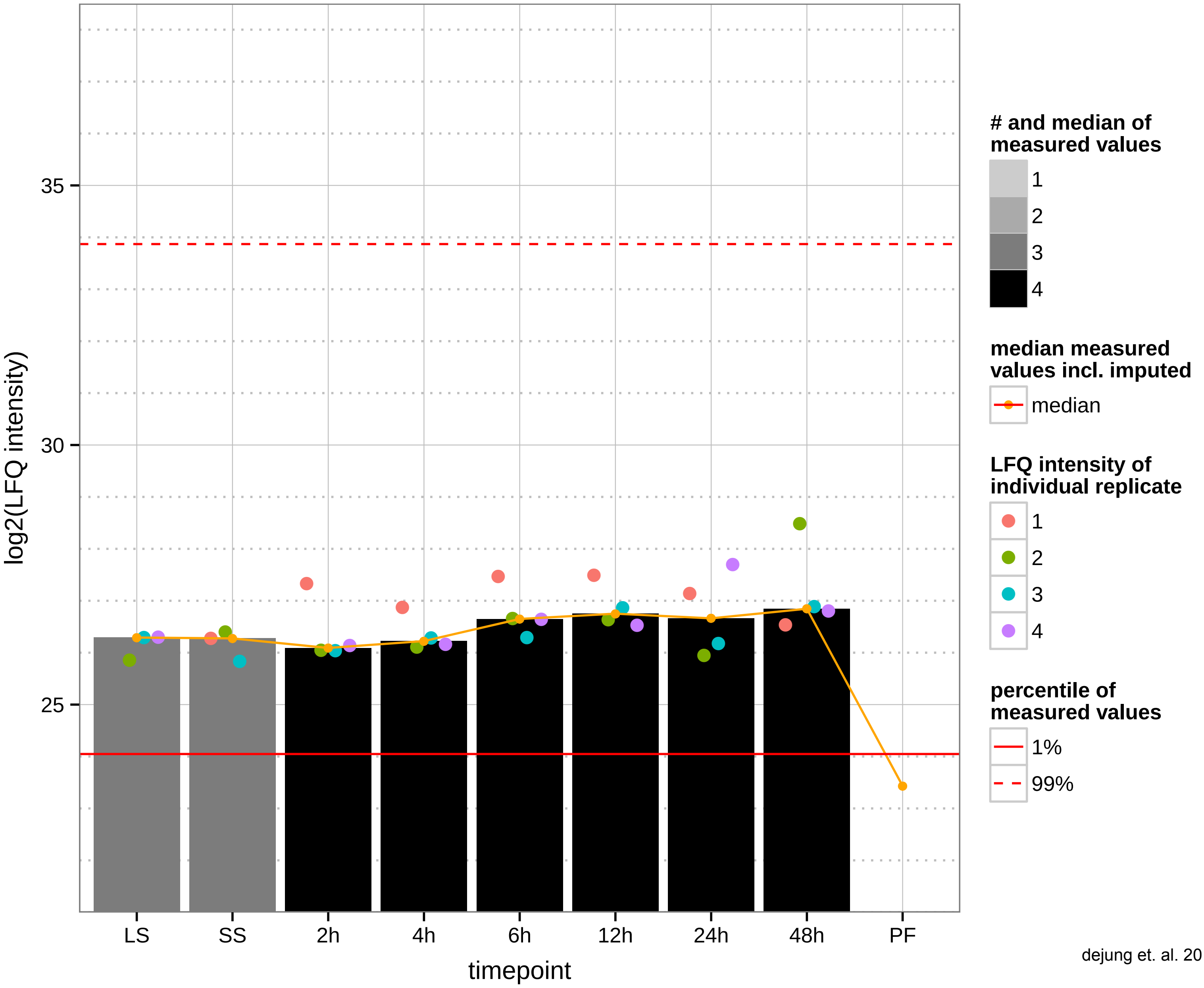




dejung et. al. 2015

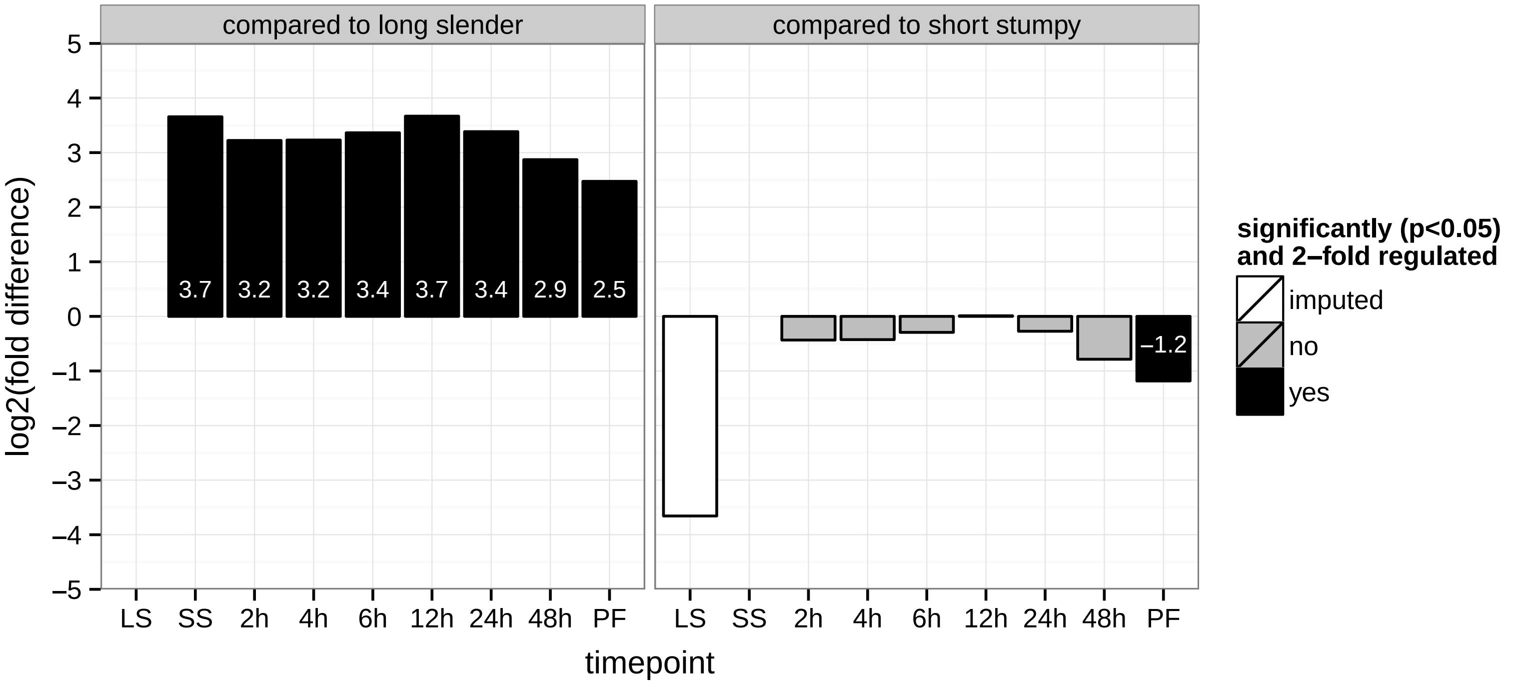
hypothetical protein, conserved
Tb927.7.7400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

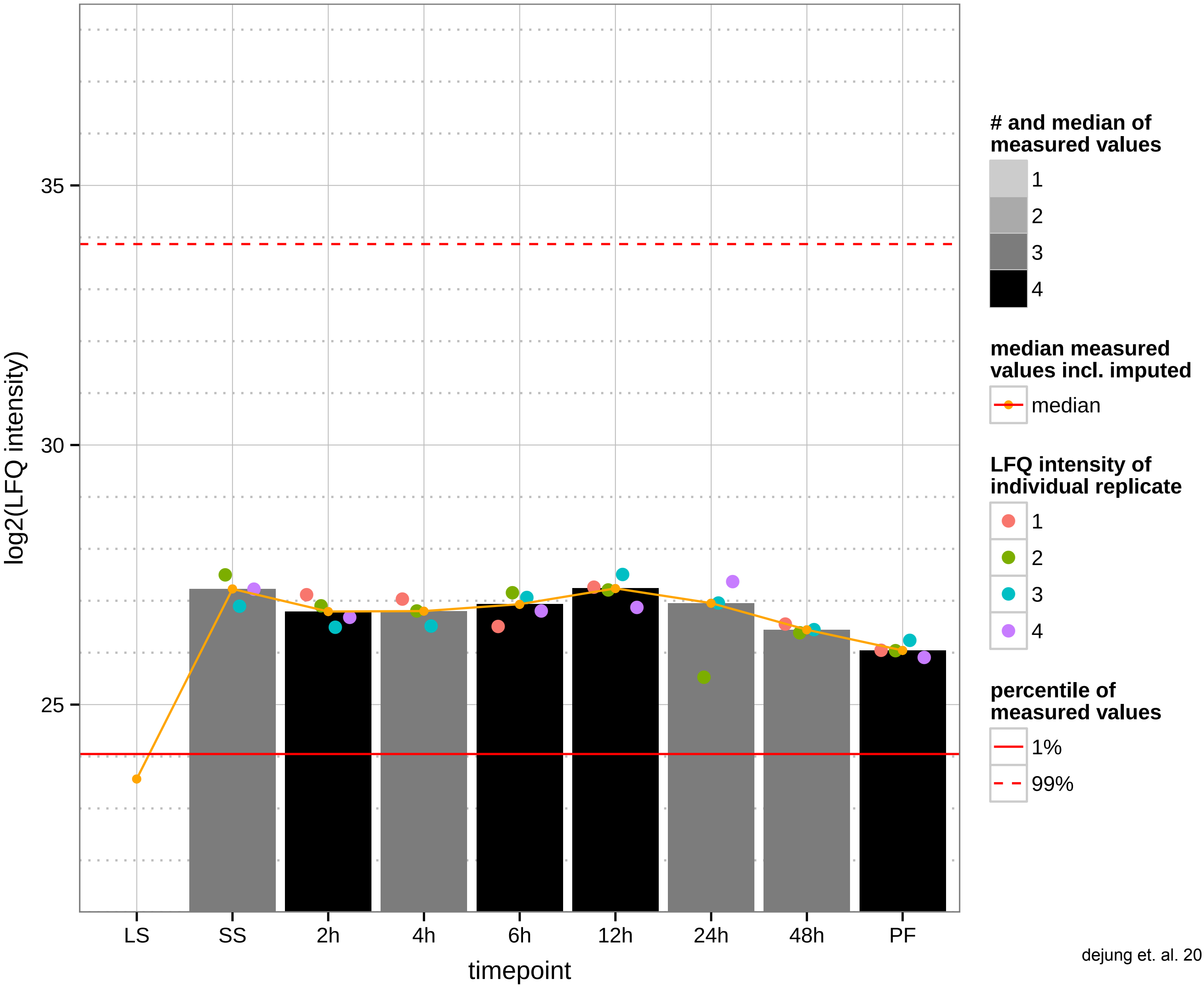




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.1140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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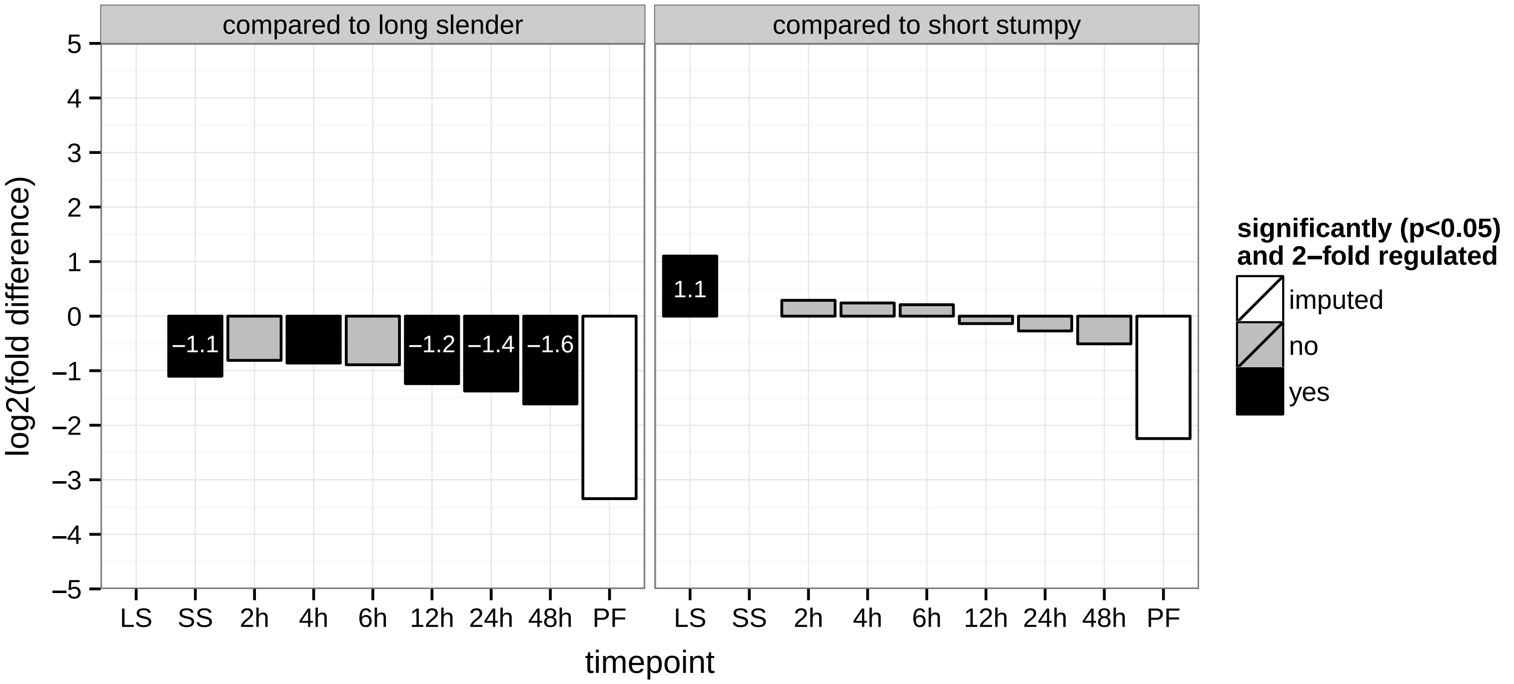
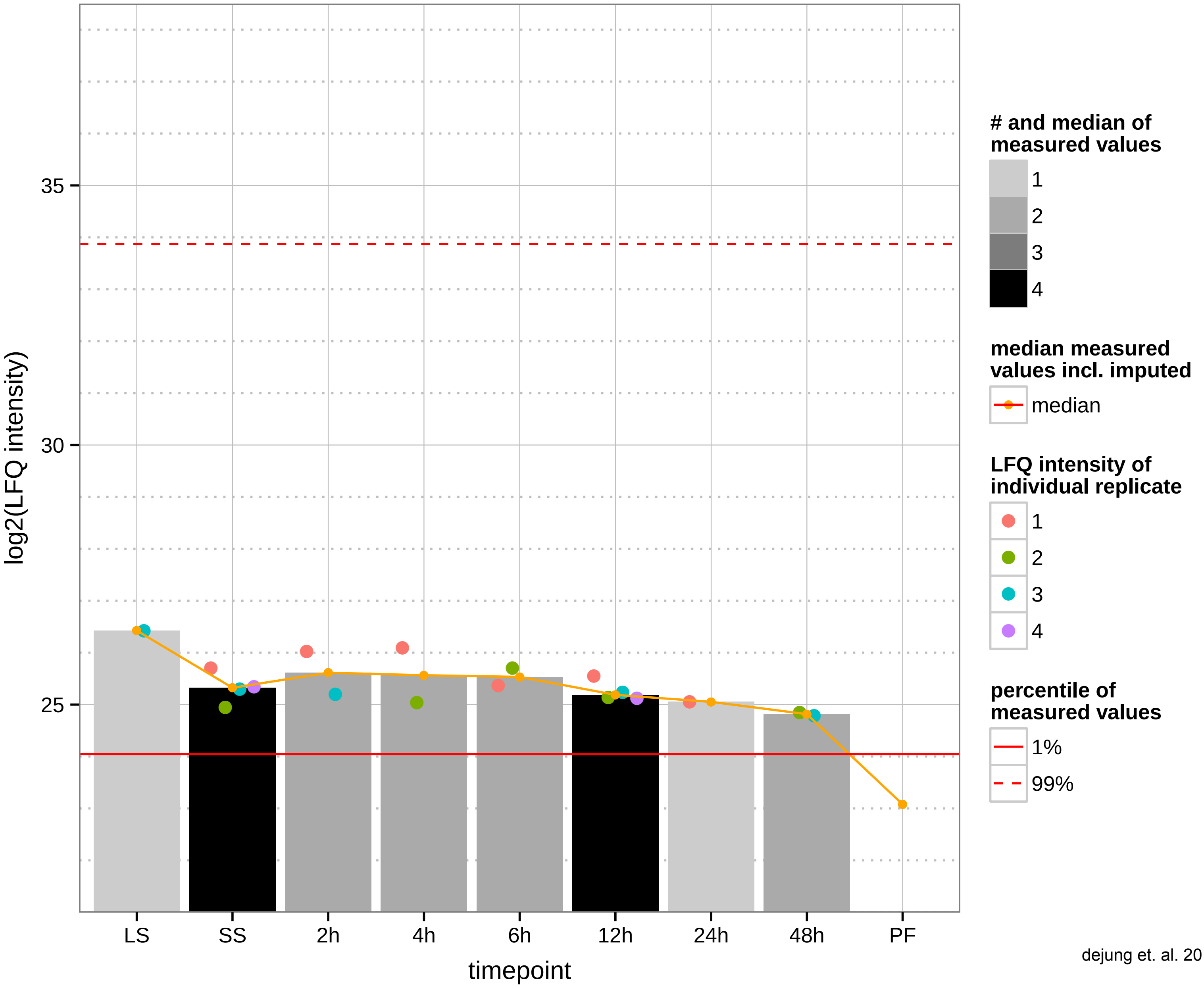
hypothetical protein, conserved
Tb927.8.1290
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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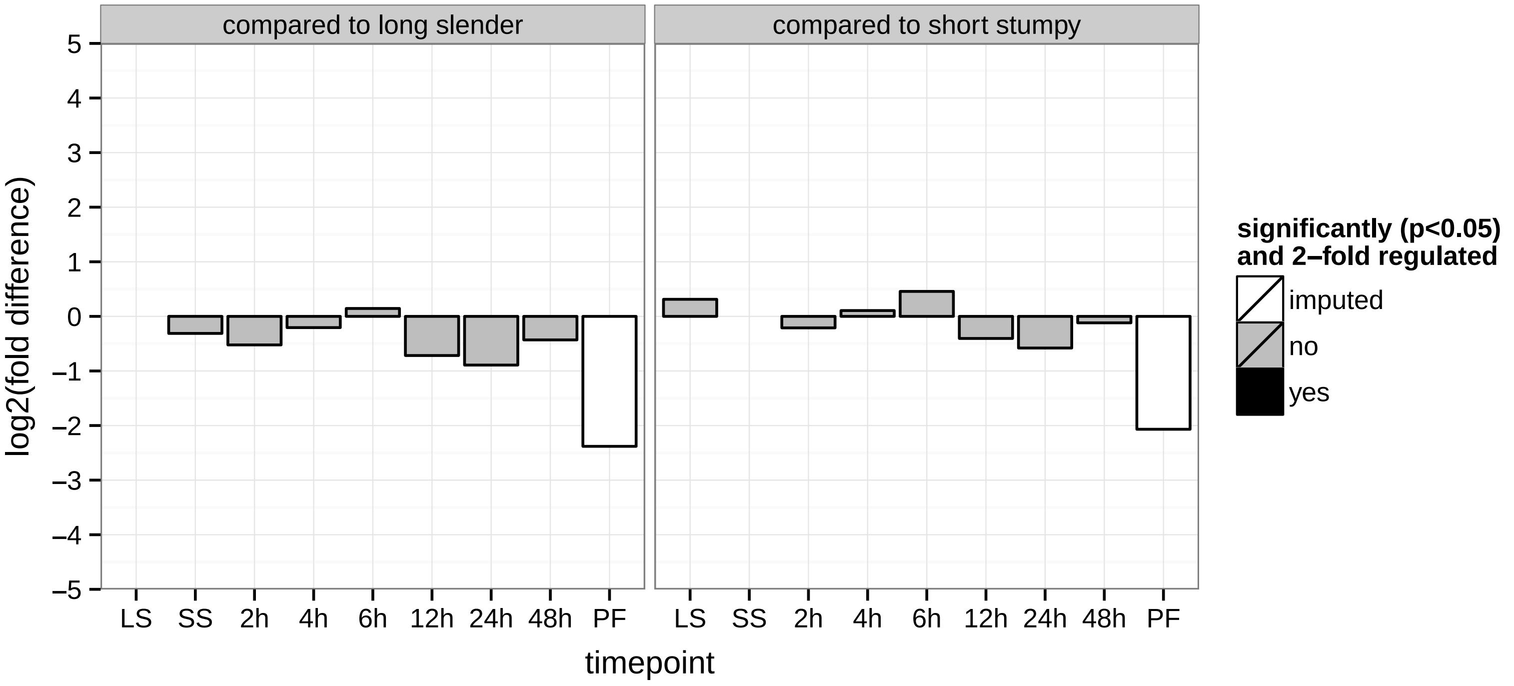
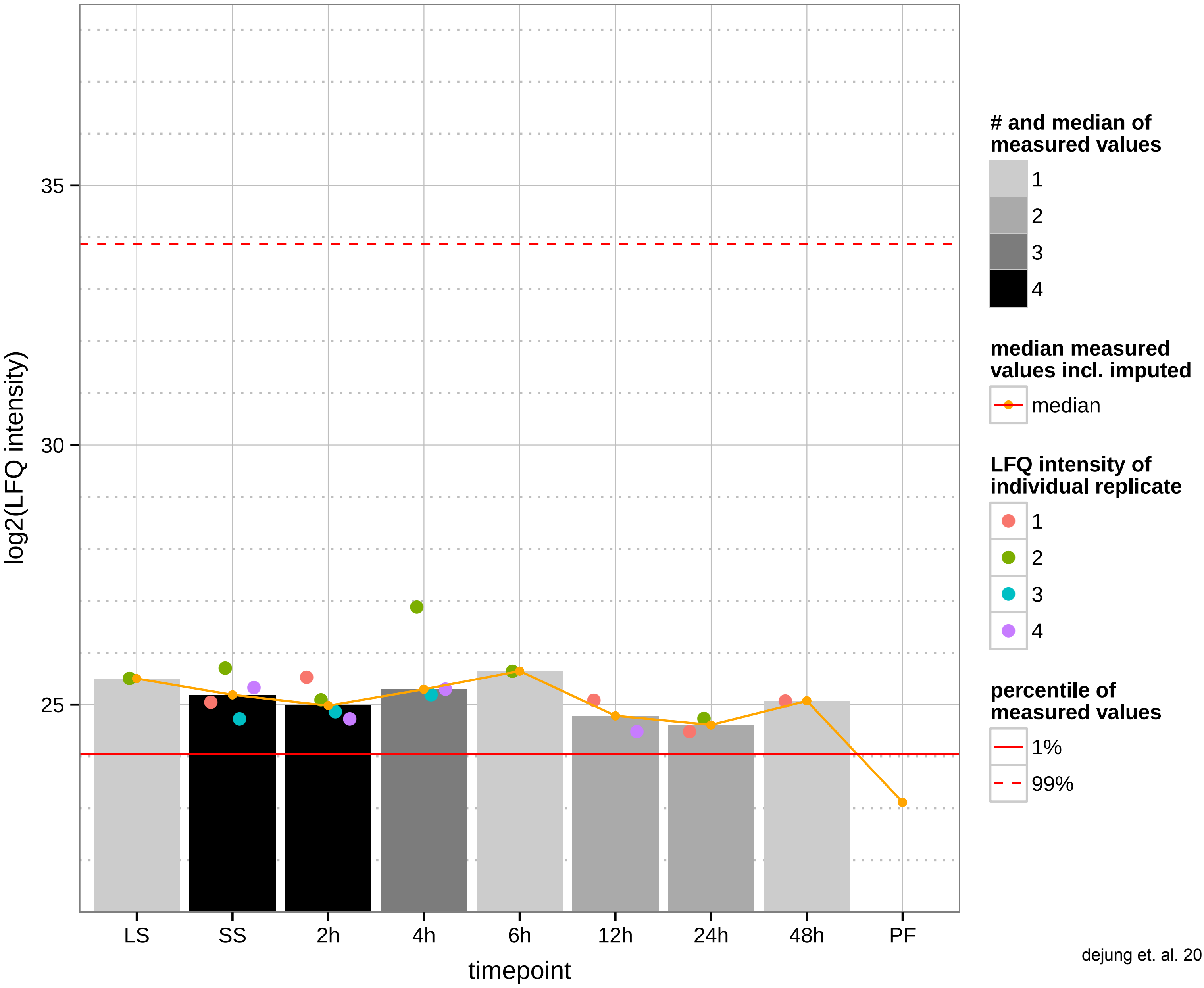
hypothetical protein, conserved
Tb927.8.1320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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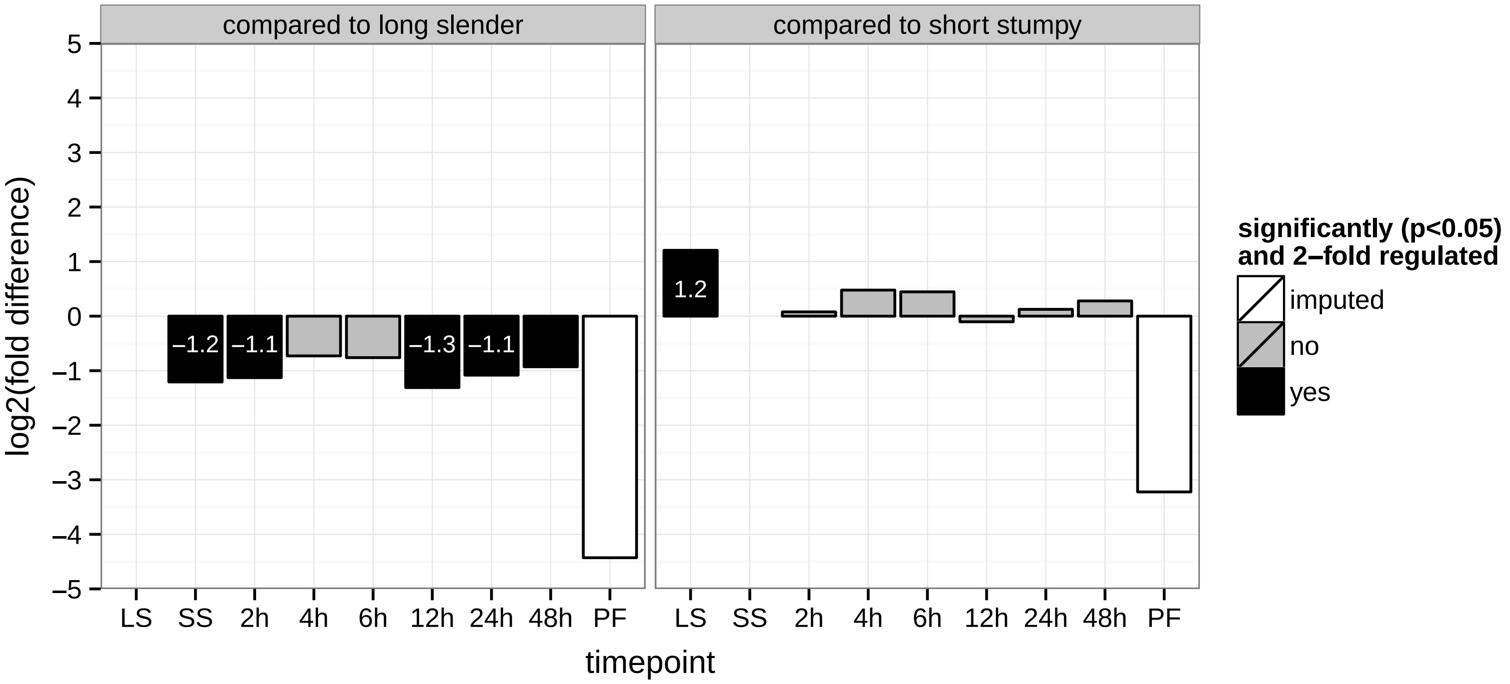
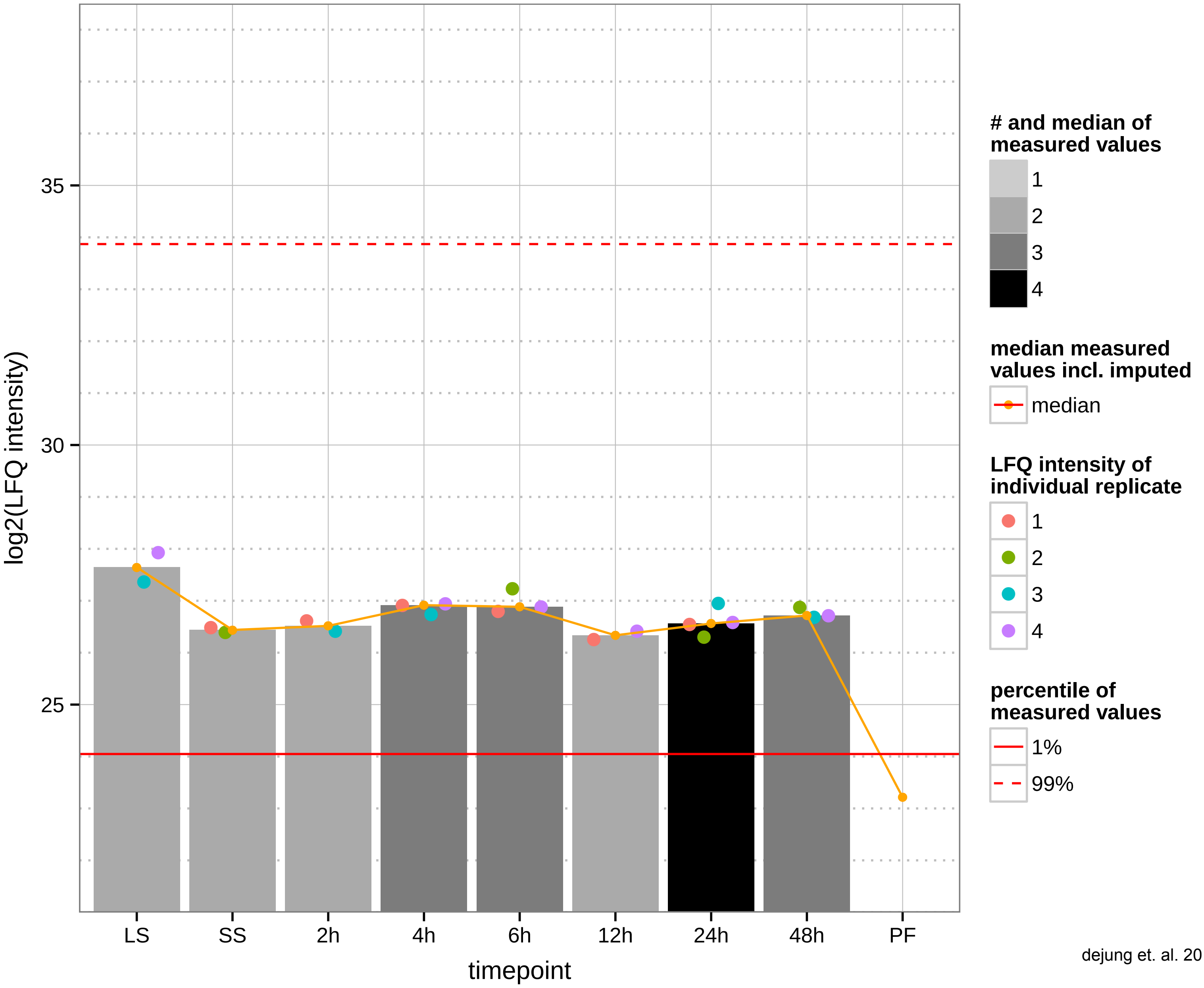
hypothetical protein, conserved
Tb927.8.1360
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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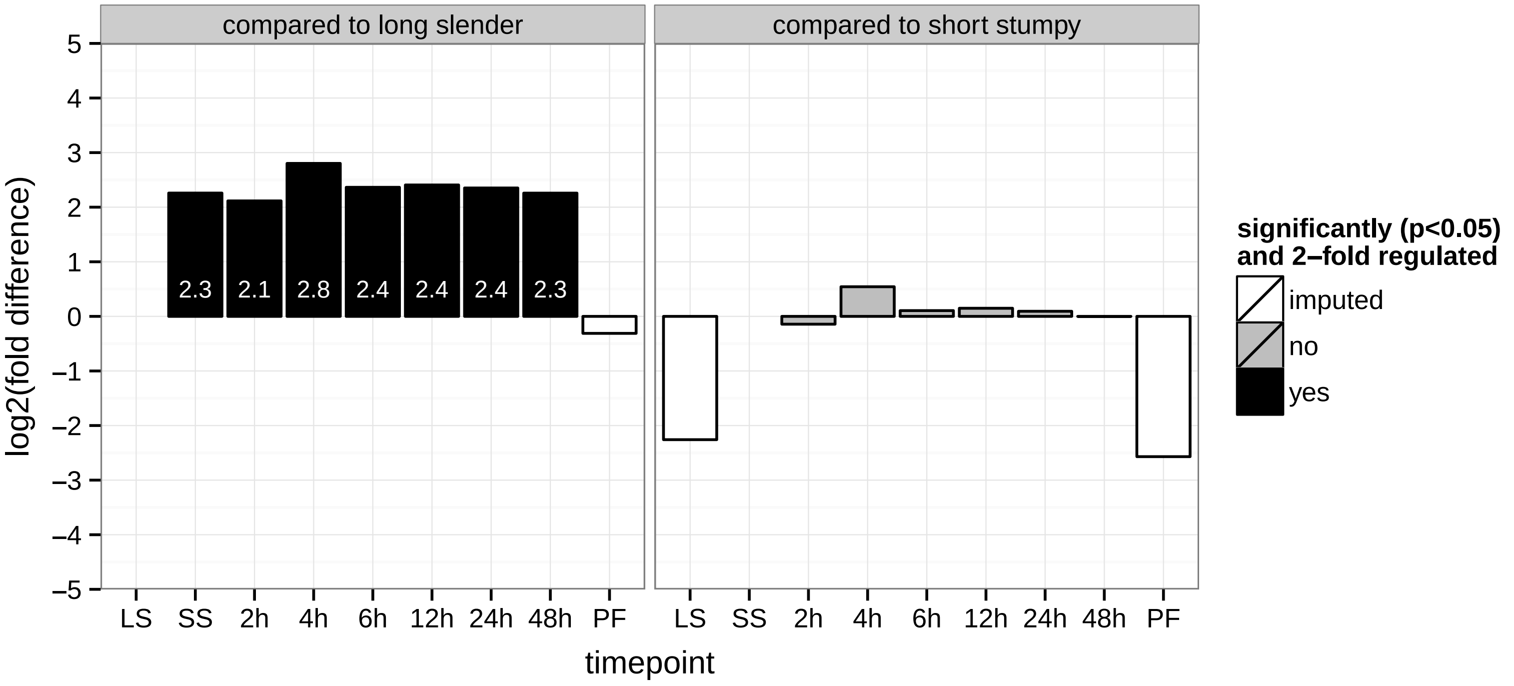
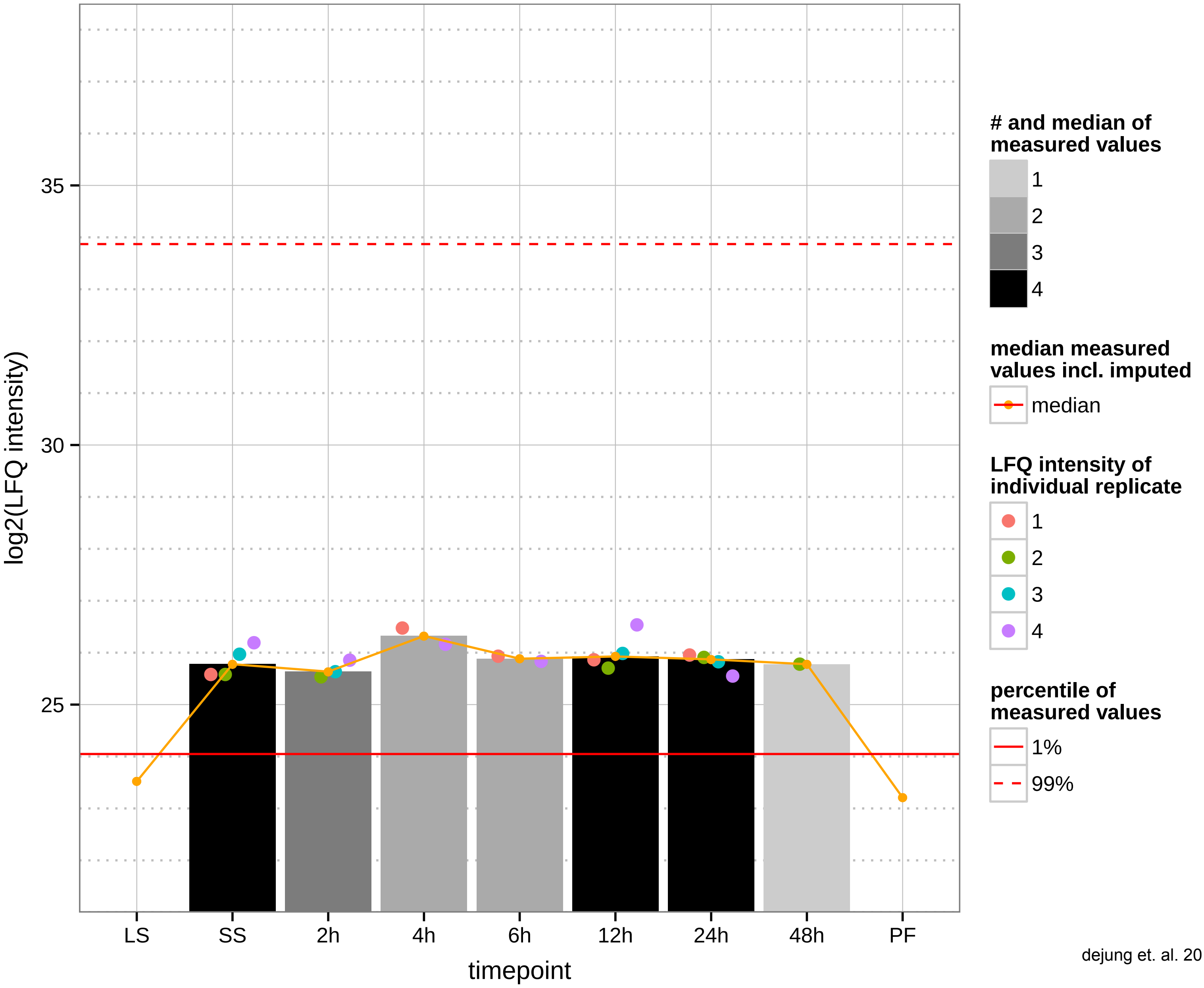
hypothetical protein, conserved
Tb927.8.1450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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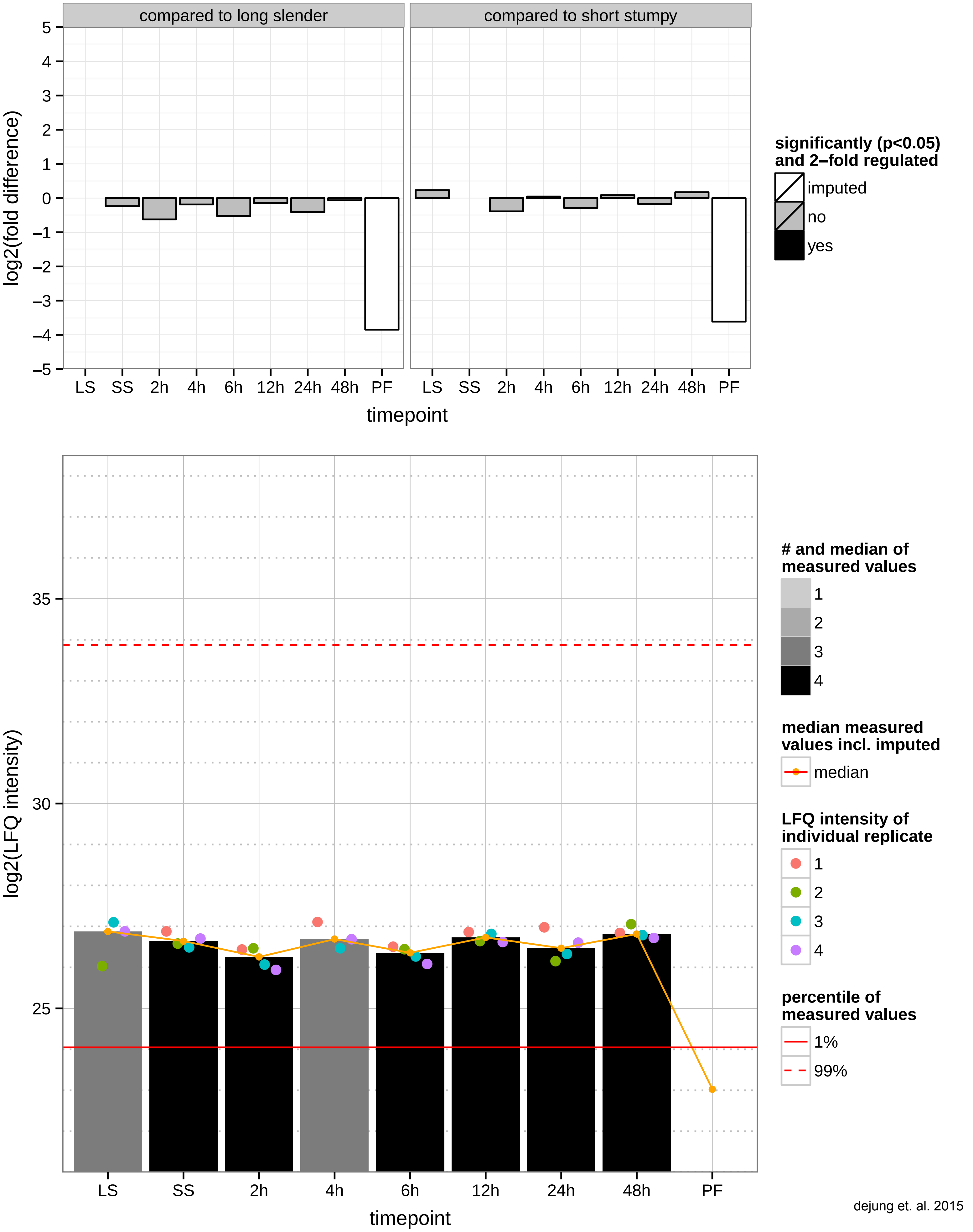
hypothetical protein, conserved
Tb927.8.1560
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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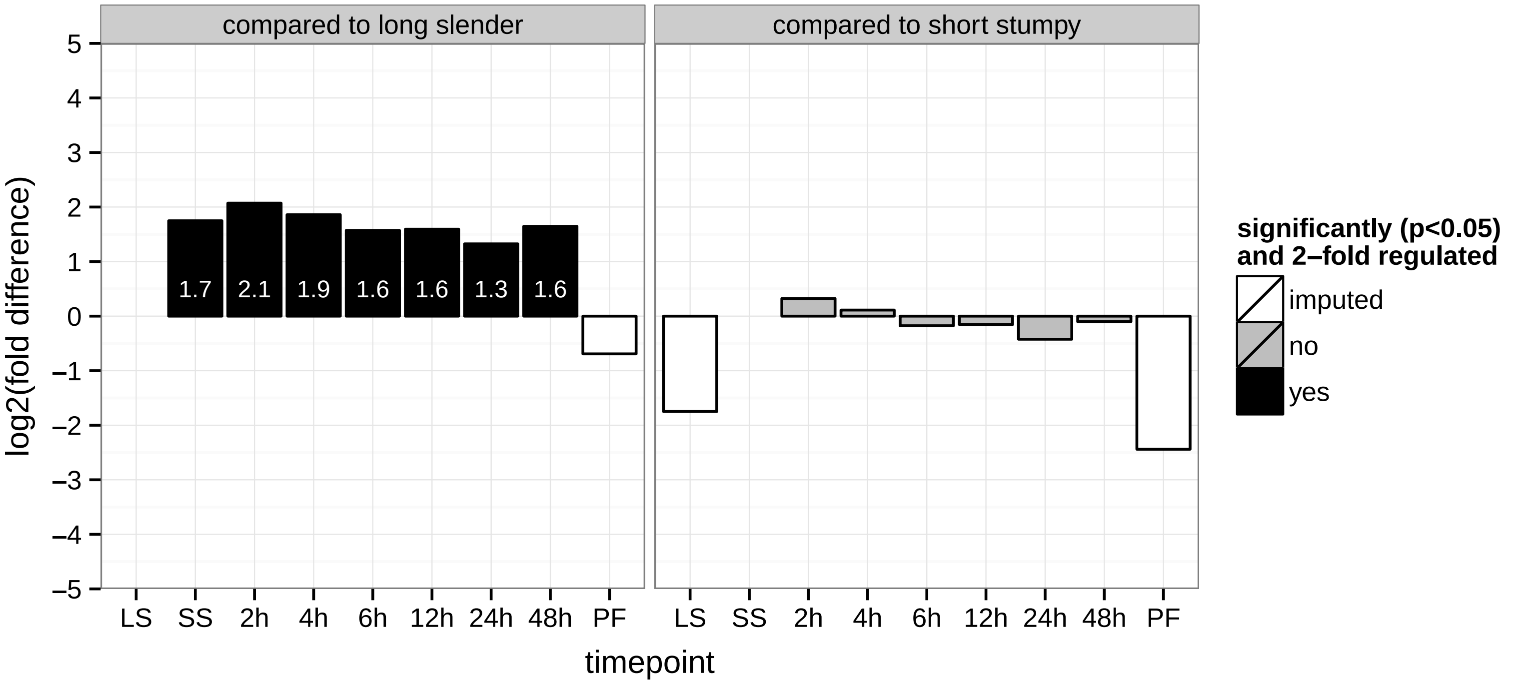
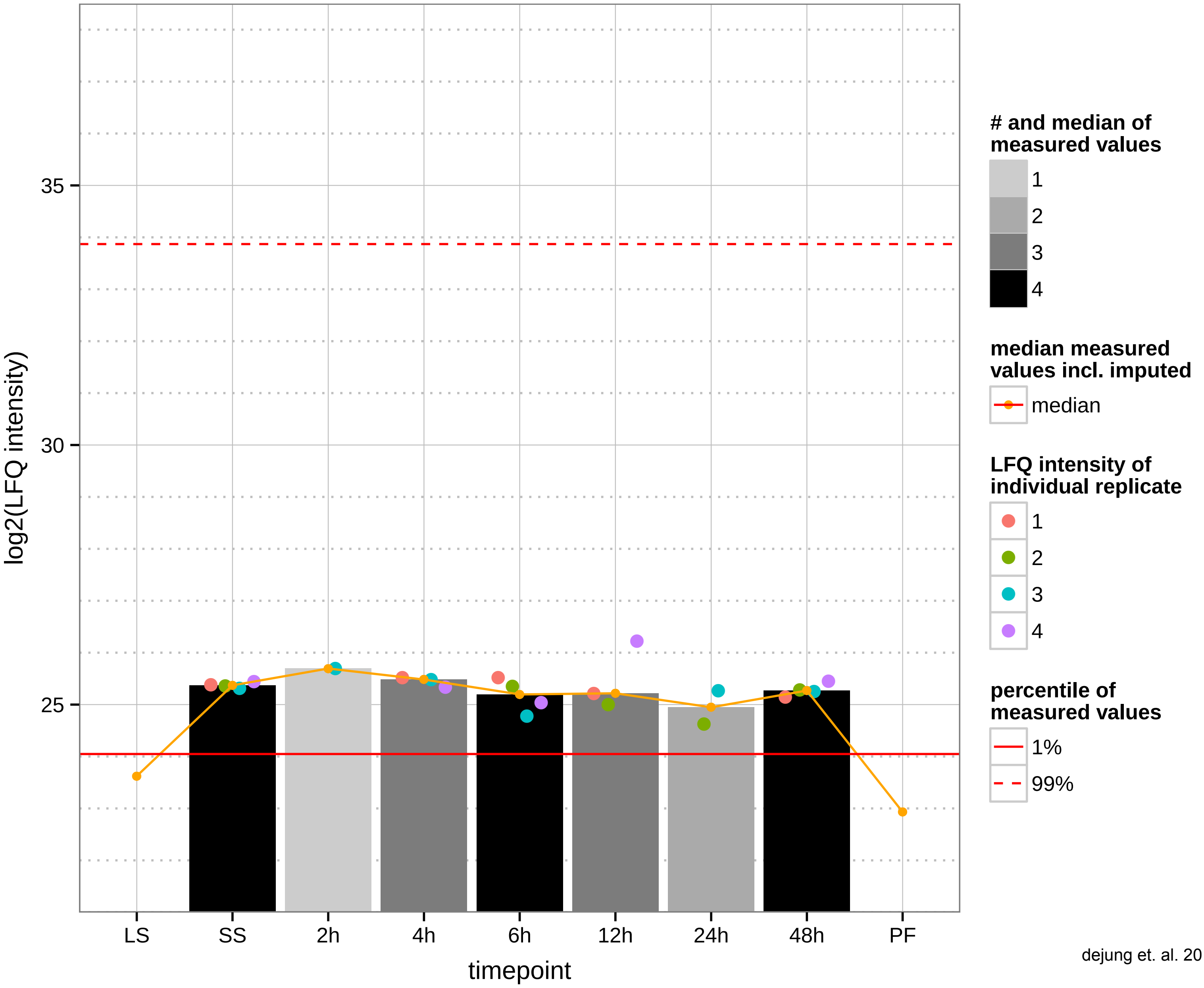
rhomboid–like protein, serine peptidase, Clan S–, family S54, putative
Tb927.8.1810
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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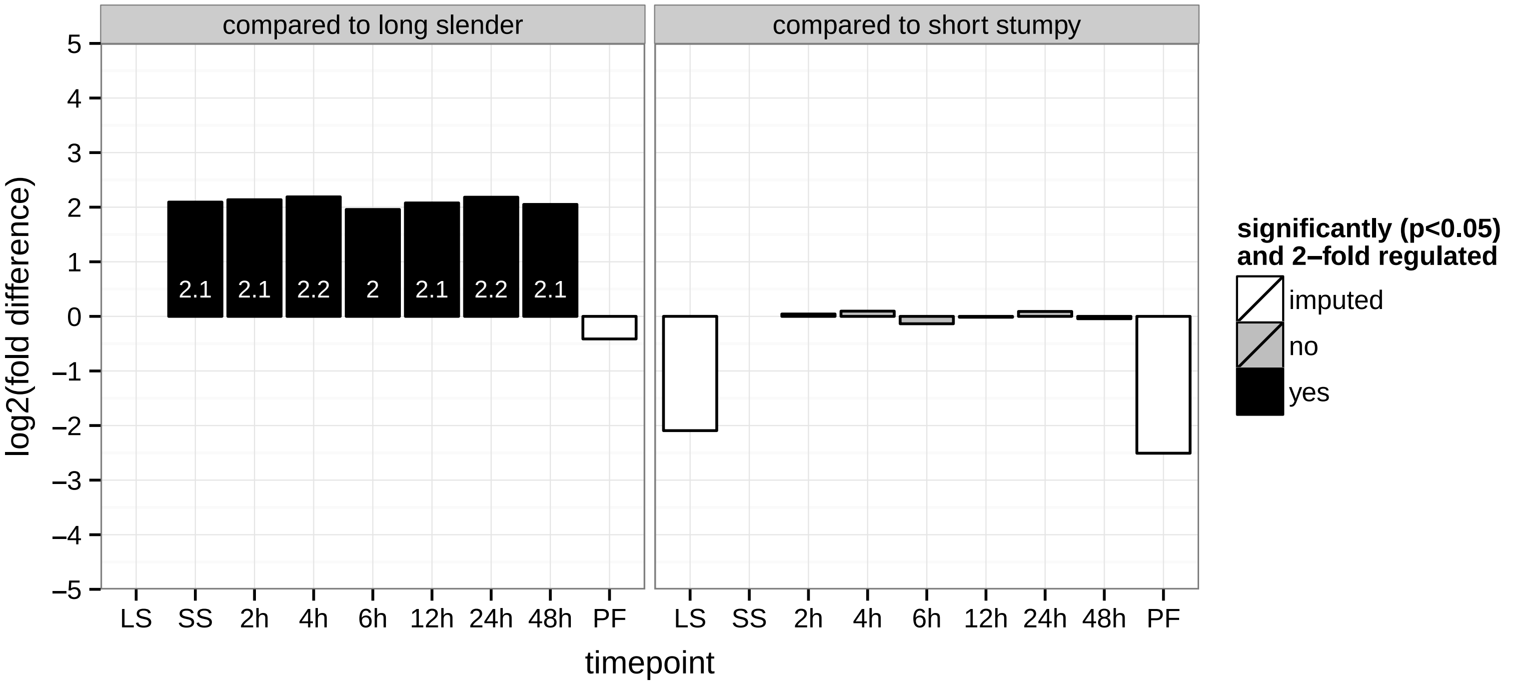
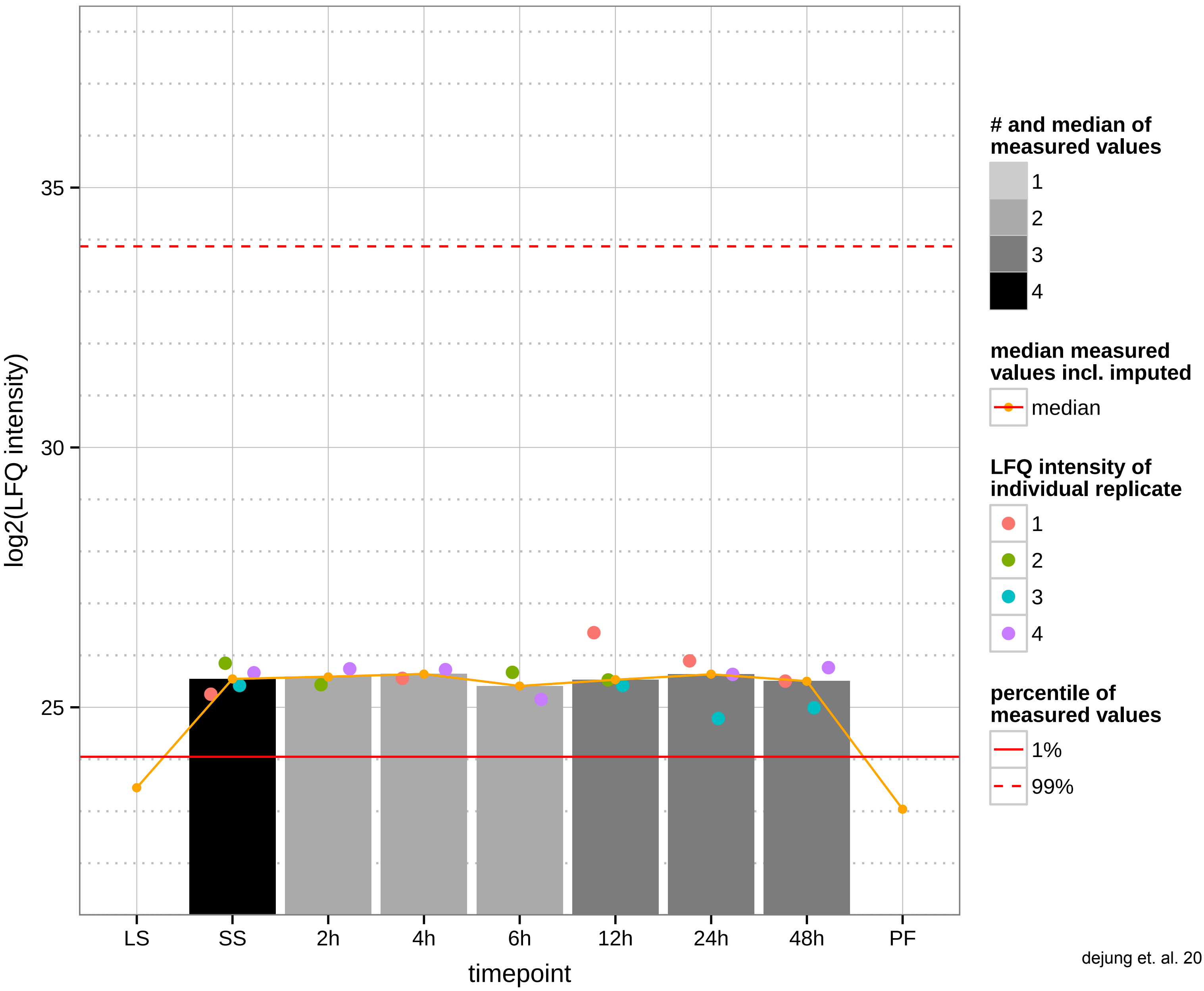
hypothetical protein, conserved
Tb927.8.2490
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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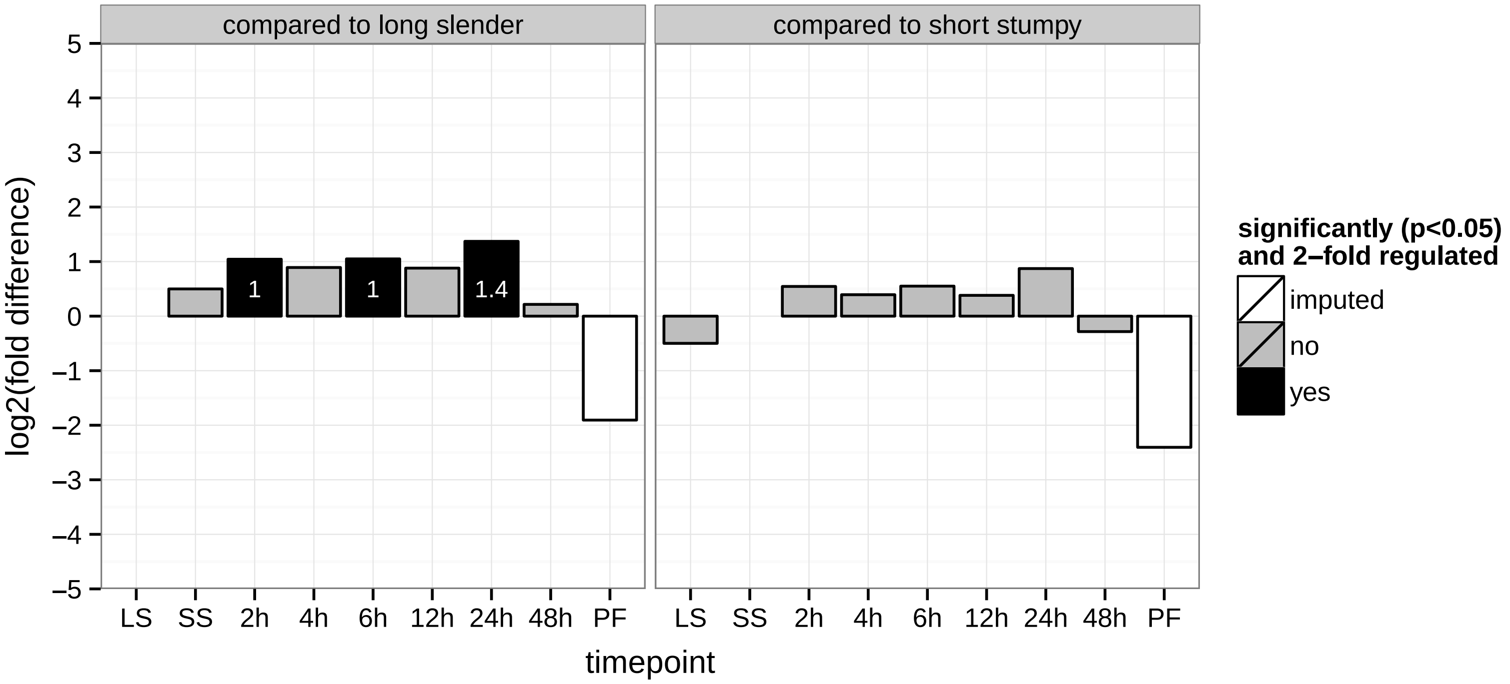
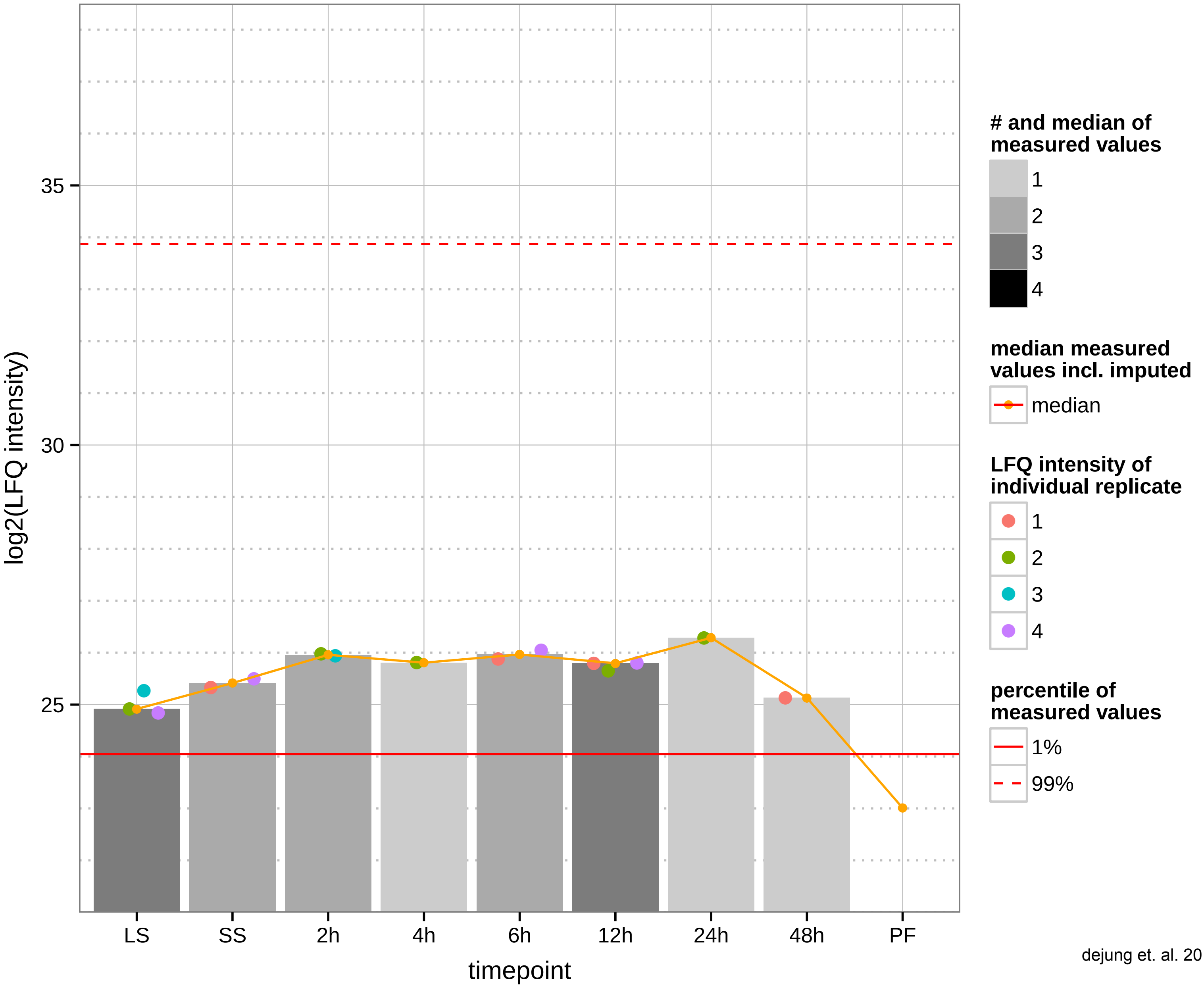
spliceosomal U5 snRNP−specific protein, putative
Tb927.8.2560
AGOF: null
AGOC: nucleus, spliceosomal complex
AGOP: RNA splicing, mitosis, nuclear migration along microfilament
PGOF: null
PGOC: spliceosomal complex
PGOP: mitosis





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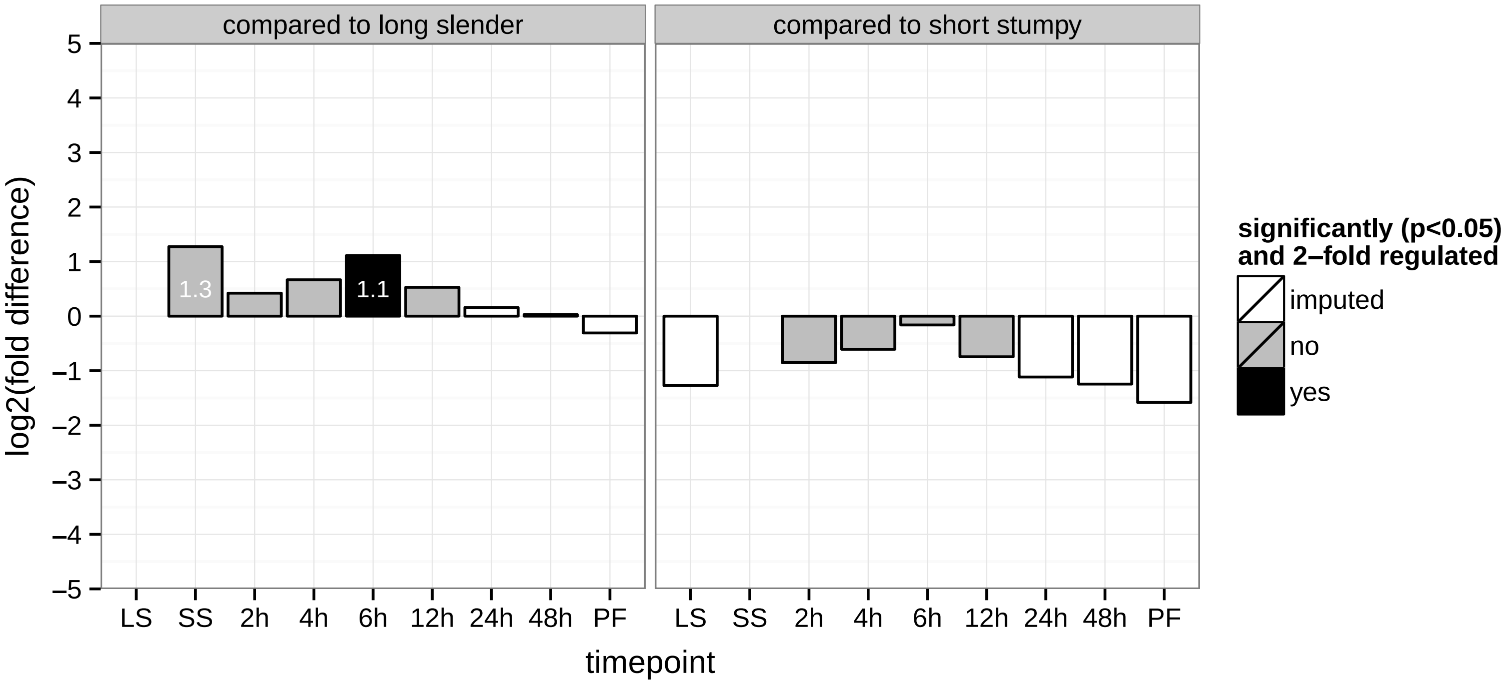
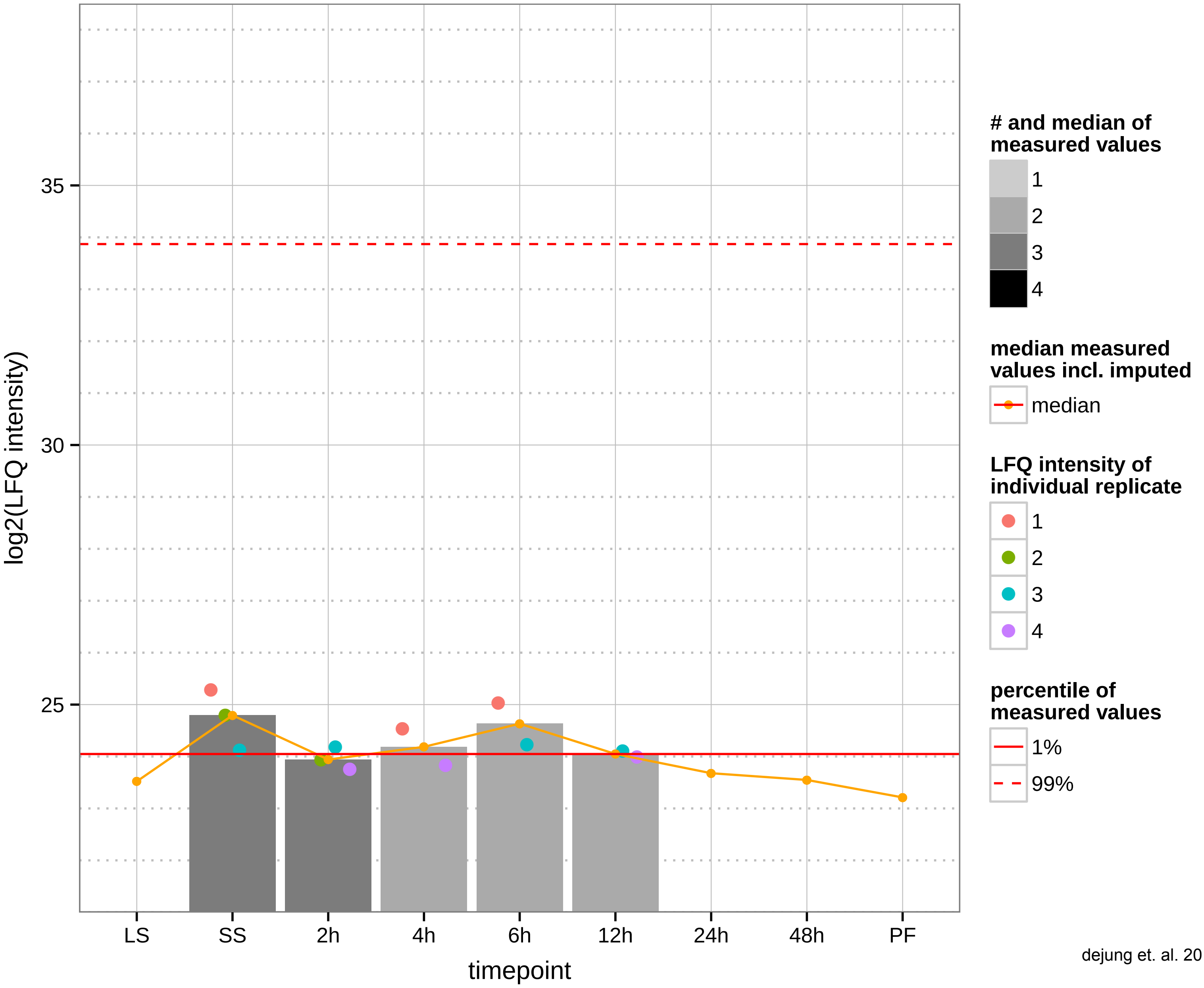
hypothetical protein, conserved
Tb927.8.2660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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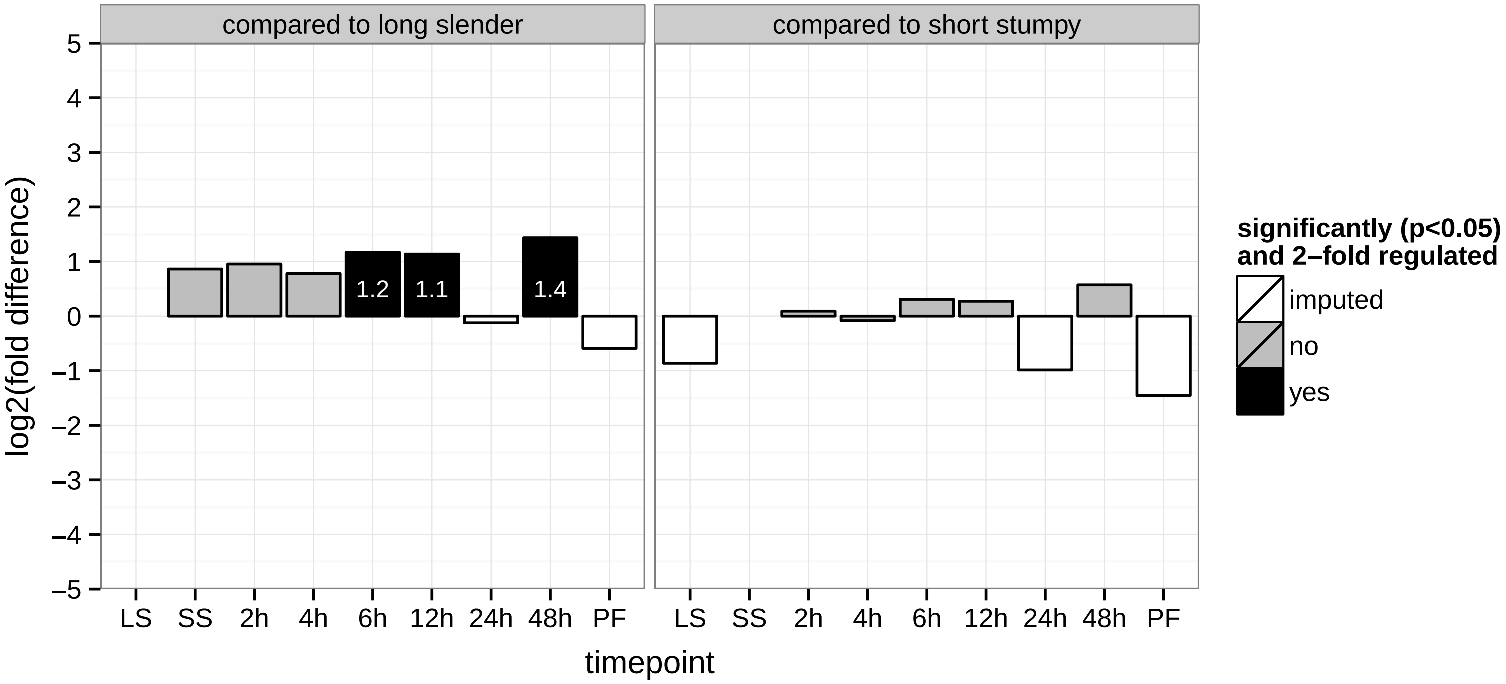
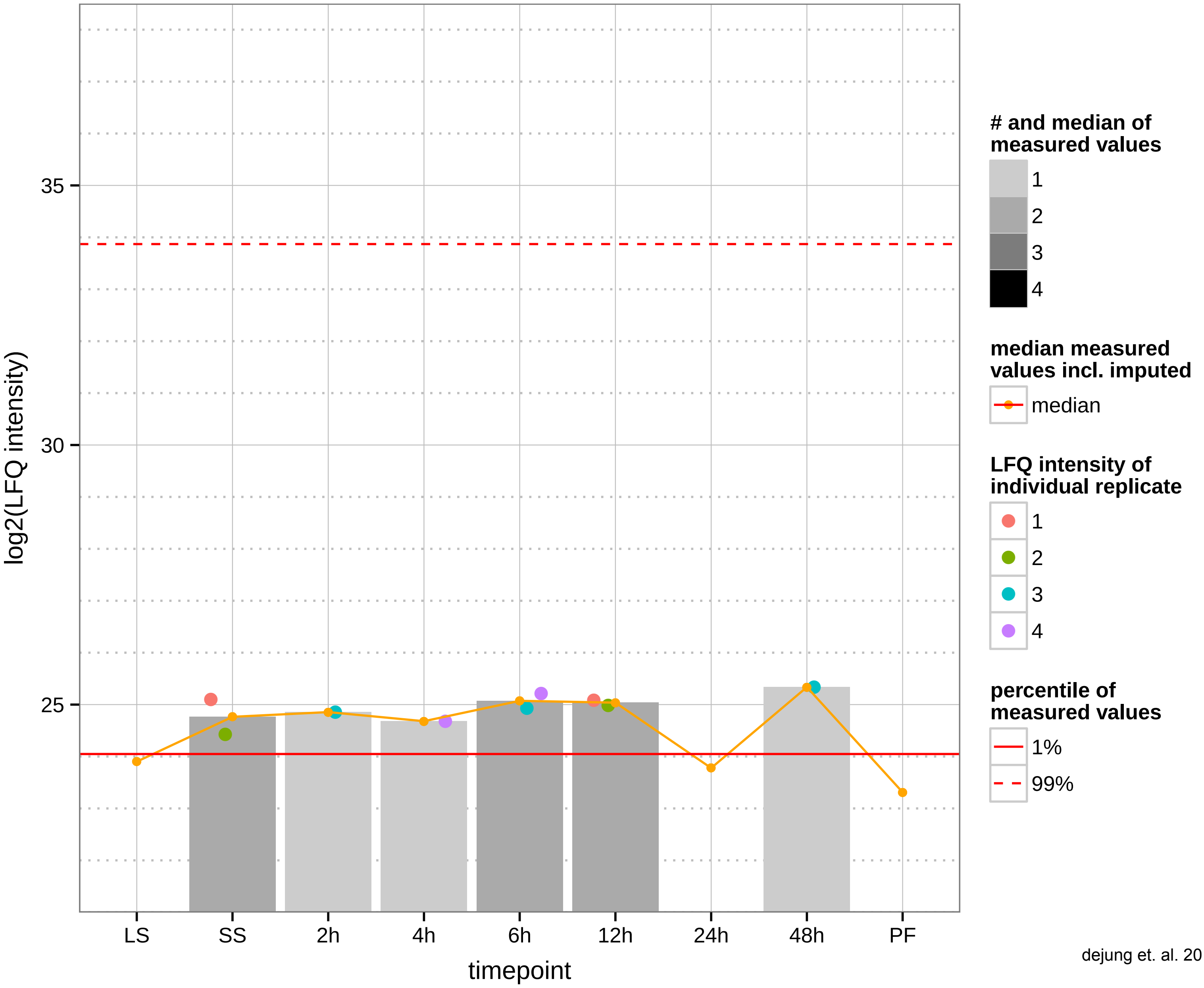
hypothetical protein, conserved
Tb927.8.2690
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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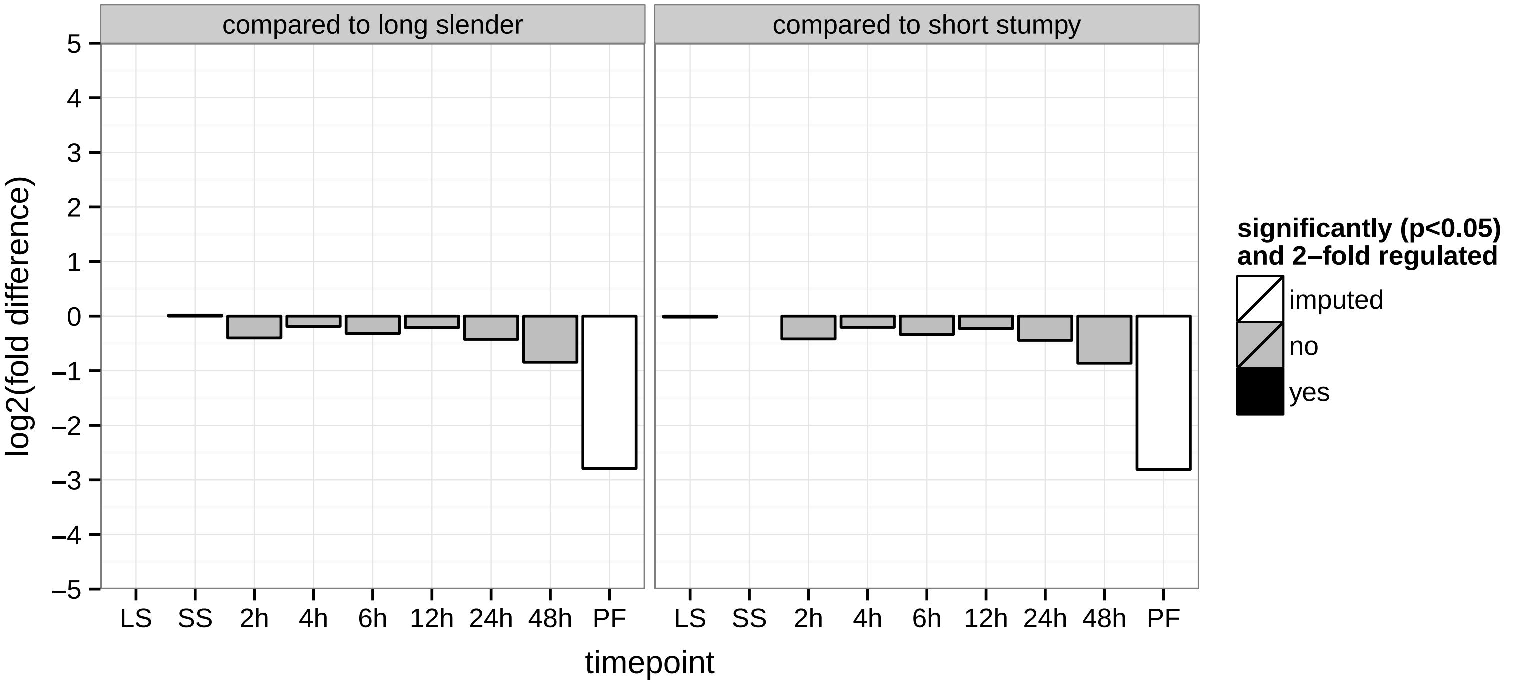
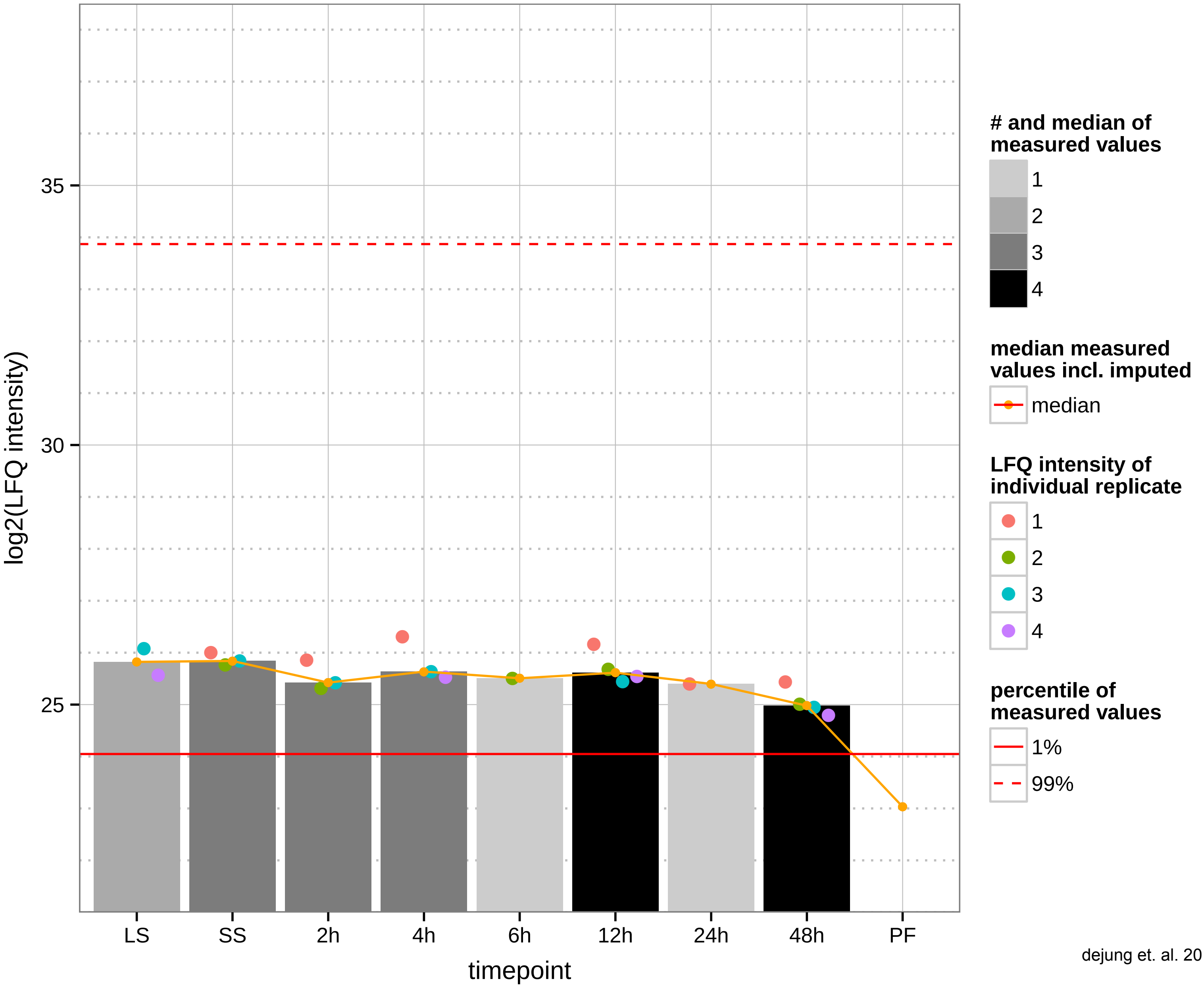
hypothetical protein, conserved
Tb927.8.3410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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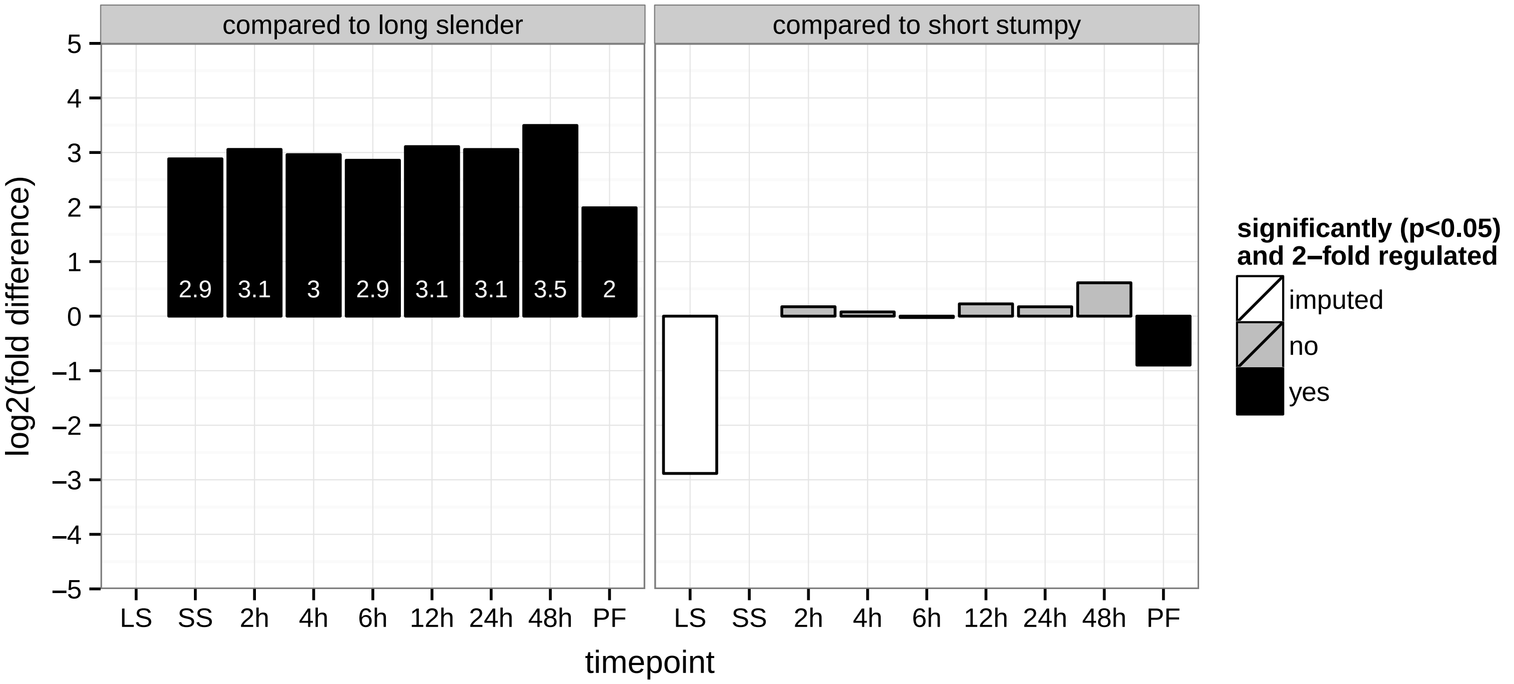
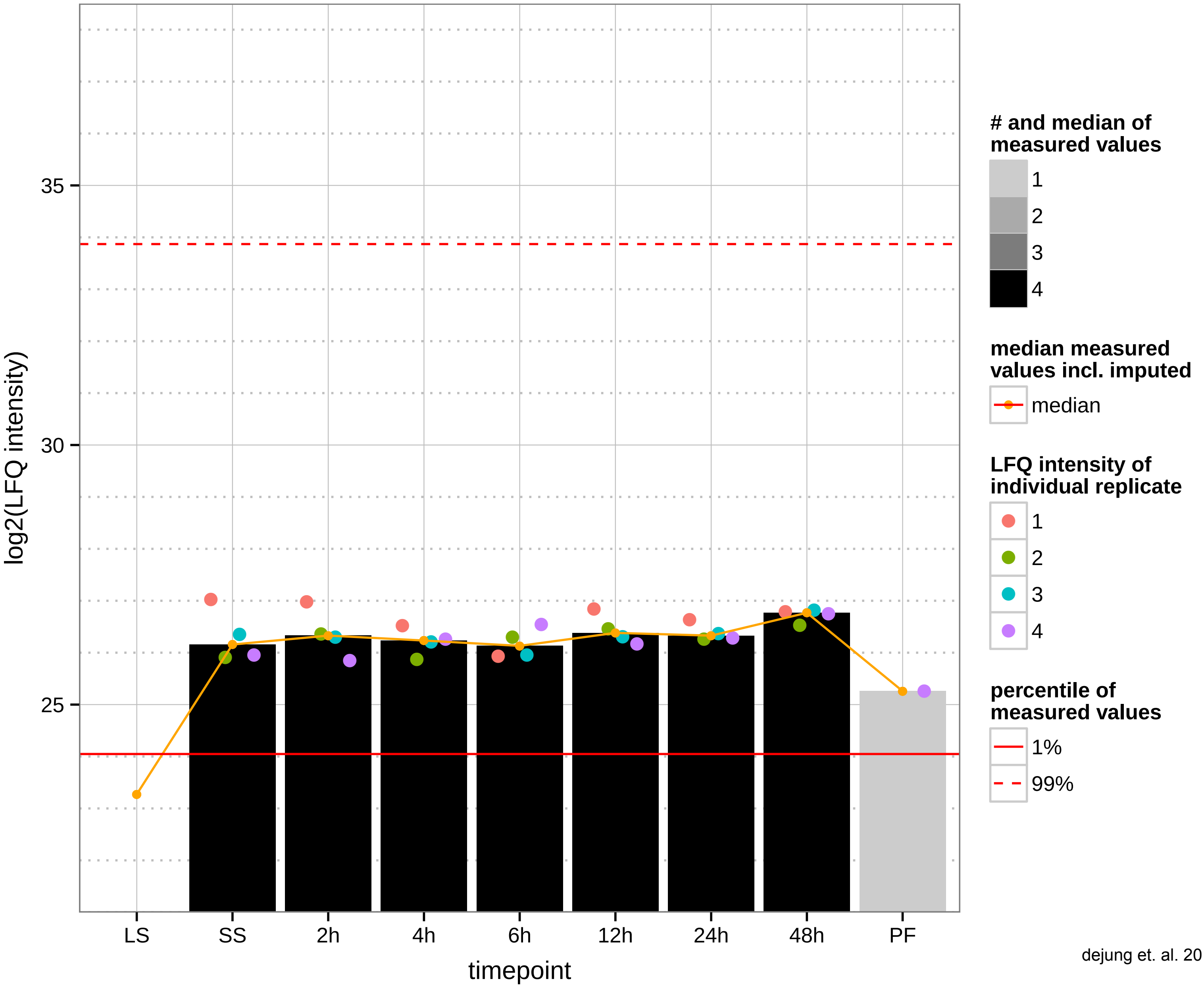
hypothetical protein, conserved
Tb927.8.3710
AGOF: exonuclease activity, nucleic acid binding
AGOC: intracellular
AGOP: null
PGOF: exonuclease activity, nucleic acid binding
PGOC: intracellular
PGOP: null





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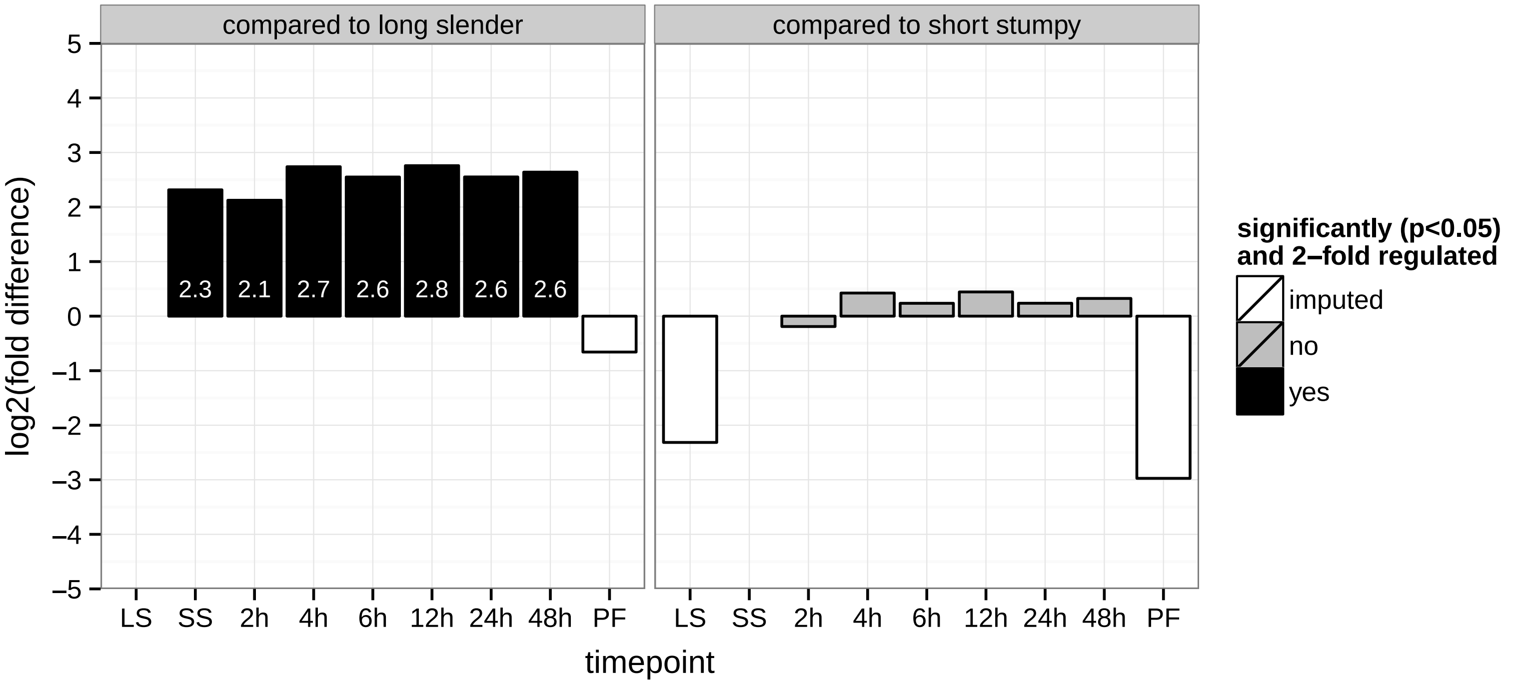
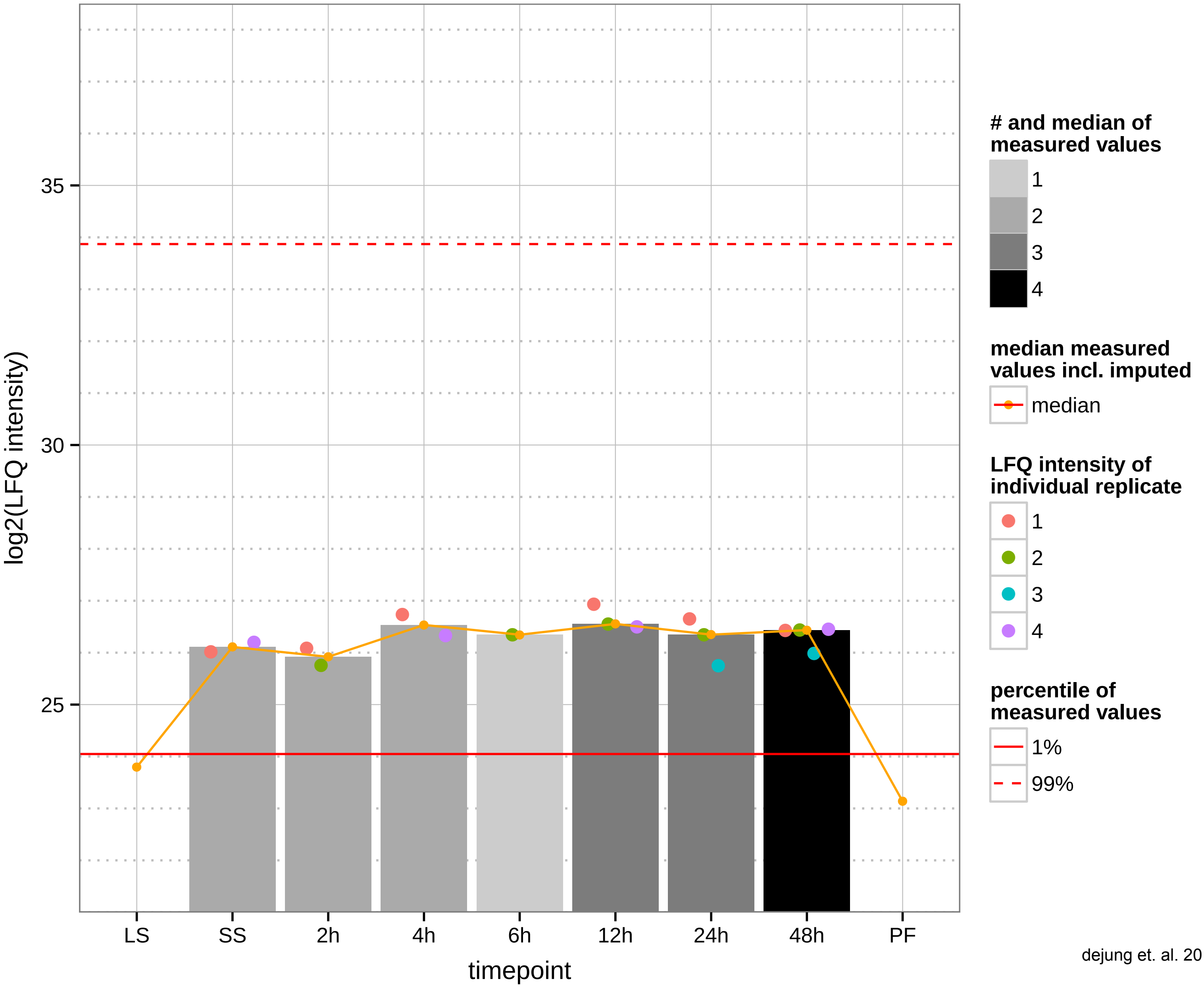
hypothetical protein, conserved
Tb927.8.4250
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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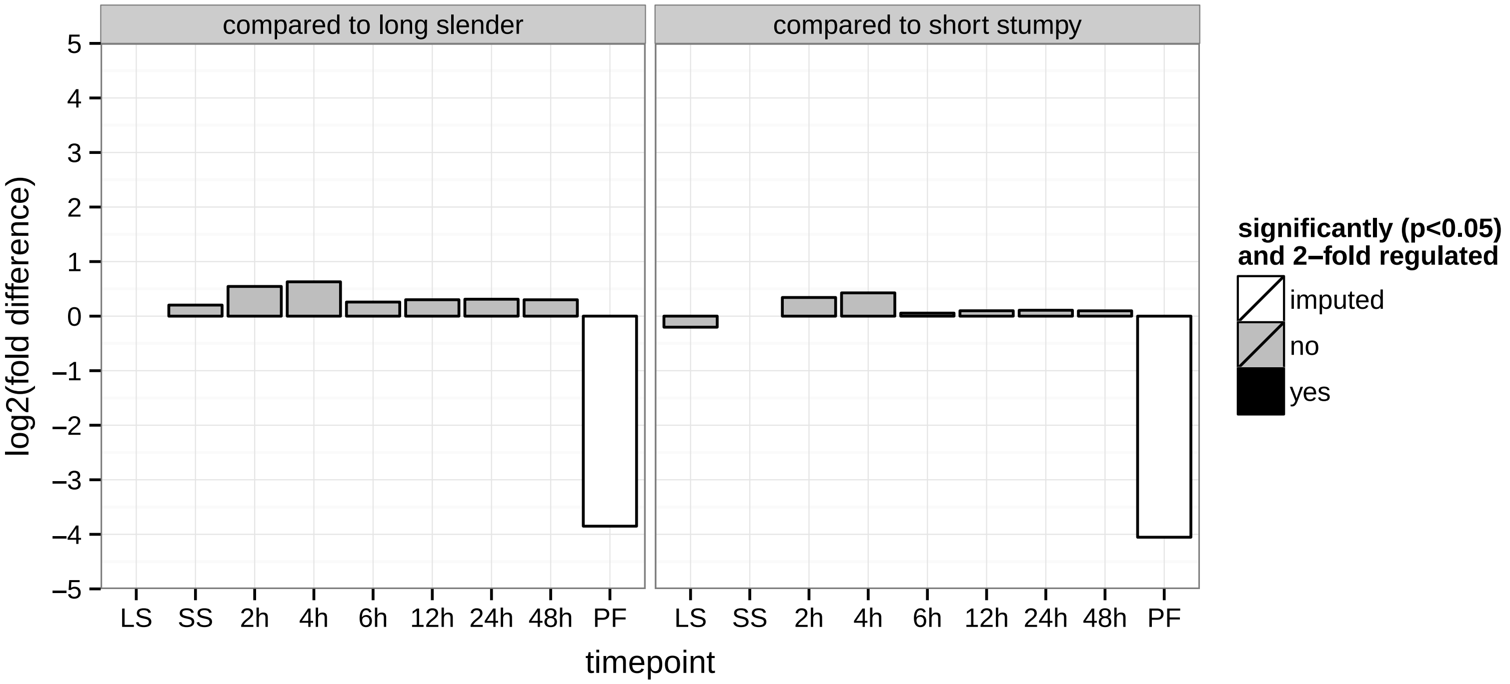
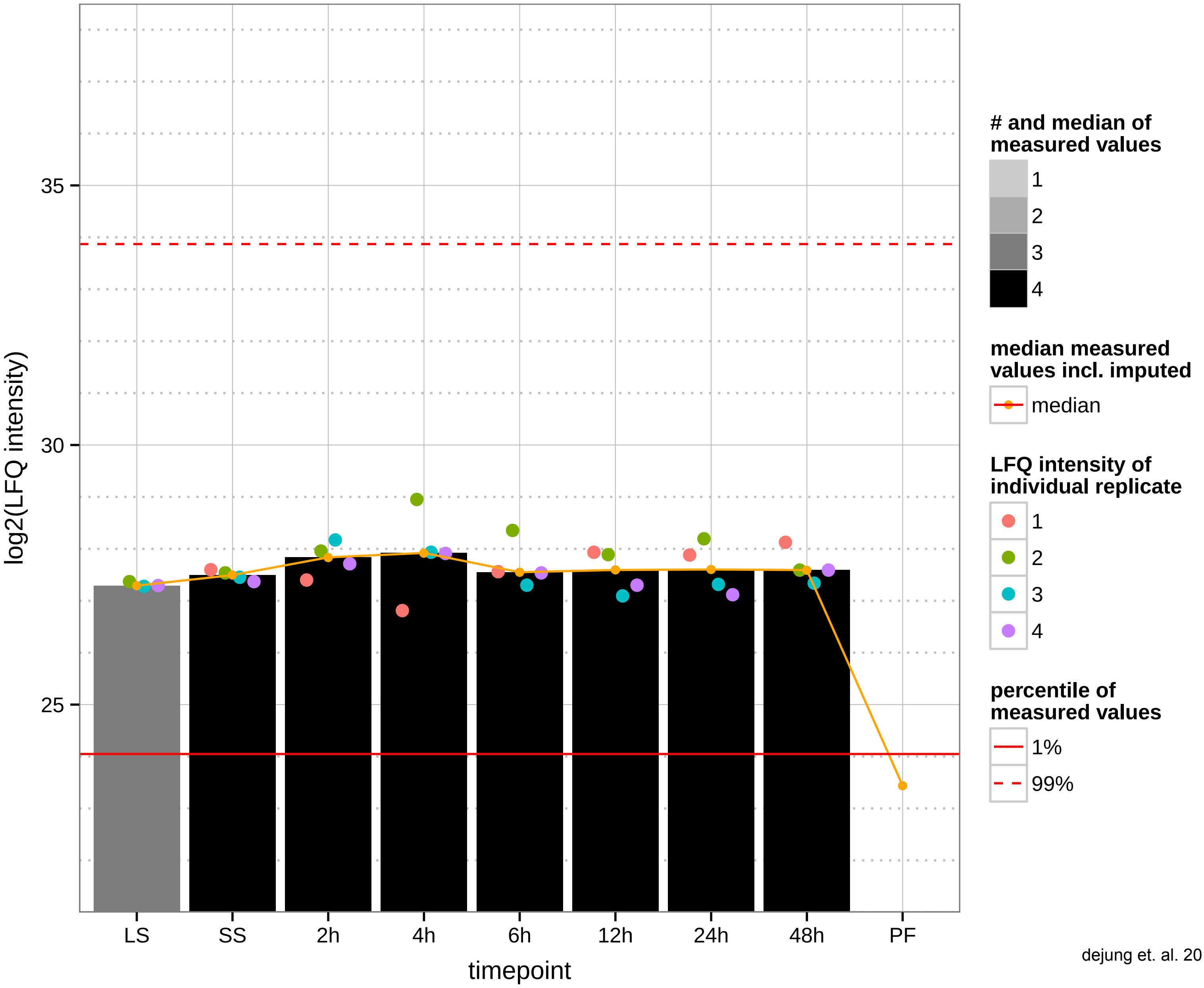
trafficking protein particle complex subunit 3, putative, TRAPP, transport protein particle (TRAPP) component, Bet3
Tb927.8.5030
AGOF: null
AGOC: TRAPP complex, integral to membrane
AGOP: ER to Golgi vesicle–mediated transport
PGOF: null
PGOC: null
PGOP: null





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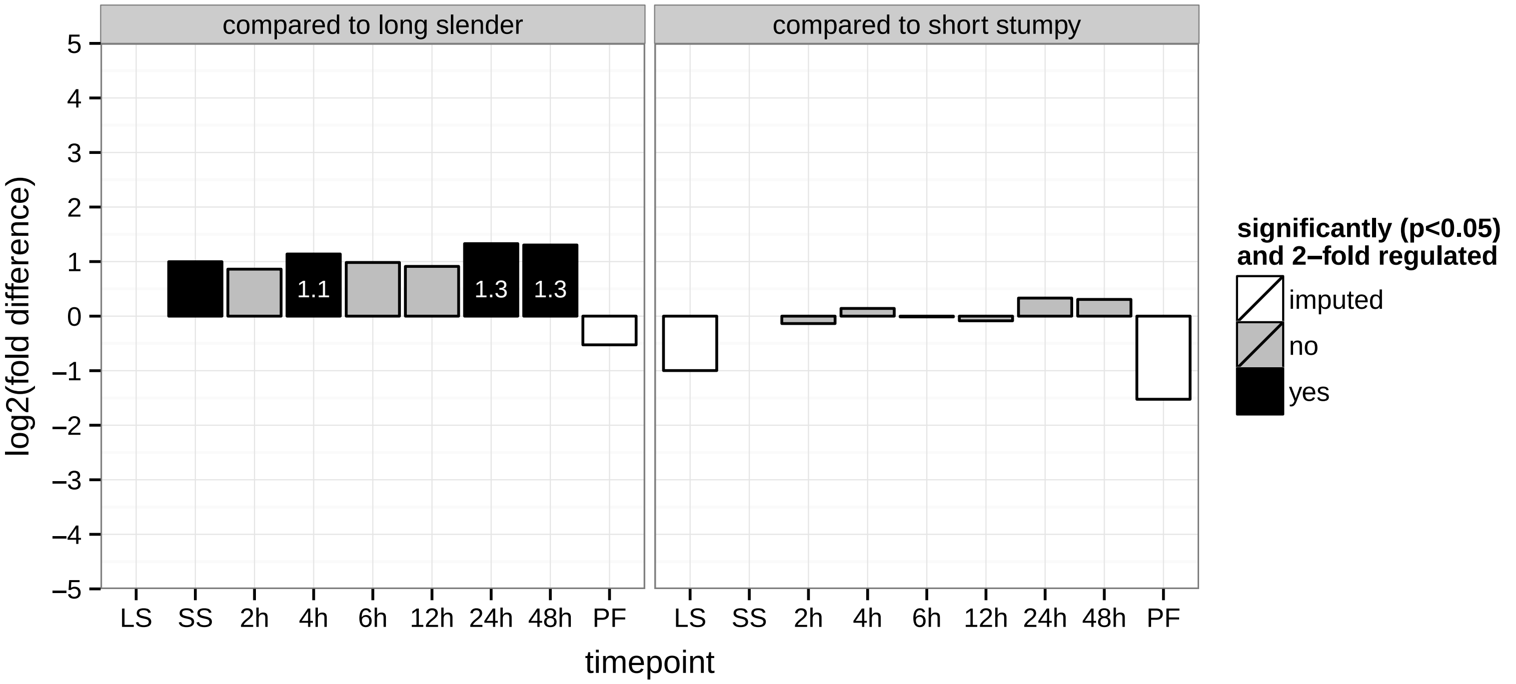
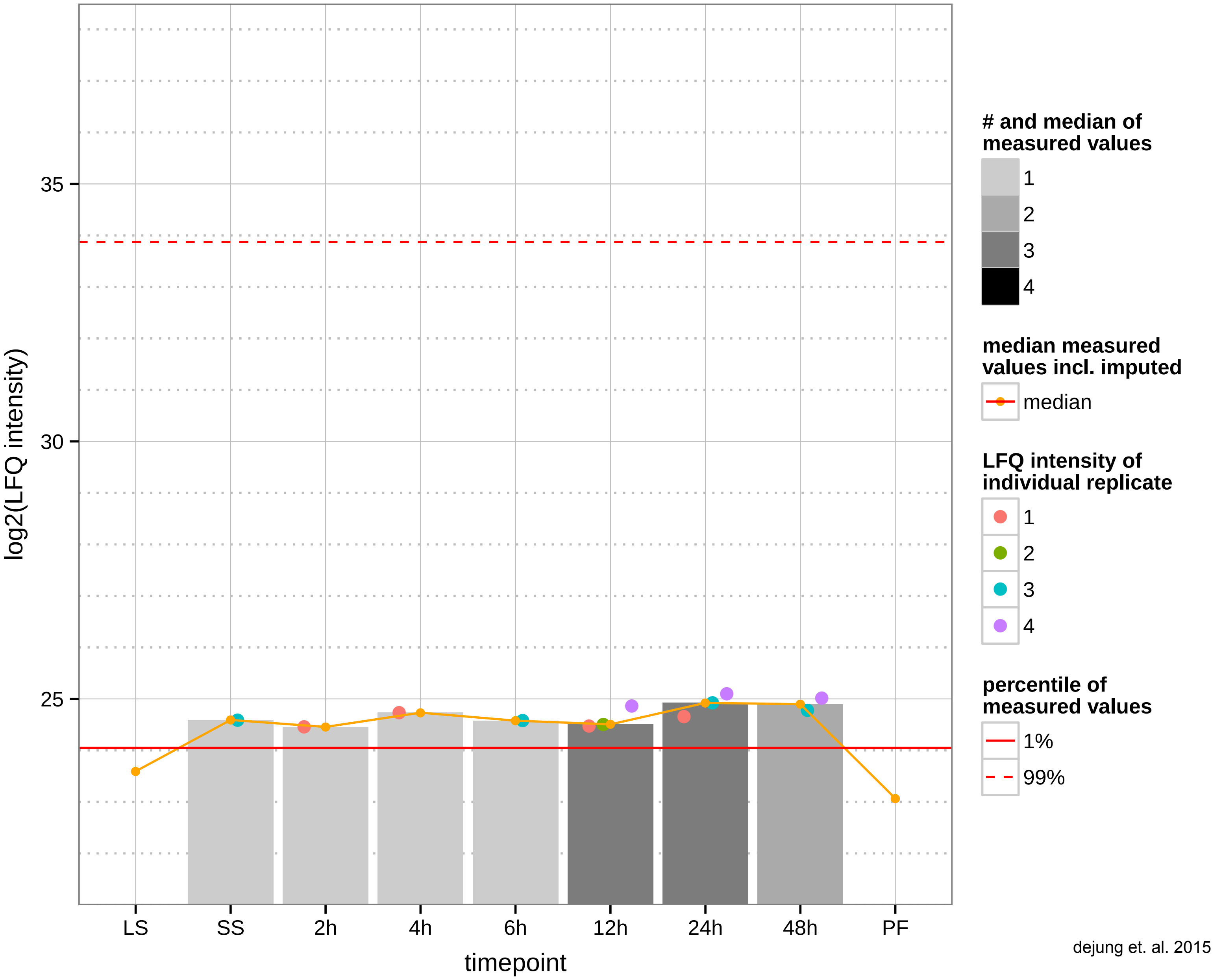
recombination initiation protein NBS1, putative
Tb927.8.5710
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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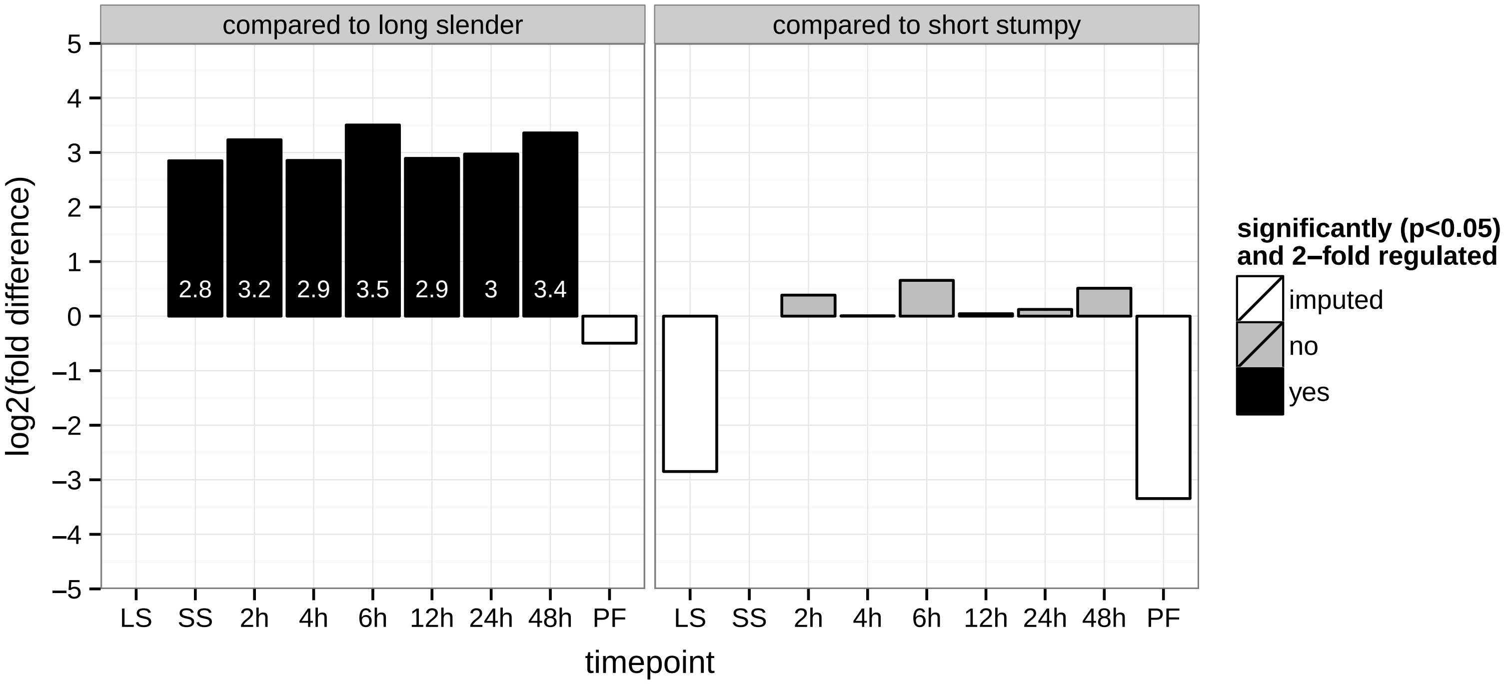
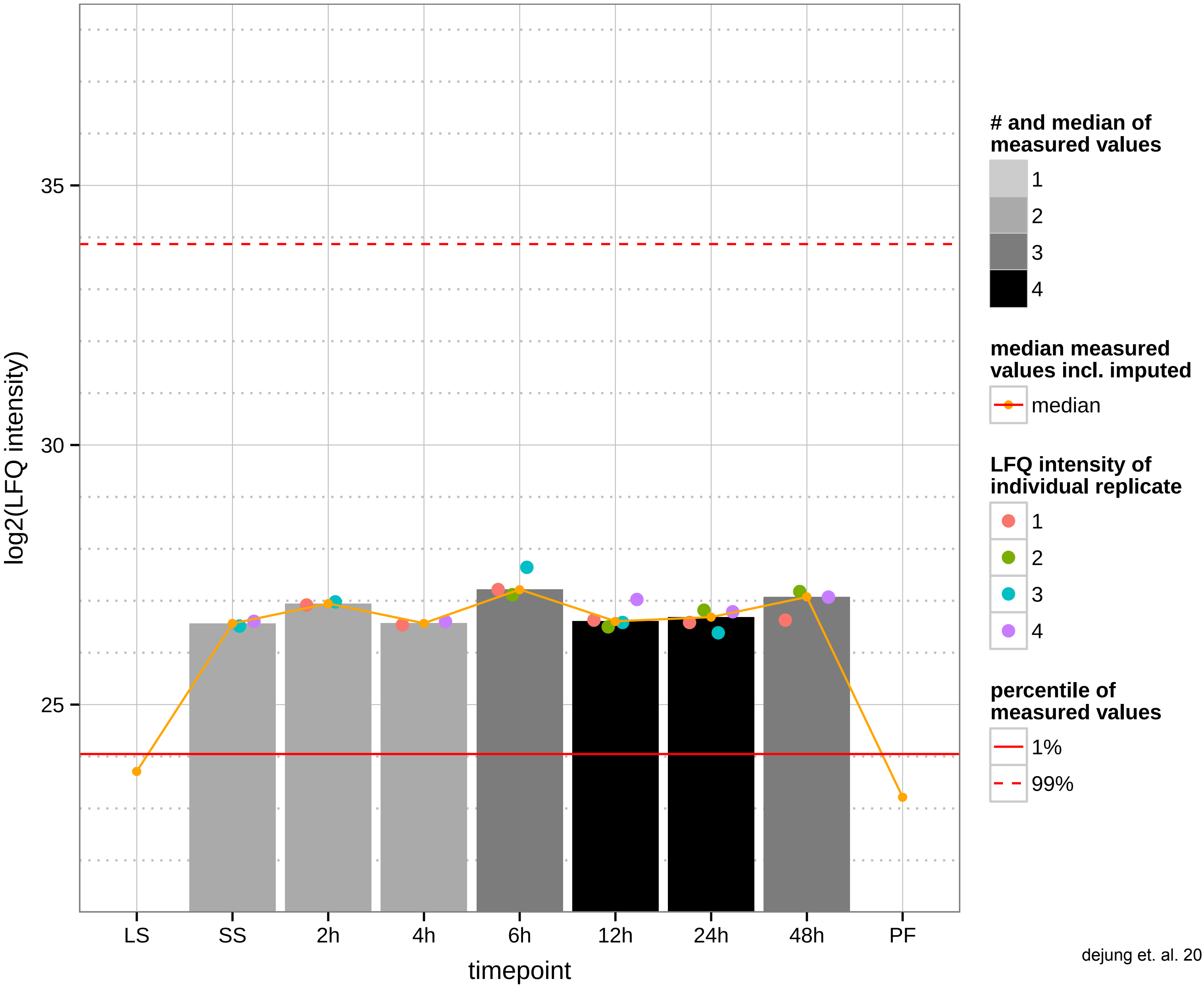
basal body component, ML protein (TBBC)
Tb927.8.6070
AGOF: null
AGOC: cilium, cilium basal body, nucleus
AGOP: cilium assembly
PGOF: null
PGOC: null
PGOP: null





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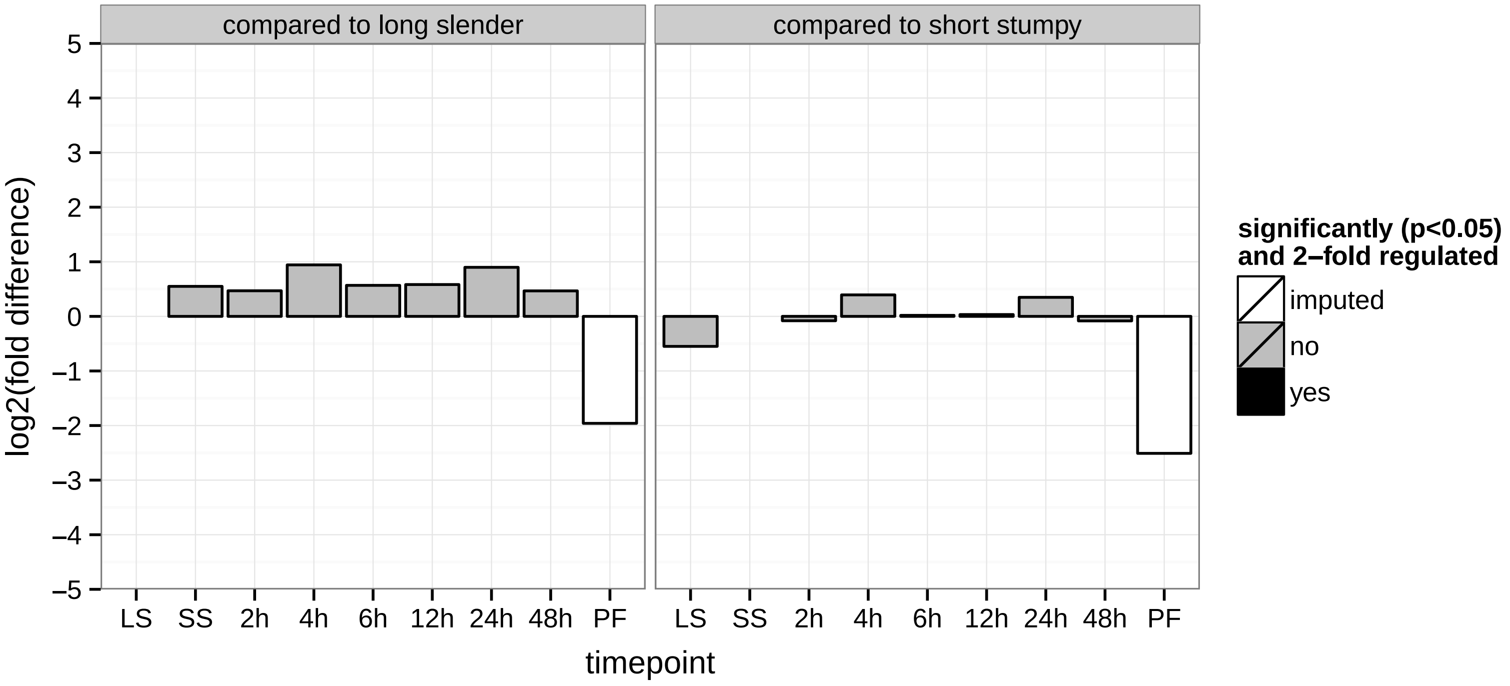
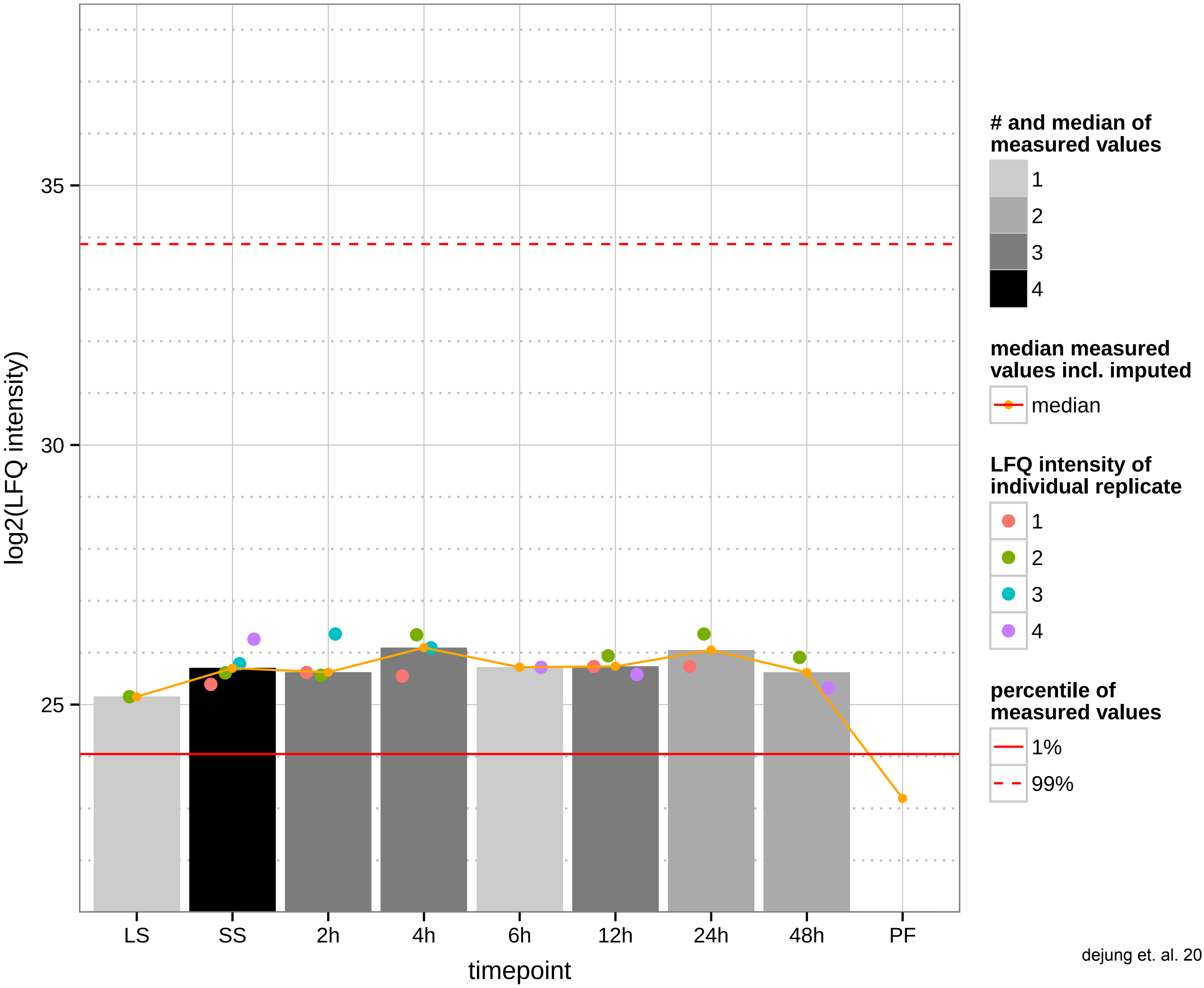
hypothetical protein, conserved
Tb927.8.6190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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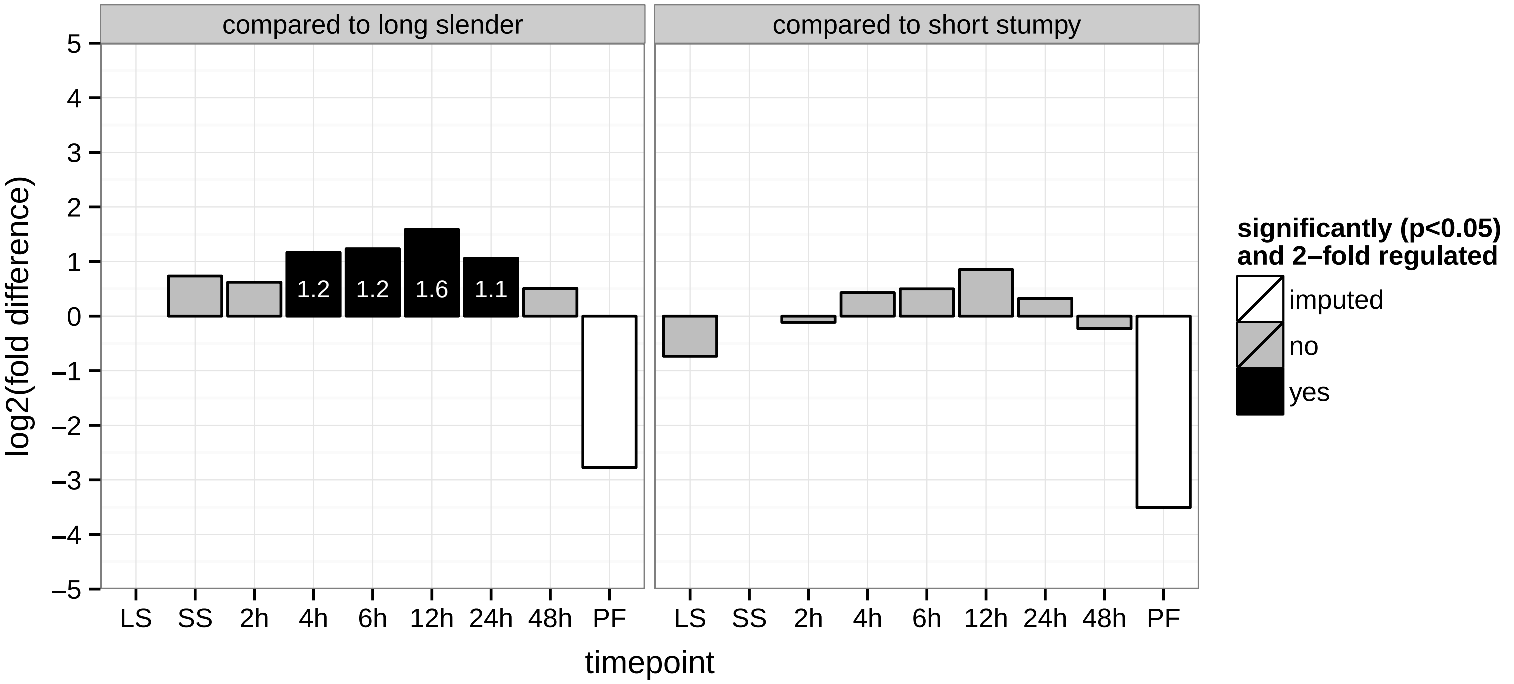
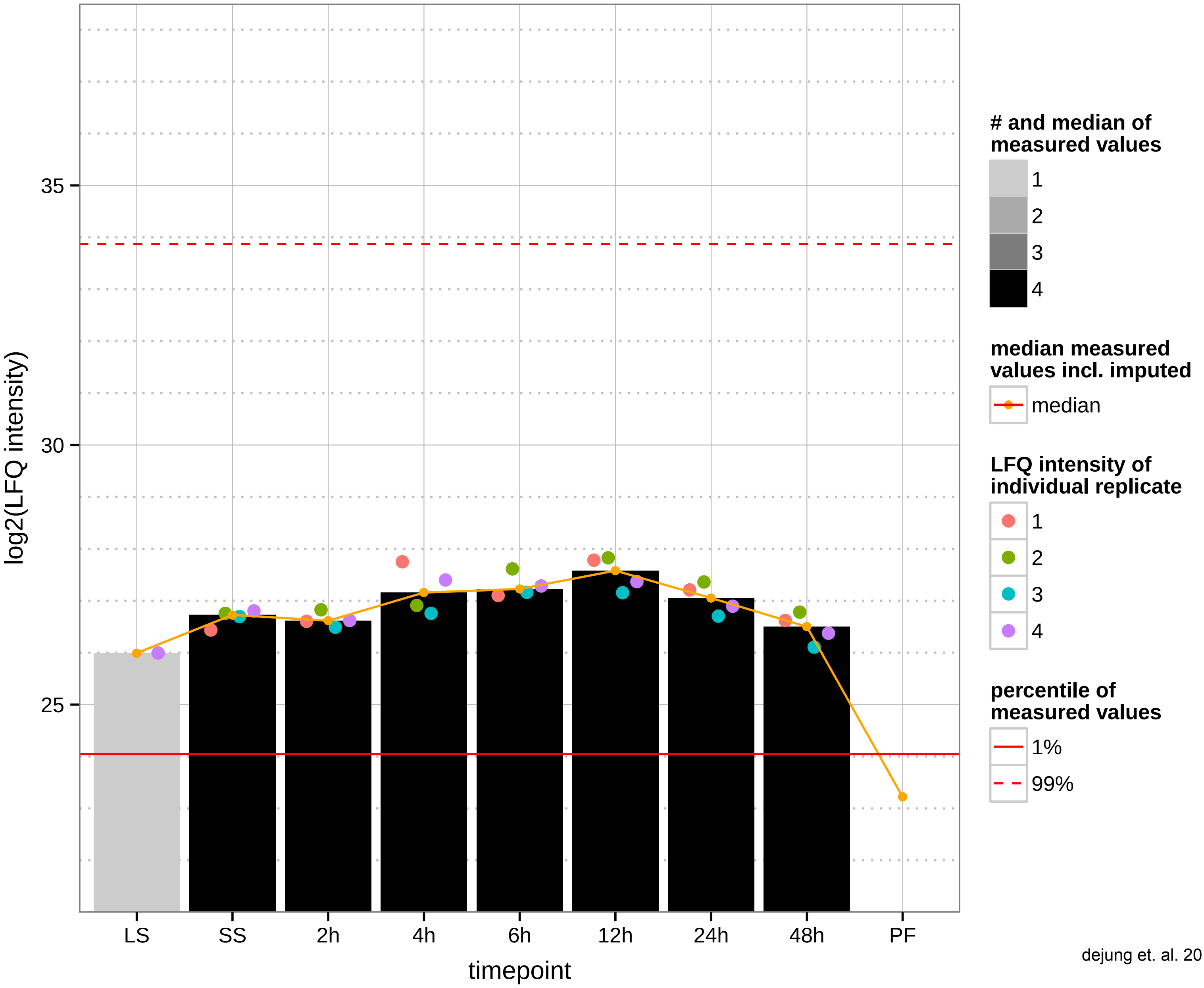
hypothetical protein, conserved
Tb927.8.7210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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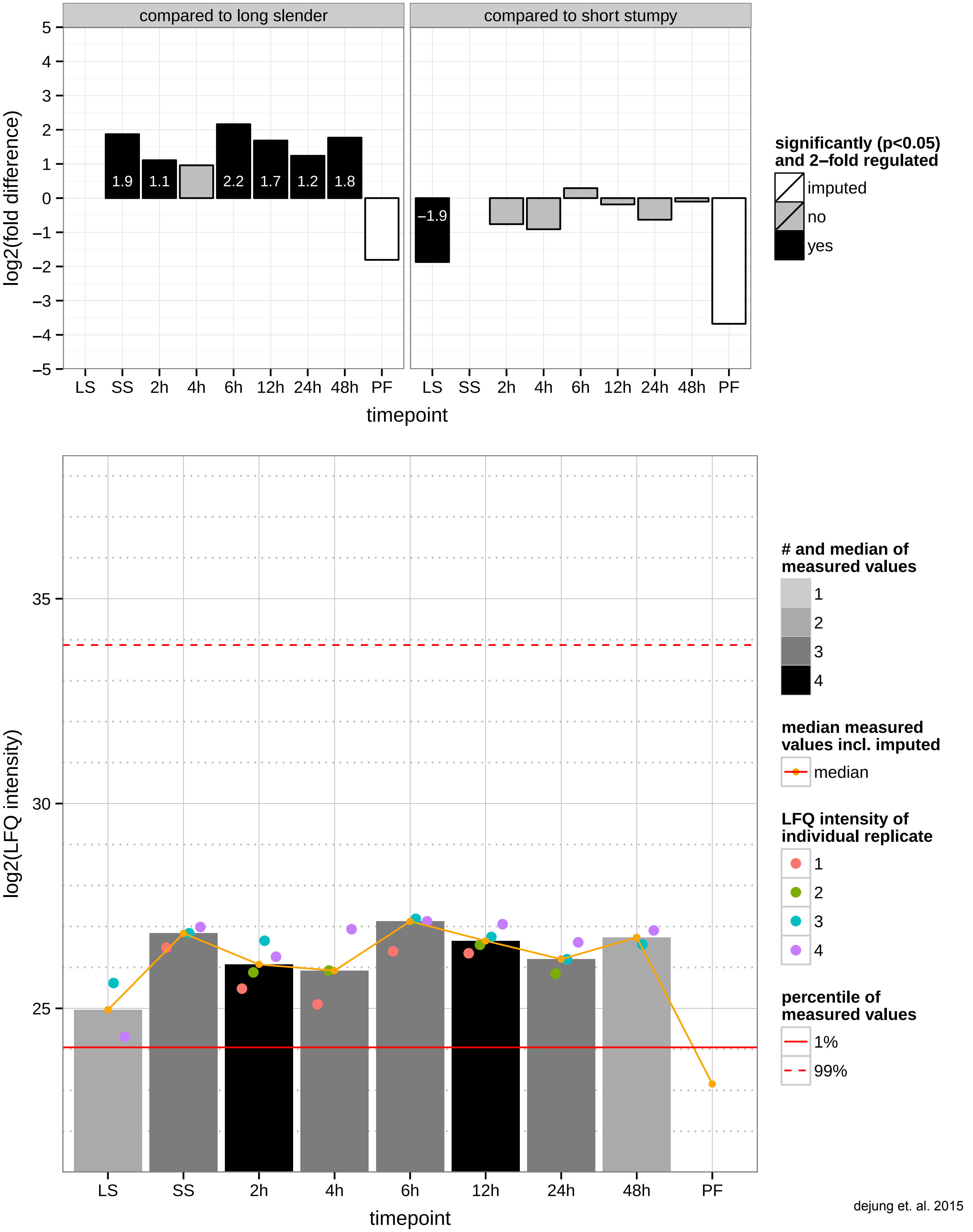
hypothetical protein, conserved
Tb927.8.7790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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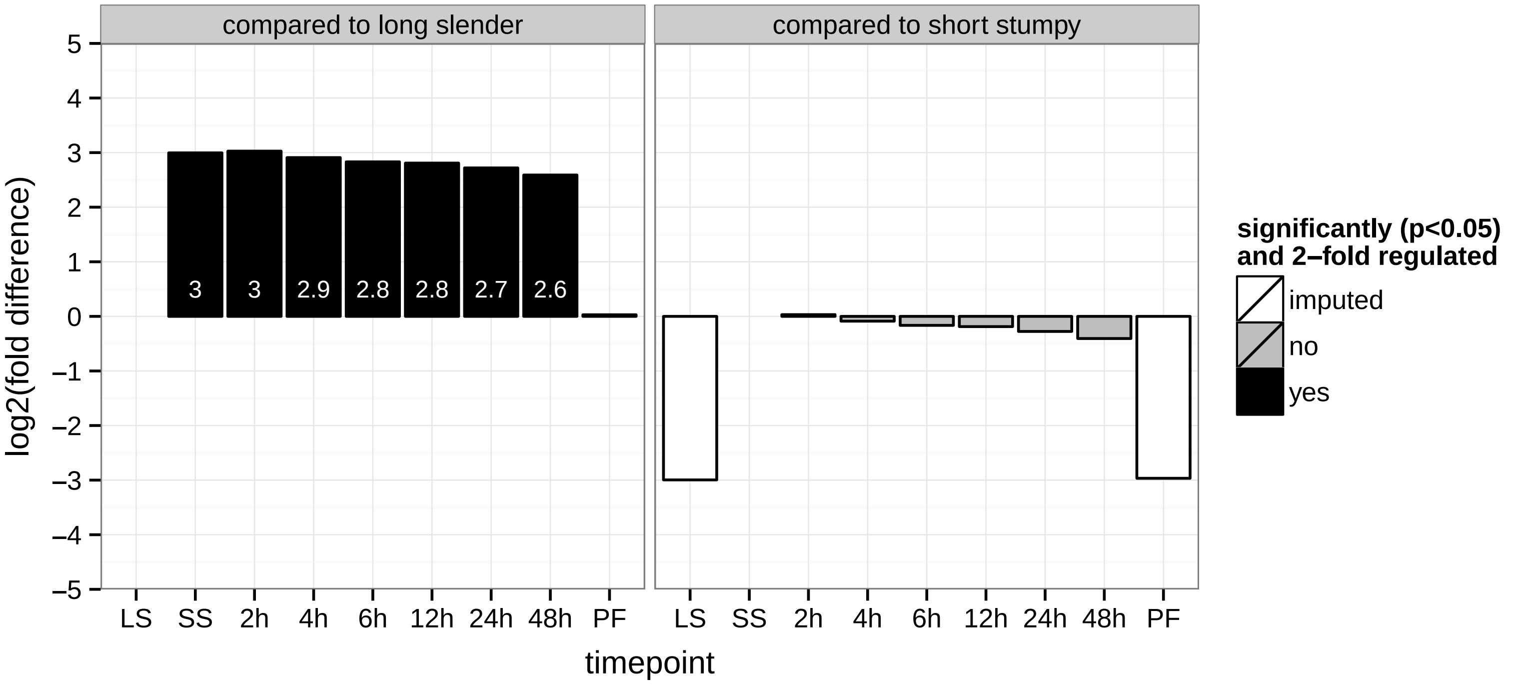
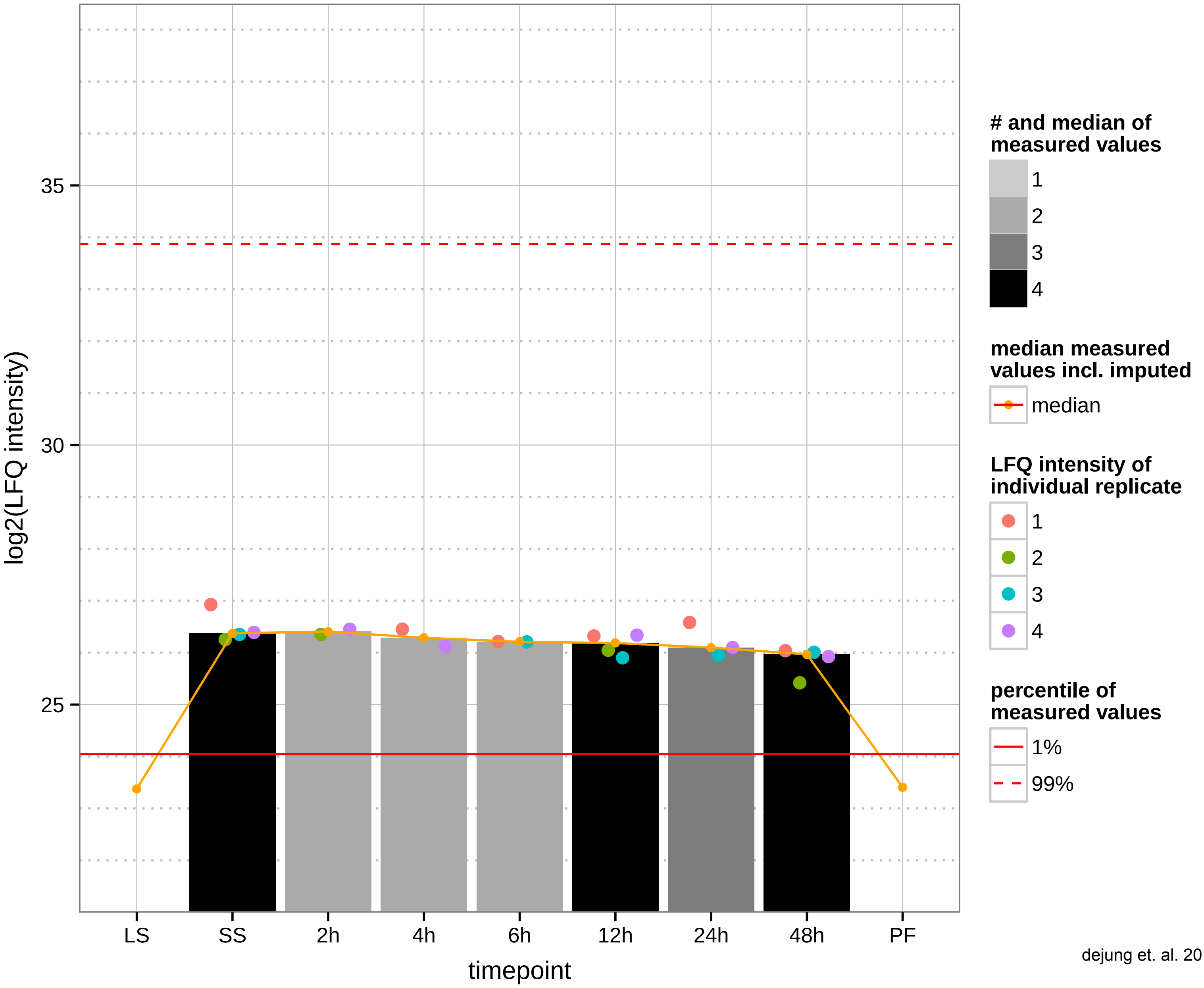
hypothetical protein, conserved
Tb927.8.7990
AGOF: zinc ion binding
AGOC: intracellular
AGOP: null
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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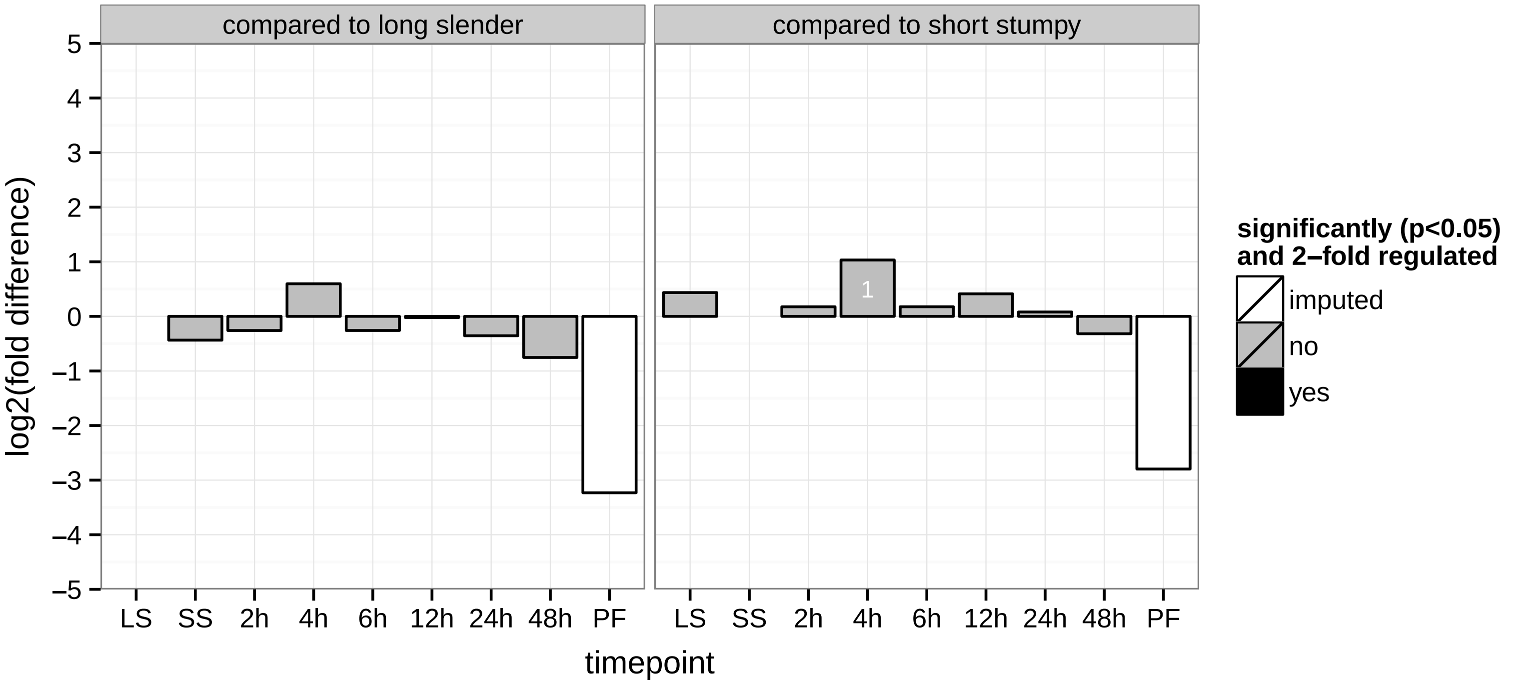
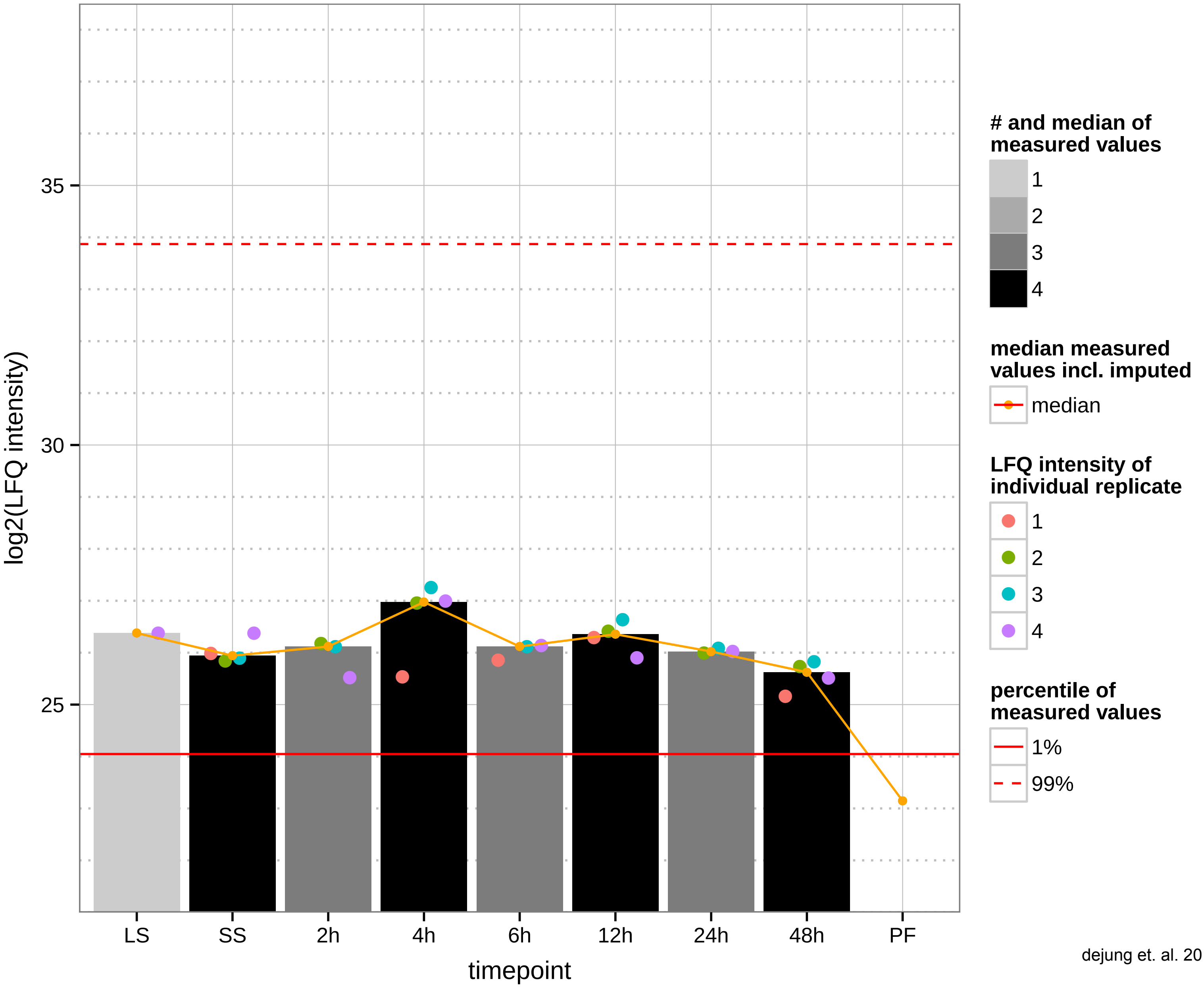
hypothetical protein, conserved
Tb927.8.8120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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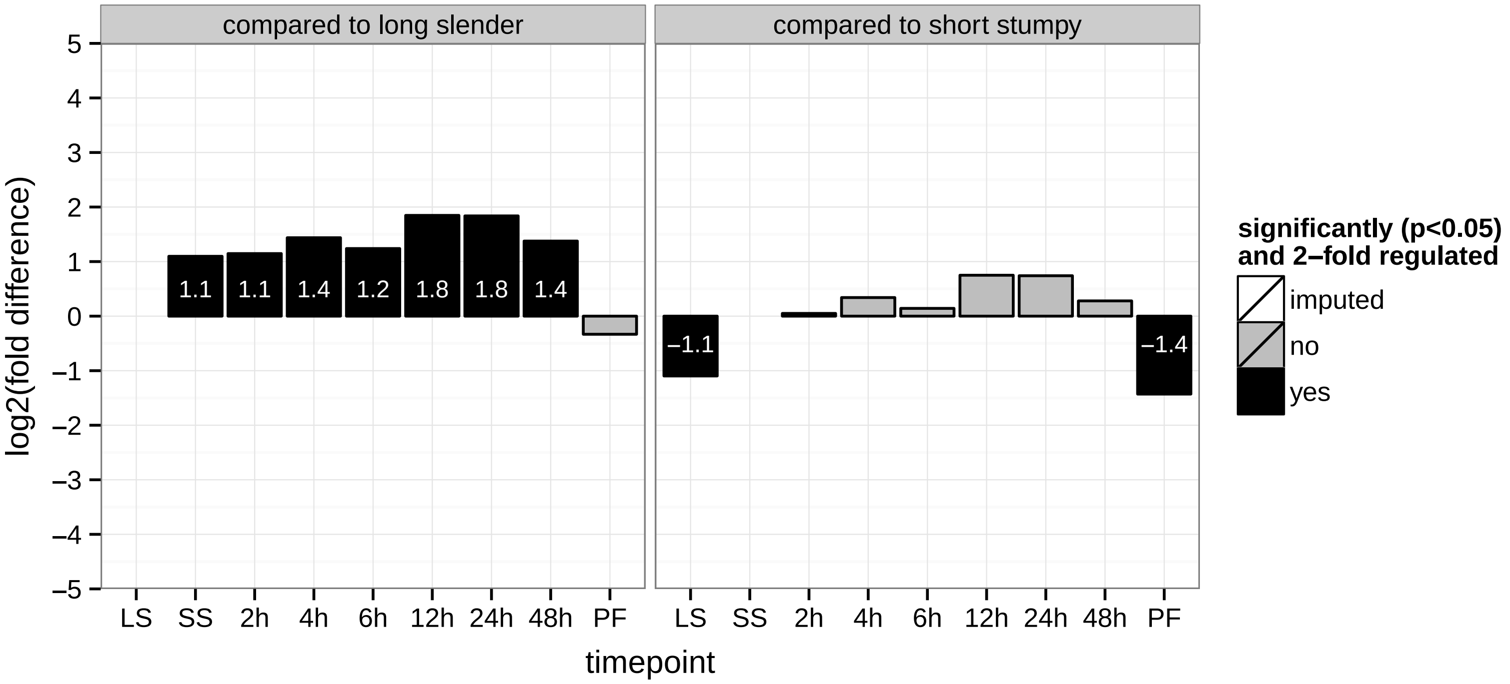
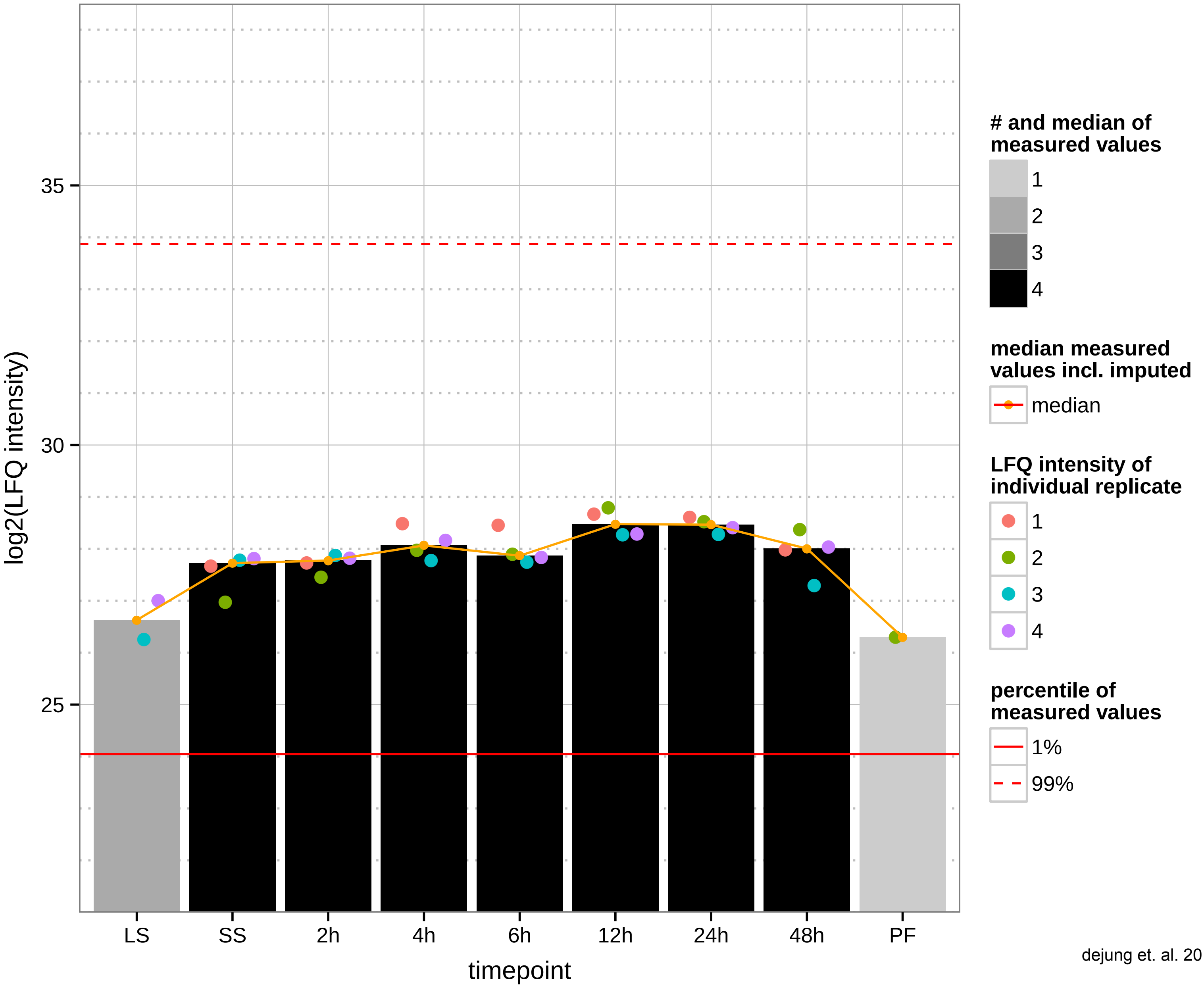
chaperone protein DNAj, putative
Tb927.8.8310
AGOF: heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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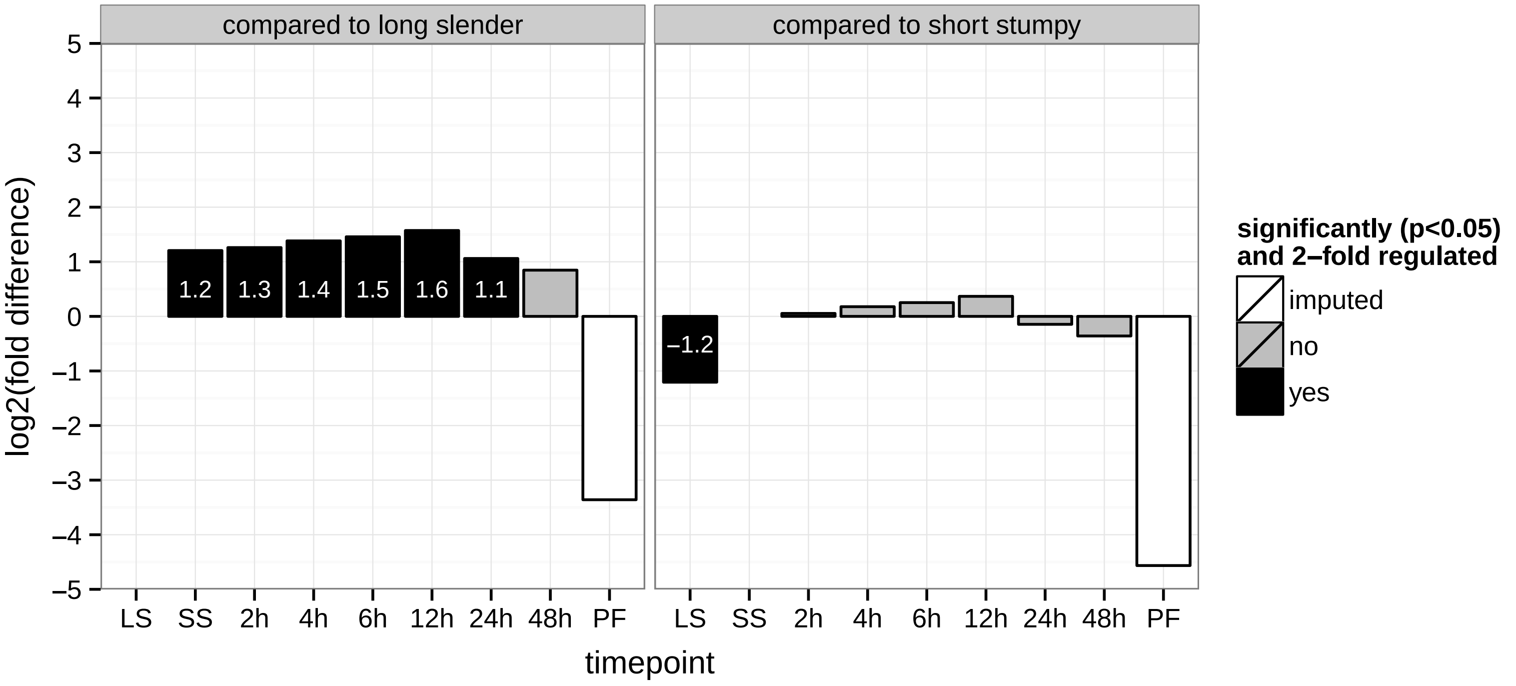
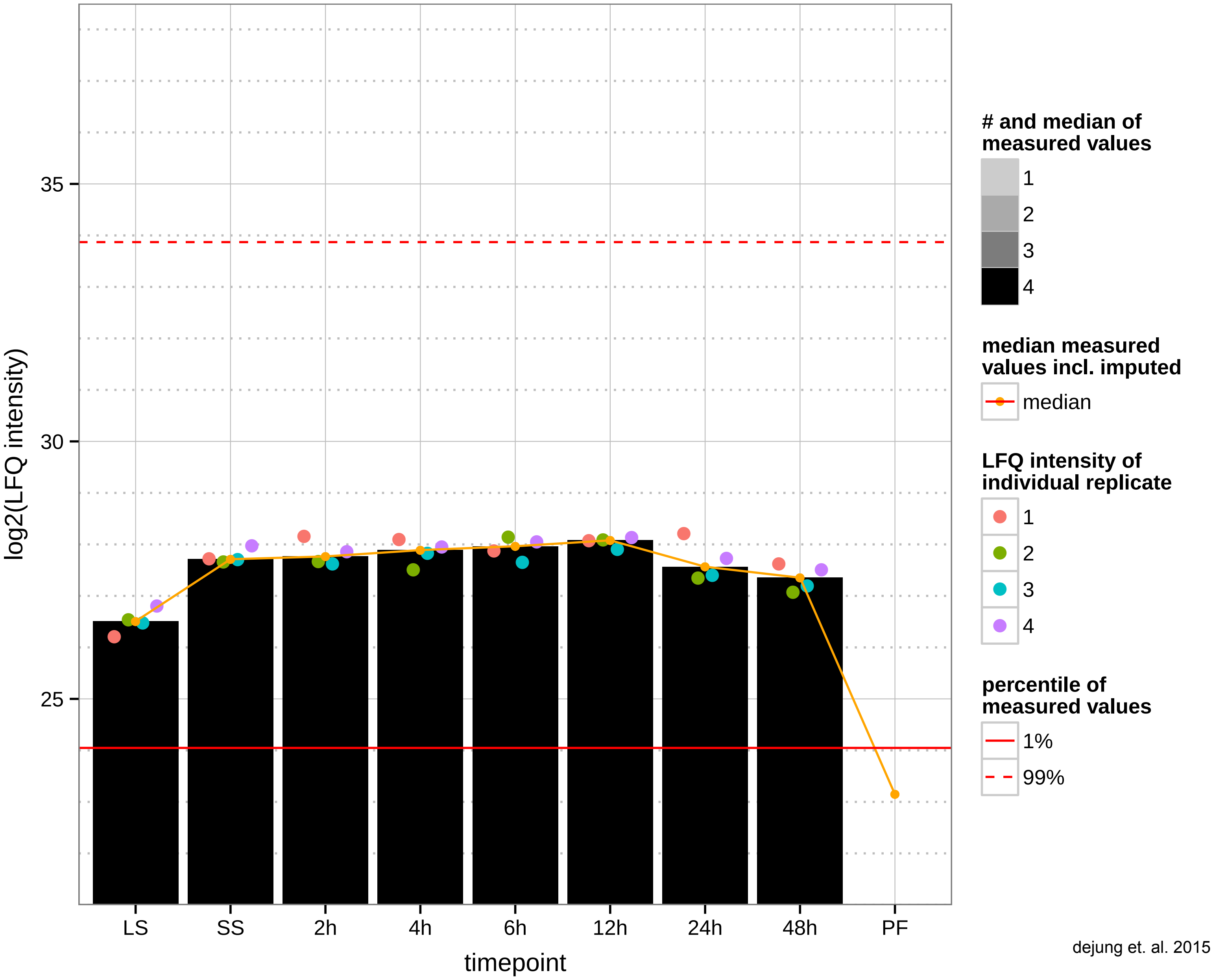
hypothetical protein, conserved
Tb927.8.8340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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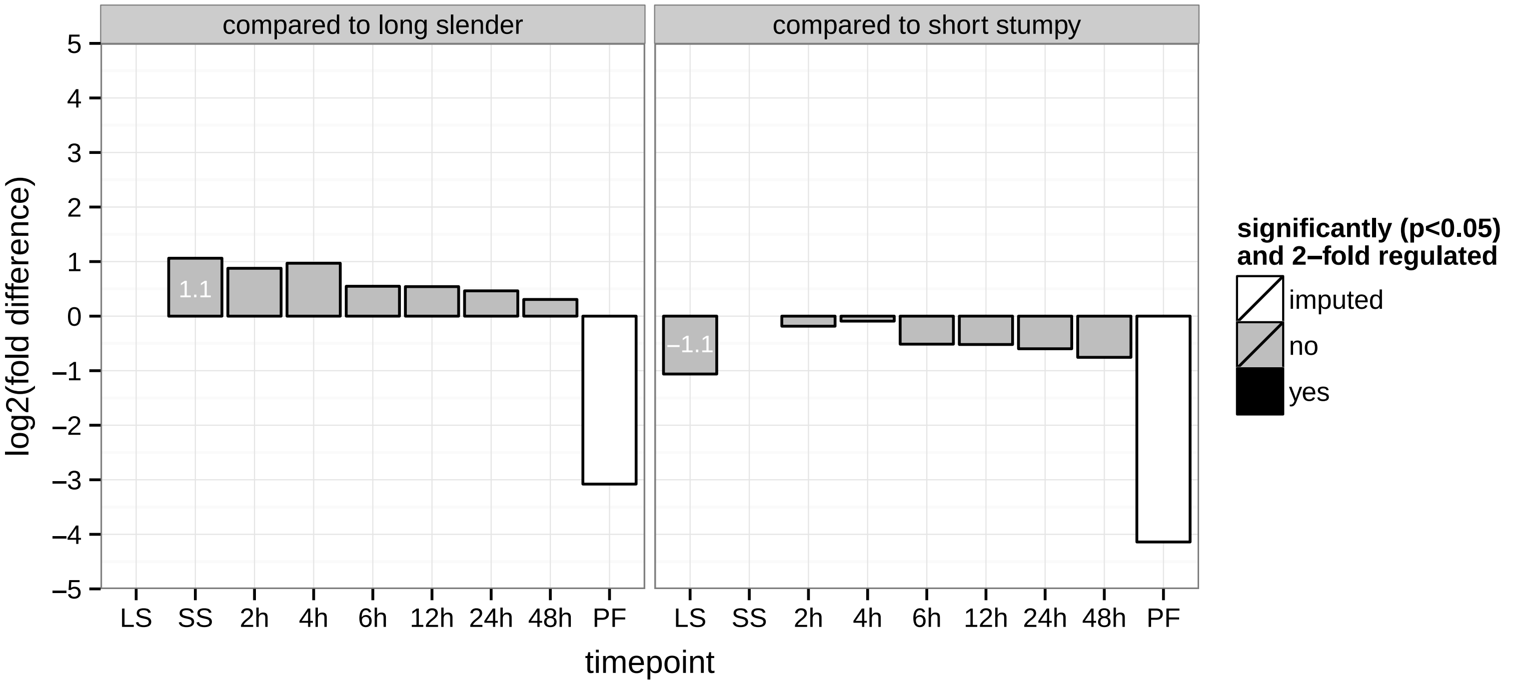
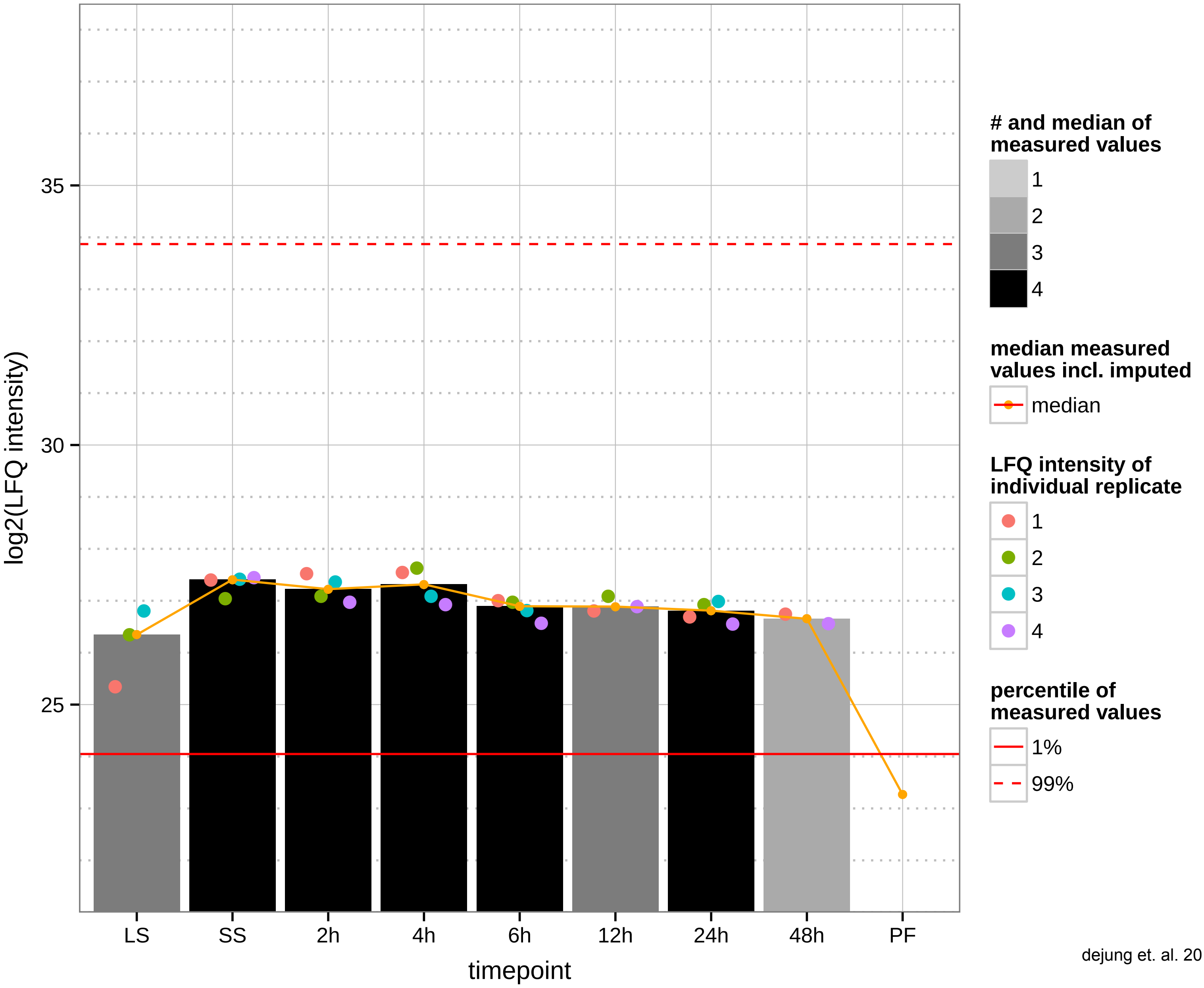
serine/threonine kinase, putative, protein kinase
Tb927.8.870
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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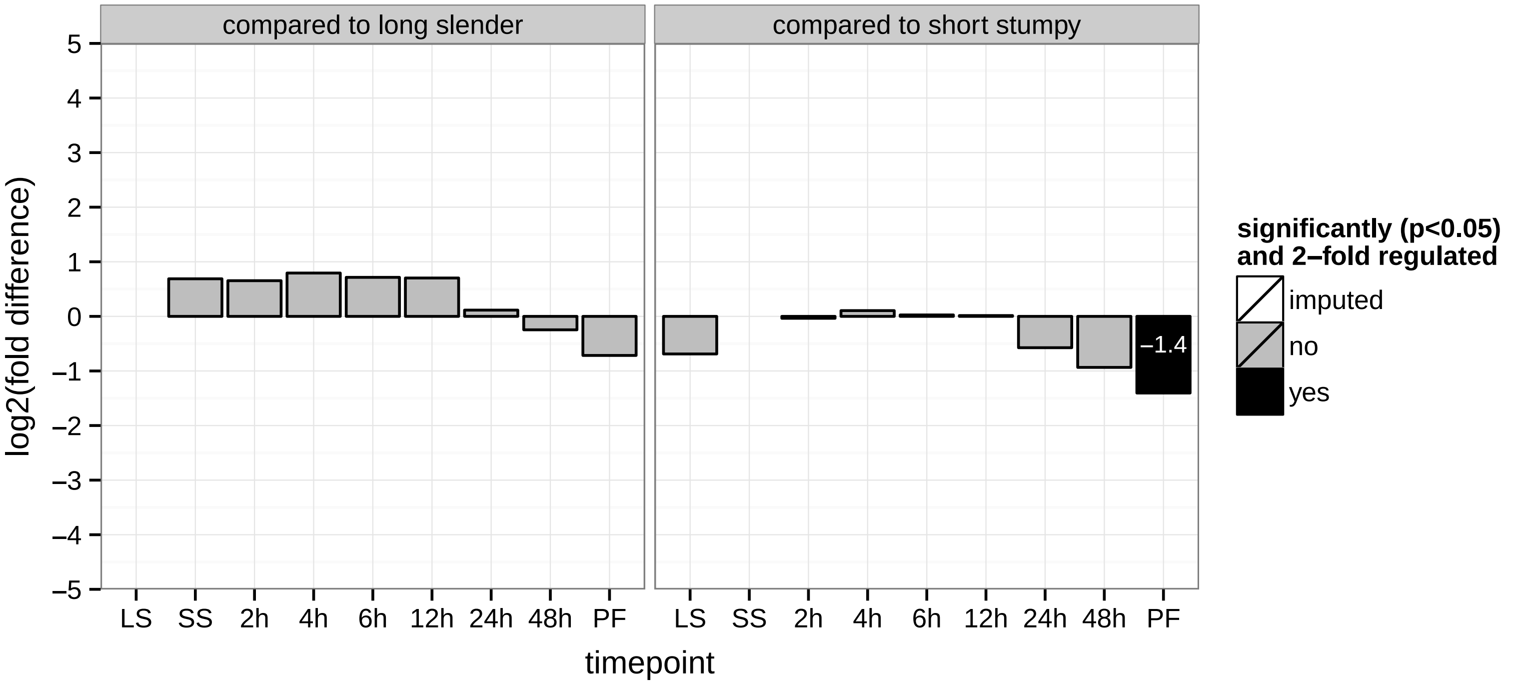
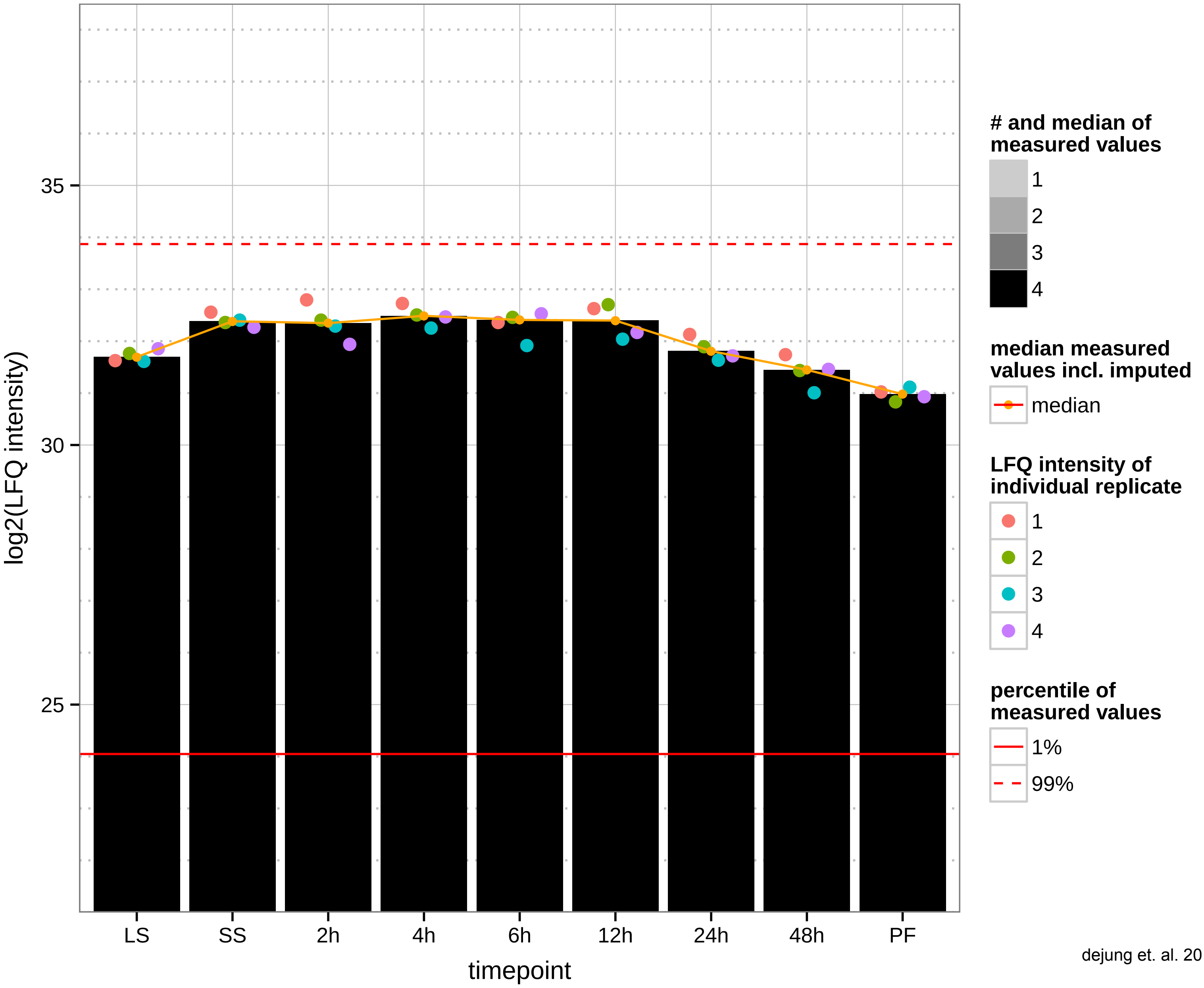
Ras−related protein Rab1A (Rab1A)
Tb927.8.890
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti





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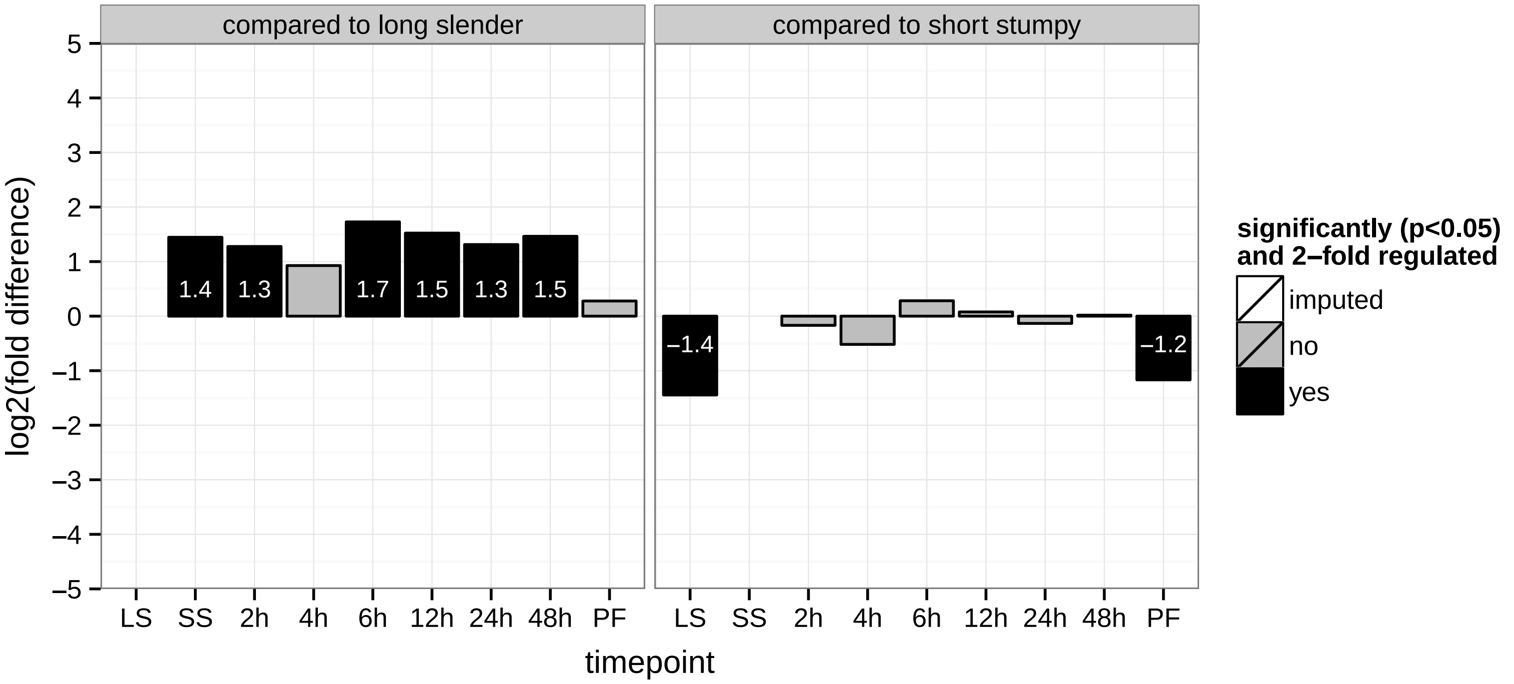
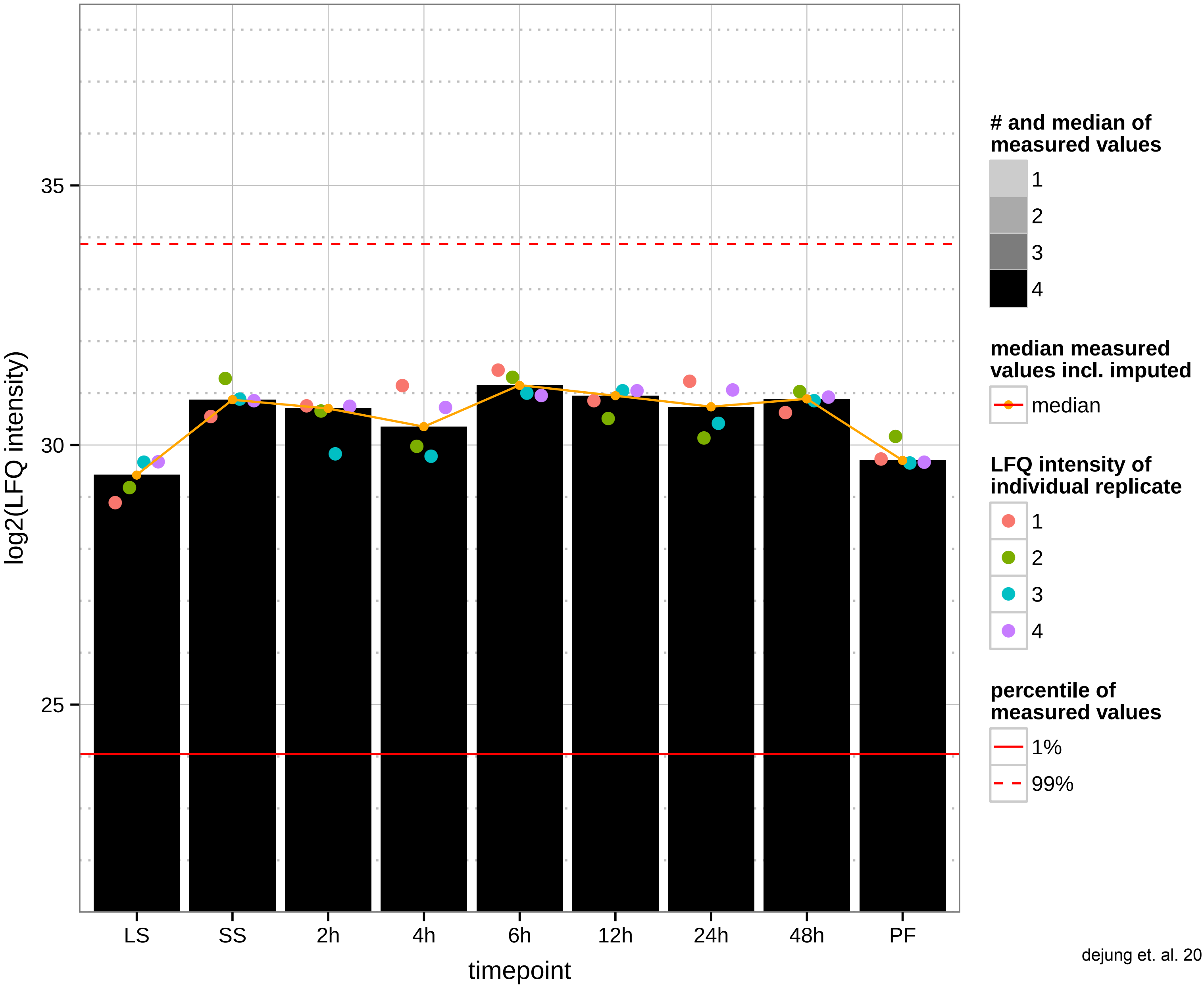
splicing factor TSR1 (TSR1)
Tb927.8.900
AGOF: RNA binding
AGOC: nucleus
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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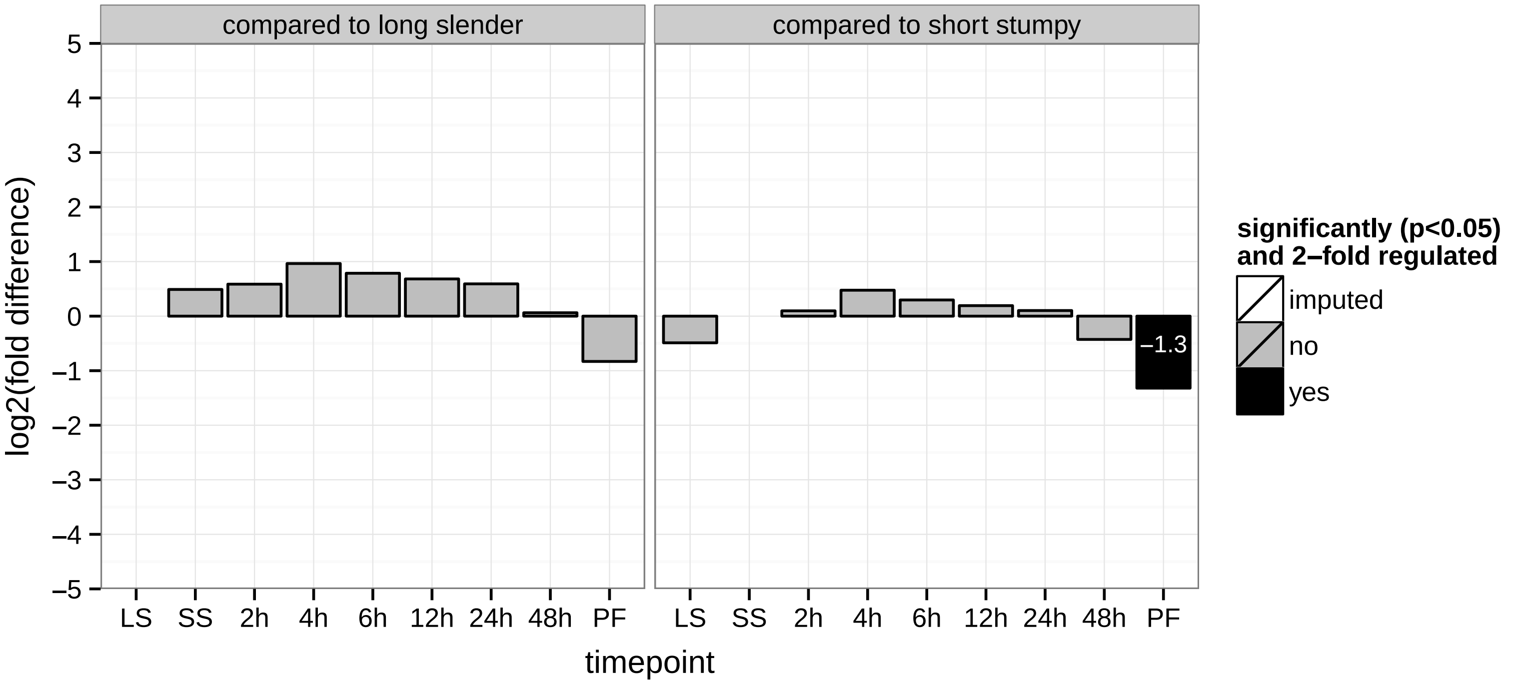
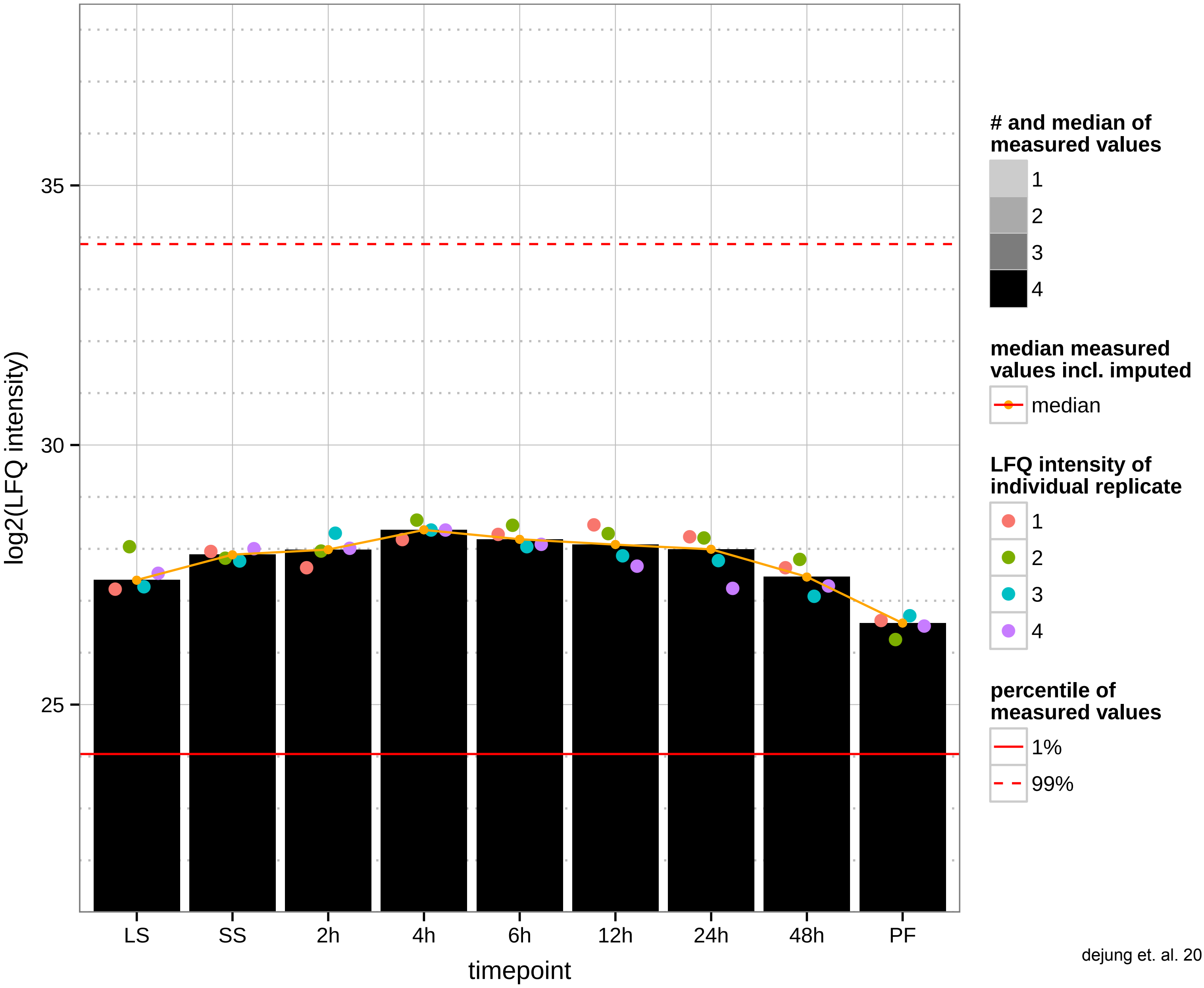
hypothetical protein, conserved
Tb927.9.10350
AGOF: null
AGOC: null
AGOP: protein transport, vesicle–mediated transport
PGOF: null
PGOC: null
PGOP: protein transport





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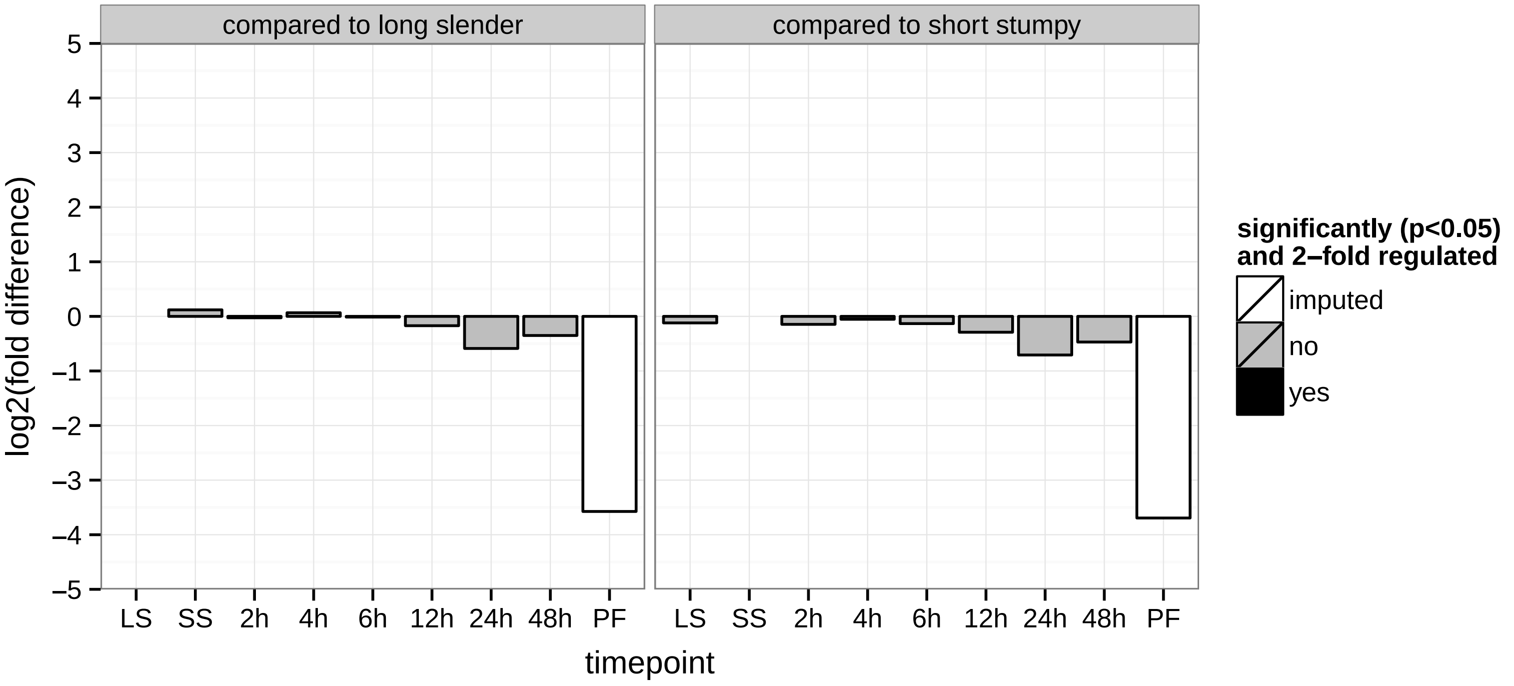
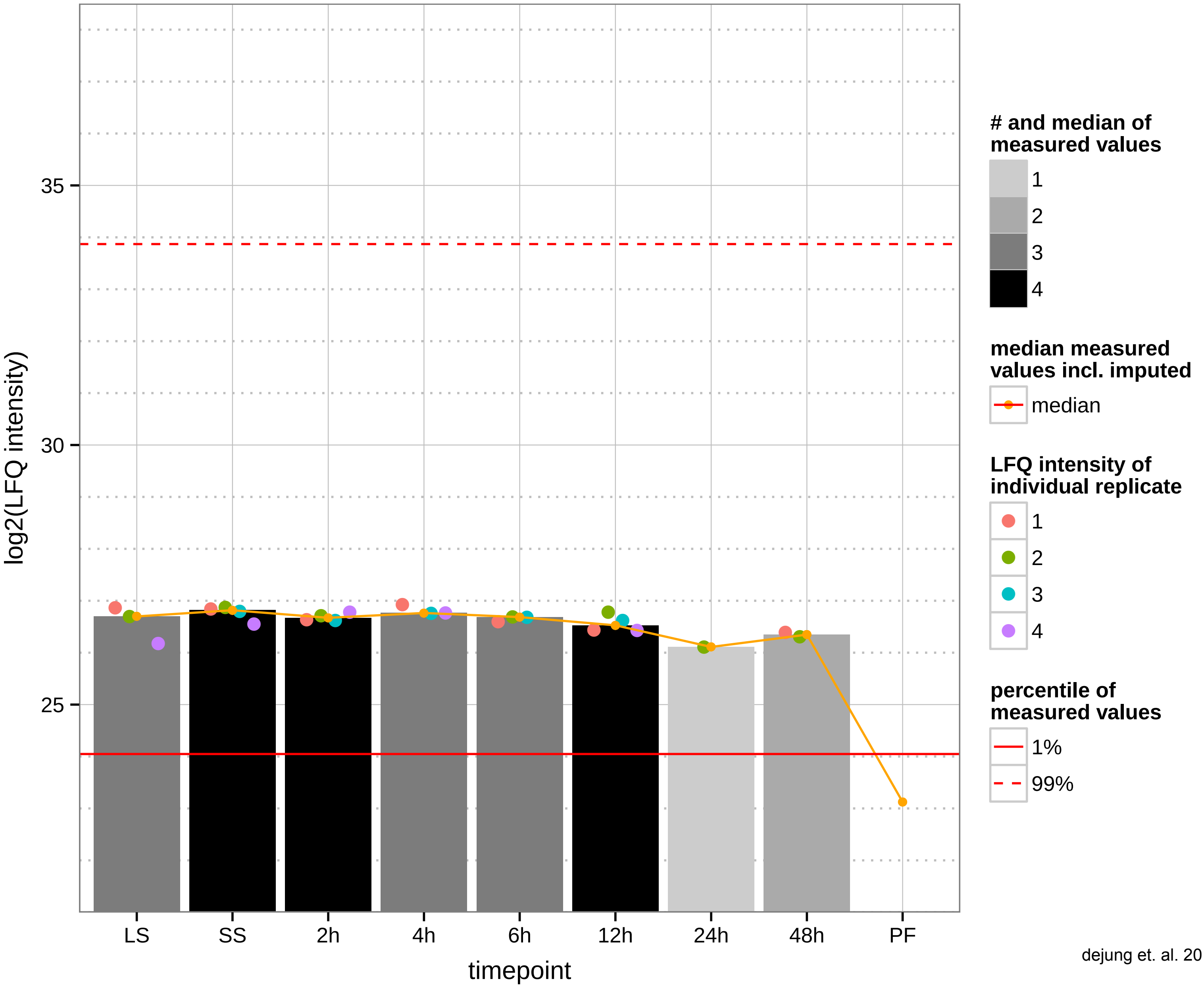
hypothetical protein, conserved
Tb927.9.10450
AGOF: hydrolase activity, acting on ester bonds
AGOC: intrinsic to endoplasmic reticulum membrane
AGOP: GPI anchor metabolic process, intracellular protein transport
PGOF: hydrolase activity, acting on ester bonds
PGOC: intrinsic to endoplasmic reticulum membrane
PGOP: GPI anchor metabolic process, intracellular protein transport





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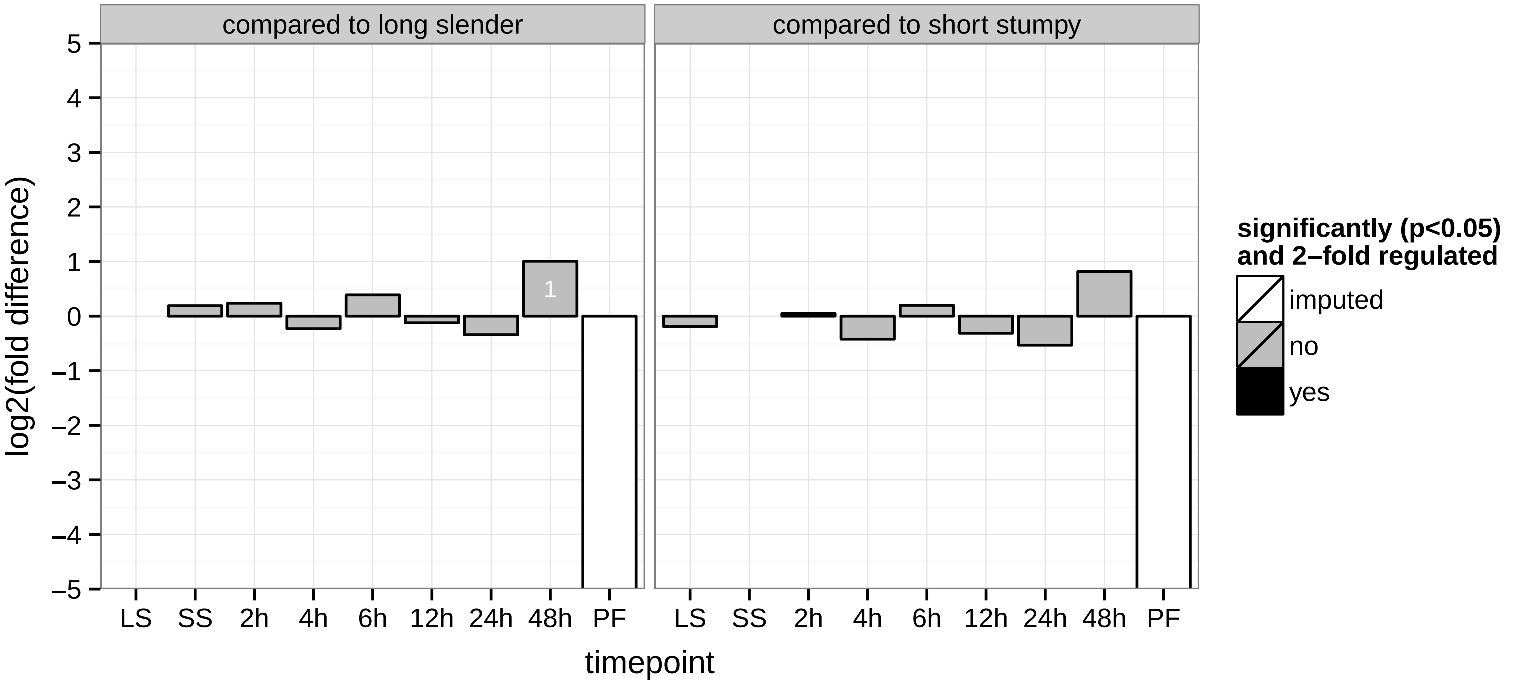
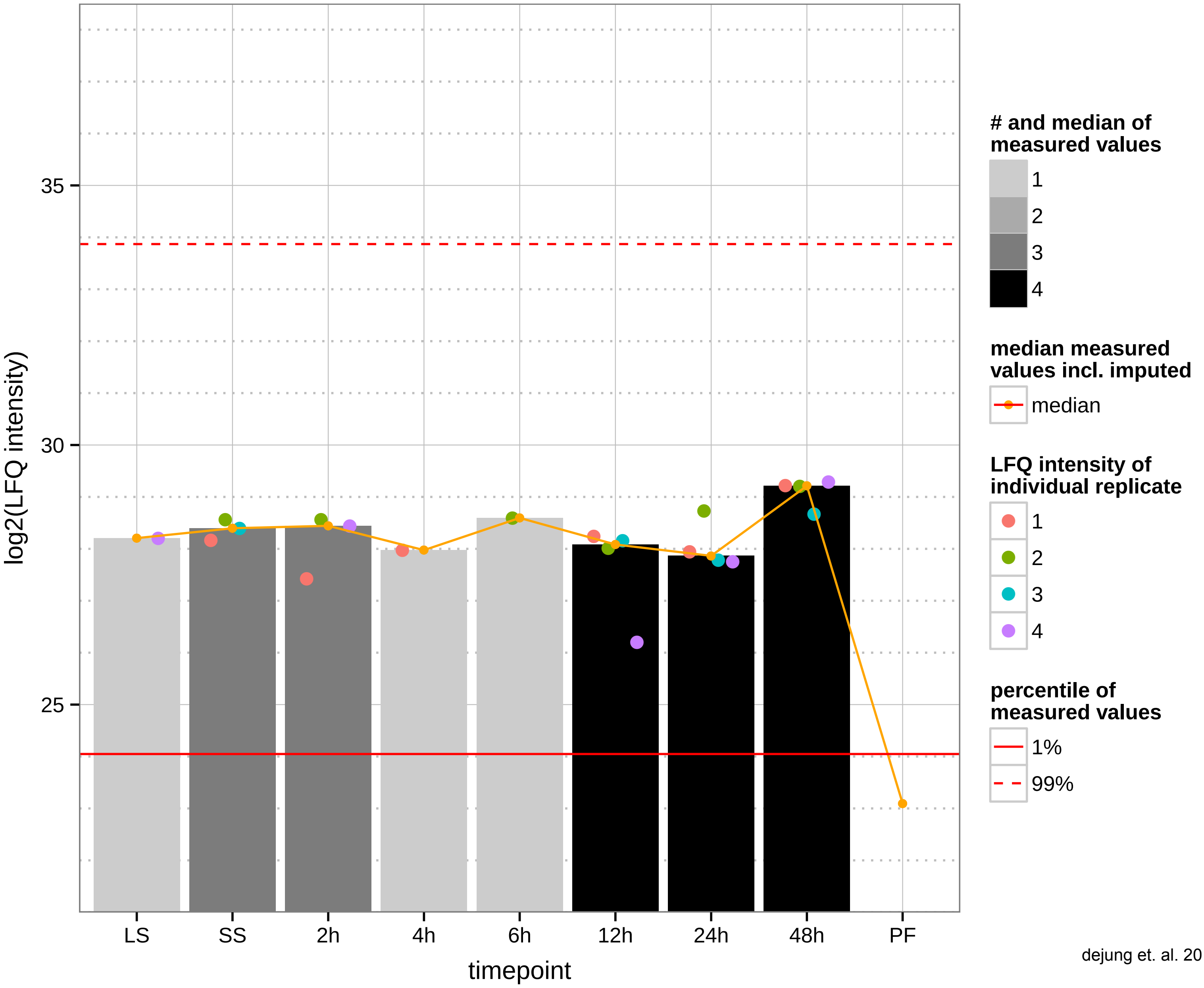
hypothetical protein, conserved
Tb927.9.10550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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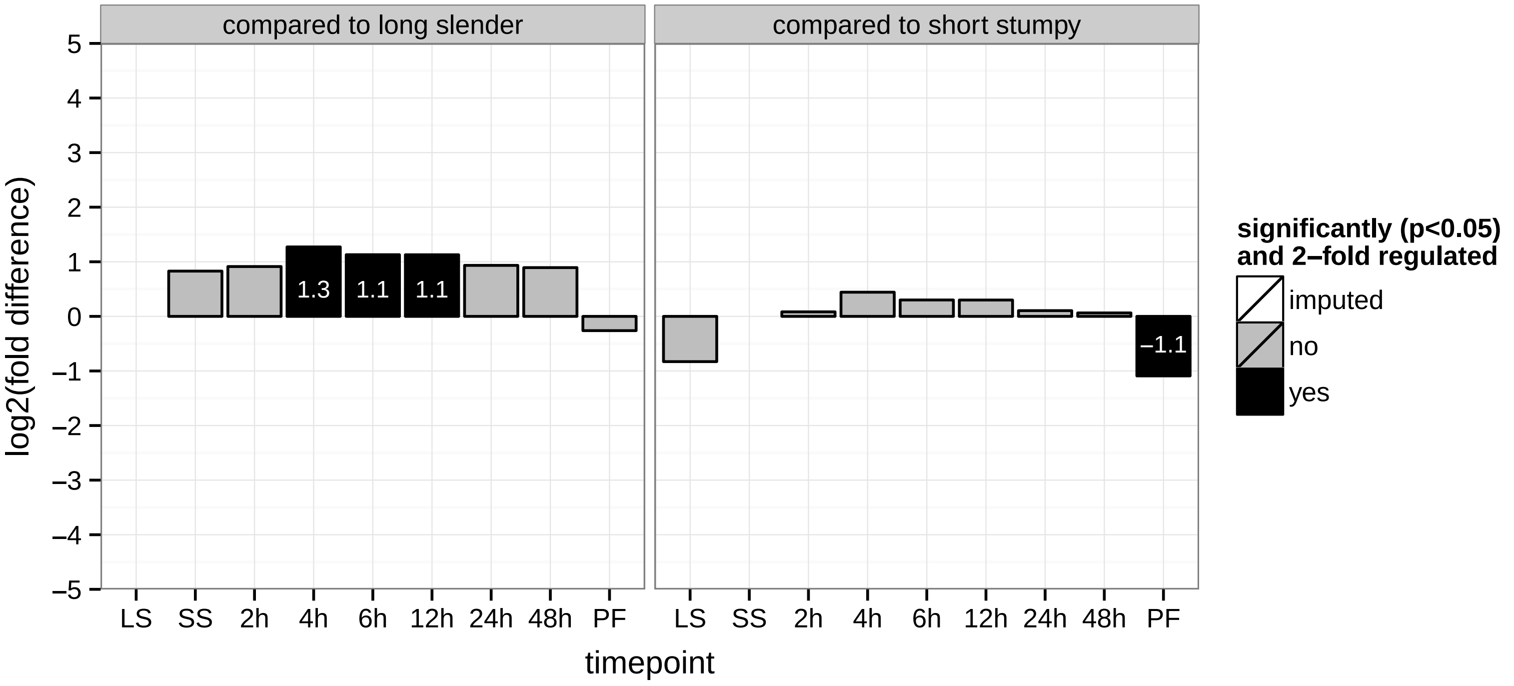
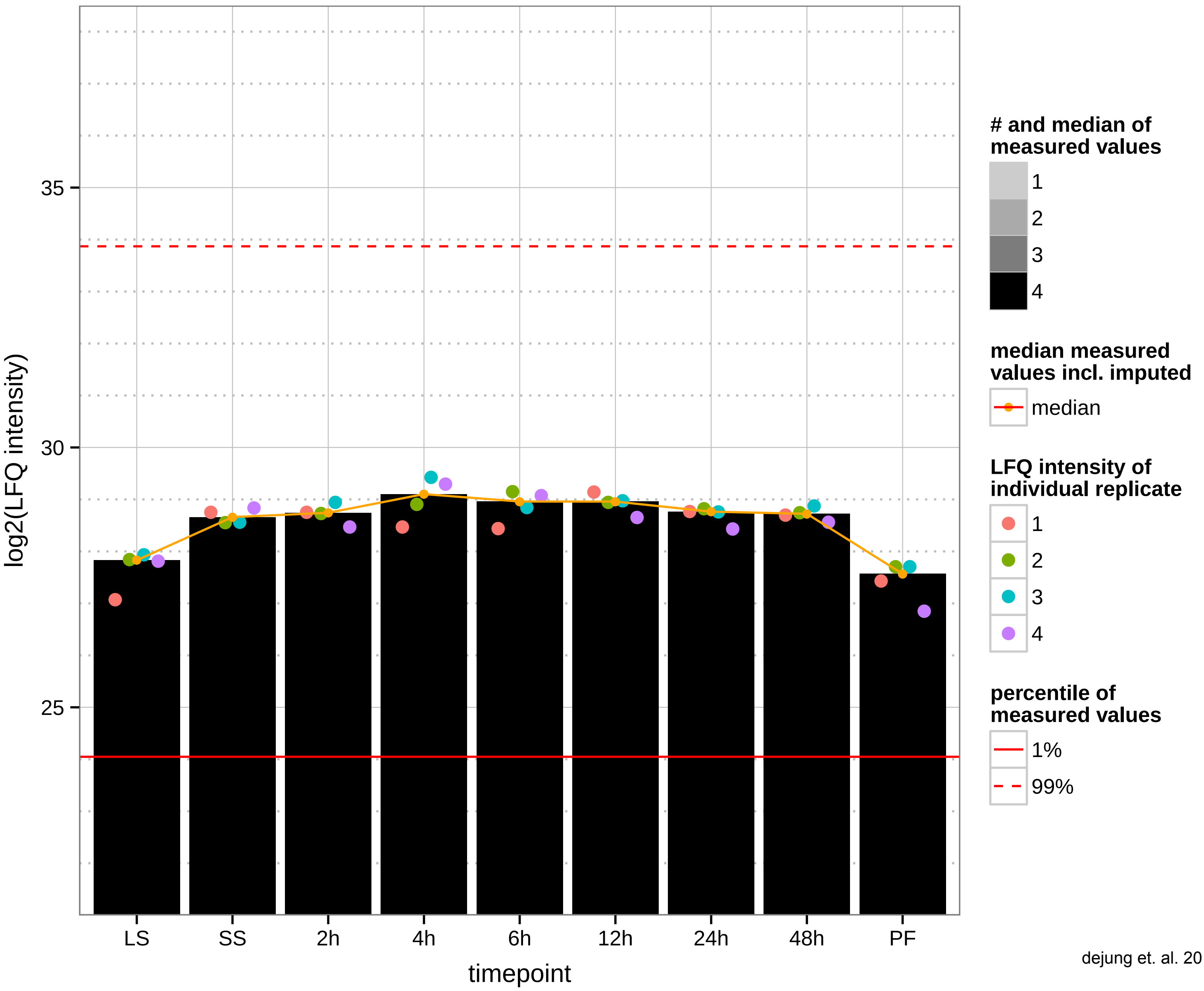
4E–interacting protein, putative
Tb927.9.11050
AGOF: translation regulator activity
AGOC: cytoplasm
AGOP: regulation of translation
PGOF: null
PGOC: null
PGOP: null





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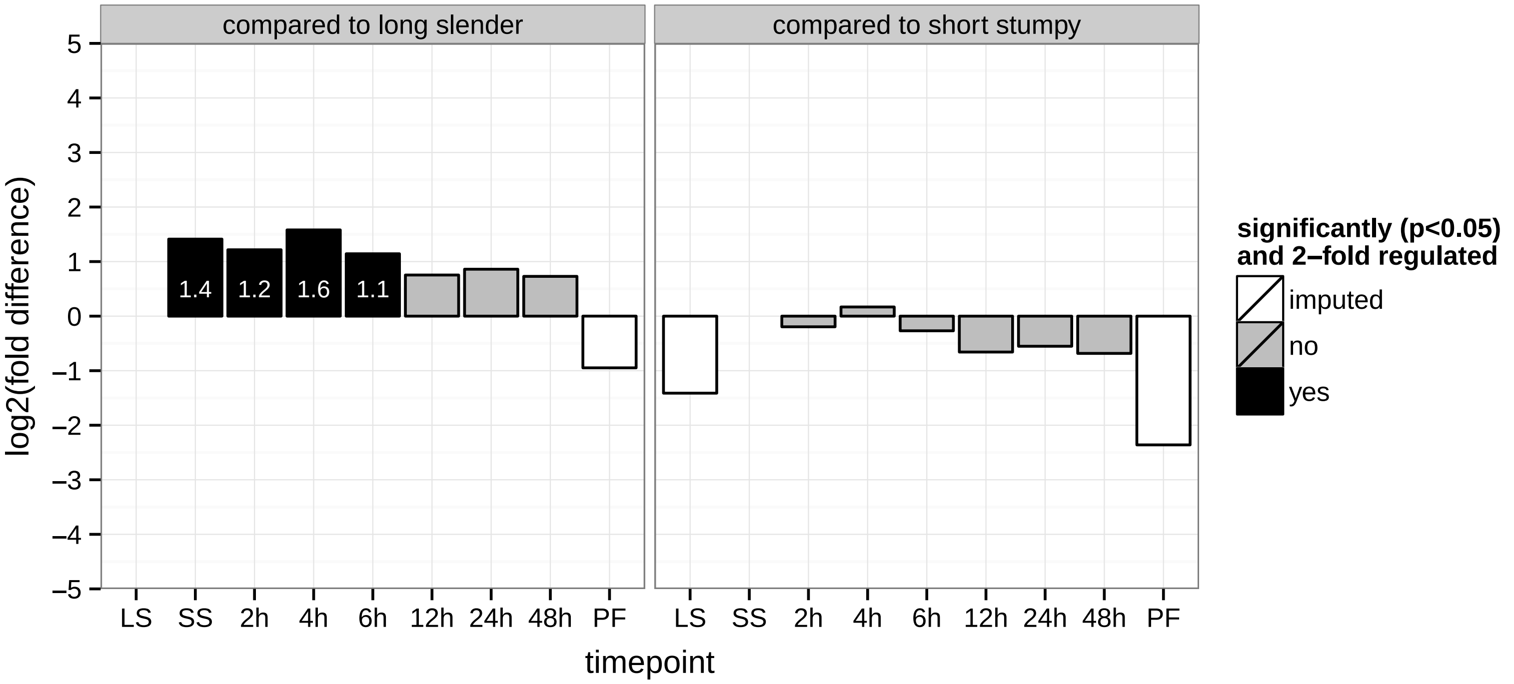
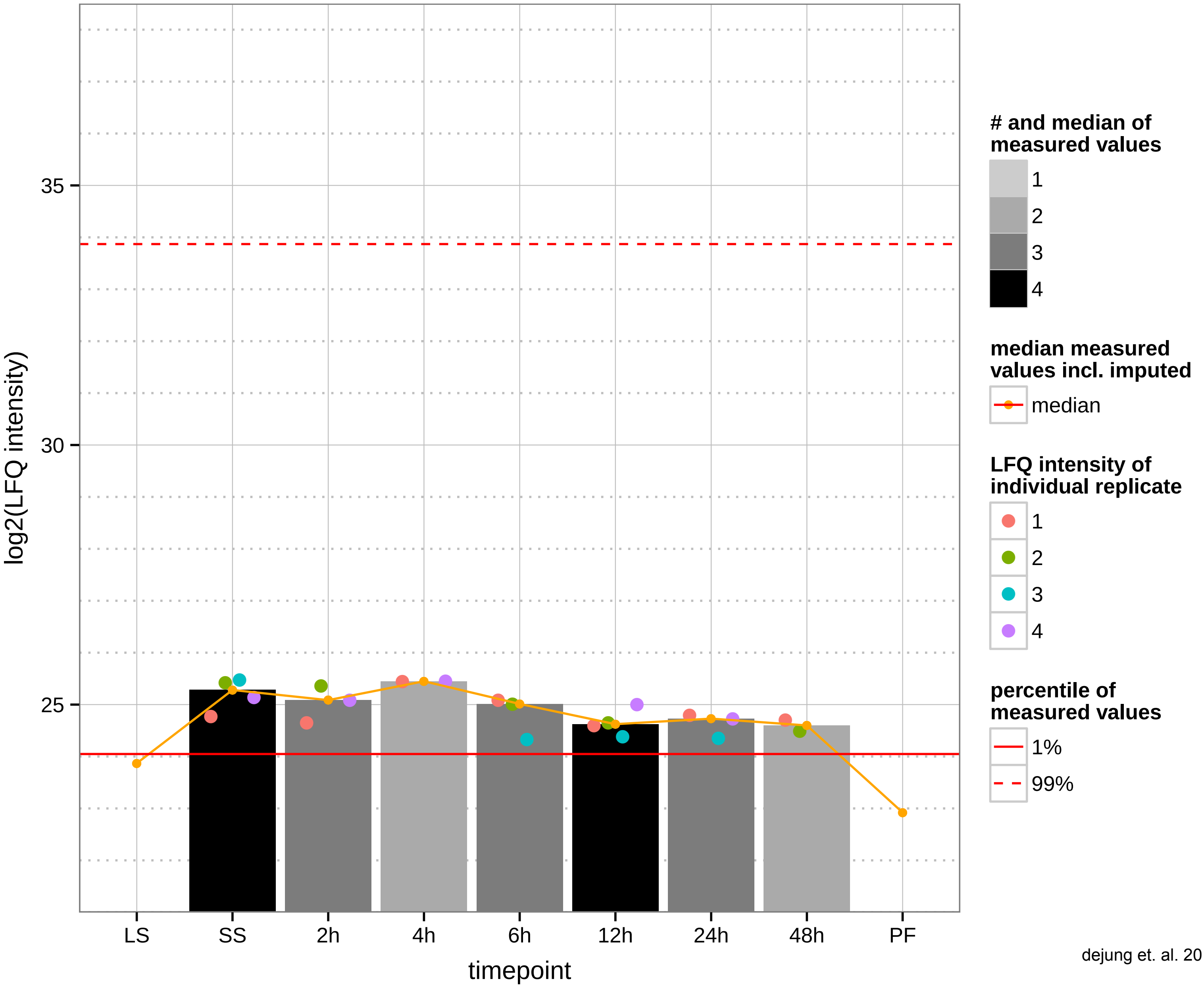
hypothetical protein, conserved
Tb927.9.12000
AGOF: null
AGOC: membrane
AGOP: null
PGOF: null
PGOC: membrane
PGOP: null





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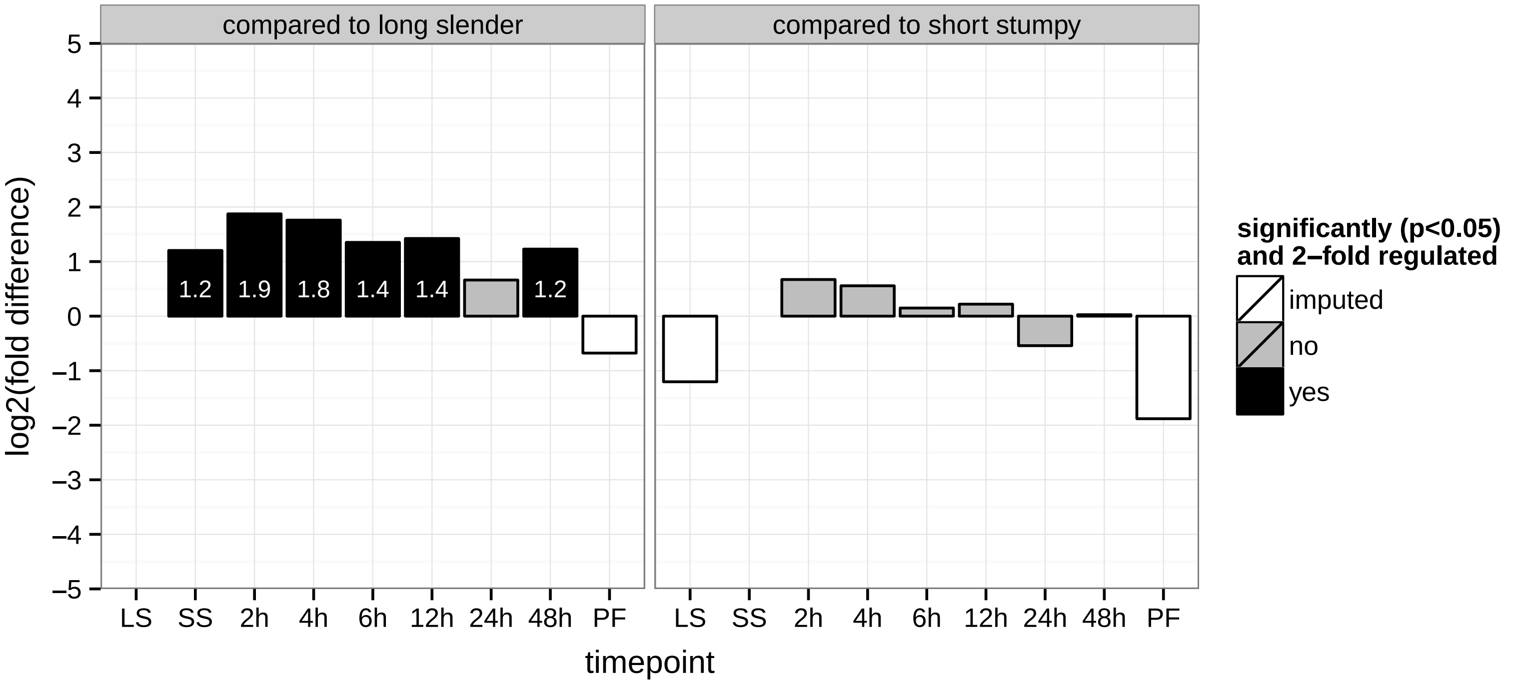
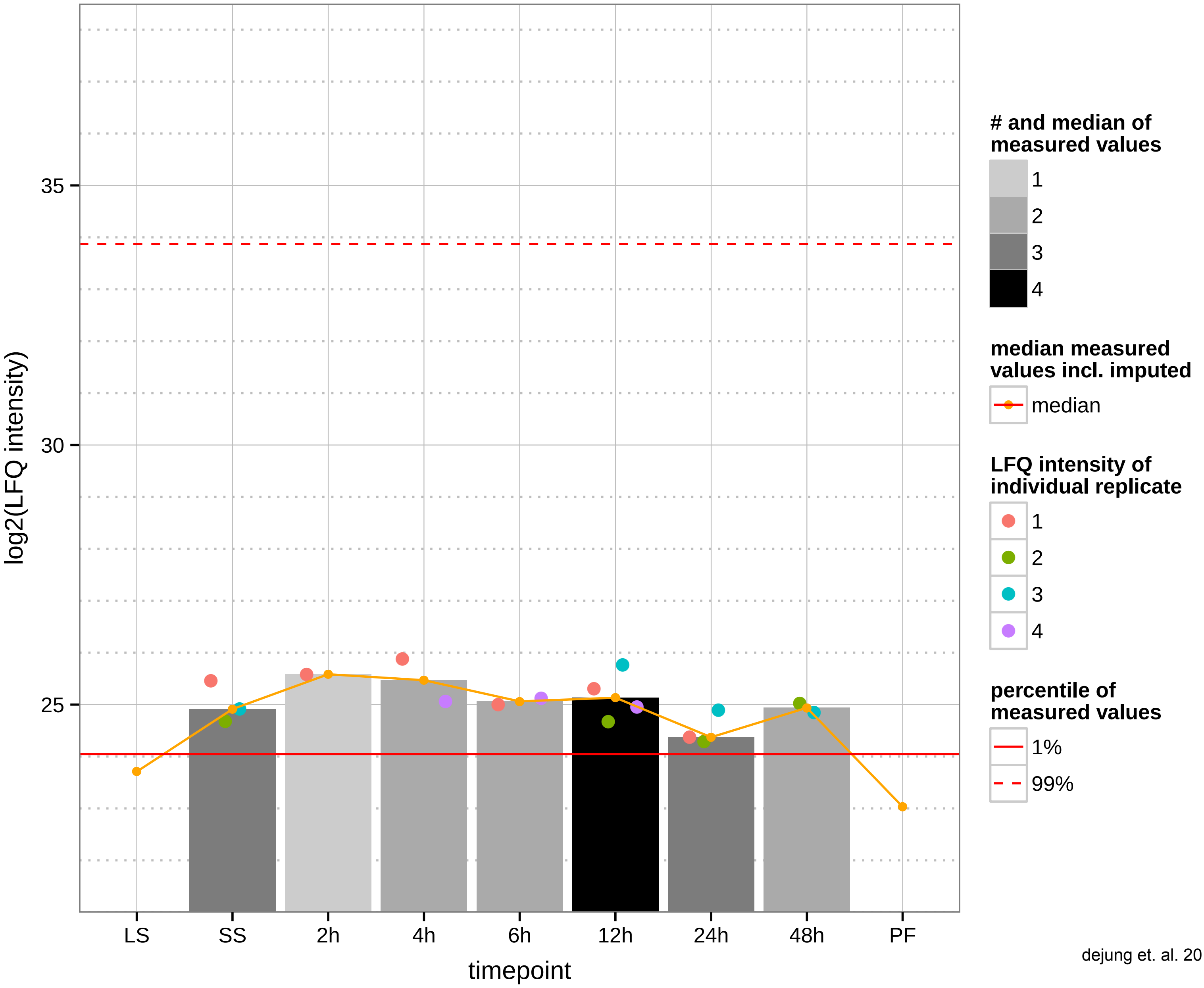
hypothetical protein, conserved
Tb927.9.12040
AGOF: mRNA (nucleoside−2'−O−)−methyltransferase activity
AGOC: null
AGOP: 7−methylguanosine mRNA capping
PGOF: null
PGOC: null
PGOP: null





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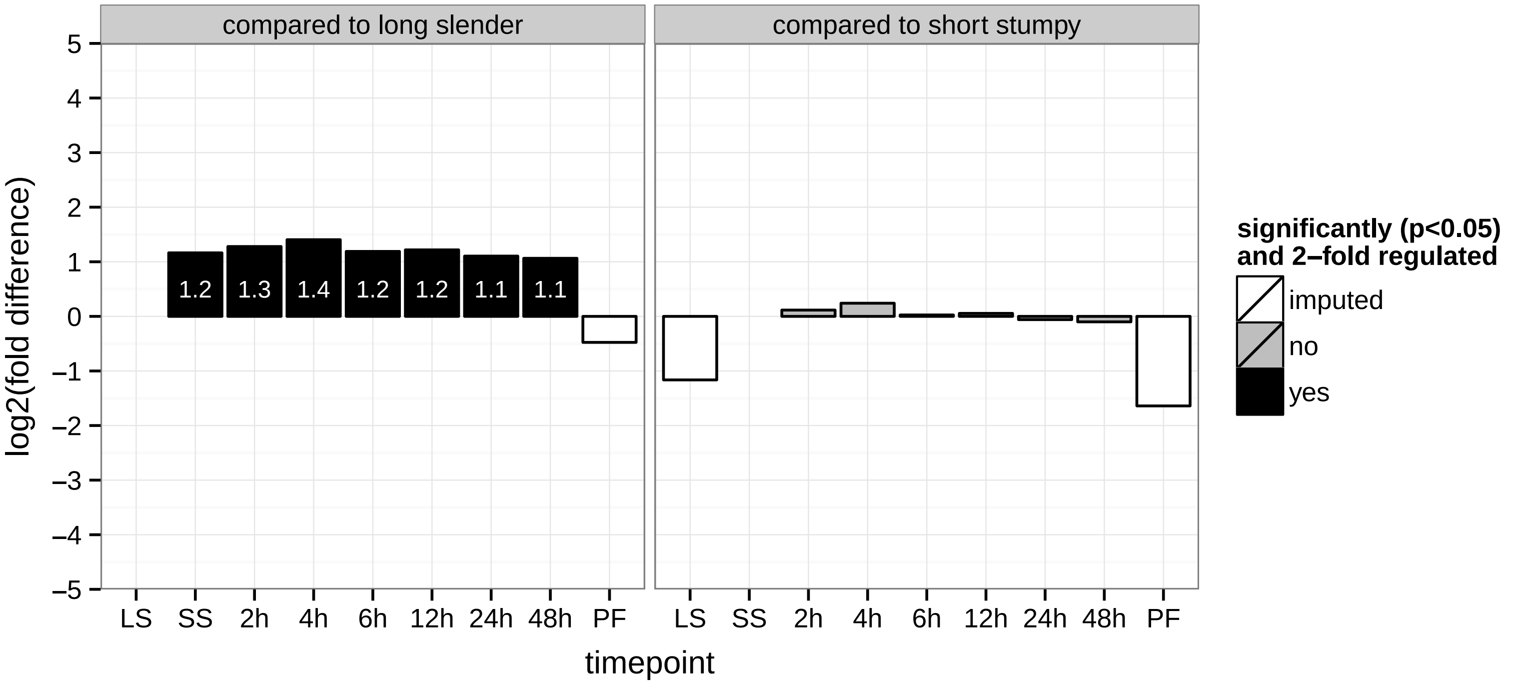
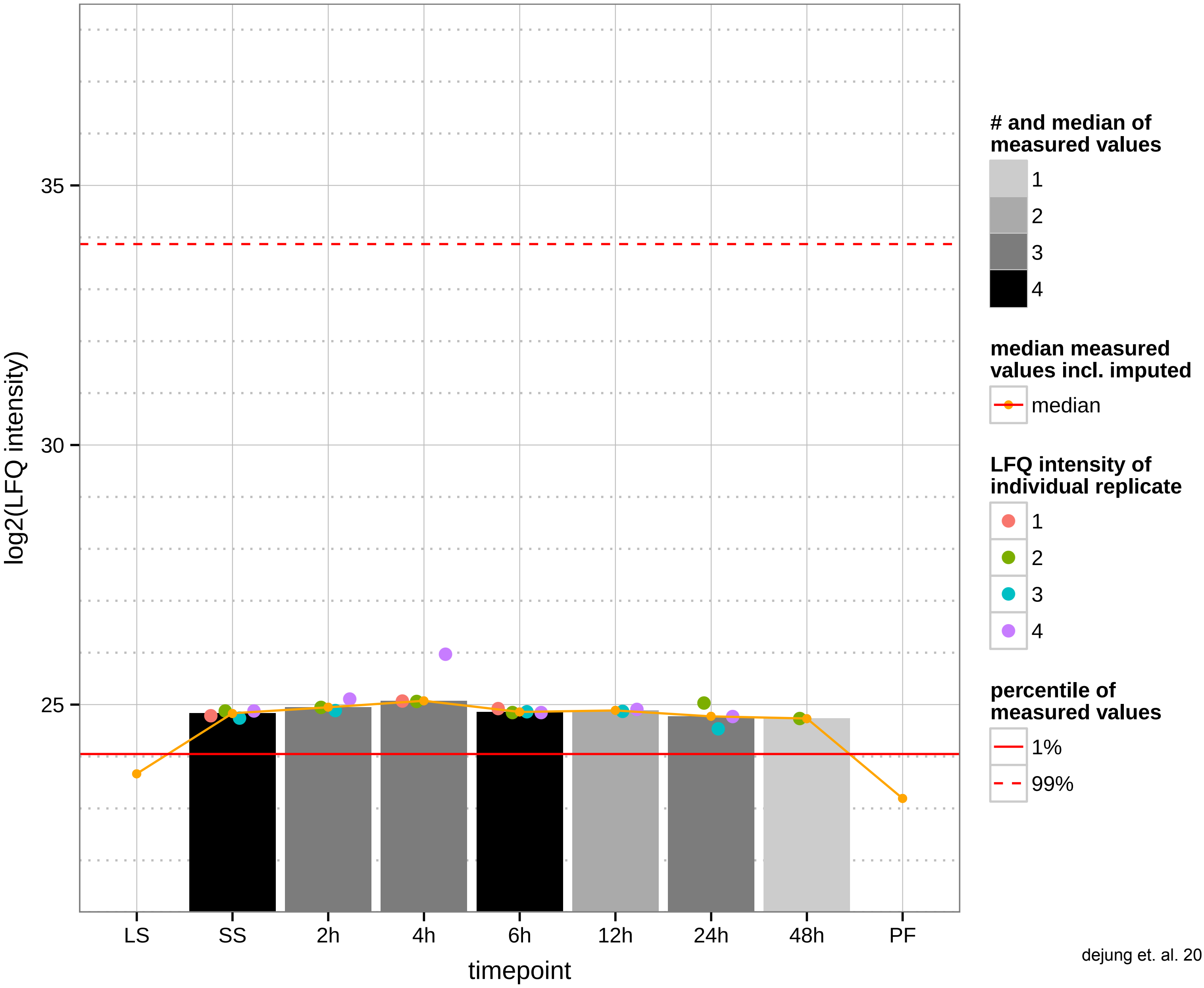
hypothetical protein, conserved
Tb927.9.12870
AGOF: null
AGOC: cis−Golgi network
AGOP: ER to Golgi vesicle−mediated transport
PGOF: null
PGOC: cis−Golgi network
PGOP: ER to Golgi vesicle−mediated transport, transport





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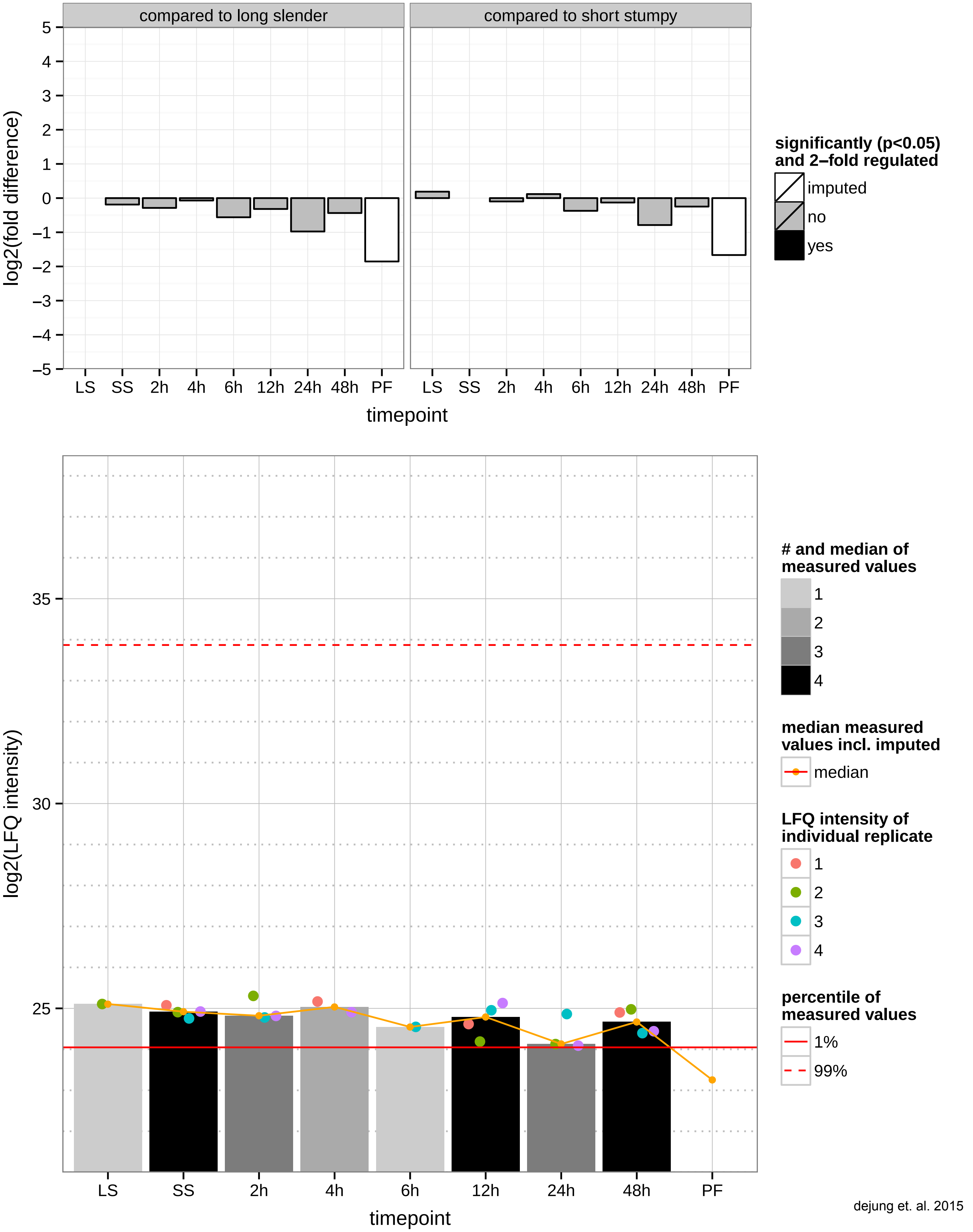
hypothetical protein, conserved
Tb927.9.13050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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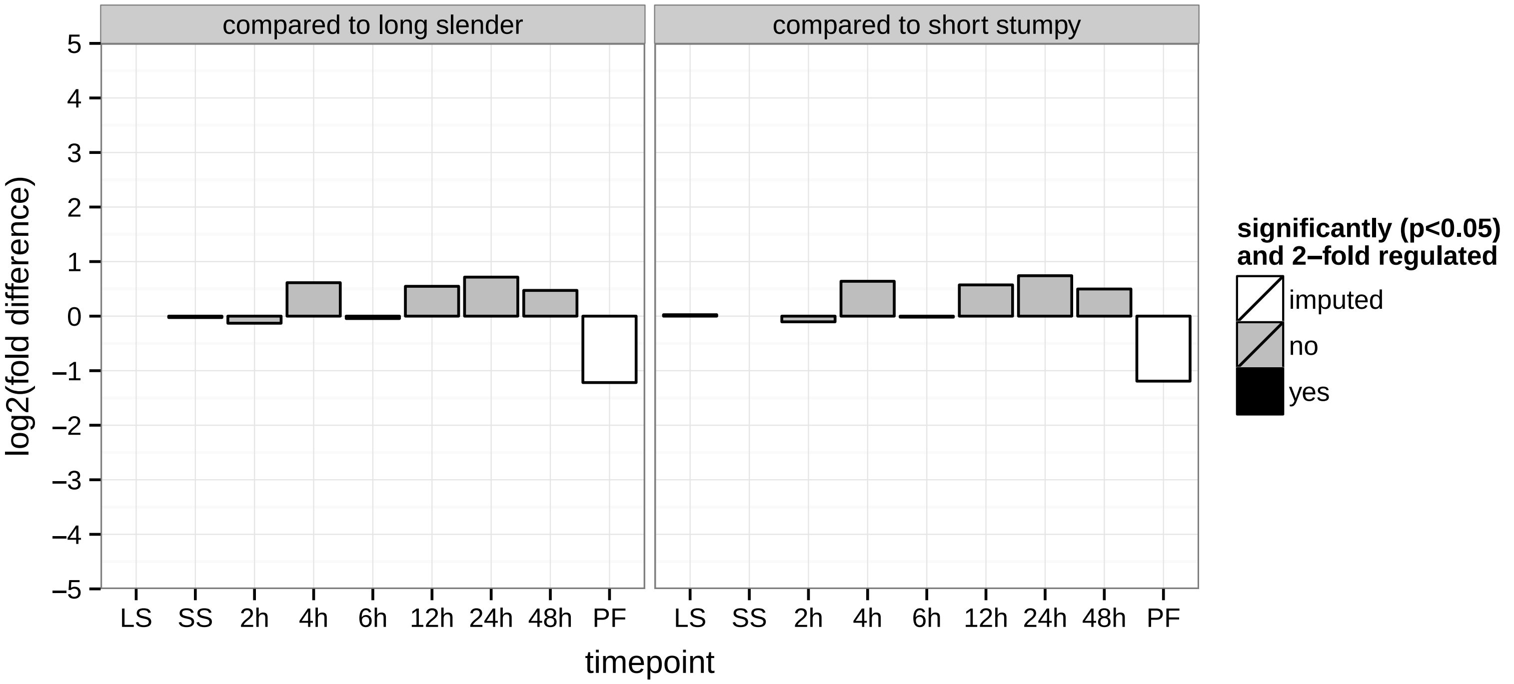
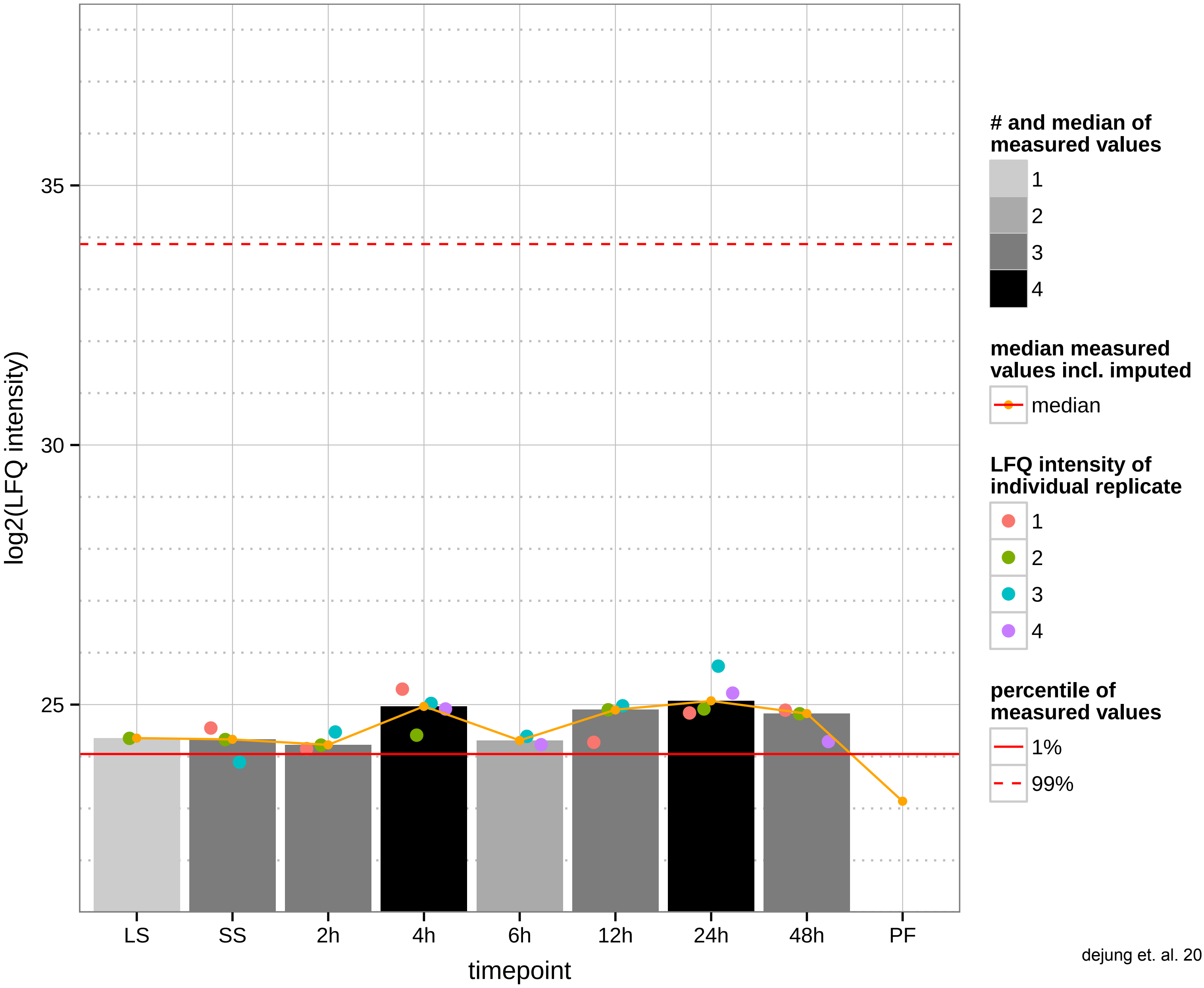
hypothetical protein, conserved
Tb927.9.13340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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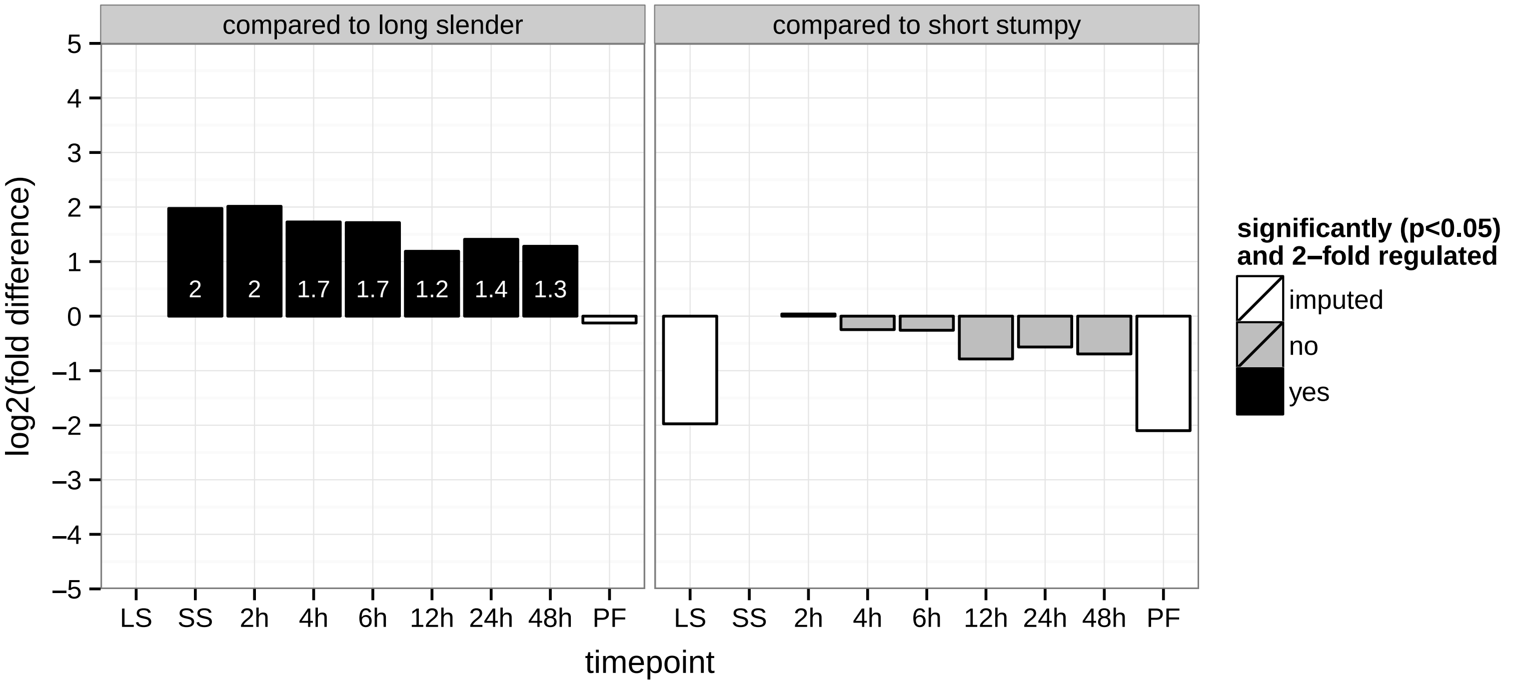
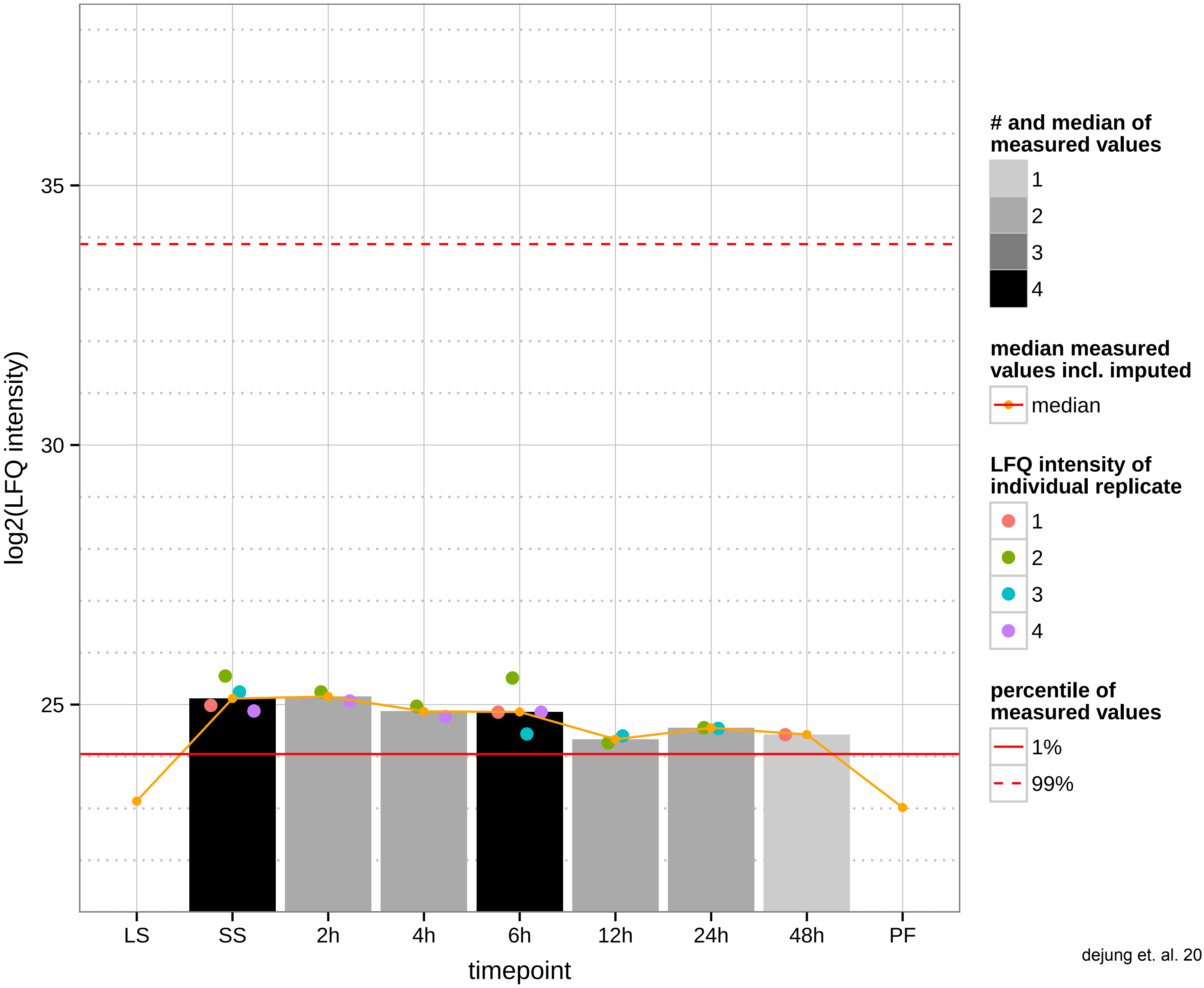
hypothetical protein, conserved
Tb927.9.2400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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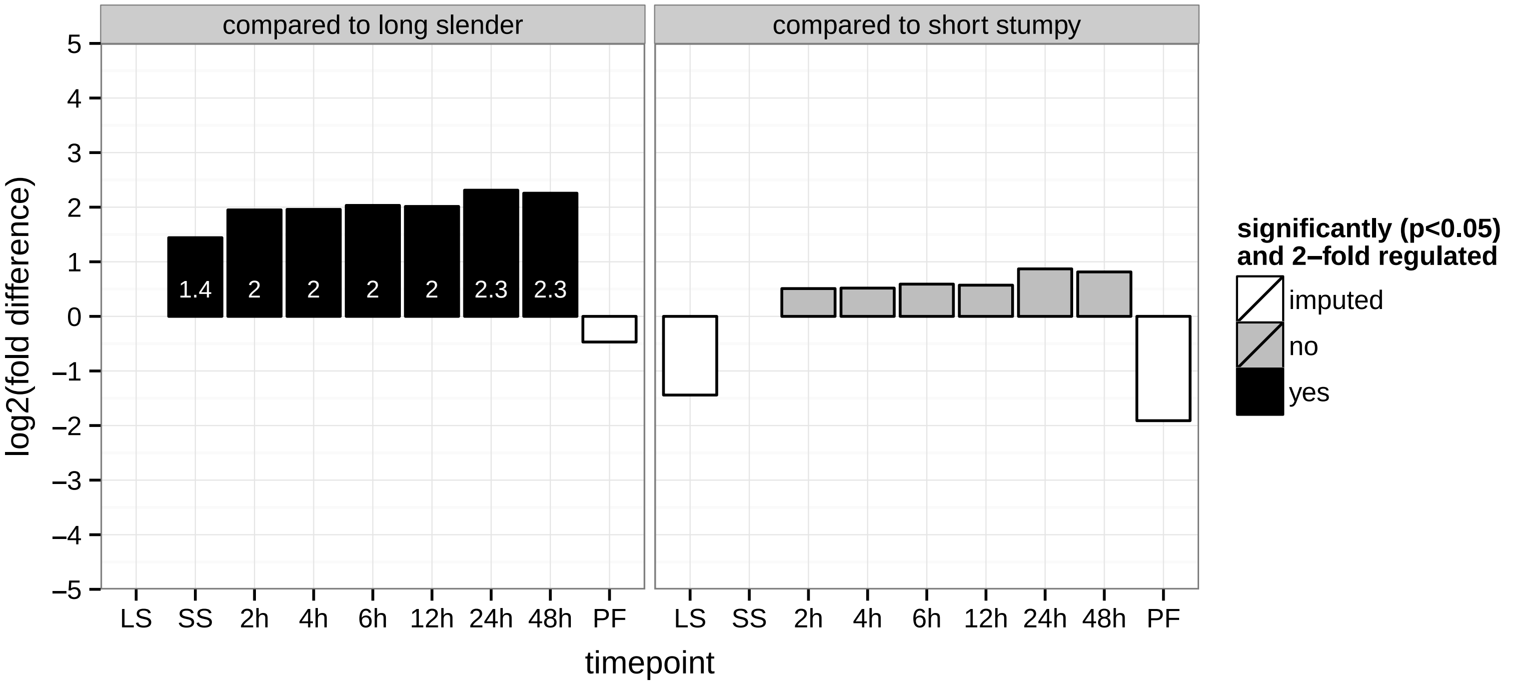
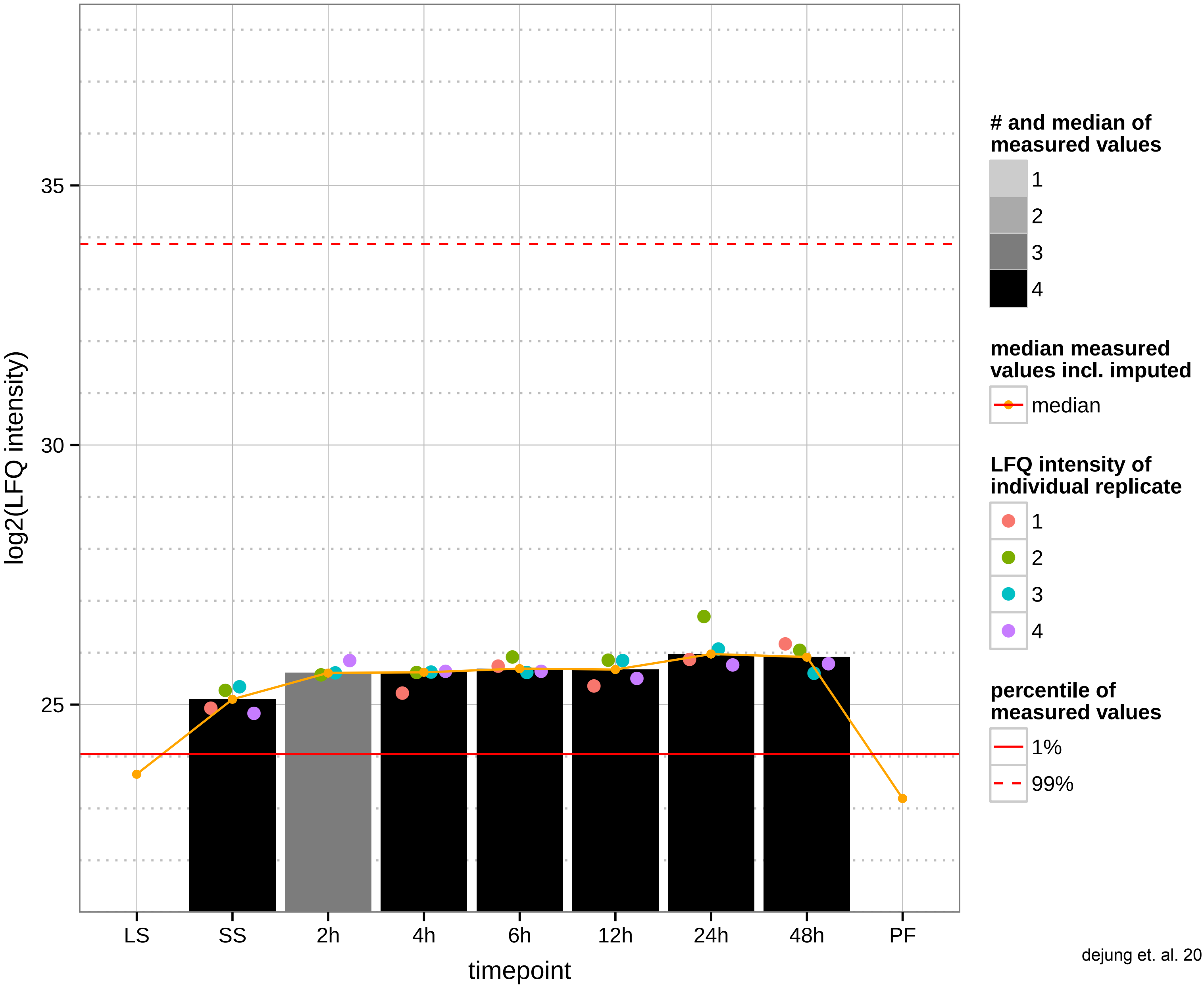
hypothetical protein, conserved
Tb927.9.3640
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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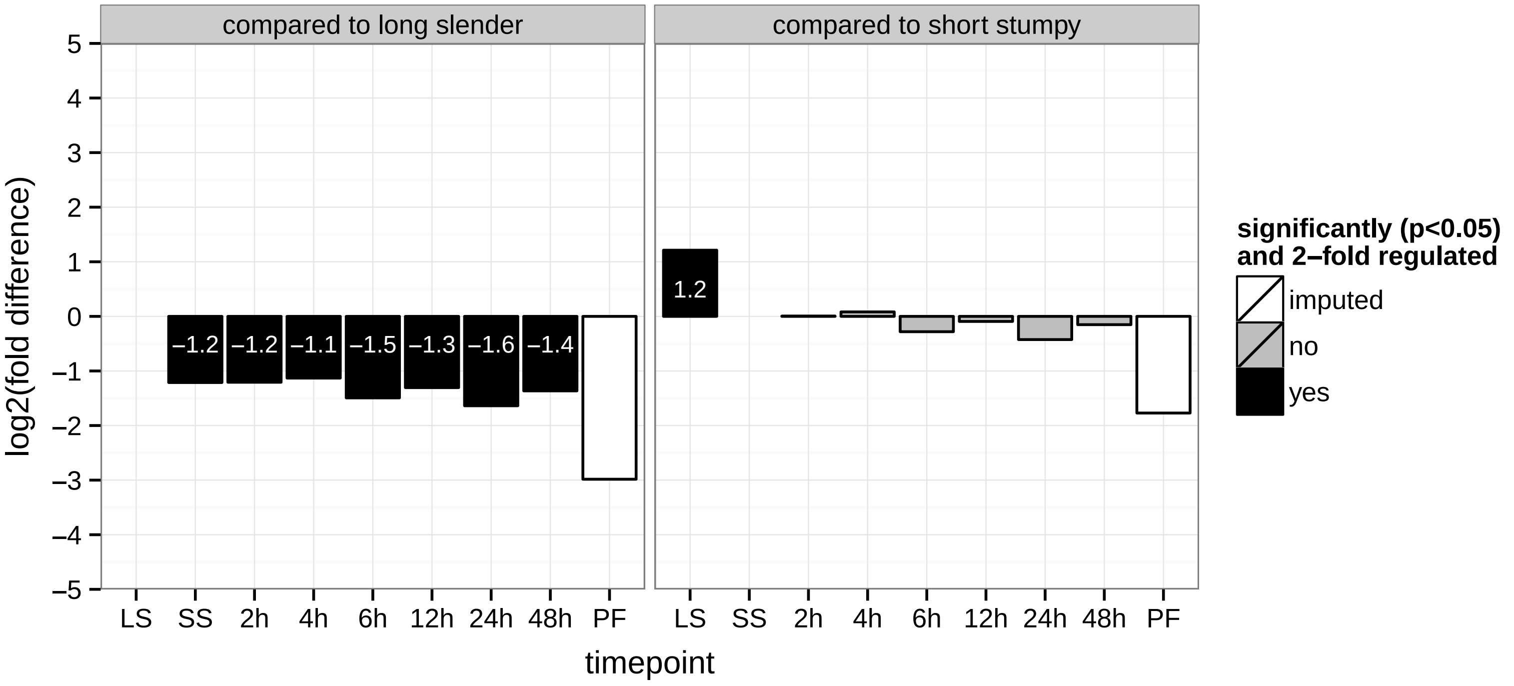
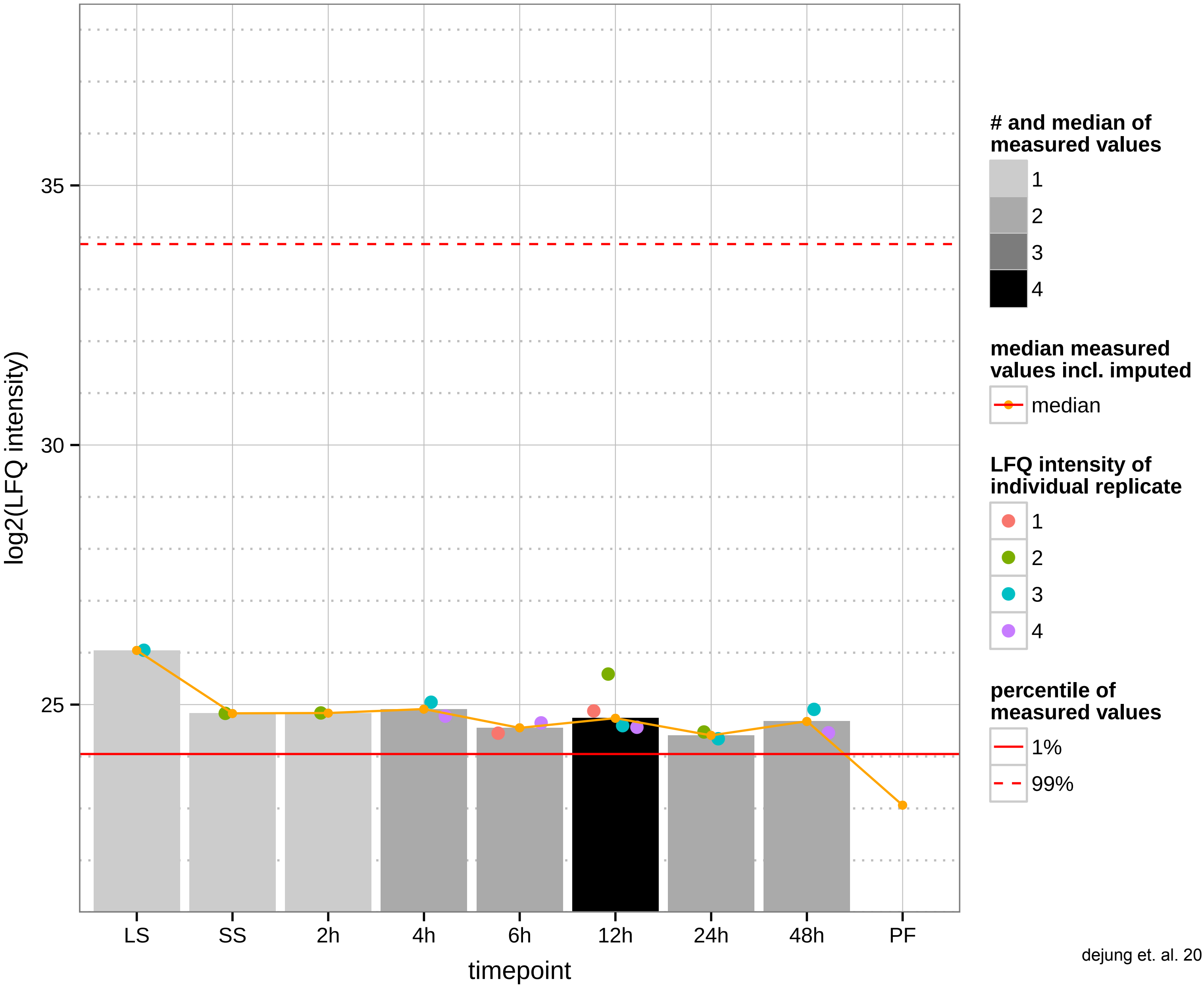
hypothetical protein, conserved
Tb927.9.3750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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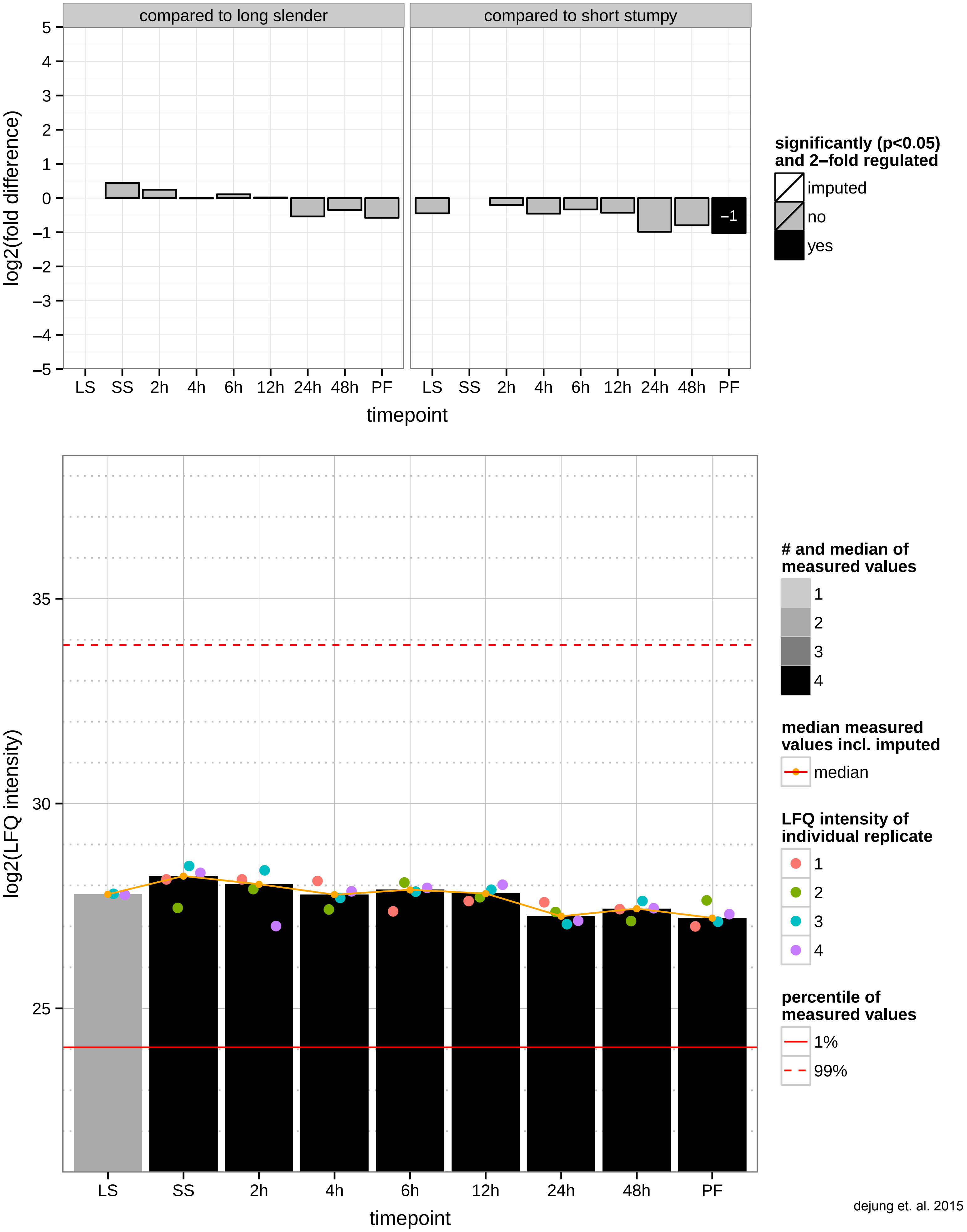
fatty acyl CoA synthetase, putative, fatty acyl CoA synthetase 3 (ACS3)
Tb927.9.4210;Tb11.v5.0561
AGOF: null, fatty−acyl−CoA synthase activity
AGOC: null, membrane
AGOP: null, fatty acid metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process



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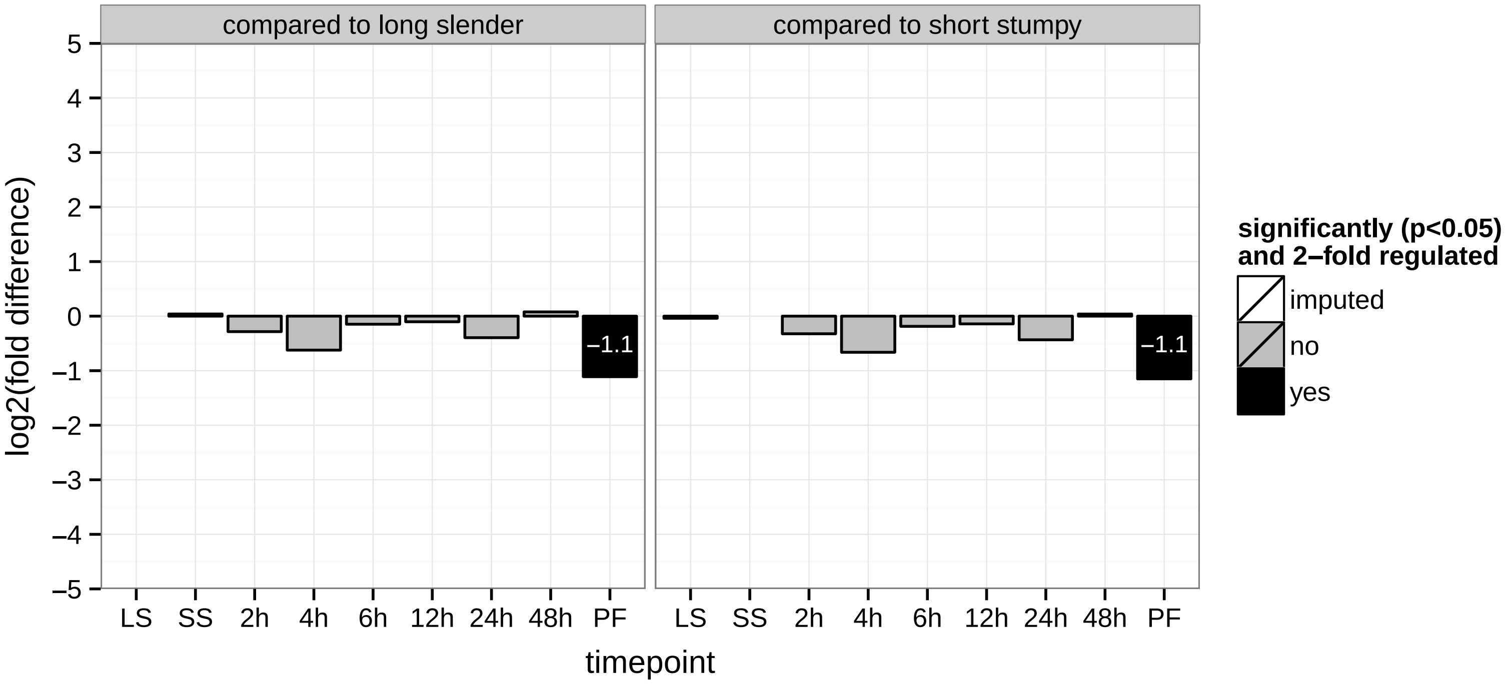
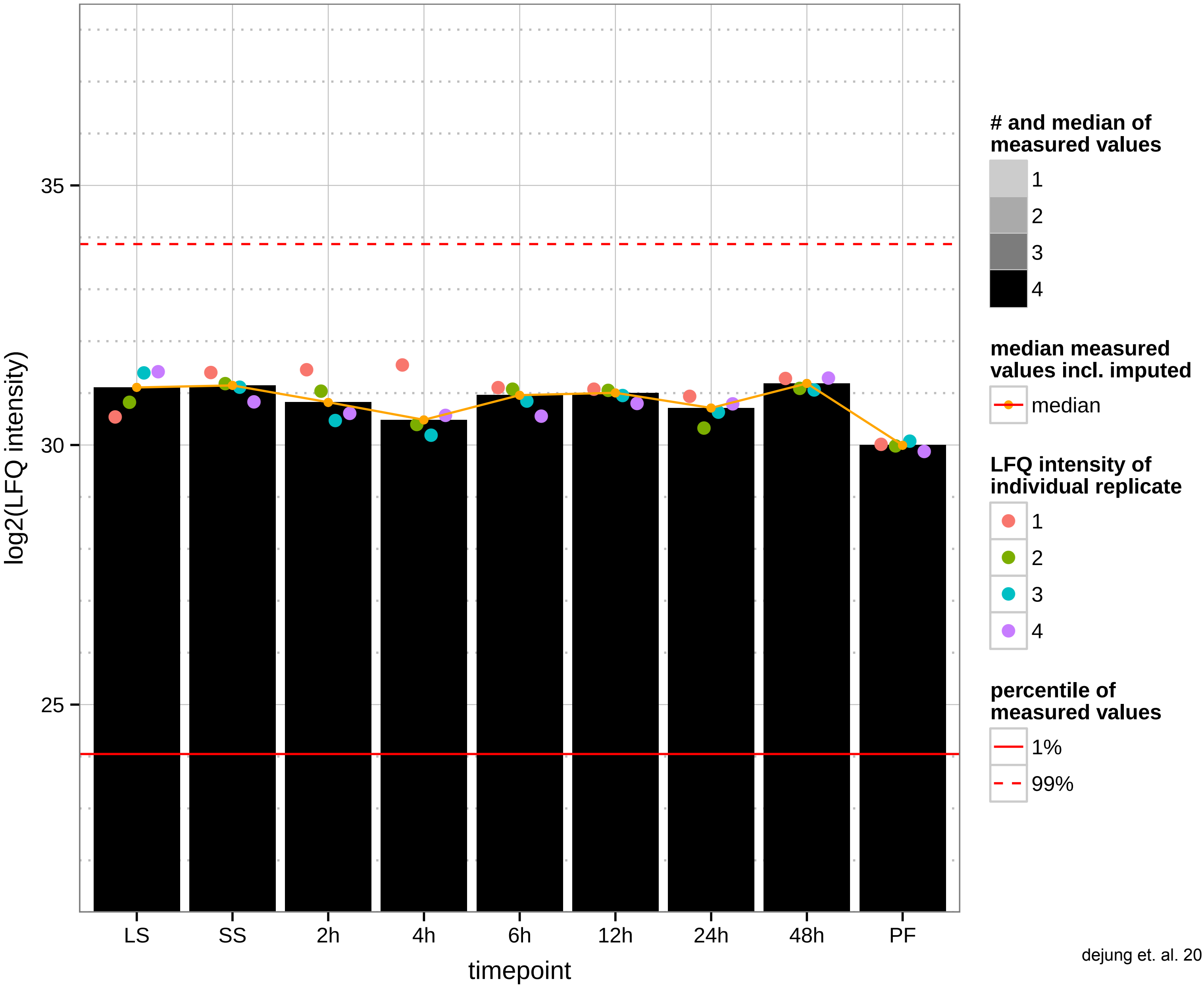
cAMP–specific phosphodiesterase (PDEB2)
Tb927.9.5100
AGOF: 3', 5'–cyclic–nucleotide phosphodiesterase activity
AGOC: cytoplasm
AGOP: cell proliferation, signal transduction
PGOF: 3', 5'–cyclic–nucleotide phosphodiesterase activity, catalytic activity, protein binding
PGOC: null
PGOP: signal transduction





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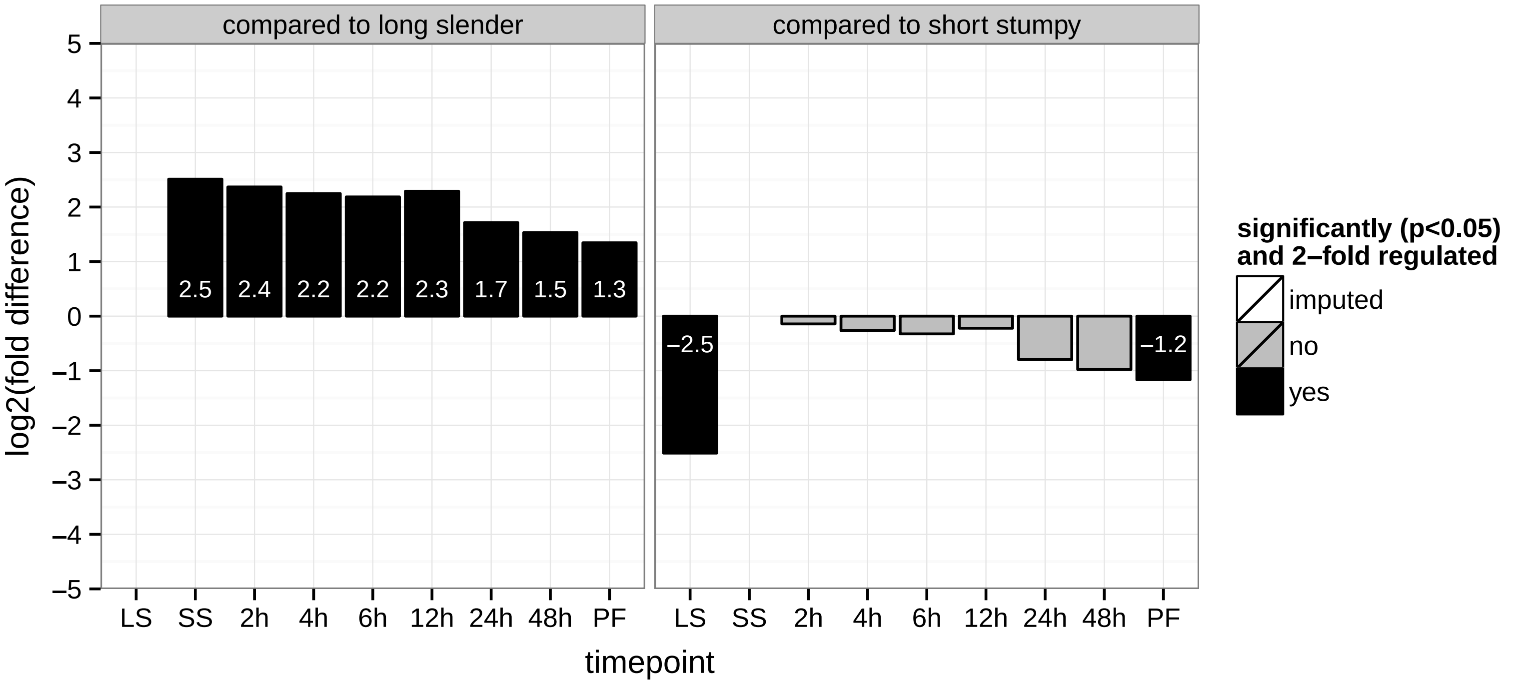
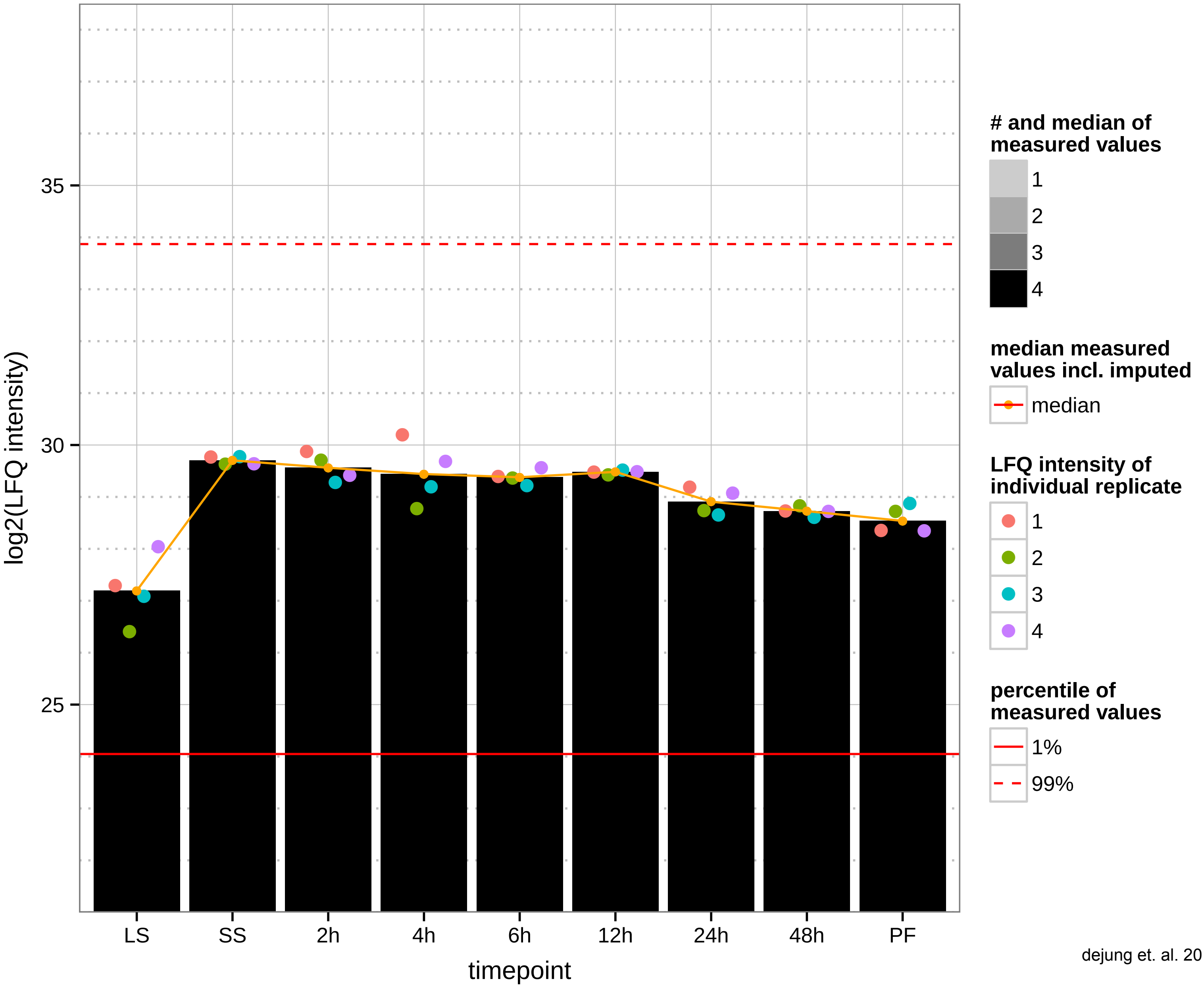
ubiquitin carboxyl–terminal hydrolase, putative, cysteine peptidase, Clan CA, family C19
Tb927.9.5520
AGOF: cysteine–type endopeptidase activity, ubiquitin thiolesterase activity
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ubiquitin thiolesterase activity
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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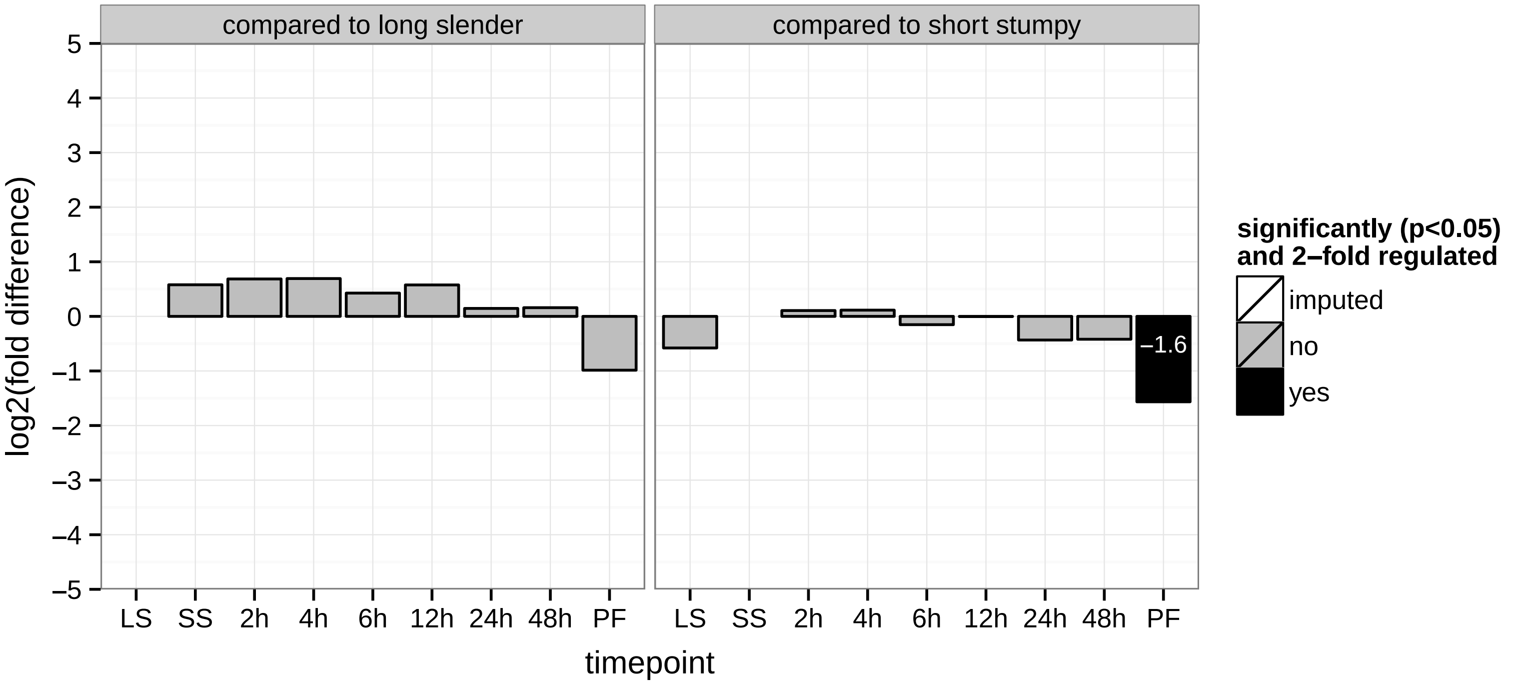
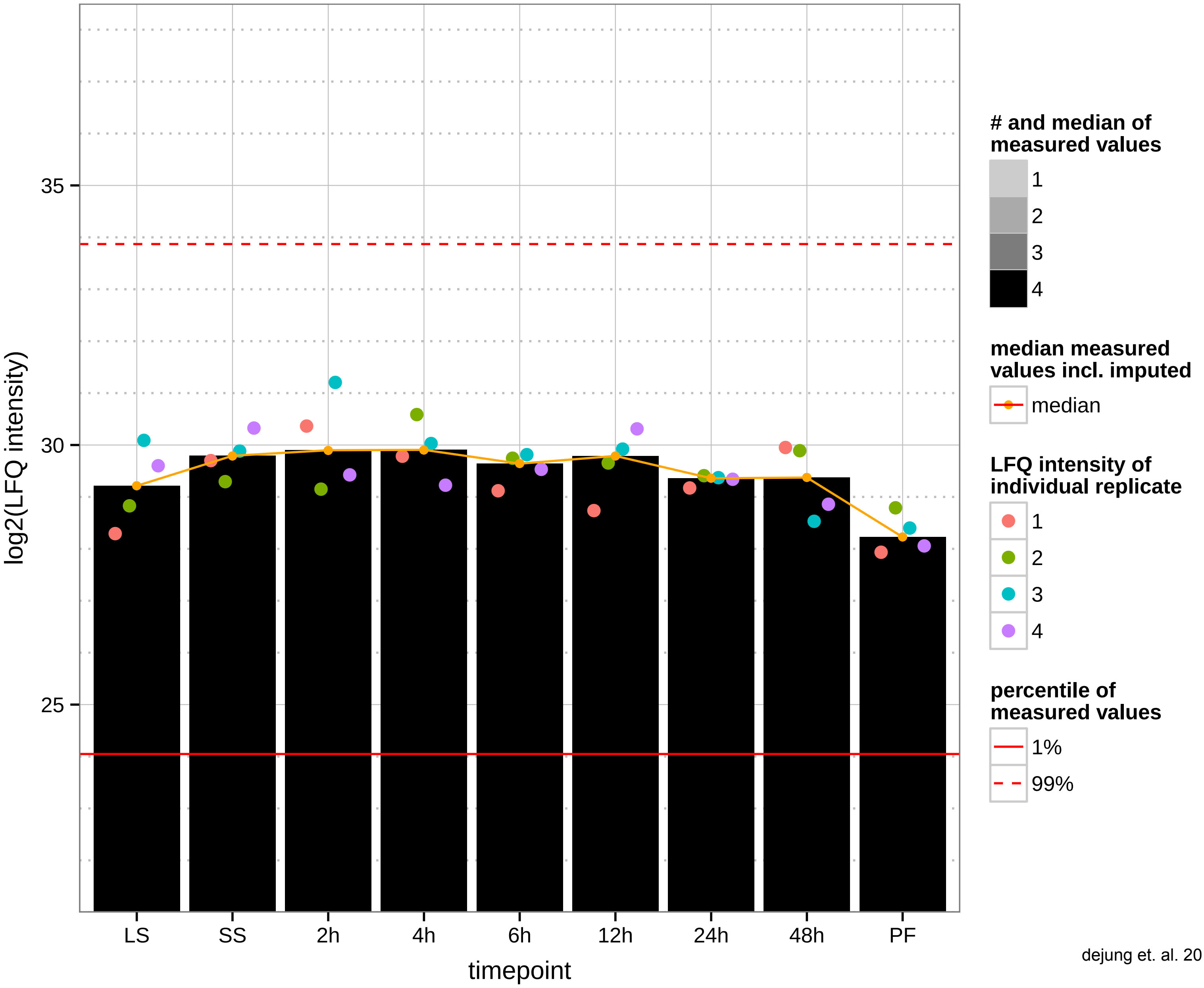
arginine kinase, AK1 (AK)
Tb927.9.6290
AGOF: ATP binding, arginine kinase activity, transferase activity, transferring phosphorus−containing groups
AGOC: cytosol
AGOP: biological_process
PGOF: kinase activity, transferase activity, transferring phosphorus−containing groups
PGOC: null
PGOP: null





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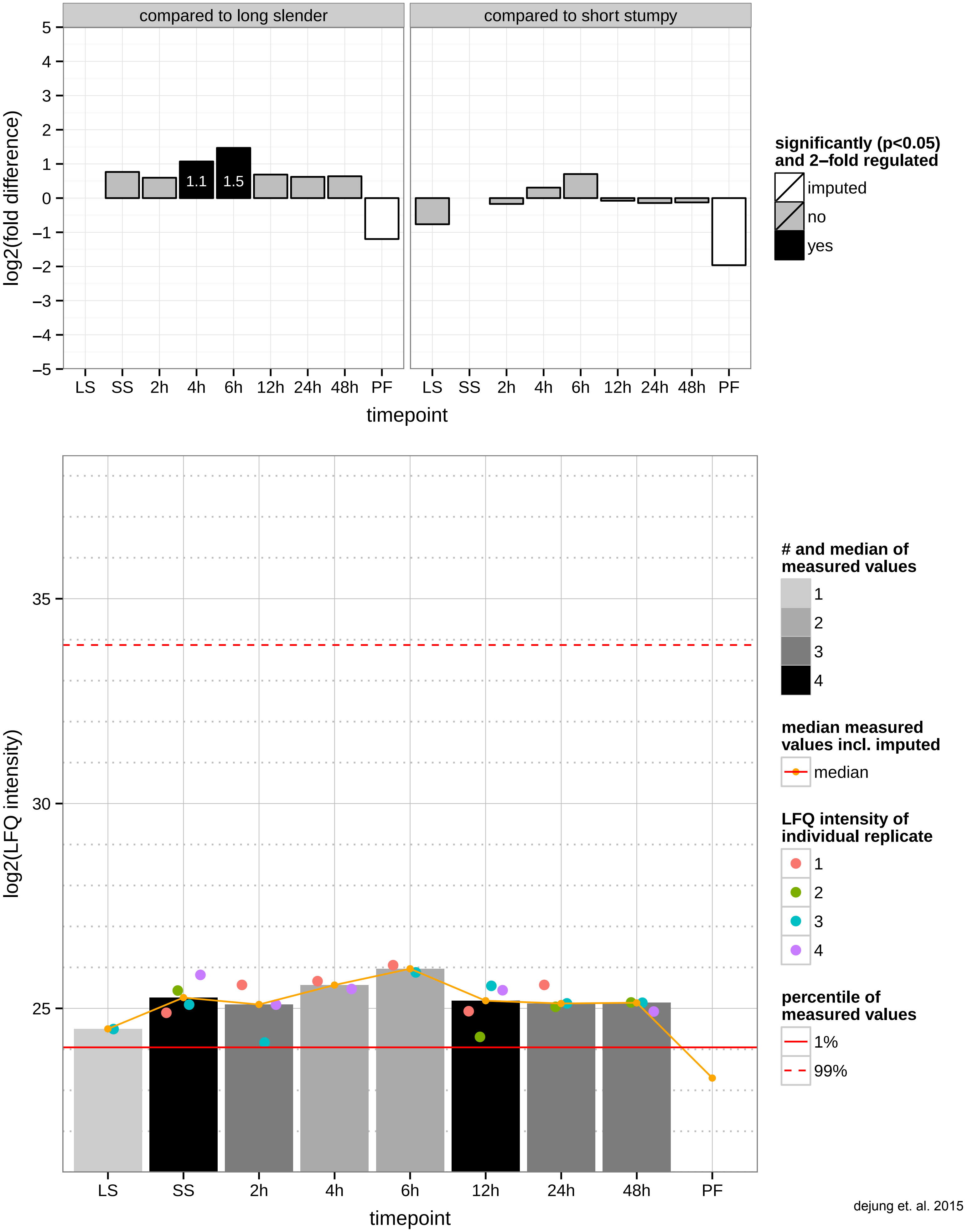
hypothetical protein, conserved
Tb927.9.7690
AGOF: nucleotidyltransferase activity
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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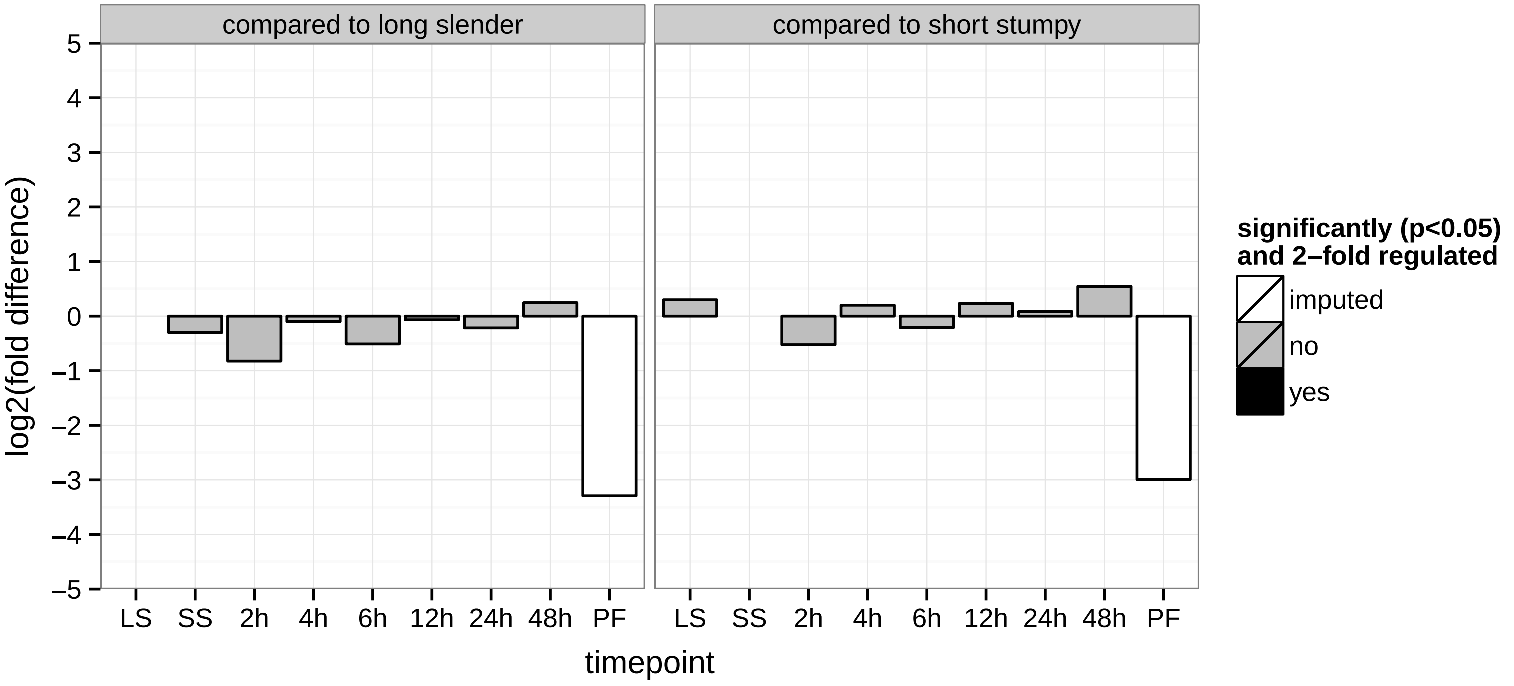
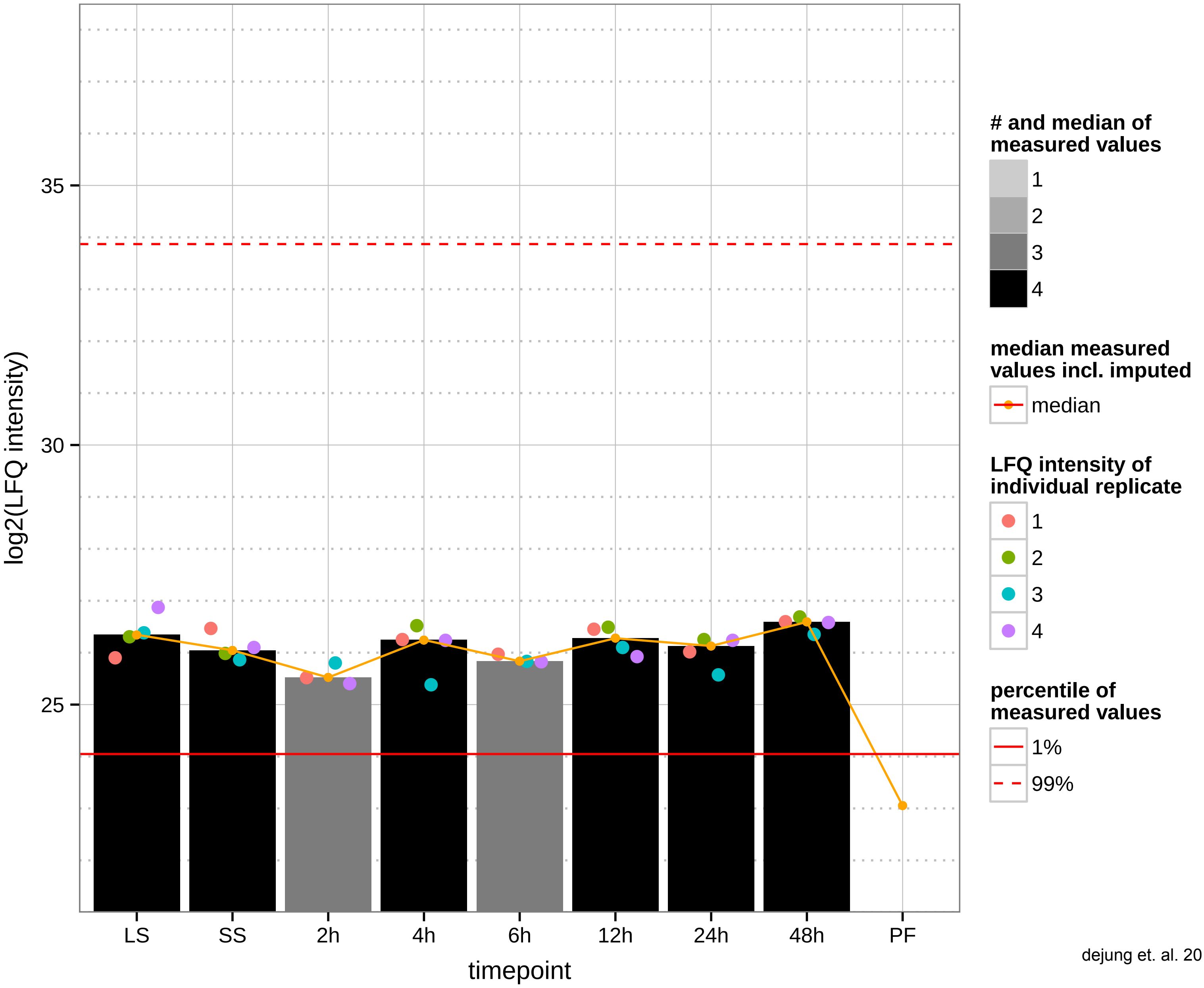
hypothetical protein, conserved
Tb927.9.9230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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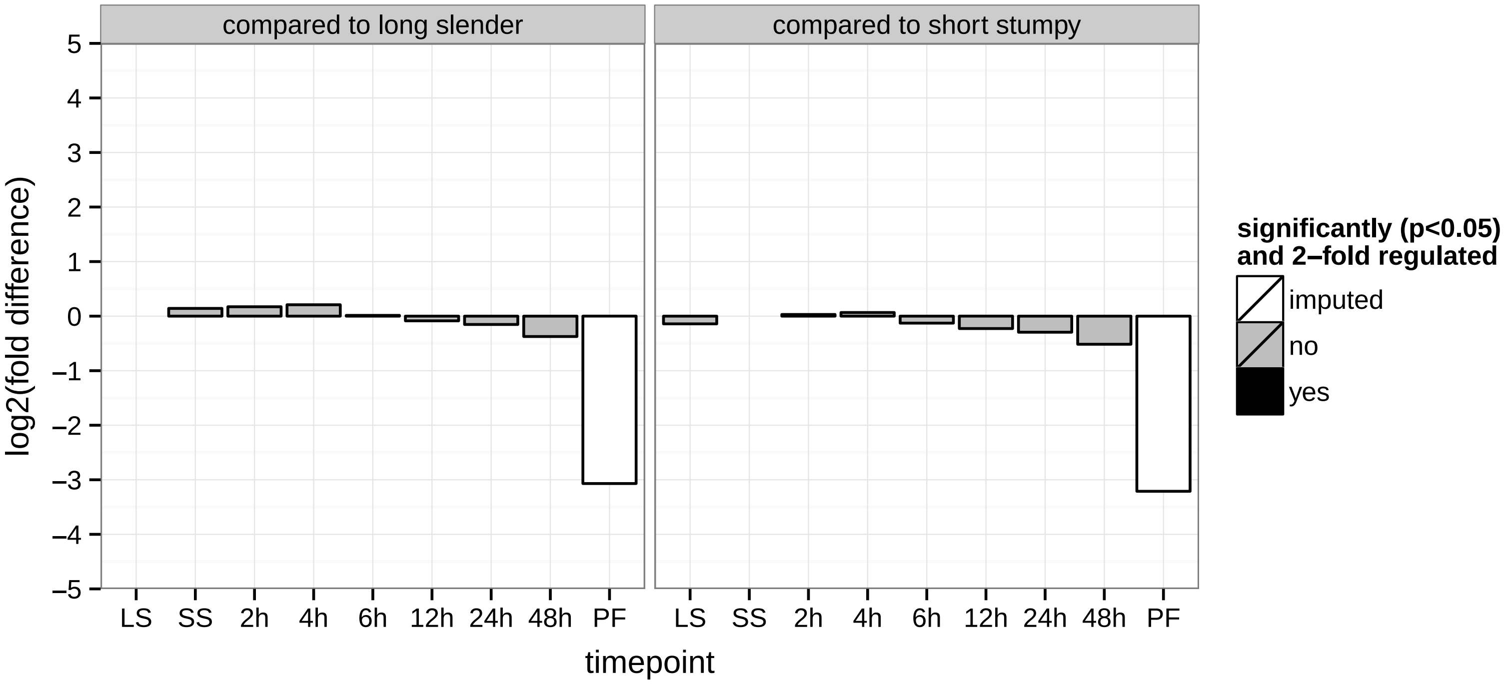
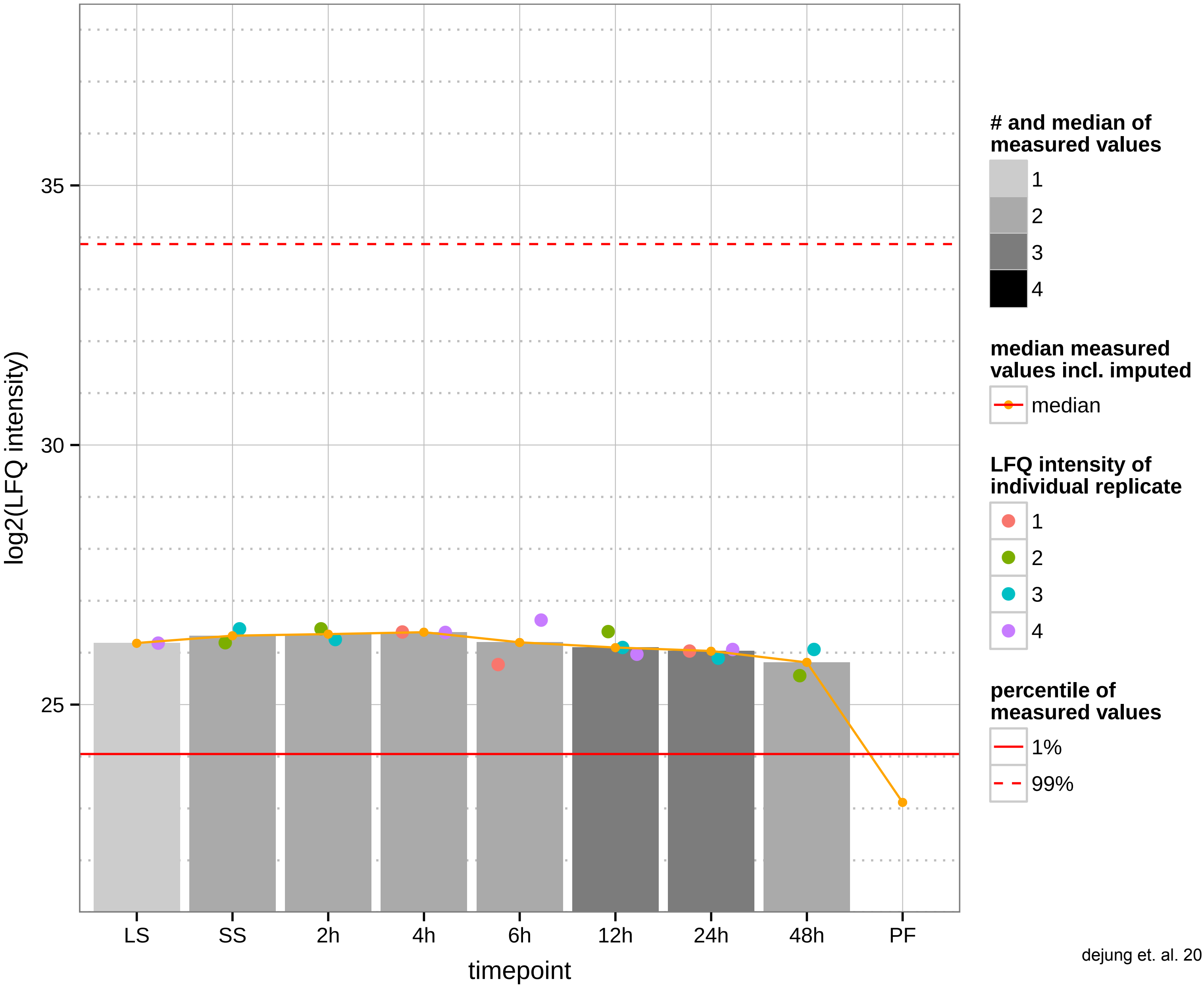
sphingomyelin/ceramide phosphorylethanolamine synthase, bifunctional, sphingomyelin synthase (SLS4), sphingomyelin synt
Tb927.9.9410;Tb927.9.9390;Tb927.9.9380;Tb927.9.9400
AGOF: ceramide cholinephosphotransferase activity, ethanolaminephosphotransferase activity, sphingomyelin synthase activi
AGOC: Golgi apparatus, membrane, membrane
AGOP: ceramide biosynthetic process, sphingomyelin biosynthetic process, ethanolamine biosynthetic process, sphingomyeli
PGOF: null
PGOC: null
PGOP: null





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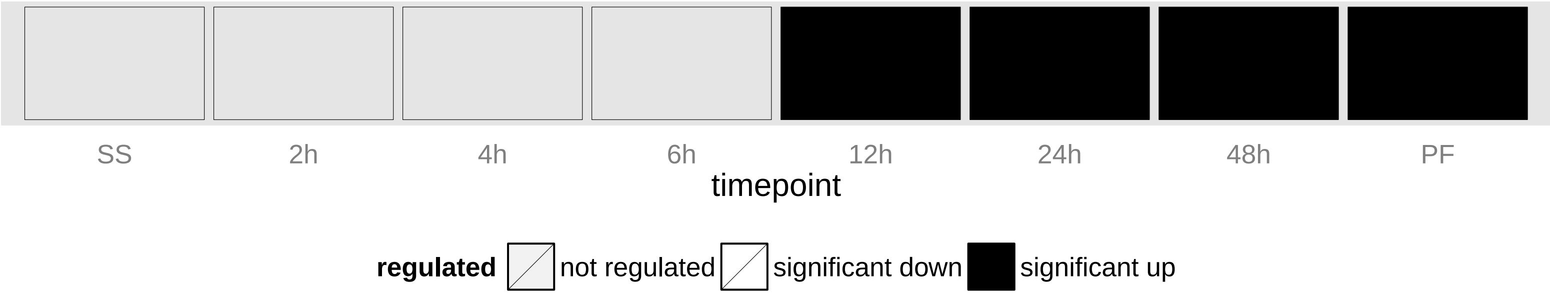

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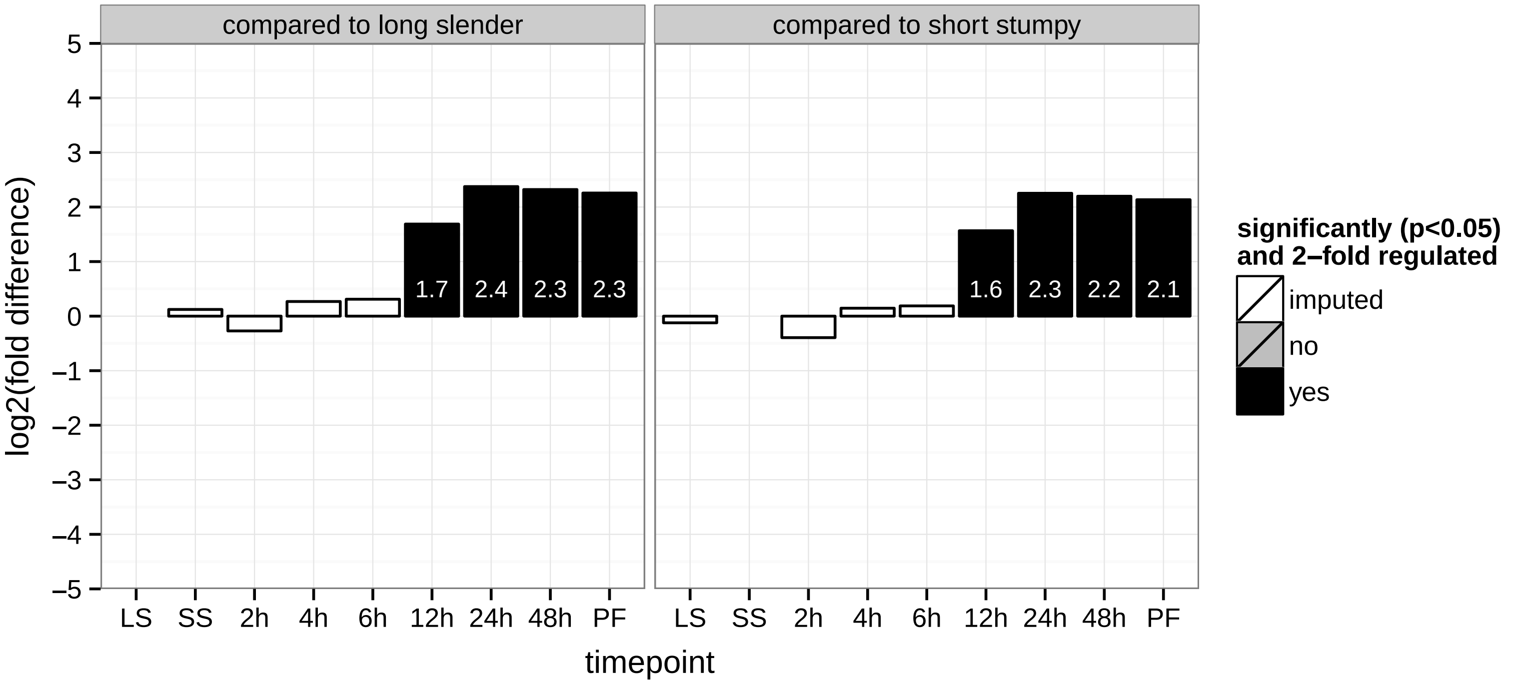
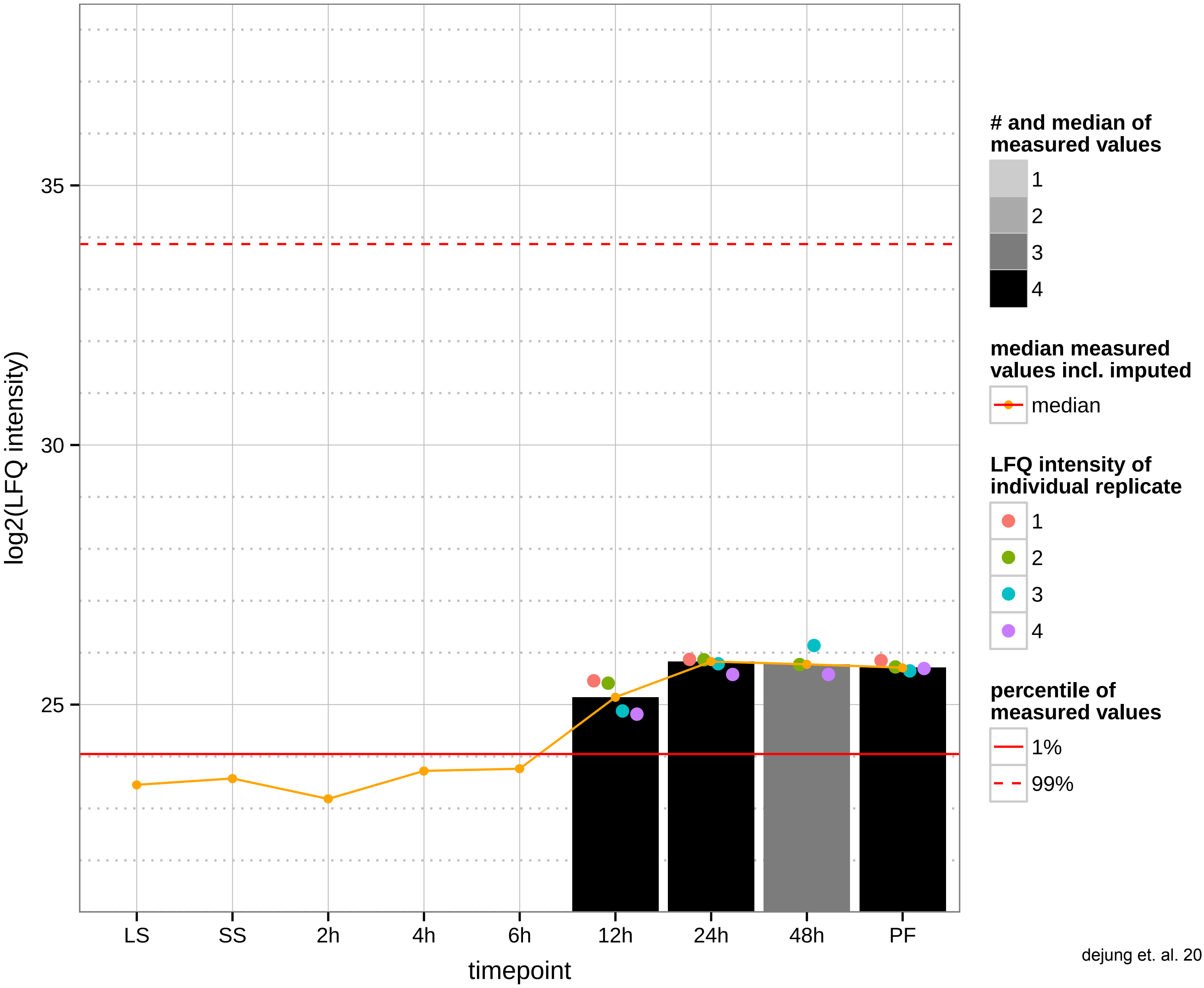
hypothetical protein, conserved
Tb11.02.5105b;Tb11.02.5105
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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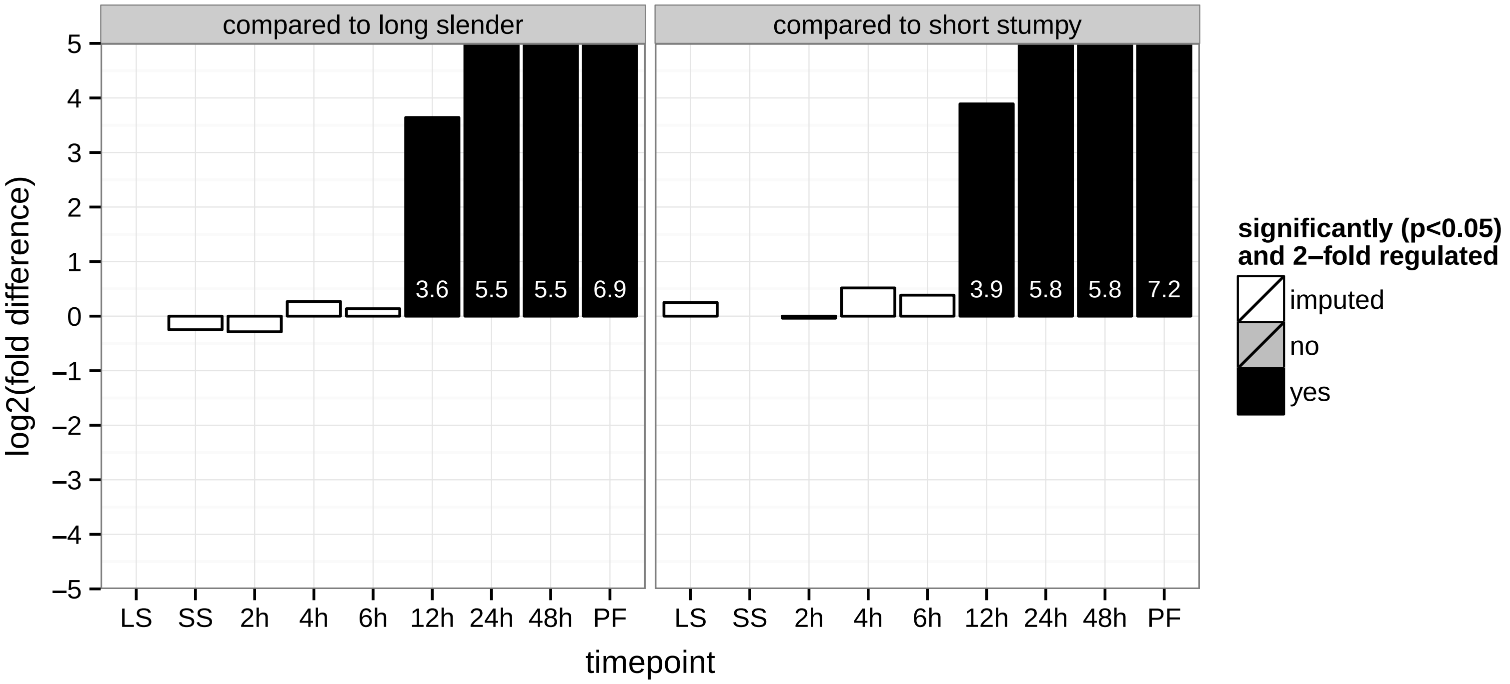
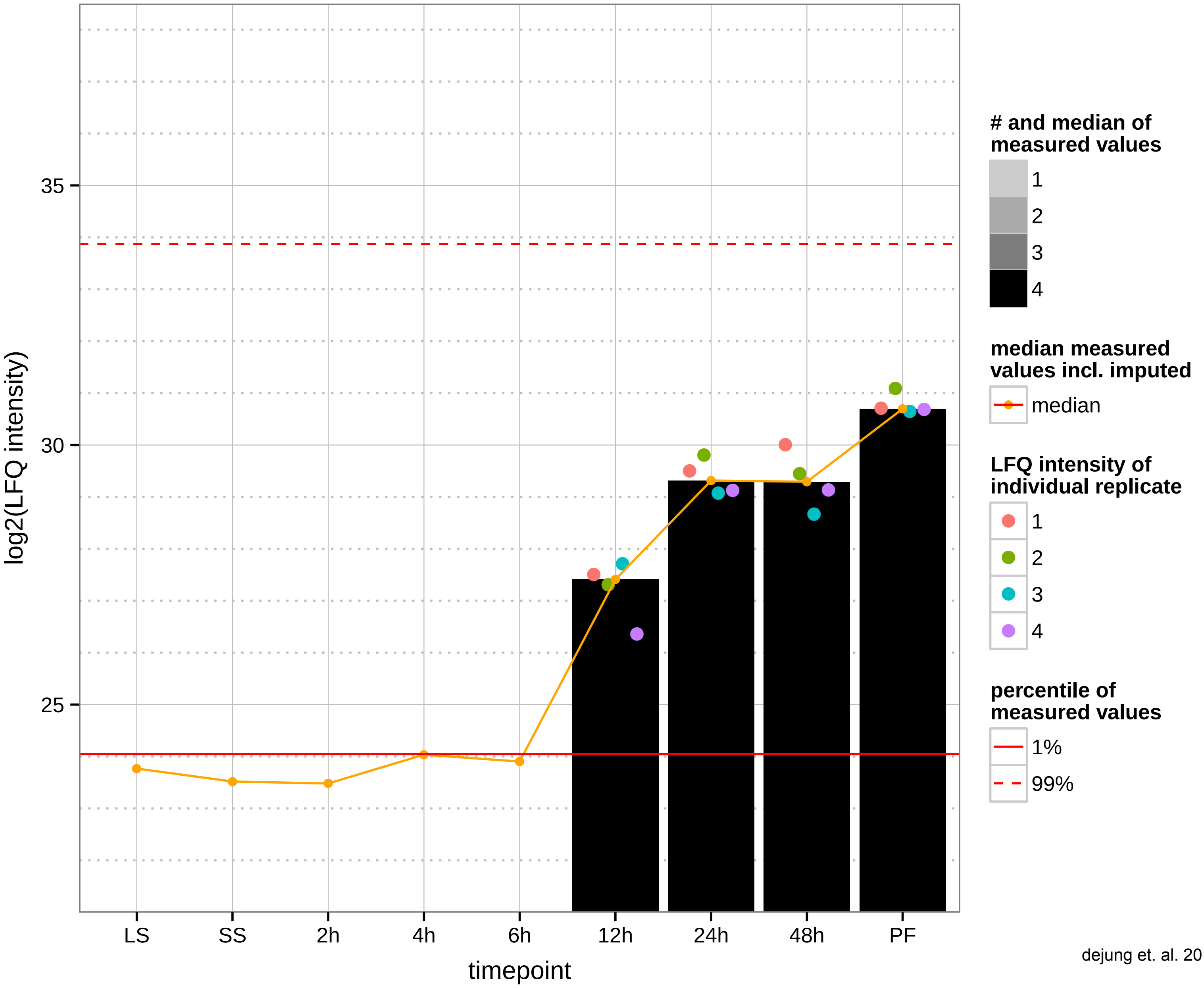
hypothetical protein, chrXI additional, unordered contigs, P27 protein, putative (P27)
Tb11.0400;Tb927.11.7700;Tb11.0300
AGOF: null
AGOC: null, cytochrome complex, mitochondrial inner membrane
AGOP: null, regulation of oxidative phosphorylation
PGOF: null
PGOC: null
PGOP: null





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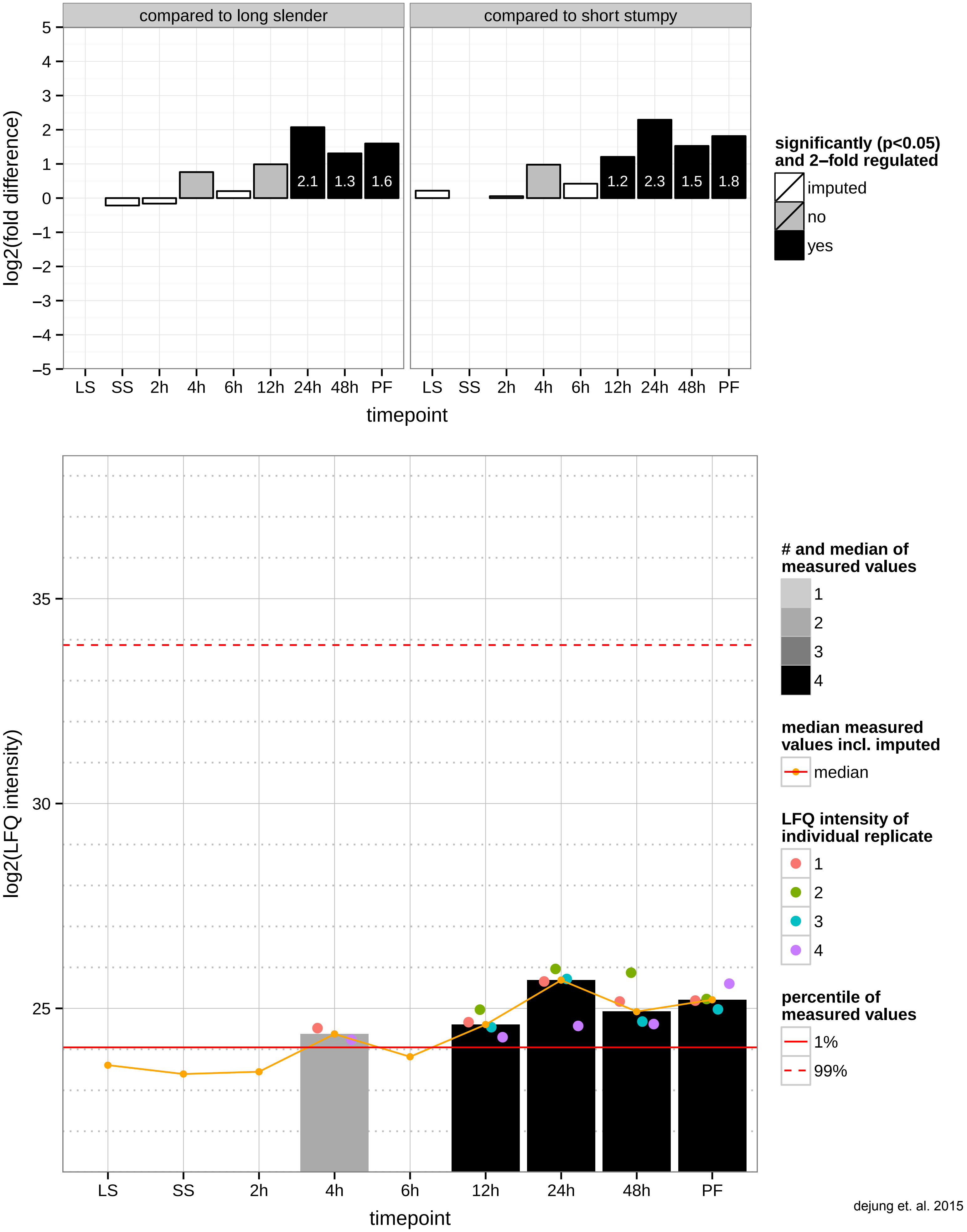
hypothetical protein, conserved
Tb927.7.4820;Tb11.v5.0164
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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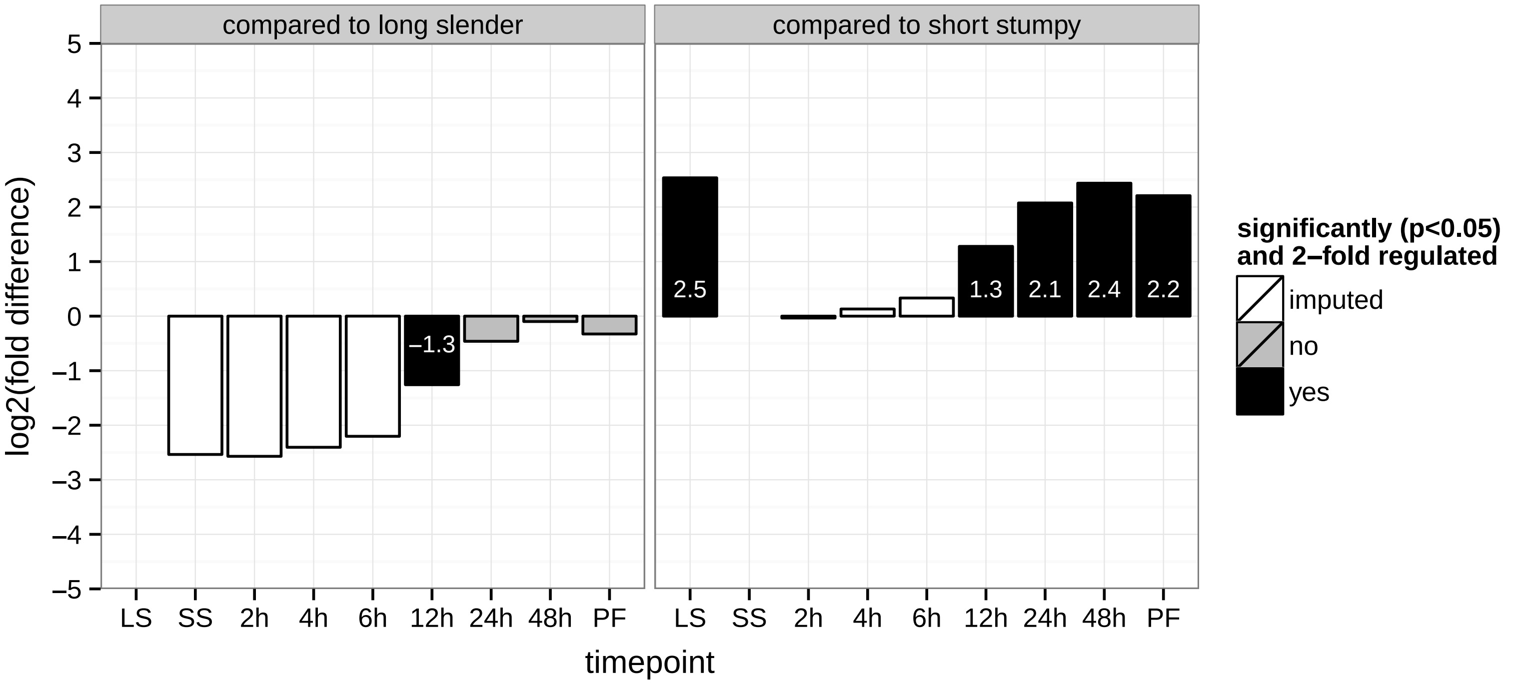
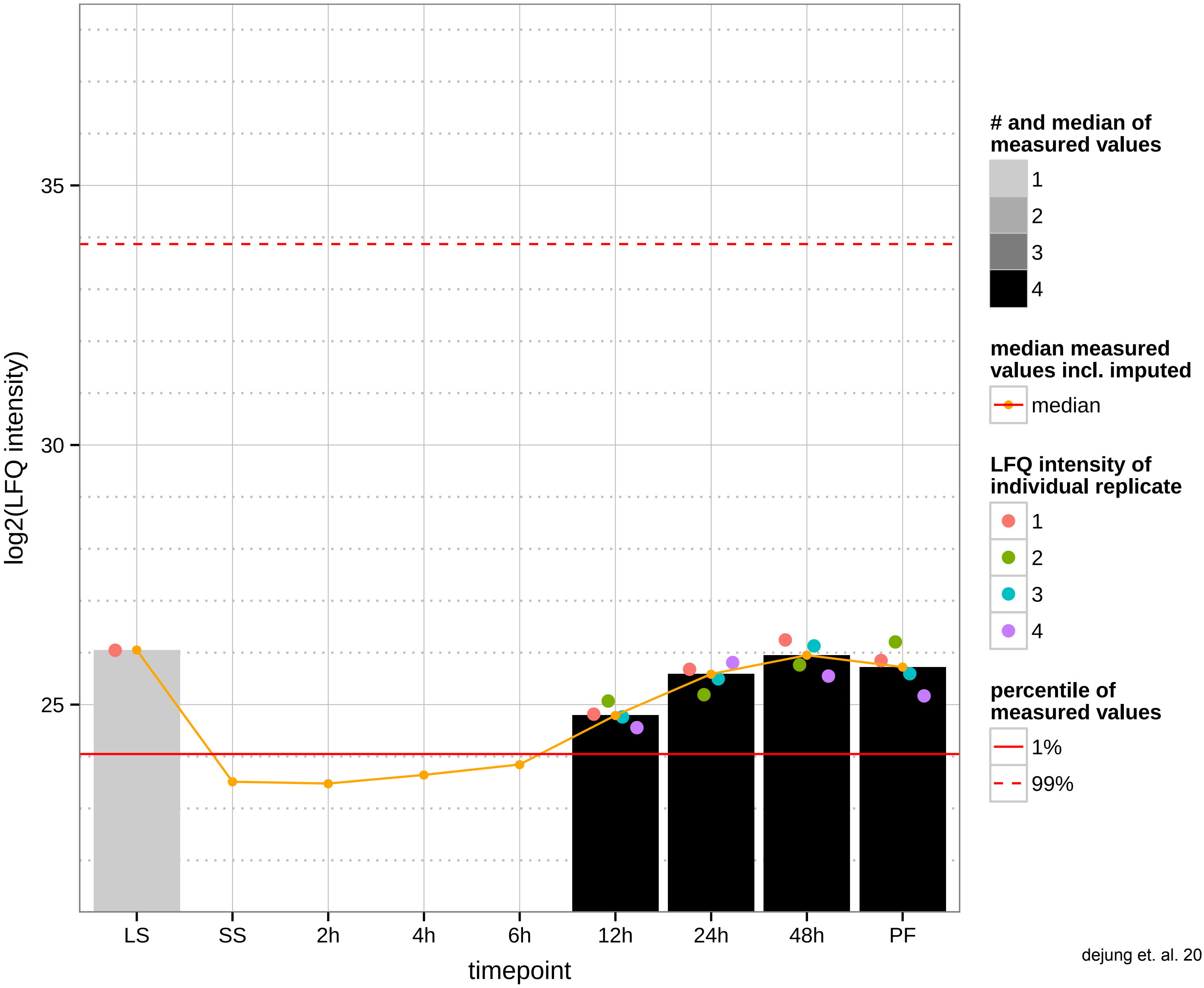
oligopeptidase B protein, putative, serine peptidase, clan SC, family S9A–like protein
Tb927.7.4940;Tb11.v5.0175
AGOF: null, serine–type endopeptidase activity
AGOC: null, mitochondrion
AGOP: null, proteolysis
PGOF: serine–type endopeptidase activity, serine–type peptidase activity
PGOC: null
PGOP: proteolysis





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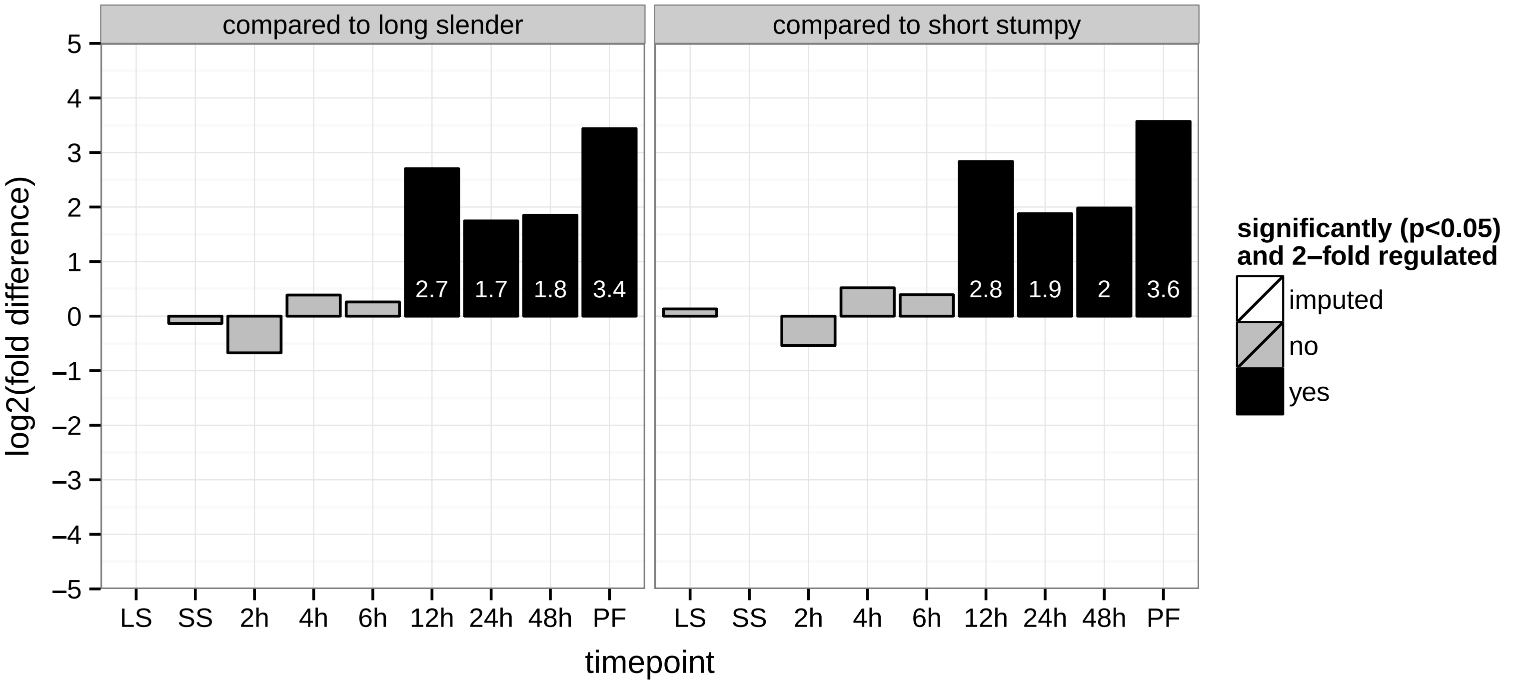
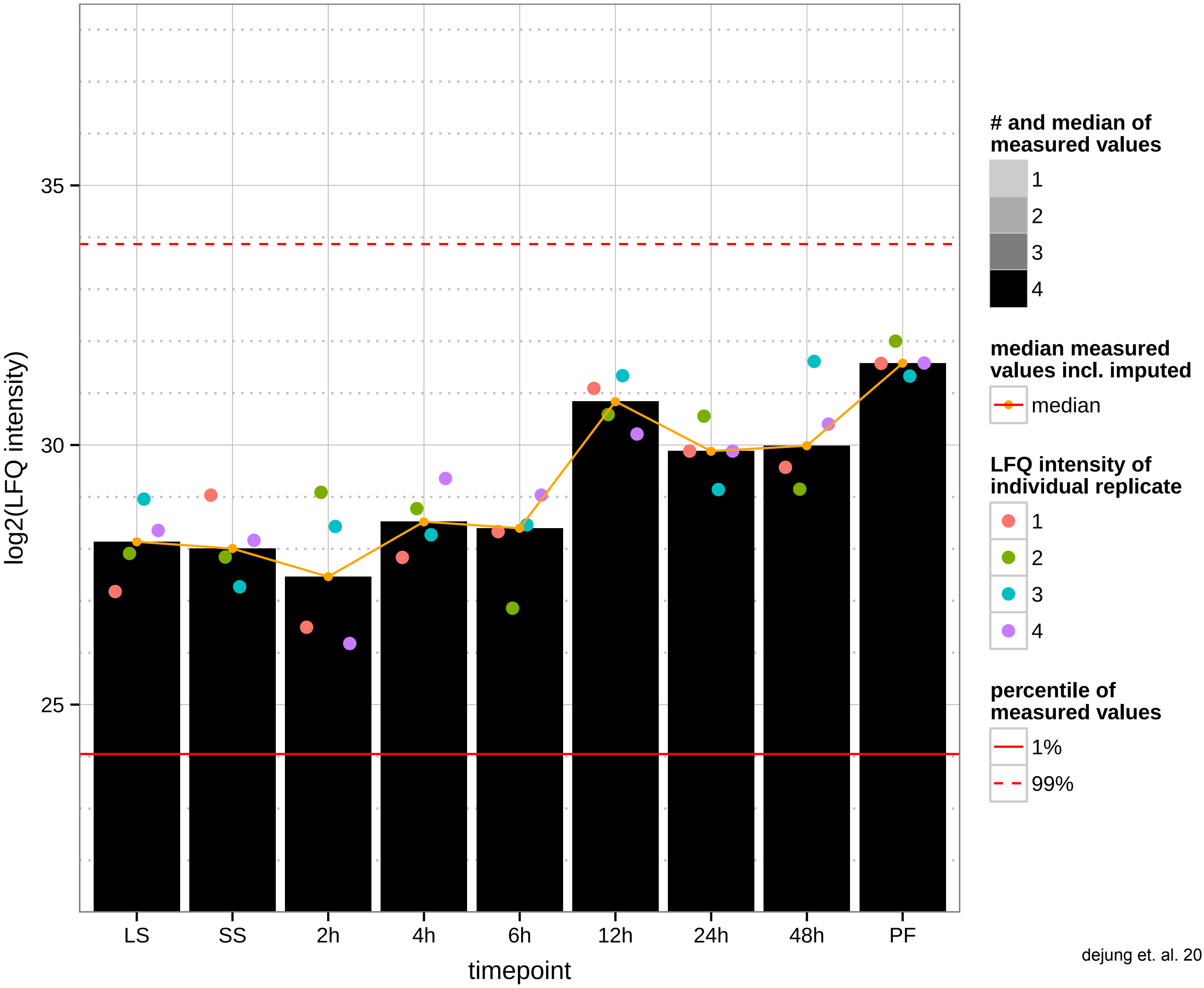
universal minicircle sequence binding protein, putative, universal minicircle sequence binding protein (UMSBP), DNA–binding
Tb927.10.6060;Tb11.v5.0199
AGOF: null, nucleic acid binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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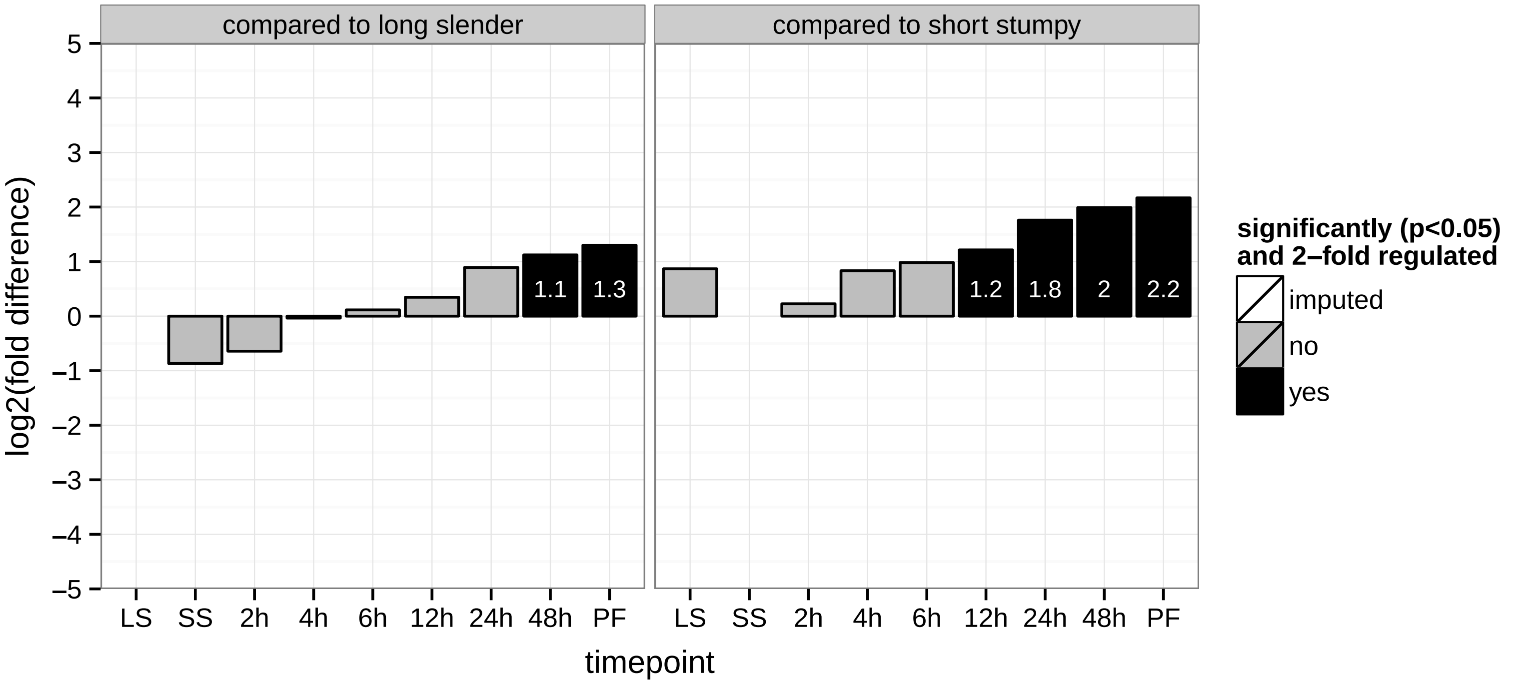
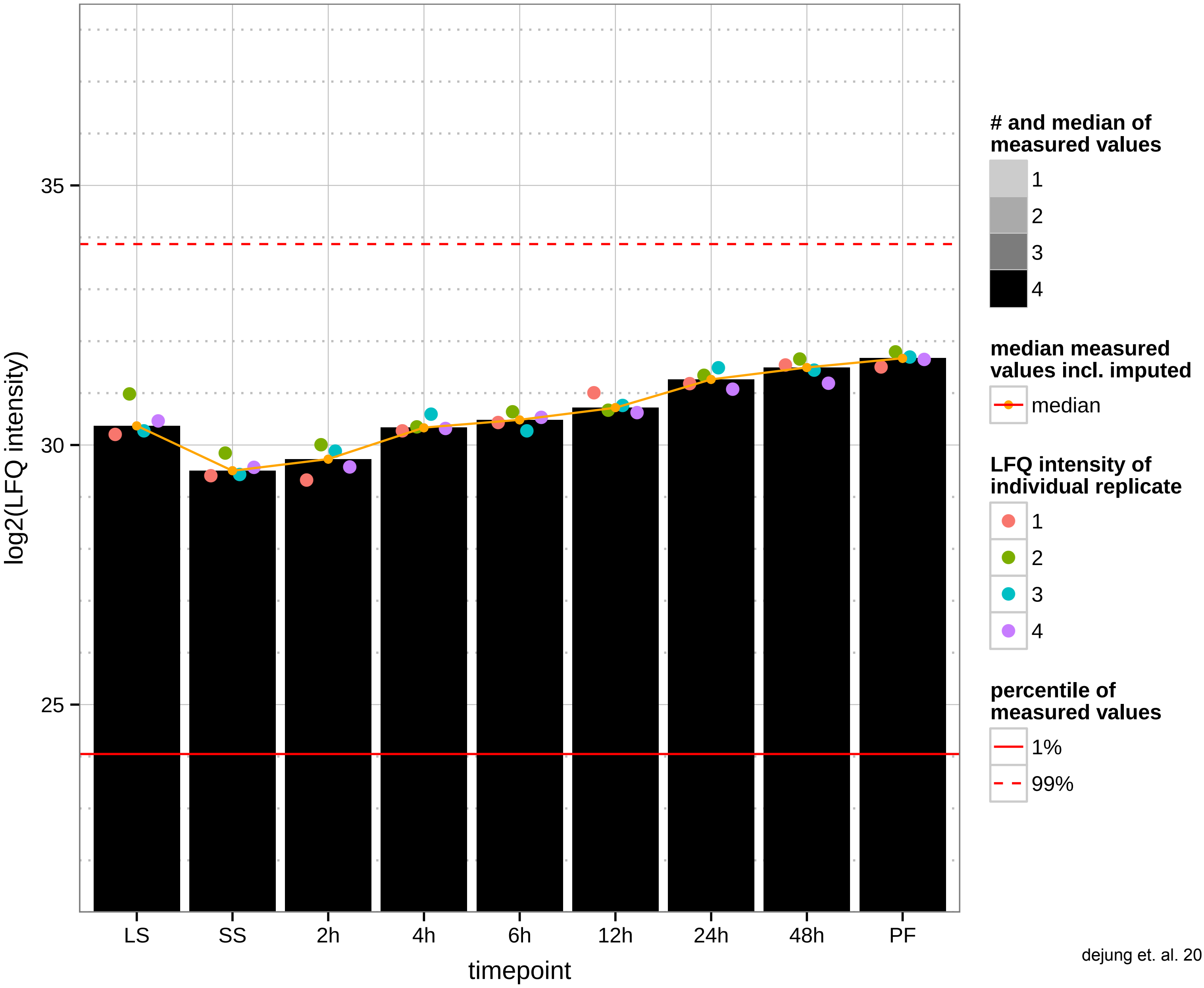
eukaryotic translation initiation factor 5, putative
Tb927.10.2770;Tb11.v5.0684
AGOF: null, translation initiation factor activity
AGOC: null
AGOP: null, translational initiation
PGOF: protein binding, translation initiation factor activity
PGOC: null
PGOP: translational initiation





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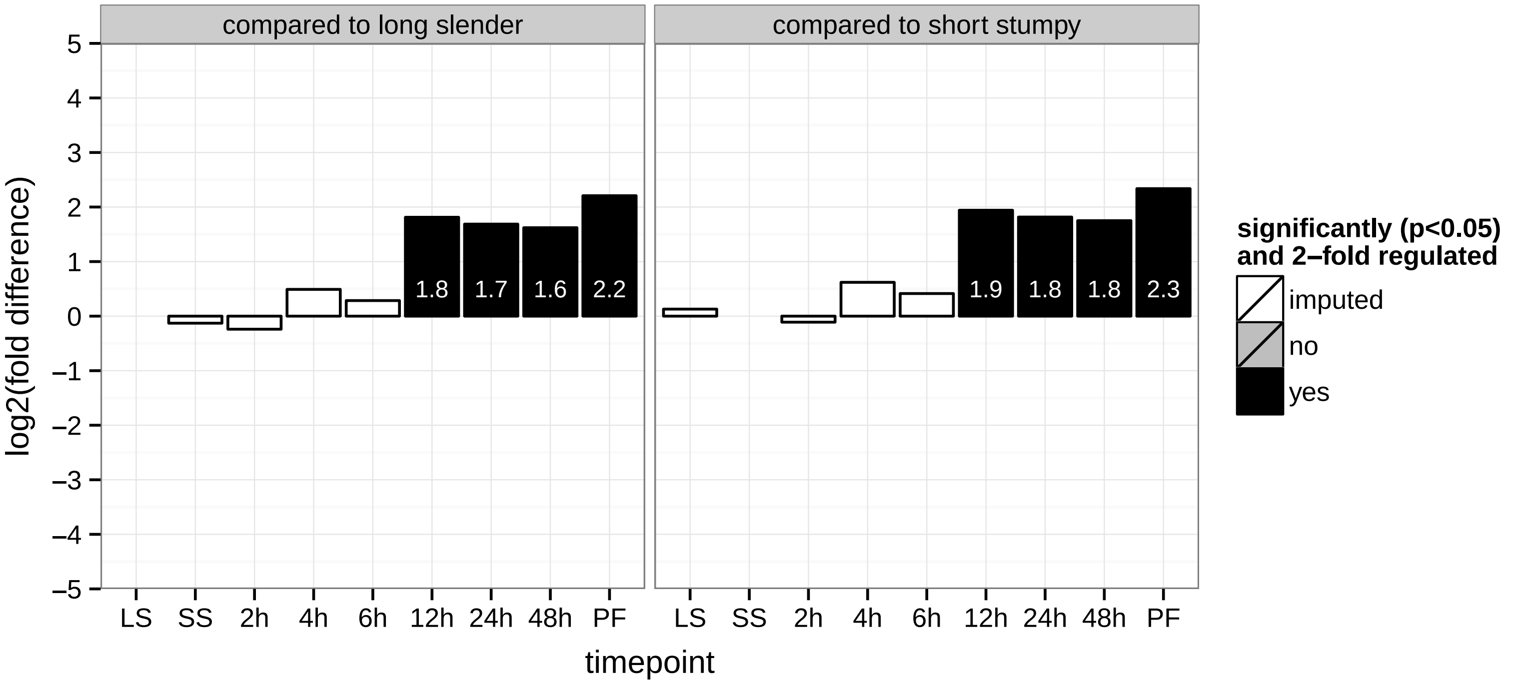
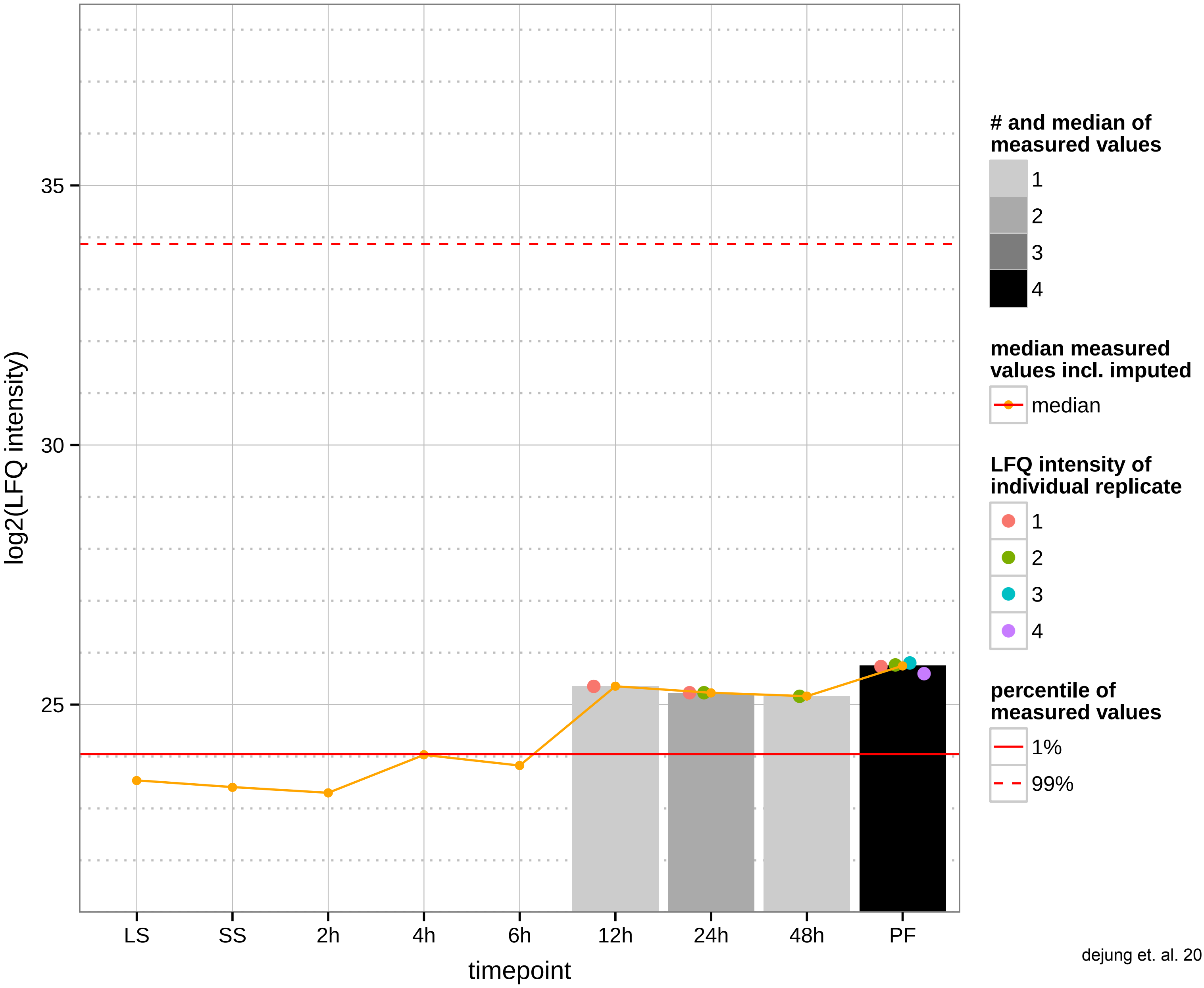
conserved protein, unknown function
Tb927.1.1210
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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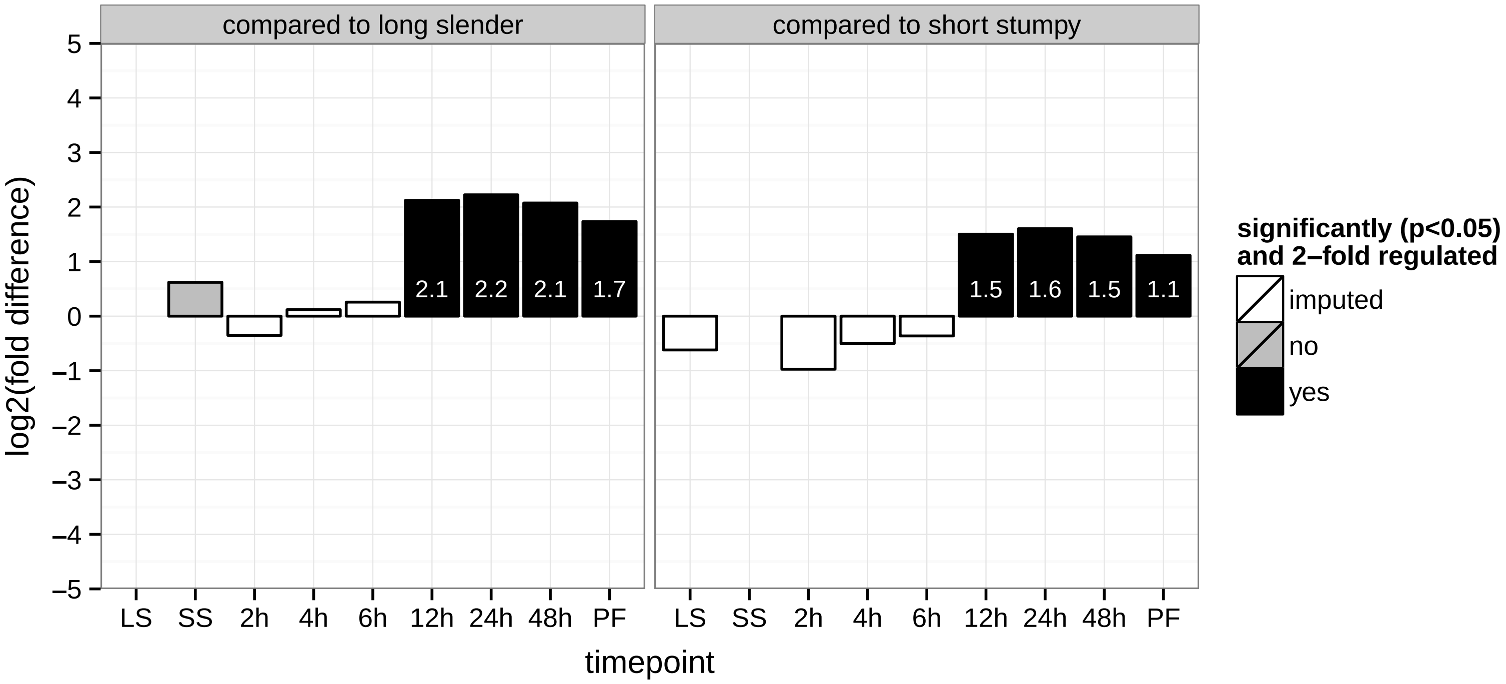
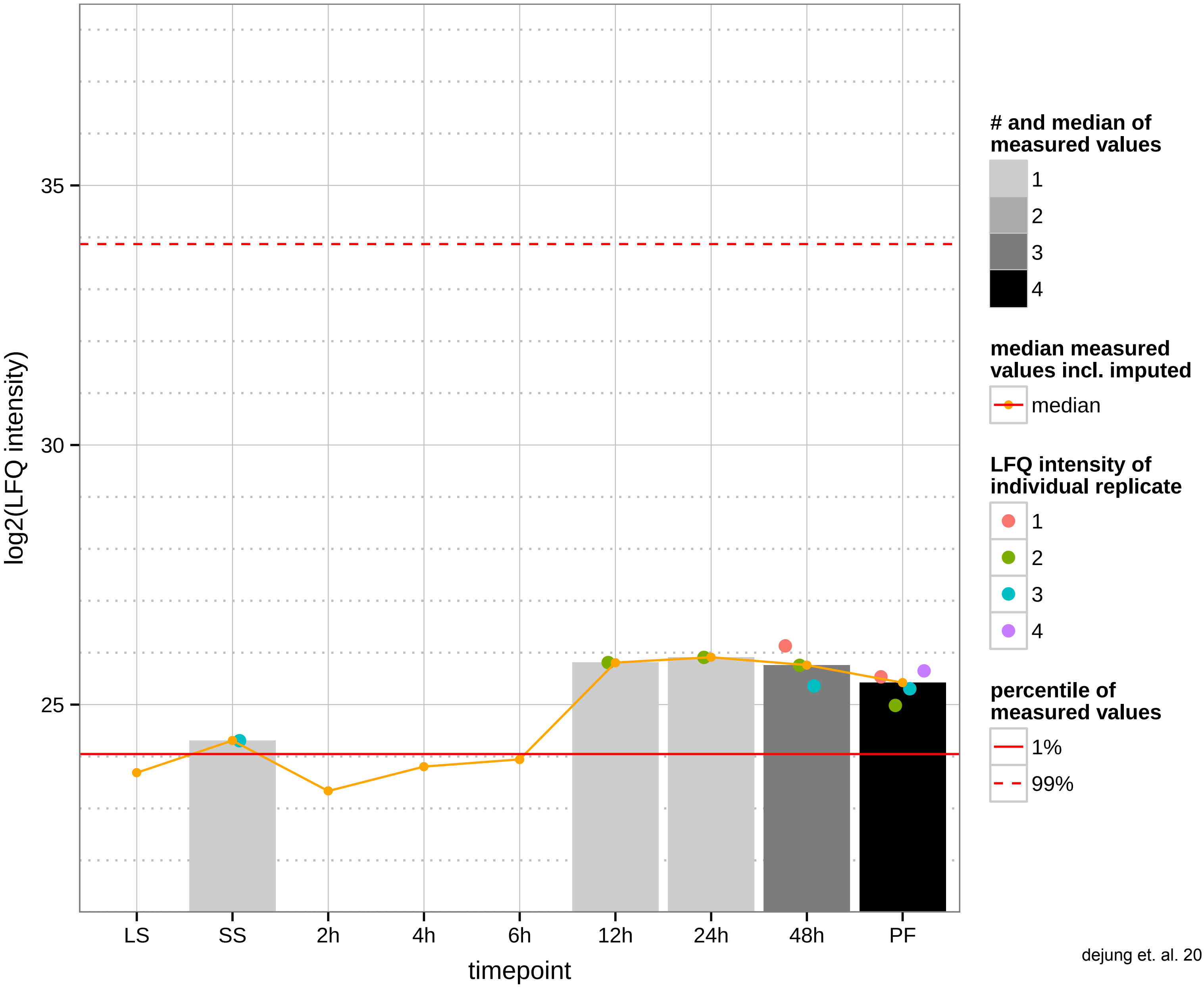
RWD domain−containing protein
Tb927.1.1220
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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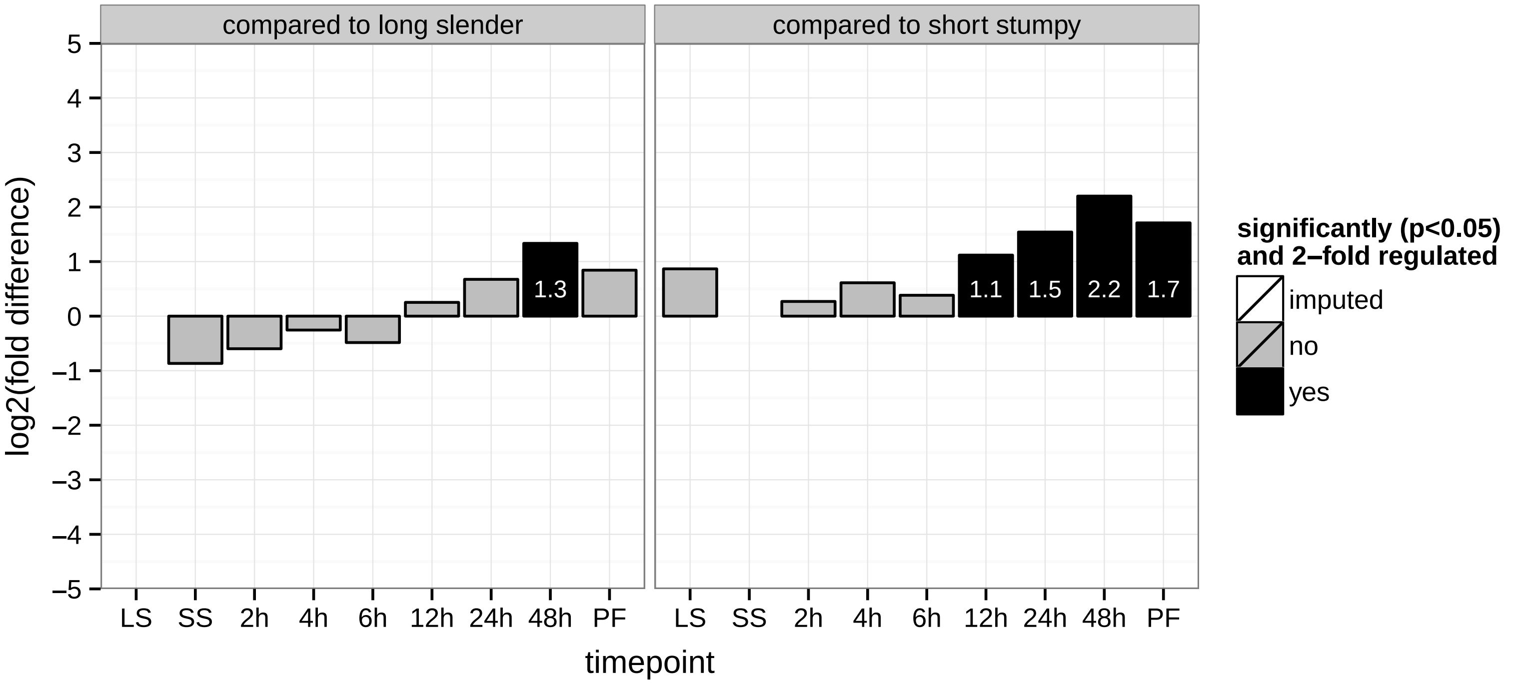
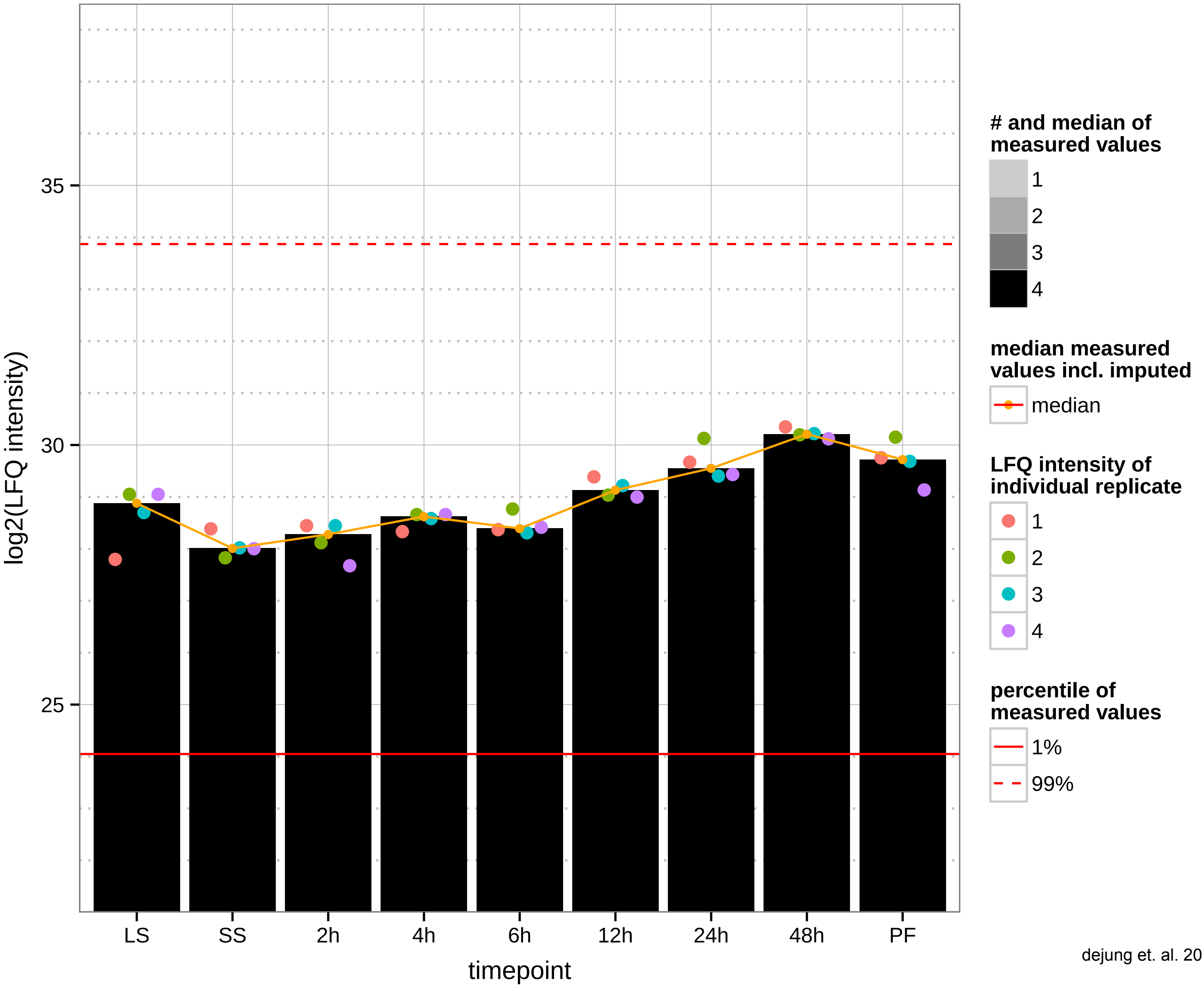
hypothetical protein, conserved
Tb927.1.3310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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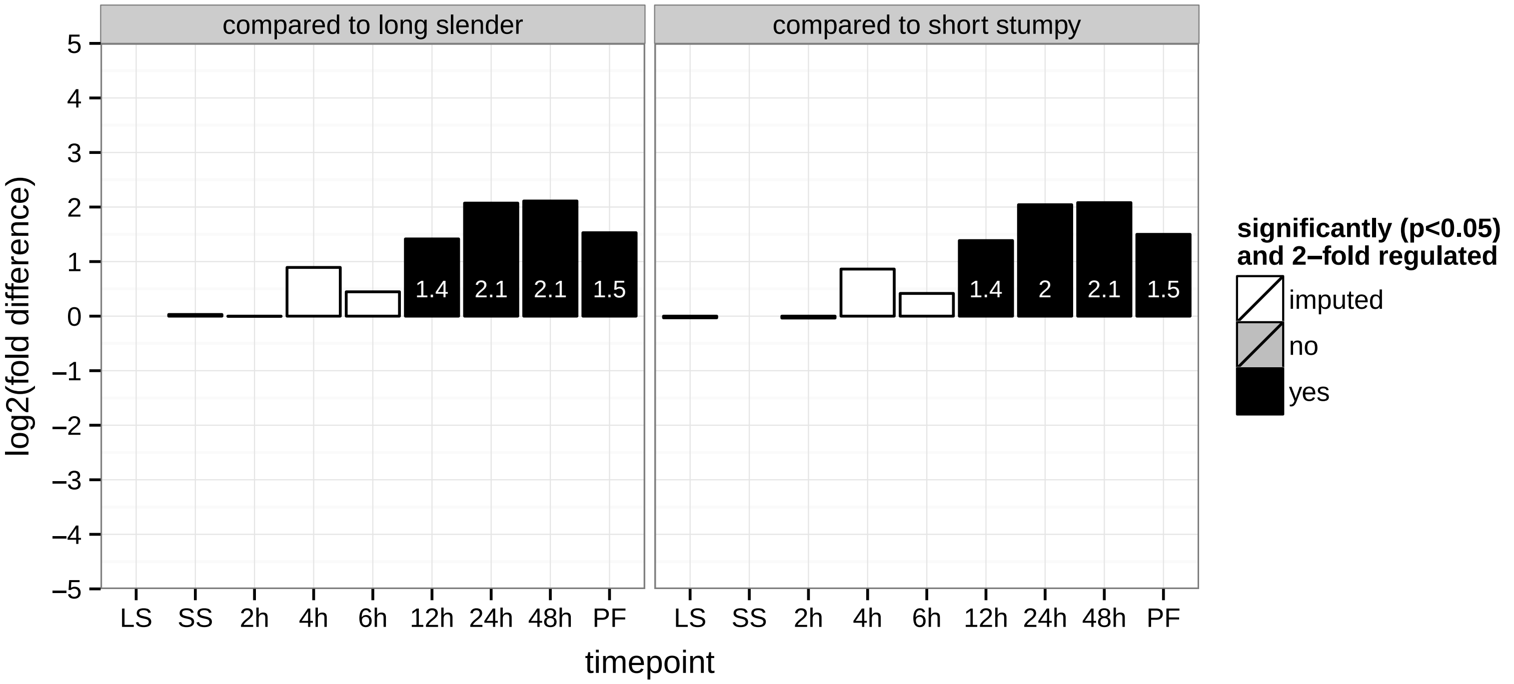
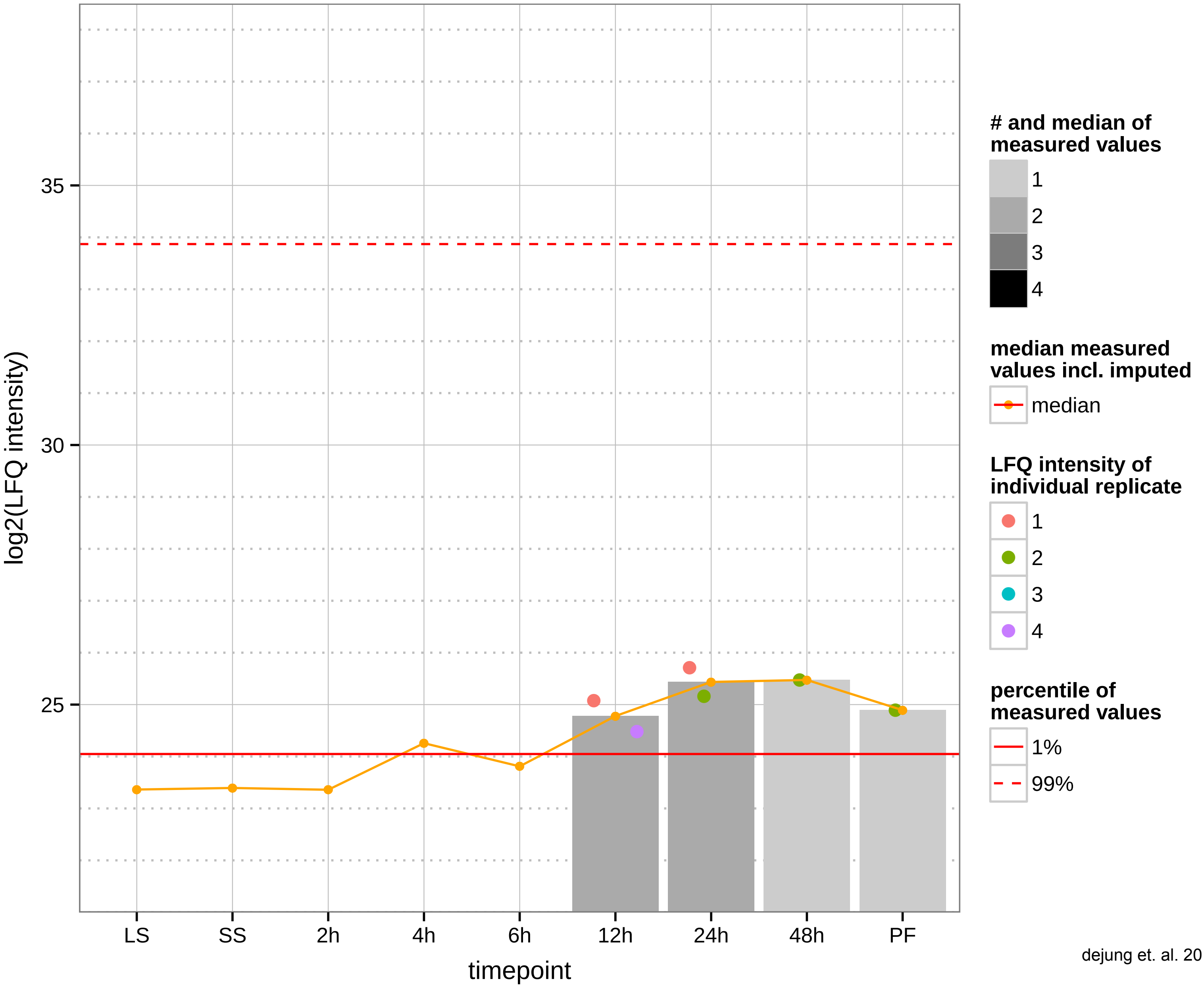
hypothetical protein, conserved
Tb927.1.4230
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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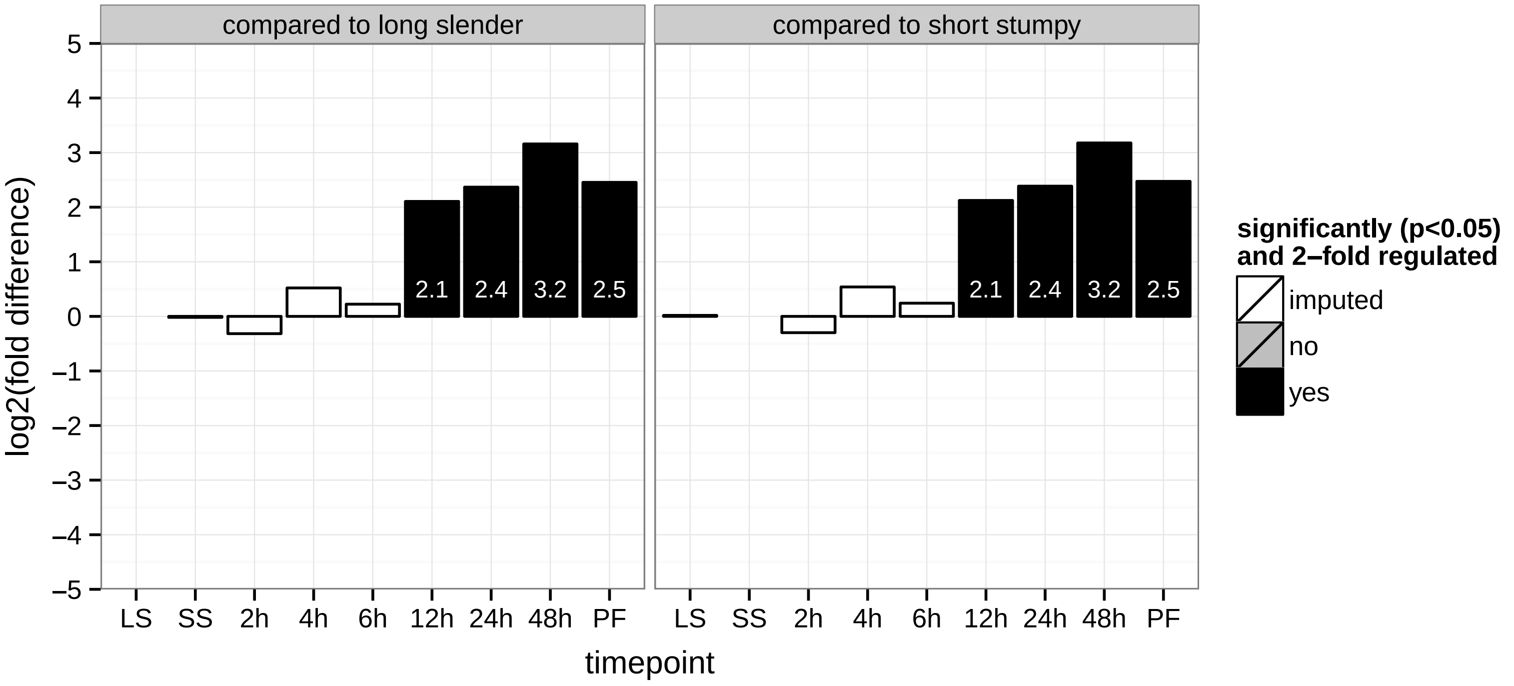
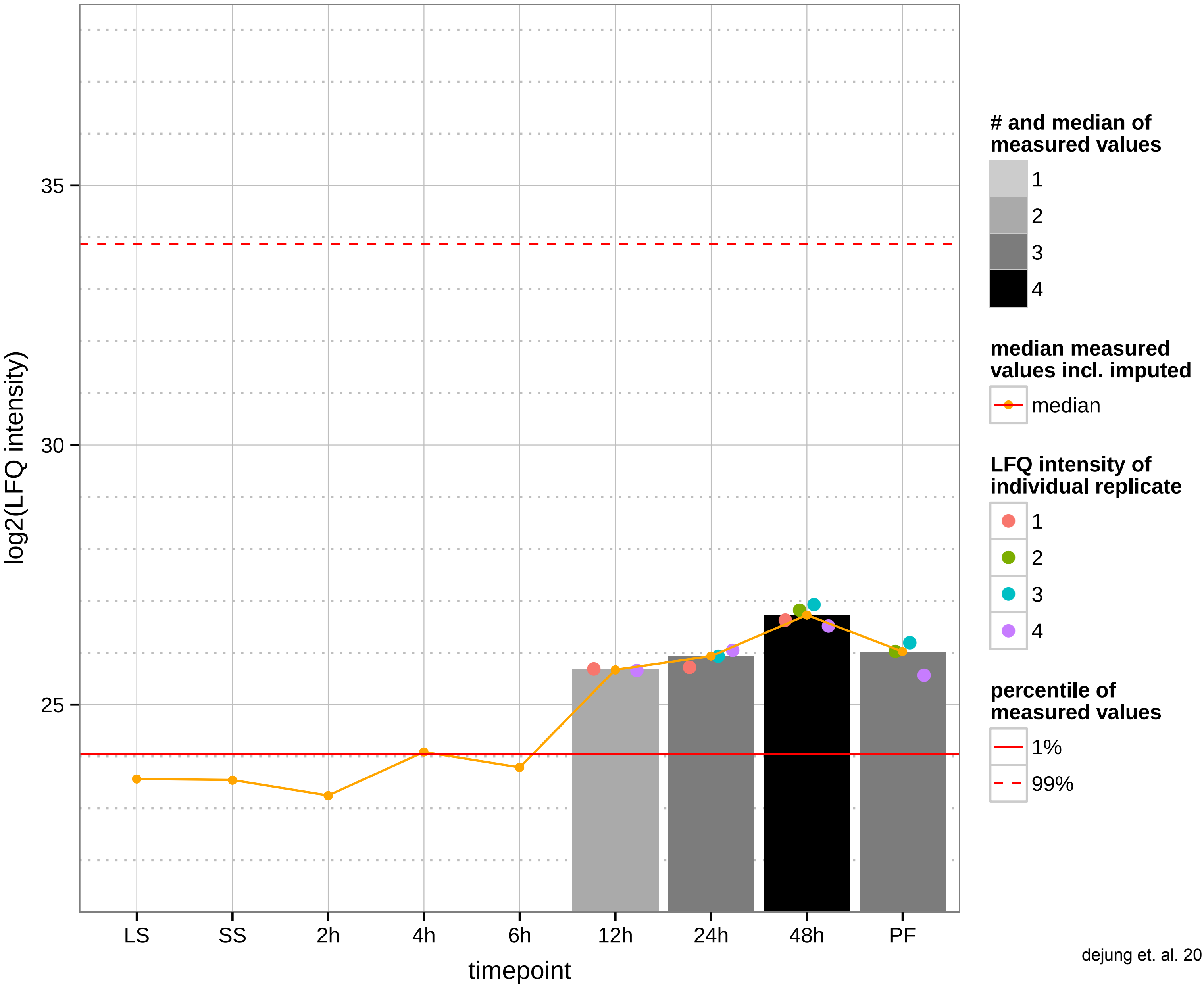
structural maintenance of chromosome 2, putative, putative (SMC2)
Tb927.10.10340;Tb11.v5.0811
AGOF: null, ATP binding
AGOC: null, chromosome, cohesin complex, nucleus
AGOP: null, chromosome organization, mitosis, mitotic sister chromatid segregation
PGOF: ATP binding, protein binding
PGOC: chromosome
PGOP: chromosome organization





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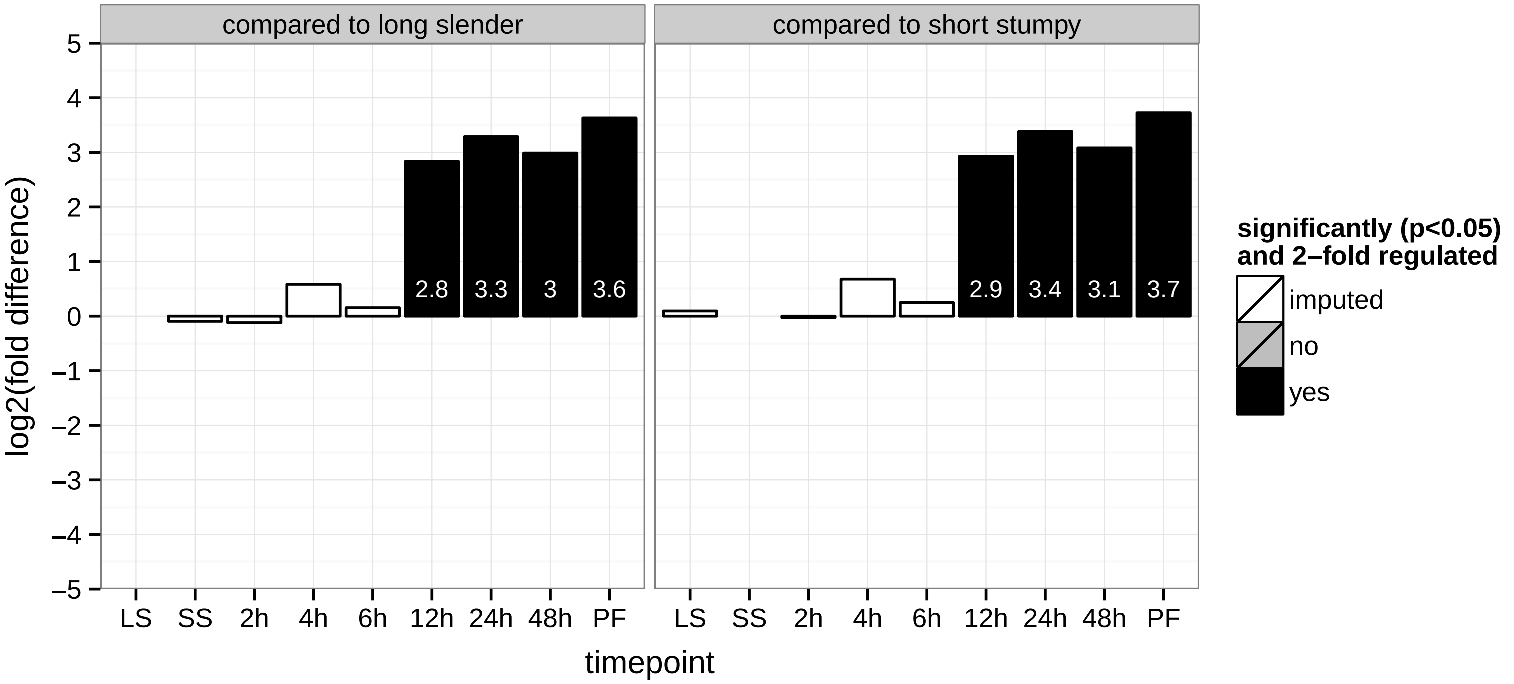
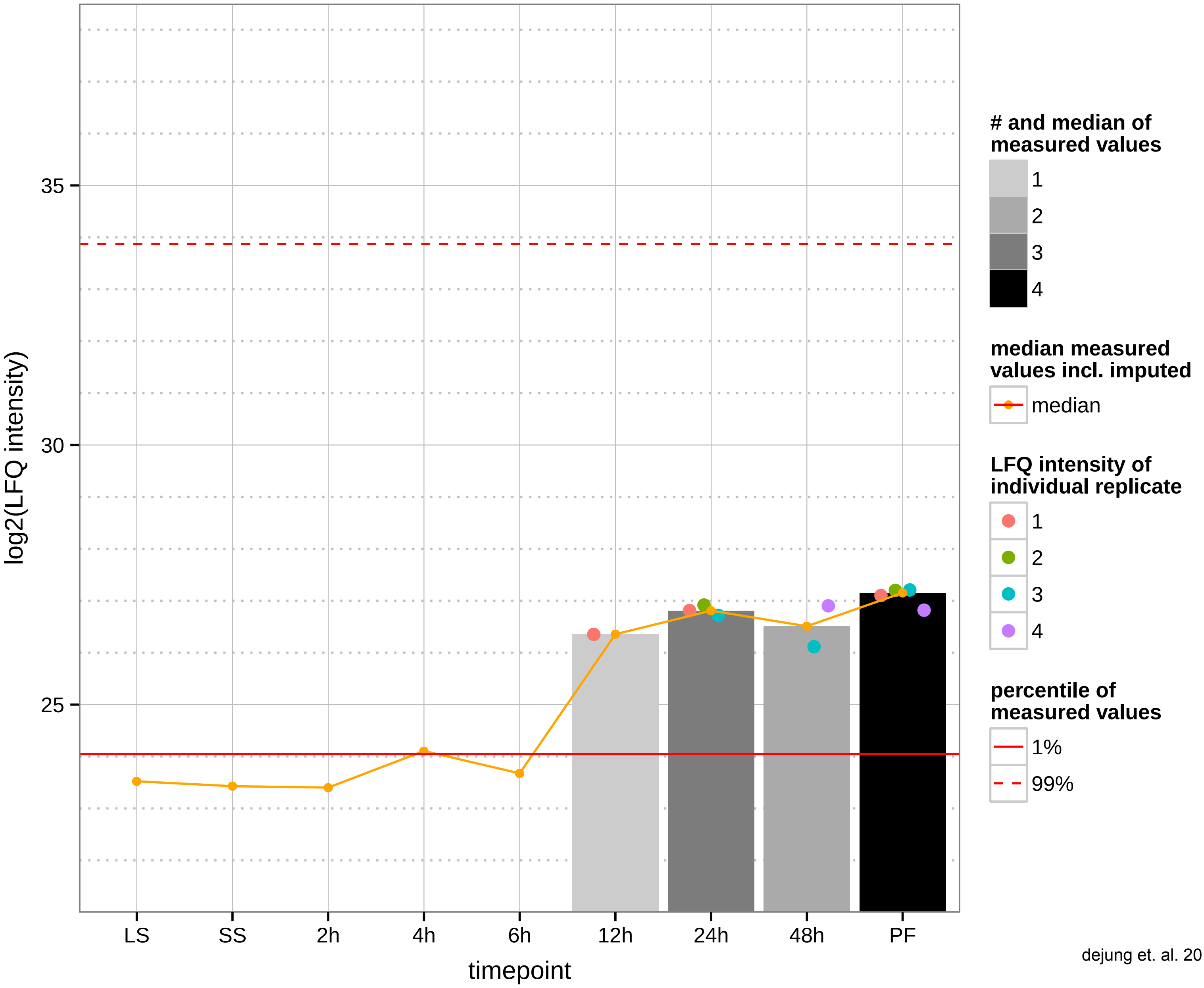
RNA–binding protein, putative (RBP23)
Tb927.10.11270
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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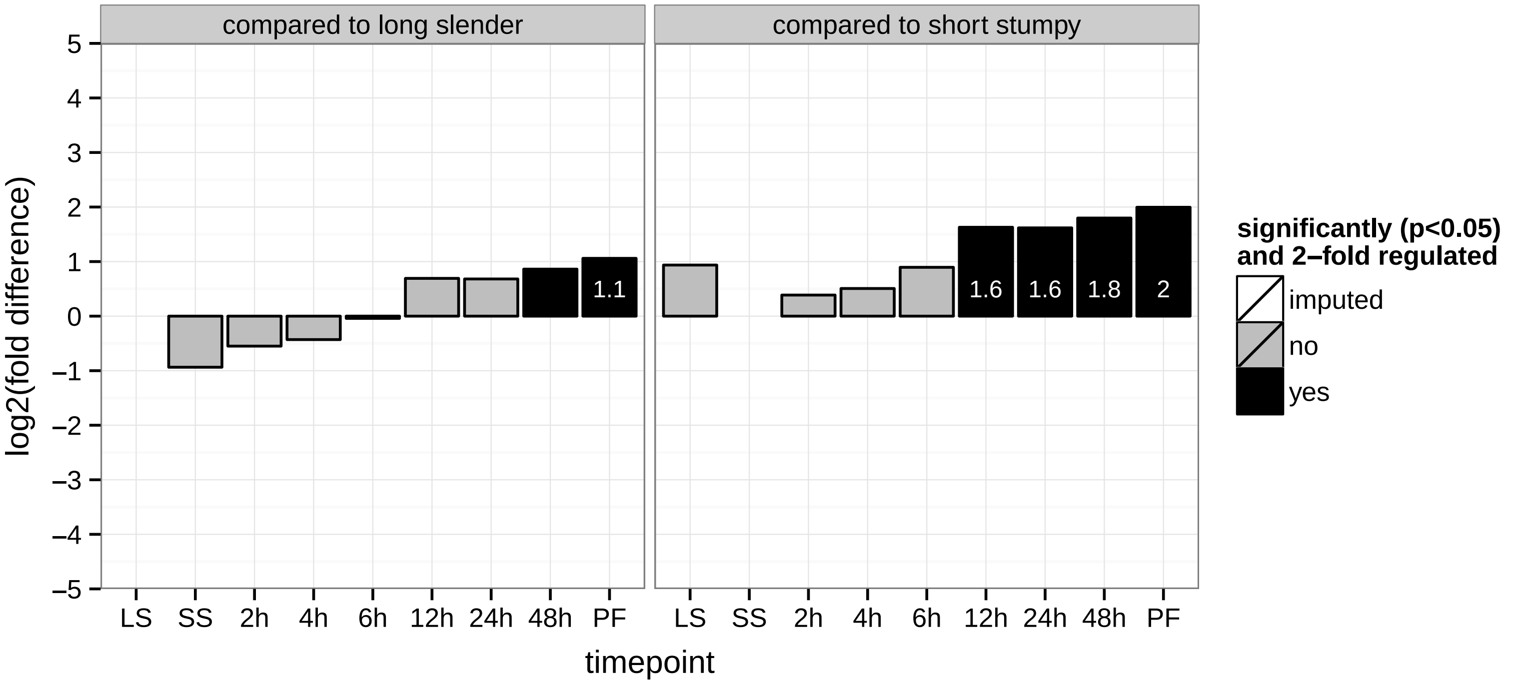
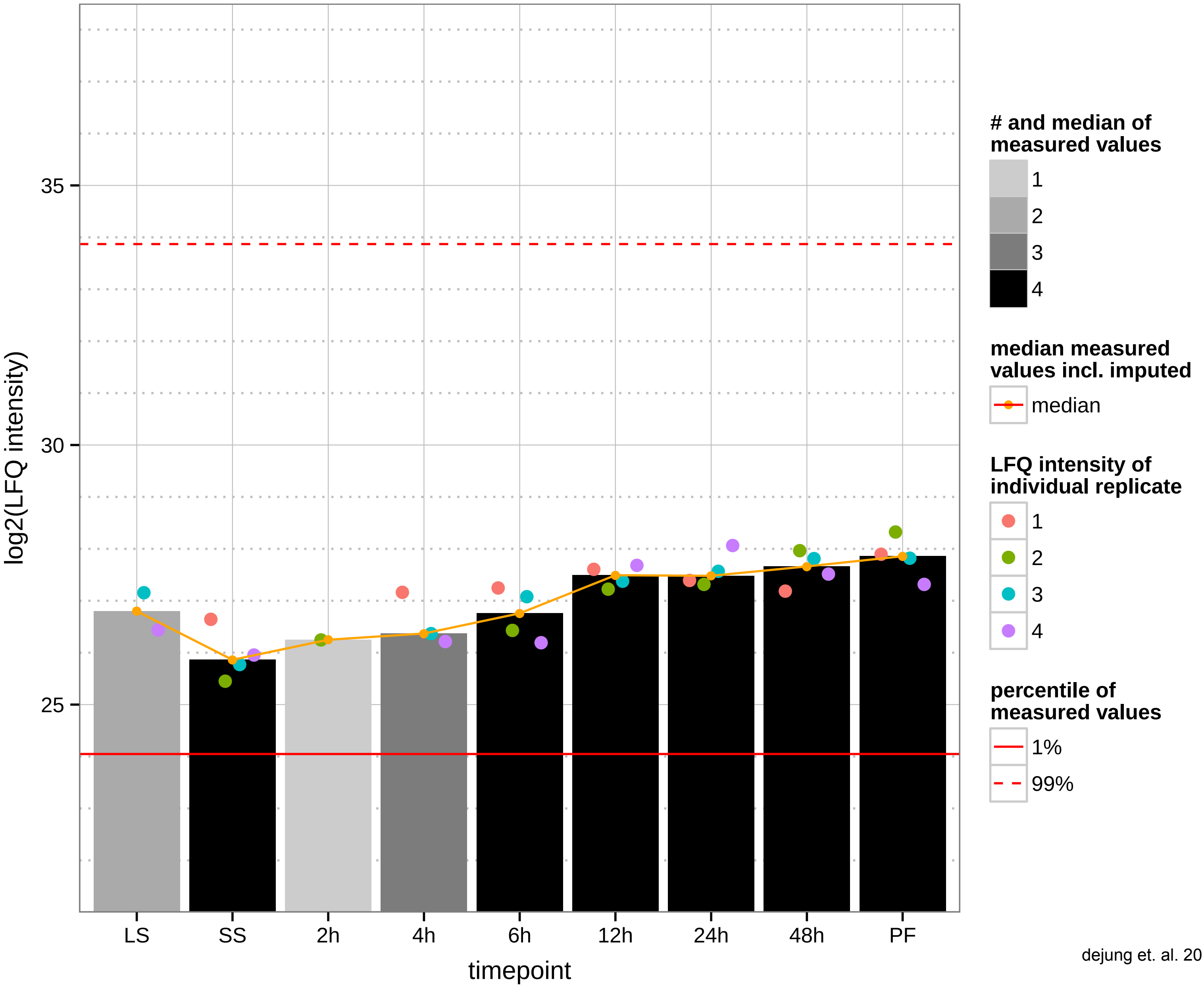
UDP−Gal or UDP−GlcNAc−dependent glycosyltransferase, putative
Tb927.10.12290
AGOF: UDP−glycosyltransferase activity, galactosyltransferase activity
AGOC: membrane
AGOP: GPI anchor biosynthetic process, protein glycosylation
PGOF: null
PGOC: null
PGOP: null





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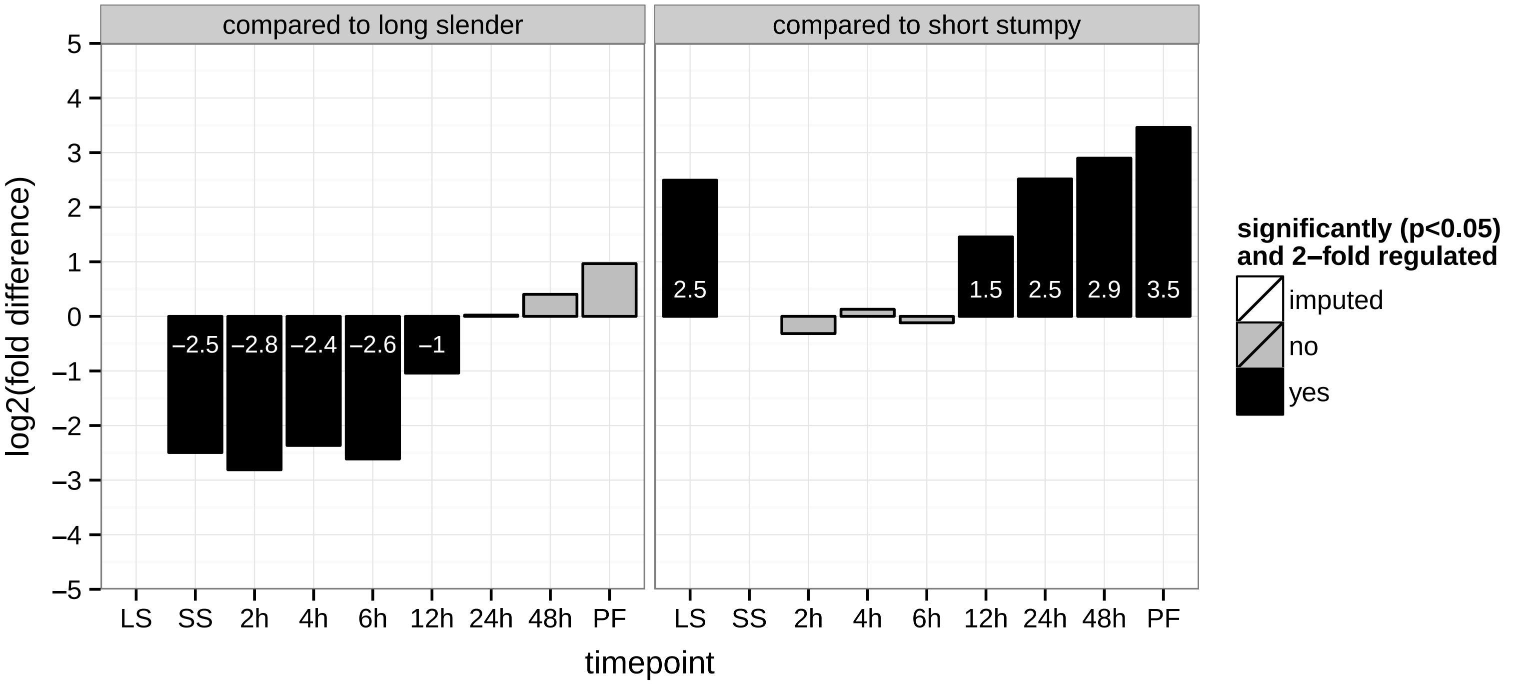
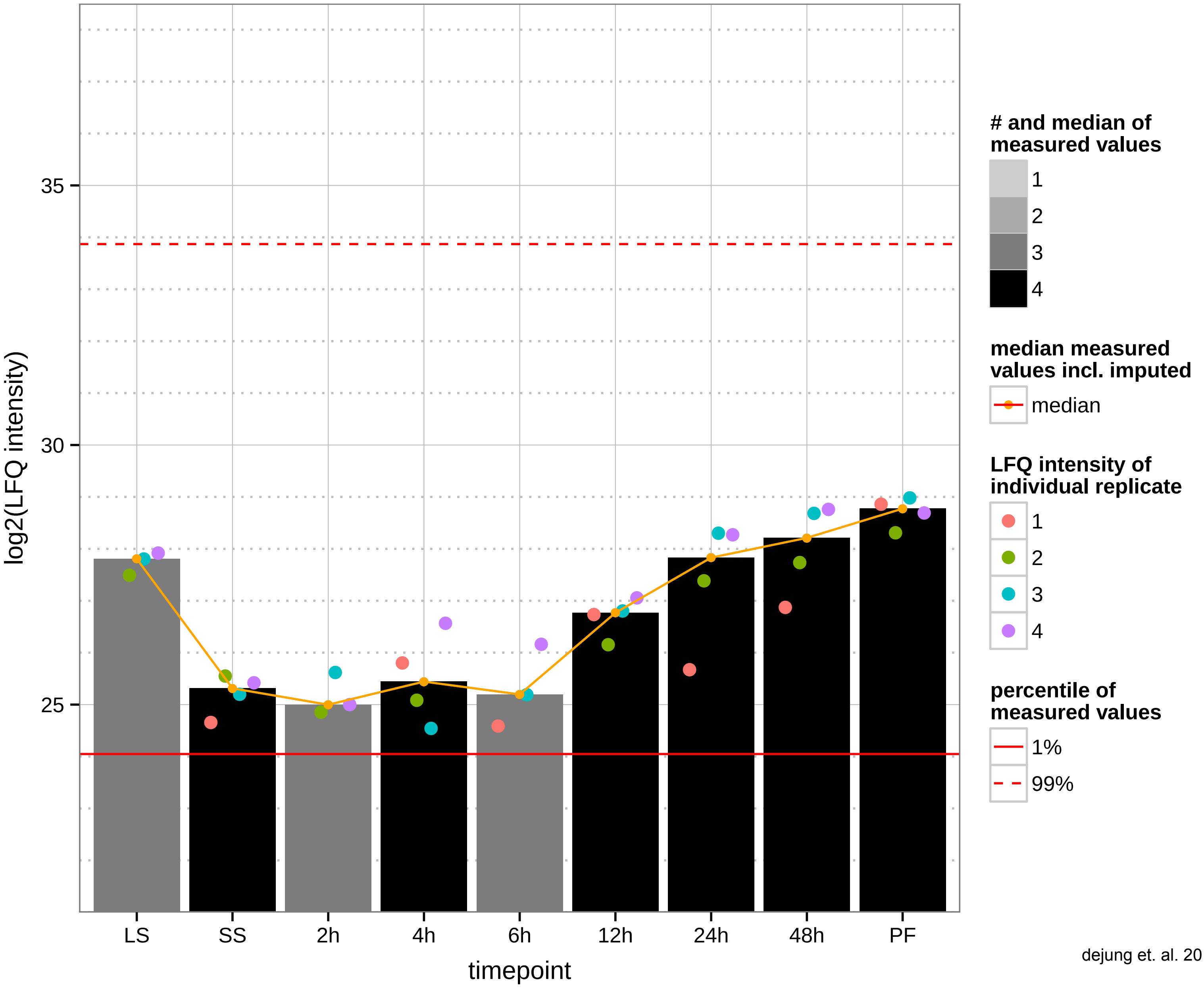
zinc finger protein family member, putative (ZC3H34)
Tb927.10.12330
AGOF: RNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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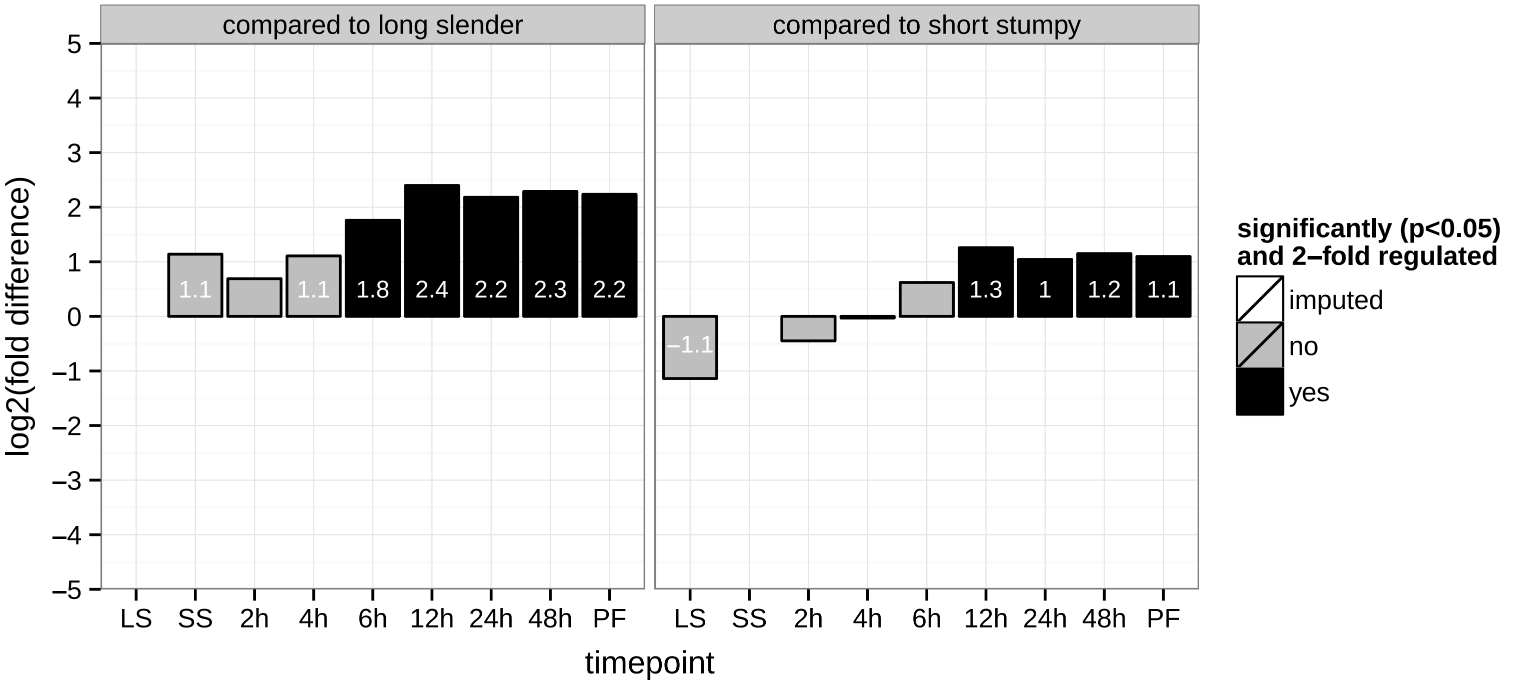
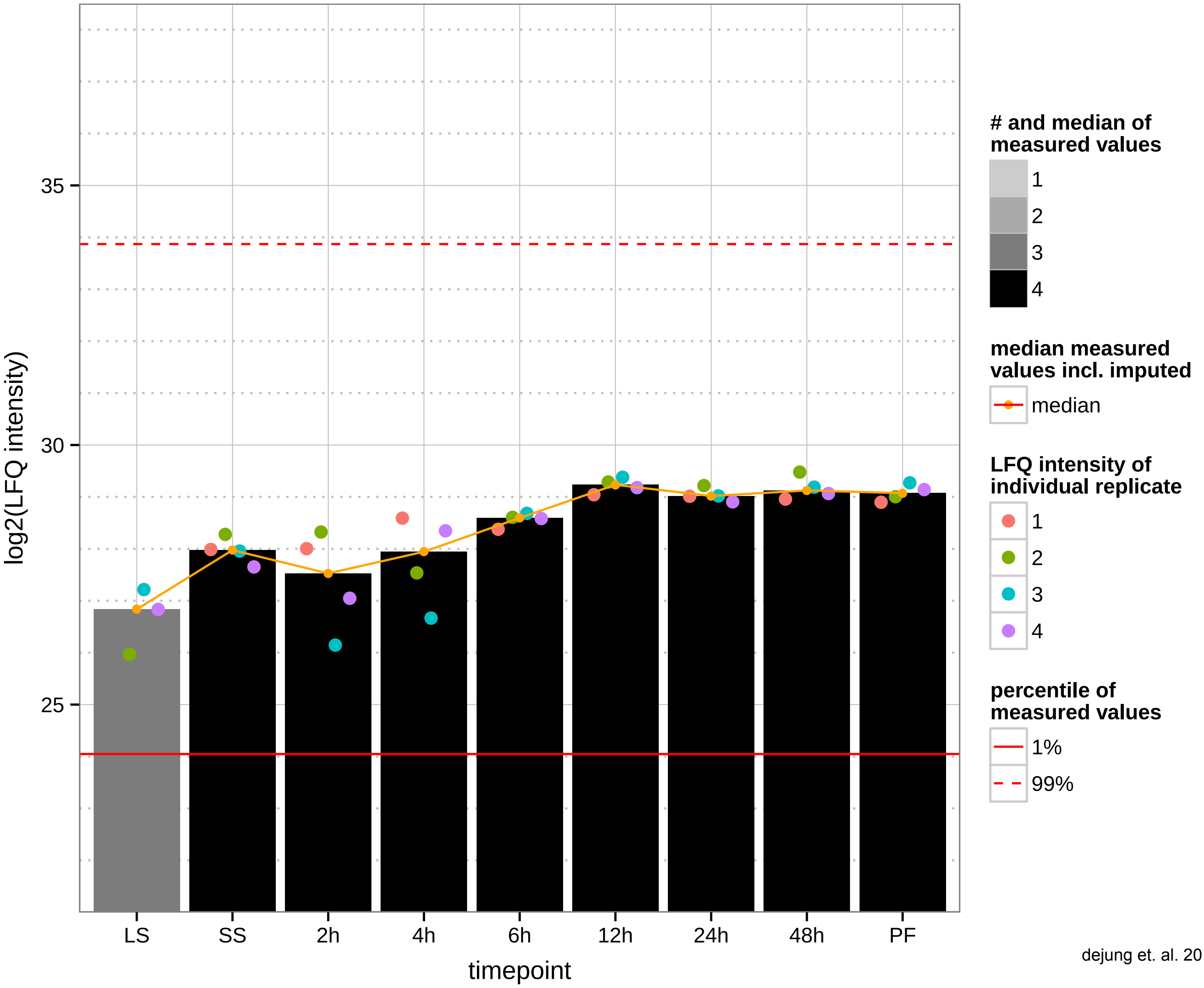
hypothetical protein, conserved
Tb927.10.1250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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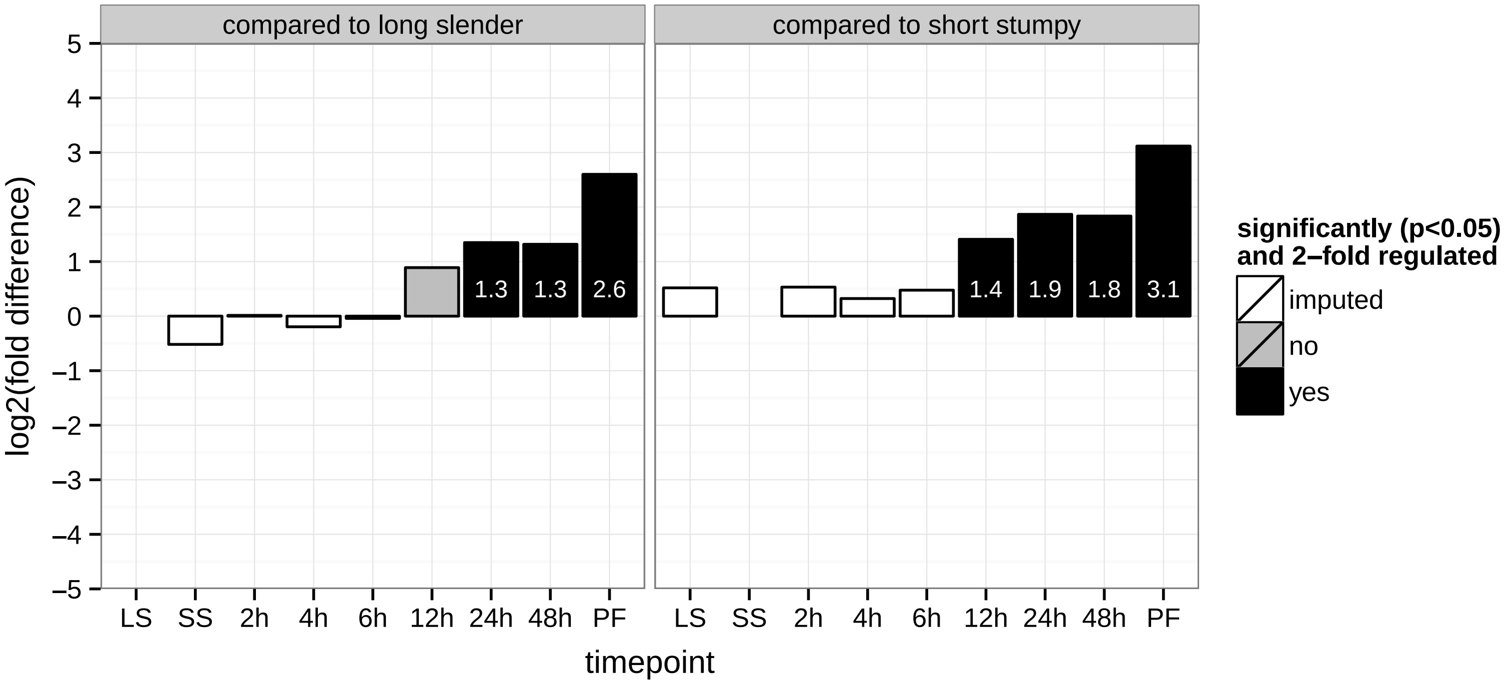
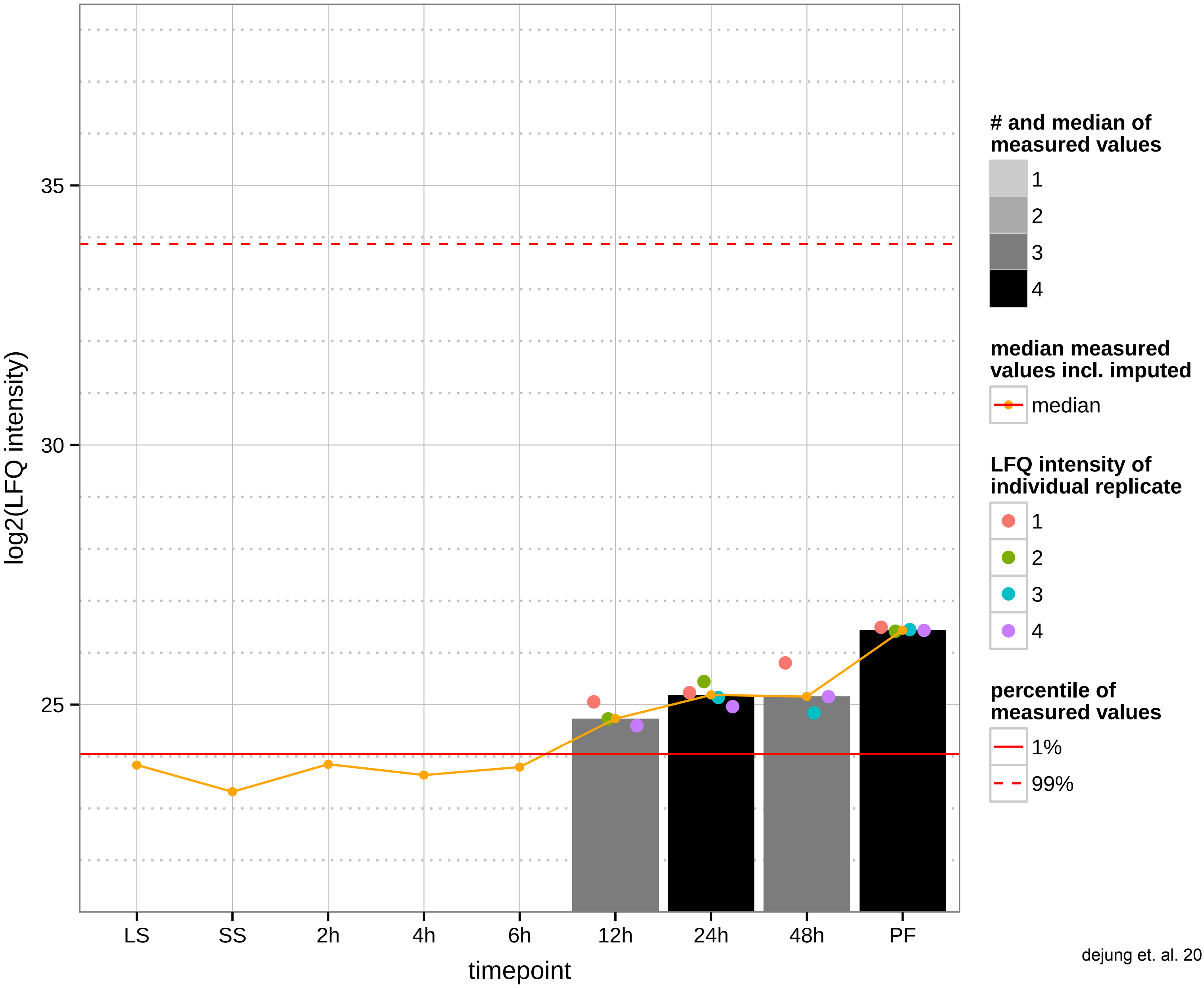
hypothetical protein, conserved
Tb927.10.1280
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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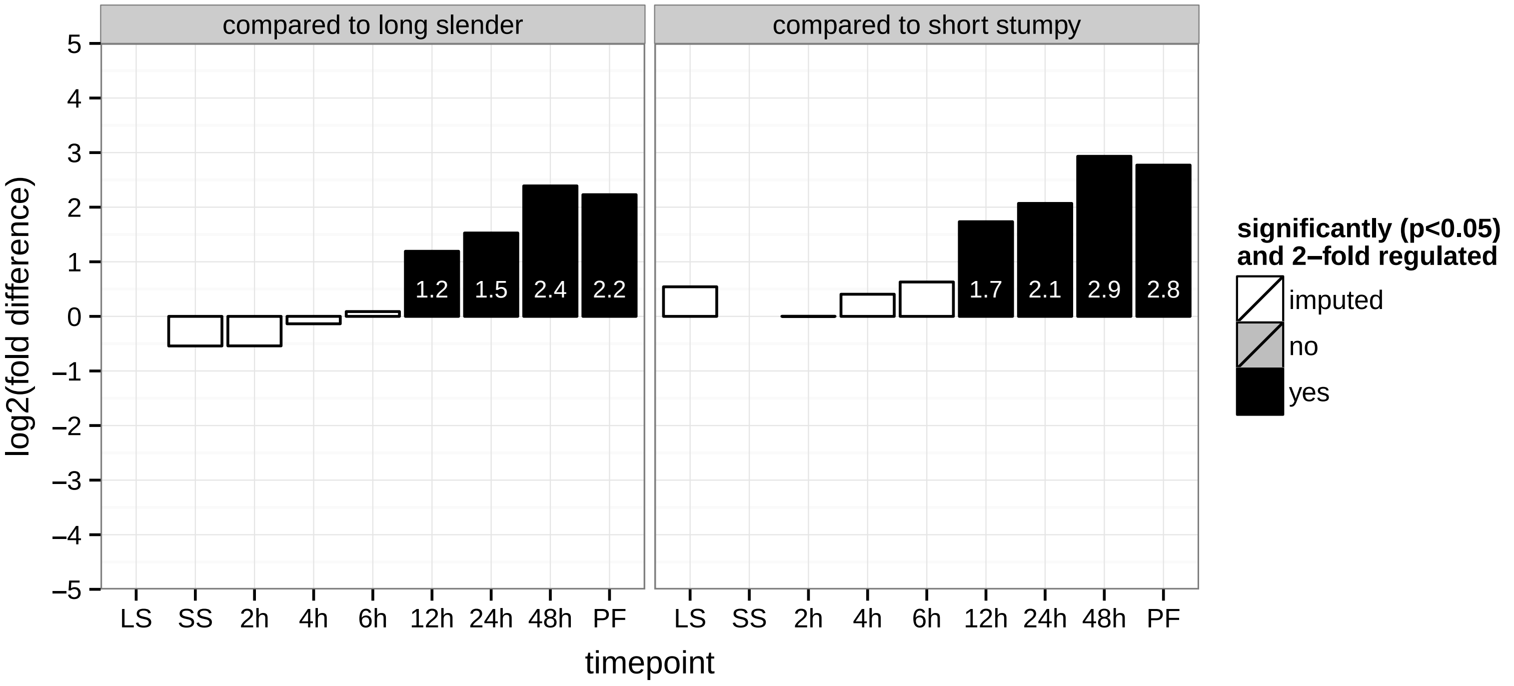
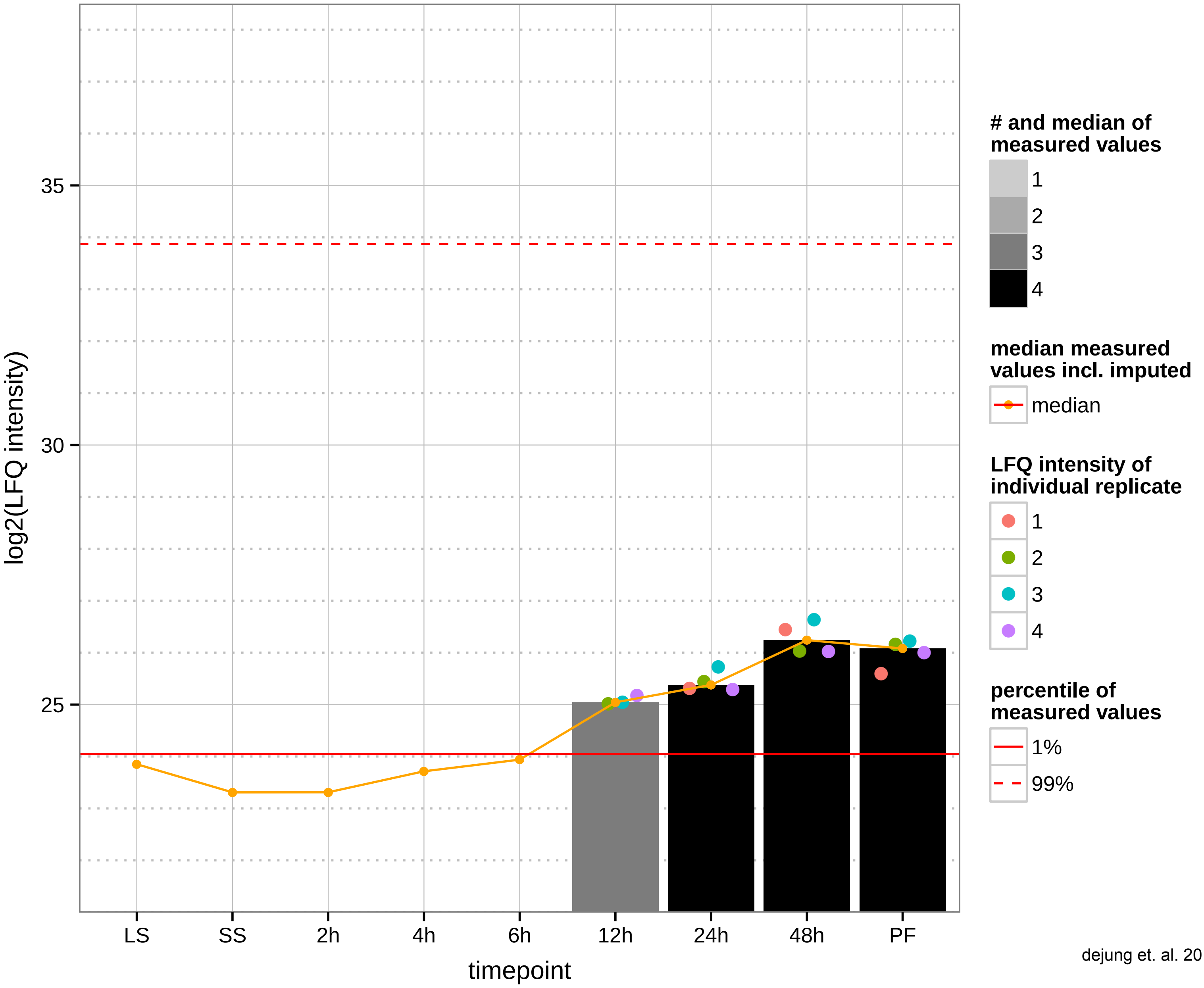
hypothetical protein, conserved
Tb927.10.12860
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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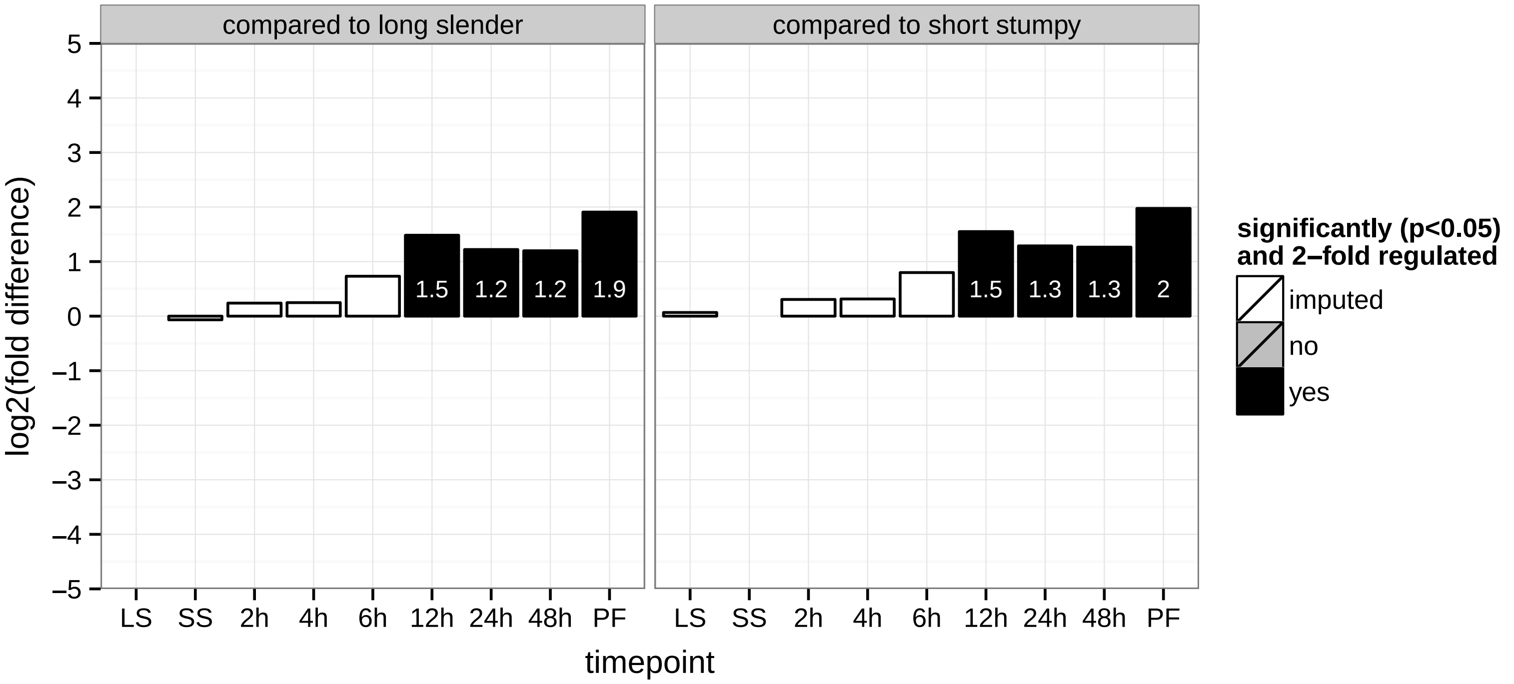
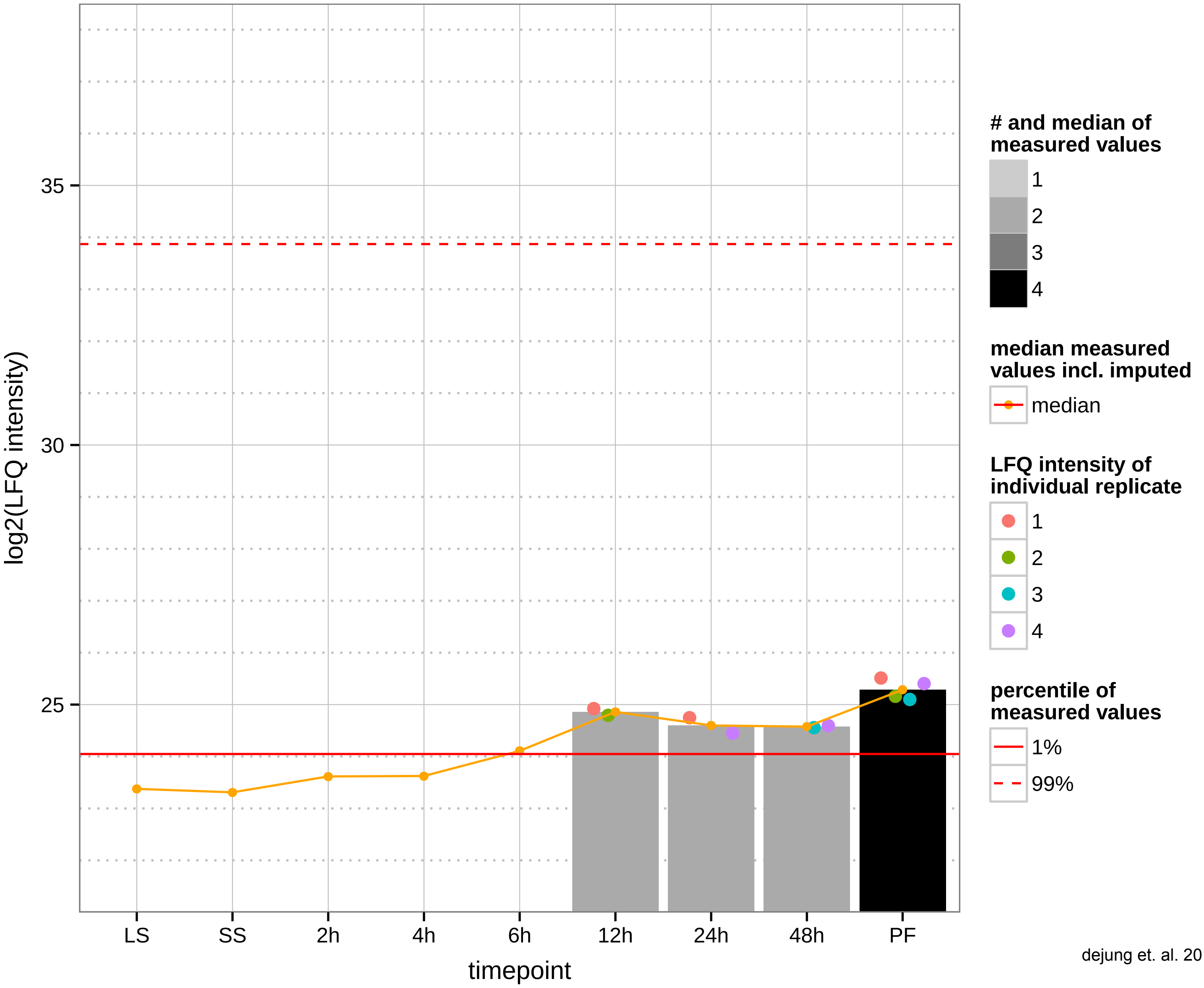
hypothetical protein, conserved
Tb927.10.13140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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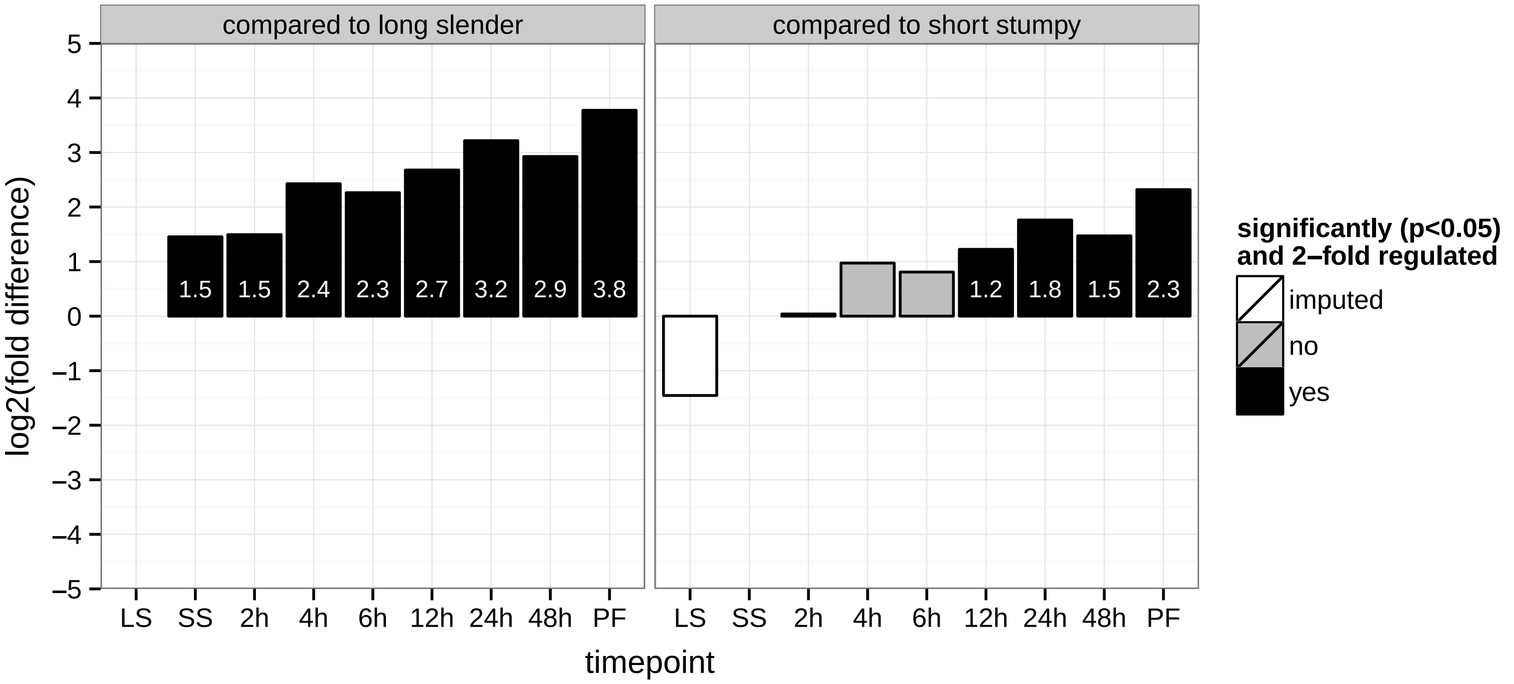
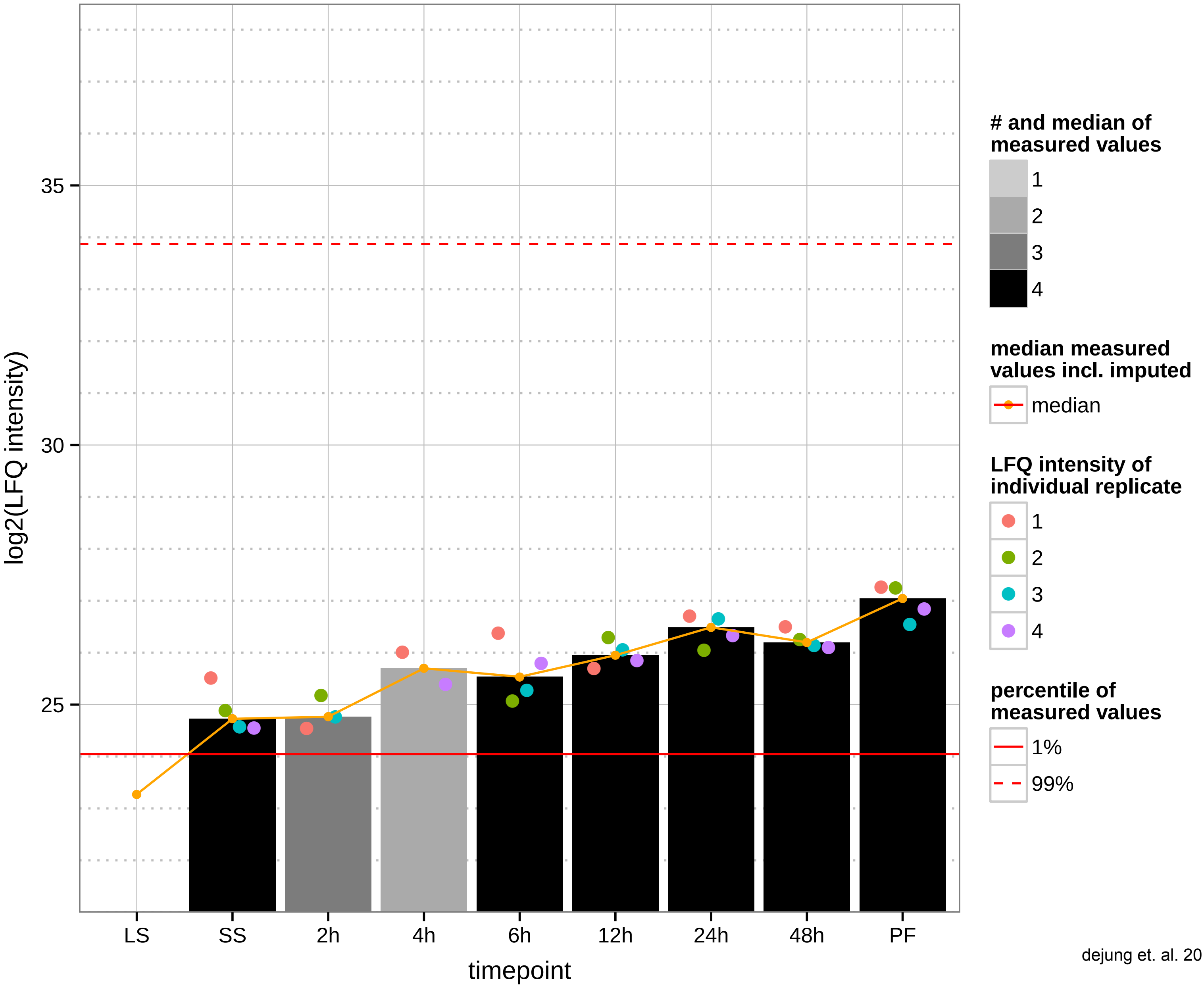
DNA–directed RNA polymerase I subunit RPB5z, putative (RPB5z)
Tb927.10.13310
AGOF: DNA binding, DNA–directed RNA polymerase activity
AGOC: nucleus
AGOP: transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: nucleus
PGOP: transcription, DNA–dependent





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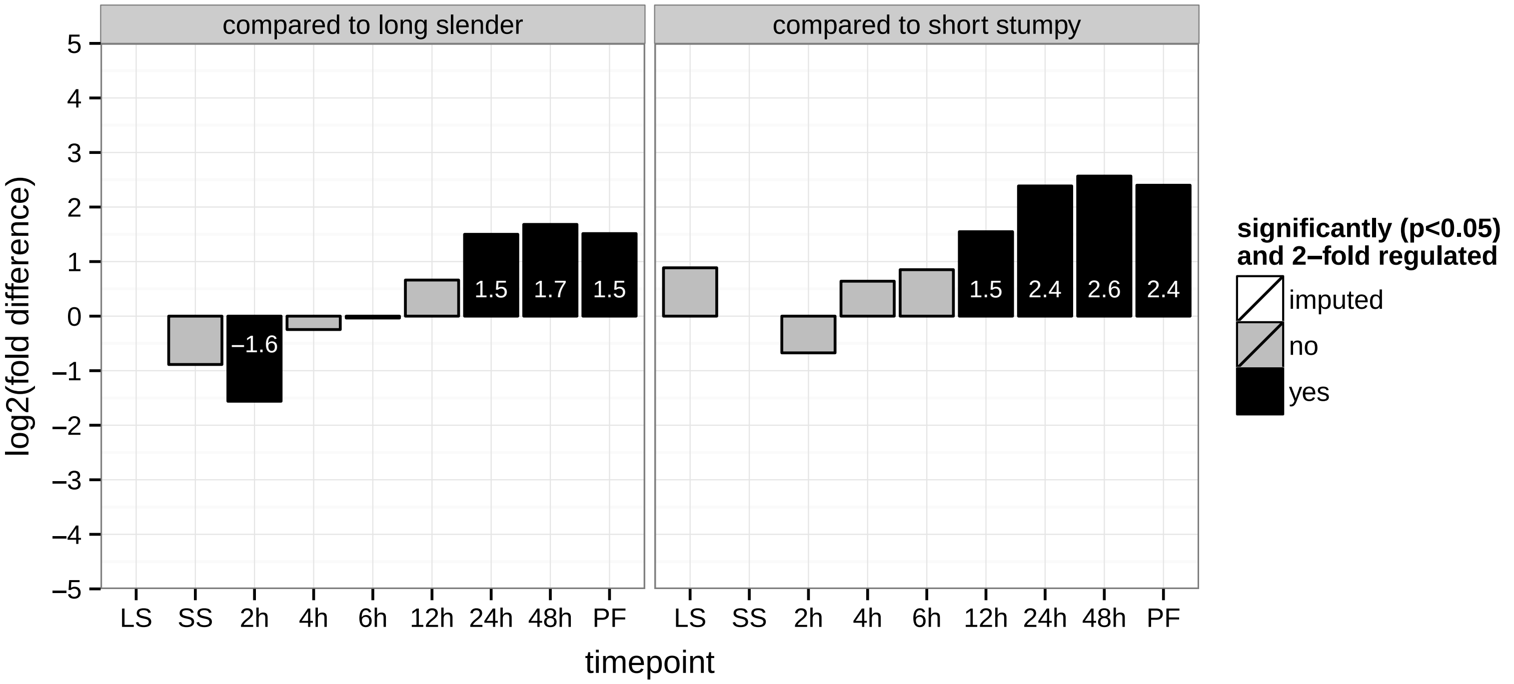
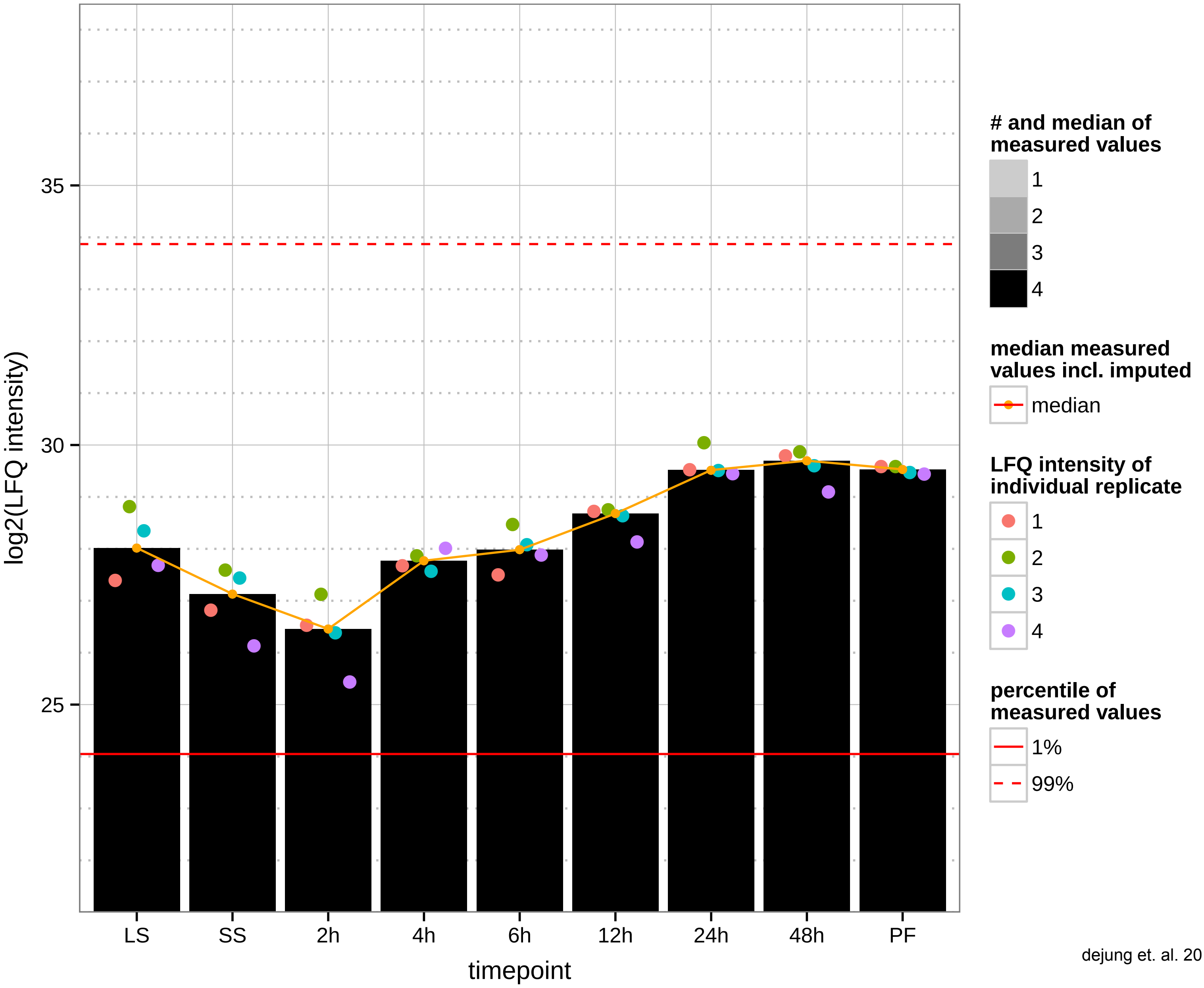
hypothetical protein, conserved
Tb927.10.13800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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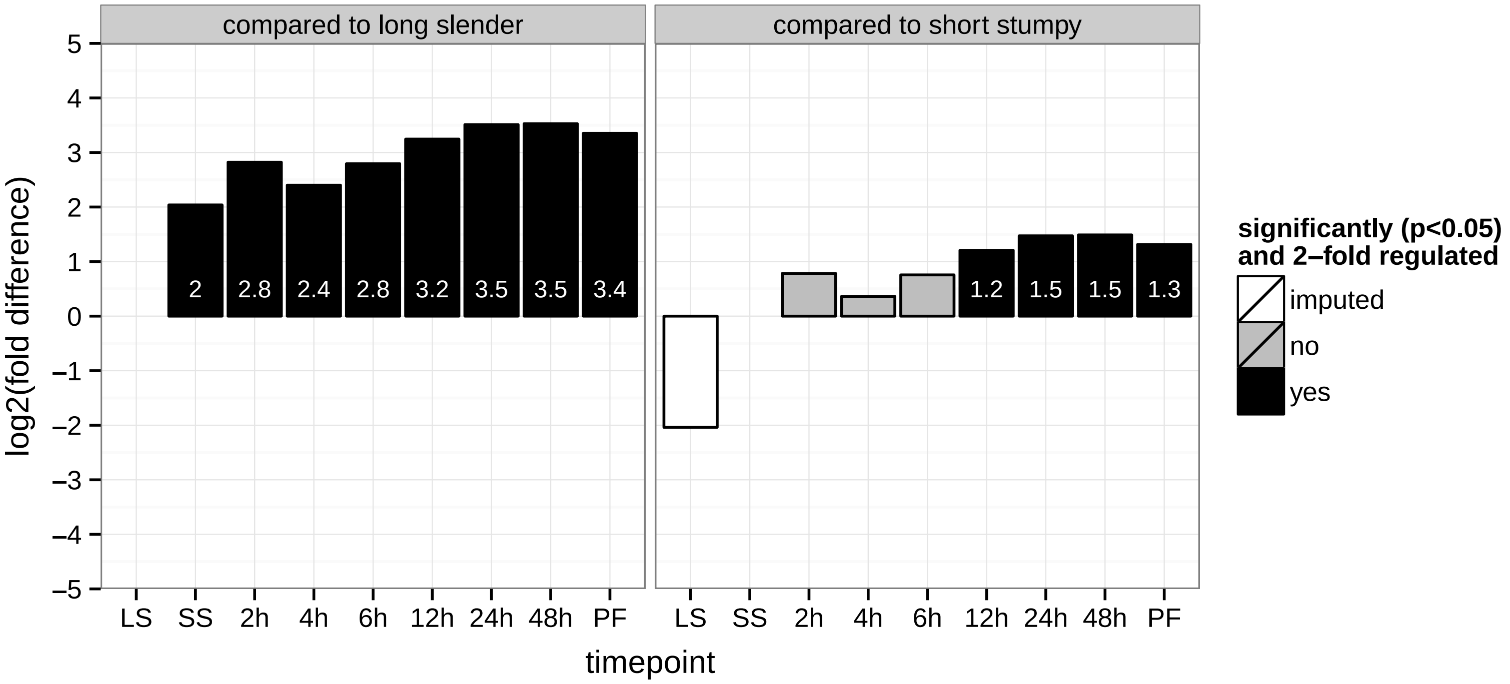
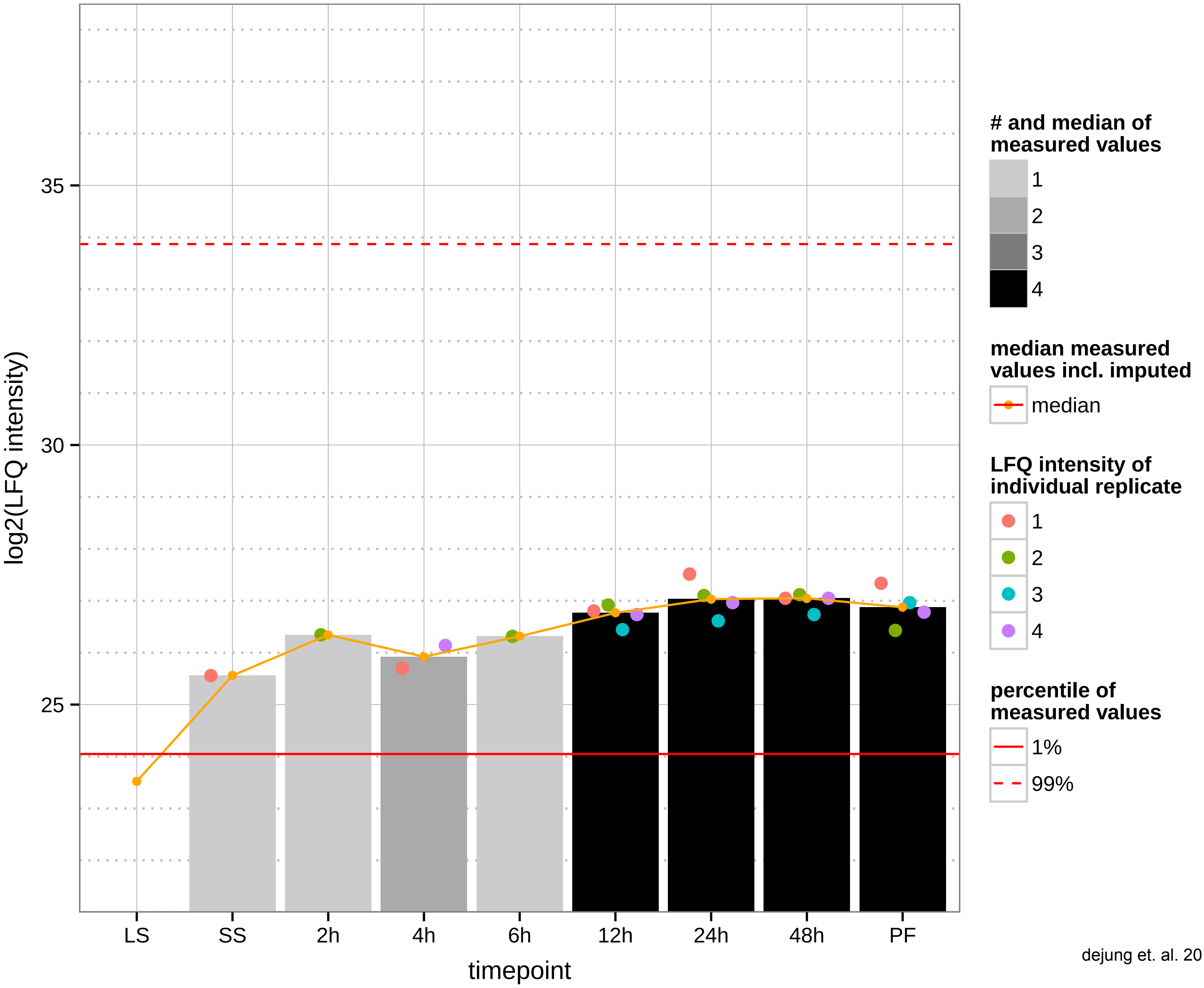
aquaglyceroporin 2 (AQP2)
Tb927.10.14170
AGOF: glycerol channel activity, water channel activity, water transmembrane transporter activity
AGOC: flagellar pocket, plasma membrane
AGOP: glycerol transport
PGOF: transporter activity
PGOC: membrane
PGOP: transport





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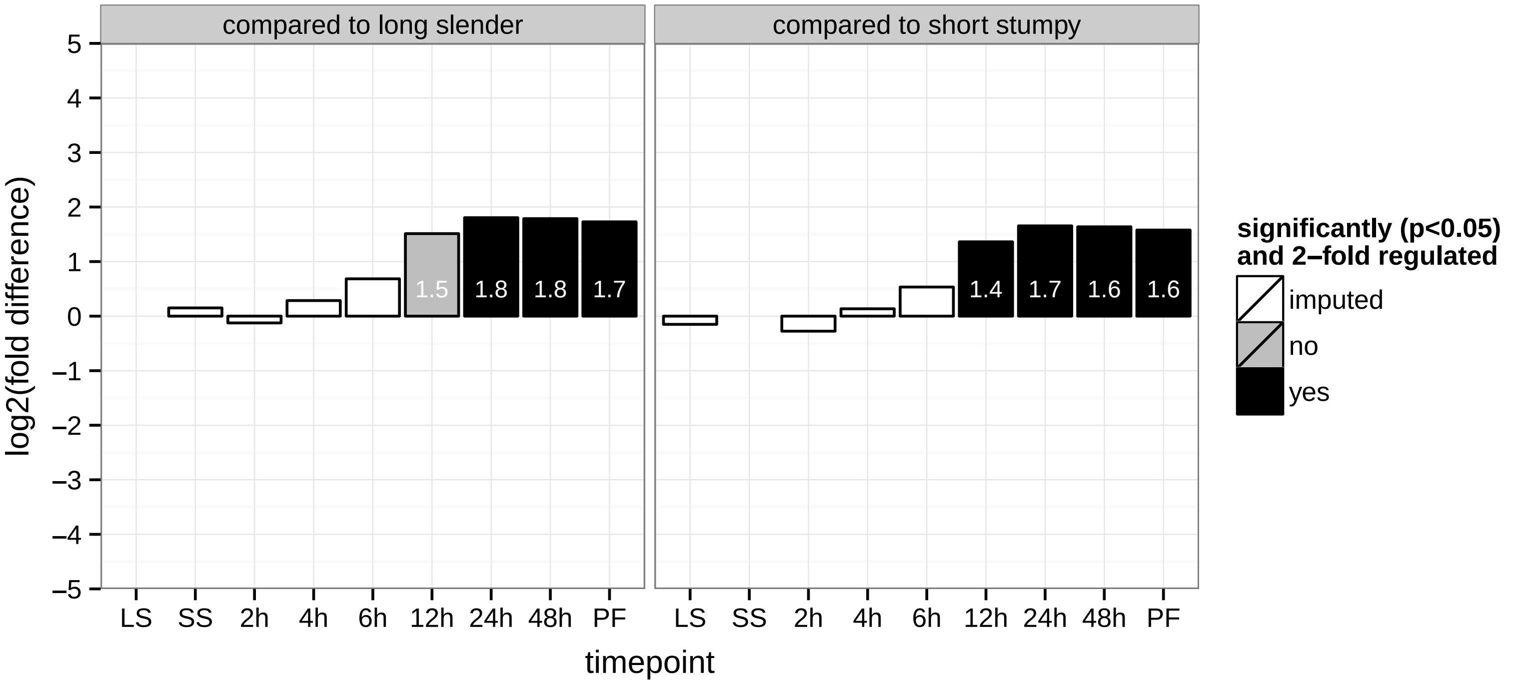
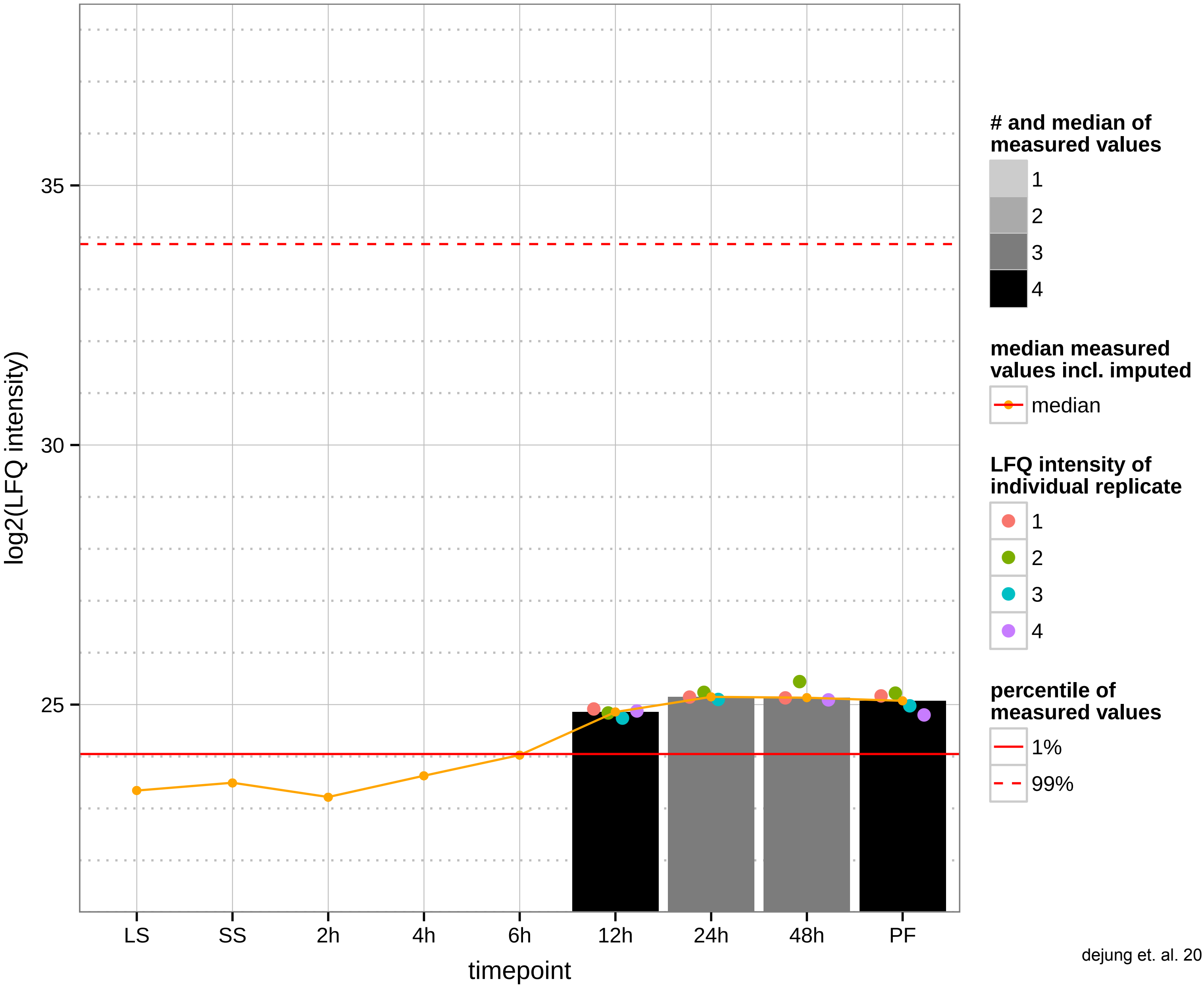
peroxin 13, SH3 domain protein, conserved (PEX13)
Tb927.10.14720
AGOF: null
AGOC: glycosome membrane
AGOP: peroxisomal membrane transport, peroxisome organization
PGOF: protein binding
PGOC: null
PGOP: null





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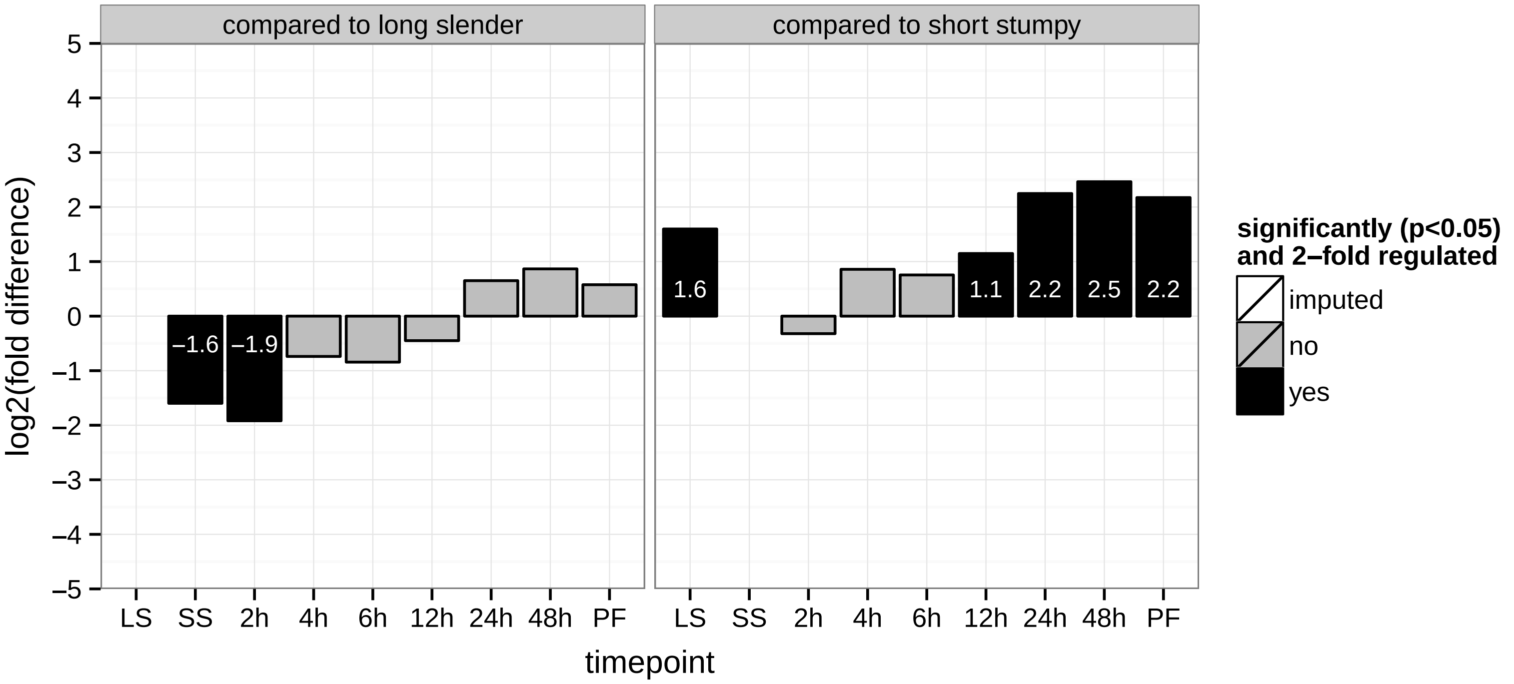
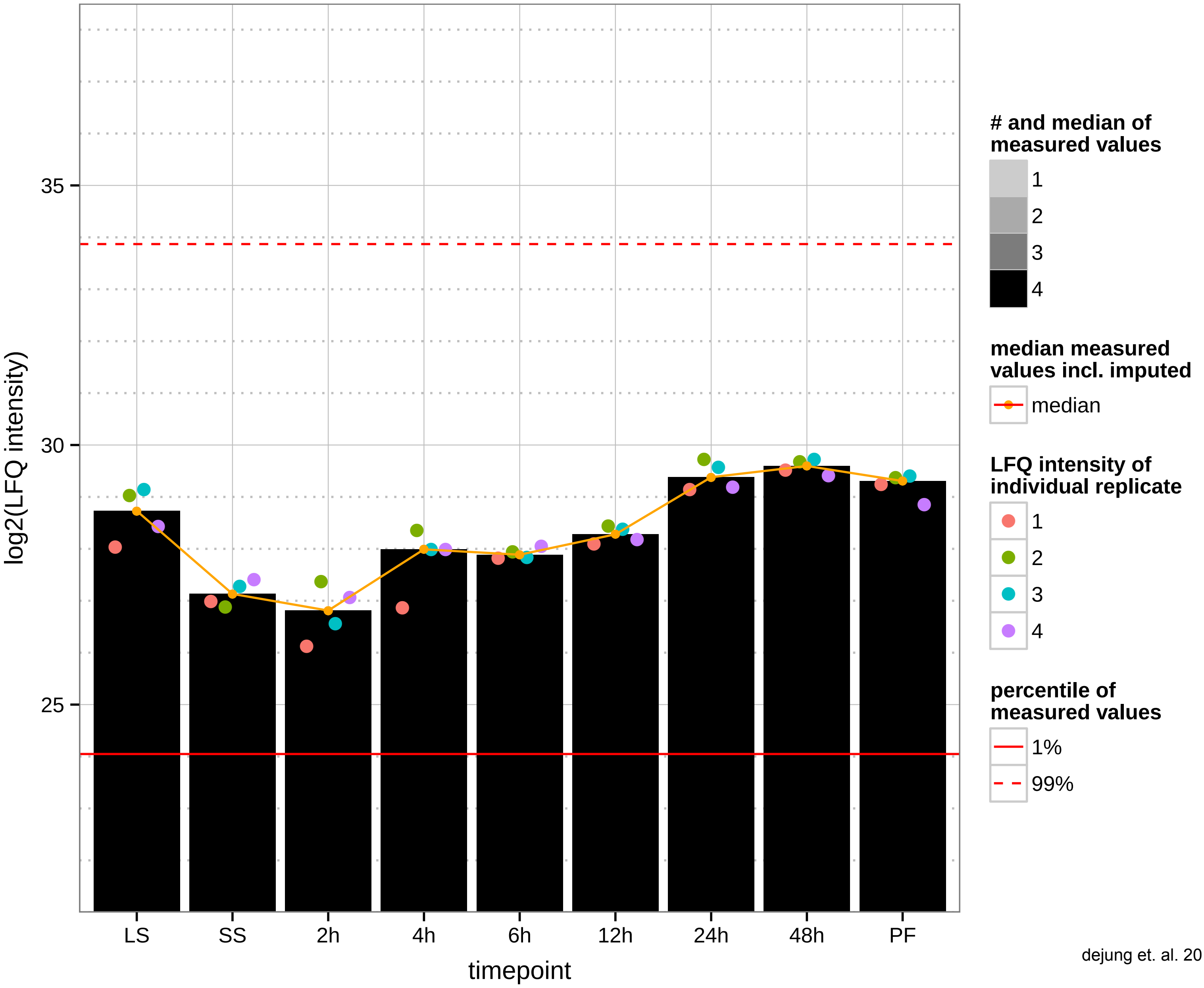
Multiprotein−bridging factor 1, putative (mbf1)
Tb927.10.14810
AGOF: DNA binding, sequence−specific DNA binding, transcription coactivator activity
AGOC: null
AGOP: positive regulation of transcription from RNA polymerase II promoter
PGOF: DNA binding, sequence−specific DNA binding
PGOC: null
PGOP: null





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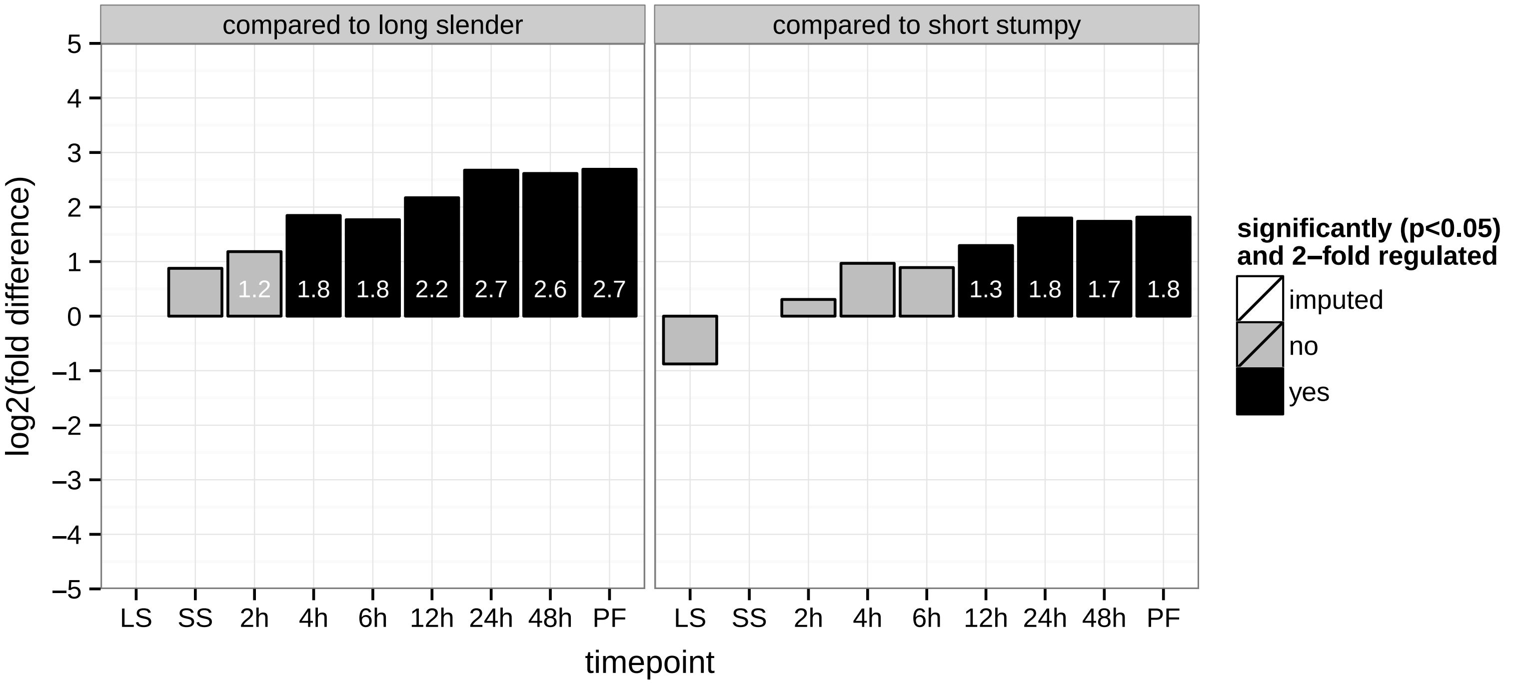
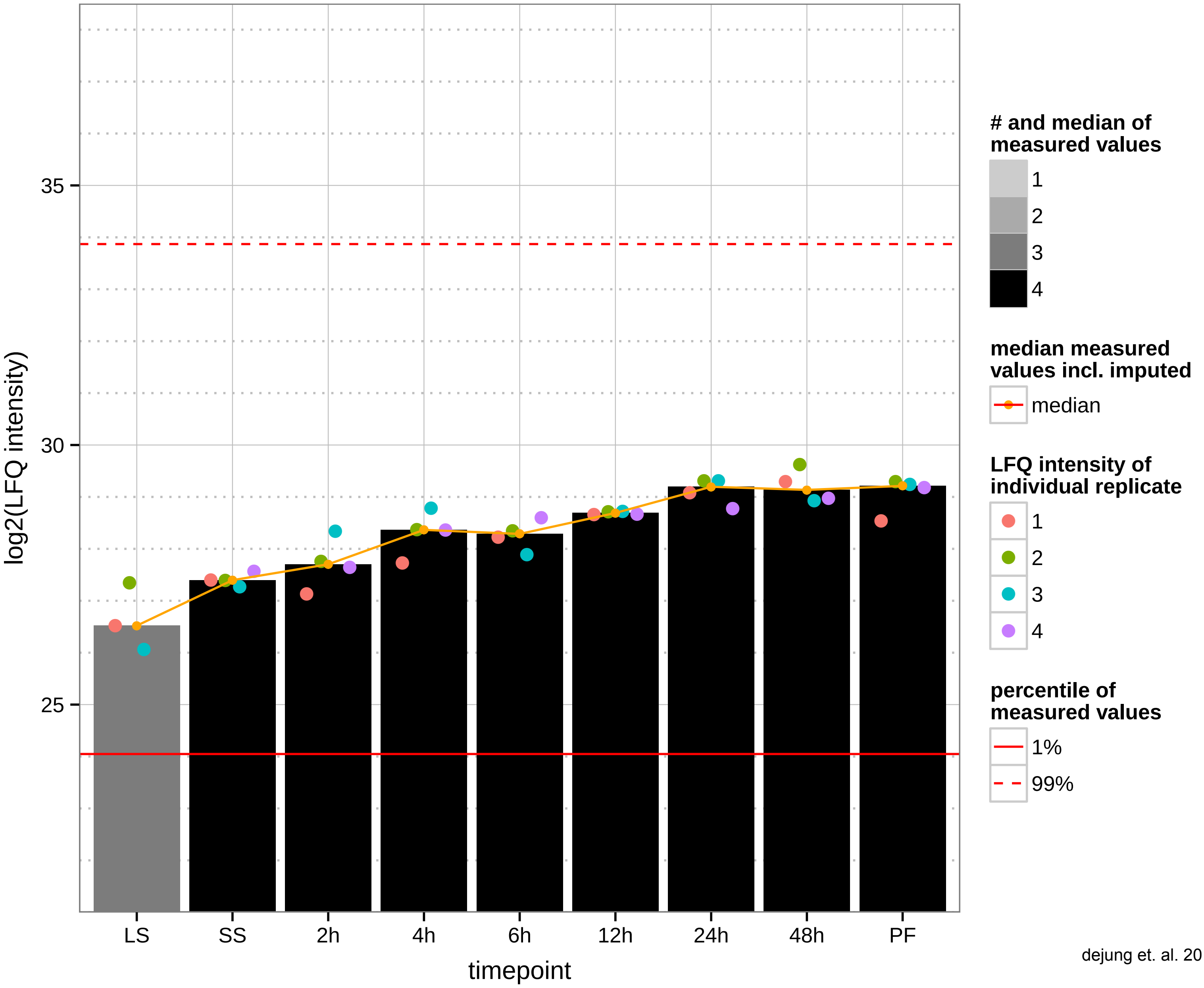
Zinc finger CCCH domain–containing protein 39 (ZC3H39)
Tb927.10.14930
AGOF: RNA binding, ubiquitin–protein ligase activity
AGOC: ubiquitin ligase complex
AGOP: protein ubiquitination
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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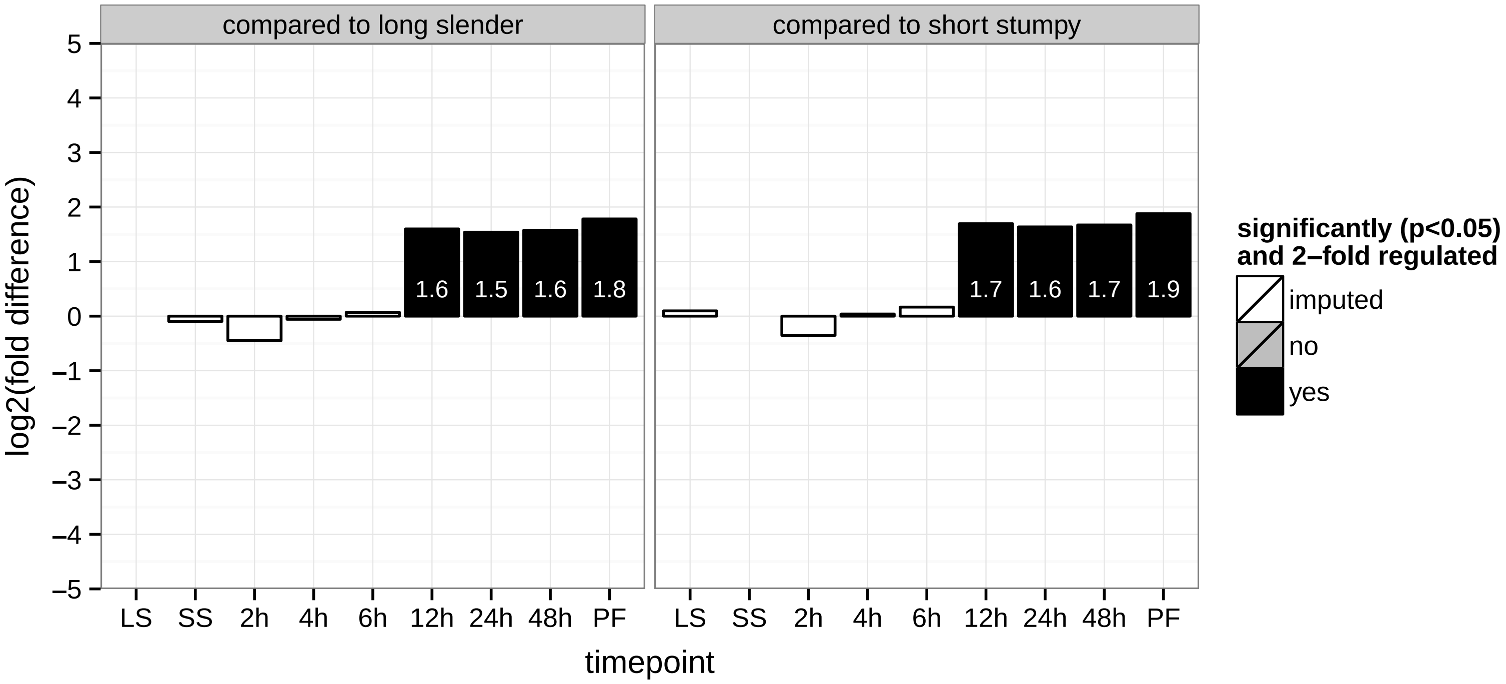
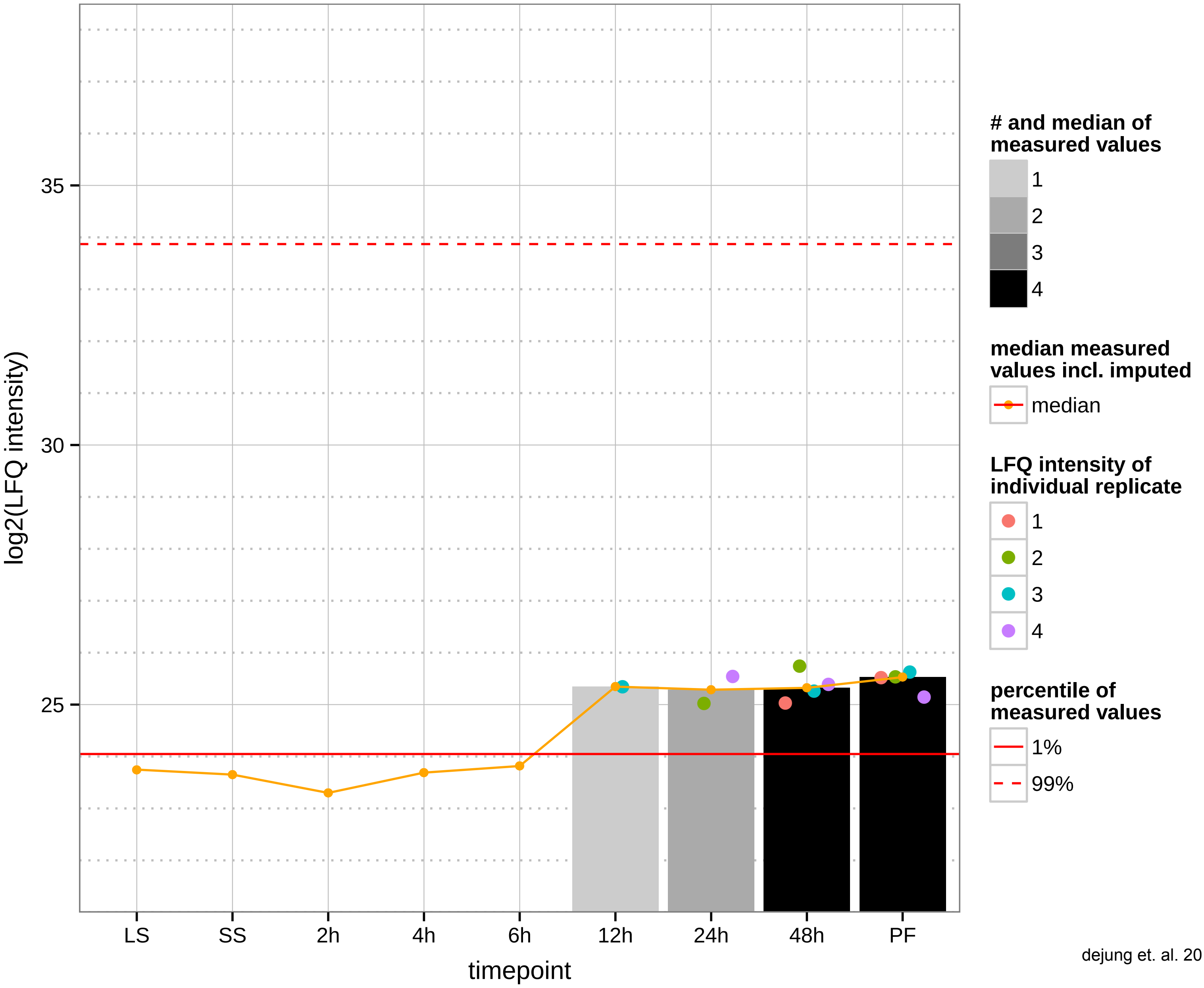
zinc finger protein family member, putative (ZC3H30)
Tb927.10.1540
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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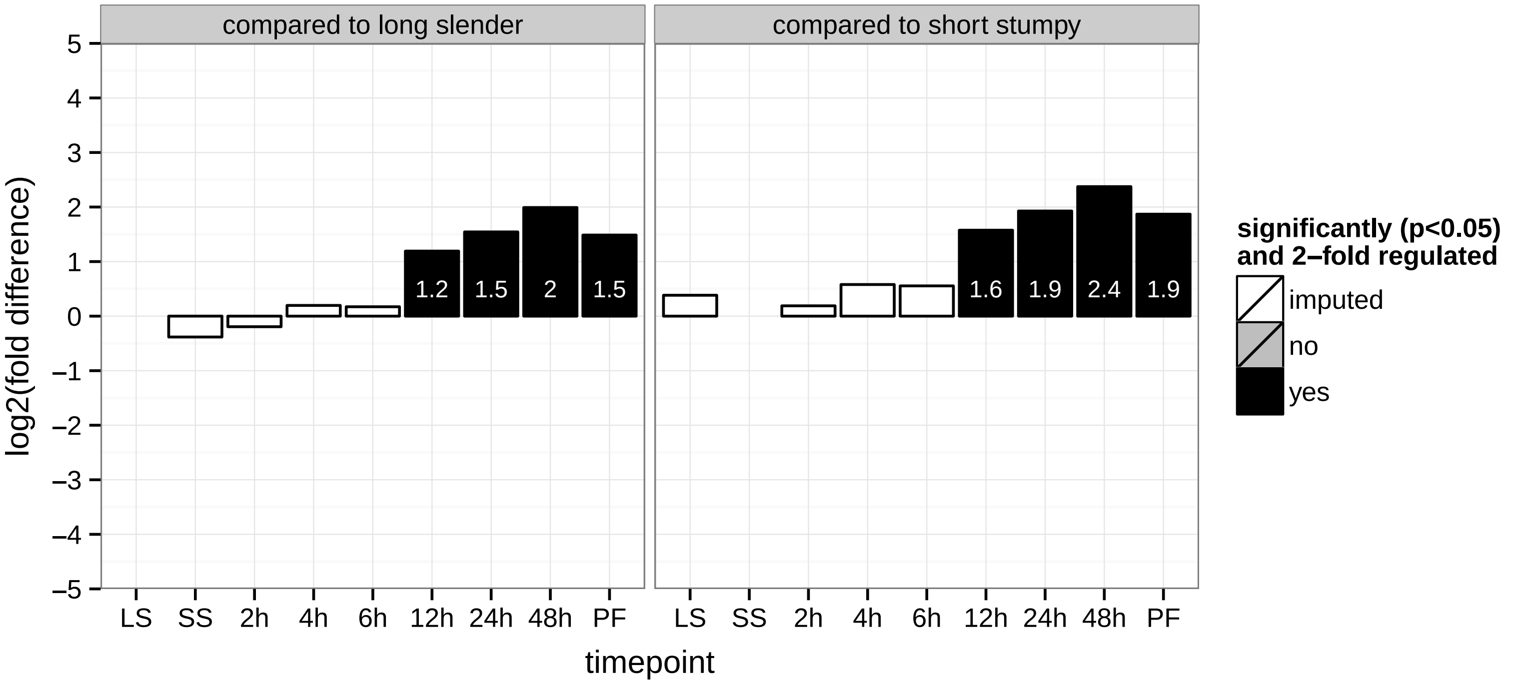
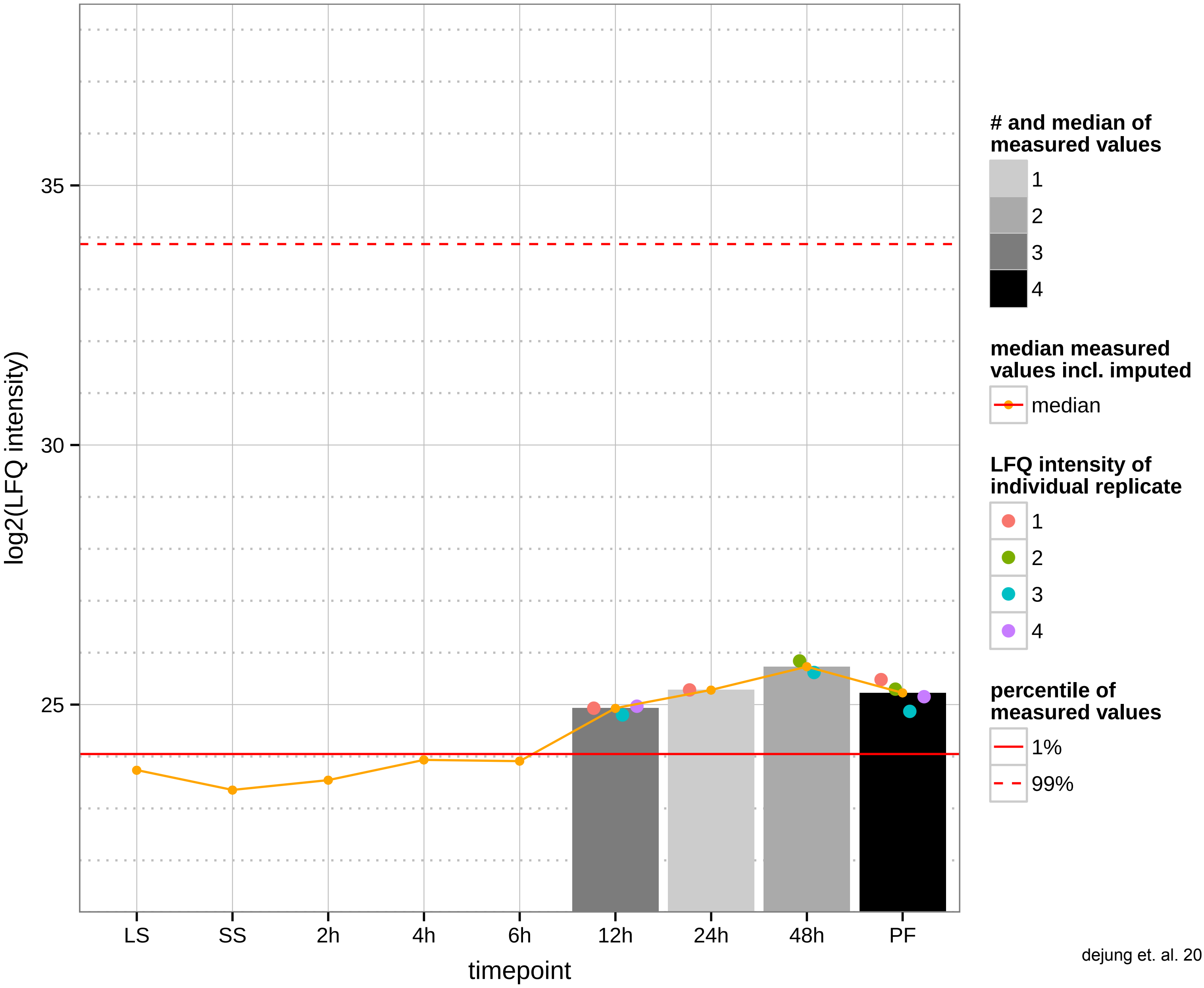
hypothetical protein, conserved
Tb927.10.2060
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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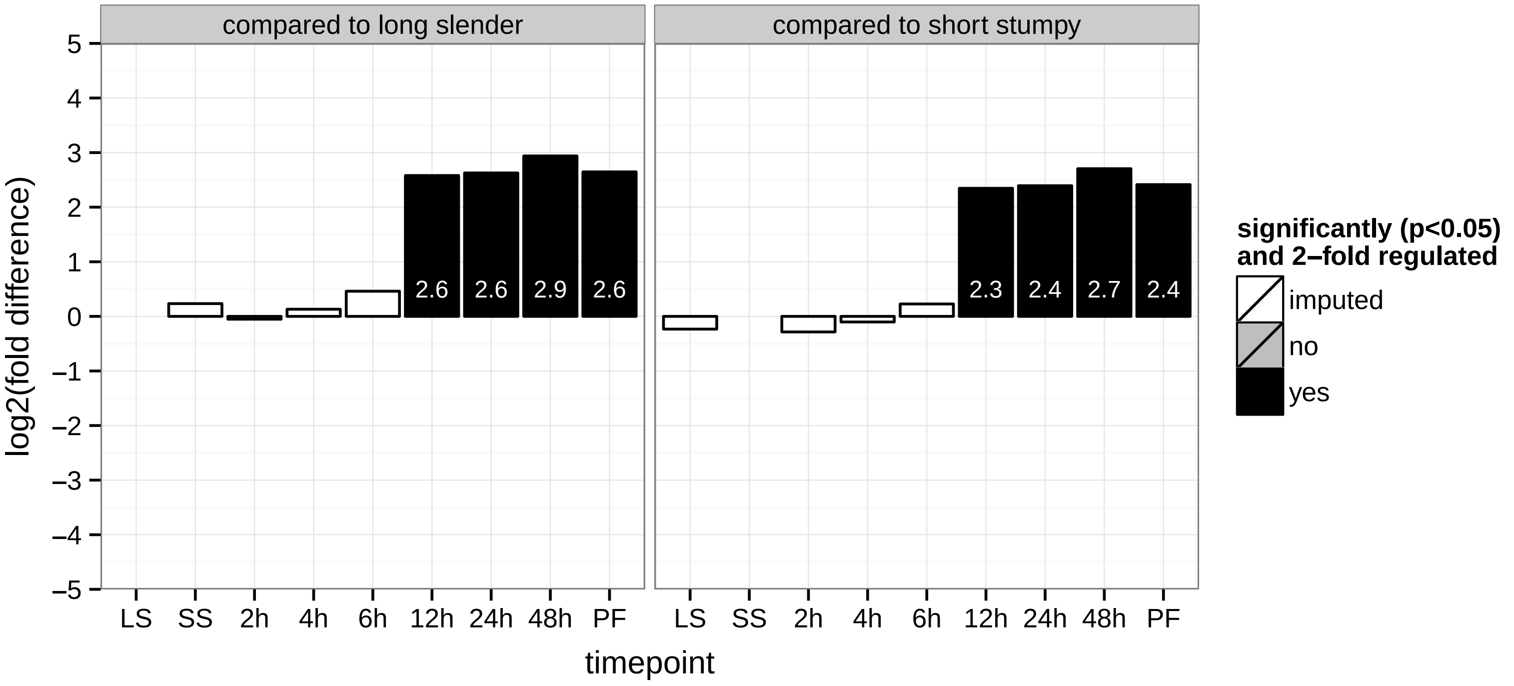
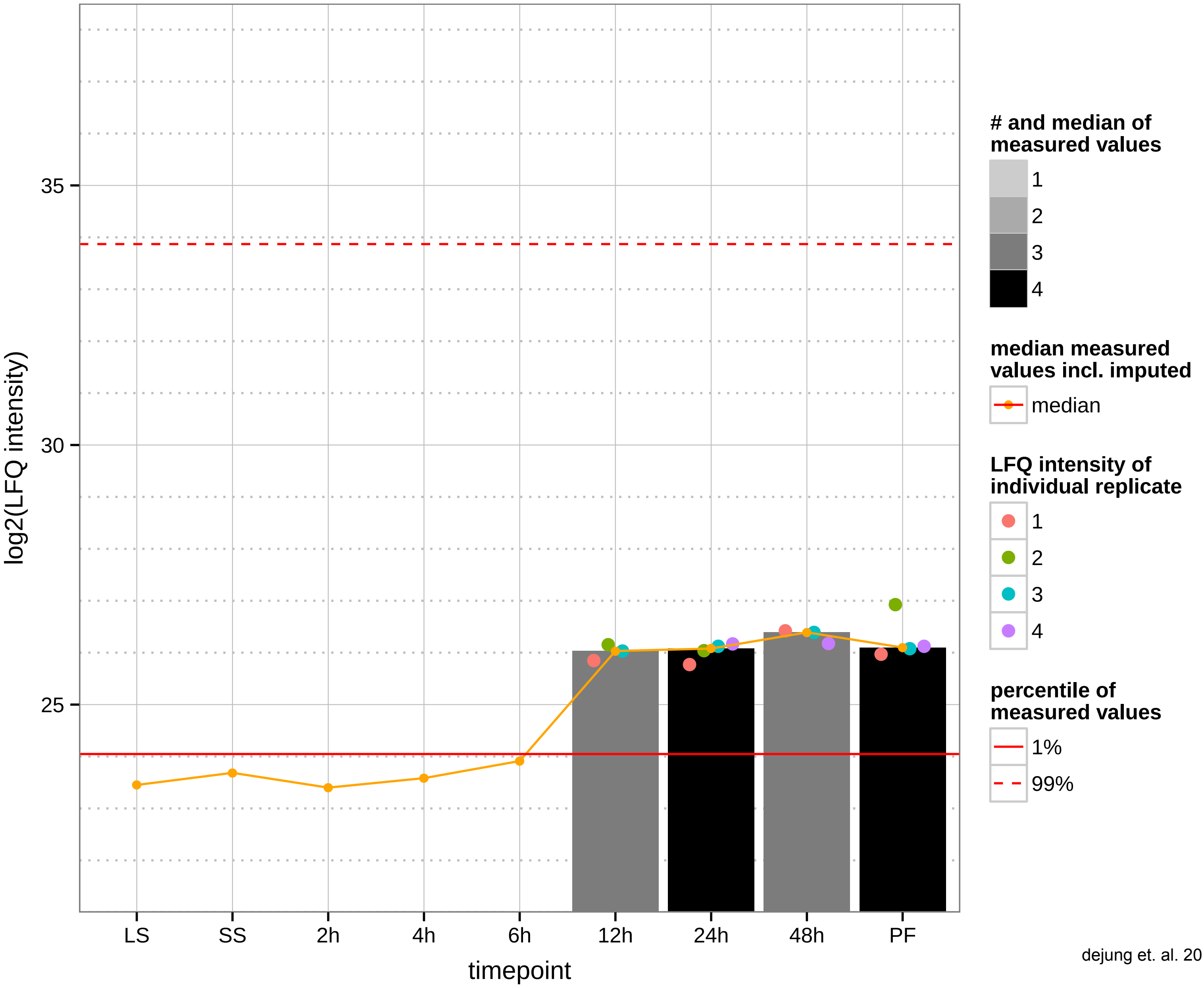
pumillio/PUF RNA binding protein 3 (PUF3)
Tb927.10.310
AGOF: RNA binding
AGOC: null
AGOP: mRNA metabolic process
PGOF: RNA binding, binding
PGOC: null
PGOP: null





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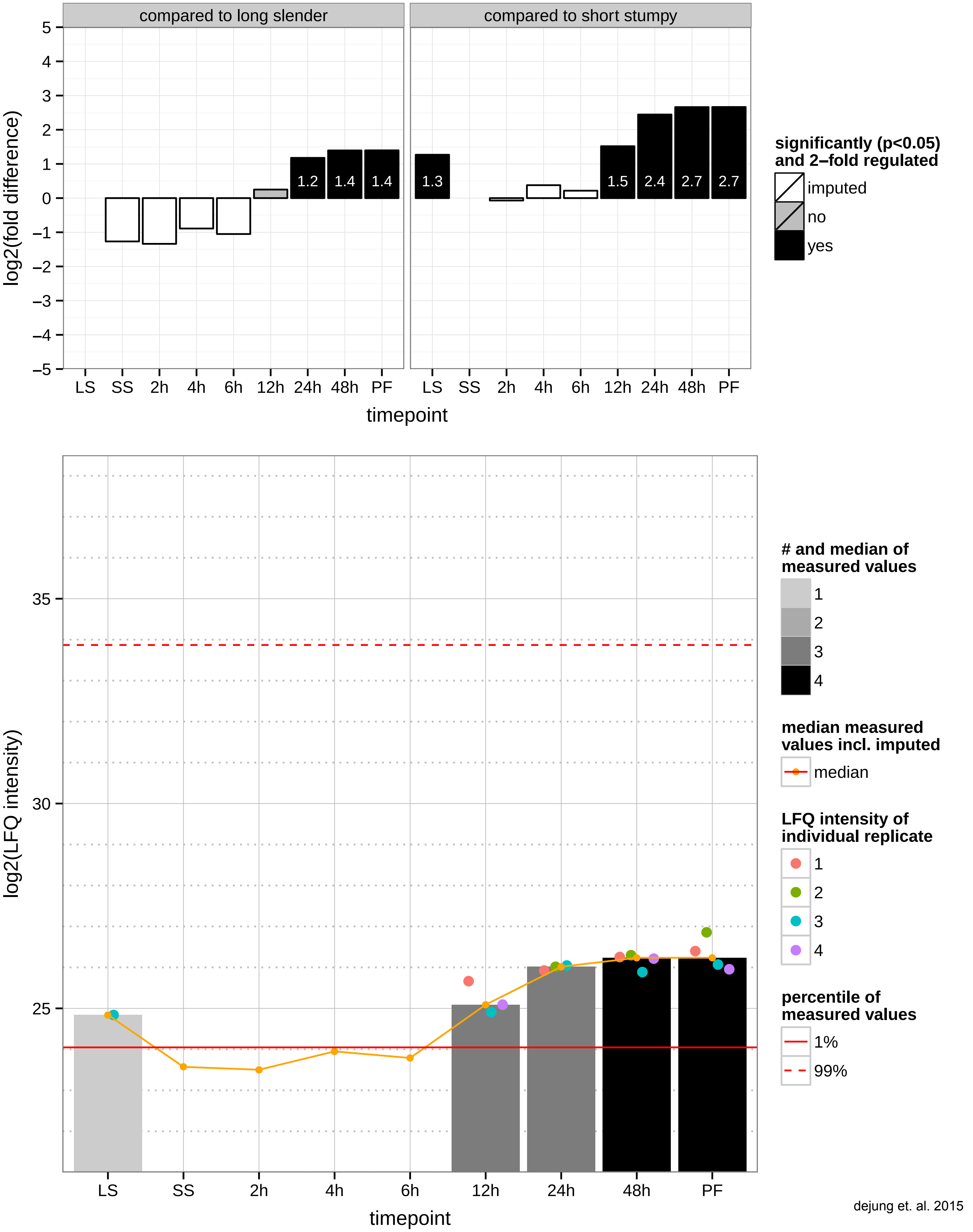
hypothetical protein, conserved
Tb927.10.3250
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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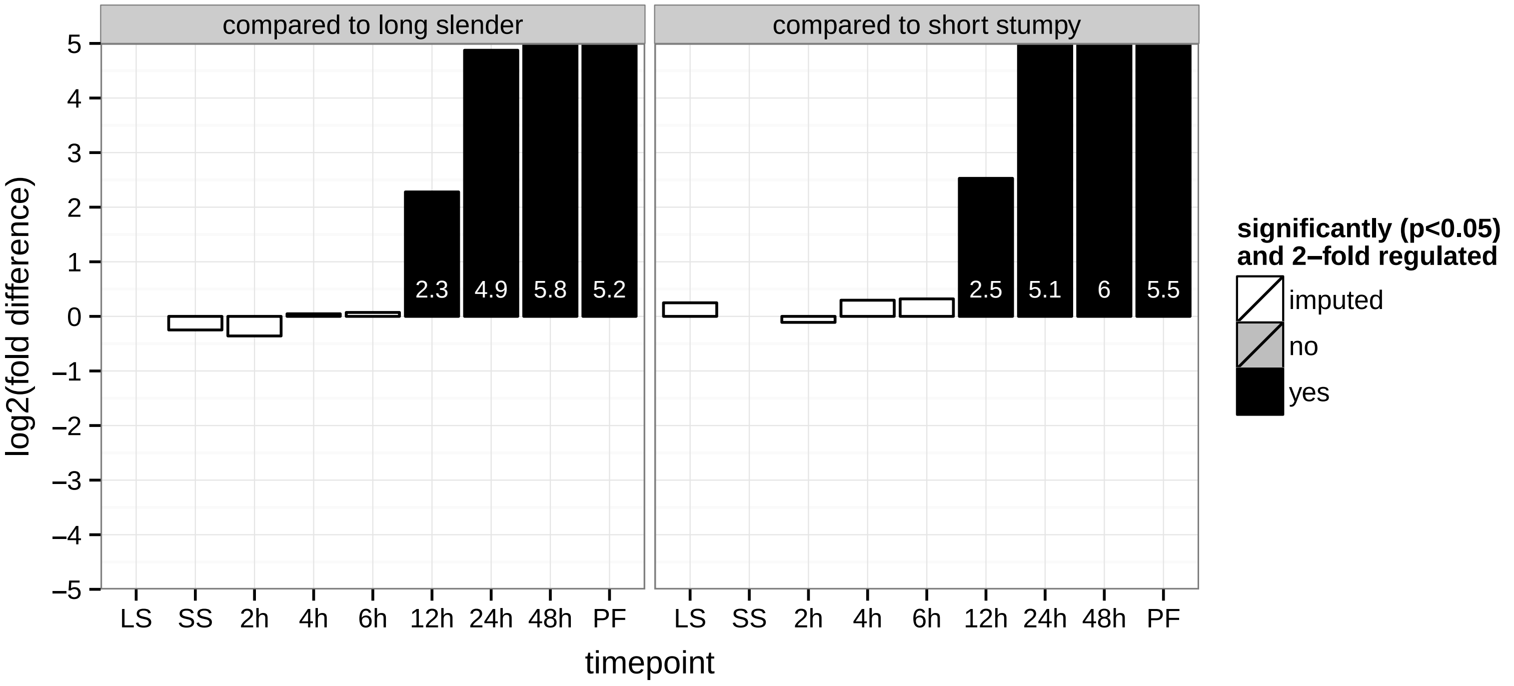
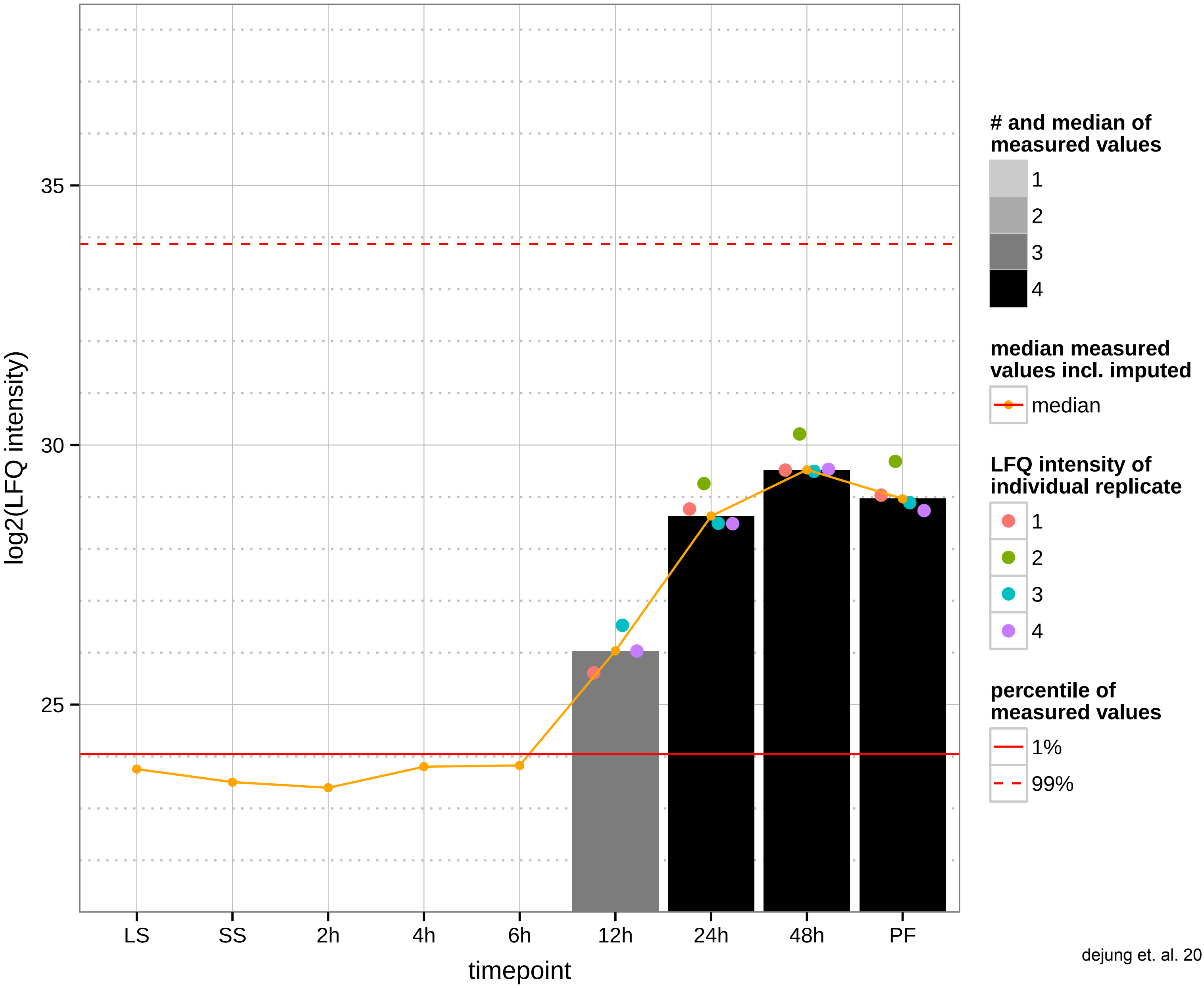
hypothetical protein, conserved
Tb927.10.4240
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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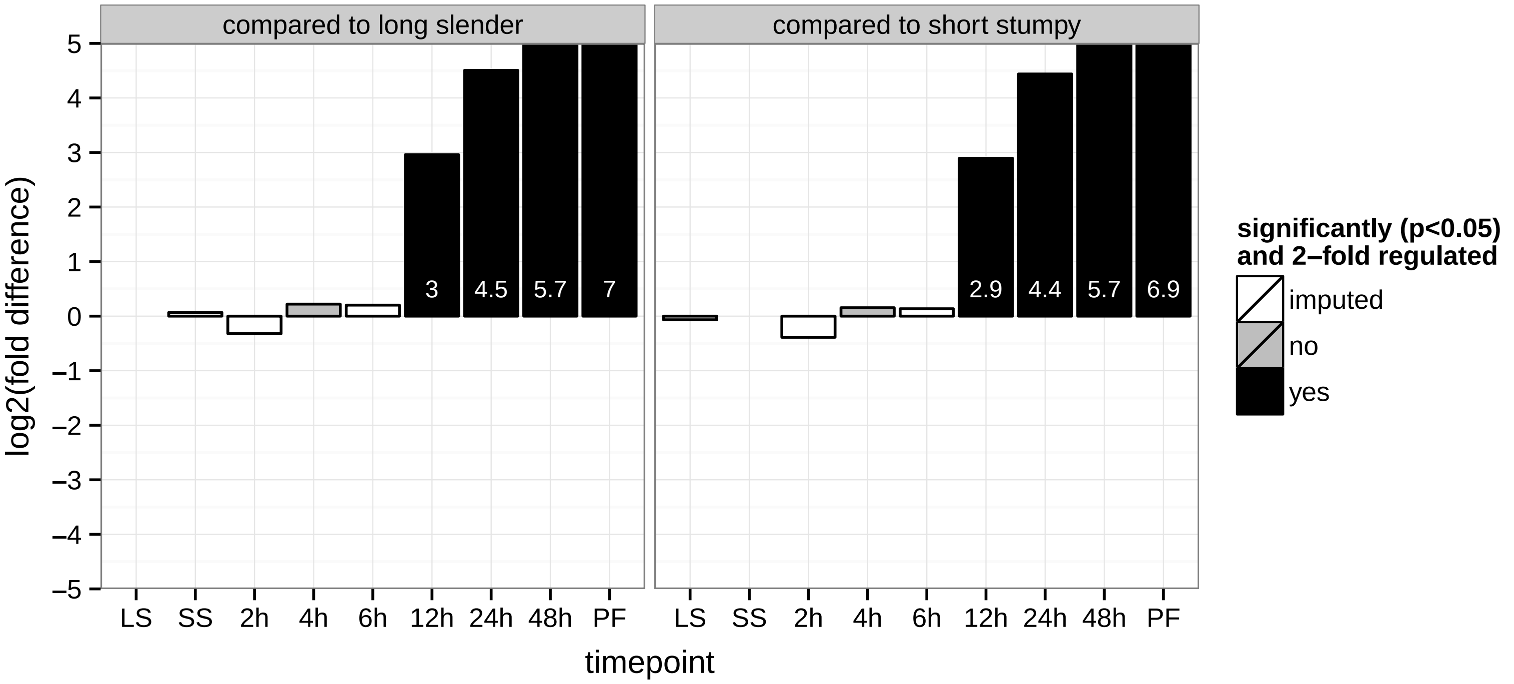
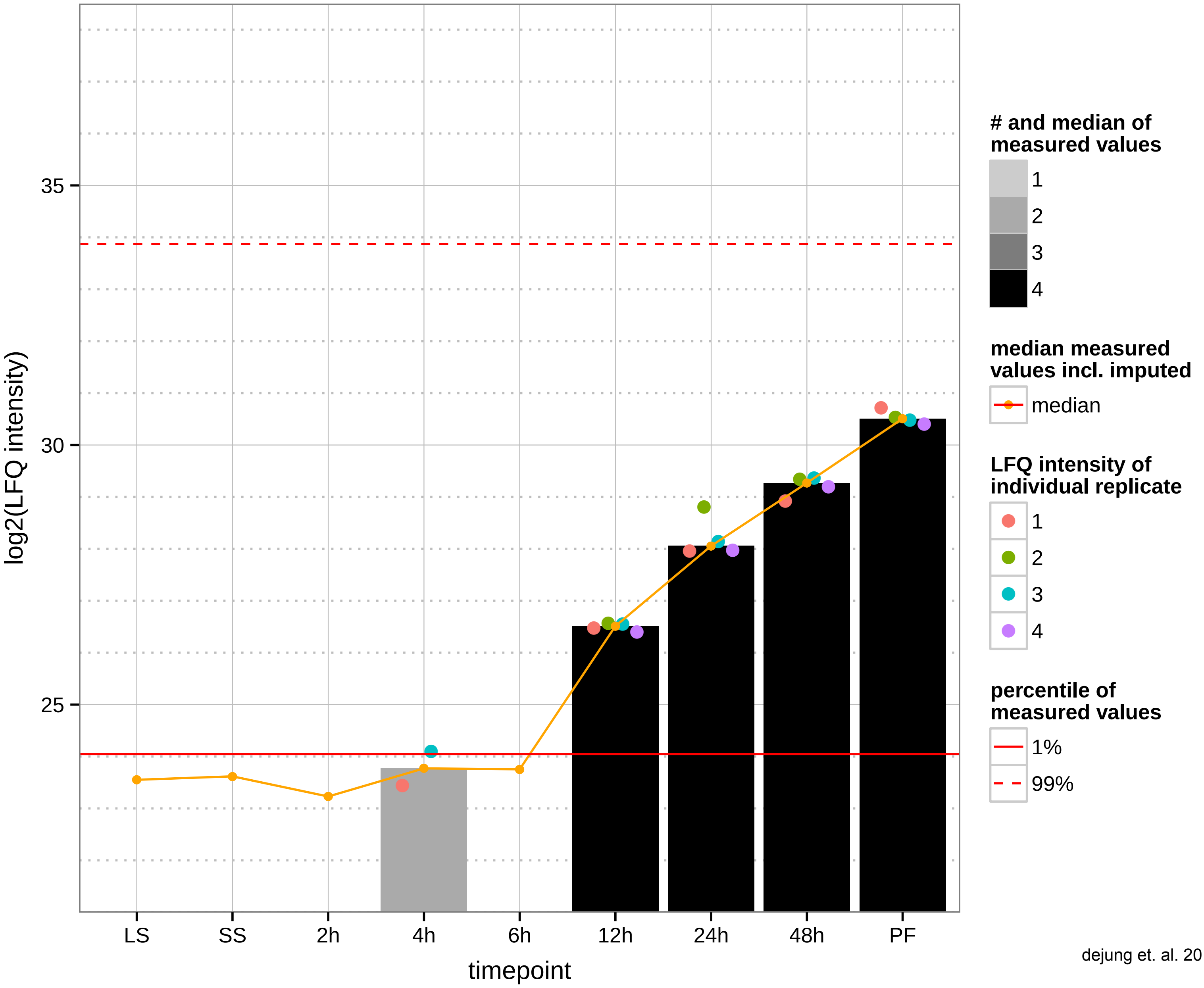
hypothetical protein, conserved
Tb927.10.4280
AGOF: ubiquinol–cytochrome–c reductase activity
AGOC: mitochondrion
AGOP: mitochondrial electron transport, ubiquinol to cytochrome c
PGOF: ubiquinol–cytochrome–c reductase activity
PGOC: null
PGOP: mitochondrial electron transport, ubiquinol to cytochrome c





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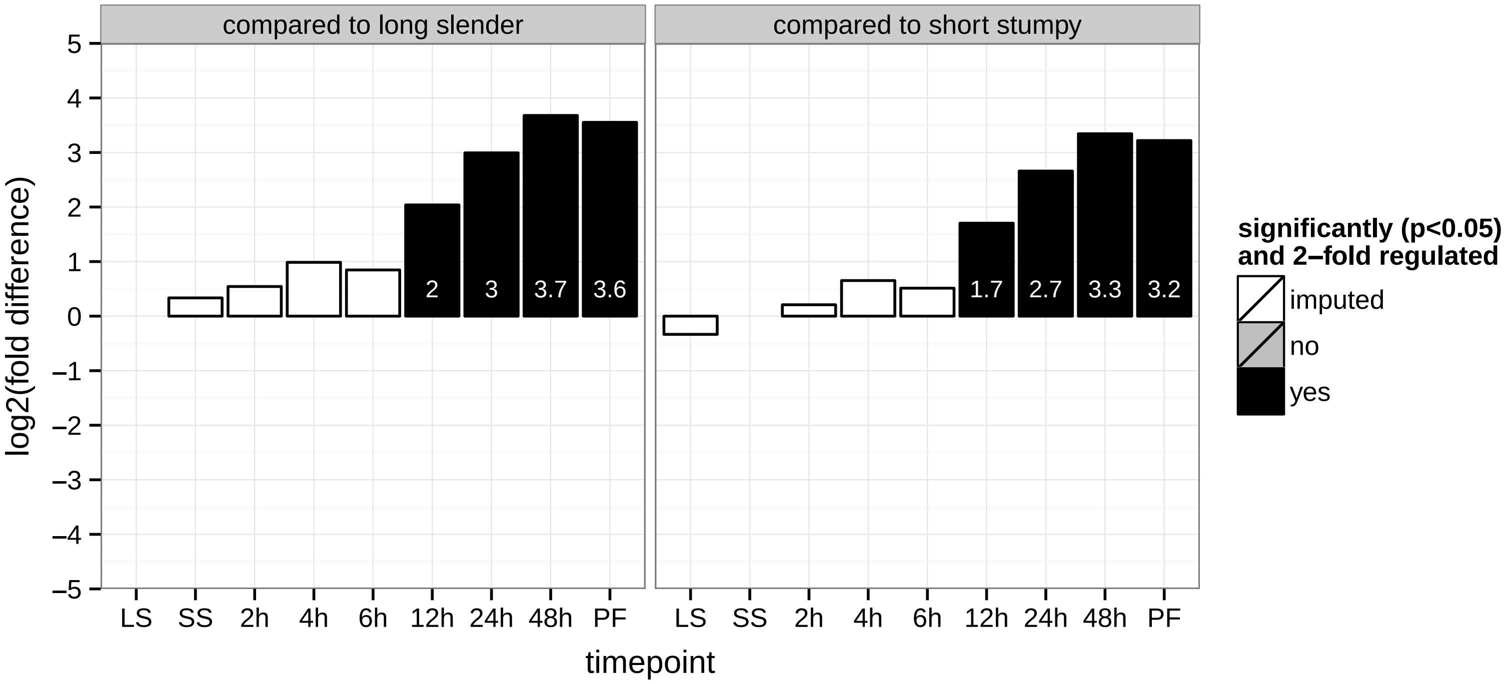
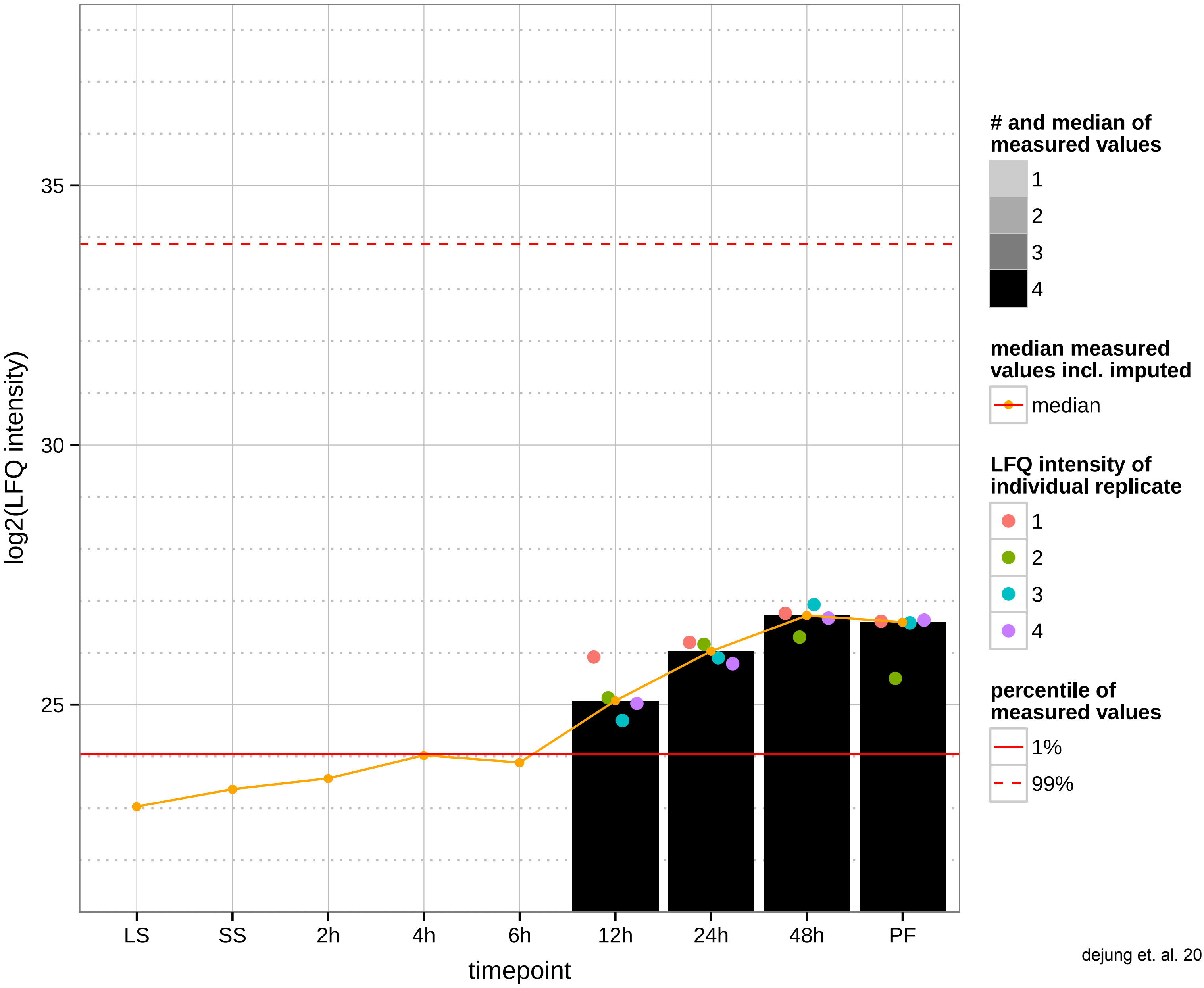
hypothetical protein, conserved
Tb927.10.430
AGOF: heme binding, peroxidase activity
AGOC: mitochondrion
AGOP: response to oxidative stress
PGOF: heme binding, peroxidase activity
PGOC: null
PGOP: oxidation–reduction process, response to oxidative stress





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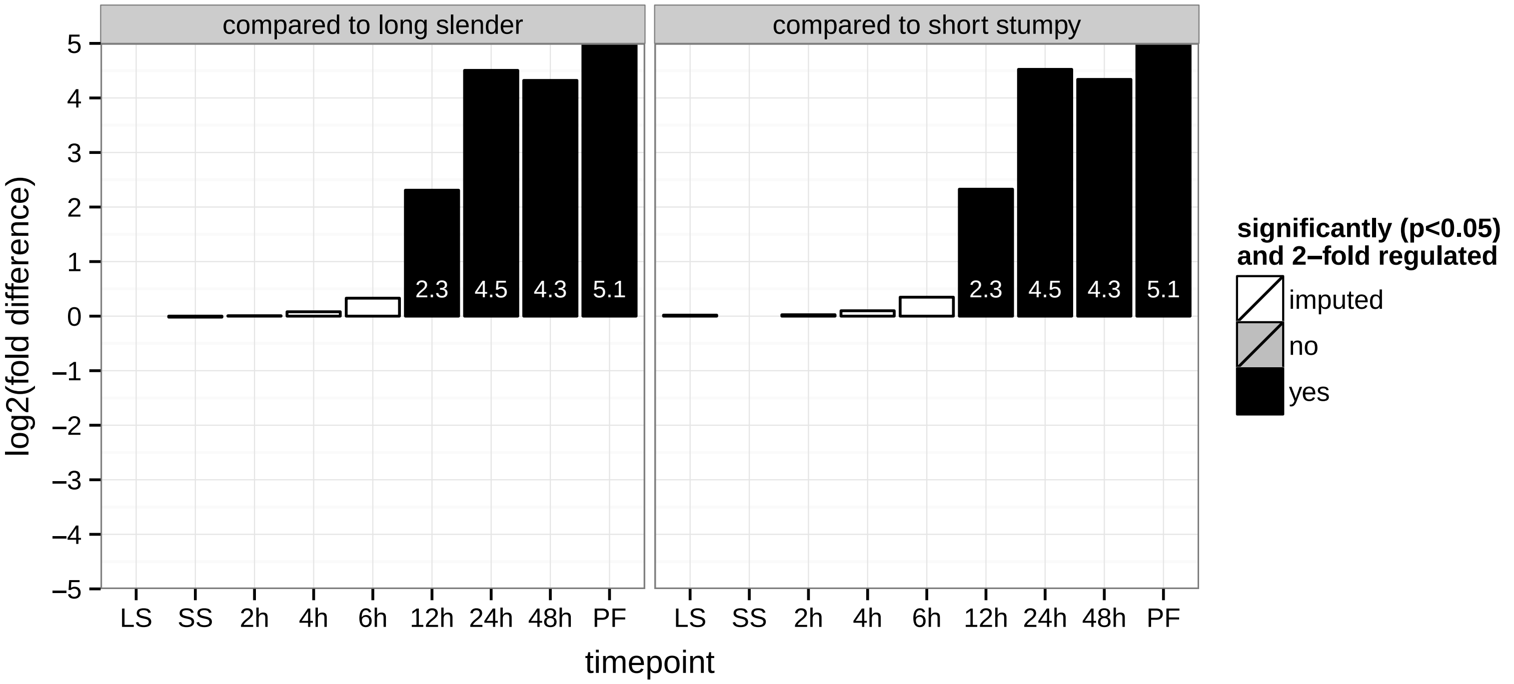
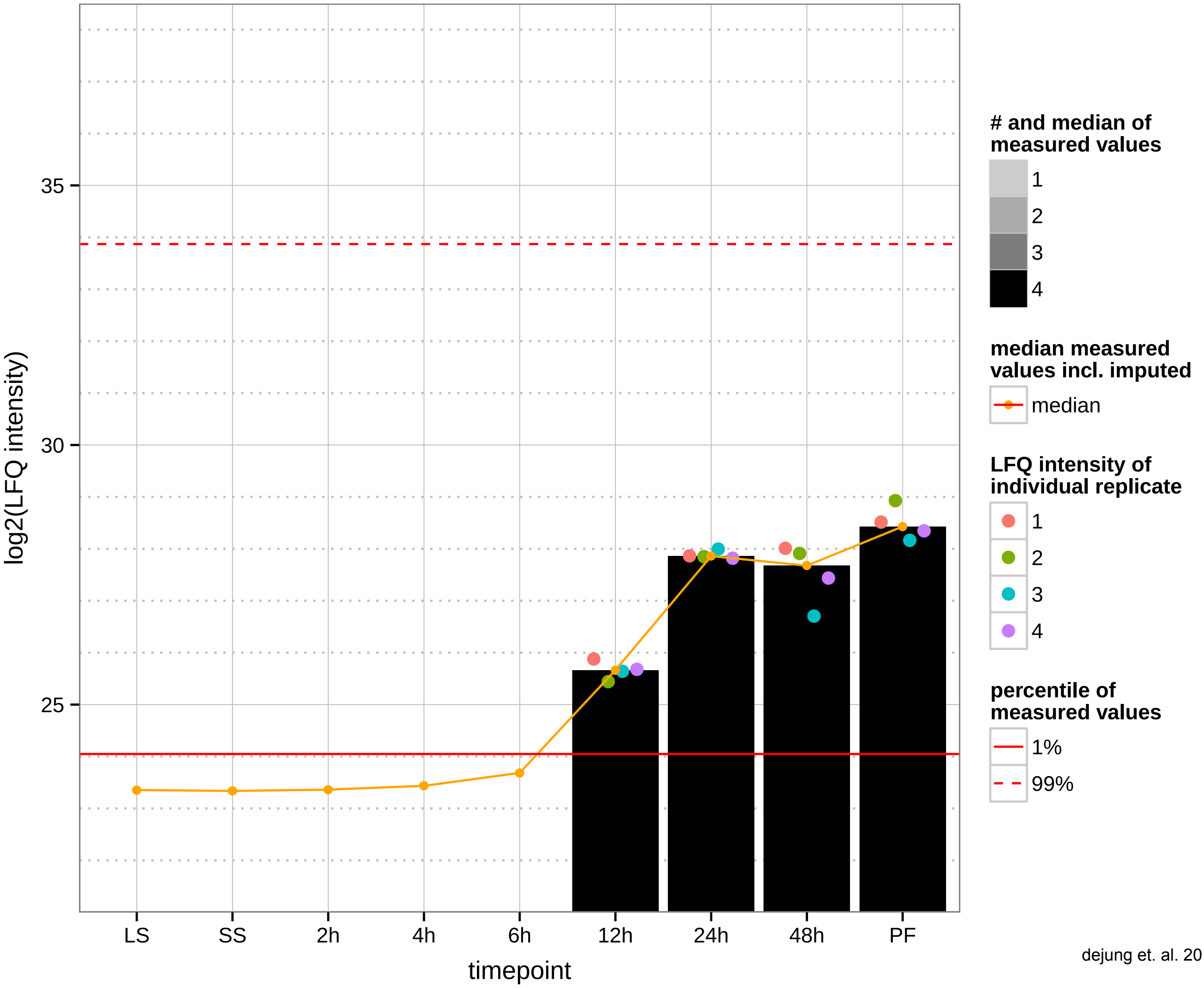
hypothetical protein, conserved
Tb927.10.4880
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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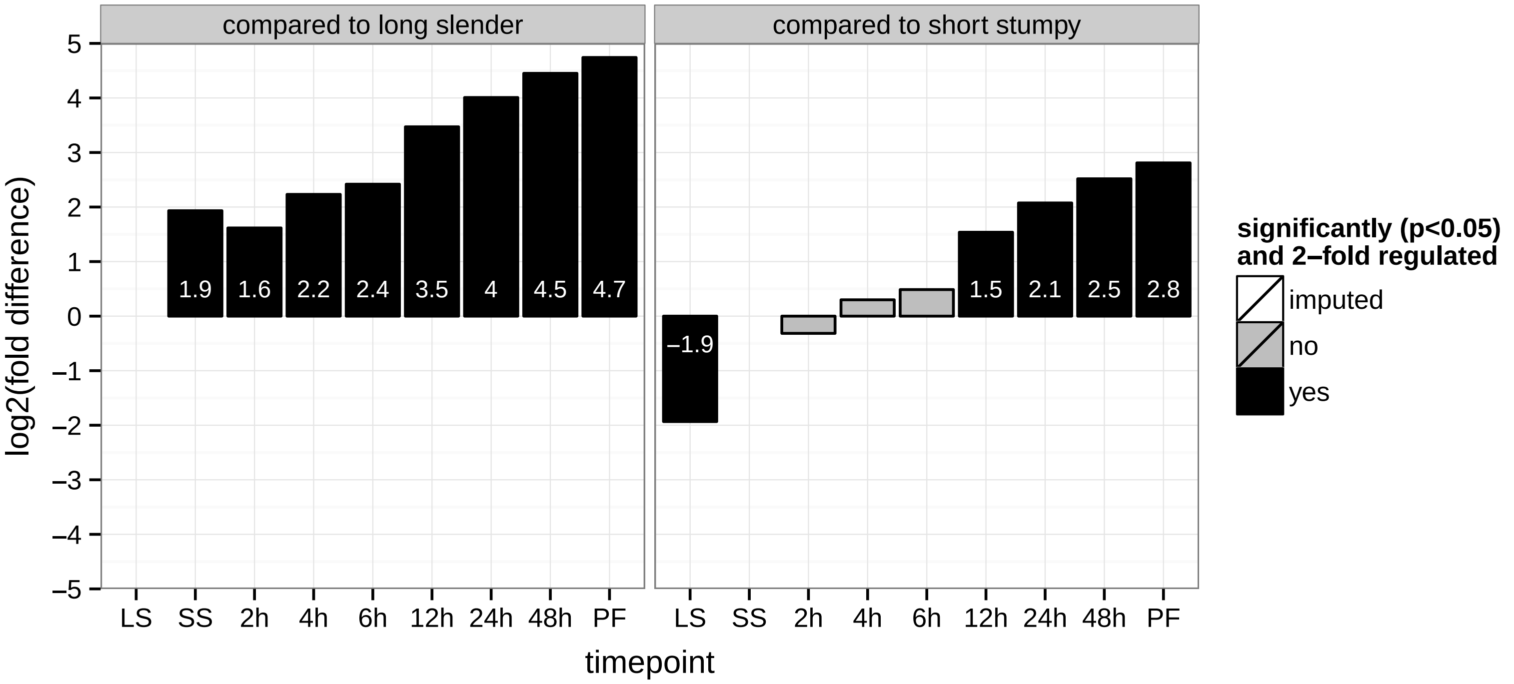
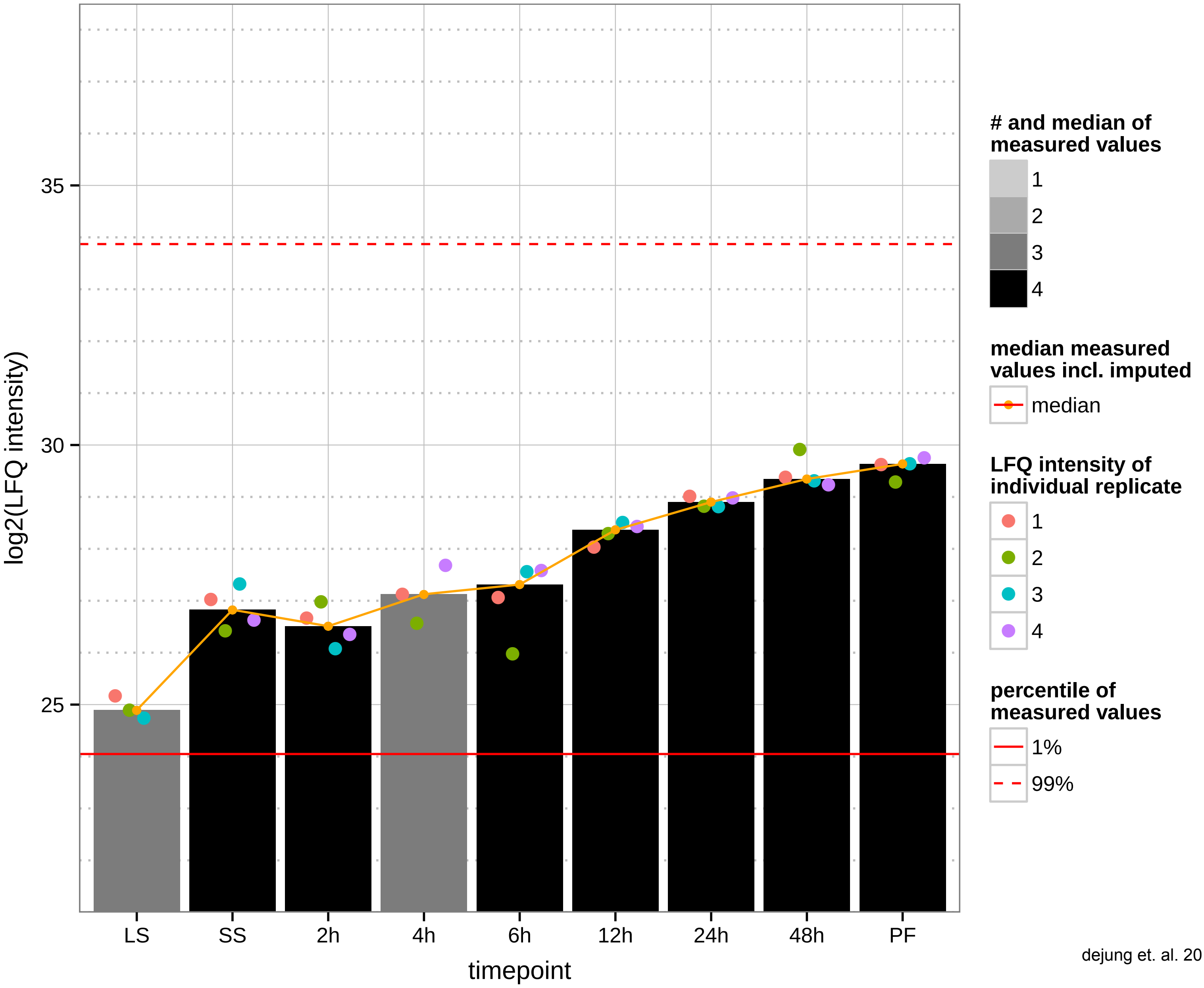
Elongation factor G1, mitochondrial, putative (EF−G1)
Tb927.10.5010
AGOF: GTP binding, GTPase activity, translation elongation factor activity
AGOC: intracellular, mitochondrion
AGOP: growth, oxidative phosphorylation, translational elongation
PGOF: GTP binding, GTPase activity, translation elongation factor activity
PGOC: intracellular
PGOP: translational elongation





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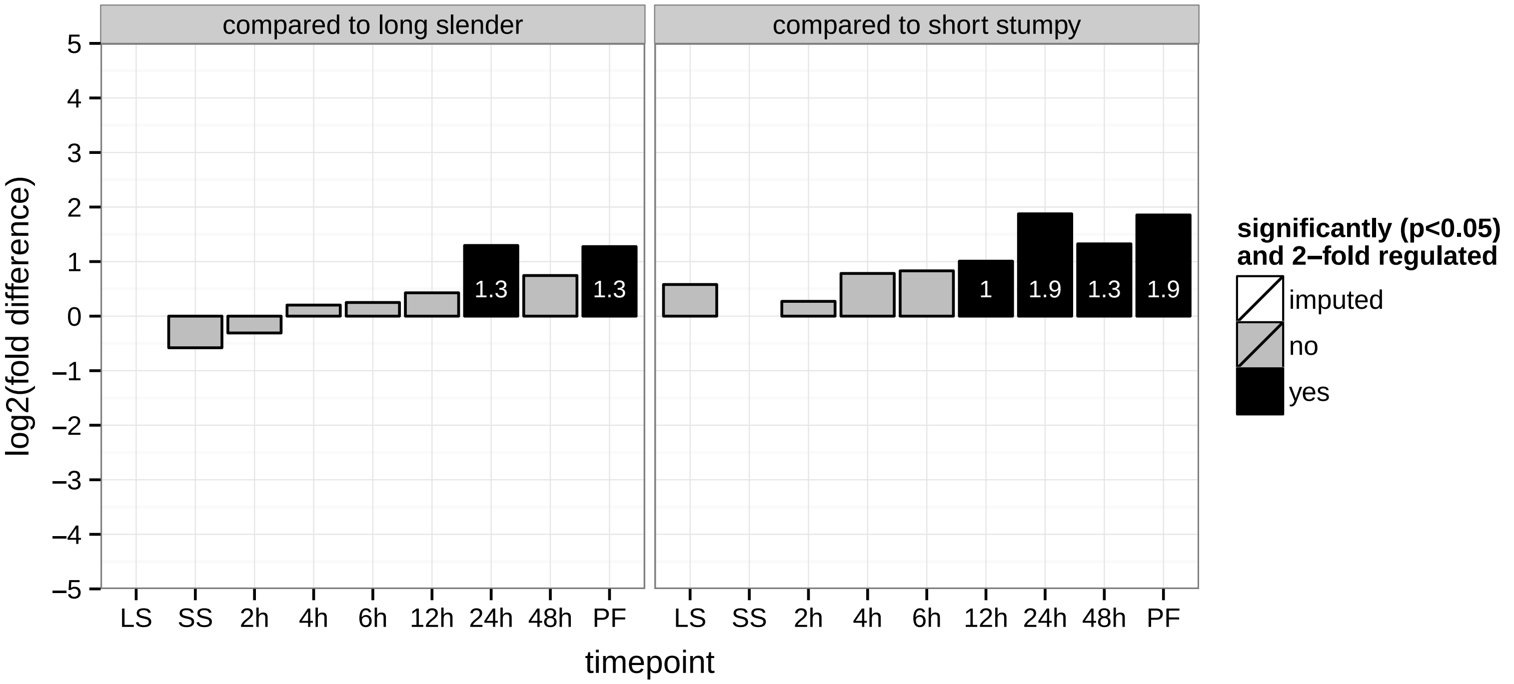
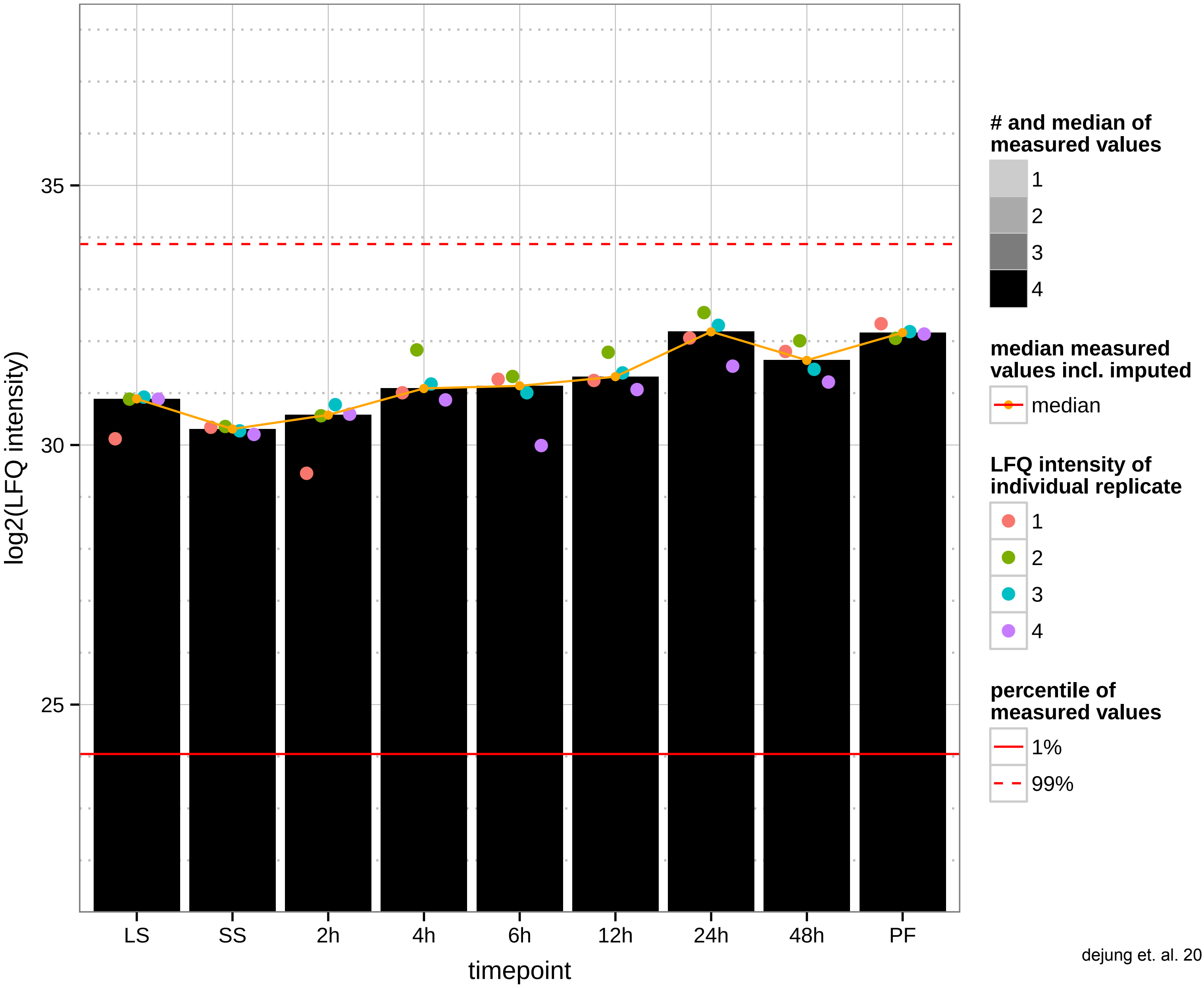
translation elongation factor 1–beta, putative
Tb927.10.5840
AGOF: translation elongation factor activity
AGOC: eukaryotic translation elongation factor 1 complex
AGOP: translational elongation
PGOF: translation elongation factor activity
PGOC: eukaryotic translation elongation factor 1 complex
PGOP: translational elongation





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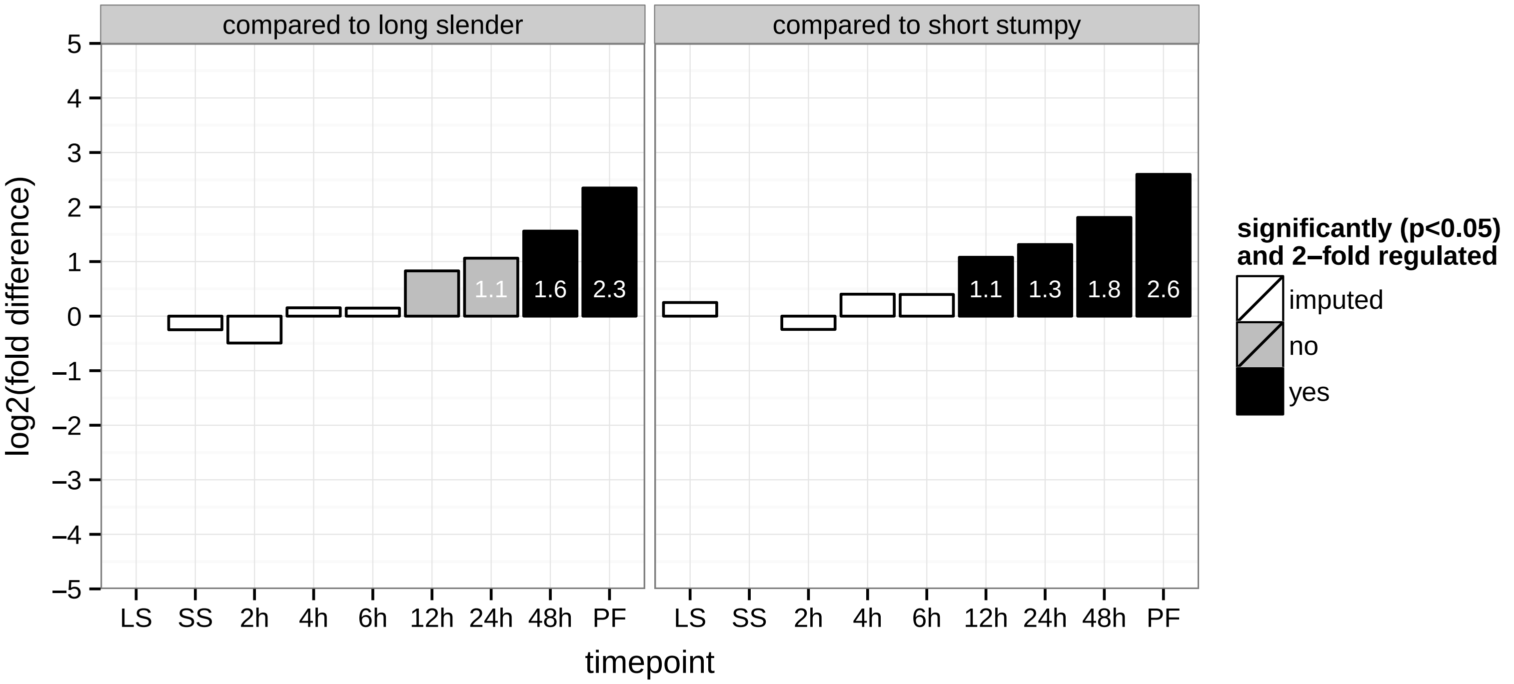
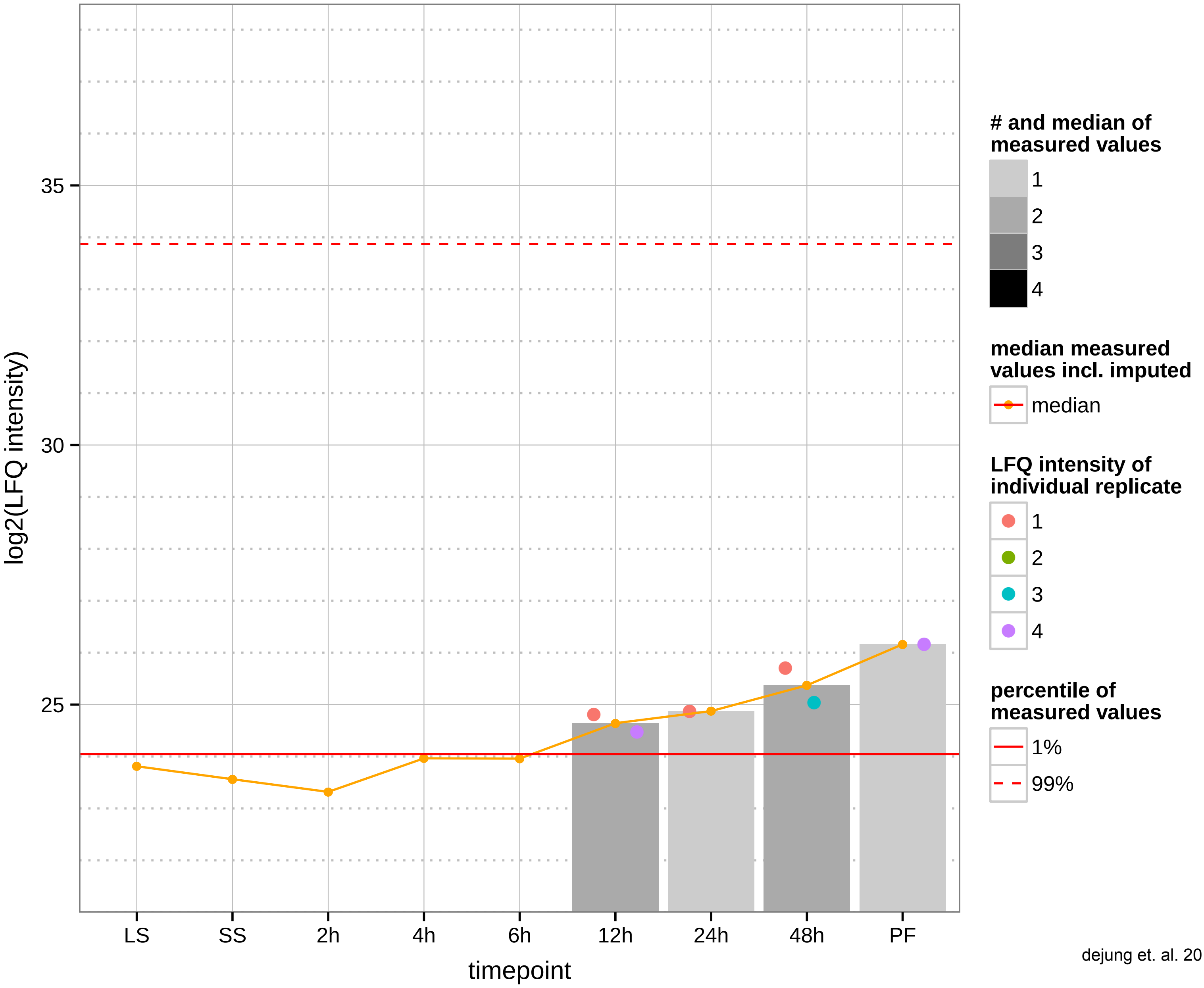
hypothetical protein, conserved
Tb927.10.6020
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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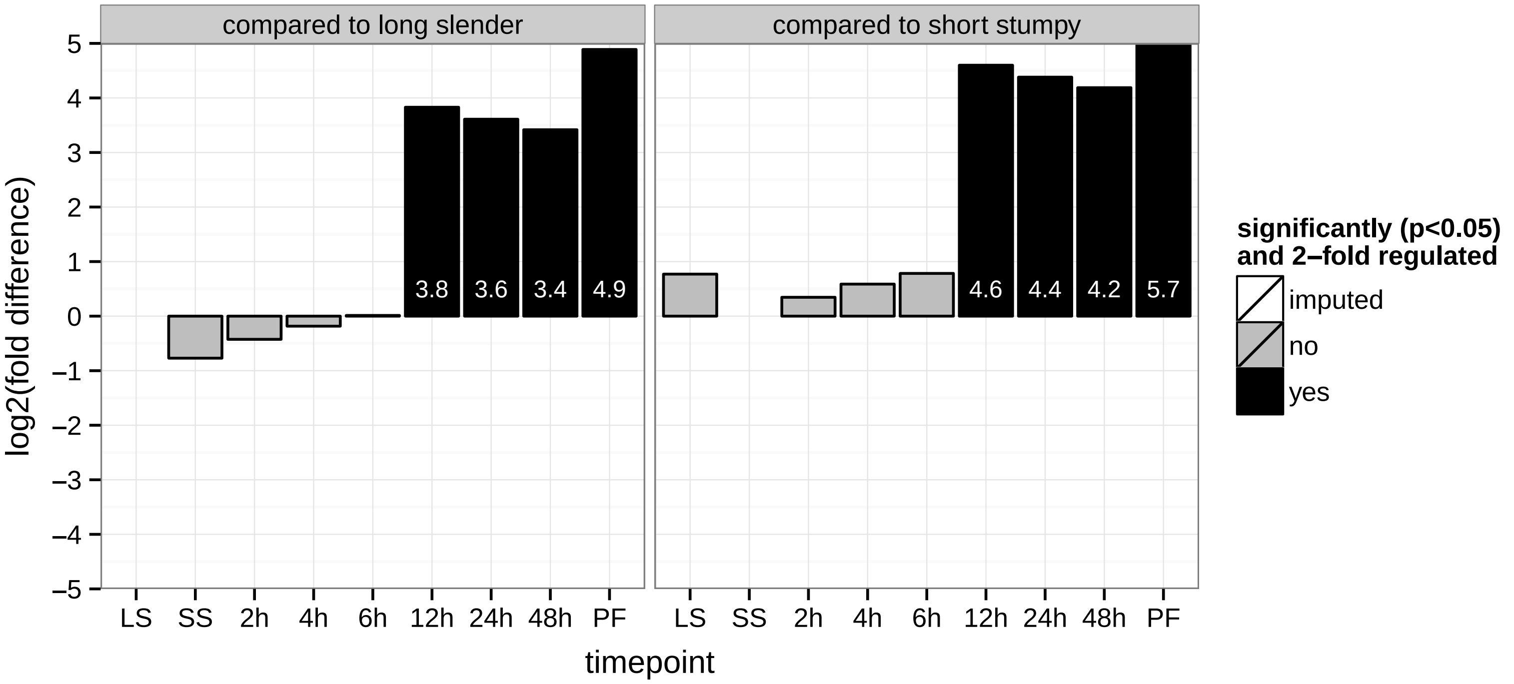
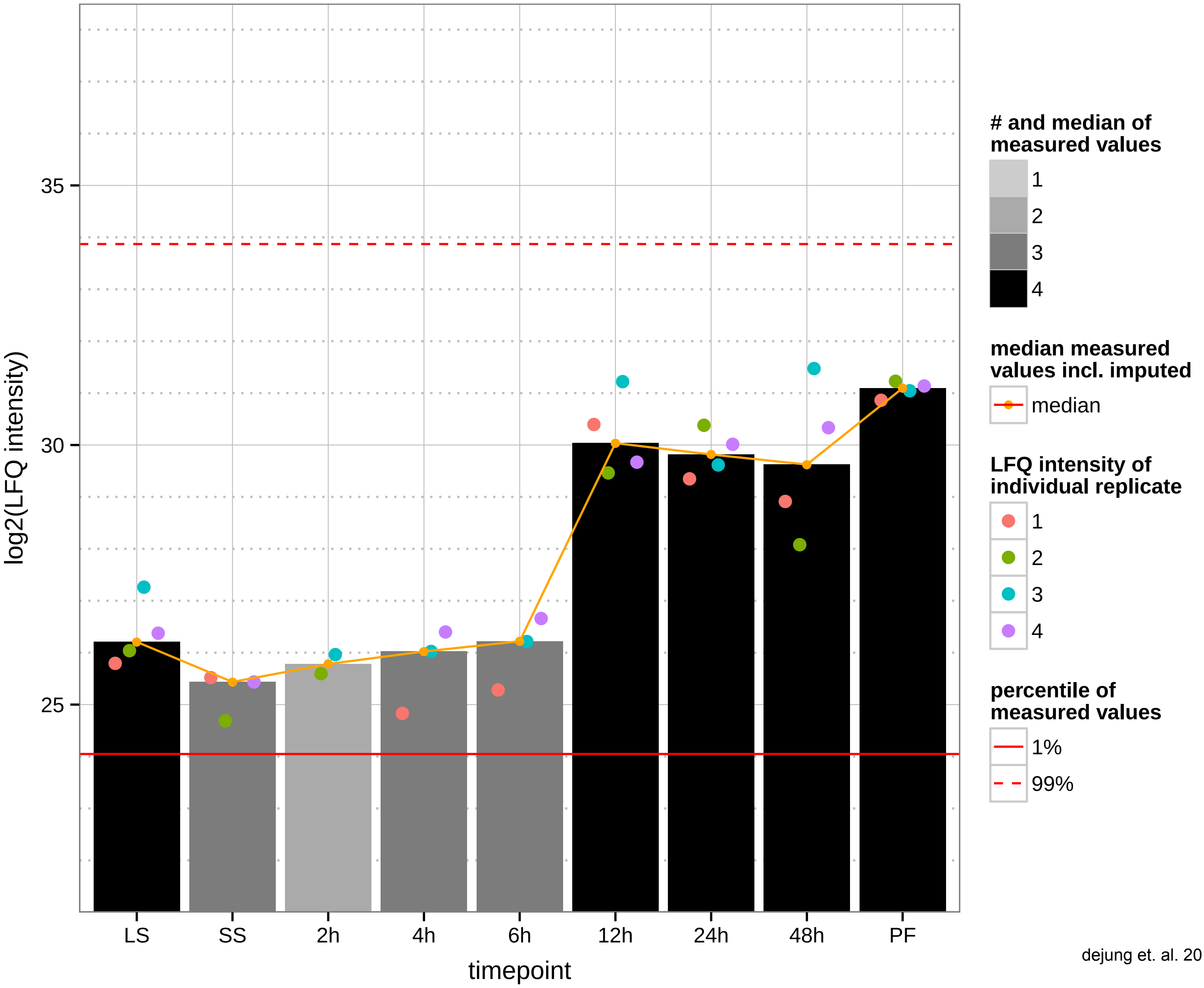
universal minicircle sequence binding protein (UMSBP), putative, predicted zinc finger protein
Tb927.10.6070
AGOF: nucleic acid binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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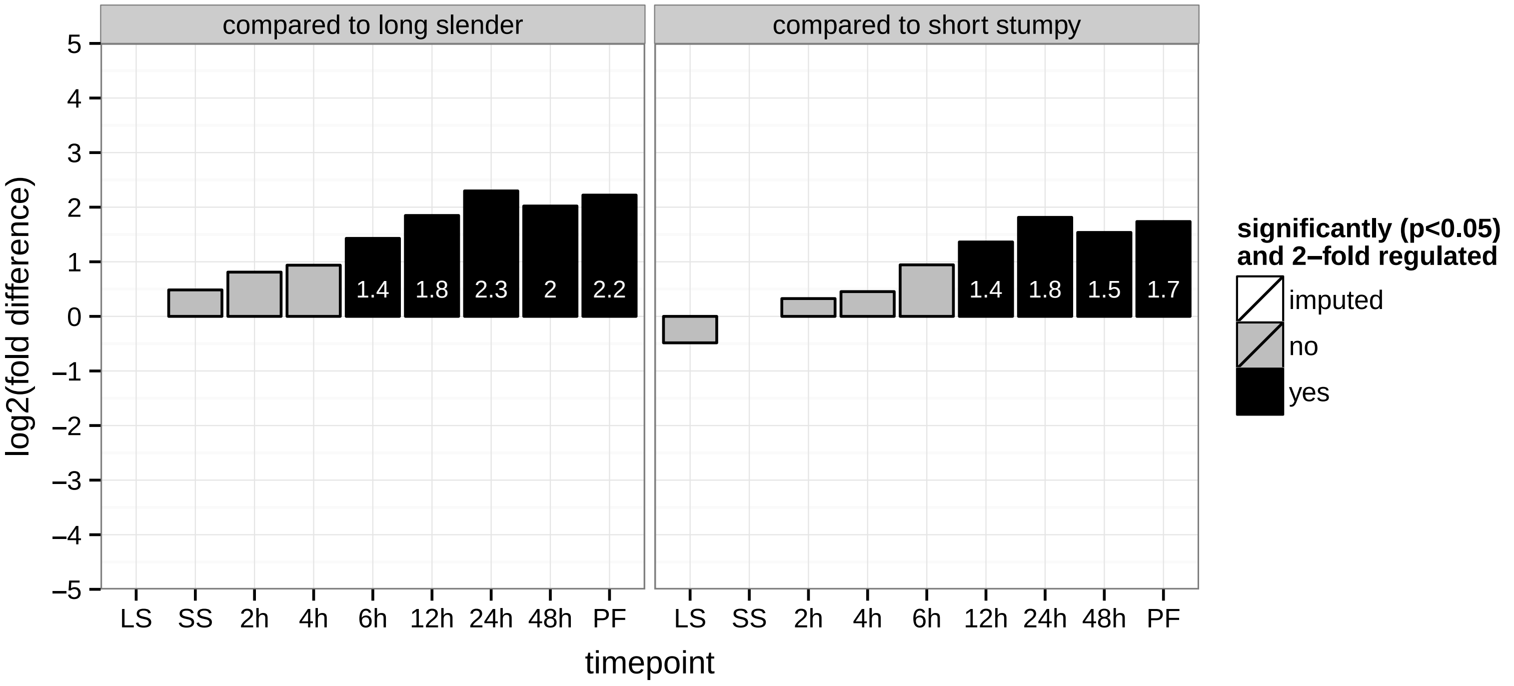
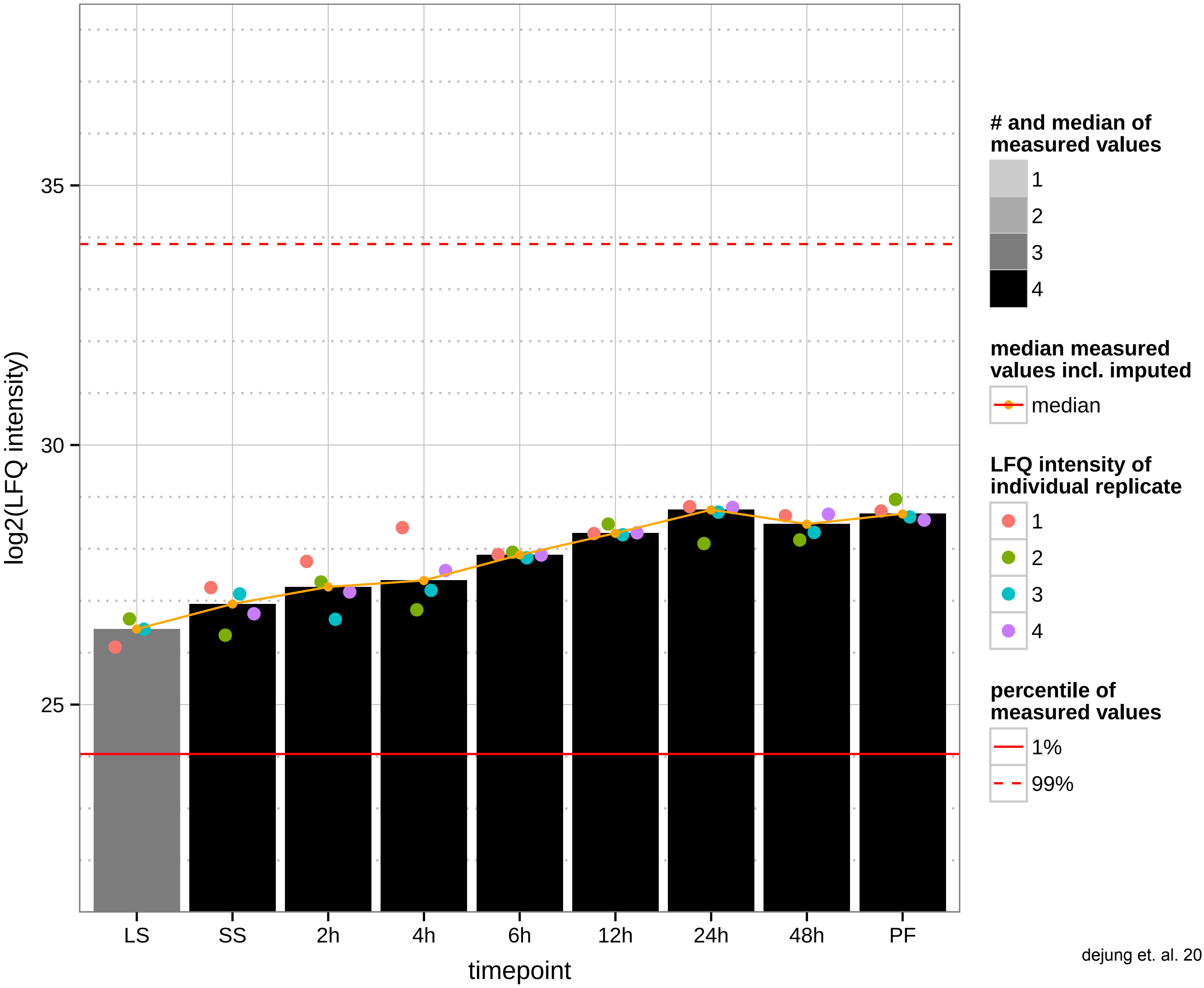
aldehyde dehydrogenase, putative (ALDH)
Tb927.10.6190
AGOF: glutathione–disulfide reductase activity
AGOC: null
AGOP: gamma–aminobutyric acid catabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process, oxidation–reduction process





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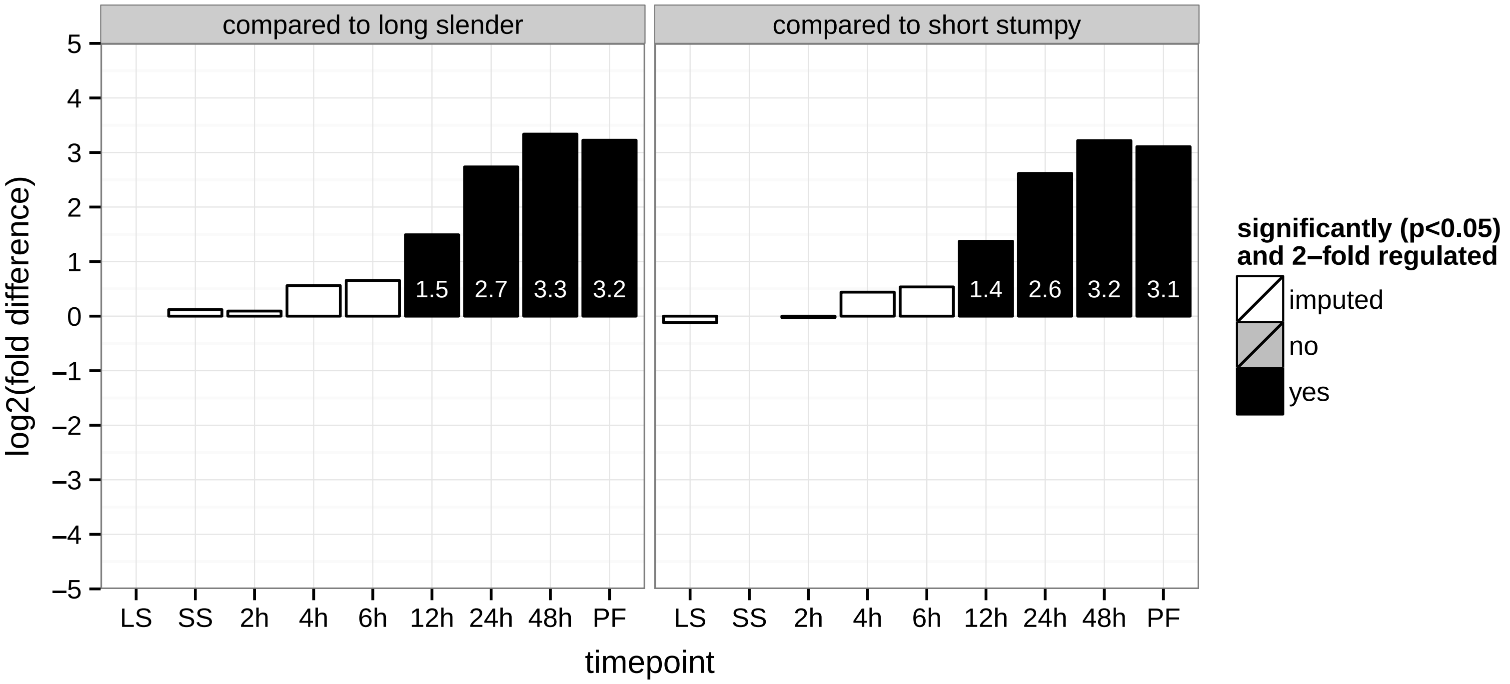
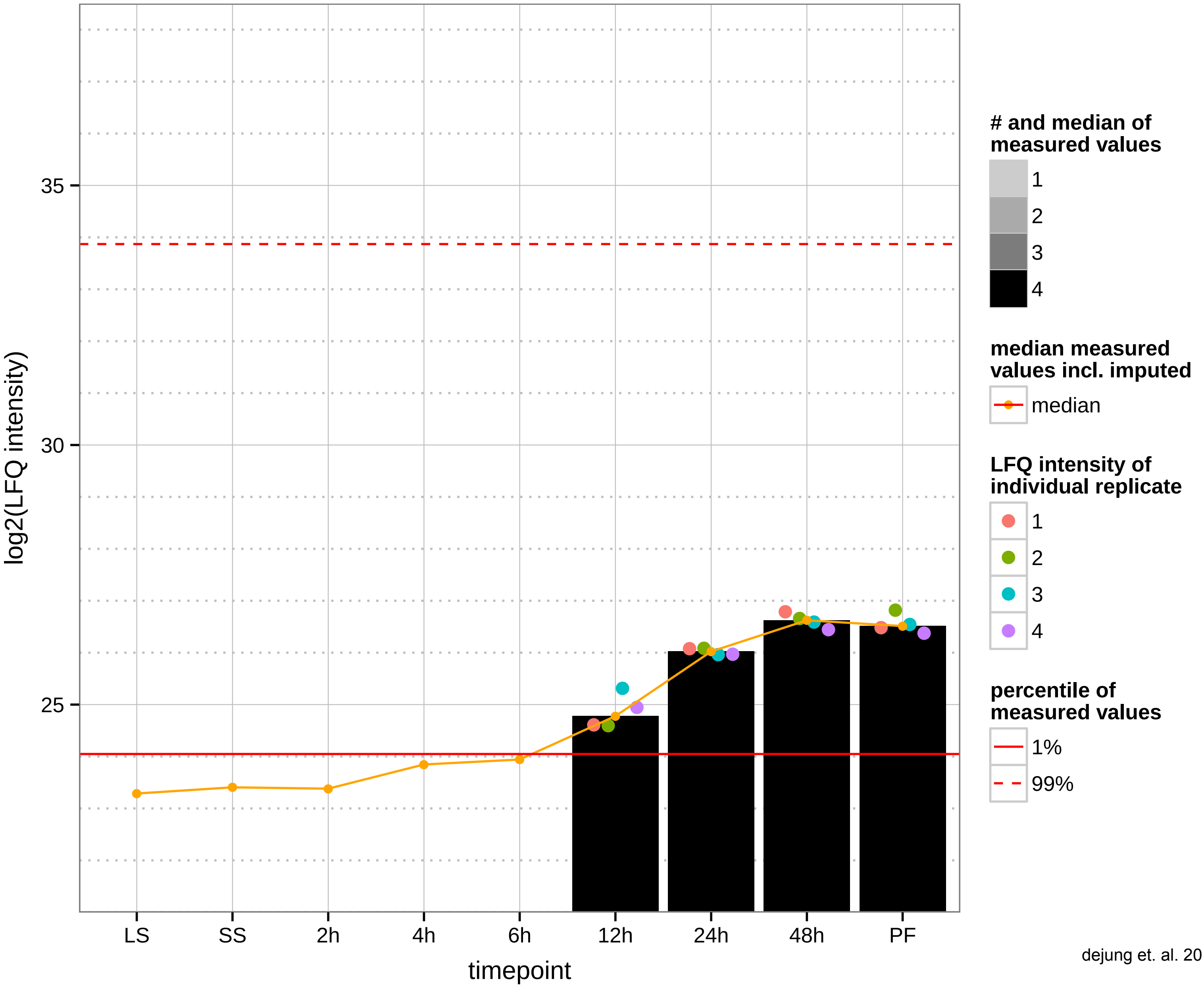
hypothetical protein, conserved
Tb927.10.760
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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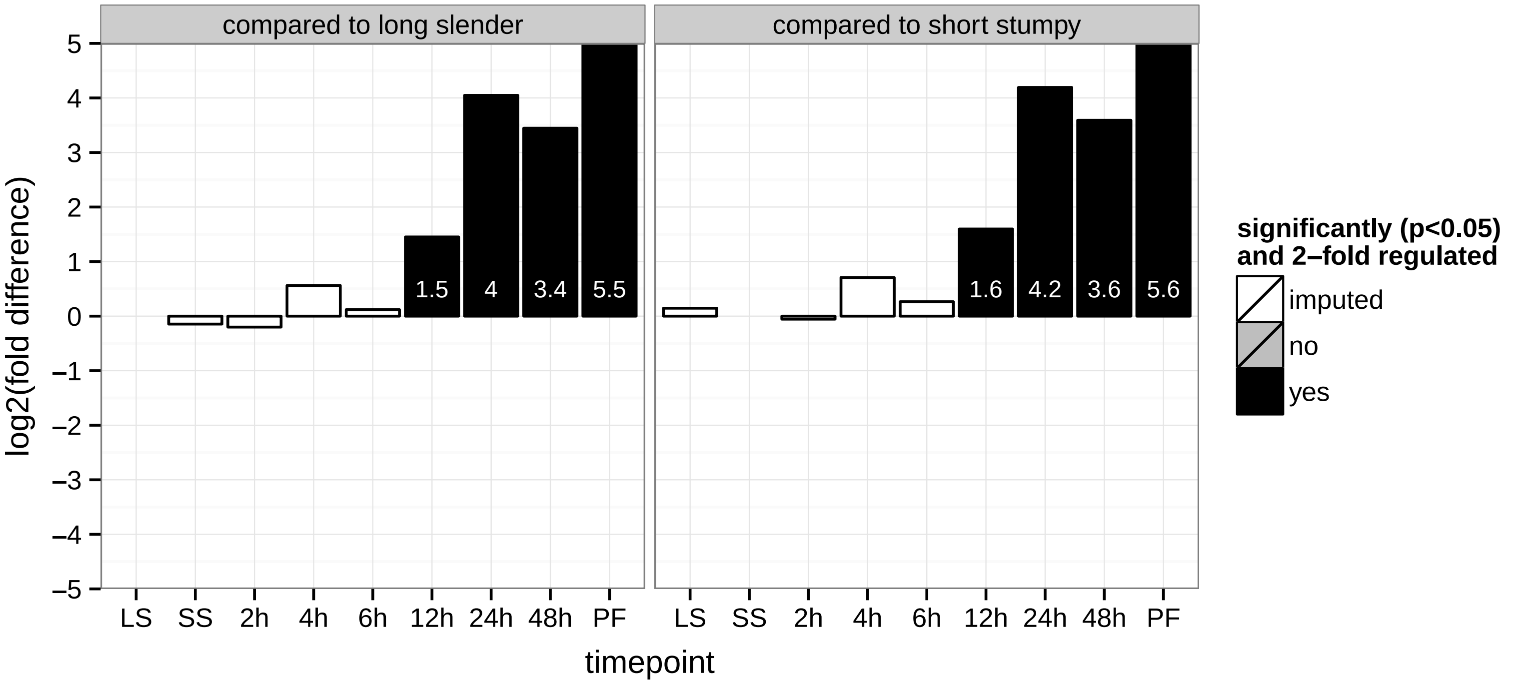
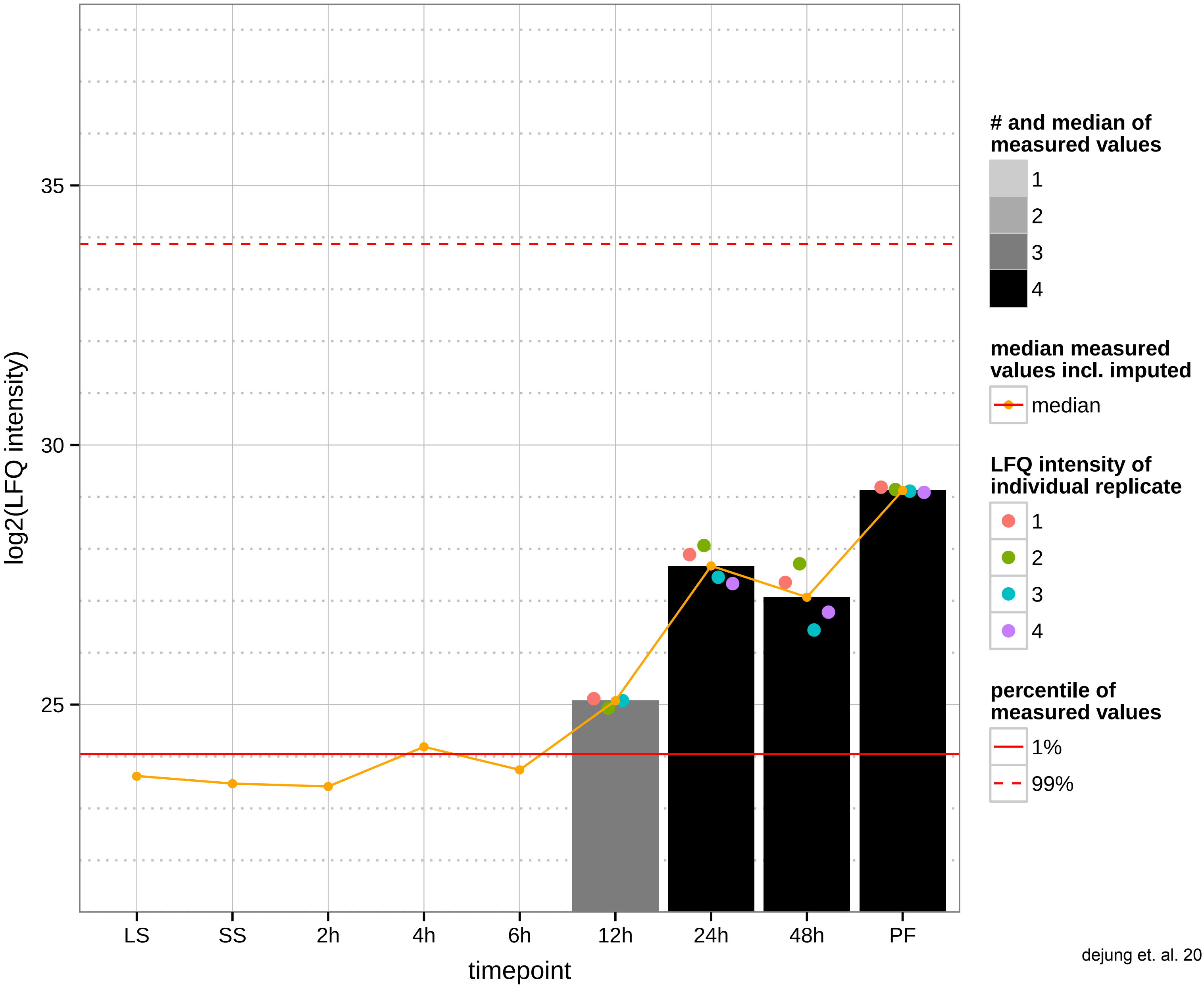
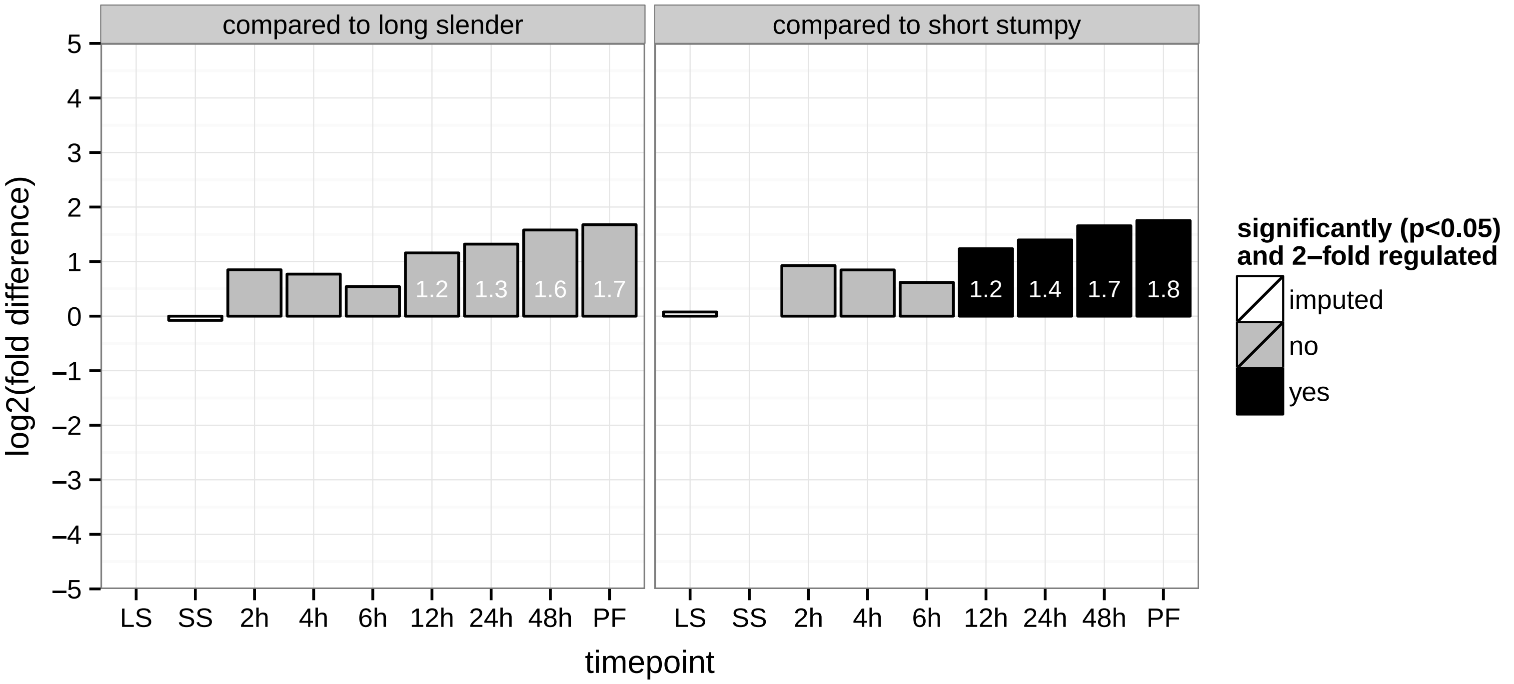
cytochrome oxidase subunit IX (COXIX)
Tb927.10.8320
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

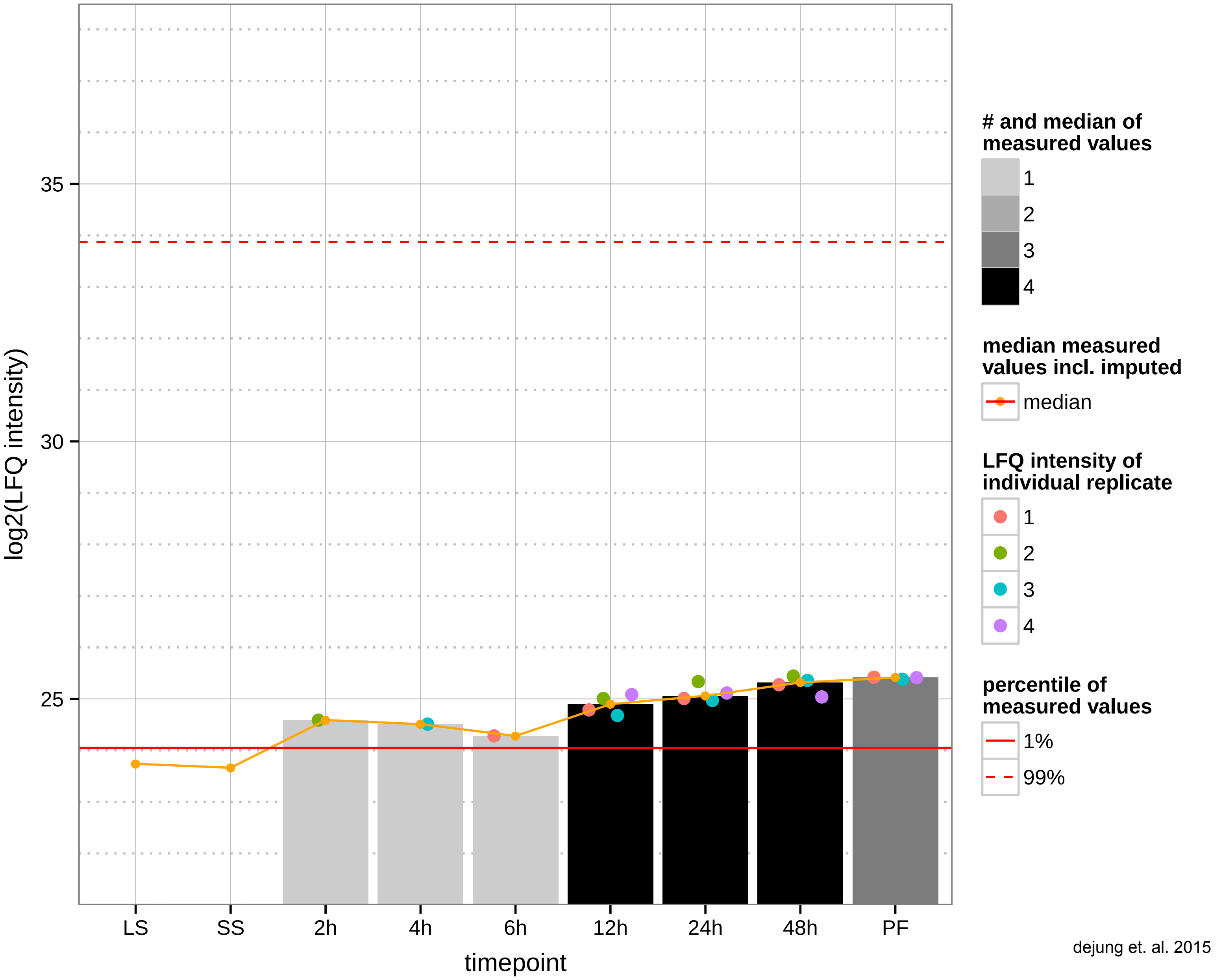




dejung et. al. 2015

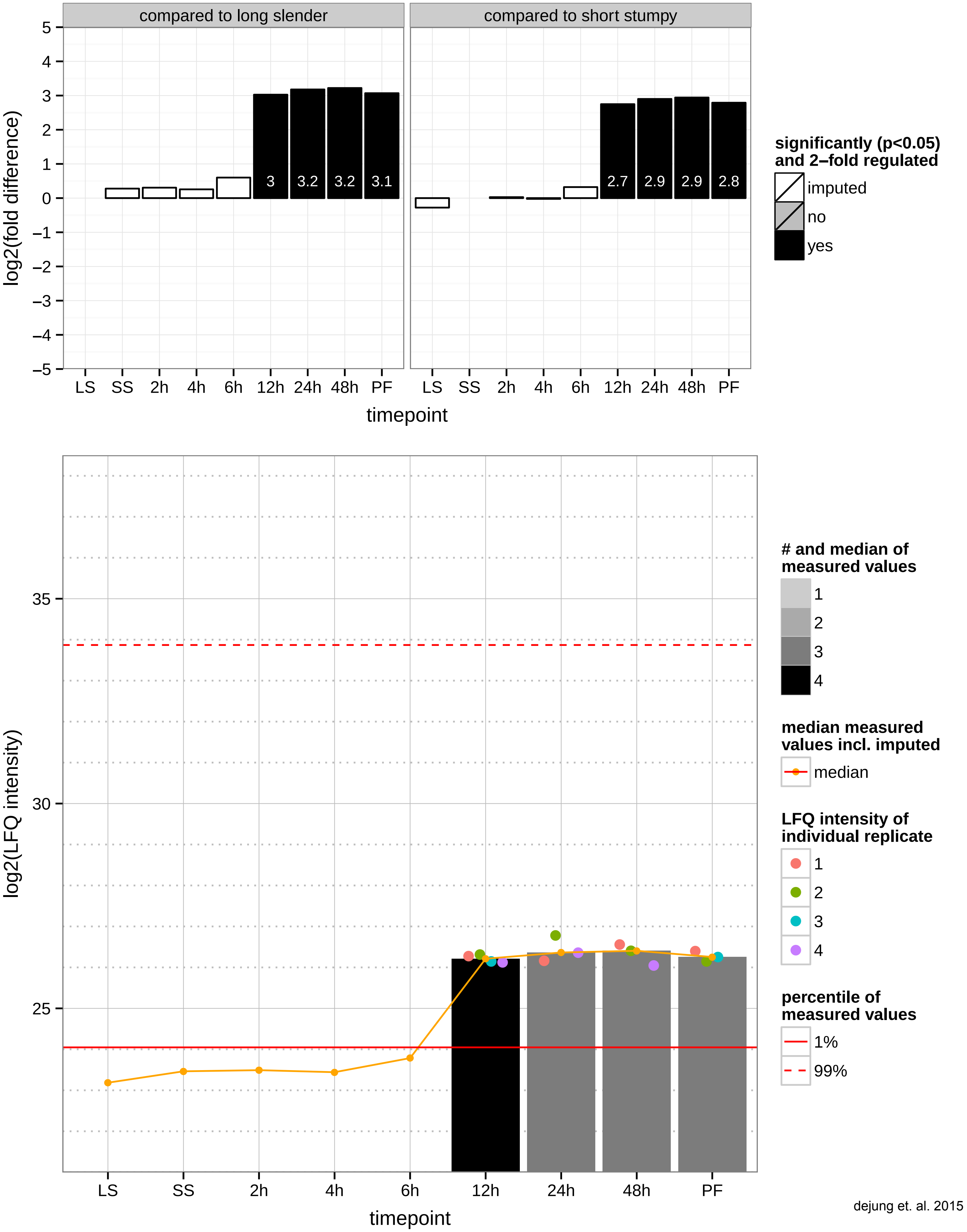
hypothetical protein, conserved
Tb927.10.8620
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.8870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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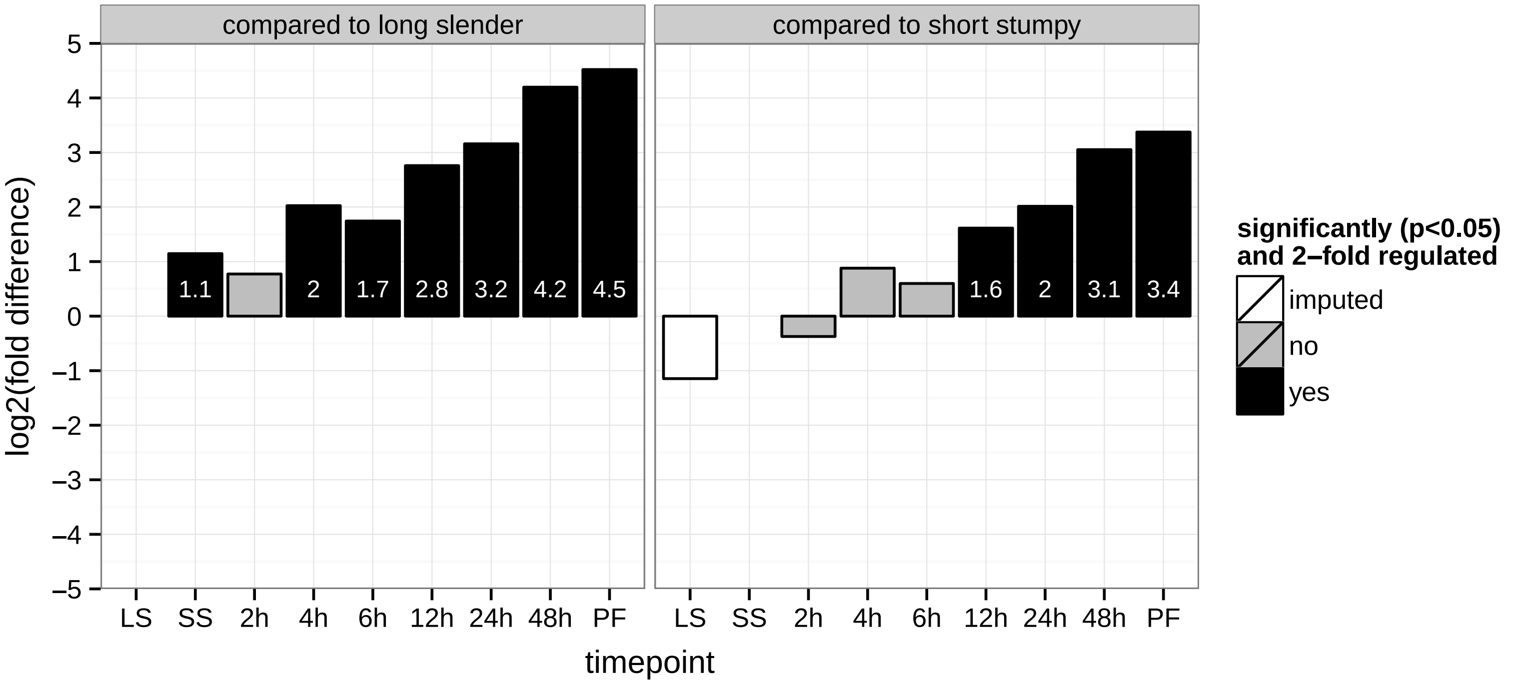
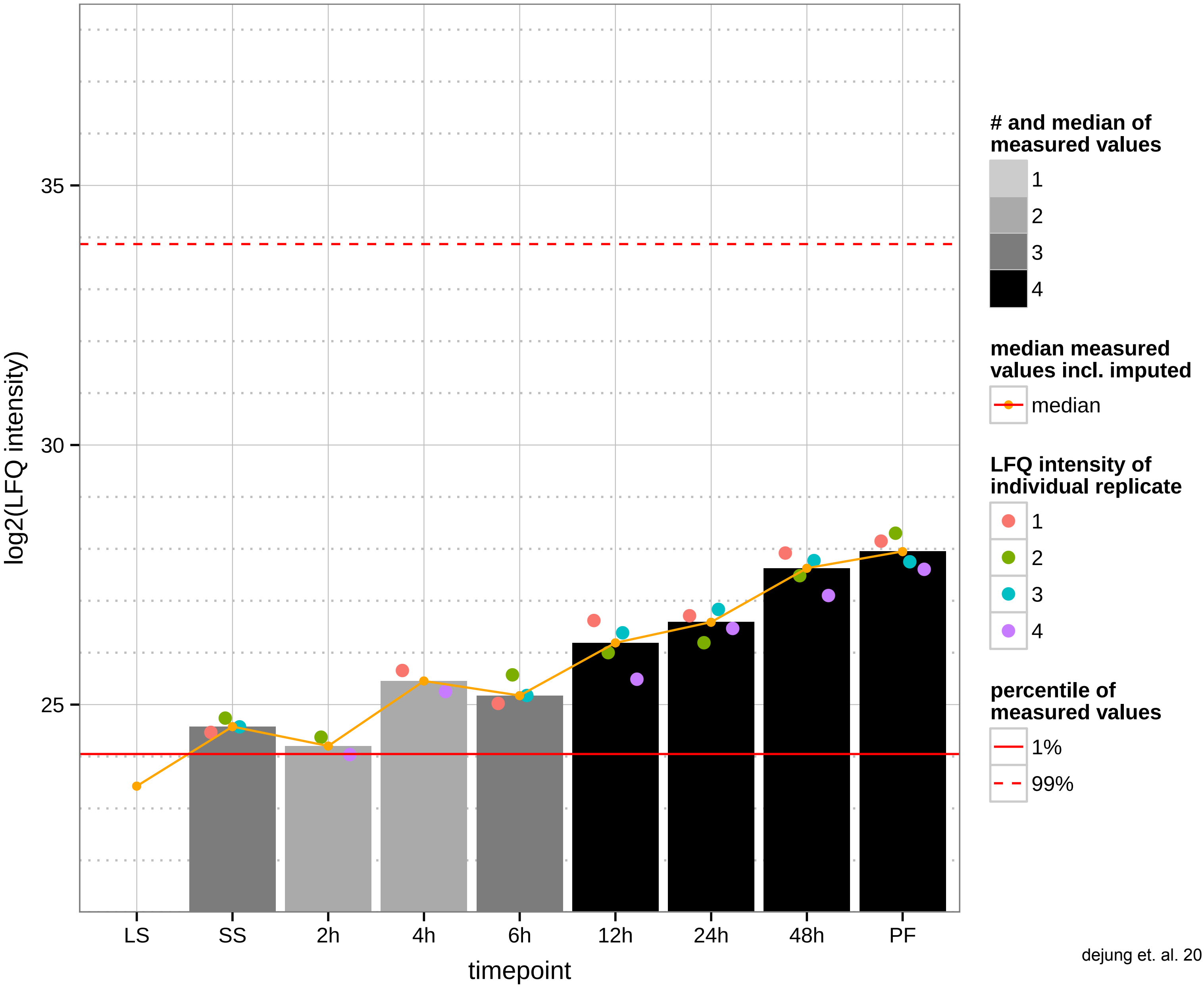
hypothetical protein, conserved
Tb927.11.10140
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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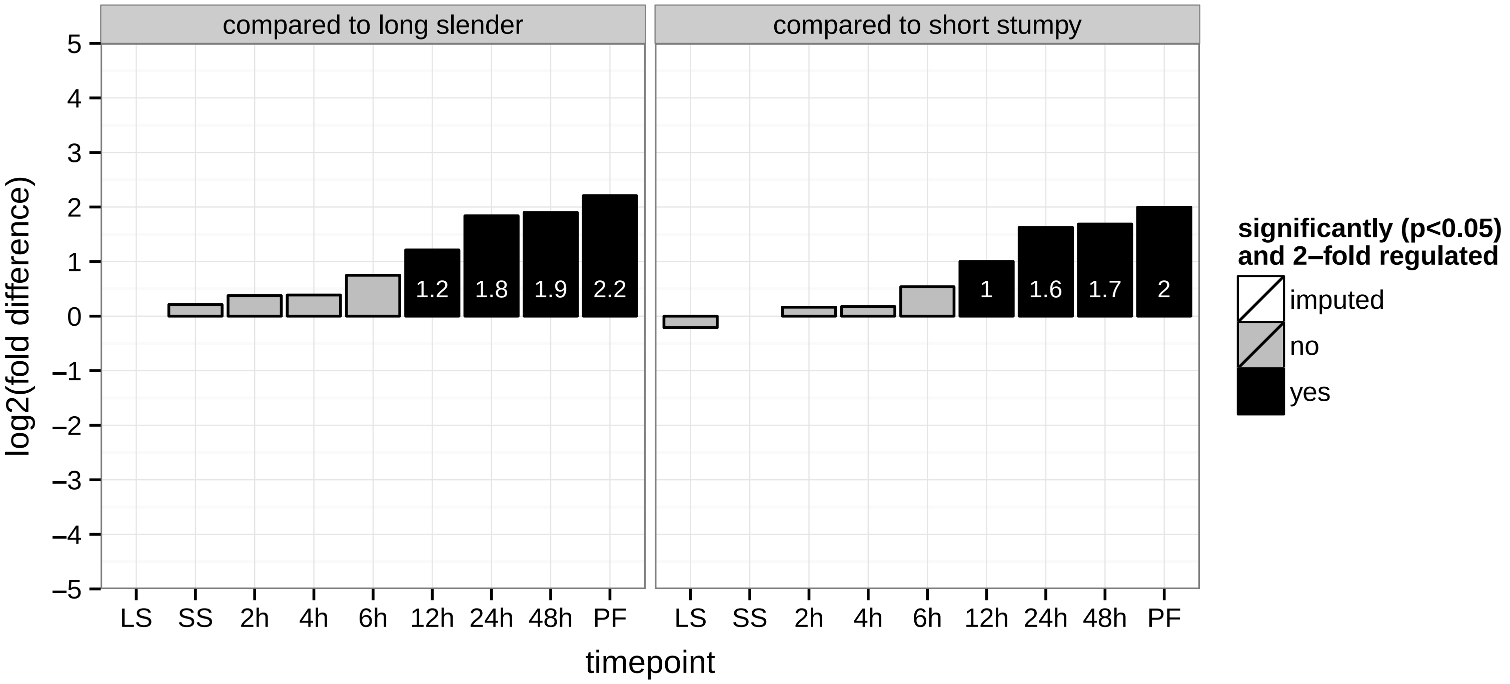
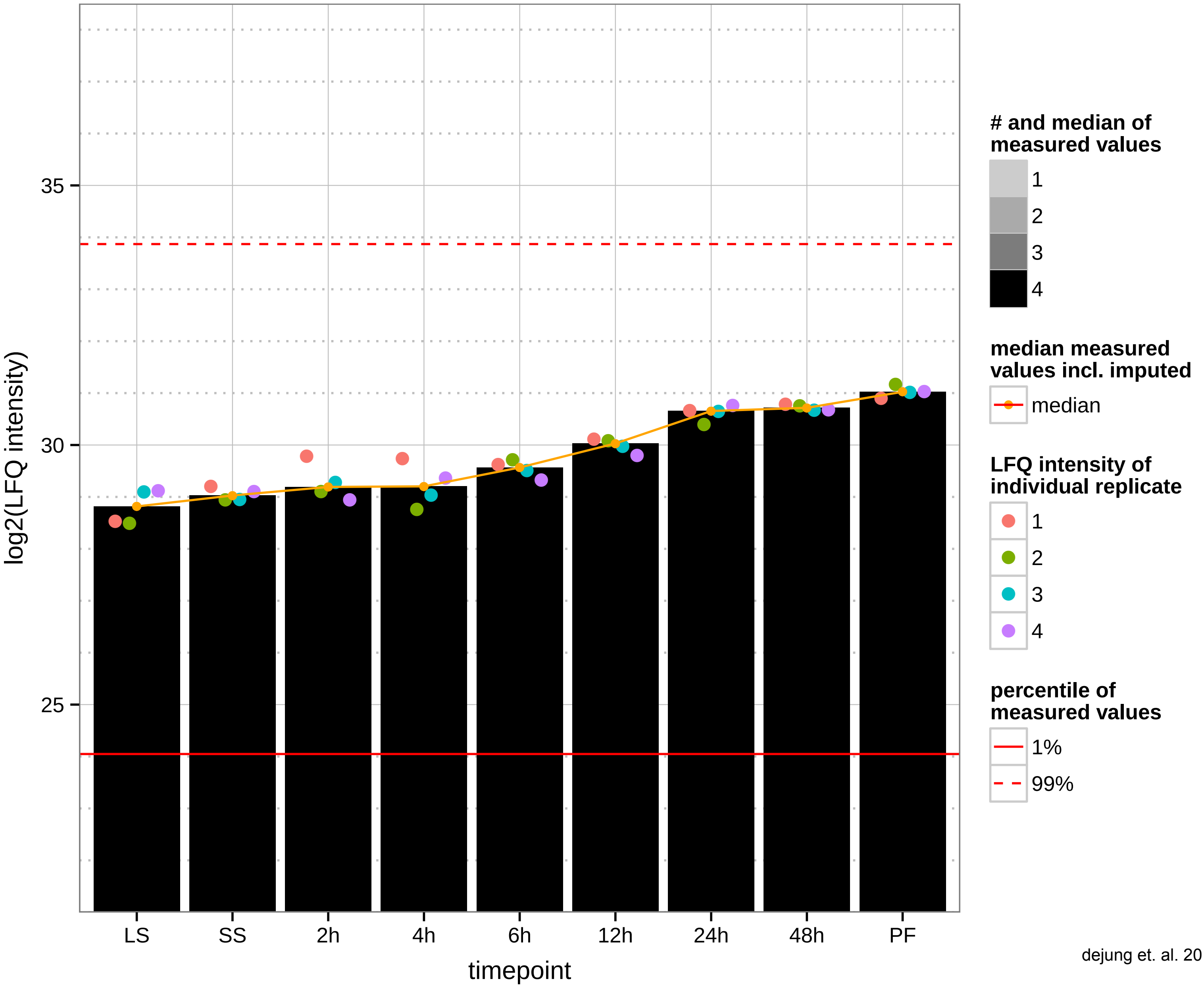
eukaryotic translation initation factor 4 gamma, putative
Tb927.11.10560
AGOF: RNA binding
AGOC: cytoplasm
AGOP: RNA metabolic process, nucleobase–containing compound metabolic process, translation
PGOF: DNA binding, RNA binding, binding, protein binding
PGOC: null
PGOP: null





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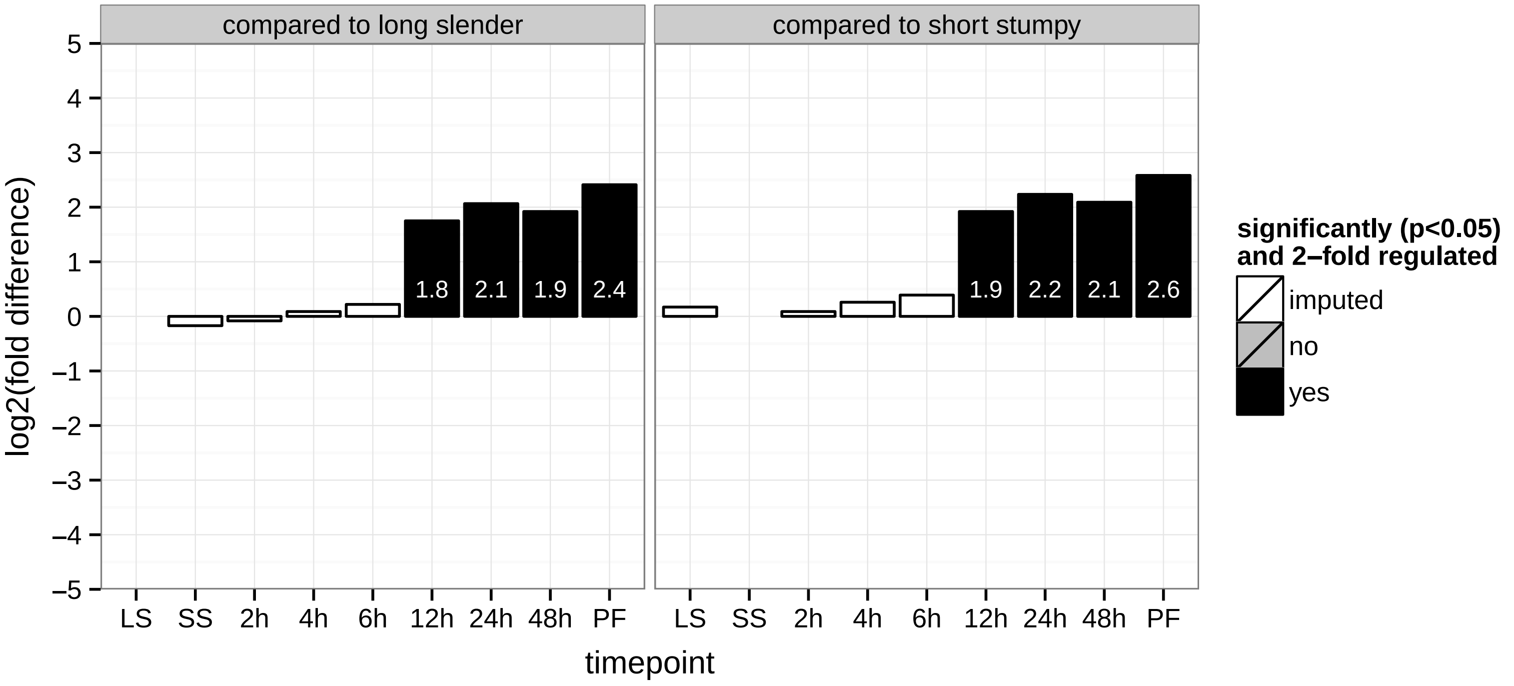
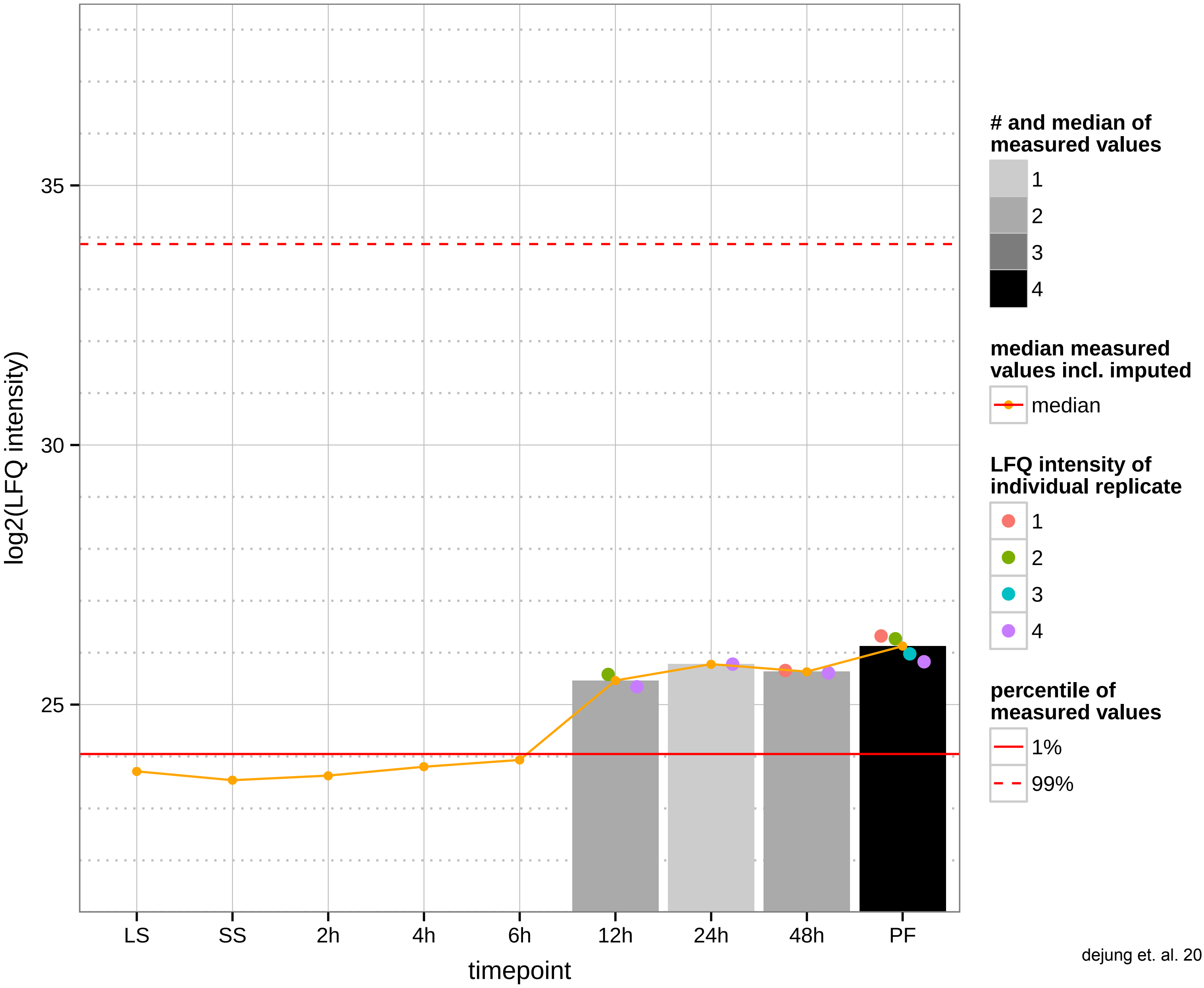
hypothetical protein, conserved
Tb927.11.11630
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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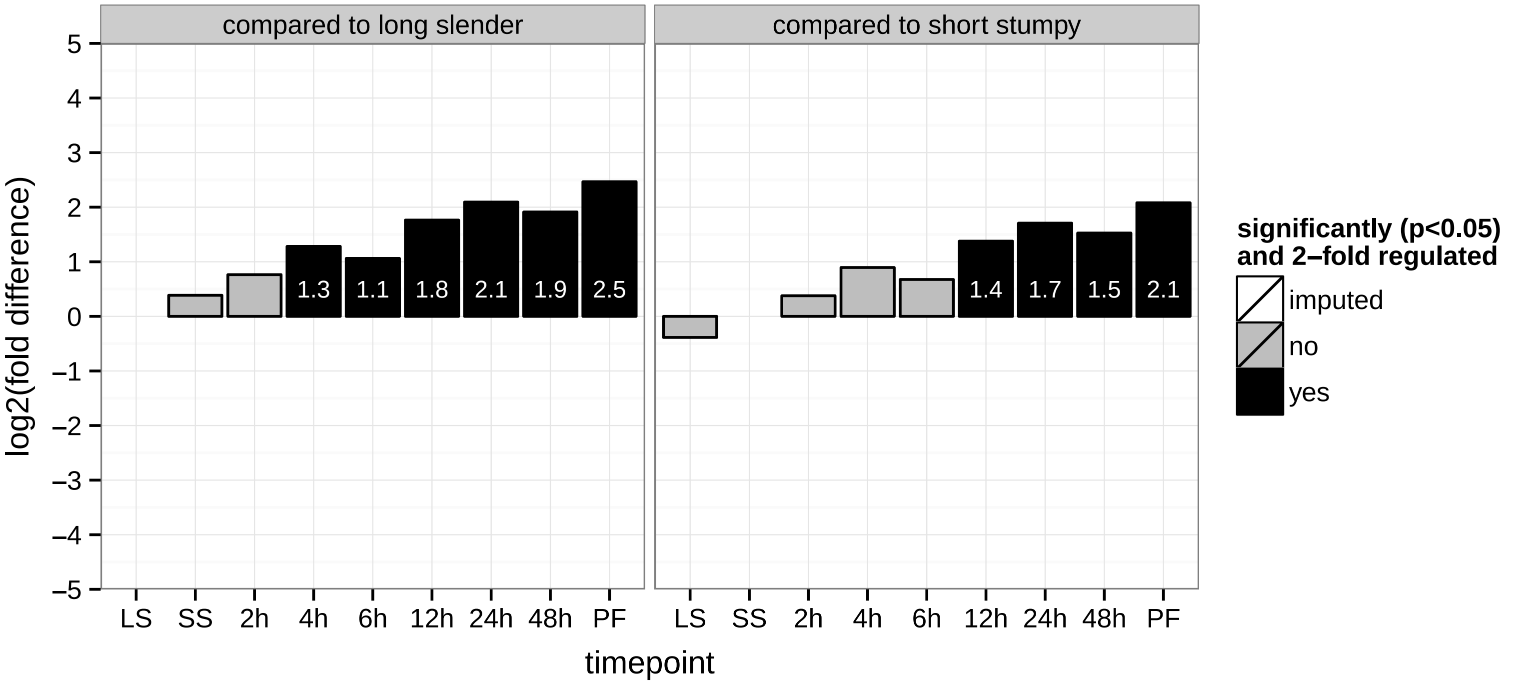
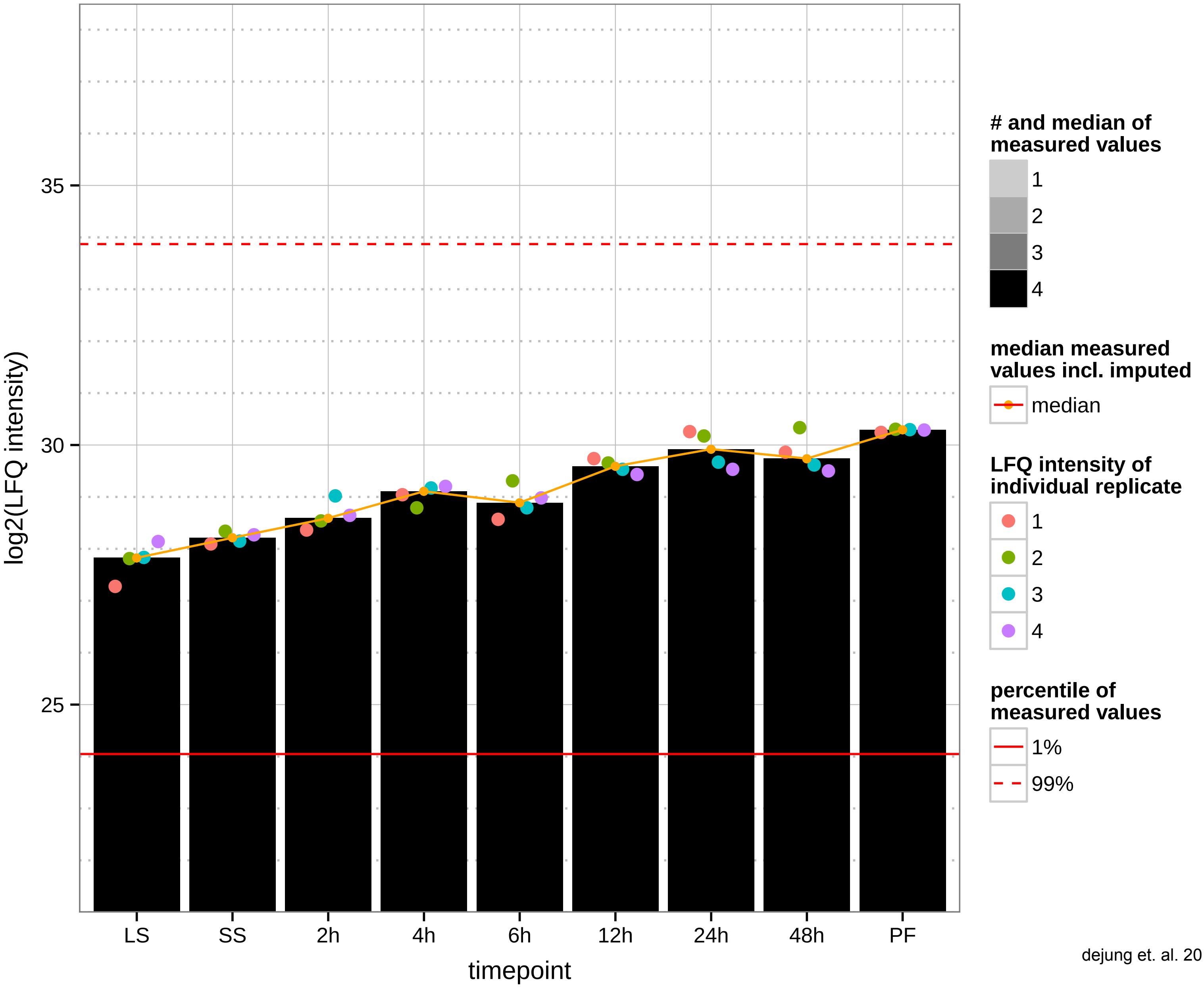
eukaryotic translation initiation factor 4e, putative
Tb927.11.11770
AGOF: RNA binding, RNA cap binding, translation initiation factor activity
AGOC: cytoplasm
AGOP: translational initiation
PGOF: RNA binding, translation initiation factor activity
PGOC: cytoplasm
PGOP: translational initiation





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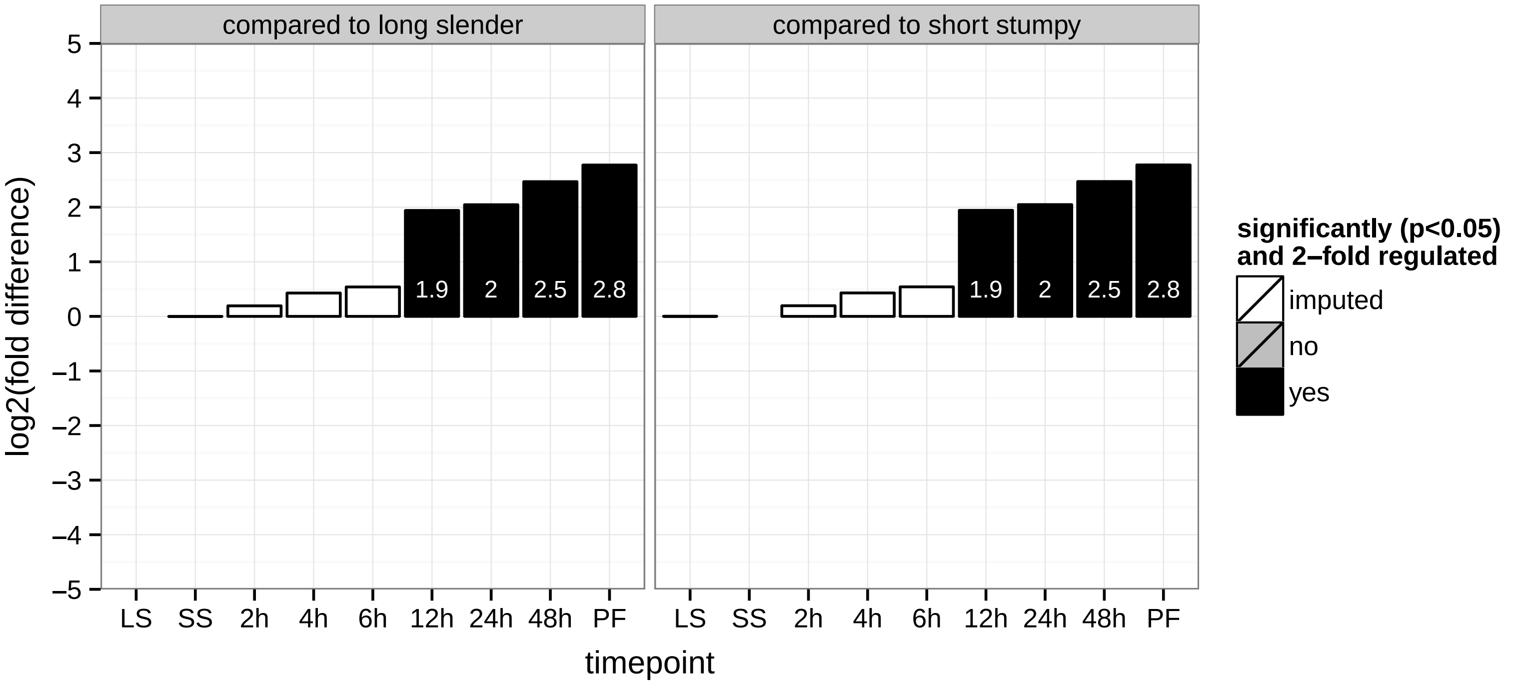
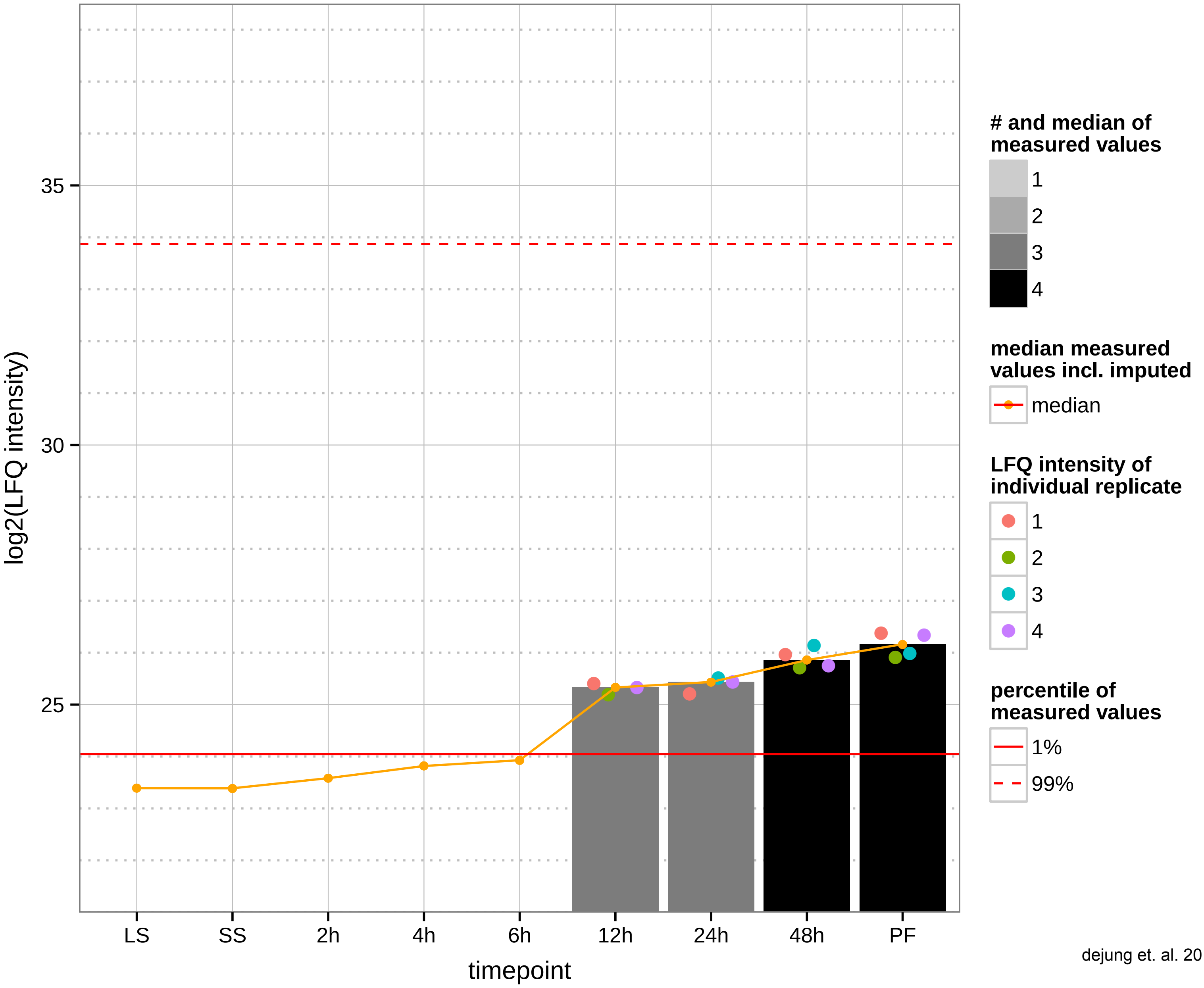
ubiquitin carboxyl–terminal hydrolase, putative, cysteine peptidase, Clan CA, family C19
Tb927.11.12240
AGOF: ubiquitin thiolesterase activity
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ubiquitin thiolesterase activity
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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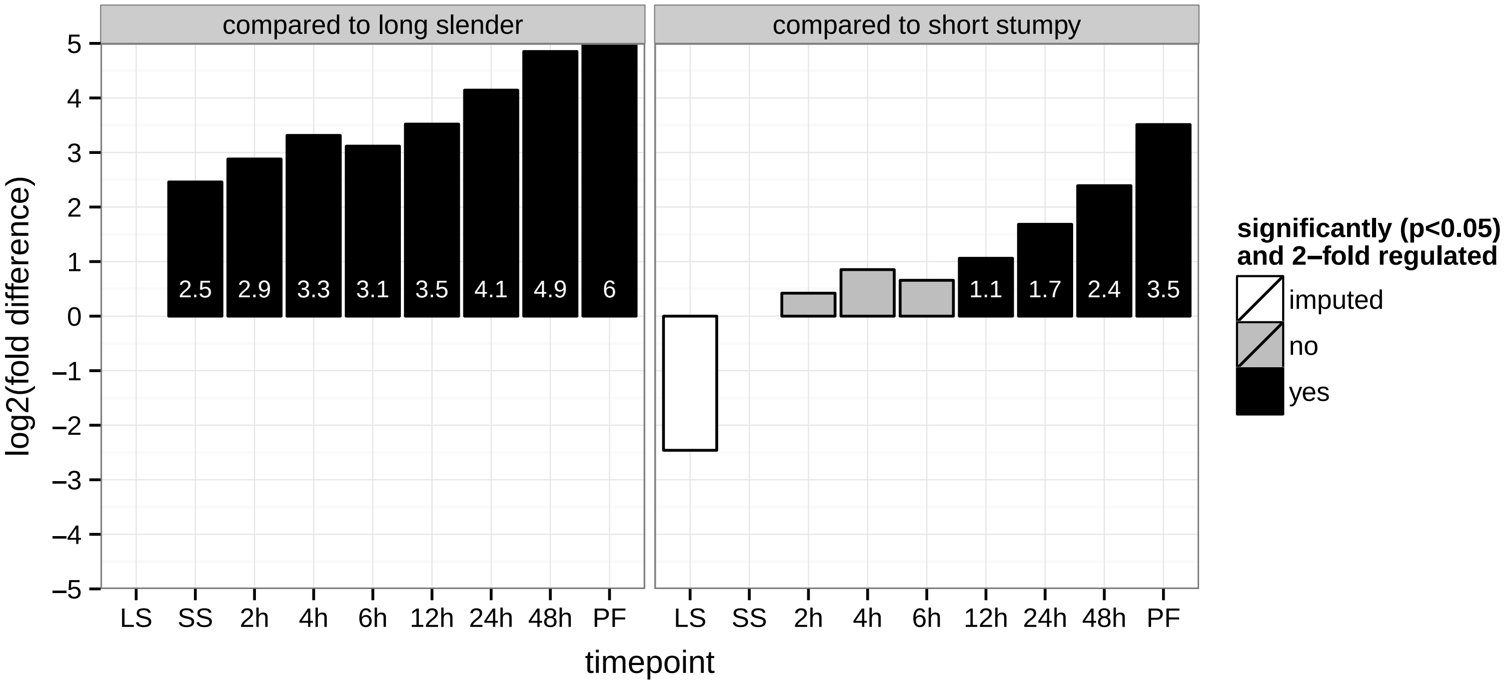
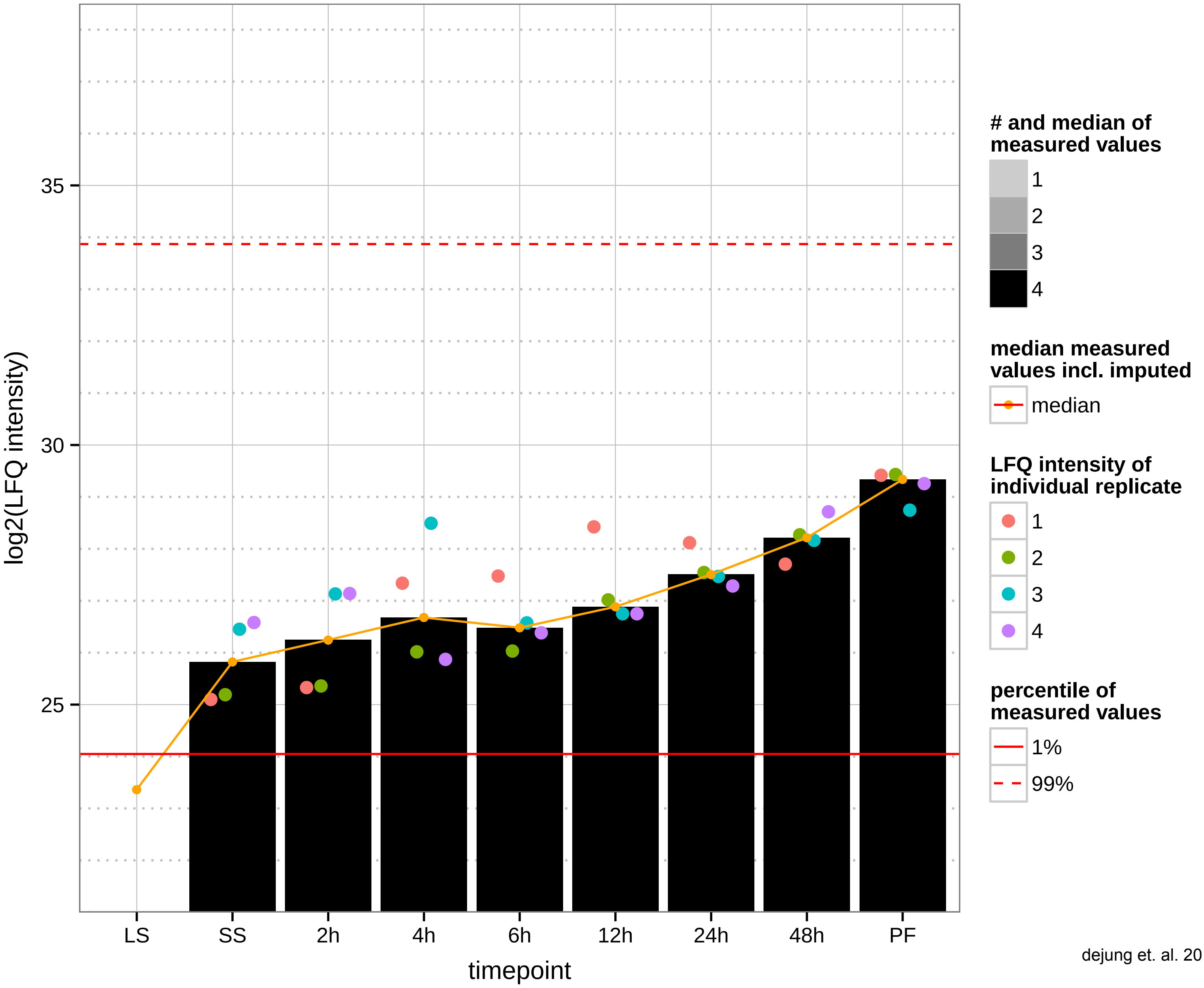
Mitochondrial SSU ribosomal protein, putative, mitochondrial edited mRNA stability factor 1 subunit, kinteoplast poly(A) polym
Tb927.11.1250
AGOF: RNA binding
AGOC: mitochondrion
AGOP: RNA polyadenylation, mRNA stabilization
PGOF: null
PGOC: null
PGOP: null





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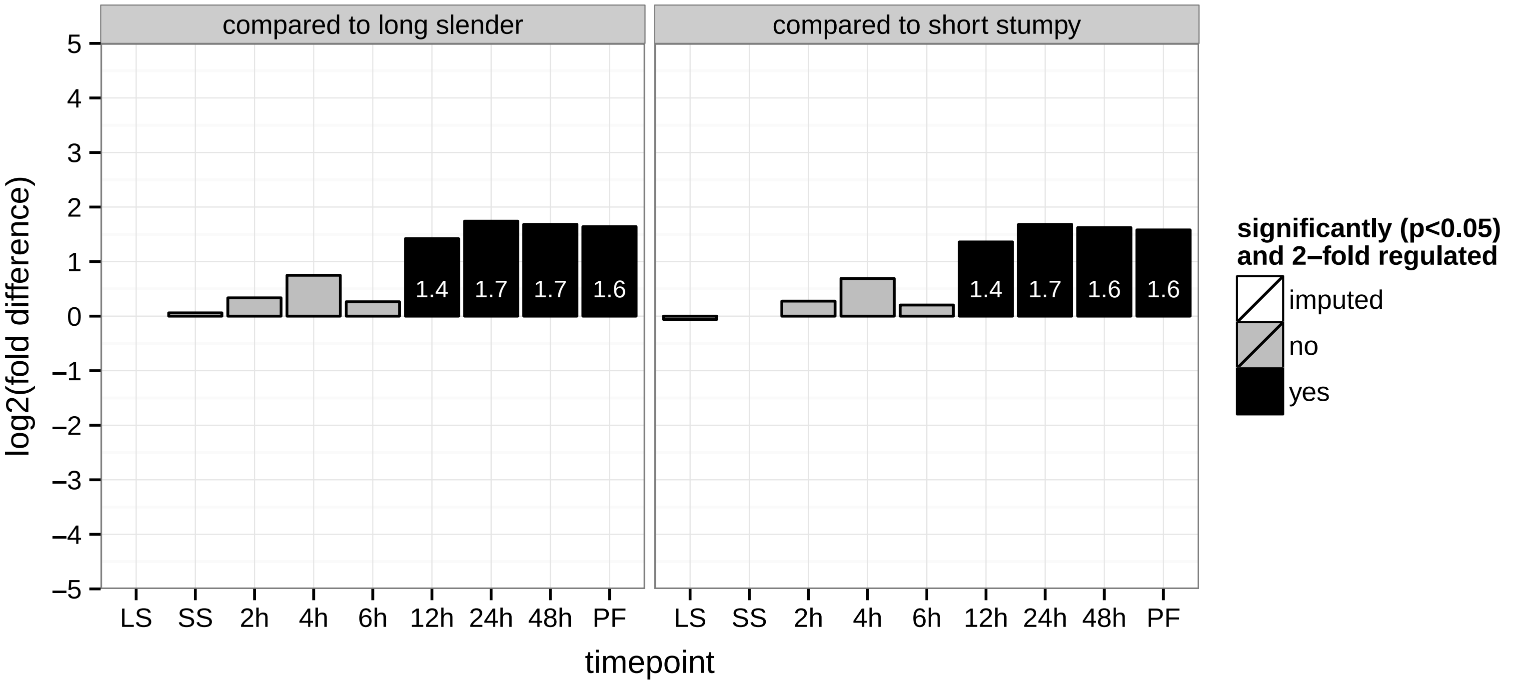
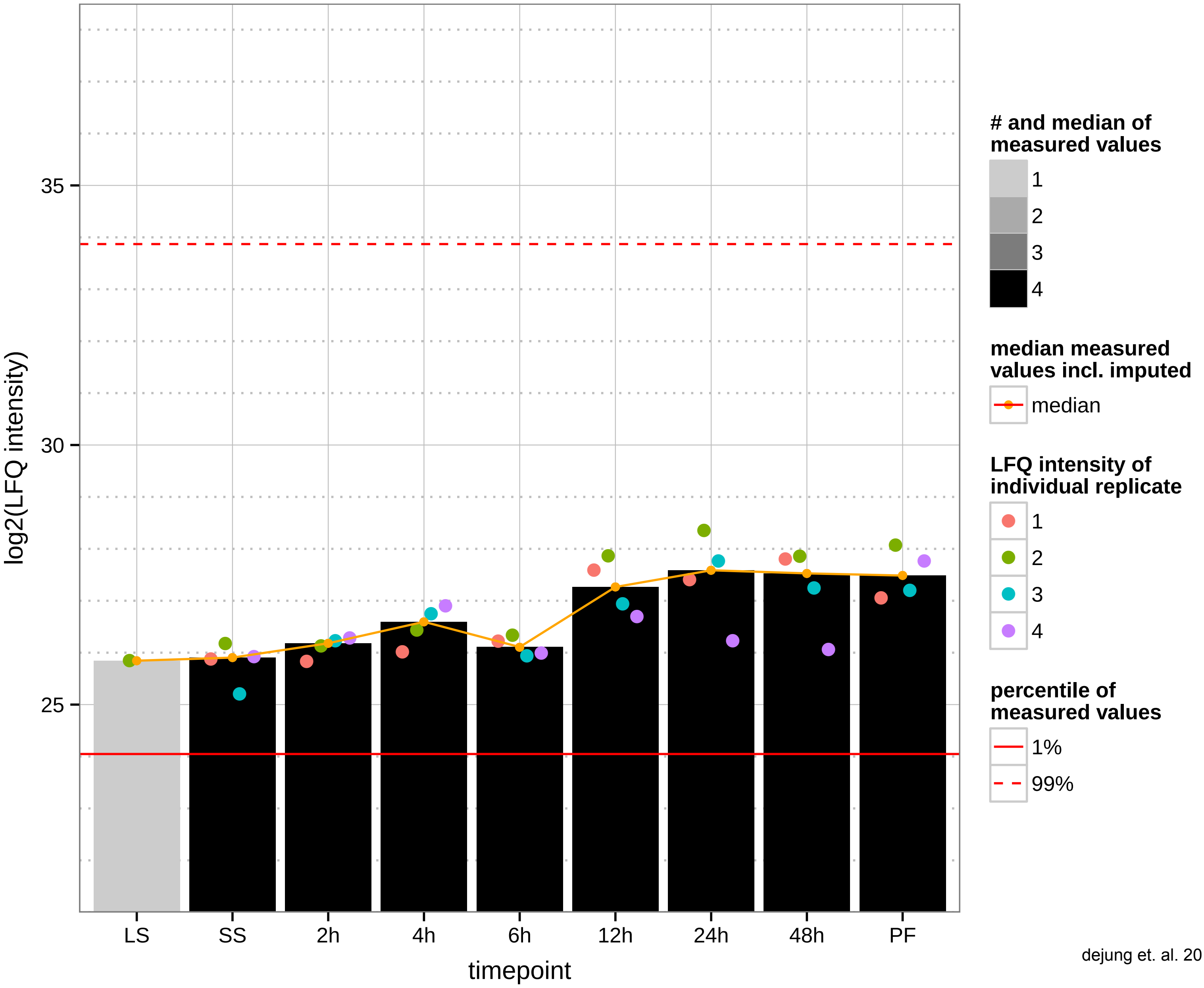
prefoldin subunit 2, putative
Tb927.11.12680
AGOF: unfolded protein binding
AGOC: prefoldin complex
AGOP: protein folding
PGOF: unfolded protein binding
PGOC: prefoldin complex
PGOP: protein folding





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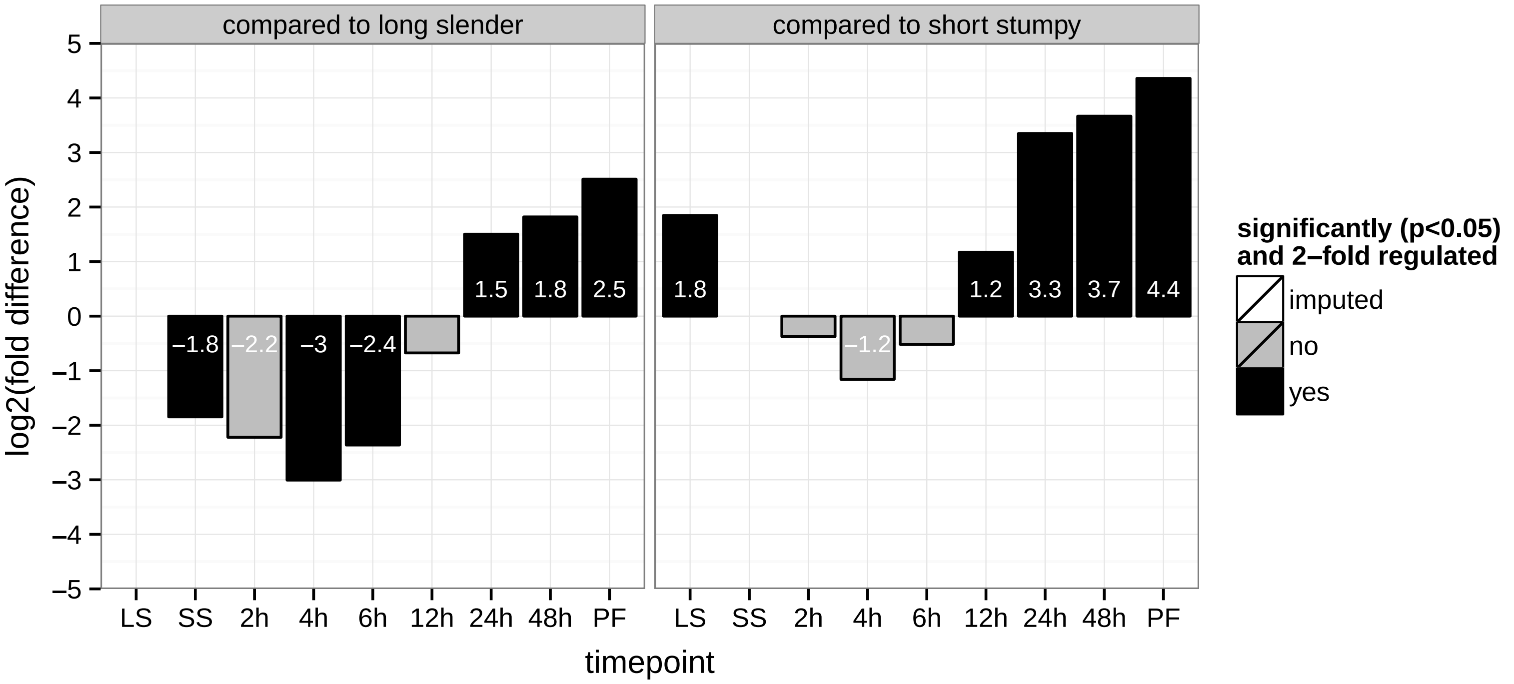
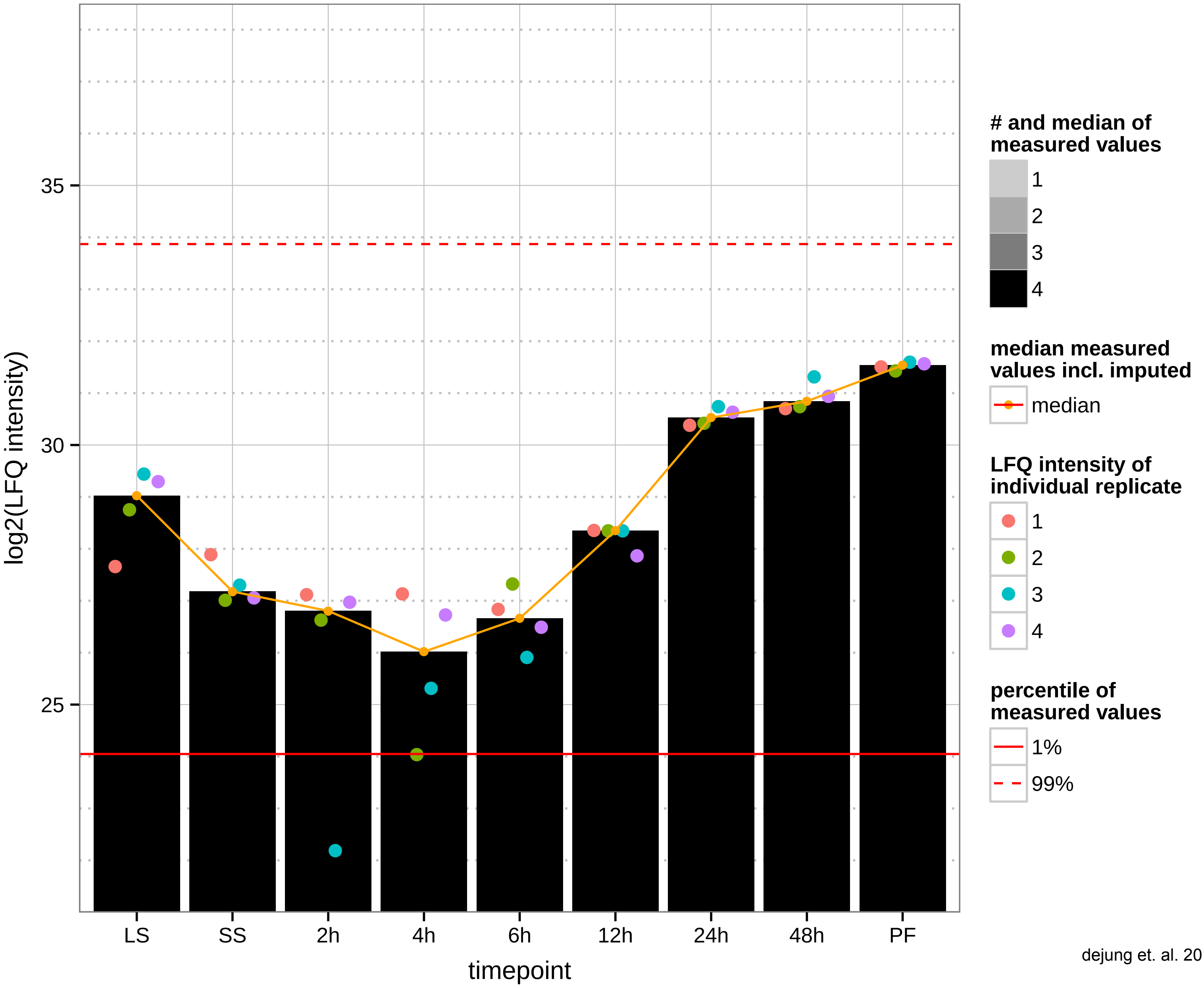
ribonucleoside–diphosphate reductase small chain, putative, ribonucleoside–diphosphate reductase small chain (RNR2)
Tb927.11.12800;Tb927.11.12790;Tb927.11.12780;Tb927.11.12820;Tb11.v5.0288;Tb927.11.12810
AGOF: null, ribonucleoside–diphosphate reductase activity, thioredoxin disulfide as acceptor, transition metal ion binding
AGOC: null
AGOP: null, deoxyribonucleoside diphosphate metabolic process
PGOF: oxidoreductase activity, ribonucleoside–diphosphate reductase activity, thioredoxin disulfide as acceptor, transition me
PGOC: null
PGOP: deoxyribonucleoside diphosphate metabolic process, oxidation–reduction process





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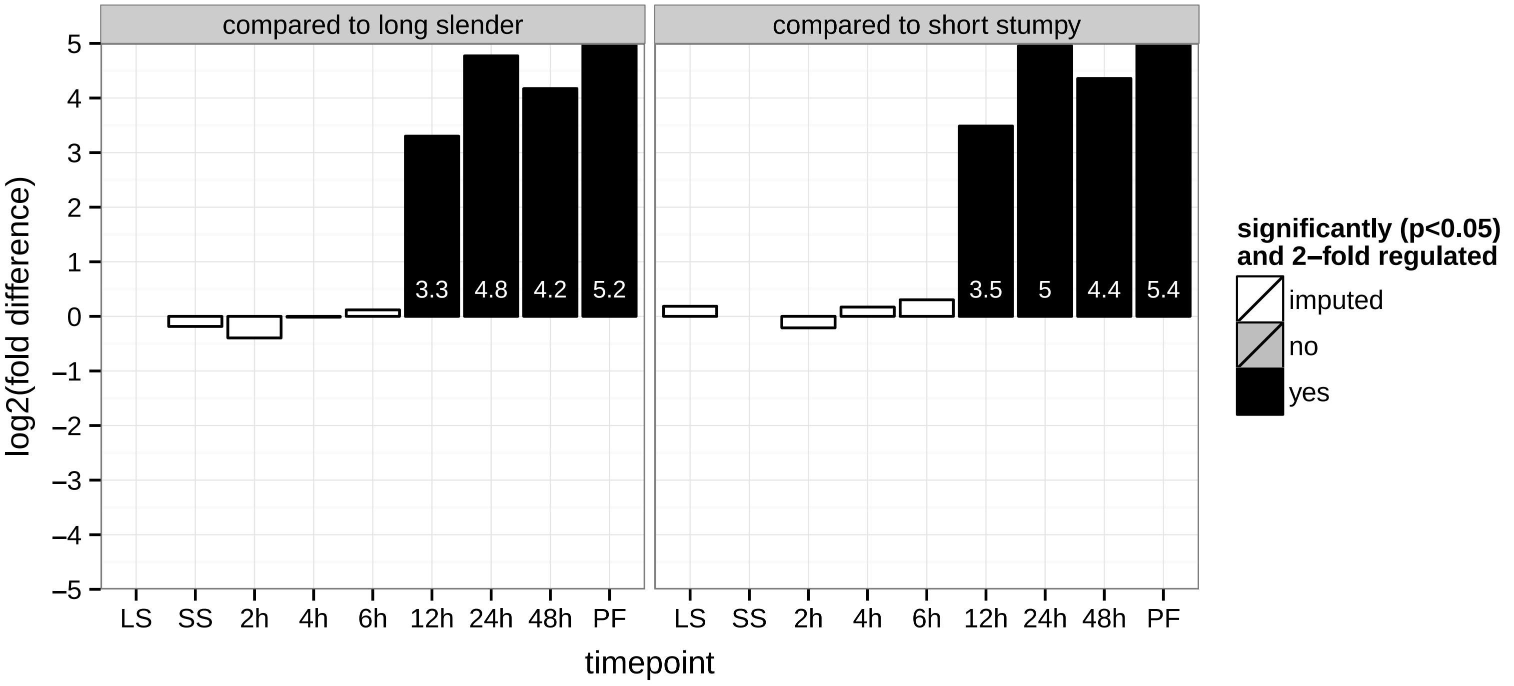
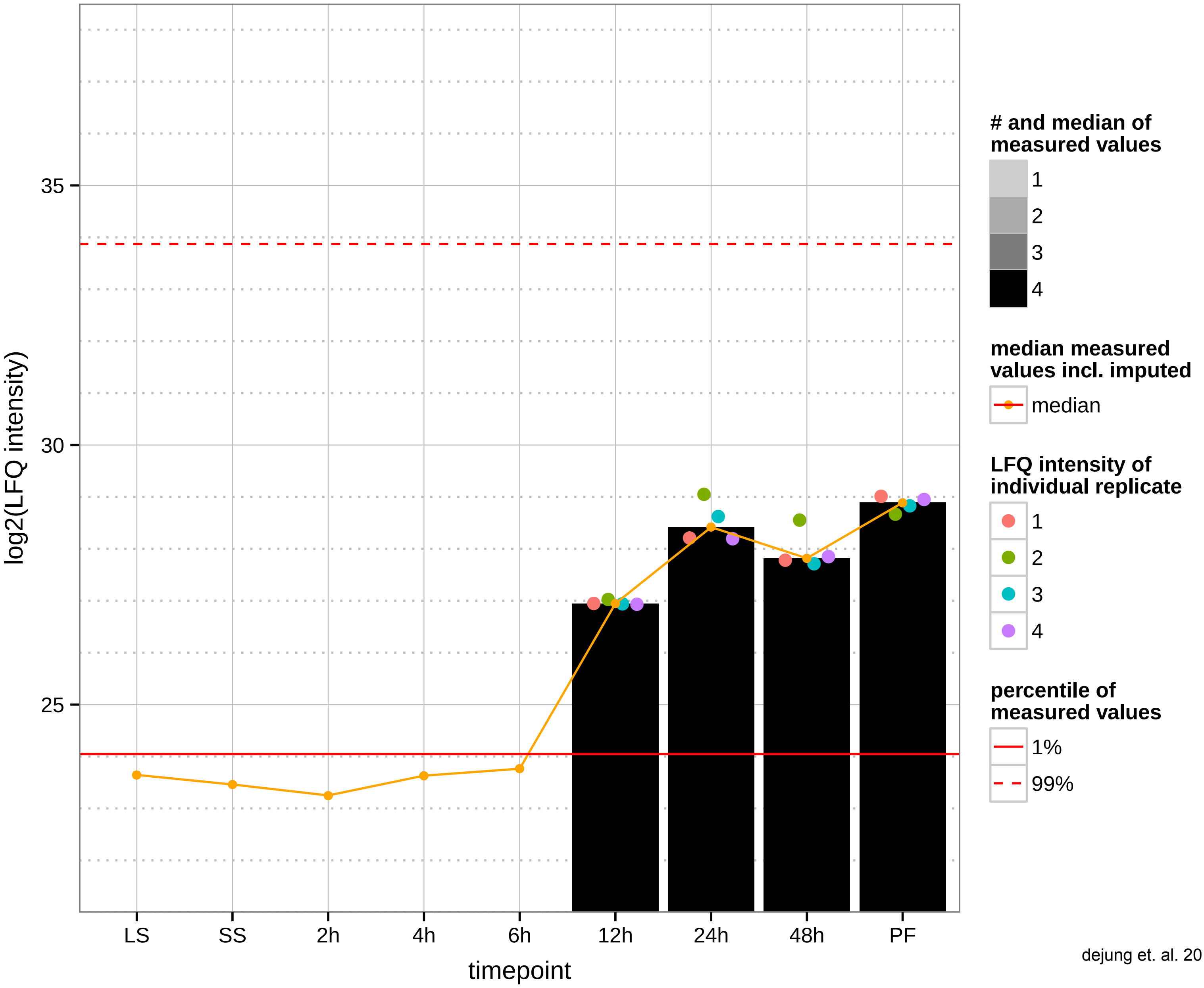
cytochrome oxidase subunit X (COXX)
Tb927.11.13140
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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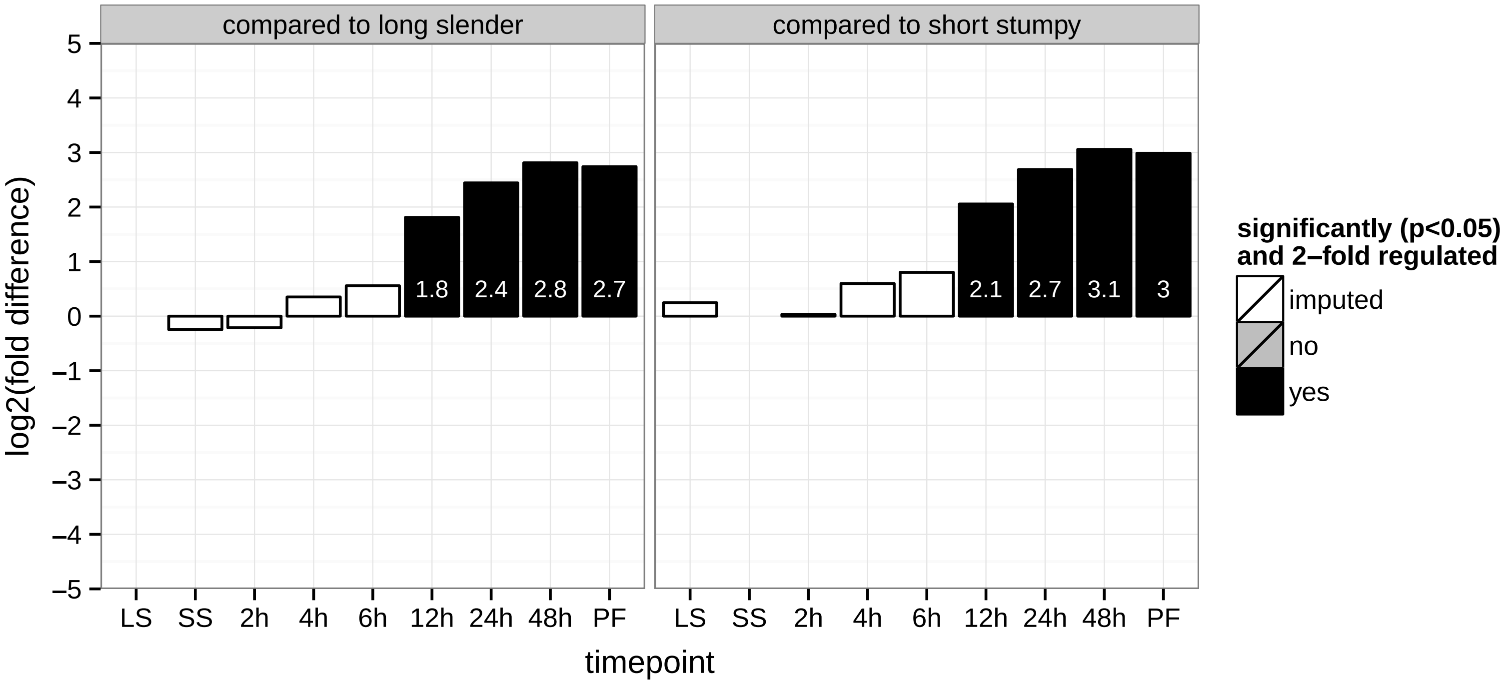
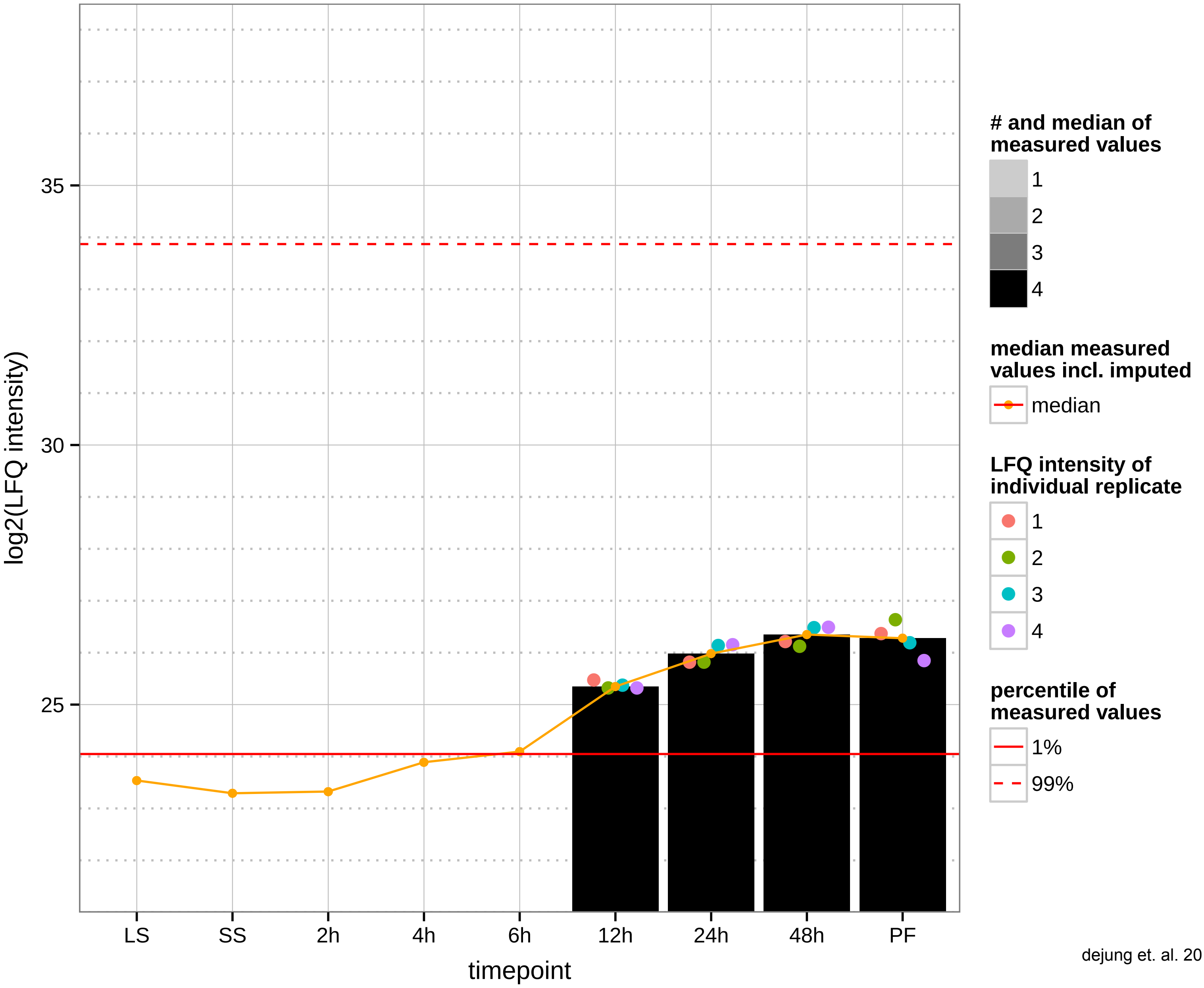
hypothetical protein, conserved
Tb927.11.13510
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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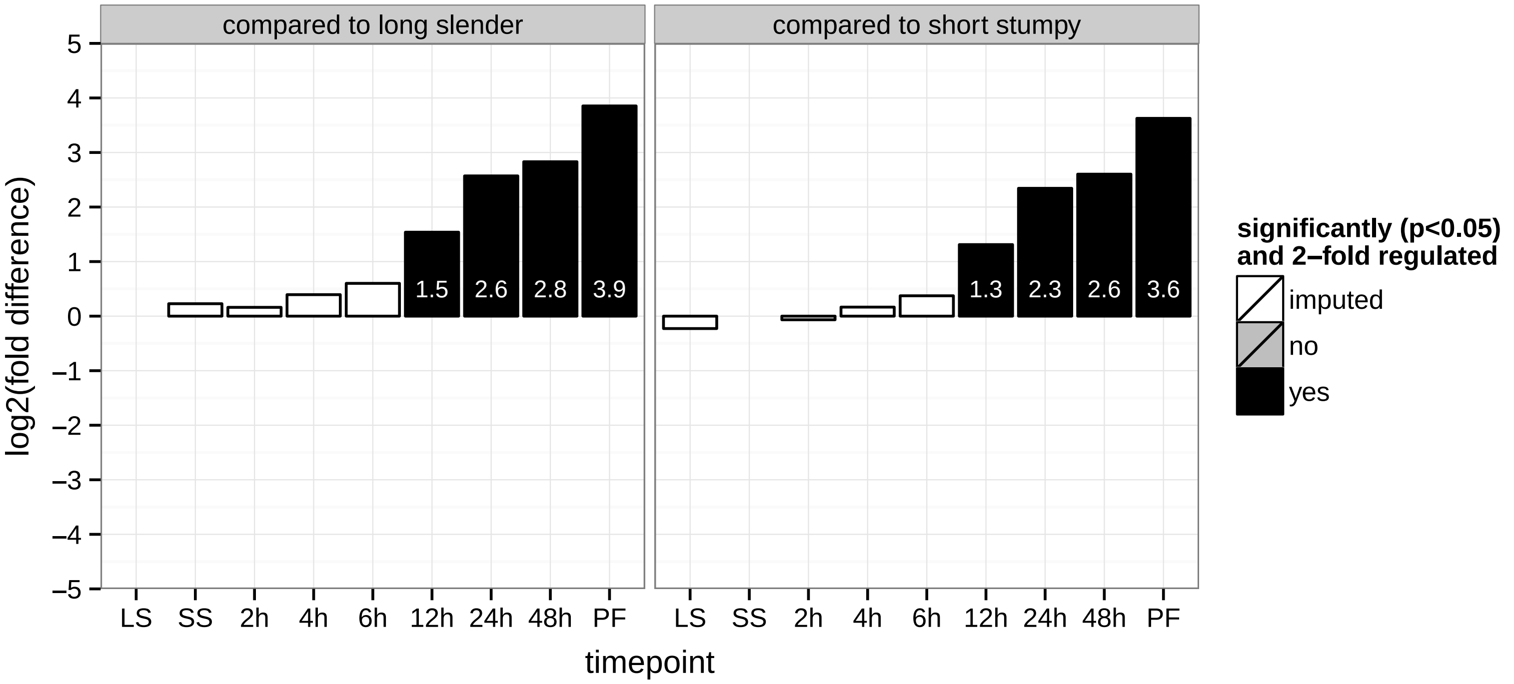
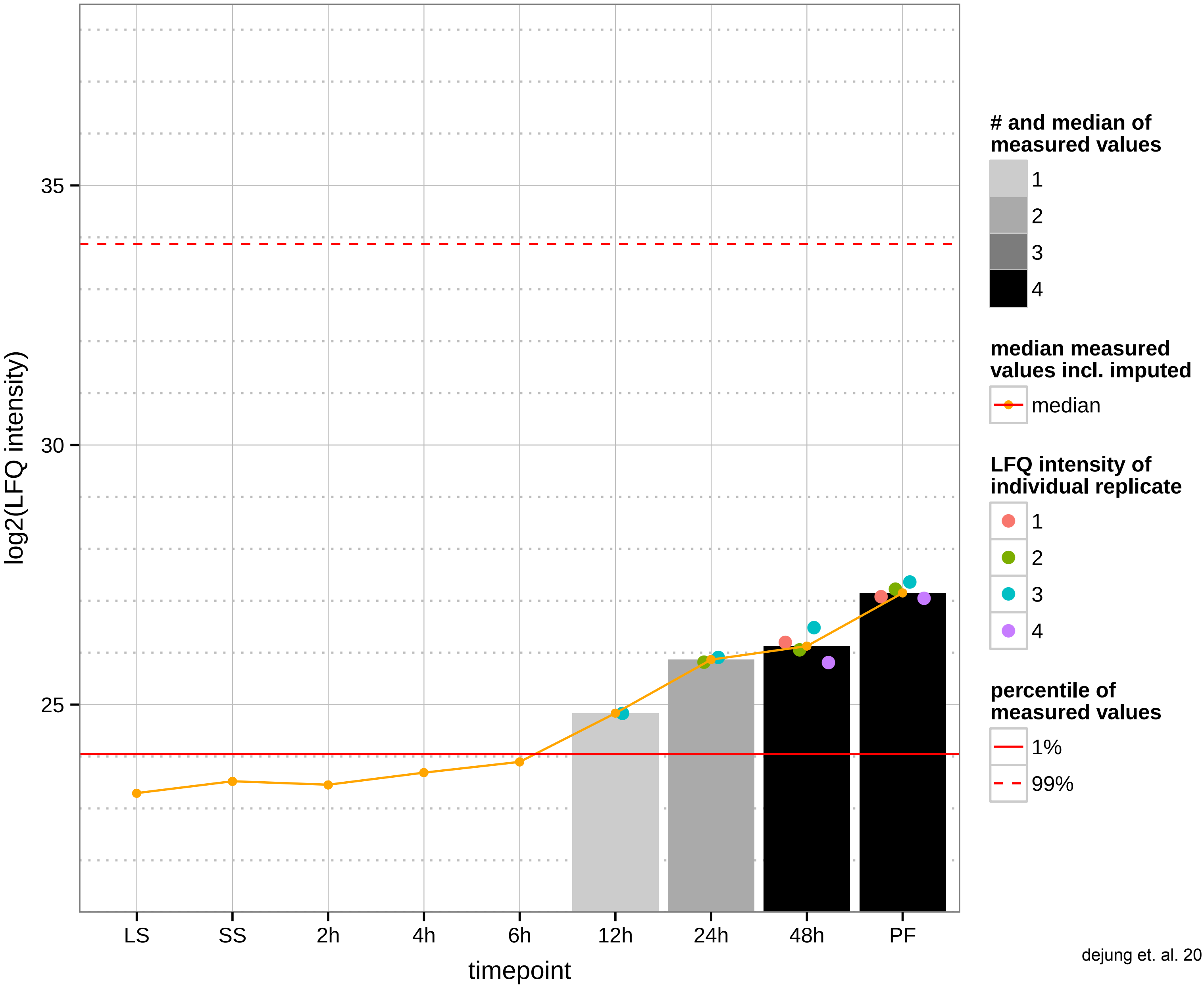
hypothetical protein, conserved
Tb927.11.13610
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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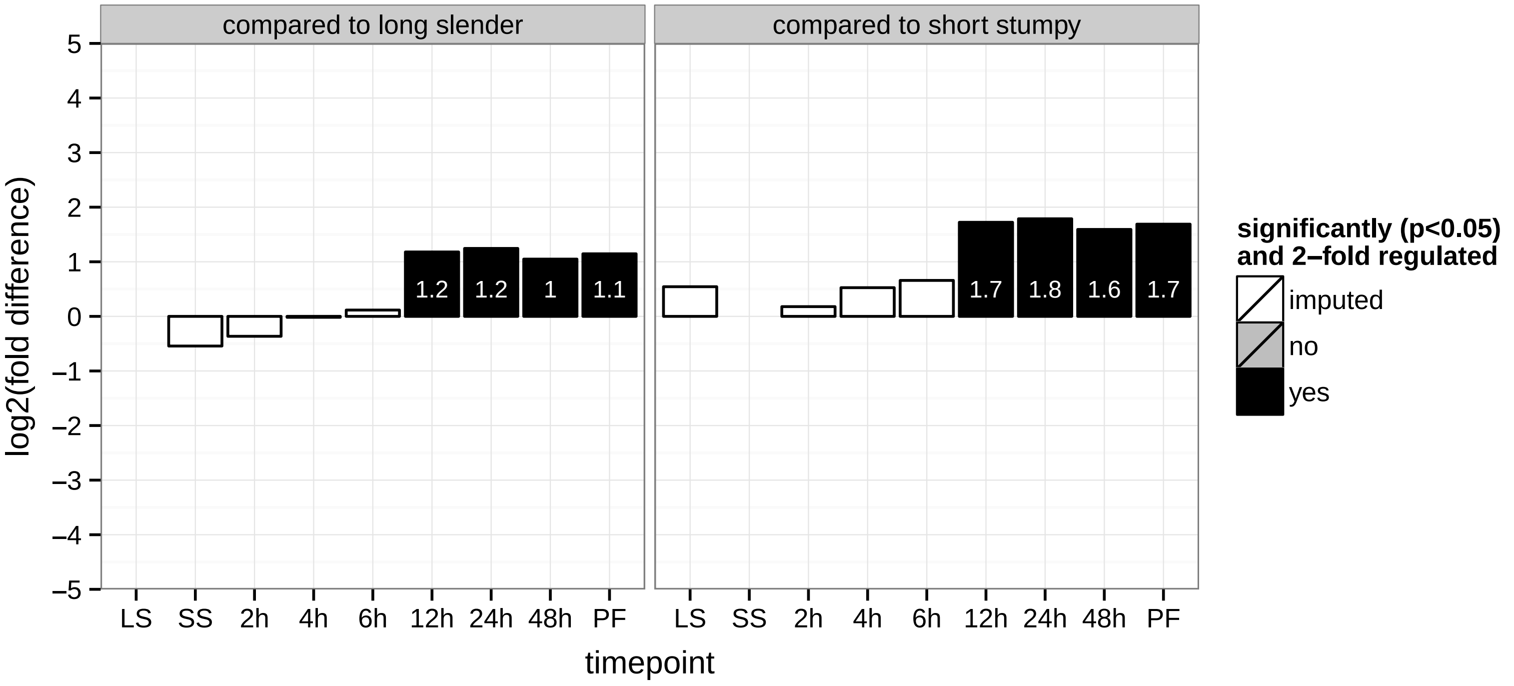
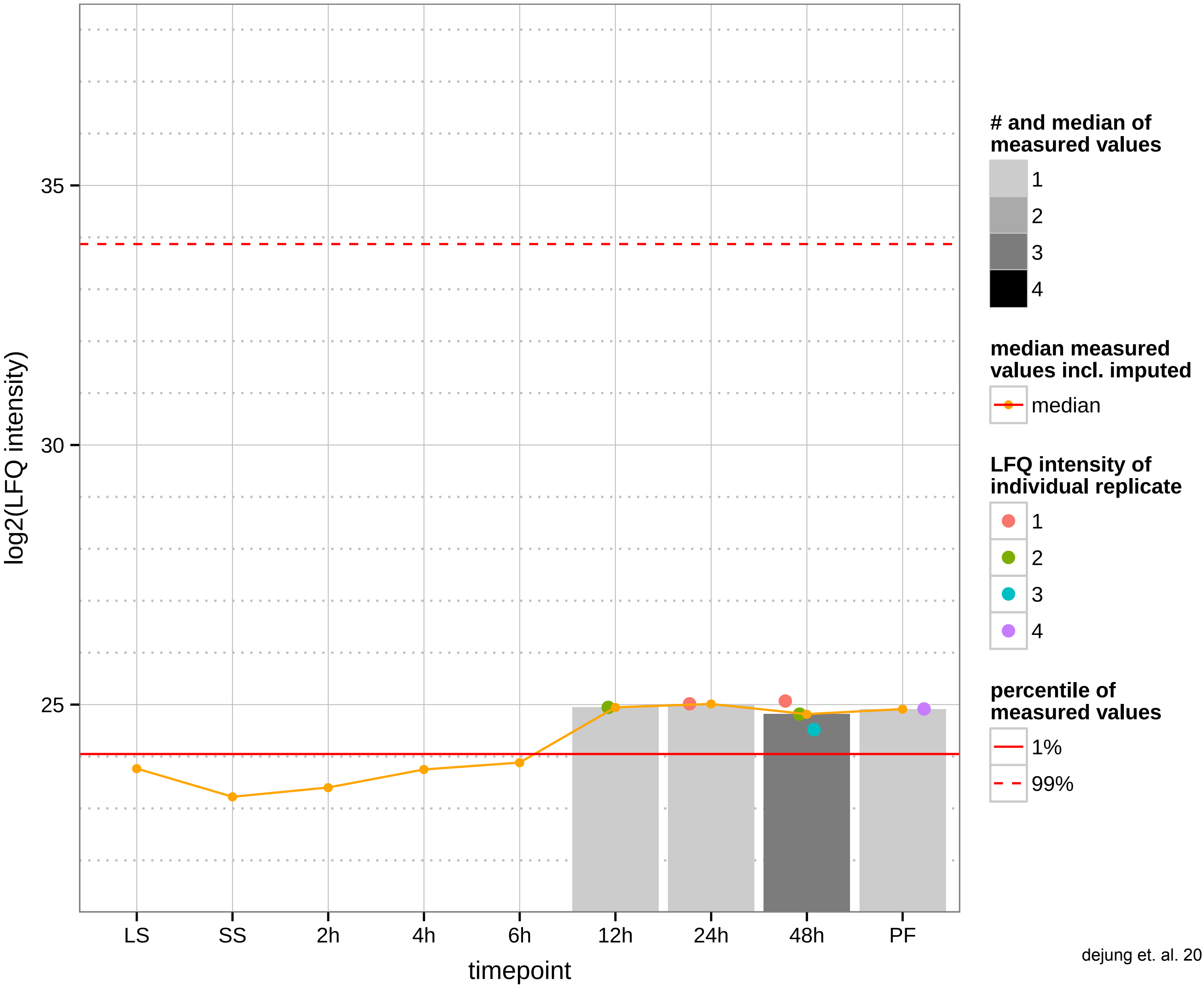
hypothetical protein, conserved
Tb927.11.13620
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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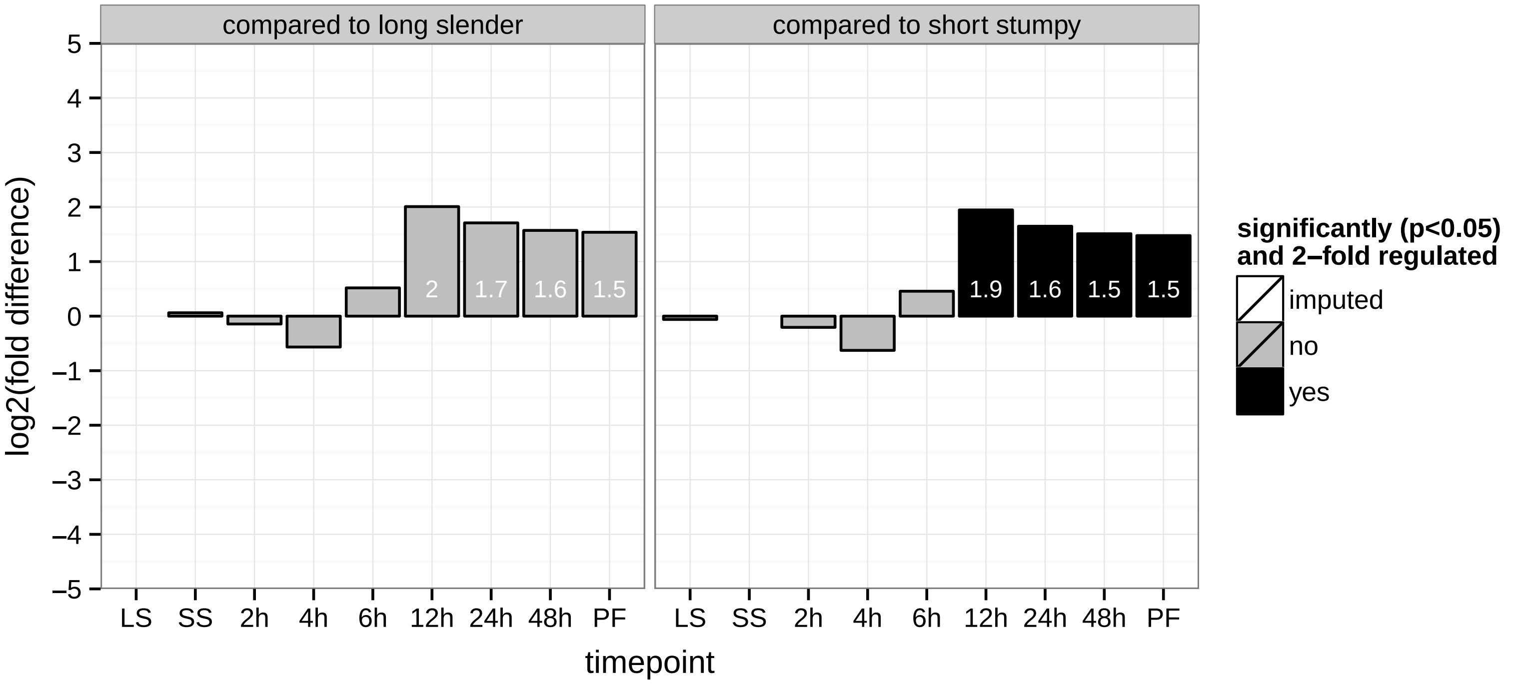
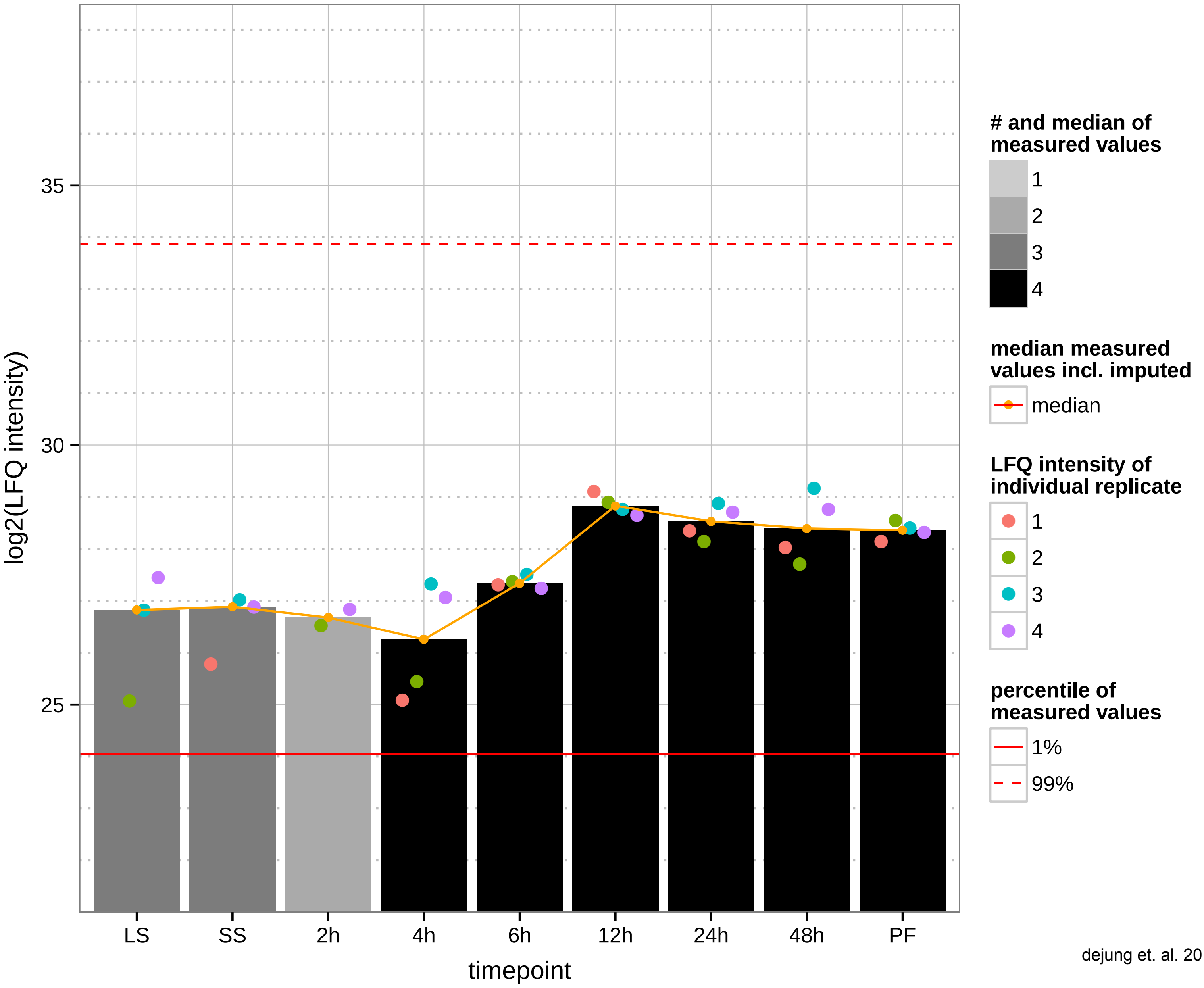
receptor–type adenylate cyclase GRESAG 4, putative
Tb927.11.13740
AGOF: adenylate cyclase activity
AGOC: integral to membrane
AGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction
PGOF: phosphorus–oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction





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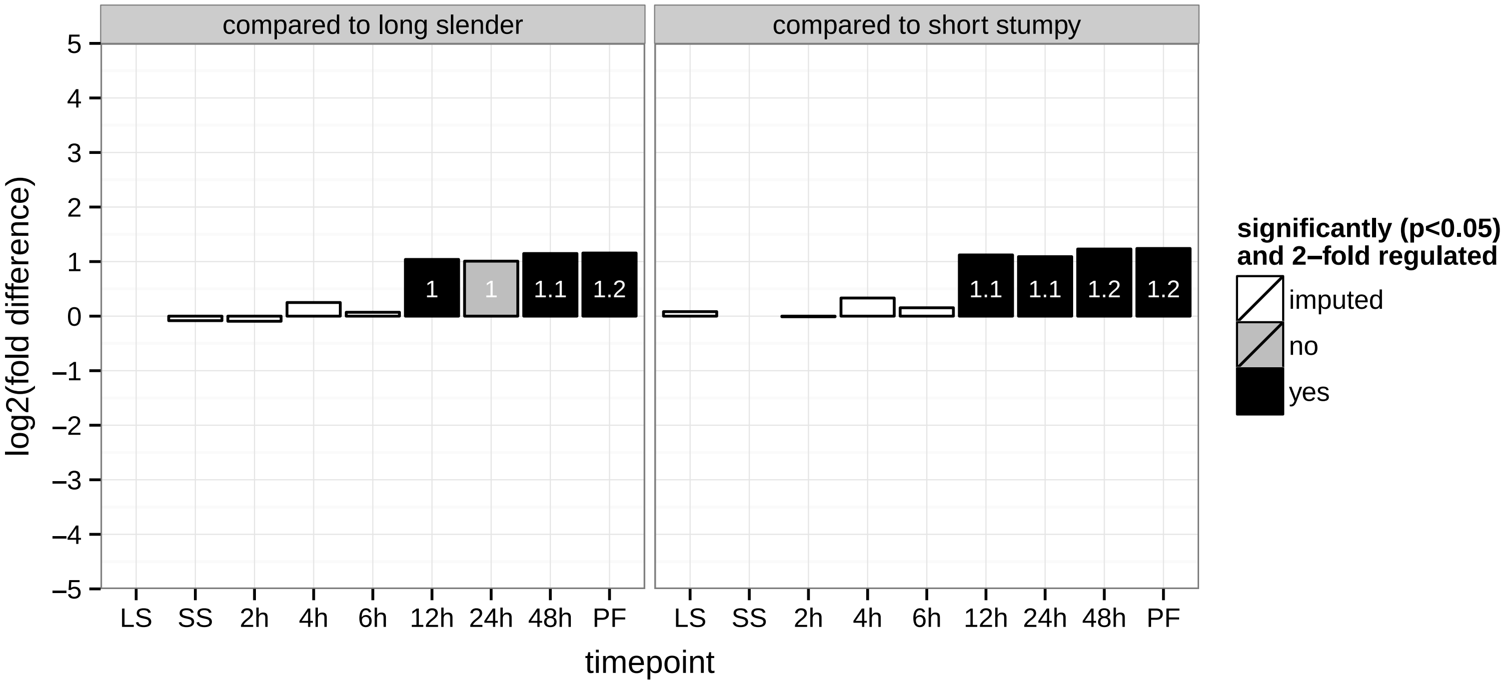
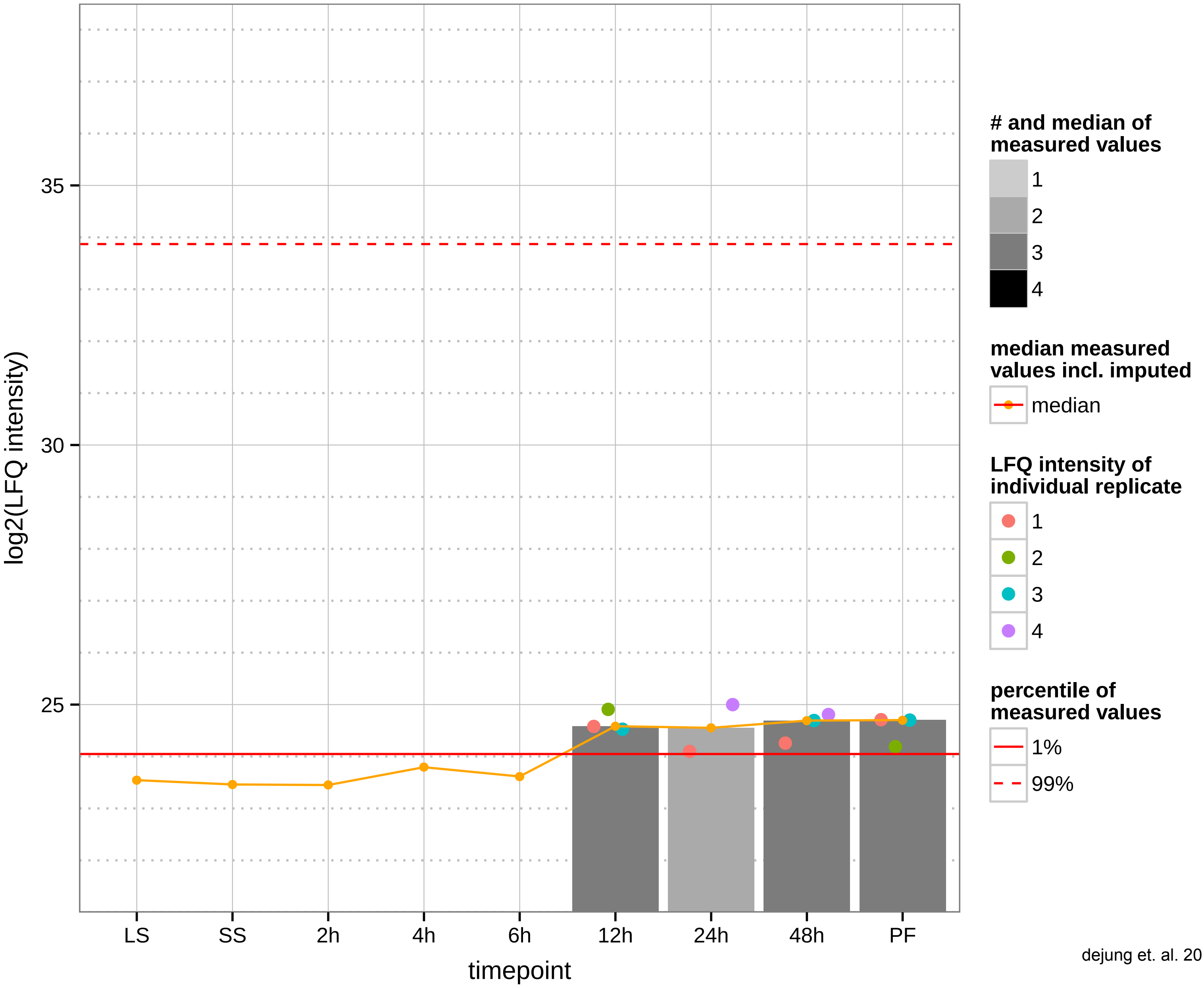
hypothetical protein, conserved
Tb927.11.13830
AGOF: heat shock protein binding
AGOC: integral to membrane, mitochondrial membrane, mitochondrion
AGOP: null
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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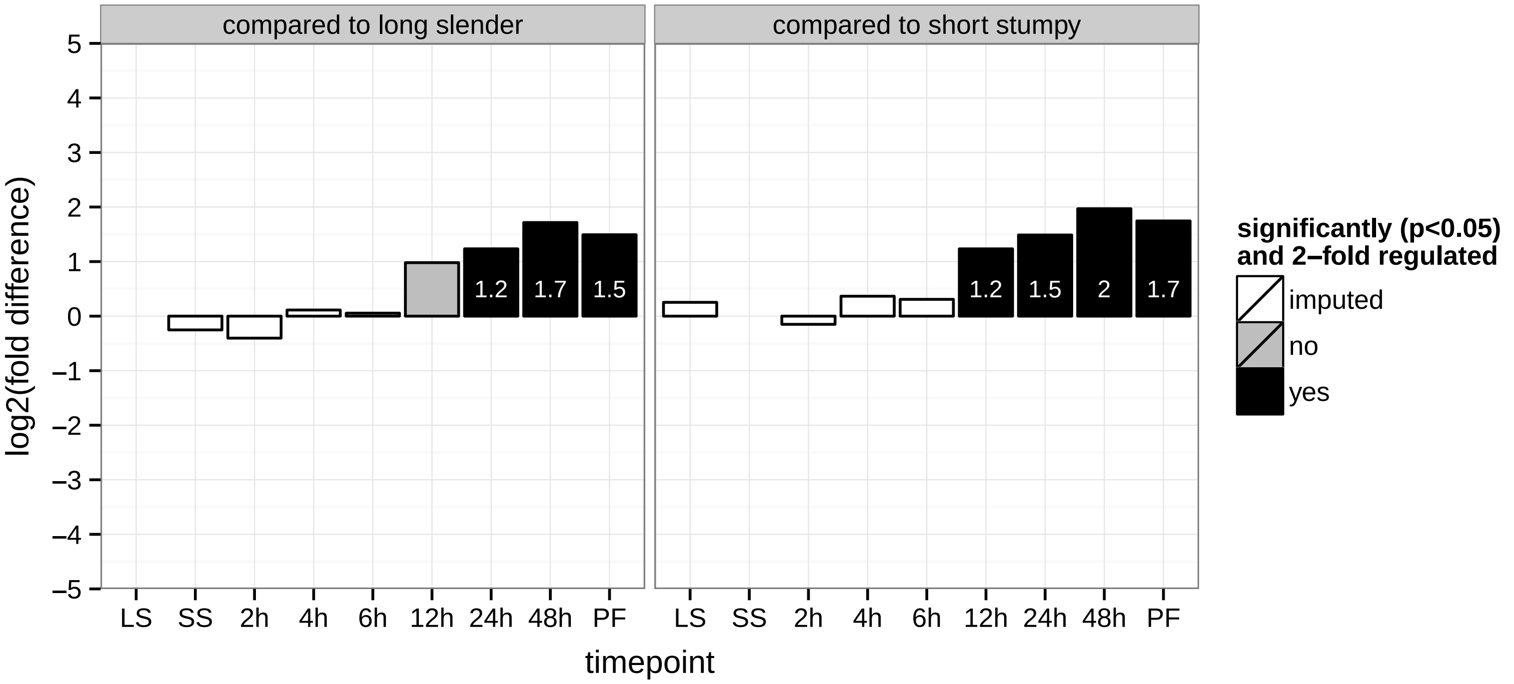
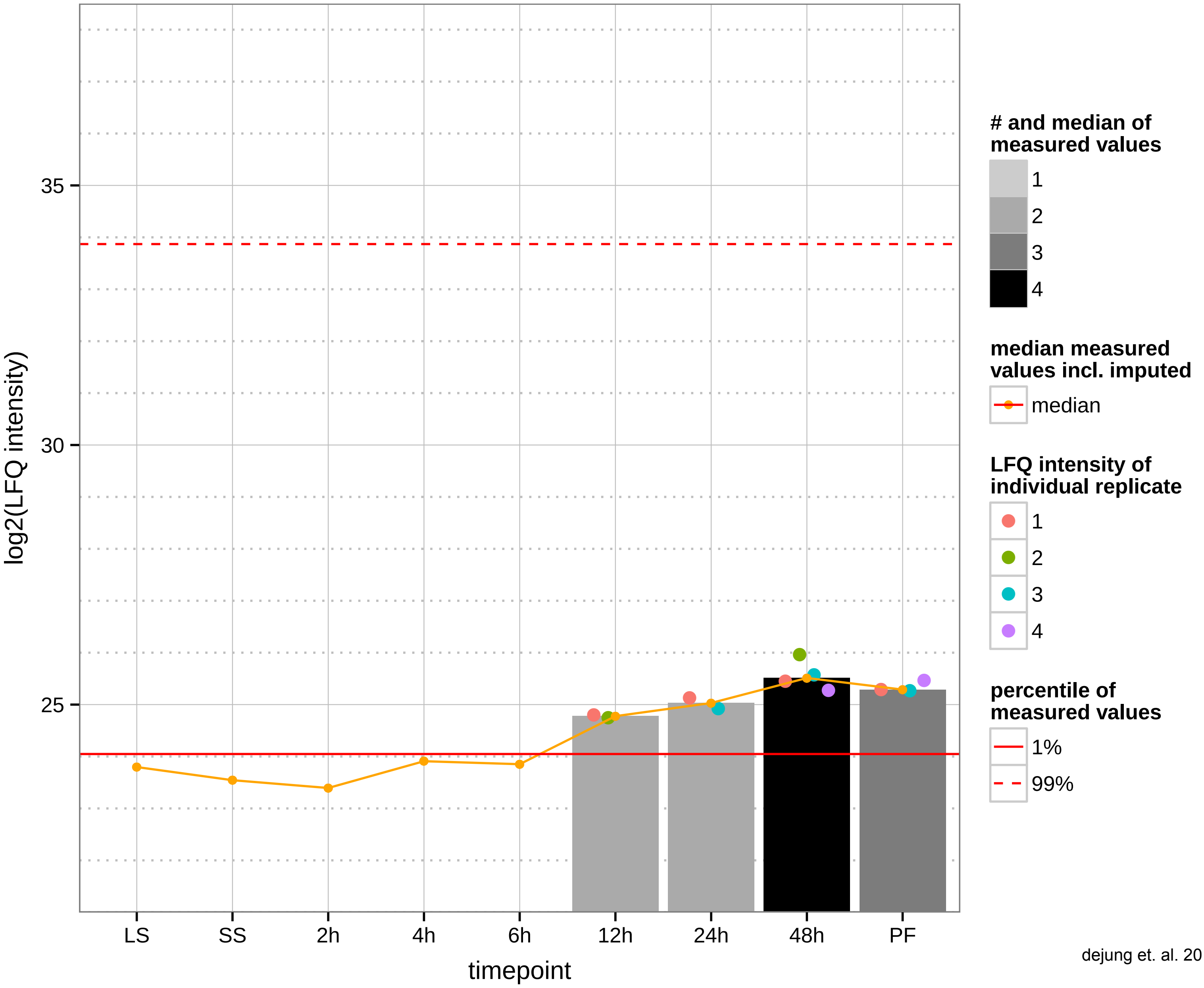
hypothetical protein, conserved
Tb927.11.13890
AGOF: catalytic activity
AGOC: intracellular, mitochondrion
AGOP: RNA metabolic process
PGOF: catalytic activity
PGOC: intracellular
PGOP: RNA metabolic process





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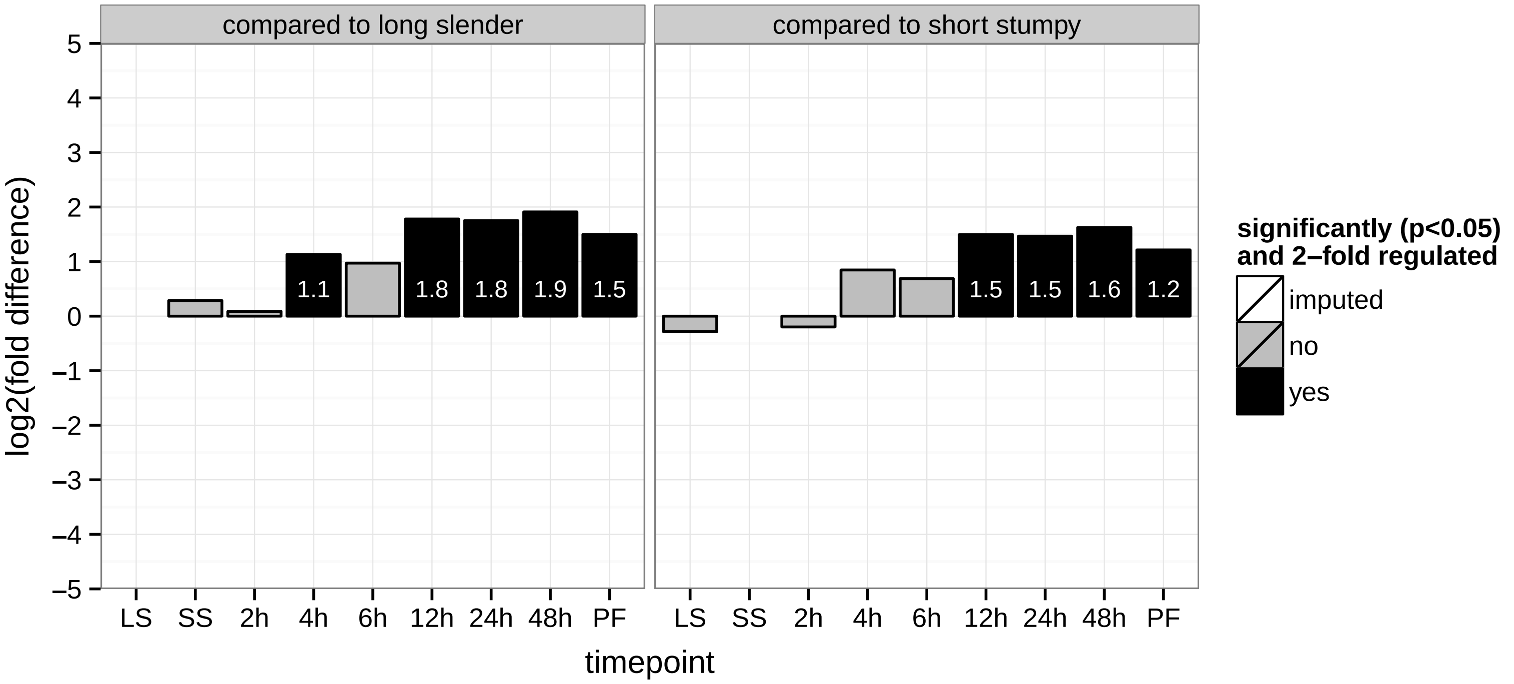
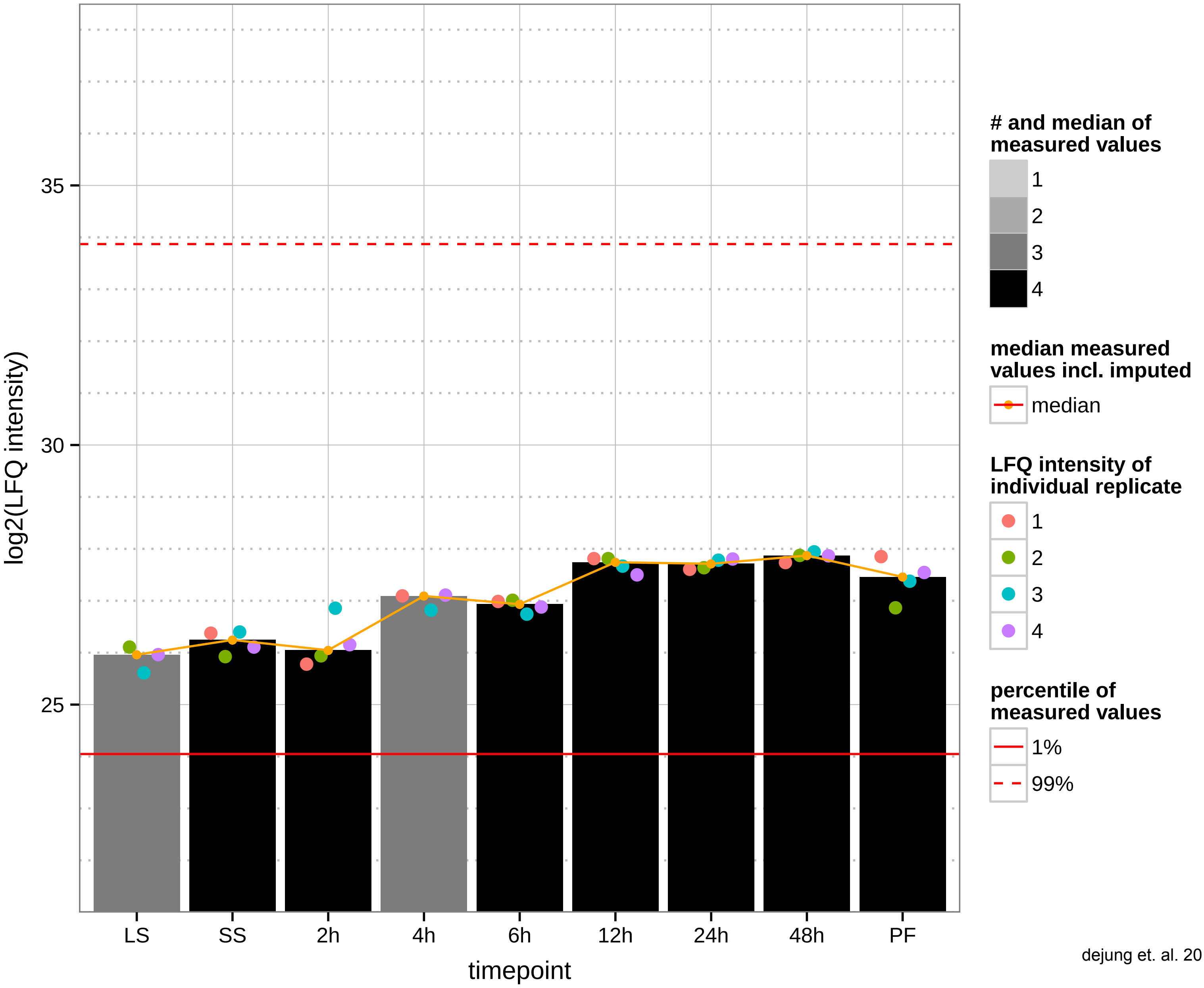
hypothetical protein, conserved
Tb927.11.14220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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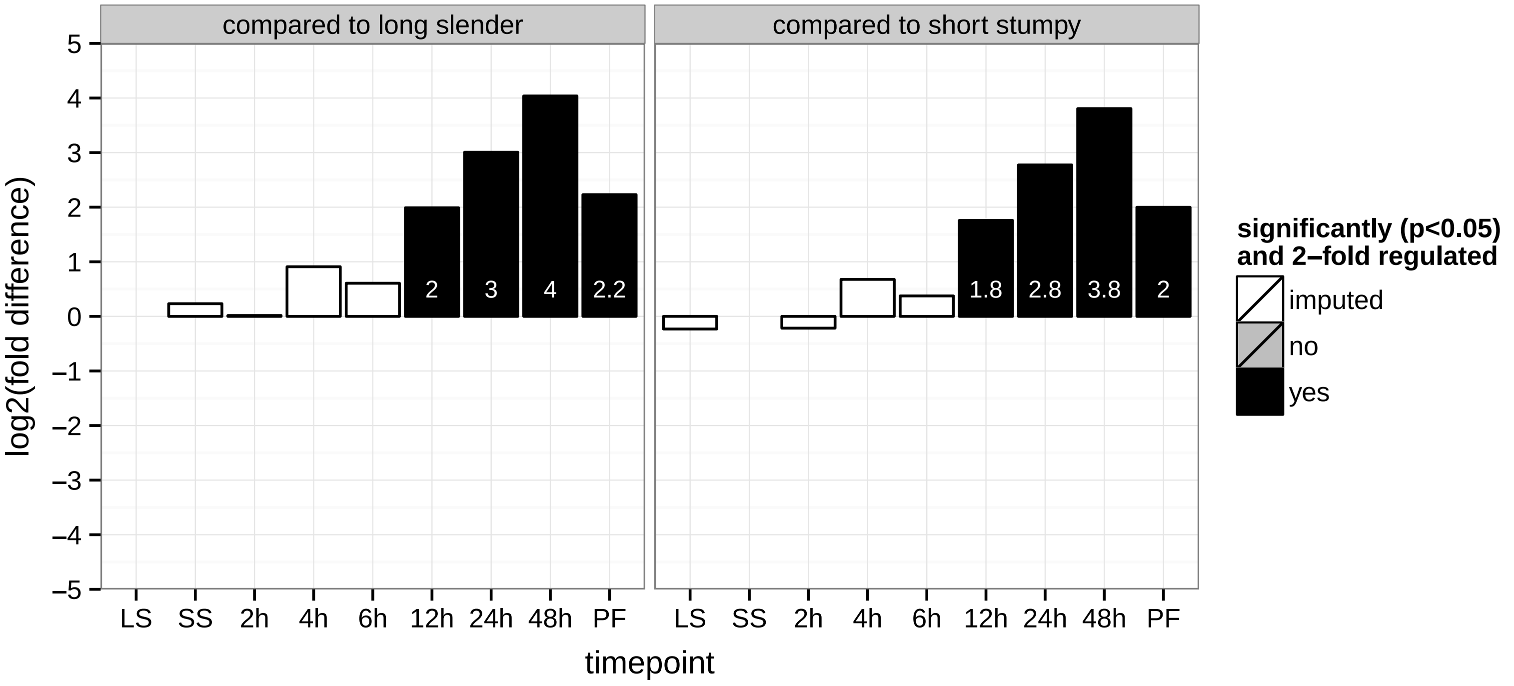
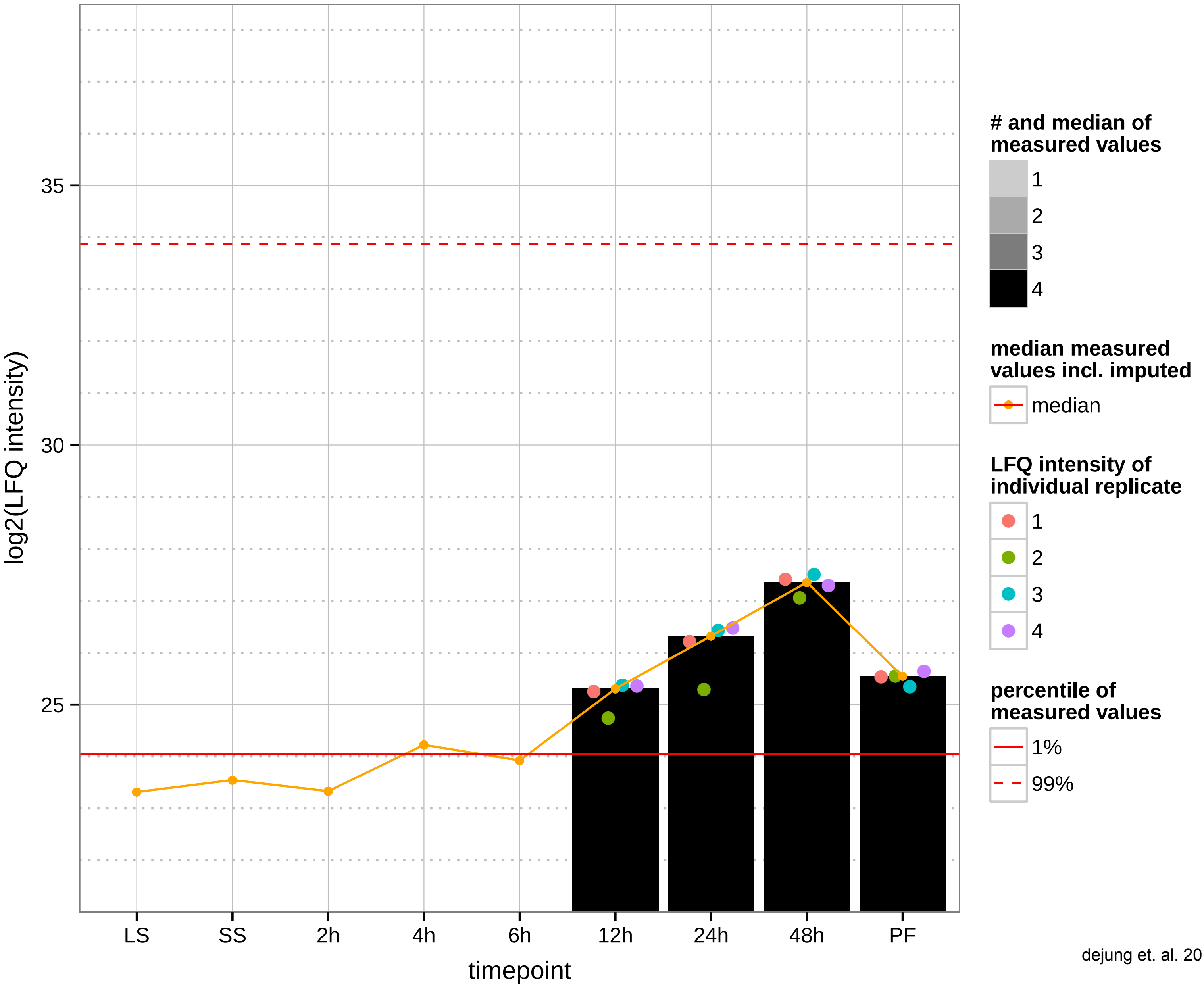
hypothetical protein, conserved
Tb927.11.14760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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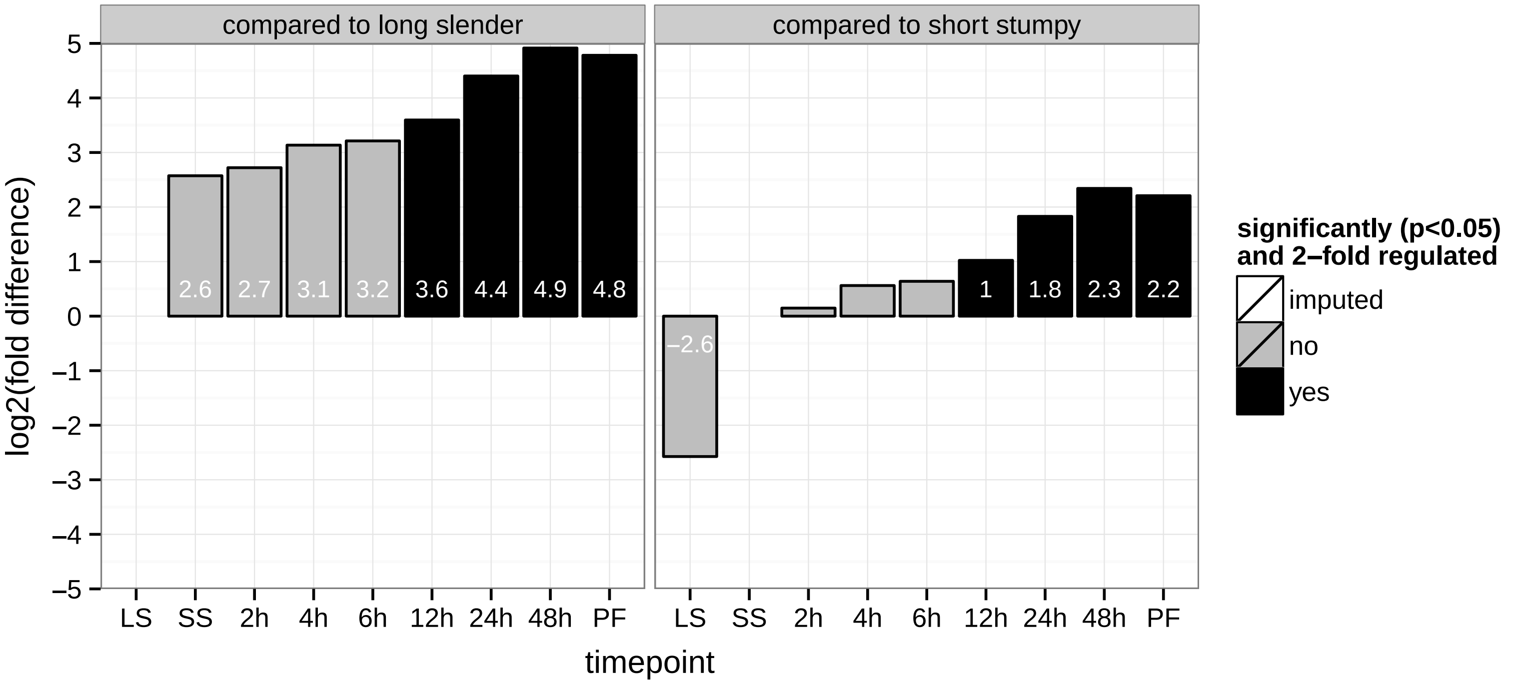
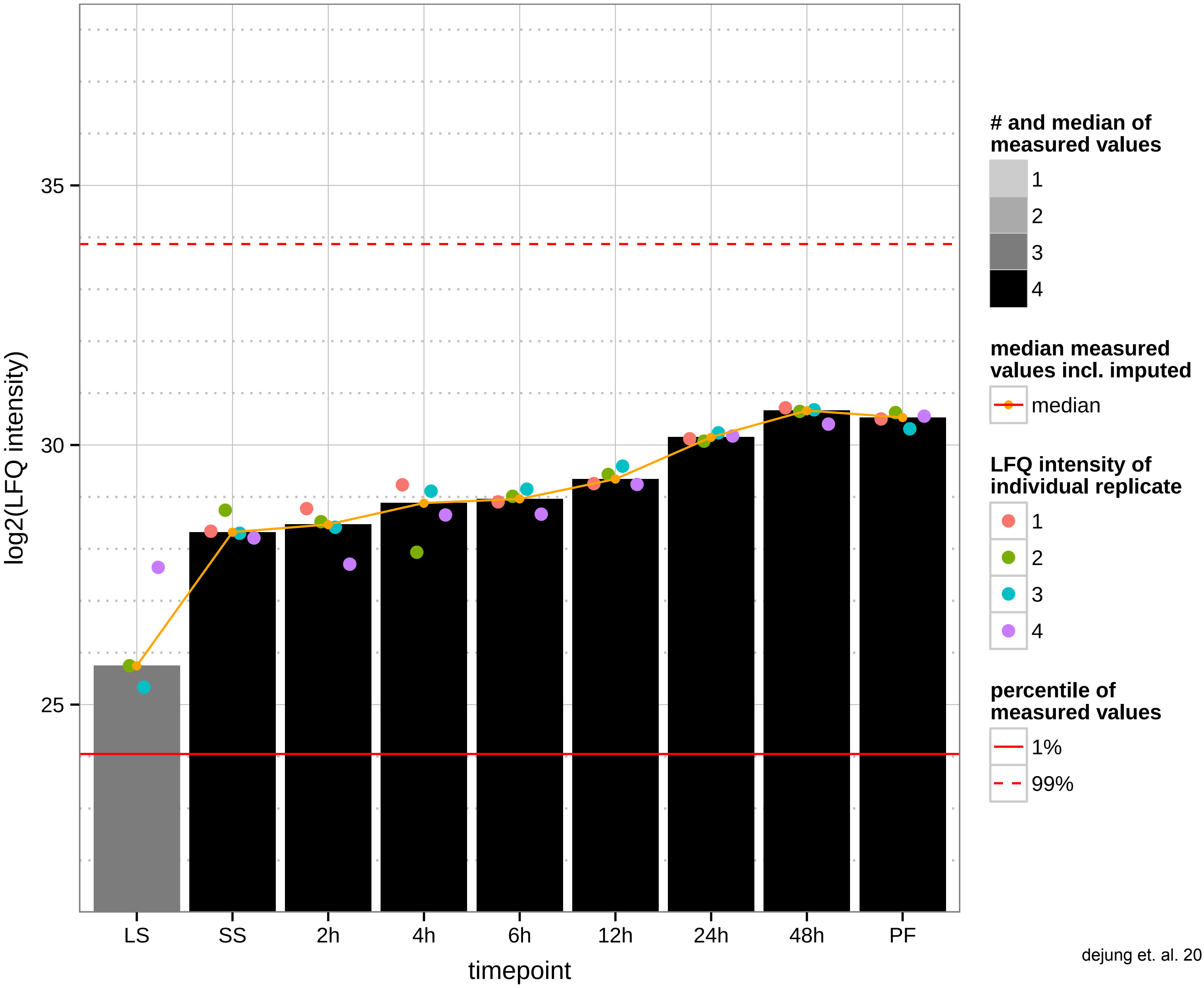
phosphomannose isomerase, putative
Tb927.11.14780
AGOF: mannose−6−phosphate isomerase activity, zinc ion binding
AGOC: cytoplasm
AGOP: carbohydrate metabolic process
PGOF: mannose−6−phosphate isomerase activity, zinc ion binding
PGOC: null
PGOP: carbohydrate metabolic process





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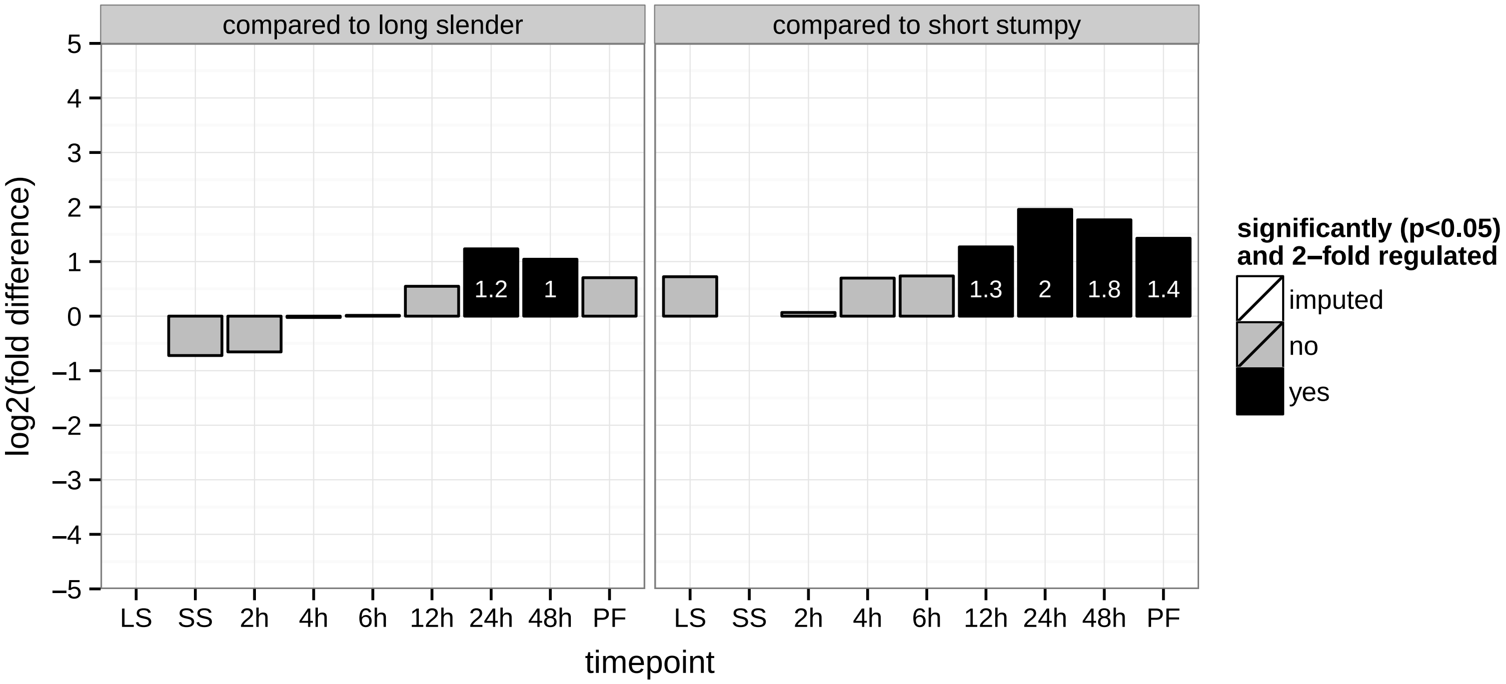
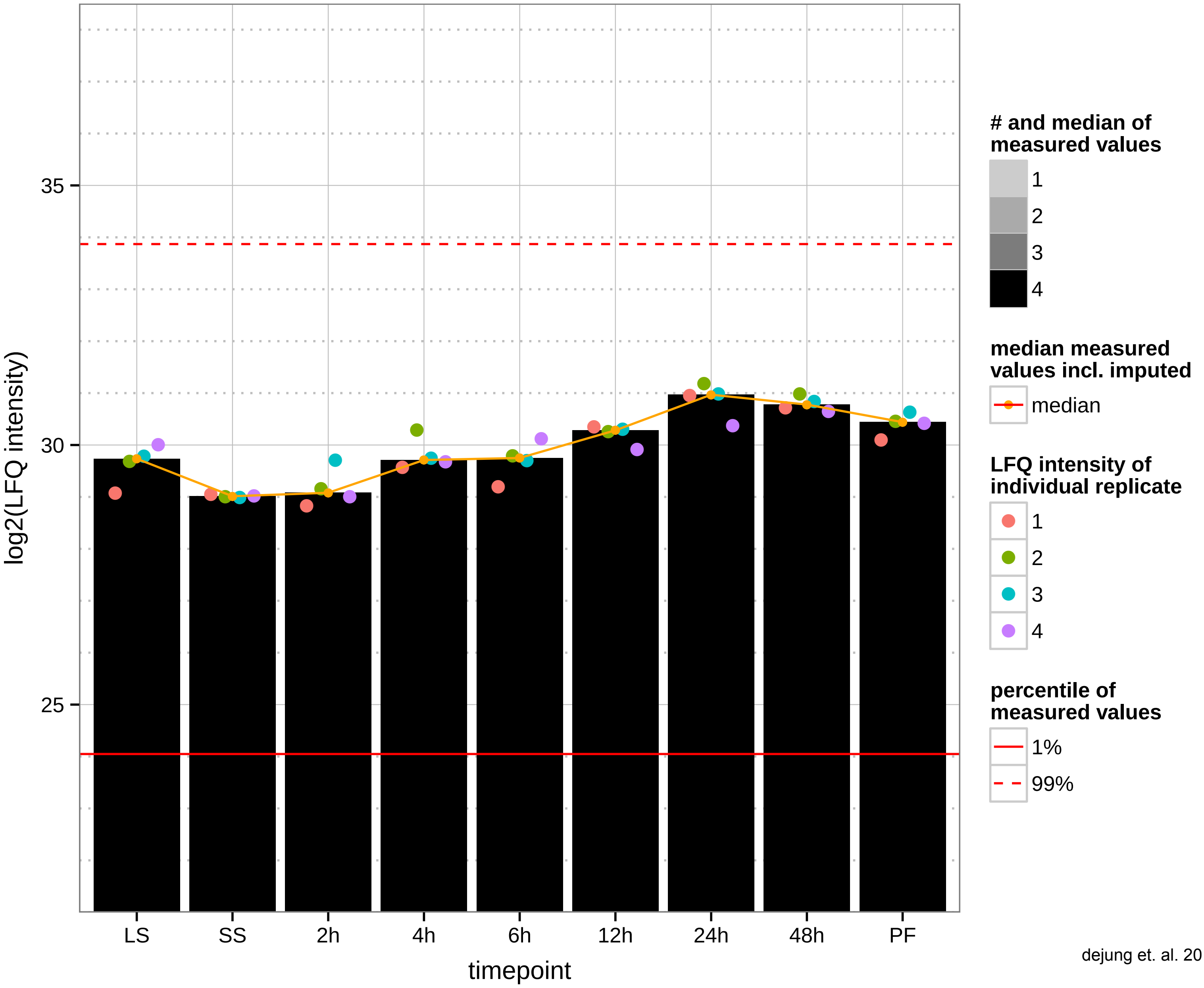
iron superoxide dismutase (TbSODB)
Tb927.11.15020
AGOF: metal ion binding, superoxide dismutase activity
AGOC: glycosome
AGOP: oxidation–reduction process, superoxide metabolic process
PGOF: metal ion binding, superoxide dismutase activity
PGOC: null
PGOP: oxidation–reduction process, superoxide metabolic process





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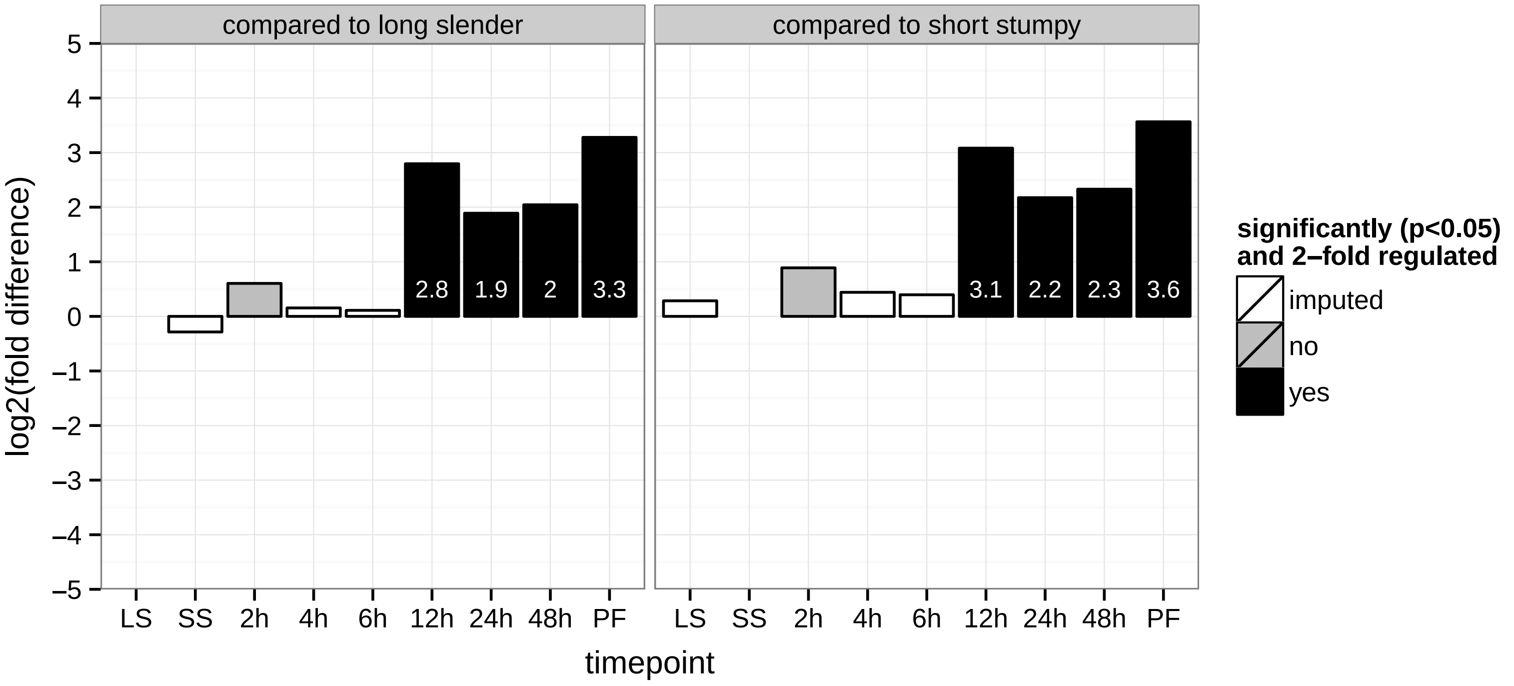
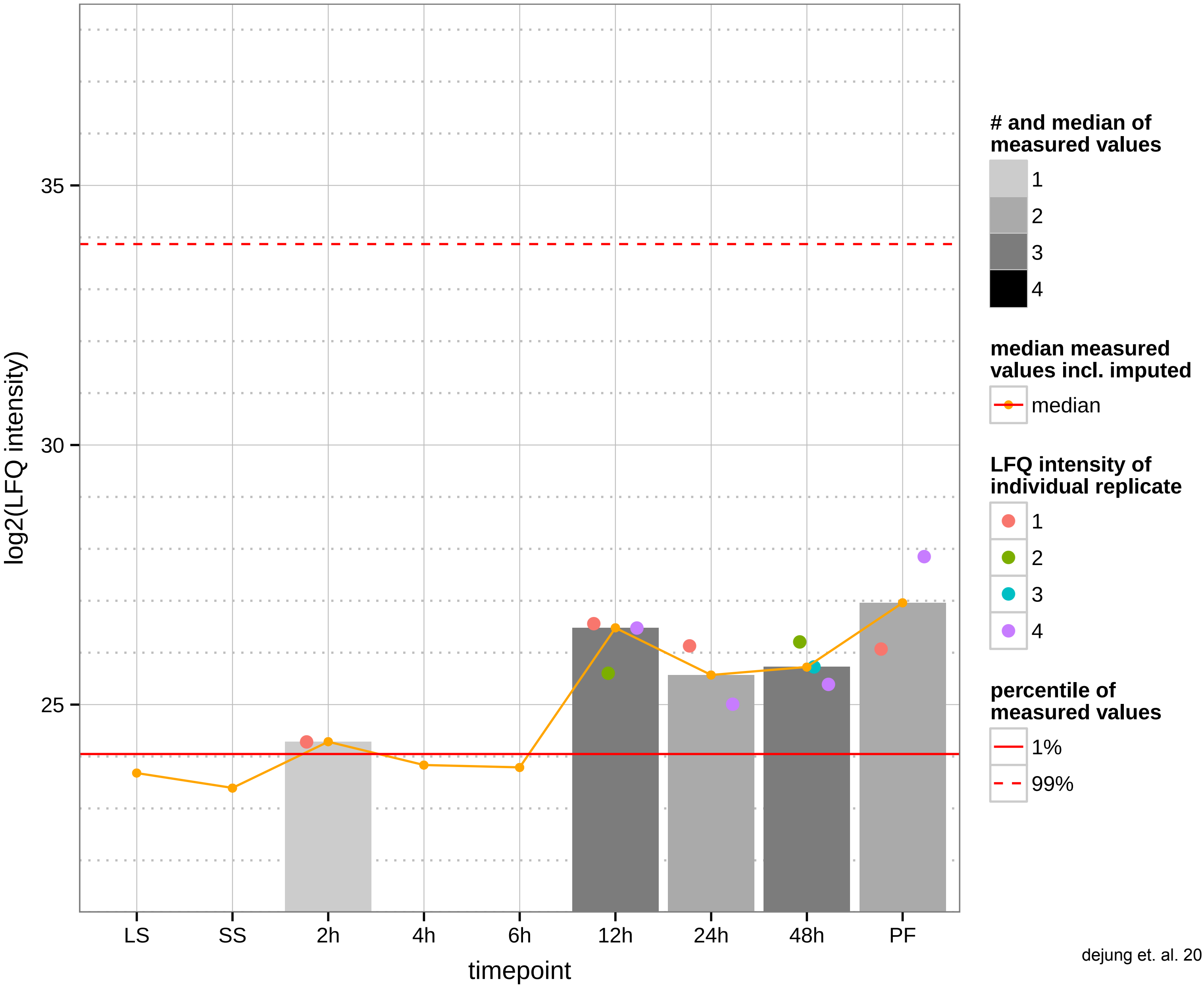
hypothetical protein
Tb927.11.15450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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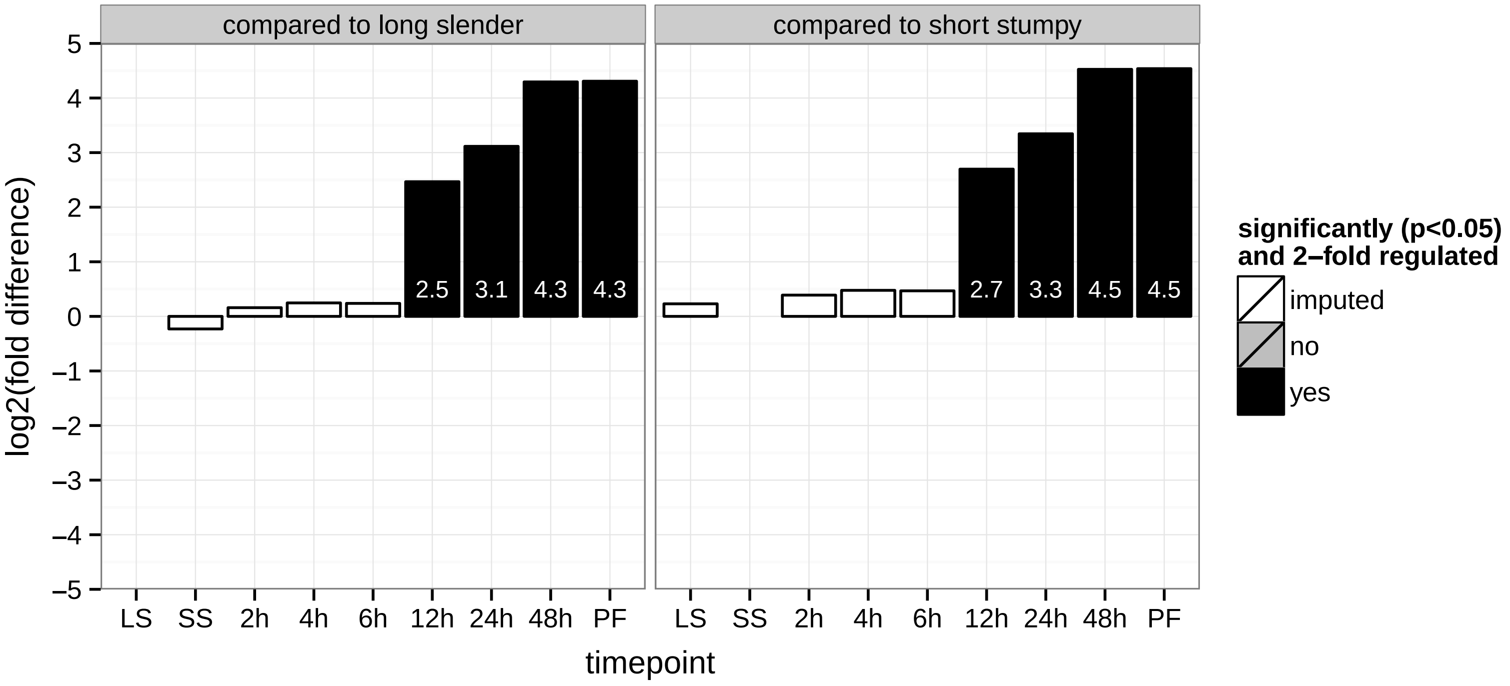
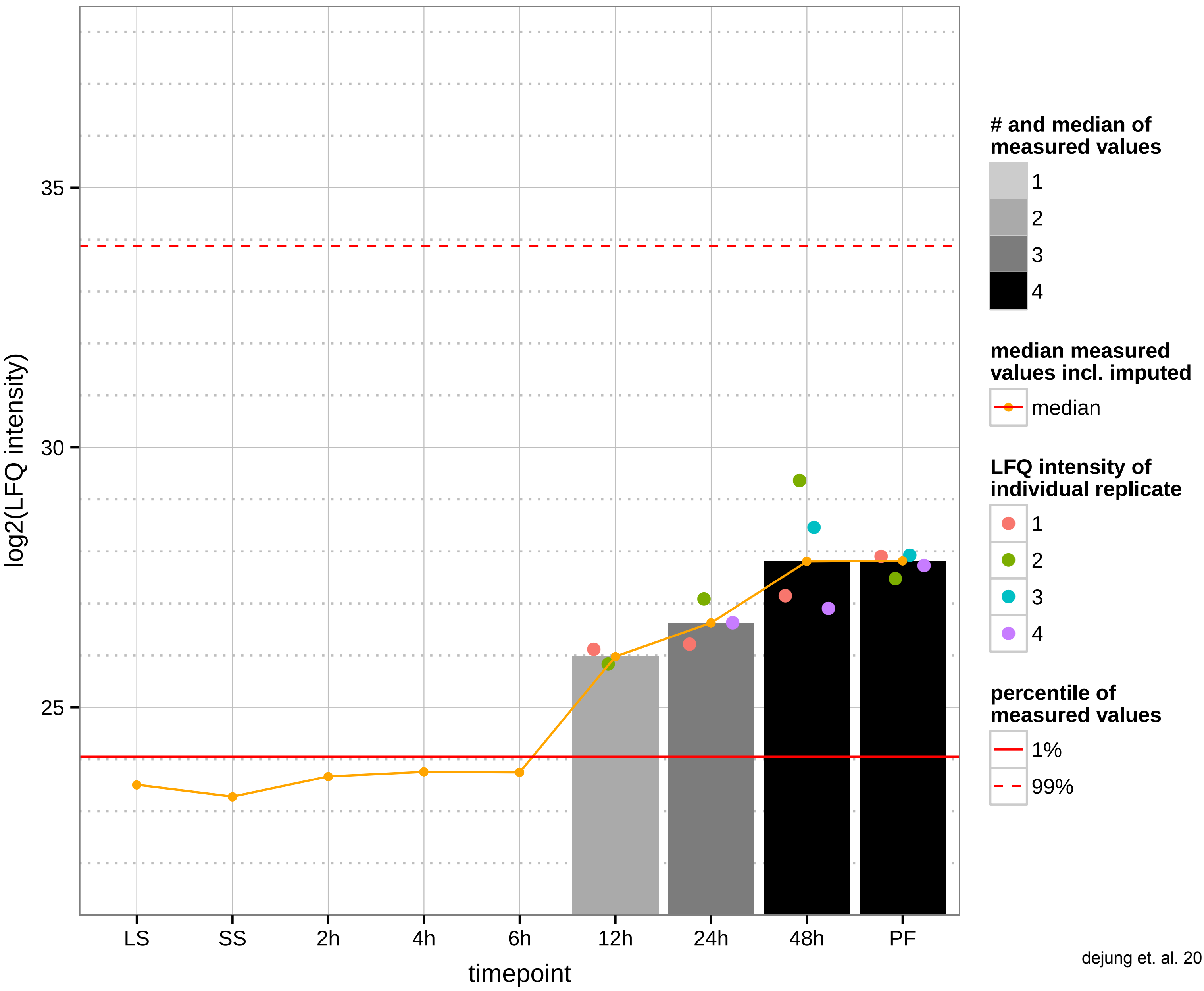
NADH–cytochrome b5 reductase, putative (B5R)
Tb927.11.15550
AGOF: cytochrome–b5 reductase activity, electron carrier activity
AGOC: null
AGOP: oxidation–reduction process
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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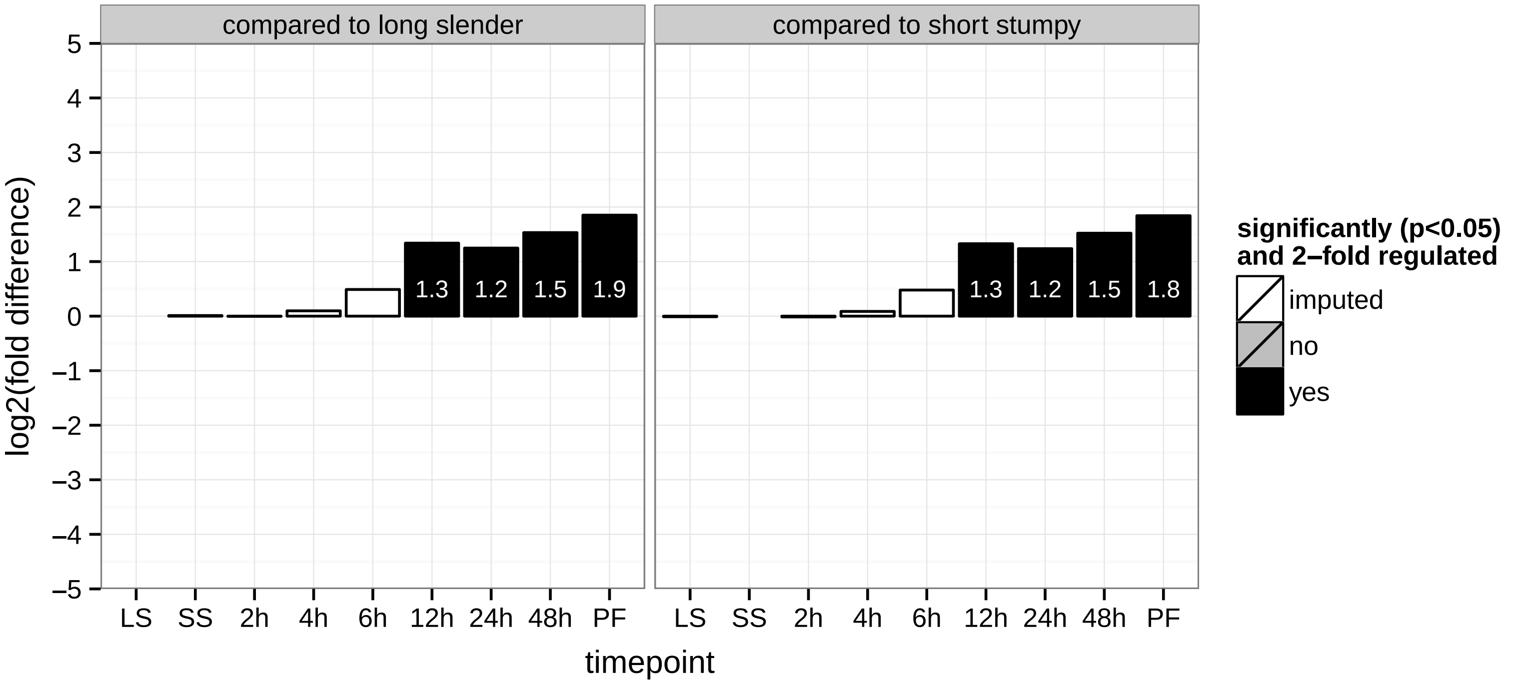
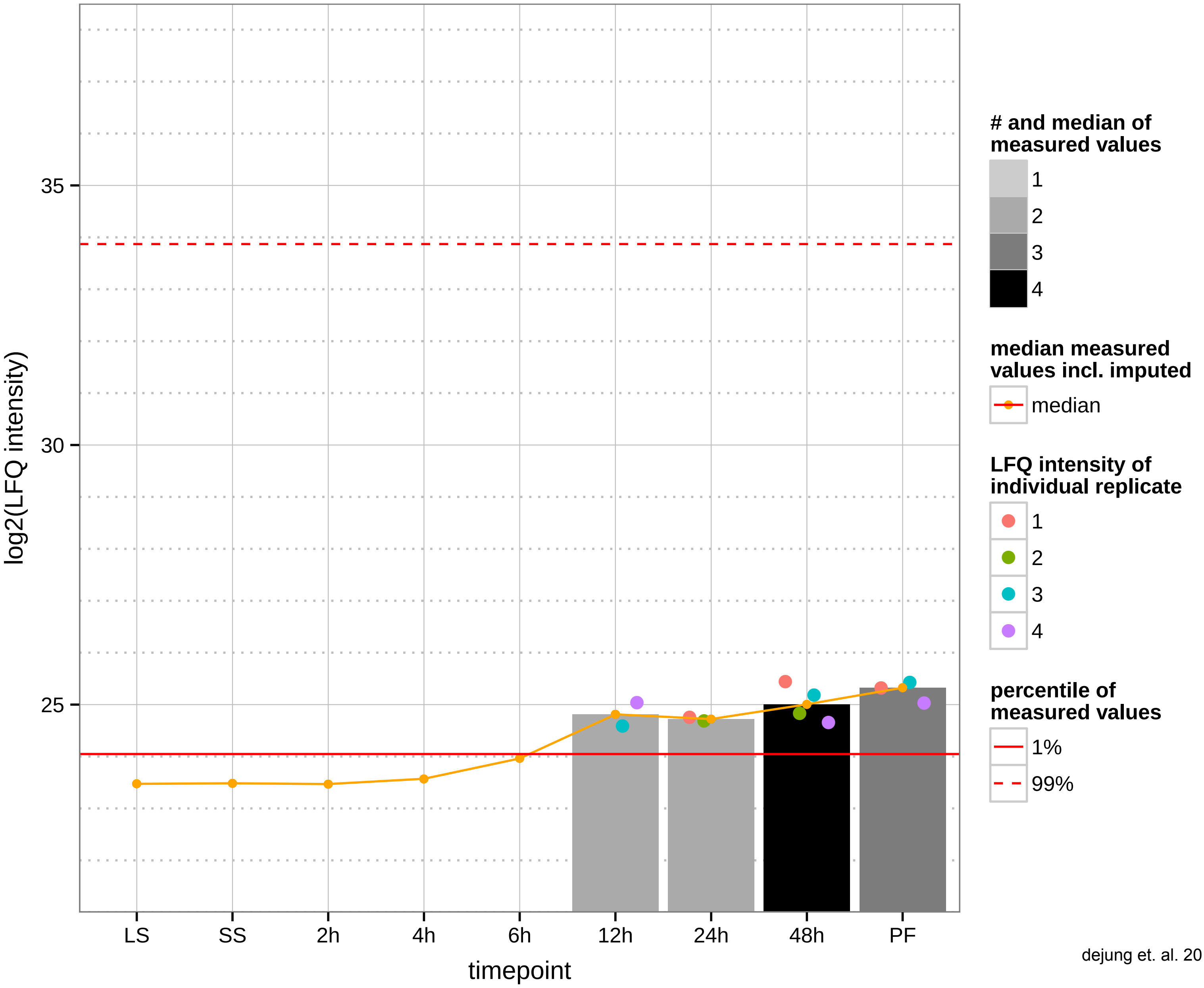
superoxide dismutase, putative
Tb927.11.15820
AGOF: metal ion binding, superoxide dismutase activity
AGOC: mitochondrion
AGOP: oxidation–reduction process, superoxide metabolic process
PGOF: metal ion binding, superoxide dismutase activity
PGOC: null
PGOP: oxidation–reduction process, superoxide metabolic process





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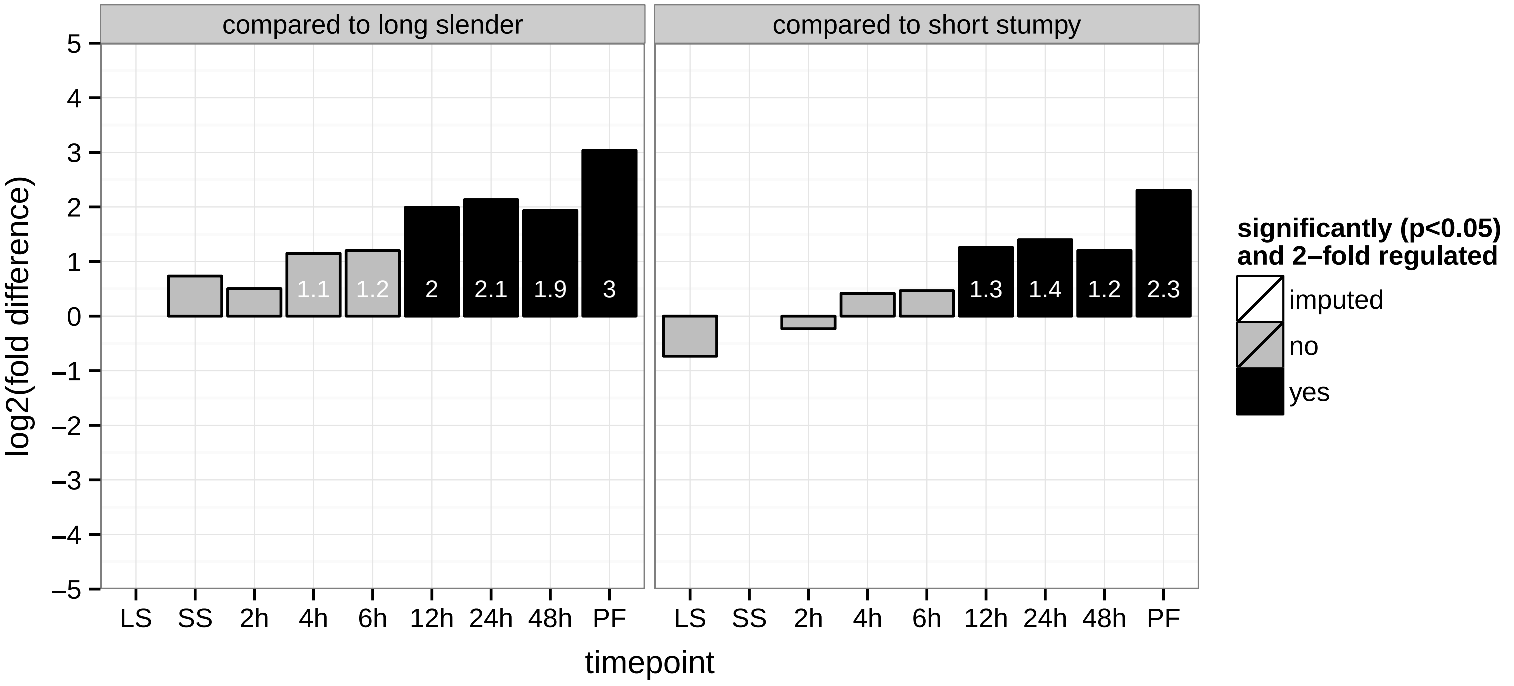
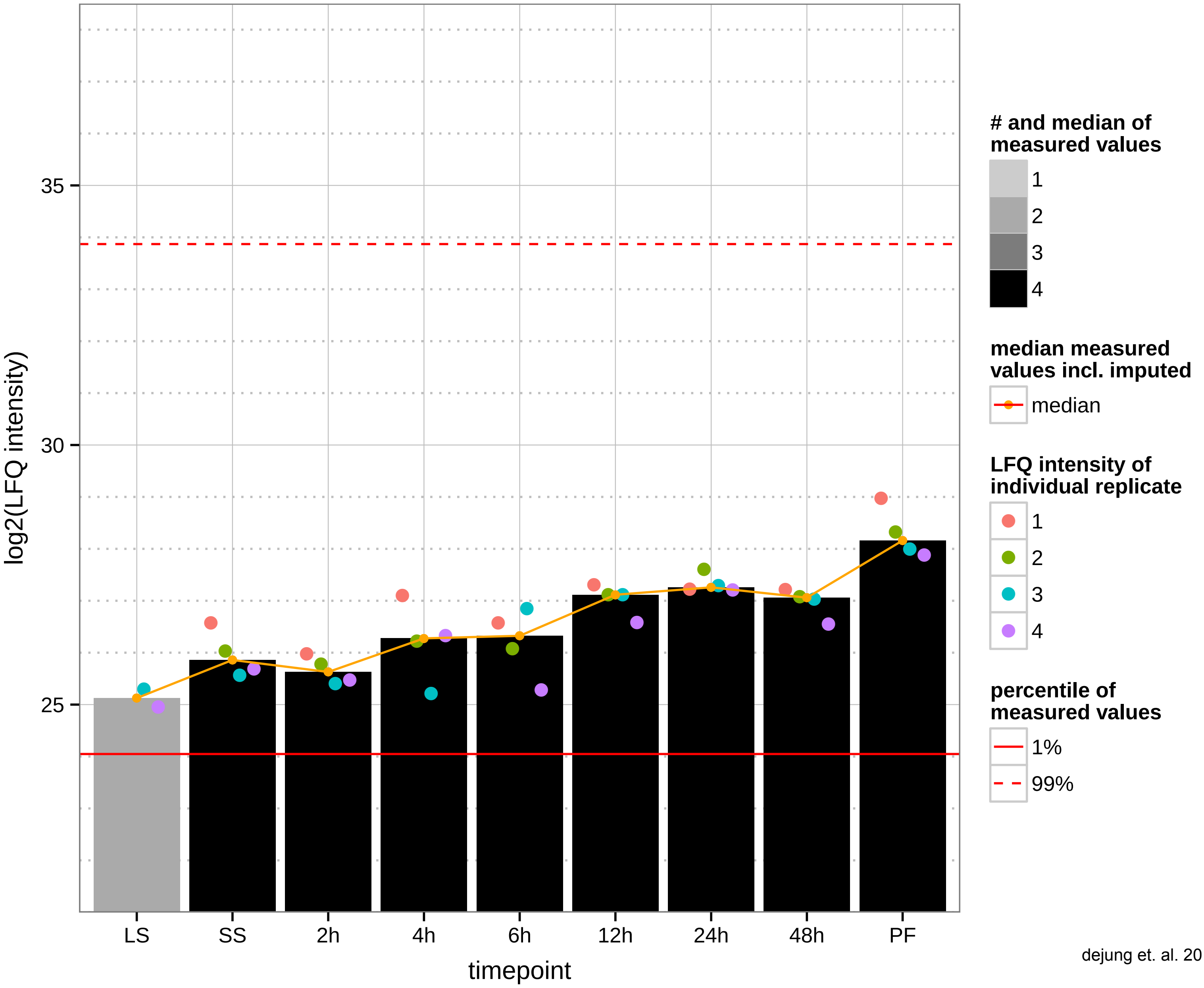
RNA–binding protein, putative (DRBD10)
Tb927.11.16020
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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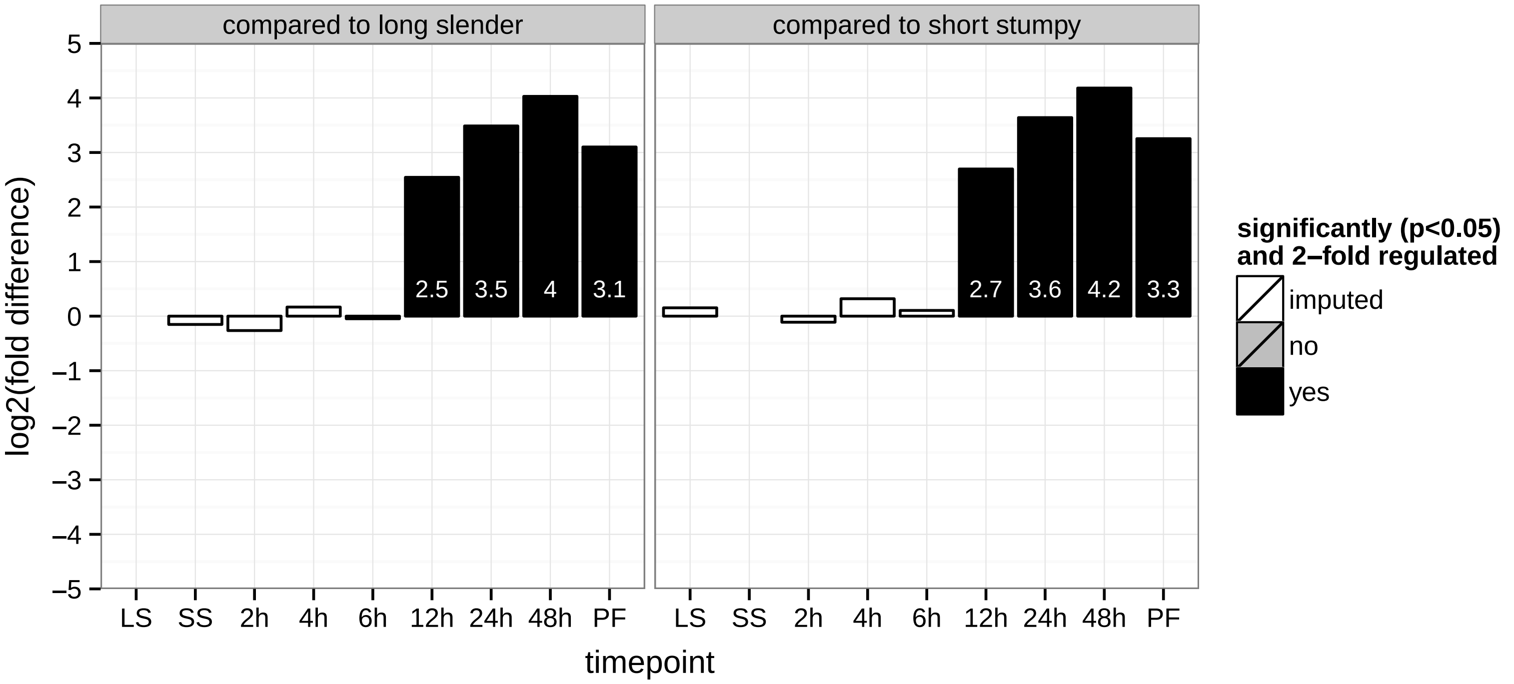
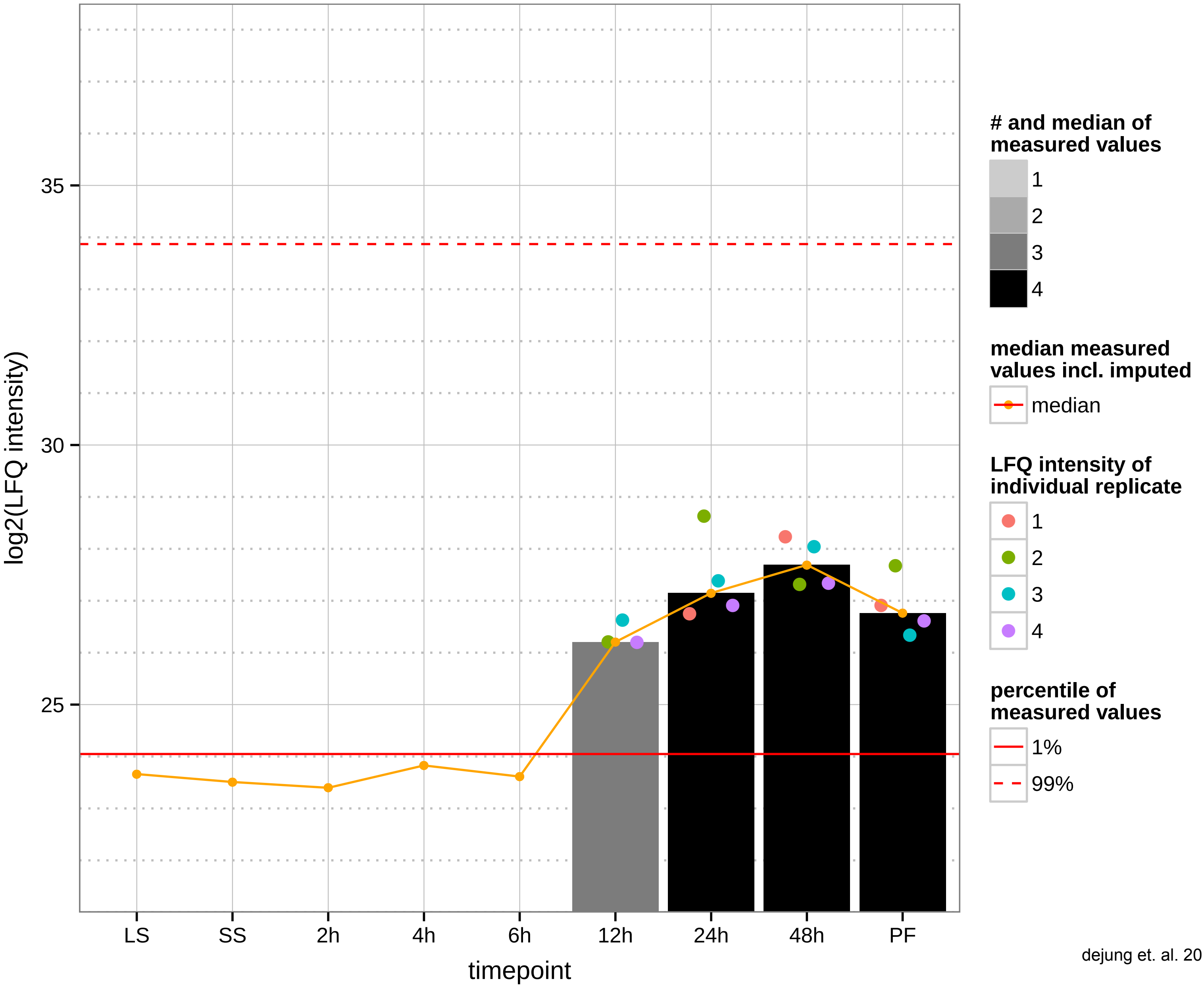
hypothetical protein, conserved
Tb927.11.16220
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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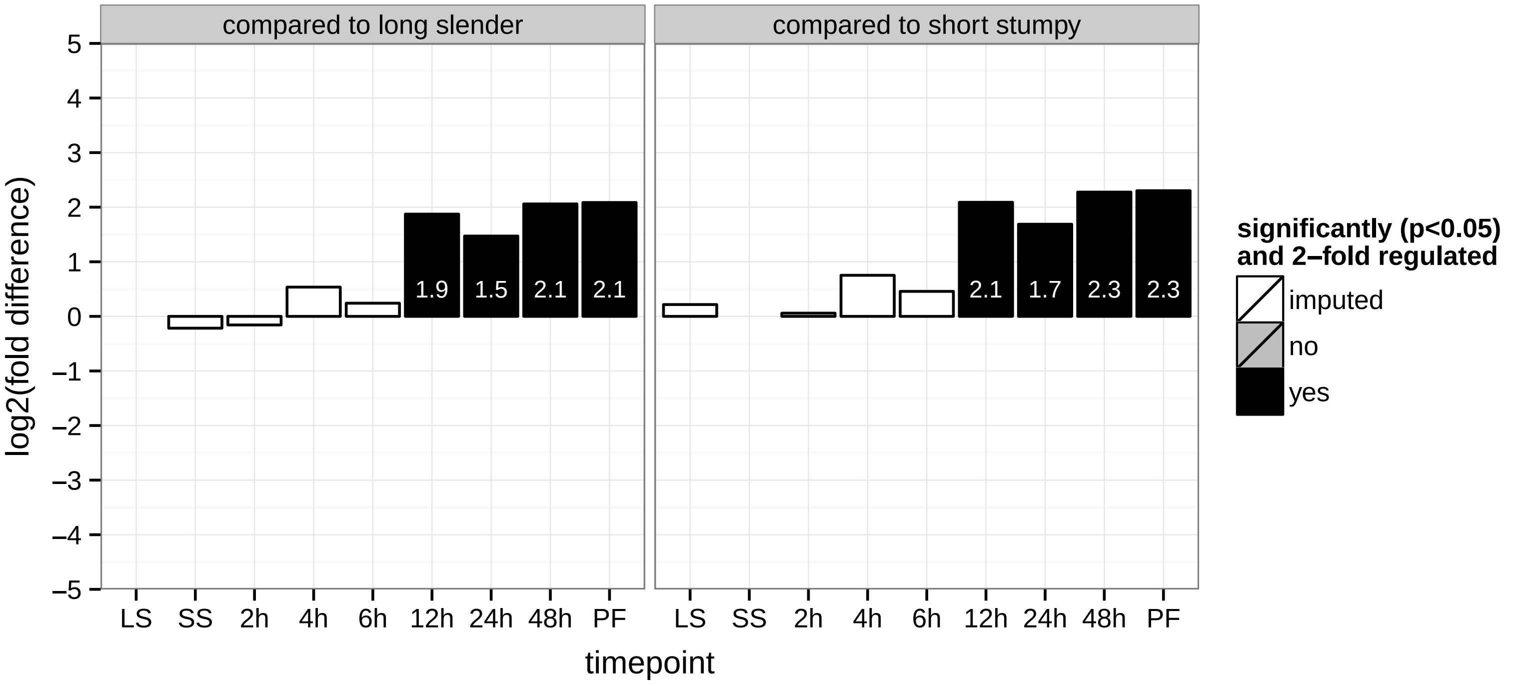
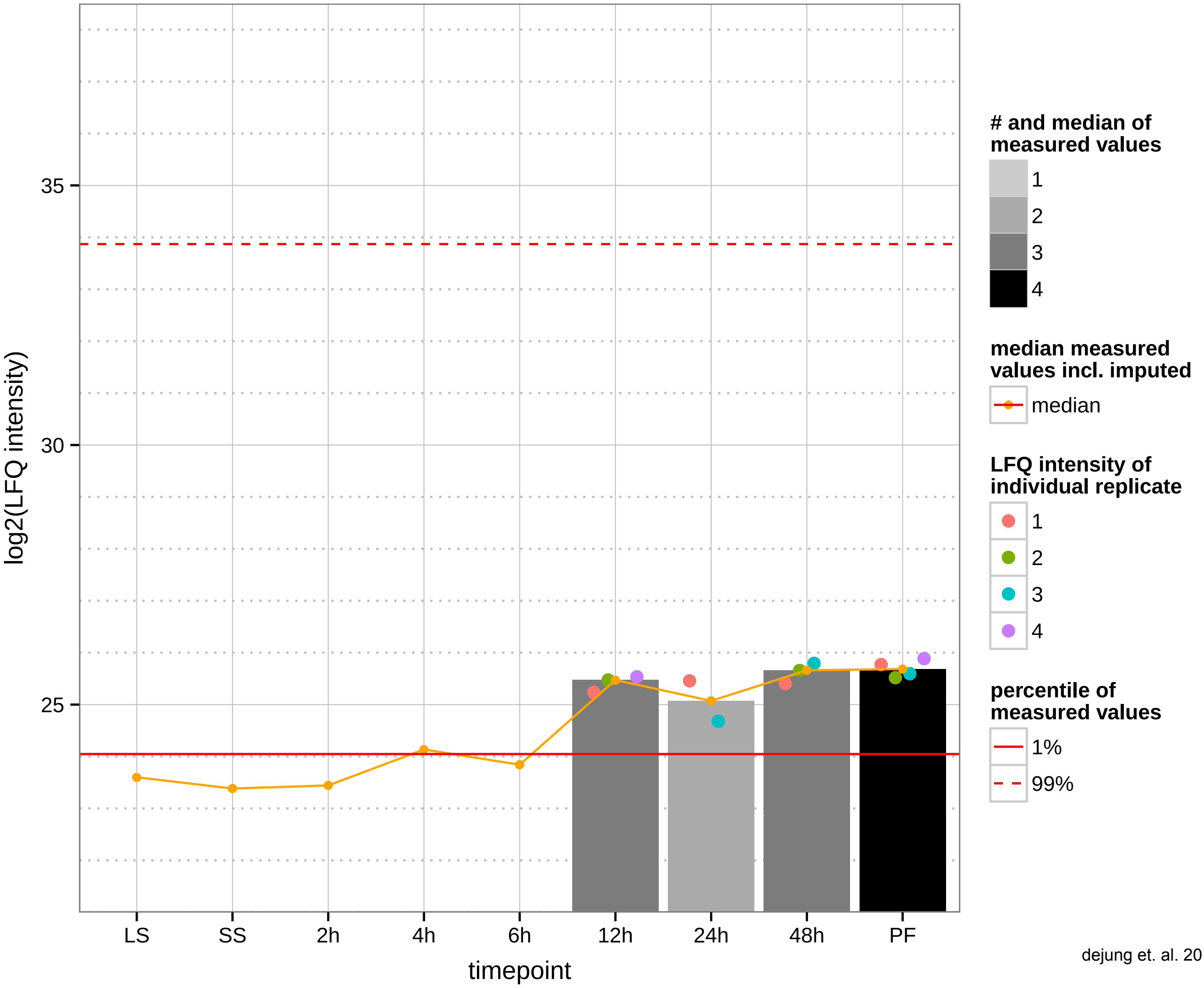
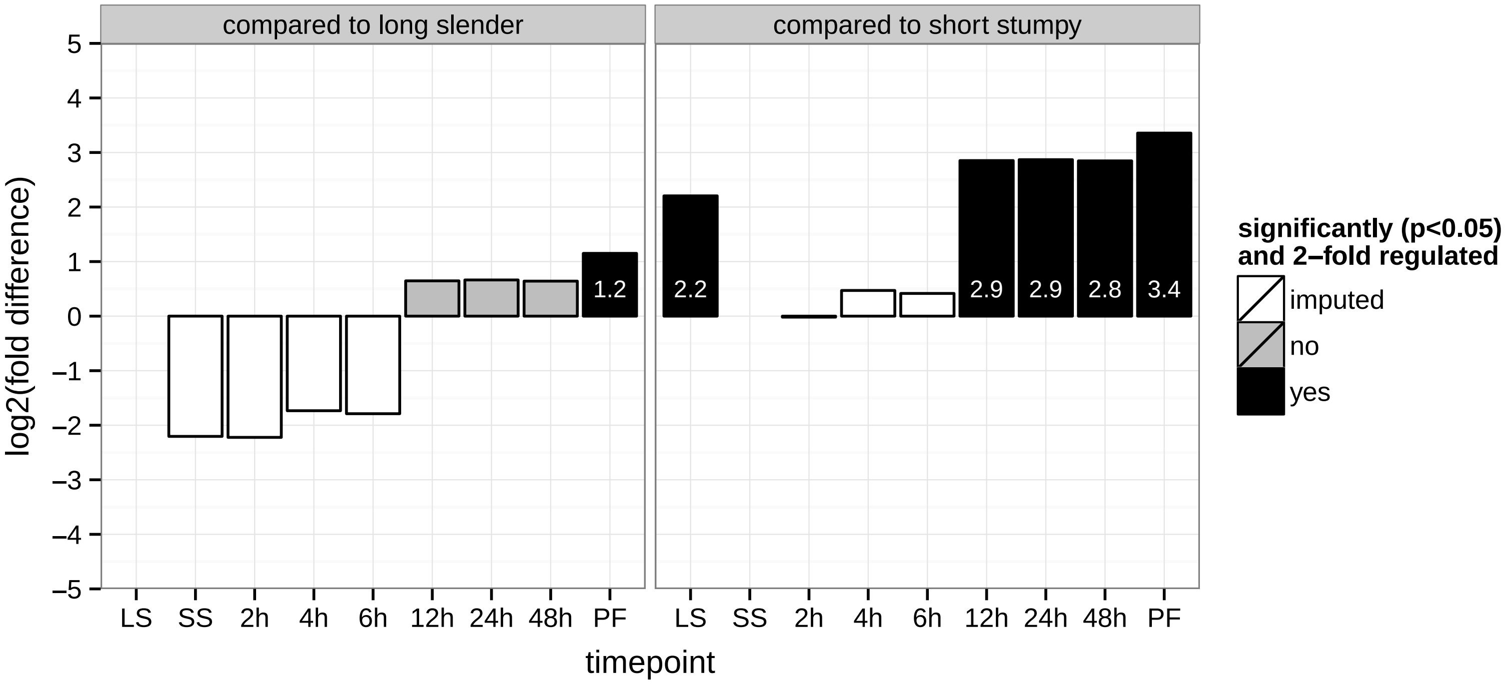
hypothetical protein, conserved
Tb927.11.16340
AGOF: protein transporter activity
AGOC: cytoplasm, nuclear pore, nucleus
AGOP: intracellular protein transport, protein import into nucleus, docking
PGOF: binding, protein transporter activity
PGOC: null
PGOP: intracellular protein transport

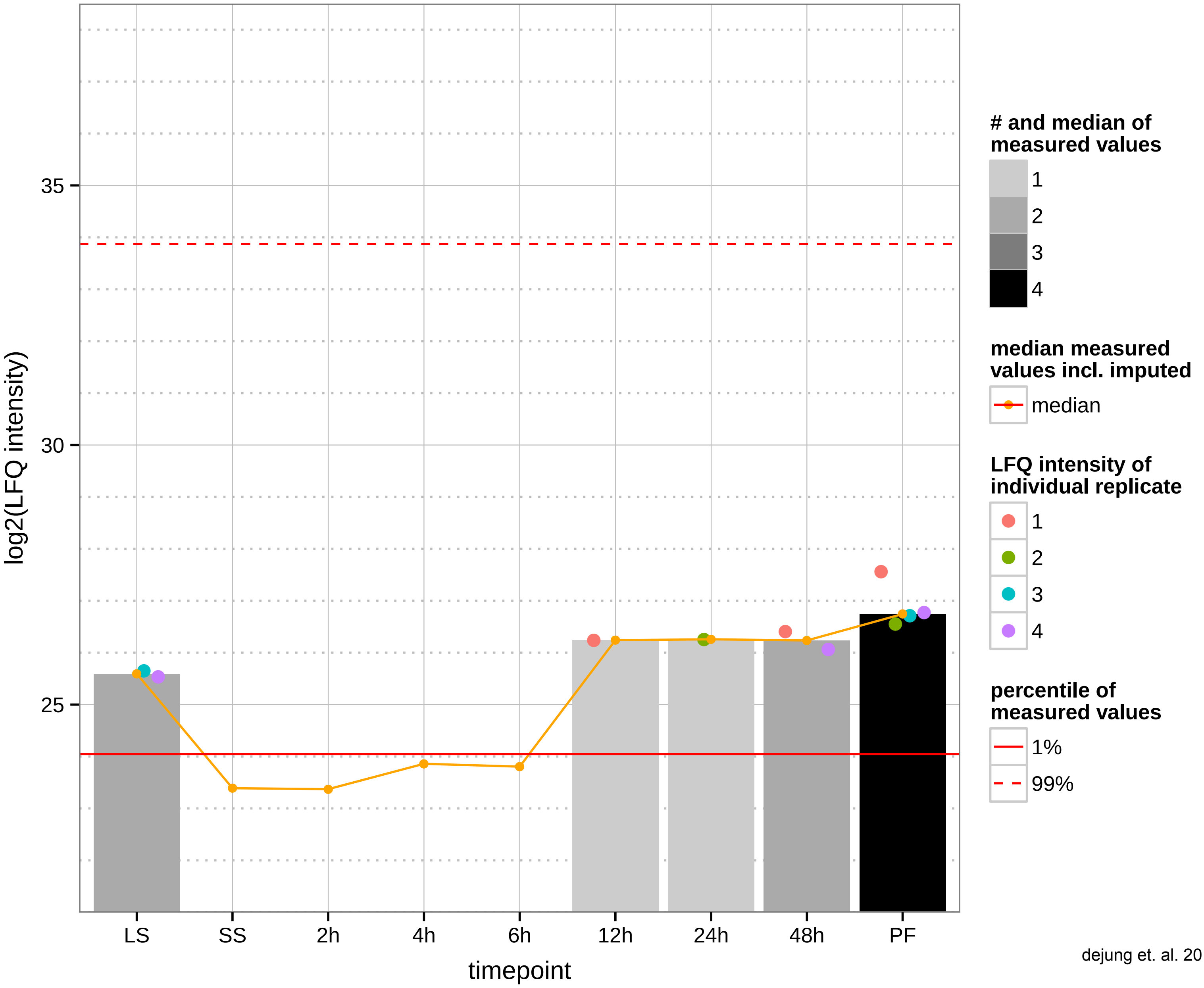




dejung et. al. 2015

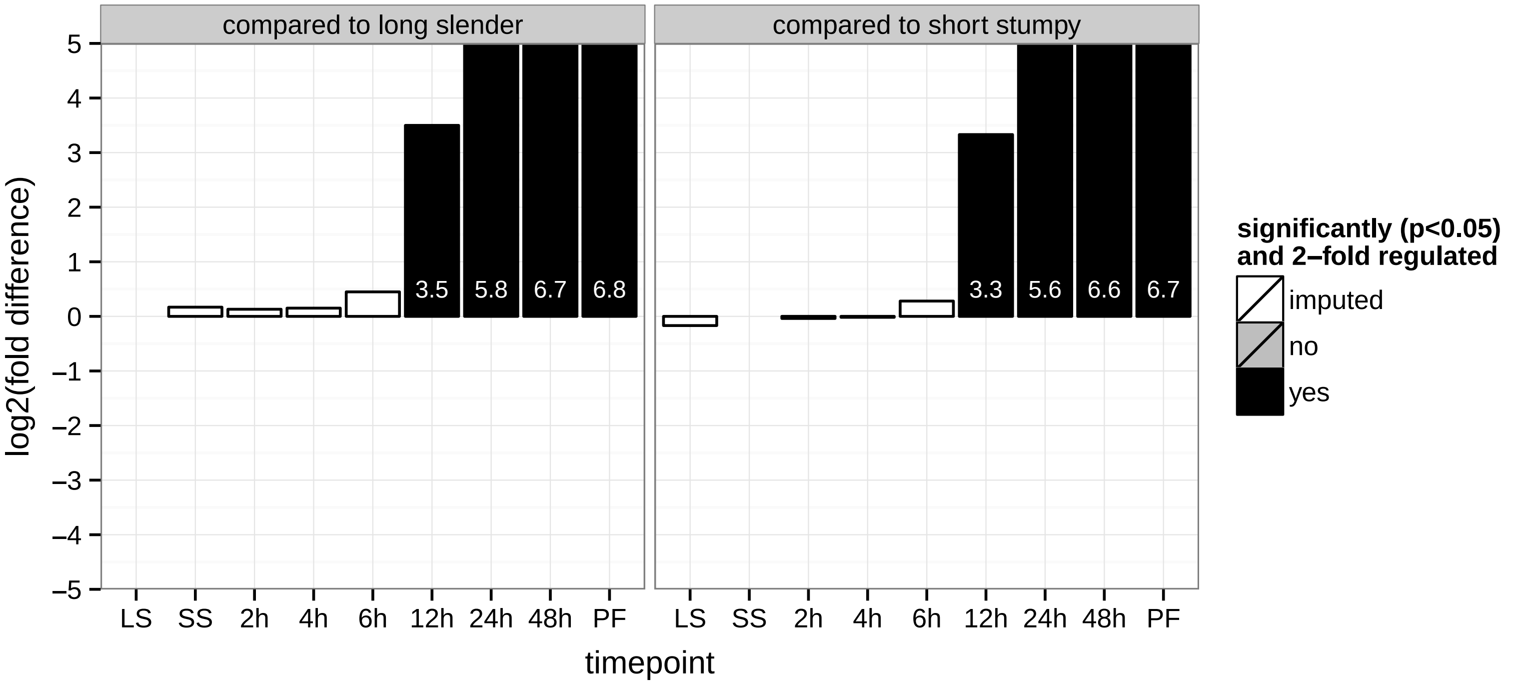
hypothetical protein, conserved
Tb927.11.16450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

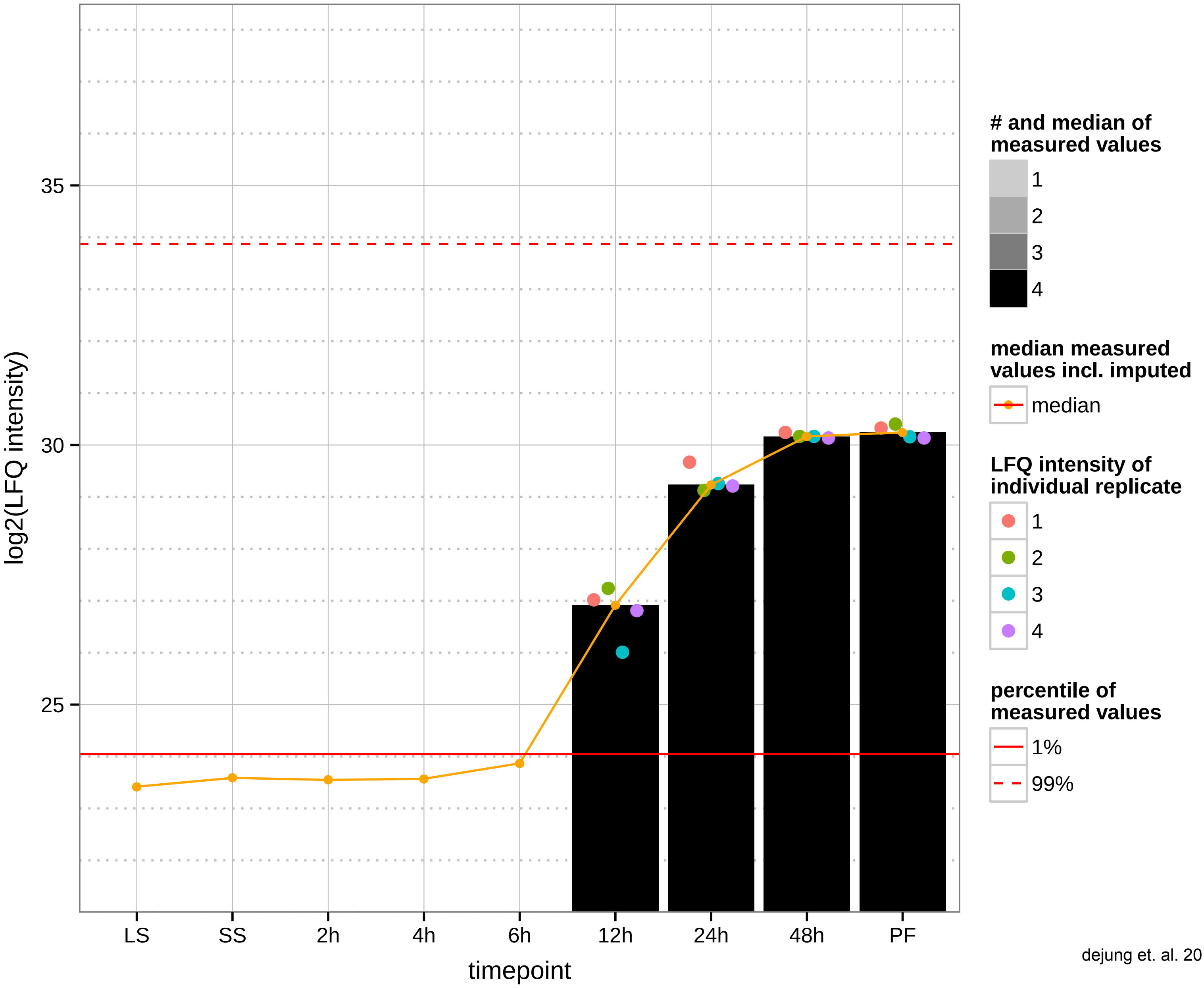




dejung et. al. 2015

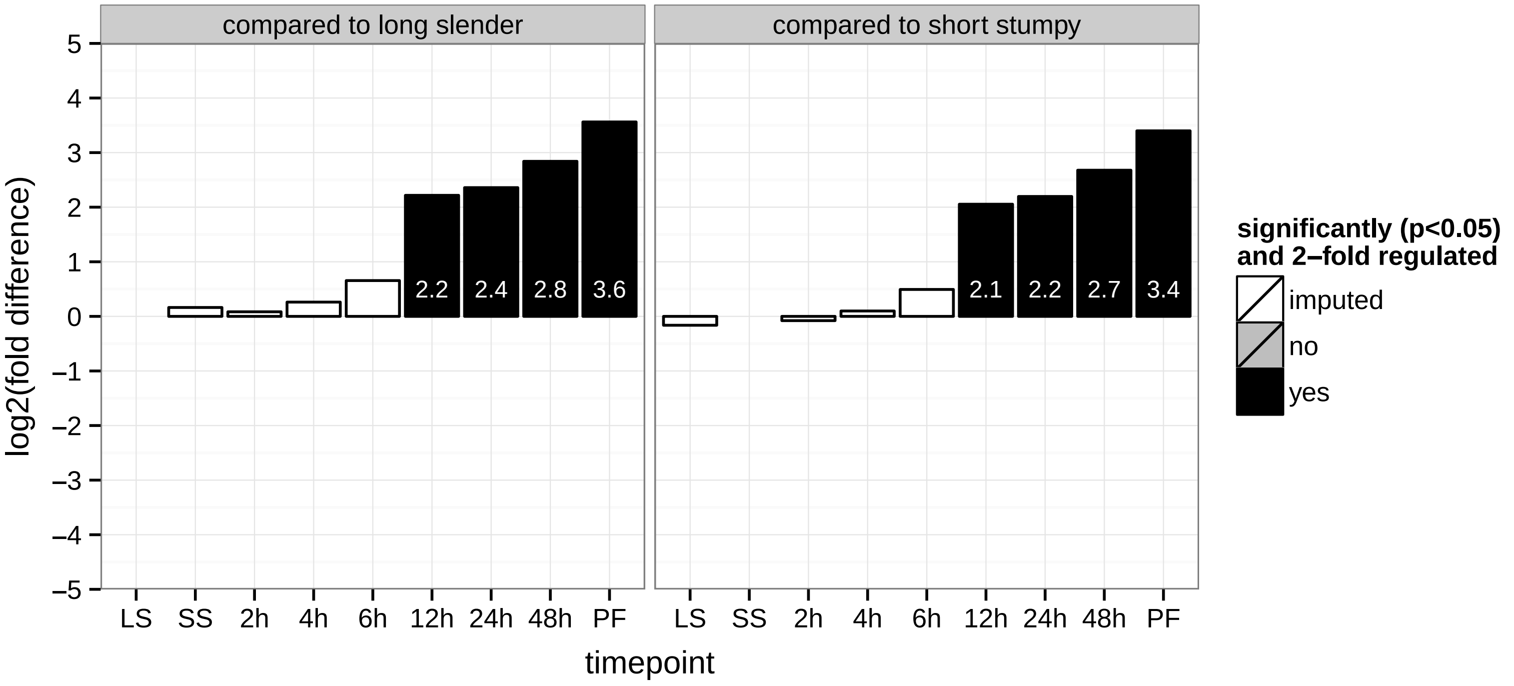
hypothetical protein, conserved
Tb927.11.16510
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

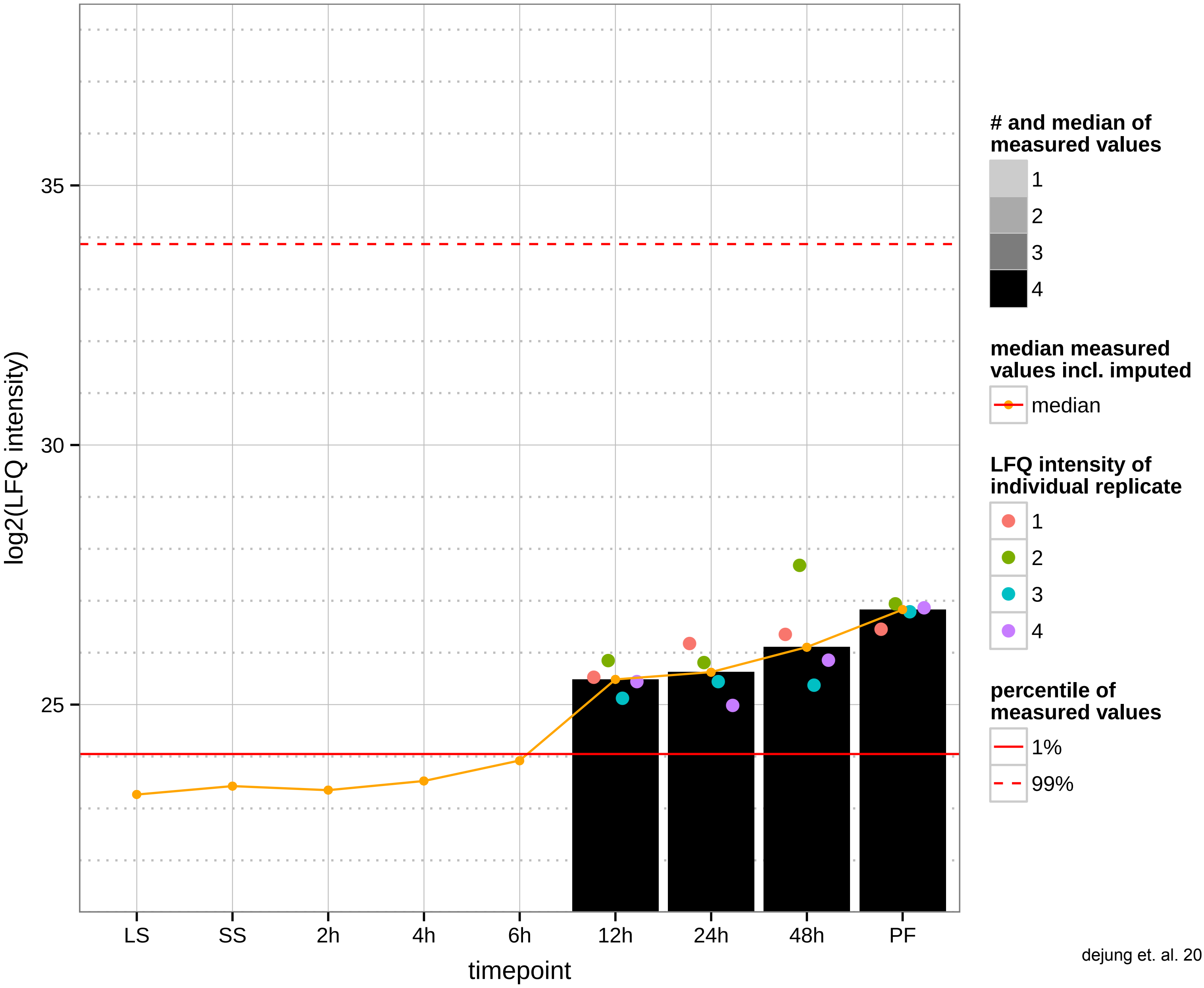




dejung et. al. 2015

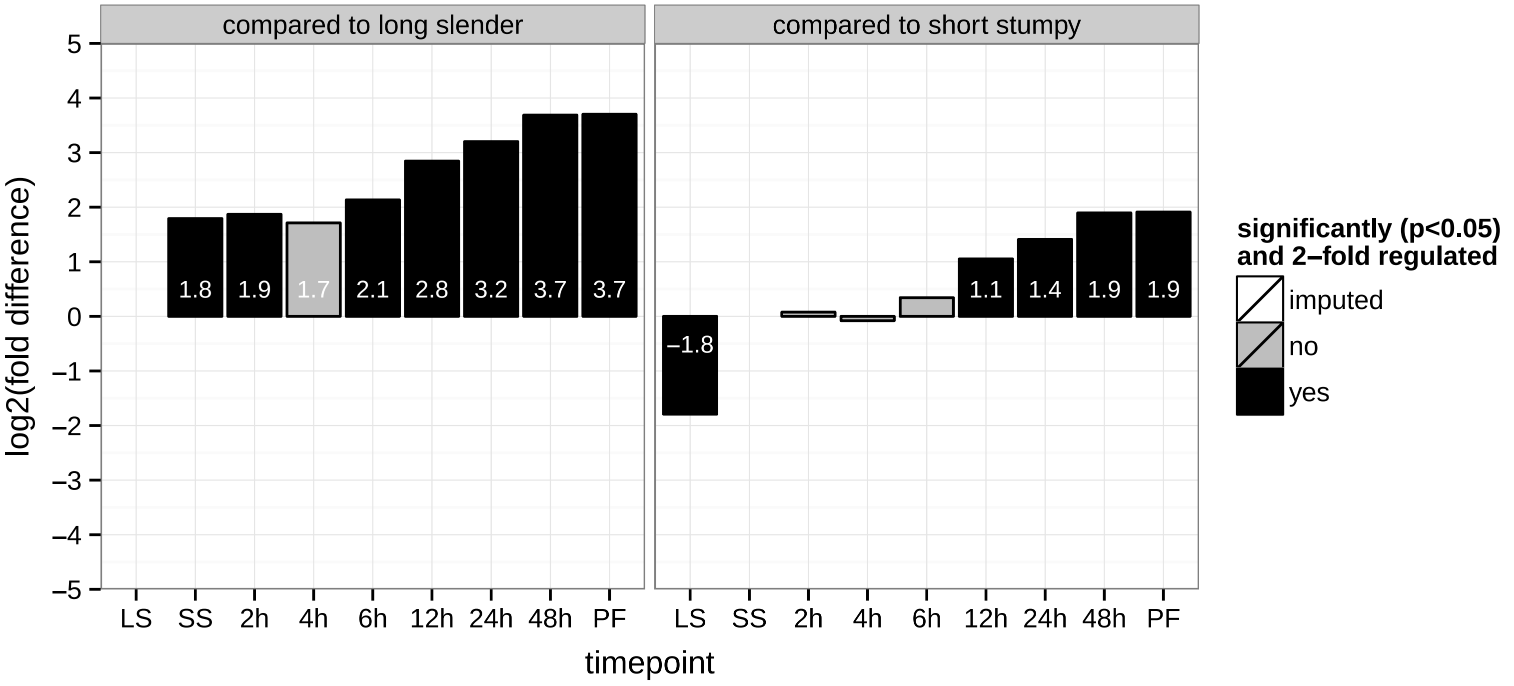
electron transfer flavoprotein, putative
Tb927.11.180
AGOF: electron carrier activity
AGOC: mitochondrion
AGOP: oxidation–reduction process
PGOF: electron carrier activity
PGOC: null
PGOP: null

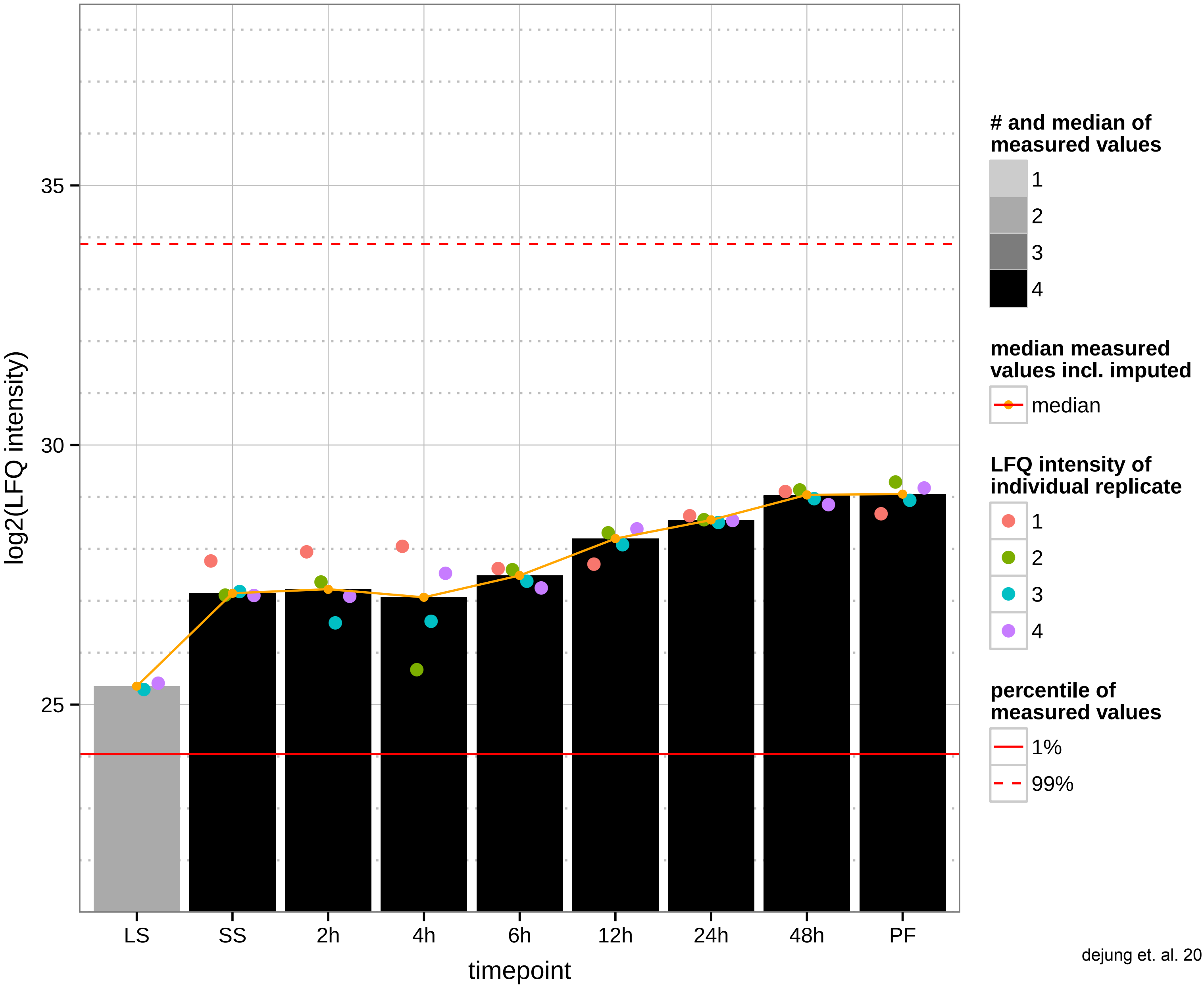




dejung et. al. 2015

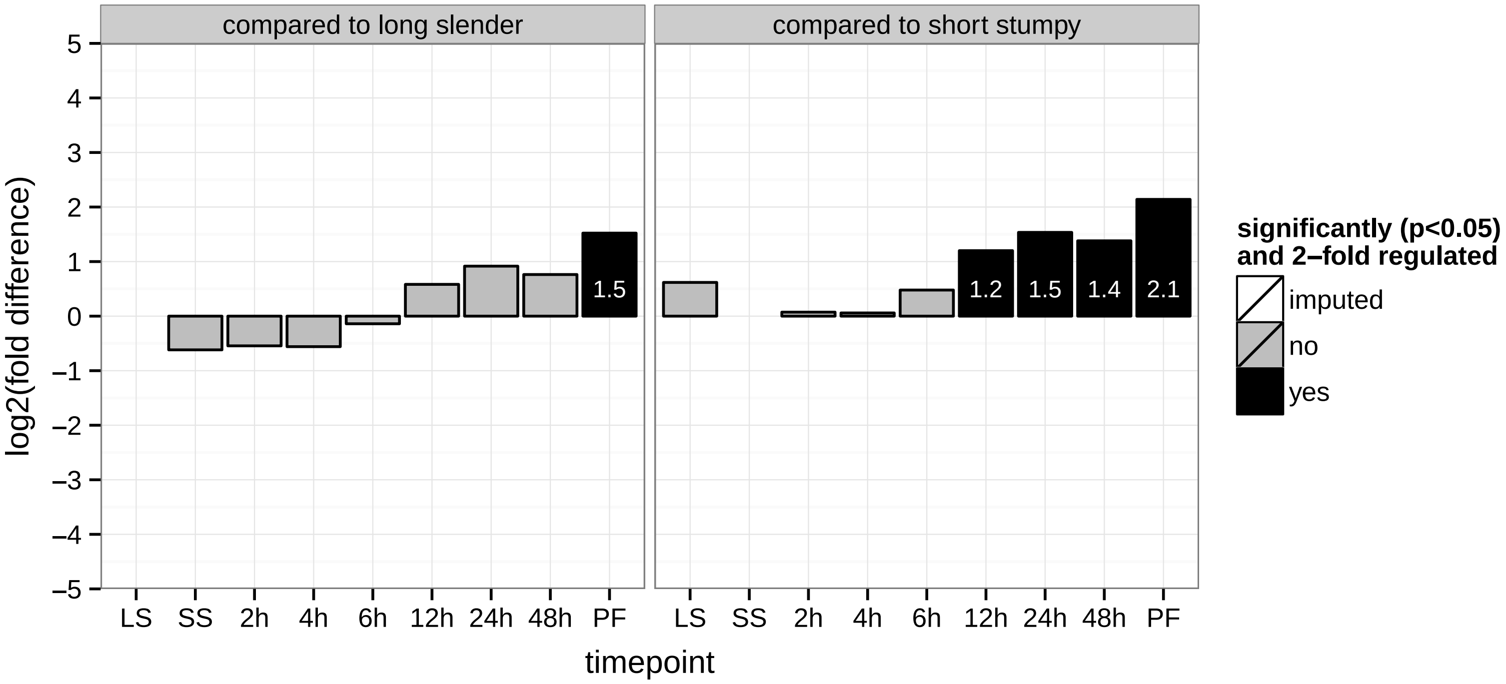
elongation factor, putative
Tb927.11.190
AGOF: GTP binding, GTPase activity
AGOC: null
AGOP: null
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null

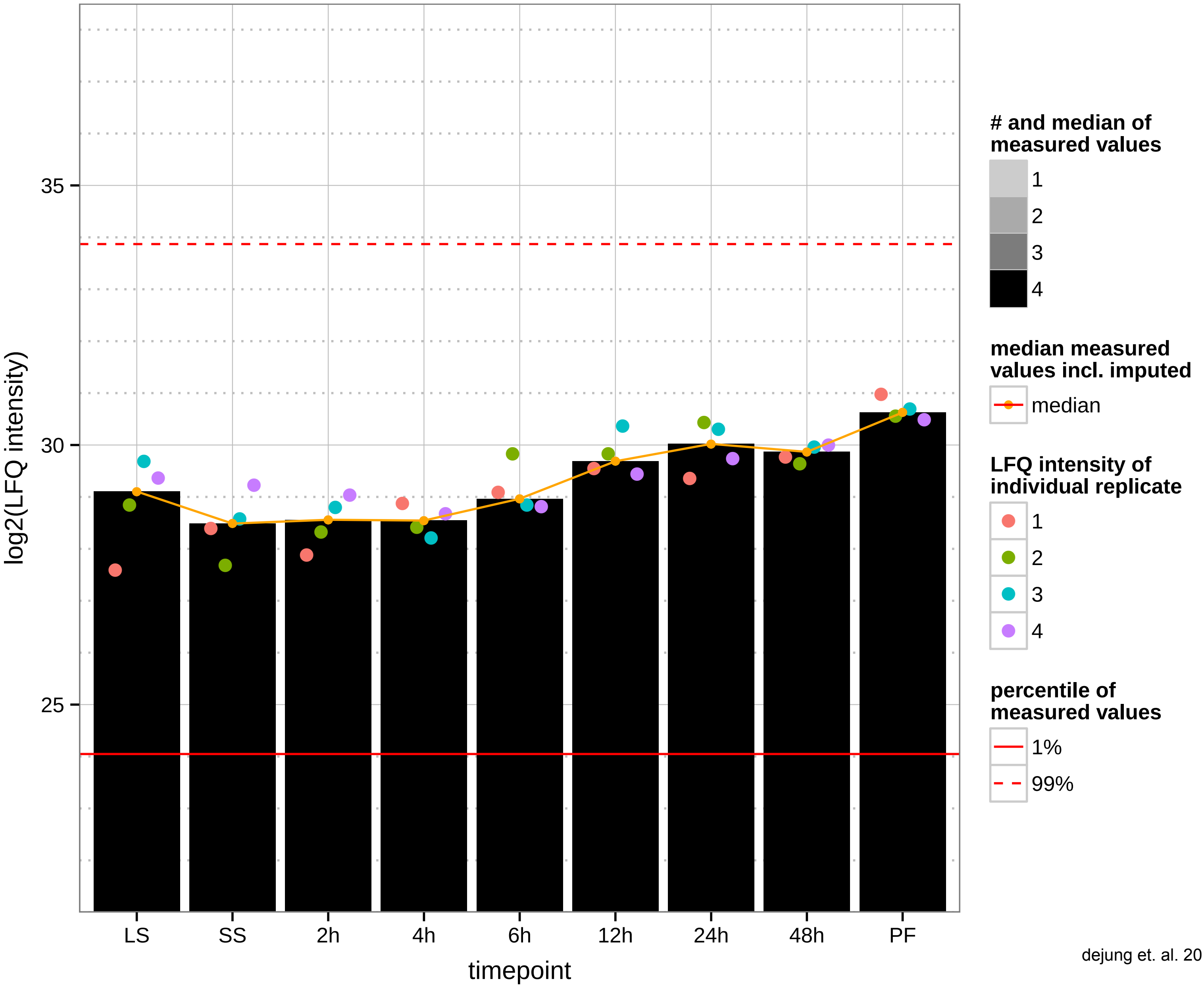




dejung et. al. 2015

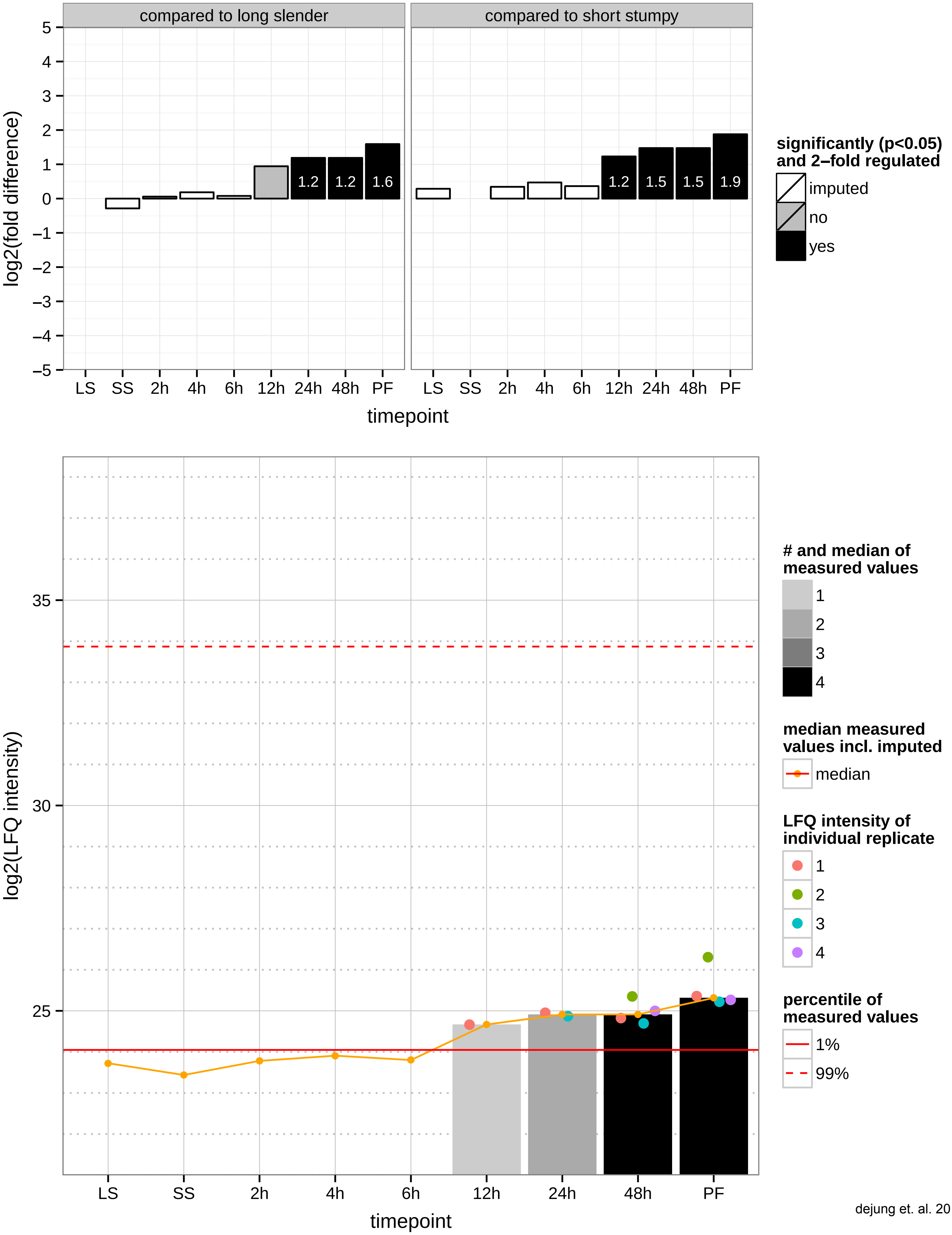
60S ribosomal protein L37, putative
Tb927.9.9210;Tb927.11.3000
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation



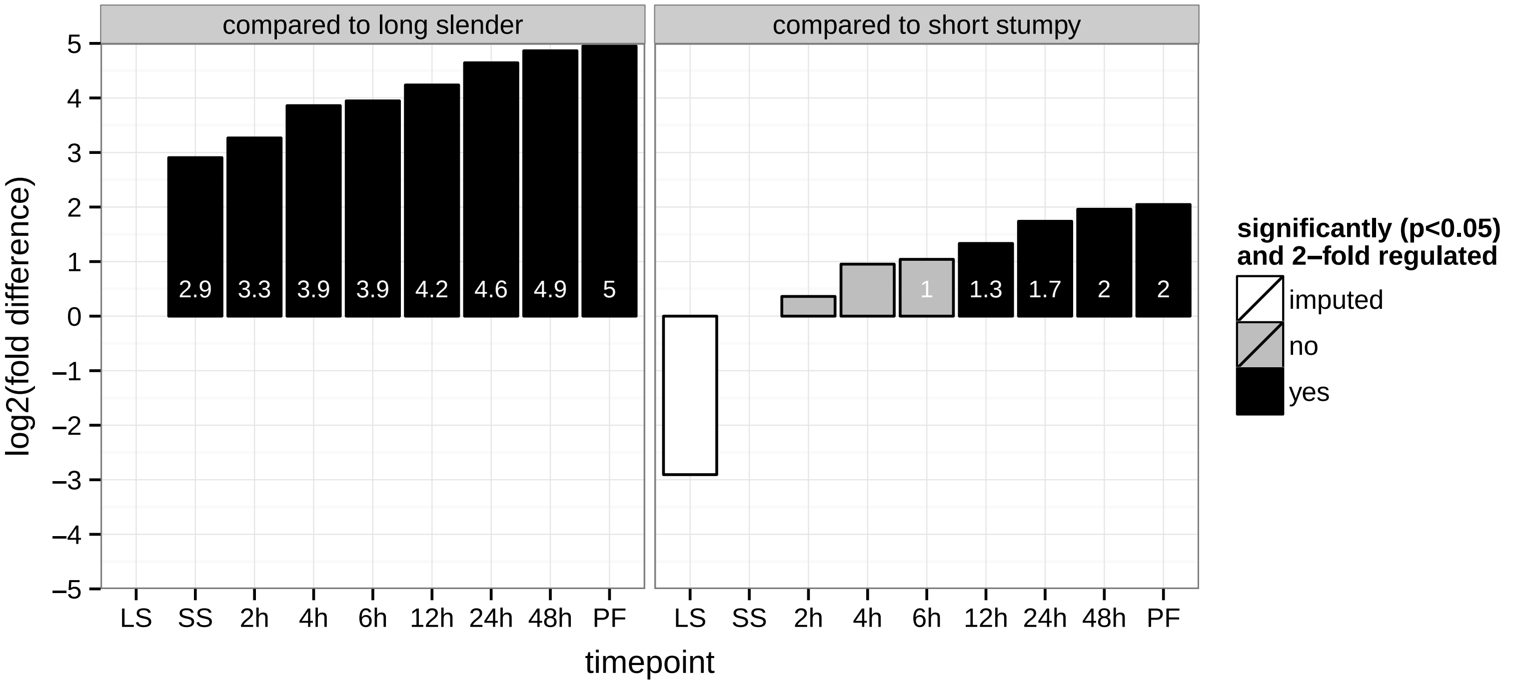


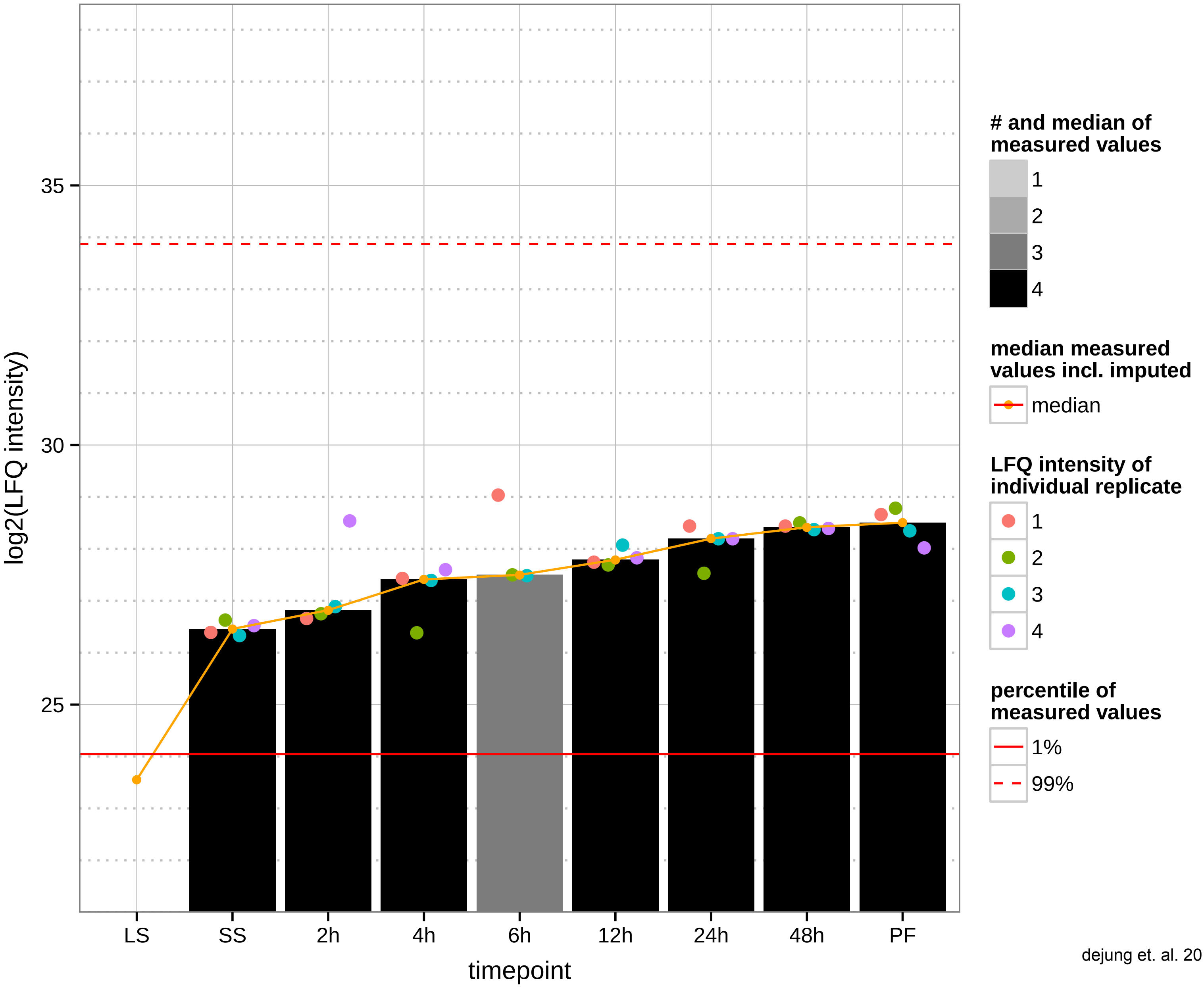
dejung et. al. 2015

mitochondrial DNA polymerase I protein D, putative (POLID)
Tb927.11.3260
AGOF: DNA binding, DNA−directed DNA polymerase activity
AGOC: mitochondrion
AGOP: DNA replication
PGOF: 3'−5' exonuclease activity, DNA binding, DNA−directed DNA polymerase activity, nucleic acid binding
PGOC: intracellular
PGOP: DNA replication, nucleobase−containing compound metabolic process



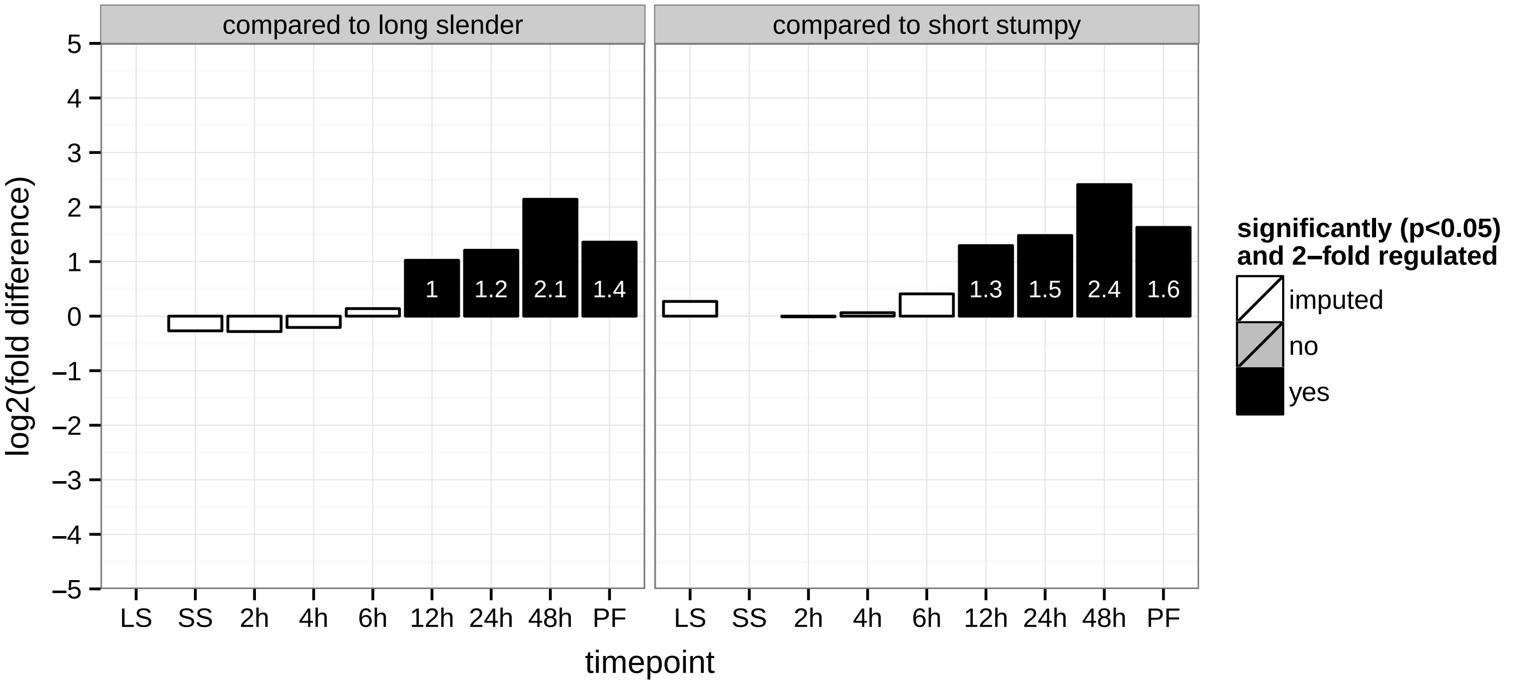
squalene monooxygenase, putative
Tb927.11.3270
AGOF: flavin adenine dinucleotide binding, monooxygenase activity, squalene monooxygenase activity
AGOC: integral to membrane
AGOP: cellular aromatic compound metabolic process, oxidation–reduction process
PGOF: flavin adenine dinucleotide binding, squalene monooxygenase activity
PGOC: integral to membrane
PGOP: oxidation–reduction process

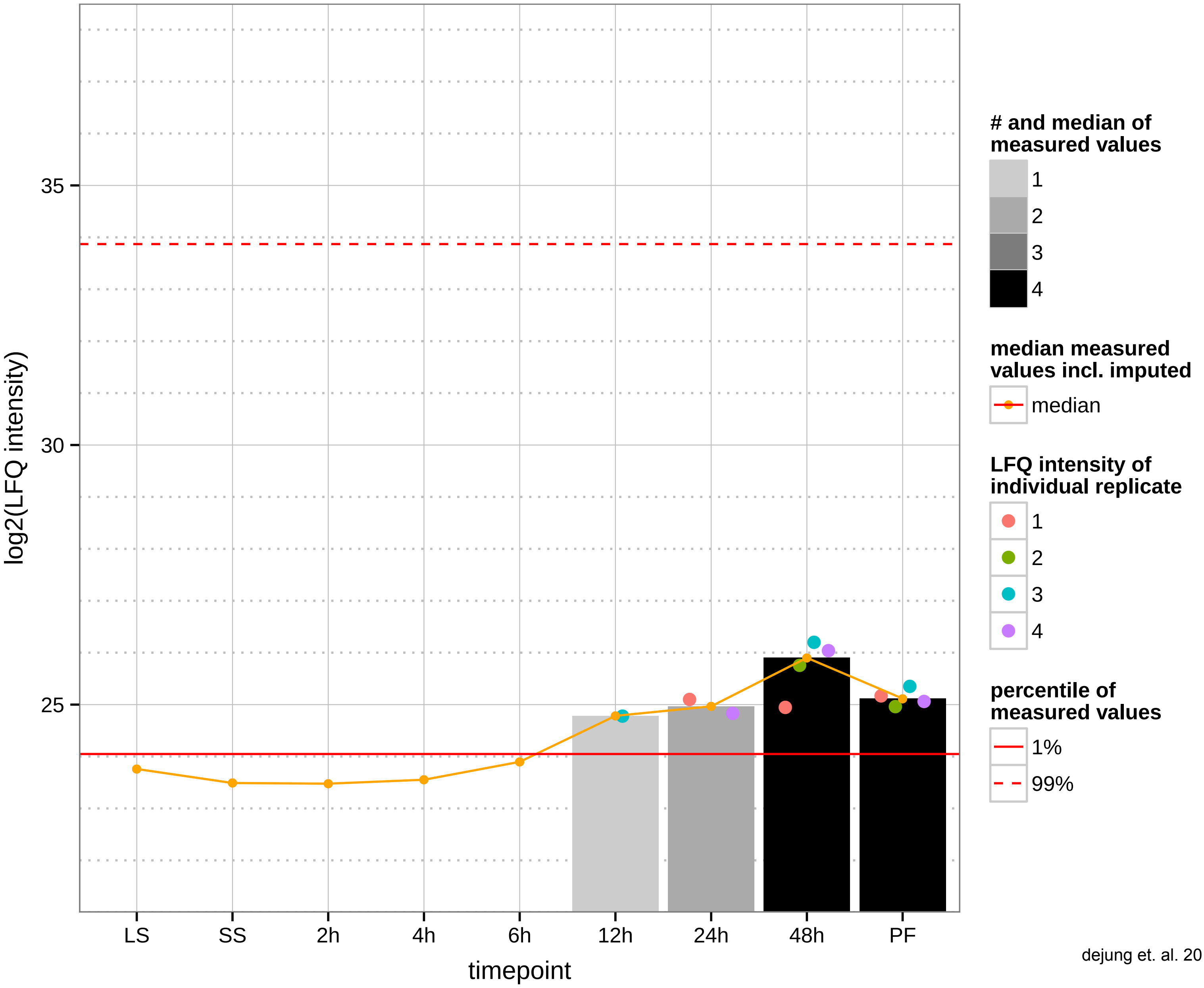




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.3400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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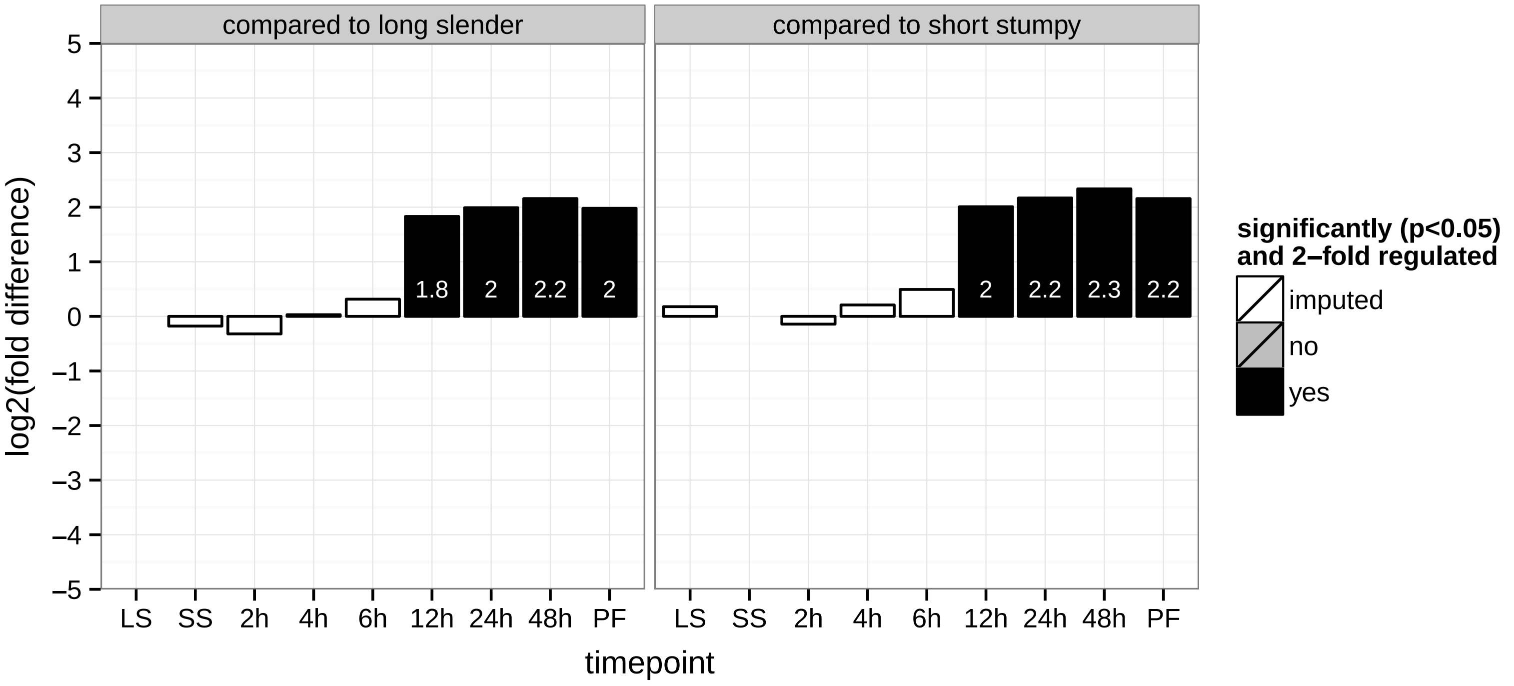
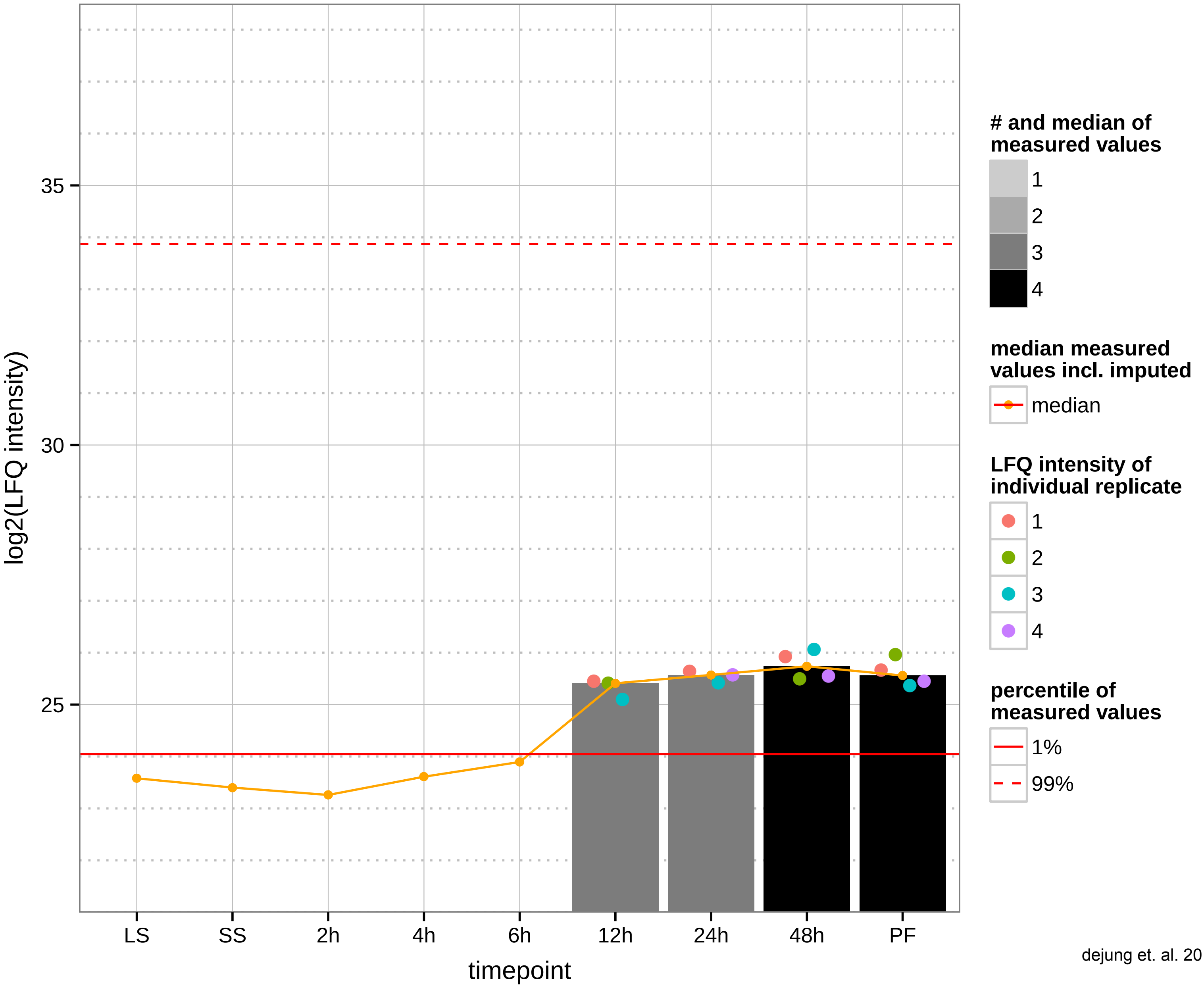
hypothetical protein, conserved
Tb927.11.5060
AGOF: methyltransferase activity
AGOC: mitochondrion
AGOP: translation
PGOF: methyltransferase activity
PGOC: null
PGOP: translation





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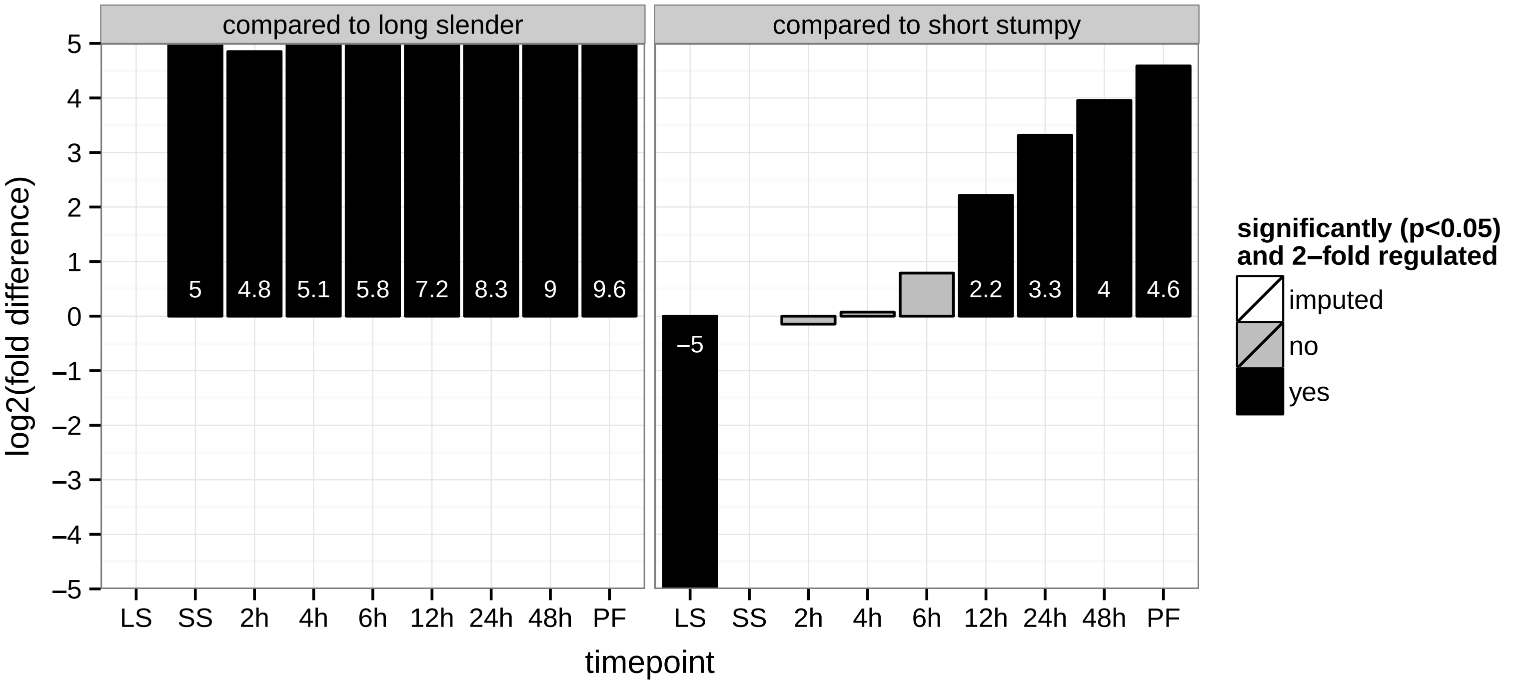
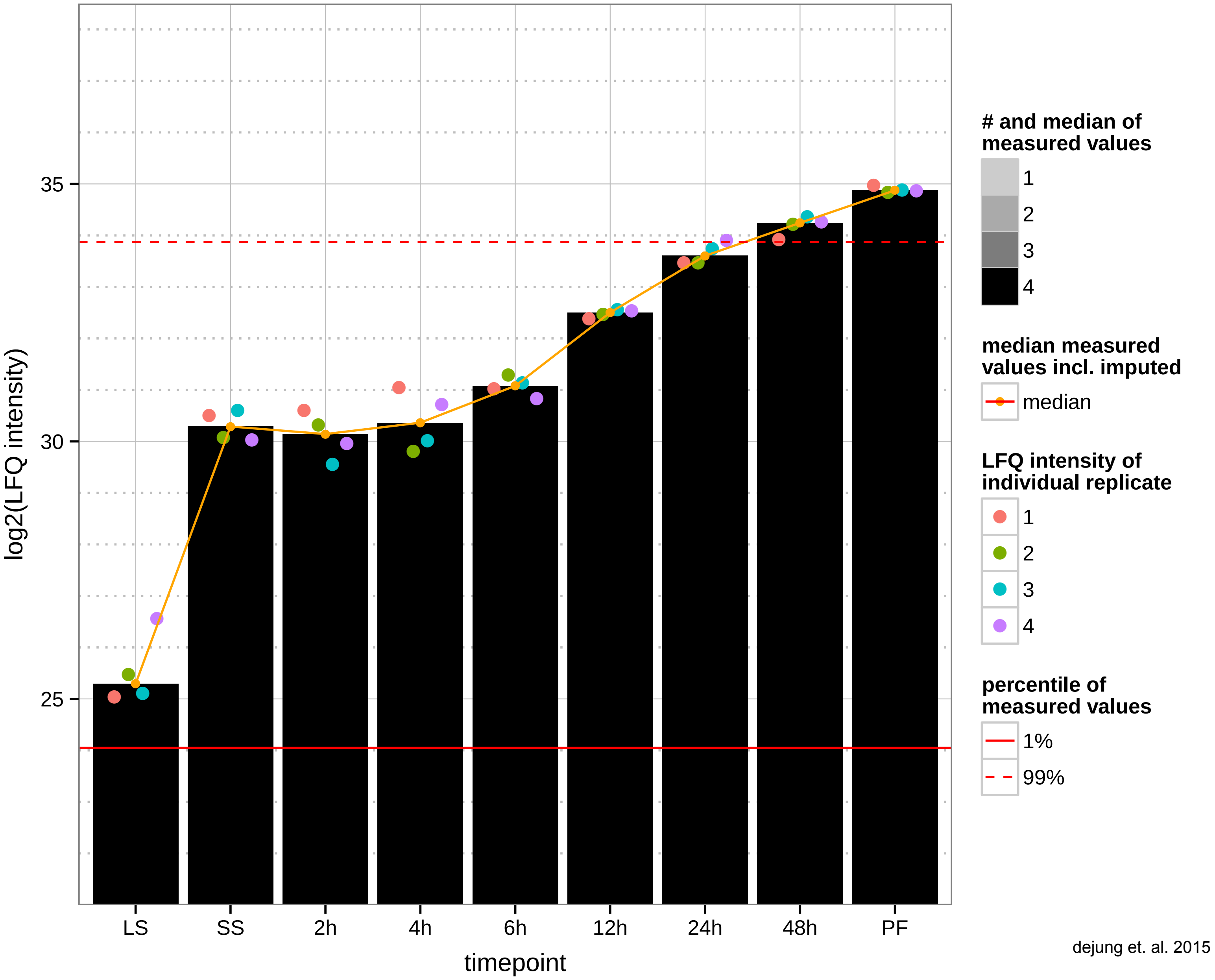
pyruvate phosphate dikinase (PPDK)
Tb927.11.6280
AGOF: ATP binding, kinase activity, pyruvate, phosphate dikinase activity
AGOC: glycosome
AGOP: phosphorylation
PGOF: ATP binding, catalytic activity, kinase activity, pyruvate, phosphate dikinase activity, transferase activity, transferring ph
PGOC: null
PGOP: phosphorylation





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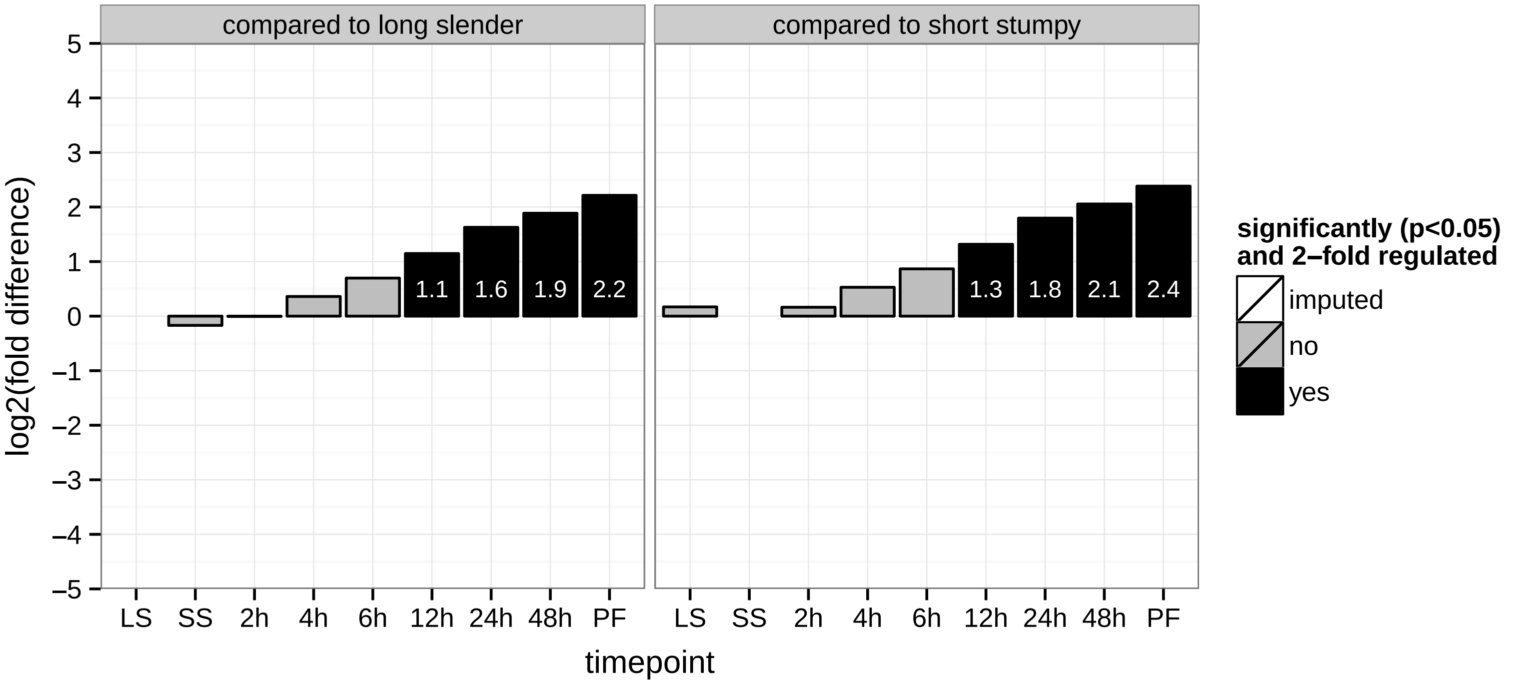
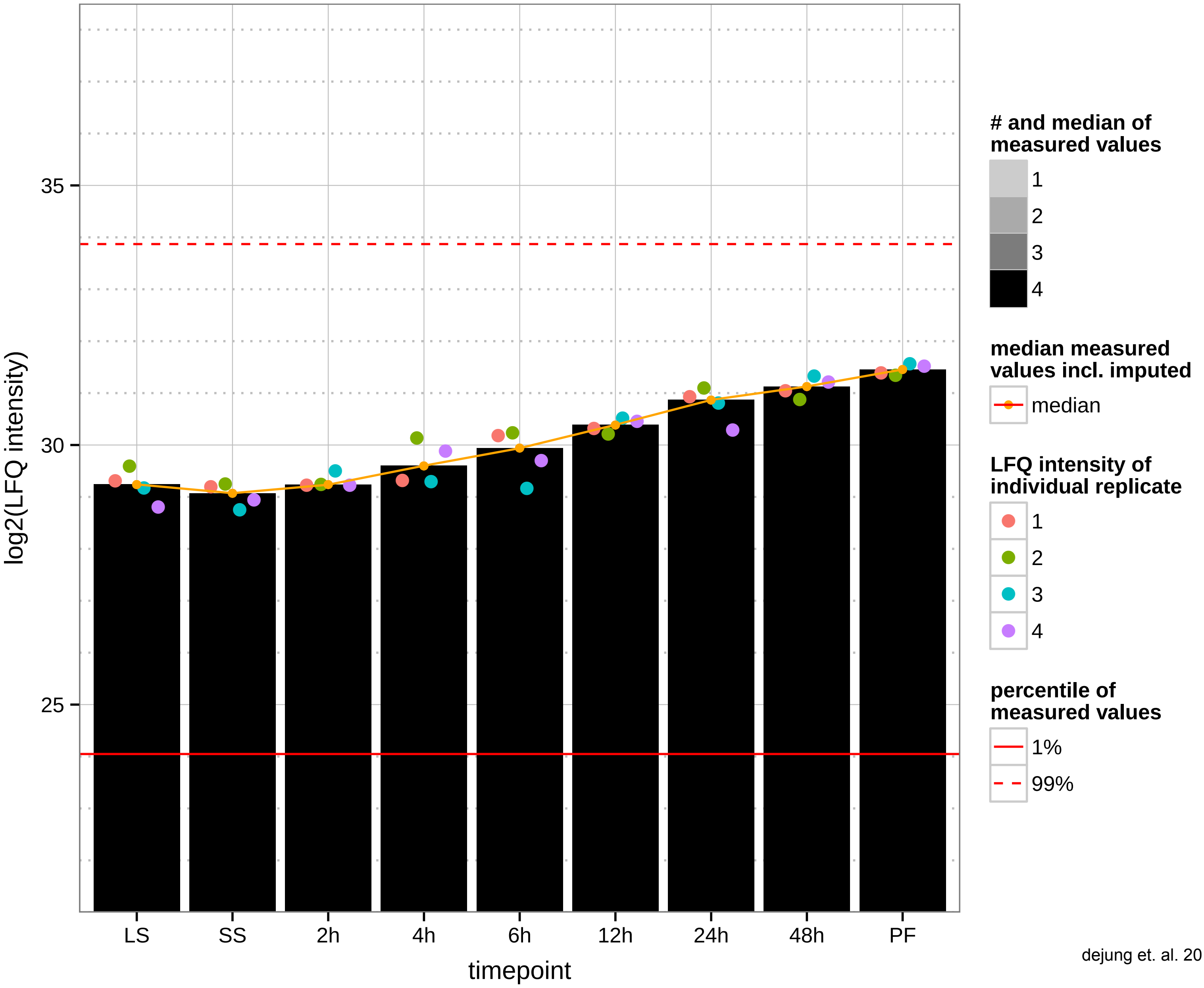
hypothetical protein, conserved
Tb927.11.6440
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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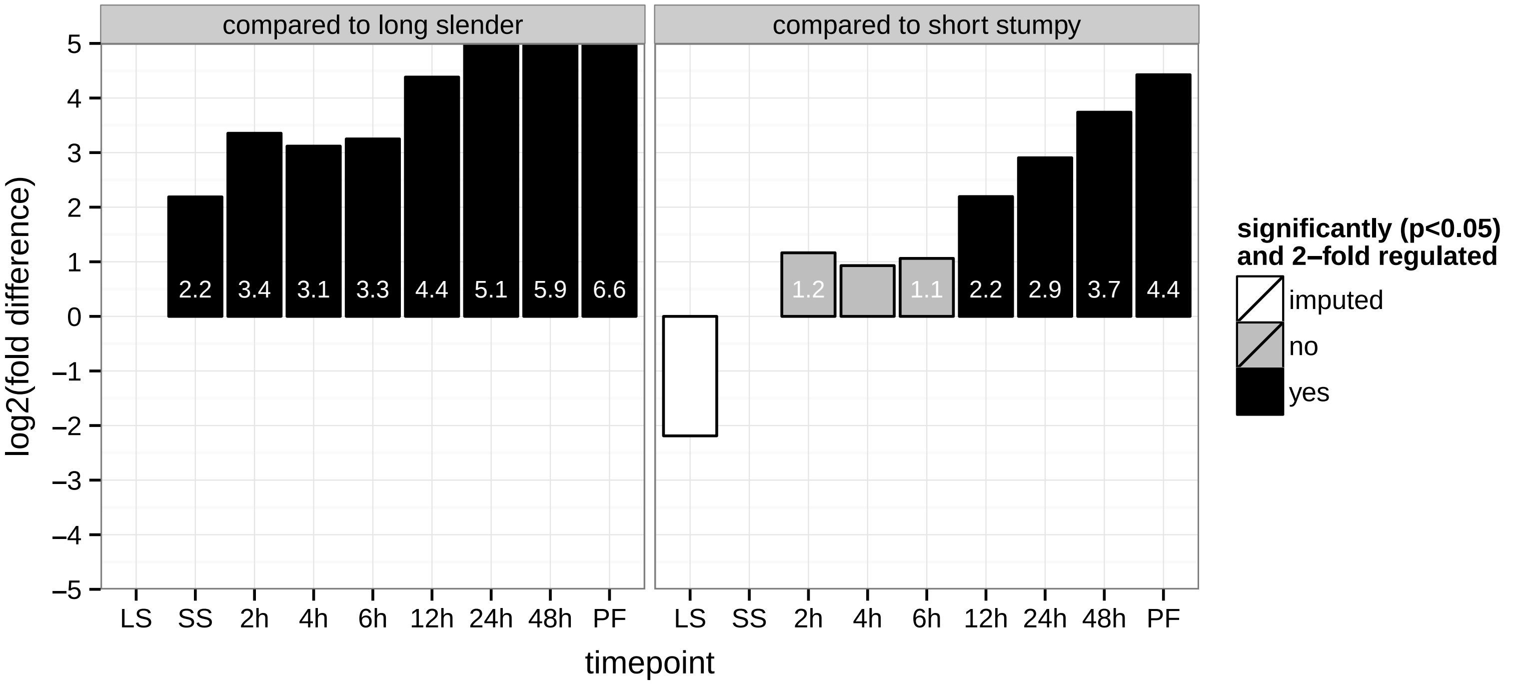
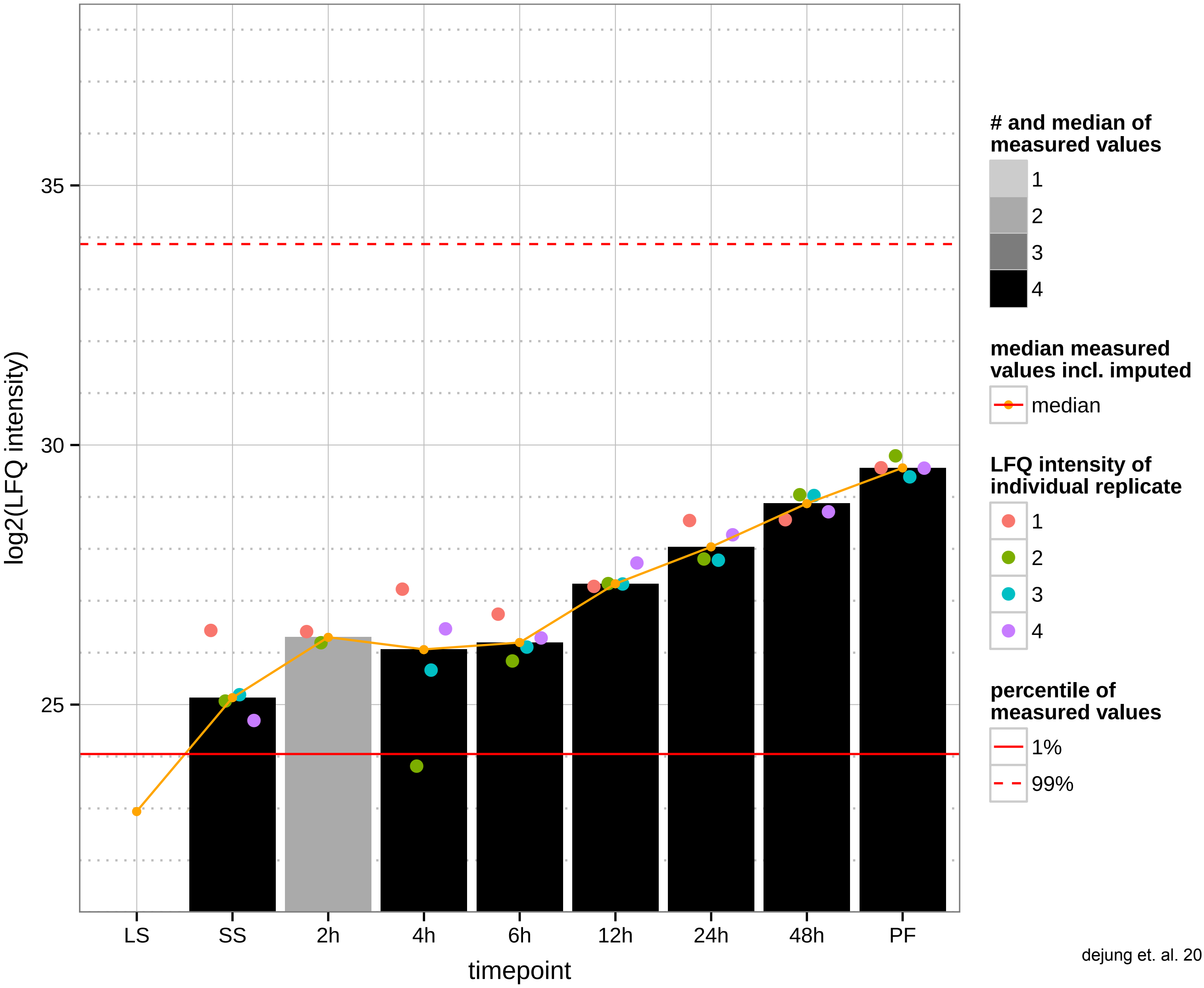
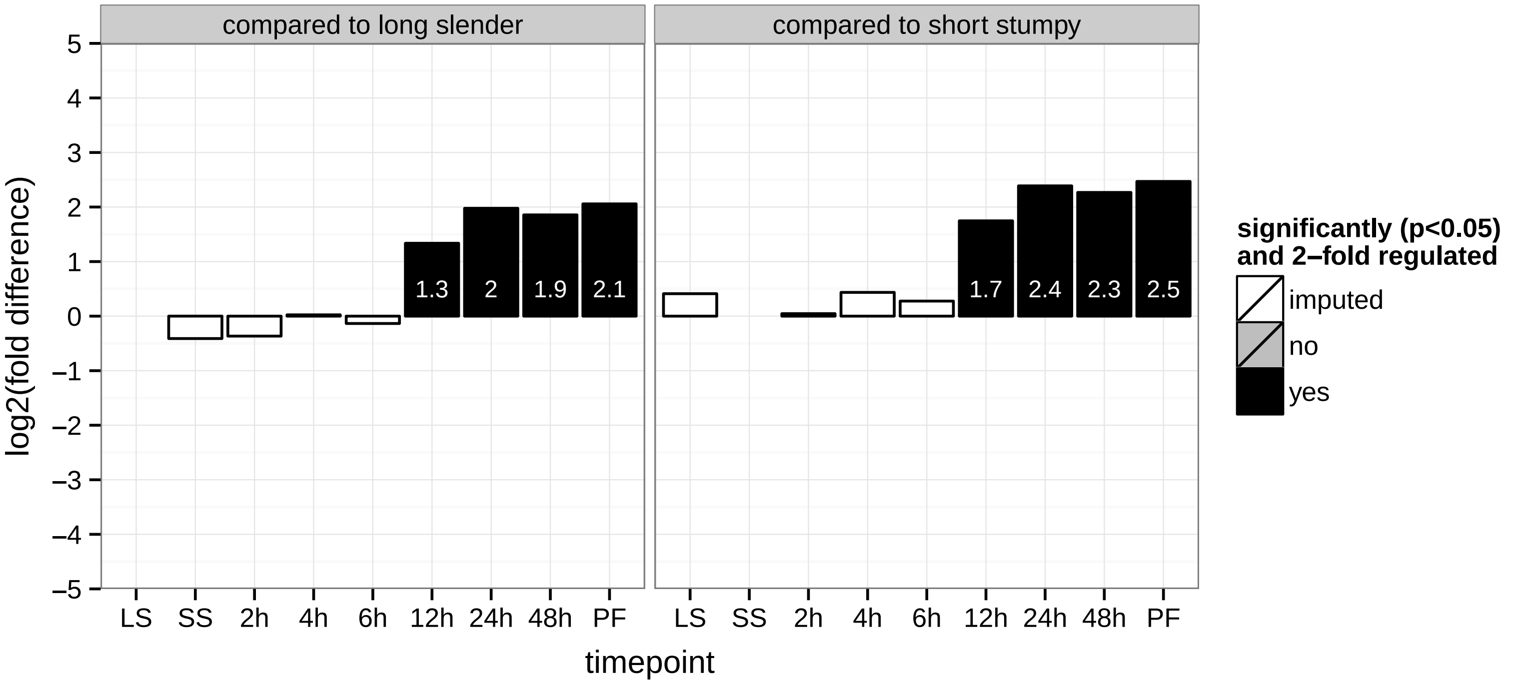
mRNA cap guanine–N7 methyltransferase, putative
Tb927.11.6720
AGOF: mRNA (guanine–N7–)–methyltransferase activity, protein binding
AGOC: eukaryotic translation initiation factor 4F complex
AGOP: null
PGOF: null
PGOC: null
PGOP: 7–methylguanosine mRNA capping

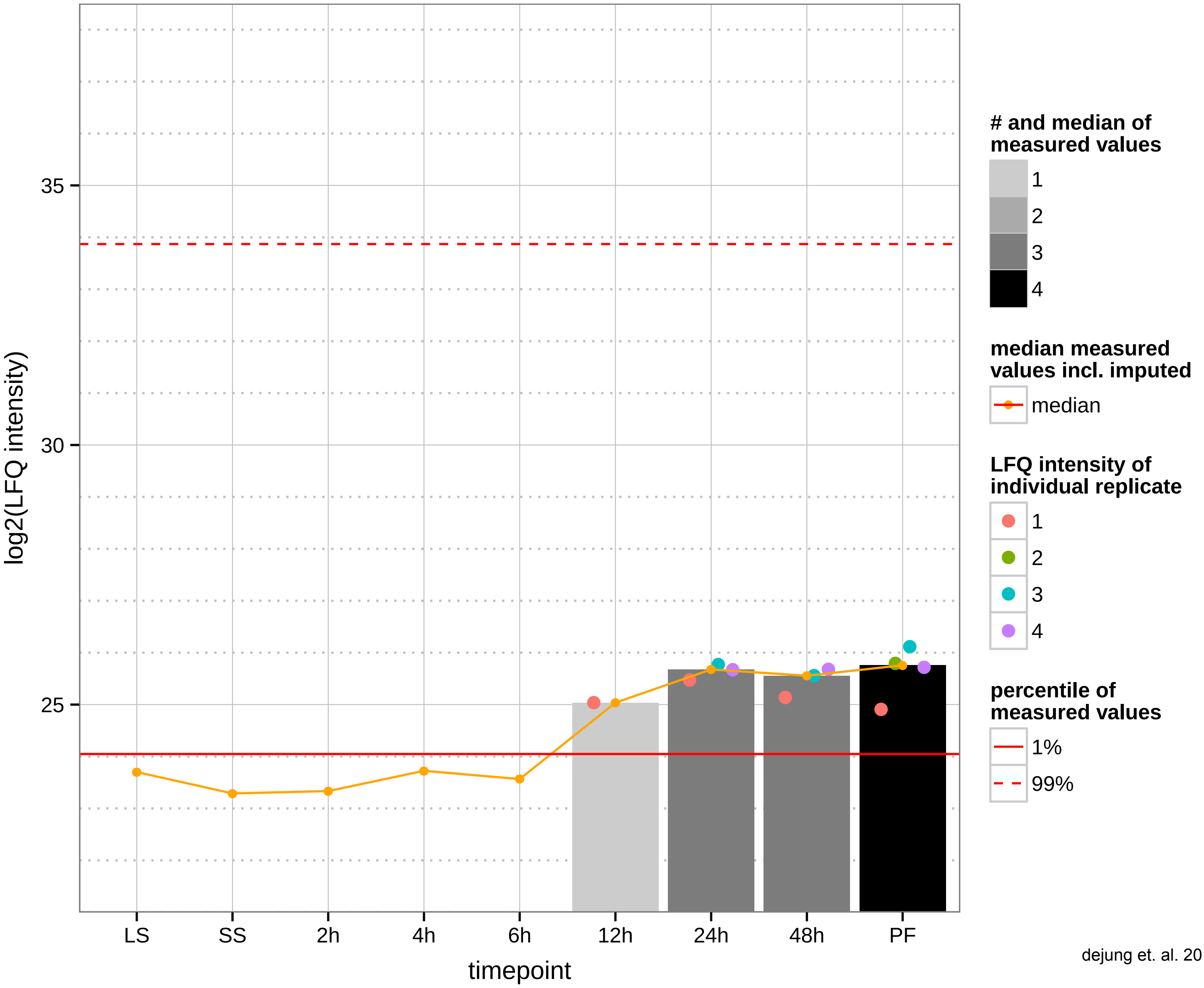




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.6850
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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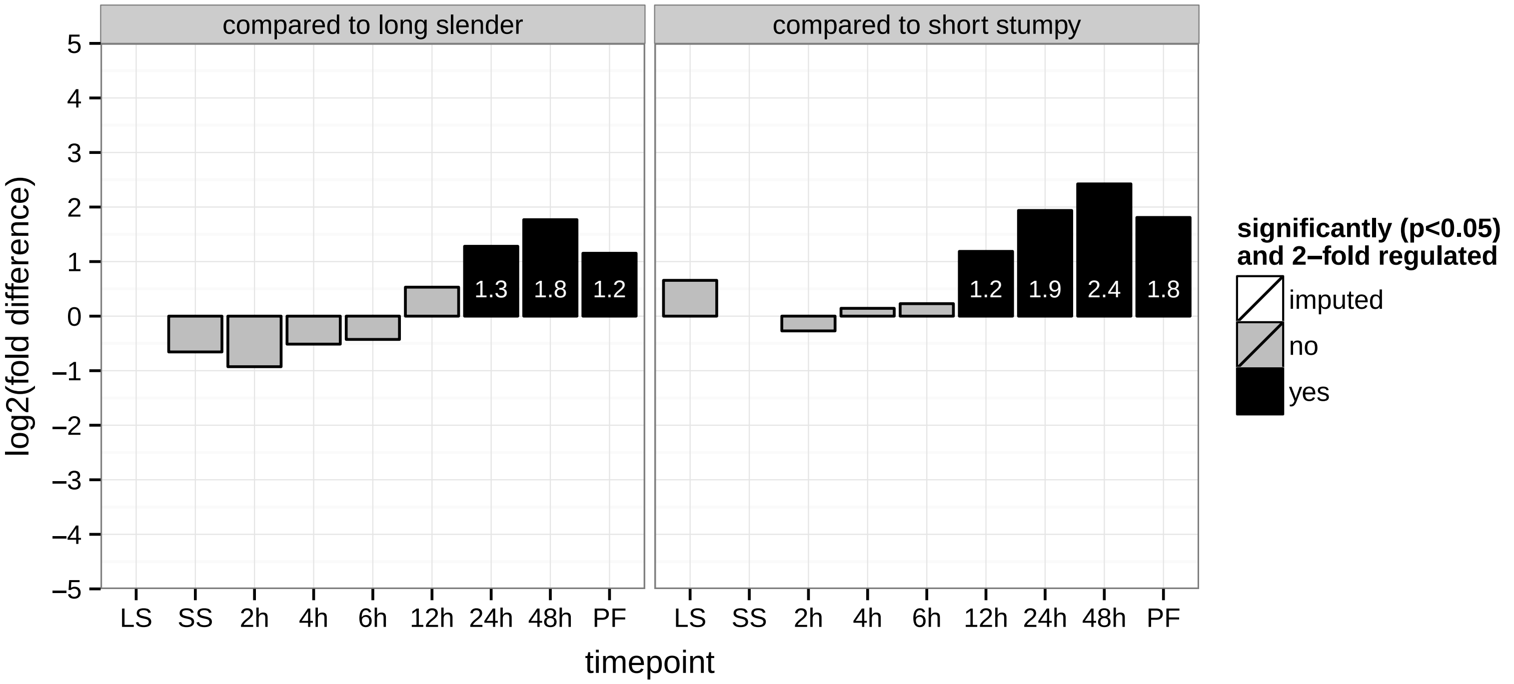
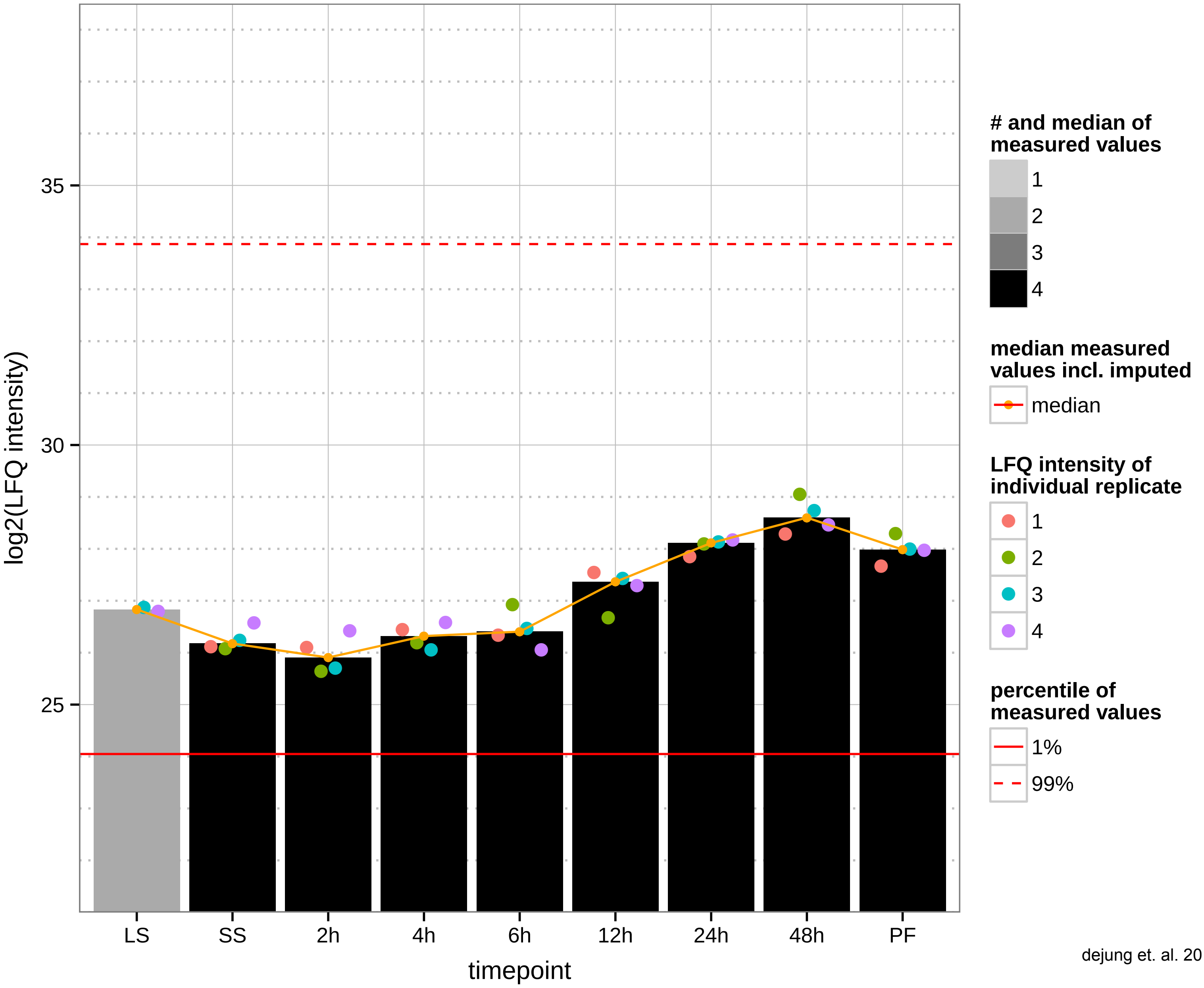
hypothetical protein, conserved
Tb927.11.7520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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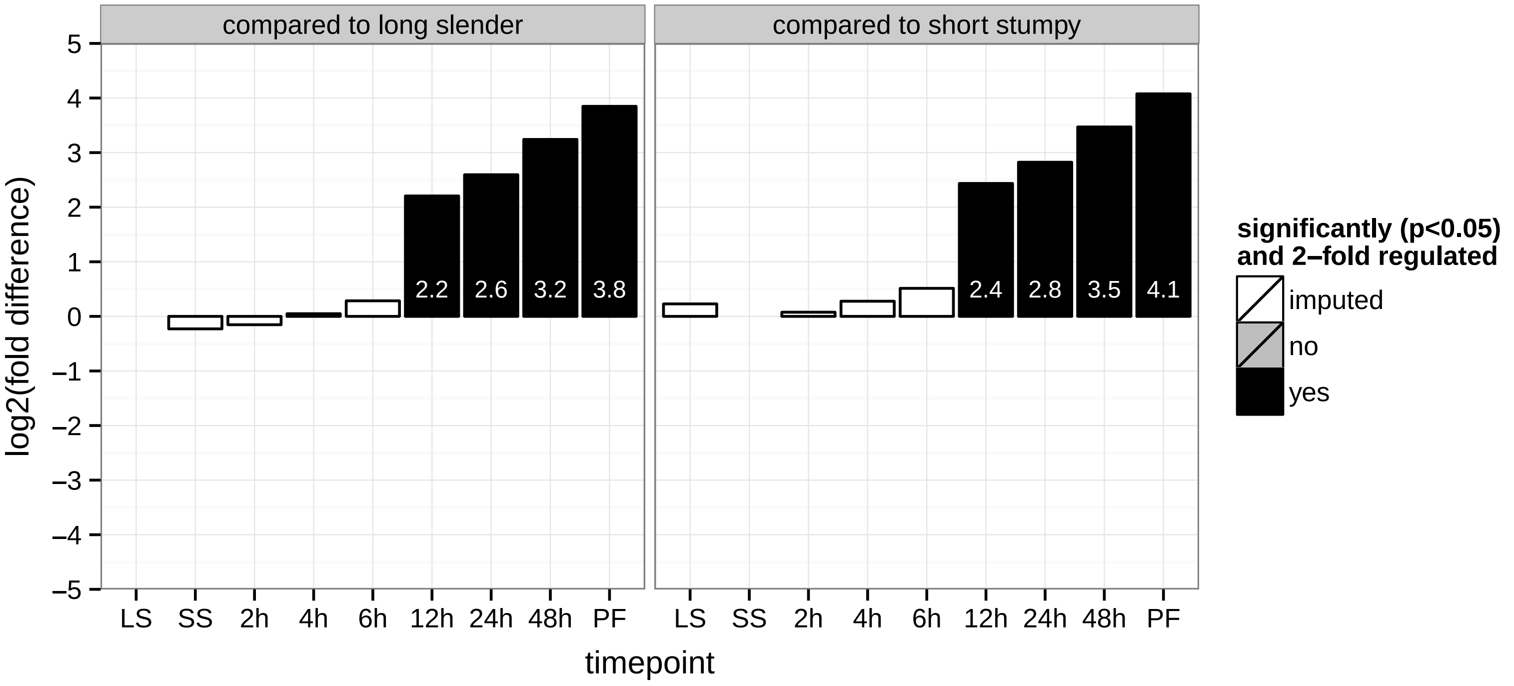
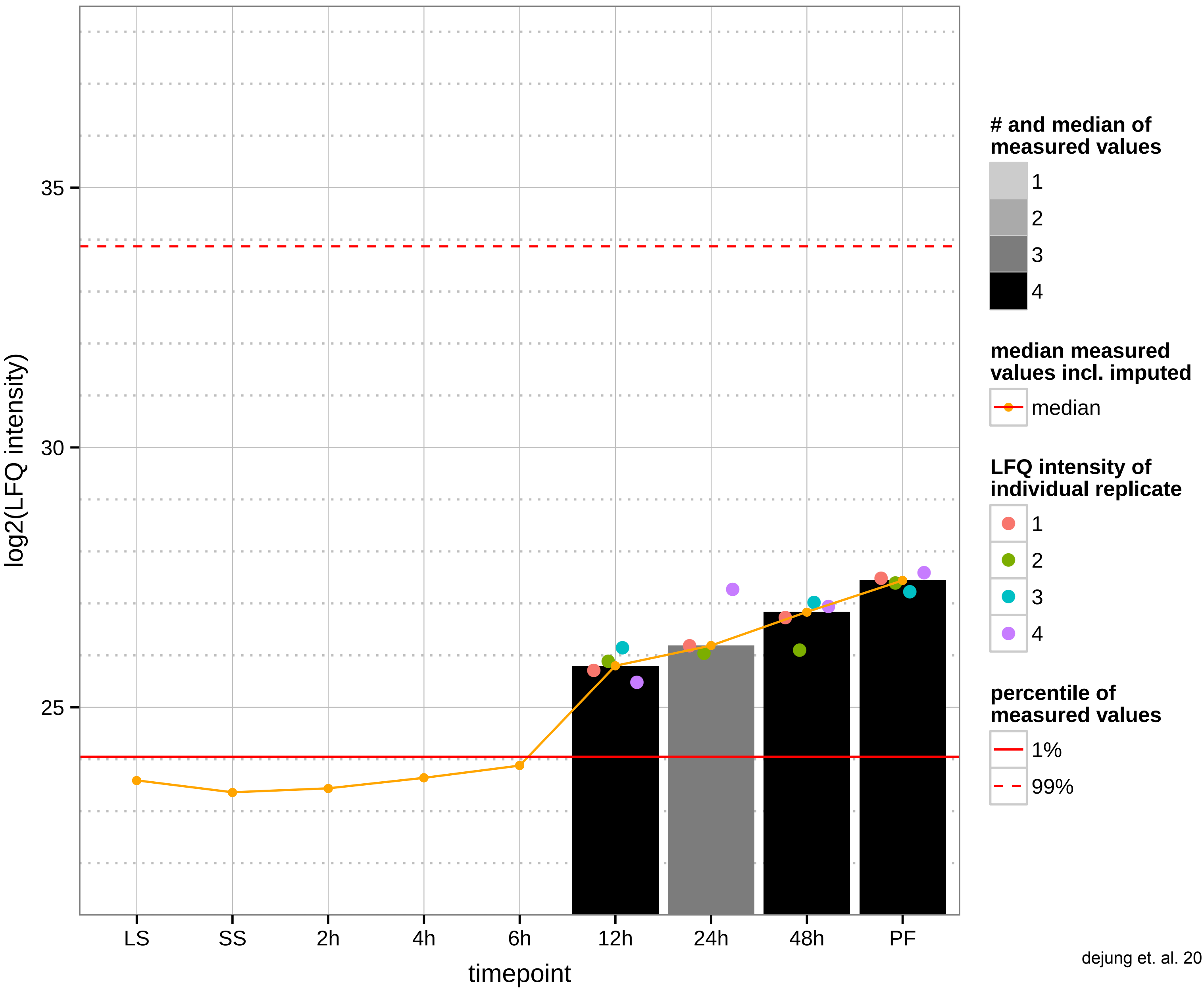
electron–transfer–flavoprotein, alpha polypeptide, putative
Tb927.11.7540
AGOF: electron carrier activity, flavin adenine dinucleotide binding
AGOC: mitochondrion
AGOP: oxidation–reduction process
PGOF: electron carrier activity, flavin adenine dinucleotide binding
PGOC: null
PGOP: null





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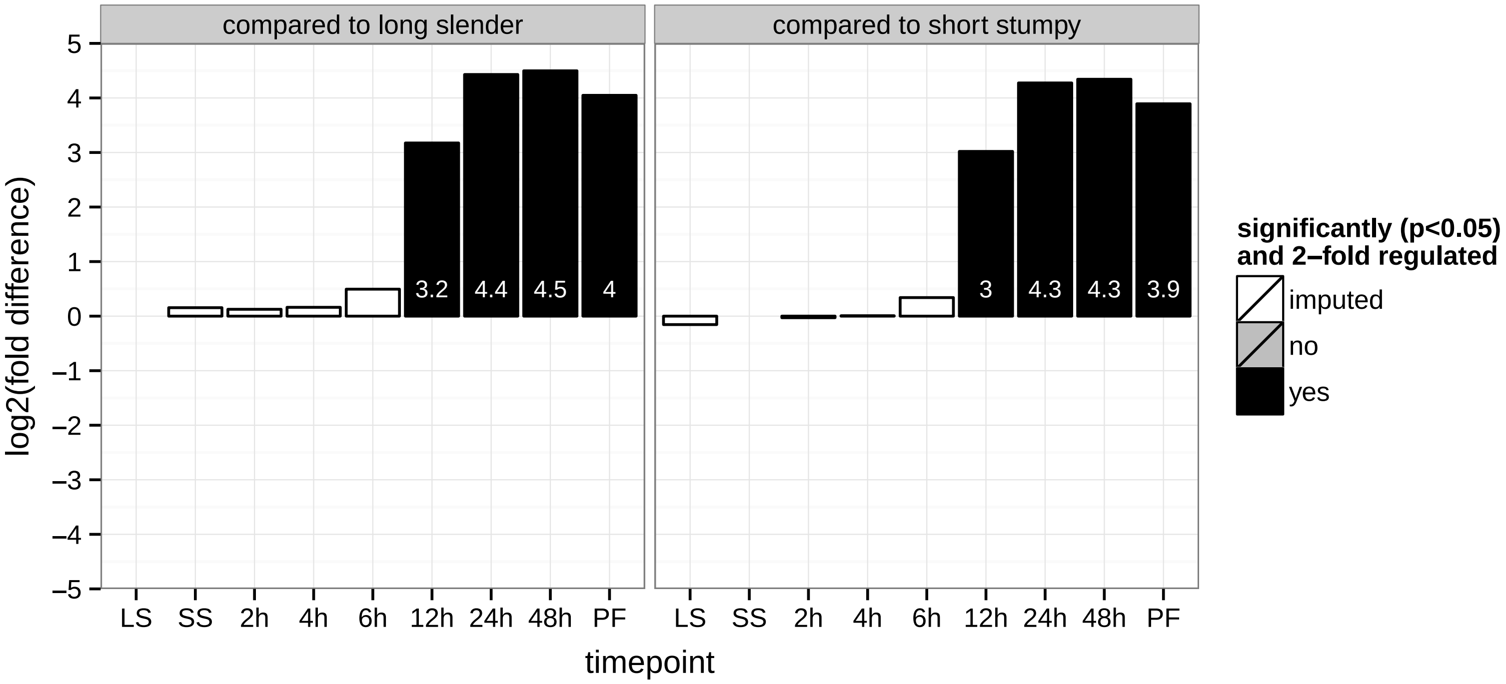
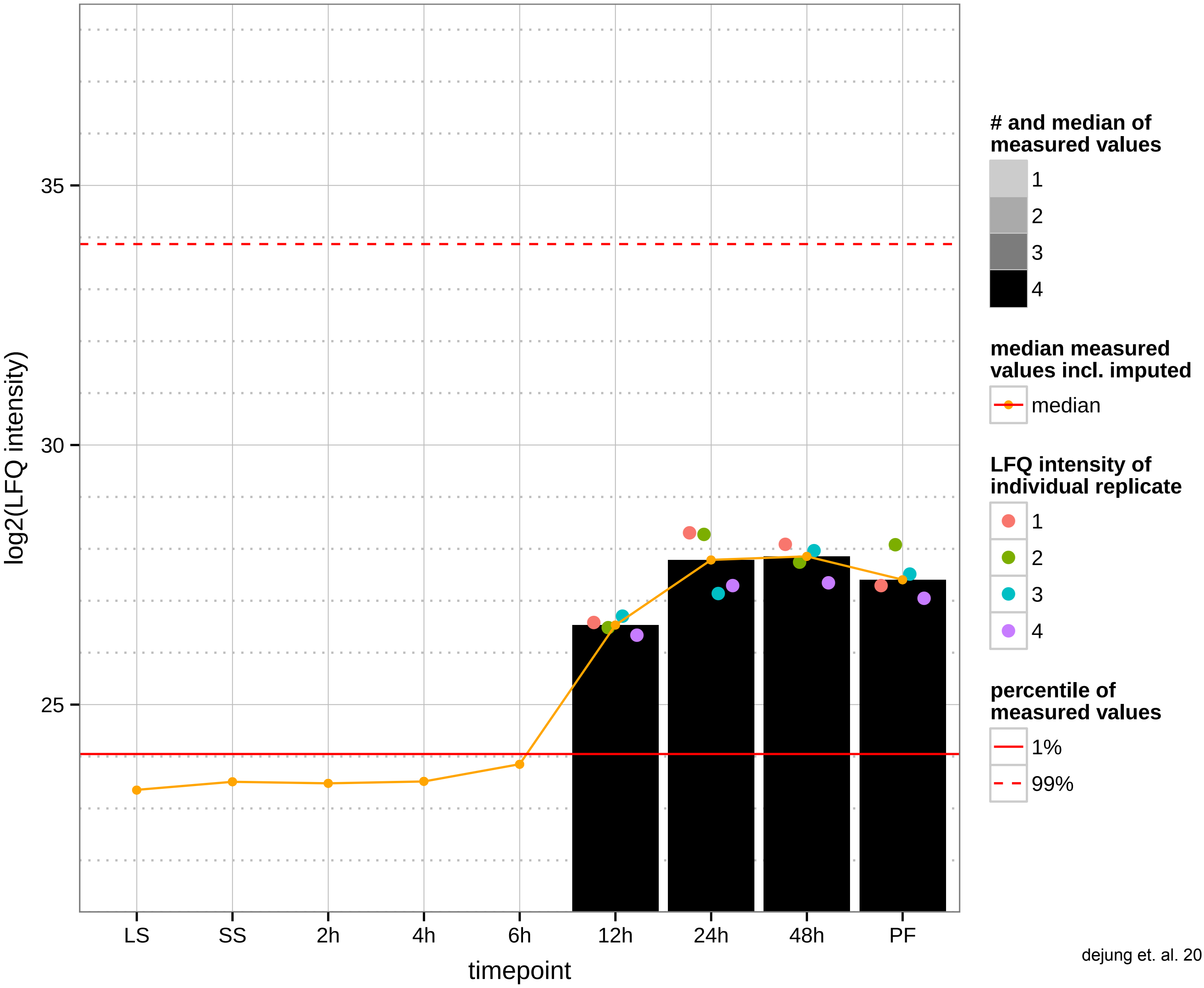
hypothetical protein, conserved
Tb927.11.7600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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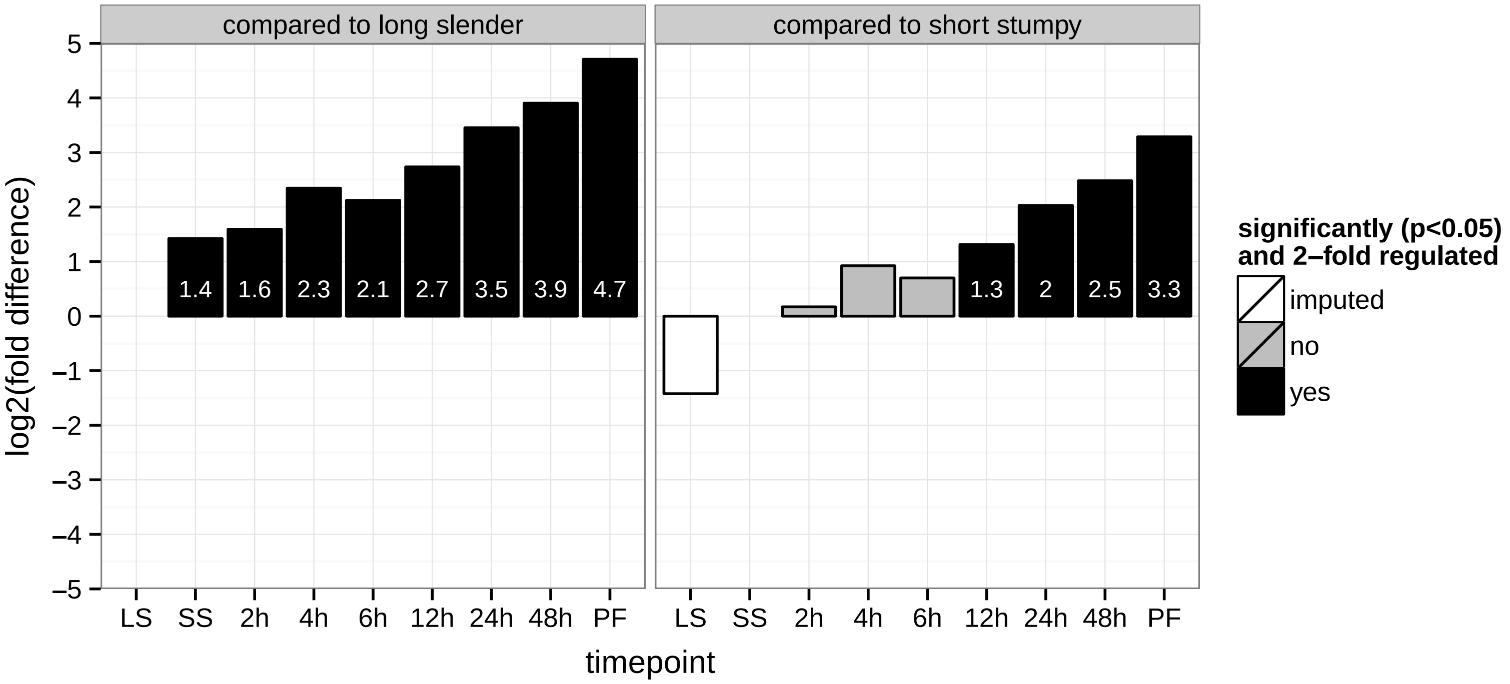
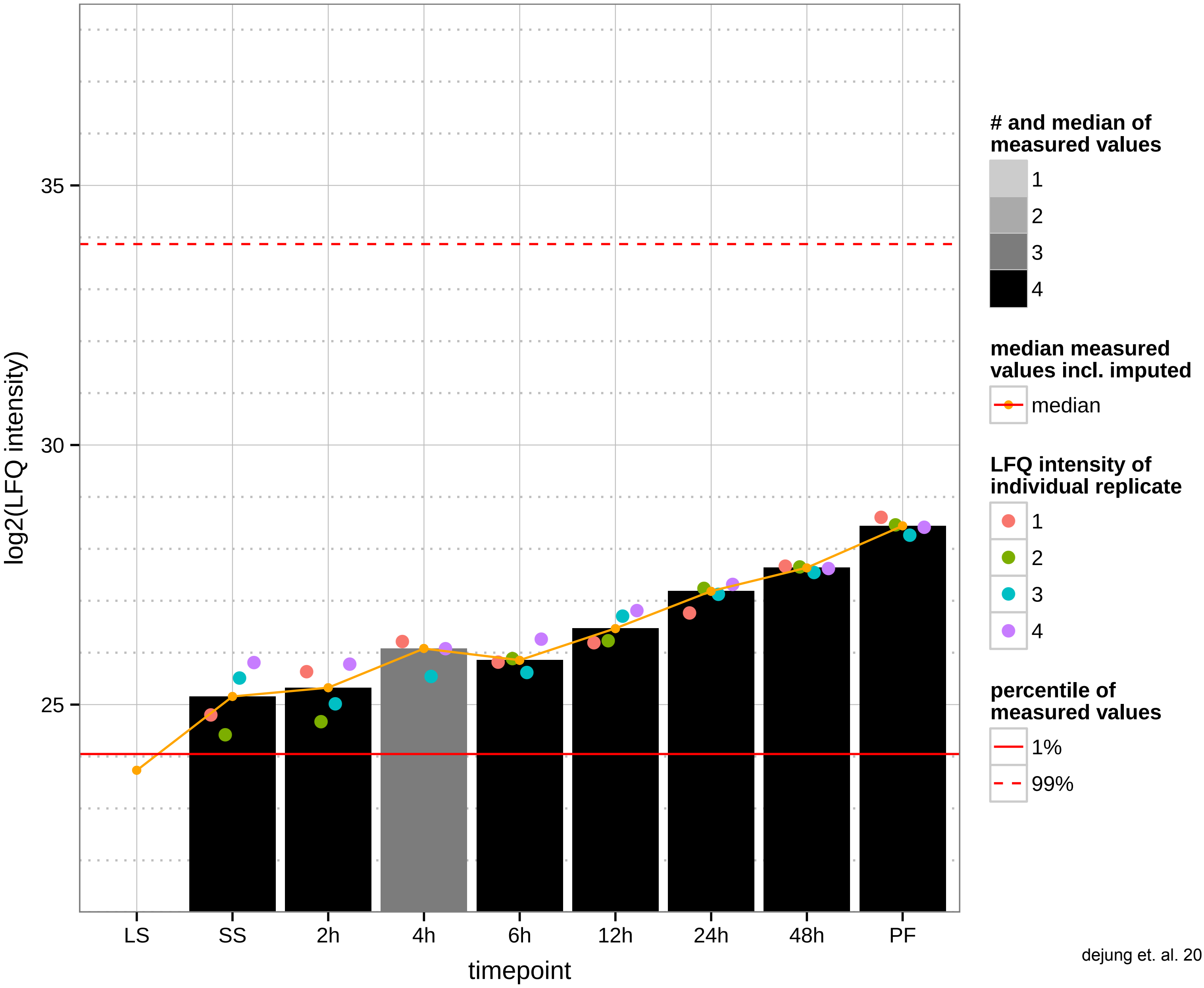
DIS3–like exonuclease, putative
Tb927.11.8290
AGOF: null, RNA binding, ribonuclease activity
AGOC: null
AGOP: null
PGOF: RNA binding, ribonuclease activity
PGOC: null
PGOP: null





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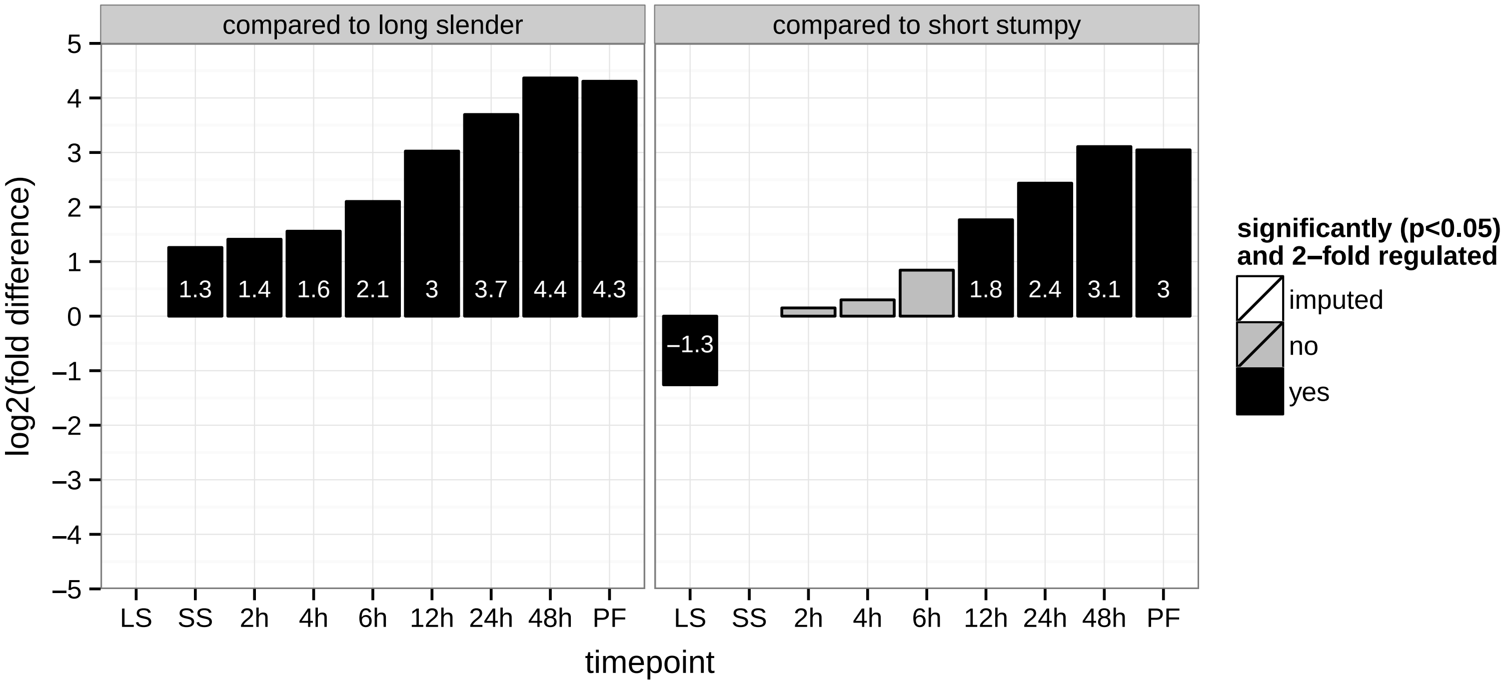
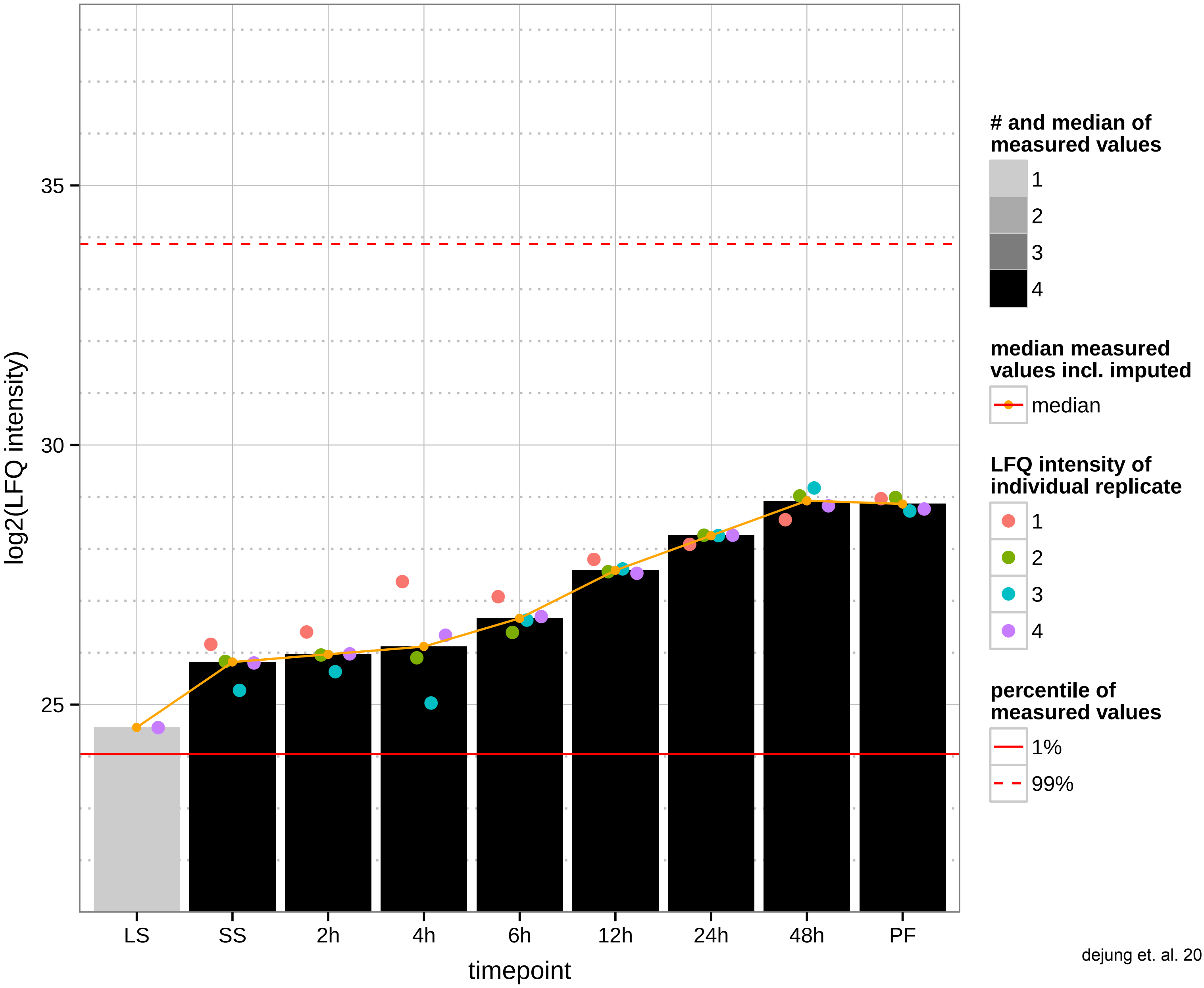
mitochondrial DEAD box protein, KREH1 (KREH1)
Tb927.11.8870
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: mitochondrion
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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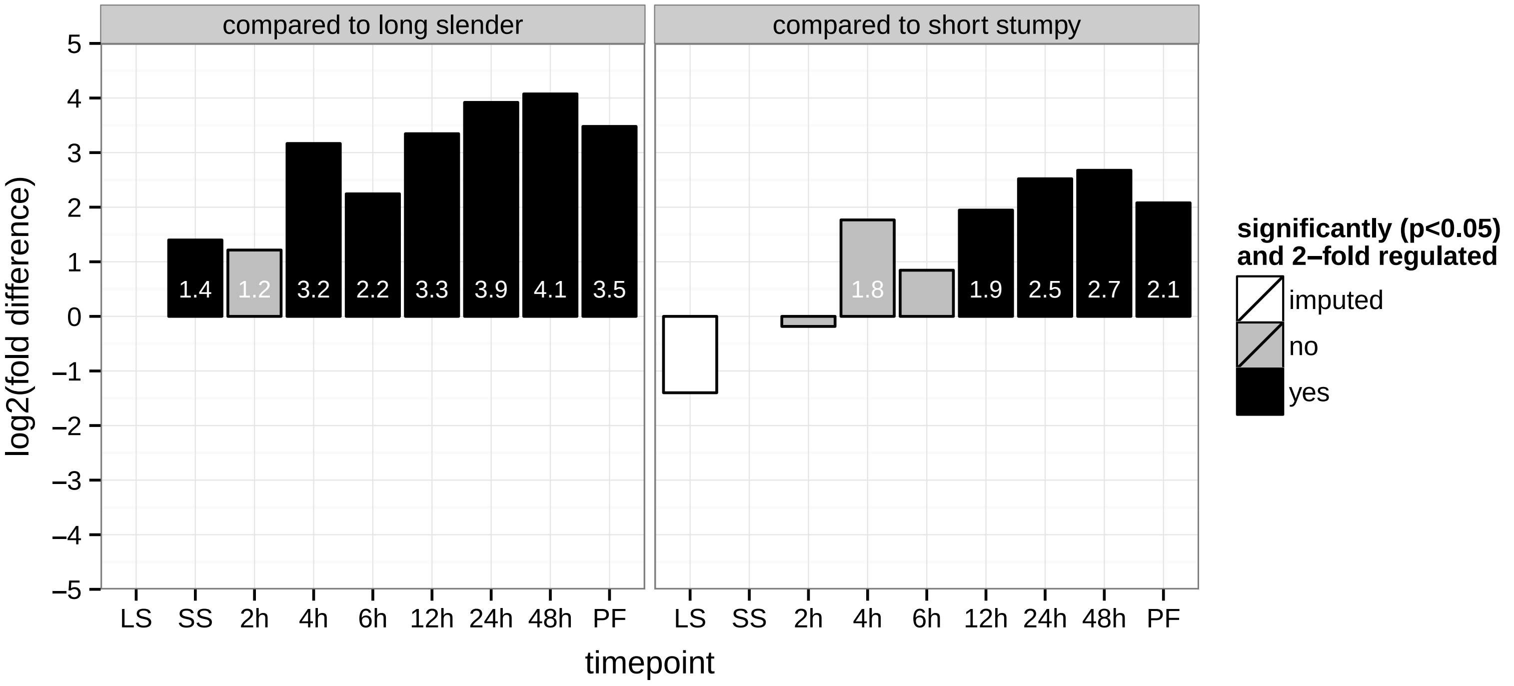
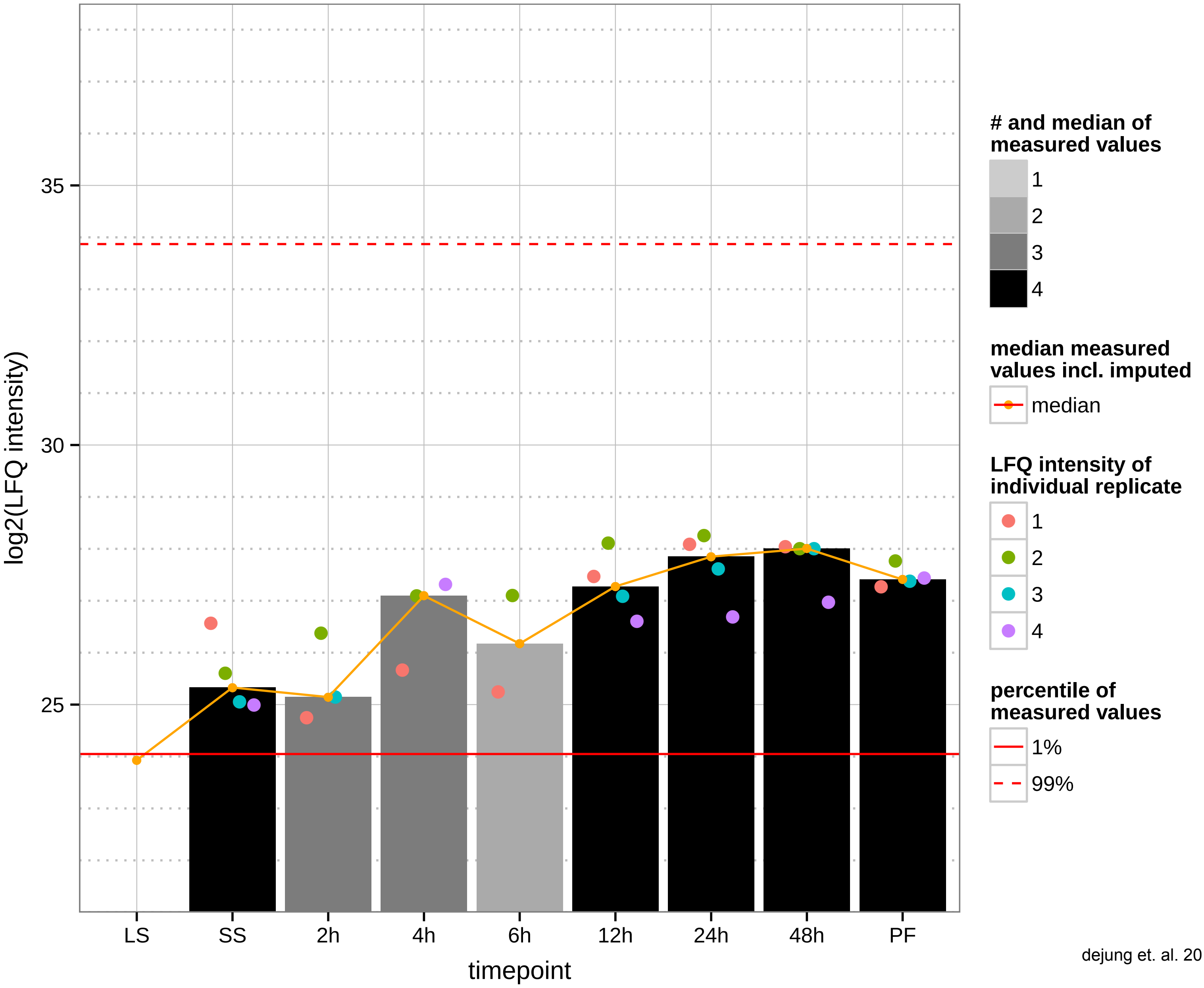
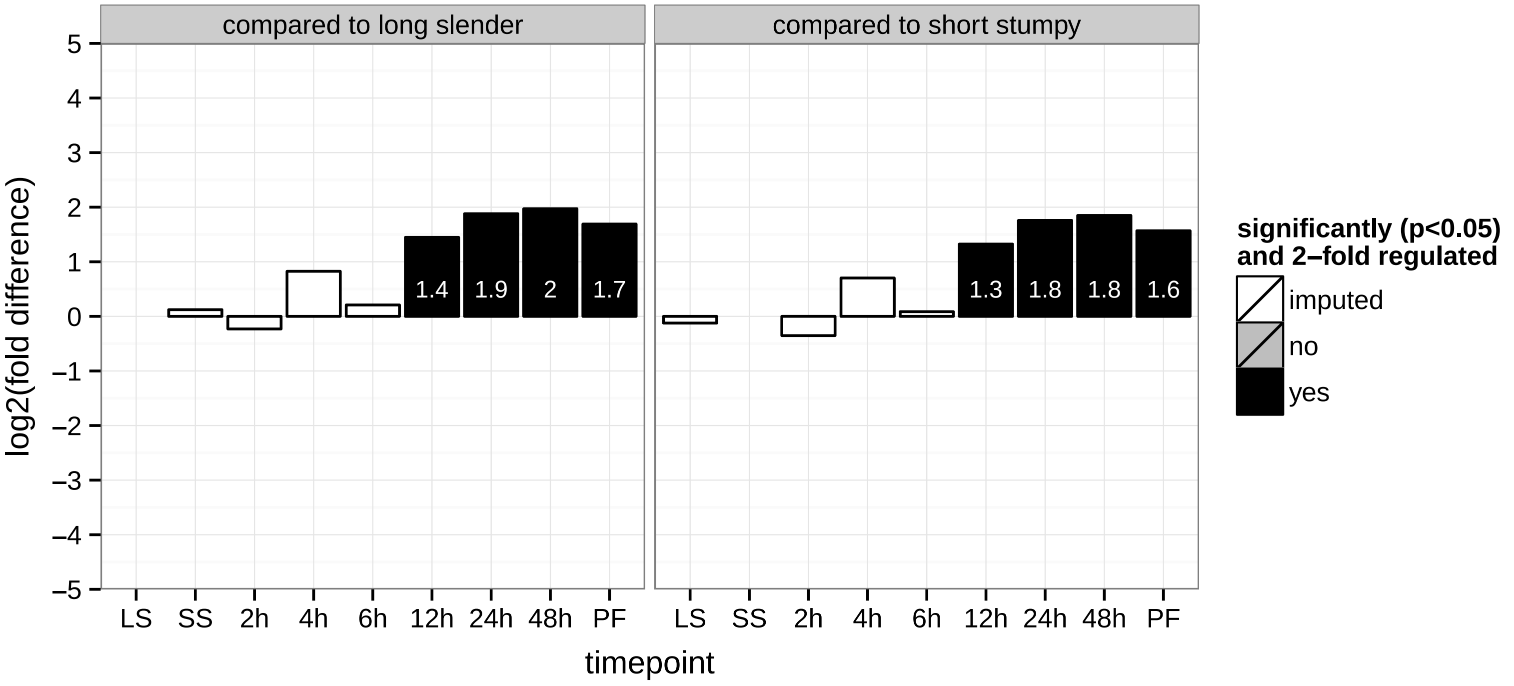
conserved protein
Tb927.11.9040
AGOF: DNA binding
AGOC: null
AGOP: null
PGOF: DNA binding
PGOC: null
PGOP: null

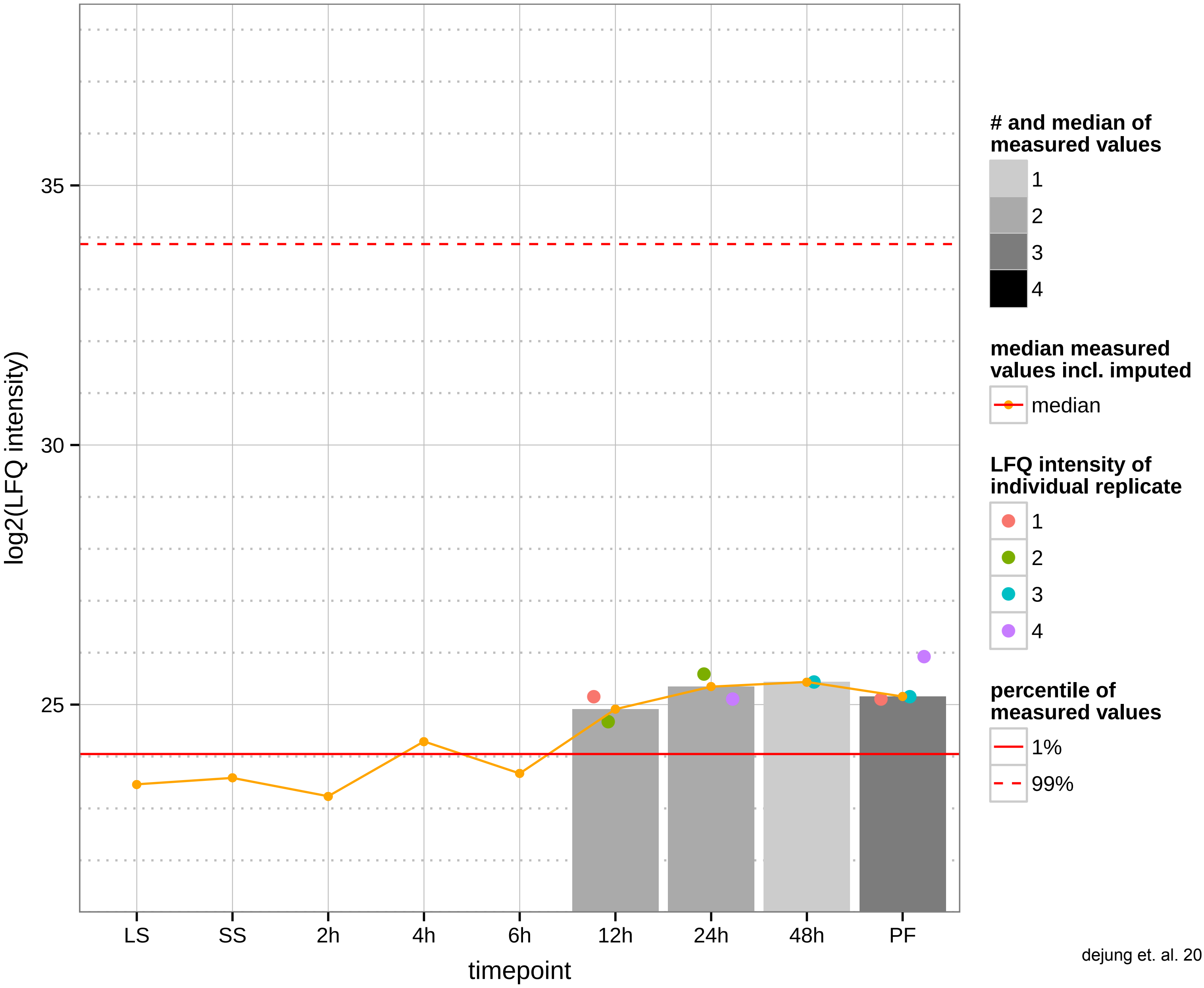




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.9280
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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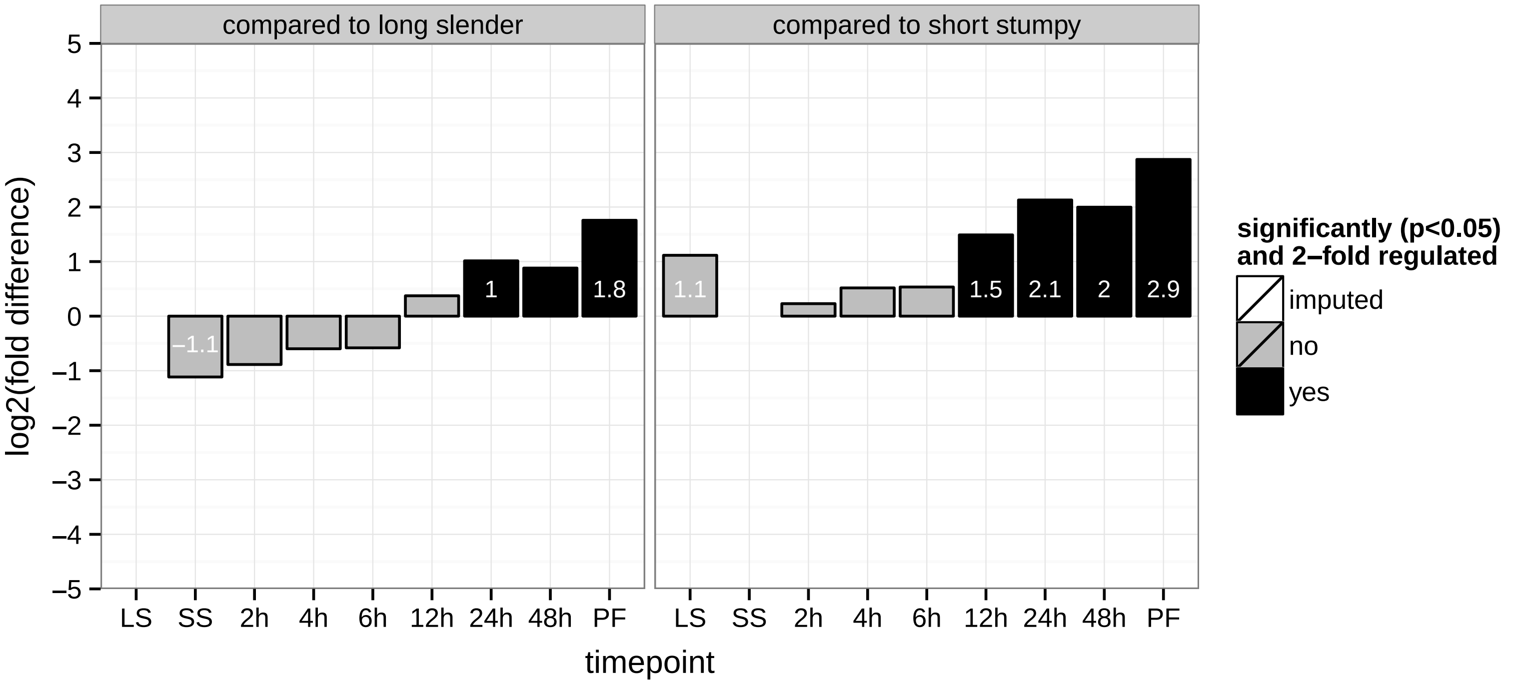
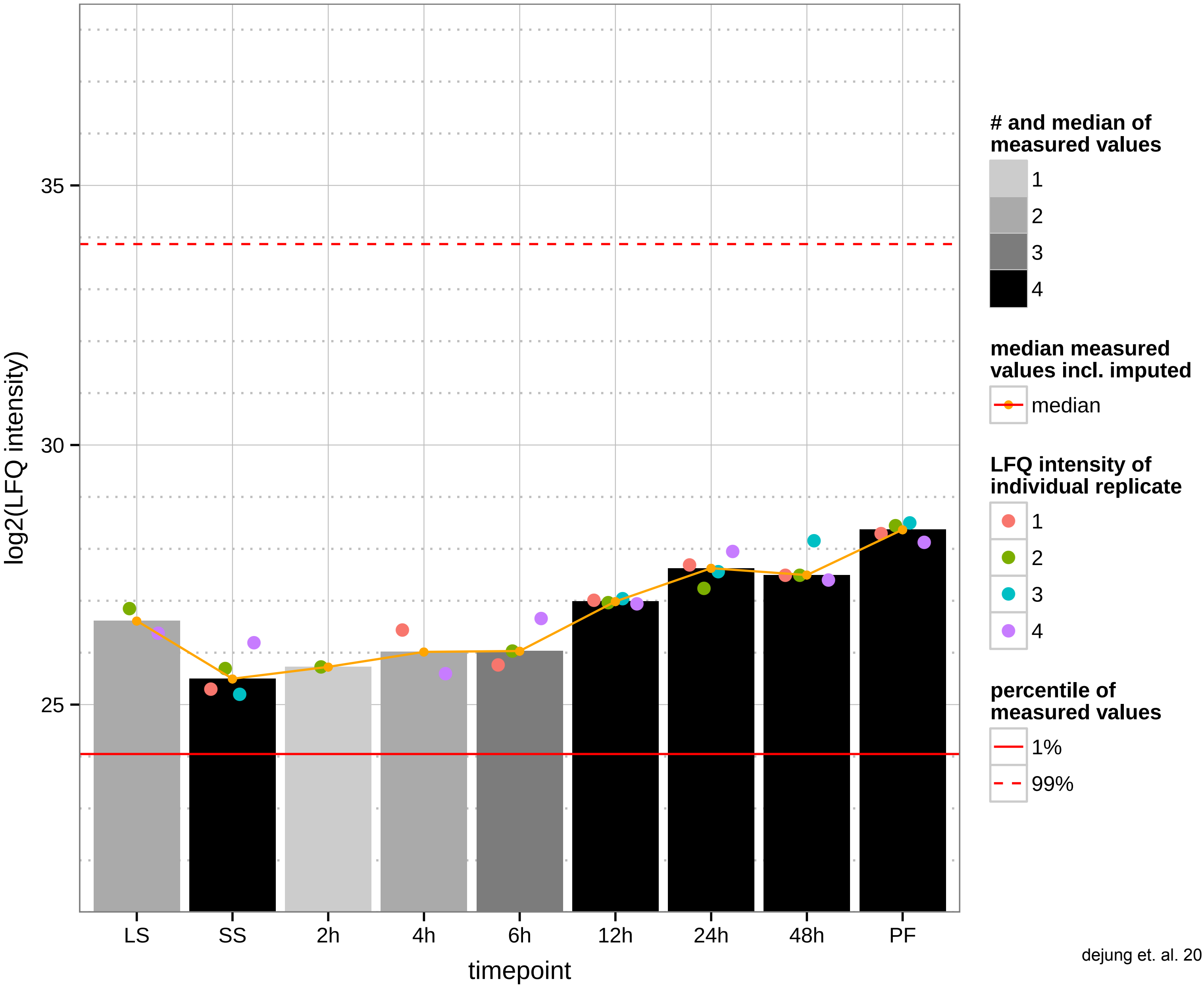
casein kinase II, alpha chain (CK2A2)
Tb927.2.2430
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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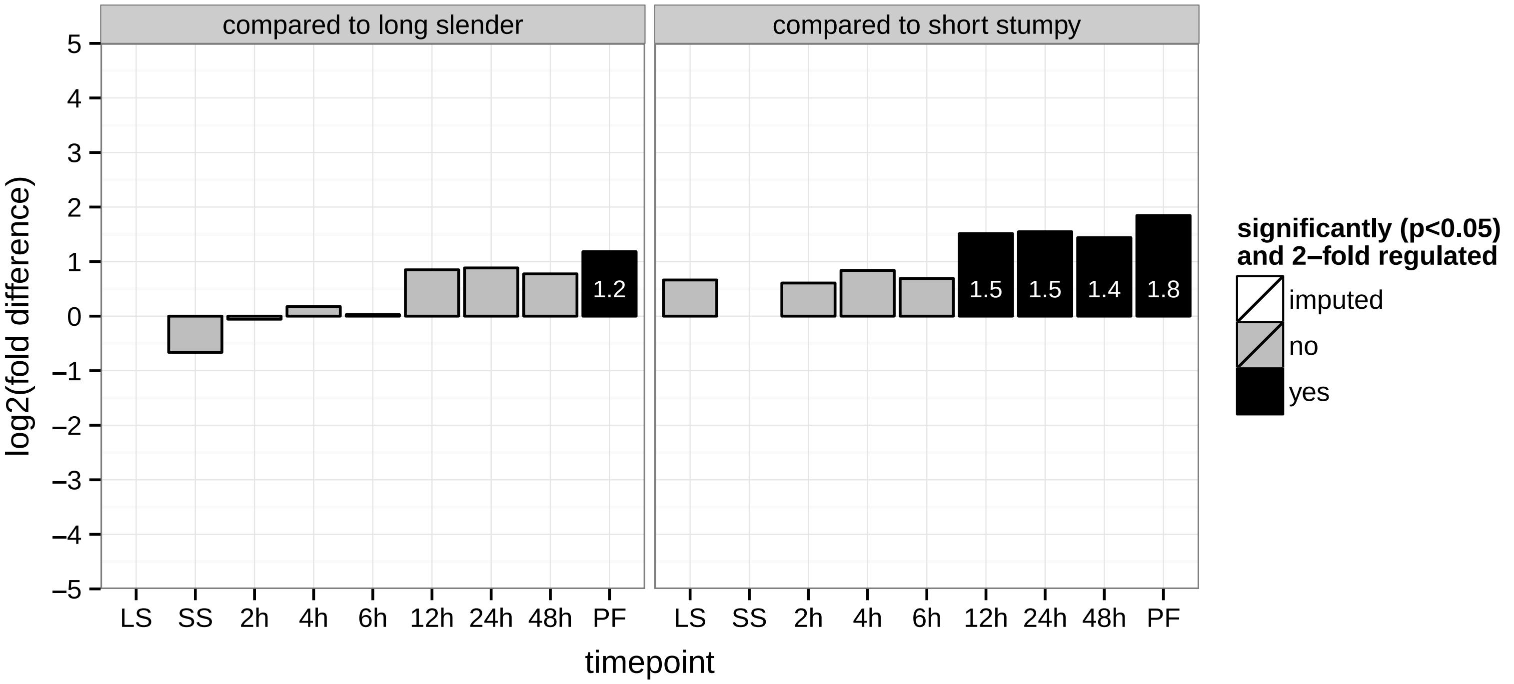
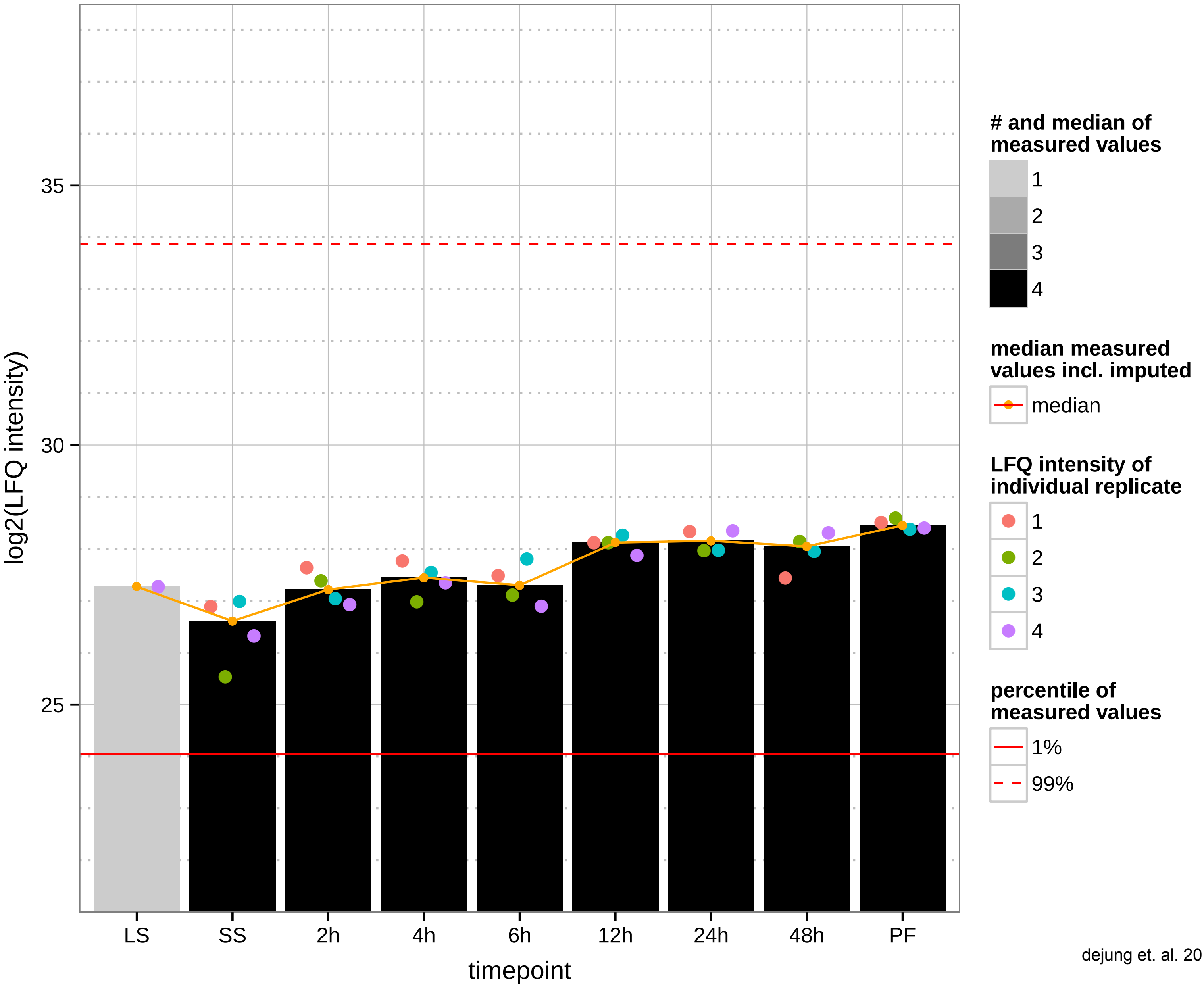
UDP−Gal or UDP−GlcNAc−dependent glycosyltransferase, putative
Tb927.2.3370
AGOF: UDP−glycosyltransferase activity, galactosyltransferase activity
AGOC: integral to membrane, membrane
AGOP: GPI anchor biosynthetic process, protein glycosylation
PGOF: null
PGOC: null
PGOP: null





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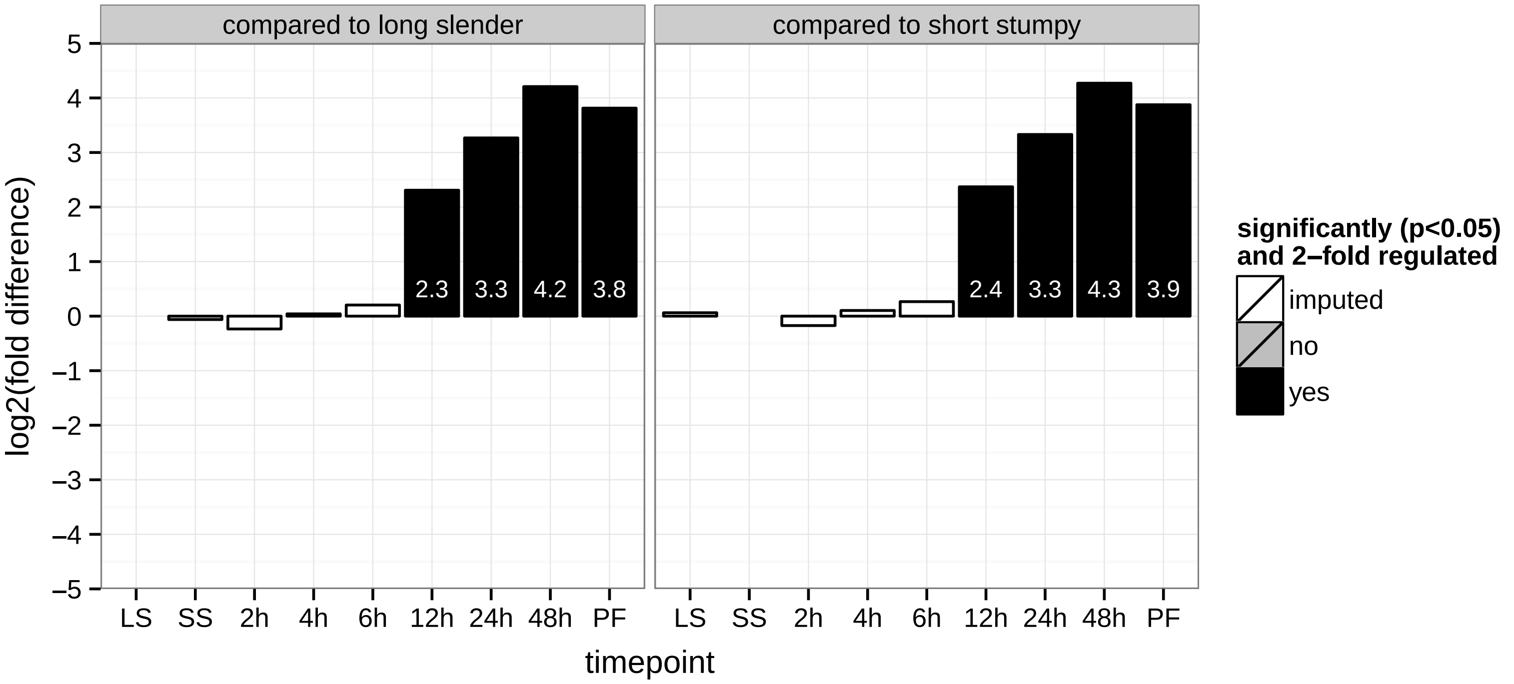
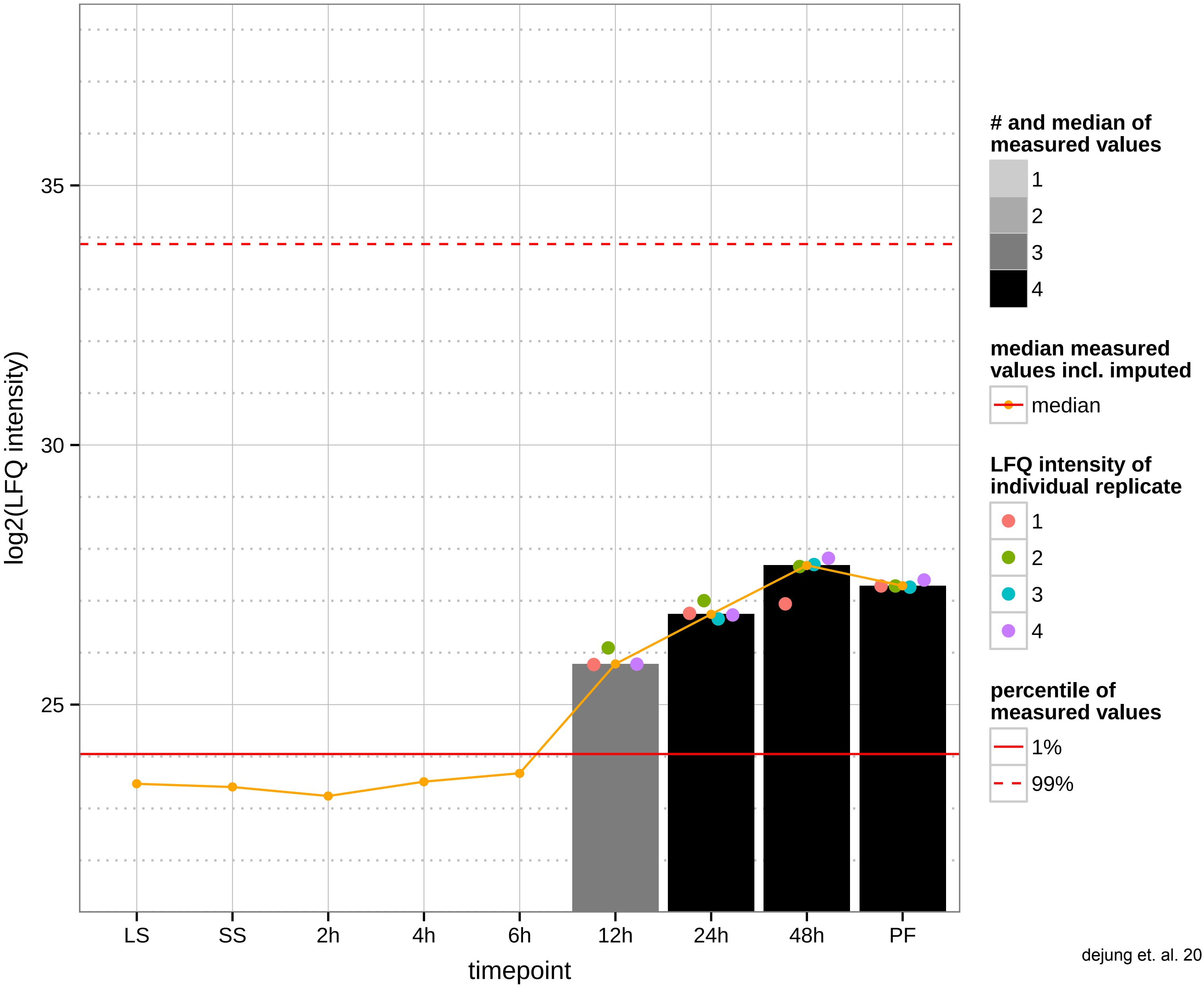
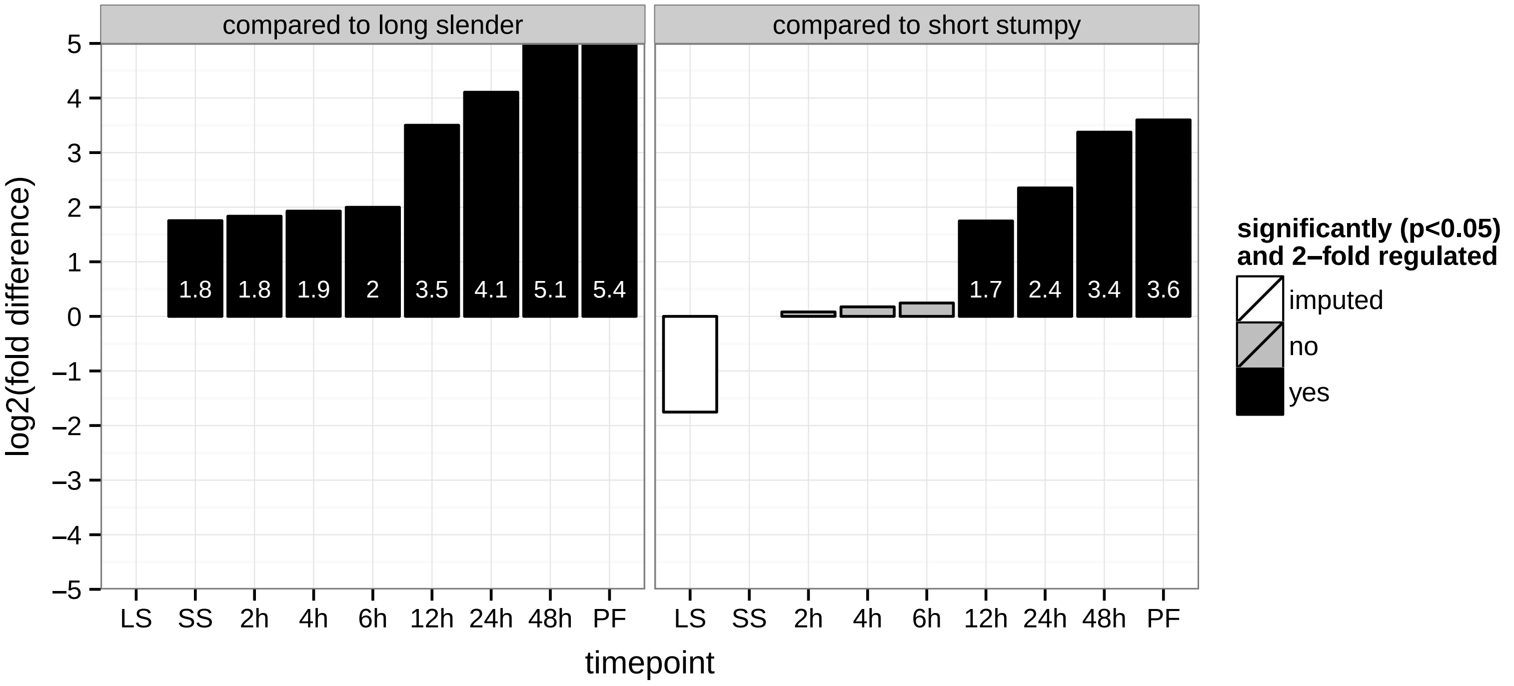
GTP binding protein, putative
Tb927.2.4240
AGOF: GTP binding
AGOC: intracellular
AGOP: null
PGOF: GTP binding
PGOC: null
PGOP: null

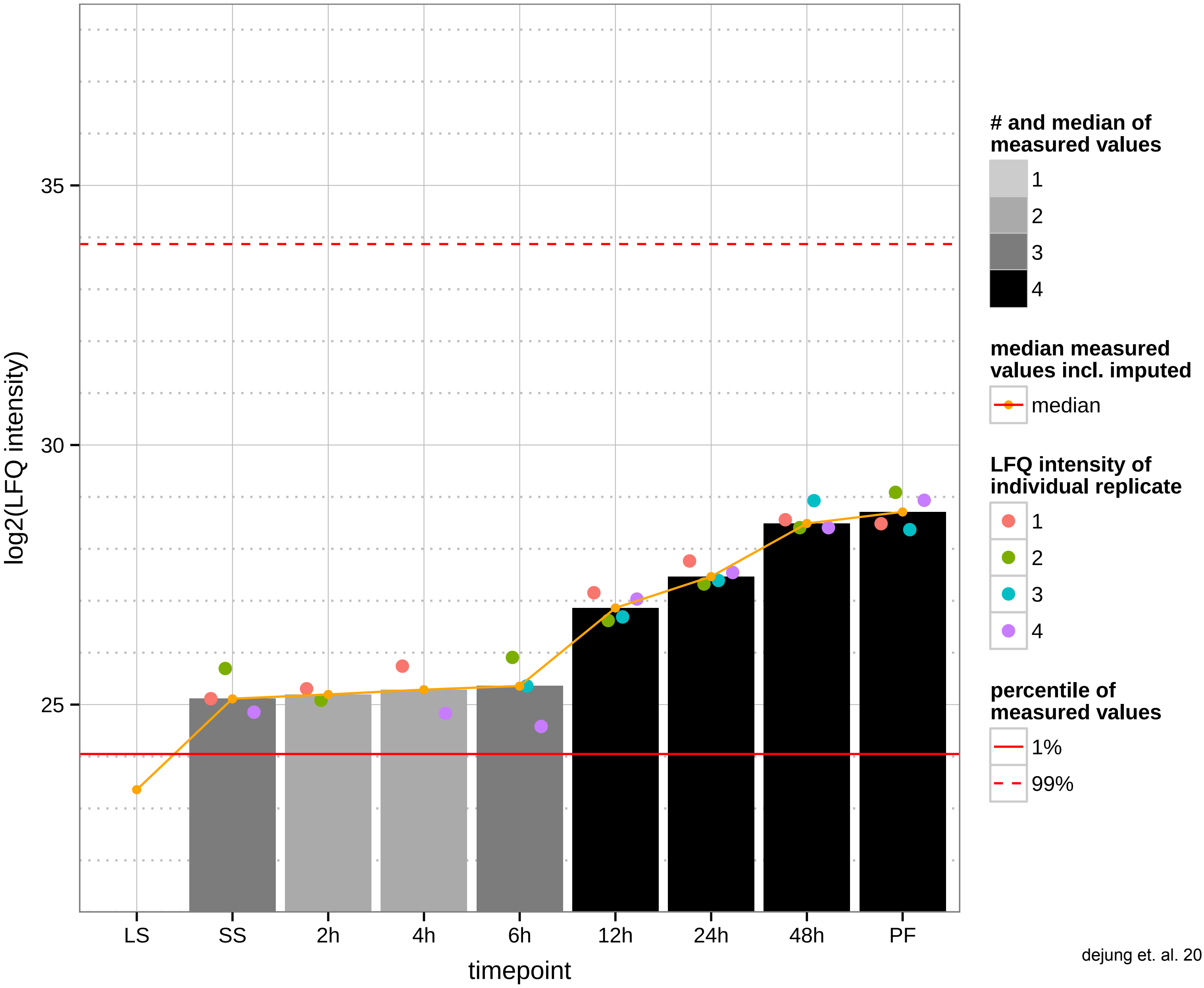




dejung et. al. 2015

hypothetical protein, conserved
Tb927.2.4400
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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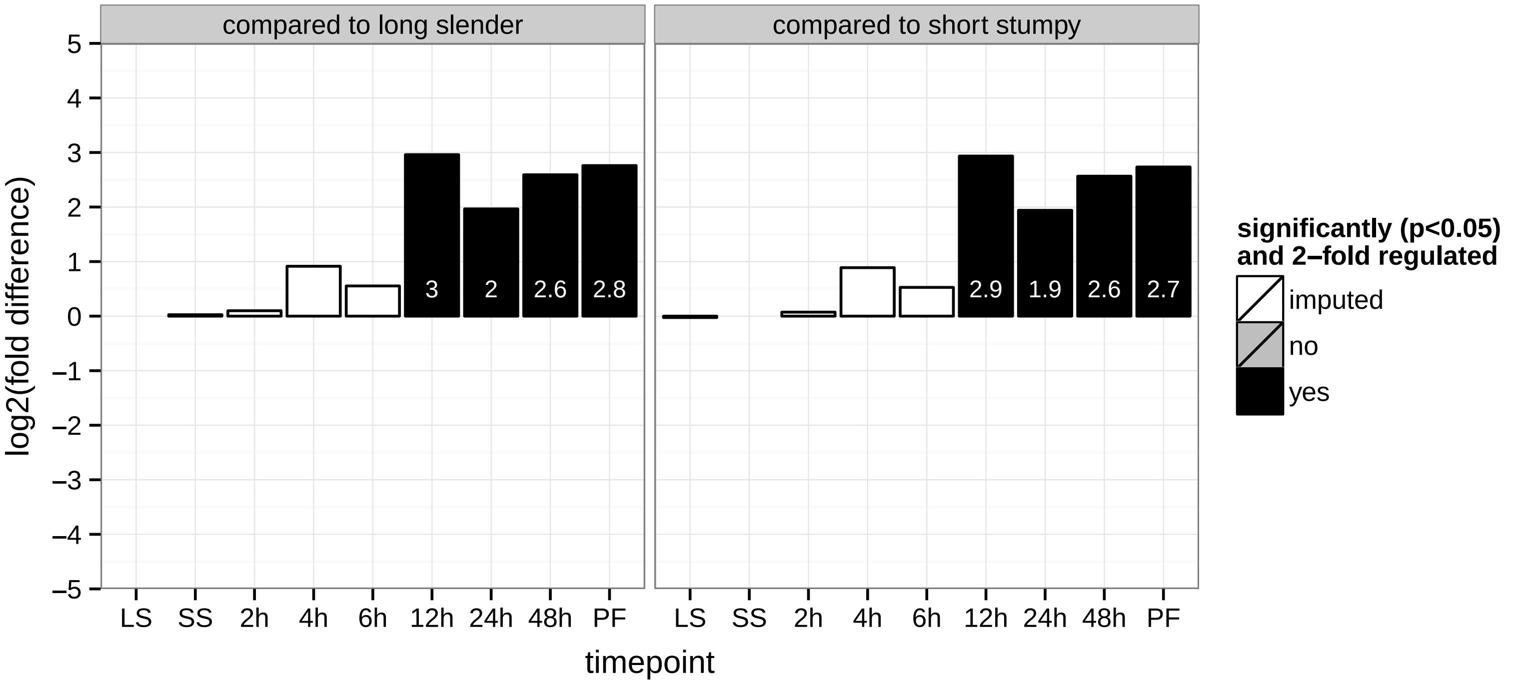
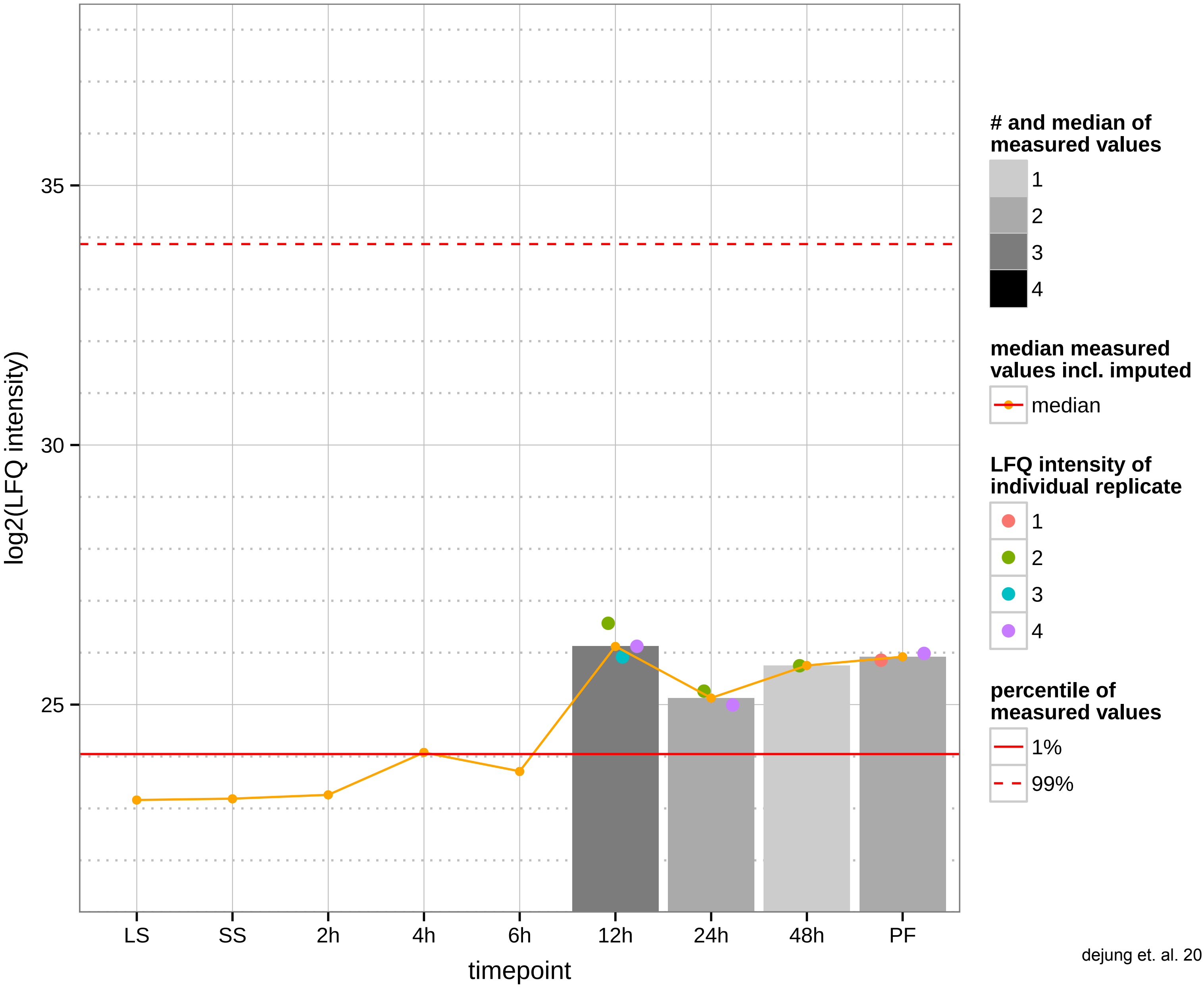
hypothetical protein, conserved
Tb927.2.4460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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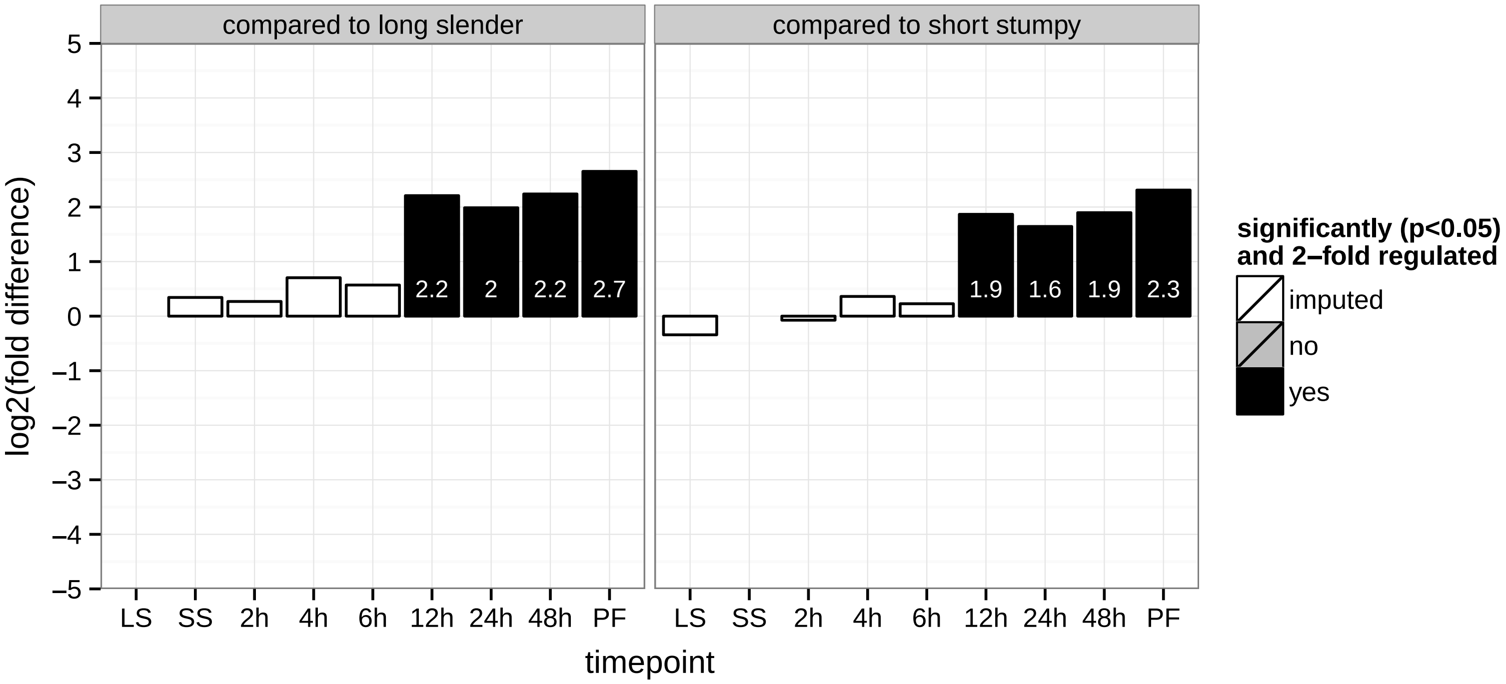
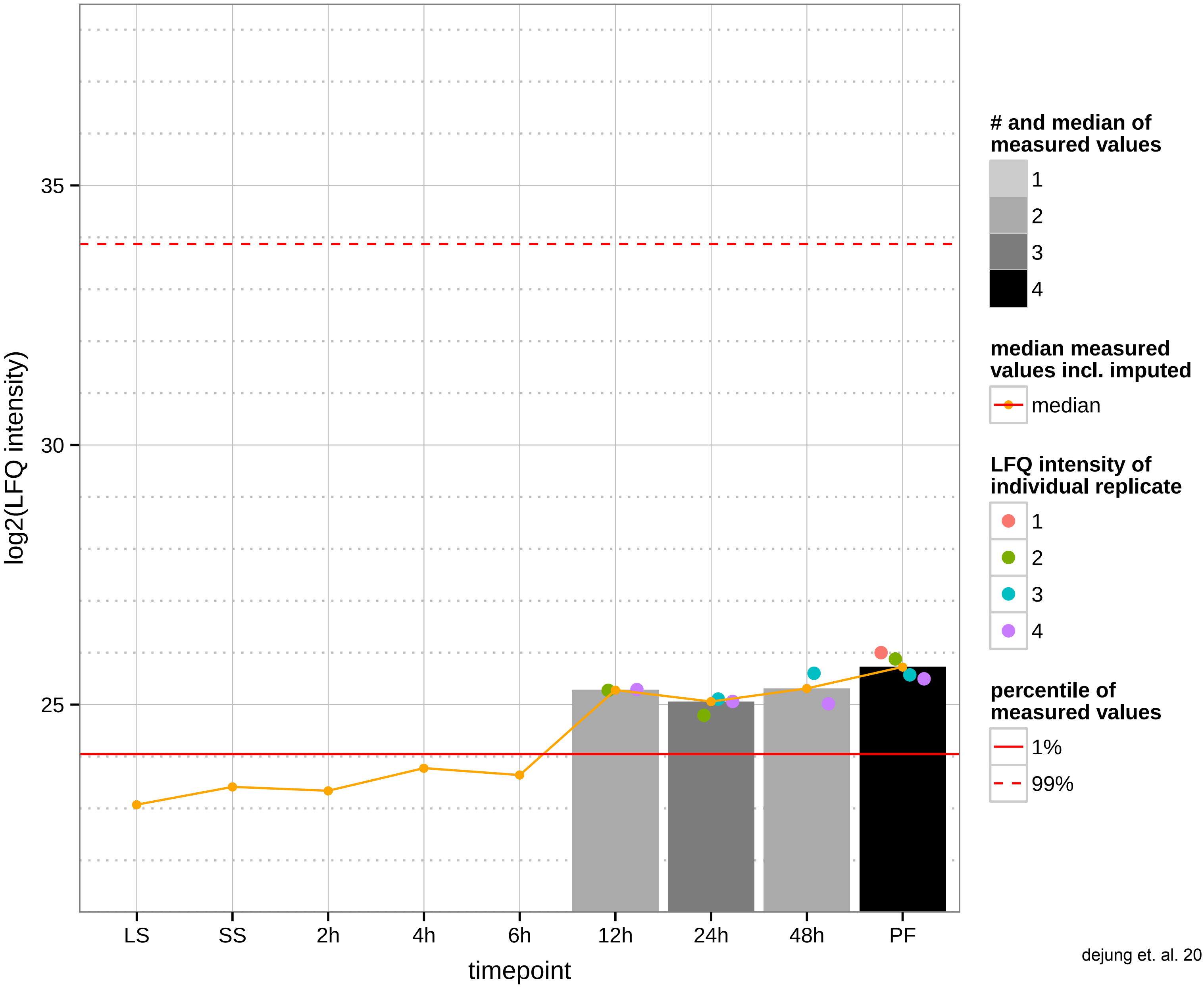
hypothetical protein, conserved
Tb927.2.4650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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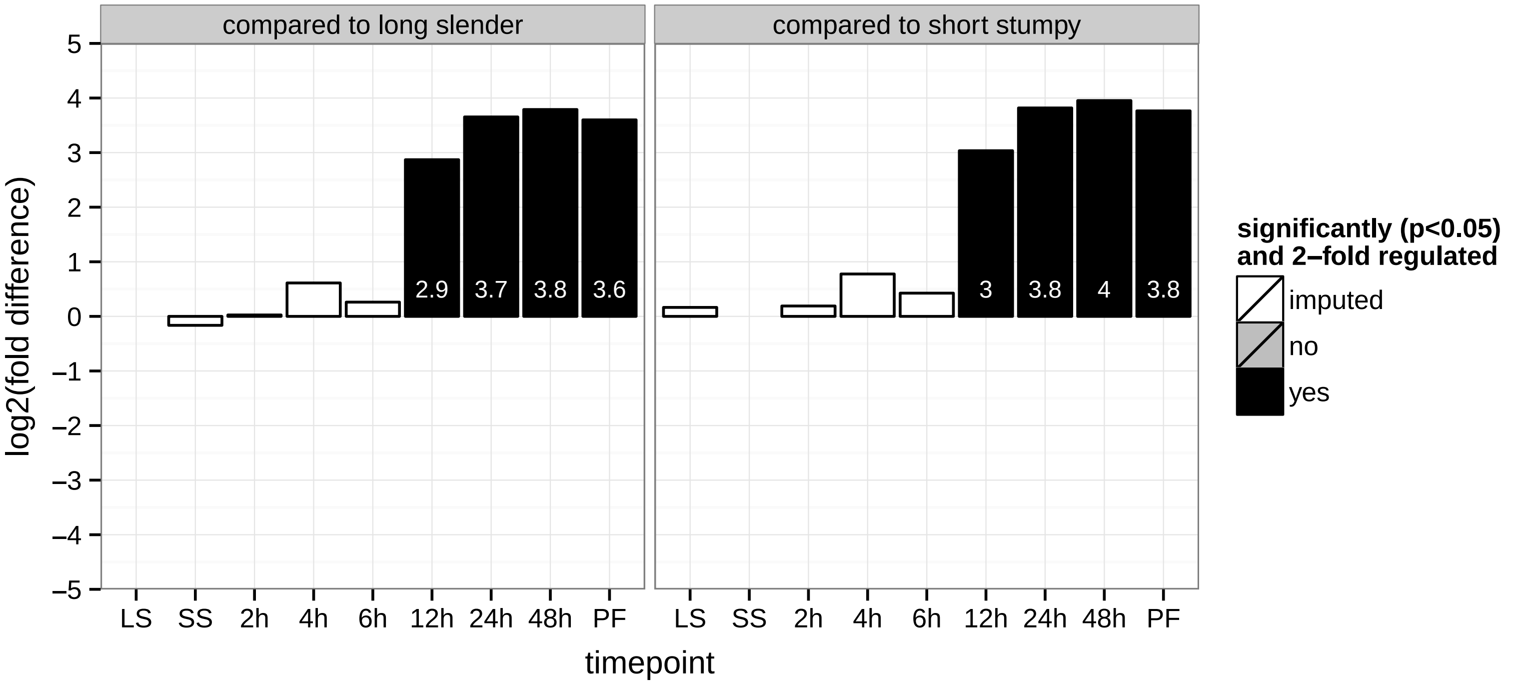
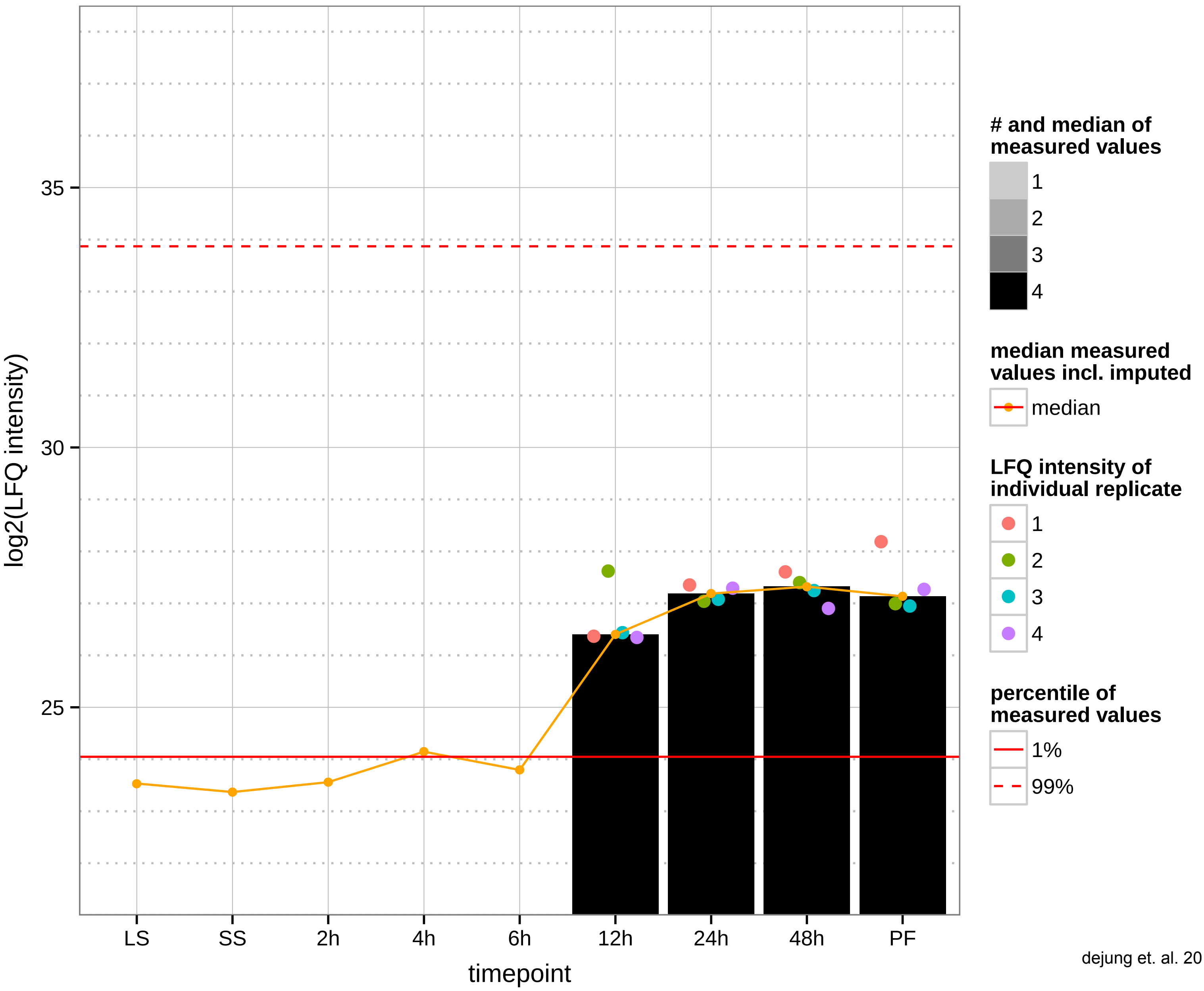
acyl–CoA oxidase, putative
Tb927.2.5020
AGOF: acyl–CoA oxidase activity
AGOC: mitochondrion, peroxisome
AGOP: fatty acid beta–oxidation
PGOF: acyl–CoA oxidase activity, oxidoreductase activity, acting on the CH–CH group of donors
PGOC: peroxisome
PGOP: fatty acid beta–oxidation, metabolic process, oxidation–reduction process





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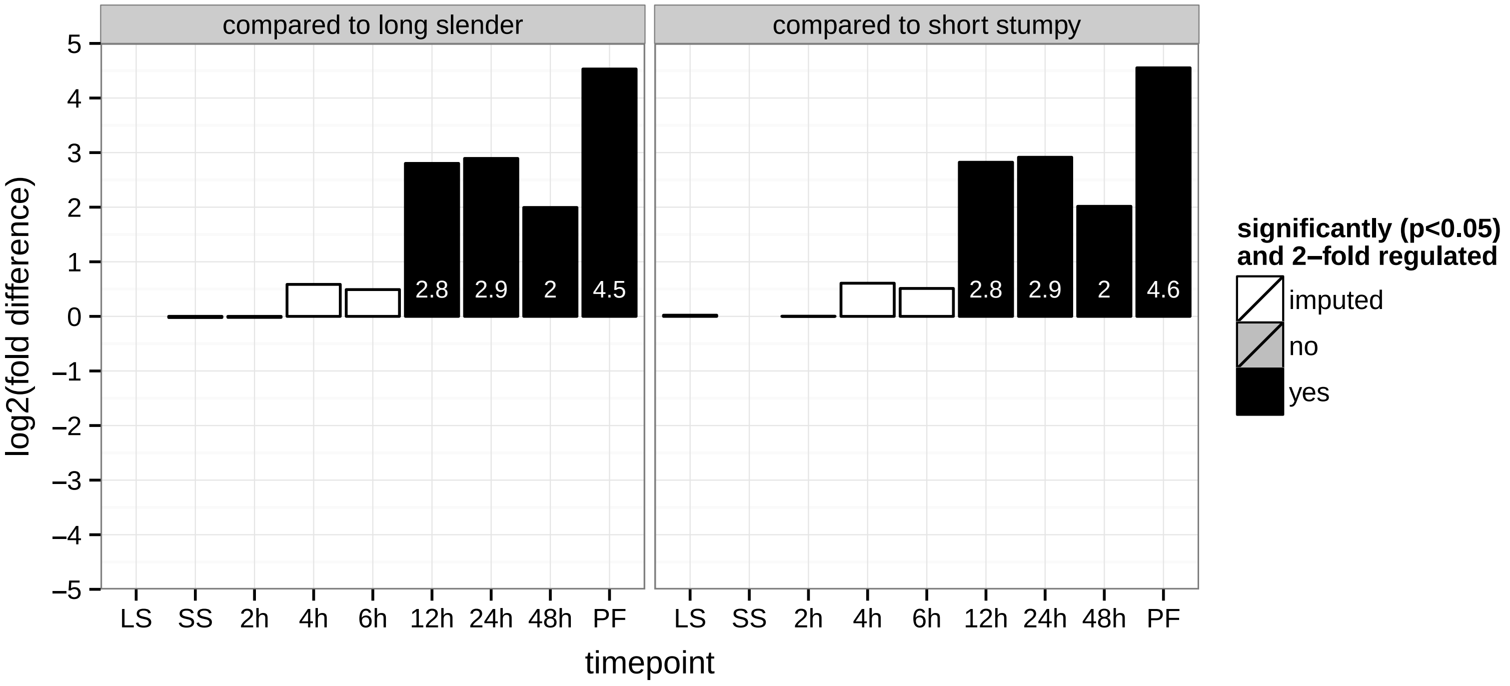
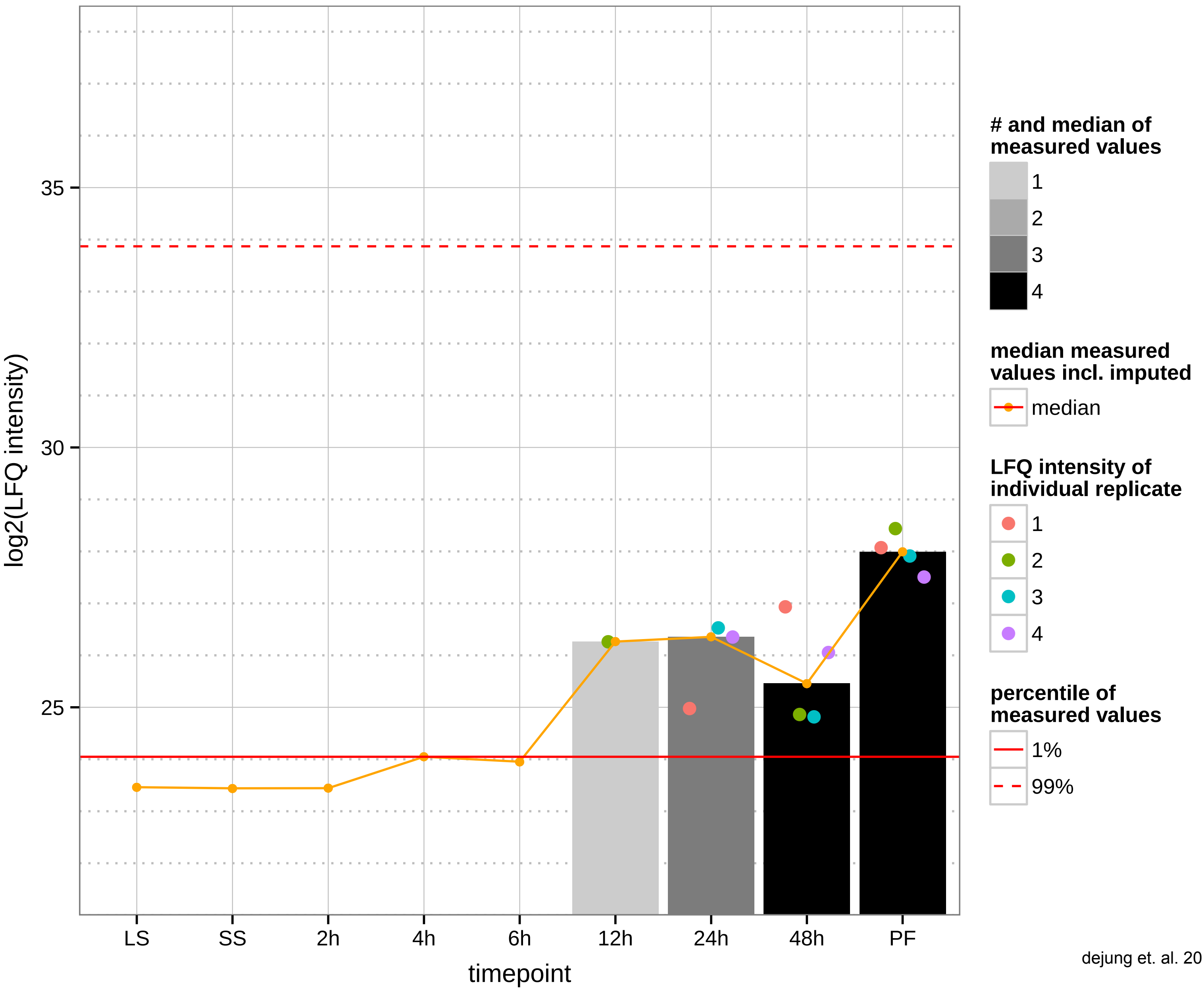
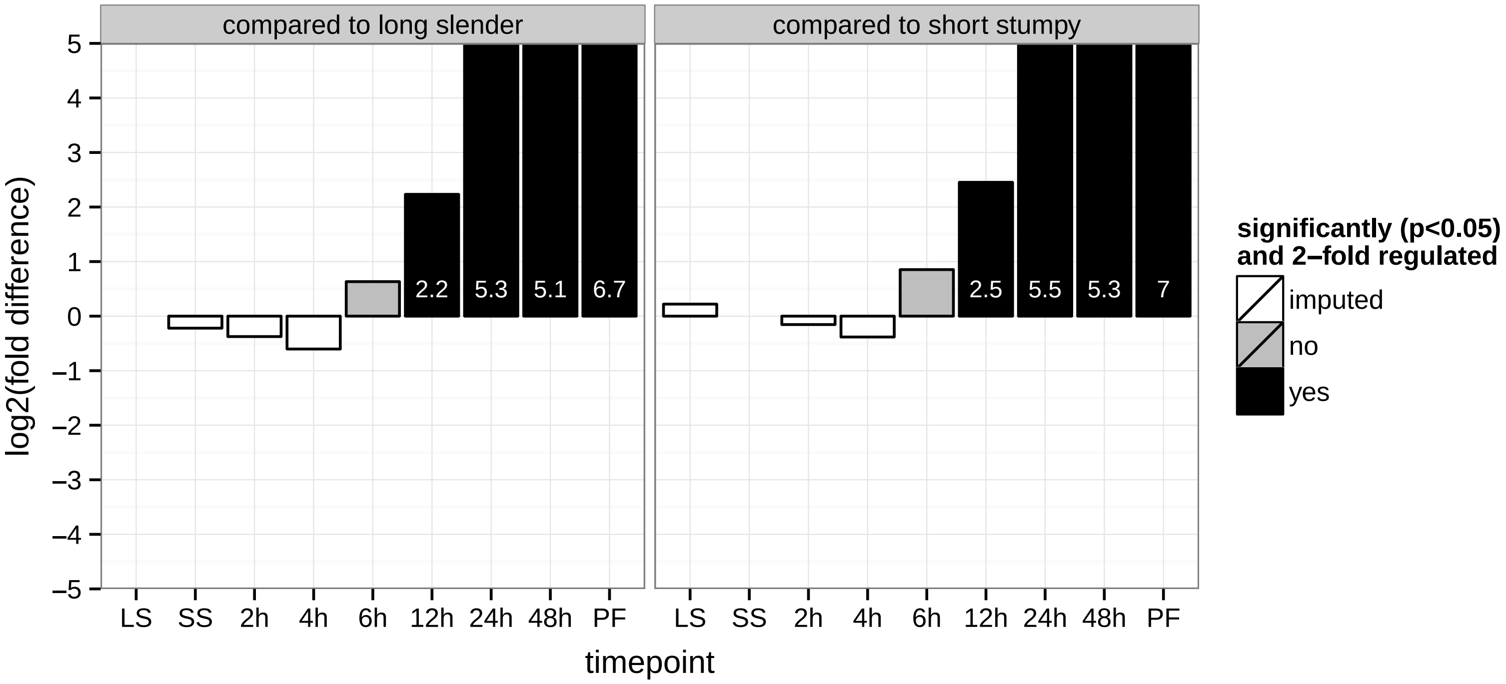
hypothetical protein, conserved
Tb927.2.5610;Tb927.2.5530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

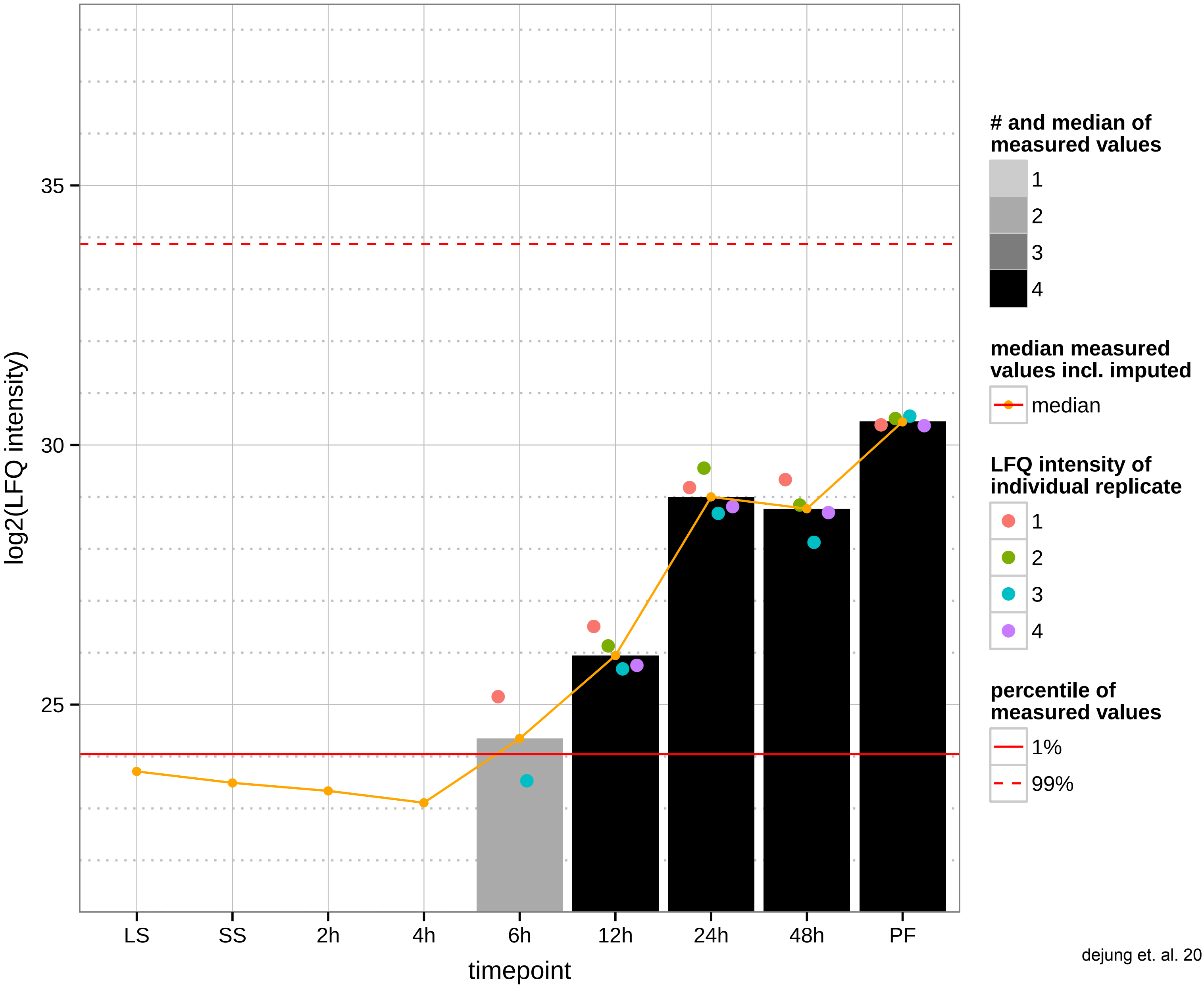




dejung et. al. 2015

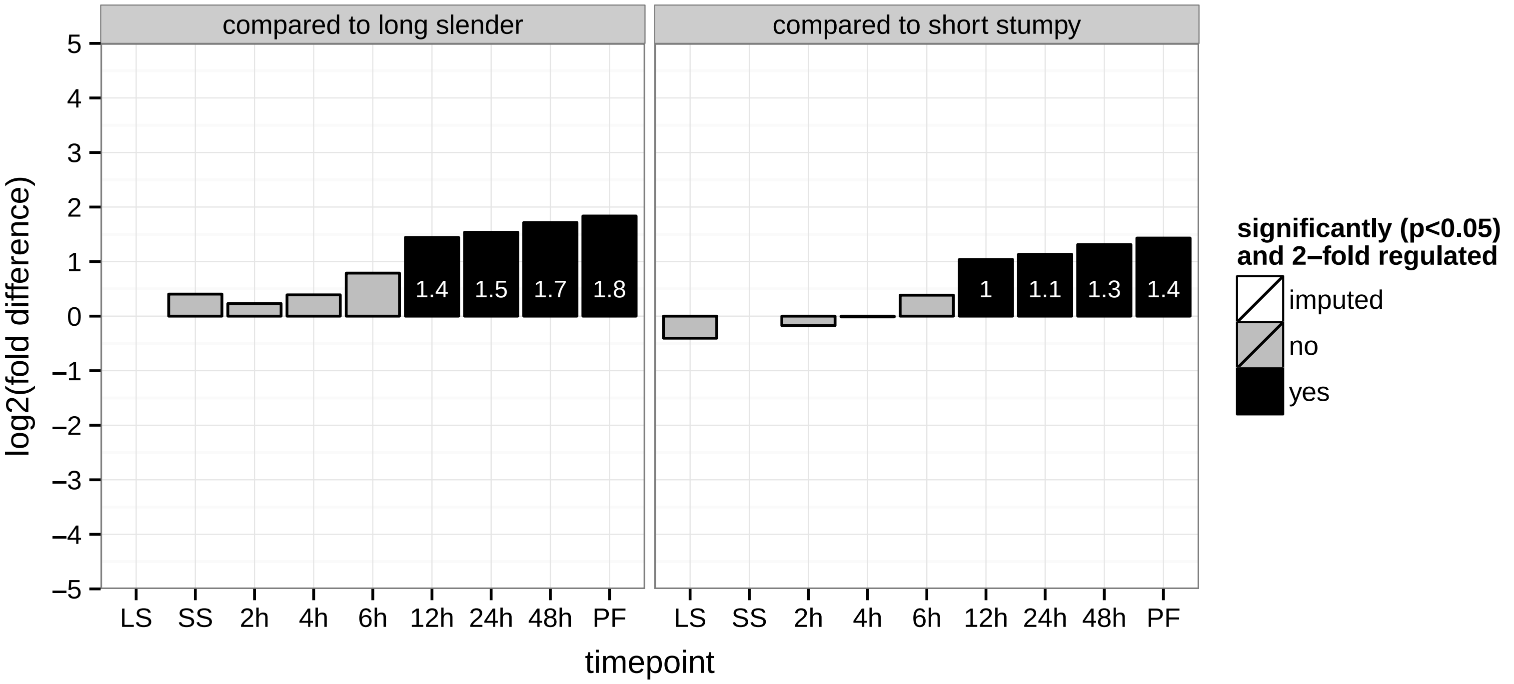
cytochrome oxidase subunit VII (COXVII)
Tb927.3.1410
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

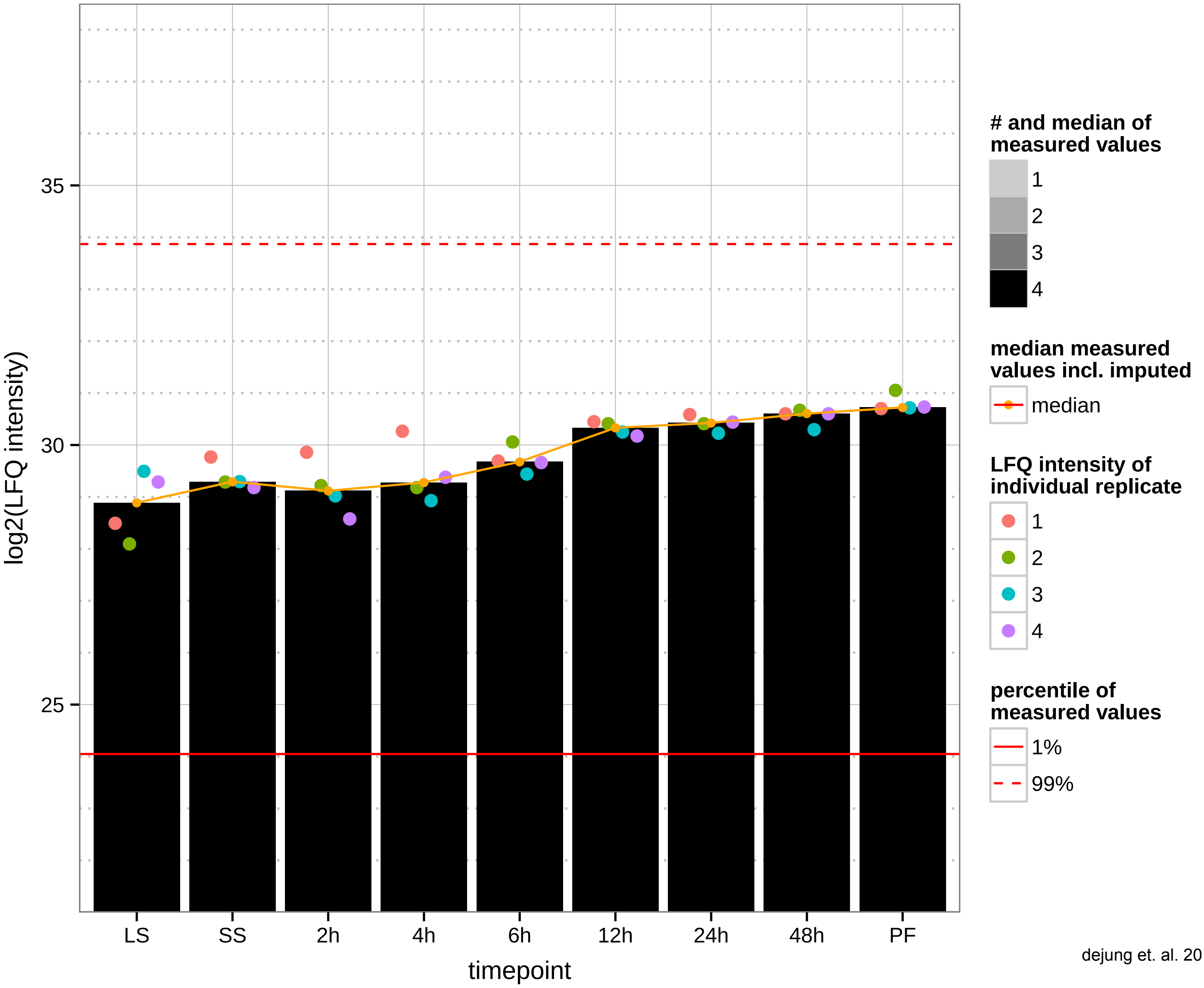




dejung et. al. 2015

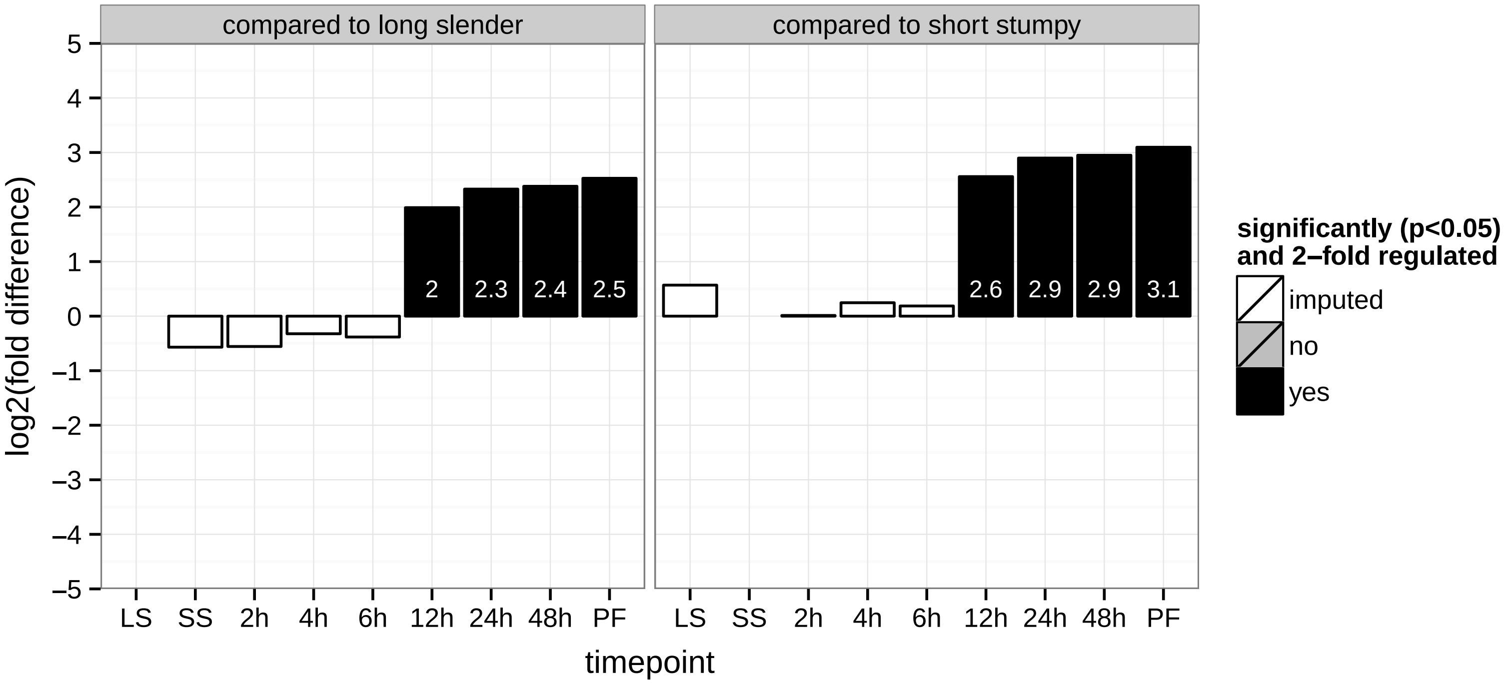
hypothetical protein, conserved
Tb927.3.1680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

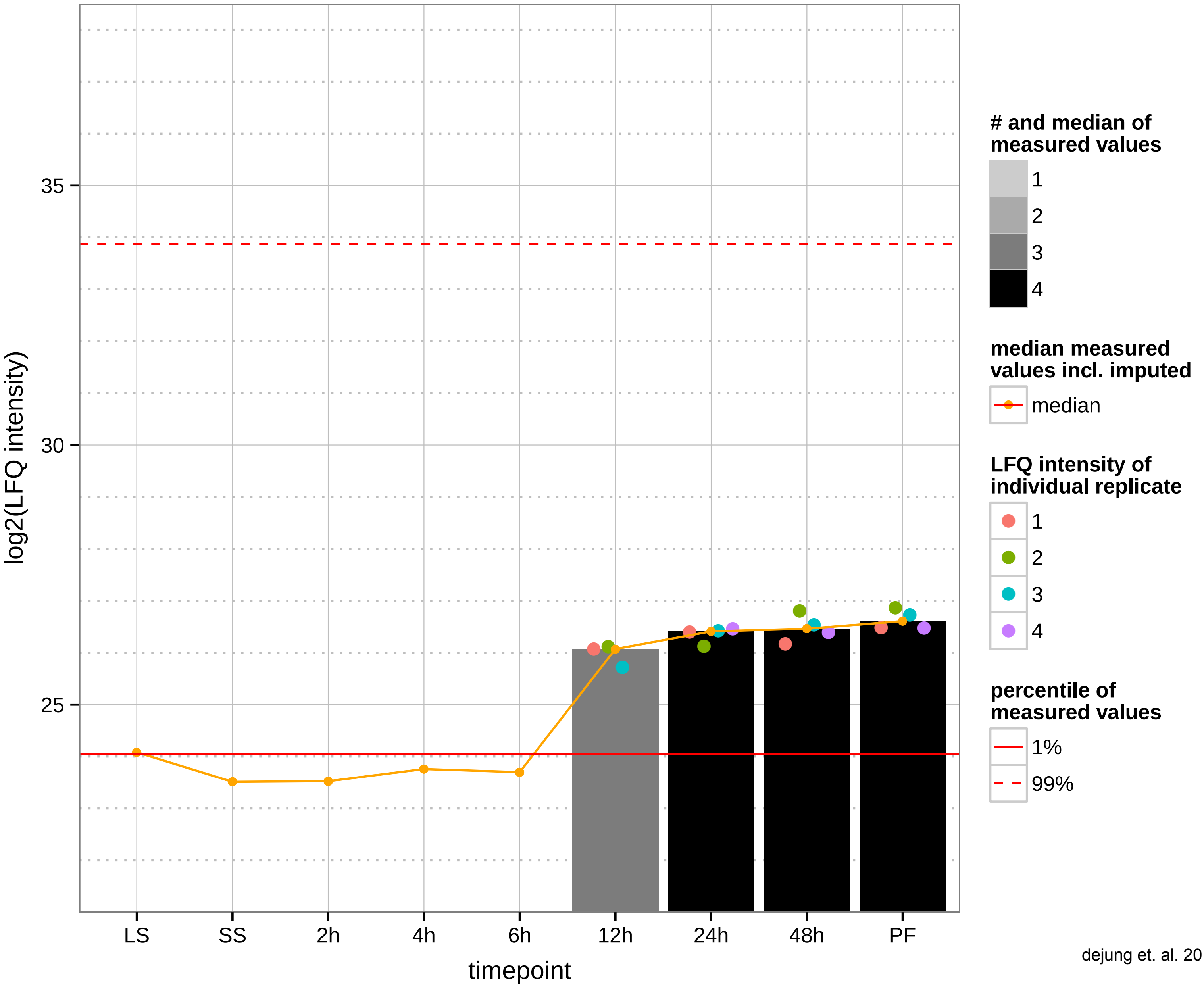




dejung et. al. 2015

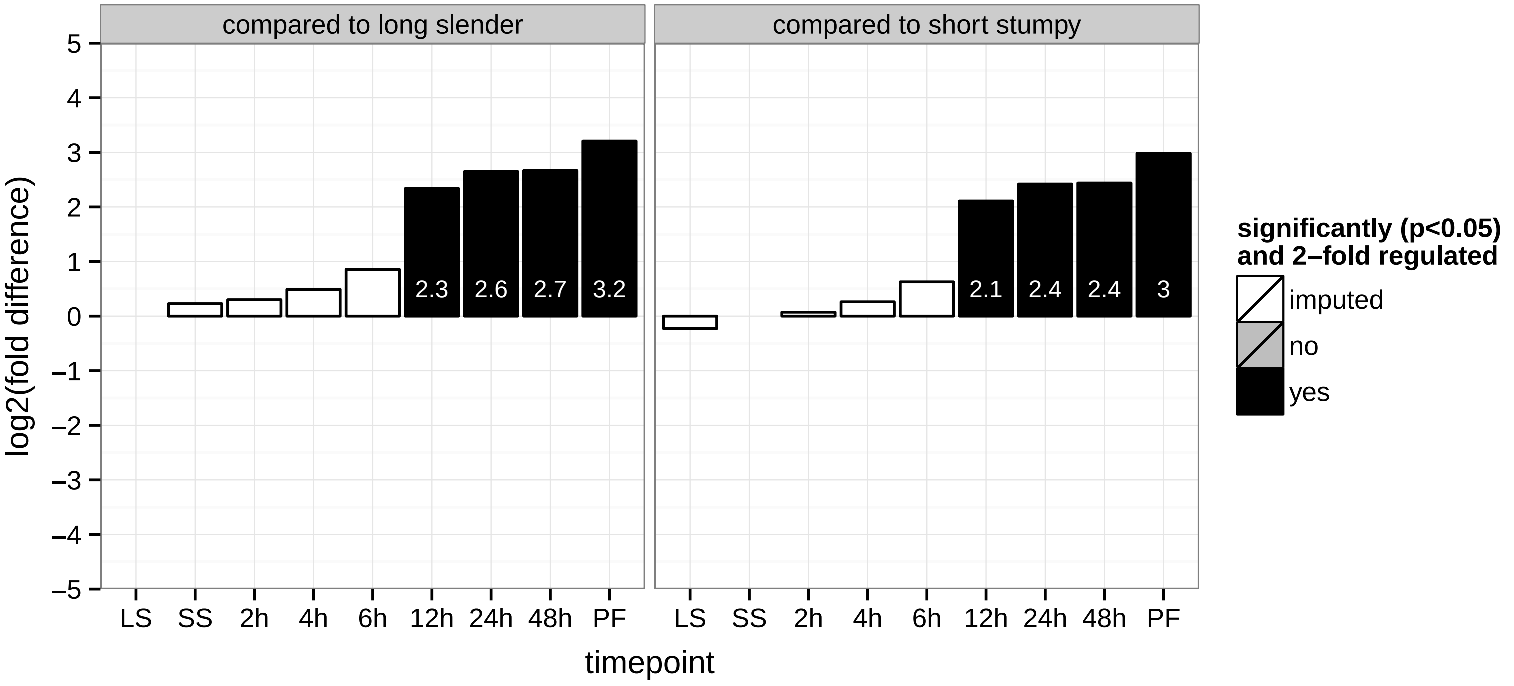
hypothetical protein, conserved
Tb927.3.1730
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

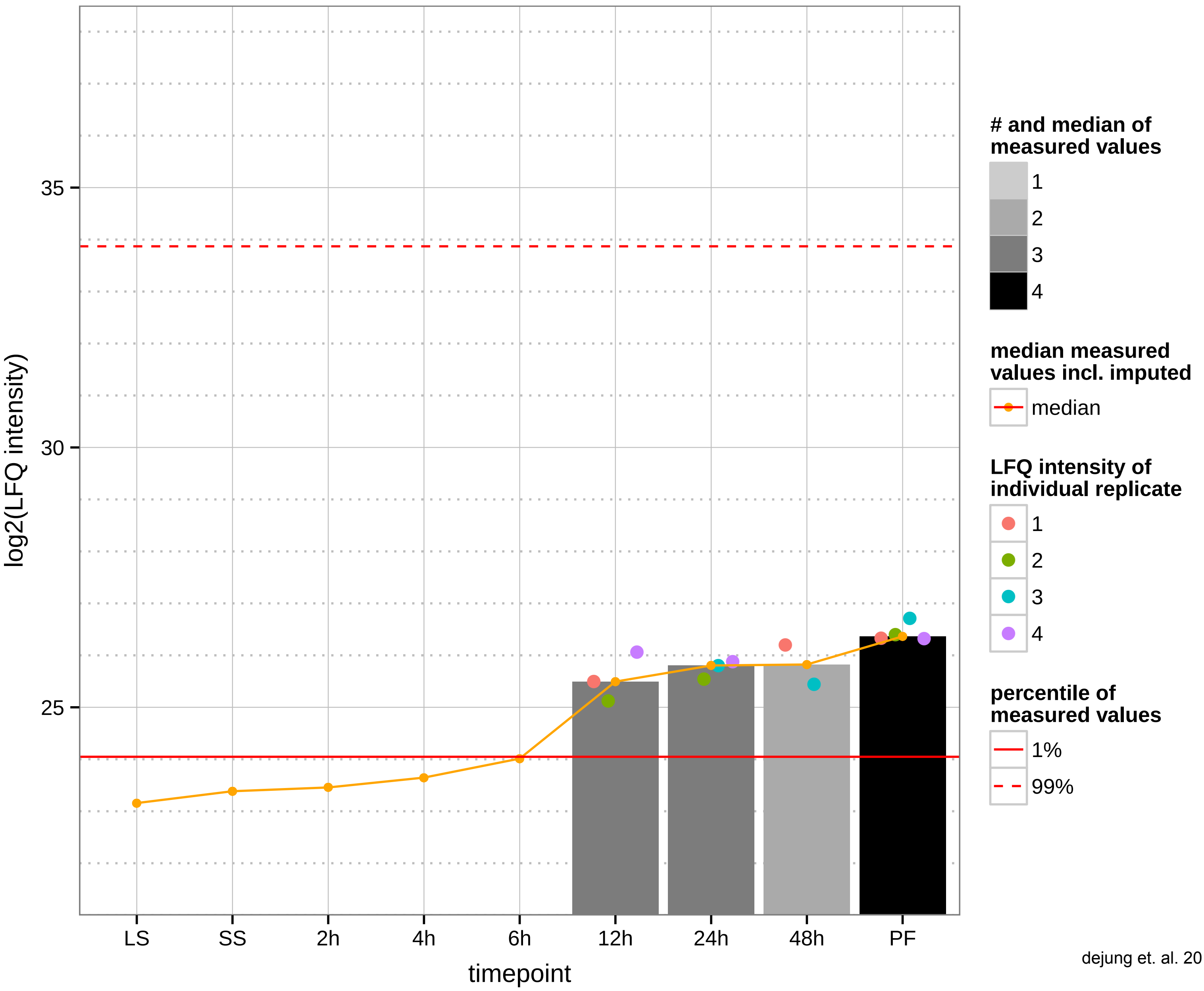




dejung et. al. 2015

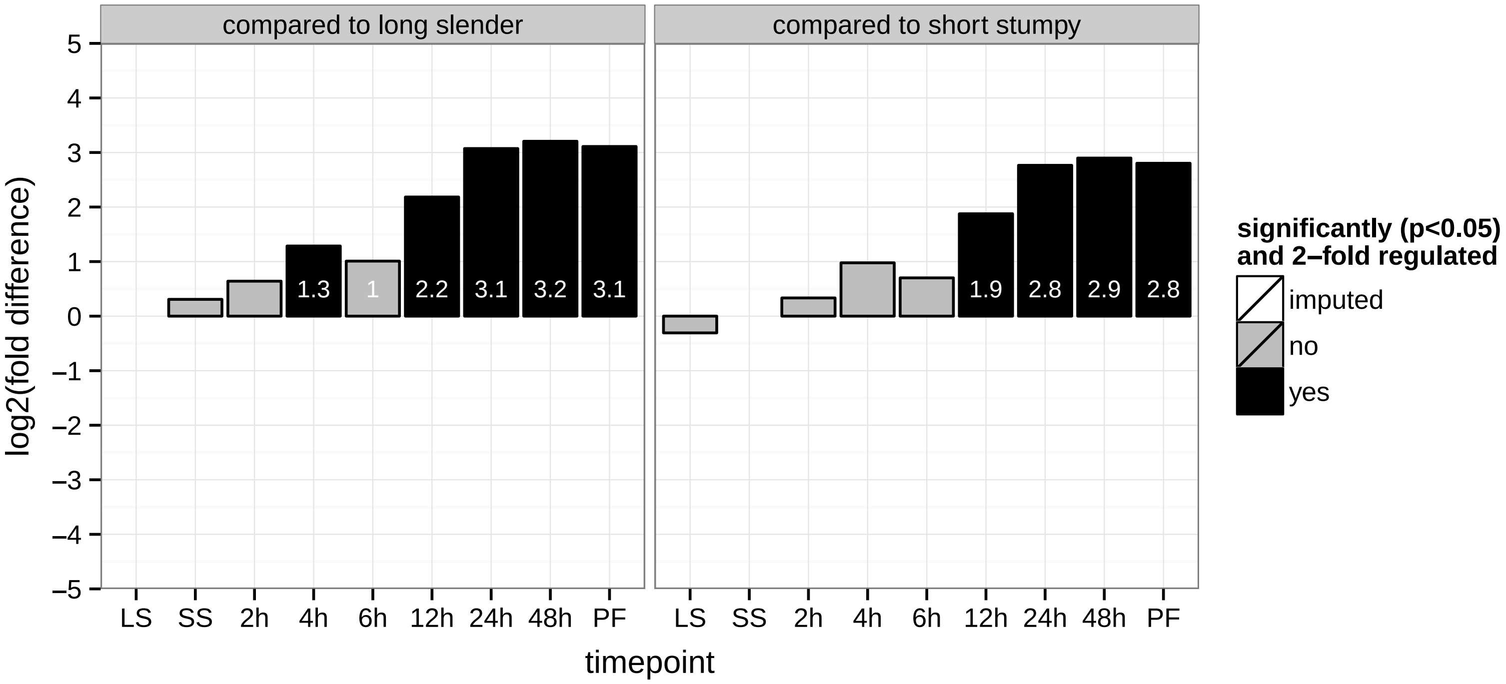
hypothetical protein, conserved
Tb927.3.1940
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

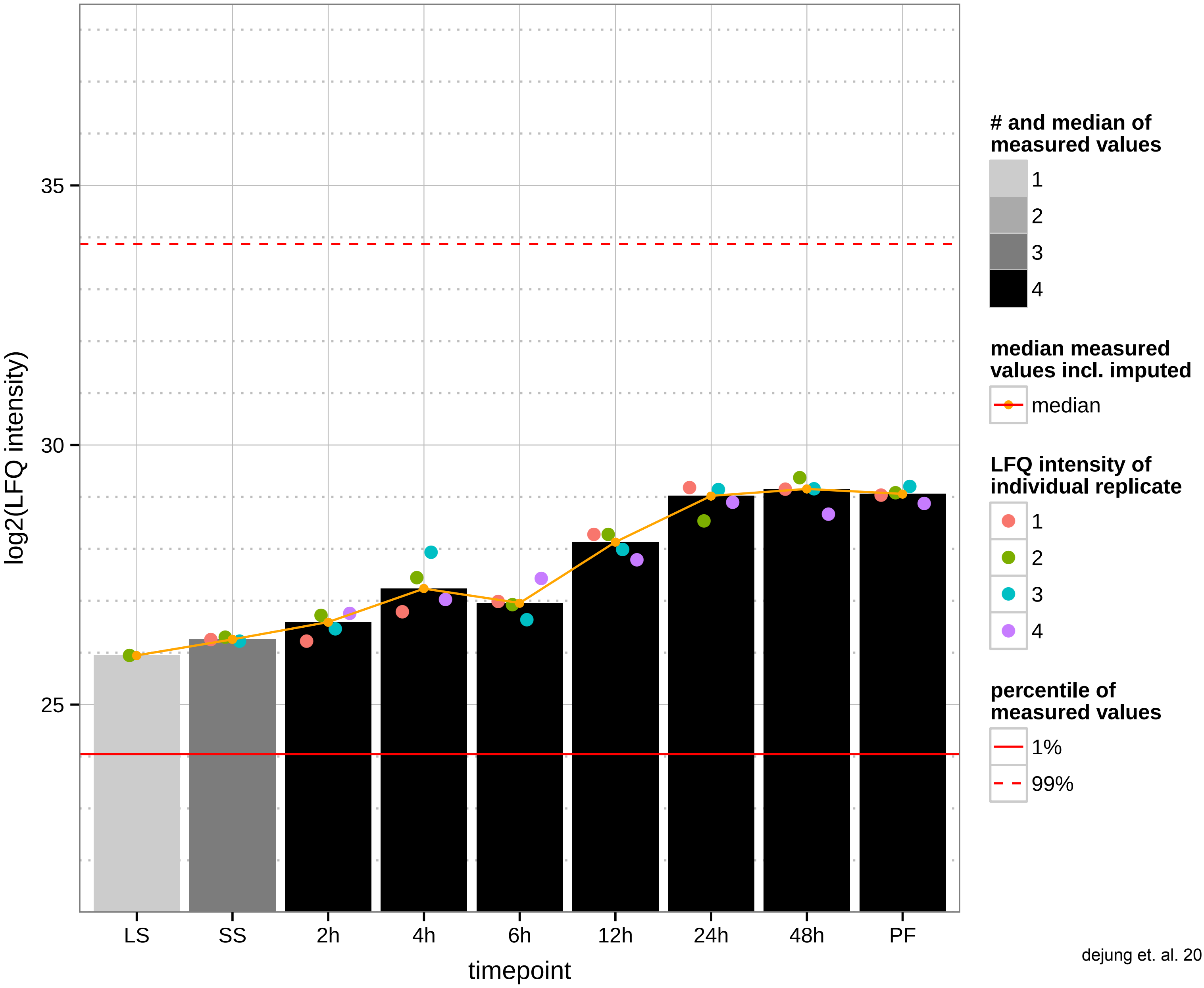




dejung et. al. 2015

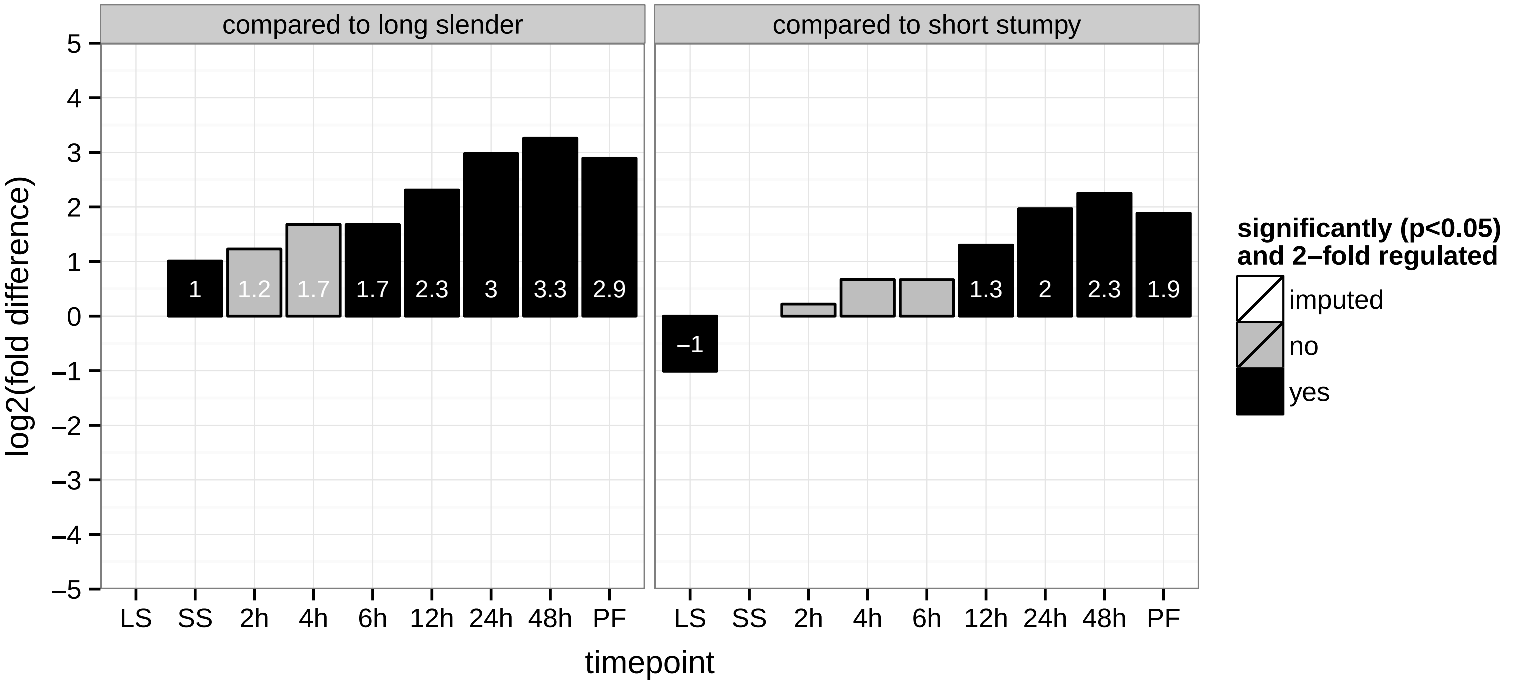
hypothetical protein, conserved
Tb927.3.2180
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

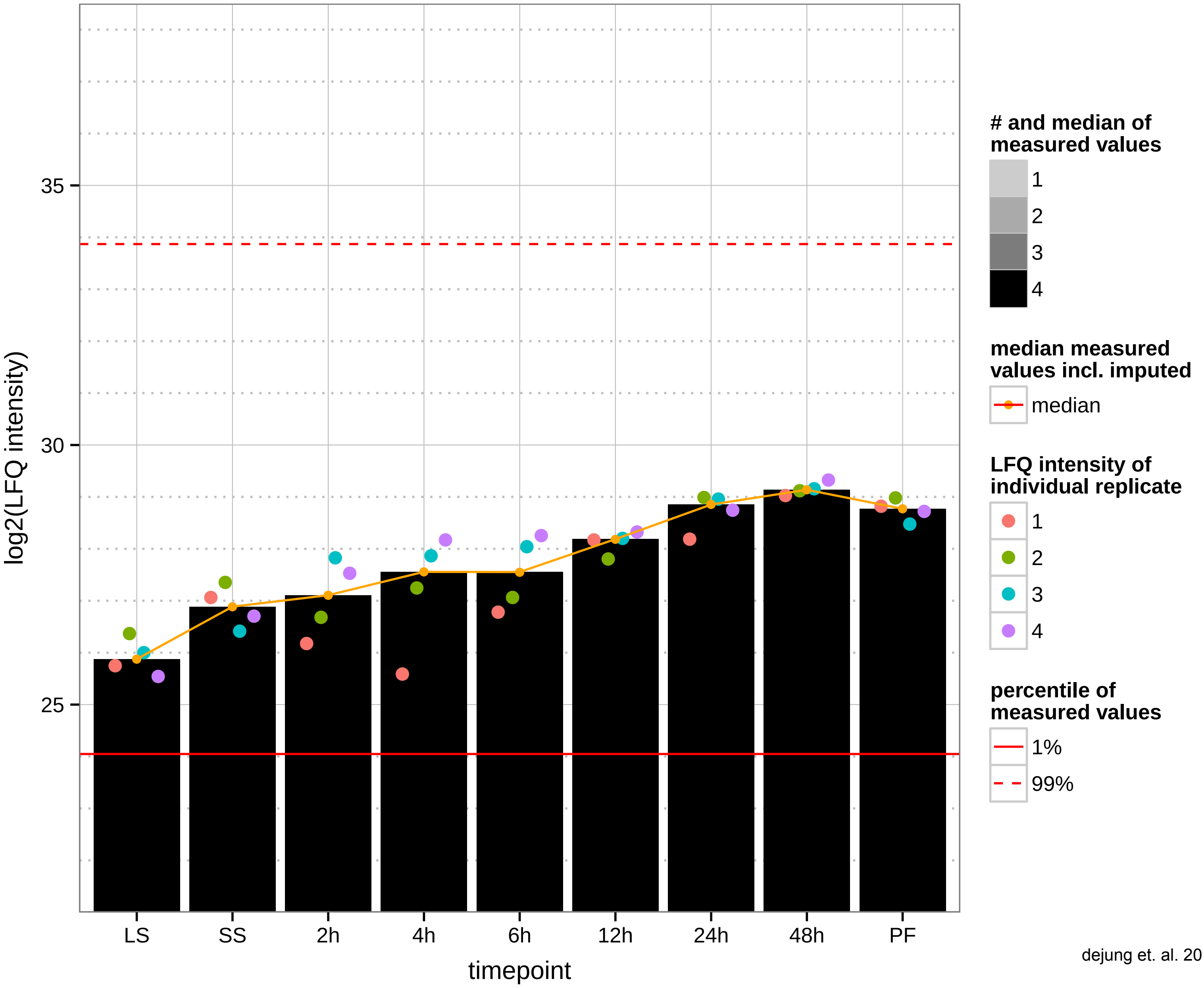




dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.2880
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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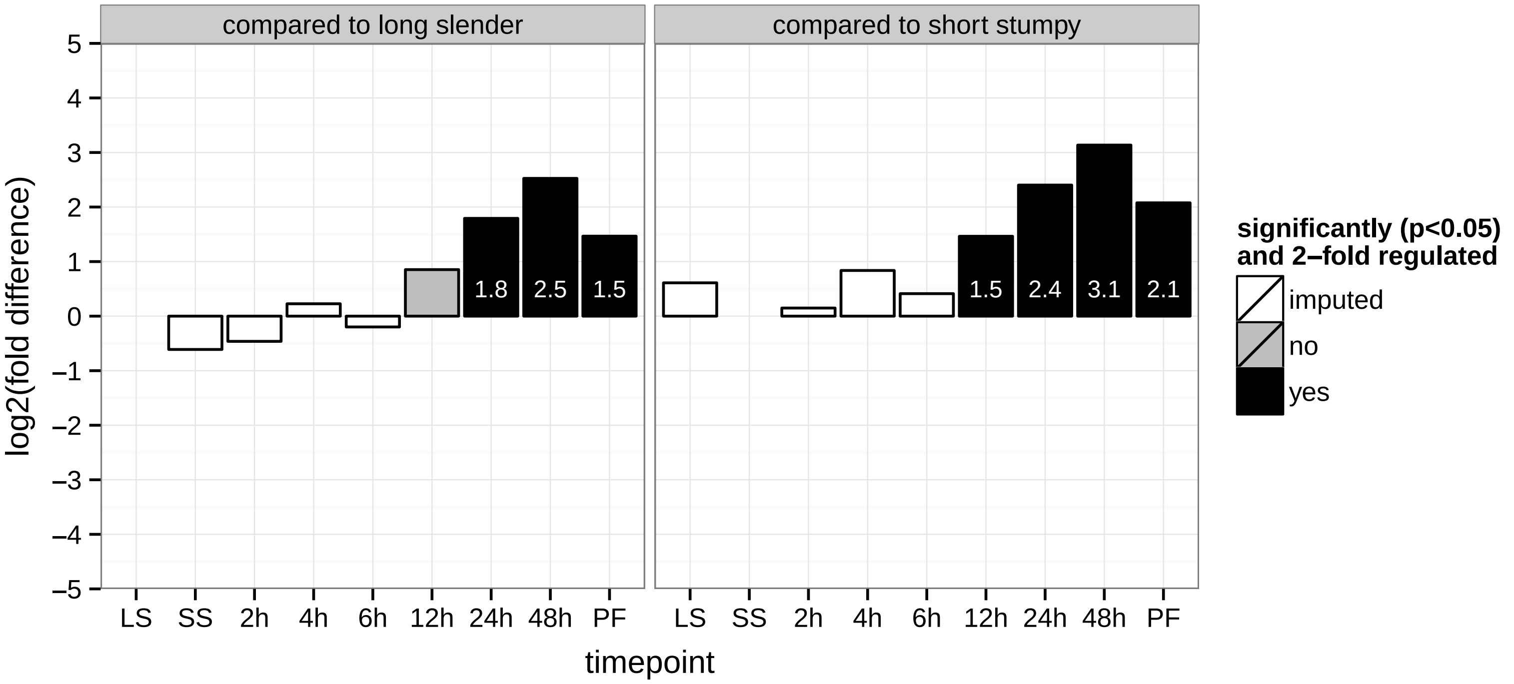
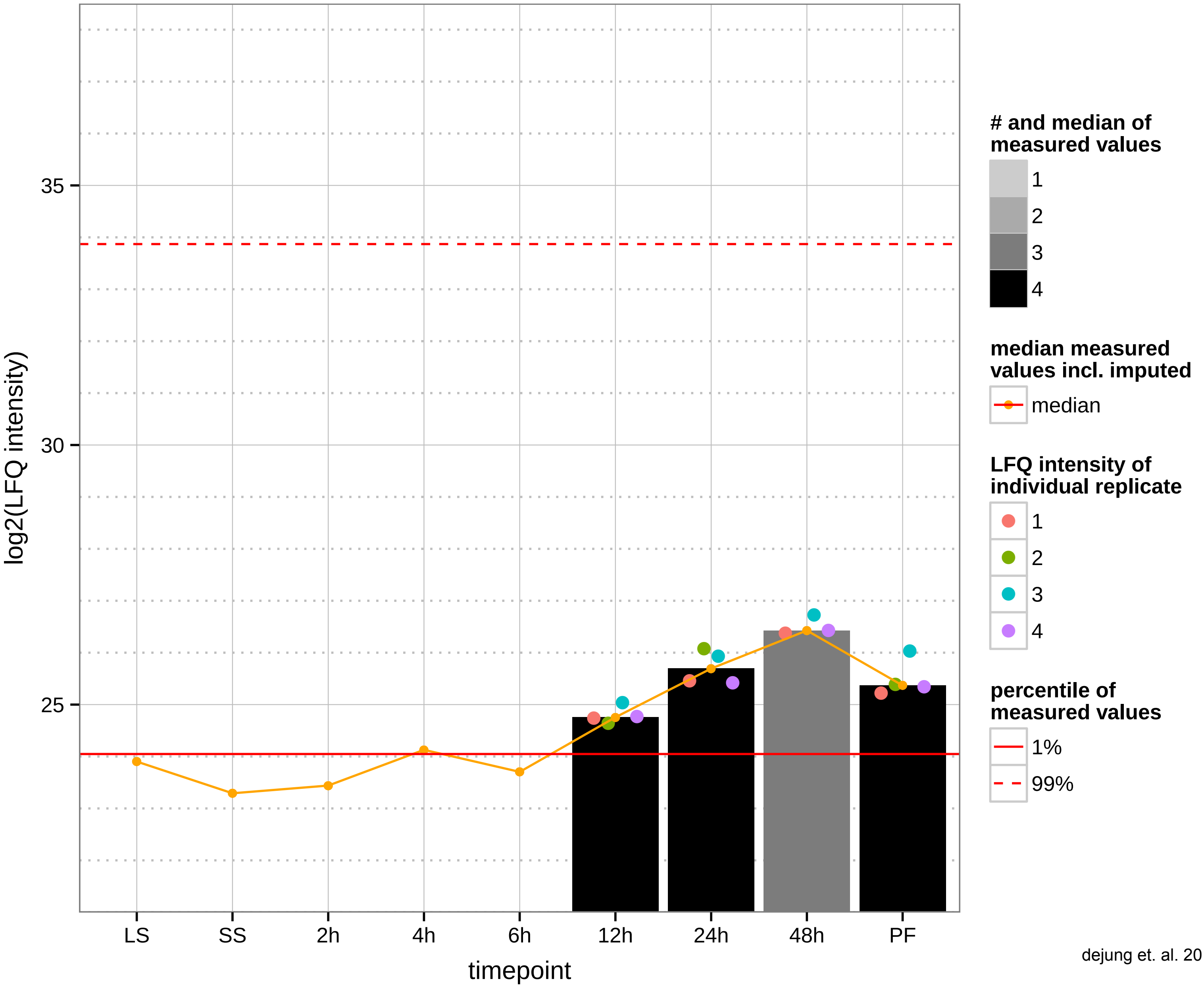
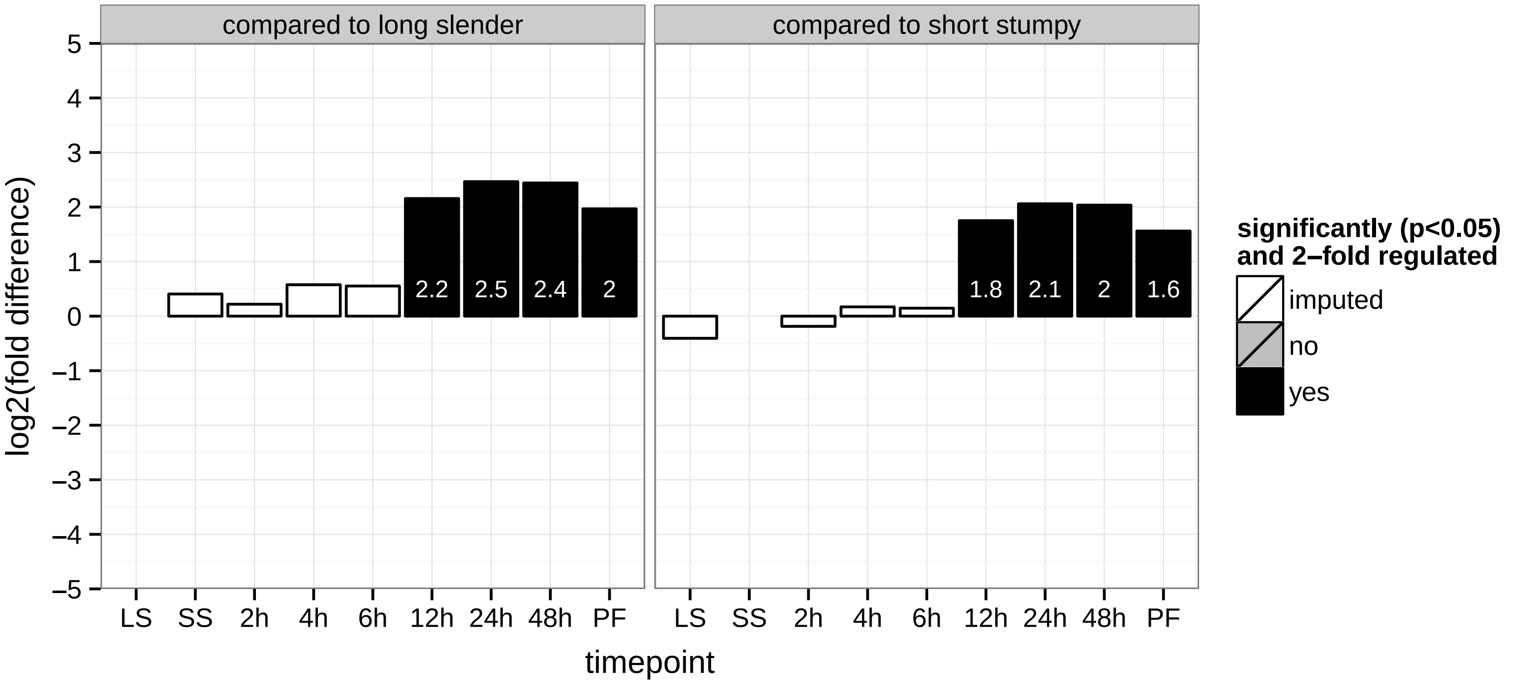
peptidyl–prolyl cis–trans isomerase NIMA–interacting 4, putative
Tb927.3.3100
AGOF: isomerase activity
AGOC: null
AGOP: null
PGOF: isomerase activity
PGOC: null
PGOP: null

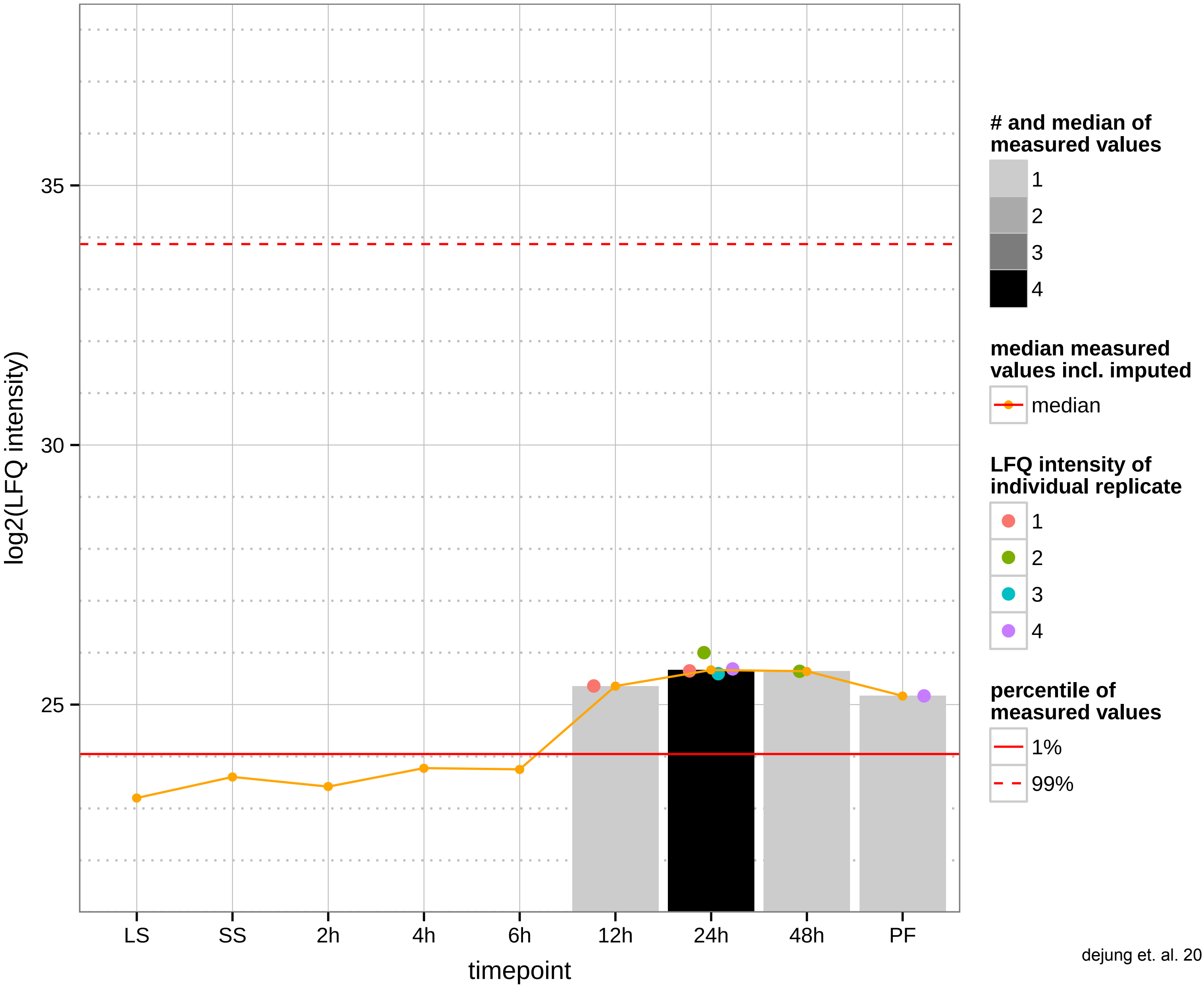




dejung et. al. 2015

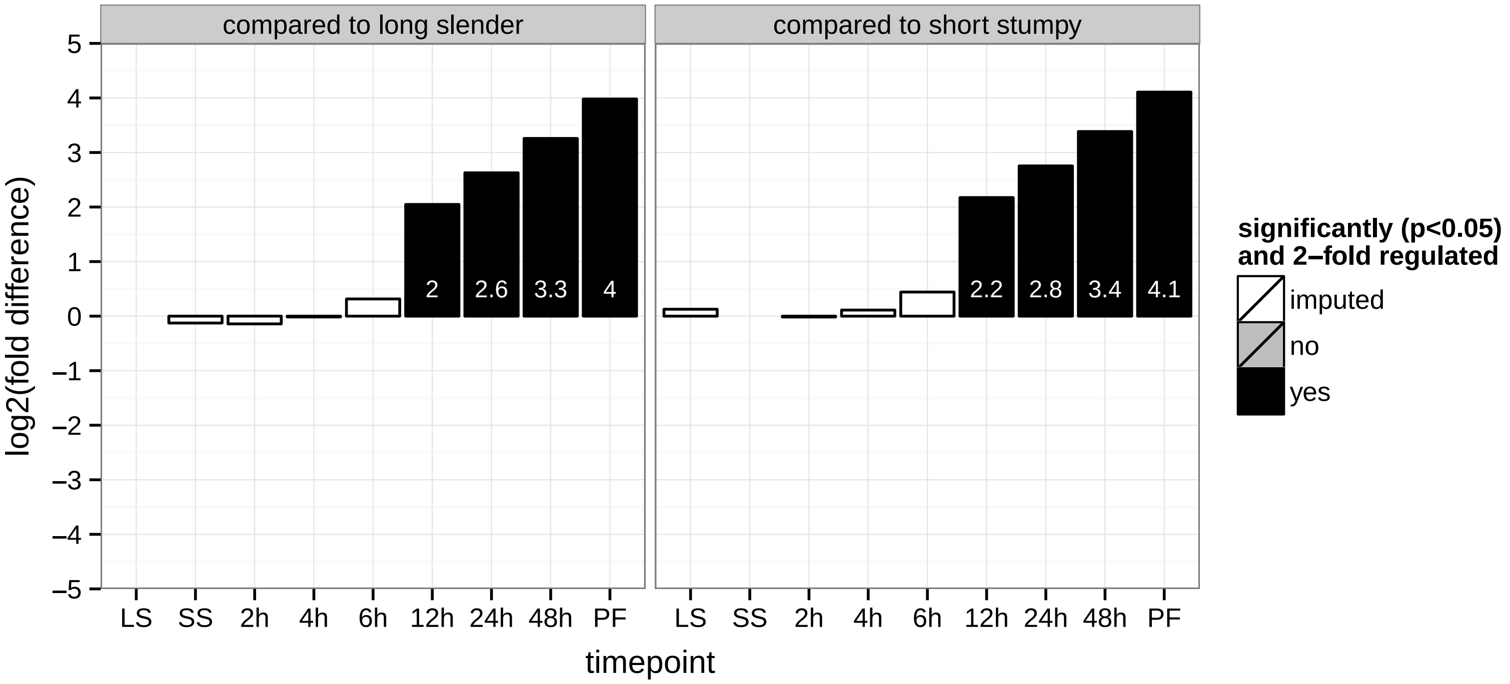
hypothetical protein, conserved
Tb927.3.3660
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

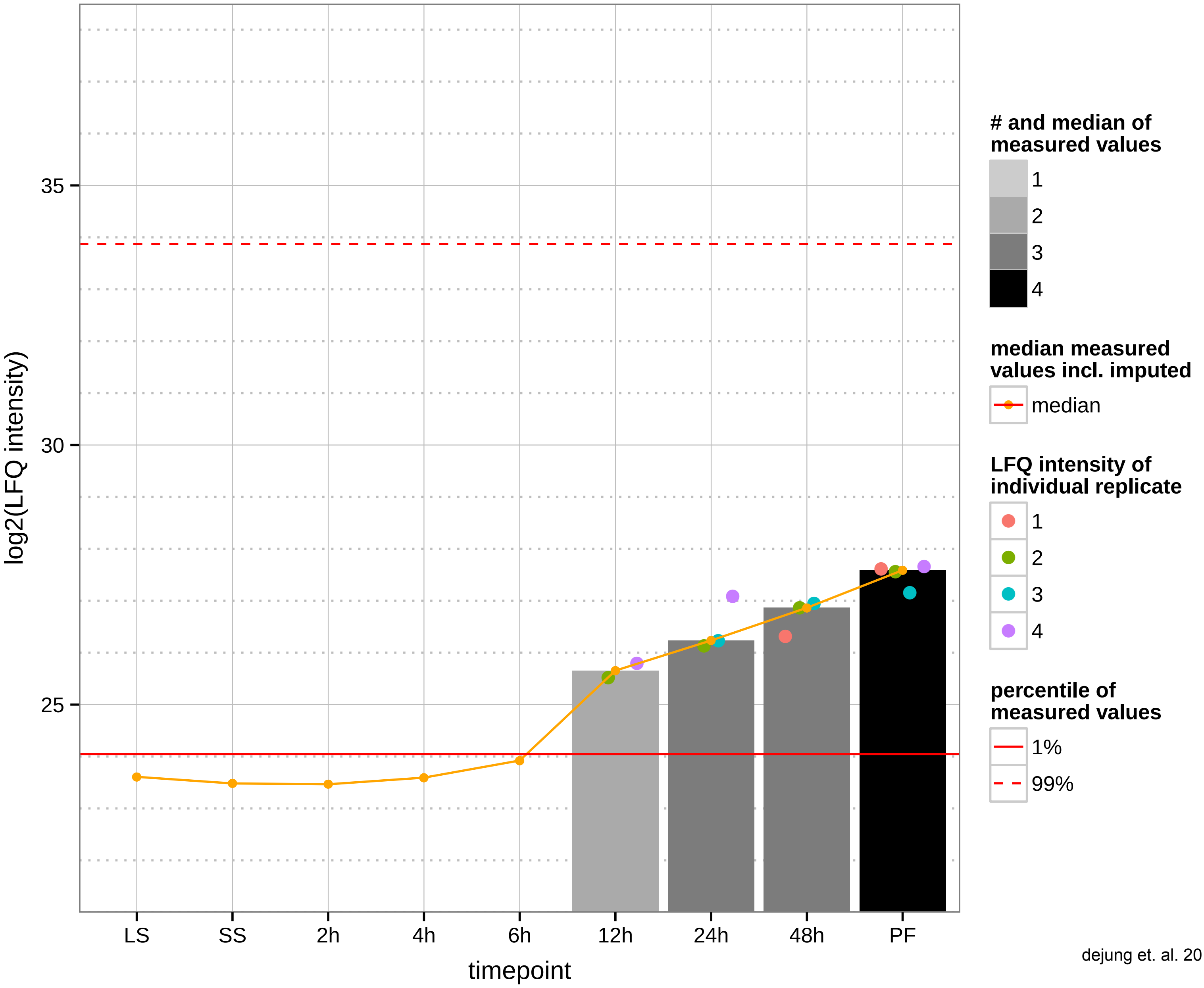




dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.3890
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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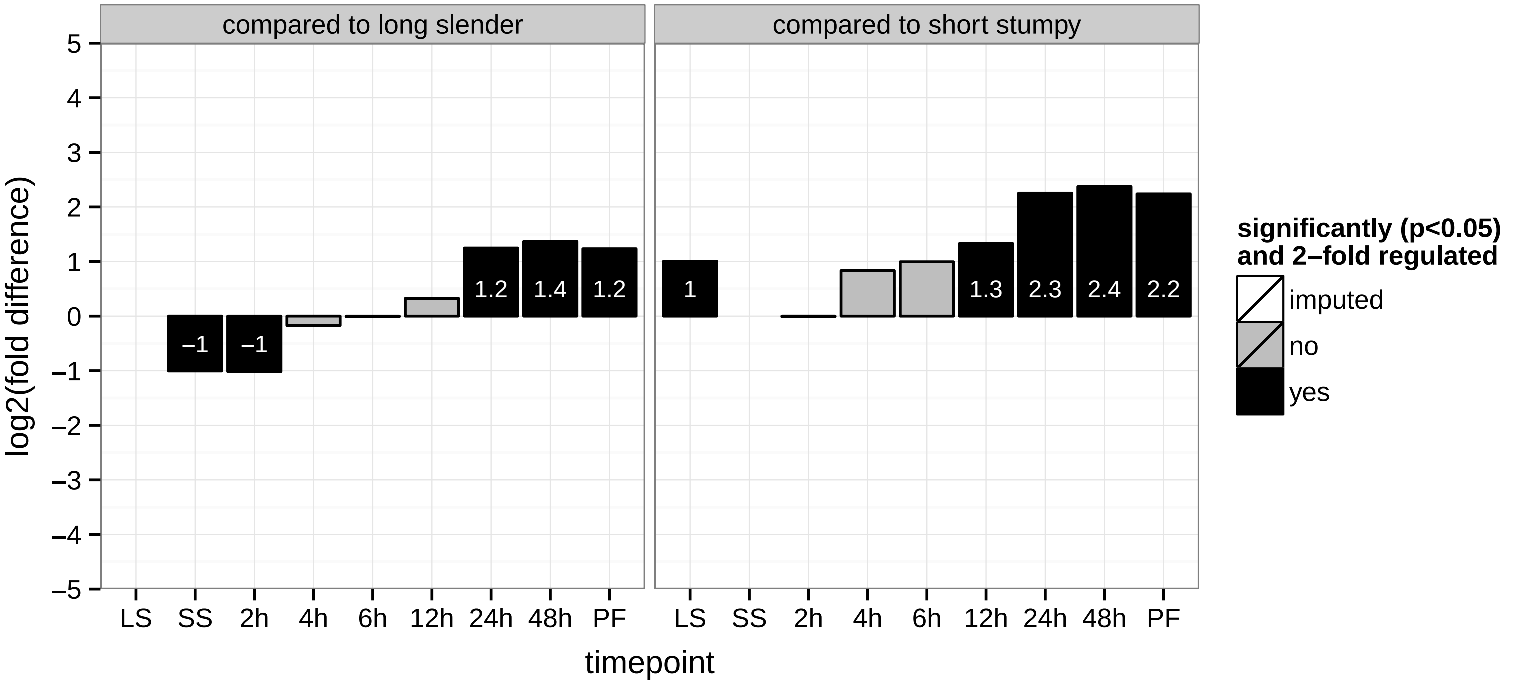
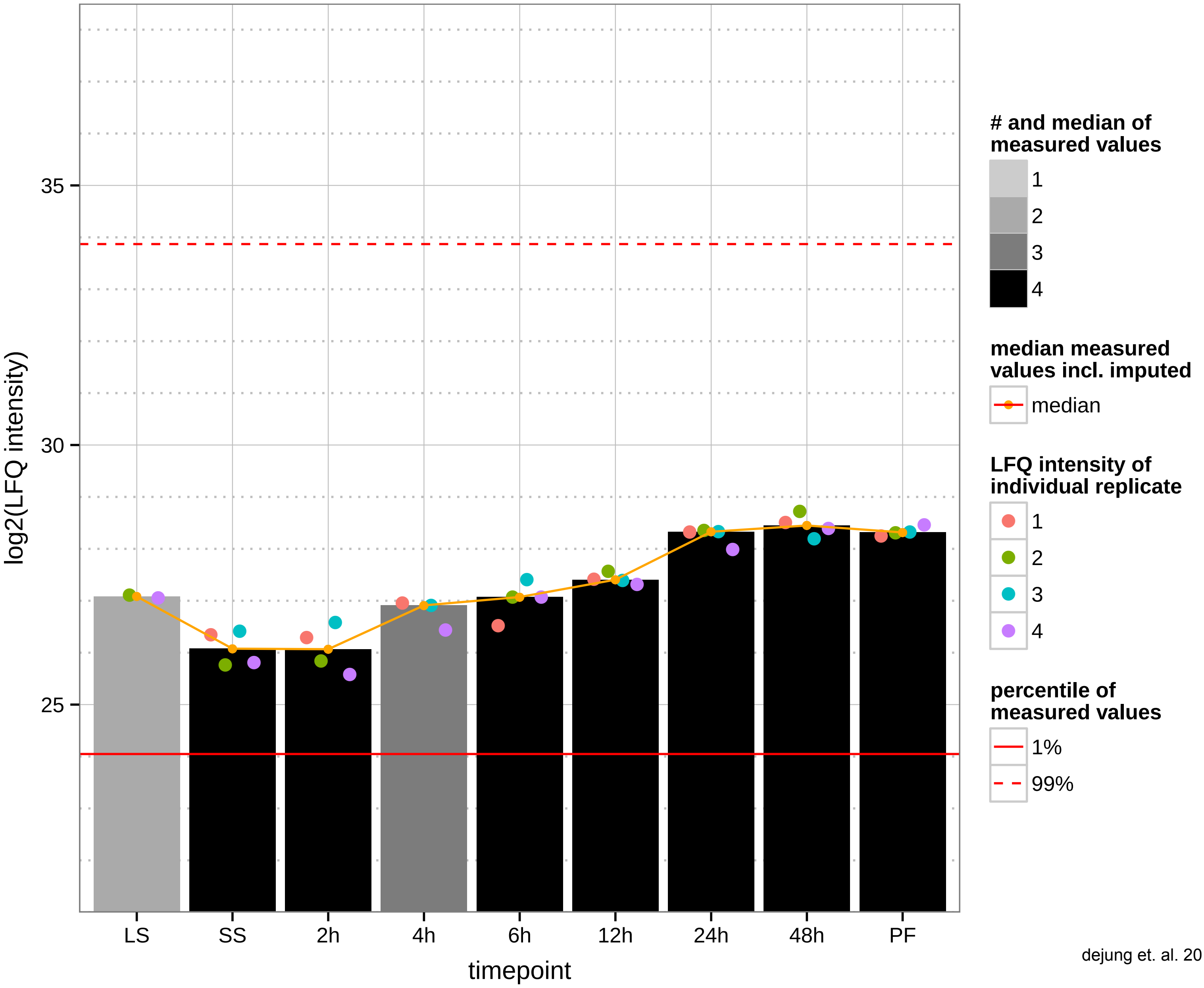
RNA–binding protein (DRBD6B), RNA–binding protein, putative (DRBD11), RNA–binding protein (DRBD6A)
Tb927.3.3940
AGOF: nucleic acid binding, RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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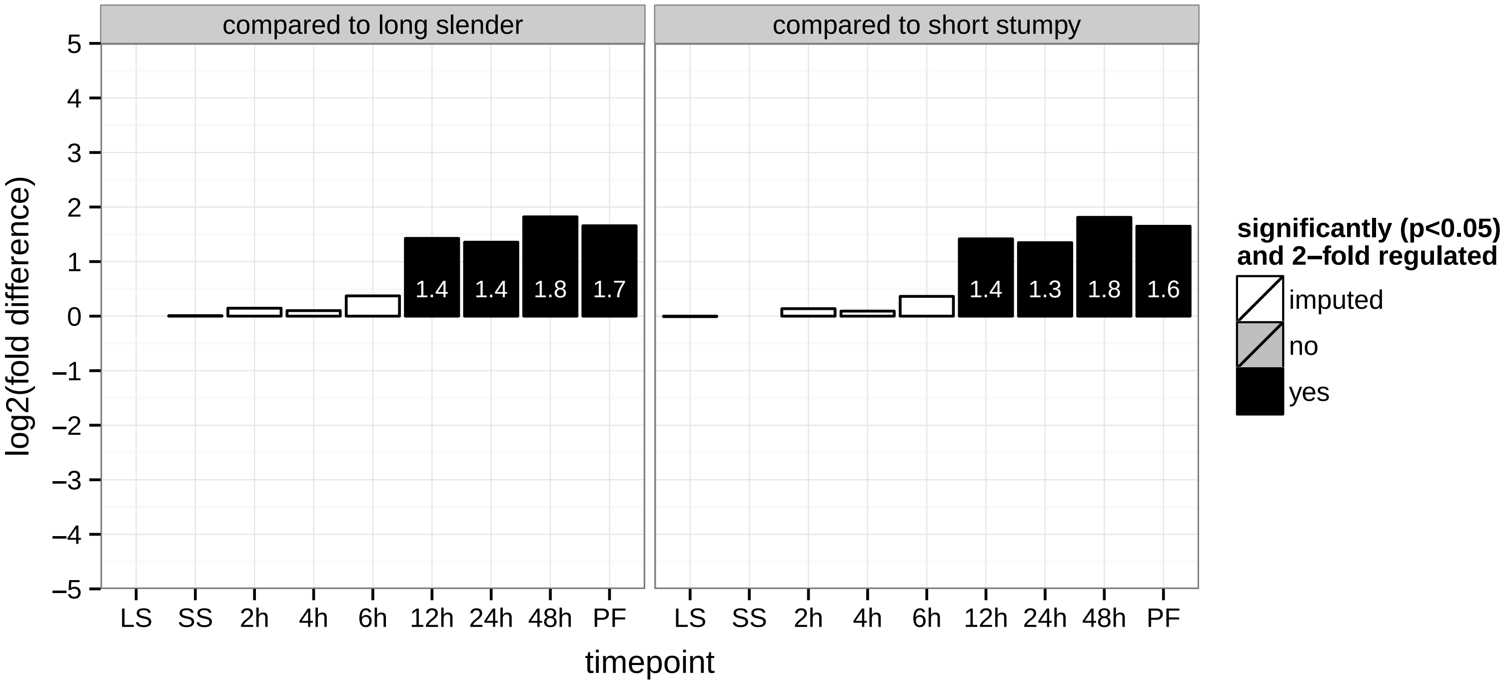
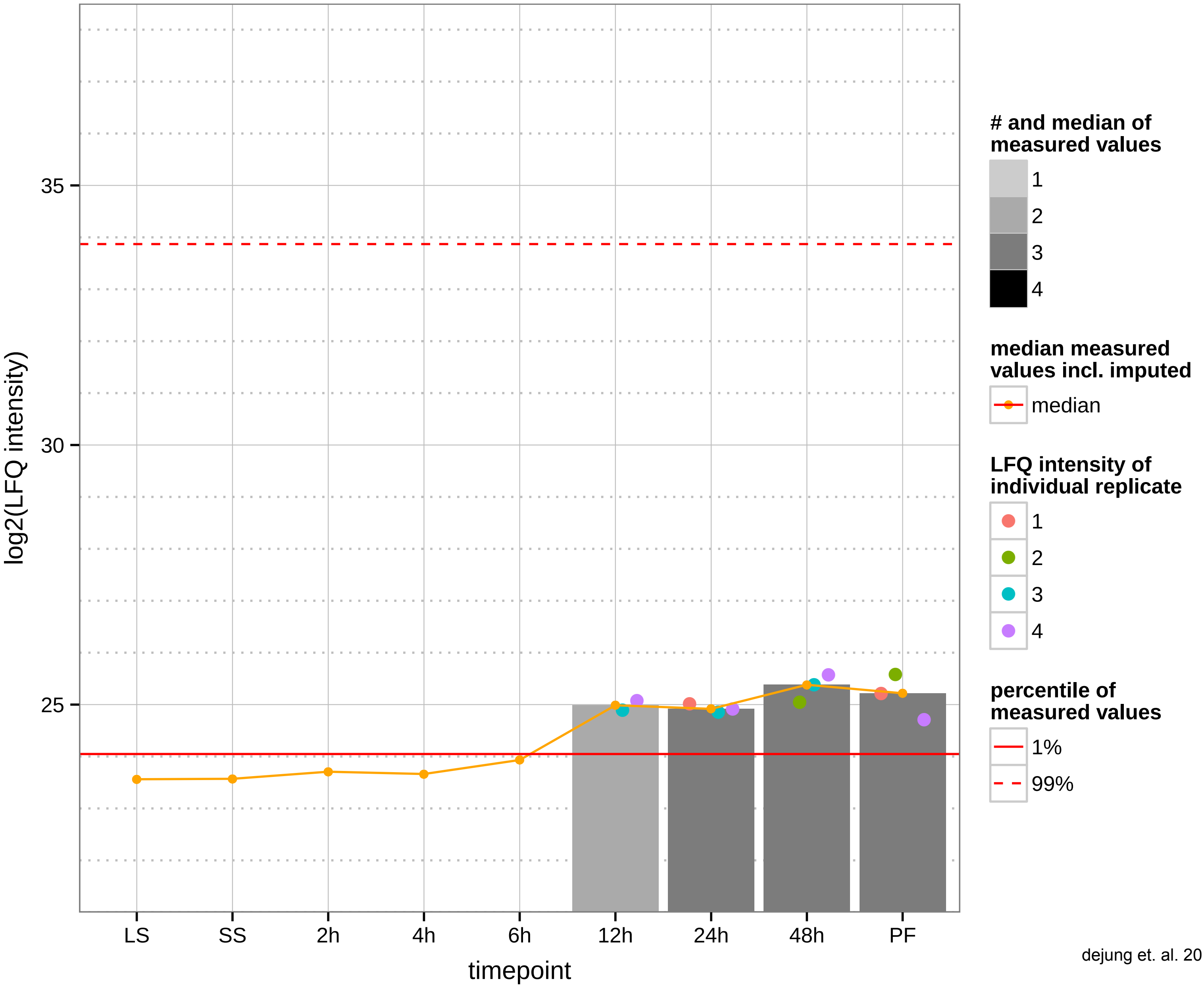
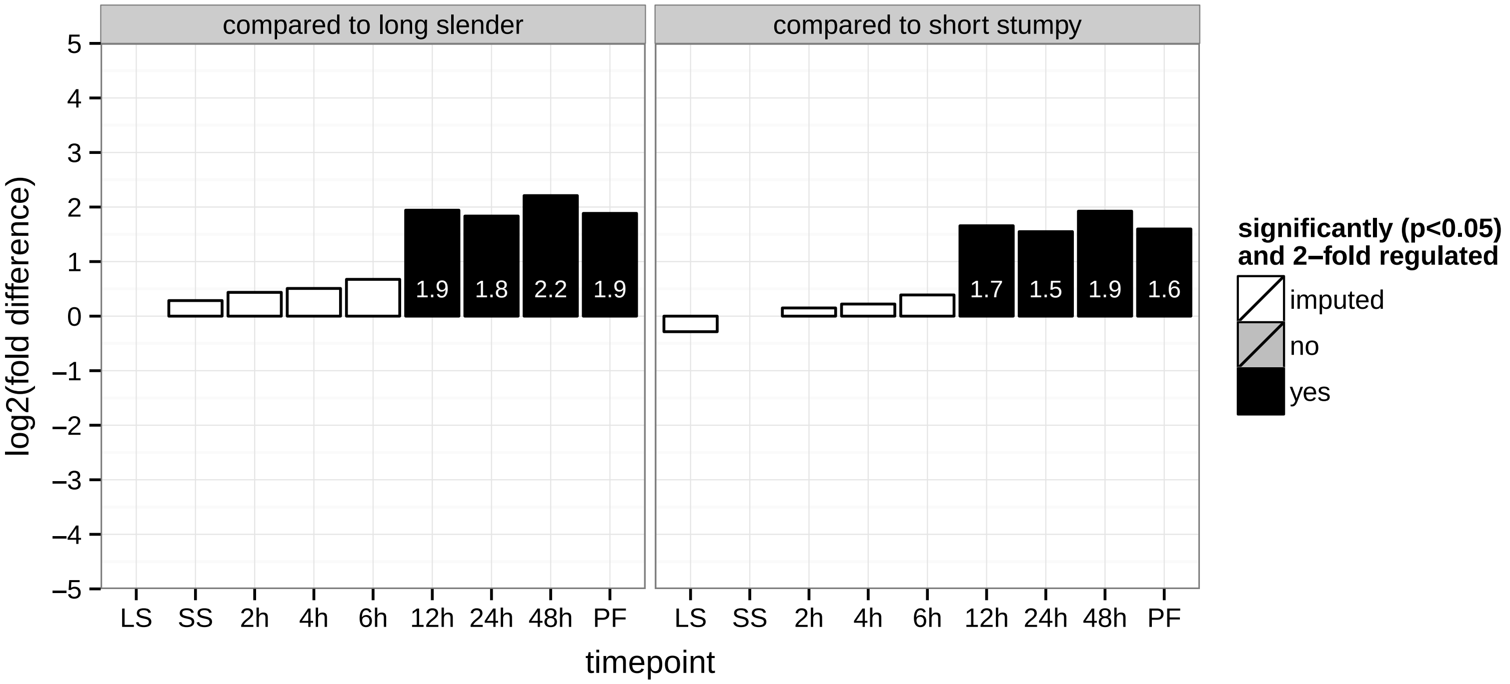
Zinc finger CCCH domain–containing protein 8 (ZC3H8)
Tb927.3.5250
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null

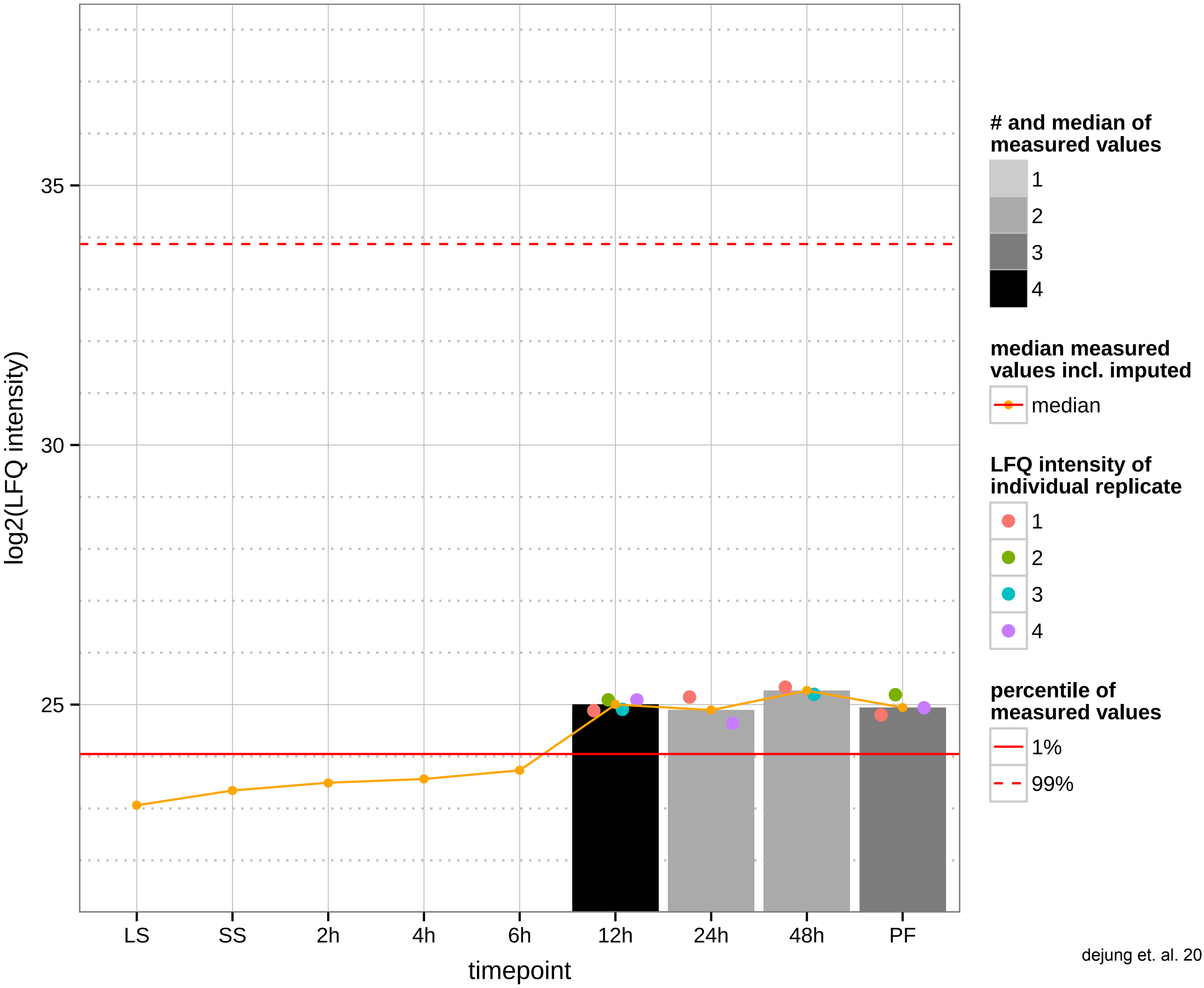




dejung et. al. 2015

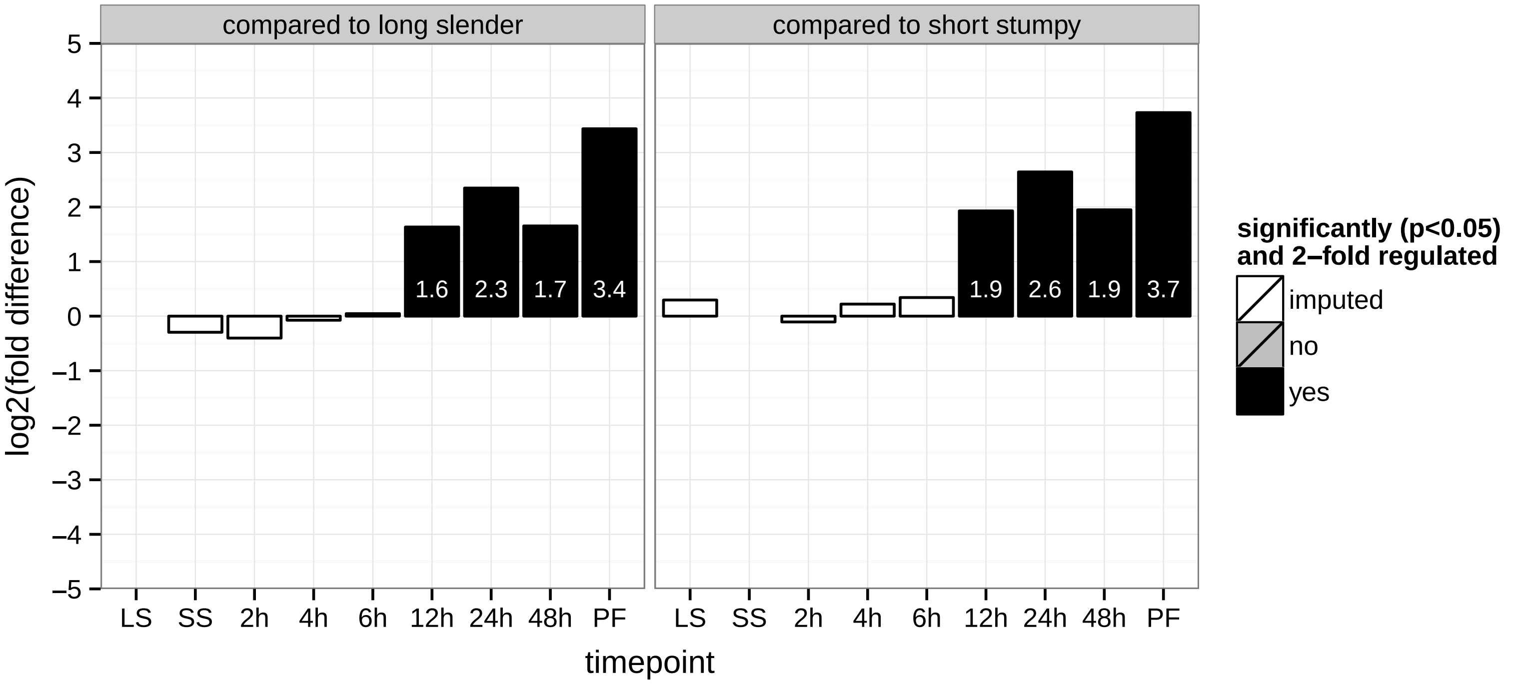
N–acetyltransferase complex ARD1 subunit, putative
Tb927.3.610
AGOF: N–acetyltransferase activity
AGOC: null
AGOP: metabolic process
PGOF: N–acetyltransferase activity
PGOC: null
PGOP: null

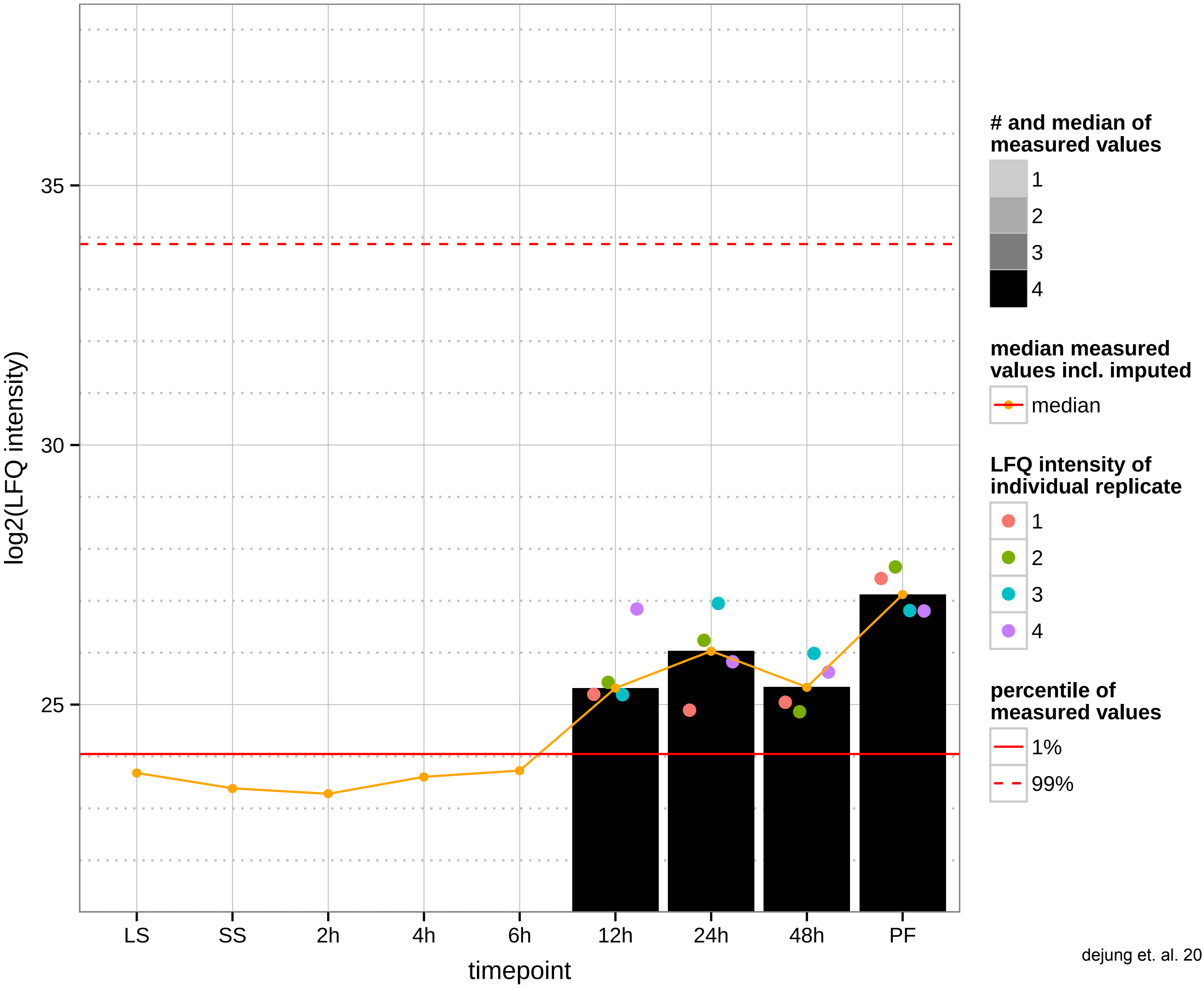




dejung et. al. 2015

zinc finger protein 3, ZFP family member, putative (ZFP3)
Tb927.3.720
AGOF: RNA binding, zinc ion binding
AGOC: ribonucleoprotein complex
AGOP: null
PGOF: nucleic acid binding, protein binding, zinc ion binding
PGOC: null
PGOP: null





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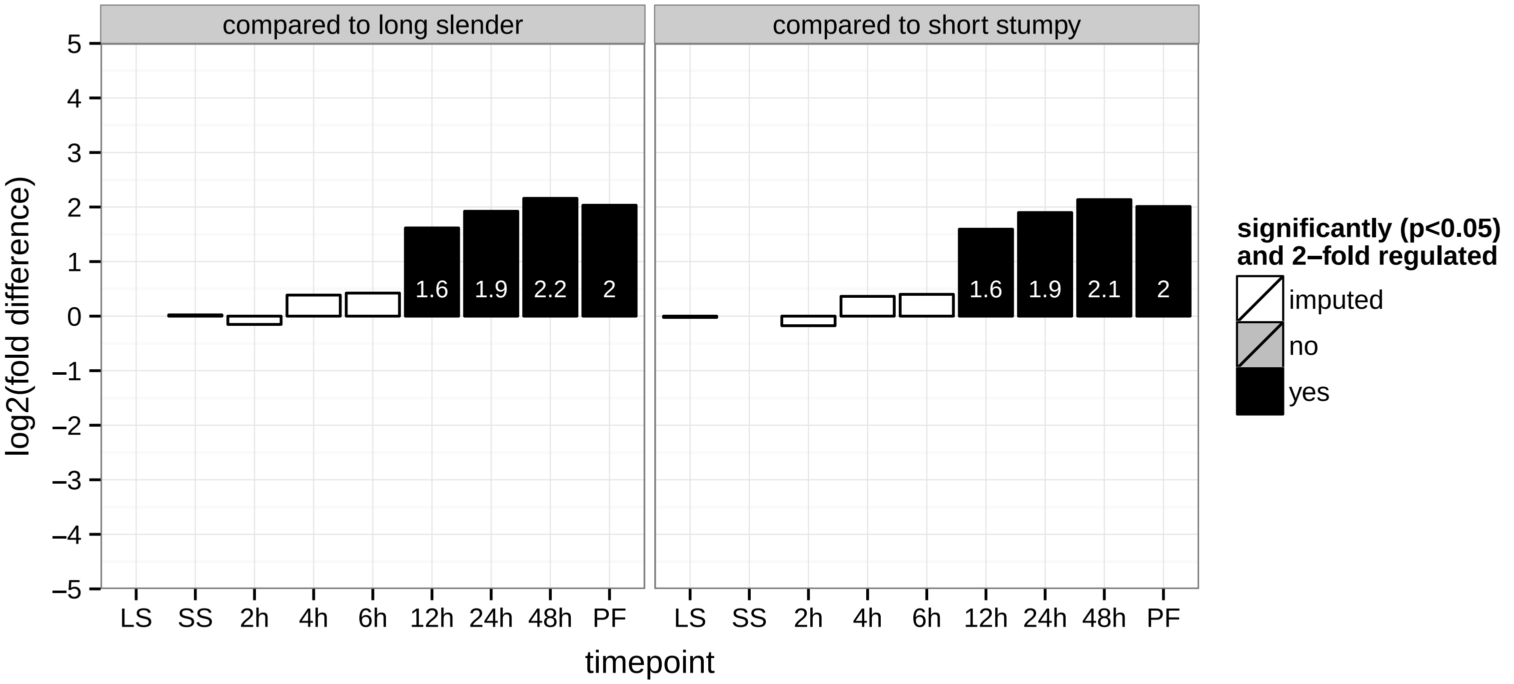
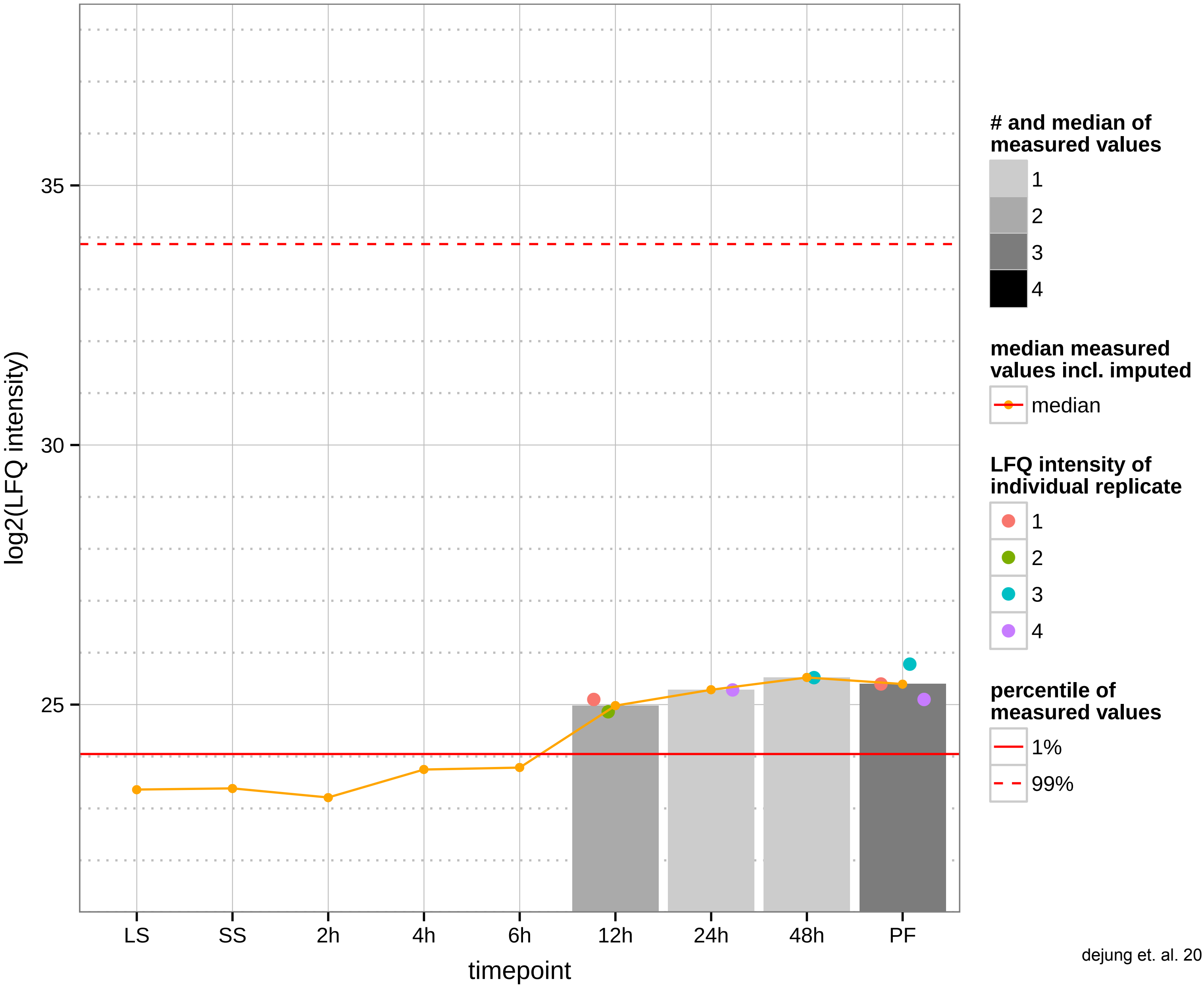
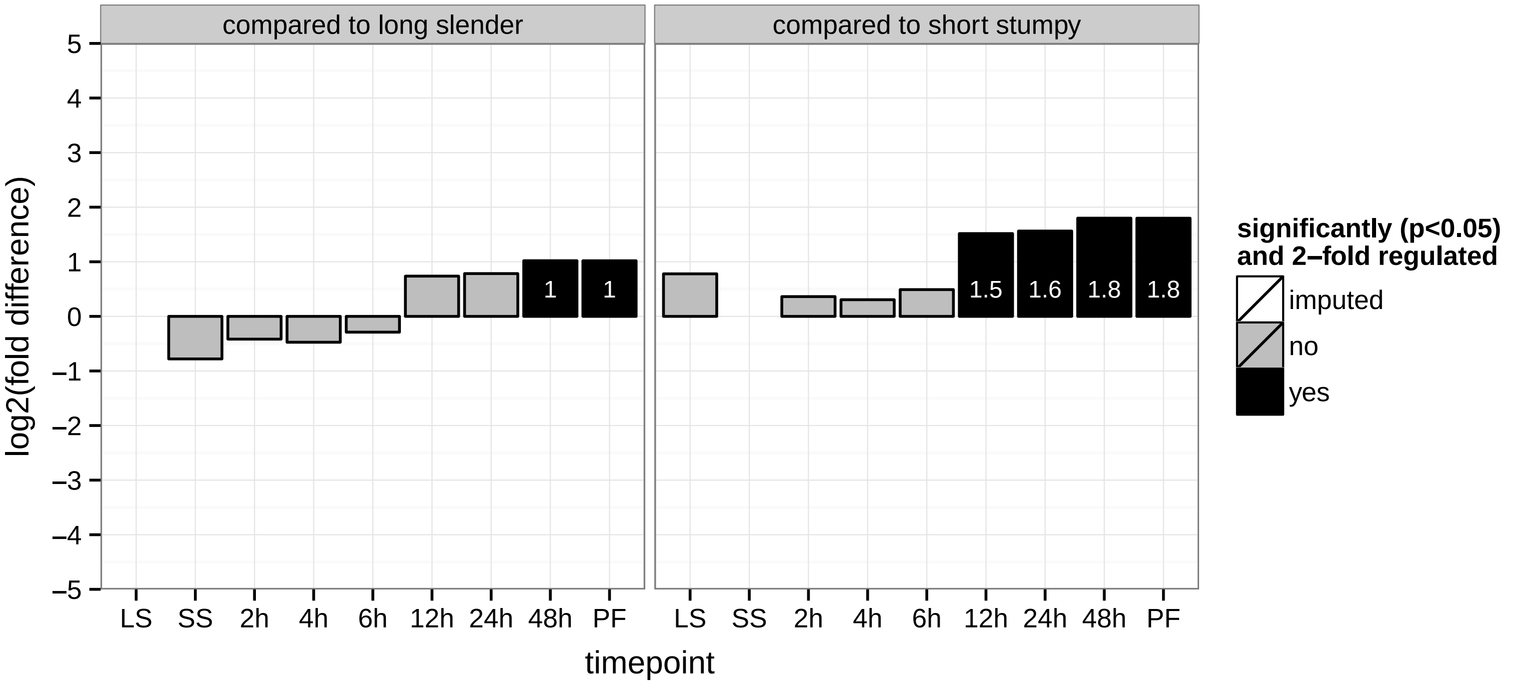
hypothetical protein, conserved
Tb927.3.950
AGOF: oxidoreductase activity
AGOC: mitochondrion
AGOP: null
PGOF: oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular o
PGOC: null
PGOP: oxidation−reduction process

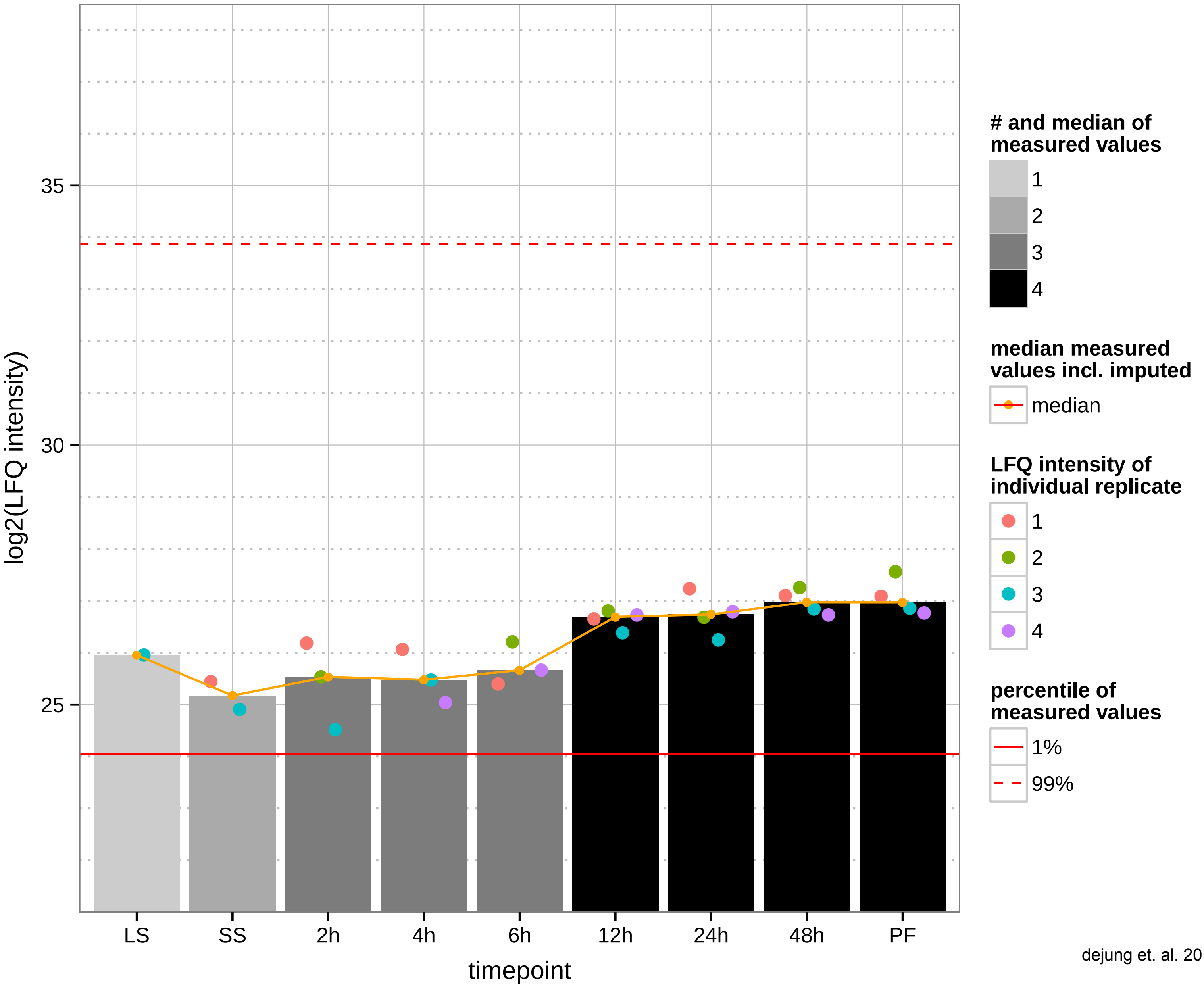




dejung et. al. 2015

ankyrin, putative
Tb927.4.1170;Tb11.v5.0430
AGOF: null
AGOC: null
AGOP: null
PGOF: null, protein binding
PGOC: null
PGOP: null





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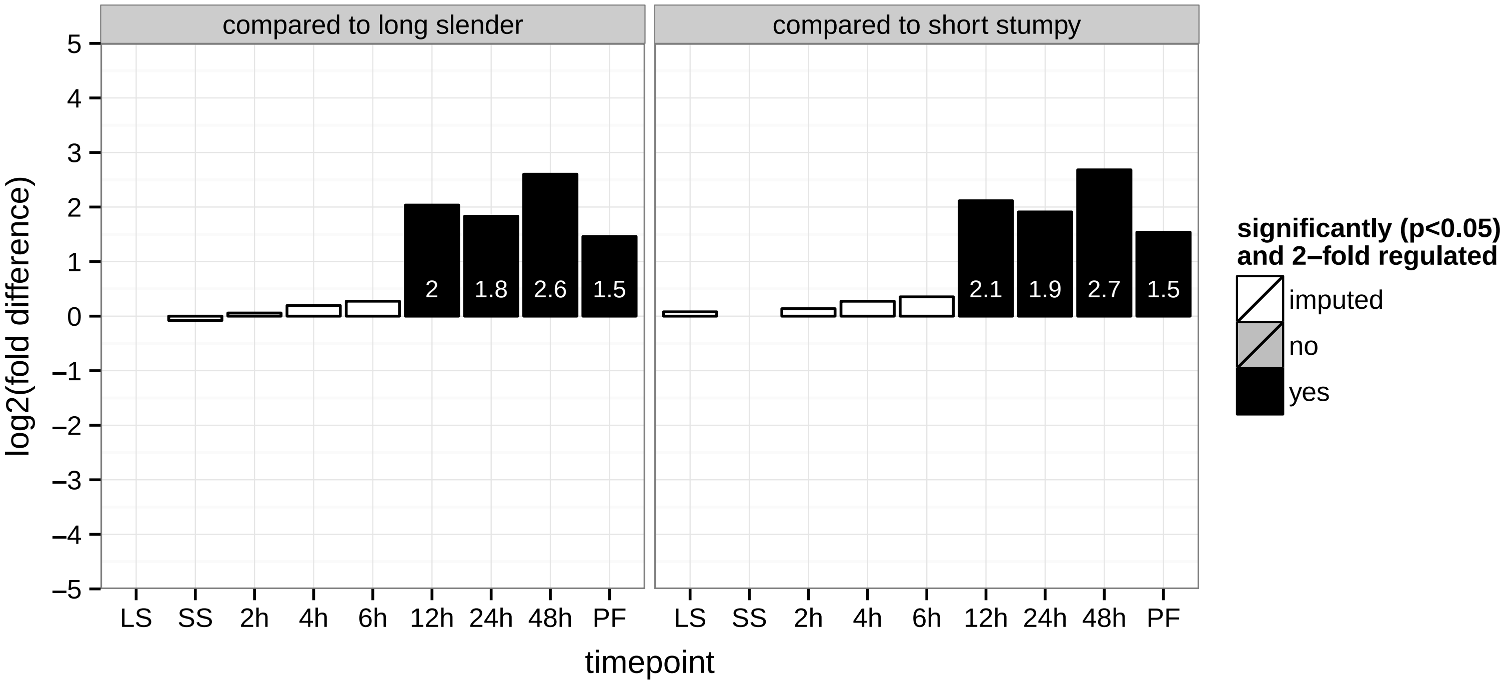
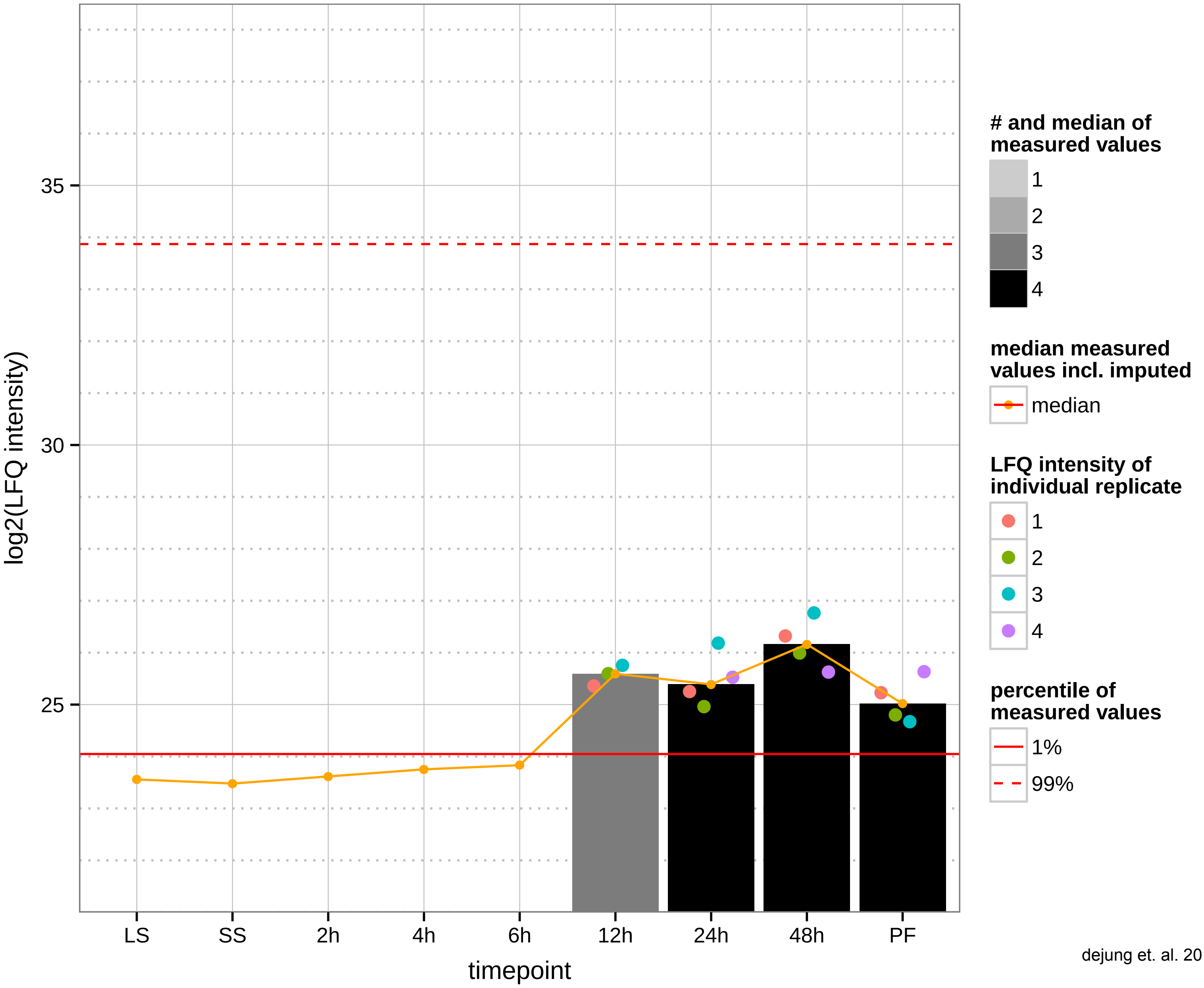
expression site−associated gene (ESAG, pseudogene), putative, expression site−associated gene 4 (ESAG4), pseudogene, n
Tb927.4.130
AGOF: phosphorus−oxygen lyase activity, null
AGOC: null
AGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction, null
PGOF: phosphorus−oxygen lyase activity, null
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction, null





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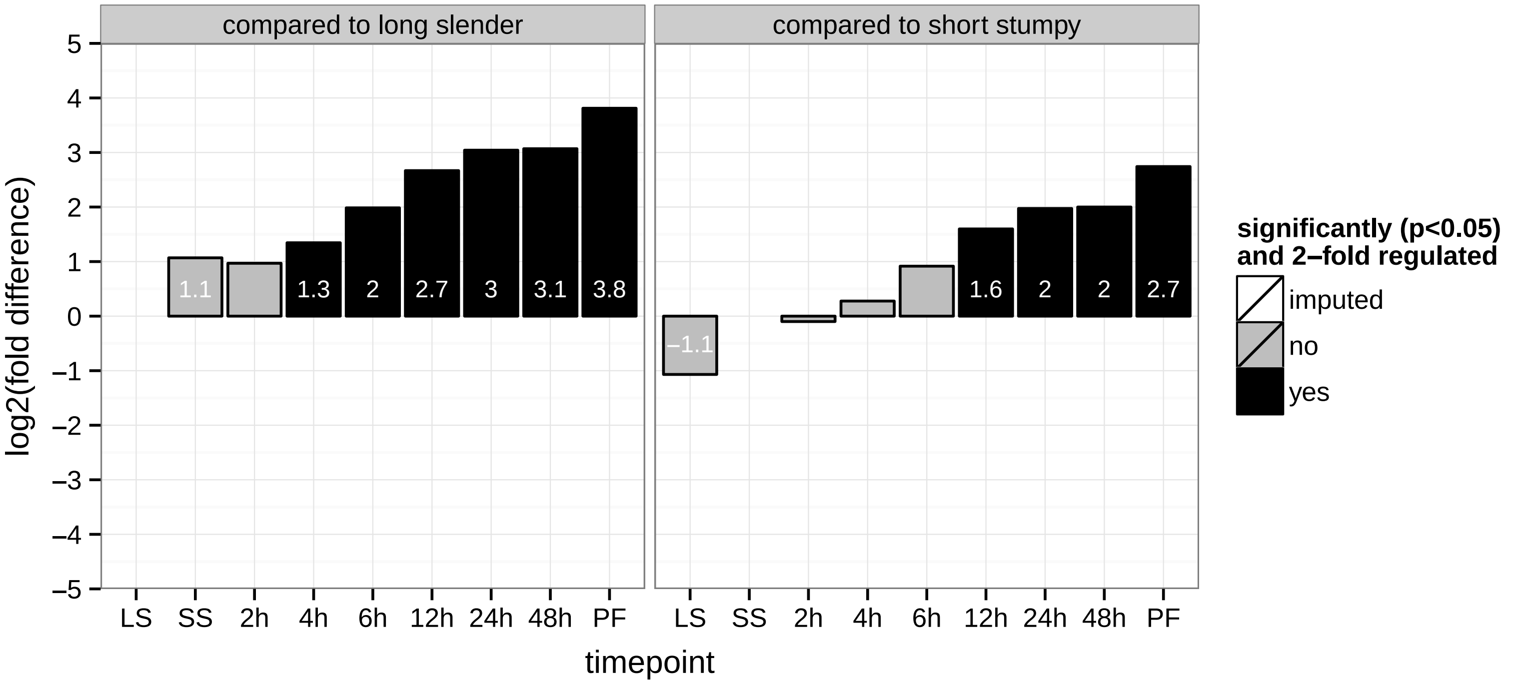
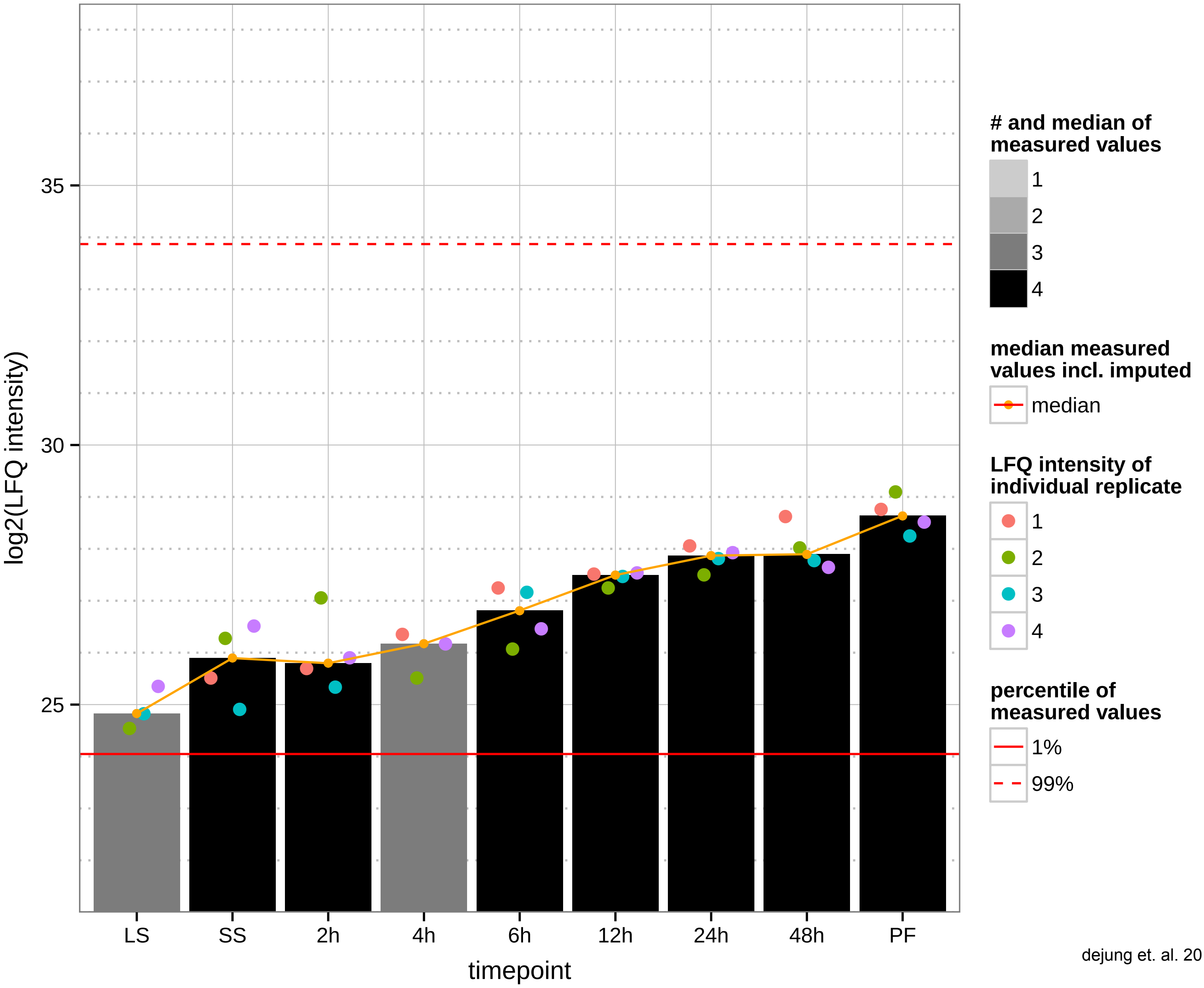
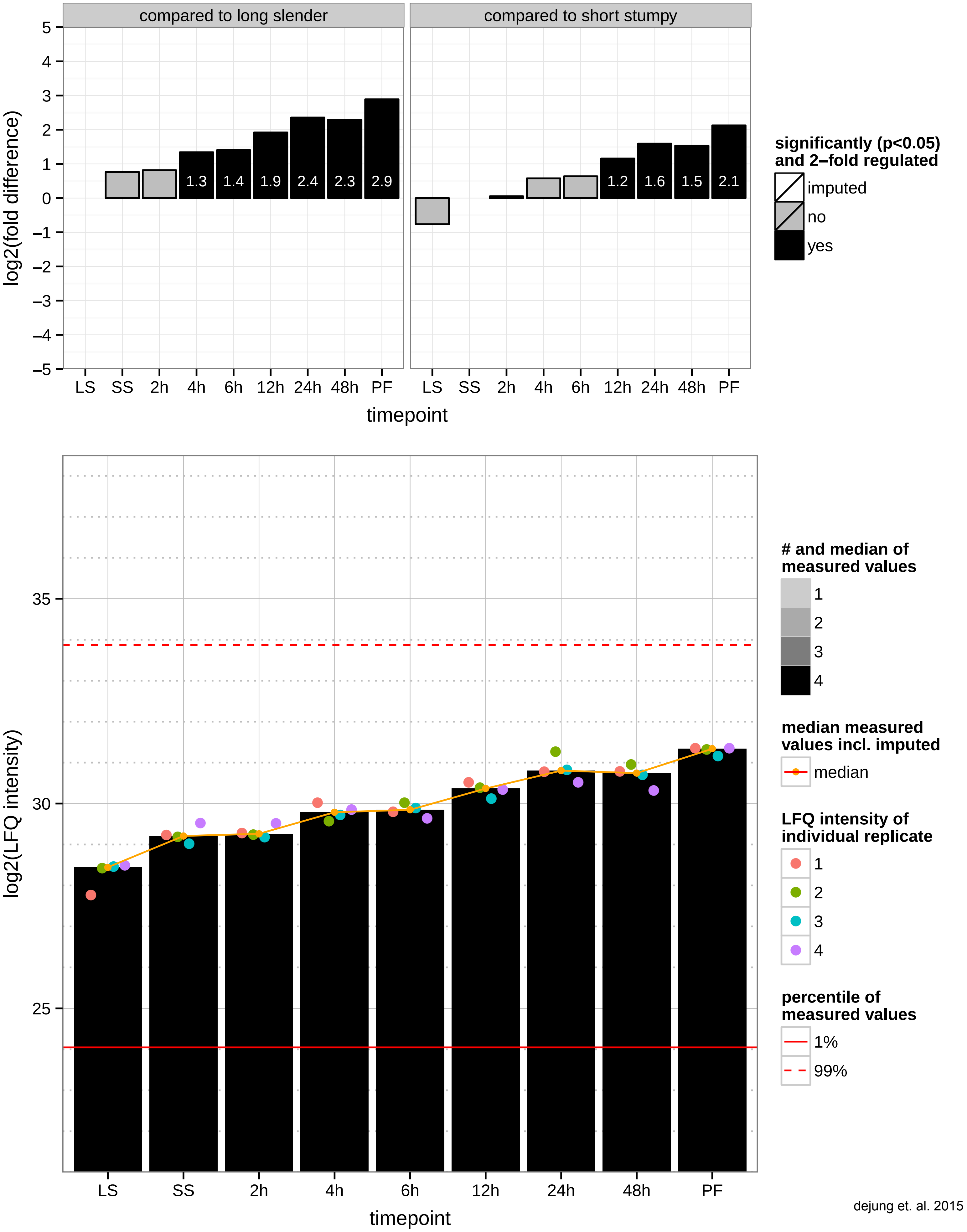
ATP−dependent DEAD/H RNA helicase, putative
Tb927.4.2630
AGOF: ATP binding, ATP−dependent helicase activity, RNA binding, helicase activity
AGOC: nucleus
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, RNA binding, helicase activity, hydrolase activity, acting on acid anhydr
PGOC: nucleus
PGOP: null





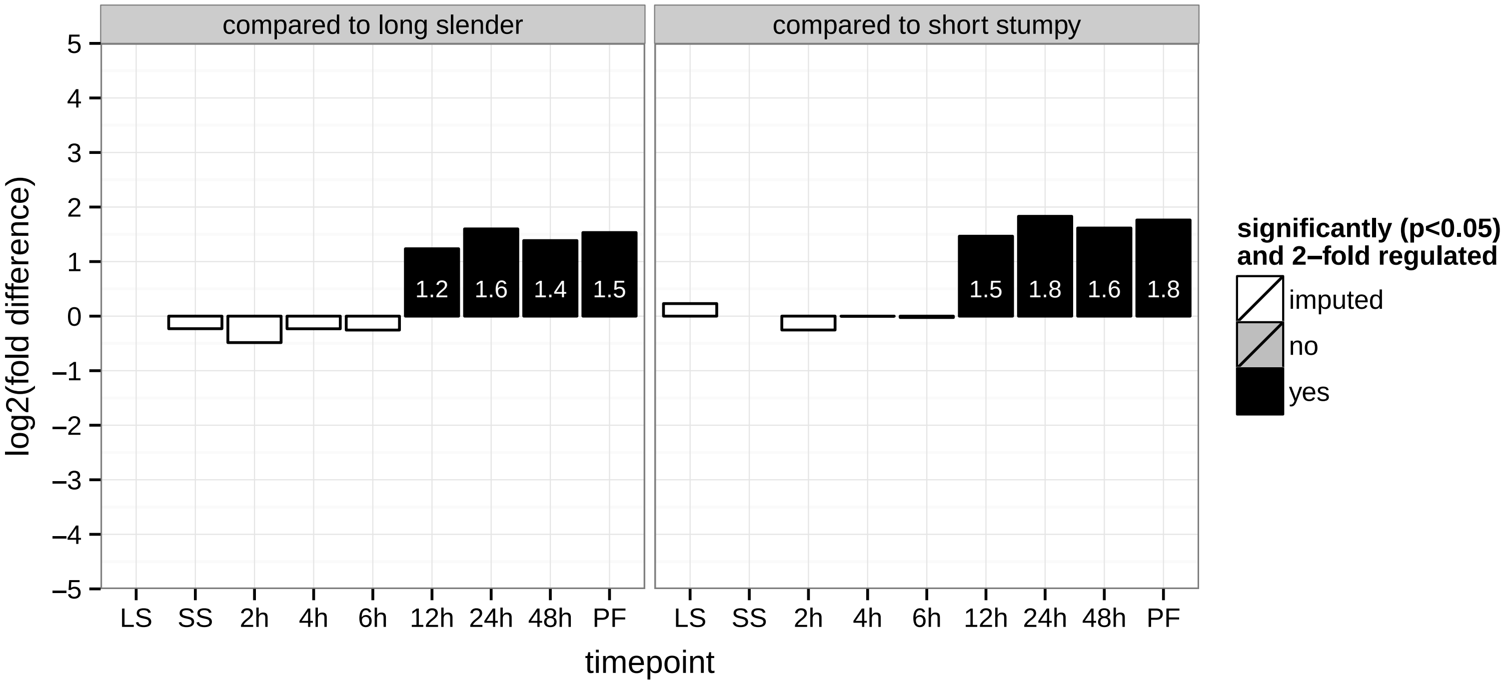
dejung et. al. 2015

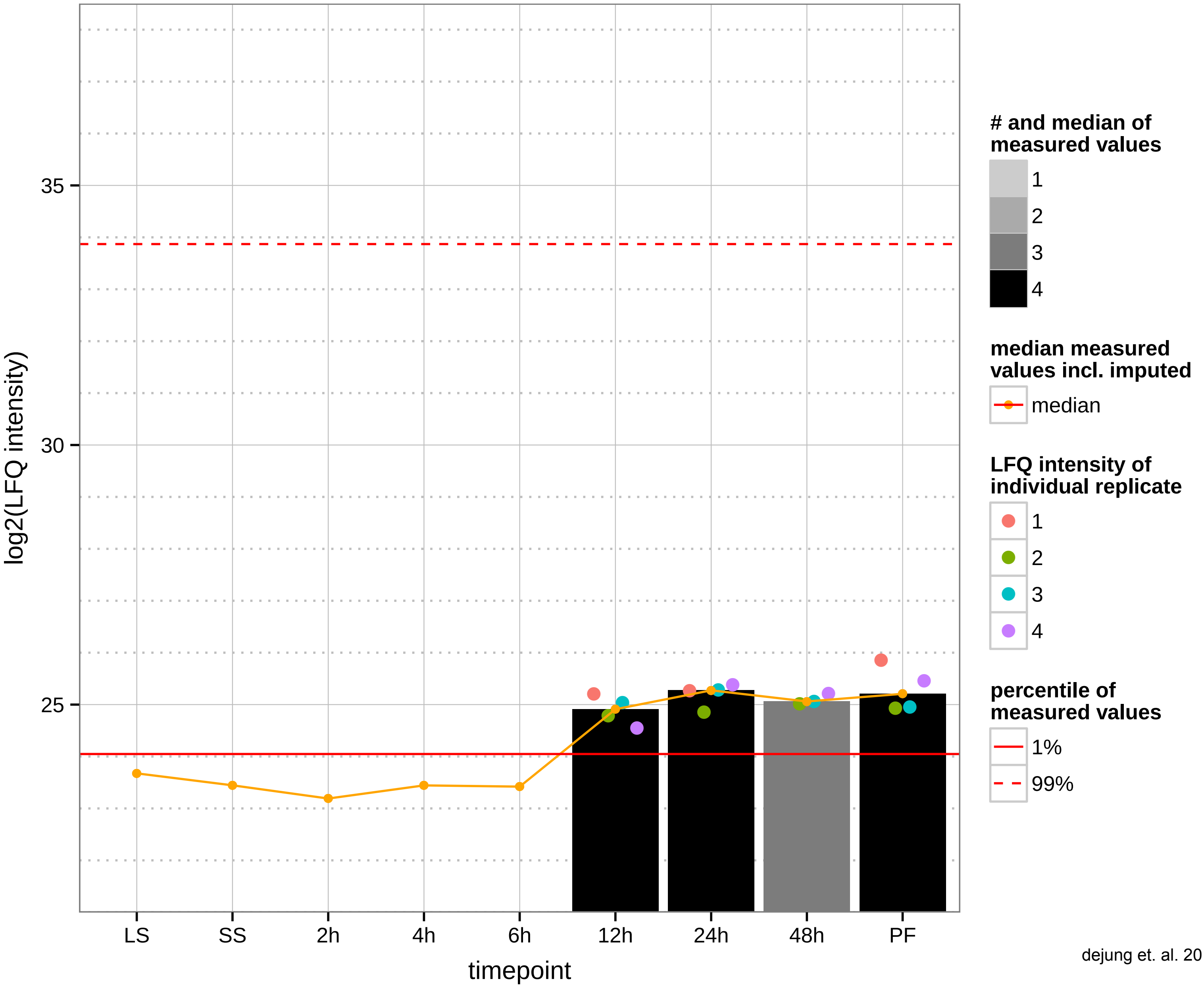
3, 2–trans–enoyl–CoA isomerase, mitochondrial precursor, putative
Tb927.4.4910
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process



dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.5120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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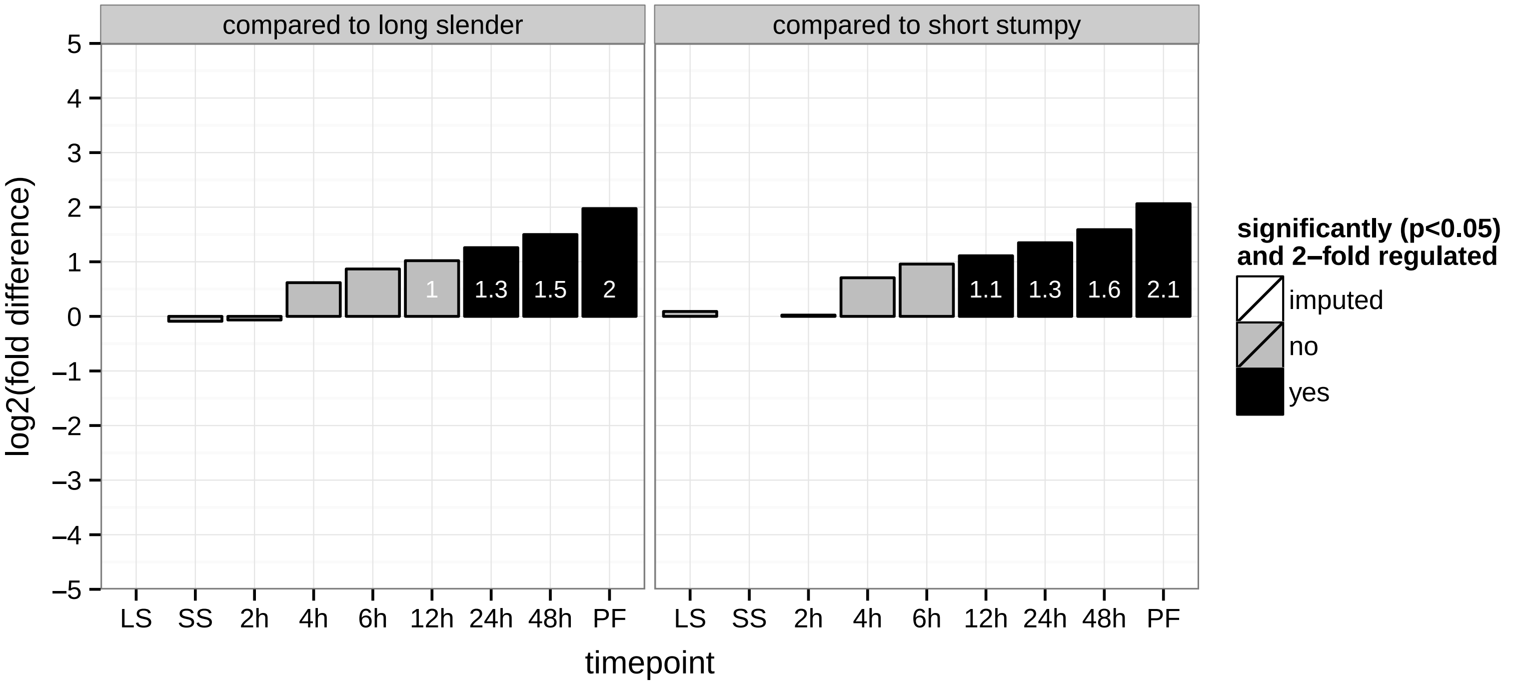
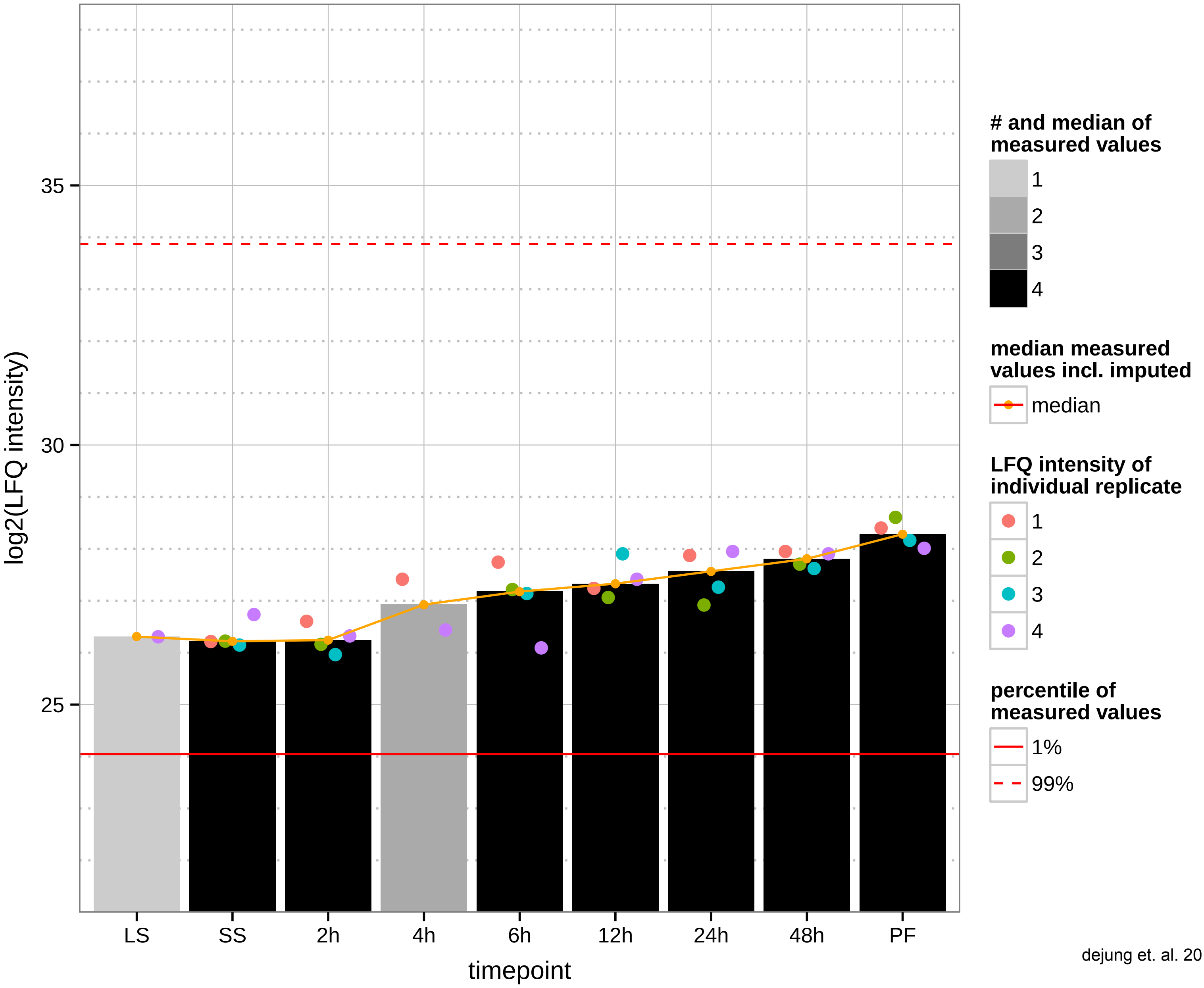
ATP−dependent DEAD/H RNA helicase, putative
Tb927.5.1560
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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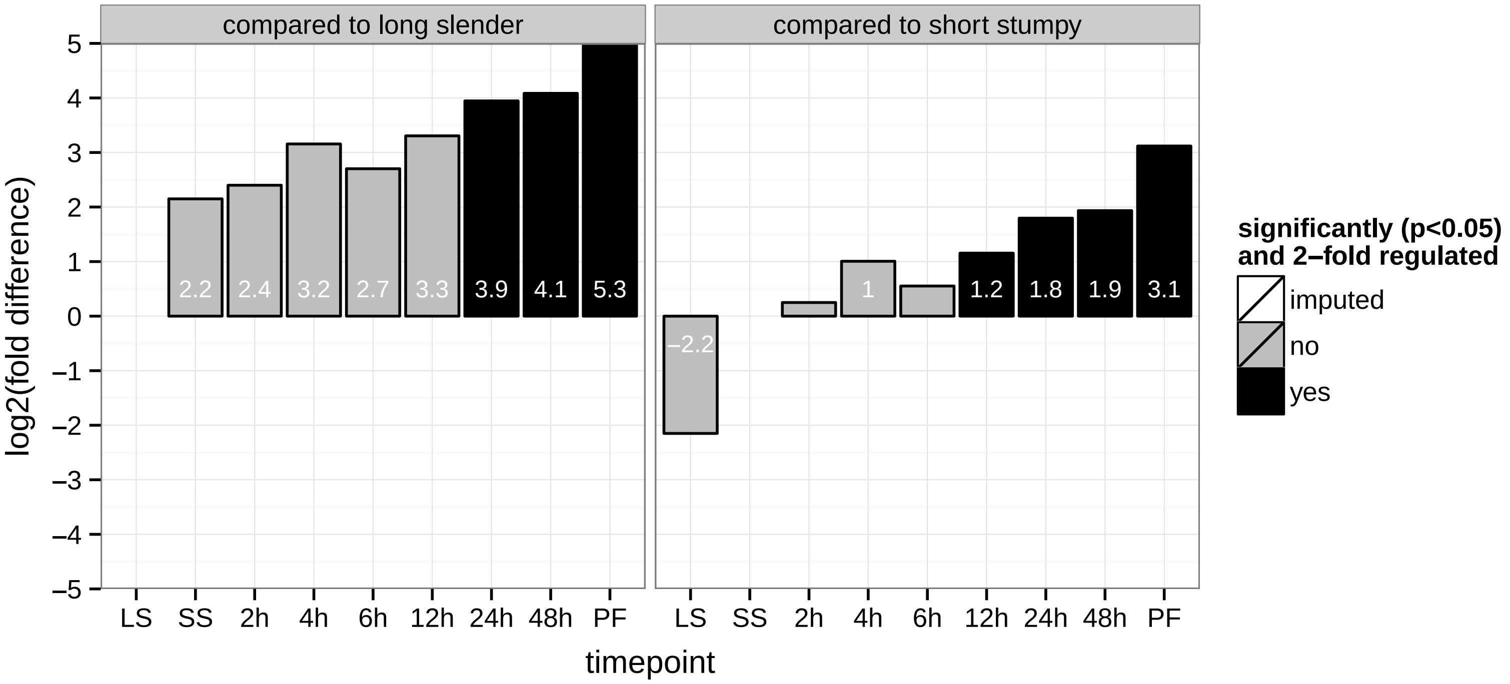
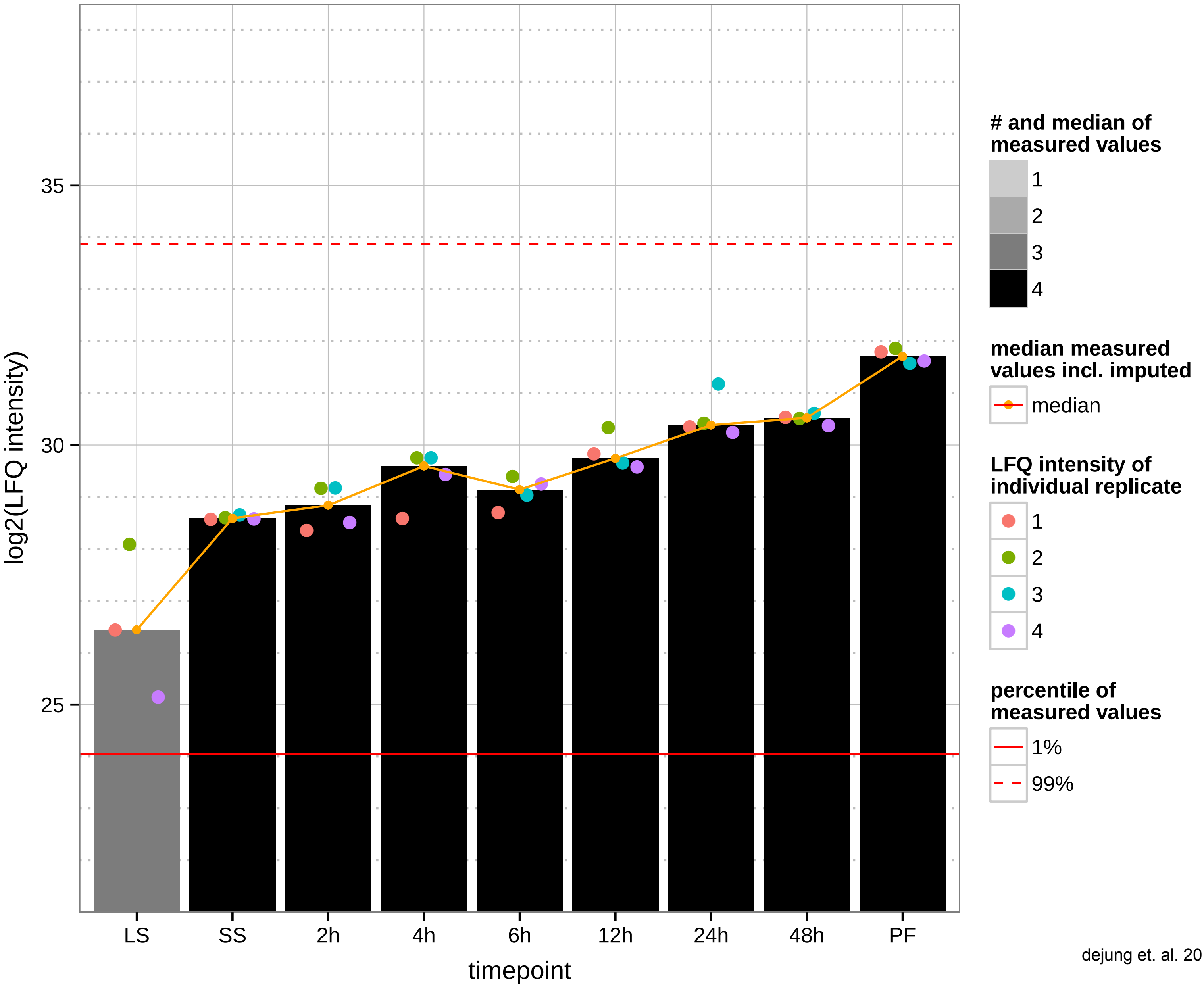
ribonucleoprotein p18, mitochondrial precursor, putative
Tb927.5.1710
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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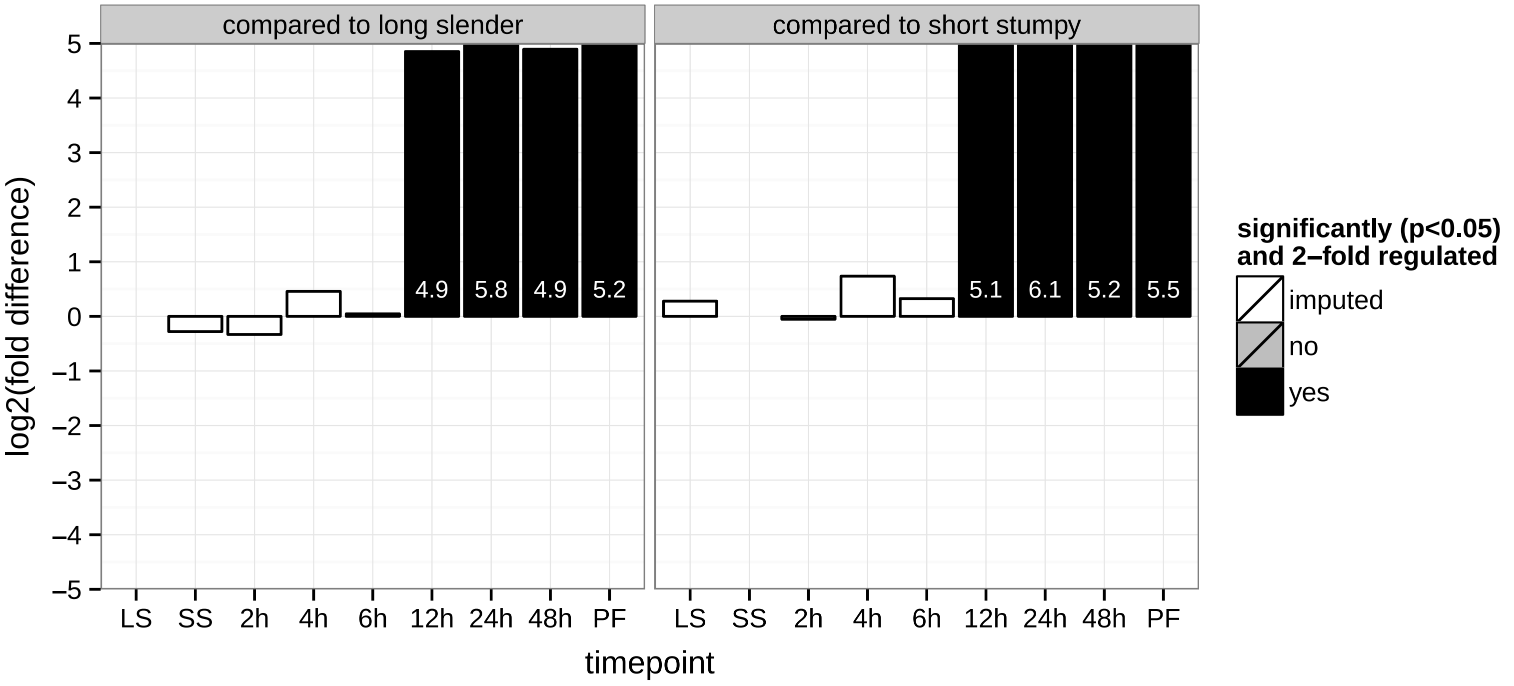
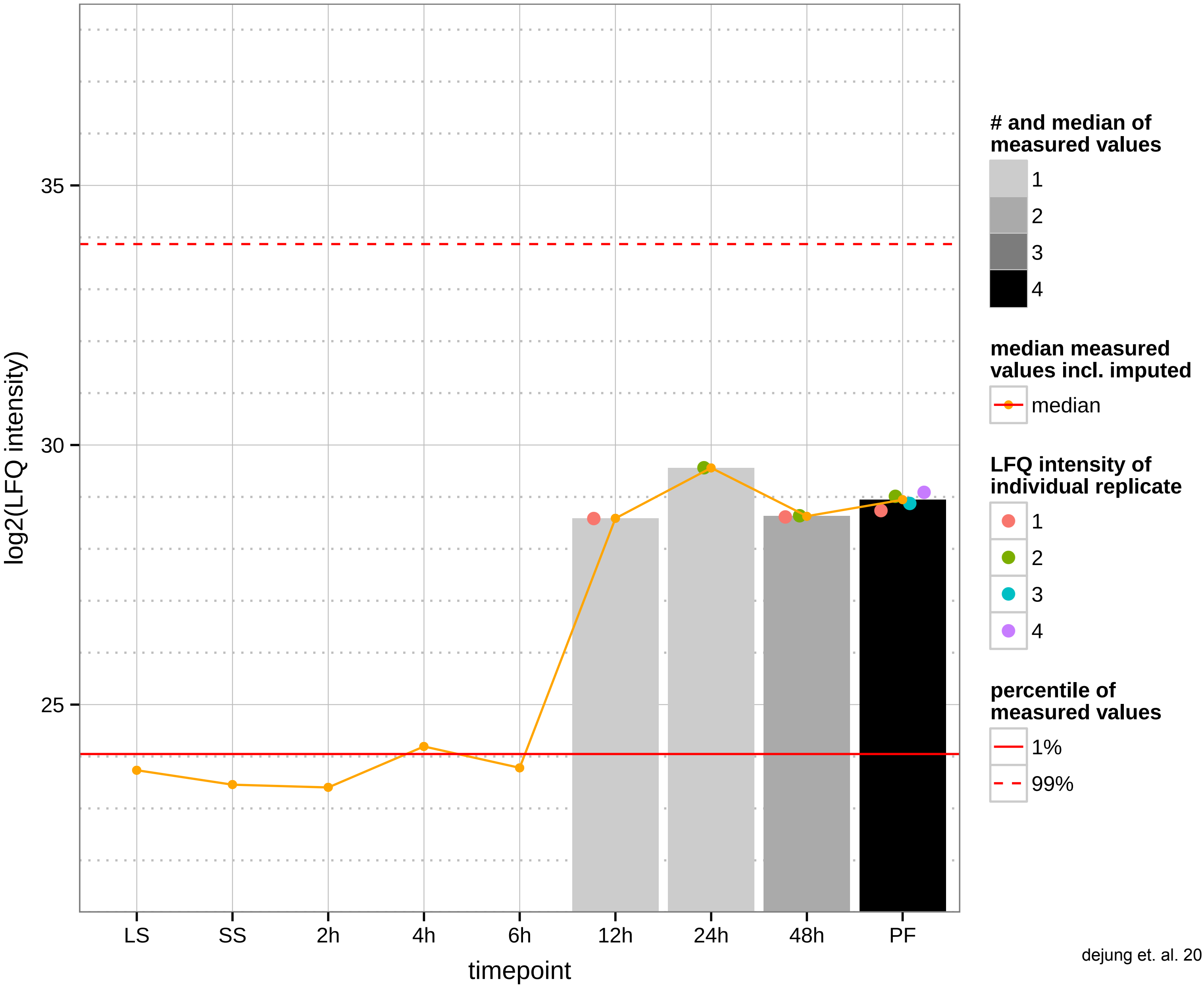
60S acidic ribosomal protein, putative
Tb927.5.1820
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation, translational elongation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translational elongation





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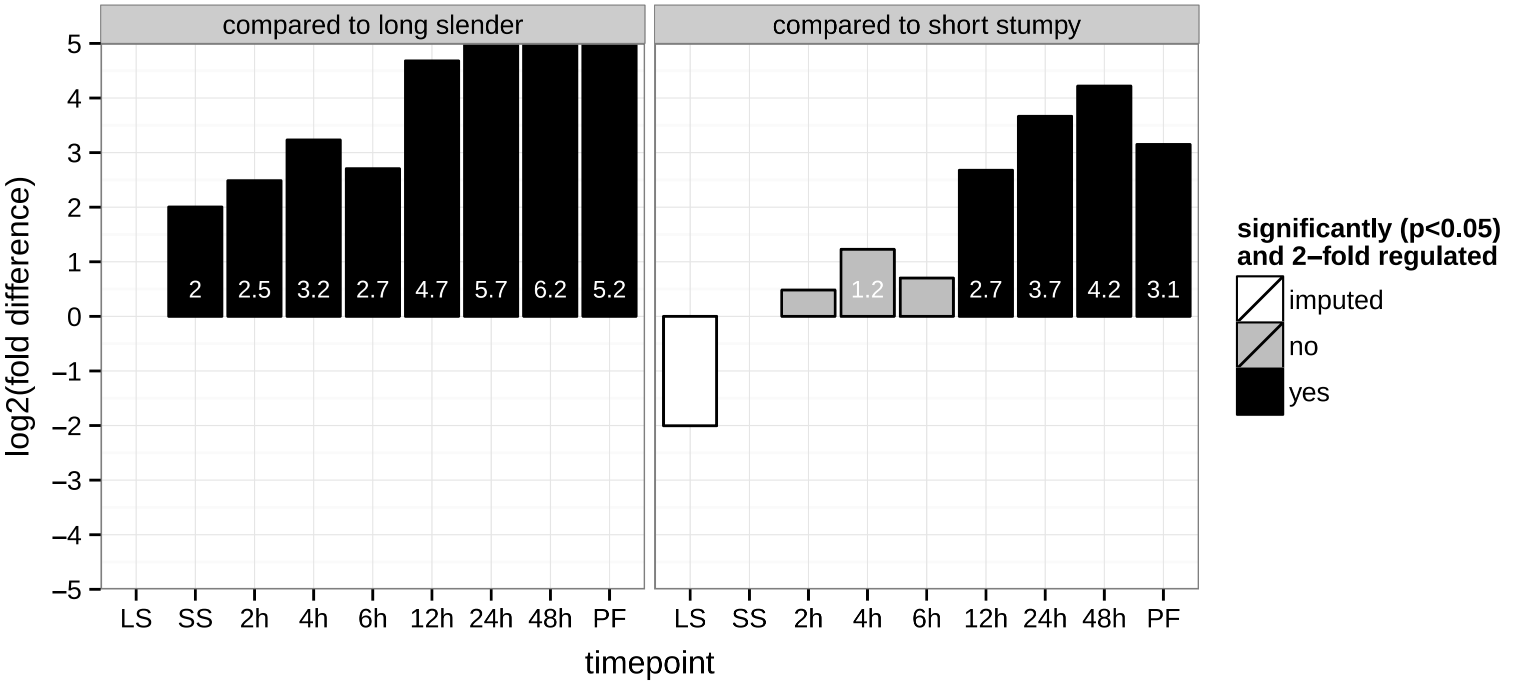
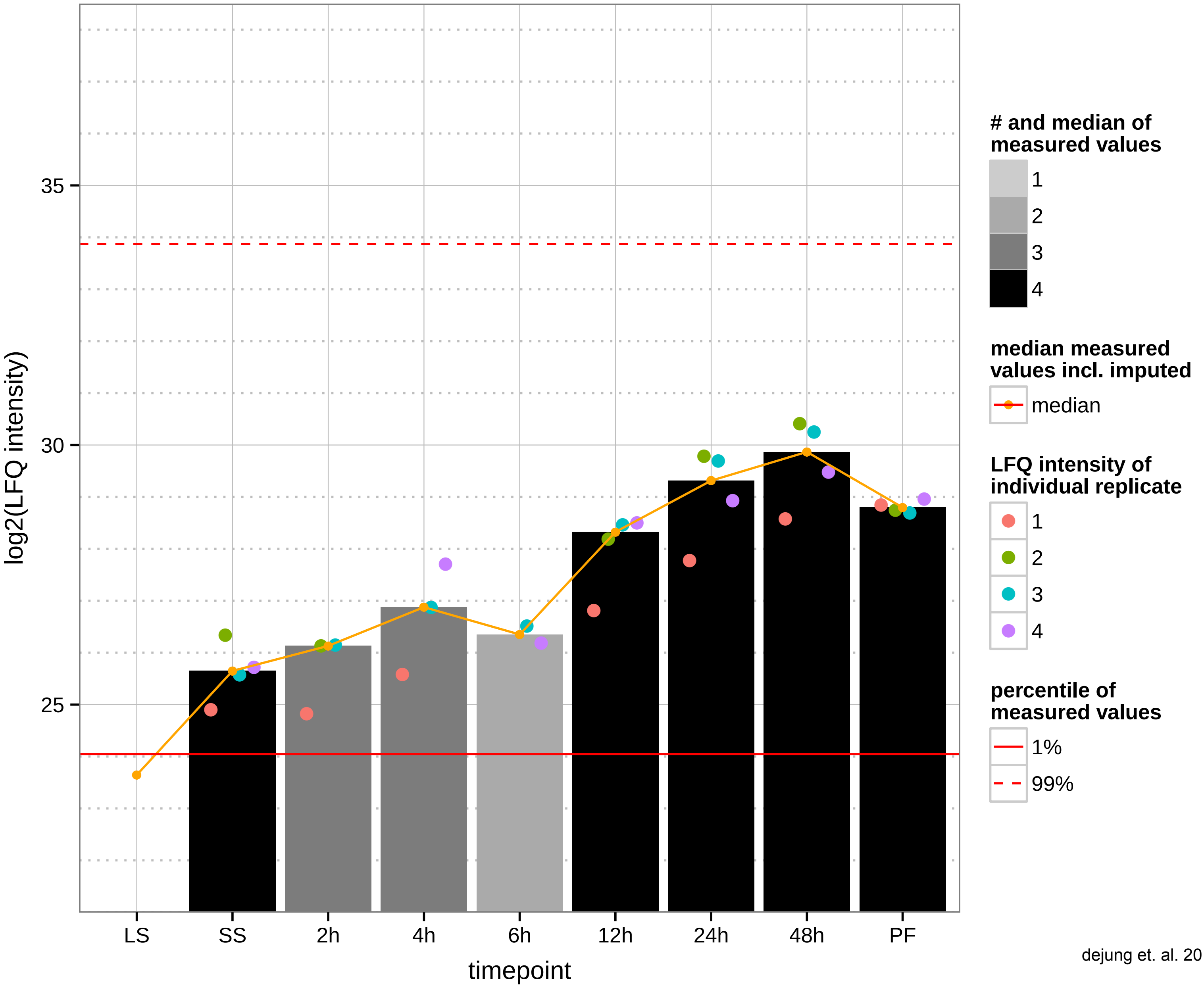
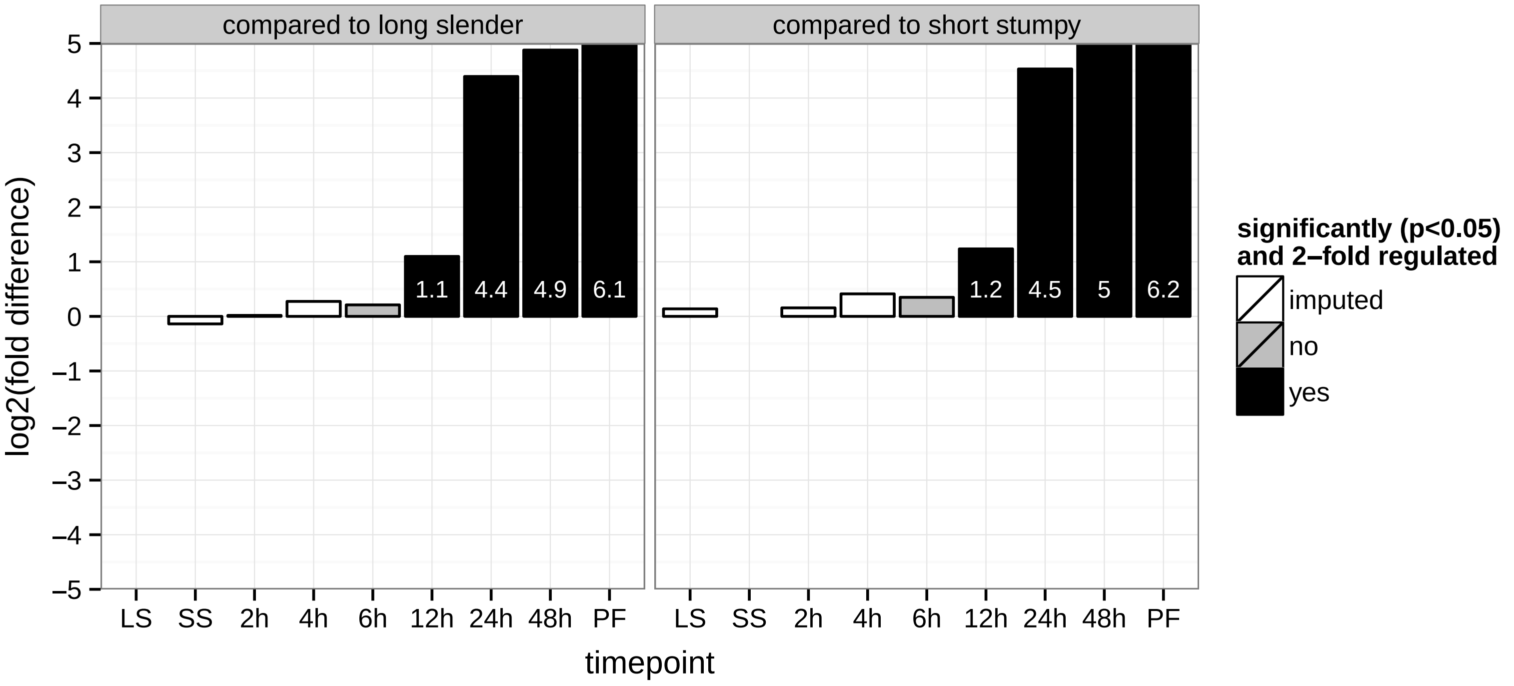
conserved protein
Tb927.5.2160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

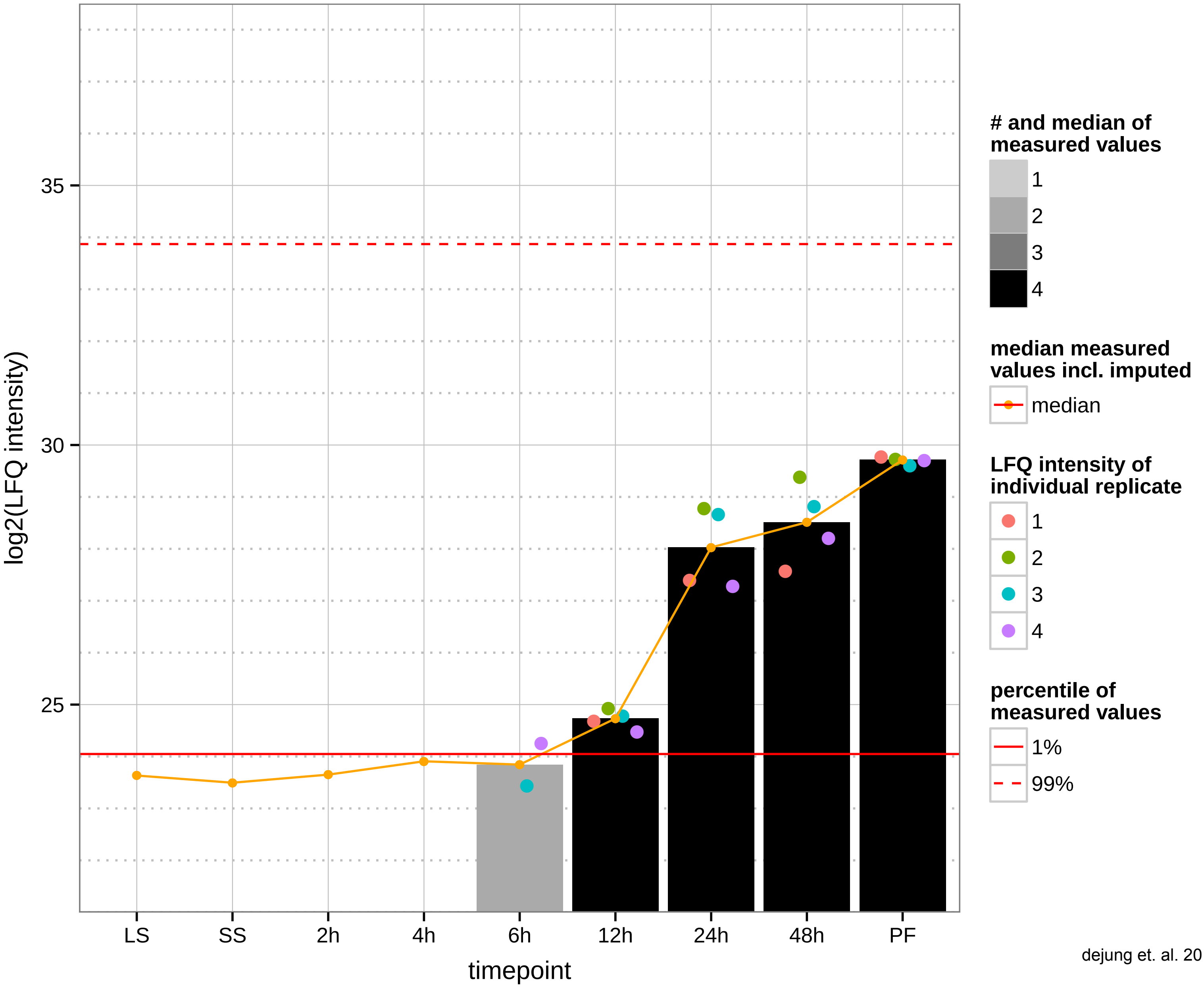




dejung et. al. 2015

hypothetical protein, conserved
Tb927.5.2560
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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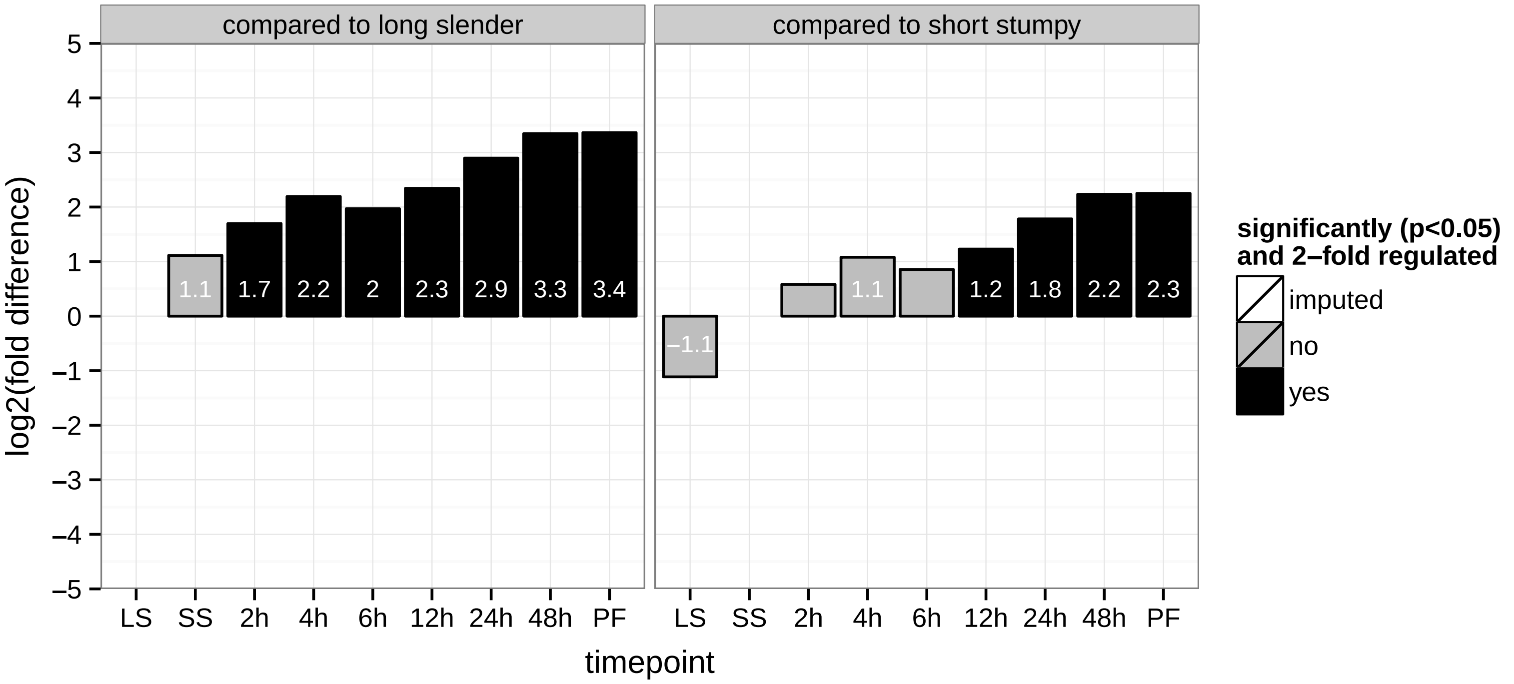
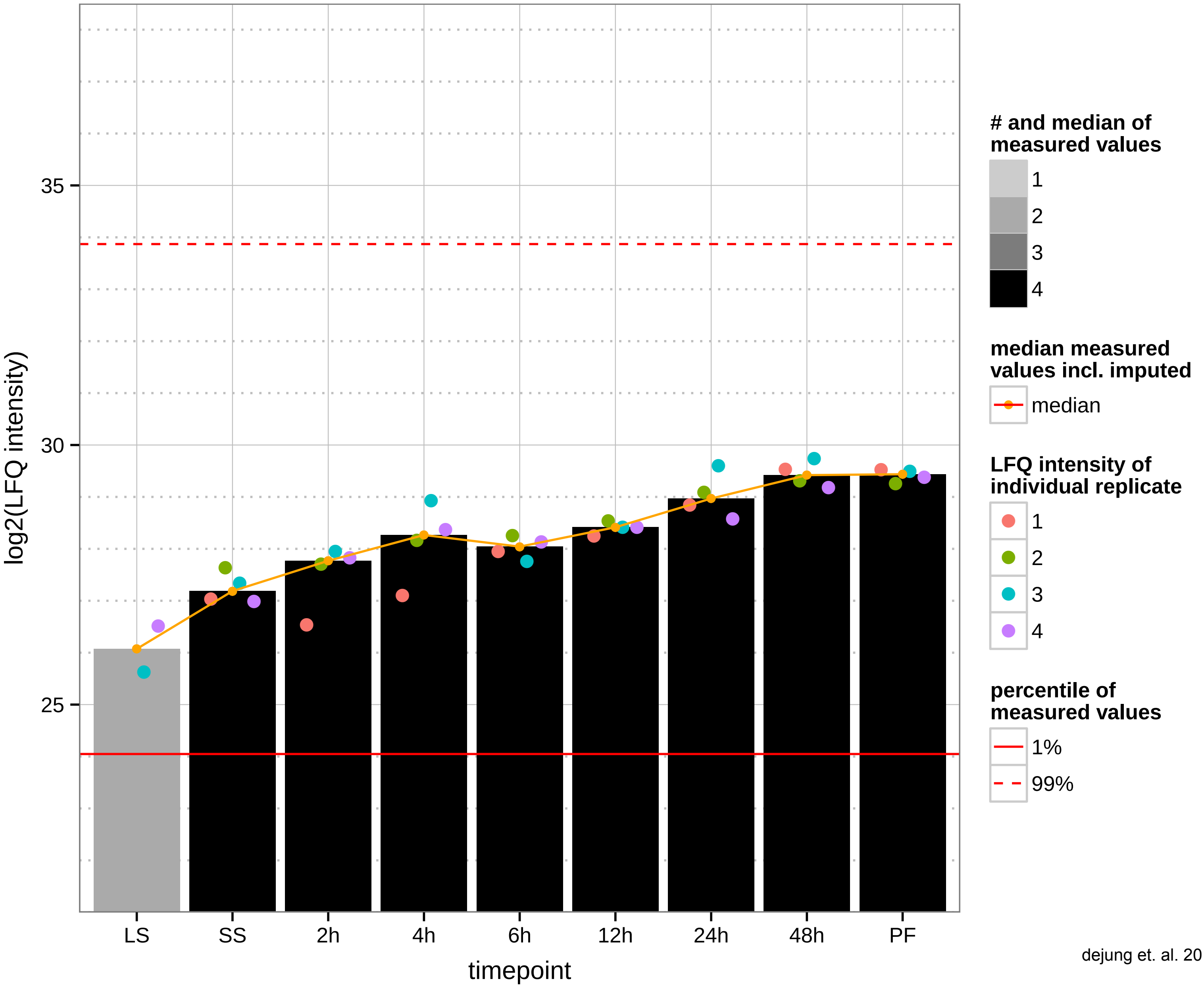
hypothetical protein, conserved
Tb927.5.3090
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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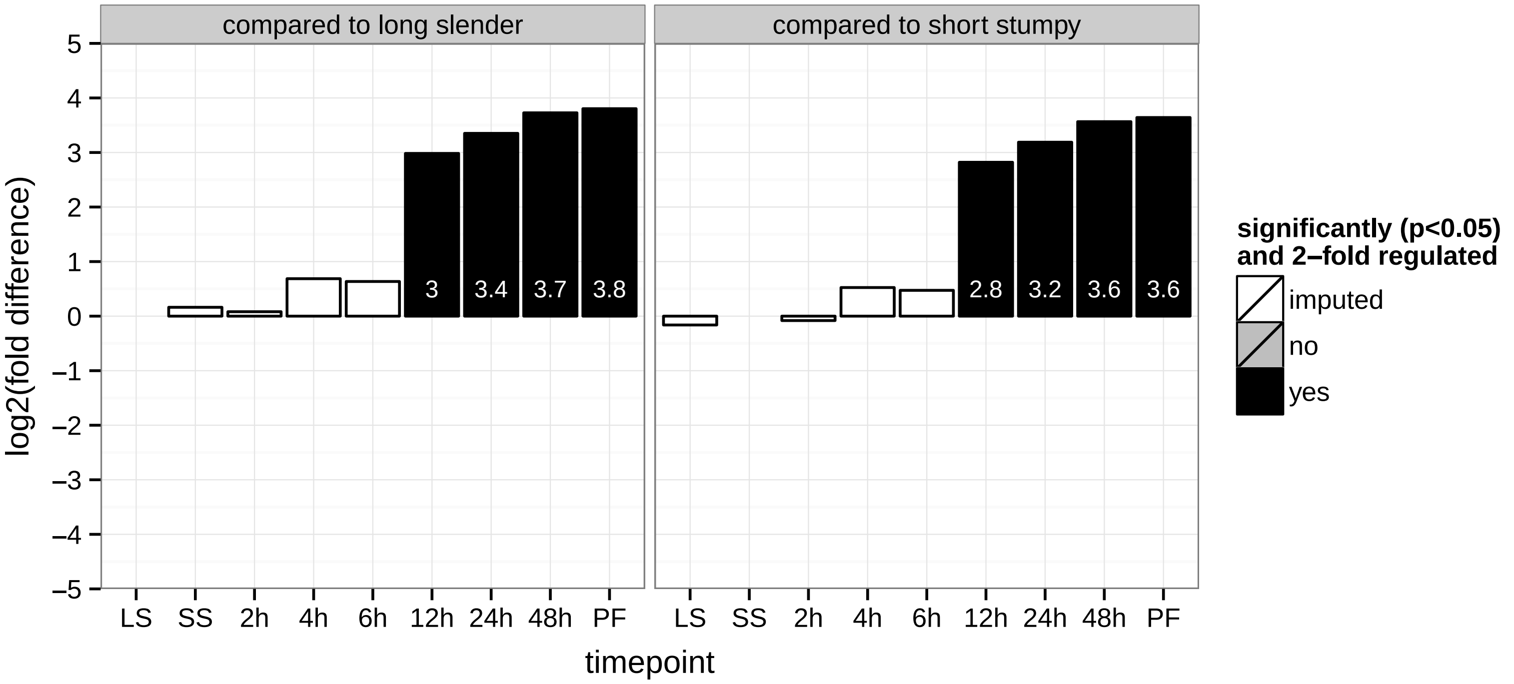
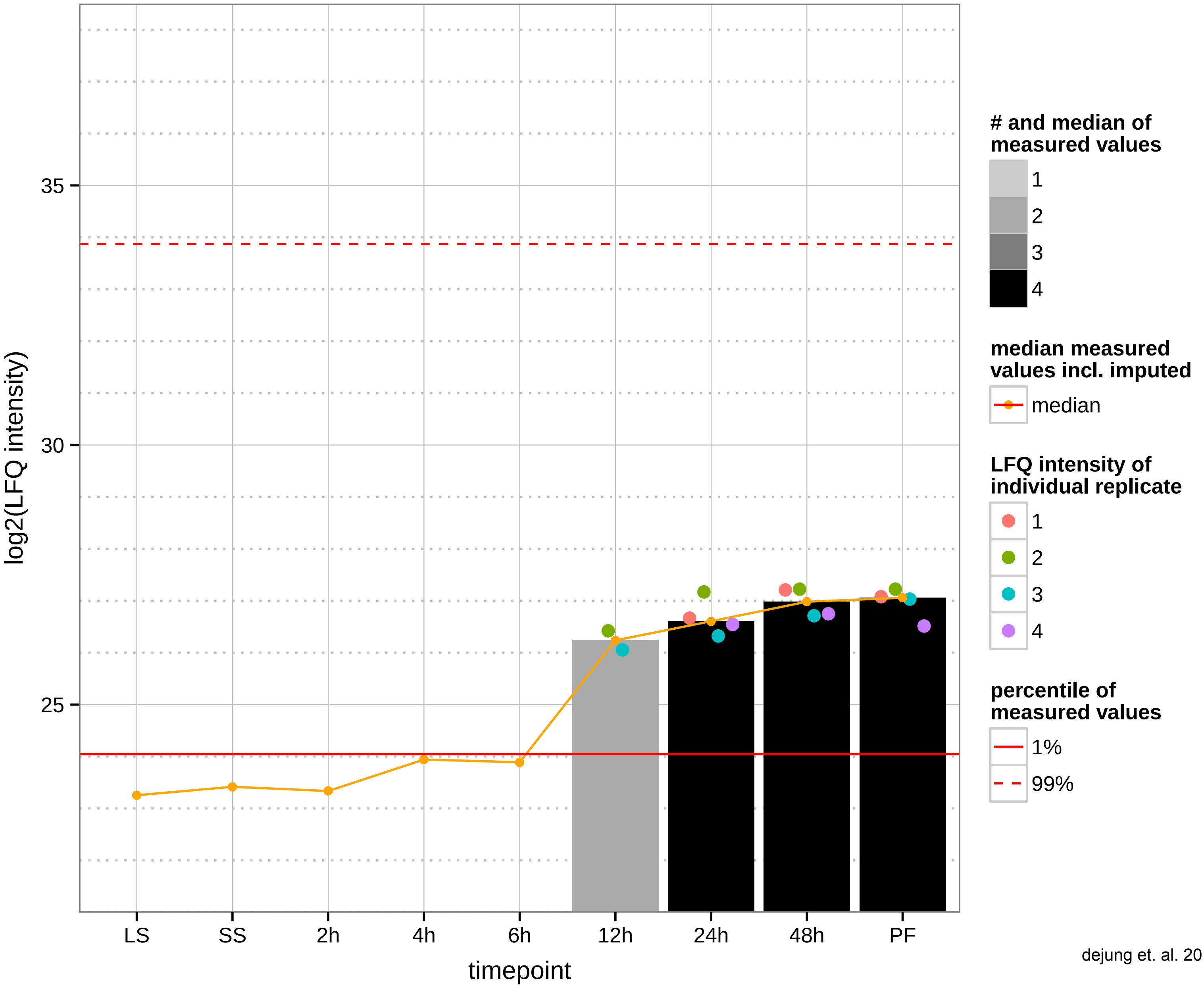
hypothetical protein, conserved
Tb927.5.3110
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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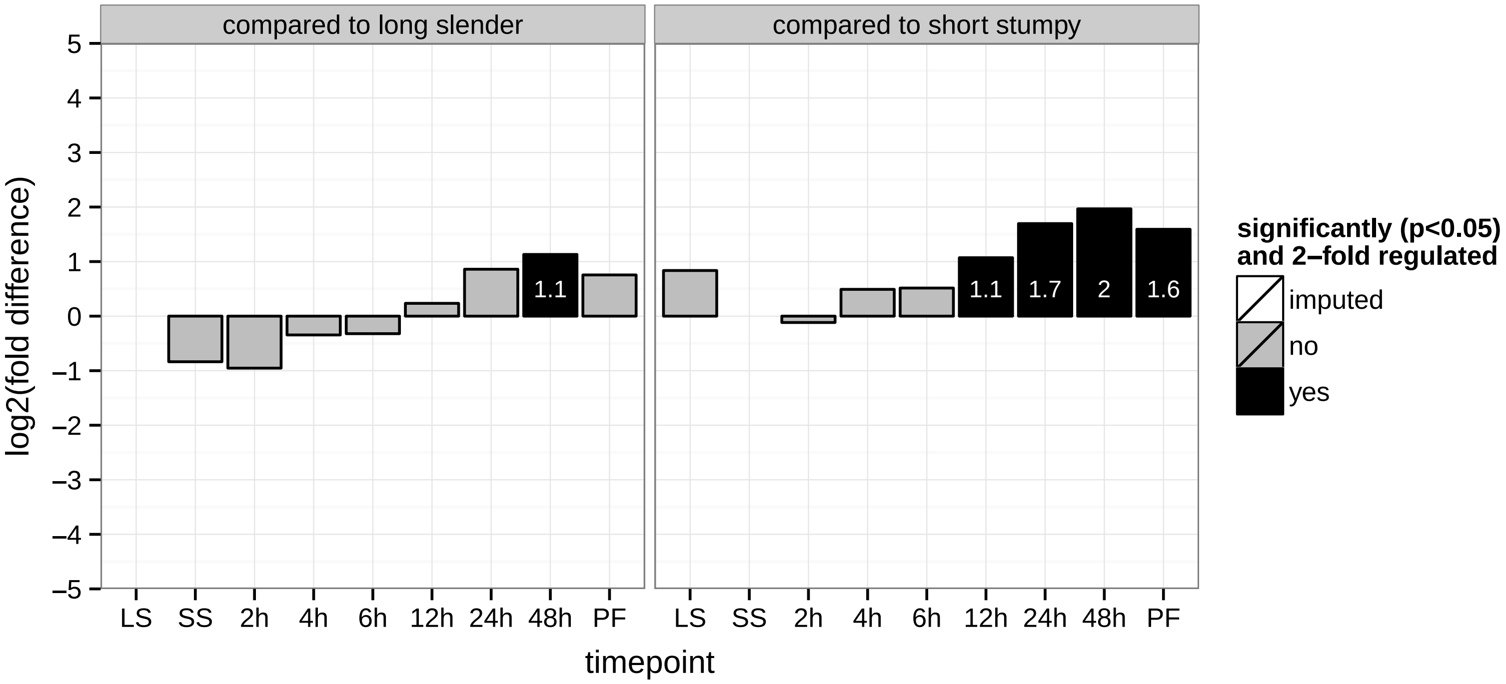
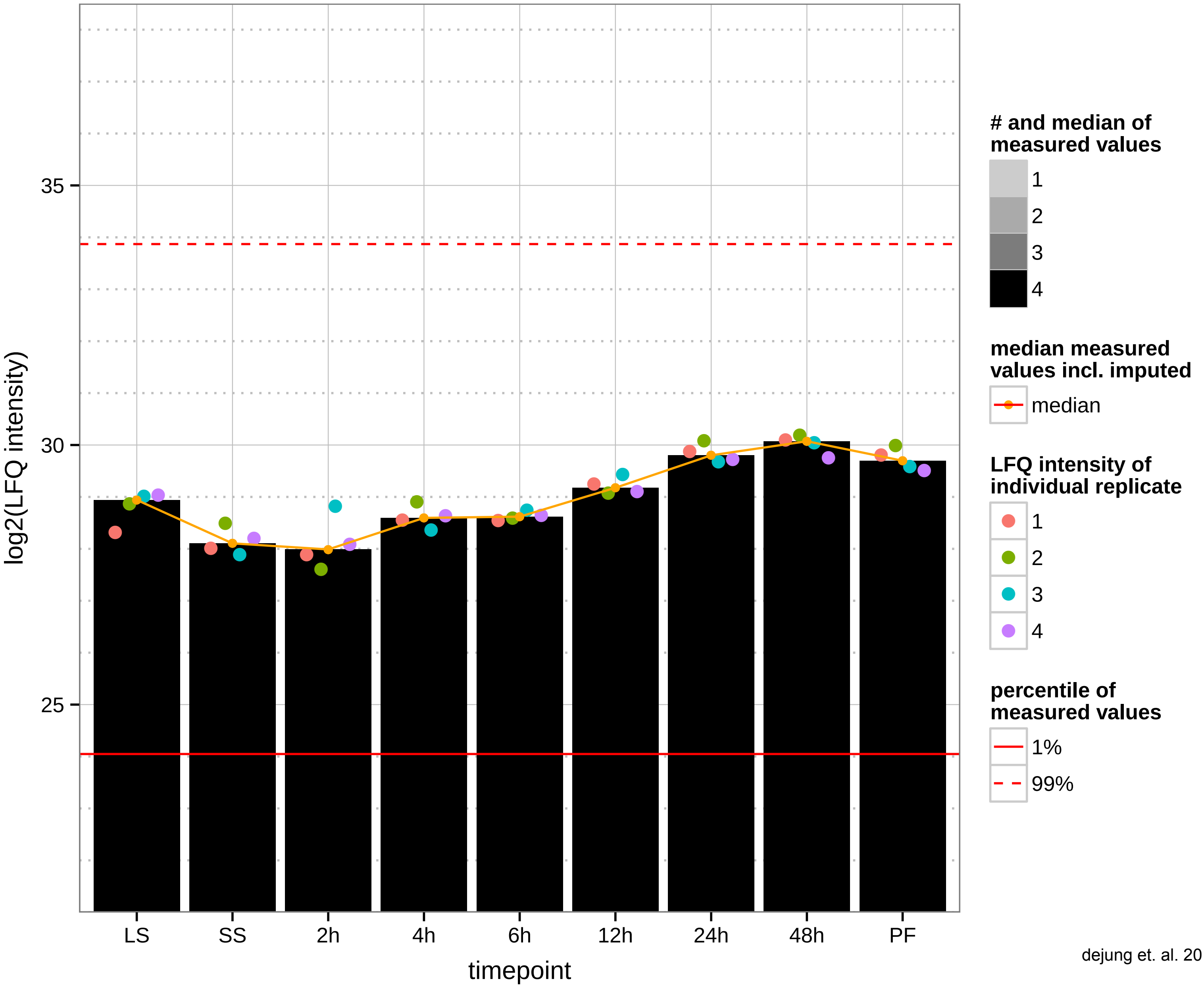
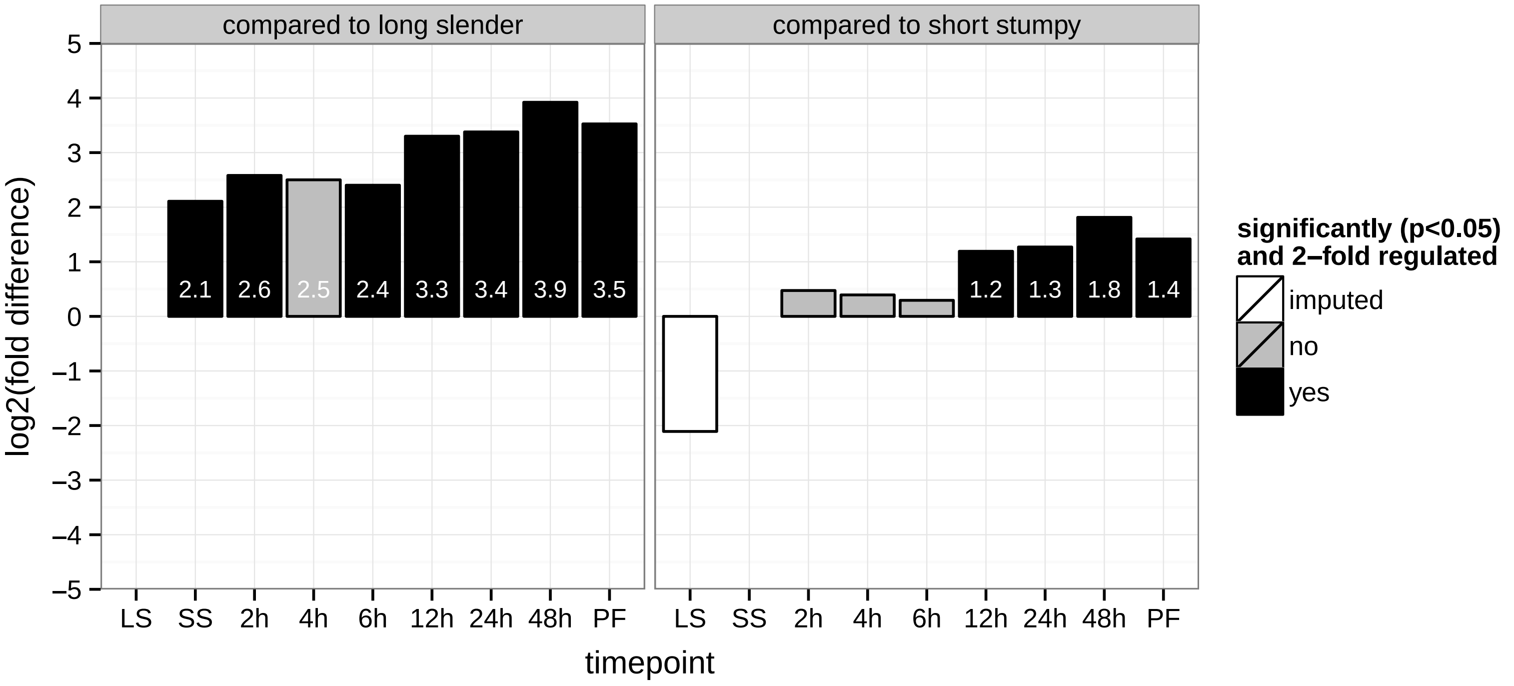
eukaryotic translation initiation factor 2 beta subunit, putative (EIF2B)
Tb927.5.3120
AGOF: translation initiation factor activity, translation initiation factor binding
AGOC: eukaryotic translation initiation factor 2 complex
AGOP: formation of translation preinitiation complex, translational initiation
PGOF: translation initiation factor activity
PGOC: null
PGOP: translational initiation

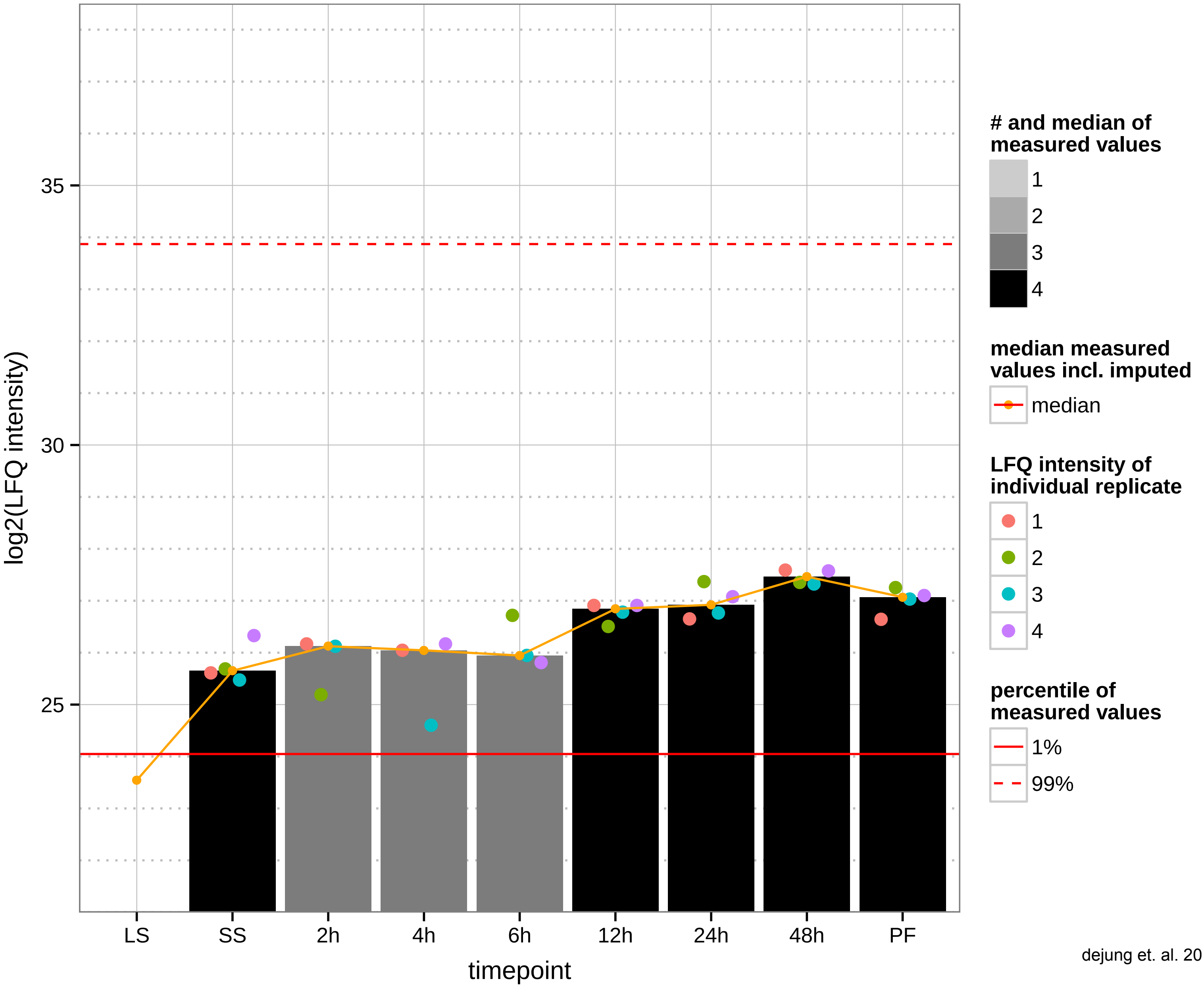




dejung et. al. 2015

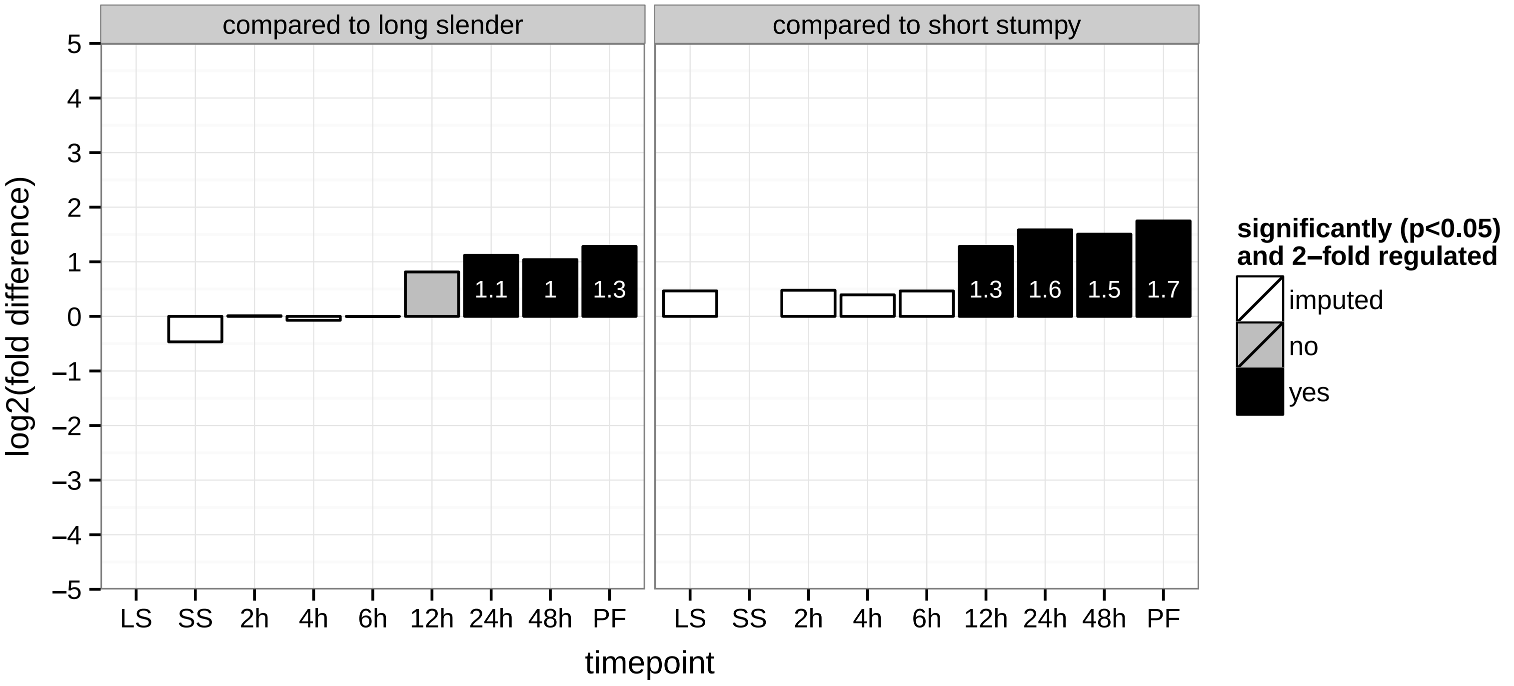
hypothetical protein, conserved
Tb927.5.3980
AGOF: structural constituent of ribosome
AGOC: large ribosomal subunit, mitochondrion
AGOP: translation
PGOF: null
PGOC: null
PGOP: null

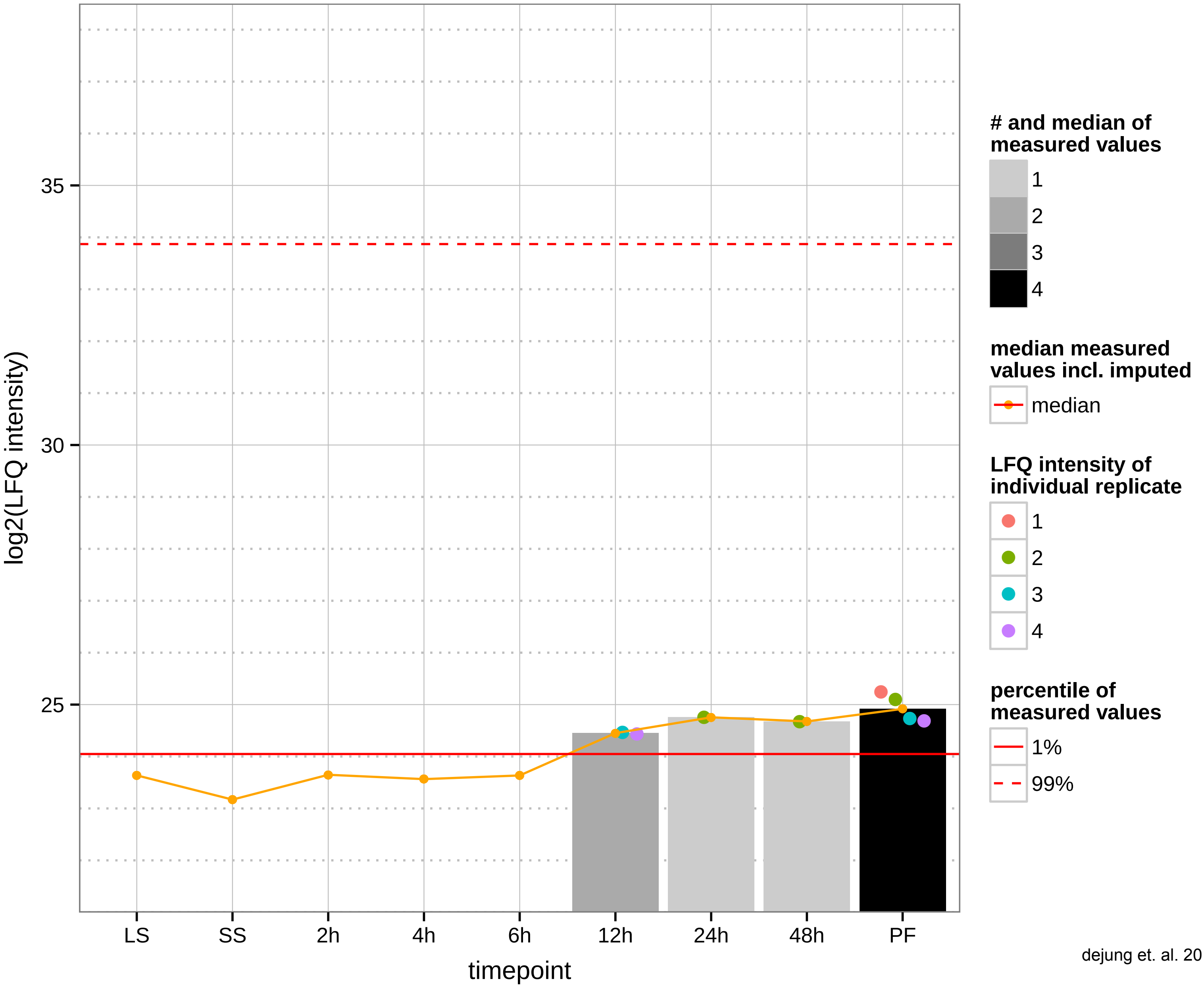




dejung et. al. 2015

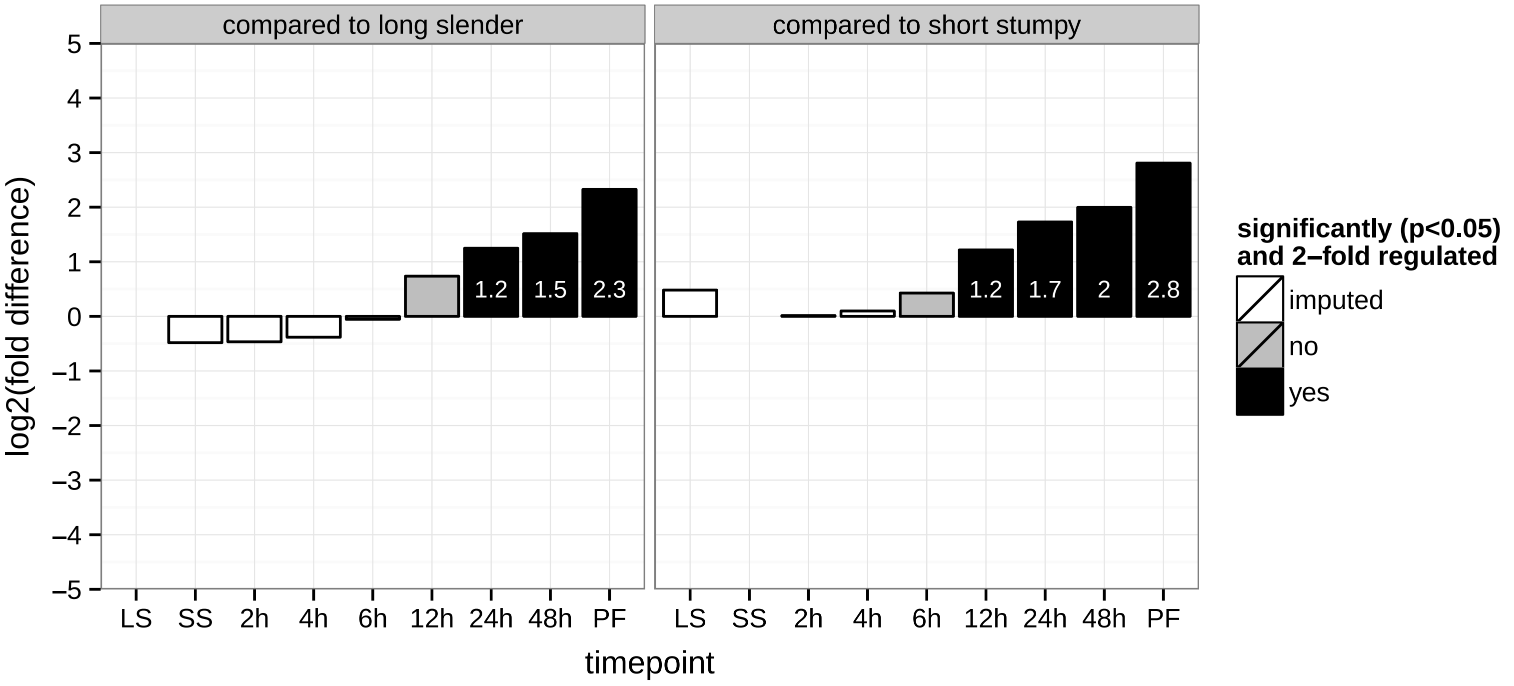
hypothetical protein, conserved
Tb927.5.4090
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

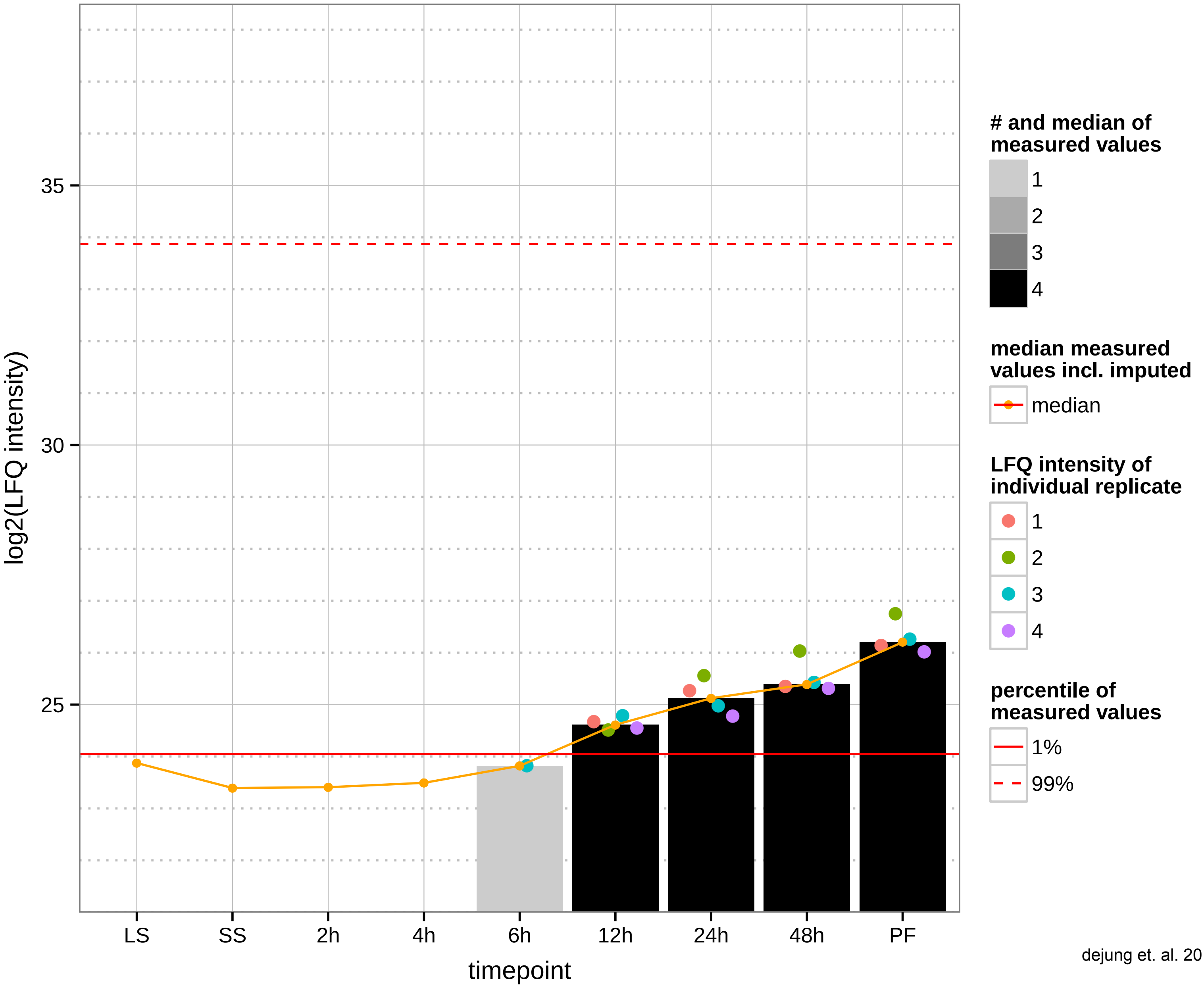




dejung et. al. 2015

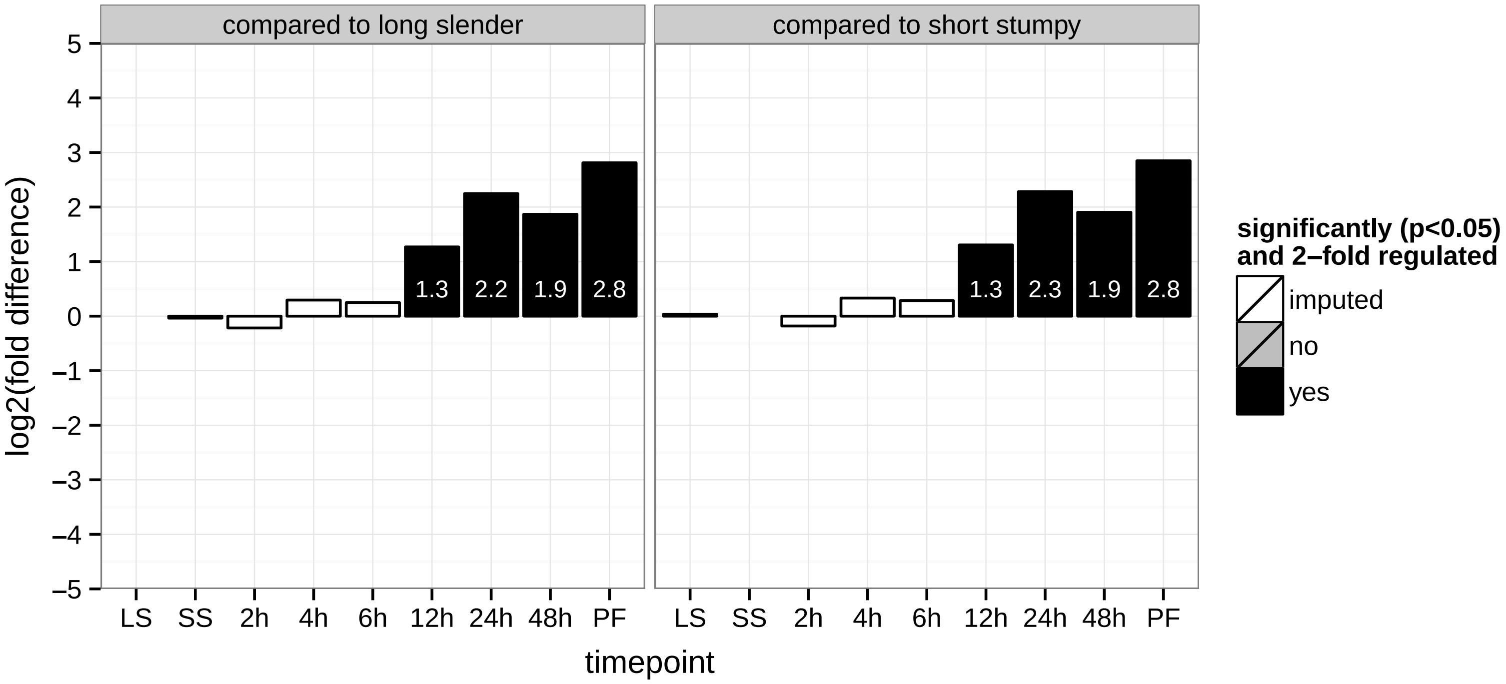
hypothetical protein, conserved
Tb927.6.1890
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

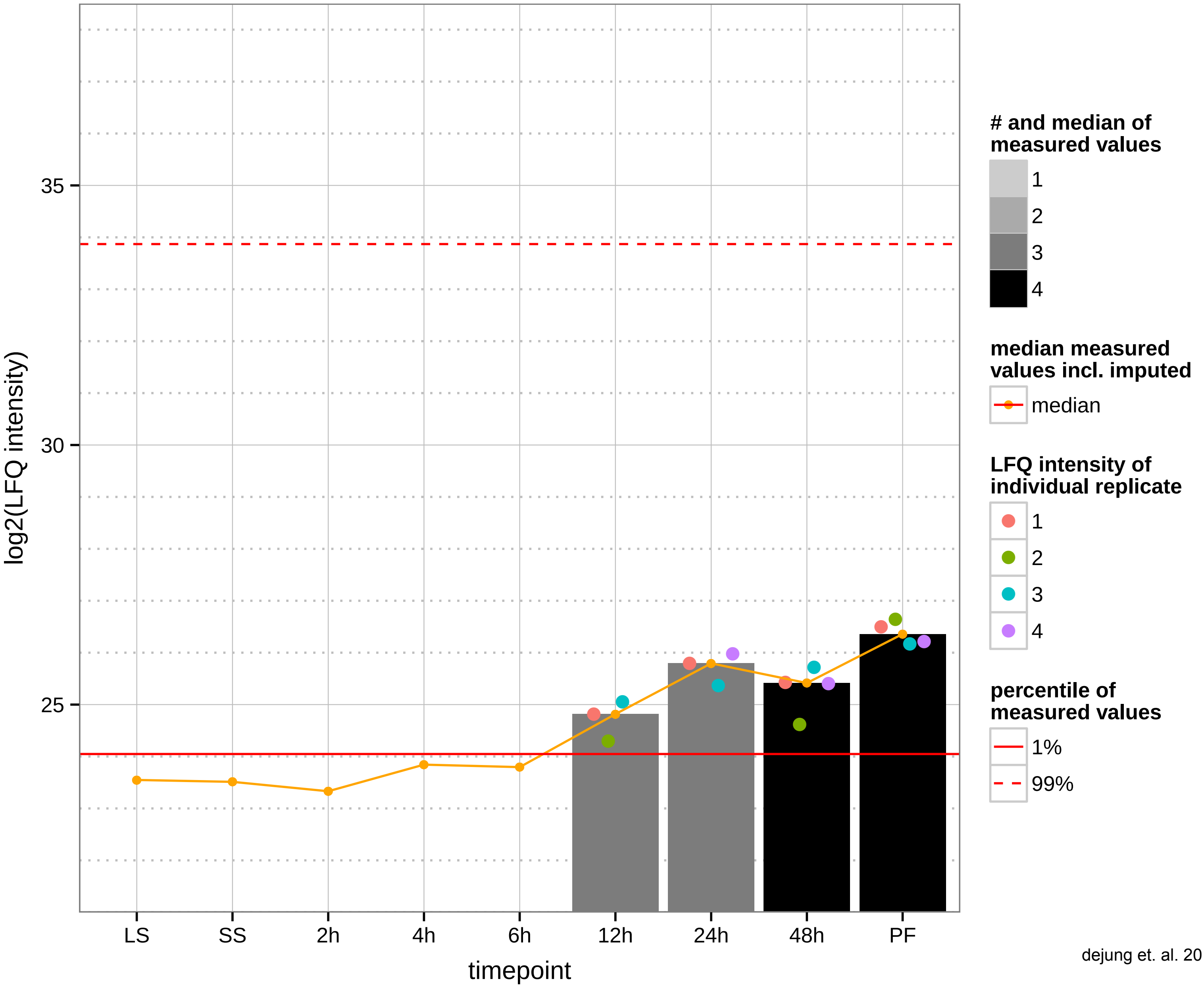




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.2080
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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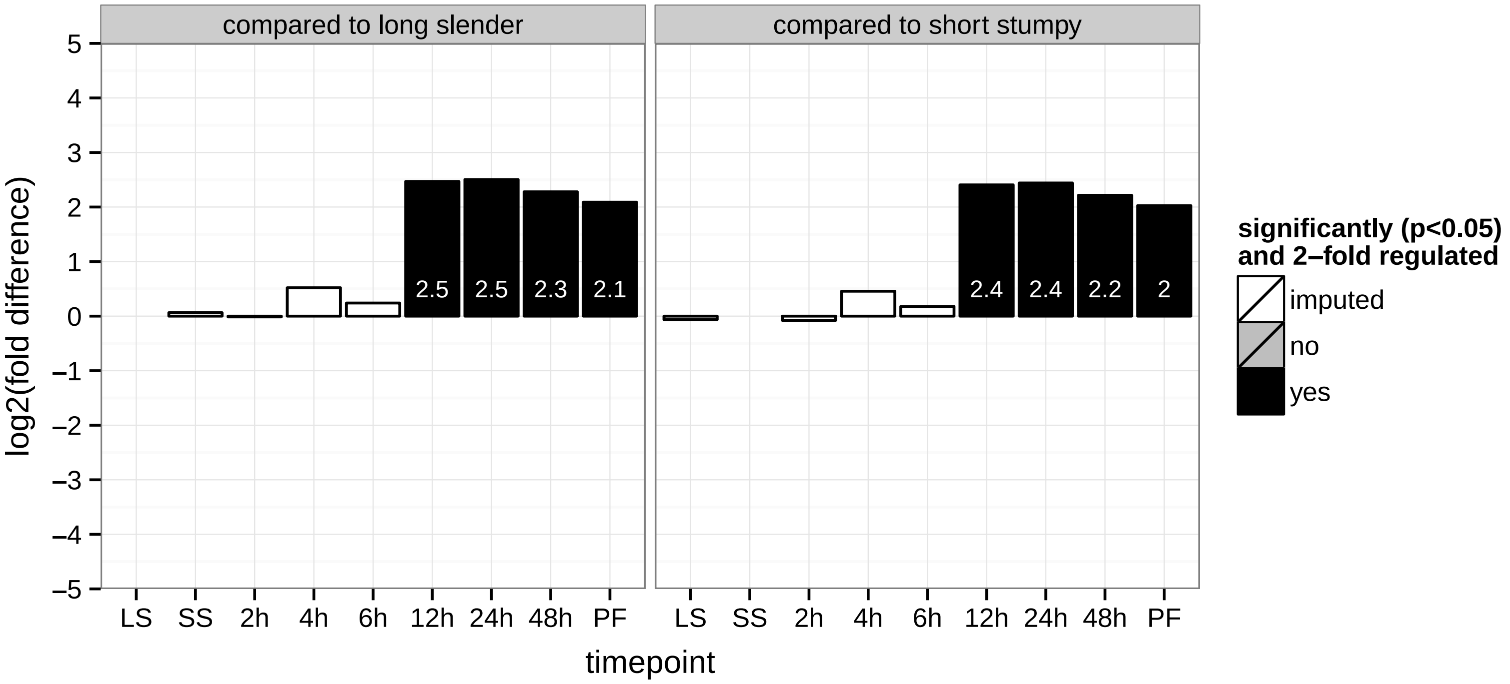
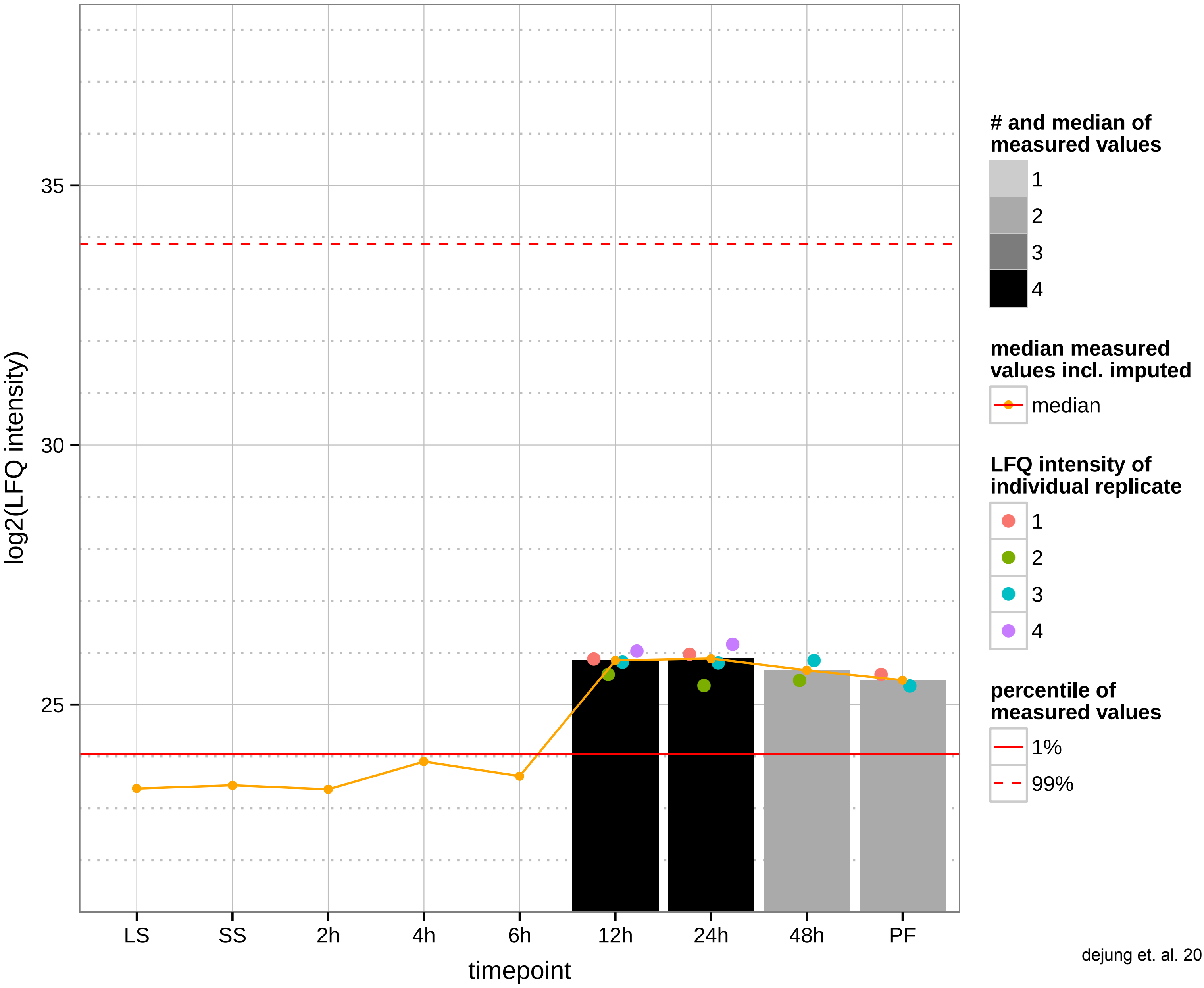
protein kinase, putative, protein kinase B kinase
Tb927.6.2450
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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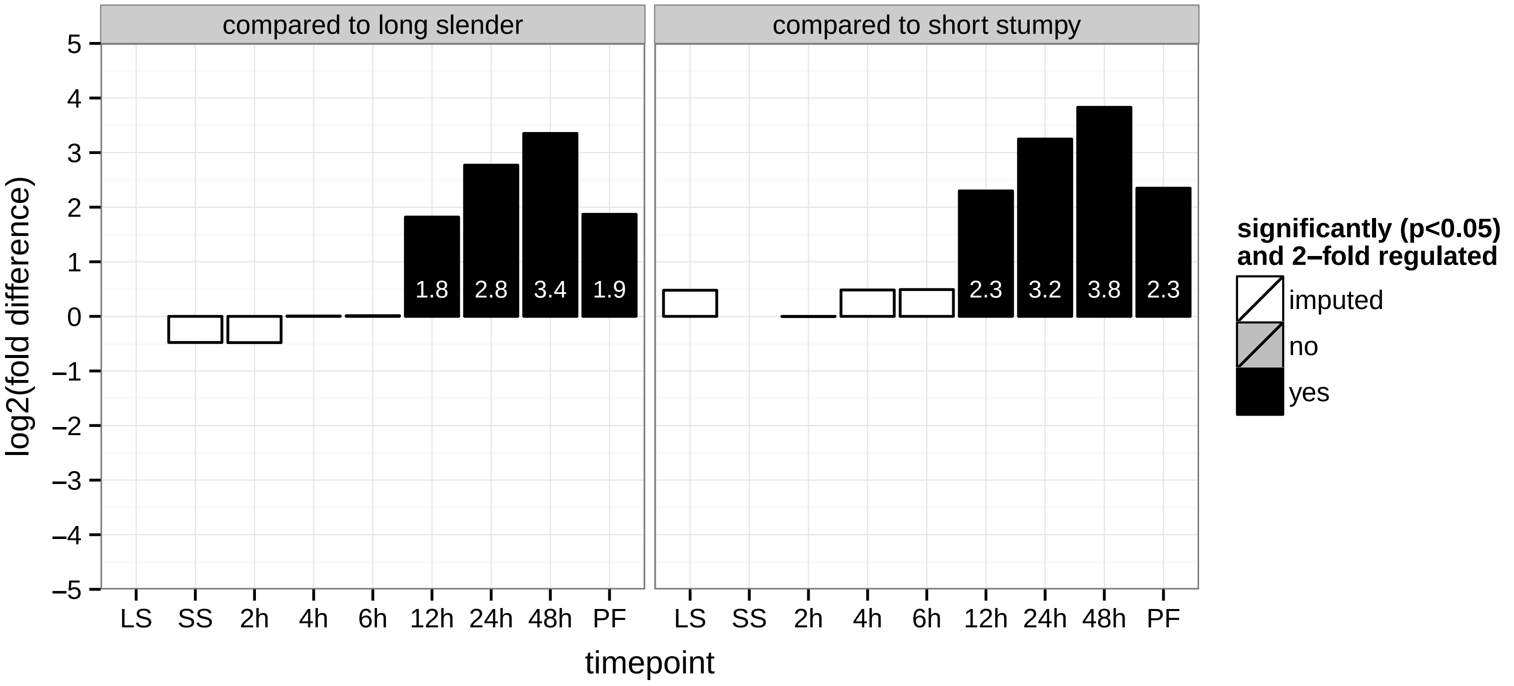
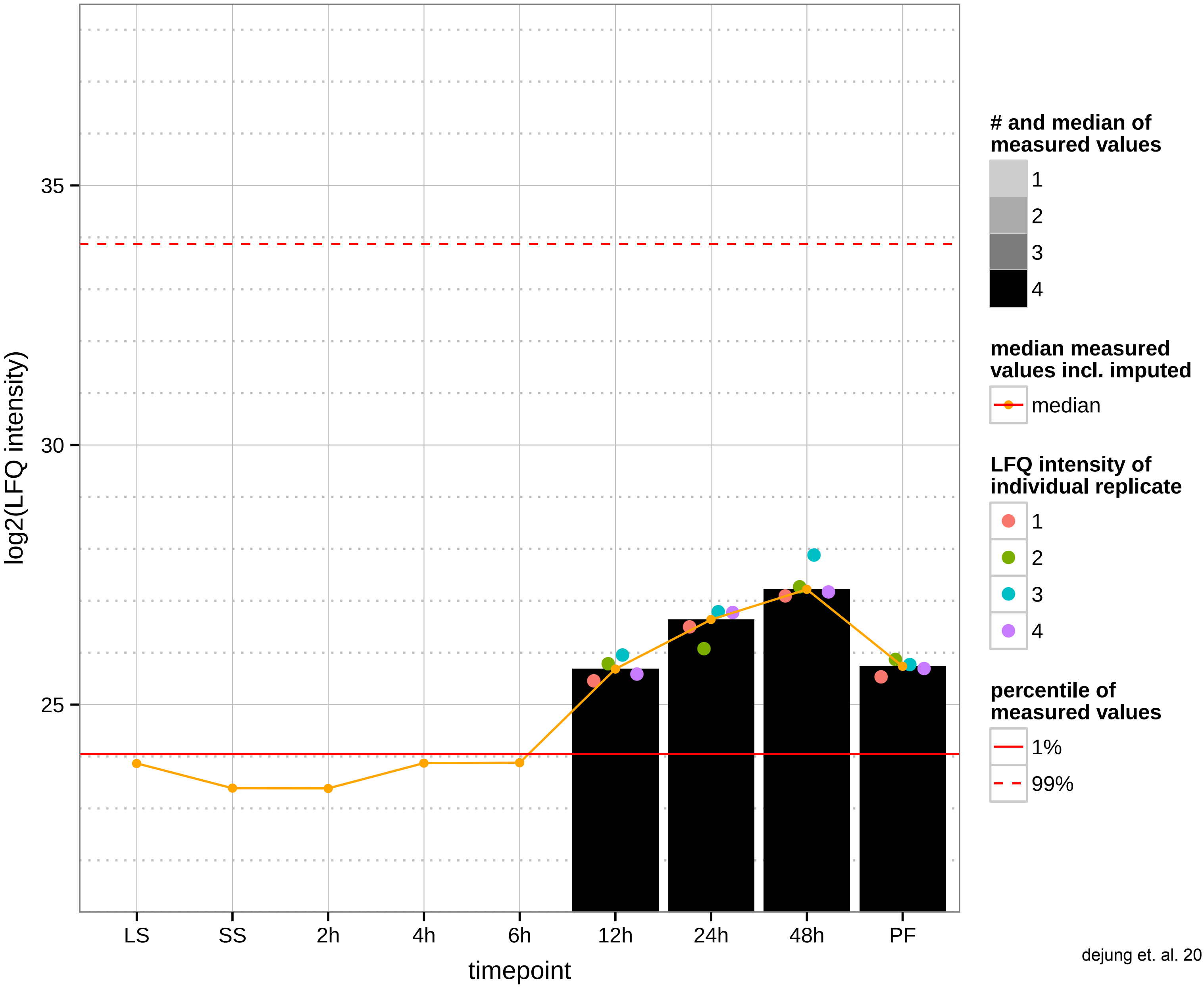
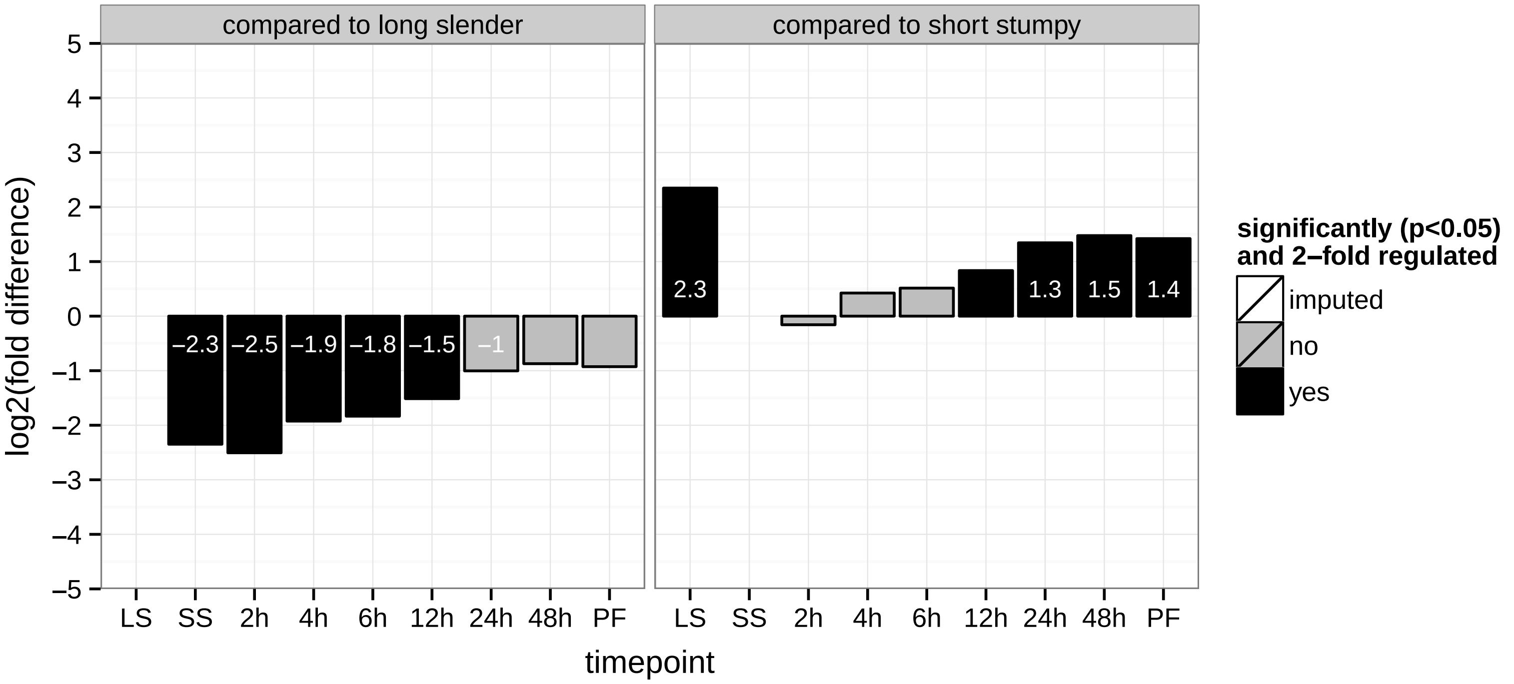
receptor–type adenylate cyclase GRESAG 4, pseudogene, putative, degenerate
Tb927.6.320
AGOF: phosphorus–oxygen lyase activity
AGOC: null
AGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction
PGOF: phosphorus–oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction

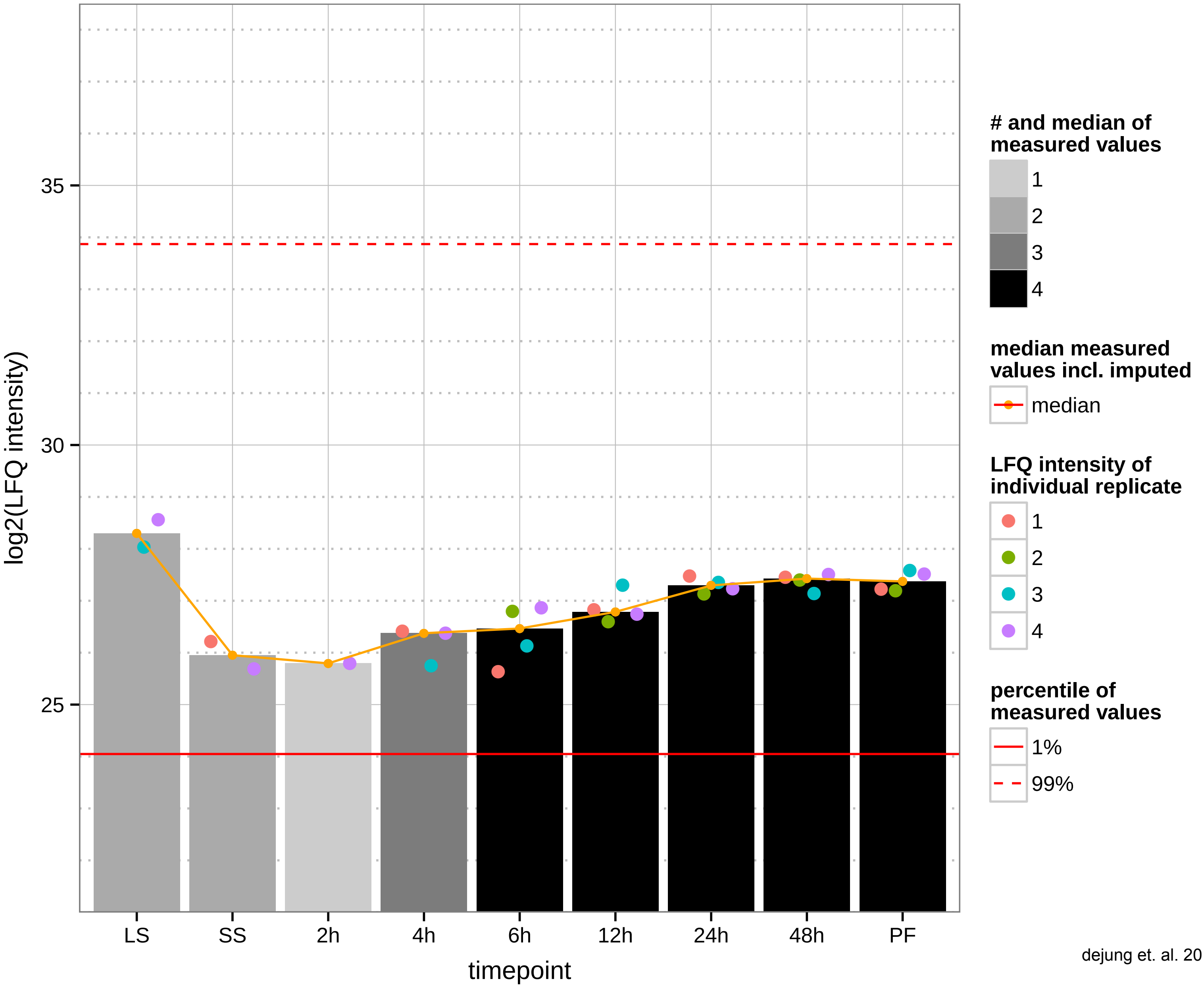




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.3250
AGOF: zinc ion binding
AGOC: intracellular
AGOP: null
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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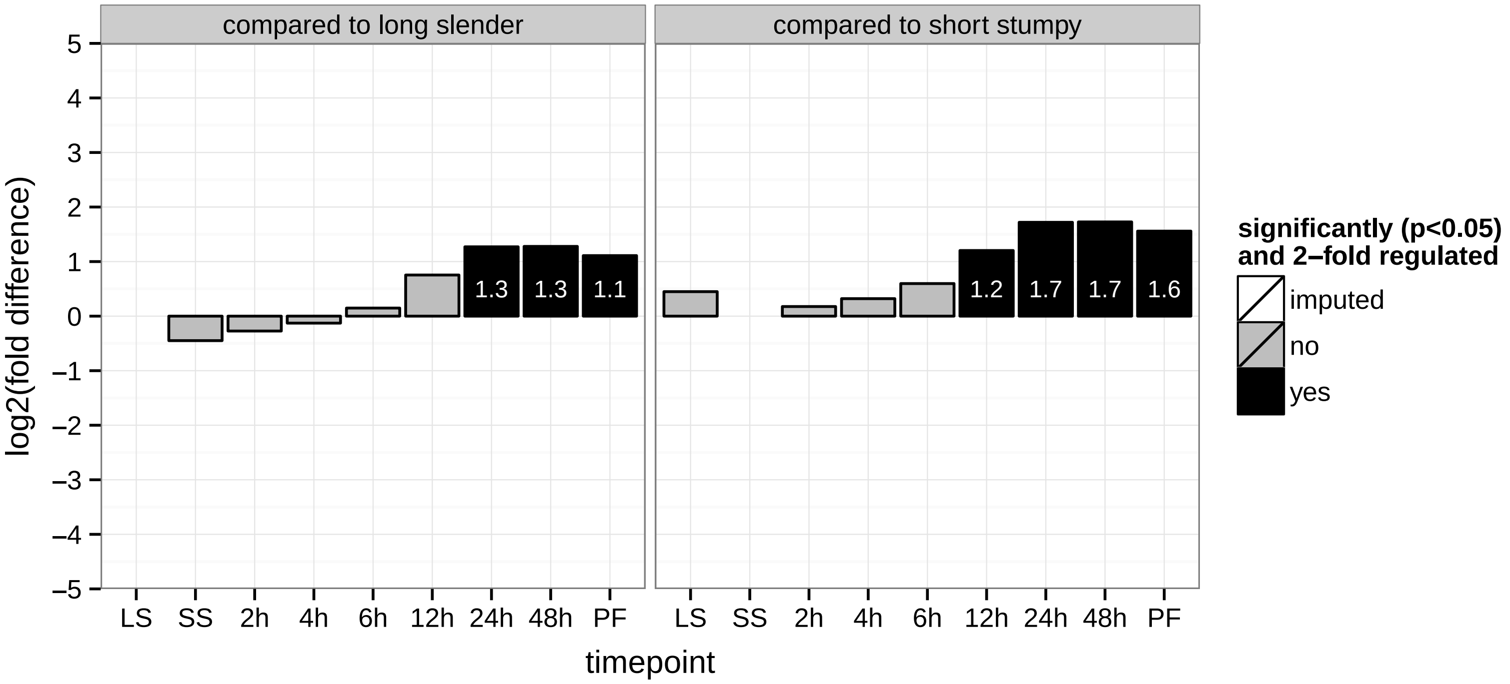
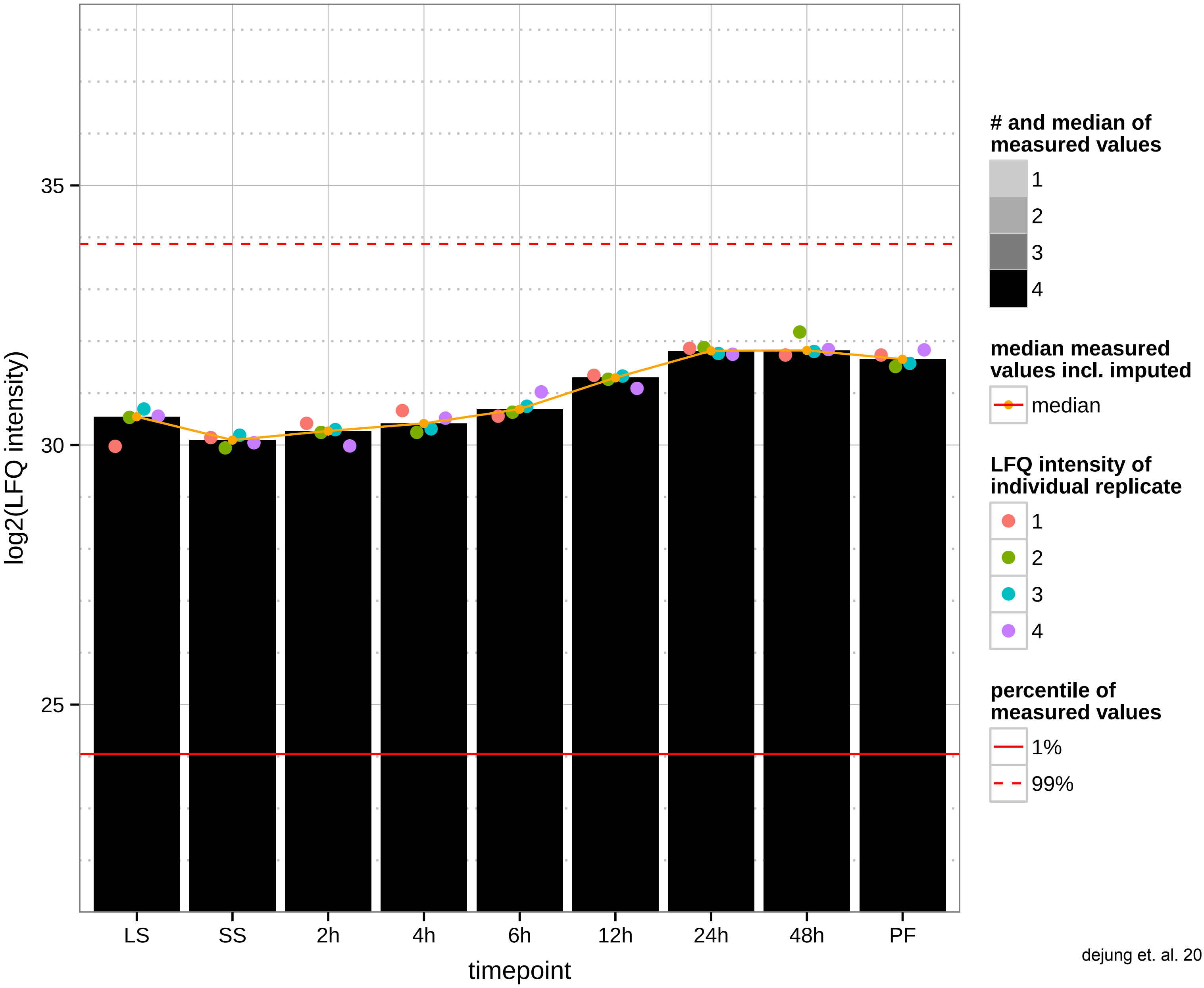
RNA–binding protein 42 (RNA–binding motif protein 42) (RBP42)
Tb927.6.4440
AGOF: RNA polymerase binding, mRNA binding
AGOC: polysome
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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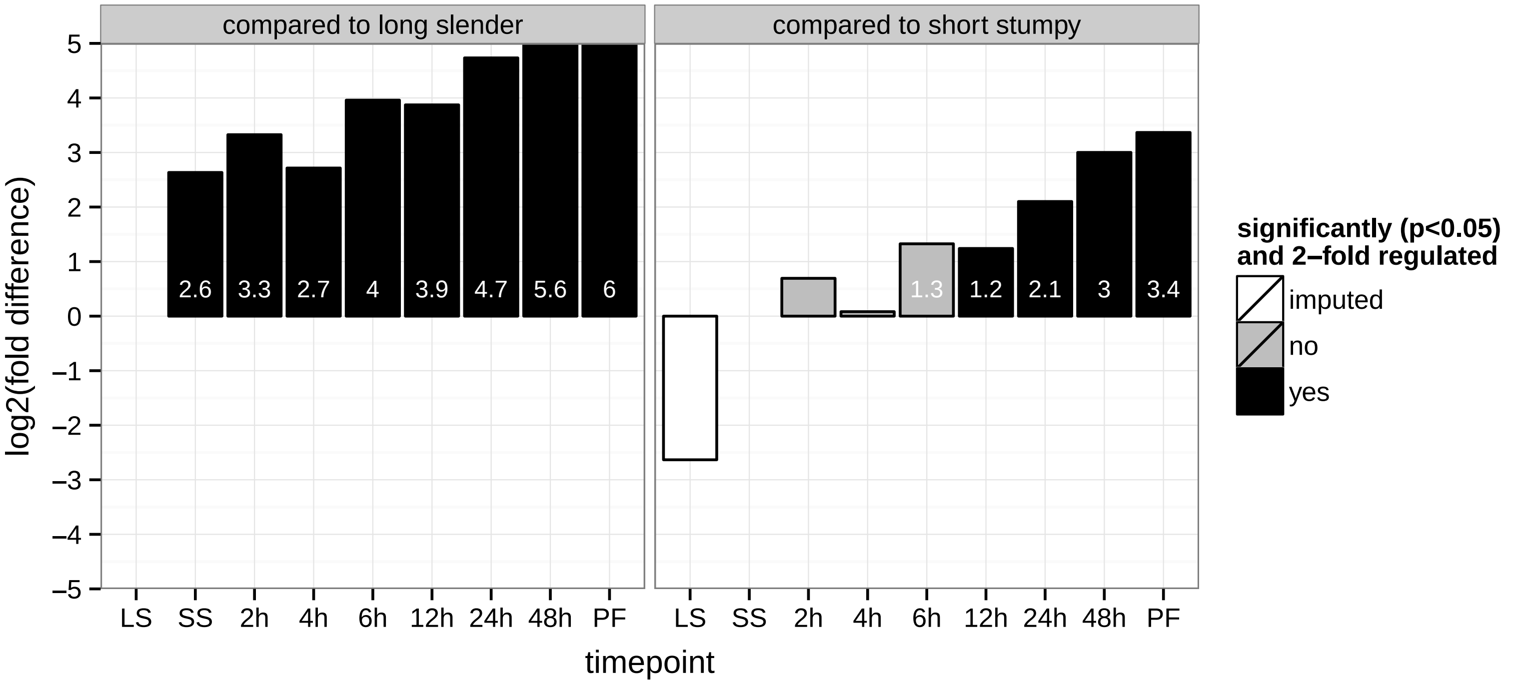
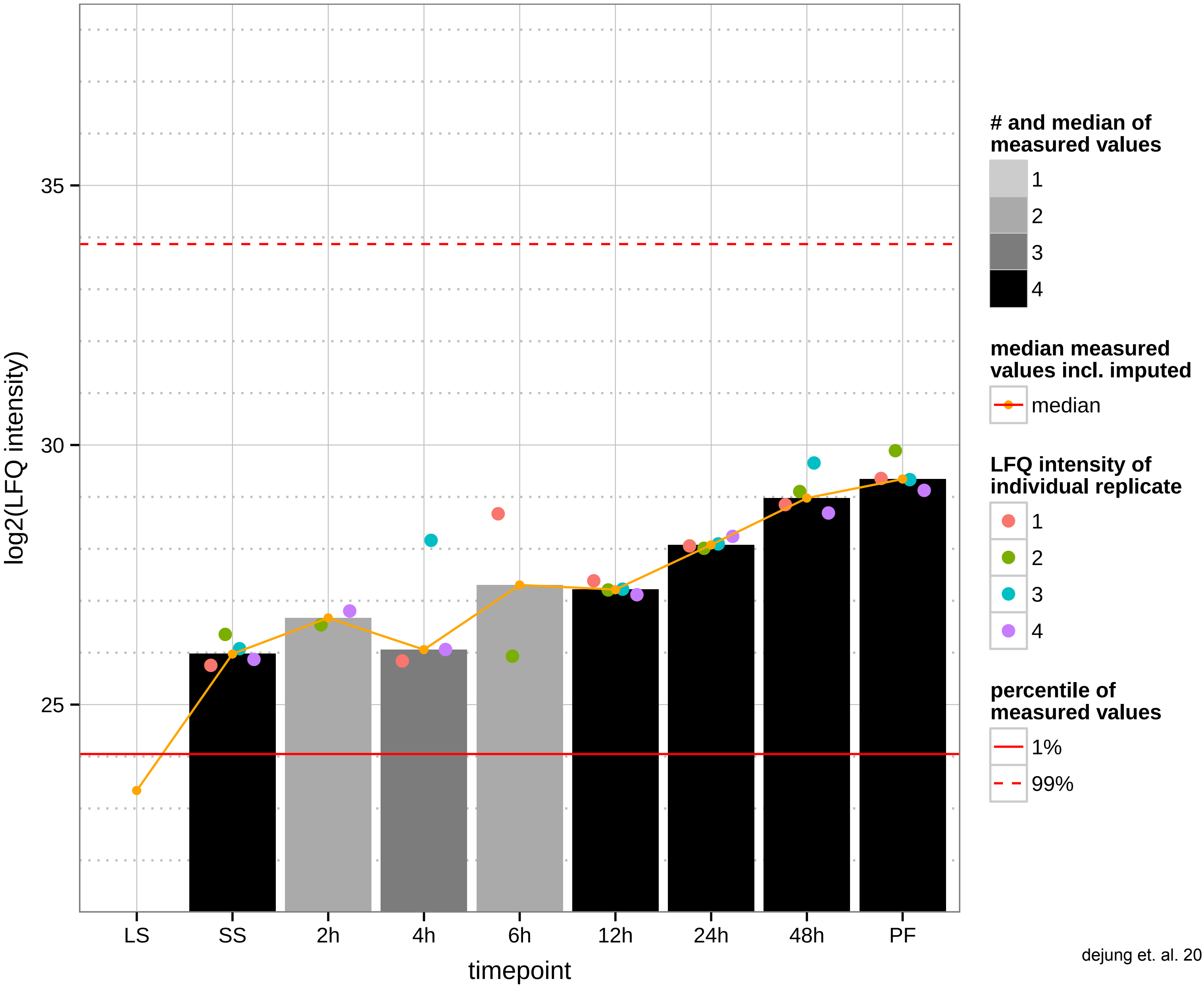
3–hydroxy–3–methylglutaryl–CoA reductase, putative
Tb927.6.4540
AGOF: NADP binding
AGOC: integral to membrane, mitochondrial inner membrane, mitochondrion
AGOP: coenzyme A metabolic process, oxidation–reduction process
PGOF: NADP binding, coenzyme binding, hydroxymethylglutaryl–CoA reductase (NADPH) activity, oxidoreductase activity, ac
PGOC: integral to membrane
PGOP: coenzyme A metabolic process, isoprenoid biosynthetic process, oxidation–reduction process





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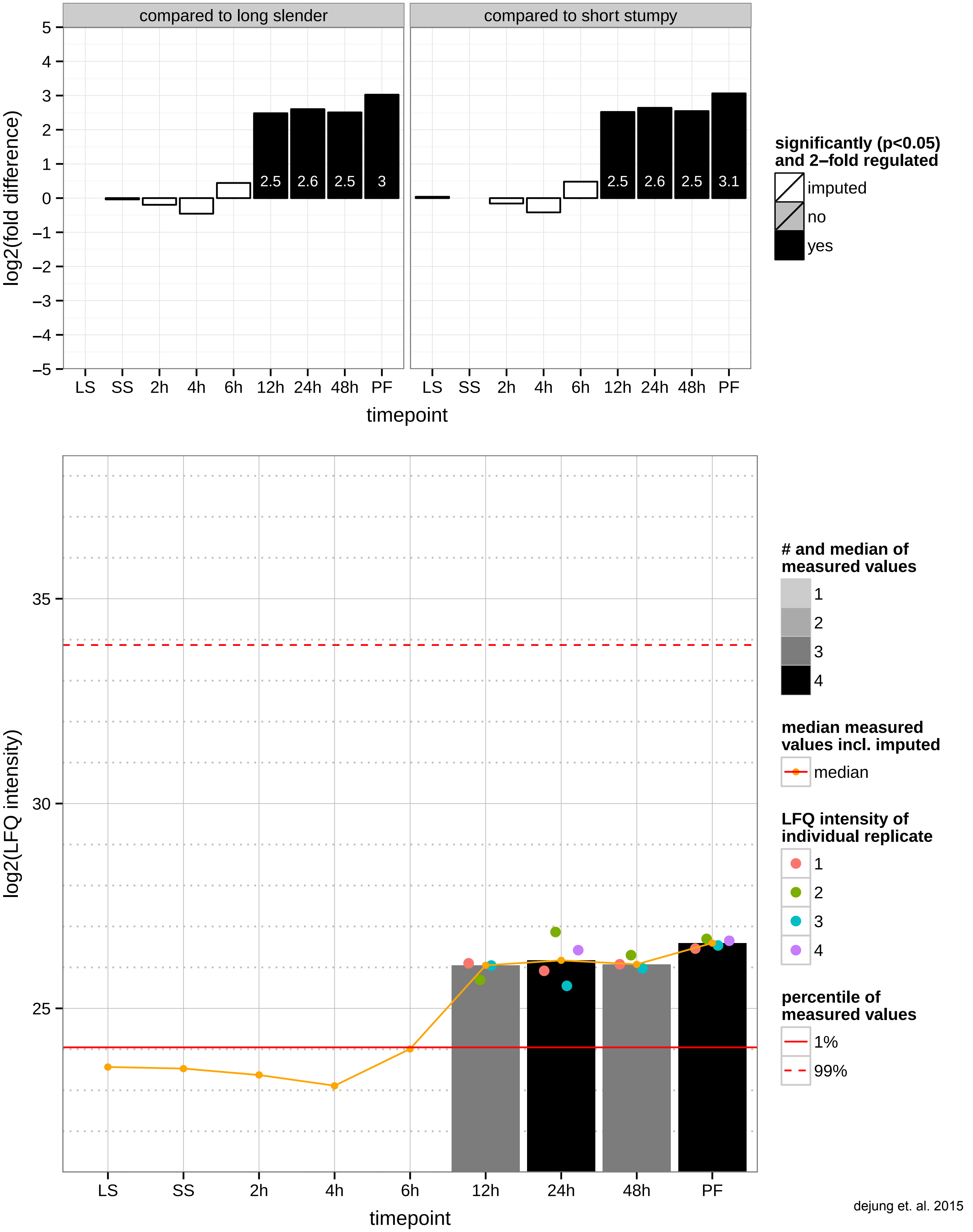
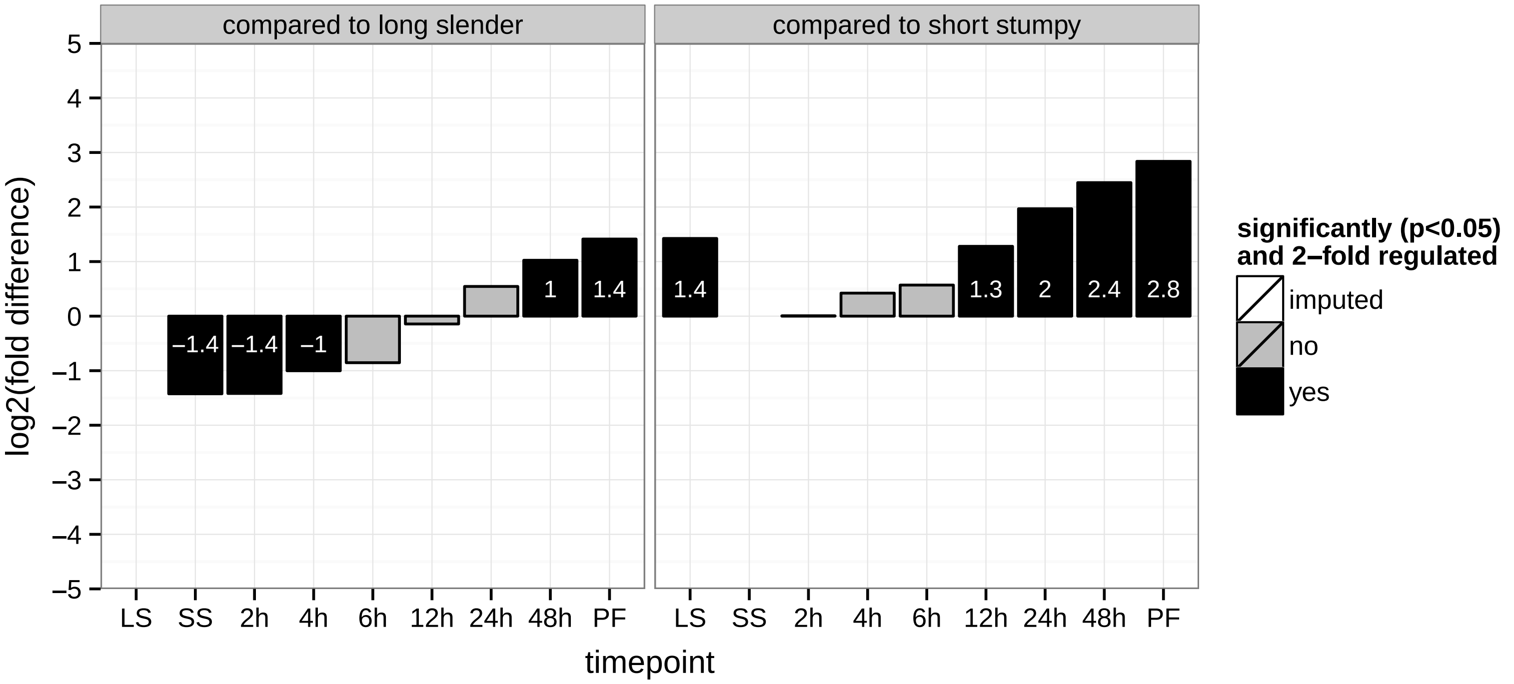
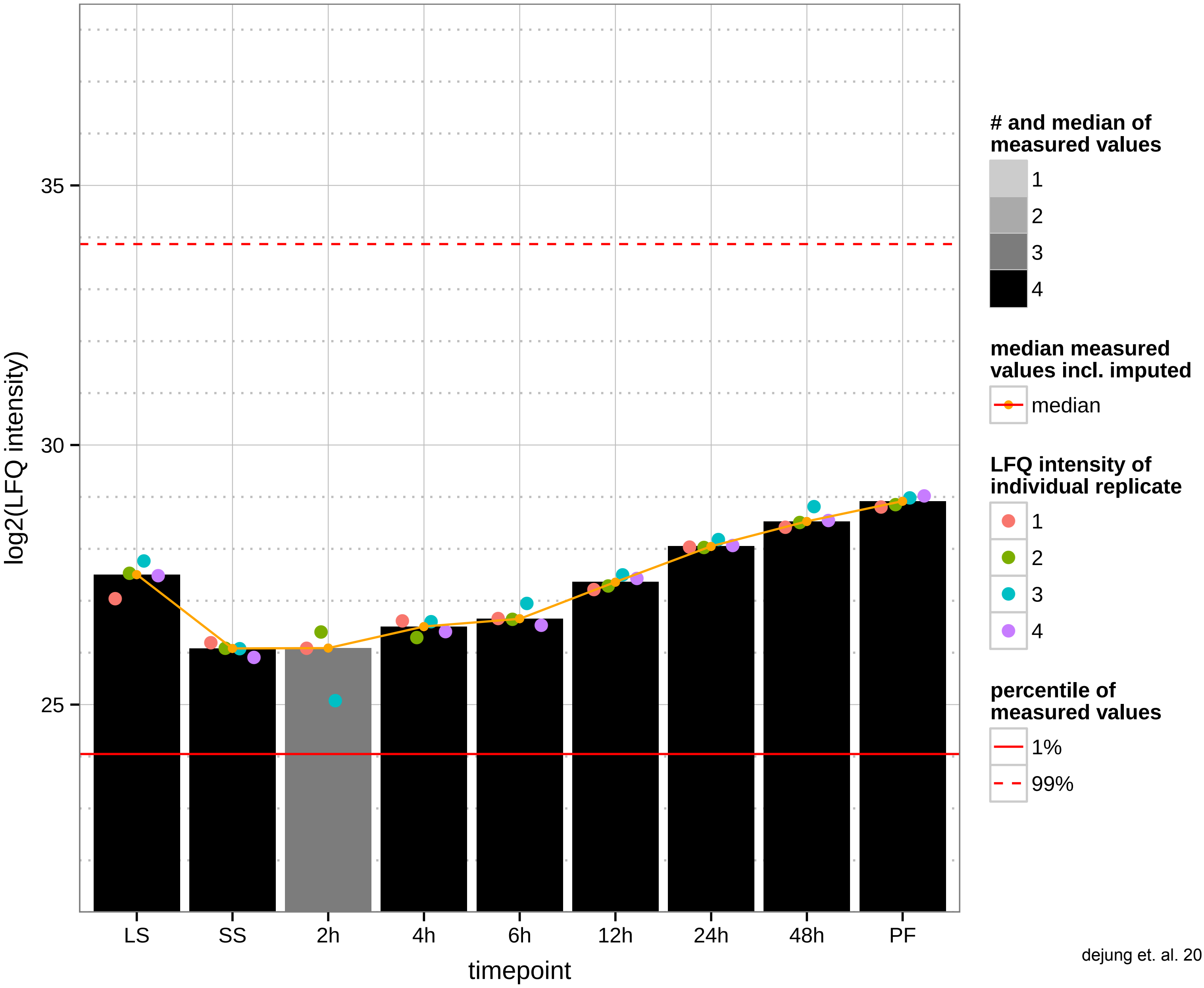
hypothetical protein, conserved
Tb927.6.4560
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



hypothetical protein, conserved
Tb927.6.4800
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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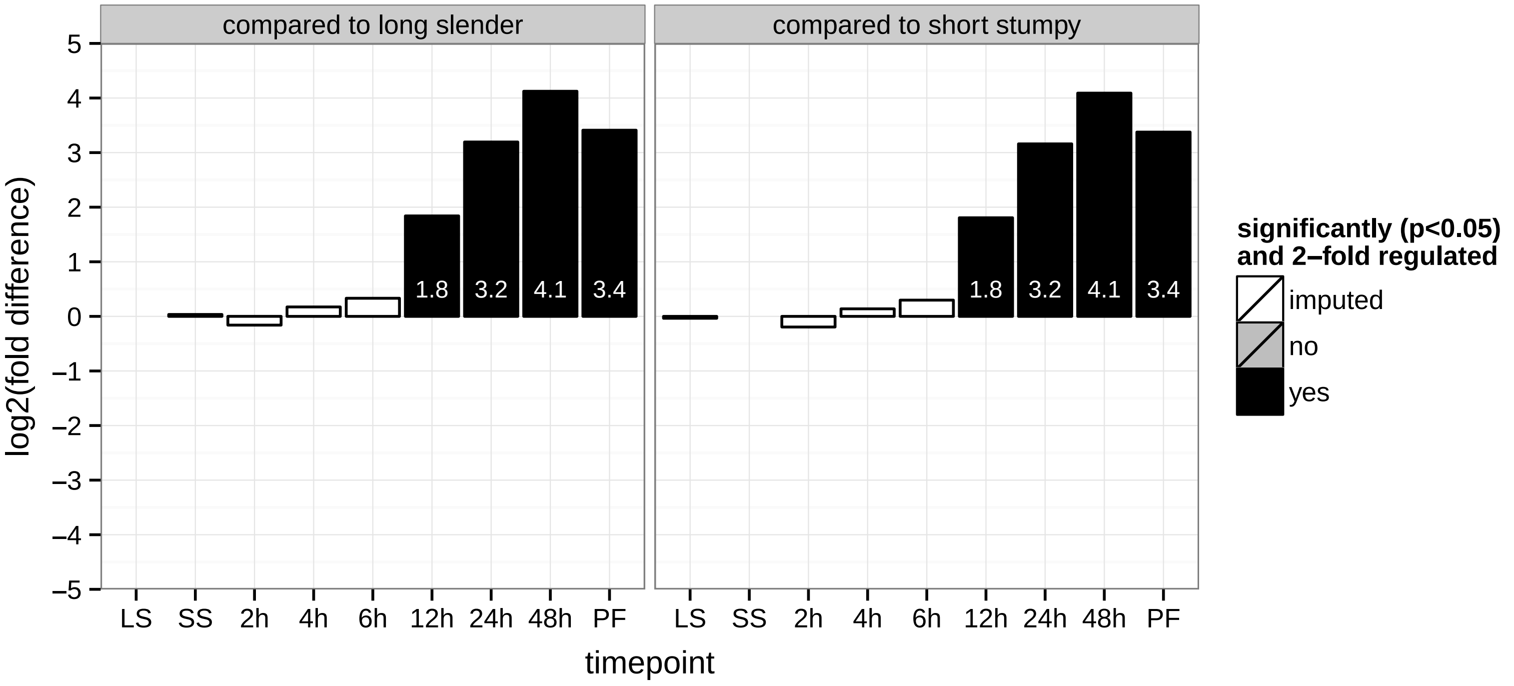
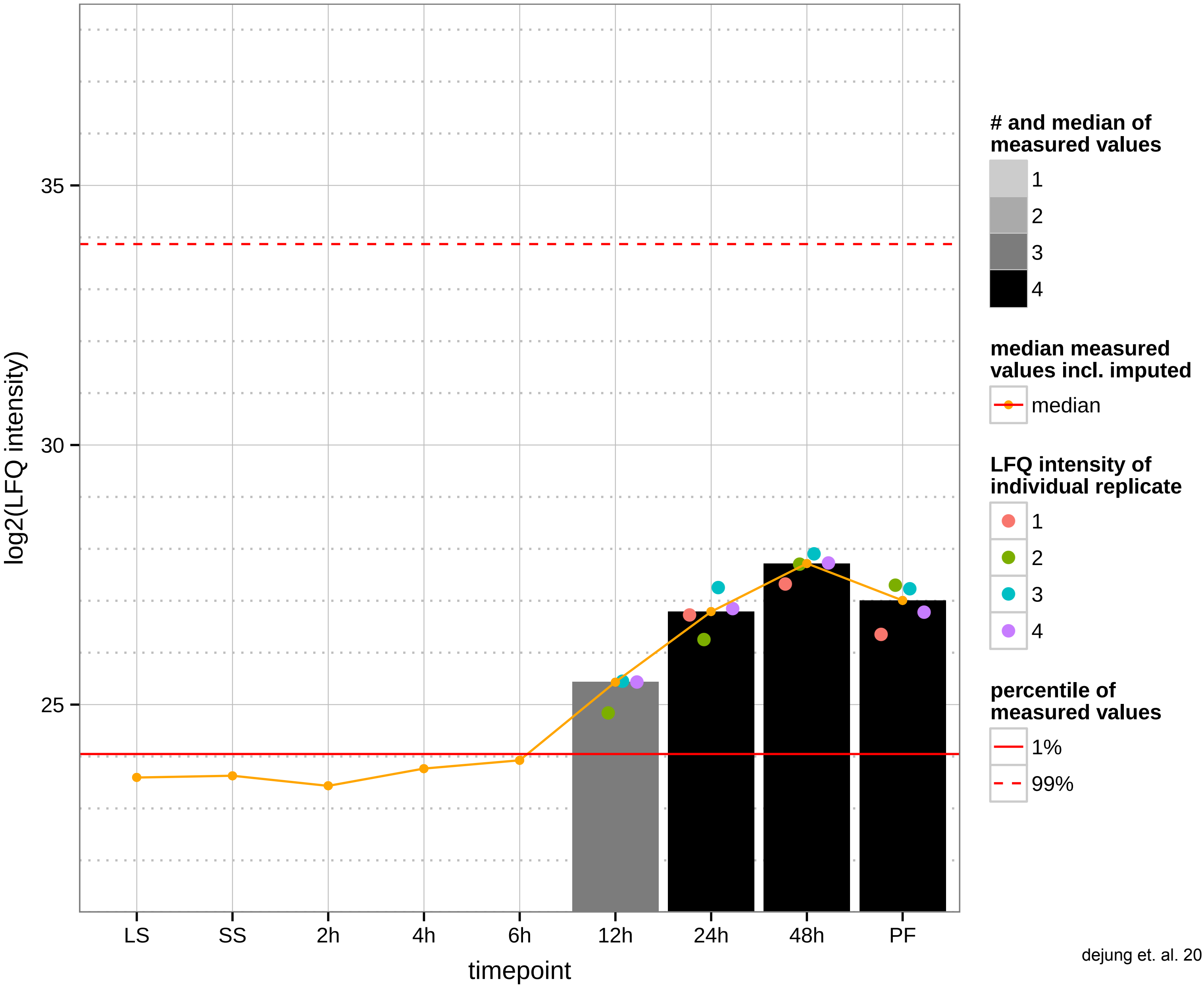
hypothetical protein, conserved
Tb927.6.5090
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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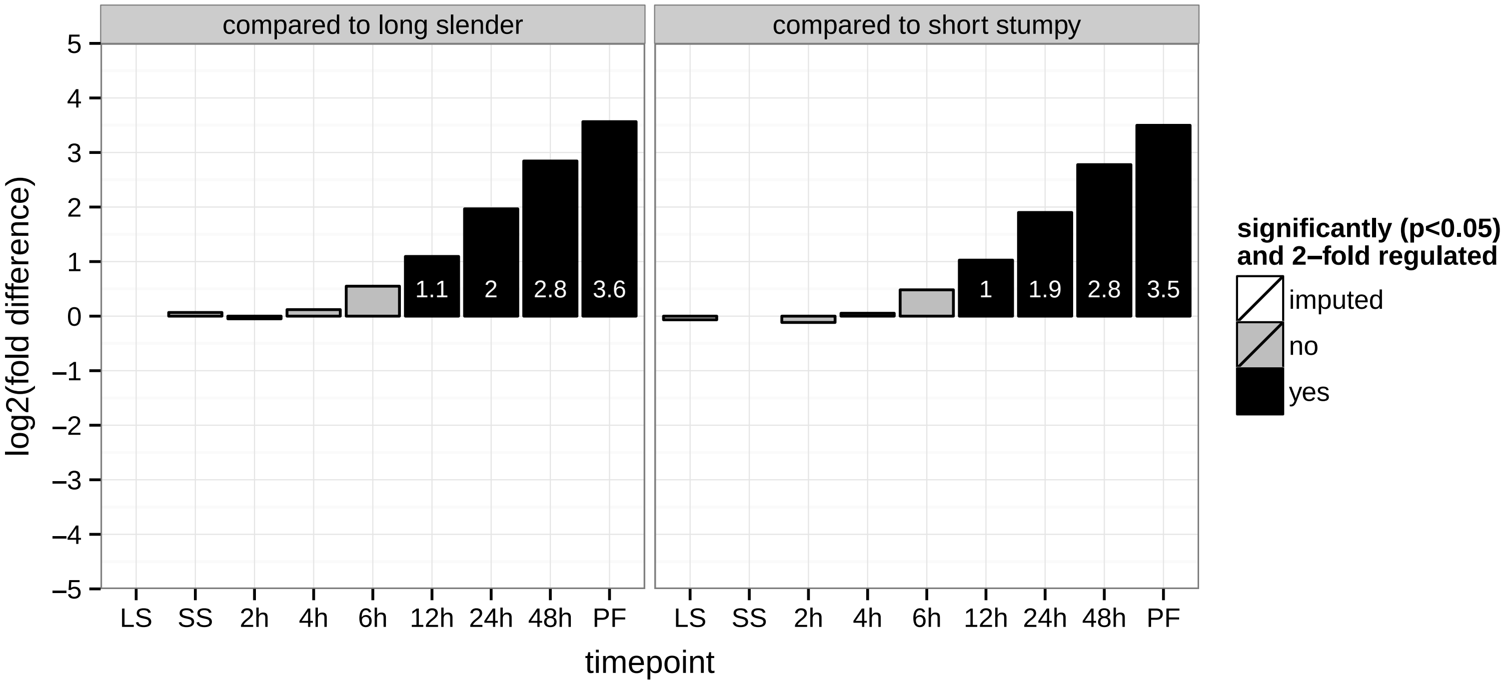
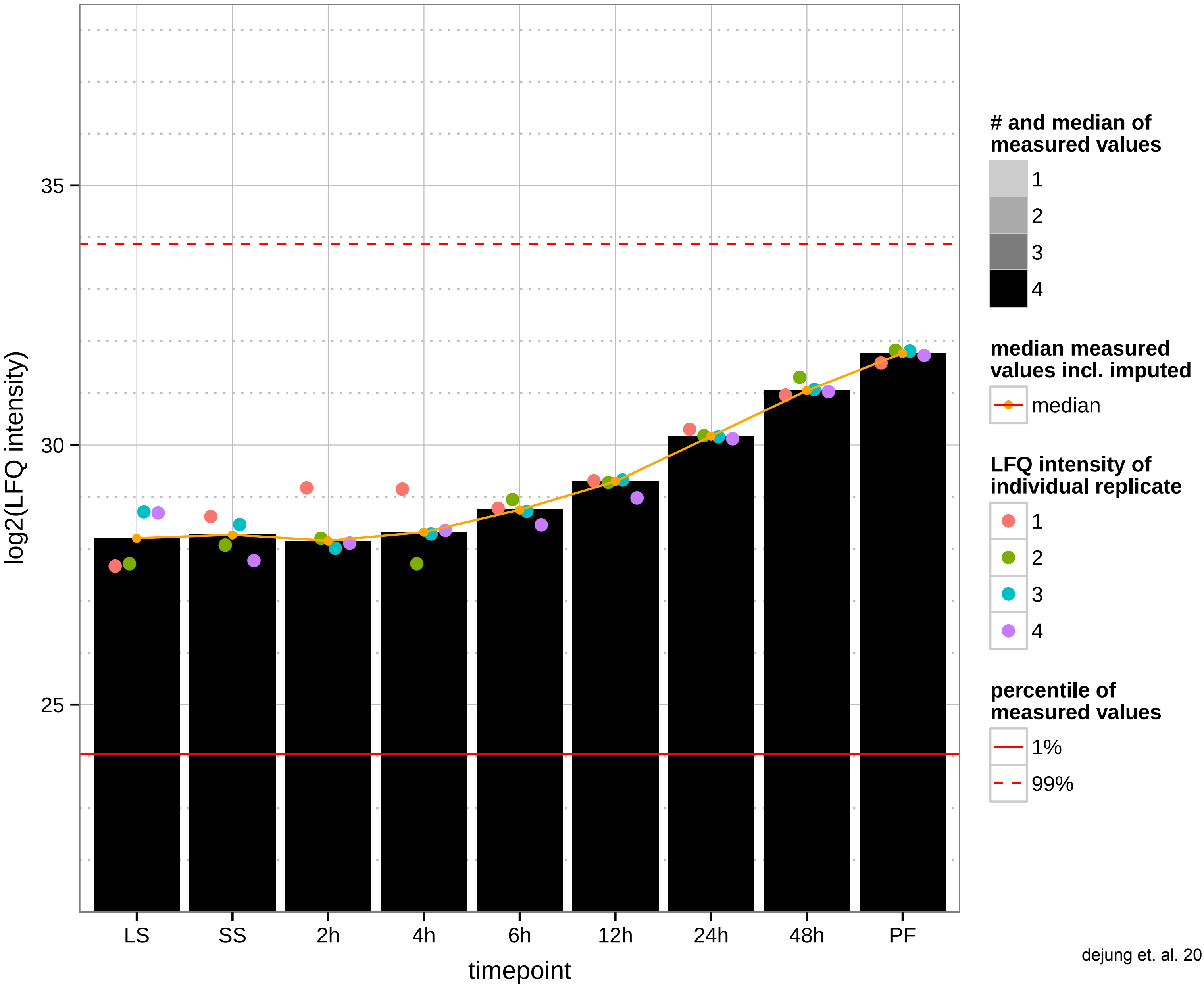
thimet oligopeptidase, putative (THOP1)
Tb927.7.190
AGOF: metalloendopeptidase activity
AGOC: null
AGOP: intracellular signal transduction, proteolysis
PGOF: metalloendopeptidase activity
PGOC: null
PGOP: proteolysis





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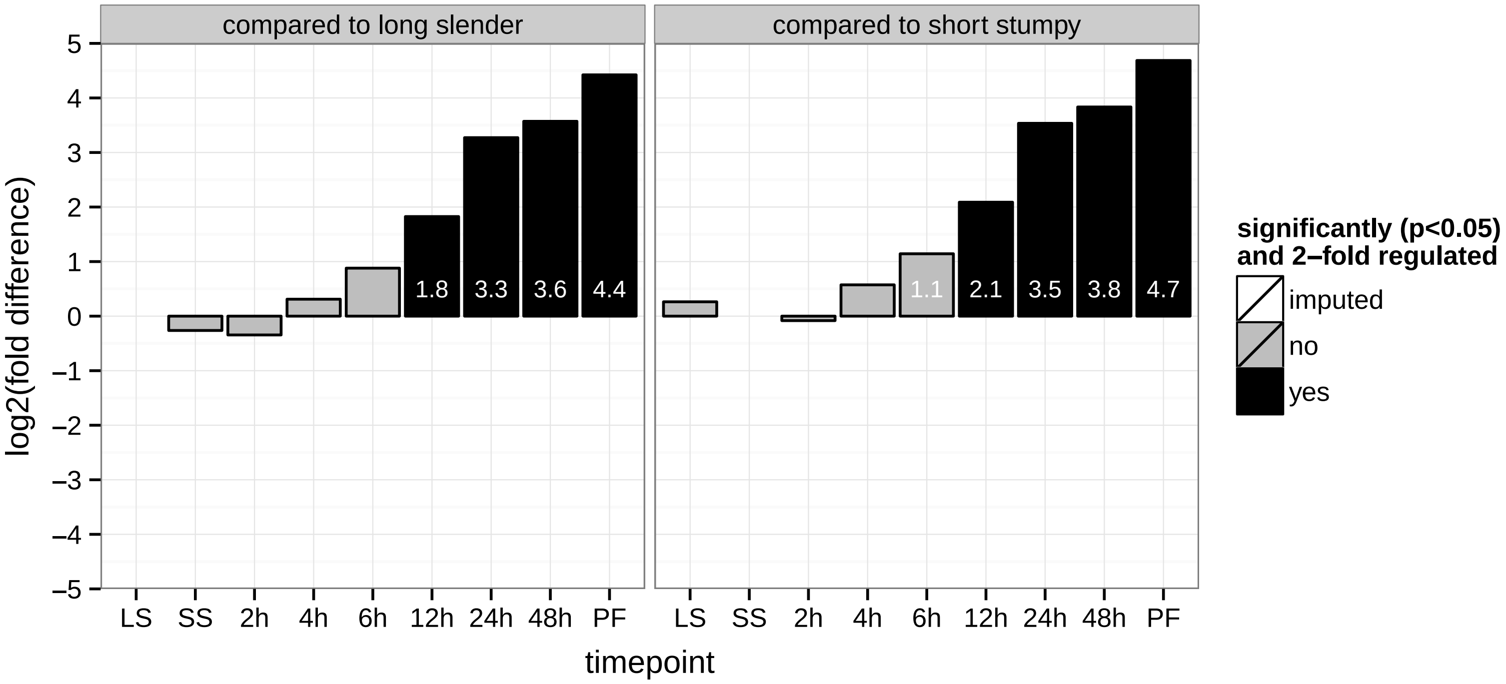
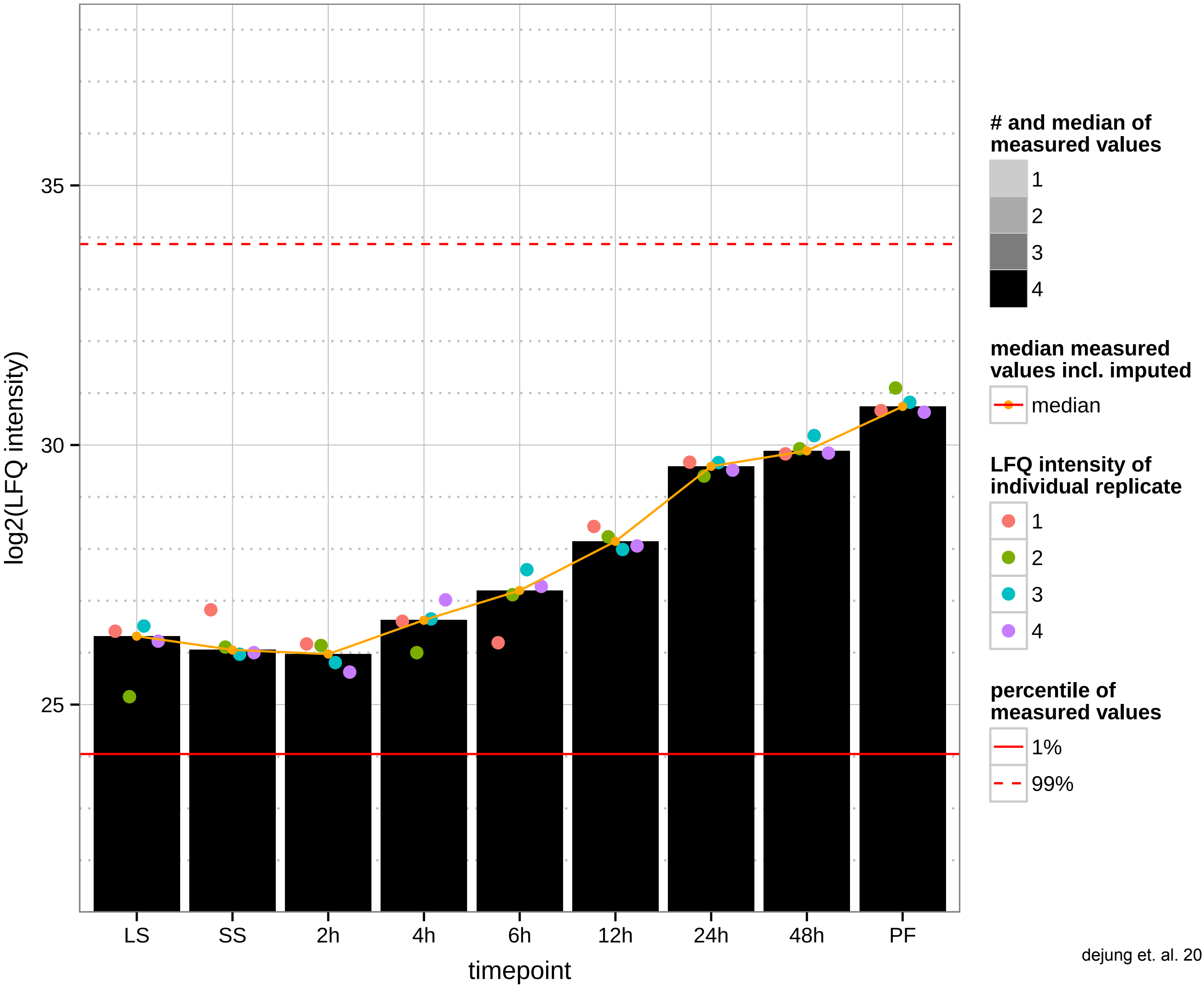
glutathione−S−transferase/glutaredoxin, putative
Tb927.7.3500
AGOF: electron carrier activity, protein disulfide oxidoreductase activity
AGOC: null
AGOP: cell redox homeostasis
PGOF: electron carrier activity, protein disulfide oxidoreductase activity
PGOC: null
PGOP: cell redox homeostasis





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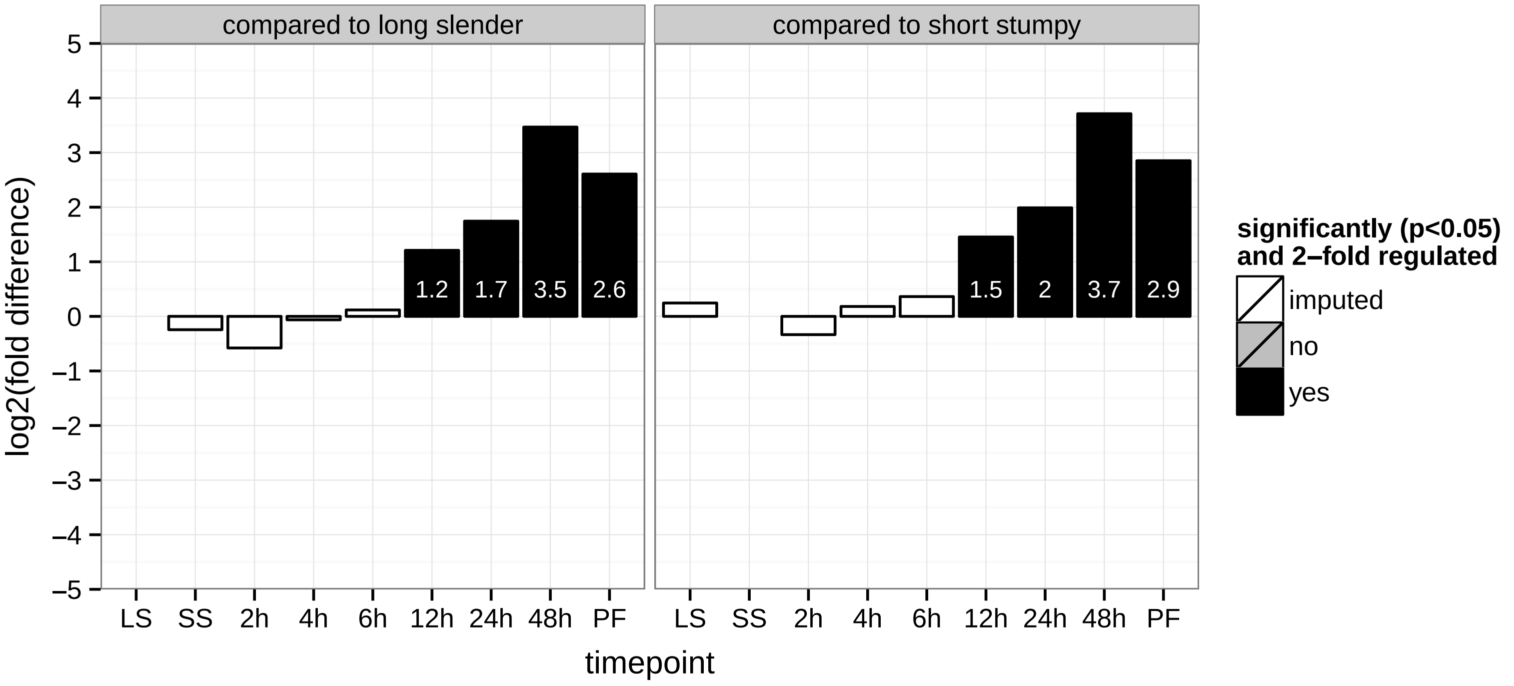
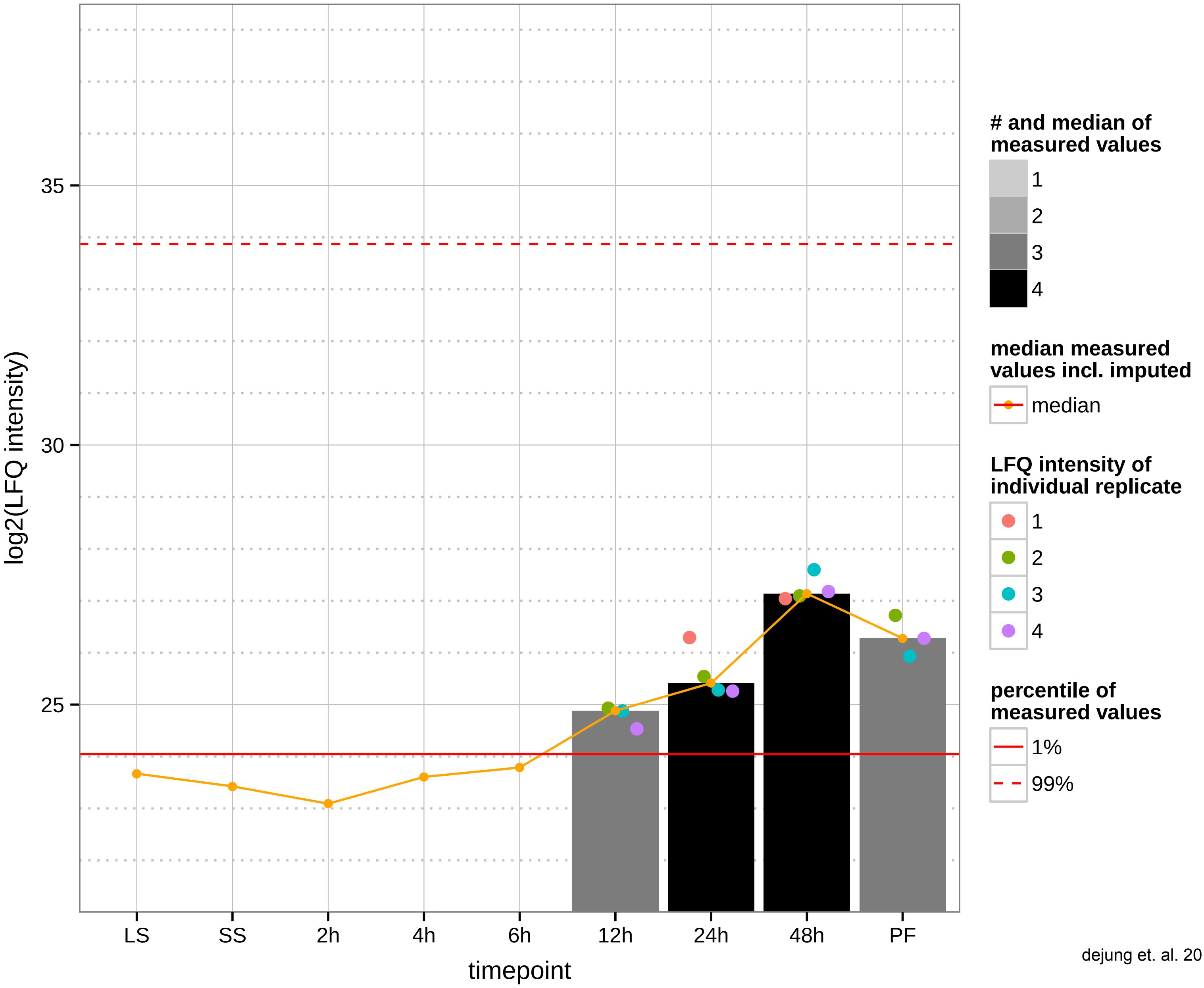
fatty acid elongase, putative
Tb927.7.4160
AGOF: fatty acid elongase activity
AGOC: integral to endoplasmic reticulum membrane
AGOP: long–chain fatty acid biosynthetic process
PGOF: null
PGOC: integral to membrane
PGOP: null





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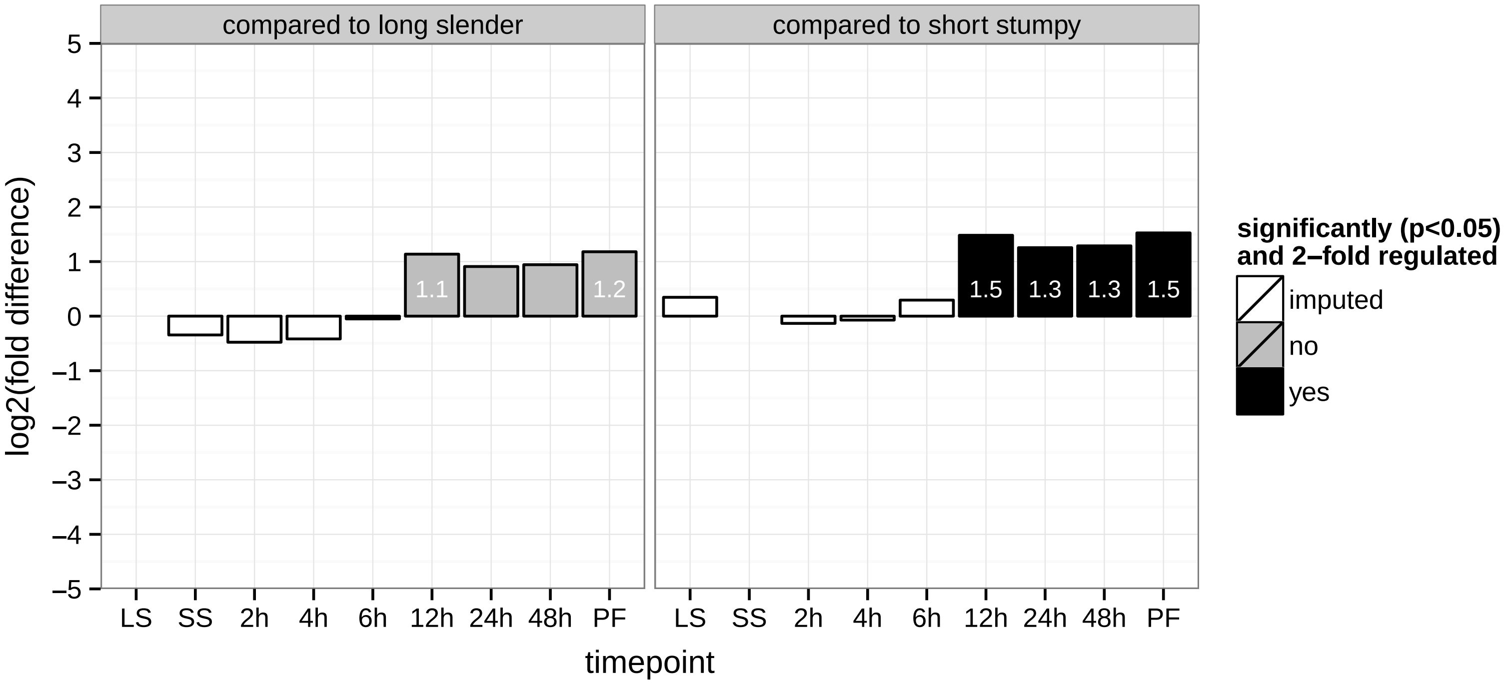
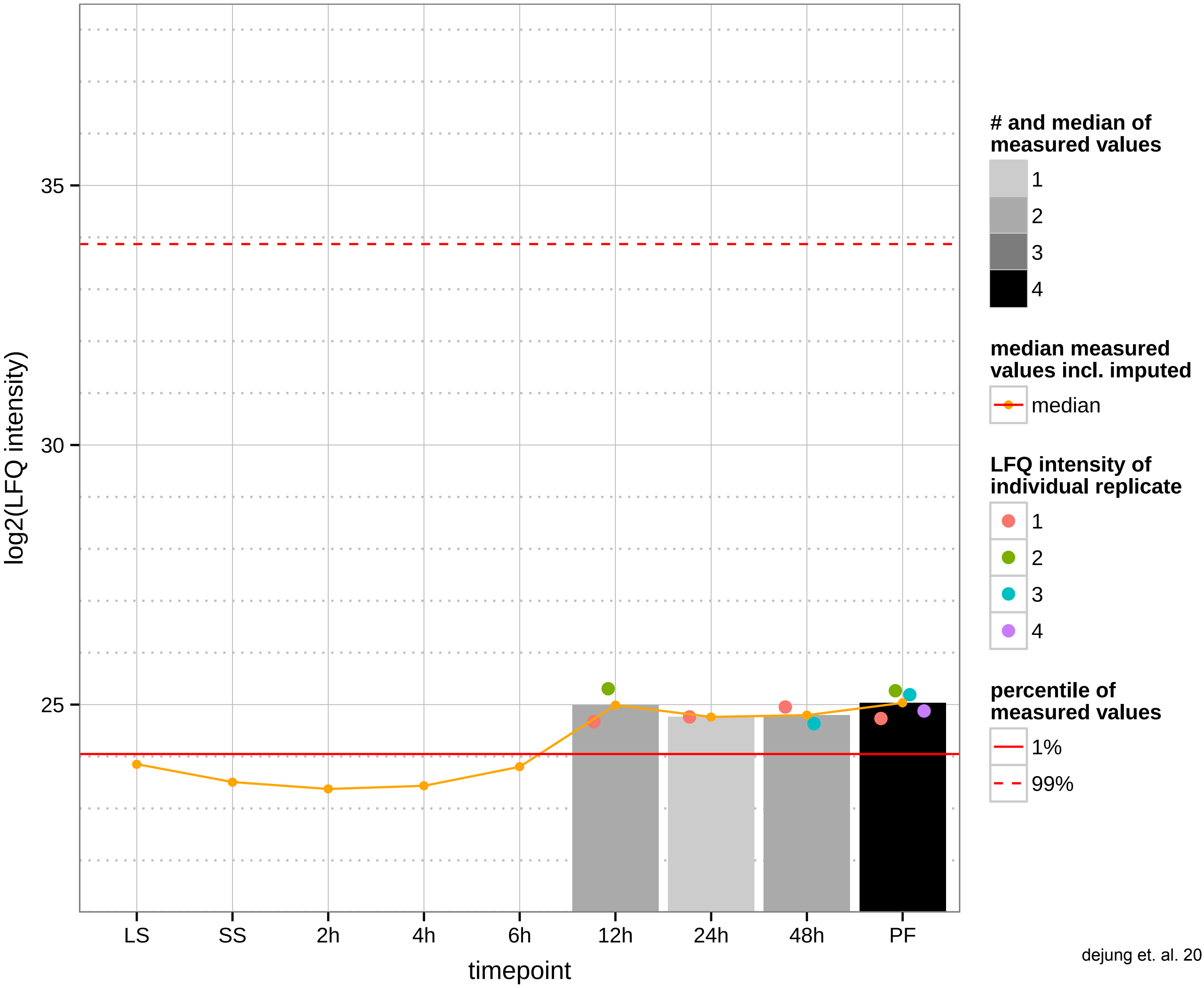
hypothetical protein, conserved
Tb927.7.5140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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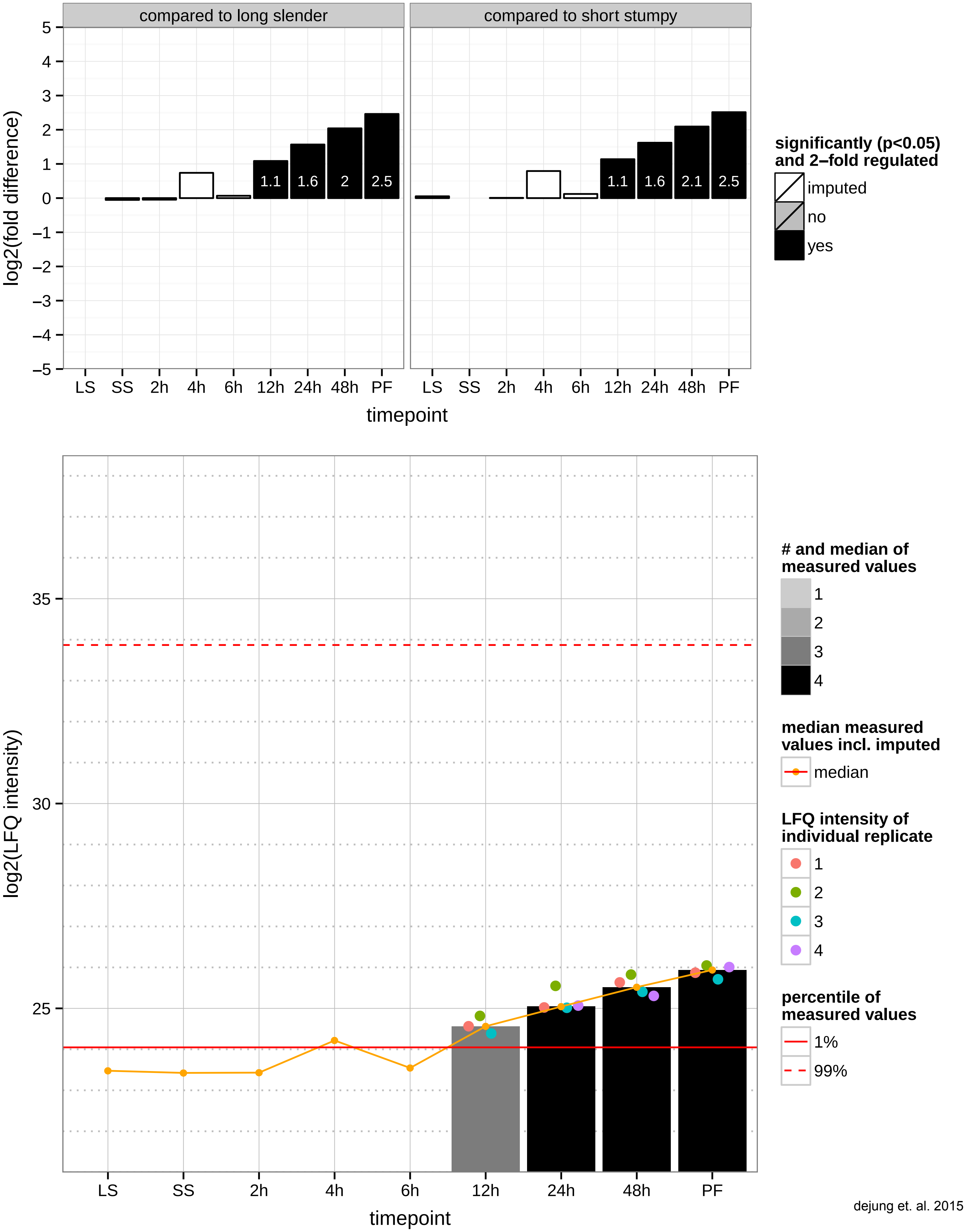
chaperone protein DNAj, putative
Tb927.7.6200
AGOF: heat shock protein binding, unfolded protein binding
AGOC: integral to membrane, mitochondrial inner membrane, mitochondrion
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null



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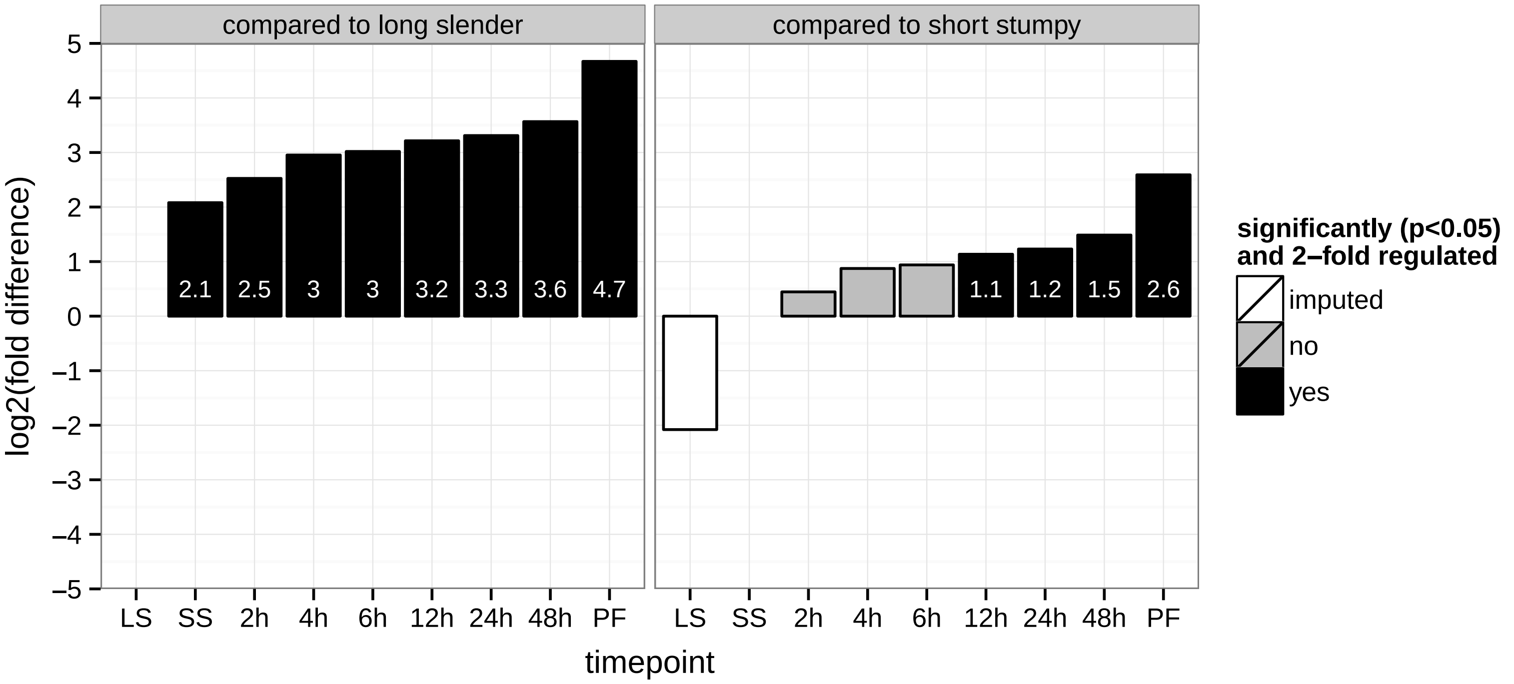
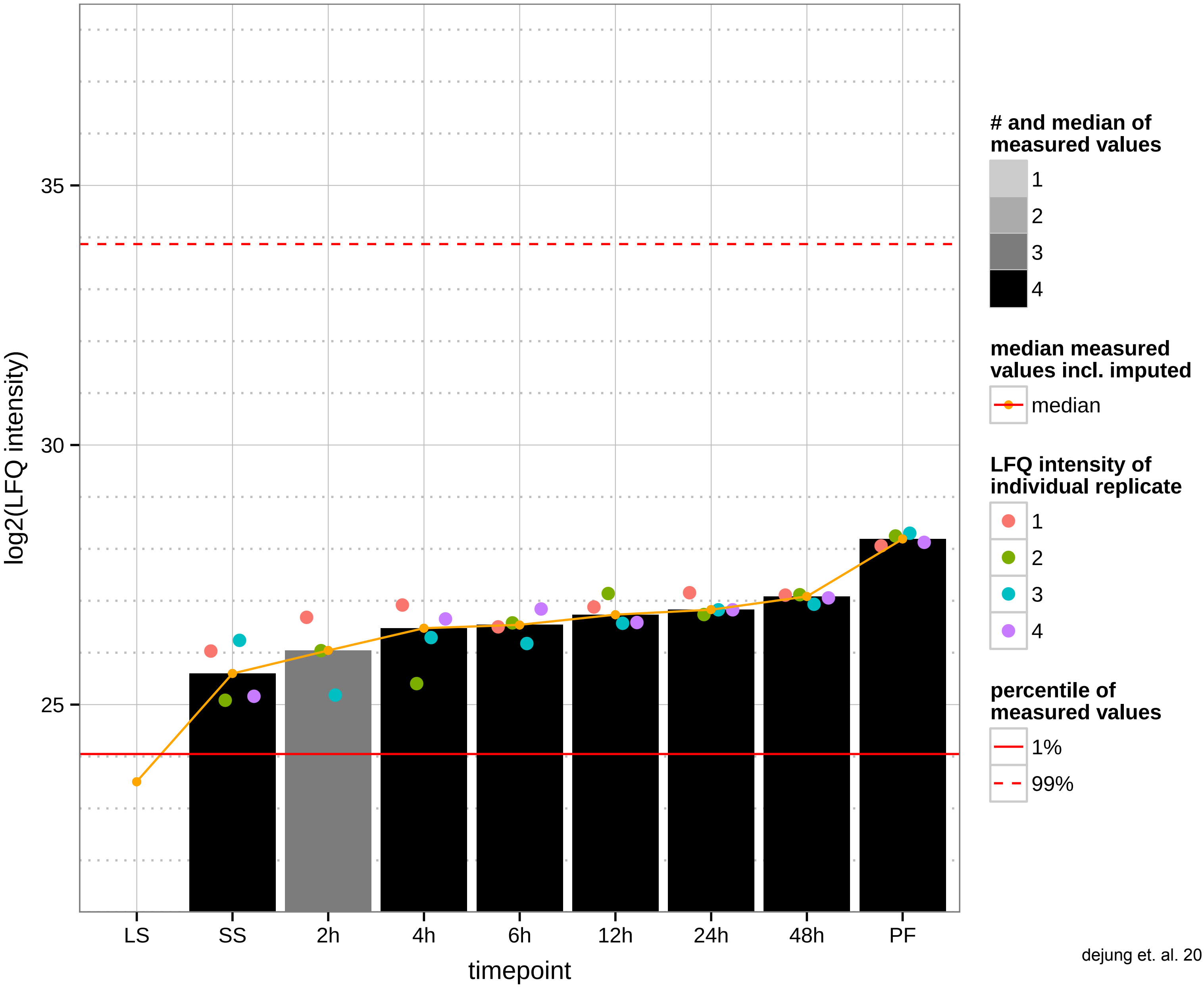
peptidase t, putative, aminotripeptidase
Tb927.7.6270
AGOF: hydrolase activity, metallopeptidase activity, protein dimerization activity, tripeptide aminopeptidase activity, zinc ion bir
AGOC: cytoplasm
AGOP: peptide metabolic process, proteolysis
PGOF: hydrolase activity, tripeptide aminopeptidase activity, zinc ion binding
PGOC: cytoplasm
PGOP: metabolic process, peptide metabolic process





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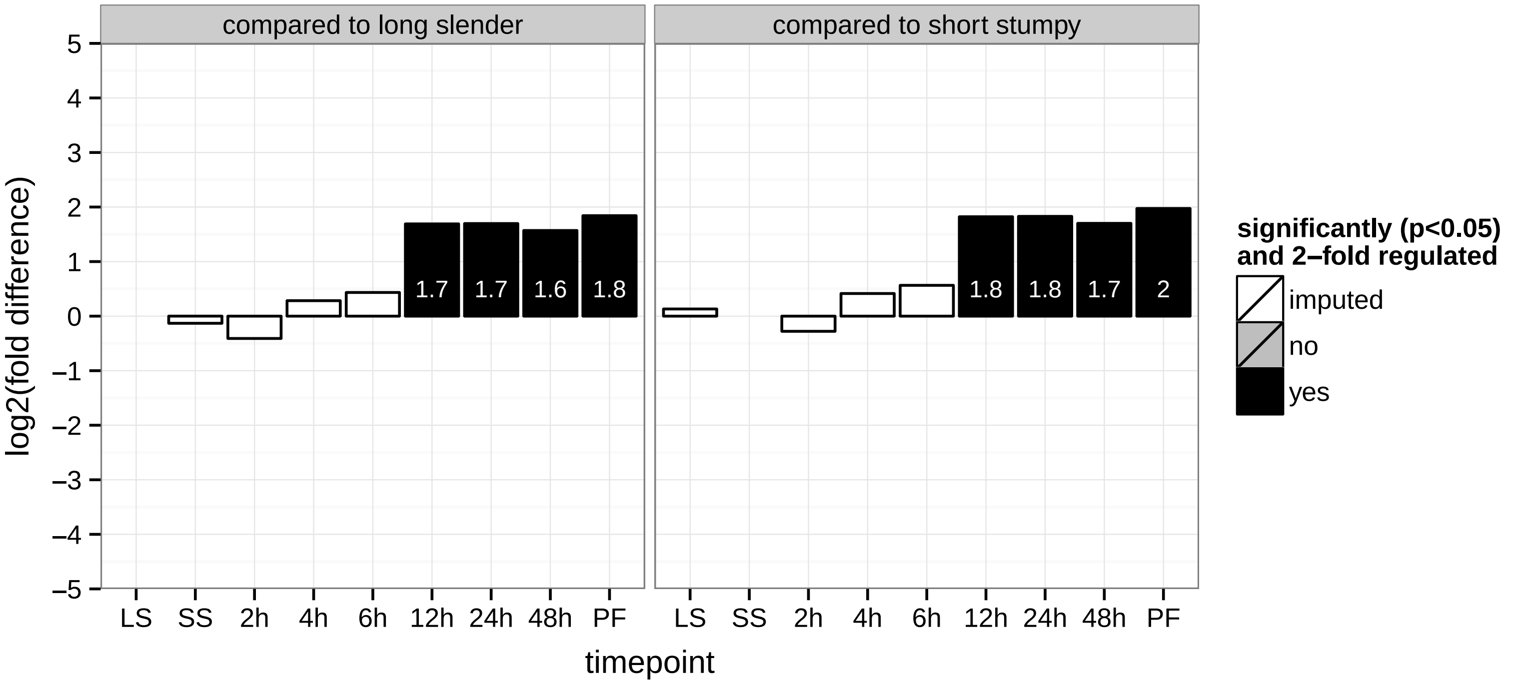
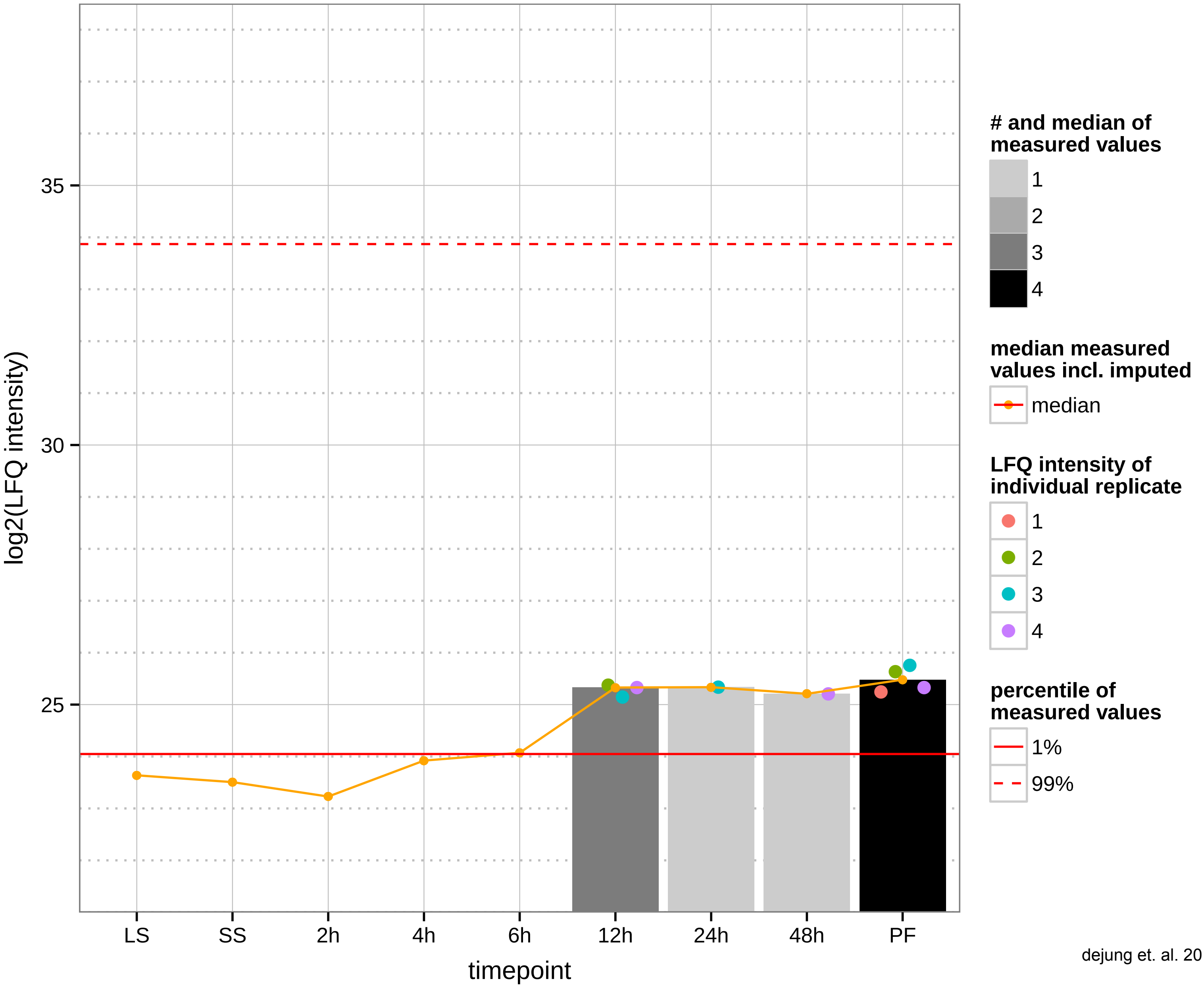
O–sialoglycoprotein endopeptidase, putative, metallo–peptidase, Clan MK, Family M67
Tb927.7.6470
AGOF: metalloendopeptidase activity, zinc ion binding
AGOC: null
AGOP: proteolysis
PGOF: metalloendopeptidase activity
PGOC: null
PGOP: proteolysis





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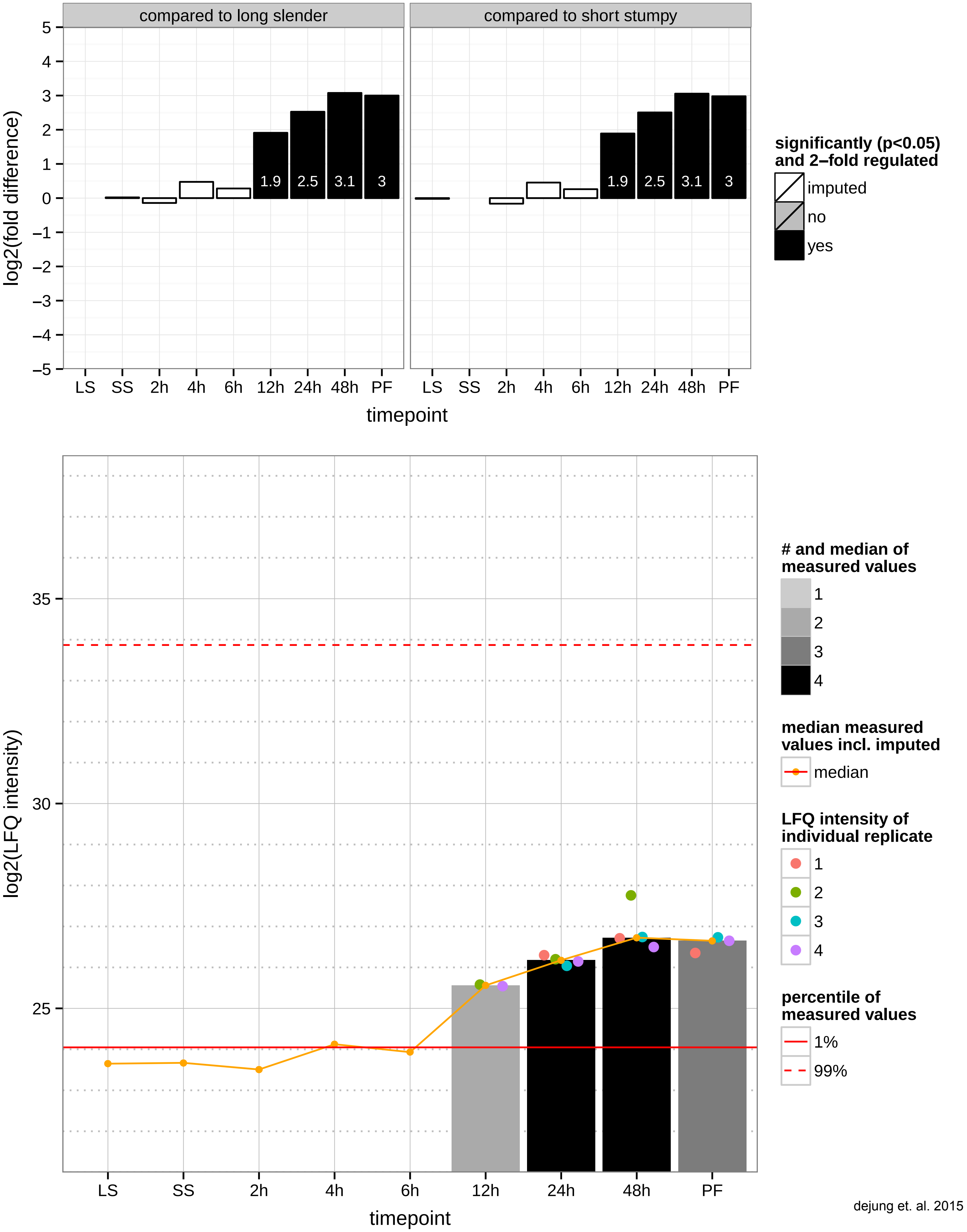
hypothetical protein, conserved
Tb927.7.6790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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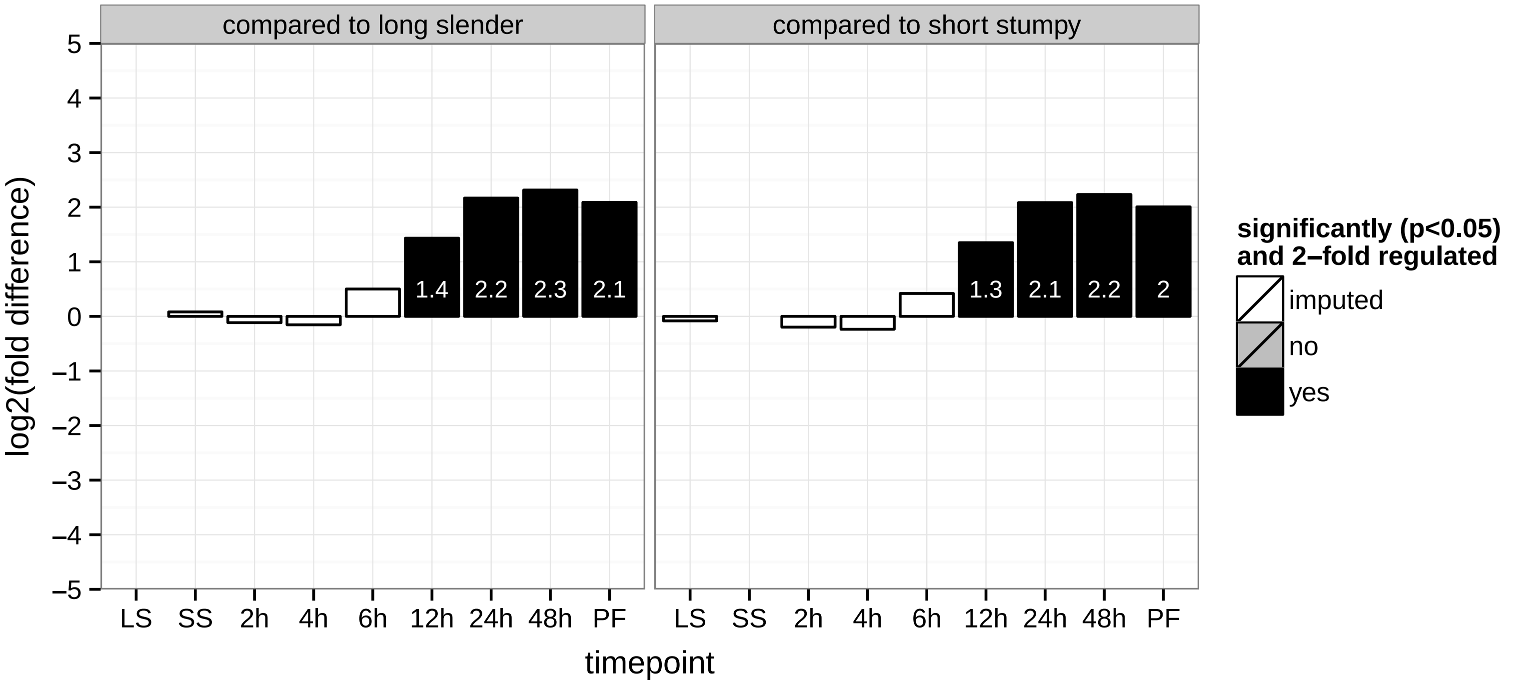
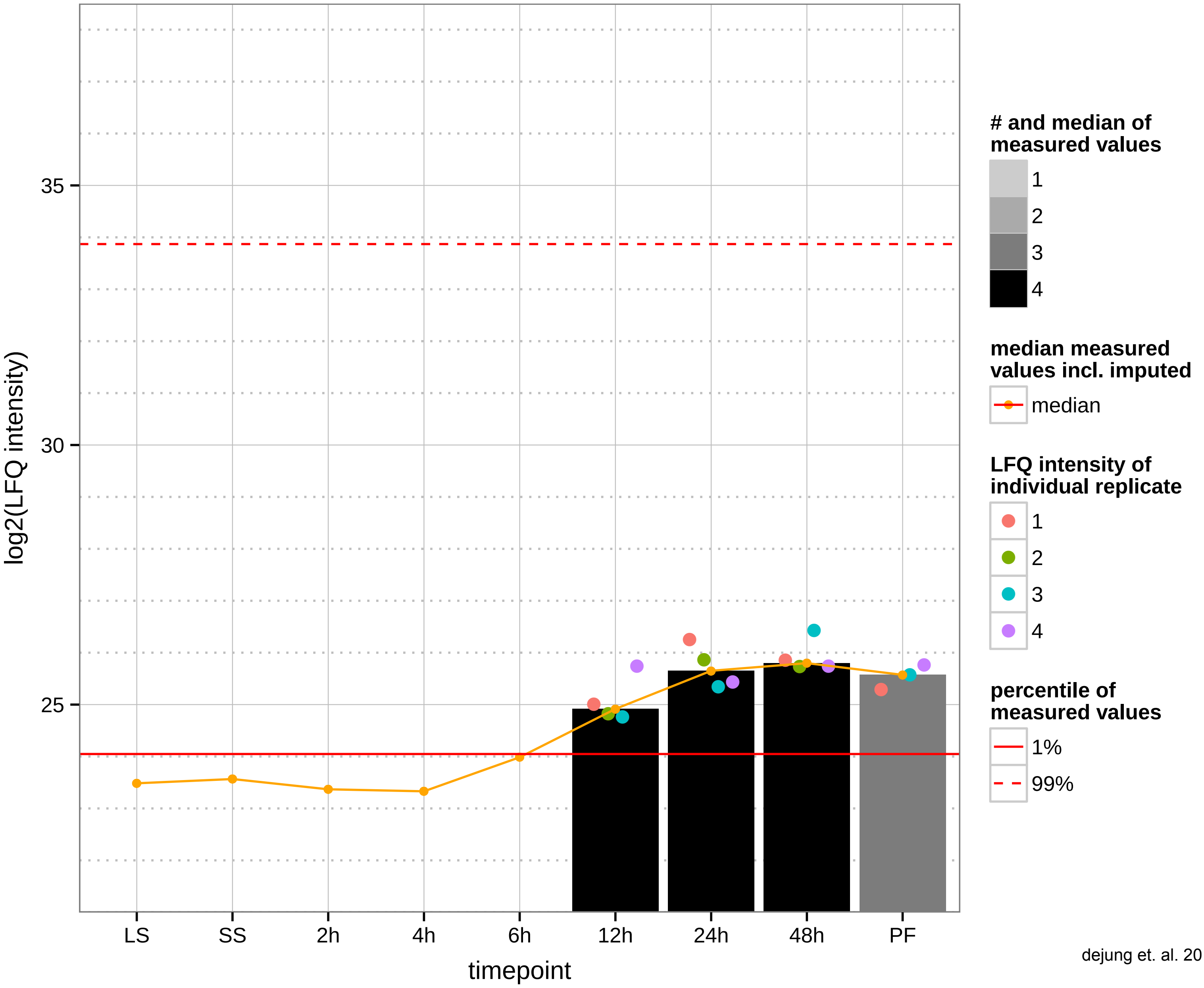
leucine−rich repeat protein (LRRP), putative, leucine−rich repeat protein 1 (LRRP1)
Tb927.7.7180;Tb927.7.7110
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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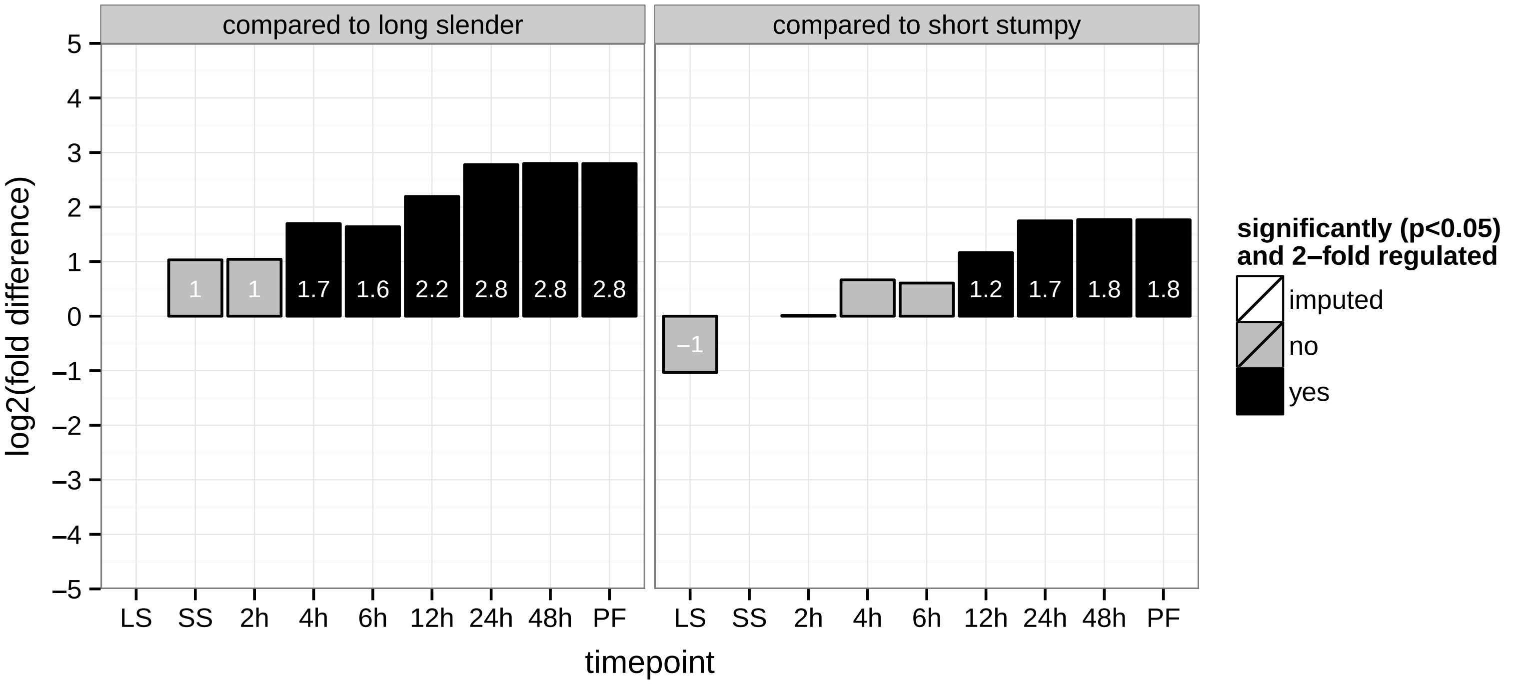
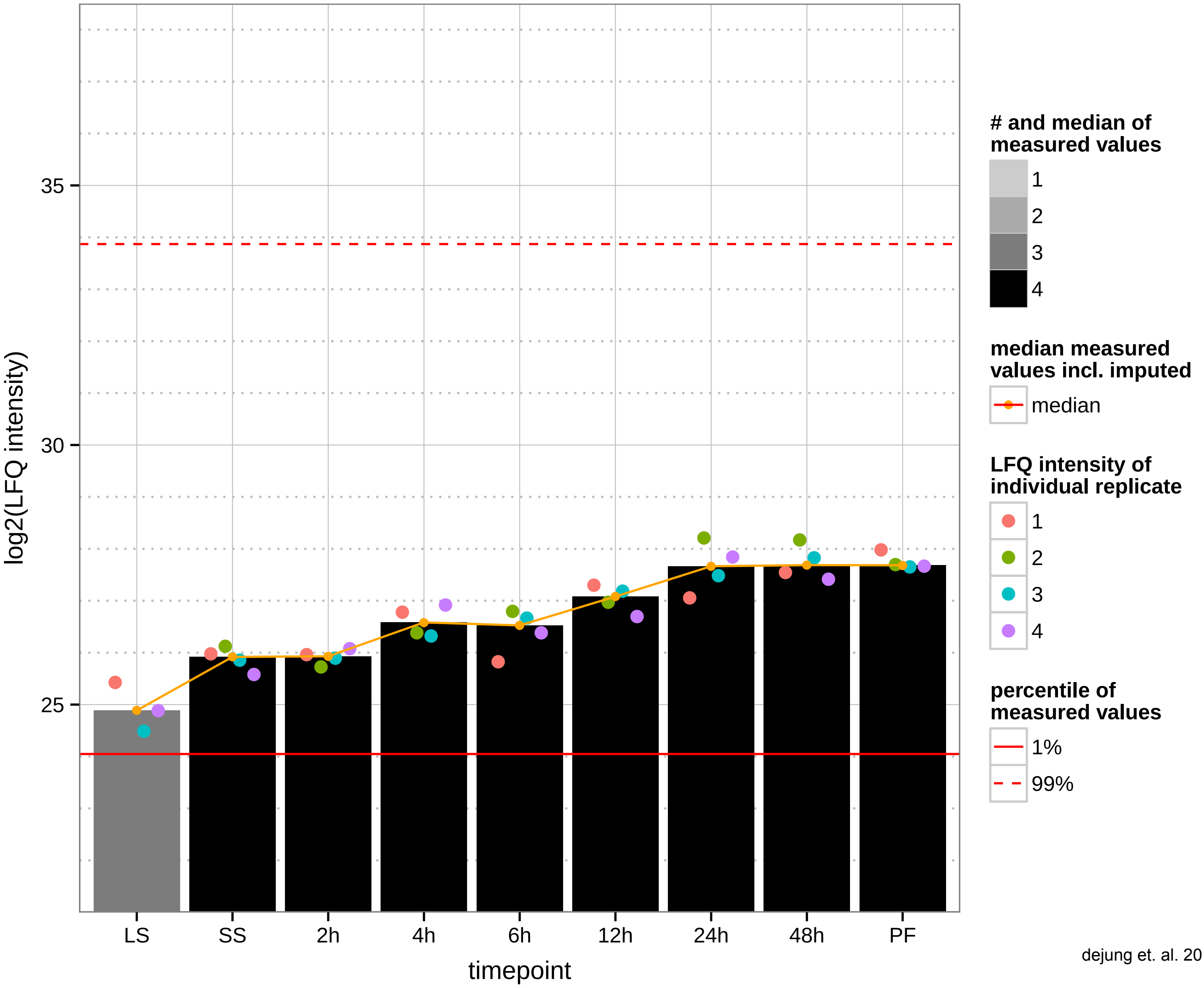
hypothetical protein, conserved
Tb927.7.7440
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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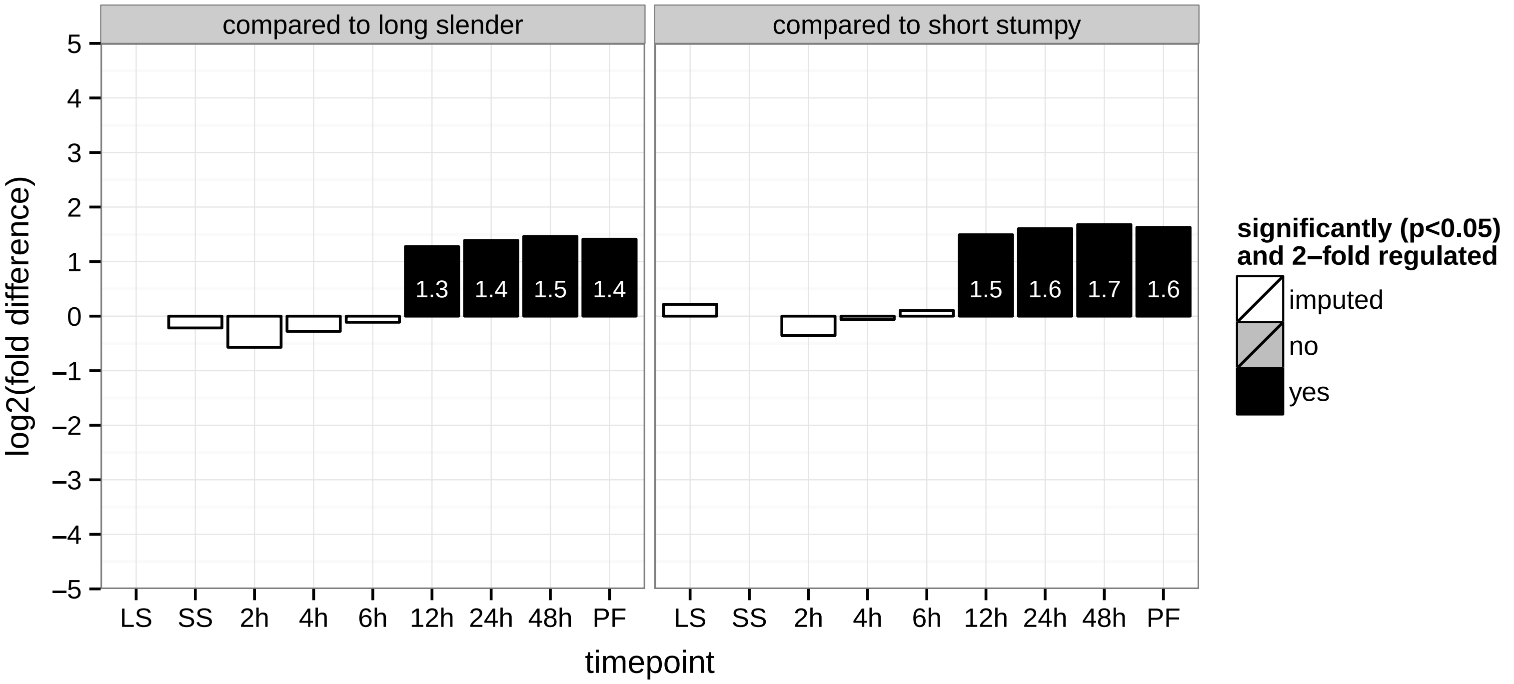
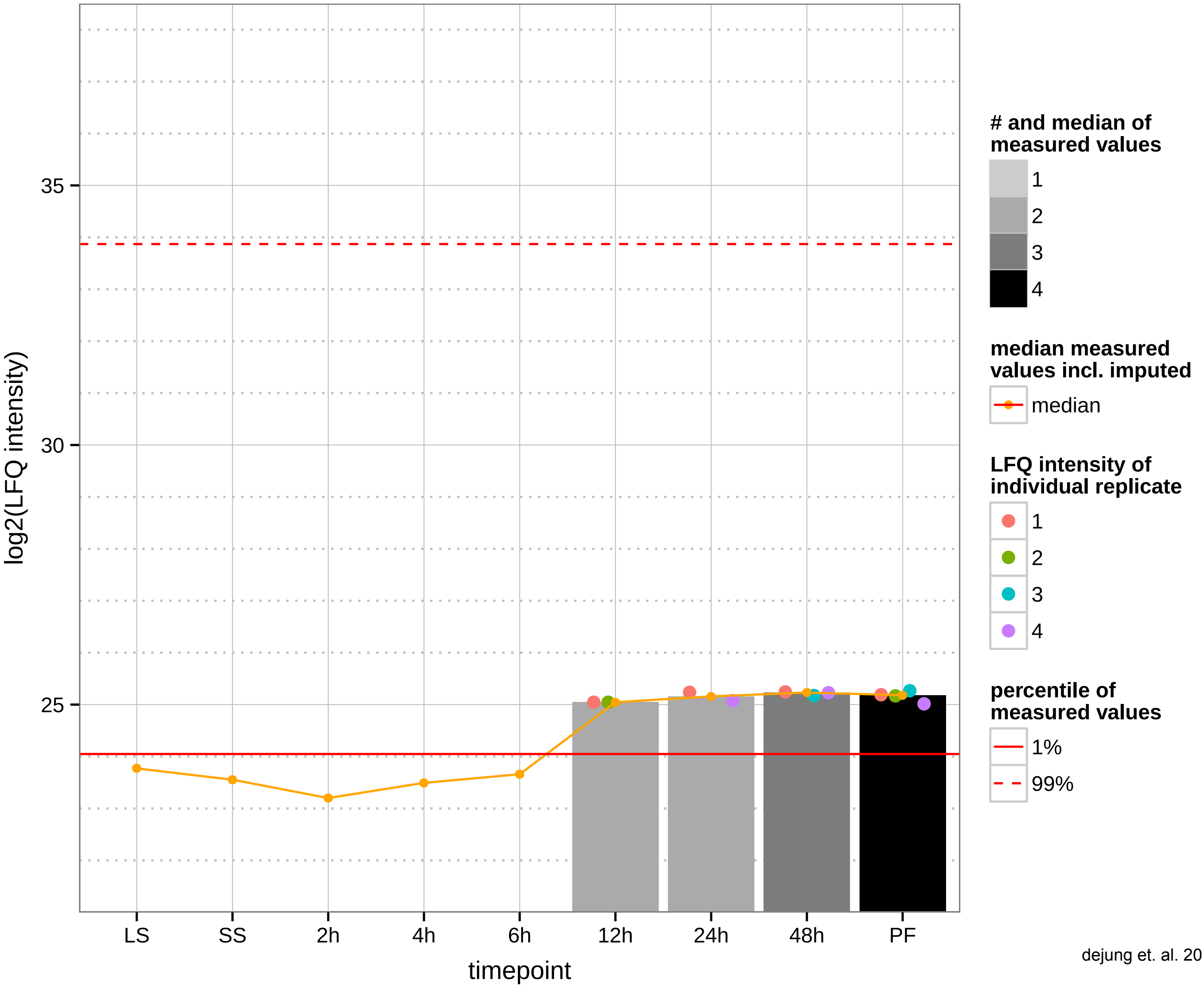
hypothetical protein, conserved
Tb927.8.1880
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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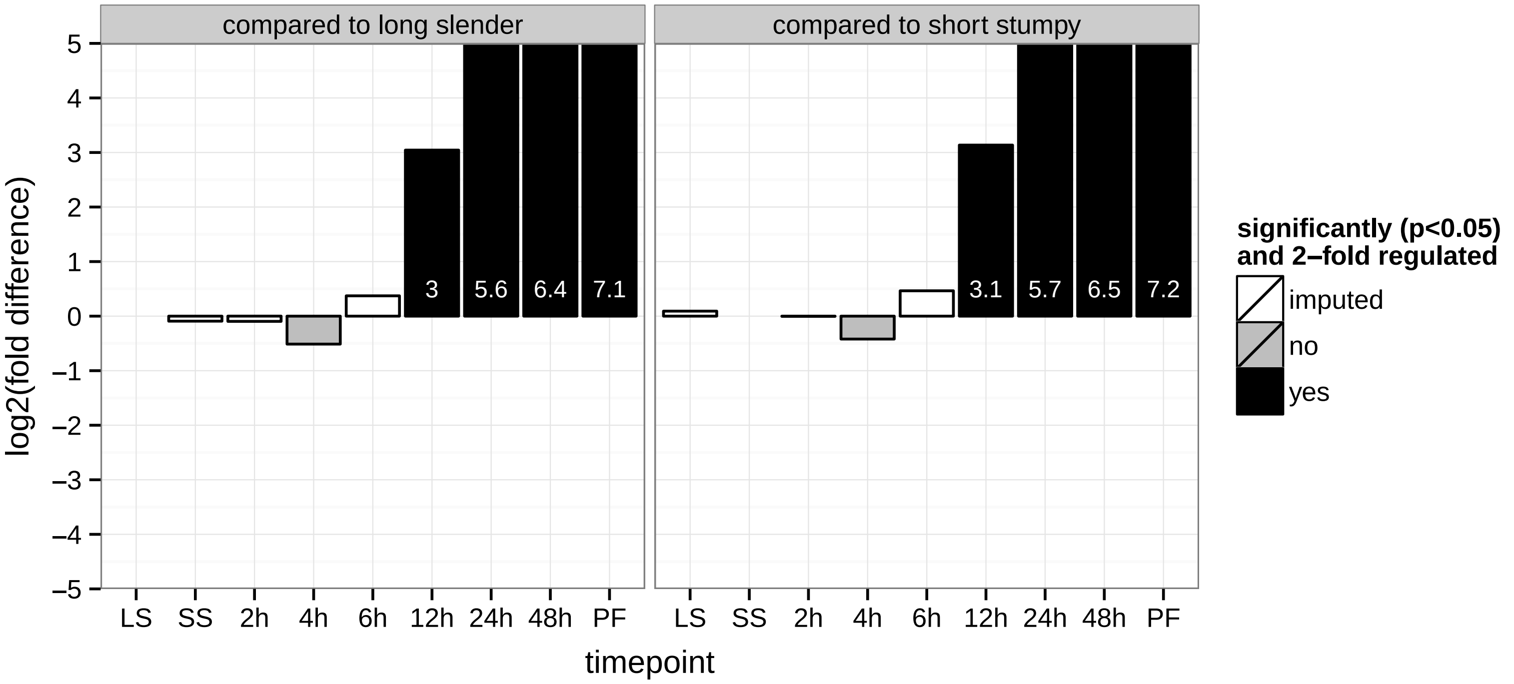
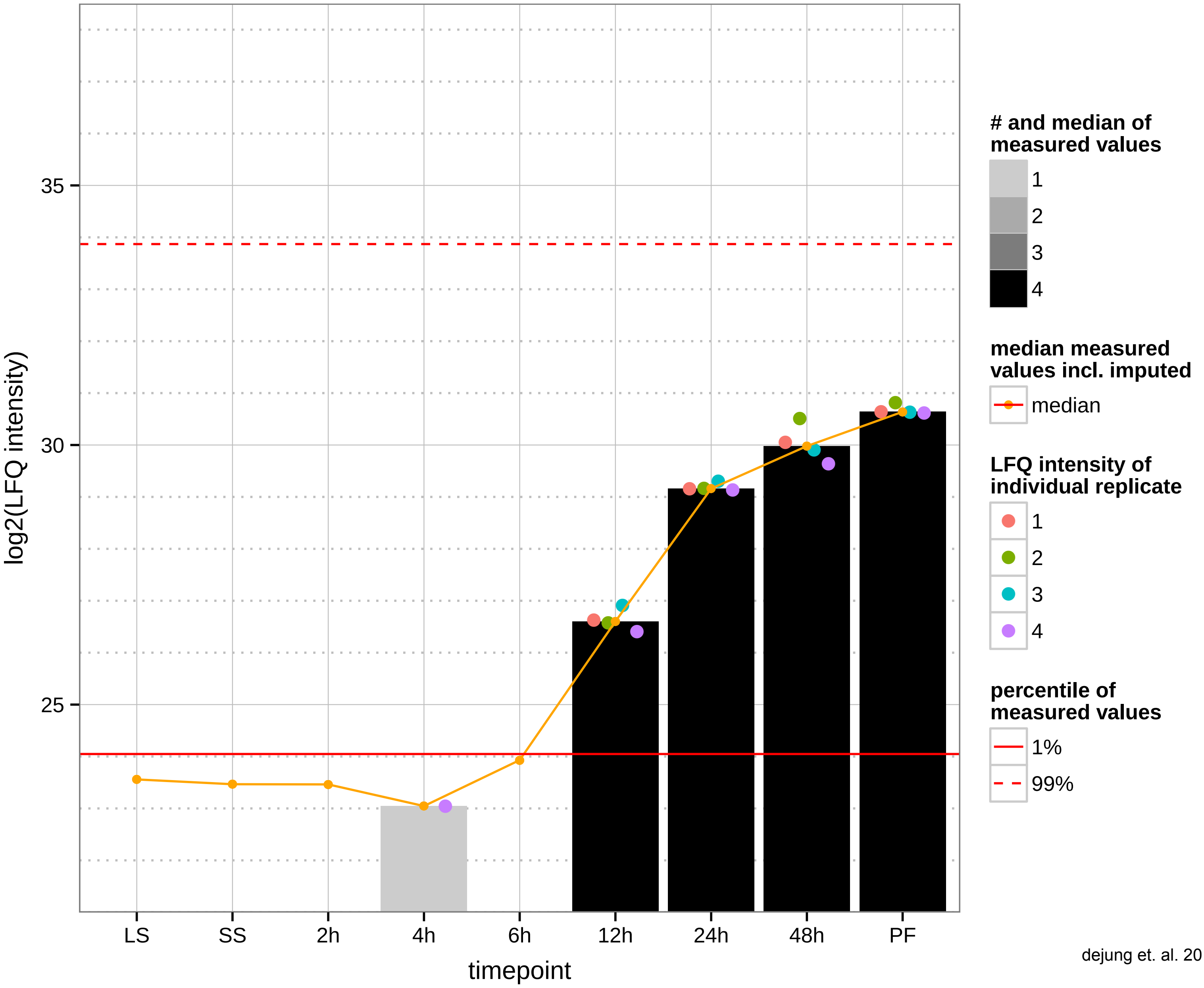
cytochrome c1, heme protein, mitochondrial precursor
Tb927.8.1890
AGOF: electron carrier activity, heme binding, iron ion binding
AGOC: mitochondrial respiratory chain, mitochondrion
AGOP: oxidation−reduction process
PGOF: electron carrier activity, heme binding, iron ion binding
PGOC: null
PGOP: null





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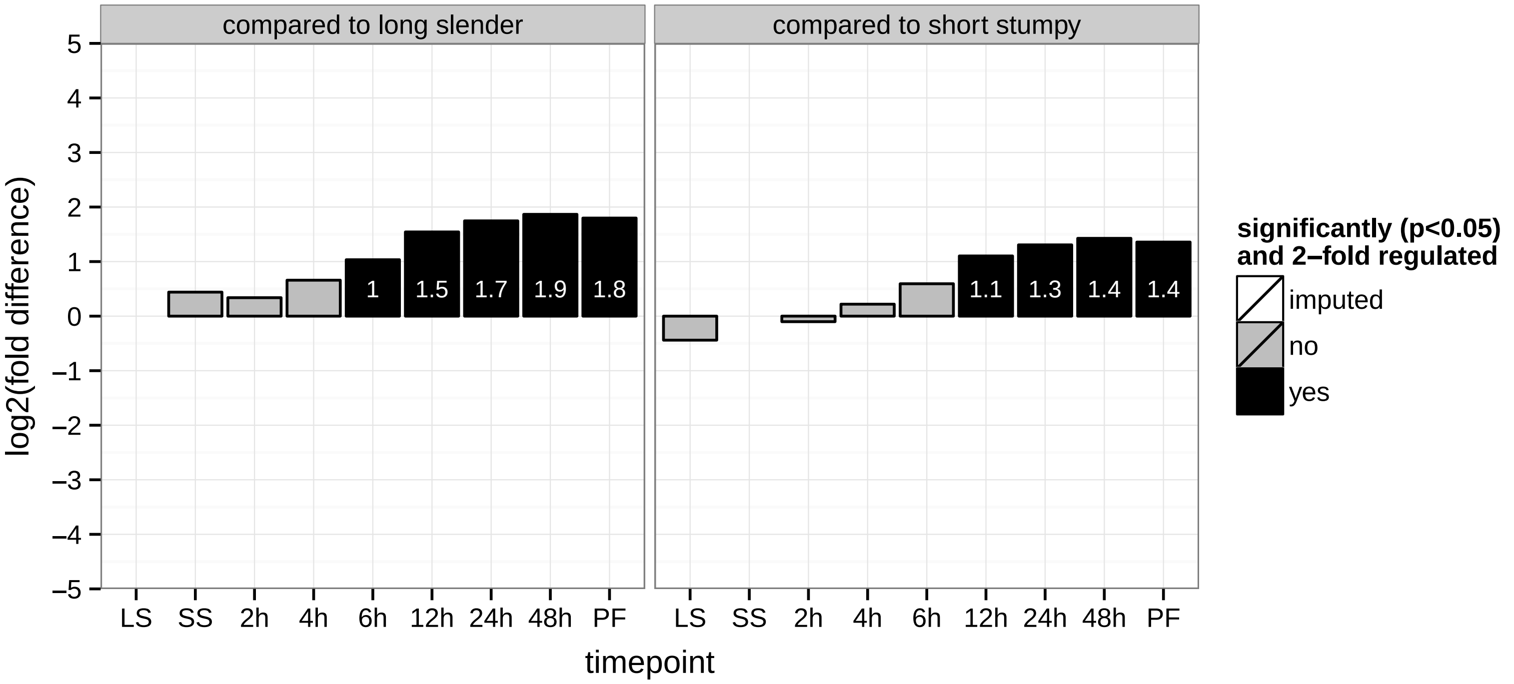
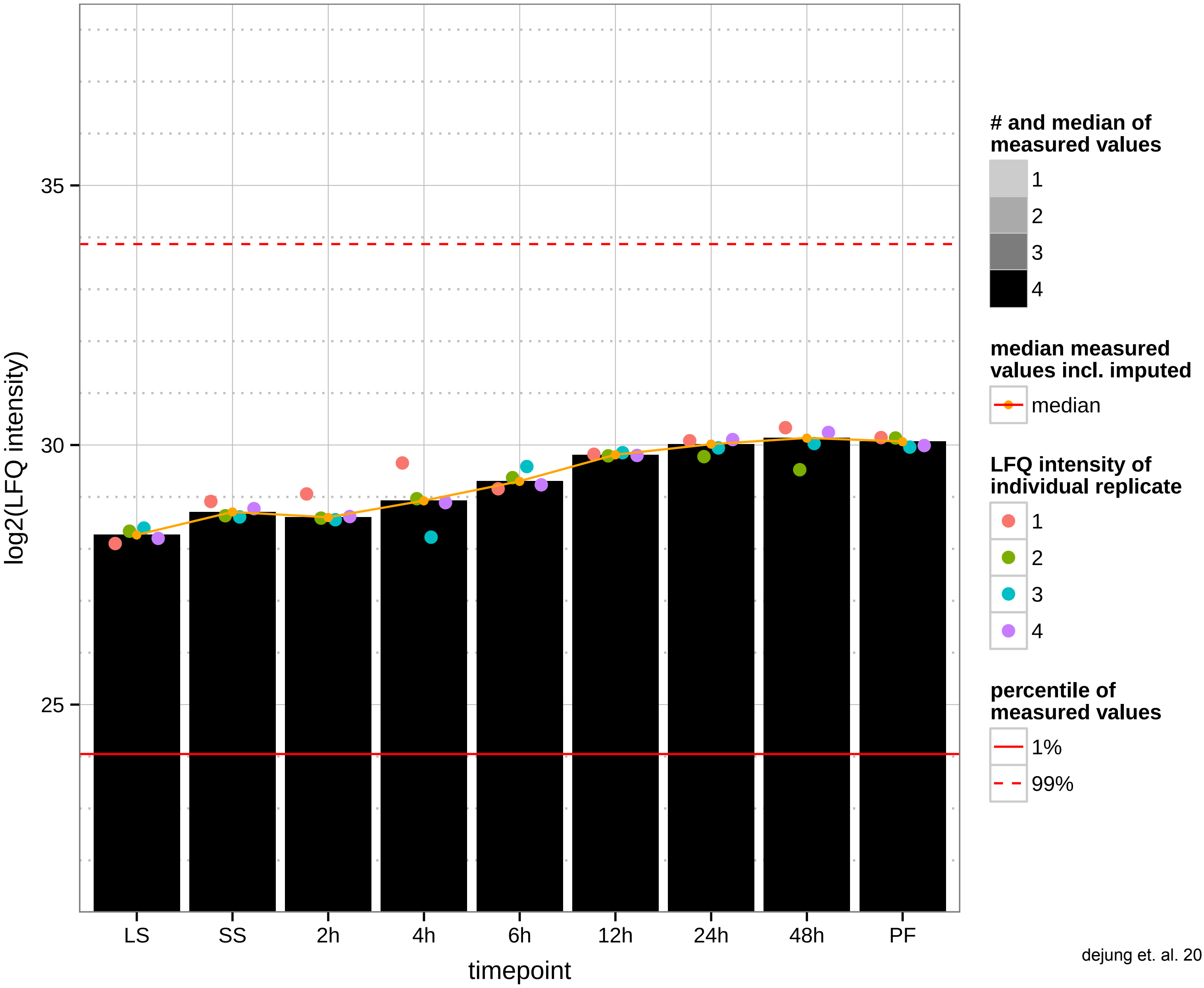
cyclophilin, putative, cyclophilin type peptidyl–prolyl cis–trans isomerase, peptidyl–prolyl cis–trans isomerase, putative (NCP1
Tb927.8.2000
AGOF: peptidyl–prolyl cis–trans isomerase activity, protein binding, rRNA binding
AGOC: nucleus
AGOP: protein folding, rRNA processing
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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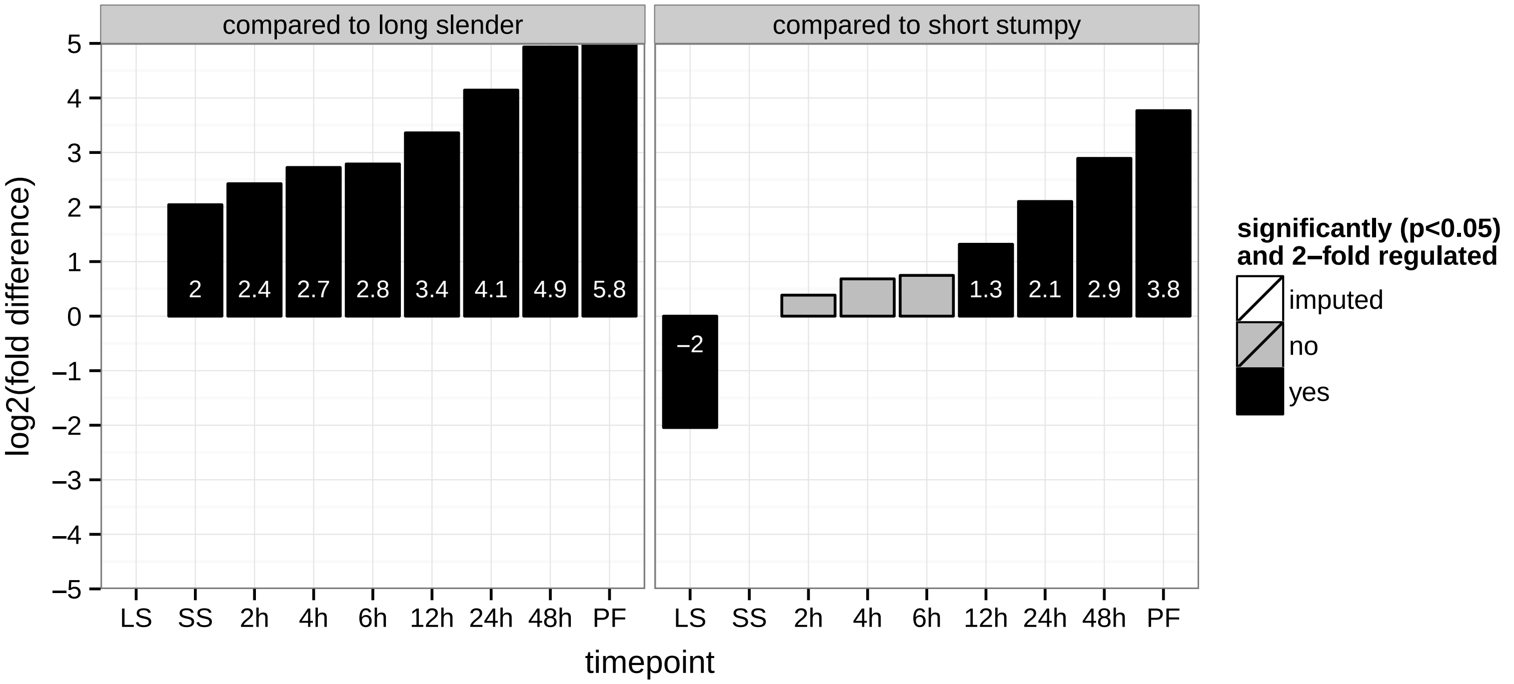
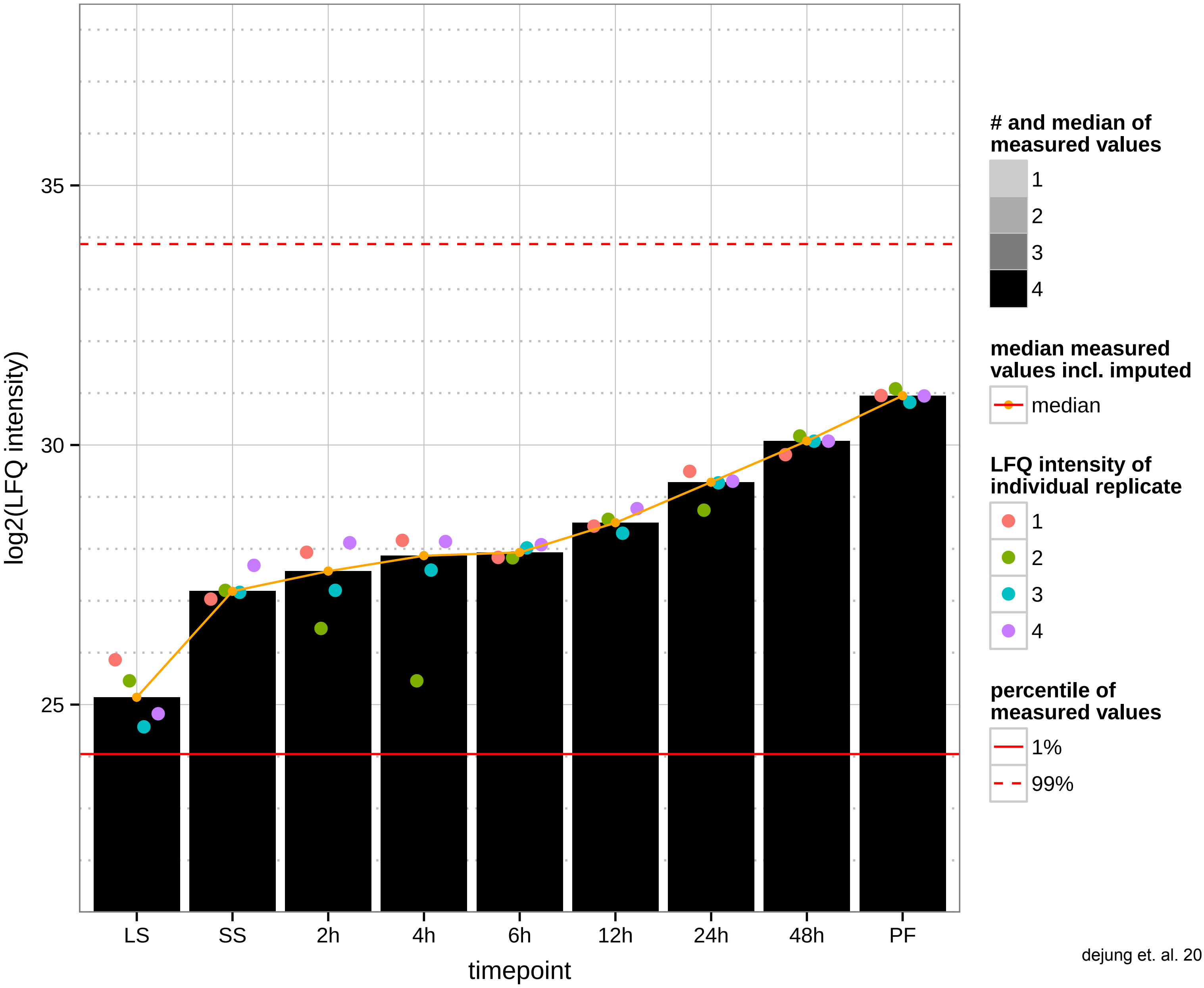
multidrug resistance protein A, p–glycoprotein (PGPA)
Tb927.8.2160
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances
AGOC: ATP–binding cassette (ABC) transporter complex, integral to membrane
AGOP: response to drug, transport
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances, nucleoside–triphosphatase activity
PGOC: integral to membrane
PGOP: transmembrane transport, transport





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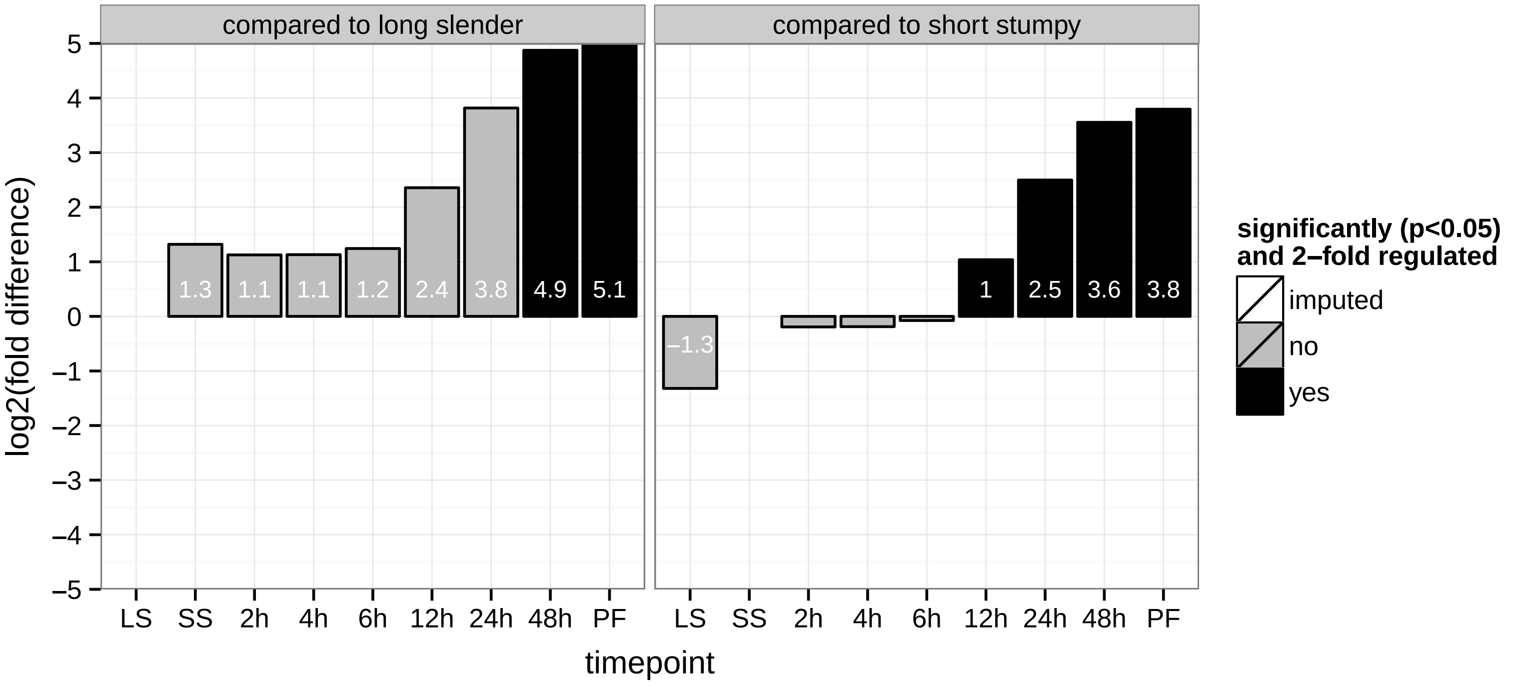
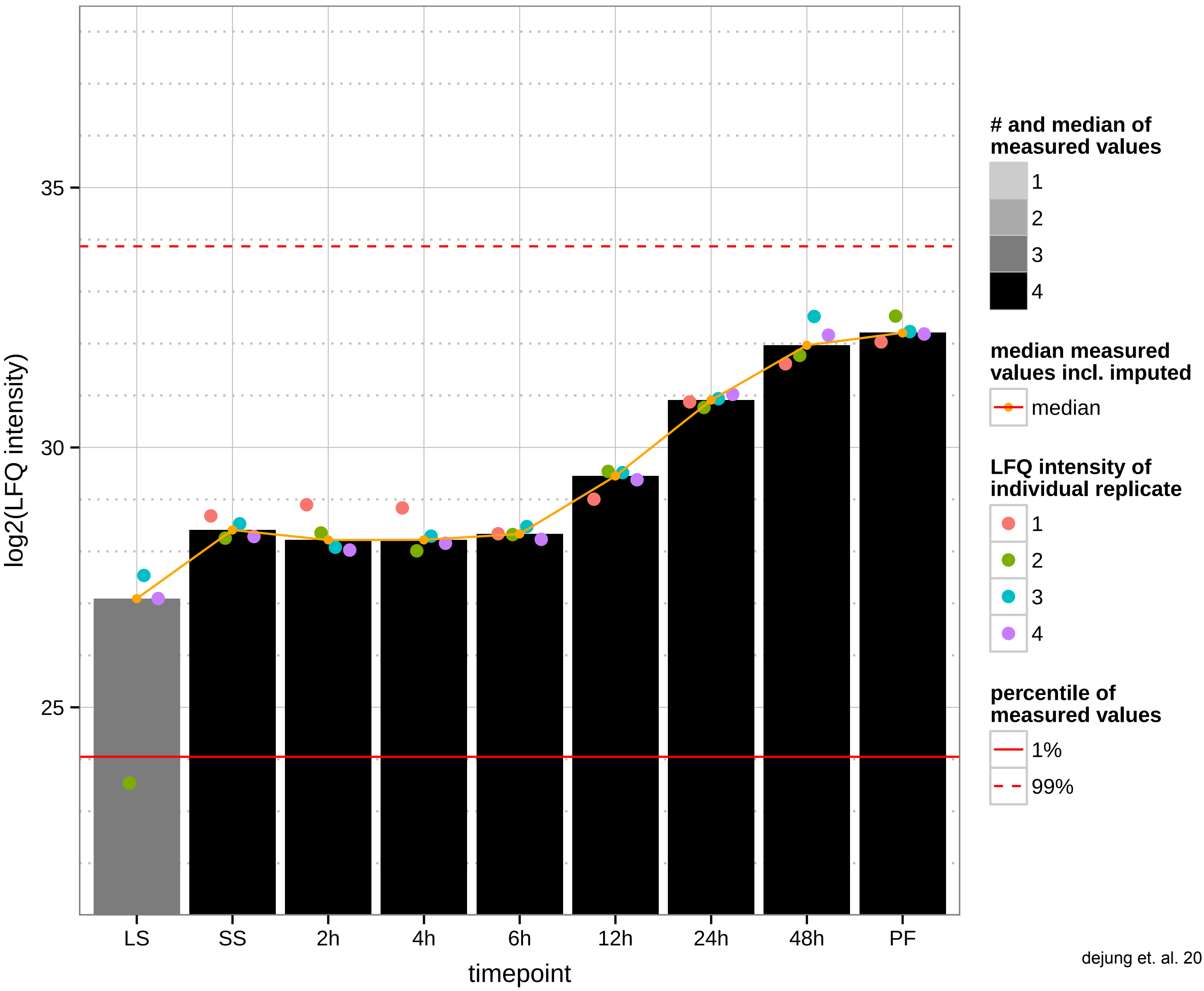
3–ketoacyl–CoA thiolase, putative, ERG10
Tb927.8.2540
AGOF: acetyl–CoA C–acyltransferase activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity, transferase activity, transferring acyl groups other than amino–acyl groups
PGOC: null
PGOP: metabolic process





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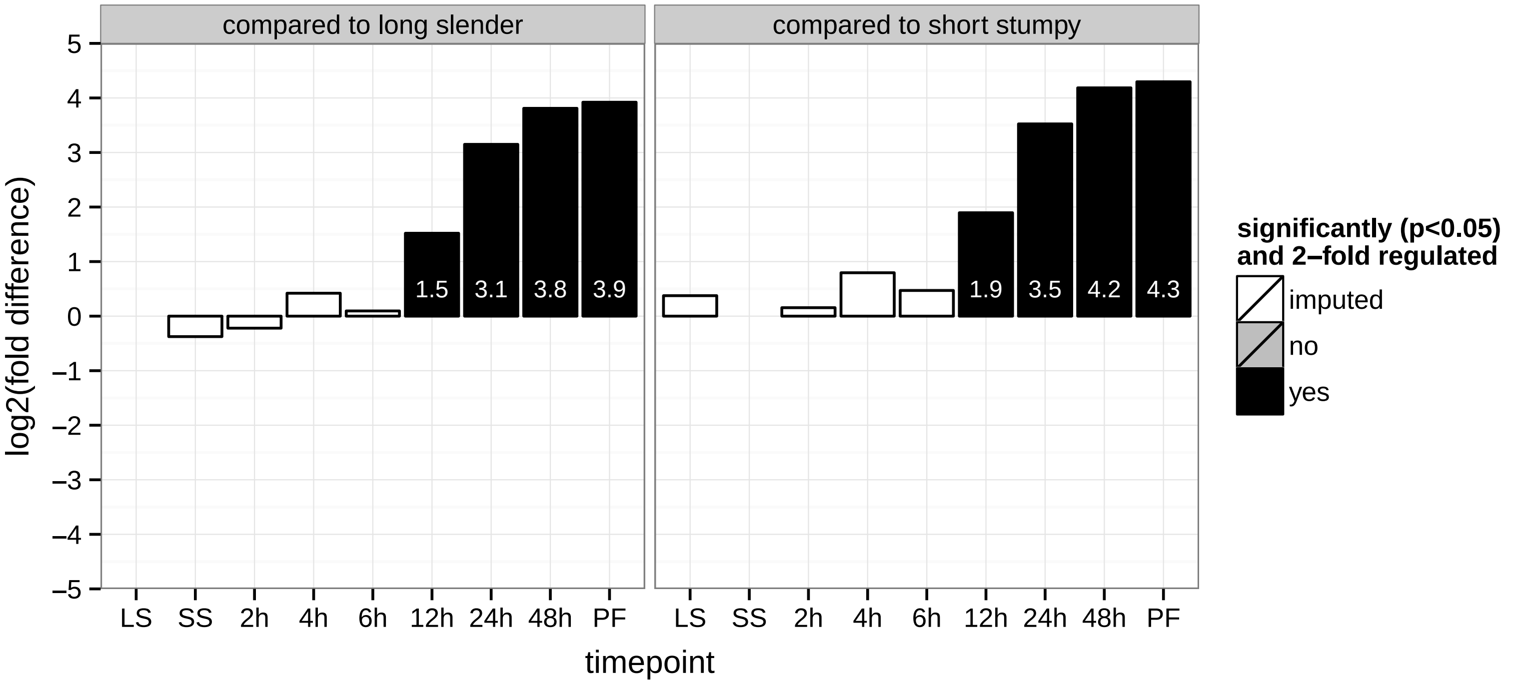
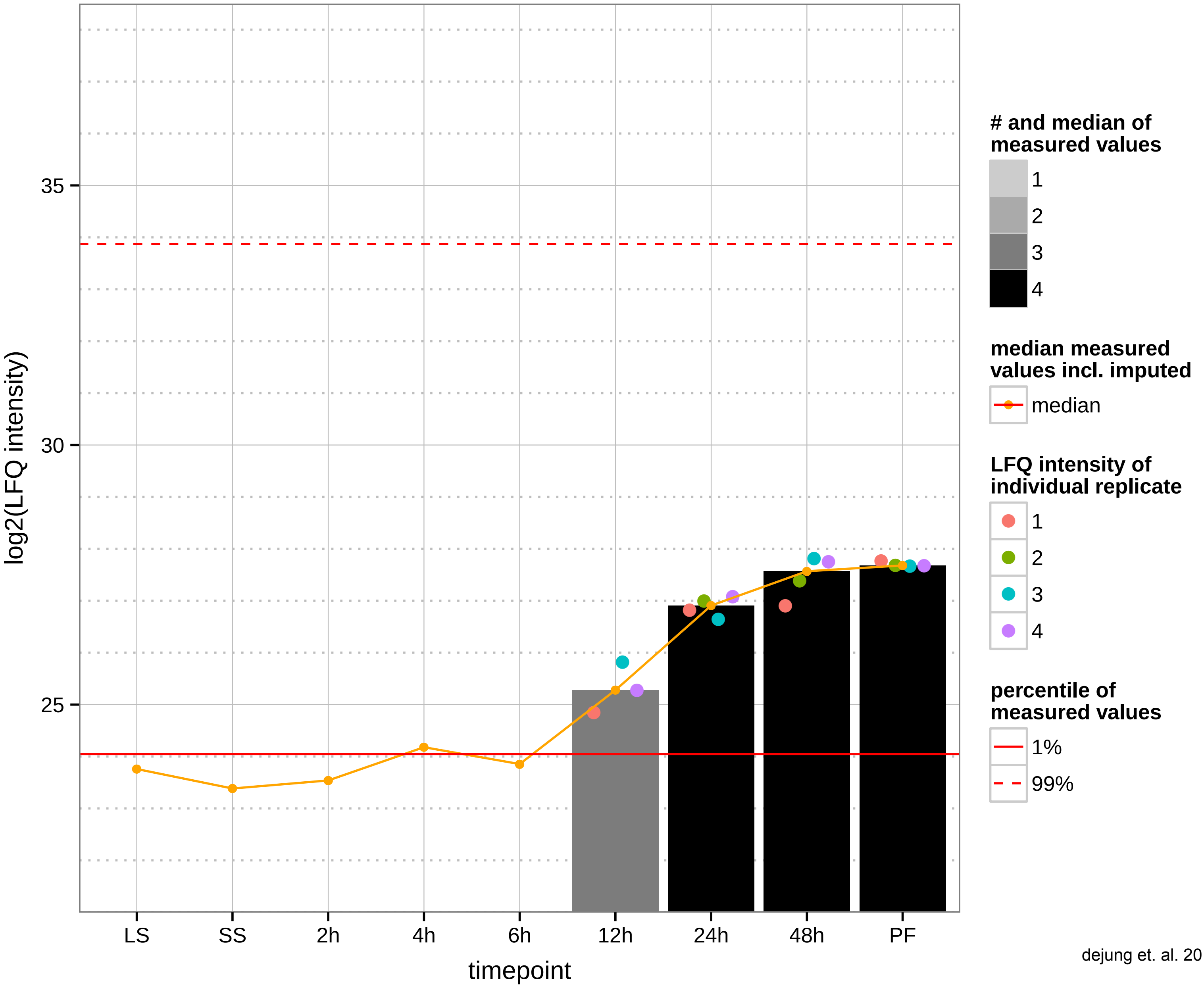
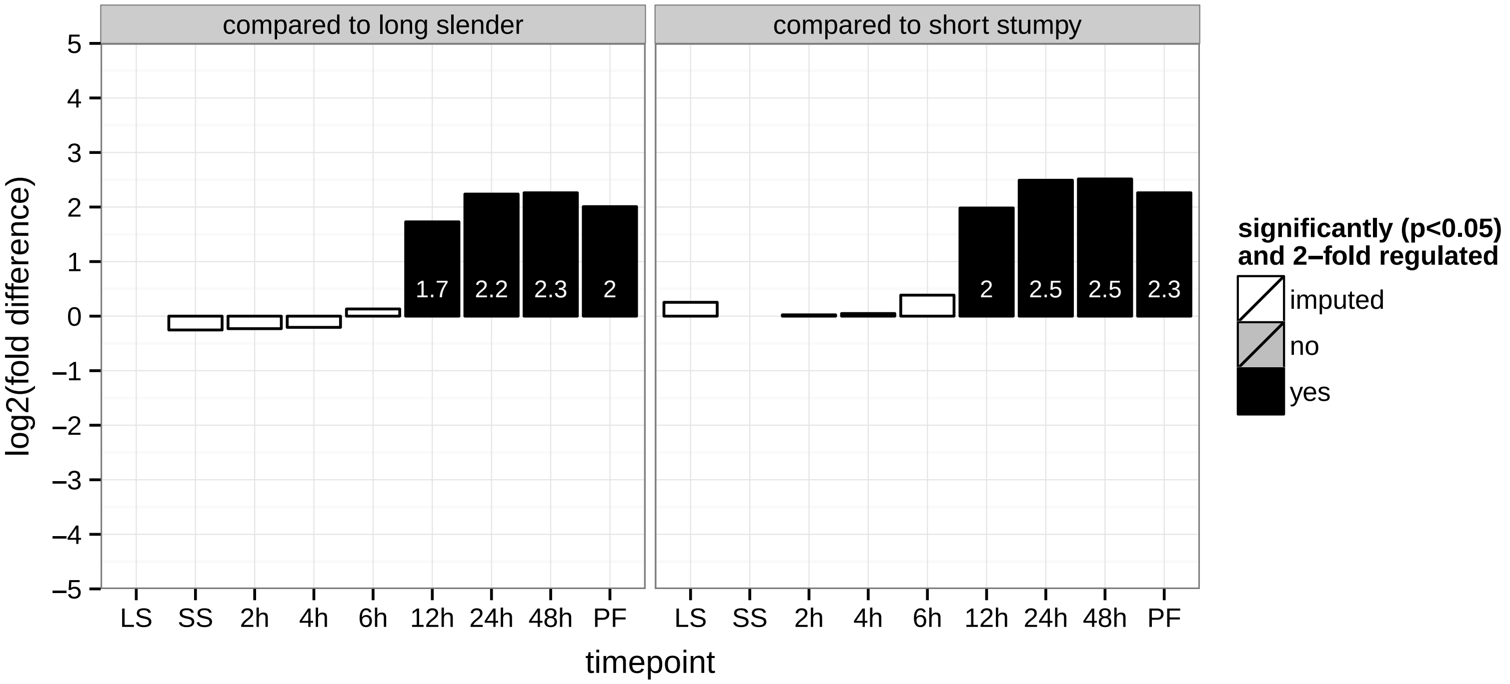
mitochondrial DNA primase (PRI1)
Tb927.8.2550
AGOF: DNA primase activity
AGOC: kinetoplast, mitochondrial matrix
AGOP: mitochondrial DNA replication
PGOF: hydrolase activity, acting on acid anhydrides
PGOC: null
PGOP: null

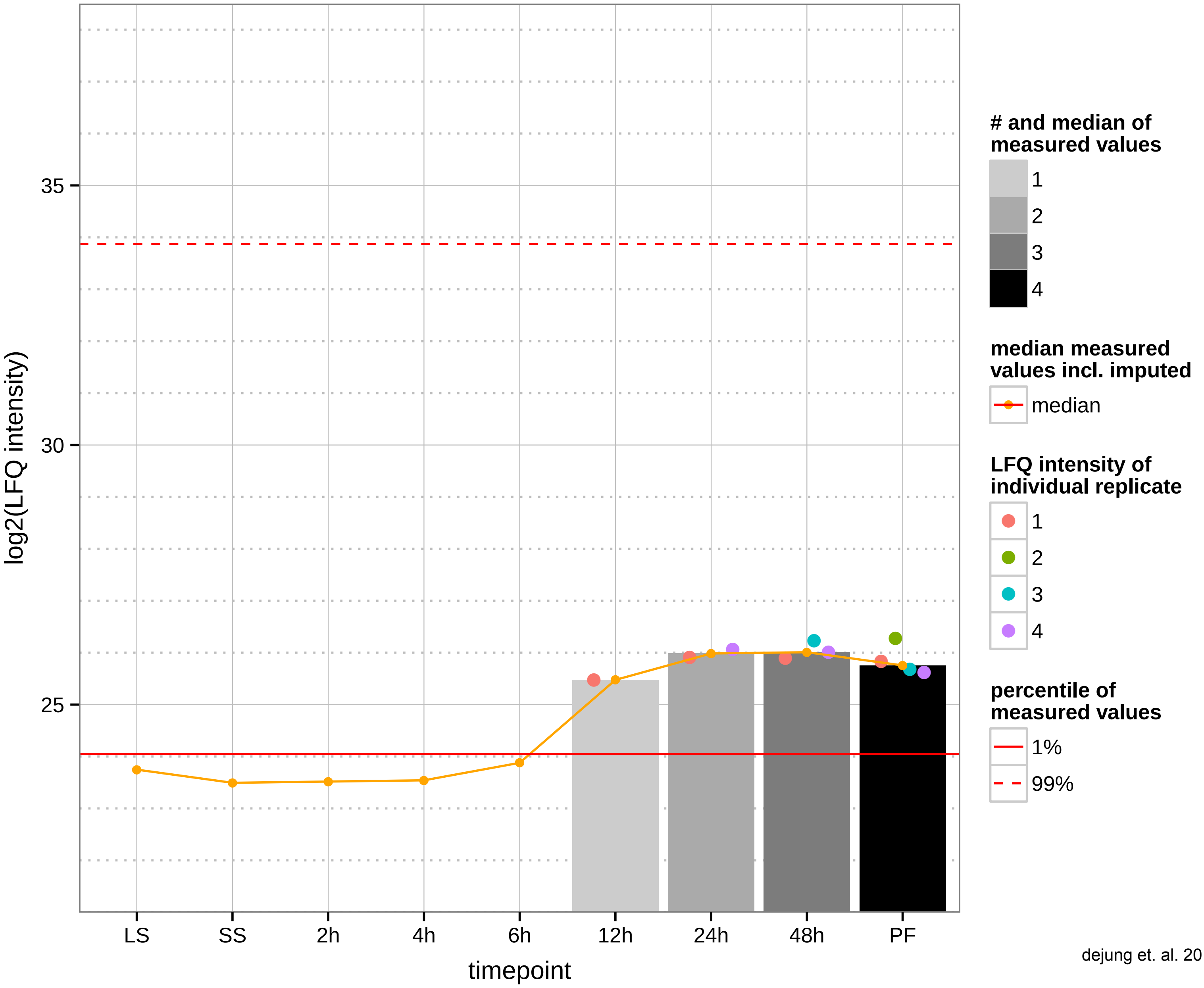




dejung et. al. 2015

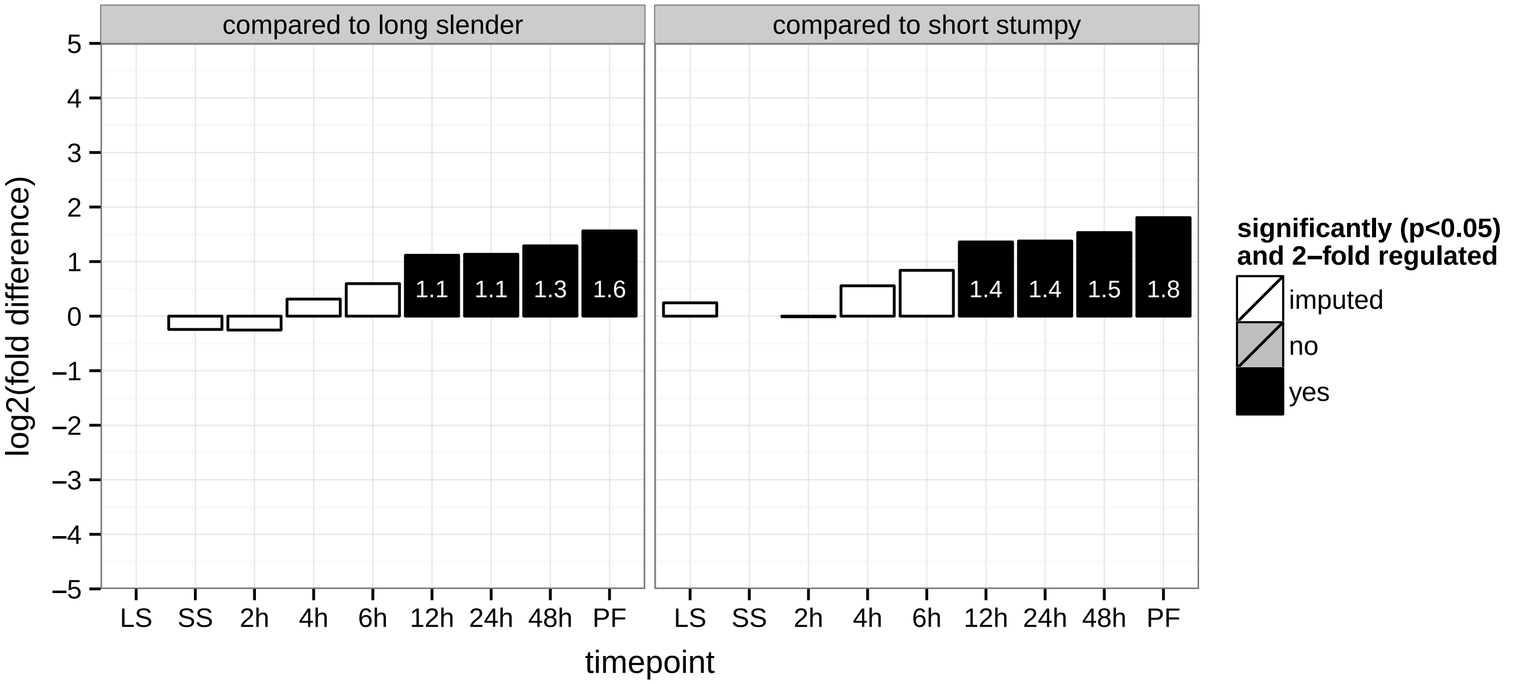
hypothetical protein, conserved
Tb927.8.2880
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

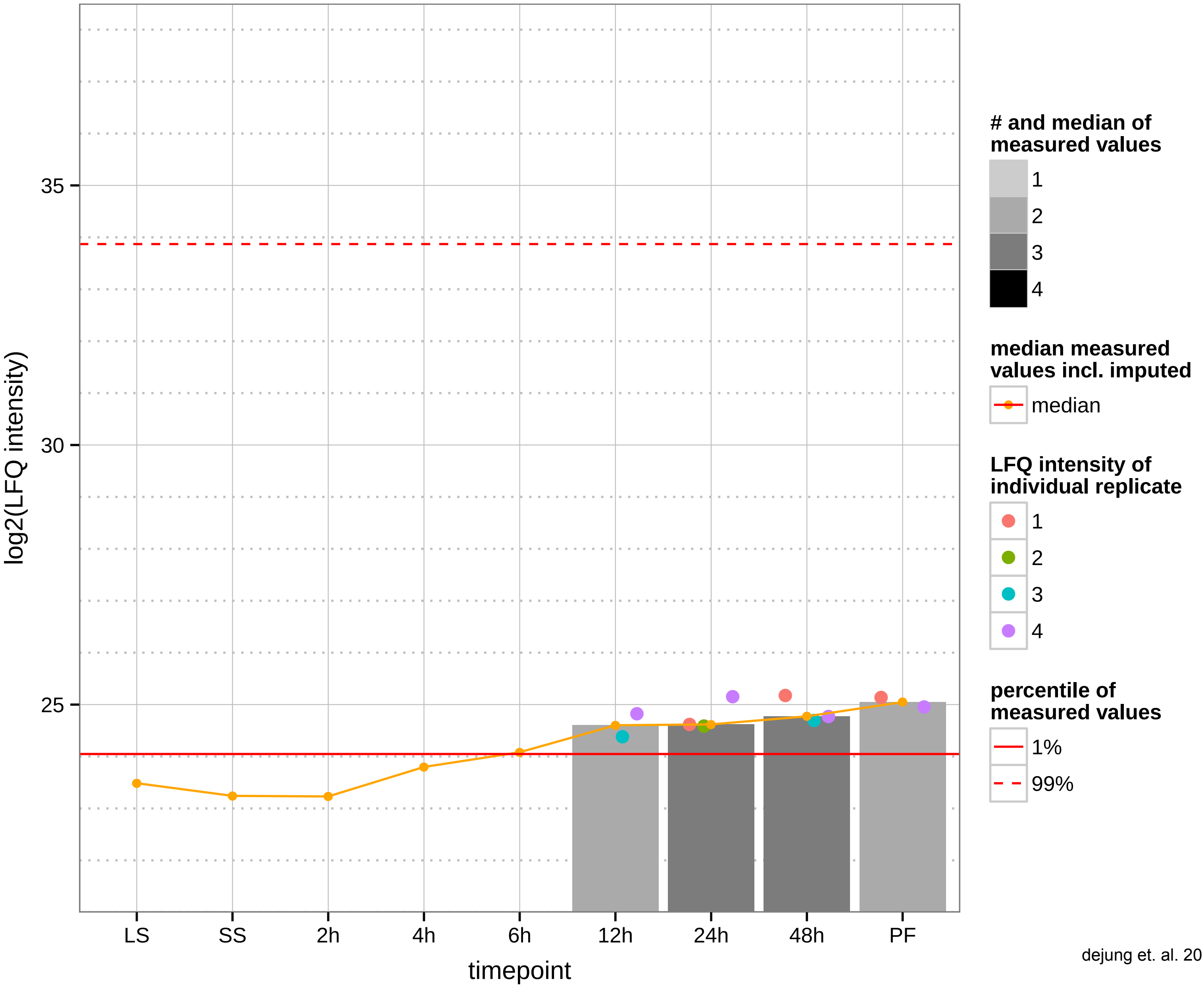




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.3010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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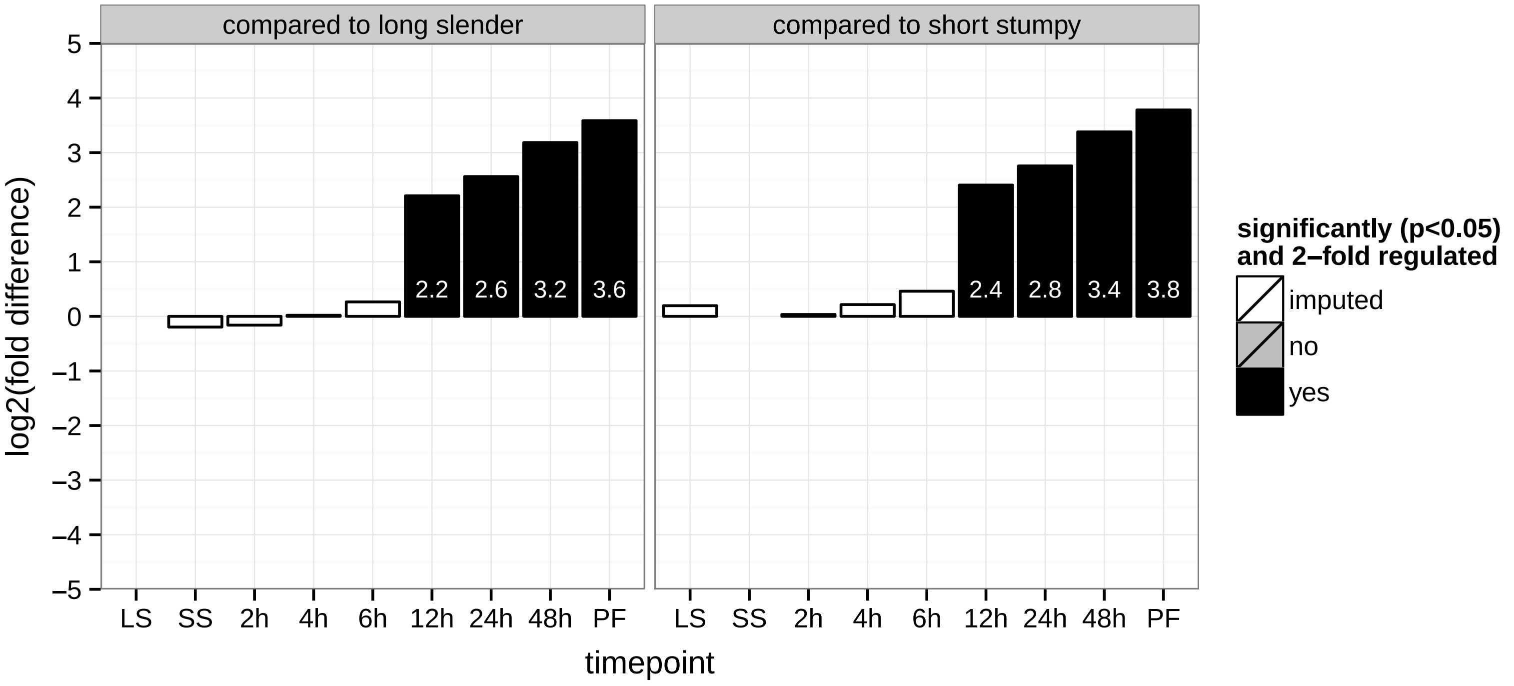
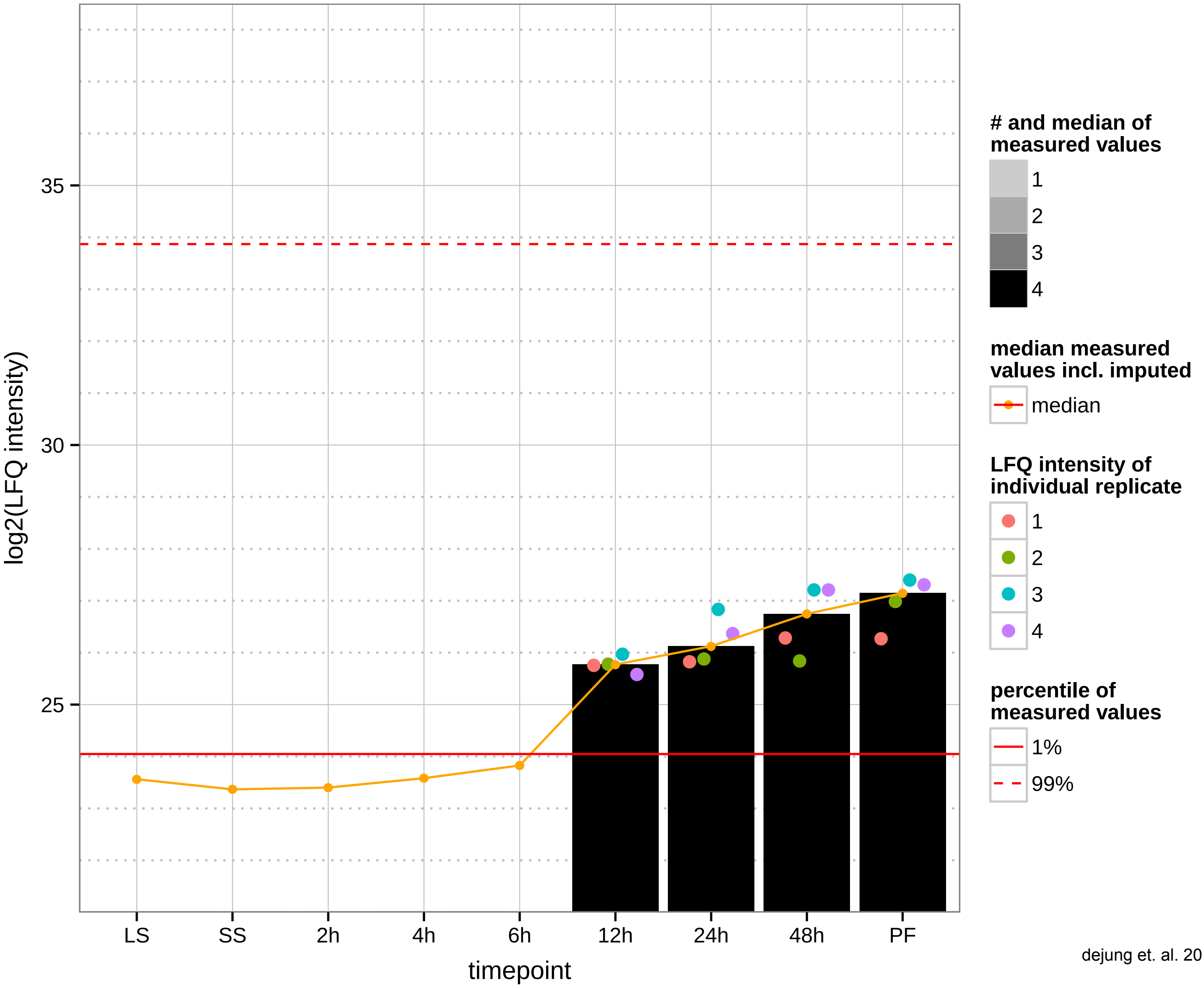
hypothetical protein, conserved
Tb927.8.3340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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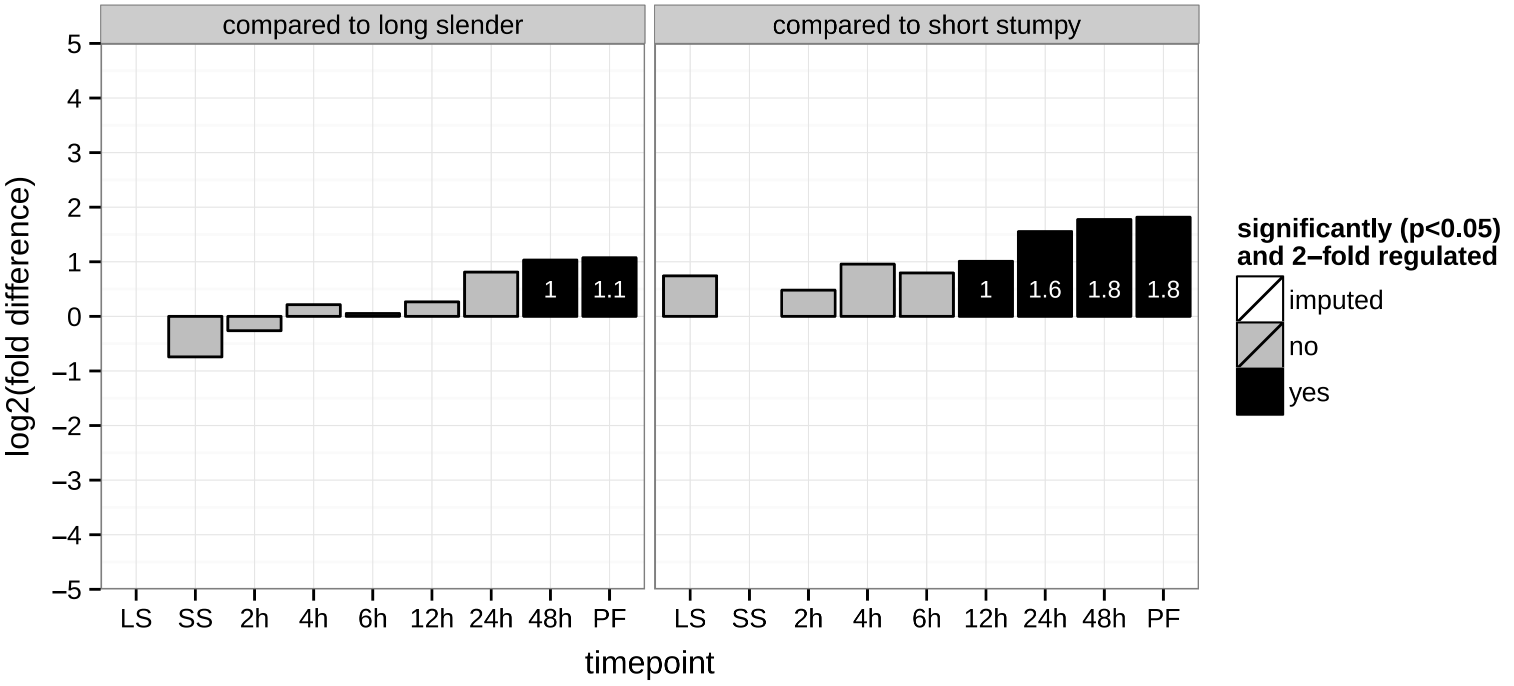
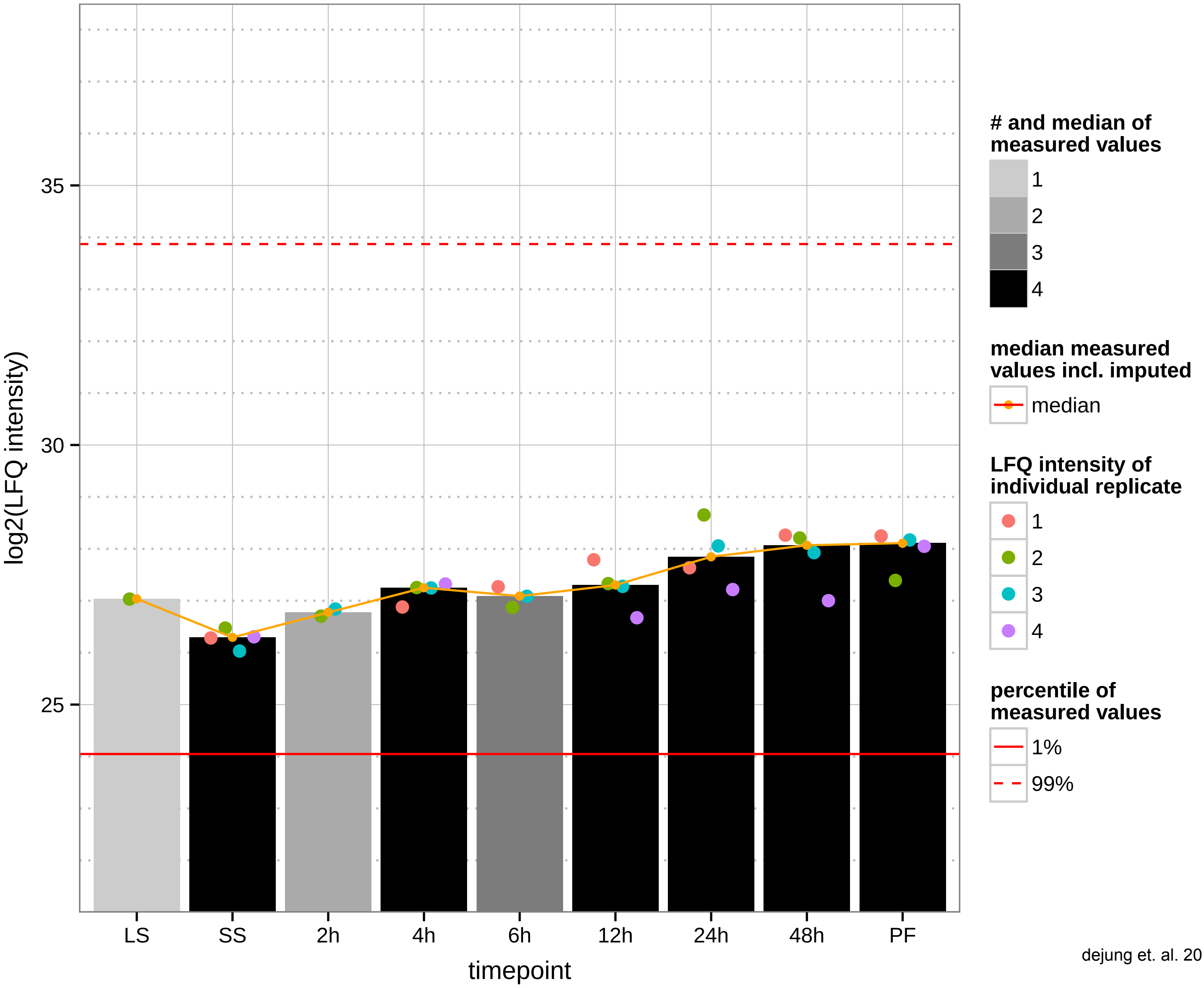
hypothetical protein, conserved
Tb927.8.5070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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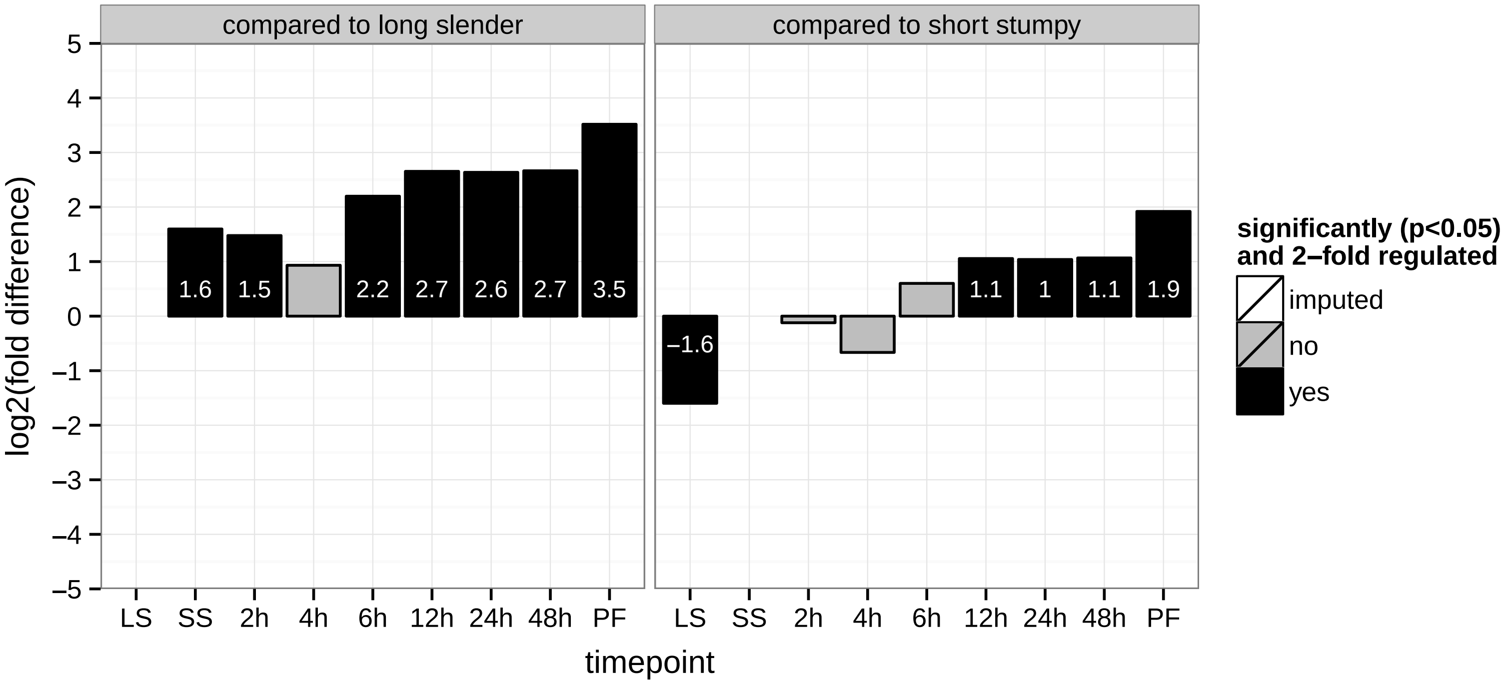
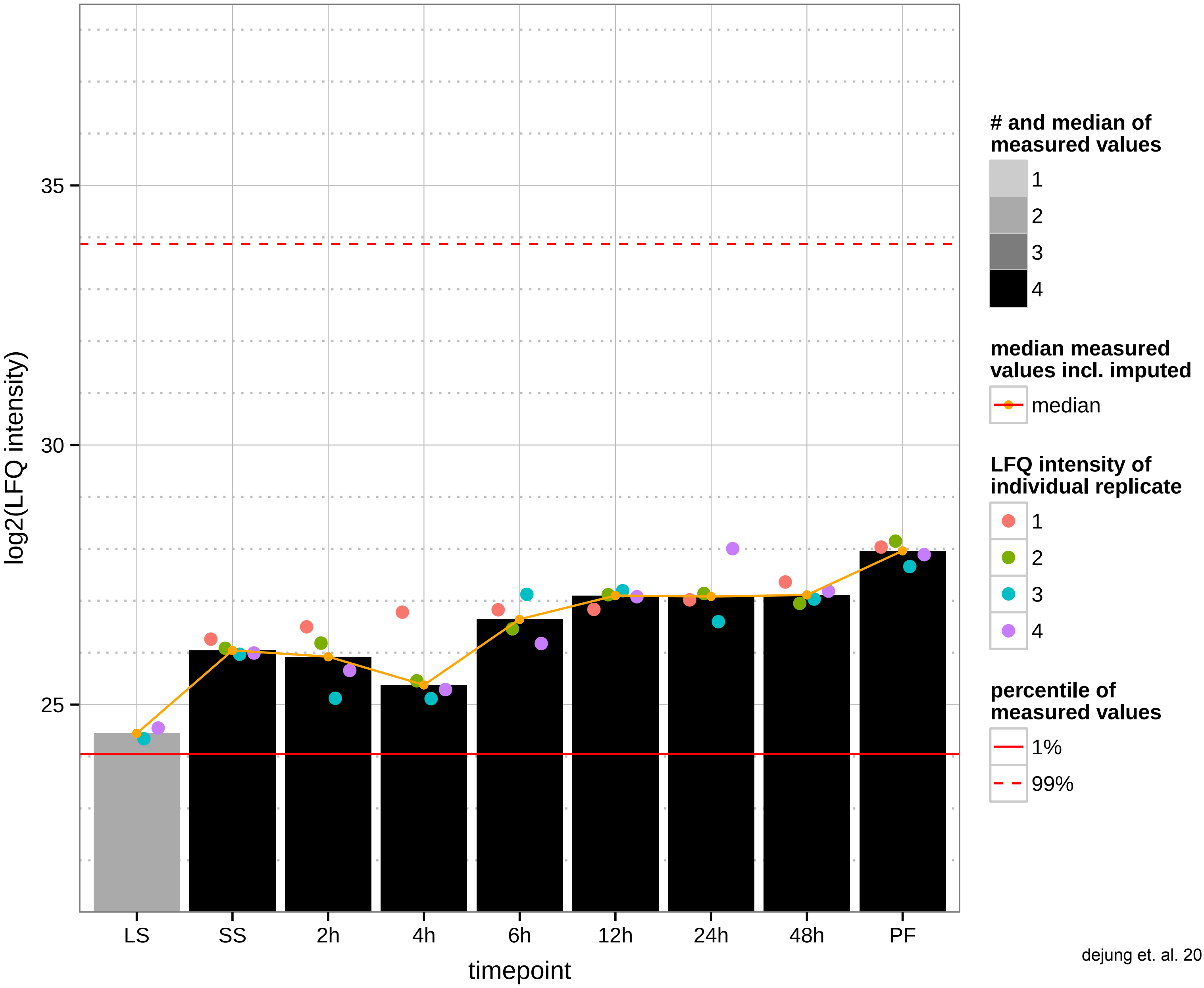
hypothetical protein, conserved
Tb927.8.5490
AGOF: null
AGOC: preribosome, small subunit precursor
AGOP: rRNA processing
PGOF: null
PGOC: preribosome, small subunit precursor
PGOP: rRNA processing





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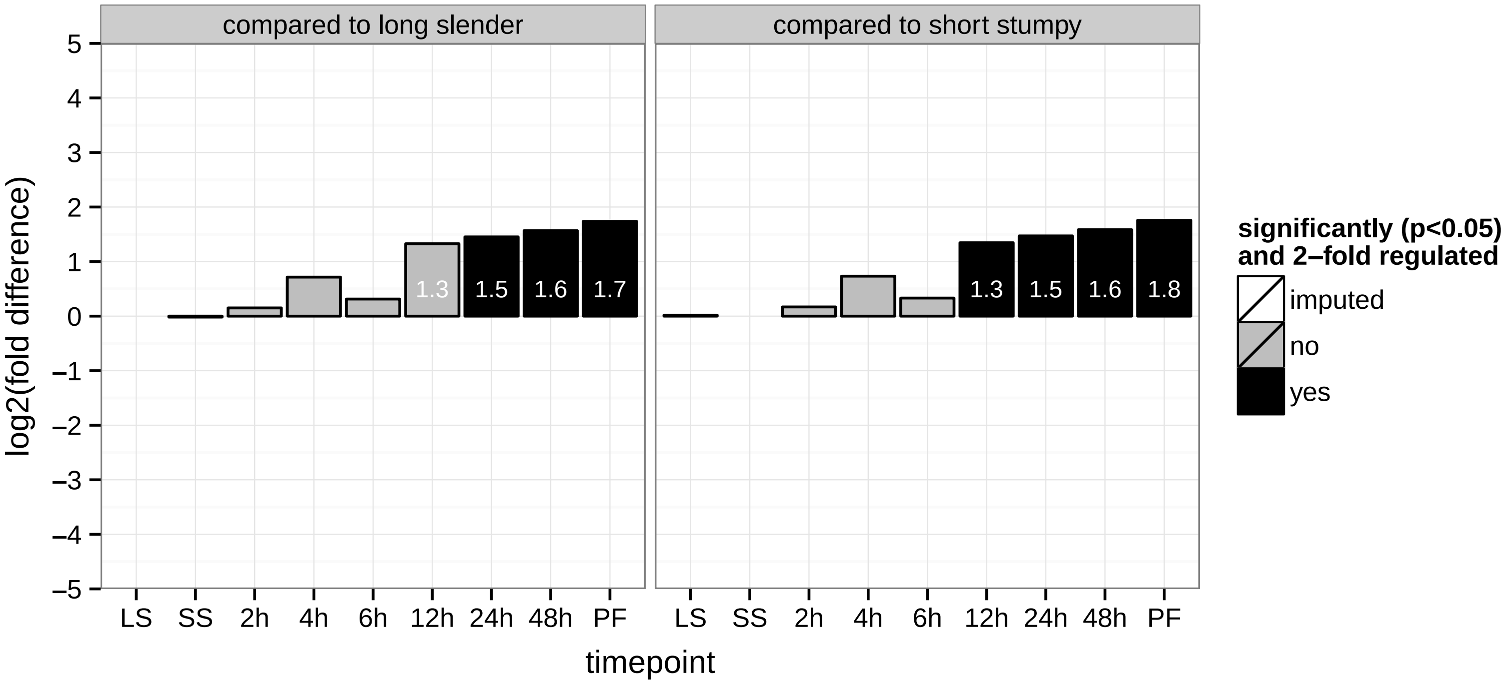
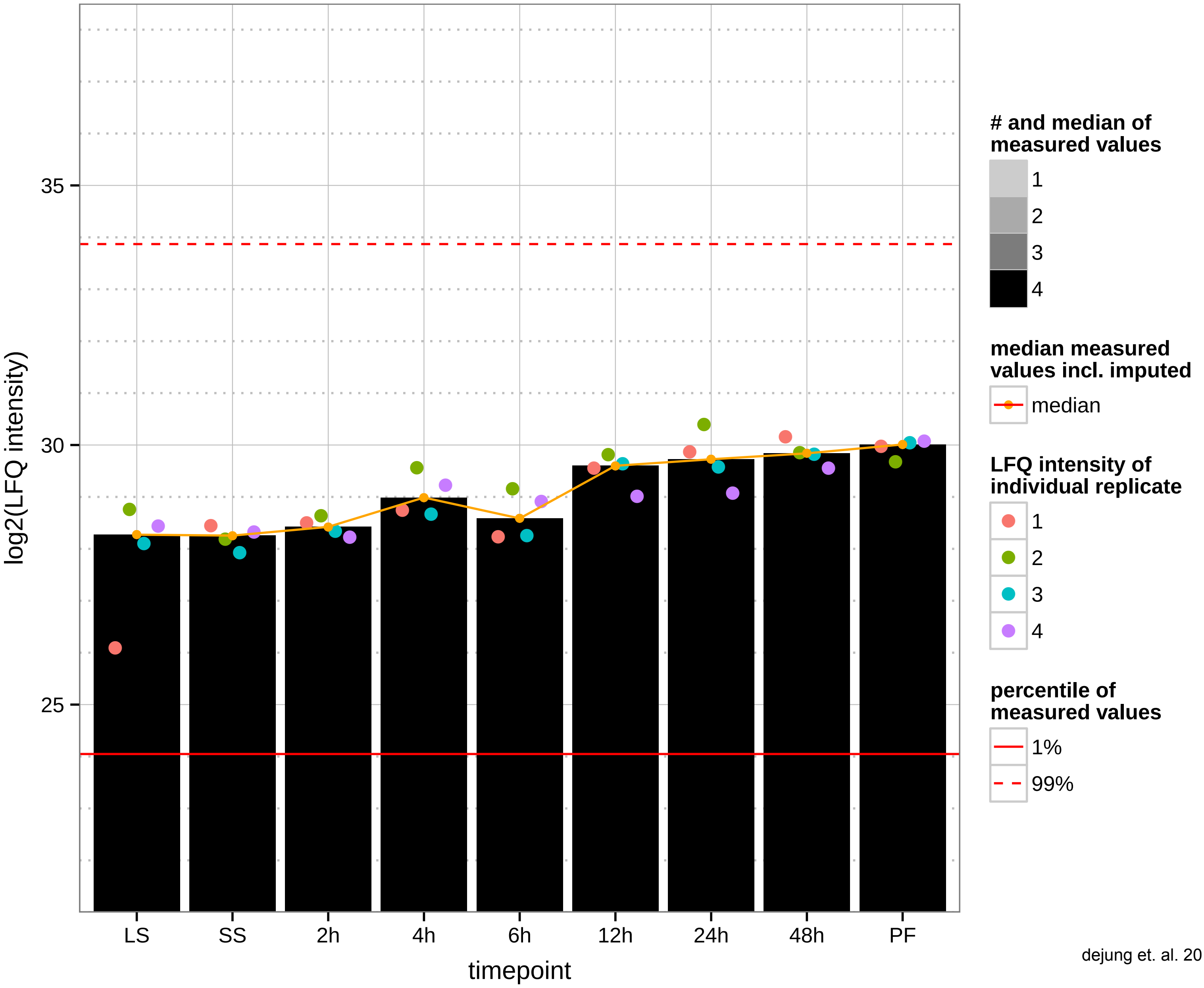
eukaryotic translation initiation factor 1A, putative
Tb927.8.5880
AGOF: RNA binding, translation initiation factor activity
AGOC: cytoplasm
AGOP: translational initiation
PGOF: RNA binding, translation initiation factor activity
PGOC: null
PGOP: translational initiation





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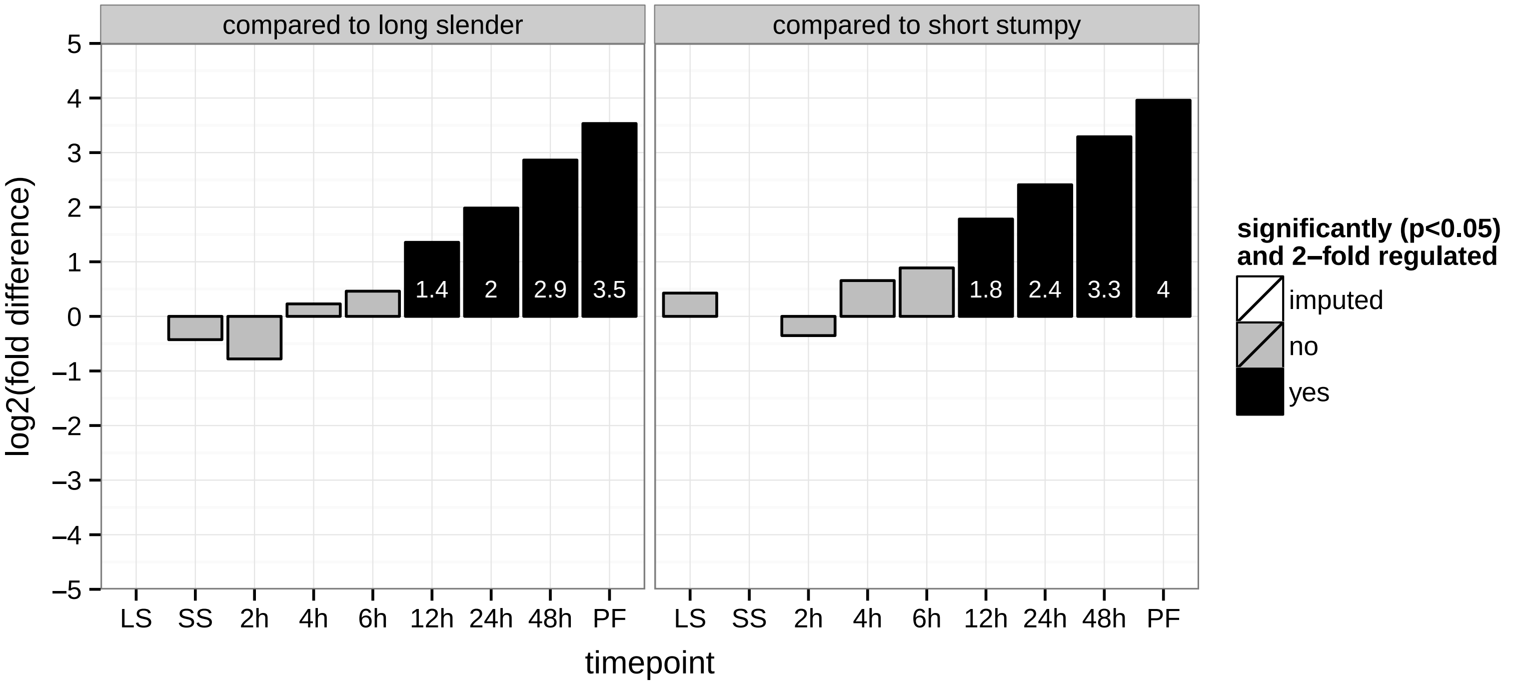
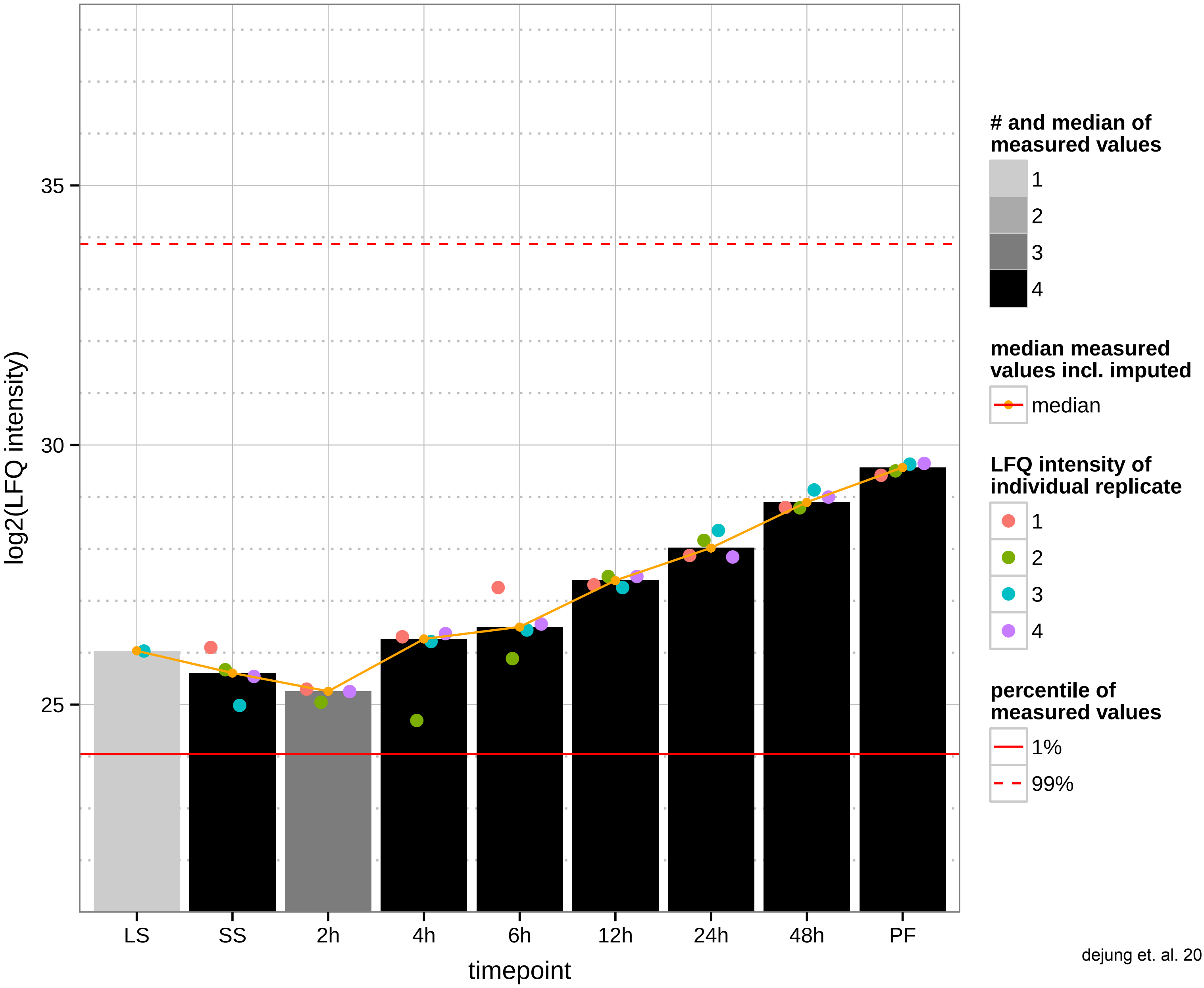
hypothetical protein, conserved
Tb927.8.6080
AGOF: glycerophosphodiester phosphodiesterase activity
AGOC: mitochondrion
AGOP: glycerol metabolic process, lipid metabolic process, phospholipid catabolic process
PGOF: glycerophosphodiester phosphodiesterase activity, phosphoric diester hydrolase activity
PGOC: null
PGOP: glycerol metabolic process, lipid metabolic process





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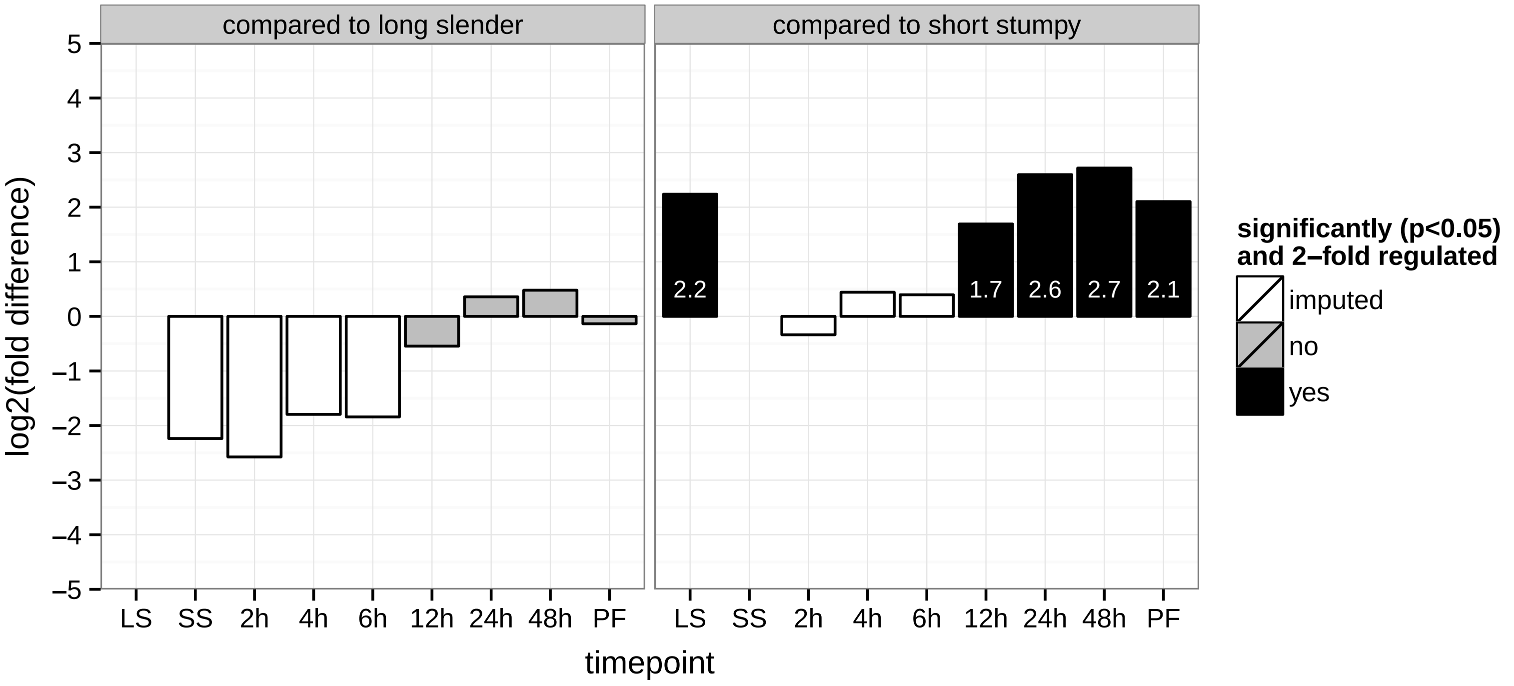
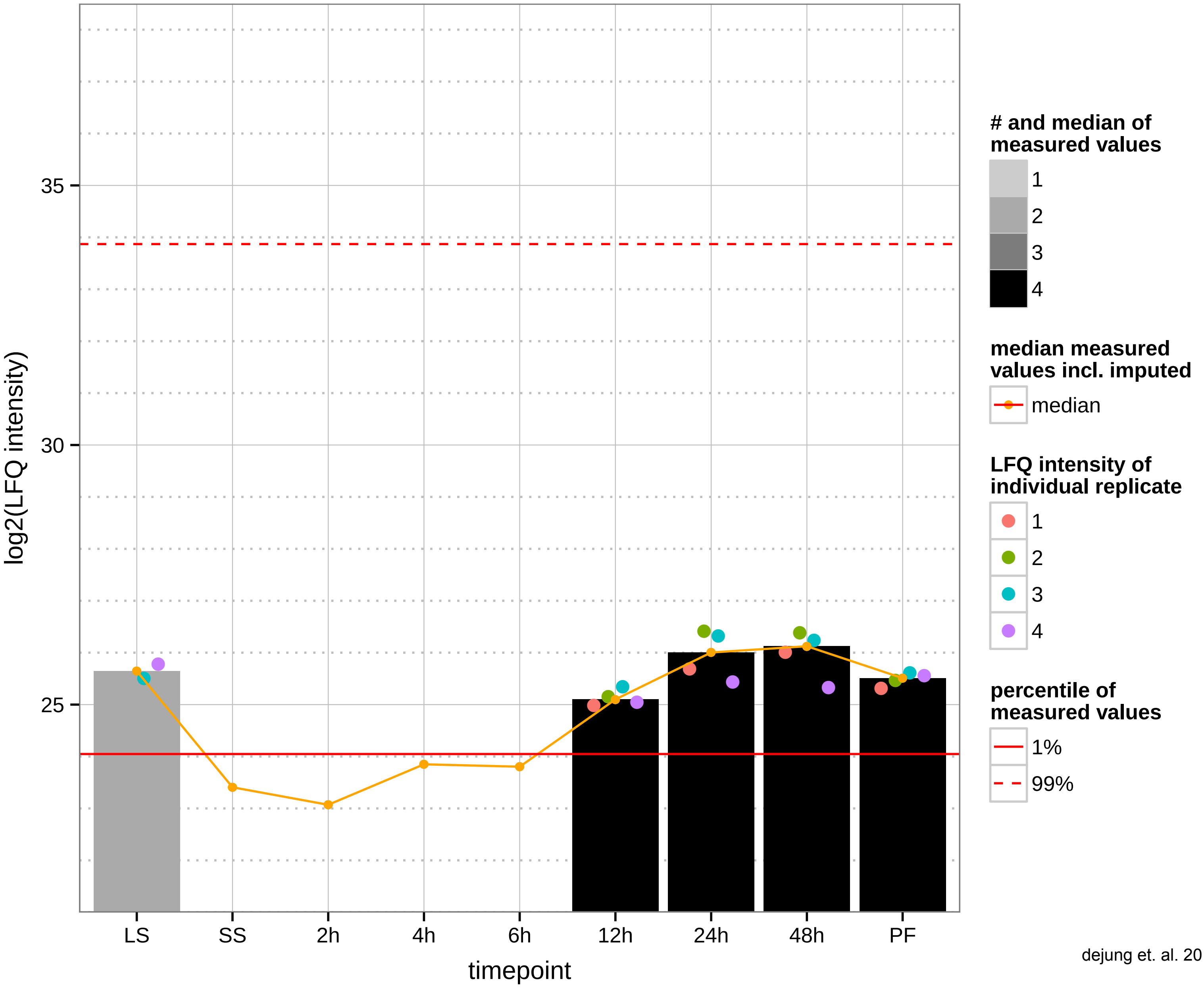
ubiquitin–conjugating enzyme E2, putative, ubiquitin–protein ligase, ubiquitin carrier protein
Tb927.8.6090
AGOF: ATP binding, ubiquitin–protein ligase activity
AGOC: null
AGOP: cellular protein modification process, post–translational protein modification, protein ubiquitination, regulation of protei
PGOF: acid–amino acid ligase activity
PGOC: null
PGOP: null





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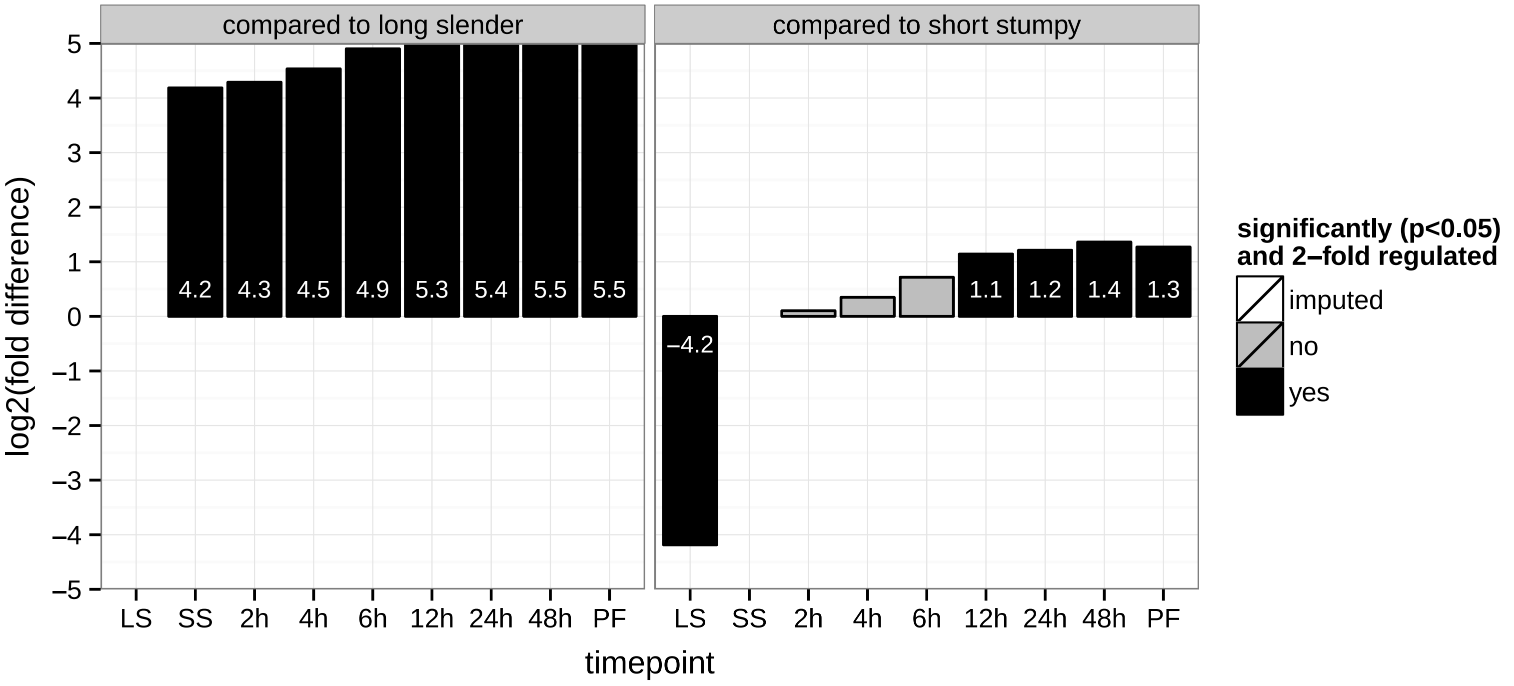
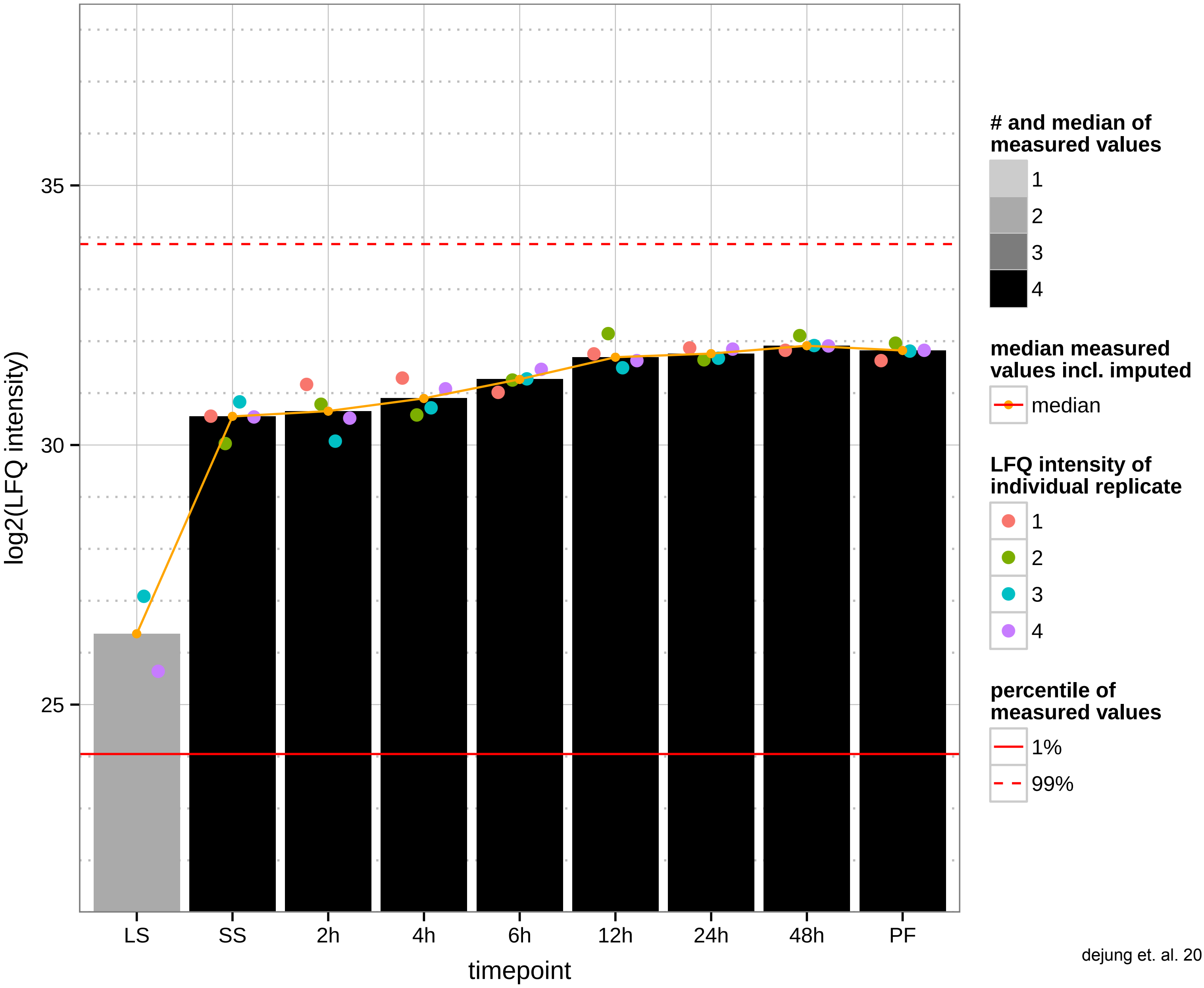
transketolase, putative (TK)
Tb927.8.6170
AGOF: transketolase activity
AGOC: cytoplasm, glycosome
AGOP: pentose−phosphate shunt
PGOF: catalytic activity, transketolase activity
PGOC: null
PGOP: metabolic process





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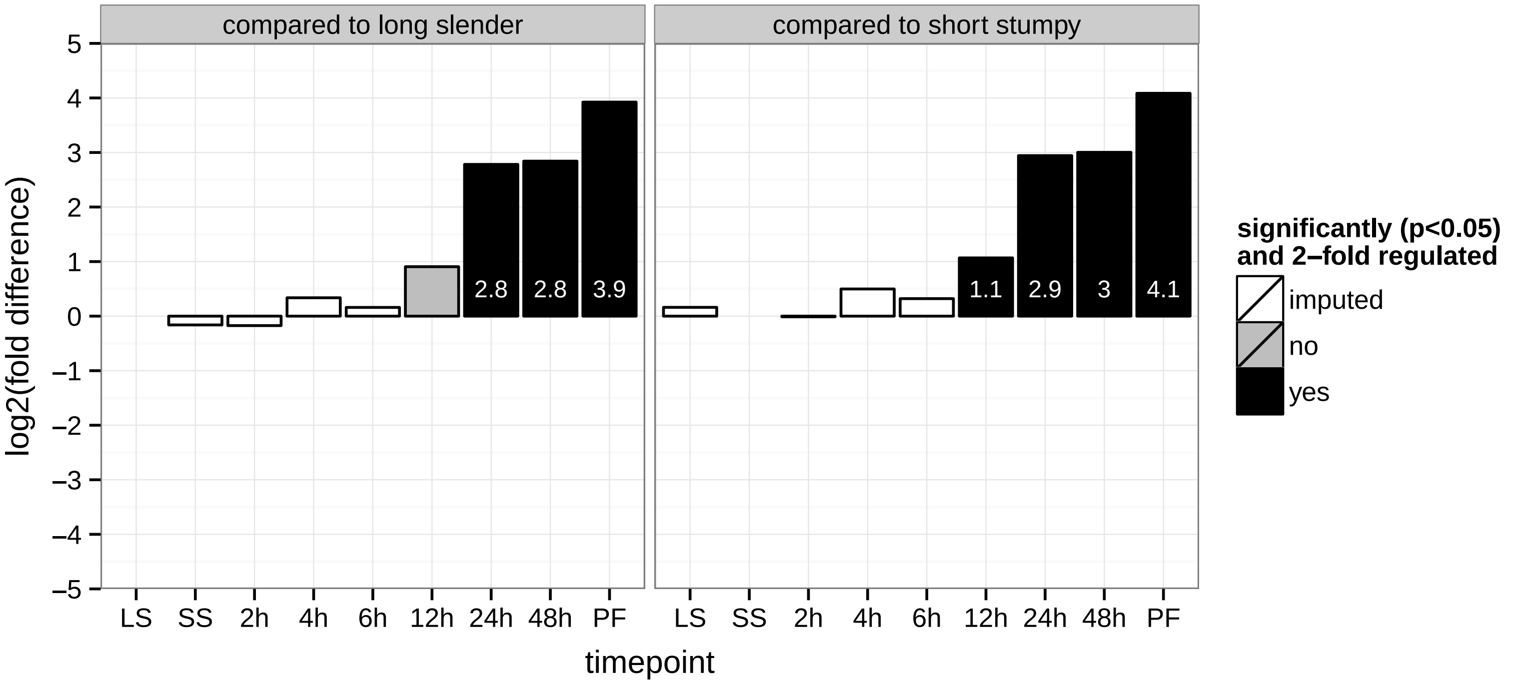
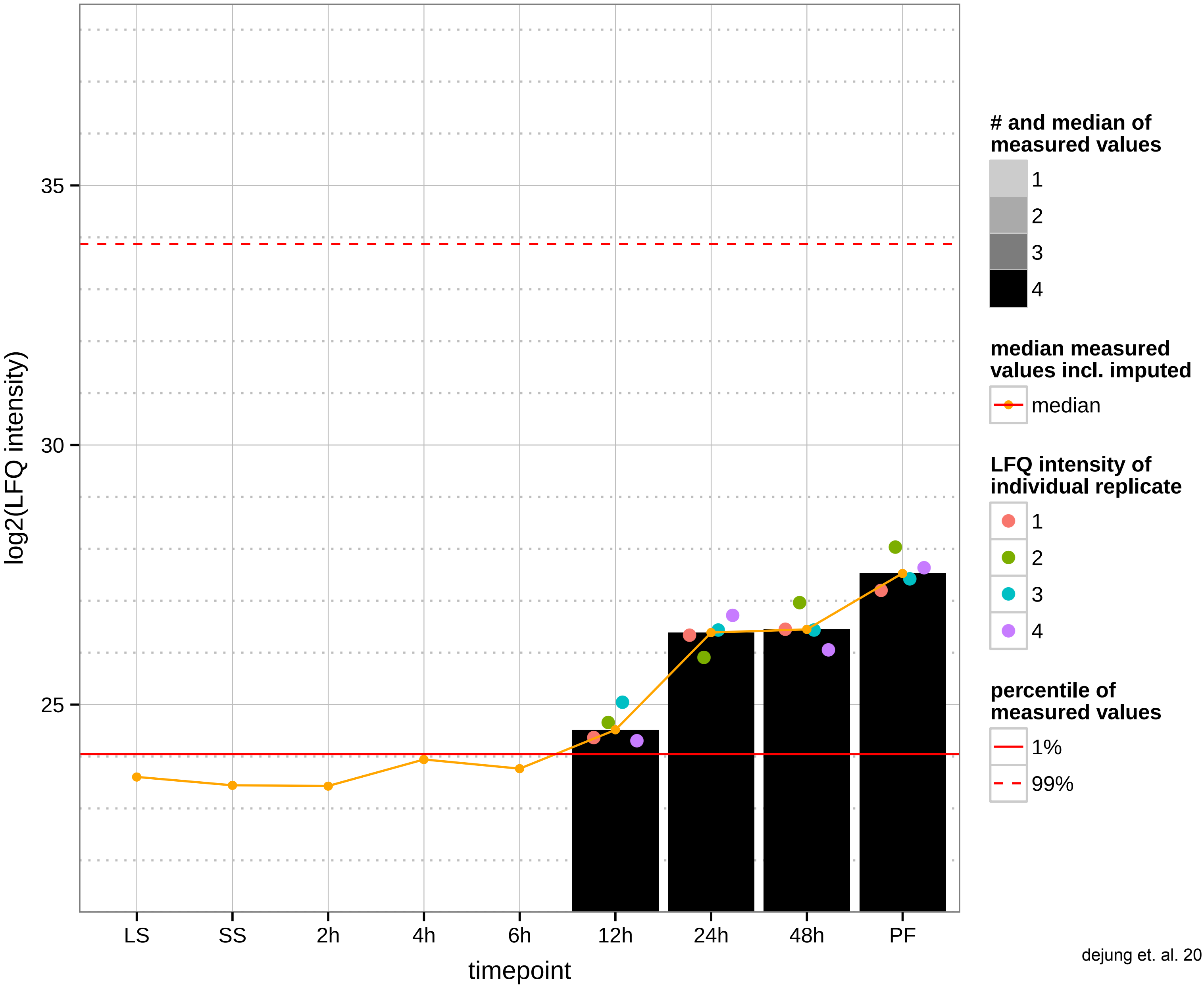
short–chain dehydrogenase, putative
Tb927.8.6410
AGOF: oxidoreductase activity
AGOC: integral to membrane, mitochondrial inner membrane, mitochondrion
AGOP: metabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process





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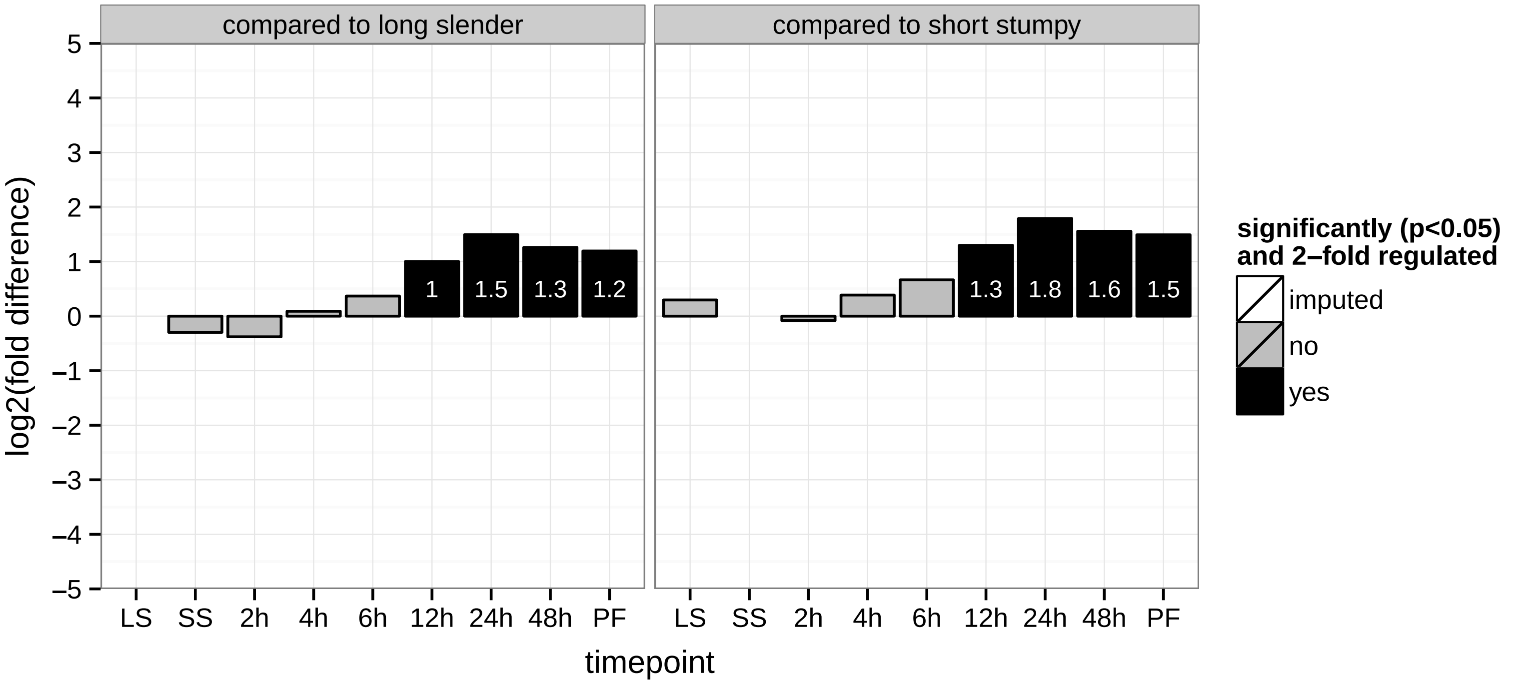
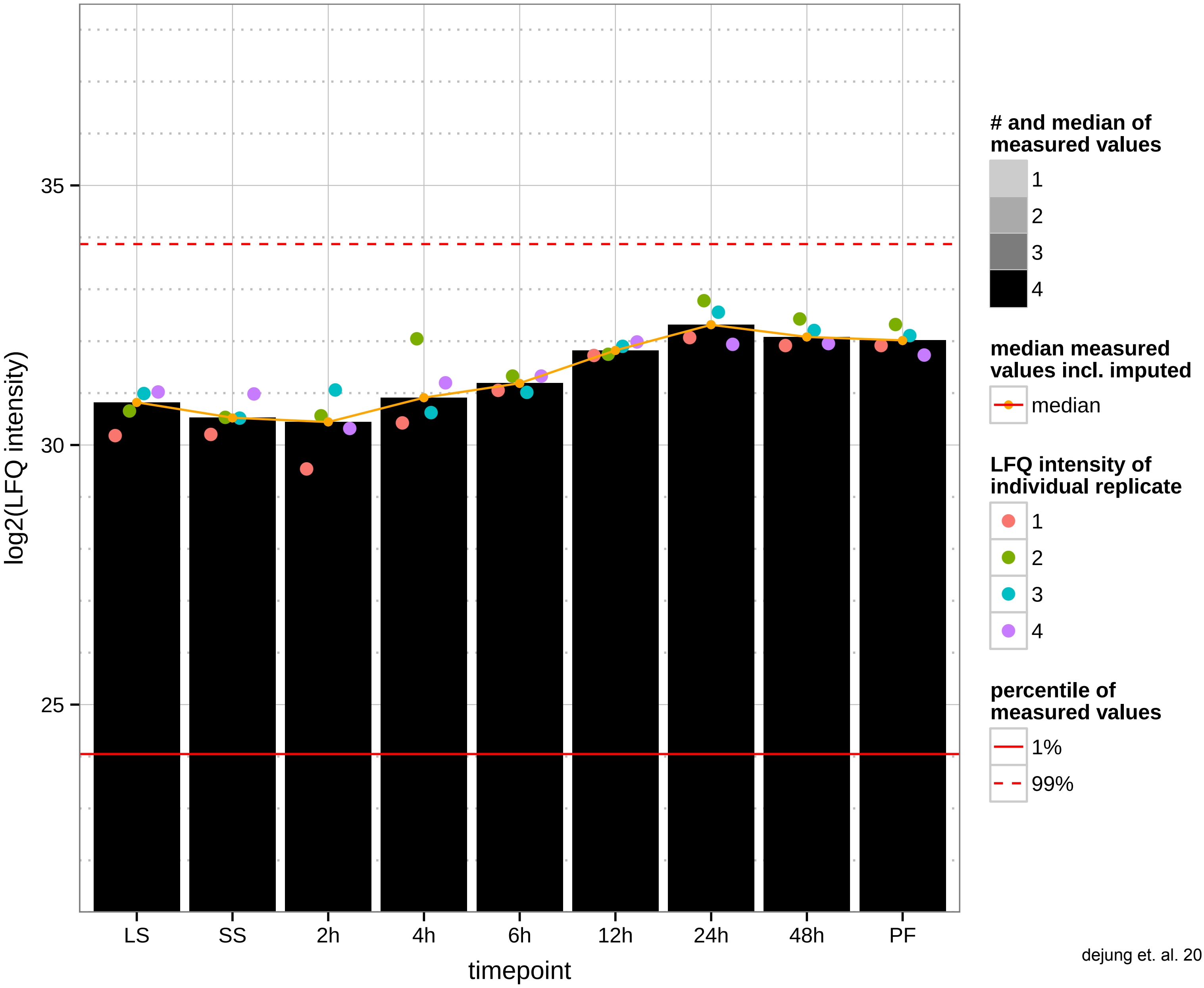
translationally controlled tumor protein (TCTP), putative
Tb927.8.6750
AGOF: null
AGOC: cytoplasm, mitochondrion
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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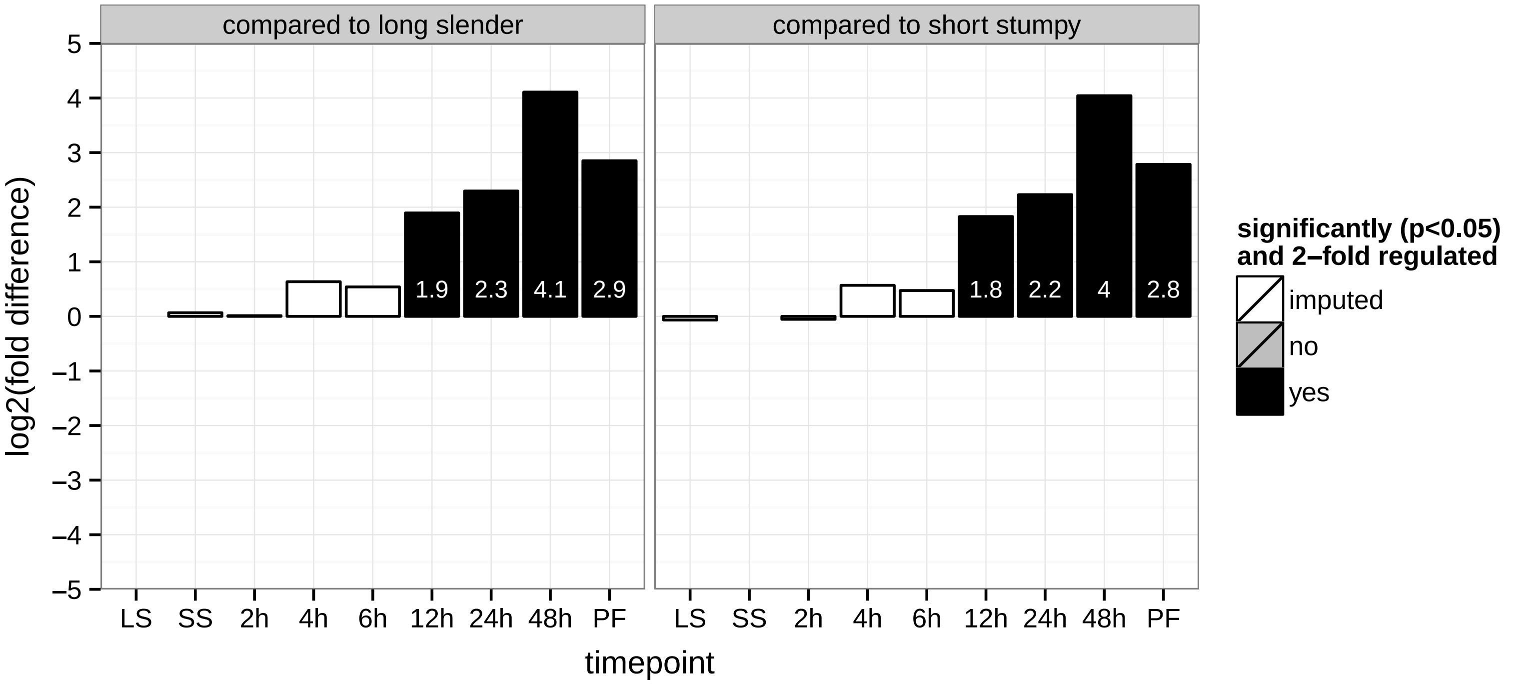
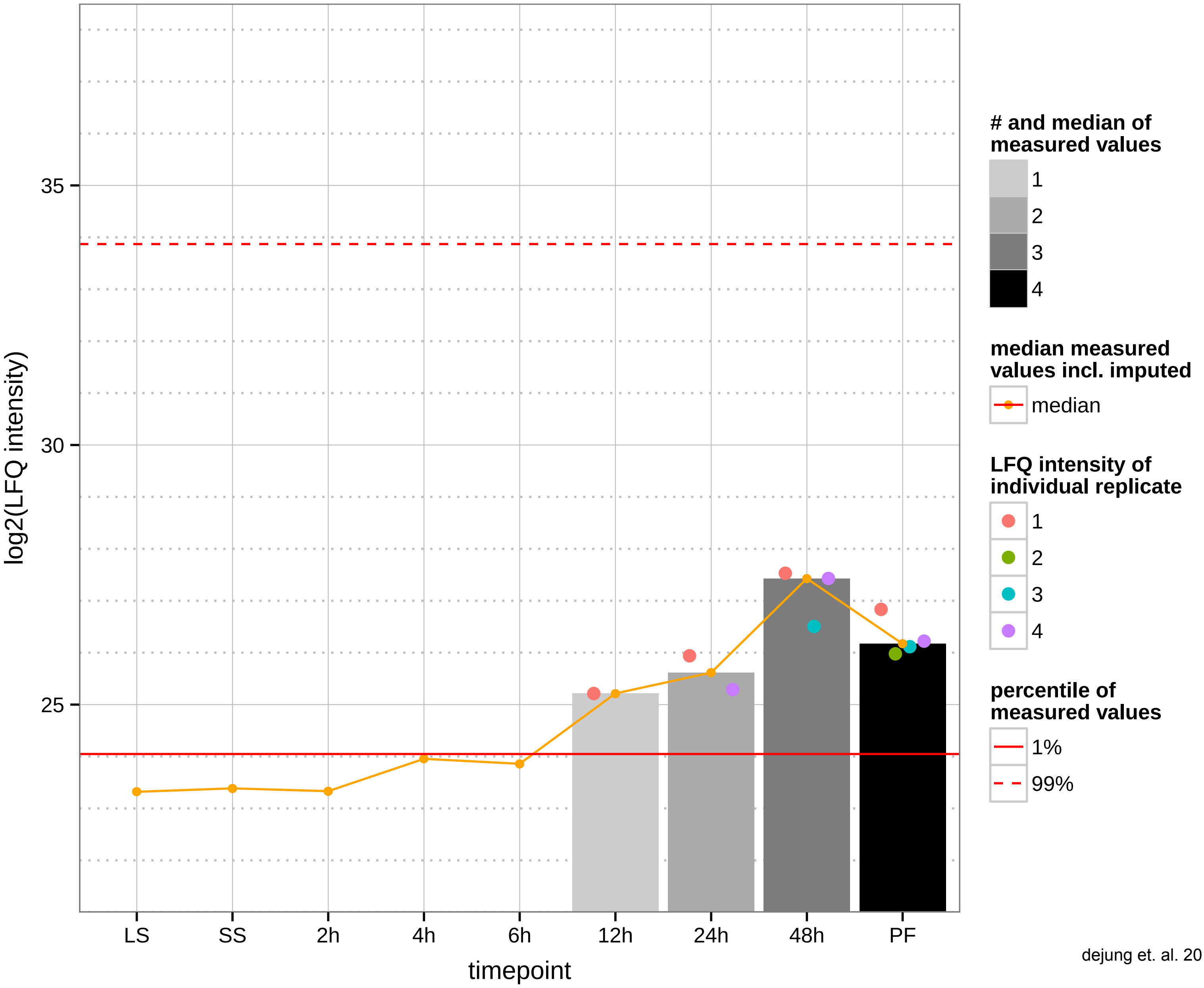
hypothetical protein, conserved
Tb927.8.6890
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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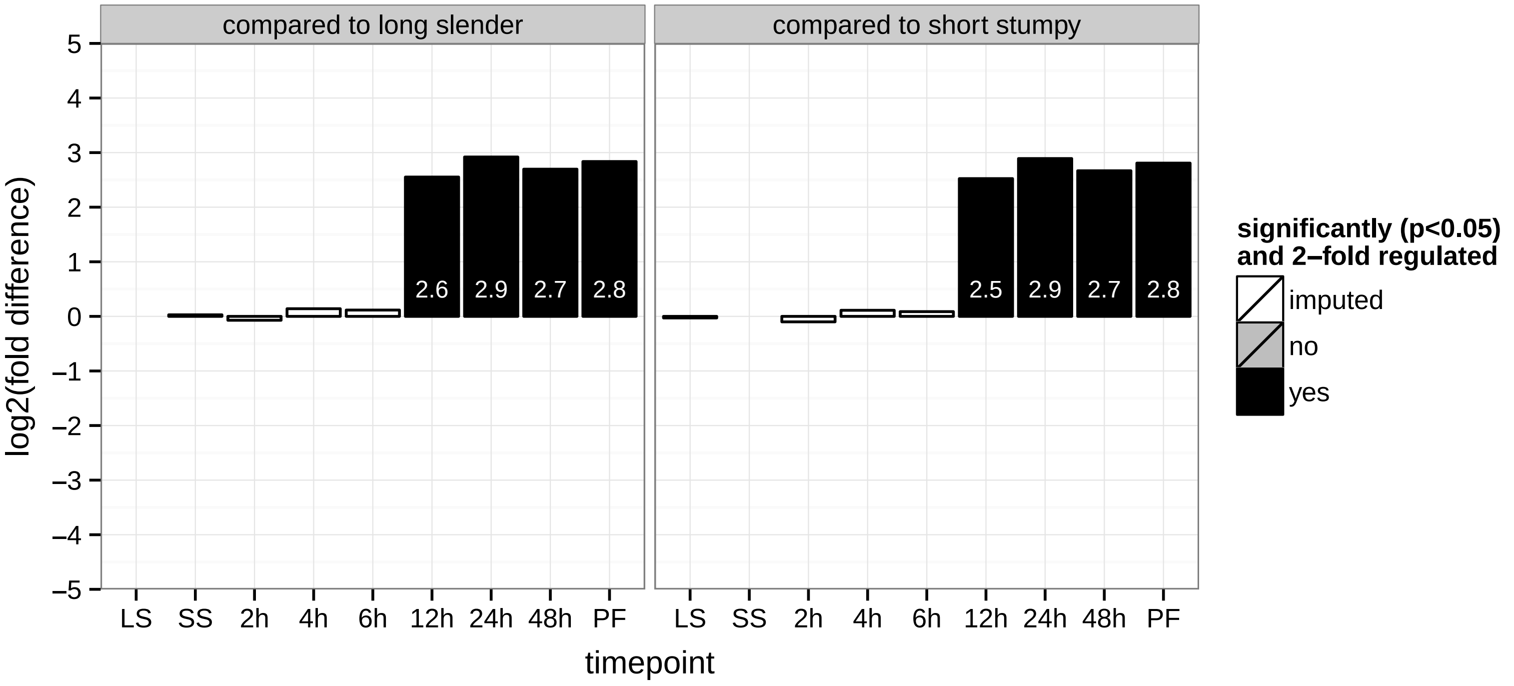
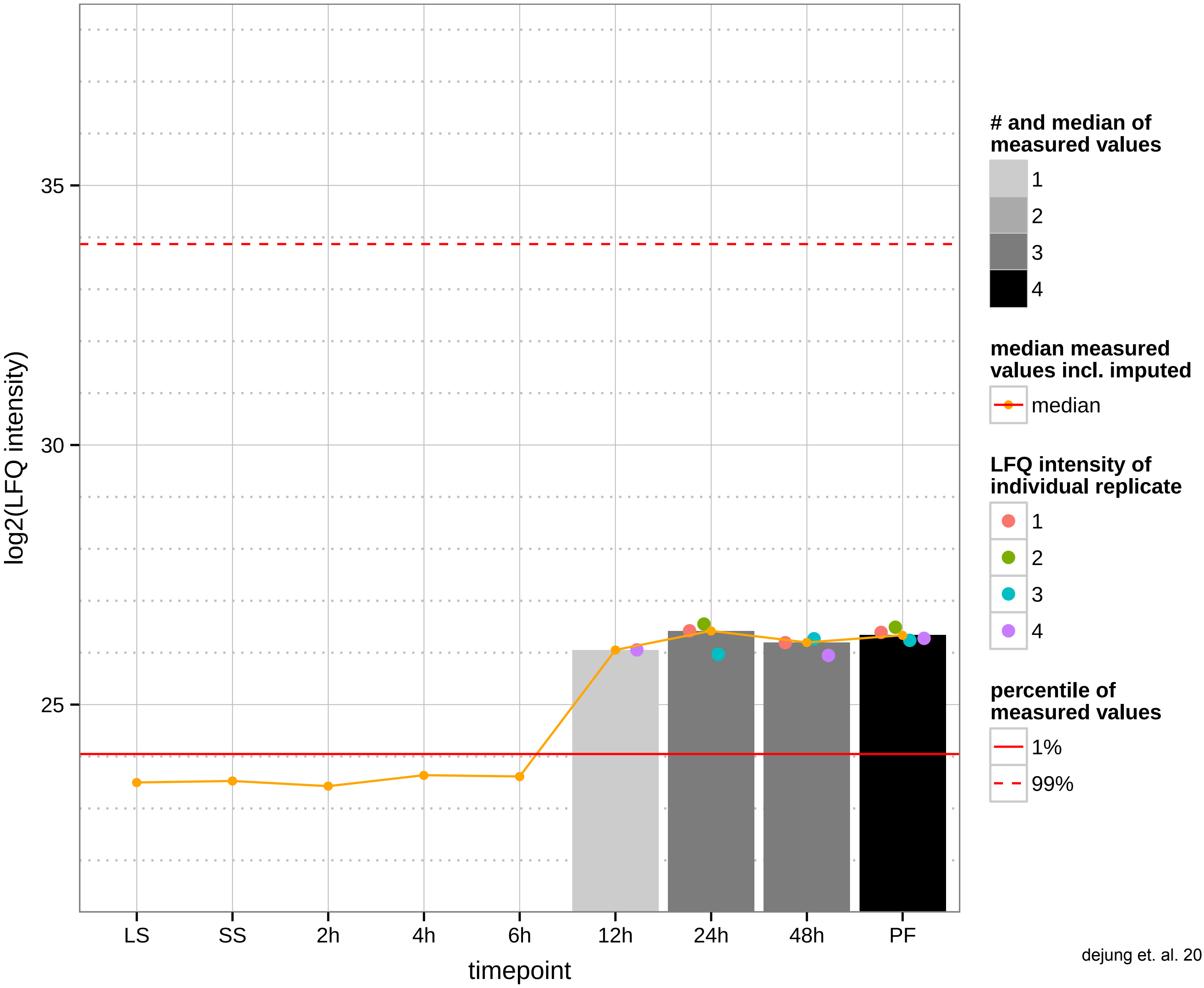
hypothetical protein, conserved
Tb927.8.6960
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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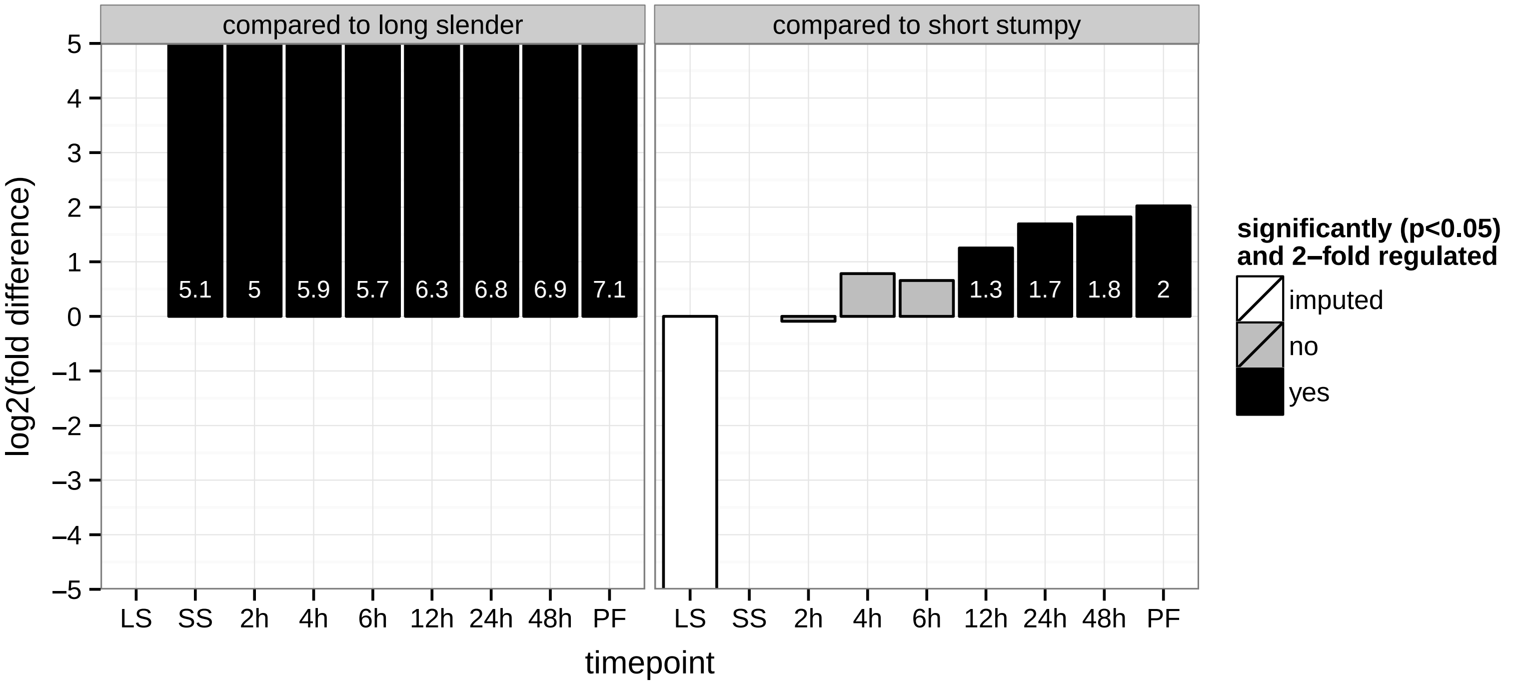
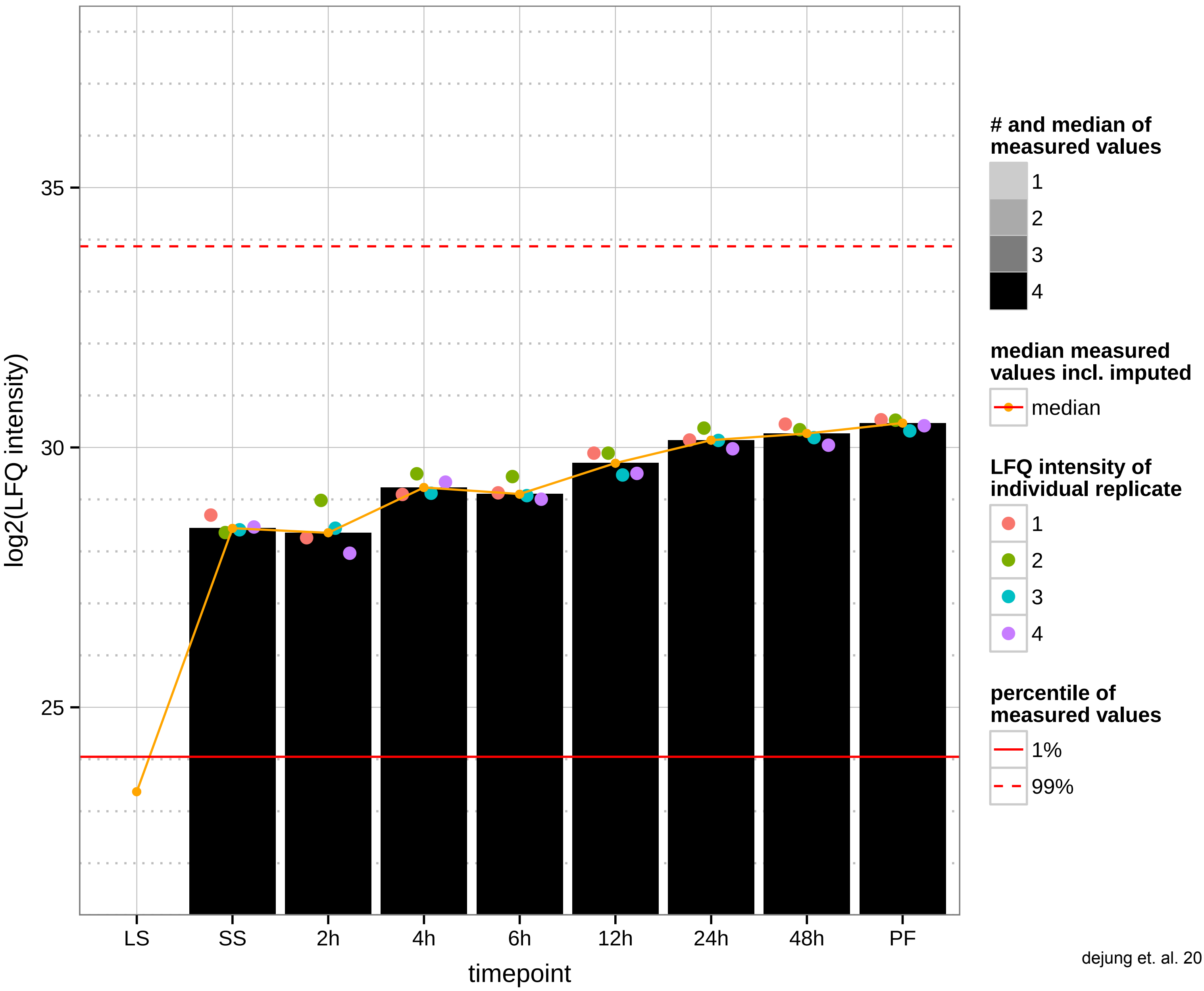
3, 2–trans–enoyl–CoA isomerase, mitochondrial precursor, putative
Tb927.8.7530
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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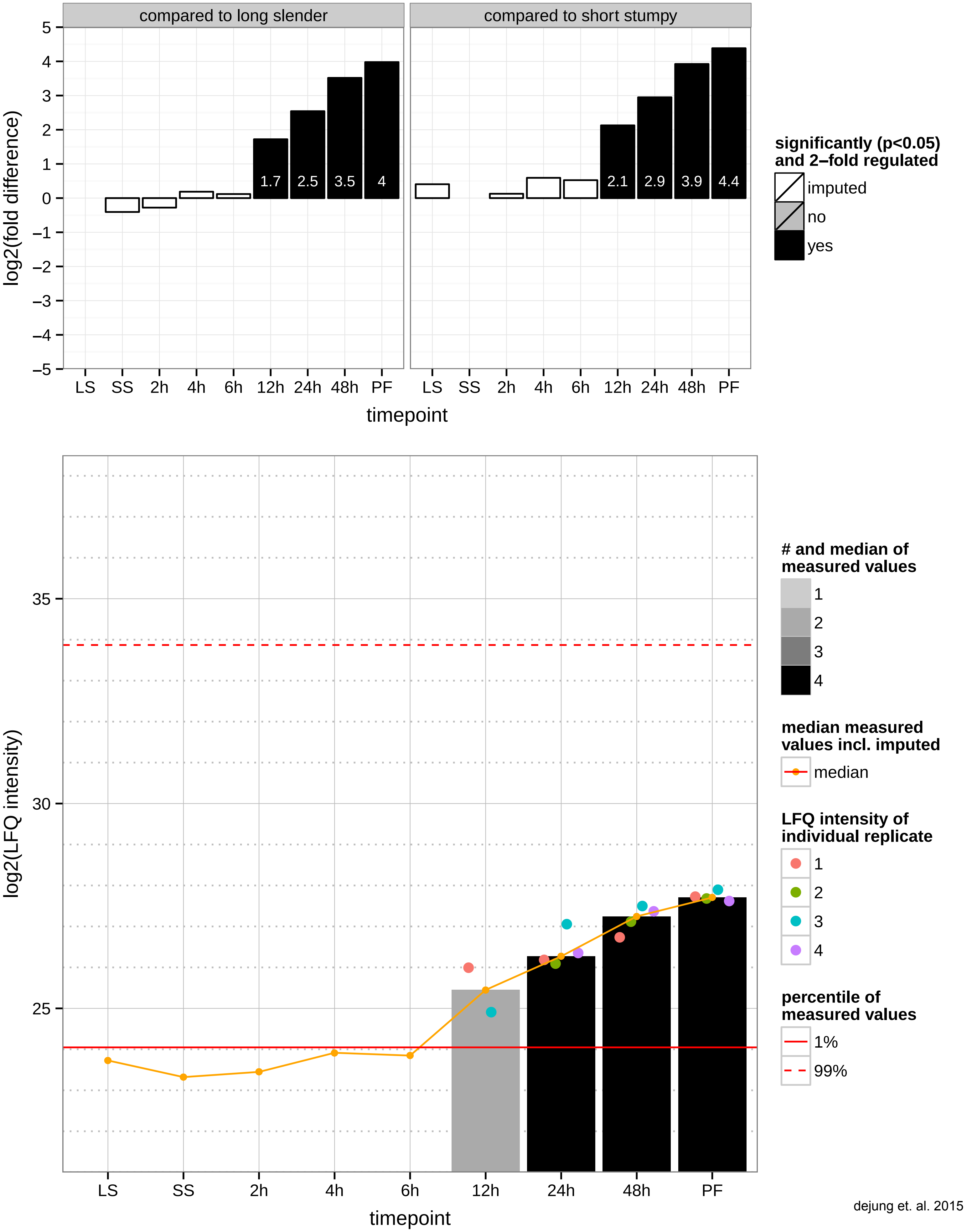
hypothetical protein, conserved
Tb927.8.960;Tb927.8.940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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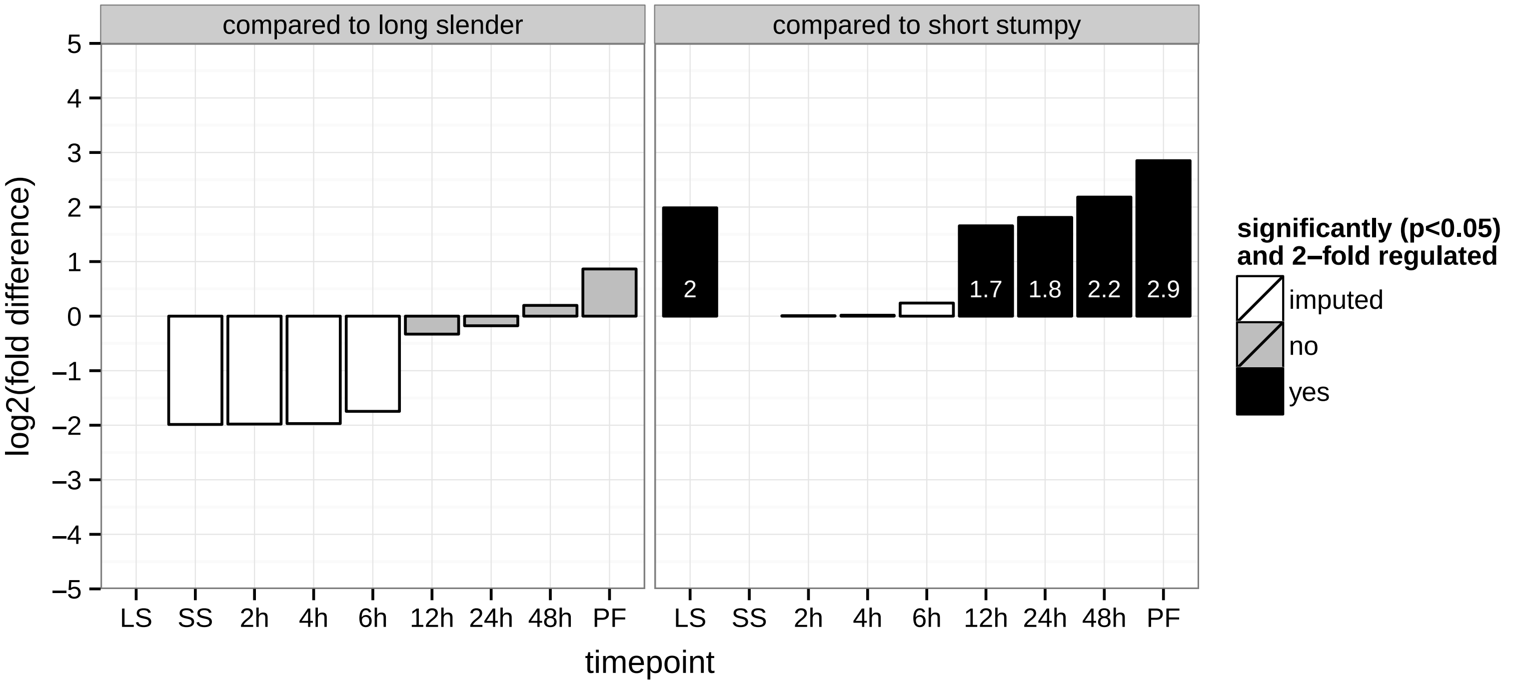
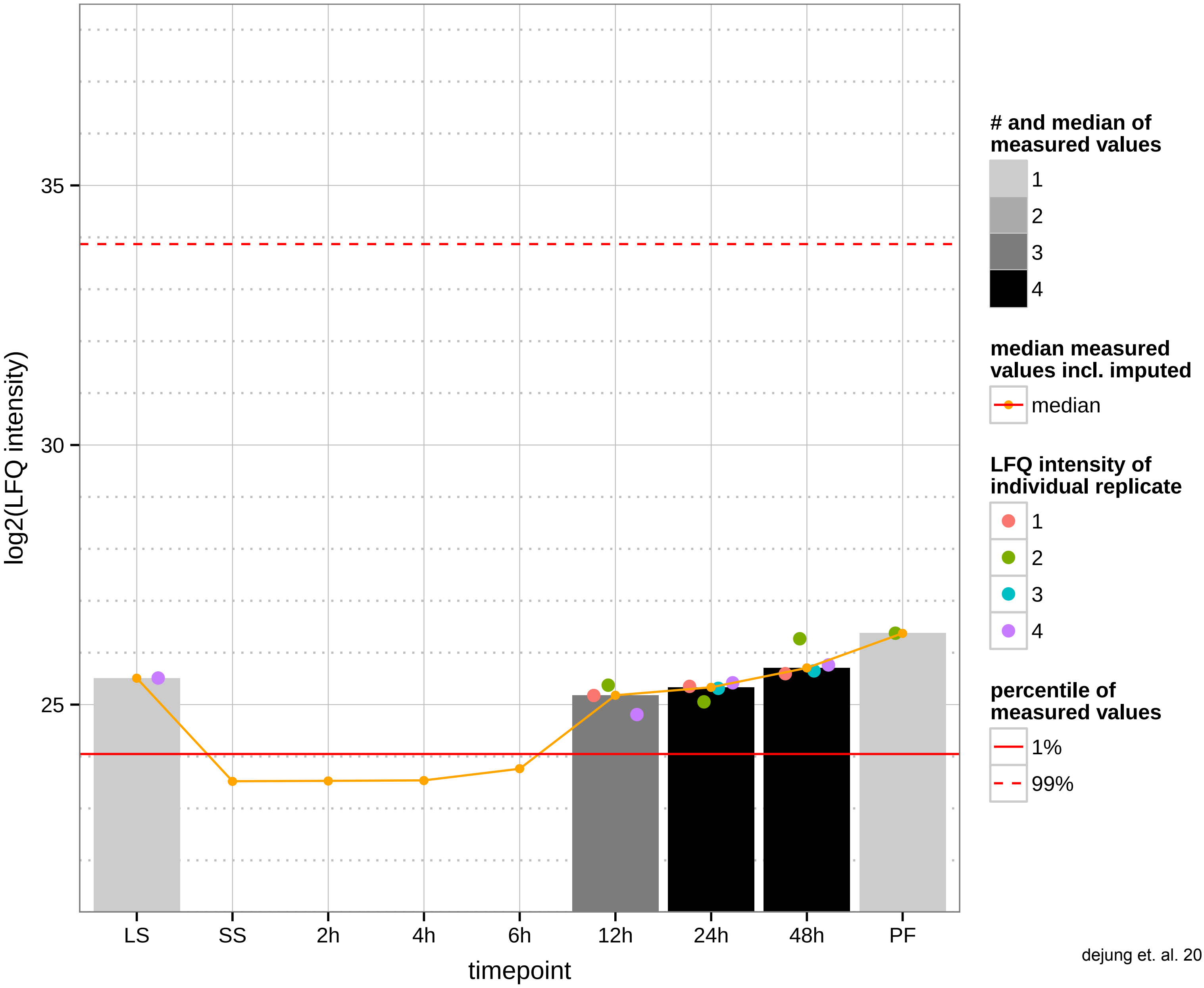
hypothetical protein, conserved
Tb927.9.10490
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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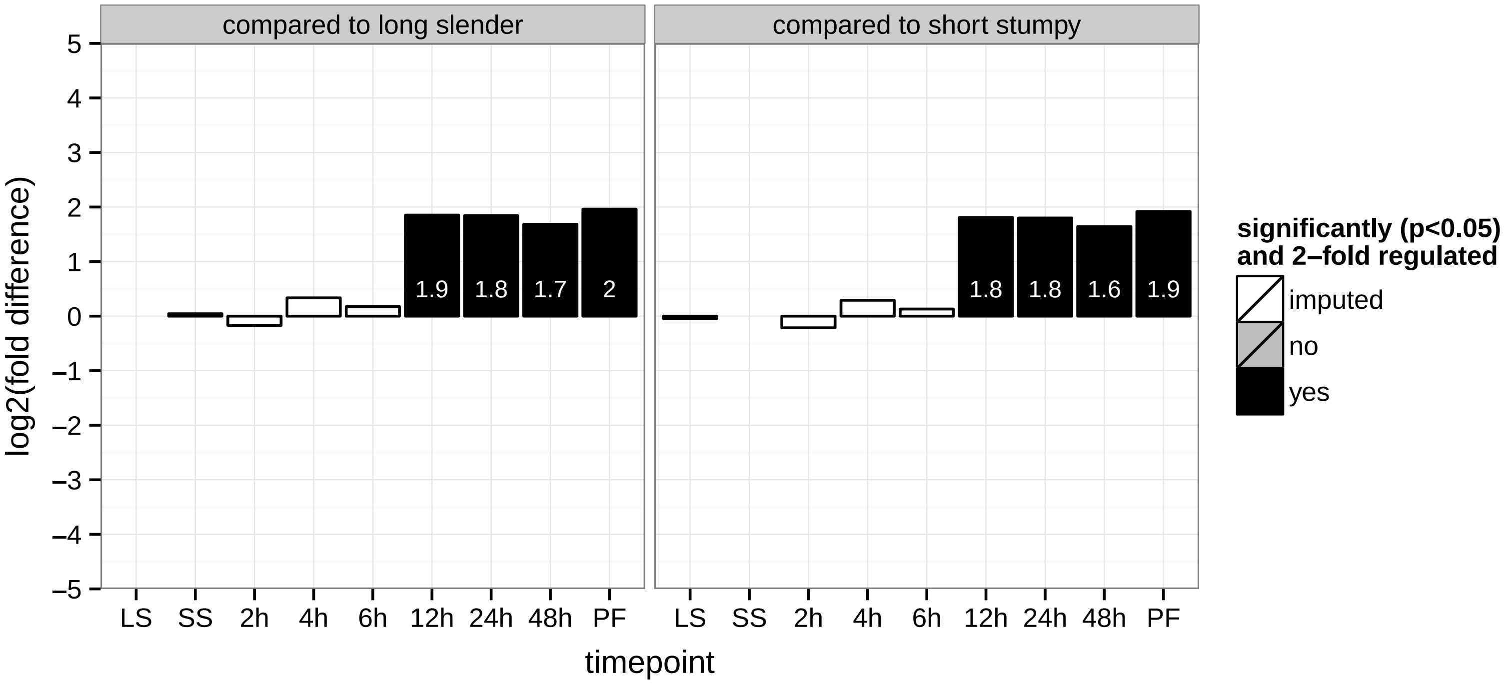
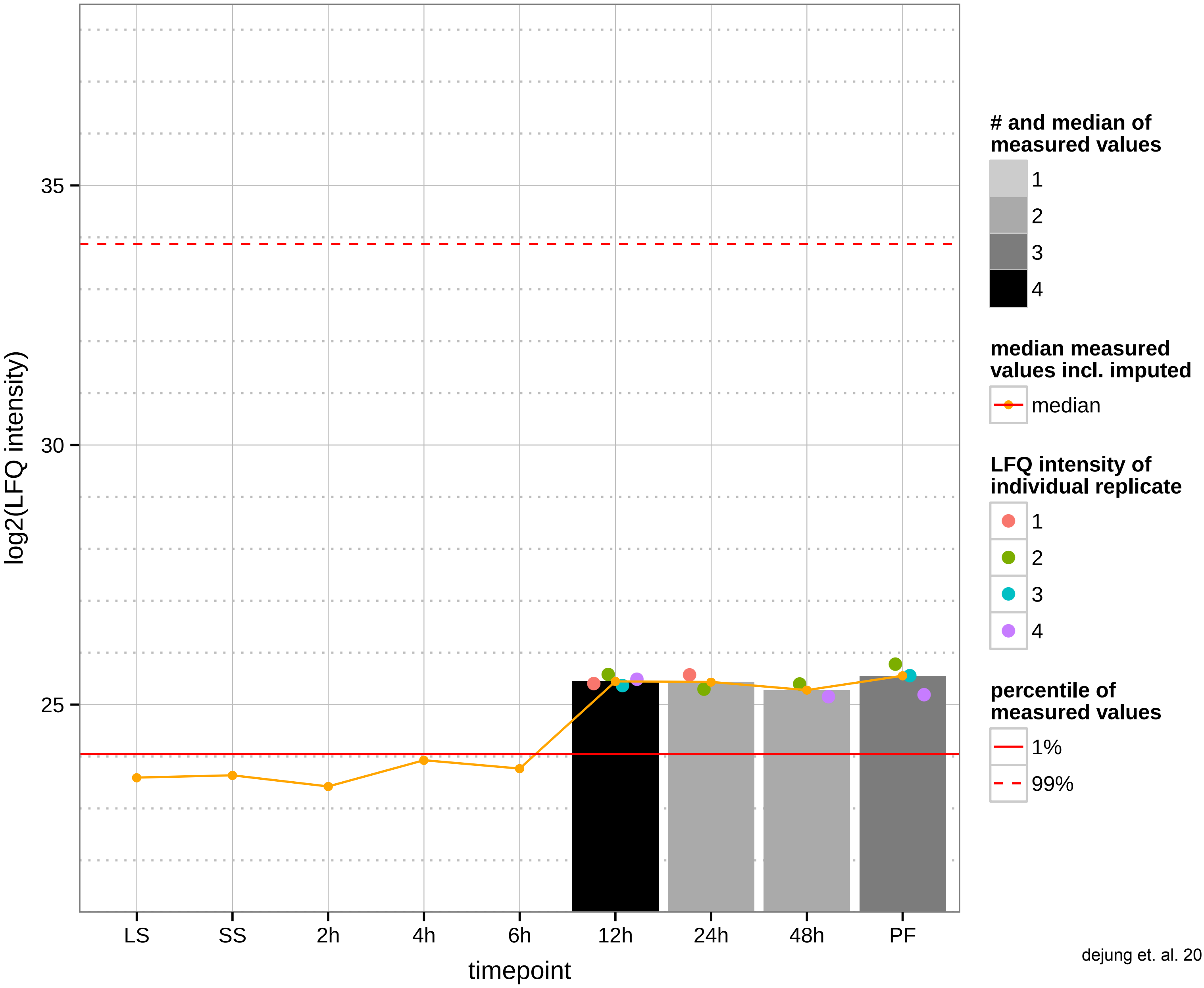
hypothetical protein, conserved
Tb927.9.10880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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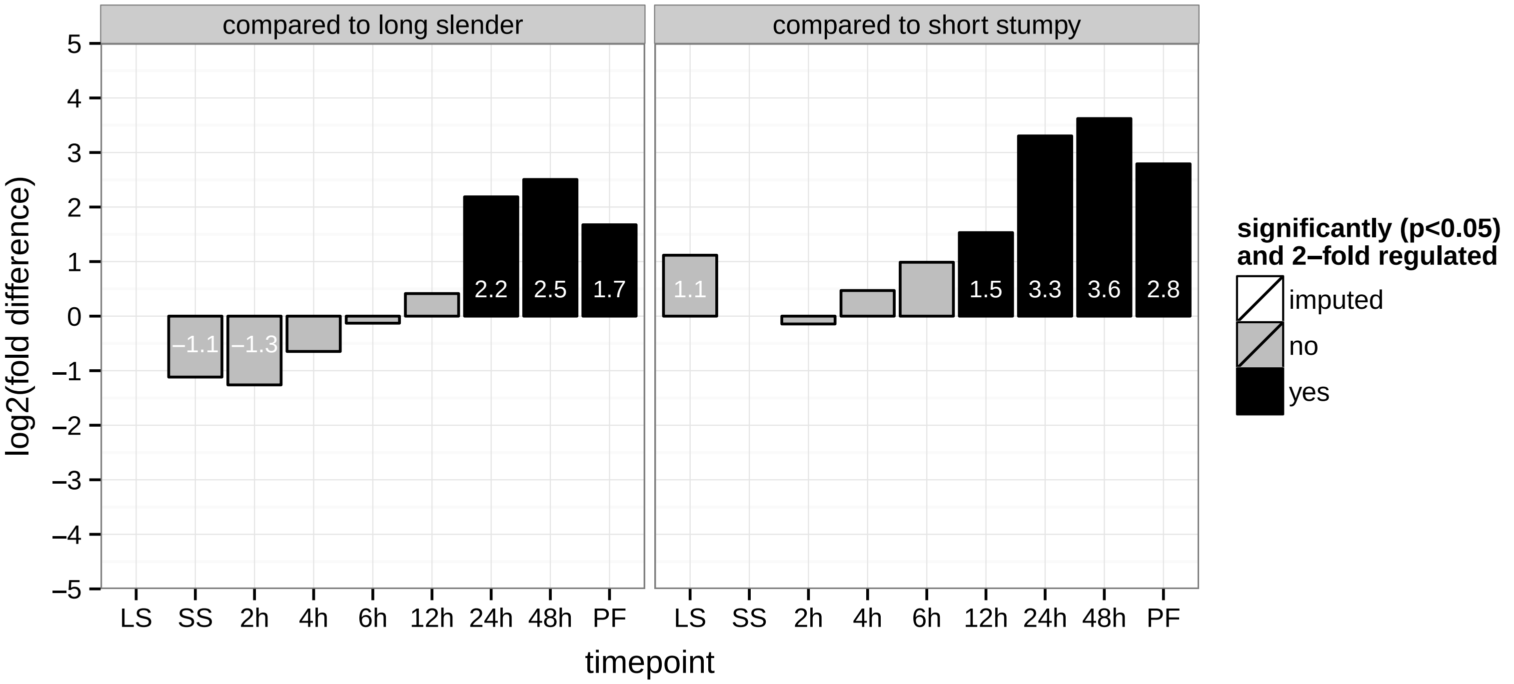
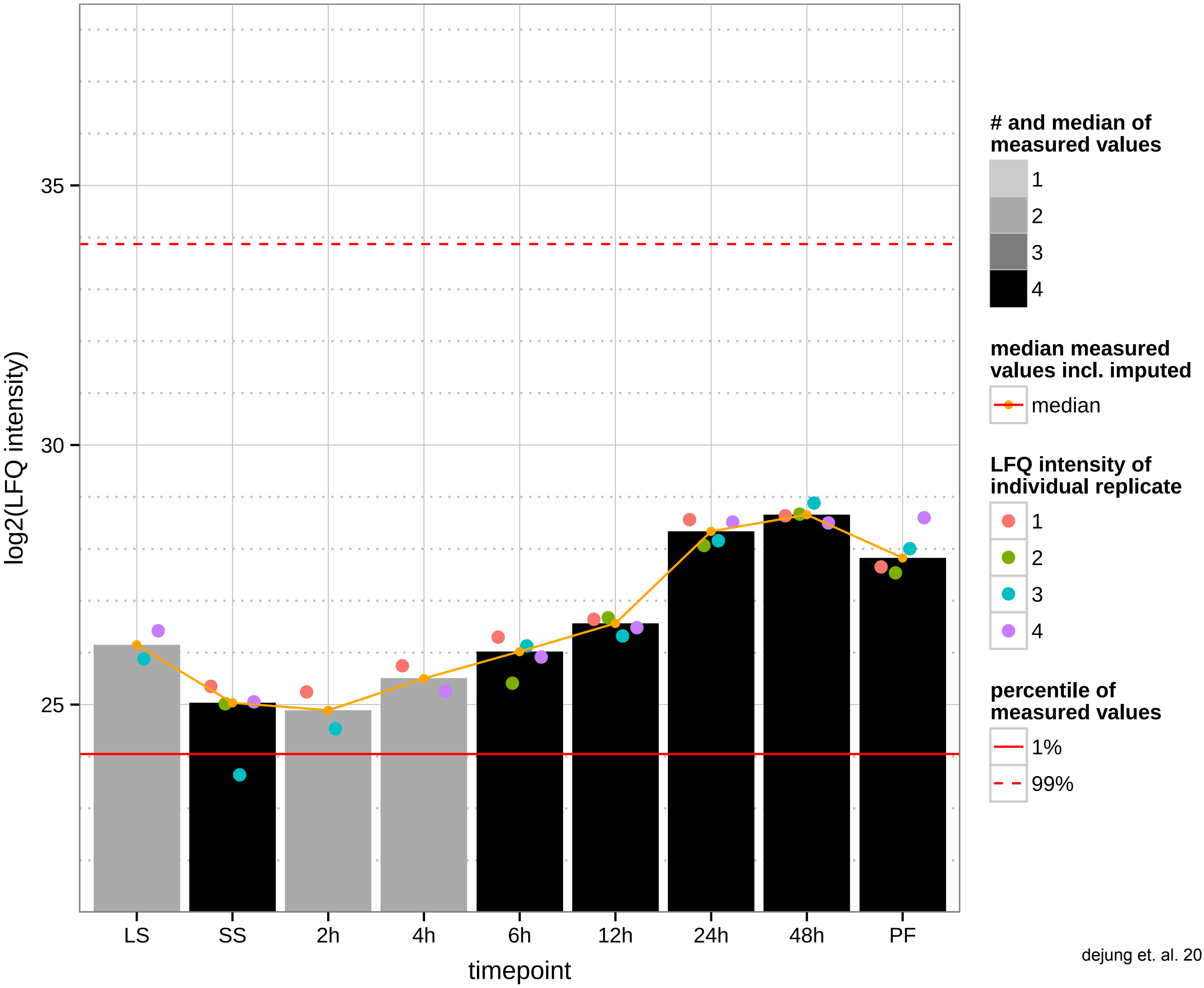
RNA–binding protein, putative (RBP35)
Tb927.9.12360
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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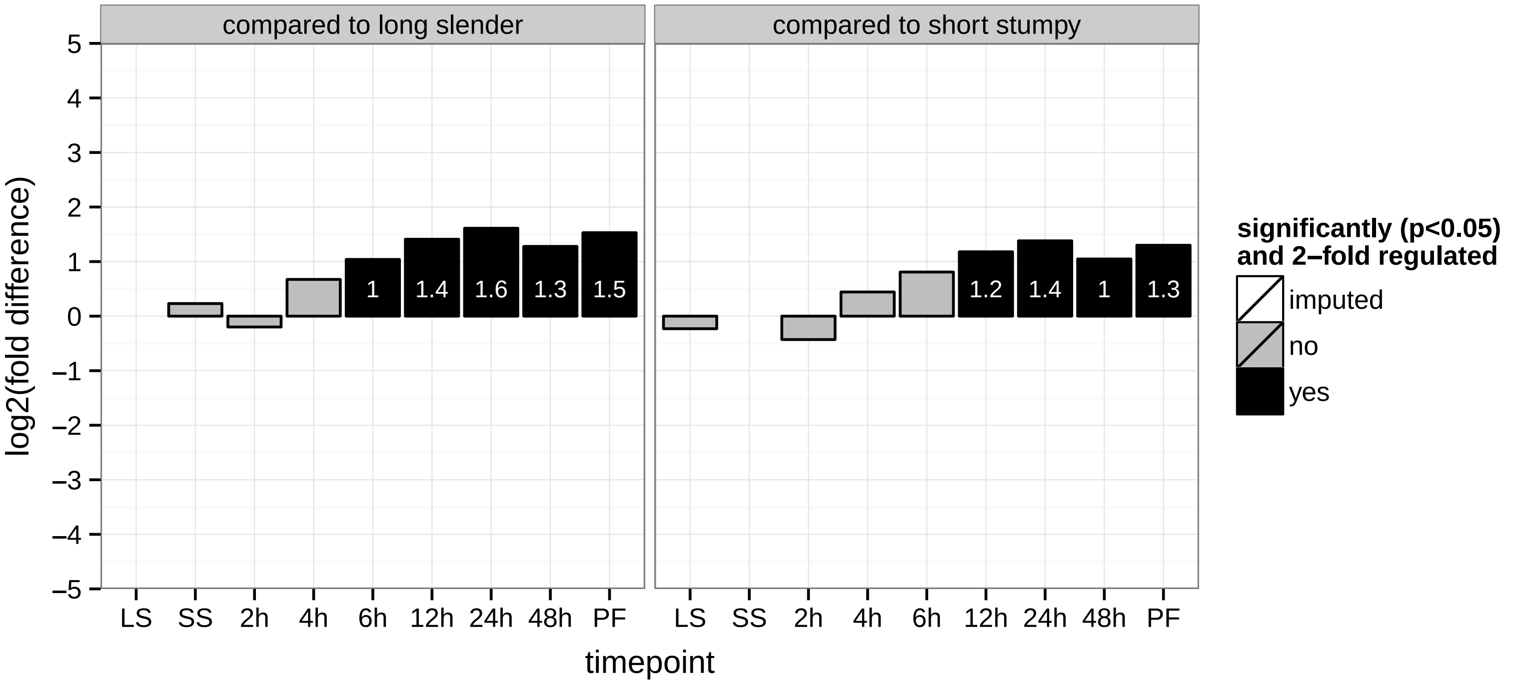
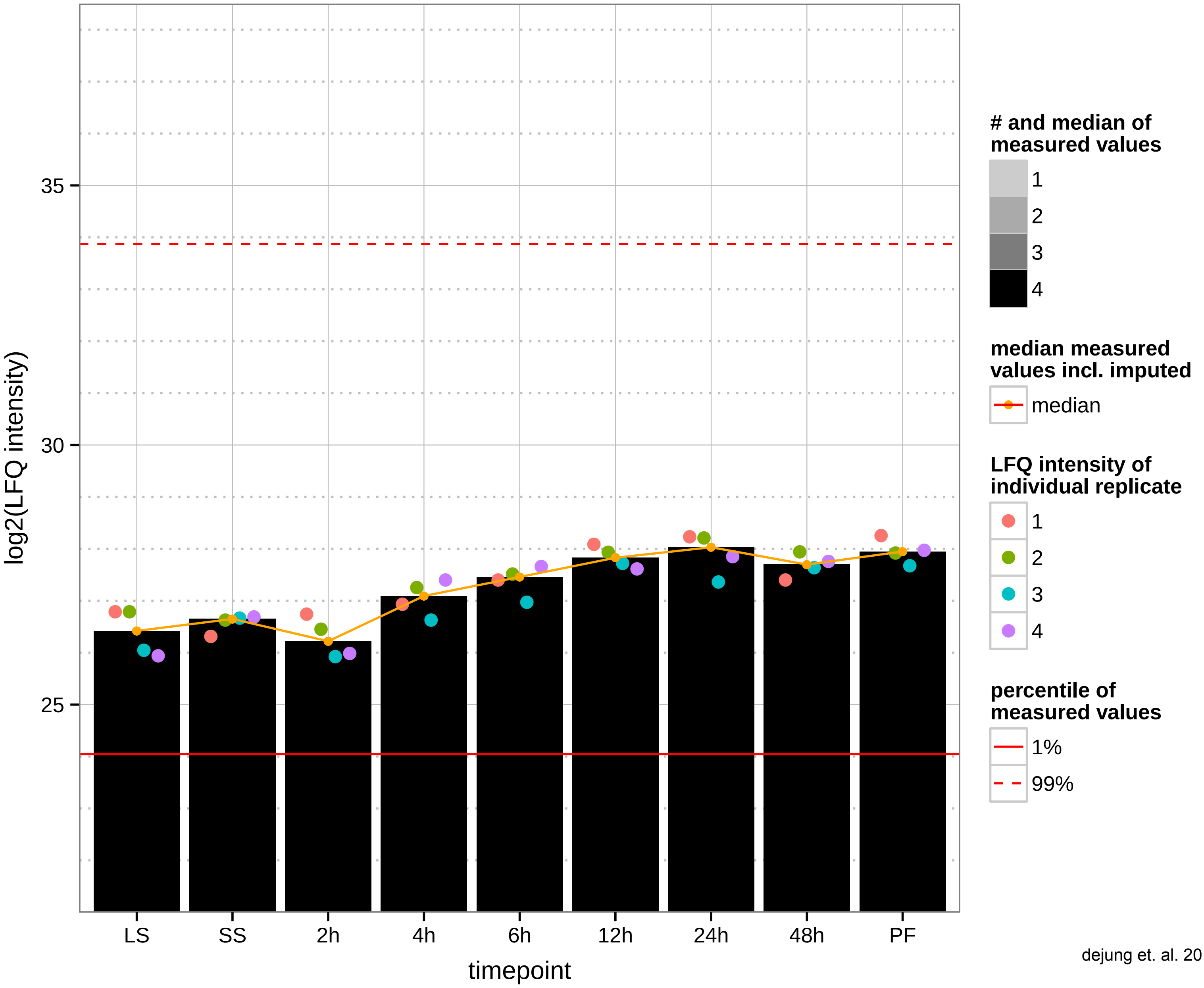
Double RNA binding domain protein 9 (DRBD9)
Tb927.9.13280
AGOF: RNA binding
AGOC: nucleus
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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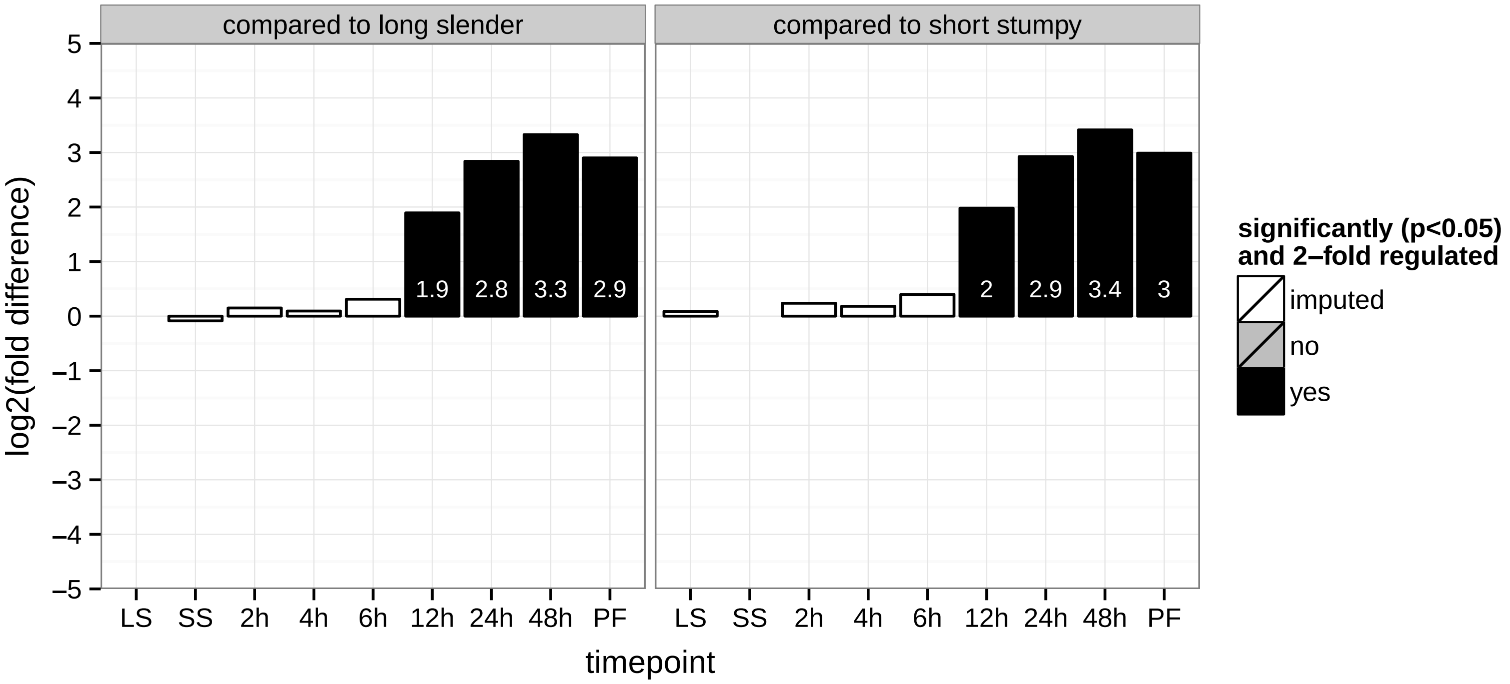
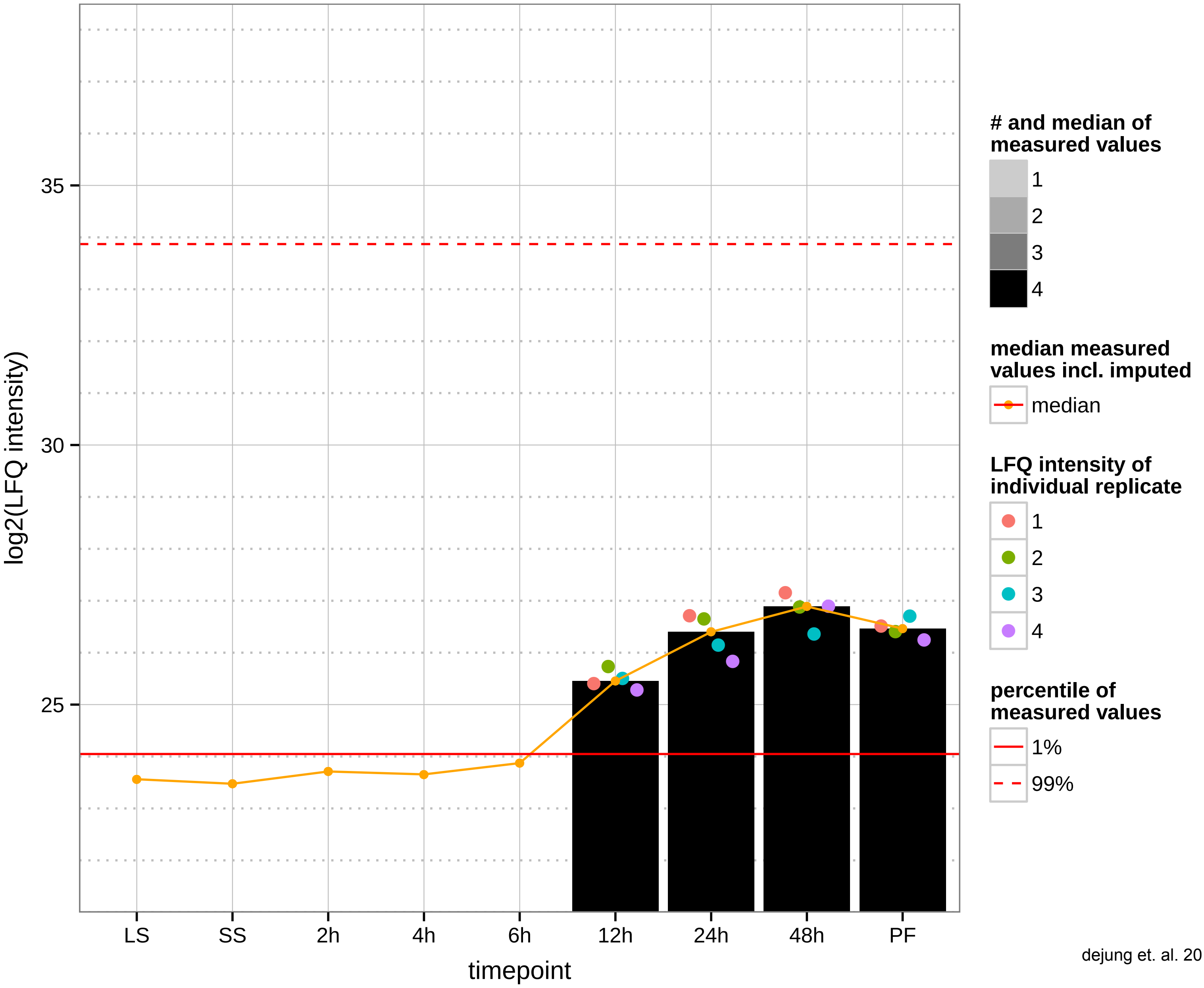
hypothetical protein, conserved
Tb927.9.14200
AGOF: methyltransferase activity
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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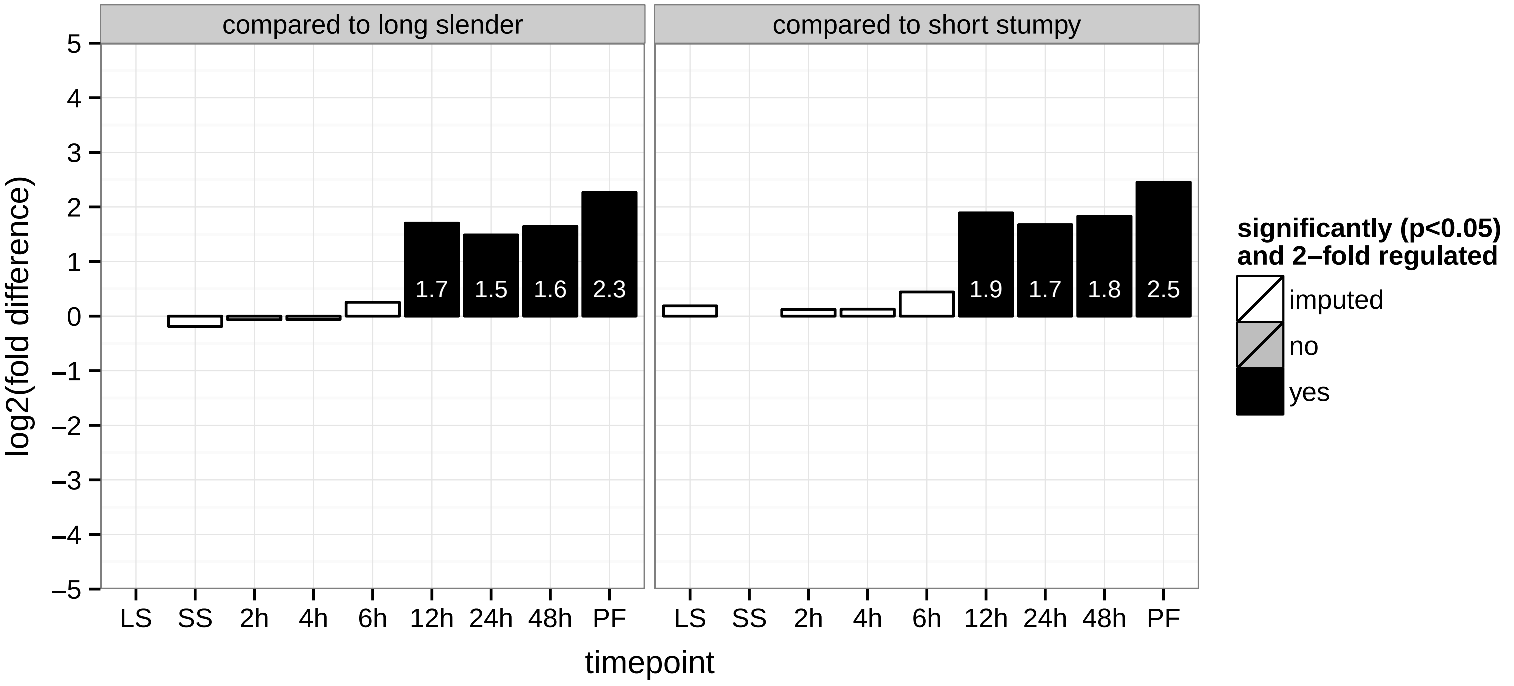
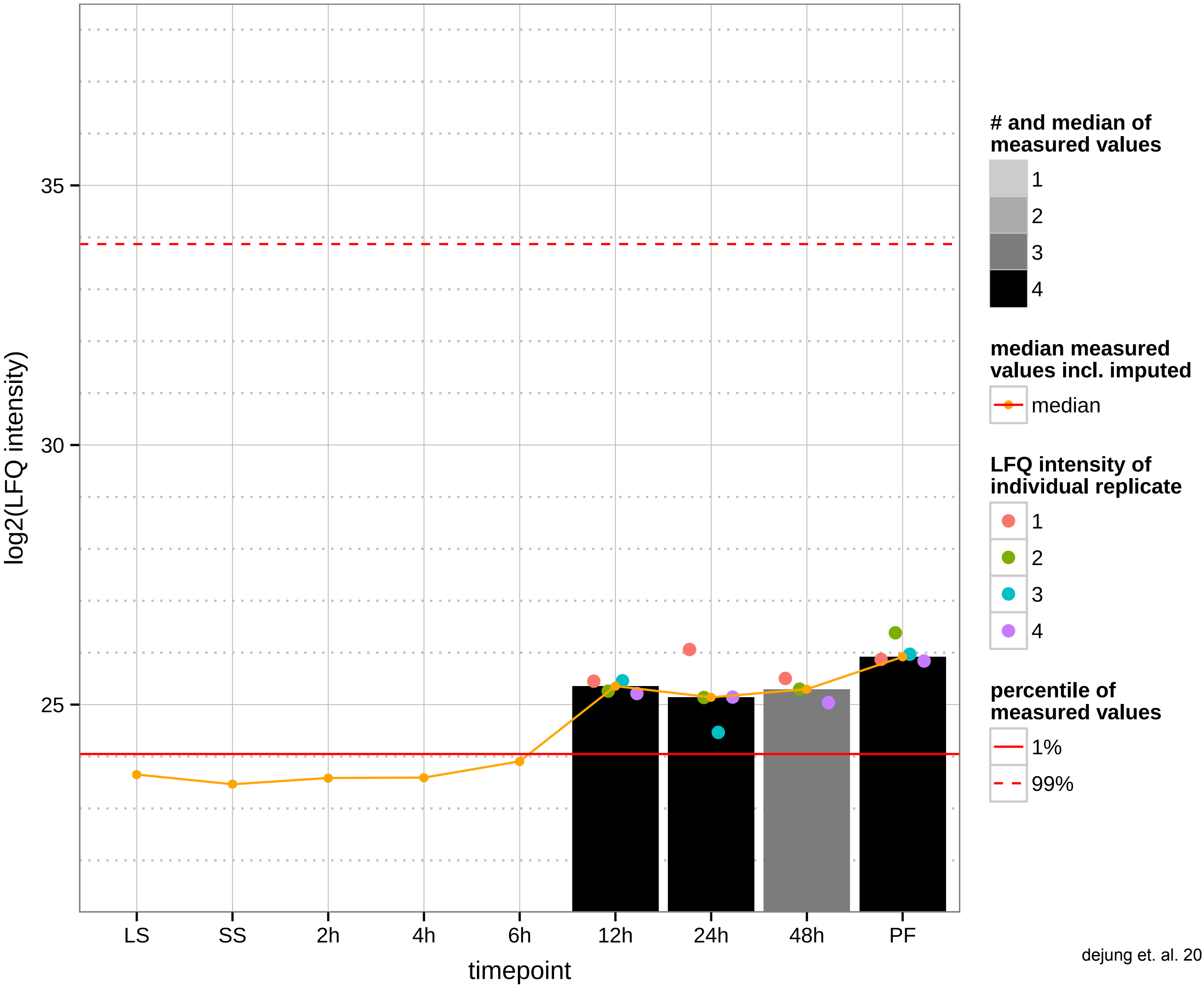
unspecified product
Tb927.9.14550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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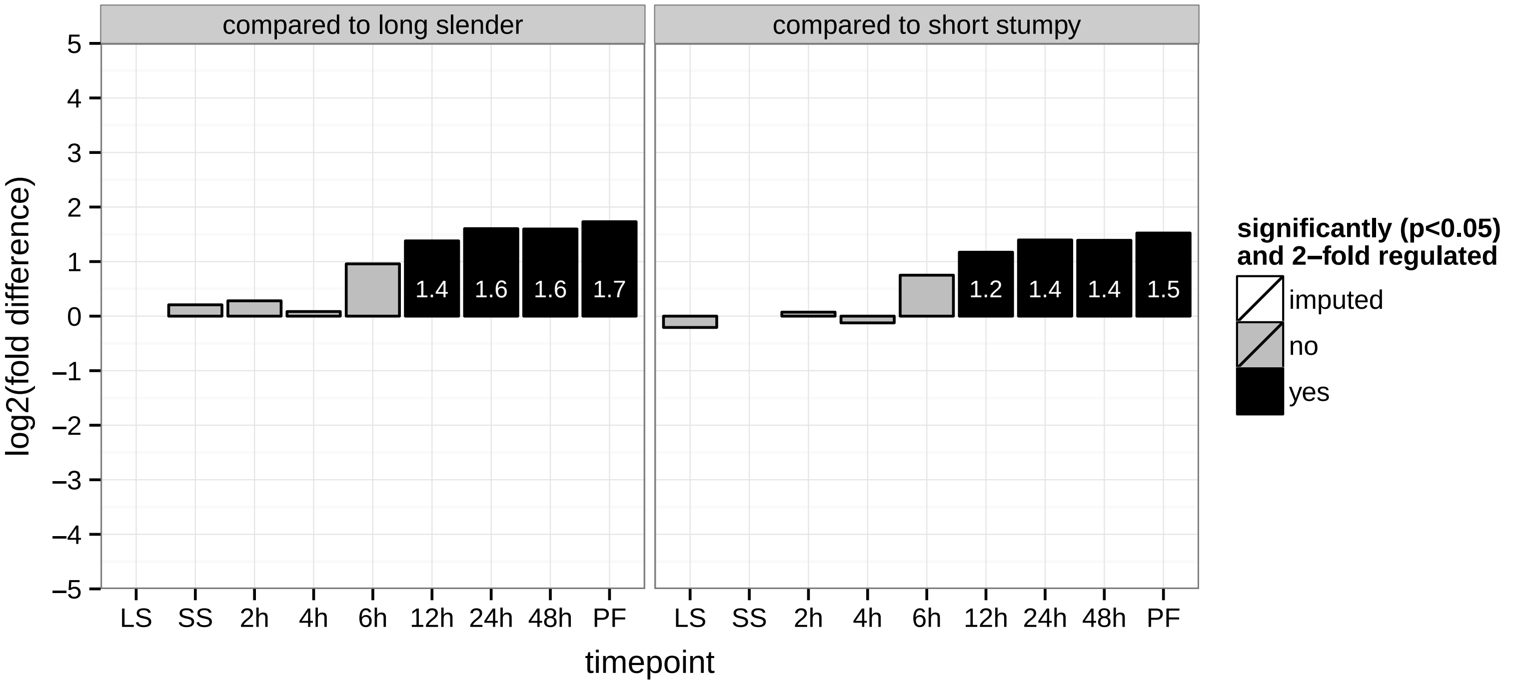
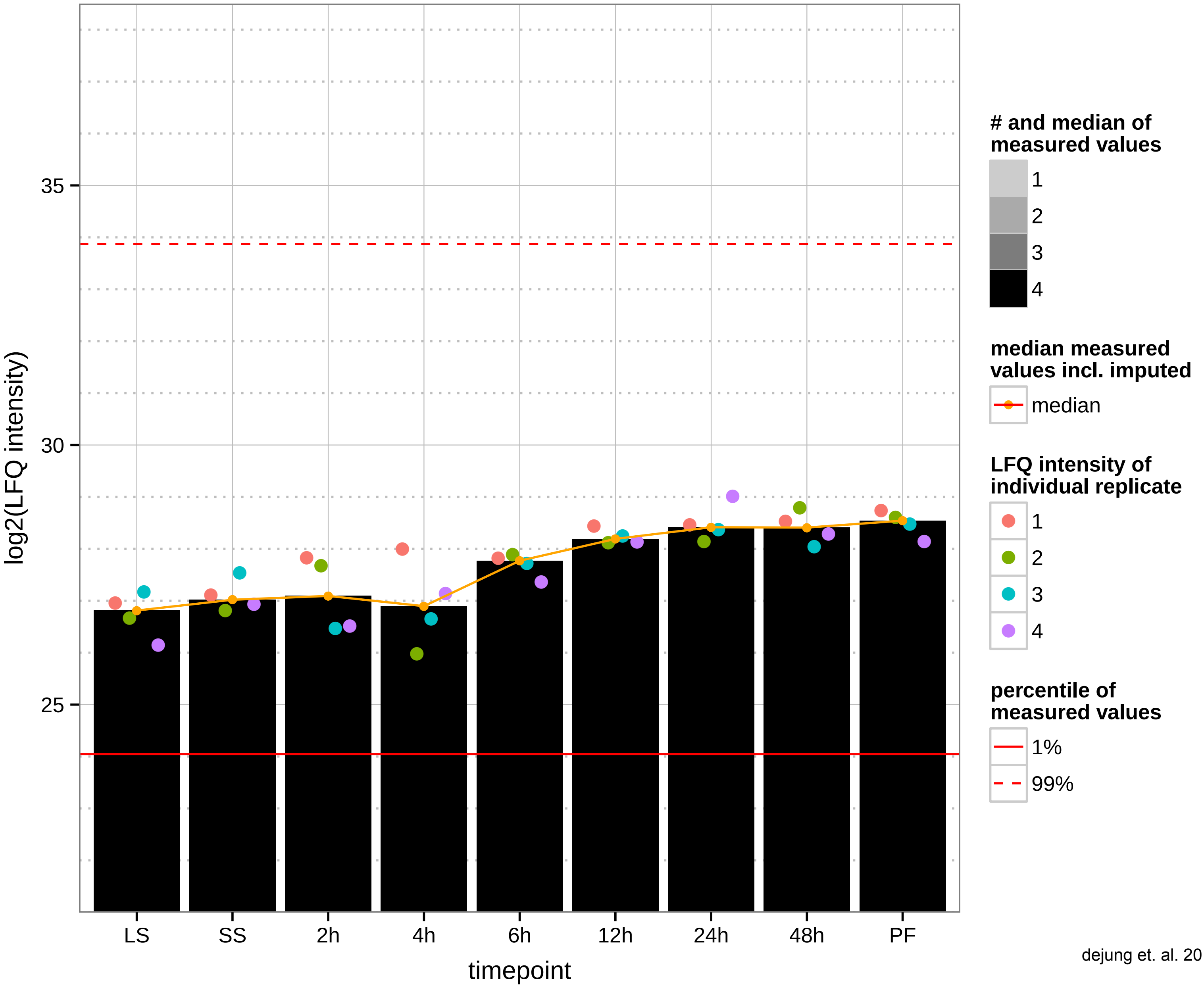
hypothetical protein, conserved
Tb927.9.15330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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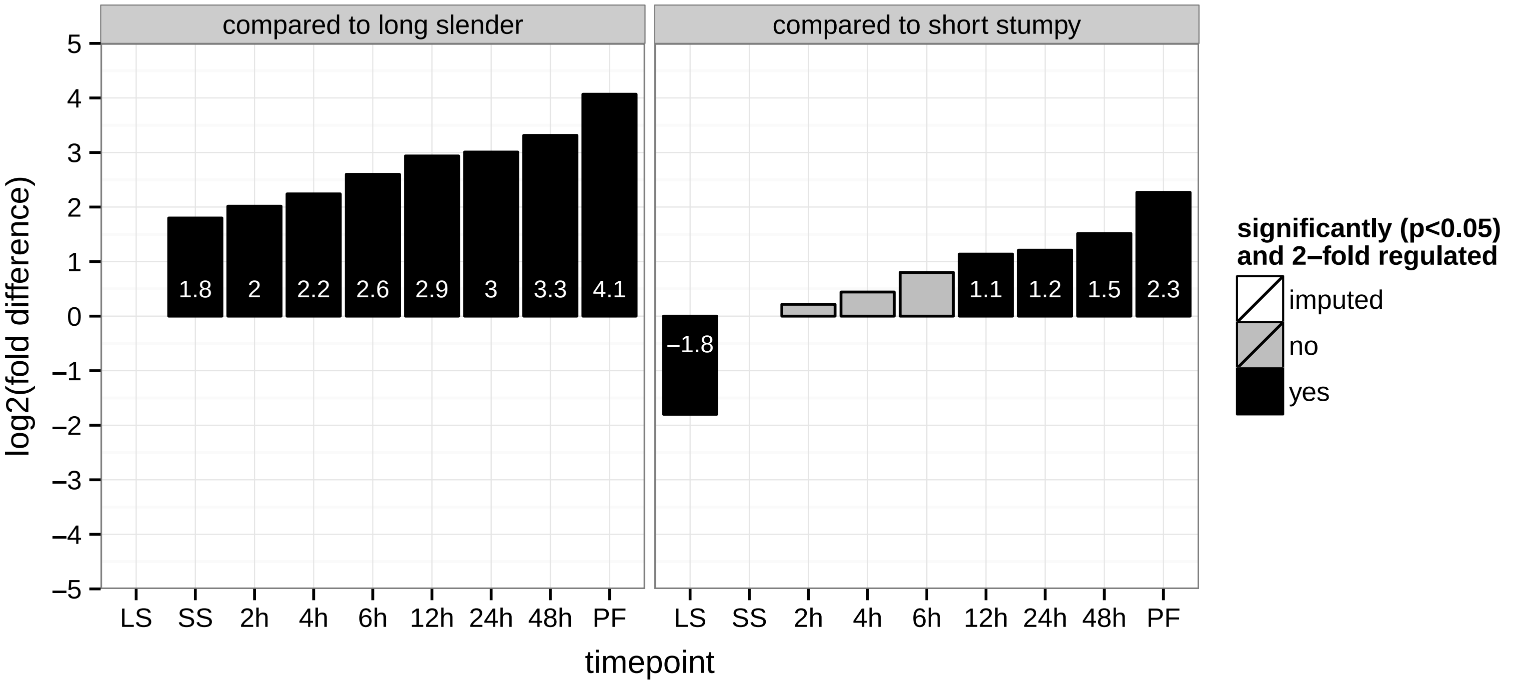
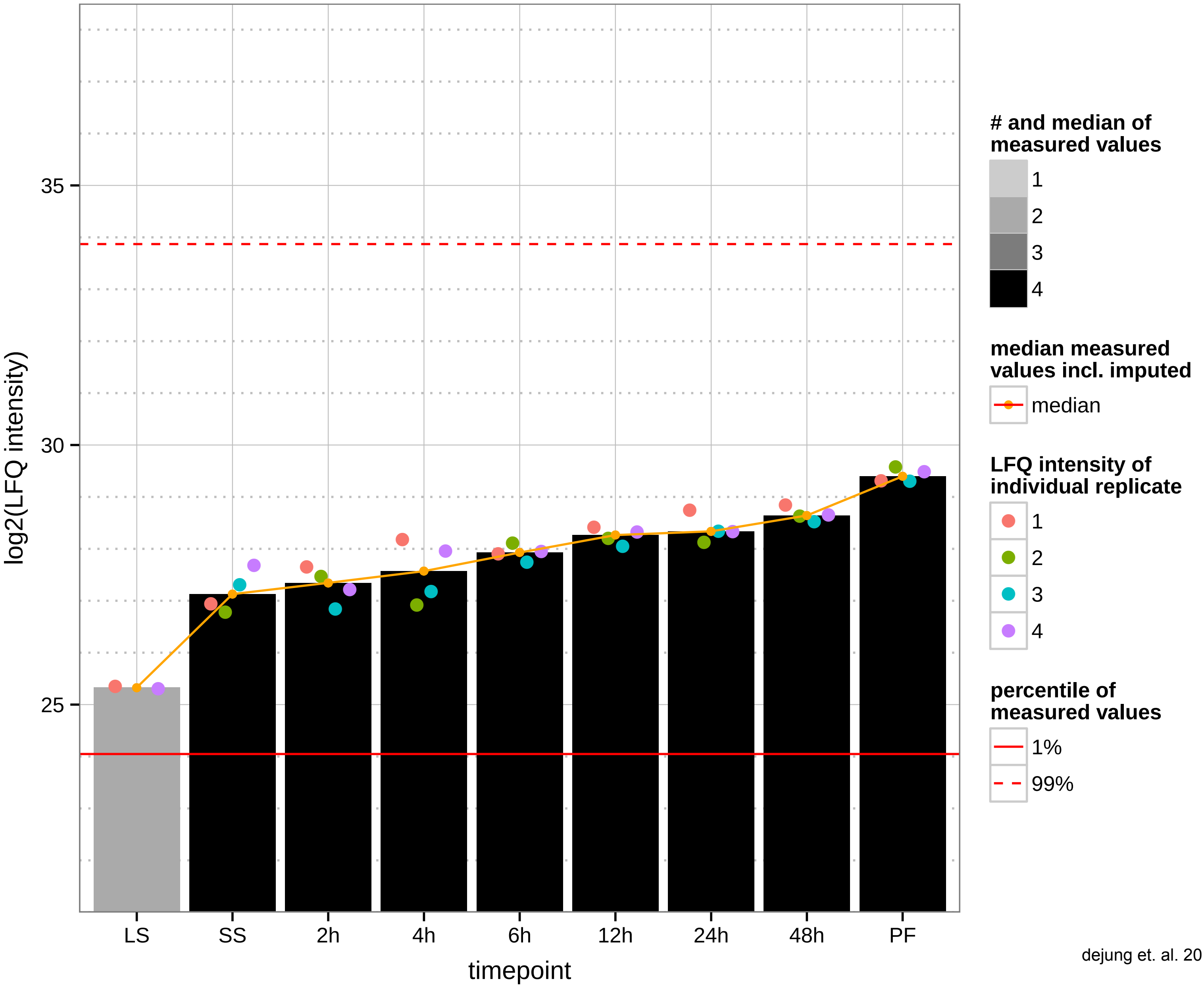
hypothetical protein, conserved
Tb927.9.2320
AGOF: methyltransferase activity
AGOC: null
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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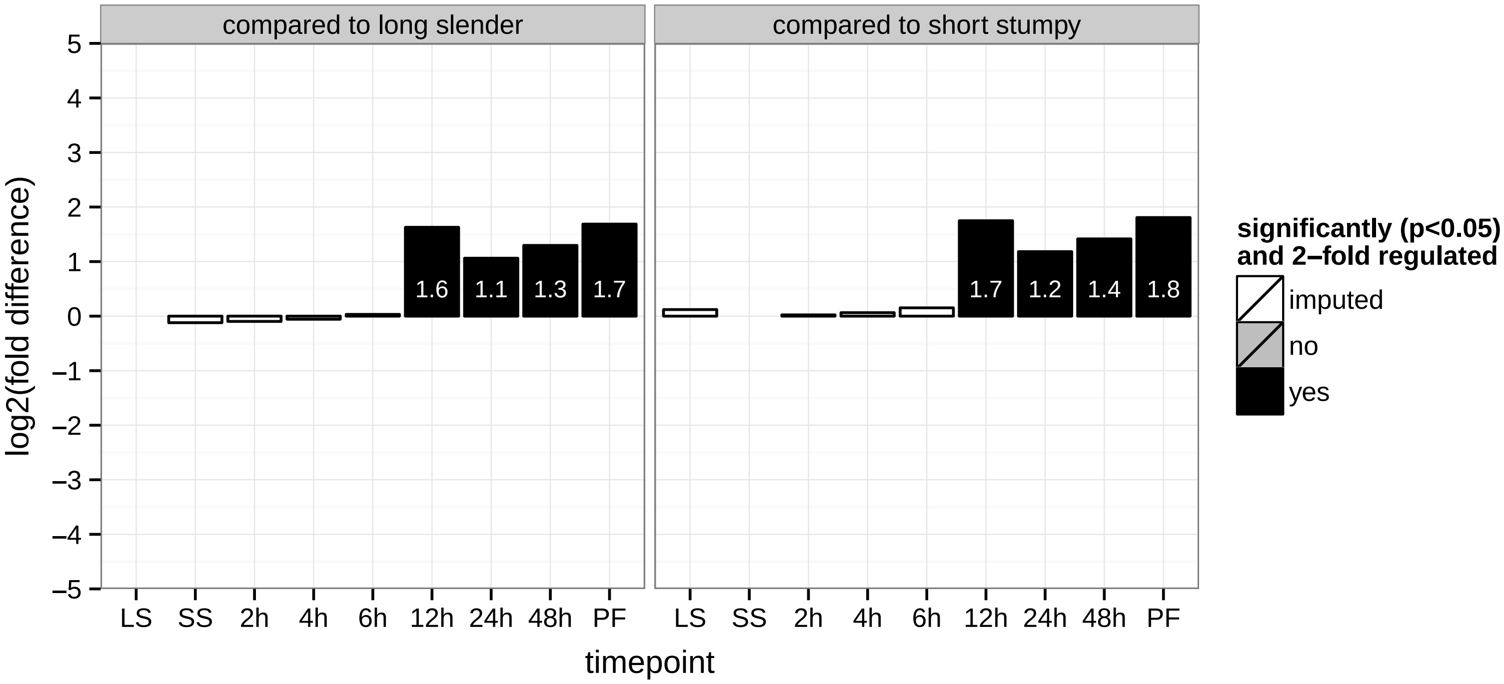
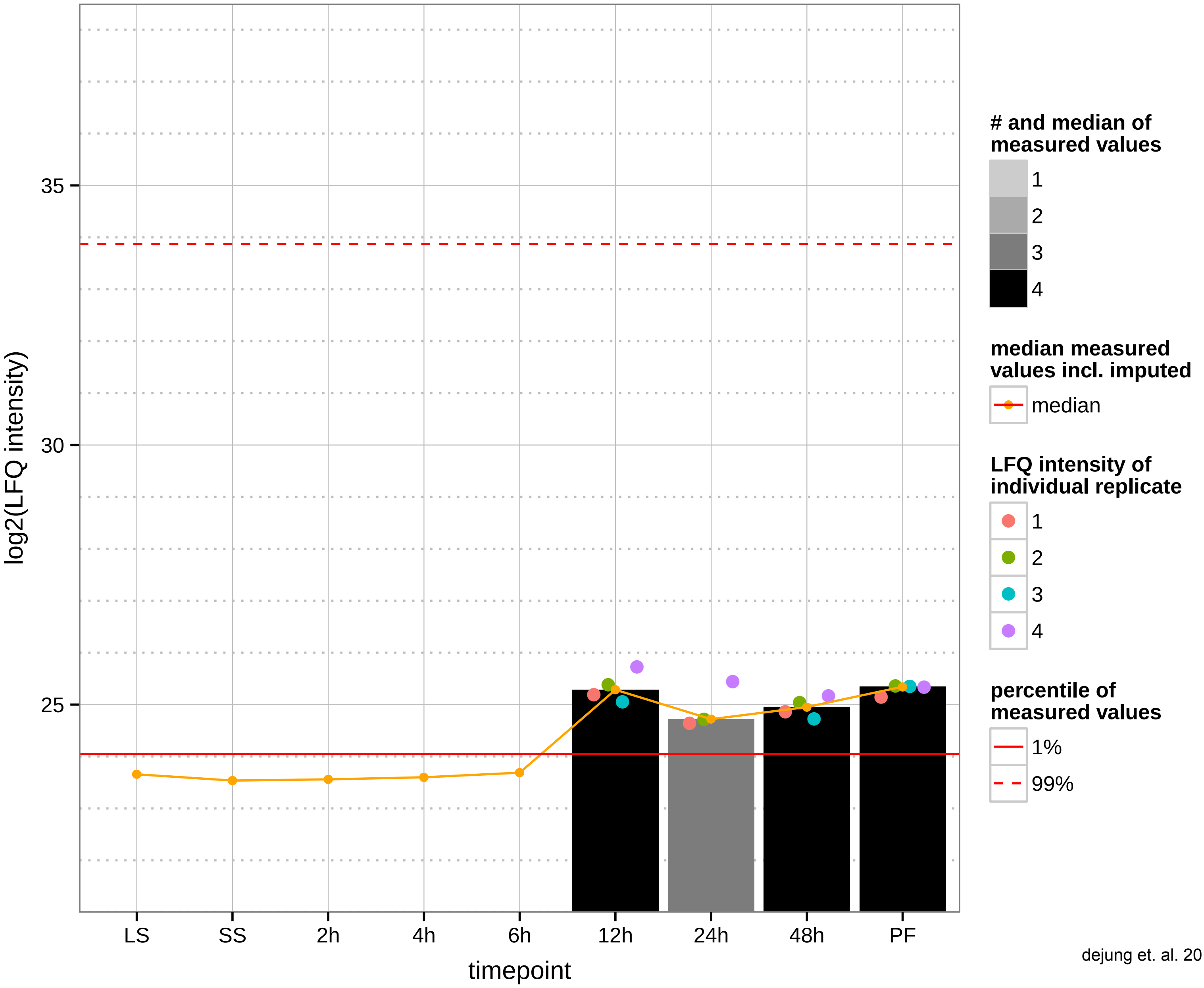
hypothetical protein, conserved
Tb927.9.3080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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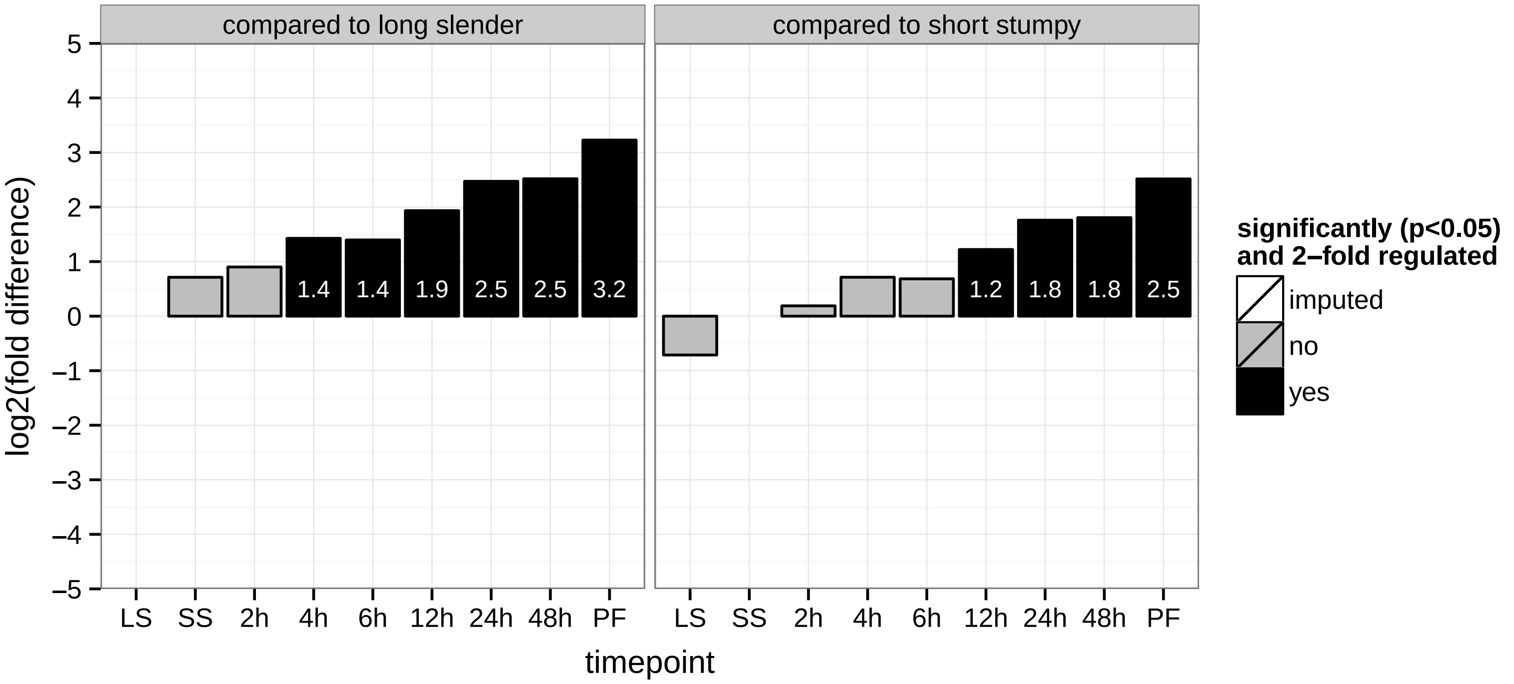
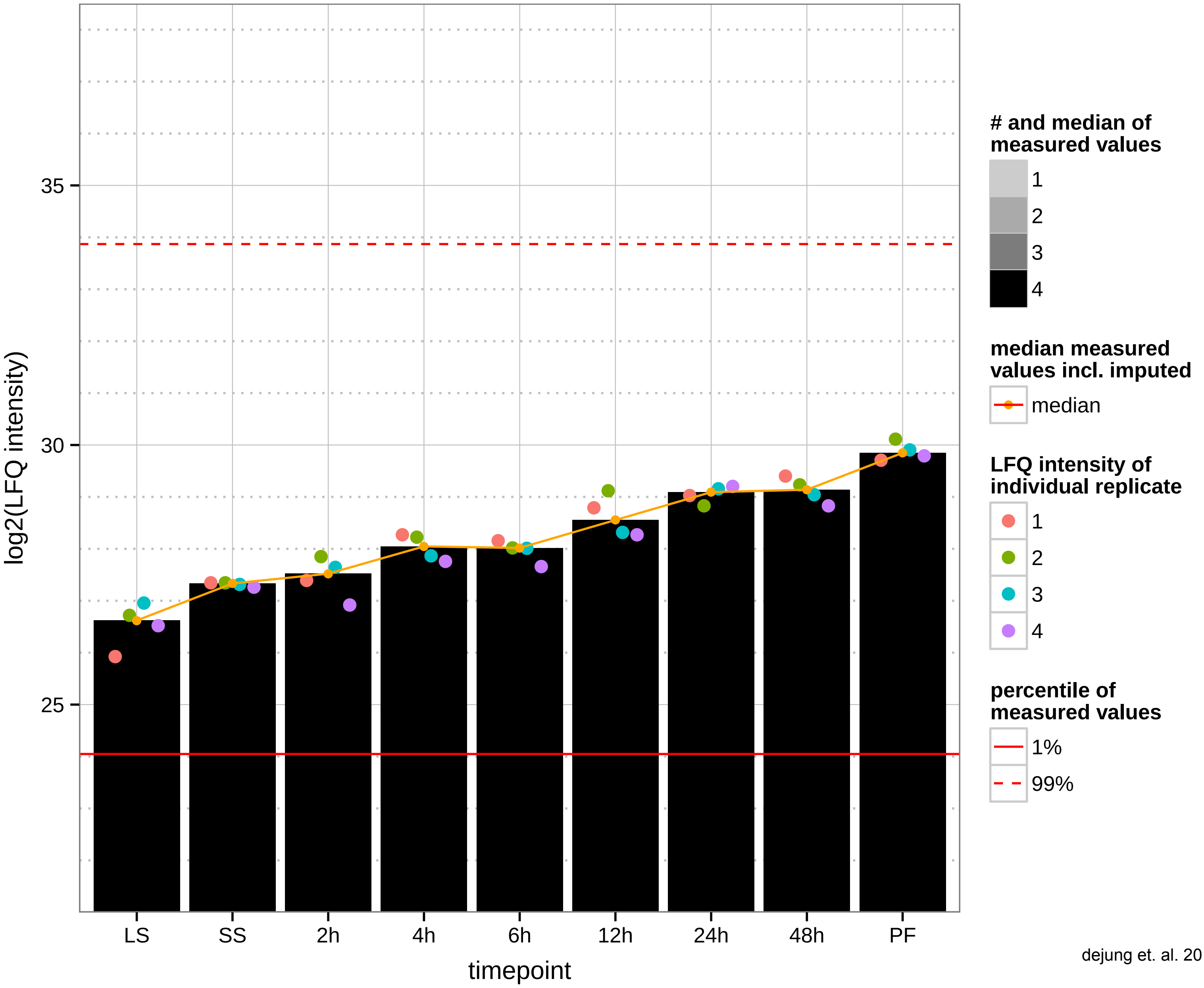
solanesyl–diphosphate synthase, putative, trans–octaprenyltranstransferase
Tb927.9.5890
AGOF: trans–hexaprenyltranstransferase activity, trans–octaprenyltranstransferase activity
AGOC: mitochondrion
AGOP: isoprenoid biosynthetic process, ubiquinone metabolic process
PGOF: null
PGOC: null
PGOP: isoprenoid biosynthetic process





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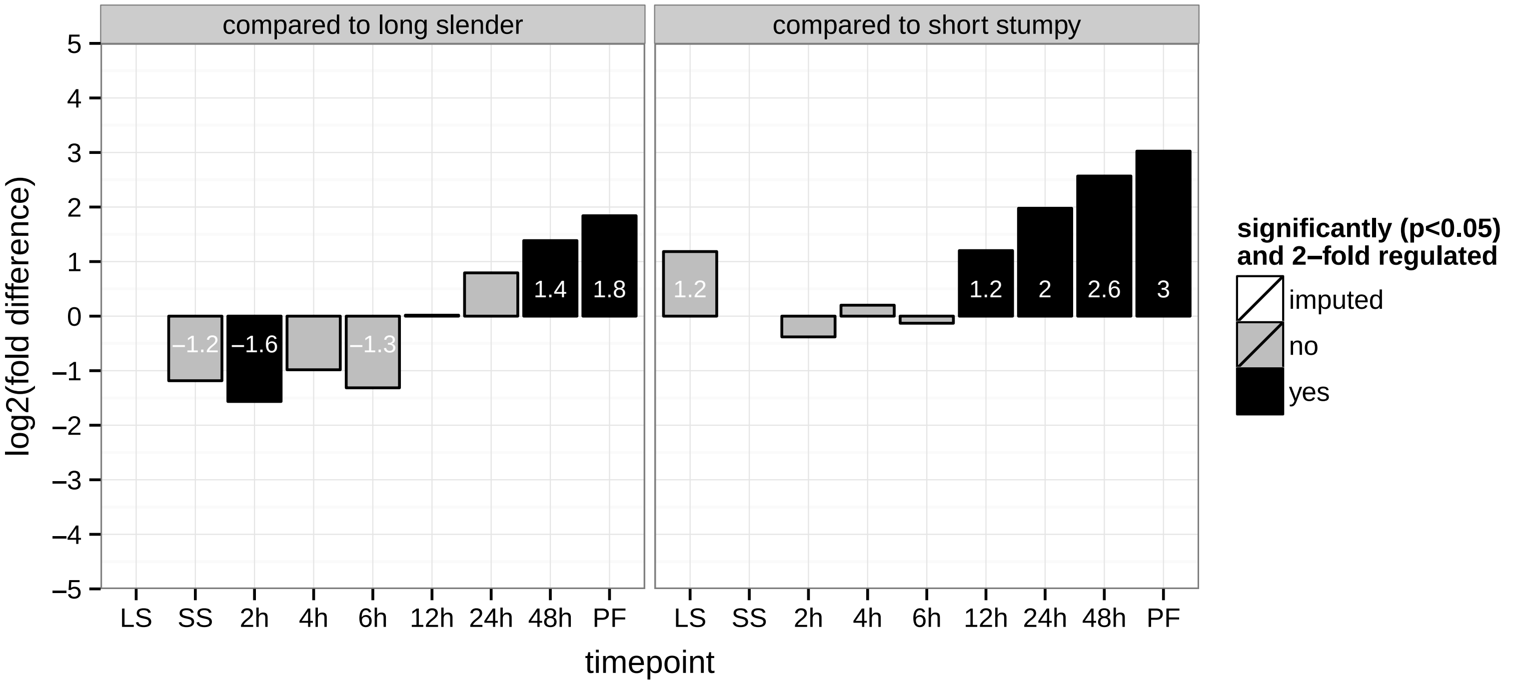
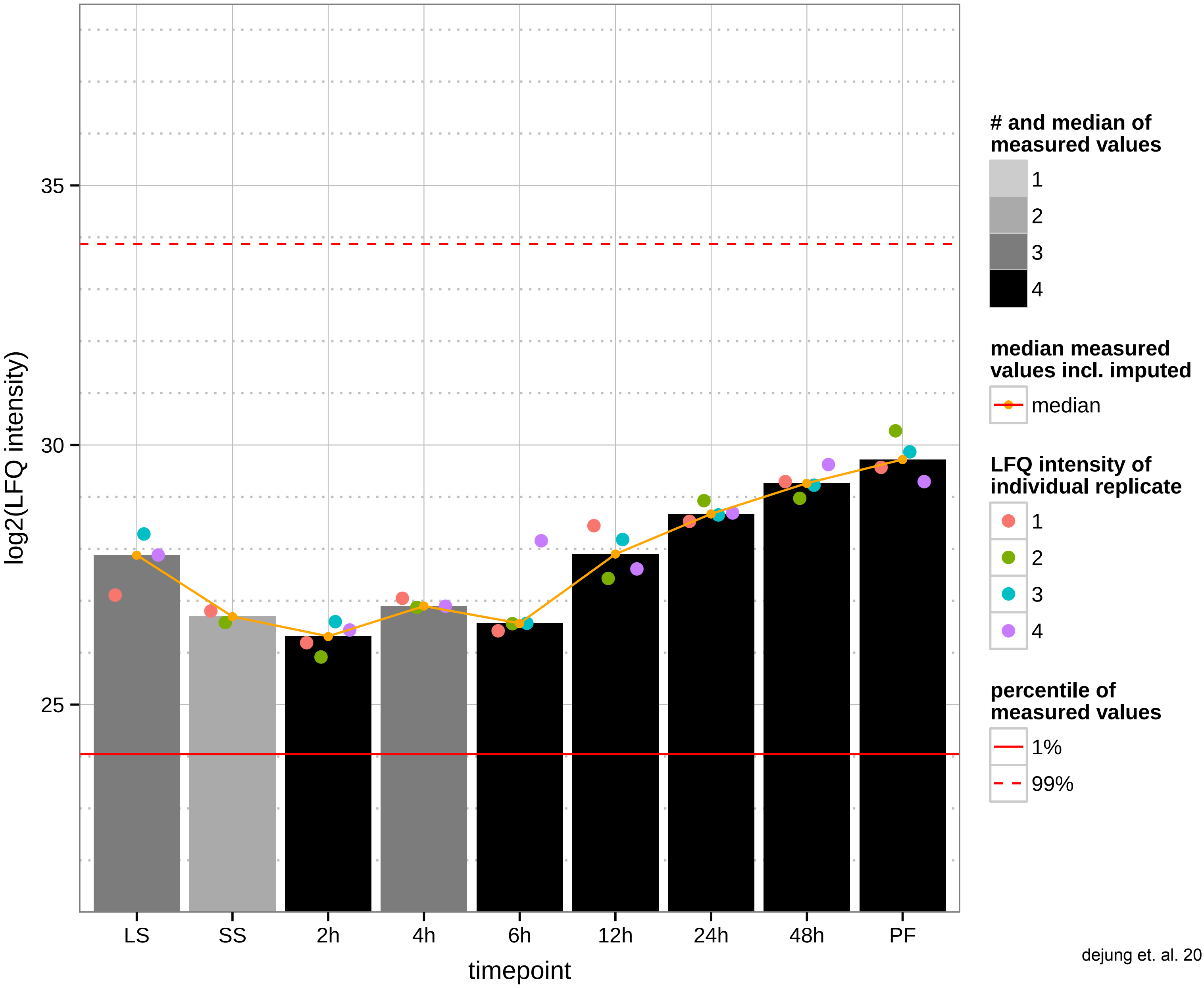
hypothetical protein, conserved
Tb927.9.6920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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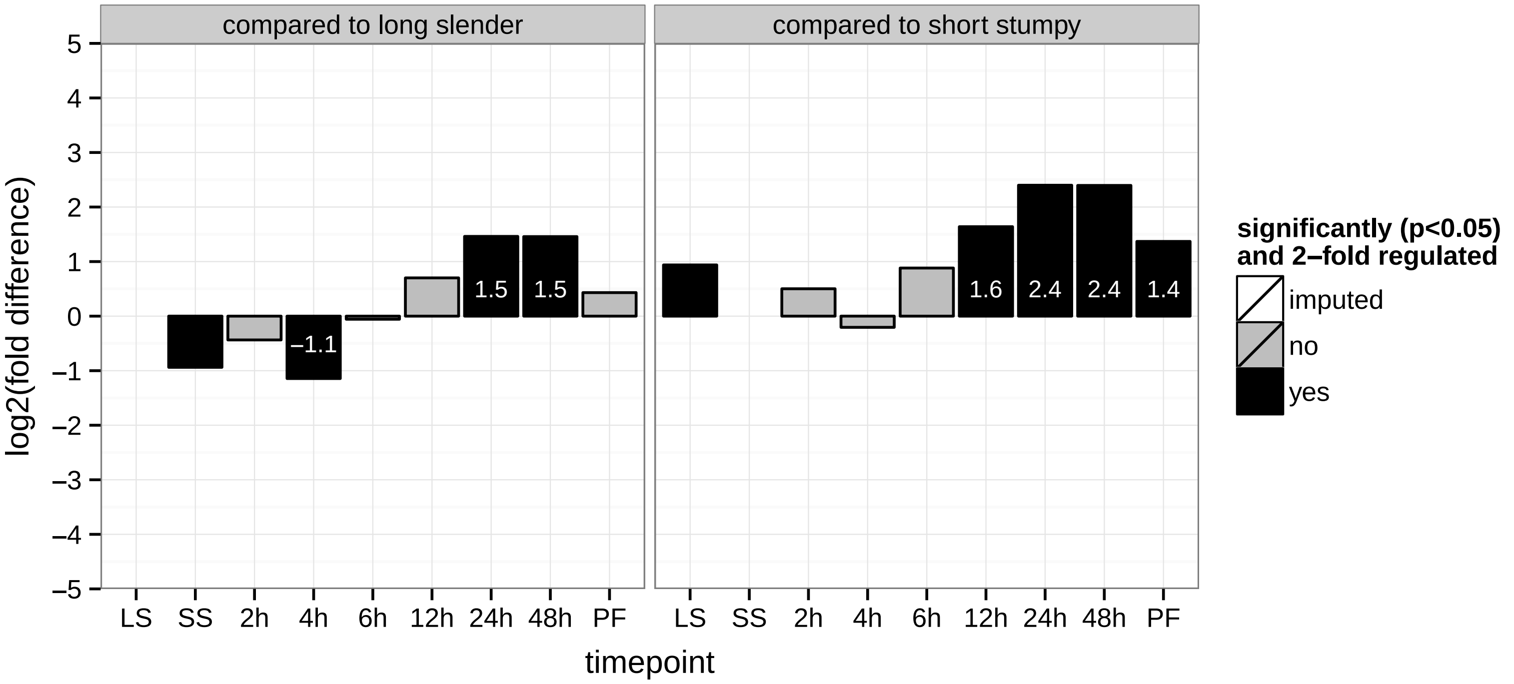
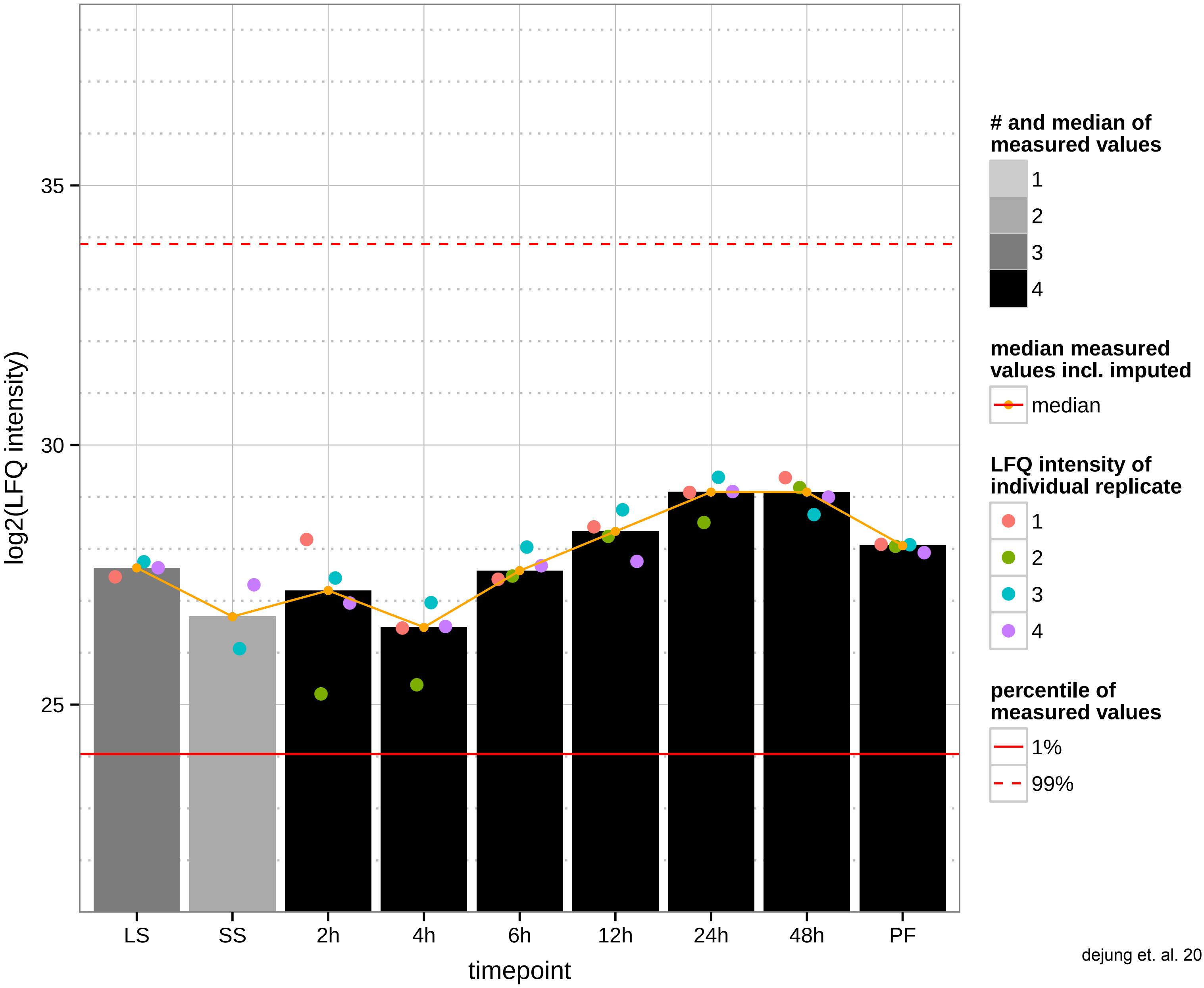
adenosine transporter 2 (TbNT2/927), adenosine transporter 2, putative (TbNT3), adenosine transporter 2 (TbNT5), putative (
Tb927.9.7470
AGOF: purine nucleoside transmembrane transporter activity, nucleoside transmembrane transporter activity, nucleoside:hydr
AGOC: integral to membrane, membrane
AGOP: purine ribonucleoside salvage, transport, nucleoside transport, adenosine transport, inosine transport, nucleoside tran
PGOF: nucleoside transmembrane transporter activity
PGOC: integral to membrane
PGOP: transport





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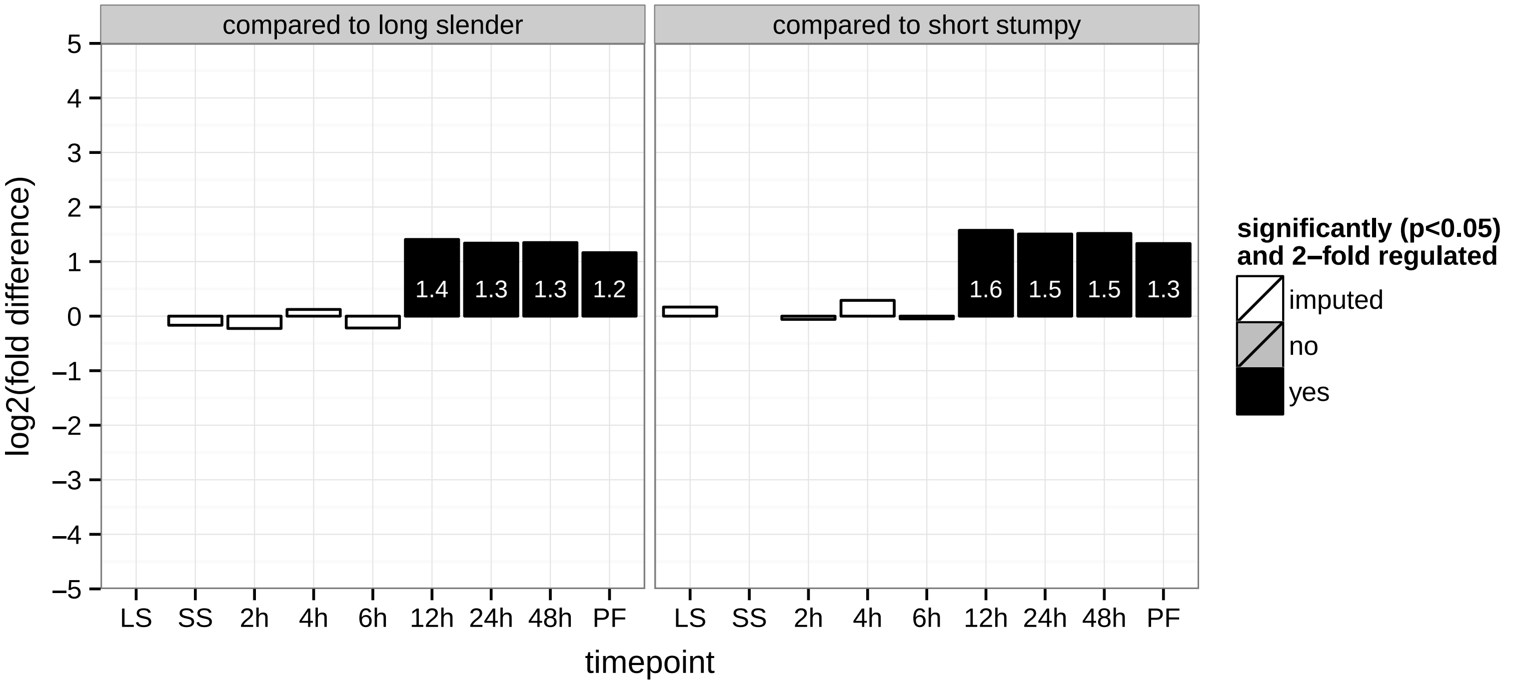
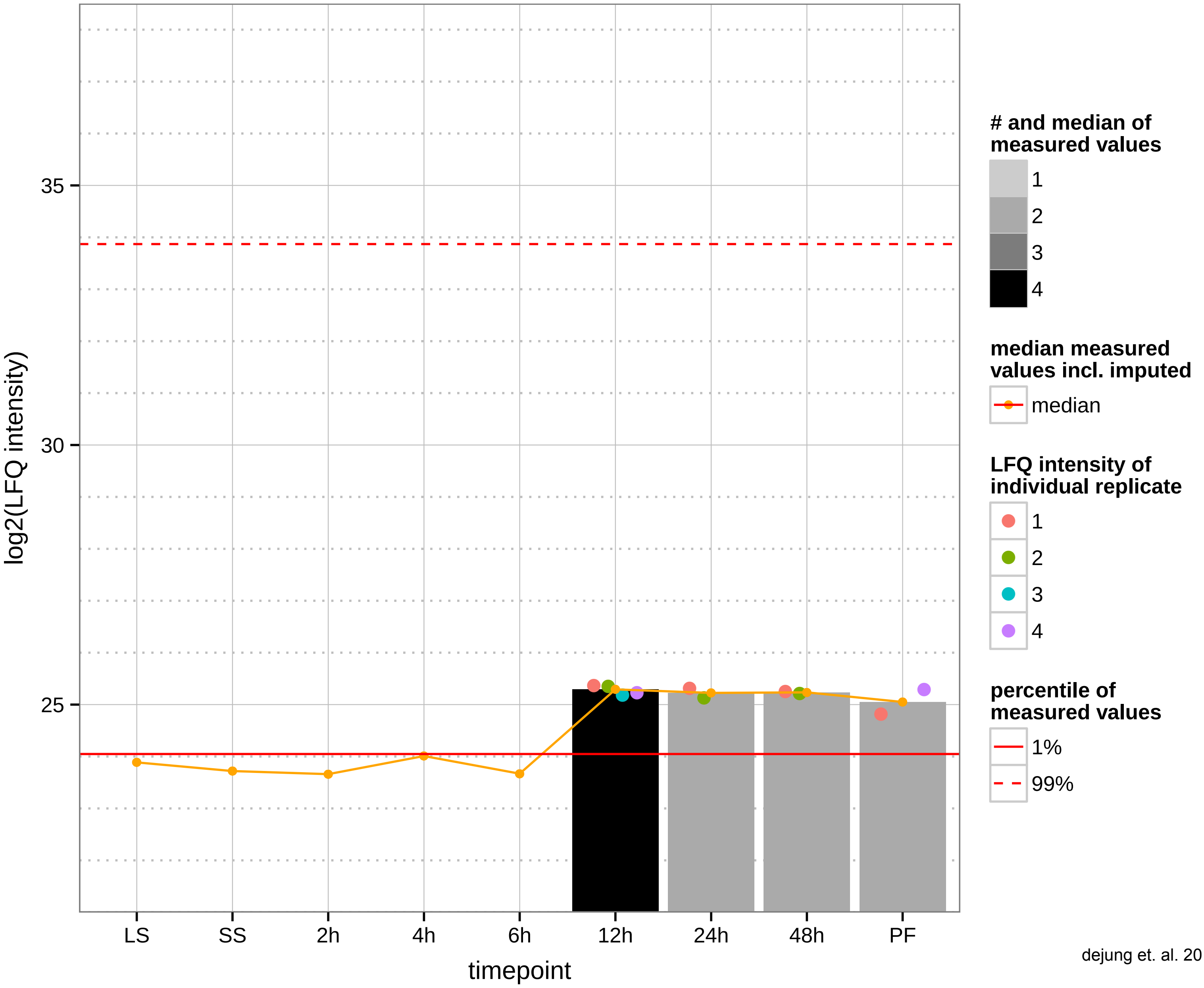
Peptide deformylase 2
Tb927.9.8210
AGOF: iron ion binding, peptide deformylase activity
AGOC: mitochondrion
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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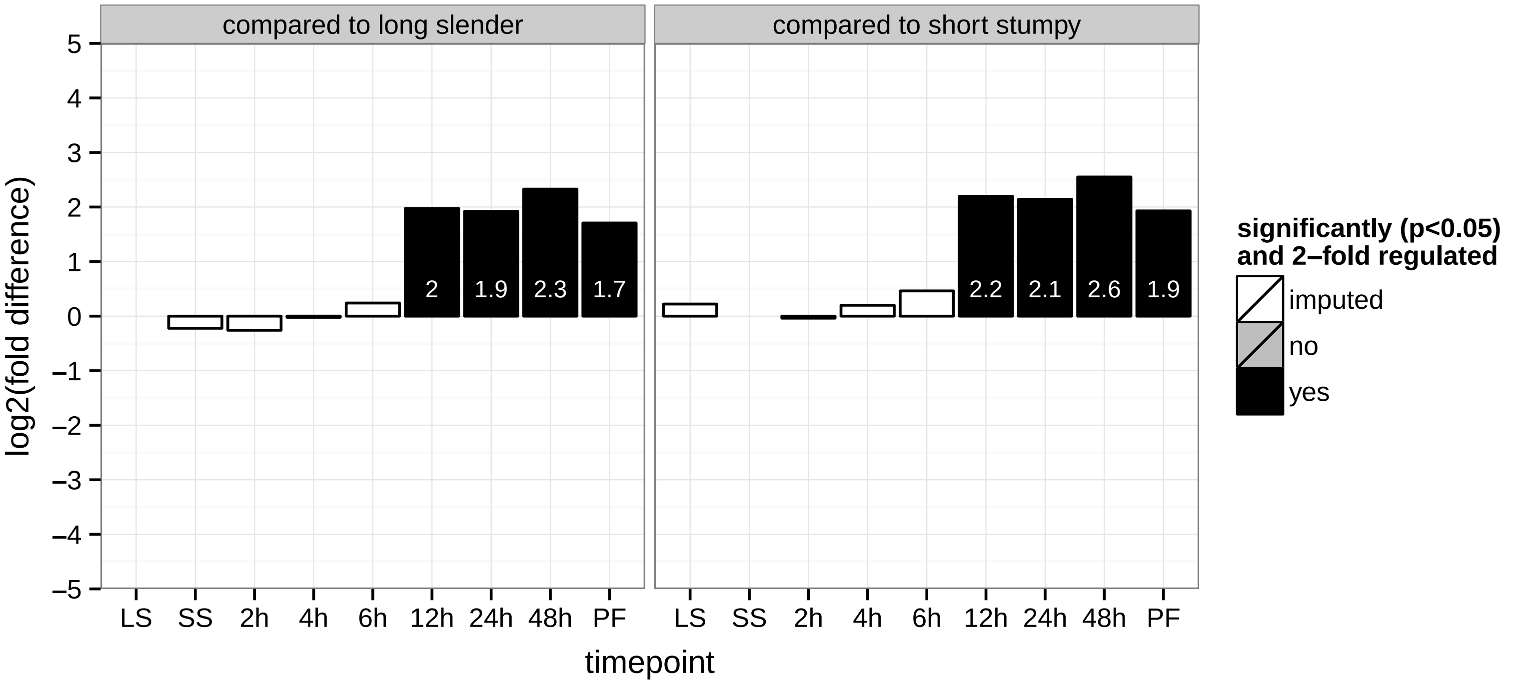
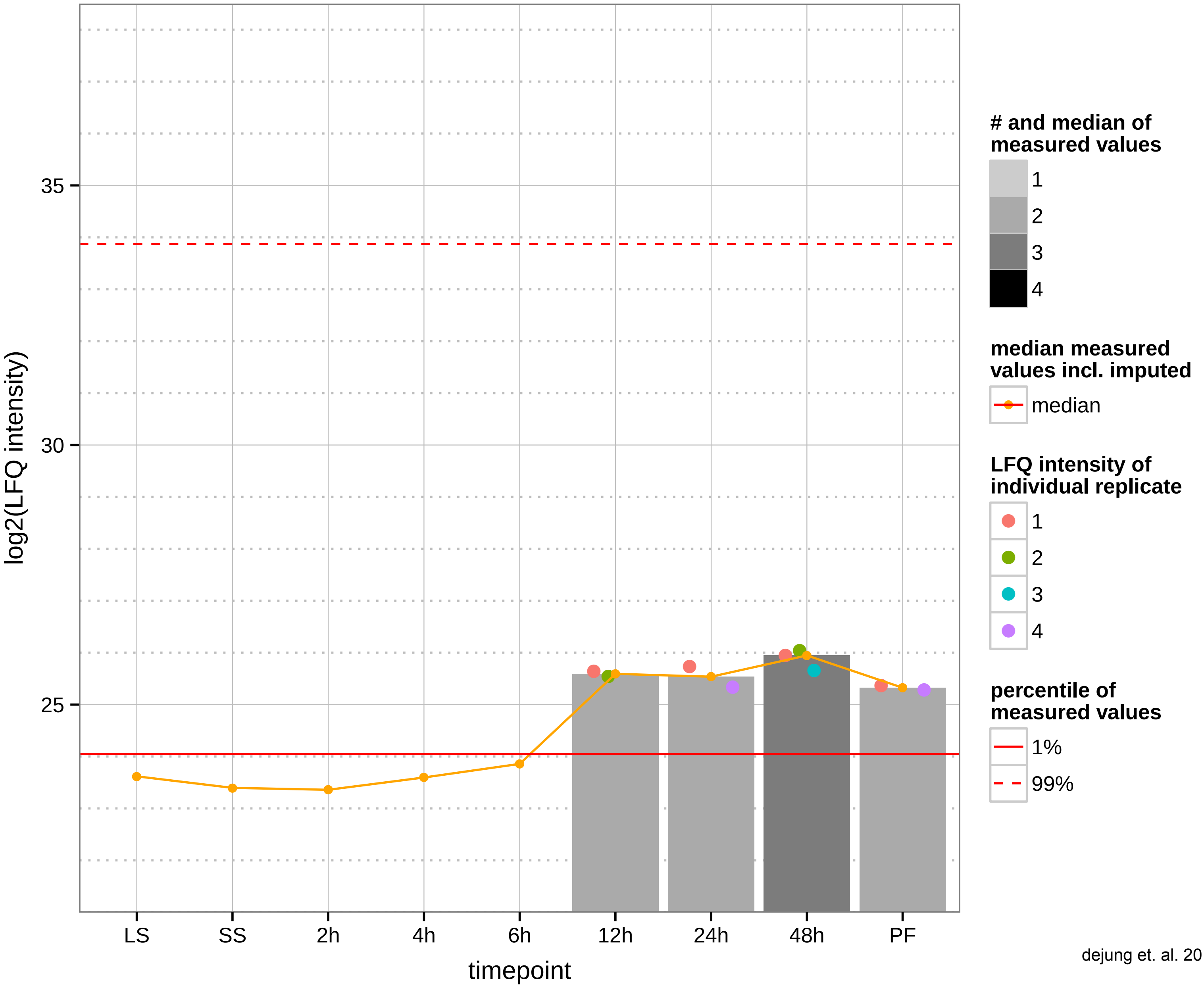
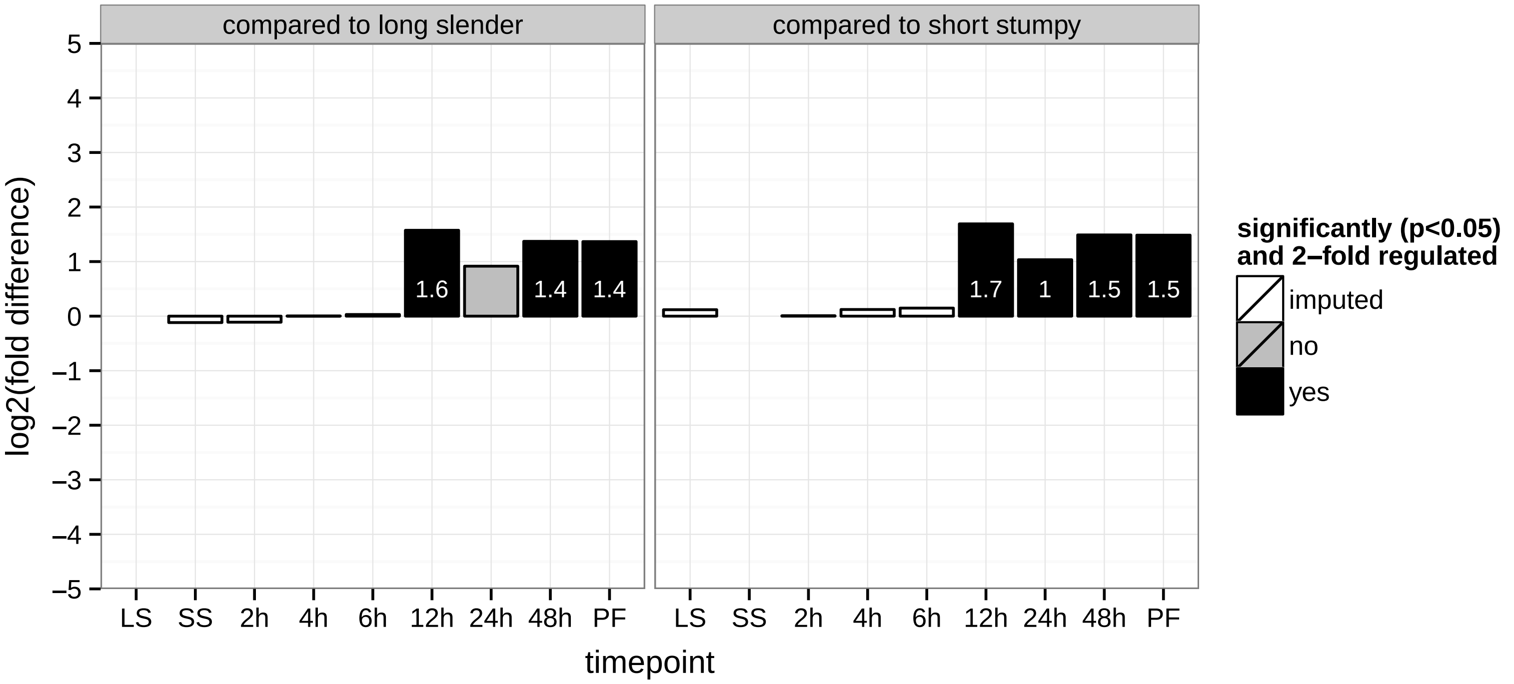
hypothetical protein, conserved
Tb927.9.8380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

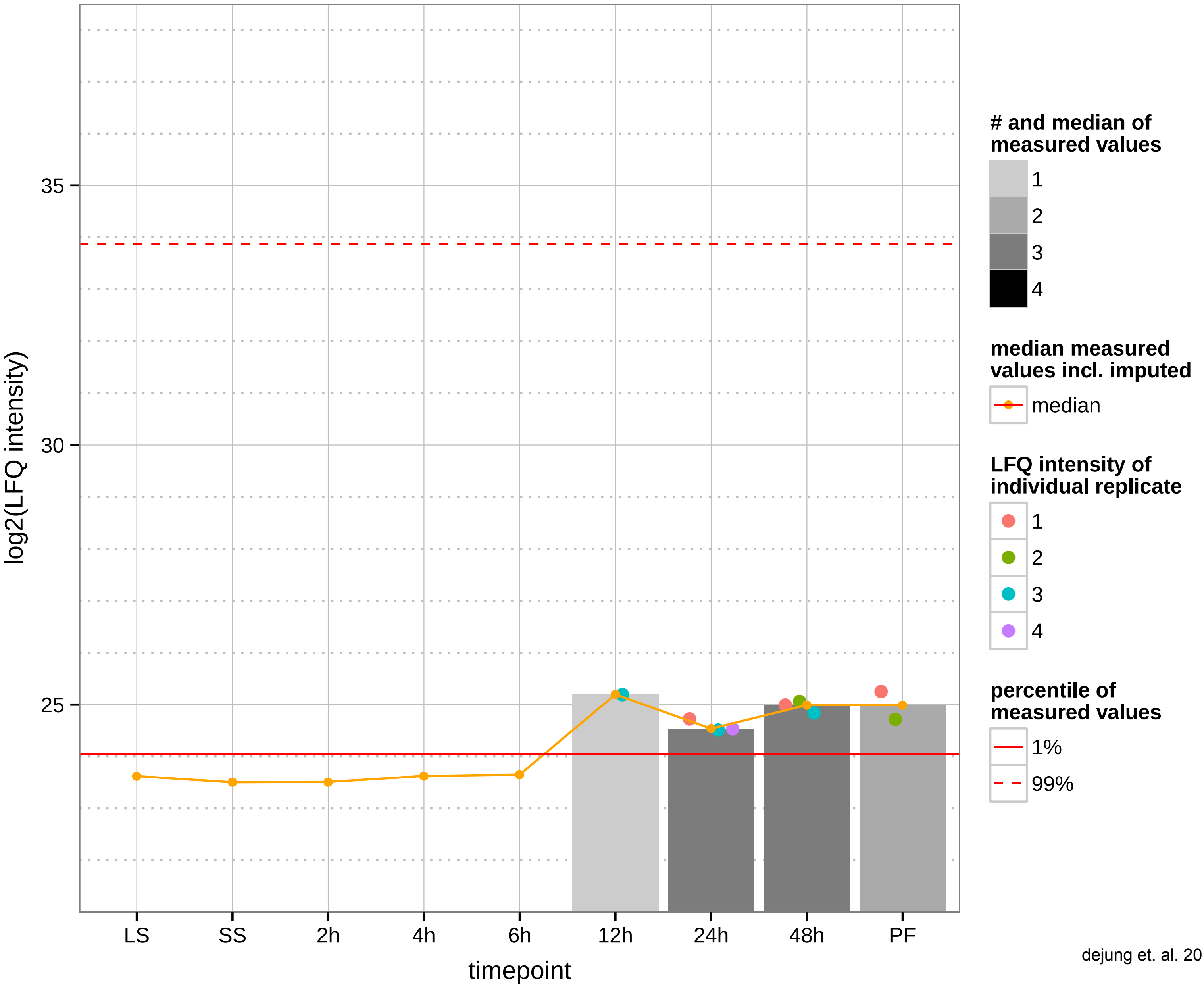




dejung et. al. 2015

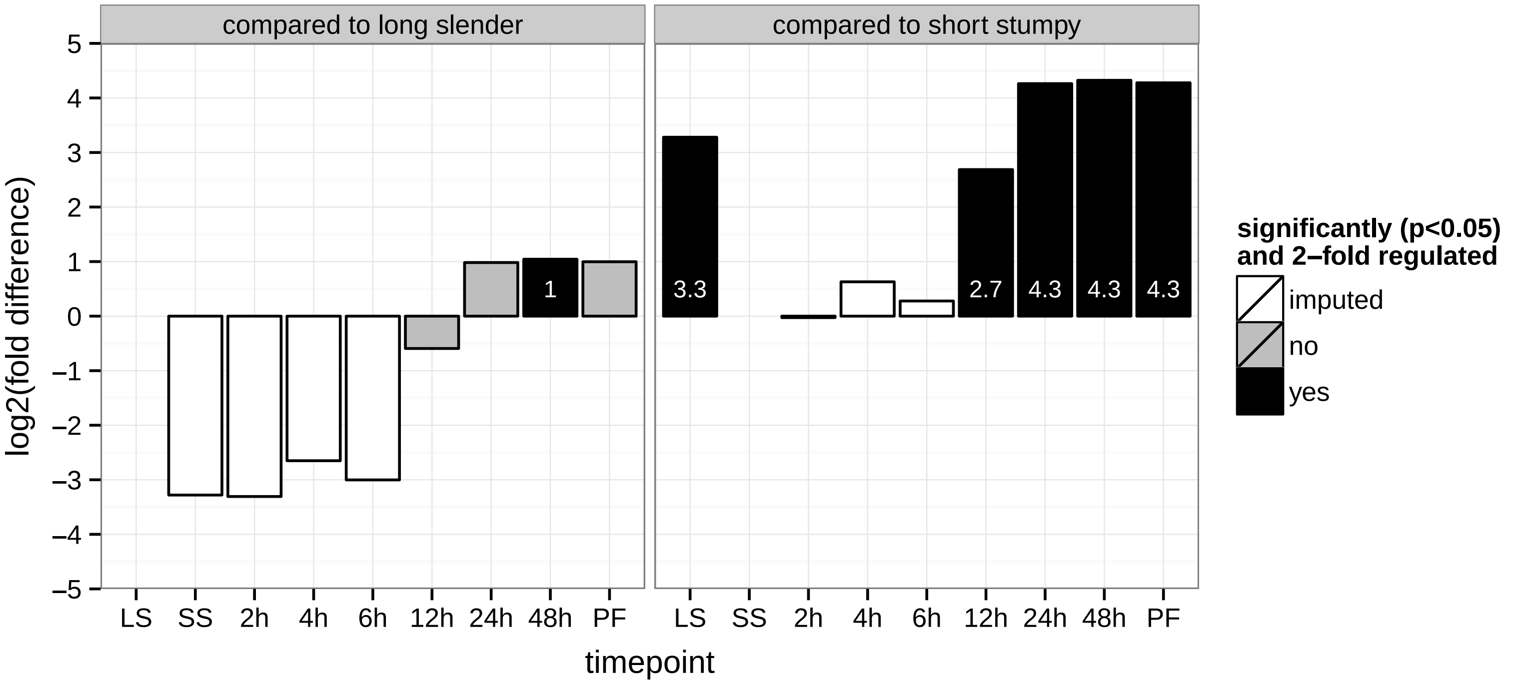
hypothetical protein, conserved
Tb927.9.9310
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

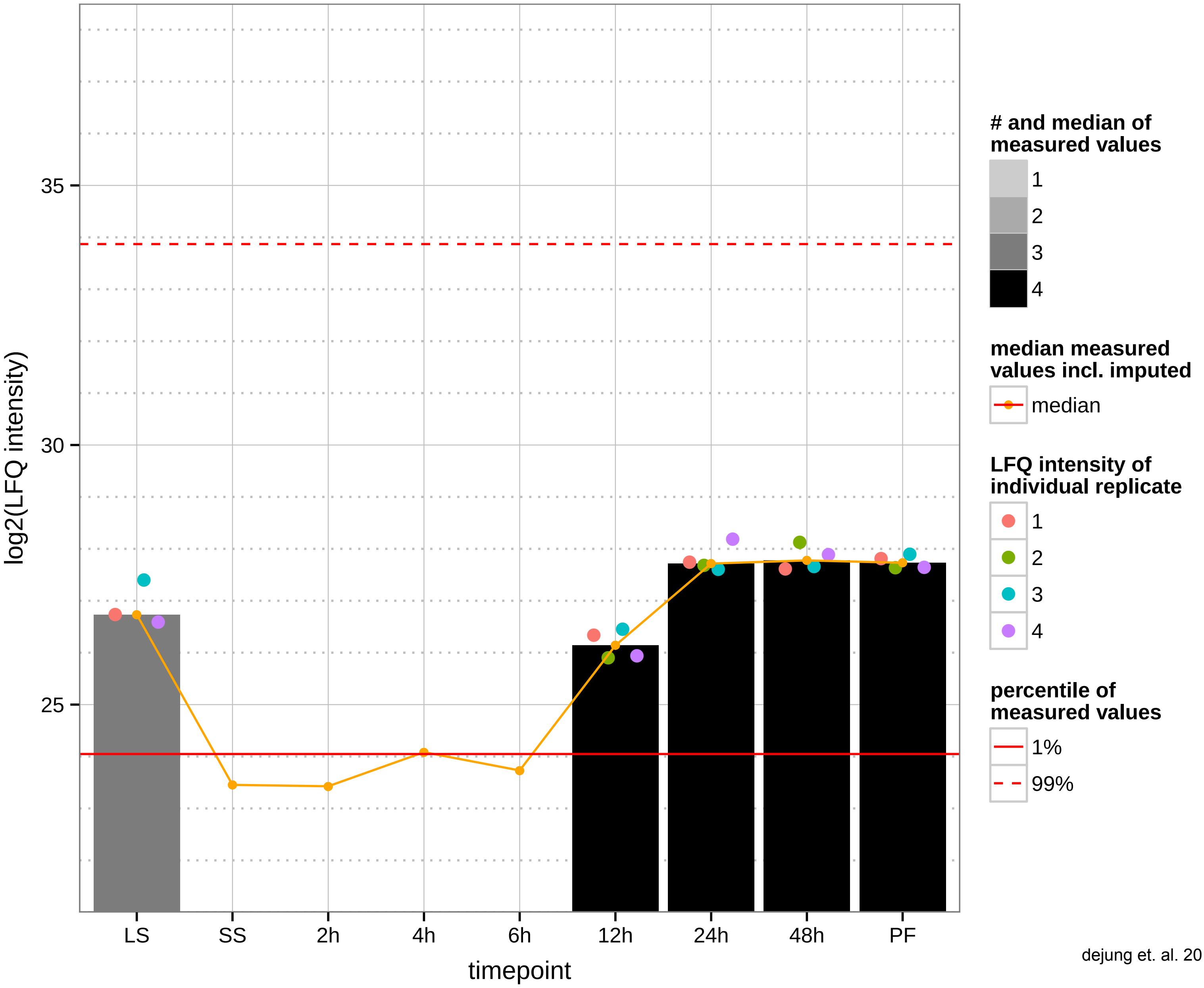




dejung et. al. 2015

zinc finger protein family member, putative (ZC3H29)
Tb927.9.9520
AGOF: RNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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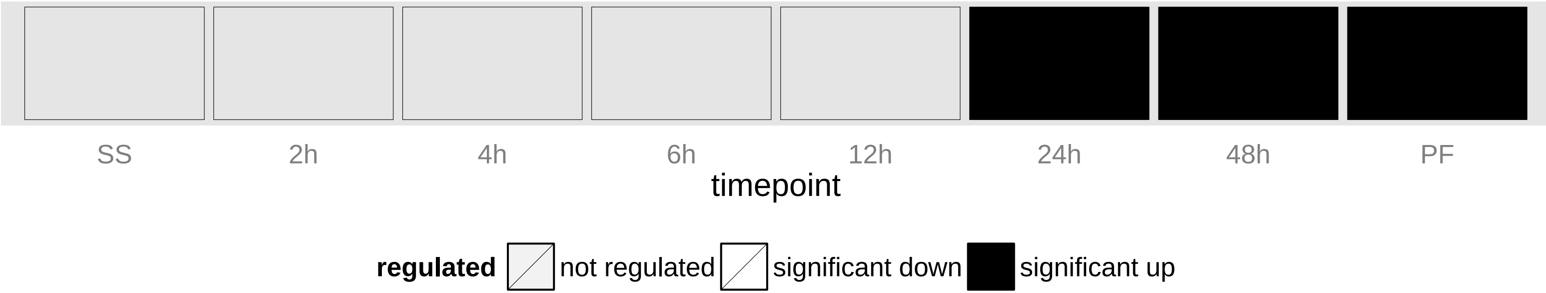

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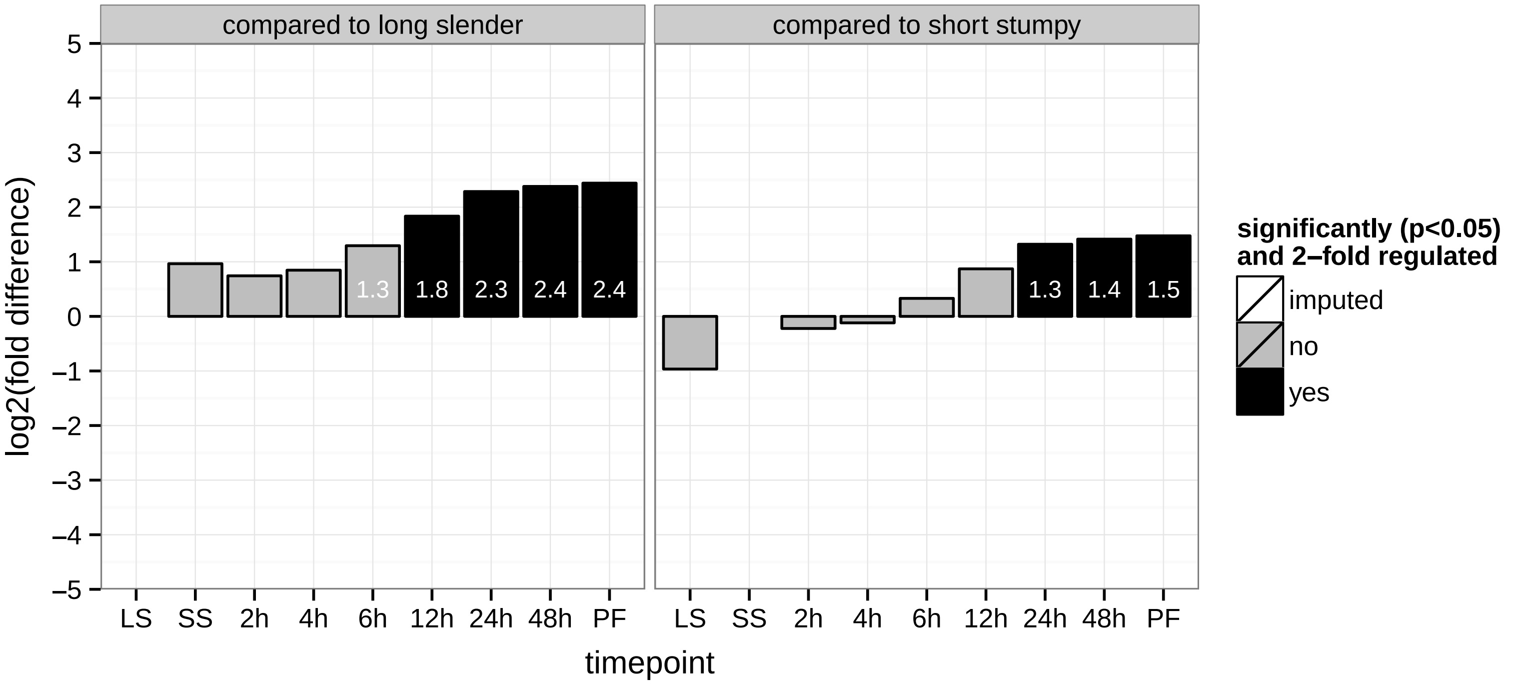
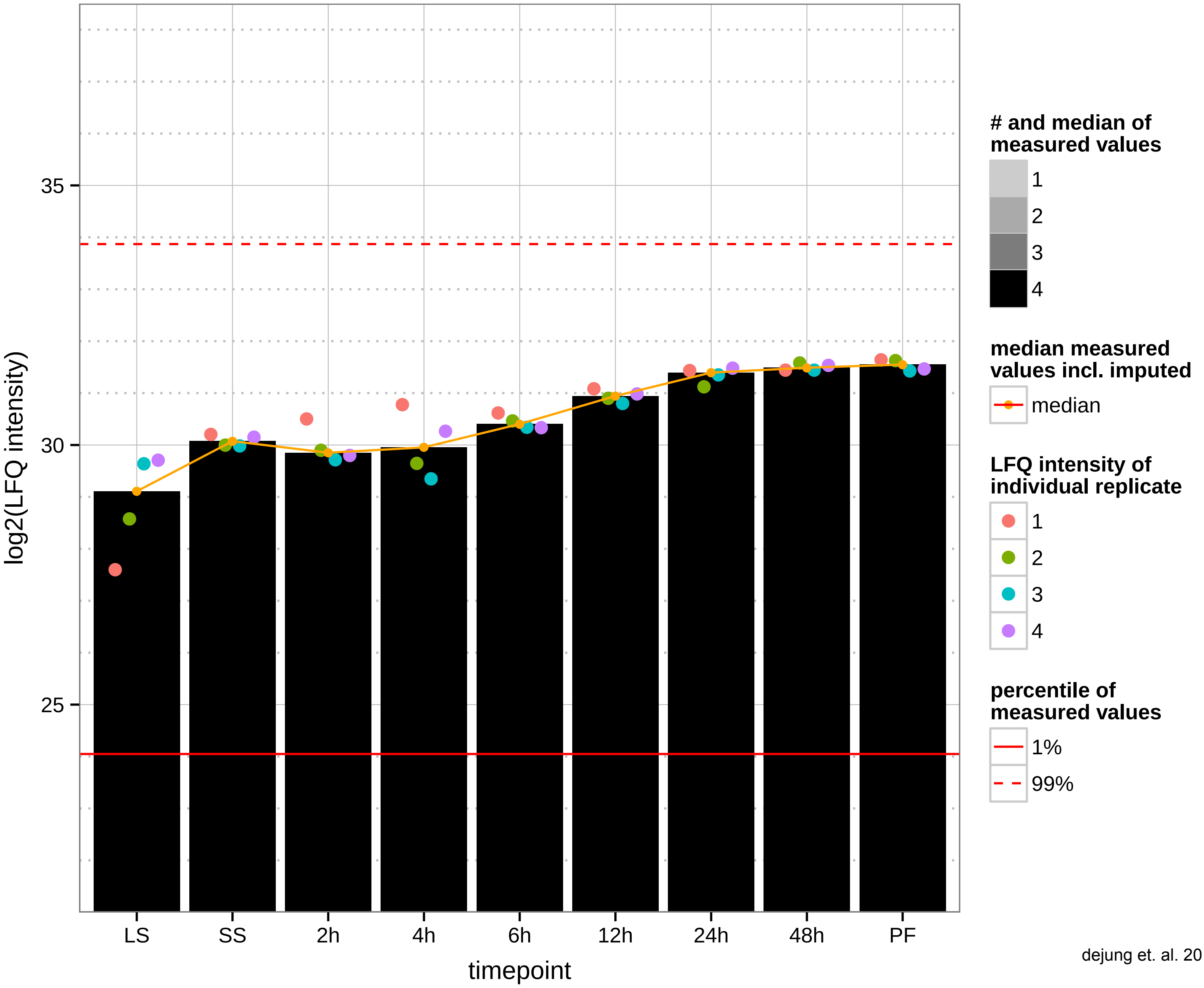
nucleolar RNA helicase II, putative, nucleolar RNA helicase Gu, BAC from homologous region on chr5
Tb927.5.4420;Tb05.5K5.70
AGOF: ATP binding, ATP–dependent helicase activity, RNA binding, helicase activity
AGOC: nucleus, nucleolus, nucleus
AGOP: null, nucleobase–containing compound metabolic process
PGOF: ATP binding, ATP–dependent helicase activity, RNA binding, helicase activity, nucleic acid binding
PGOC: nucleus
PGOP: null





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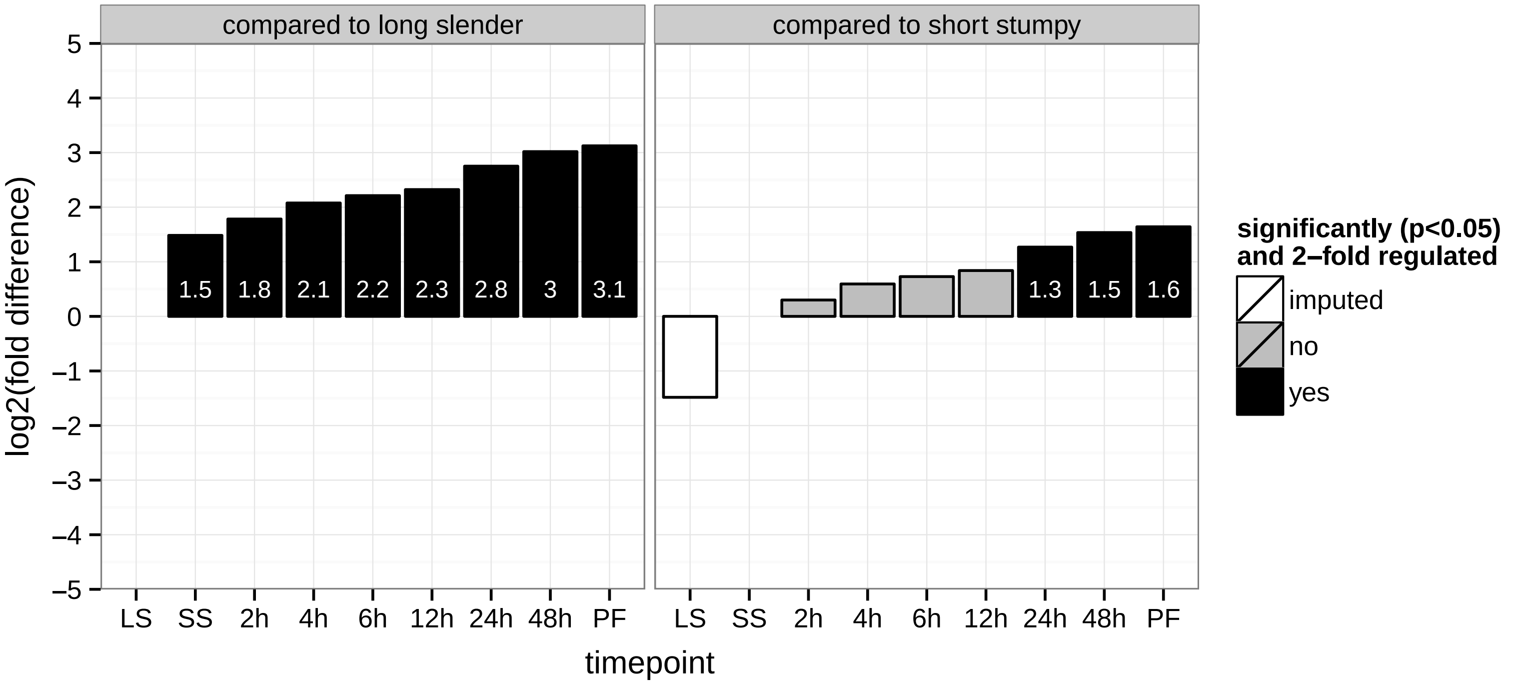
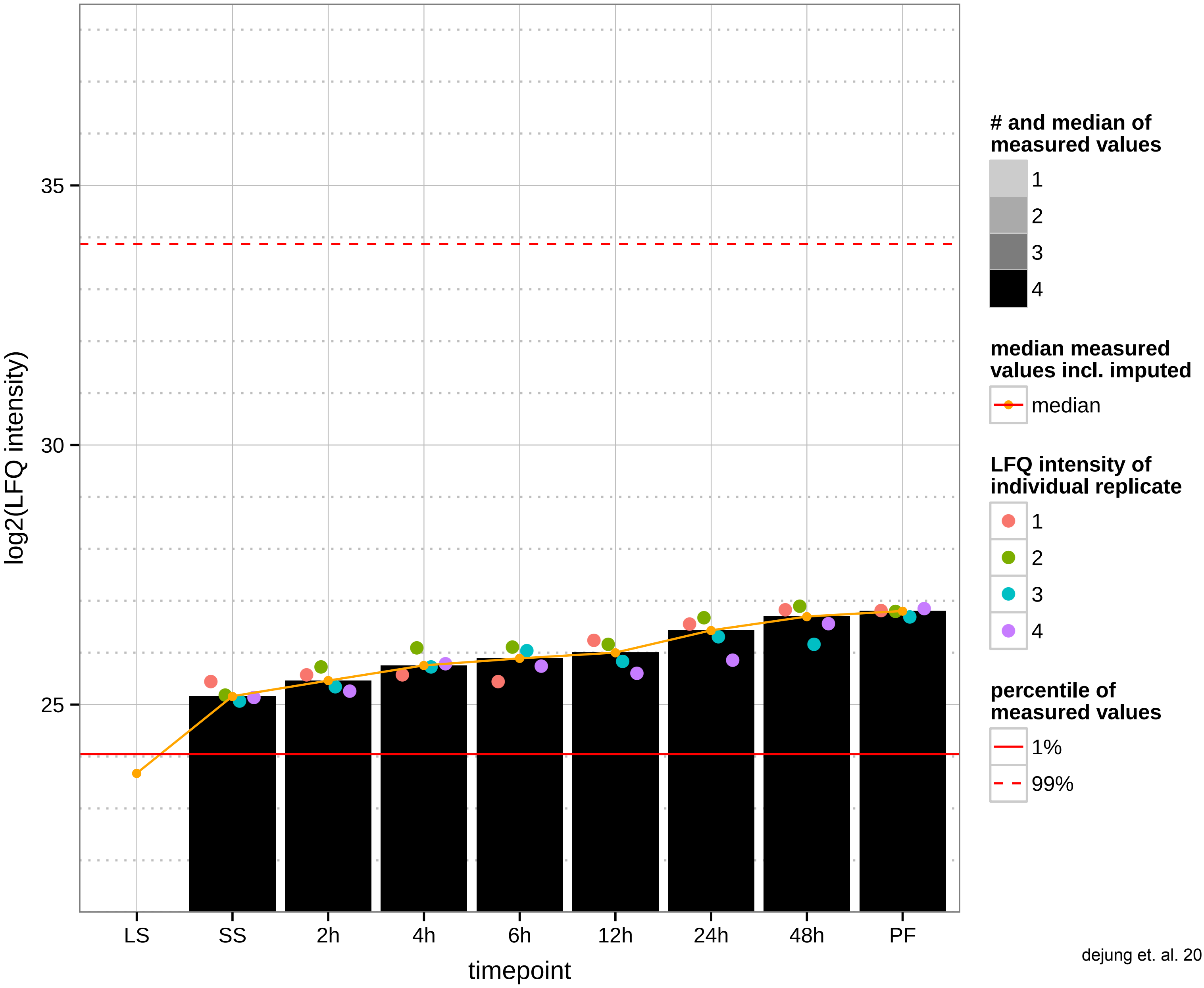
hypothetical protein, conserved, chrXI additional, unordered contigs
Tb11.1420;Tb11.1370;Tb927.11.1850
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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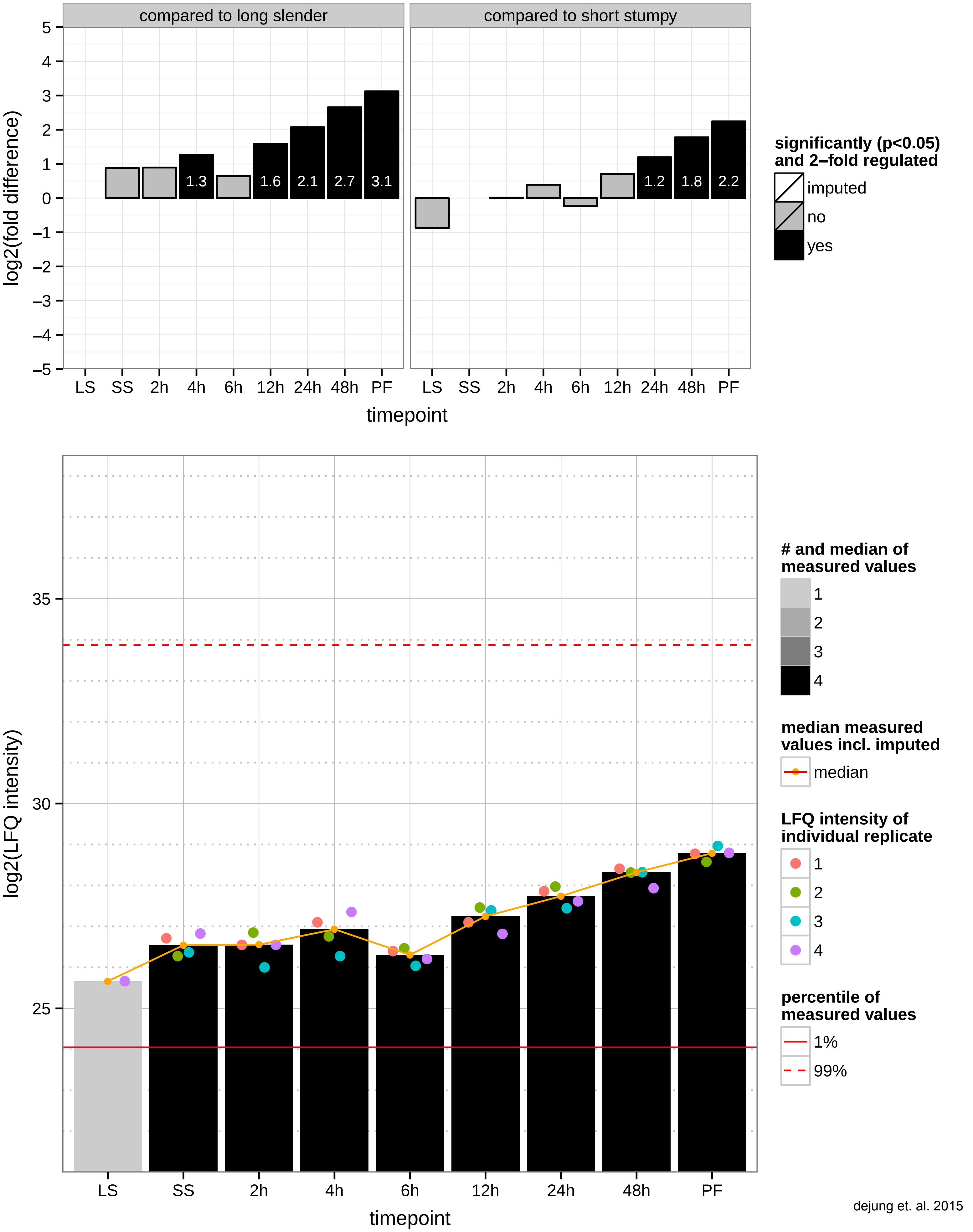
2–oxoisovalerate dehydrogenase alpha subunit, putative
Tb927.10.660;Tb11.v5.0500
AGOF: null, 2–oxoisovalerate dehydrogenase (acylating) activity, oxidoreductase activity, acting on the aldehyde or oxo group
AGOC: null, mitochondrion
AGOP: null, metabolic process
PGOF: oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor
PGOC: null
PGOP: metabolic process



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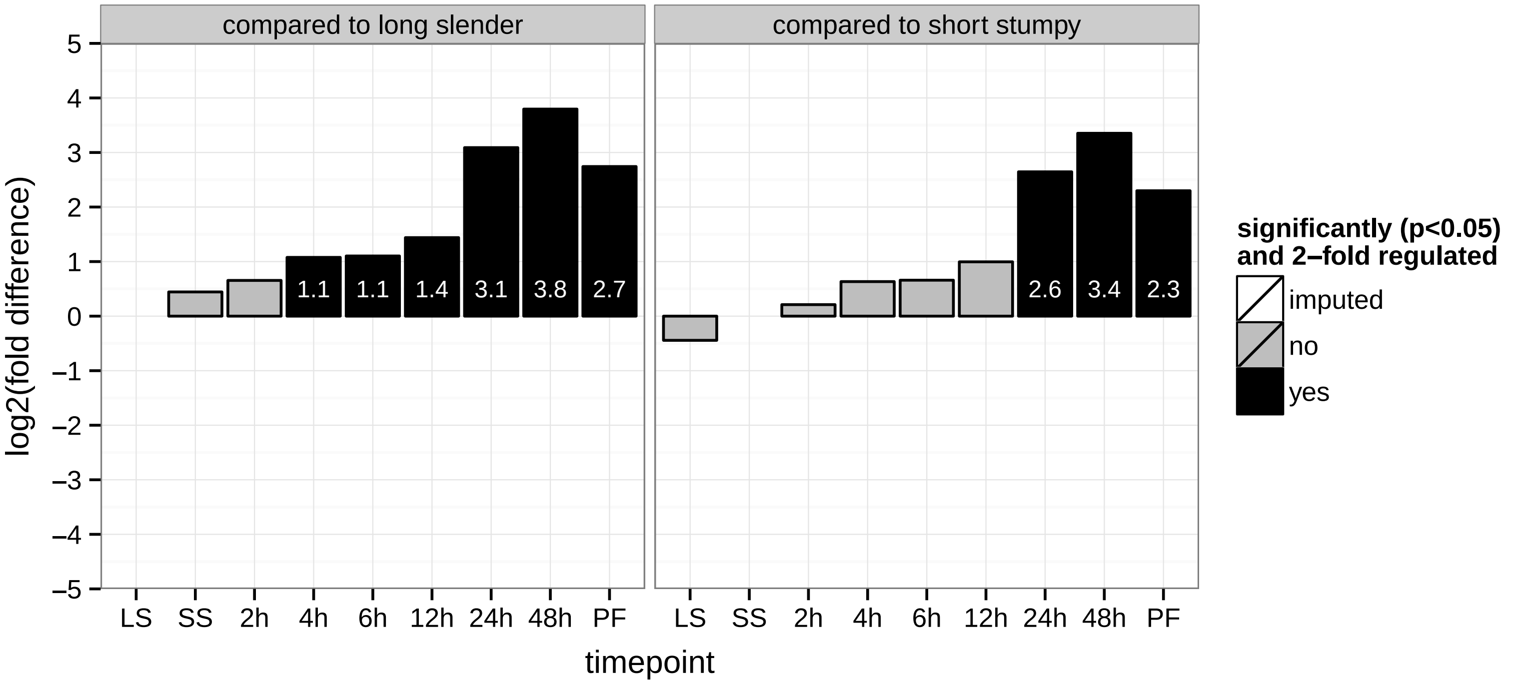
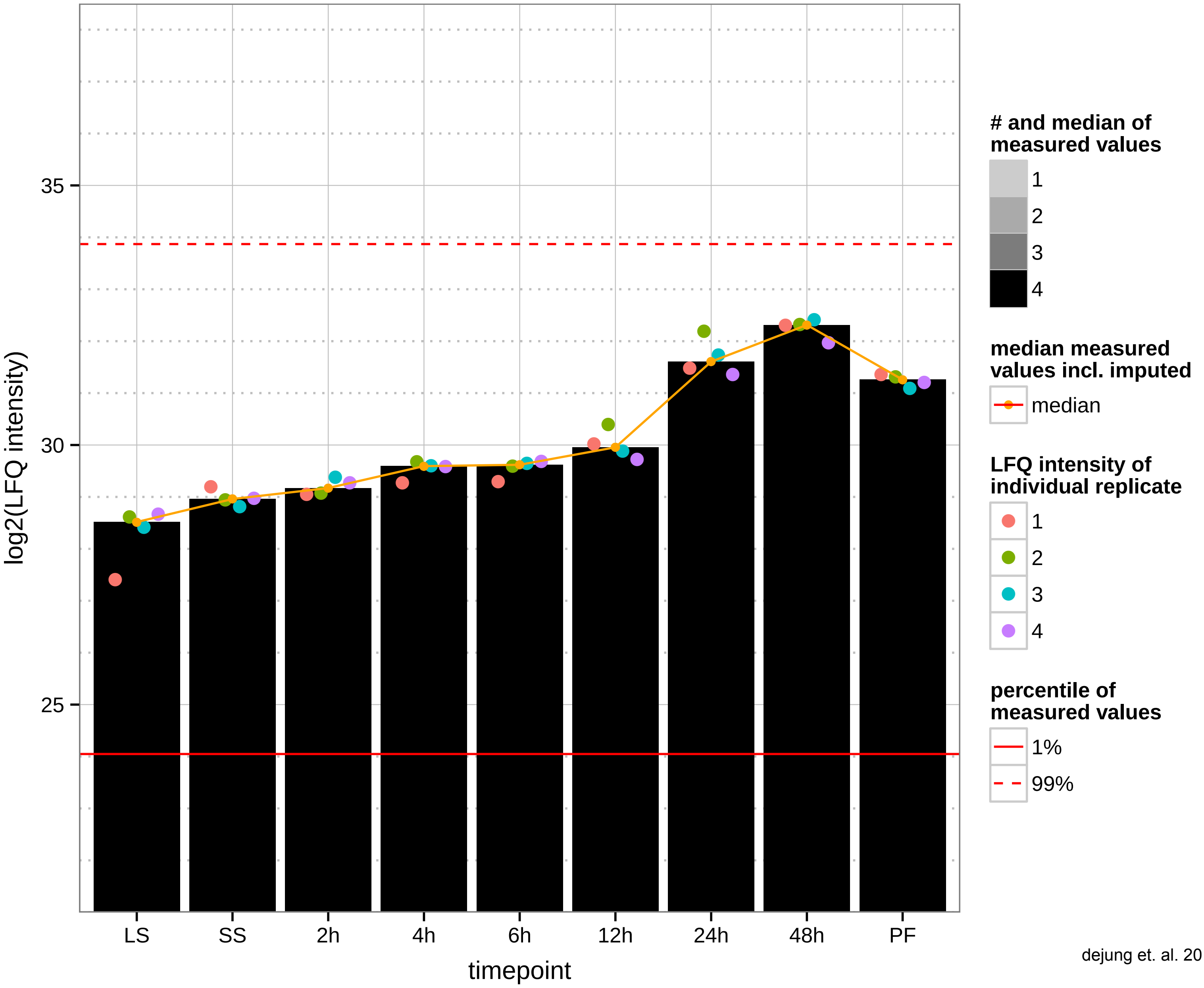
calpain–like protein fragment, putative
Tb927.1.2260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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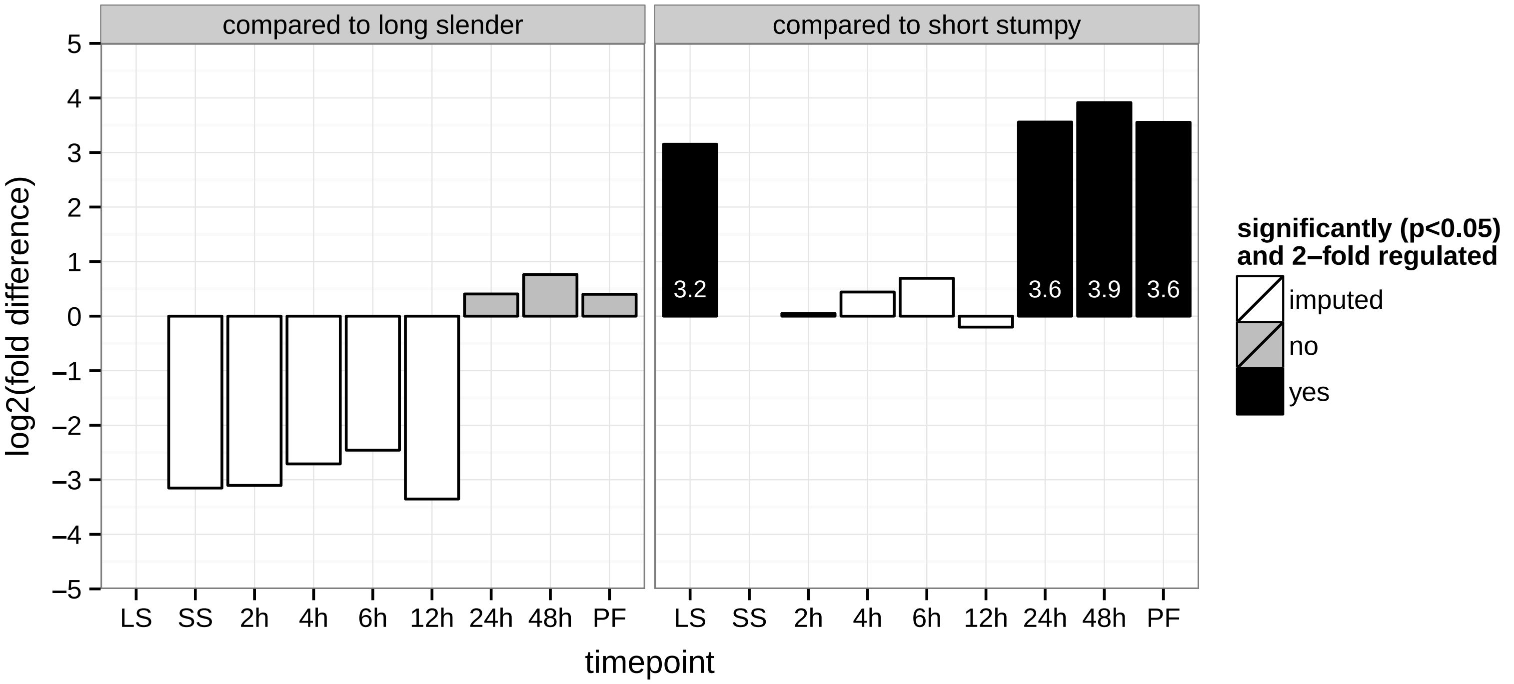
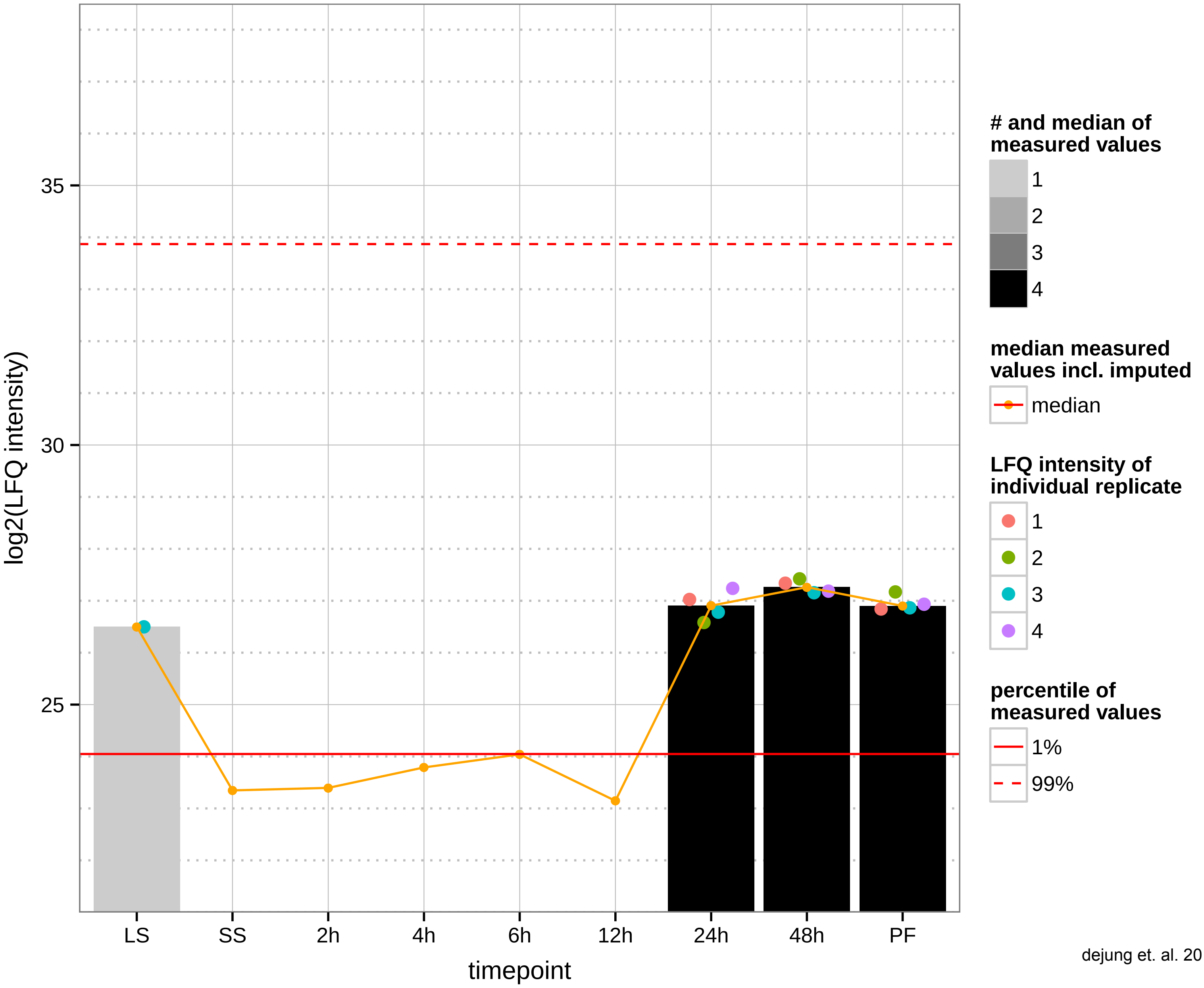
pumilio/PUF RNA binding protein 9 (PUF9)
Tb927.1.2600
AGOF: mRNA binding
AGOC: null
AGOP: regulation of mRNA stability
PGOF: RNA binding, binding
PGOC: null
PGOP: null





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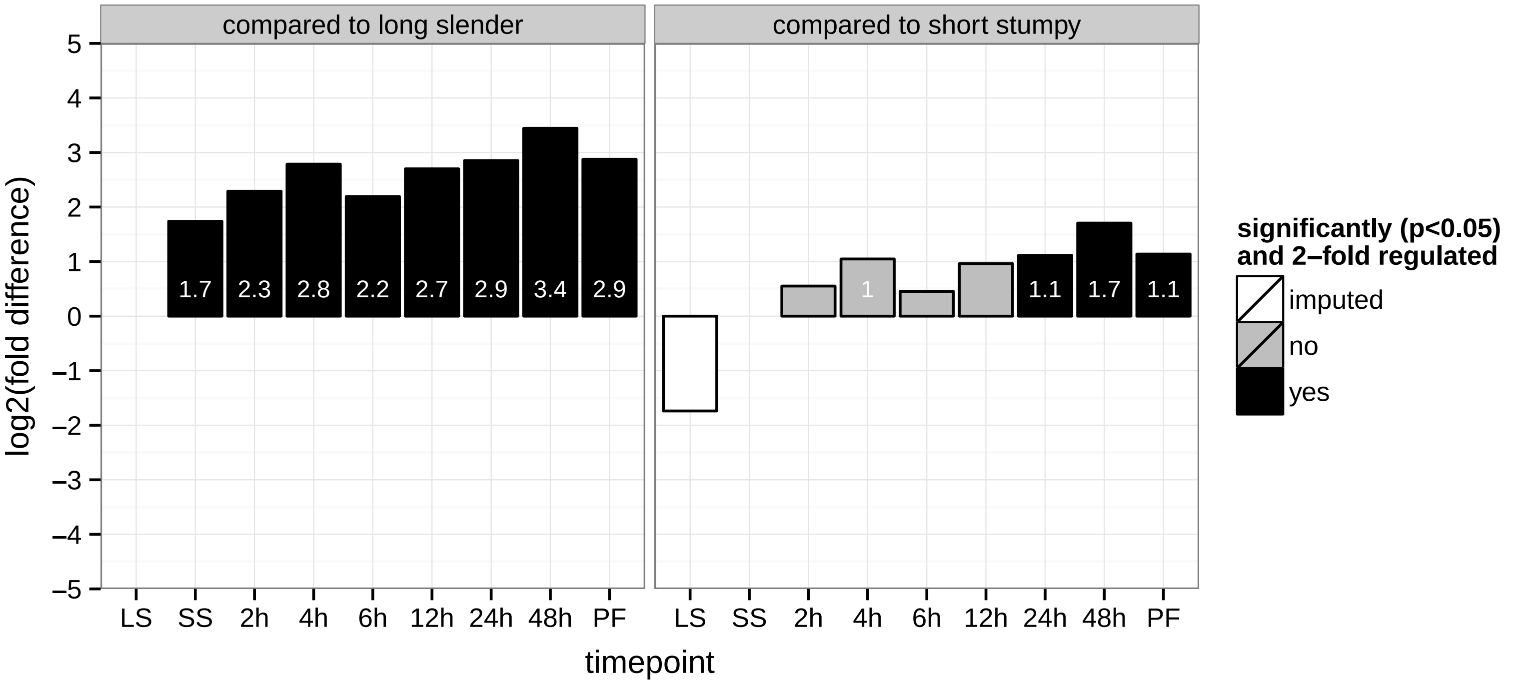
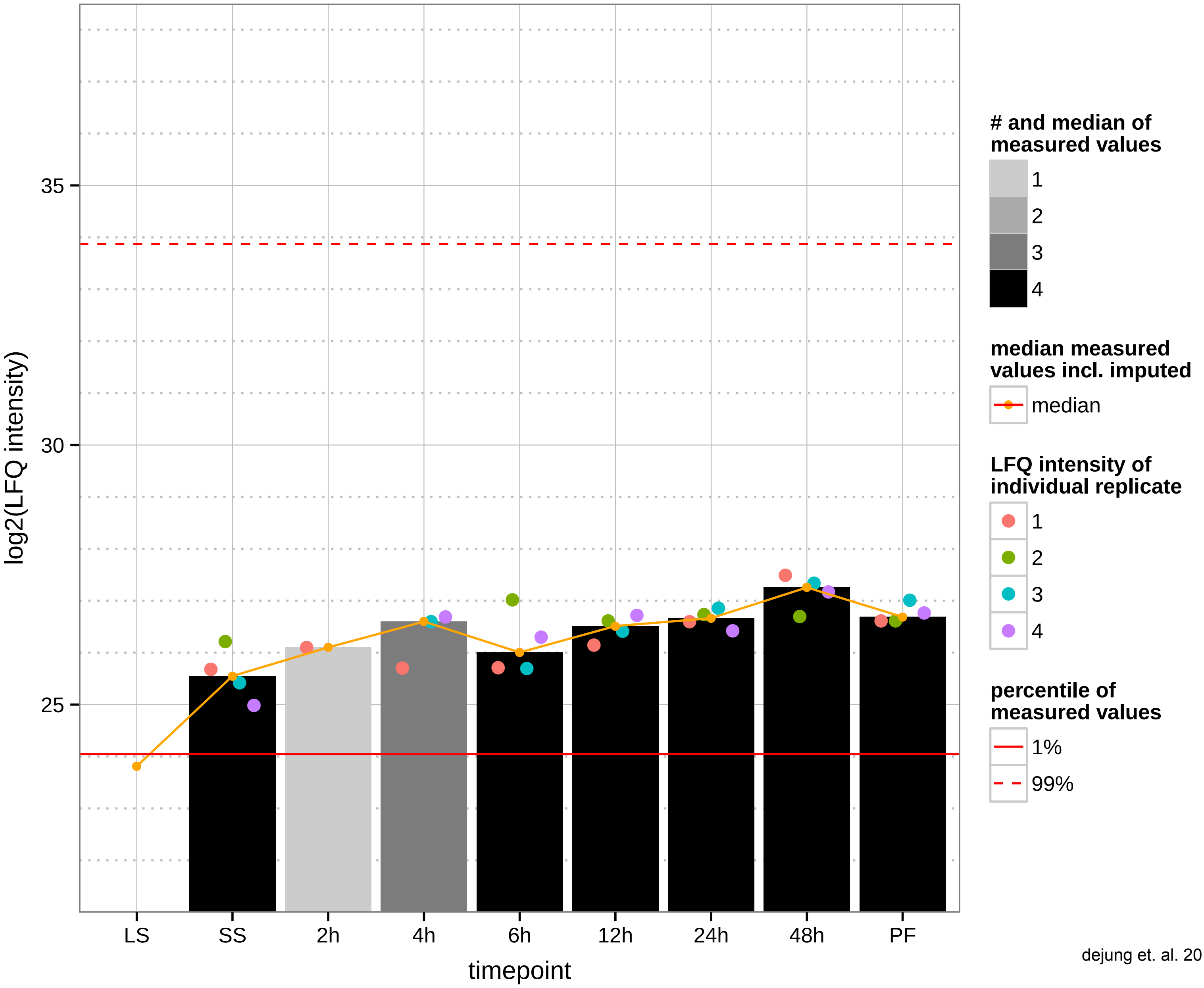
monothiol glutaredoxin, putative
Tb927.10.10420
AGOF: electron carrier activity, protein disulfide isomerase activity, protein disulfide oxidoreductase activity
AGOC: mitochondrion
AGOP: cell redox homeostasis, oxidation–reduction process
PGOF: electron carrier activity, protein disulfide oxidoreductase activity
PGOC: null
PGOP: cell redox homeostasis





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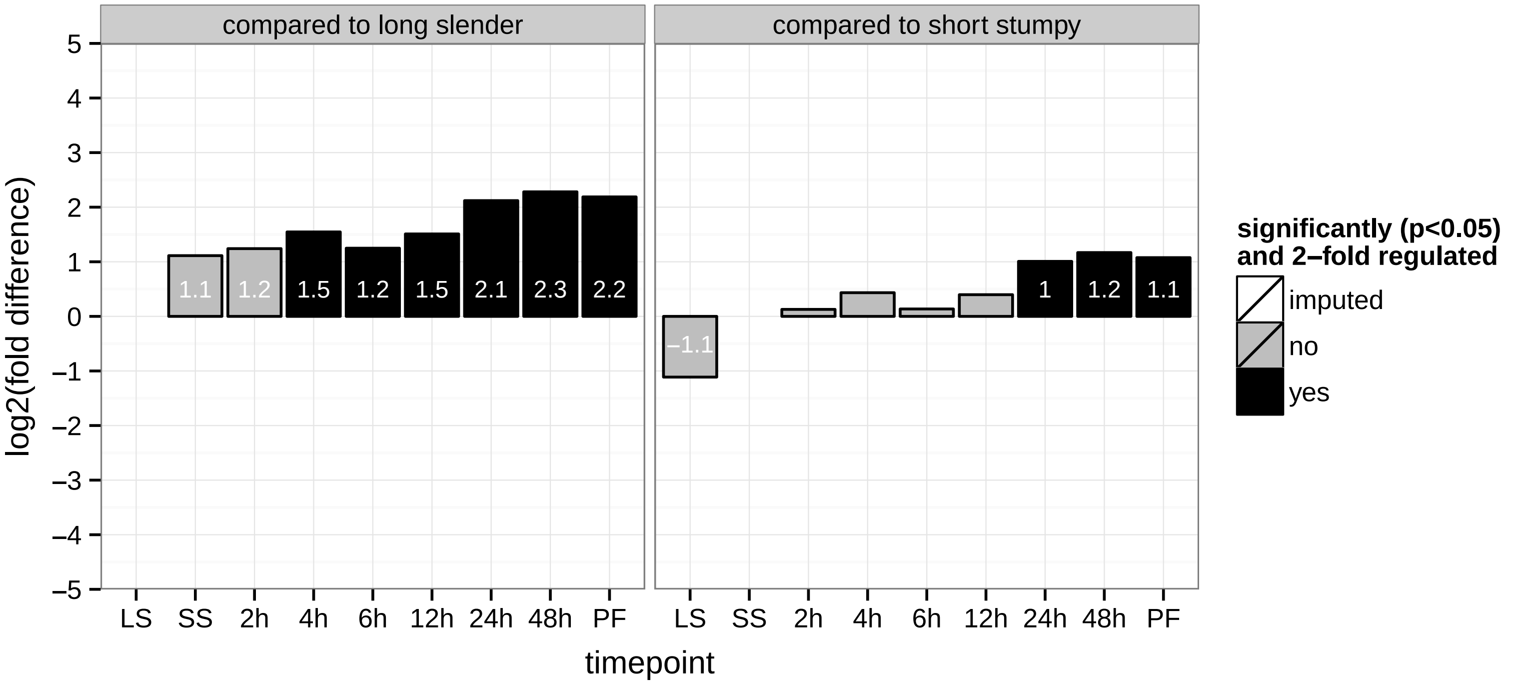
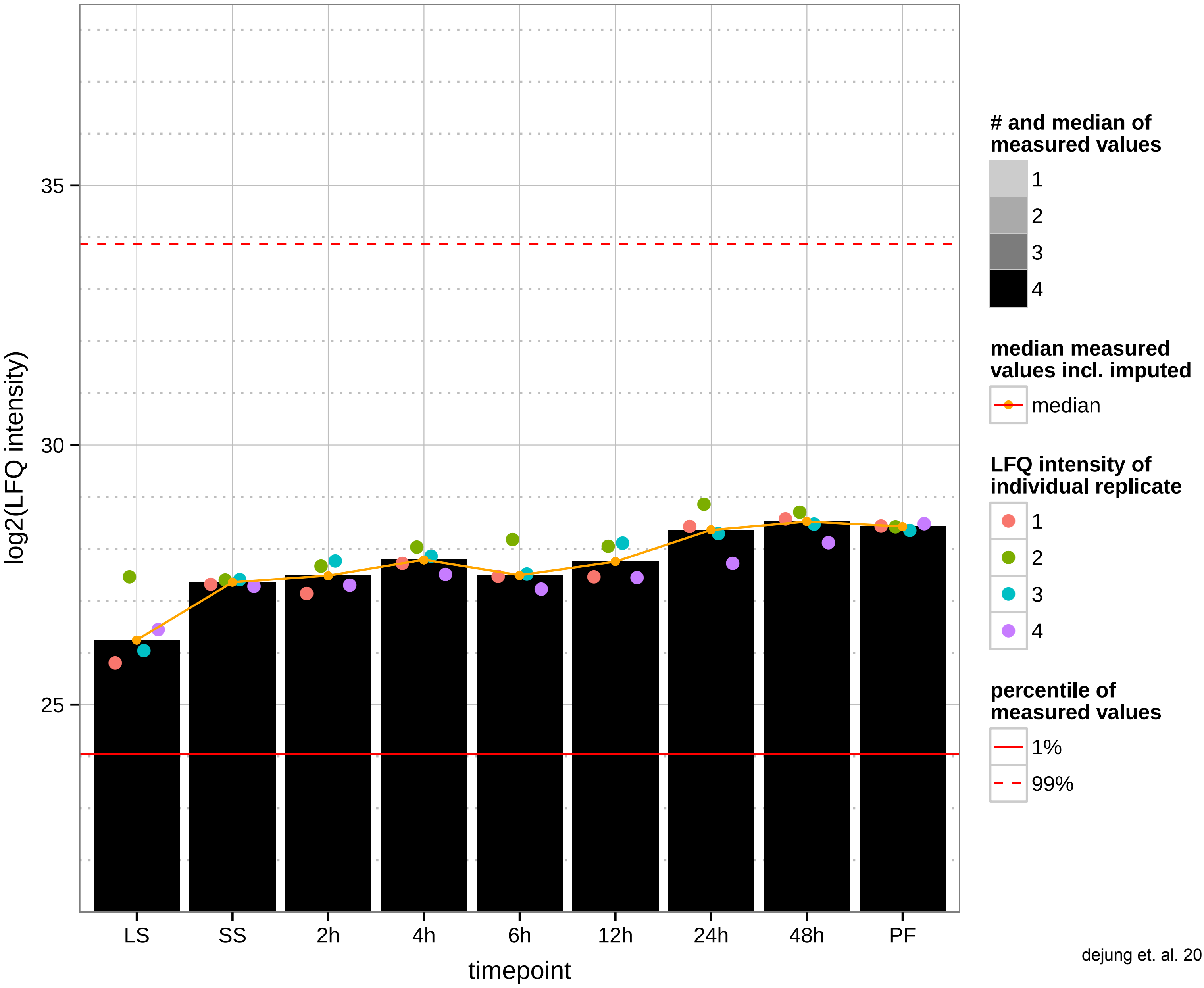
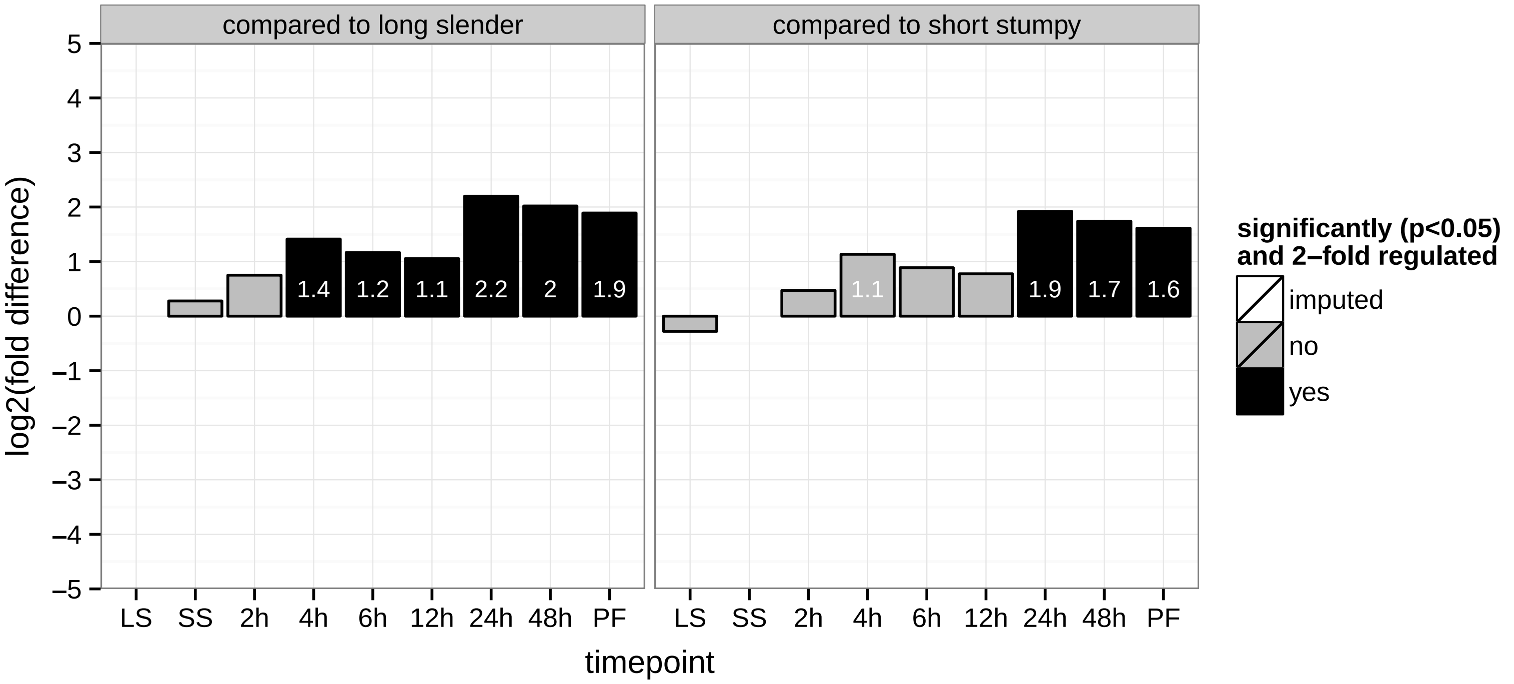
RGG−containing protein 2, MRB1−associated protein, RGGm (RGG2)
Tb927.10.10830
AGOF: mRNA binding
AGOC: external side of mitochondrial outer membrane, mitochondrion
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null

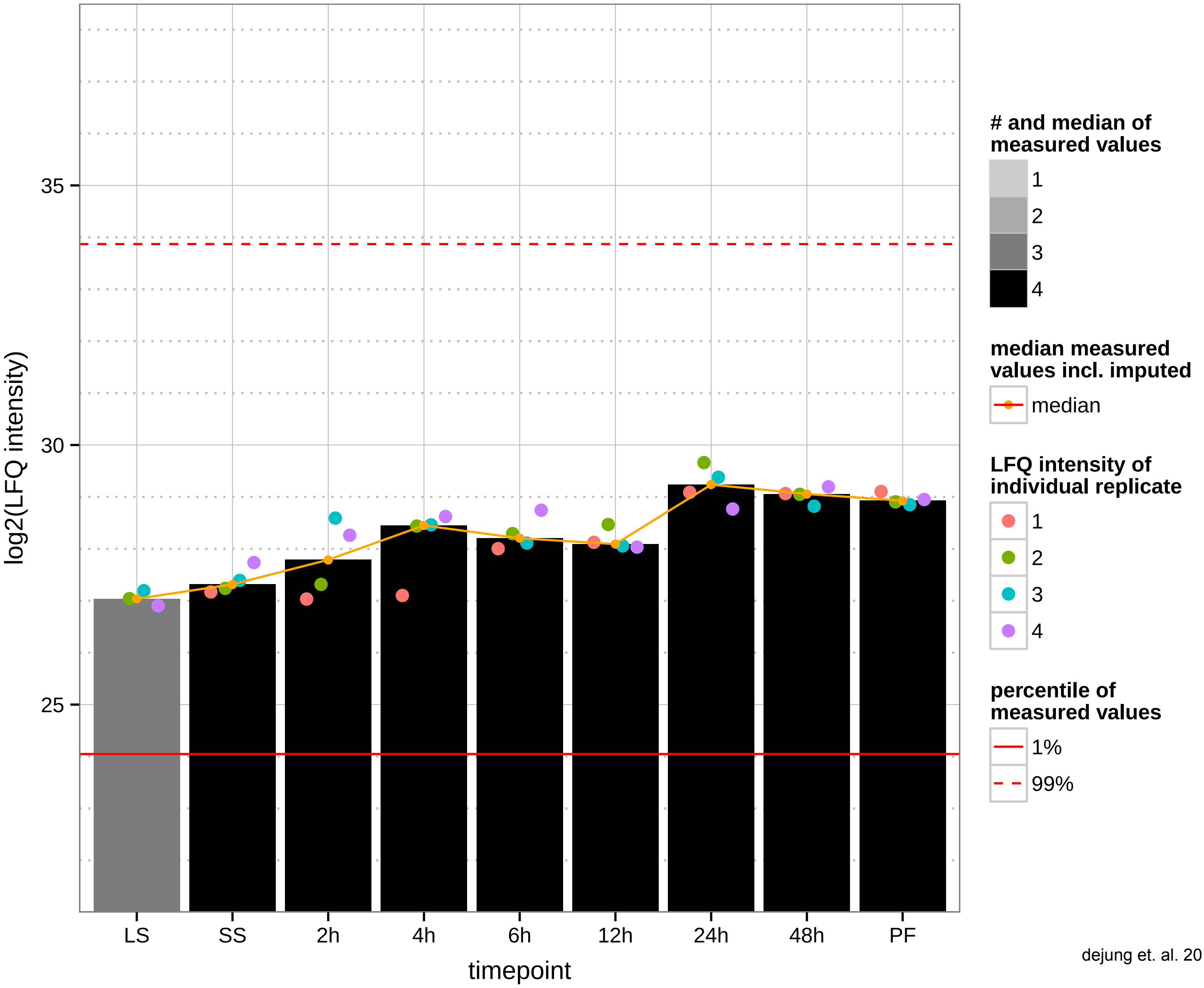




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.11030
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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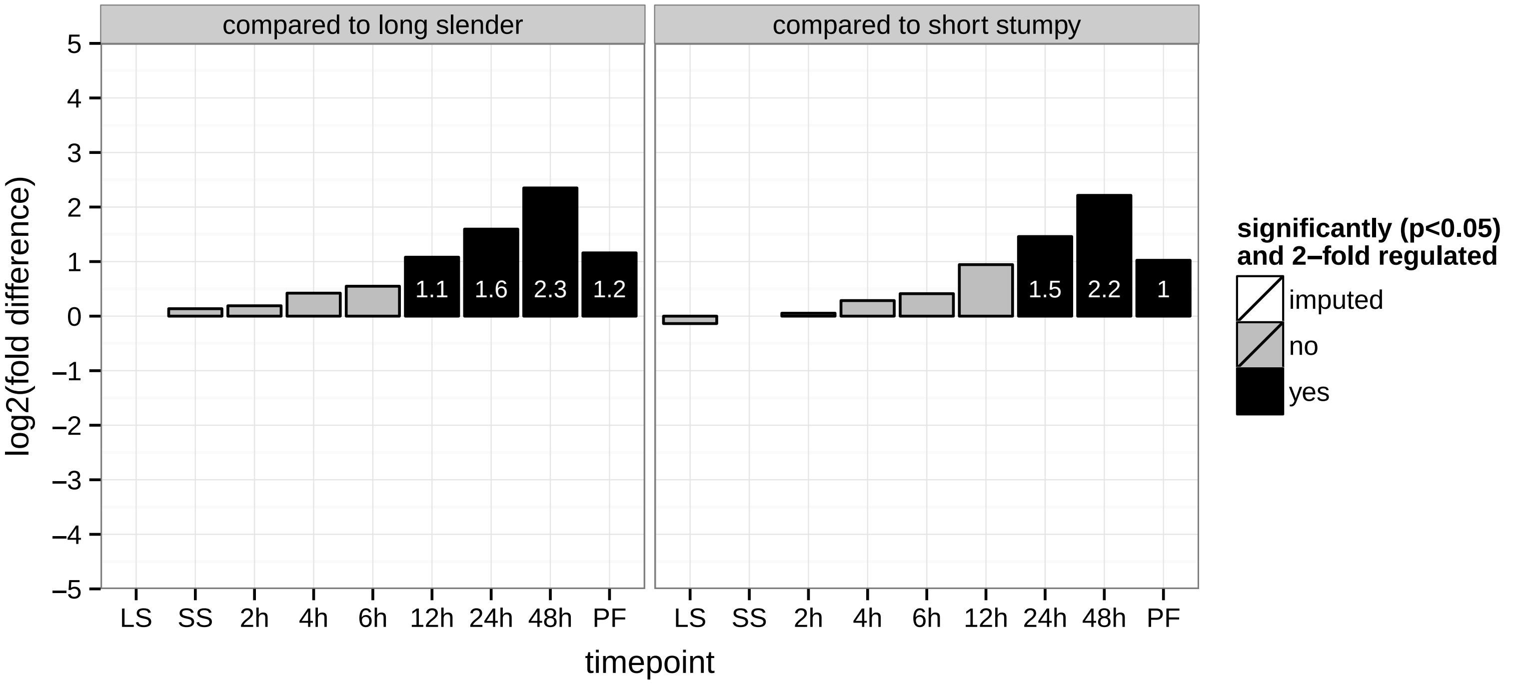
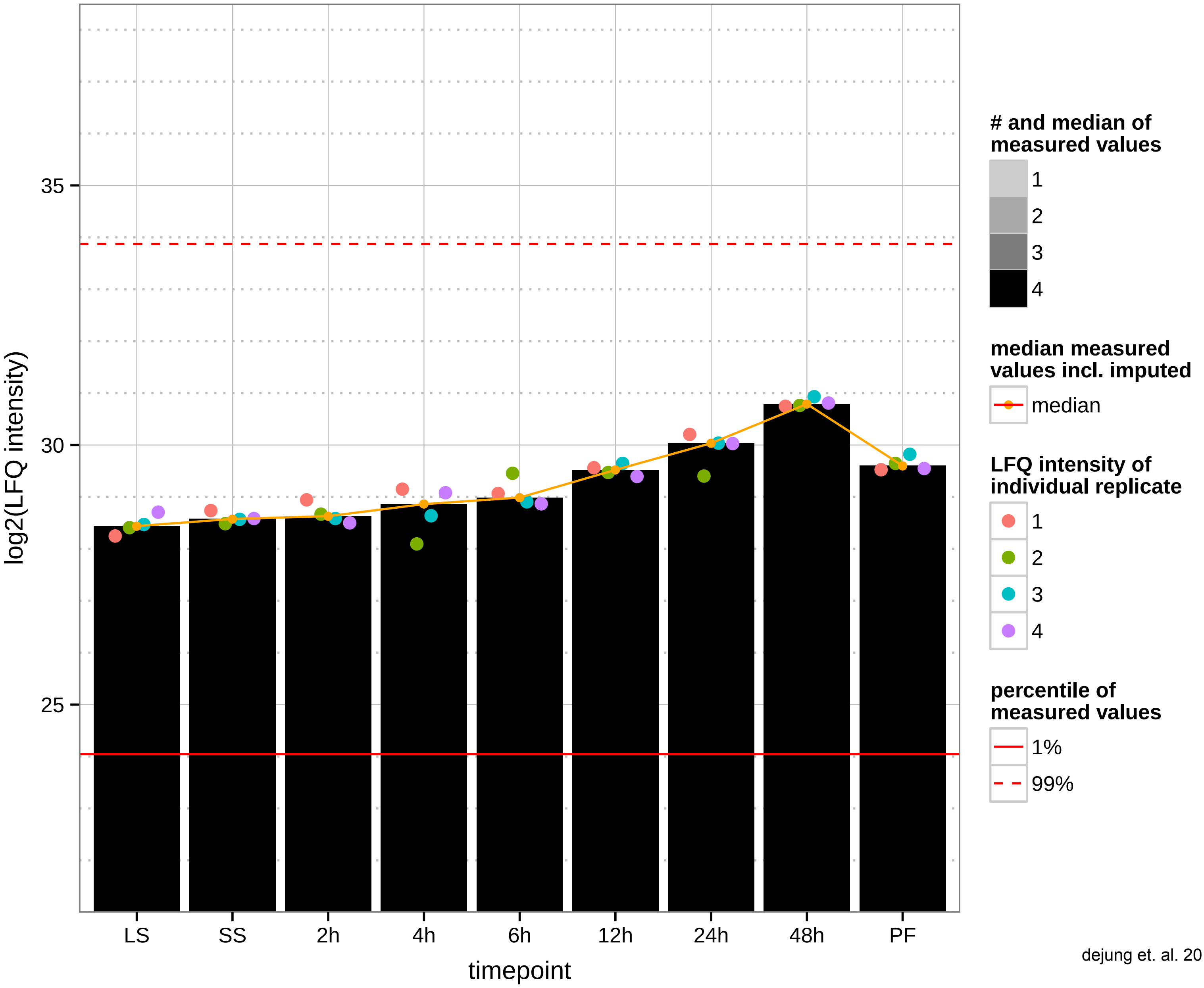
pumilio/PUF RNA binding protein 6 (PUF6)
Tb927.10.11760
AGOF: RNA binding
AGOC: null
AGOP: mRNA metabolic process
PGOF: RNA binding, binding
PGOC: null
PGOP: null





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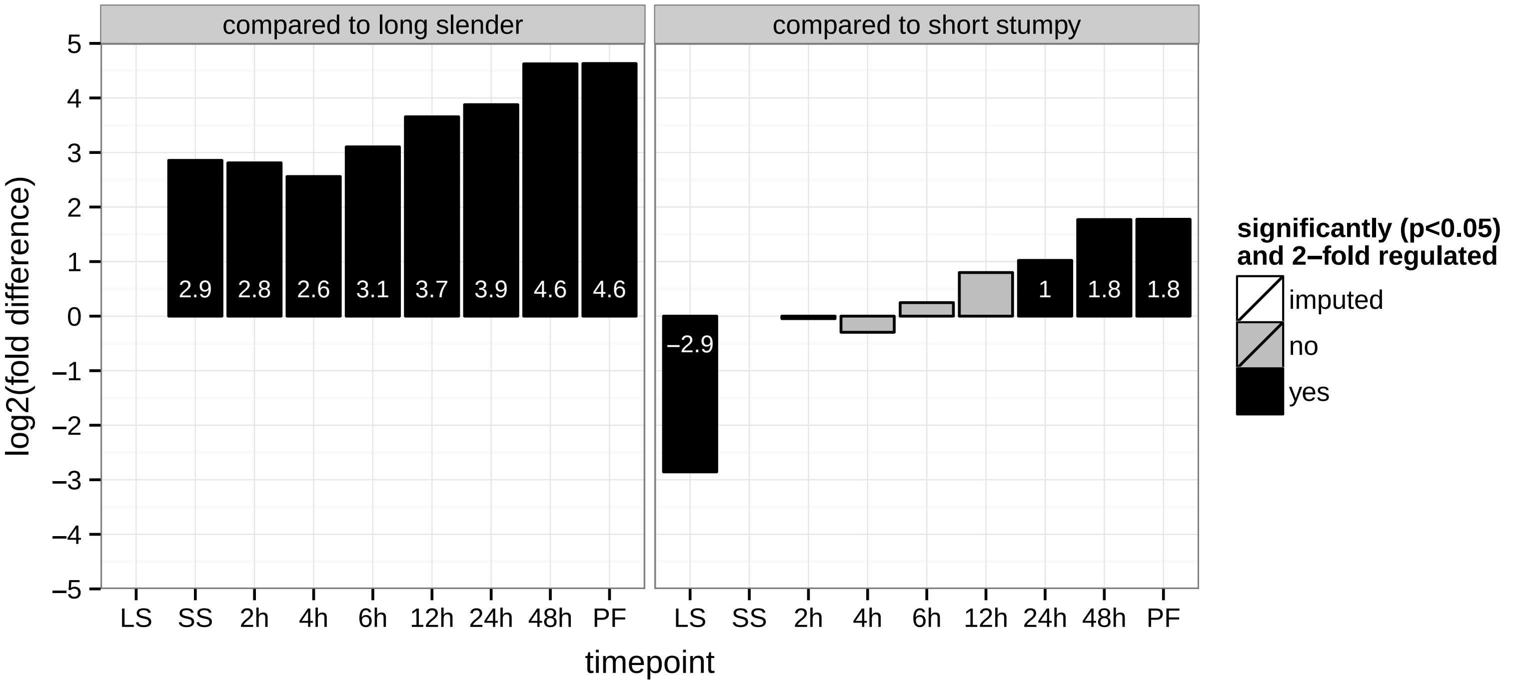
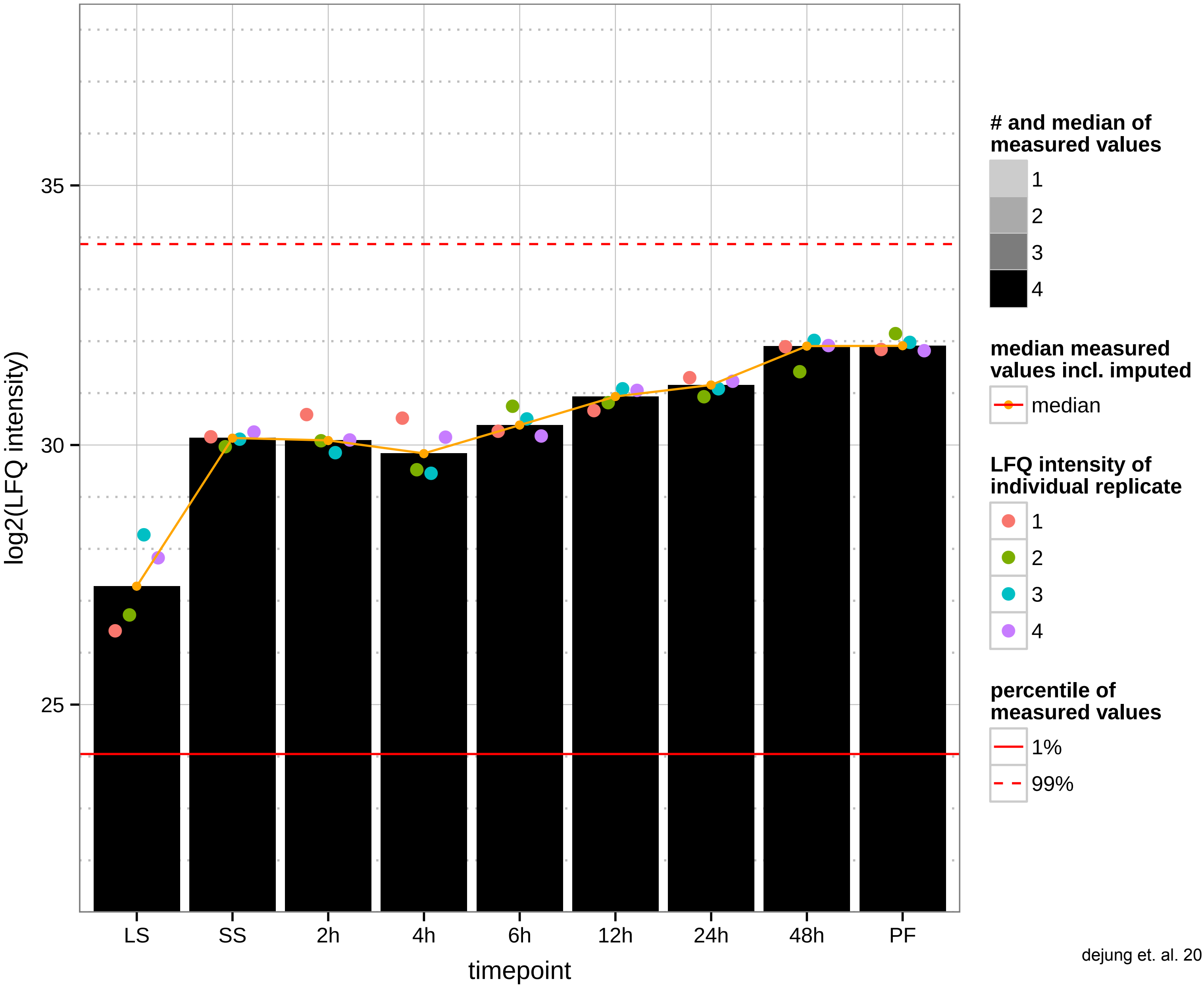
Elongation factor Tu, mitochondrial (EF−Tu)
Tb927.10.13360
AGOF: GTP binding, GTPase activity, translation elongation factor activity
AGOC: intracellular, mitochondrion
AGOP: growth, mitochondrial translation, oxidative phosphorylation, translational elongation
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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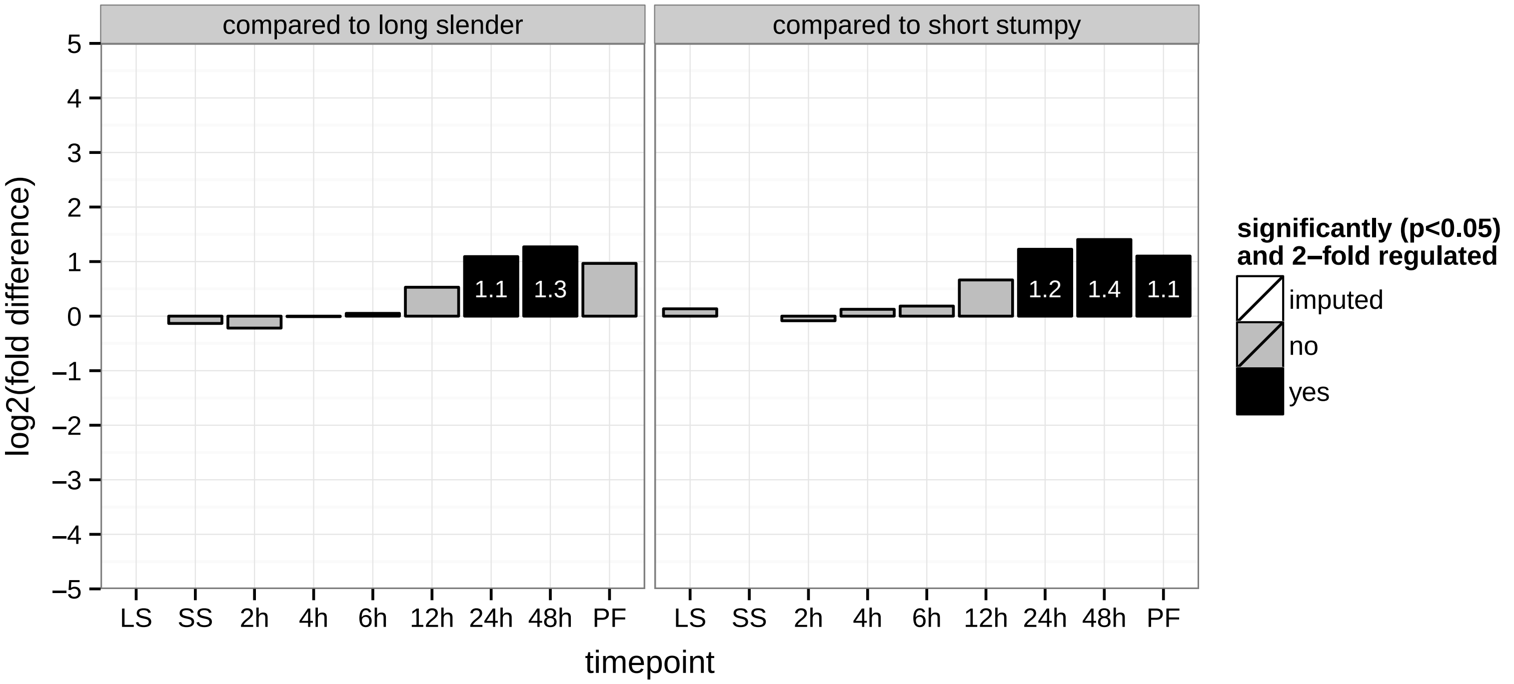
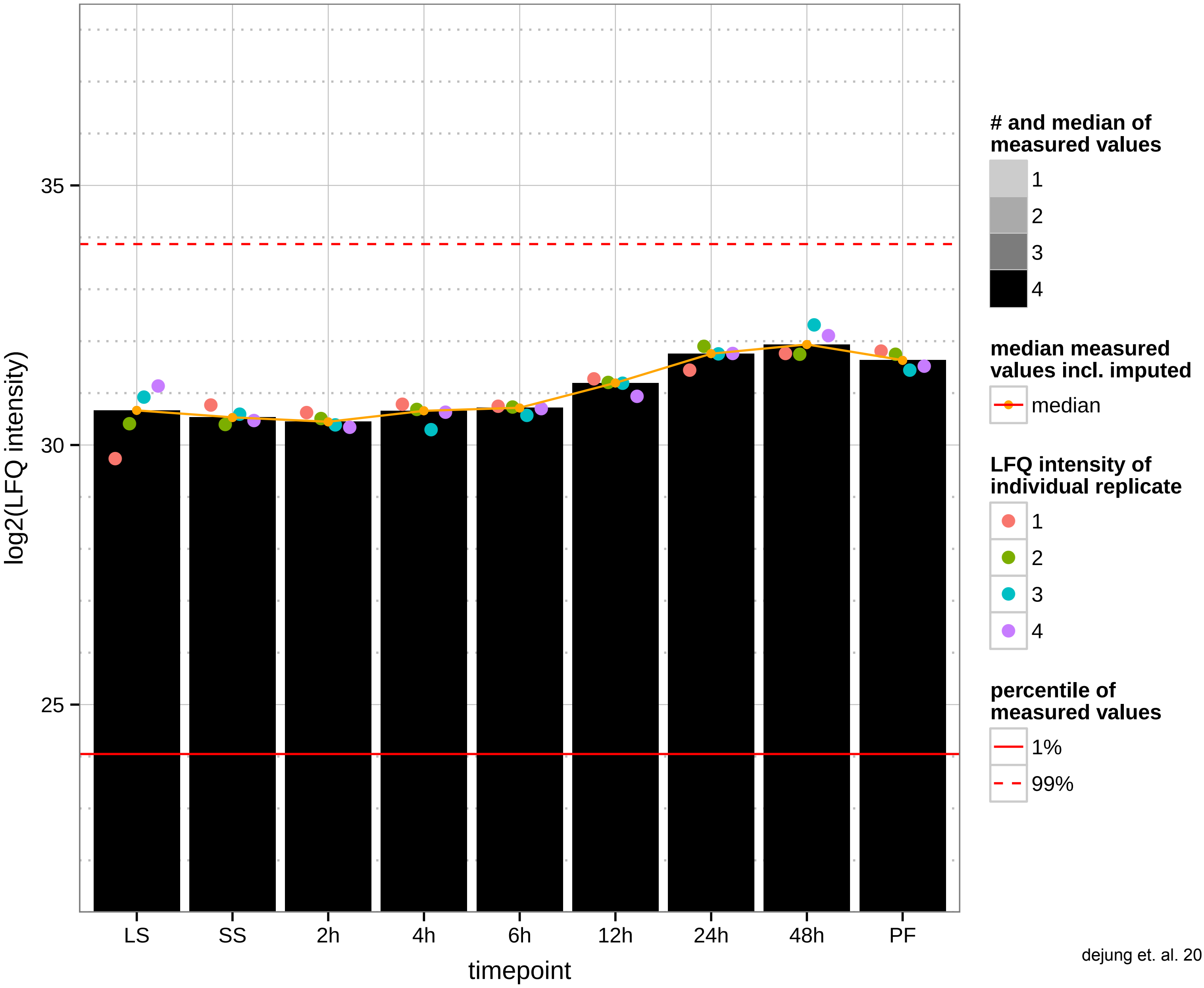
hypoxanthine–guanine phosphoribosyltransferase, putative
Tb927.10.1390
AGOF: hypoxanthine phosphoribosyltransferase activity
AGOC: cytoplasm
AGOP: purine ribonucleoside salvage
PGOF: null
PGOC: null
PGOP: nucleoside metabolic process





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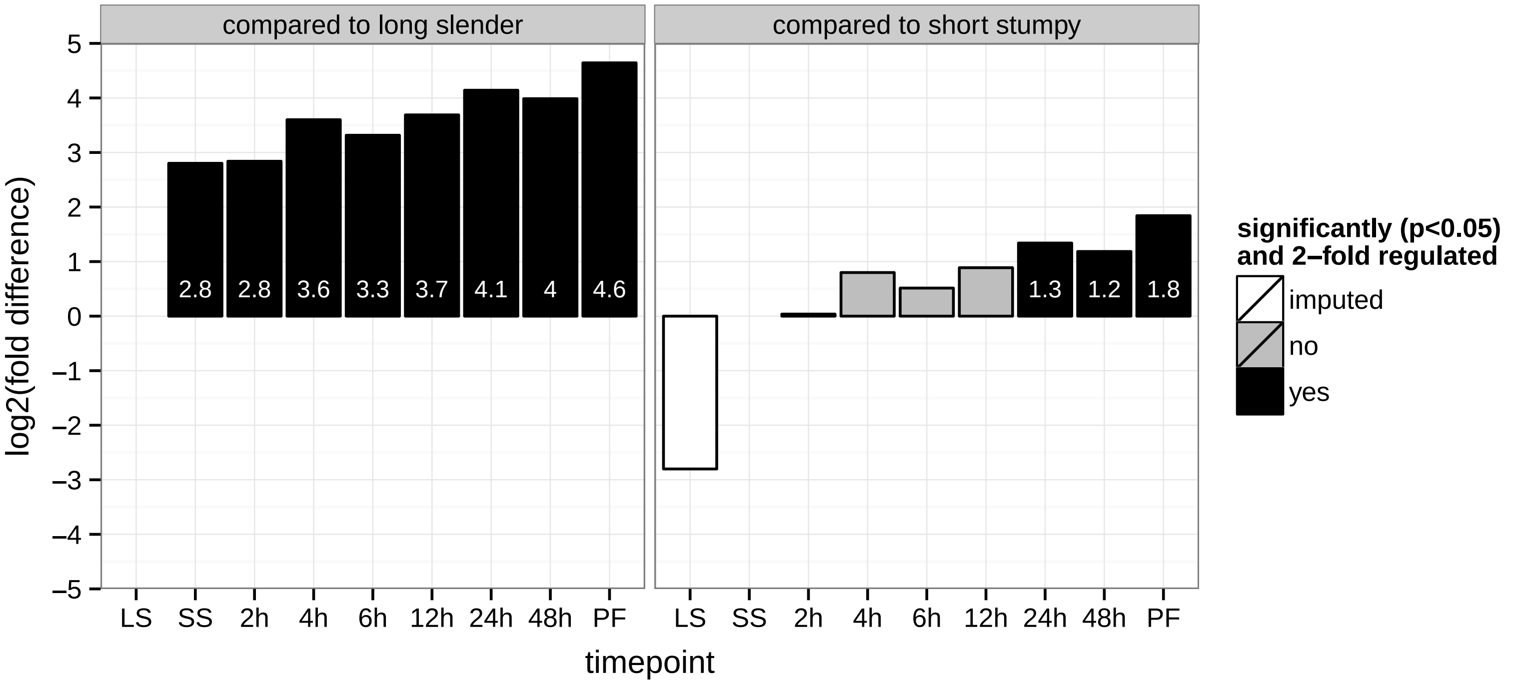
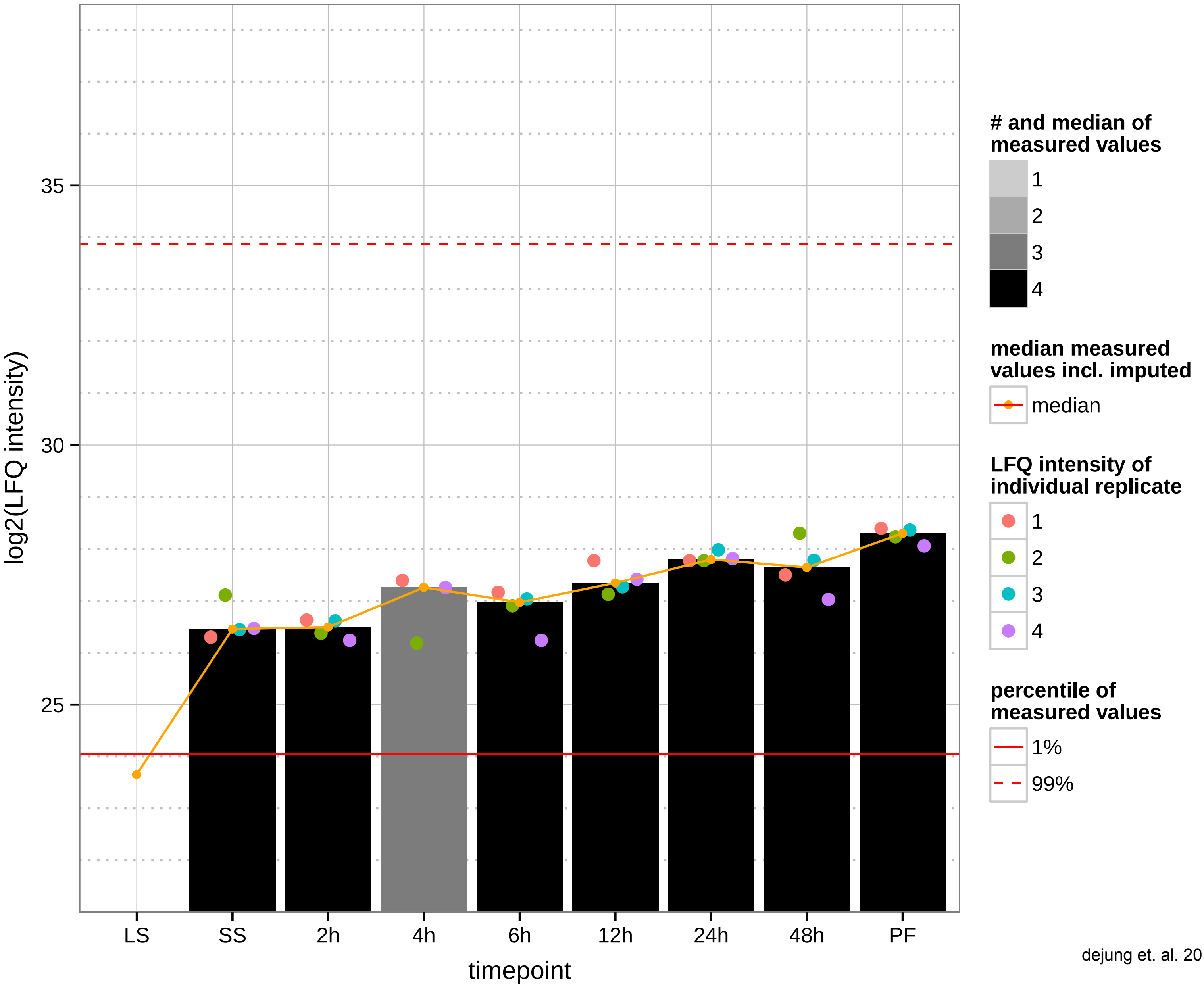
hypothetical protein, conserved
Tb927.10.14860
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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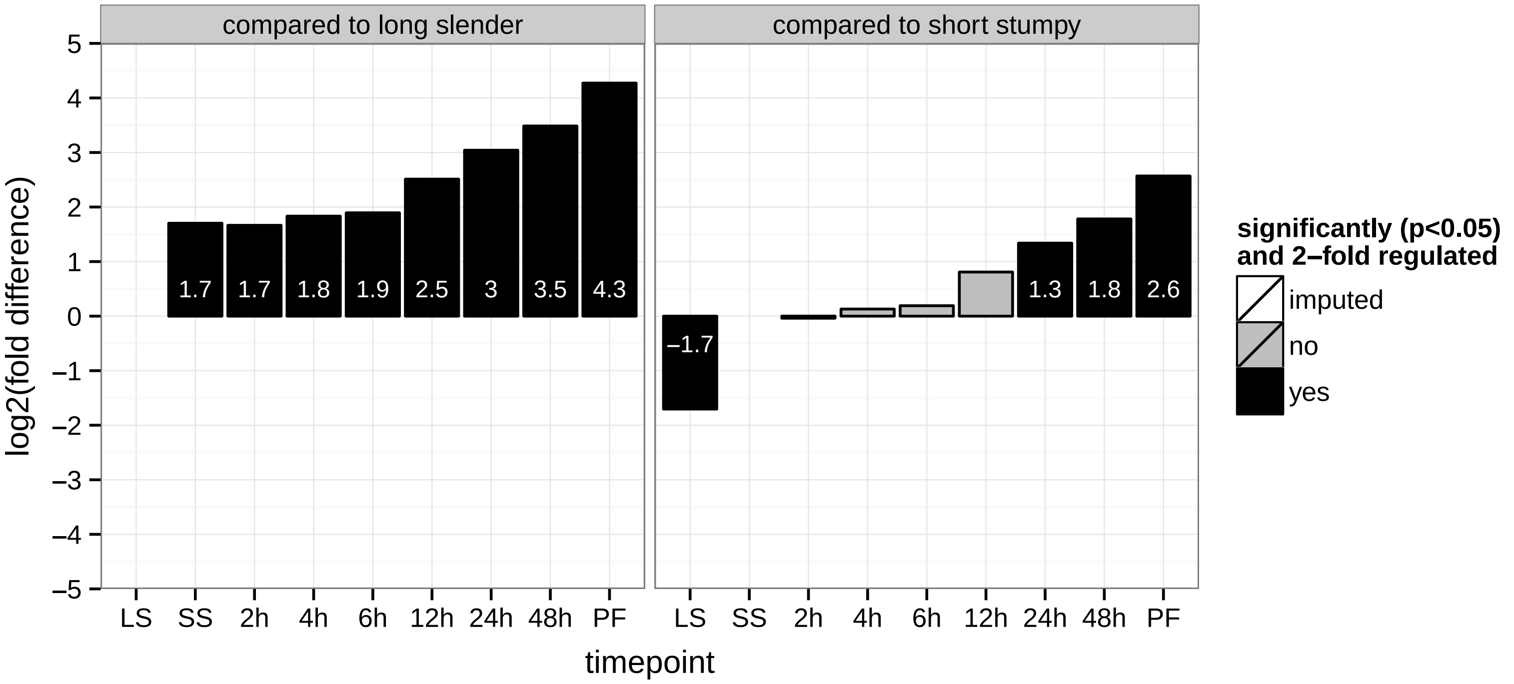
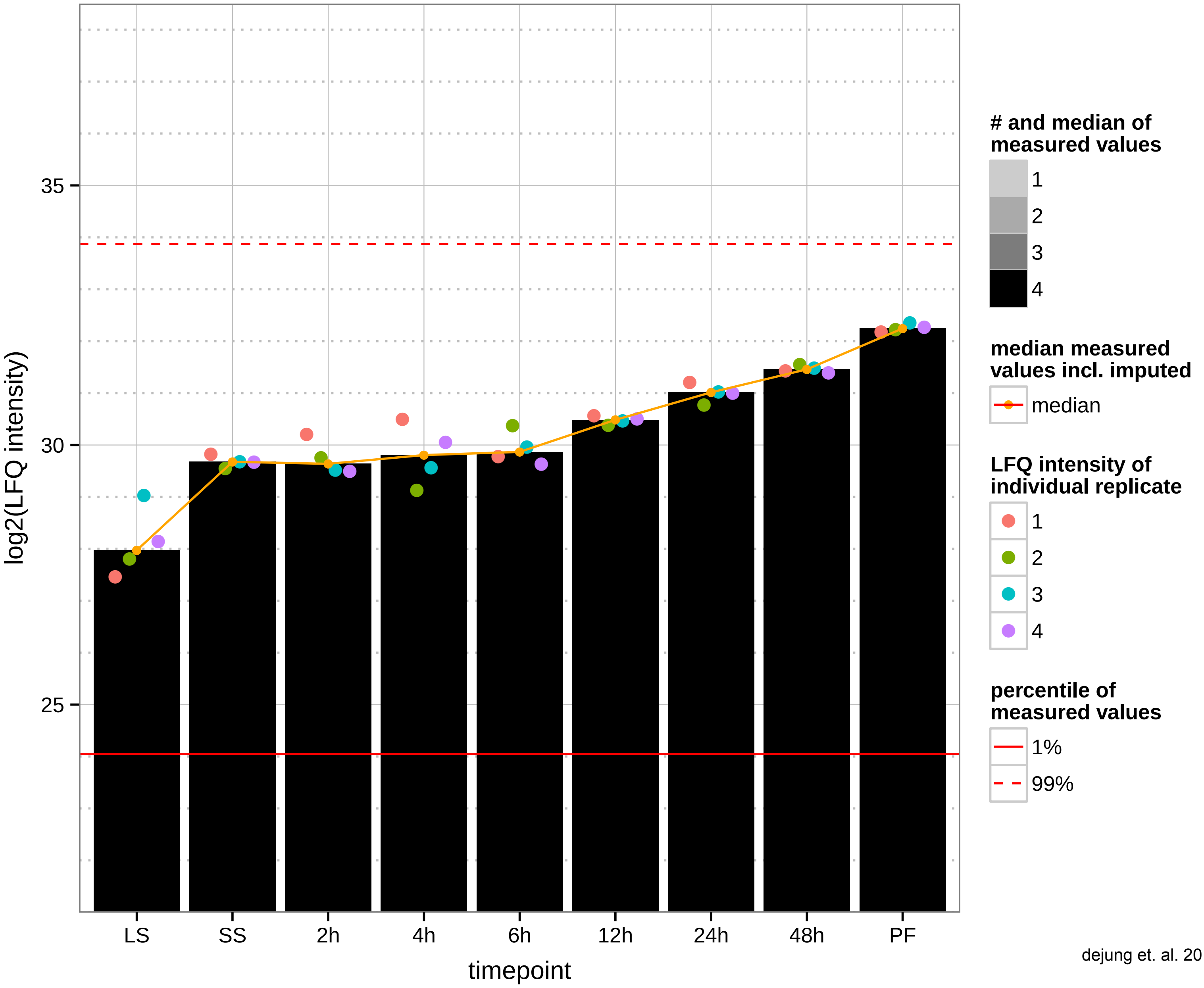
methionyl–tRNA synthetase, putative (MetRS)
Tb927.10.1500
AGOF: ATP binding, methionine–tRNA ligase activity
AGOC: cytoplasm
AGOP: methionyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, methionine–tRNA ligase activity, nucleotide binding
PGOC: cytoplasm
PGOP: methionyl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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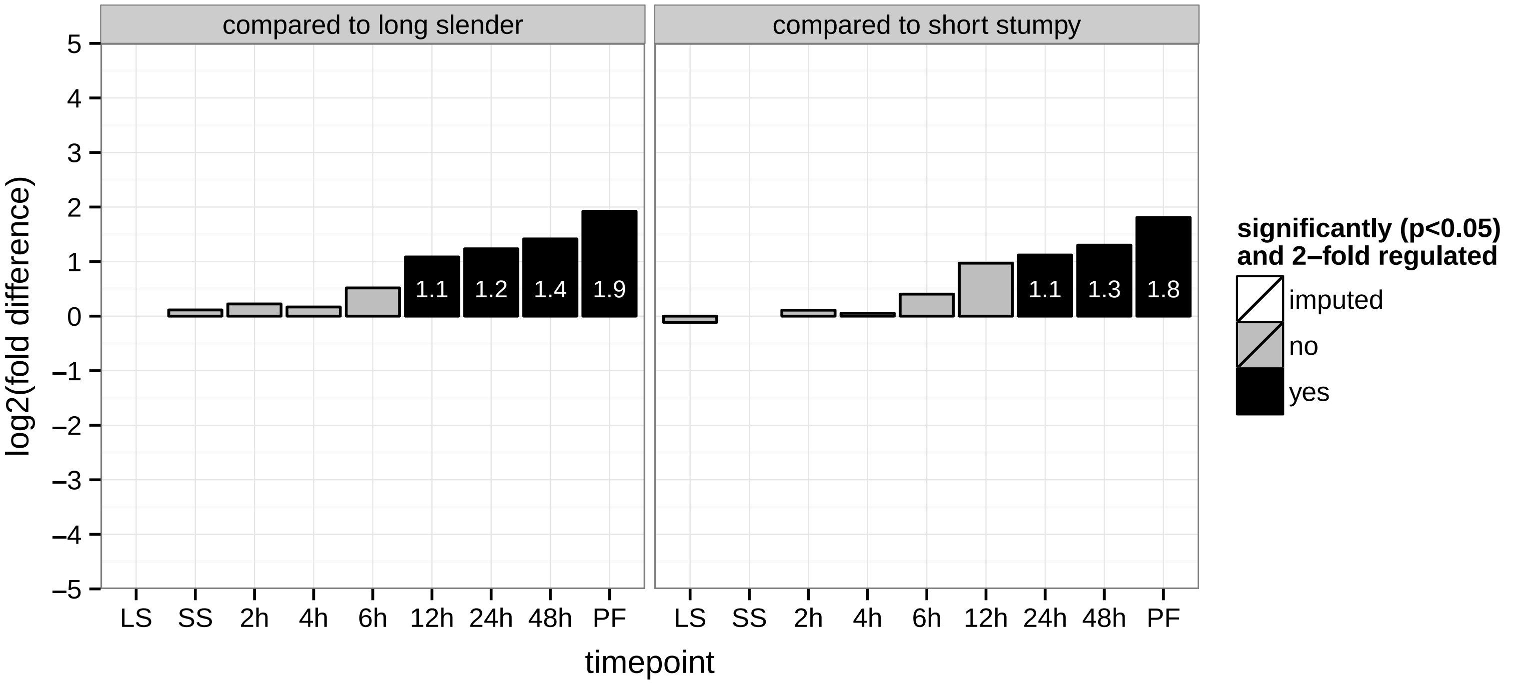
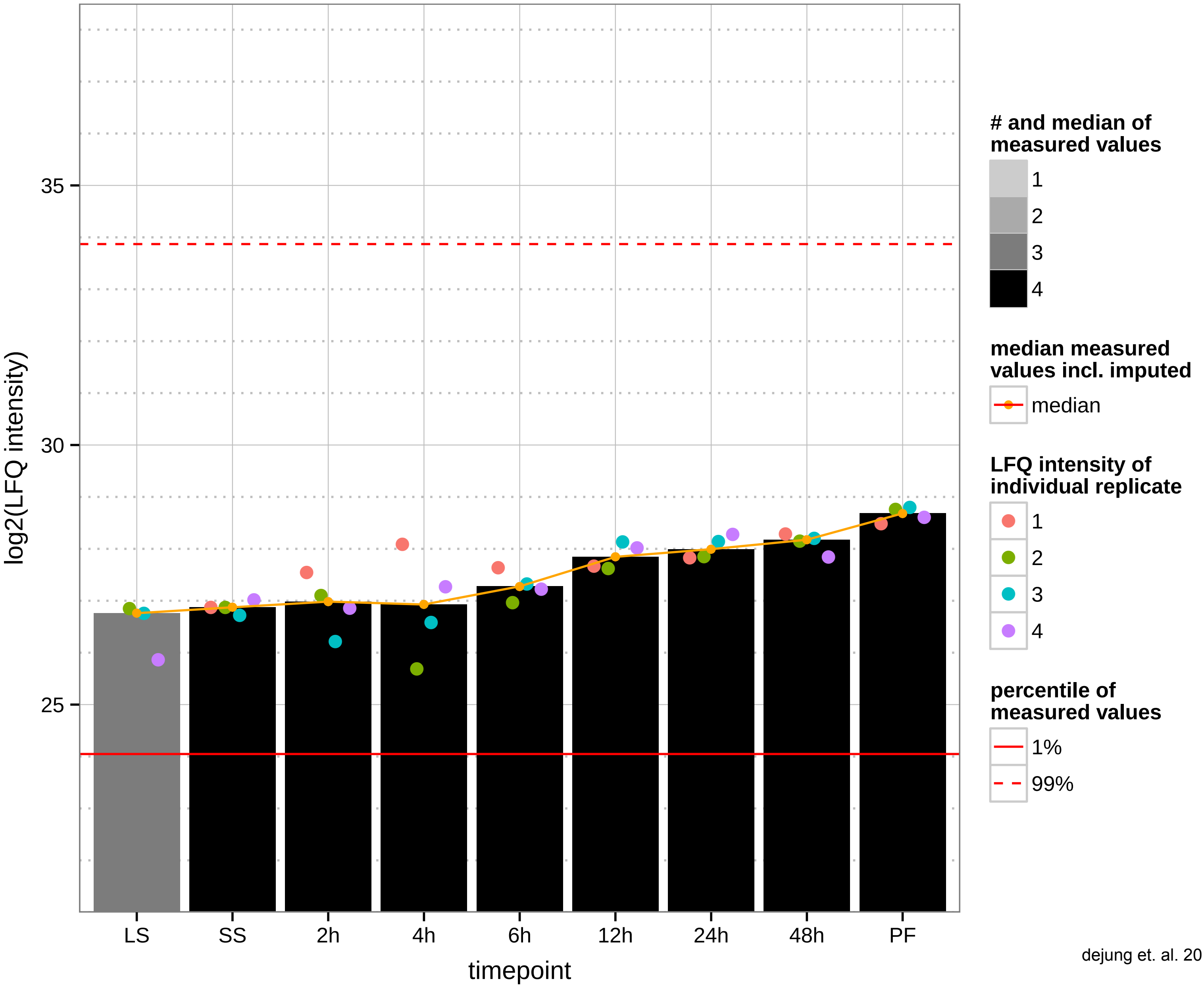
hypothetical protein, conserved
Tb927.10.15170
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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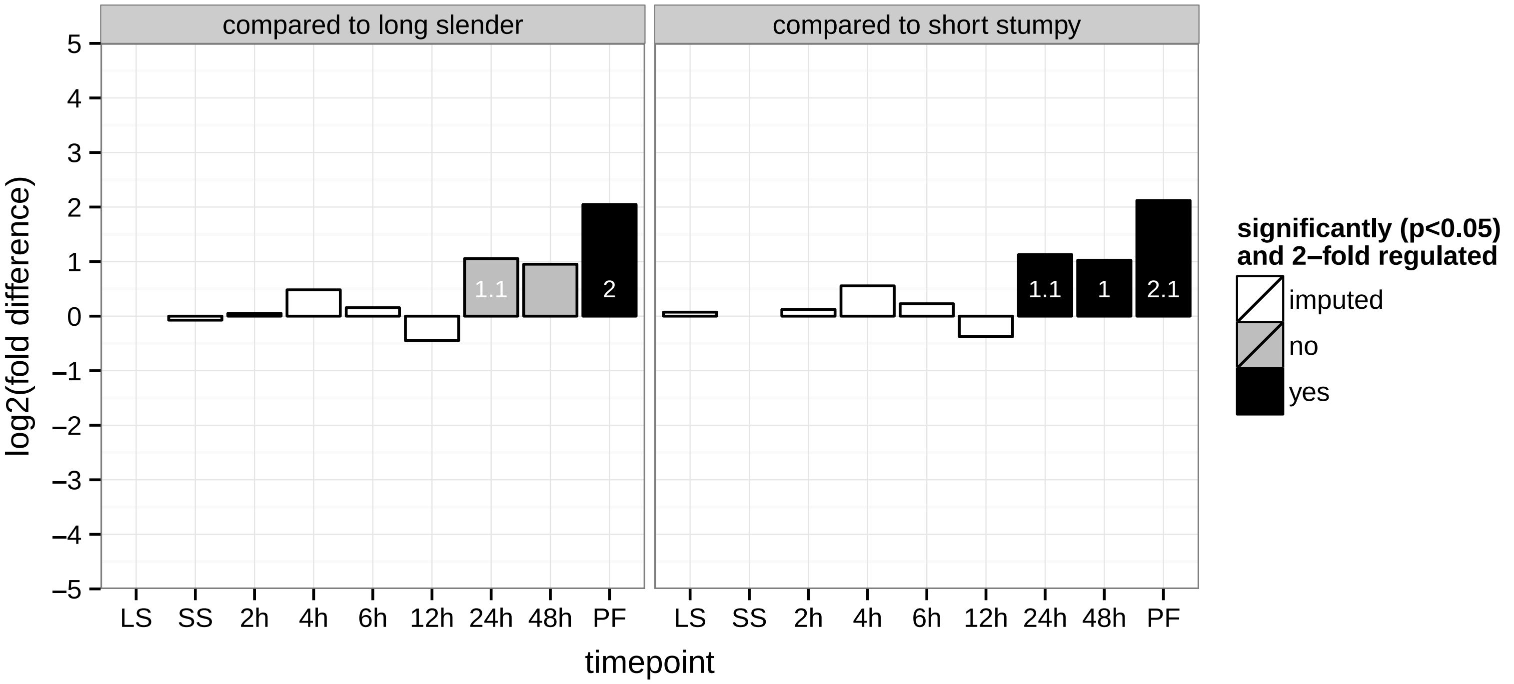
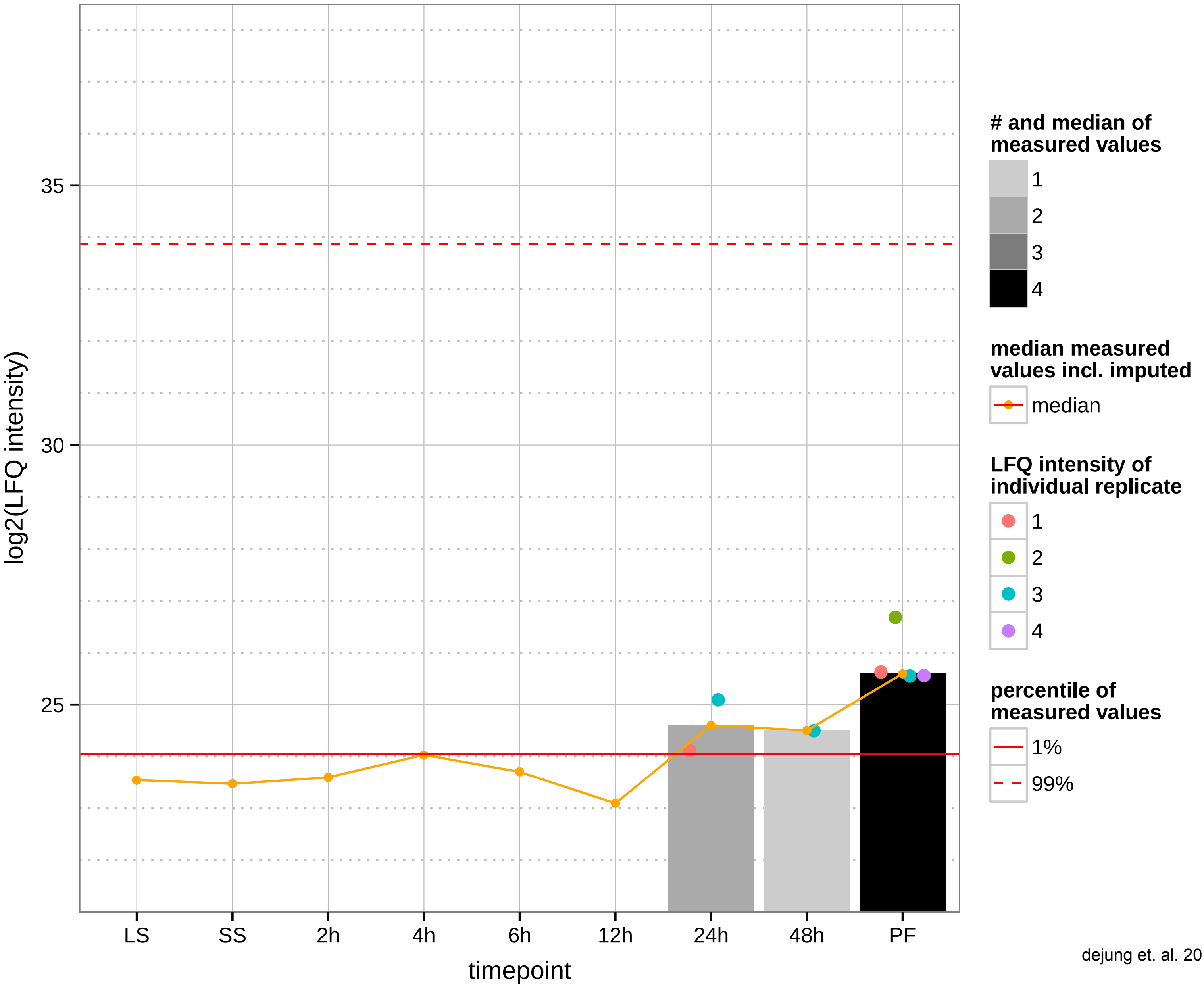
hypothetical protein, conserved
Tb927.10.15790
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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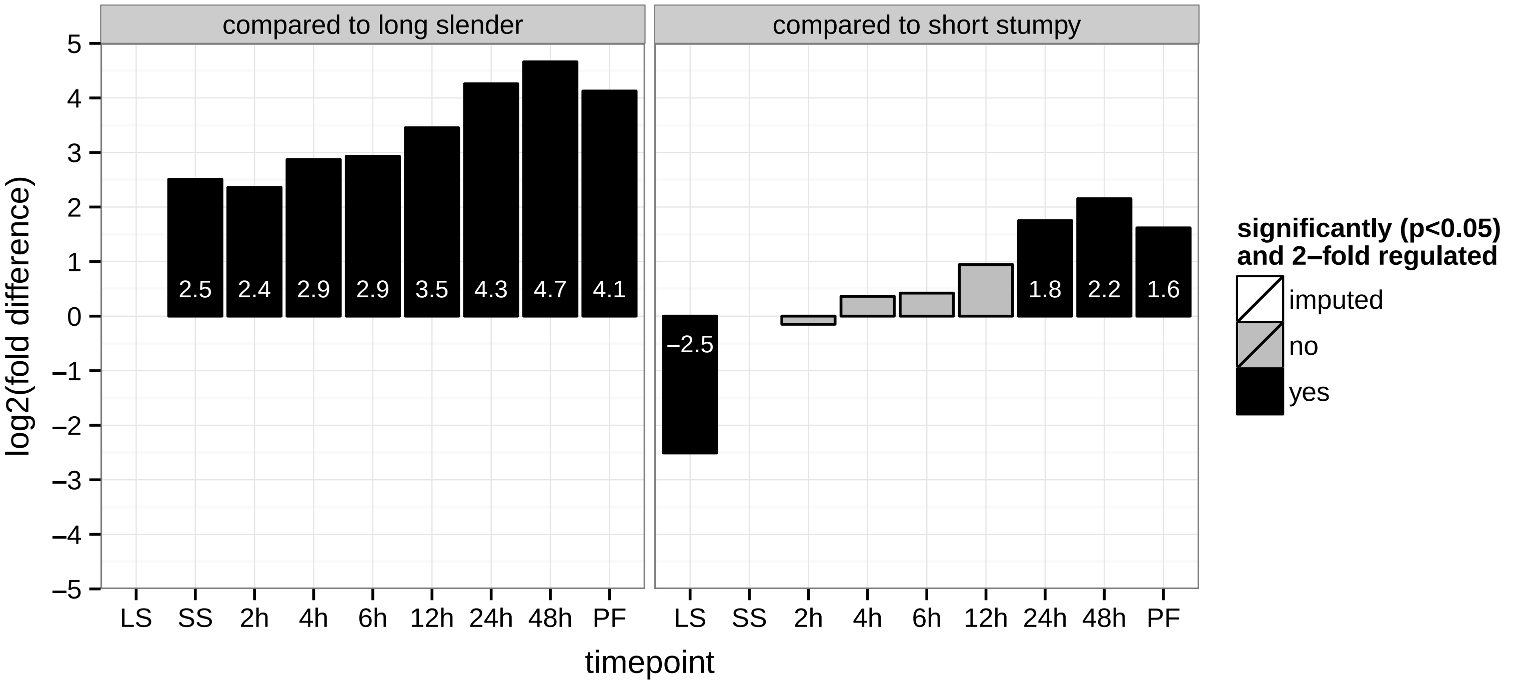
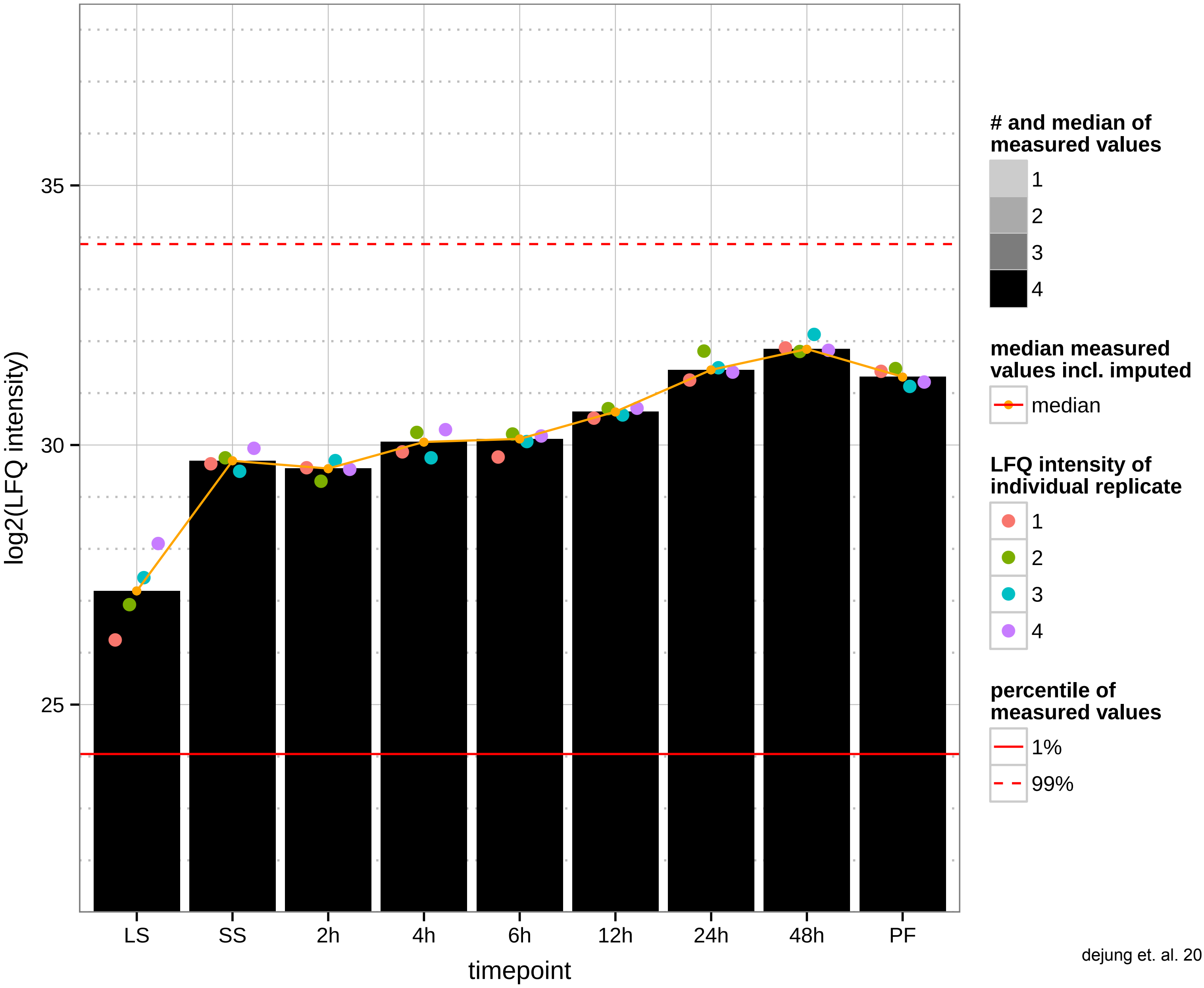
ATP synthase F1 subunit gamma protein, putative
Tb927.10.180
AGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, proton−transporting ATPase activity
AGOC: mitochondrion, proton−transporting ATP synthase complex, catalytic core F(1), proton−transporting two−sector ATPas
AGOP: ATP synthesis coupled proton transport
PGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, proton−transporting ATPase activity
PGOC: proton−transporting ATP synthase complex, catalytic core F(1)
PGOP: ATP synthesis coupled proton transport





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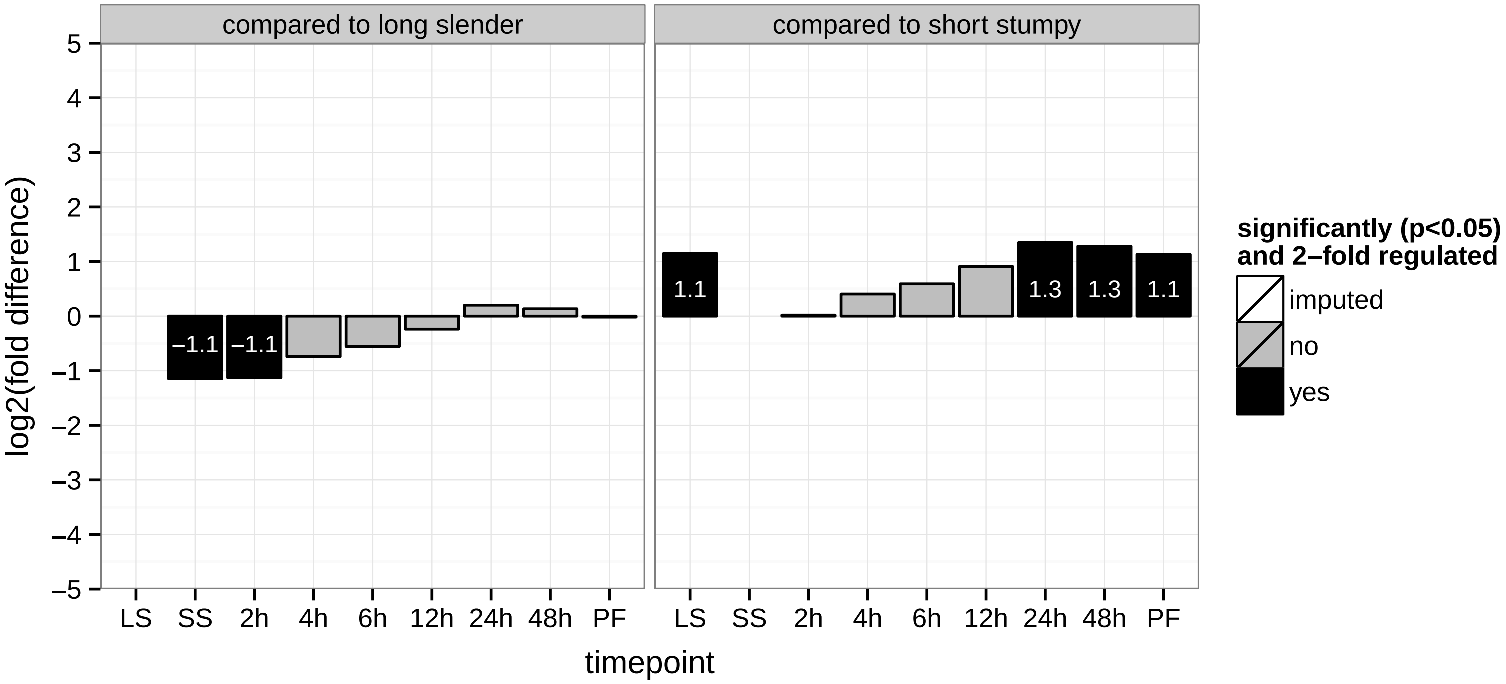
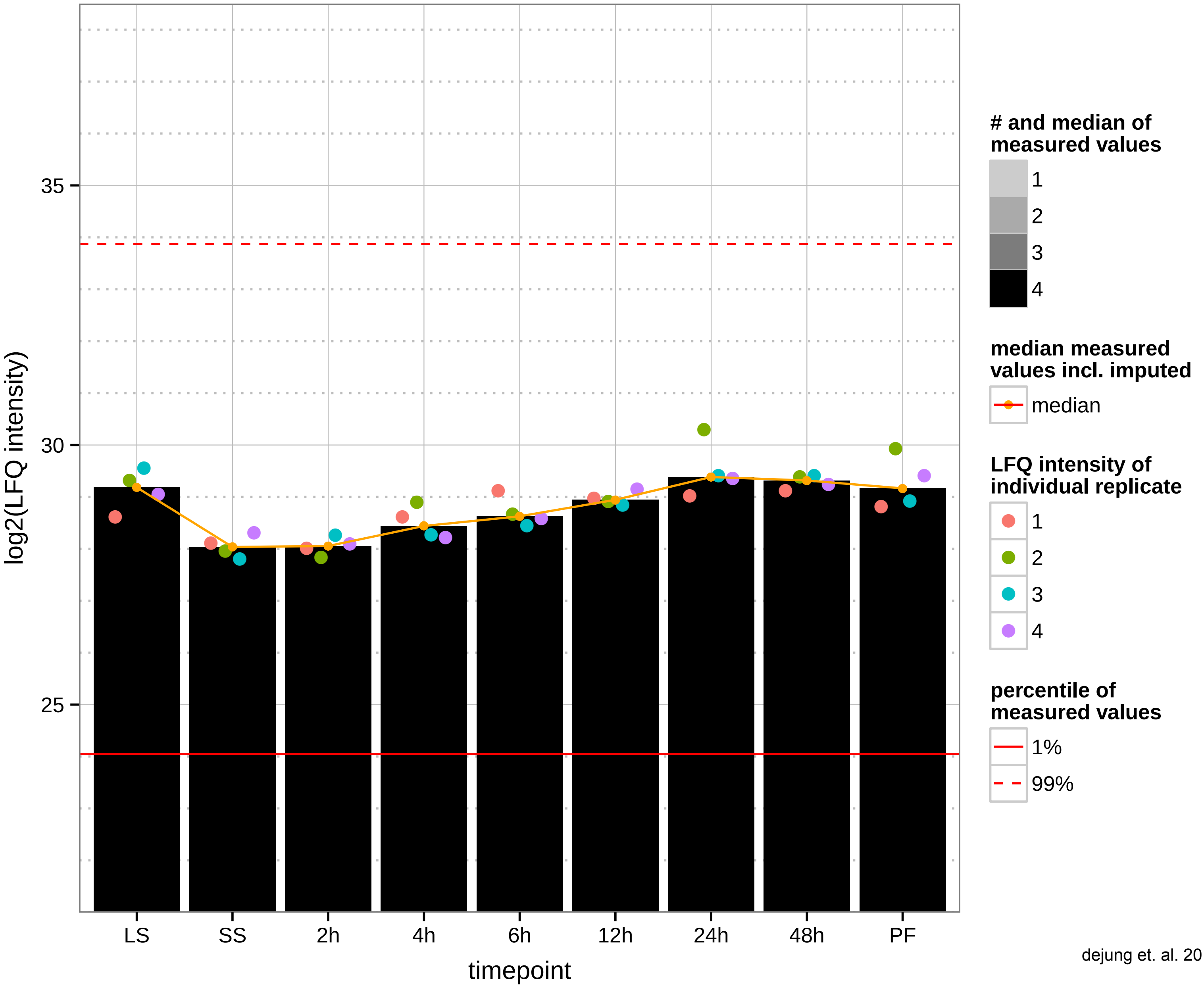
NA, 40S ribosomal protein S6, putative
Tb927.10.190
AGOF: NA, structural constituent of ribosome
AGOC: NA, intracellular, ribosome
AGOP: NA, regulation of cell growth, regulation of cell proliferation, translation
PGOF: NA, structural constituent of ribosome
PGOC: NA, intracellular, ribosome
PGOP: NA, translation





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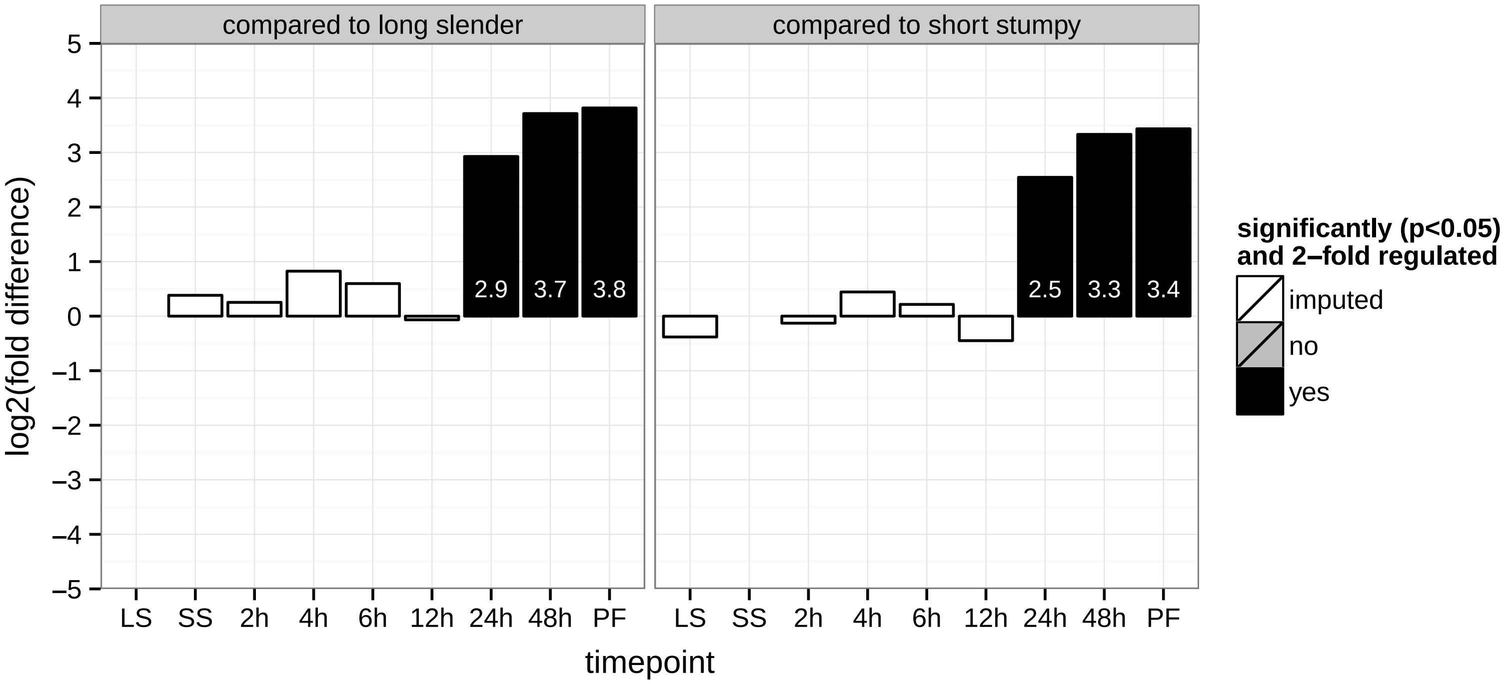
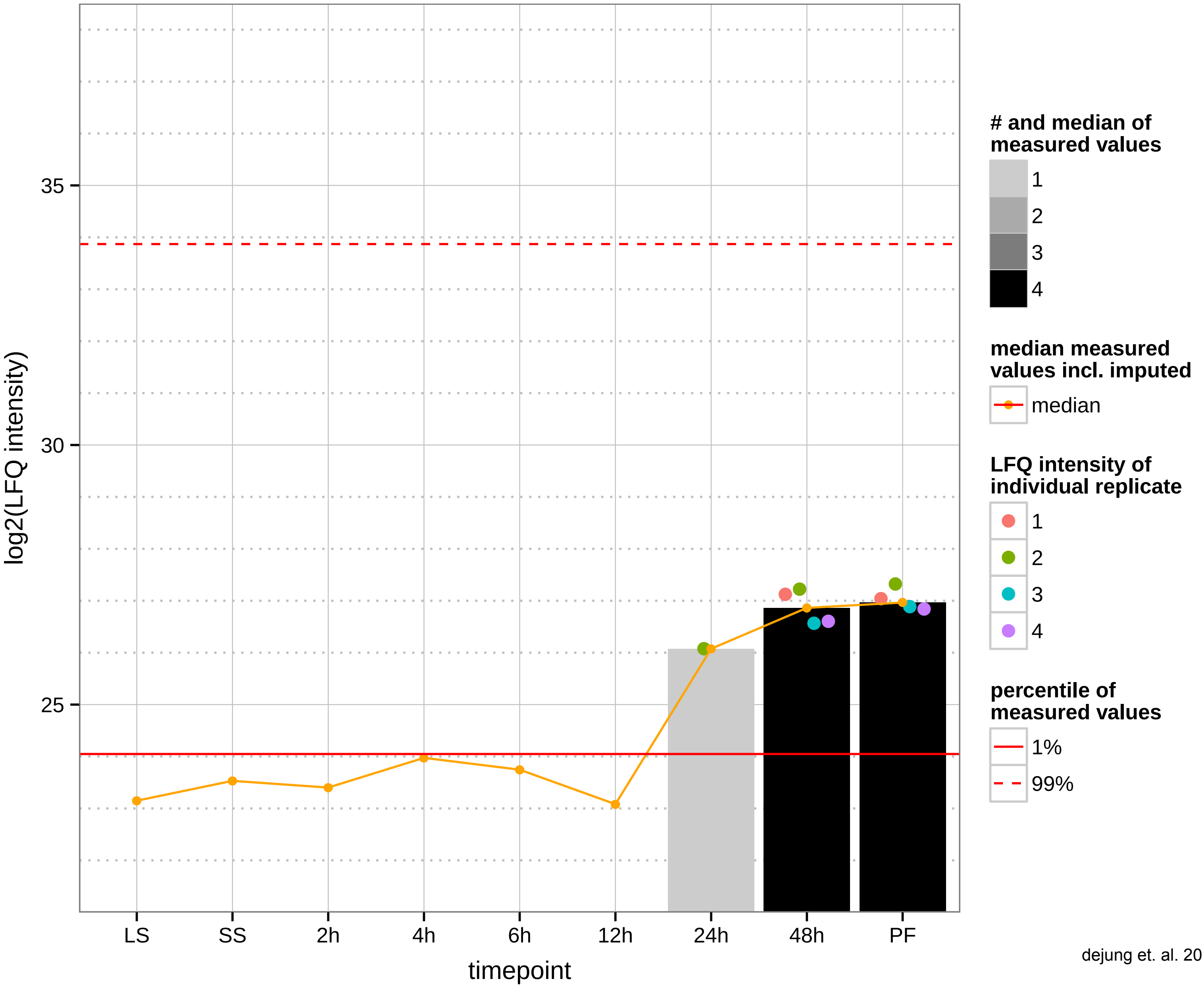
DNA topoisomerase IA, putative
Tb927.10.1900
AGOF: DNA binding, DNA topoisomerase type I activity
AGOC: chromosome
AGOP: DNA modification, DNA topological change
PGOF: DNA binding, DNA topoisomerase activity
PGOC: chromosome
PGOP: DNA topological change





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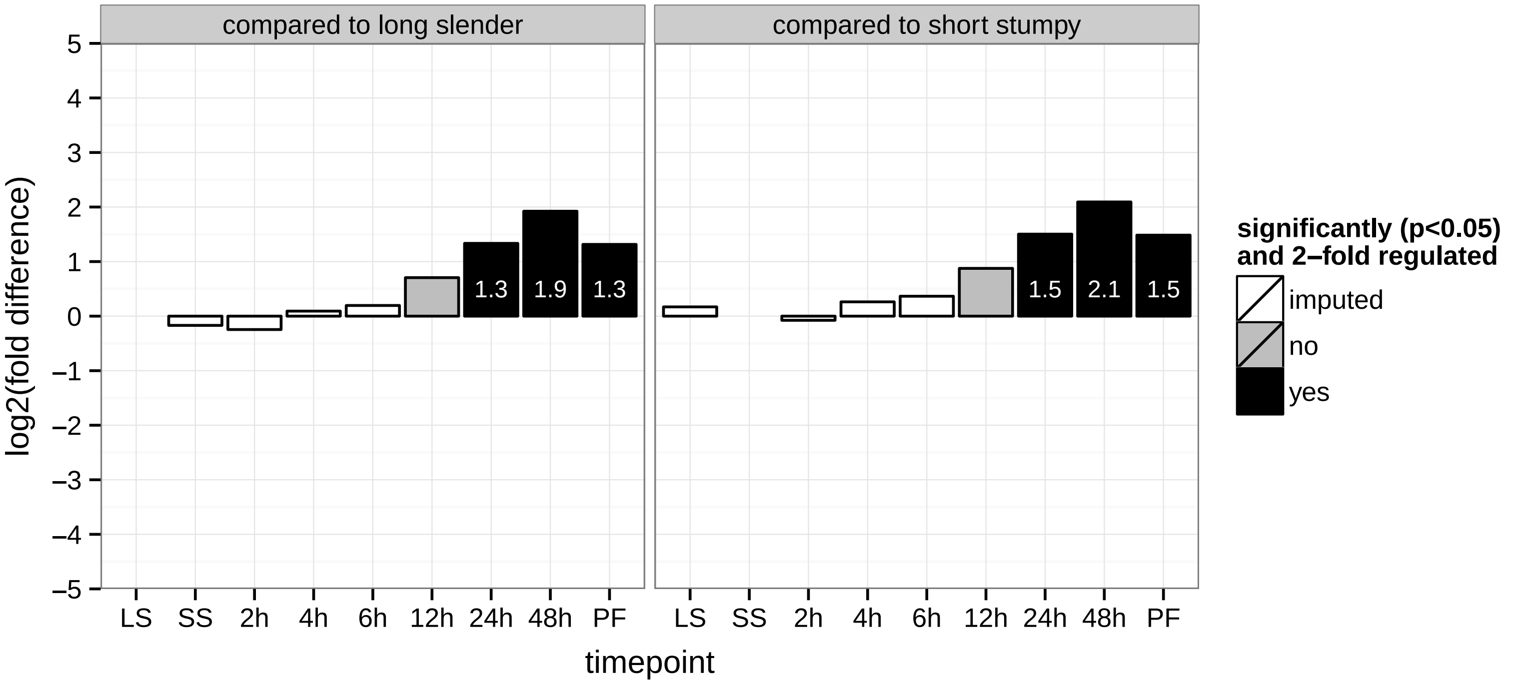
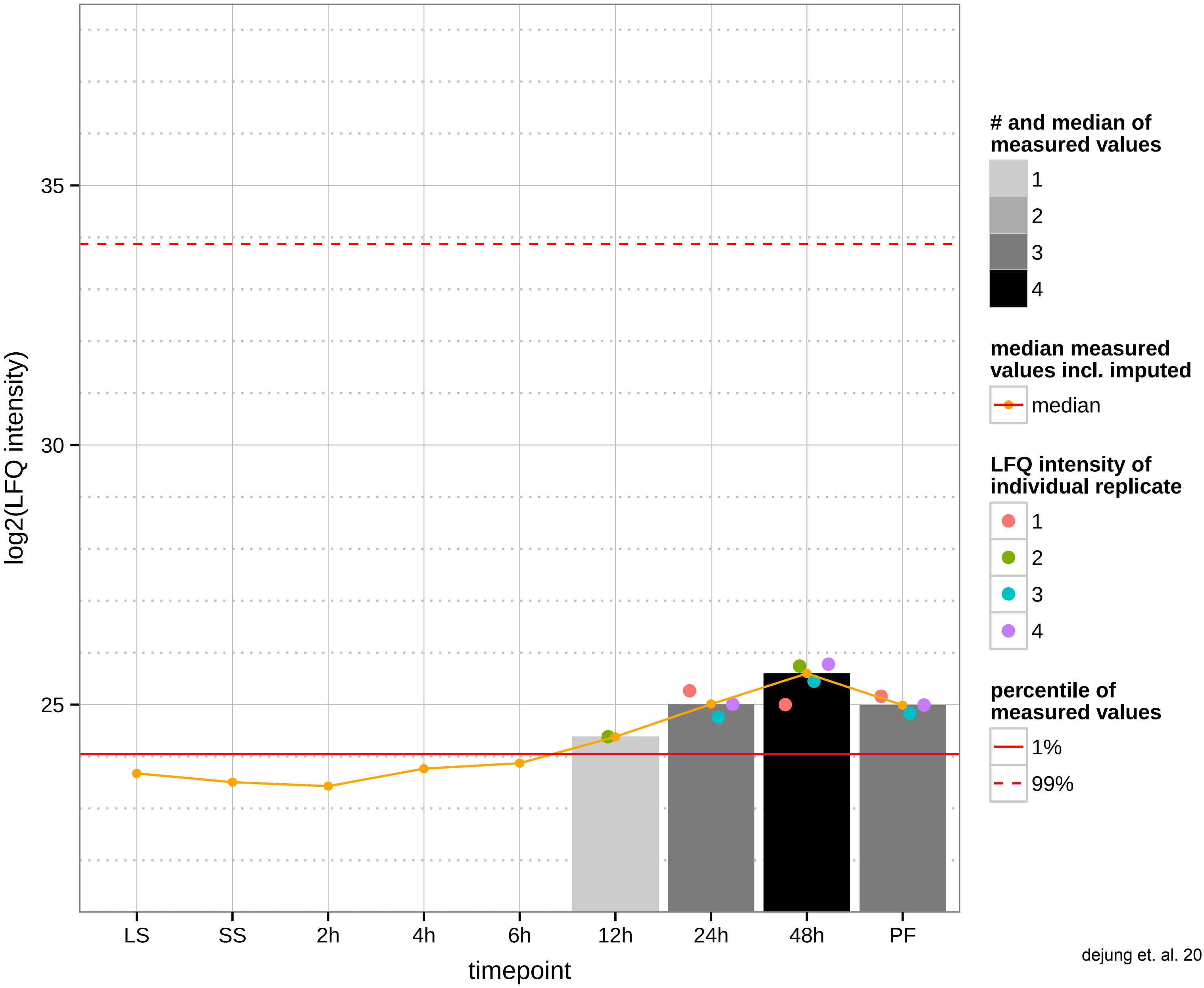
hypothetical protein, conserved
Tb927.10.2070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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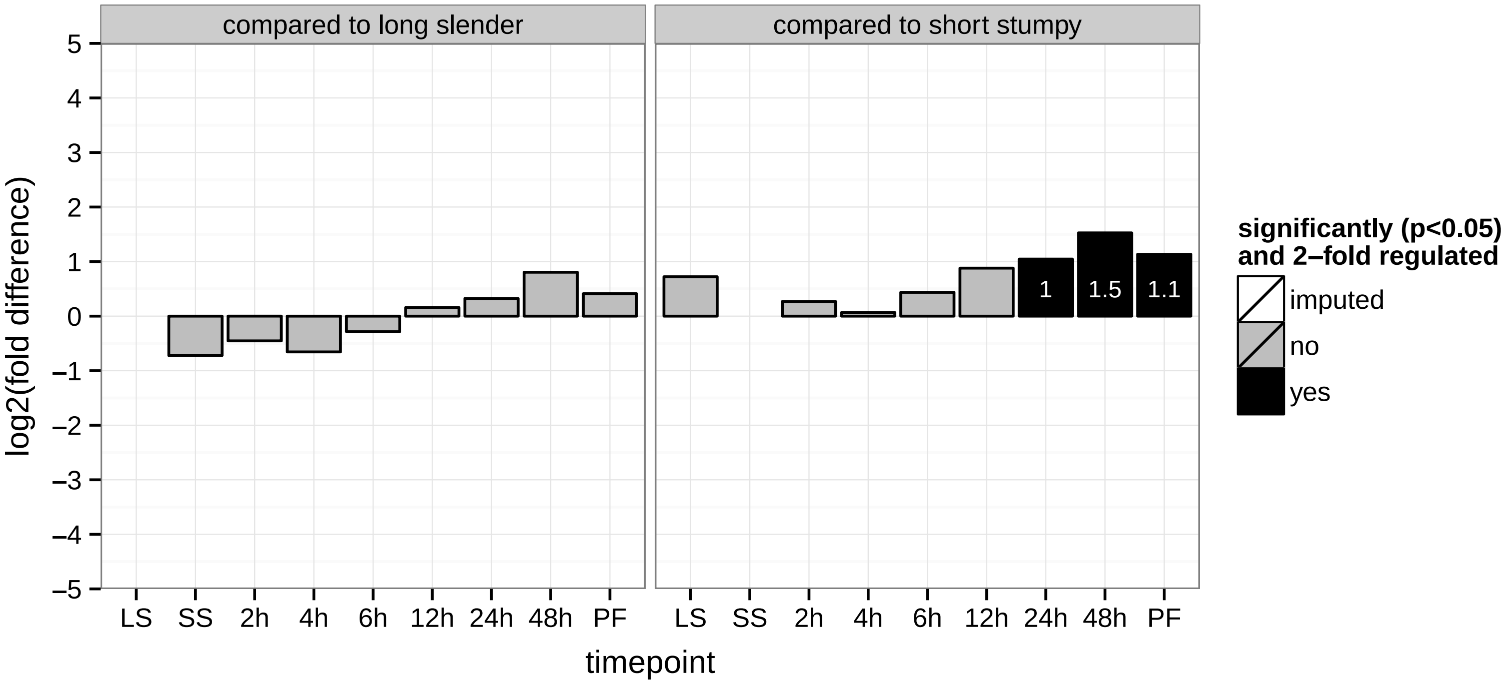
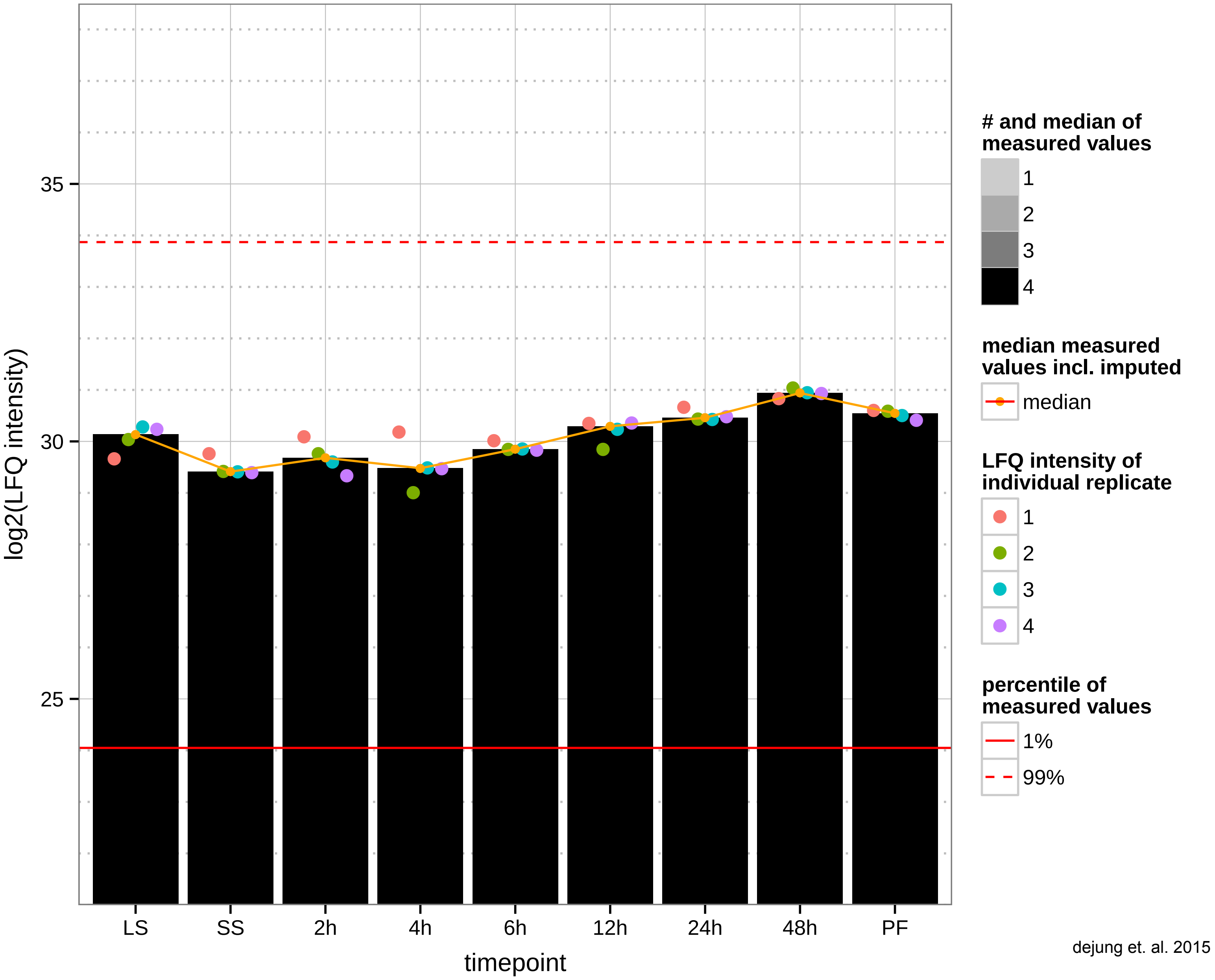
hypothetical protein, conserved
Tb927.10.2240
AGOF: null
AGOC: intracellular
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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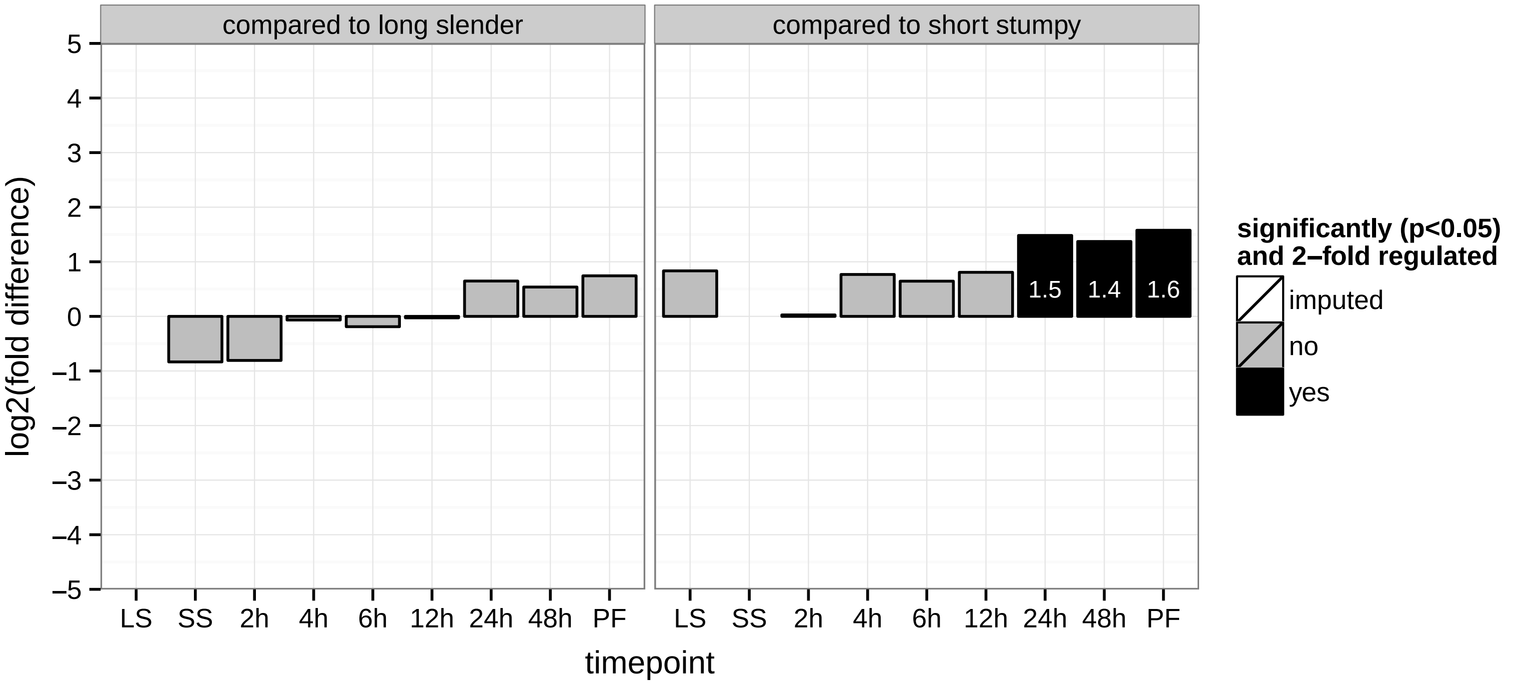
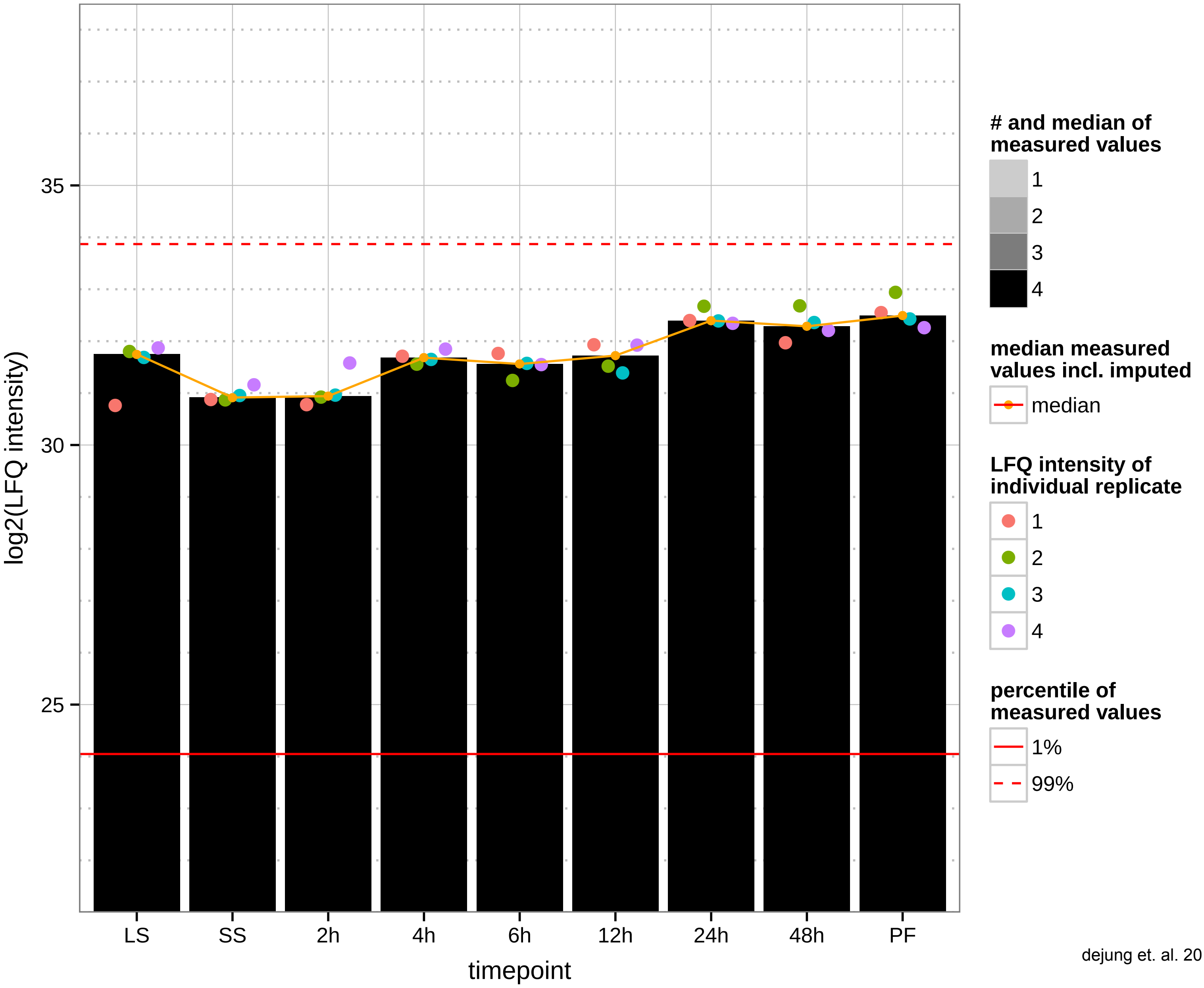
60S ribosomal protein L32, putative, unspecified product
Tb927.9.15420;Tb927.10.270
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: null, translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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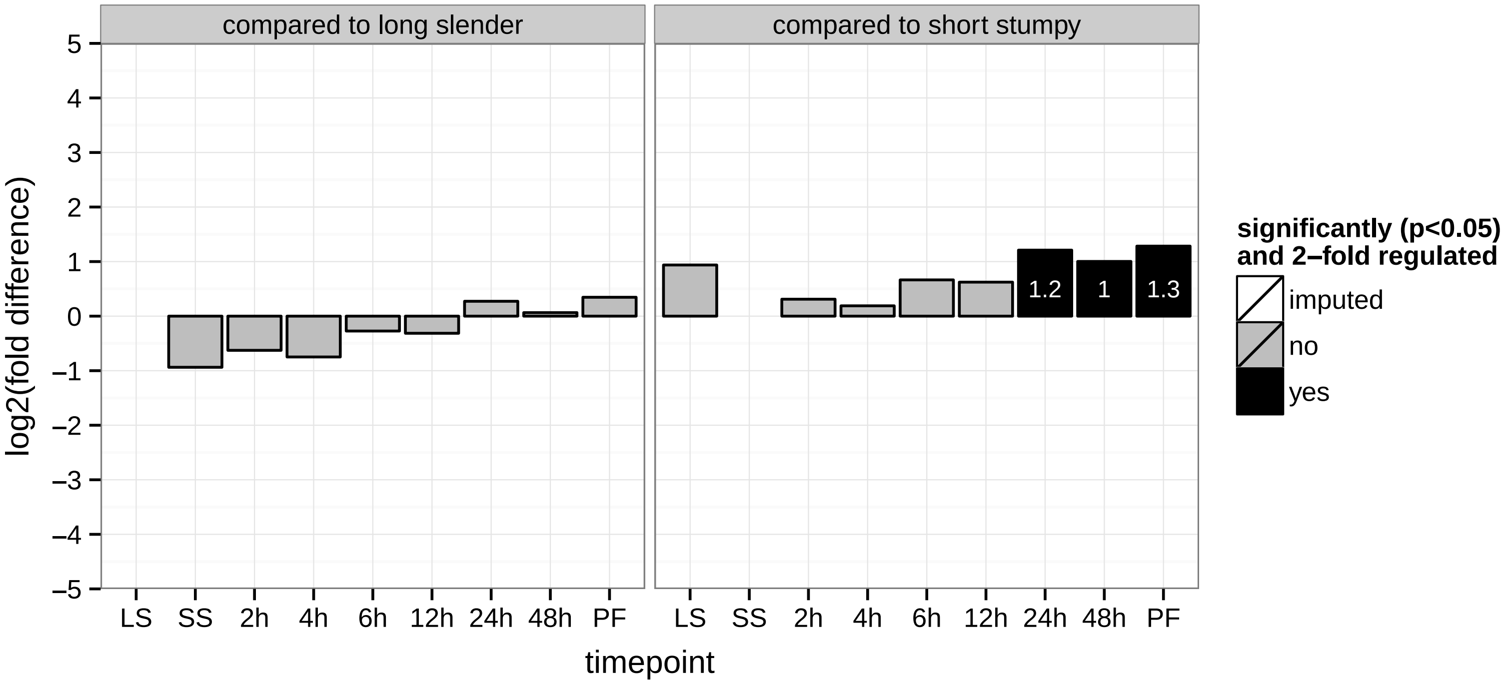
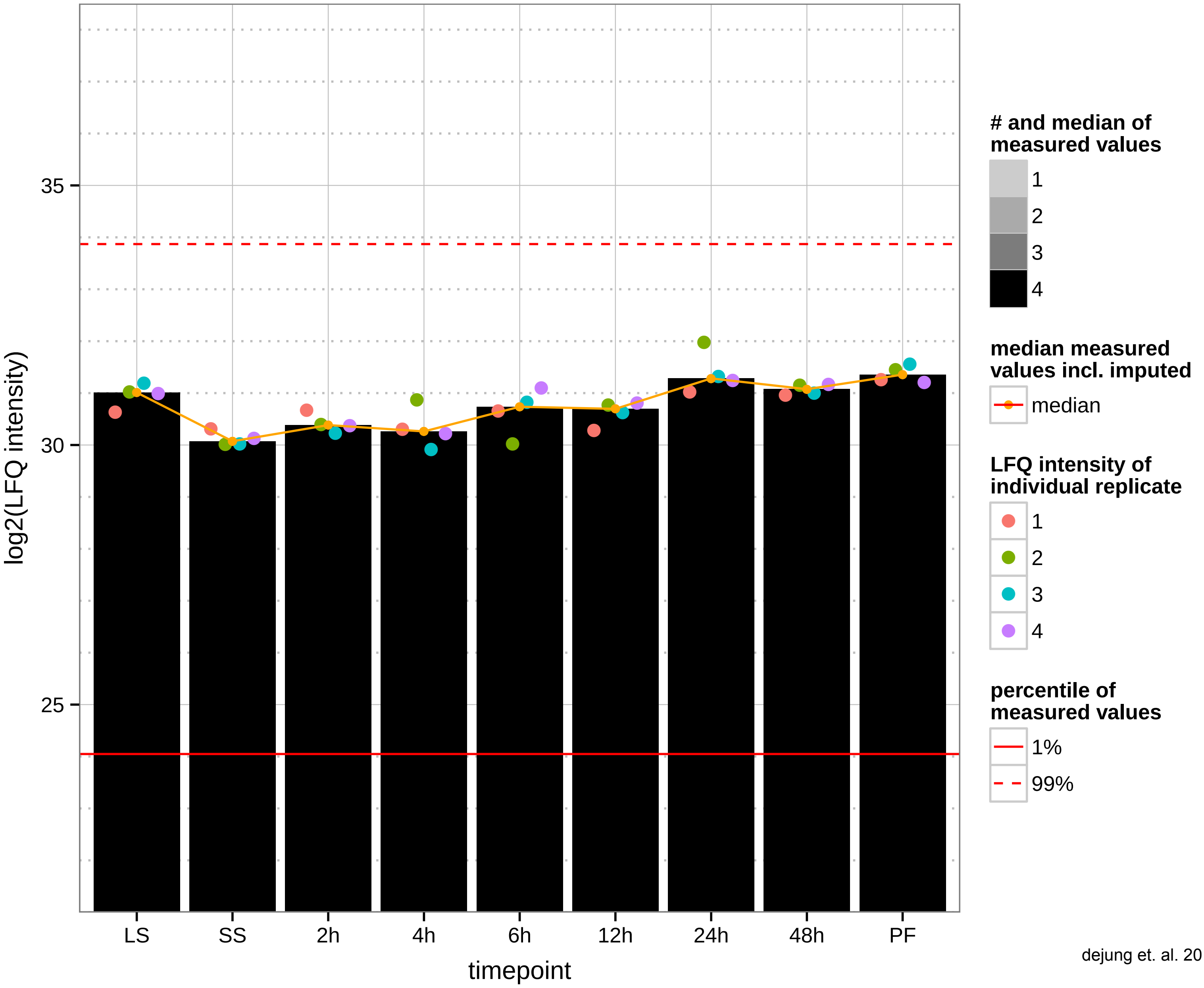
60S ribosomal proteins L38, putative
Tb927.10.3280
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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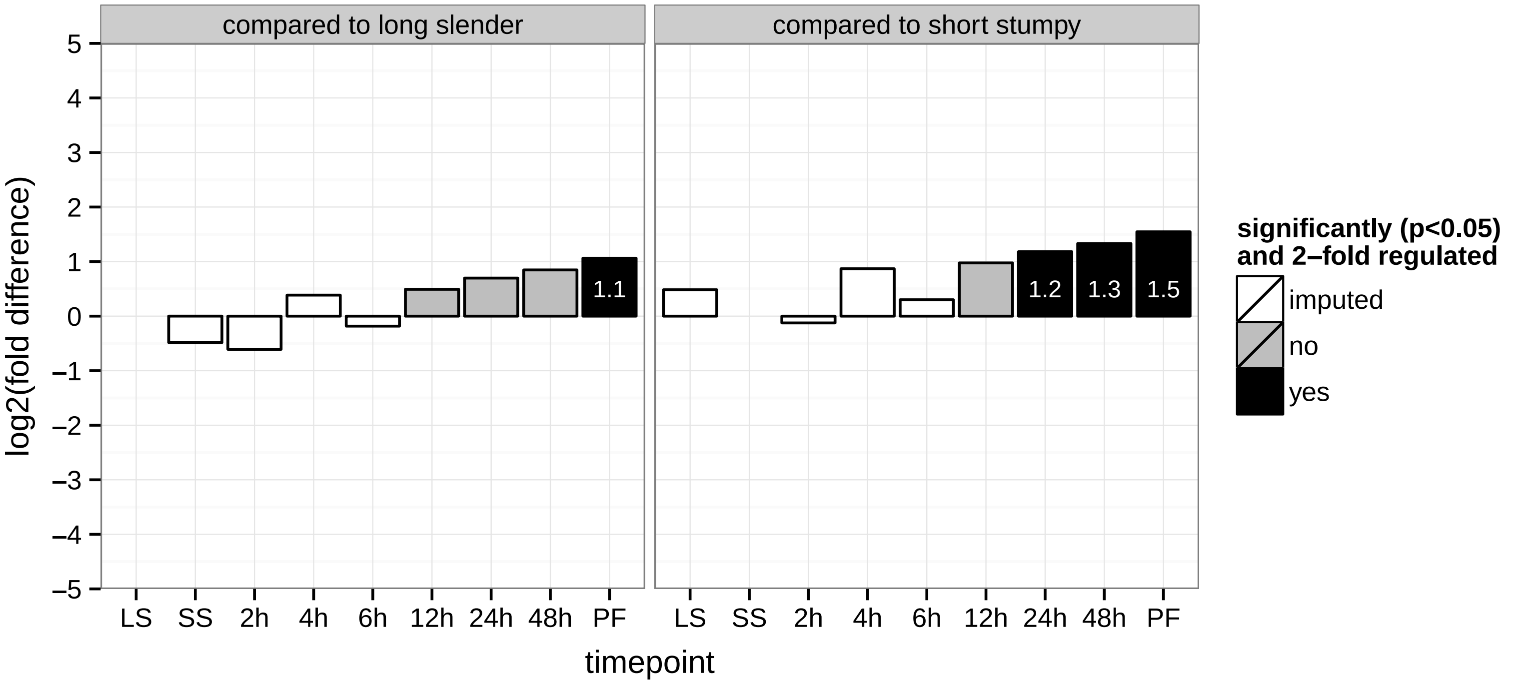
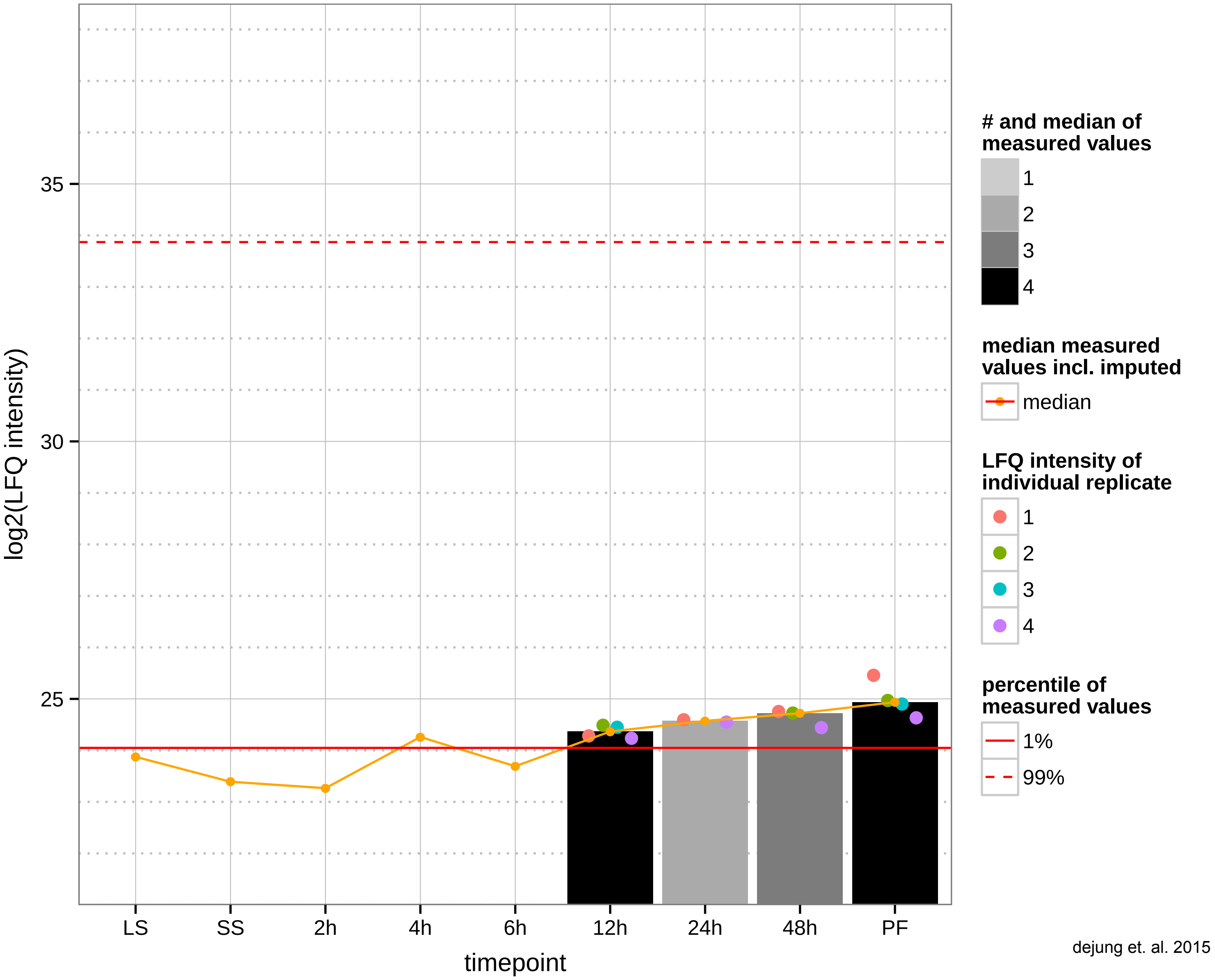
mitochondrial structure specific endonuclease I (SSE−1), putative
Tb927.10.340
AGOF: 5'−3' exonuclease activity, DNA binding
AGOC: mitochondrion
AGOP: DNA catabolic process
PGOF: 5'−3' exonuclease activity, DNA binding, catalytic activity
PGOC: null
PGOP: null





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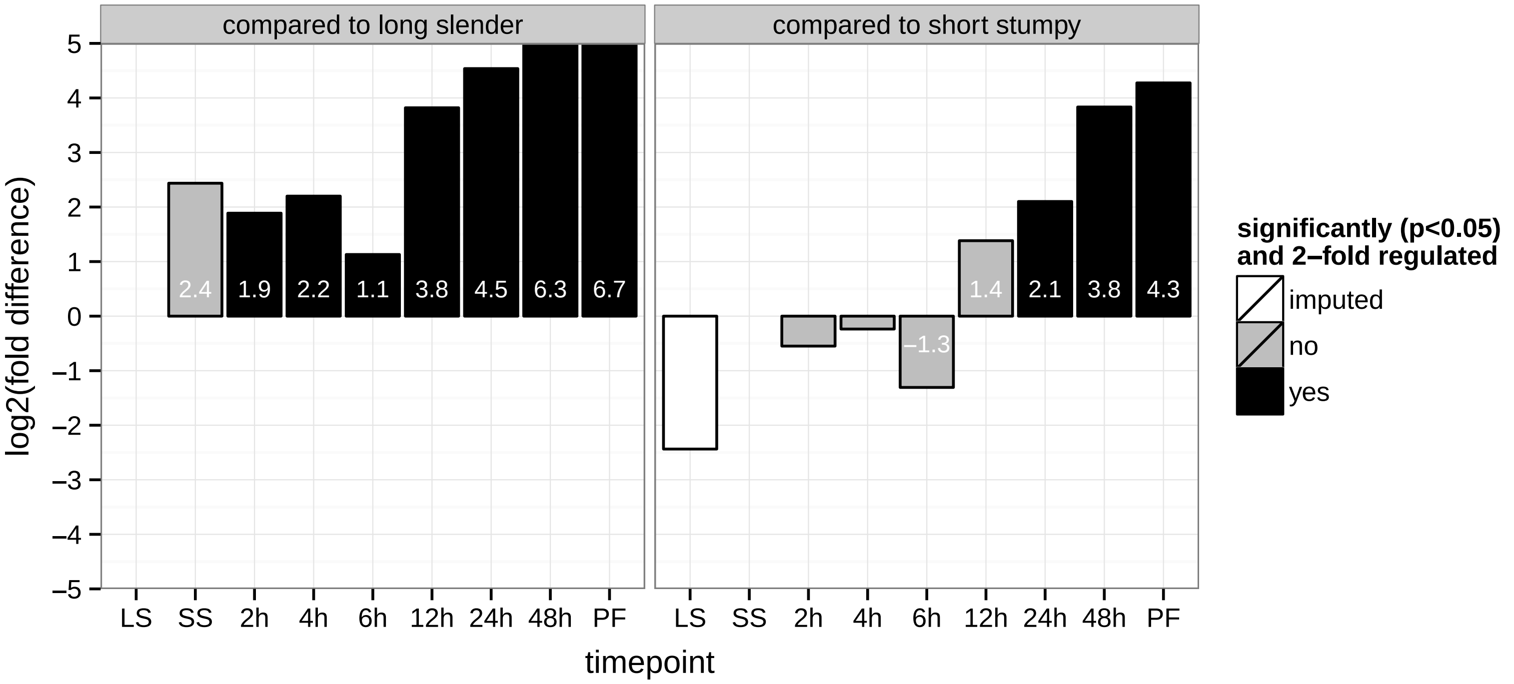
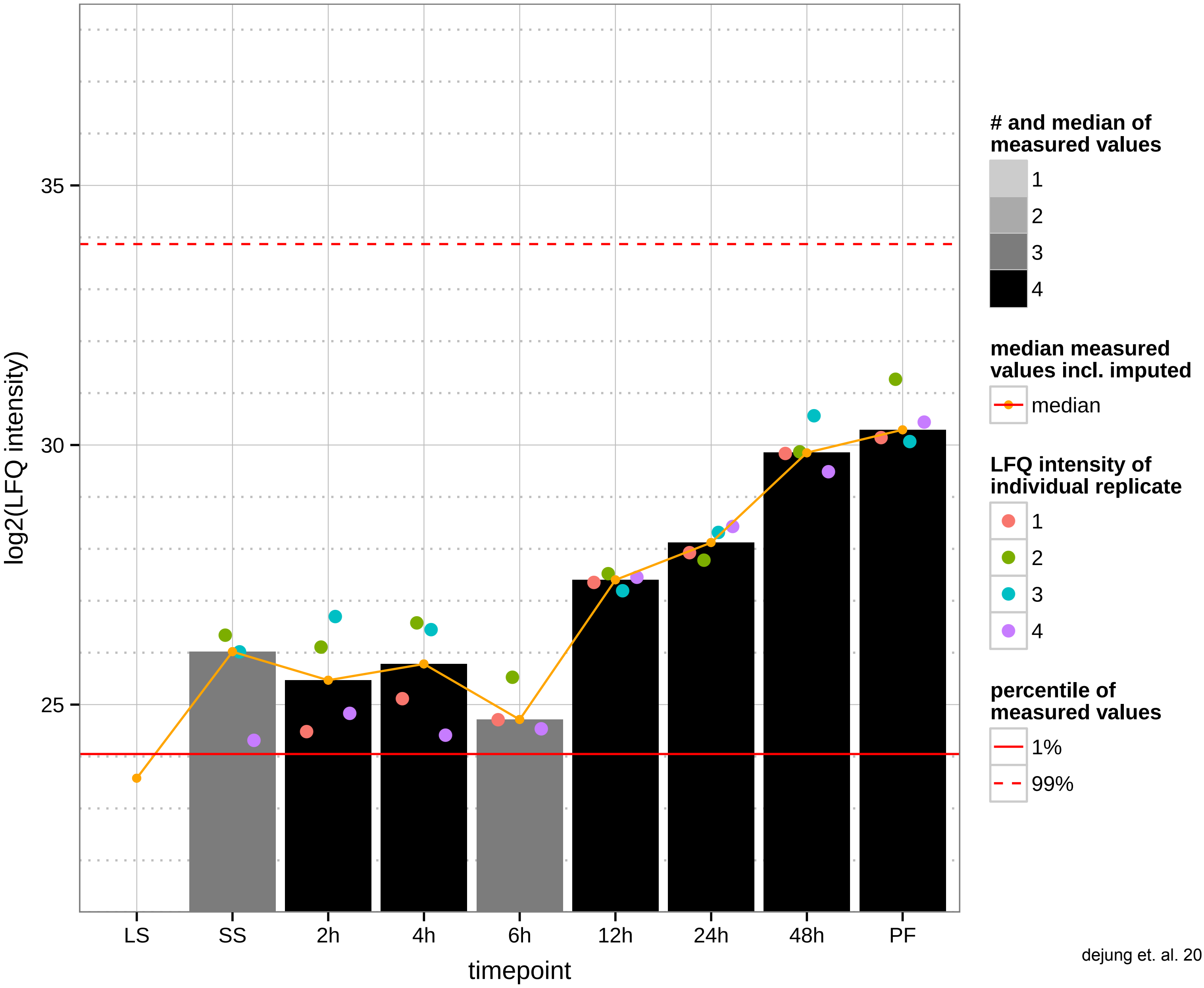
NADH–dependent fumarate reductase, putative
Tb927.10.3650
AGOF: electron carrier activity, succinate dehydrogenase activity
AGOC: null
AGOP: thiamine biosynthetic process
PGOF: oxidoreductase activity, succinate dehydrogenase activity
PGOC: null
PGOP: oxidation–reduction process





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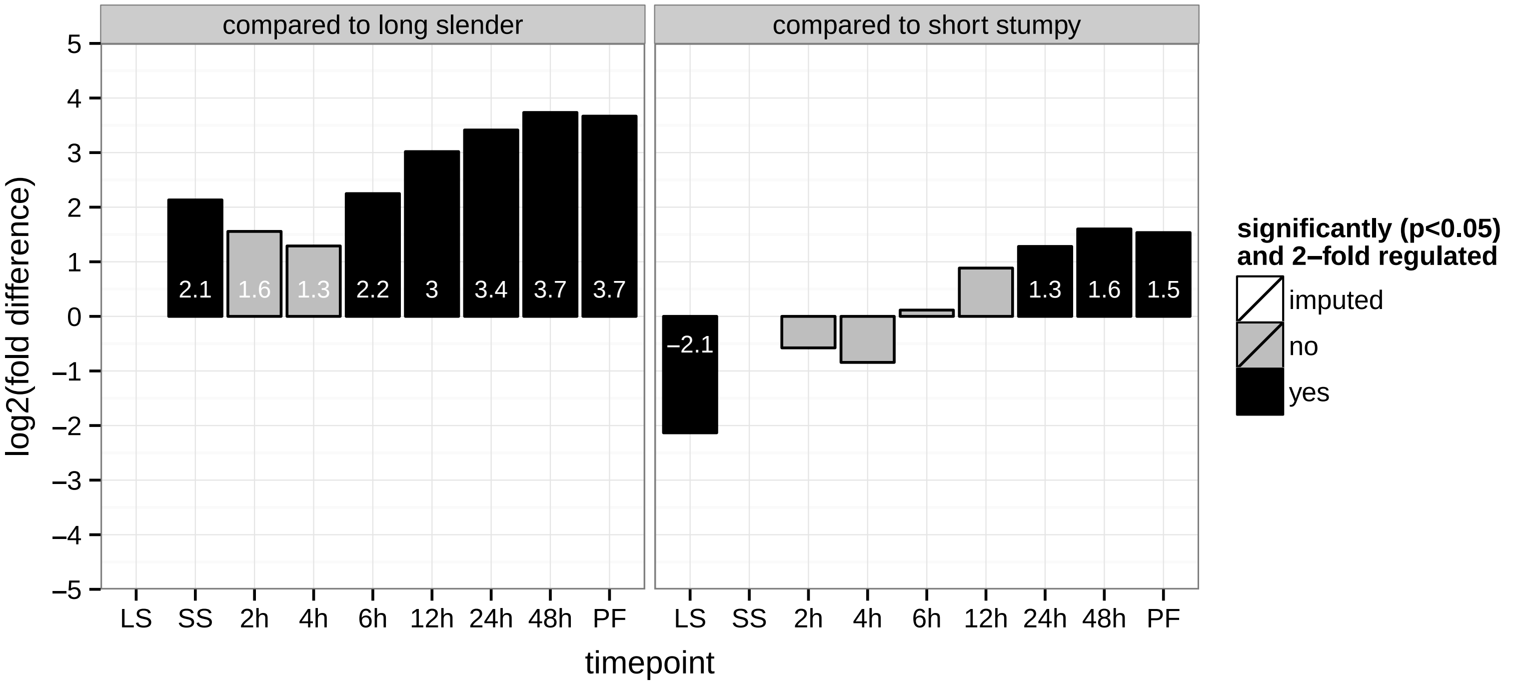
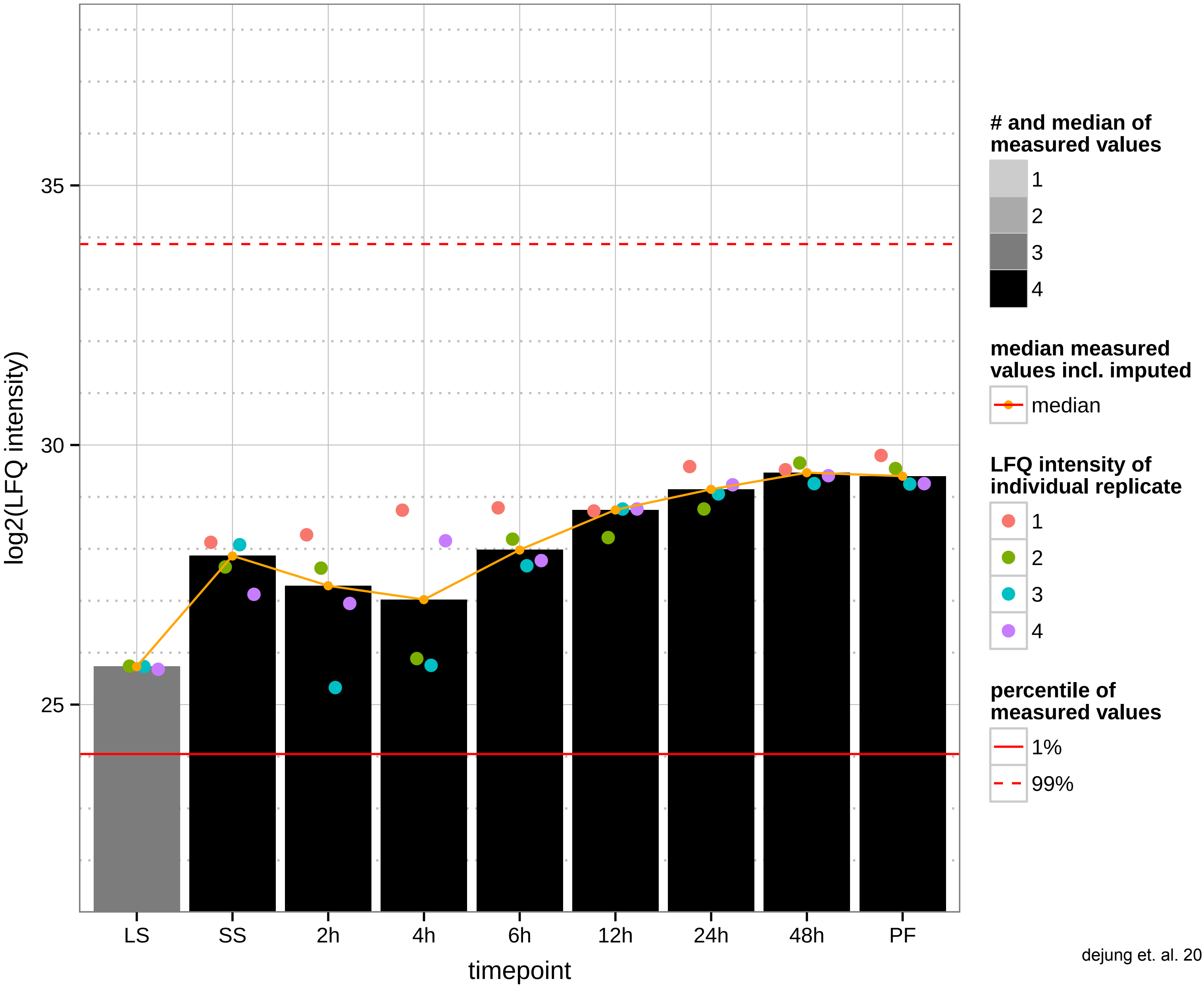
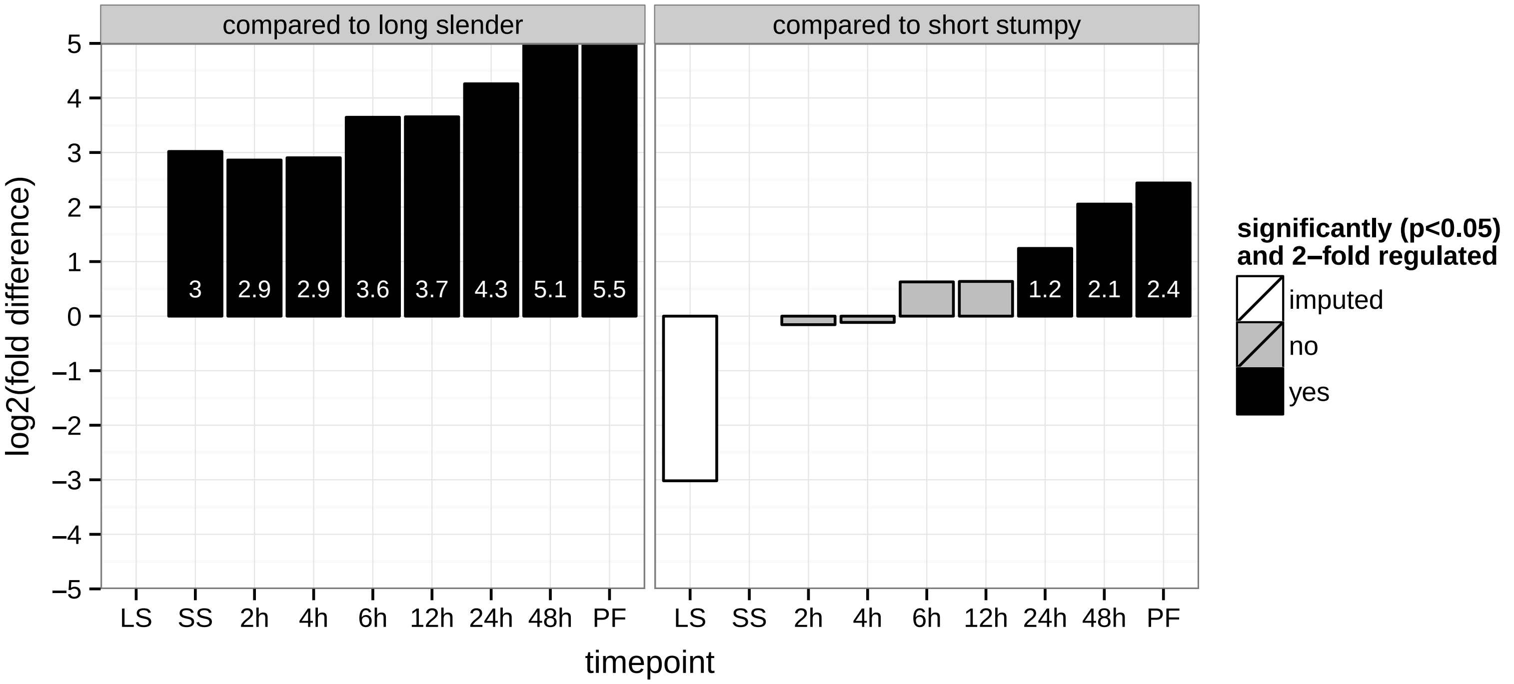
hypothetical protein, conserved
Tb927.10.3790
AGOF: null
AGOC: null
AGOP: null
PGOF: binding, null
PGOC: null
PGOP: null

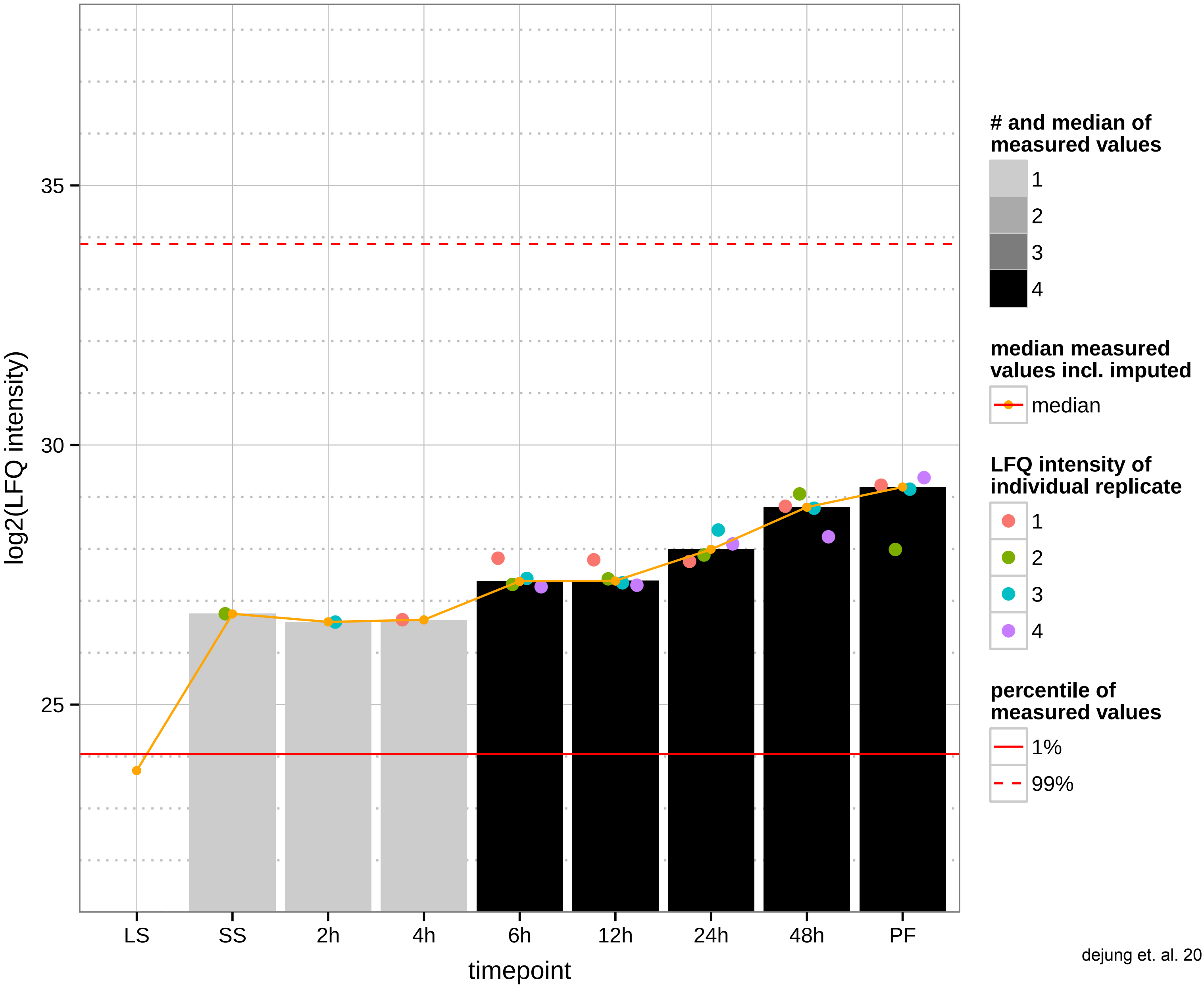




dejung et. al. 2015

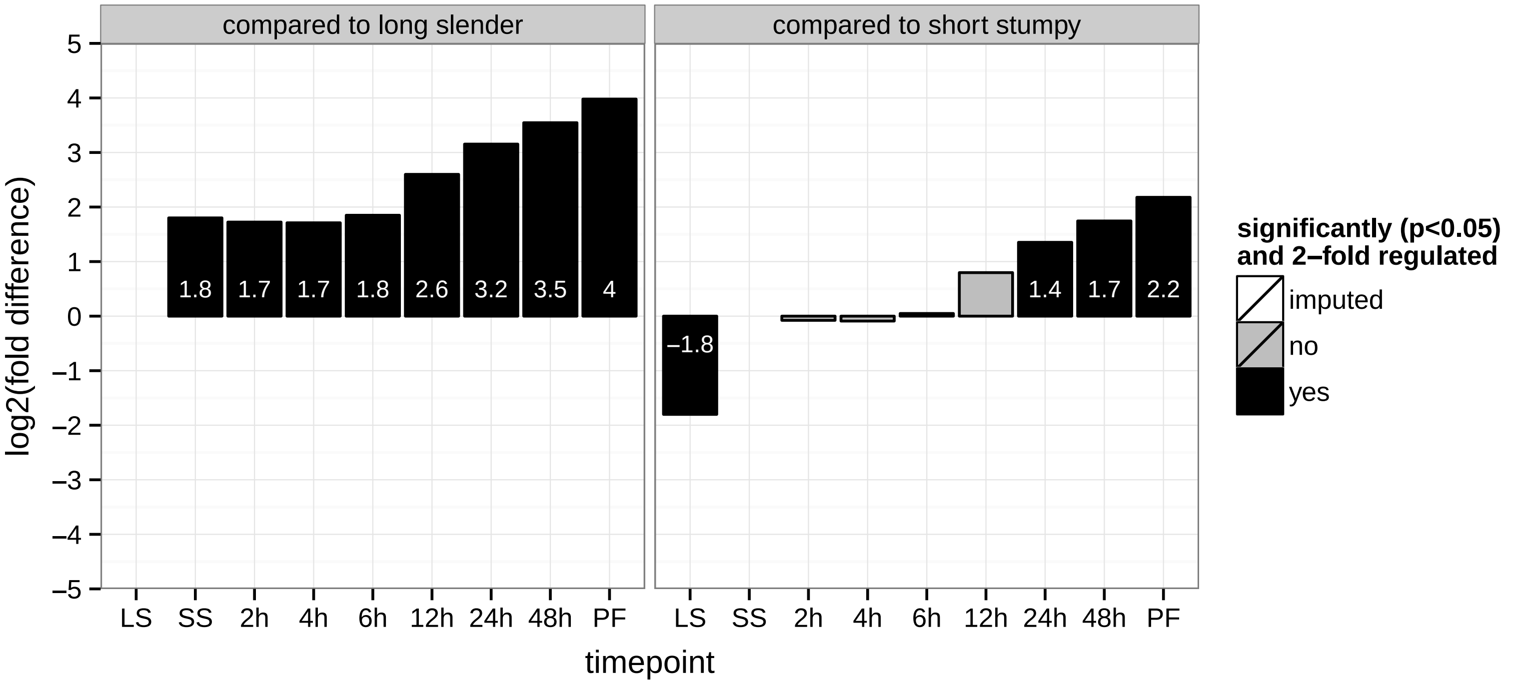
hypothetical protein, conserved
Tb927.10.4080
AGOF: oxidoreductase activity
AGOC: mitochondrion
AGOP: fatty acid metabolic process
PGOF: null
PGOC: null
PGOP: oxidation−reduction process

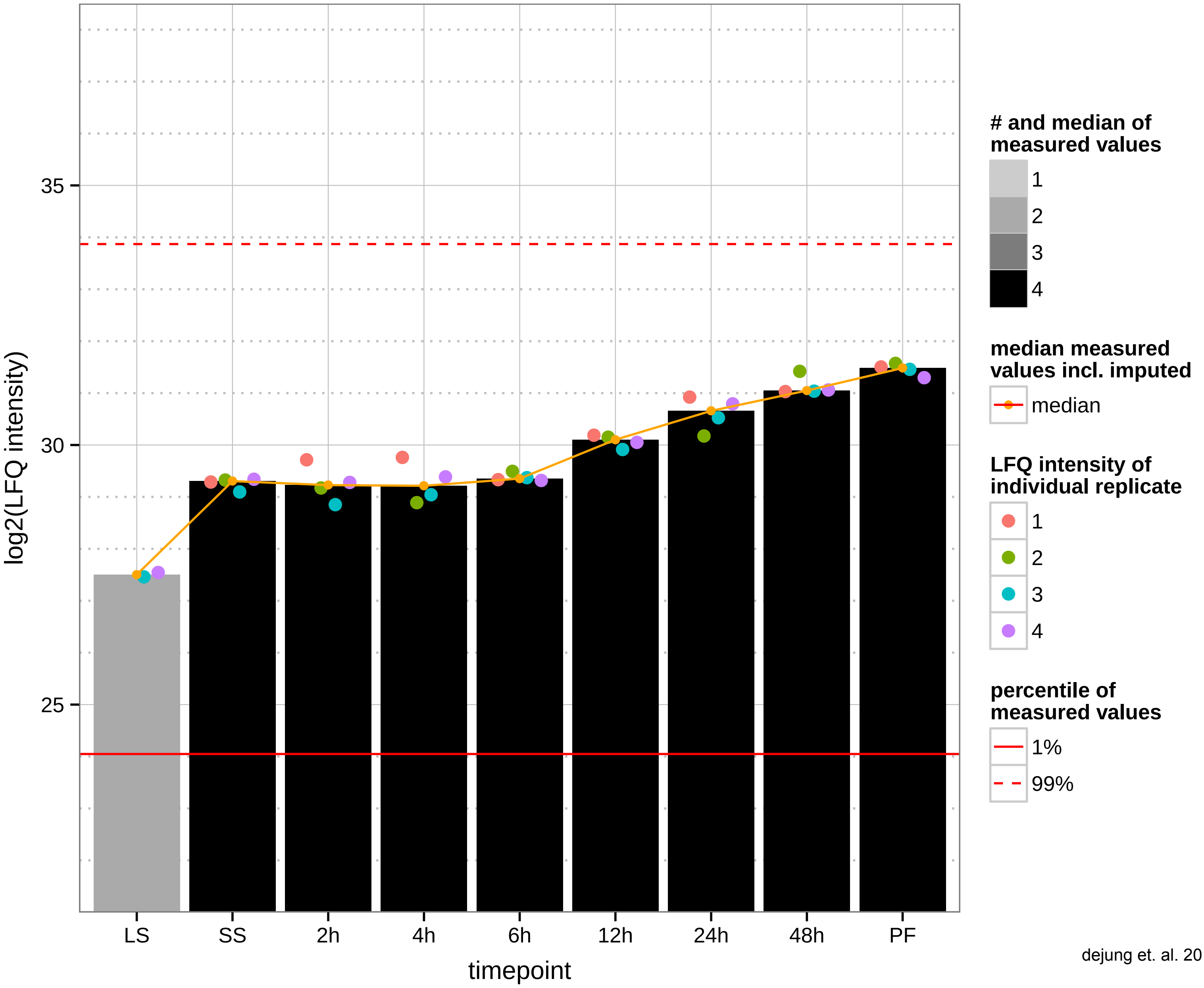




dejung et. al. 2015

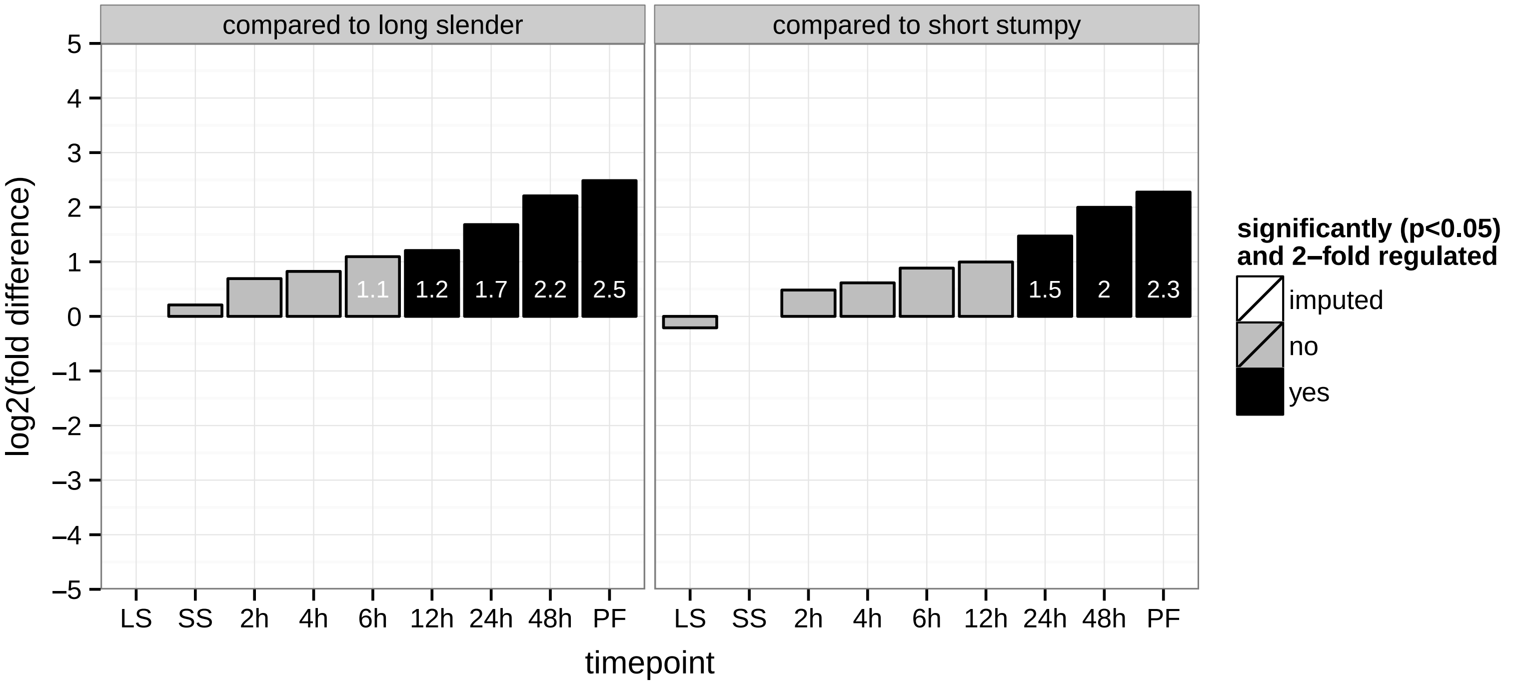
hypothetical protein, conserved
Tb927.10.520
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

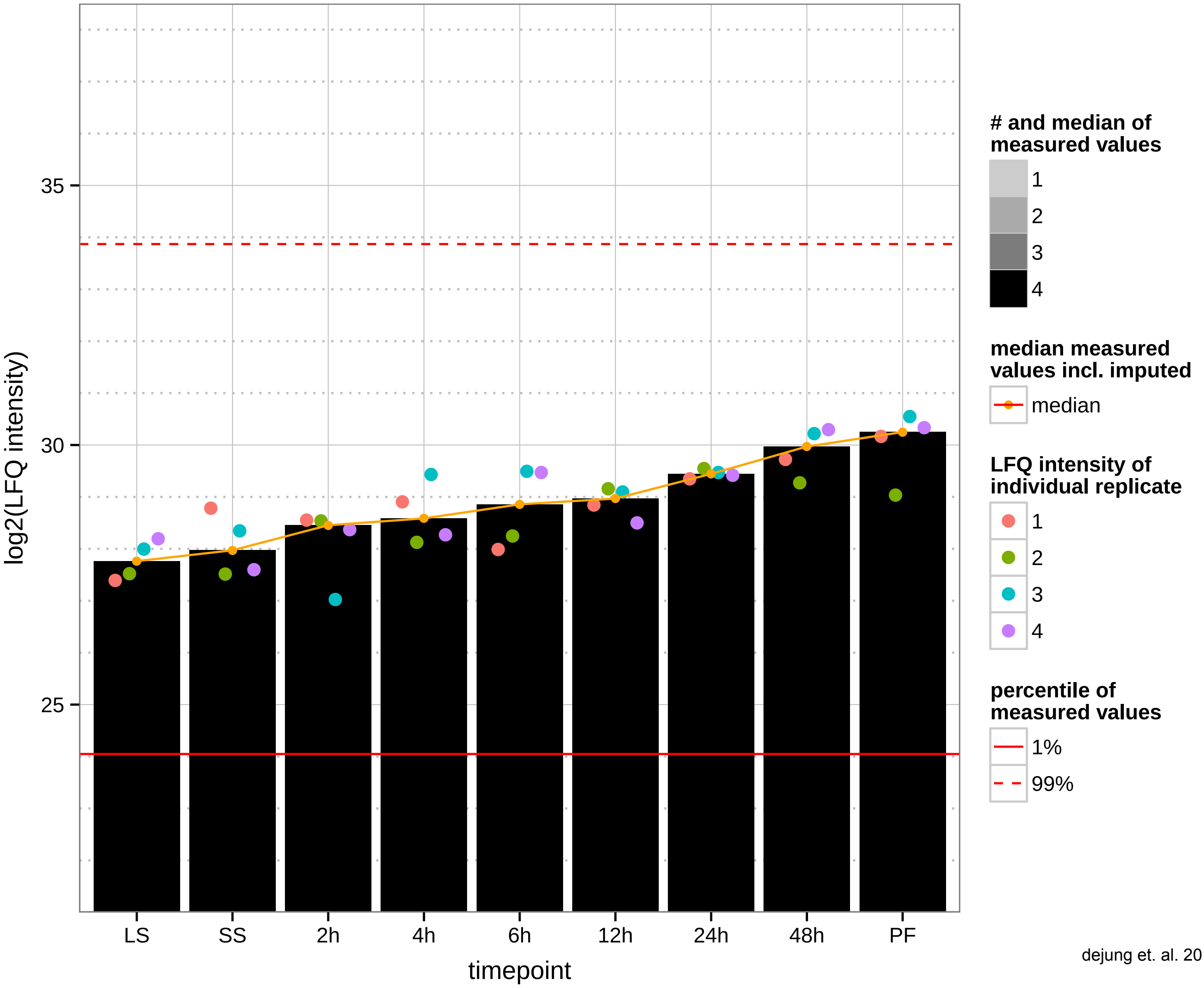




dejung et. al. 2015

40S ribosomal proteins S11, putative
Tb927.10.560
AGOF: structural constituent of ribosome
AGOC: intracellular, organellar small ribosomal subunit, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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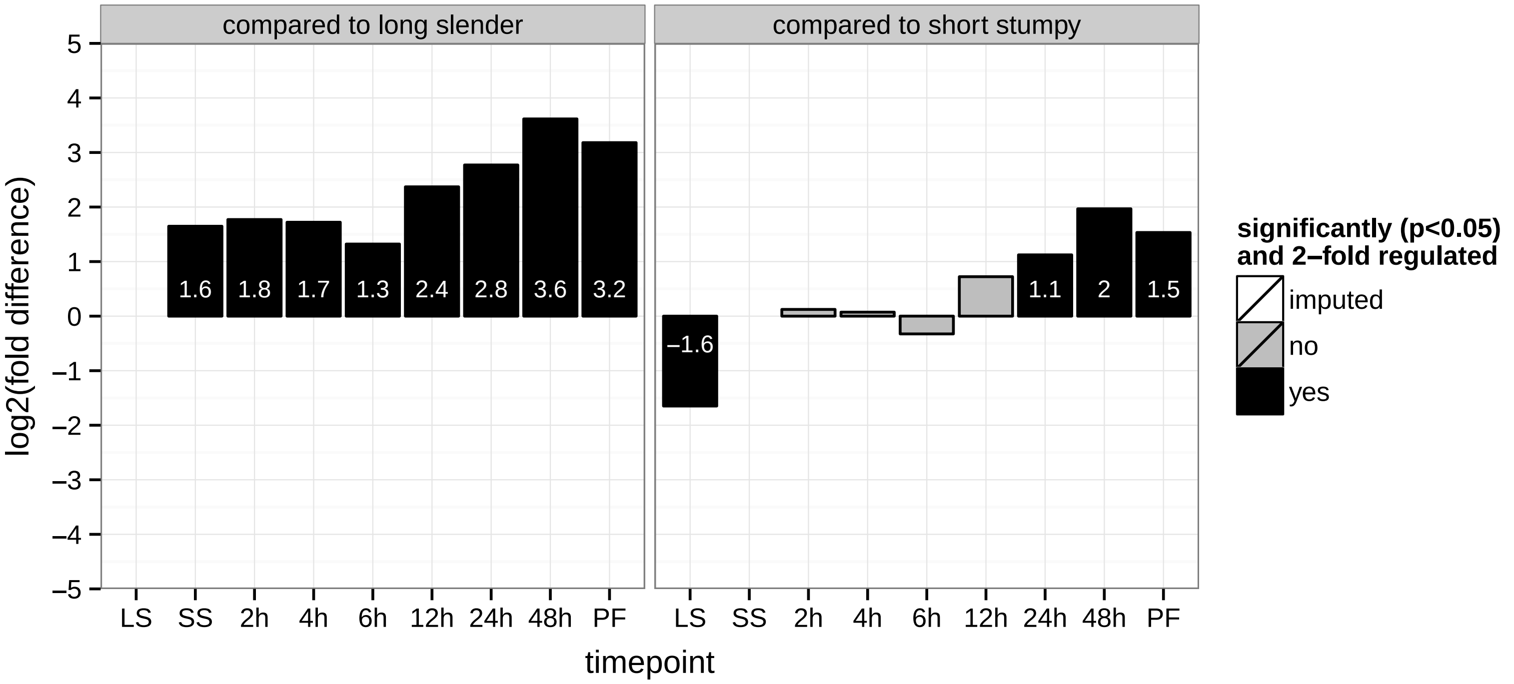
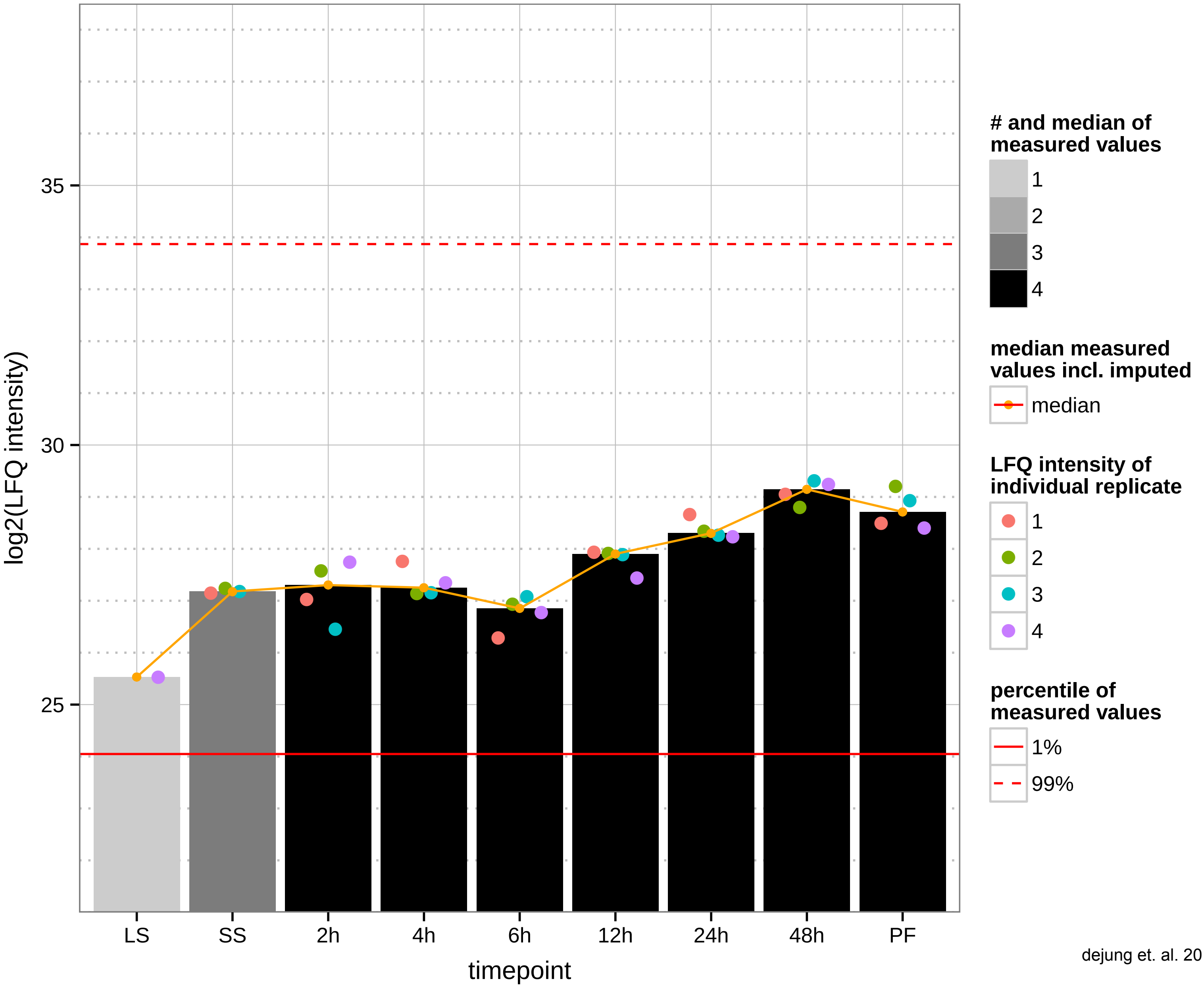
adenylate kinase, putative
Tb927.10.5760
AGOF: ATP binding, adenylate kinase activity
AGOC: null
AGOP: nucleobase−containing compound metabolic process, nucleobase−containing small molecule interconversion
PGOF: ATP binding, nucleobase−containing compound kinase activity, nucleotide kinase activity, phosphotransferase activity,
PGOC: null
PGOP: nucleobase−containing compound metabolic process, nucleotide phosphorylation





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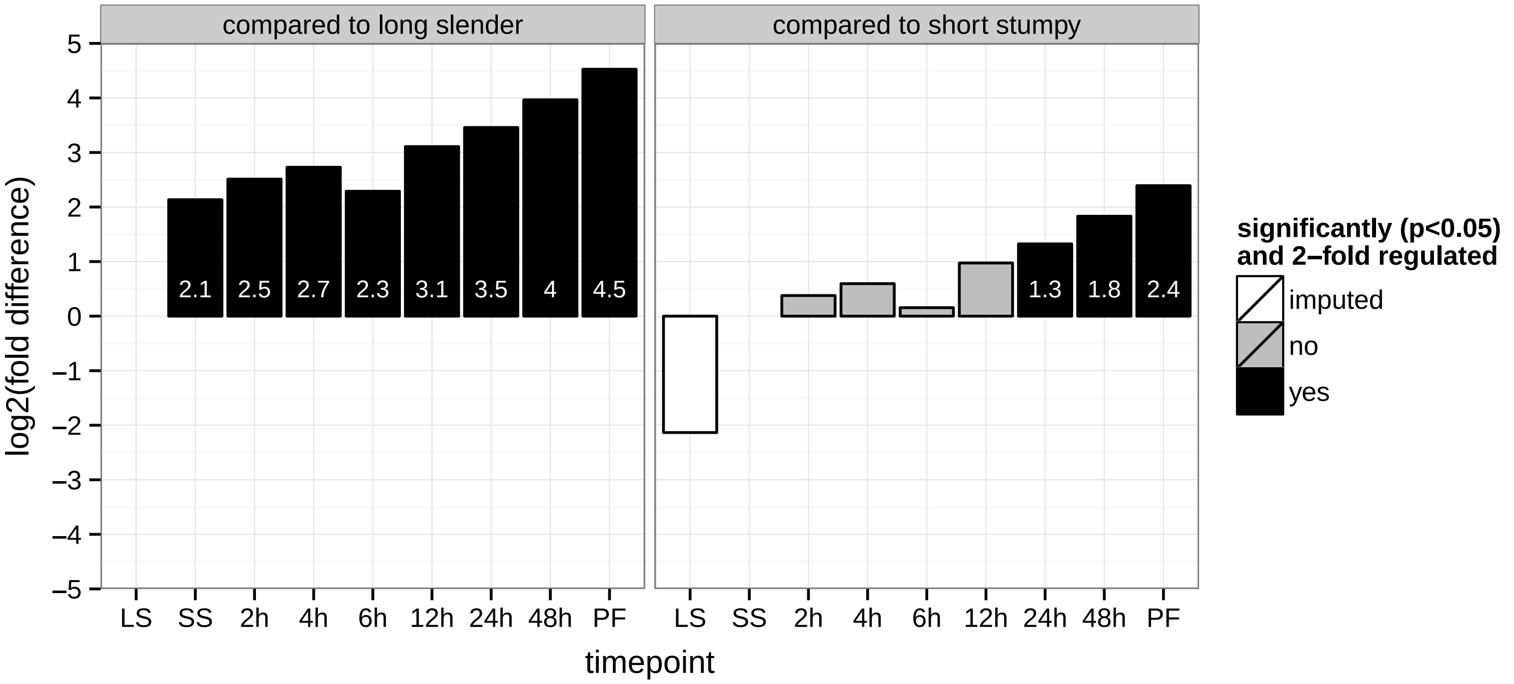
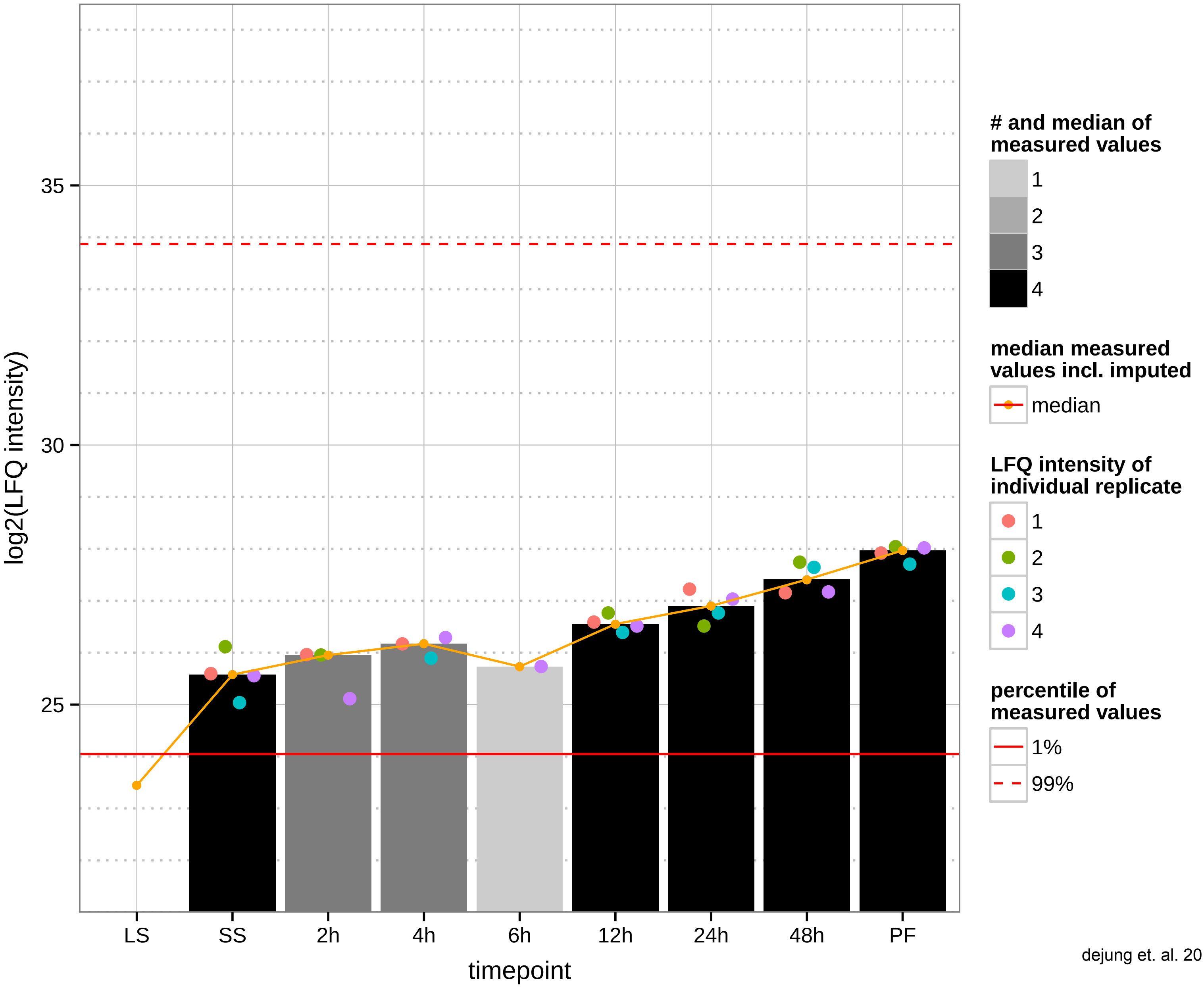
hypothetical protein, conserved
Tb927.10.600
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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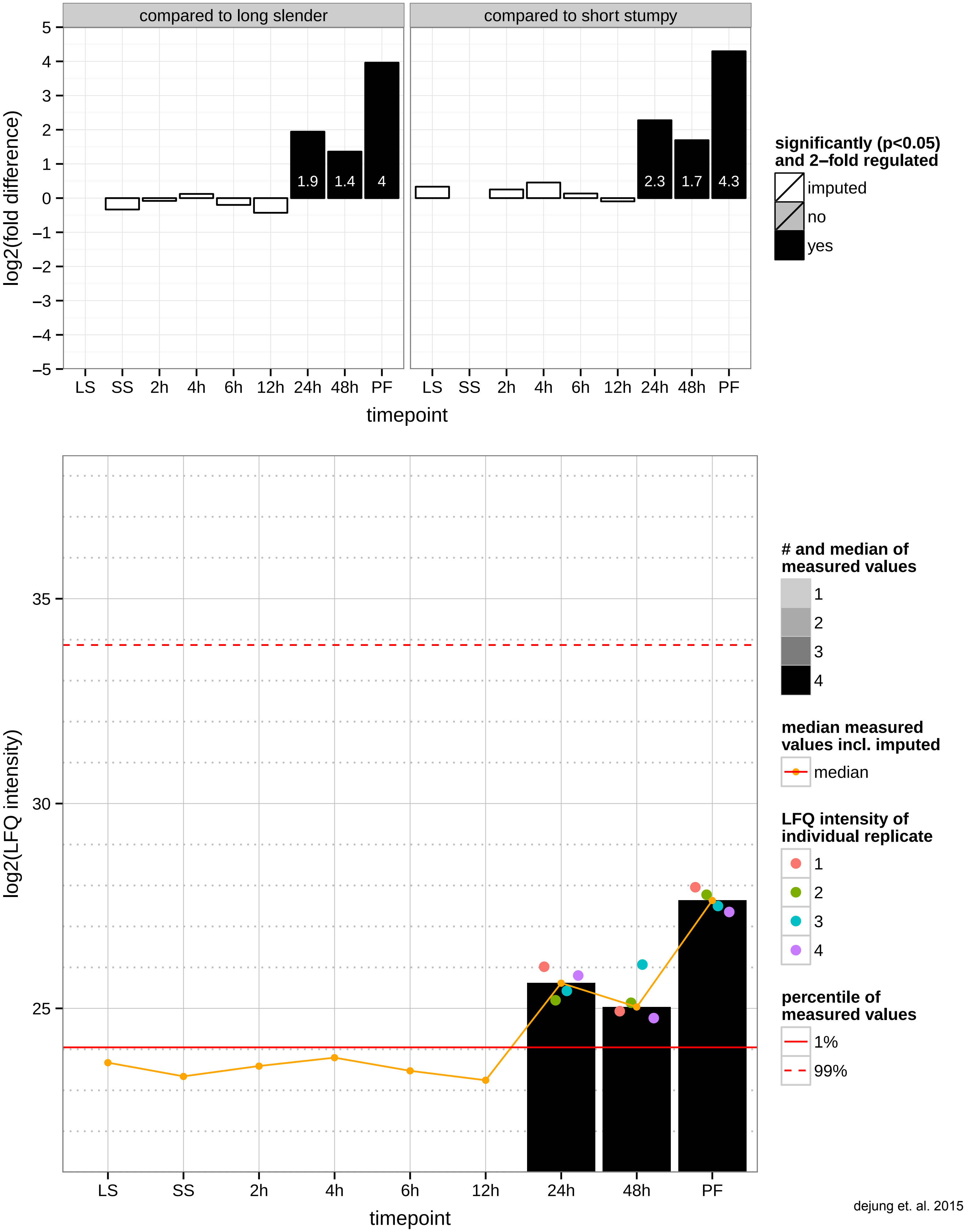
hypothetical protein, conserved
Tb927.10.6200
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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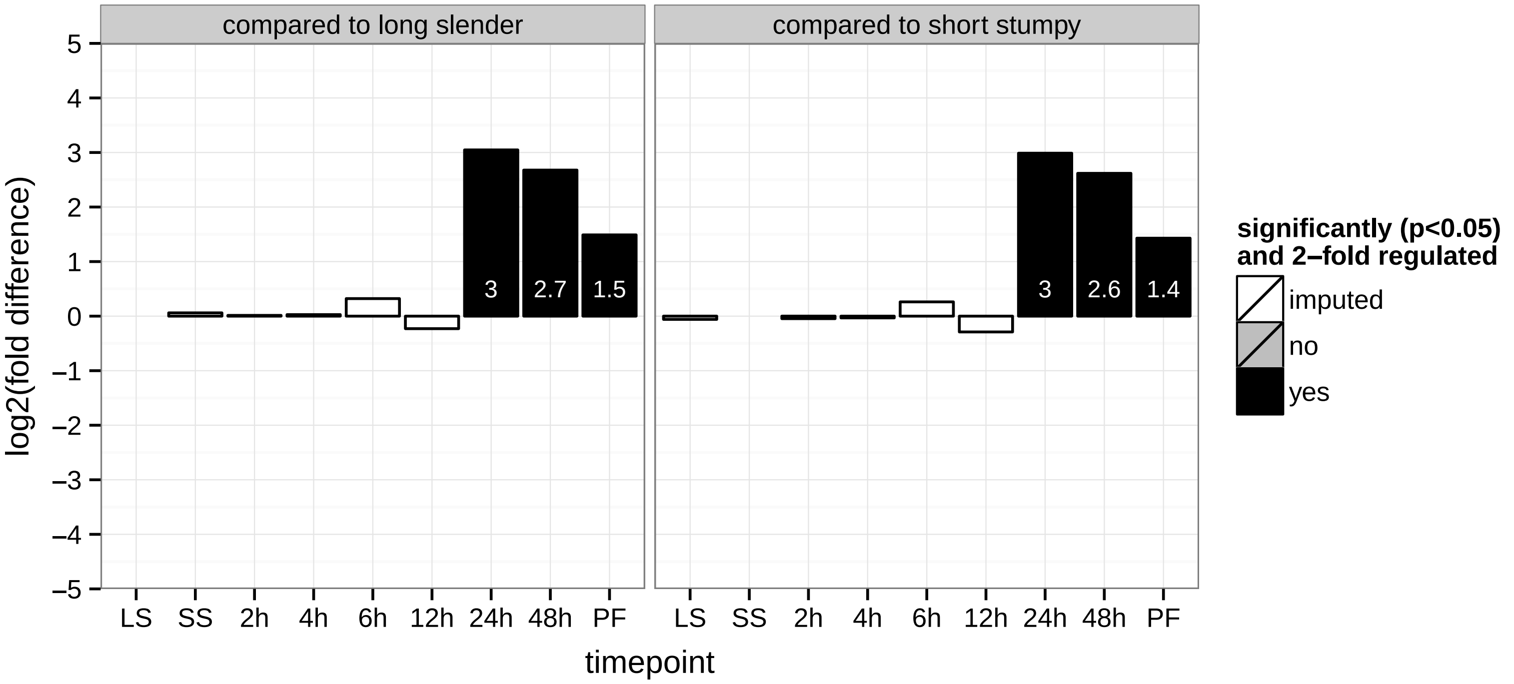
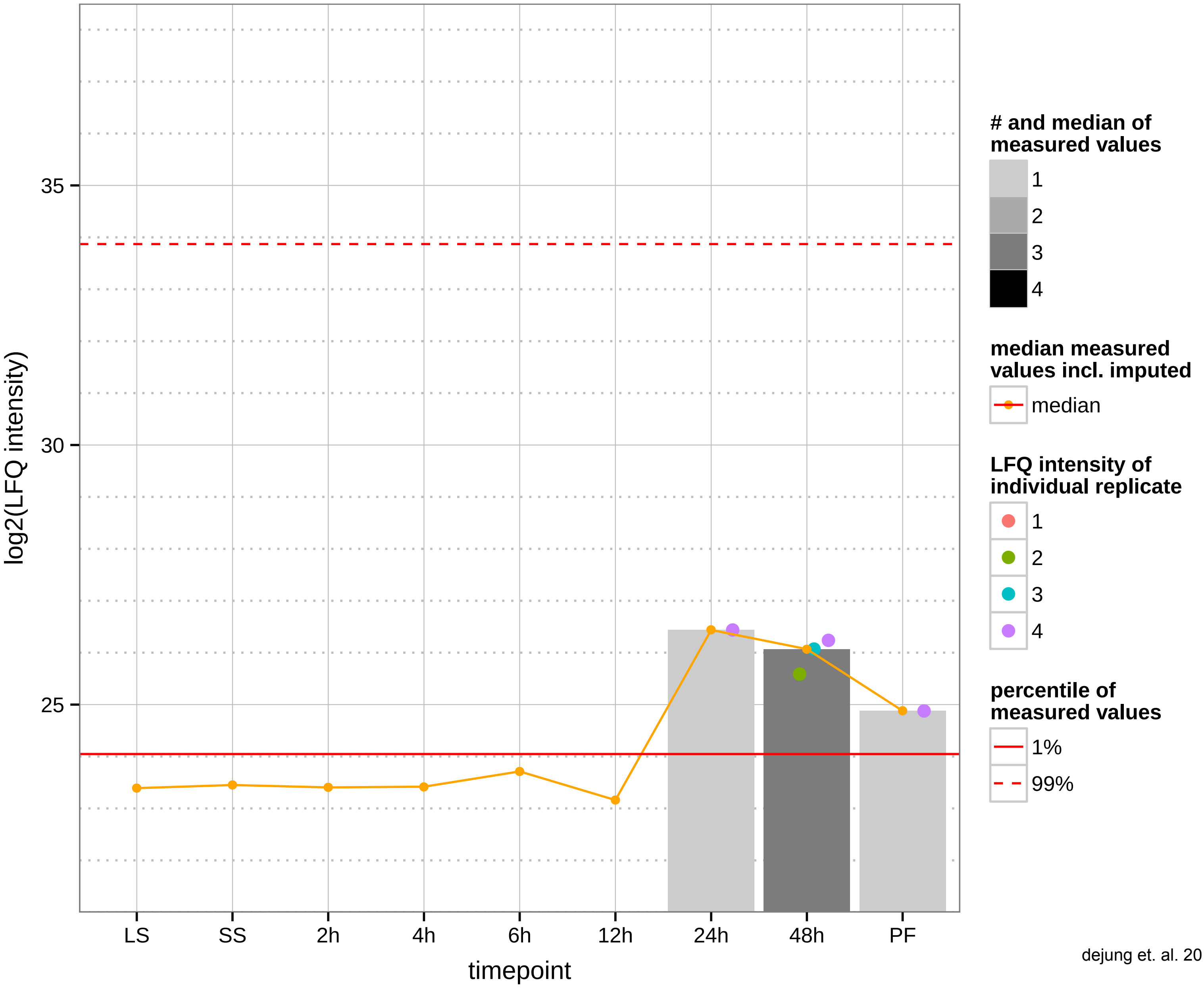
thymidine kinase, putative
Tb927.10.880
AGOF: ATP binding, thymidine kinase activity
AGOC: mitochondrion
AGOP: nucleobase−containing small molecule interconversion
PGOF: ATP binding, thymidine kinase activity
PGOC: null
PGOP: null





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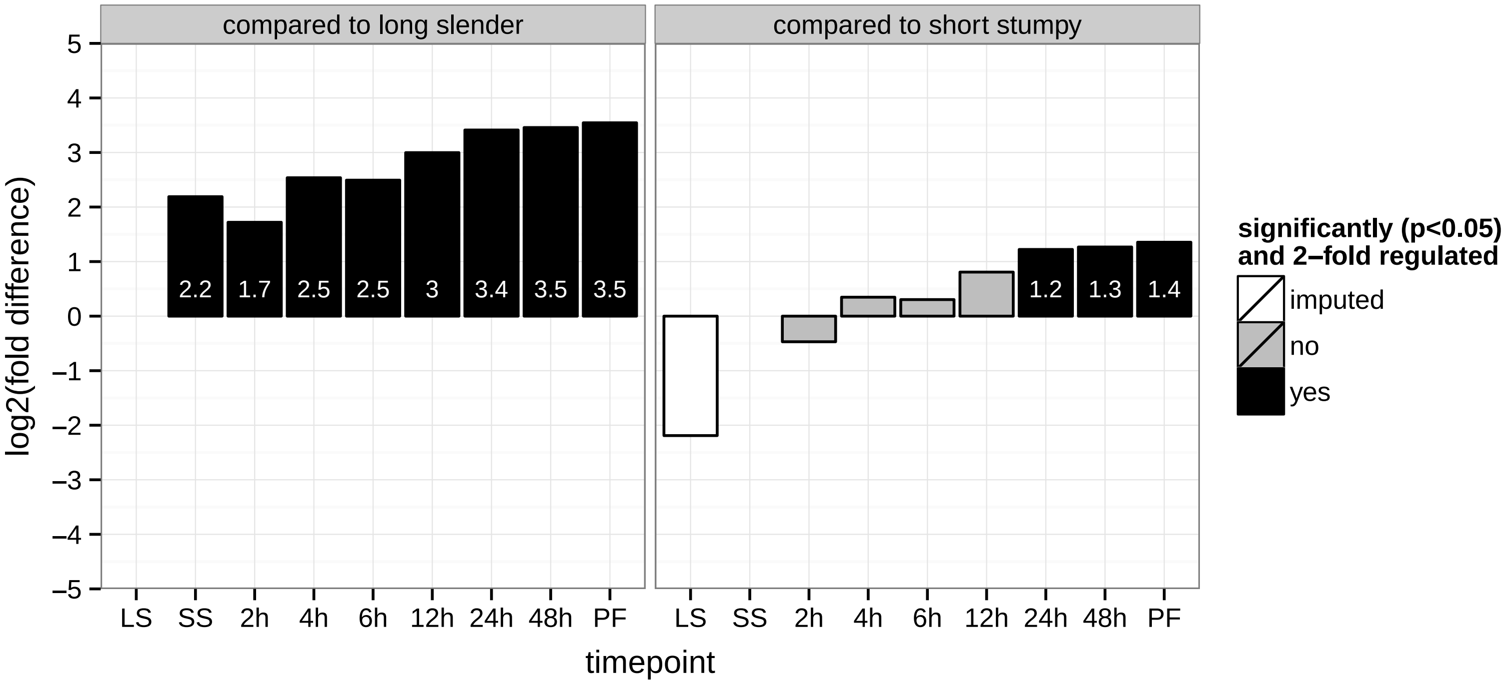
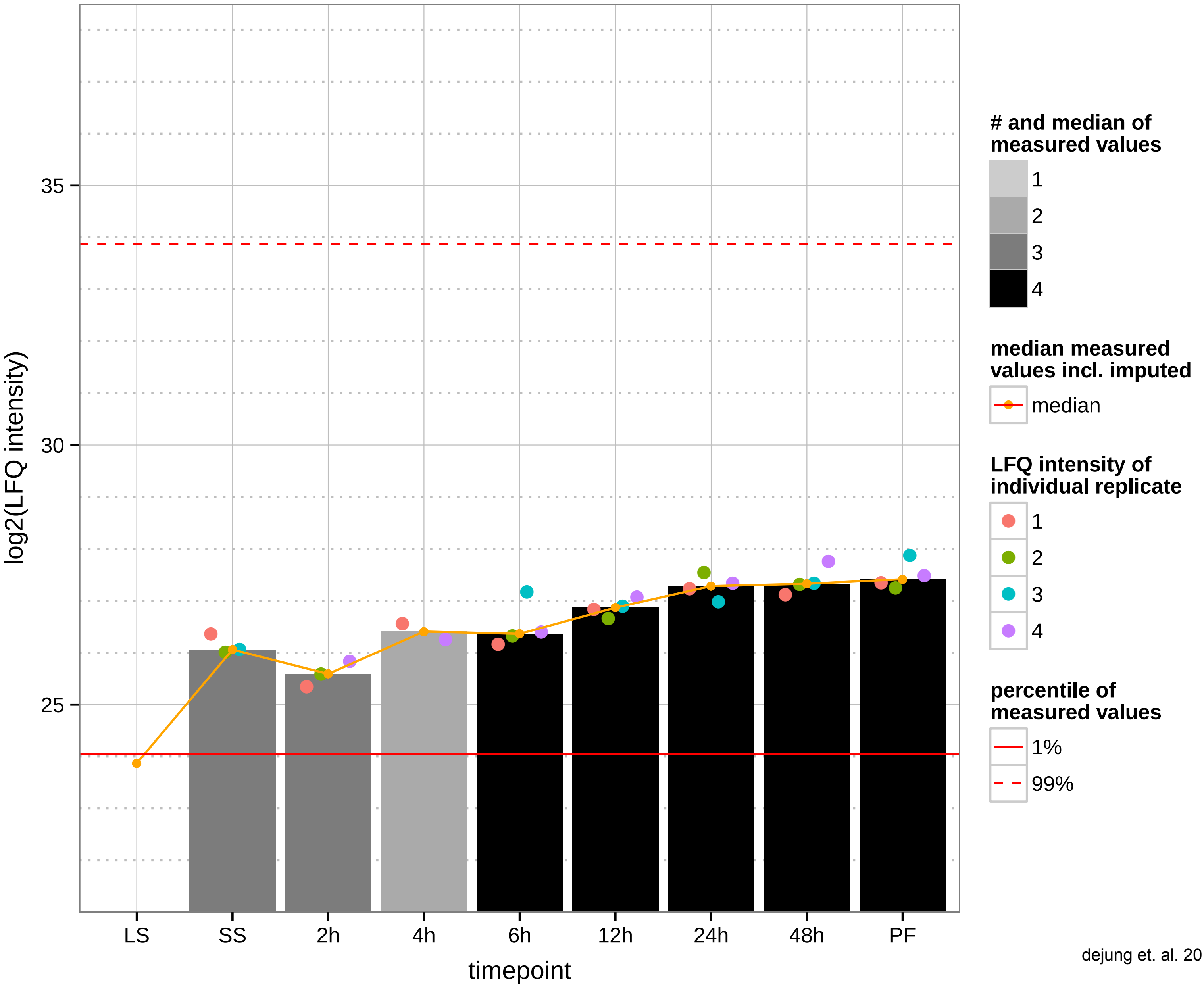
ras–like small GTPase, putative (TbGRP)
Tb927.10.8920
AGOF: GTP binding
AGOC: cytoplasm, nucleus
AGOP: null
PGOF: GTP binding
PGOC: cytoplasm, nucleus
PGOP: null





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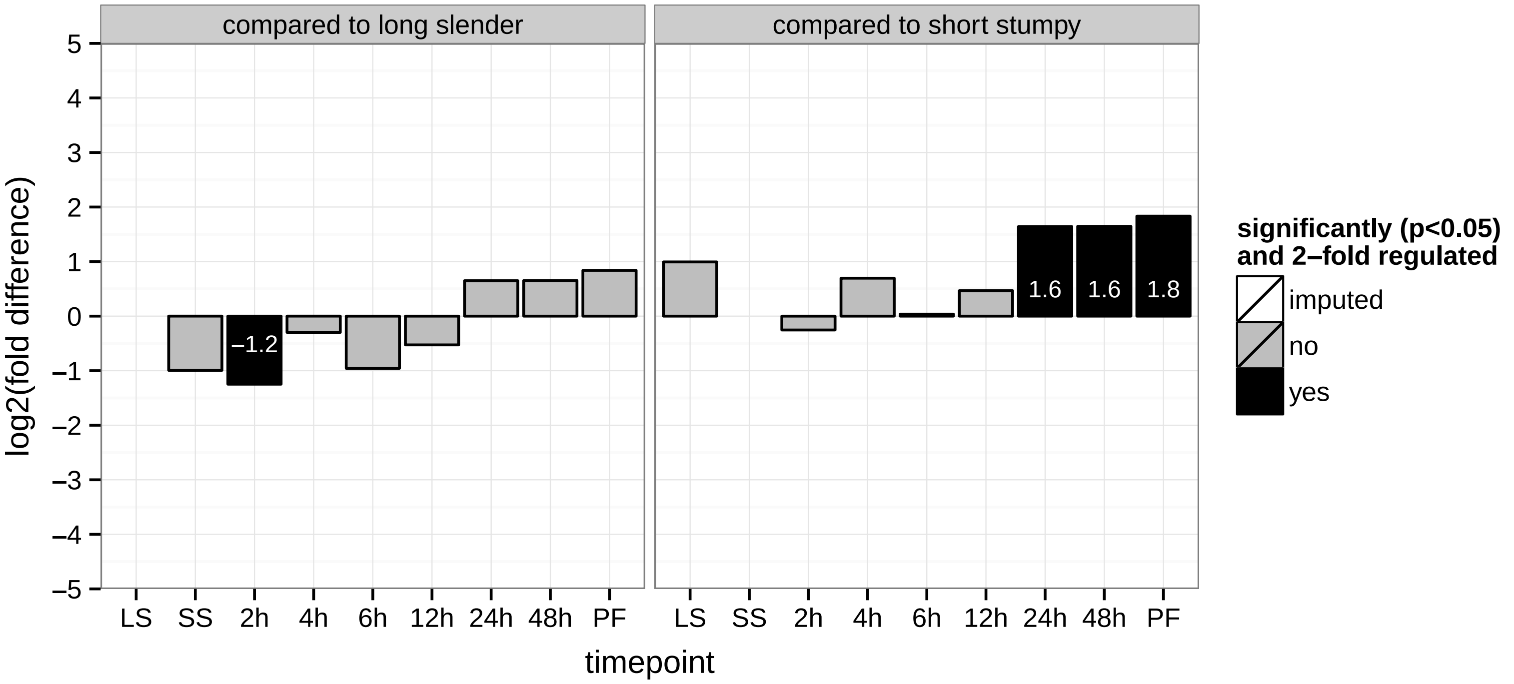
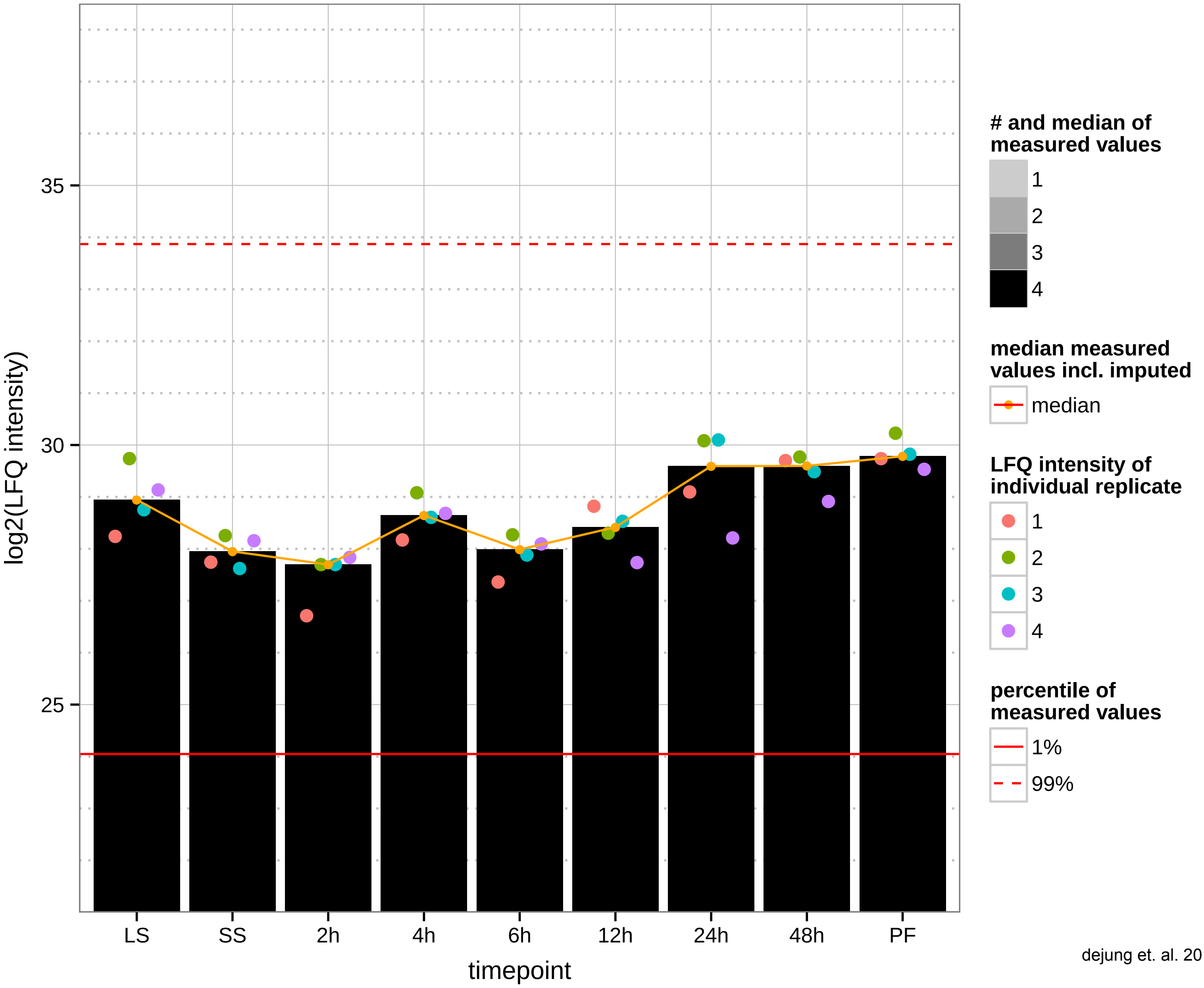
hypothetical protein, conserved
Tb927.10.8980
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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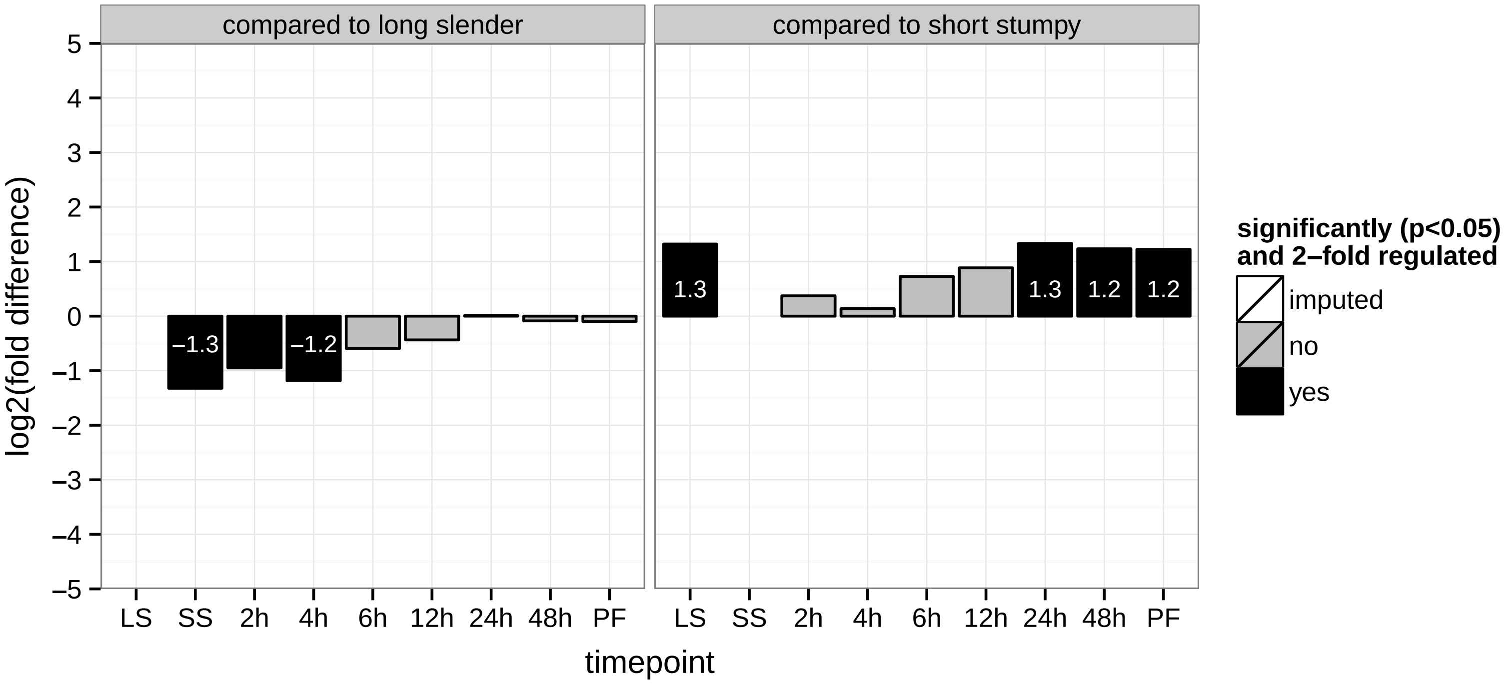
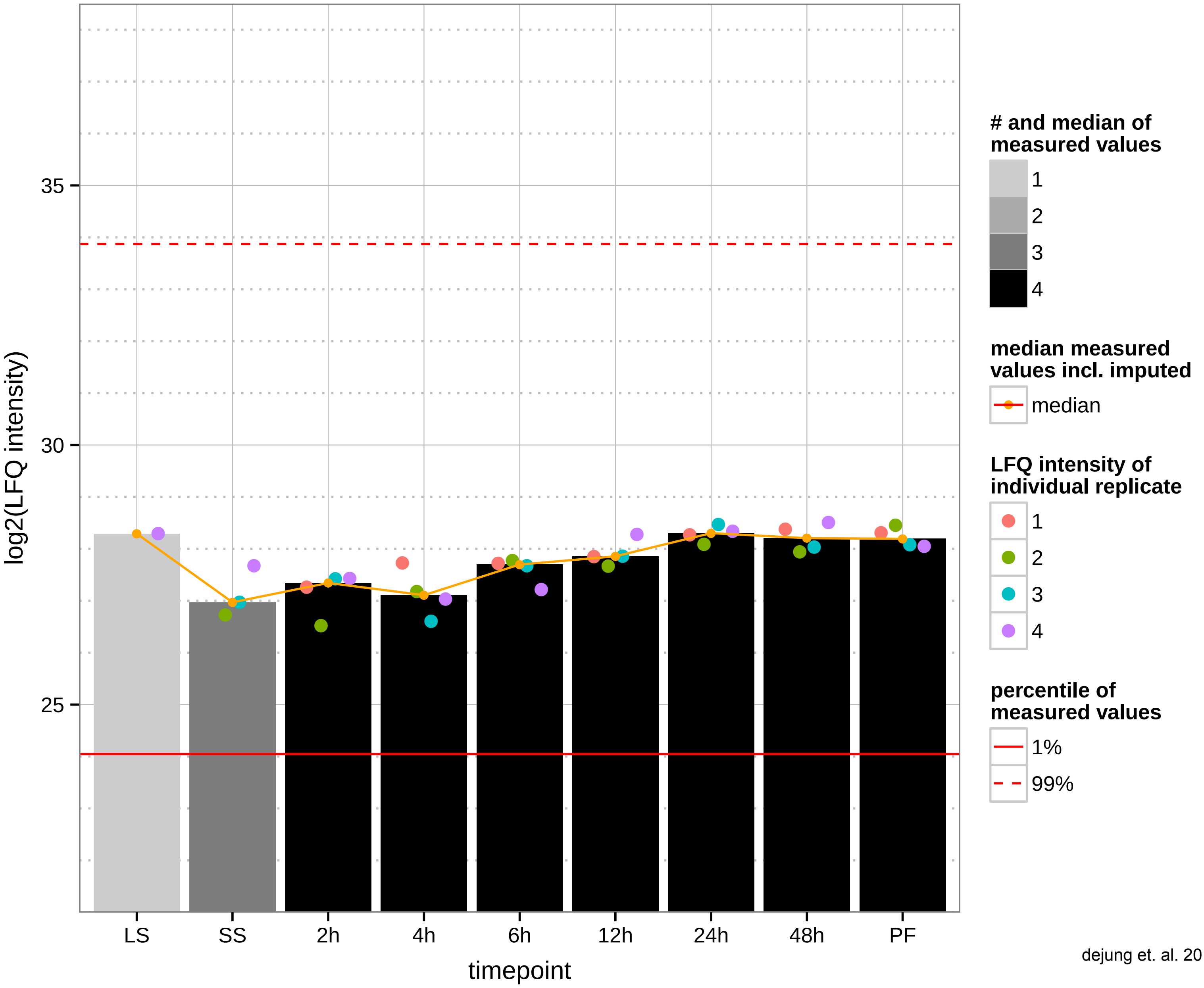
hypothetical protein, conserved
Tb927.10.920
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: RNA binding, structural constituent of ribosome
PGOC: large ribosomal subunit
PGOP: translation





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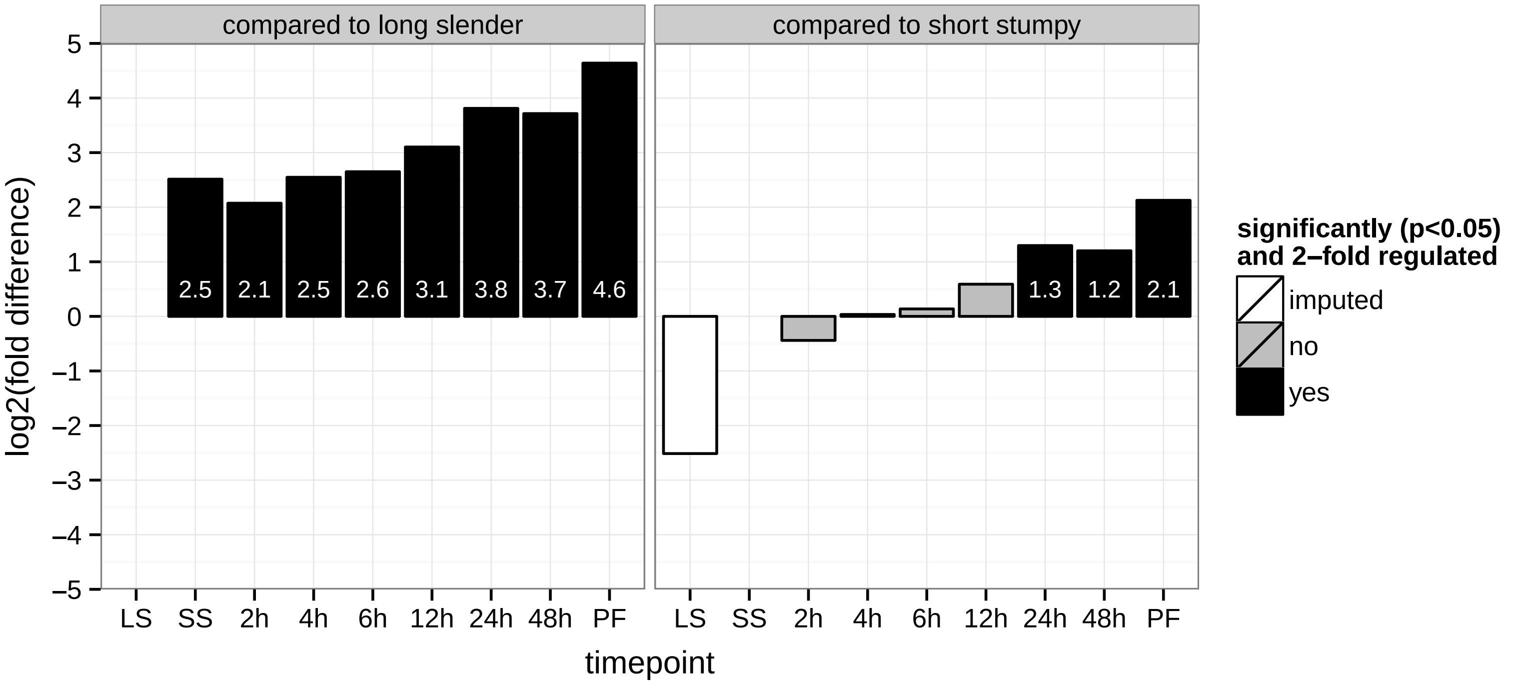
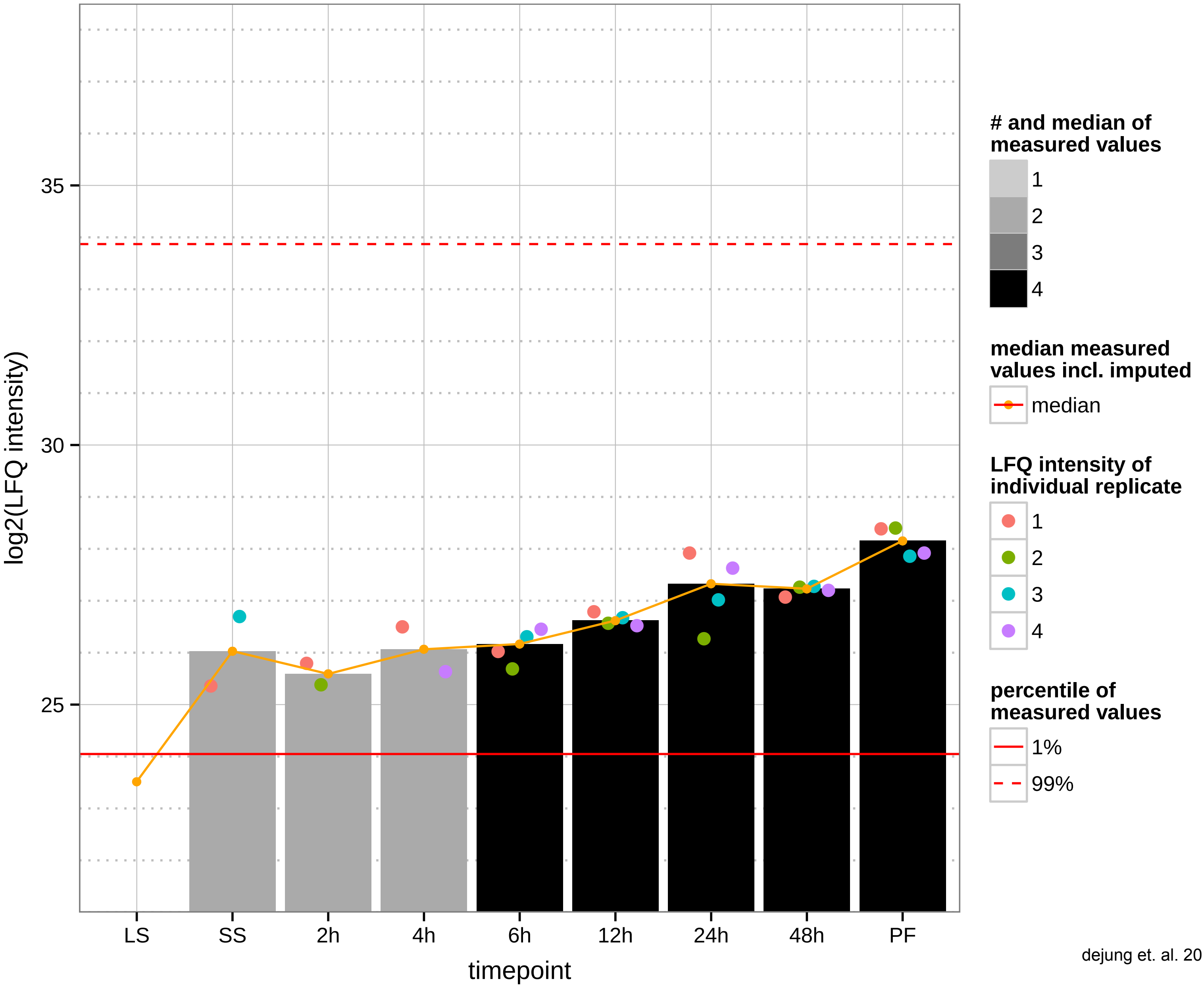
ATP−dependent DEAD/H RNA helicase, putative, ATP− dependent RNA helicase
Tb927.10.9780
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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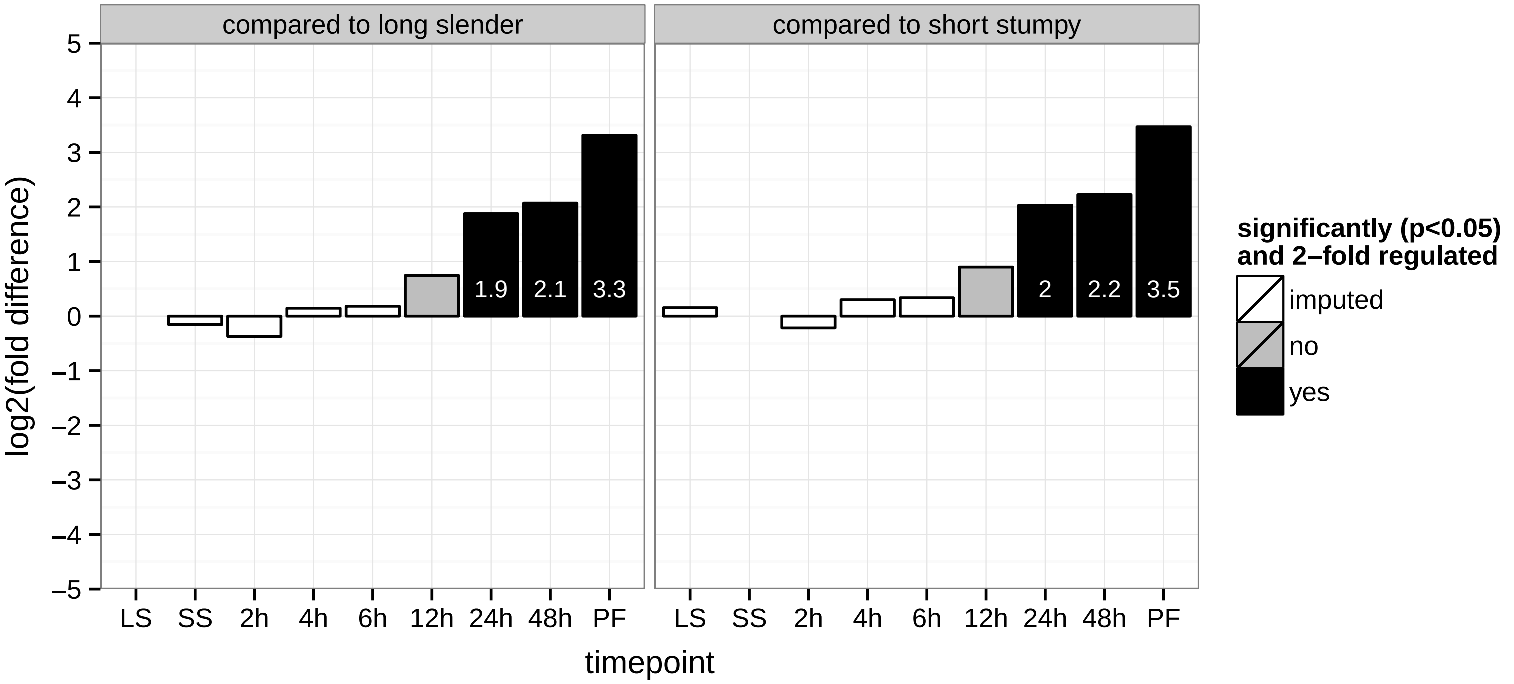
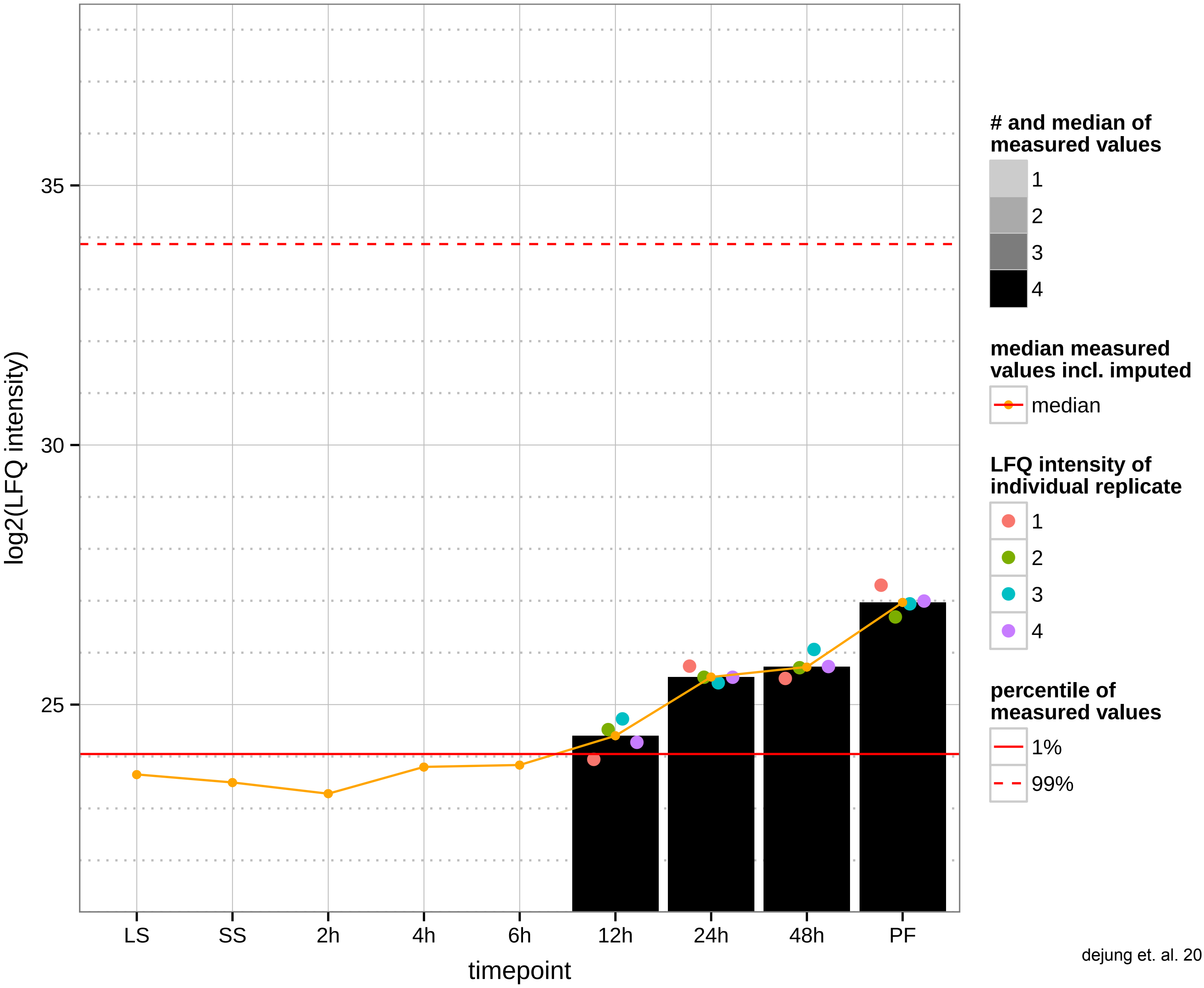
hypothetical protein, conserved
Tb927.10.9810
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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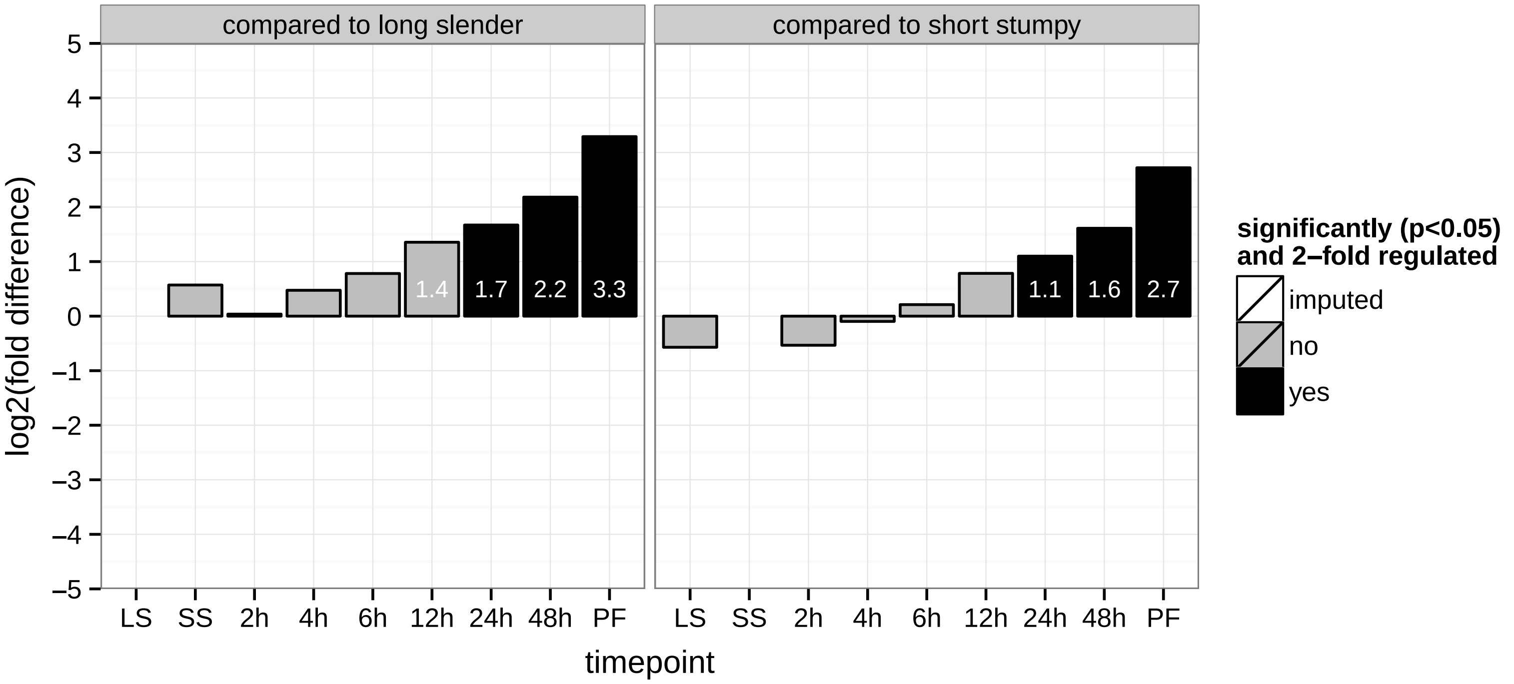
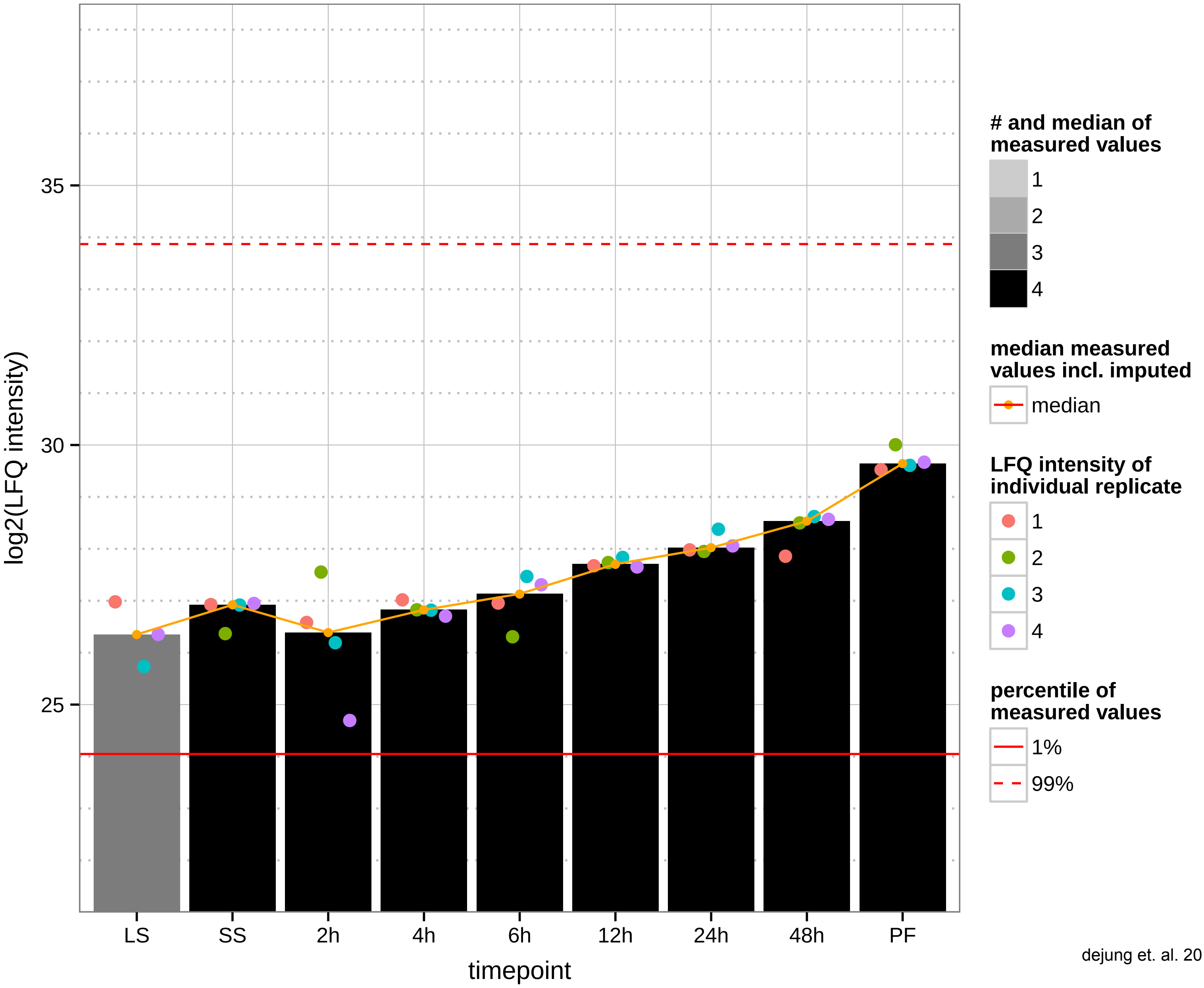
mitochondrial intermediate peptidase, putative, metallo–peptidase, Clan MA(E) Family M3
Tb927.10.9820;Tb11.v5.0565
AGOF: null, metalloendopeptidase activity
AGOC: null, mitochondrion
AGOP: null, proteolysis
PGOF: metalloendopeptidase activity
PGOC: null
PGOP: proteolysis





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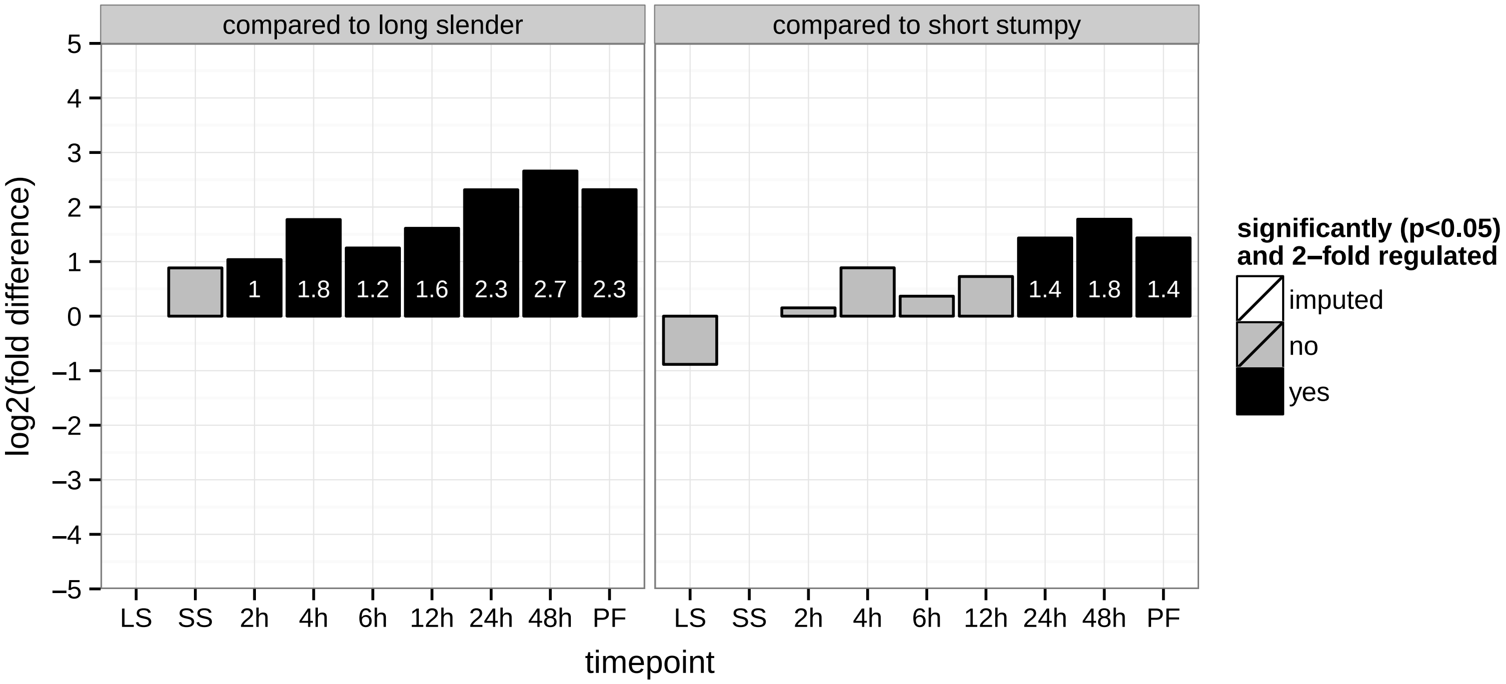
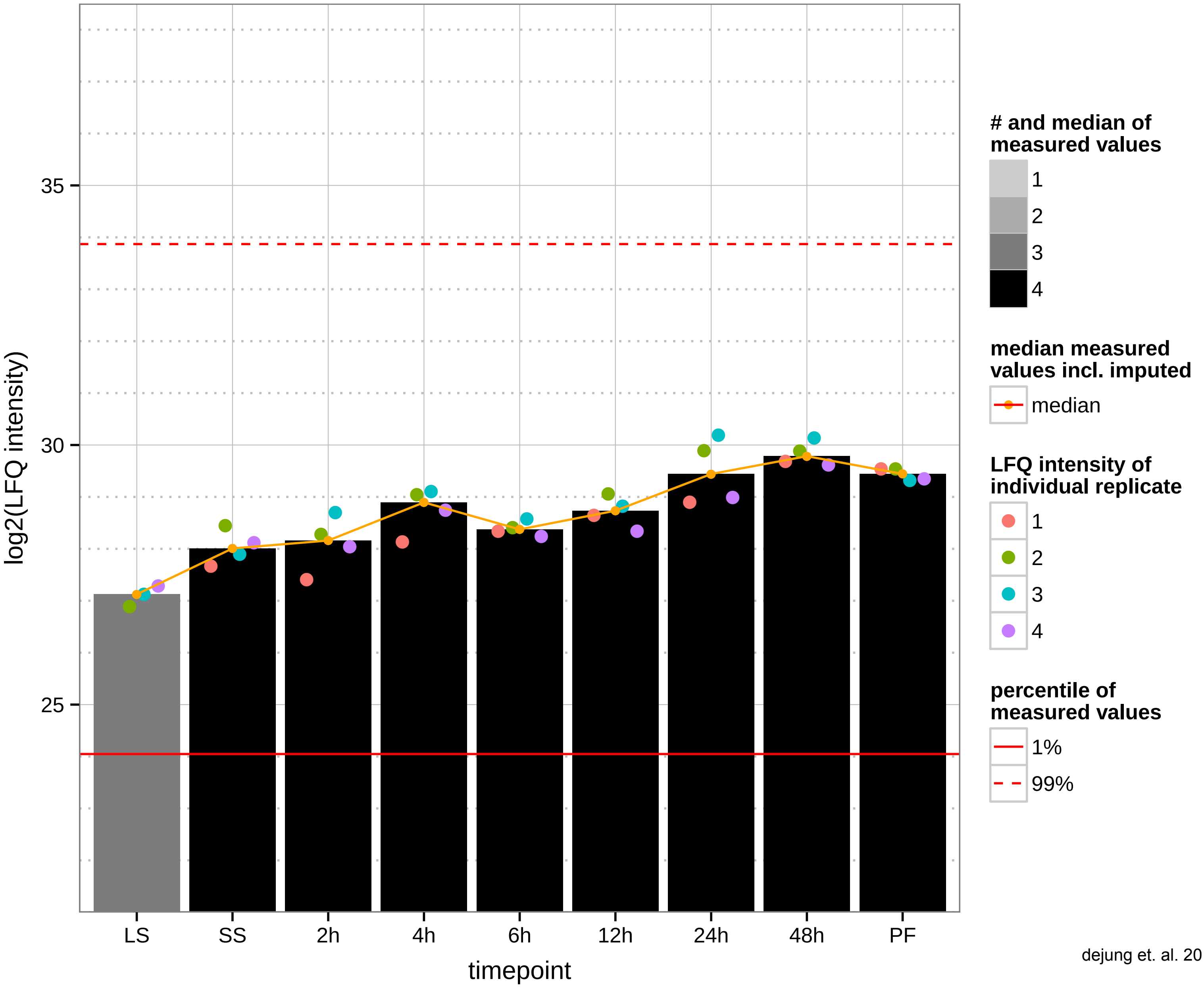
hypothetical protein, conserved
Tb927.10.9830
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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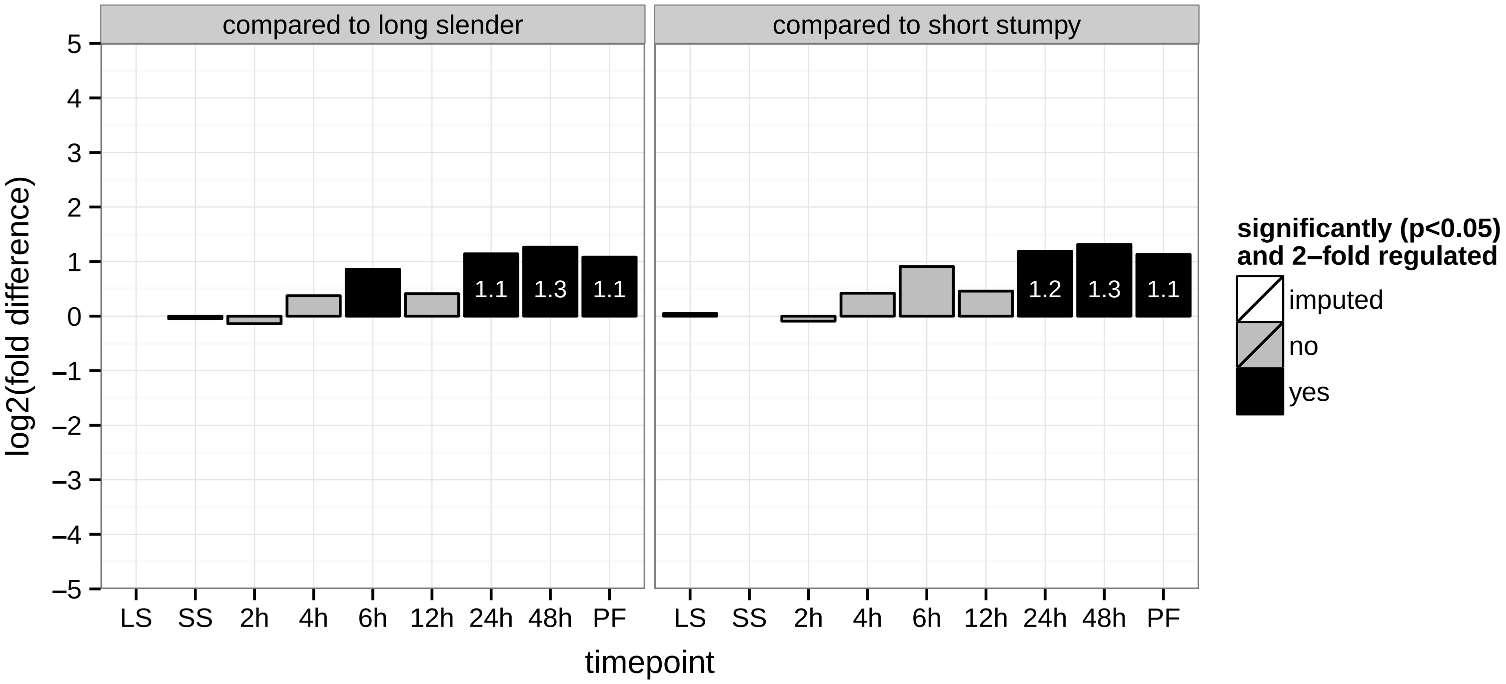
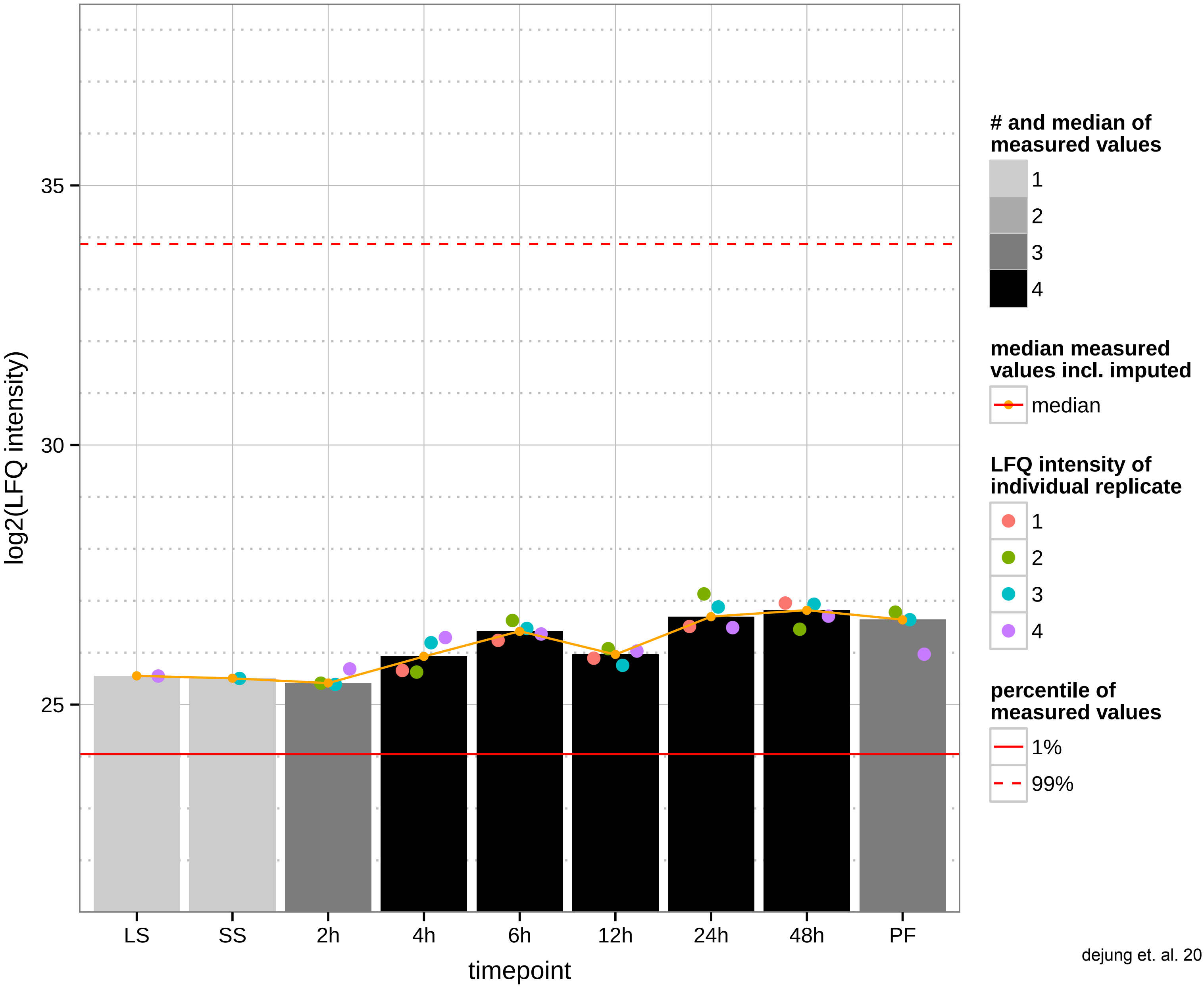
hypothetical protein, conserved
Tb927.10.9990
AGOF: hydrolase activity
AGOC: null
AGOP: null
PGOF: hydrolase activity
PGOC: null
PGOP: null





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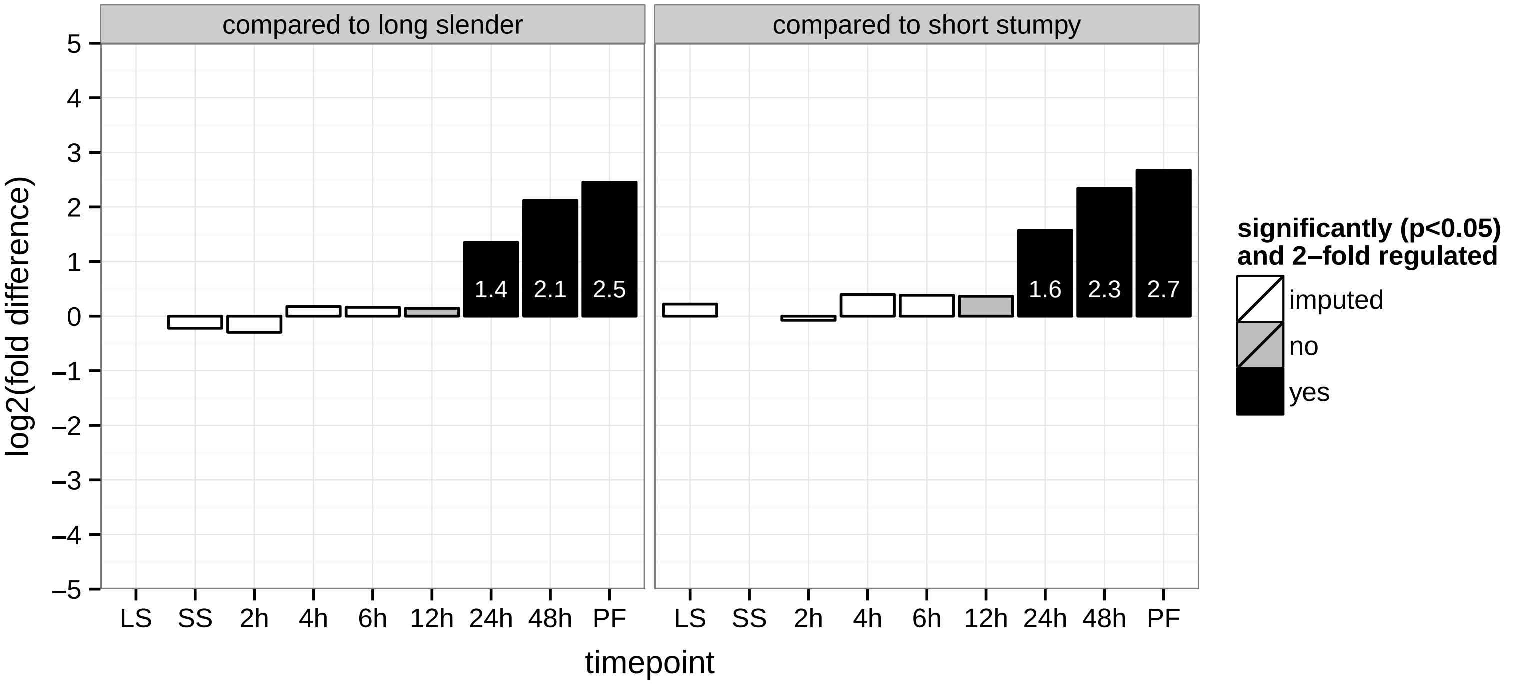
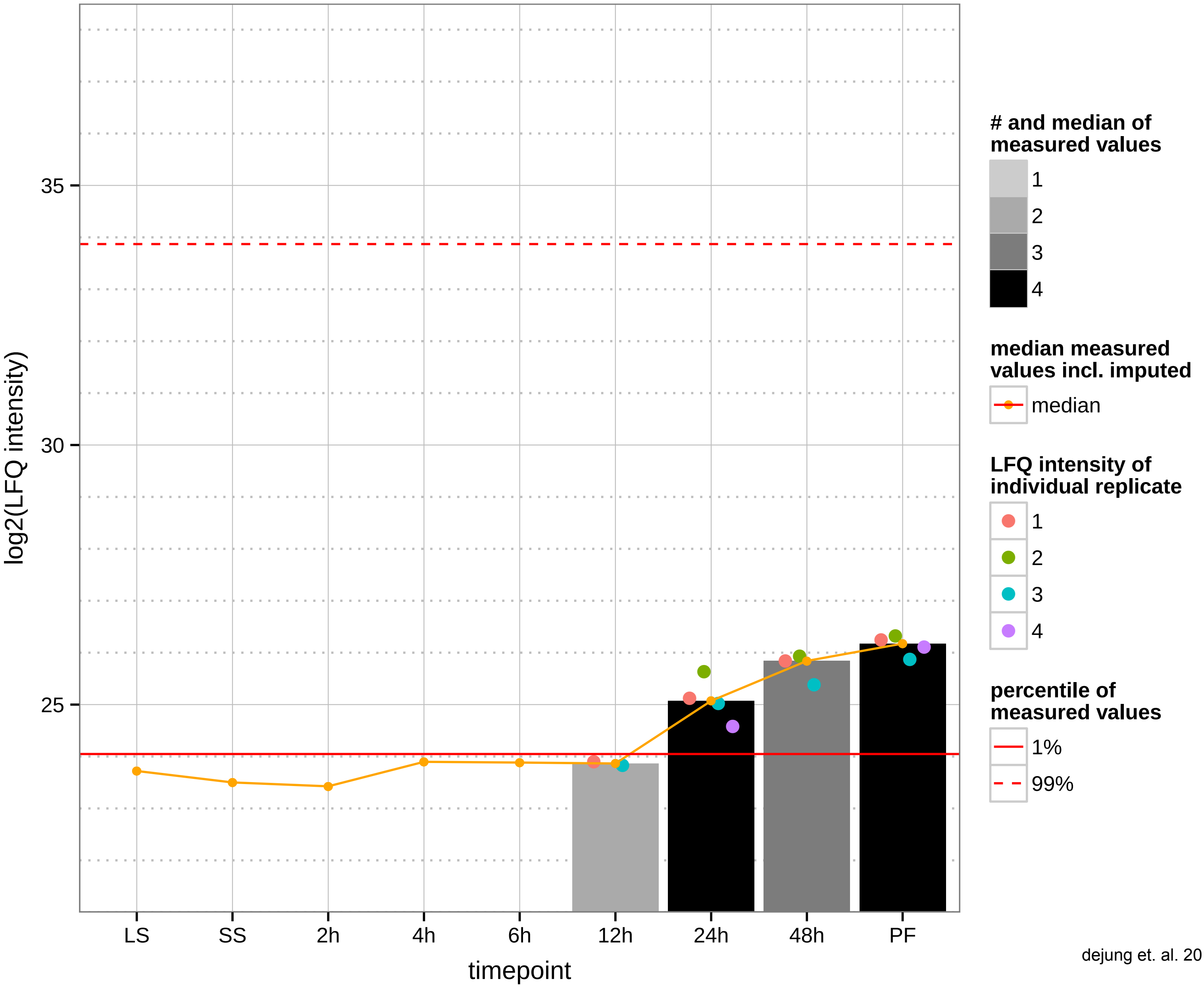
hypothetical protein, conserved
Tb927.11.10400
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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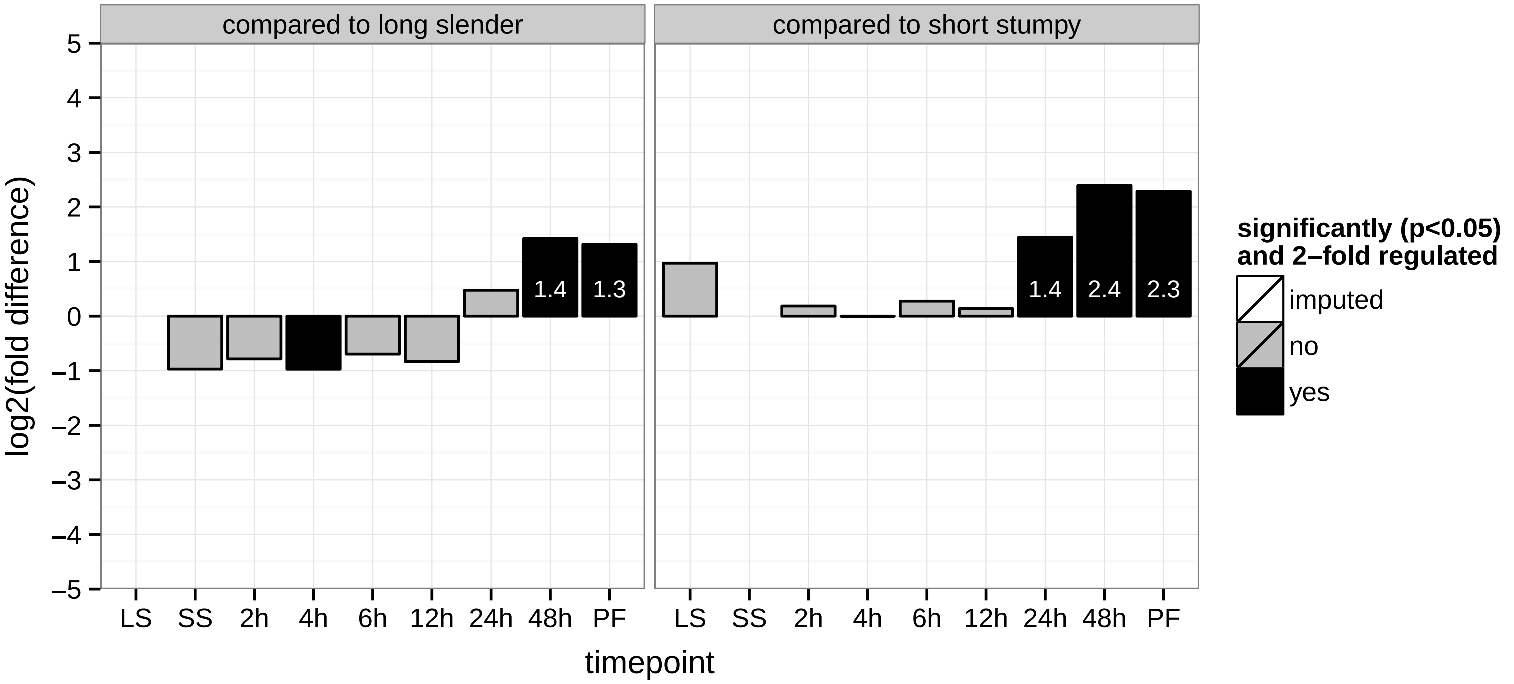
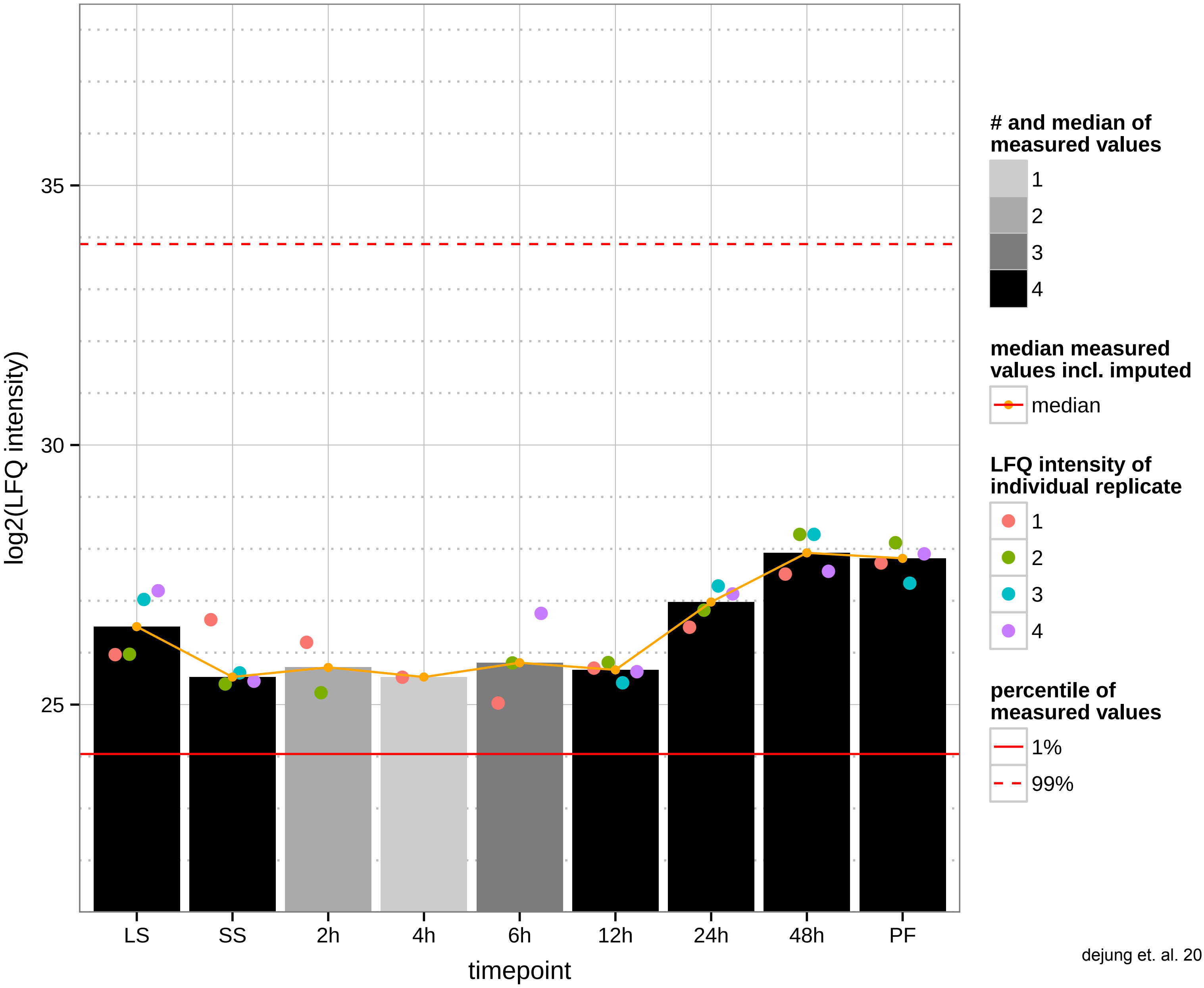
glycosomal transporter (GAT3), putative (gat3)
Tb927.11.1070
AGOF: ATP binding, ATPase activity
AGOC: ATP−binding cassette (ABC) transporter complex, integral to membrane, membrane
AGOP: transport
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances, nucleoside−triphosphatase activity
PGOC: integral to membrane, membrane
PGOP: transmembrane transport, transport





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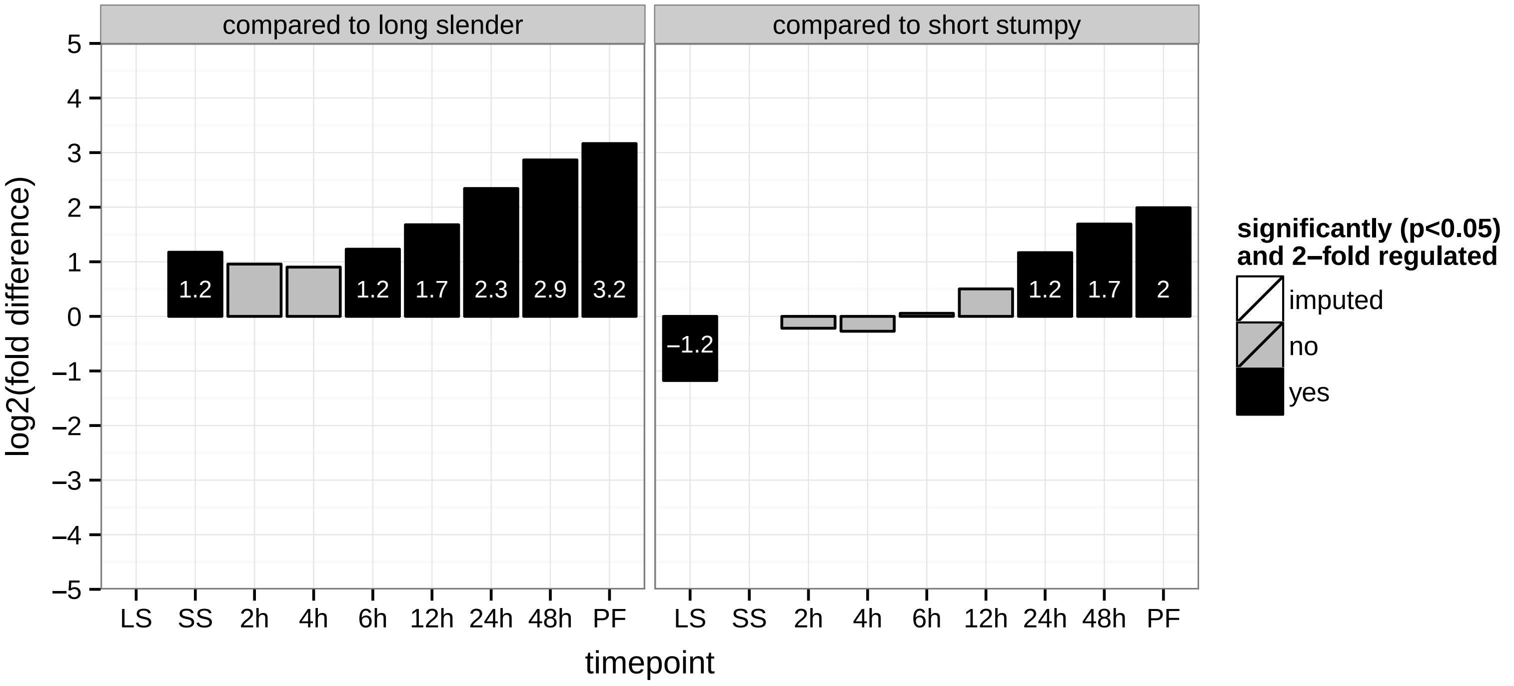
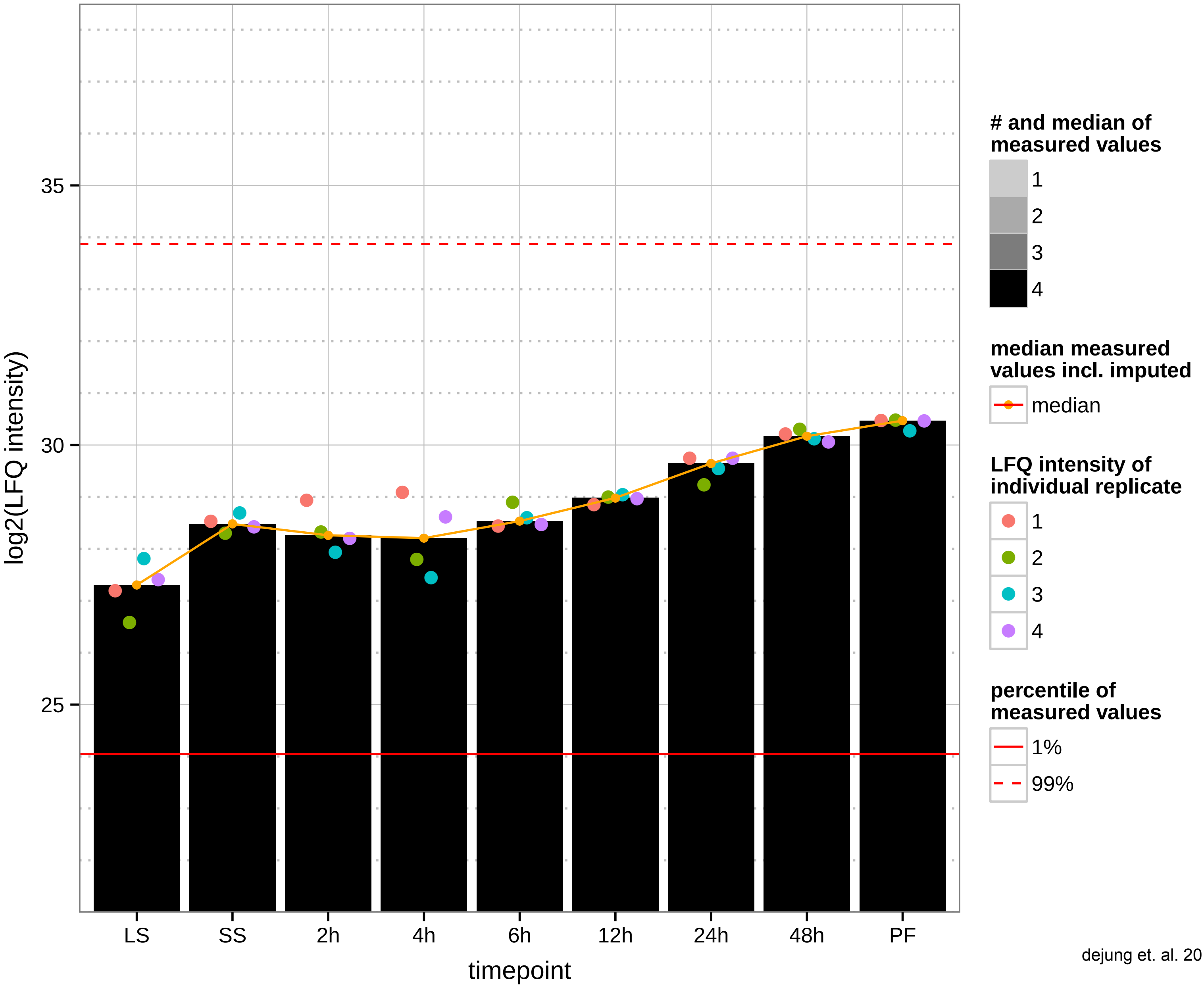
kinesin–like protein, putative
Tb927.11.10760
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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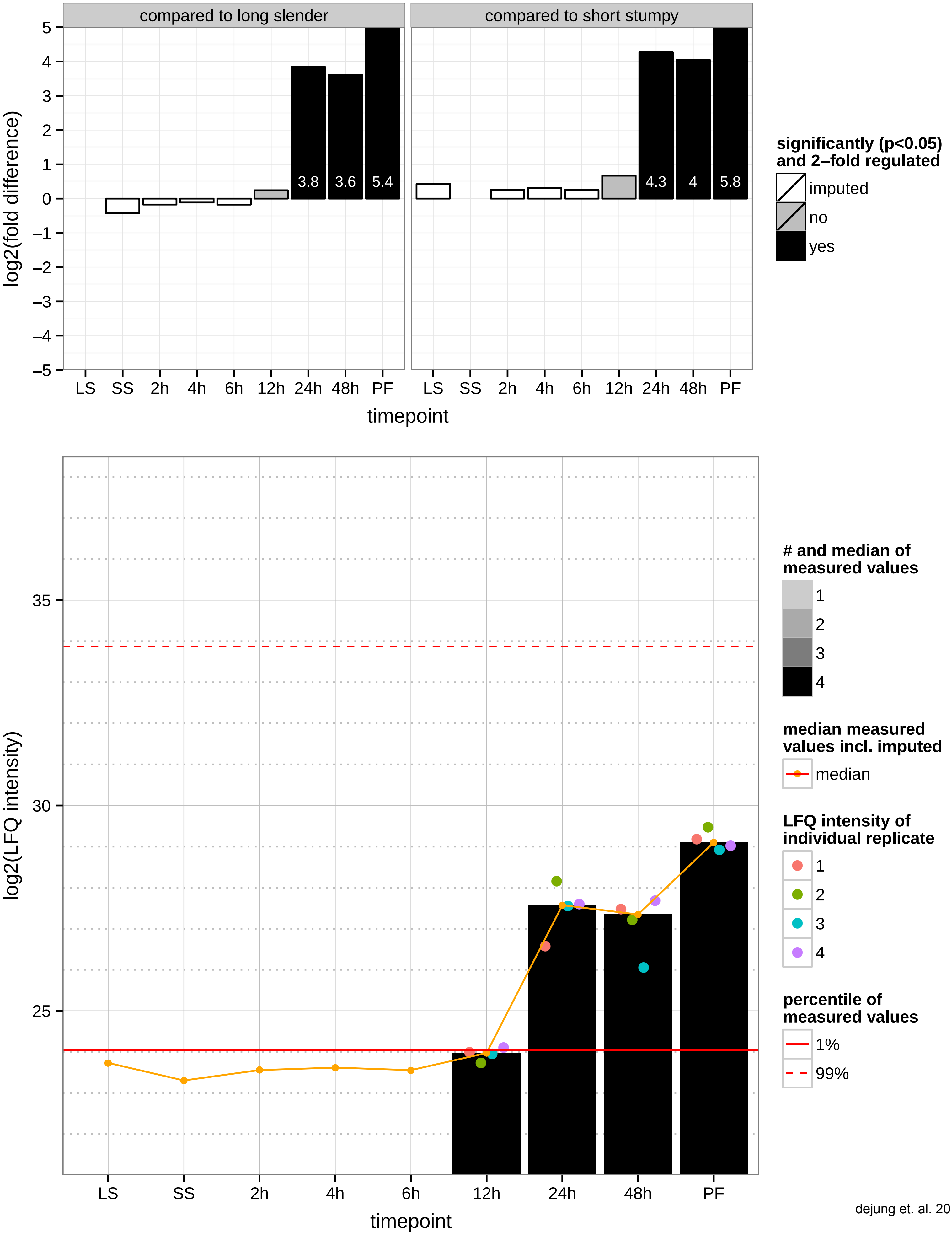
hypothetical protein, conserved
Tb927.11.12040
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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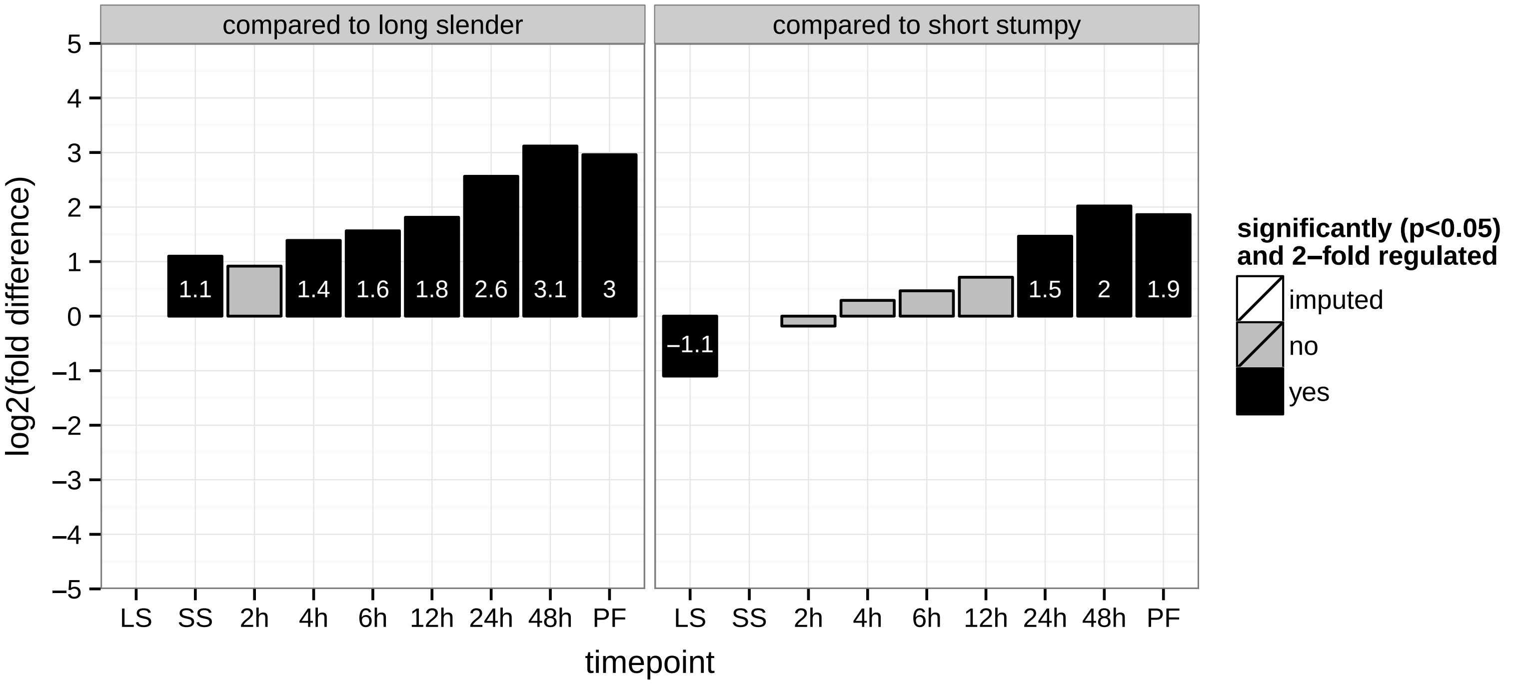
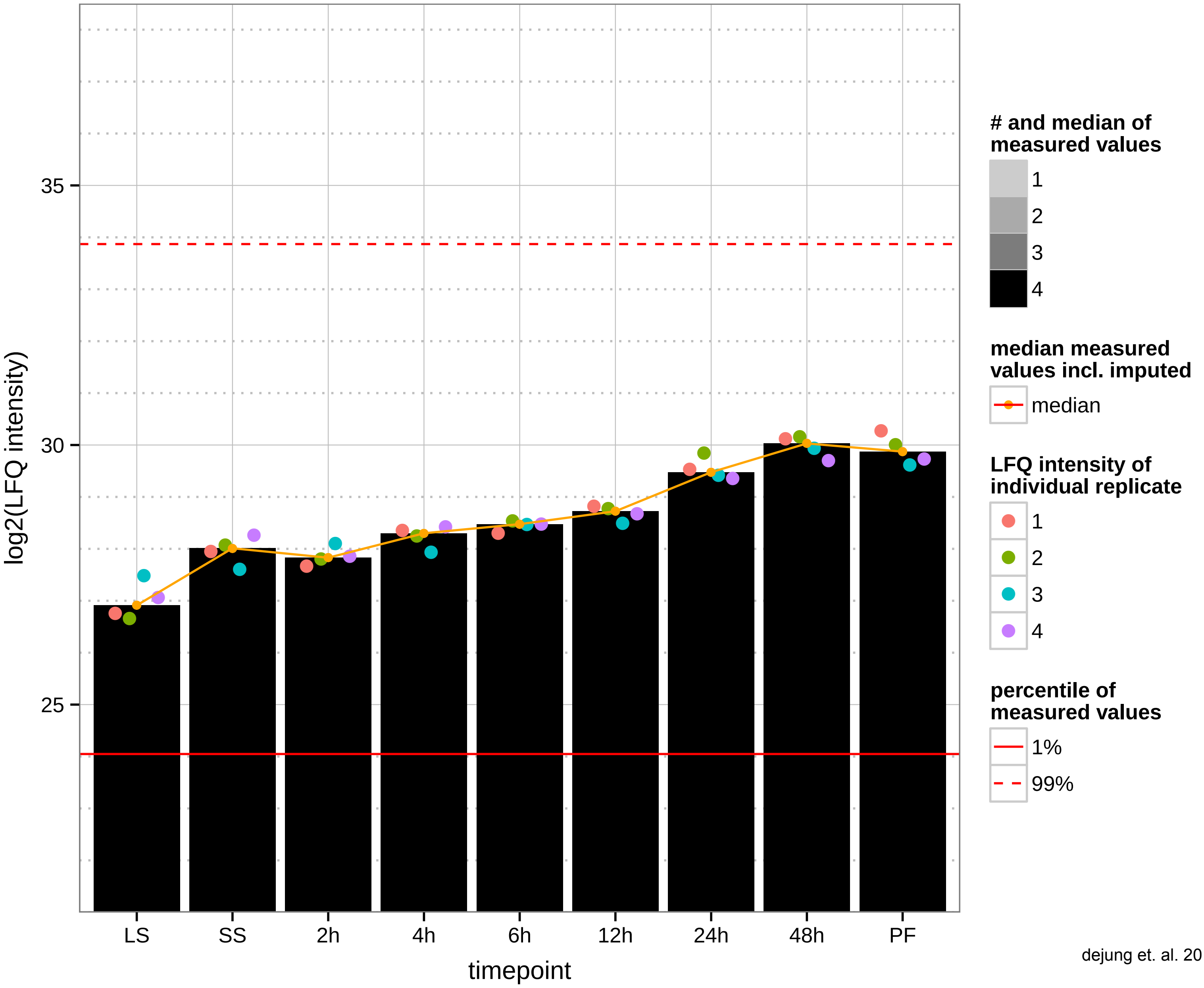
hypothetical protein, conserved
Tb927.11.1270
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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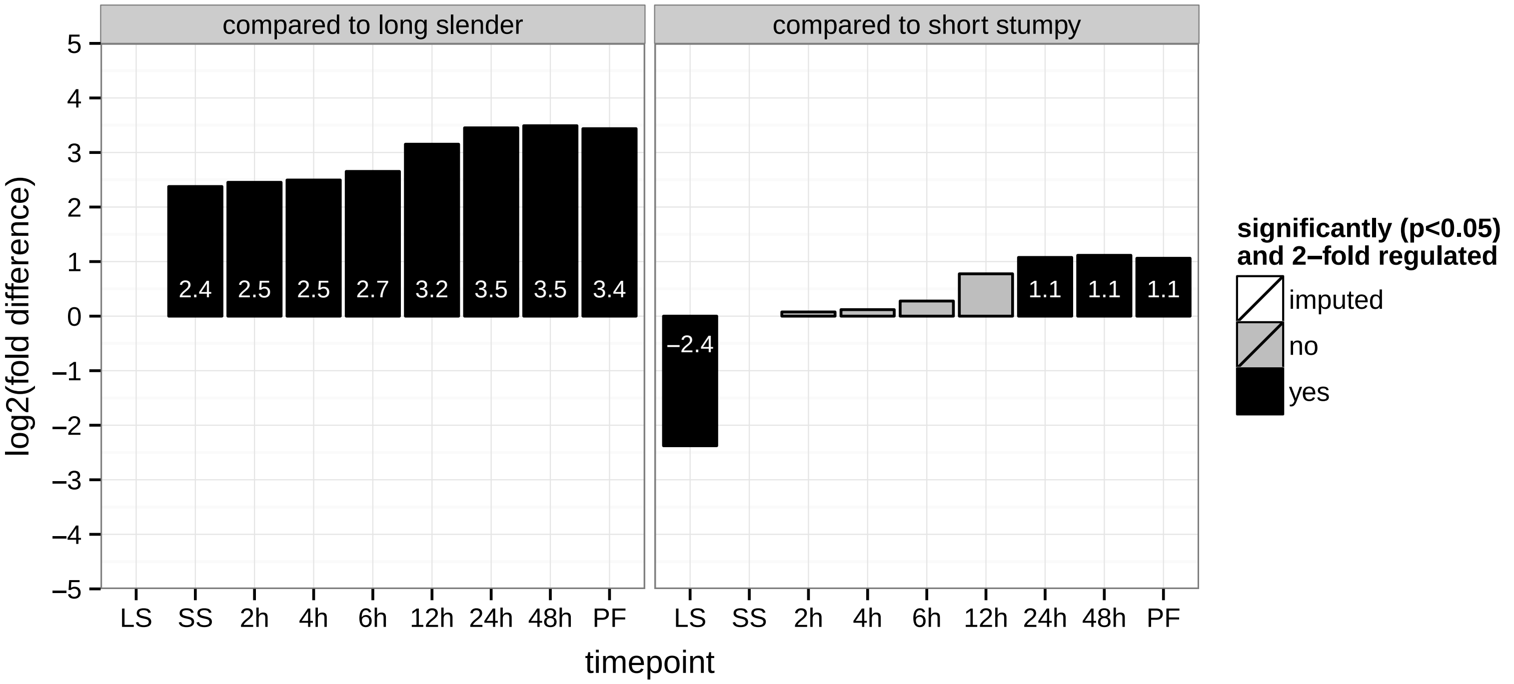
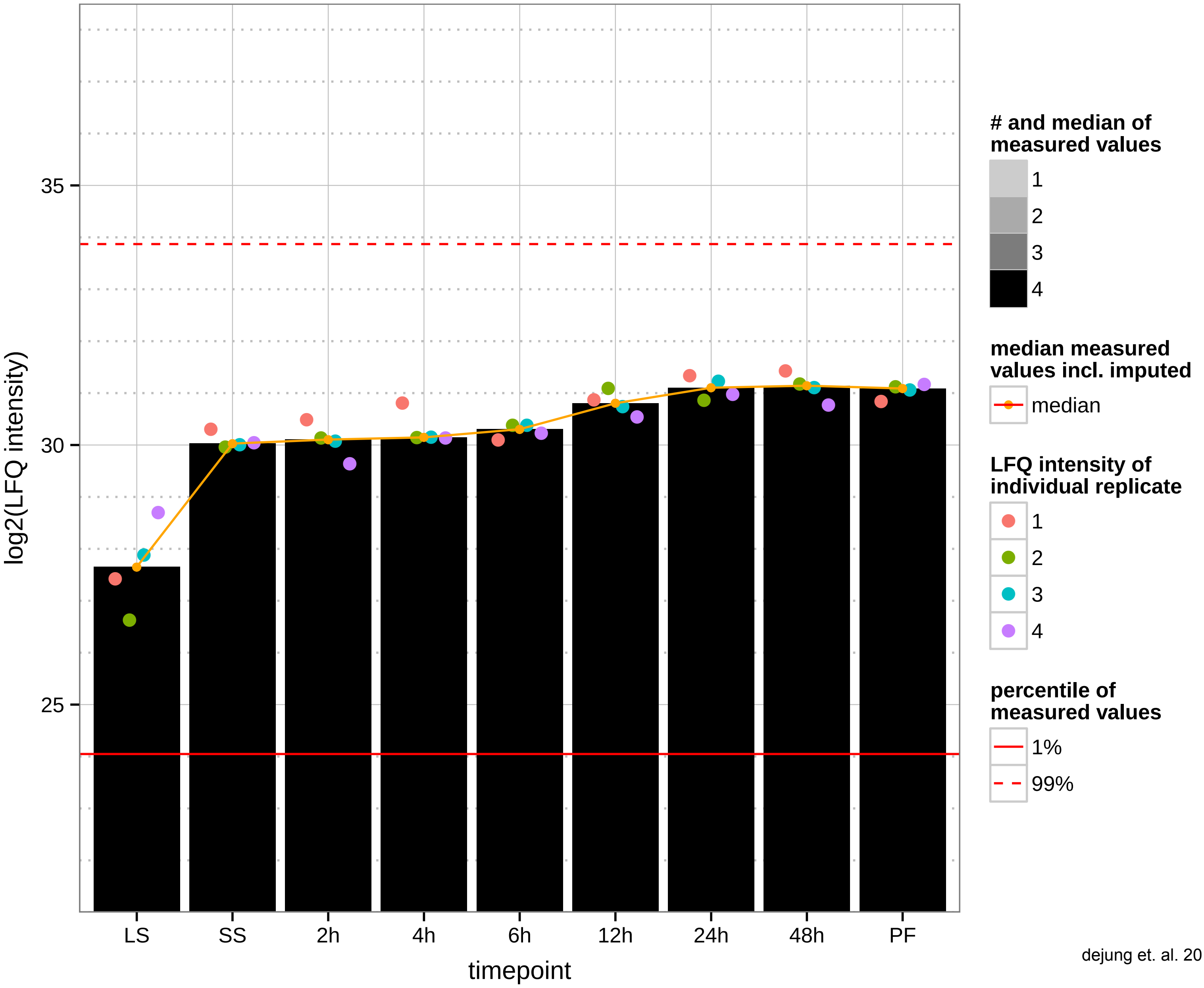
hypothetical protein conserved
Tb927.11.13180
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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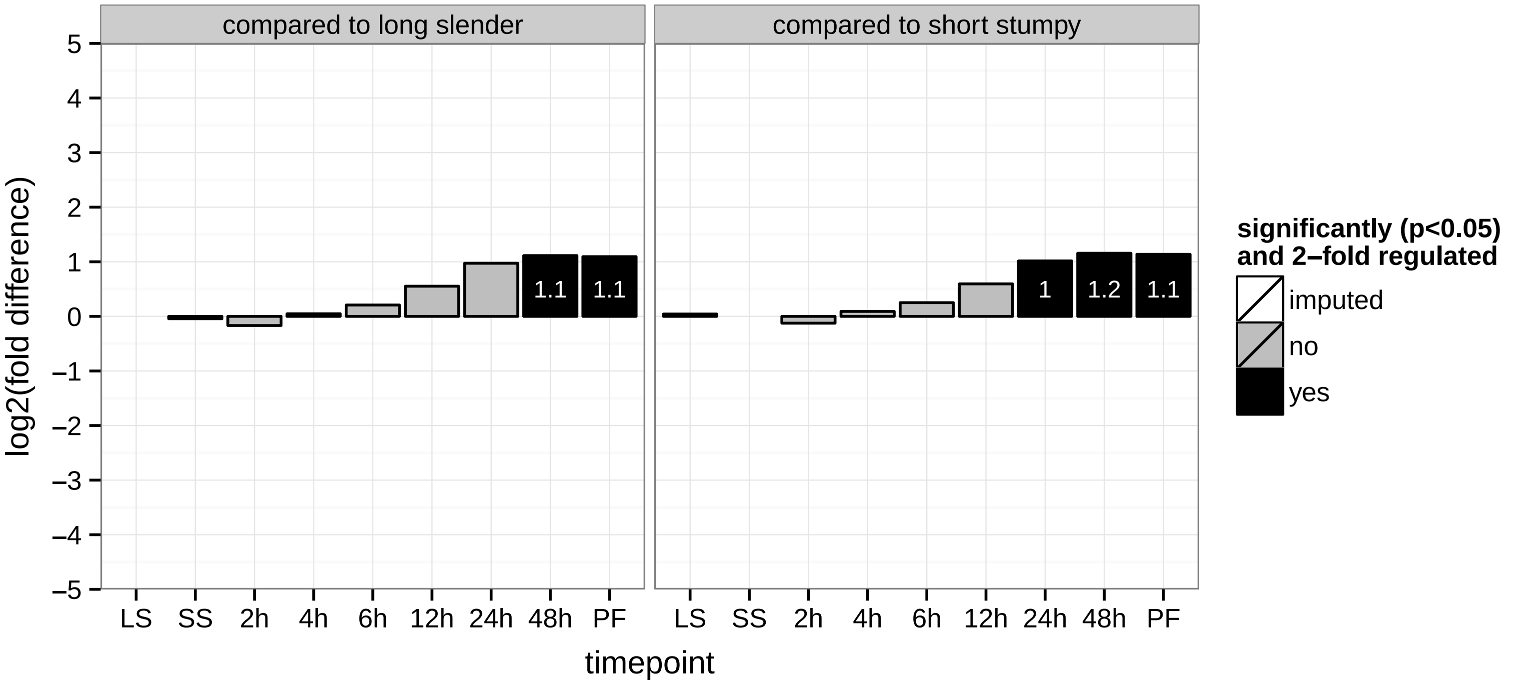
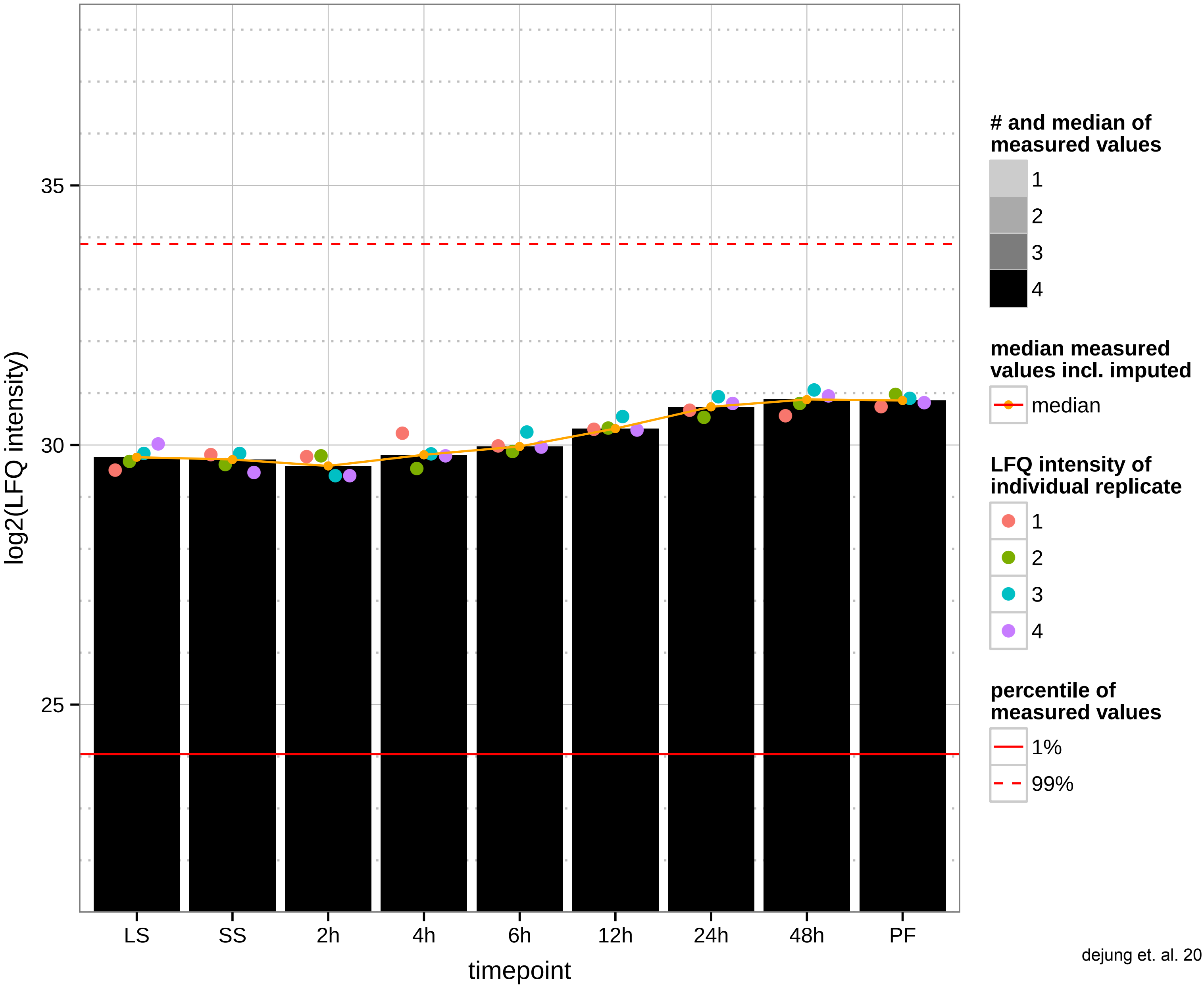
eukaryotic translation initiation factor 2 gamma, putative (eIF−2−gamma)
Tb927.11.13250
AGOF: GTP binding, GTPase activity, histone methyltransferase activity, translation initiation factor activity
AGOC: eukaryotic 43S preinitiation complex
AGOP: translation, translational initiation
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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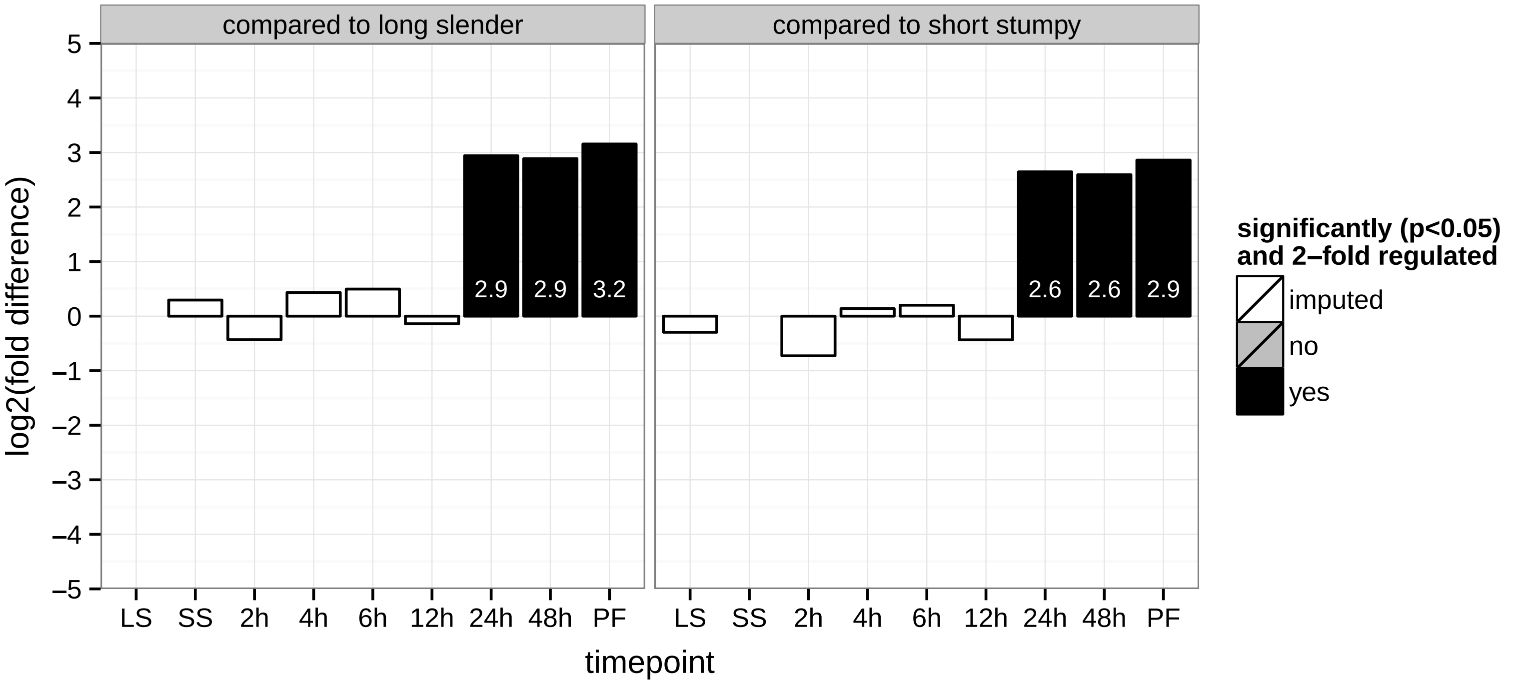
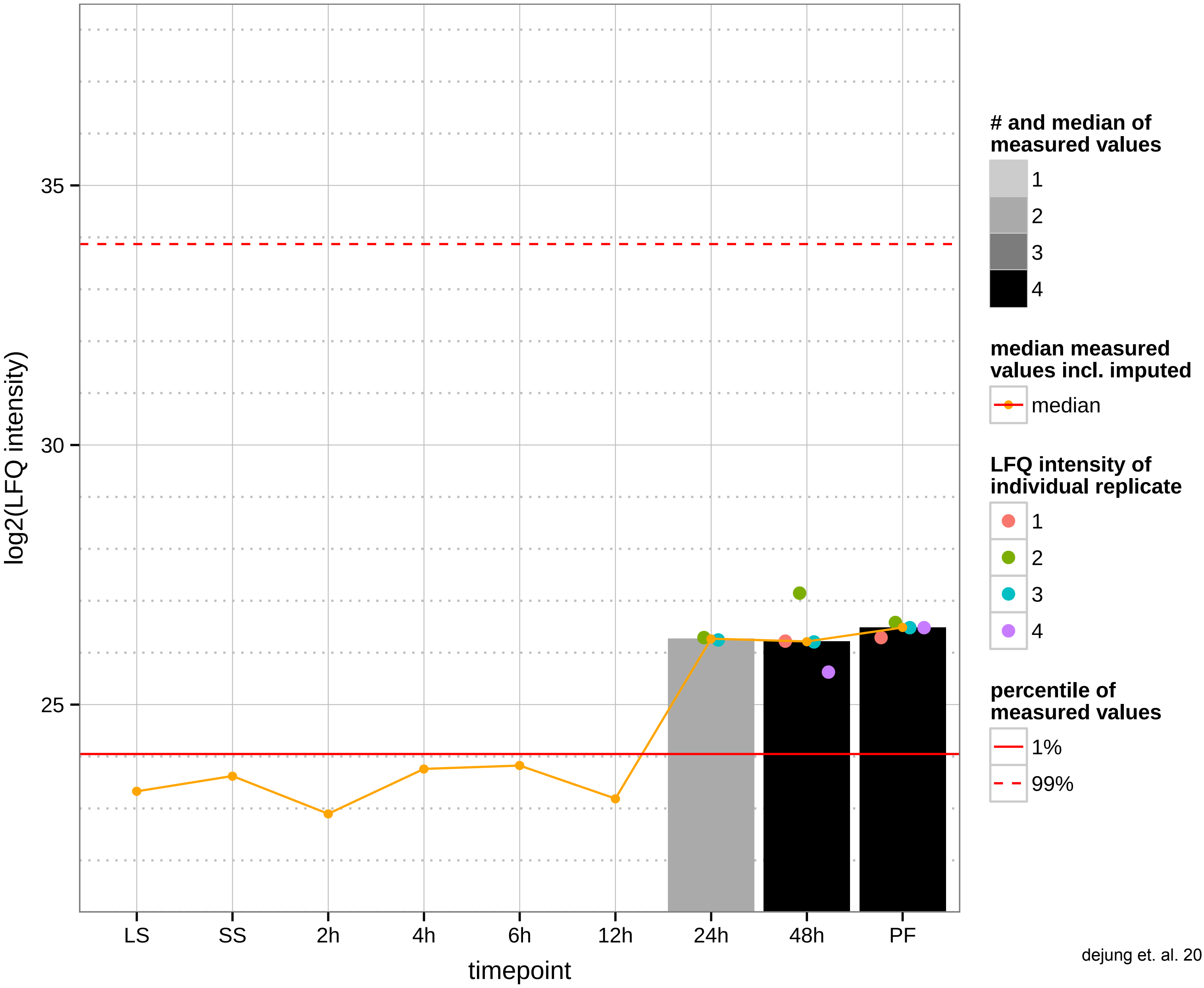
hypothetical protein, conserved
Tb927.11.1340
AGOF: null
AGOC: null
AGOP: null
PGOF: transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: null





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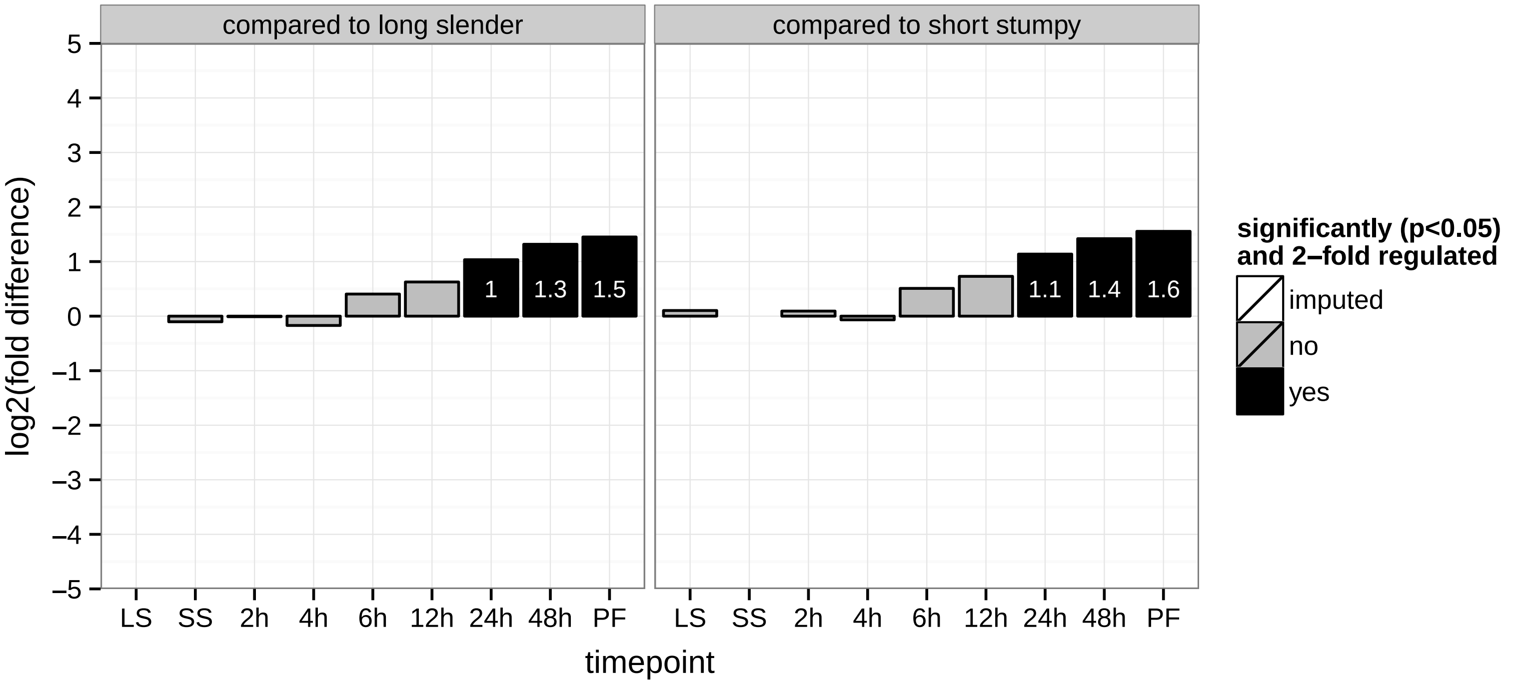
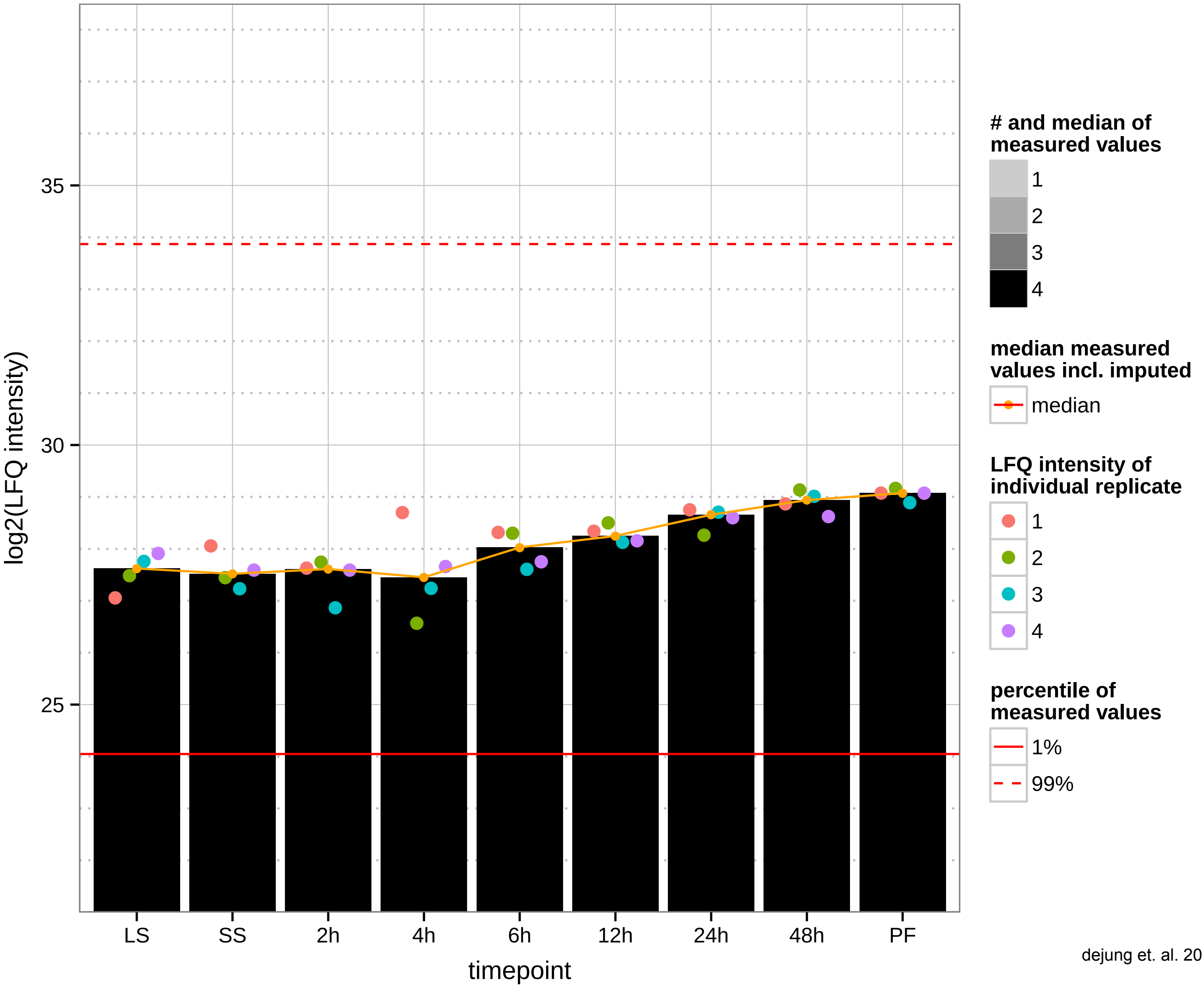
G5–interacting protein (G5–IP)
Tb927.11.14590
AGOF: protein binding
AGOC: cytoplasm, eukaryotic translation initiation factor 4F complex
AGOP: RNA capping
PGOF: null
PGOC: null
PGOP: null





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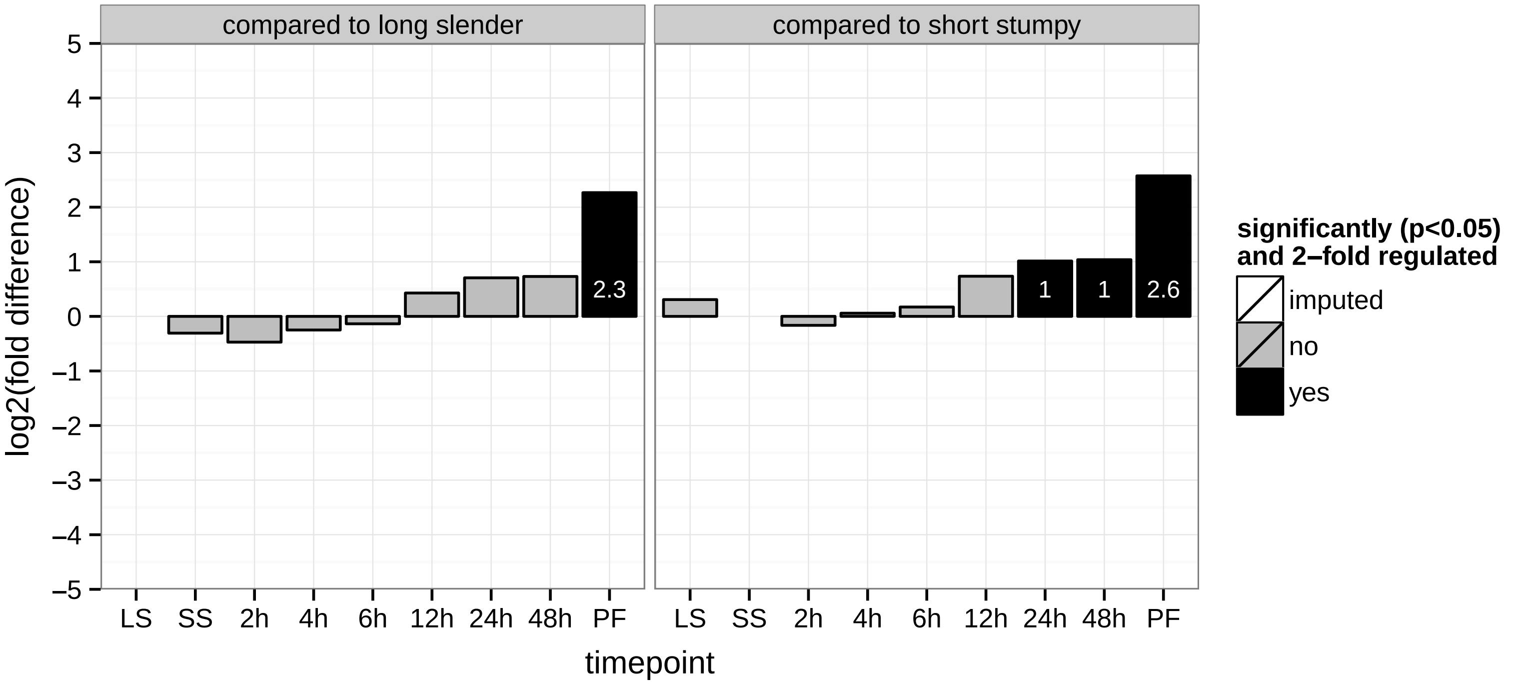
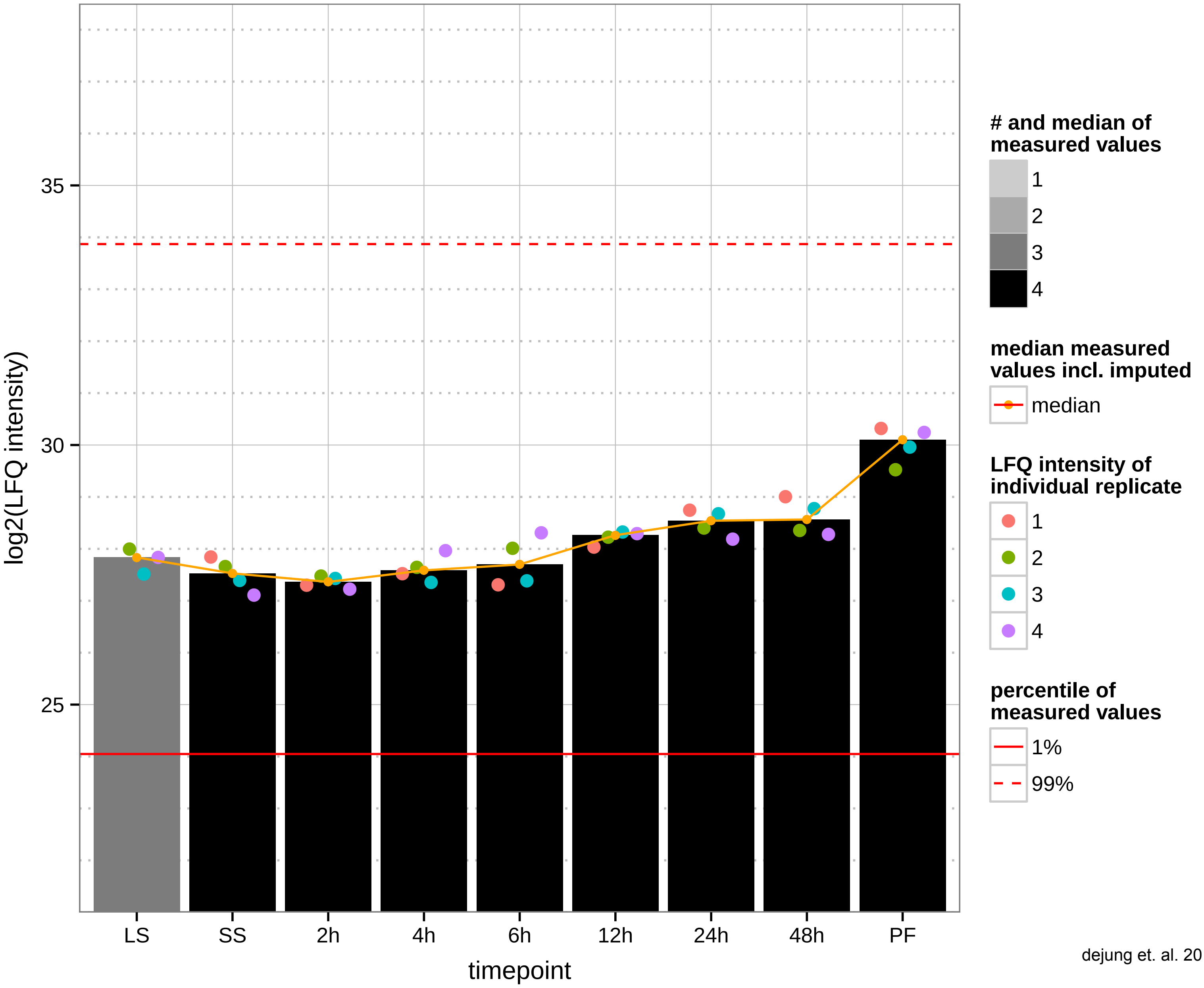
zinc finger protein 2 (ZFP2)
Tb927.11.14950
AGOF: RNA binding, nucleic acid binding, zinc ion binding
AGOC: cytoplasm
AGOP: cell differentiation, microtubule polymerization
PGOF: nucleic acid binding, protein binding, zinc ion binding
PGOC: null
PGOP: null





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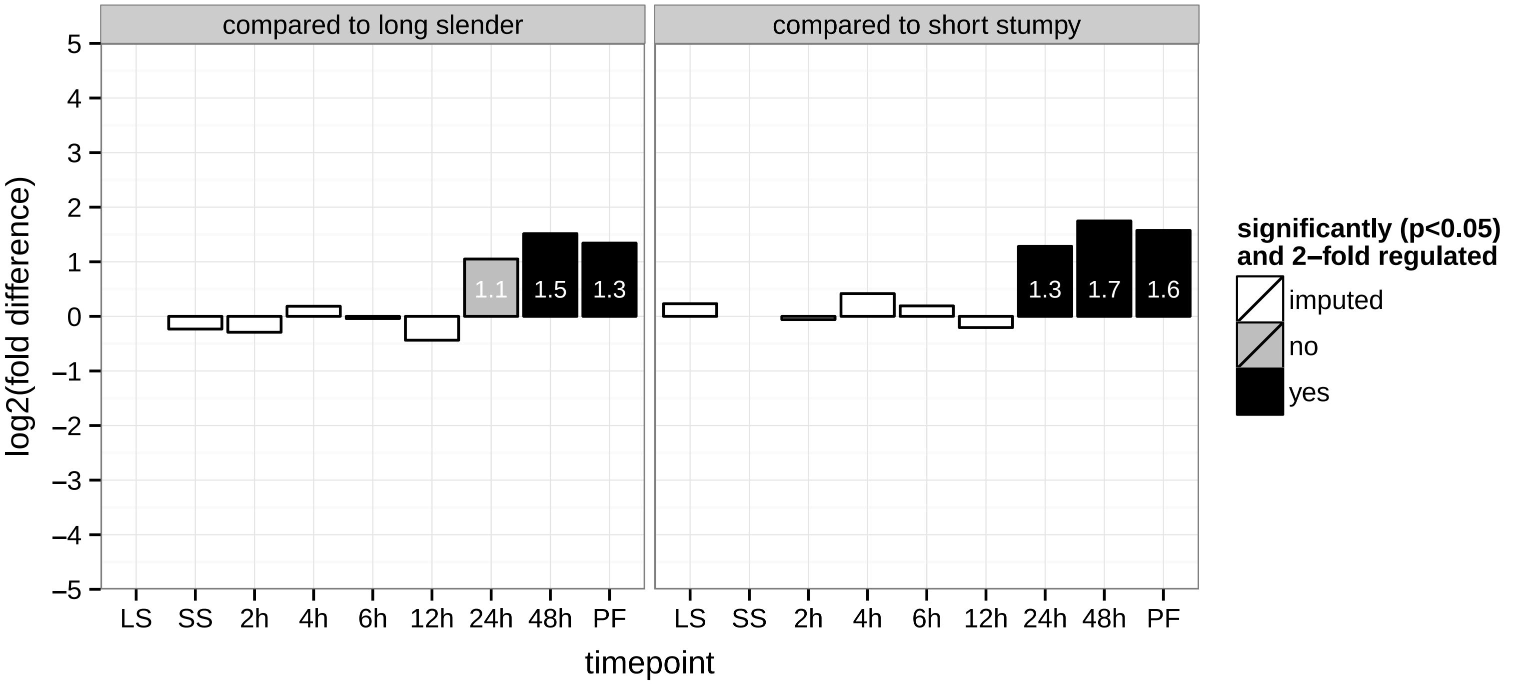
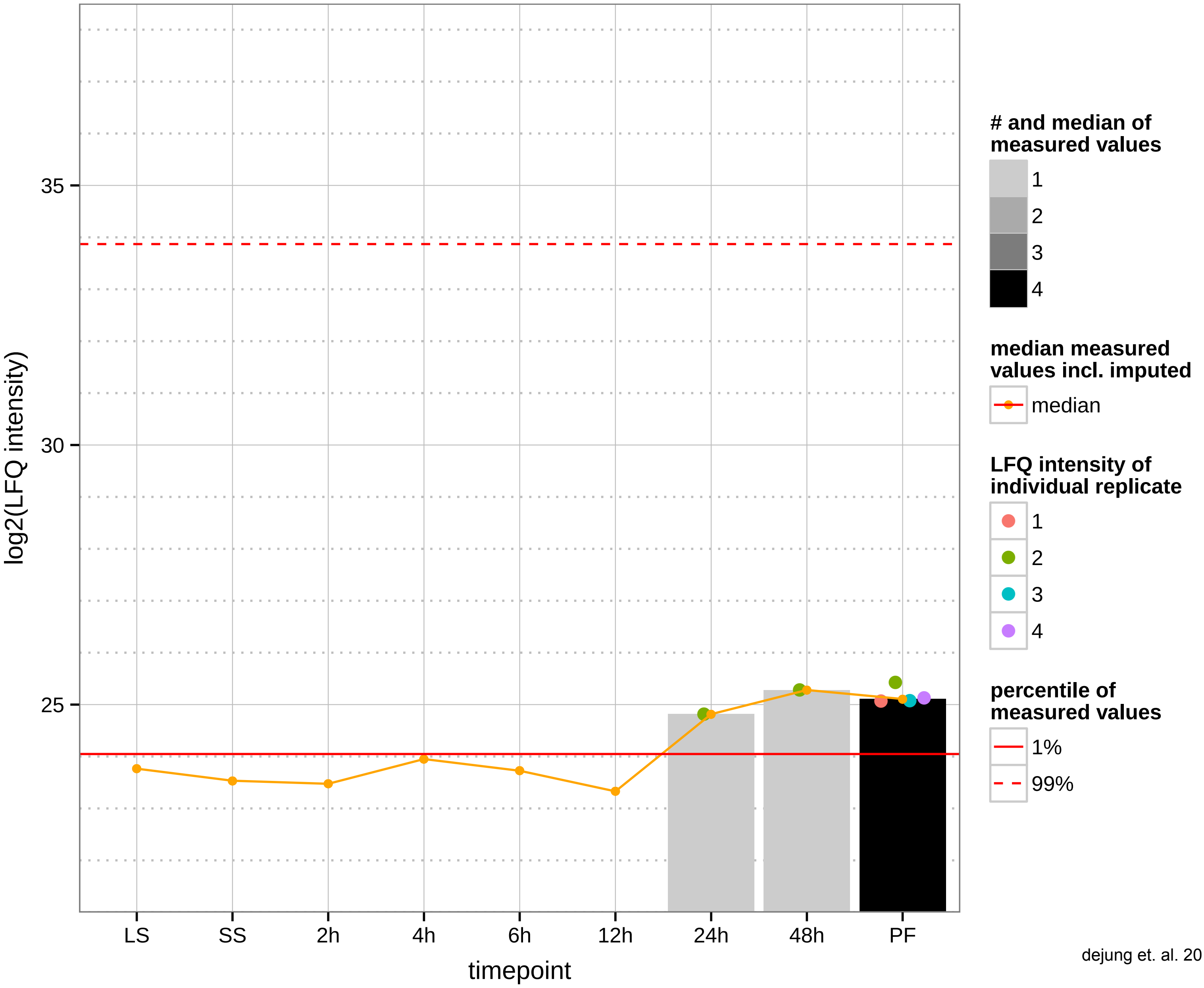
hypothetical protein, conserved
Tb927.11.15500
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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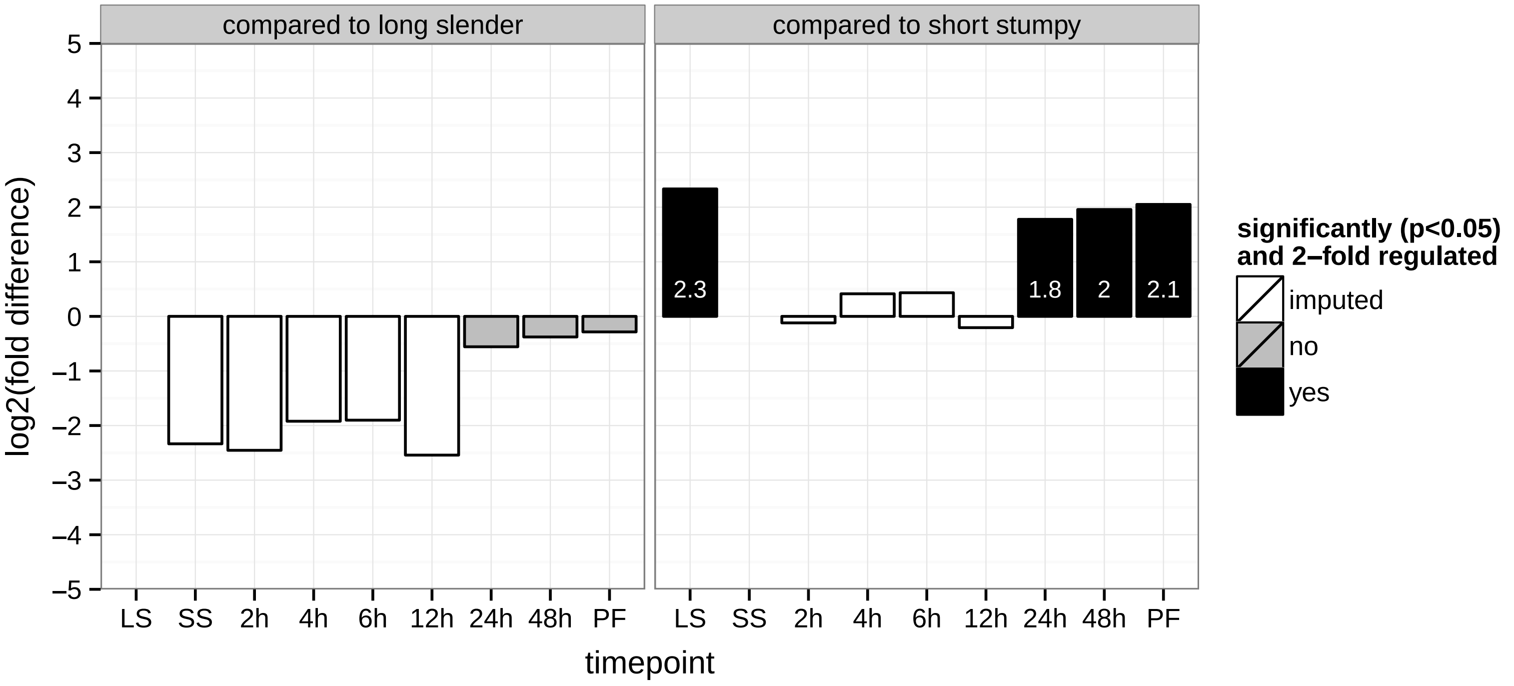
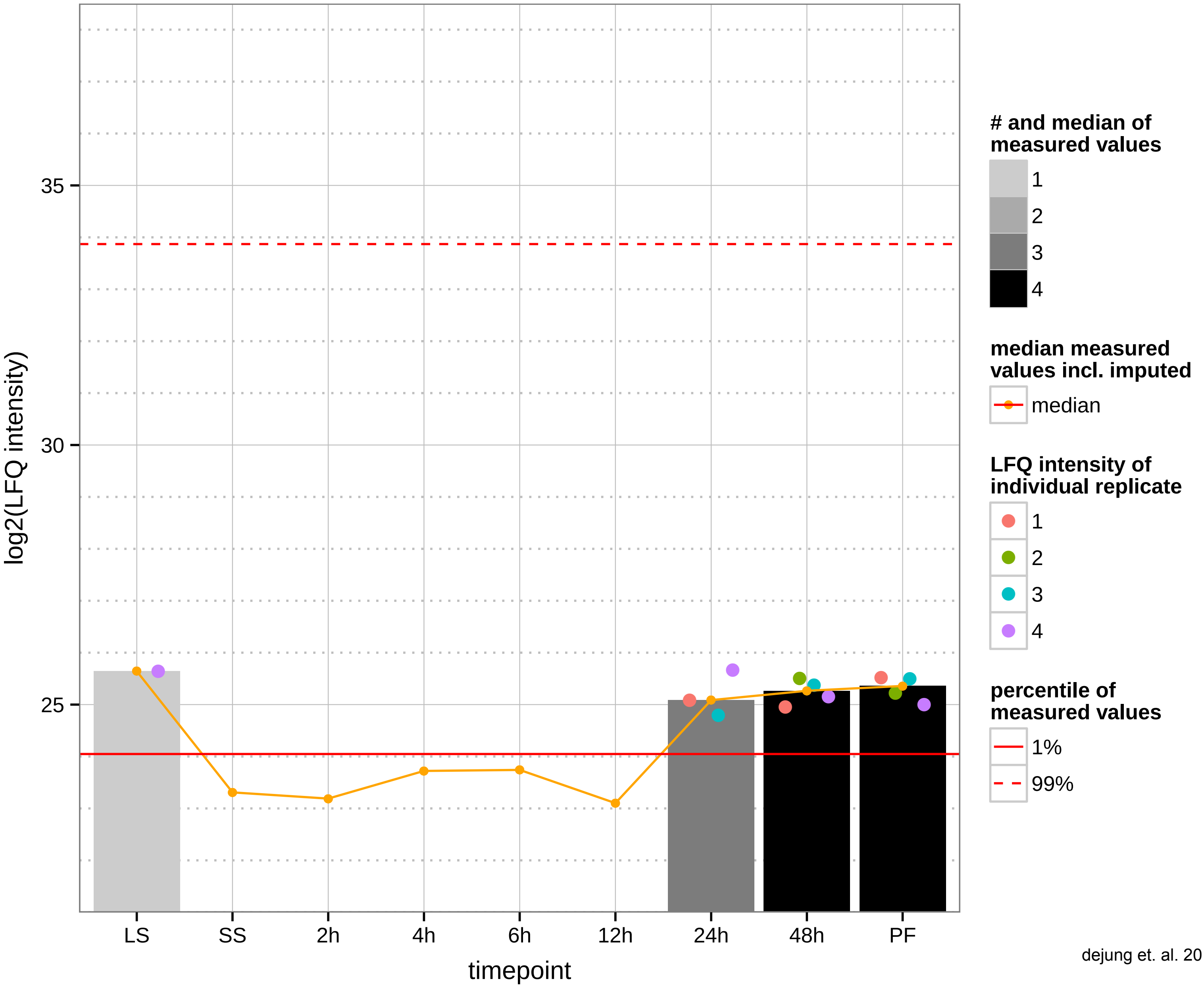
hypothetical protein, conserved
Tb927.11.15800
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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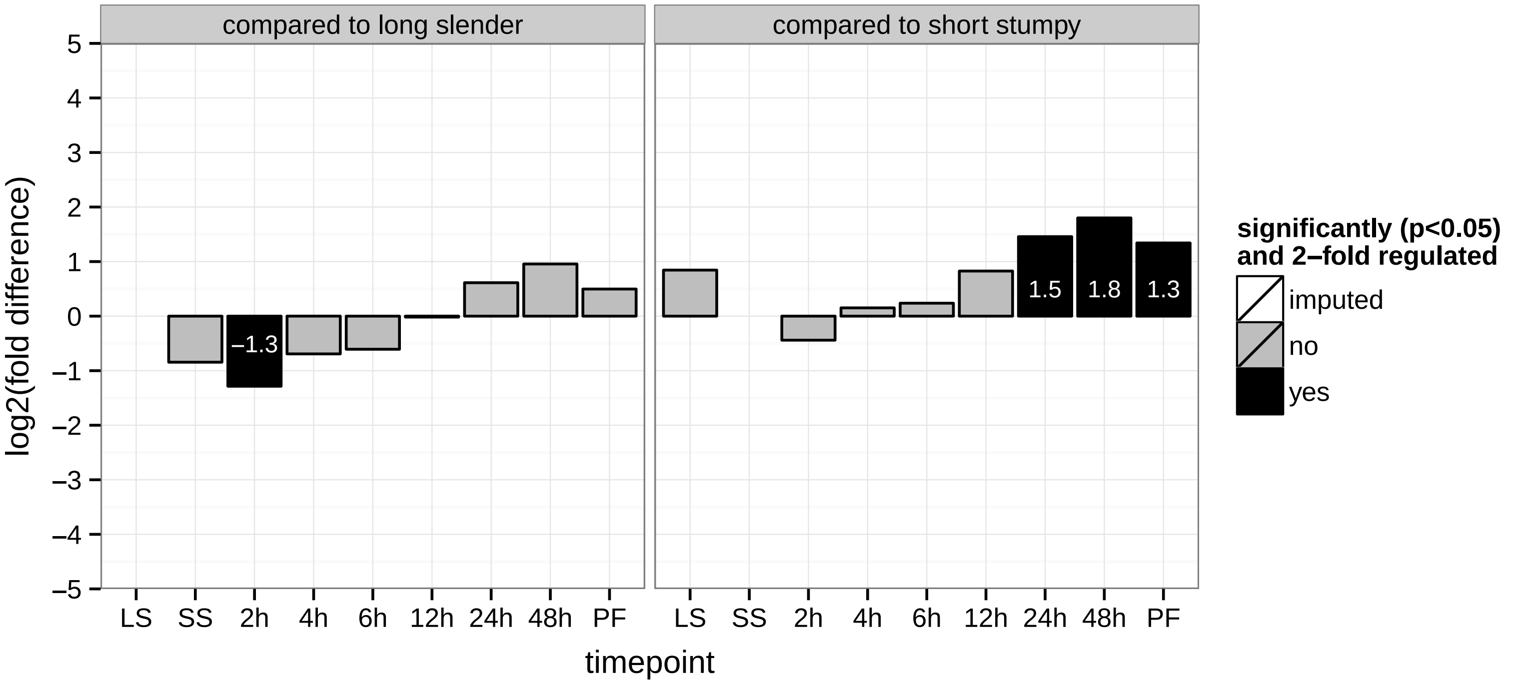
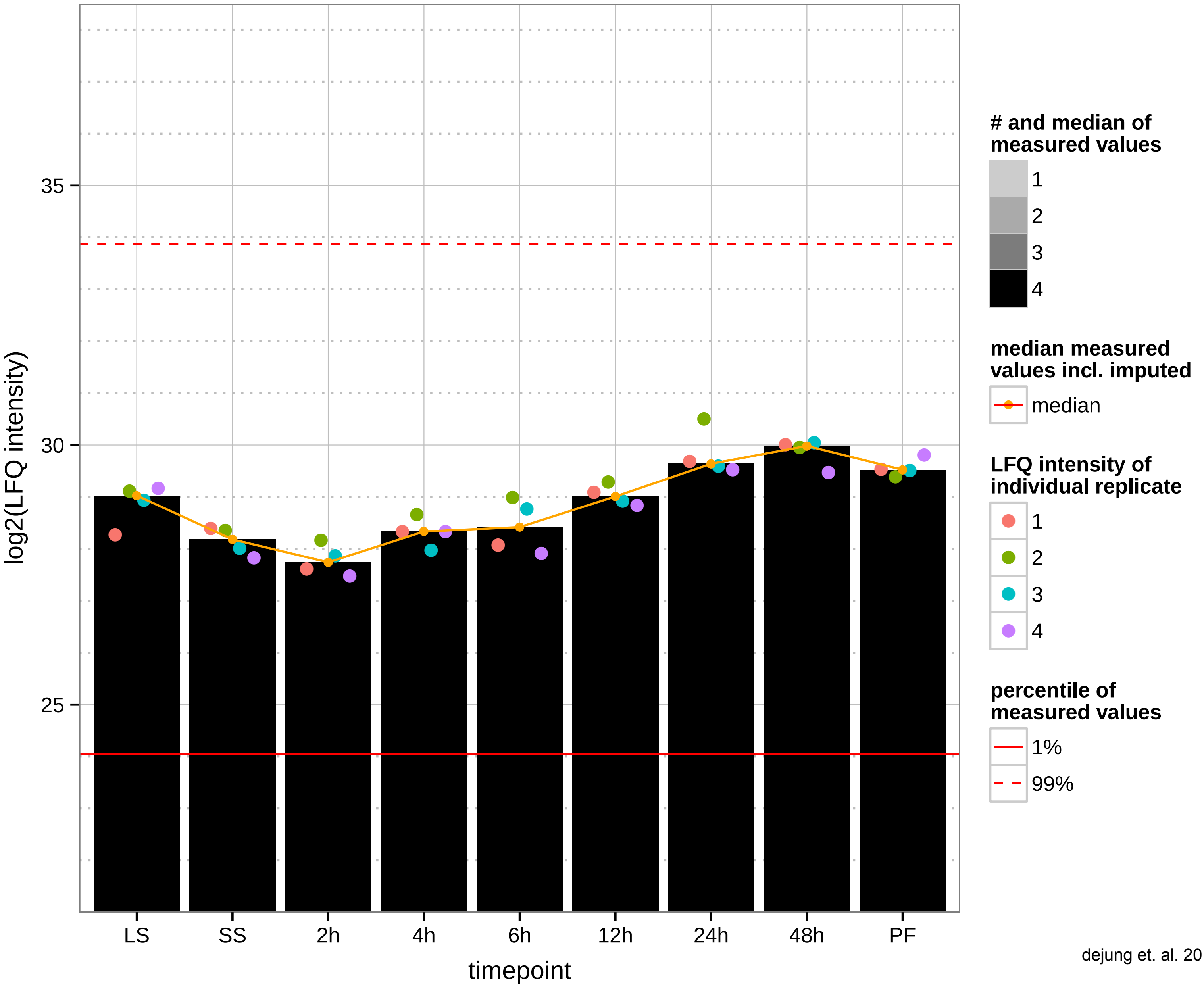
ATP binding protein–like protein
Tb927.11.16160
AGOF: glutathione–disulfide reductase activity
AGOC: null
AGOP: oxidation–reduction process
PGOF: null
PGOC: null
PGOP: null





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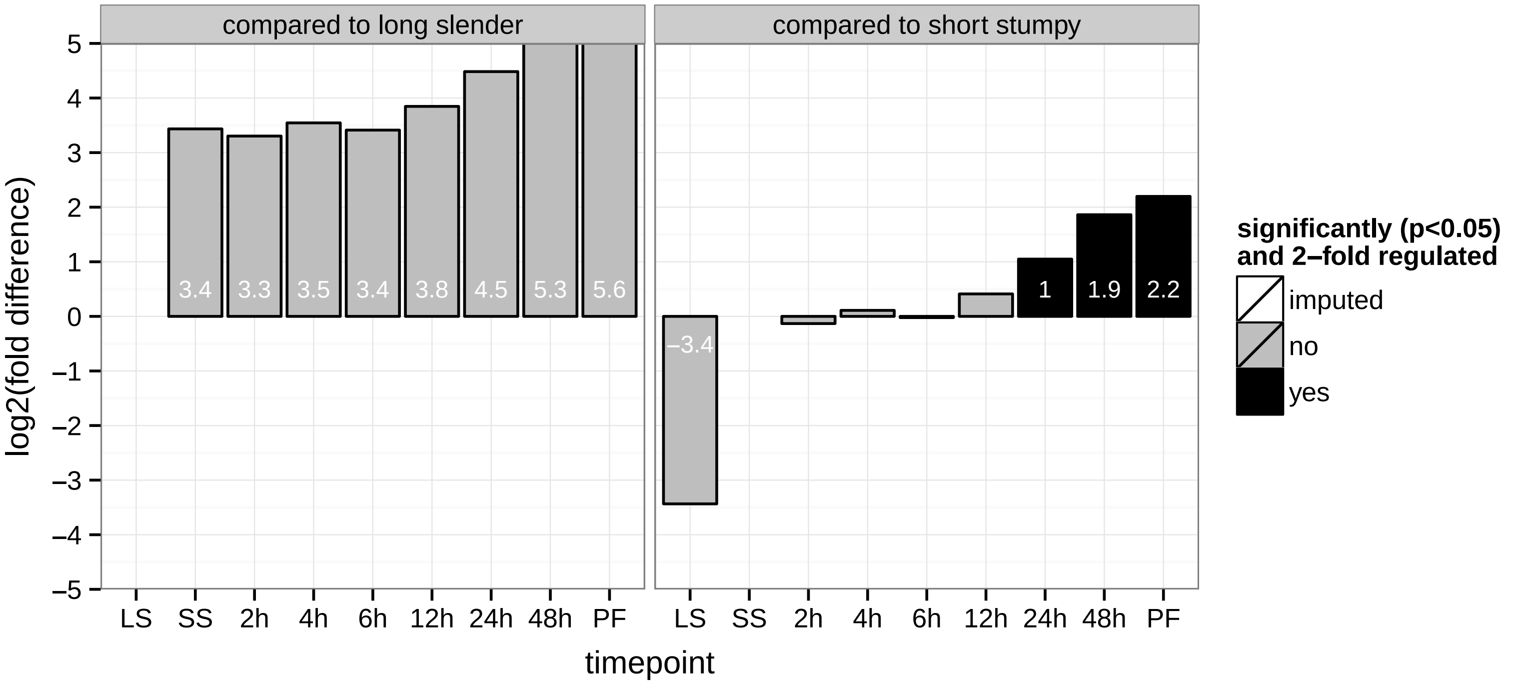
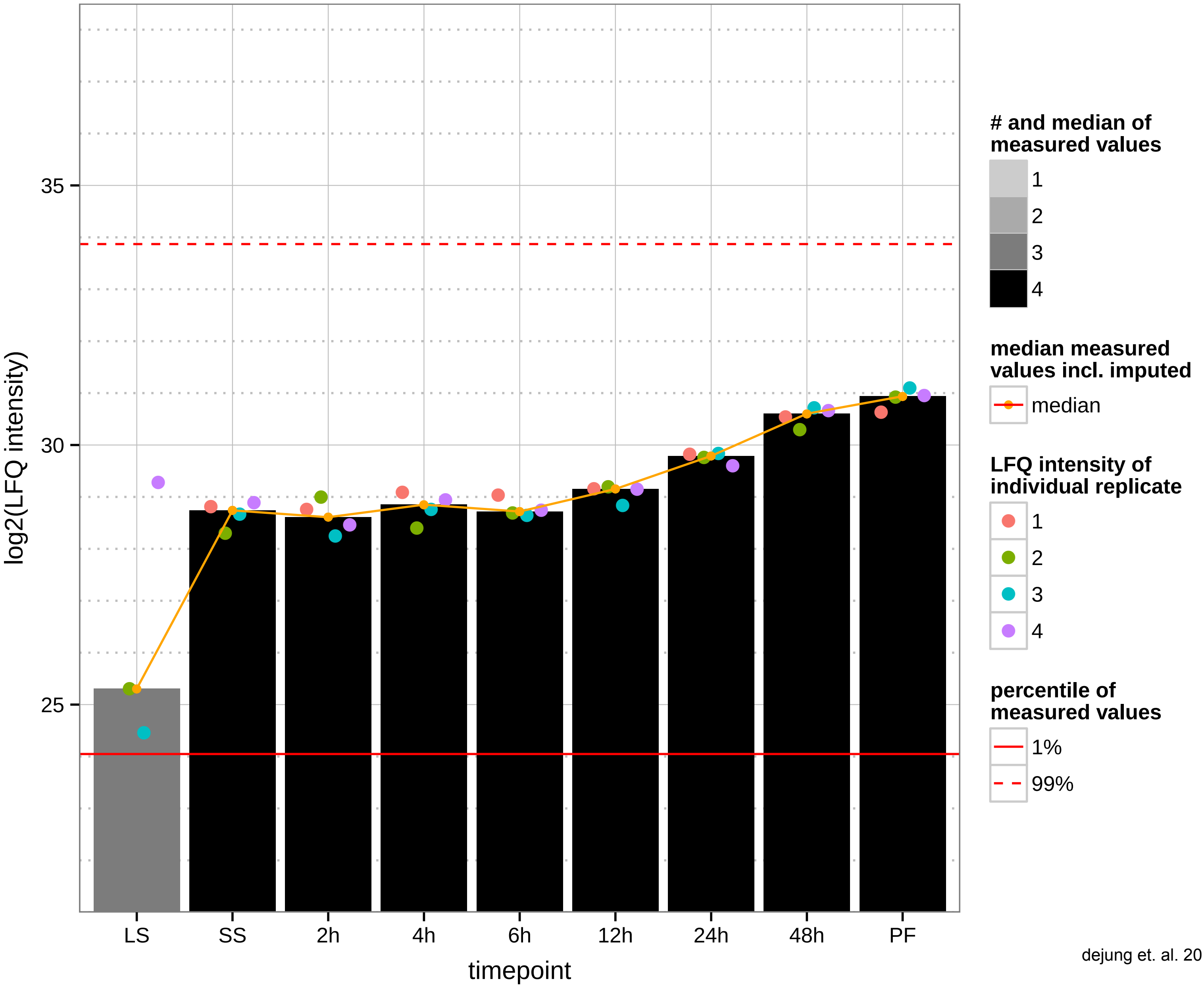
enoyl–CoA hydratase/isomerase family protein, putative
Tb927.11.16480
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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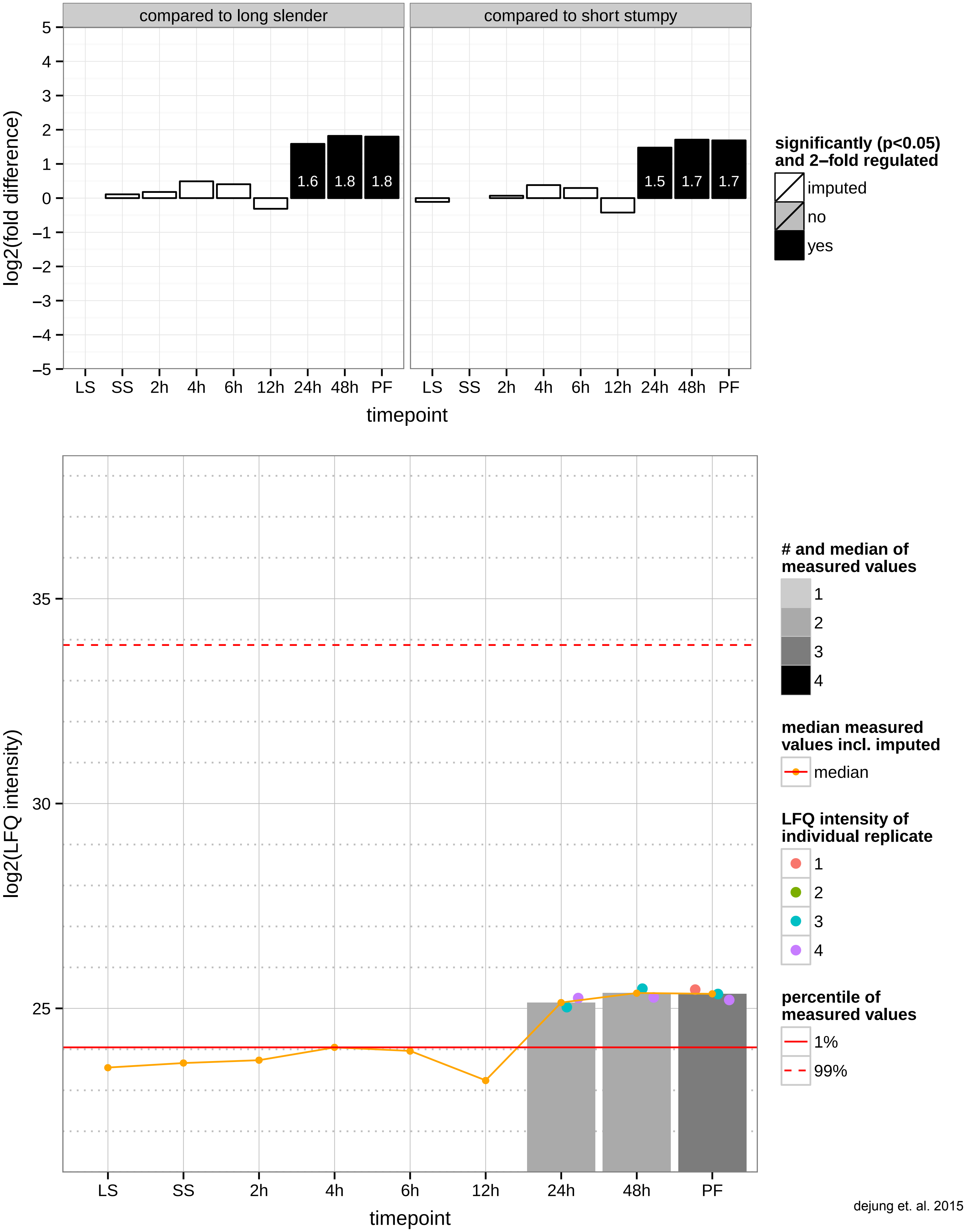
NADH dehydrogenase subunit NI8M, putative, NADH–ubiquinone oxidoreductase chain NI8M
Tb927.11.16870
AGOF: null
AGOC: mitochondrion
AGOP: mitochondrial electron transport, NADH to ubiquinone
PGOF: null
PGOC: null
PGOP: null



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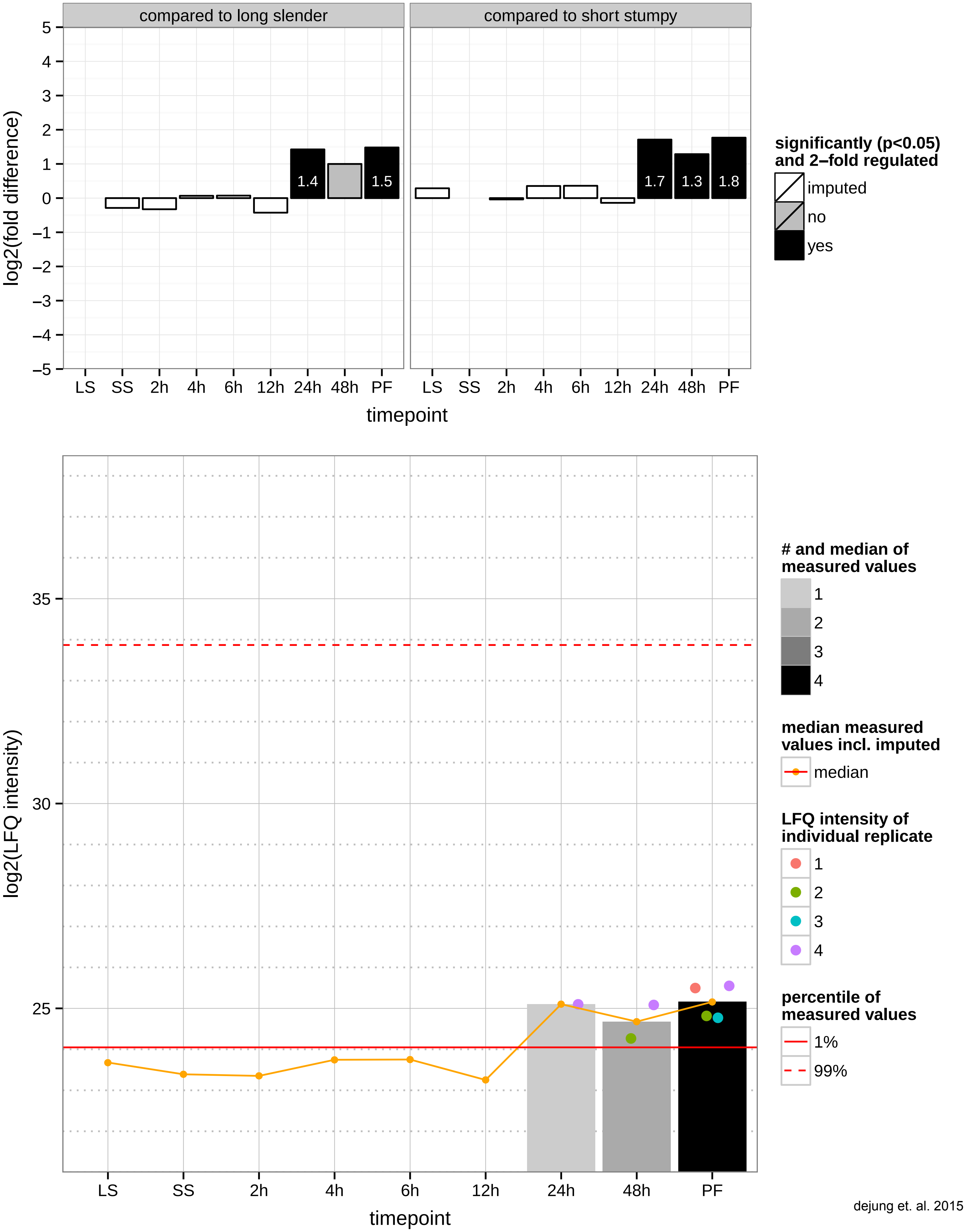
hypothetical protein, conserved
Tb927.11.16910
AGOF: null, GTP binding
AGOC: null, intracellular
AGOP: null
PGOF: GTP binding, protein binding
PGOC: null
PGOP: null



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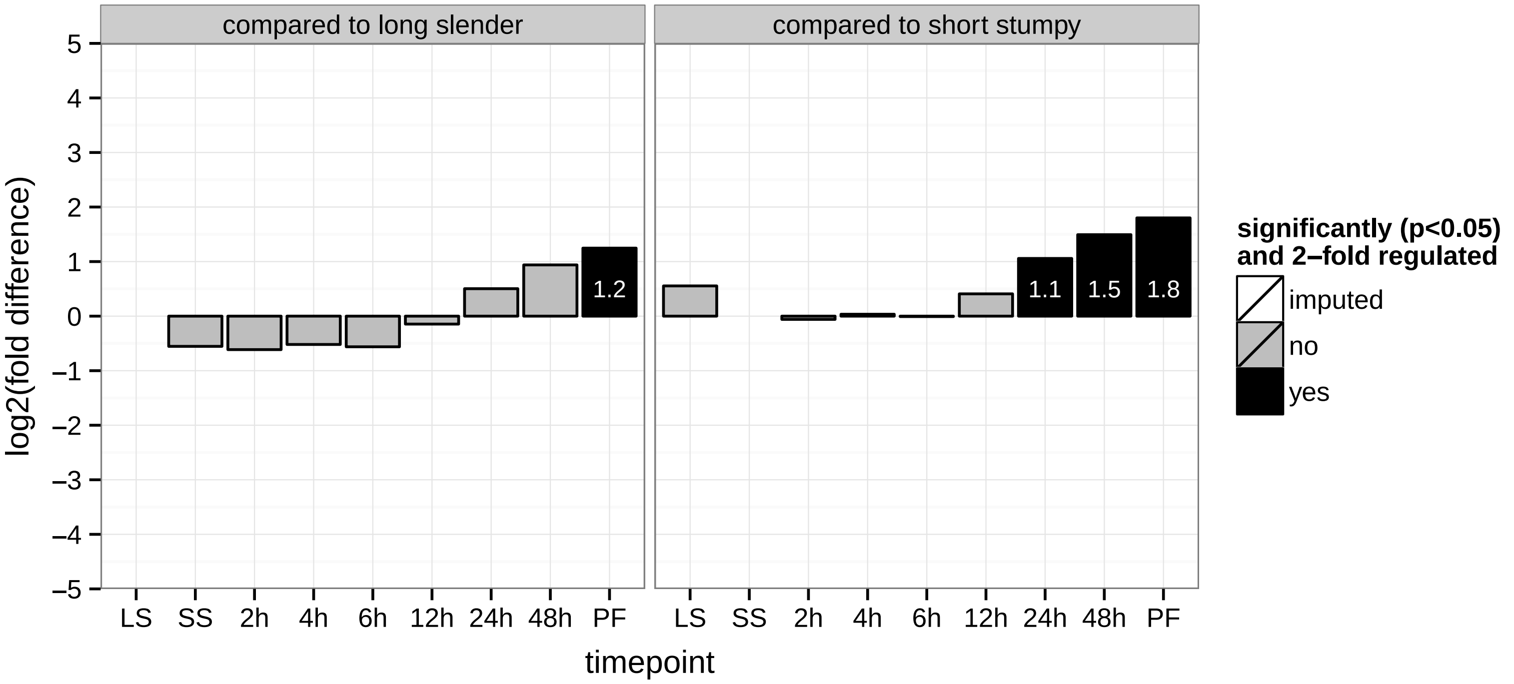
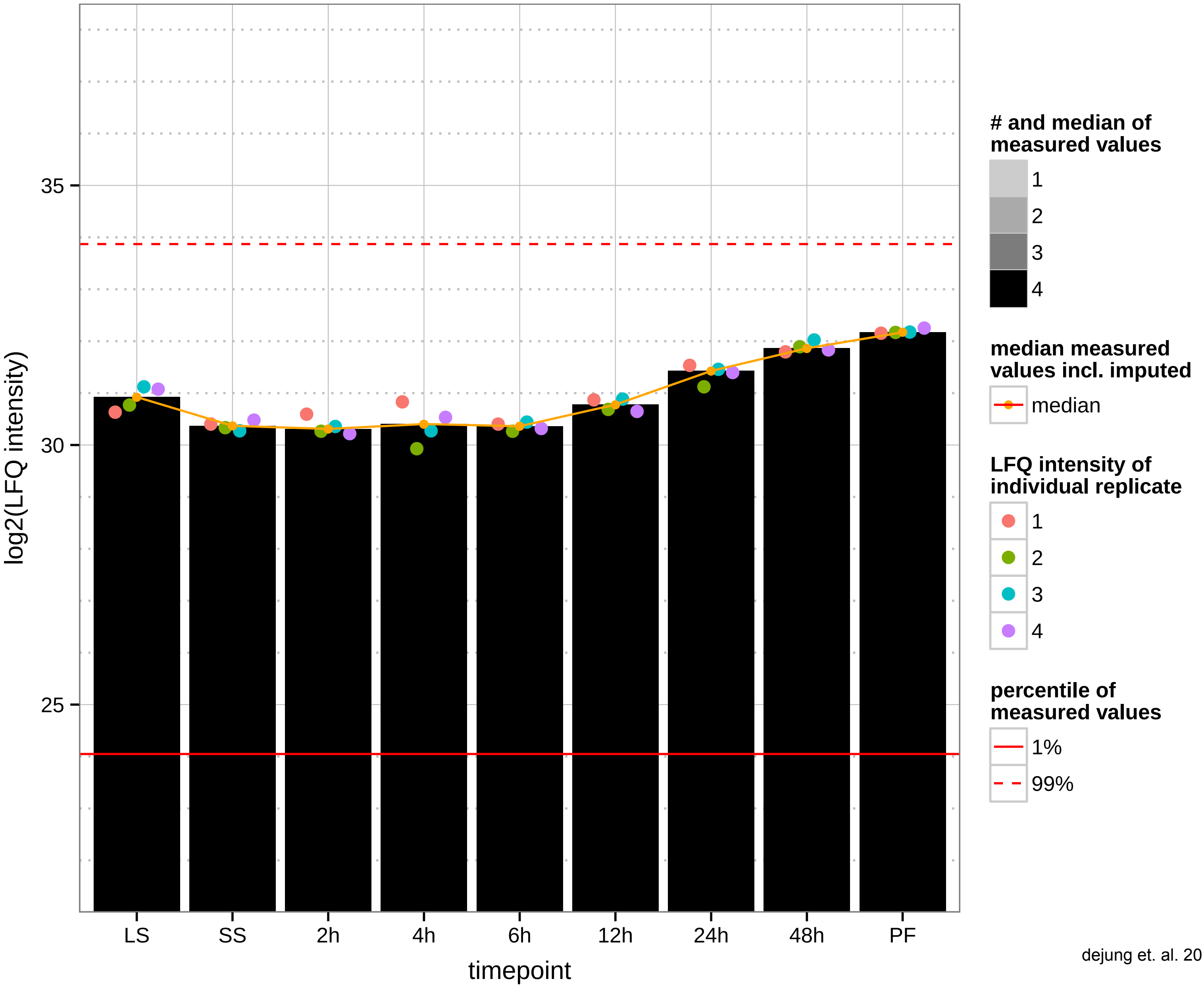
zinc finger protein family member, putative (ZC3H41)
Tb927.11.1980
AGOF: ATP binding, RNA binding, helicase activity, zinc ion binding
AGOC: null
AGOP: null
PGOF: ATP binding, helicase activity, nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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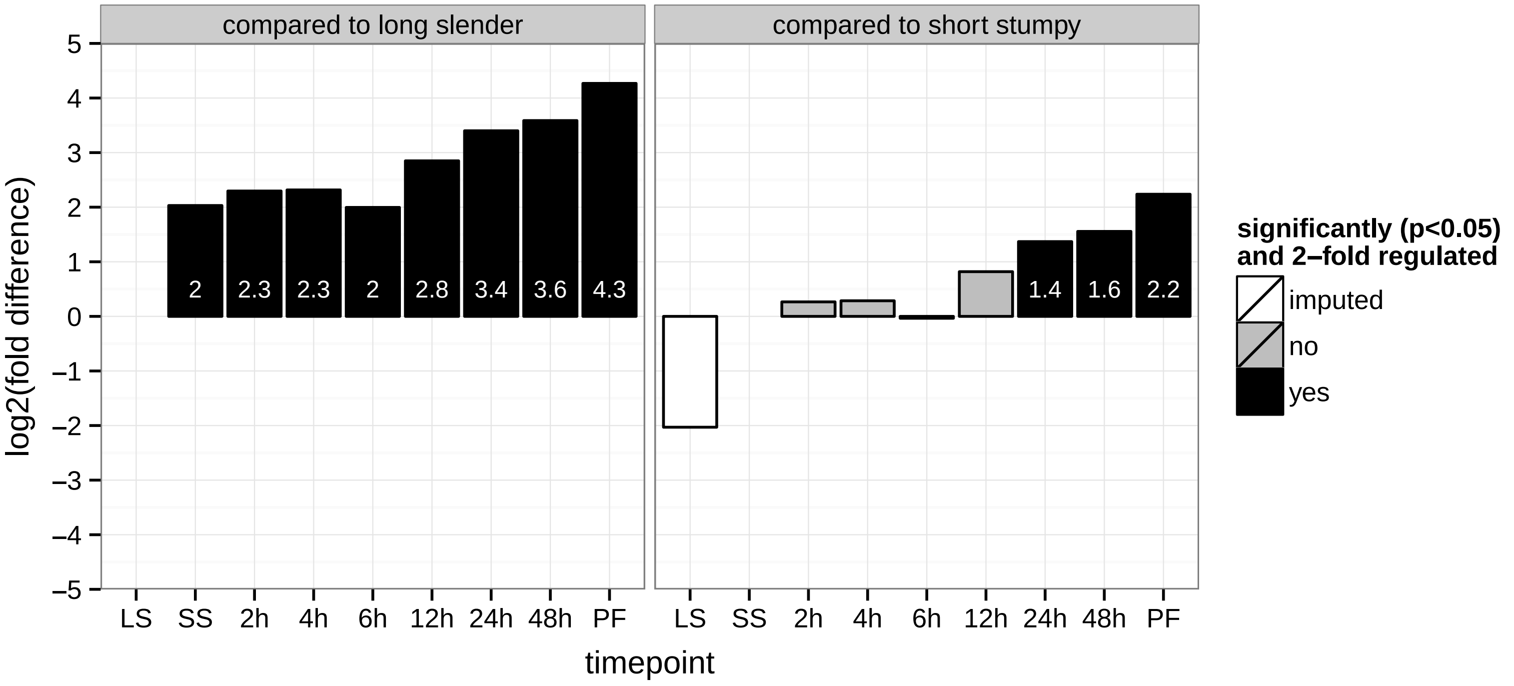
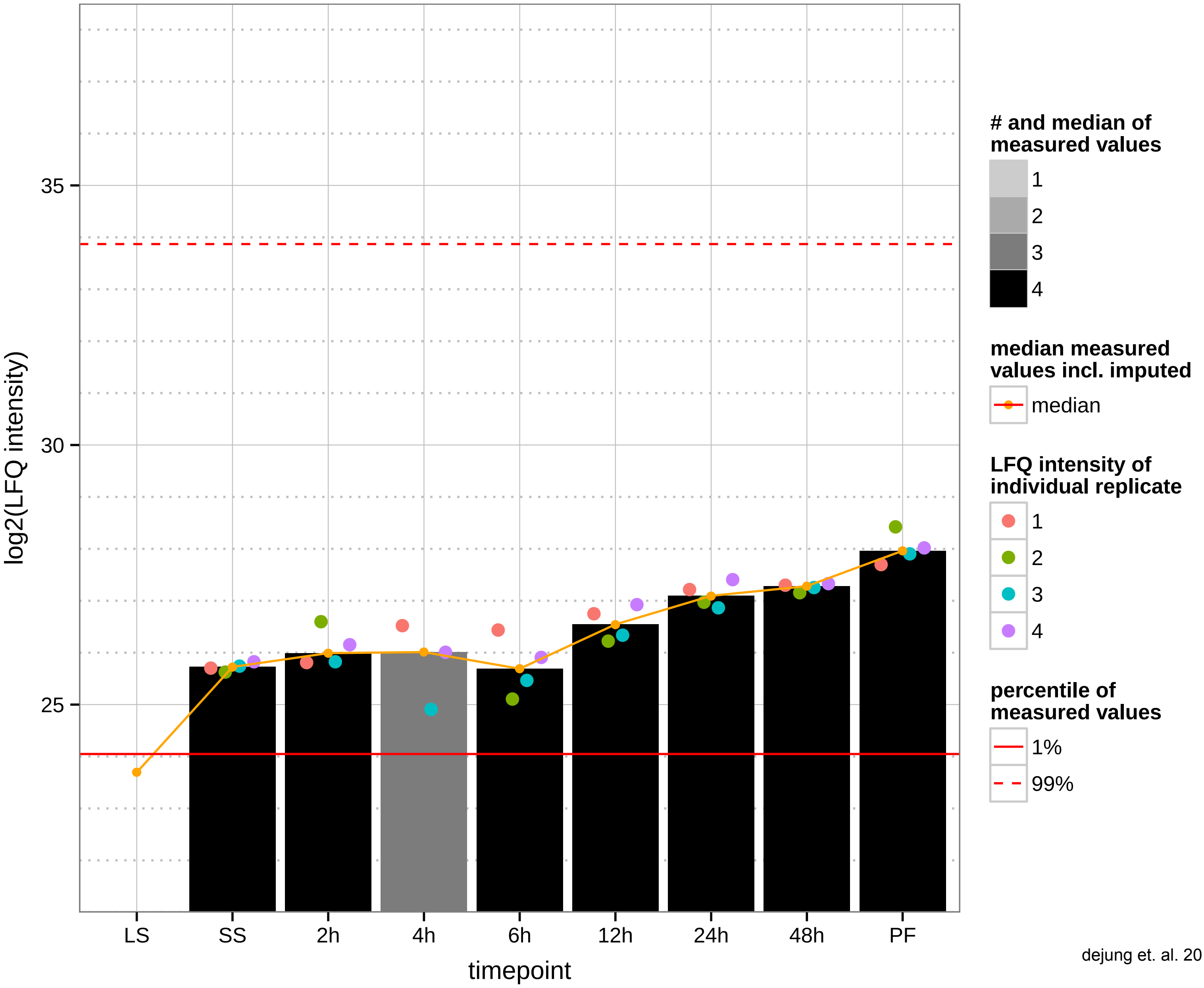
mitochondrial RNA binding complex 1 subunit, kinteoplast poly(A) polymerase complex 1 subunit, mitochondrial edited mRNA
Tb927.11.2530
AGOF: RNA binding
AGOC: mitochondrion
AGOP: RNA polyadenylation, mRNA stabilization
PGOF: null
PGOC: null
PGOP: null





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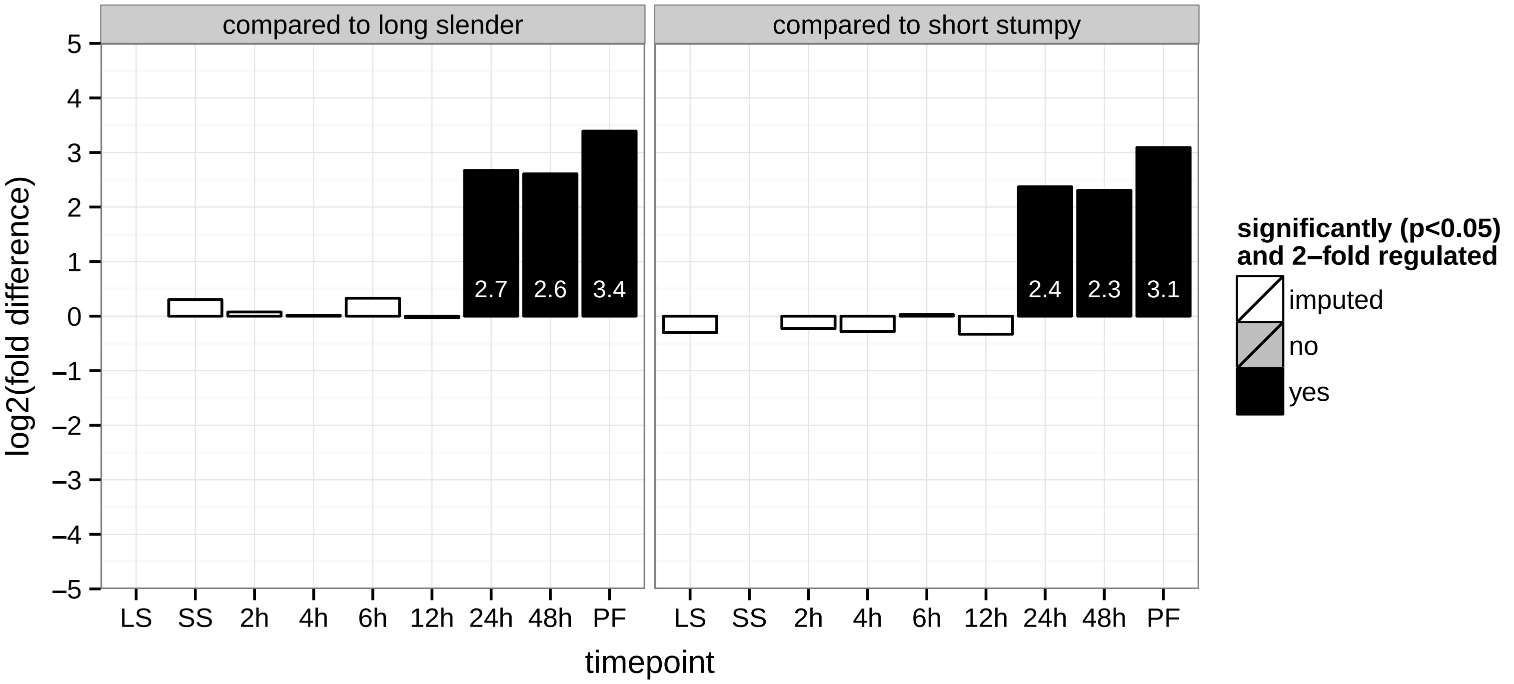
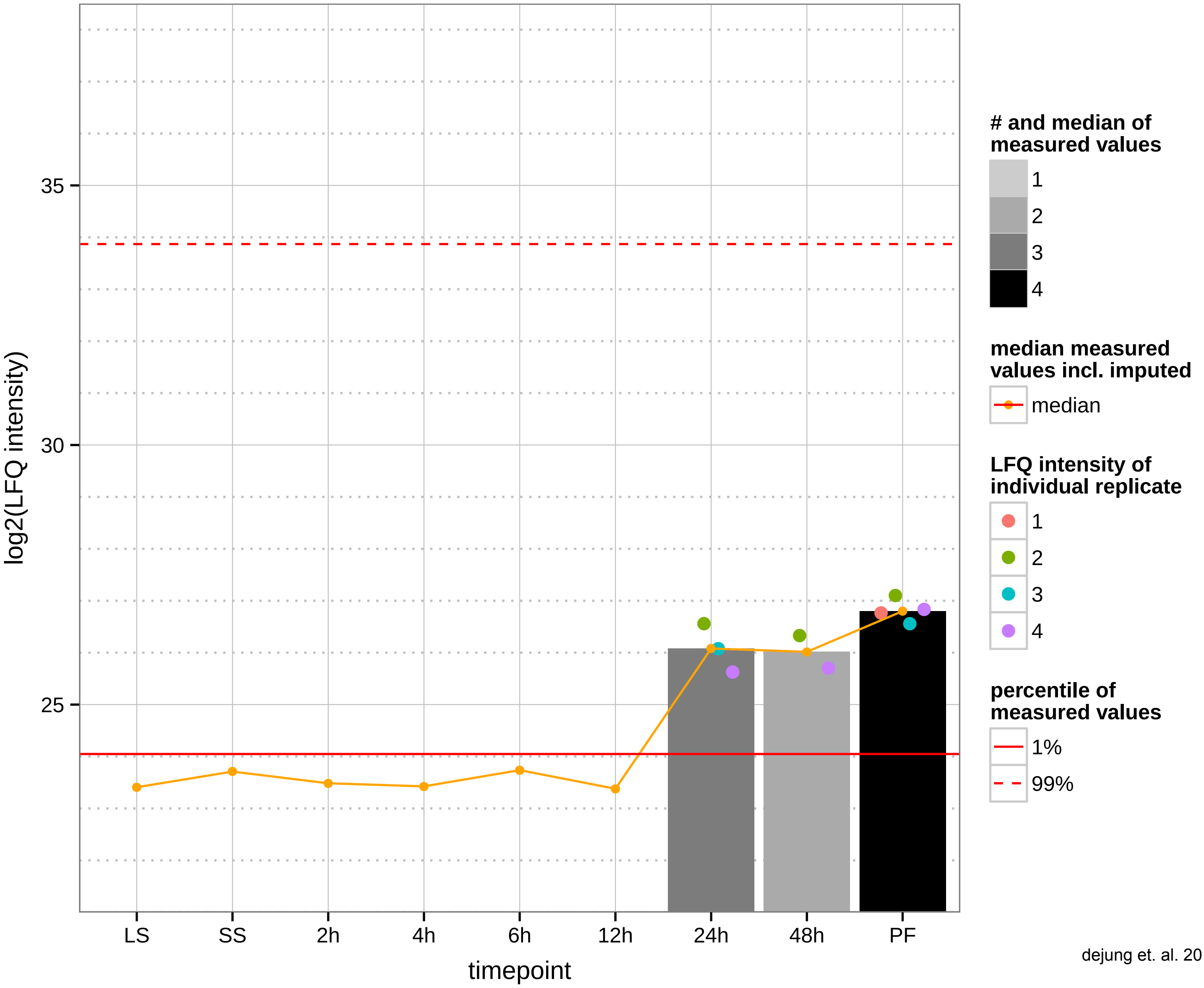
hypothetical protein, conserved
Tb927.11.2930
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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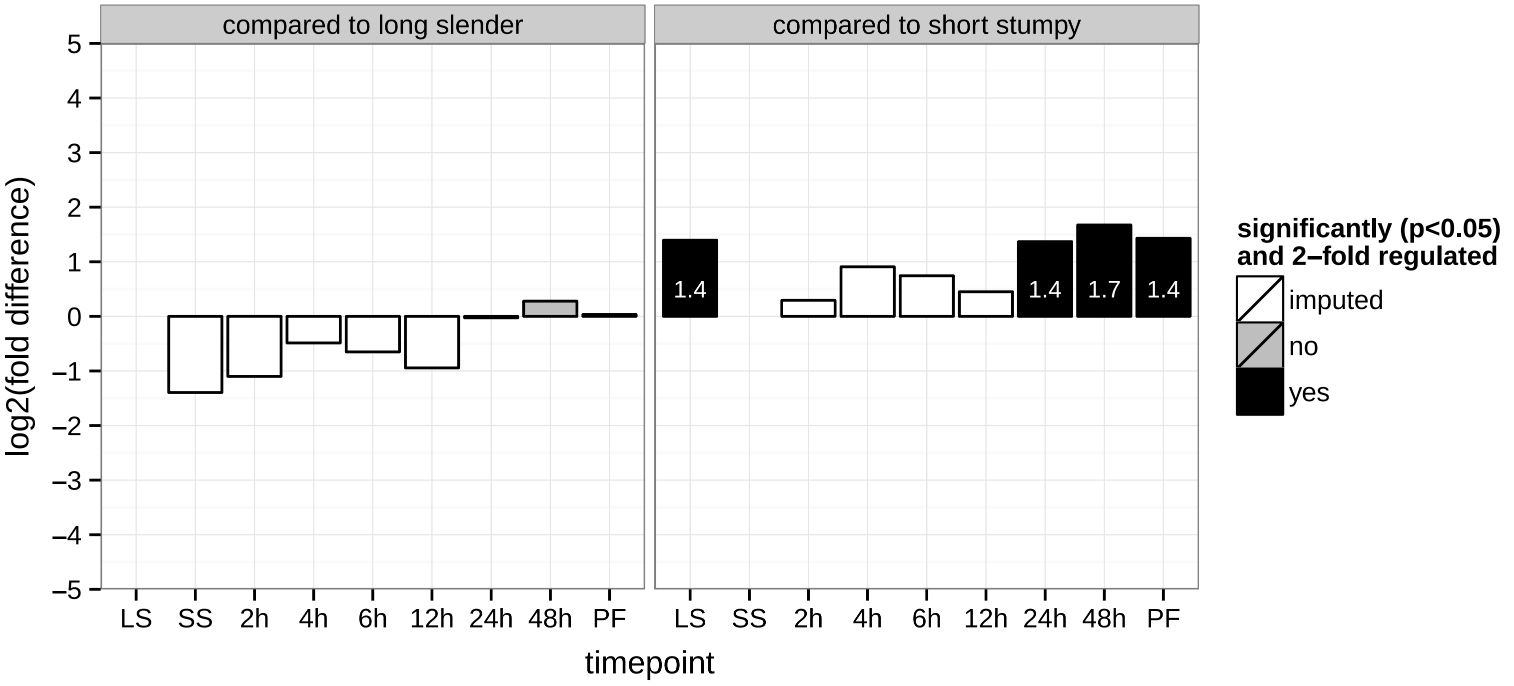
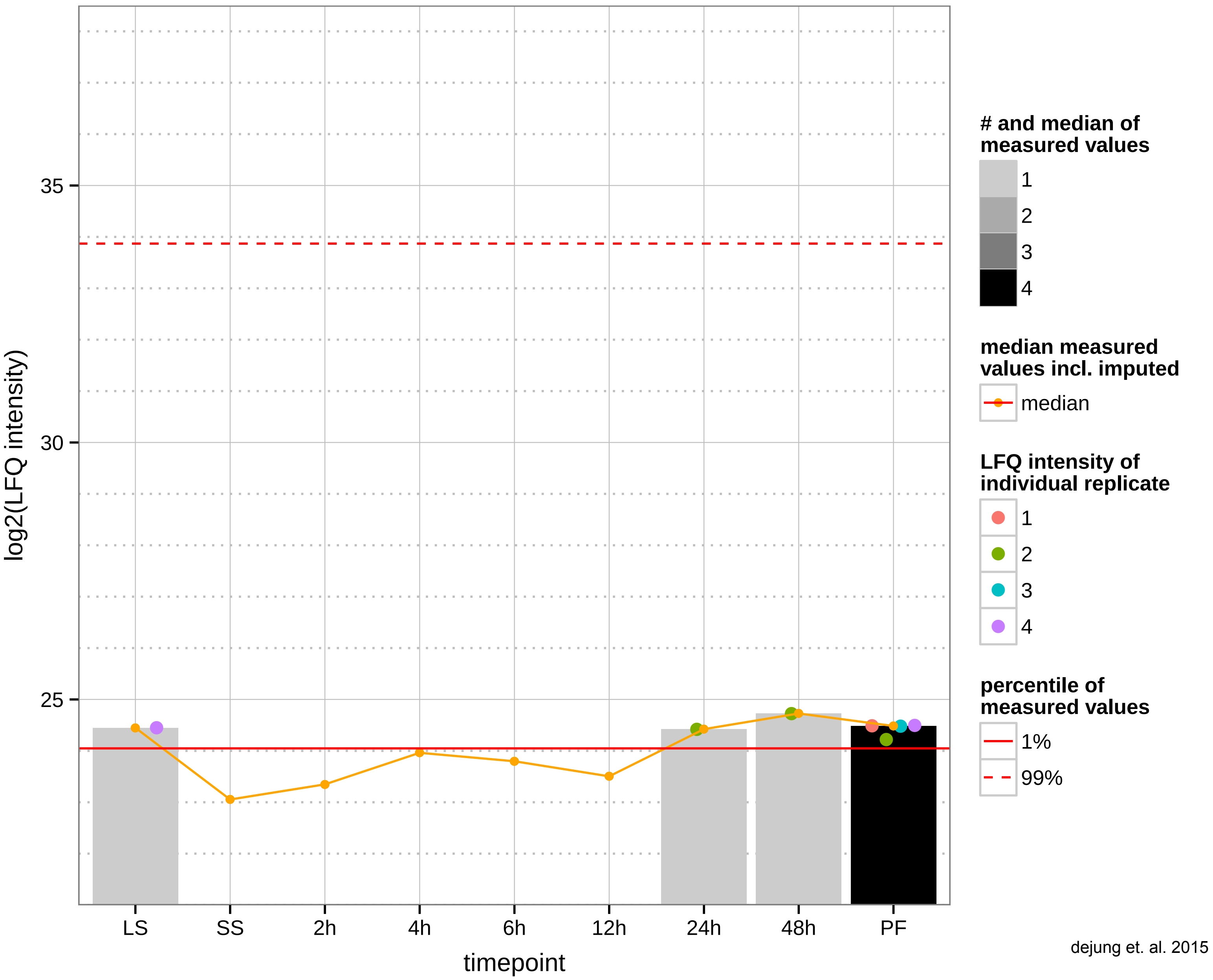
hypothetical protein, conserved
Tb927.11.4180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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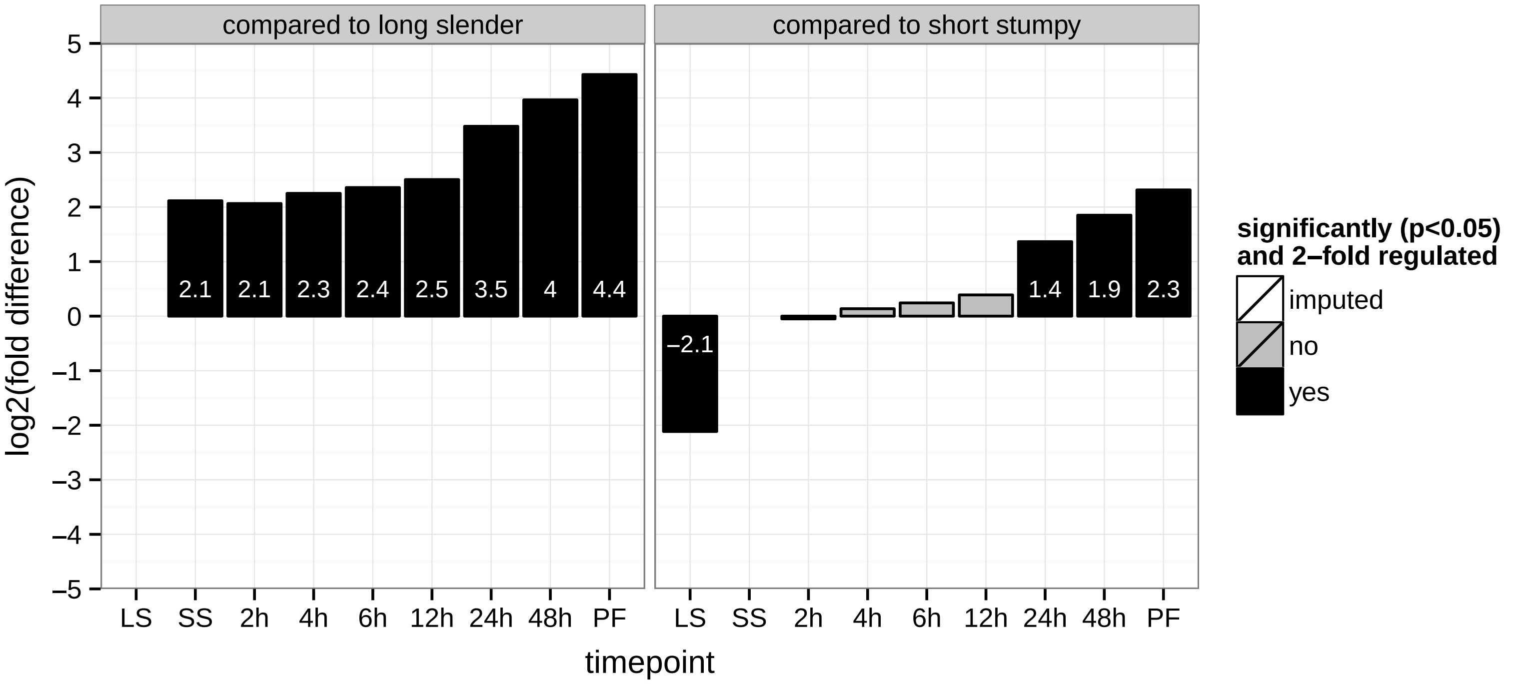
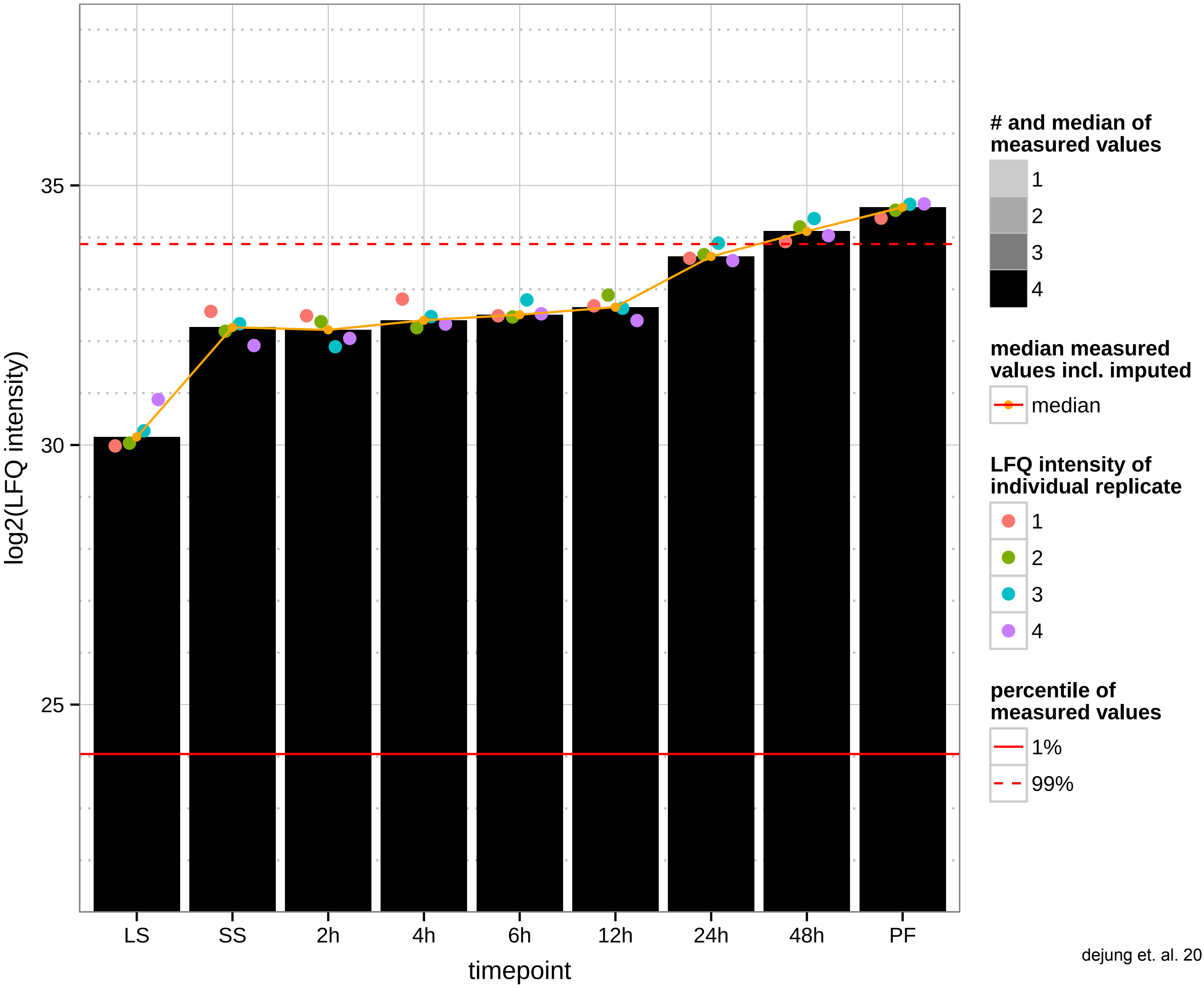
prostaglandin f synthase
Tb927.11.4700
AGOF: D–arabinose 1–dehydrogenase [NAD(P)+] activity, aldo–keto reductase (NADP) activity
AGOC: null
AGOP: D–arabinose catabolic process, oxidation–reduction process
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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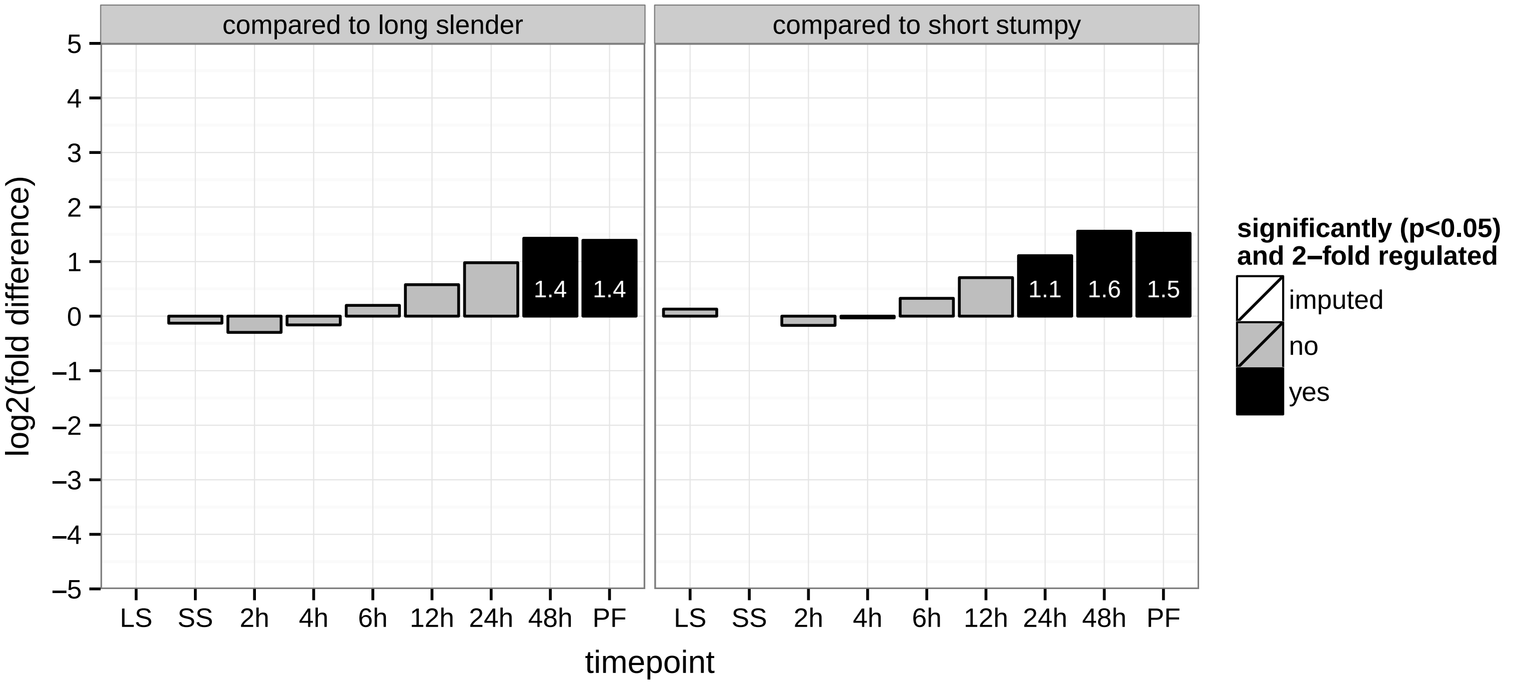
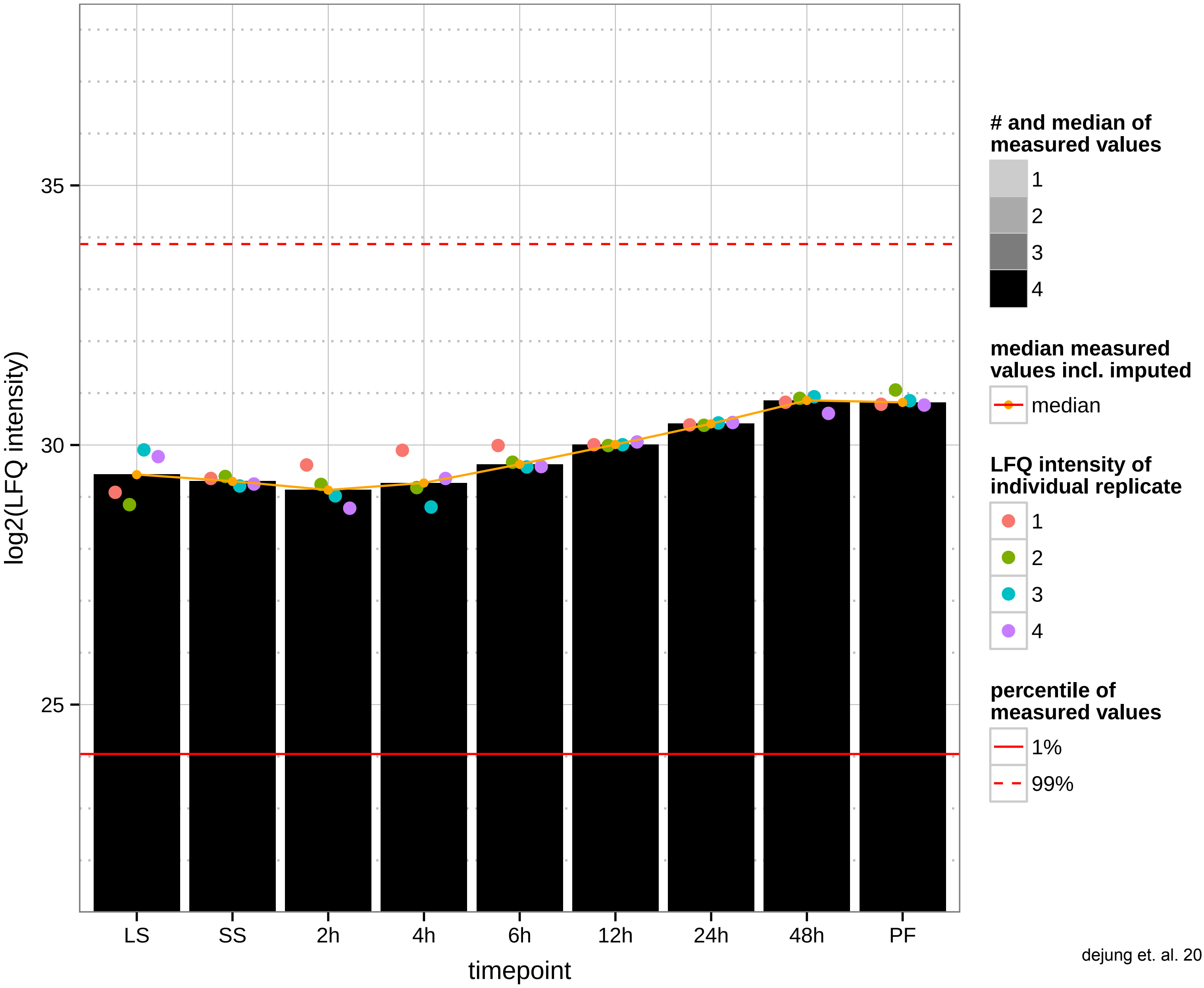
predicted ankyrin repeat family protein
Tb927.11.4910
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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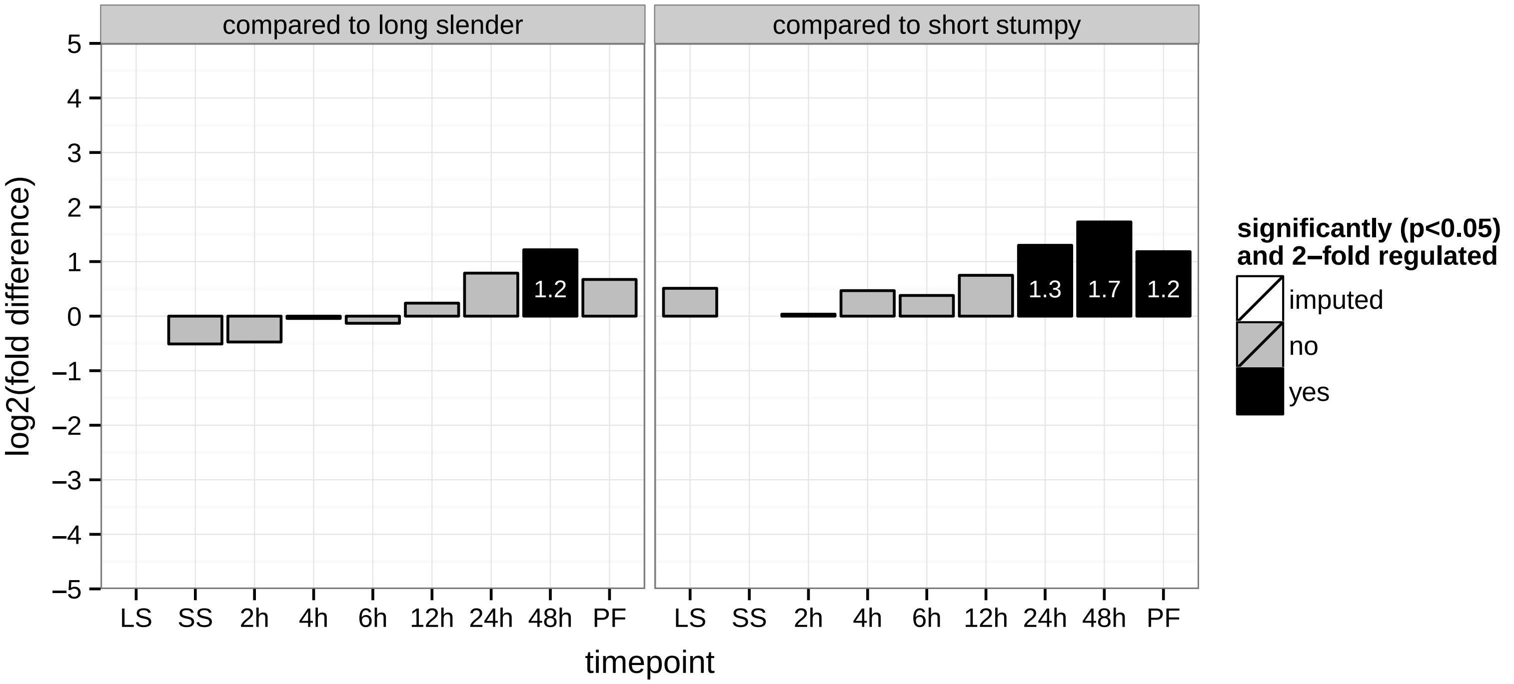
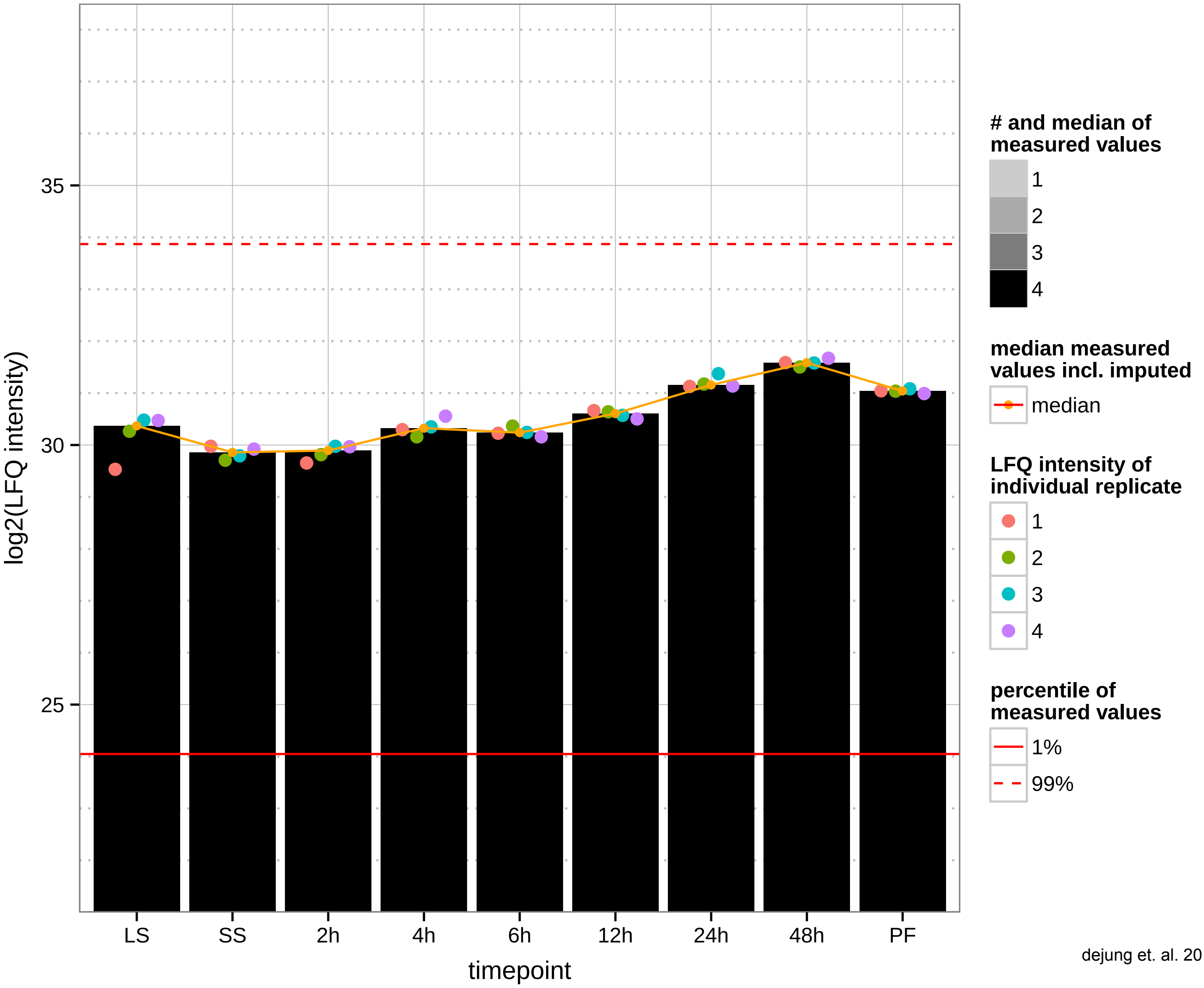
RNA–binding protein, UBP2 (UBP2)
Tb927.11.510
AGOF: RNA binding, mRNA binding
AGOC: cytoplasm, nucleus
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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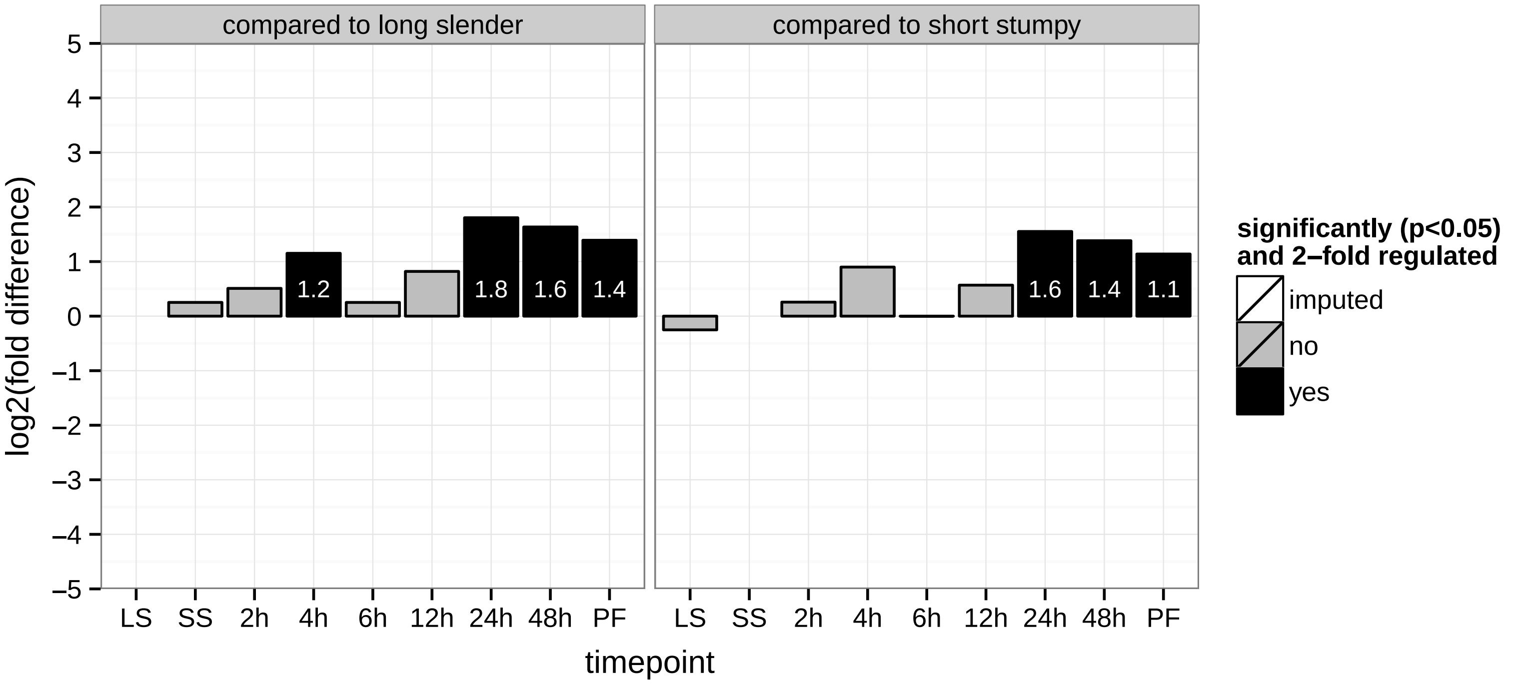
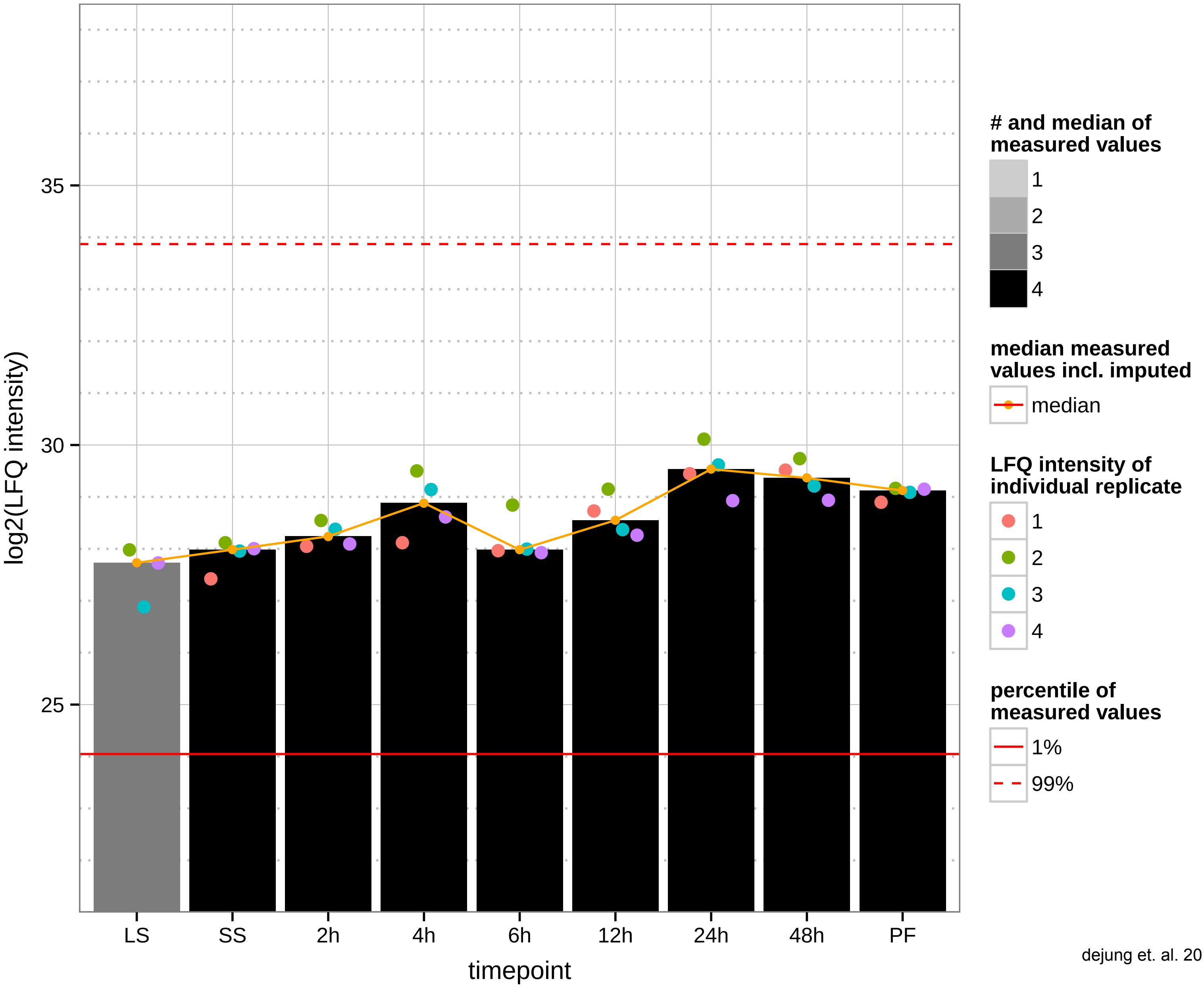
hypothetical protein, conserved
Tb927.11.5600
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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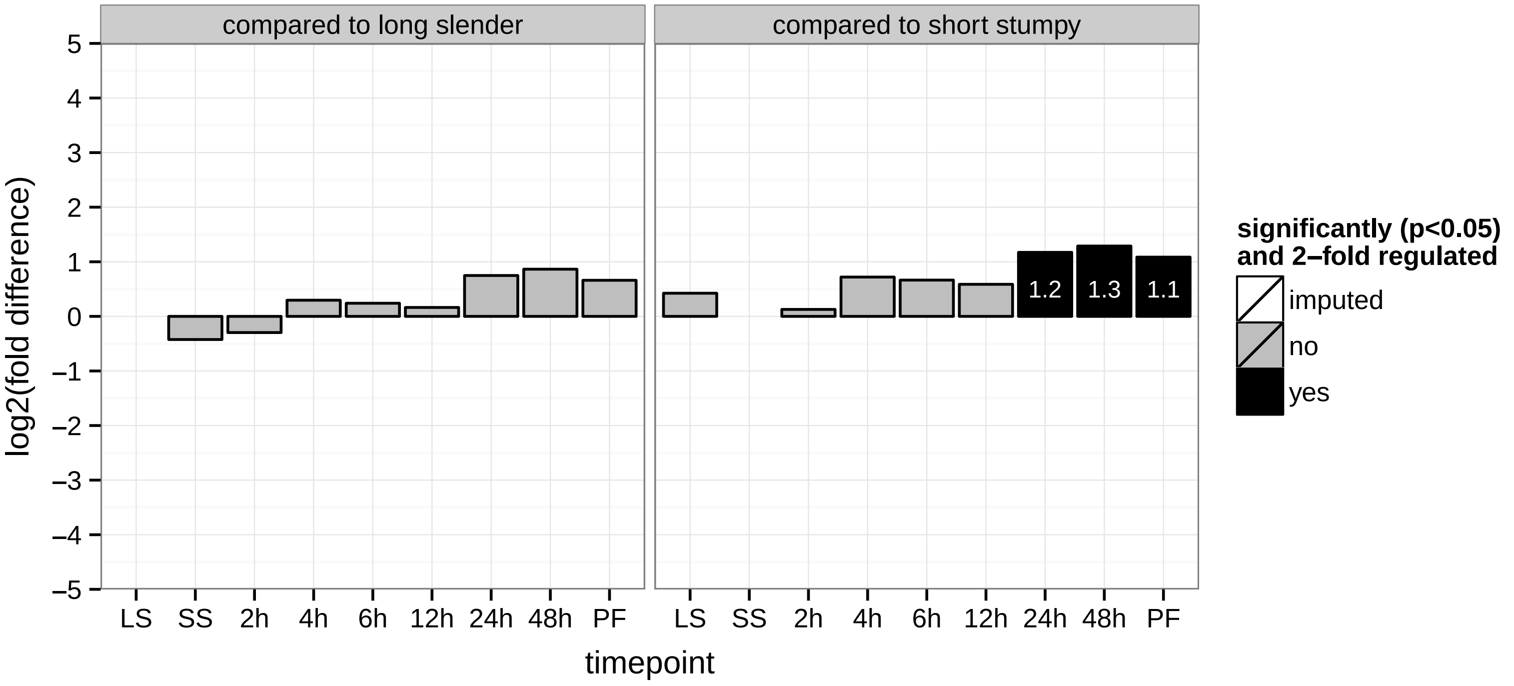
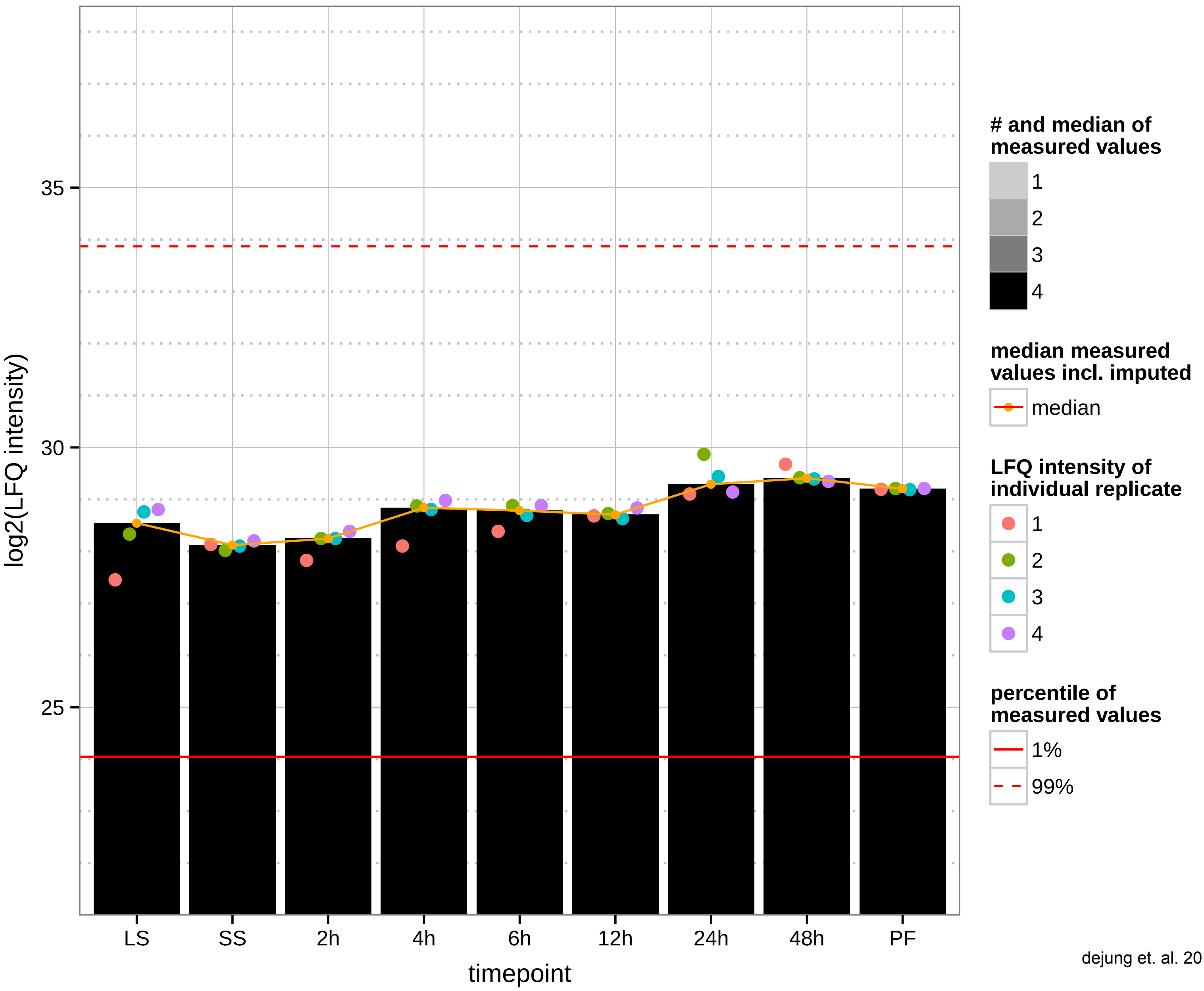
Protein translation factor SUI1 homolog, putative
Tb927.11.5840
AGOF: translation initiation factor activity
AGOC: null
AGOP: translation, translational initiation
PGOF: translation initiation factor activity
PGOC: null
PGOP: translational initiation





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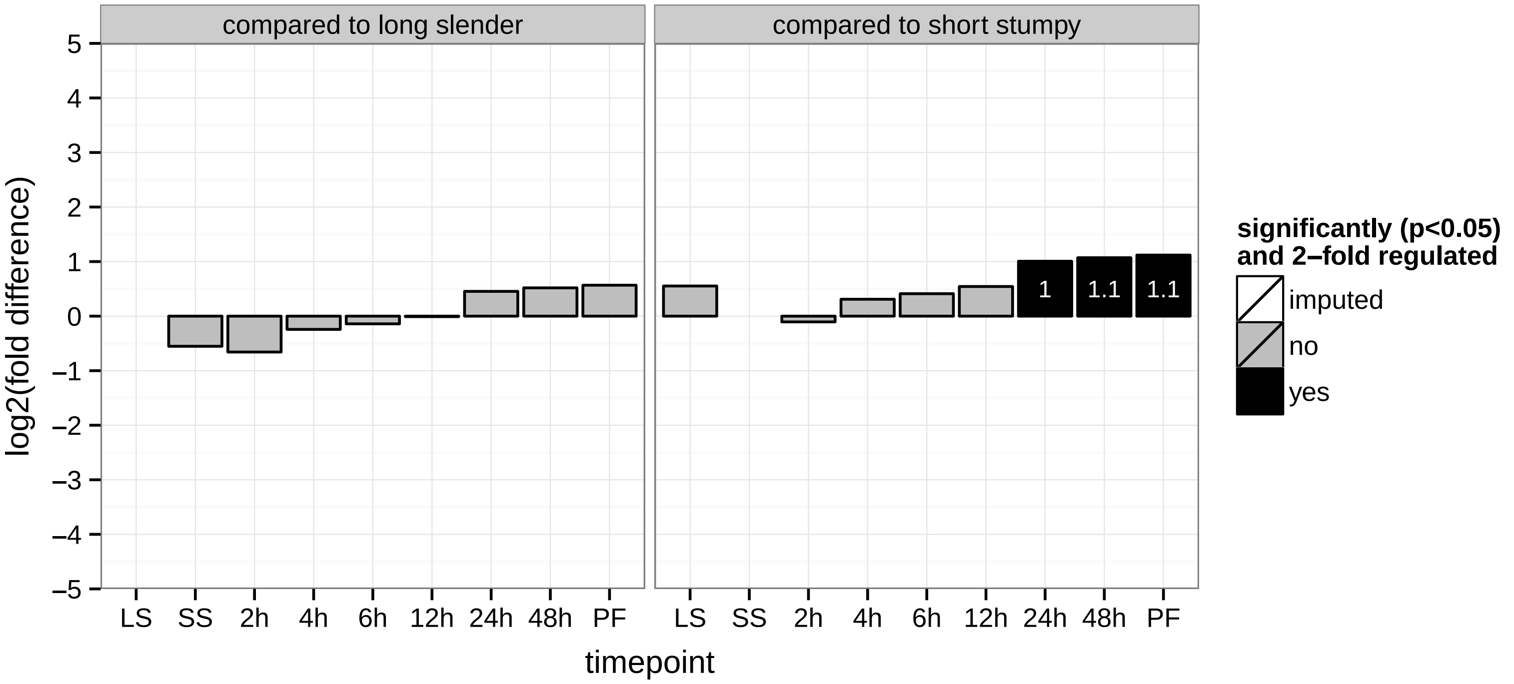
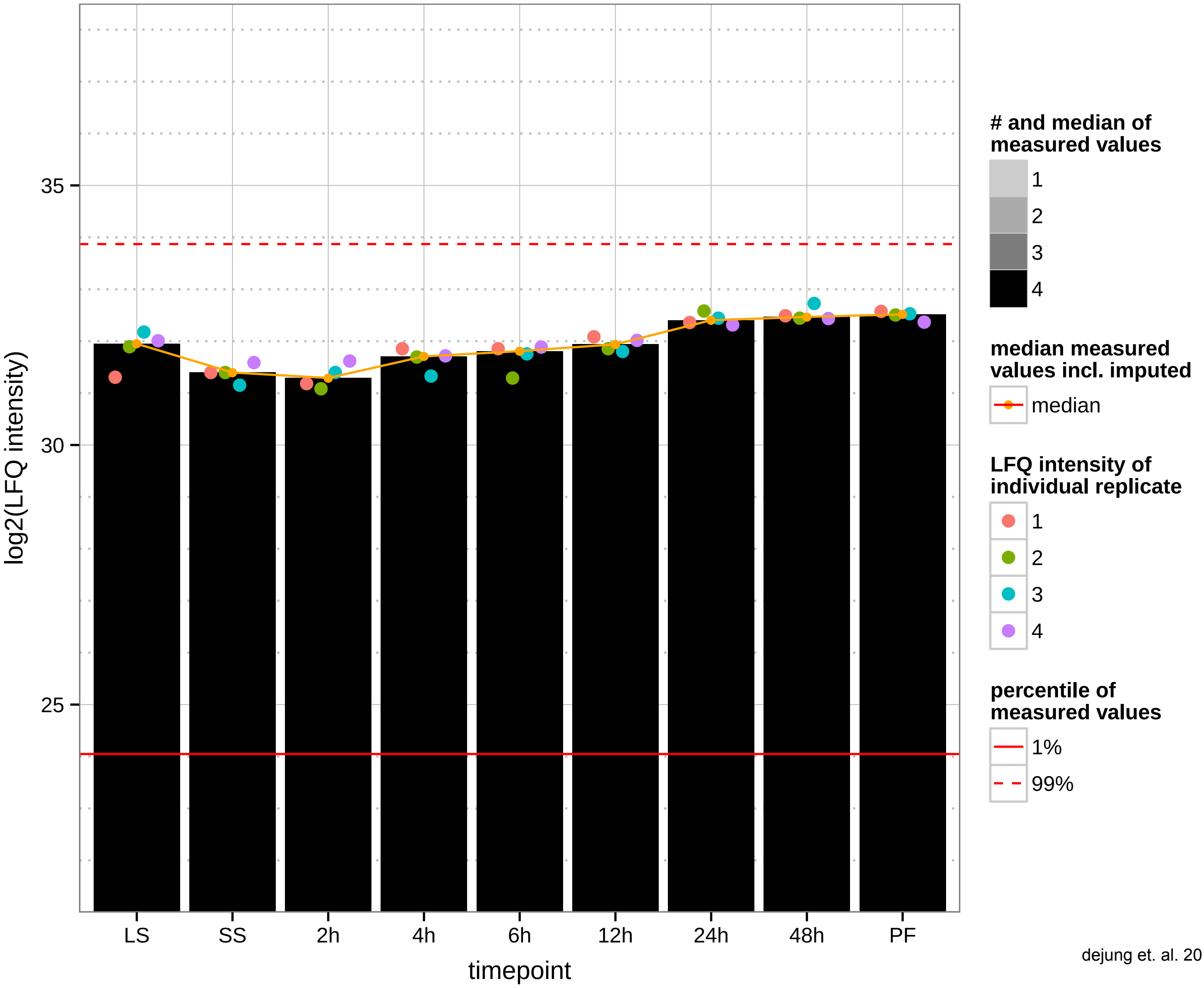
60S ribosomal protein L28, putative
Tb927.11.6200;Tb927.11.6180
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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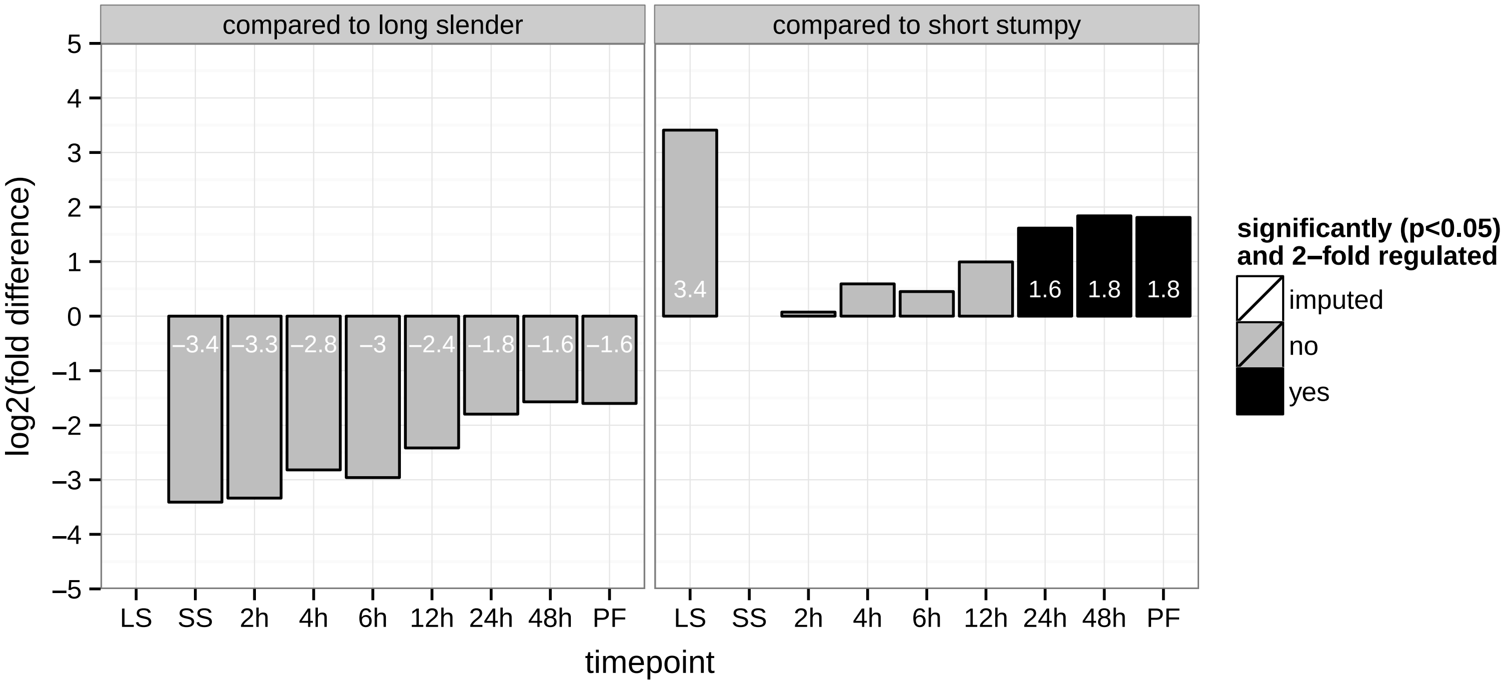
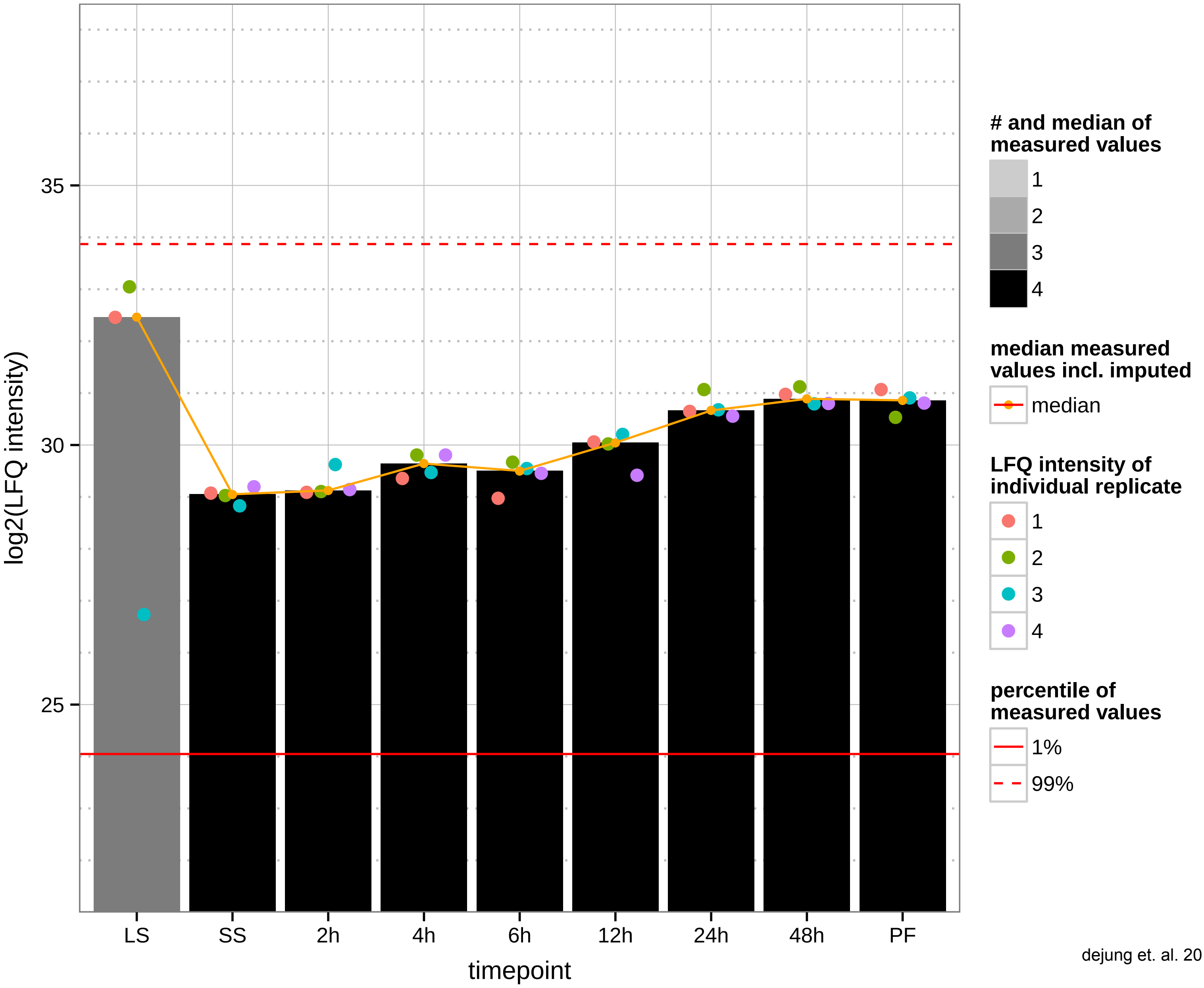
hypothetical protein, conserved
Tb927.11.6250
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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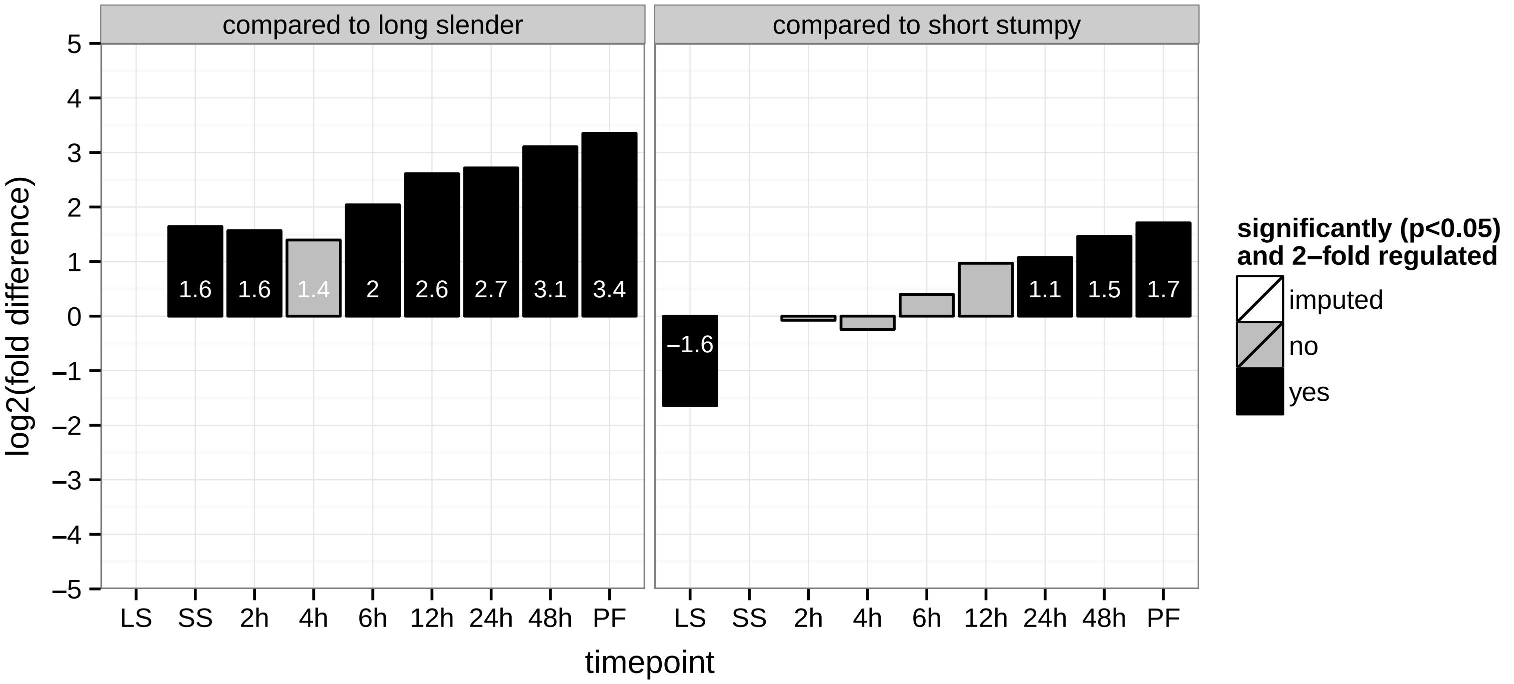
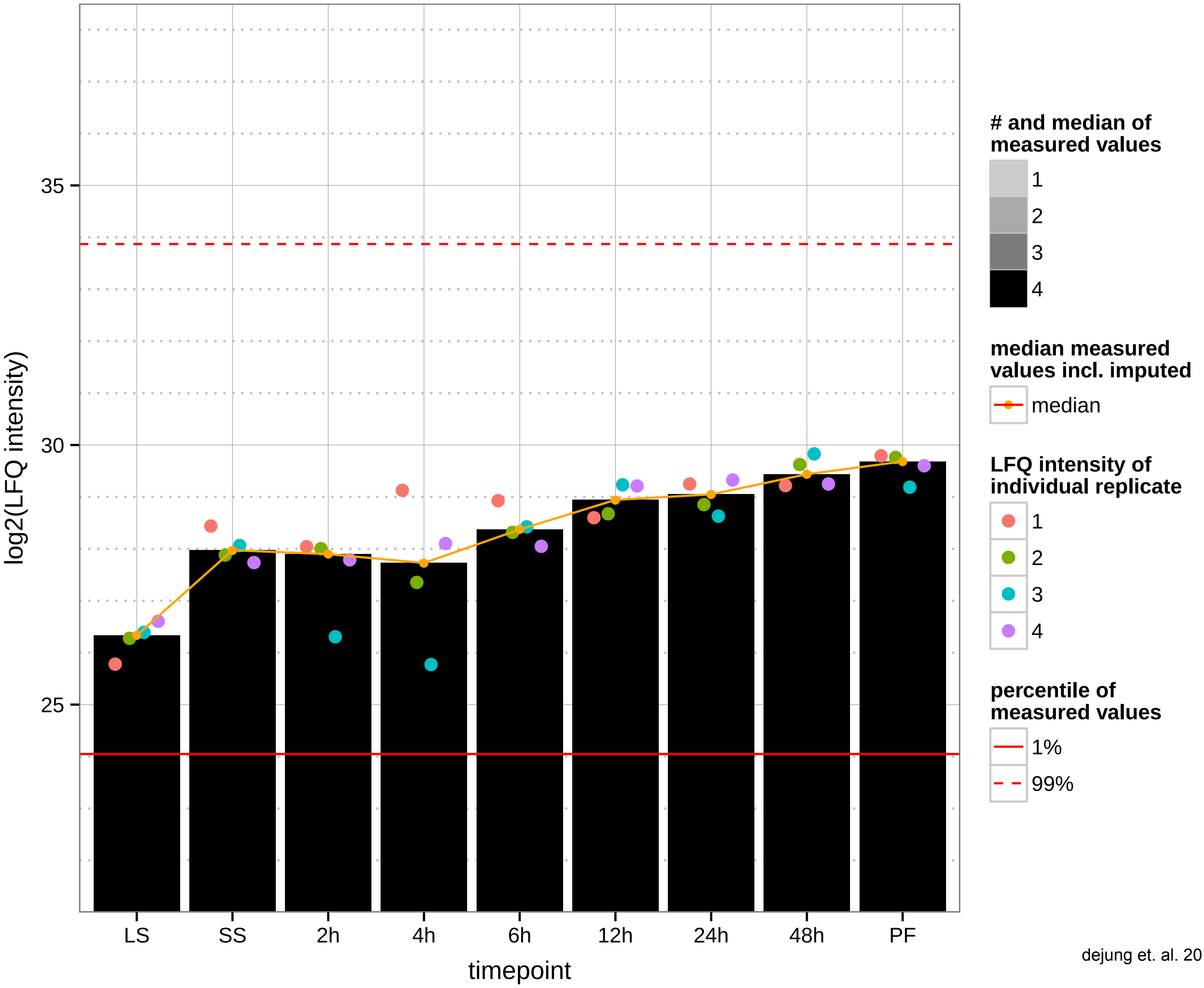
pumilio/PUF RNA binding protein 10, putative
Tb927.11.6740
AGOF: RNA binding
AGOC: null
AGOP: mRNA metabolic process
PGOF: RNA binding, binding
PGOC: null
PGOP: null





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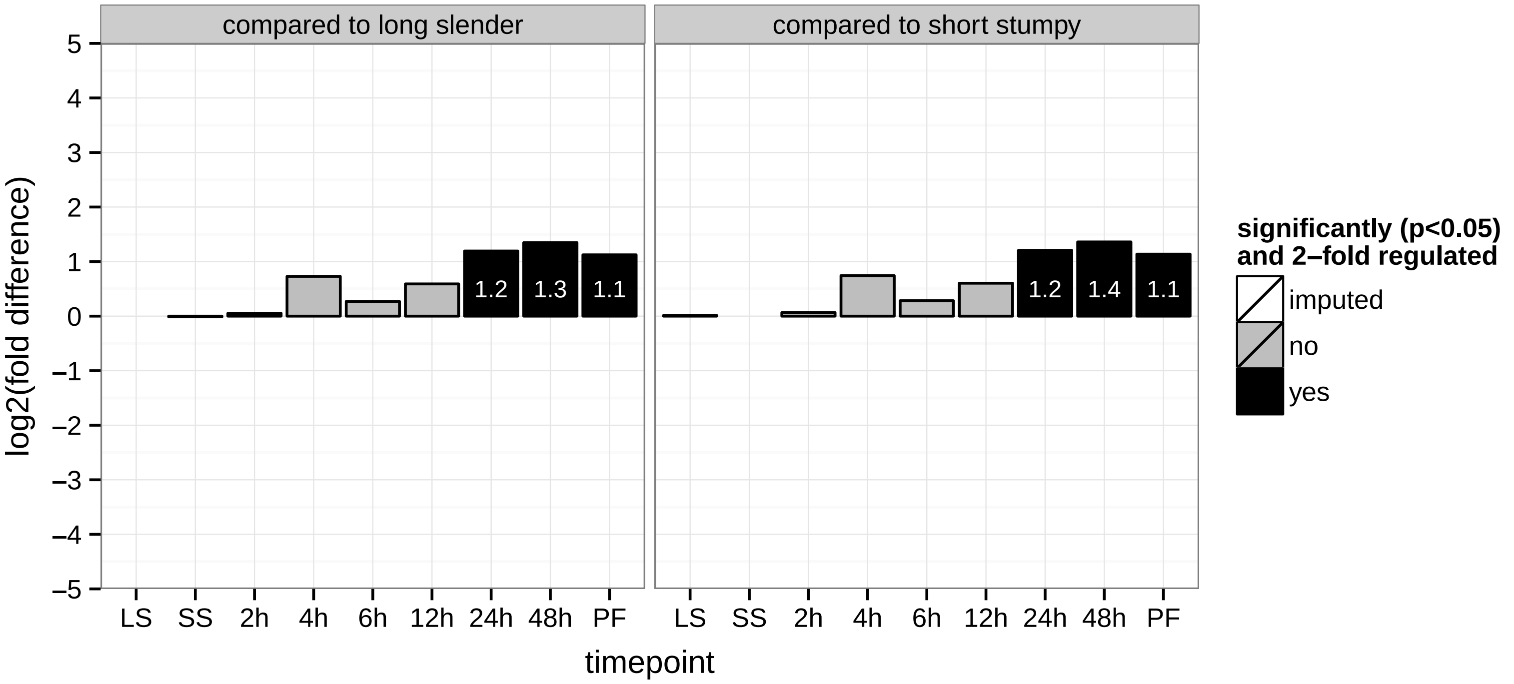
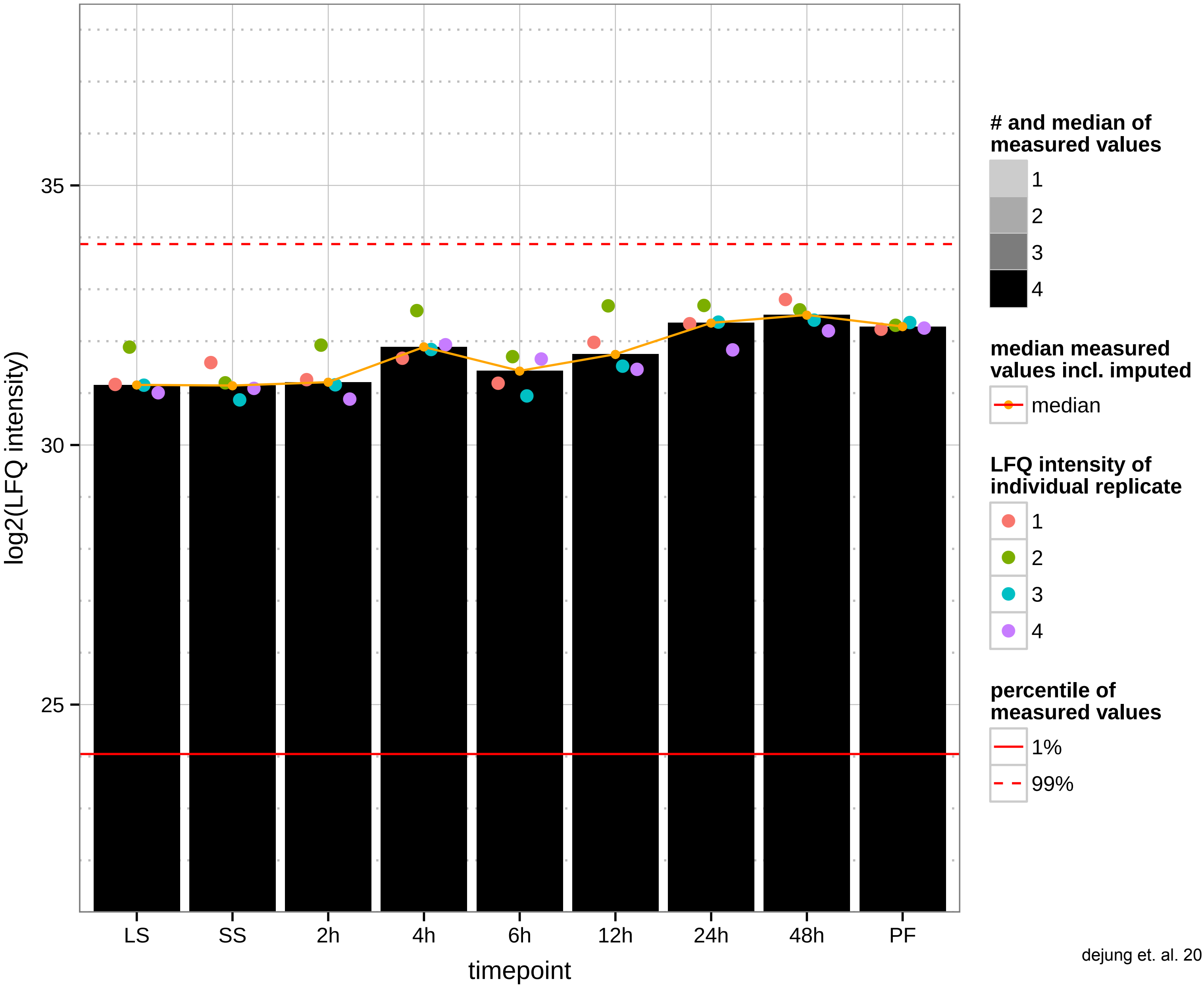
eukaryotic translation initiation factor 5A, putative (eIF–5A)
Tb927.11.740
AGOF: RNA binding, ribosome binding, translation elongation factor activity, translation initiation factor activity
AGOC: cytoplasm
AGOP: peptidyl–lysine modification to hypusine, positive regulation of translational elongation, positive regulation of translatio
PGOF: RNA binding, ribosome binding, translation elongation factor activity
PGOC: null
PGOP: peptidyl–lysine modification to hypusine, positive regulation of translational elongation, positive regulation of translatio





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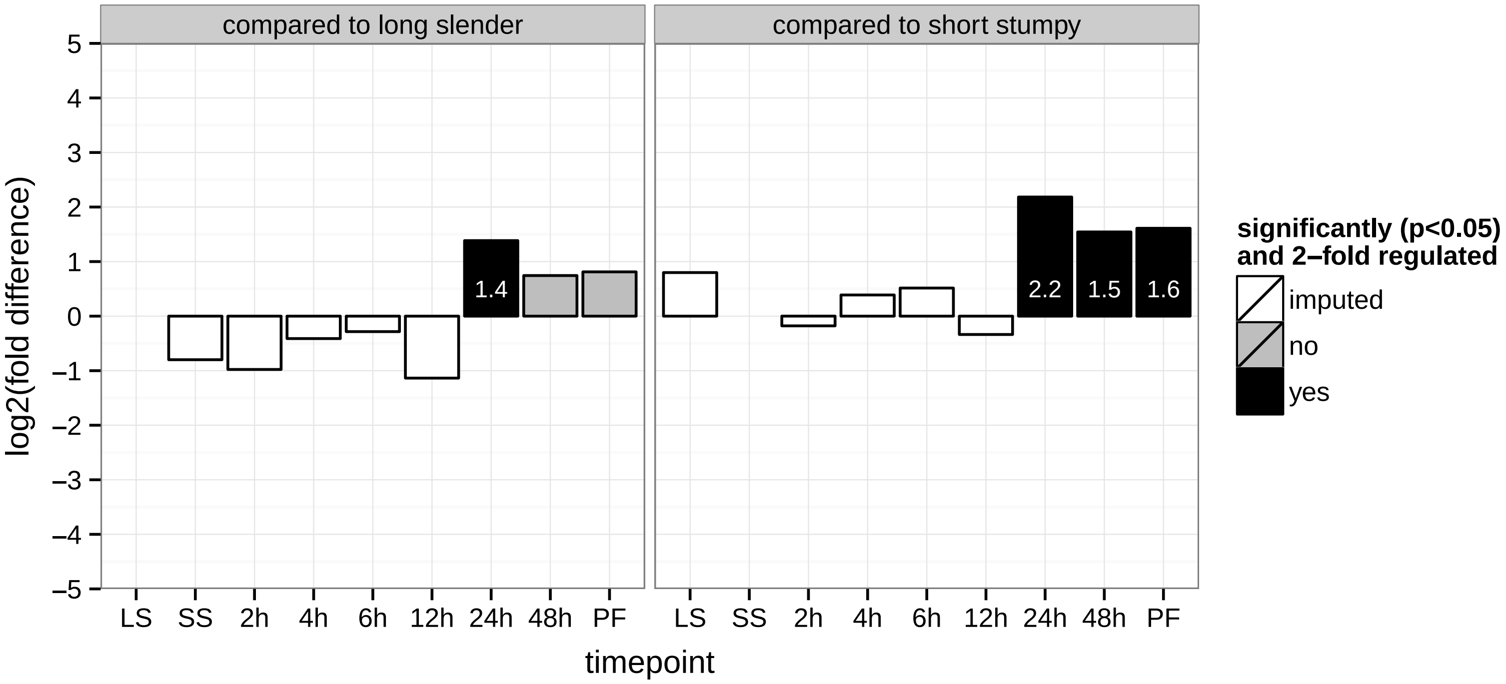
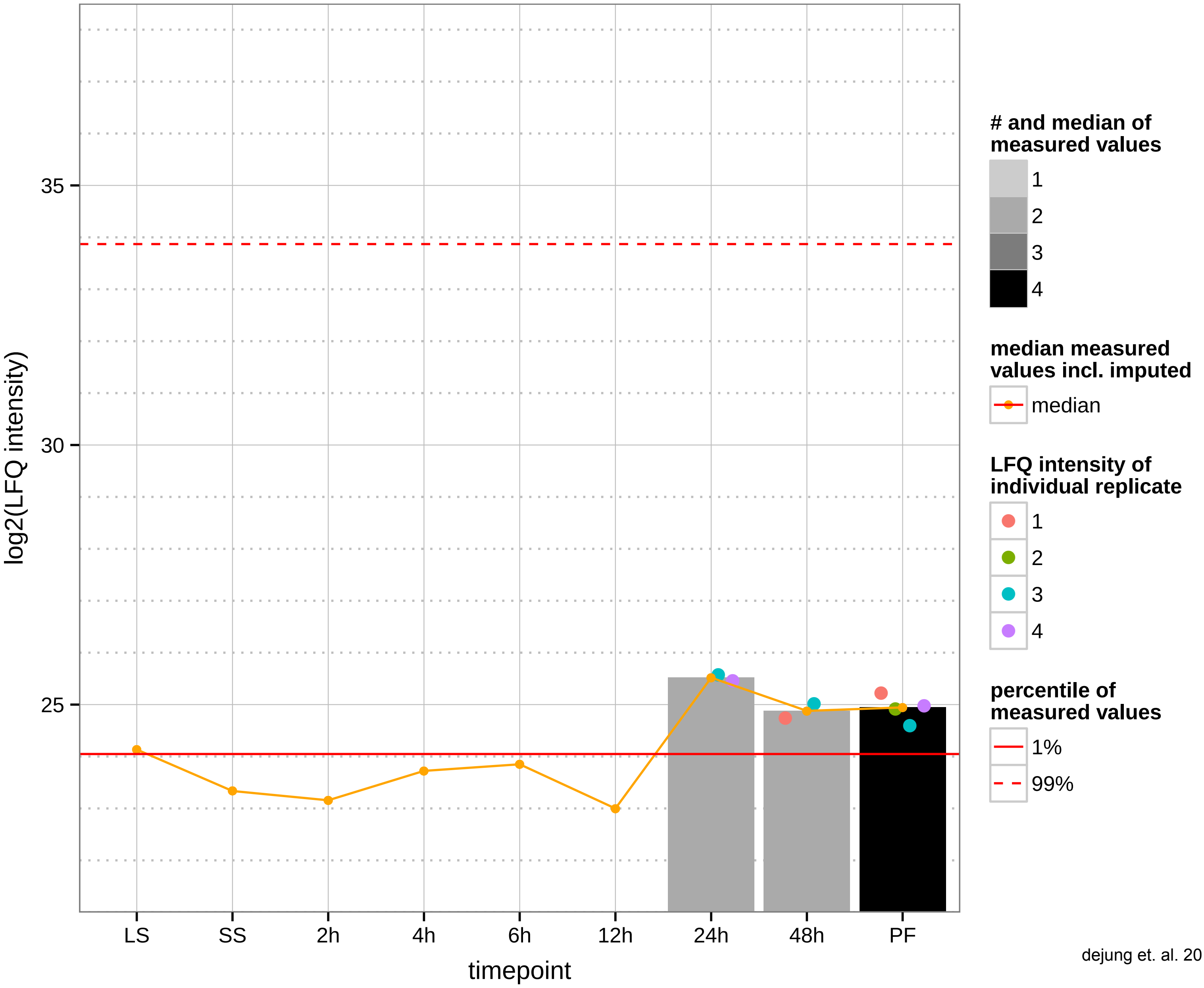
hypothetical protein, conserved
Tb927.11.7790
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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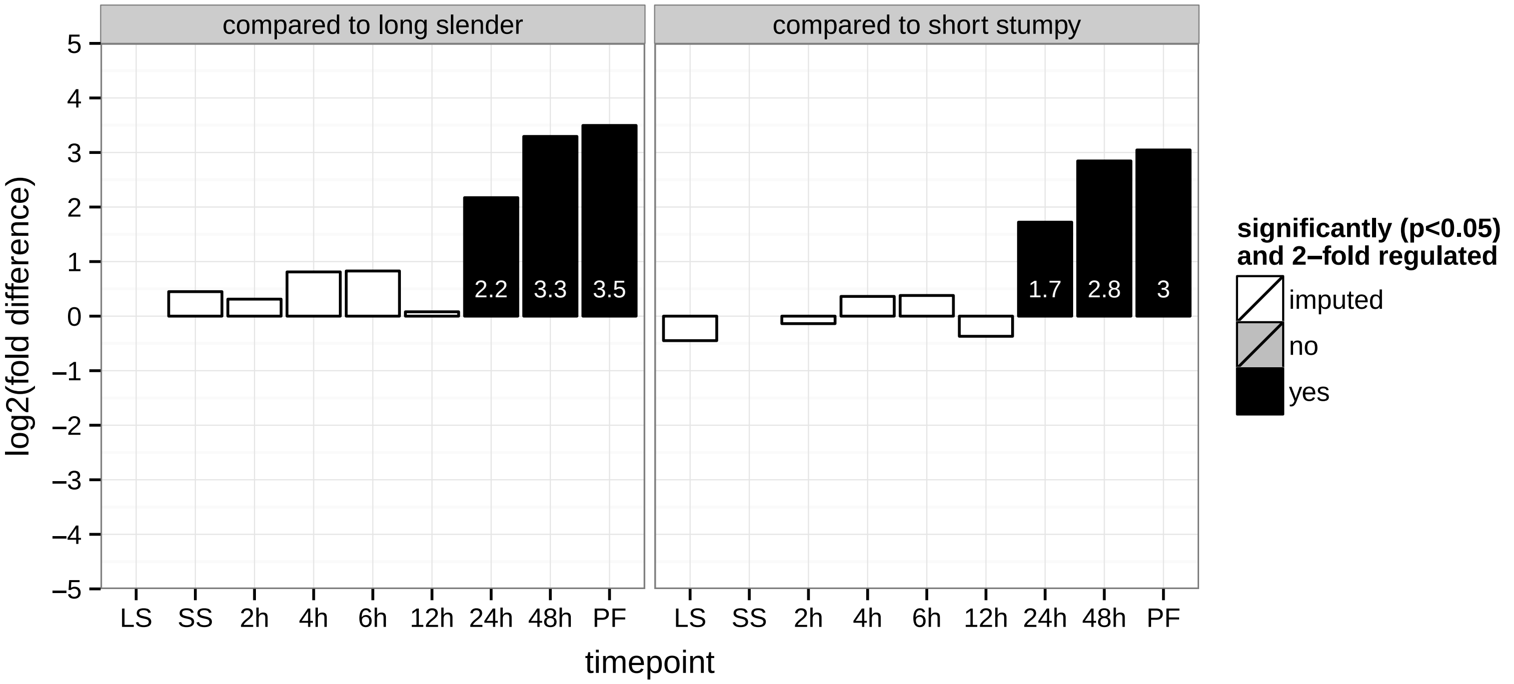
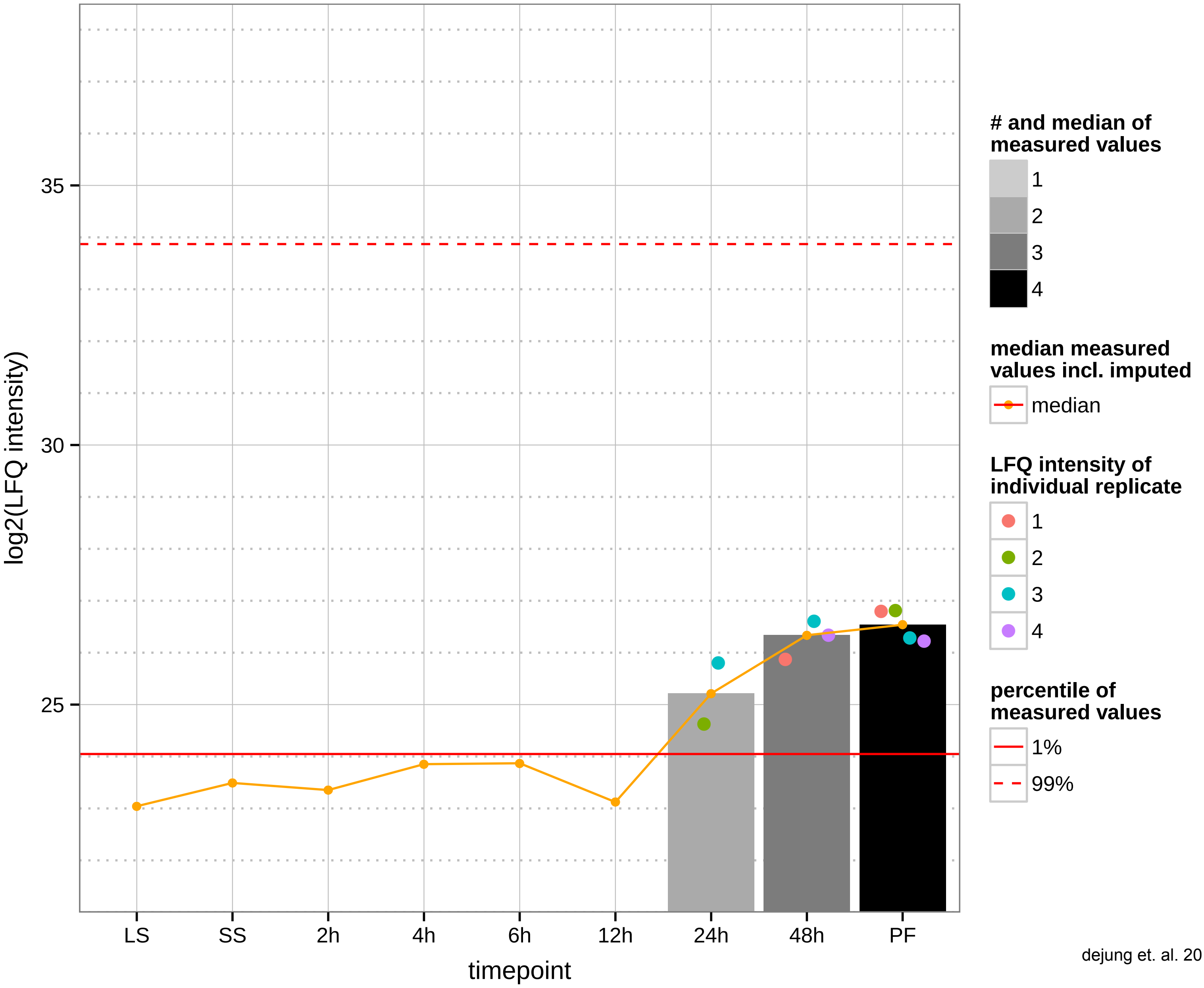
hypothetical protein, conserved
Tb927.11.9570
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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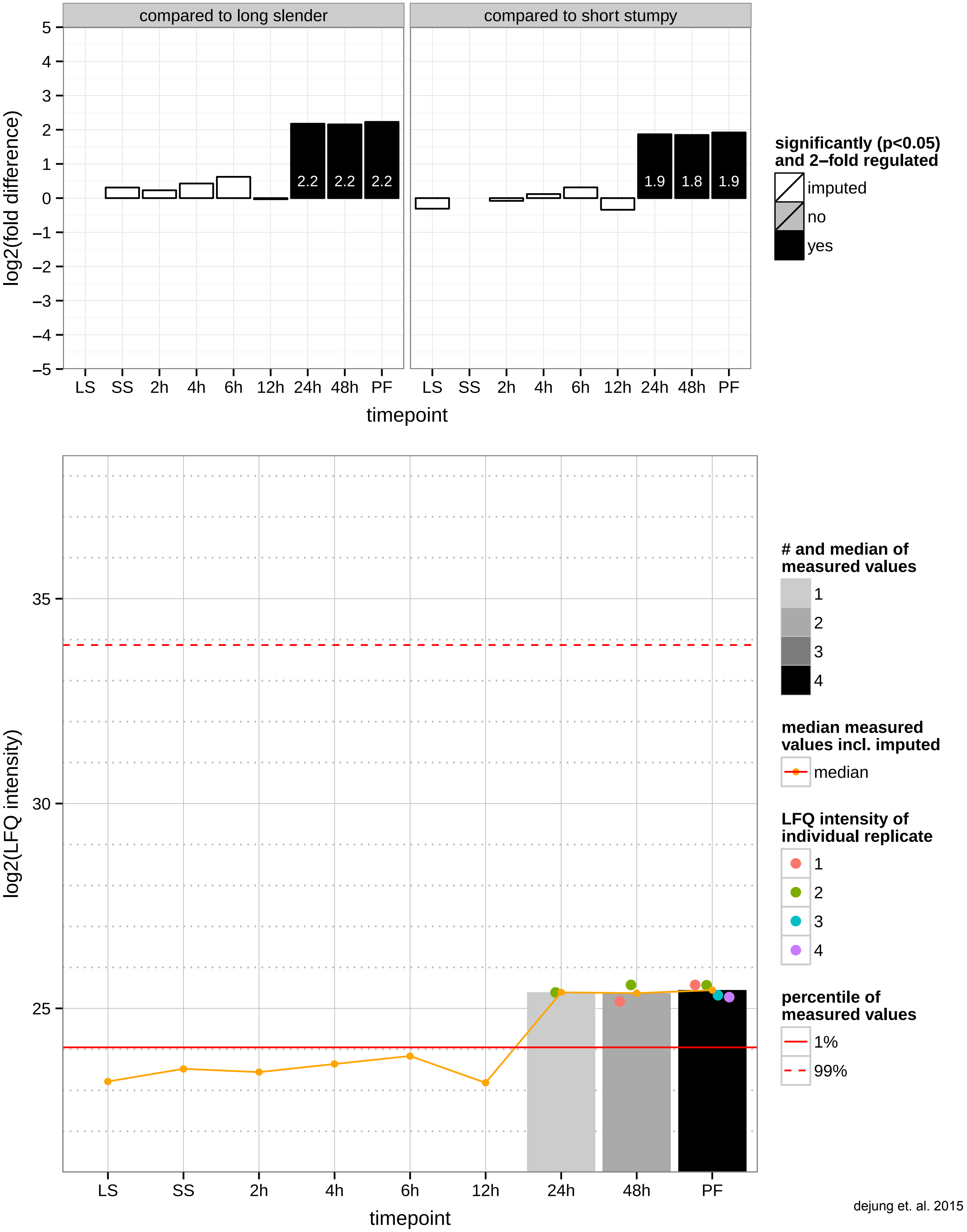
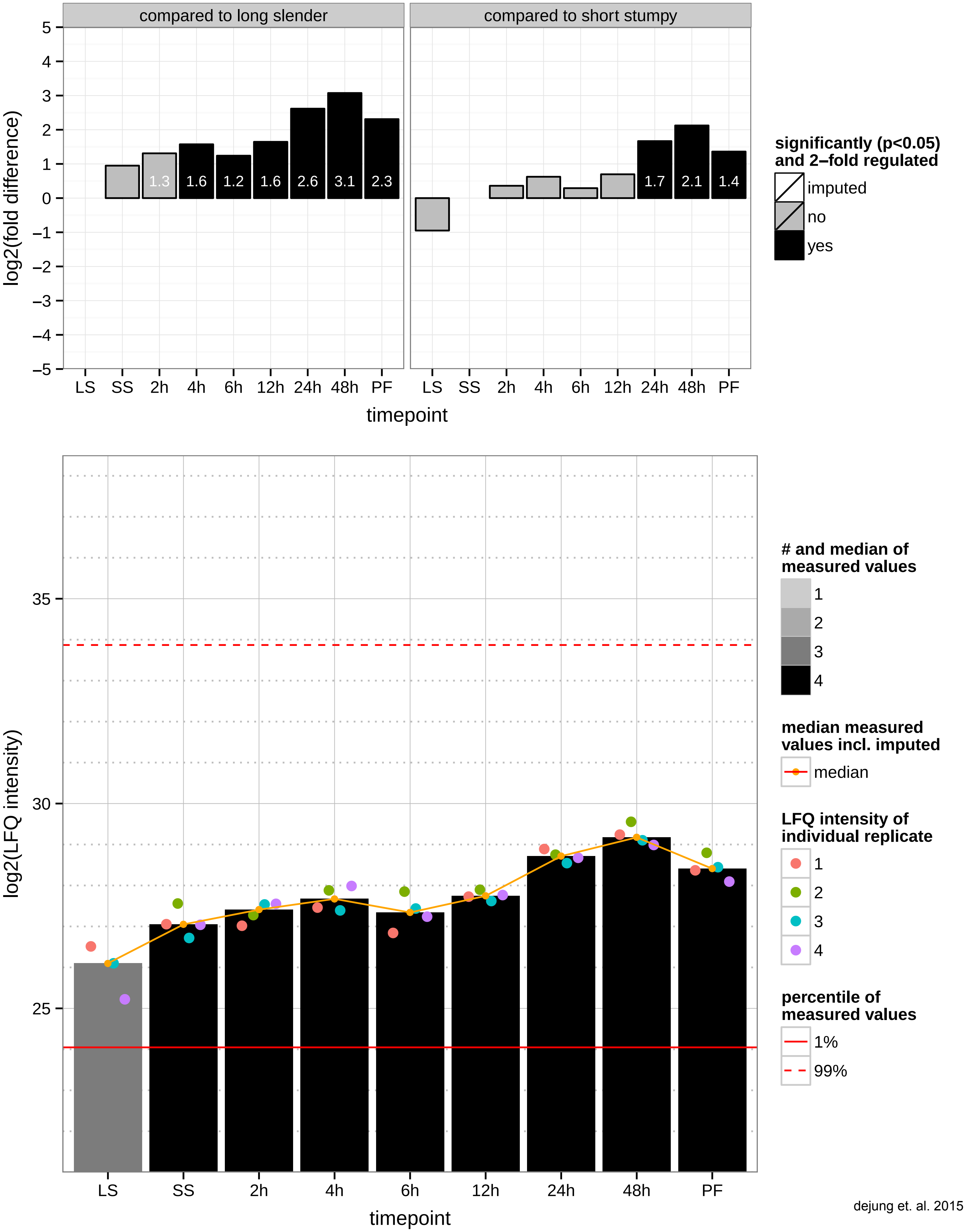
hypothetical protein, conserved
Tb927.11.9970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



hypothetical protein, conserved
Tb927.2.3610
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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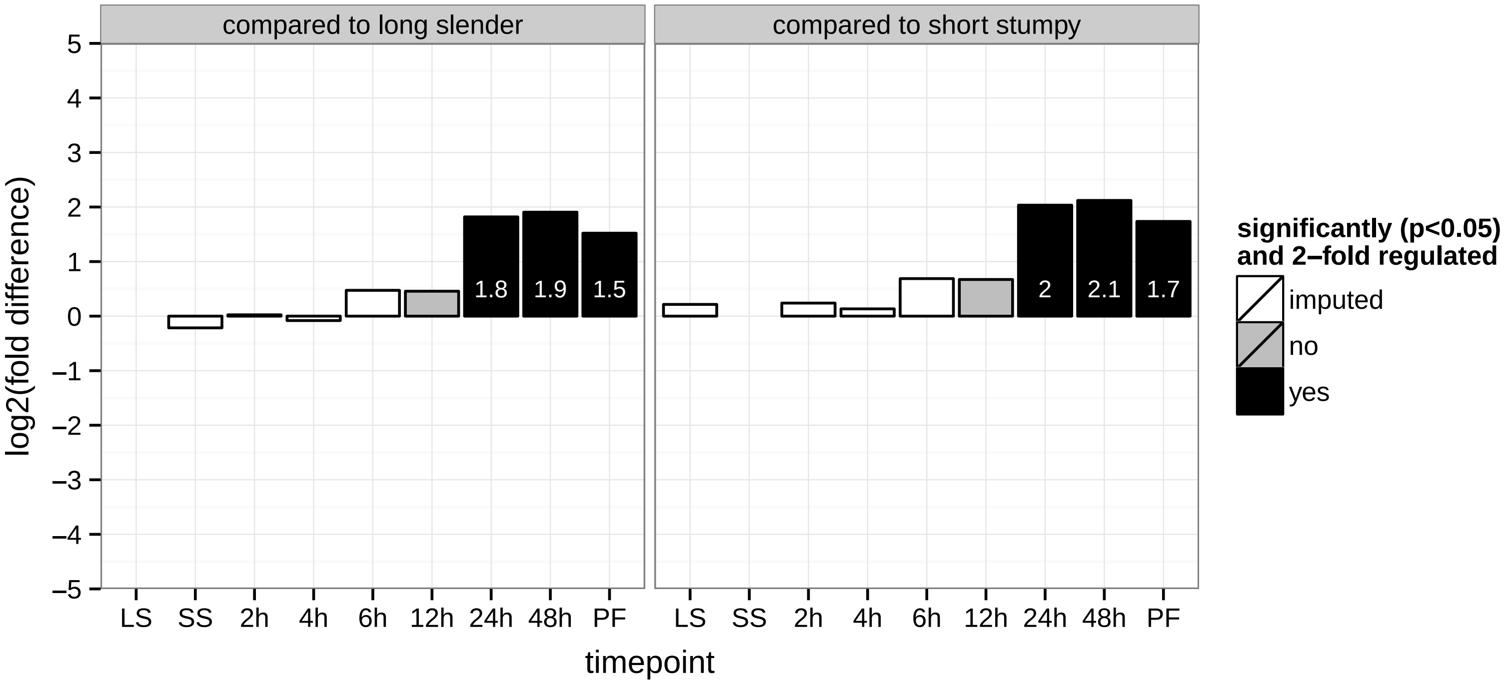
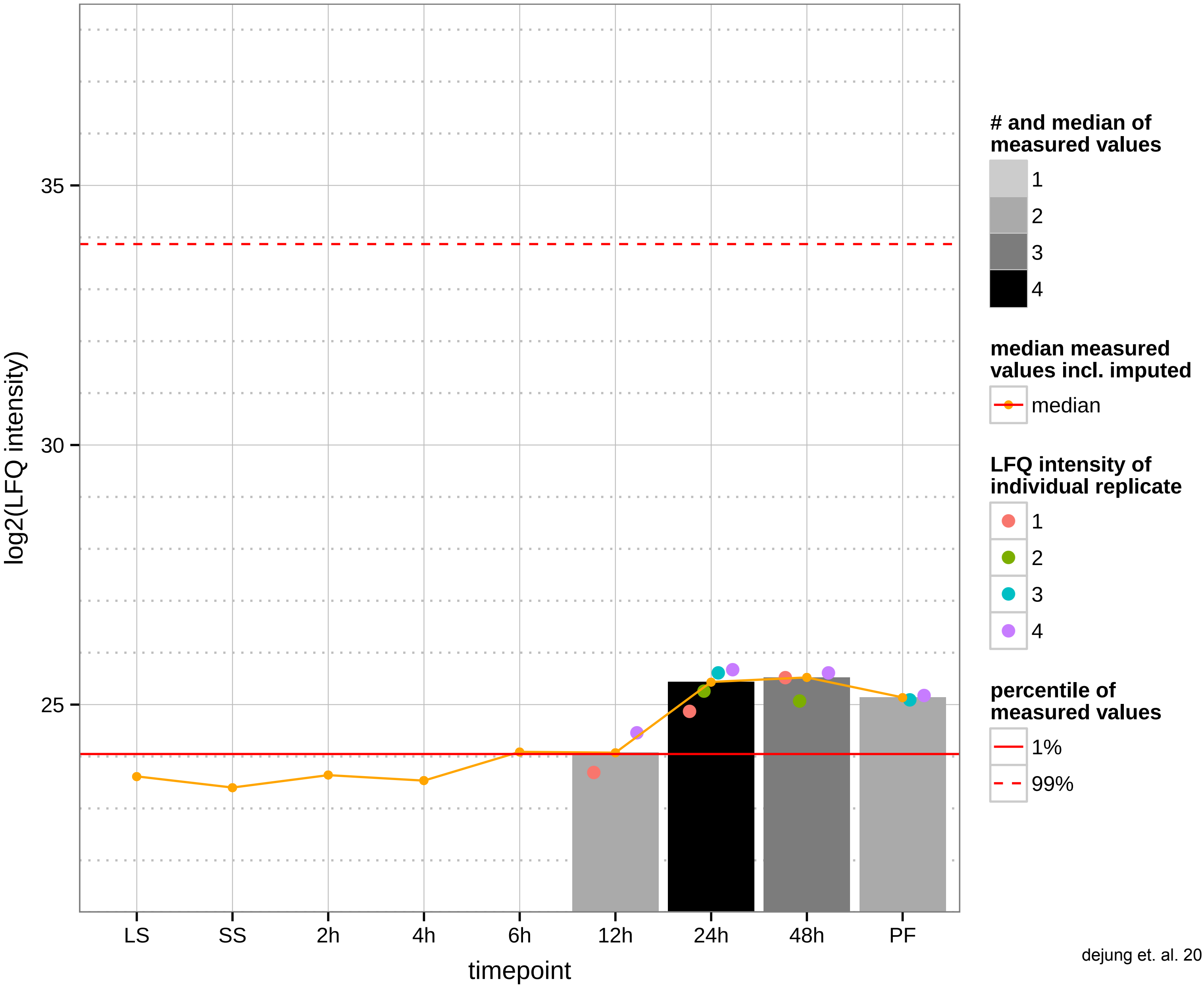
ubiquitin–conjugating enzyme, putative
Tb927.2.3720
AGOF: ubiquitin–protein ligase activity
AGOC: nucleus
AGOP: cellular protein modification process, post–translational protein modification, regulation of protein metabolic process
PGOF: acid–amino acid ligase activity
PGOC: null
PGOP: null





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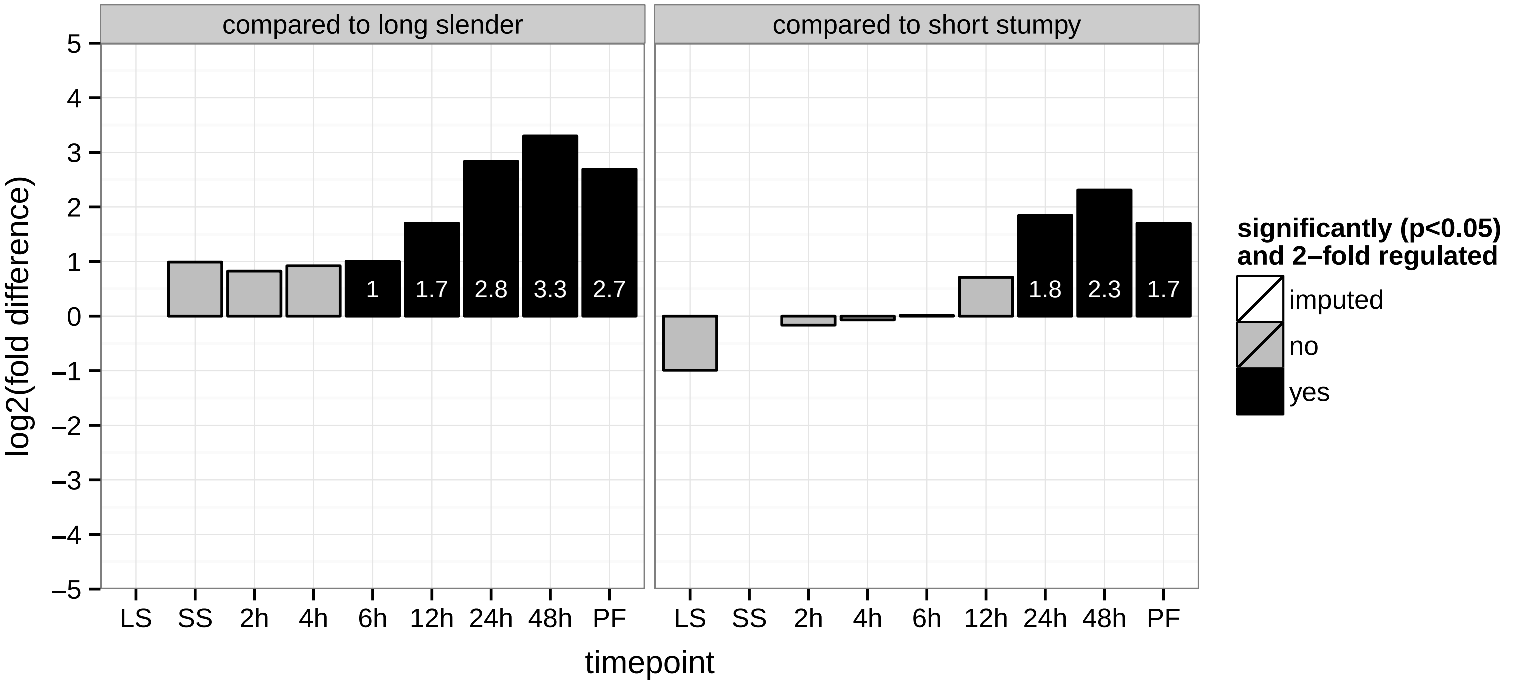
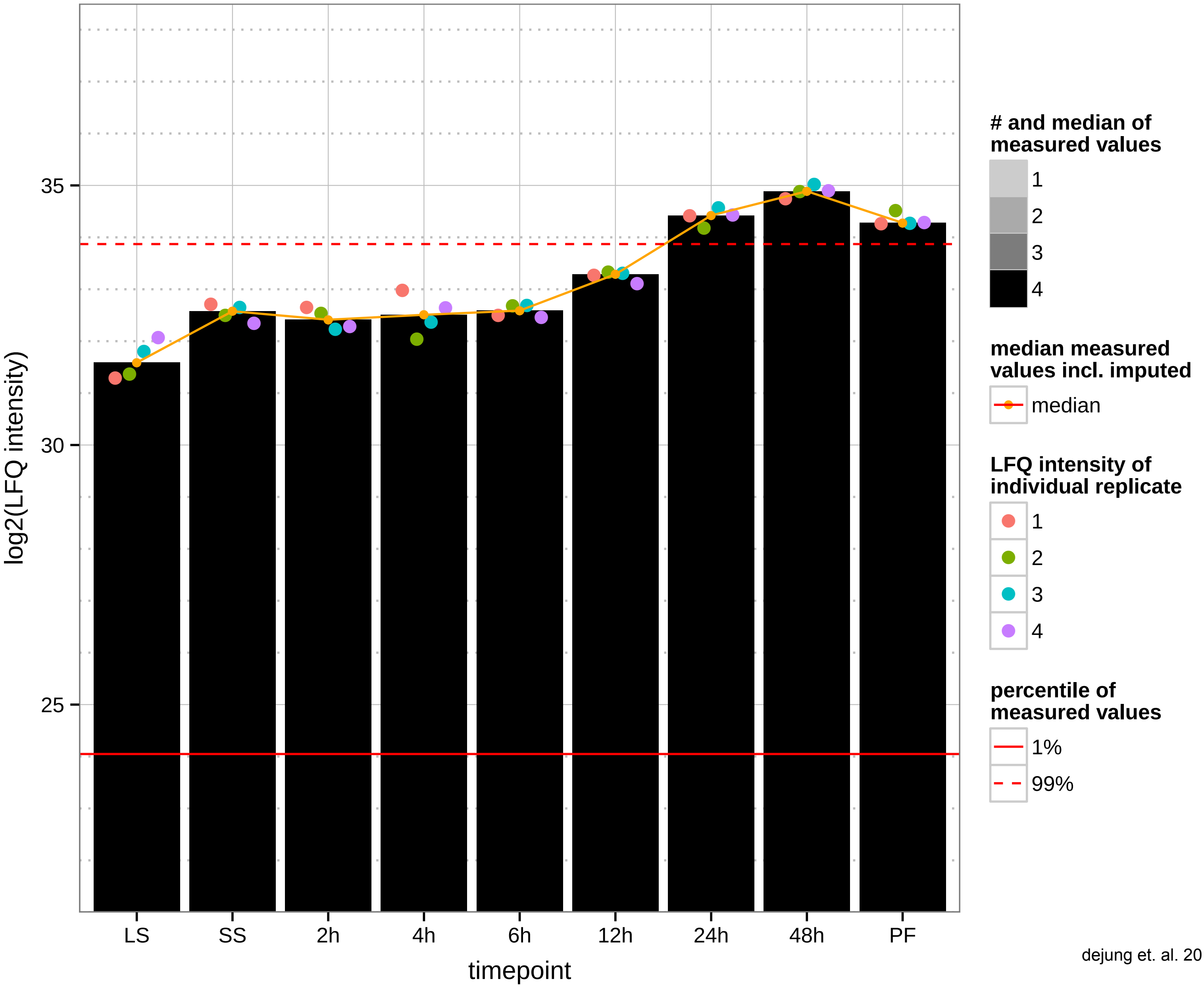
glycosomal phosphoenolpyruvate carboxykinase (PEPCK)
Tb927.2.4210
AGOF: ATP binding, microtubule binding, phosphoenolpyruvate carboxykinase (ATP) activity
AGOC: glycosome, vesicle membrane
AGOP: gluconeogenesis
PGOF: ATP binding, phosphoenolpyruvate carboxykinase (ATP) activity, phosphoenolpyruvate carboxykinase activity, purine r
PGOC: null
PGOP: gluconeogenesis





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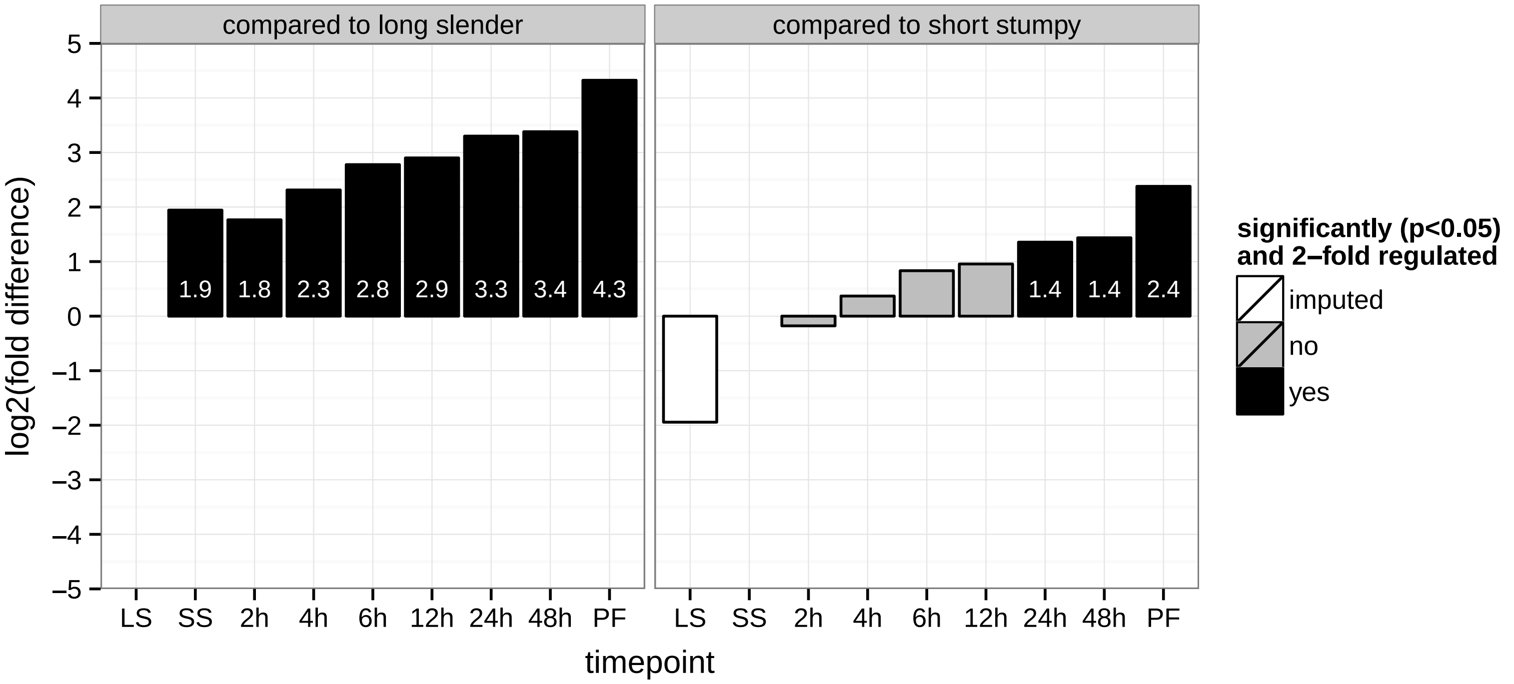
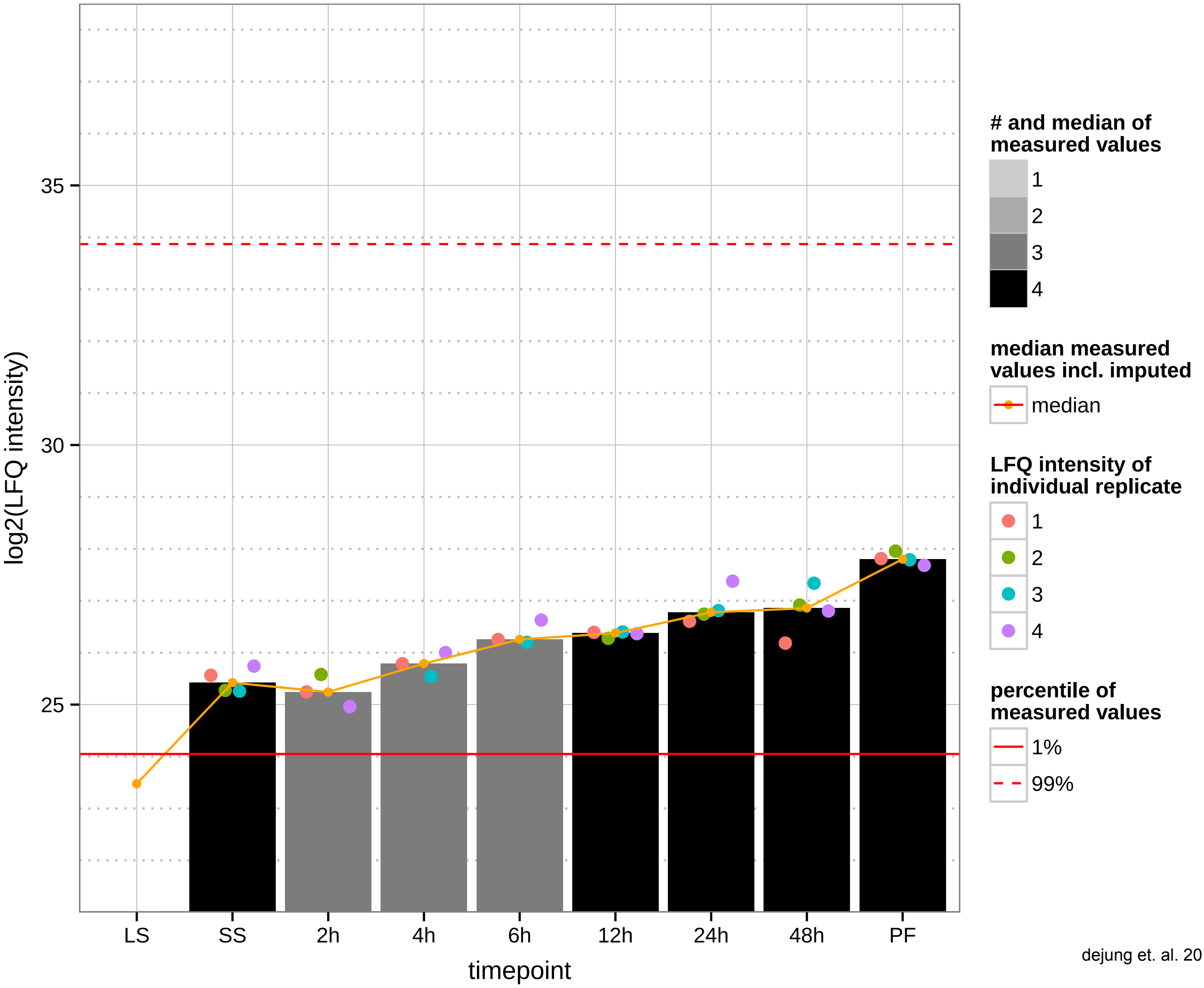
hypothetical protein, conserved
Tb927.2.4980
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: methyltransferase activity
PGOC: null
PGOP: null





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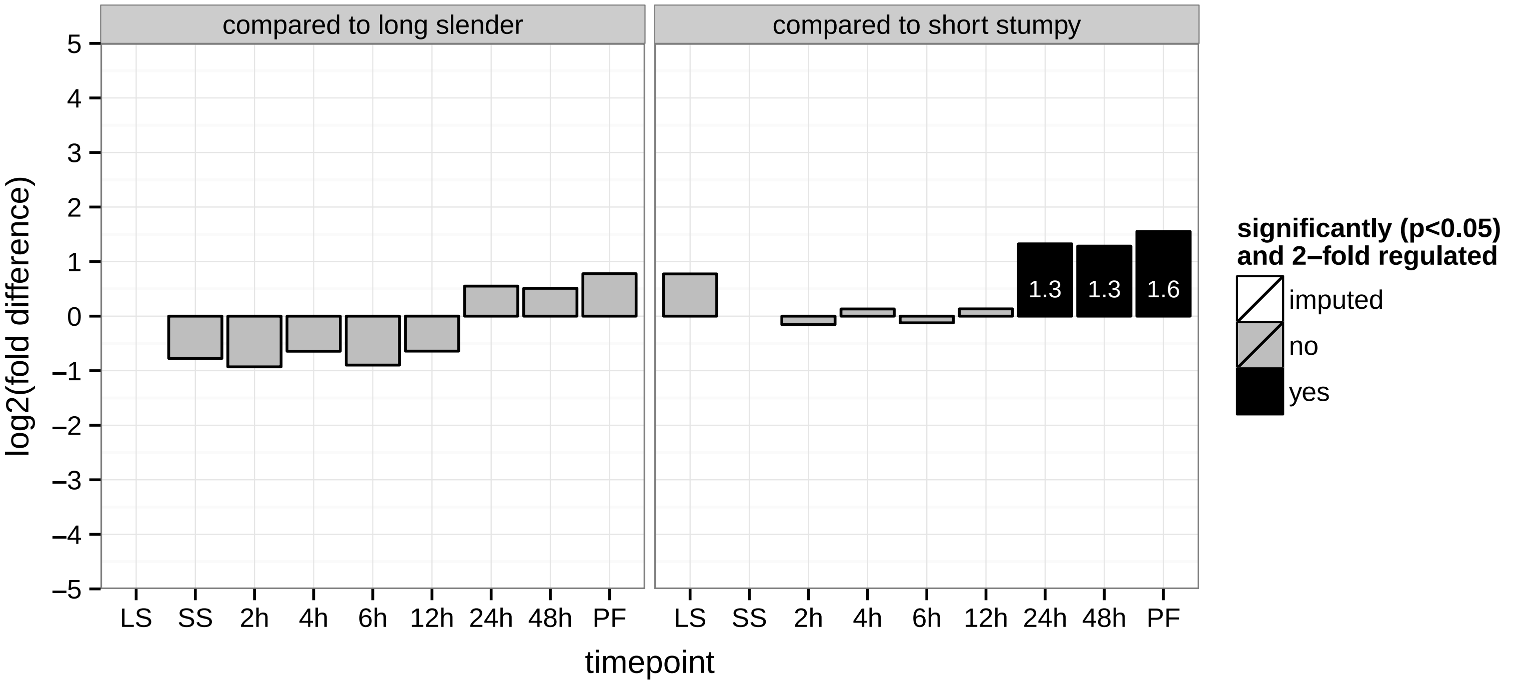
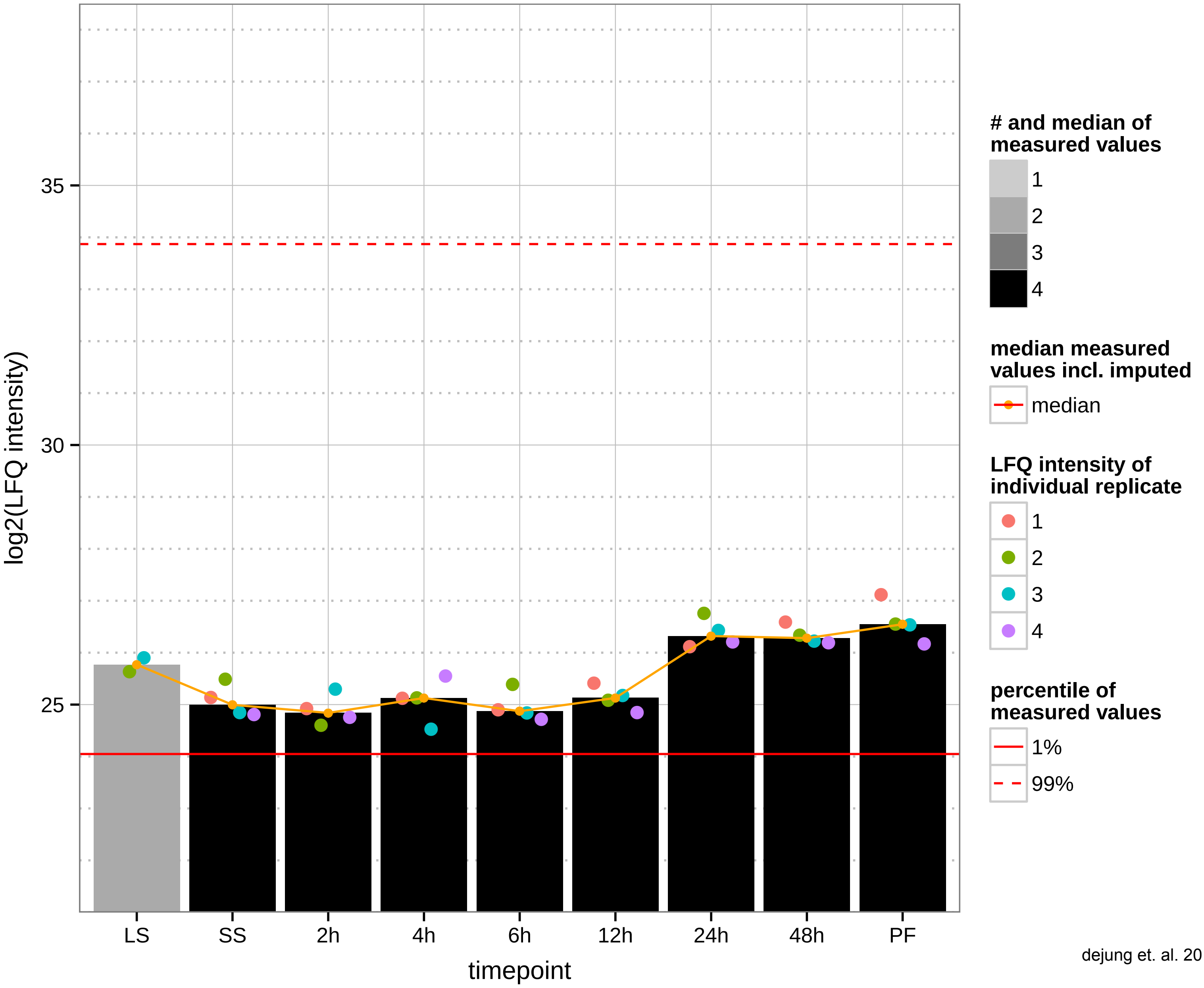
hypothetical protein, conserved
Tb927.2.6100
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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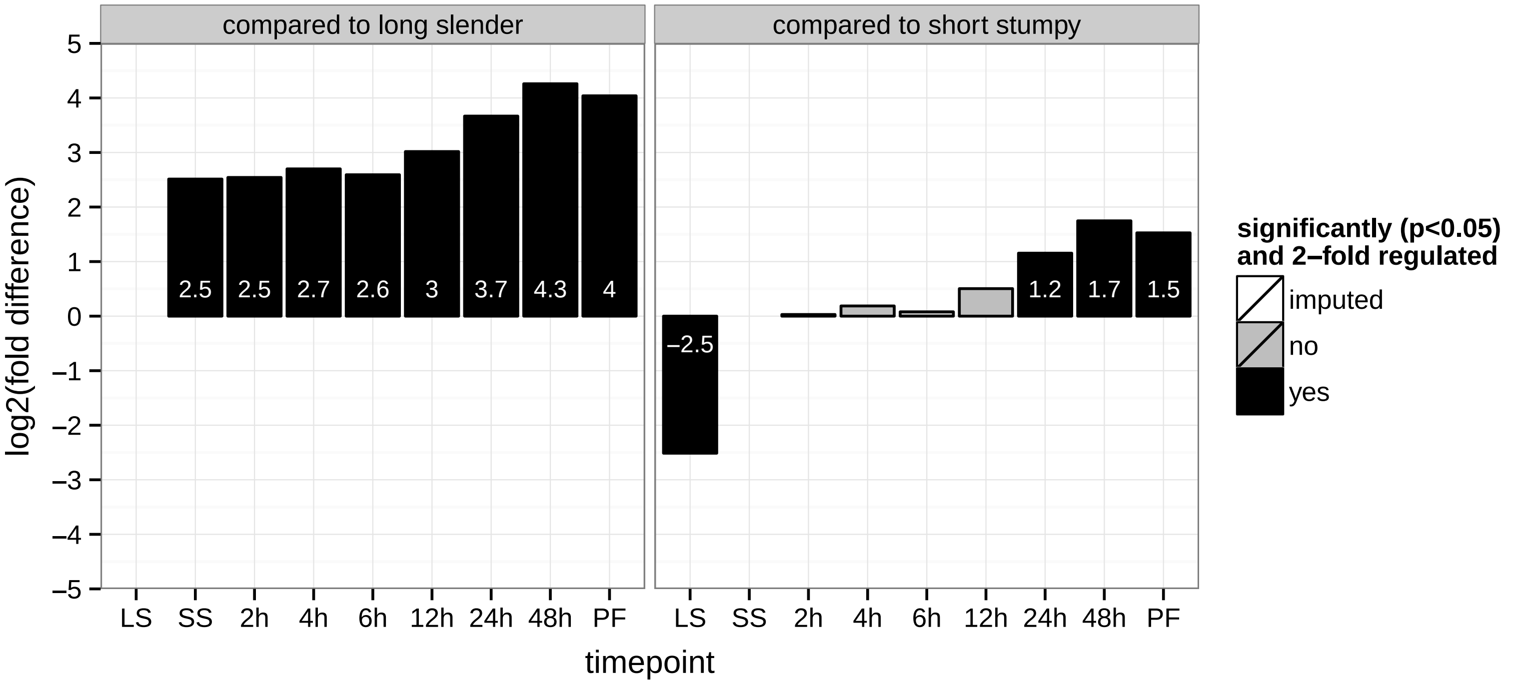
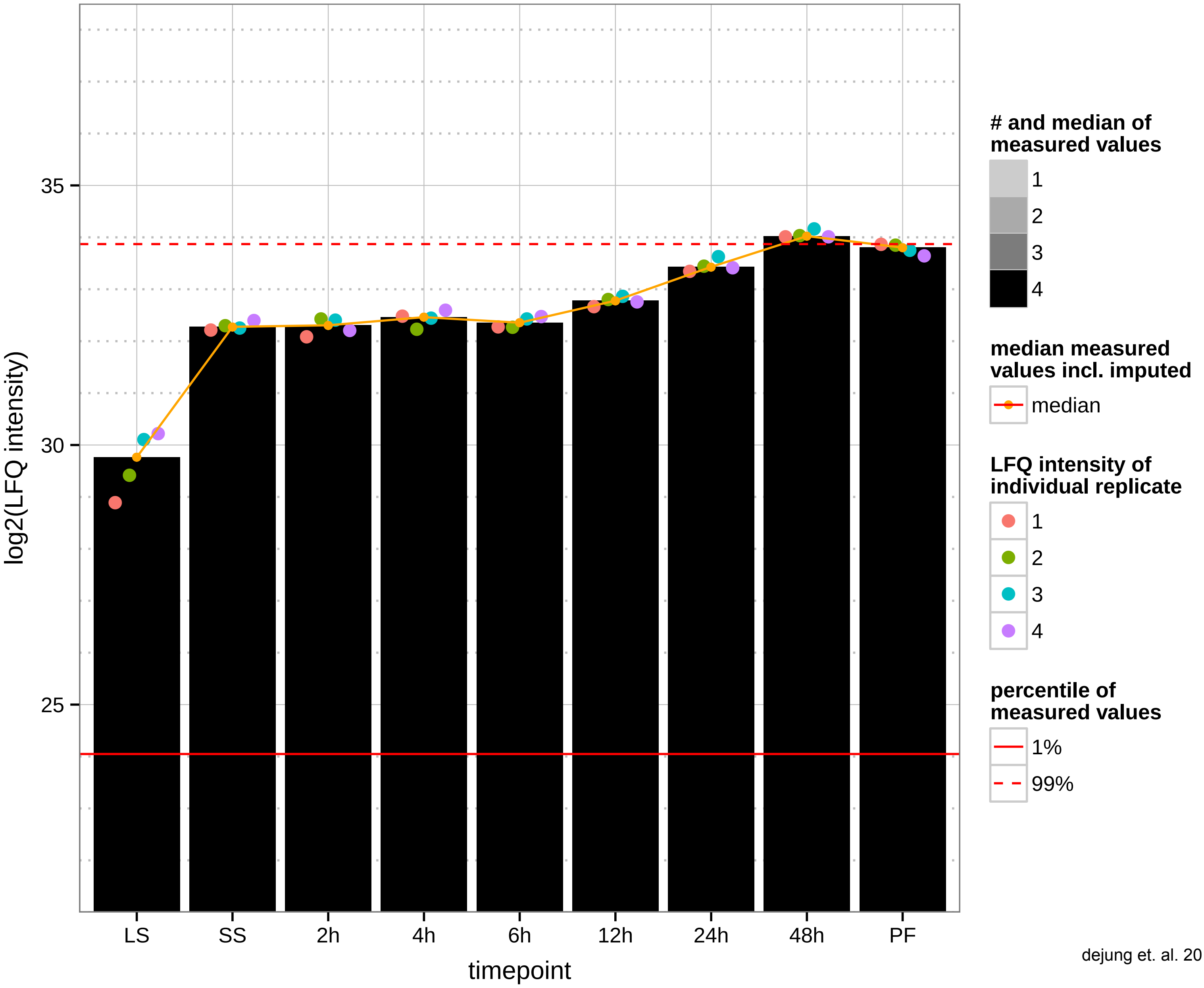
ATP synthase beta chain, mitochondrial precursor, ATP synthase F1, beta subunit
Tb927.3.1380
AGOF: ATP binding, GTP binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen−exporting
AGOC: mitochondrial inner membrane, mitochondrial proton−transporting ATP synthase complex, catalytic core F(1), mitocho
AGOP: ATP synthesis coupled proton transport, proton transport
PGOF: ATP binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen−exporting ATPase activ
PGOC: proton−transporting ATP synthase complex, catalytic core F(1), proton−transporting two−sector ATPase complex, cata
PGOP: ATP hydrolysis coupled proton transport, ATP metabolic process, ATP synthesis coupled proton transport, proton trans





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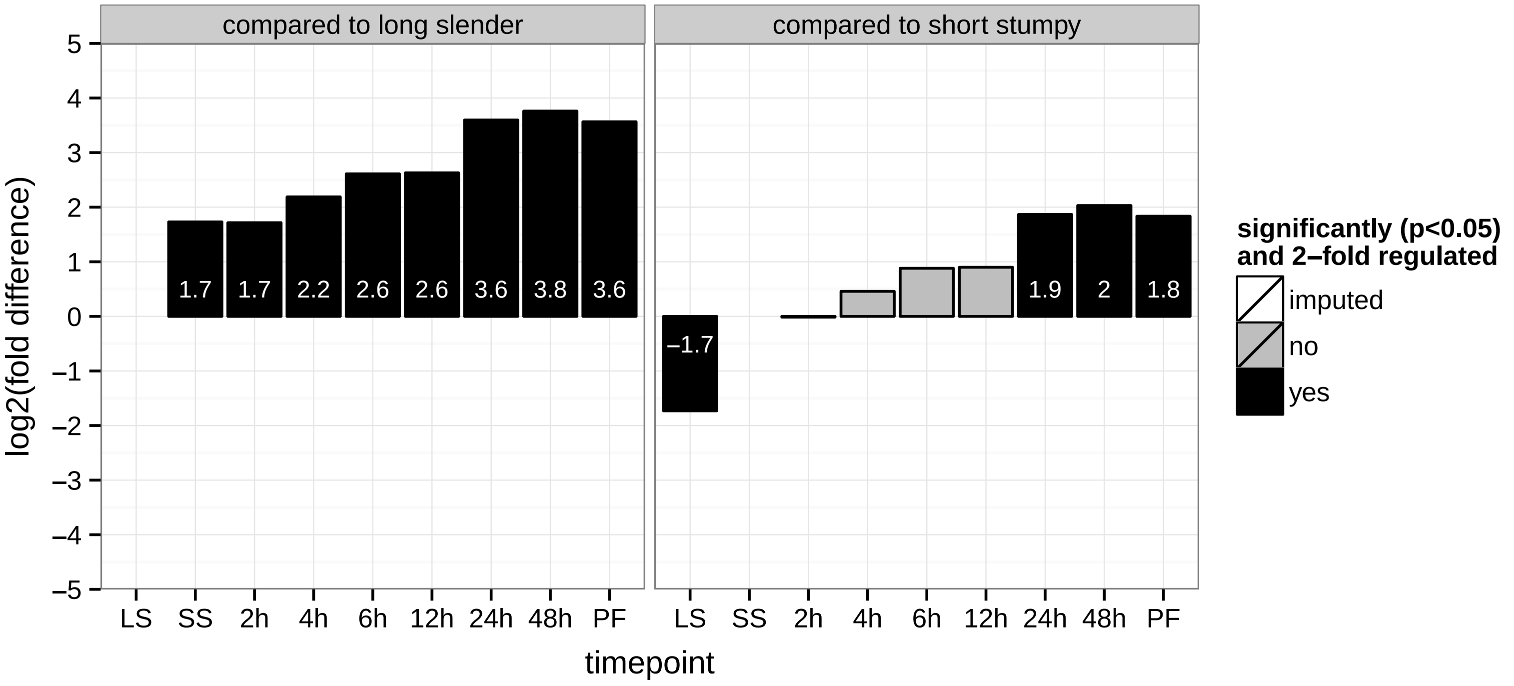
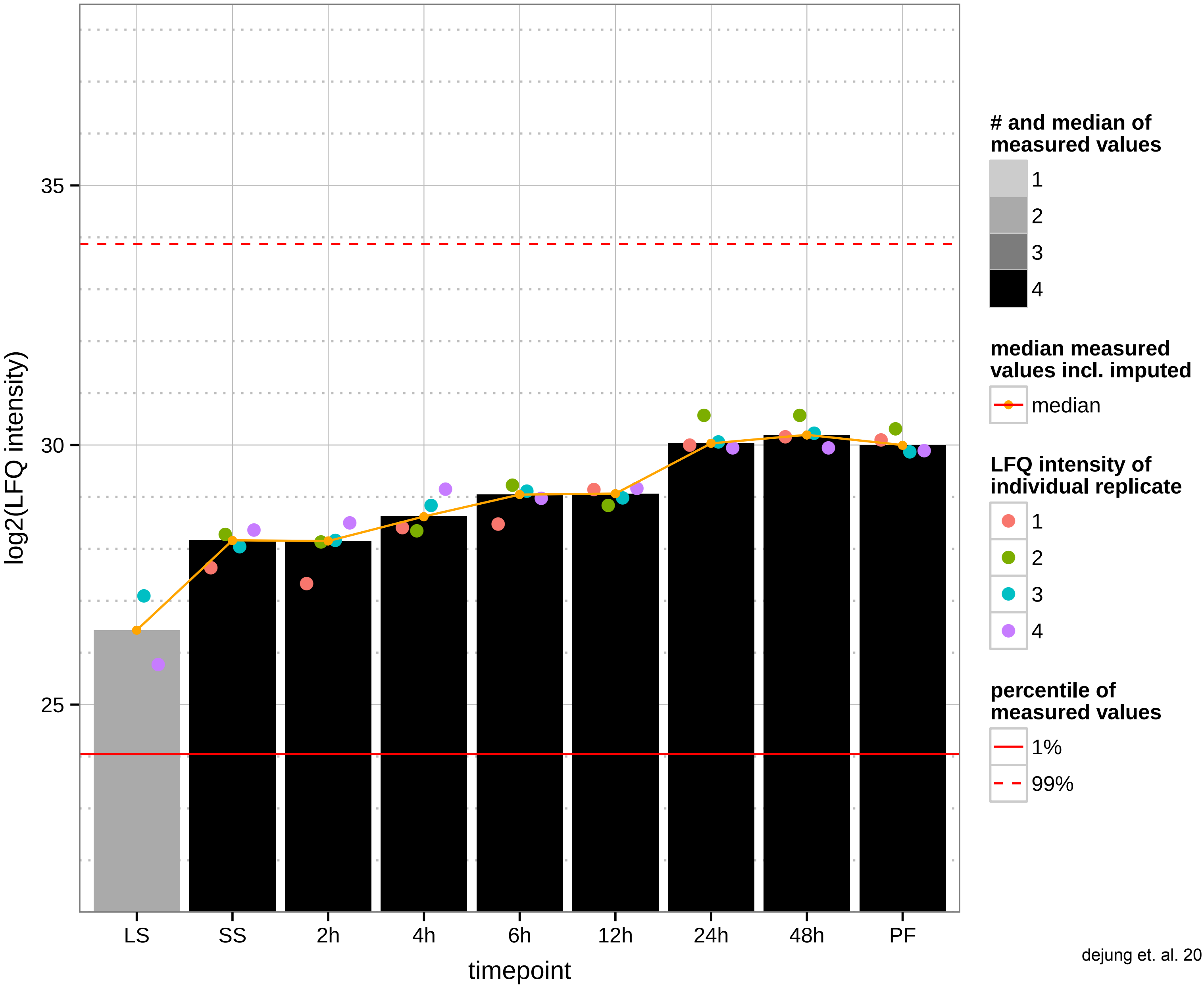
hypothetical protein, conserved
Tb927.3.1690
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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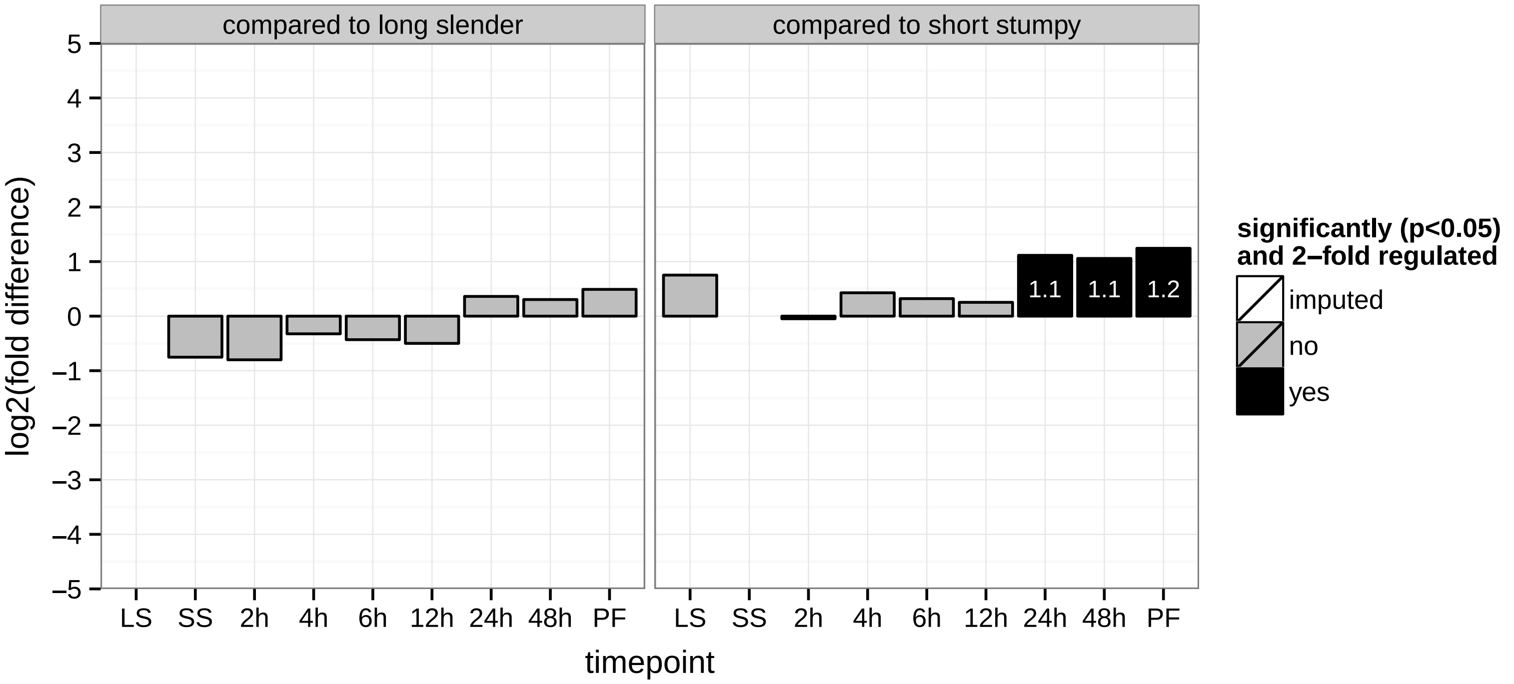
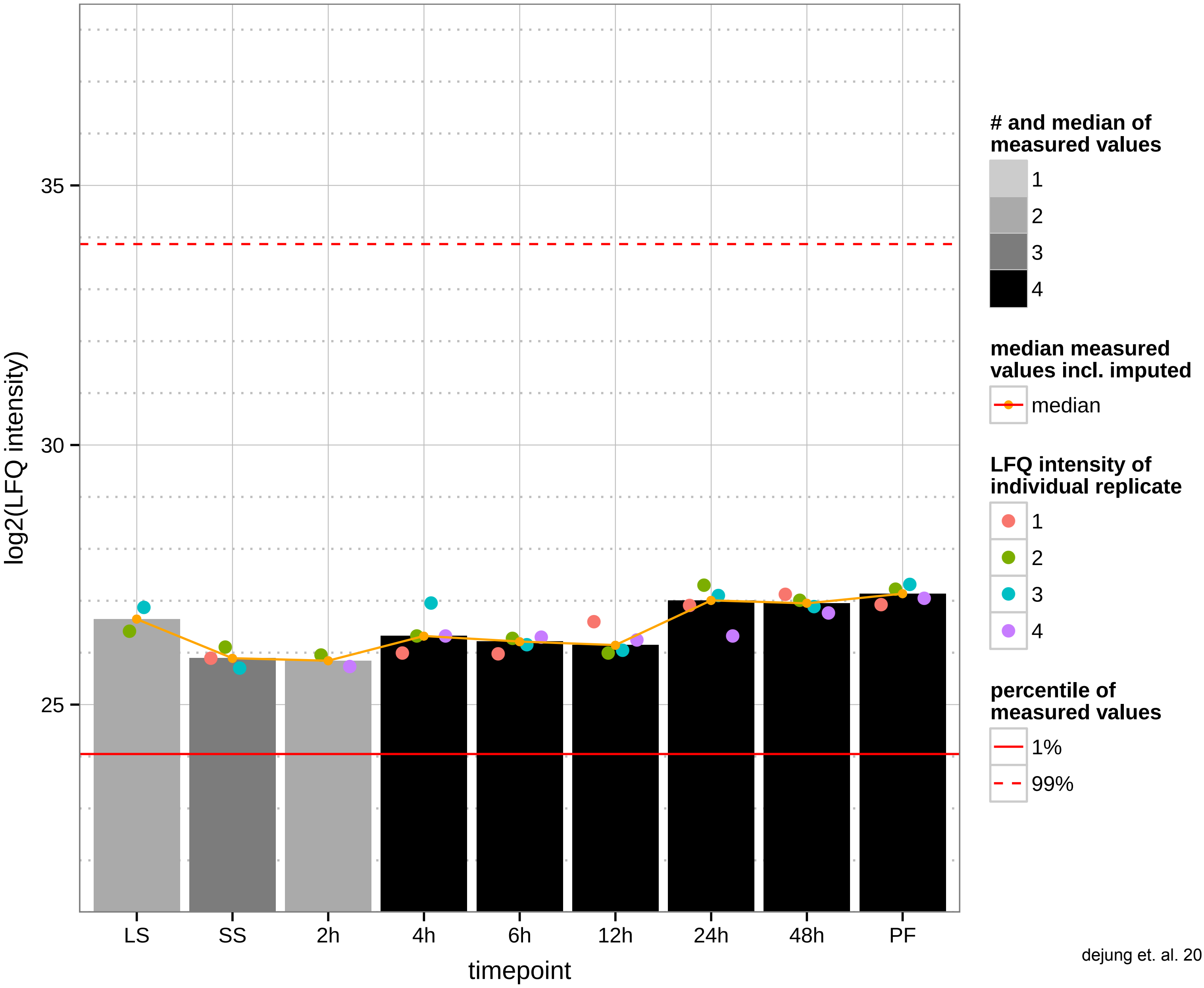
hypothetical protein, conserved
Tb927.3.1810
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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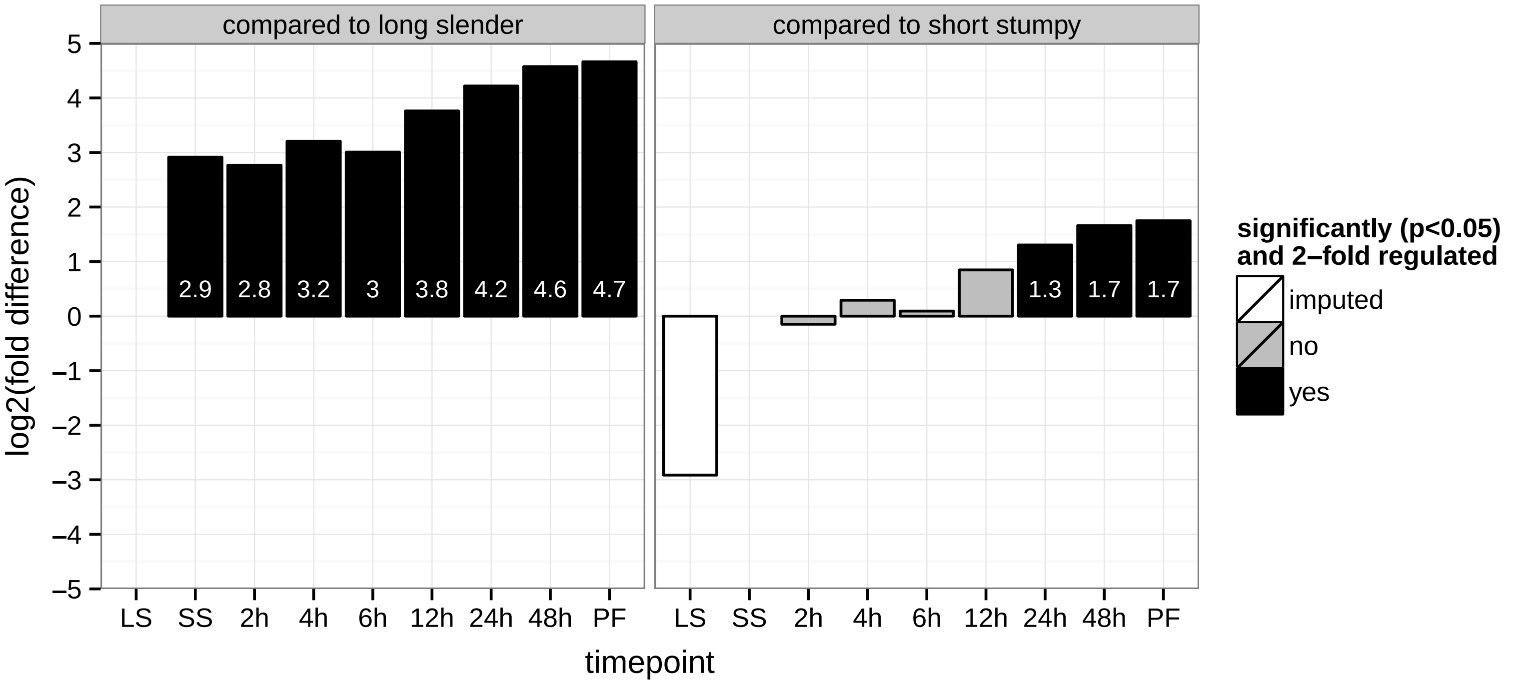
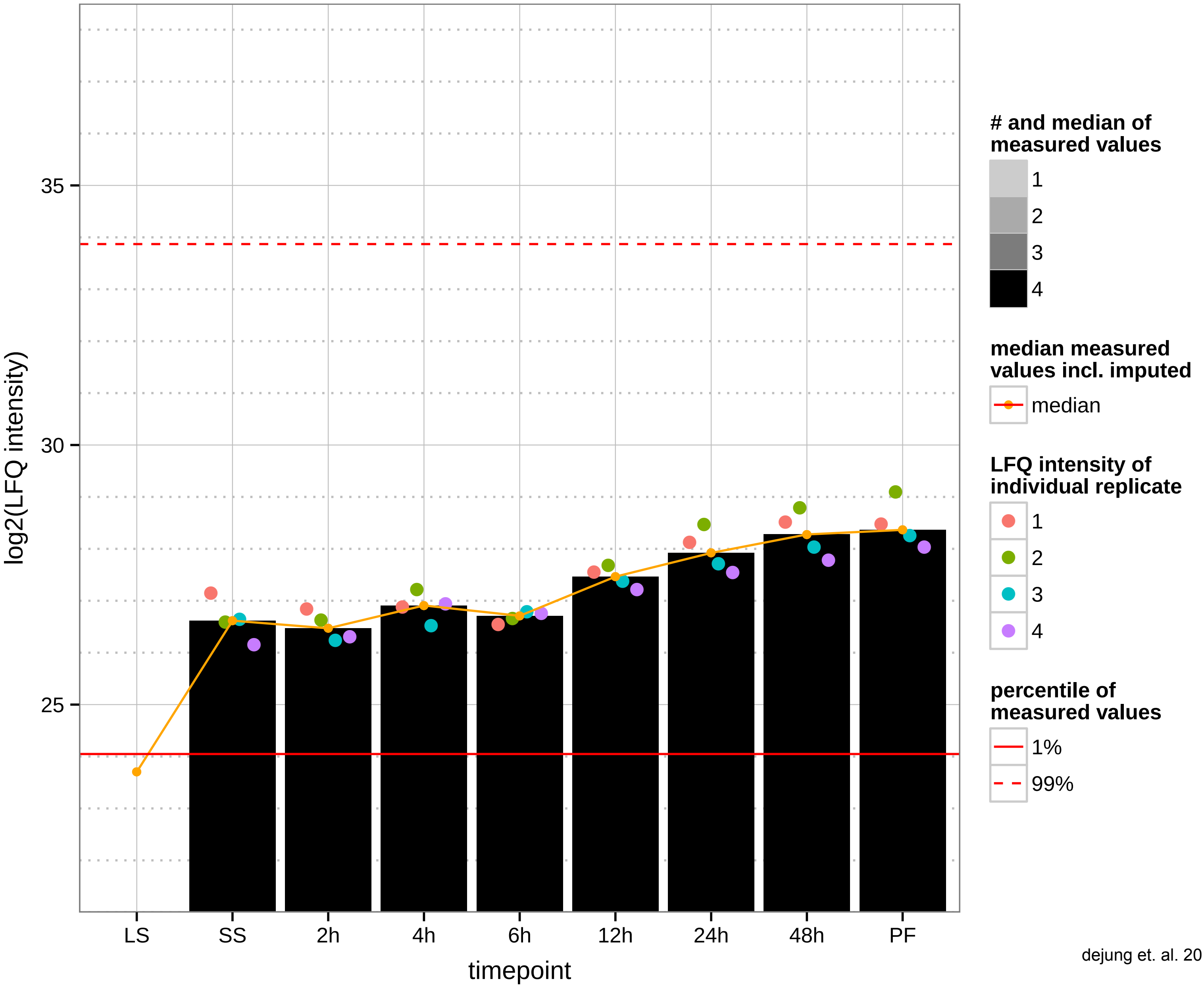
protein phosphatase 2C, putative
Tb927.3.2150
AGOF: phosphoprotein phosphatase activity
AGOC: null
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null





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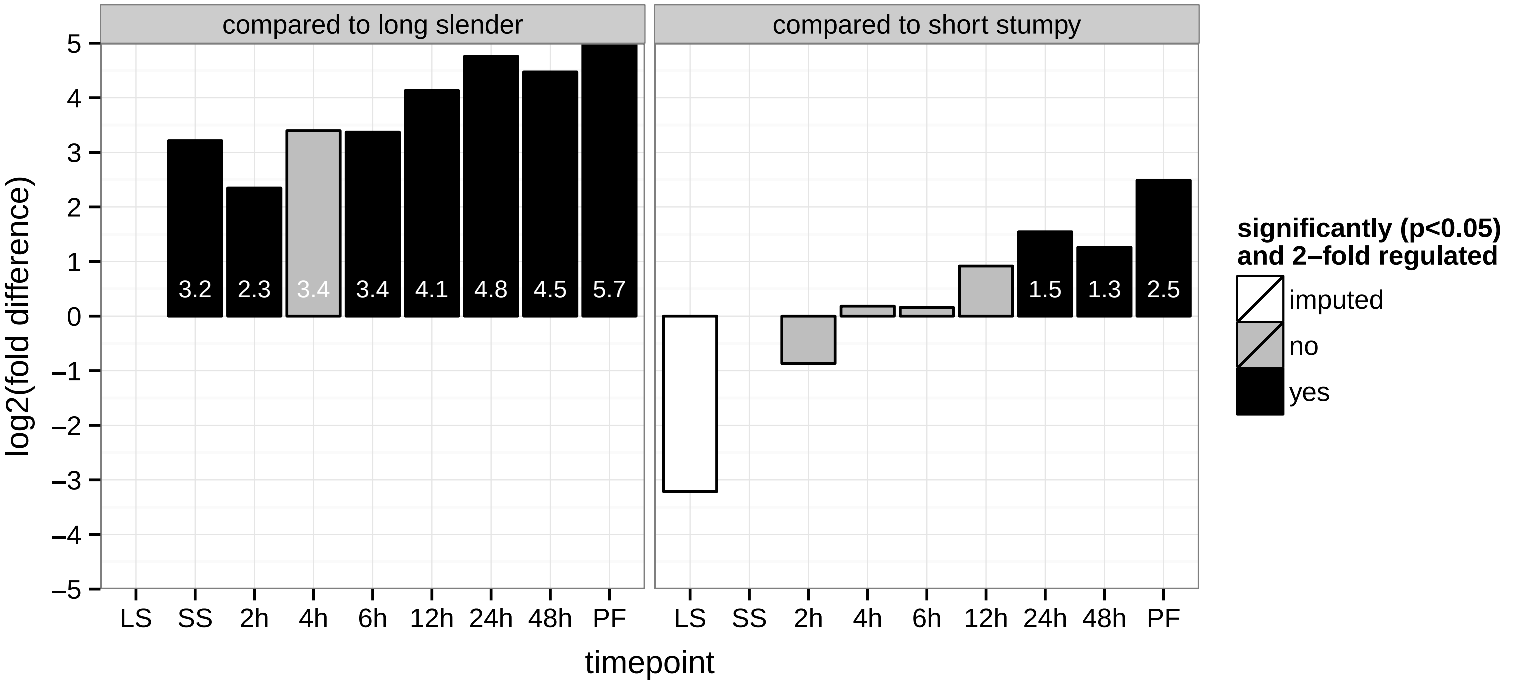
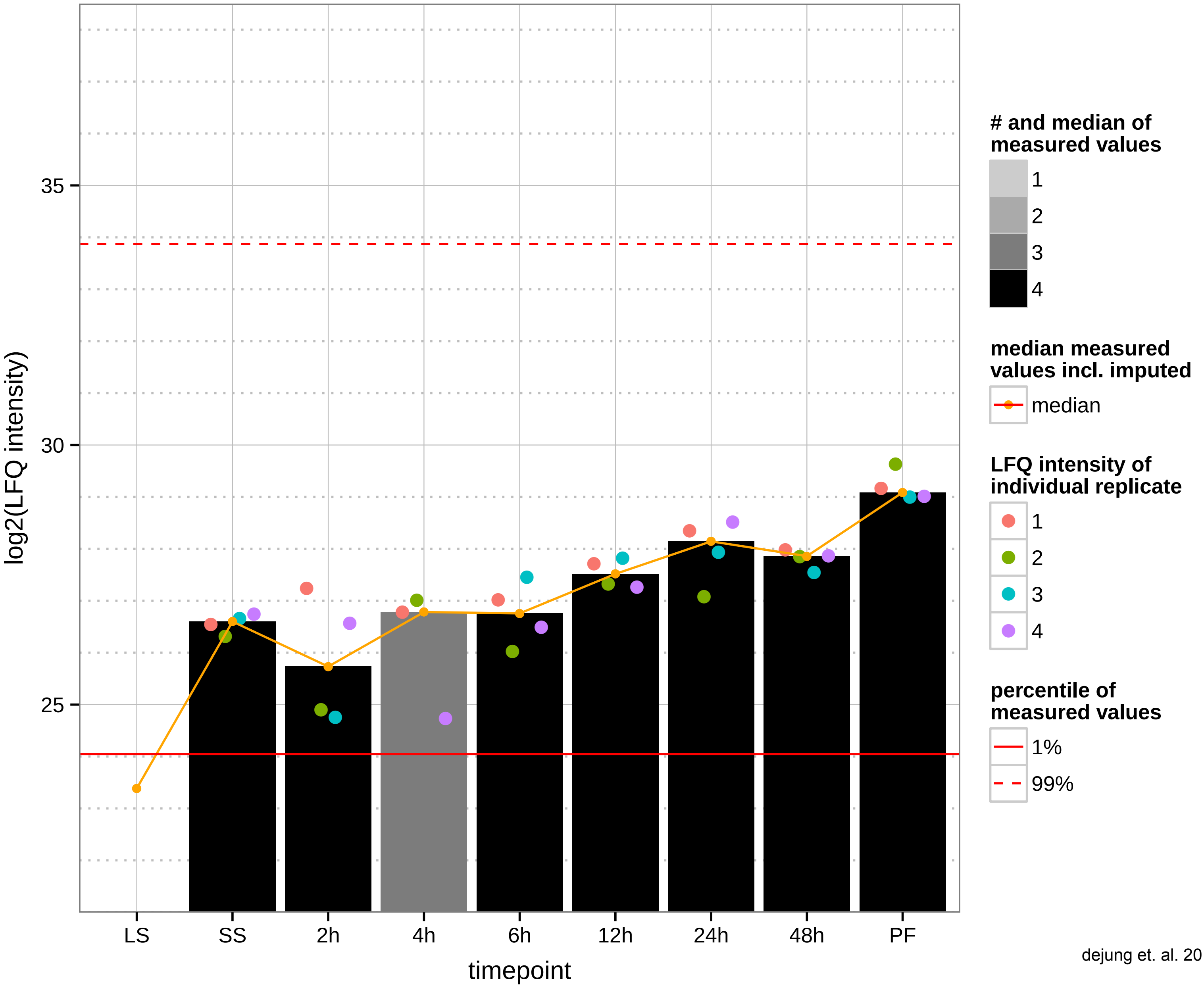
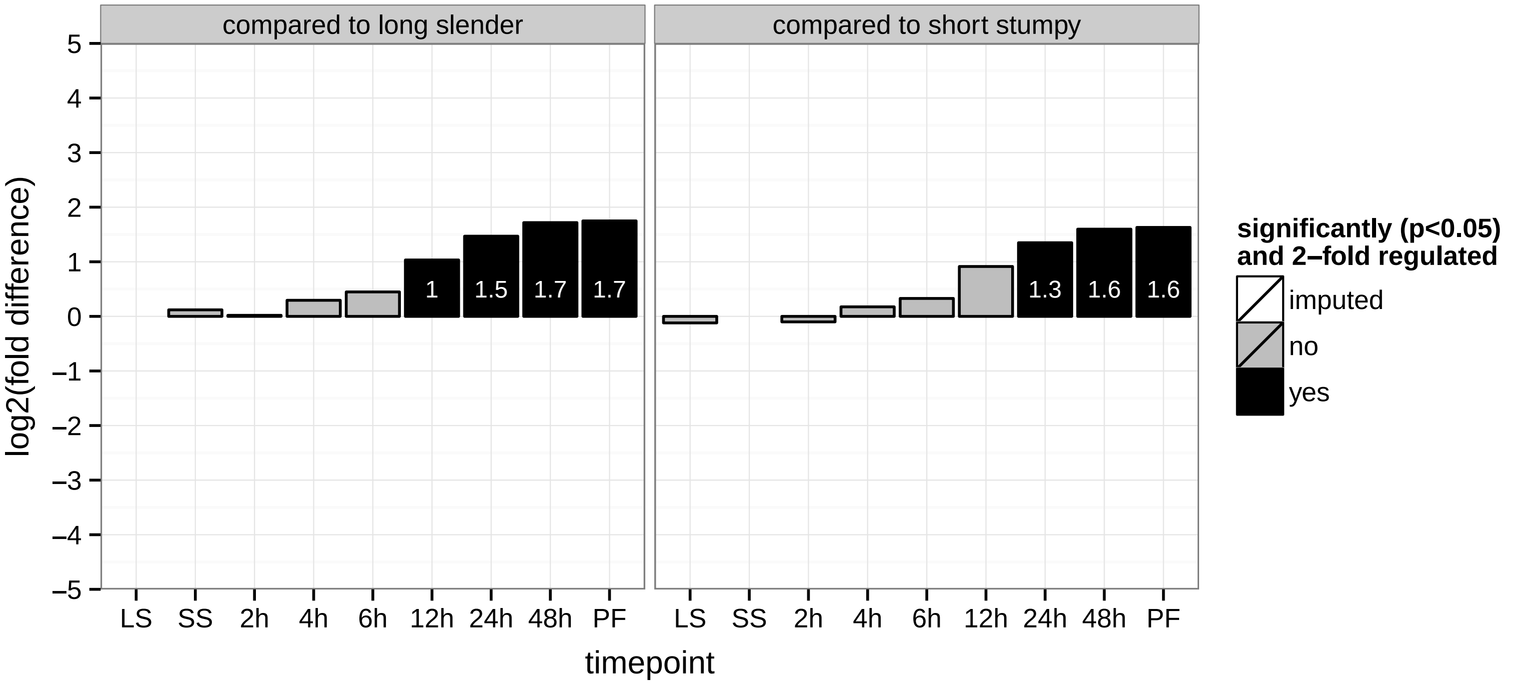
hypothetical protein, conserved
Tb927.3.2750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

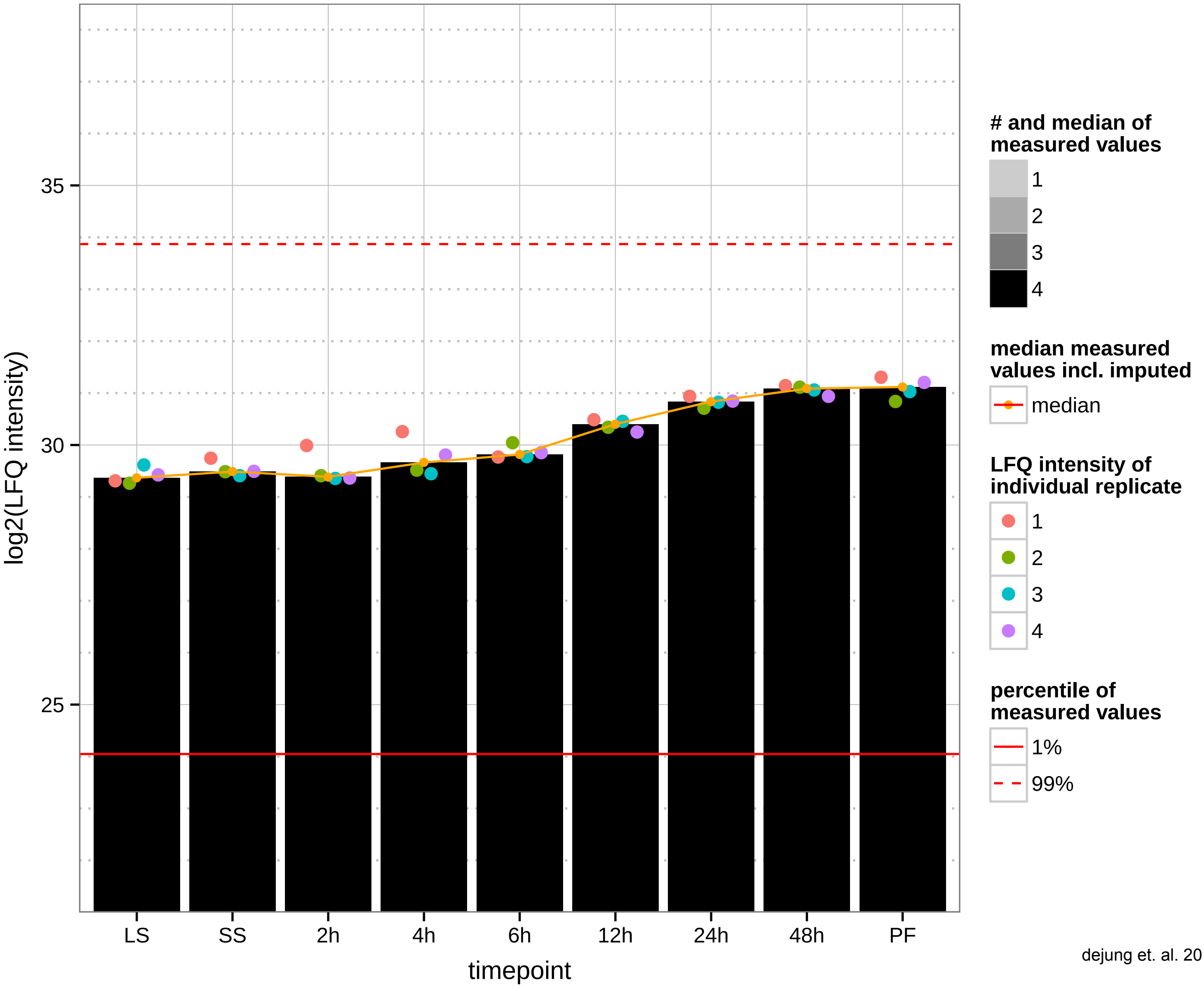




dejung et. al. 2015

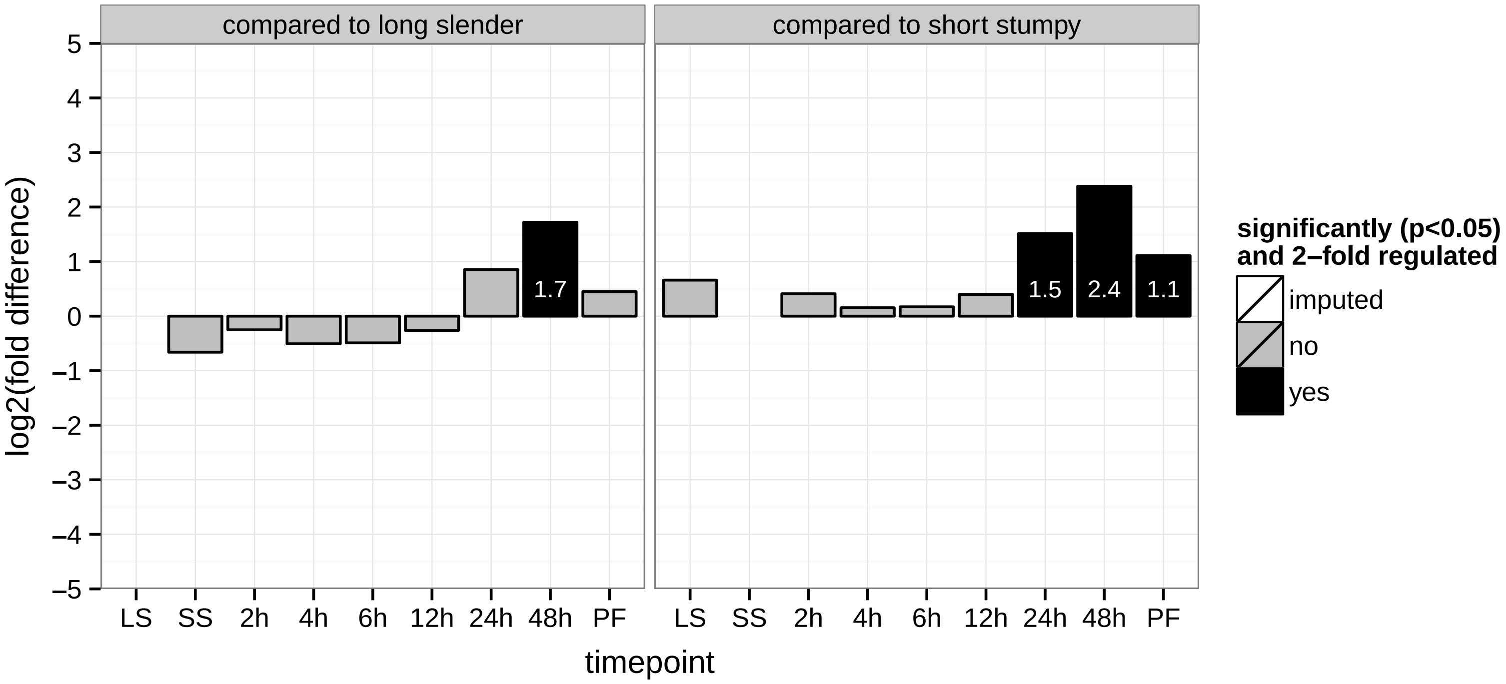
eukaryotic initiation factor 2a, putative
Tb927.3.2900
AGOF: RNA binding, translation initiation factor activity
AGOC: eukaryotic translation initiation factor 2 complex
AGOP: translation
PGOF: RNA binding, translation initiation factor activity
PGOC: eukaryotic translation initiation factor 2 complex
PGOP: null

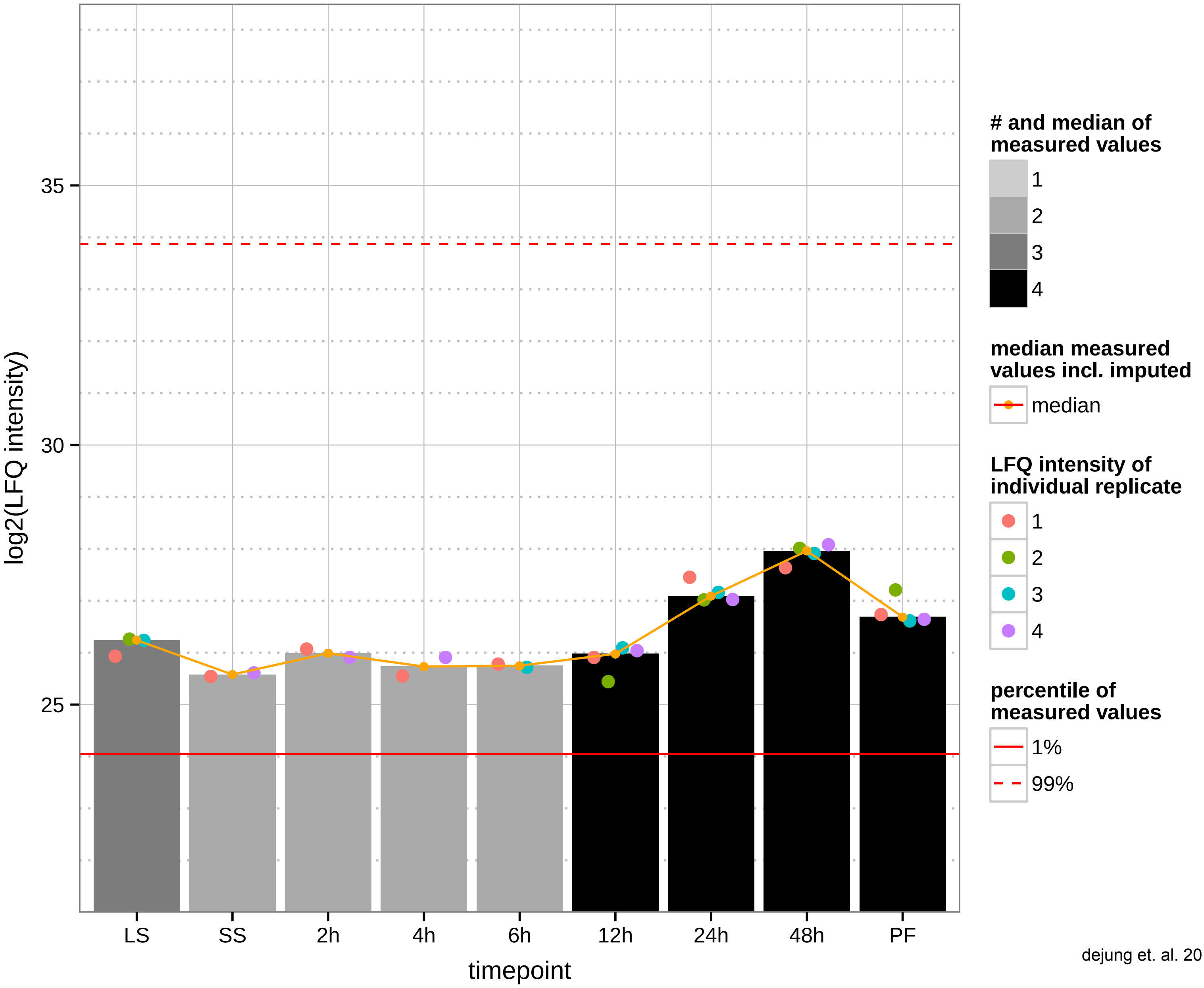




dejung et. al. 2015

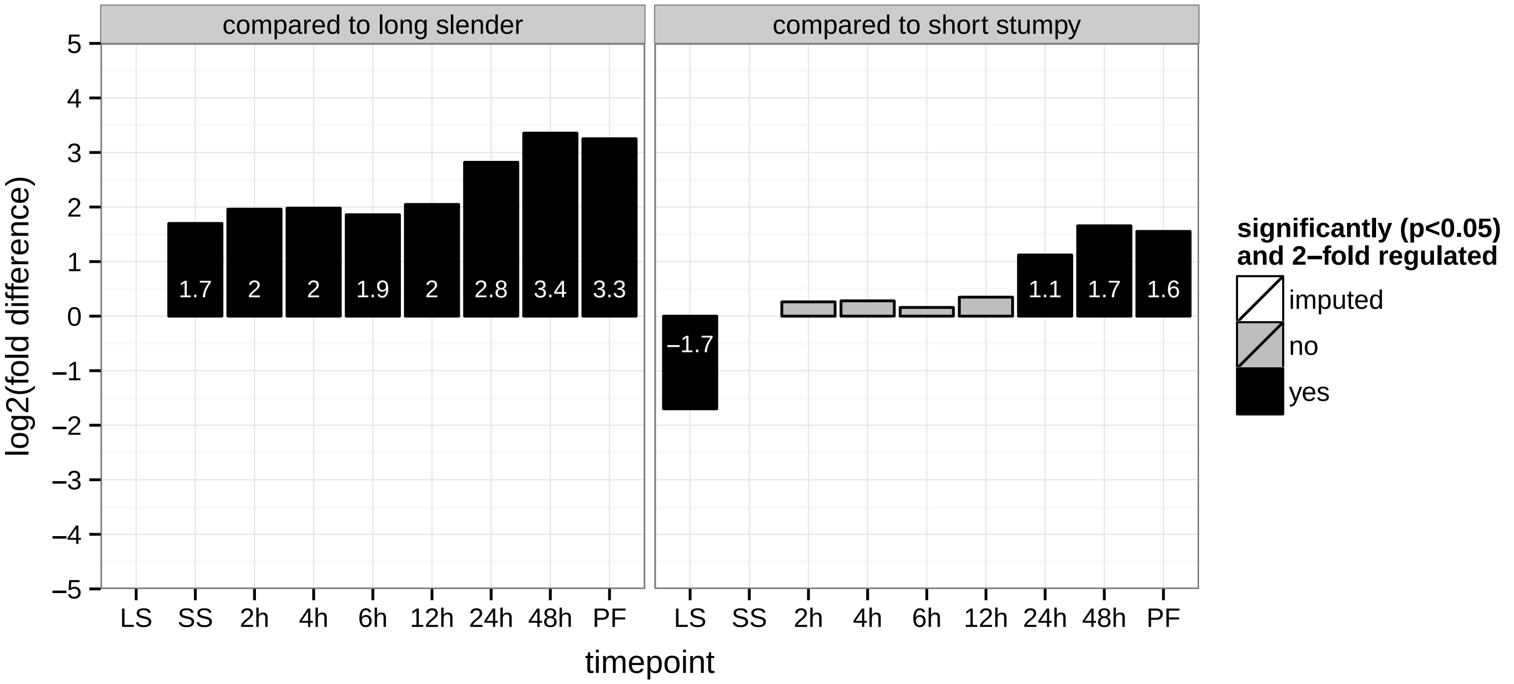
hypothetical protein, conserved
Tb927.3.3170
AGOF: null
AGOC: null
AGOP: intracellular signal transduction
PGOF: null
PGOC: null
PGOP: intracellular signal transduction

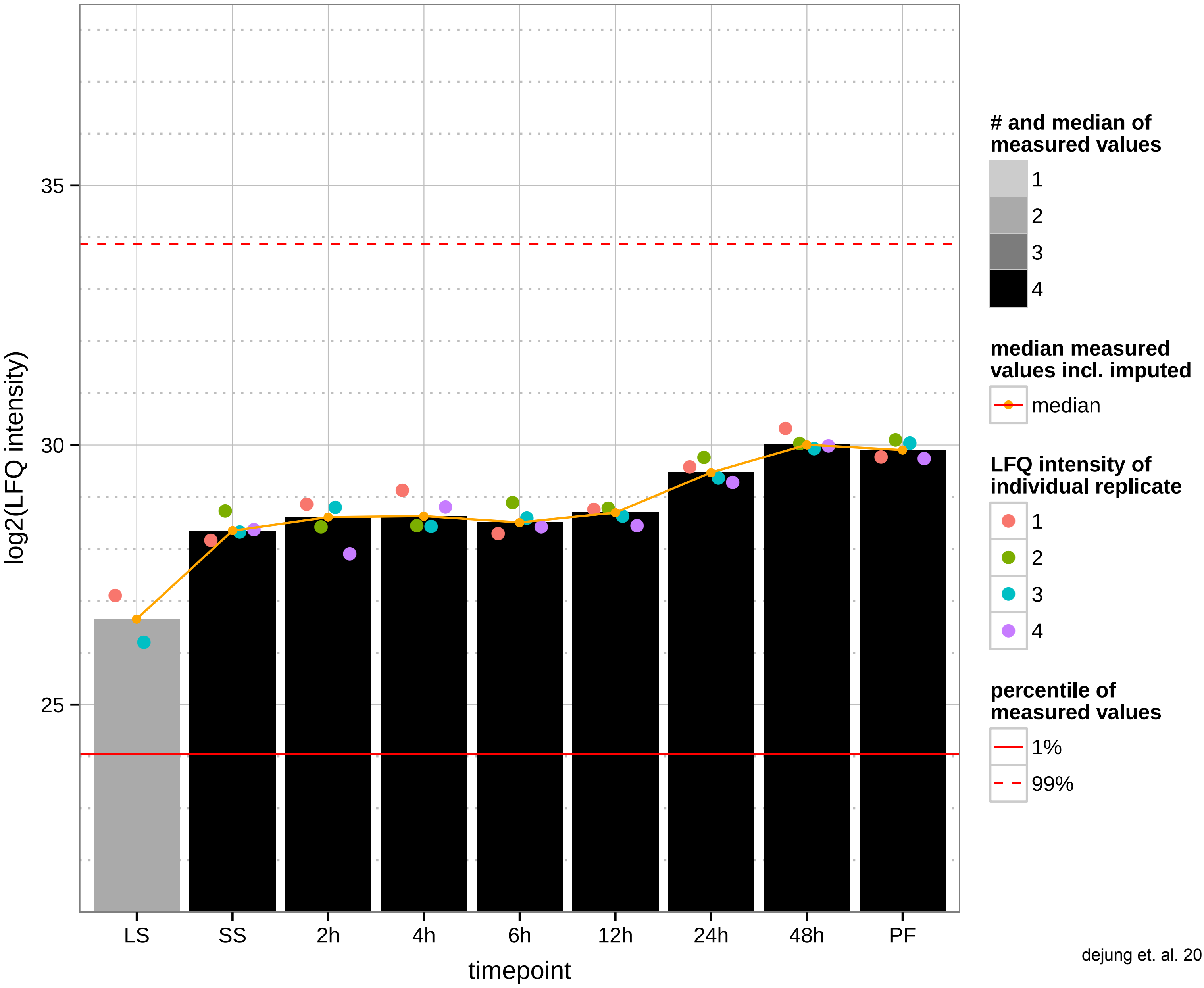




dejung et. al. 2015

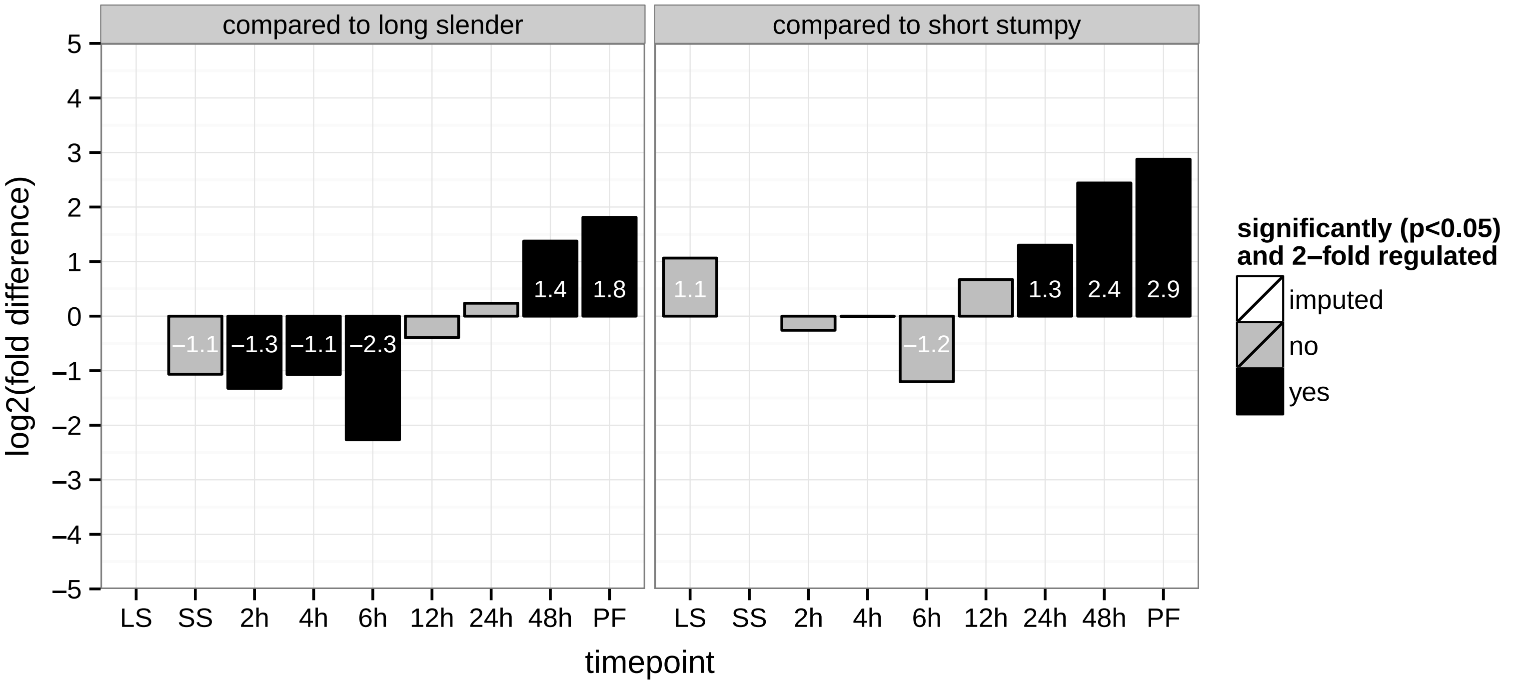
hypothetical protein, conserved
Tb927.3.3460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

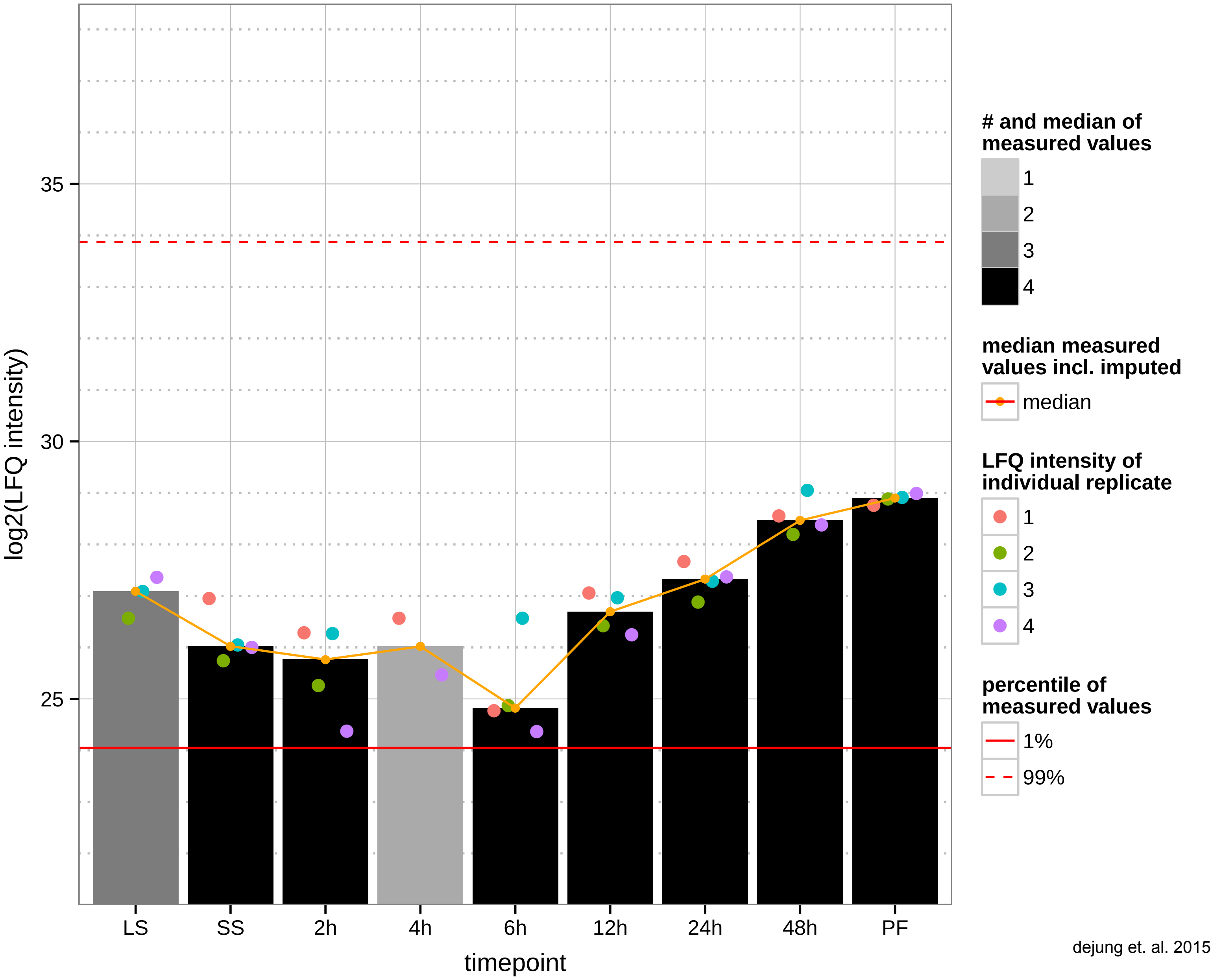




dejung et. al. 2015

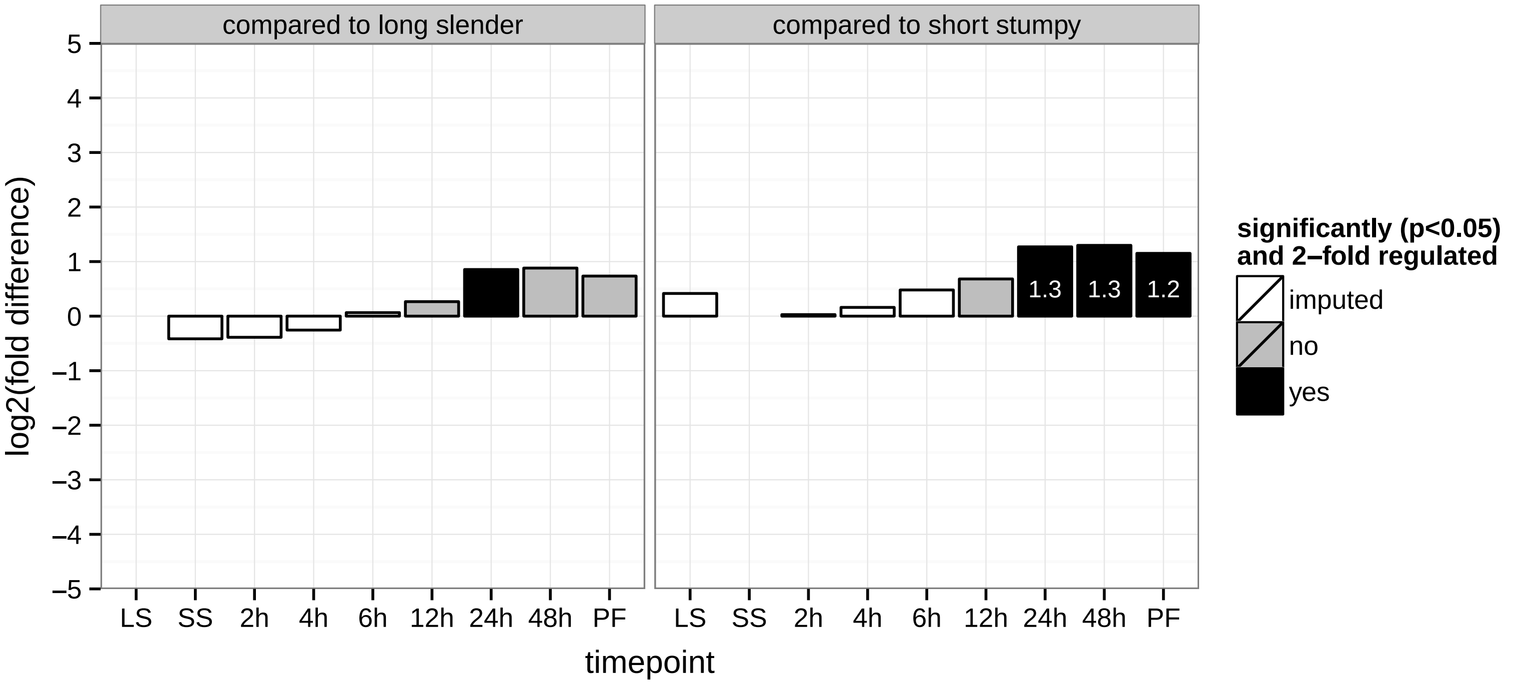
peroxisomal targeting signal type 2 receptor, putative, peroxin 7, peroxin 7 (PEX7)
Tb927.3.3610
AGOF: peroxisome matrix targeting signal−2 binding
AGOC: cytoplasm, peroxisome
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

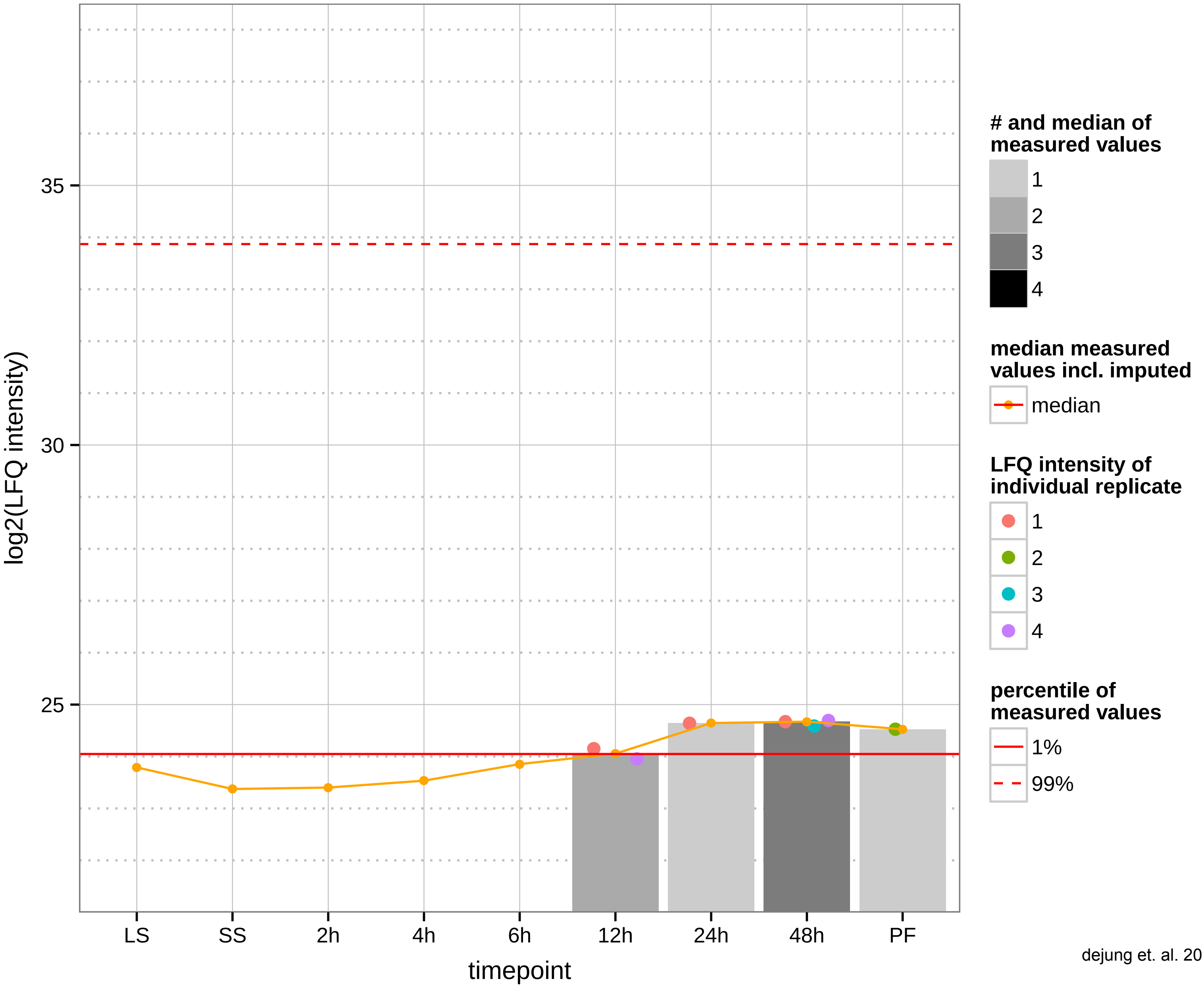




dejung et. al. 2015

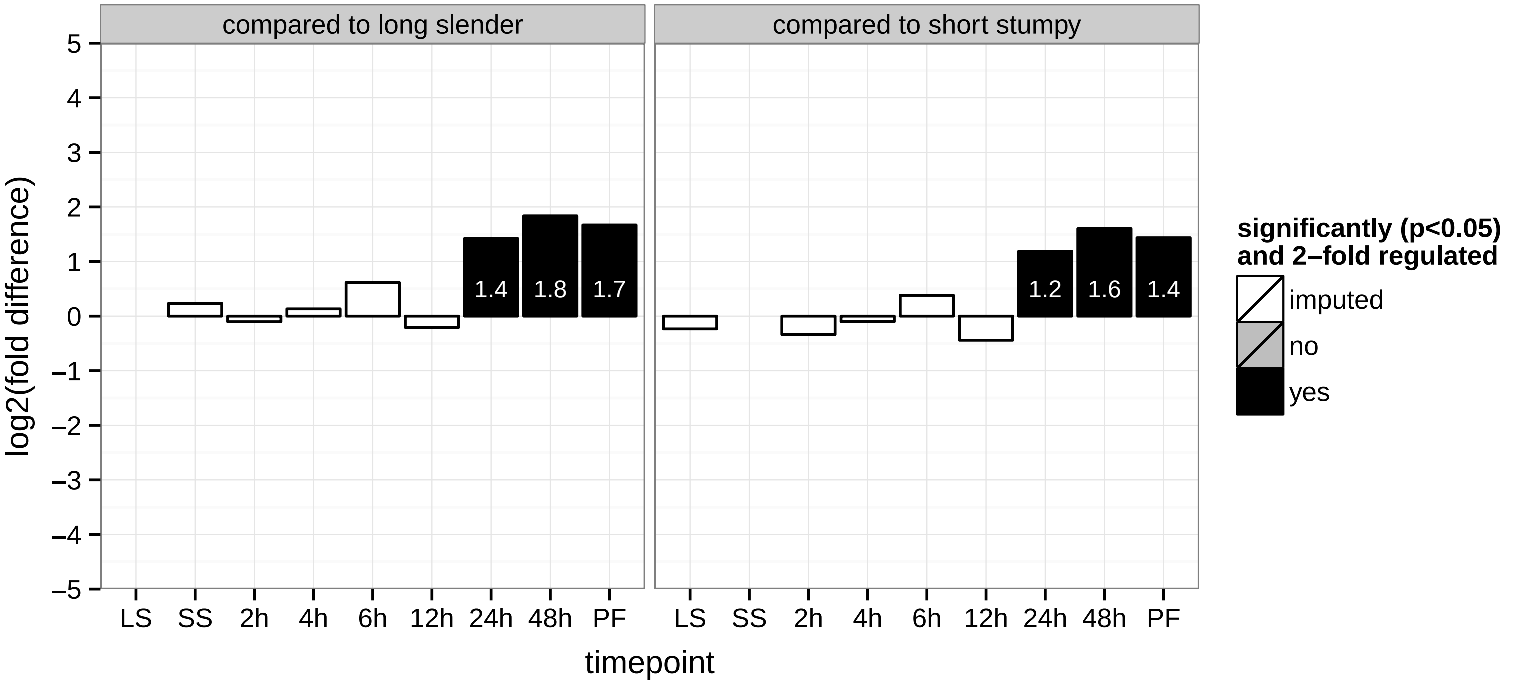
SNF1/AMP–activated kinase catalytic subunit, putative
Tb927.3.4560
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, protein phosphorylation, quorum sensing invo
PGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity, transferring phosphoru
PGOC: null
PGOP: protein phosphorylation

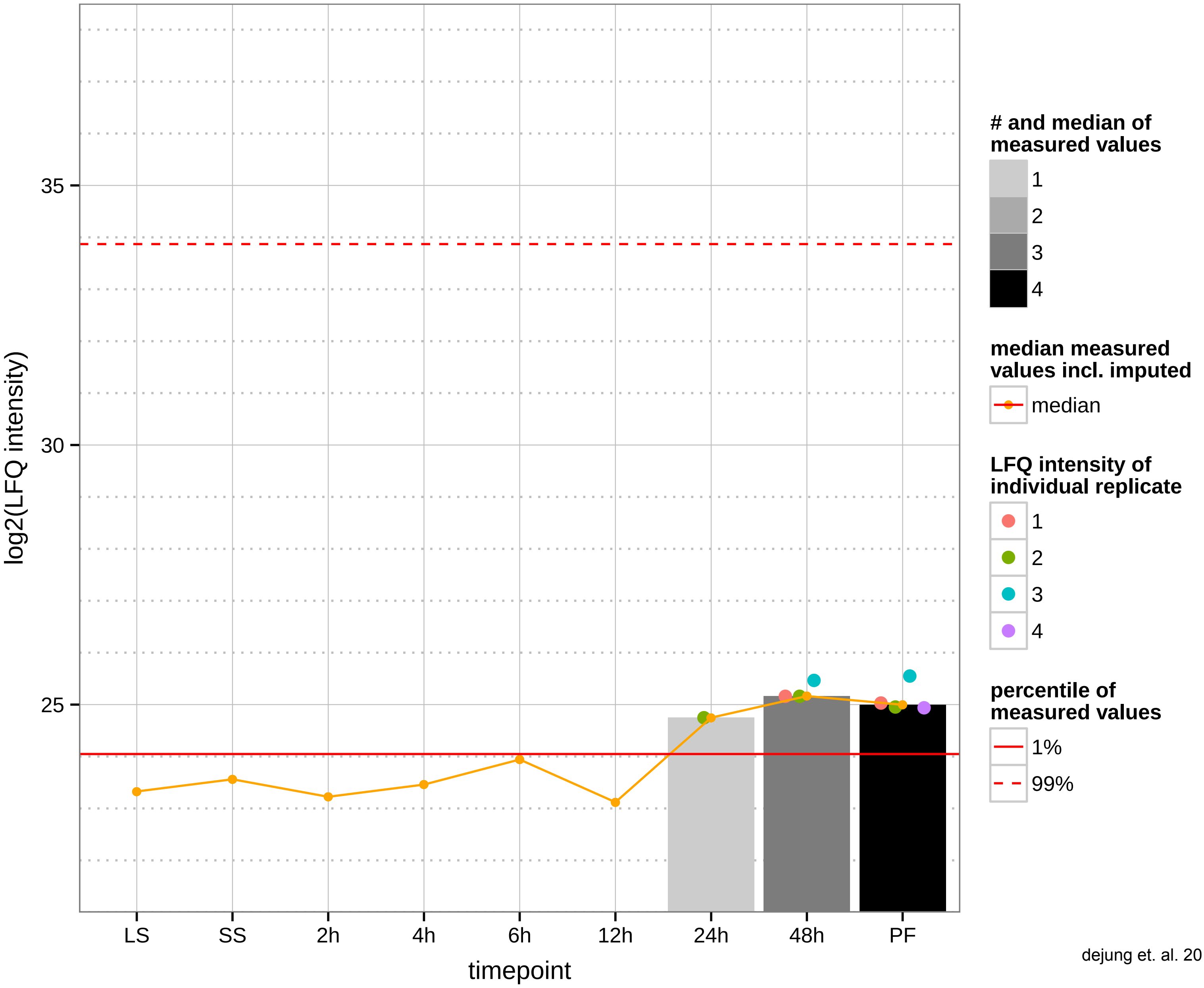




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.1280
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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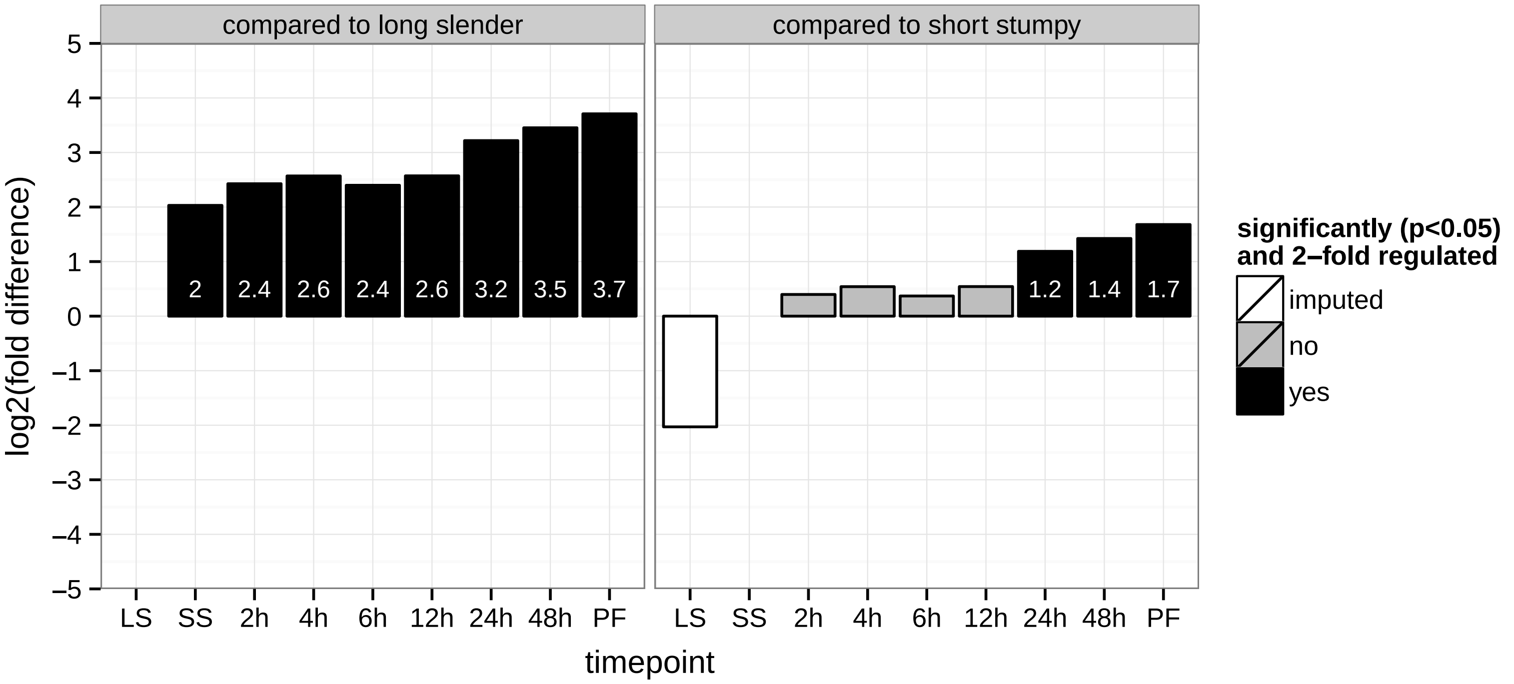
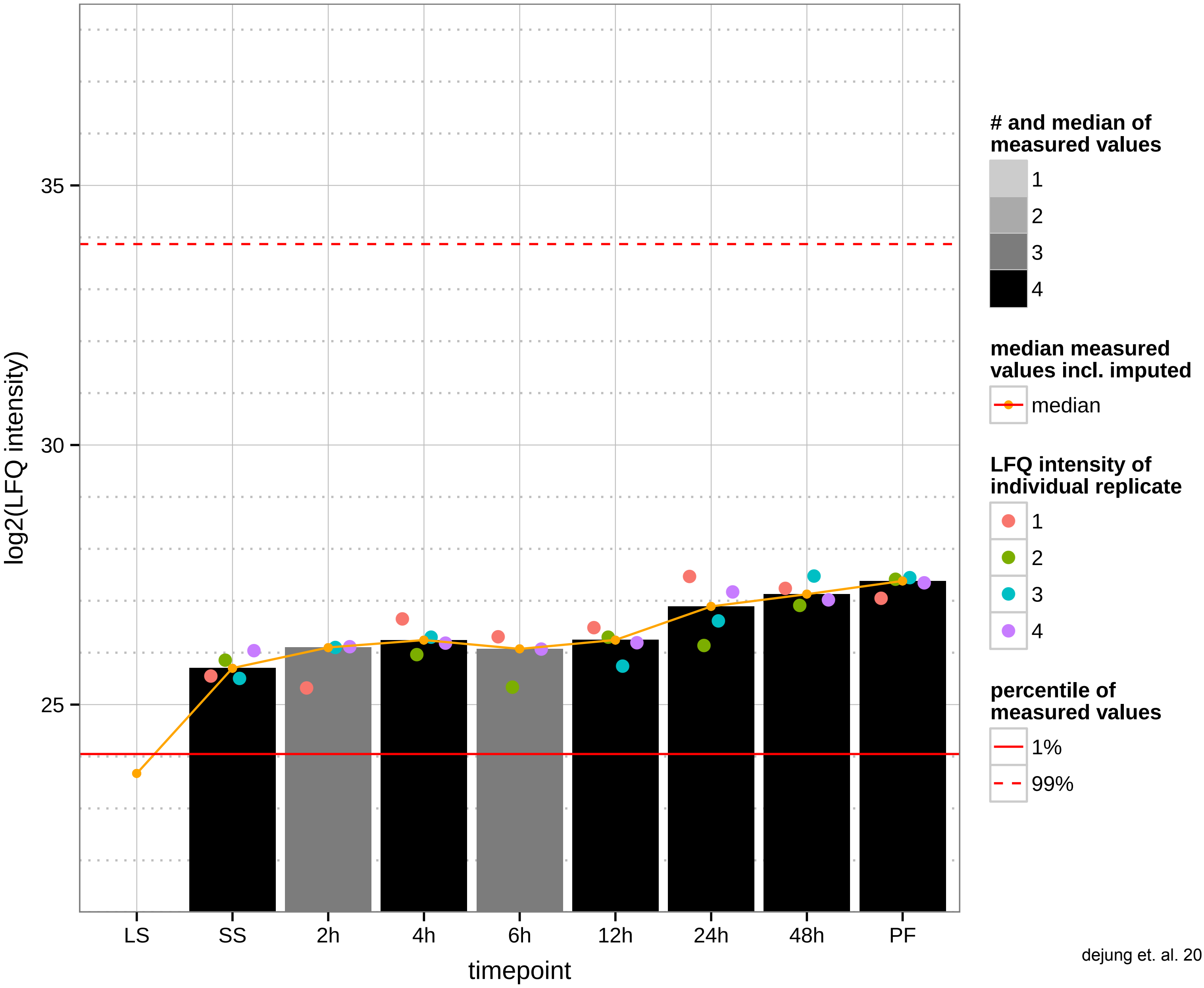
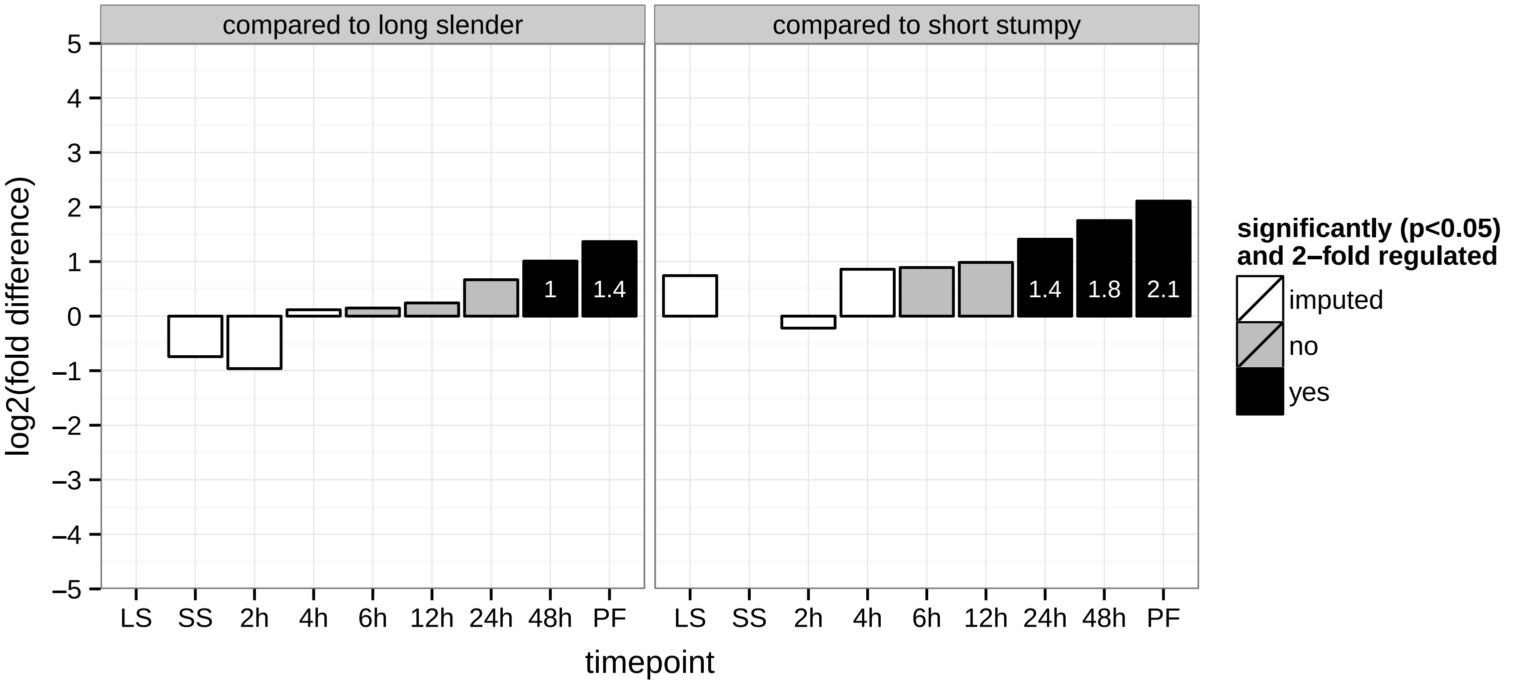
RNA editing associated helicase 2, mitochondrial RNA binding complex 1 subunit (REH2)
Tb927.4.1500
AGOF: 3'−5' RNA helicase activity, ATP binding, RNA binding, double−stranded RNA binding, helicase activity, mRNA binding
AGOC: intracellular, mitochondrial mRNA editing complex, mitochondrion
AGOP: cytidine to uridine editing, mRNA modification, mRNA stabilization
PGOF: ATP binding, ATP−dependent helicase activity, double−stranded RNA binding, helicase activity, nucleic acid binding
PGOC: intracellular
PGOP: null

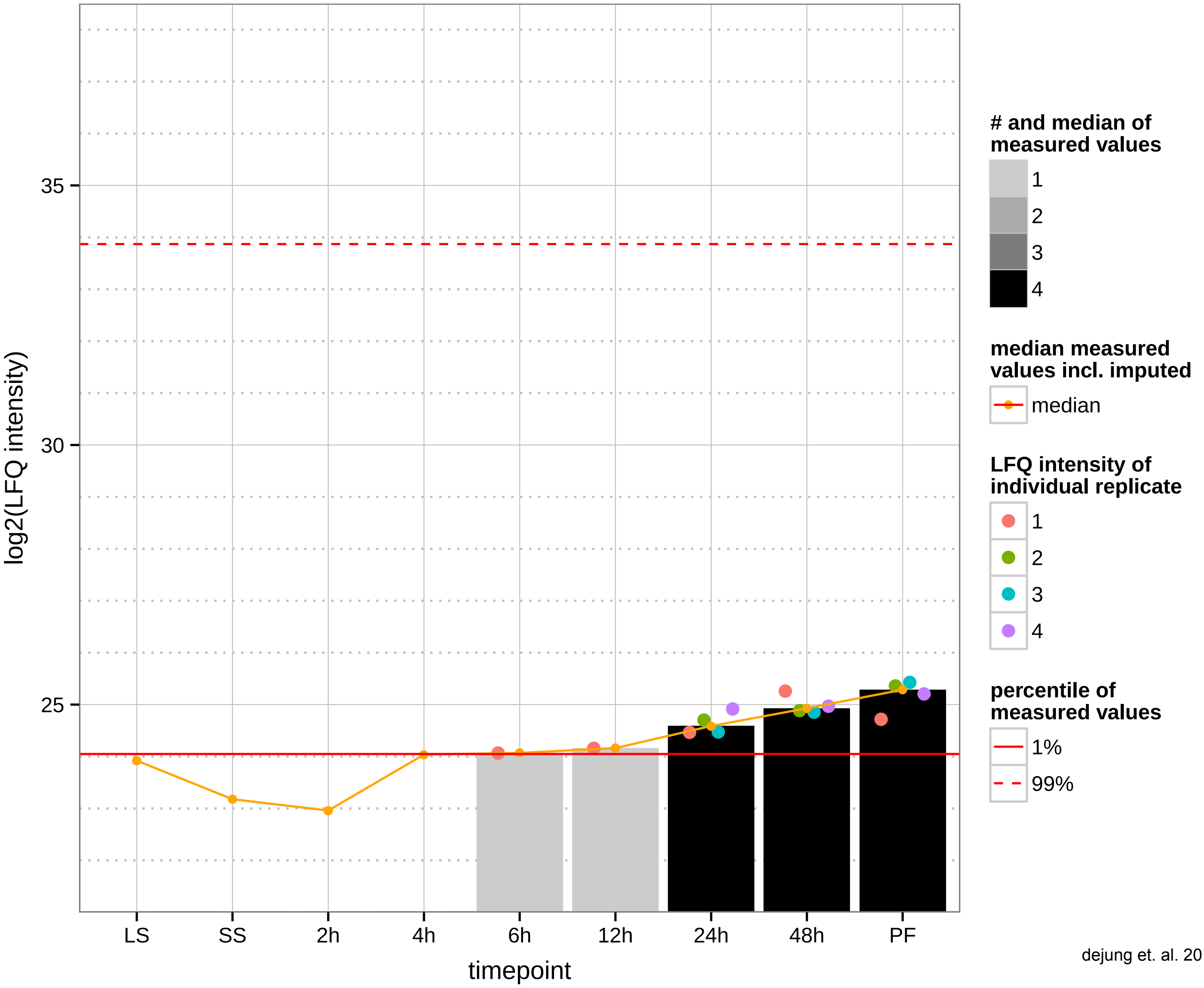




dejung et. al. 2015

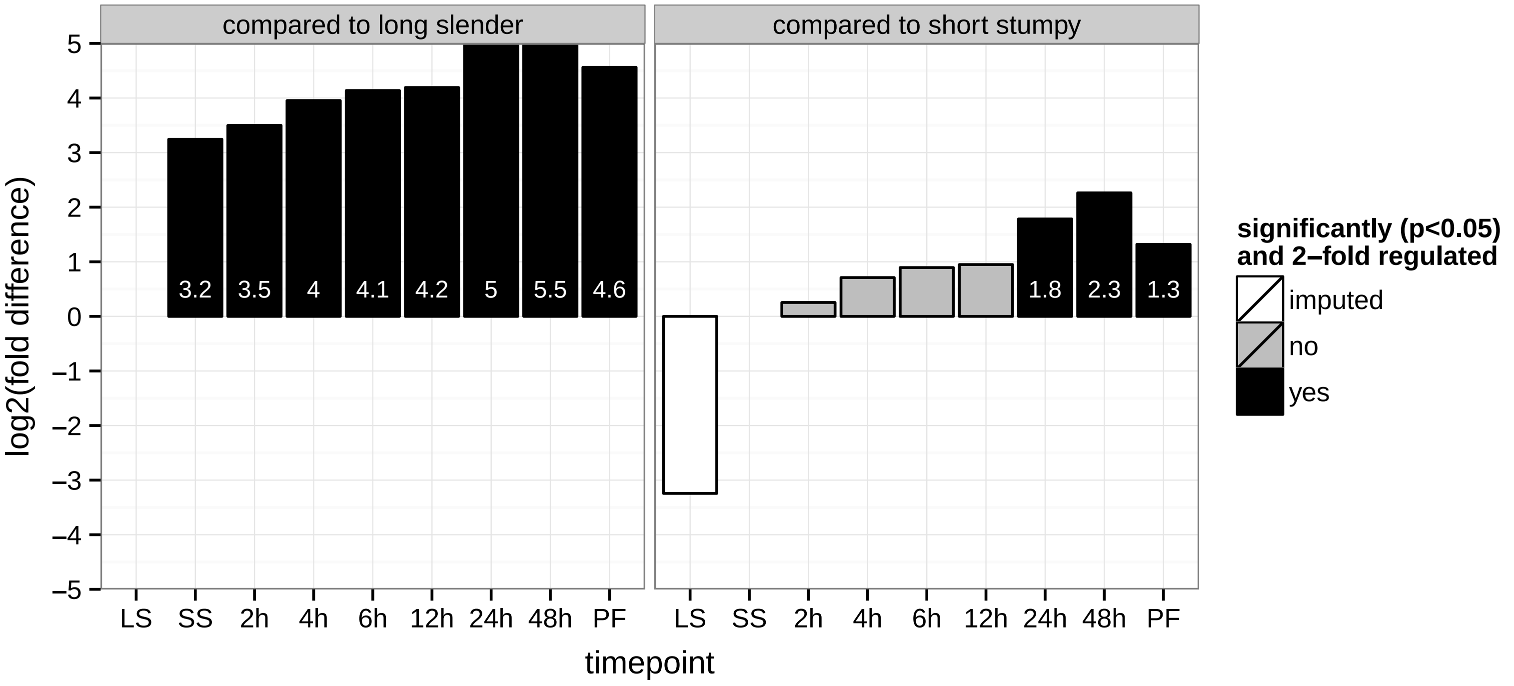
hypothetical protein, conserved
Tb927.4.2680
AGOF: null
AGOC: null
AGOP: null
PGOF: ATP binding, kinase activity
PGOC: null
PGOP: null

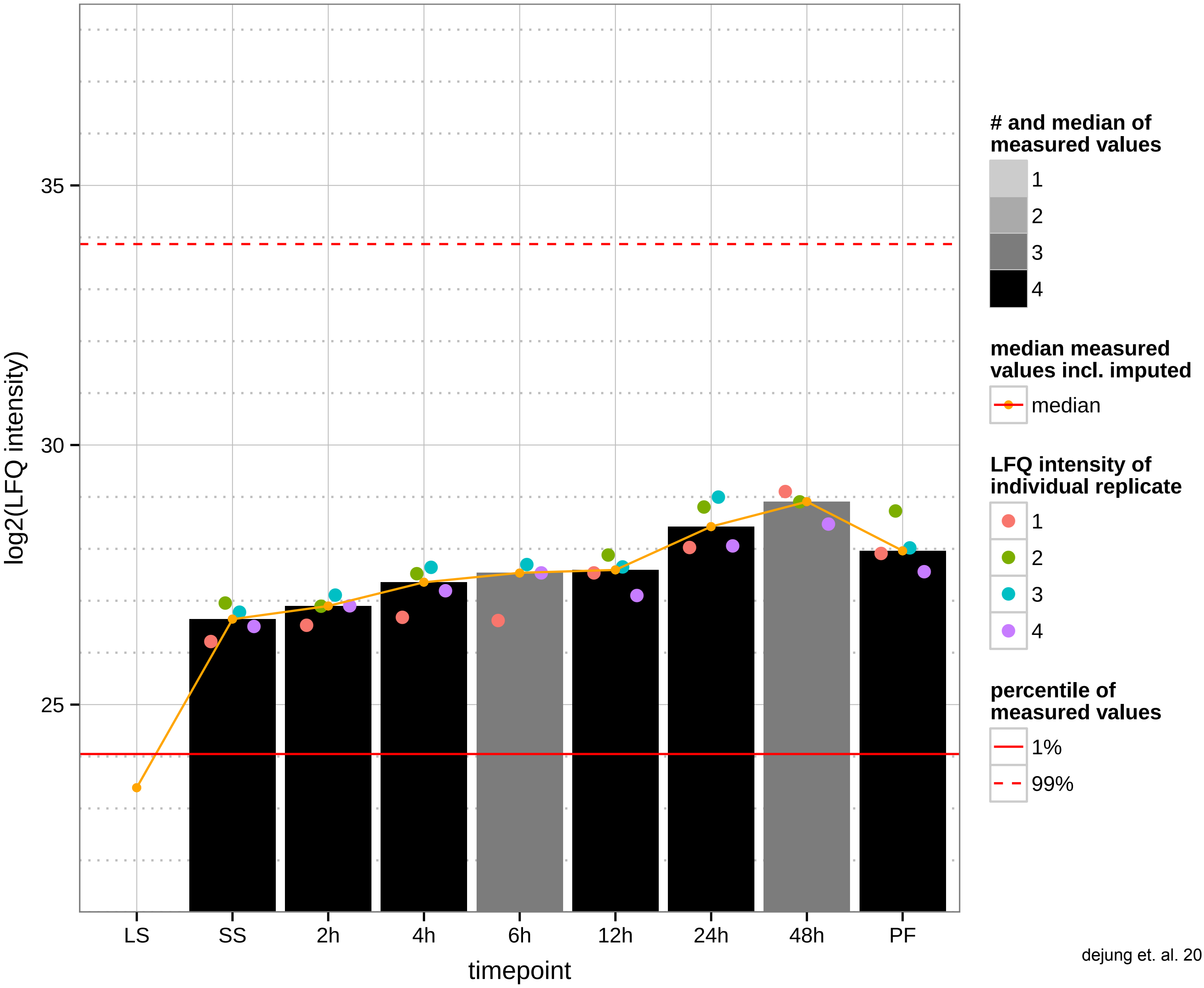




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.3450
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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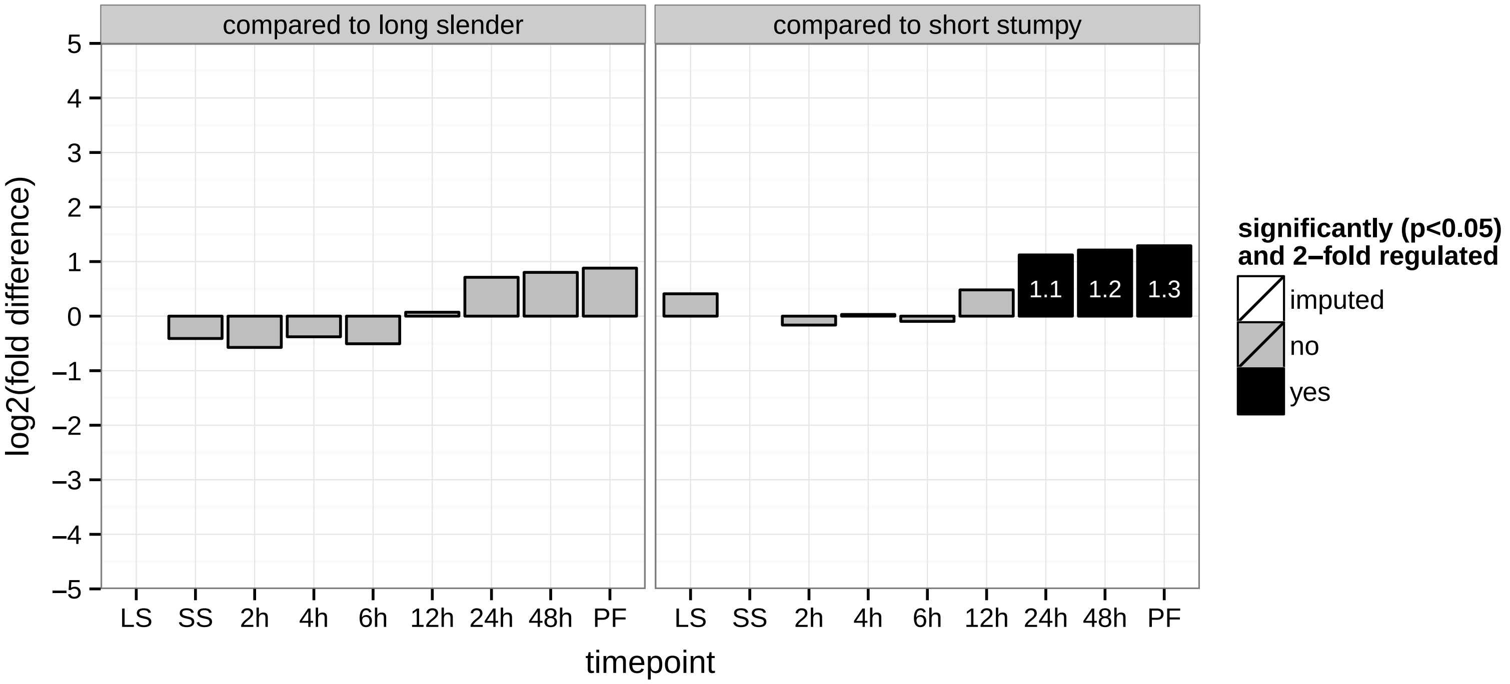
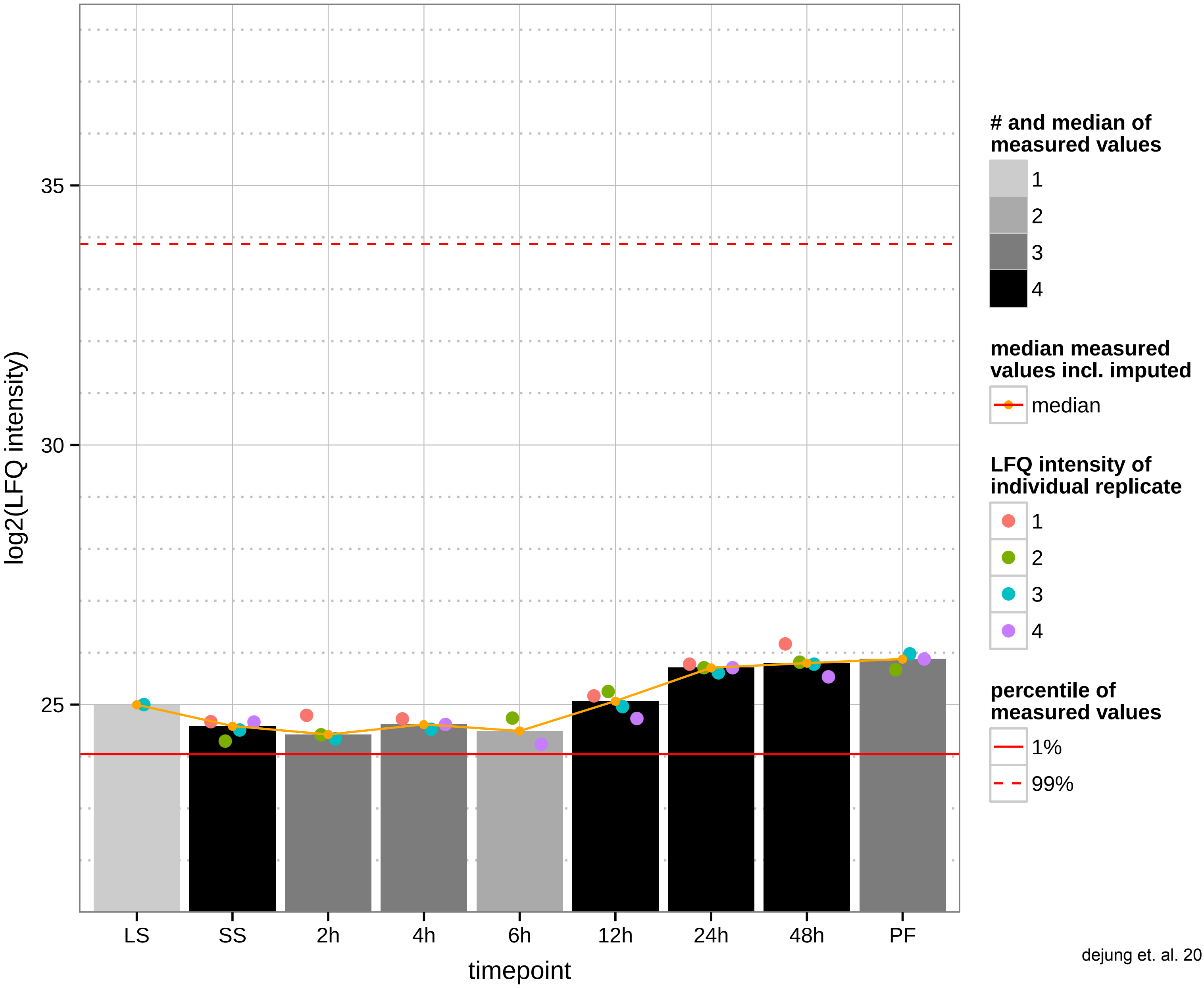
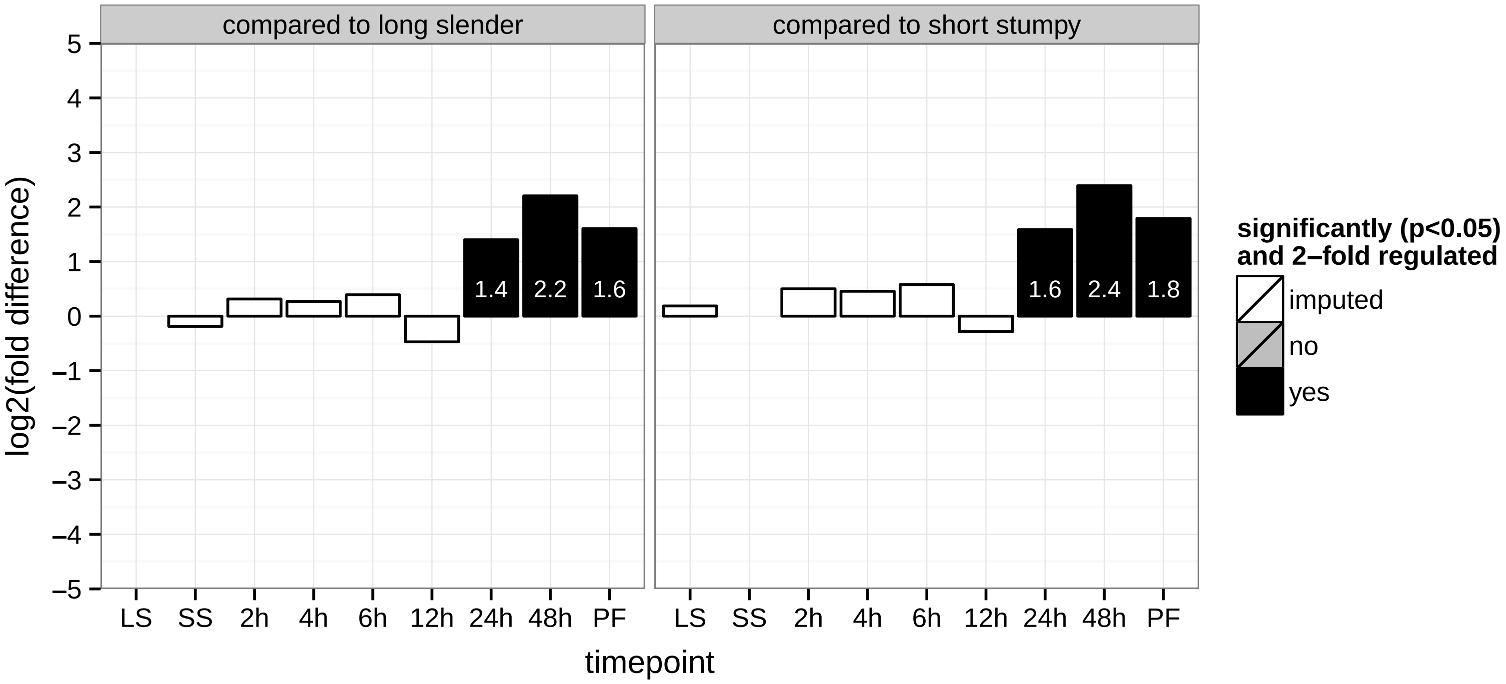
Double RNA binding domain protein 7 (DRBD7)
Tb927.4.400
AGOF: RNA binding
AGOC: cytoplasm
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null

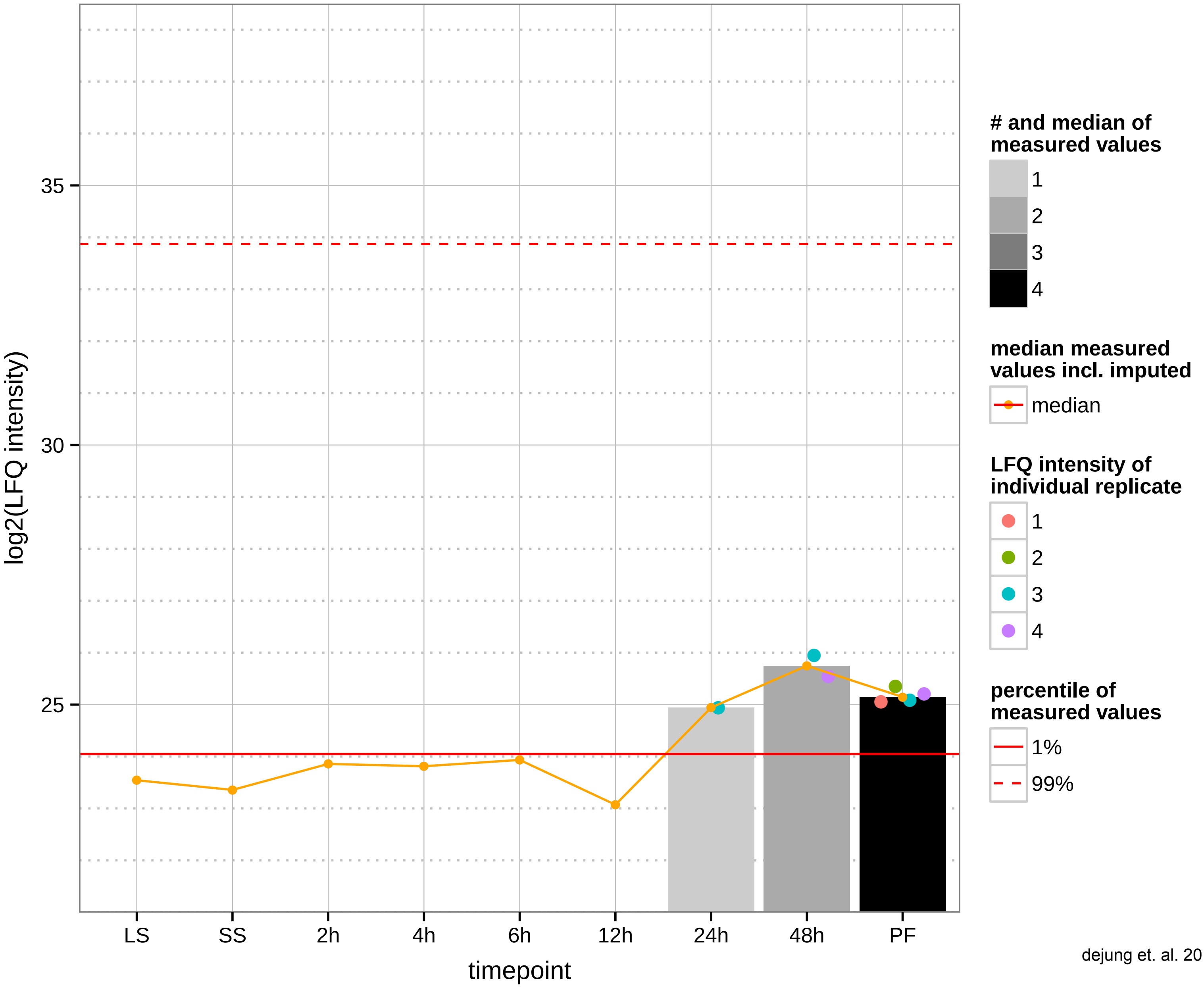




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.4570
AGOF: sequence−specific DNA binding transcription factor activity
AGOC: null
AGOP: regulation of transcription, DNA−dependent
PGOF: null
PGOC: null
PGOP: null





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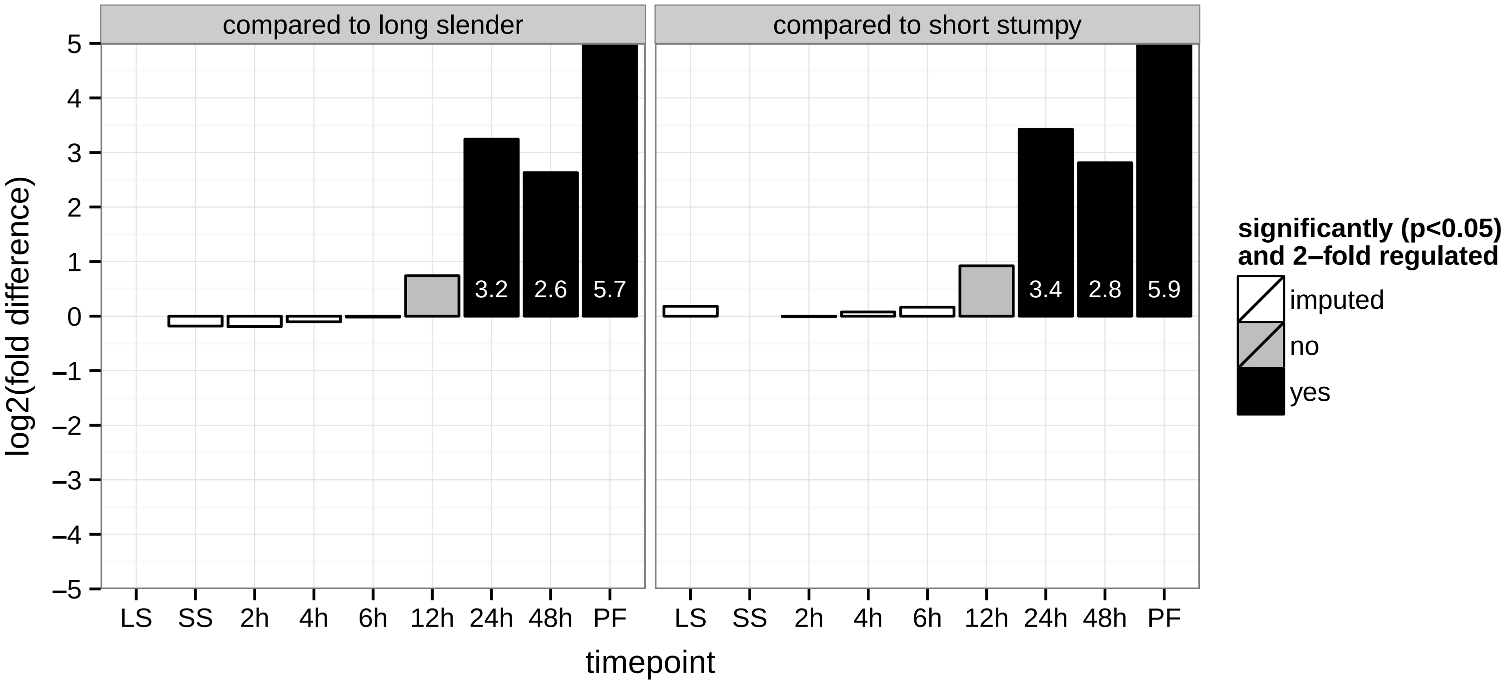
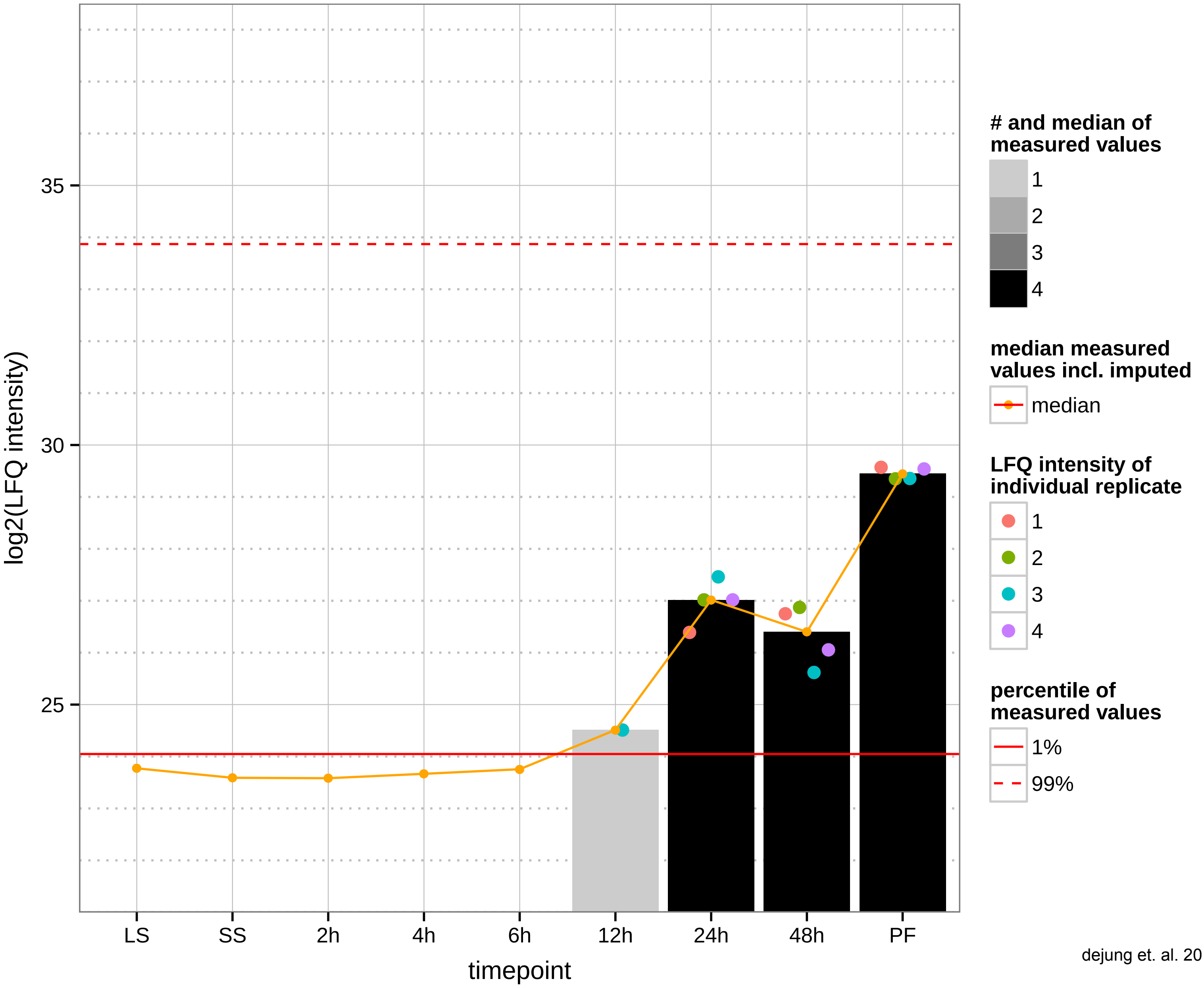
cytochrome oxidase subunit VIII (COXVIII)
Tb927.4.4620
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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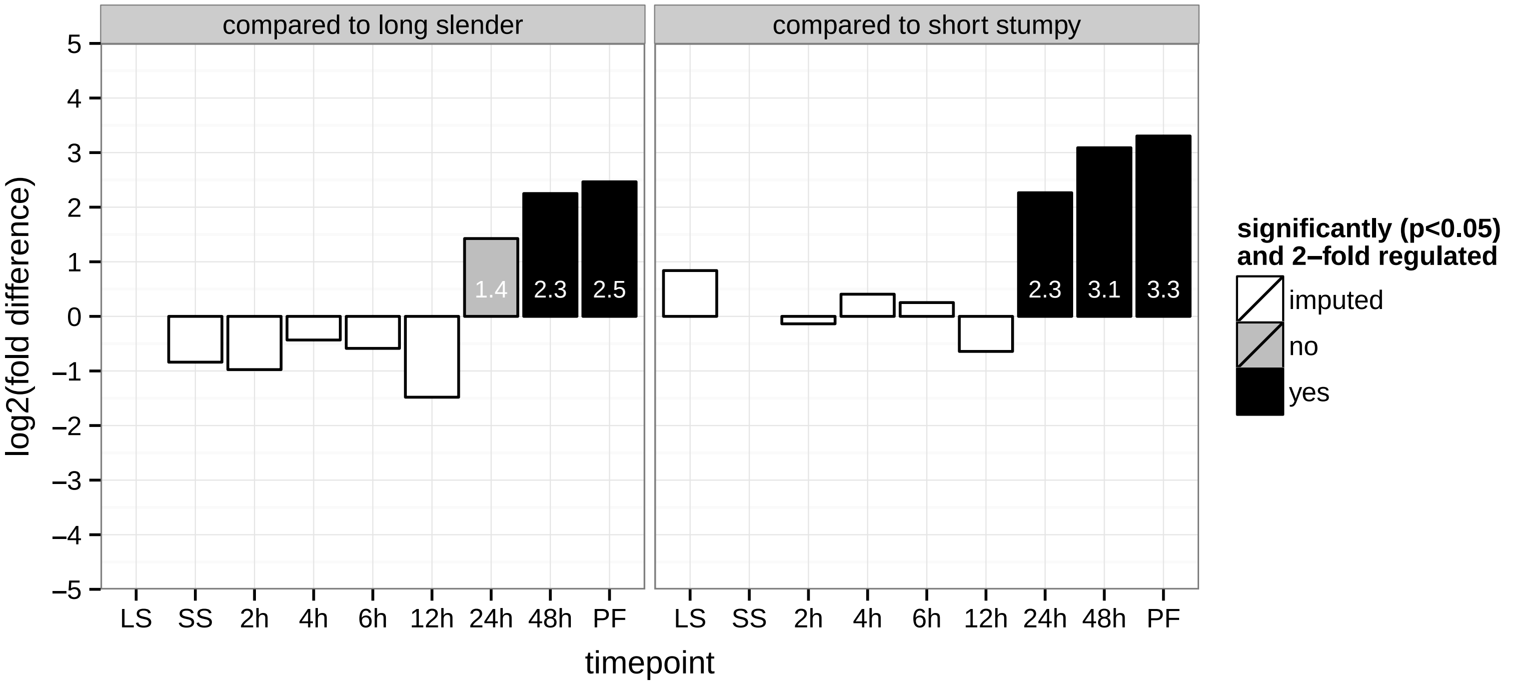
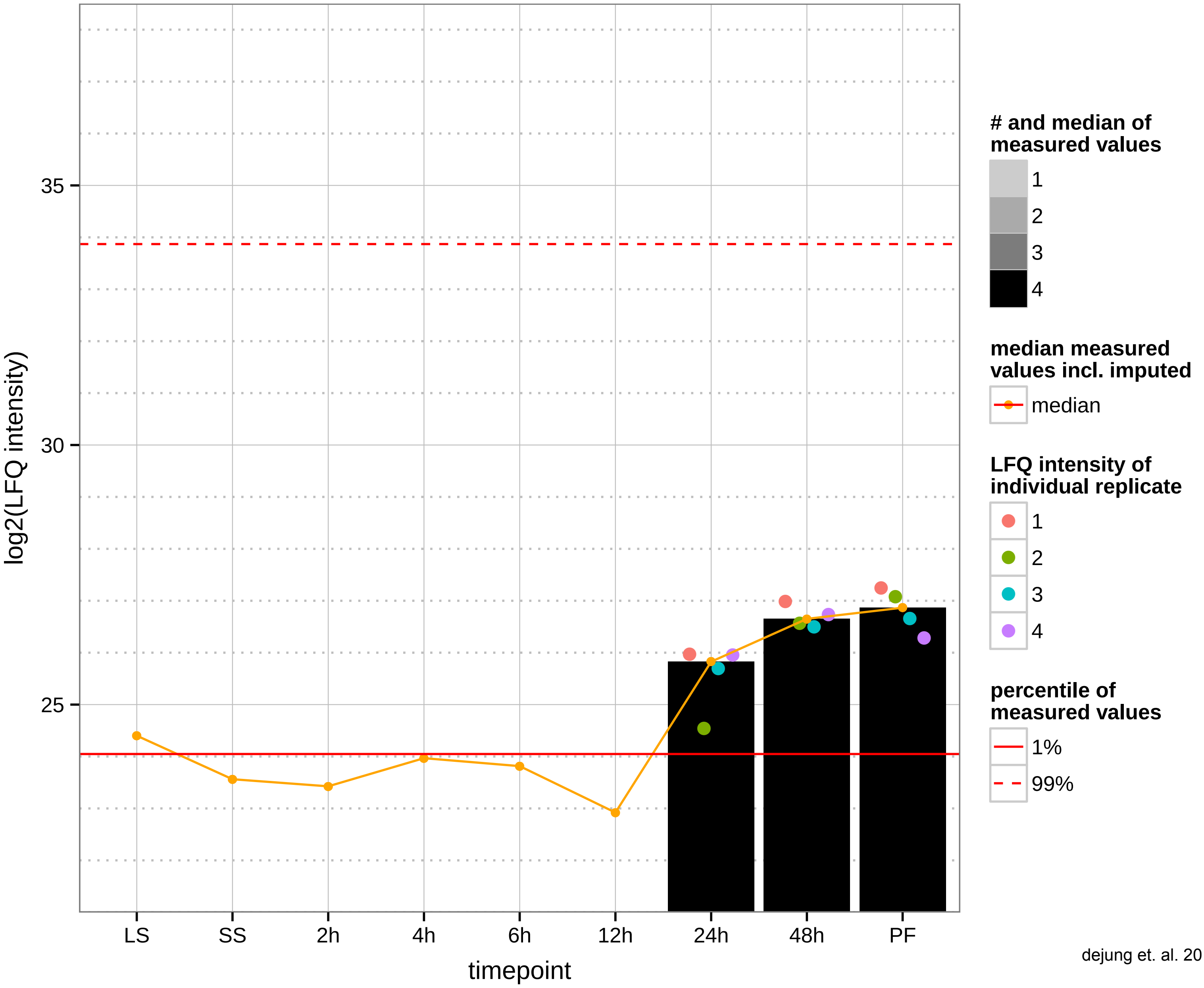
hypothetical protein, conserved
Tb927.4.4940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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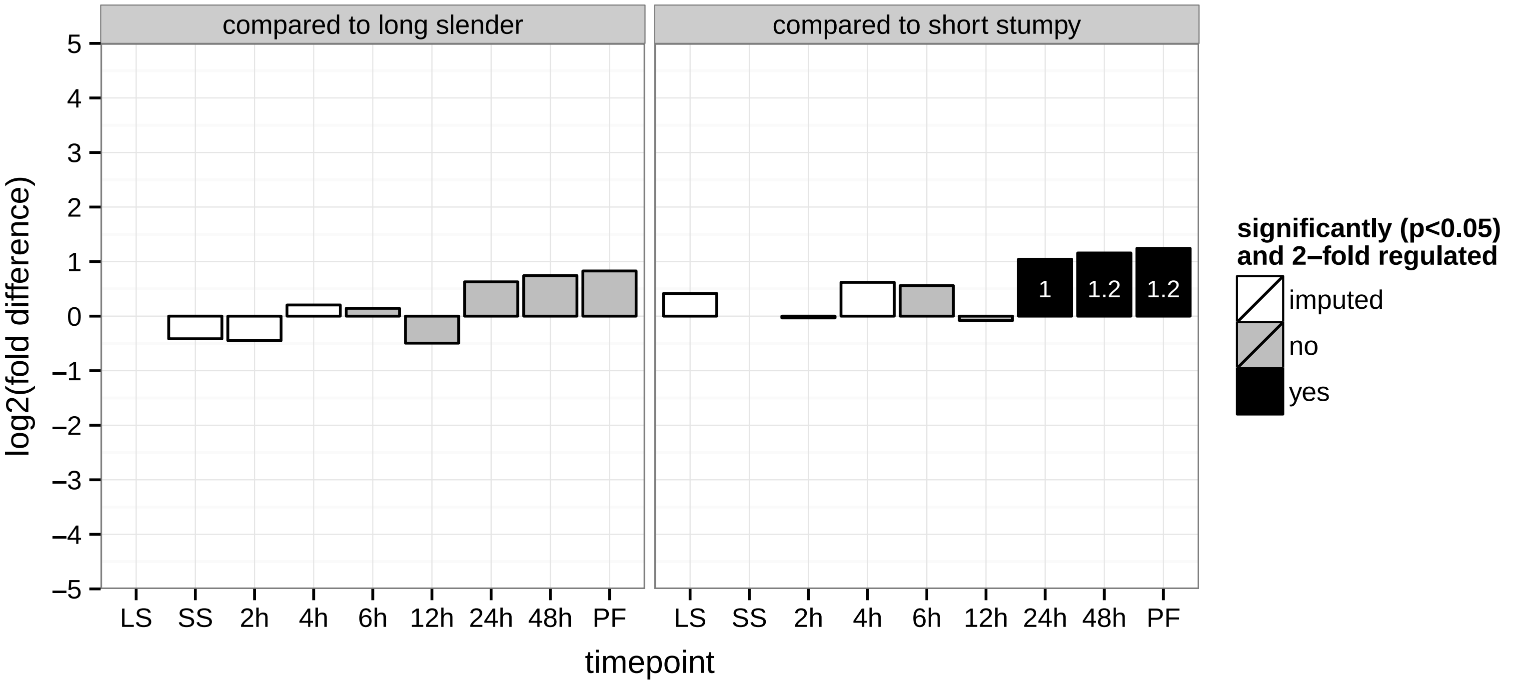
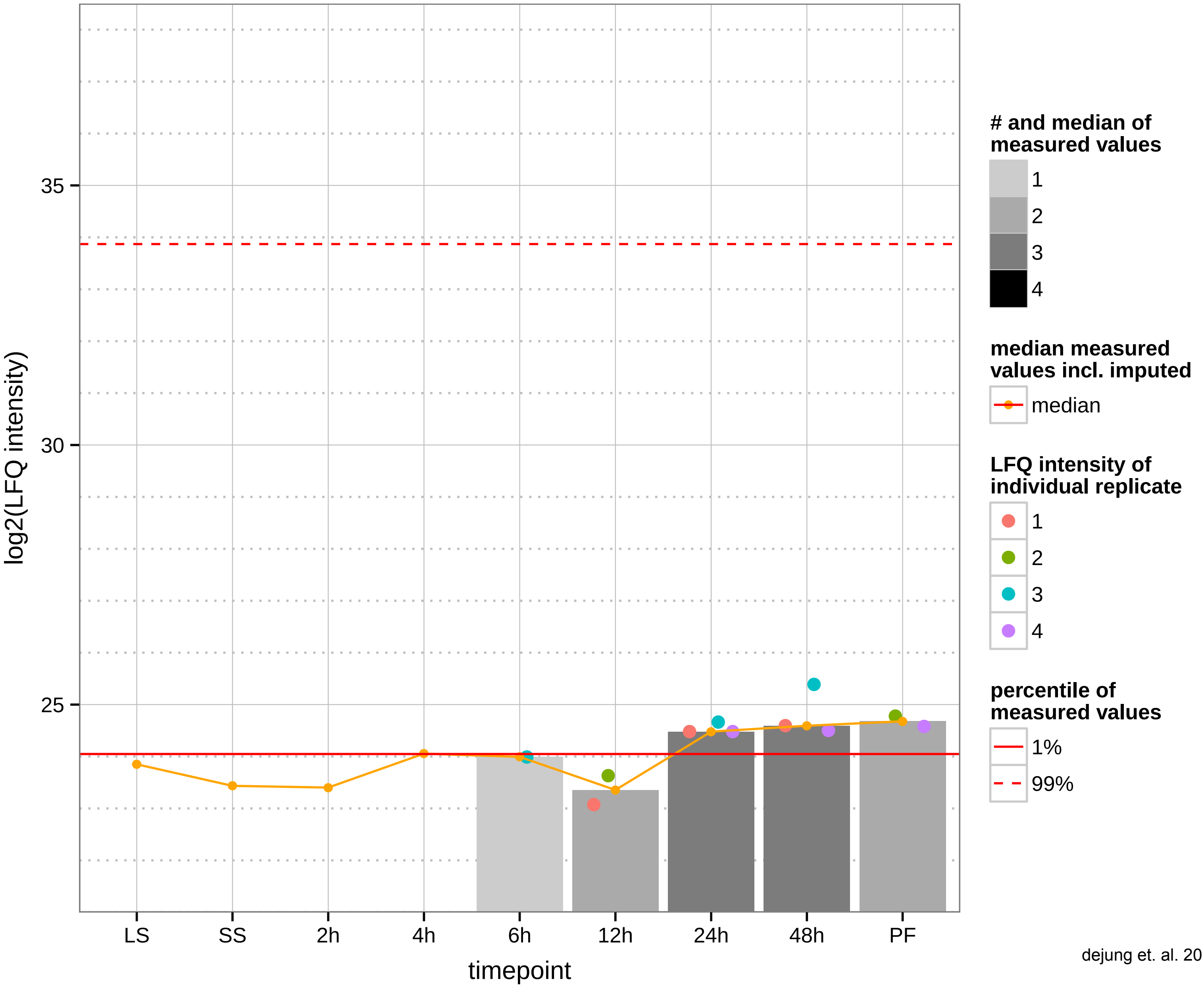
50S ribosomal protein L14, putative
Tb927.4.930
AGOF: structural constituent of ribosome
AGOC: intracellular, large ribosomal subunit, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: ribosome
PGOP: translation





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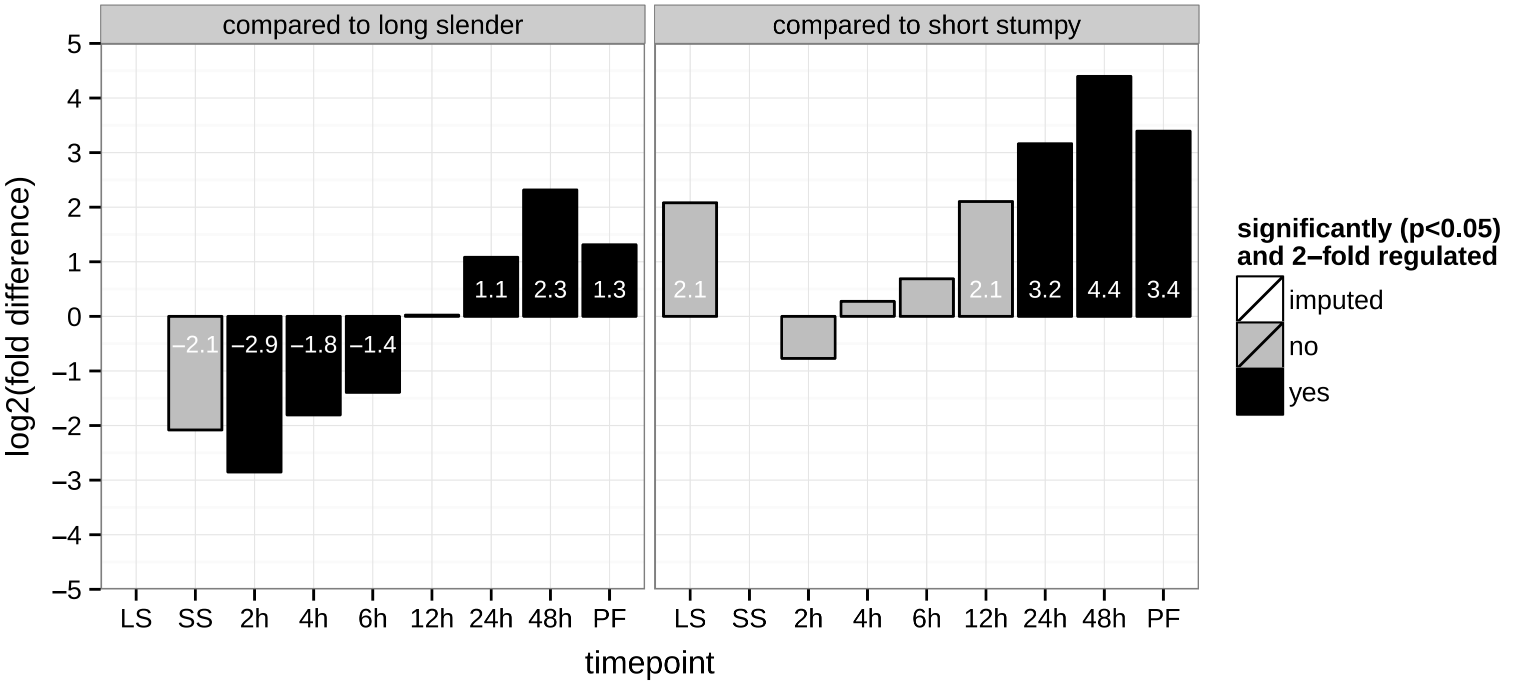
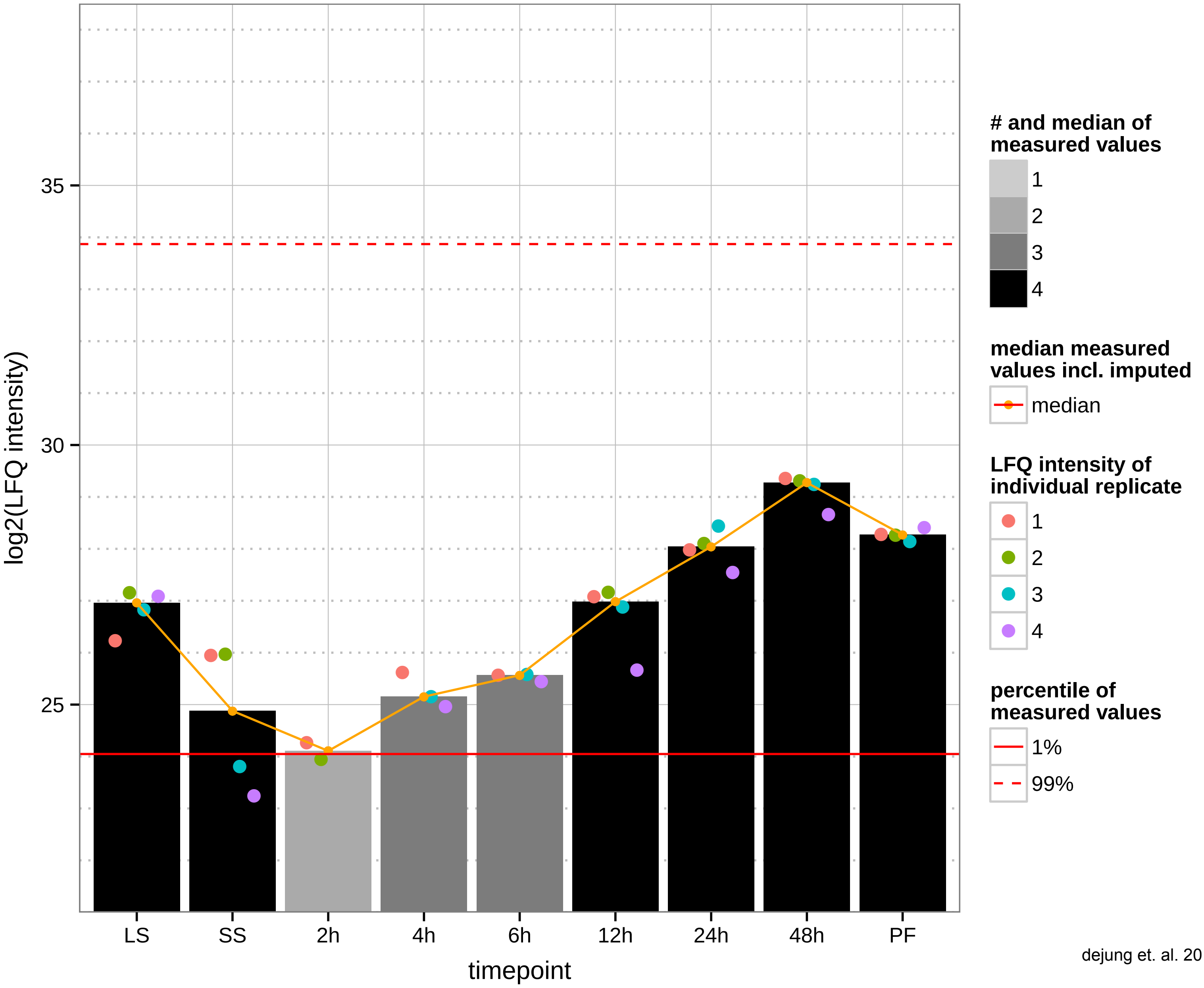
peroxisome targeting signal 1 receptor (TbPEX5)
Tb927.5.1100
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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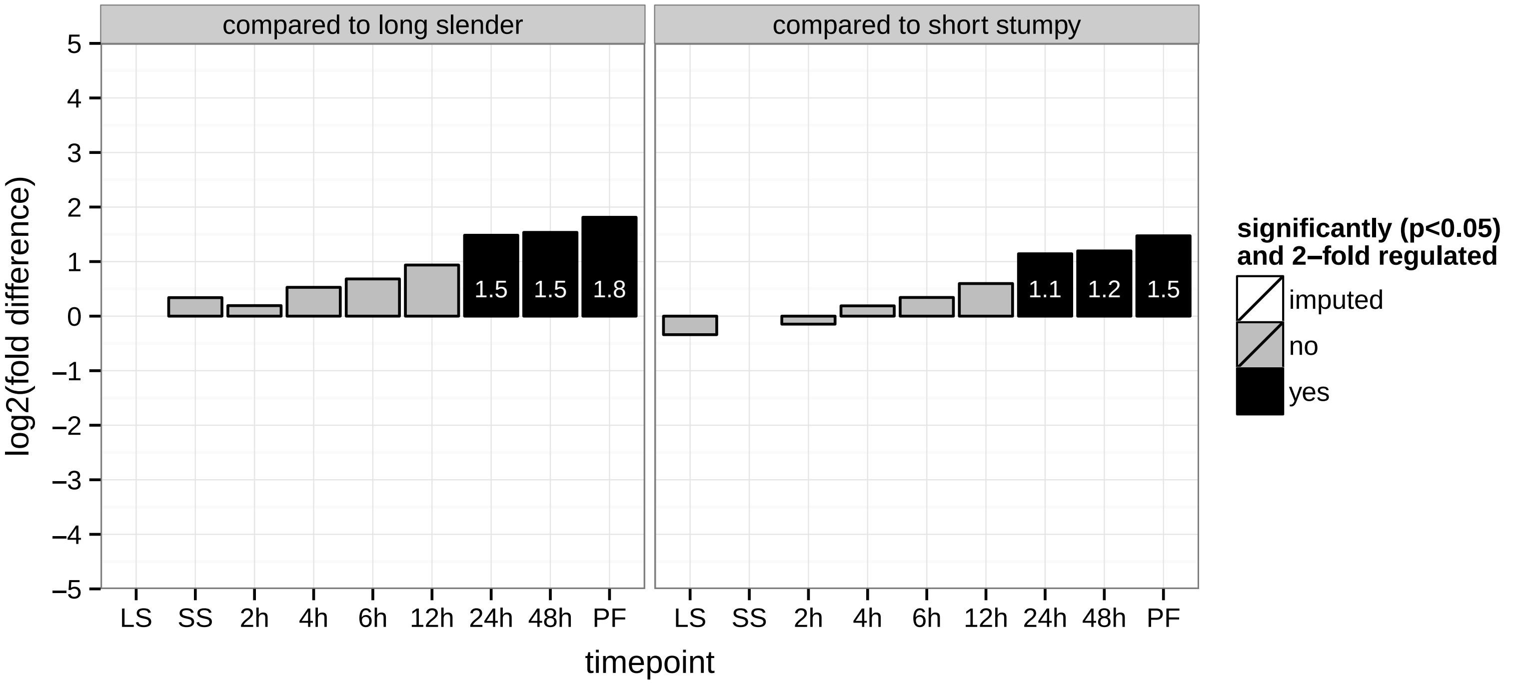
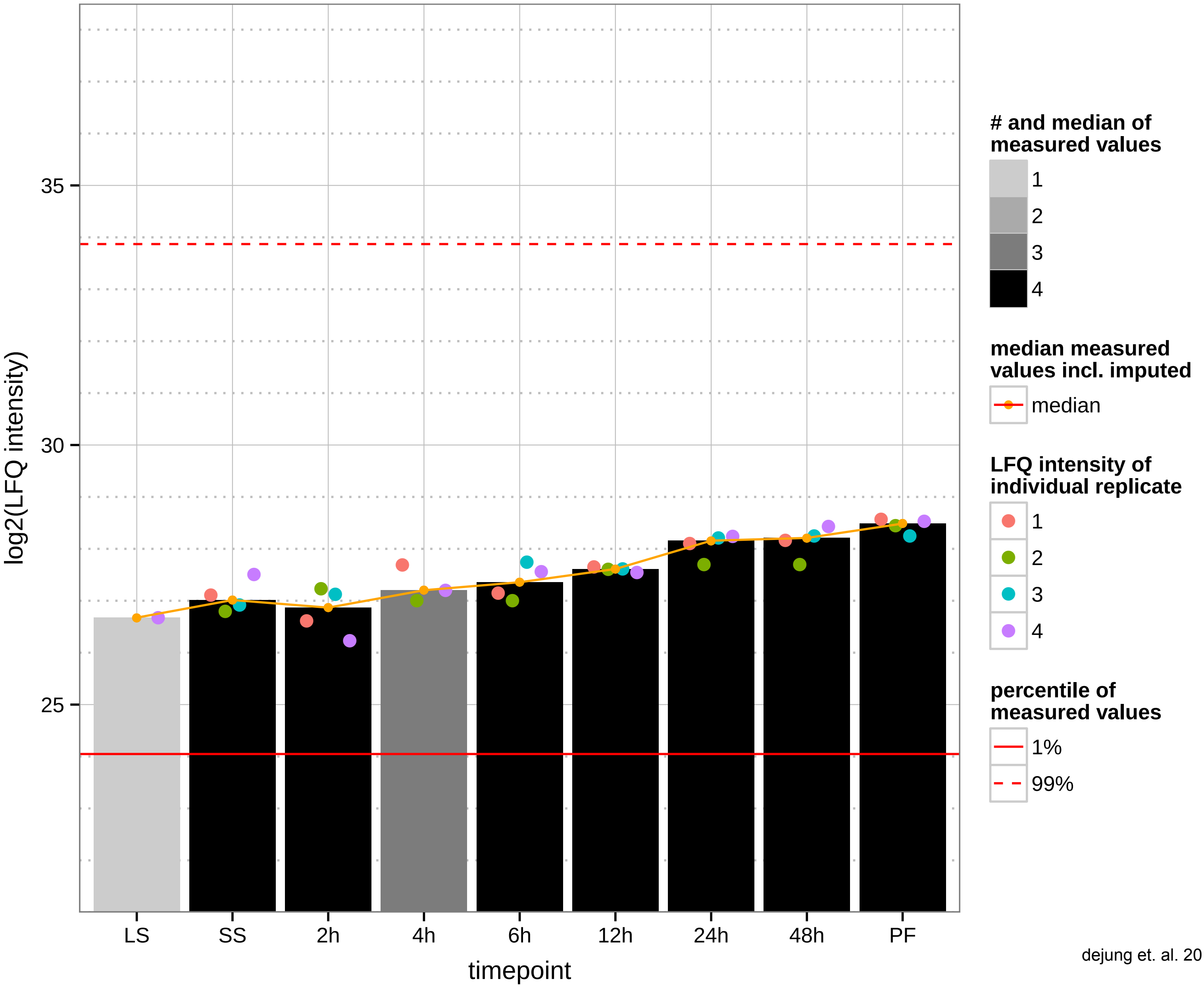
RNA helicase Prp43
Tb927.5.1150
AGOF: ATP binding, helicase activity, nucleic acid binding, nucleoside–triphosphatase activity
AGOC: null
AGOP: RNA splicing
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding, nucleoside–triphosphatase activi
PGOC: null
PGOP: null





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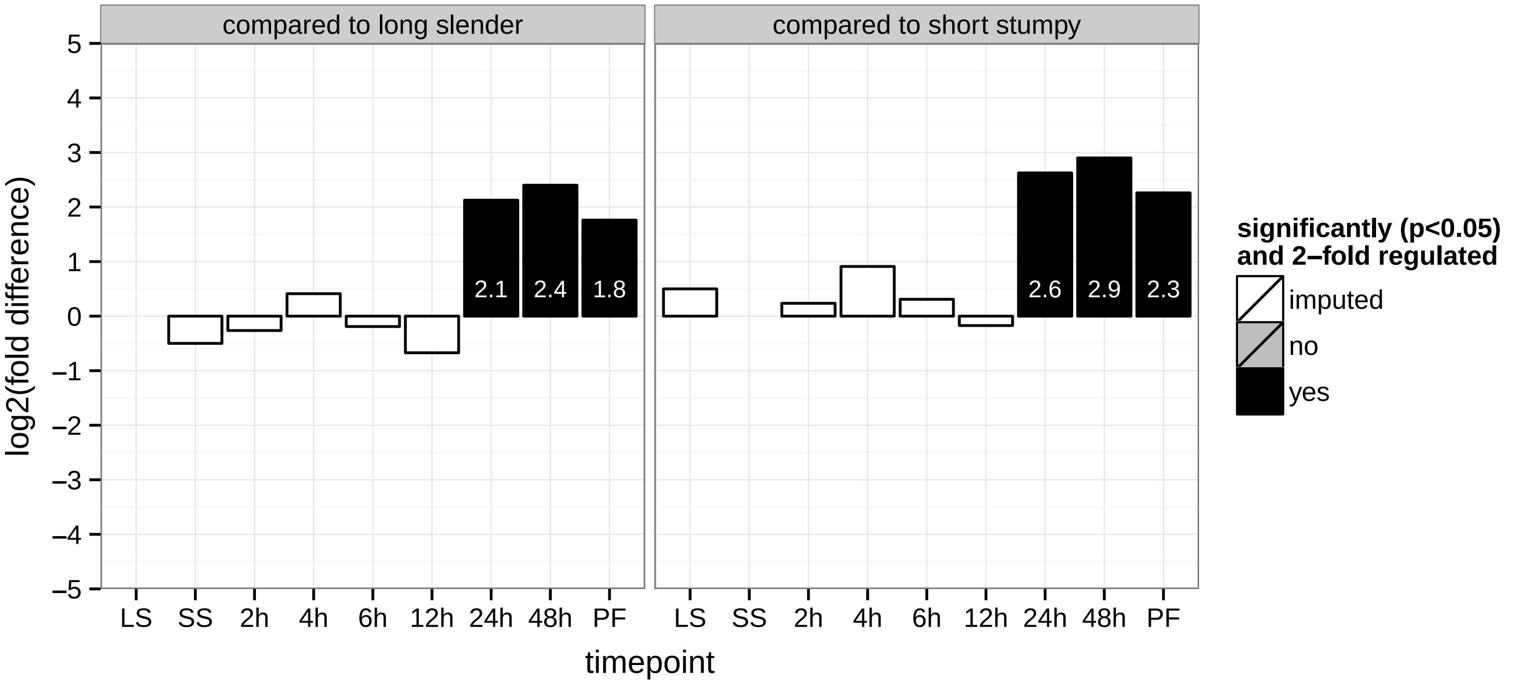
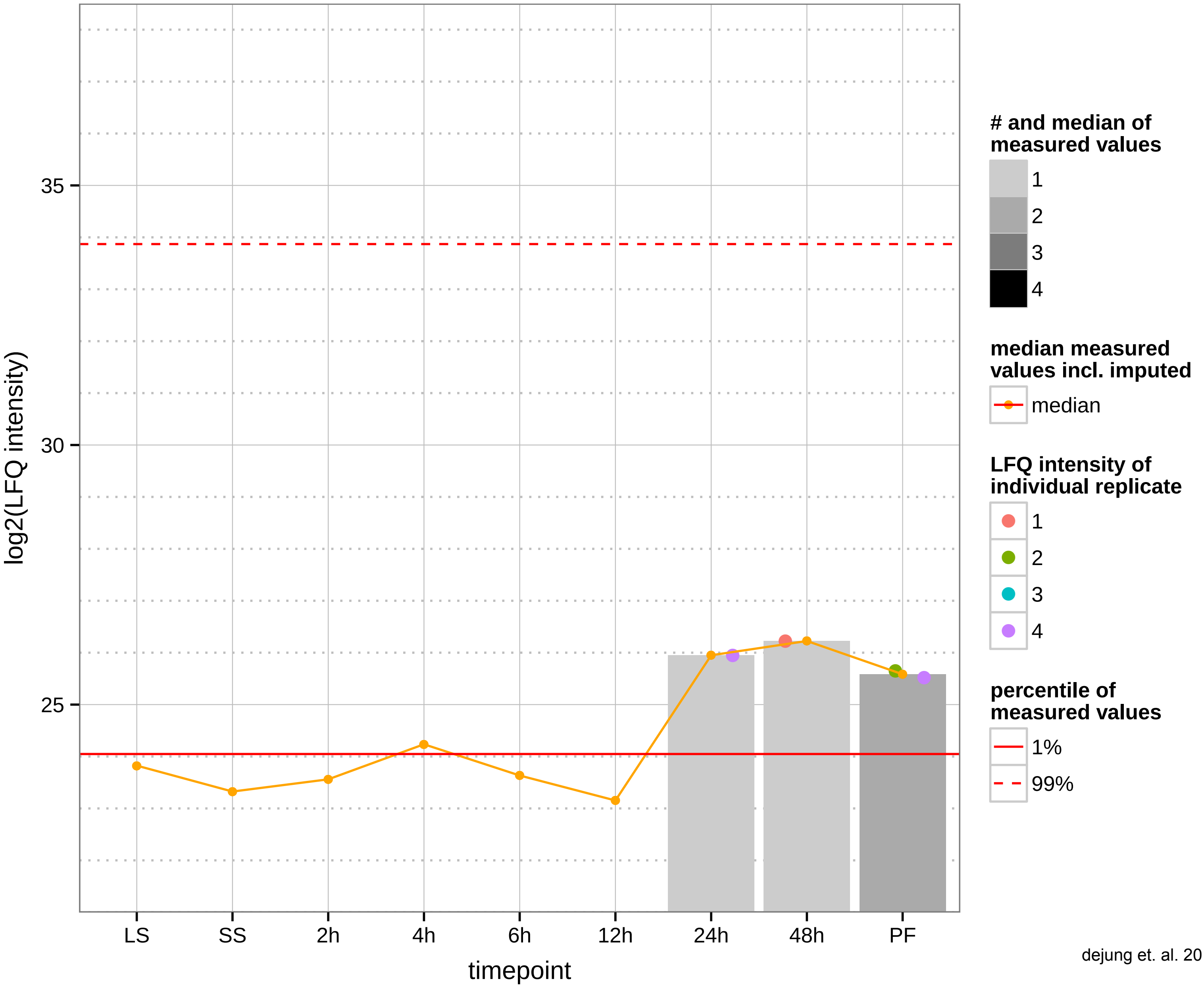
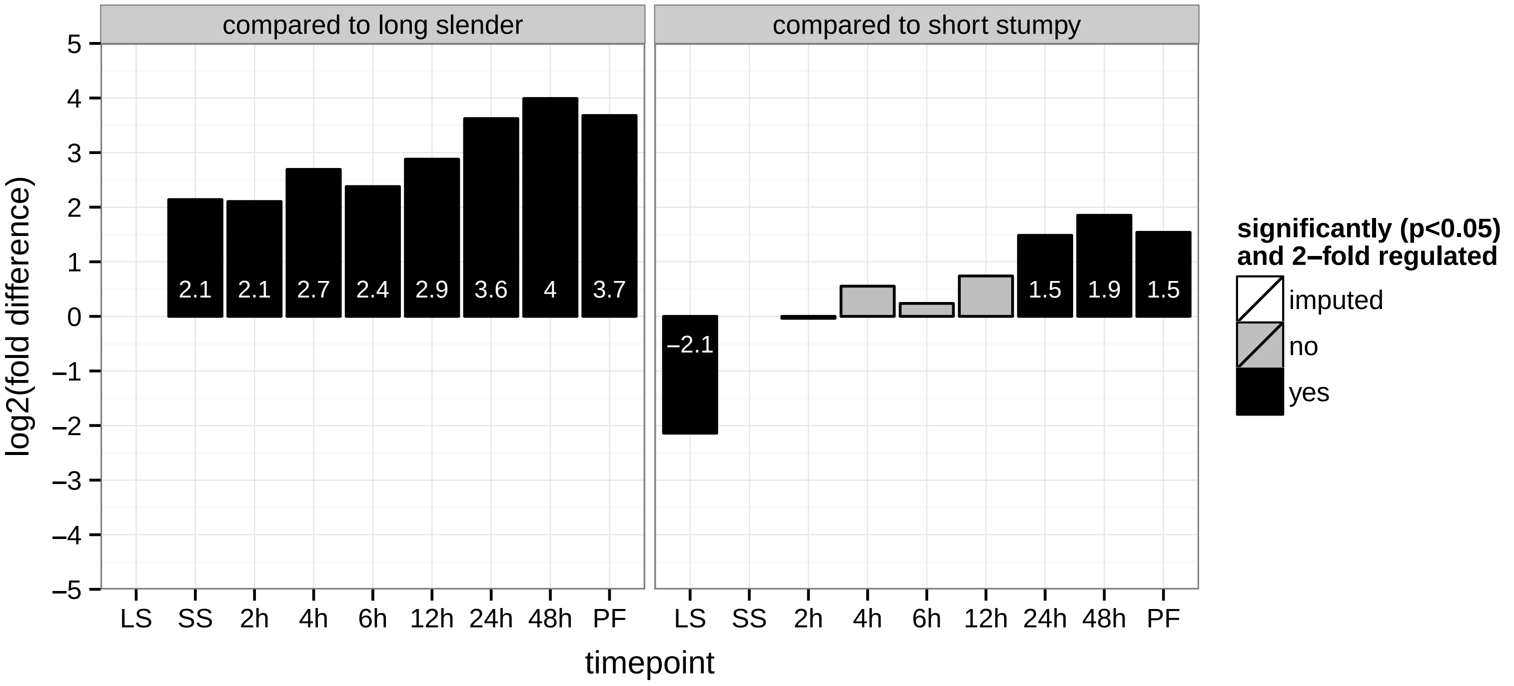
hypothetical protein, conserved
Tb927.5.2800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

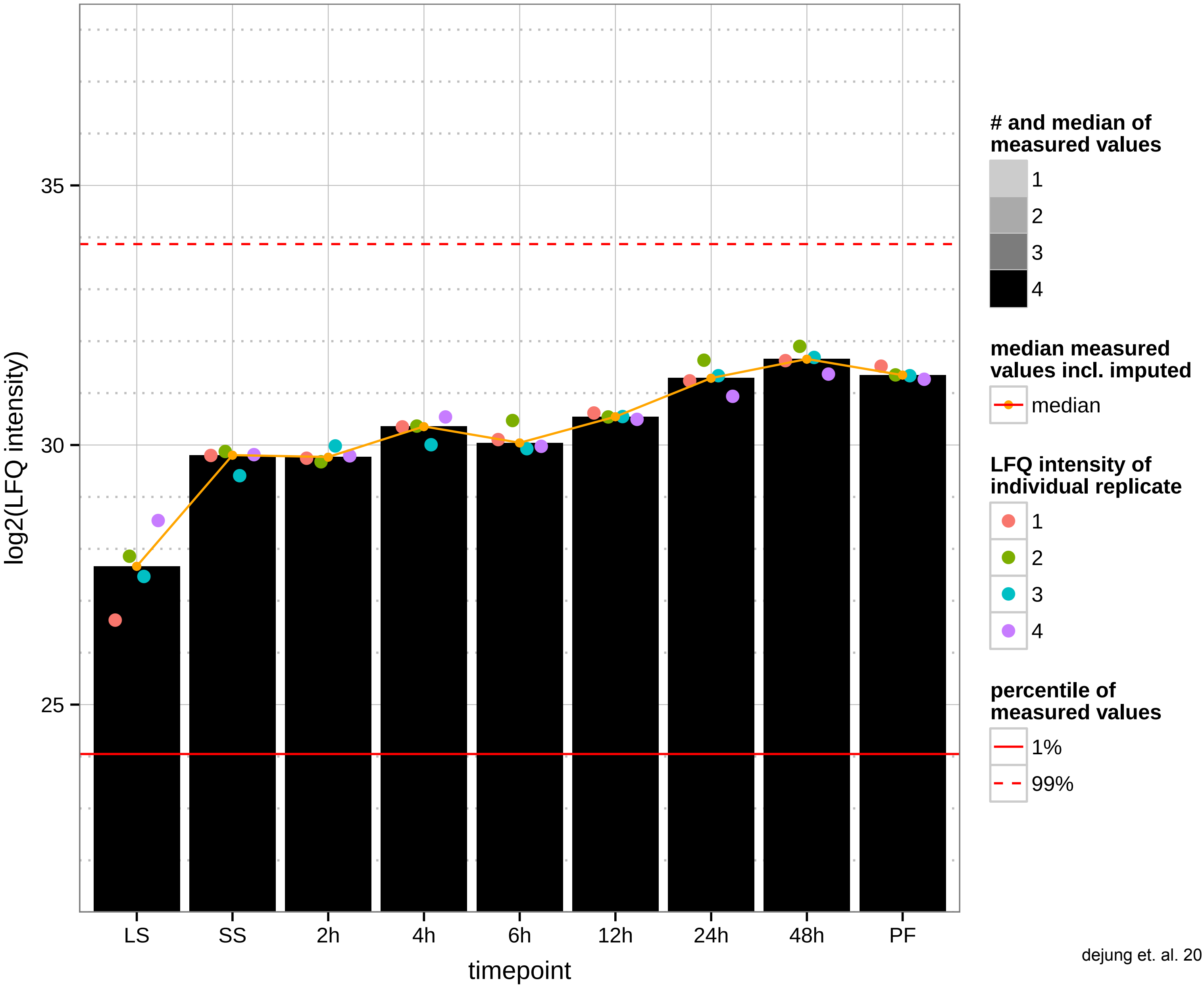




dejung et. al. 2015

hypothetical protein, conserved
Tb927.5.2930
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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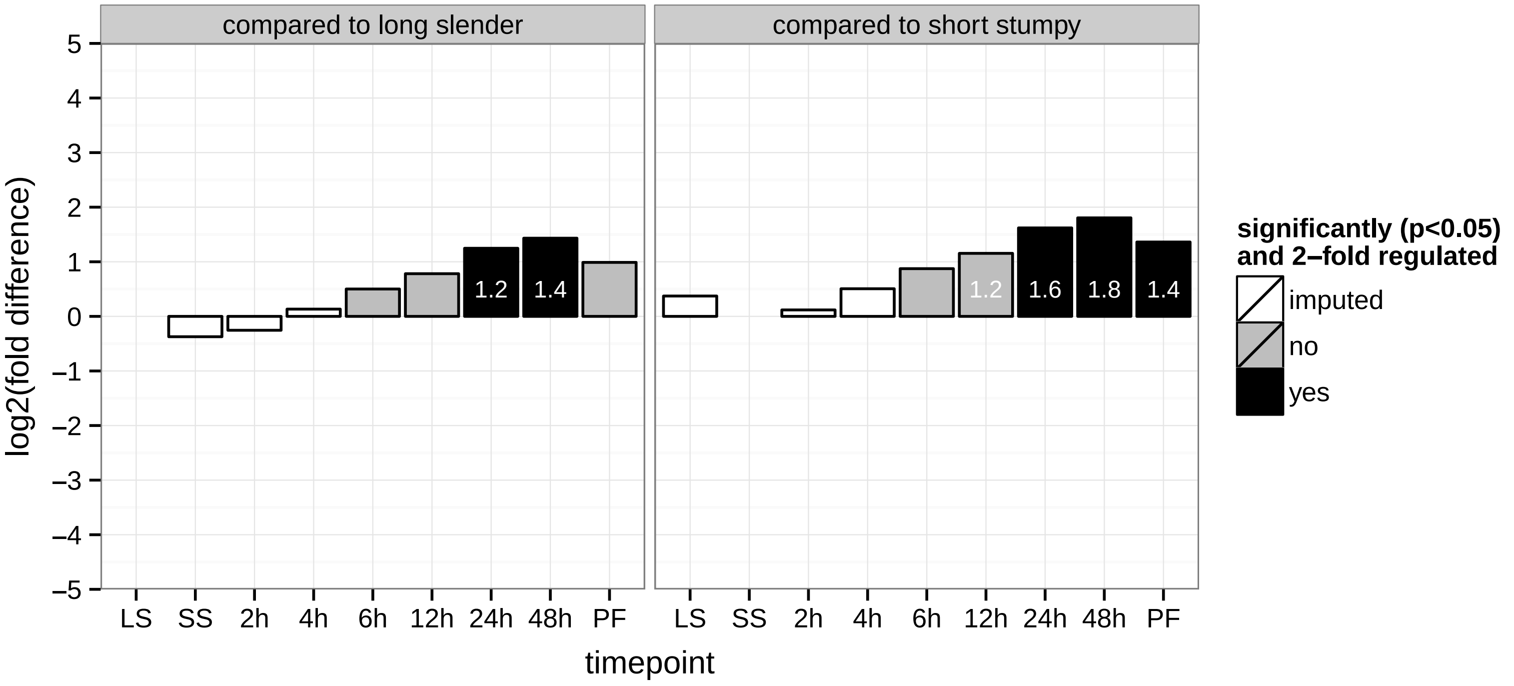
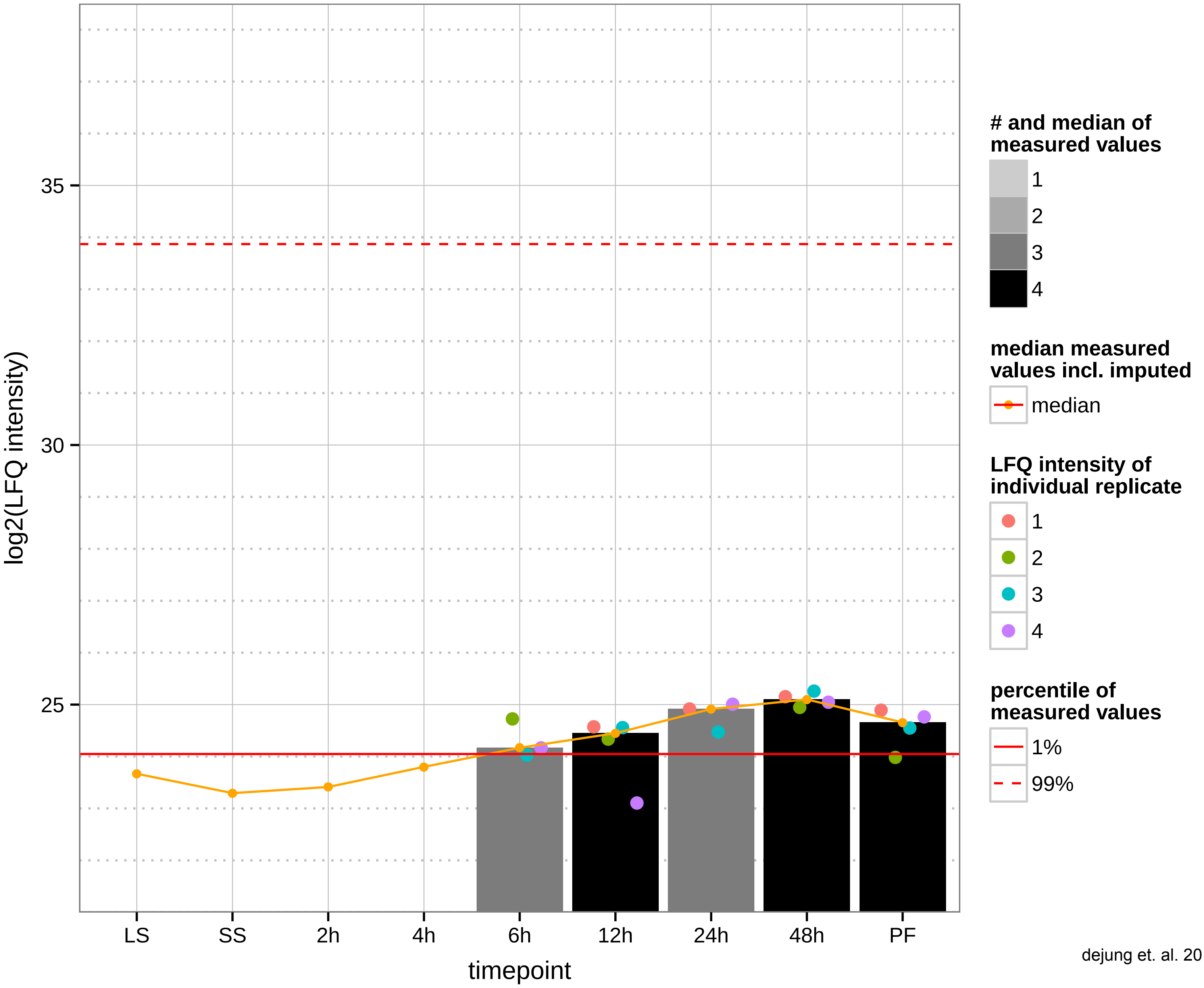
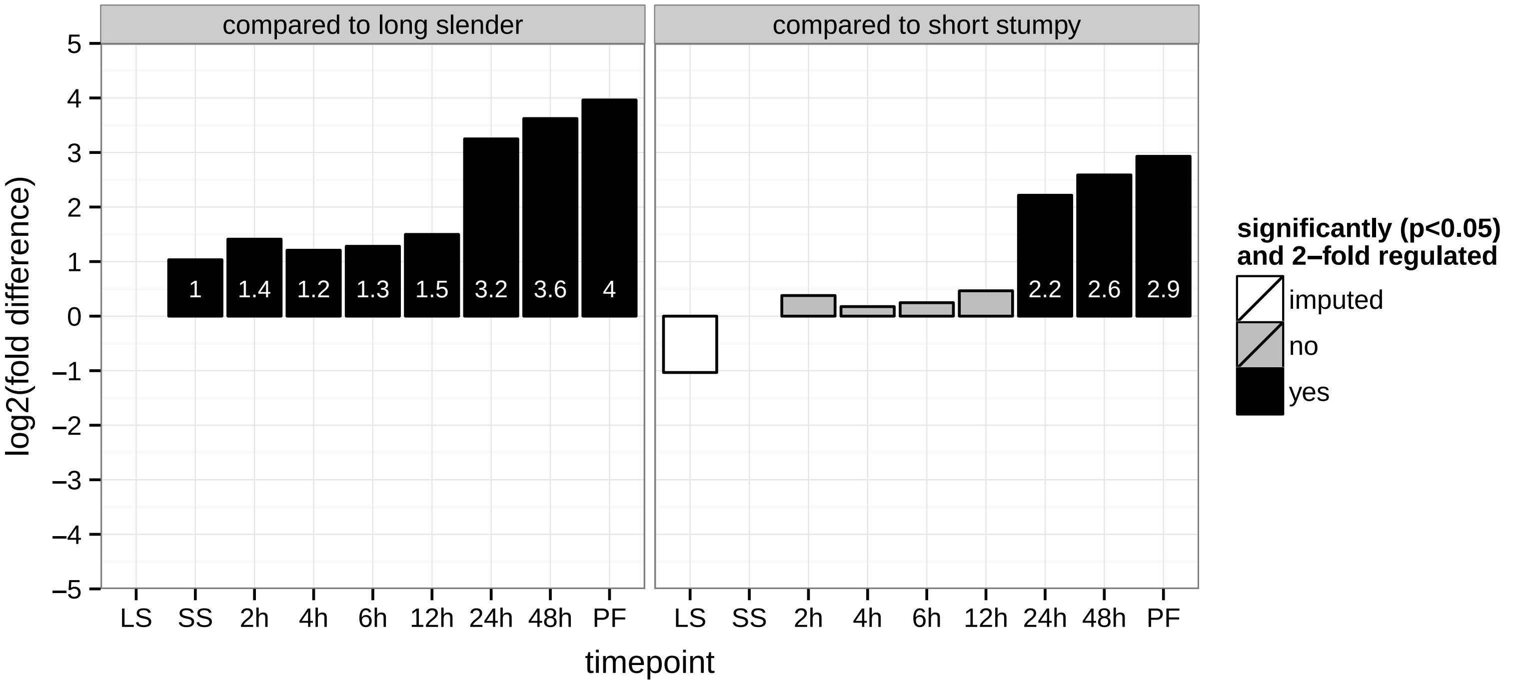
poly(ADP–ribose) polymerase, putative
Tb927.5.3050
AGOF: NAD+ ADP–ribosyltransferase activity
AGOC: nucleus
AGOP: protein ADP–ribosylation
PGOF: NAD+ ADP–ribosyltransferase activity
PGOC: null
PGOP: protein ADP–ribosylation

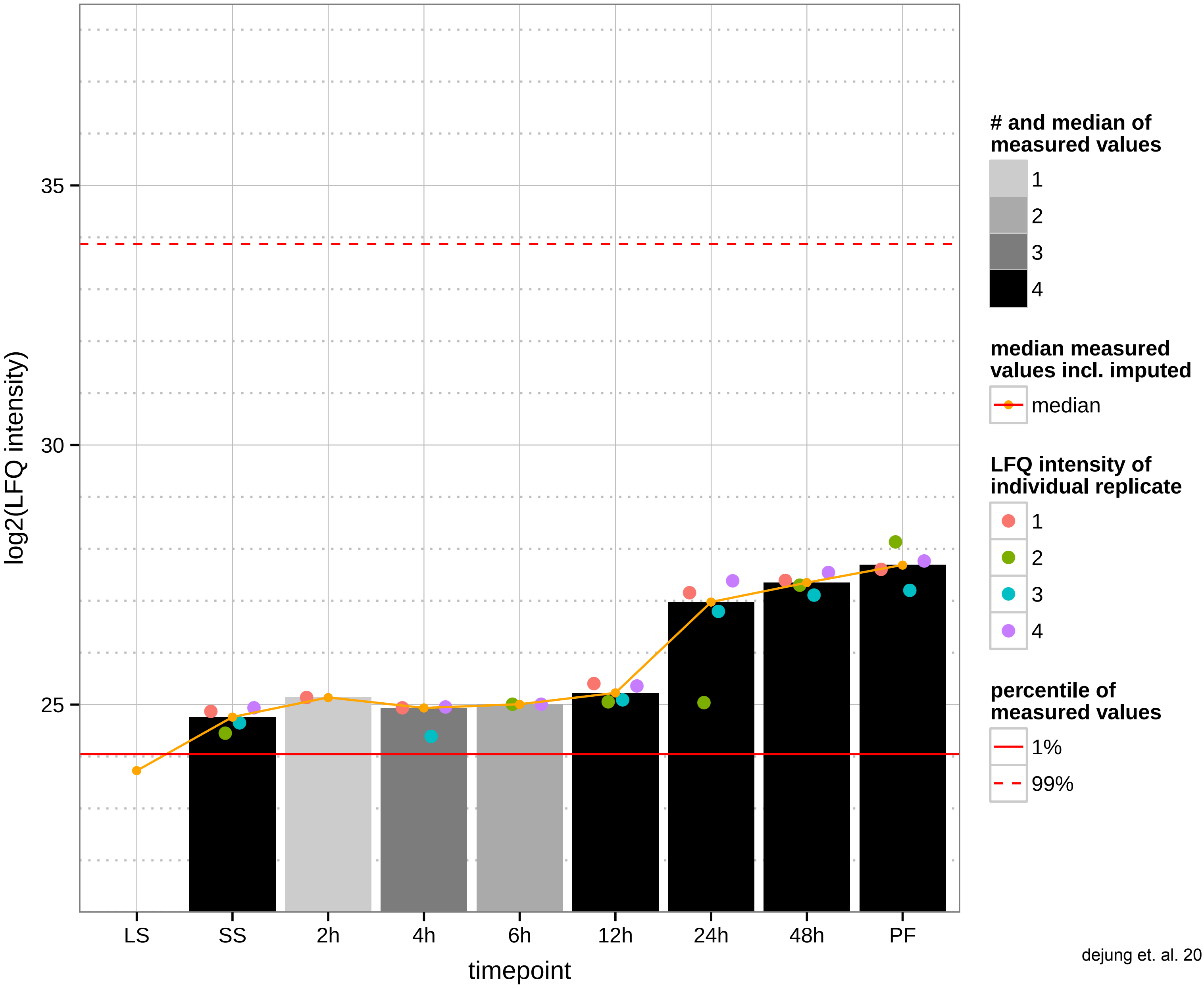




dejung et. al. 2015

hypothetical protein, conserved
Tb927.5.4040
AGOF: null
AGOC: mitochondrion
AGOP: cell wall macromolecule catabolic process
PGOF: null
PGOC: null
PGOP: cell wall macromolecule catabolic process





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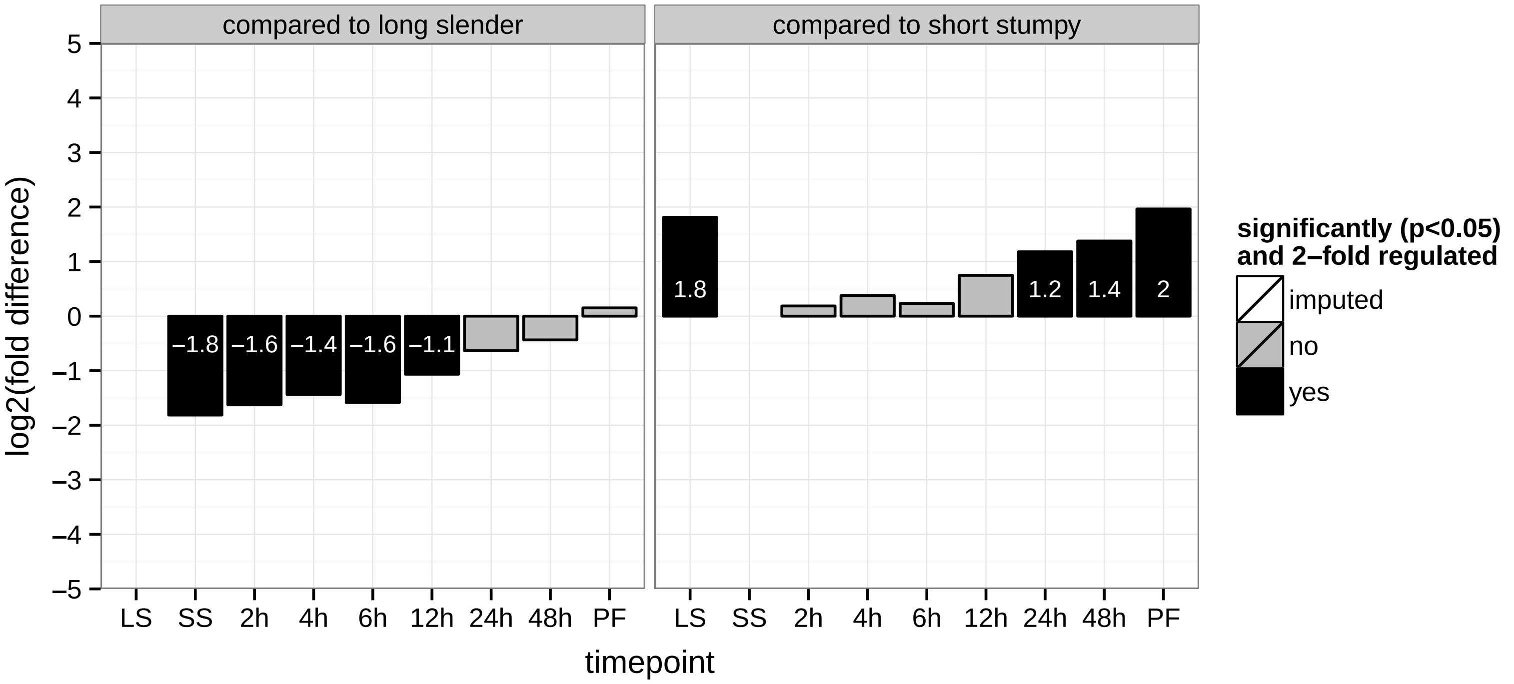
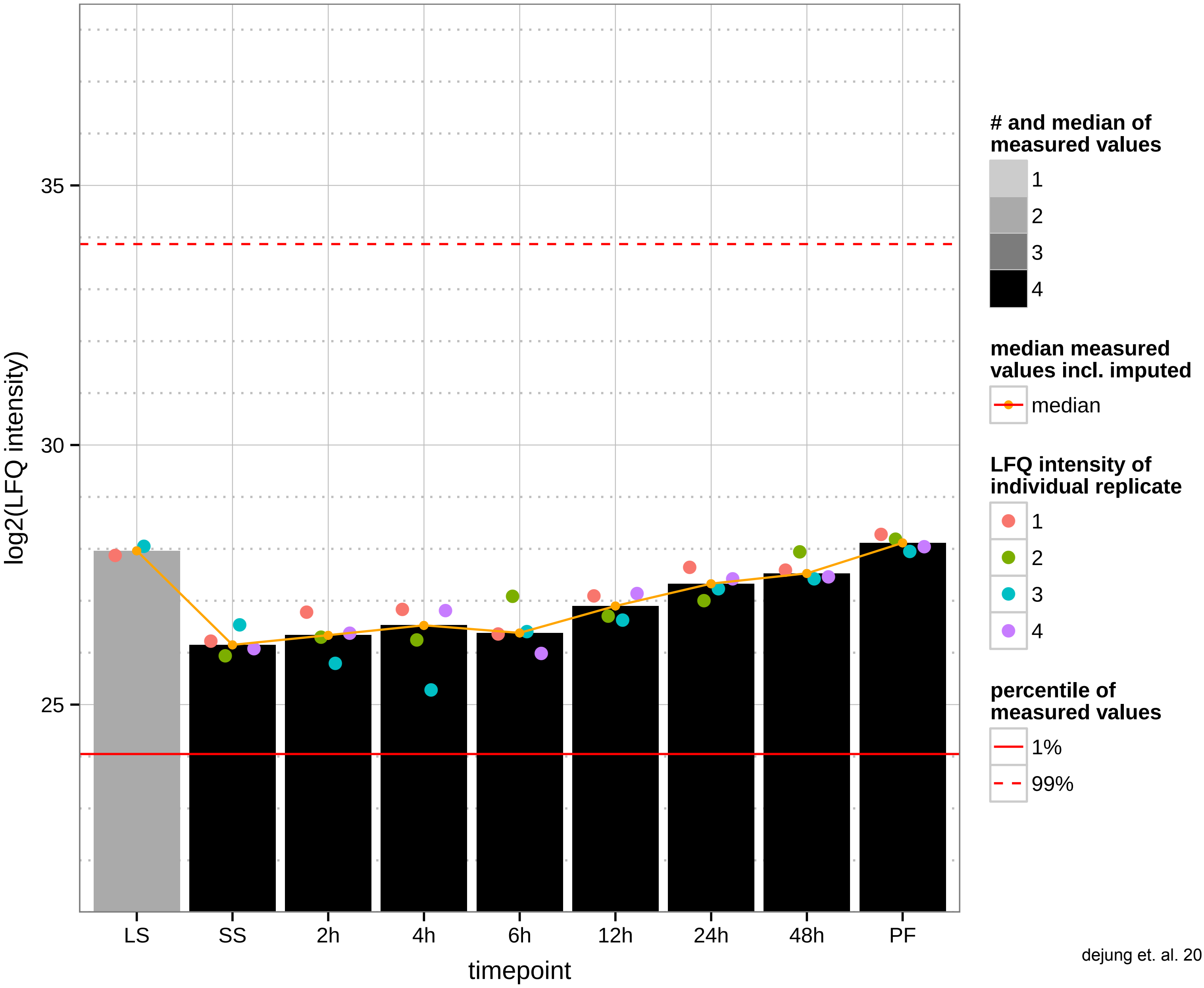
dihydrolipoamide branched chain transacylase, putative
Tb927.5.4330
AGOF: cofactor binding, dihydrolipoyllysine–residue (2–methylpropanoyl)transferase activity, transferase activity, transferring a
AGOC: mitochondrion
AGOP: fatty–acyl–CoA biosynthetic process
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: metabolic process





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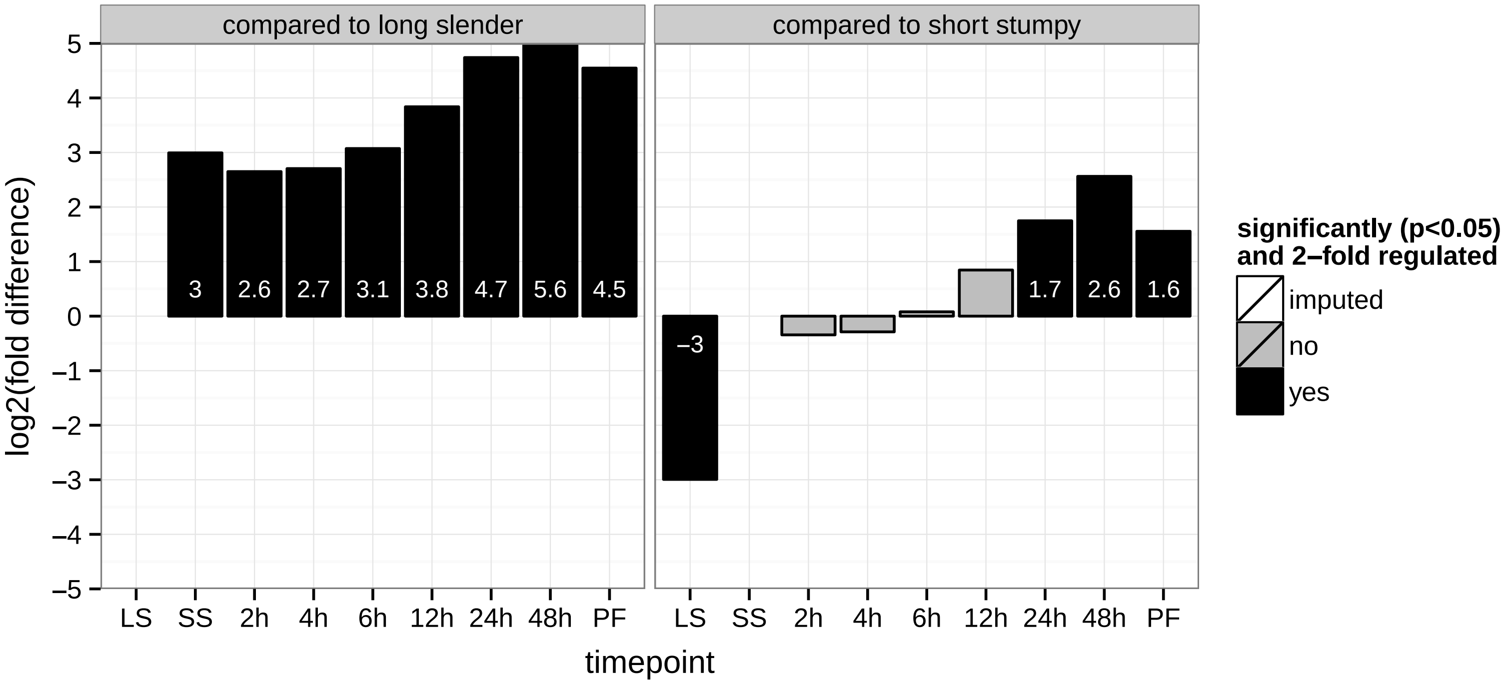
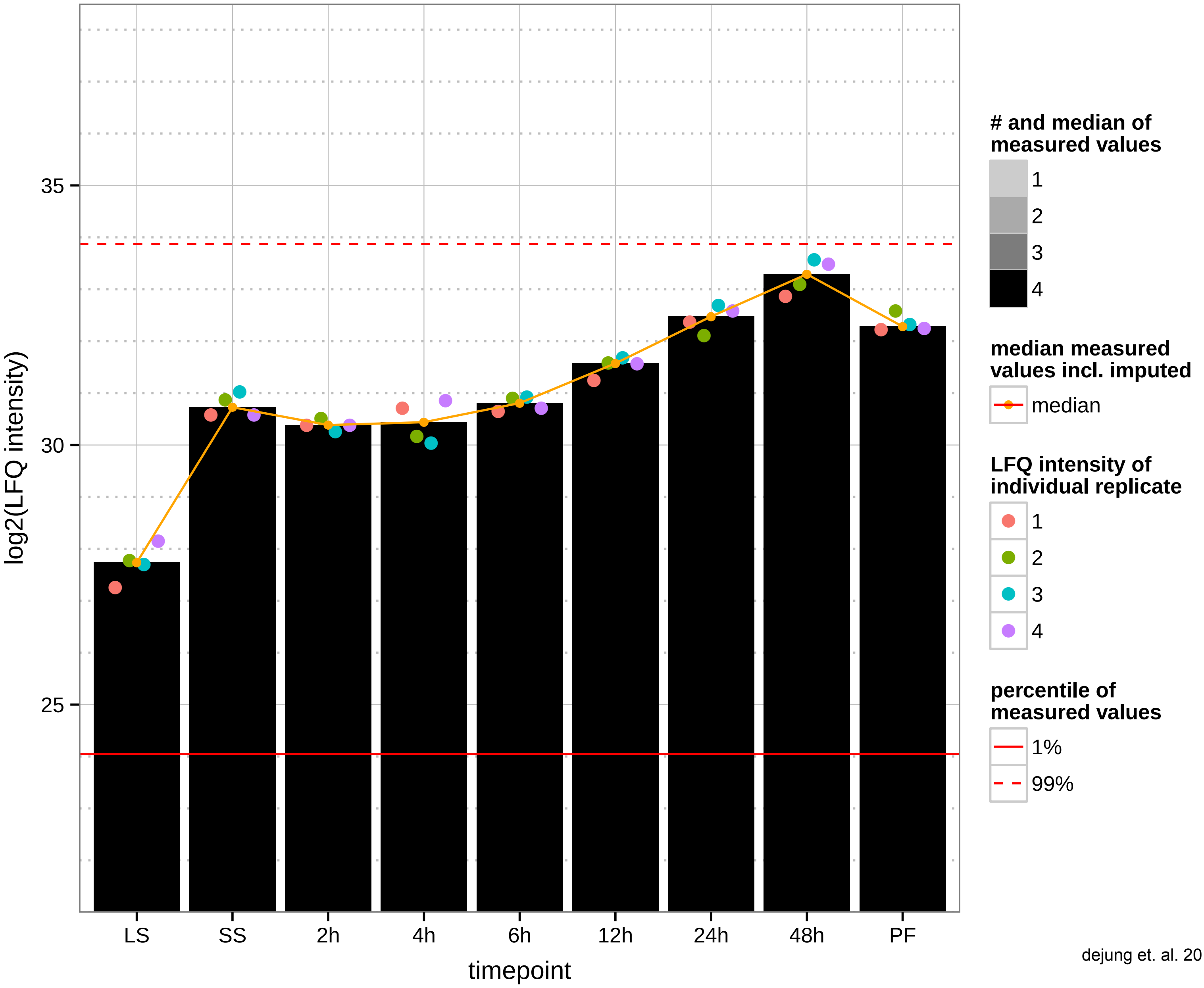
NADH–dependent fumarate reductase, putative, hypothetical protein, NADH–dependent fumarate reductase (FRDg)
Tb927.5.930;Tb11.v5.0613
AGOF: null, electron carrier activity, fumarate reductase (NADH) activity, succinate dehydrogenase activity
AGOC: null, glycosome
AGOP: null, metabolic process, thiamine biosynthetic process
PGOF: oxidoreductase activity, null, succinate dehydrogenase activity
PGOC: null
PGOP: oxidation–reduction process, null





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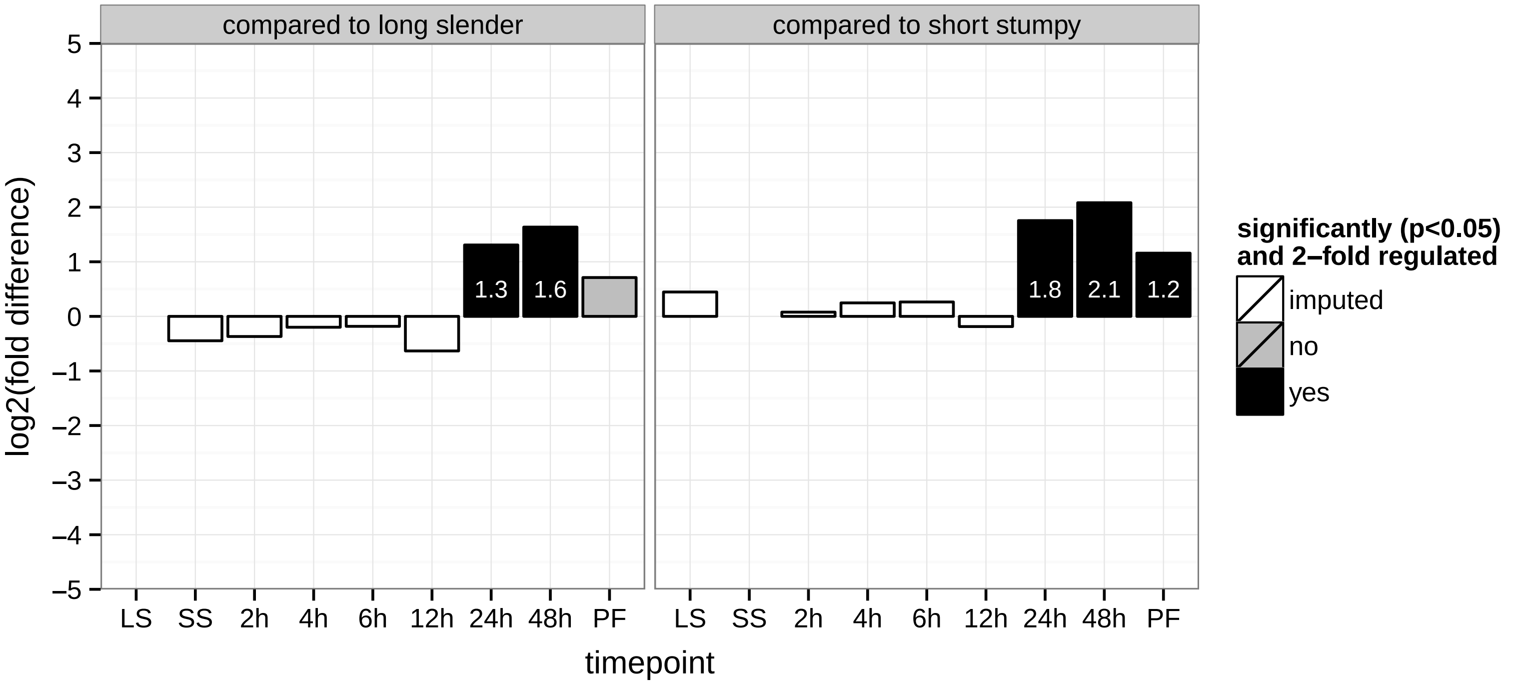
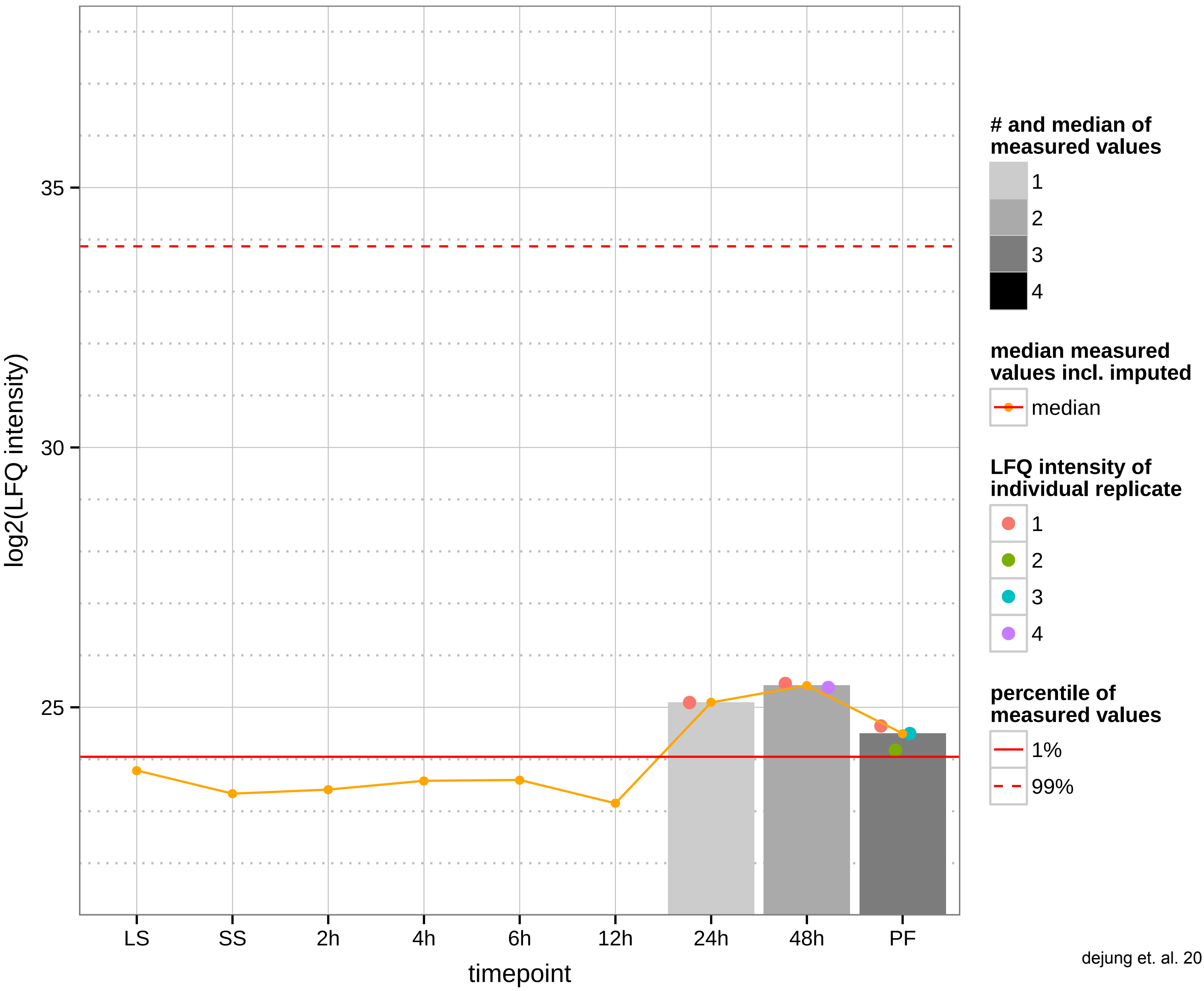
hypothetical protein, conserved
Tb927.6.2180
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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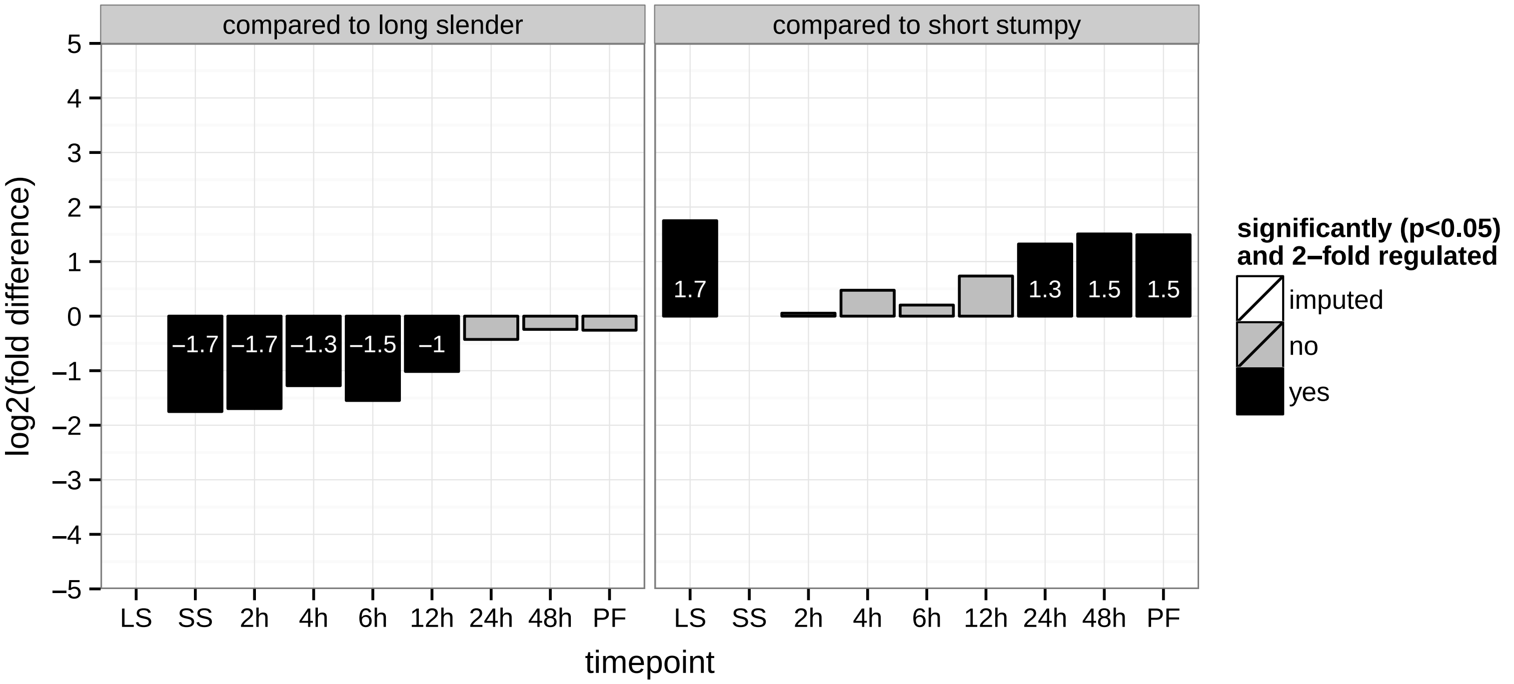
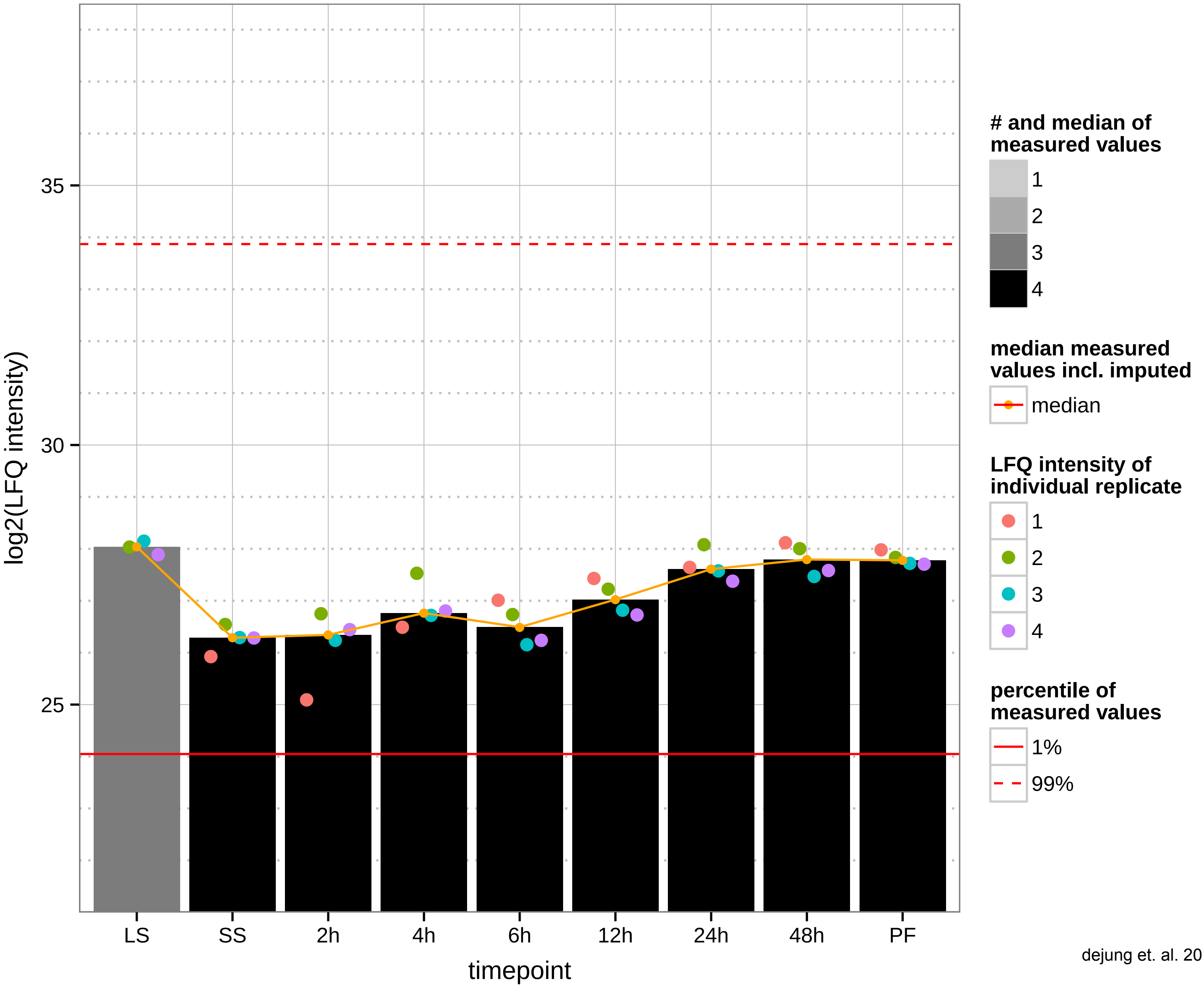
hypothetical protein, conserved
Tb927.6.2320;Tb927.6.2260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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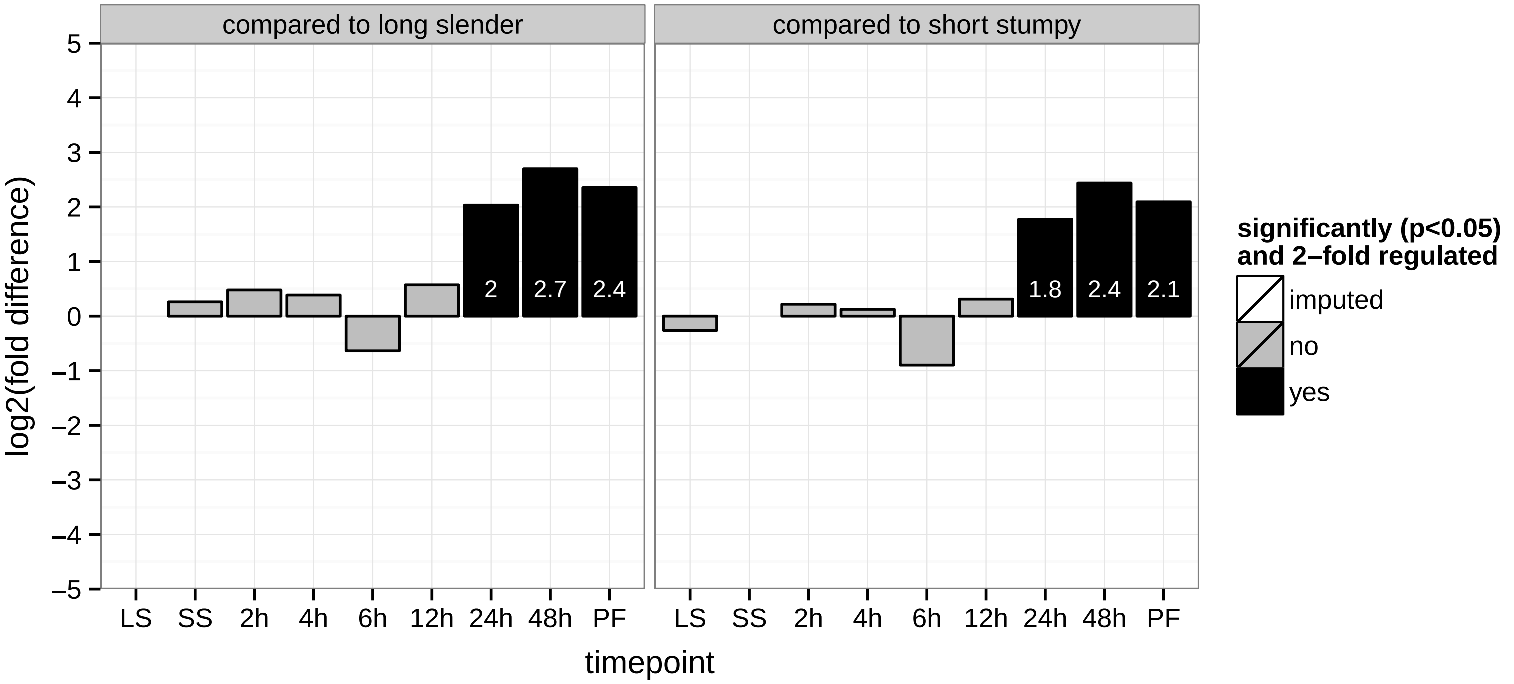
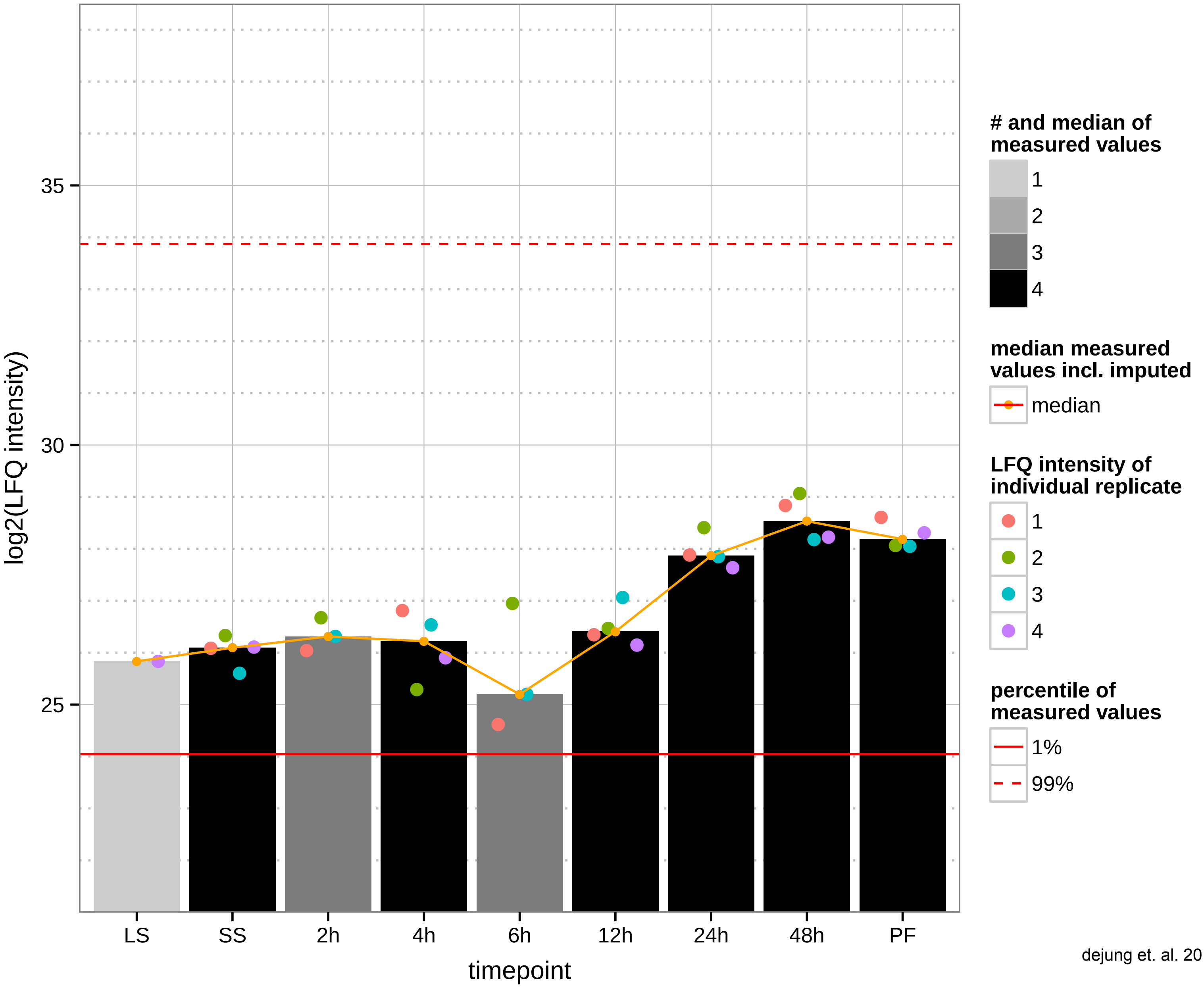
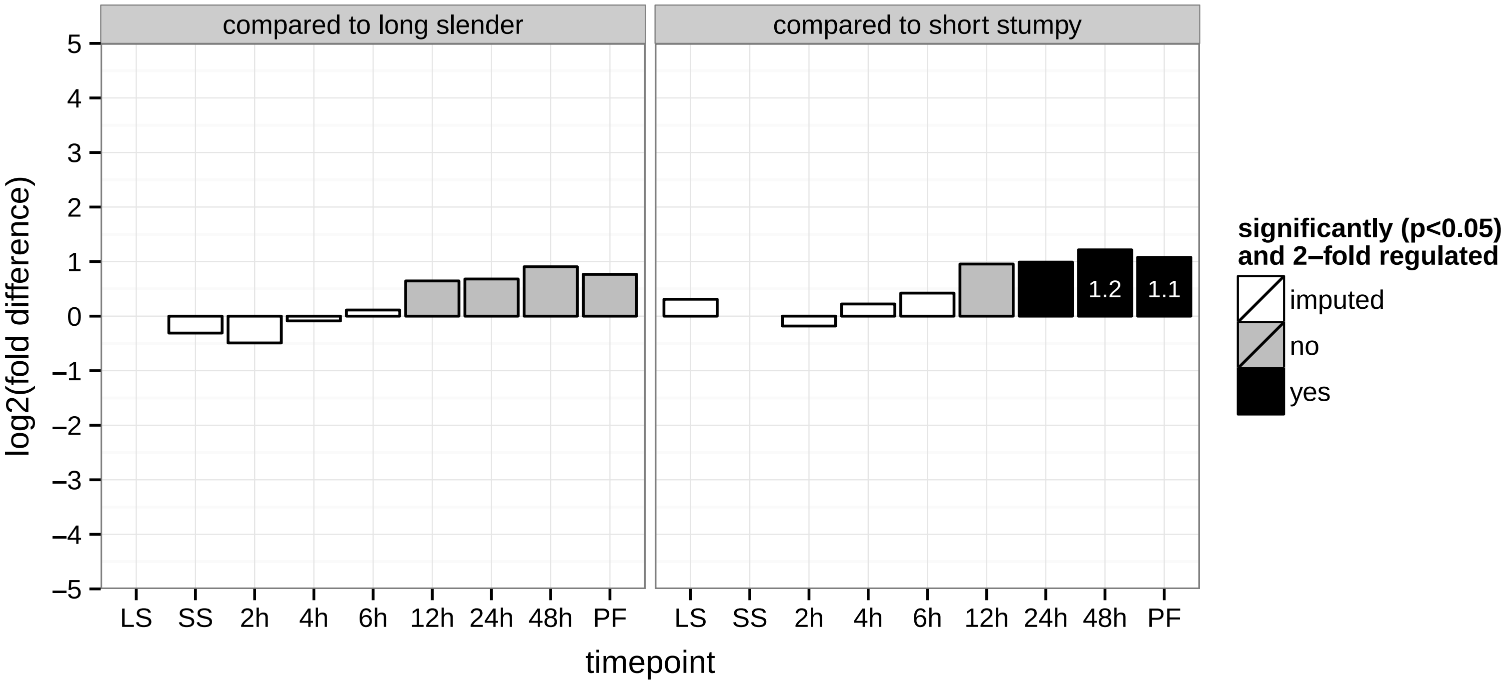
hypothetical protein, conserved
Tb927.6.2490
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

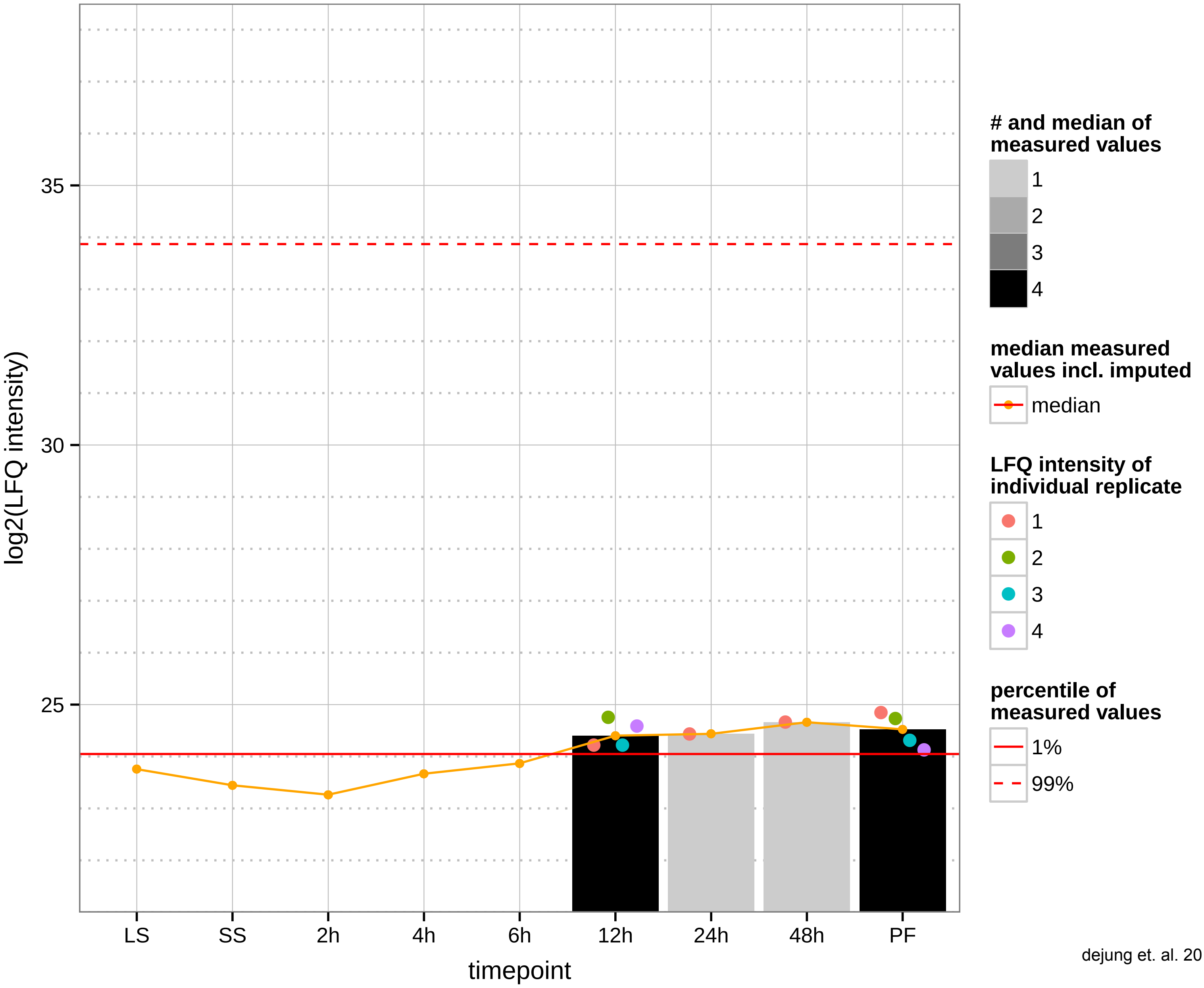




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.2570
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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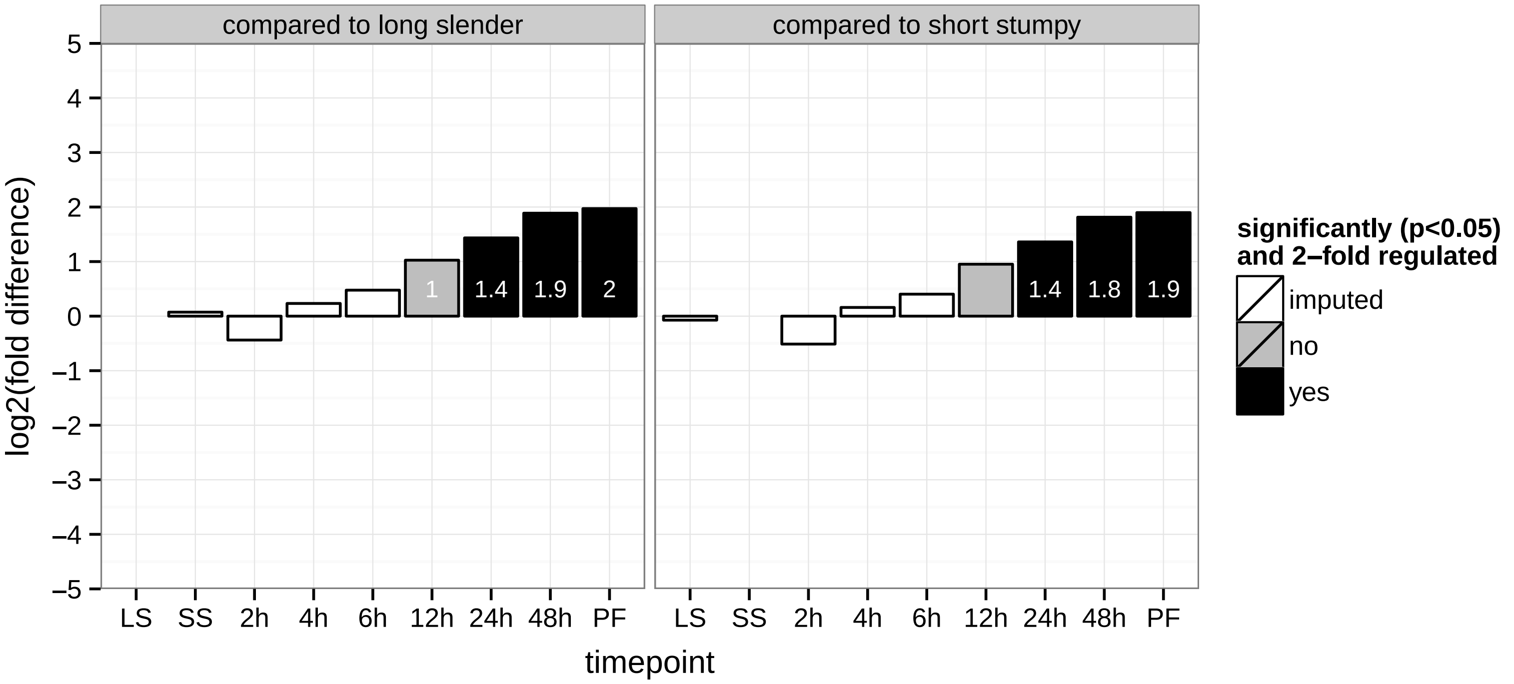
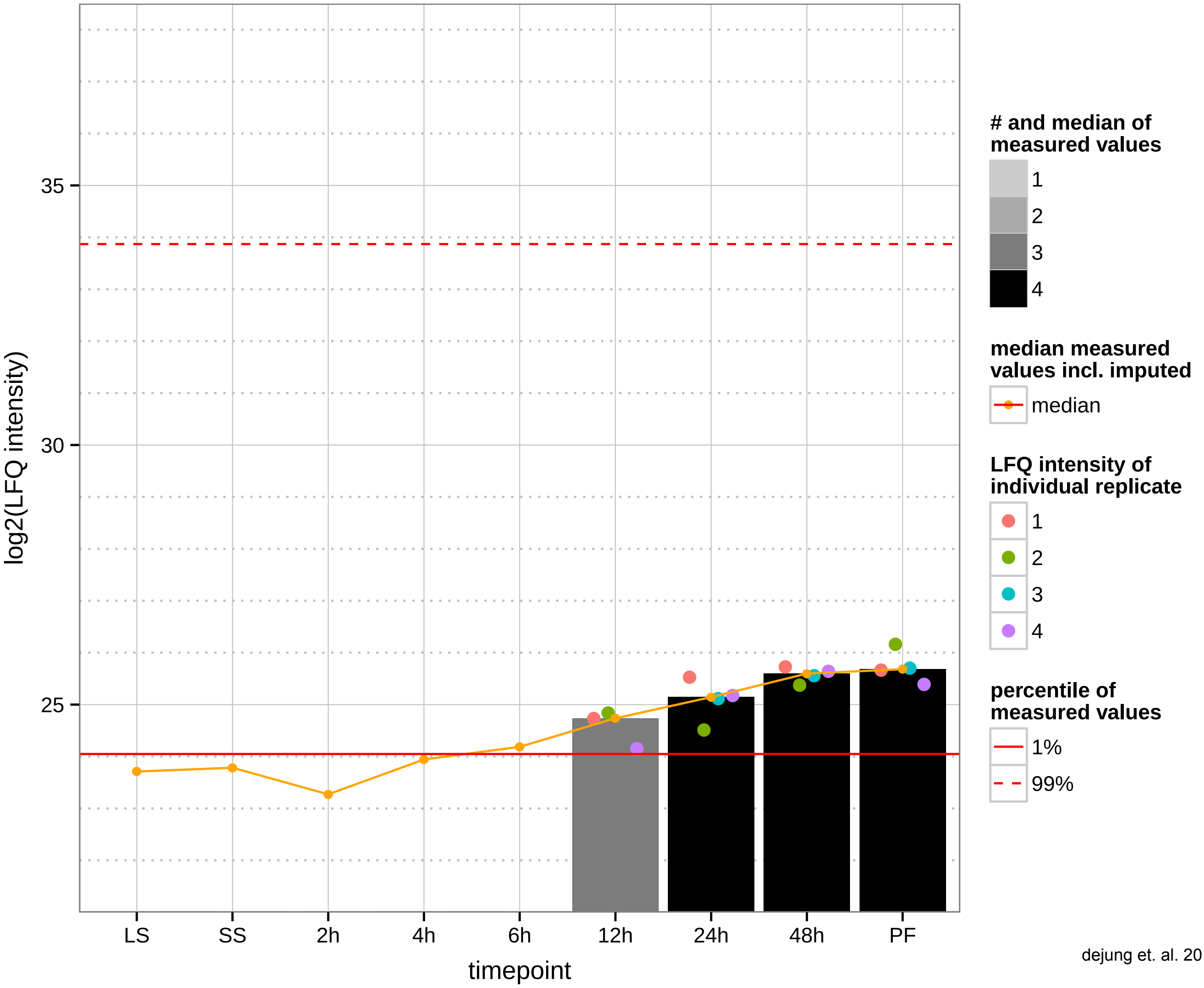
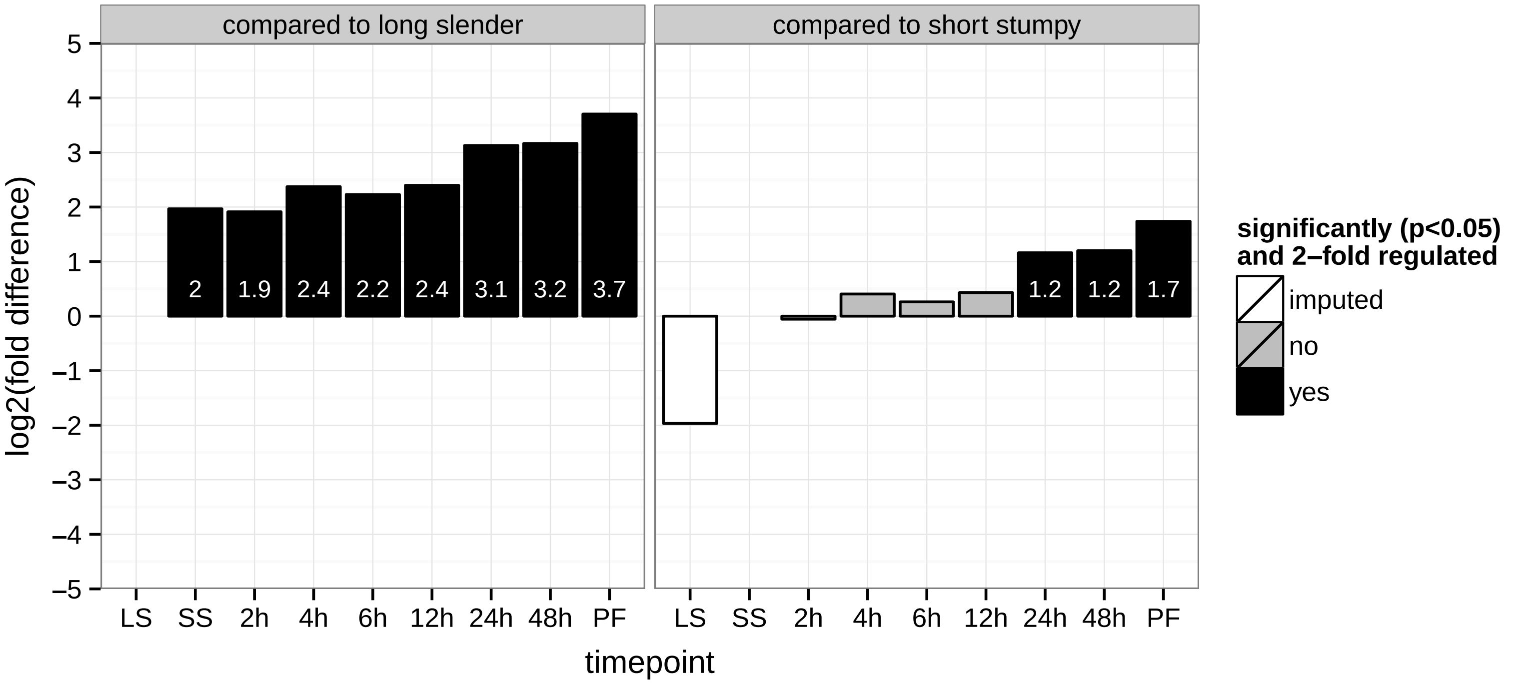
superoxide dismutase, putative
Tb927.6.4030
AGOF: metal ion binding, superoxide dismutase activity
AGOC: mitochondrion
AGOP: oxidation–reduction process, superoxide metabolic process
PGOF: metal ion binding, superoxide dismutase activity
PGOC: null
PGOP: oxidation–reduction process, superoxide metabolic process

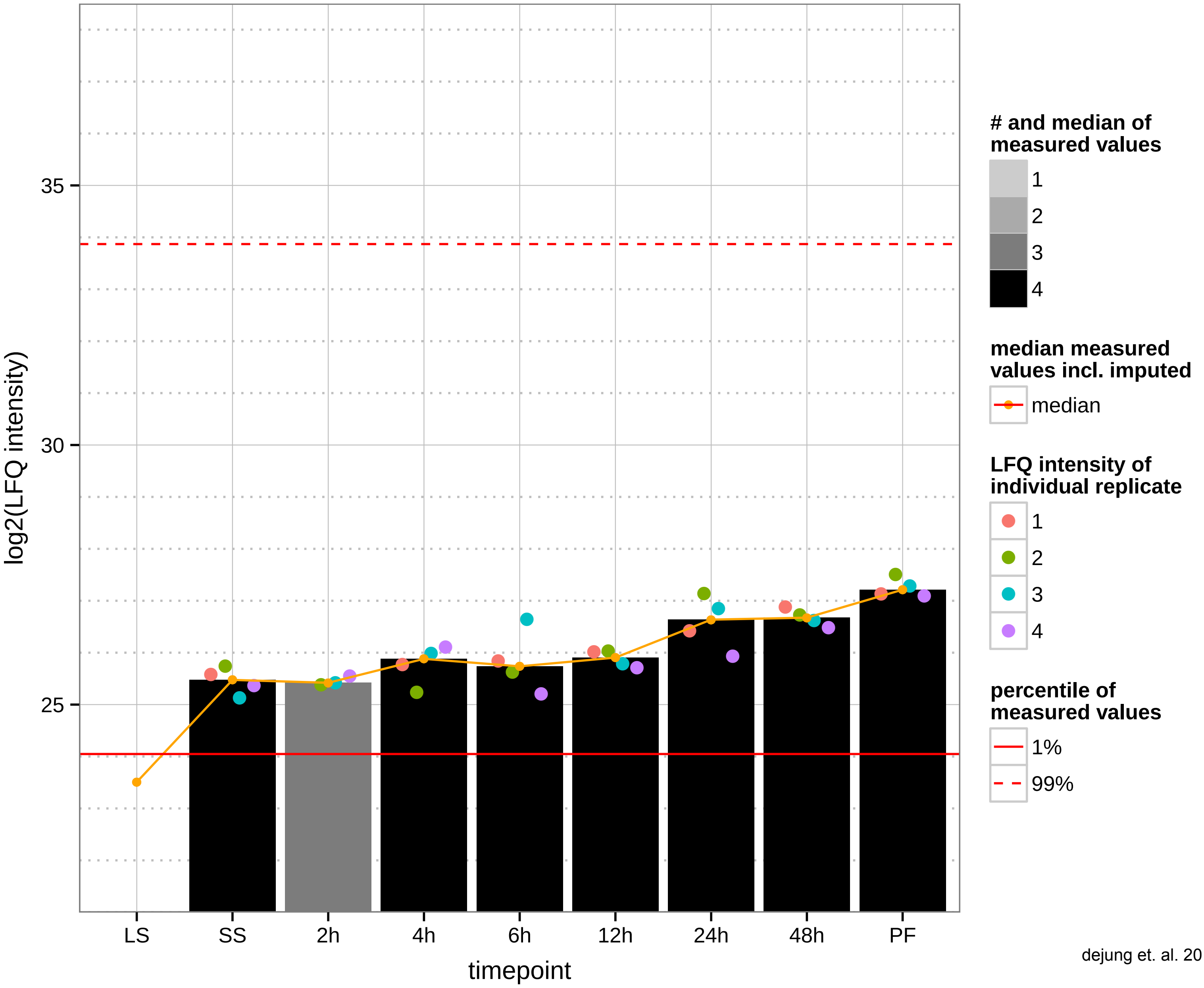




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.4070
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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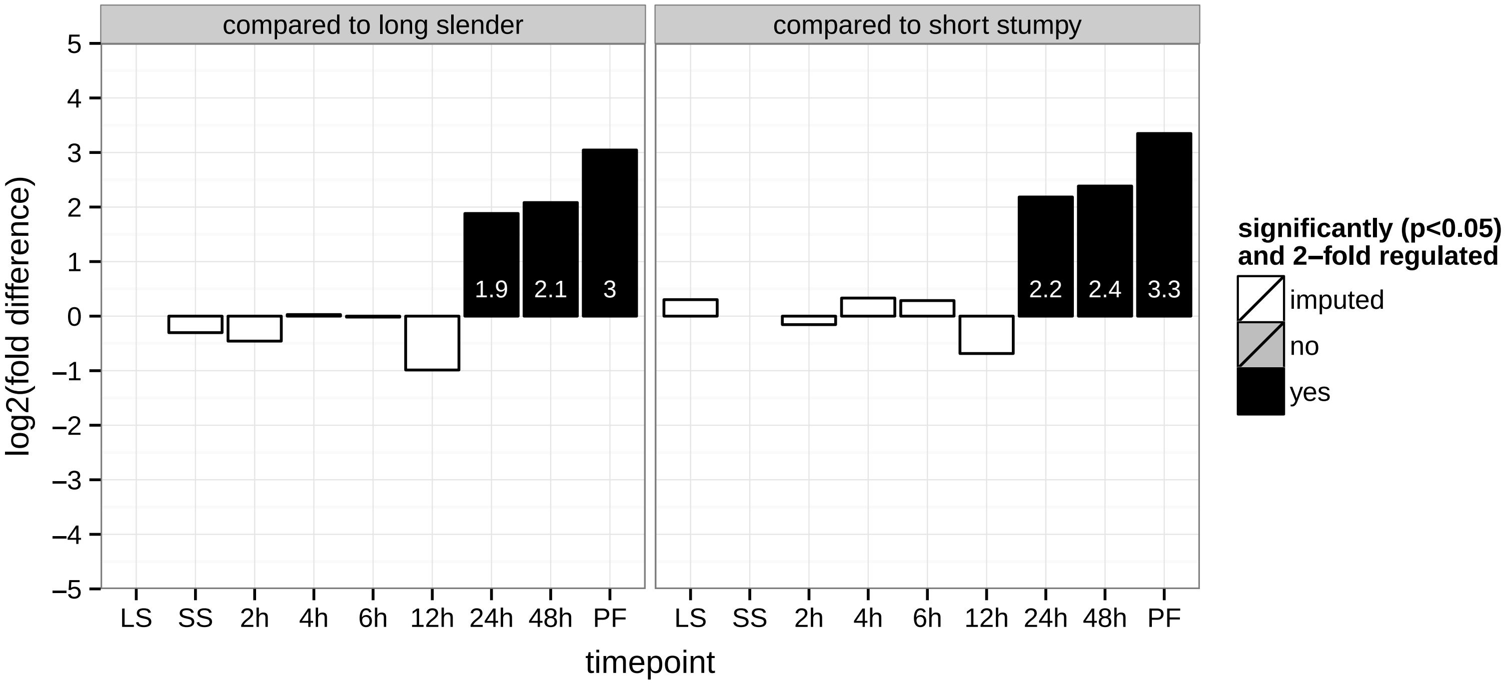
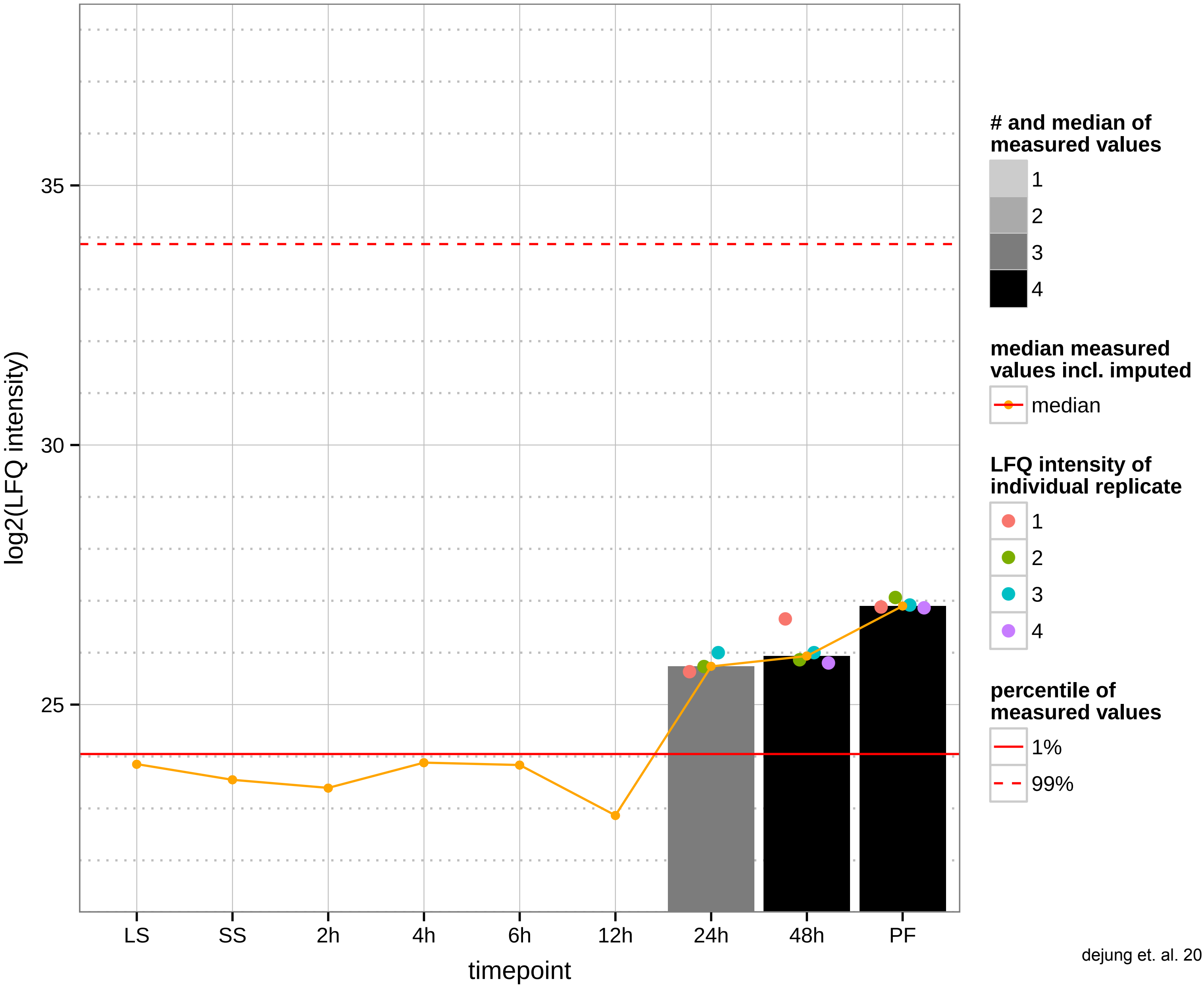
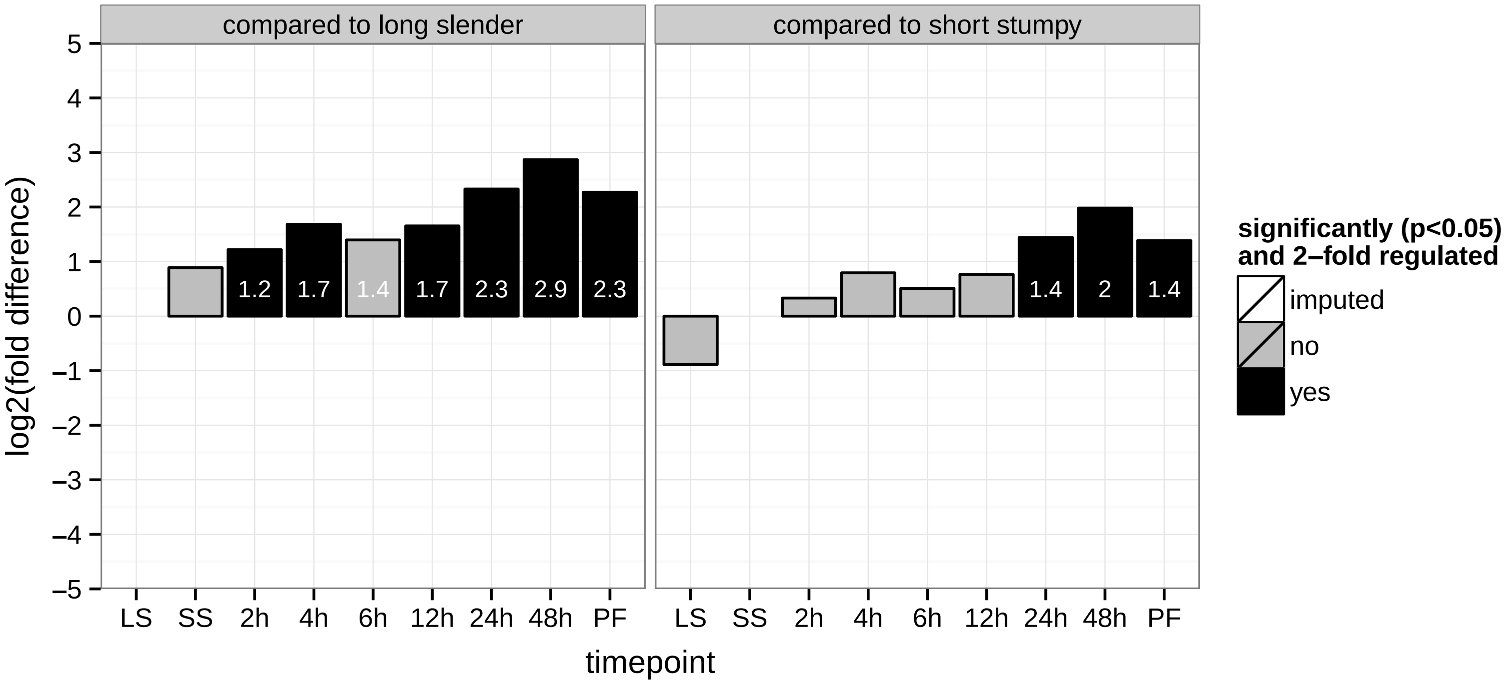
RNA–binding protein, putative (RBP17)
Tb927.6.4530
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null

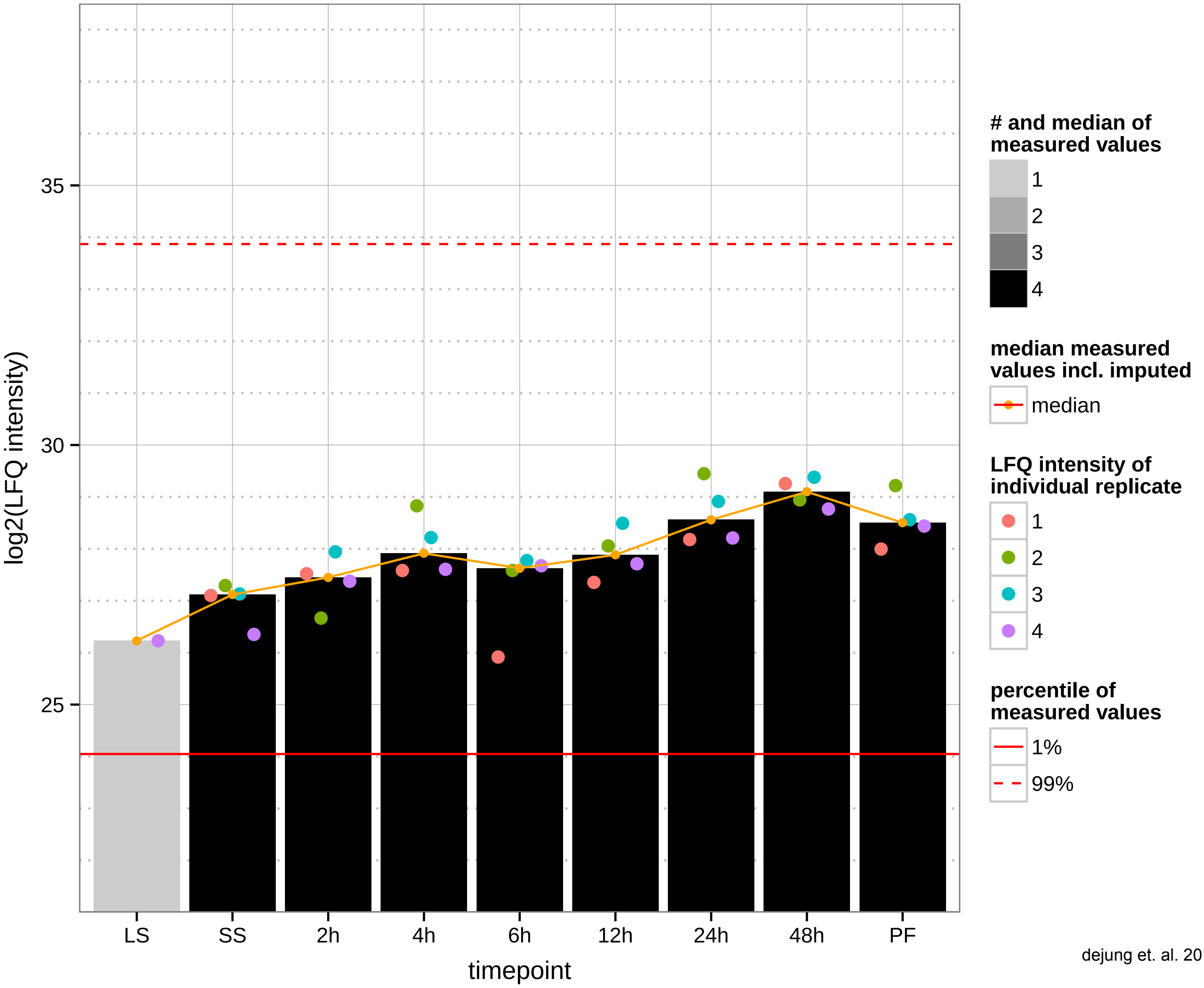




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.590
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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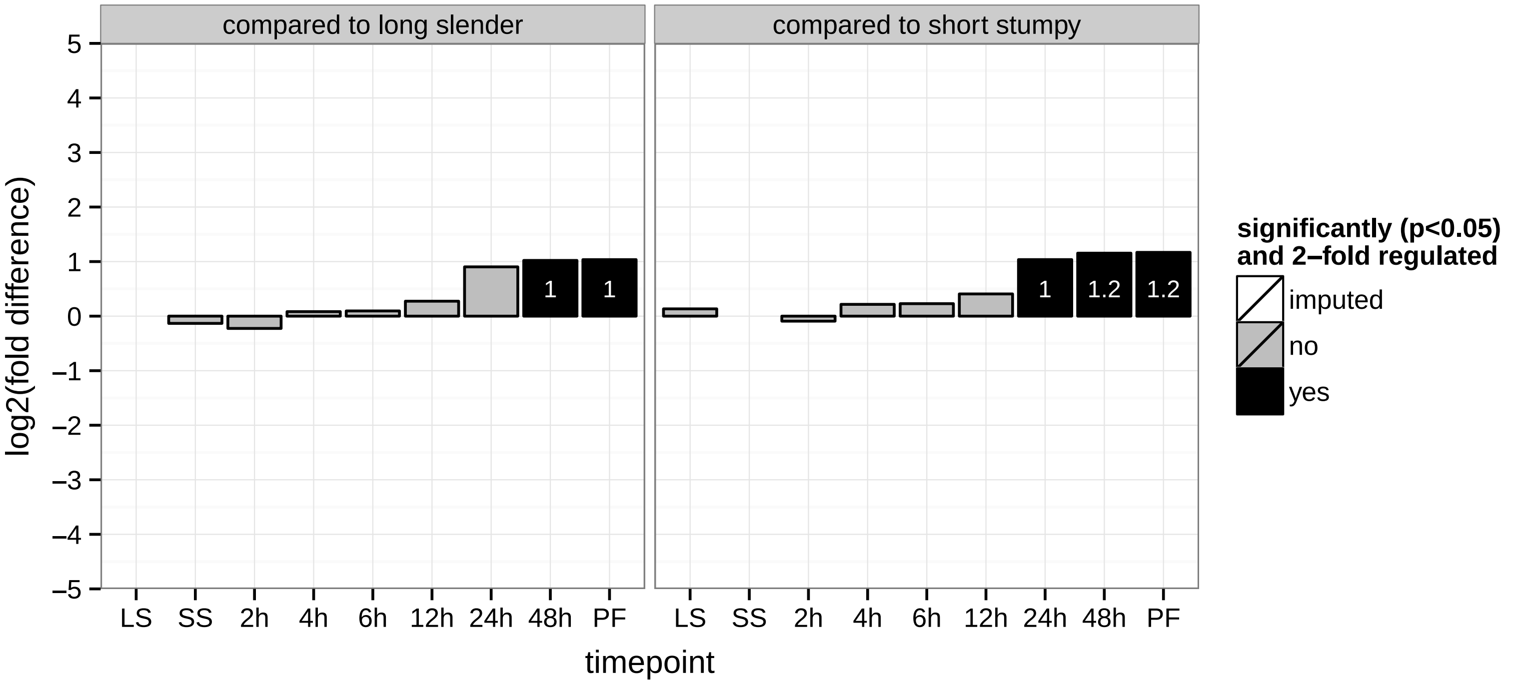
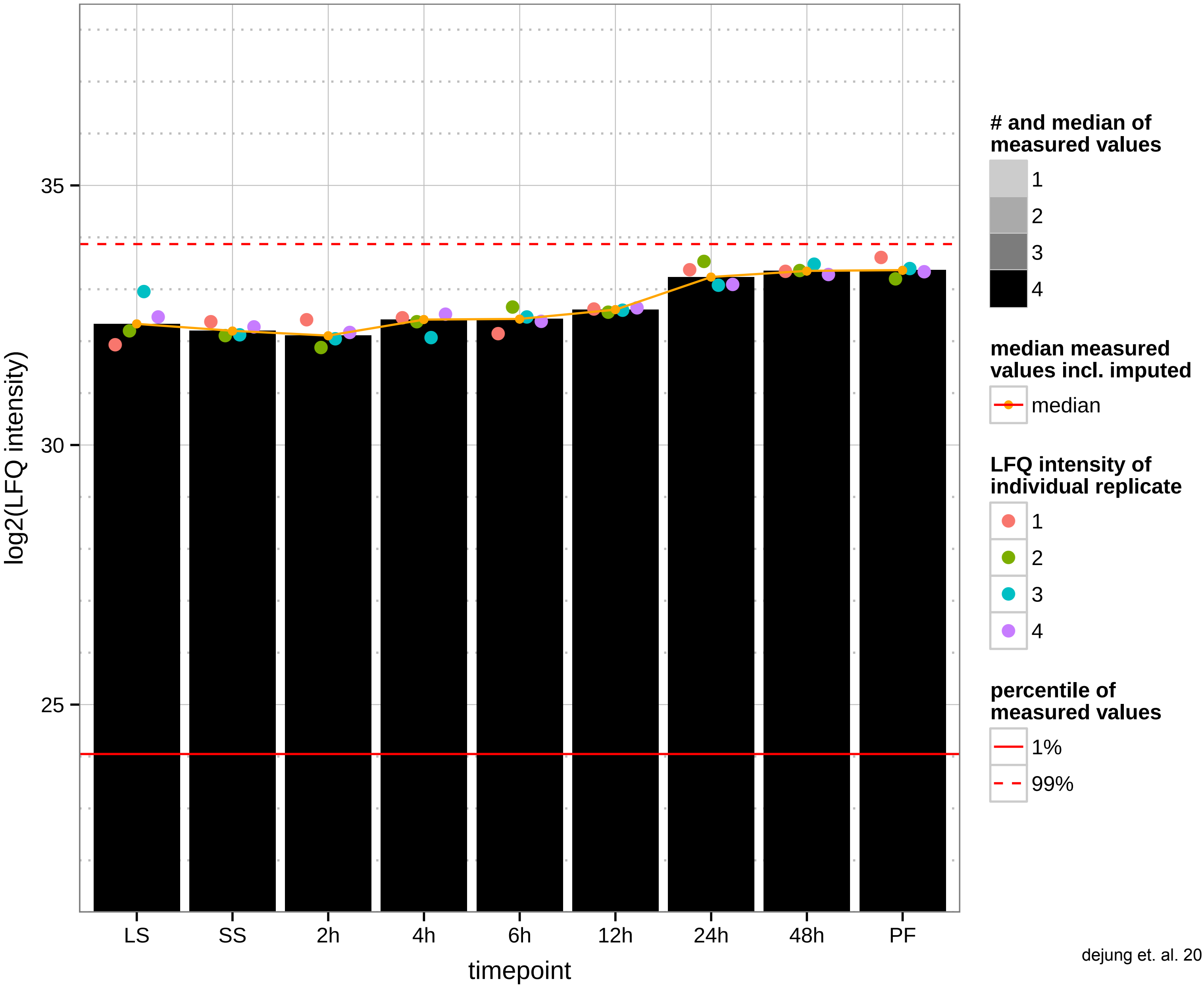
60S ribosomal protein L7, putative
Tb927.7.1730;Tb927.7.1750;Tb927.7.1740
AGOF: structural constituent of ribosome
AGOC: intracellular, large ribosomal subunit, ribosome
AGOP: ribosome biogenesis, translation
PGOF: null
PGOC: null
PGOP: null





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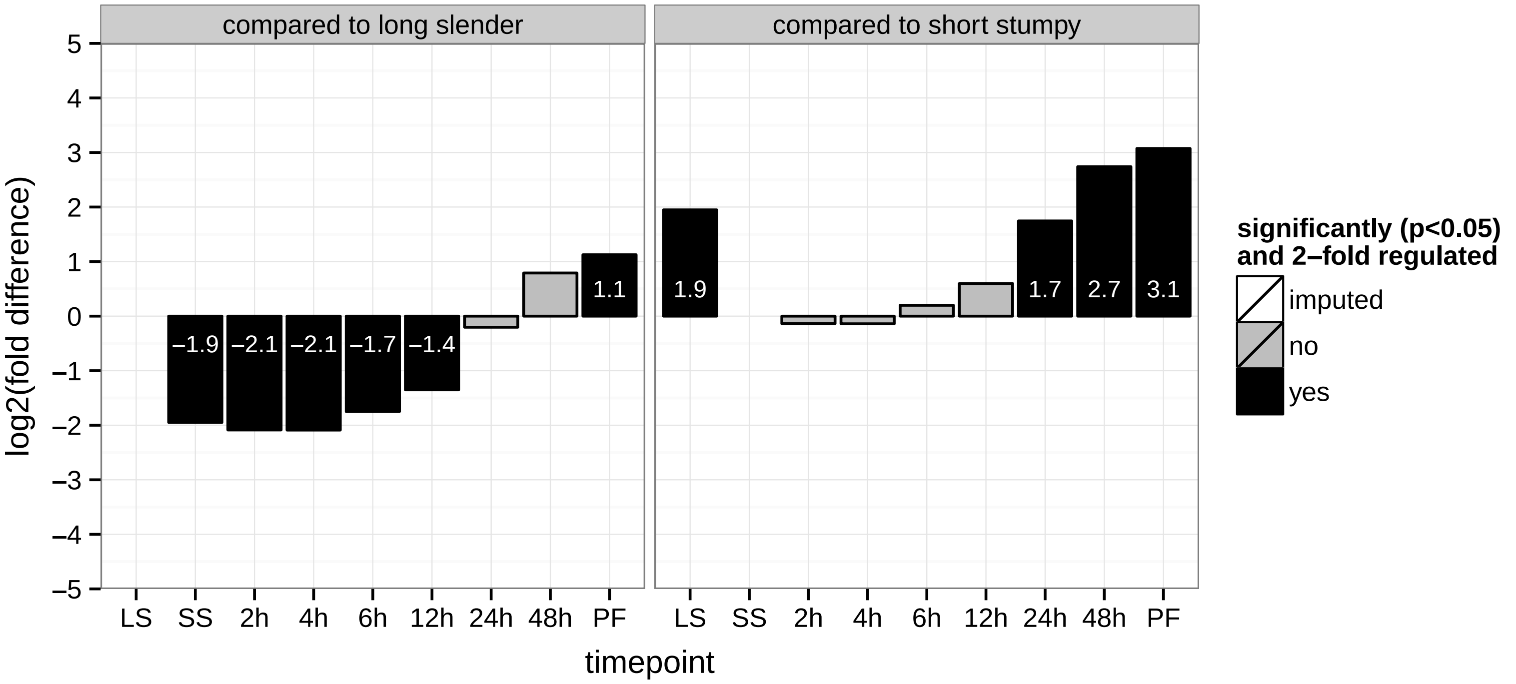
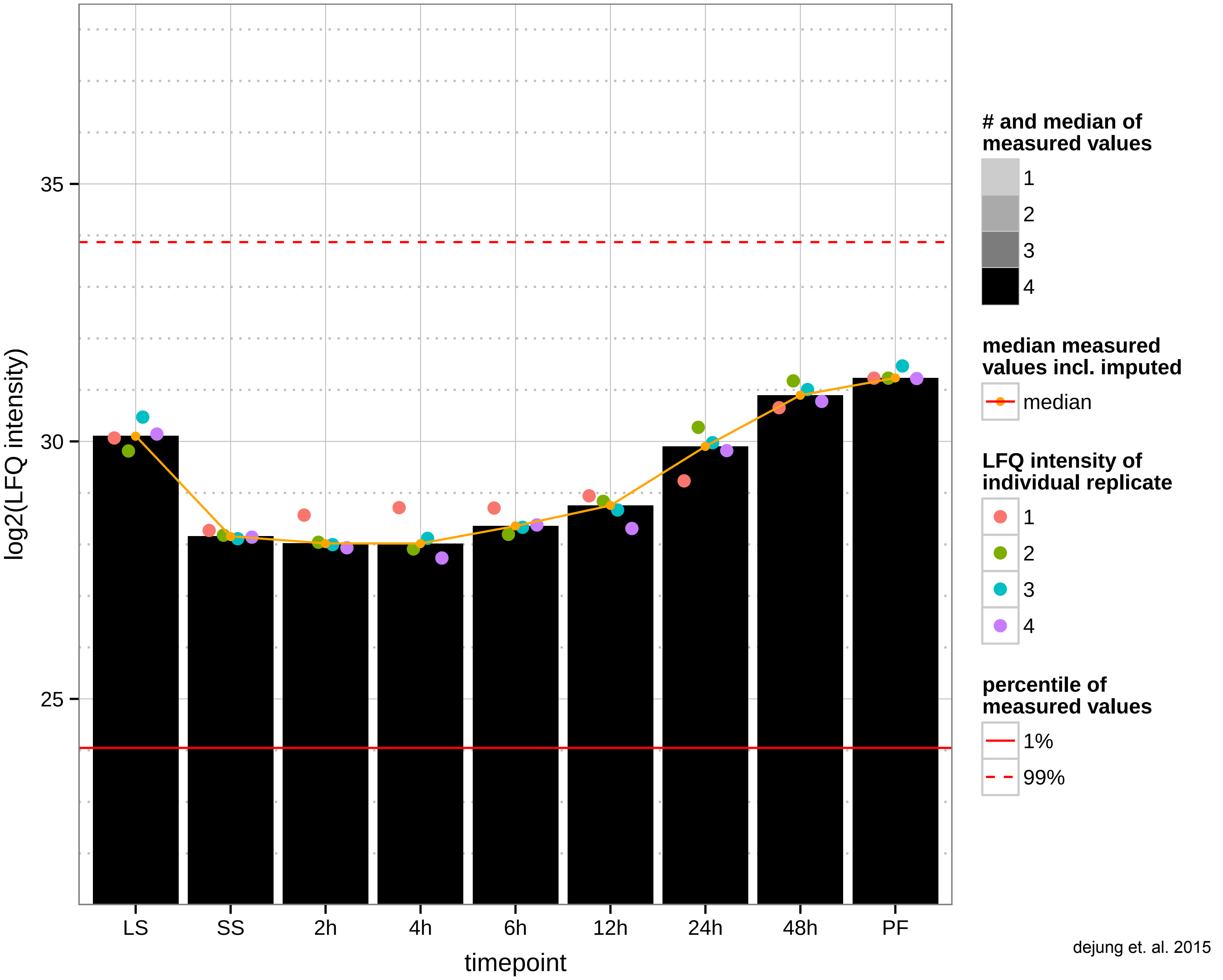
Adenine phosphoribosyltransferase, putative
Tb927.7.1780
AGOF: null
AGOC: null
AGOP: purine ribonucleoside salvage
PGOF: null
PGOC: null
PGOP: nucleoside metabolic process





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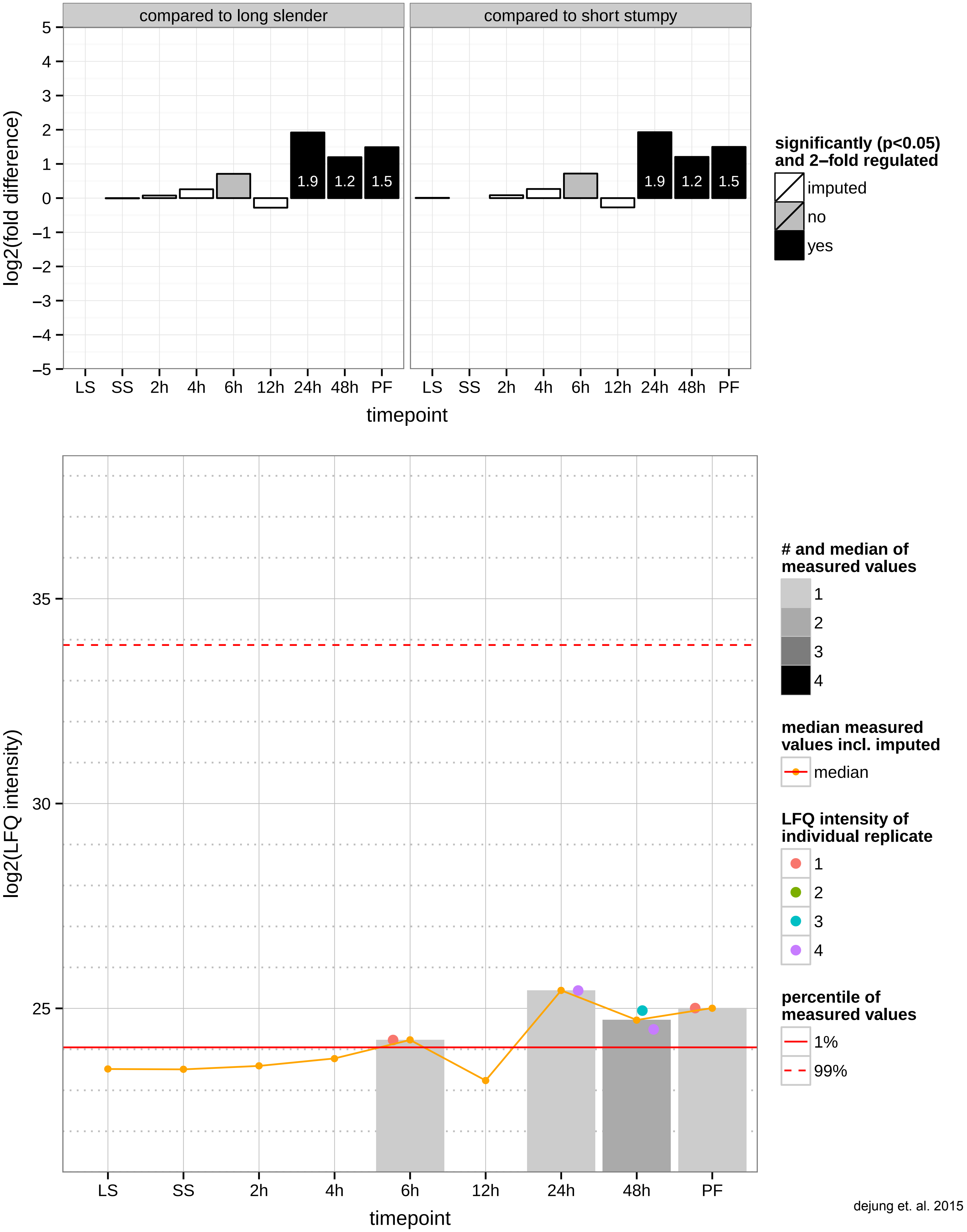
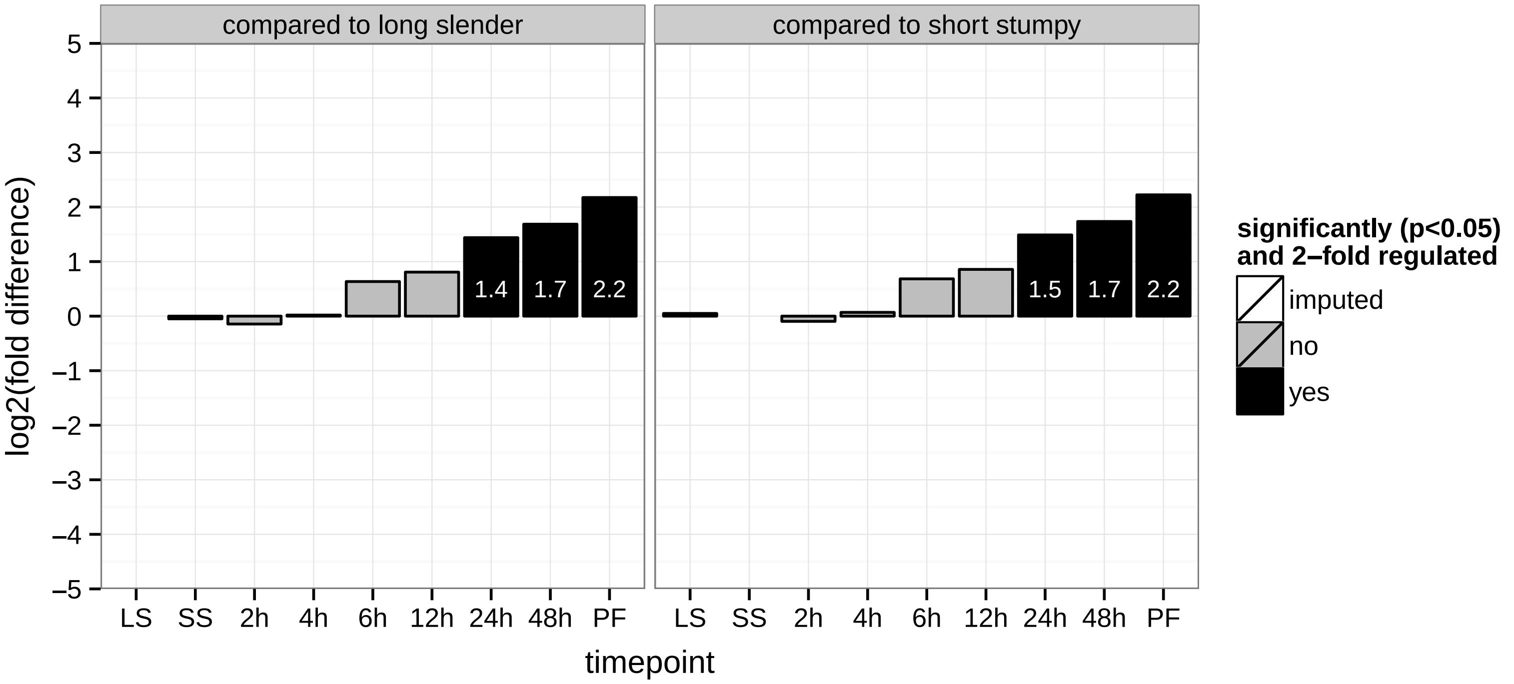
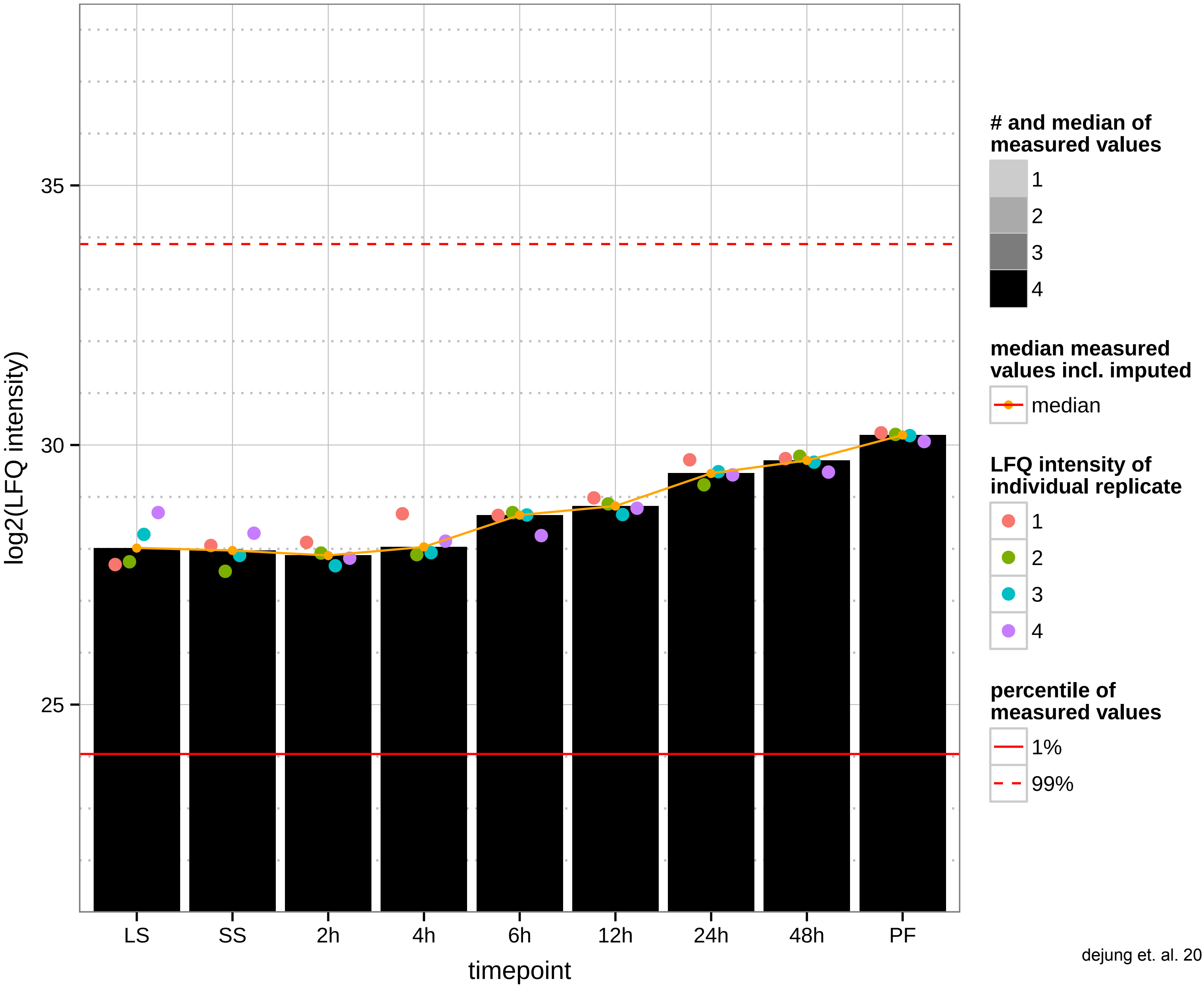
hypothetical protein, conserved
Tb927.7.2220
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



tyrosyl–tRNA synthetase, putative
Tb927.7.2400
AGOF: tRNA binding
AGOC: null
AGOP: null
PGOF: tRNA binding
PGOC: null
PGOP: null





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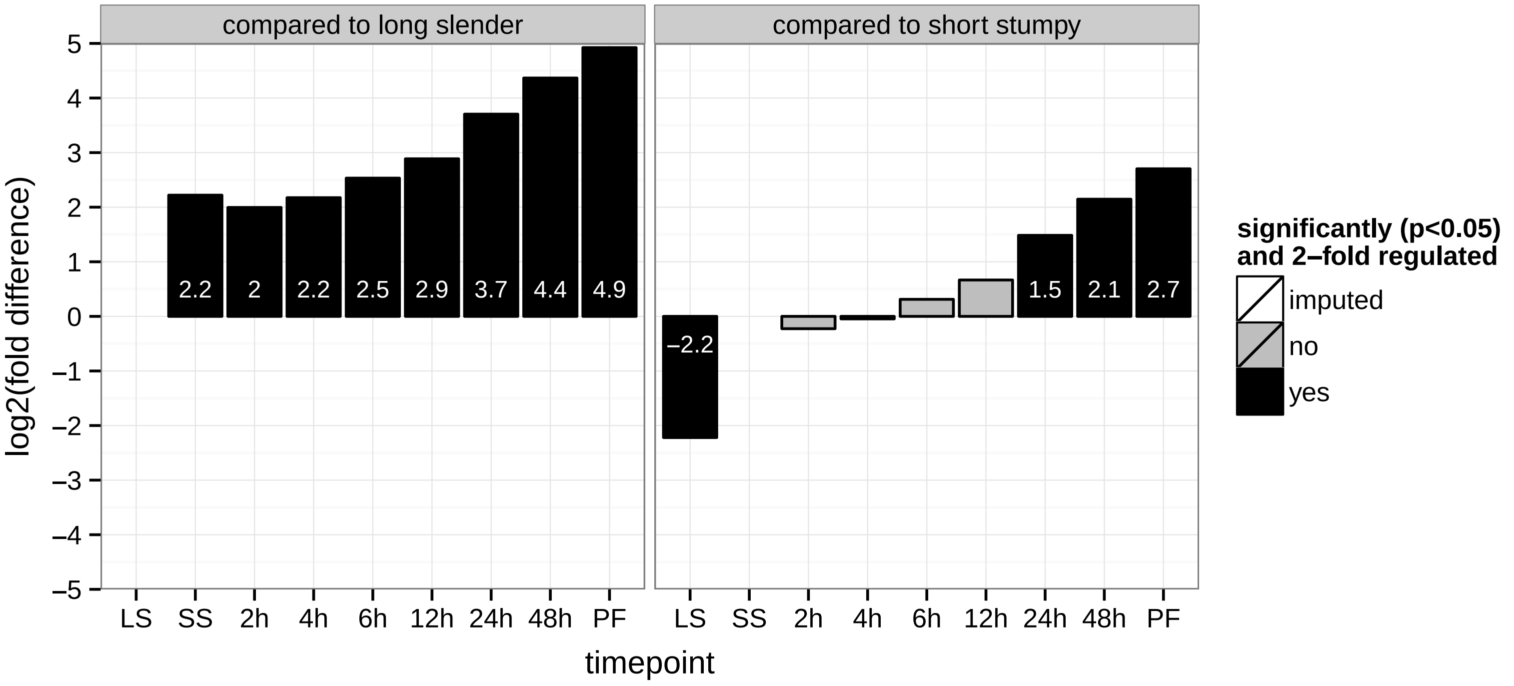
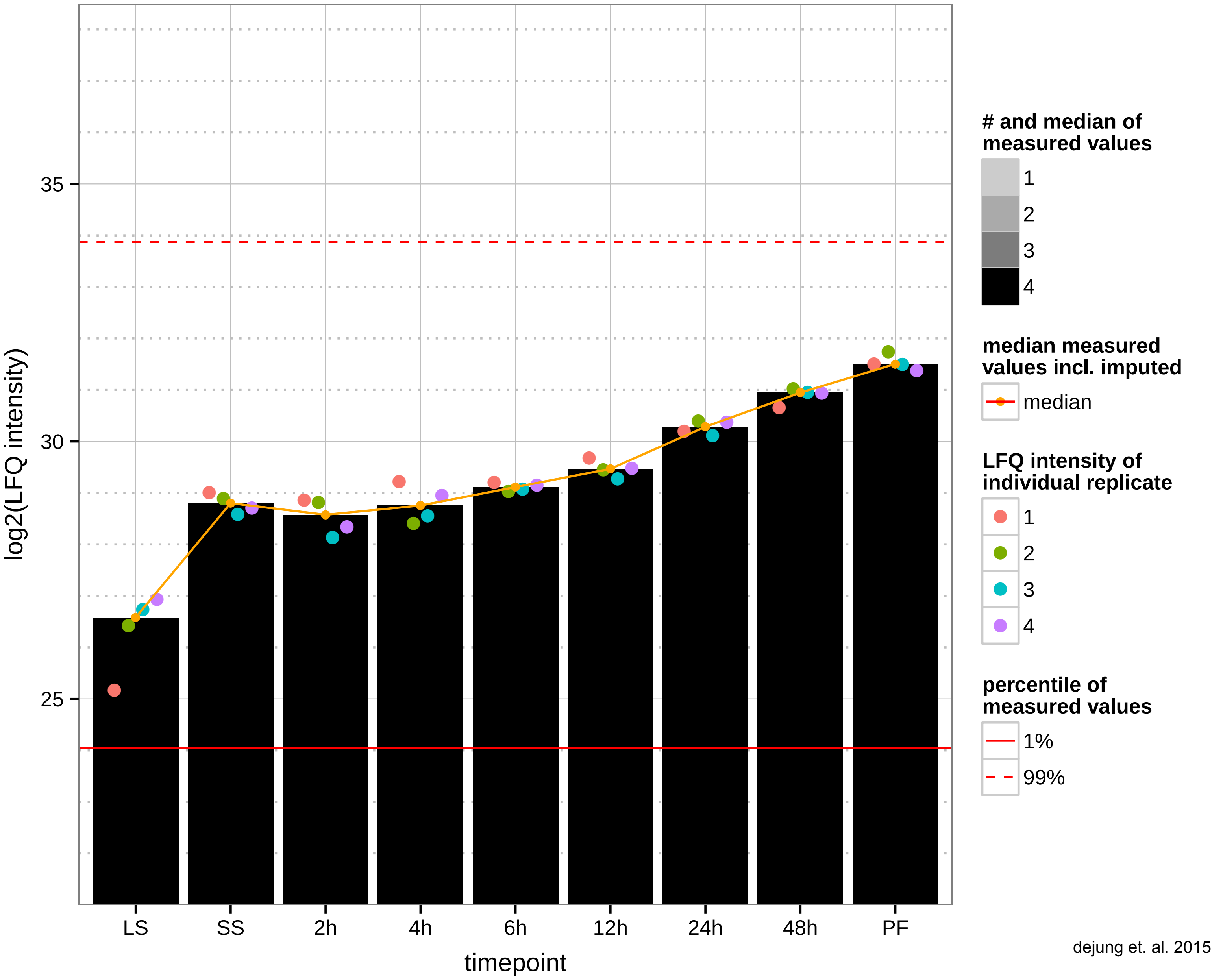
NADH–cytochrome b5 reductase, putative (B5R)
Tb927.7.2700
AGOF: electron carrier activity, oxidoreductase activity
AGOC: mitochondrion
AGOP: null
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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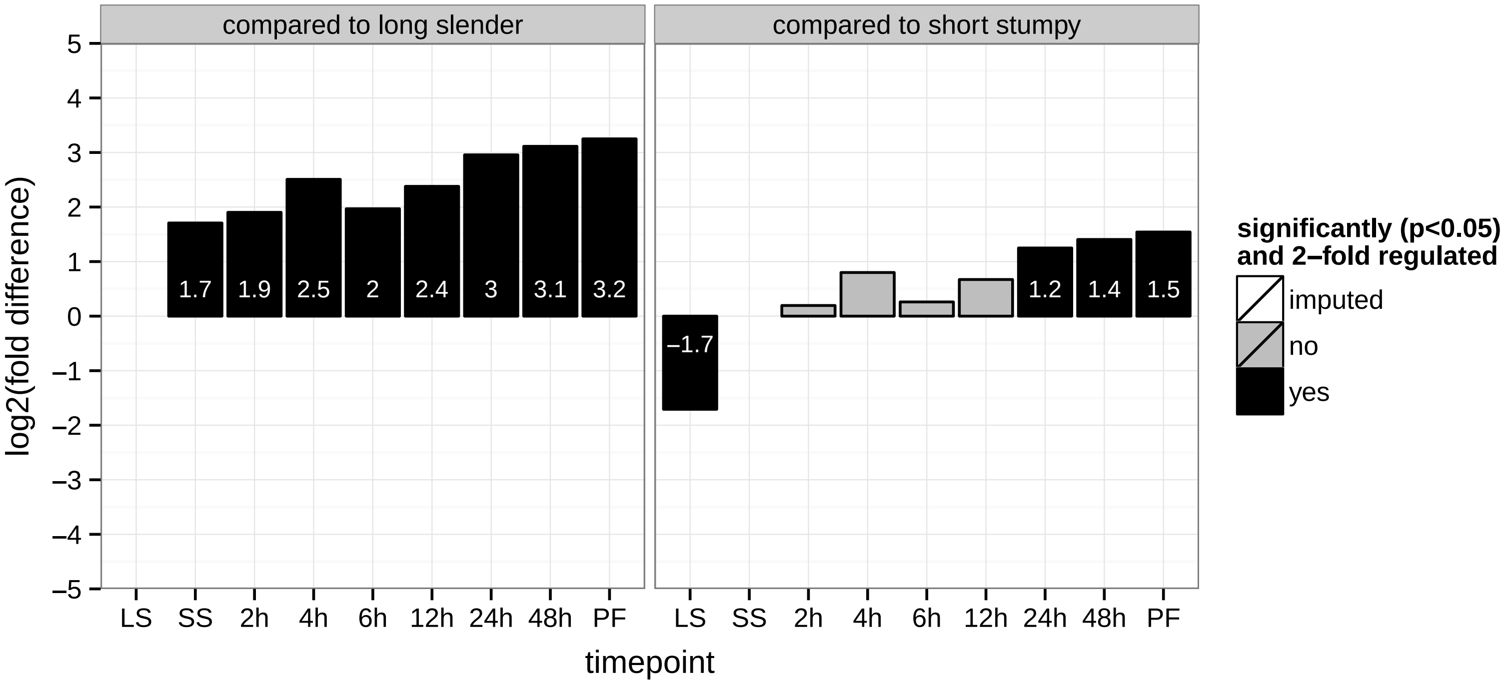
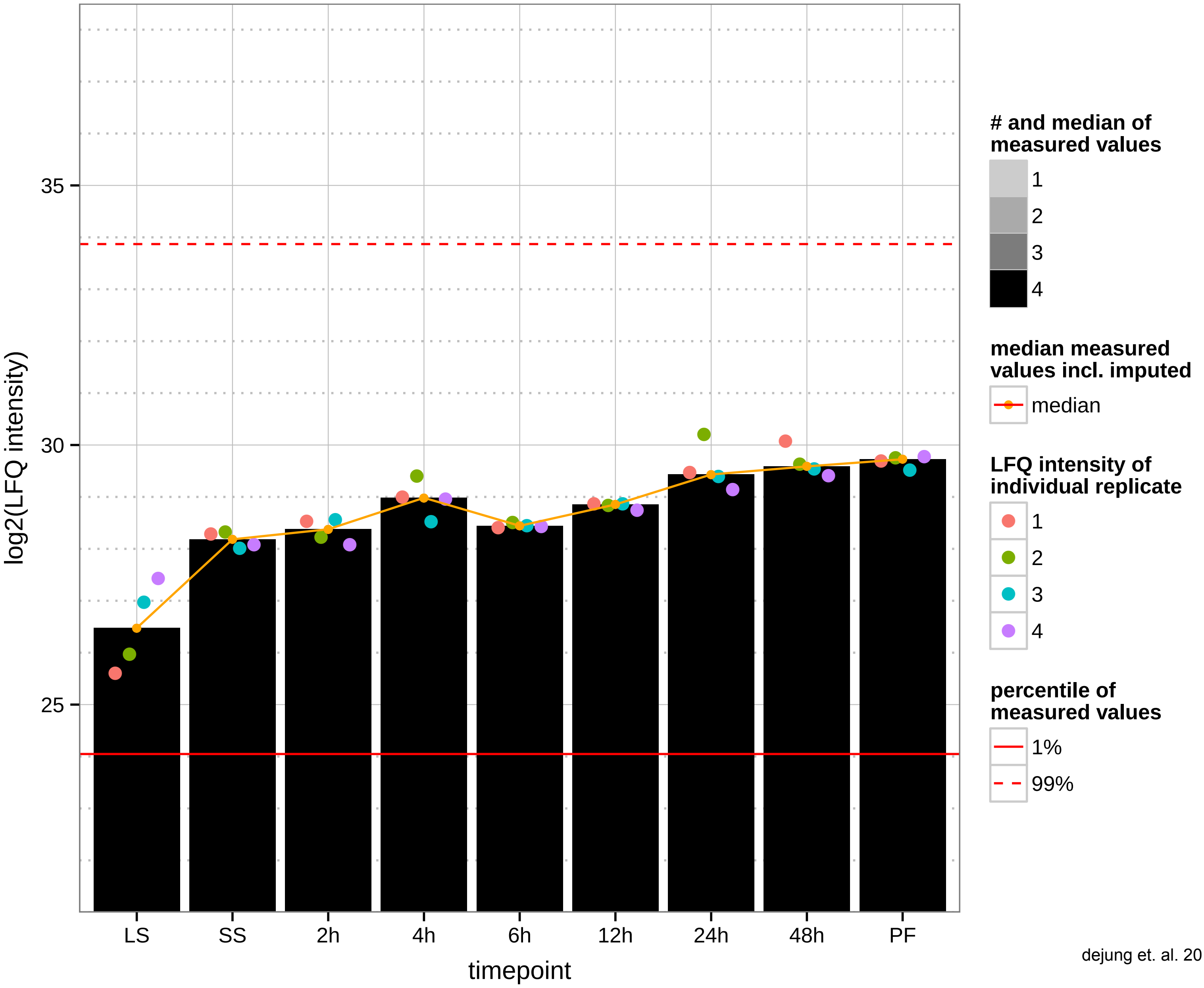
NADH–cytochrome b5 reductase, putative
Tb927.7.2710
AGOF: electron carrier activity, oxidoreductase activity
AGOC: null
AGOP: null
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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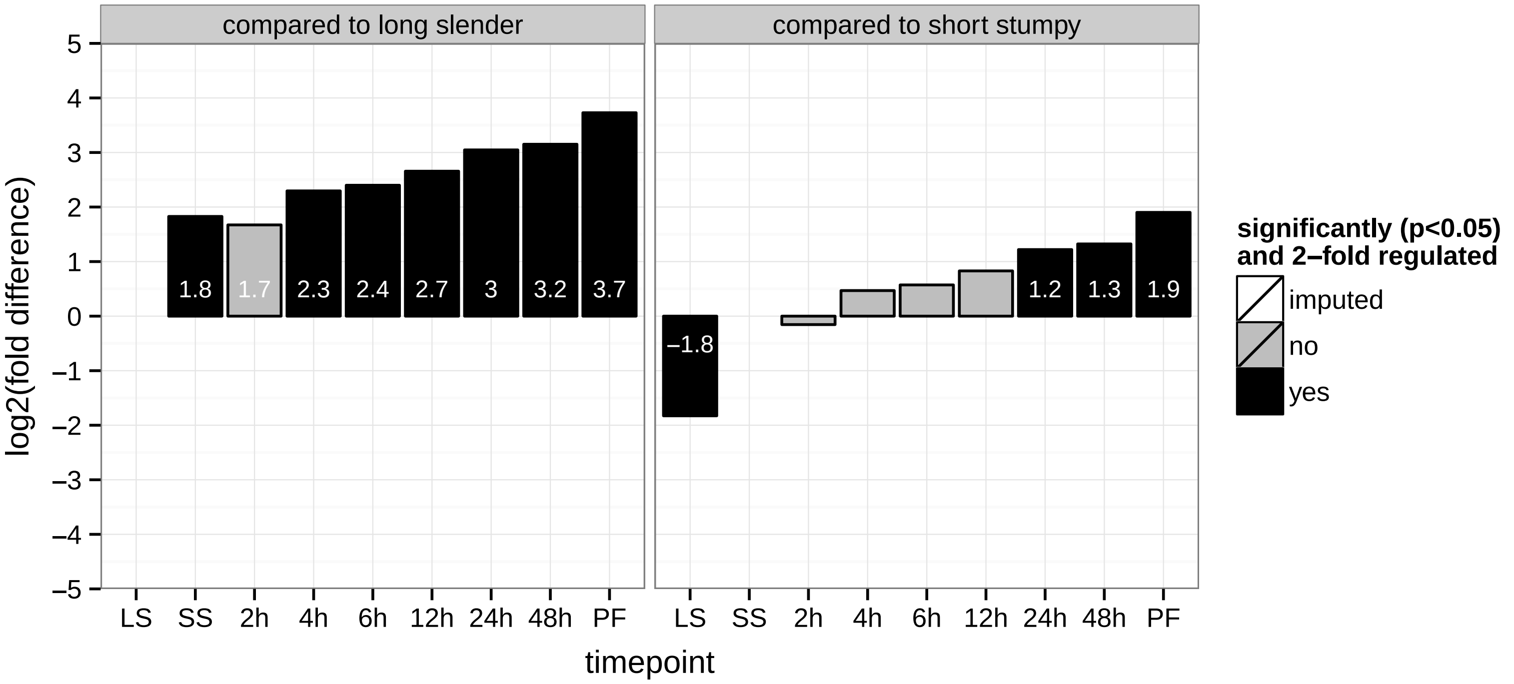
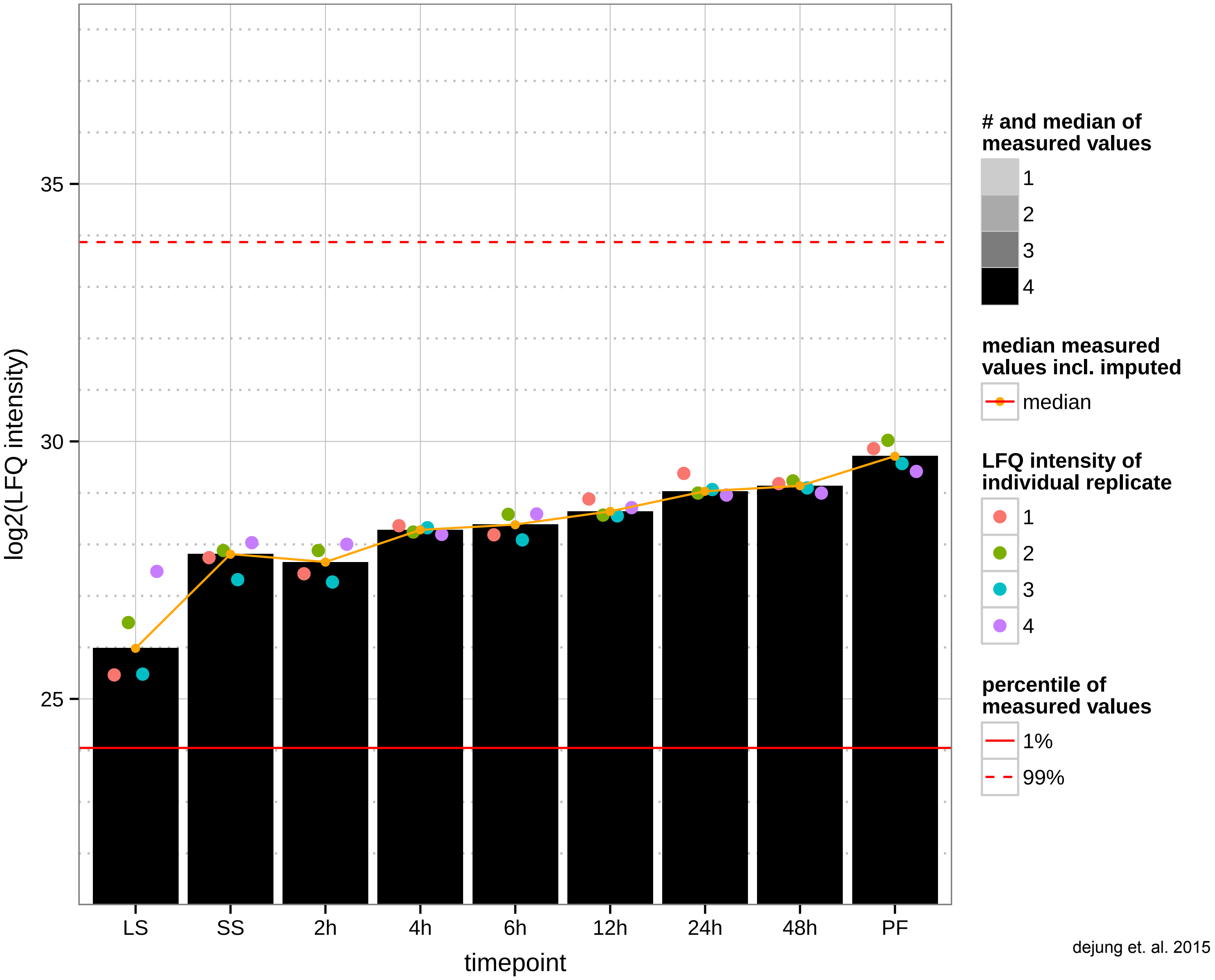
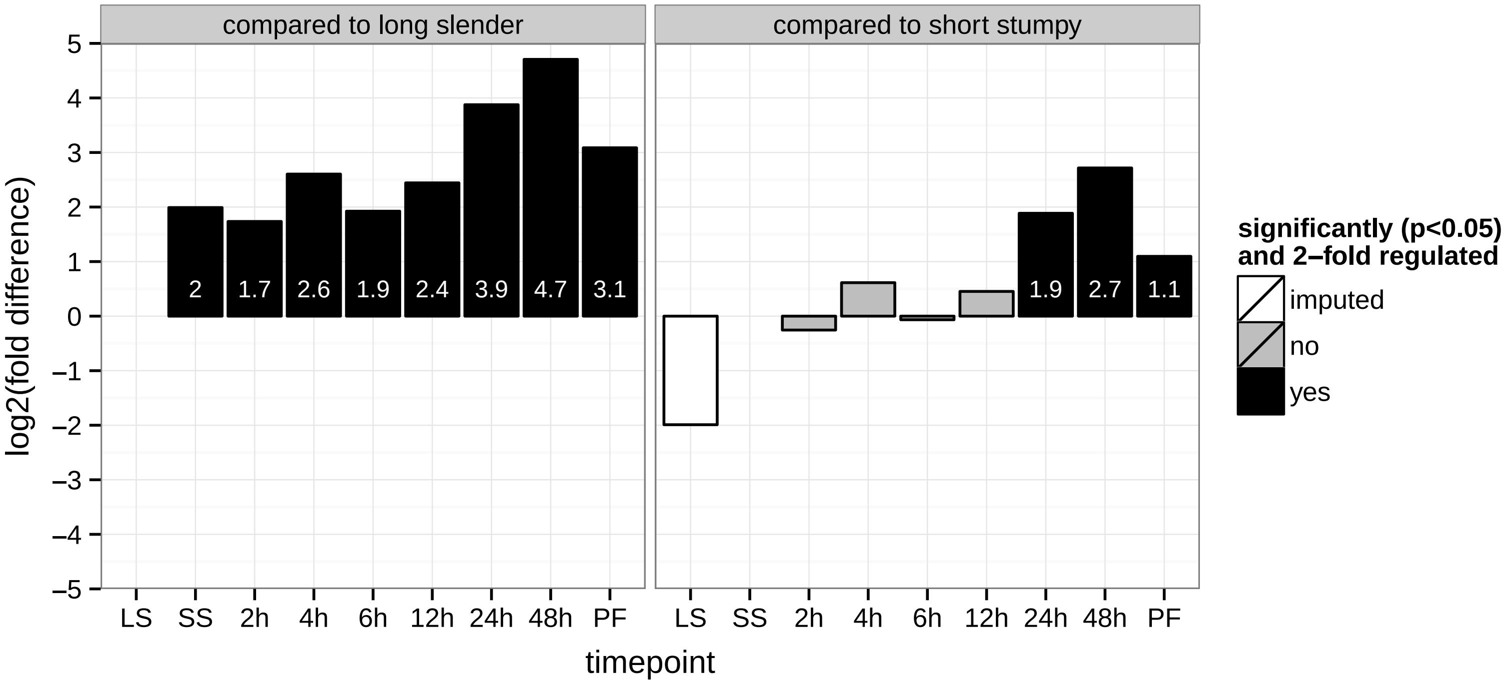
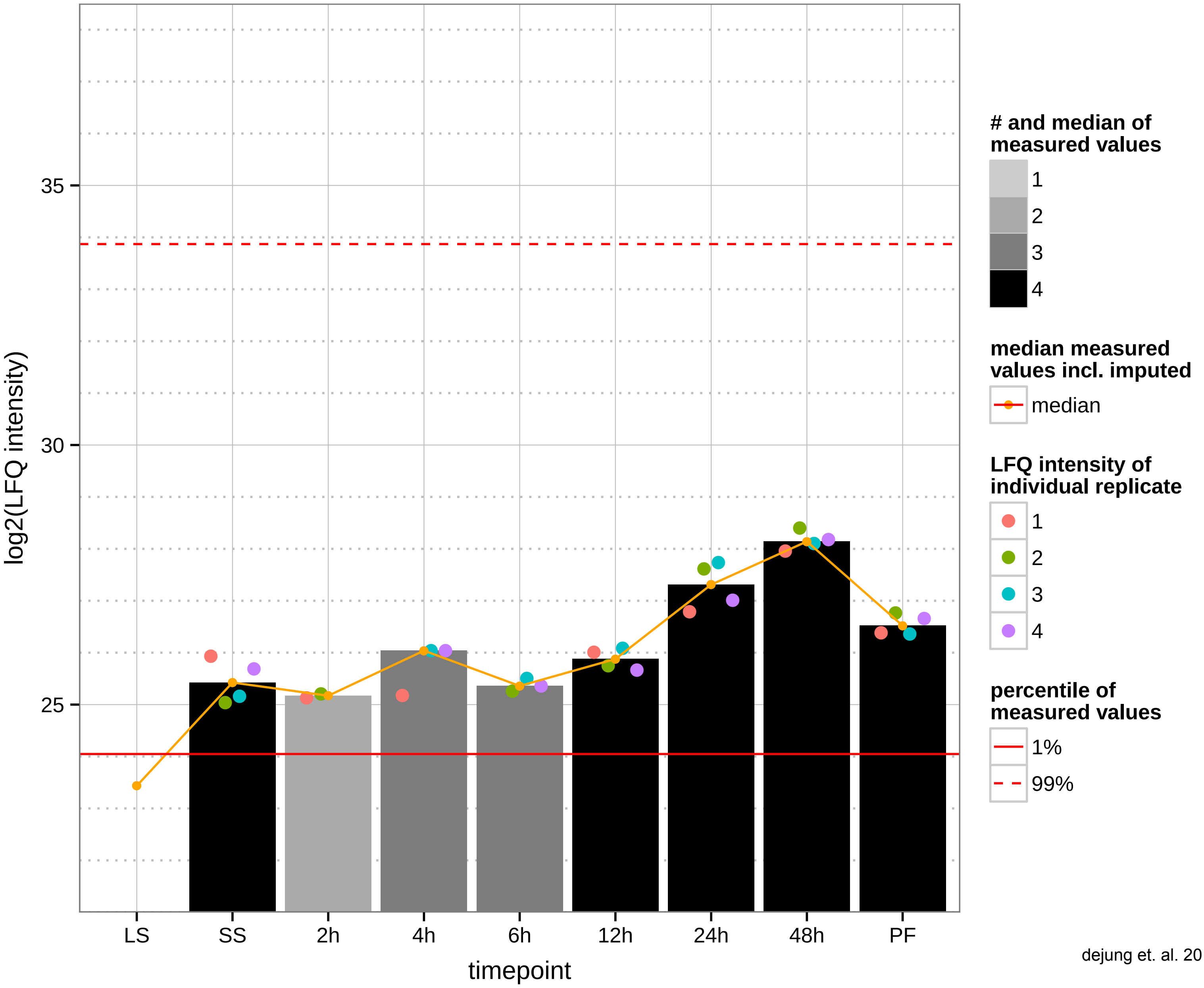
cyclophilin–type peptidyl–prolyl cis–trans isomerase, putative (PPIase)
Tb927.7.280
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





hypothetical protein, conserved
Tb927.7.3590
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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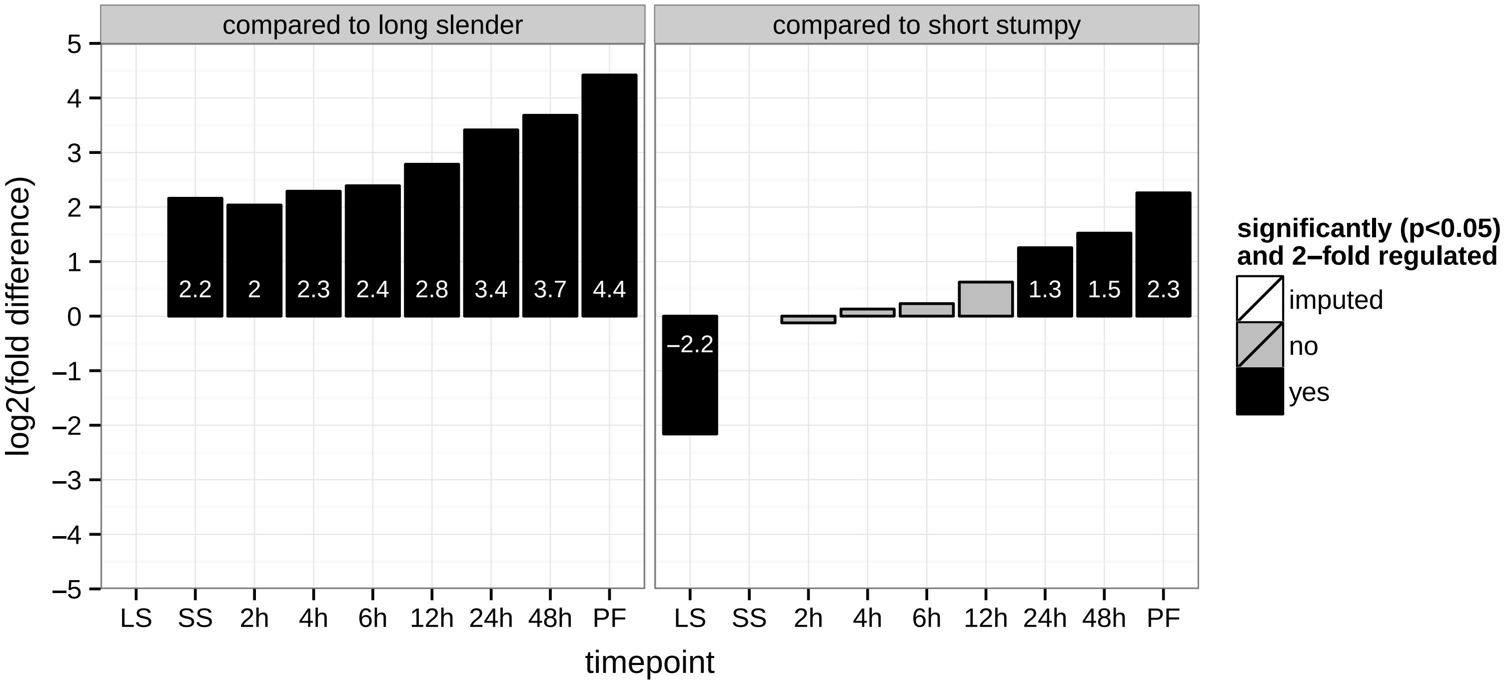
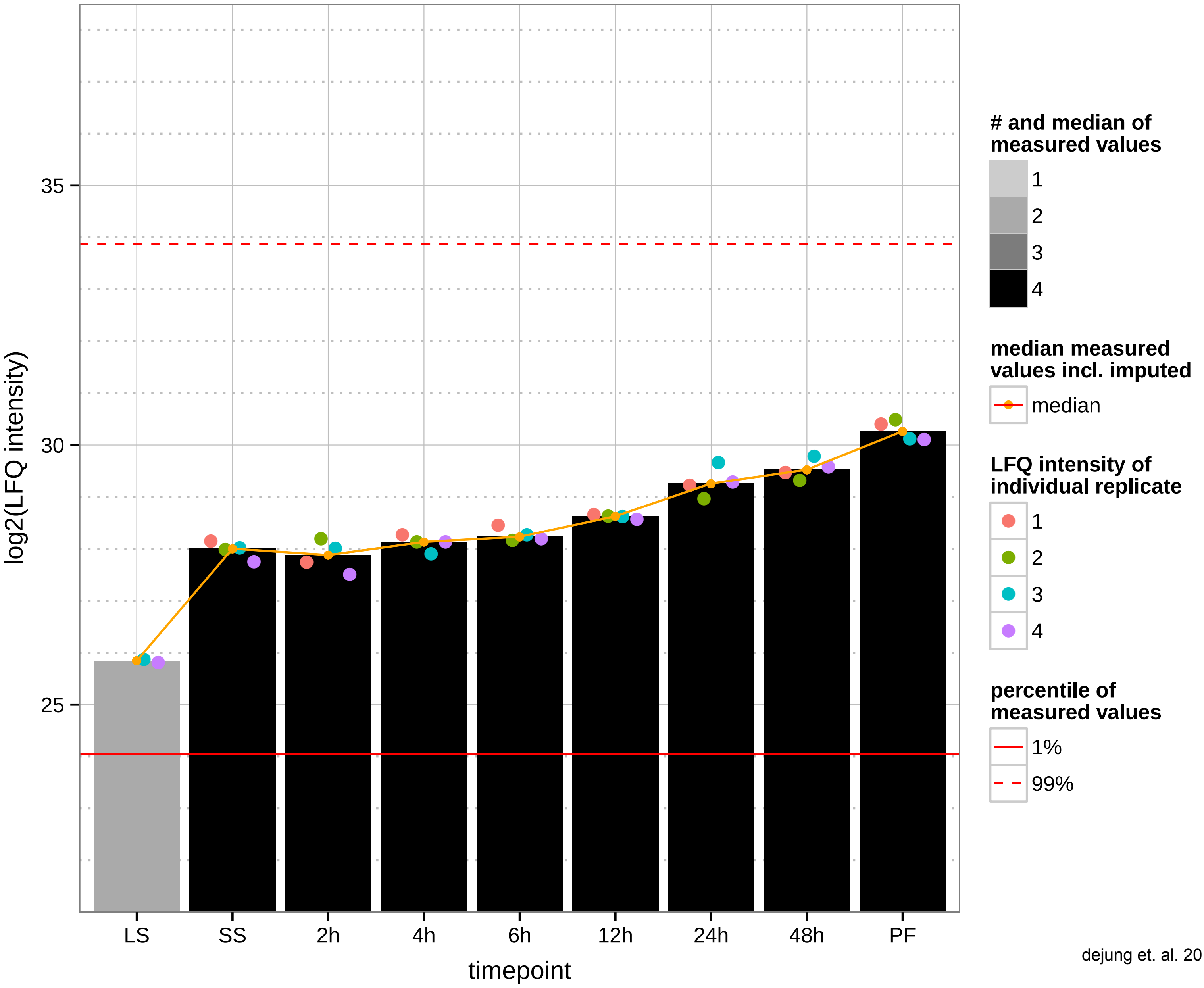
mitochondrial carrier protein, ADP/ATP mitochondrial translocase, putative, adenine nucleotide mitochondrial translocator, put
Tb927.7.3940
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrial part
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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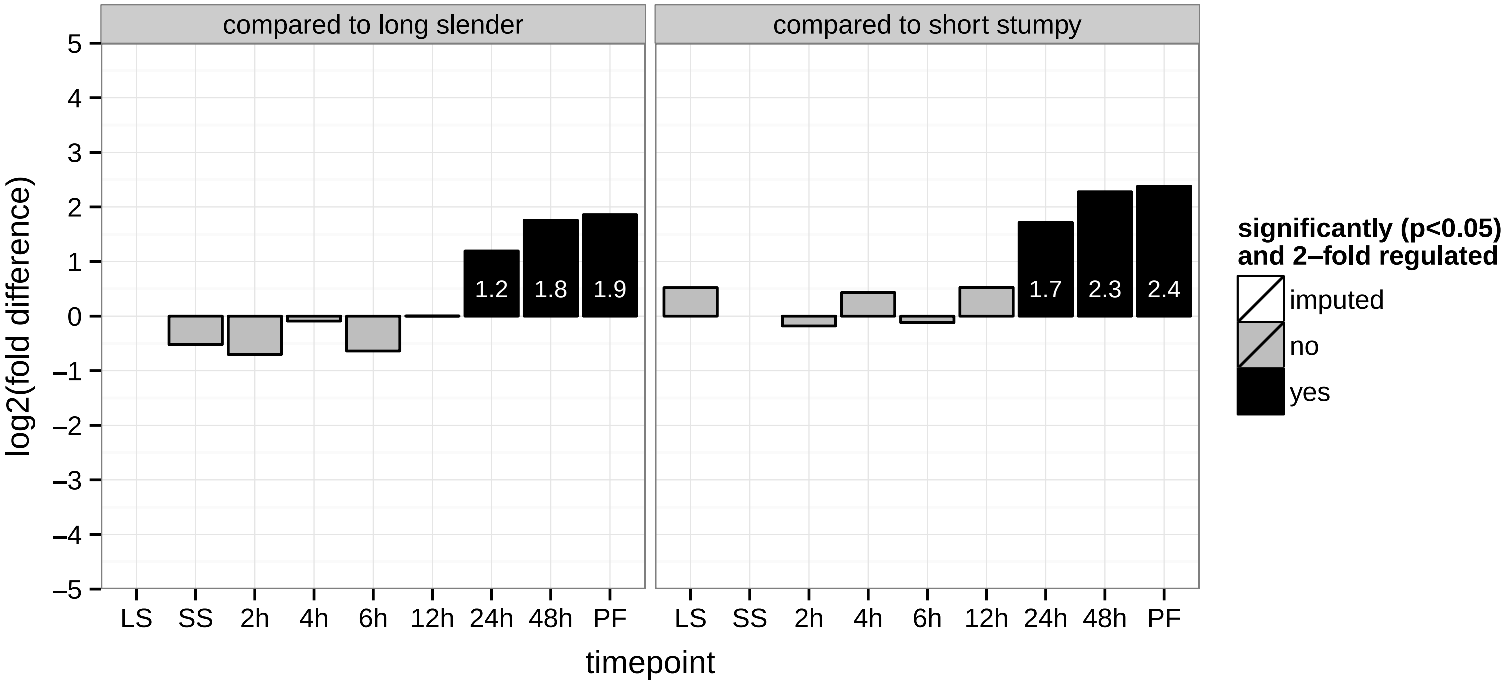
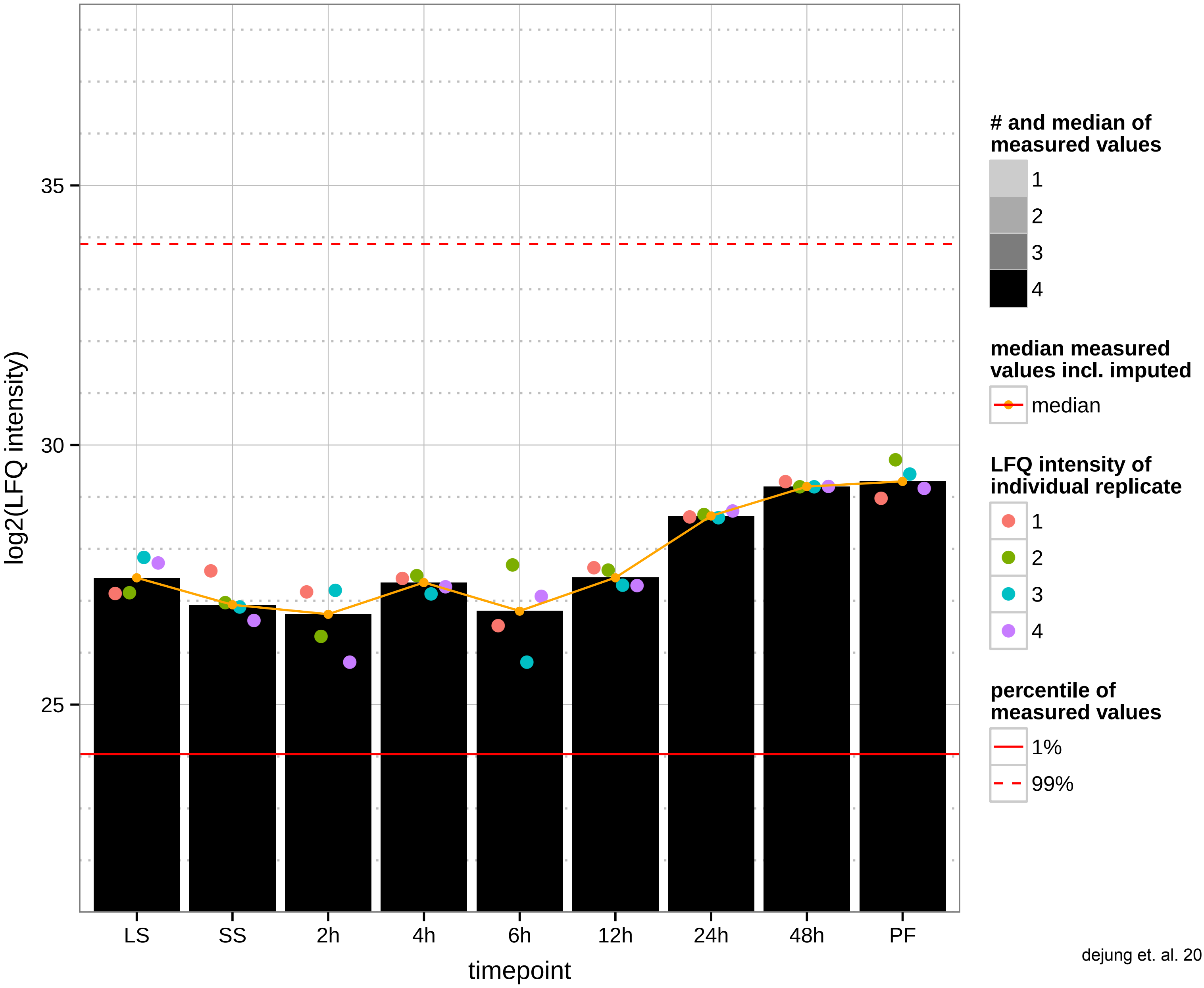
deoxyuridine triphosphatase, putative, dUTP diphosphatase
Tb927.7.5160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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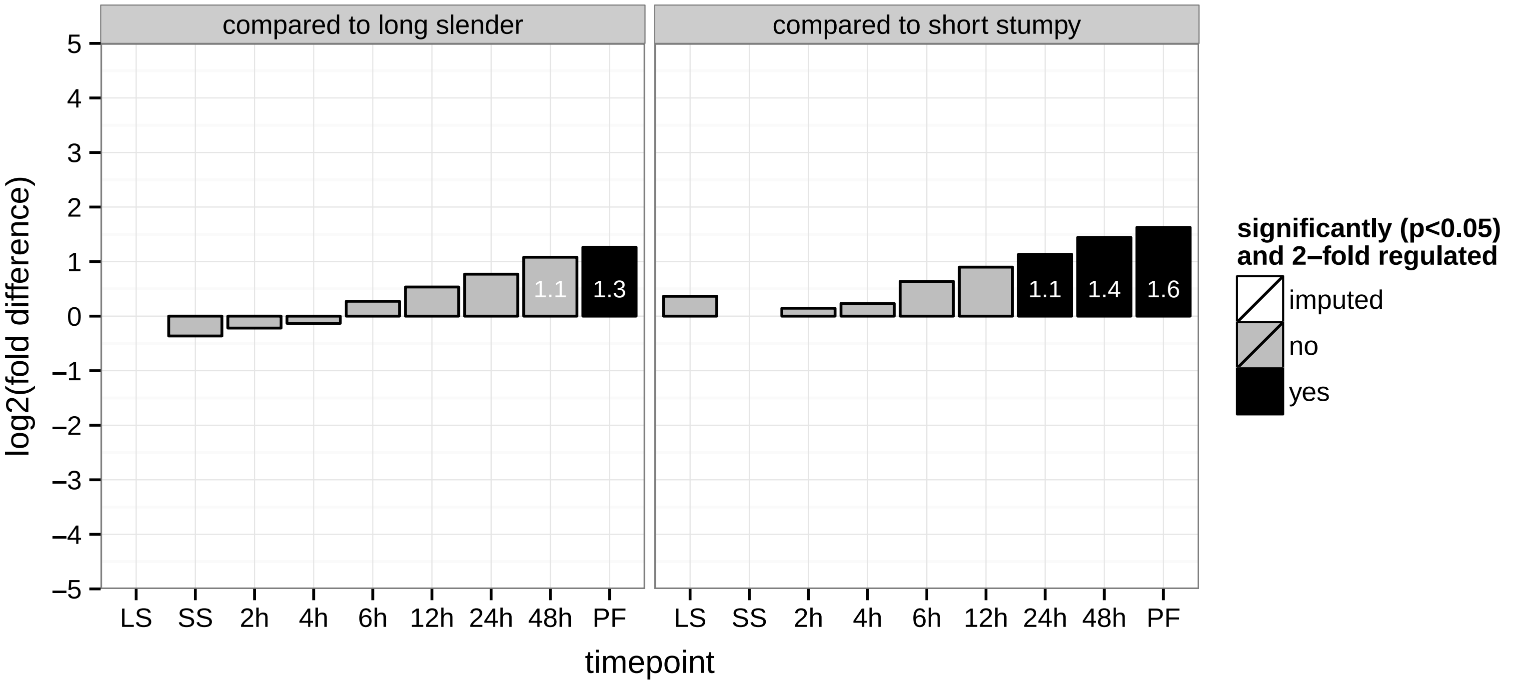
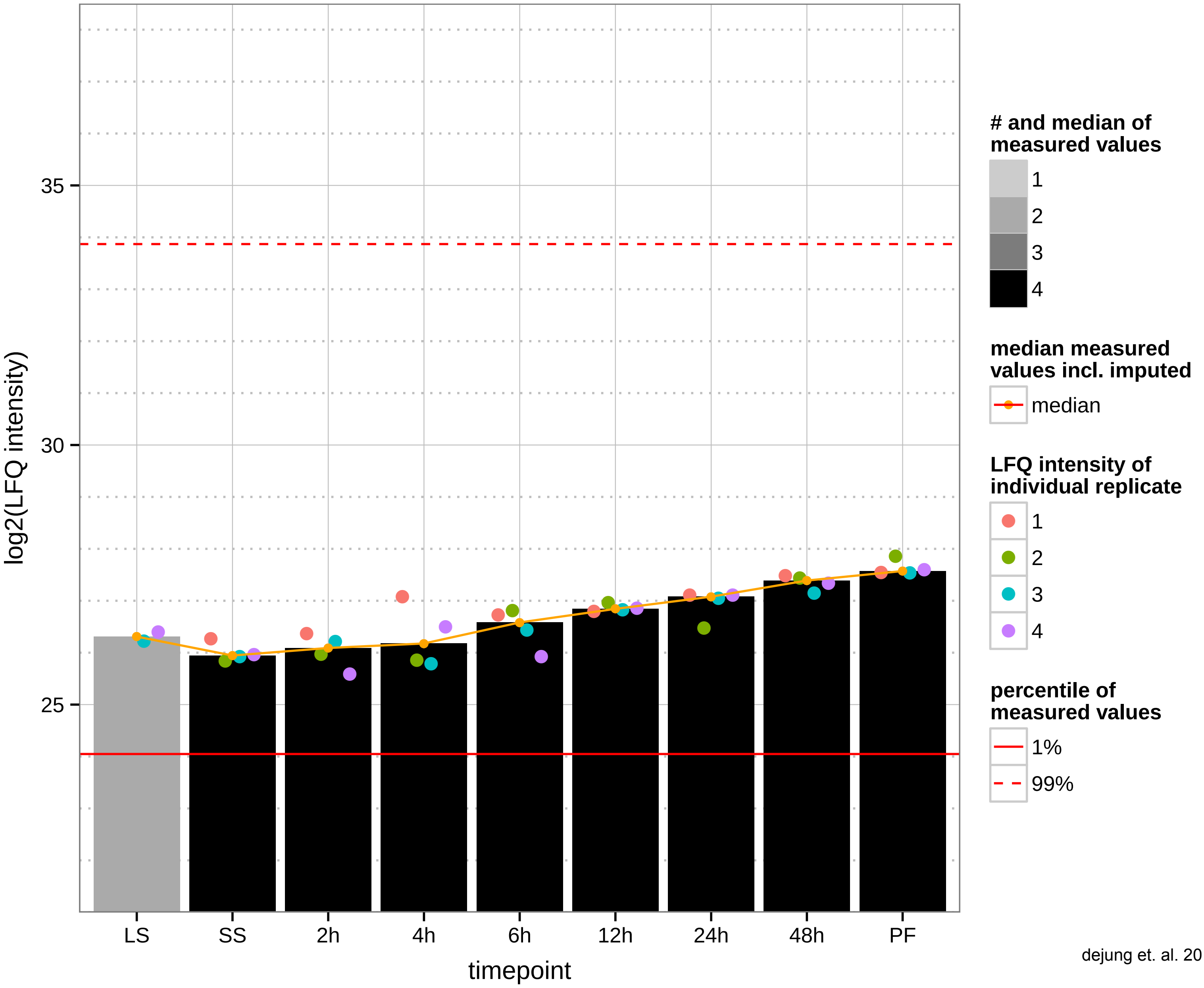
hypothetical protein, conserved
Tb927.7.6670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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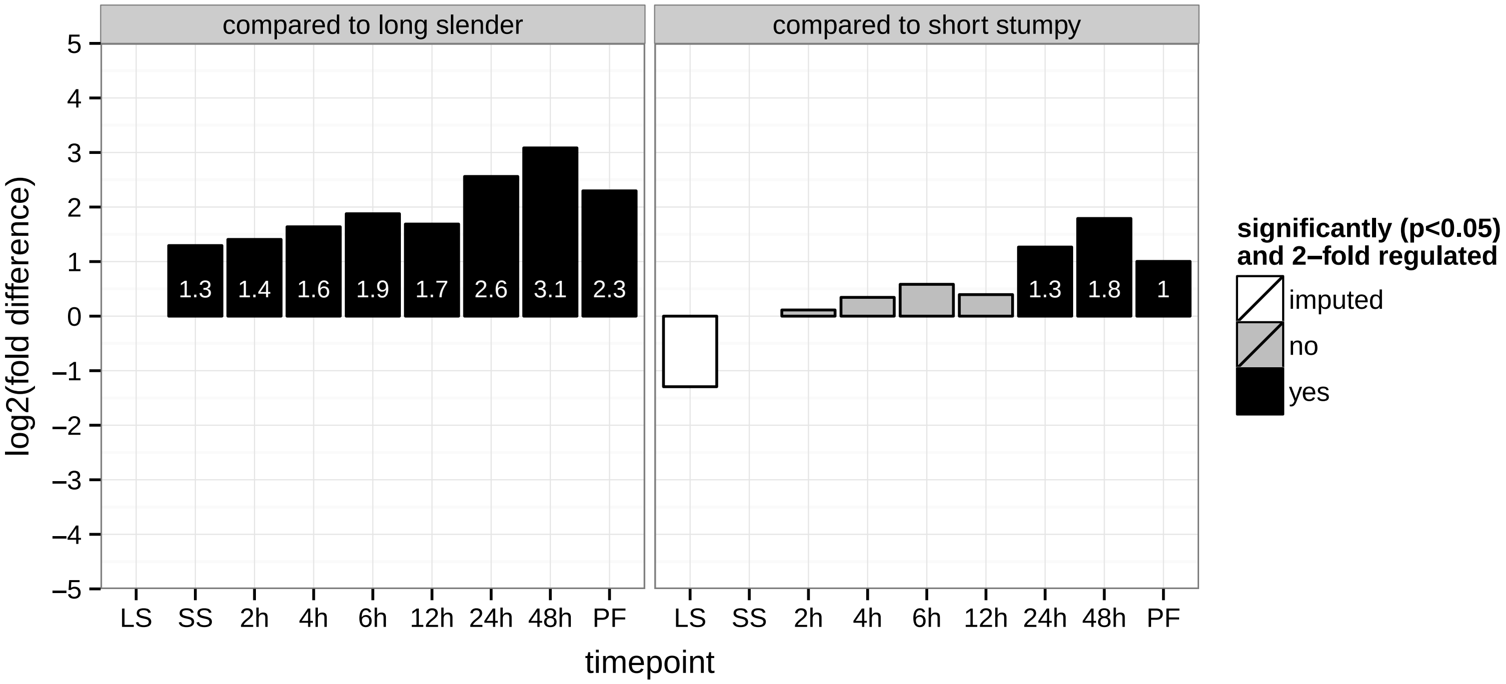
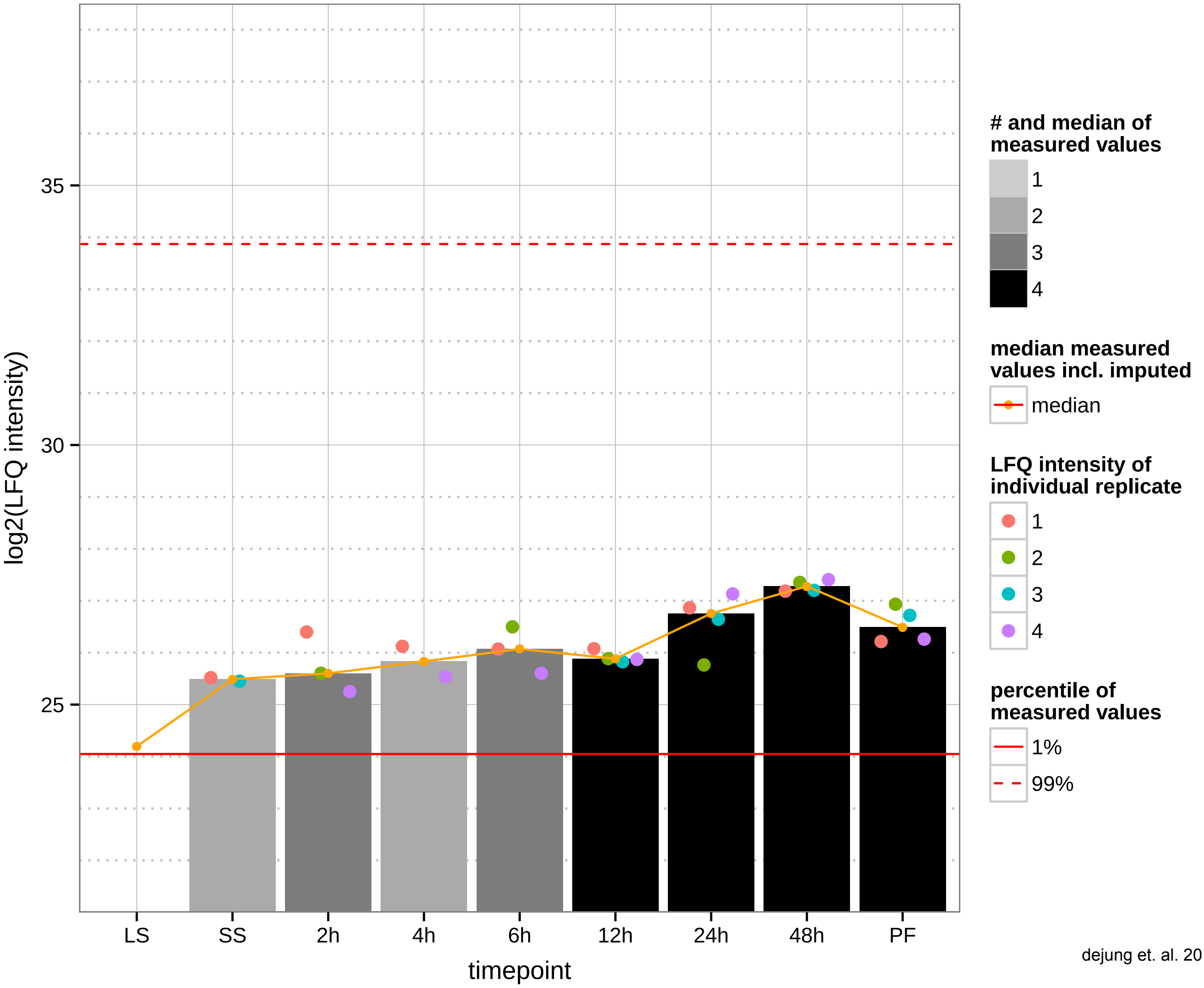
hypothetical protein, conserved
Tb927.7.6800
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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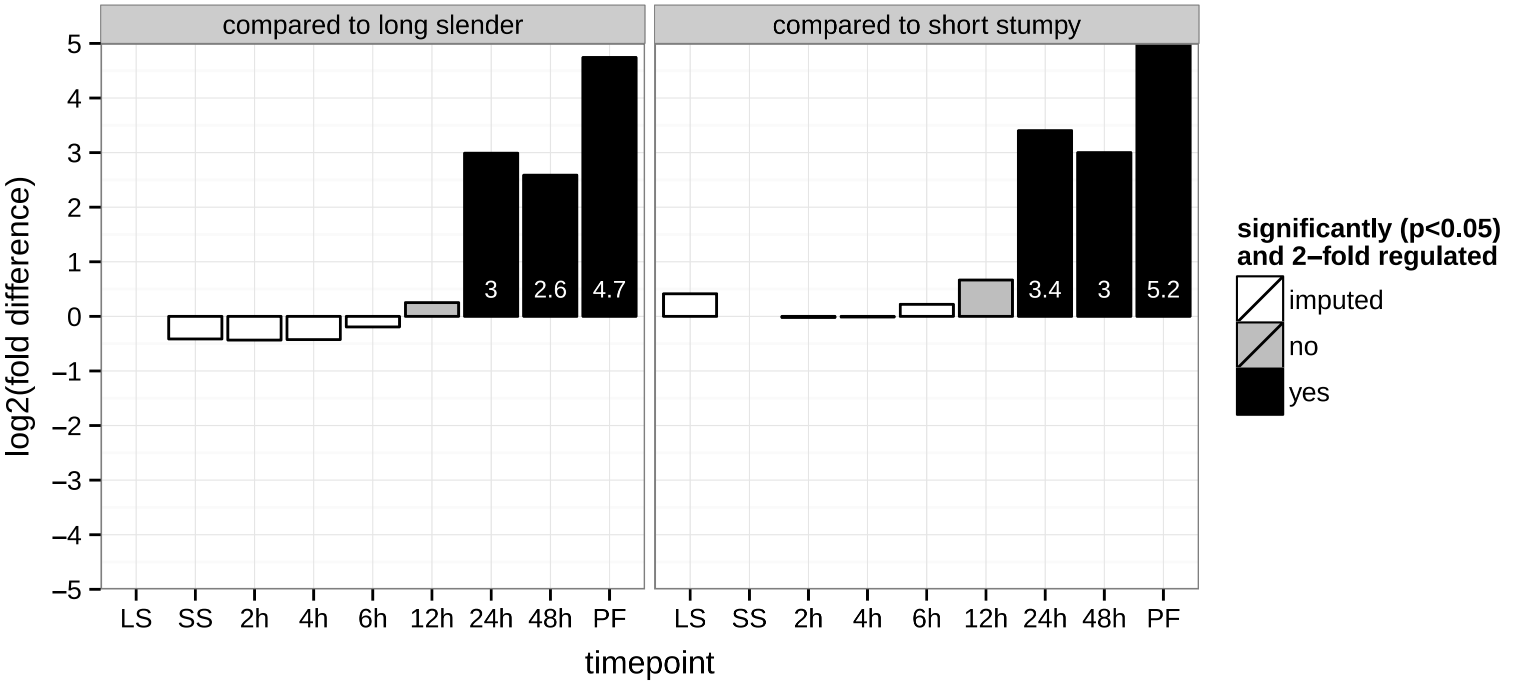
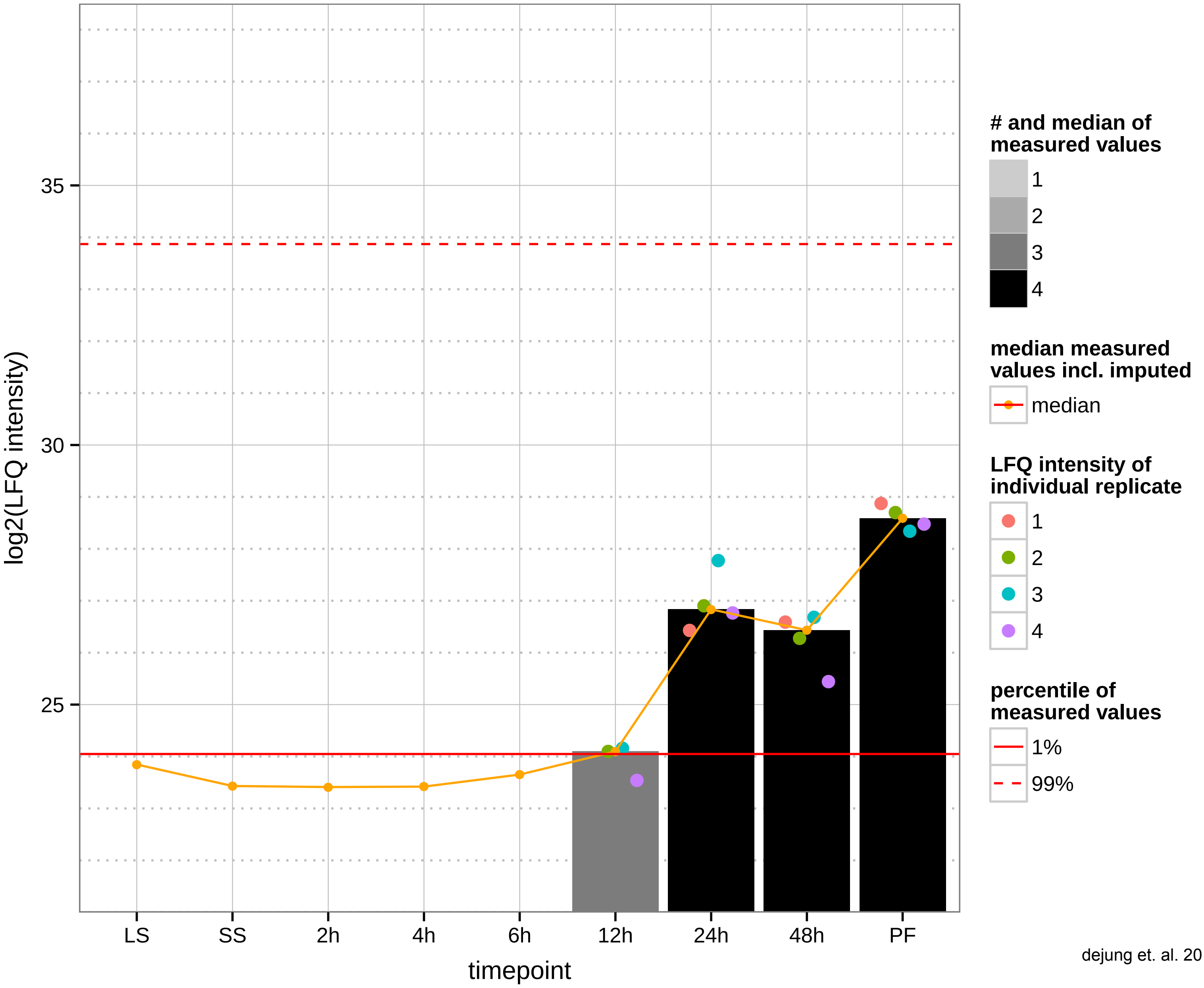
hypothetical protein, conserved
Tb927.7.7090
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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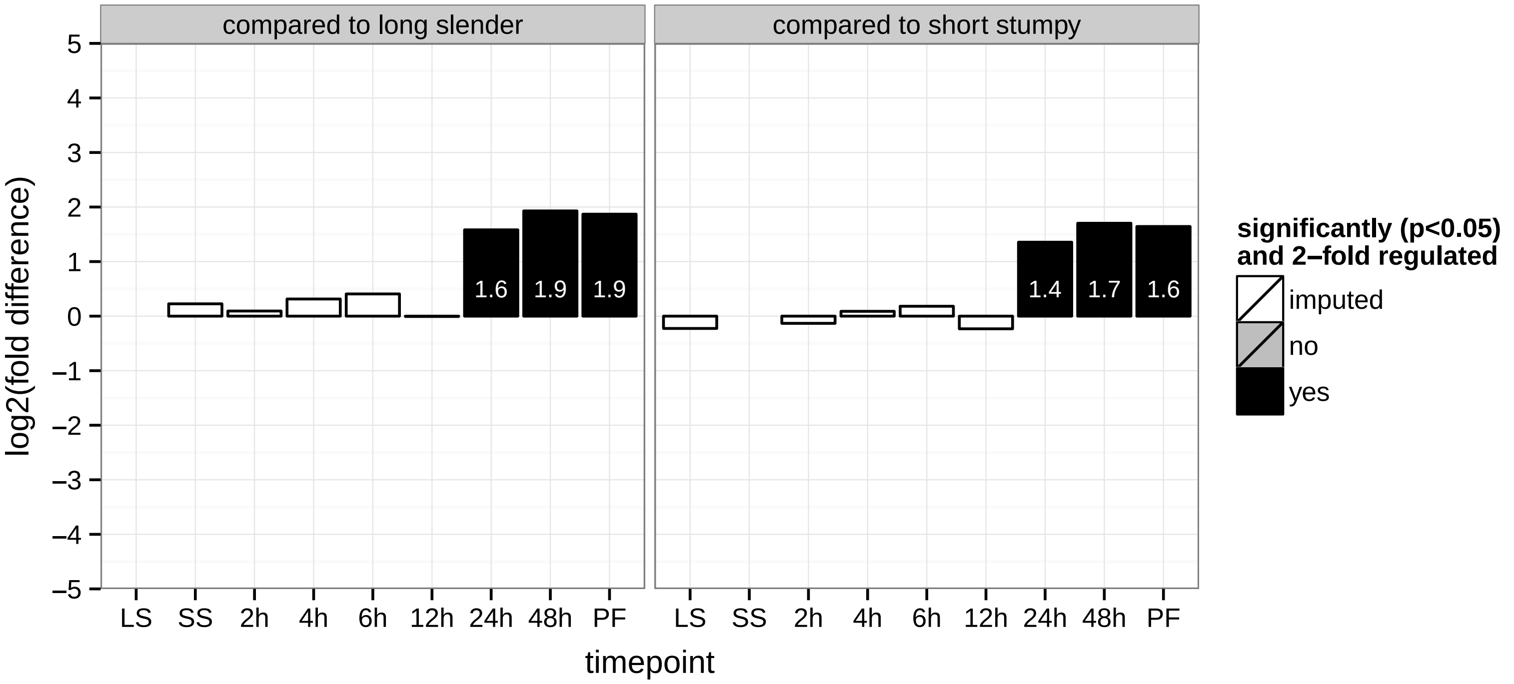
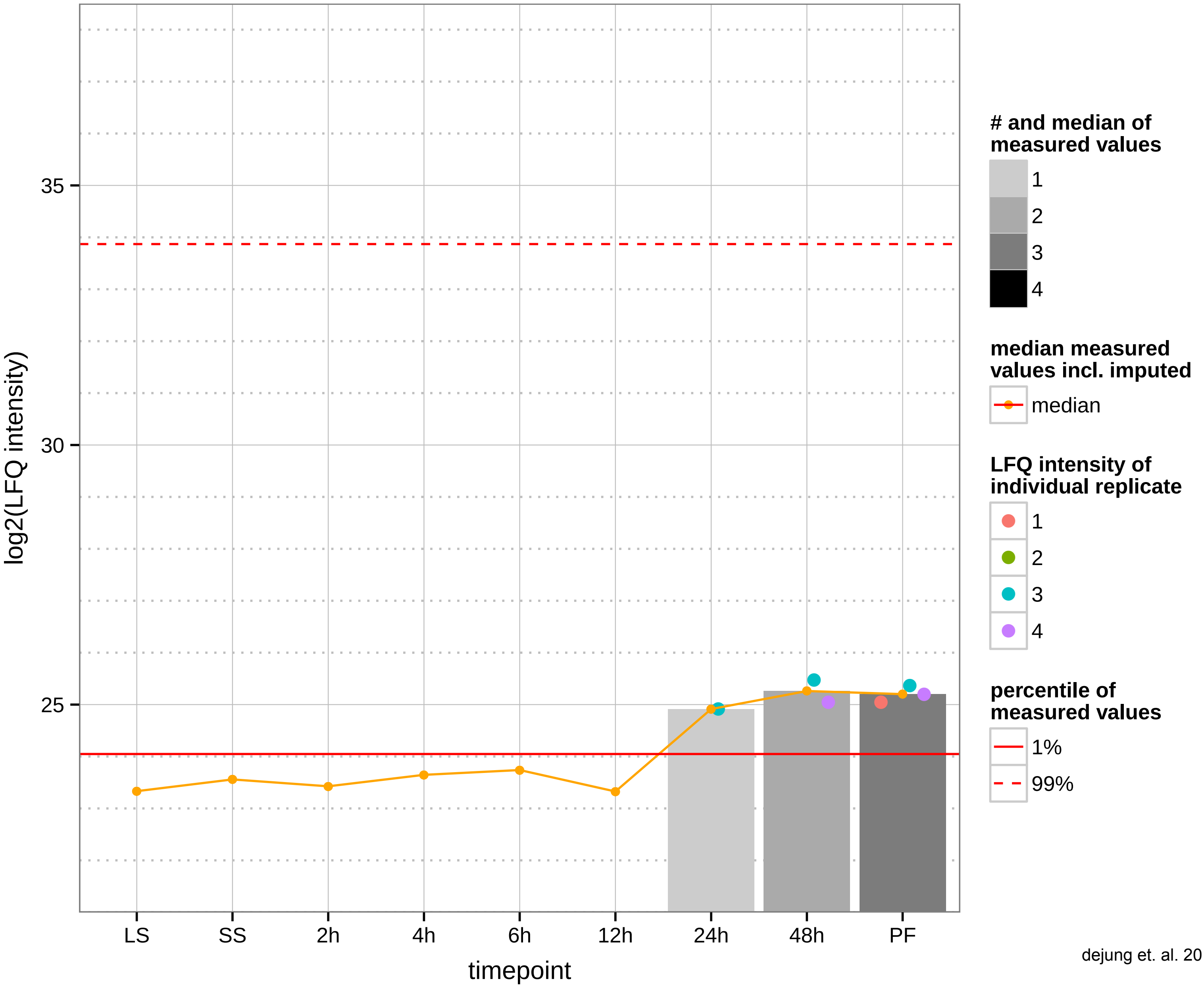
hypothetical protein, conserved
Tb927.7.730
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null





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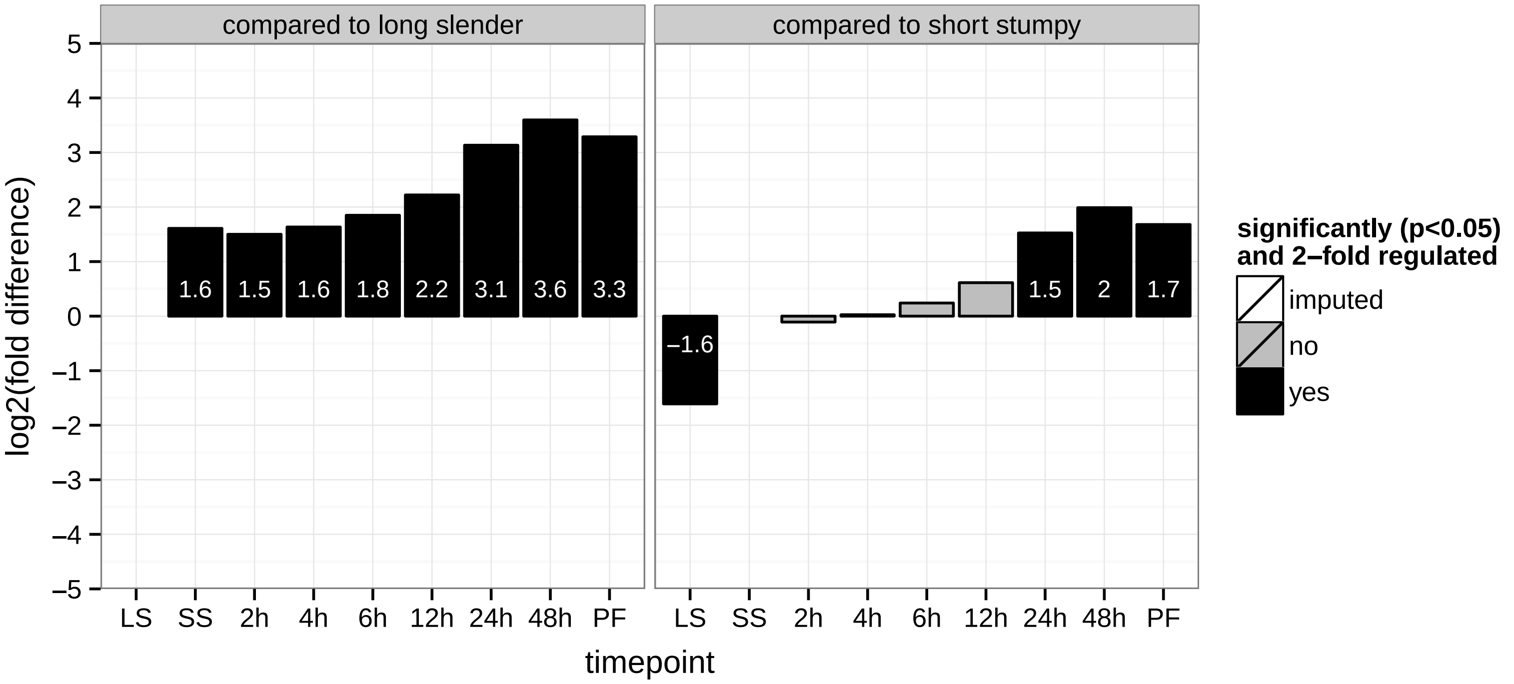
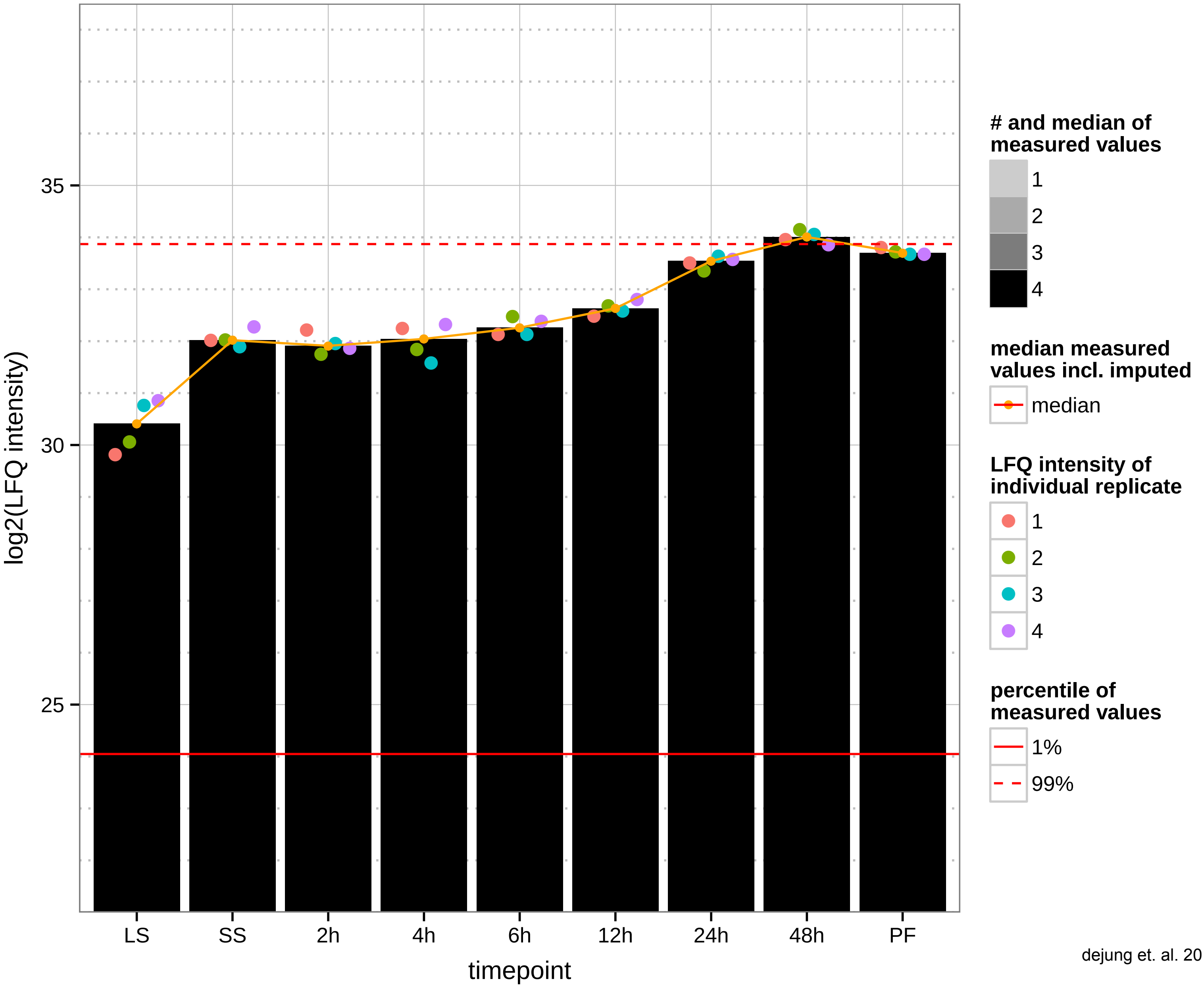
ATP synthase alpha chain, mitochondrial precursor, ATP synthase F1, alpha subunit
Tb927.7.7430;Tb927.7.7420
AGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, proton−transporting ATPase activity
AGOC: mitochondrial inner membrane, mitochondrion, proton−transporting ATP synthase complex, catalytic core F(1), proton
AGOP: ATP synthesis coupled proton transport
PGOF: ATP binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrolase activity, acting on acid
PGOC: proton−transporting ATP synthase complex, catalytic core F(1), proton−transporting two−sector ATPase complex, cata
PGOP: ATP hydrolysis coupled proton transport, ATP synthesis coupled proton transport





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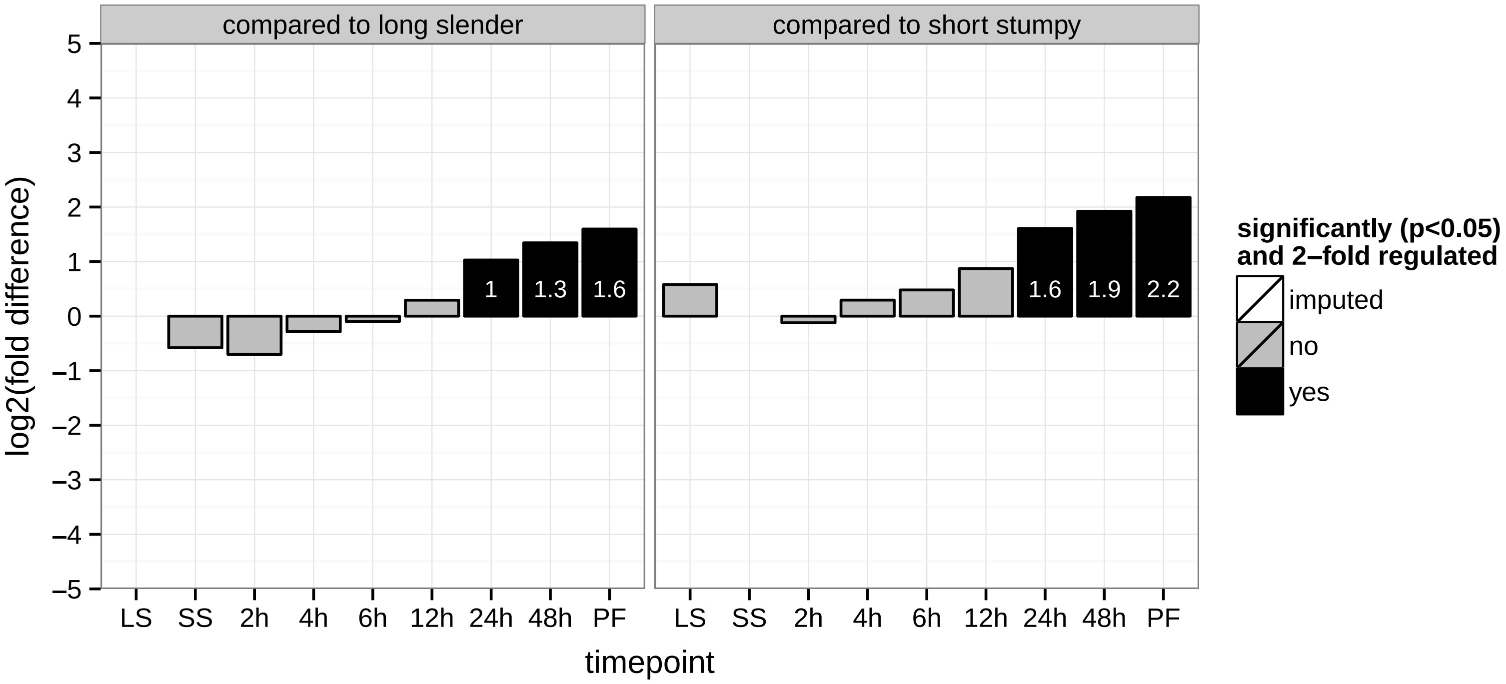
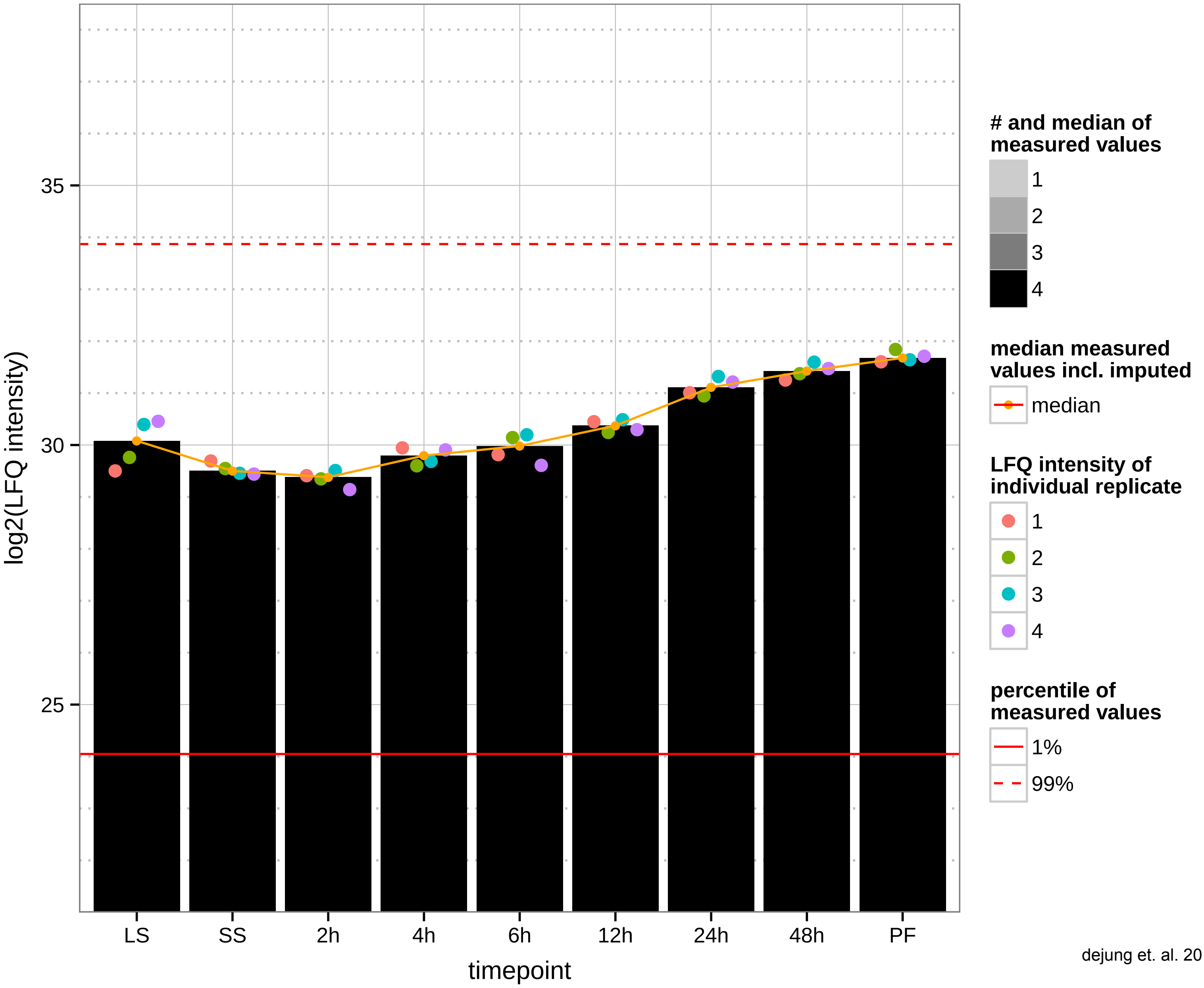
hypothetical protein, conserved
Tb927.7.7460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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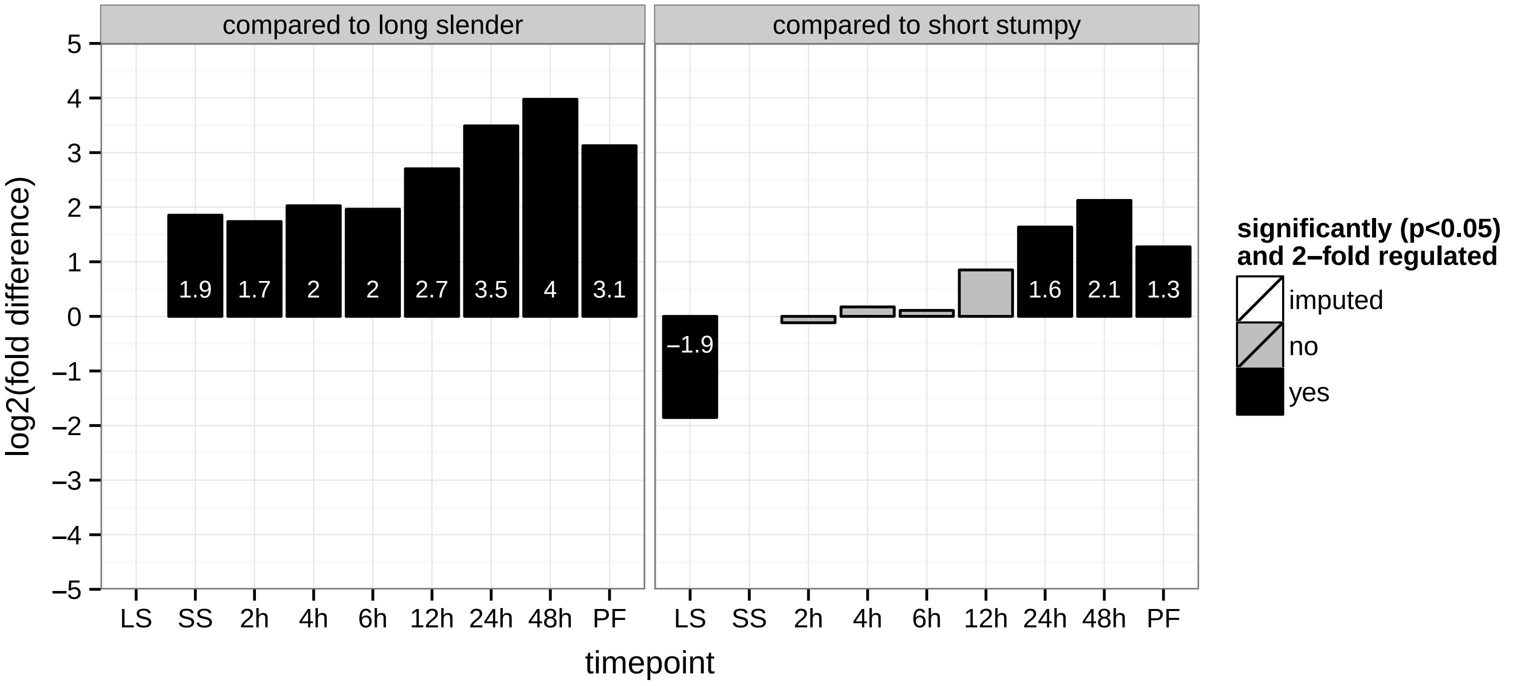
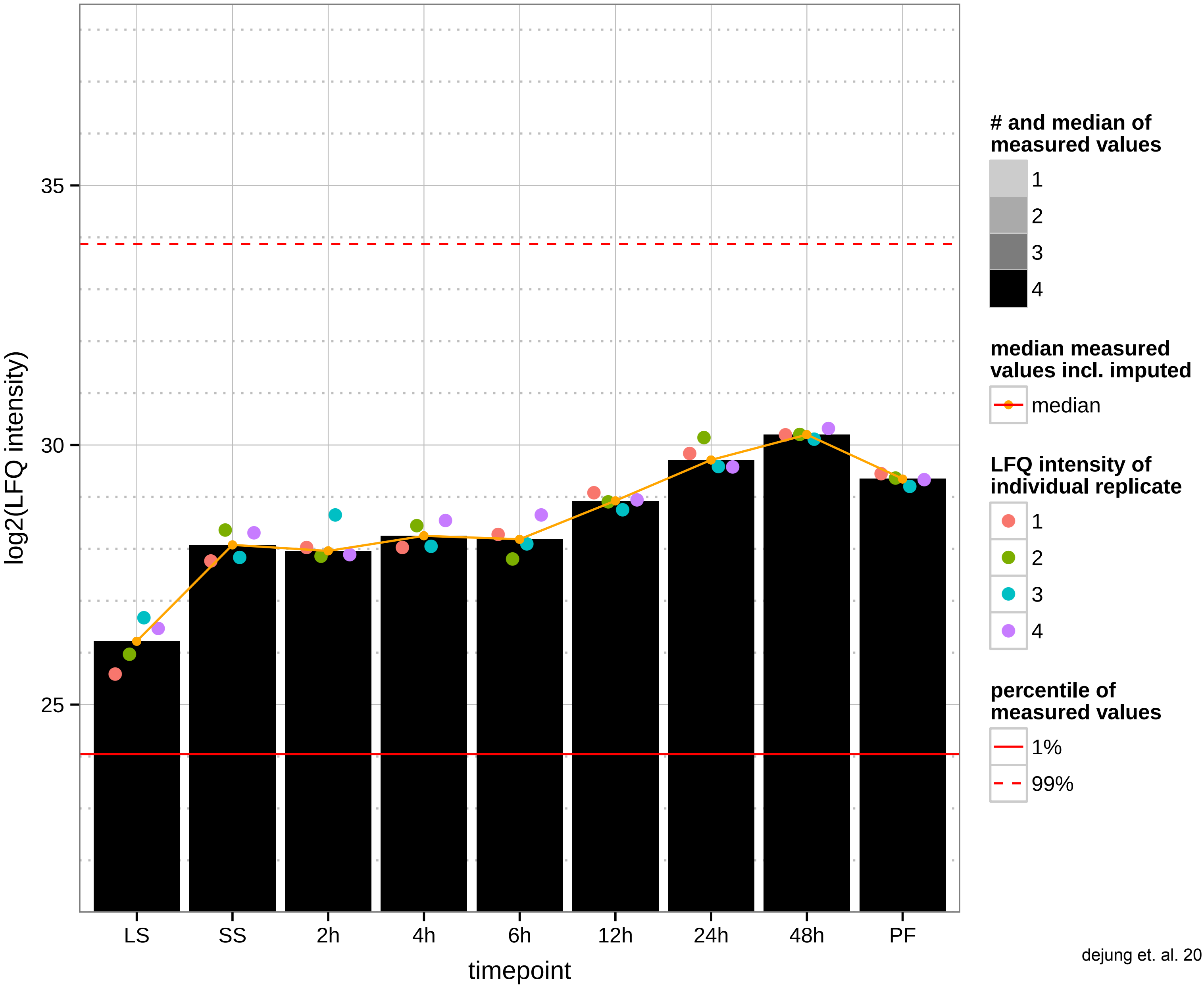
hypothetical protein, conserved
Tb927.7.840
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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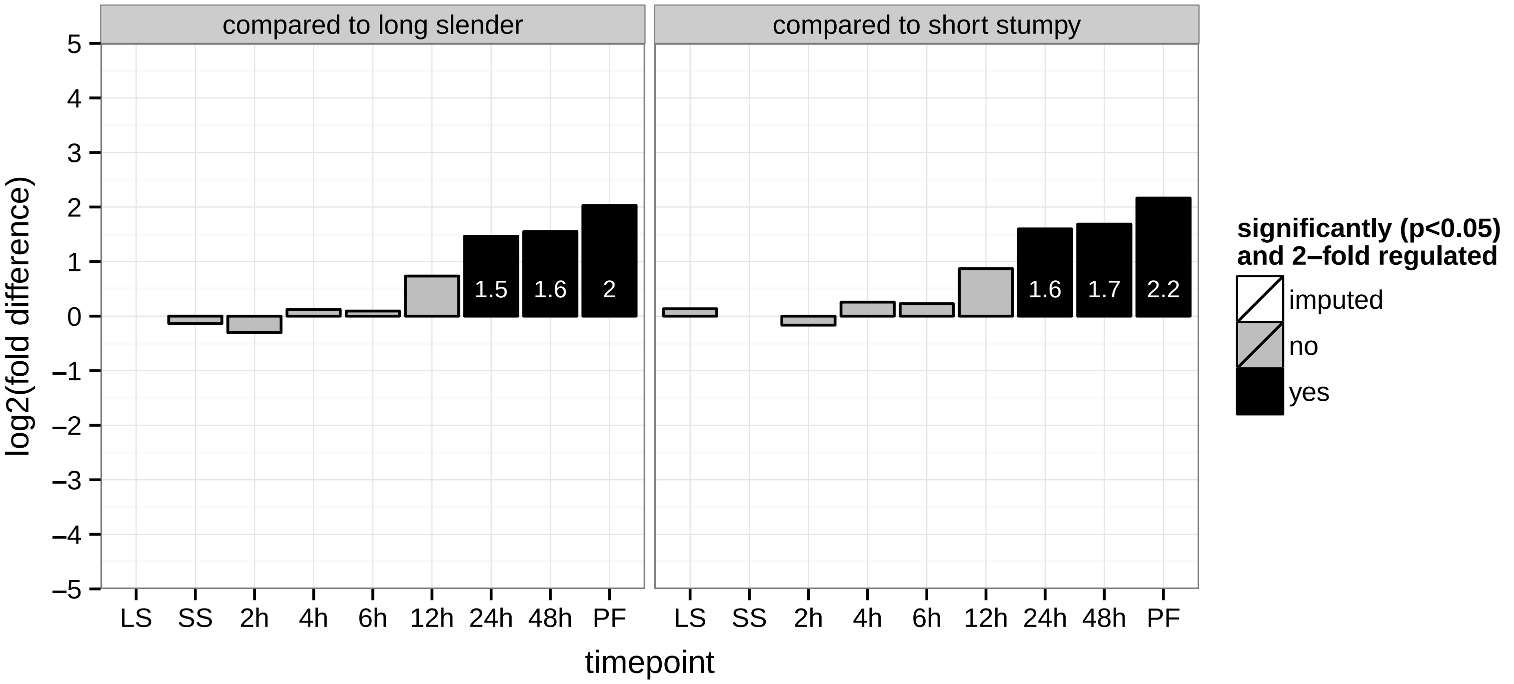
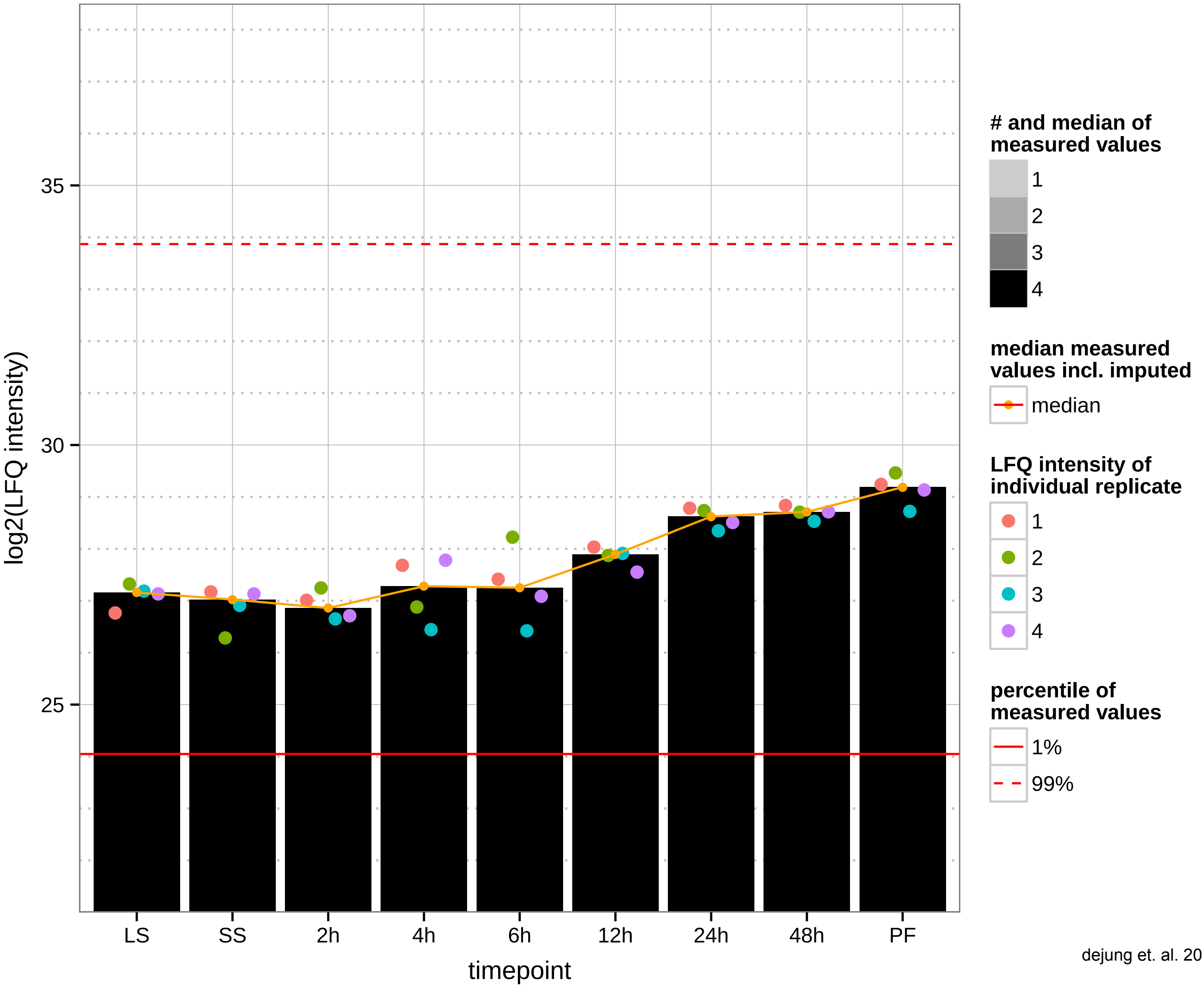
hypothetical protein, conserved
Tb927.7.900
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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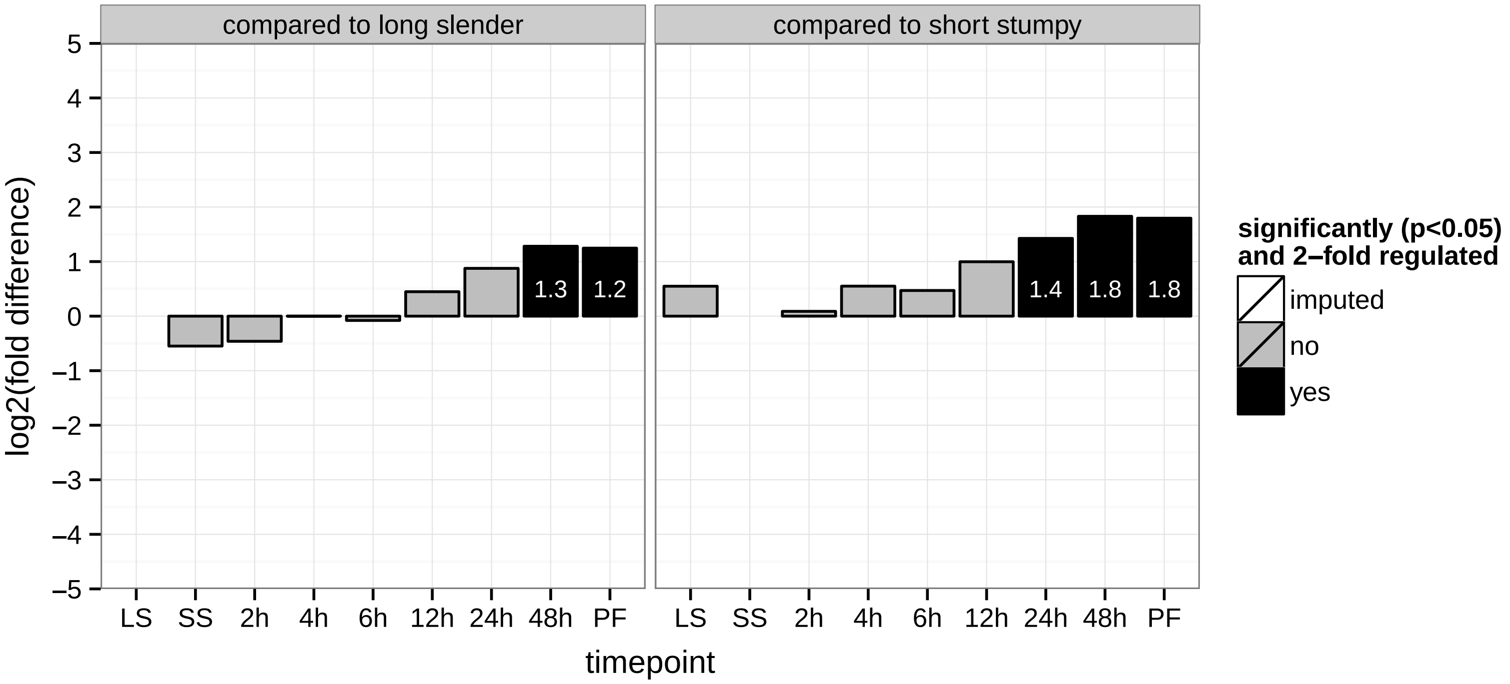
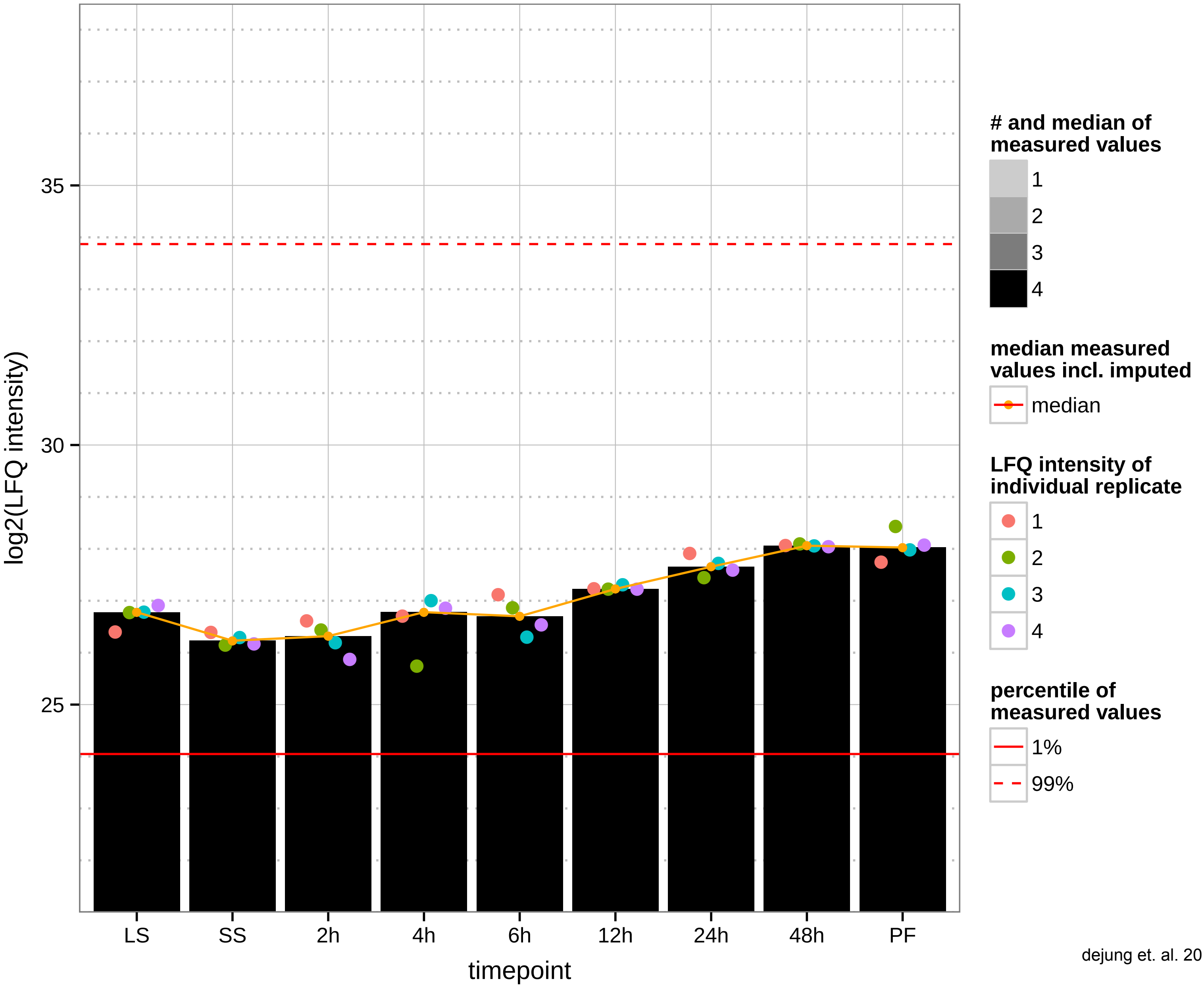
hypothetical protein, conserved
Tb927.8.1500
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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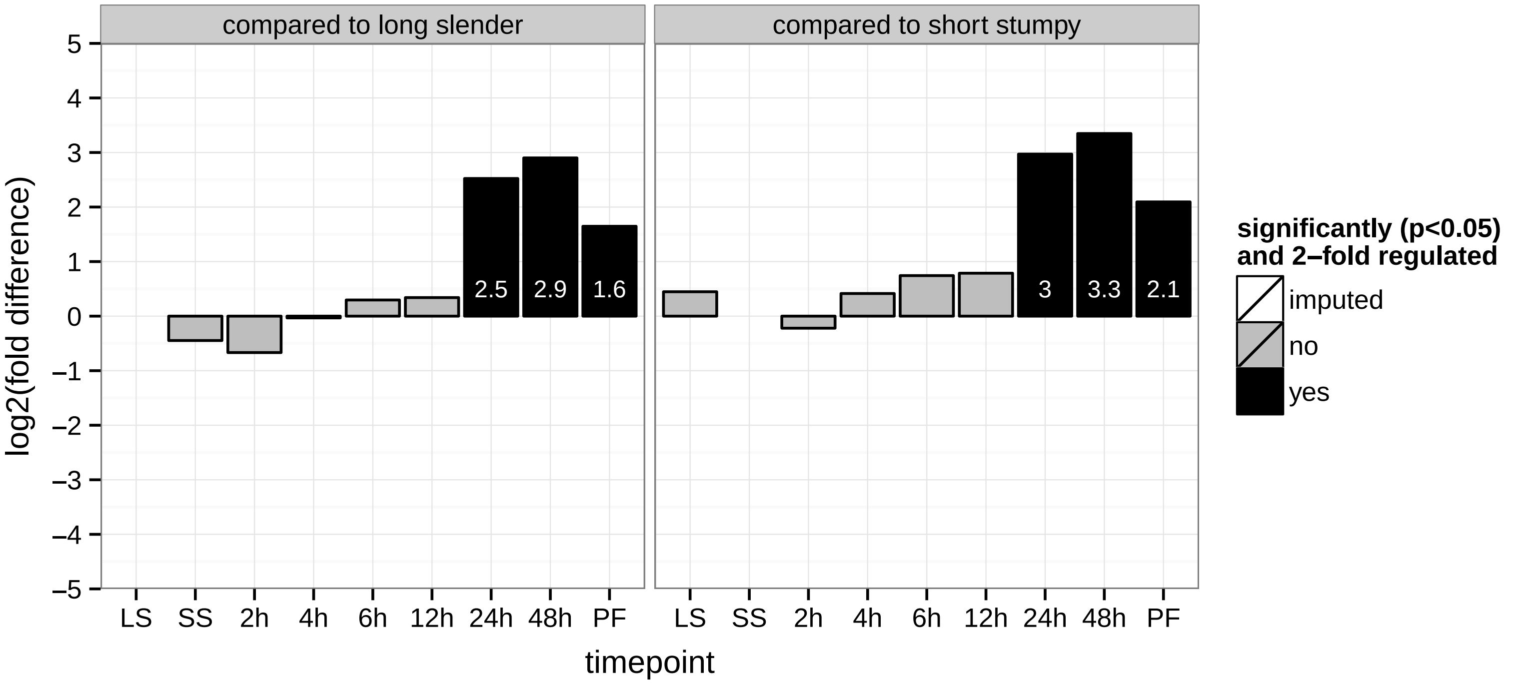
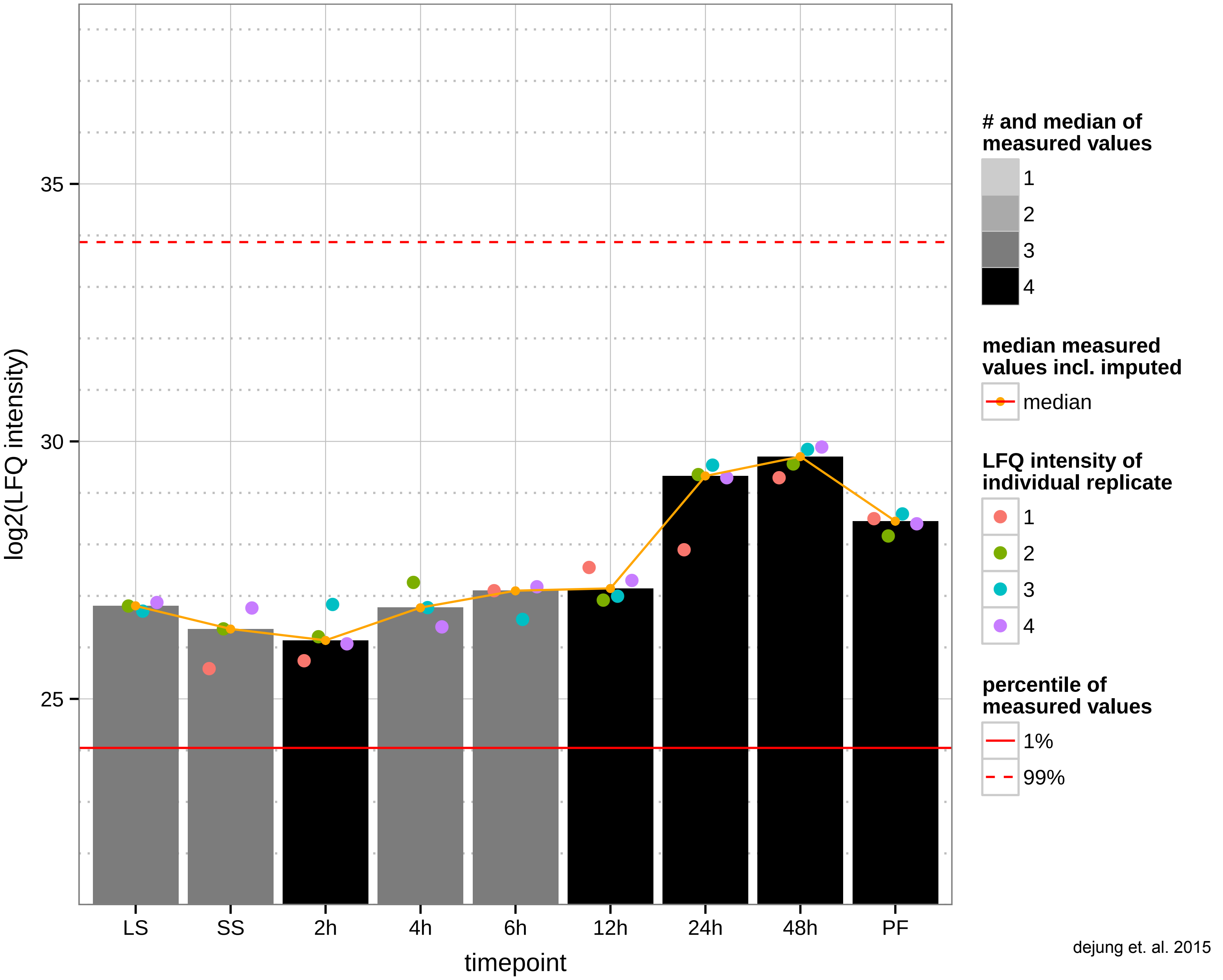
hypothetical protein, conserved
Tb927.8.1790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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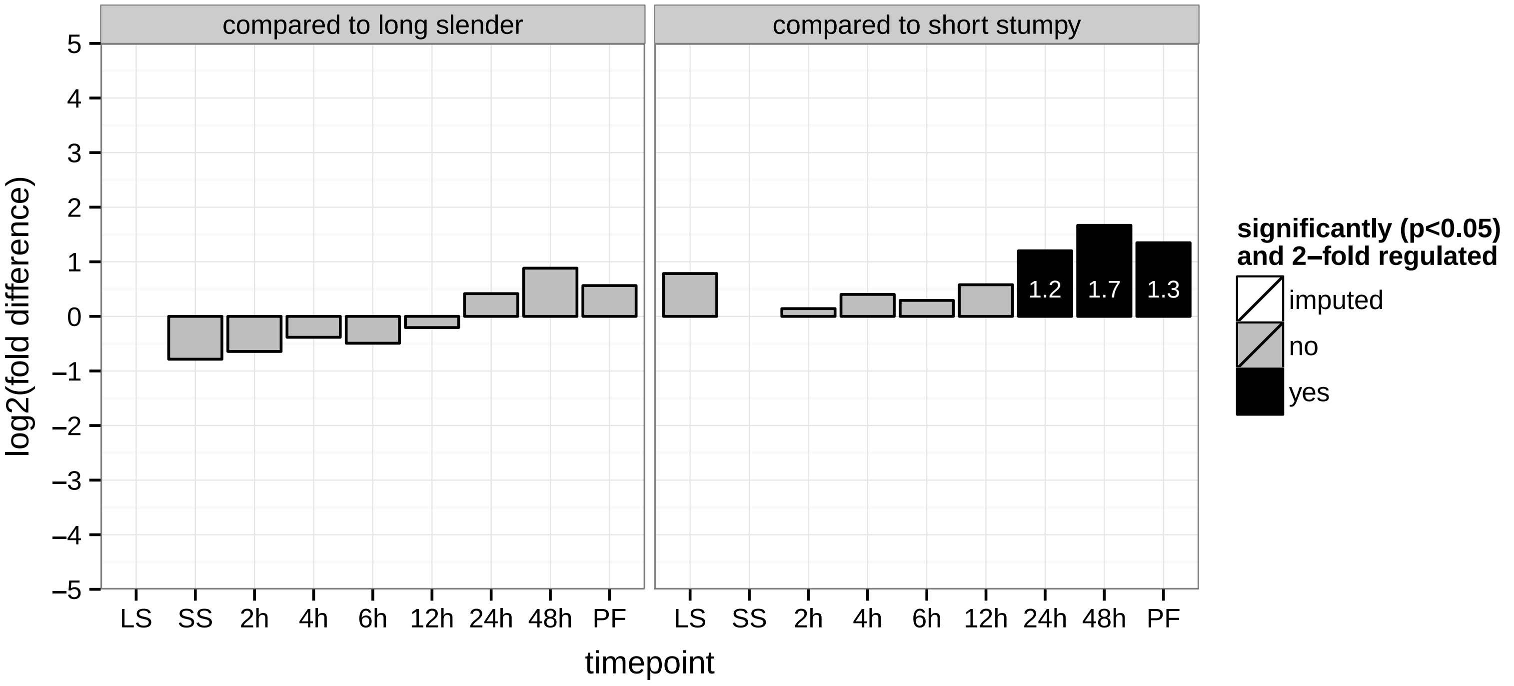
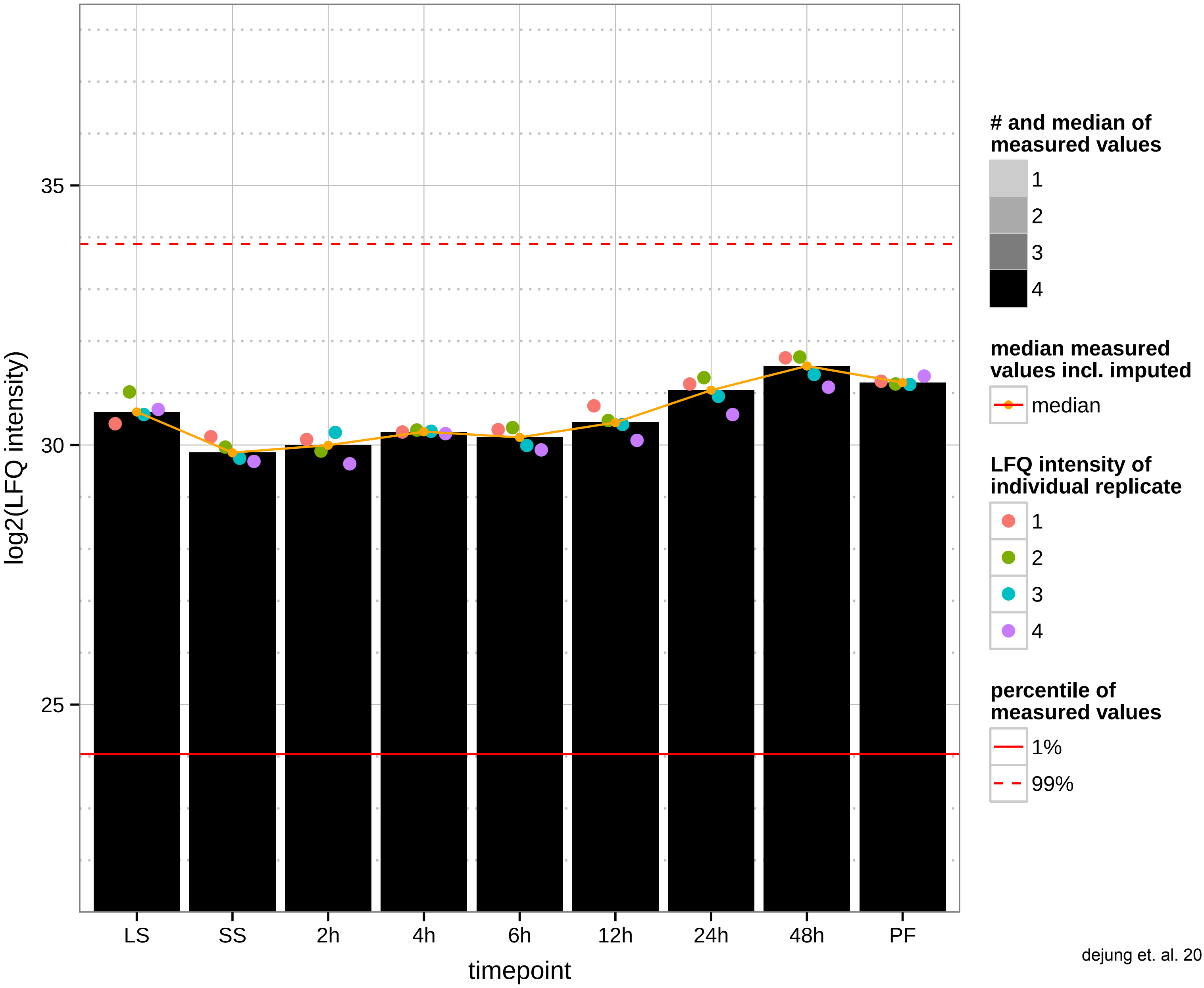
hypothetical protein, conserved
Tb927.8.2030
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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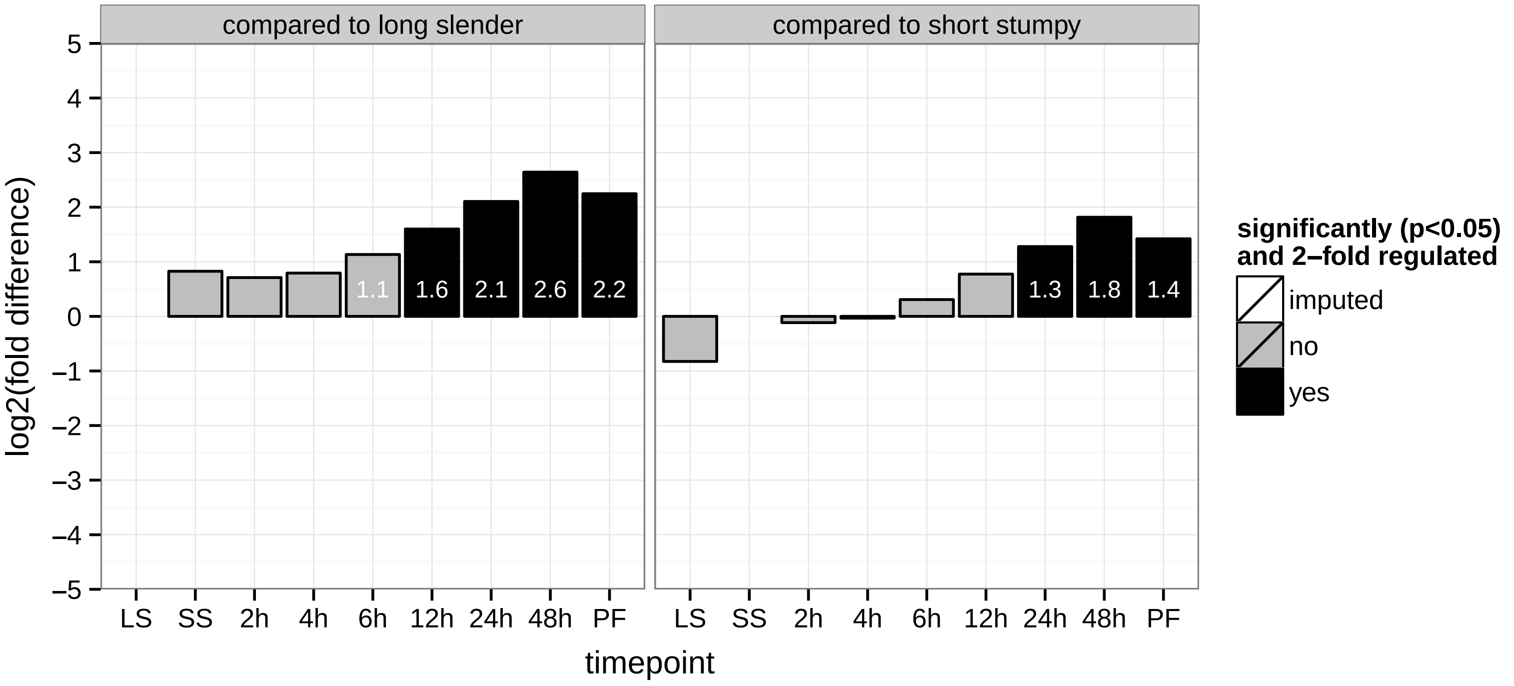
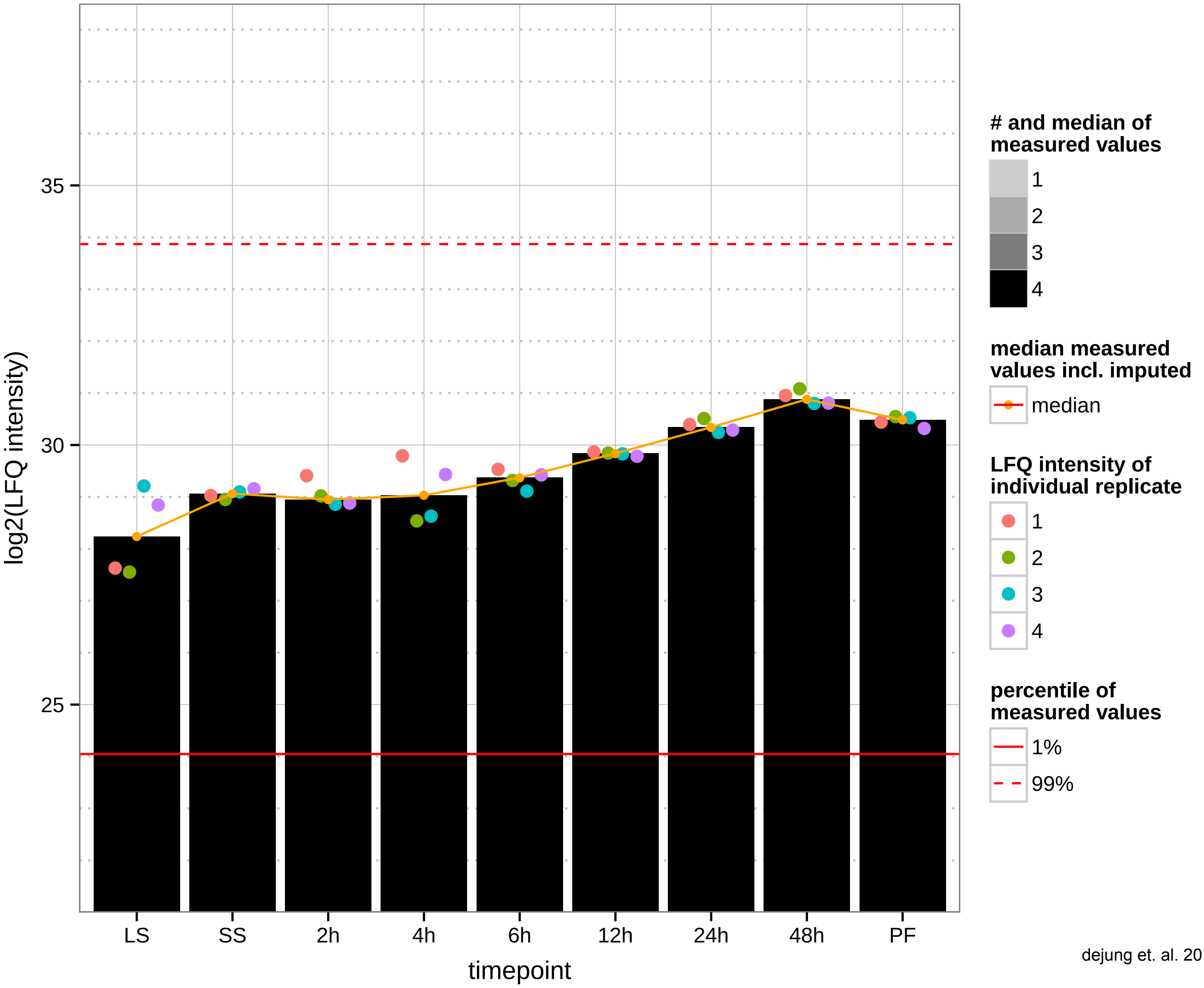
kinesin, putative
Tb927.8.2630
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: kinesin complex, microtubule associated complex
AGOP: microtubule−based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule−based movement





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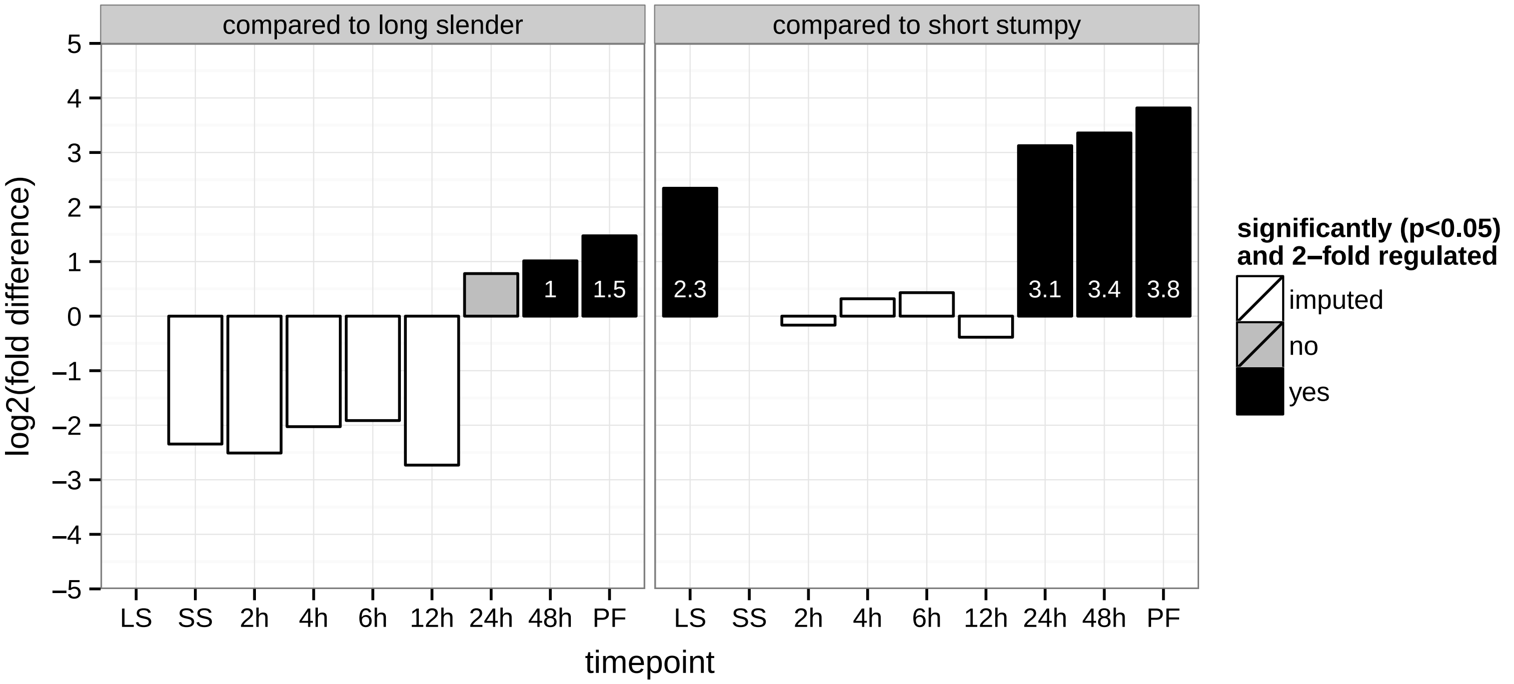
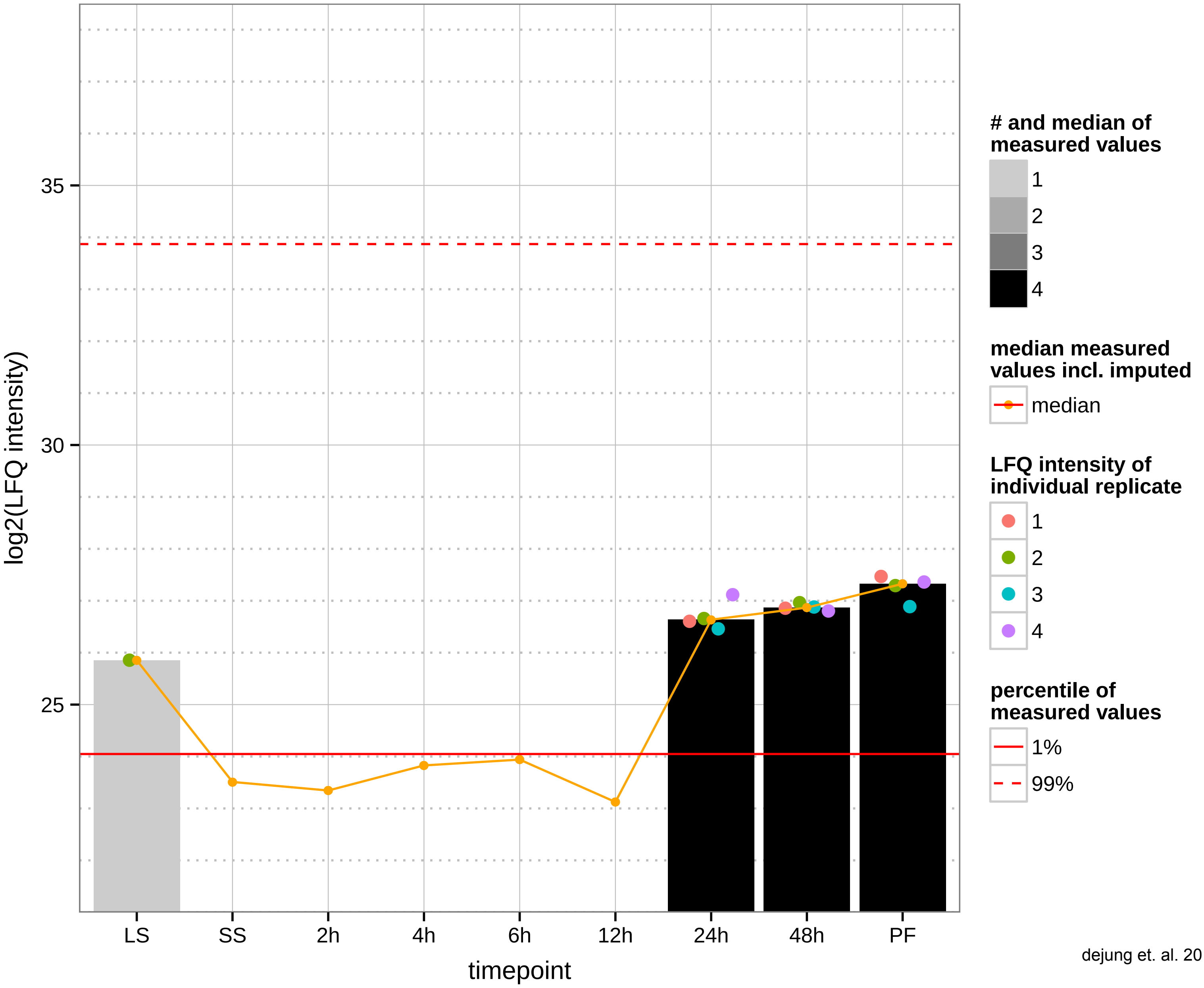
DNA repair and recombination helicase protein PIF5 (PIF5)
Tb927.8.3560
AGOF: 5'–3' DNA helicase activity, nucleoside–triphosphatase activity, nucleotide binding
AGOC: mitochondrion
AGOP: DNA replication, Okazaki fragment processing, DNA replication, removal of RNA primer
PGOF: nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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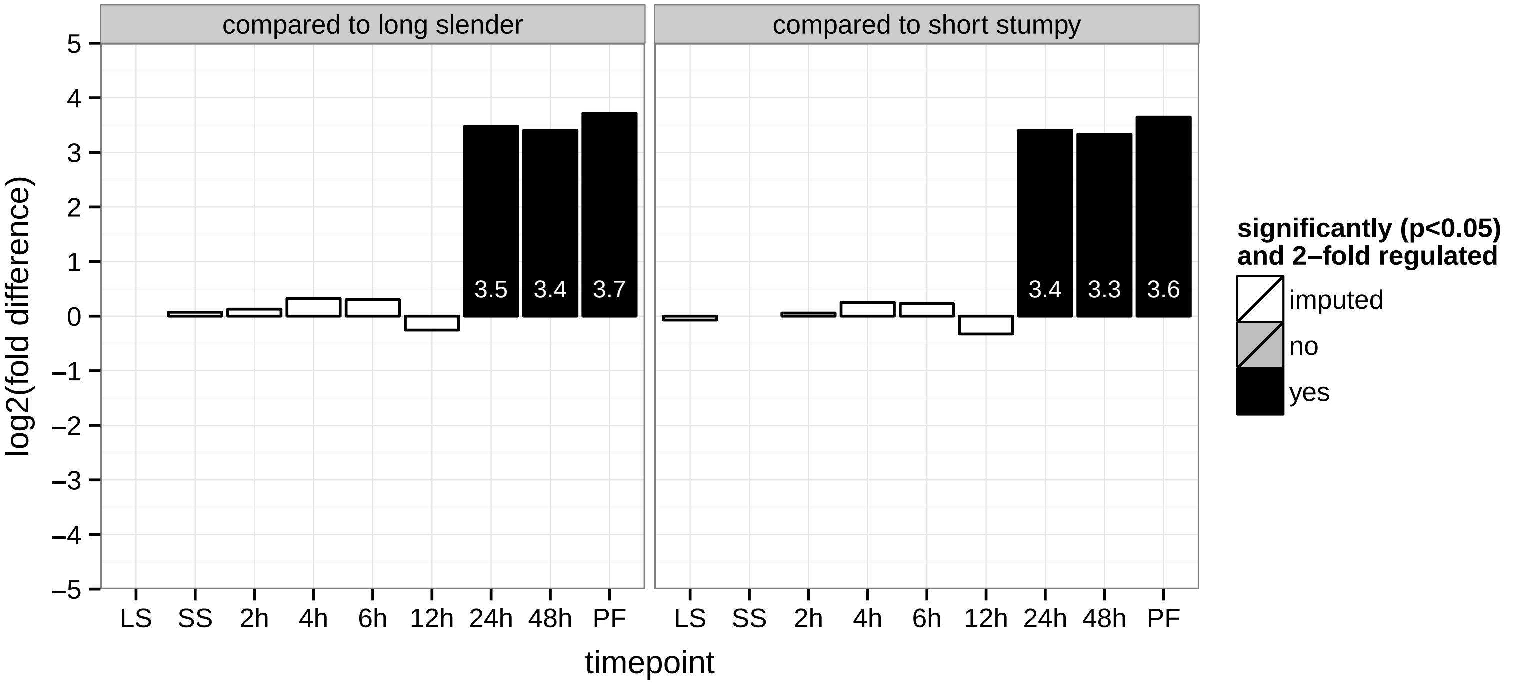
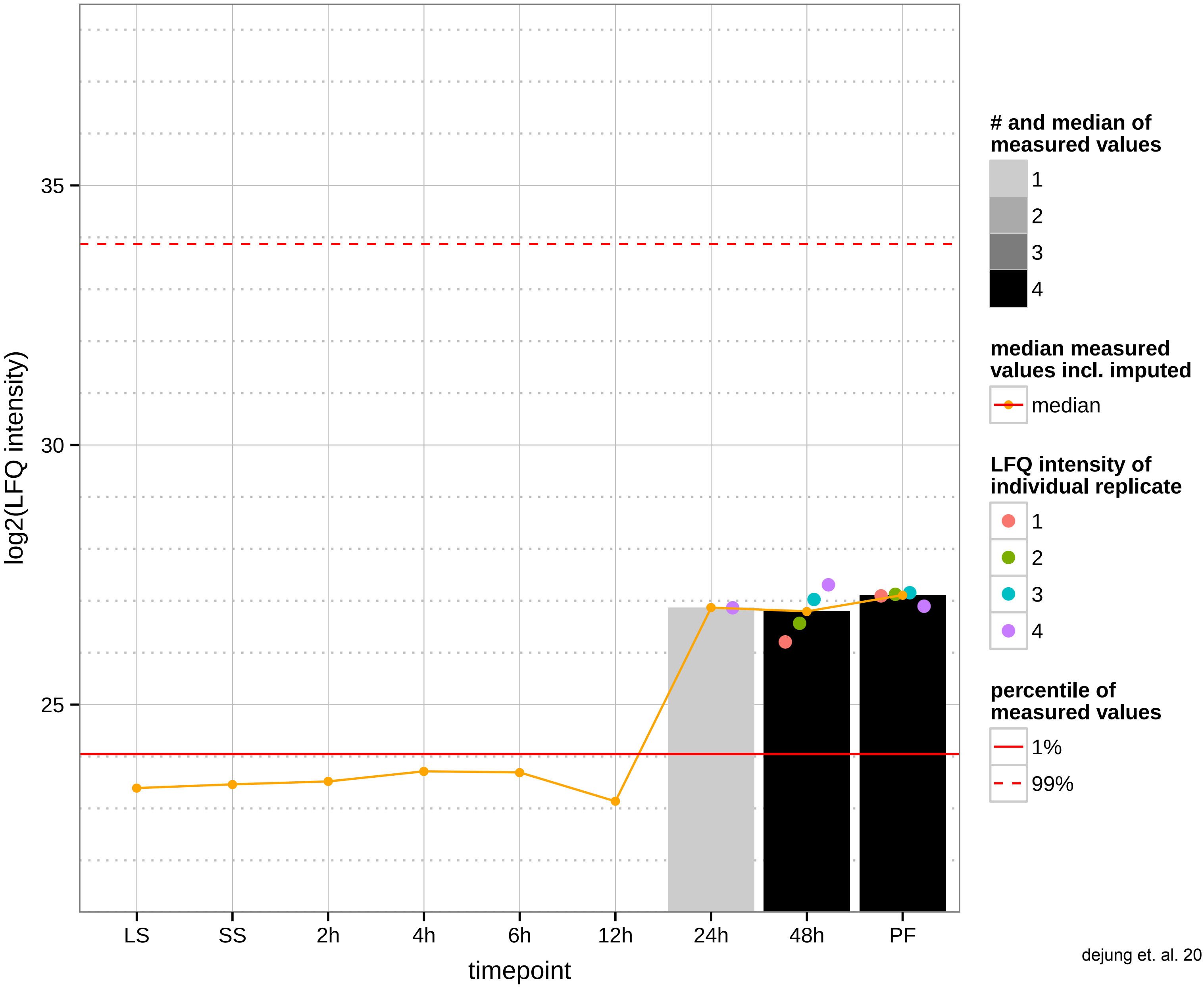
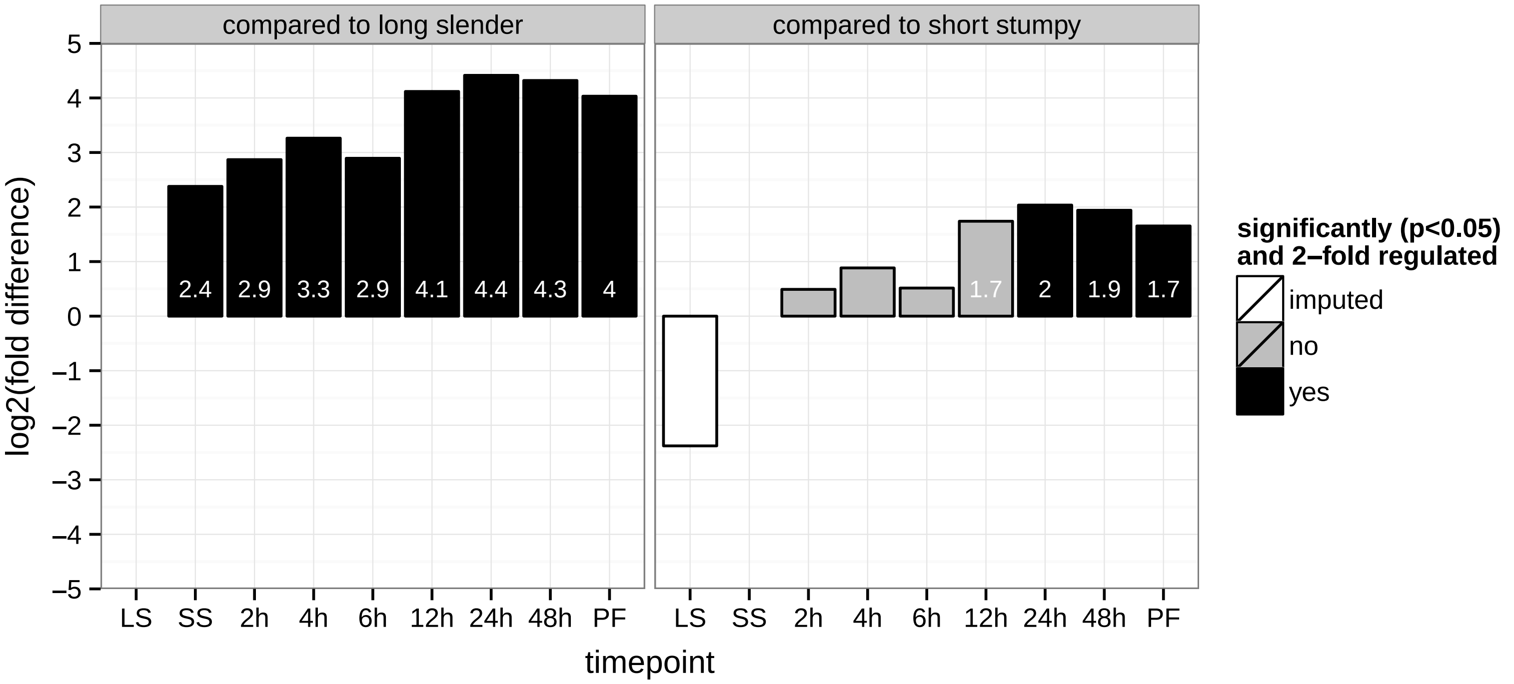
hypothetical protein, conserved
Tb927.8.4230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

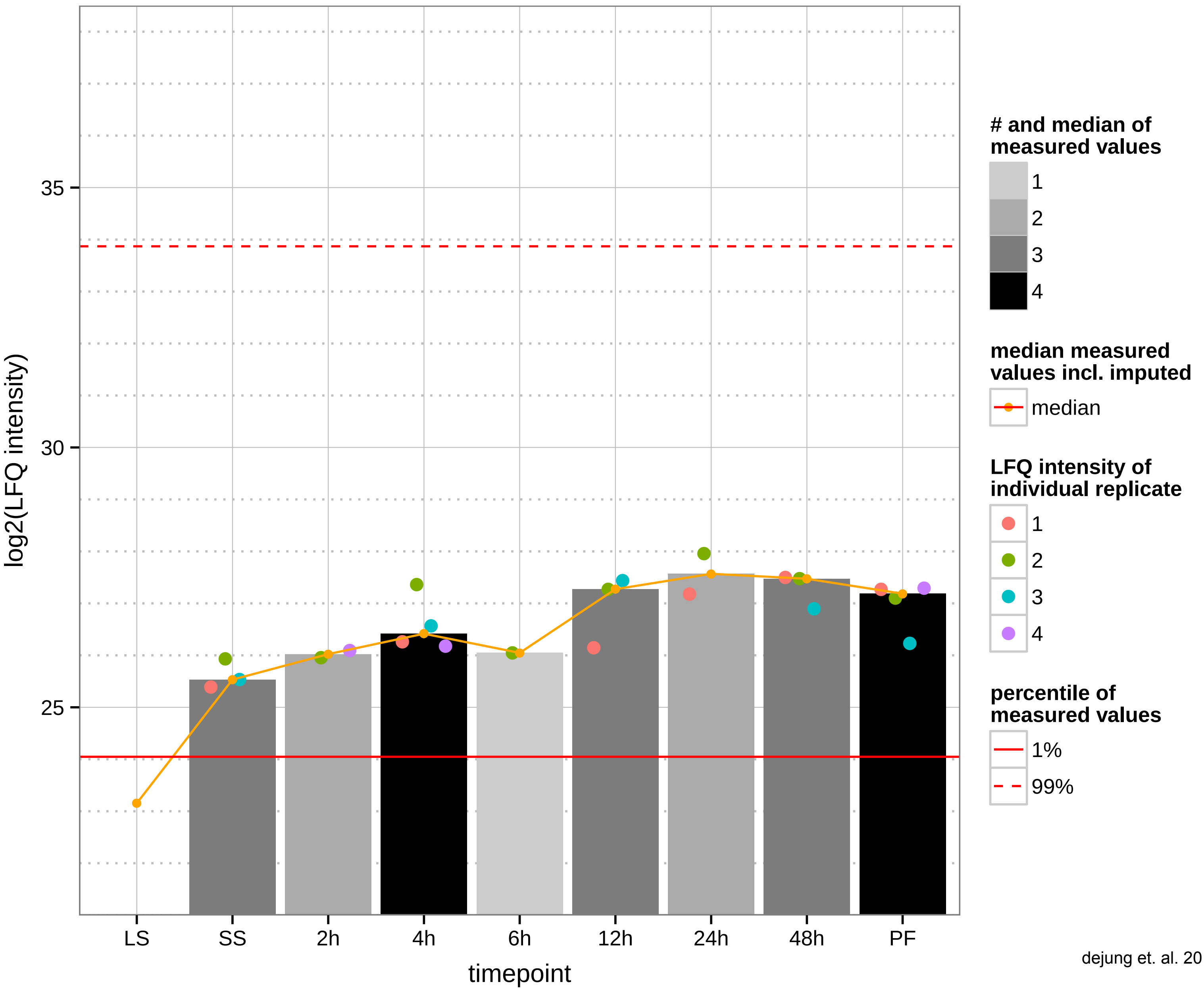




dejung et. al. 2015

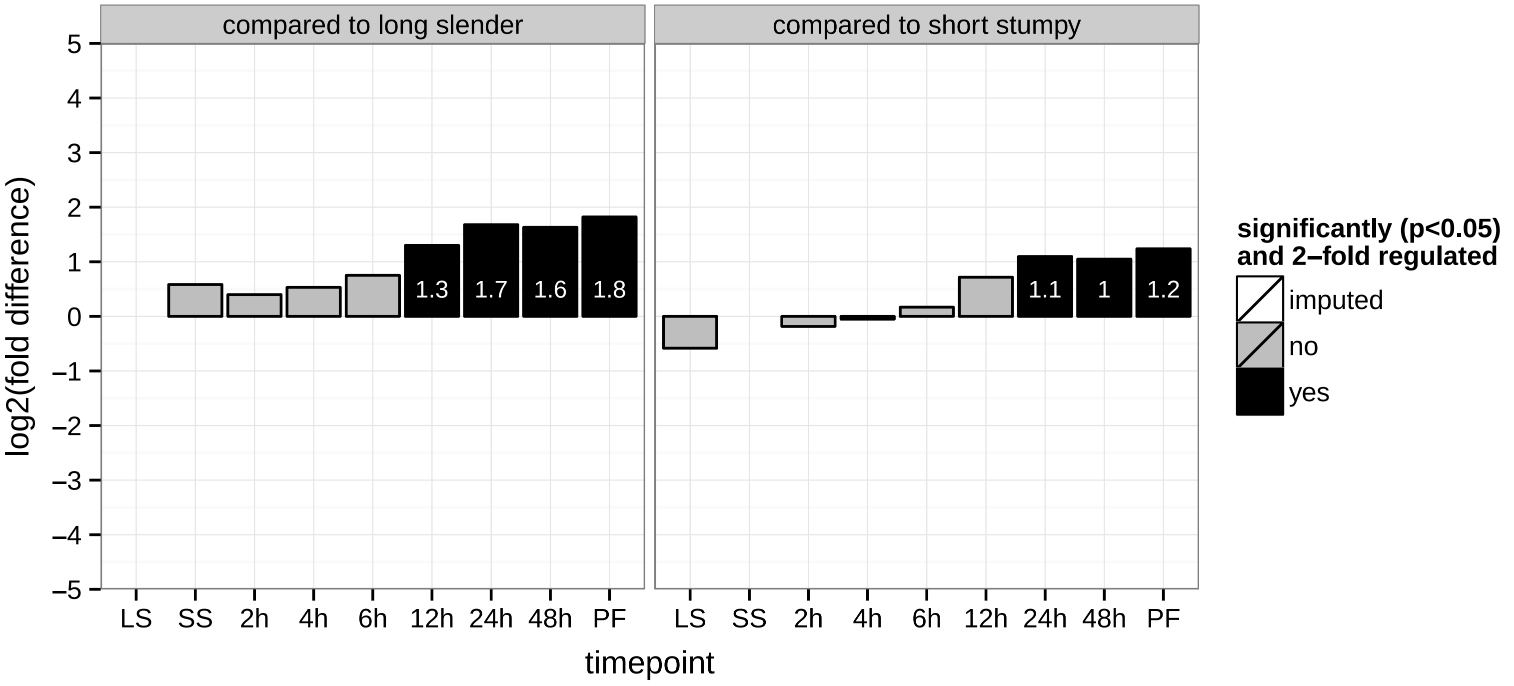
hypothetical protein, conserved
Tb927.8.4380
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

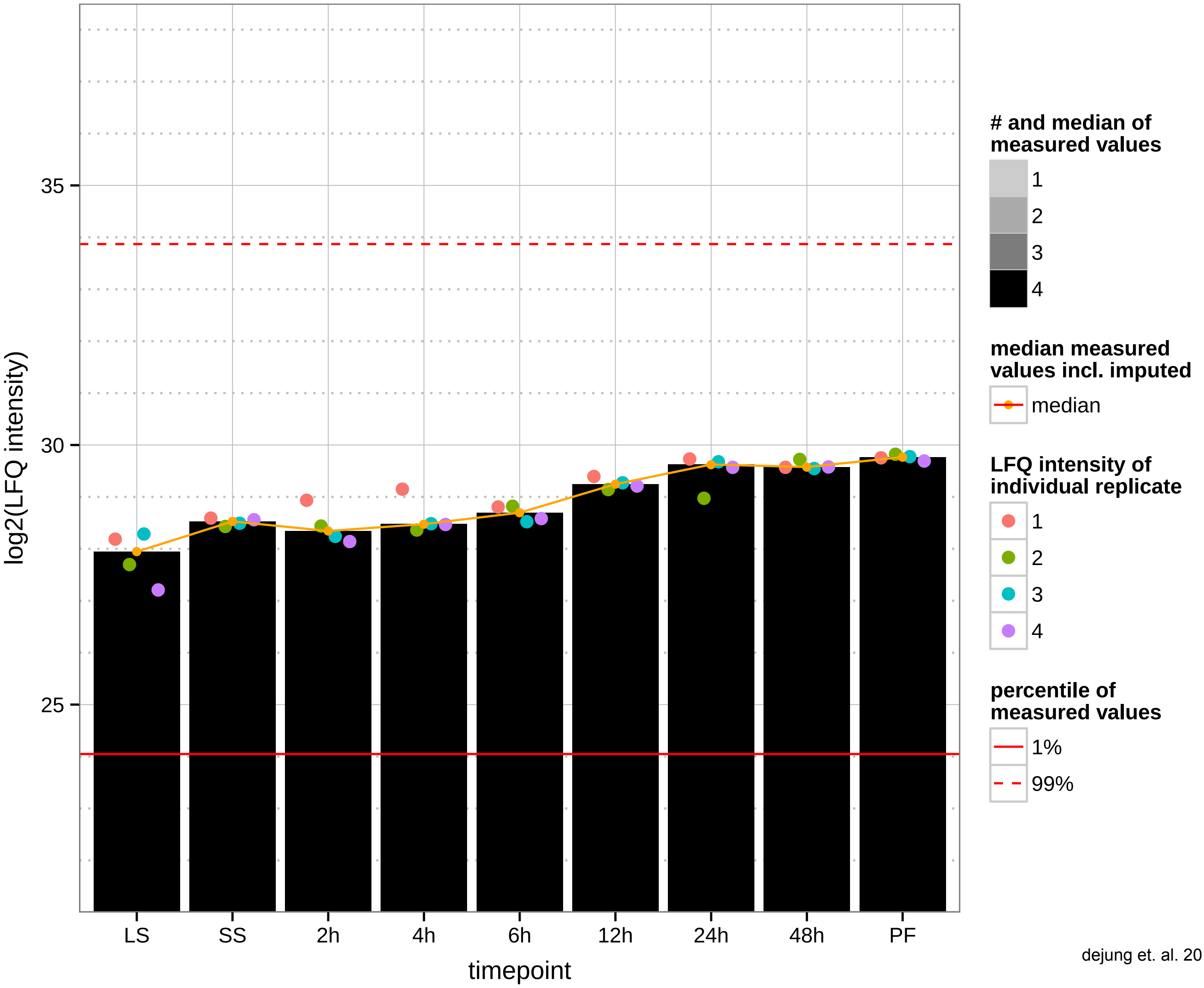




dejung et. al. 2015

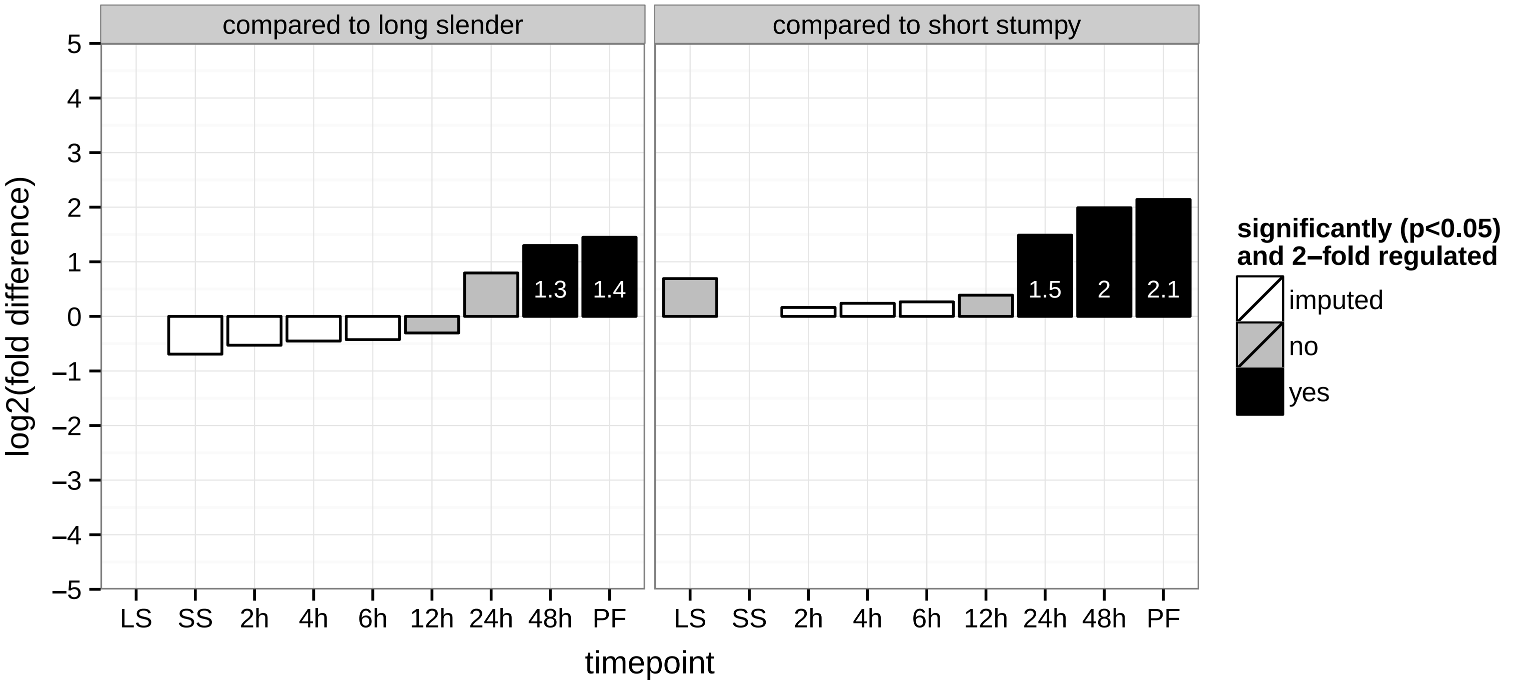
hypothetical protein, conserved, eukaryotic translation initation factor 4 gamma, putative (eIF4G3)
Tb927.8.4820;Tb11.v5.0659
AGOF: null
AGOC: null
AGOP: null, RNA metabolic process, translation
PGOF: DNA binding, RNA binding, binding, protein binding
PGOC: null
PGOP: null

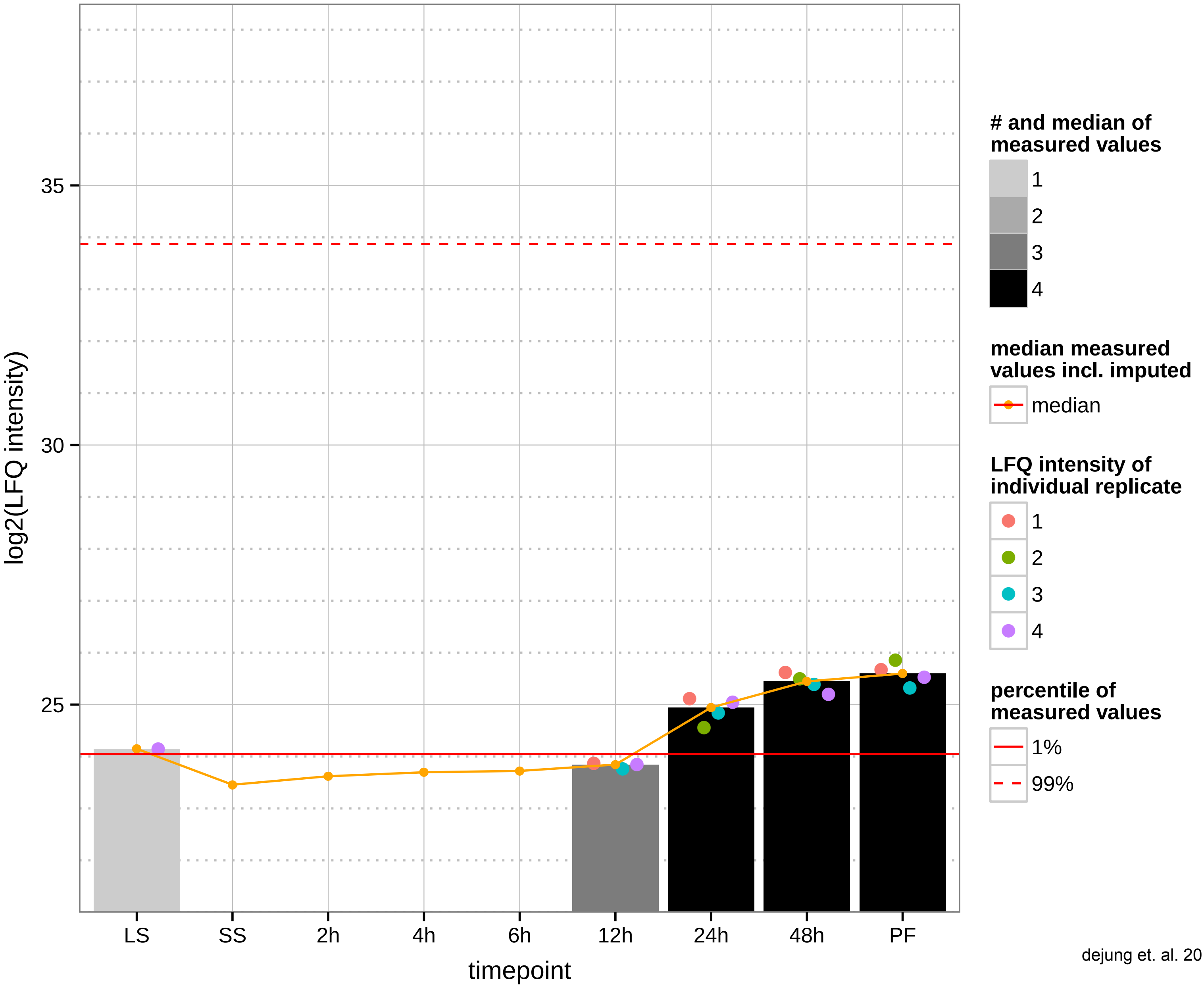




dejung et. al. 2015

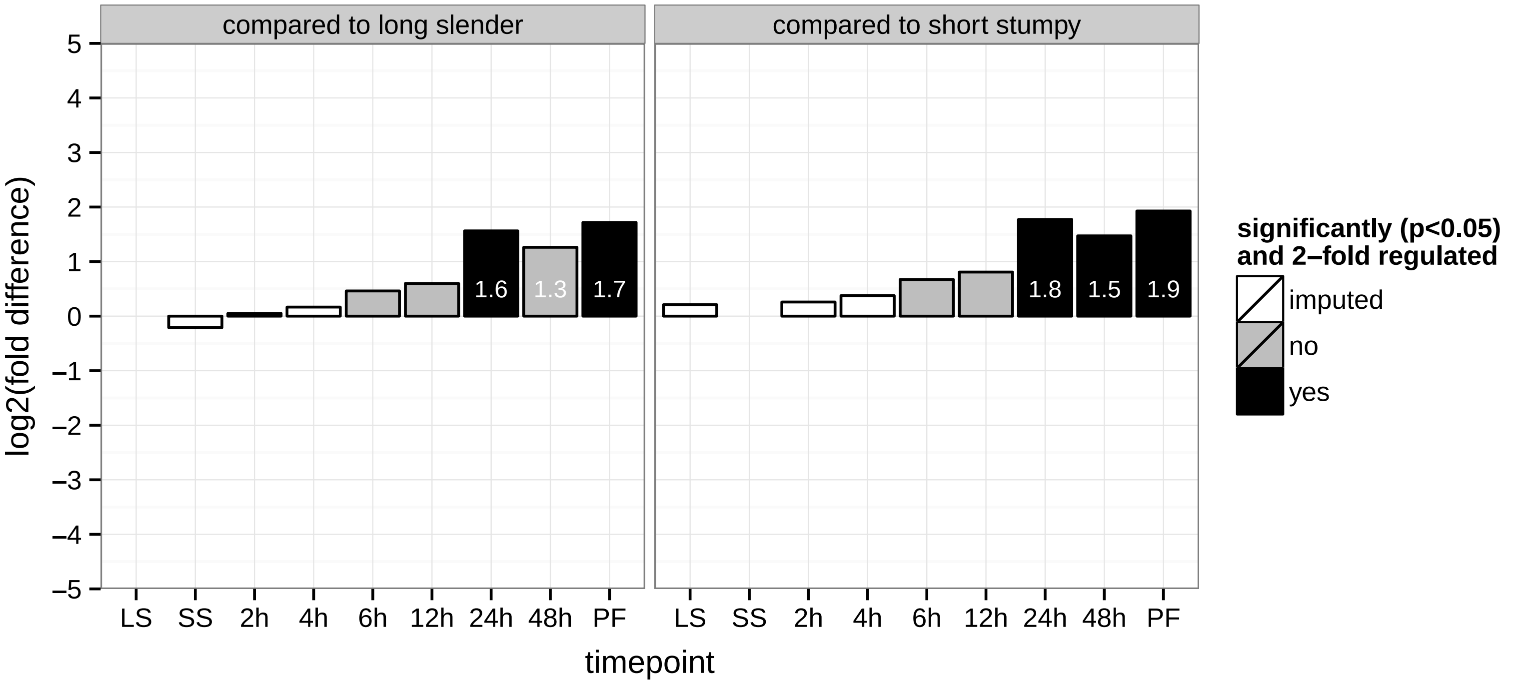
DNA polymerase alpha catalytic subunit, DNA polymerase I
Tb927.8.4880
AGOF: DNA binding, DNA−directed DNA polymerase activity, nucleotide binding
AGOC: DNA−directed RNA polymerase I complex, nucleus
AGOP: DNA replication, lagging strand elongation
PGOF: DNA binding, DNA−directed DNA polymerase activity, nucleic acid binding, nucleotide binding
PGOC: null
PGOP: DNA replication, nucleobase−containing compound metabolic process

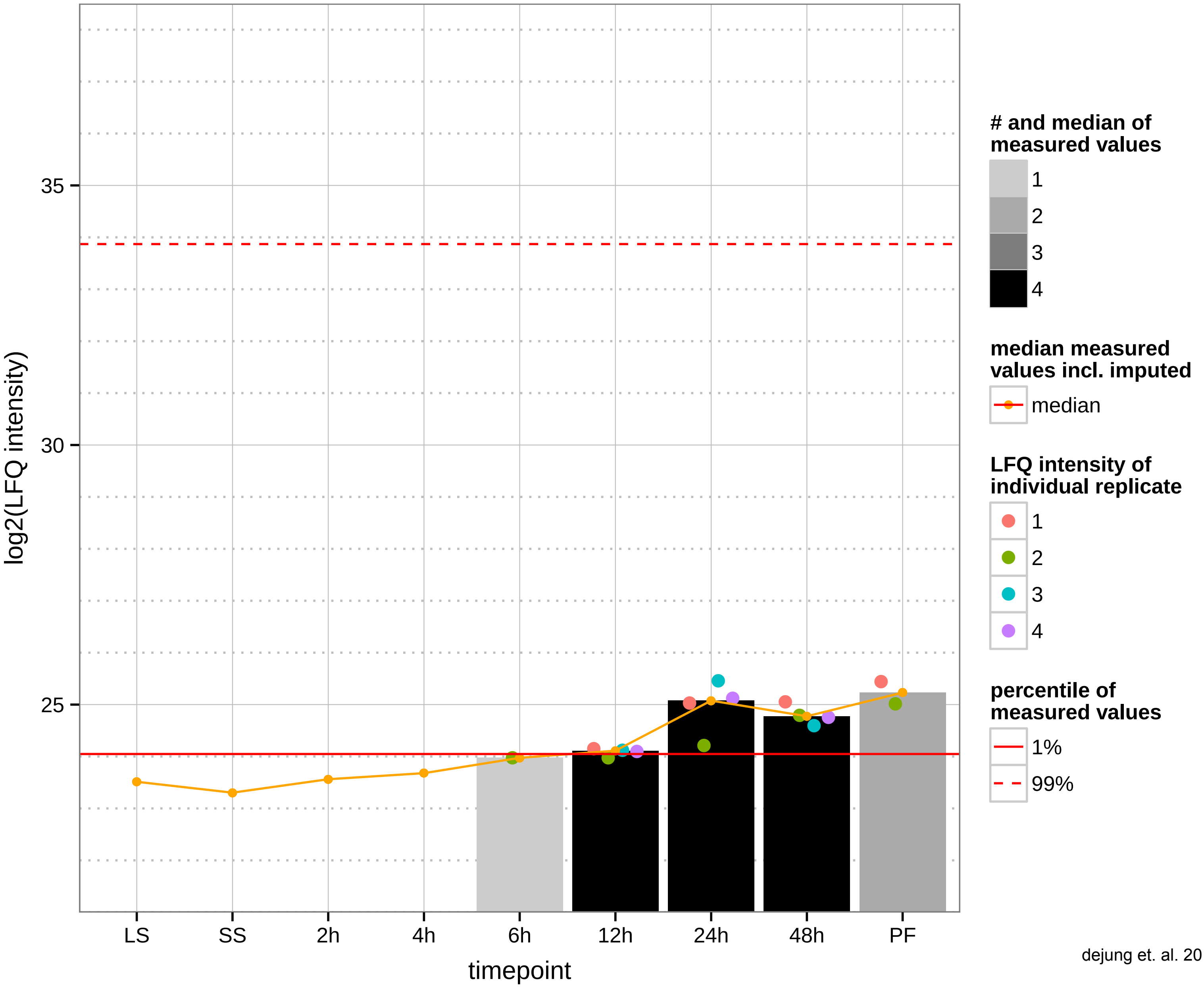




dejung et. al. 2015

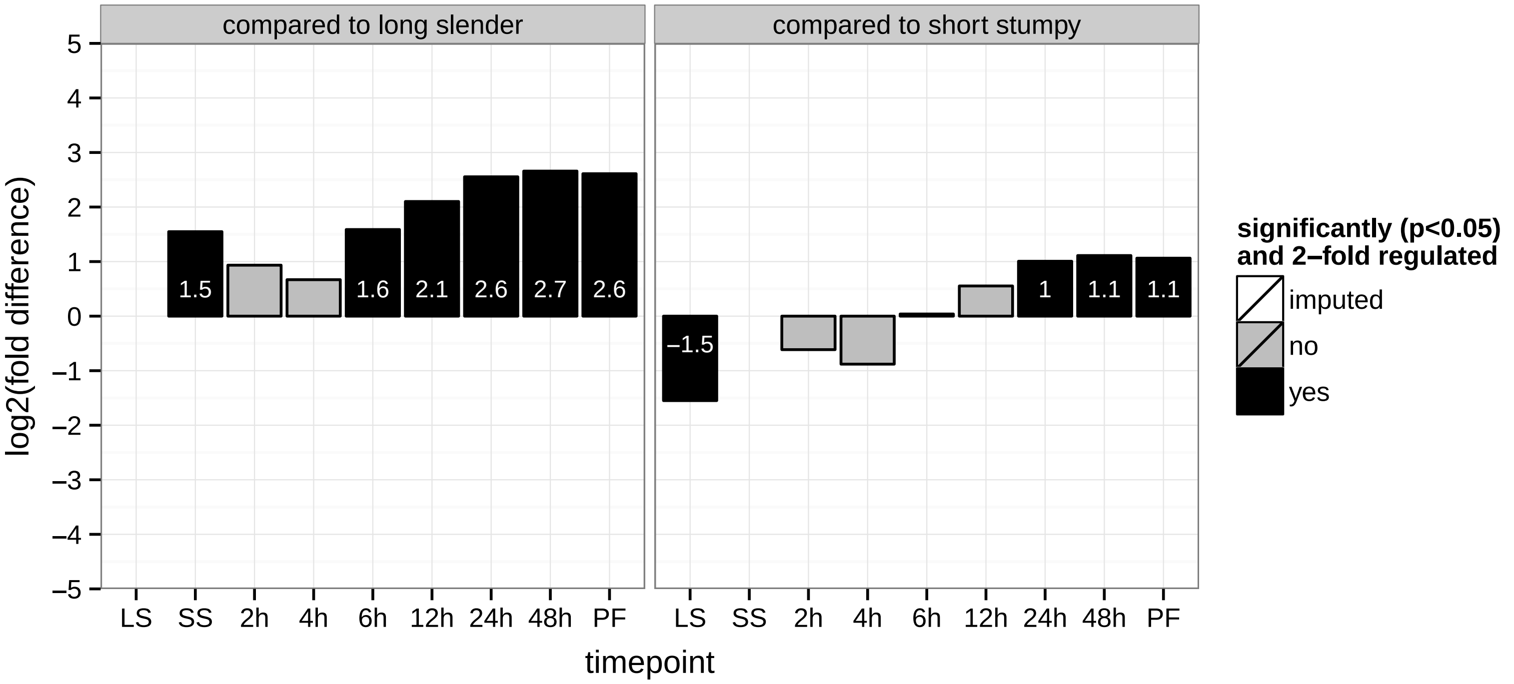
hypothetical protein, conserved
Tb927.8.4920
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

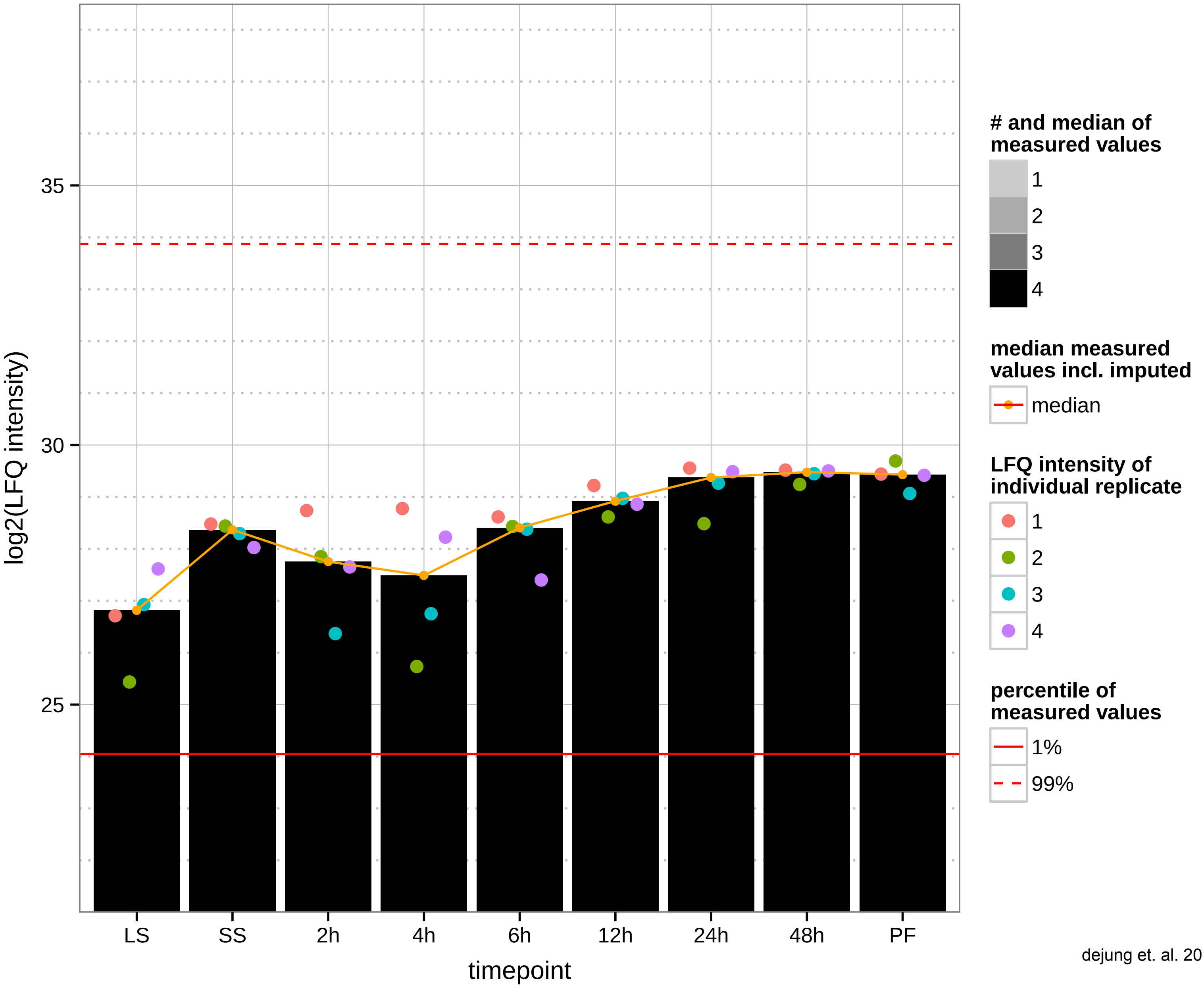




dejung et. al. 2015

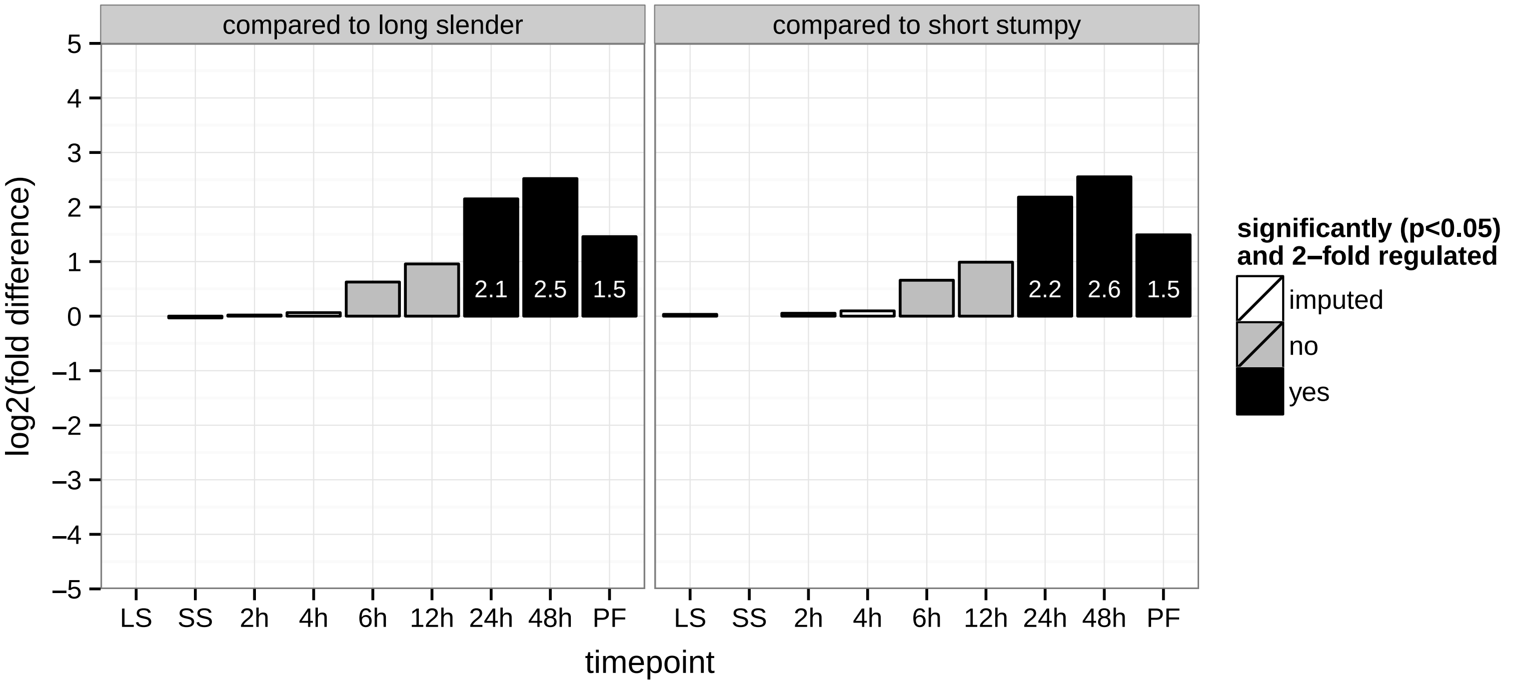
DNA–directed rna polymerase I largest subunit, putative, DNA–directed RNA polymerase I largest subunit (RPA190)
Tb927.8.5090
AGOF: null, DNA binding, DNA–directed RNA polymerase activity, zinc ion binding
AGOC: null, nucleus
AGOP: null, transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA–dependent

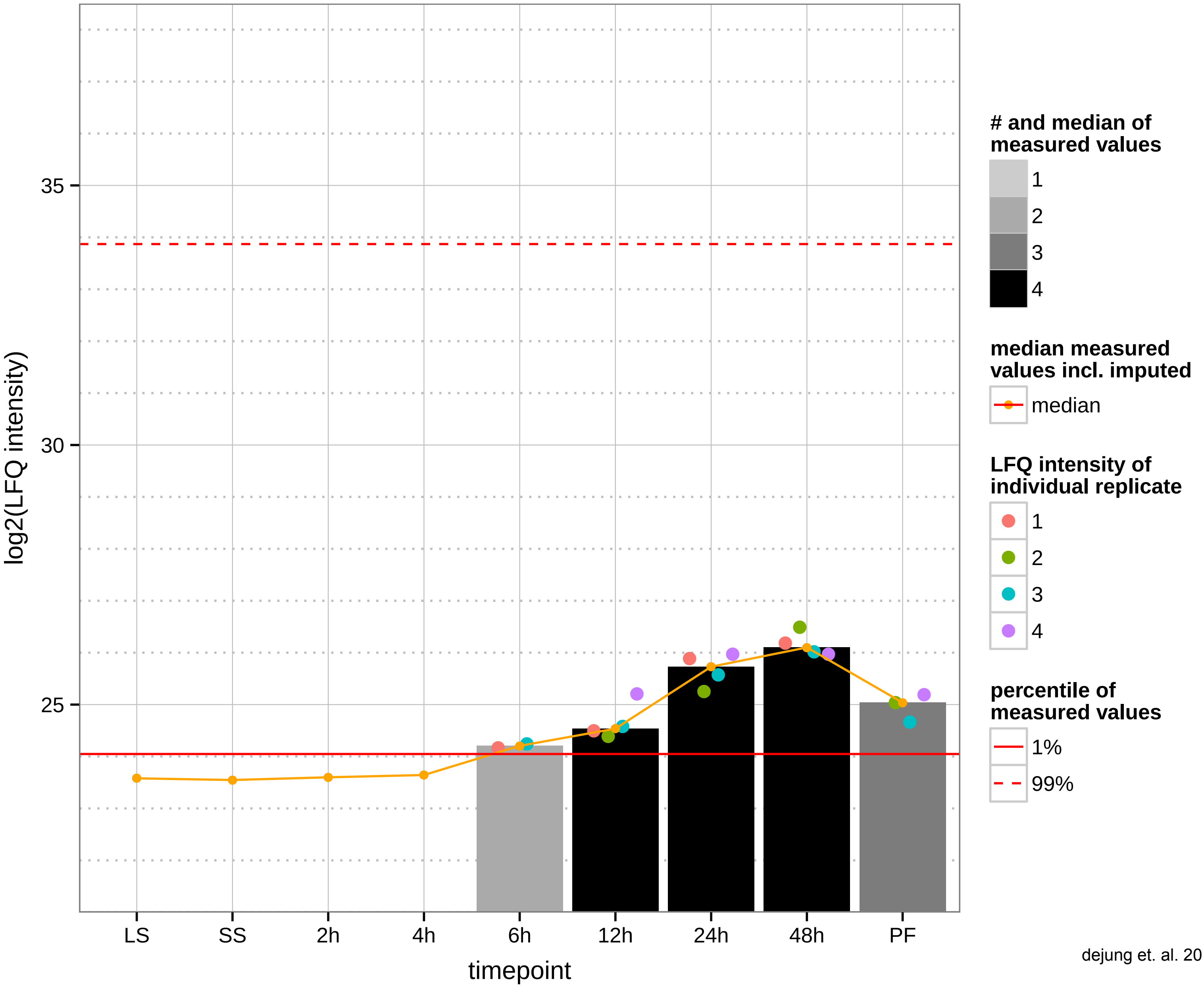




dejung et. al. 2015

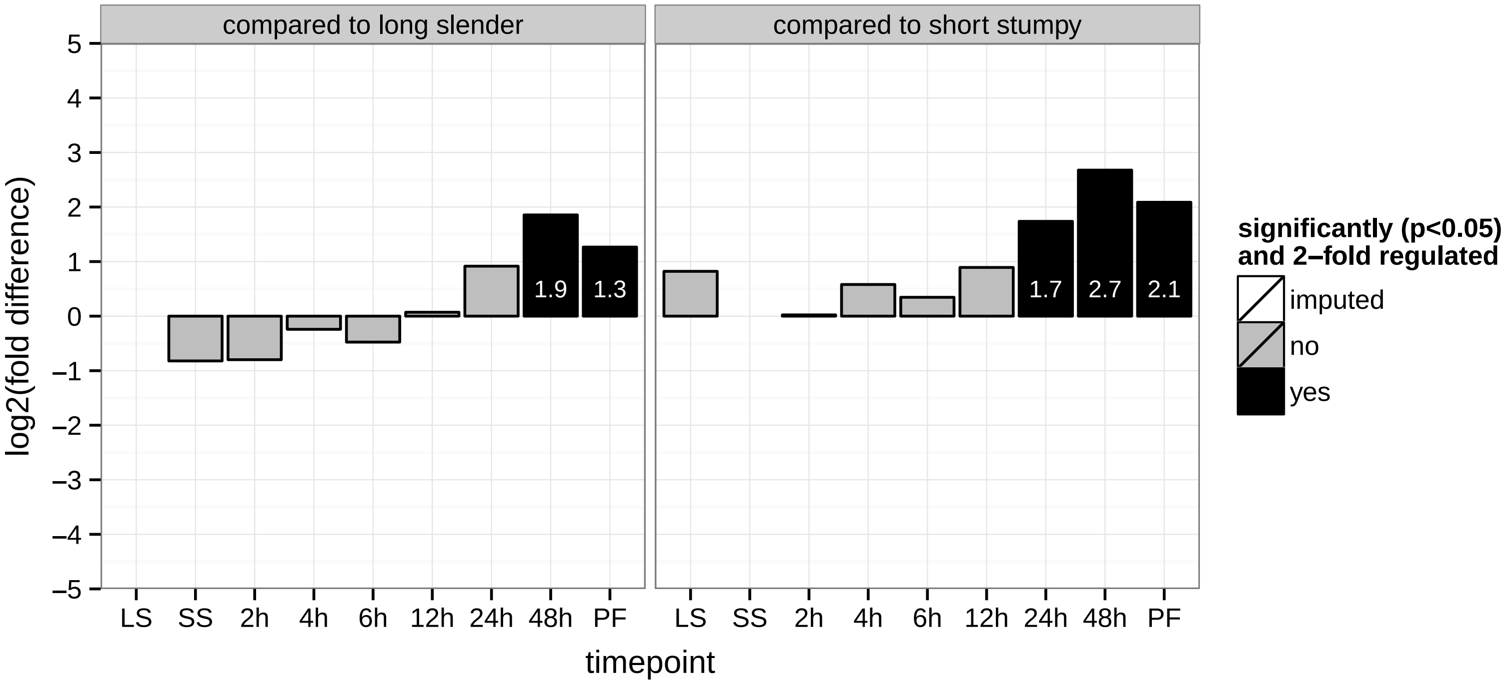
hypothetical protein, conserved
Tb927.8.5420
AGOF: methyltransferase activity
AGOC: integral to membrane, mitochondrion
AGOP: metabolic process
PGOF: methyltransferase activity
PGOC: null
PGOP: metabolic process

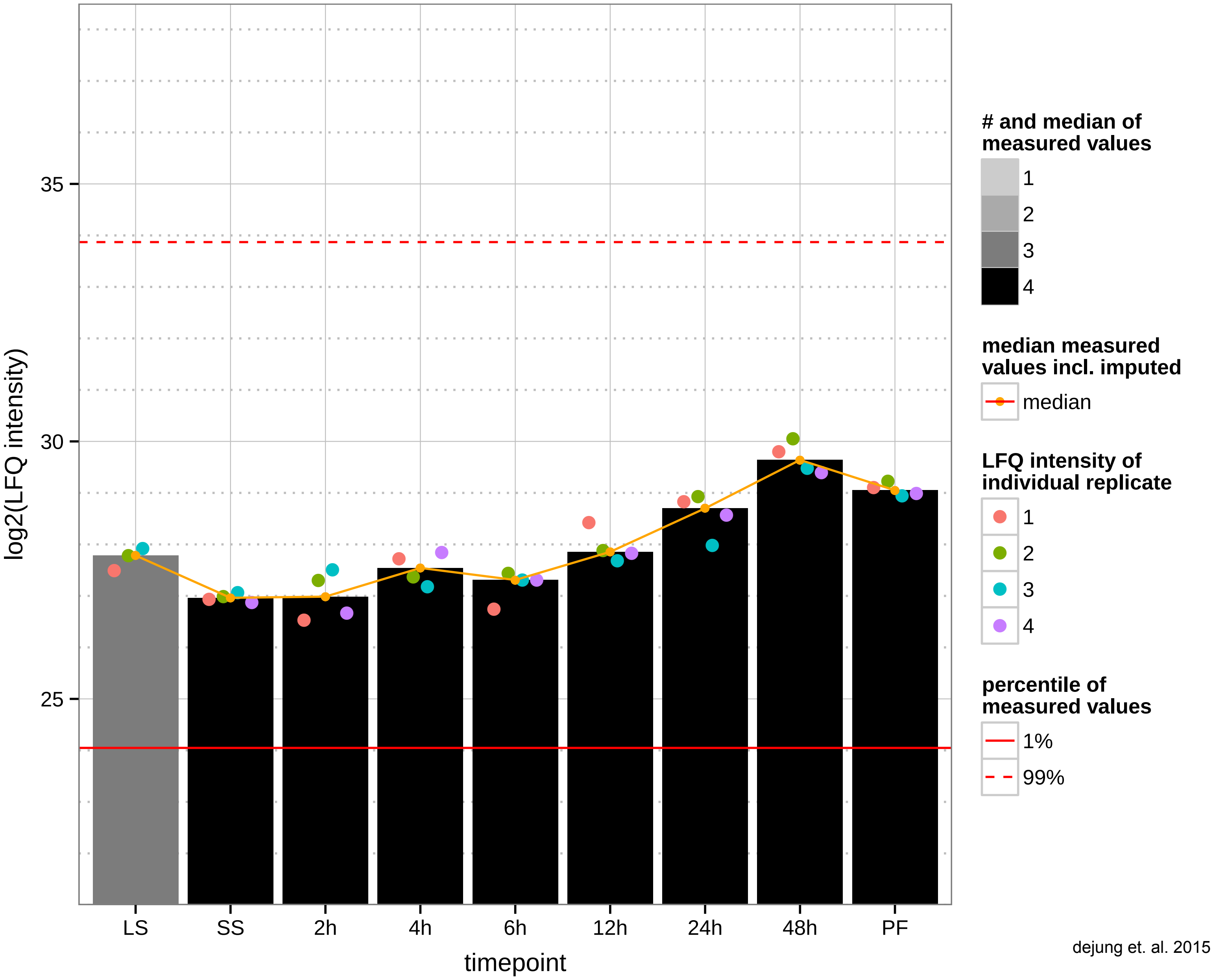




dejung et. al. 2015

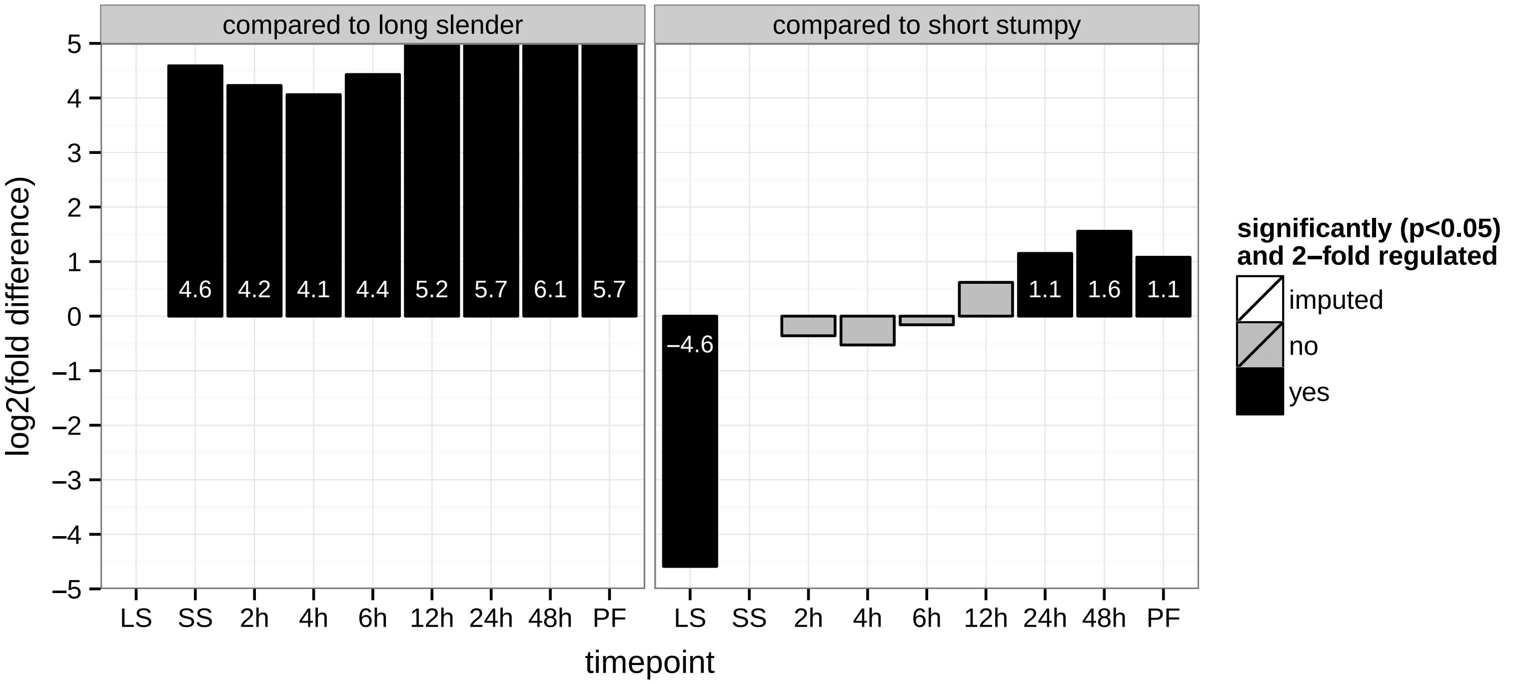
hypothetical protein, conserved
Tb927.8.5640
AGOF: sequence−specific DNA binding transcription factor activity
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

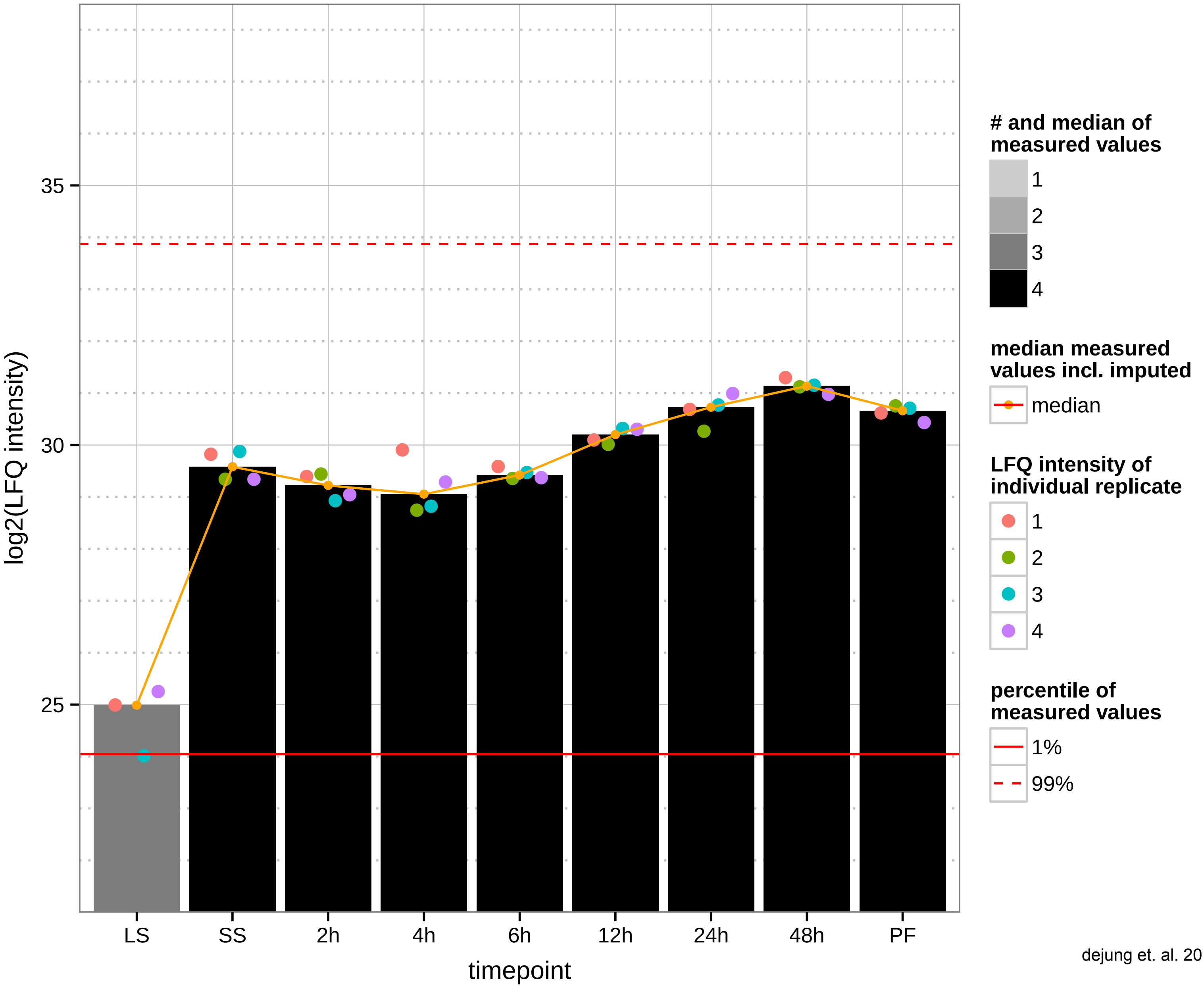




dejung et. al. 2015

succinate dehydrogenase flavoprotein, putative
Tb927.8.6580
AGOF: electron carrier activity, flavin adenine dinucleotide binding, succinate dehydrogenase activity
AGOC: mitochondrion
AGOP: electron transport chain, oxidation–reduction process, tricarboxylic acid cycle
PGOF: flavin adenine dinucleotide binding, oxidoreductase activity, acting on the CH–CH group of donors
PGOC: null
PGOP: electron transport chain, oxidation–reduction process, tricarboxylic acid cycle





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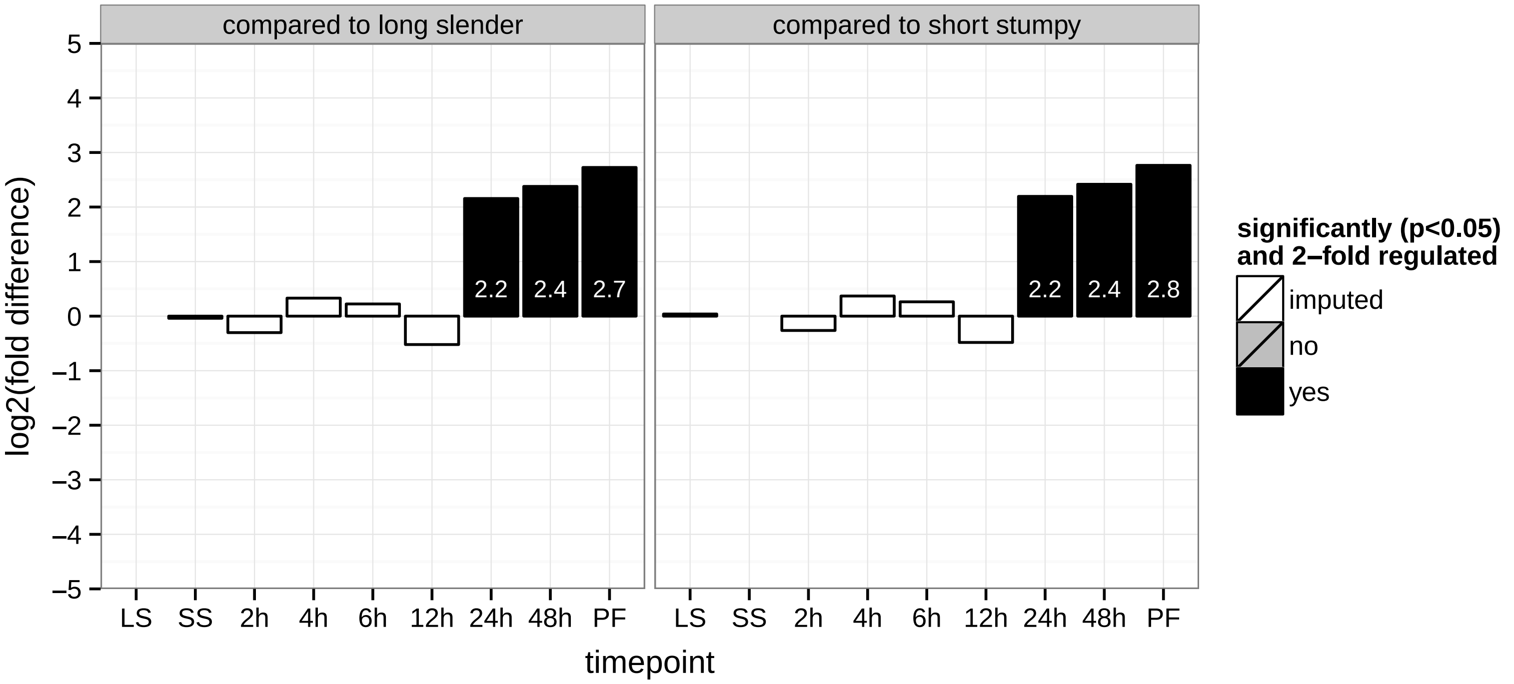
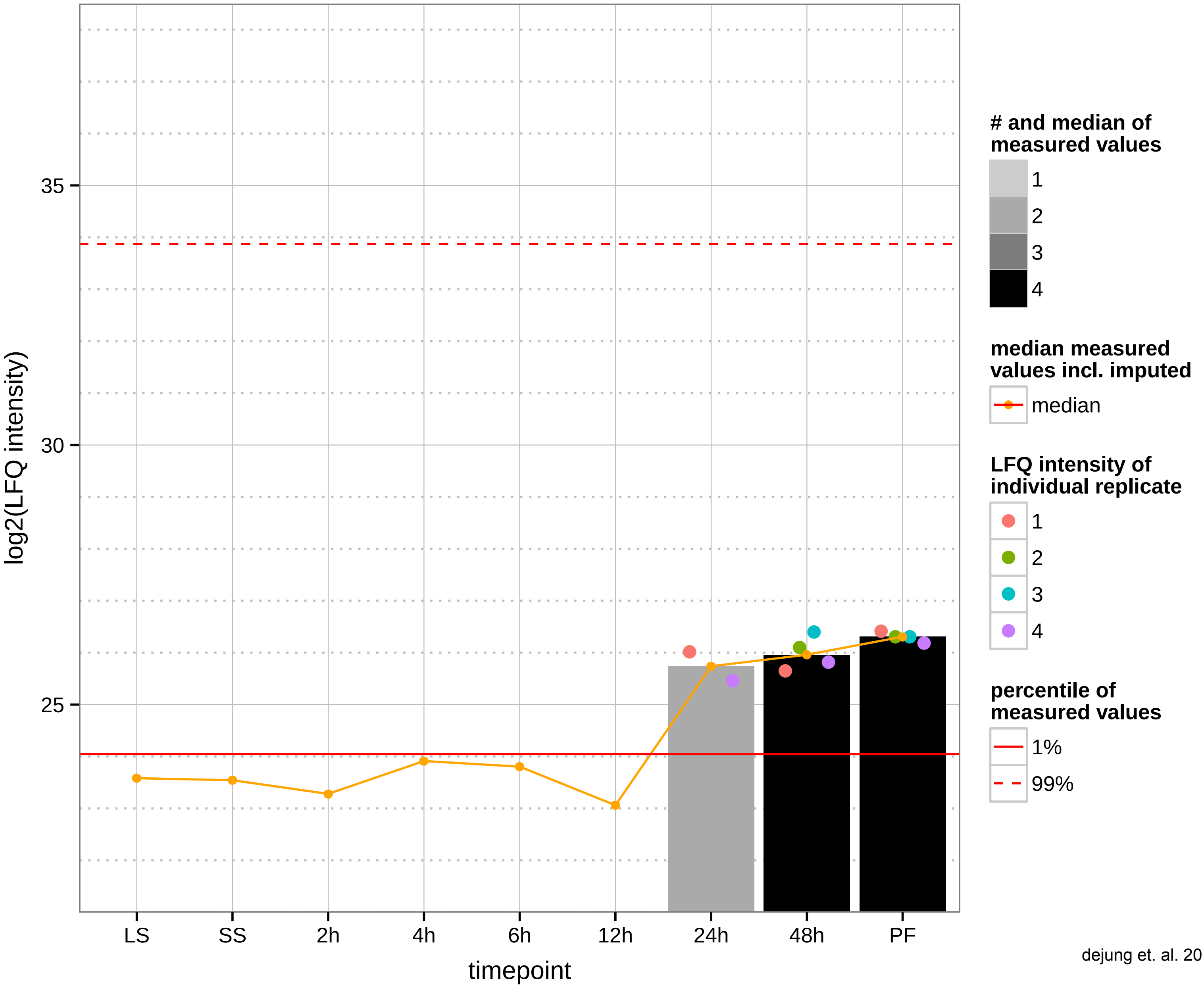
dihydroceramide synthase, putative
Tb927.8.7730
AGOF: very long−chain fatty acid−CoA ligase activity
AGOC: cytosol, integral to membrane
AGOP: ceramide biosynthetic process
PGOF: null
PGOC: integral to membrane
PGOP: null





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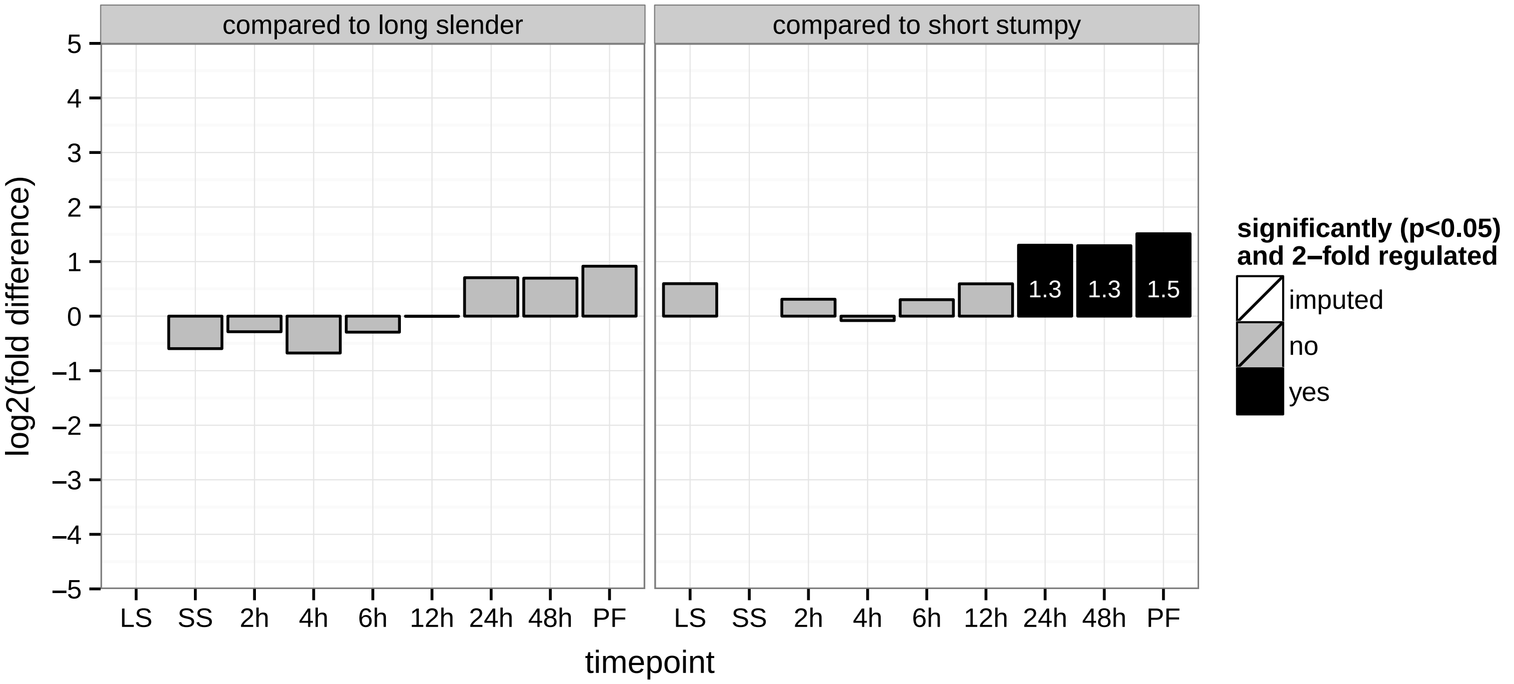
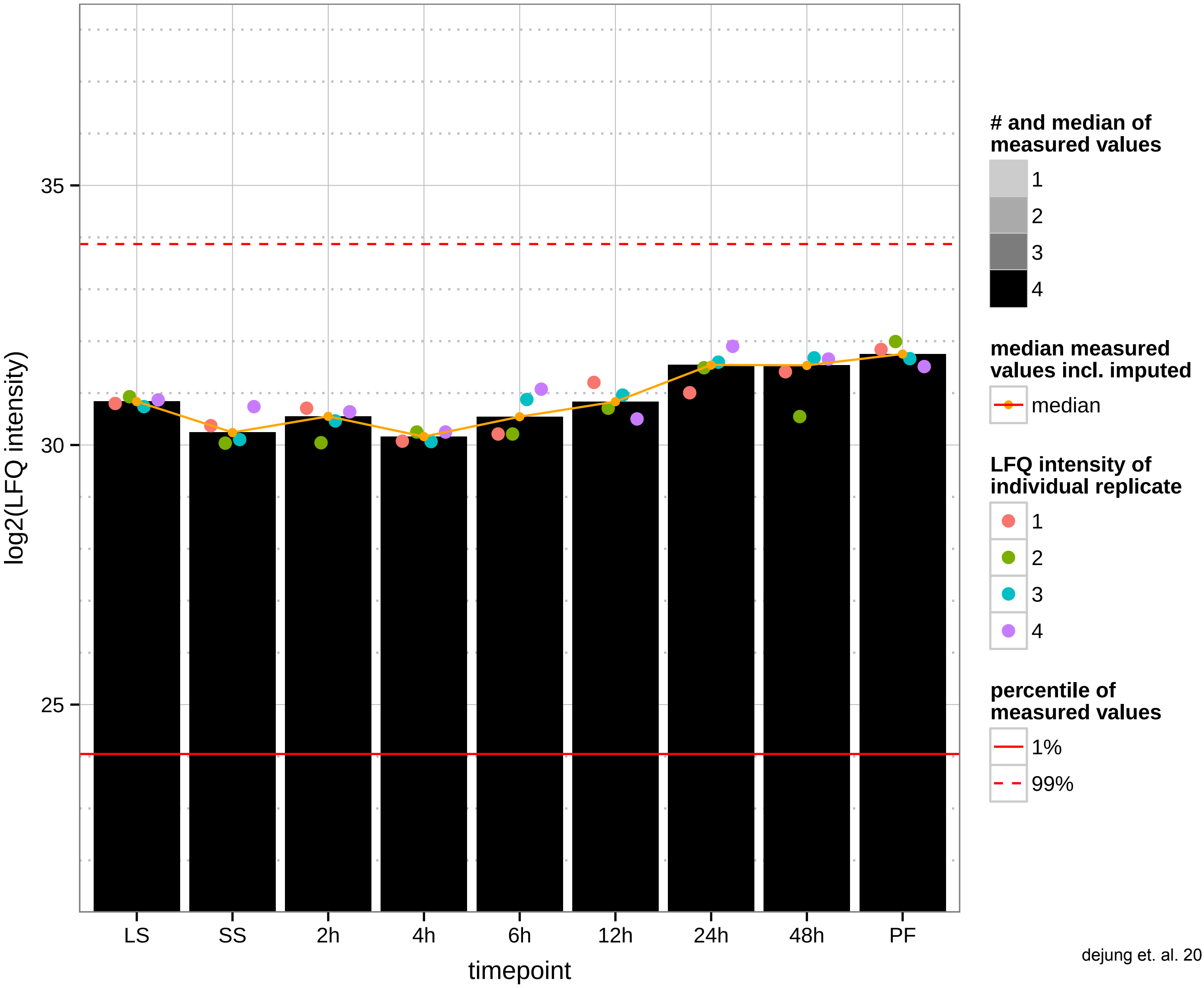
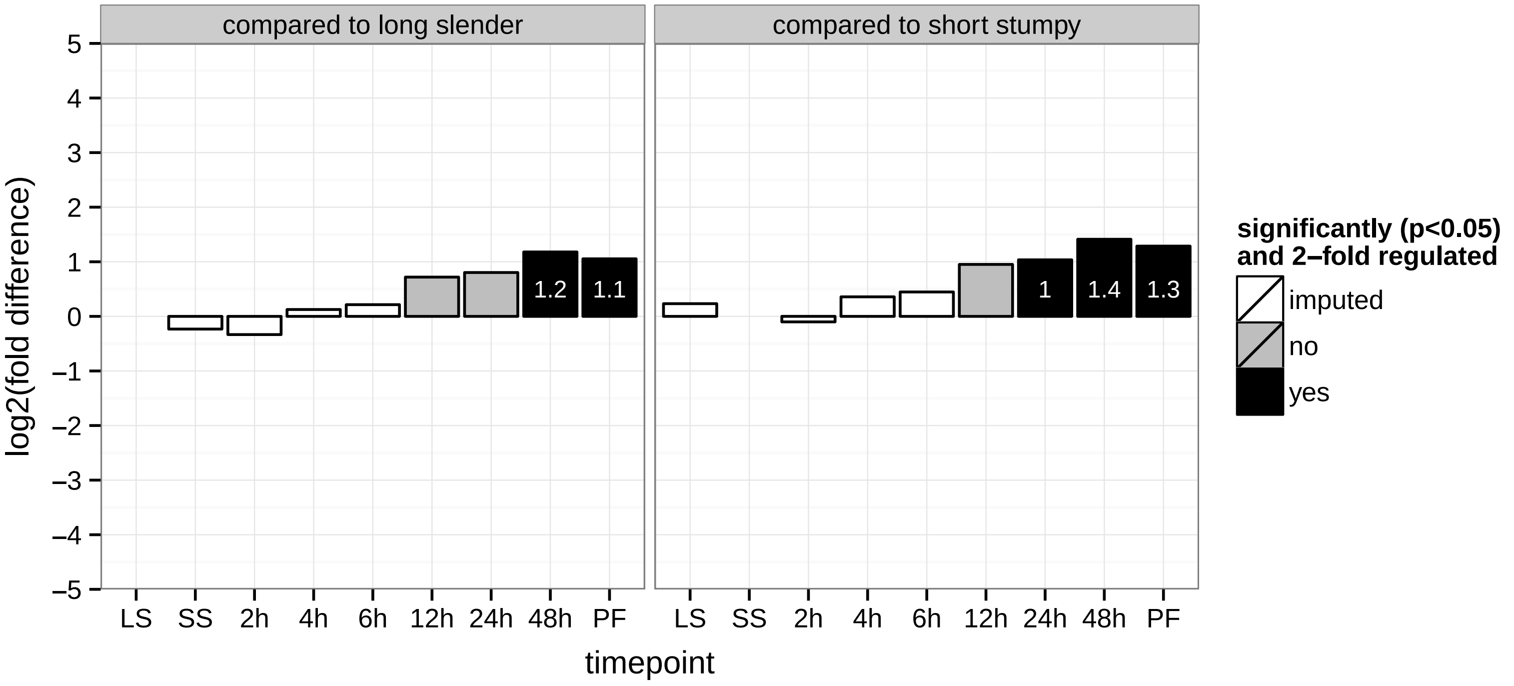
60S ribosomal protein L27a, 60S ribosomal protein L28, 60S ribosomal protein L29, 60S ribosomal protein L29 (RPL27A)
Tb927.9.11490;Tb927.9.11470
AGOF: RNA binding, structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation, null
PGOF: null
PGOC: null
PGOP: null

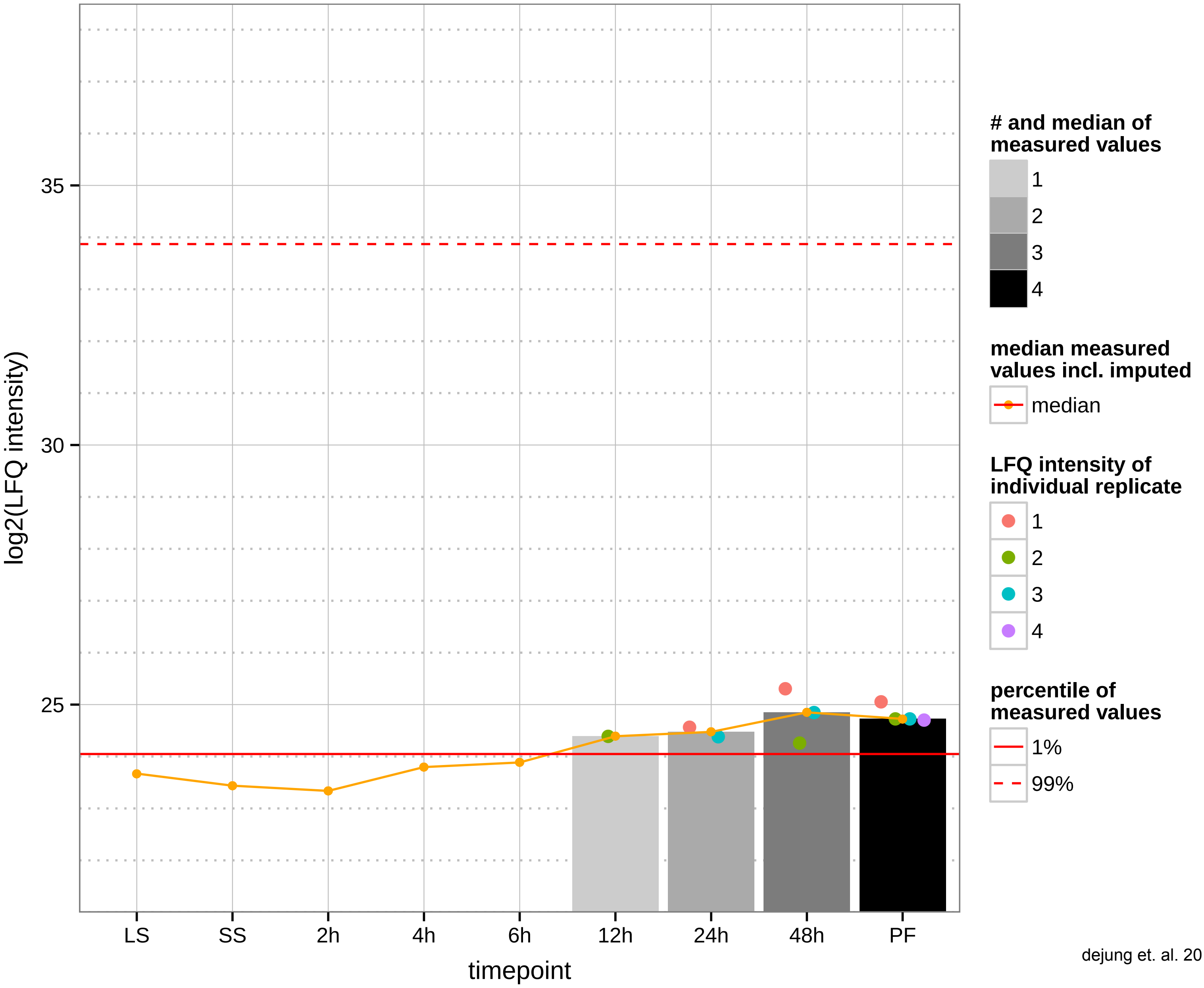




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.12160
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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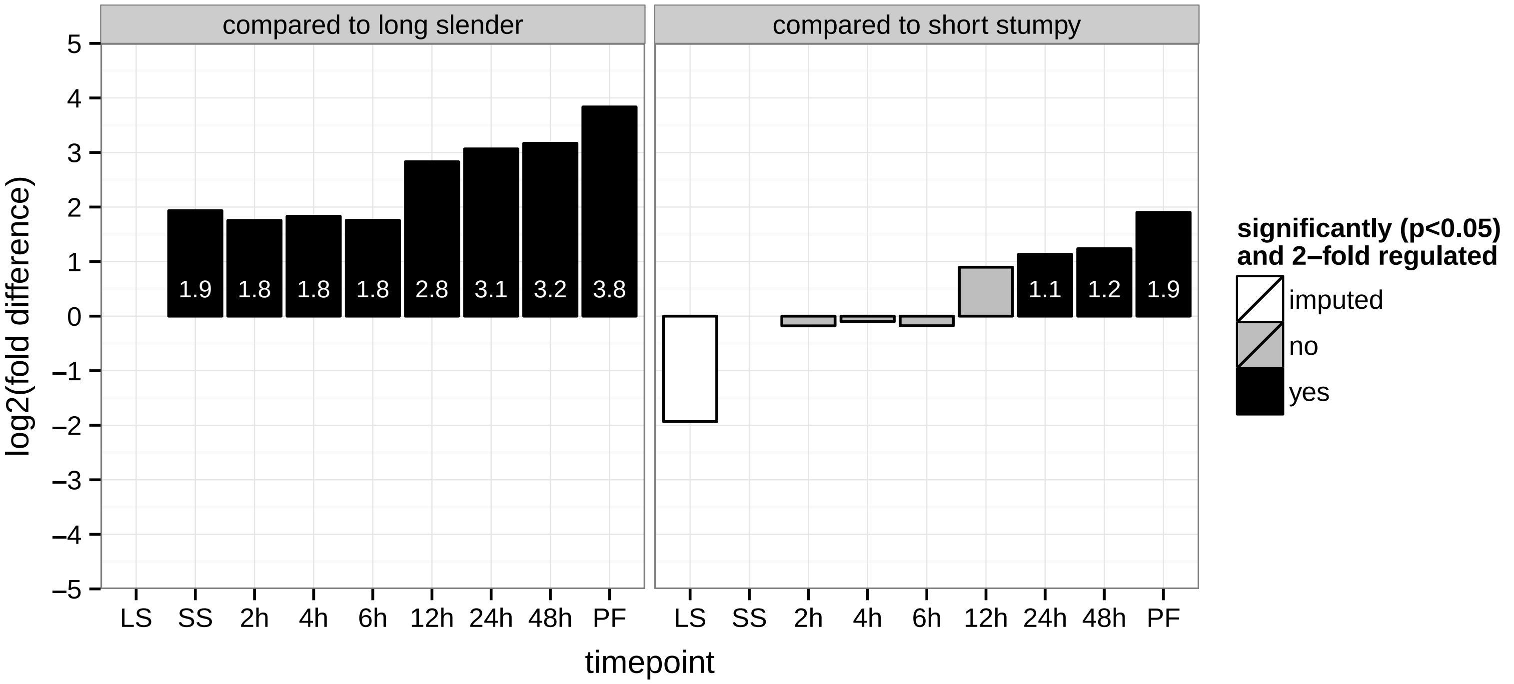
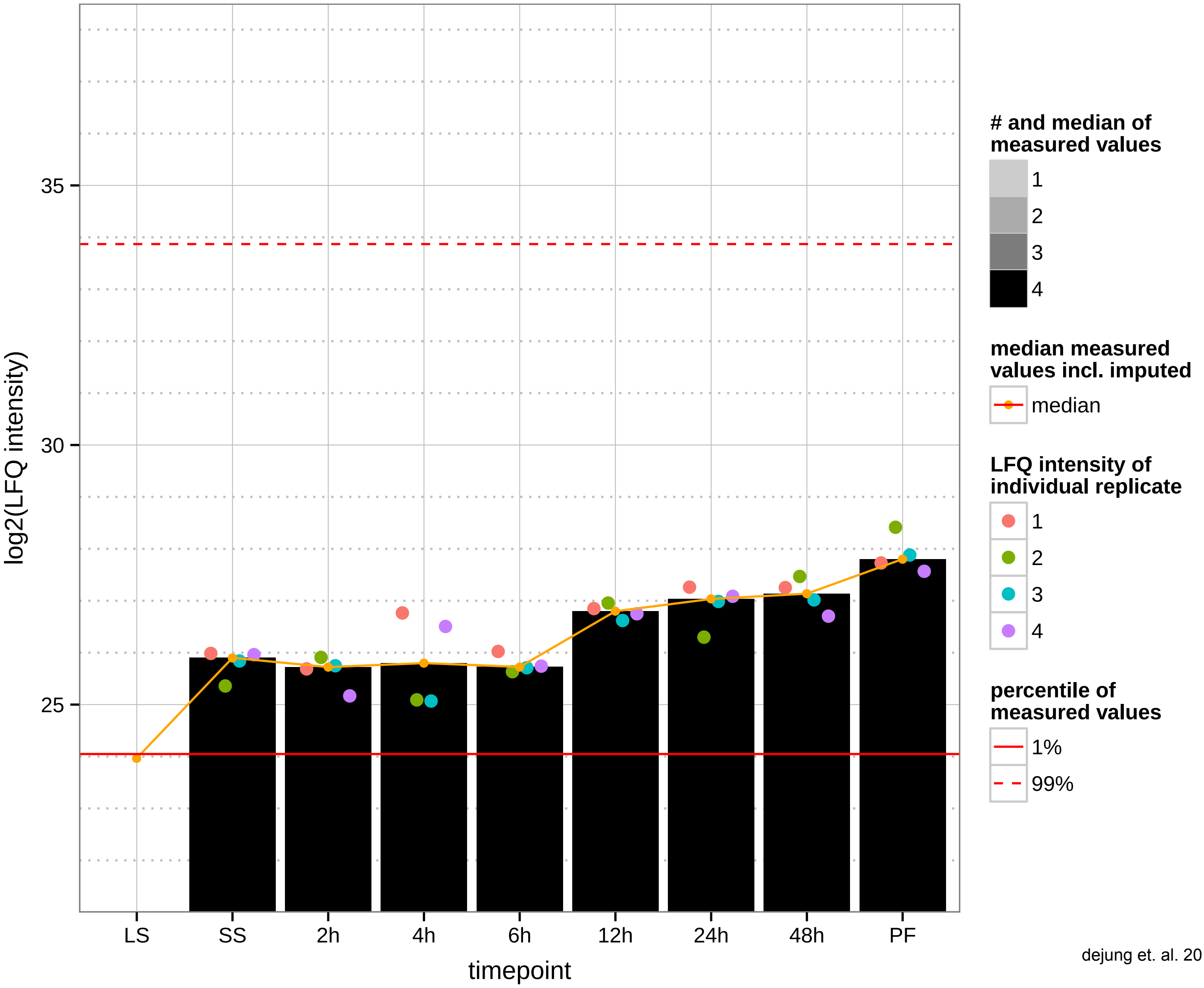
hypothetical protein, conserved
Tb927.9.12770
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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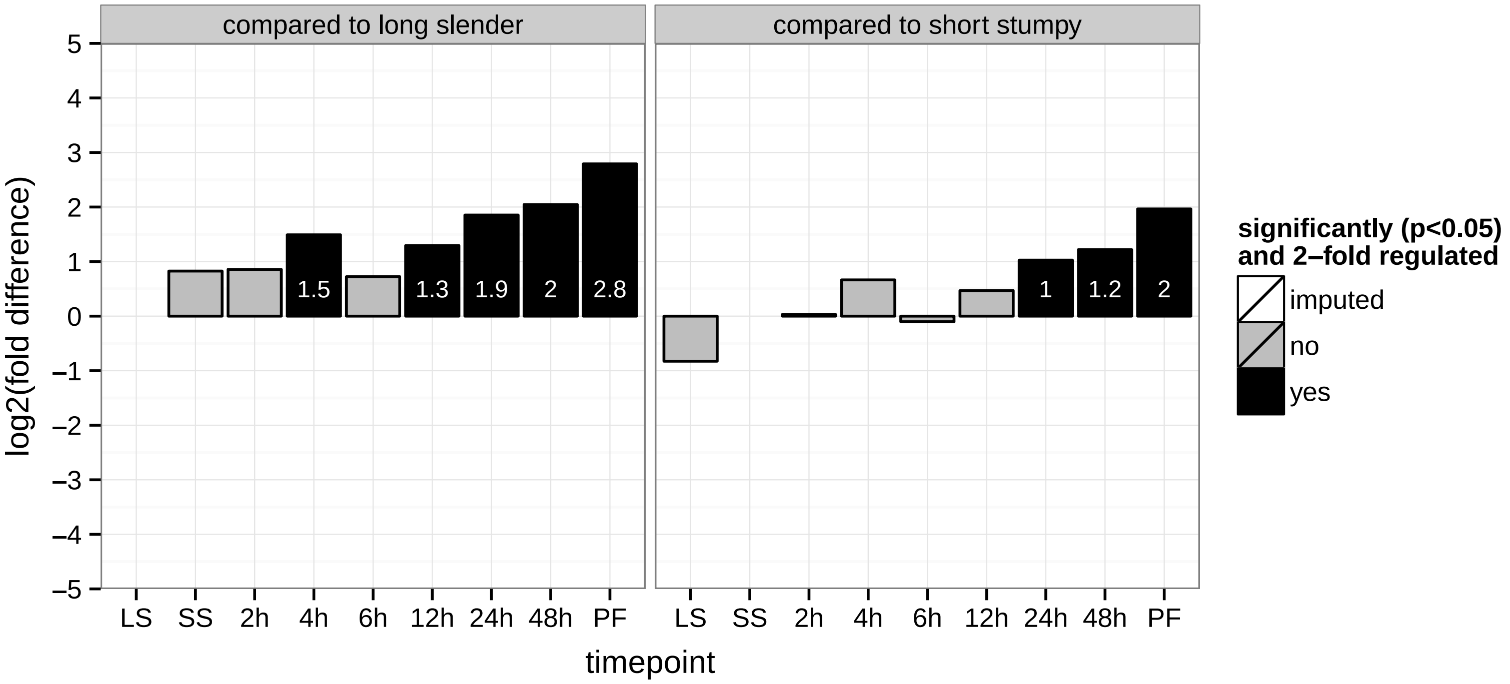
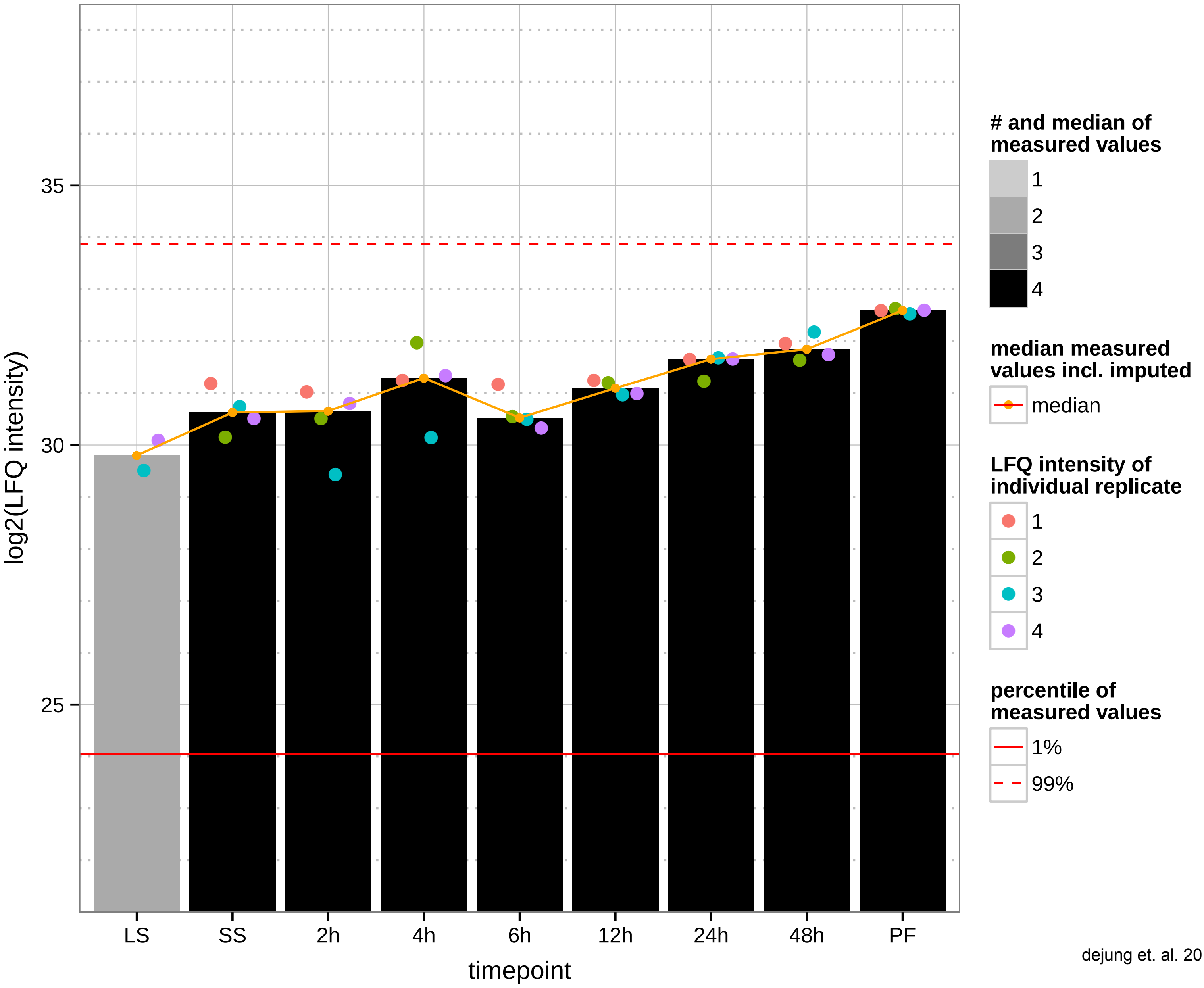
aminopeptidase P, putative, metallo−peptidase, Clan MG, Family M24
Tb927.9.13490
AGOF: aminopeptidase activity, manganese ion binding
AGOC: null
AGOP: cellular process
PGOF: aminopeptidase activity, manganese ion binding
PGOC: null
PGOP: cellular process





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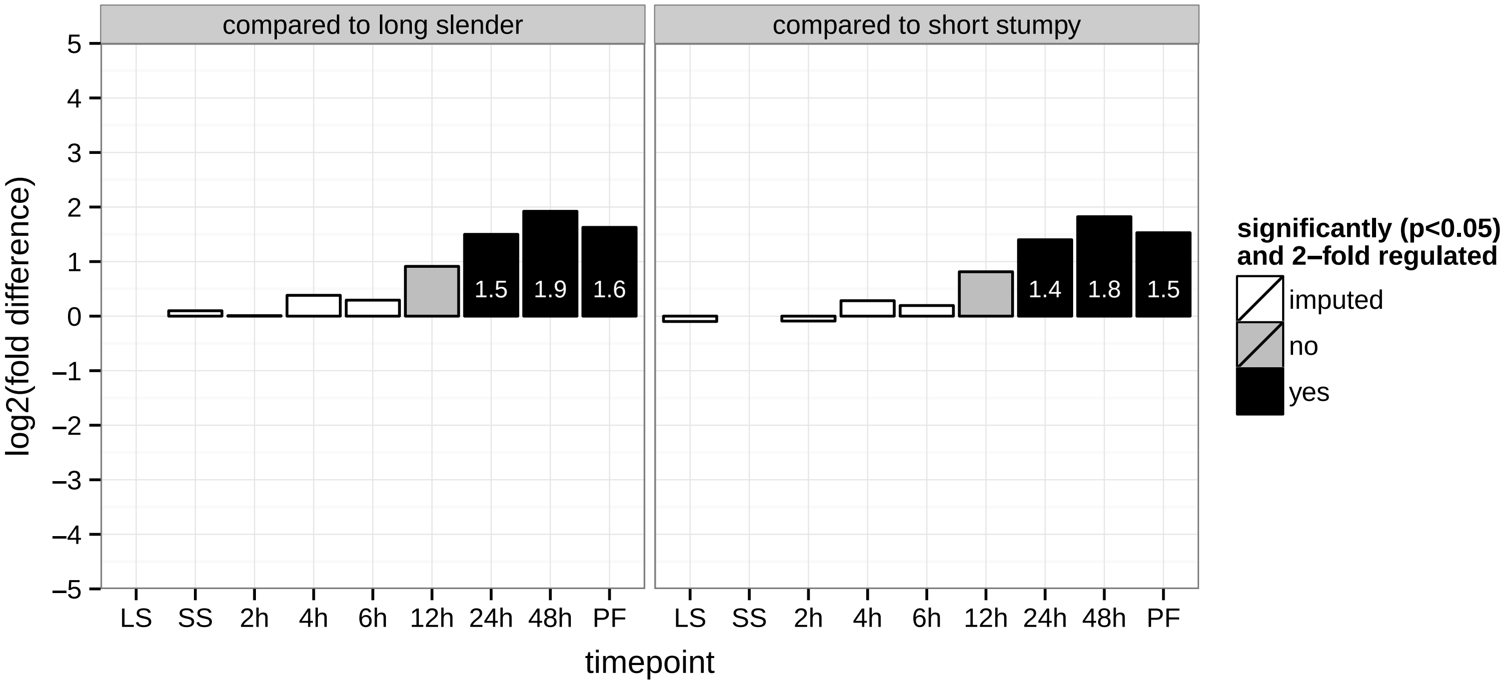
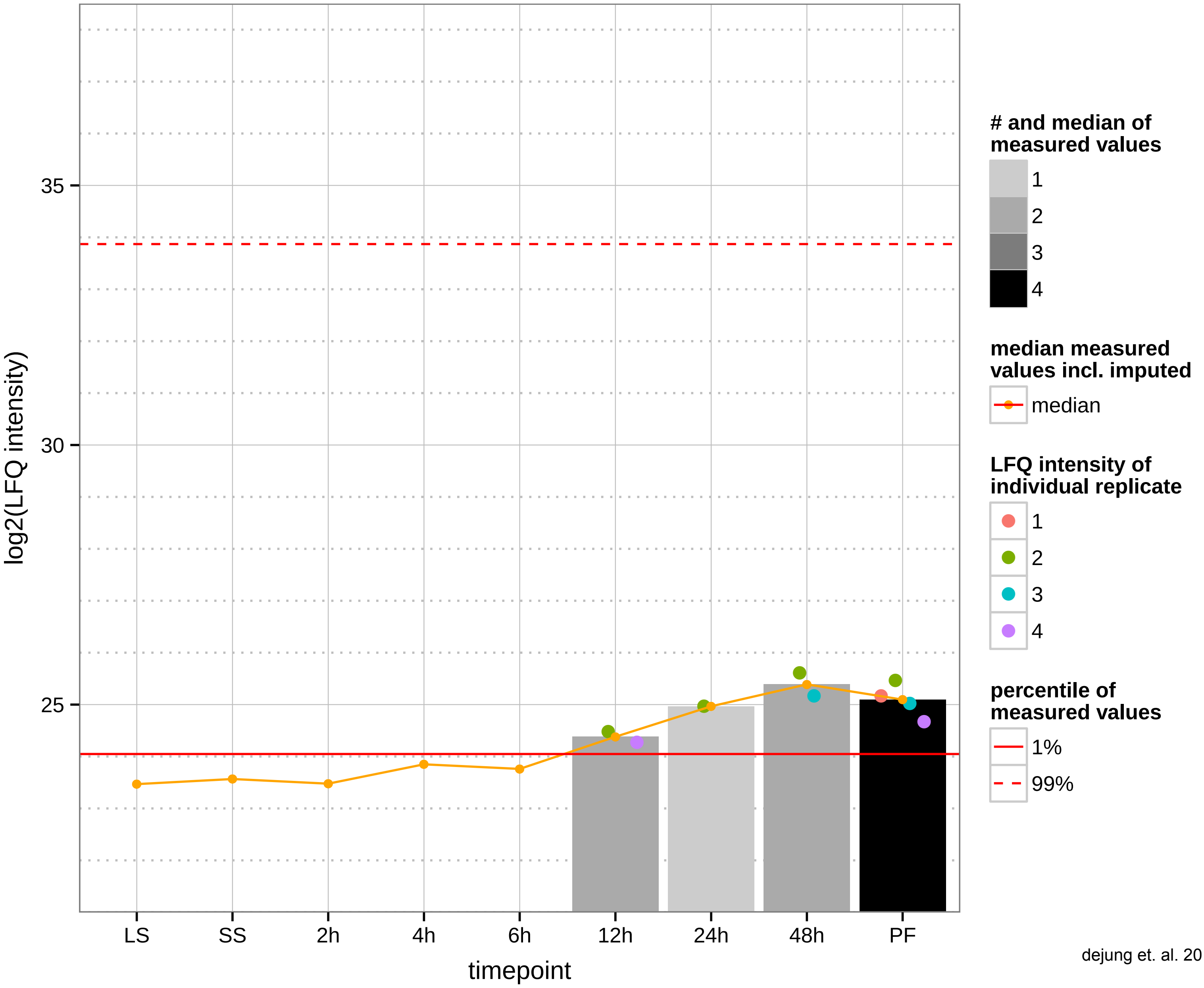
hypothetical protein, conserved
Tb927.9.13580
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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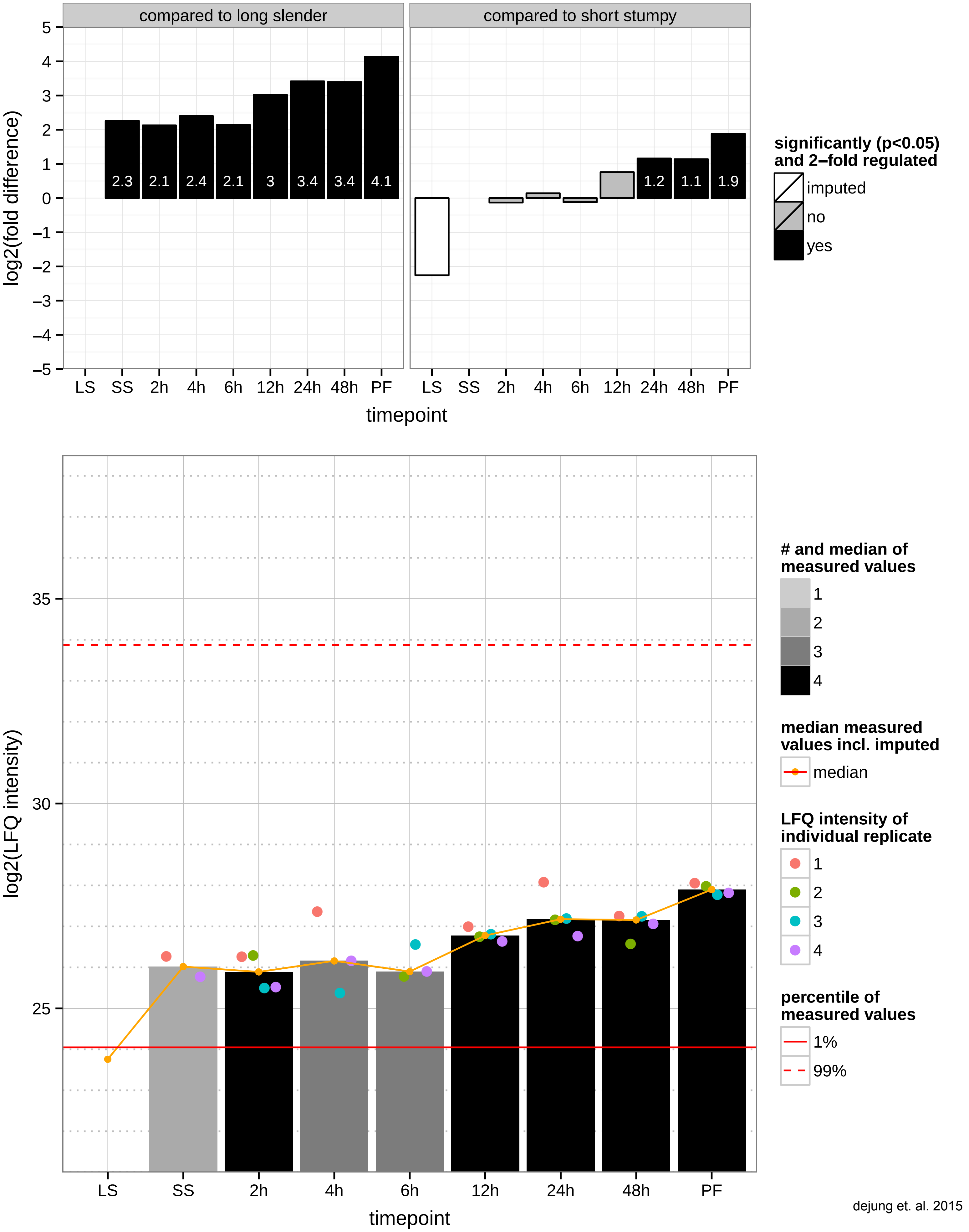
RNA 3'–terminal phosphate cyclase–like protein
Tb927.9.14410
AGOF: RNA–3'–phosphate cyclase activity
AGOC: nucleus
AGOP: null
PGOF: catalytic activity
PGOC: nucleolus
PGOP: RNA processing, ribosome biogenesis



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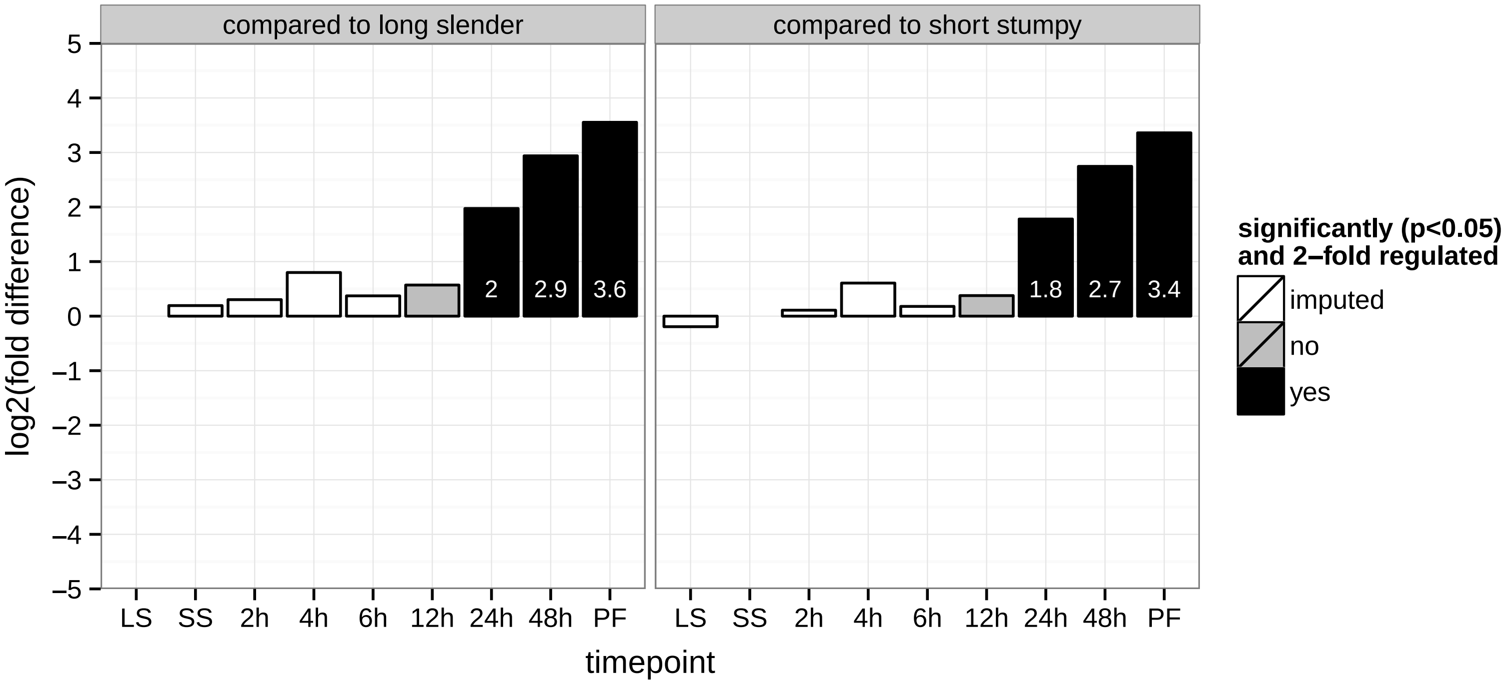
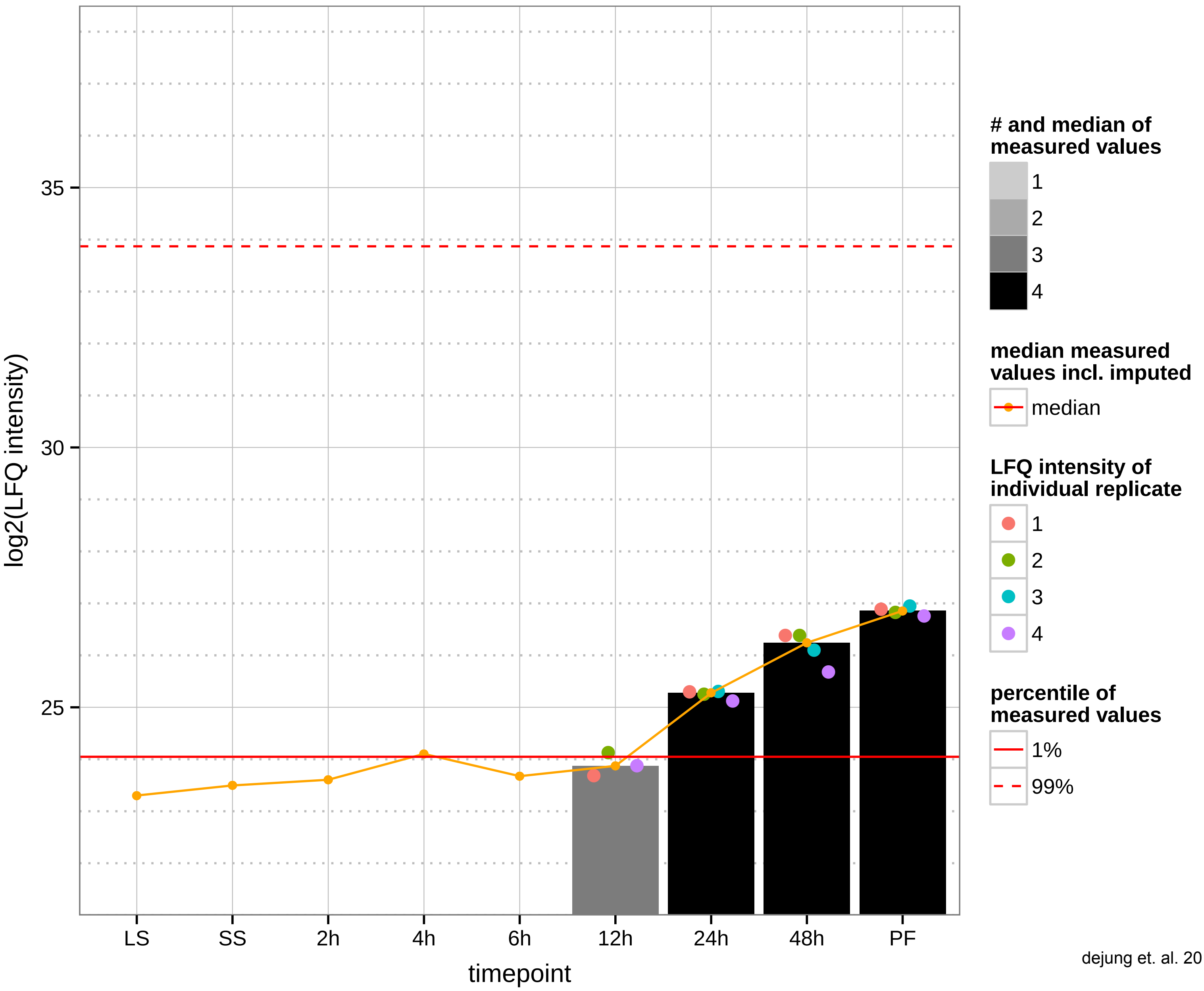
cyclophilin–like protein, putative (PPIase)
Tb927.9.14420
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: integral to membrane, mitochondrion
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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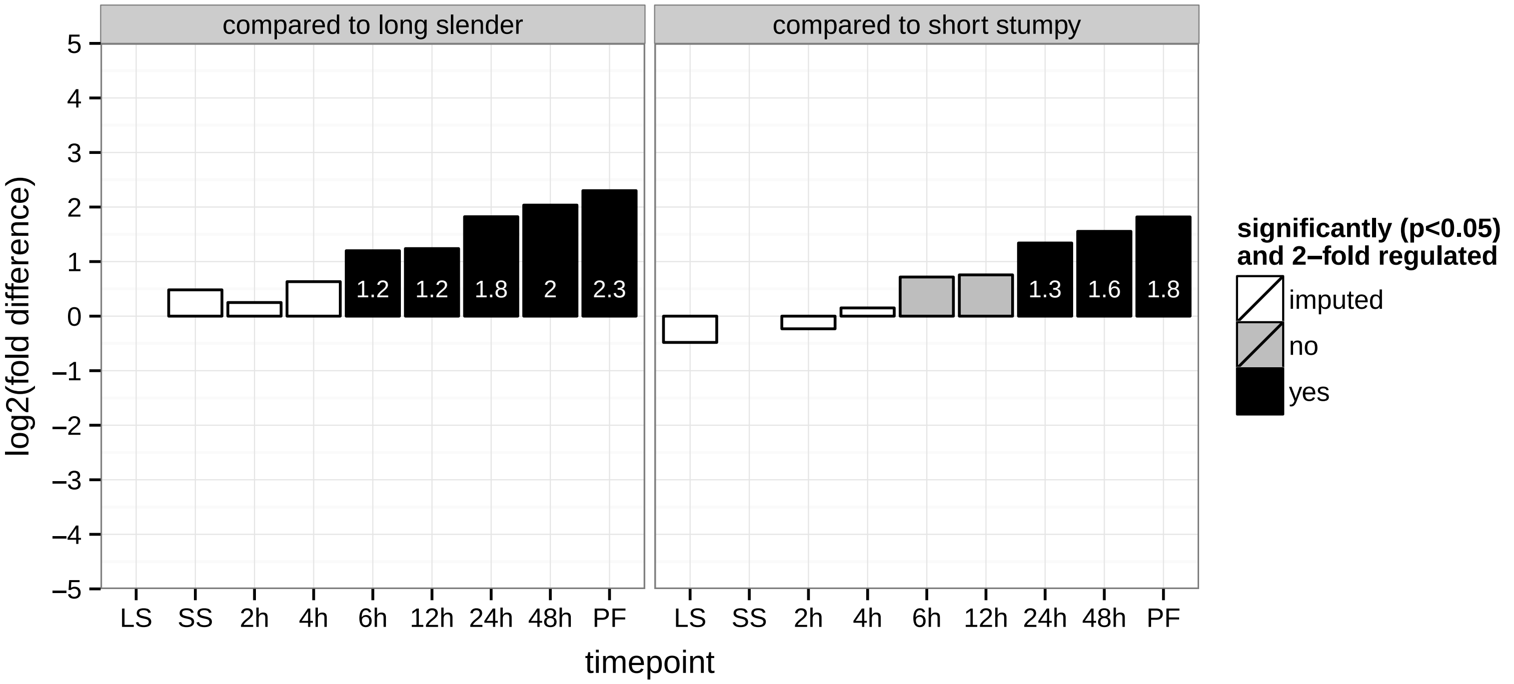
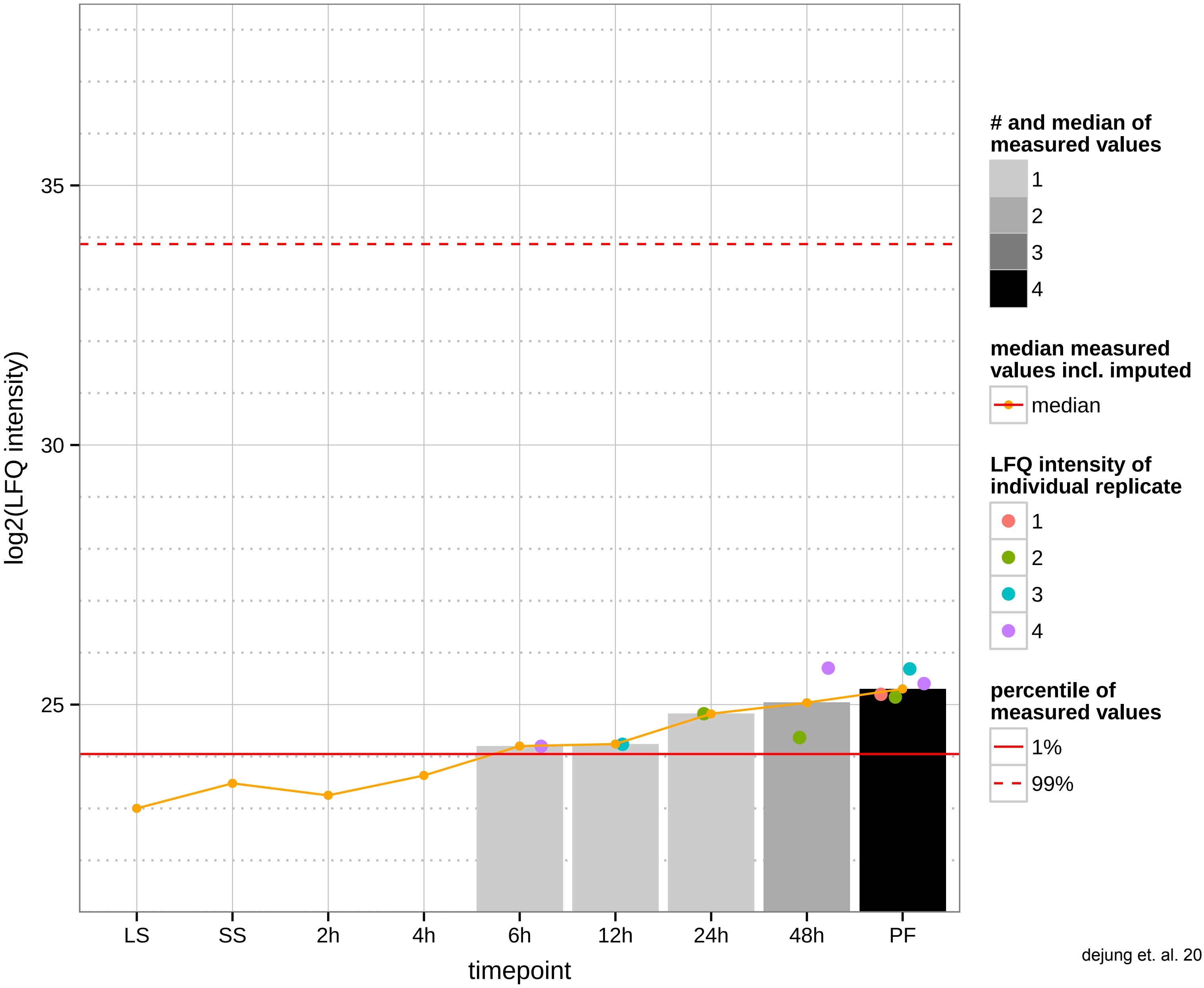
hypothetical protein, conserved
Tb927.9.1510
AGOF: ATP binding, catalytic activity
AGOC: null
AGOP: null
PGOF: ATP binding, D–alanine–D–alanine ligase activity, metal ion binding, protein binding
PGOC: null
PGOP: null





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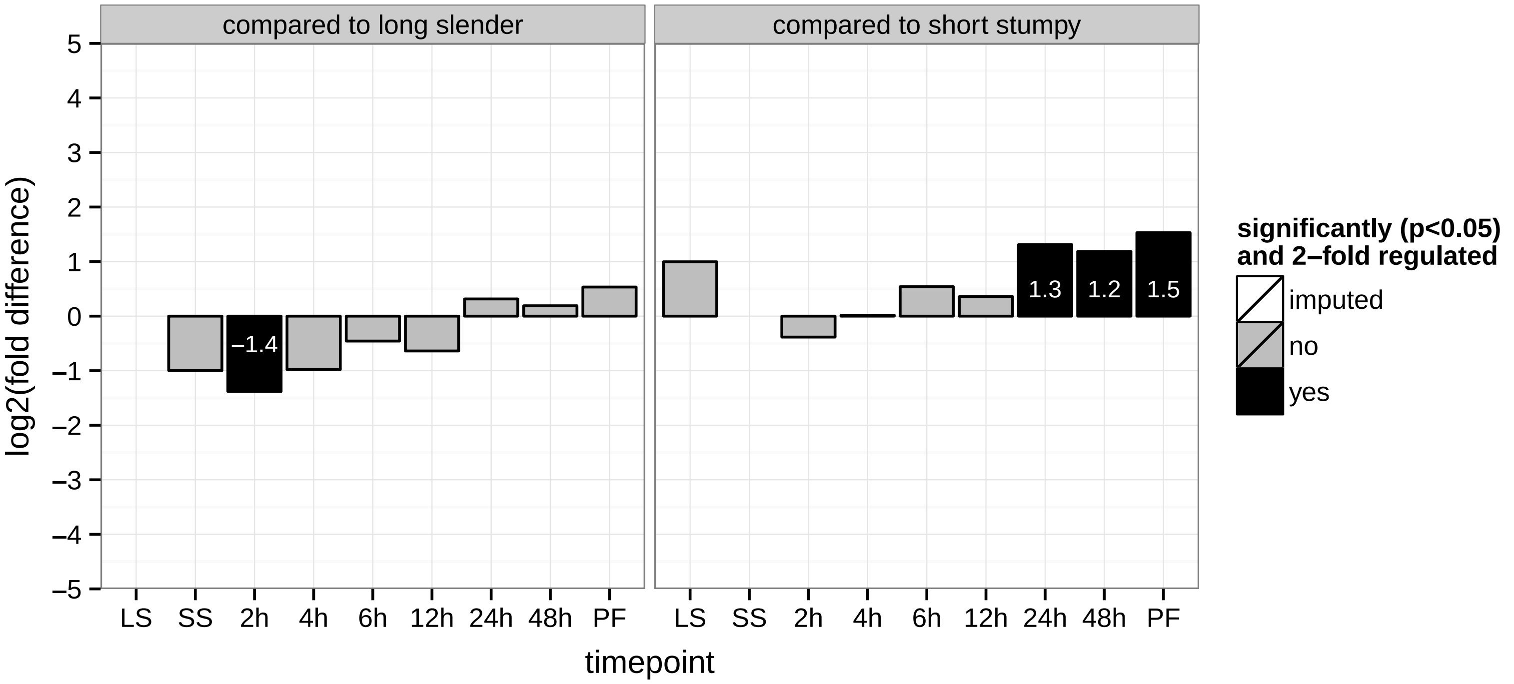
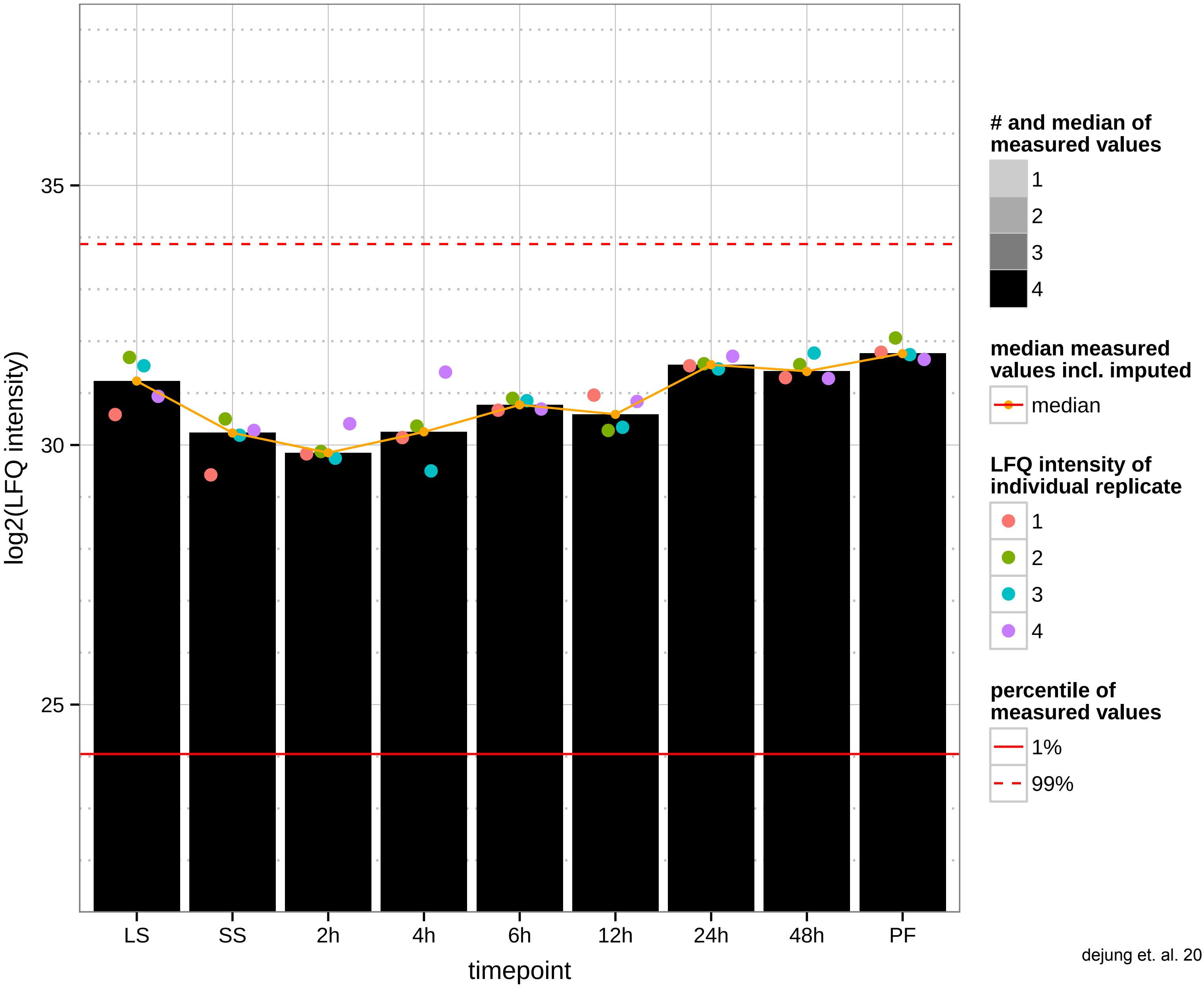
60S ribosomal protein L35, putative
Tb927.9.1850;Tb927.9.1810
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null, structural constituent of ribosome
PGOC: null, intracellular, ribosome
PGOP: null, translation





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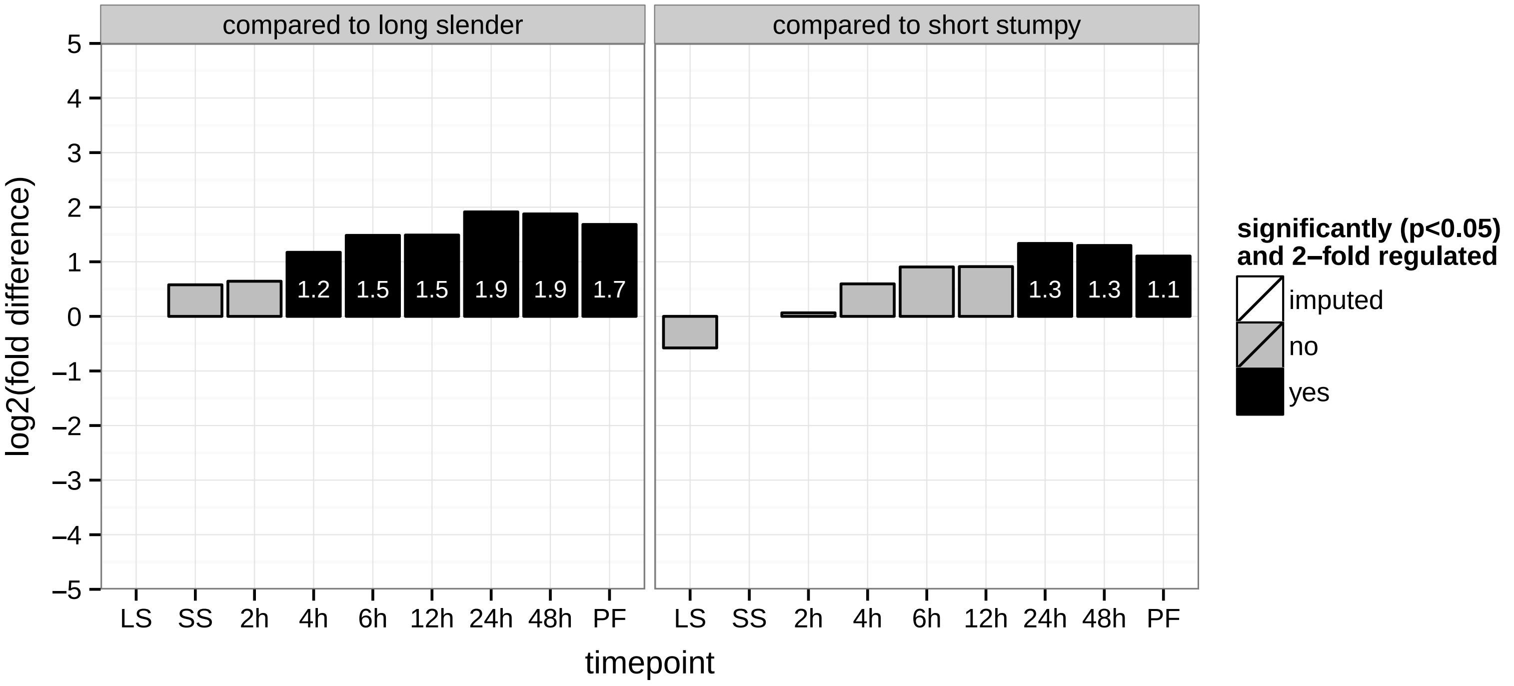
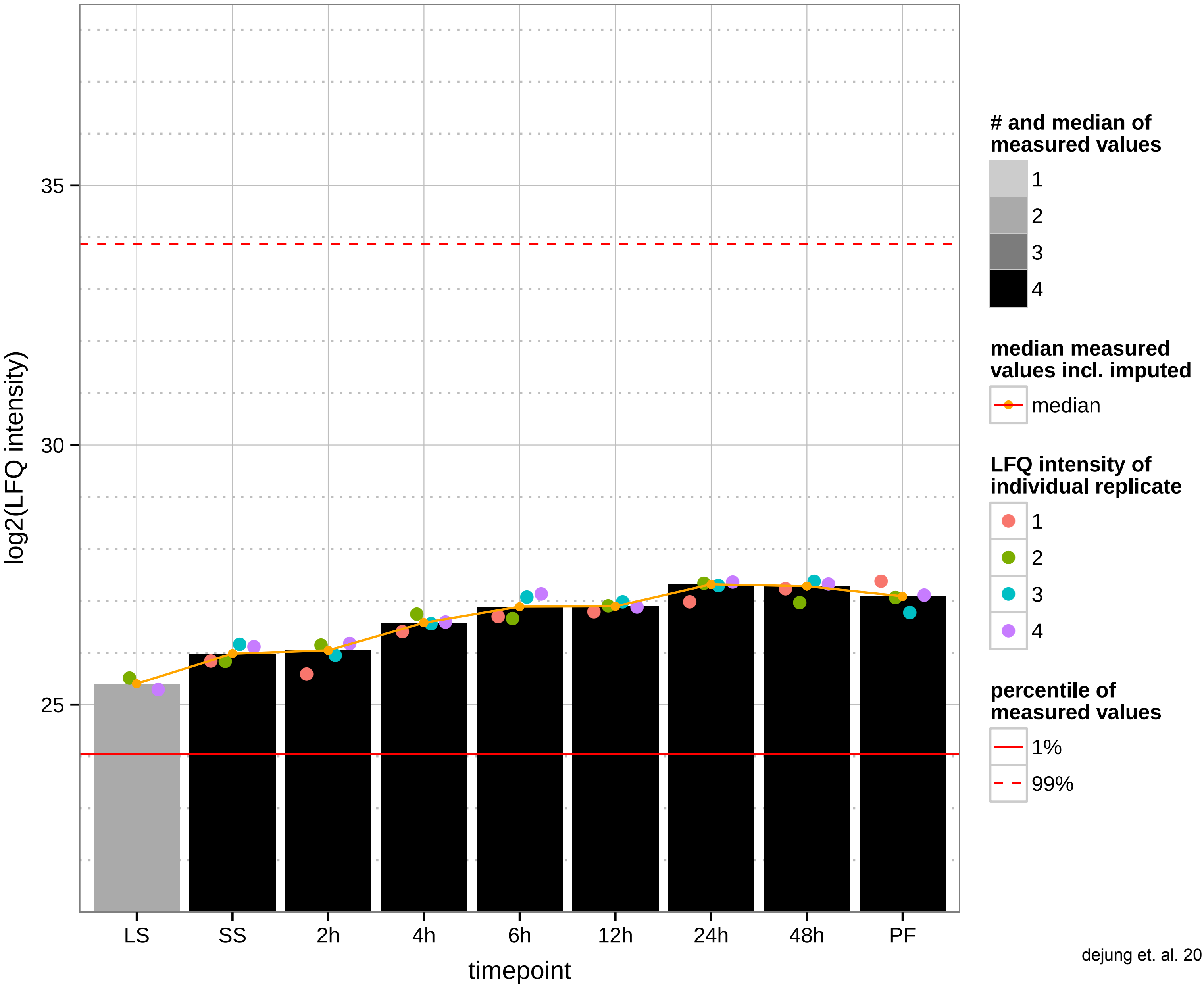
hypothetical protein, conserved
Tb927.9.2120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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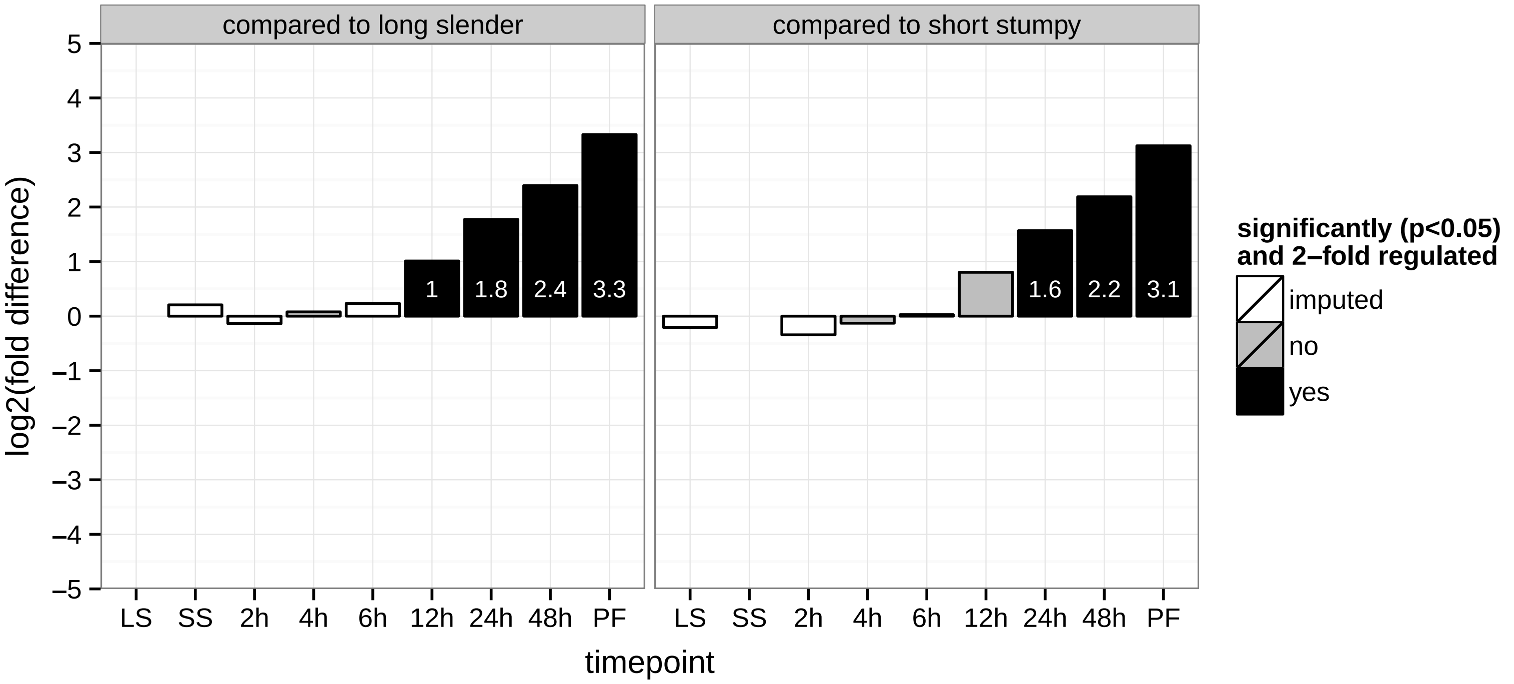
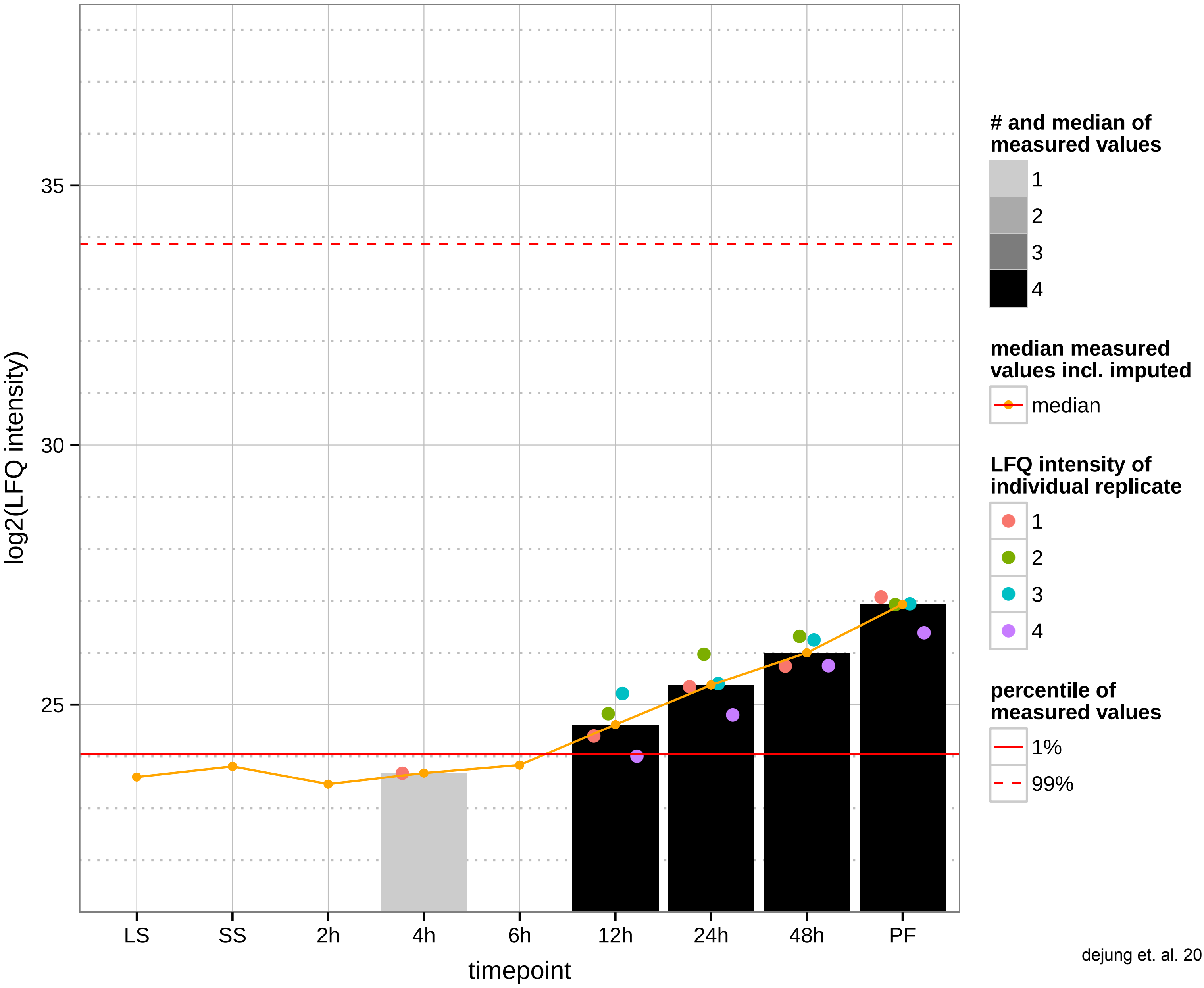
electon transport protein SCO1/SCO2, putative
Tb927.9.2450
AGOF: copper ion binding
AGOC: mitochondrial inner membrane
AGOP: oxidation−reduction process
PGOF: null
PGOC: null
PGOP: null





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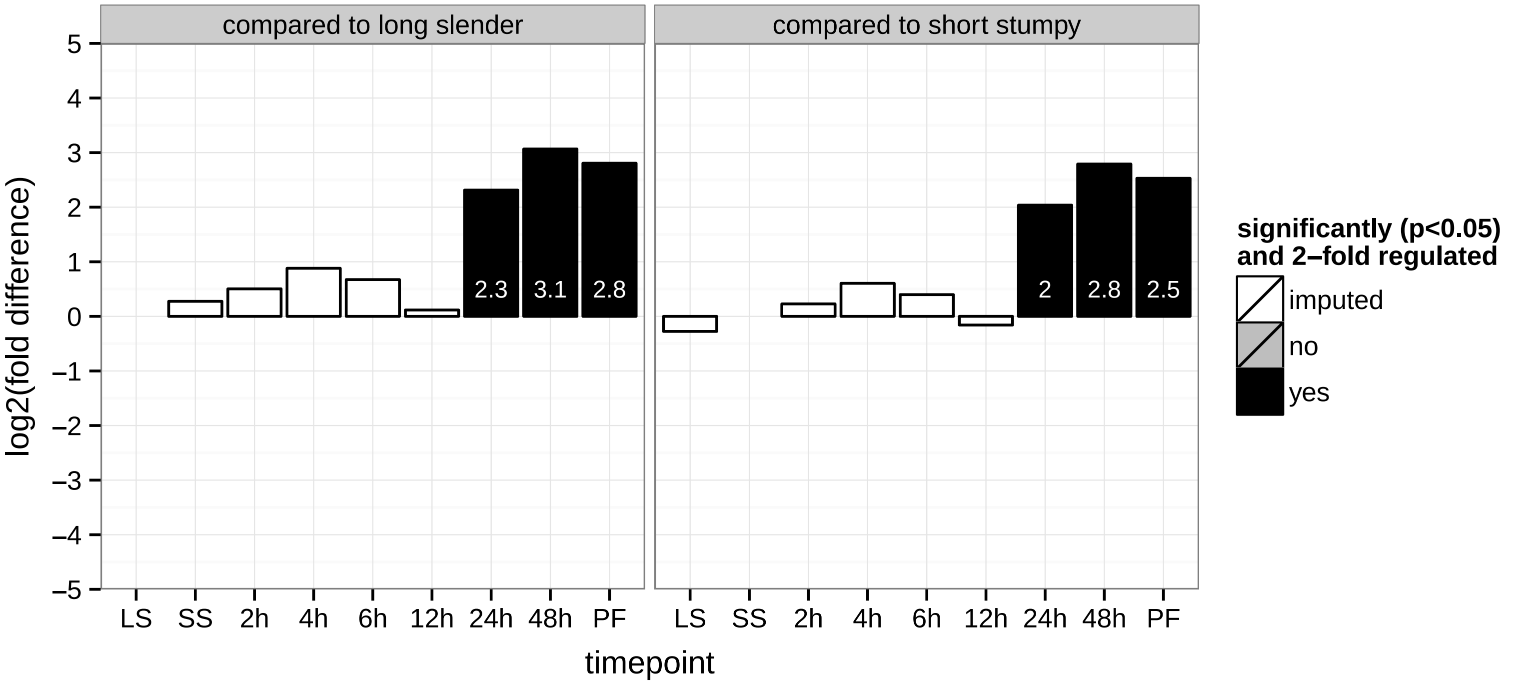
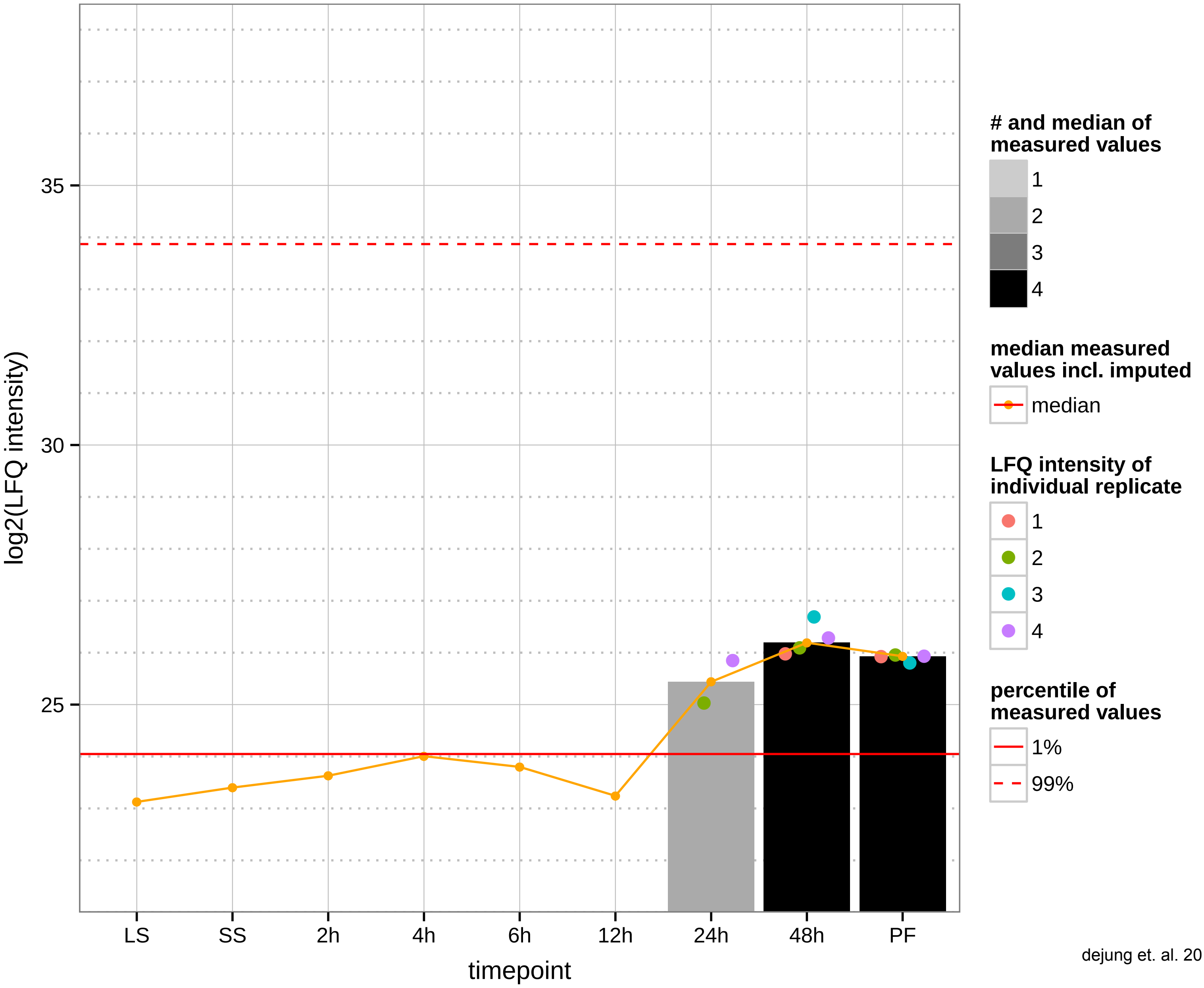
fatty acyl CoA synthetase 2 (ACS2)
Tb927.9.4200
AGOF: fatty–acyl–CoA synthase activity
AGOC: membrane
AGOP: fatty acid metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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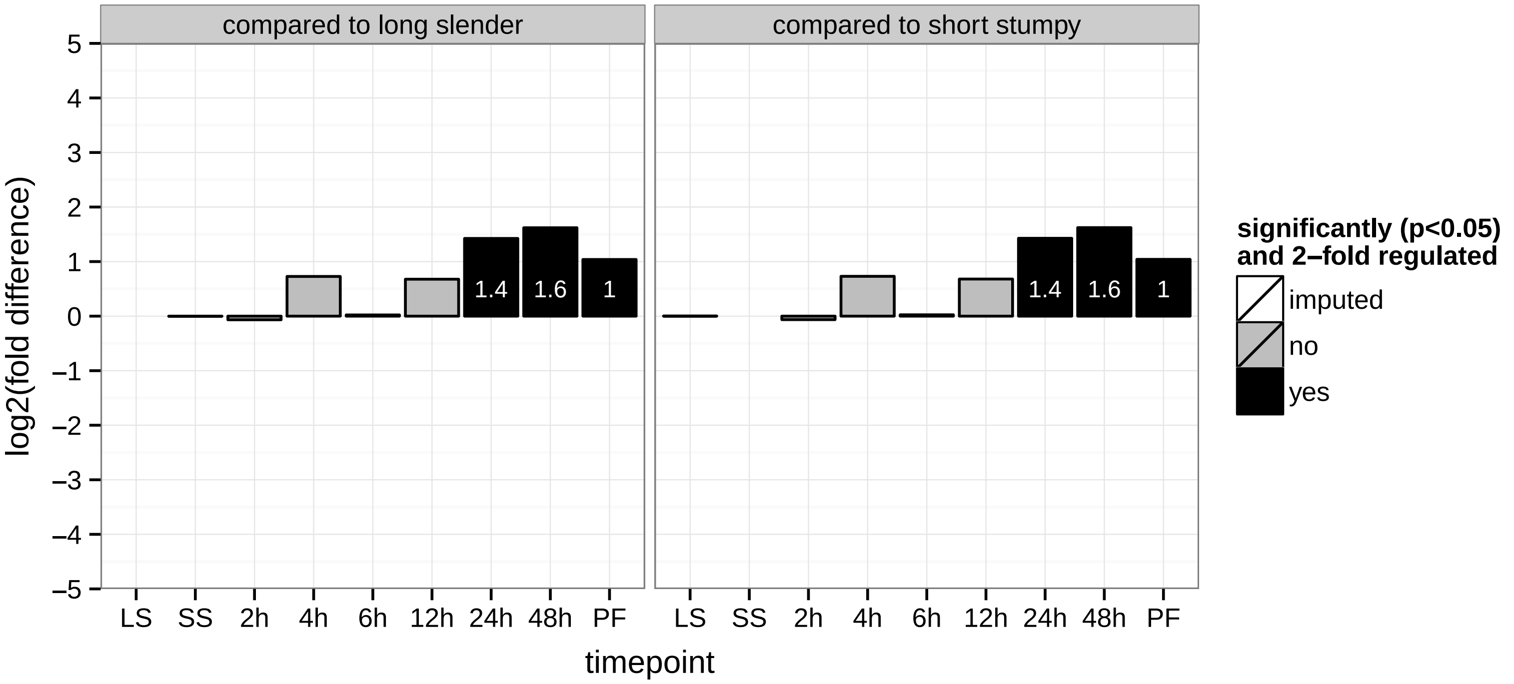
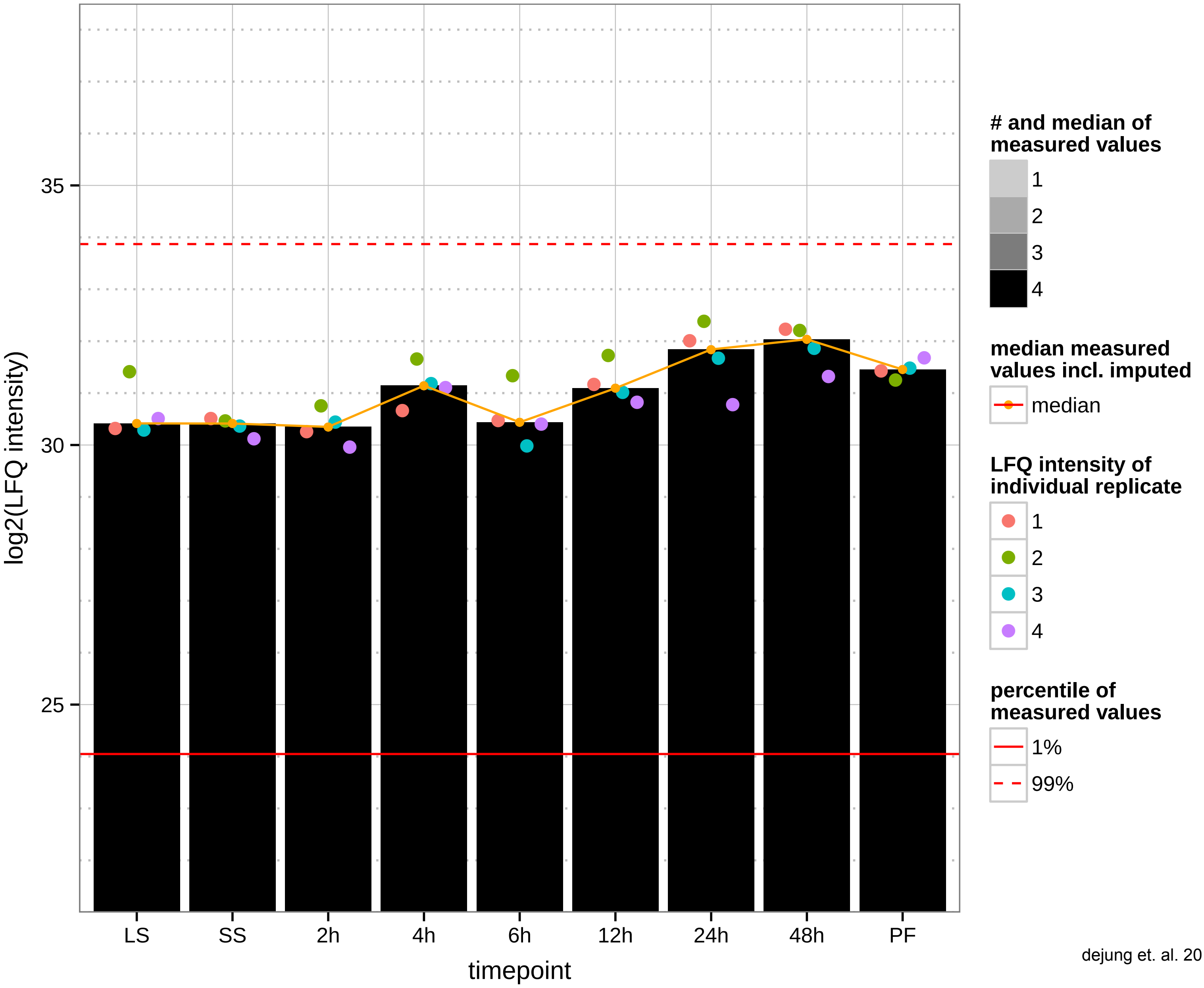
60S acidic ribosomal protein, putative
Tb927.9.5690
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation, translational elongation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translational elongation





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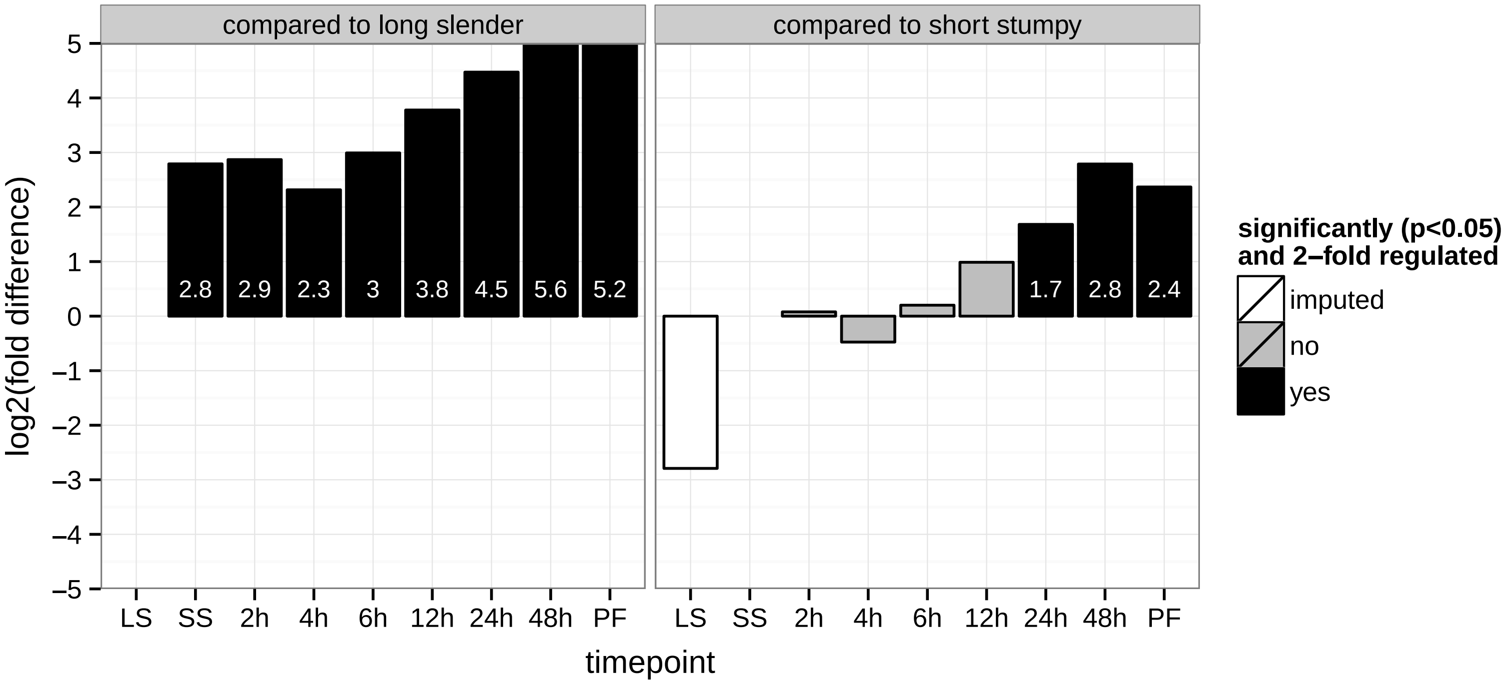
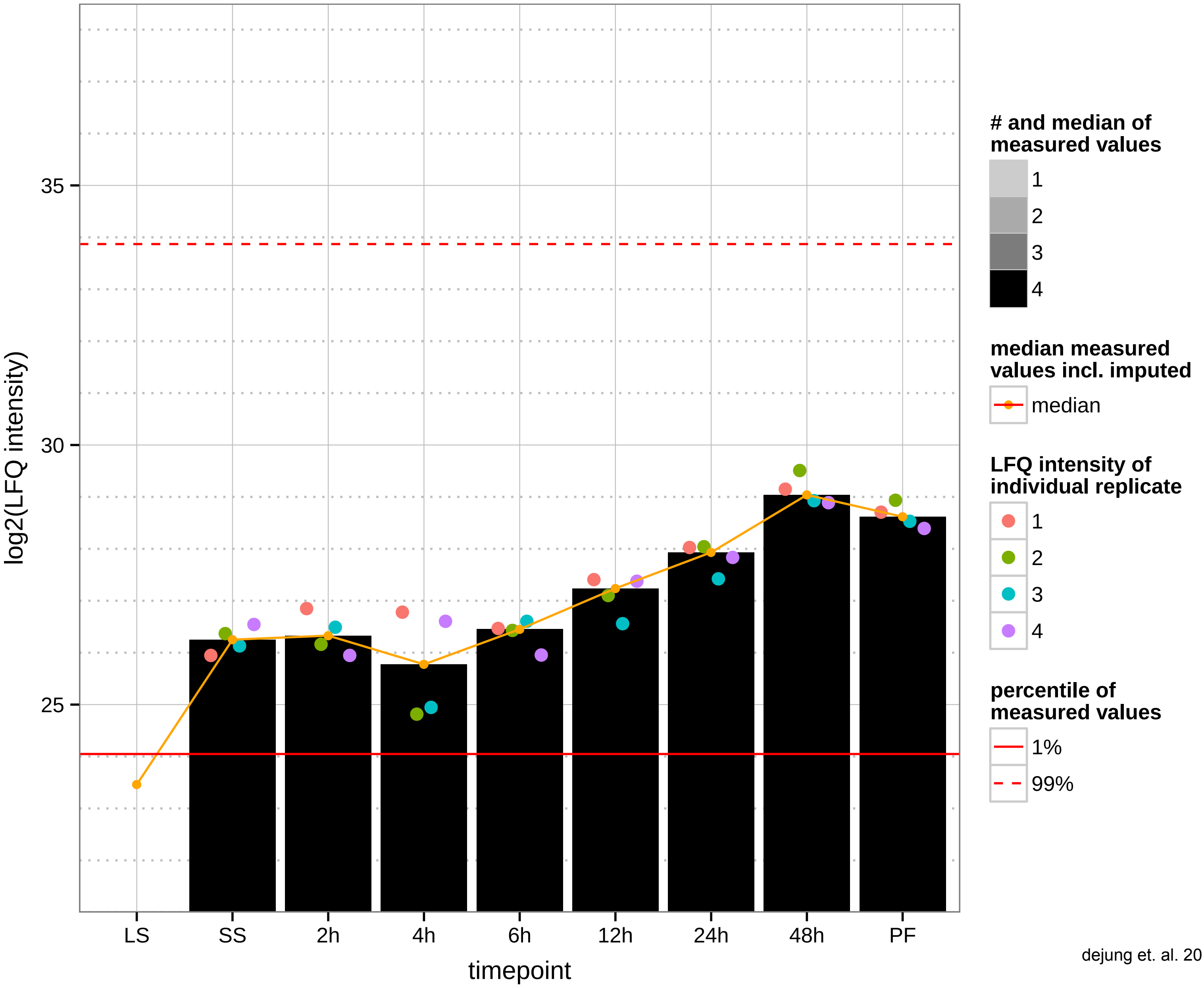
succinate dehydrogenase, putative
Tb927.9.5960
AGOF: iron–sulfur cluster binding, oxidoreductase activity
AGOC: mitochondrion
AGOP: null
PGOF: iron–sulfur cluster binding
PGOC: null
PGOP: null





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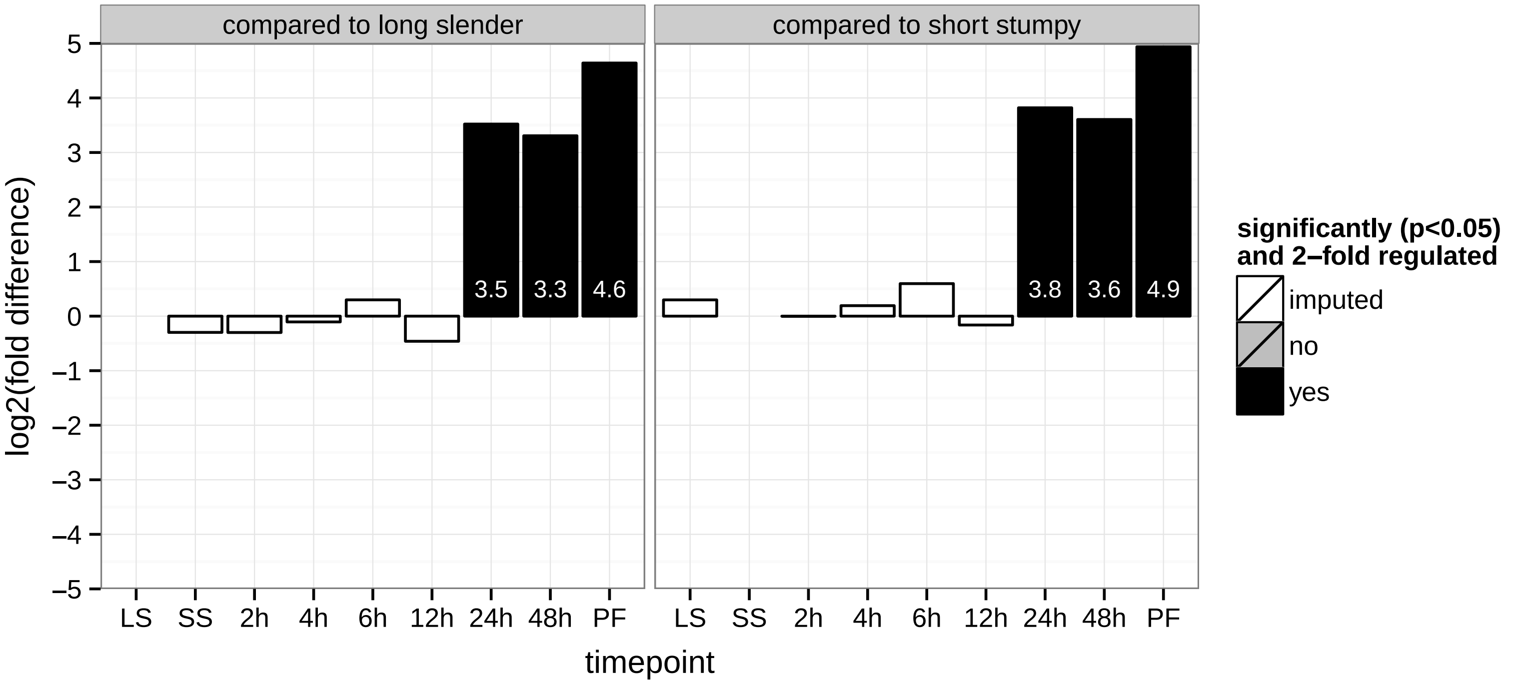
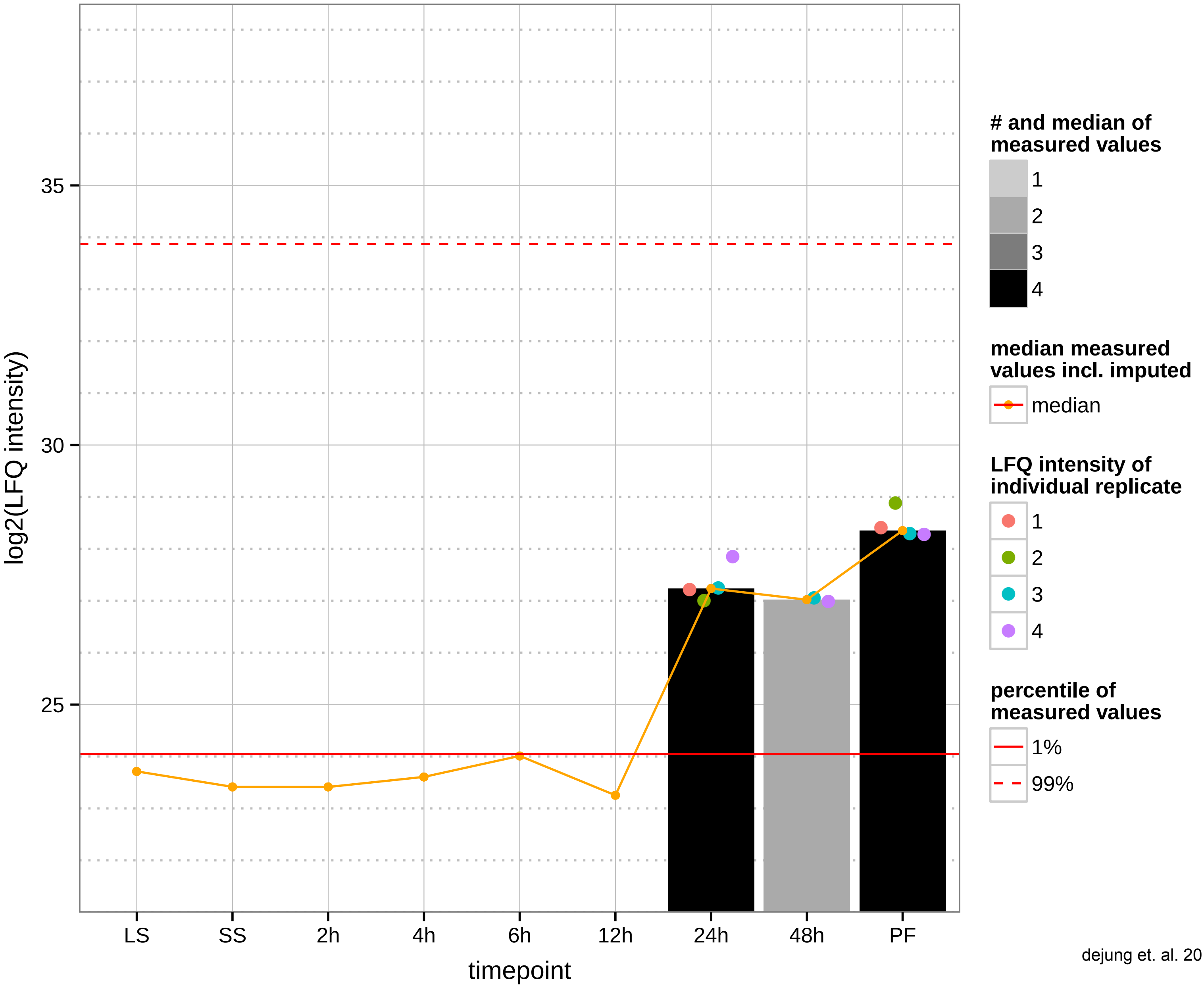
hypothetical protein, conserved
Tb927.9.7830
AGOF: null
AGOC: mitochondrial membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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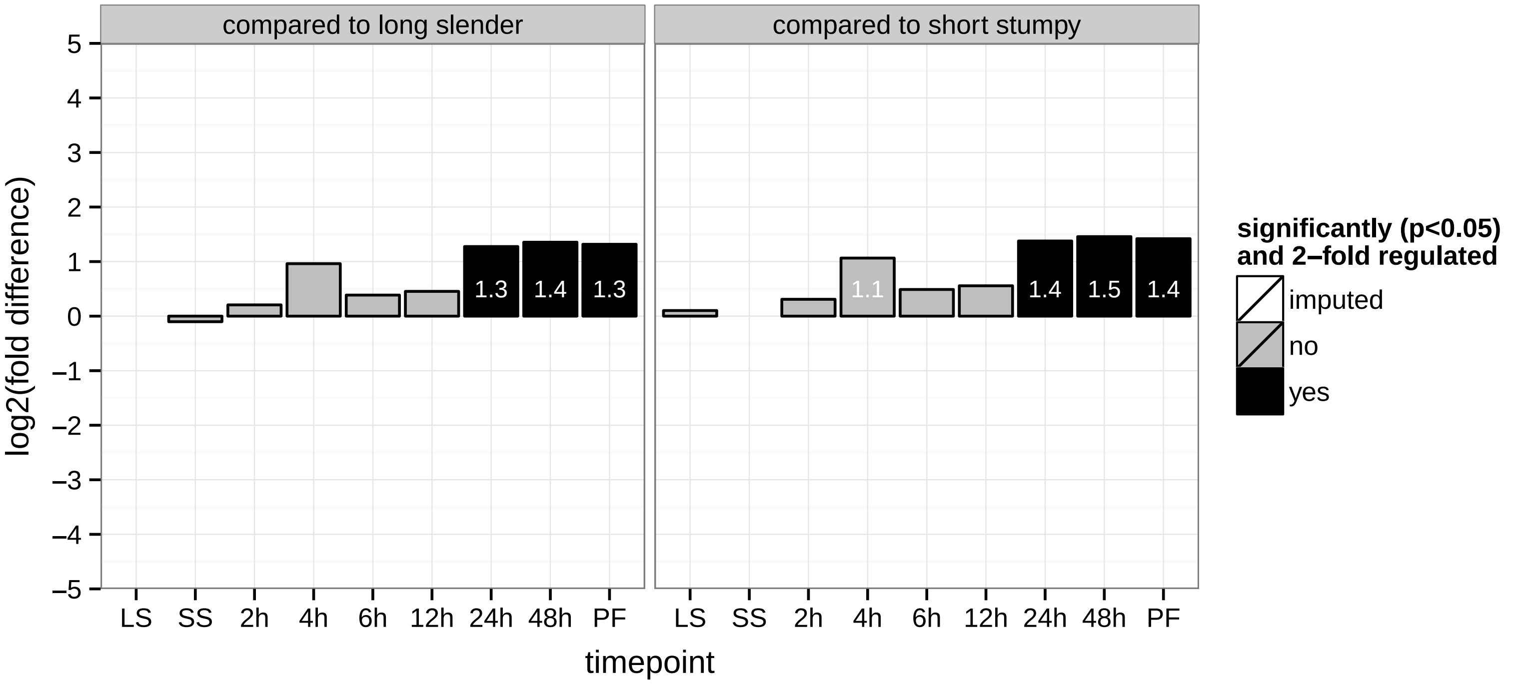
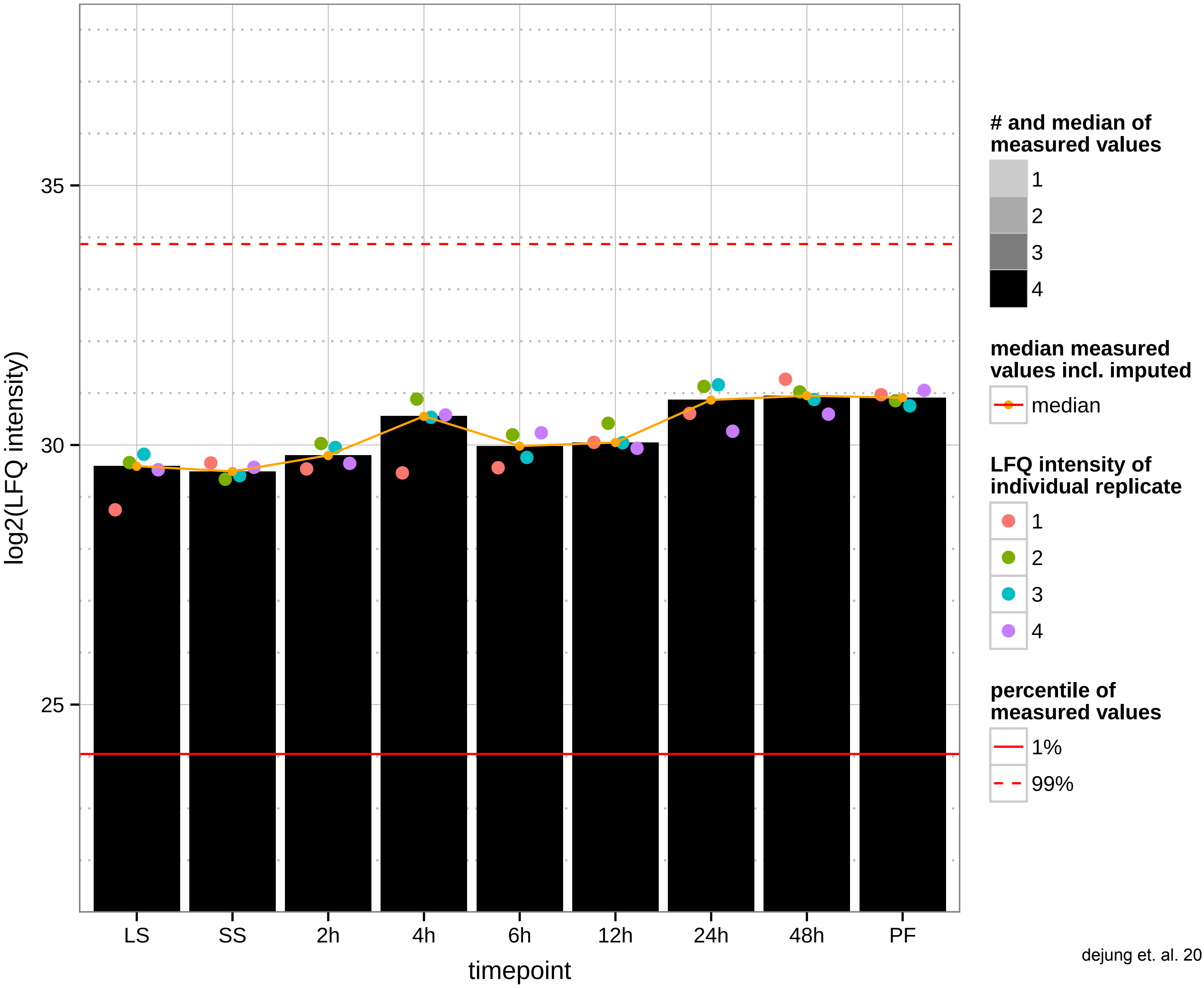
nascent polypeptide associated complex subunit, putative
Tb927.9.8130;Tb927.9.8100
AGOF: transcription coactivator activity
AGOC: nascent polypeptide–associated complex
AGOP: 'de novo' cotranslational protein folding, translation
PGOF: null
PGOC: null
PGOP: null





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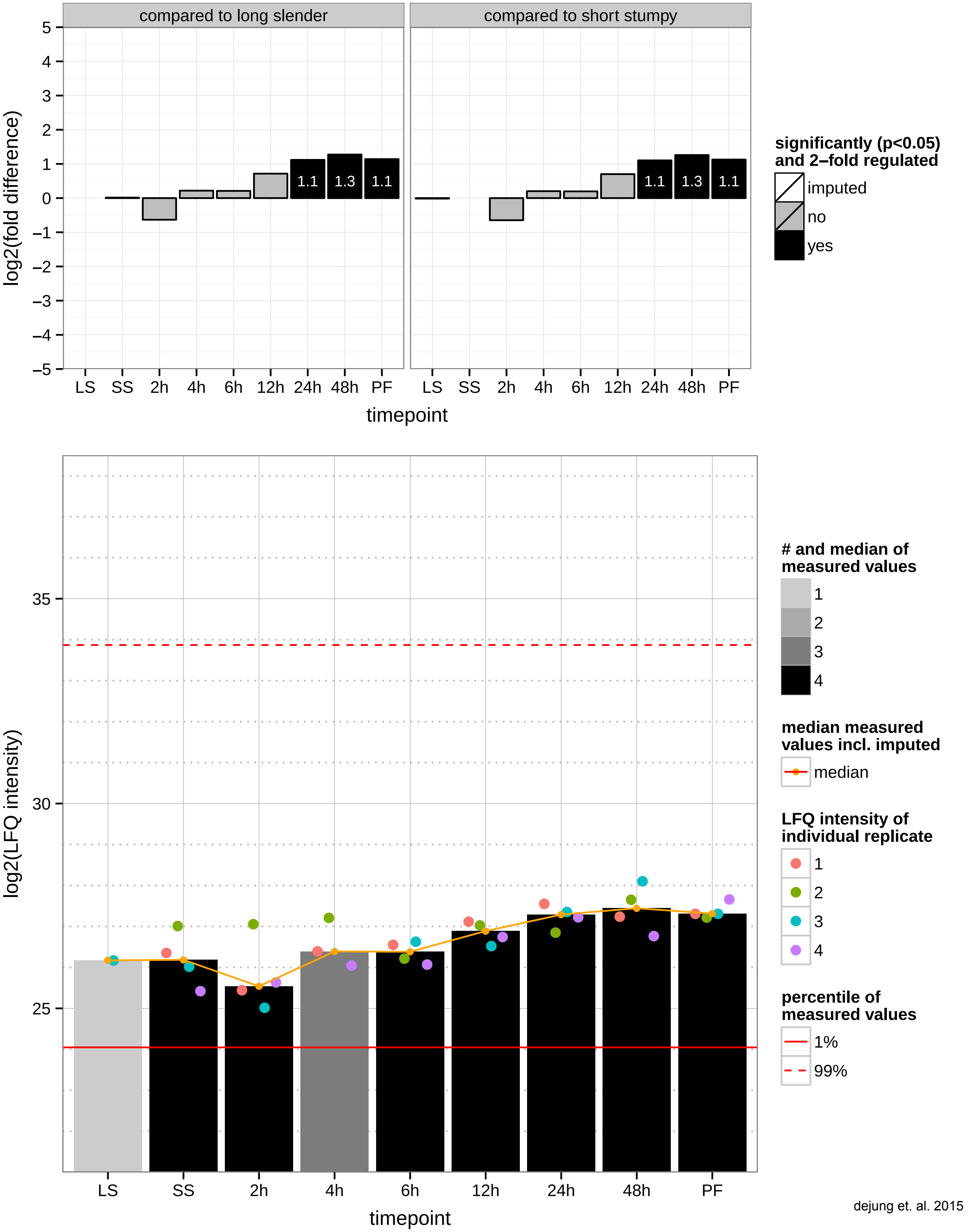
ribosome–interacting GTPase 2, putative (RBG2)
Tb927.9.9020
AGOF: GTP binding
AGOC: cytoplasm, intracellular
AGOP: cytoplasmic translation
PGOF: GTP binding
PGOC: null
PGOP: null



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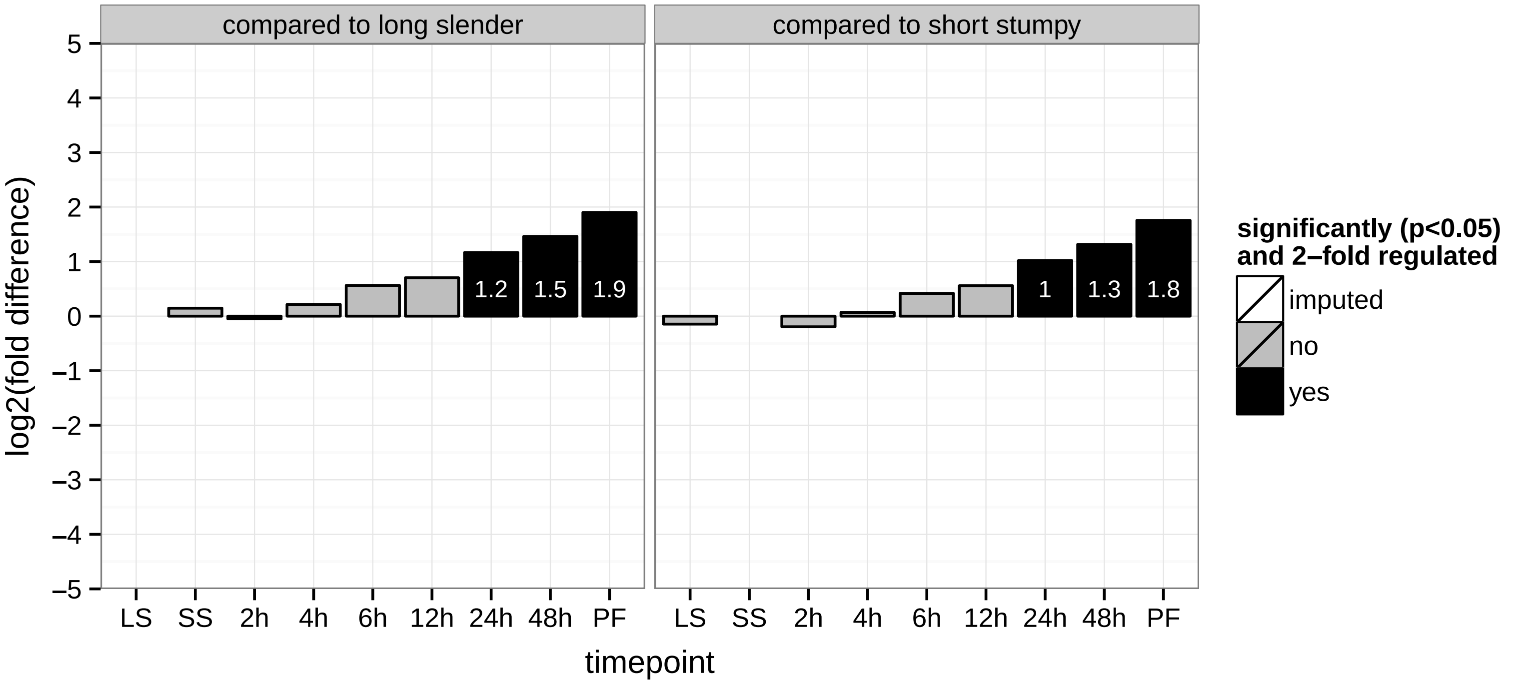
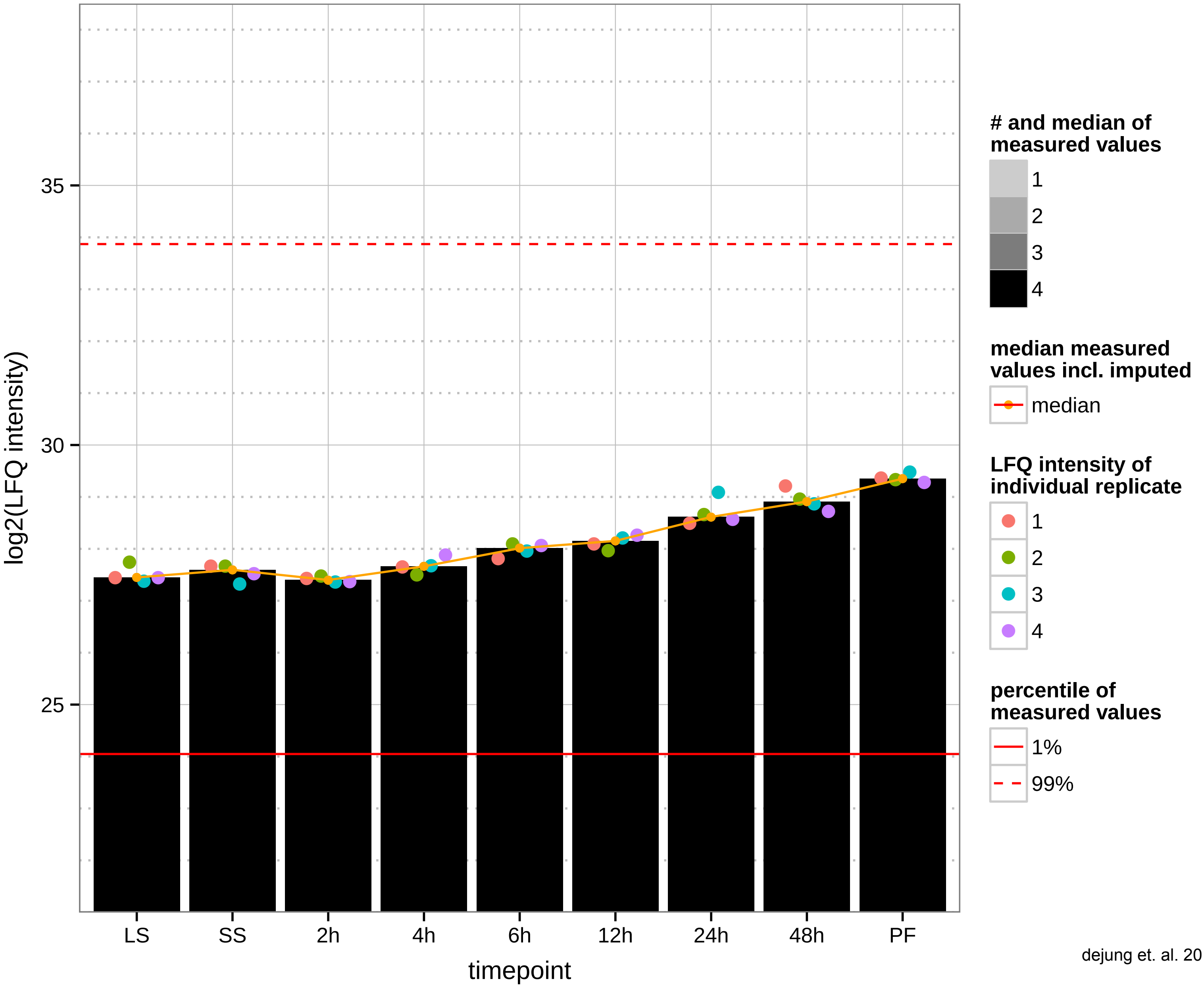
zinc finger protein family member, putative (ZC3H28)
Tb927.9.9450
AGOF: RNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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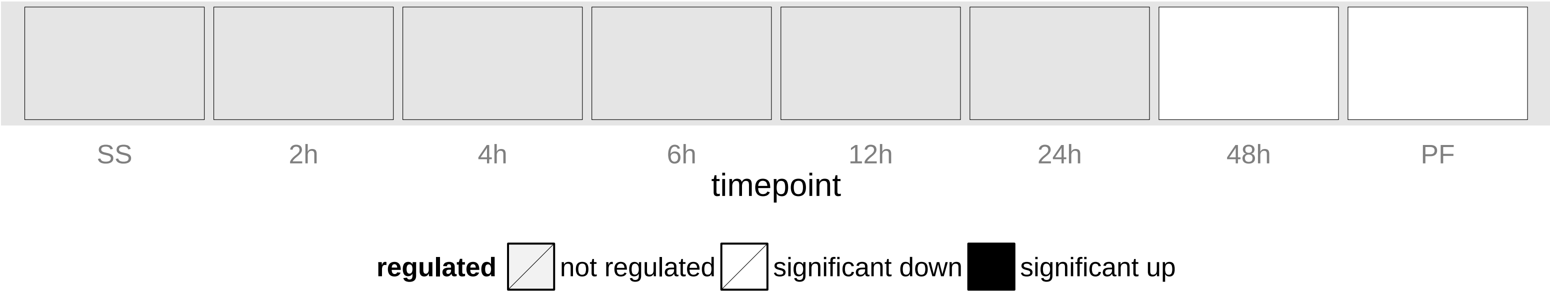

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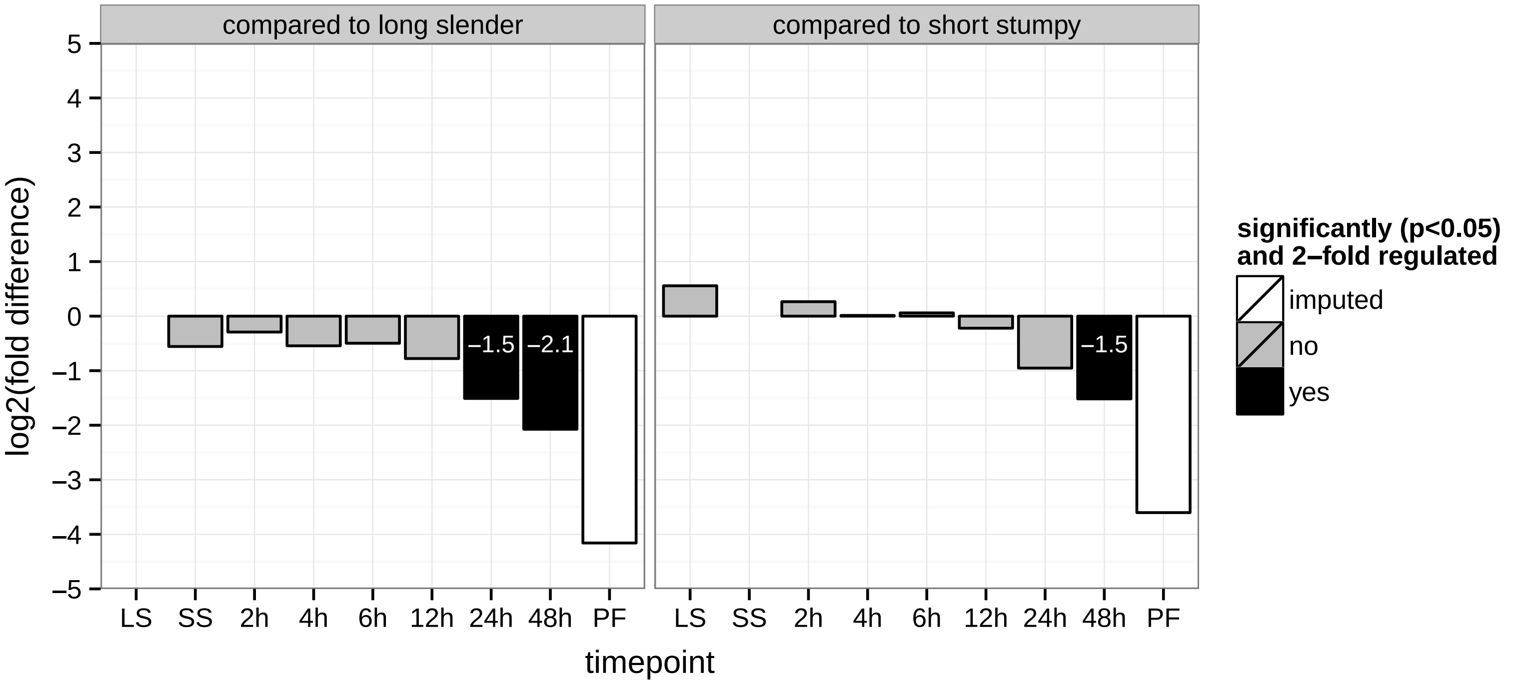
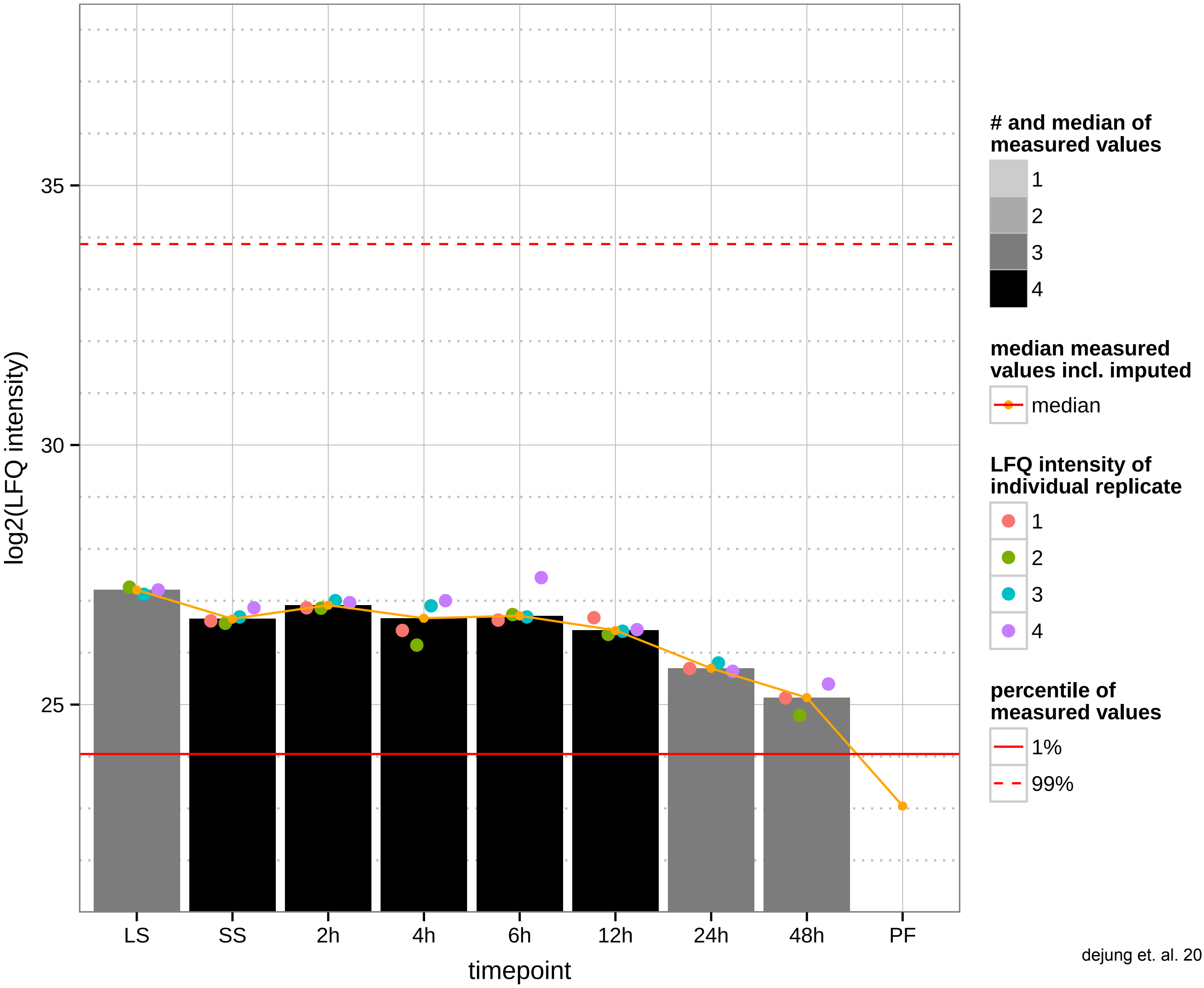
hypothetical protein, BAC from homologous region on chr5, conserved
Tb927.5.4570;Tb05.5K5.210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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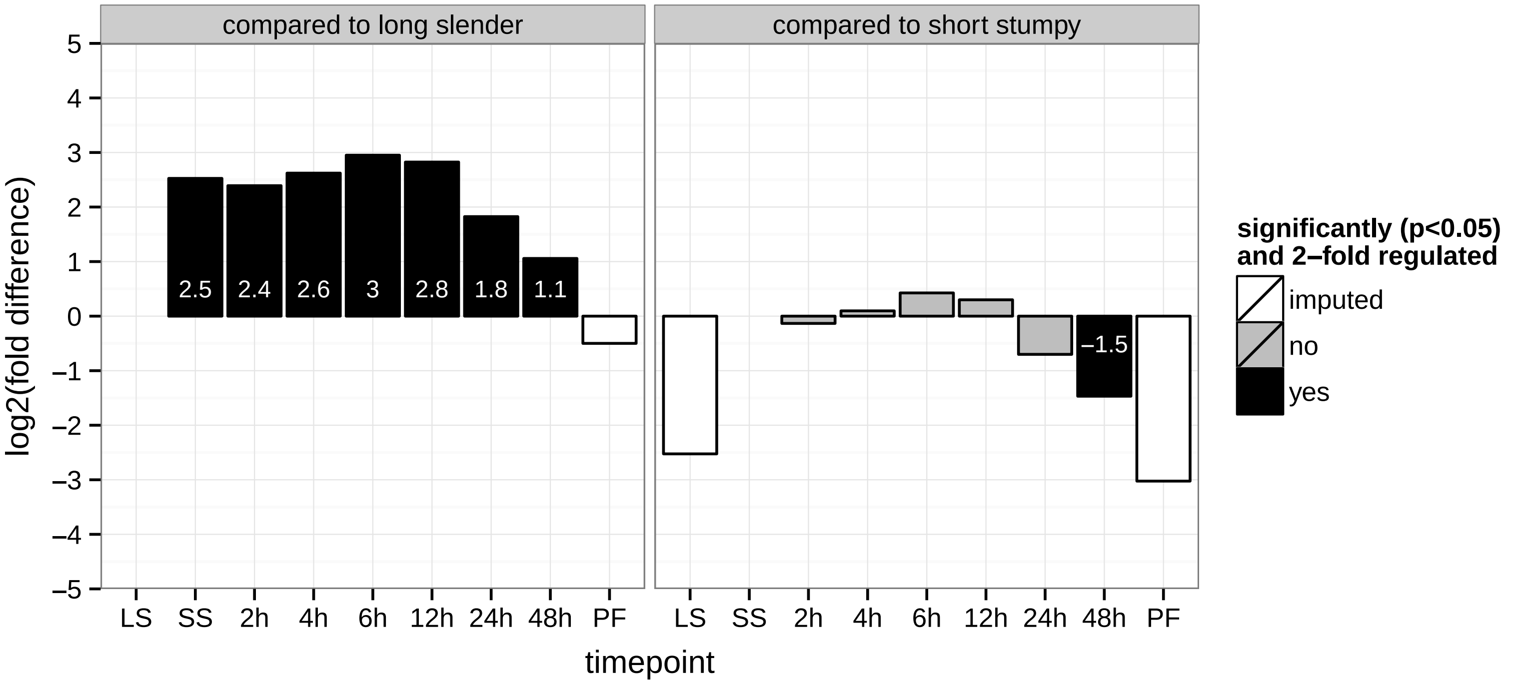
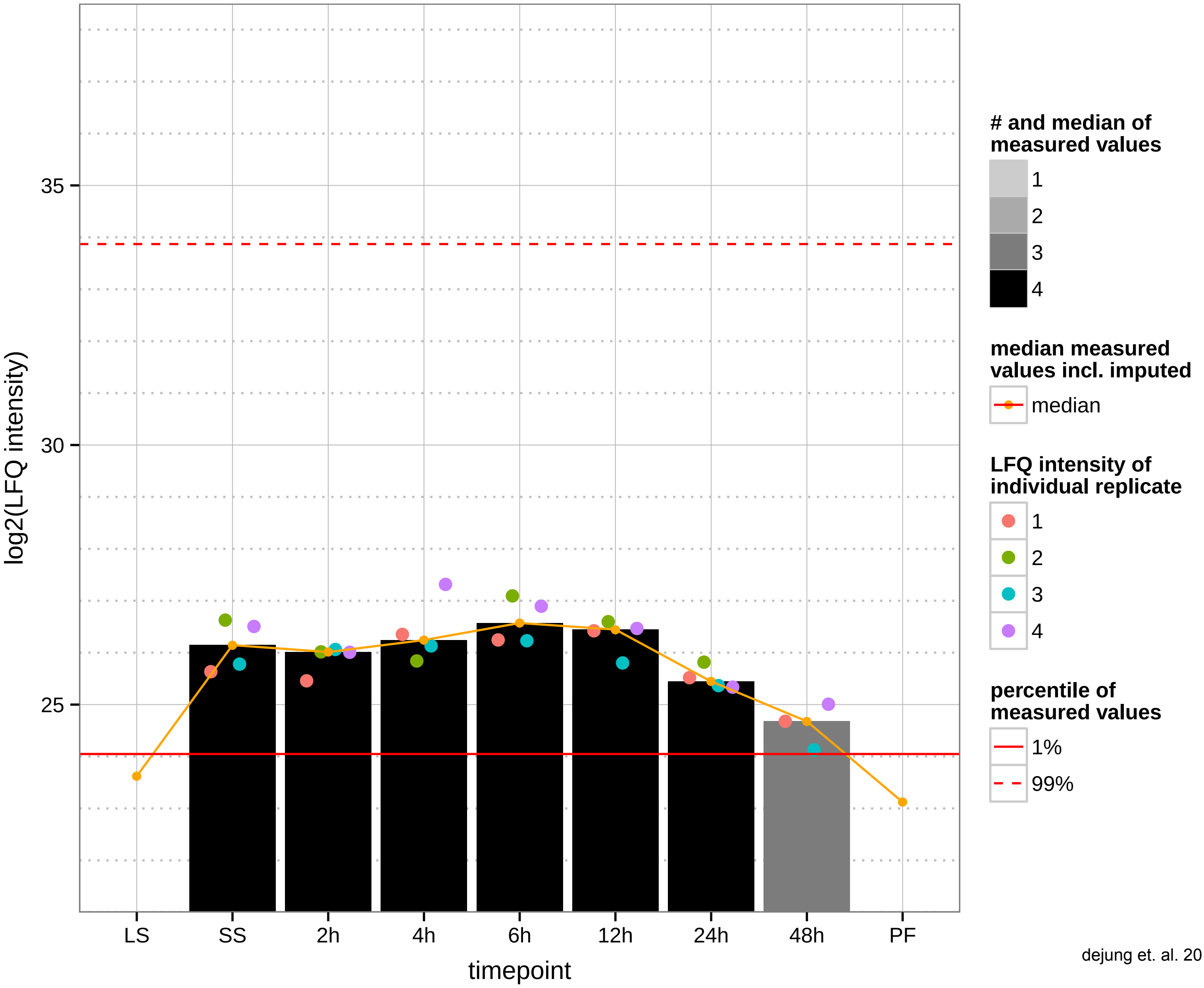
hypothetical protein, chrIX additional, unordered contigs
Tb927.9.15870;Tb09.v4.0015
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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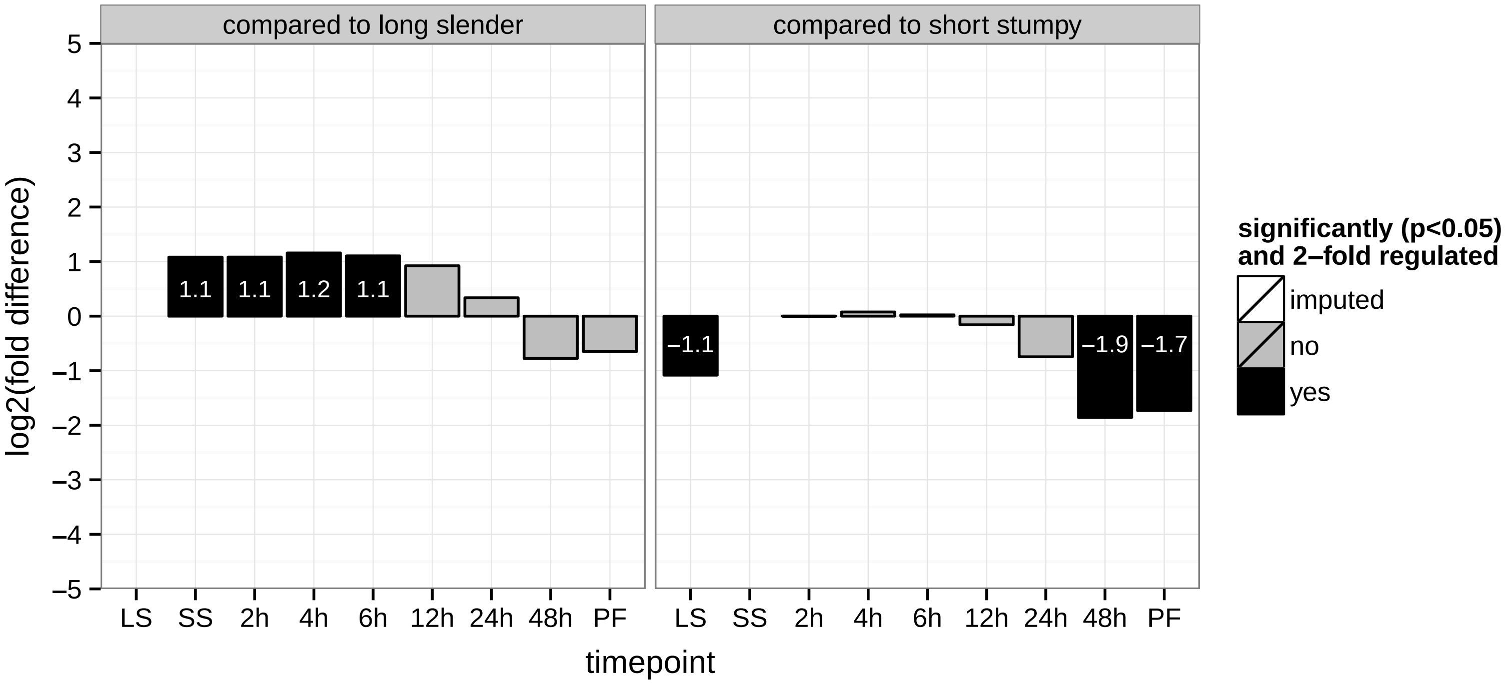
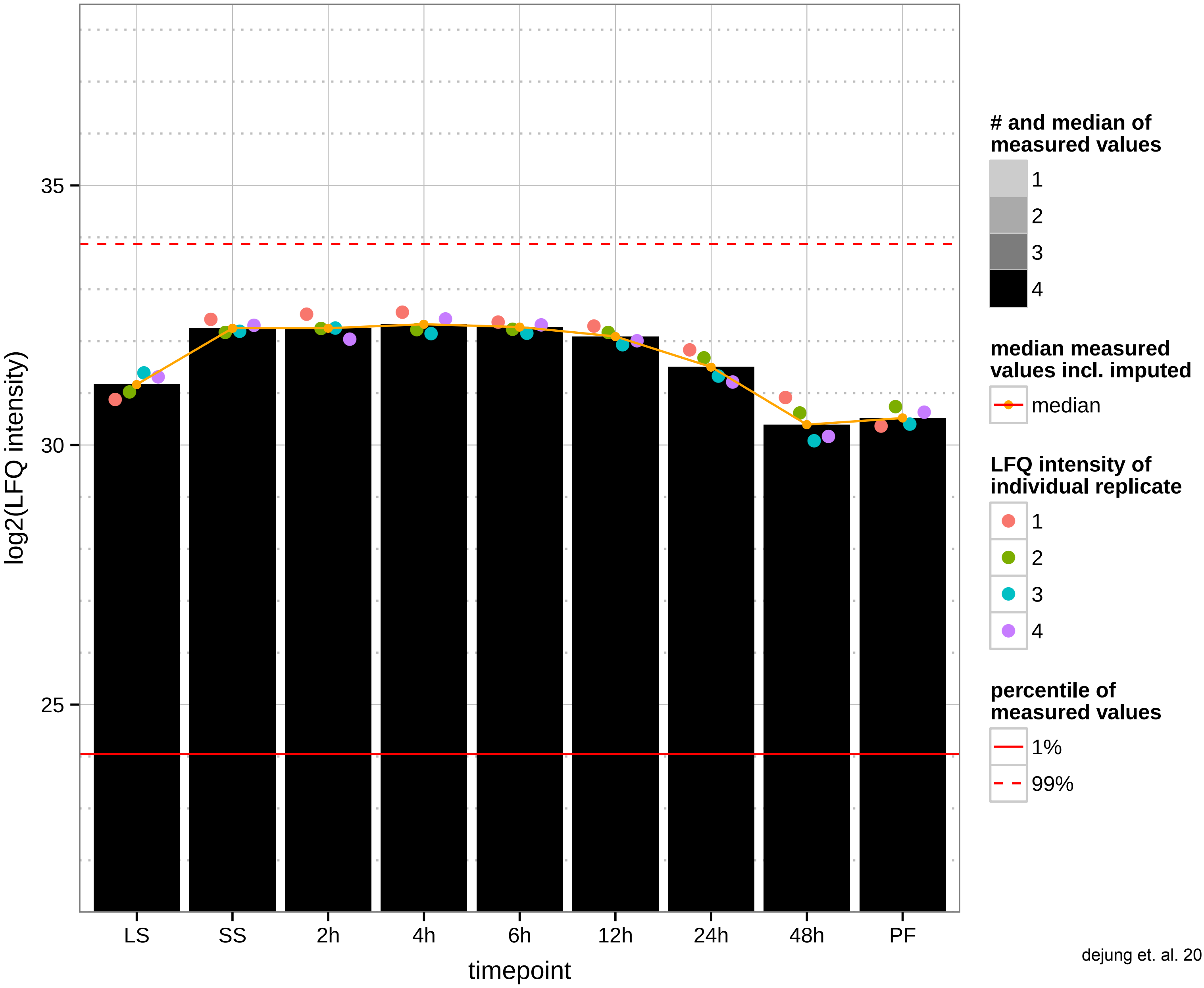
hypothetical protein, conserved
Tb927.7.4500;Tb11.v5.0263
AGOF: null, phosphatidylinositol binding
AGOC: null
AGOP: null, cell communication
PGOF: phosphatidylinositol binding, protein binding
PGOC: null
PGOP: cell communication





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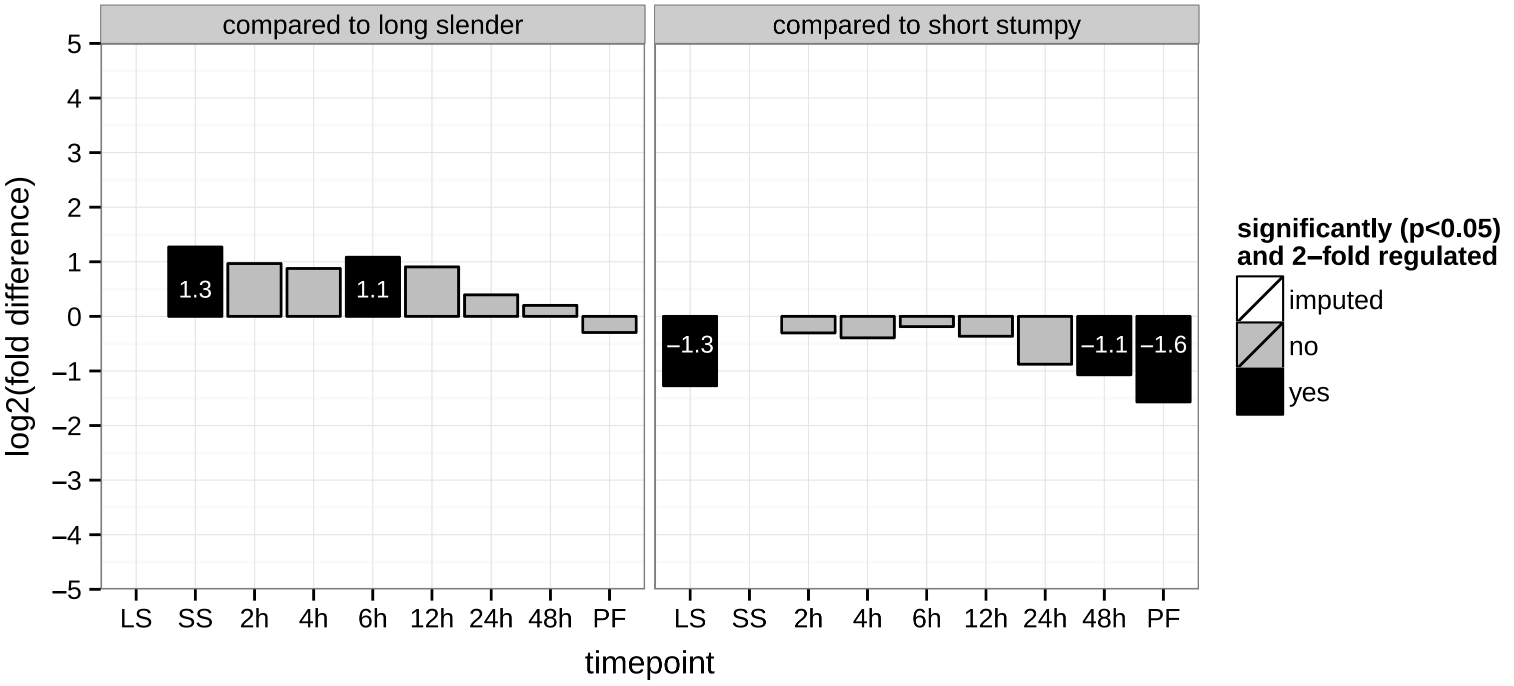
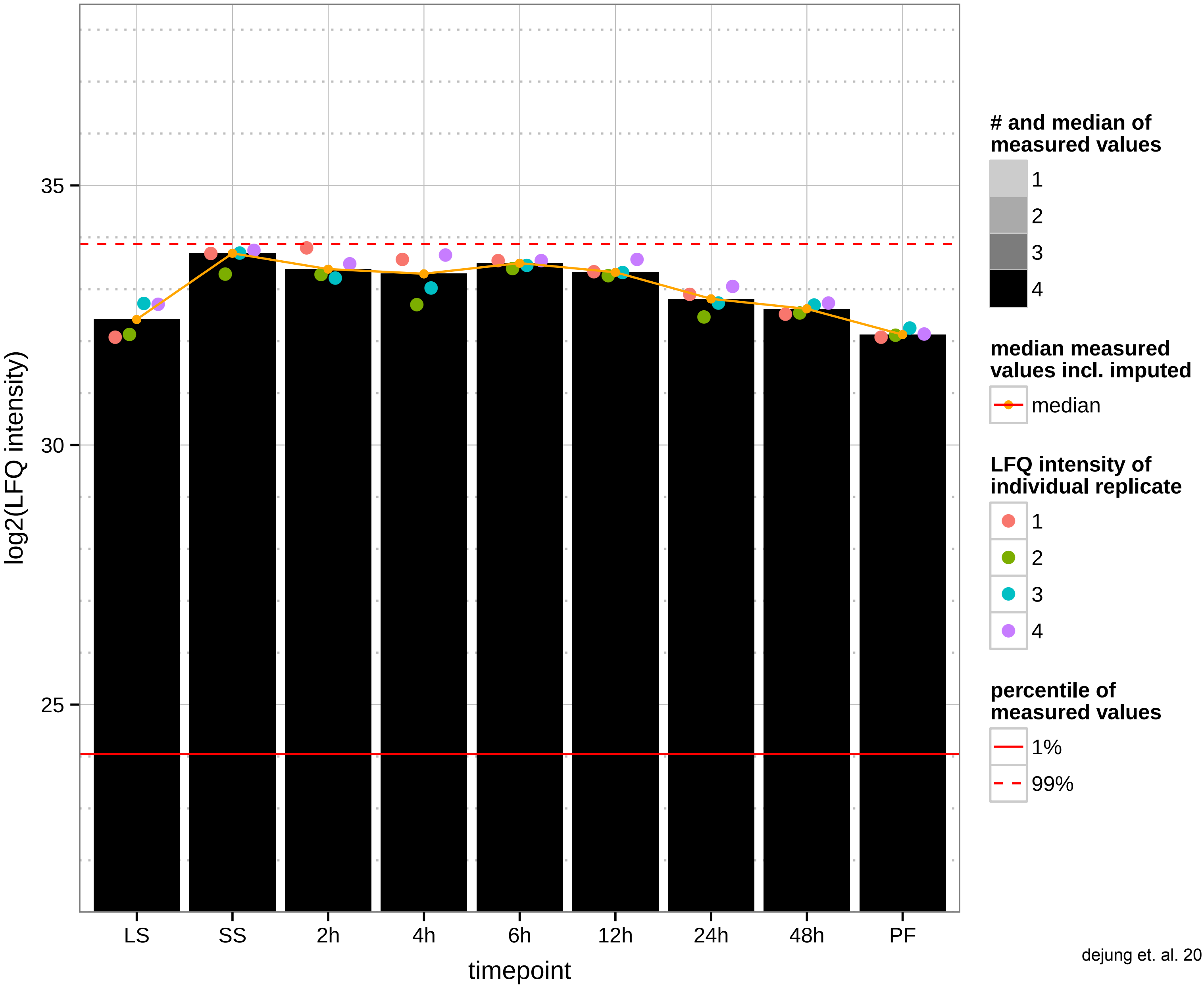
adenylosuccinate synthetase, putative
Tb927.11.3650;Tb11.v5.0435
AGOF: null, GTP binding, adenylosuccinate synthase activity, magnesium ion binding
AGOC: null
AGOP: null, purine nucleotide biosynthetic process
PGOF: GTP binding, adenylosuccinate synthase activity, magnesium ion binding
PGOC: cytoplasm
PGOP: purine nucleotide biosynthetic process





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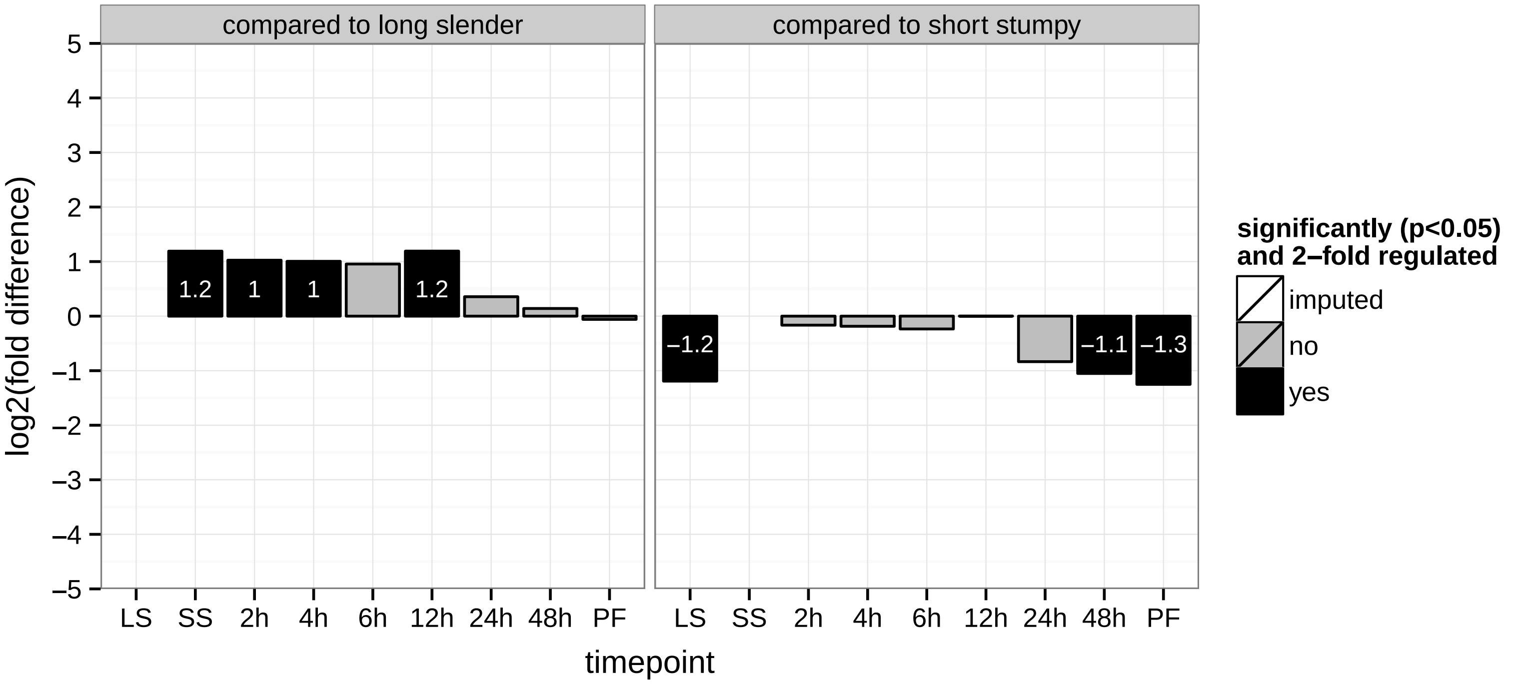
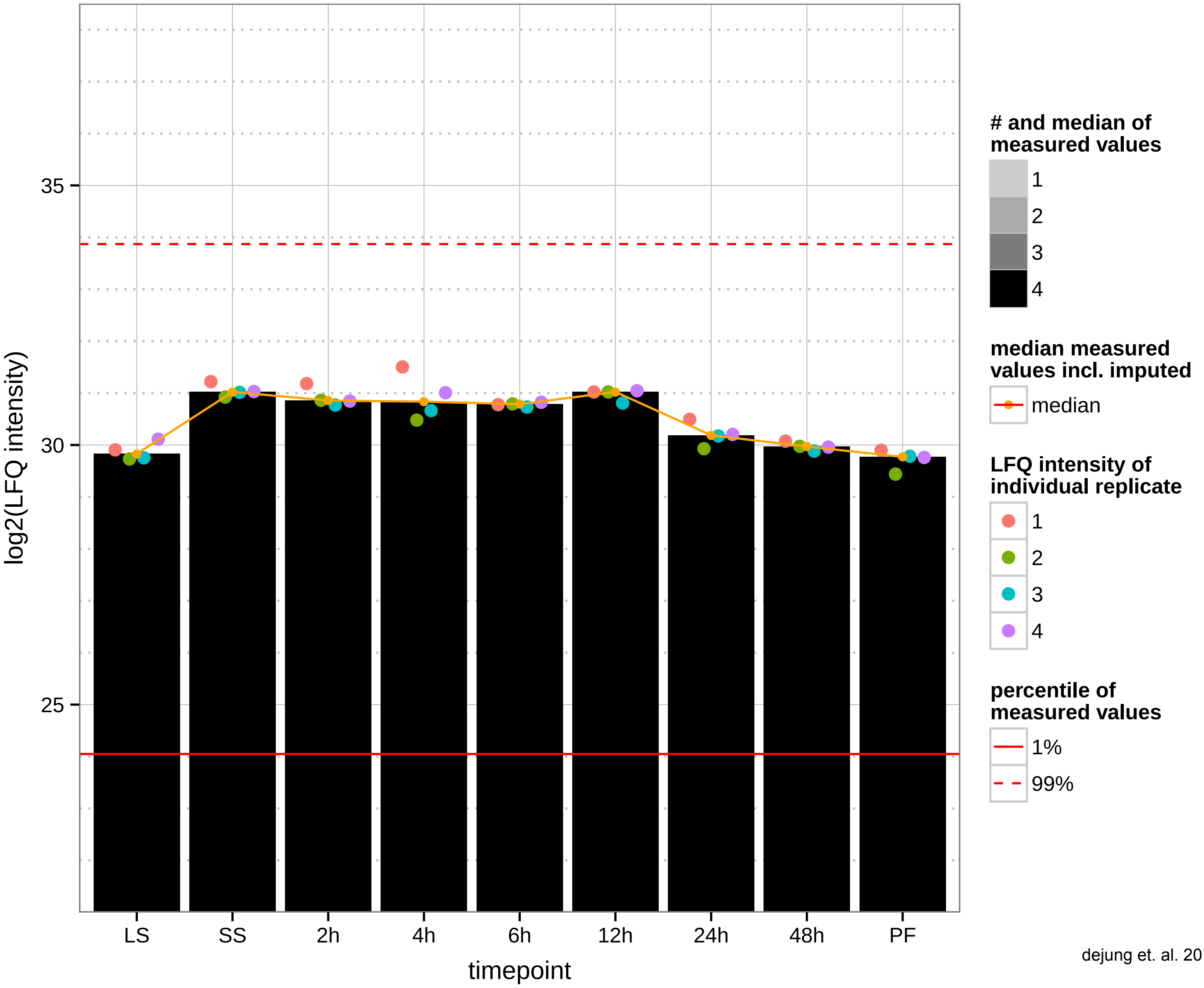
vesicular−fusion protein nsf, putative, N−ethylmaleimide sensitive factor (NsF)
Tb927.1.1560;Tb11.v5.0464
AGOF: null, ATP binding, ATPase activity
AGOC: null
AGOP: null, exocytosis
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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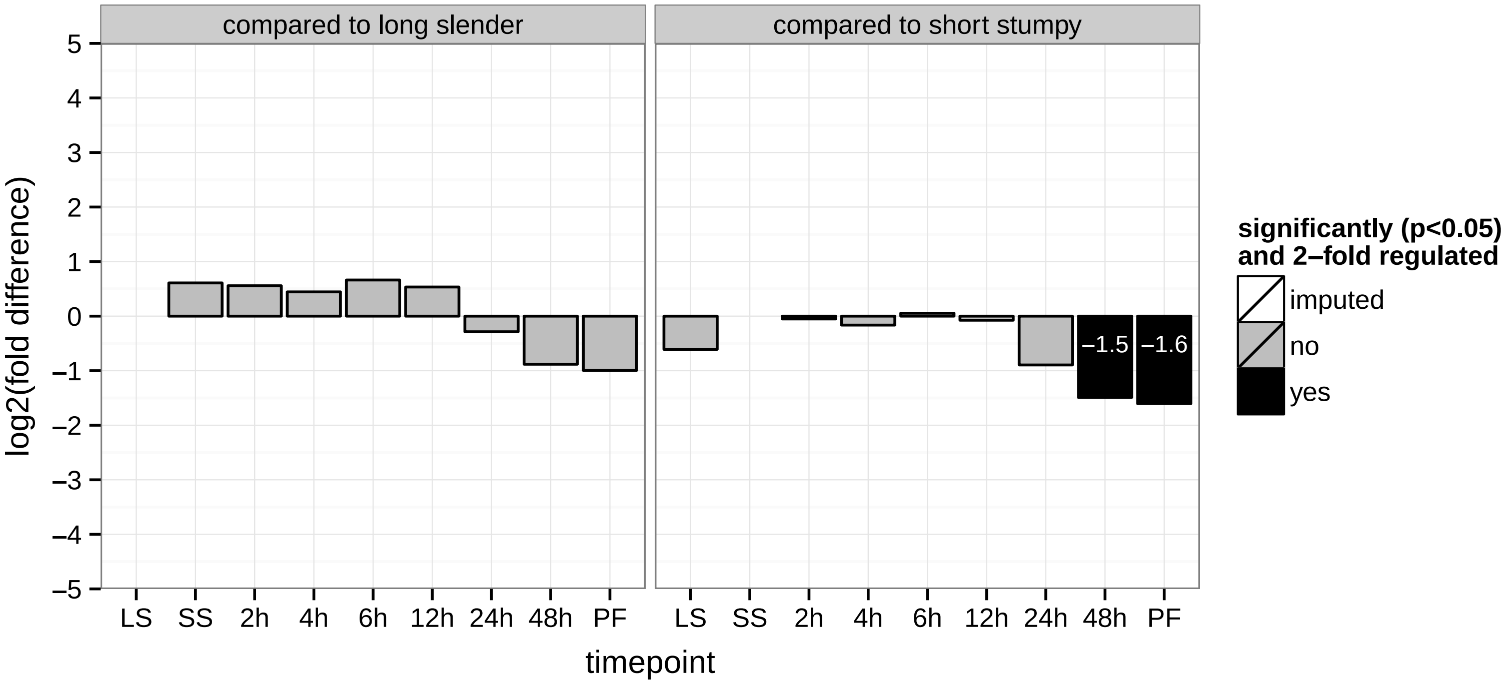
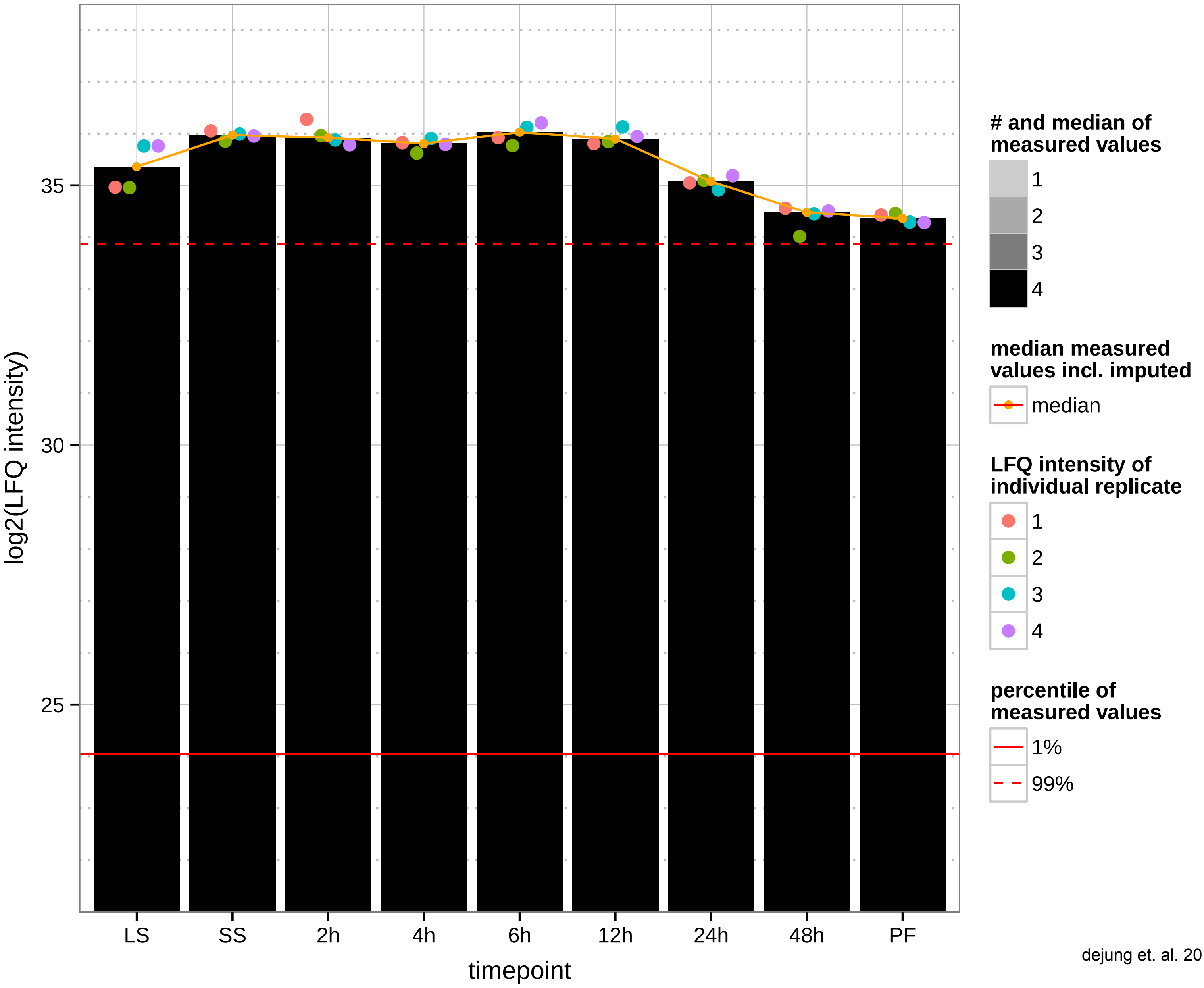
fructose–bisphosphate aldolase, glycosomal, putative, glycosomal (ALD)
Tb927.10.5620;Tb11.v5.0531
AGOF: null, fructose–bisphosphate aldolase activity
AGOC: null, glycosome
AGOP: null, glycolysis
PGOF: fructose–bisphosphate aldolase activity
PGOC: null
PGOP: glycolysis





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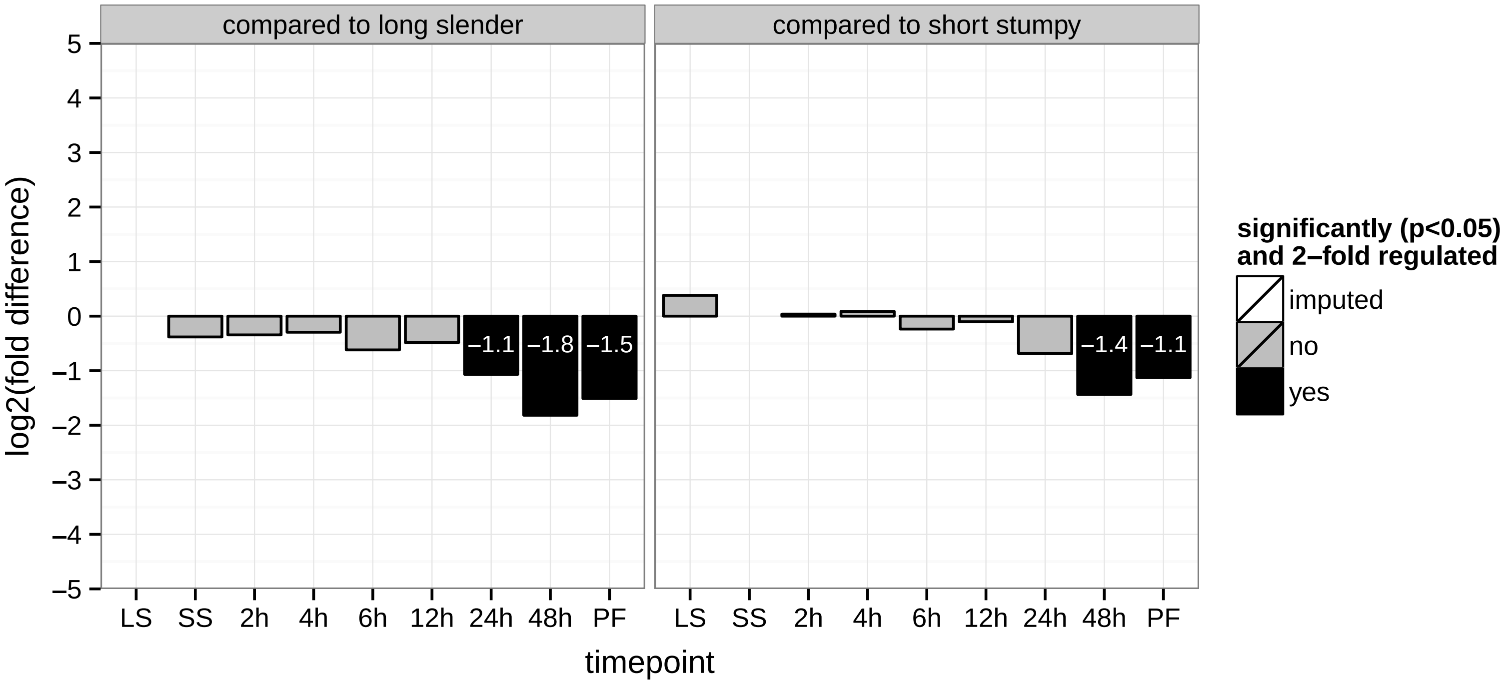
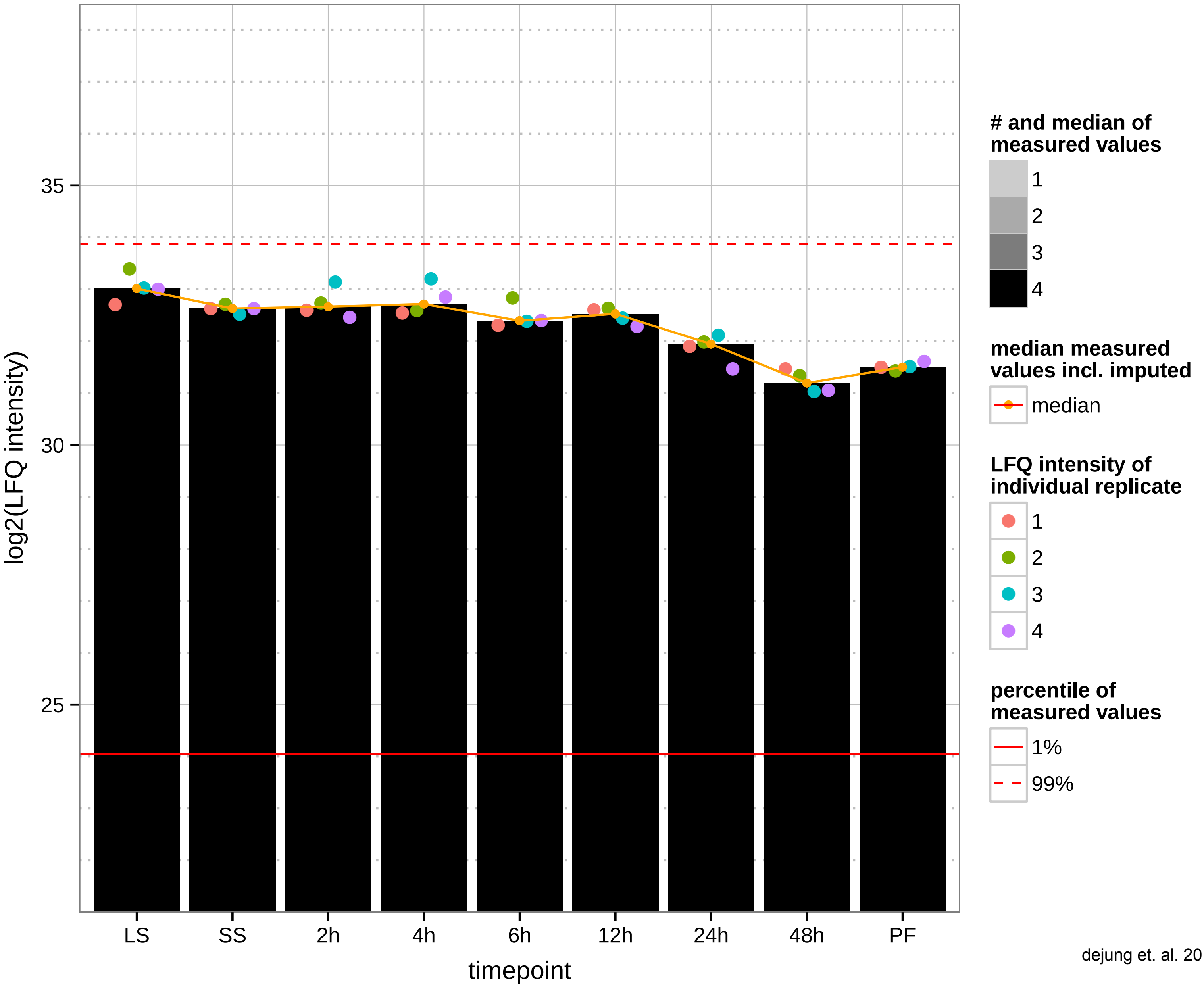
protein disulfide isomerase, bloodstream– specific protein 2 precursor
Tb927.10.8230;Tb11.v5.0668
AGOF: null, protein disulfide isomerase activity
AGOC: null, cytoplasm
AGOP: null, cell redox homeostasis, protein folding
PGOF: isomerase activity
PGOC: null
PGOP: cell redox homeostasis





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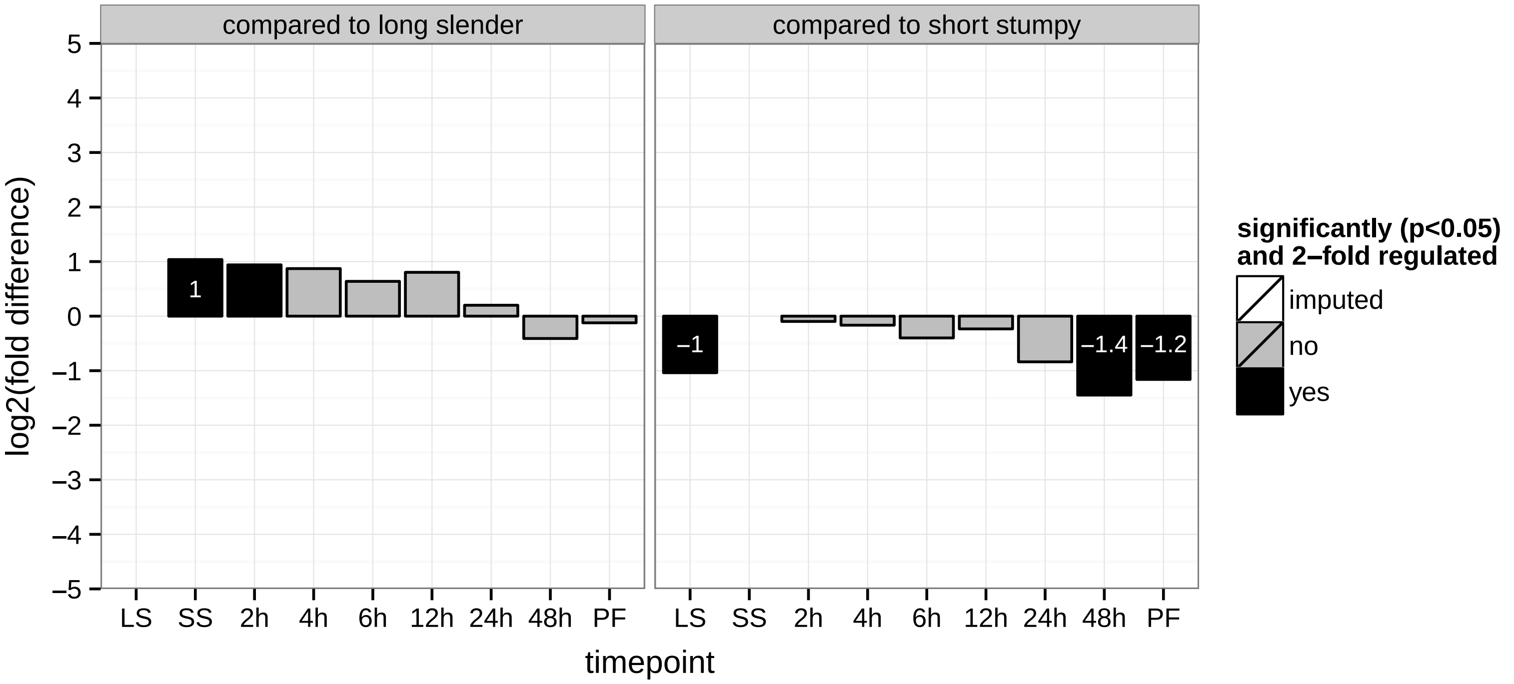
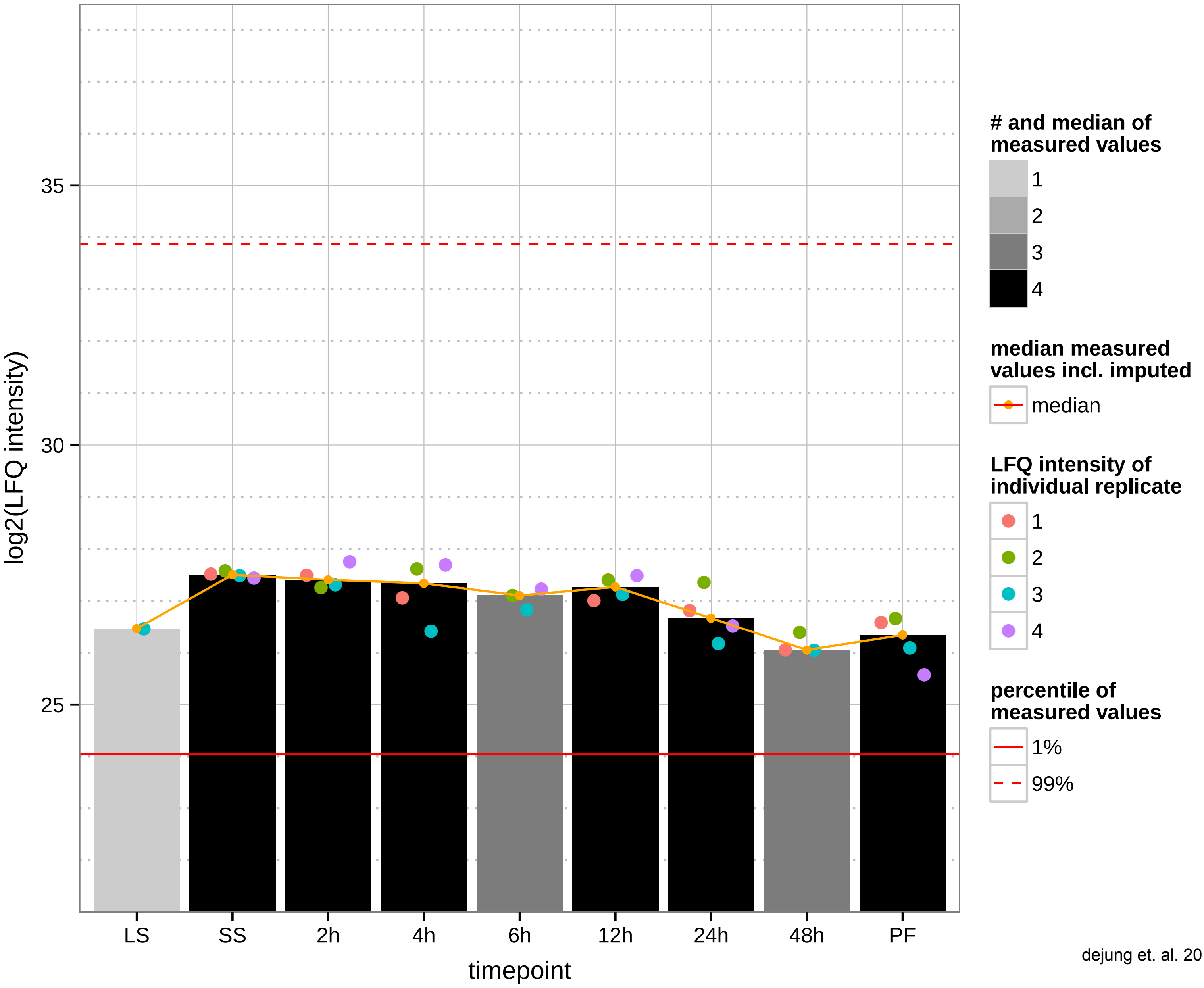
hypothetical protein, conserved
Tb927.1.2970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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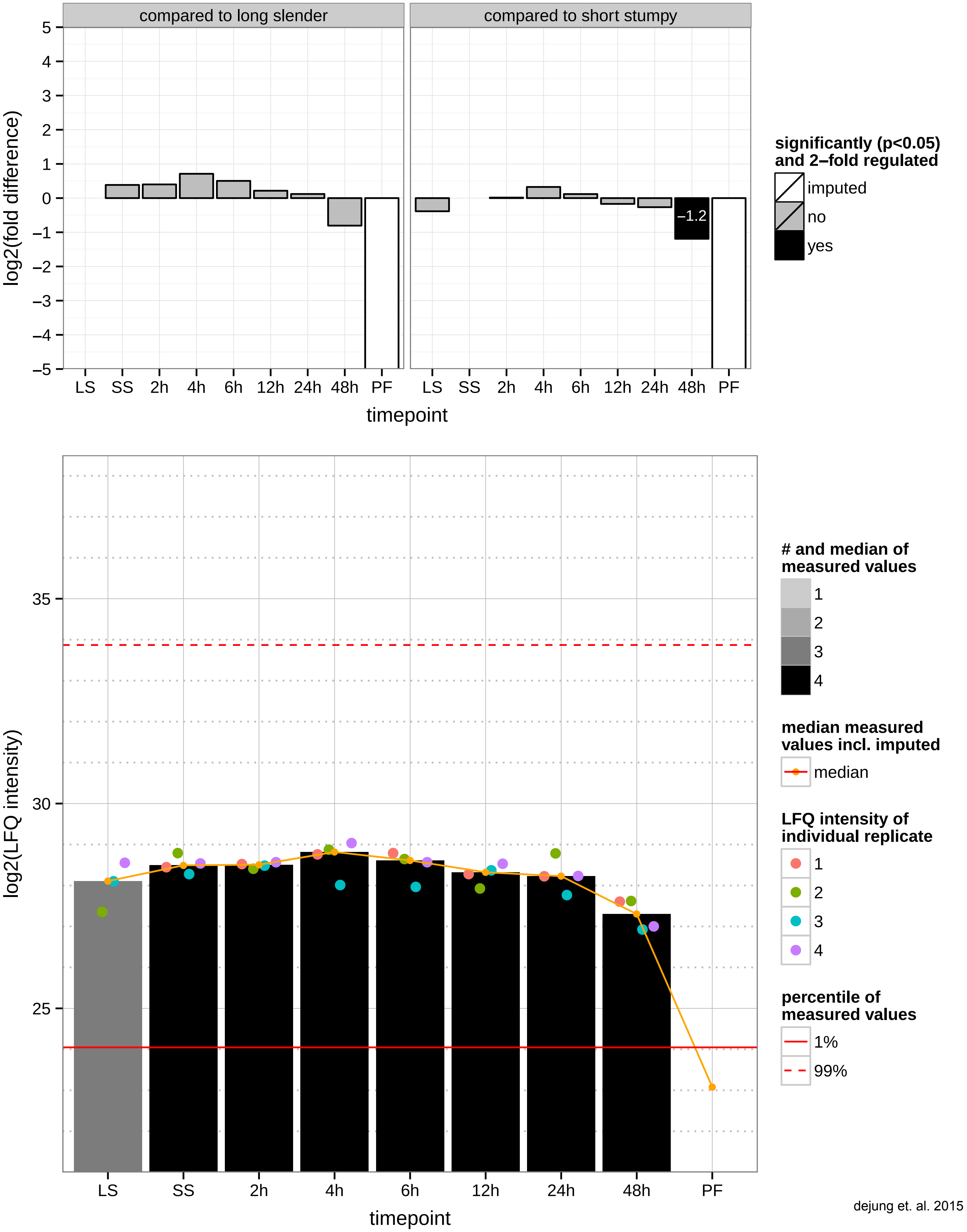
acetyltransferase, putative
Tb927.1.4490
AGOF: N–acetyltransferase activity, palmitoyl–CoA oxidase activity
AGOC: null
AGOP: metabolic process
PGOF: N–acetyltransferase activity
PGOC: null
PGOP: null



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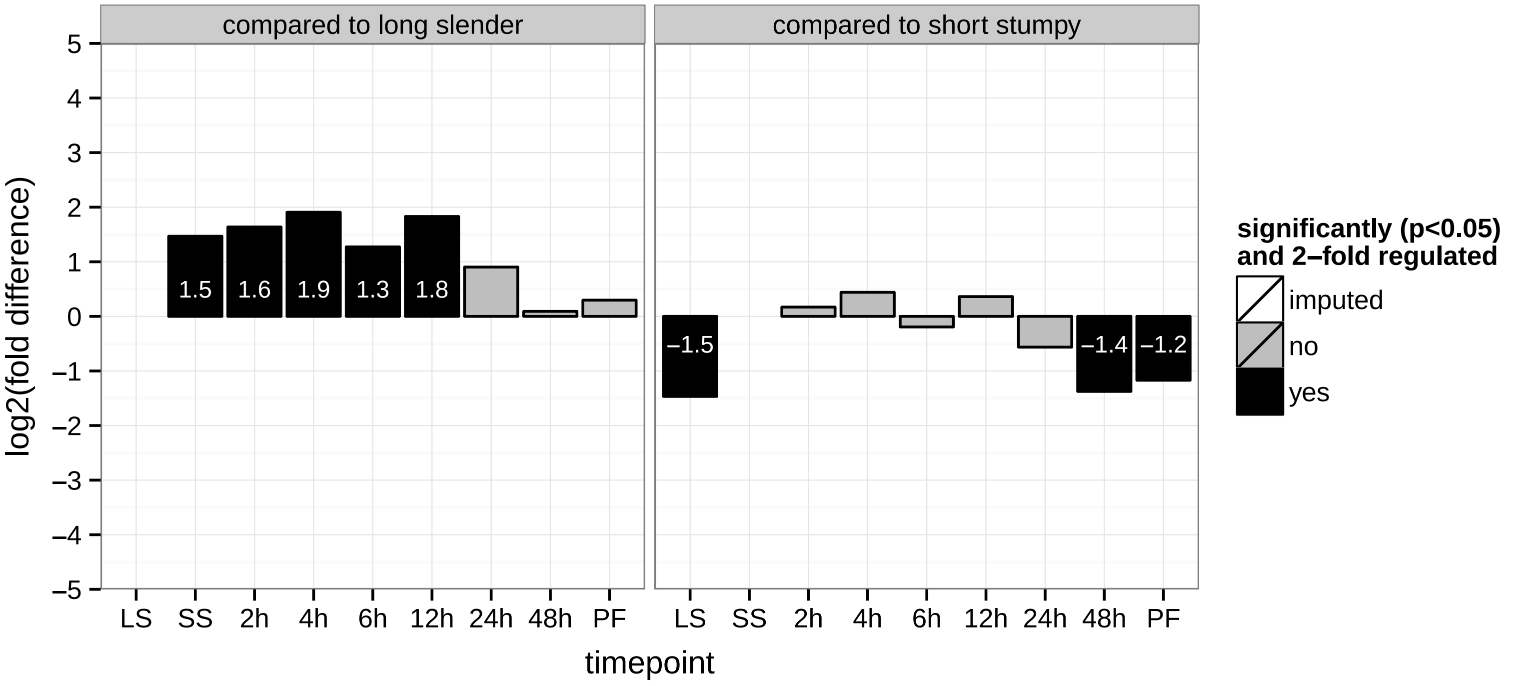
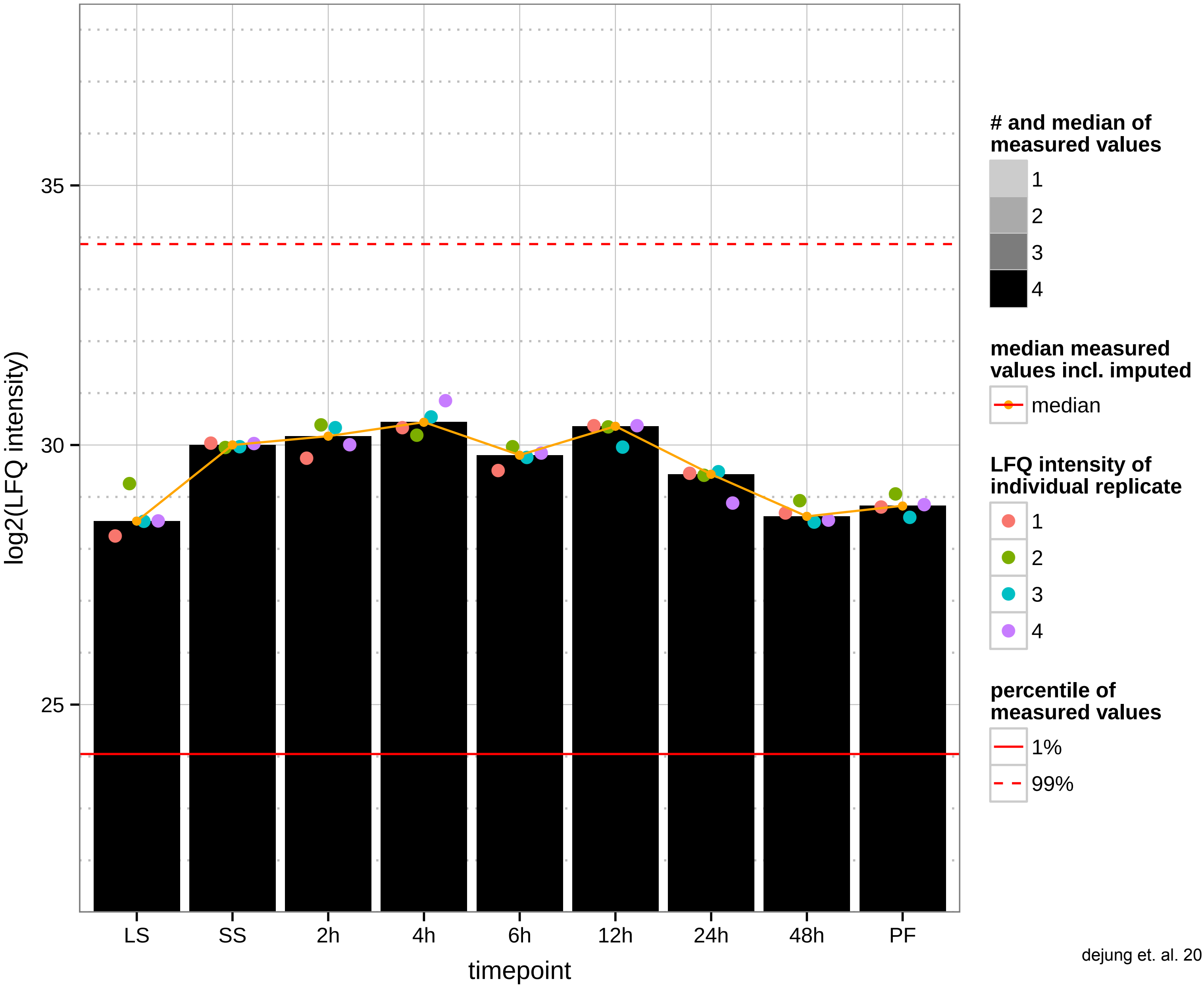
serine carboxypeptidase III precursor, putative (CBP1), serine peptidase, Clan SC, Family S10
Tb927.10.1040;Tb11.v5.0638;Tb927.10.1050
AGOF: null, serine−type carboxypeptidase activity
AGOC: null
AGOP: null, proteolysis
PGOF: serine−type carboxypeptidase activity
PGOC: null
PGOP: proteolysis





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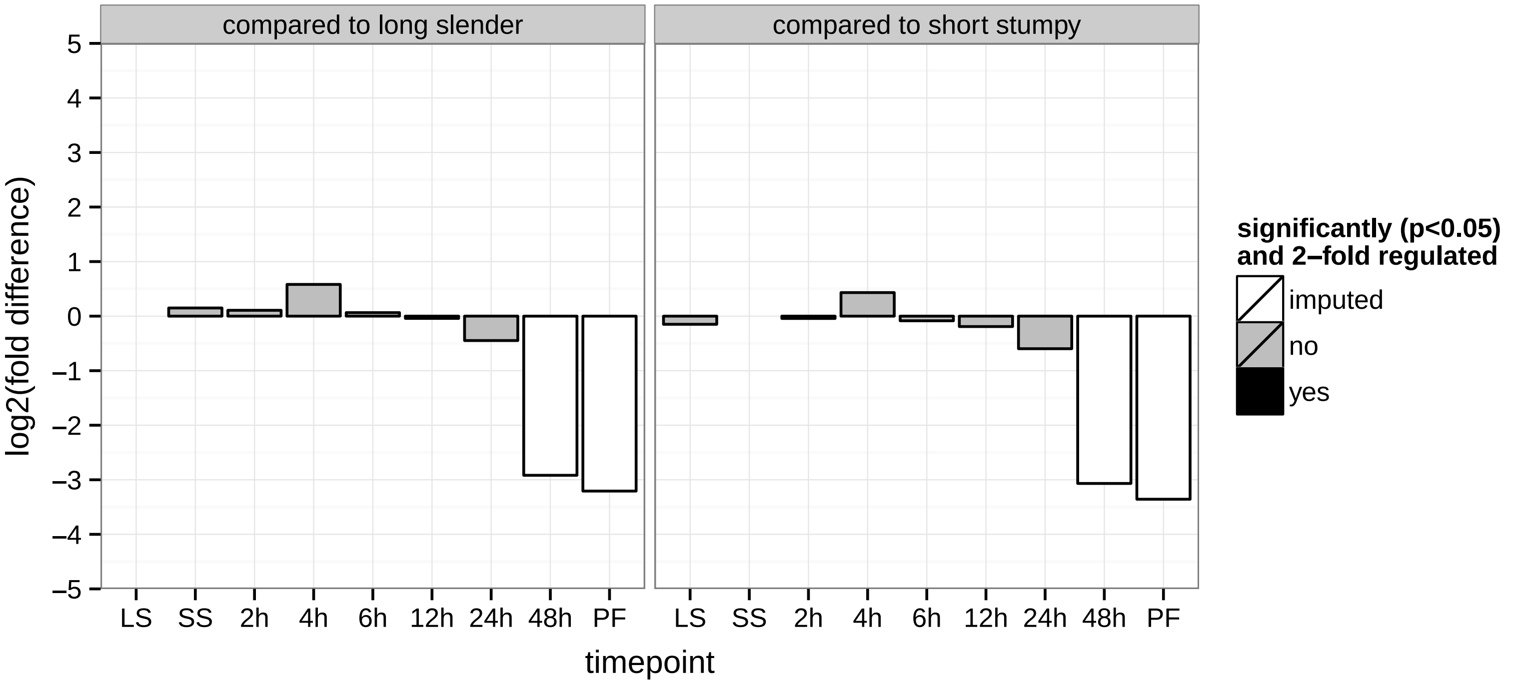
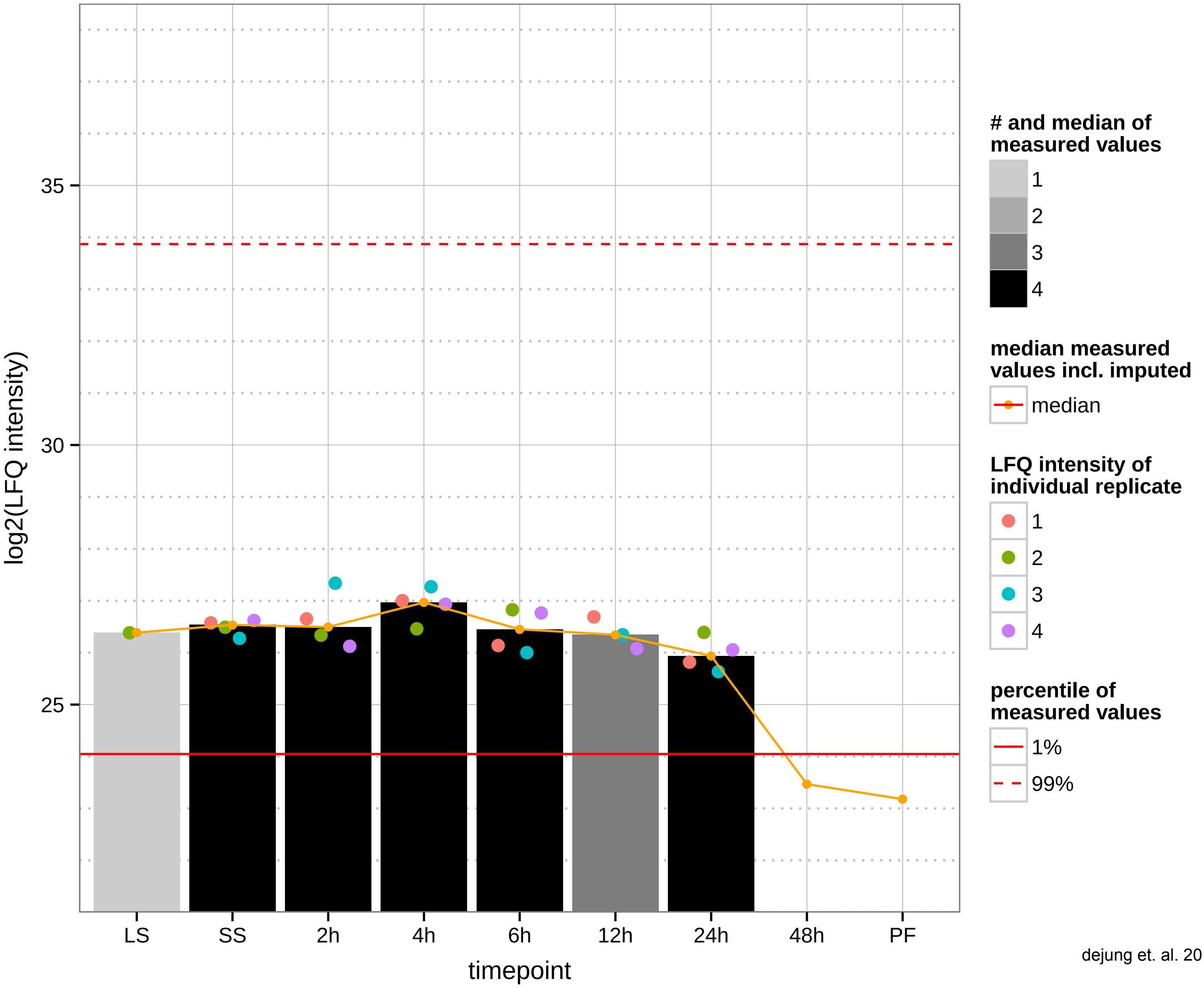
hypothetical protein, conserved
Tb927.10.11140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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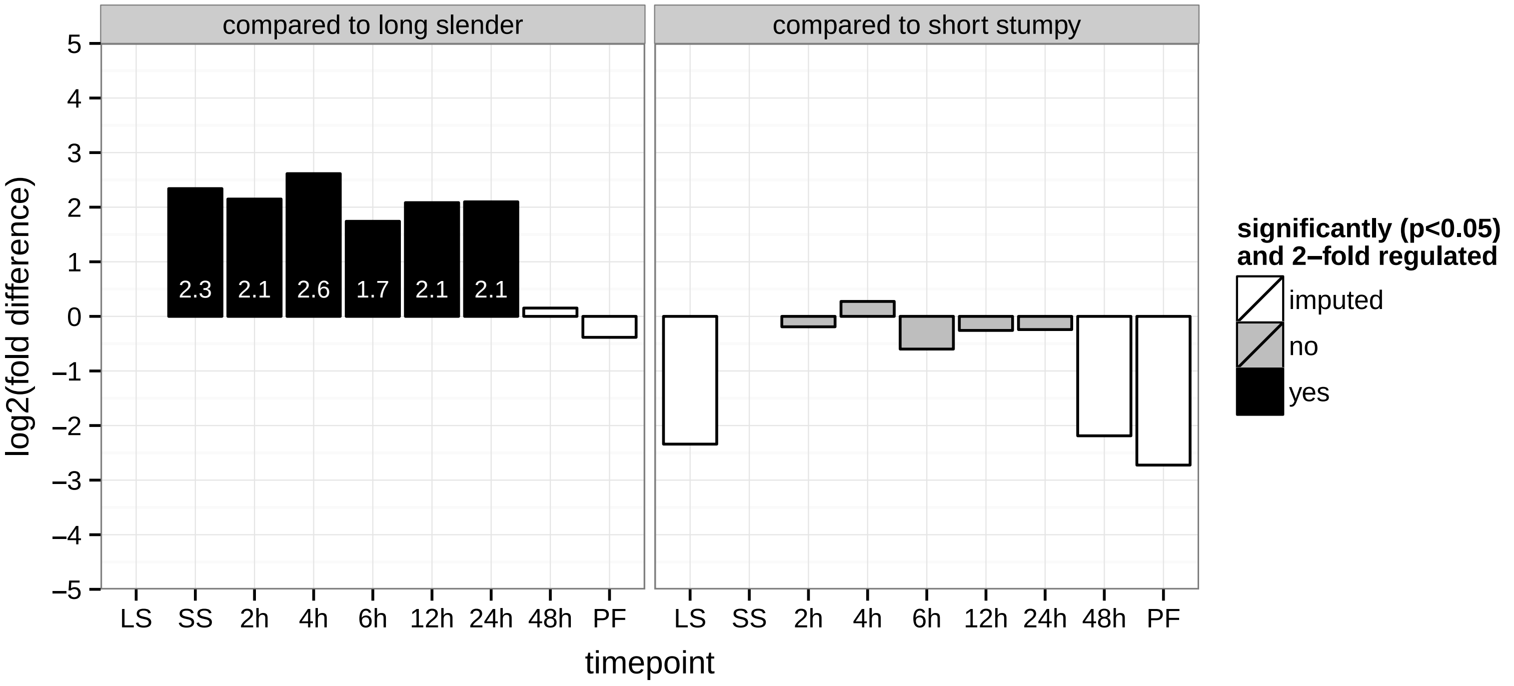
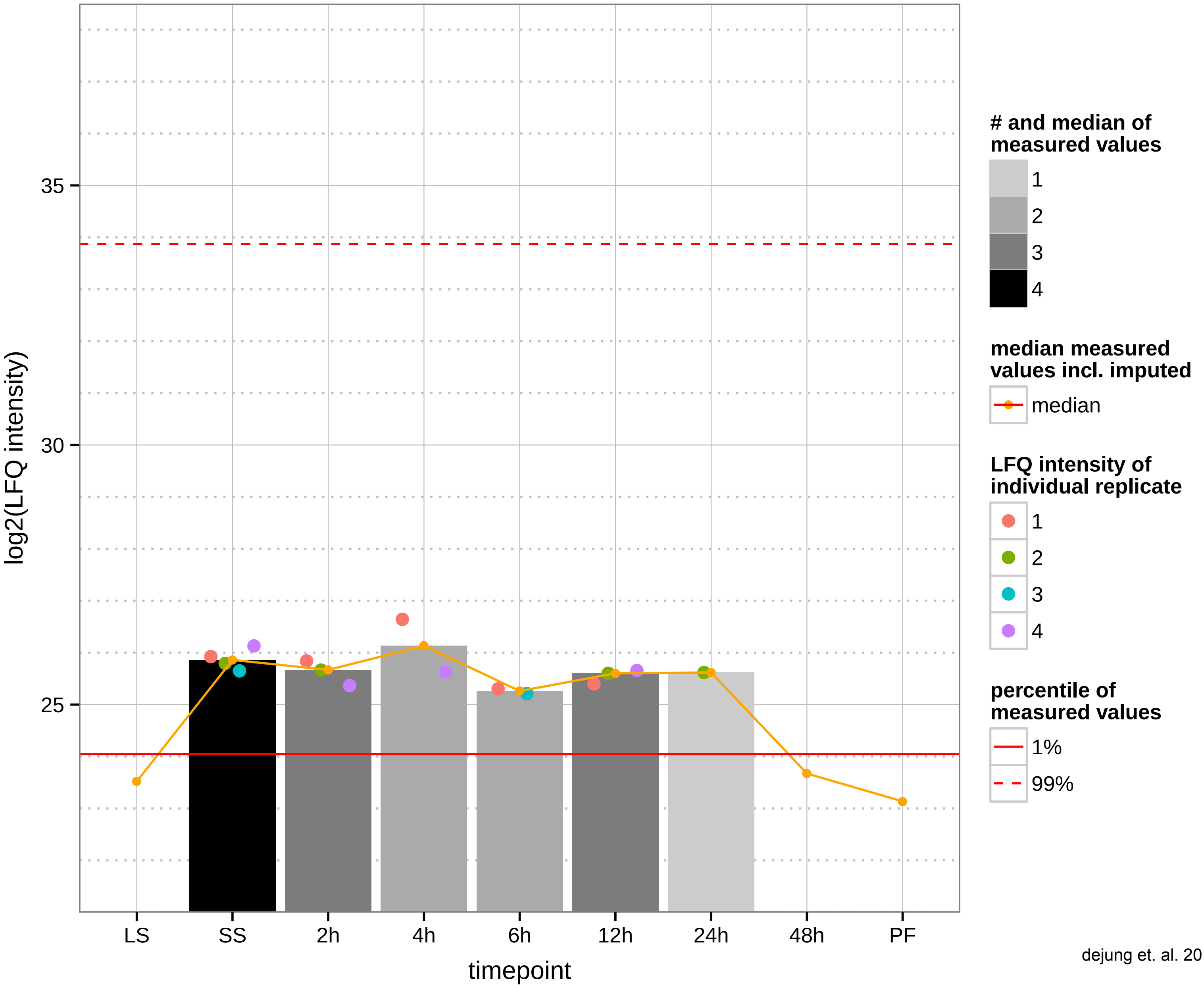
chloride channel protein, putative
Tb927.10.11680
AGOF: hormone activity, voltage–gated chloride channel activity
AGOC: extracellular region, membrane
AGOP: chloride transport
PGOF: ion channel activity, protein binding, voltage–gated chloride channel activity
PGOC: membrane
PGOP: chloride transport, transmembrane transport





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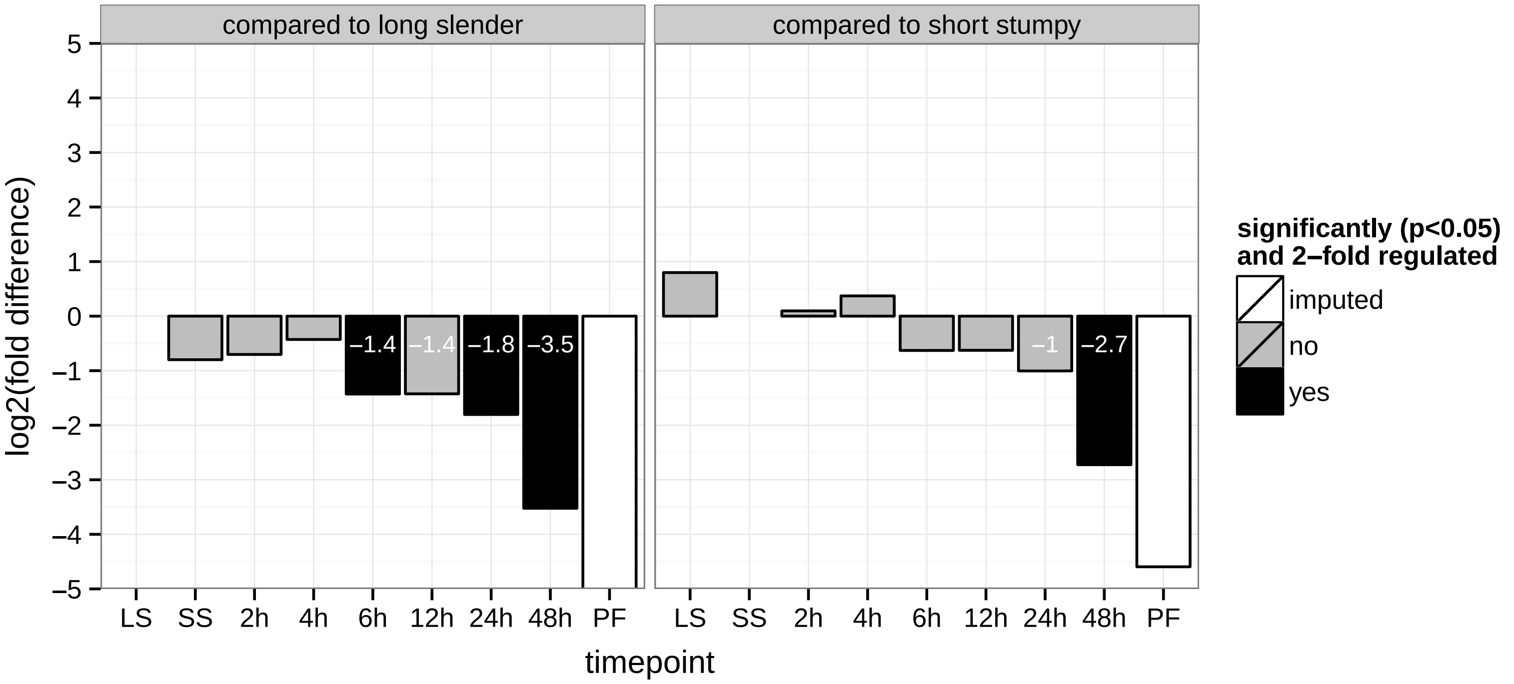
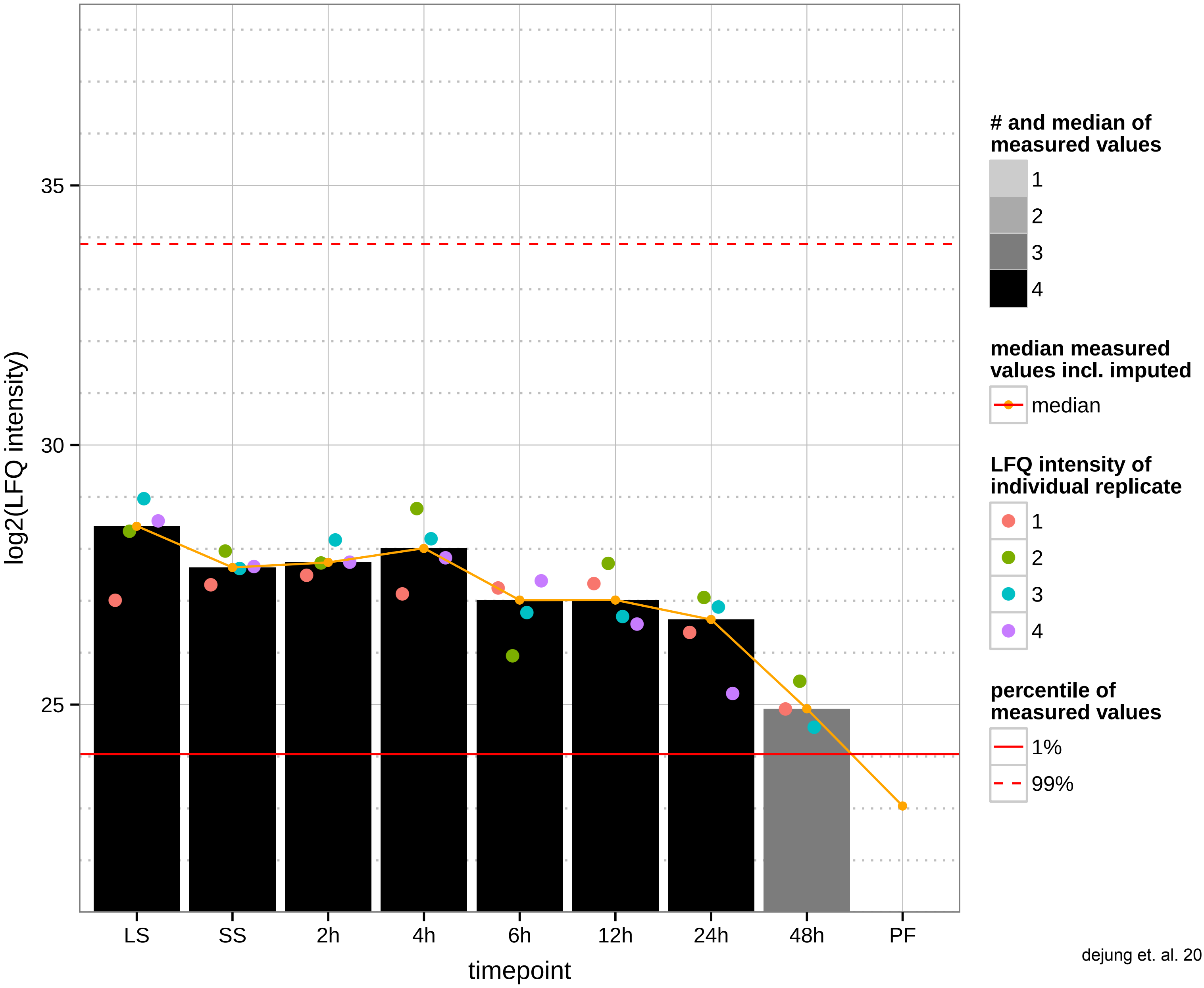
hypothetical protein, conserved
Tb927.10.12010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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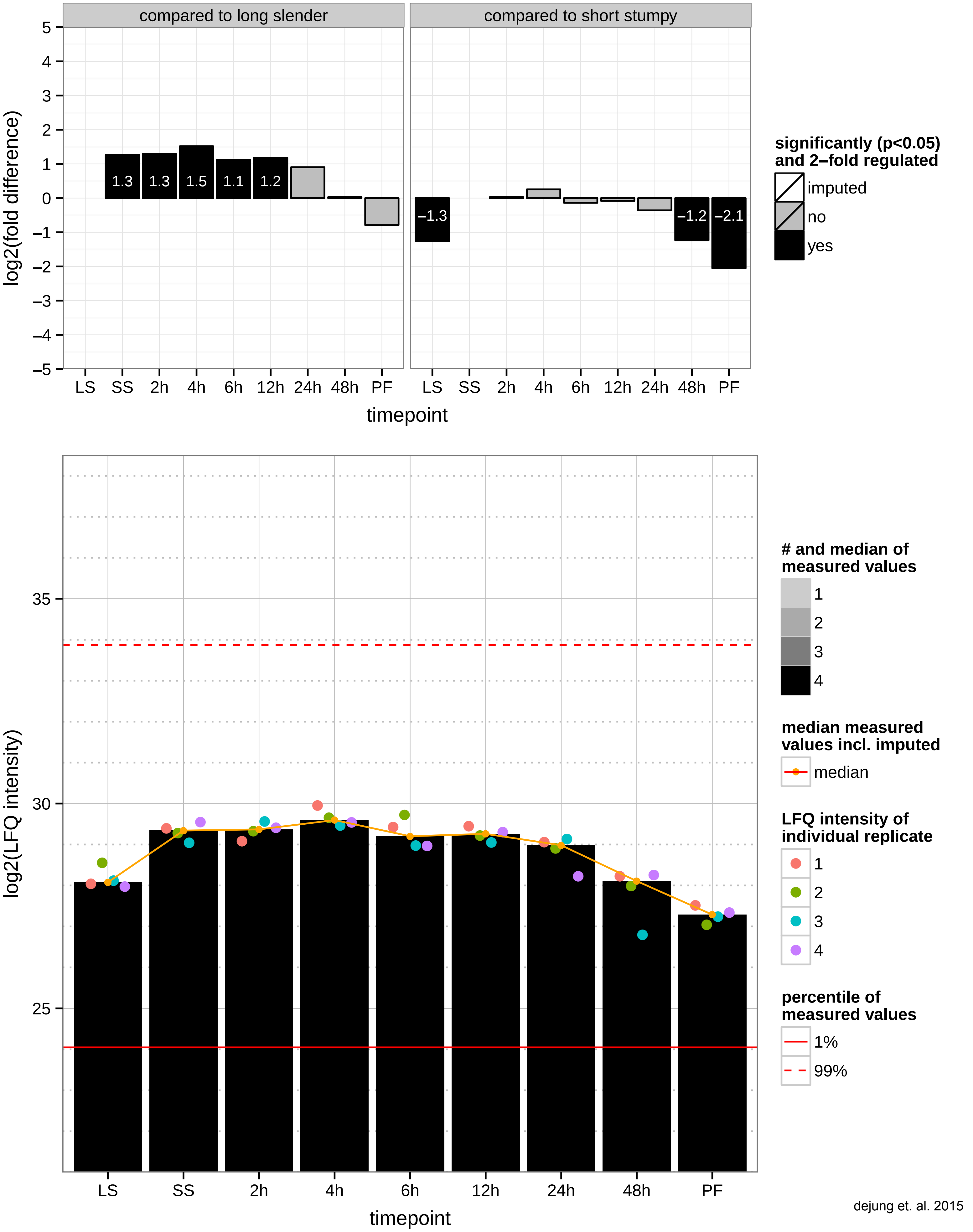
hypothetical protein, conserved
Tb927.10.1230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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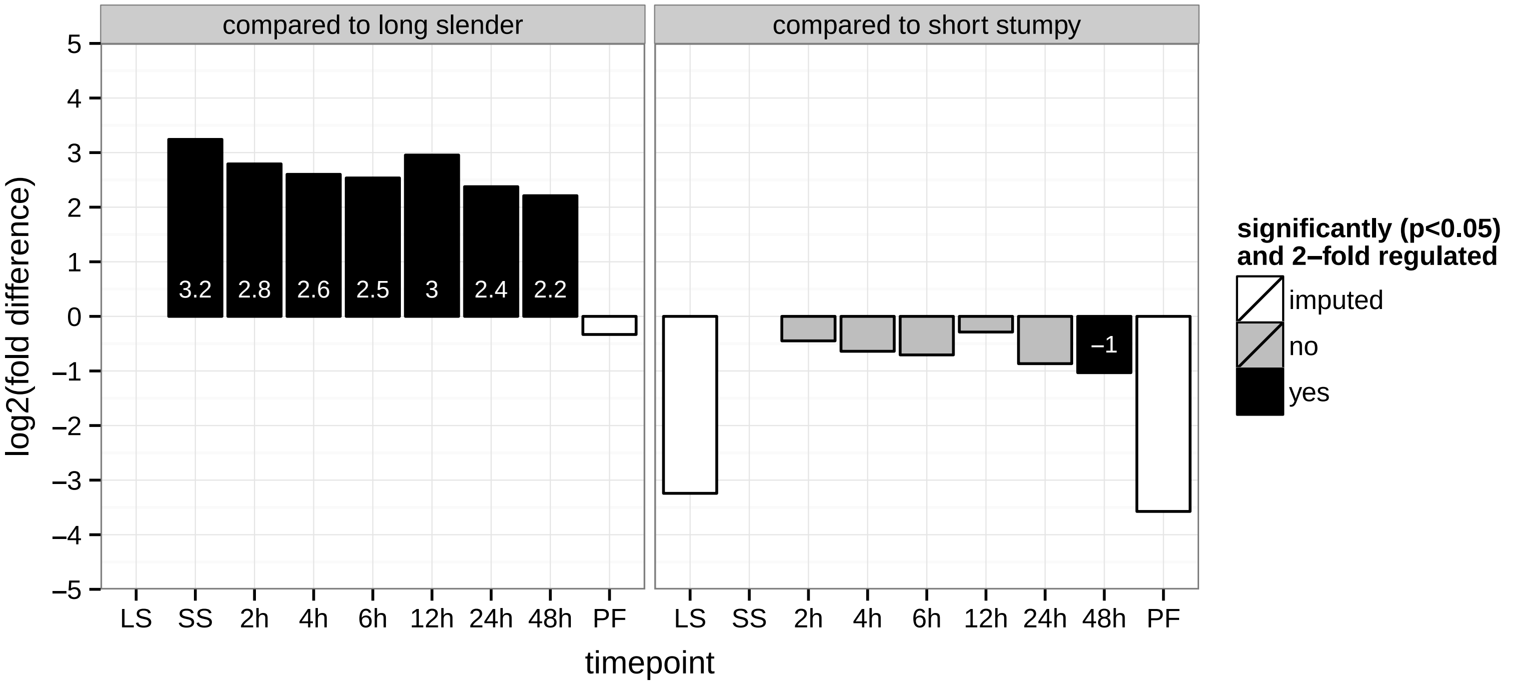
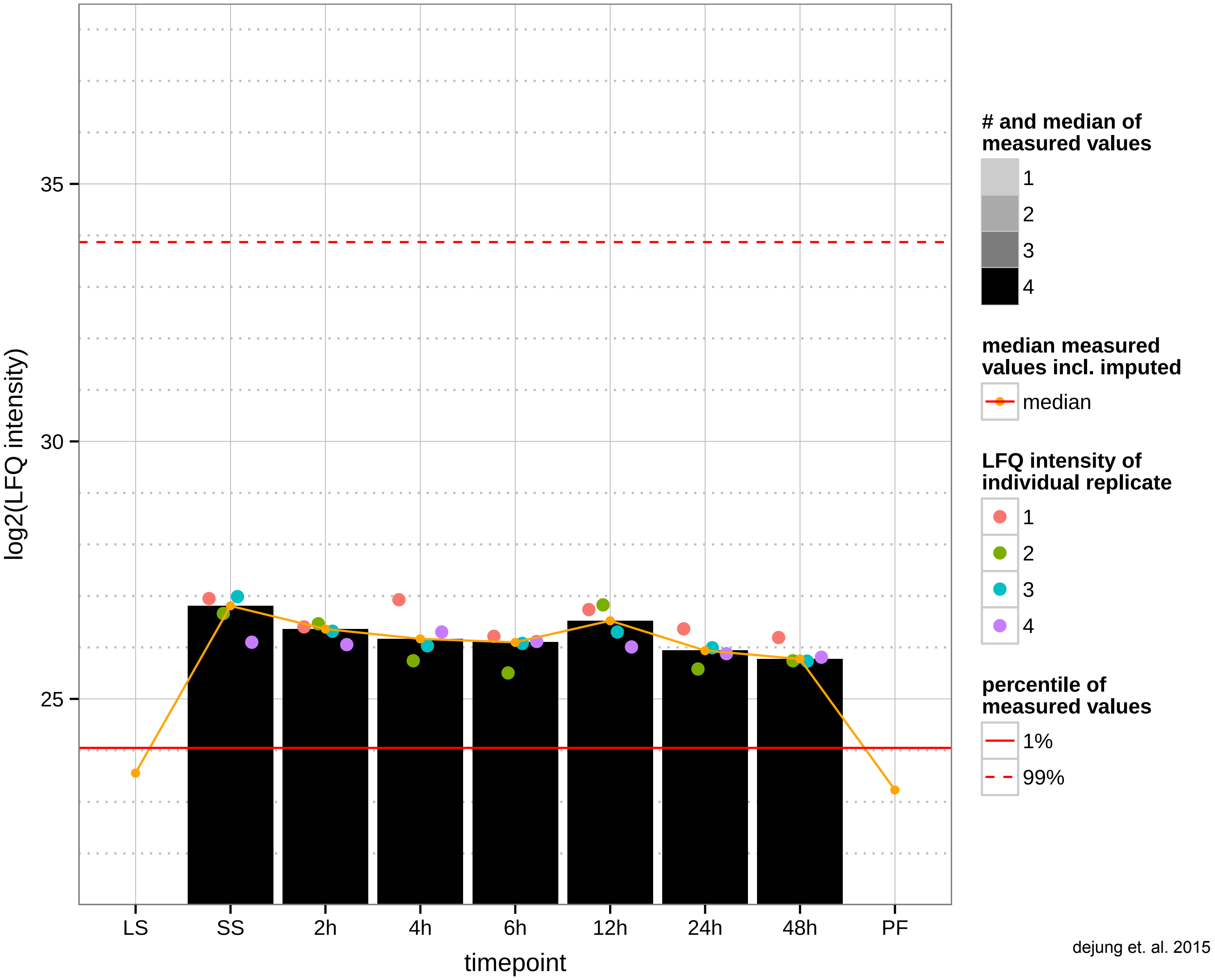
cholinephosphate cytidylyltransferase A, putative
Tb927.10.12810
AGOF: cytidylyltransferase activity, nucleotidyltransferase activity
AGOC: cytosol
AGOP: biosynthetic process, phosphatidylcholine biosynthetic process
PGOF: catalytic activity, nucleotidyltransferase activity, phosphotransferase activity, for other substituted phosphate groups
PGOC: membrane
PGOP: biosynthetic process, phospholipid biosynthetic process





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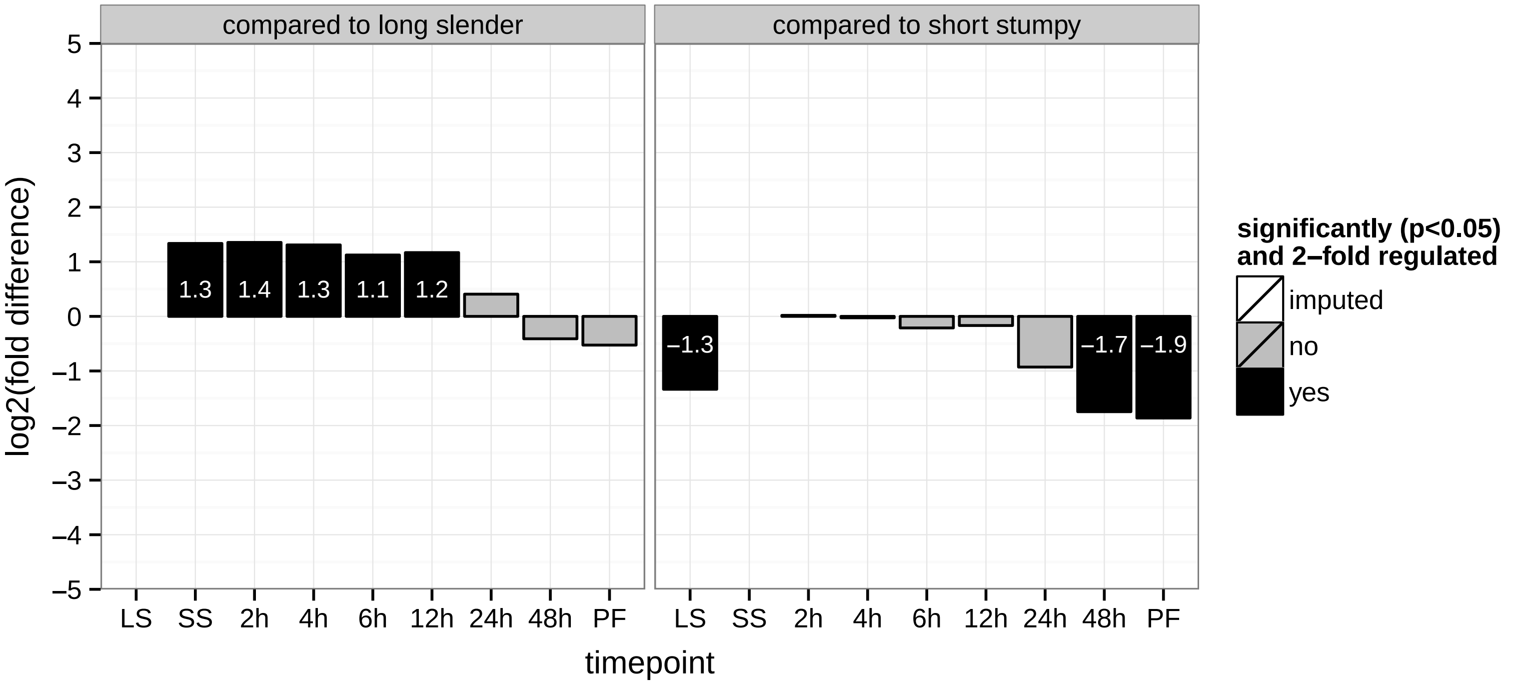
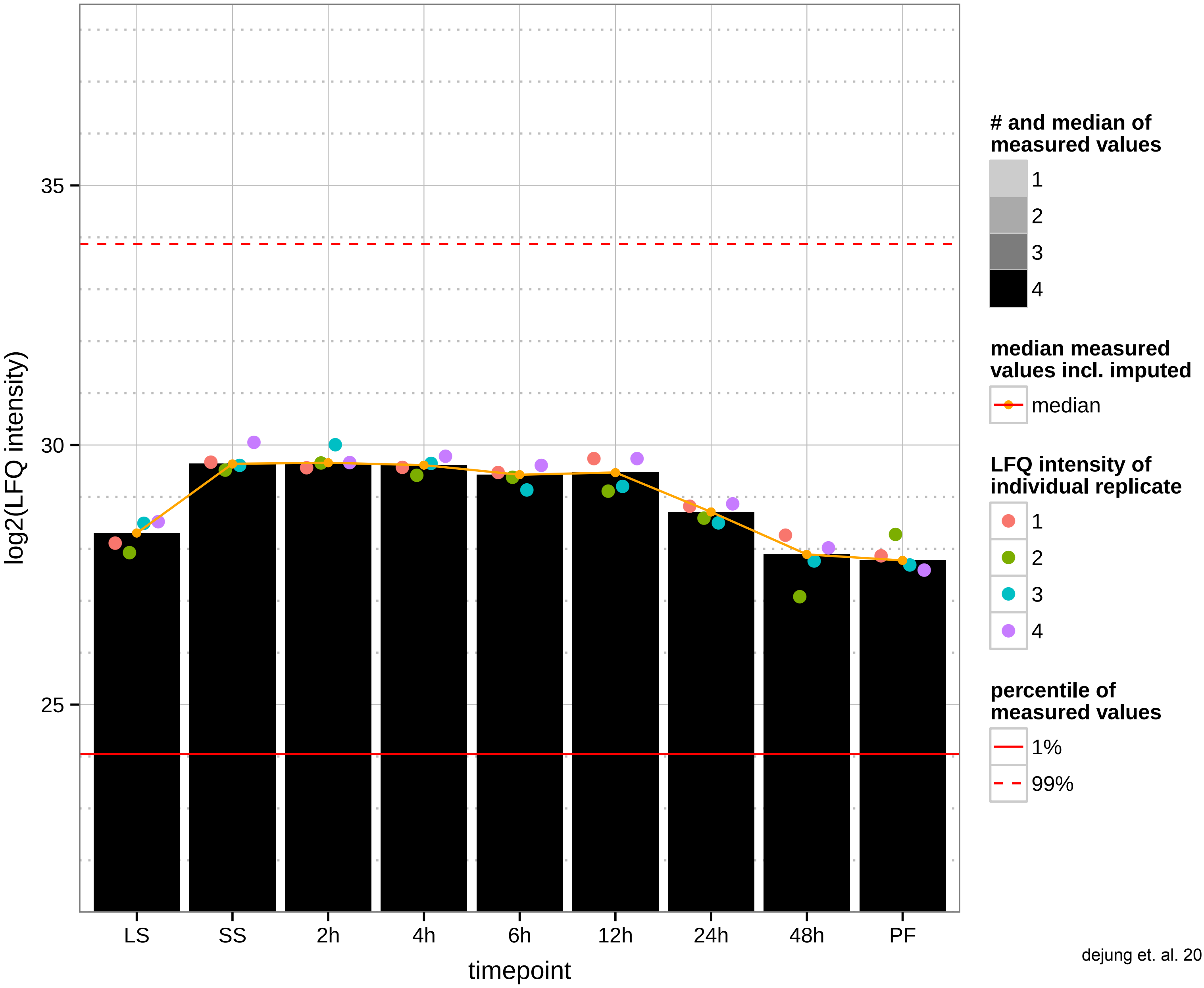
predicted zinc finger protein
Tb927.10.12940
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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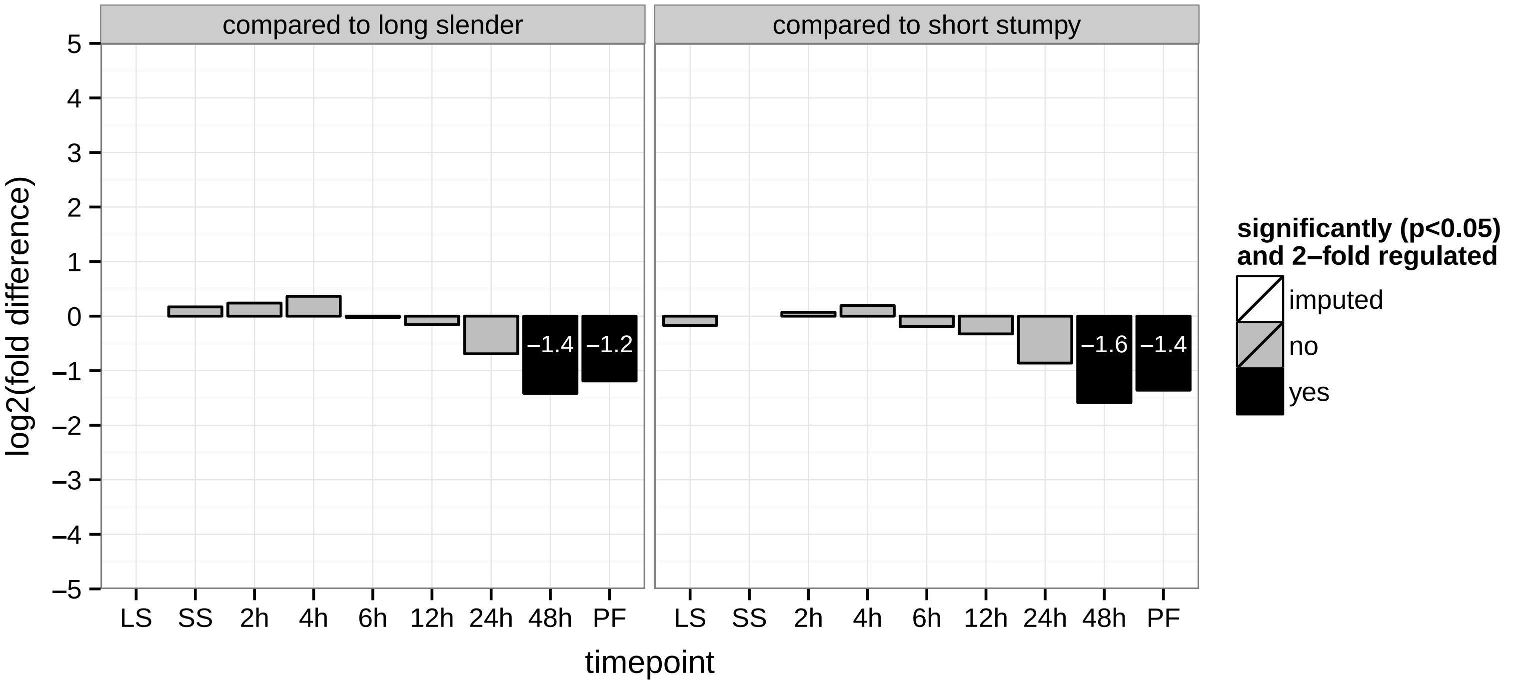
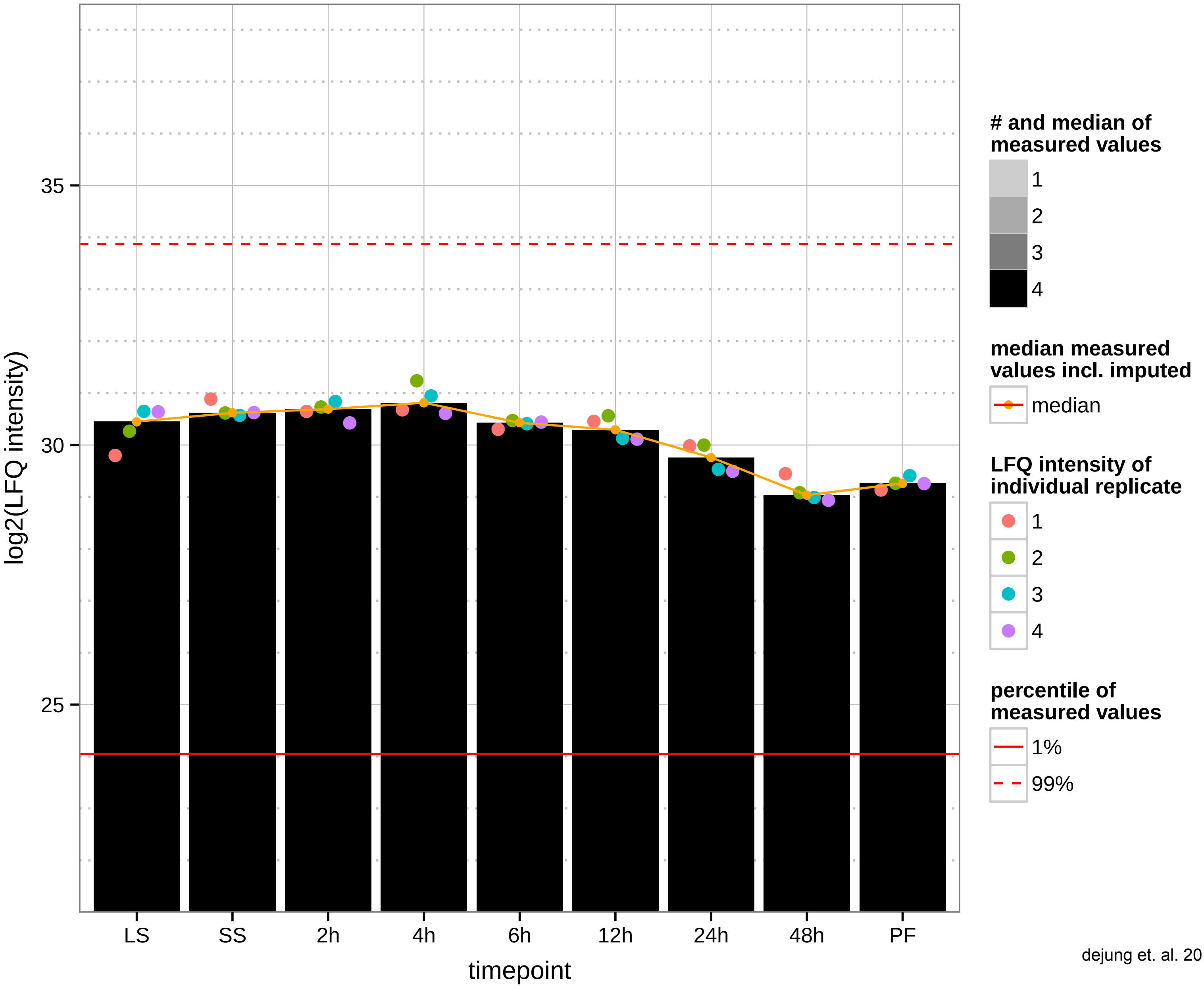
Ras–related protein Rab5A (RAB5A)
Tb927.10.12960
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti





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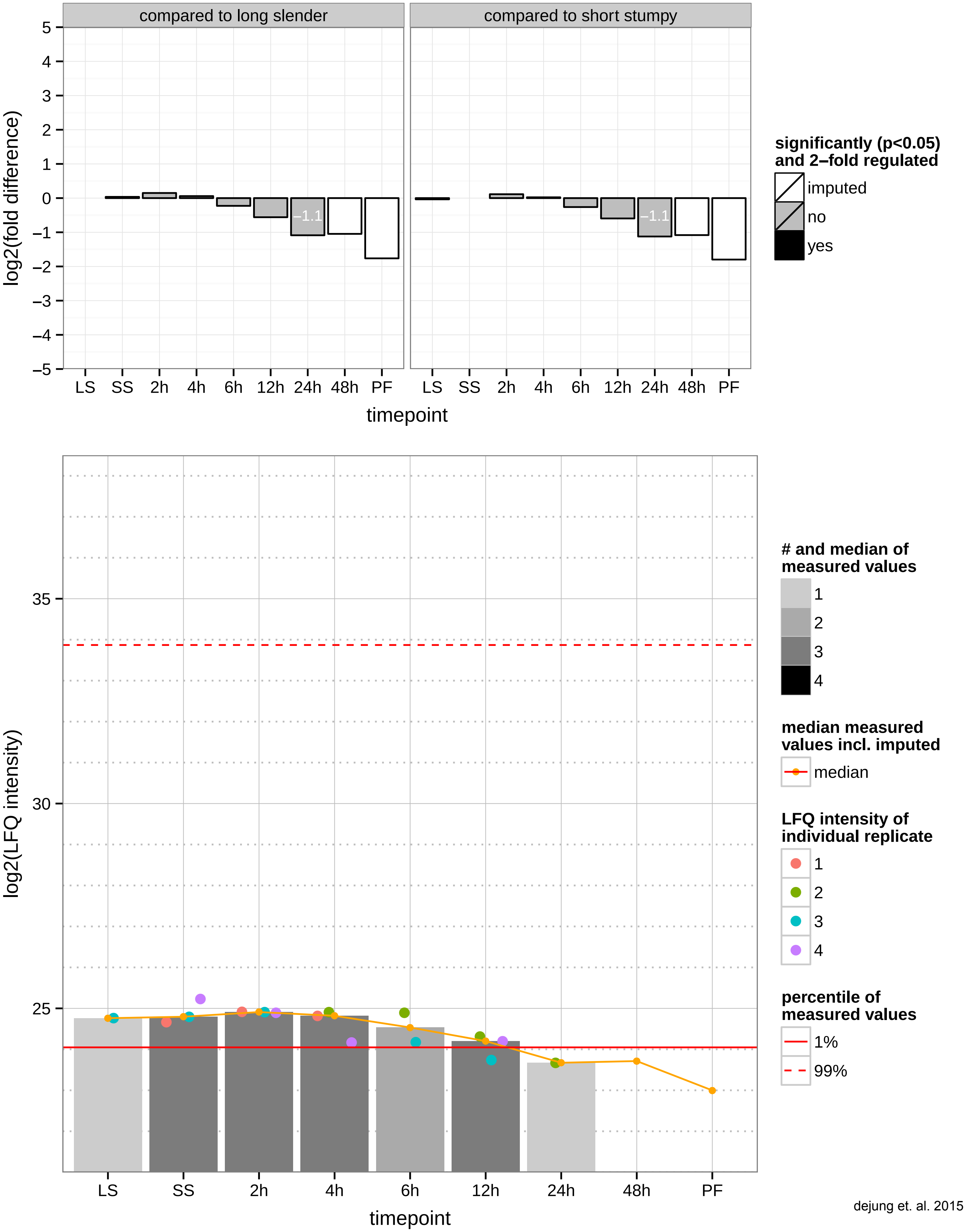
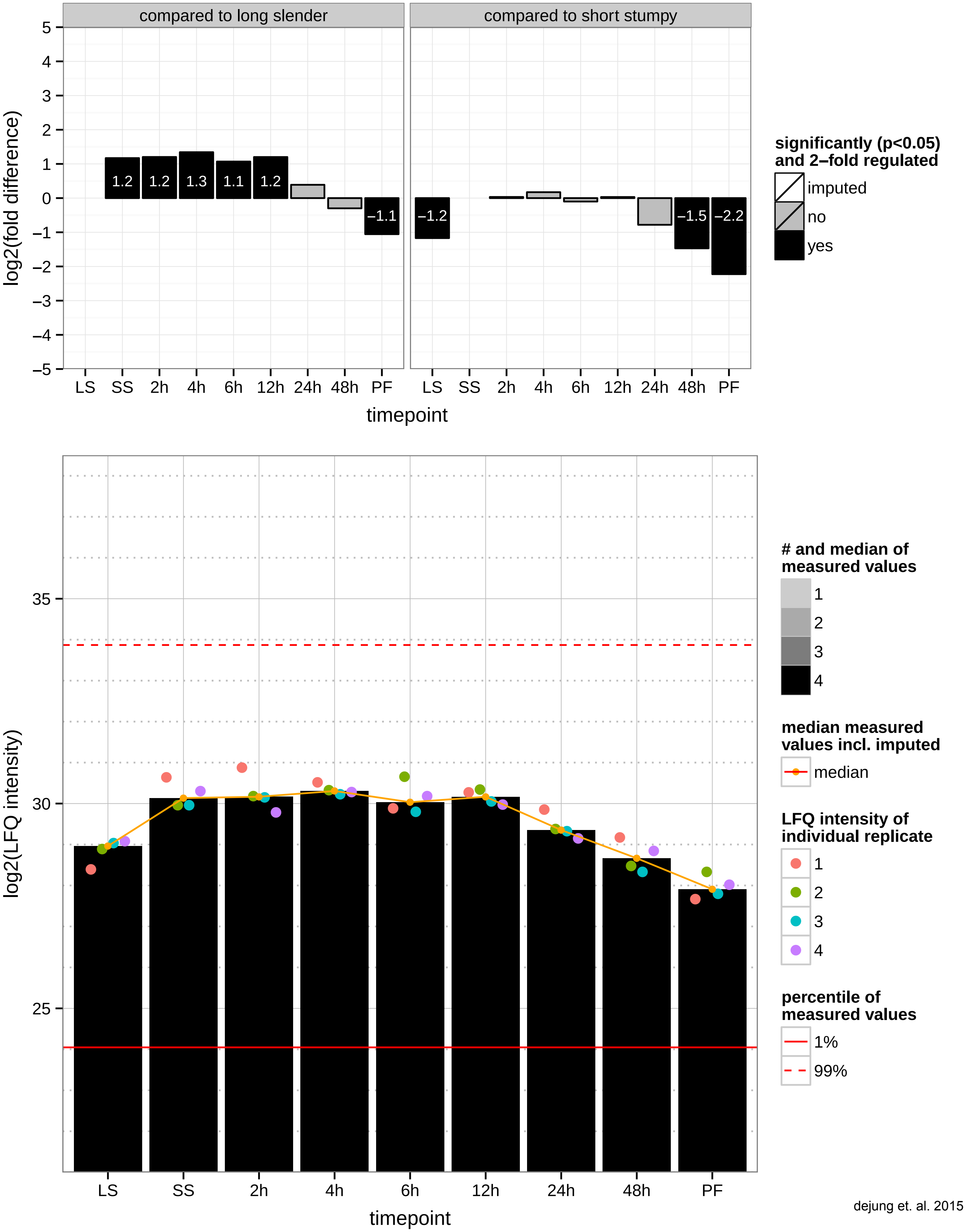
RNA–binding protein, putative (RBP12)
Tb927.10.13540
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null



hypothetical protein, conserved
Tb927.10.1430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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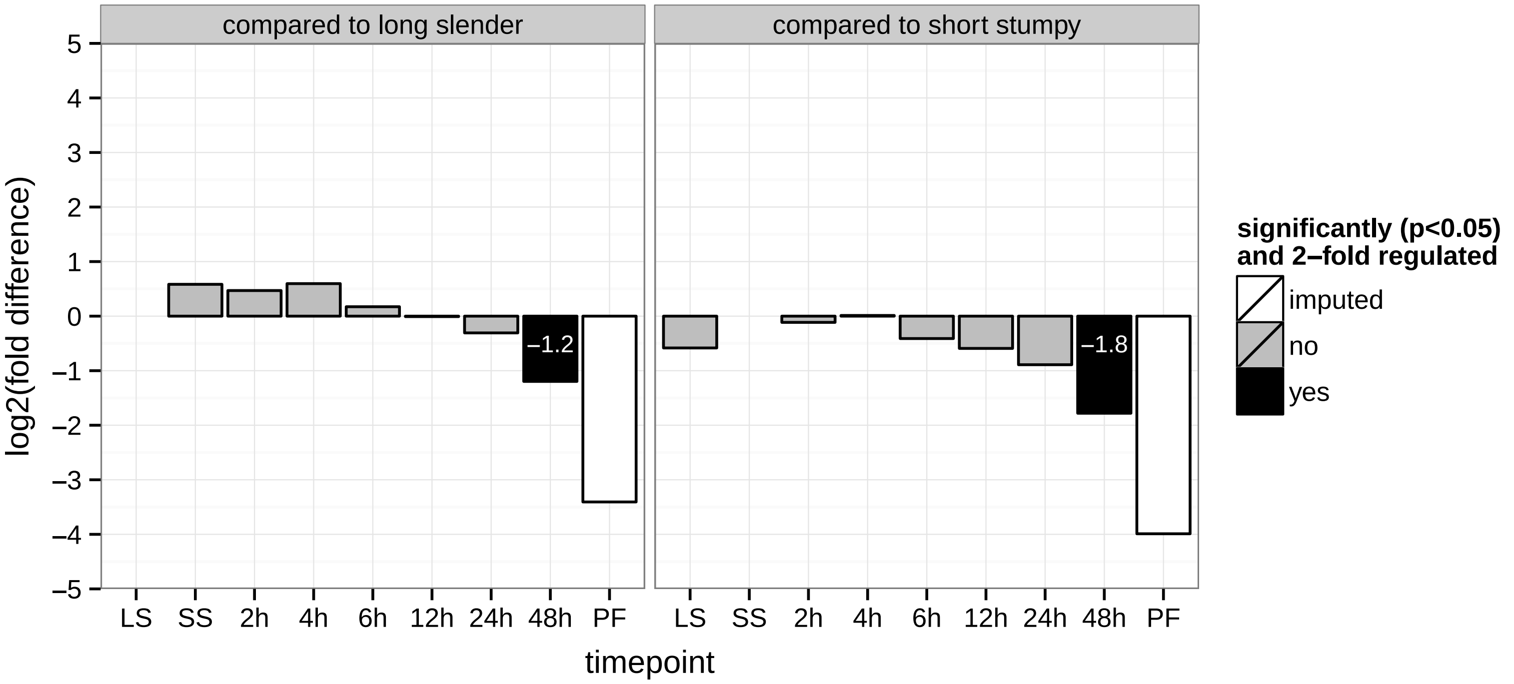
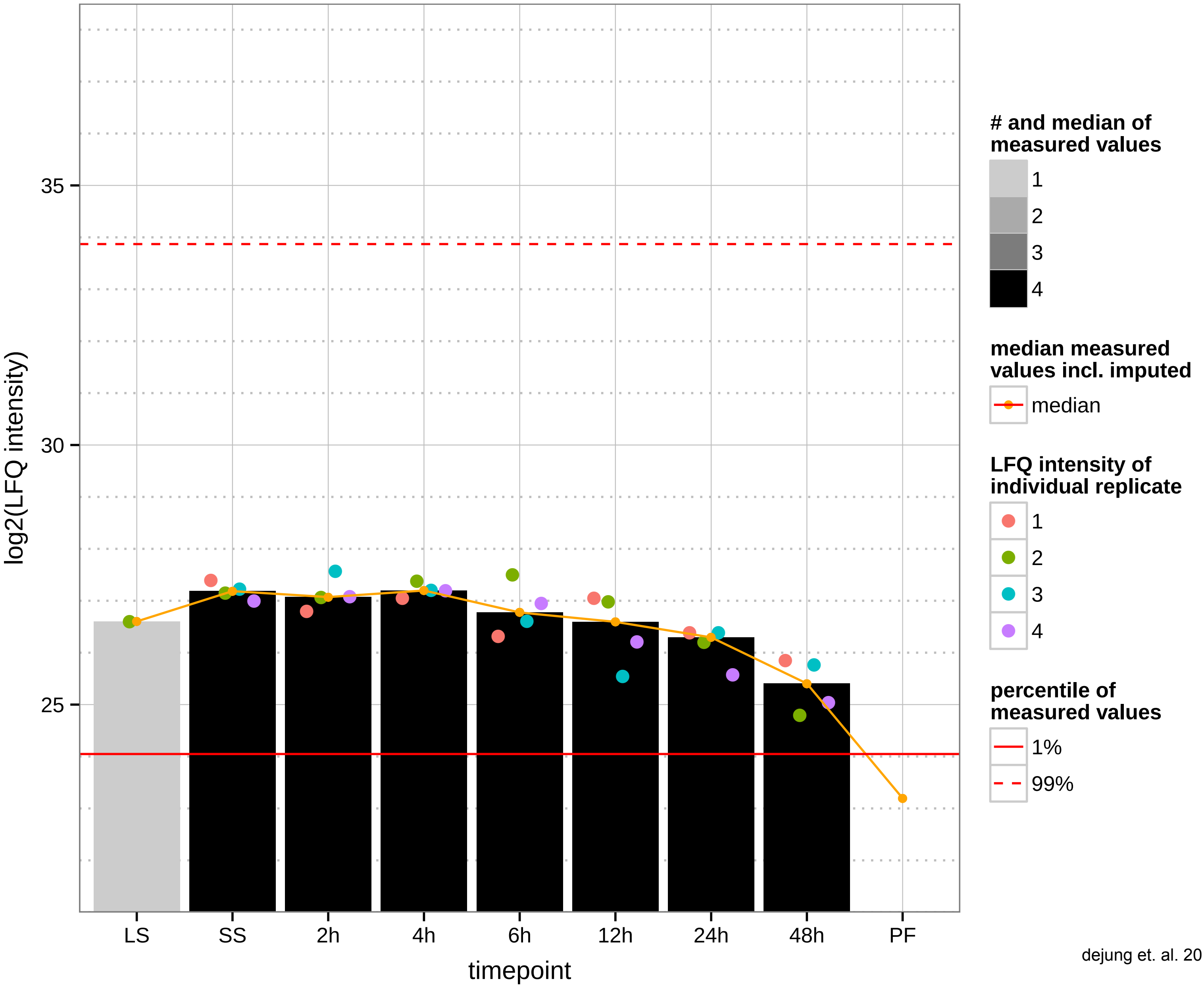
syntaxin, putative
Tb927.10.14690
AGOF: transporter activity
AGOC: membrane
AGOP: vesicle−mediated transport
PGOF: protein binding
PGOC: null
PGOP: null





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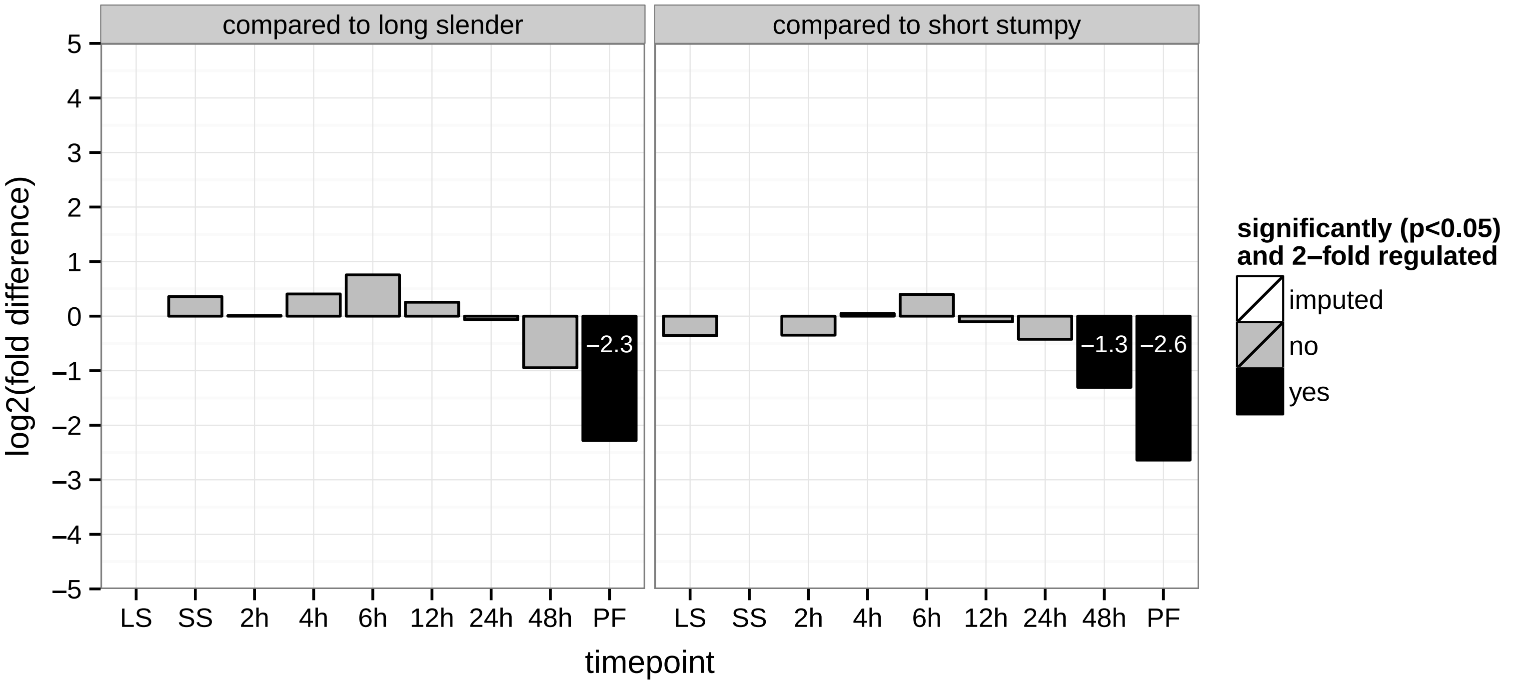
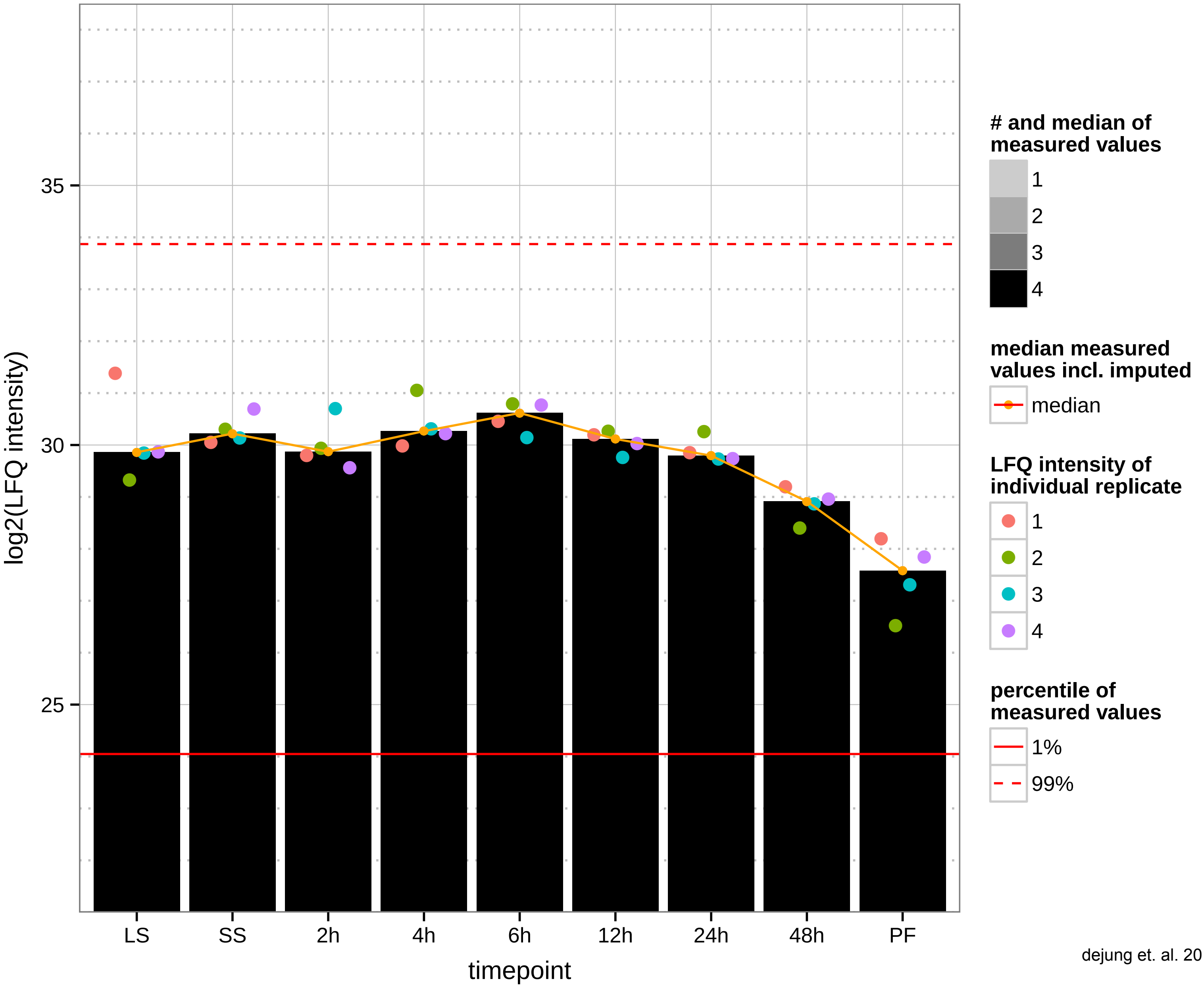
ras–related protein Rab21, putative (RAB21)
Tb927.10.1520
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti





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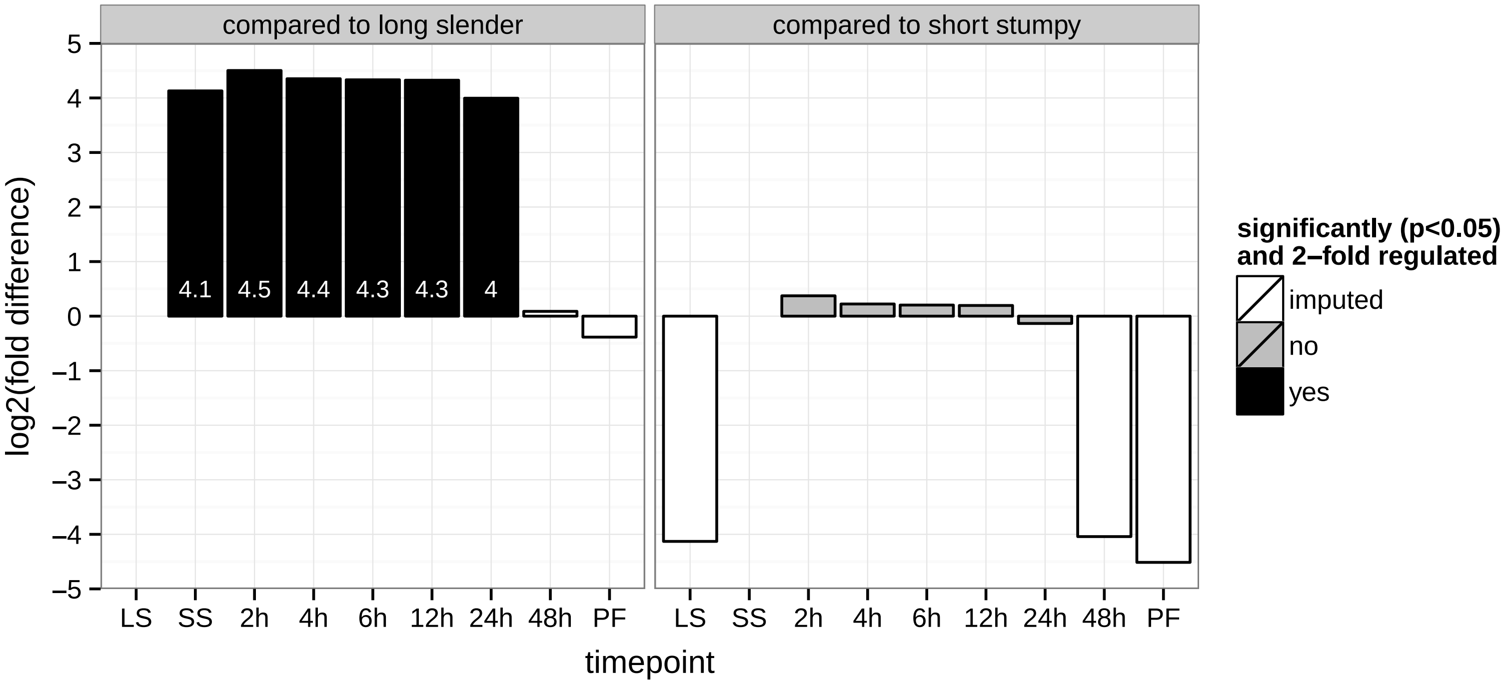
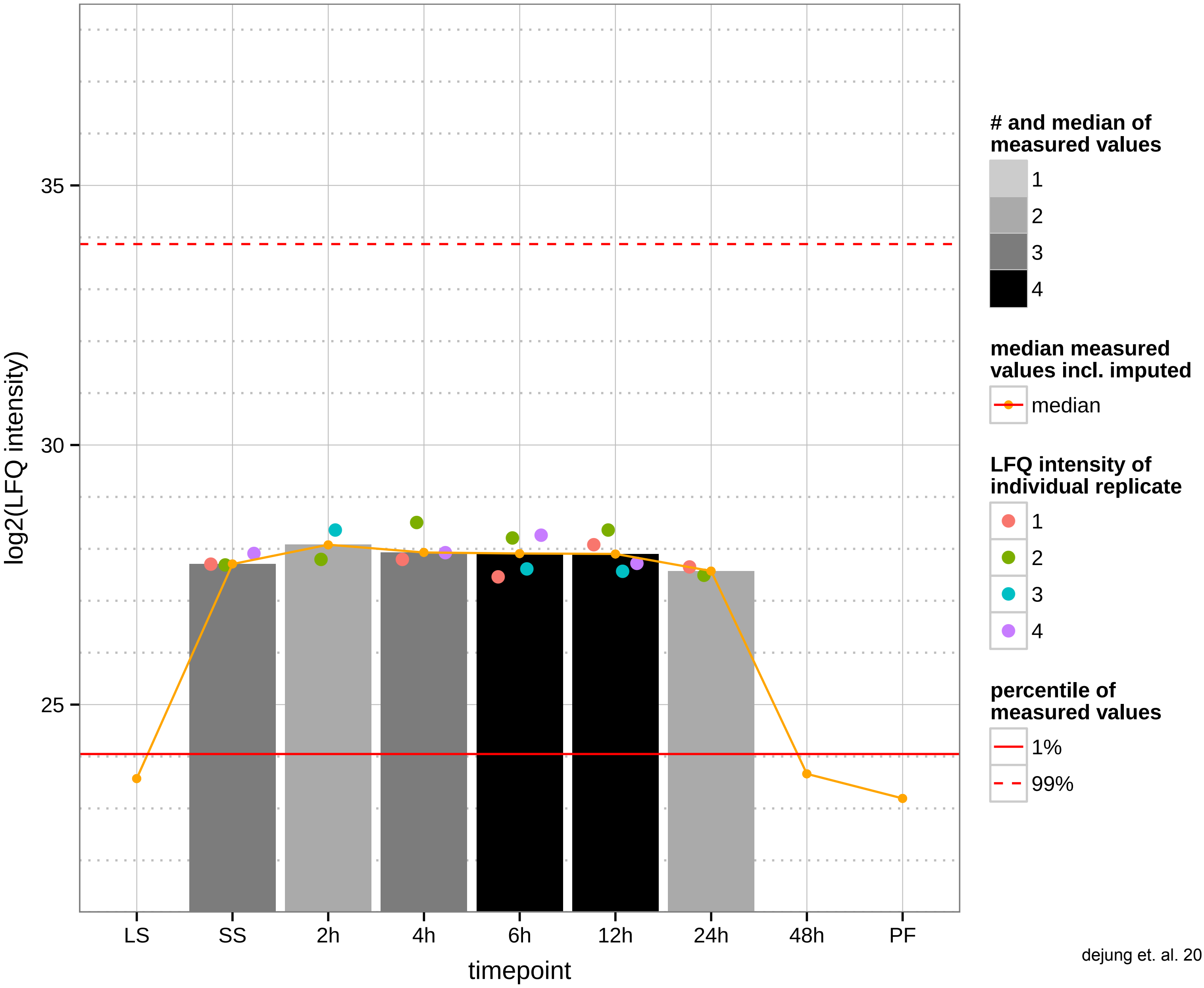
hypothetical protein, conserved
Tb927.10.15200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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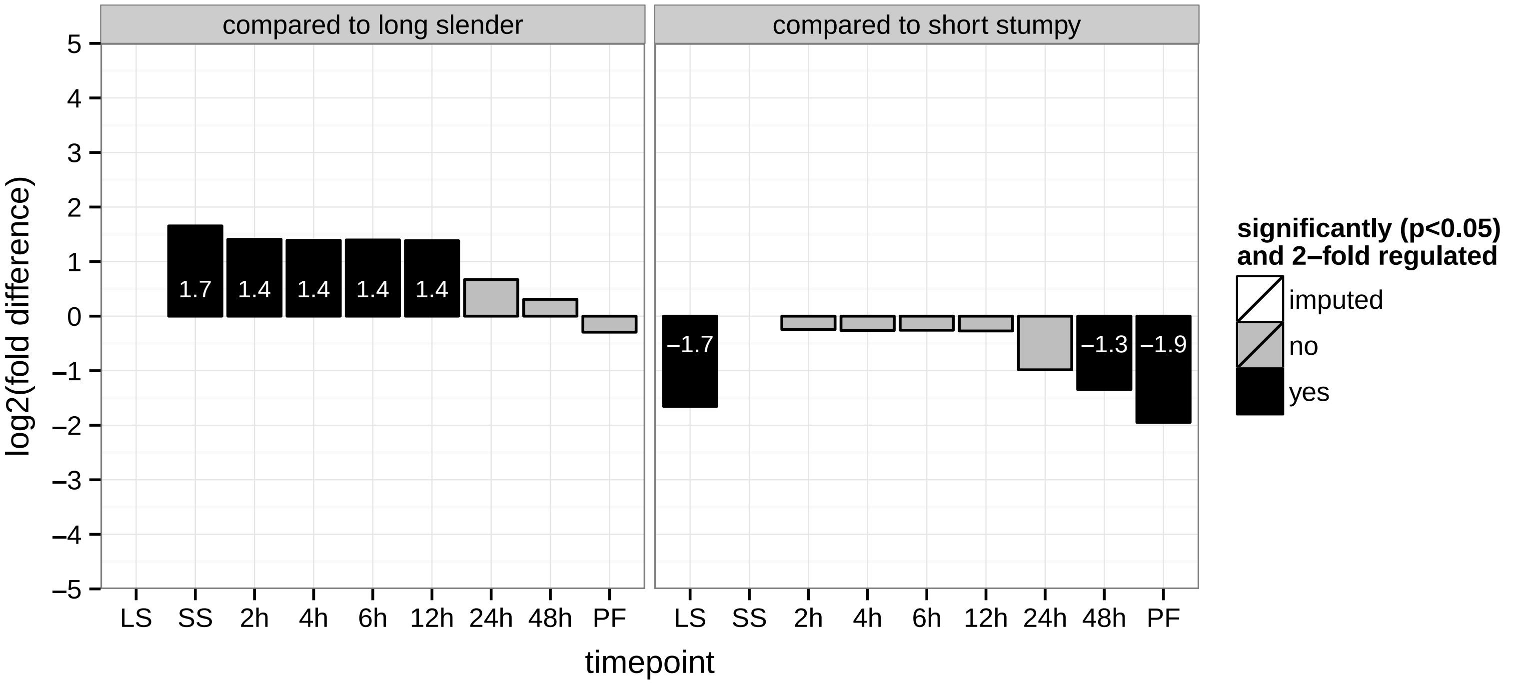
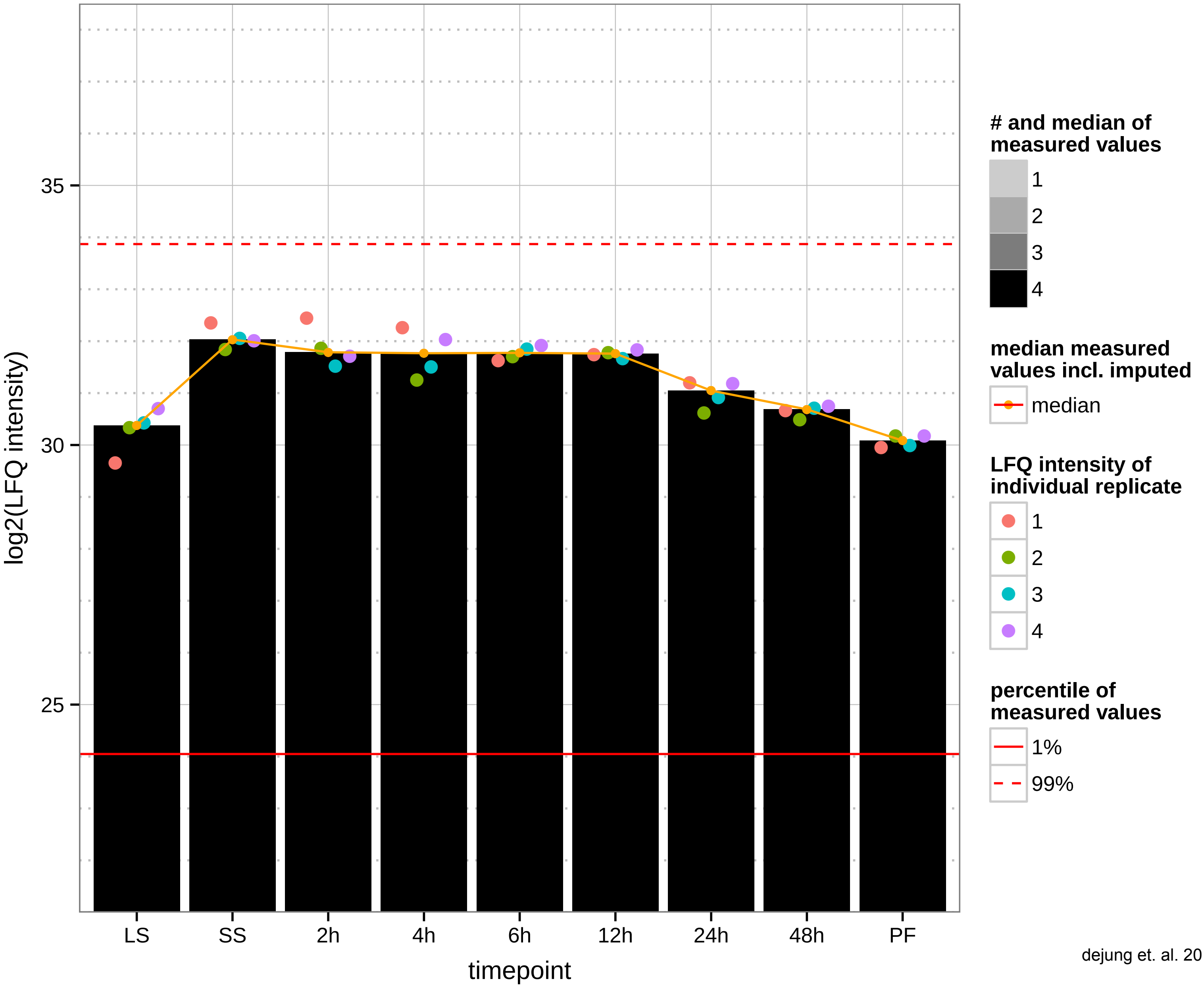
fatty acyl CoA synthetase, putative, Long−chain−fatty−acid−−CoA ligase 5 (EC 6.2.1.3) (Long−chain acyl−CoA synthetase 5)
Tb927.10.3260
AGOF: null, catalytic activity, long−chain fatty acid−CoA ligase activity
AGOC: null
AGOP: null, fatty acid elongation
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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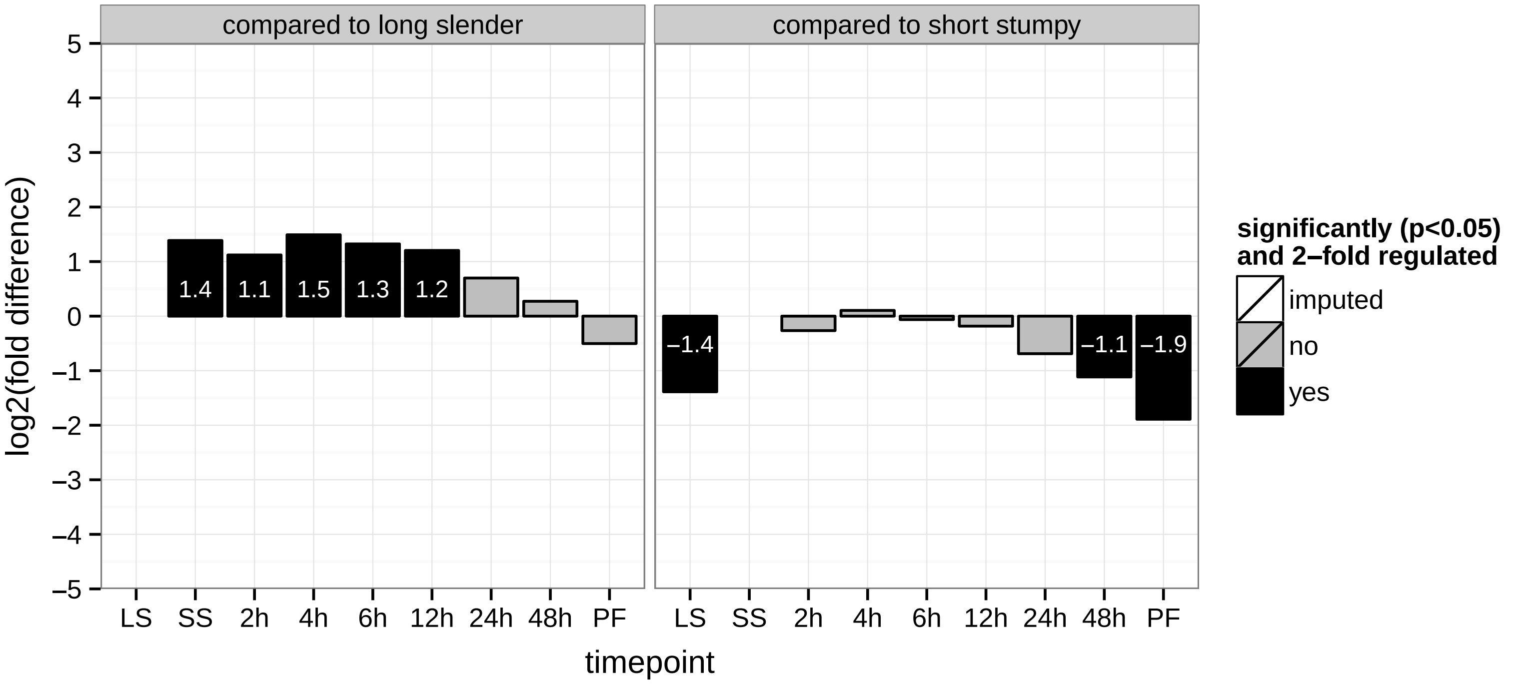
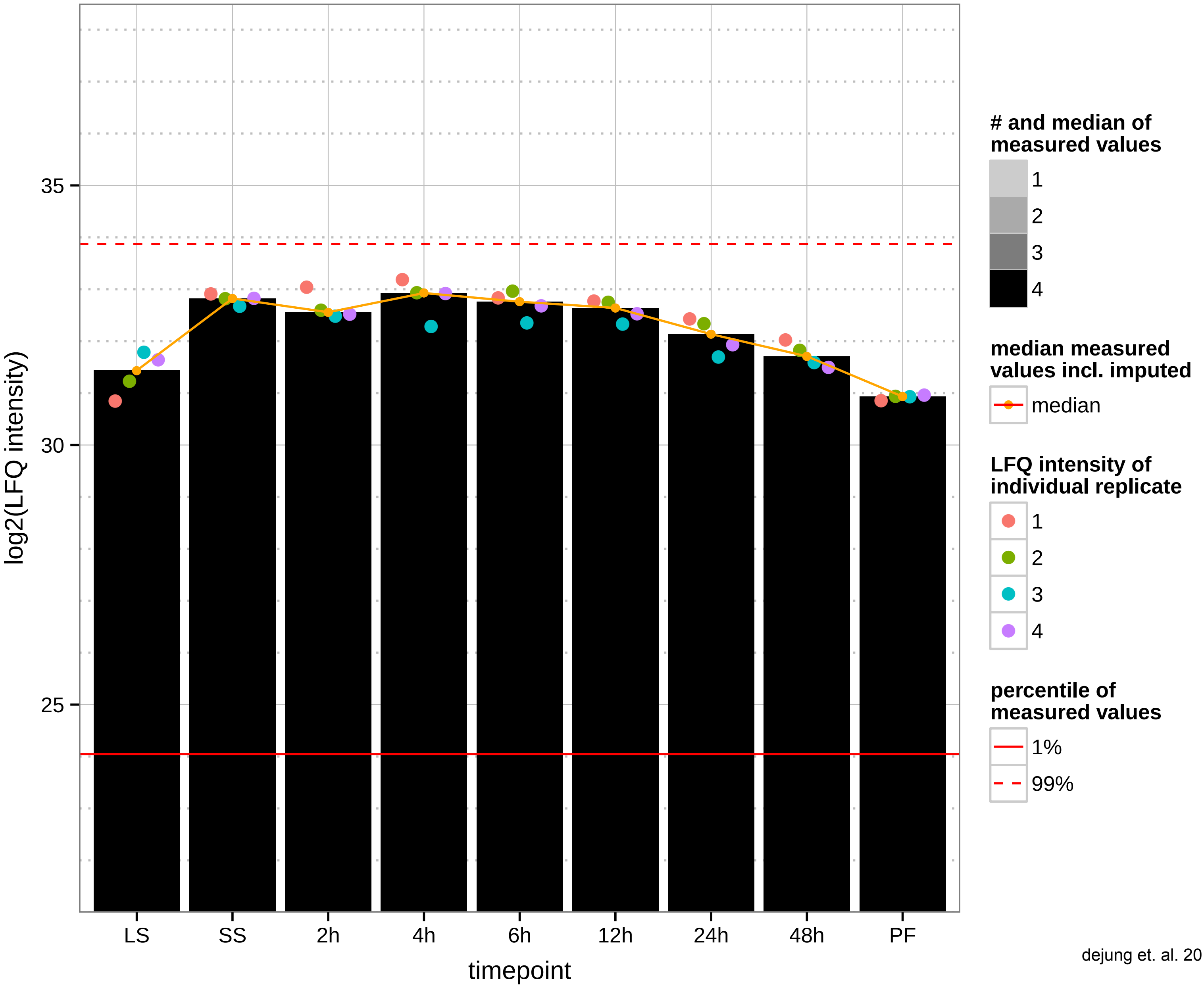
aspartate aminotransferase
Tb927.10.3660
AGOF: L–aspartate:2–oxoglutarate aminotransferase activity, pyridoxal phosphate binding
AGOC: cytoplasm
AGOP: L–methionine salvage from methylthioadenosine, biosynthetic process
PGOF: pyridoxal phosphate binding, transferase activity
PGOC: null
PGOP: biosynthetic process





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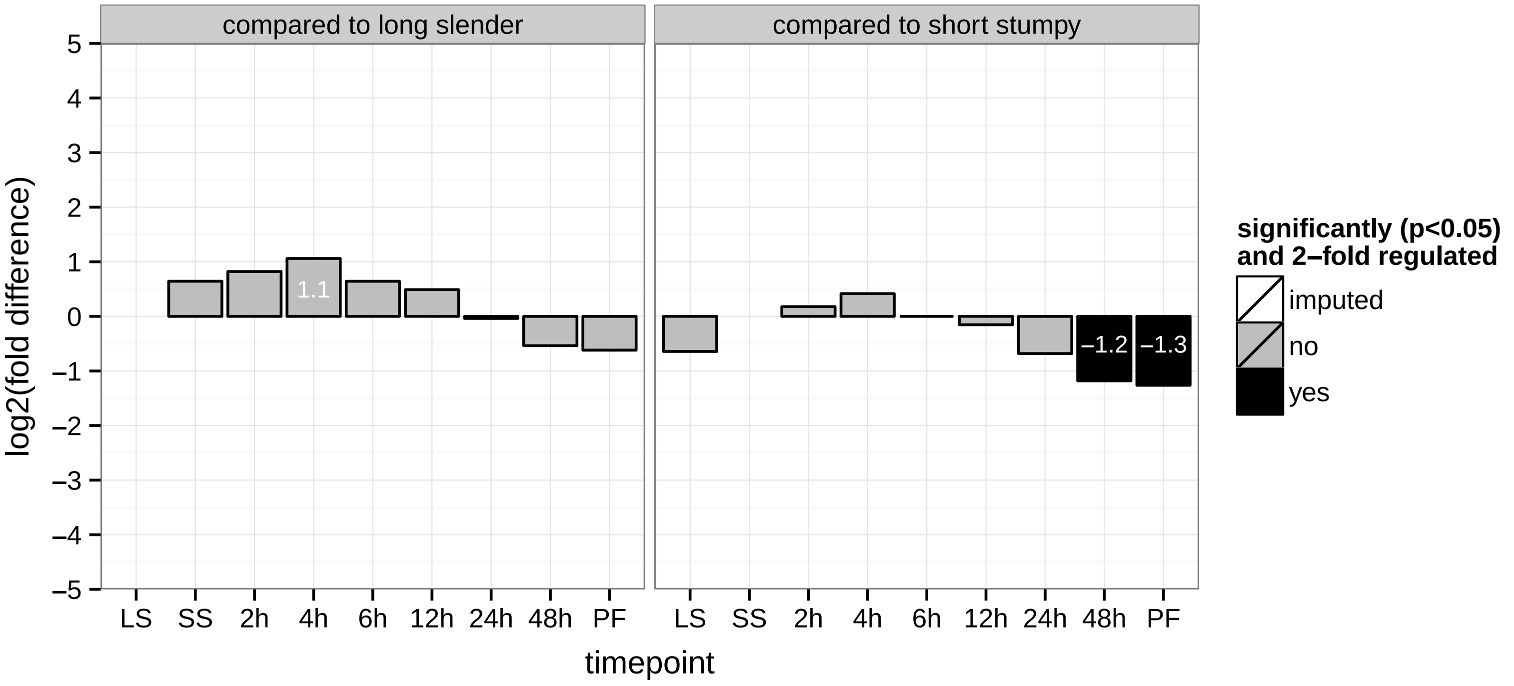
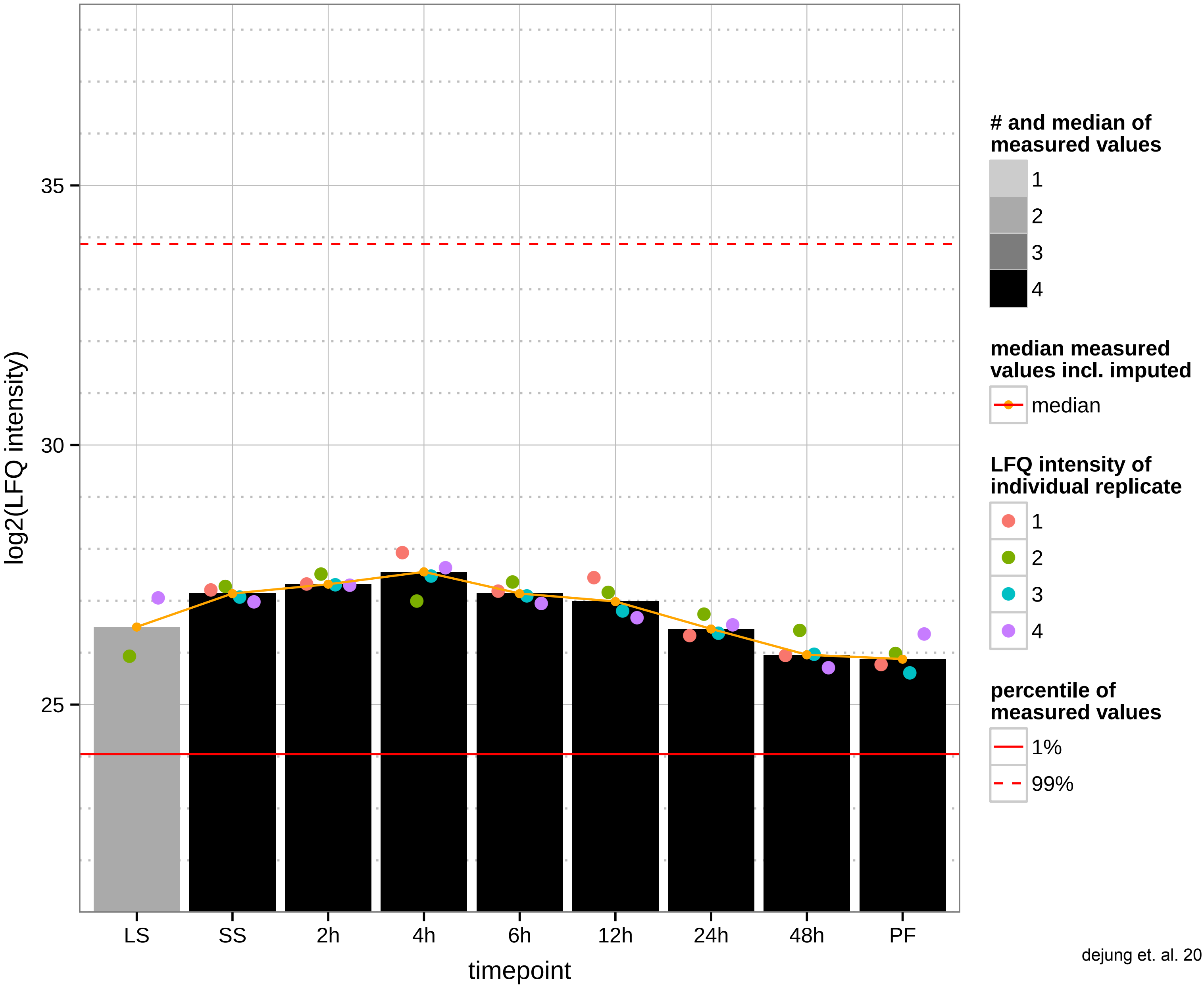
hypothetical protein, conserved
Tb927.10.3670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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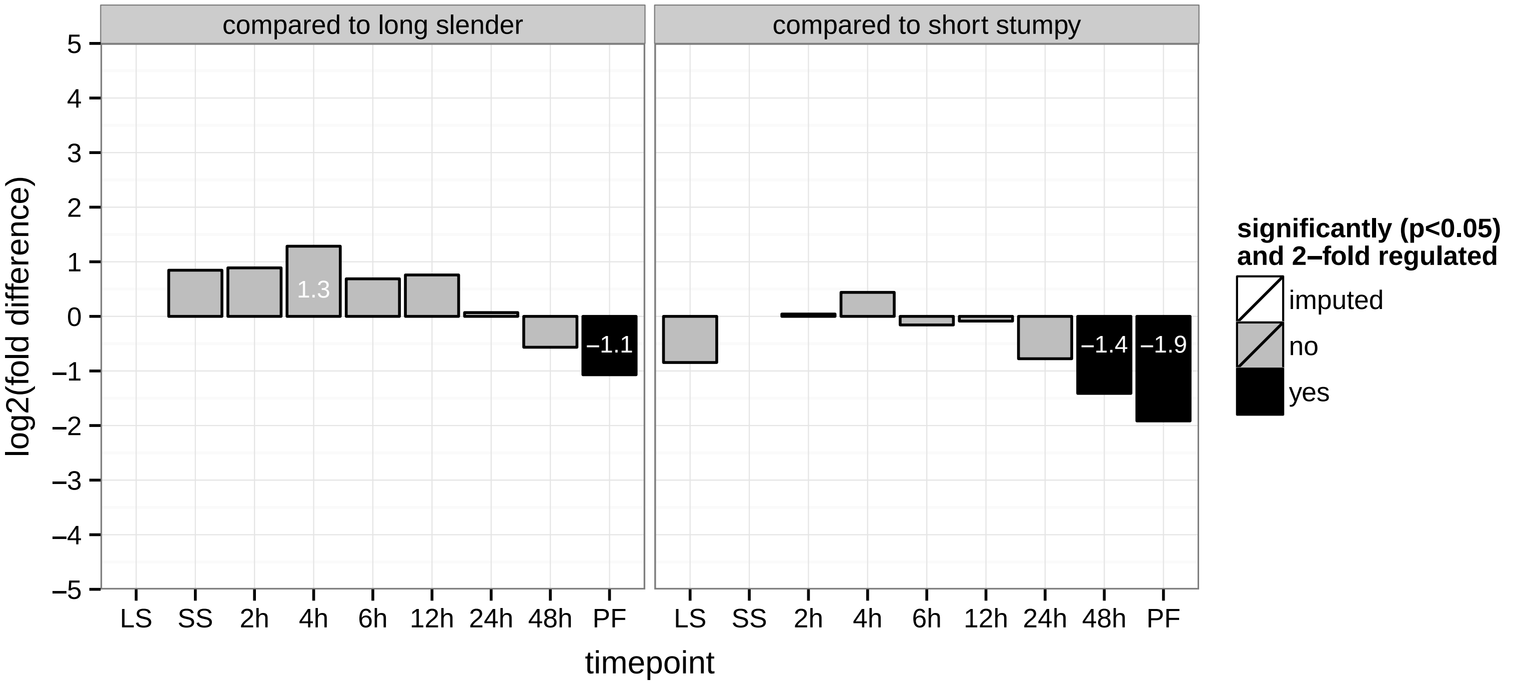
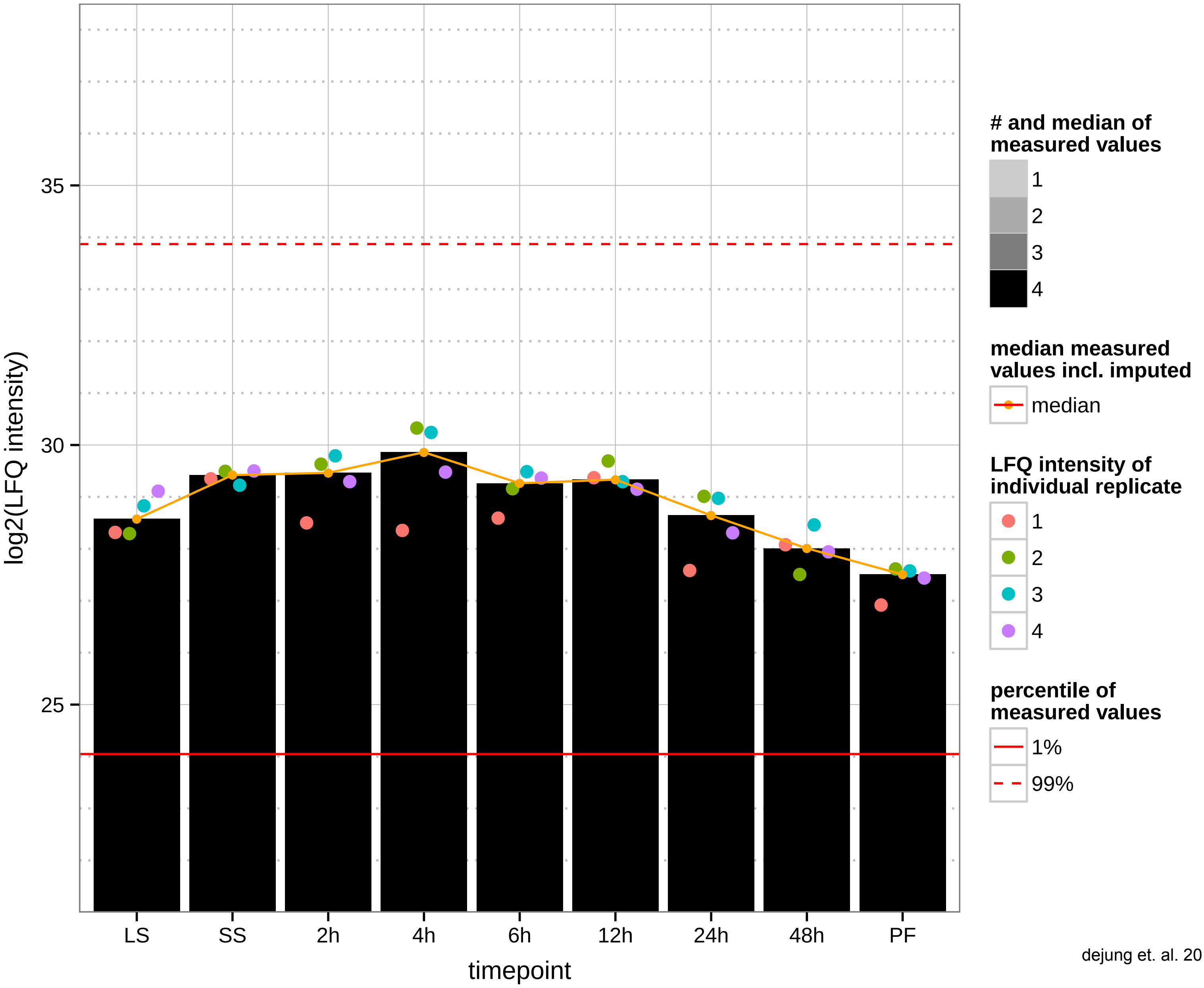
hypothetical protein, conserved
Tb927.10.390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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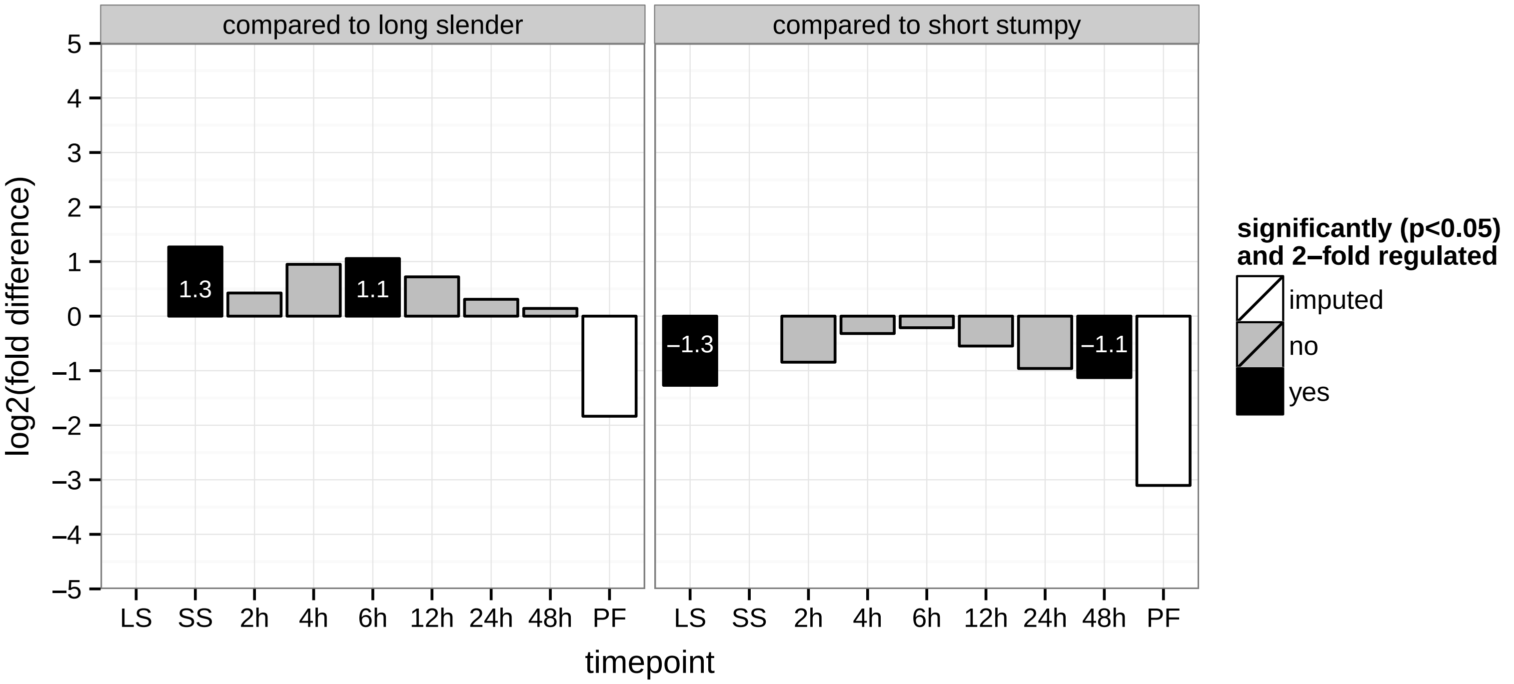
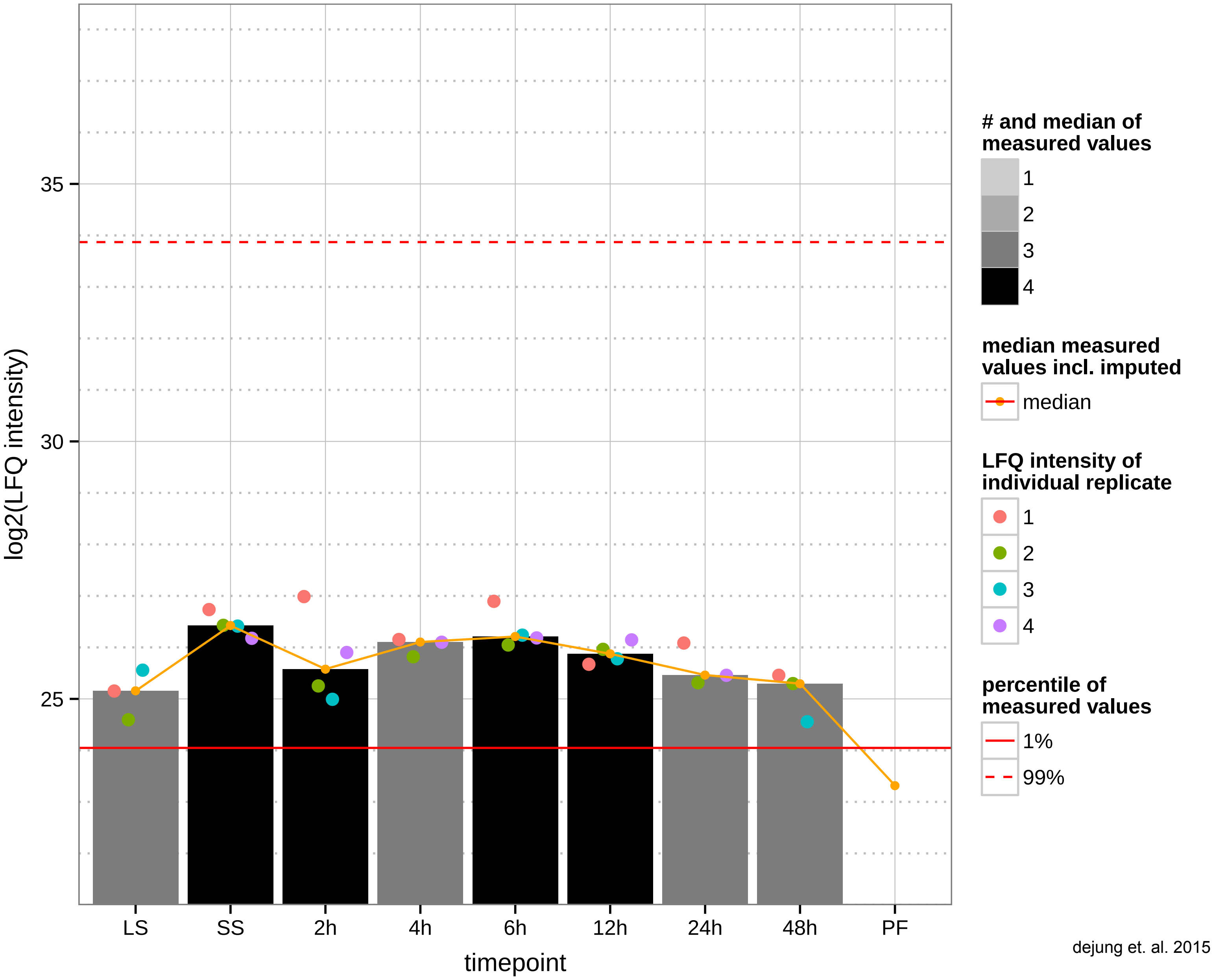
phosphatidylinositol–4–phosphate 5–kinase, putative
Tb927.10.4770
AGOF: 1–phosphatidylinositol–4–phosphate 5–kinase activity
AGOC: null
AGOP: phosphatidylinositol metabolic process
PGOF: phosphatidylinositol phosphate kinase activity
PGOC: null
PGOP: phosphatidylinositol metabolic process





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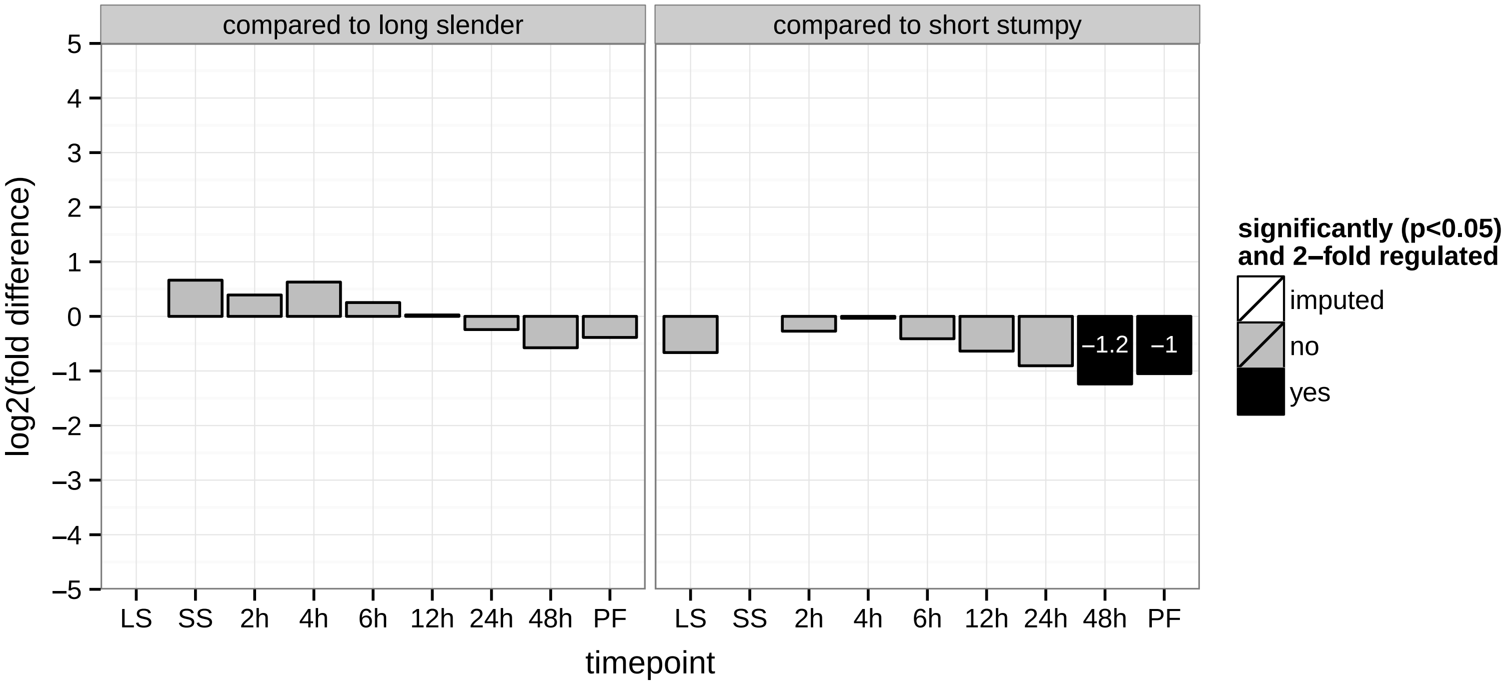
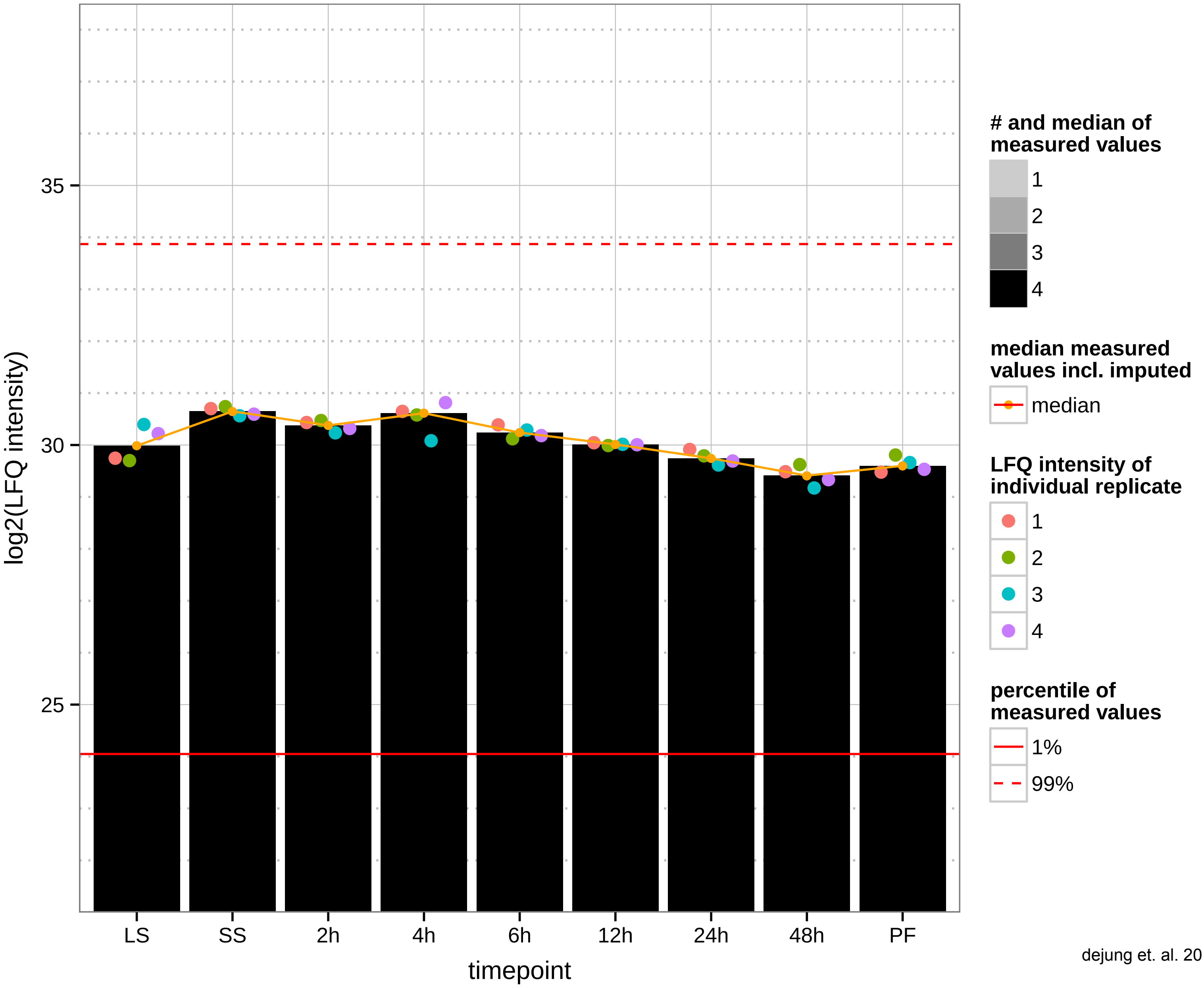
mitogen–activated protein kinase 2, putative (MPK2)
Tb927.10.5140
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: cytokinesis after mitosis, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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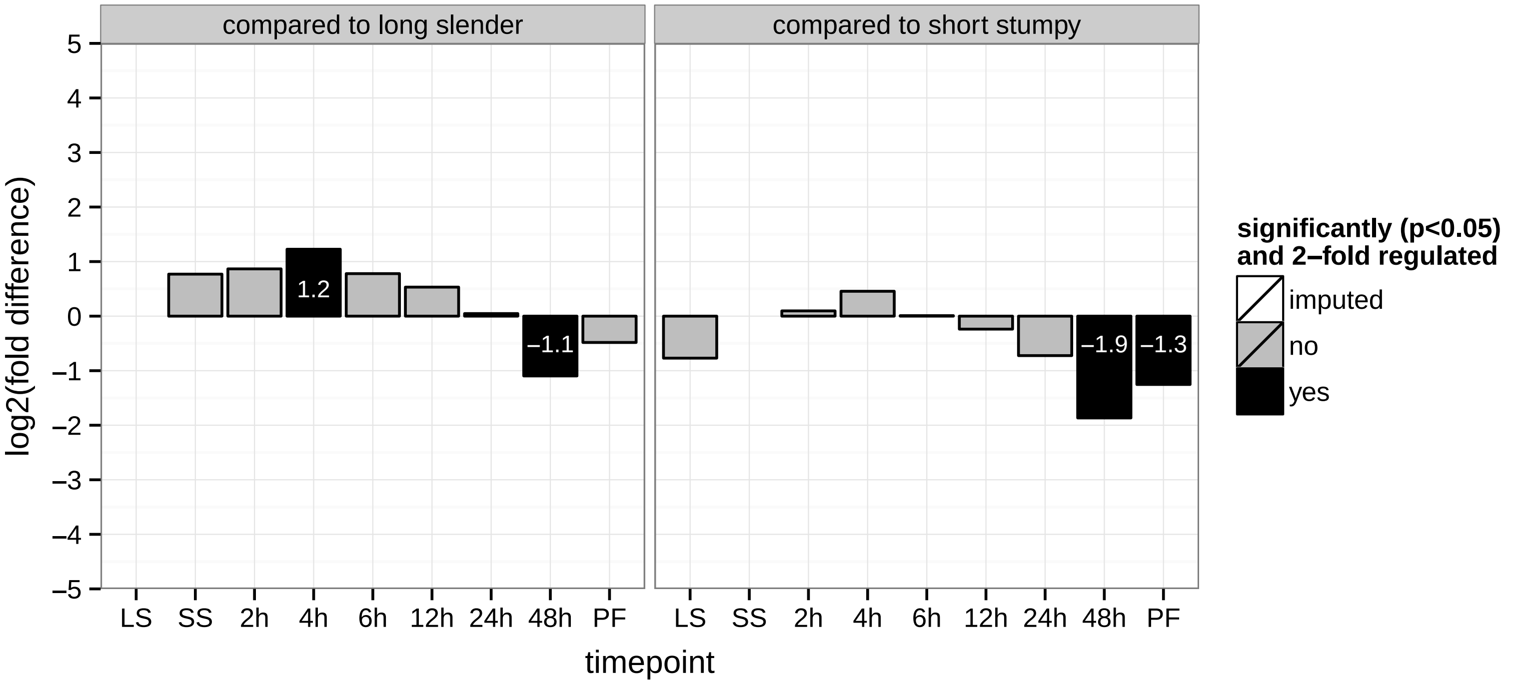
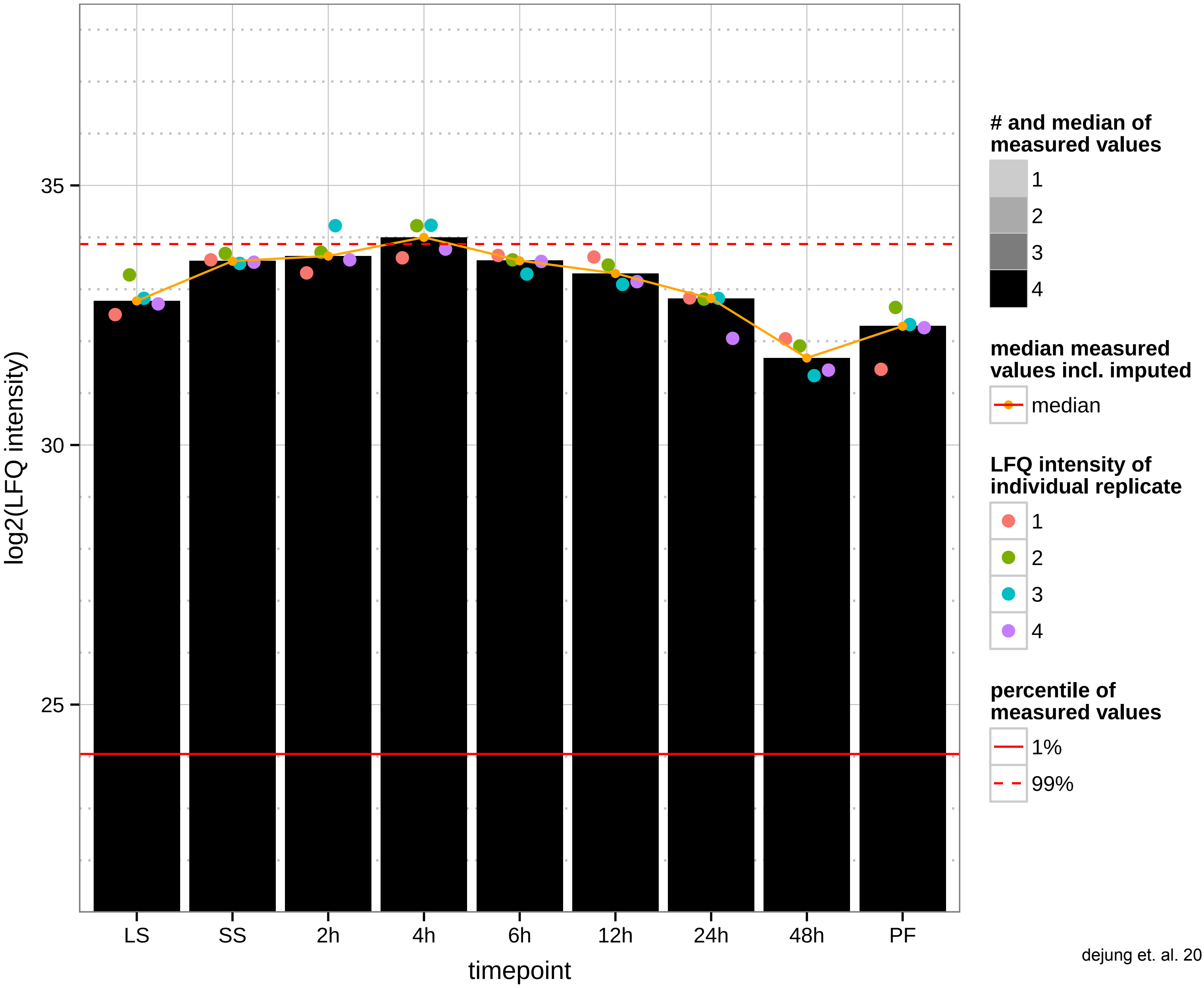
hypothetical protein, conserved
Tb927.10.5810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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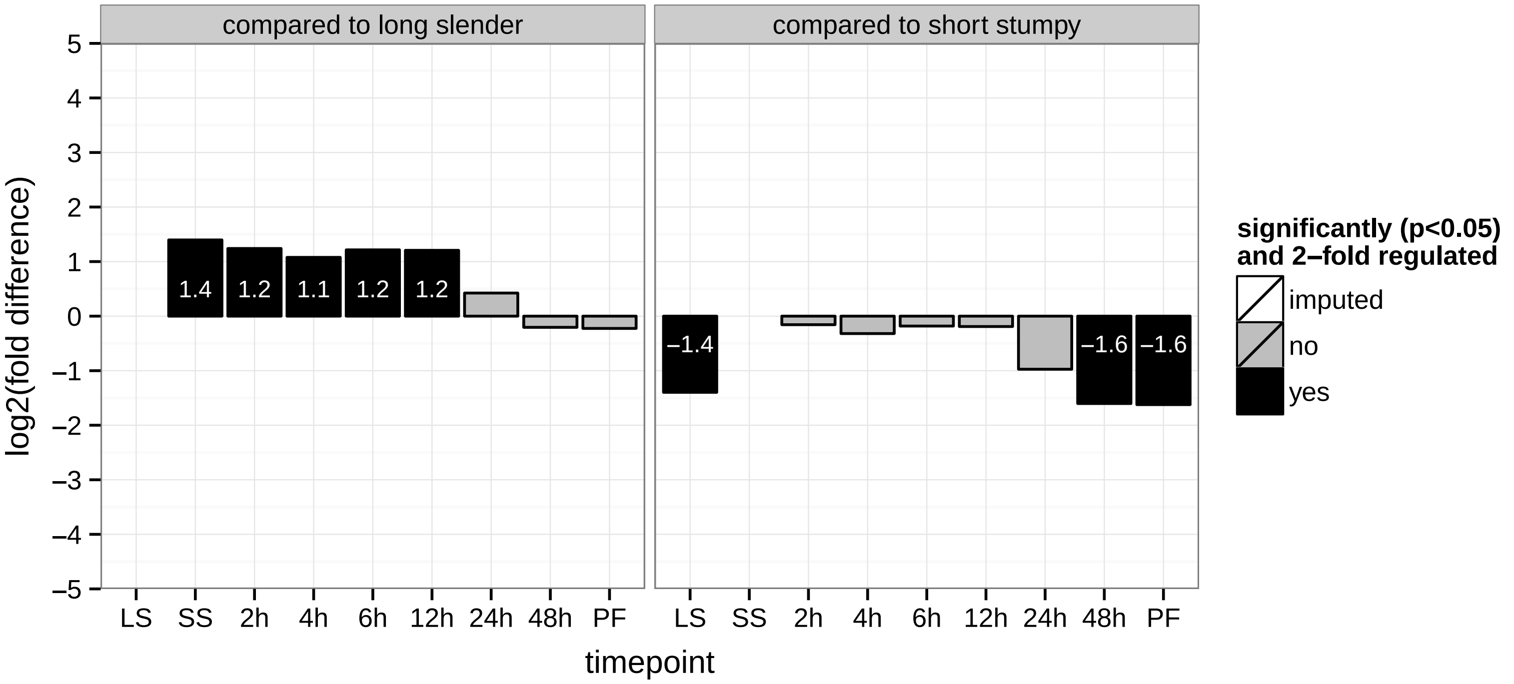
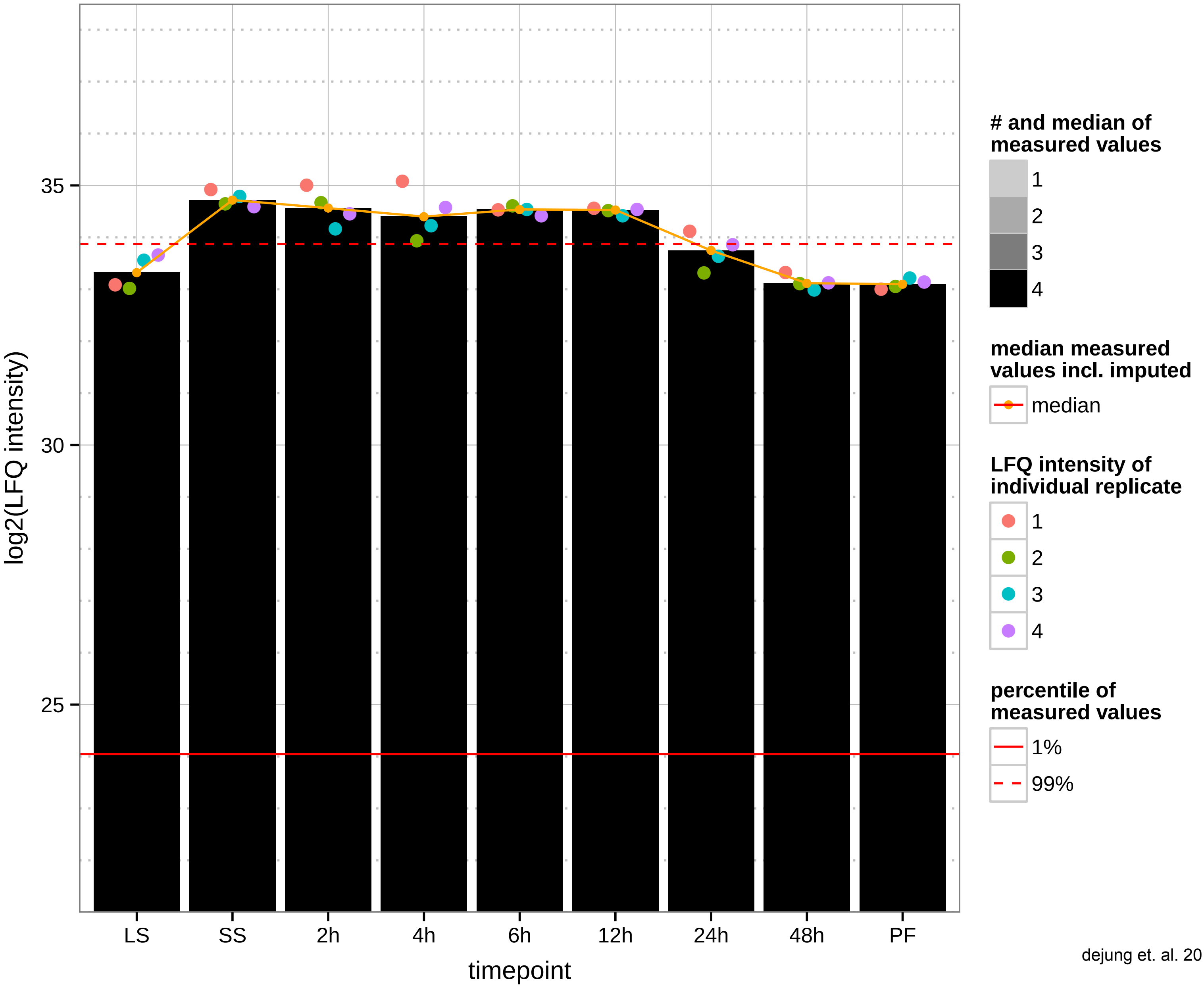
clathrin heavy chain, putative, clathrin heavy chain (CHC)
Tb927.10.6050;Tb11.v5.0198
AGOF: null, structural molecule activity
AGOC: null, clathrin coat of coated pit, clathrin coat of trans−Golgi network vesicle
AGOP: null, intracellular protein transport, vesicle−mediated transport
PGOF: binding, structural molecule activity
PGOC: null, clathrin coat of coated pit, clathrin coat of trans−Golgi network vesicle
PGOP: intracellular protein transport, vesicle−mediated transport





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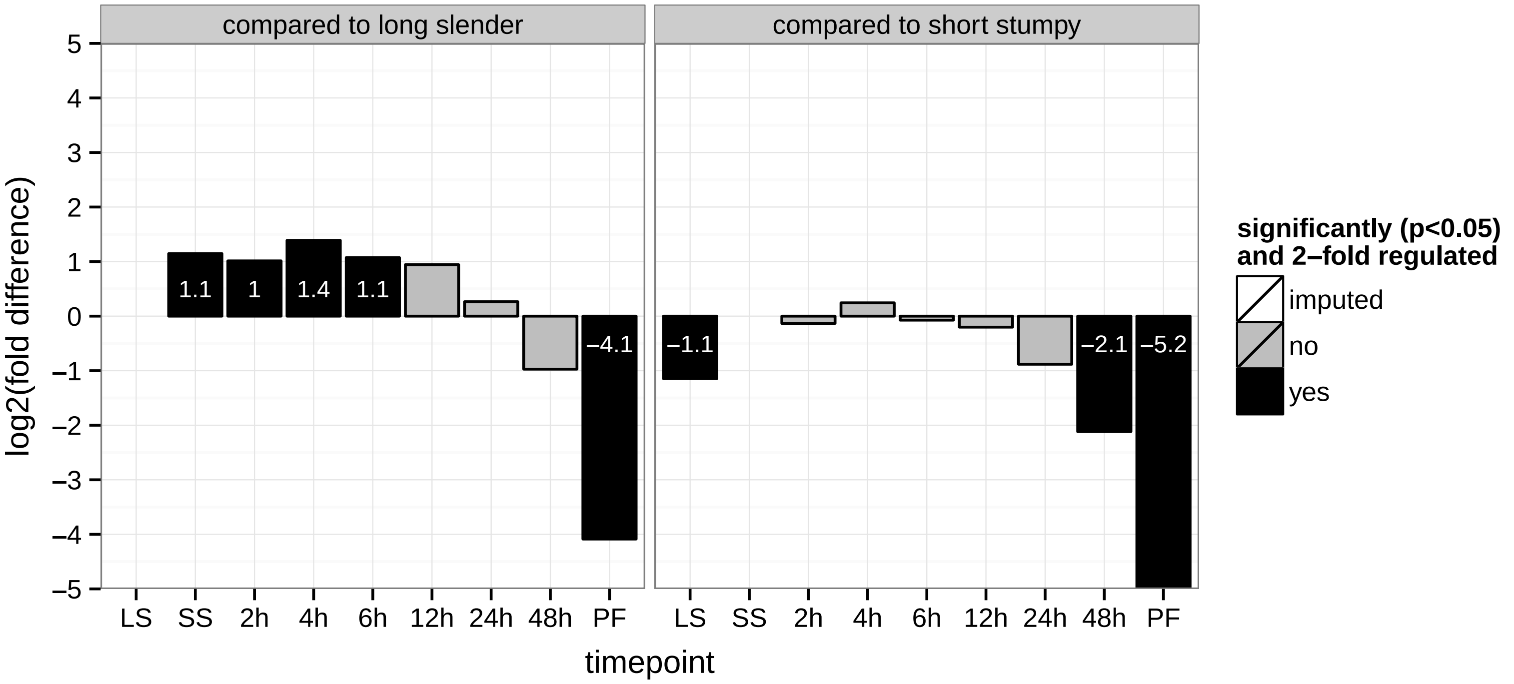
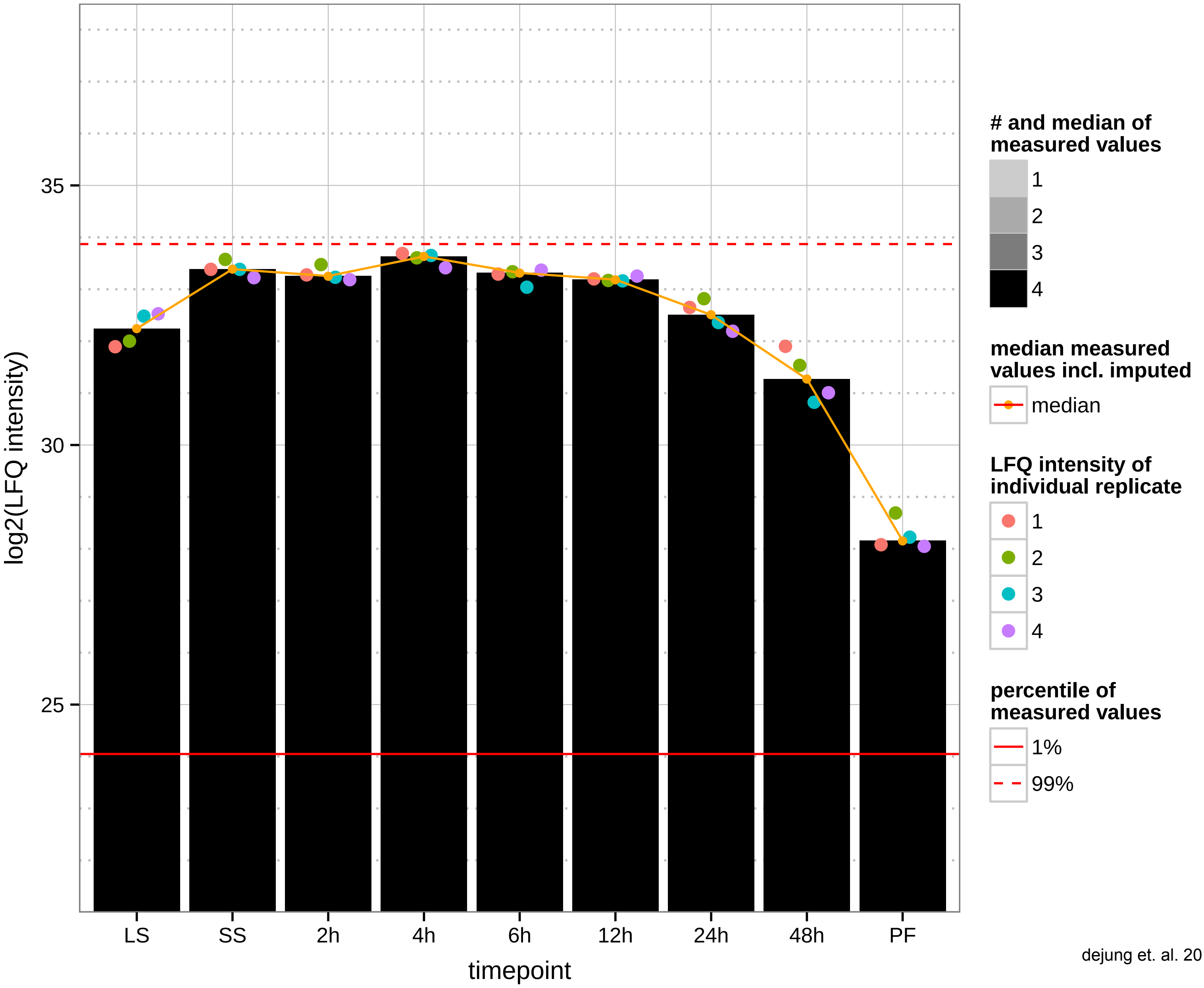
alternative oxidase (AOX)
Tb927.10.7090
AGOF: alternative oxidase activity, ferric iron binding, oxidoreductase activity
AGOC: mitochondrial envelope, mitochondrial inner membrane, mitochondrion
AGOP: oxidation–reduction process, respiratory gaseous exchange
PGOF: null
PGOC: mitochondrial envelope
PGOP: oxidation–reduction process, respiratory gaseous exchange





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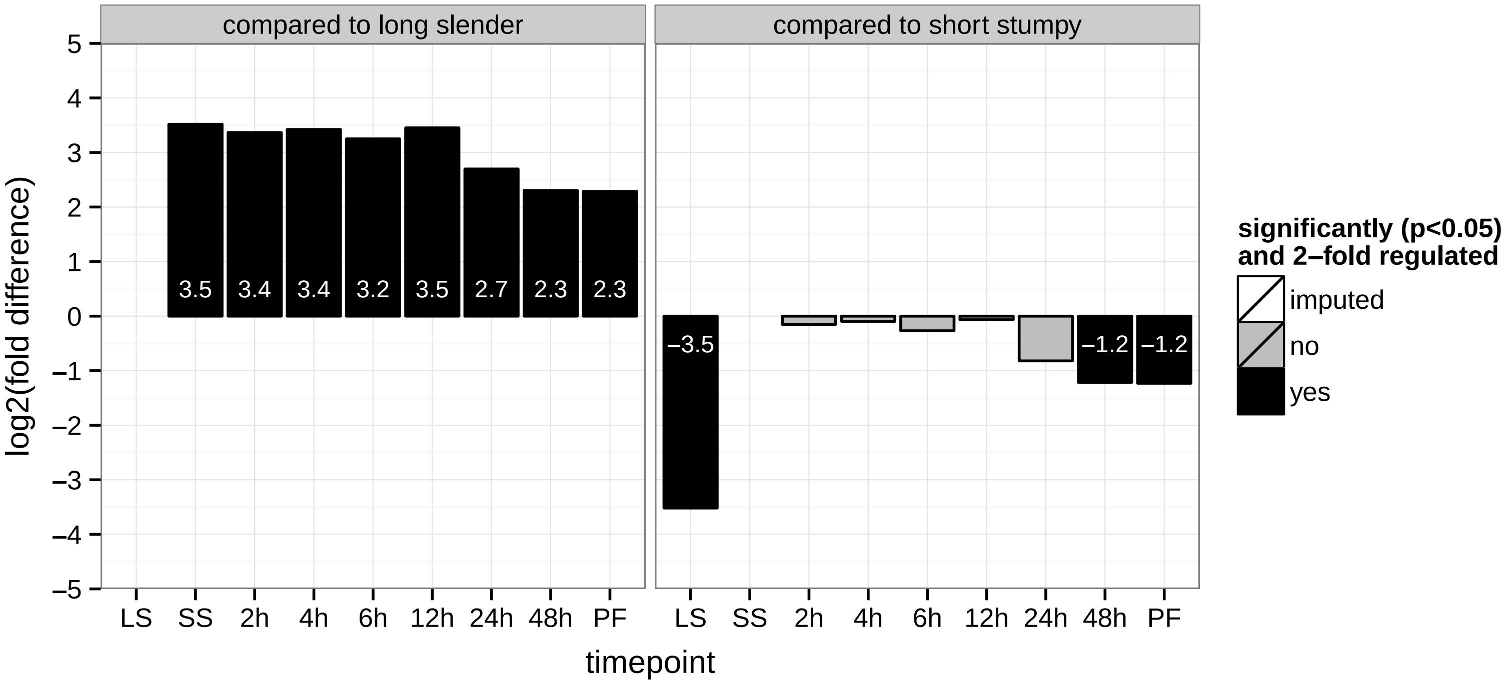
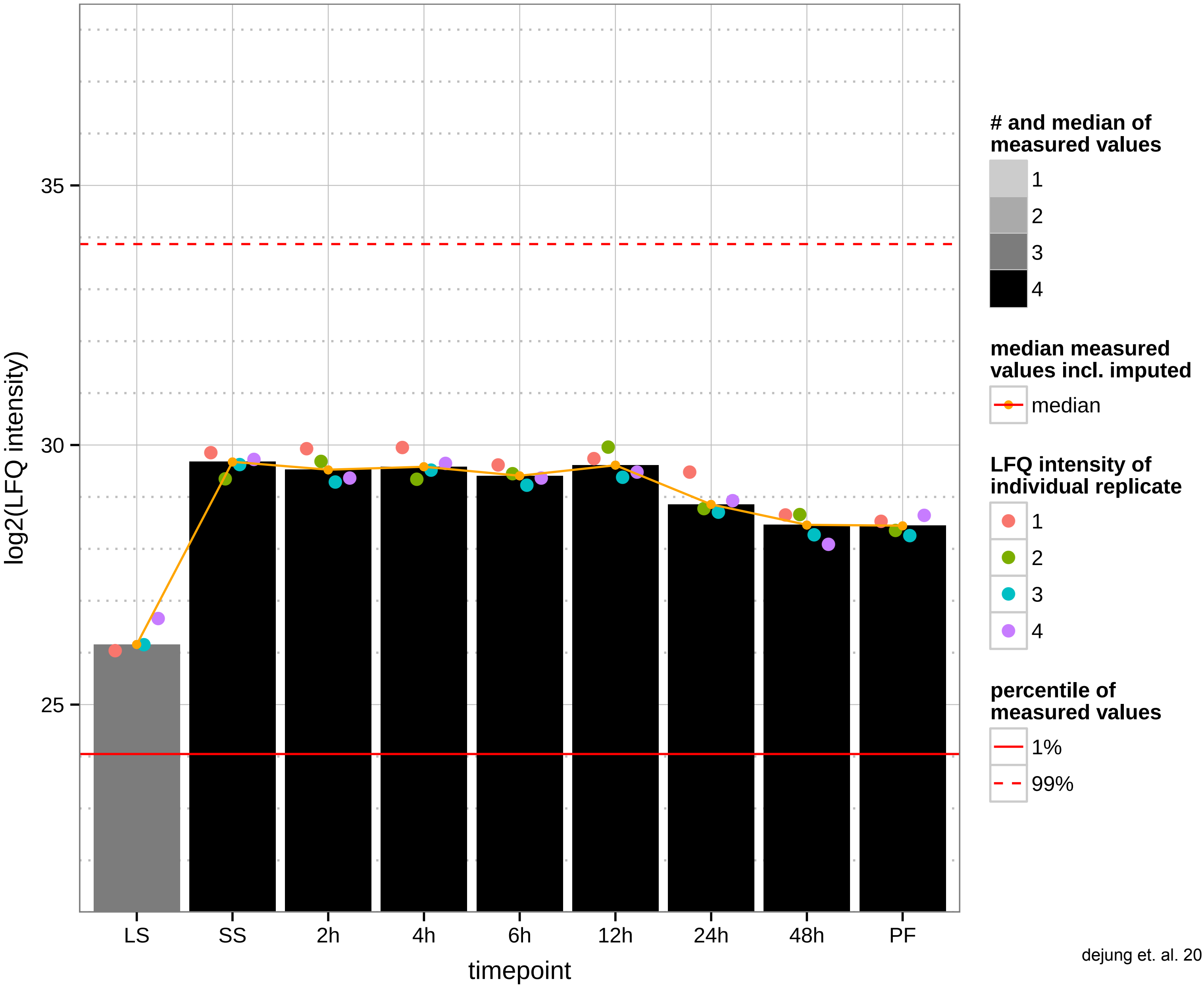
inositol–3–phosphate synthase, putative
Tb927.10.7110
AGOF: inositol–3–phosphate synthase activity
AGOC: null
AGOP: inositol biosynthetic process, metabolic process, phospholipid biosynthetic process
PGOF: inositol–3–phosphate synthase activity
PGOC: null
PGOP: inositol biosynthetic process, phospholipid biosynthetic process





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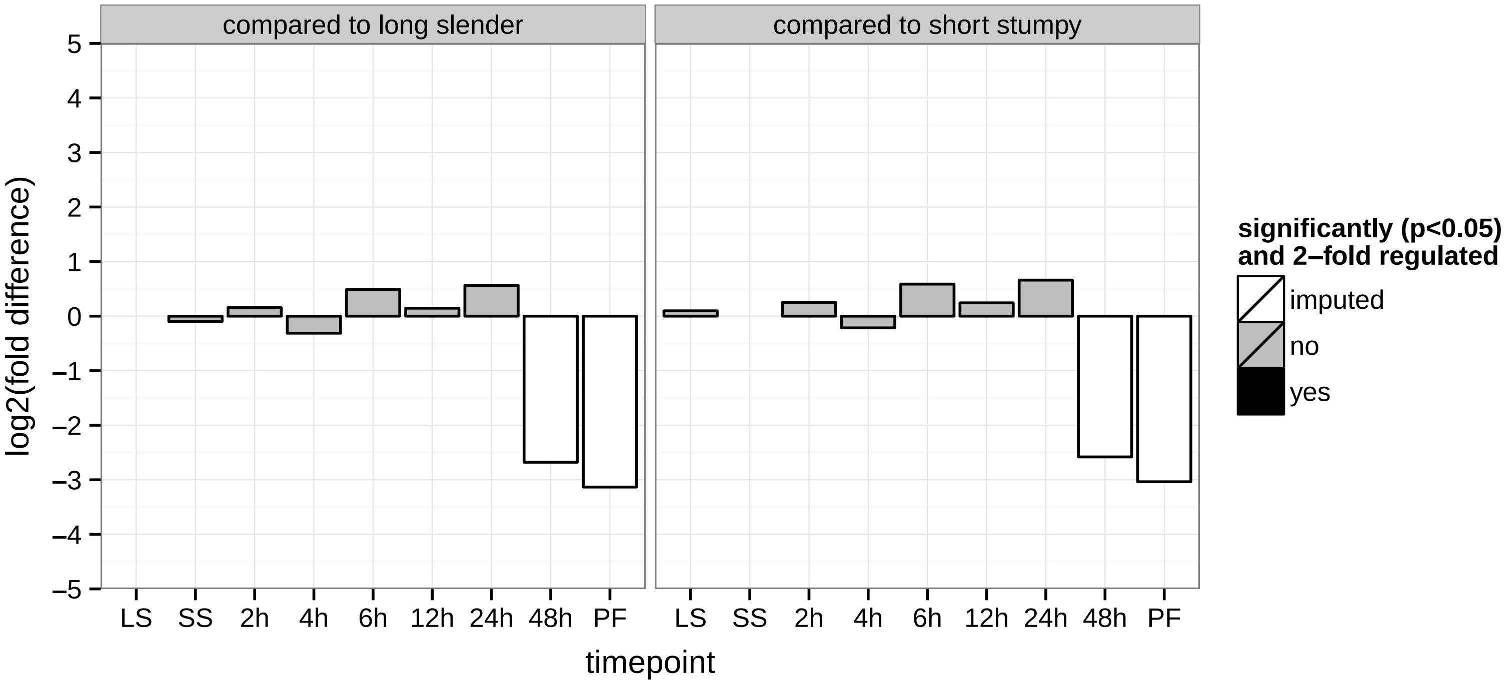
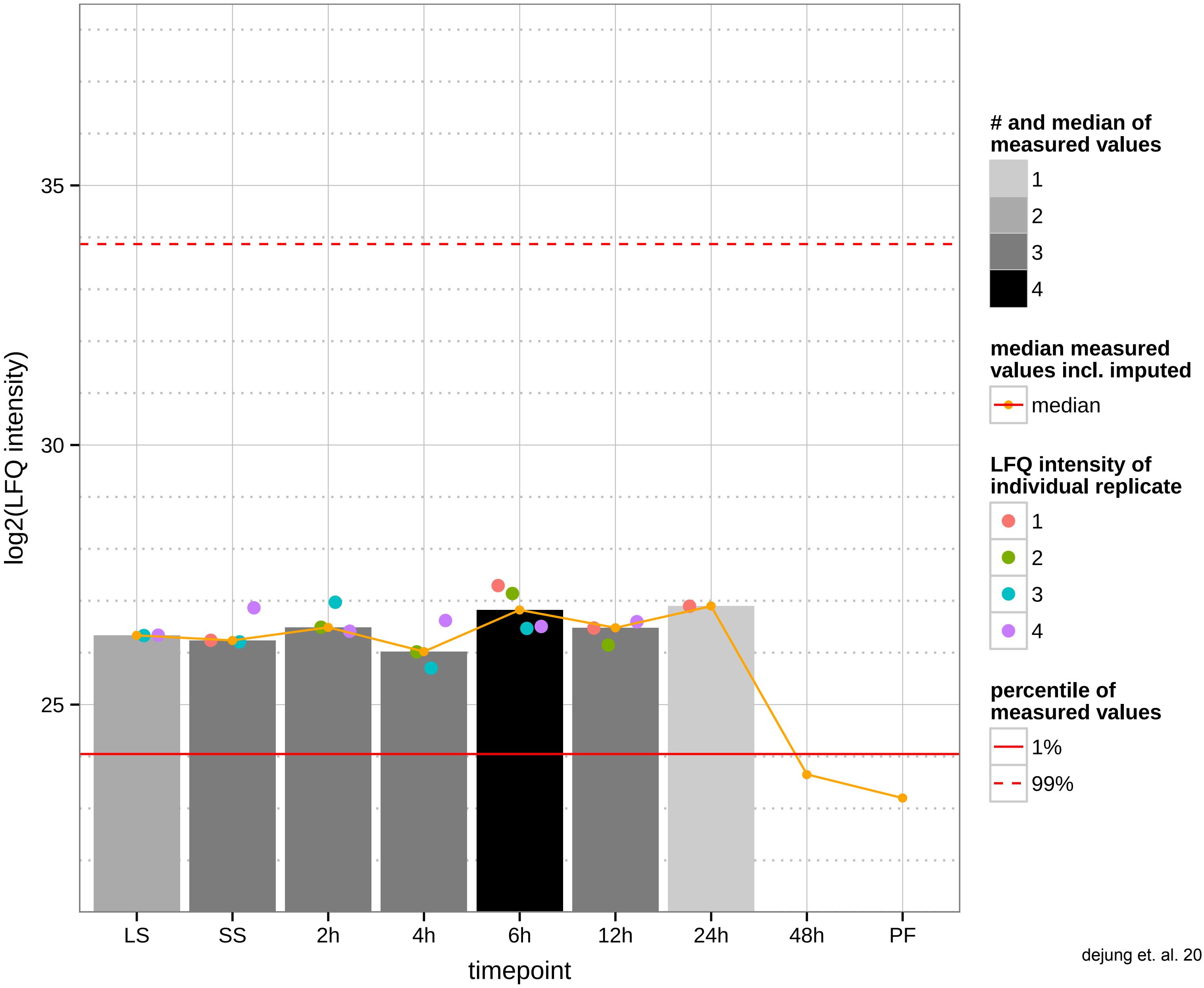
hypothetical protein, conserved
Tb927.10.7820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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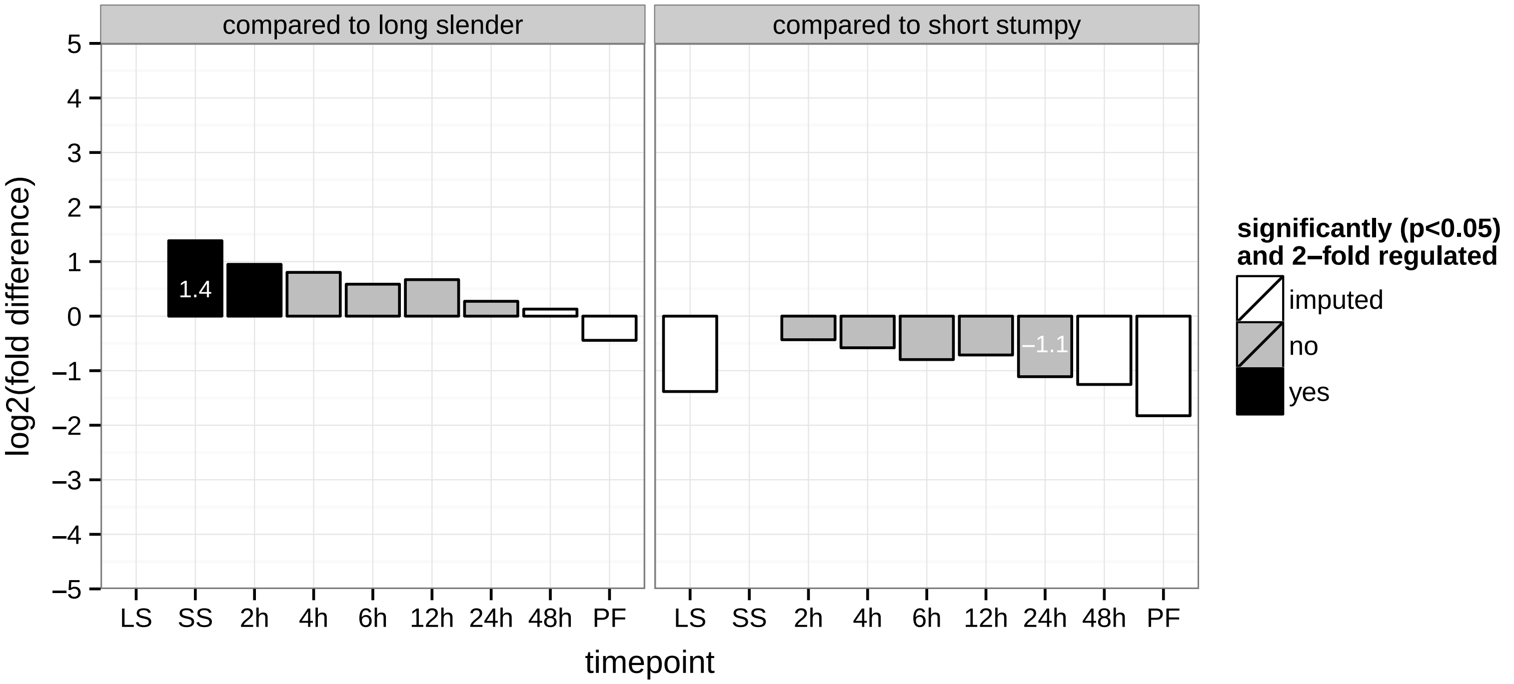
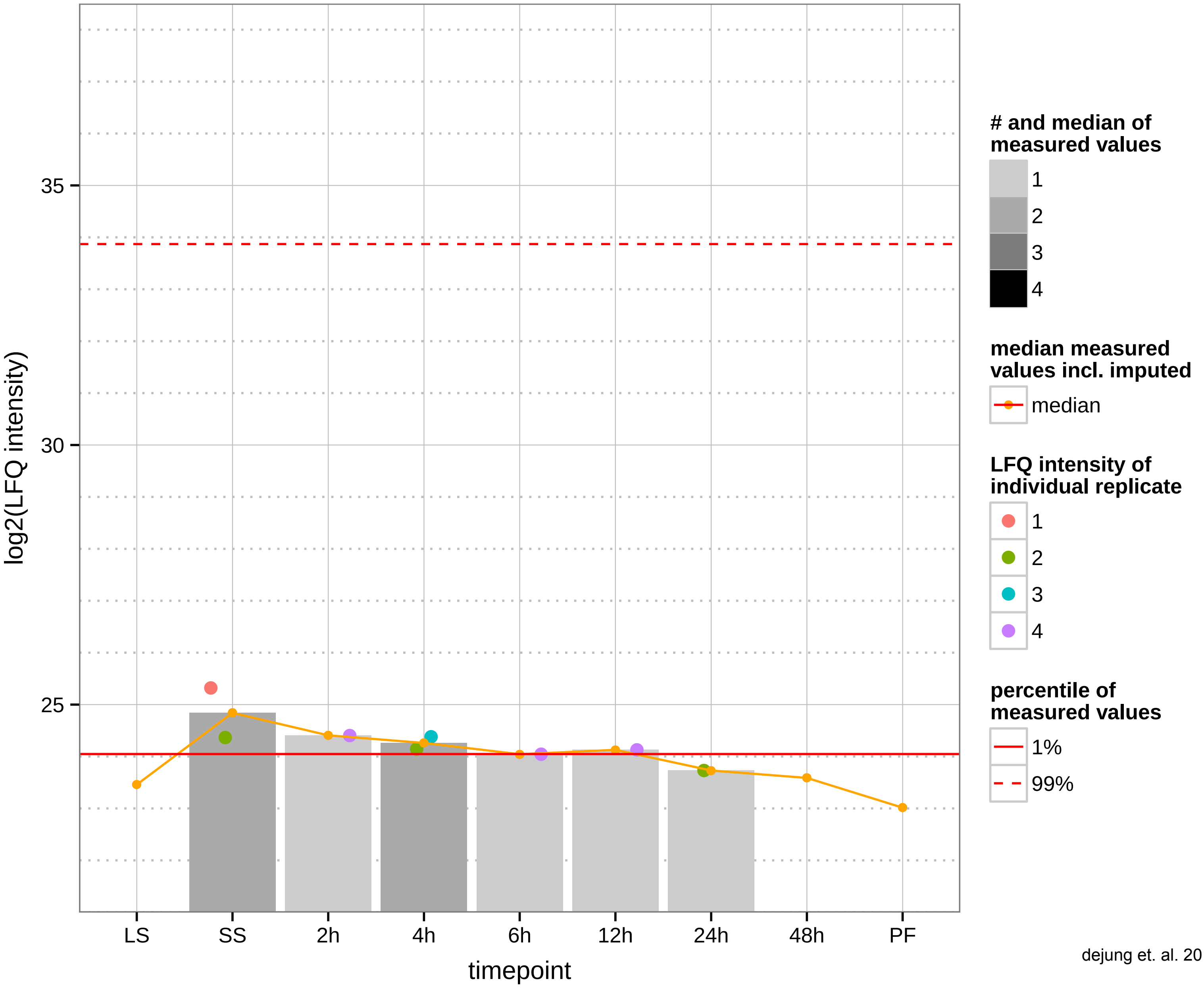
DNA–(apurinic or apyrimidinic site) lyase, putative
Tb927.11.10640
AGOF: endonuclease activity
AGOC: null
AGOP: DNA repair
PGOF: nuclease activity
PGOC: null
PGOP: DNA repair





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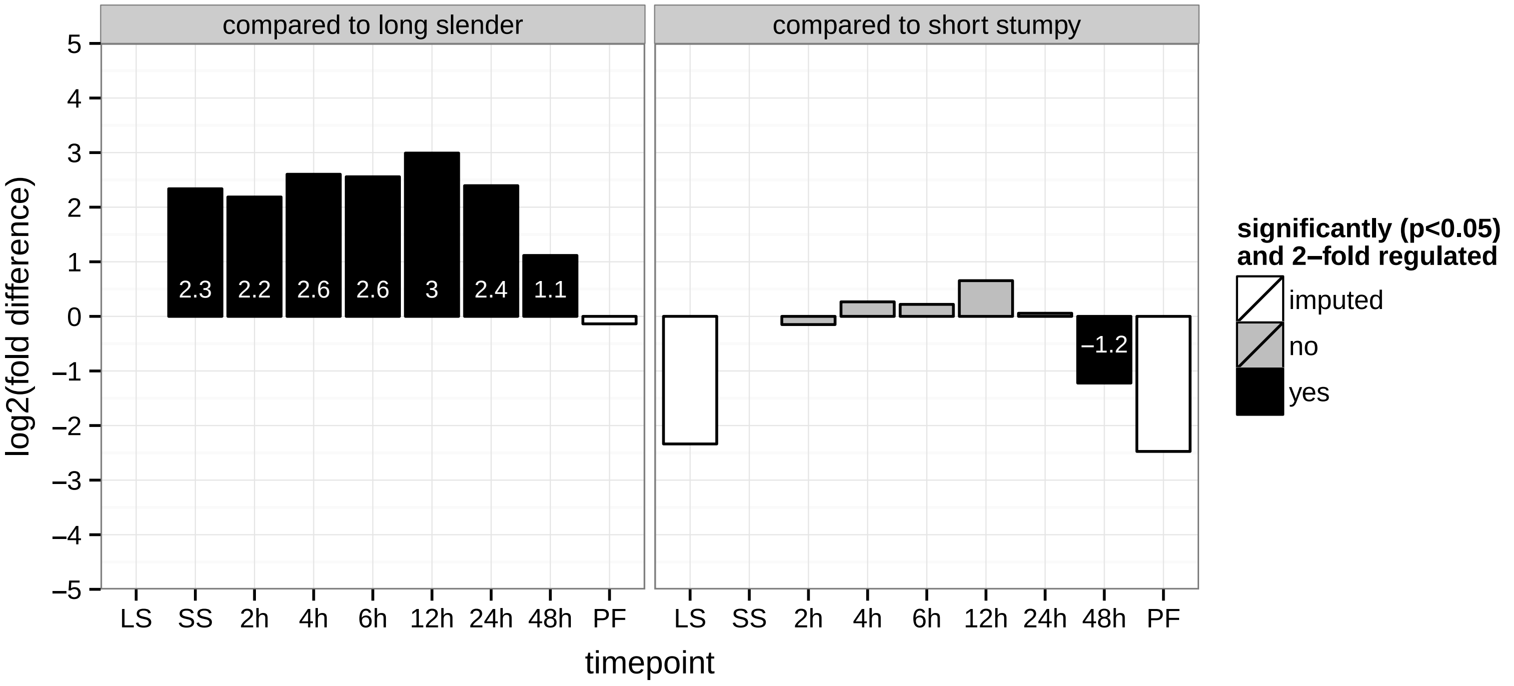
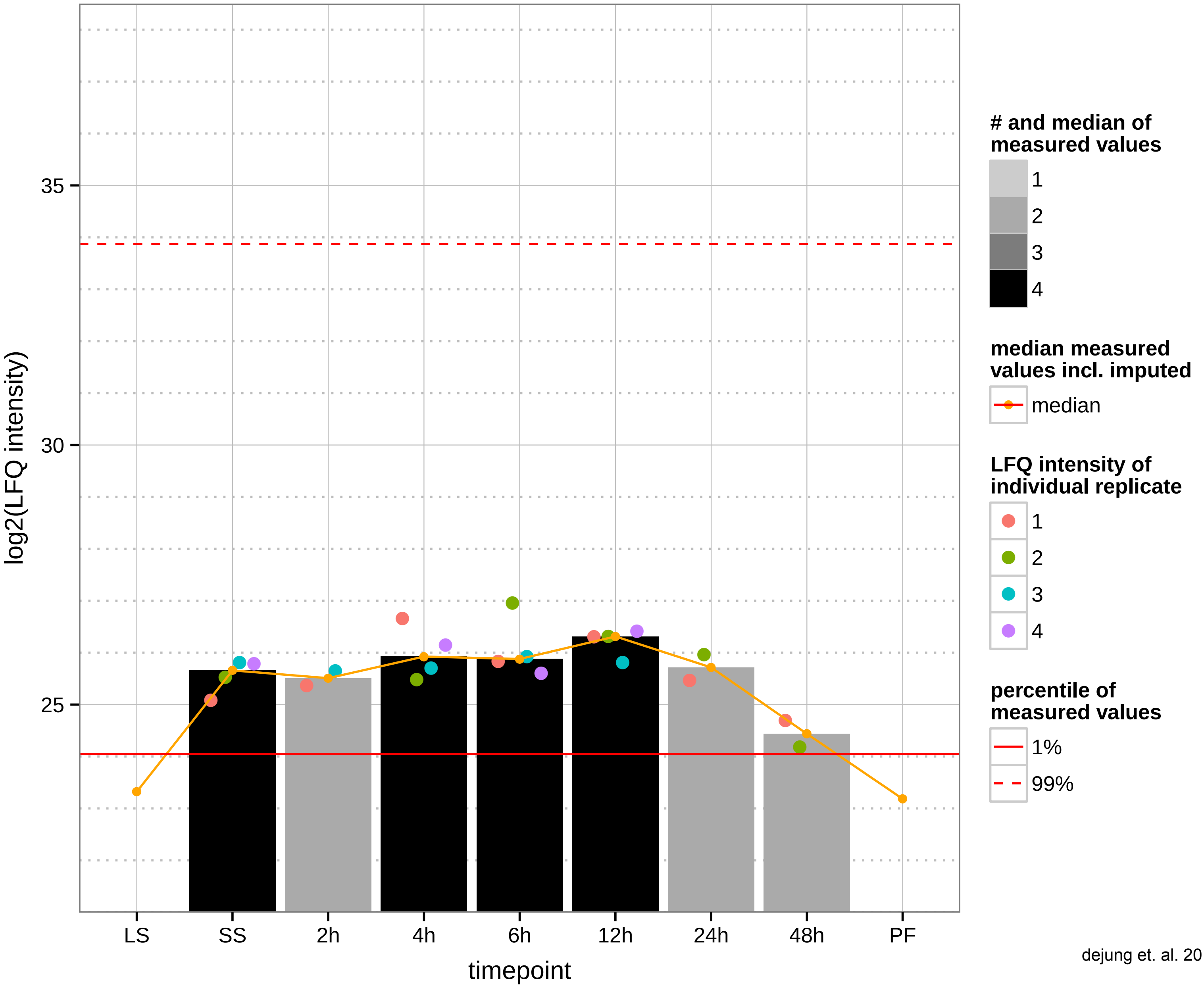
trans−sialidase, putative
Tb927.11.11410
AGOF: exo−alpha−sialidase activity
AGOC: null
AGOP: pathogenesis
PGOF: null
PGOC: null
PGOP: null





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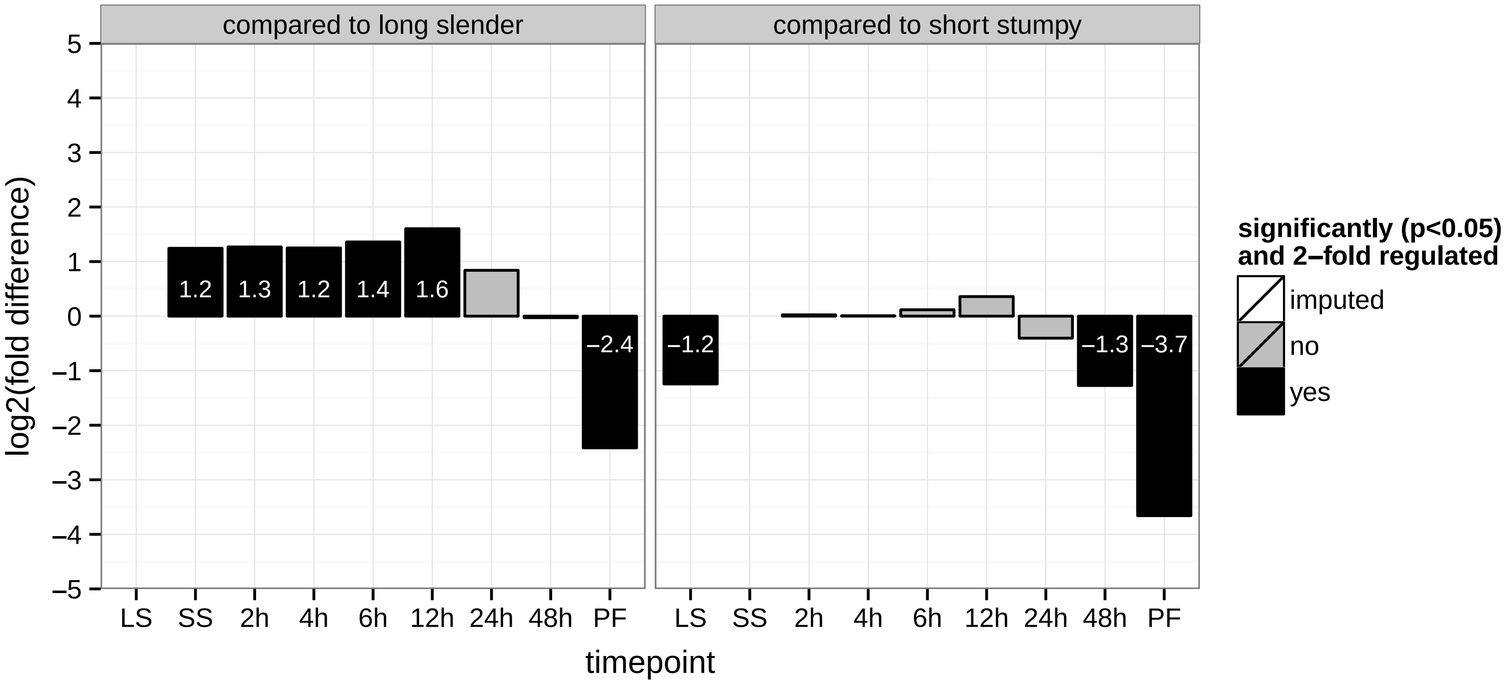
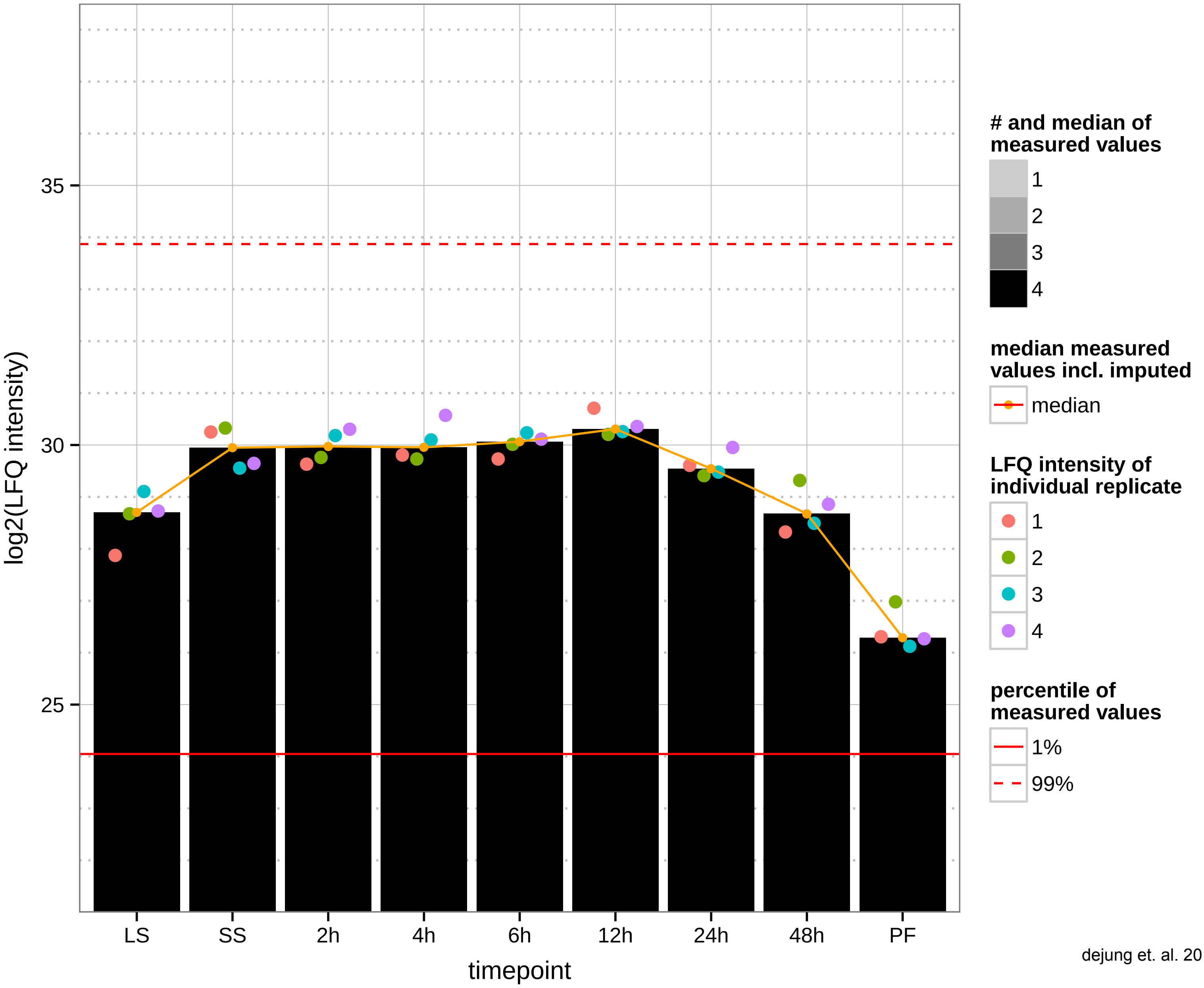
Trichohyalin, putative
Tb927.11.11480
AGOF: null
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, quorum sensing involved in interaction with ho
PGOF: null
PGOC: null
PGOP: null





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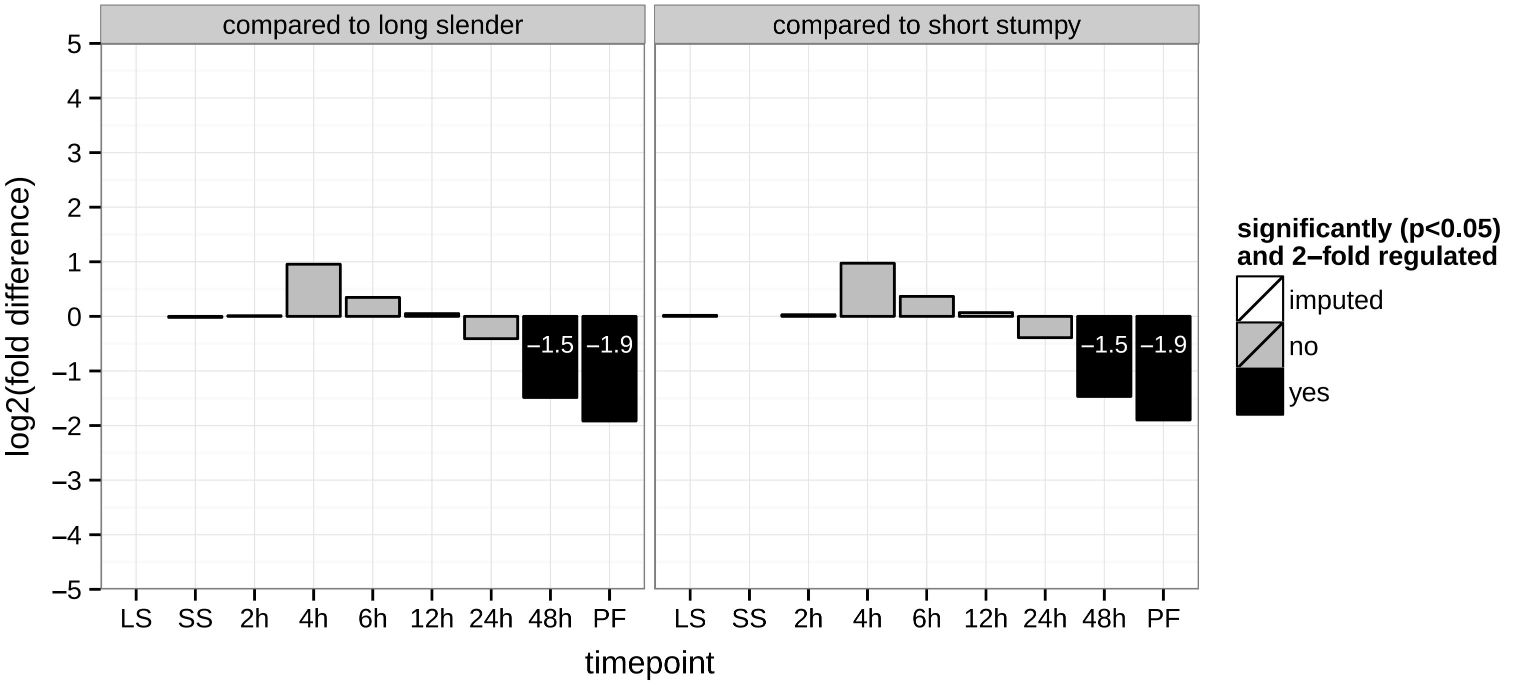
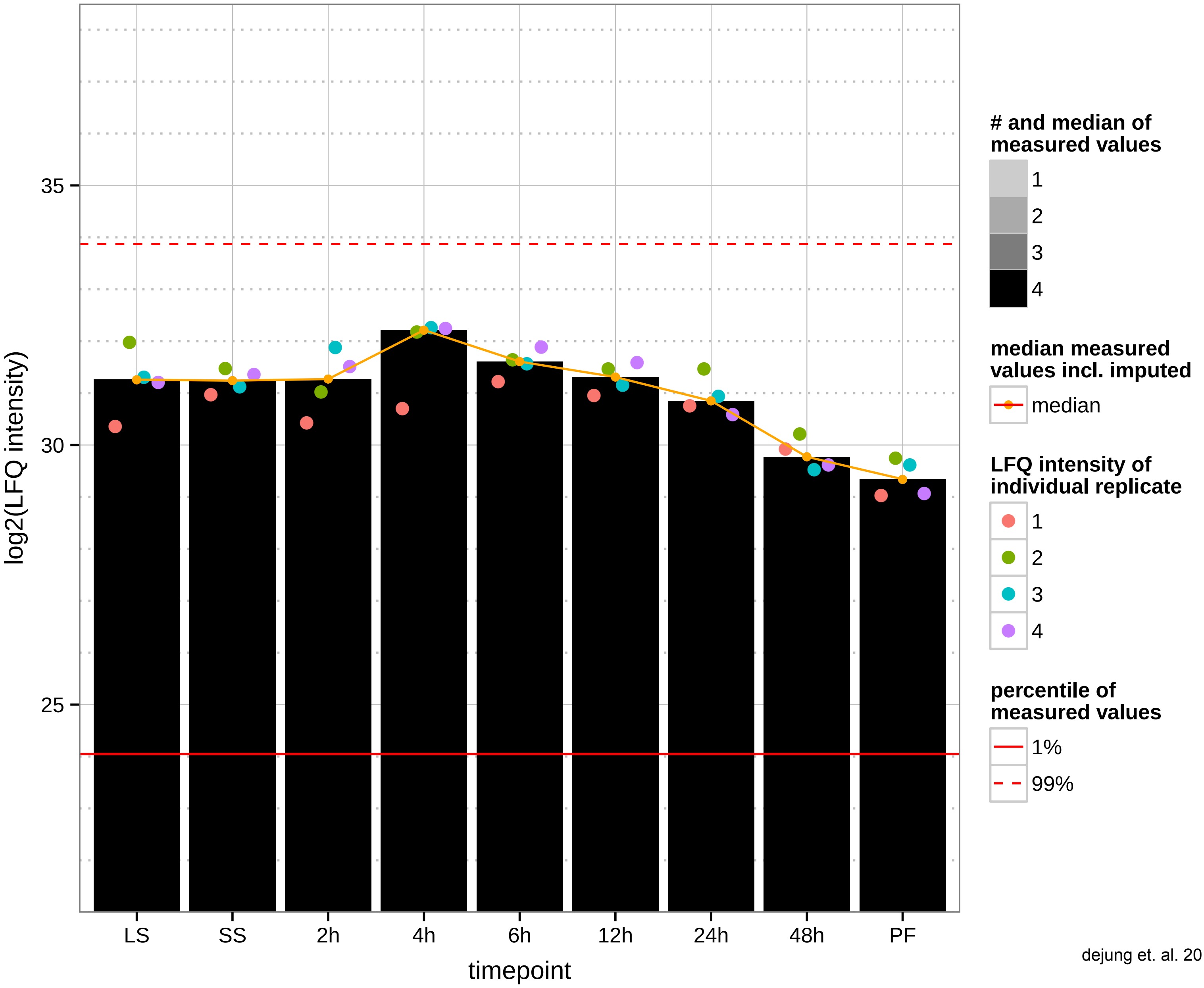
microtubule–associated protein, corset–associated protein 15 (CAP15)
Tb927.11.11980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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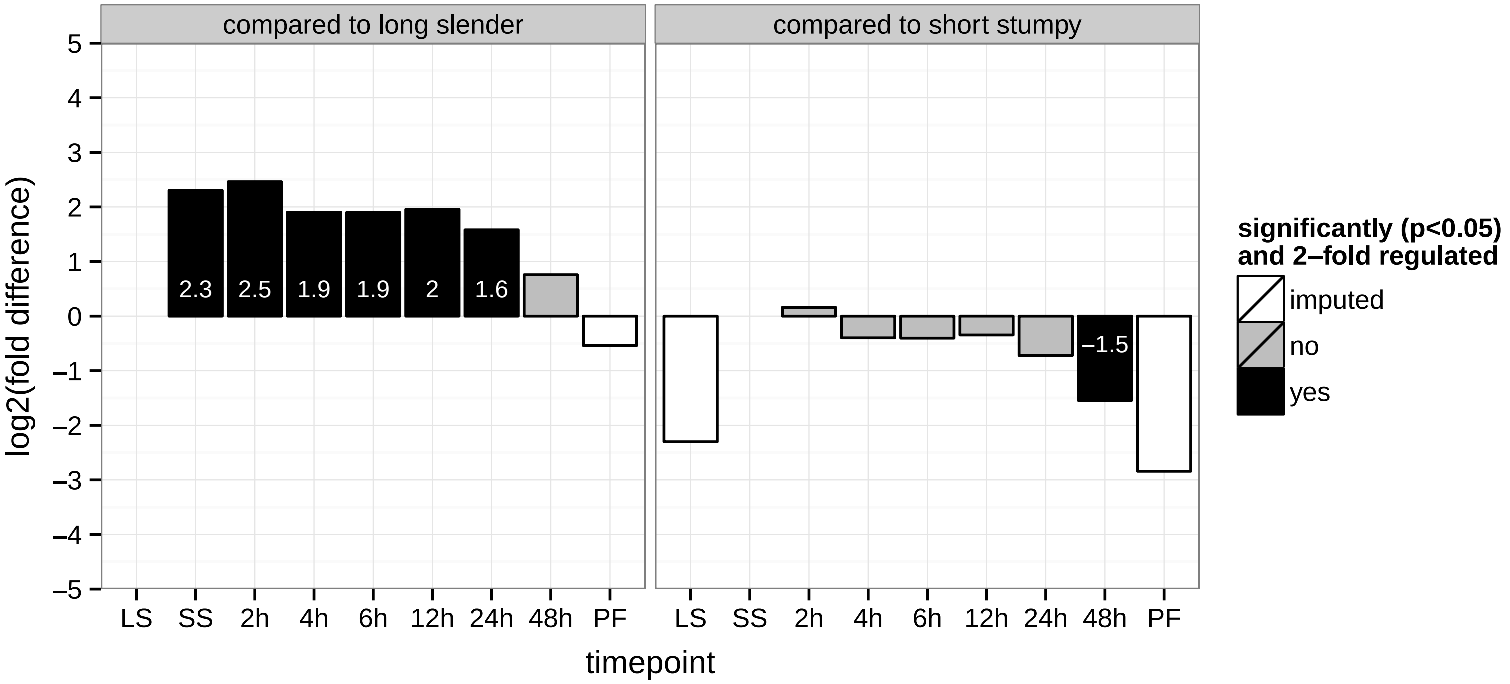
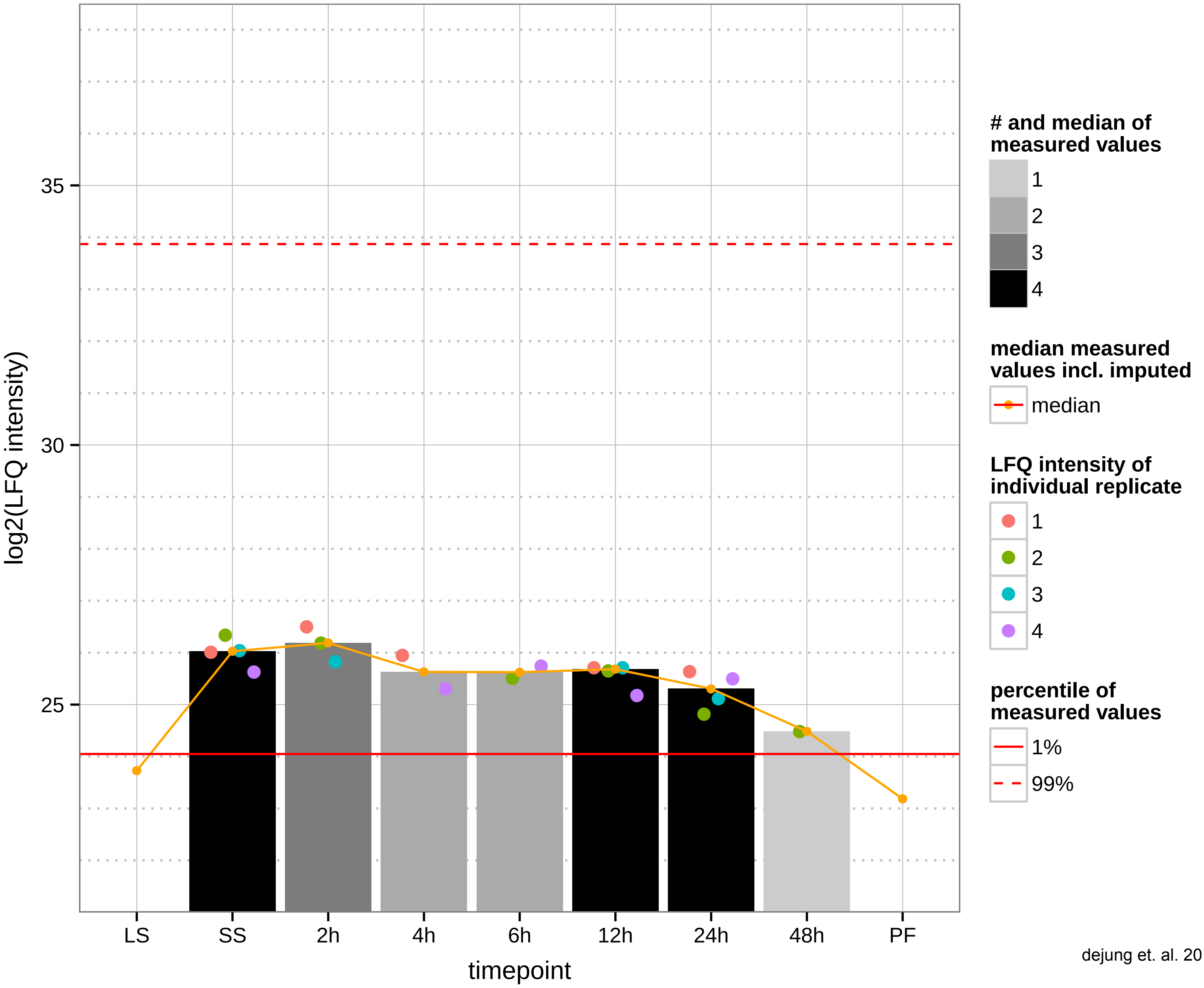
hypothetical protein, conserved
Tb927.11.12060
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: integral to peroxisomal membrane
PGOP: peroxisome fission





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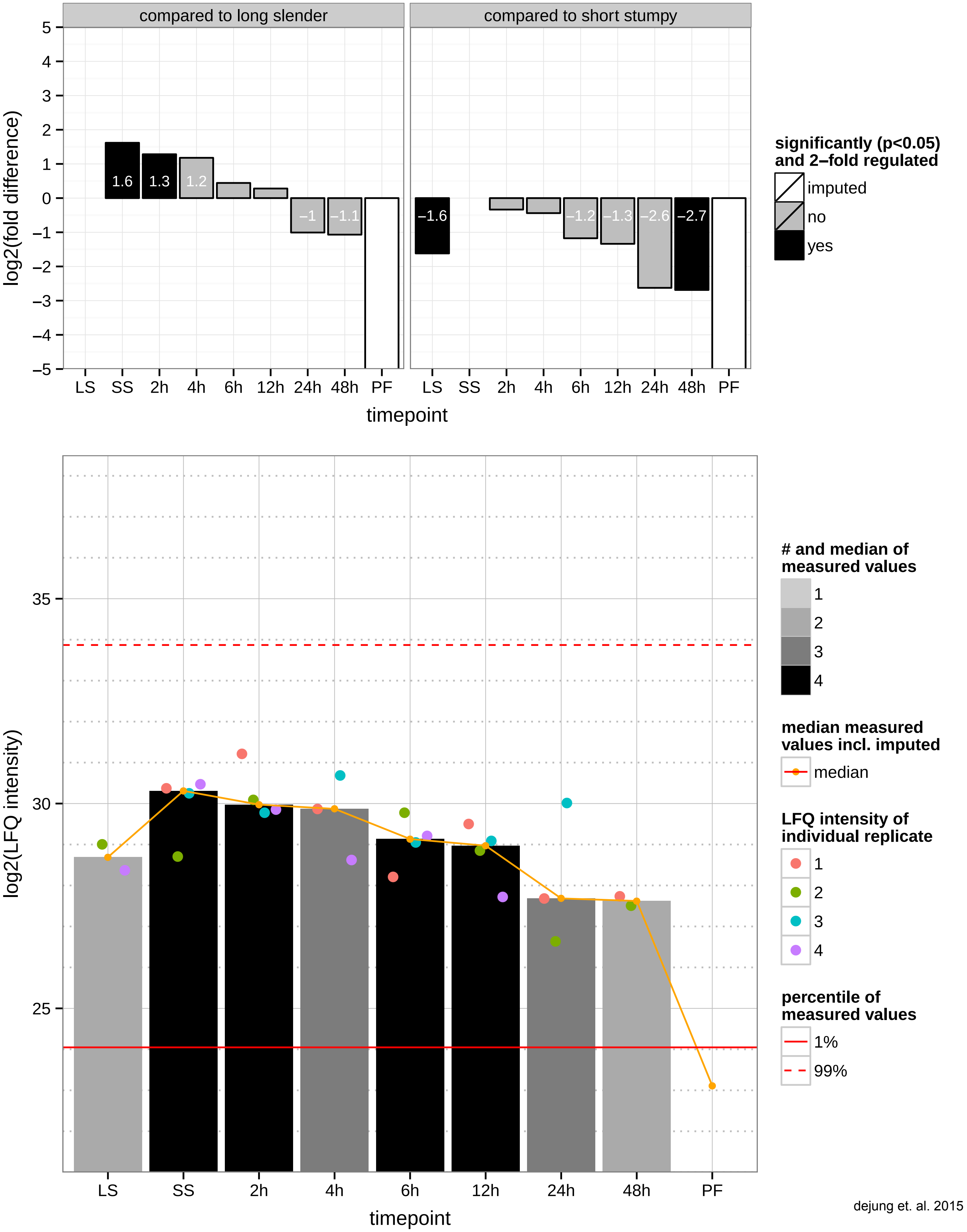
hypothetical protein, conserved
Tb927.11.12870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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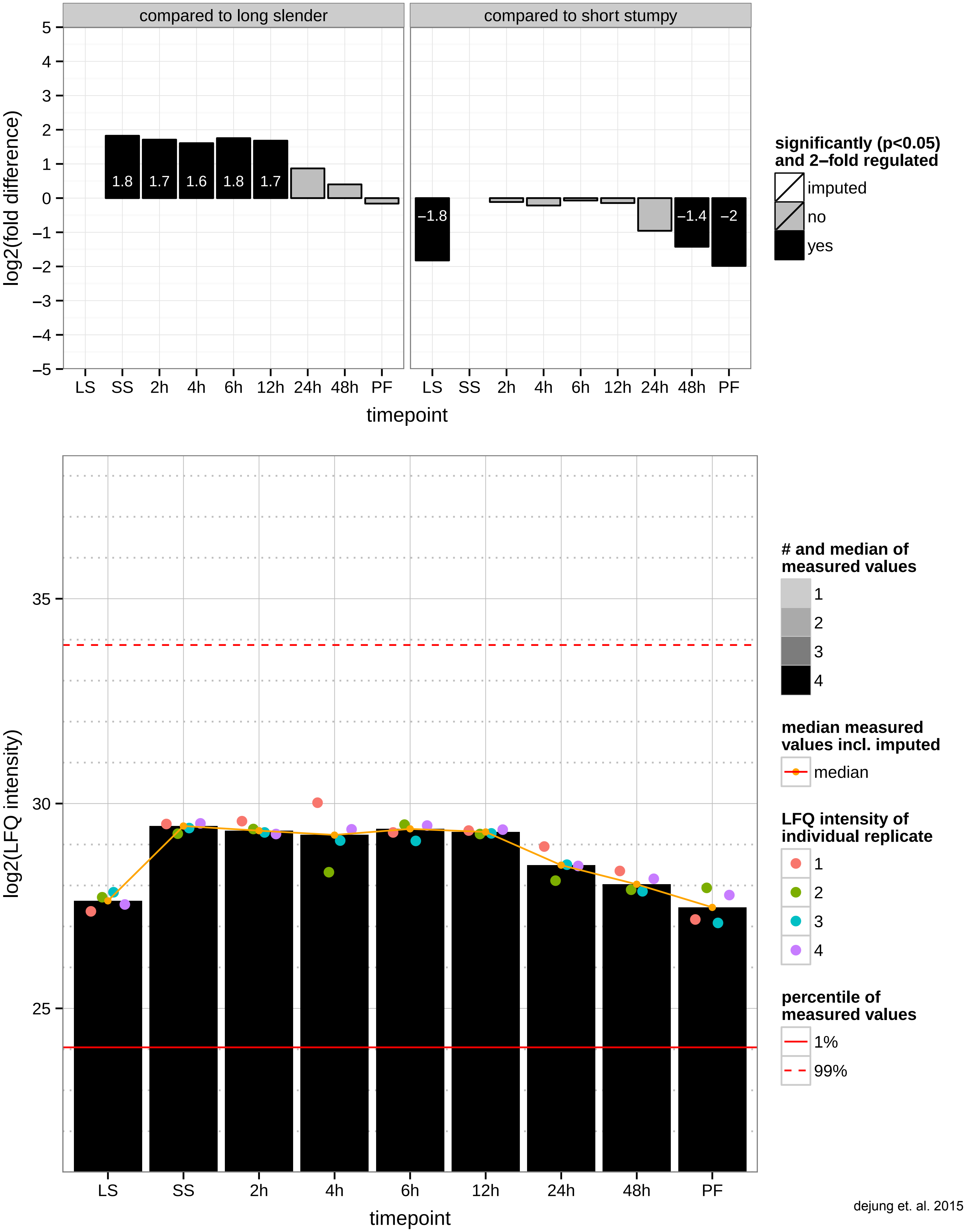
kinesin–II 85 Kd subunit, putative
Tb927.11.13920
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: kinesin complex, microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement



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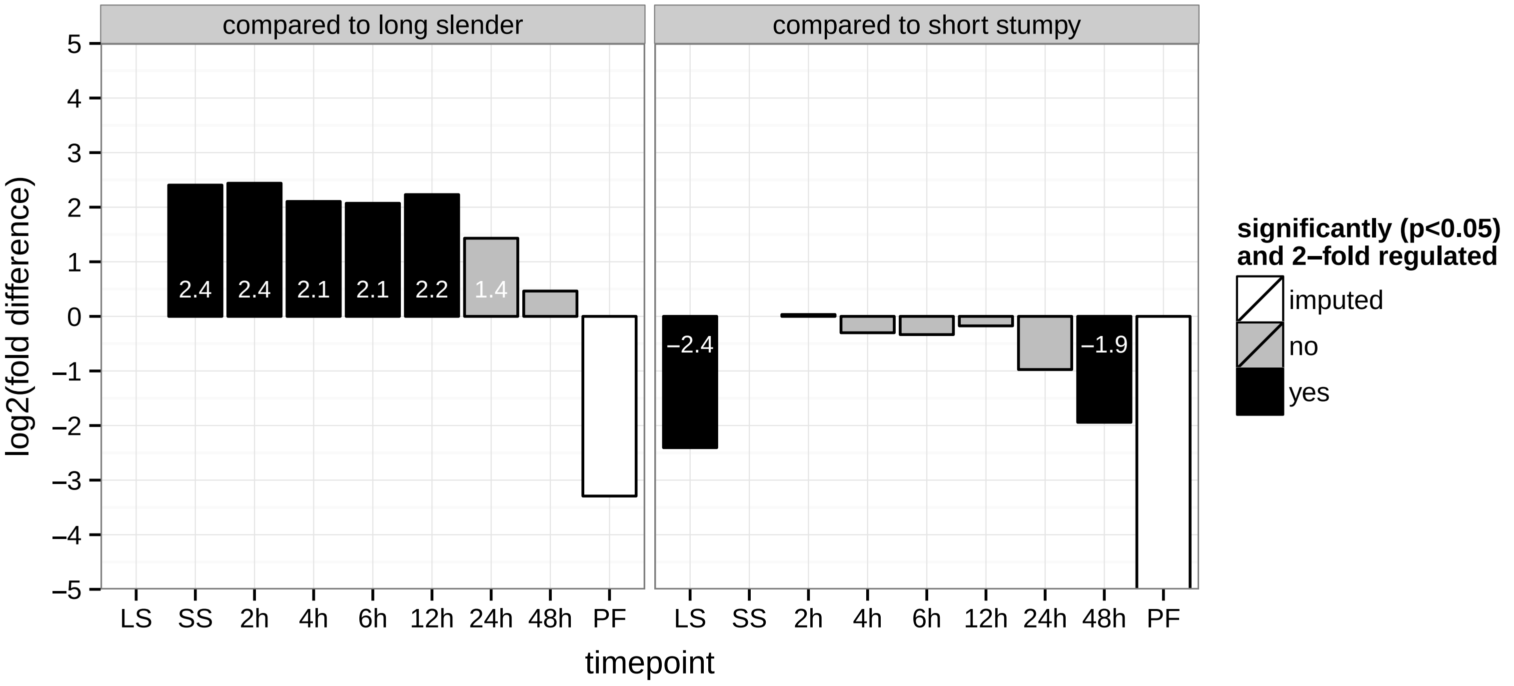
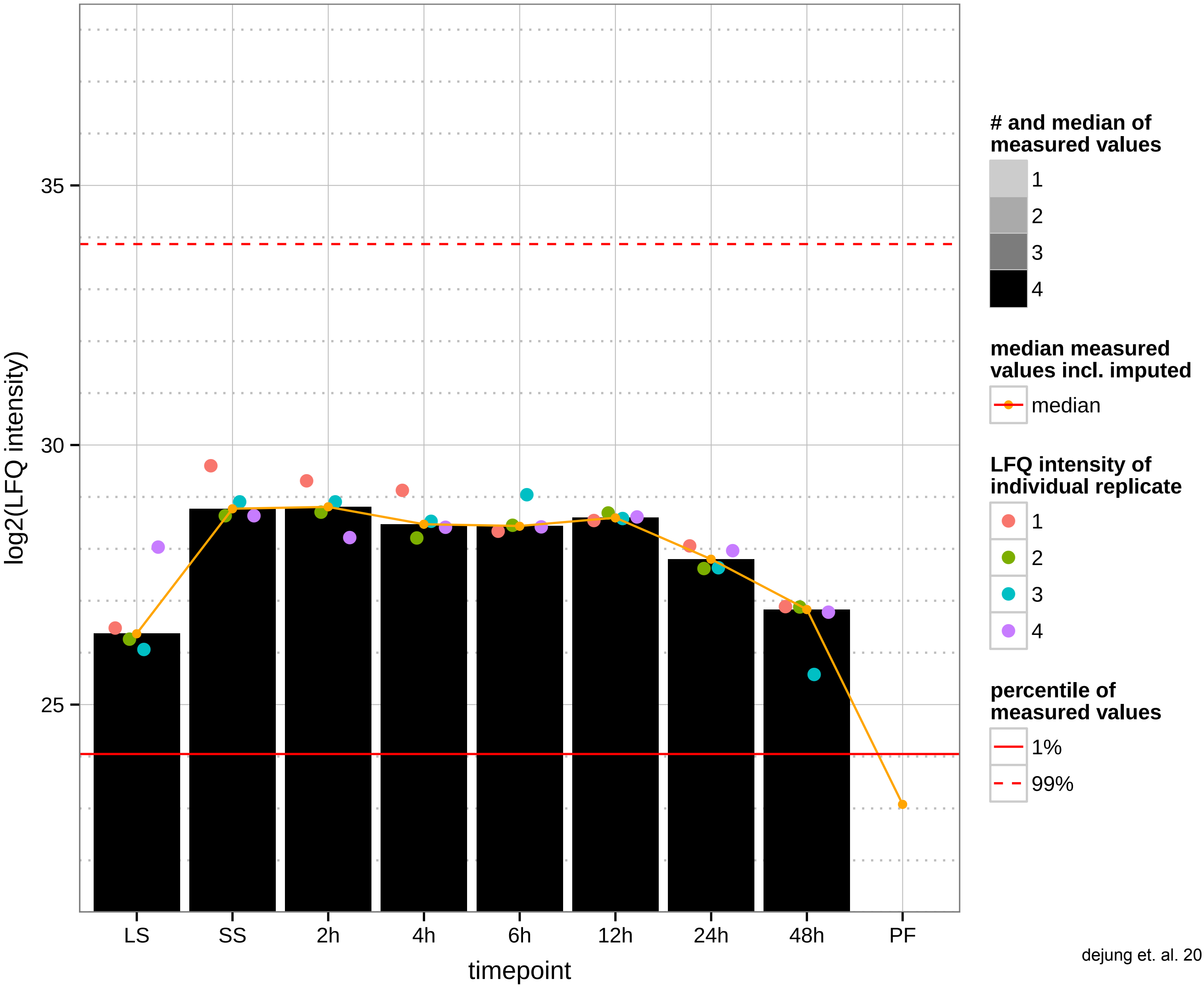
hypothetical protein, conserved
Tb927.11.2320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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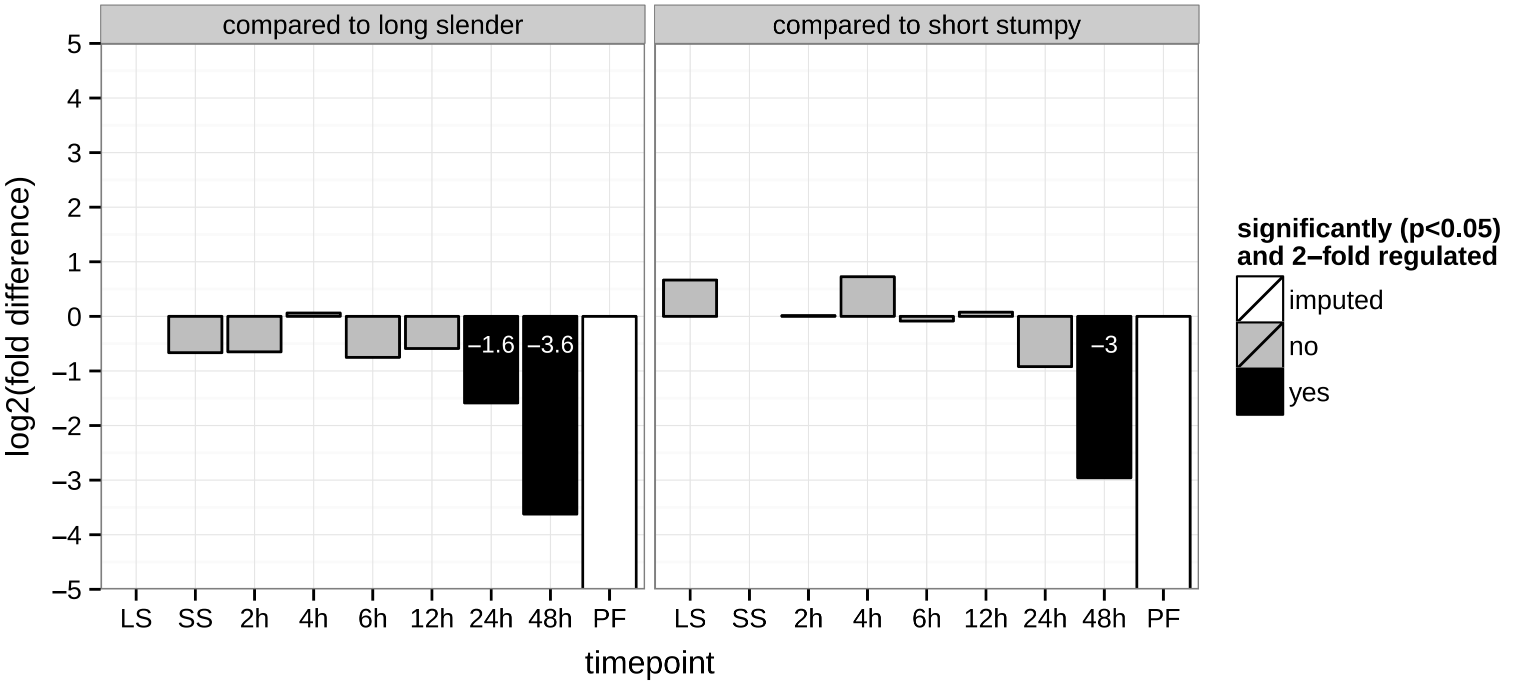
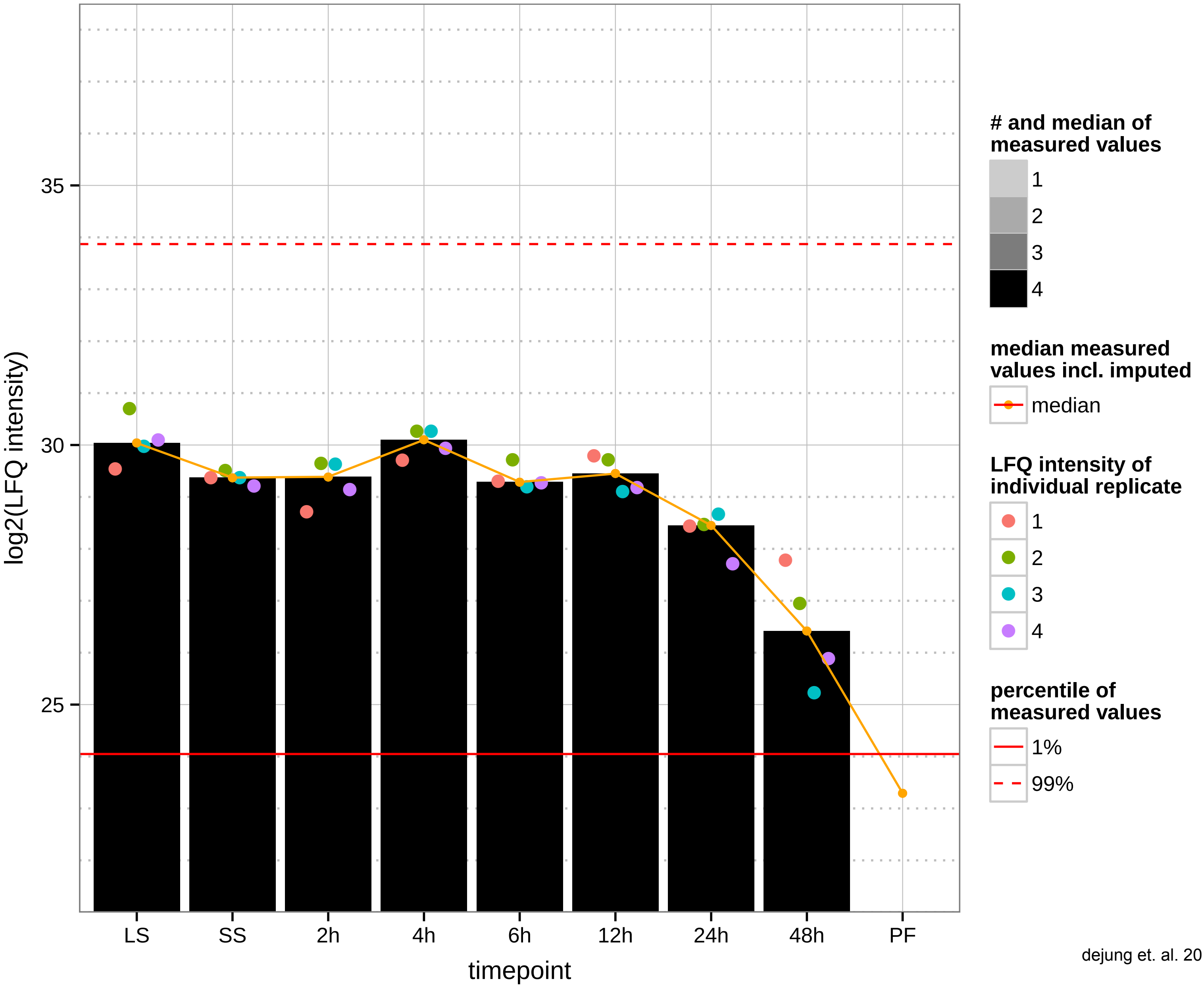
hypothetical protein, conserved
Tb927.11.2400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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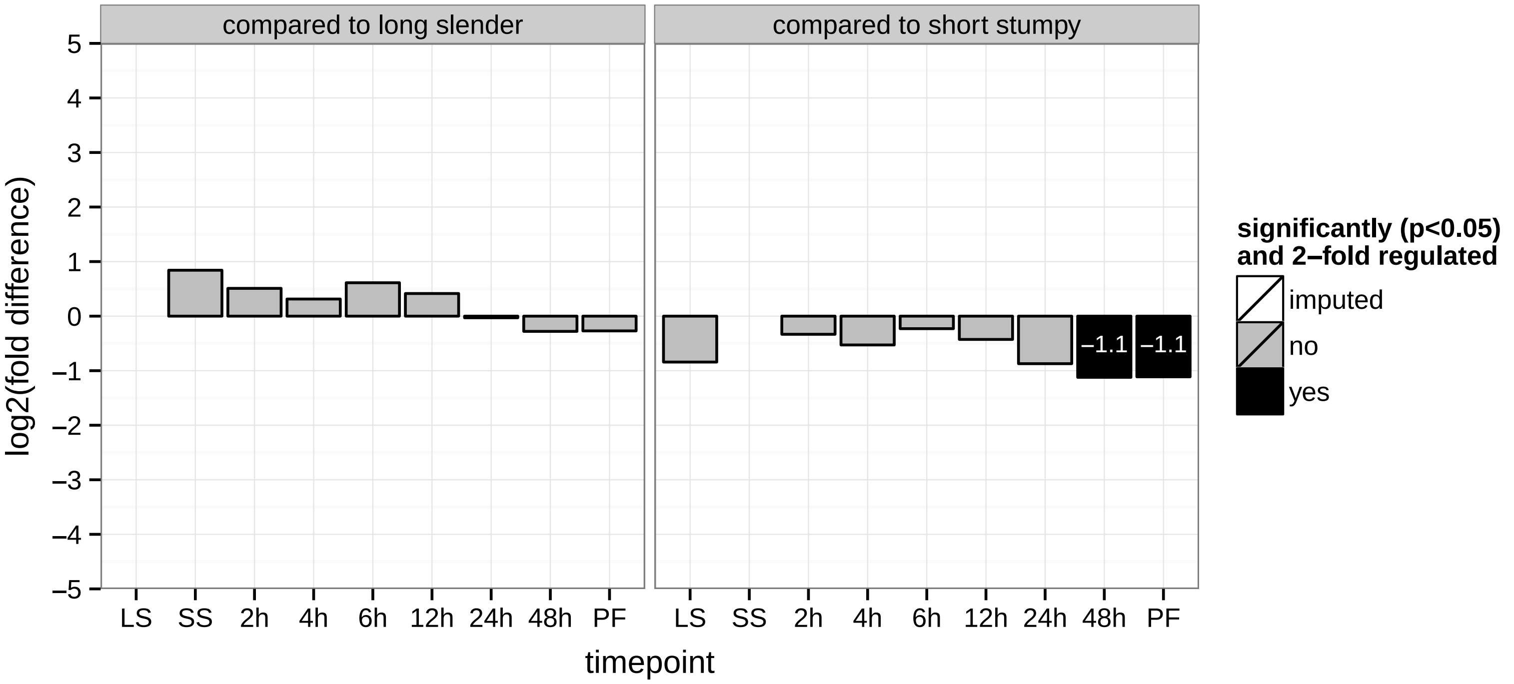
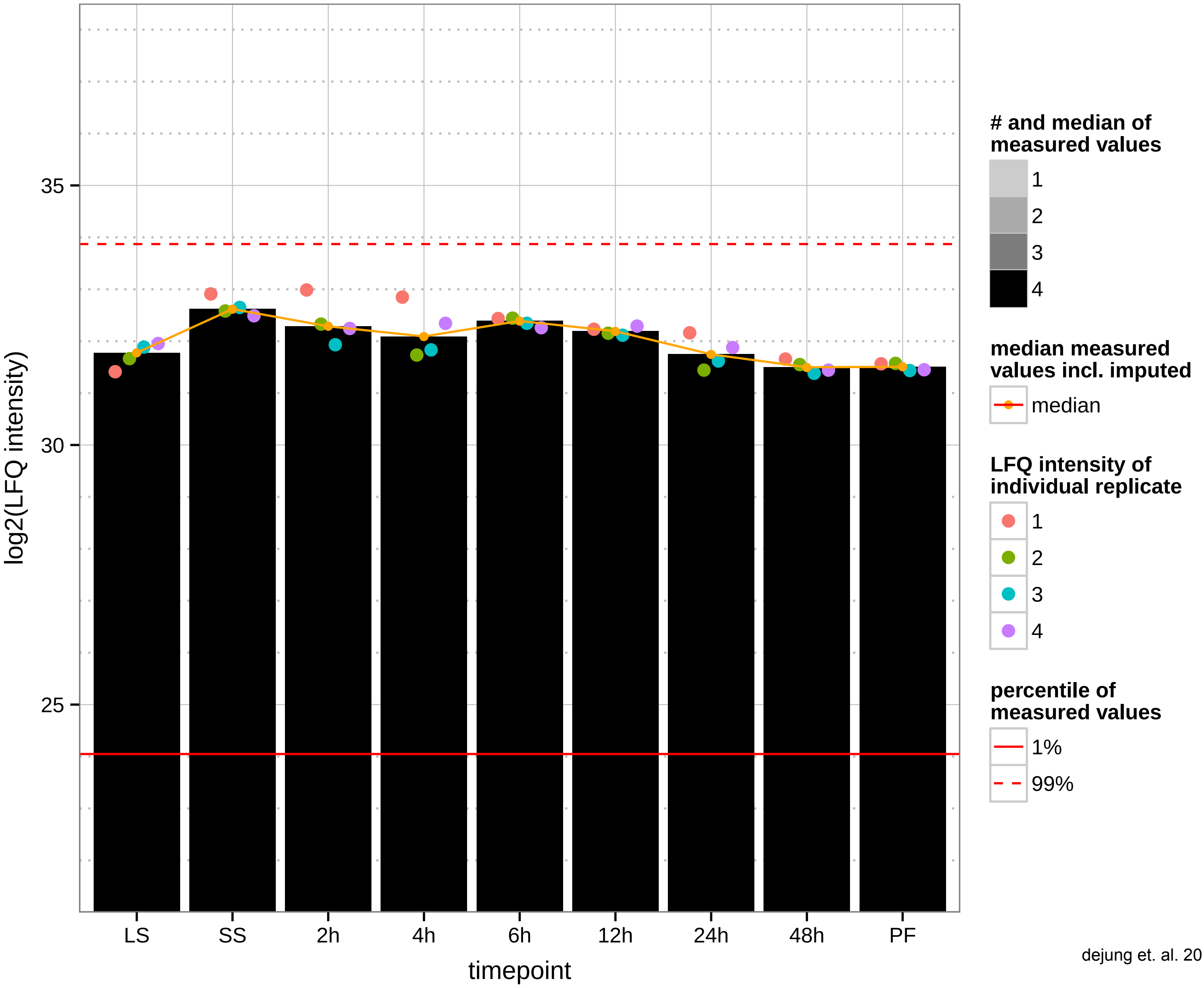
Cytoplasmic dynein 2 heavy chain (DYNC2H1), putative, Cytoplasmic dynein 2 heavy chain (DYNC2H2), putative (DHC1b)
Tb927.11.2430
AGOF: ATP binding, ATPase activity, microtubule motor activity
AGOC: dynein complex
AGOP: chromosome segregation, microtubule–based movement, minus–end–directed vesicle transport along microtubule, m
PGOF: ATP binding, ATPase activity, microtubule motor activity
PGOC: dynein complex
PGOP: microtubule–based movement





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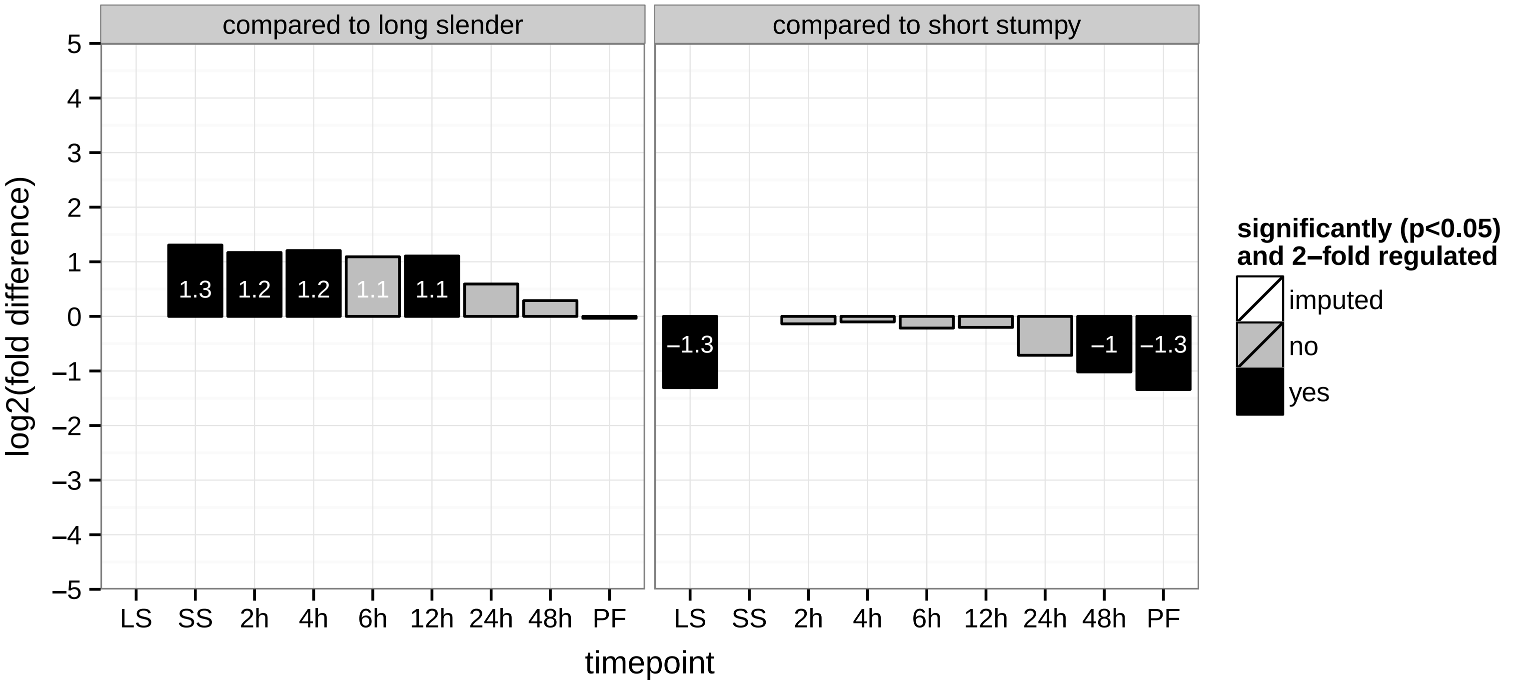
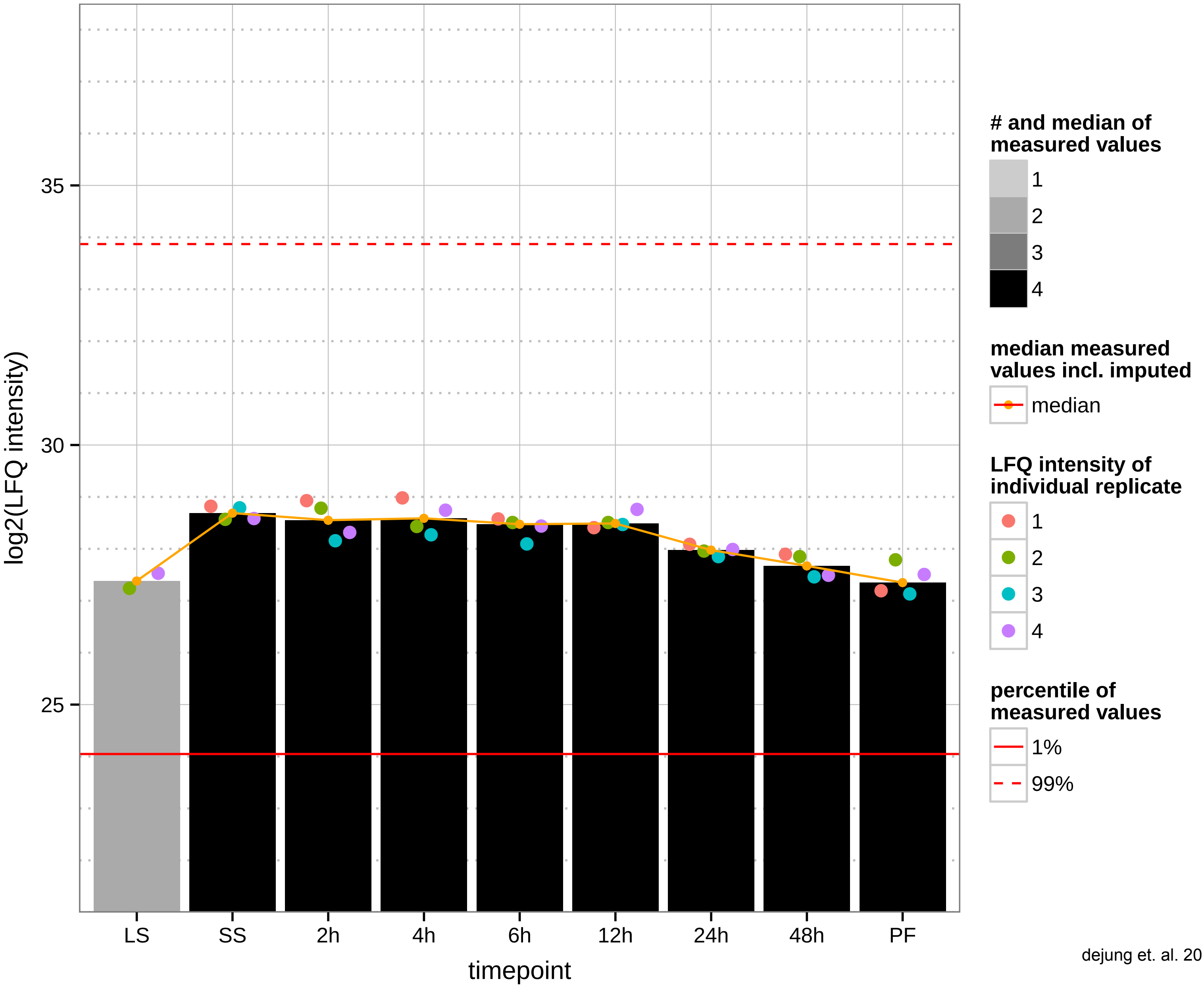
UDP−galactose 4−epimerase (galE)
Tb927.11.2730
AGOF: UDP−glucose 4−epimerase activity, coenzyme binding
AGOC: null
AGOP: galactose metabolic process
PGOF: UDP−glucose 4−epimerase activity, catalytic activity, coenzyme binding
PGOC: null
PGOP: cellular metabolic process, galactose metabolic process





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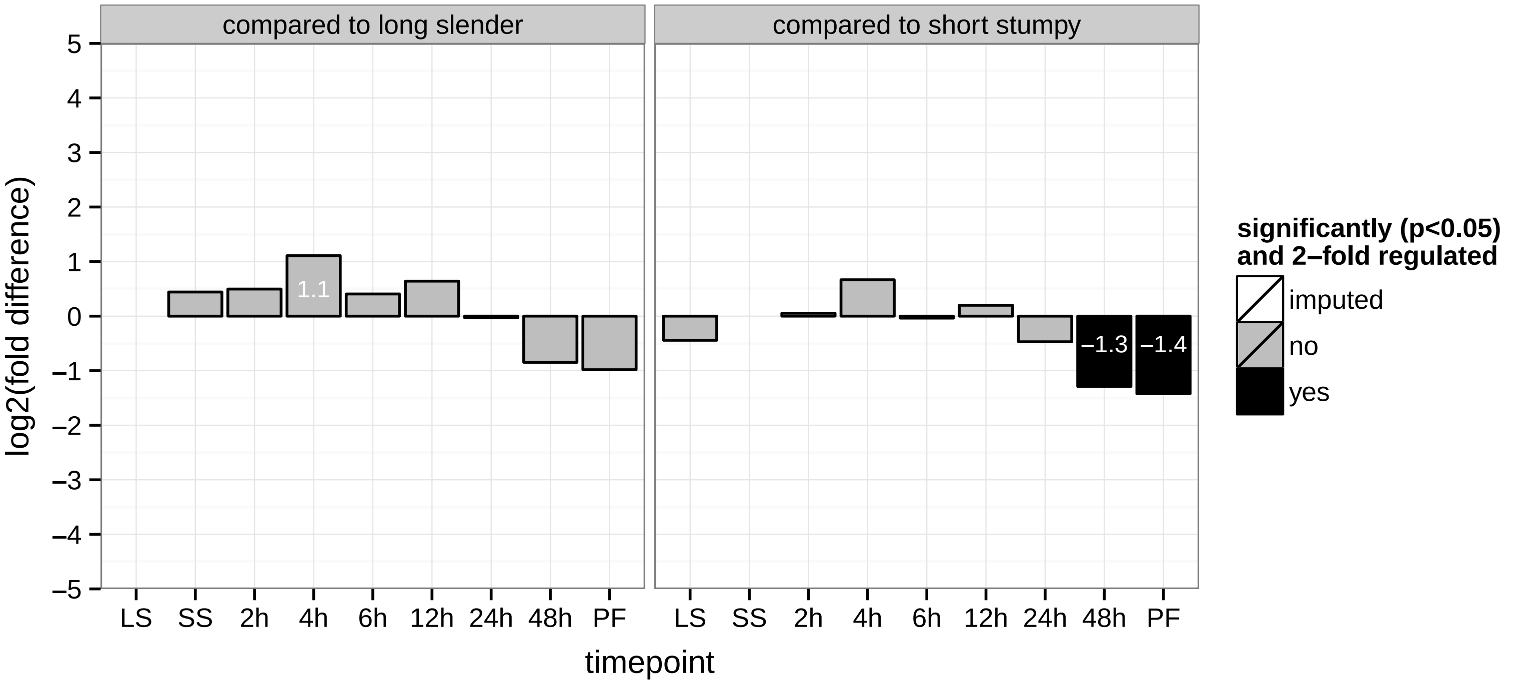
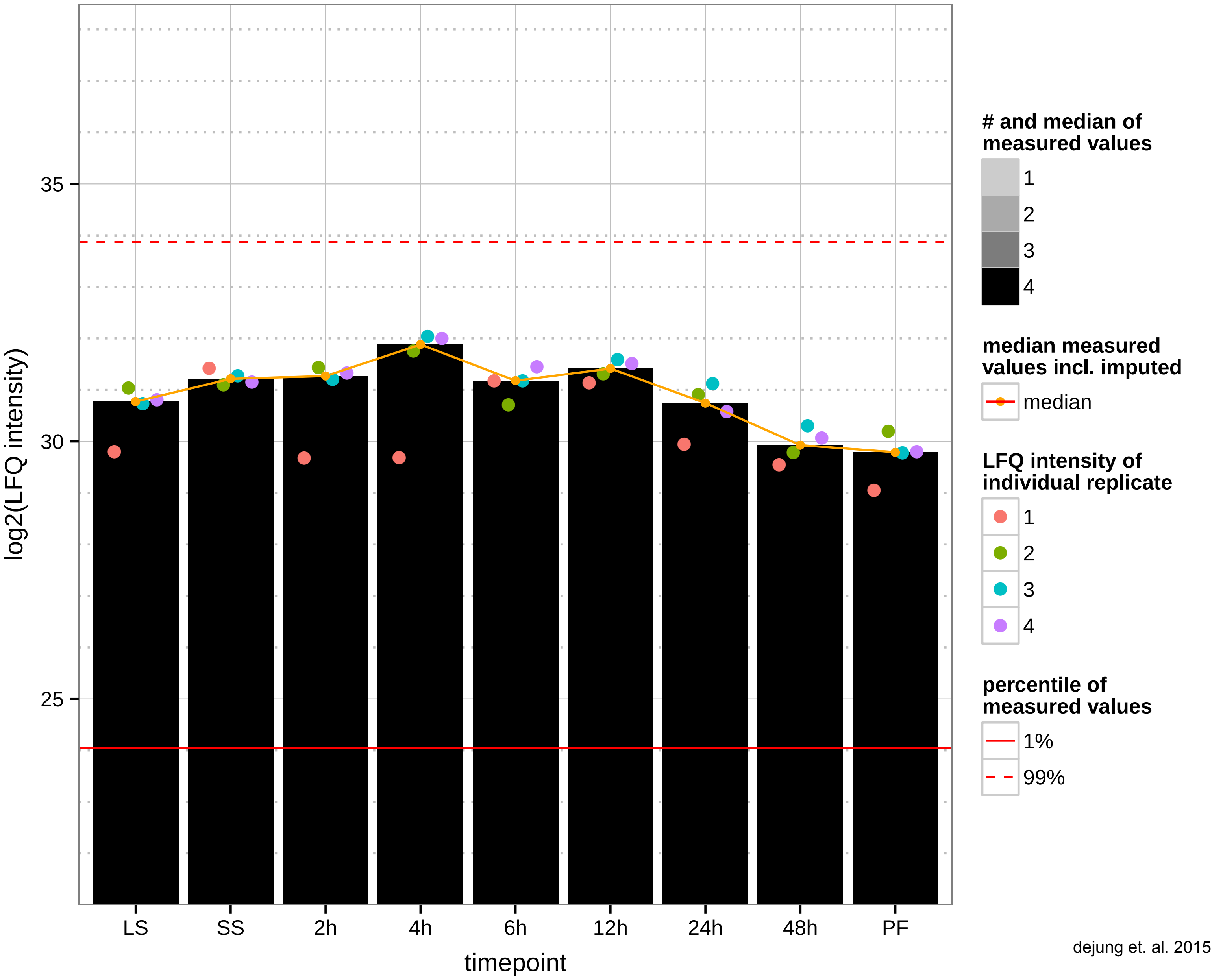
ubiquitin–conjugating enzyme, putative, ubiquitin–conjugating enzyme–like protein
Tb927.11.3310
AGOF: ubiquitin–protein ligase activity
AGOC: null
AGOP: cellular protein modification process, post–translational protein modification, regulation of protein metabolic process
PGOF: acid–amino acid ligase activity
PGOC: null
PGOP: null





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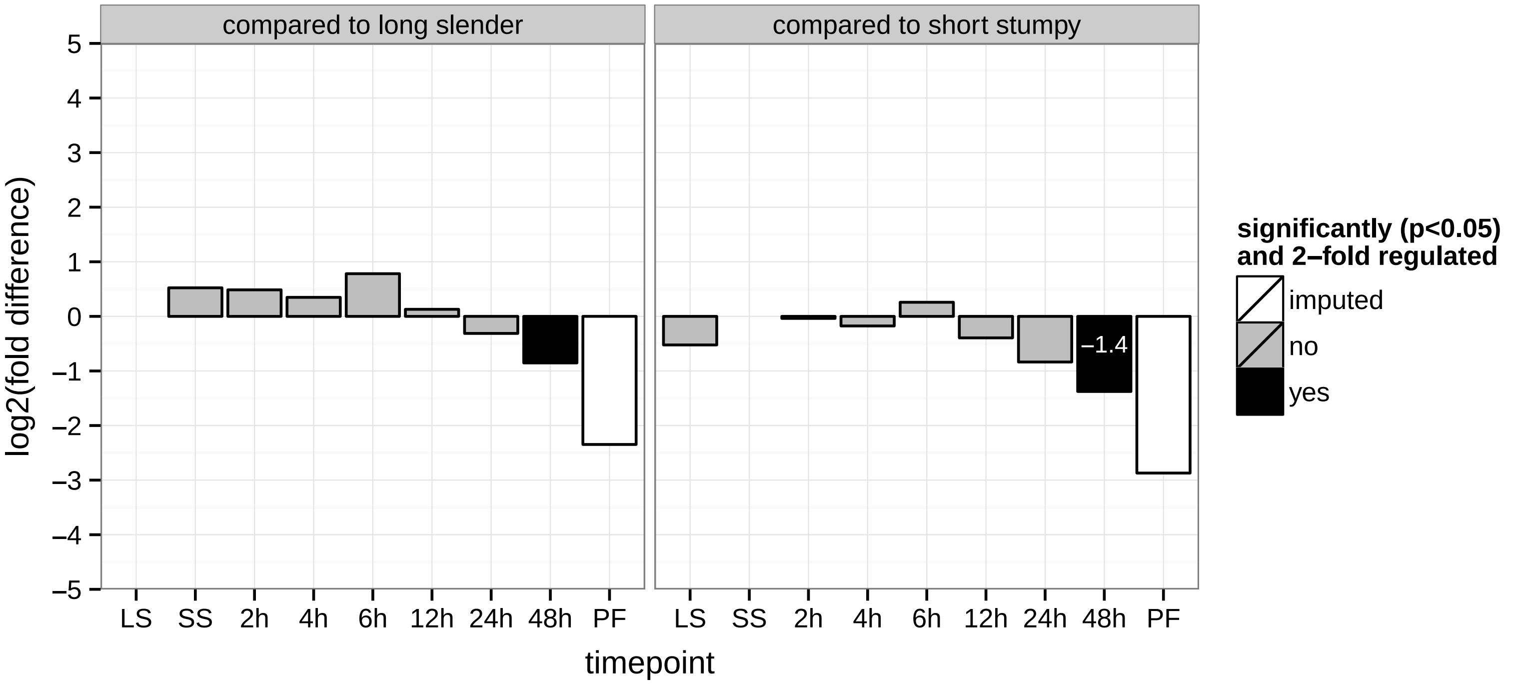
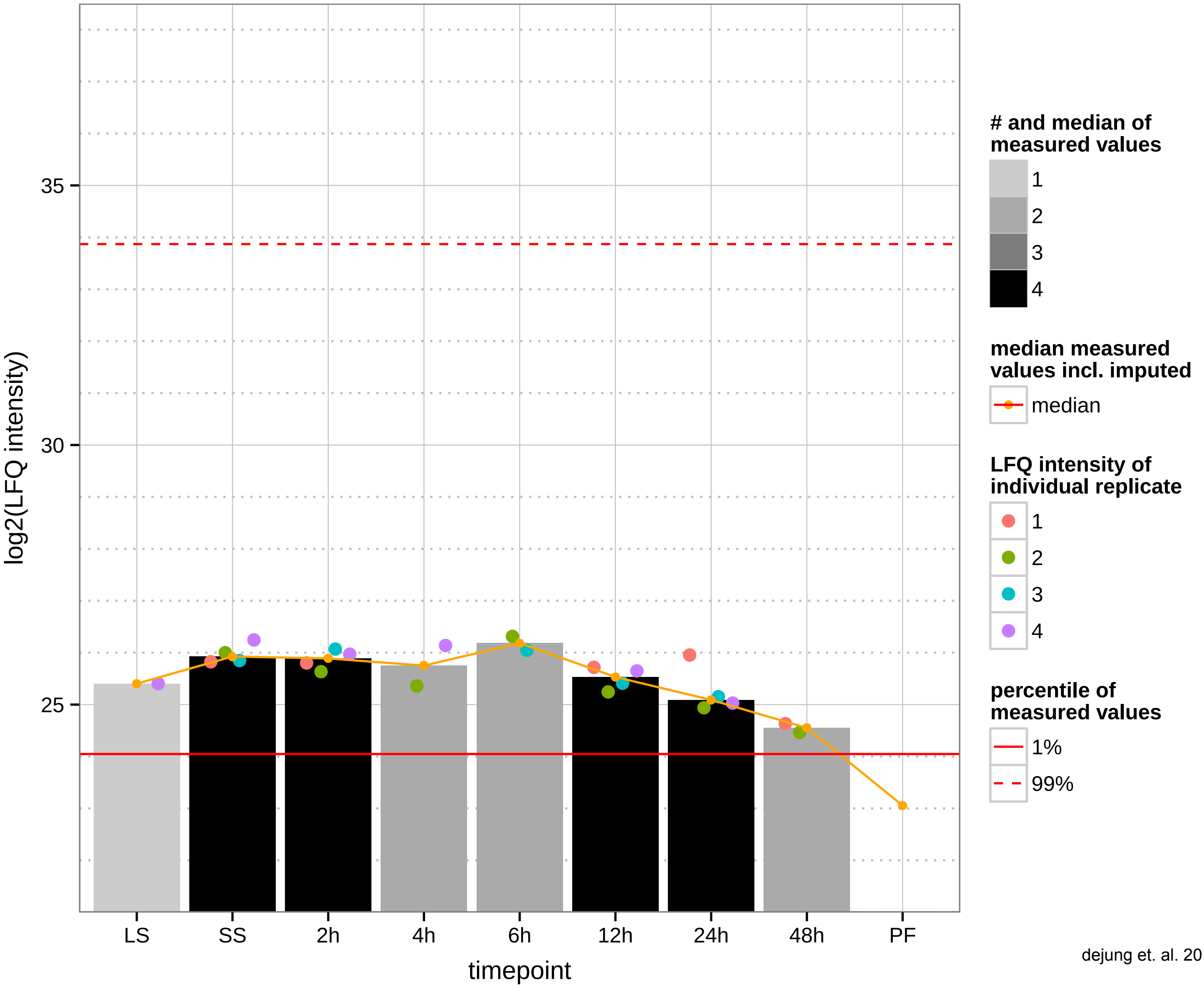
kinetoplastid–specific dual specificity phosphatase, putative
Tb927.11.4170
AGOF: protein tyrosine/serine/threonine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: phosphatase activity, protein tyrosine/serine/threonine phosphatase activity
PGOC: null
PGOP: dephosphorylation, protein dephosphorylation





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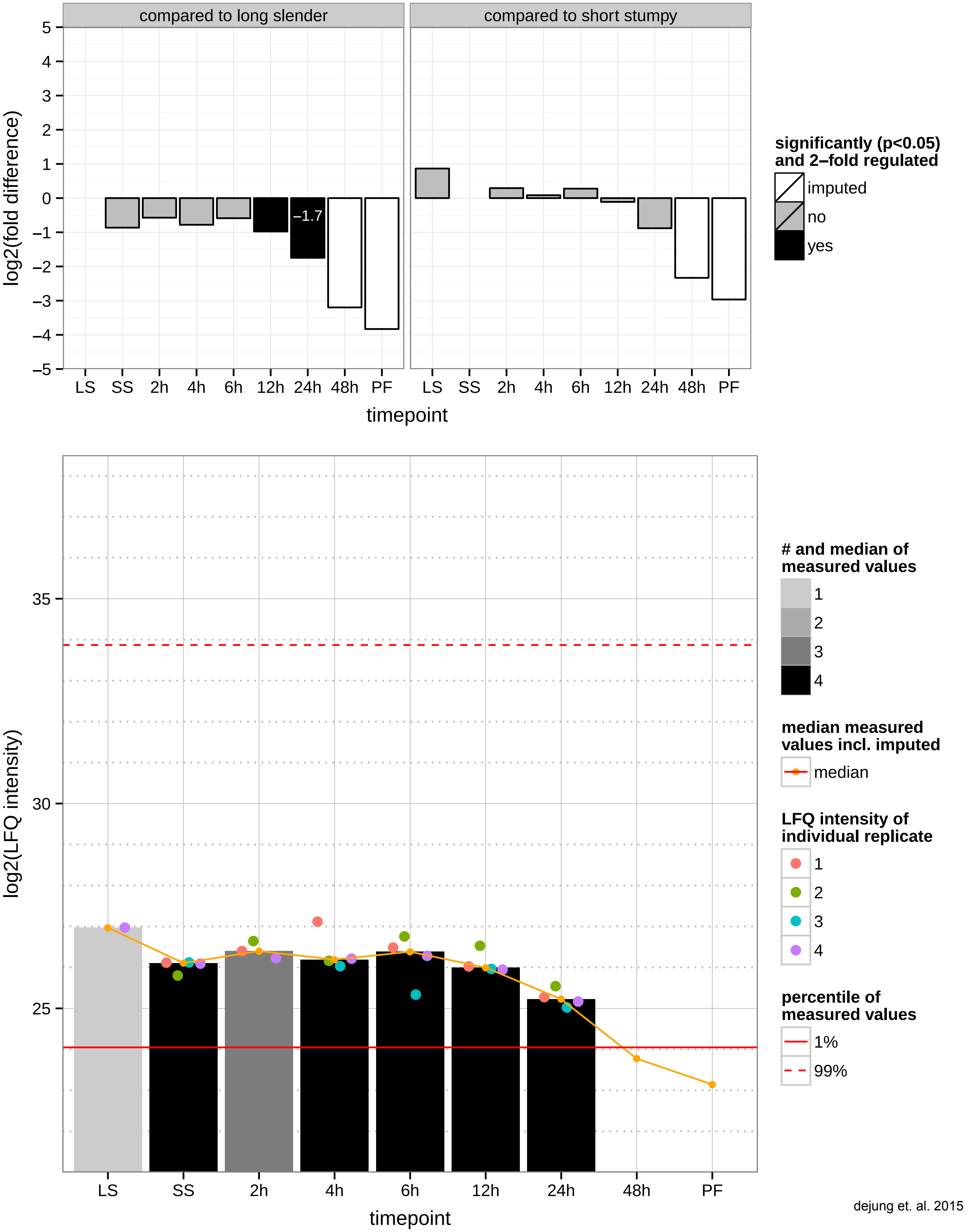
Ras−related protein Rab5B (RAB5B)
Tb927.11.4570
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti



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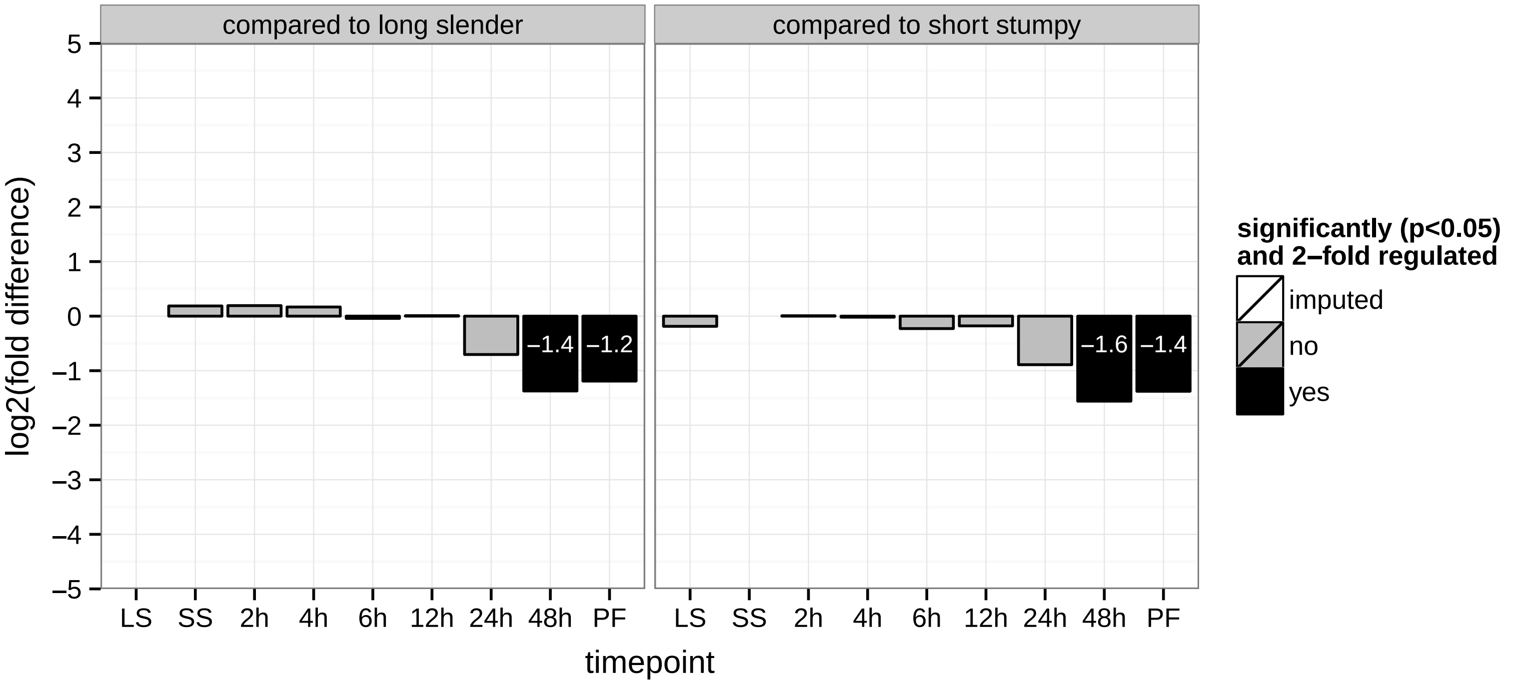
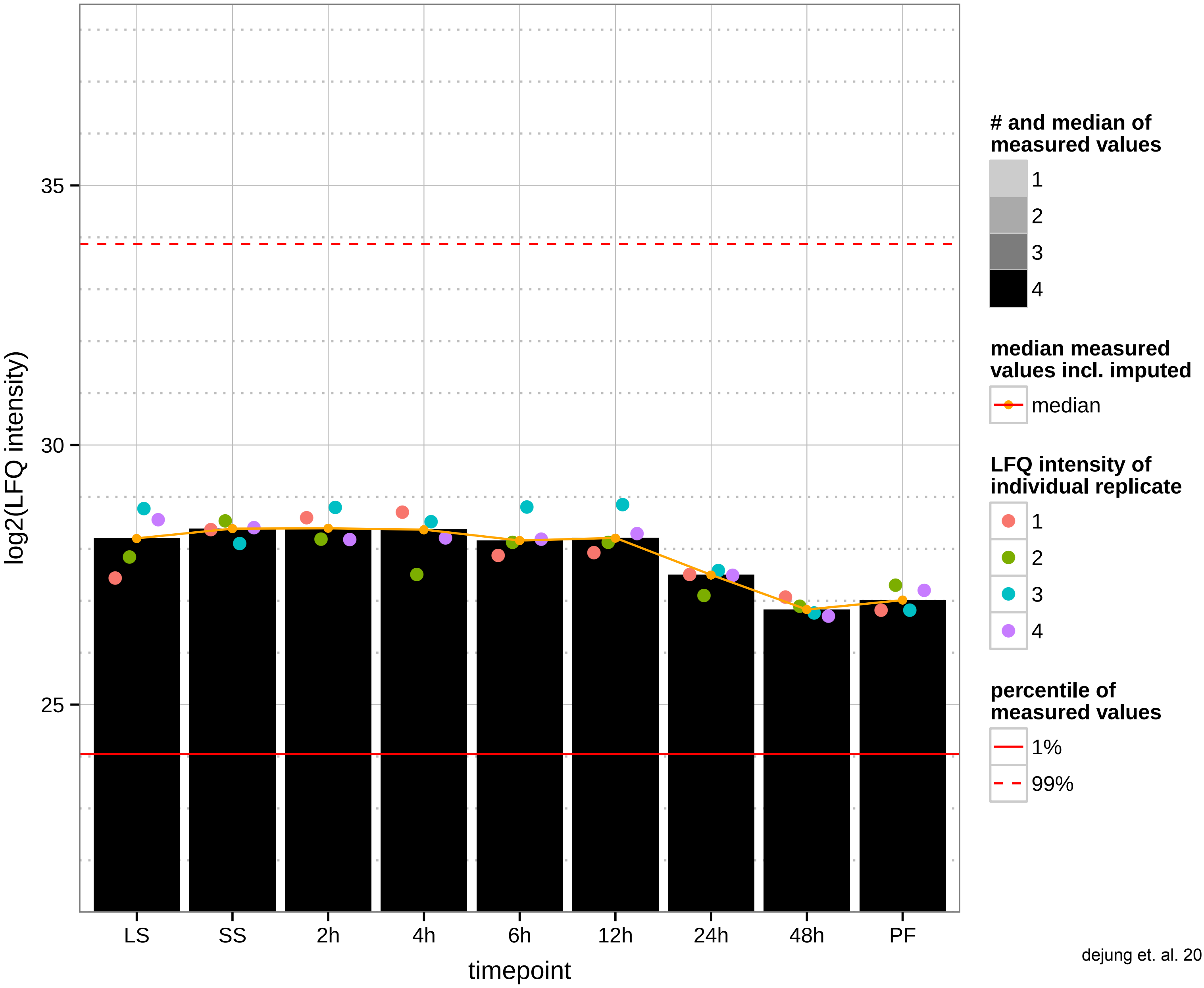
hypothetical protein, conserved
Tb927.11.4860
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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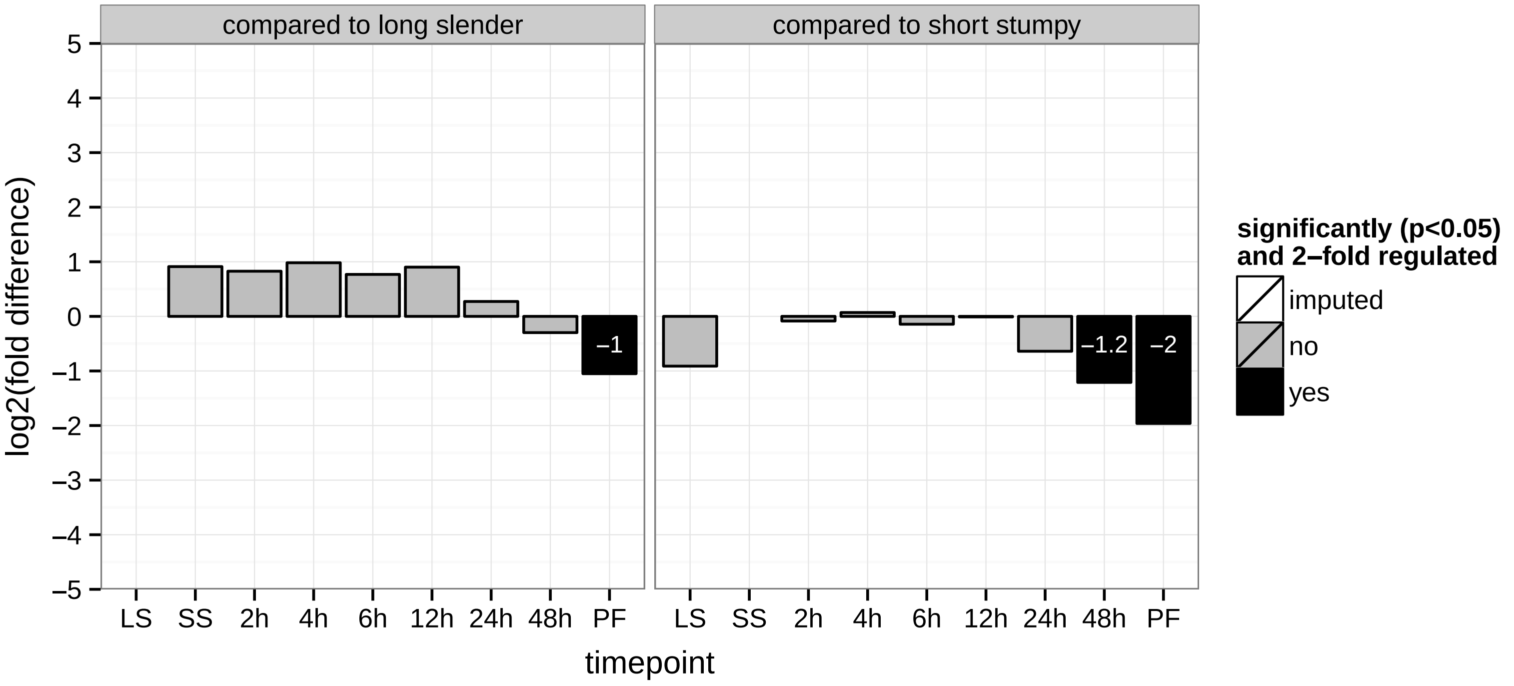
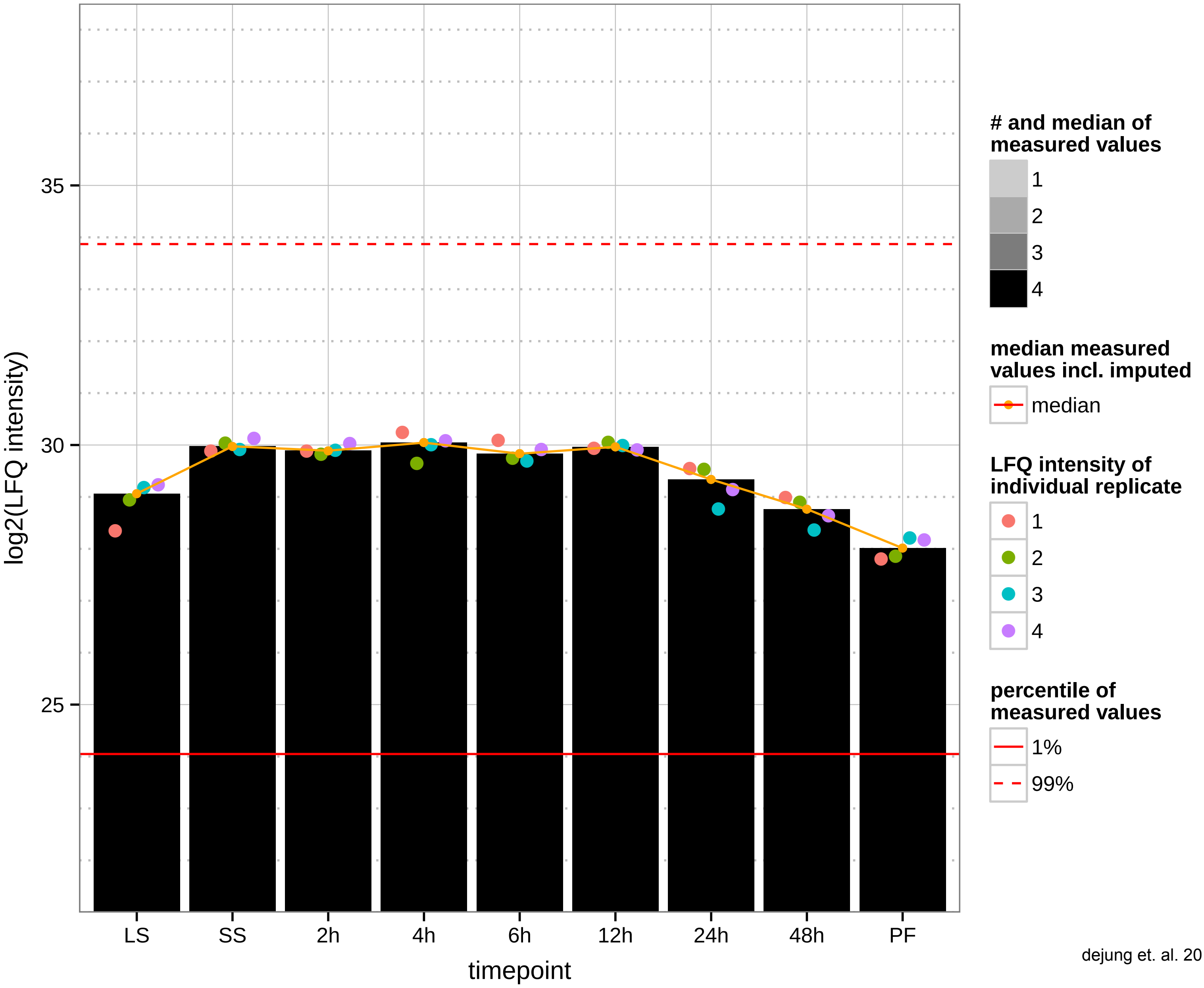
hypothetical protein, conserved
Tb927.11.6390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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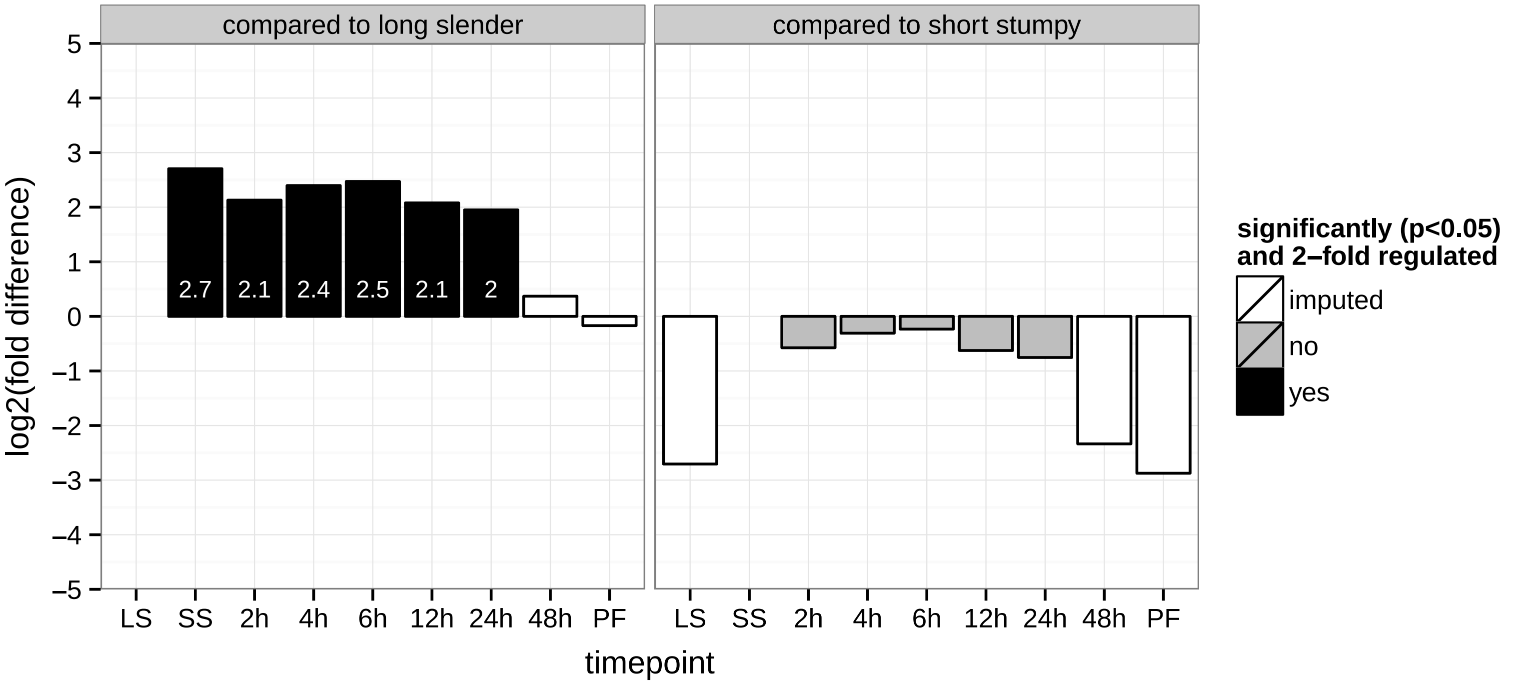
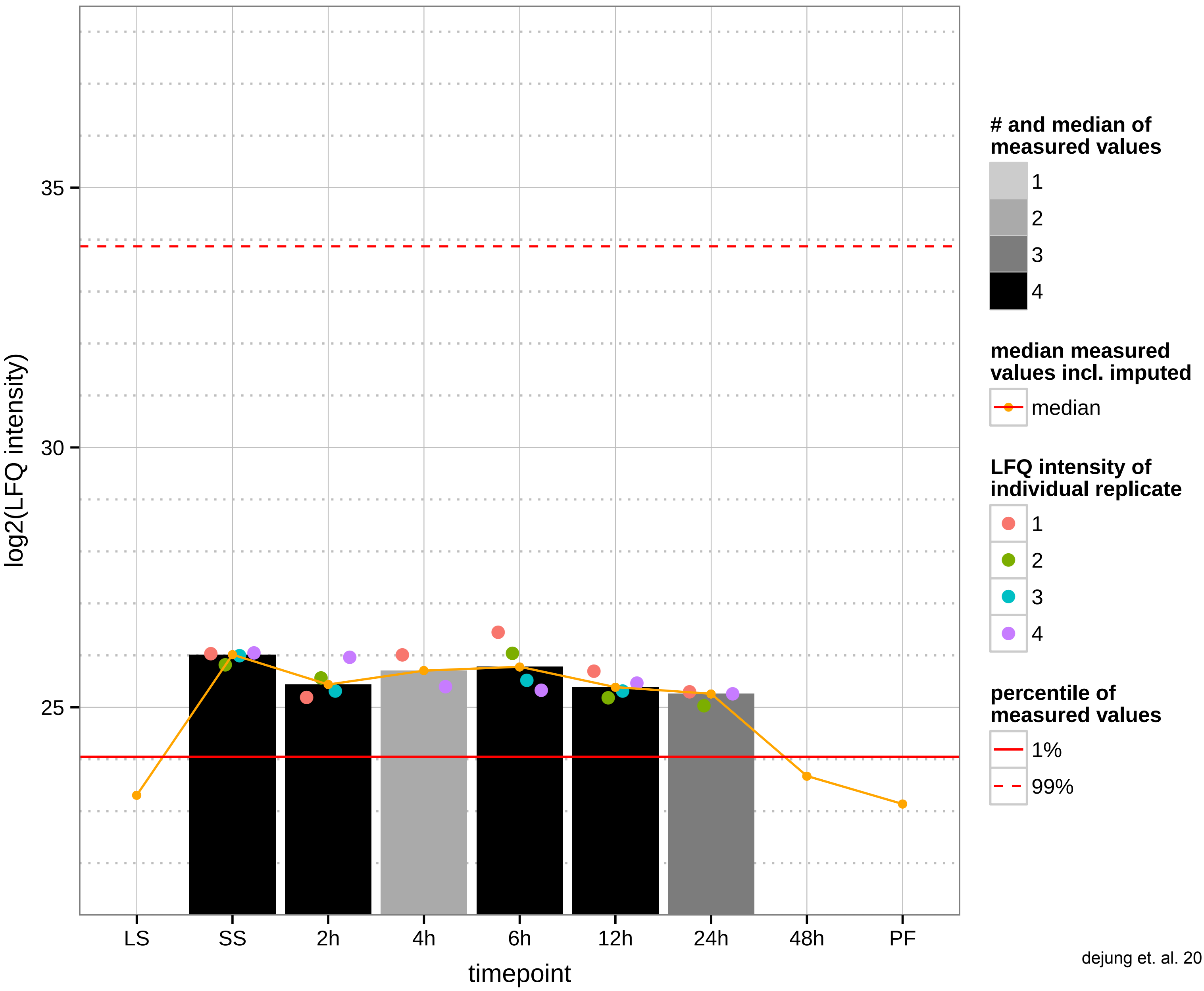
hypothetical protein, conserved
Tb927.11.7570
AGOF: ATP binding, catalytic activity
AGOC: null
AGOP: null
PGOF: ATP binding, metal ion binding
PGOC: null
PGOP: null





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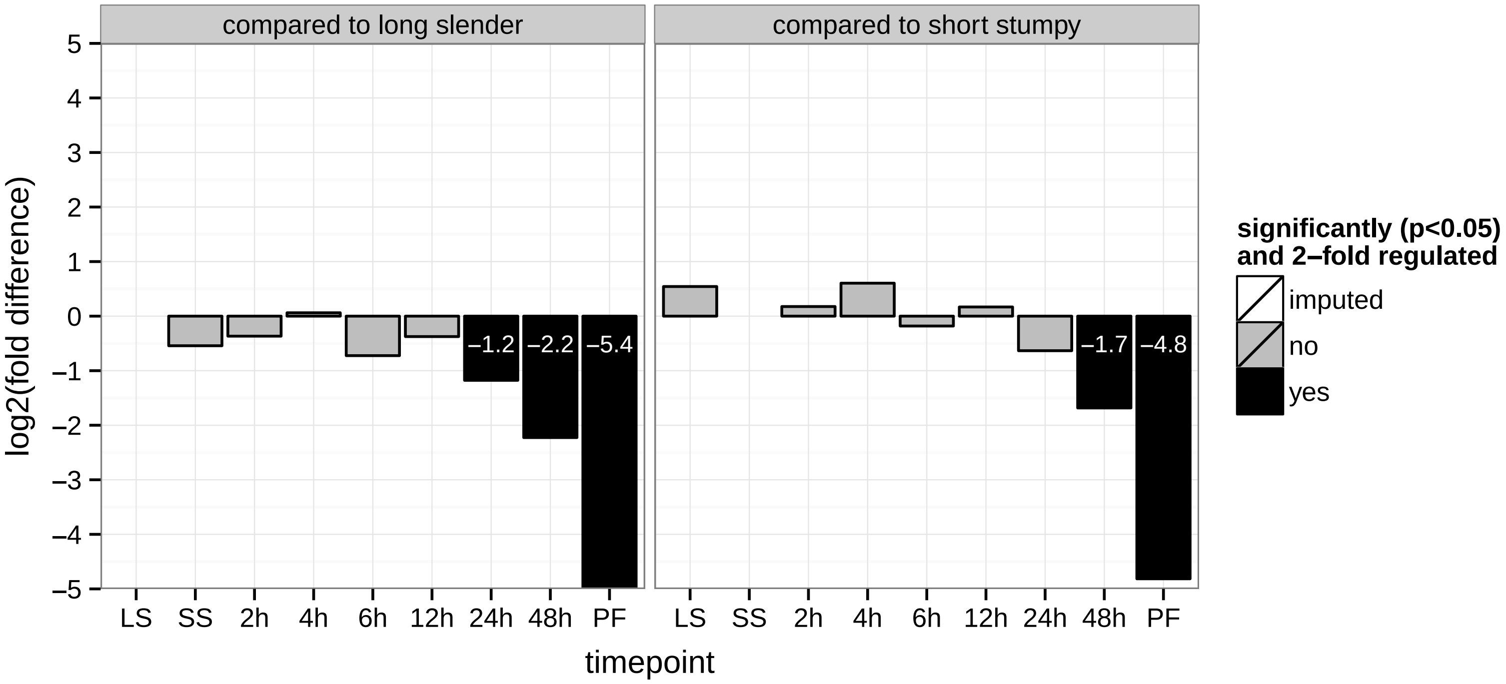
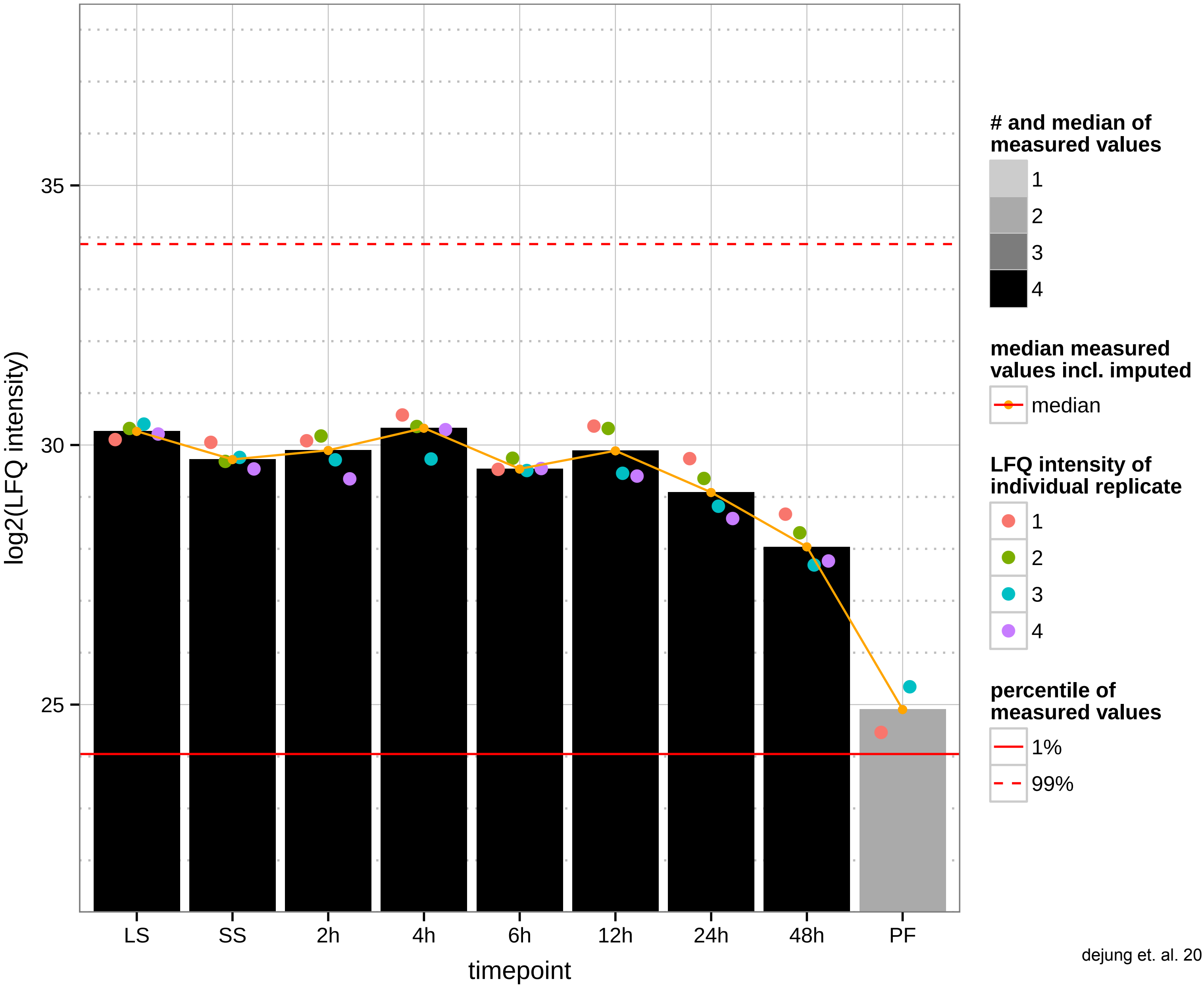
haloacid dehalogenase–like hydrolase, putative
Tb927.11.8440
AGOF: hydrolase activity
AGOC: null
AGOP: metabolic process
PGOF: catalytic activity, hydrolase activity
PGOC: null
PGOP: metabolic process





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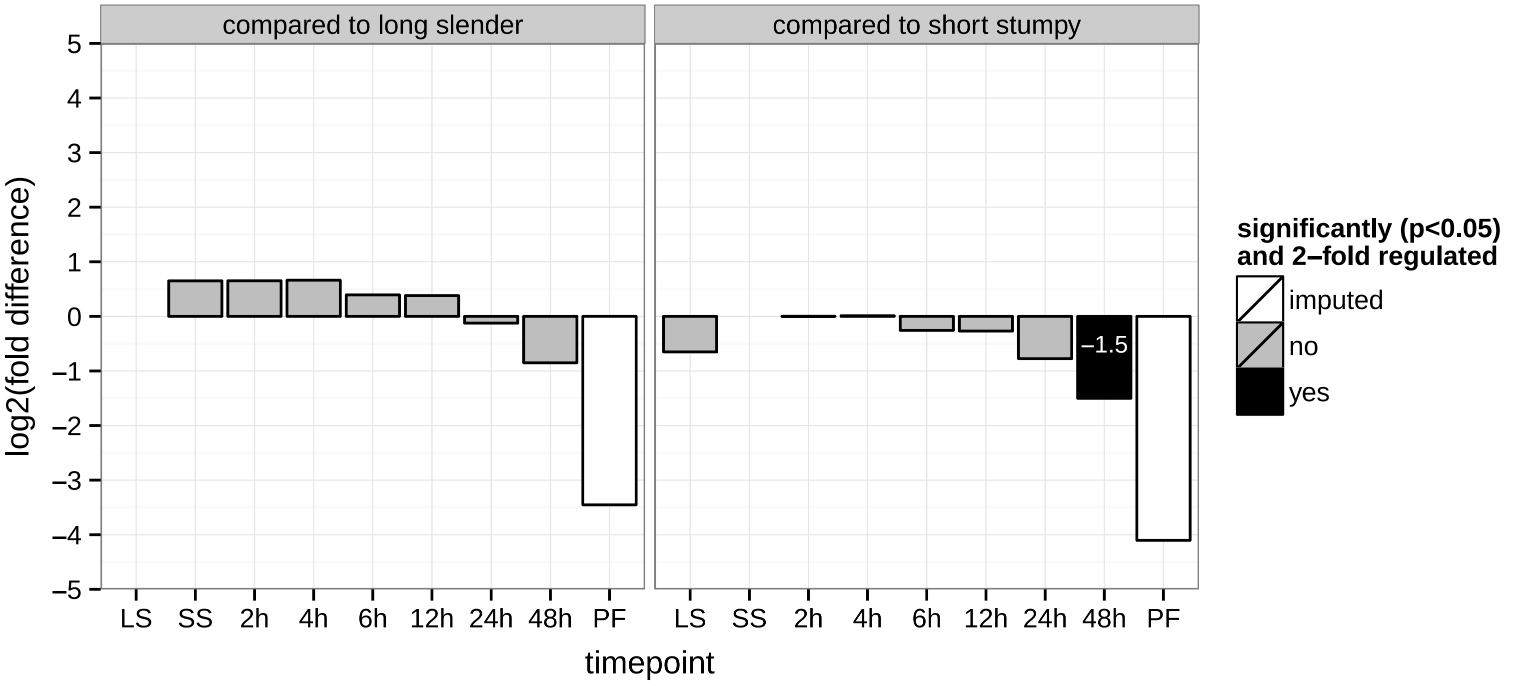
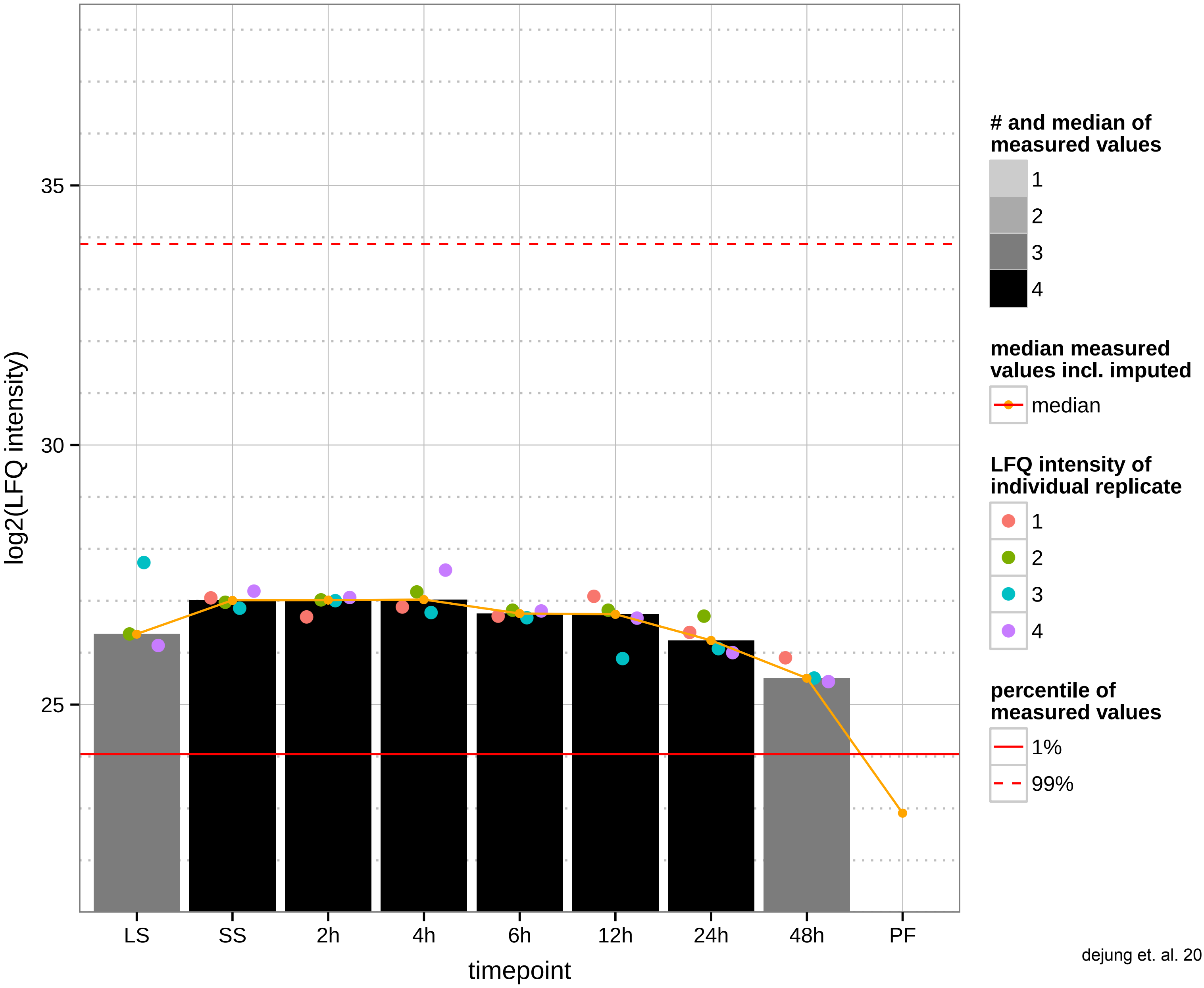
target SNARE, putative
Tb927.11.8790
AGOF: SNAP receptor activity
AGOC: integral to membrane, membrane
AGOP: membrane fusion, vesicle–mediated transport
PGOF: protein binding
PGOC: membrane
PGOP: vesicle–mediated transport





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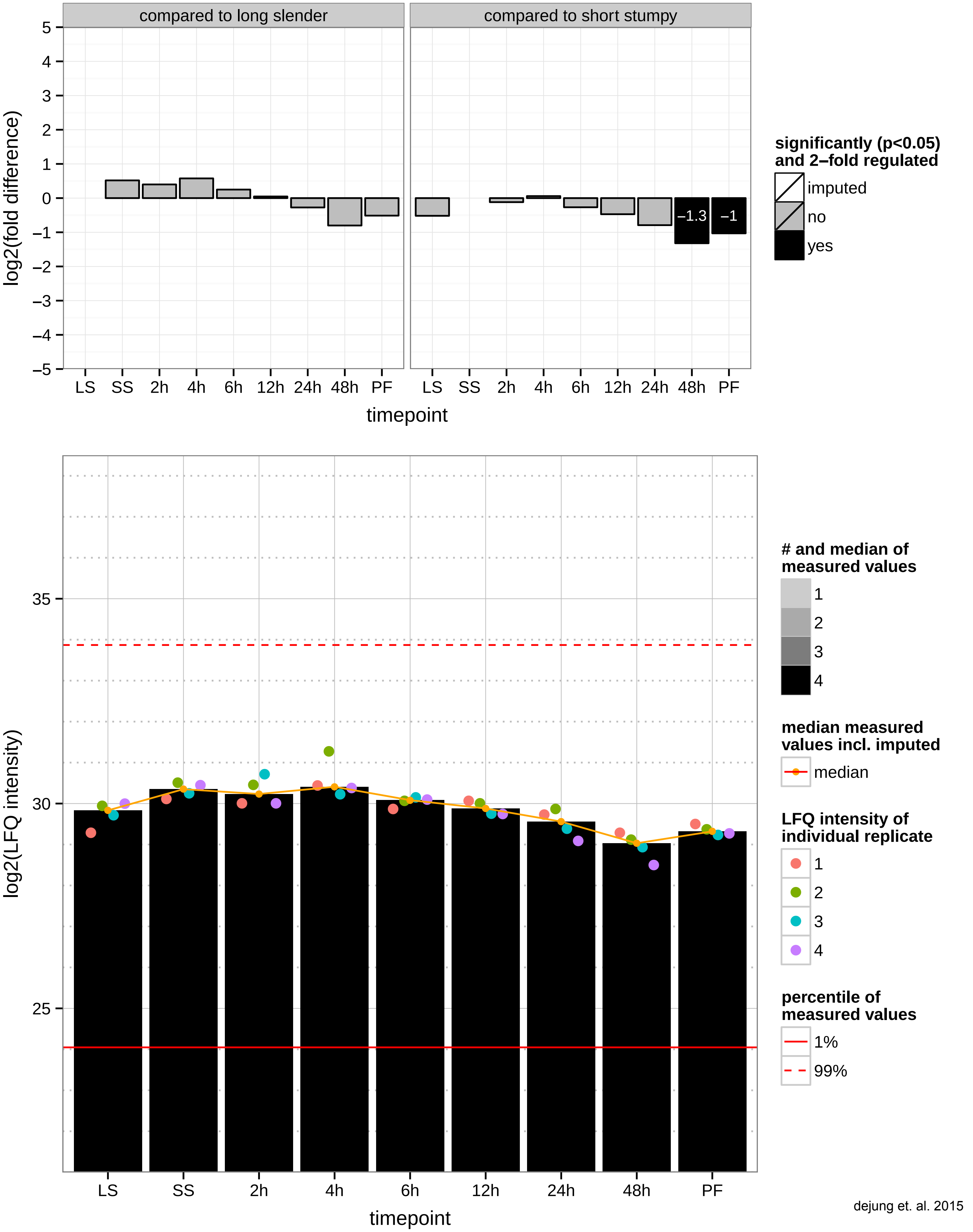
ATP synthase, putative
Tb927.11.9420
AGOF: proton−transporting ATPase activity, rotational mechanism
AGOC: proton−transporting two−sector ATPase complex, catalytic domain
AGOP: ATP synthesis coupled proton transport
PGOF: proton−transporting ATPase activity, rotational mechanism
PGOC: proton−transporting two−sector ATPase complex, catalytic domain
PGOP: ATP hydrolysis coupled proton transport



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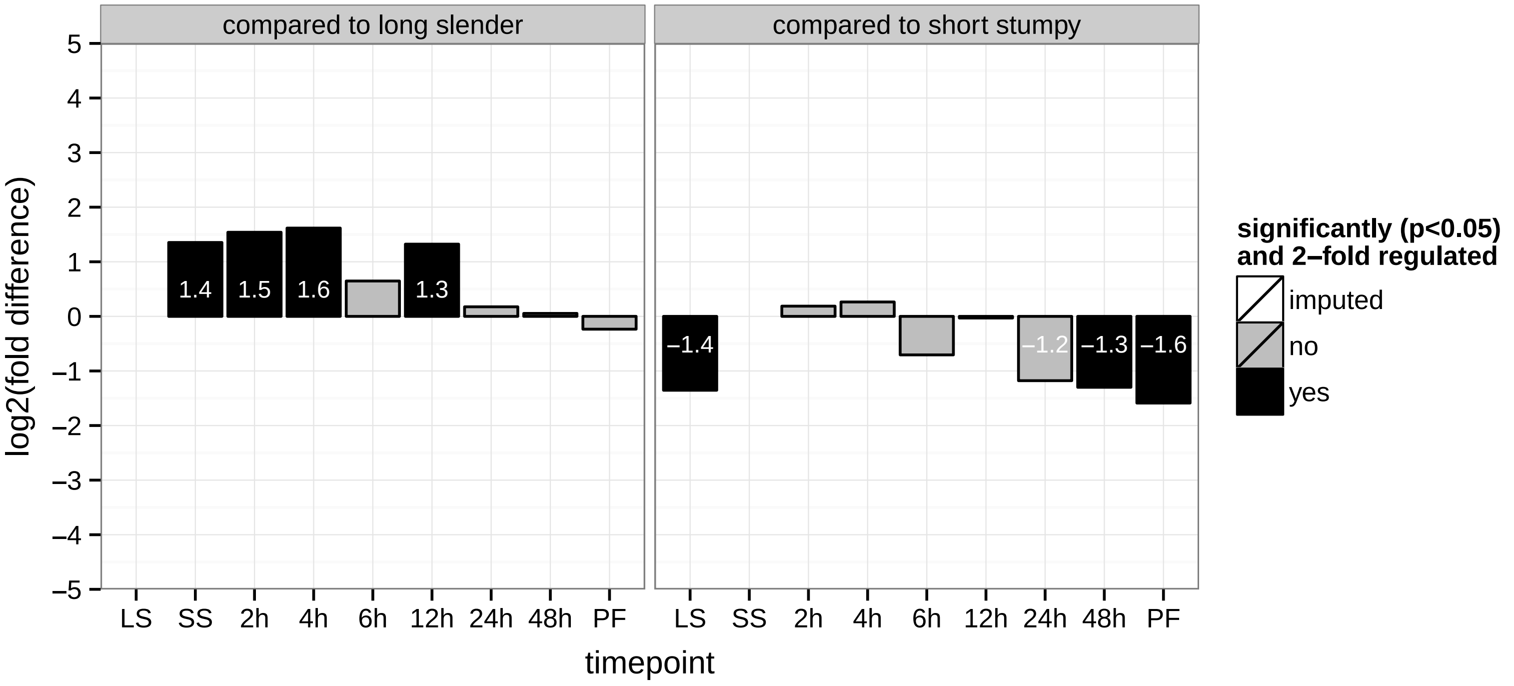
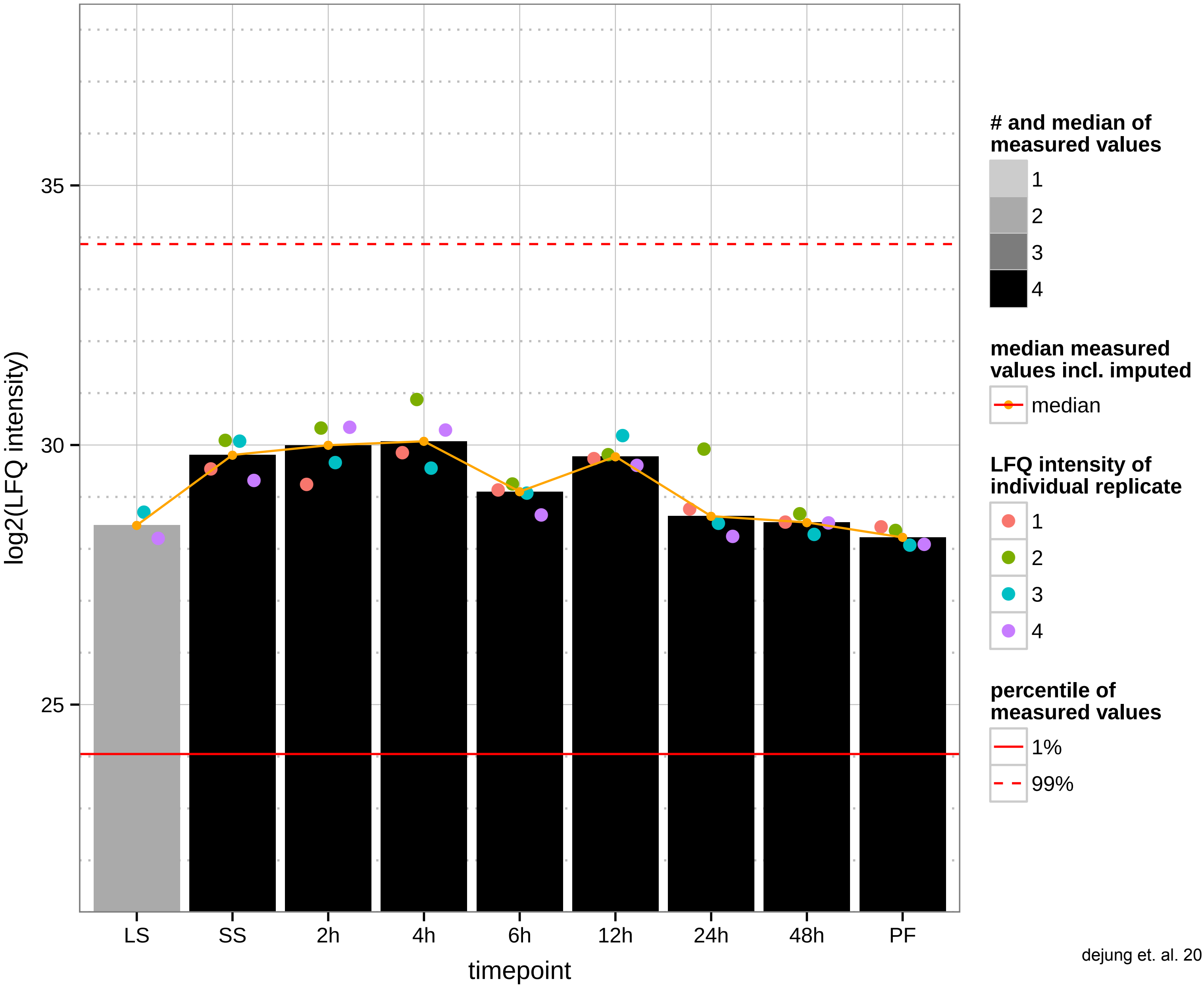
histone H4 variant
Tb927.2.2670
AGOF: DNA binding
AGOC: nucleosome, nucleus
AGOP: chromosome organization, nucleosome assembly
PGOF: DNA binding
PGOC: nucleosome, nucleus
PGOP: nucleosome assembly





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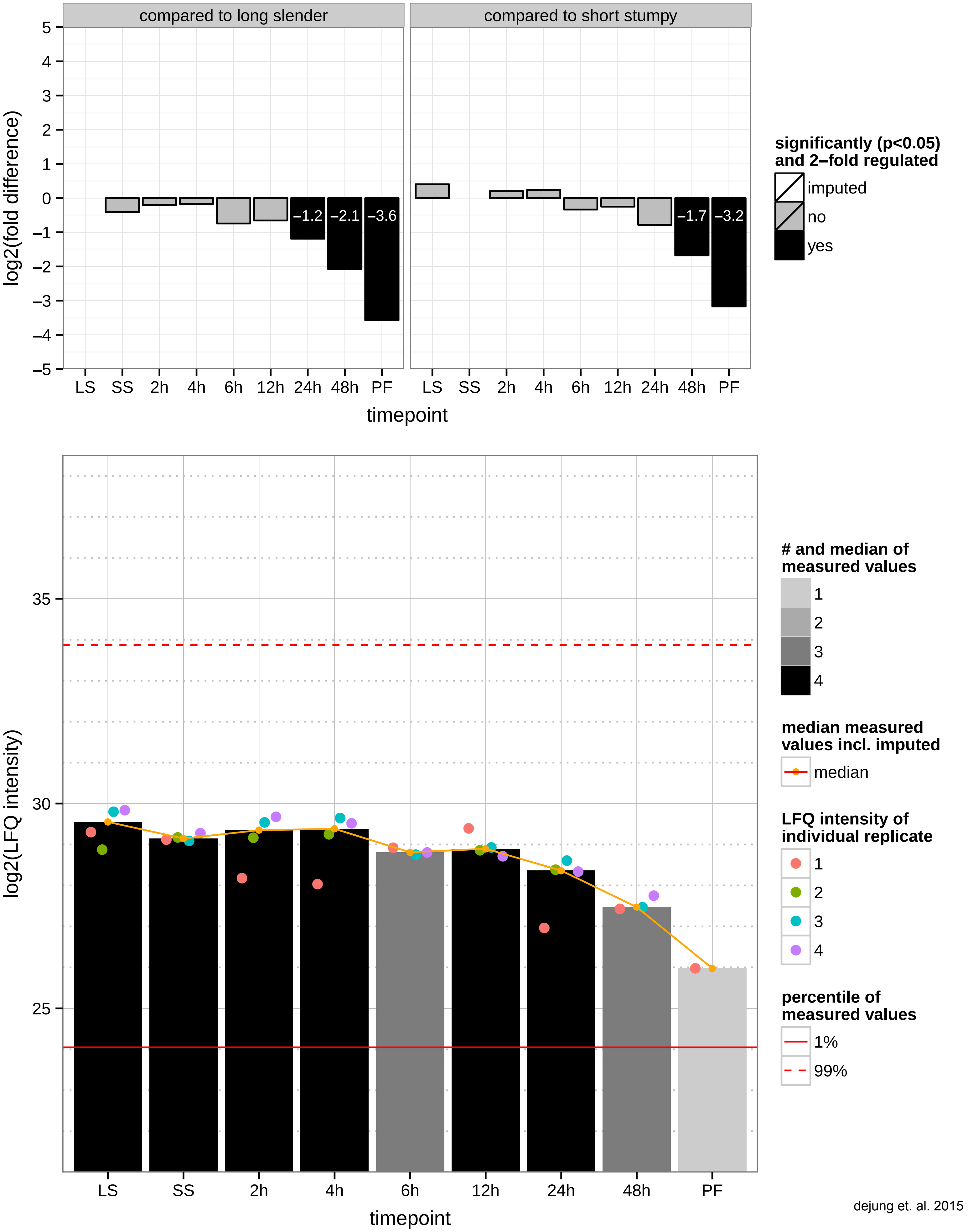
hypothetical protein, conserved
Tb927.2.2770
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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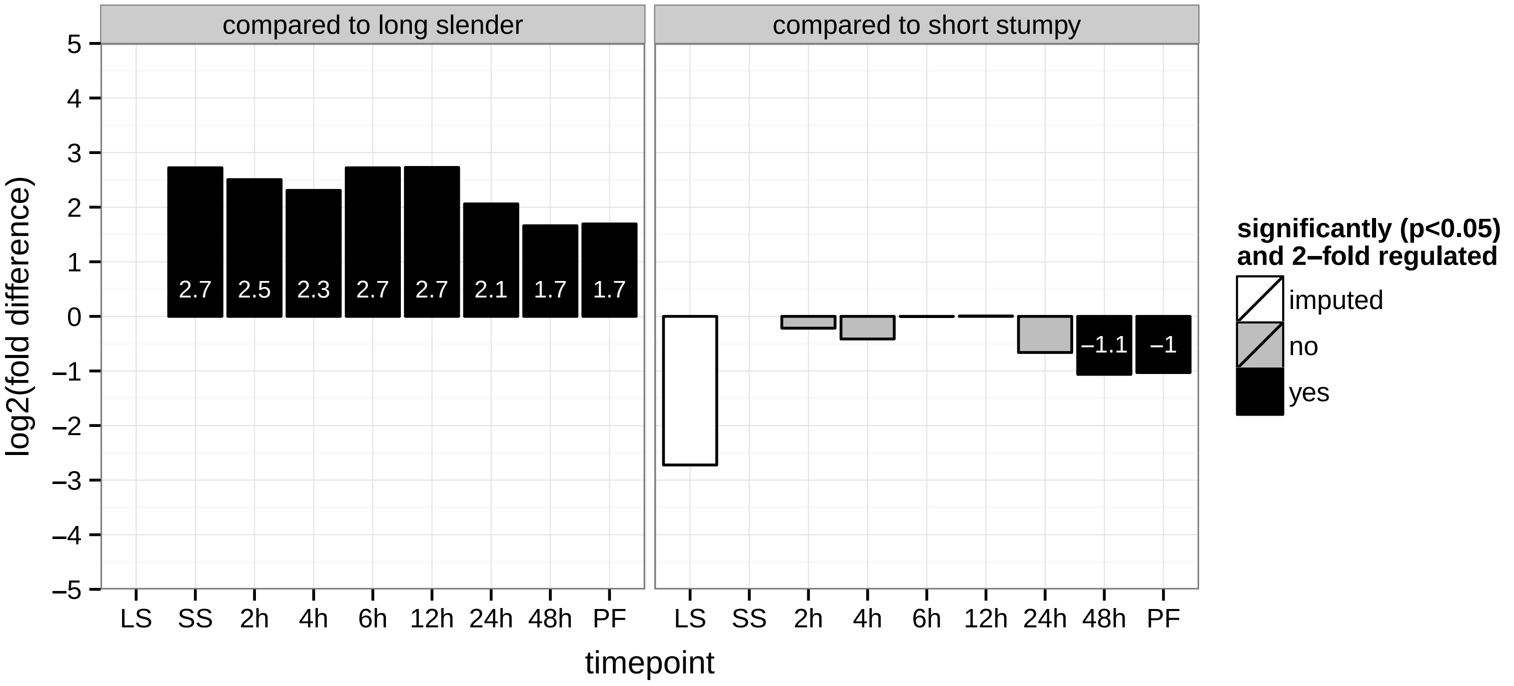
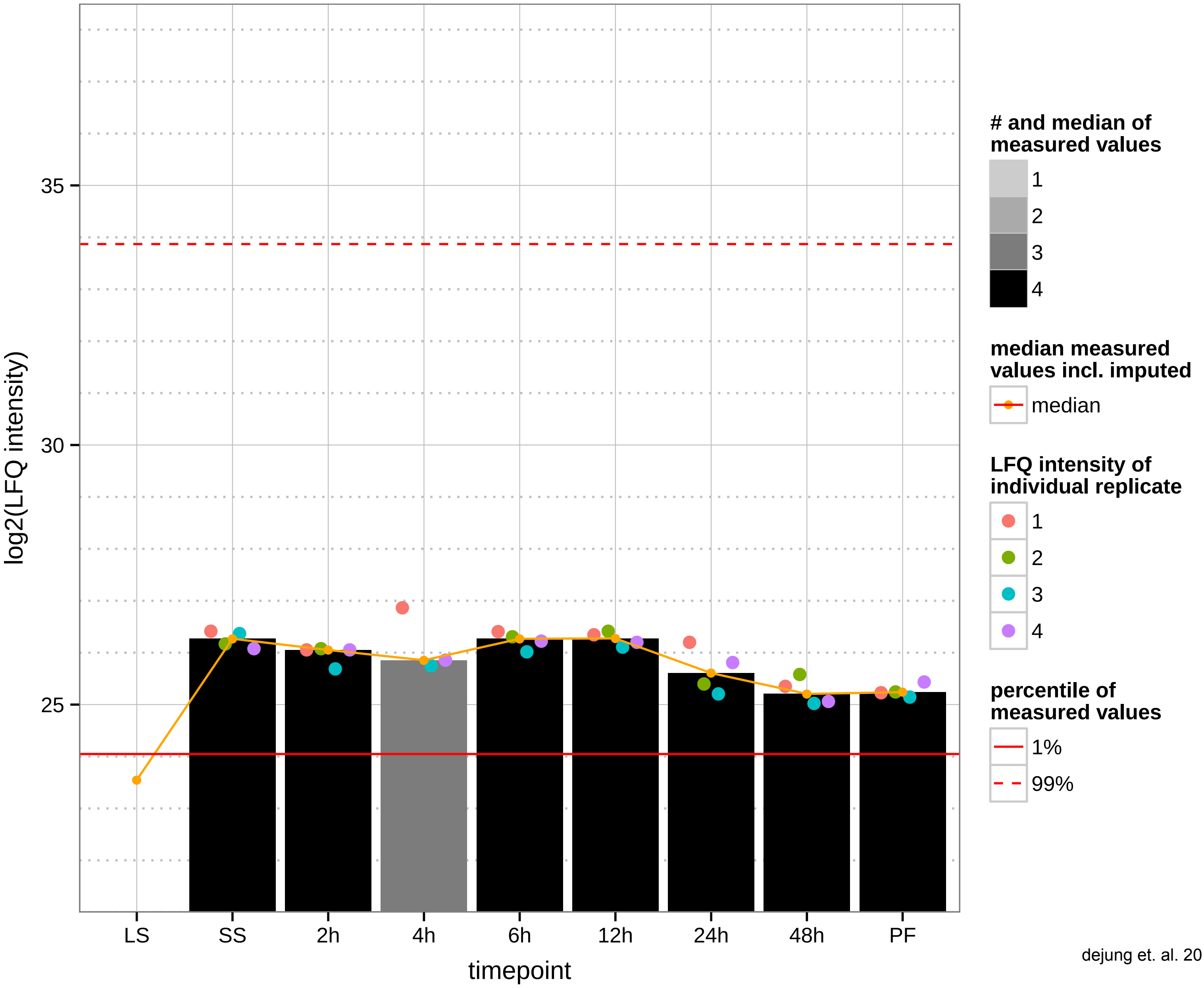
GTP–binding elongation factor Tu family, putative
Tb927.2.3620
AGOF: GTP binding, GTPase activity, translation elongation factor activity
AGOC: null
AGOP: translational elongation
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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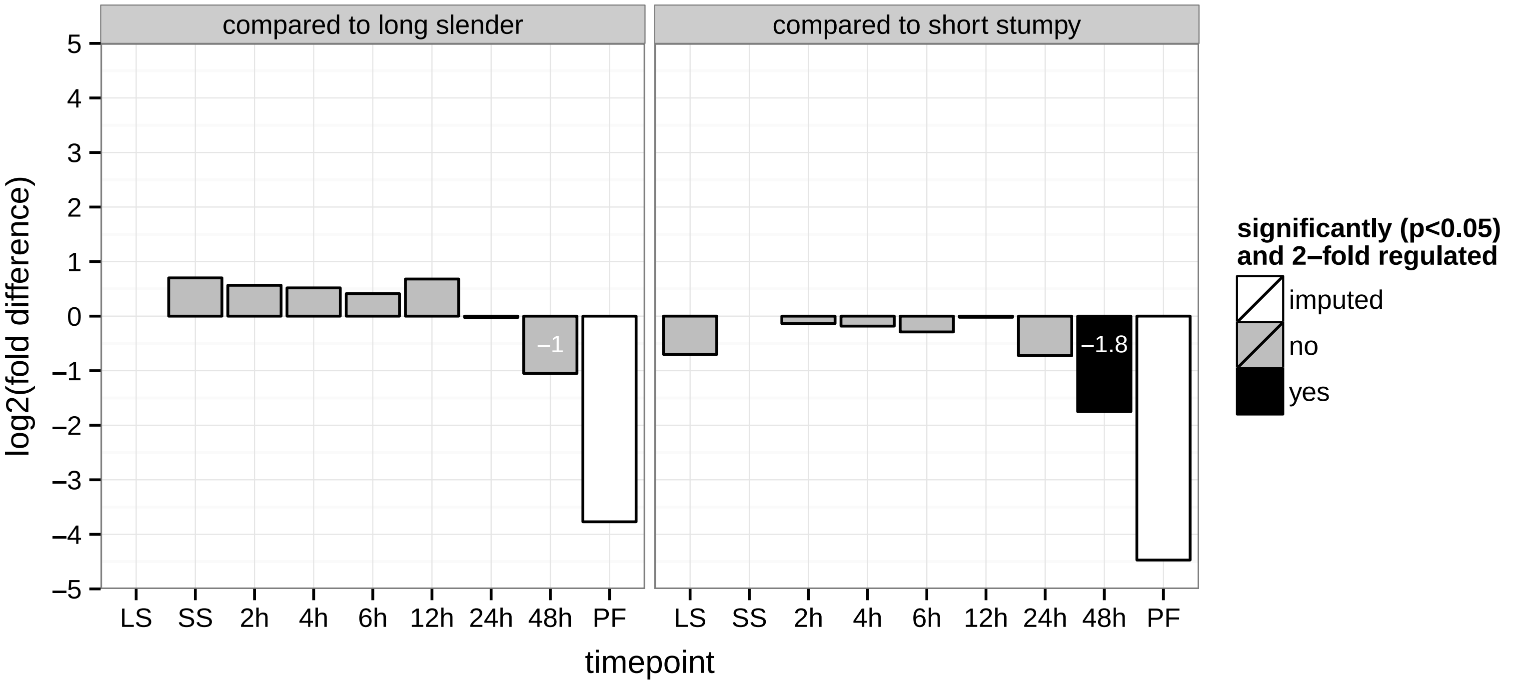
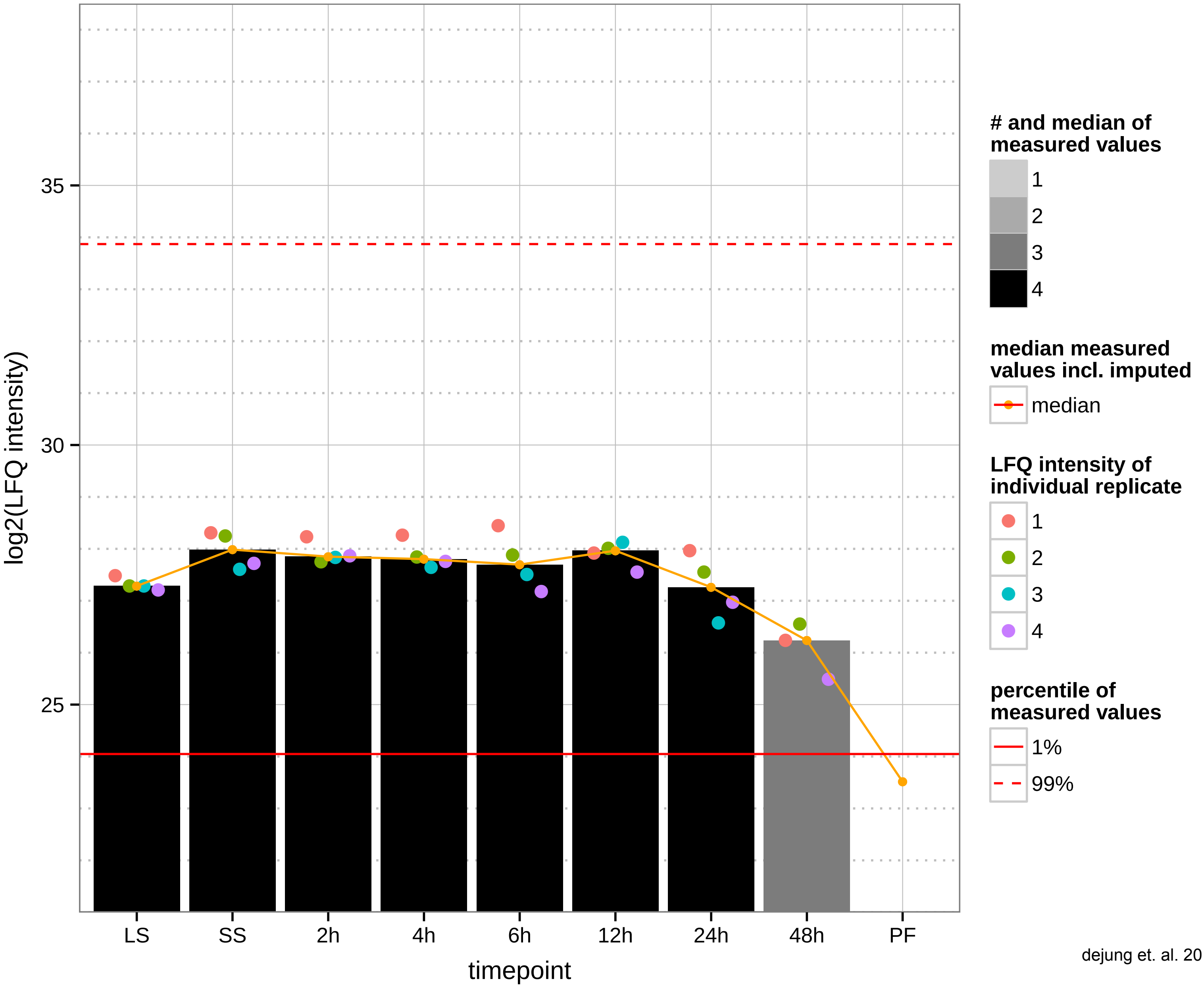
heterogeneous nuclear ribonucleoprotein H/F, putative (HNRNPH)
Tb927.2.3880
AGOF: mRNA binding
AGOC: nucleus
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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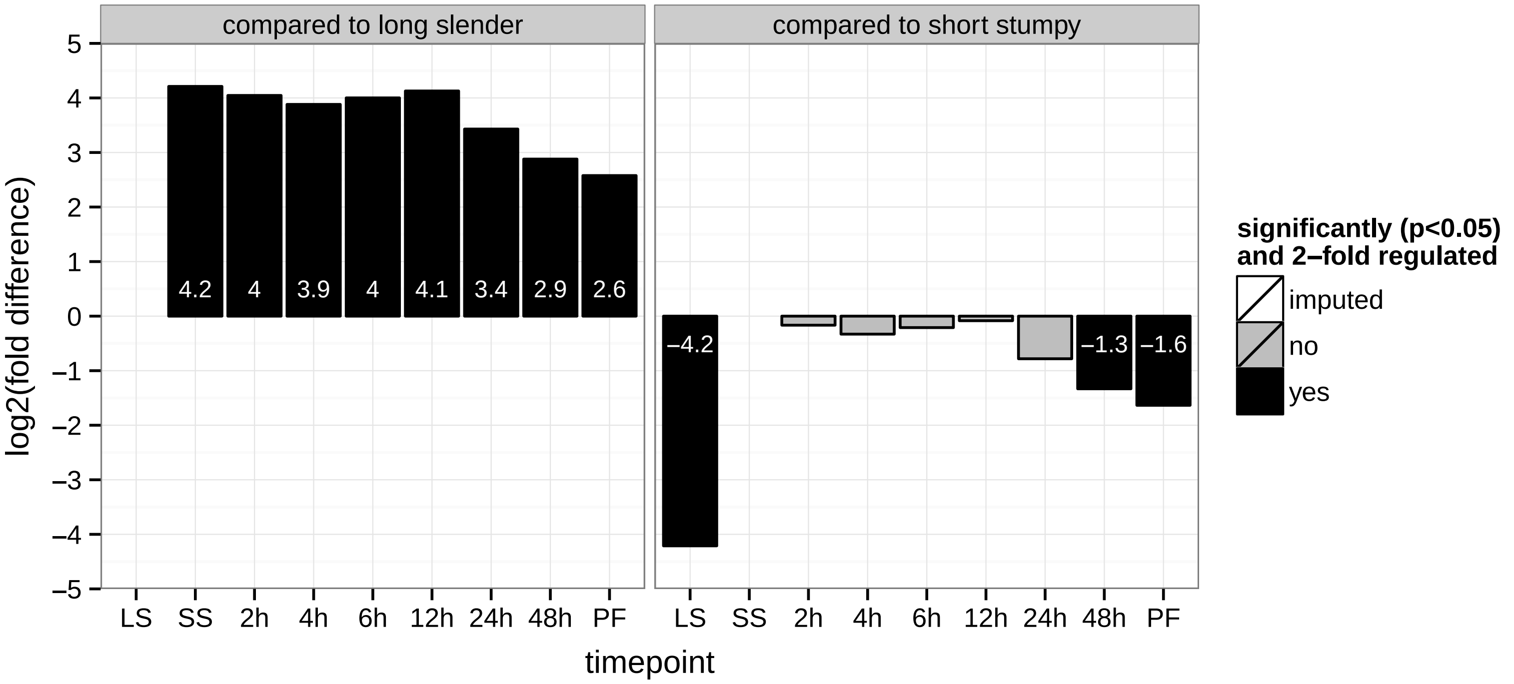
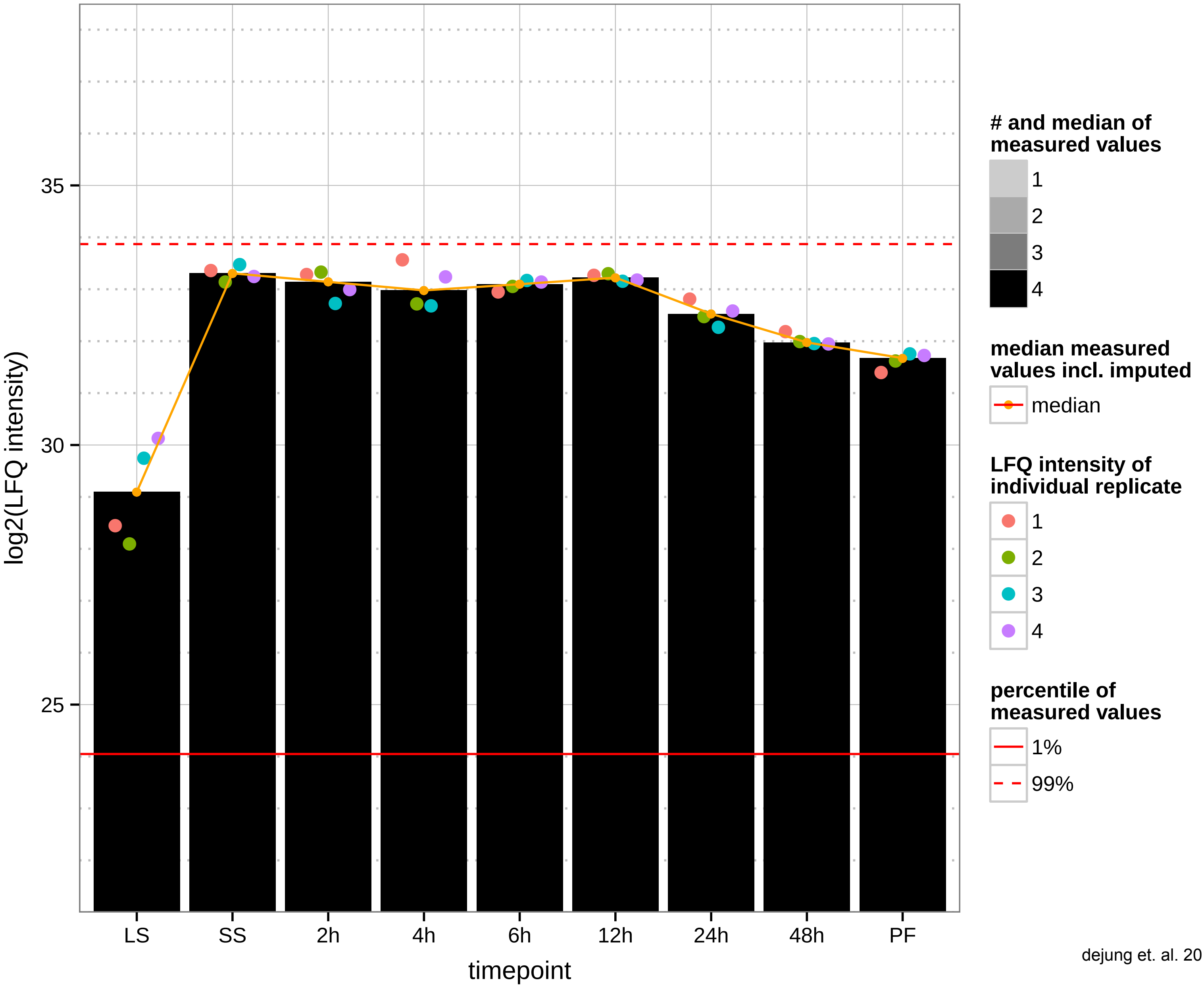
trypanothione synthetase, putative, trypanothione synthetase (TRYS)
Tb927.2.4370;Tb11.v5.0653
AGOF: null, trypanothione−disulfide reductase activity
AGOC: null, cytosol
AGOP: null, trypanothione biosynthetic process
PGOF: null
PGOC: null
PGOP: null





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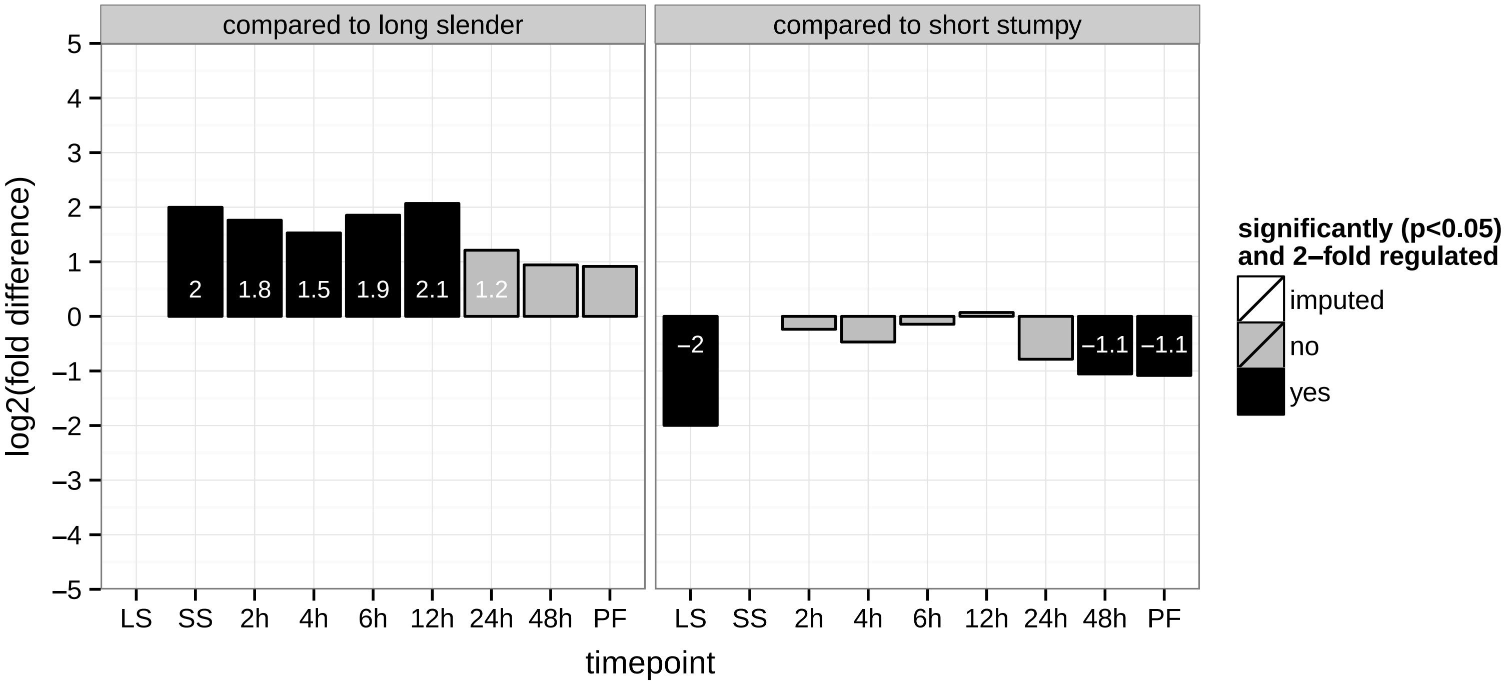
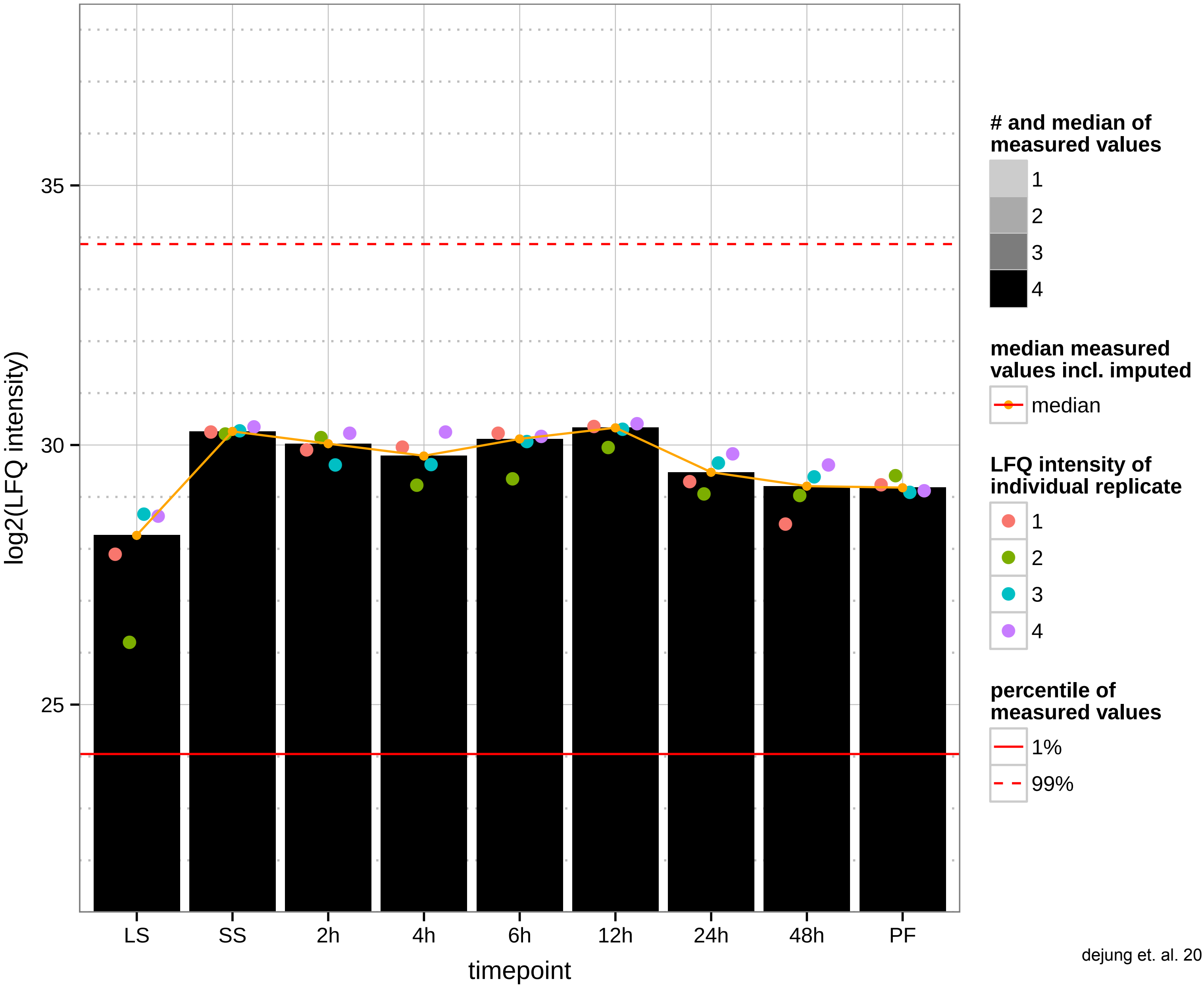
sedoheptulose−1, 7−bisphosphatase (SBPase)
Tb927.2.5800
AGOF: molecular_function, phosphoric ester hydrolase activity
AGOC: glycosome
AGOP: carbohydrate metabolic process
PGOF: phosphoric ester hydrolase activity
PGOC: null
PGOP: carbohydrate metabolic process





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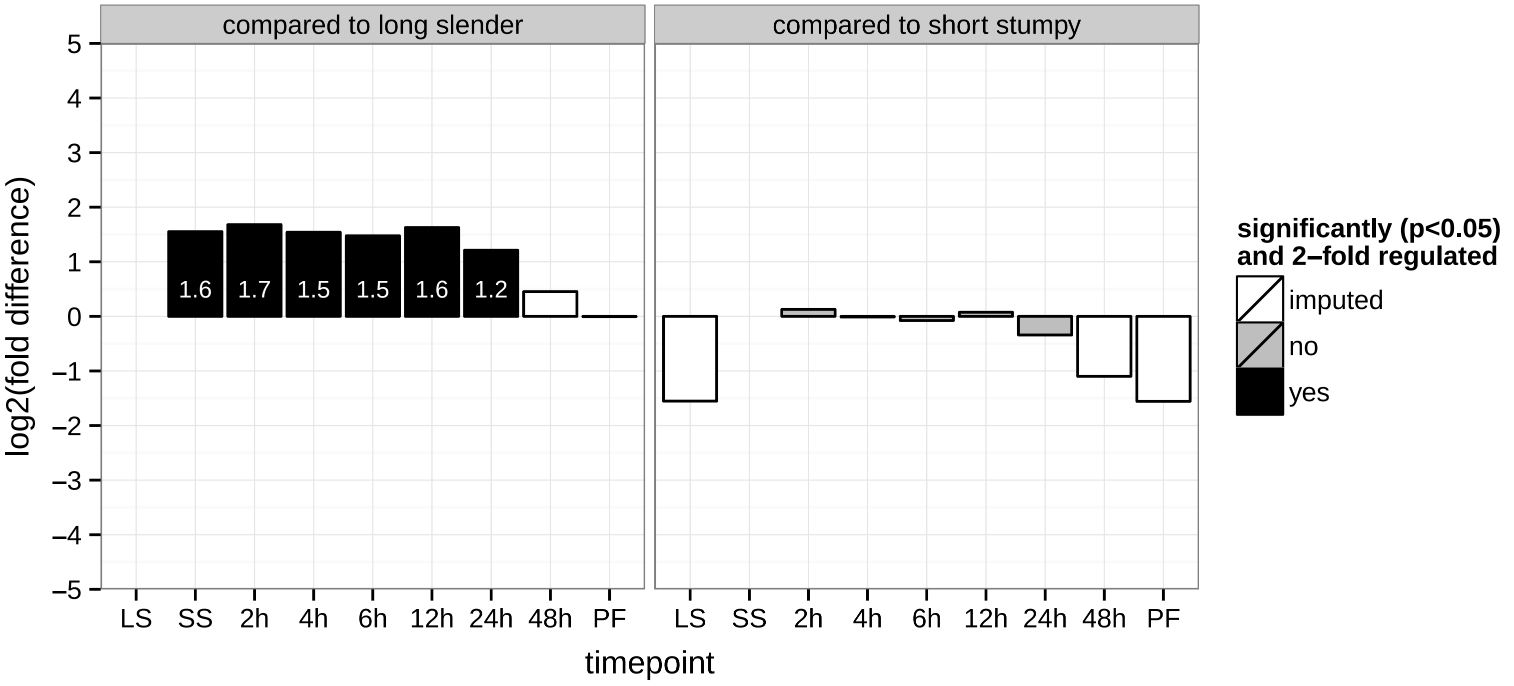
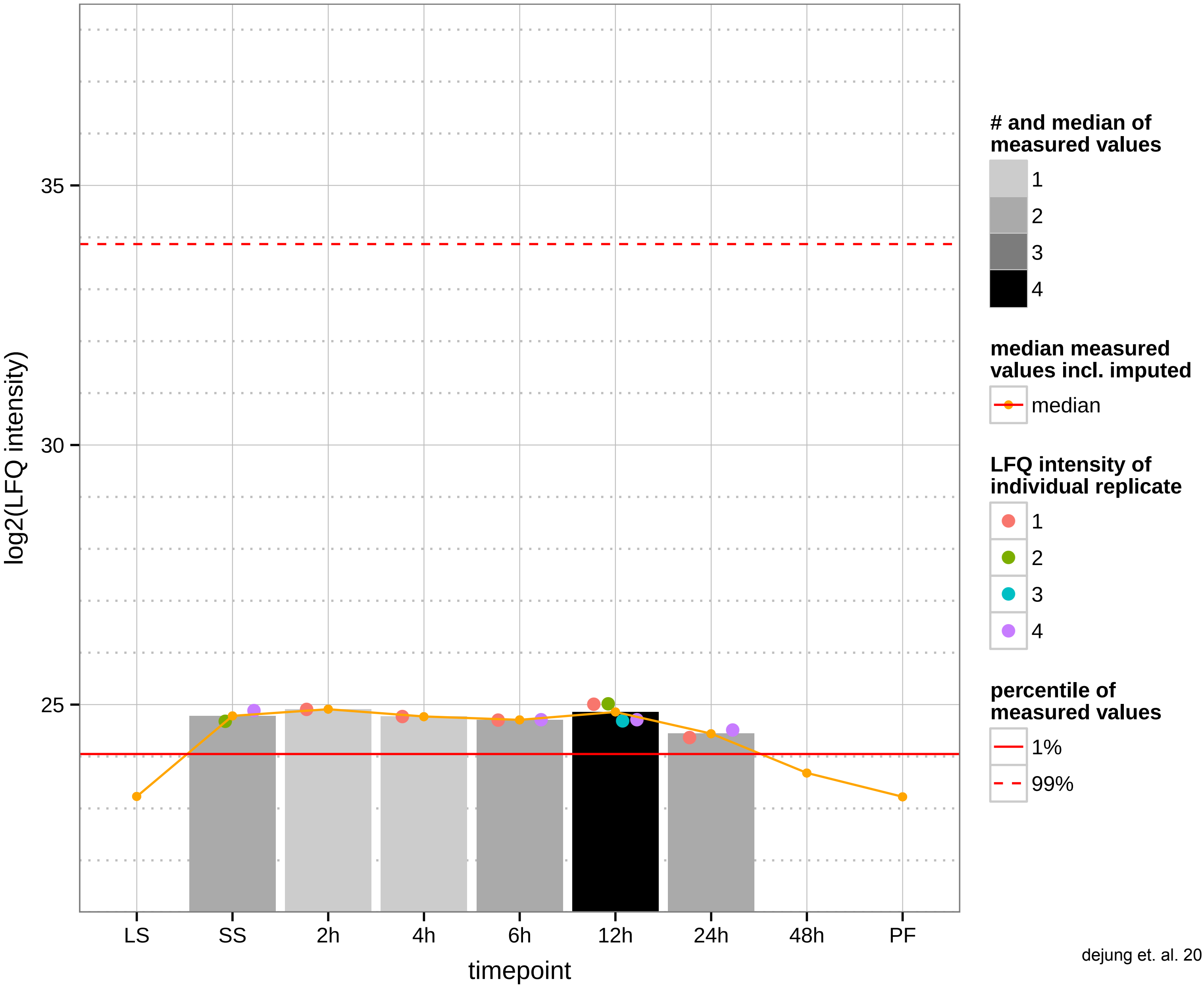
hypothetical protein, conserved
Tb927.3.1390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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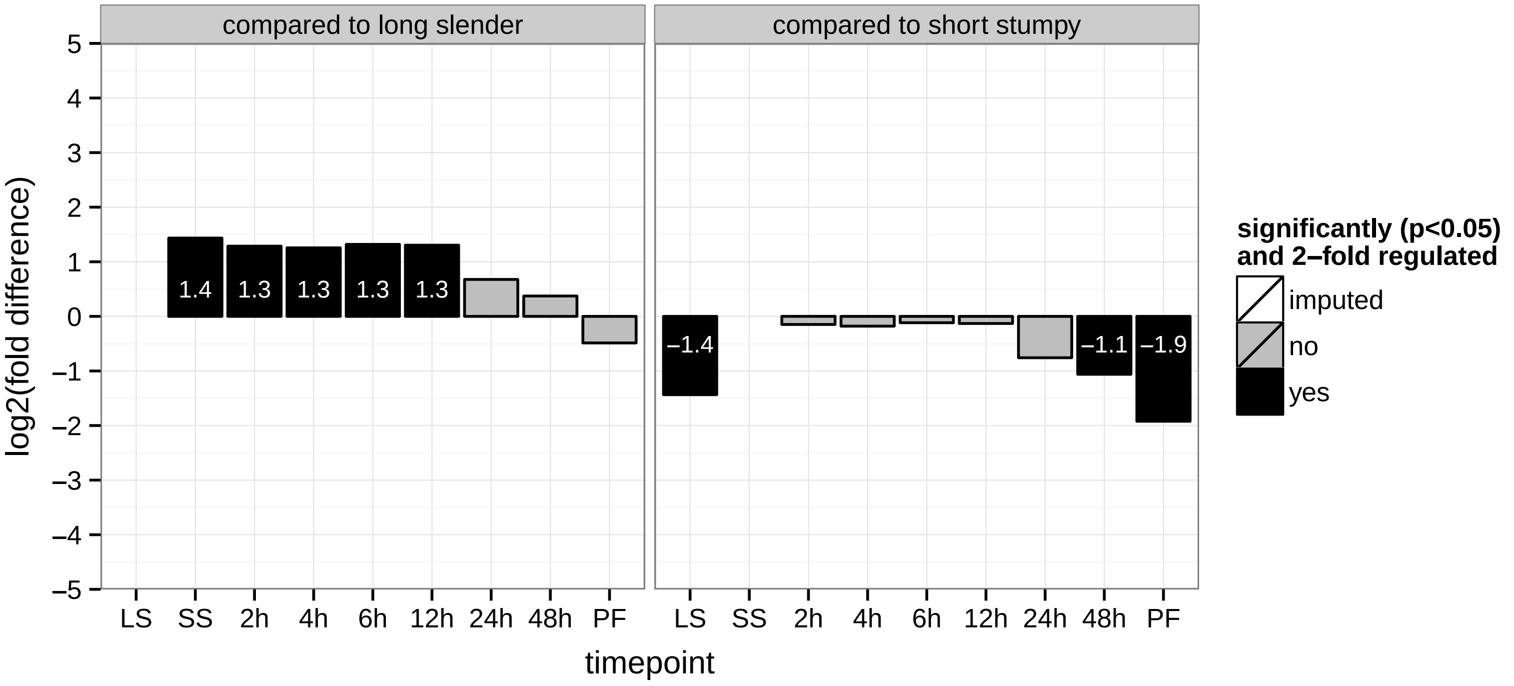
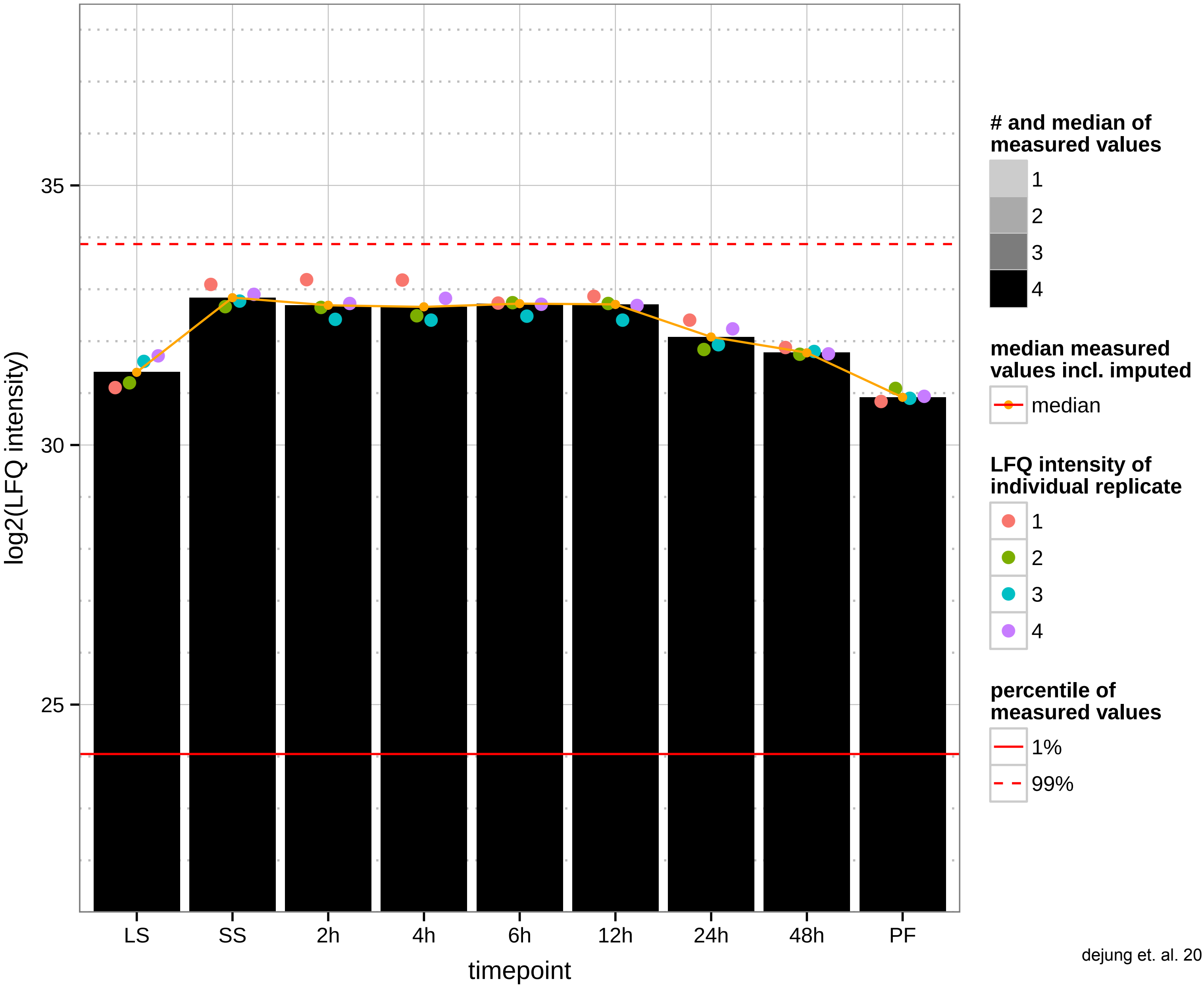
dynamin, putative, vacuolar sortin protein 1
Tb927.3.4720
AGOF: GTP binding, GTPase activity
AGOC: null
AGOP: null
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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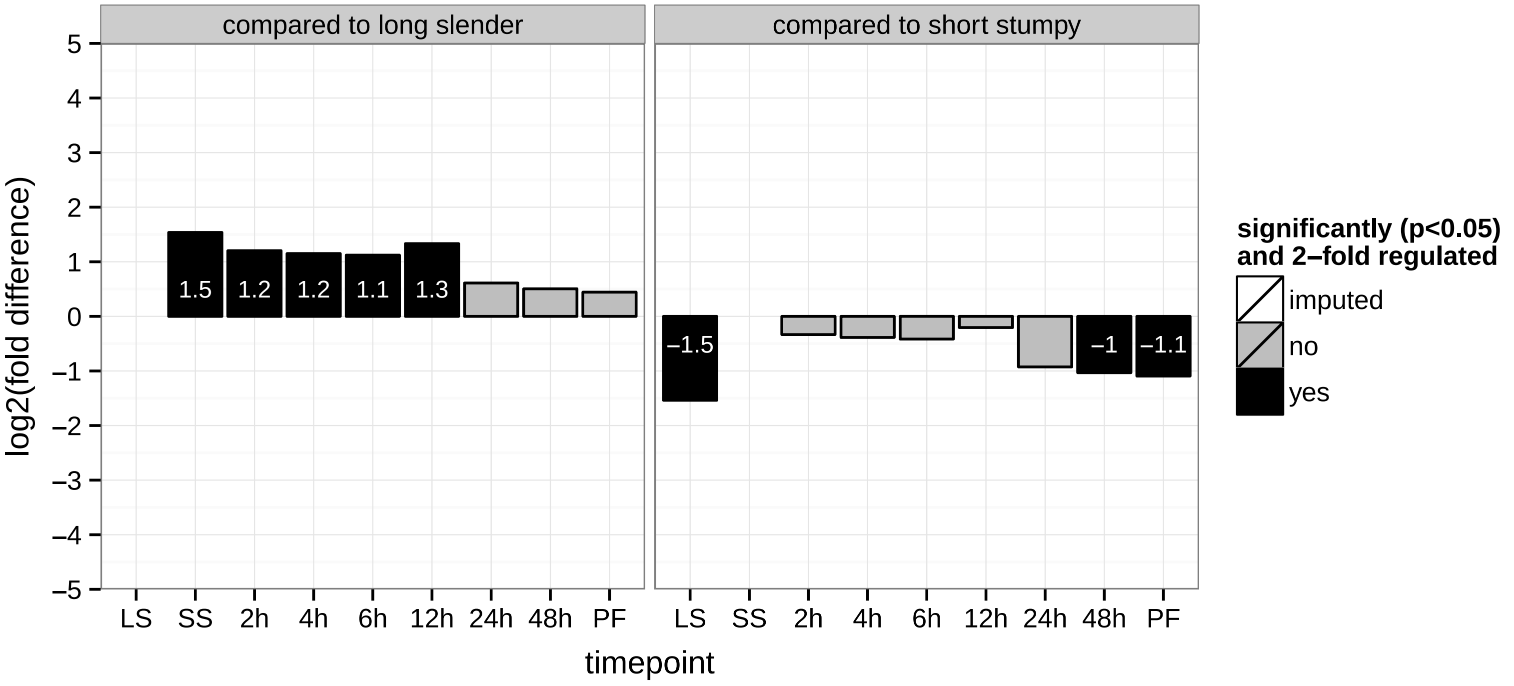
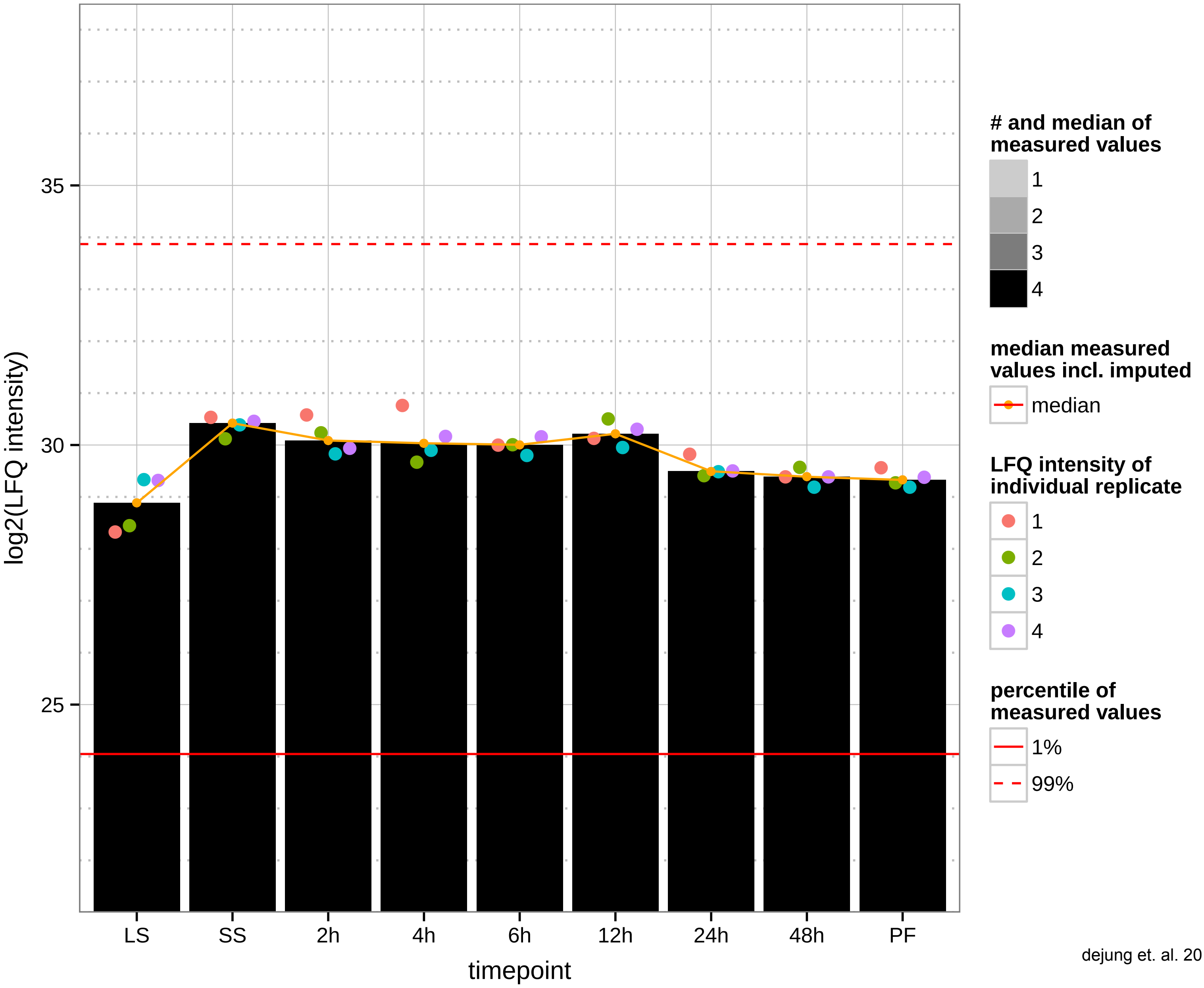
flagellar transport protein, putative (PIFTB2)
Tb927.3.5490
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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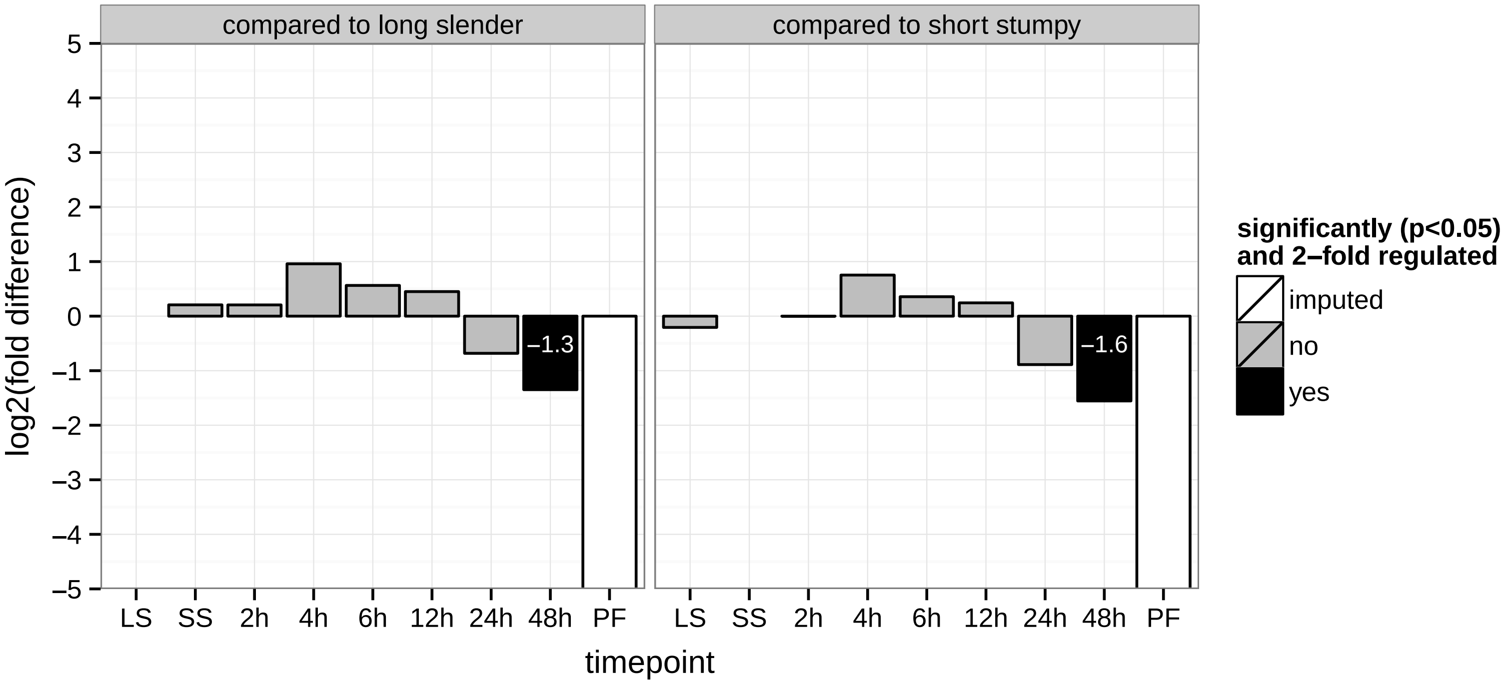
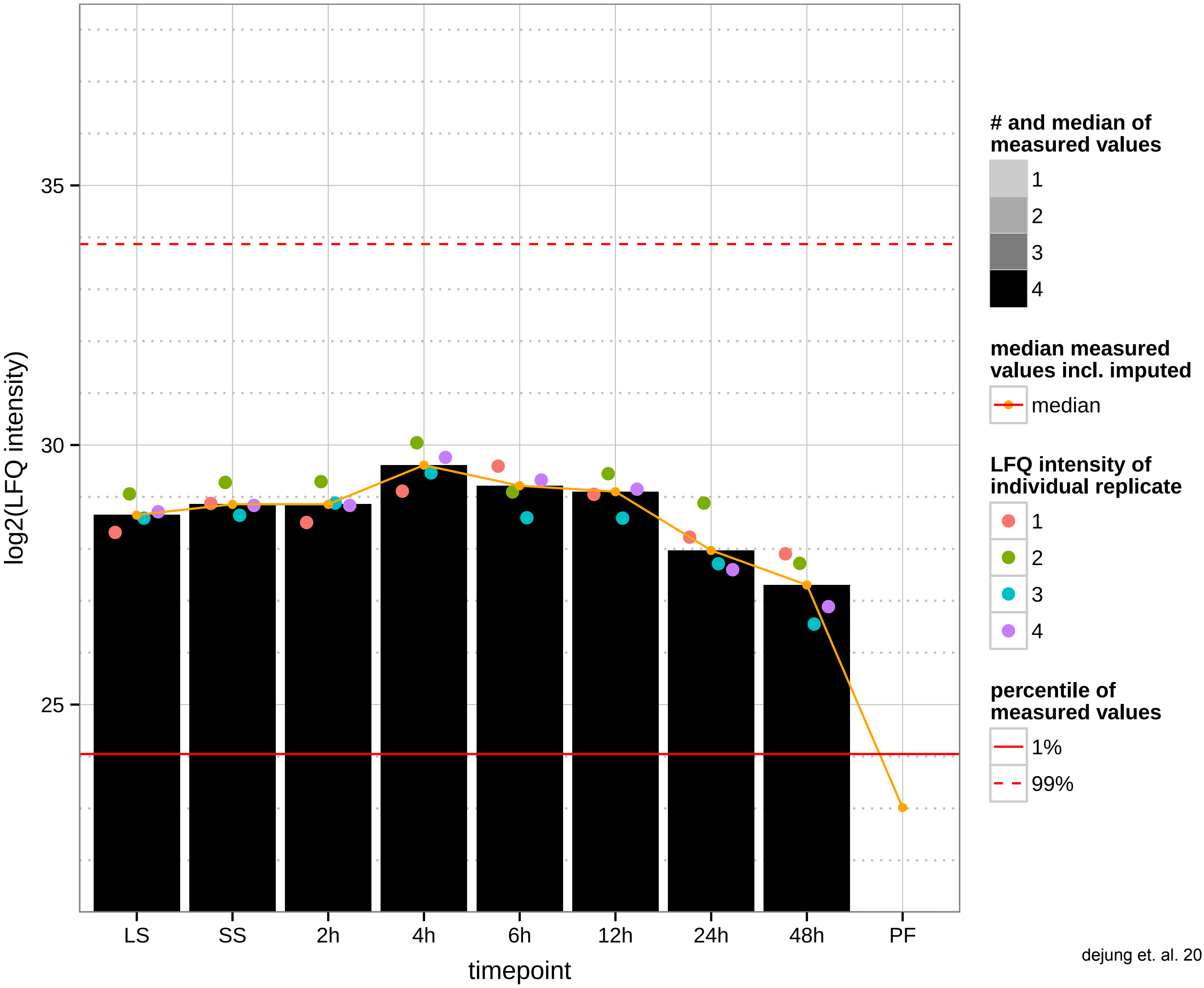
ALBA–Domain Protein (ALBA4)
Tb927.4.2030
AGOF: nucleic acid binding
AGOC: cytoplasm, cytoplasmic stress granule
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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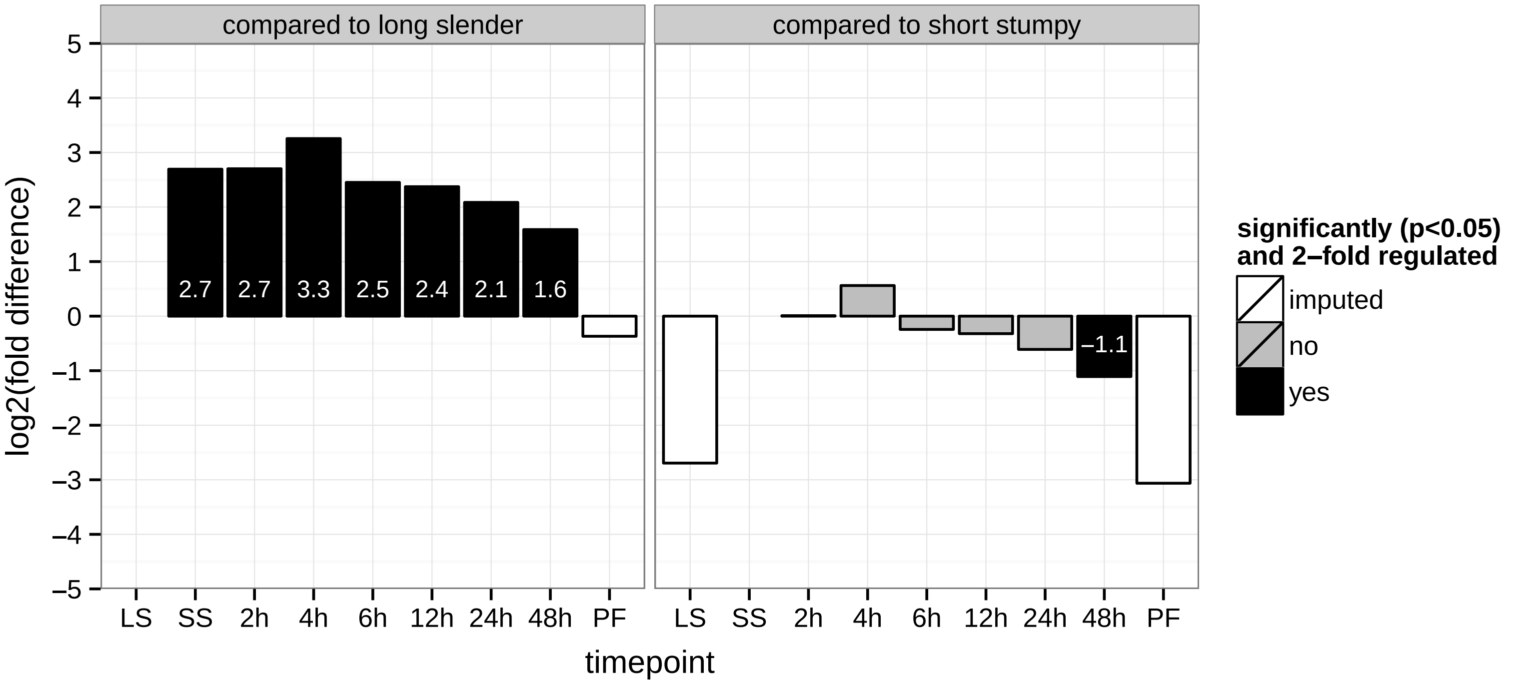
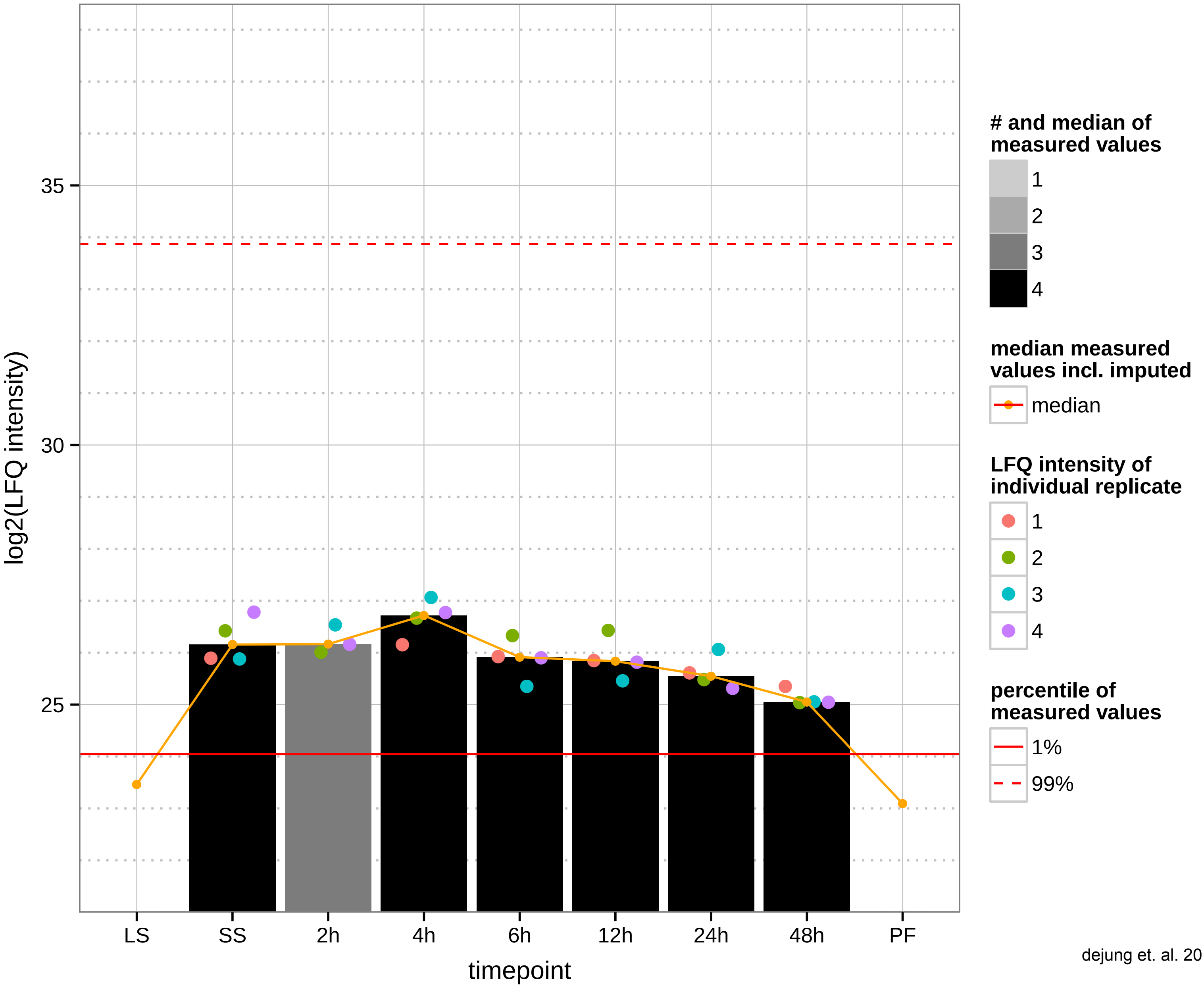
hypothetical protein, conserved
Tb927.4.2170
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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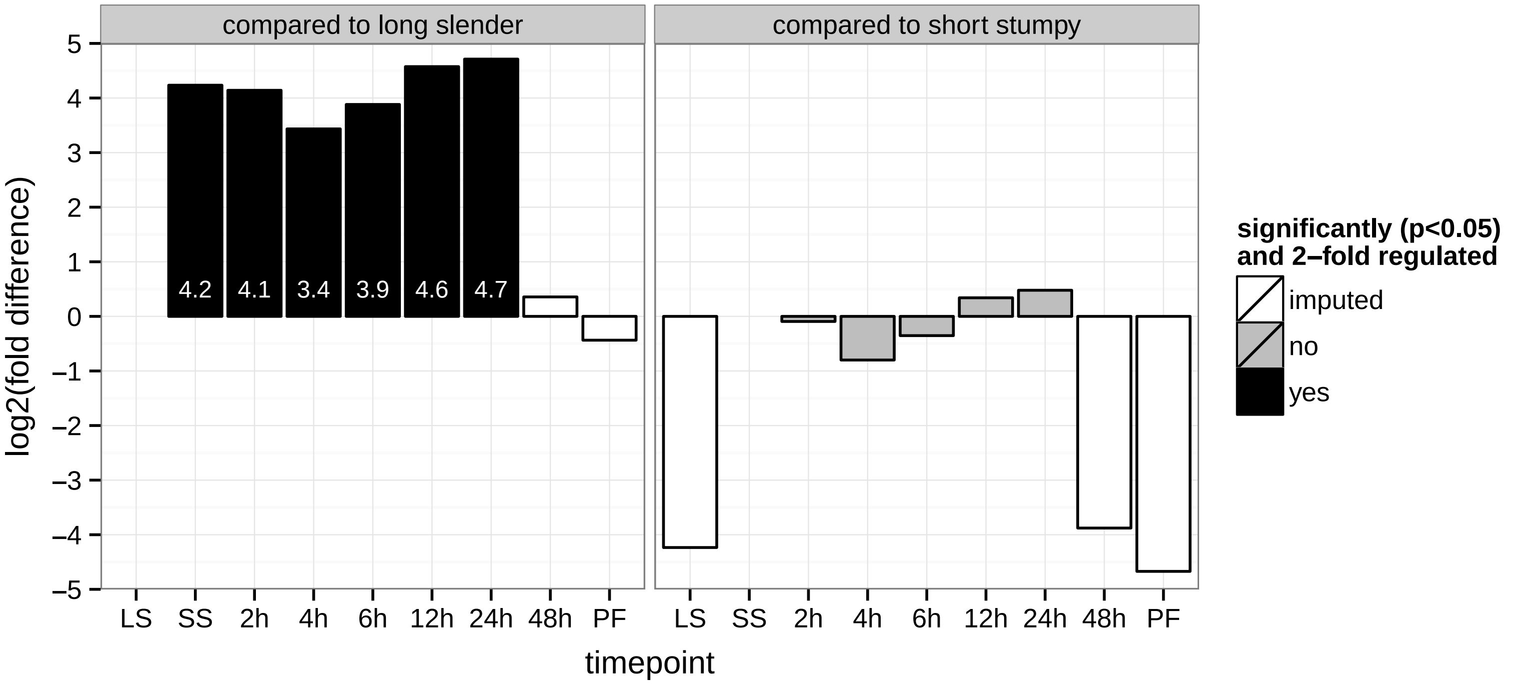
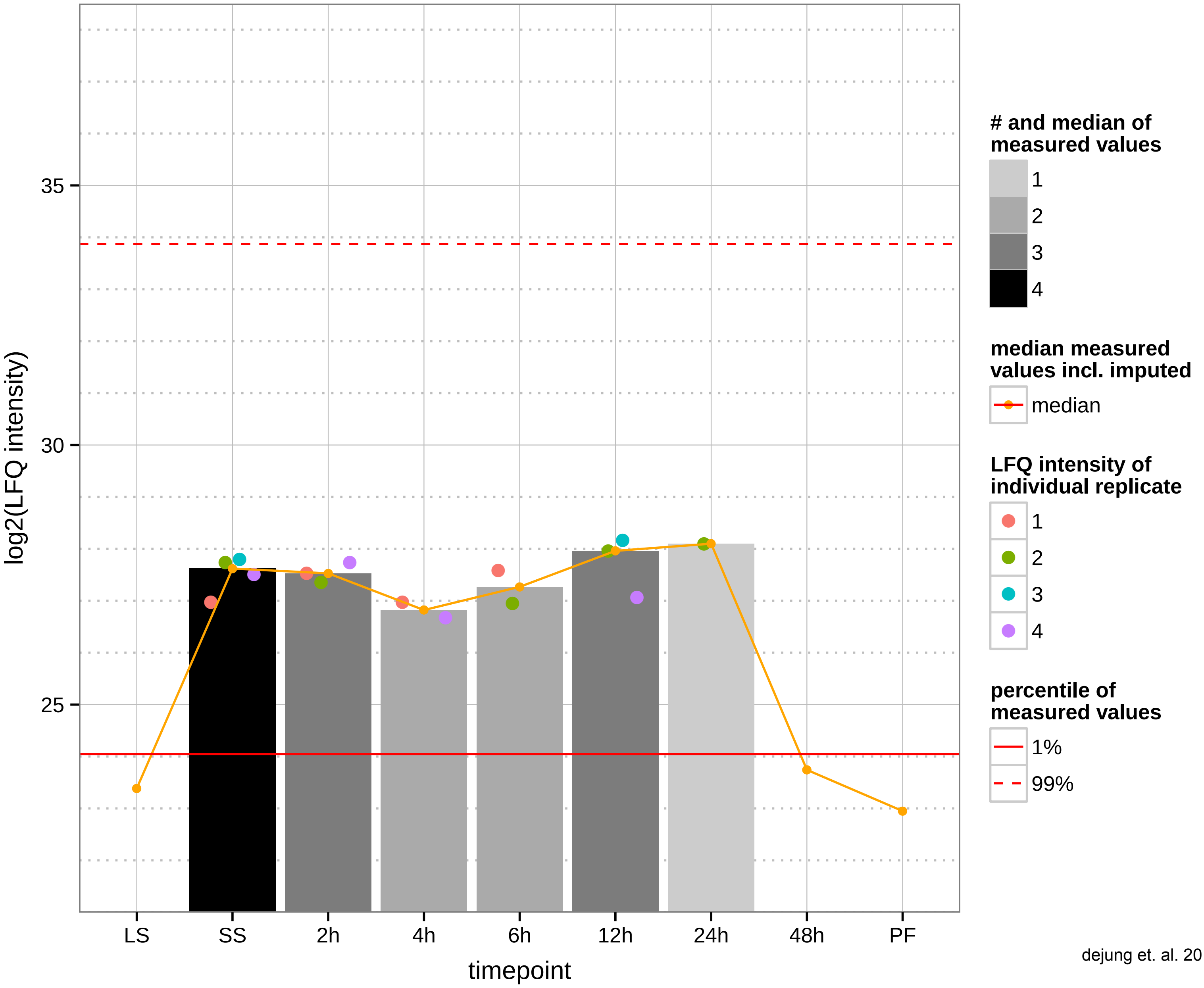
hypothetical protein, conserved
Tb927.4.2640
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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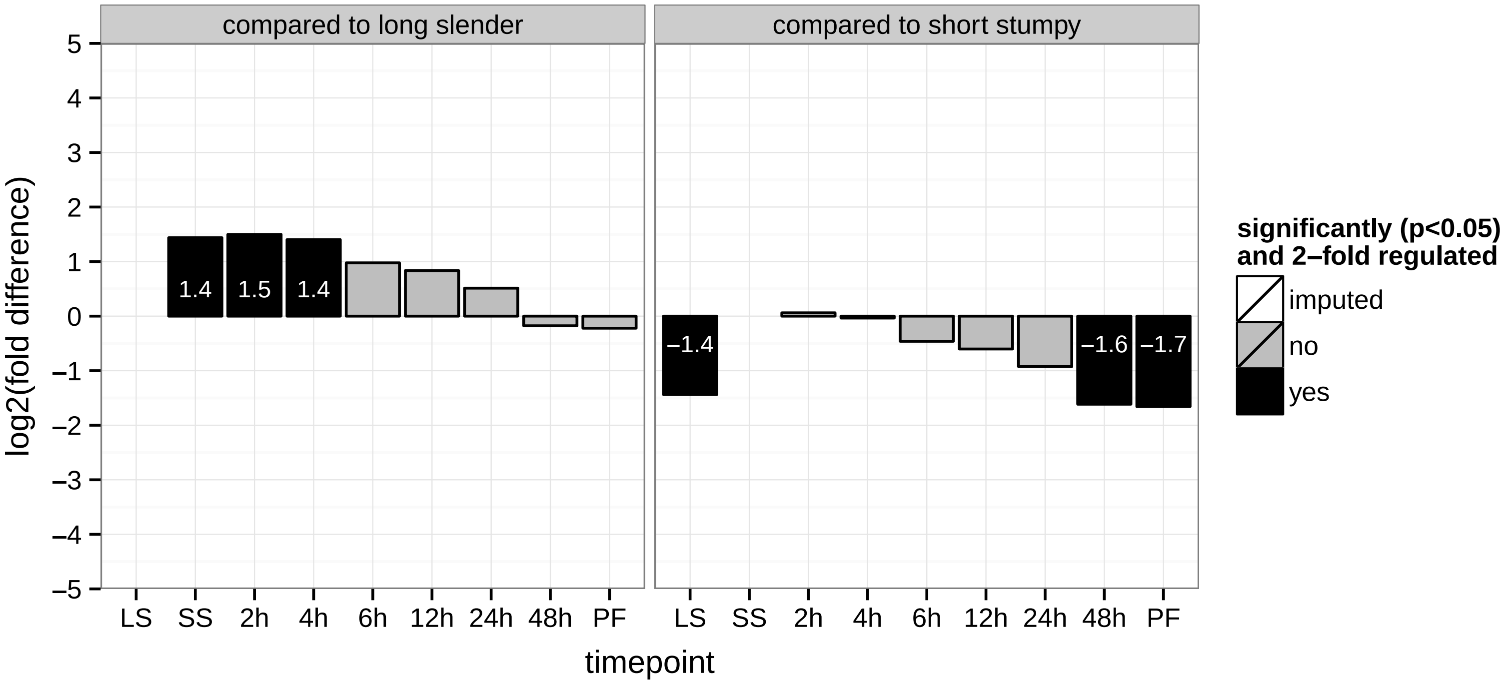
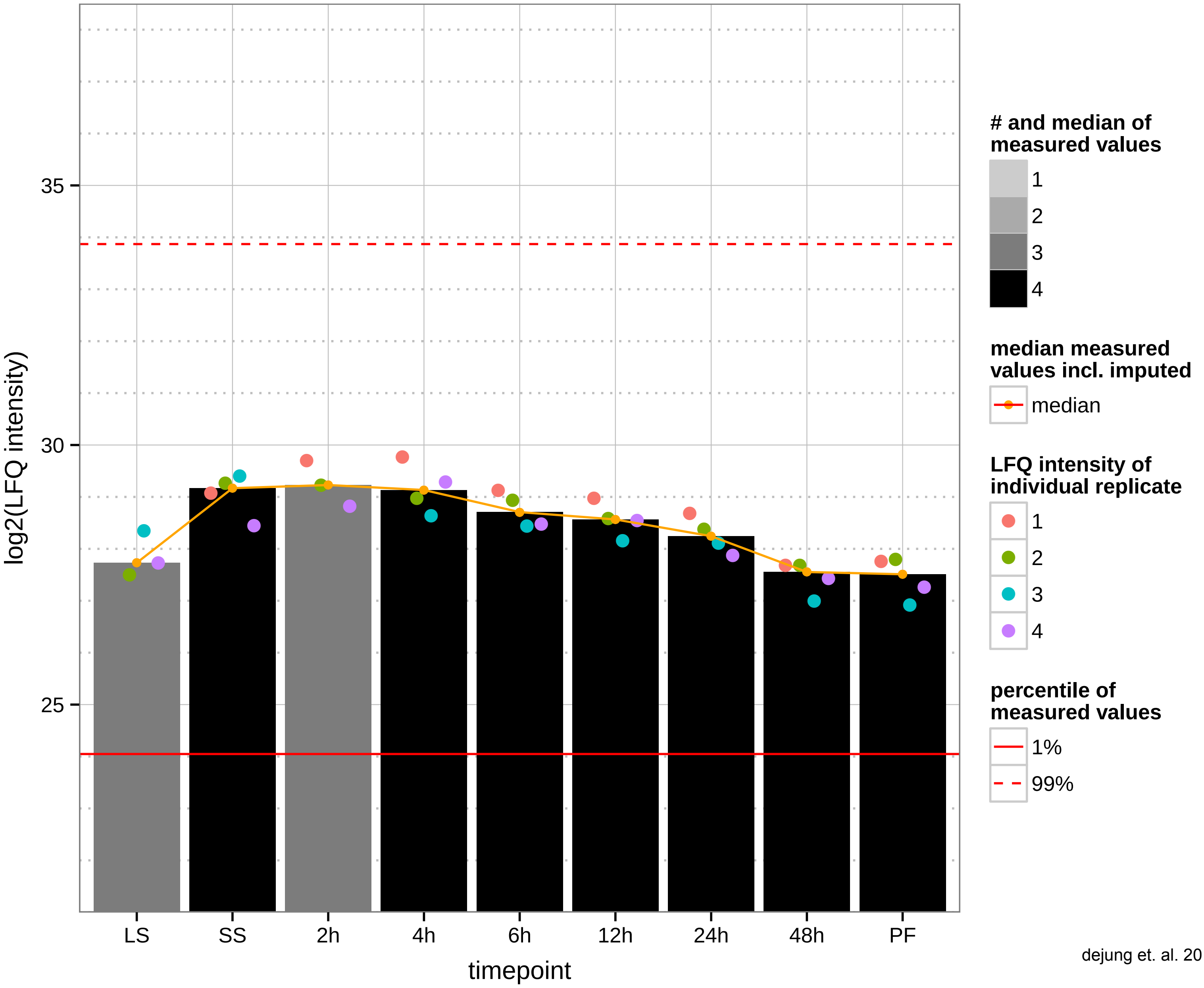
hypothetical protein, conserved
Tb927.4.2760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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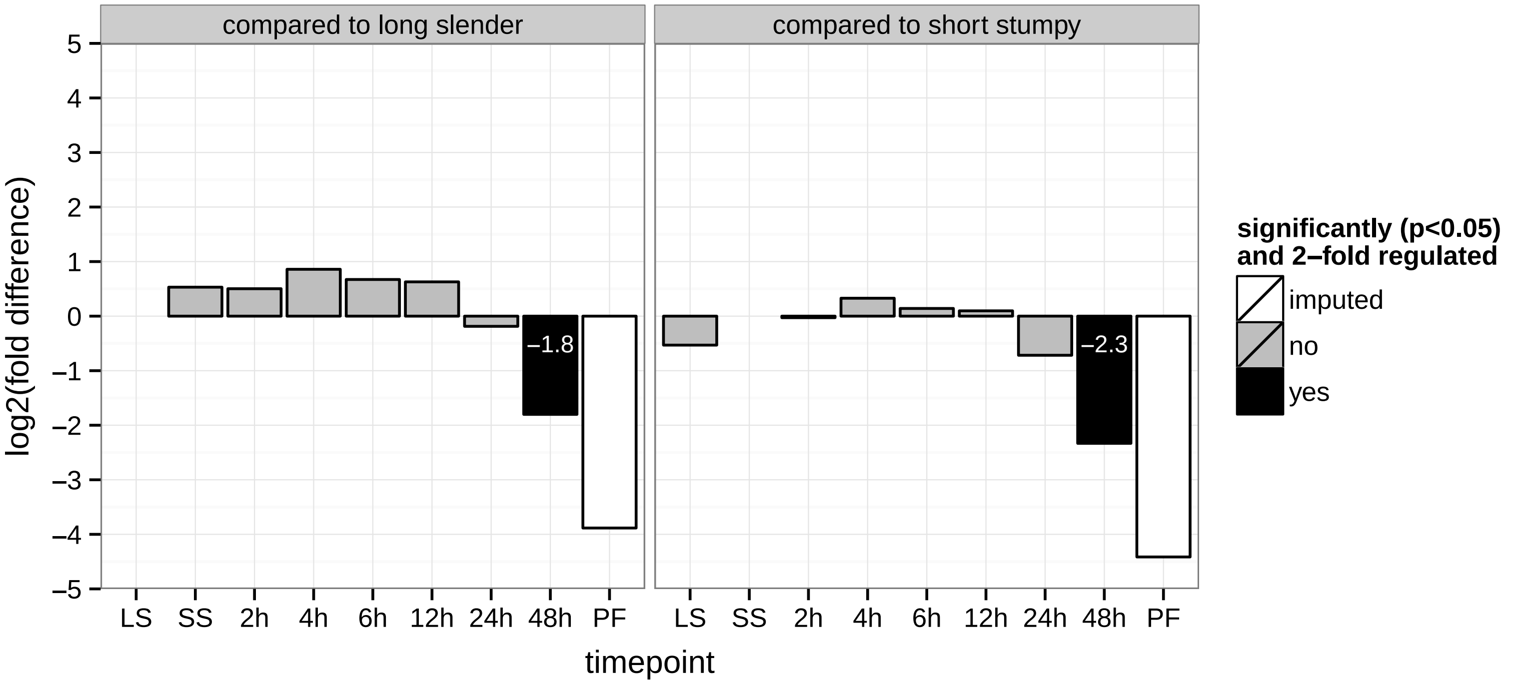
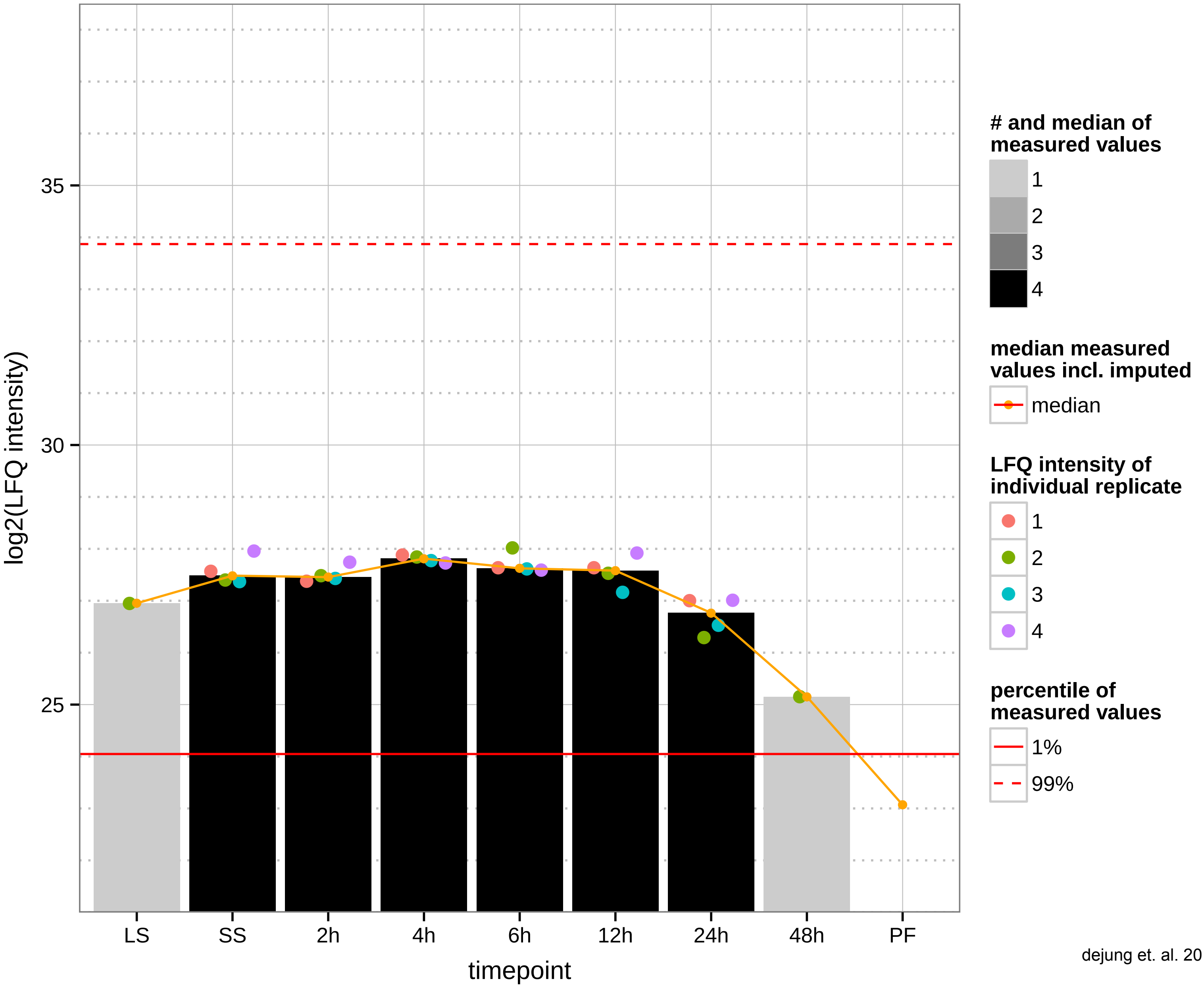
hypothetical protein, conserved
Tb927.4.3400
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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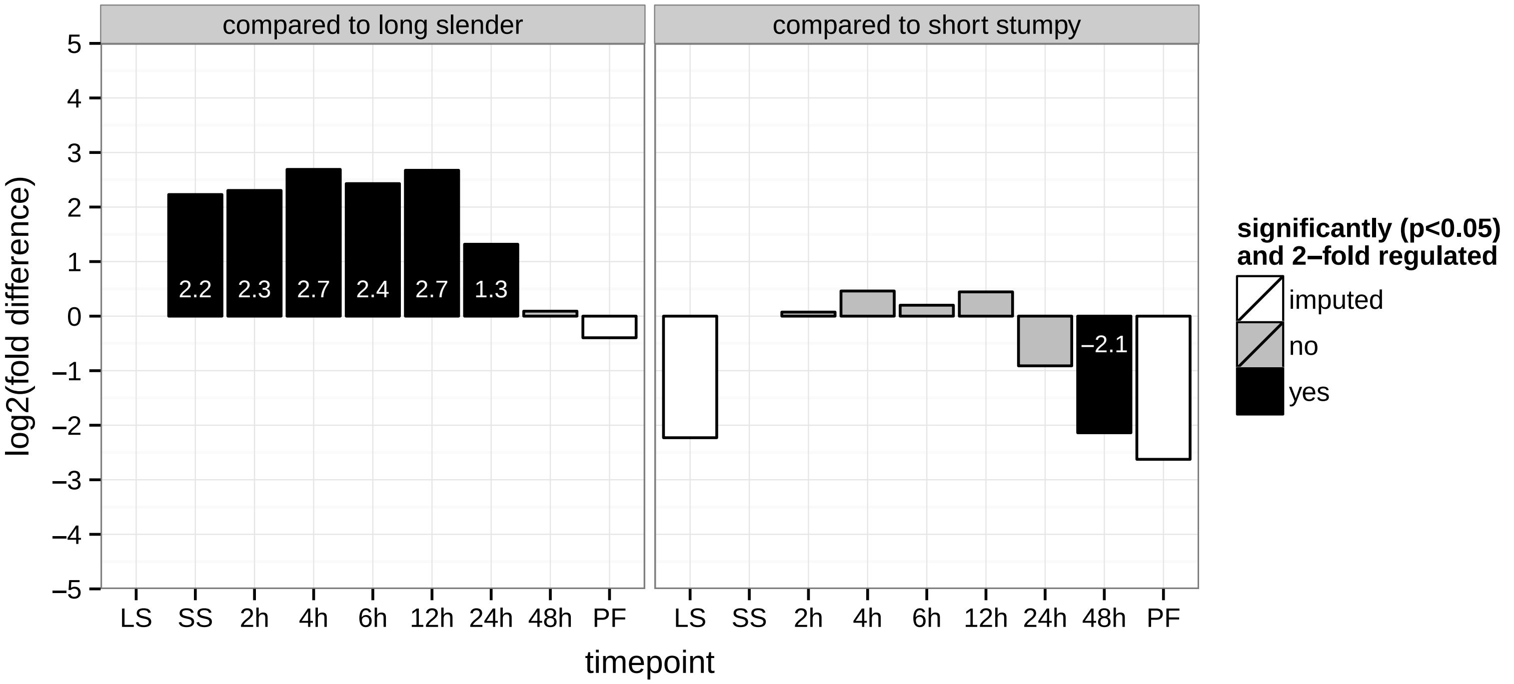
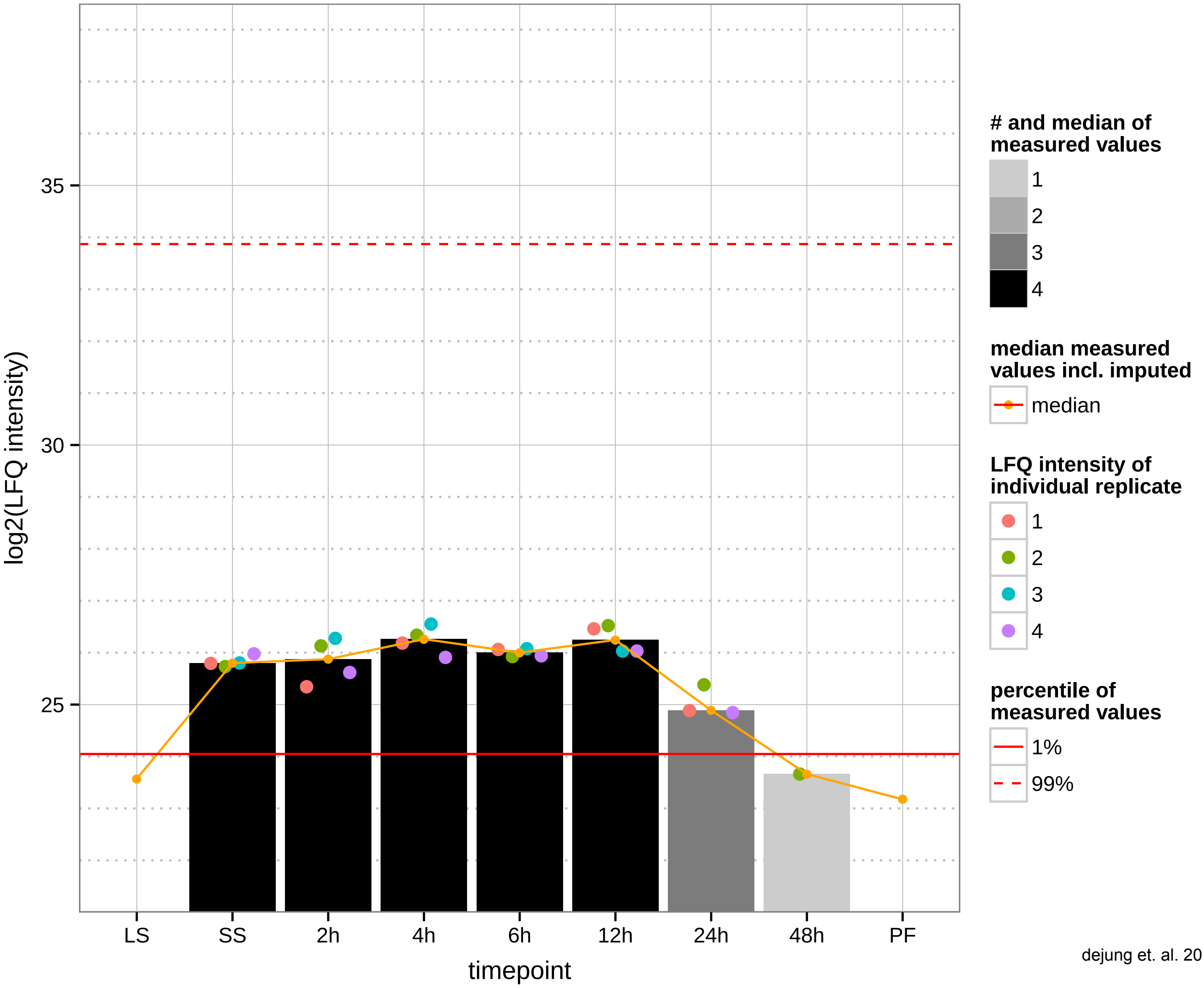
hypothetical protein, conserved
Tb927.4.3970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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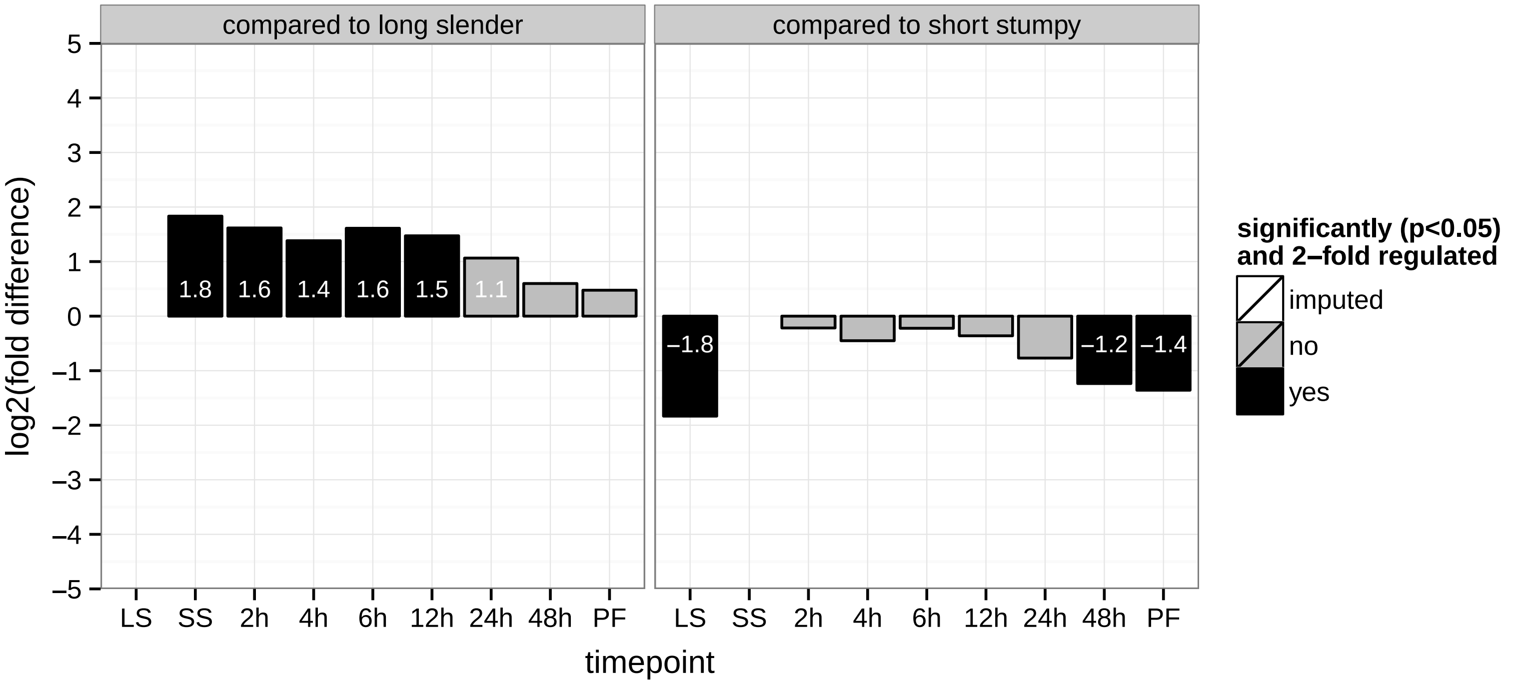
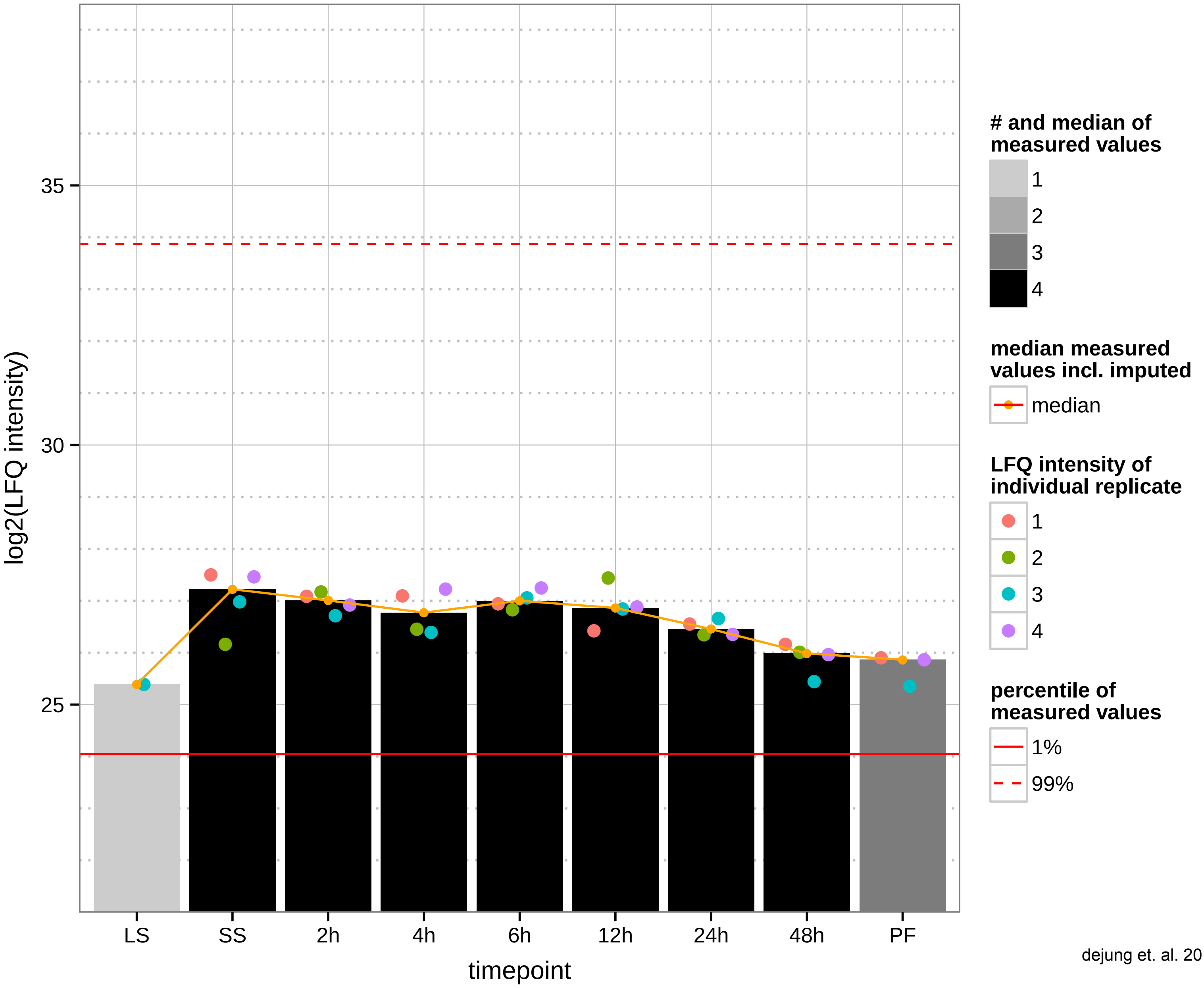
hypothetical protein, conserved
Tb927.4.610
AGOF: phosphatidylinositol binding
AGOC: null
AGOP: cell communication
PGOF: phosphatidylinositol binding, protein binding
PGOC: null
PGOP: cell communication





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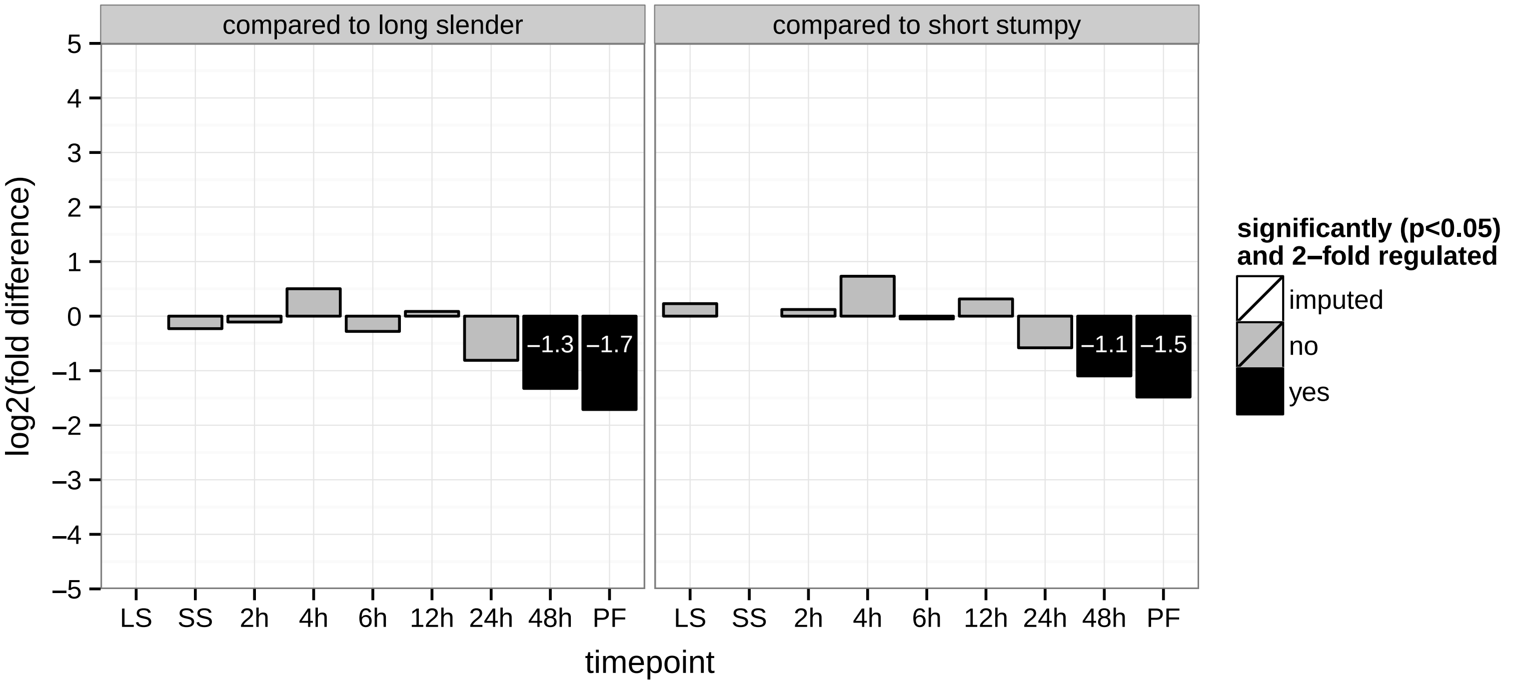
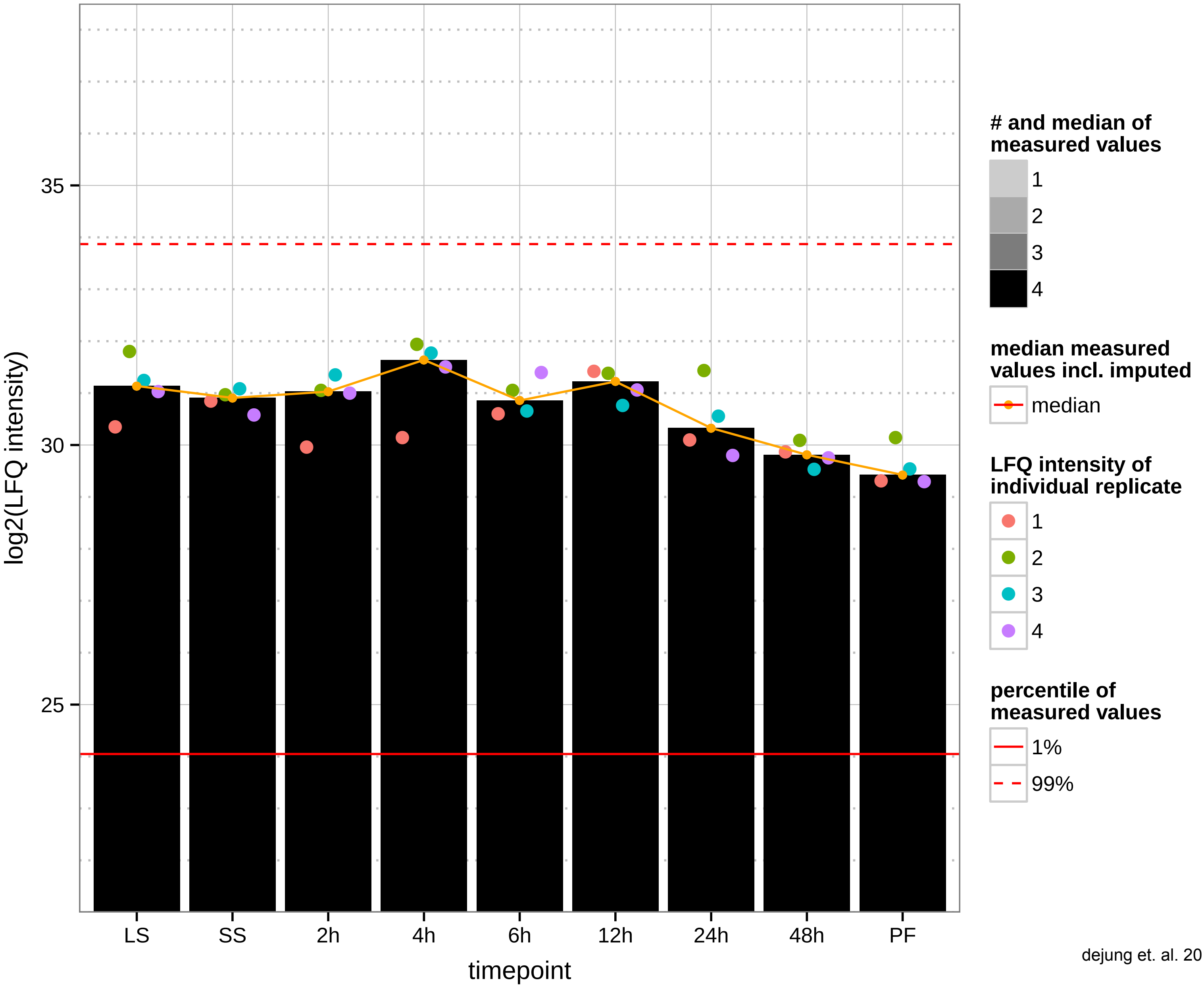
hypothetical protein, conserved
Tb927.5.1160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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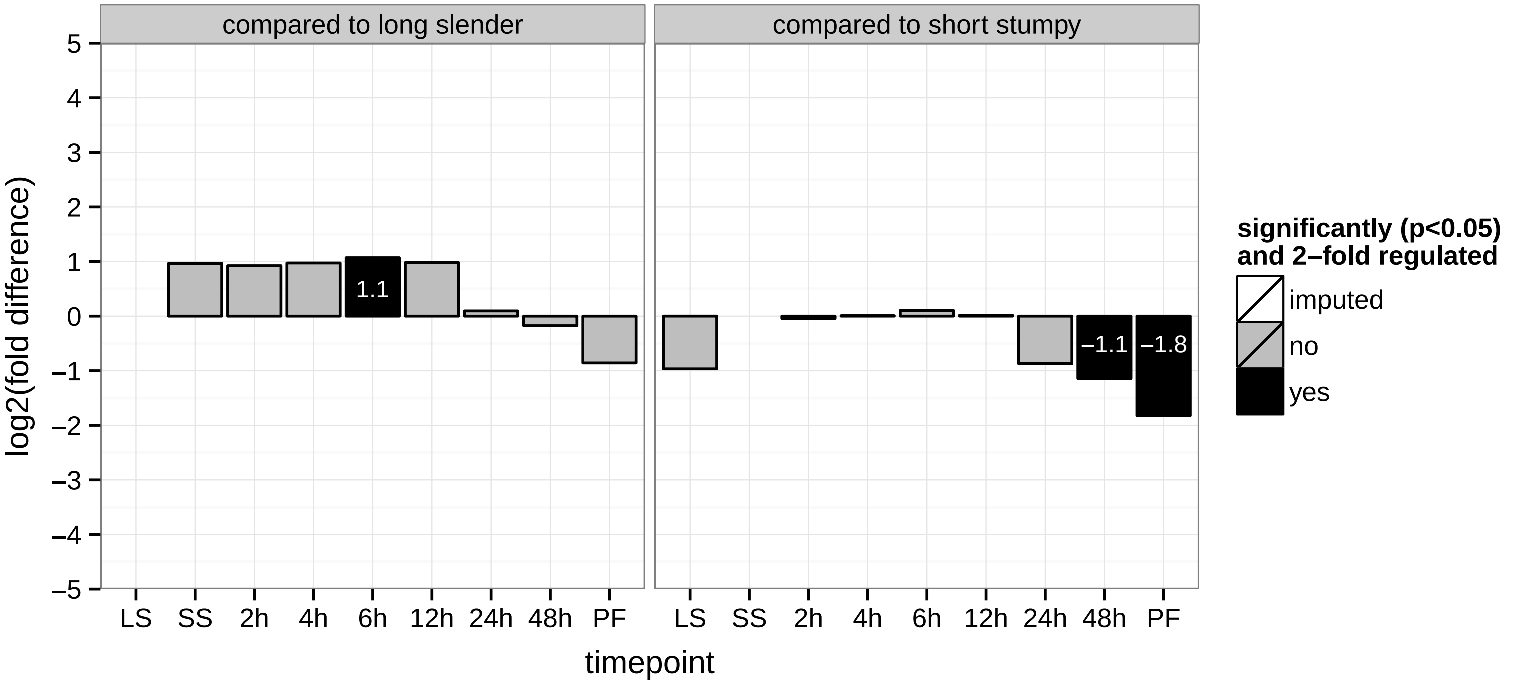
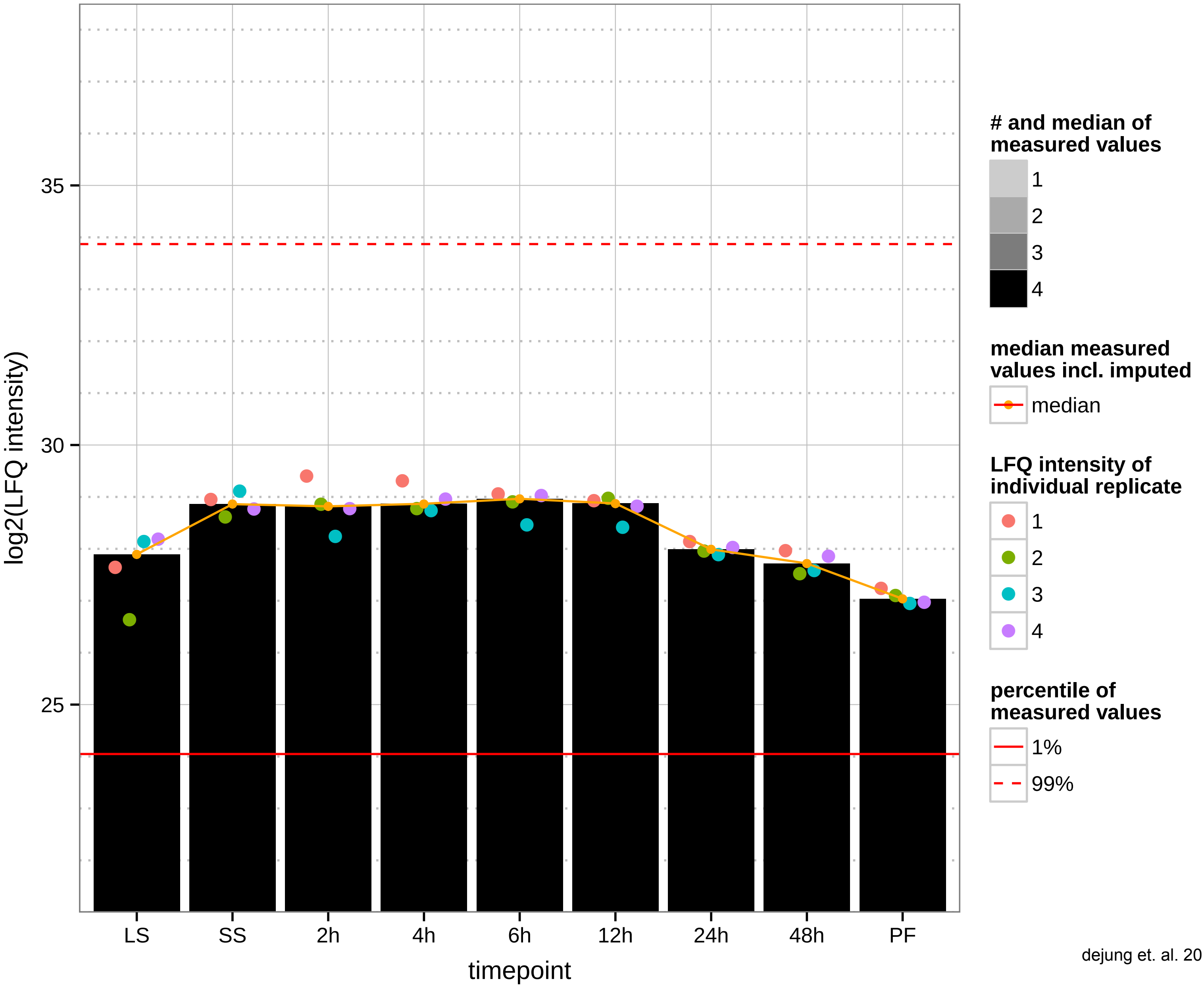
hypothetical protein, conserved
Tb927.5.1260
AGOF: transporter activity
AGOC: integral to membrane
AGOP: transport
PGOF: sulfate transmembrane transporter activity
PGOC: integral to membrane
PGOP: sulfate transport





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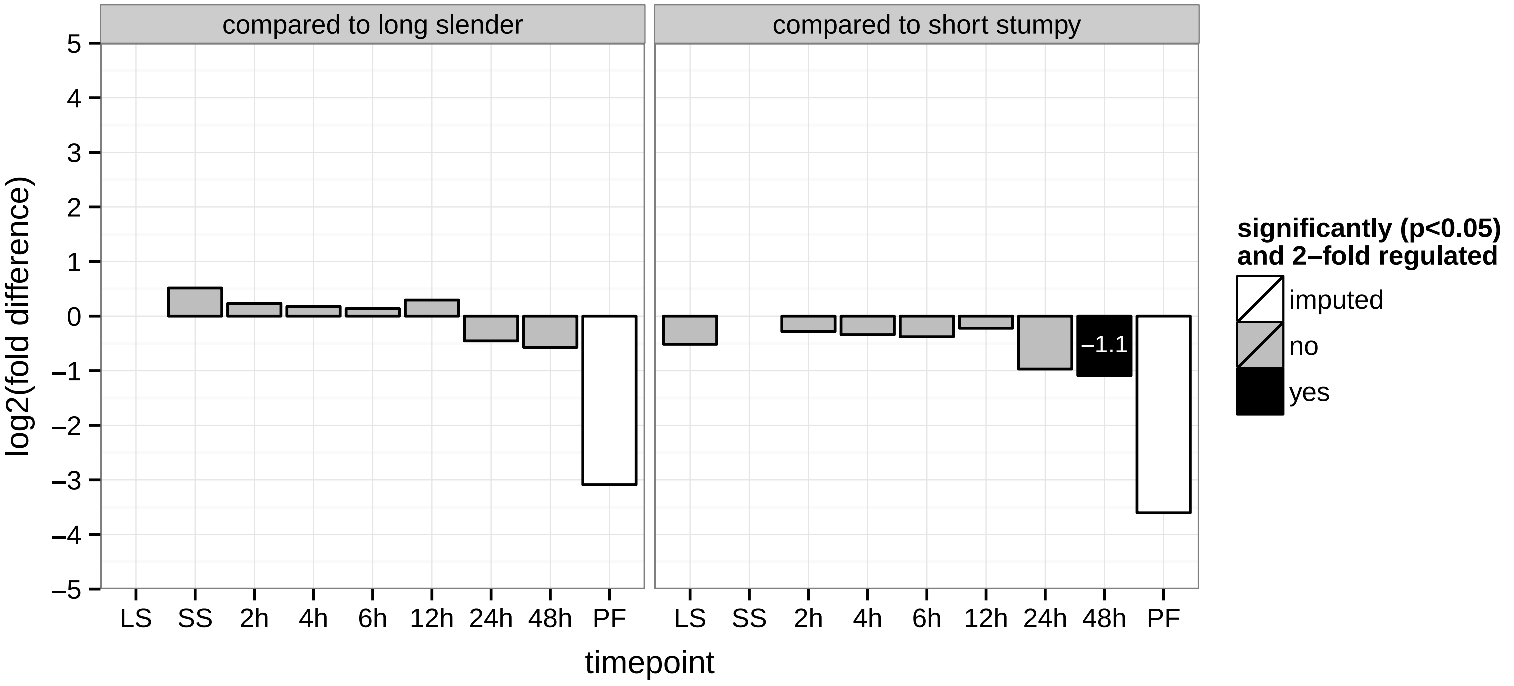
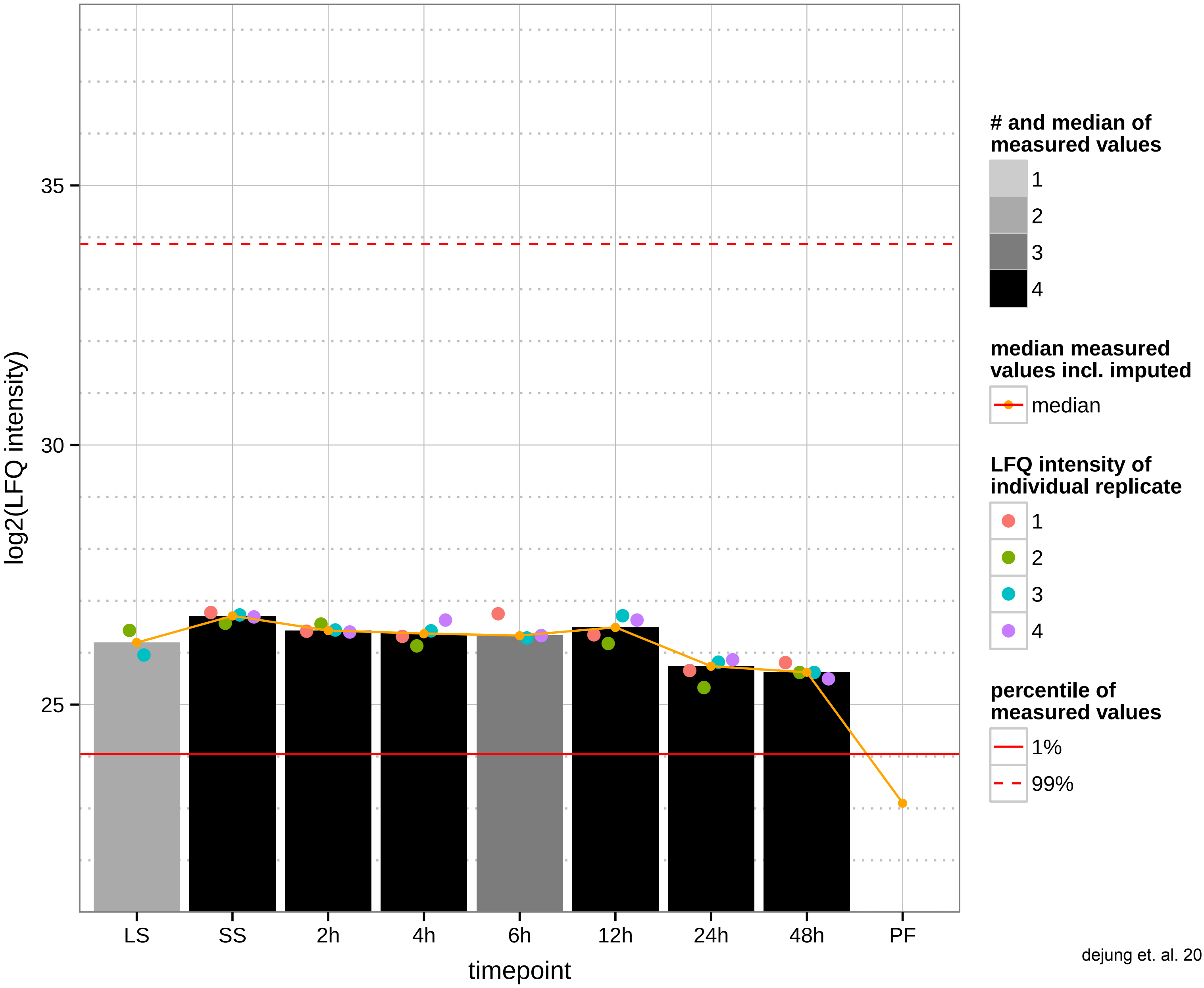
inositol–1(or 4)–monophosphatase 1, putative (IMPase 1)
Tb927.5.2690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: phosphatidylinositol phosphorylation





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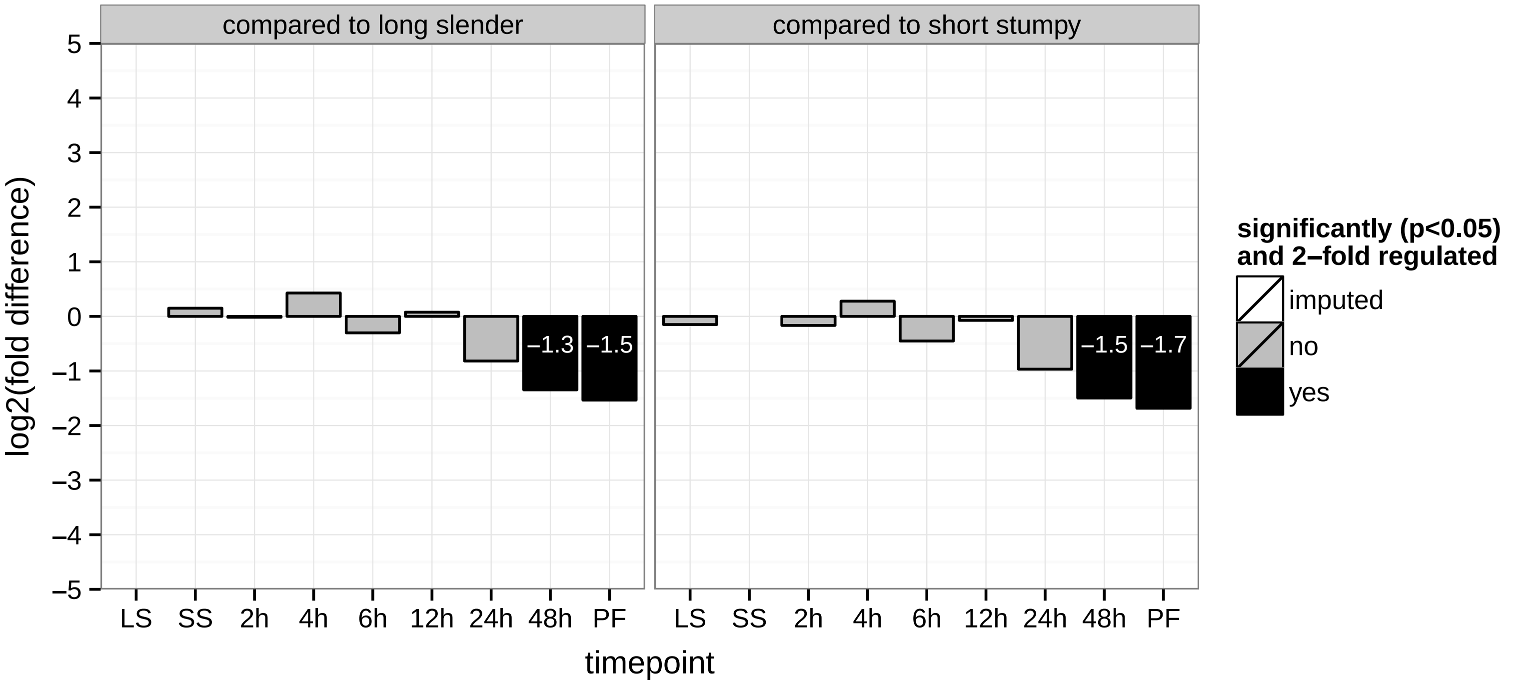
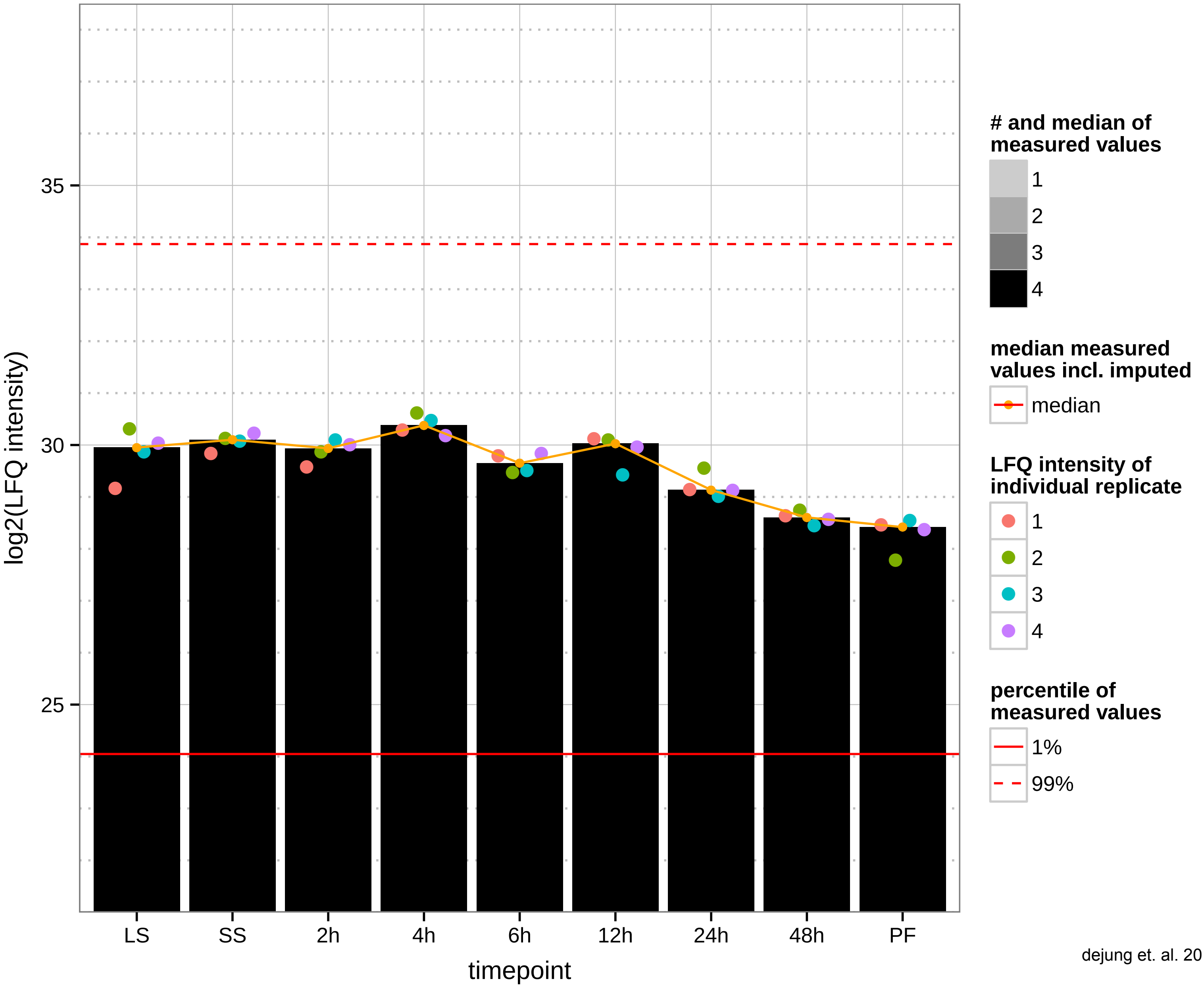
vesicle–associated membrane protein, putative, synaptobrevin, putative (VAMP)
Tb927.5.3560
AGOF: null
AGOC: integral to membrane
AGOP: vesicle–mediated transport
PGOF: null
PGOC: integral to membrane
PGOP: transport, vesicle–mediated transport





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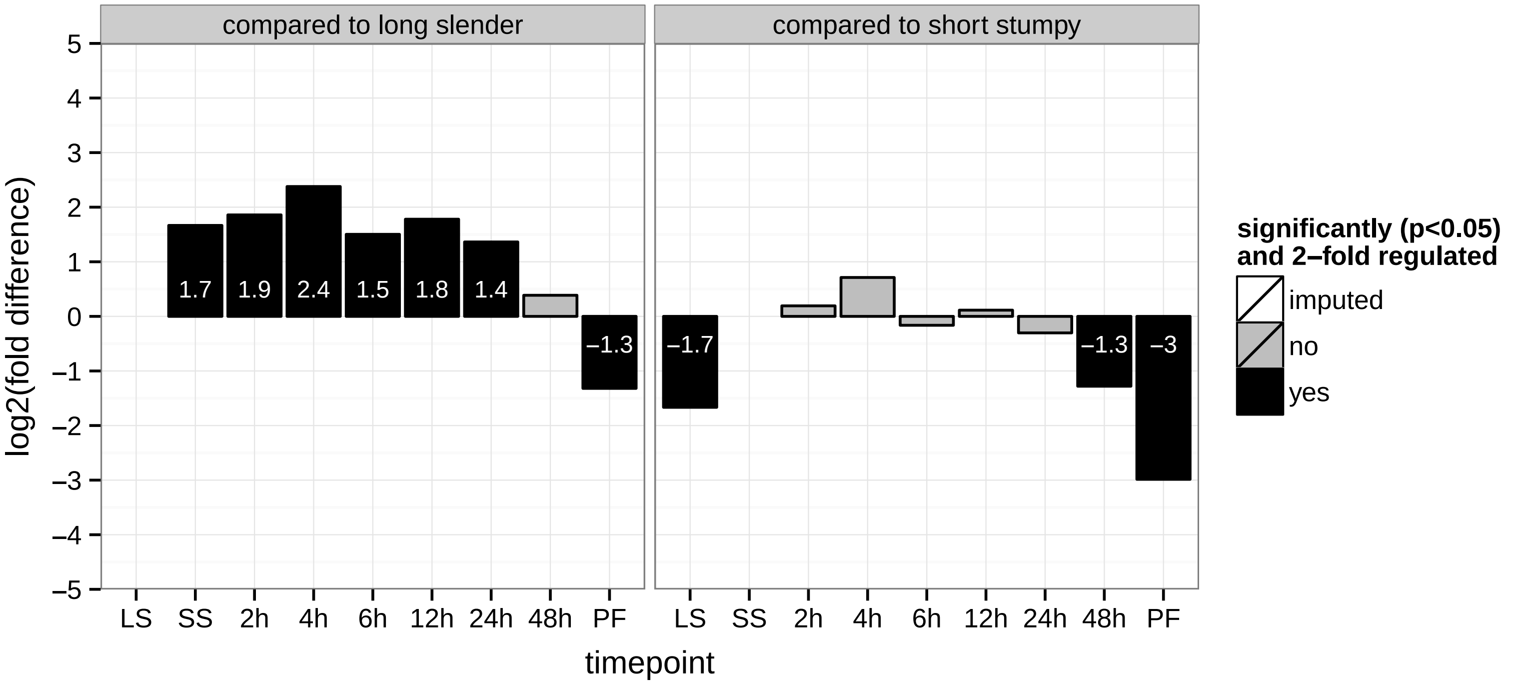
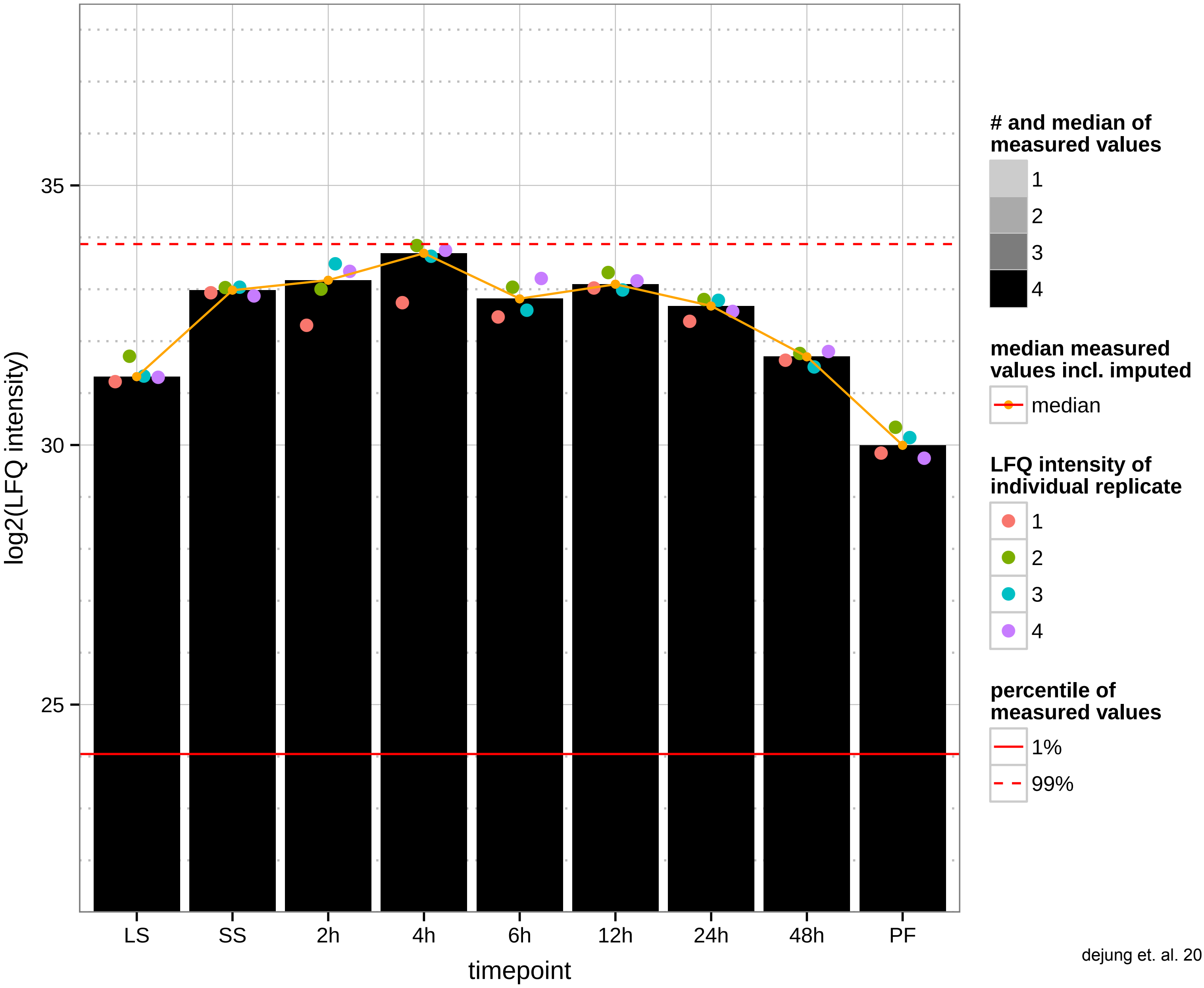
cysteine peptidase, Clan CA, family C1, Cathepsin L−like (CP), Cathepsin L−like (Rhodesain)
Tb927.6.980;Tb927.6.970;Tb927.6.960;Tb927.6.1020;Tb927.6.1010
AGOF: cysteine−type peptidase activity
AGOC: null
AGOP: proteolysis
PGOF: cysteine−type endopeptidase activity, cysteine−type peptidase activity, null
PGOC: null
PGOP: proteolysis, null





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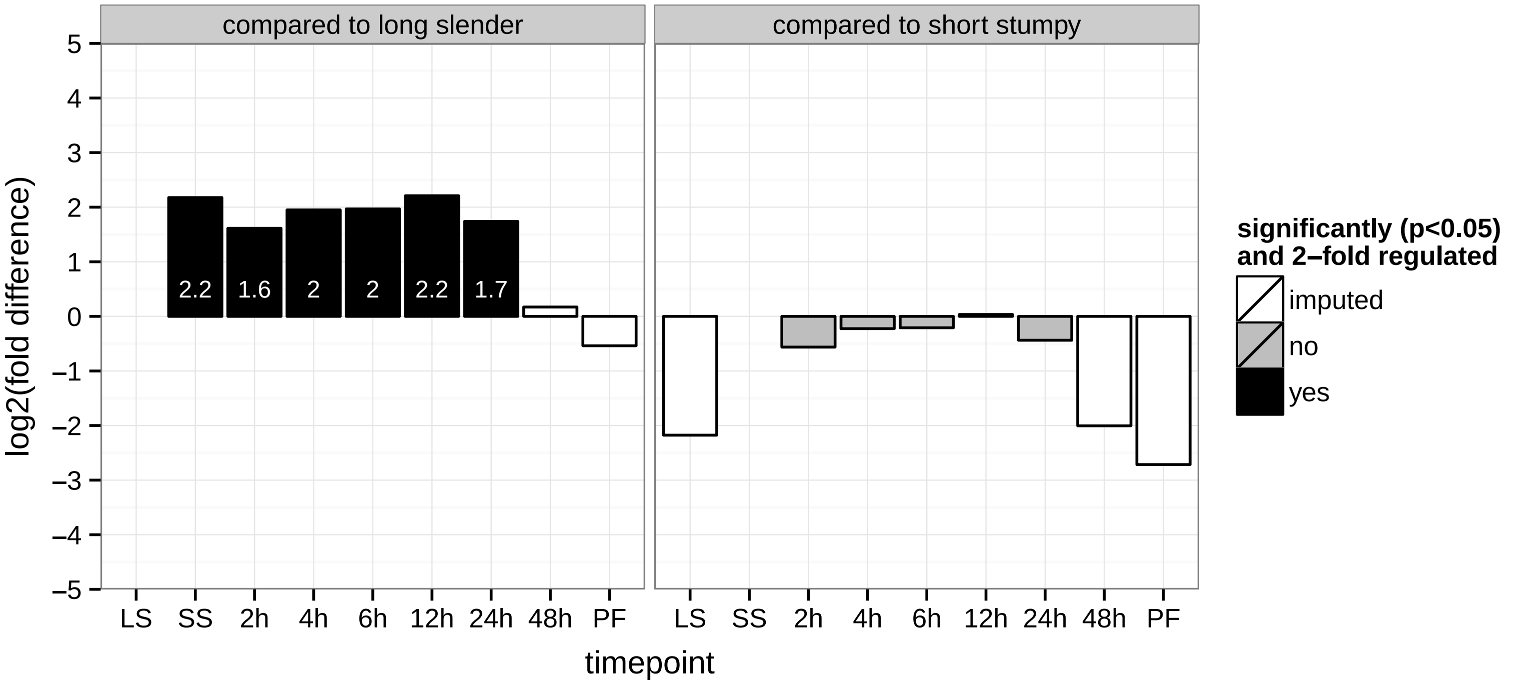
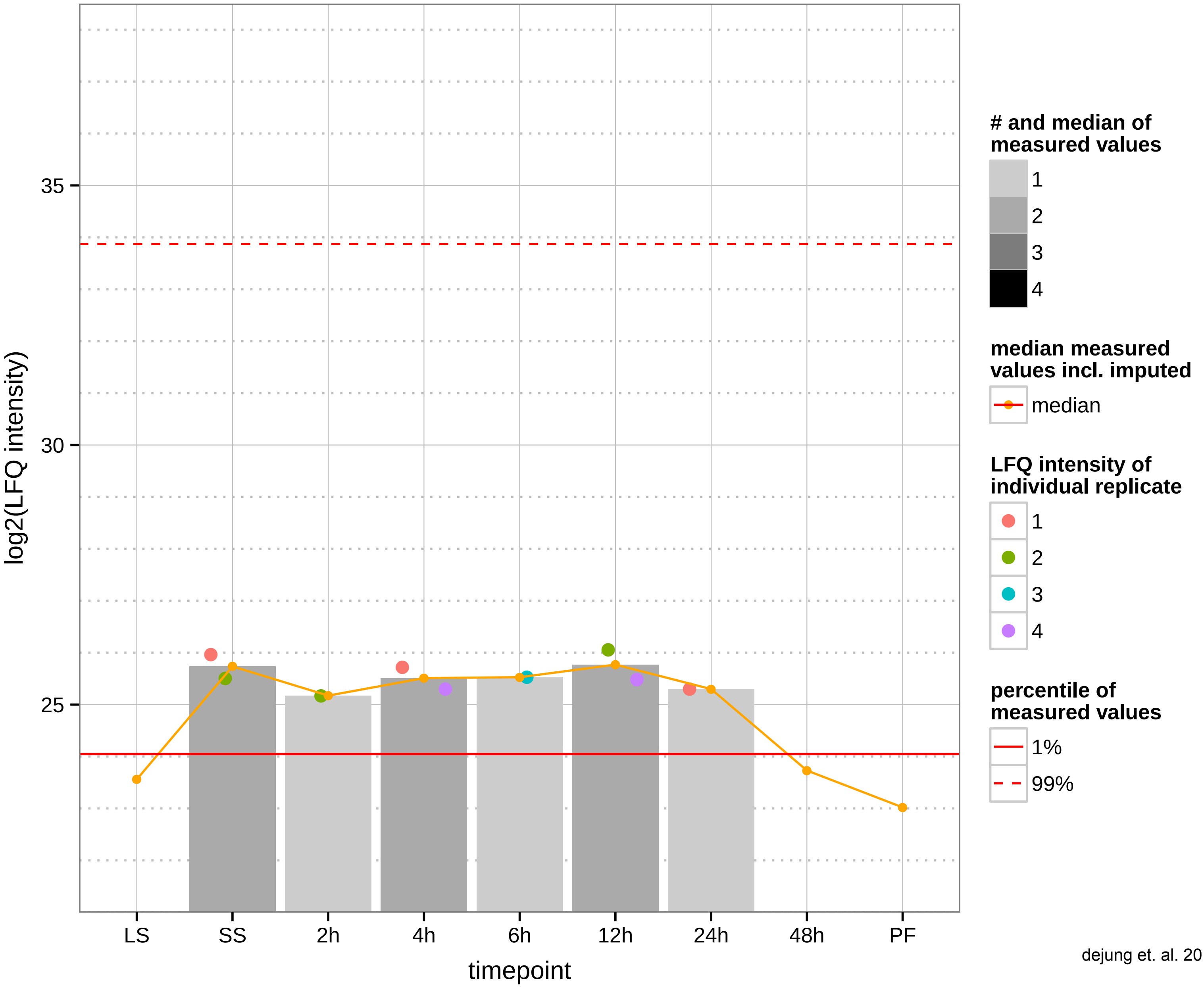
cyclin 3, mitotic cyclin, putative (CYC3)
Tb927.6.1460
AGOF: molecular_function
AGOC: null
AGOP: G1/S transition of mitotic cell cycle
PGOF: null
PGOC: null
PGOP: null





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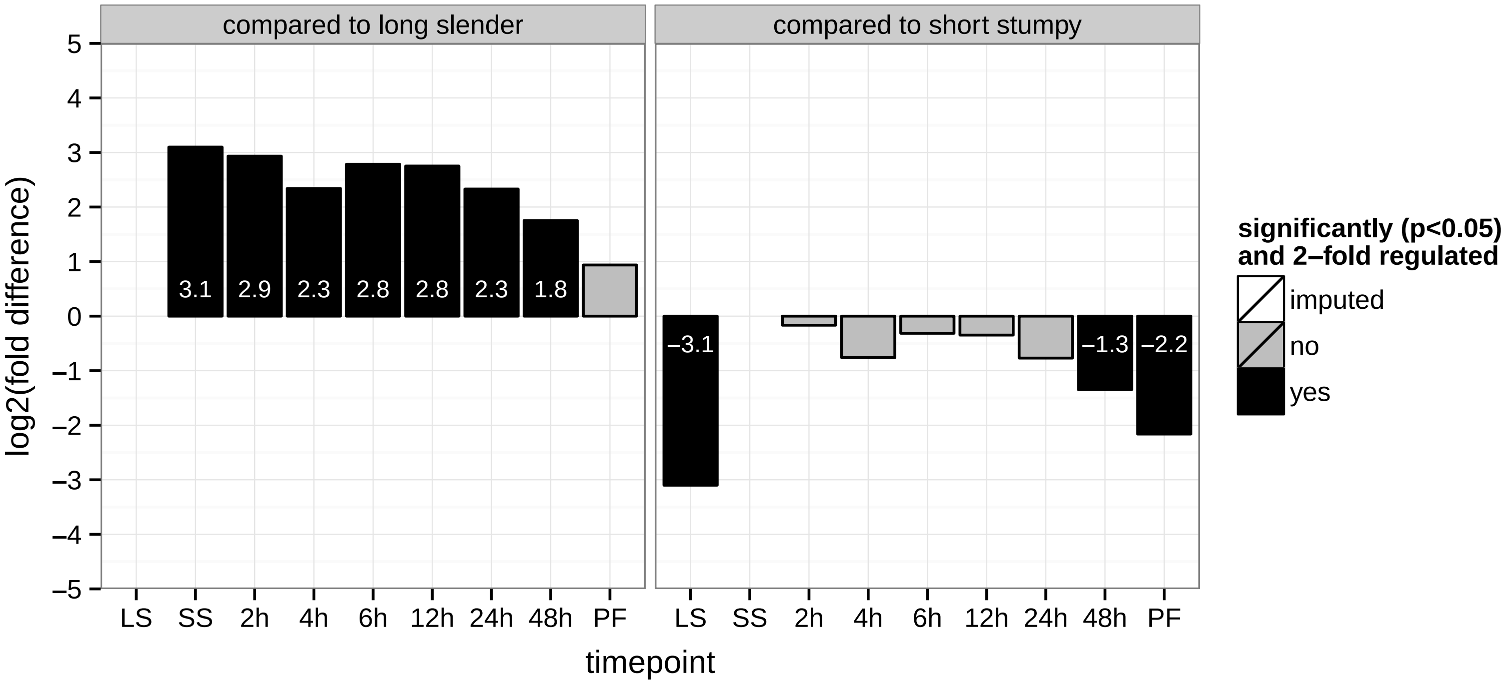
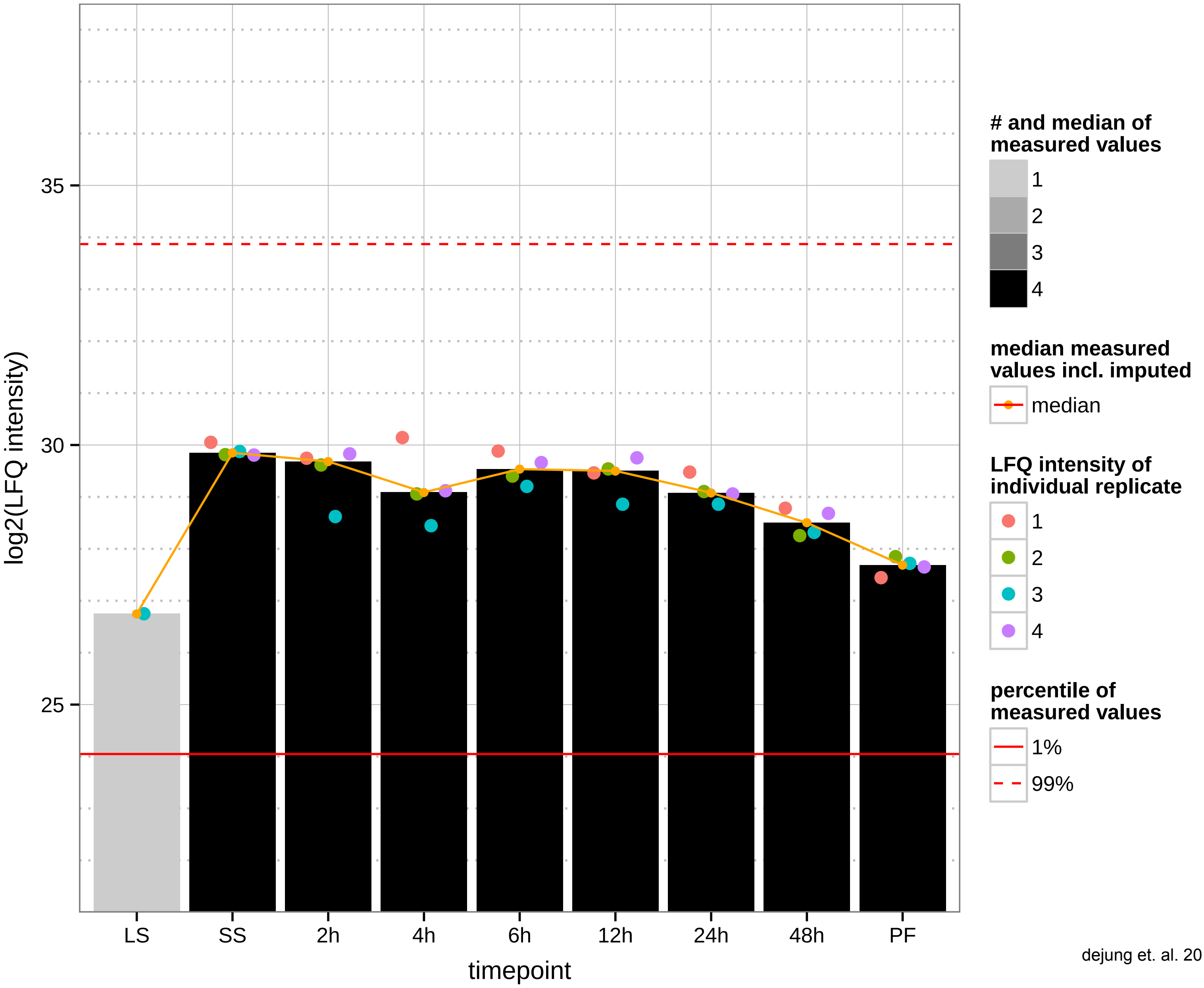
hypothetical protein, conserved
Tb927.6.1530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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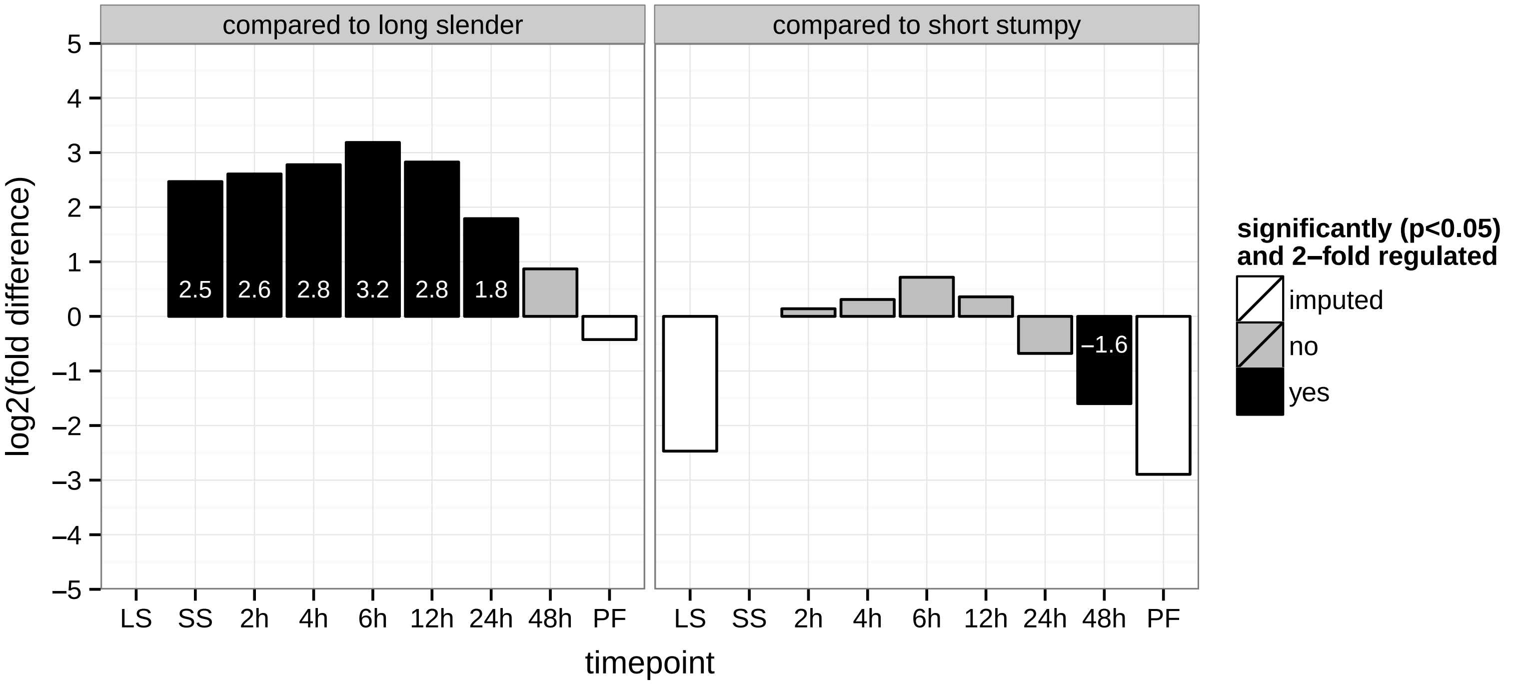
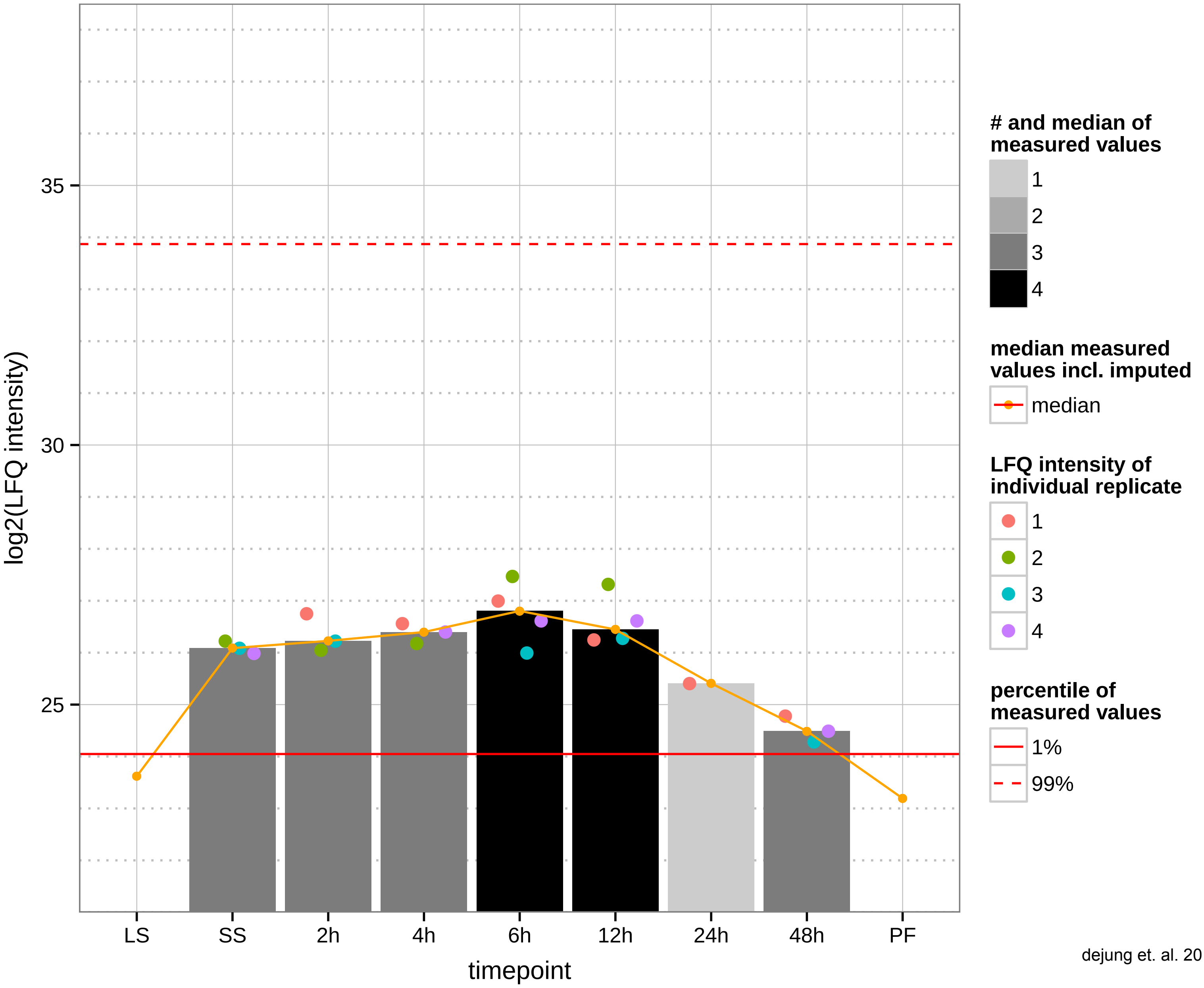
hypothetical protein, conserved
Tb927.6.3240
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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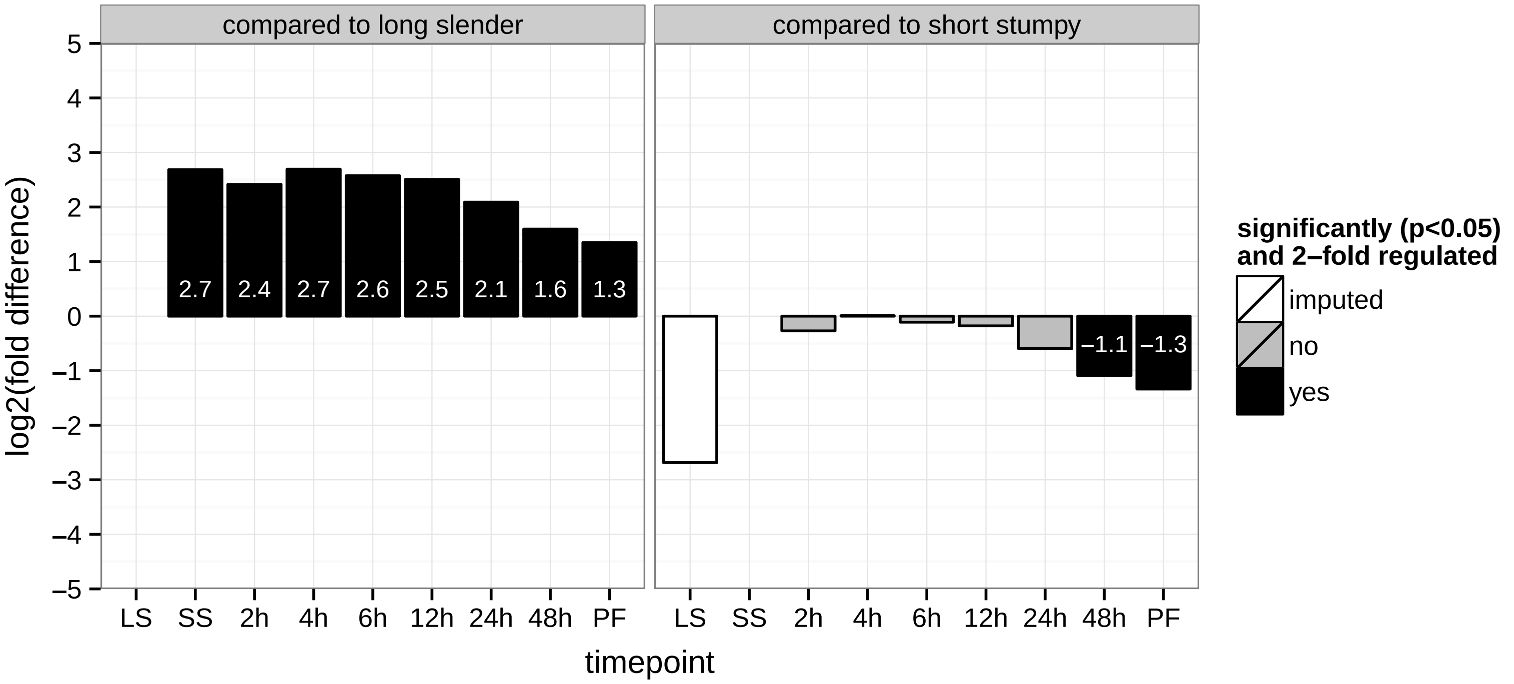
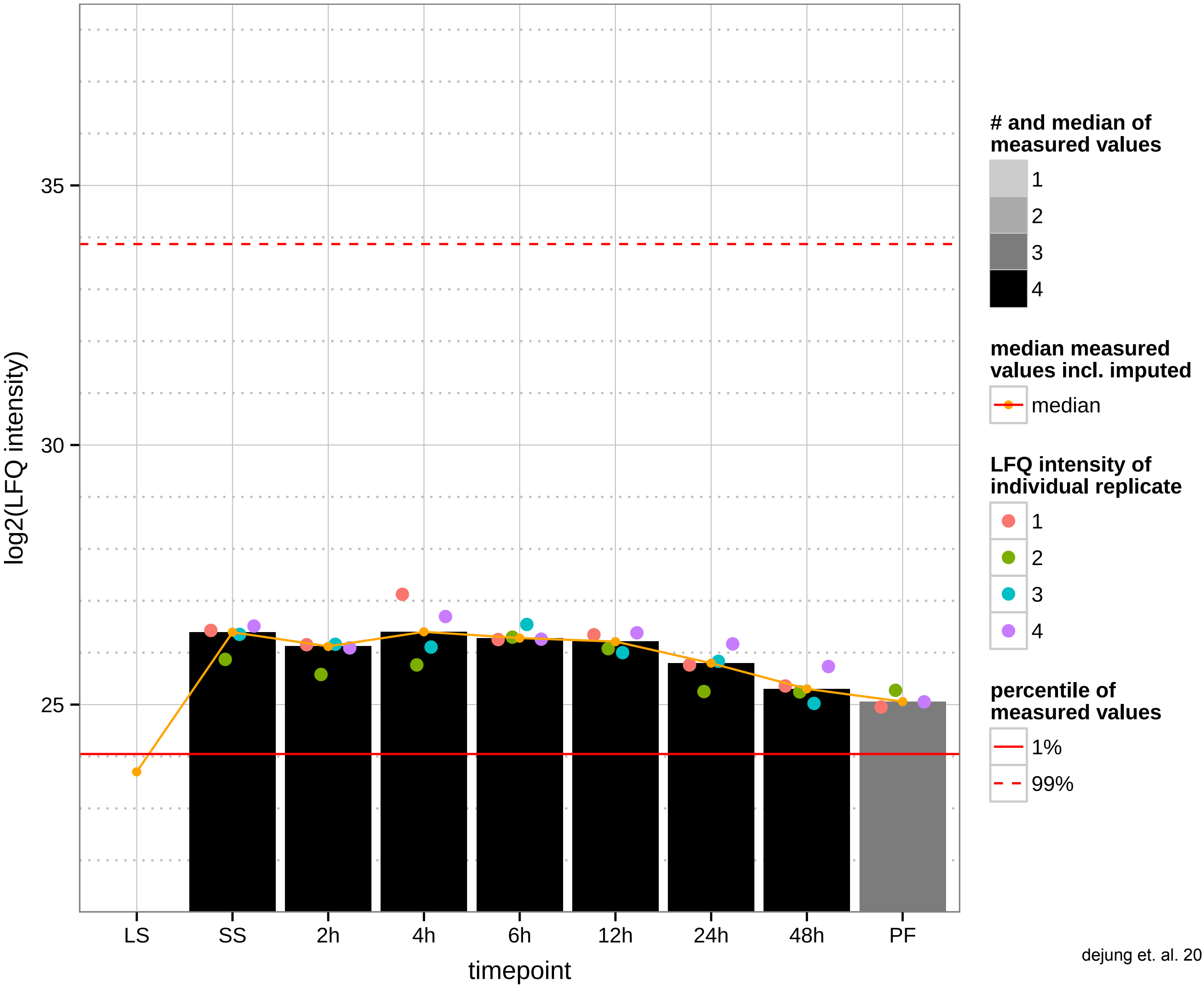
hypothetical protein, conserved
Tb927.6.3720
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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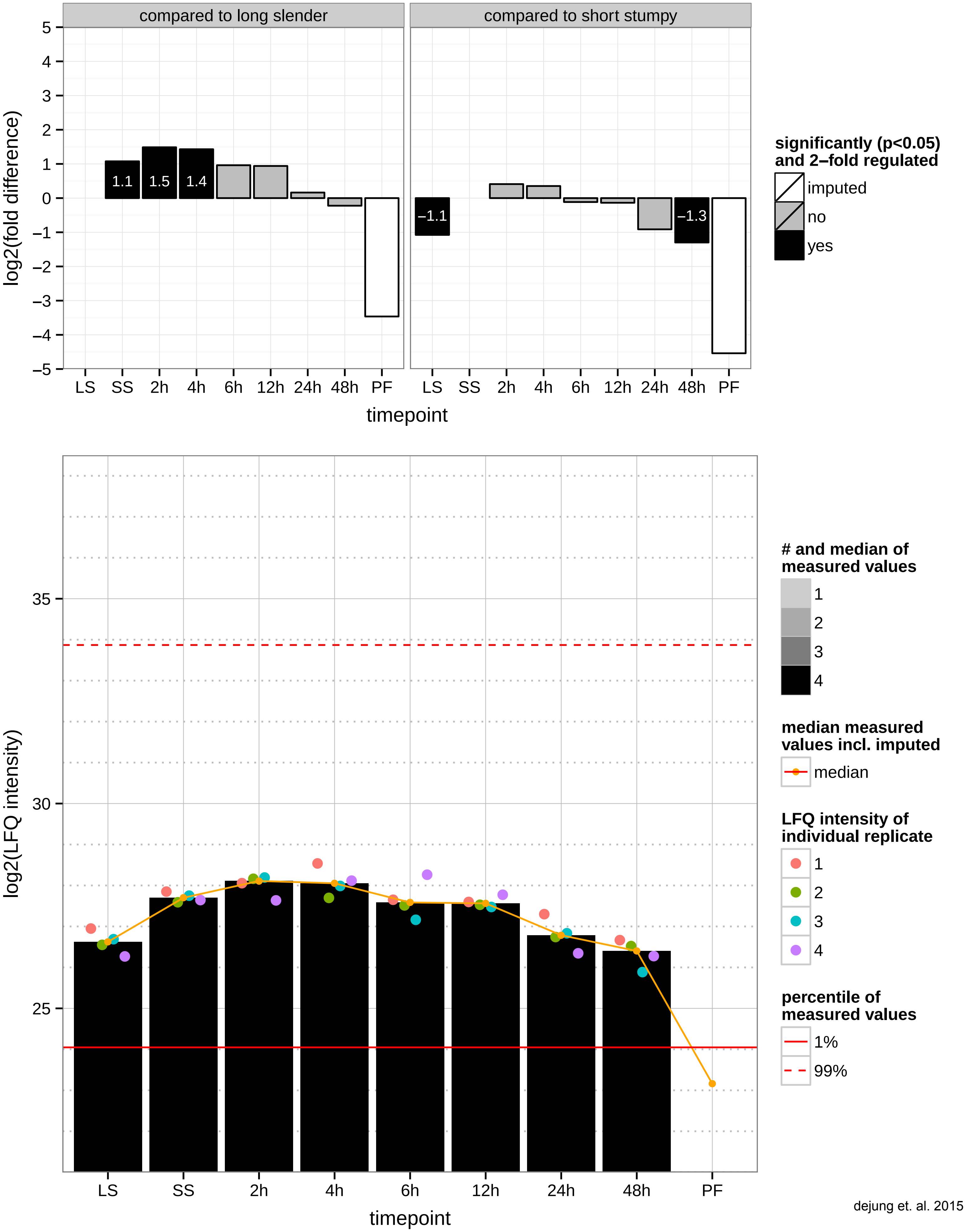
hypothetical protein, conserved
Tb927.6.4550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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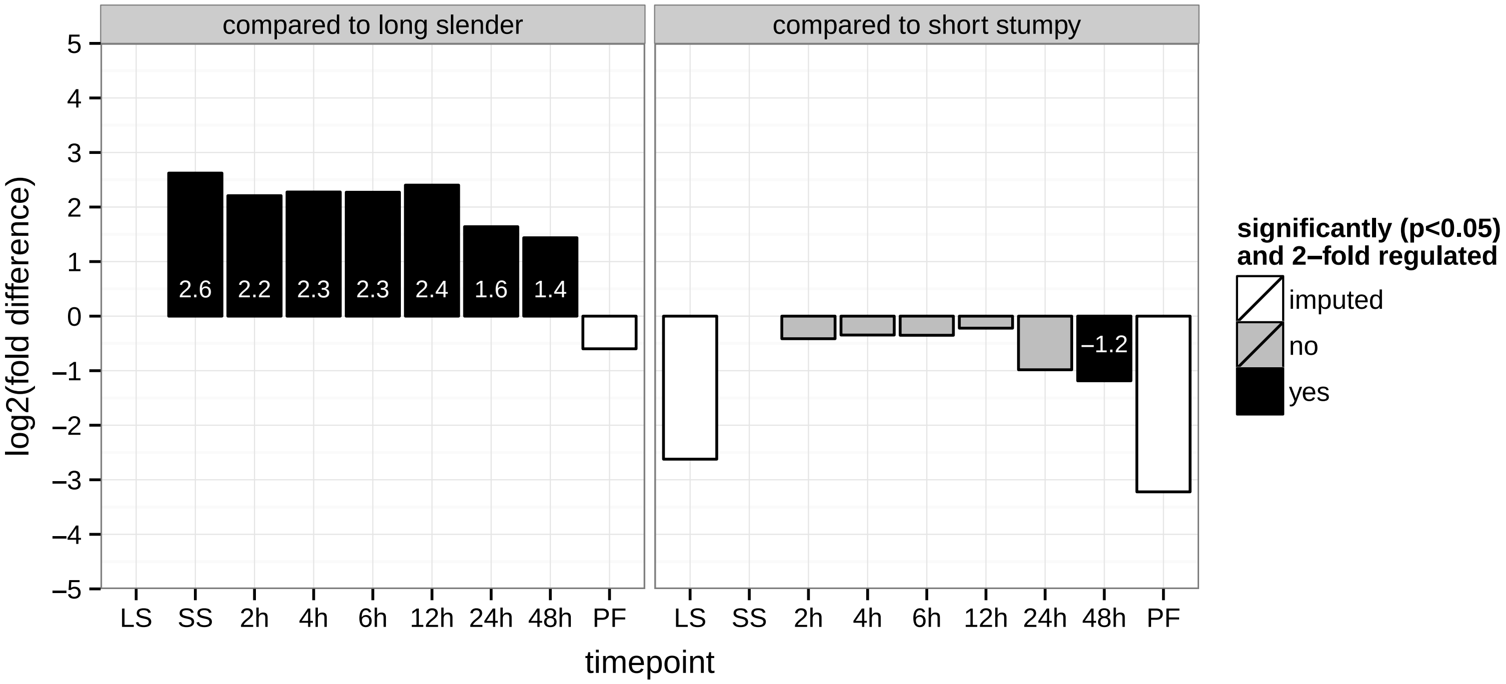
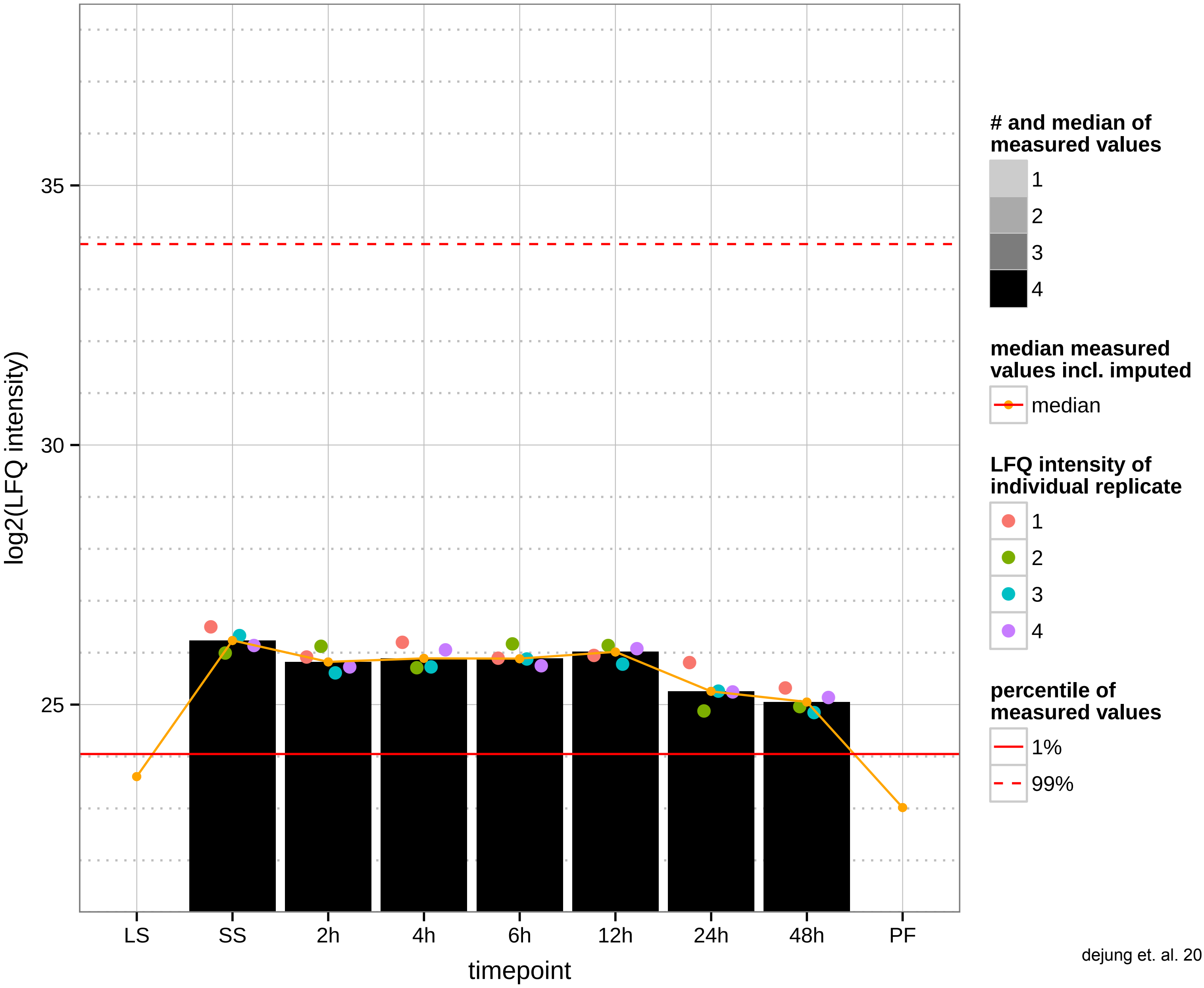
C–1–tetrahydrofolate synthase, cytoplasmic, putative
Tb927.7.1600
AGOF: catalytic activity
AGOC: null
AGOP: folic acid–containing compound biosynthetic process
PGOF: catalytic activity, methylenetetrahydrofolate dehydrogenase (NADP+) activity
PGOC: null
PGOP: folic acid–containing compound biosynthetic process, oxidation–reduction process





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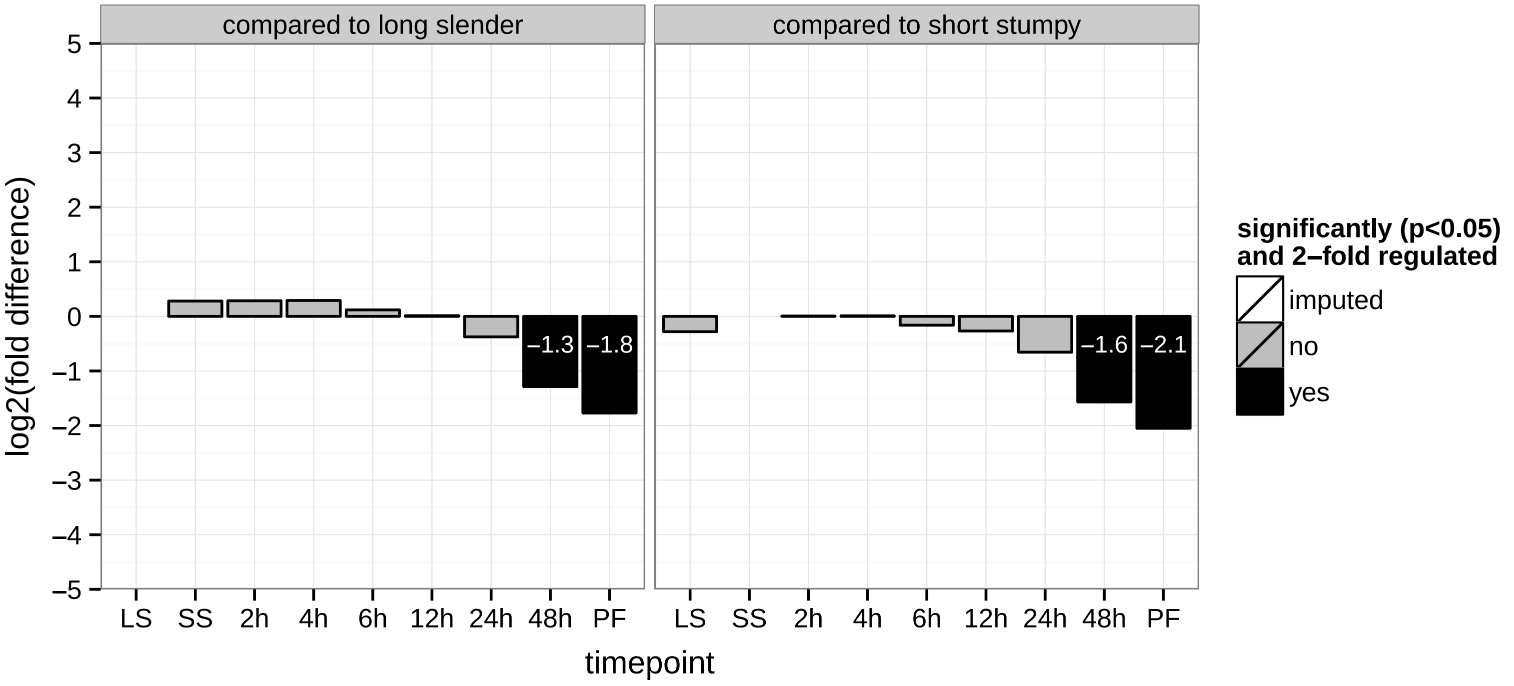
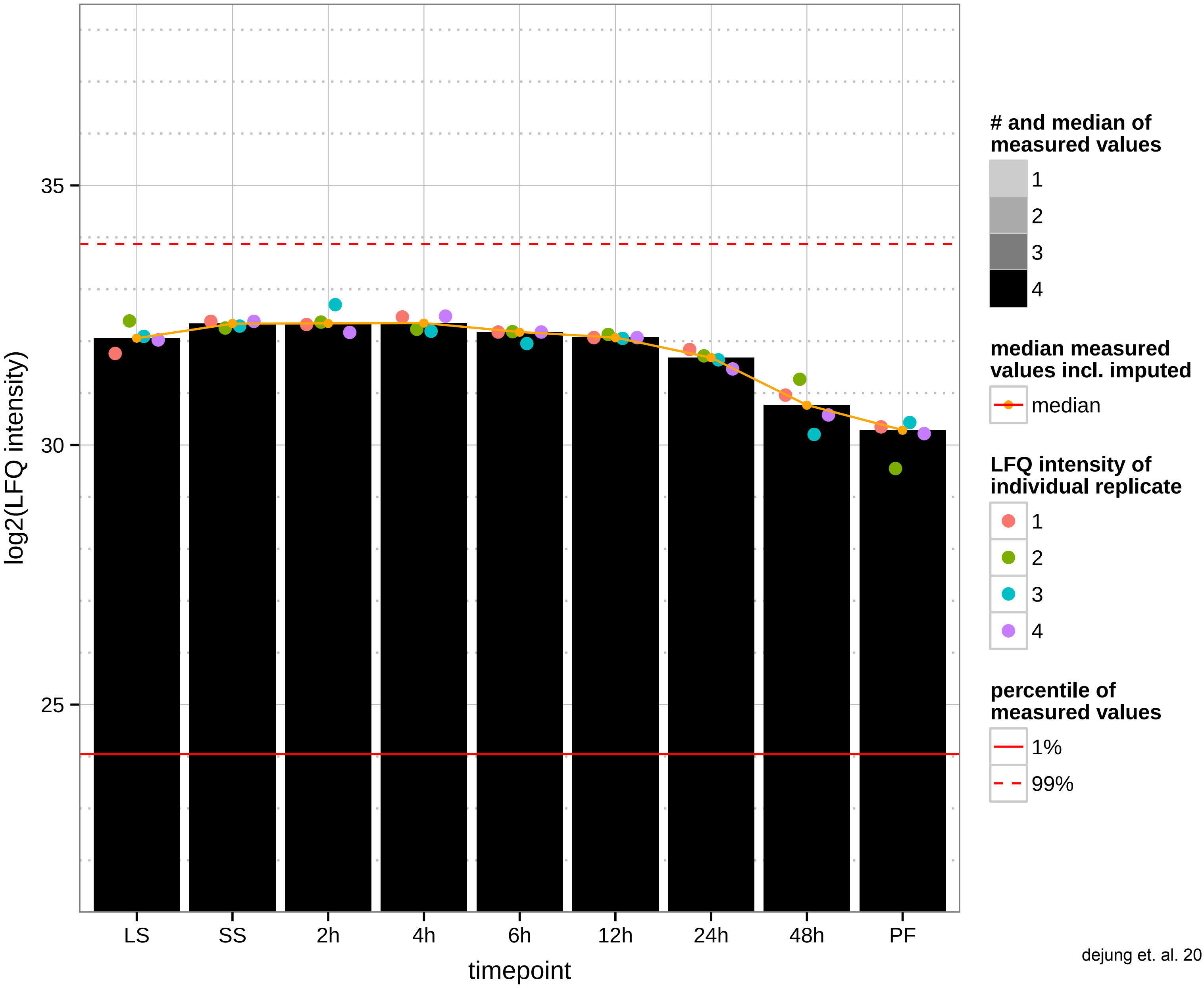
hypothetical protein, conserved
Tb927.7.2650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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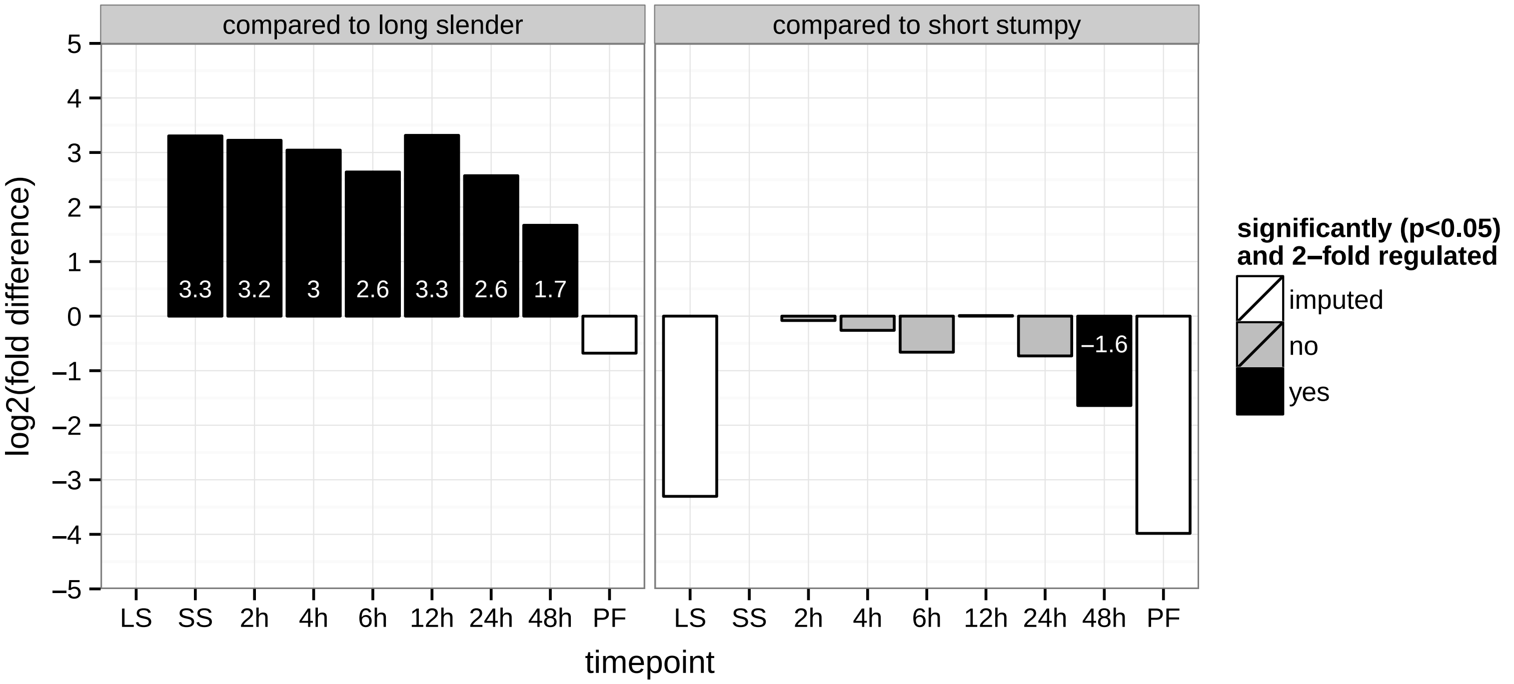
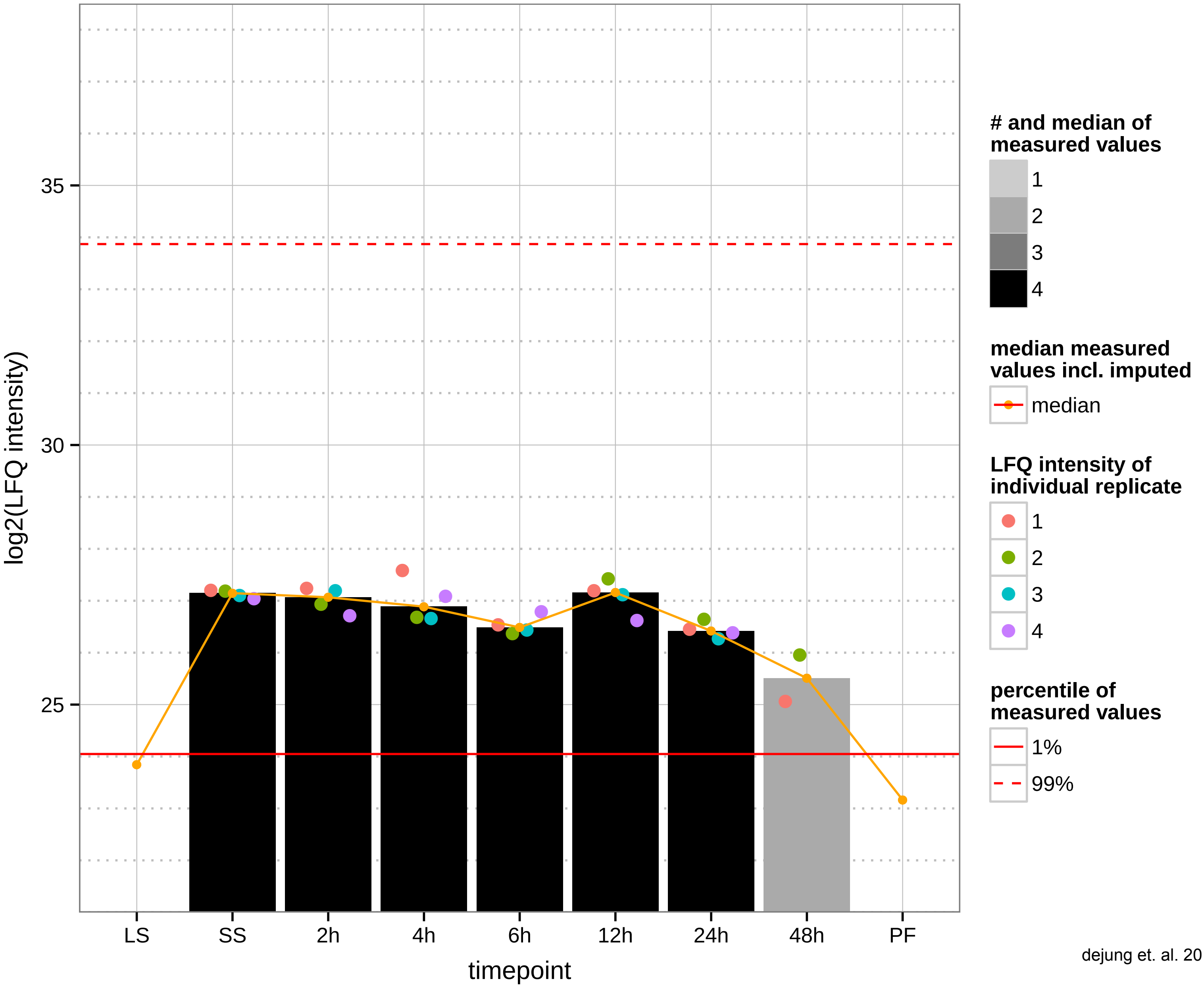
hypothetical protein, conserved
Tb927.7.510;Tb11.v5.0890
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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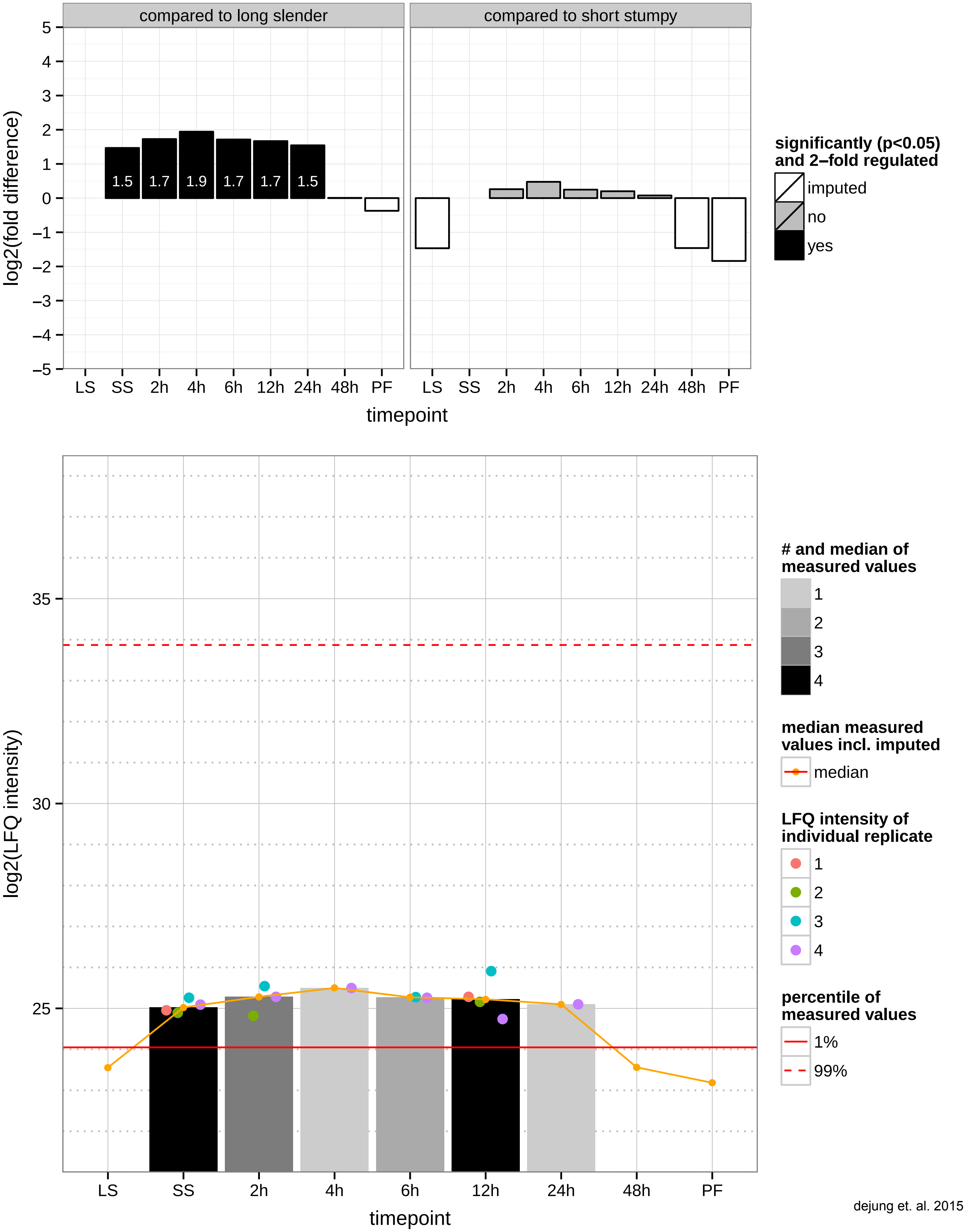
hypothetical protein, conserved
Tb927.7.530
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: metal ion binding
PGOC: null
PGOP: null



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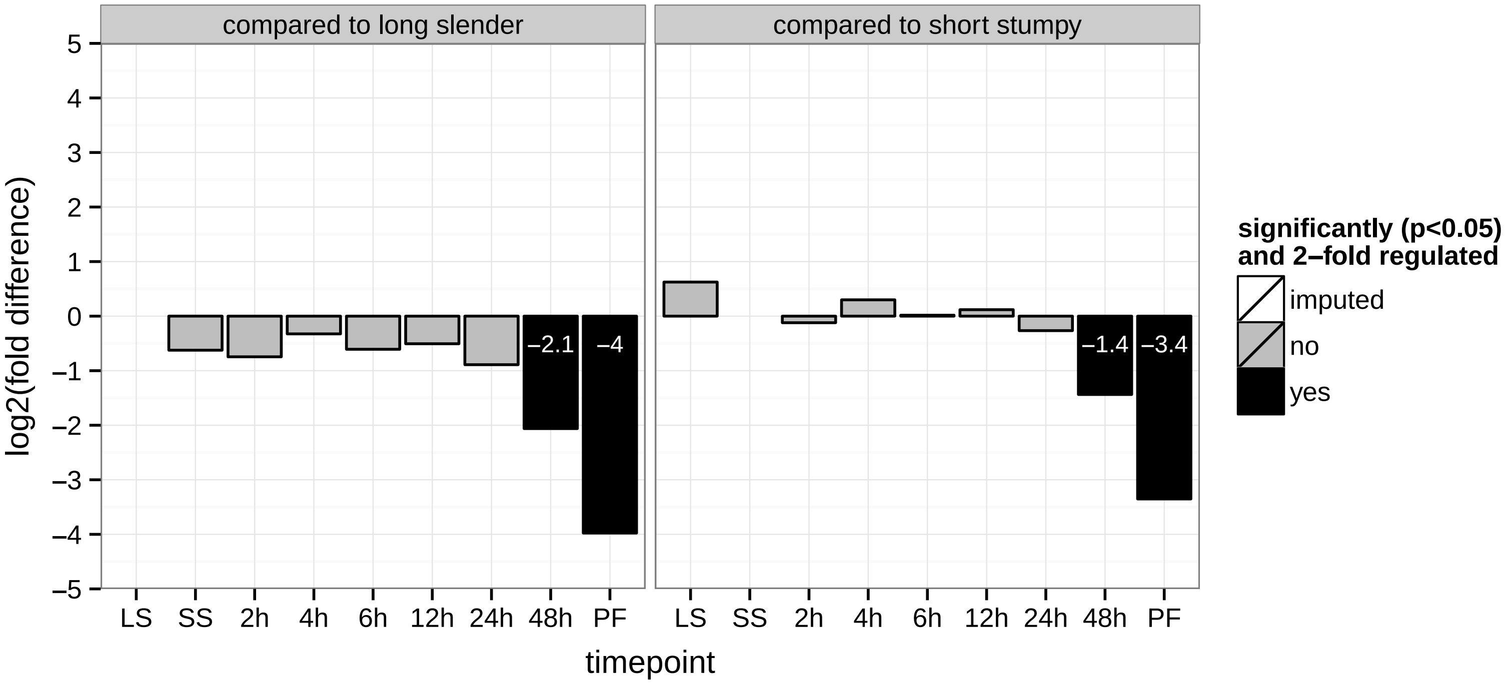
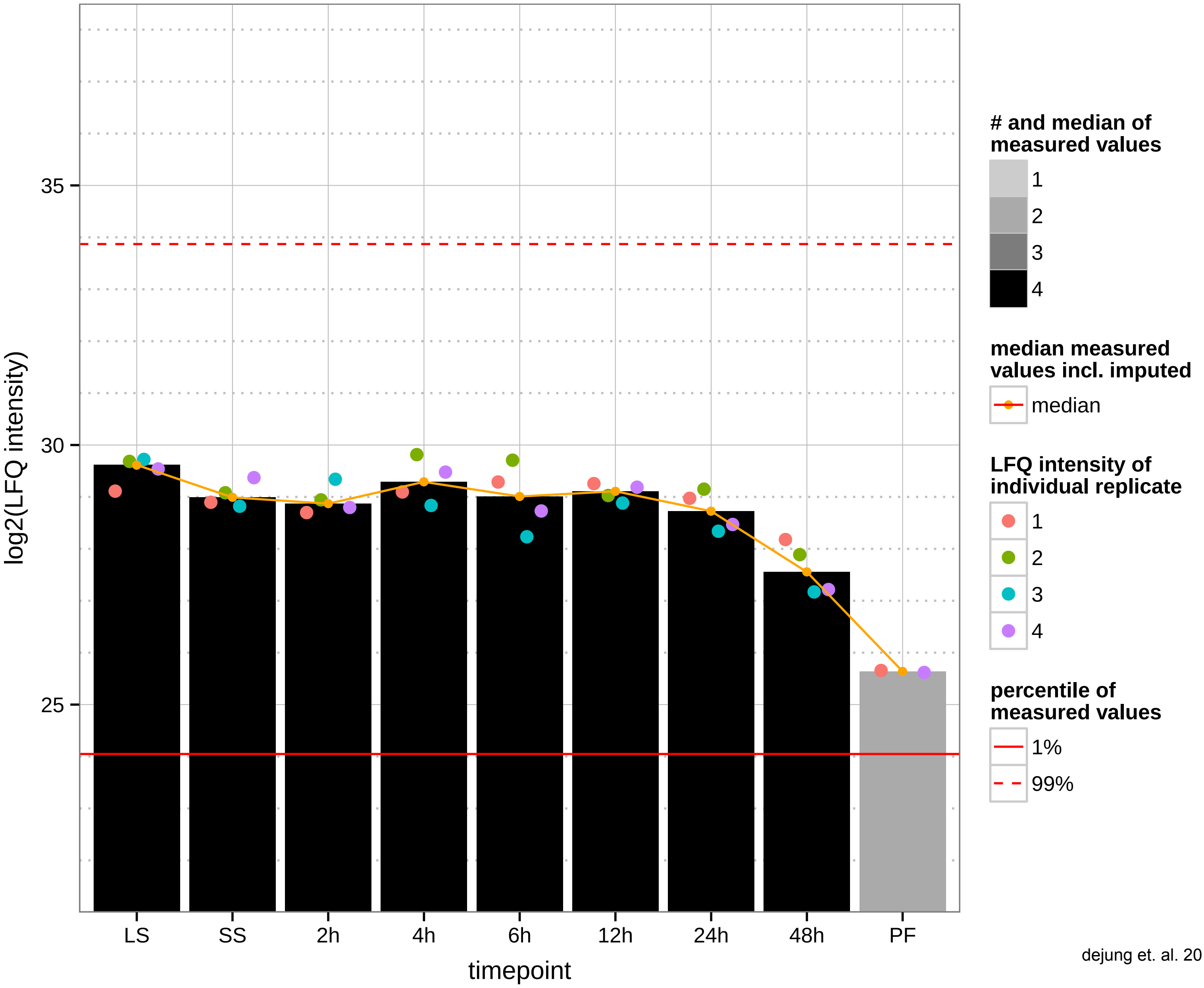
hypothetical protein, conserved
Tb927.8.2080
AGOF: null
AGOC: null
AGOP: null
PGOF: ATP binding, RNA ligase (ATP) activity
PGOC: null
PGOP: tRNA splicing, via endonucleolytic cleavage and ligation





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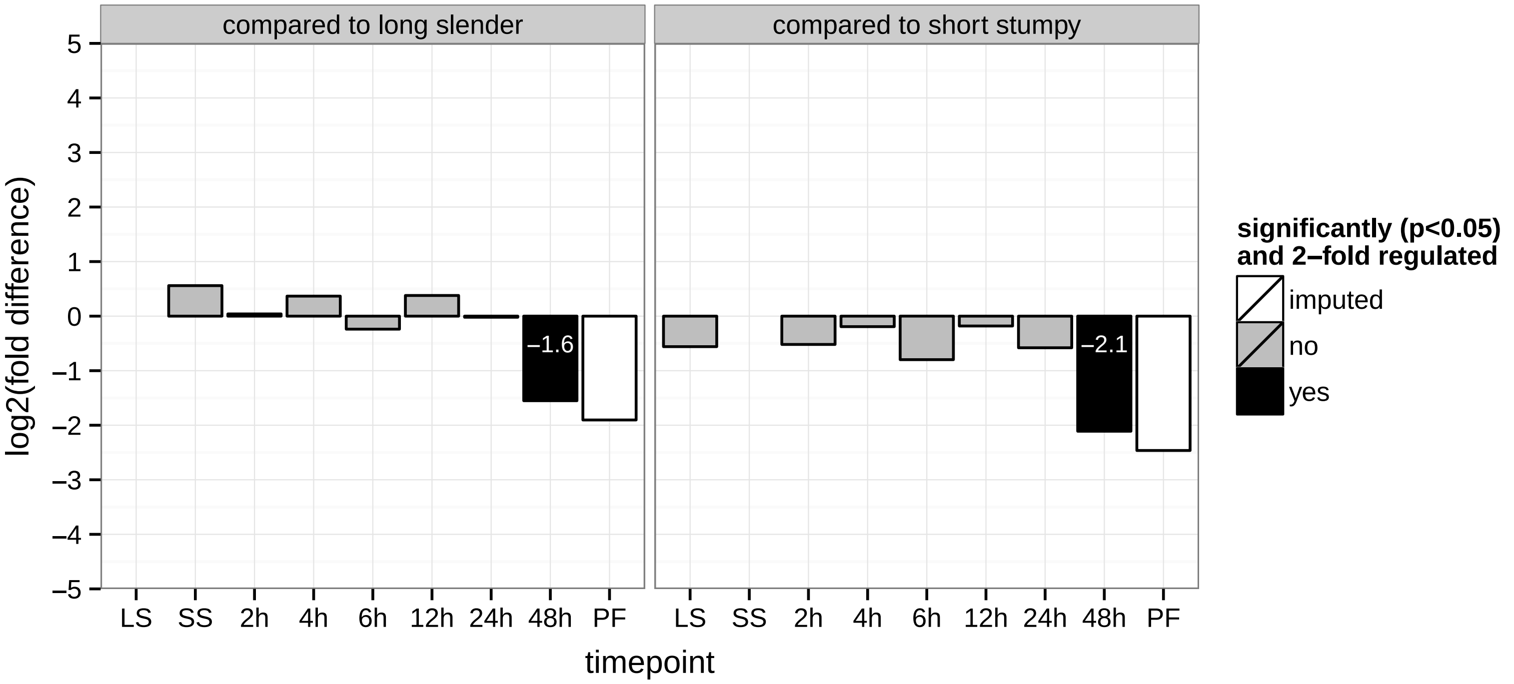
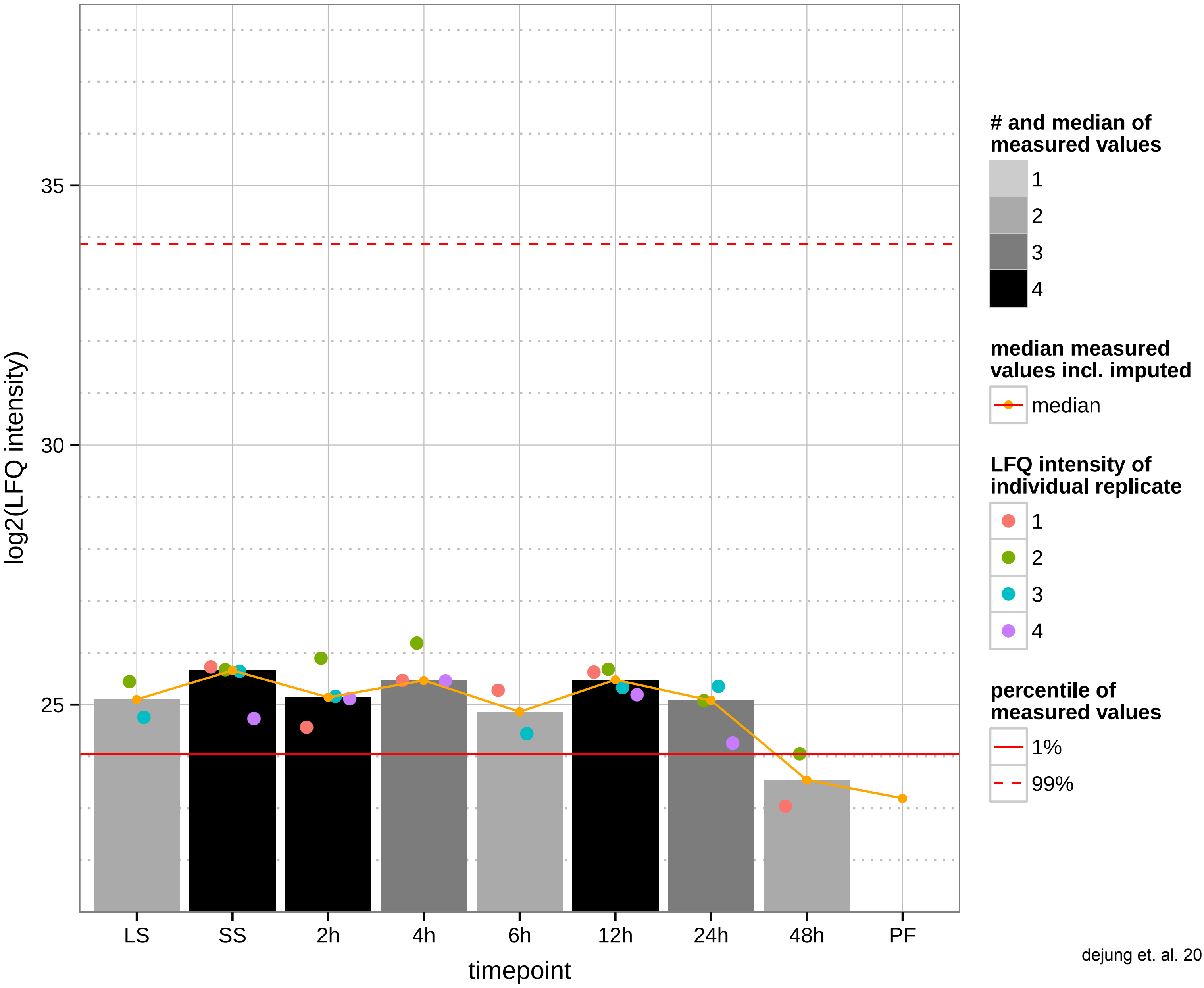
hypothetical protein, conserved
Tb927.8.2250
AGOF: null
AGOC: null
AGOP: null
PGOF: ATP binding, RNA ligase (ATP) activity
PGOC: null
PGOP: tRNA splicing, via endonucleolytic cleavage and ligation





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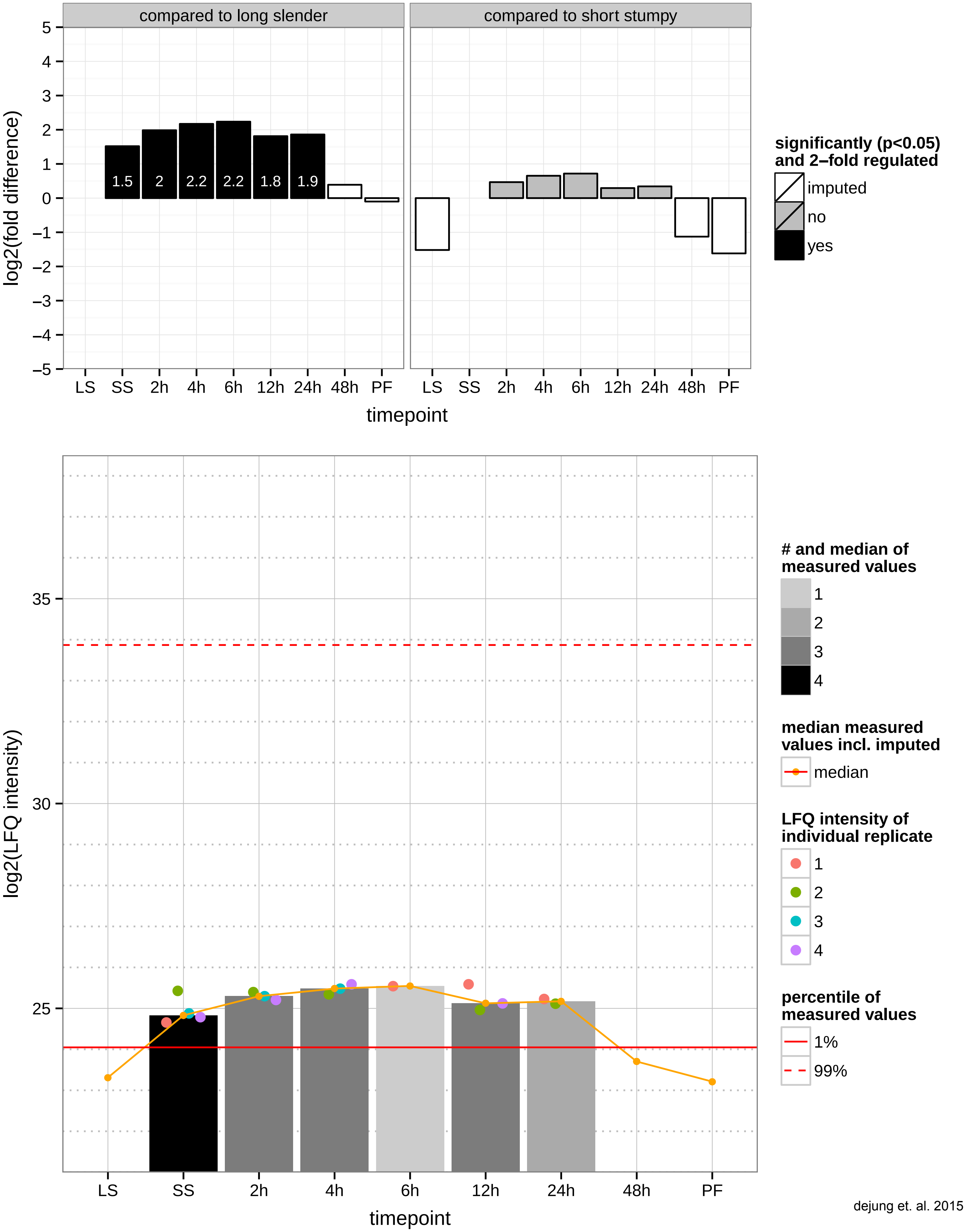
hypothetical protein, conserved
Tb927.8.3520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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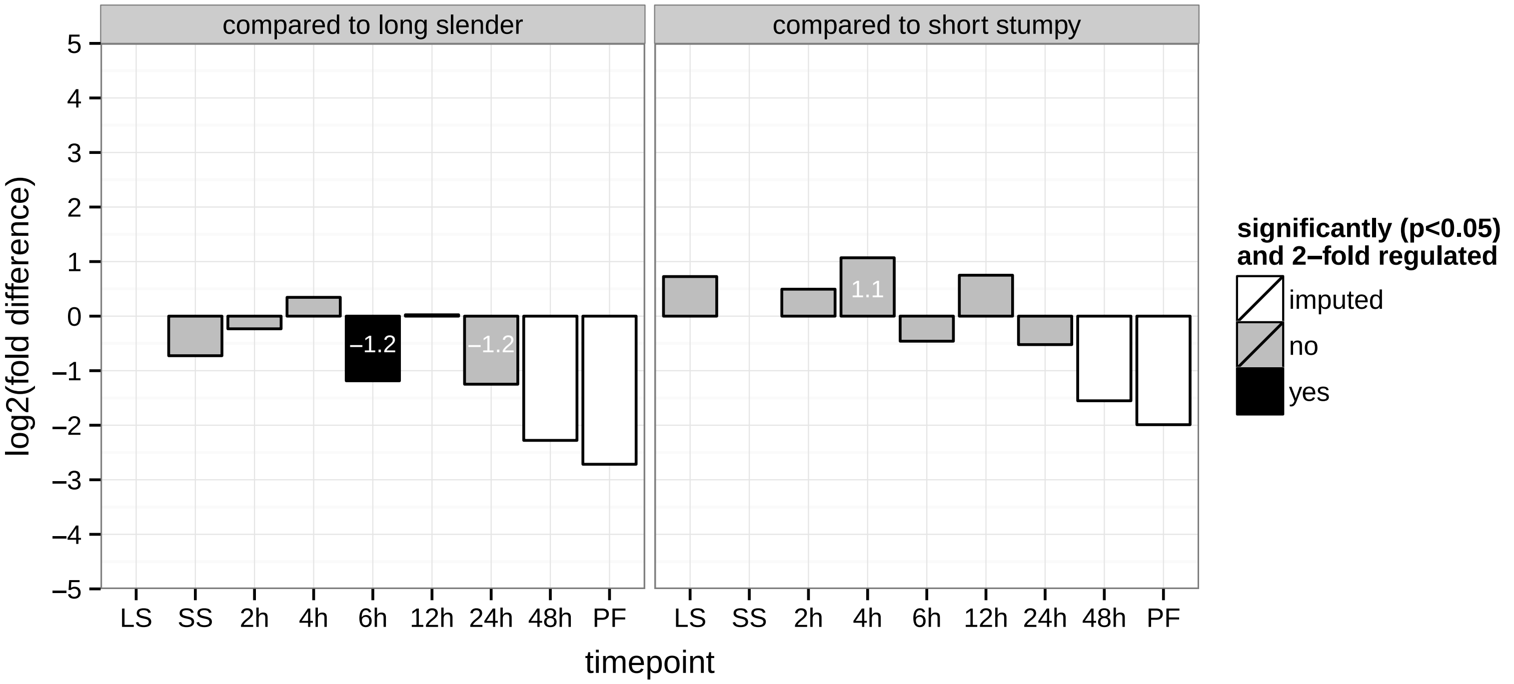
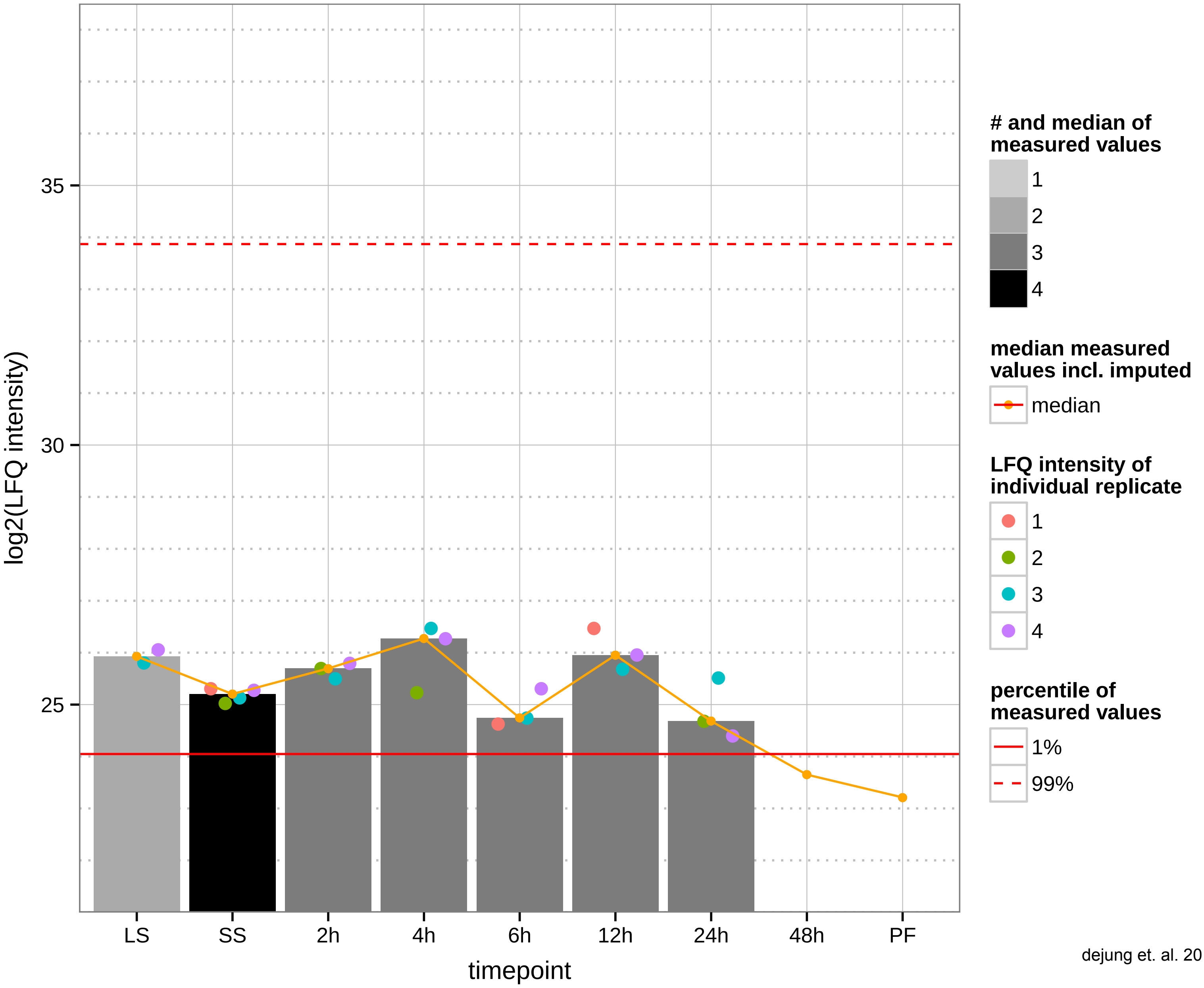
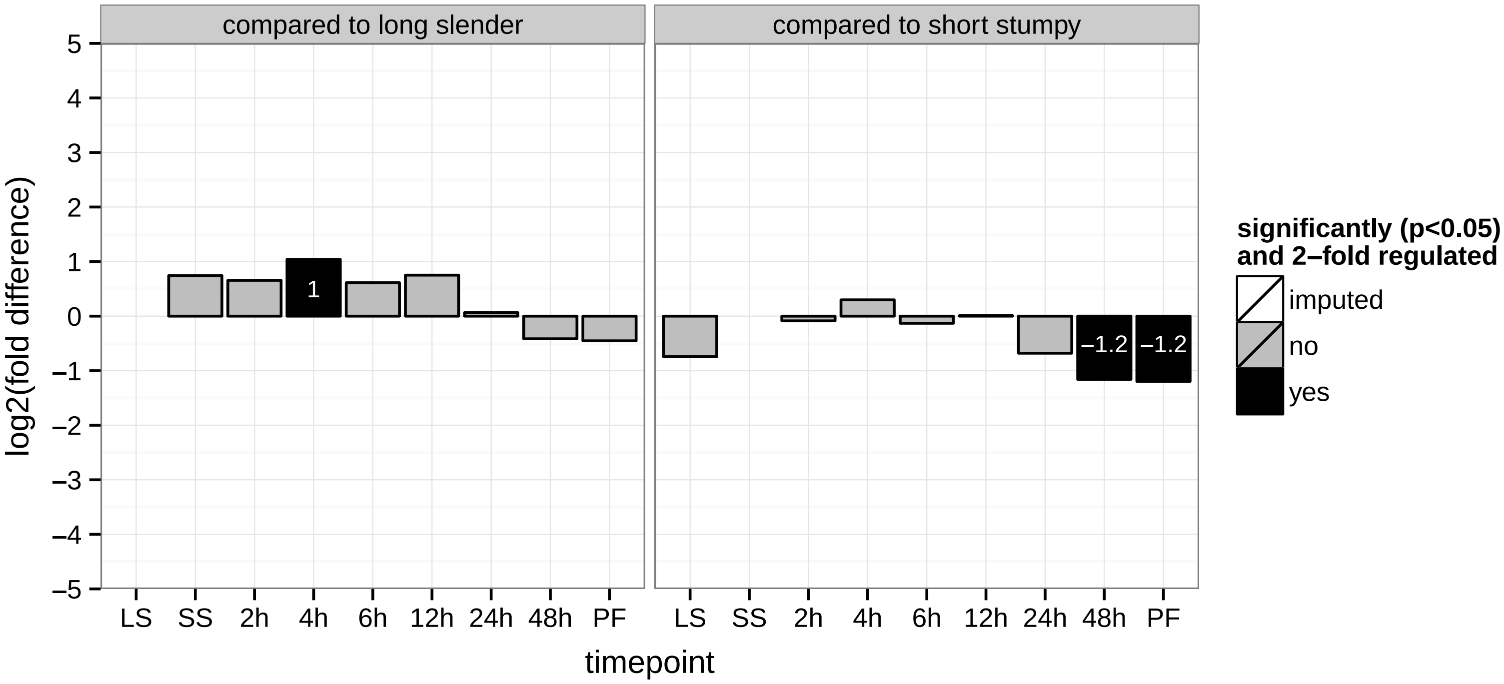
flagellum–adhesion glycoprotein, putative
Tb927.8.4060
AGOF: null
AGOC: flagellar pocket, integral to membrane, motile cilium
AGOP: null
PGOF: null
PGOC: null
PGOP: null

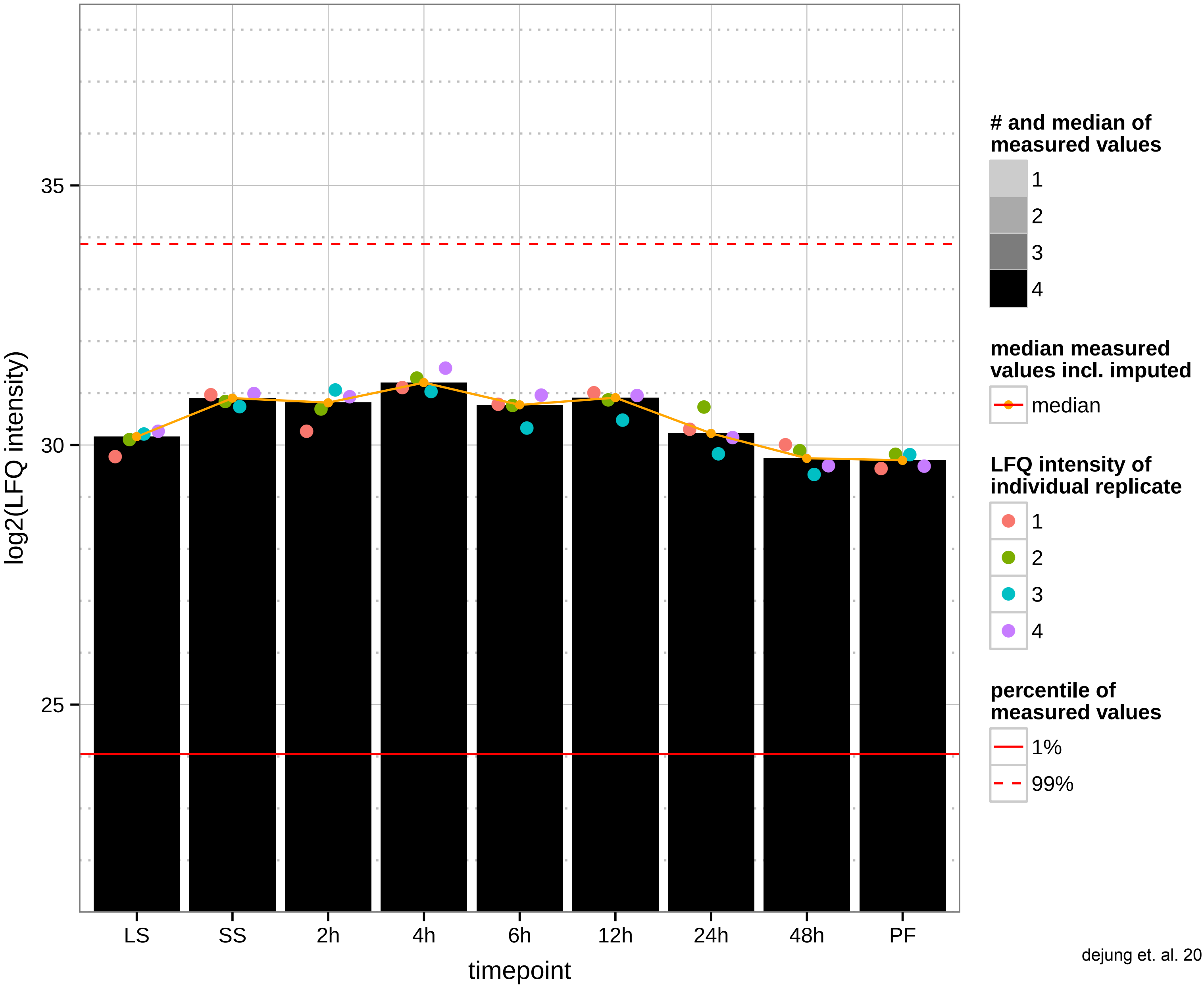




dejung et. al. 2015

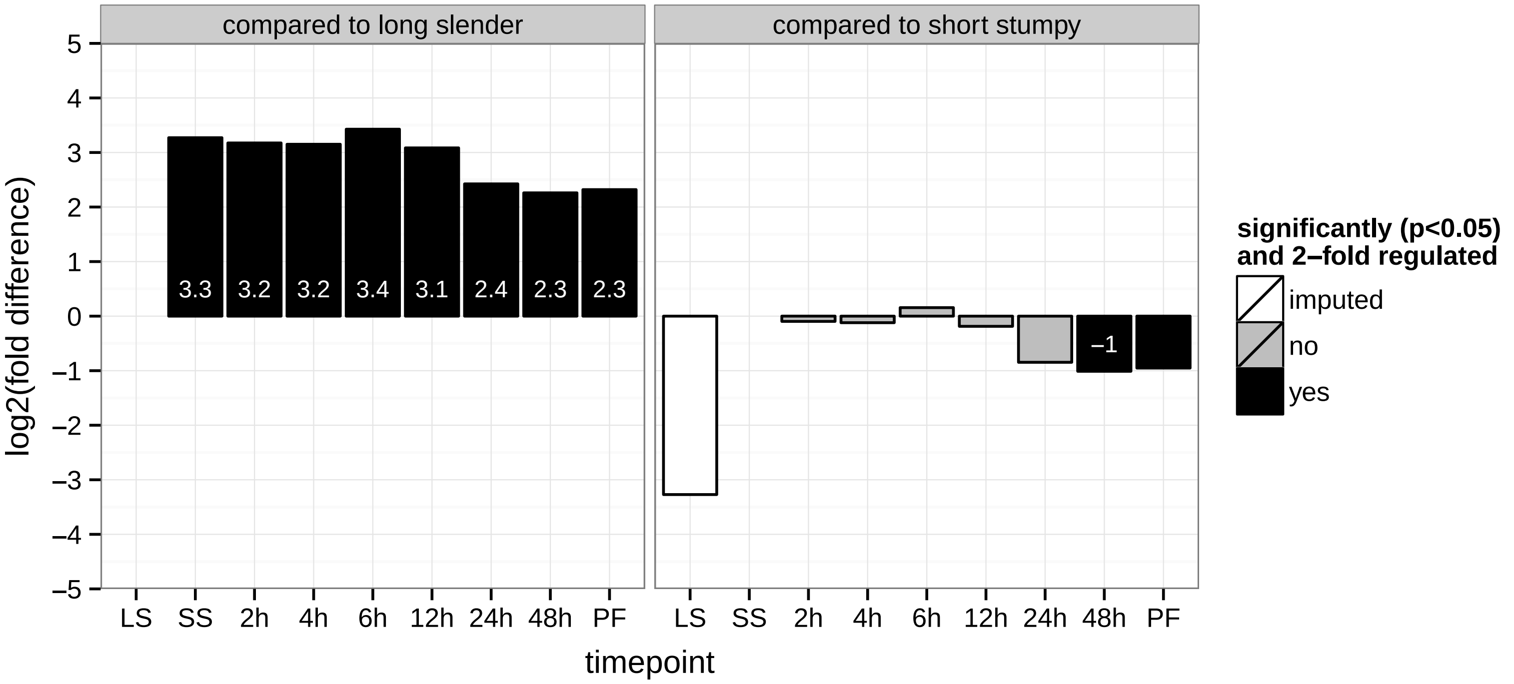
small GTP–binding protein Rab11, Rab11A GTPase (RAB11)
Tb927.8.4330
AGOF: GTP binding, GTPase activity
AGOC: contractile vacuole, endomembrane system, endosome, intracellular
AGOP: endosomal transport, intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal trans
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti

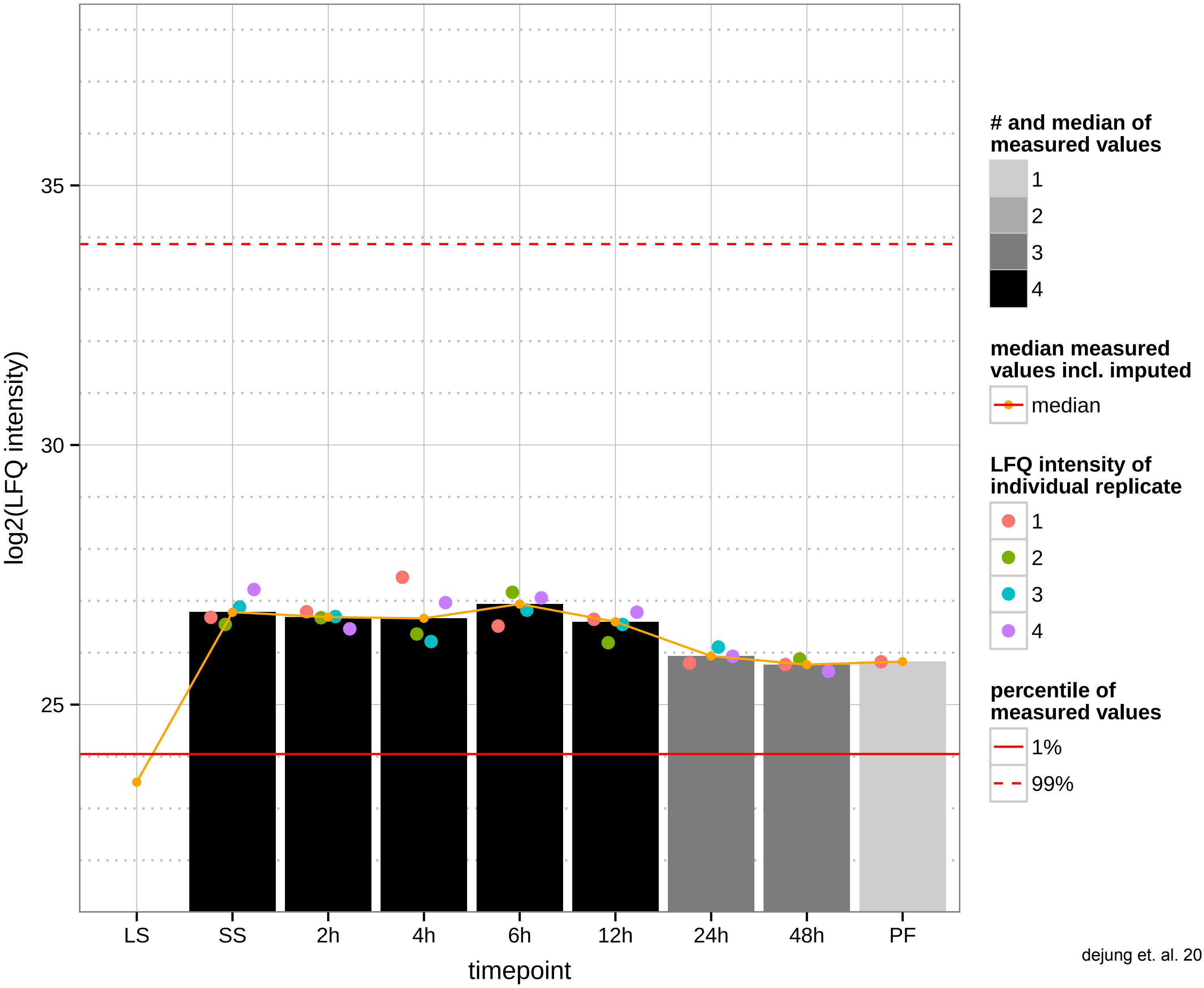




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.5240
AGOF: null
AGOC: membrane
AGOP: null
PGOF: null
PGOC: membrane
PGOP: null





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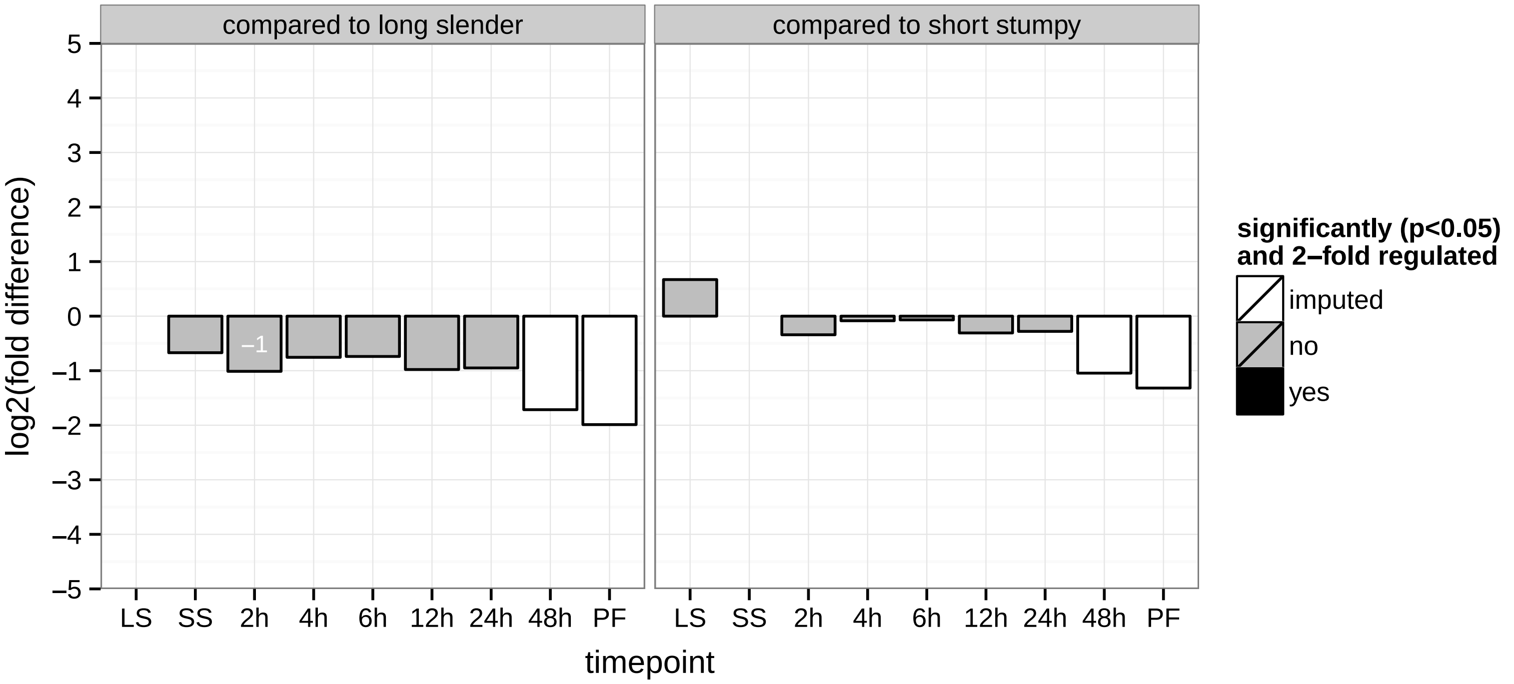
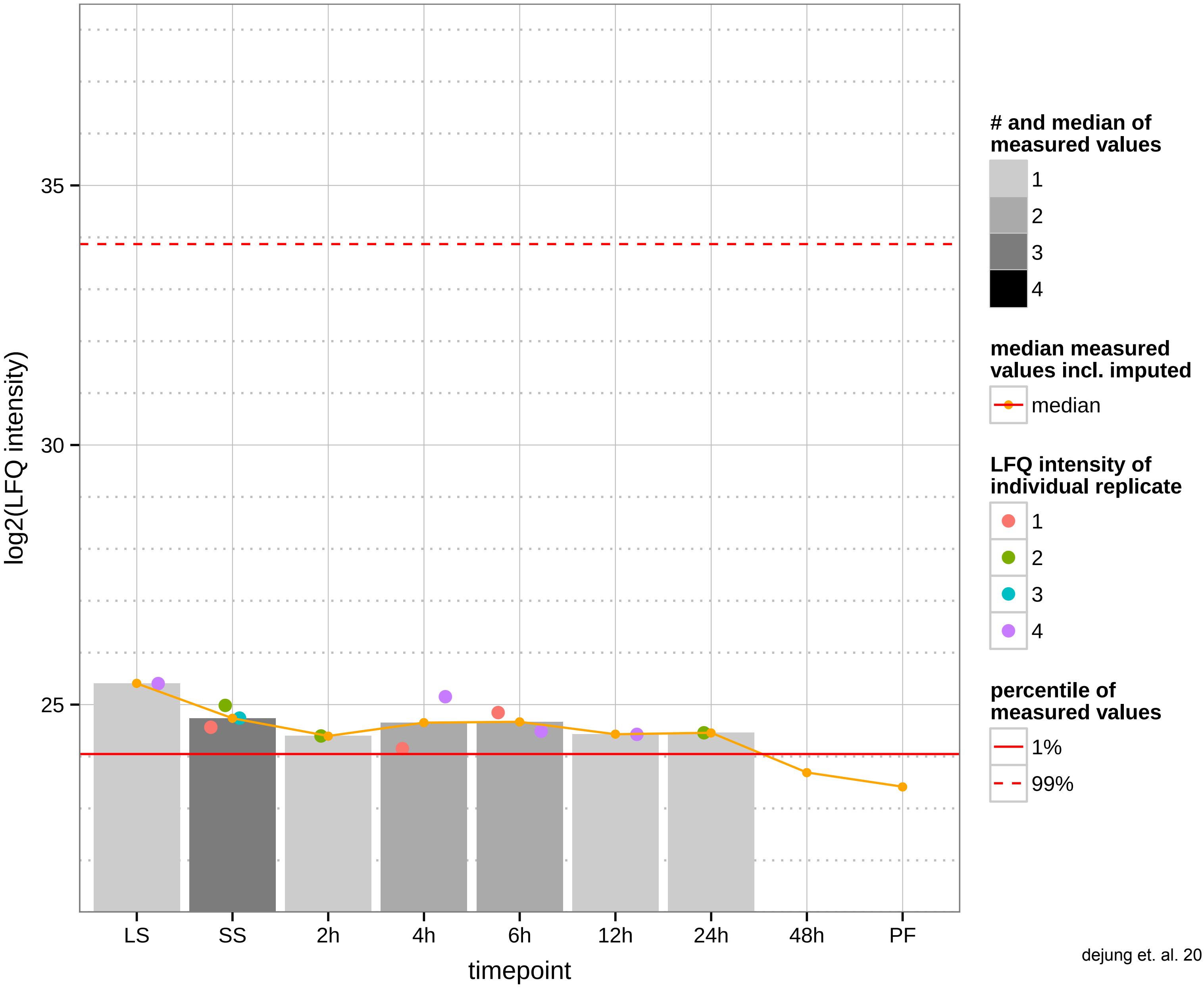
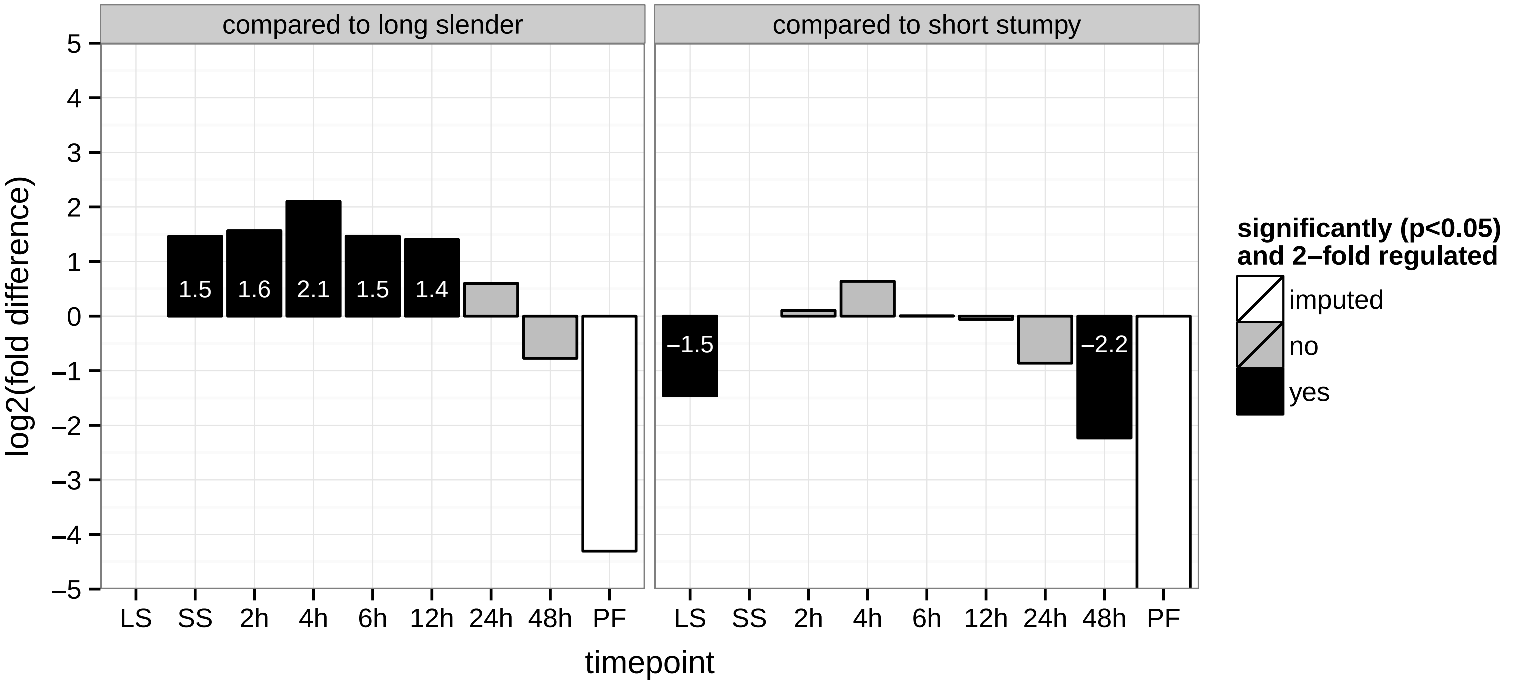
hypothetical protein, conserved
Tb927.8.6620
AGOF: null
AGOC: integral to membrane, mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

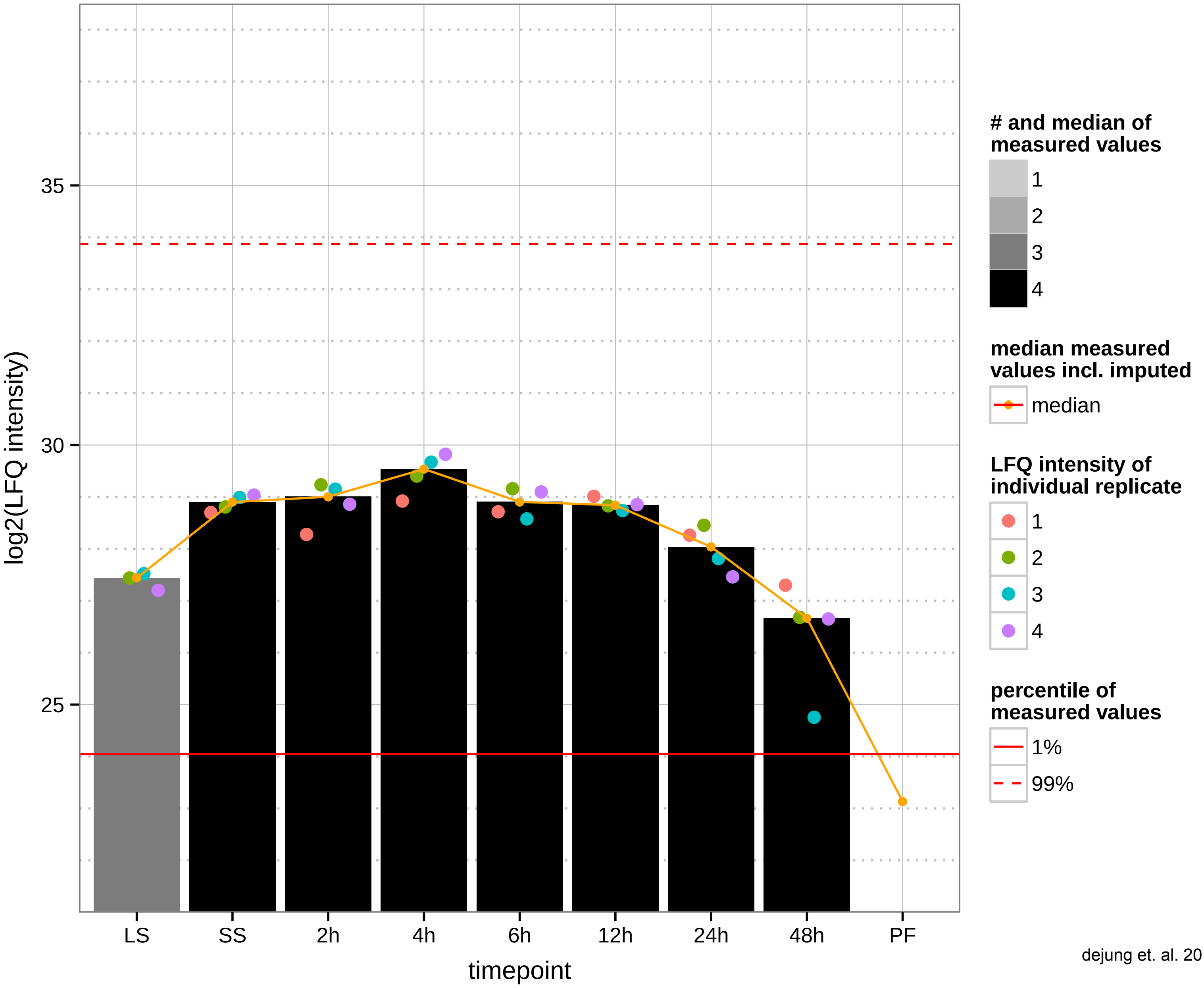




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.7720
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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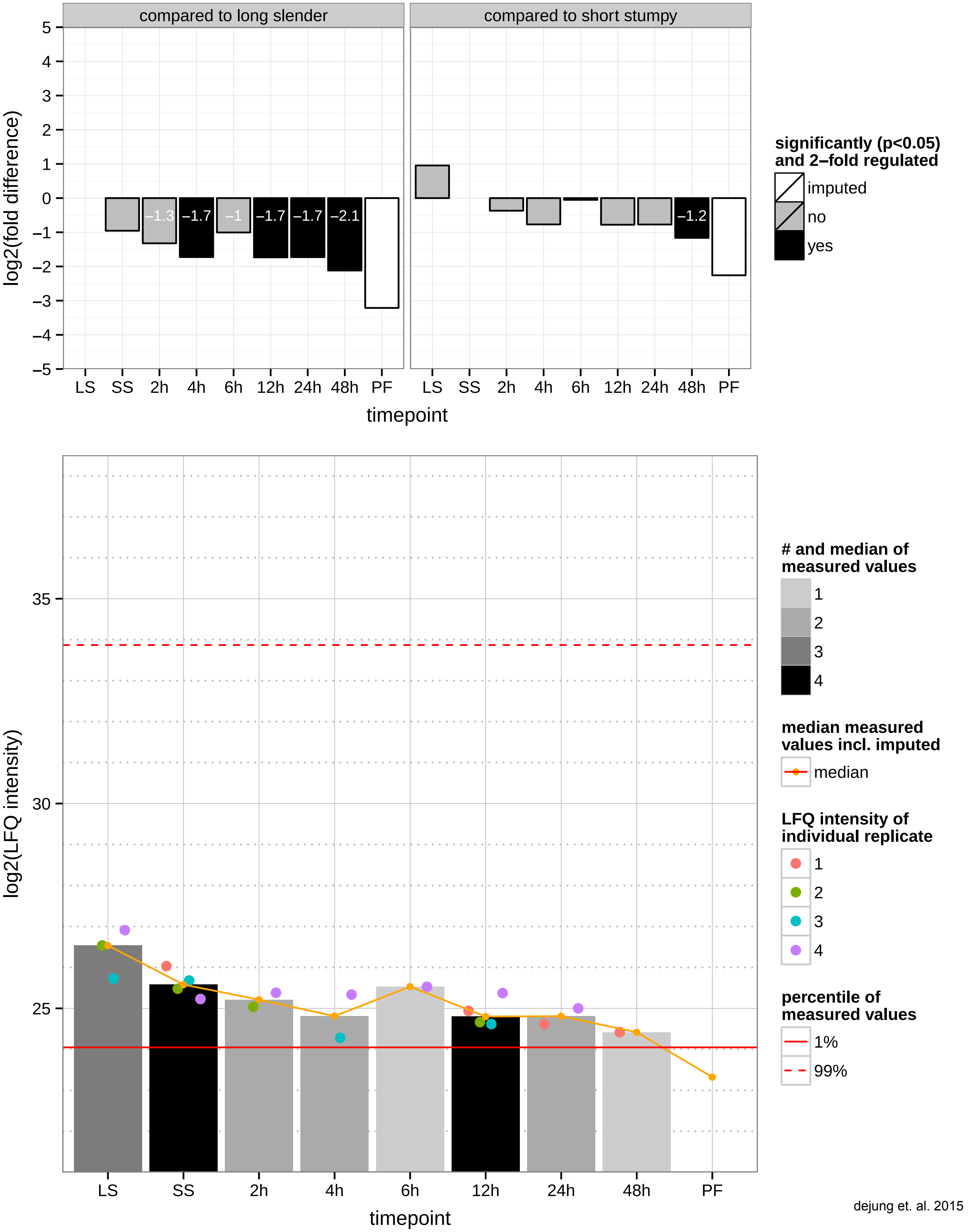
hypothetical protein, conserved
Tb927.8.8000
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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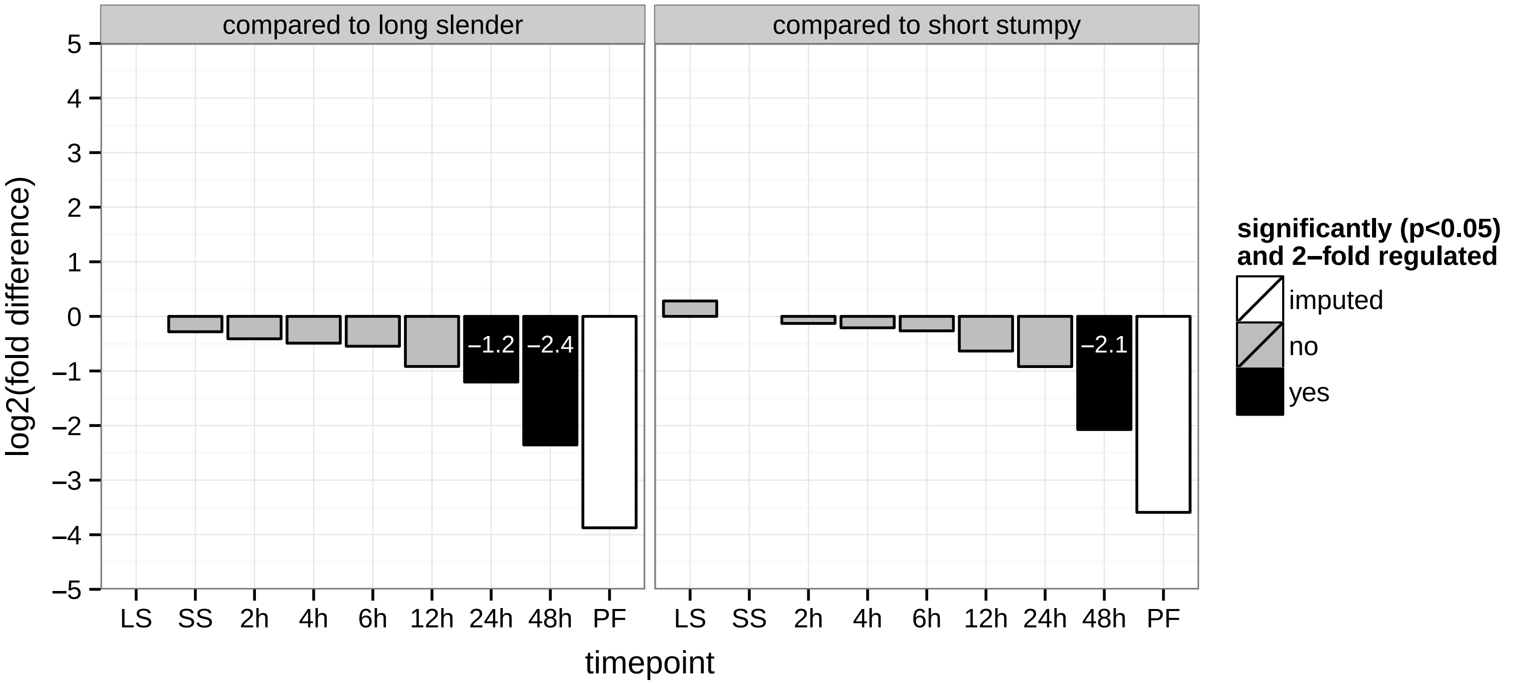
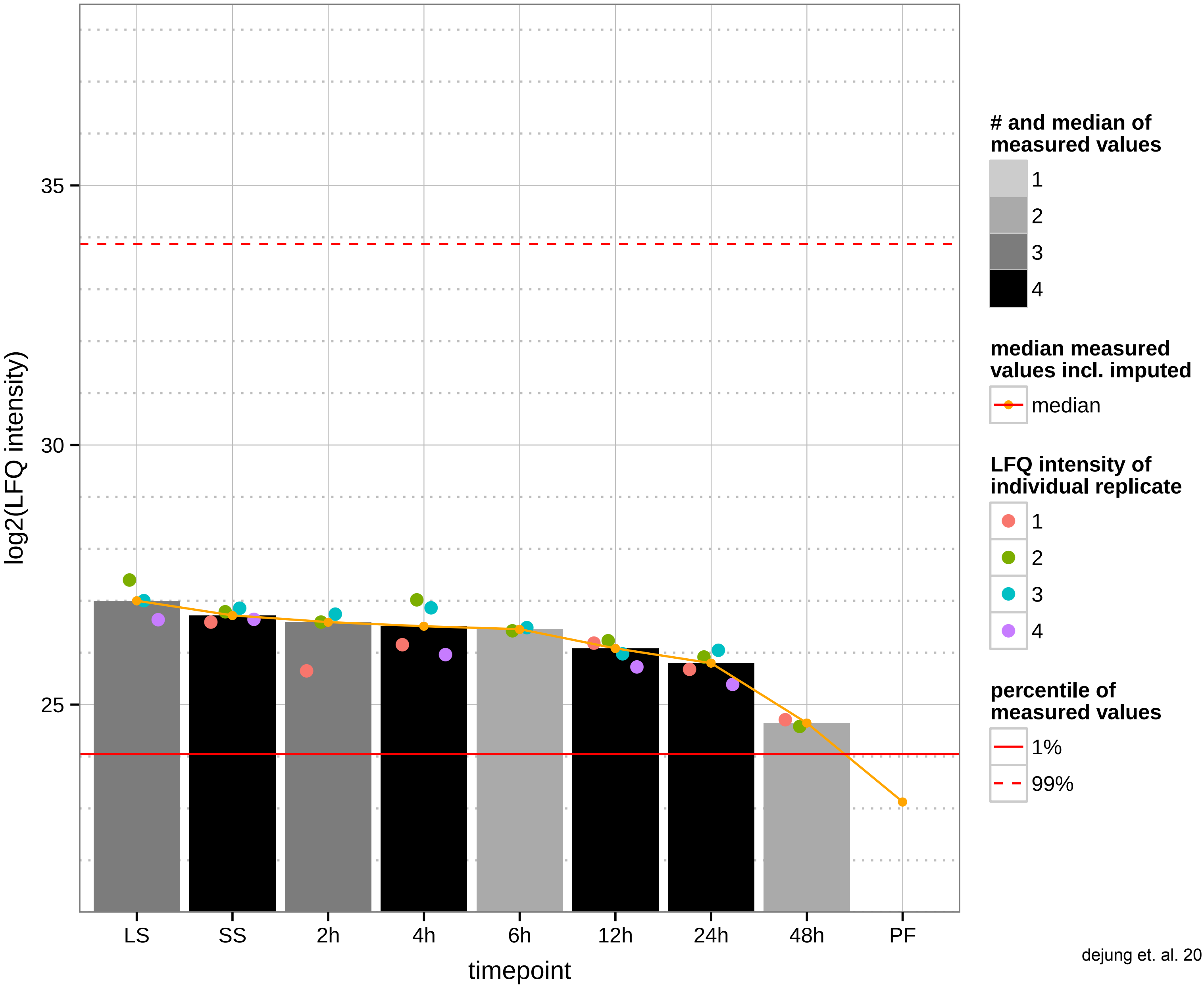
hypothetical protein, conserved
Tb927.8.8030
AGOF: null
AGOC: integral to membrane
AGOP: transport
PGOF: null
PGOC: integral to membrane
PGOP: transport





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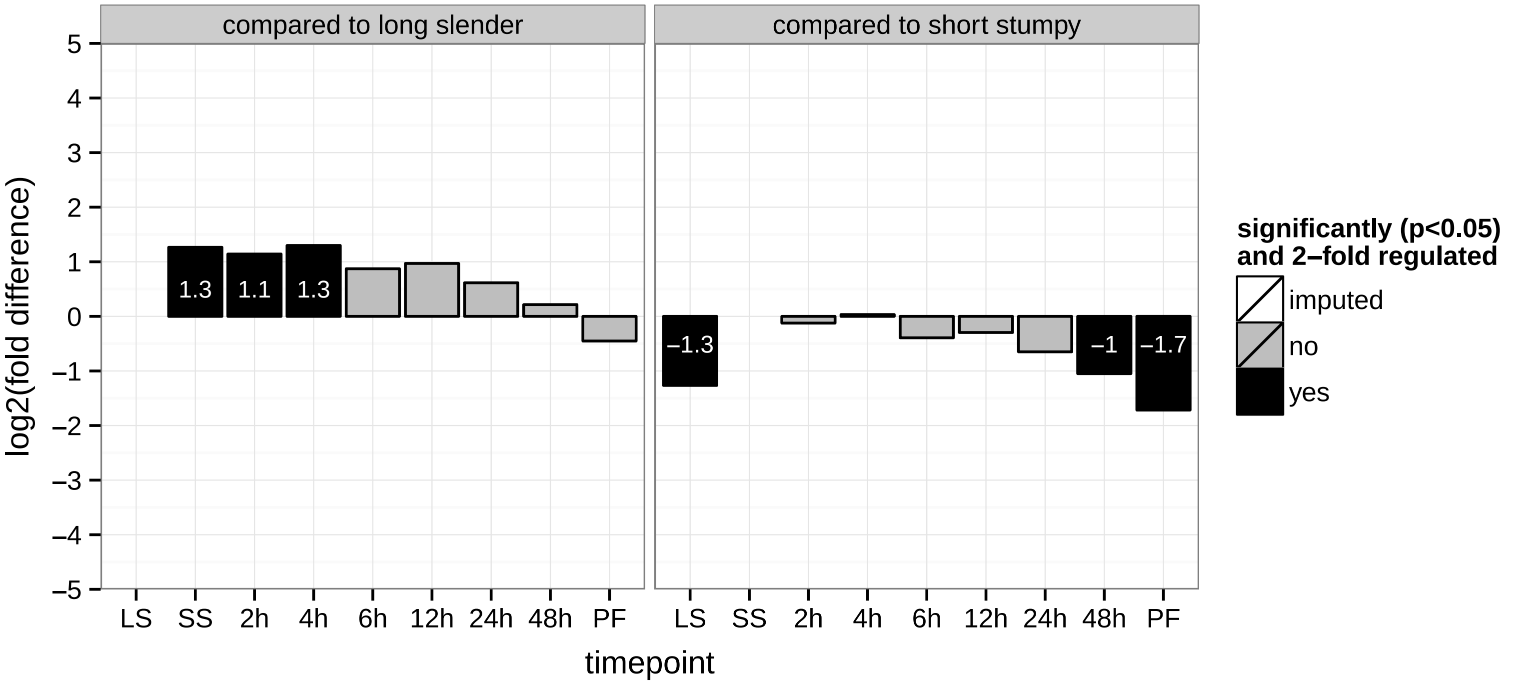
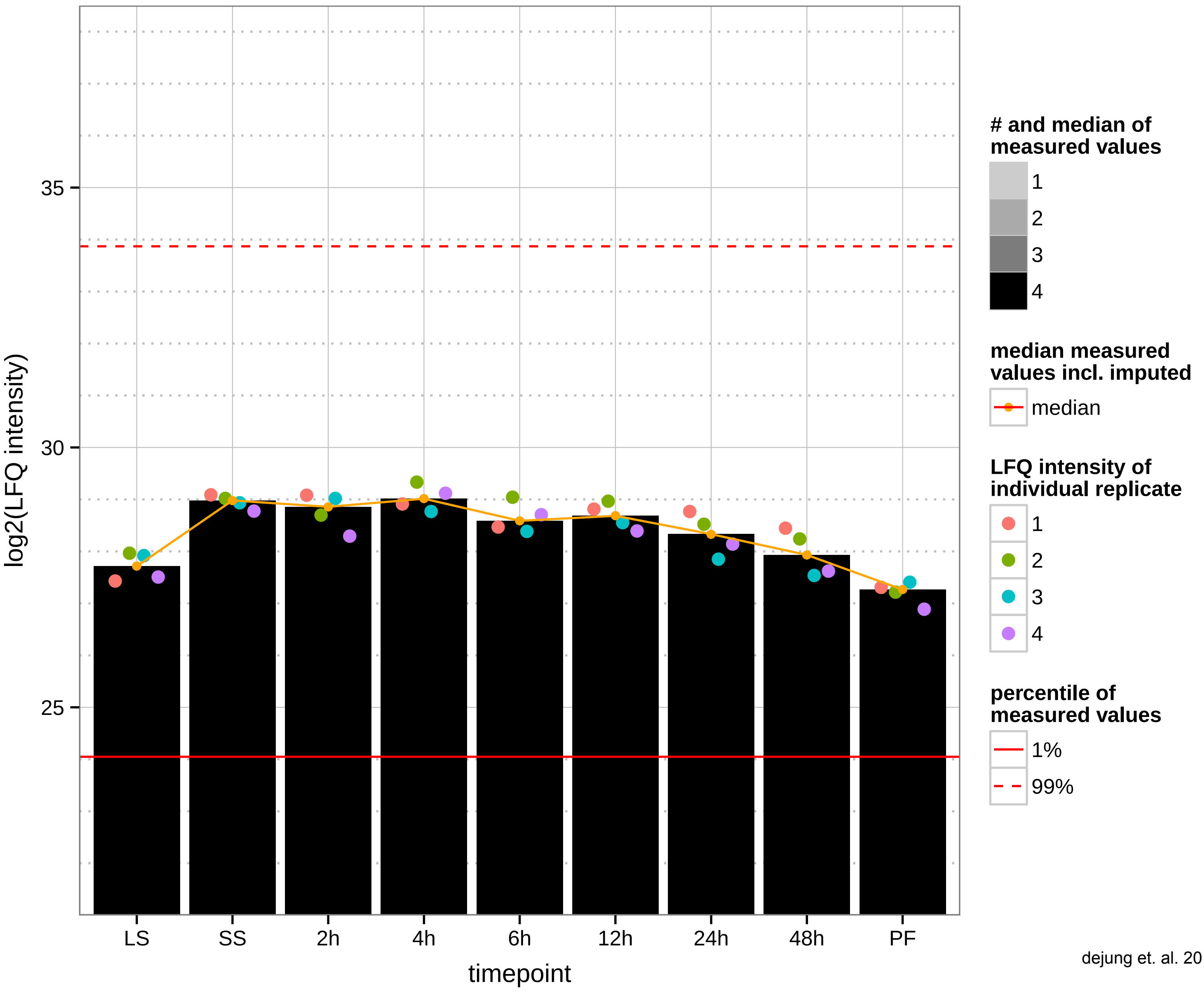
small GTPase, putative, GTP−binding protein, putative (RAB7)
Tb927.9.11000
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: protein transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: membrane
PGOP: GTP catabolic process, protein transport, signal transduction, small GTPase mediated signal transduction





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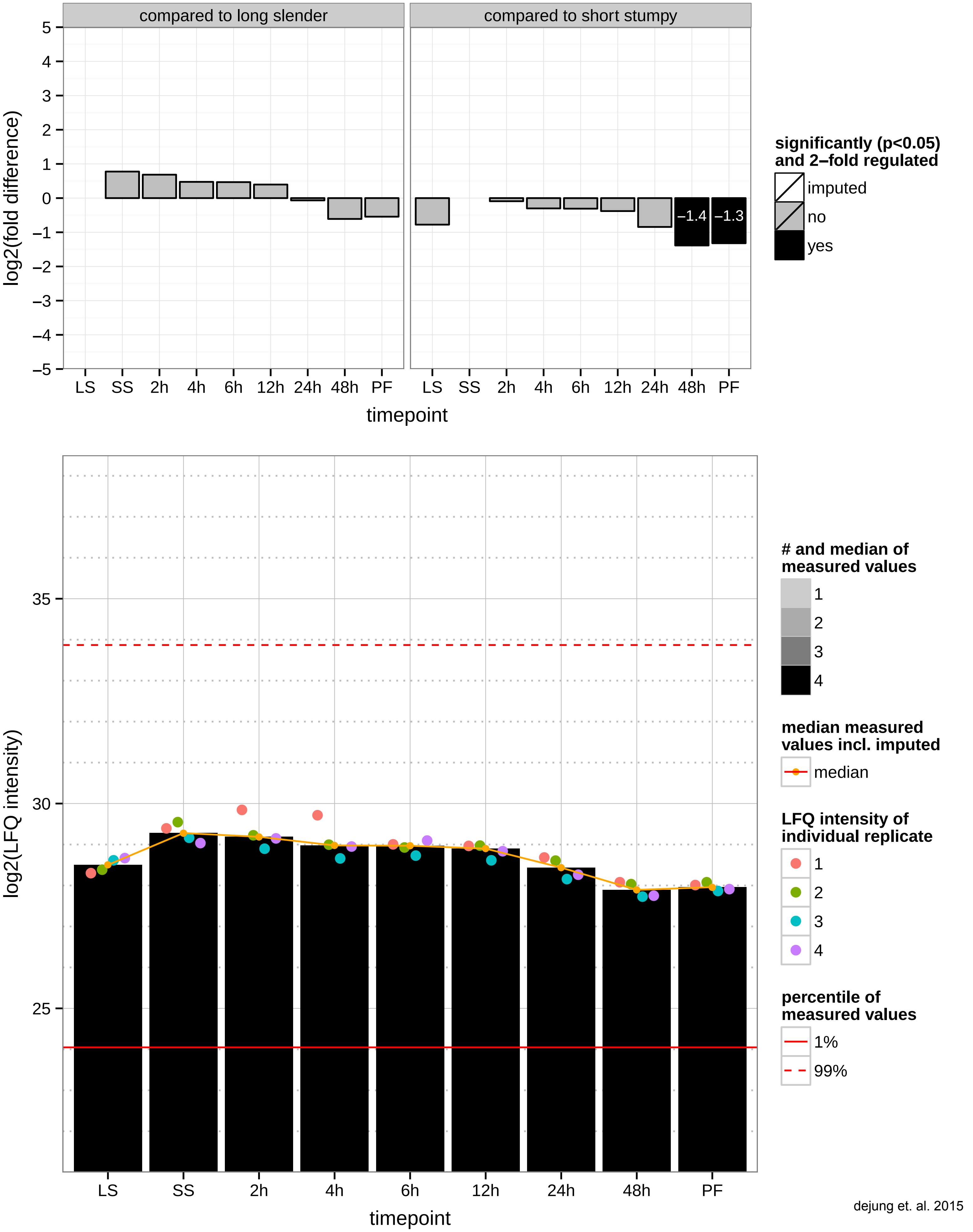
cAMP–dependent protein kinase catalytic subunit 2 (PKAC2)
Tb927.9.11030
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null
PGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity, transferring phosphoru
PGOC: null
PGOP: protein phosphorylation



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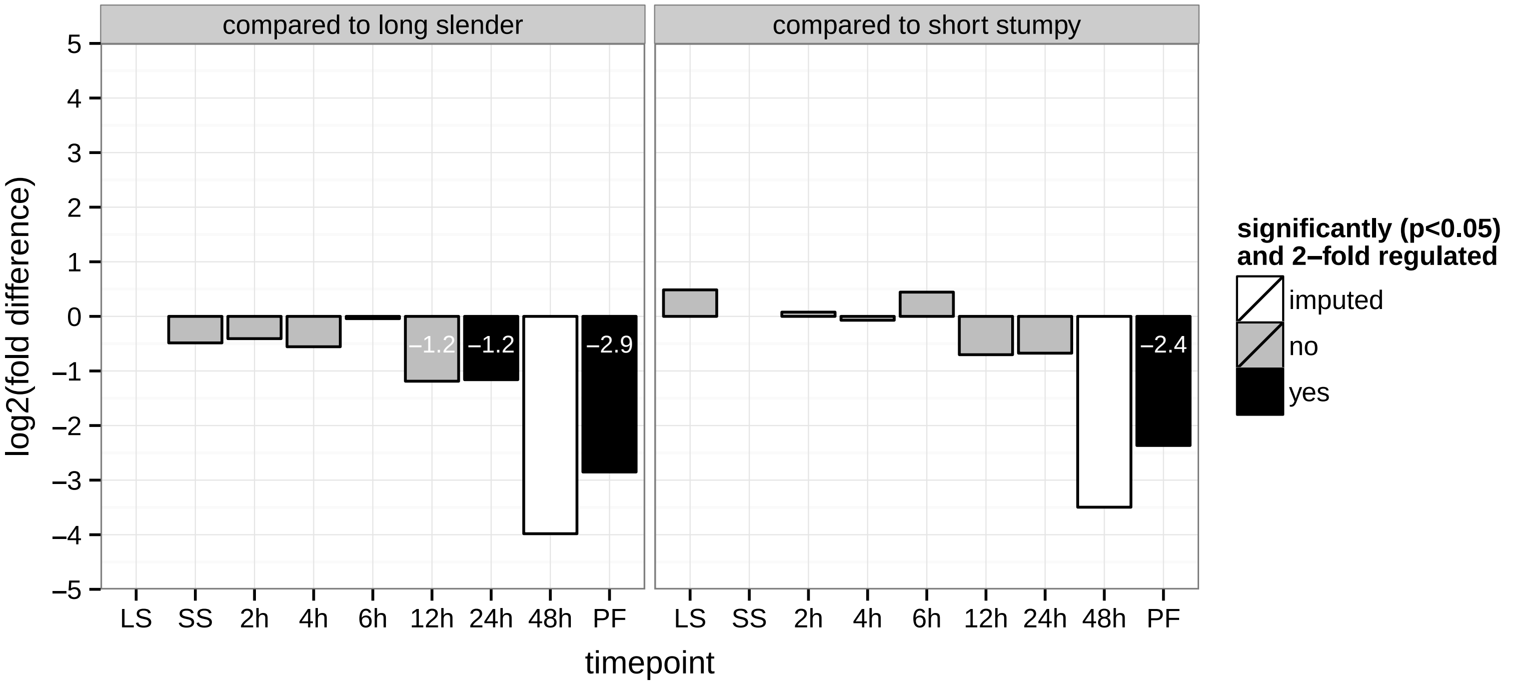
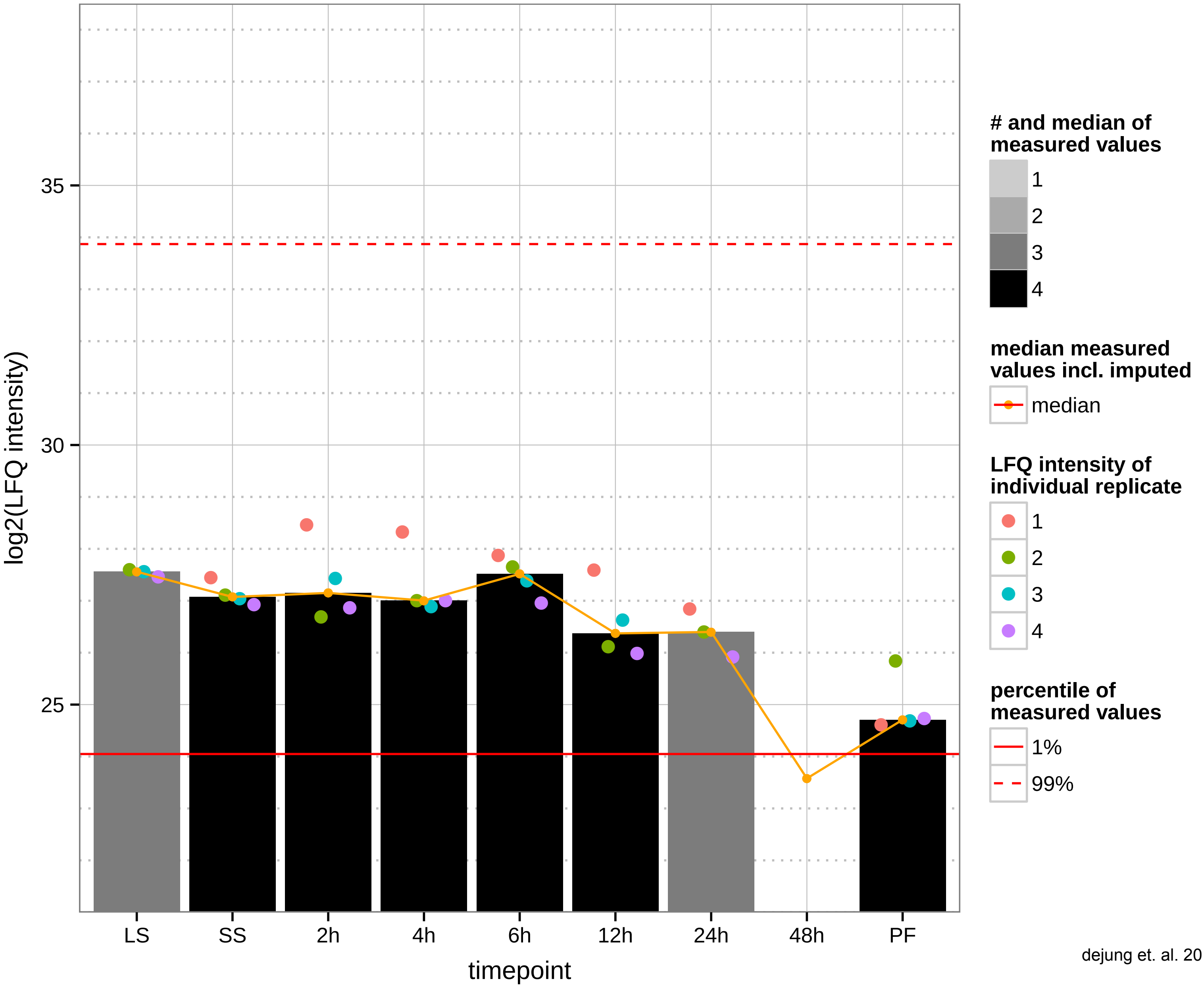
cAMP–dependent protein kinase catalytic subunit 1 (PKAC1)
Tb927.9.11100
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity, transferring phosphoru
PGOC: null
PGOP: protein phosphorylation





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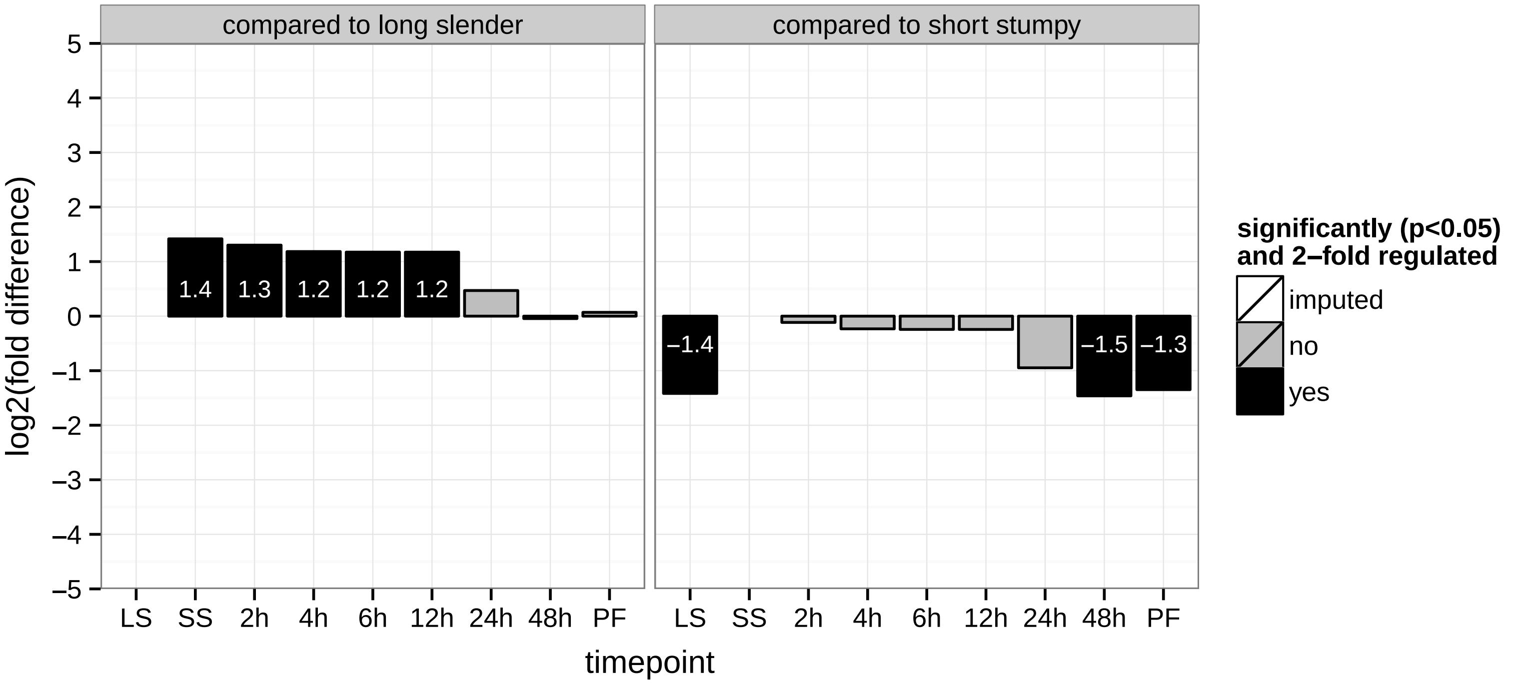
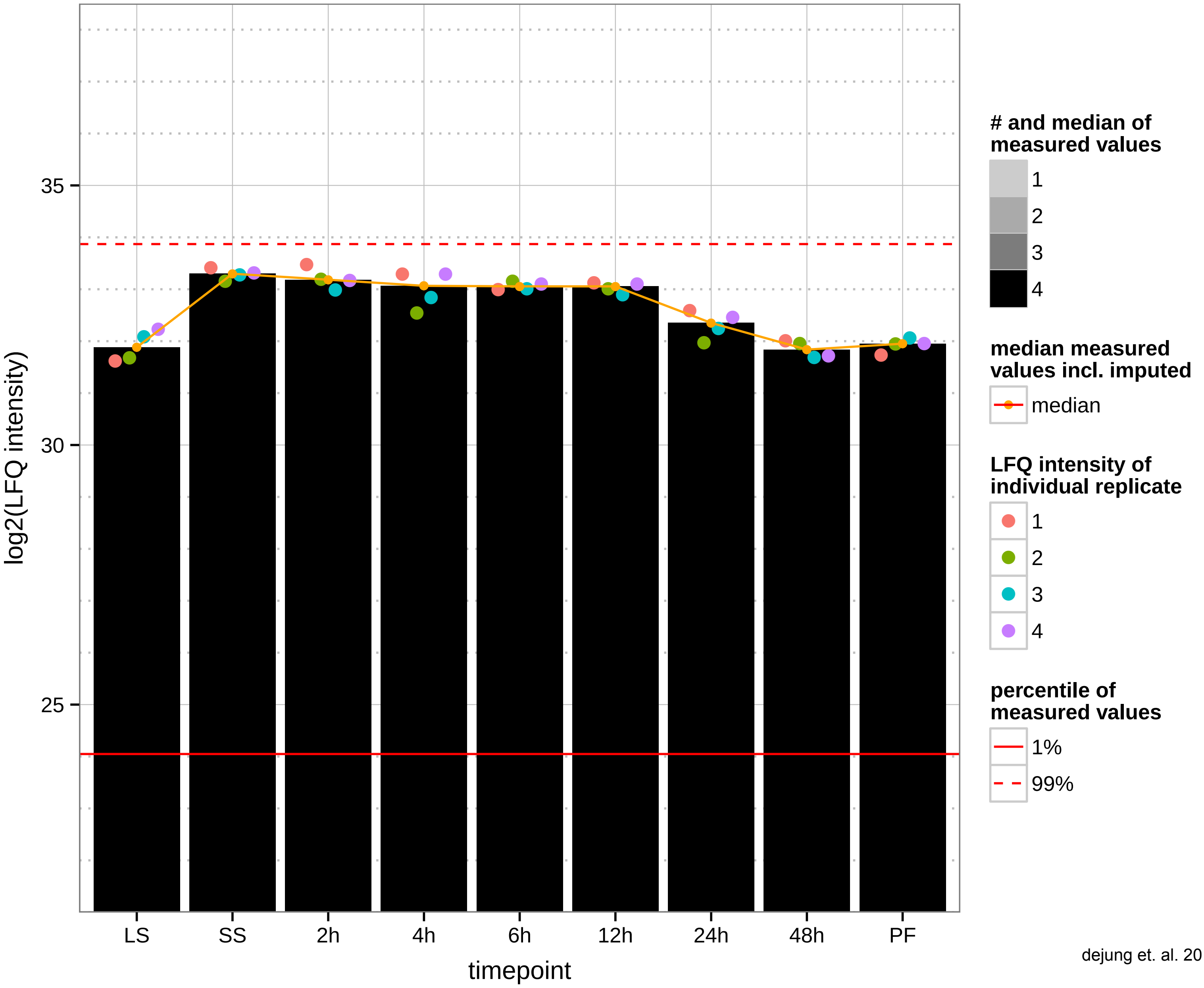
ubiquitin–activating enzyme E1, putative, putative (UBA2)
Tb927.9.12650
AGOF: null, ATP binding, small protein activating enzyme activity, ubiquitin–protein ligase activity
AGOC: null, mitochondrion
AGOP: null, cellular protein modification process
PGOF: catalytic activity, ATP binding, catalytic activity, small protein activating enzyme activity
PGOC: null
PGOP: null, cellular protein modification process





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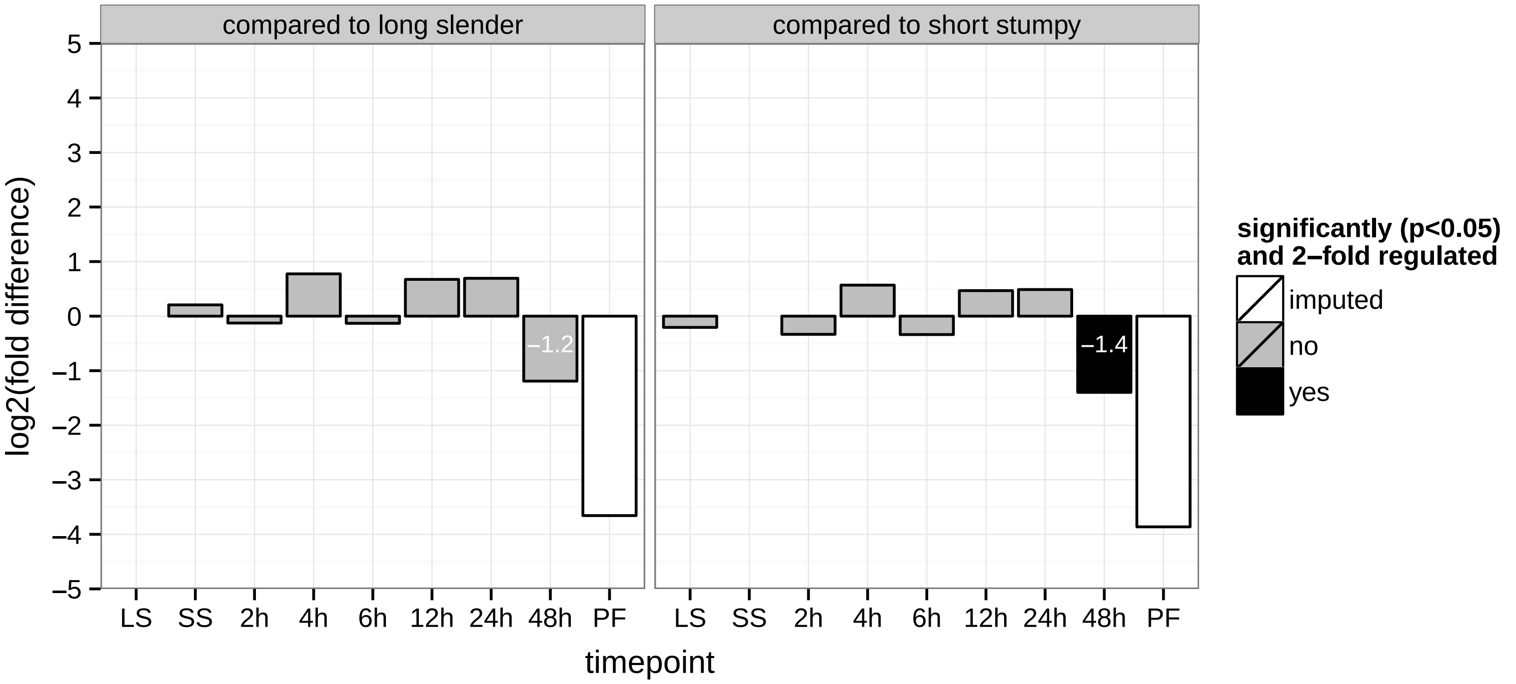
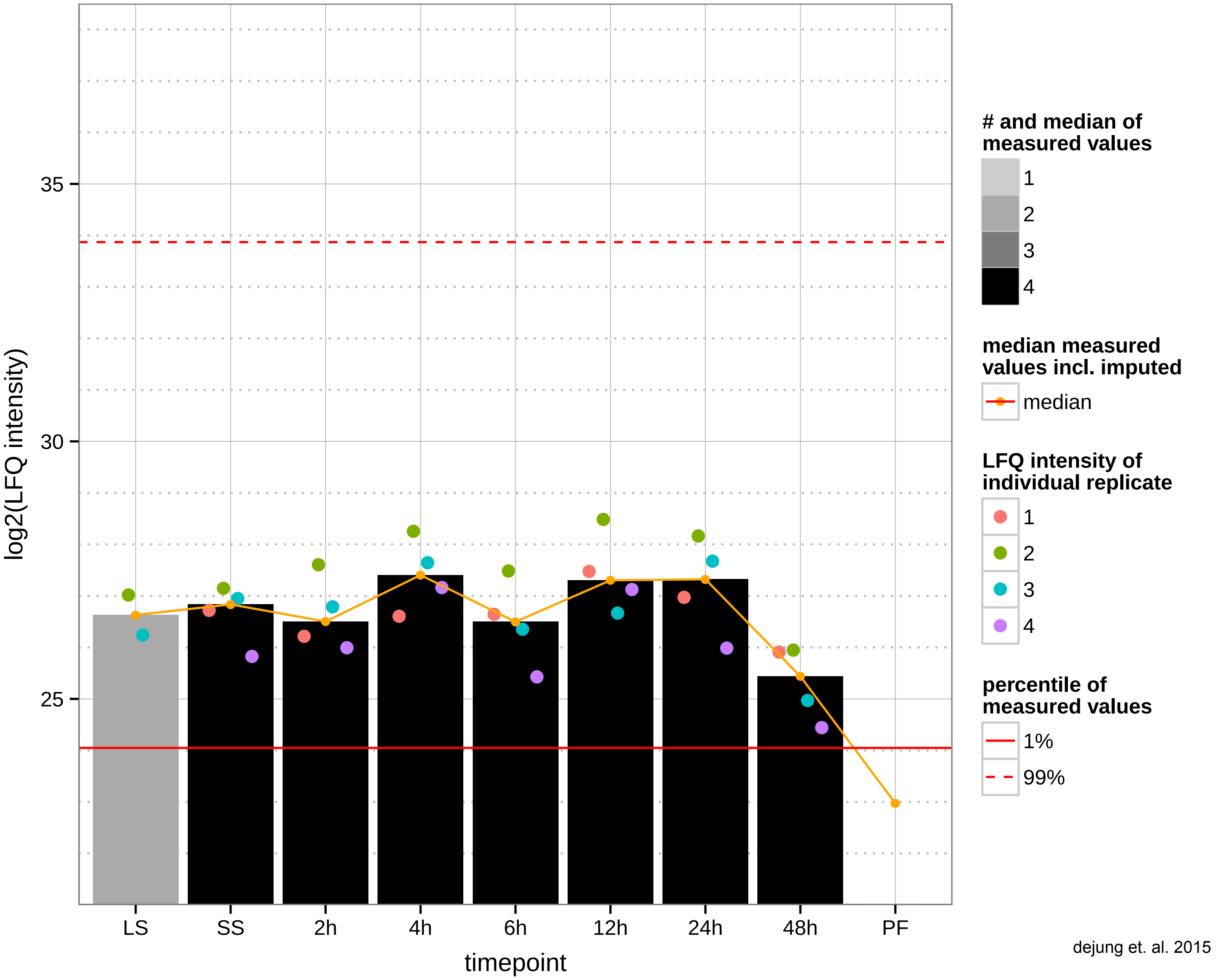
predicted heat shock factor binding protein
Tb927.9.13070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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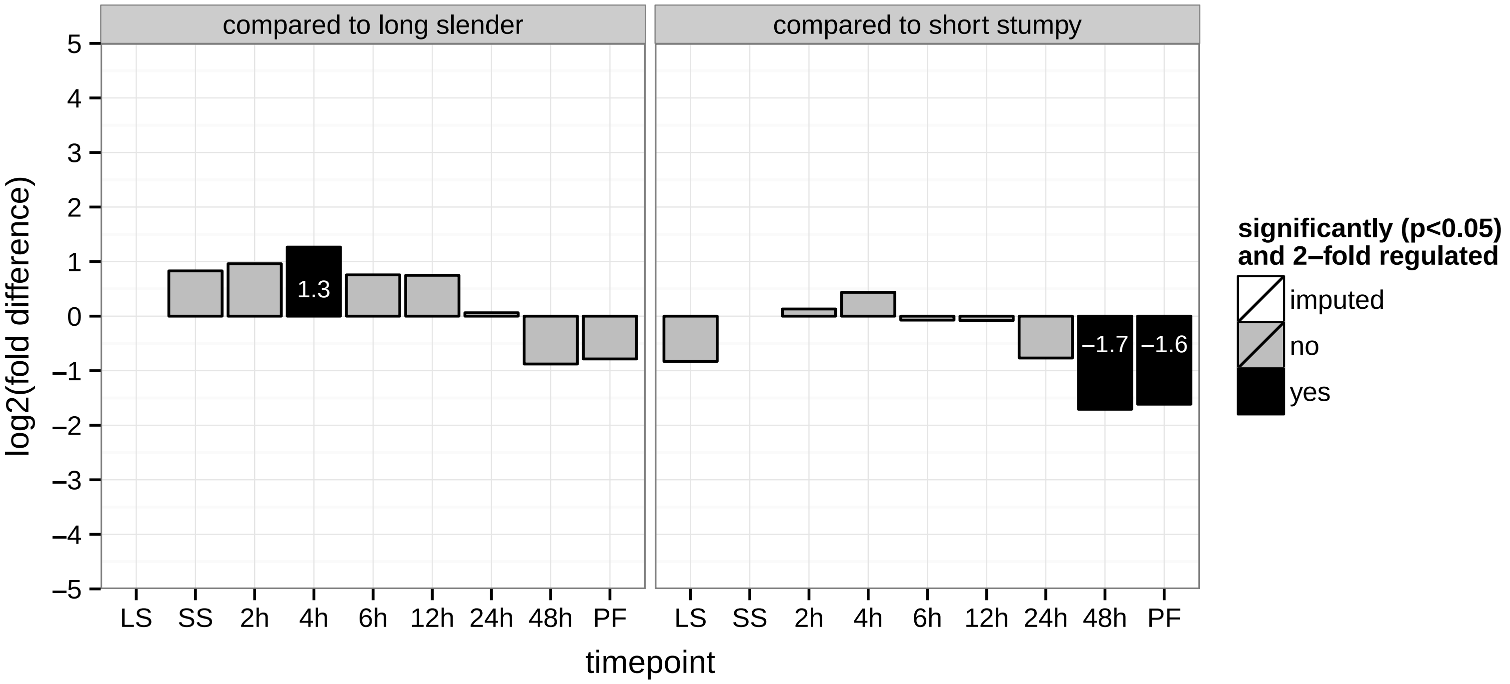
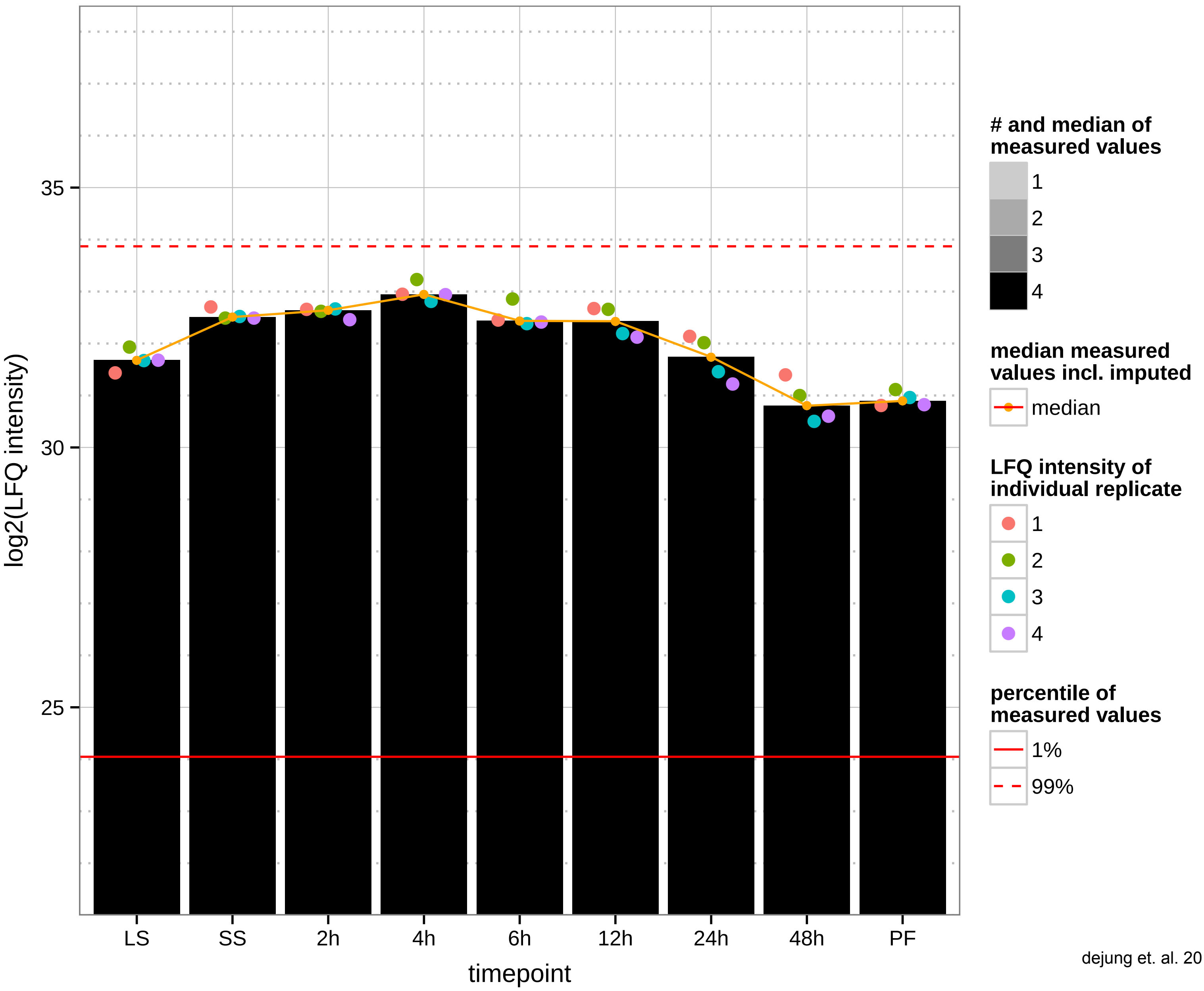
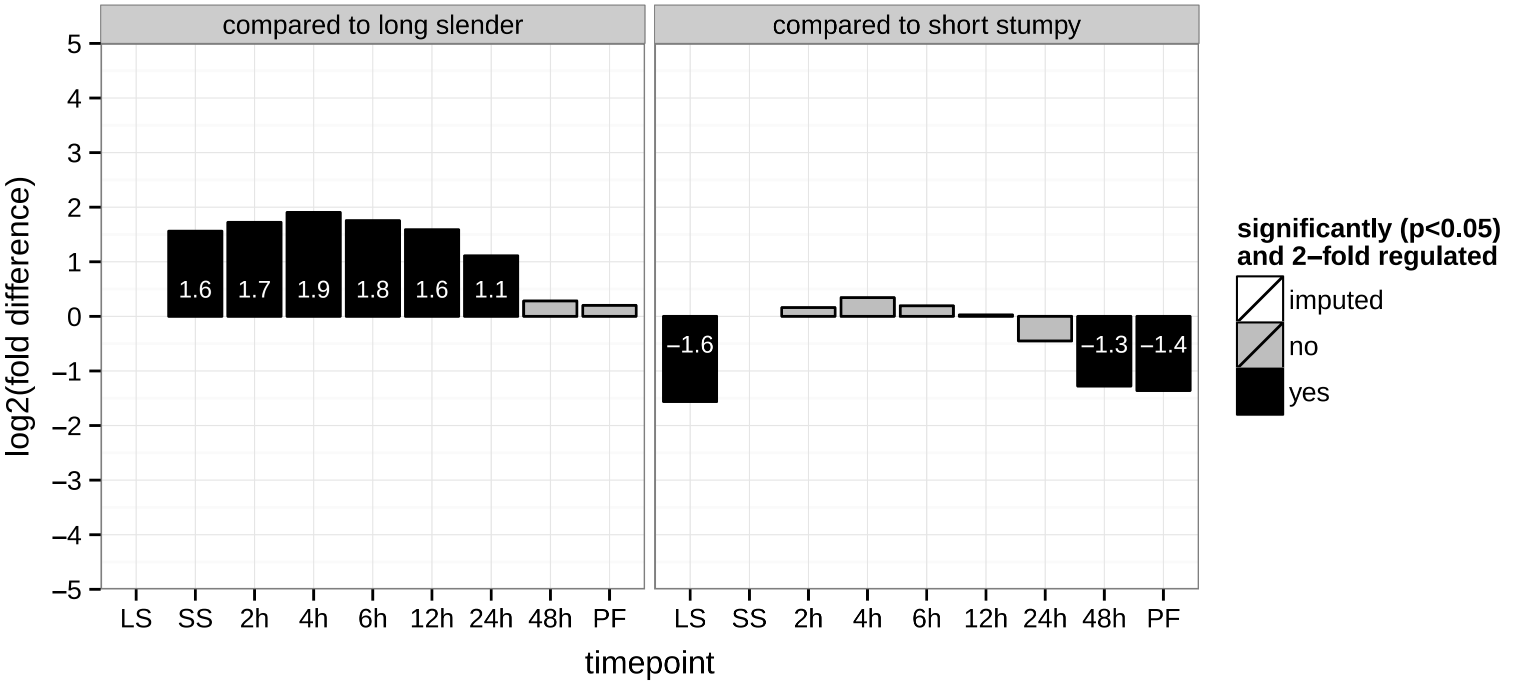
phosphoinositide–binding protein, putative
Tb927.9.13380
AGOF: oxidoreductase activity, phosphatidylinositol binding, transition metal ion binding
AGOC: null
AGOP: cell communication, intracellular signal transduction
PGOF: phosphatidylinositol binding, protein binding
PGOC: null
PGOP: cell communication

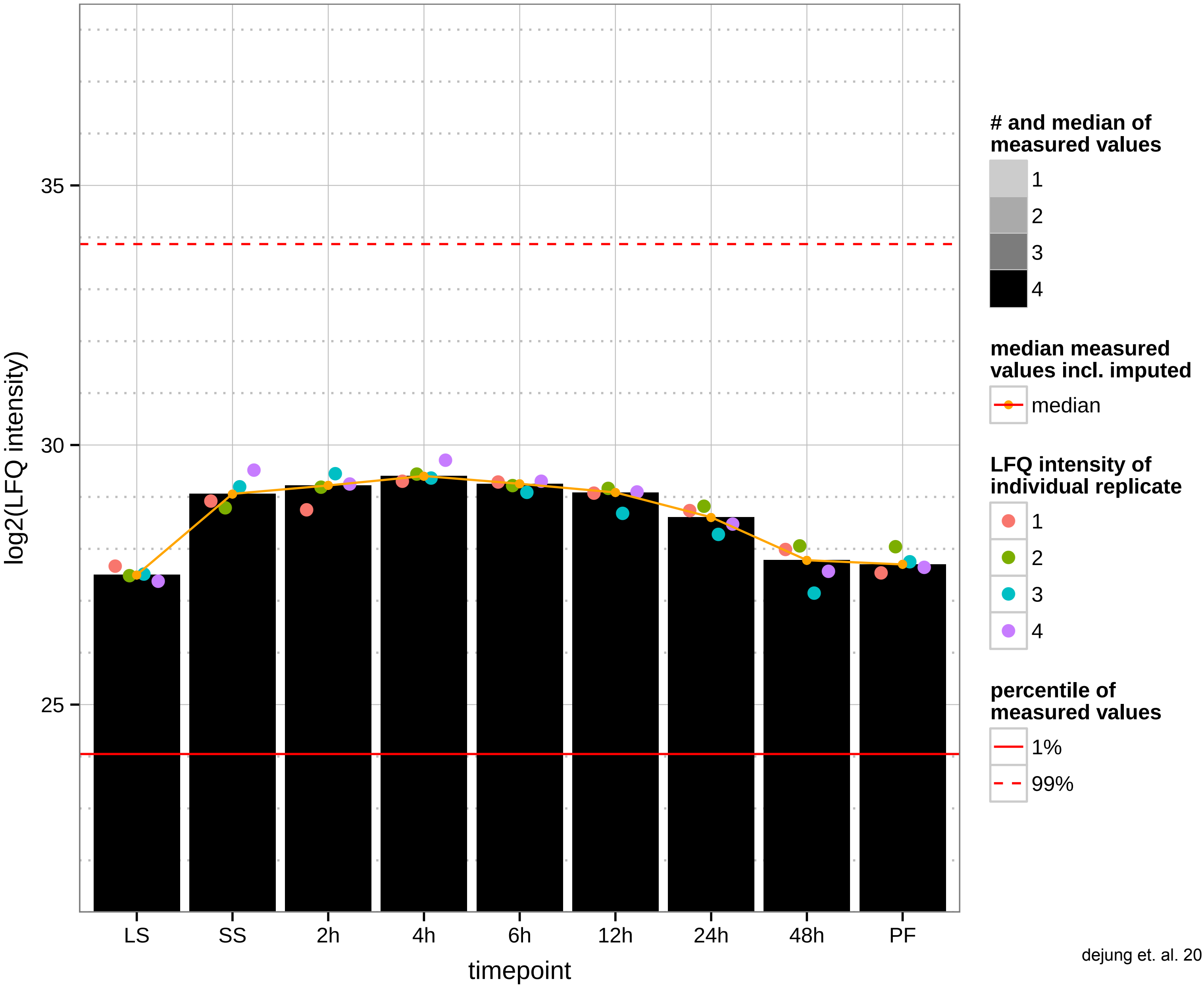




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.14100
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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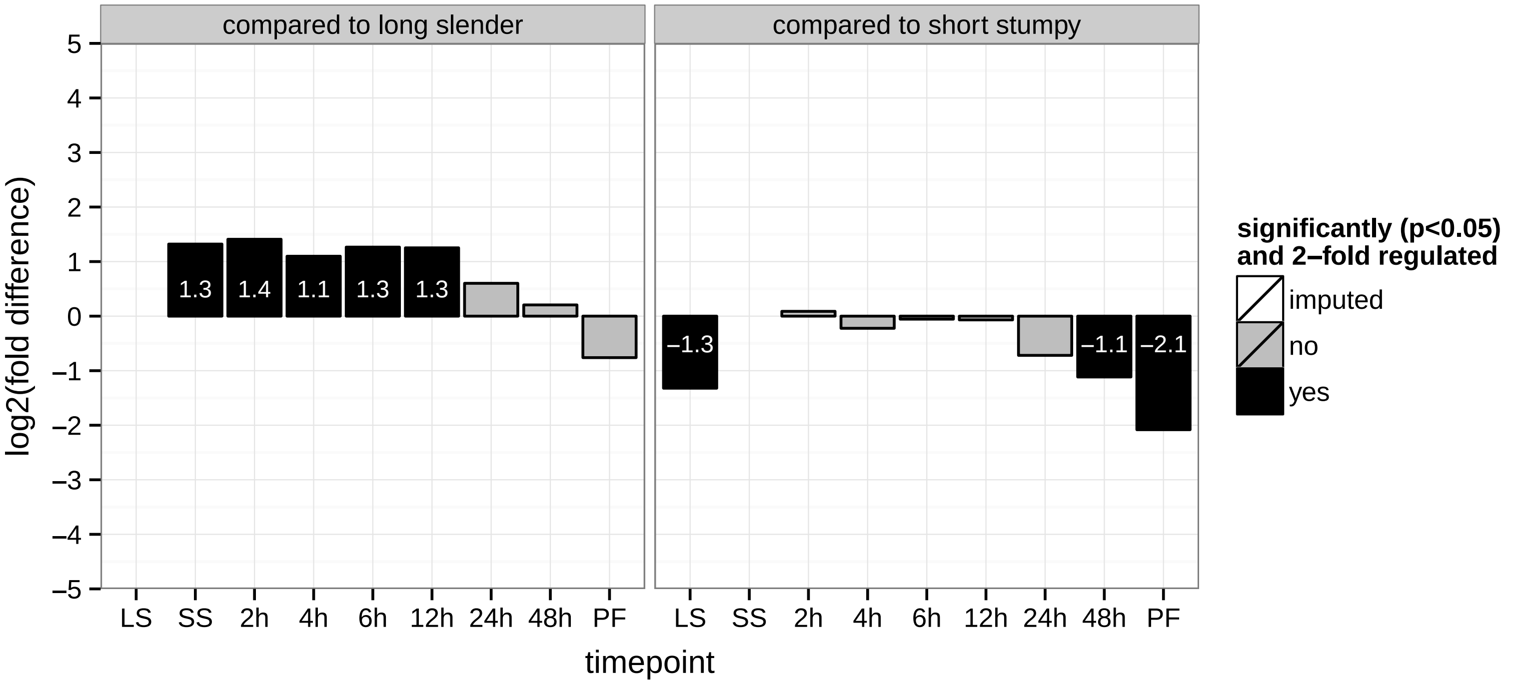
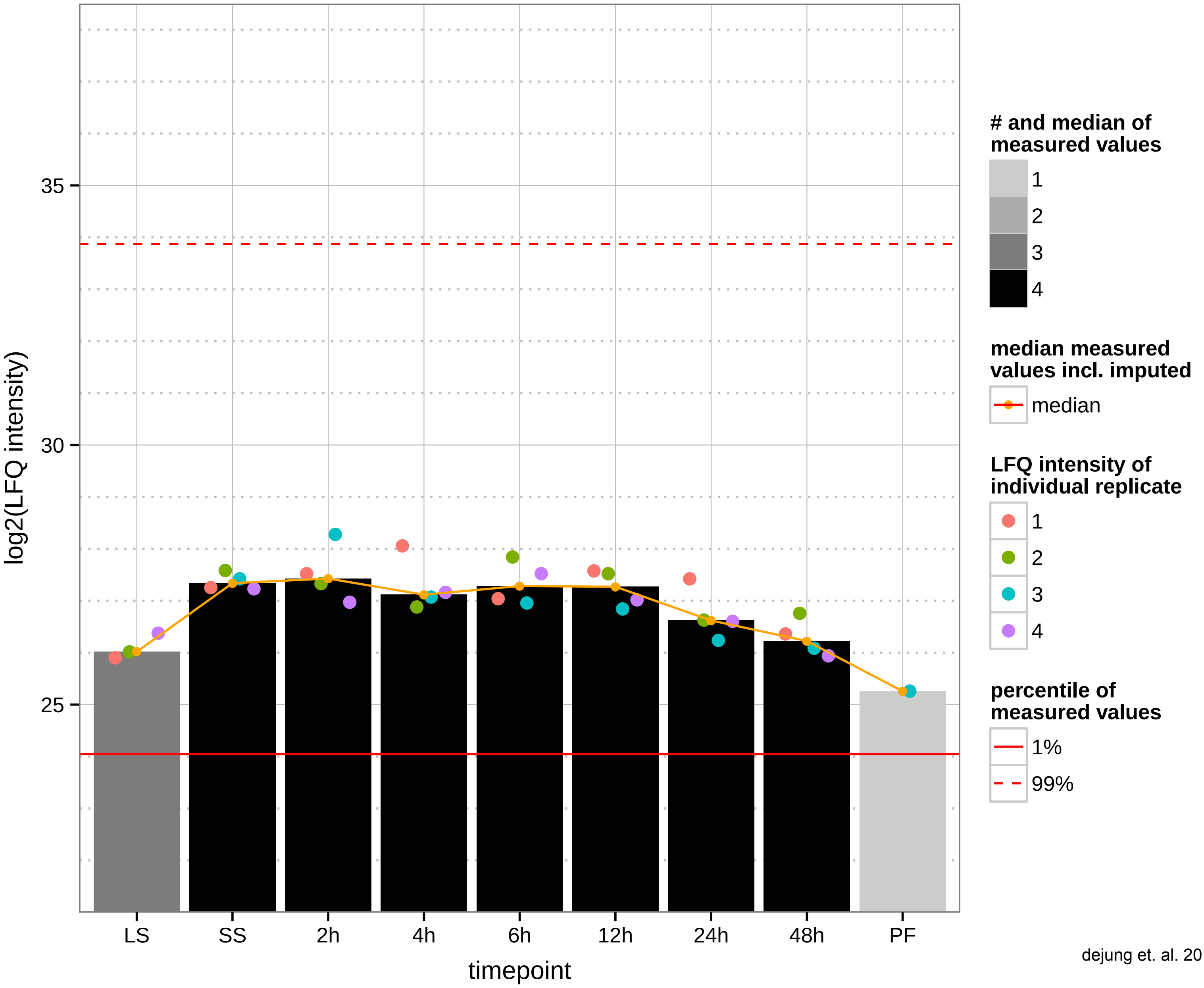
Lys–63–specific deubiquitinase BRCC36, putative, JAB–MPN domain protein
Tb927.9.1680
AGOF: metallopeptidase activity, polyubiquitin binding, ubiquitin thiolesterase activity
AGOC: BRCA1–A complex, BRISC complex, nuclear ubiquitin ligase complex, nucleus
AGOP: G2/M transition DNA damage checkpoint, double–strand break repair, histone H2A K63–linked deubiquitination, prote
PGOF: protein binding
PGOC: null
PGOP: null





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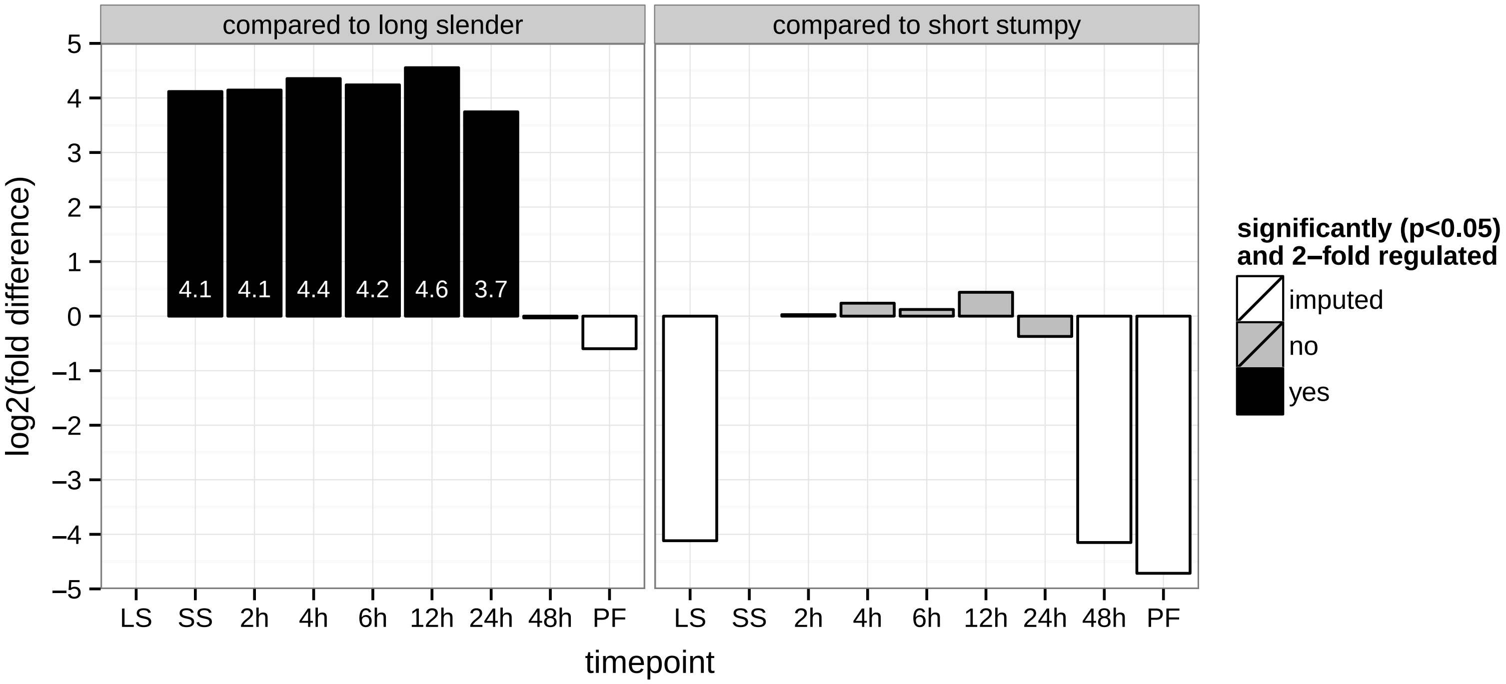
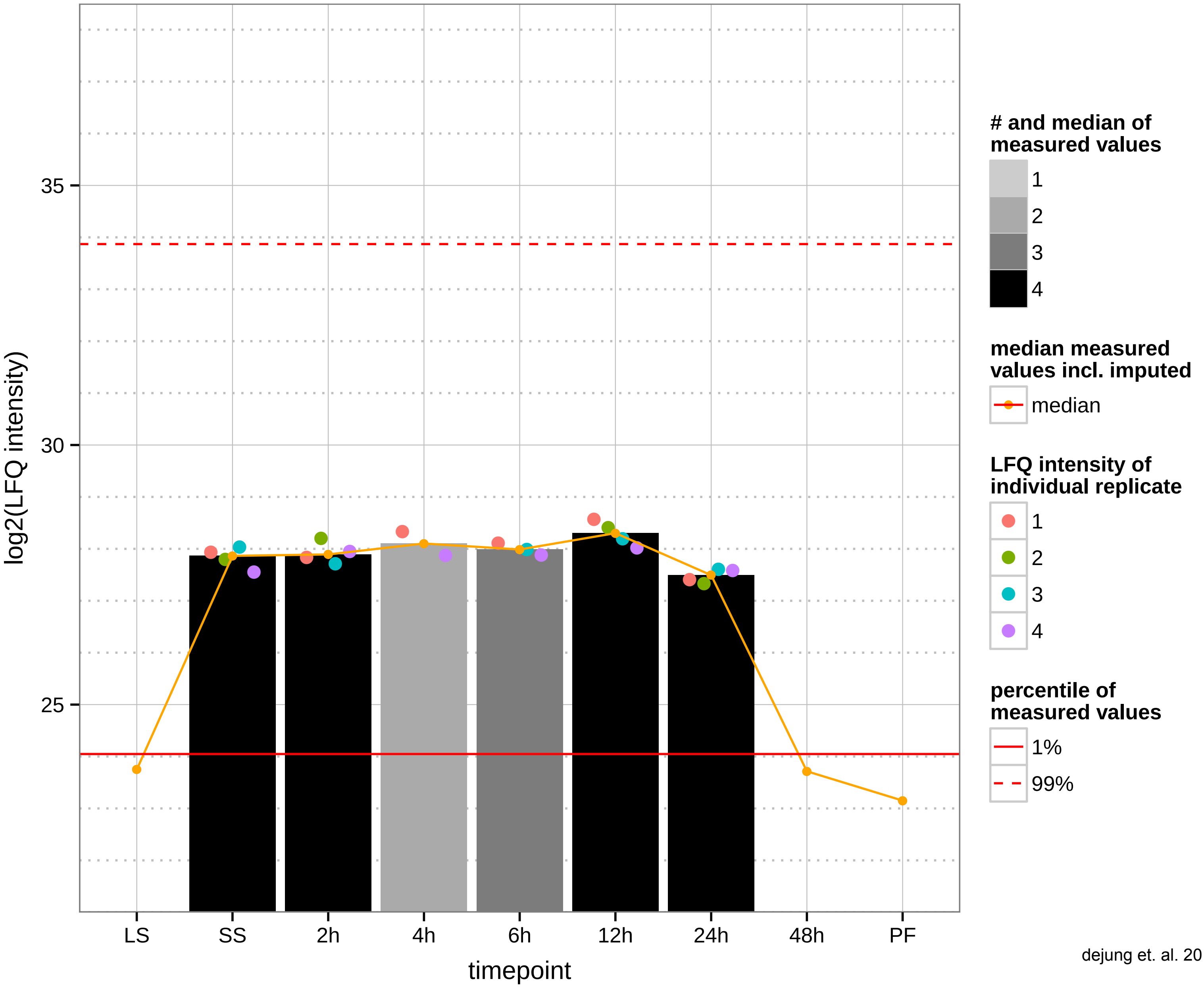
GTPase activating protein, putative
Tb927.9.4370
AGOF: Rab GTPase activator activity, protein kinase activity
AGOC: intracellular
AGOP: regulation of Rab GTPase activity
PGOF: Rab GTPase activator activity
PGOC: intracellular
PGOP: regulation of Rab GTPase activity





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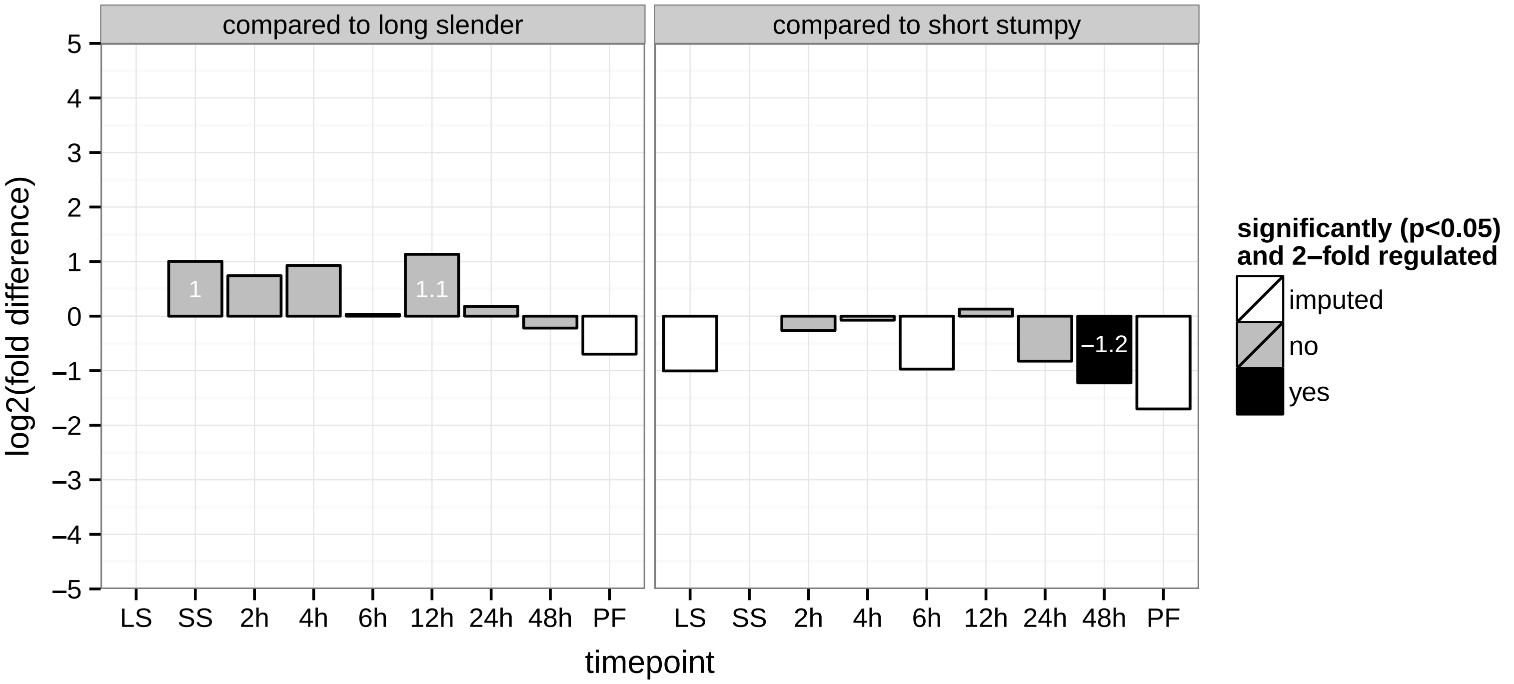
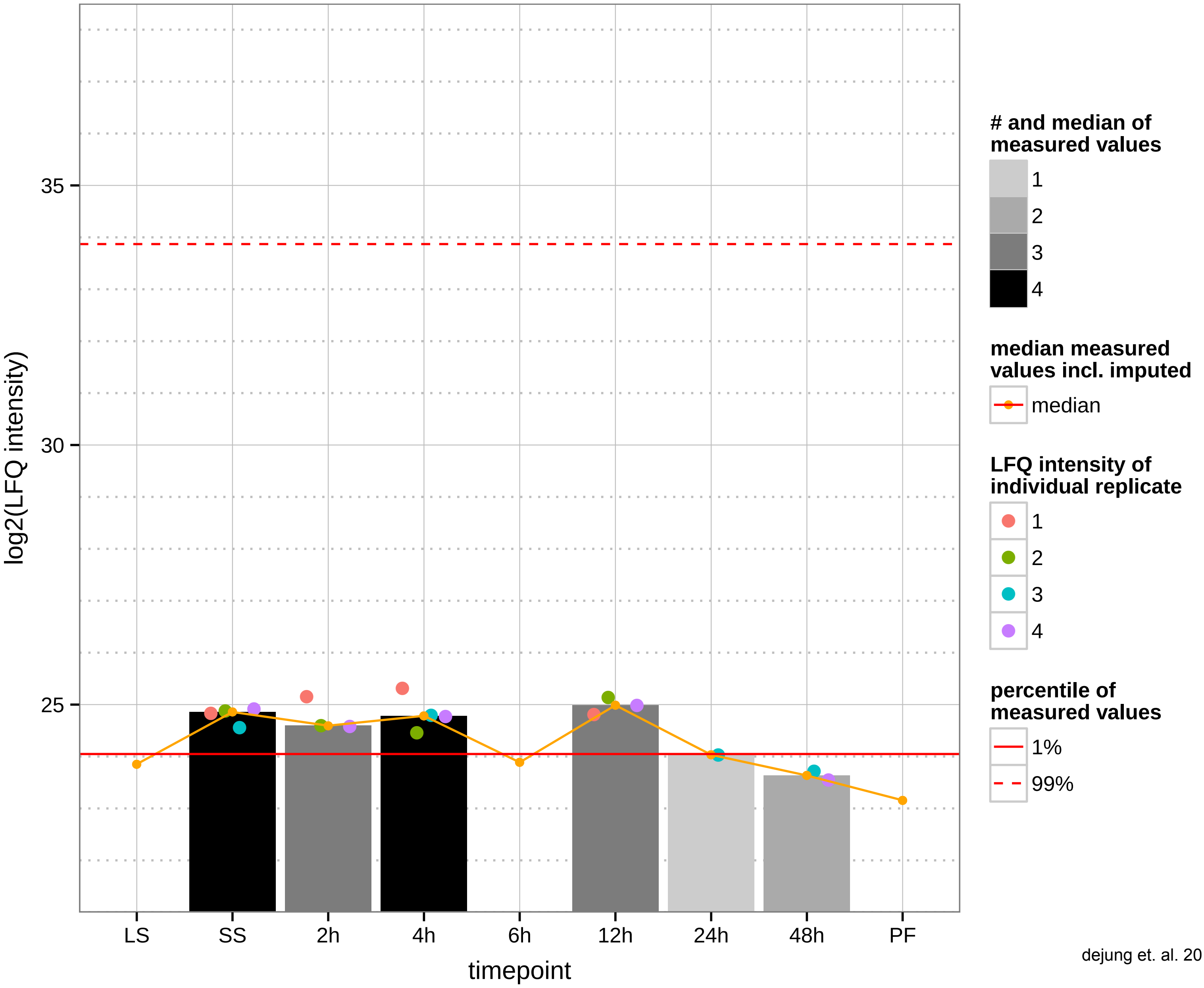
inositol/phosphatidylinositol phosphatase, putative
Tb927.9.5680
AGOF: null
AGOC: intracellular
AGOP: signal transduction
PGOF: null
PGOC: intracellular
PGOP: phosphatidylinositol phosphorylation, signal transduction





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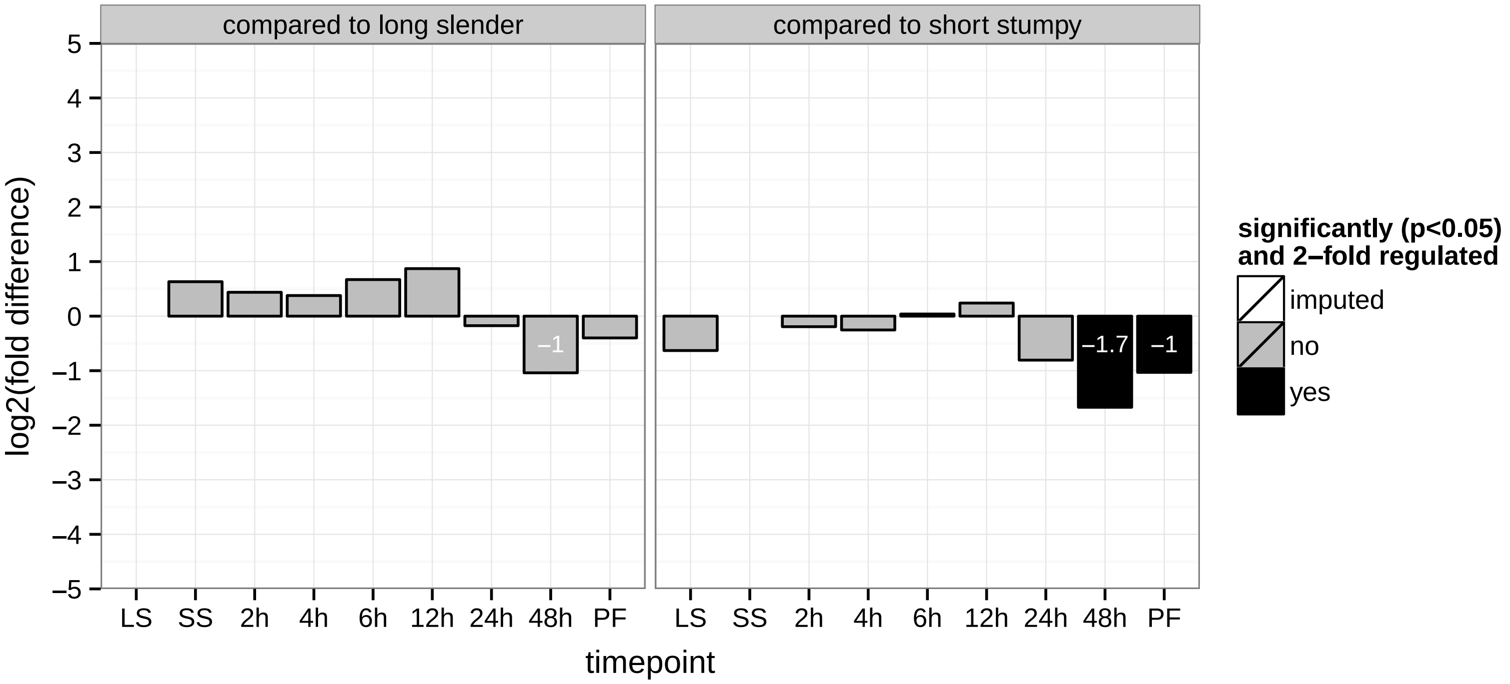
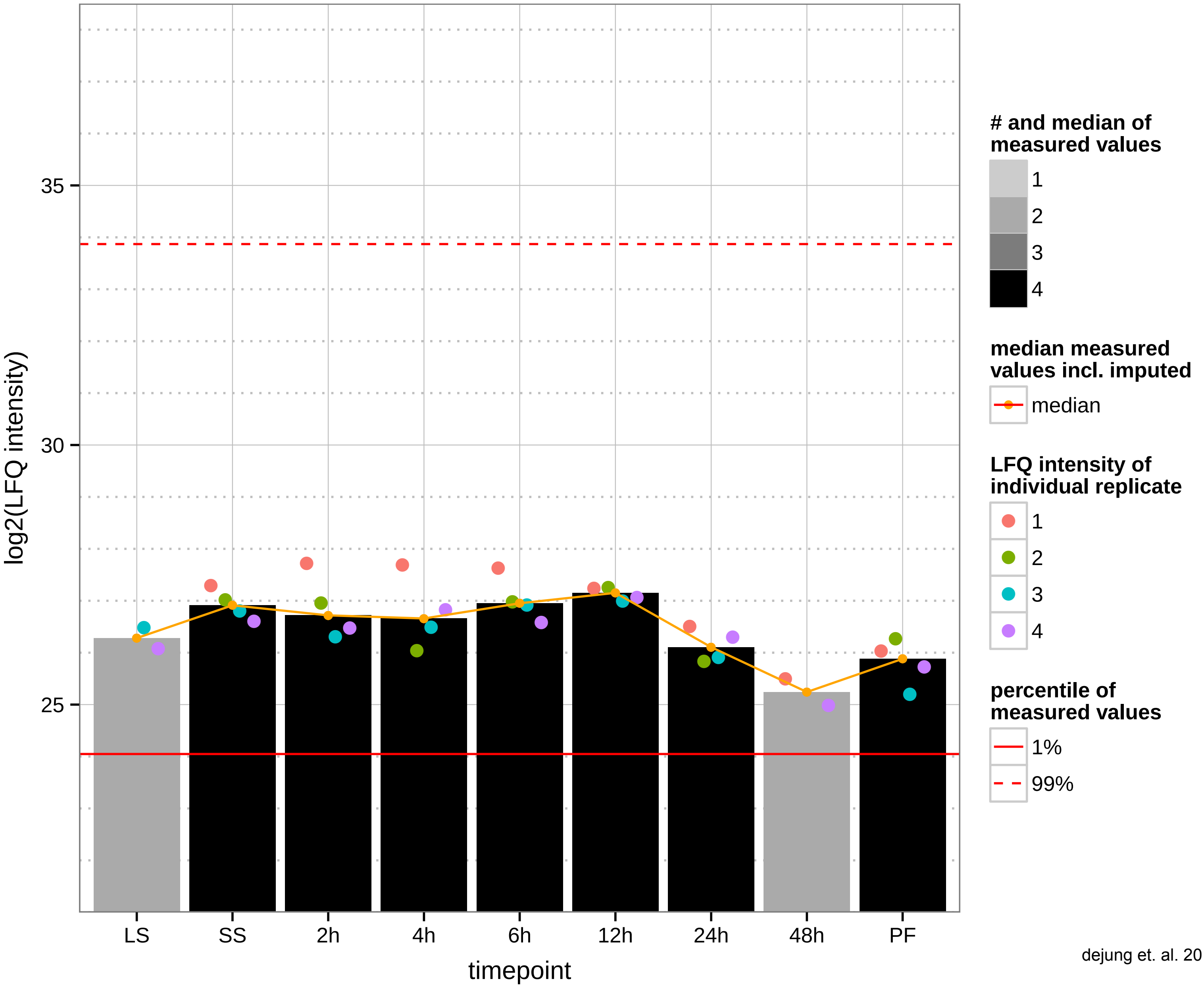
hypothetical protein
Tb927.9.6530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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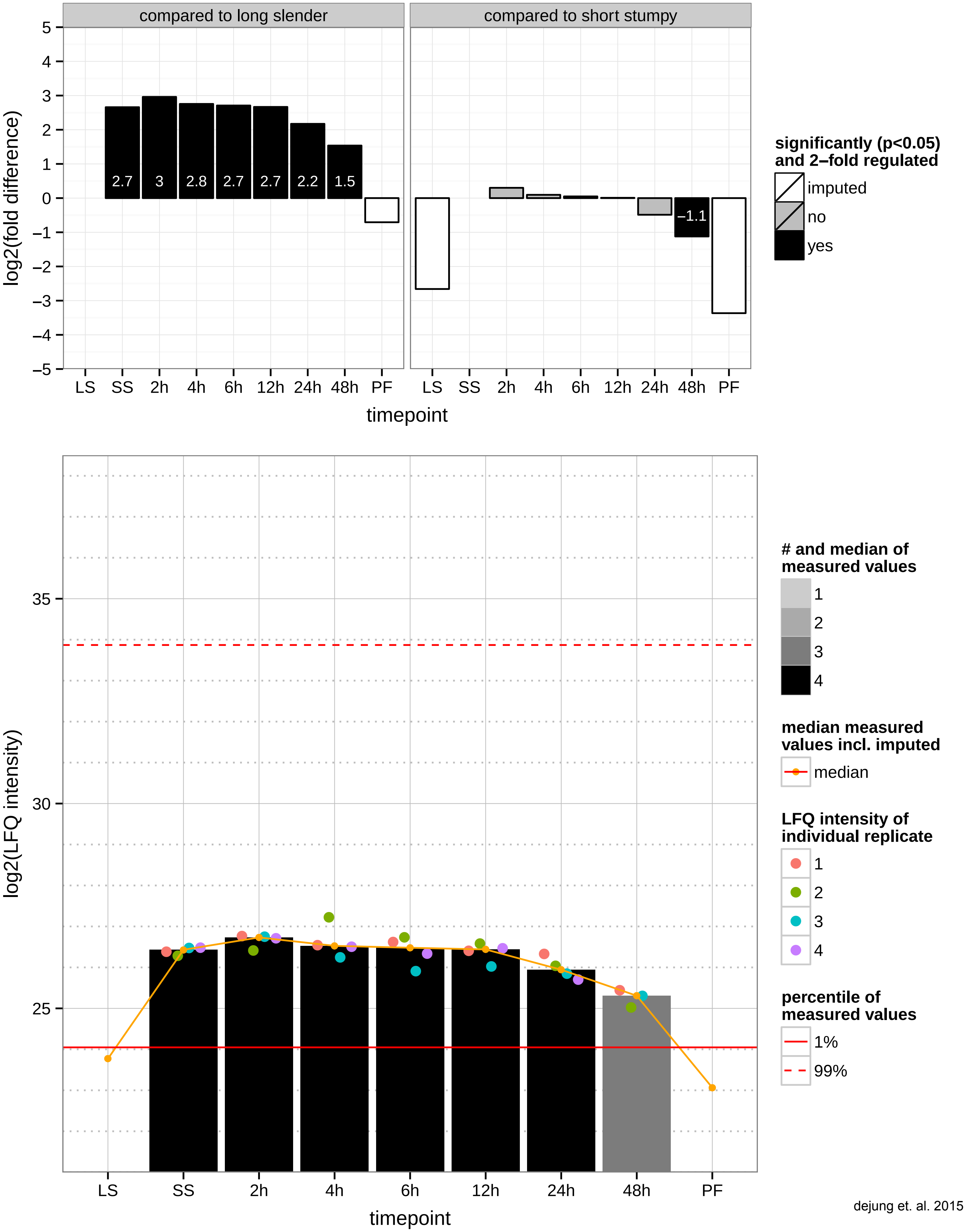
ADP–ribosylation factor–like protein, putative (ARL1B)
Tb927.9.7230
AGOF: GTP binding
AGOC: intracellular
AGOP: intracellular protein transport, small GTPase mediated signal transduction
PGOF: GTP binding
PGOC: intracellular
PGOP: intracellular protein transport, protein transport, small GTPase mediated signal transduction



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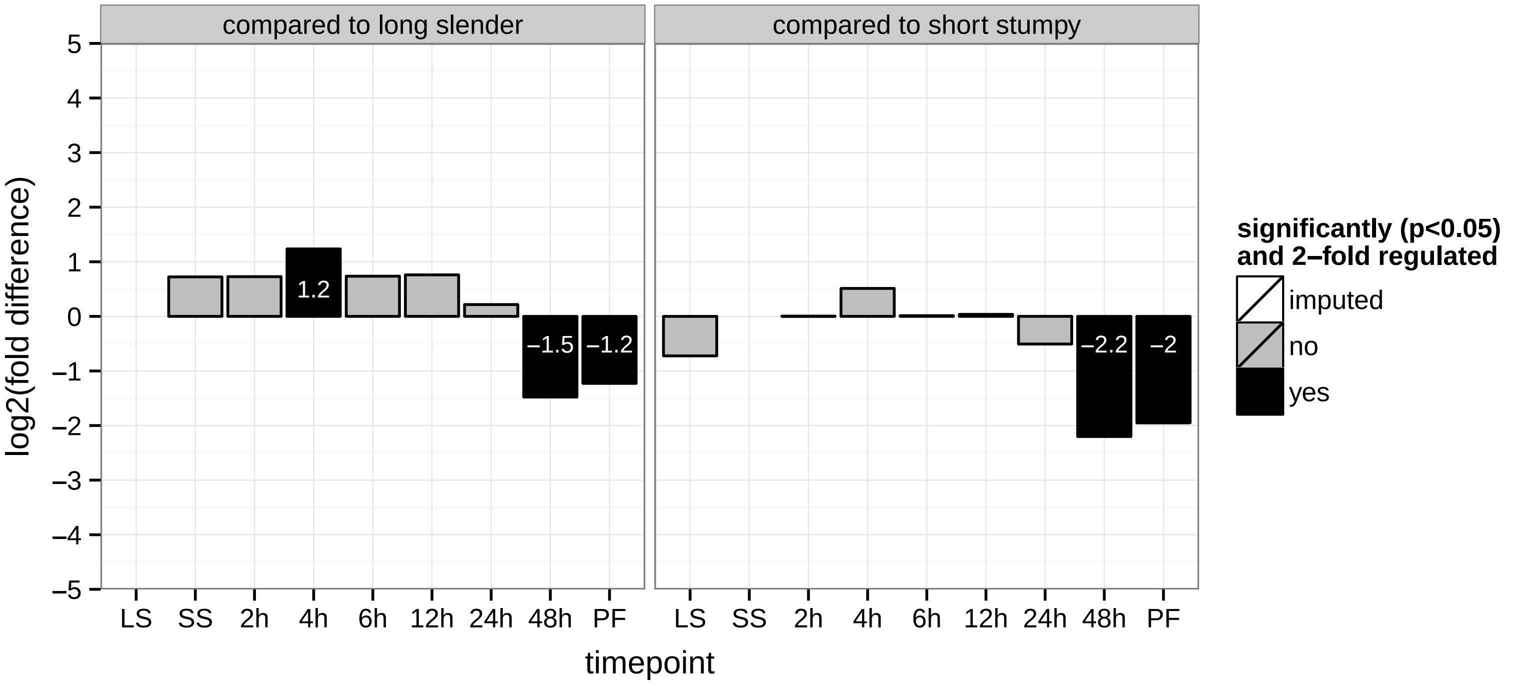
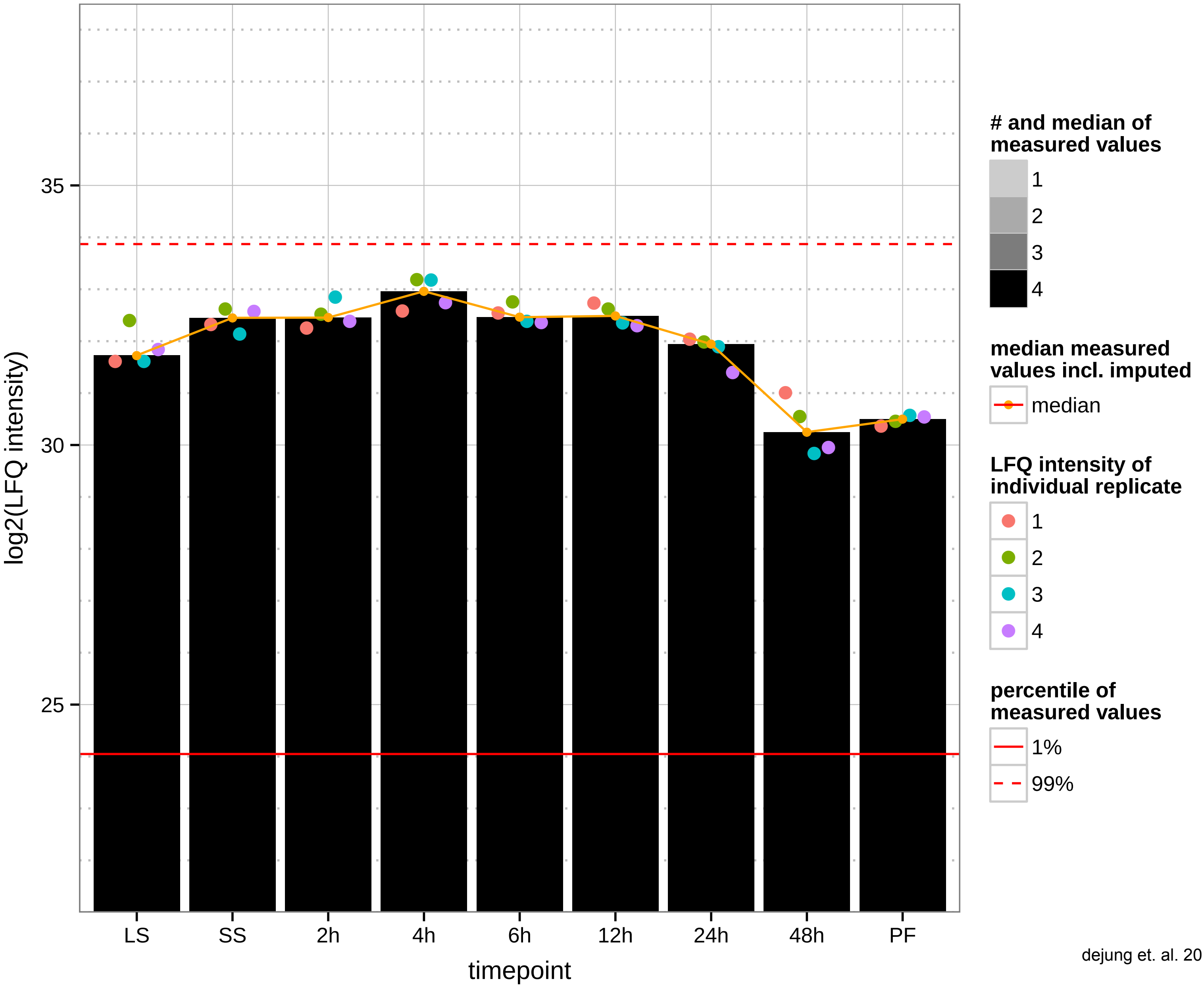
hypothetical protein, conserved
Tb927.9.7520
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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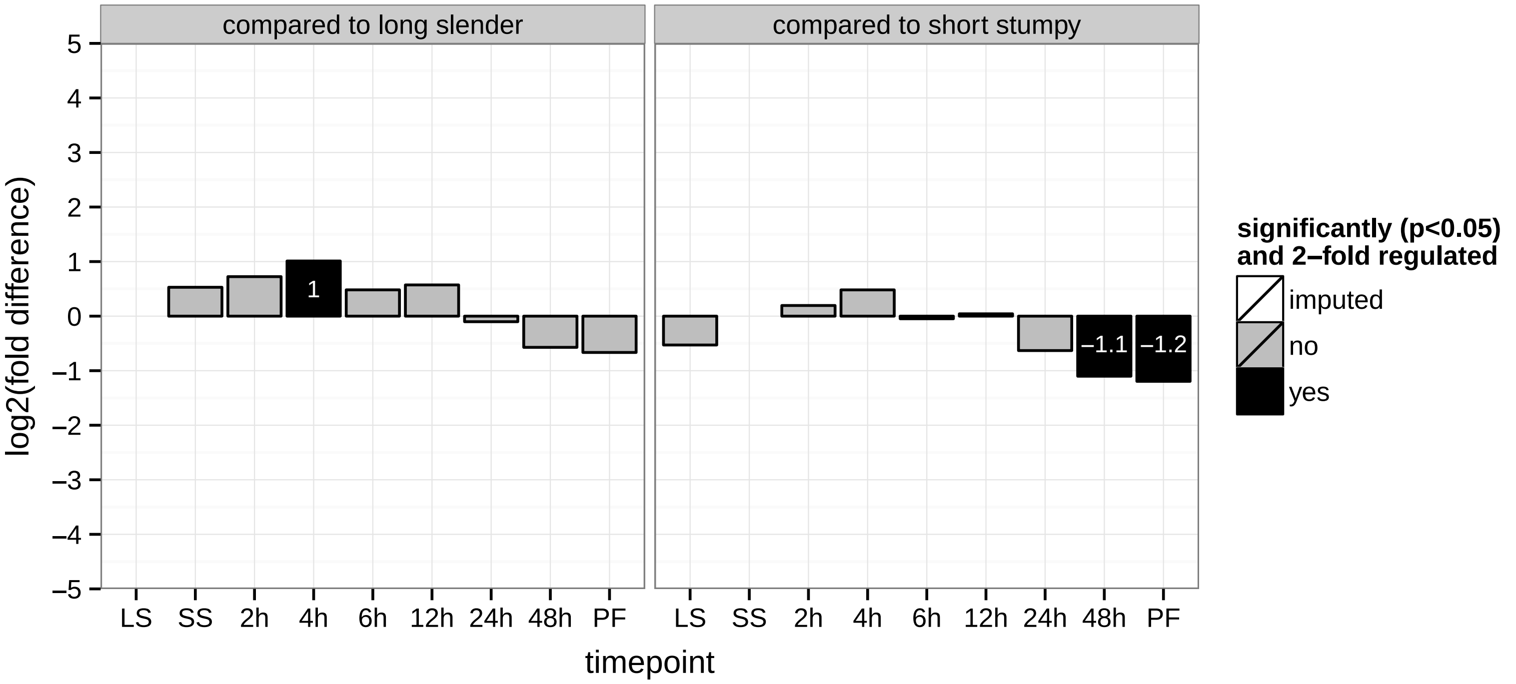
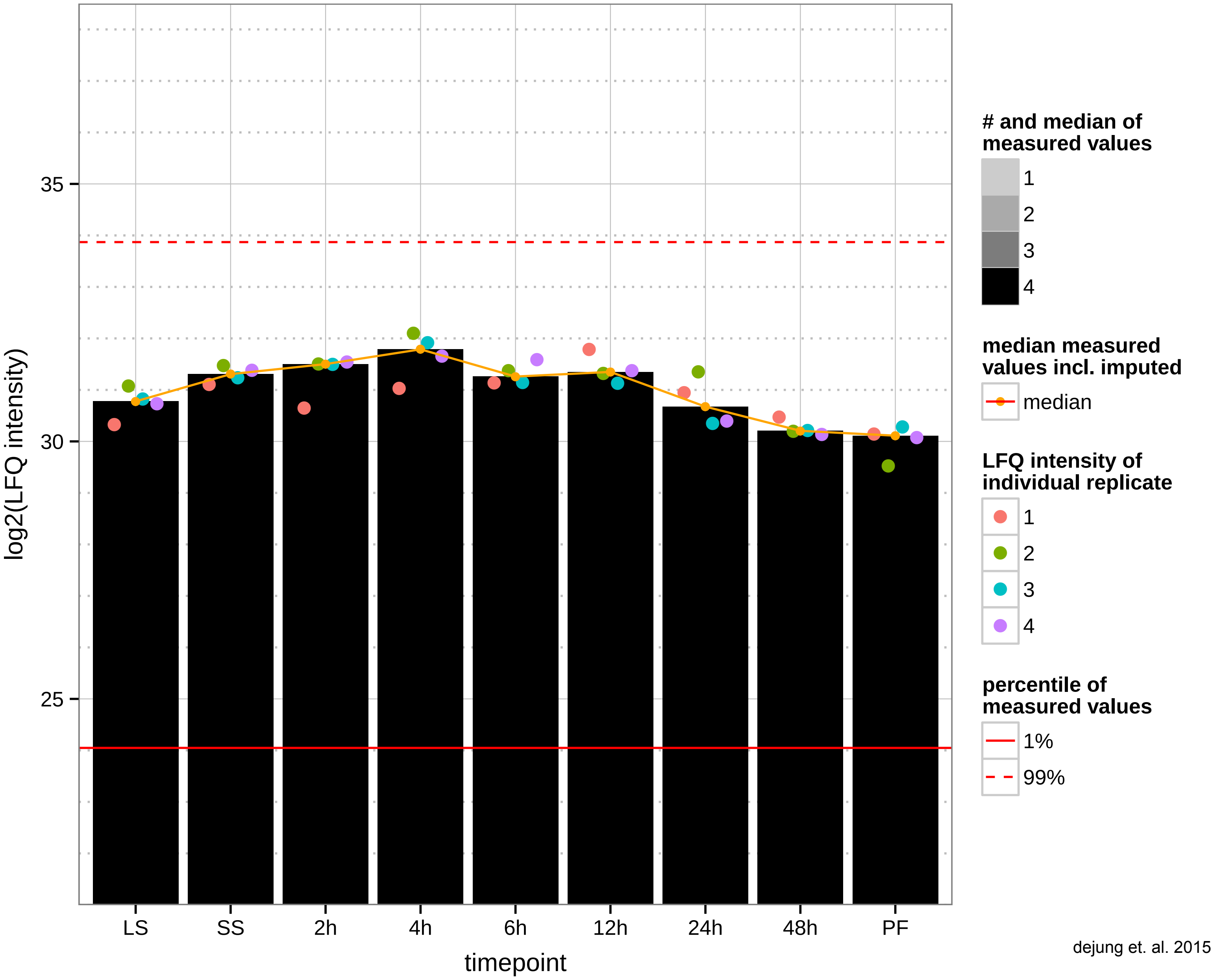
ubiquitin–conjugating enzyme E2, putative, ubiquitin carrier protein, ubiquitin–protein ligase
Tb927.9.8000
AGOF: ubiquitin–protein ligase activity
AGOC: null
AGOP: cellular protein modification process, post–translational protein modification, regulation of protein metabolic process
PGOF: acid–amino acid ligase activity
PGOC: null
PGOP: null





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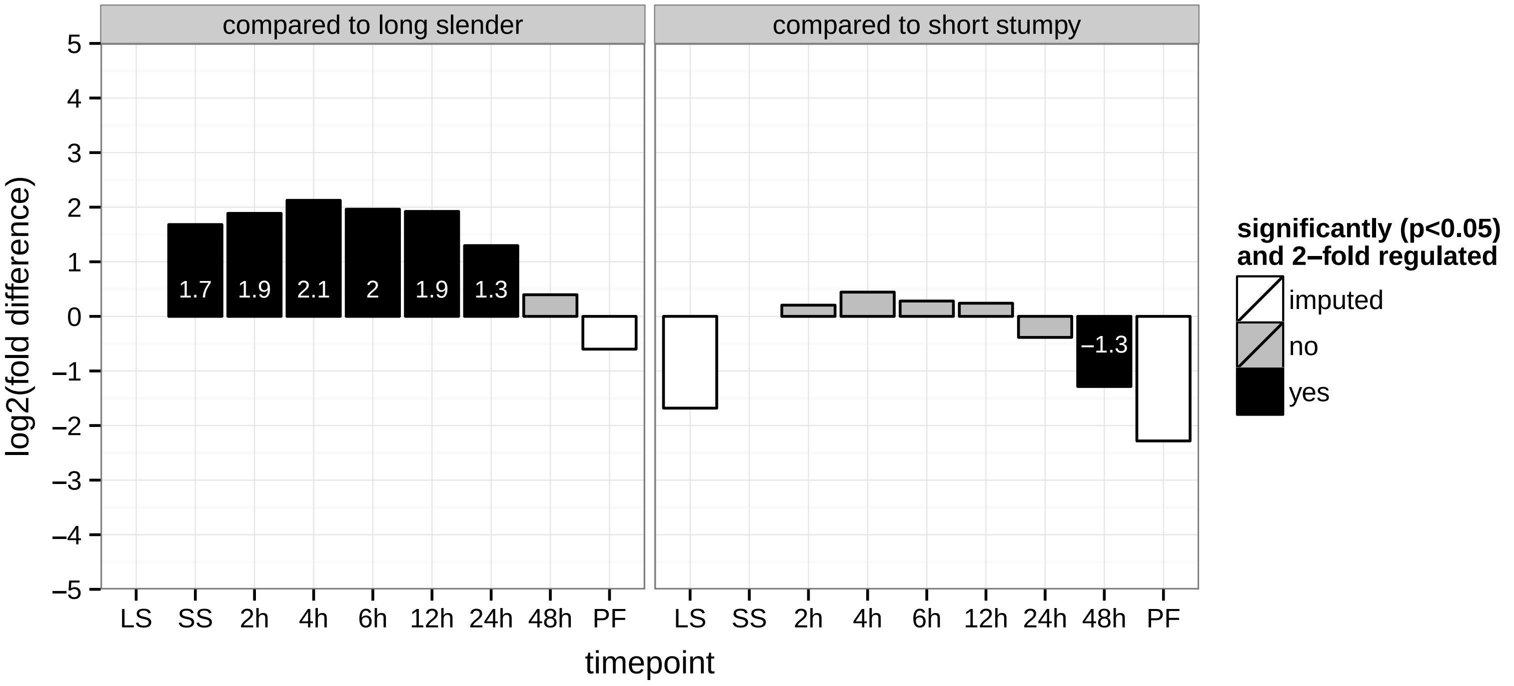
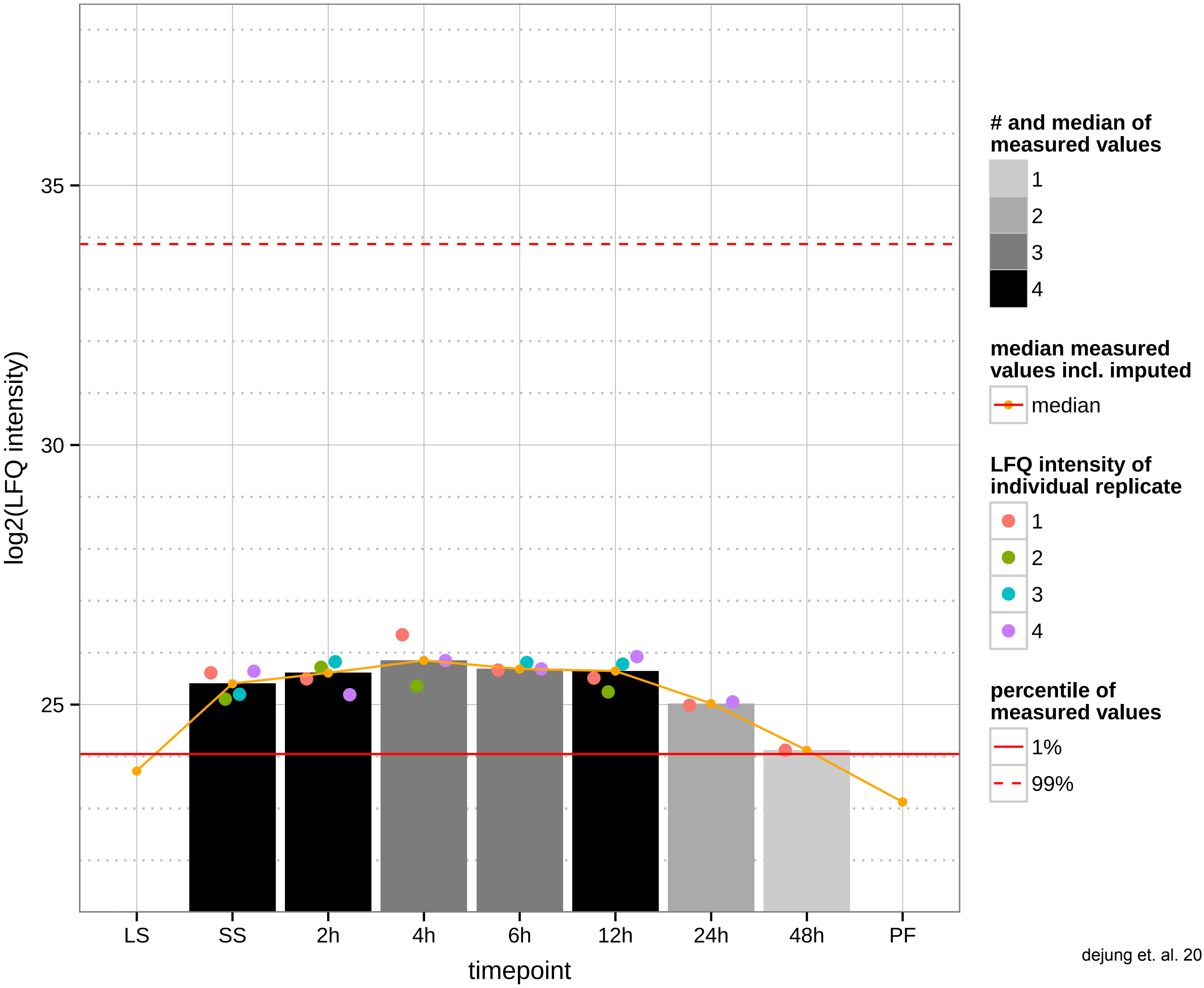
hypothetical protein, conserved
Tb927.9.8060
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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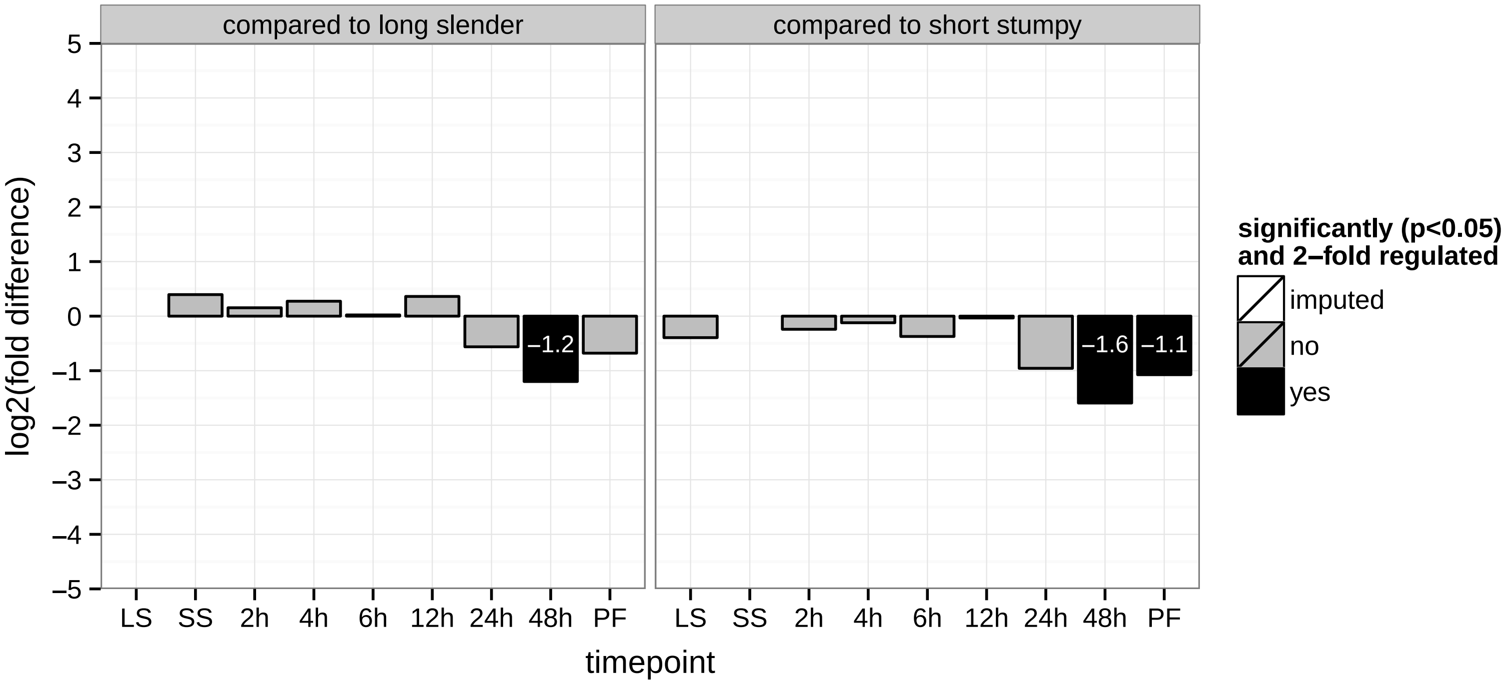
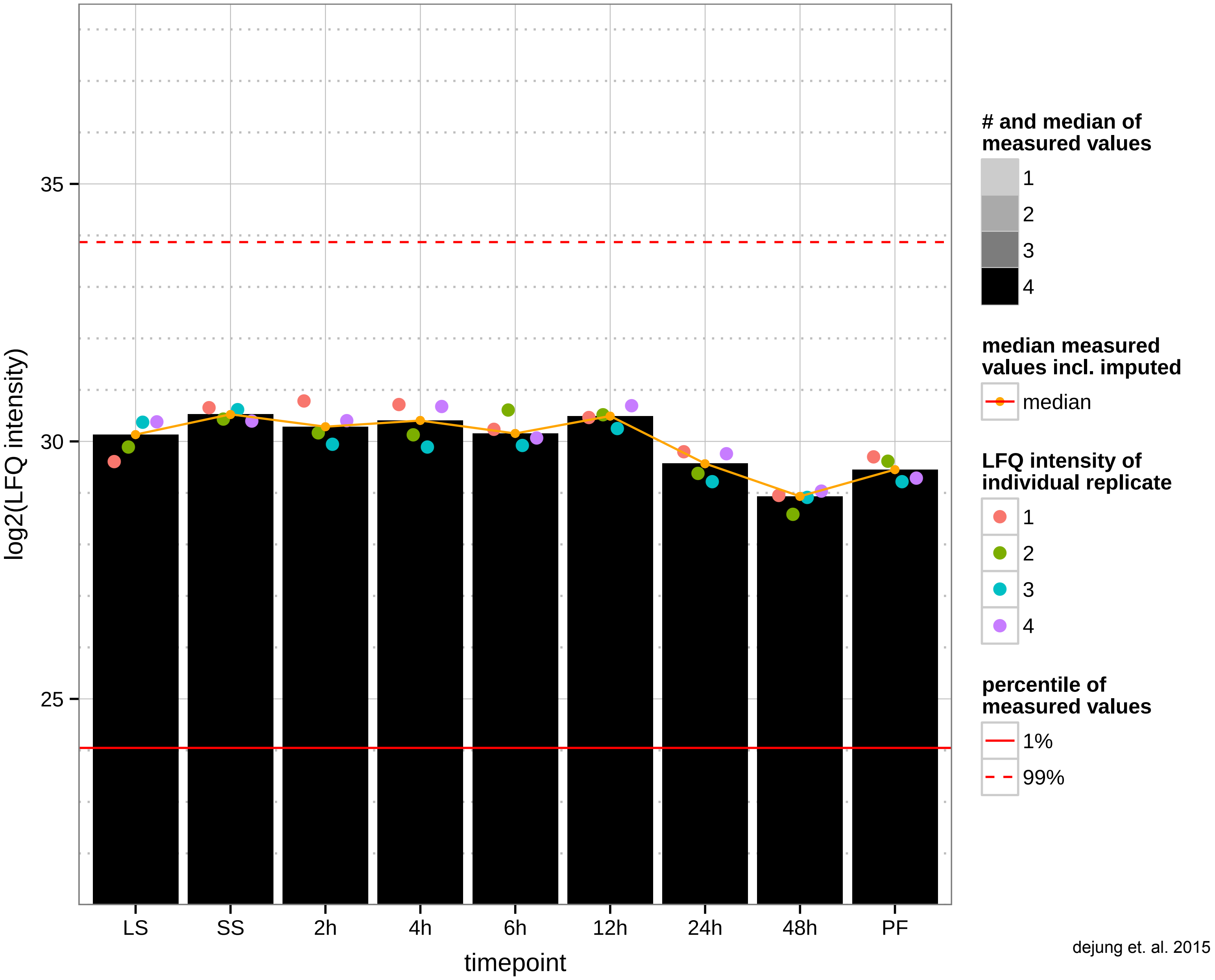
fructose–1, 6–bisphosphatase (FBPase)
Tb927.9.8720
AGOF: fructose 1, 6–bisphosphate 1–phosphatase activity
AGOC: null
AGOP: carbohydrate metabolic process
PGOF: phosphoric ester hydrolase activity
PGOC: null
PGOP: carbohydrate metabolic process





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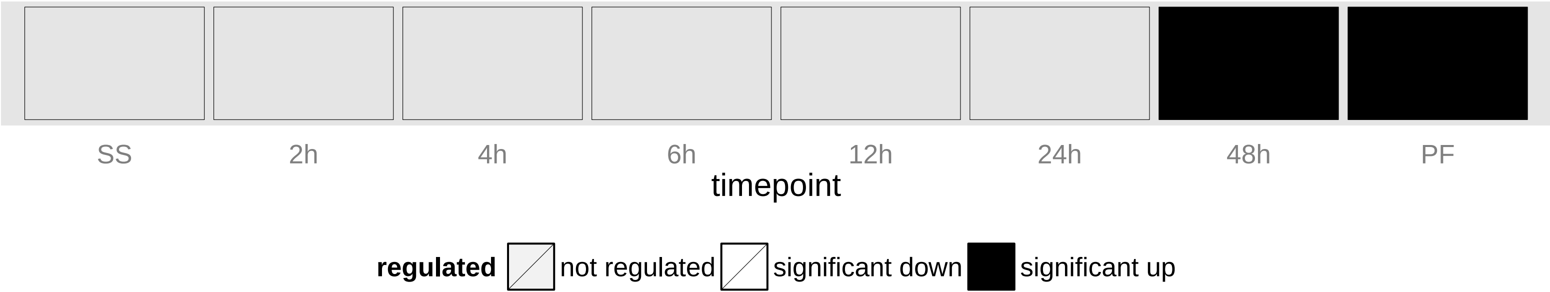

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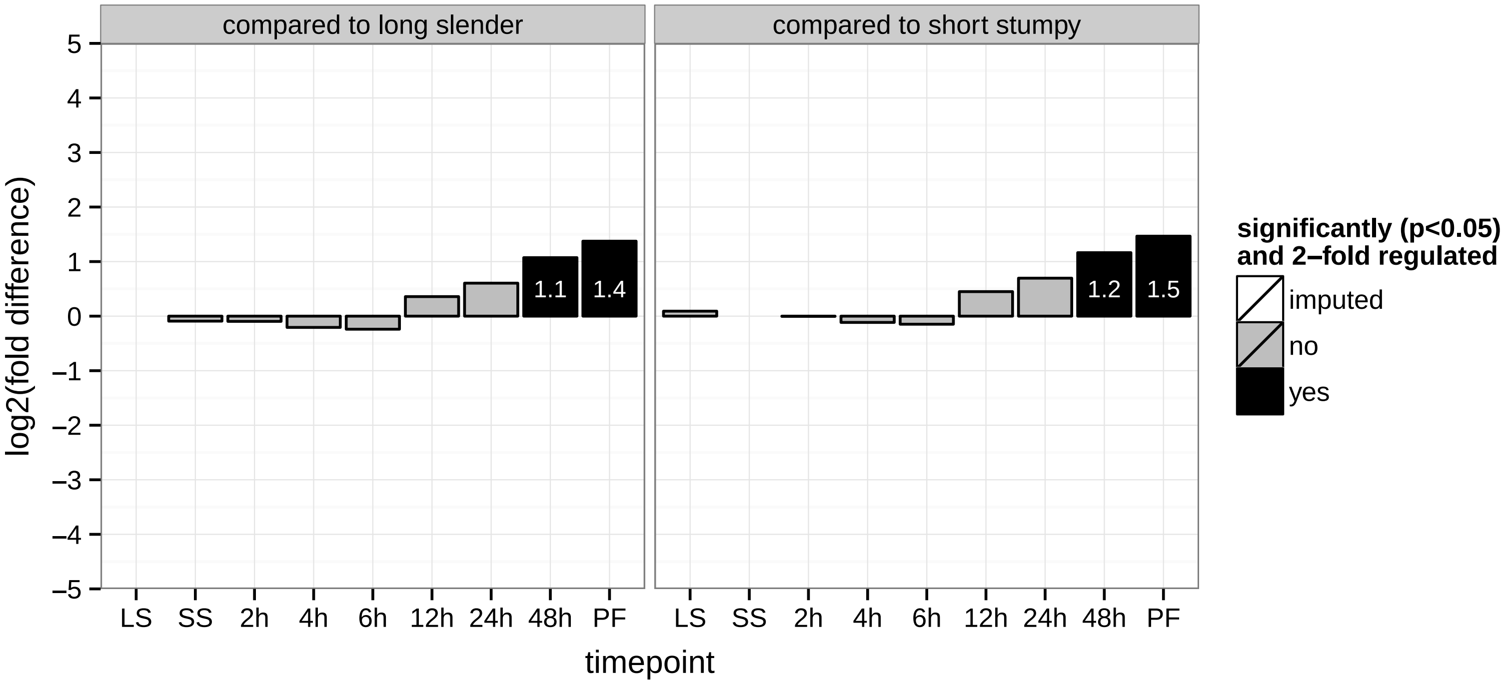
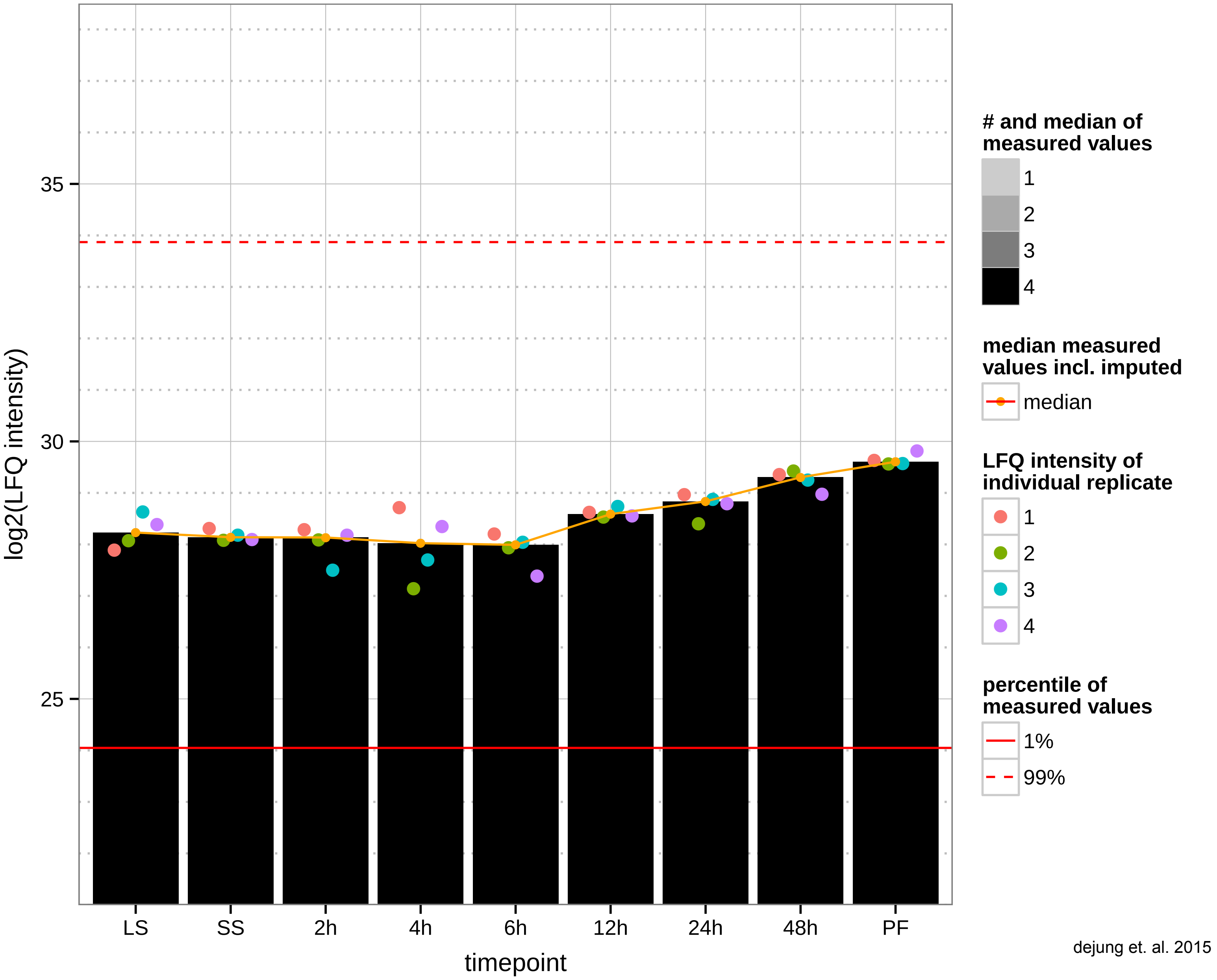
serine/threonine protein phosphatase, putative, BAC from homologous region on chr5, kinetoplastid−specific phospho−protei
Tb927.5.4380;Tb05.5K5.30
AGOF: hydrolase activity, protein serine/threonine phosphatase activity
AGOC: null
AGOP: null, protein dephosphorylation
PGOF: hydrolase activity
PGOC: null
PGOP: null





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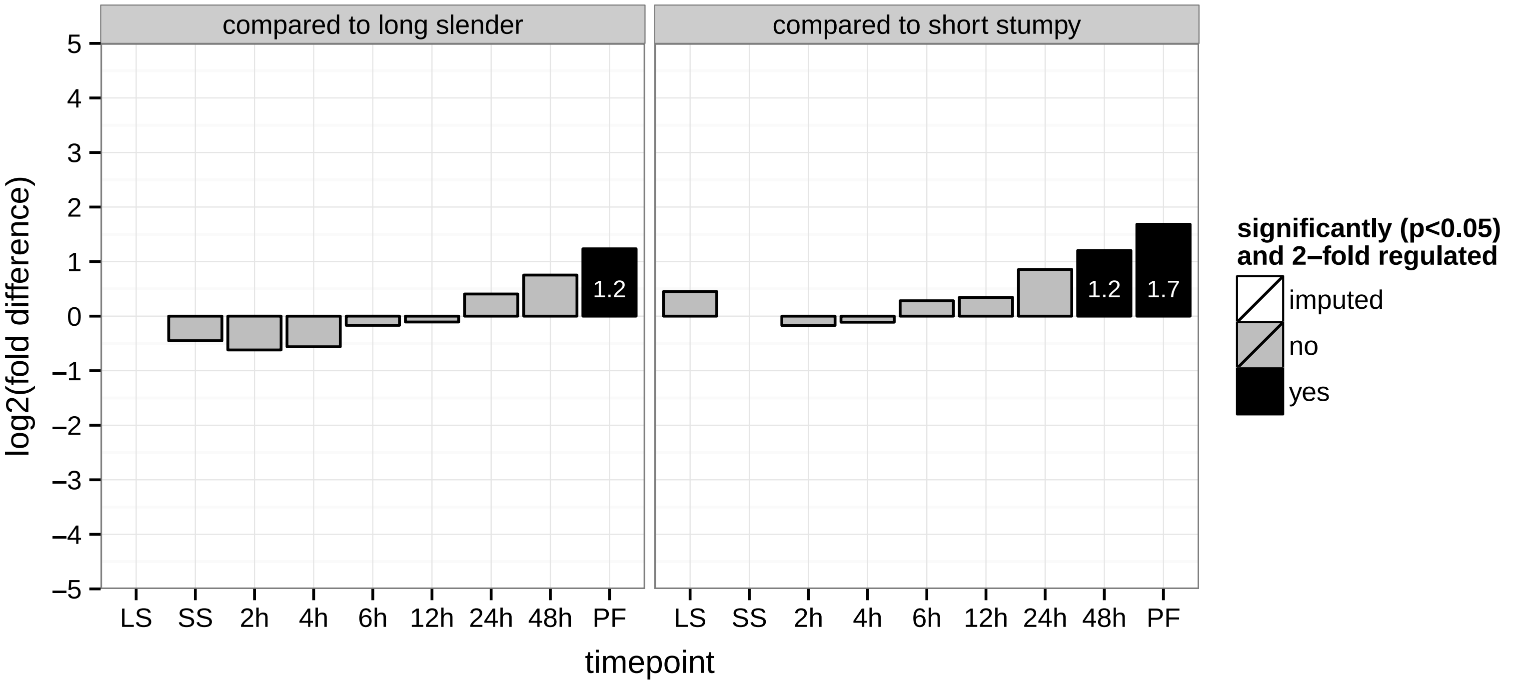
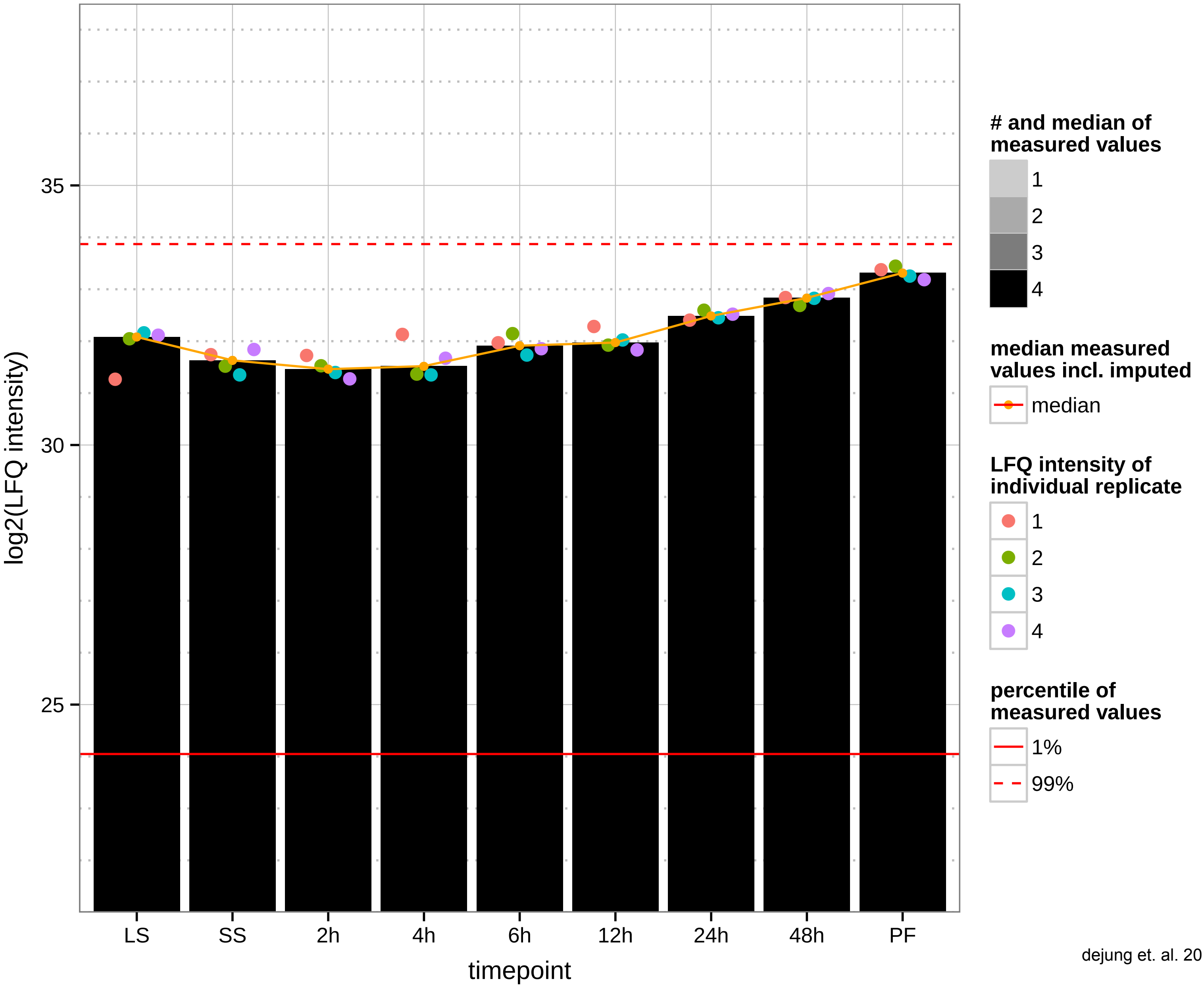
60S ribosomal protein L21e, putative, chrXI additional, unordered contigs, ribosomal protein L21E (60S)
Tb927.4.1100;Tb927.11.680;Tb11.0880
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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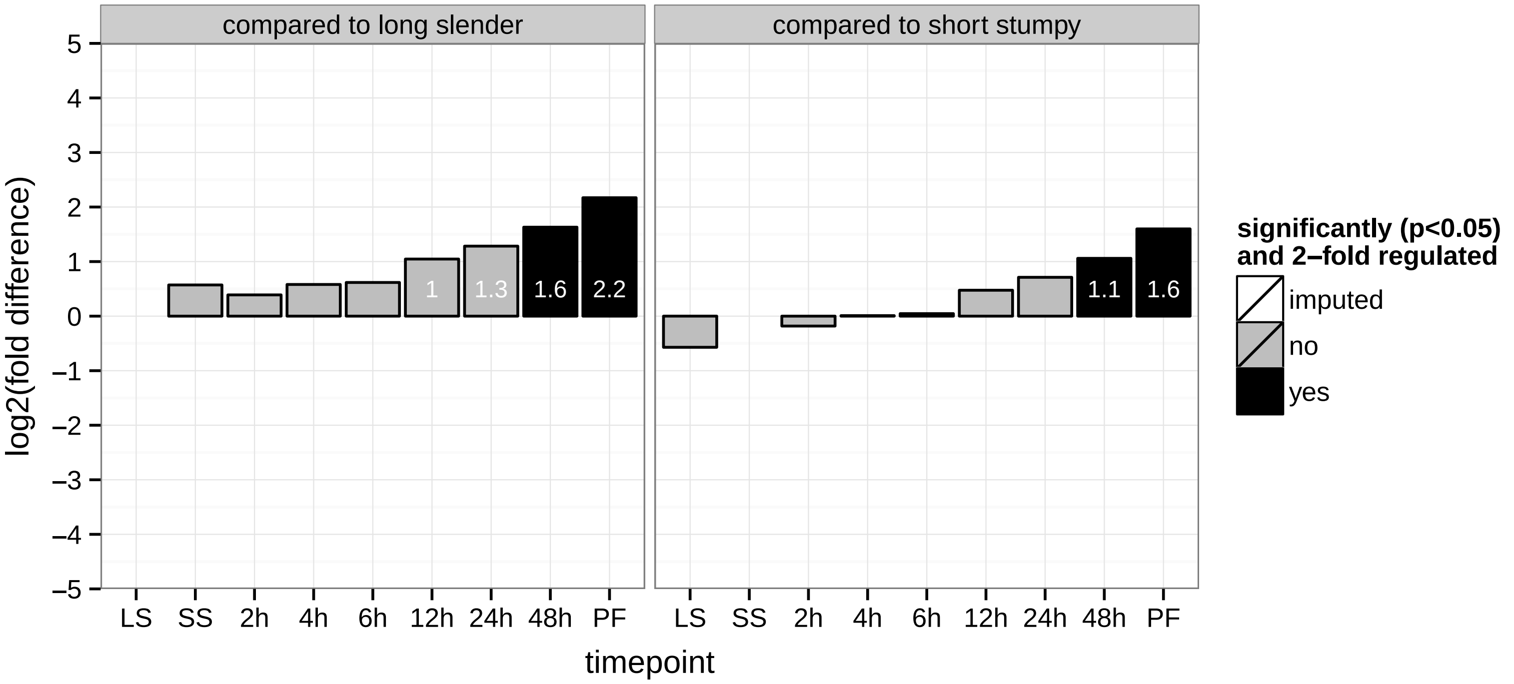
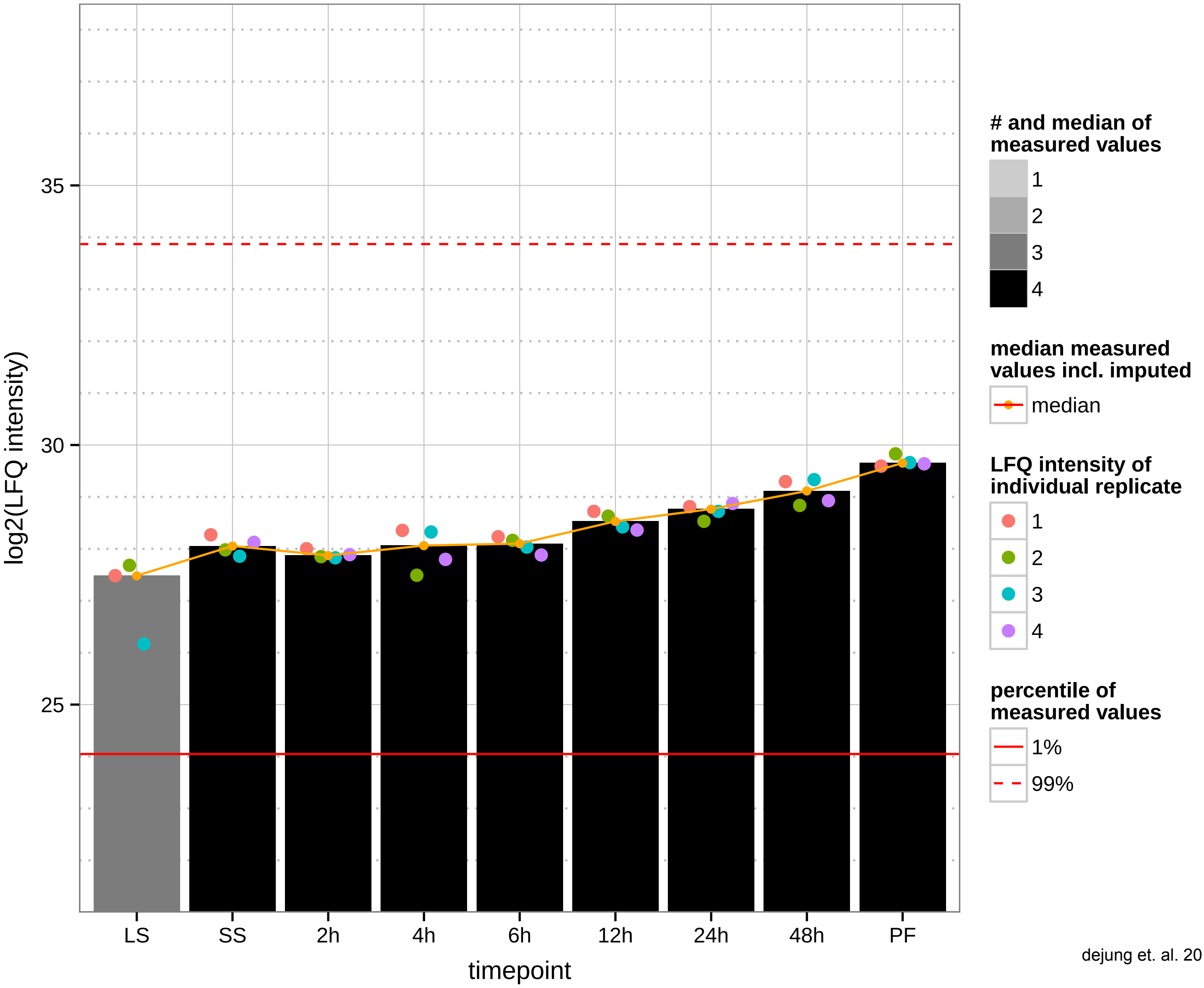
hypothetical protein, chrXI additional, unordered contigs, methionine aminopeptidase, putative, metallo– peptidase, Clan MG,
Tb927.10.15270;Tb11.v5.0998;Tb11.1240
AGOF: aminopeptidase activity, metalloexopeptidase activity, null
AGOC: null
AGOP: cellular process, proteolysis, null
PGOF: aminopeptidase activity, metalloexopeptidase activity, zinc ion binding
PGOC: null
PGOP: cellular process, proteolysis





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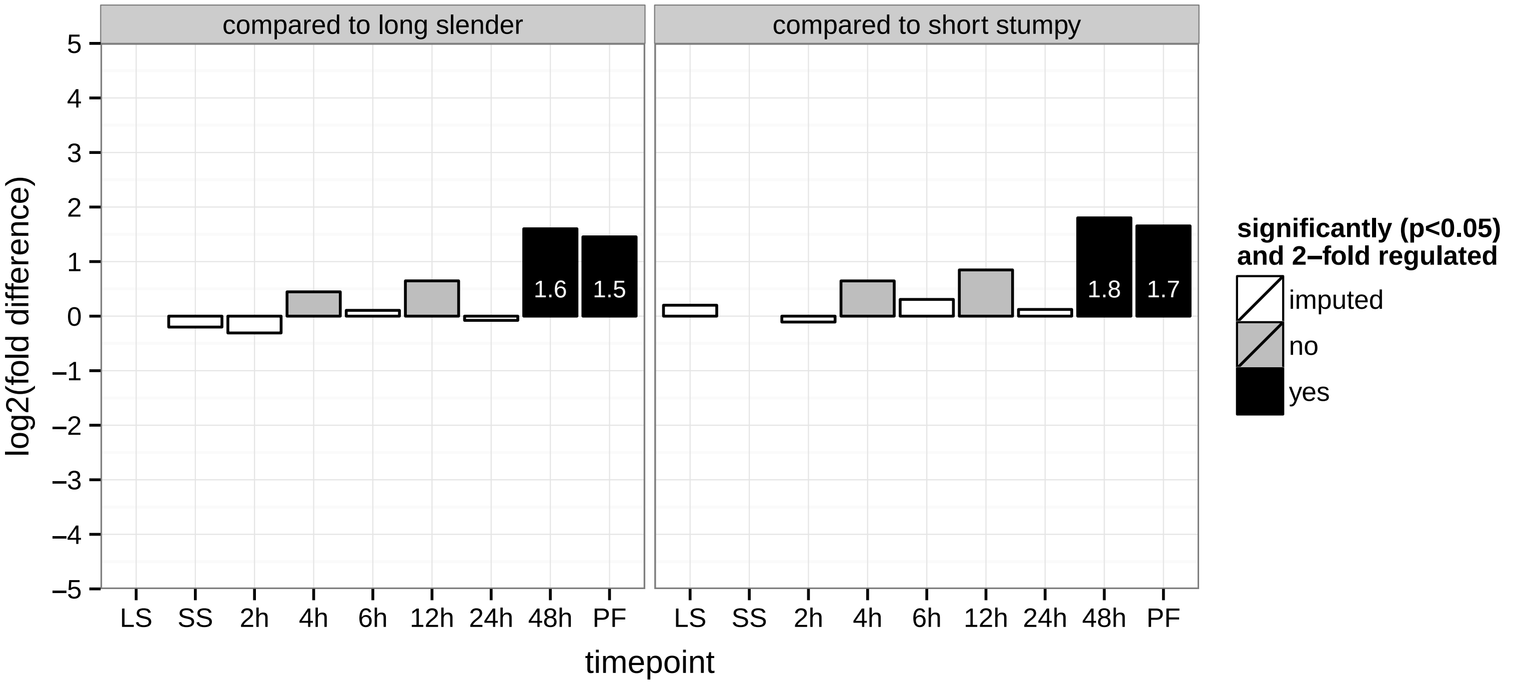
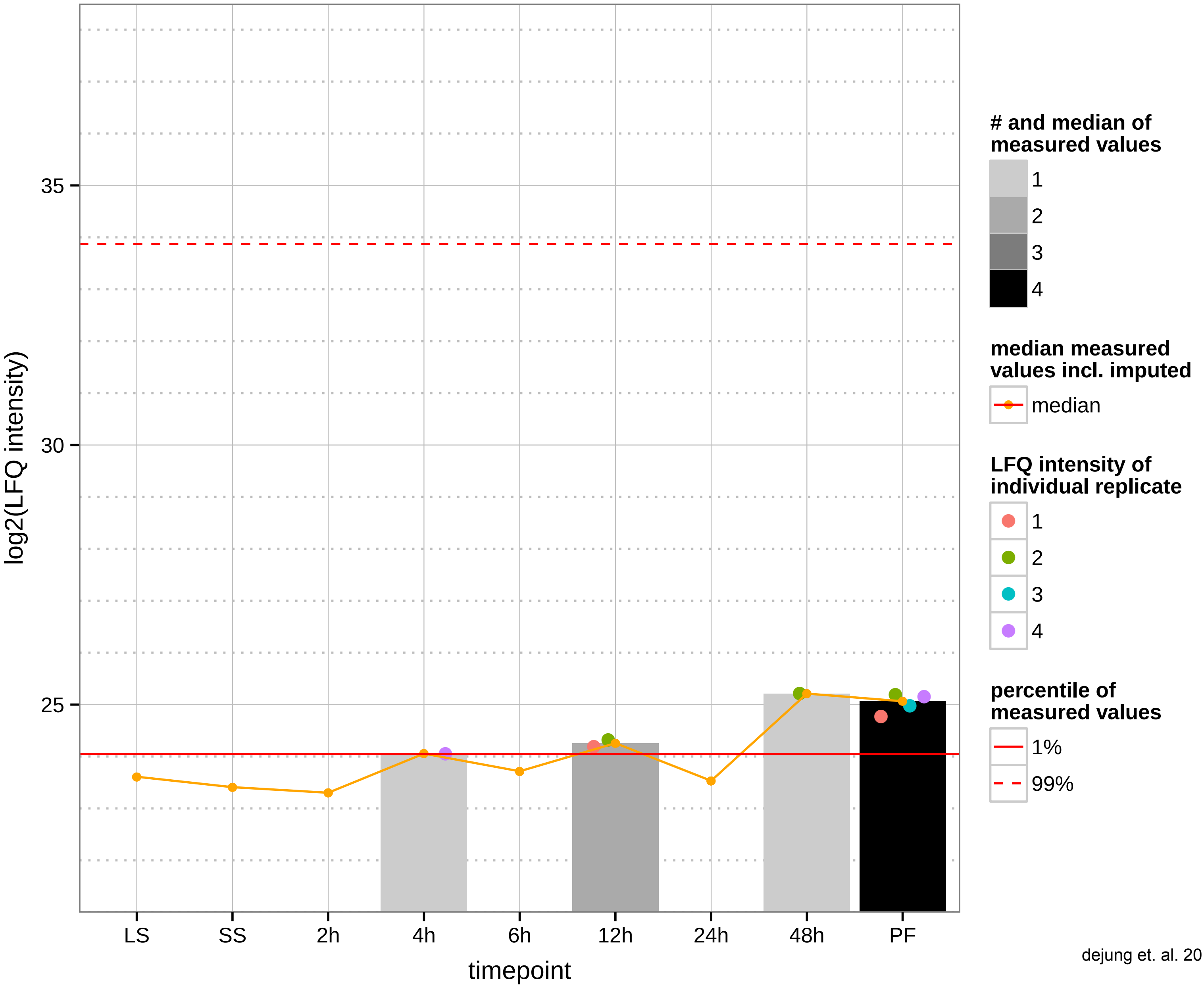
hypothetical protein, conserved
Tb927.7.4890;Tb11.v5.0170
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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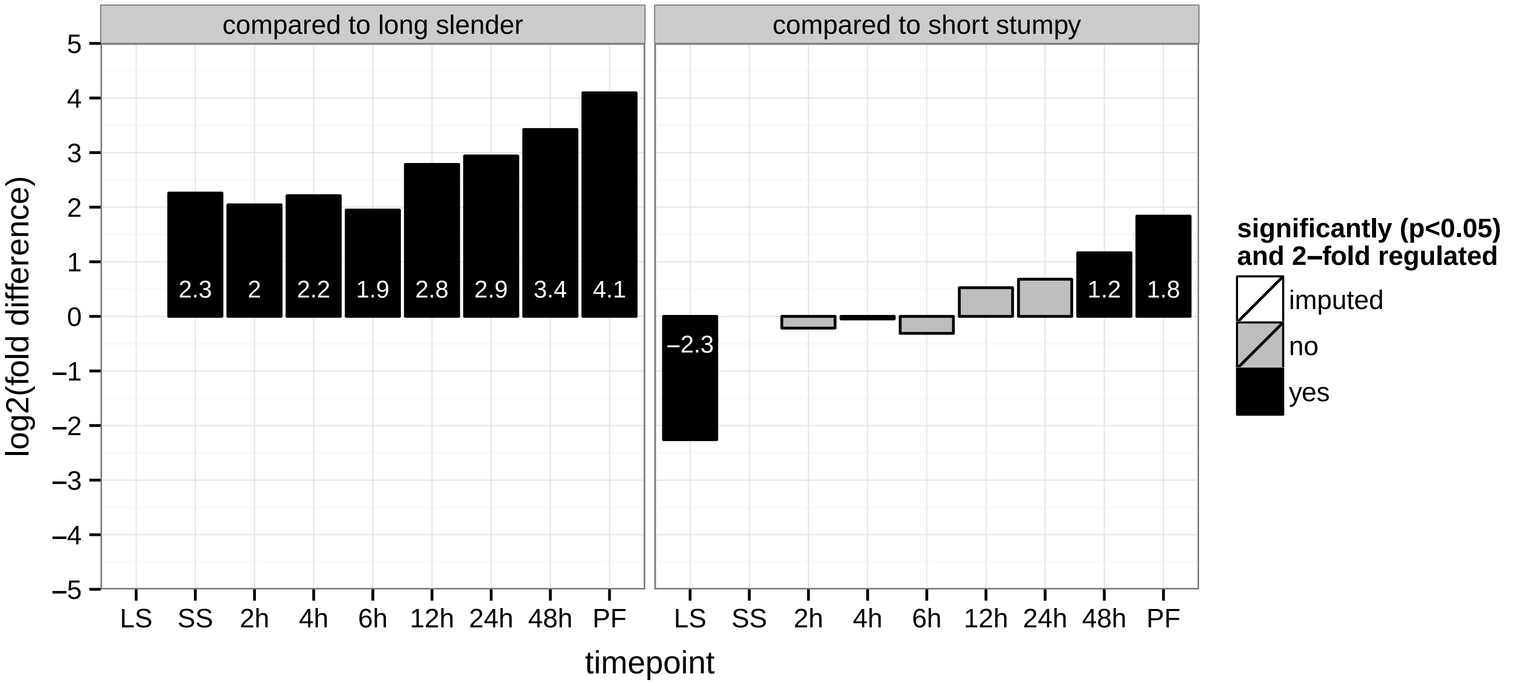
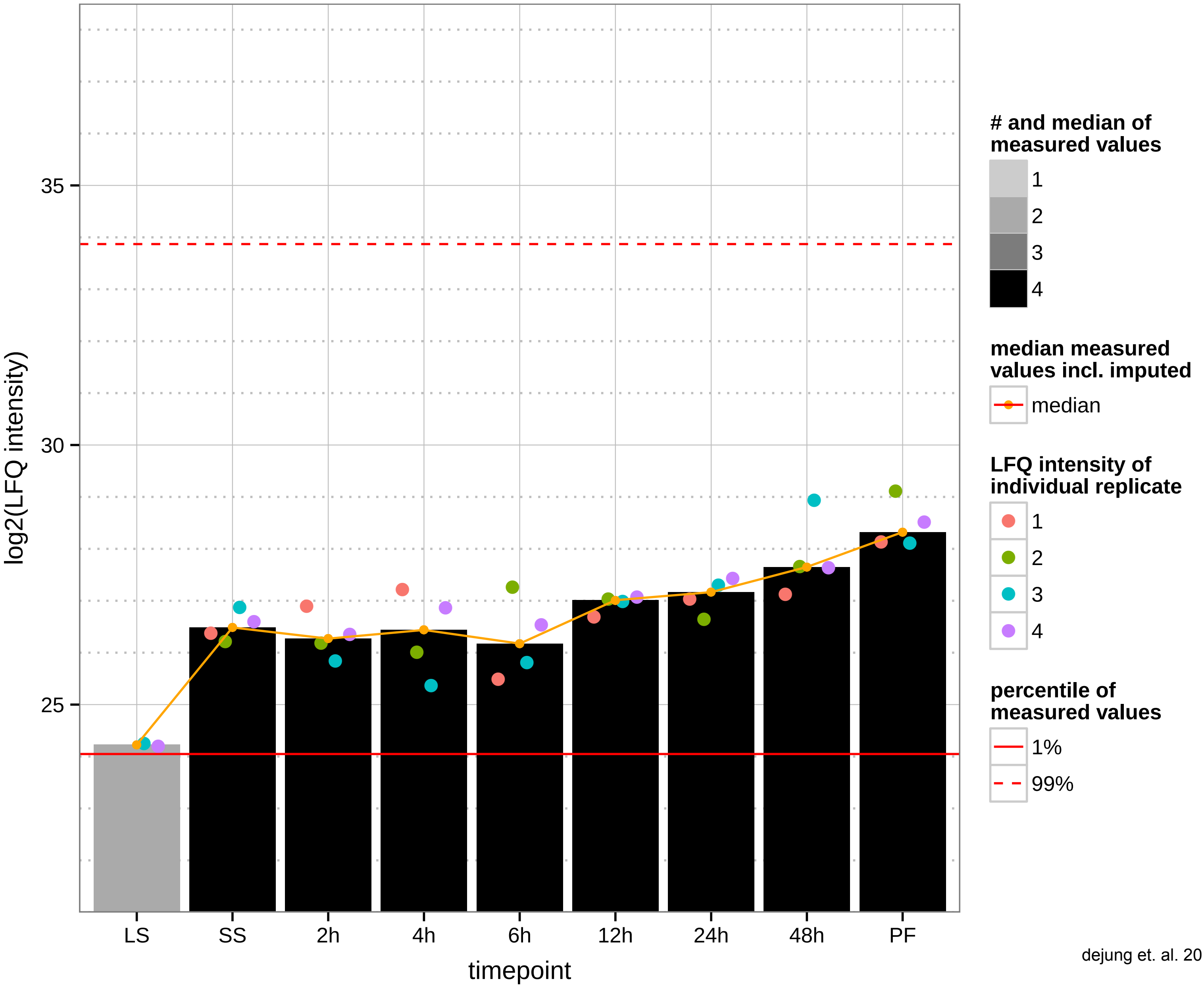
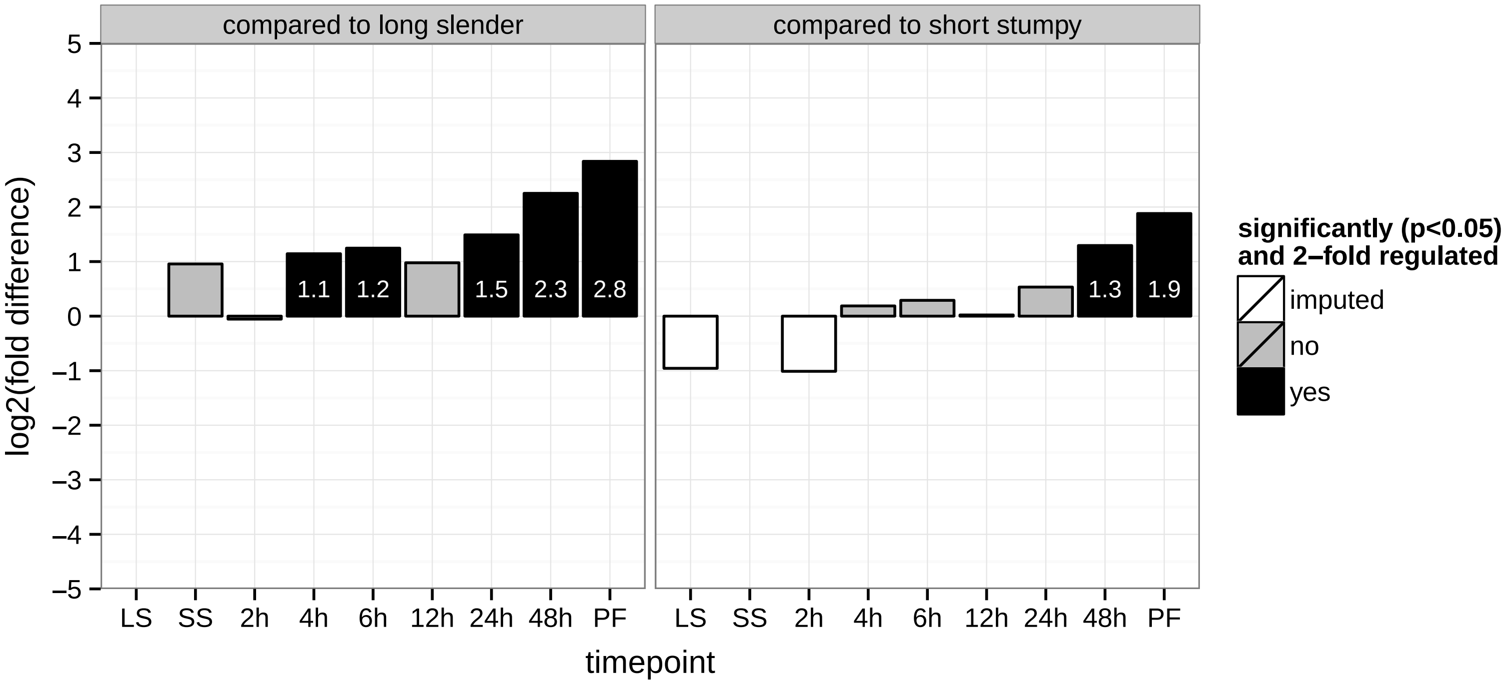
pantothenate kinase subunit, putative
Tb927.11.7290;Tb11.v5.0254
AGOF: null, ATP binding, pantothenate kinase activity
AGOC: null
AGOP: null, coenzyme A biosynthetic process
PGOF: ATP binding, catalytic activity, pantothenate kinase activity
PGOC: null
PGOP: coenzyme A biosynthetic process, metabolic process

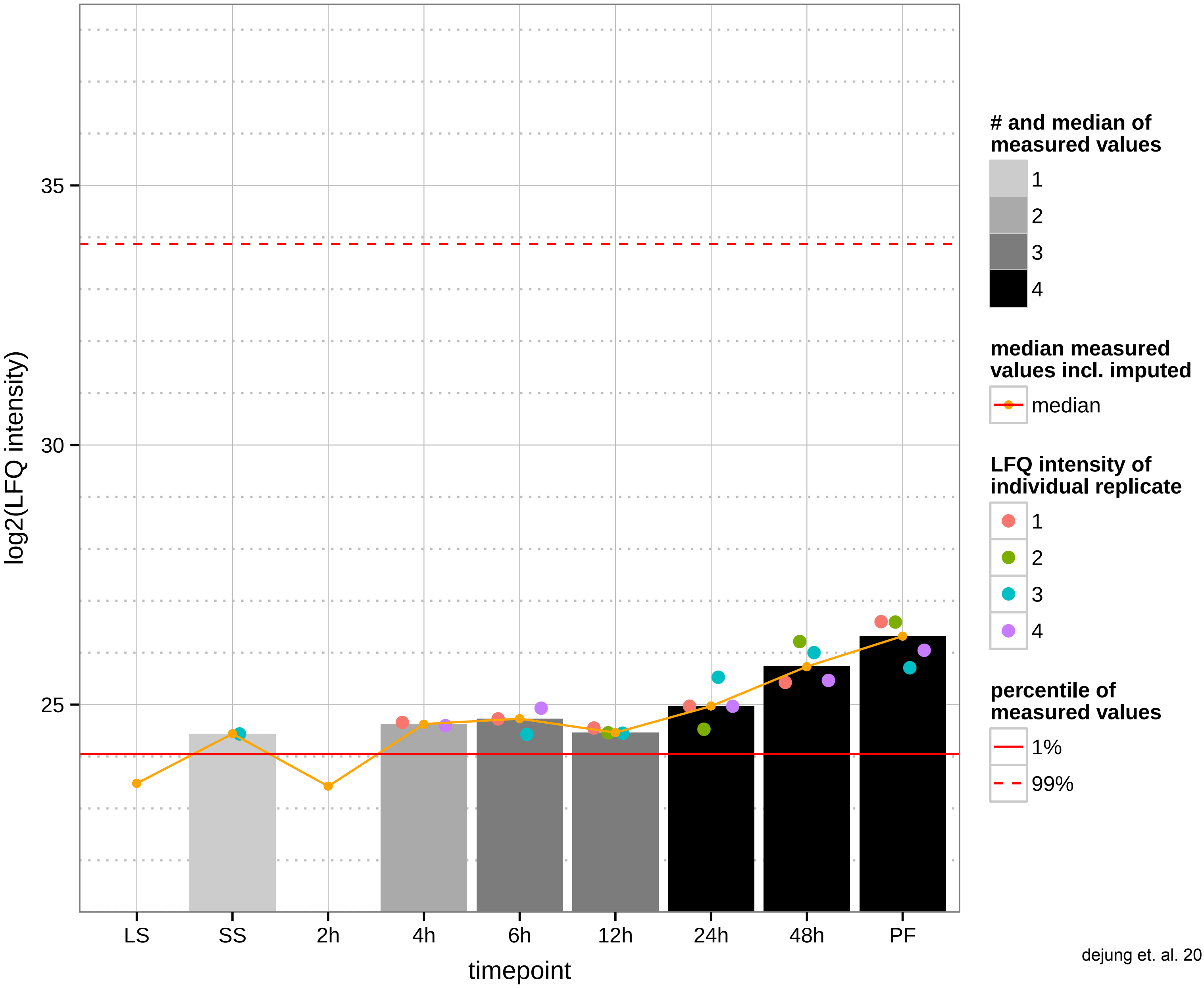




dejung et. al. 2015

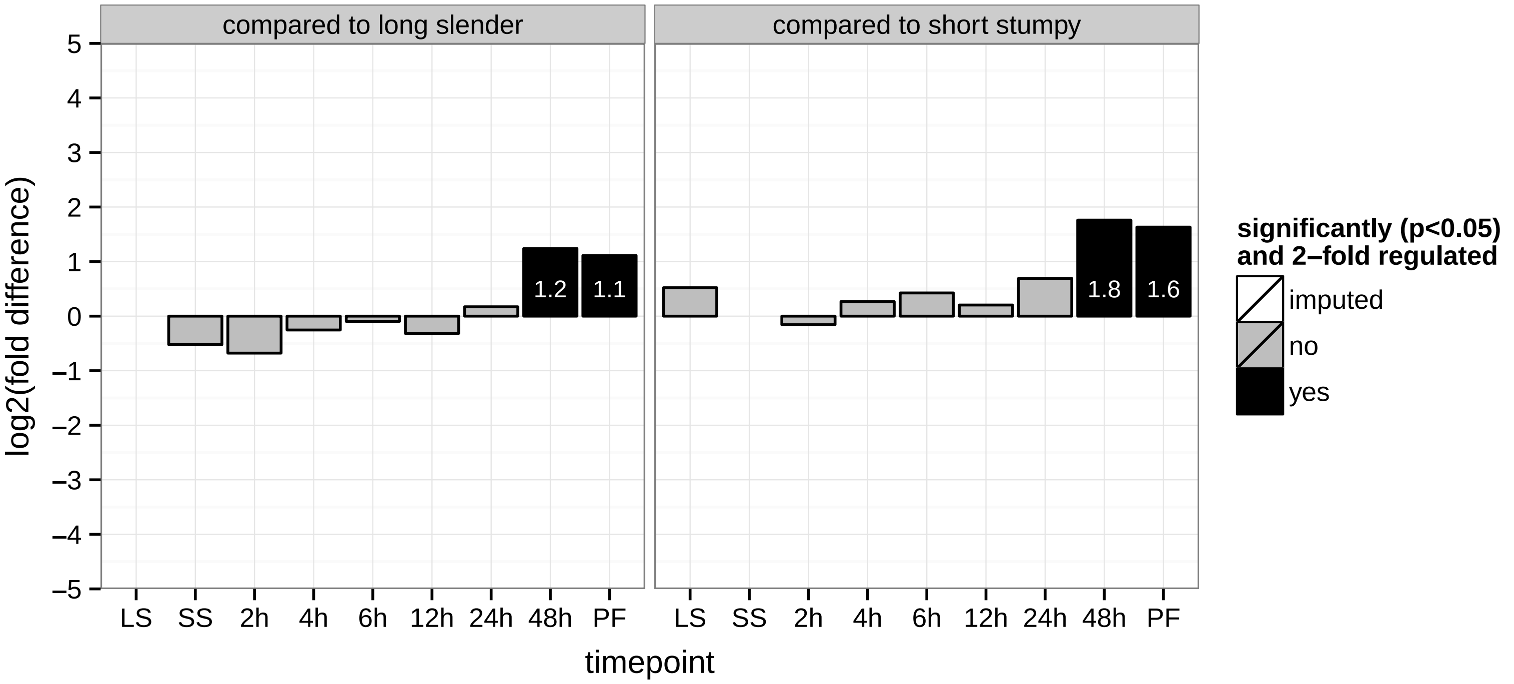
hypothetical protein, conserved
Tb927.1.3270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

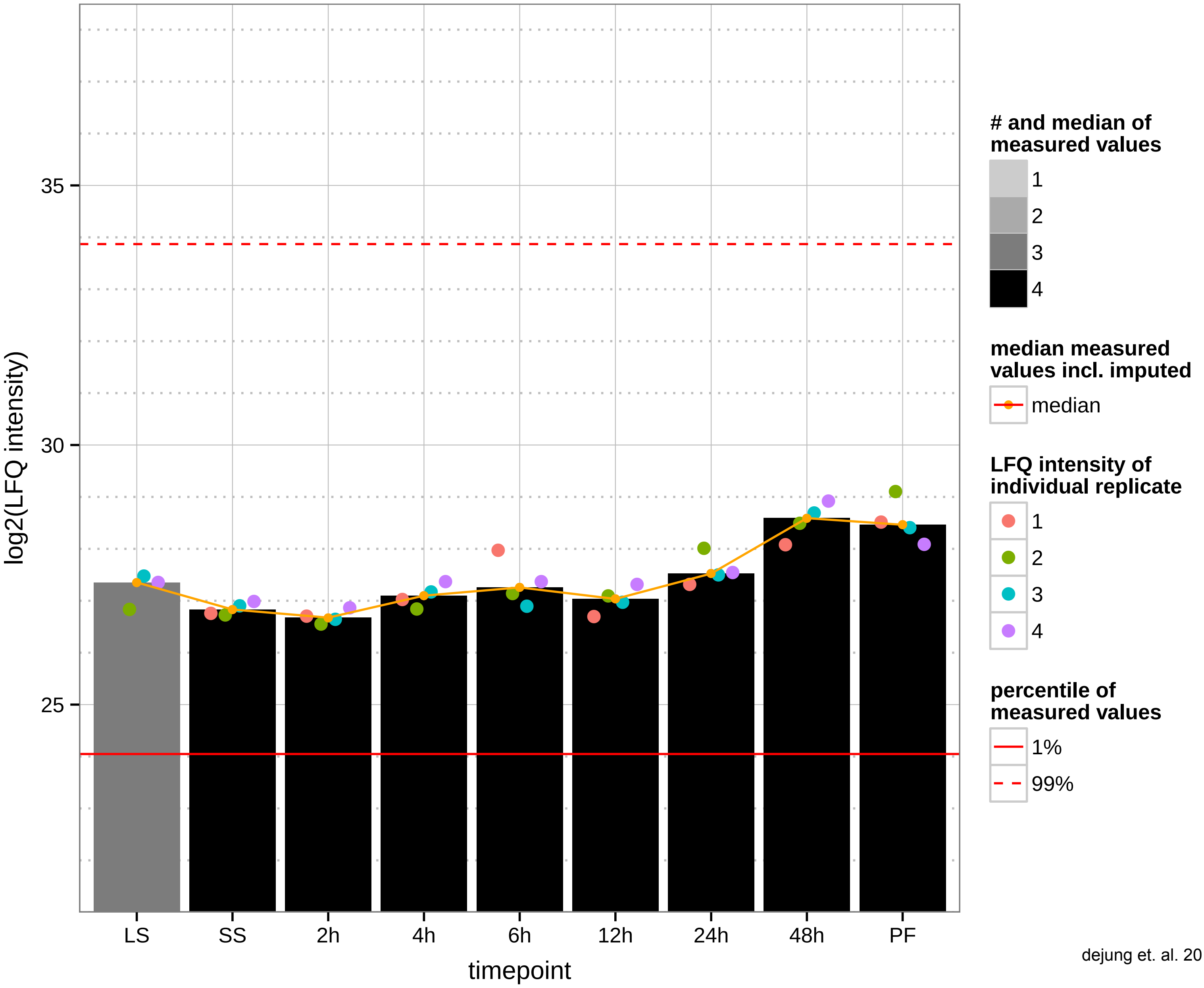




dejung et. al. 2015

protein tyrosine phosphatase, putative
Tb927.10.10610
AGOF: protein tyrosine phosphatase activity
AGOC: membrane, mitochondrial inner membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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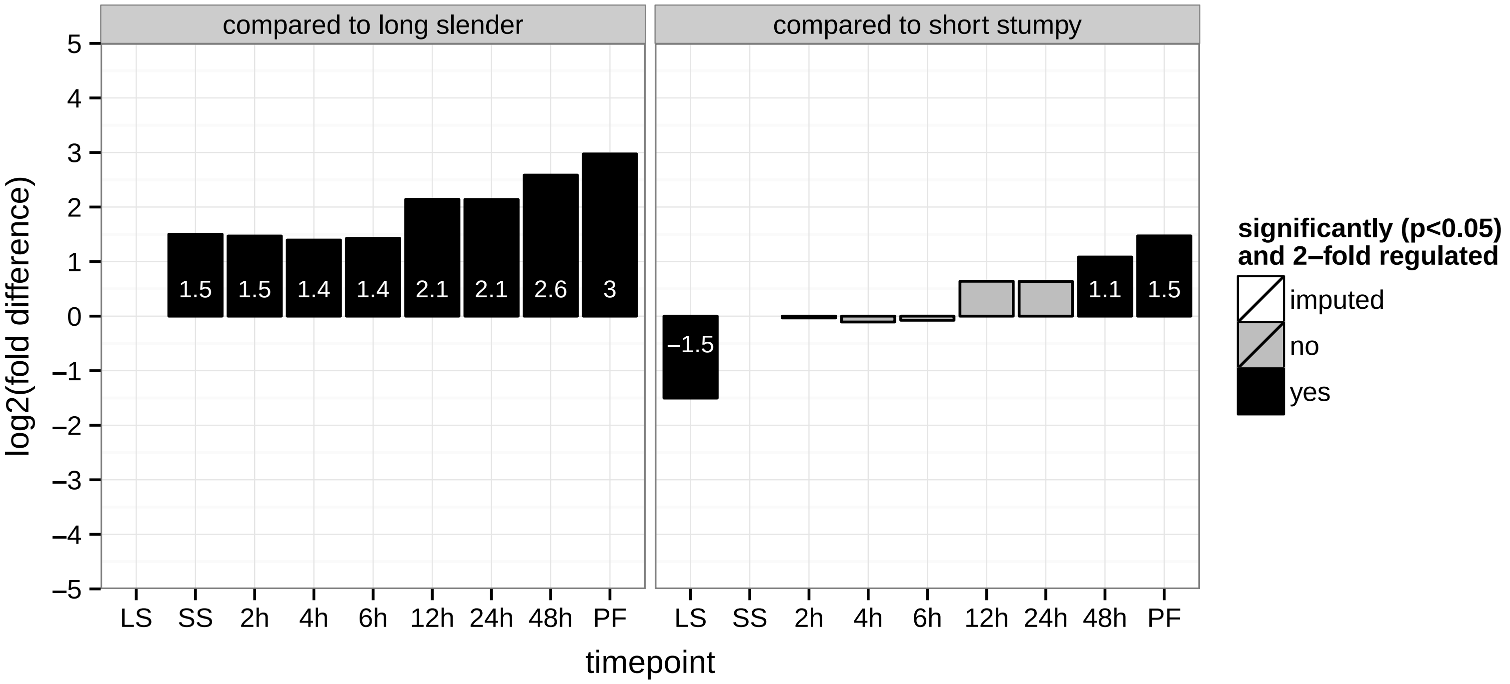
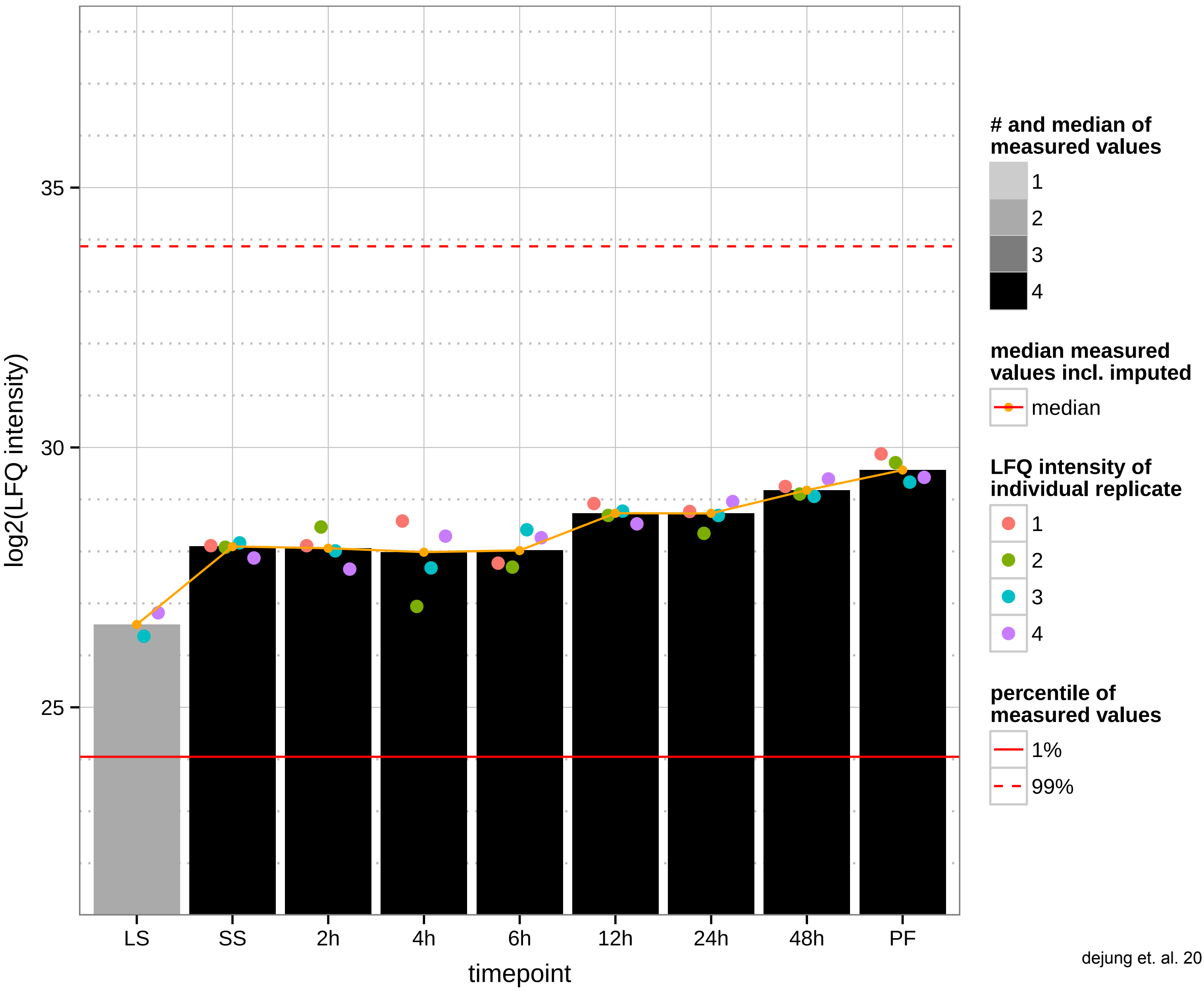
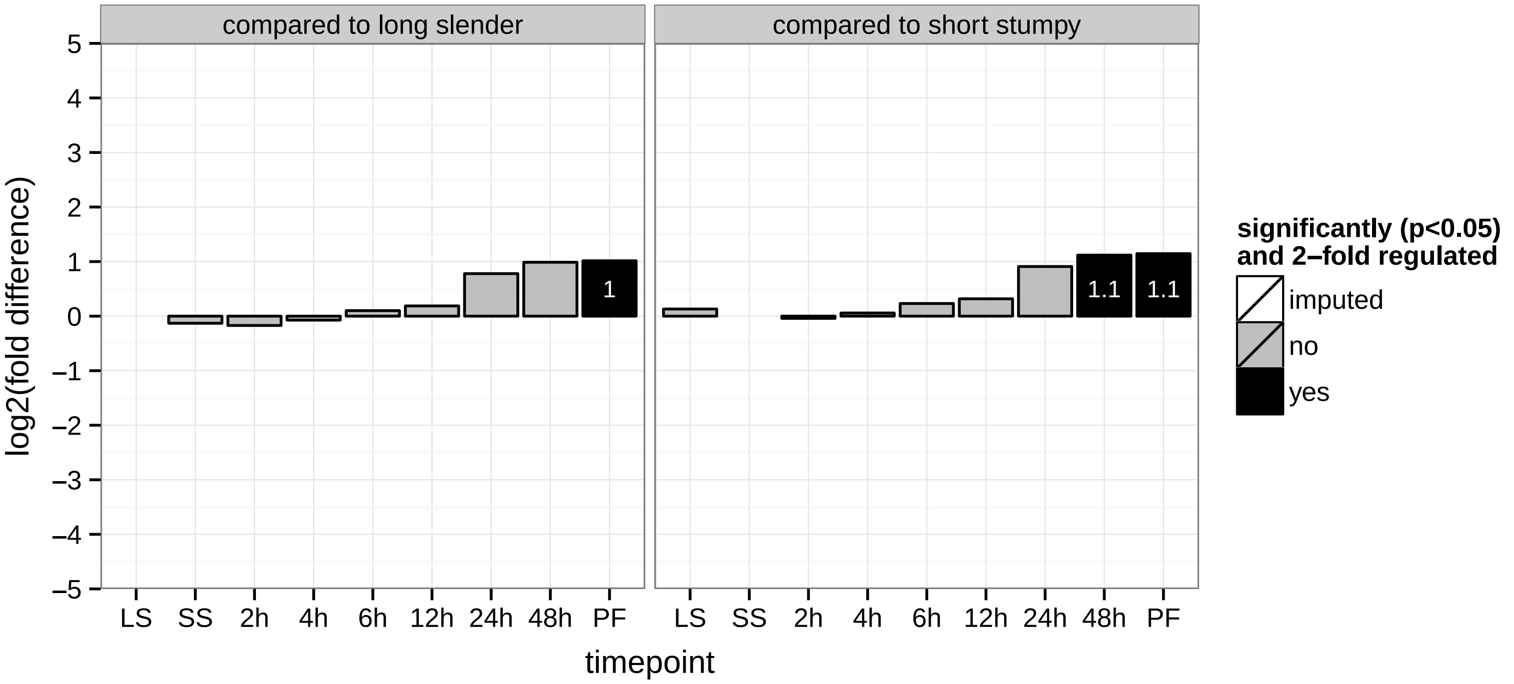
ATP−binding cassette sub−family F member 1, putative, ATPase, putative (ABCF1)
Tb927.10.10880
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances
AGOC: ATP−binding cassette (ABC) transporter complex, integral to membrane, internal side of plasma membrane
AGOP: transport
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null

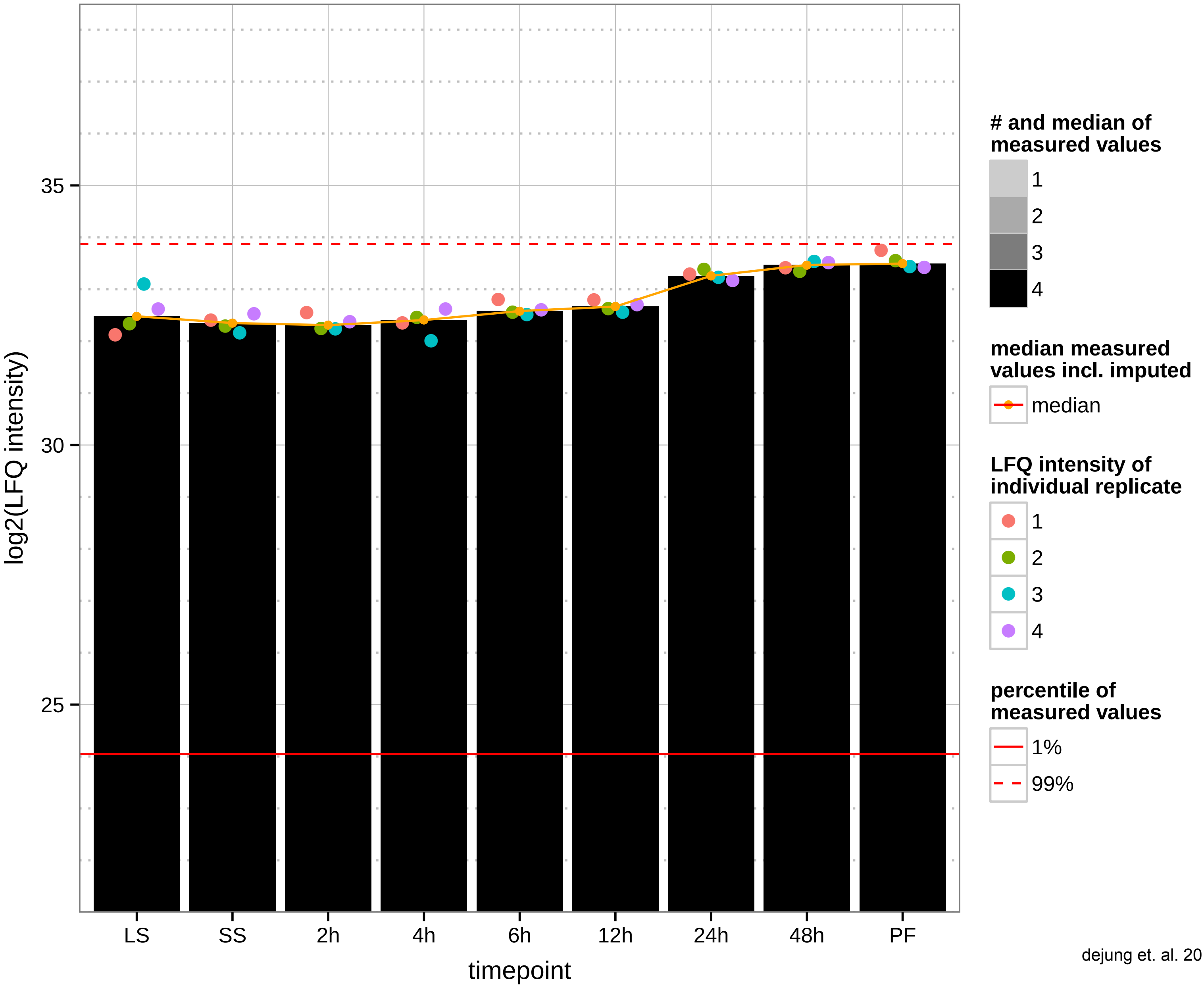




dejung et. al. 2015

60S ribosomal protein L6, putative
Tb927.10.11390
AGOF: structural constituent of ribosome
AGOC: intracellular, organellar large ribosomal subunit, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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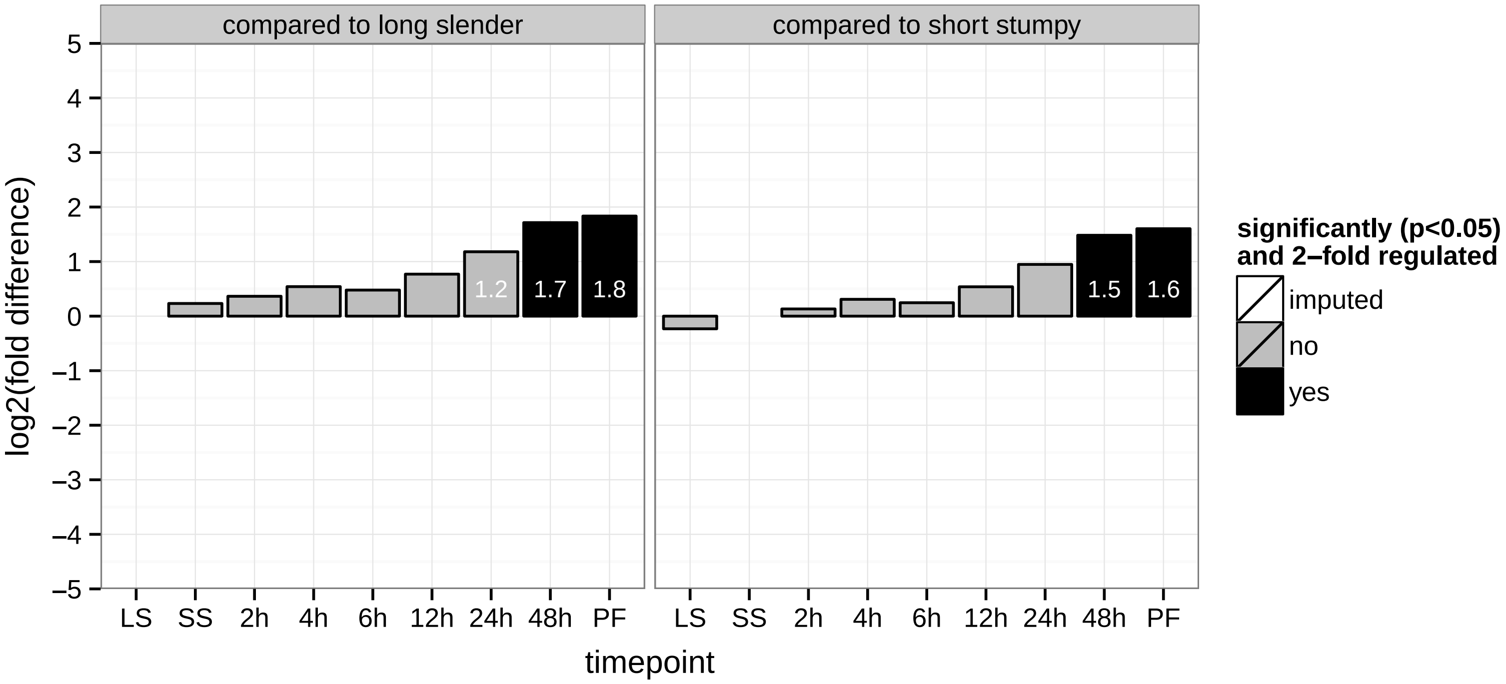
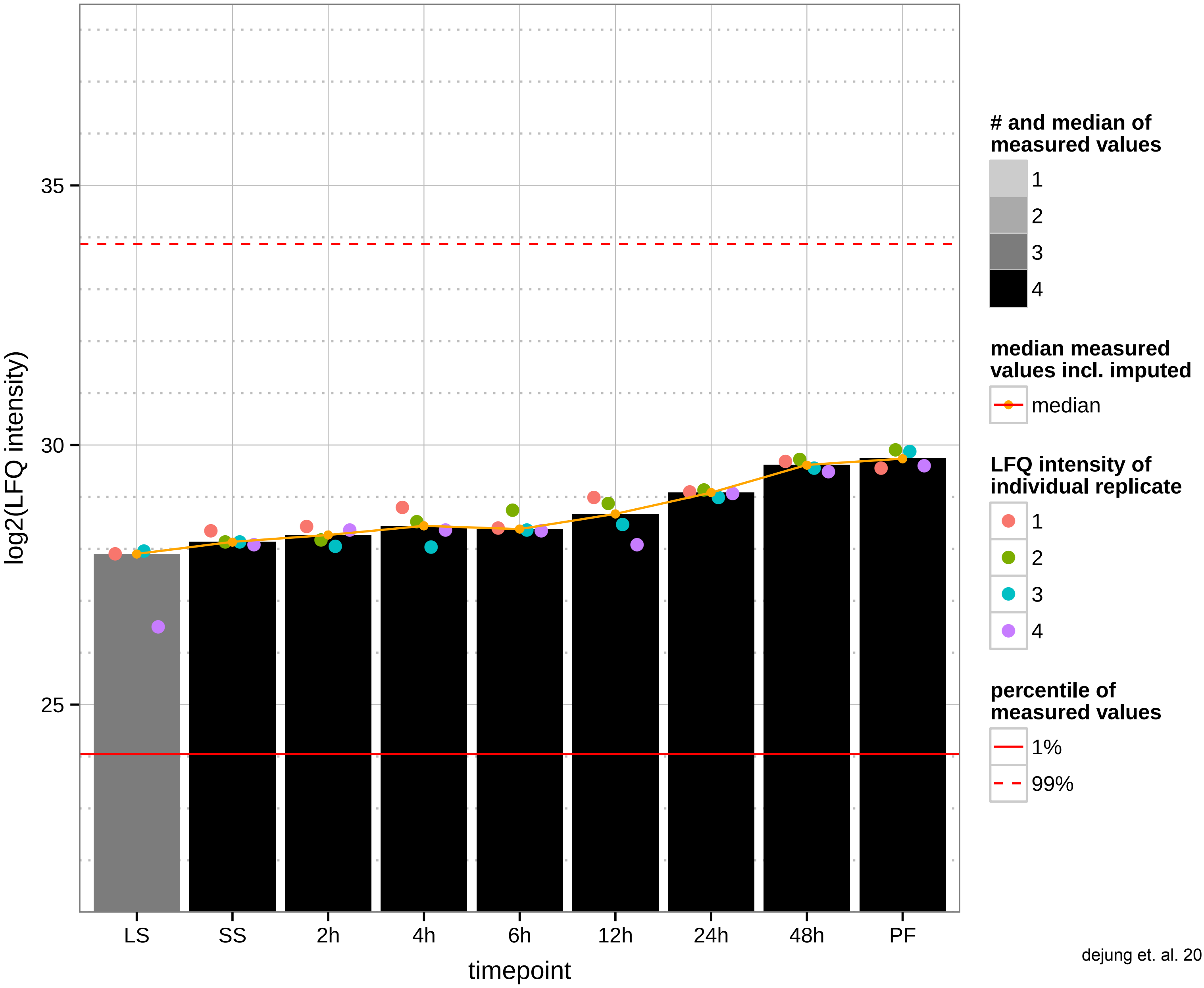
3–ketoacyl–CoA reductase, putative
Tb927.10.12240
AGOF: oxidoreductase activity
AGOC: endoplasmic reticulum
AGOP: metabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process





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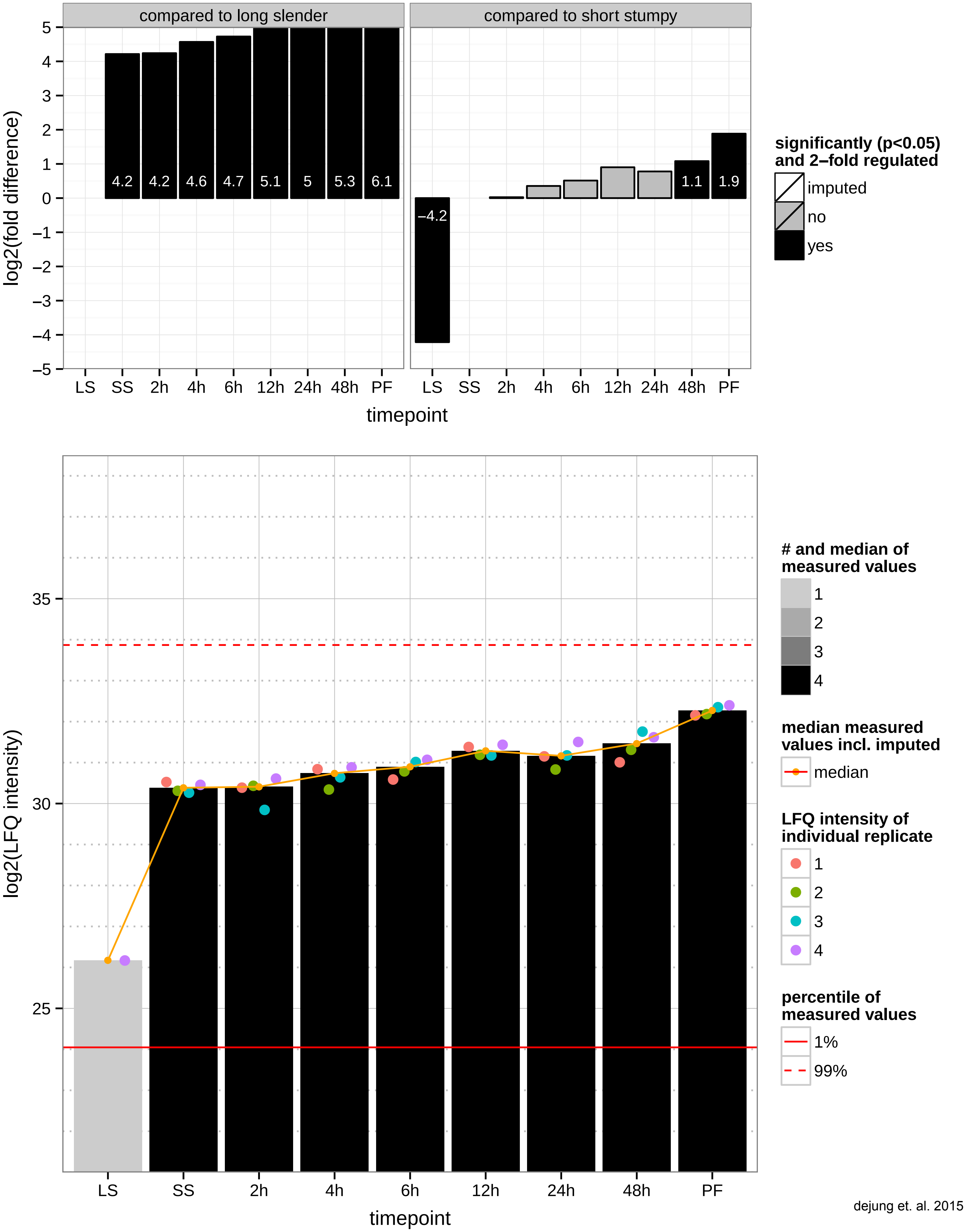
cytosolic nonspecific dipeptidase, putative, peptidase (M20/M25/M40 family)
Tb927.10.12260
AGOF: hydrolase activity, metallopeptidase activity, protein dimerization activity
AGOC: null
AGOP: proteolysis
PGOF: hydrolase activity
PGOC: null
PGOP: metabolic process



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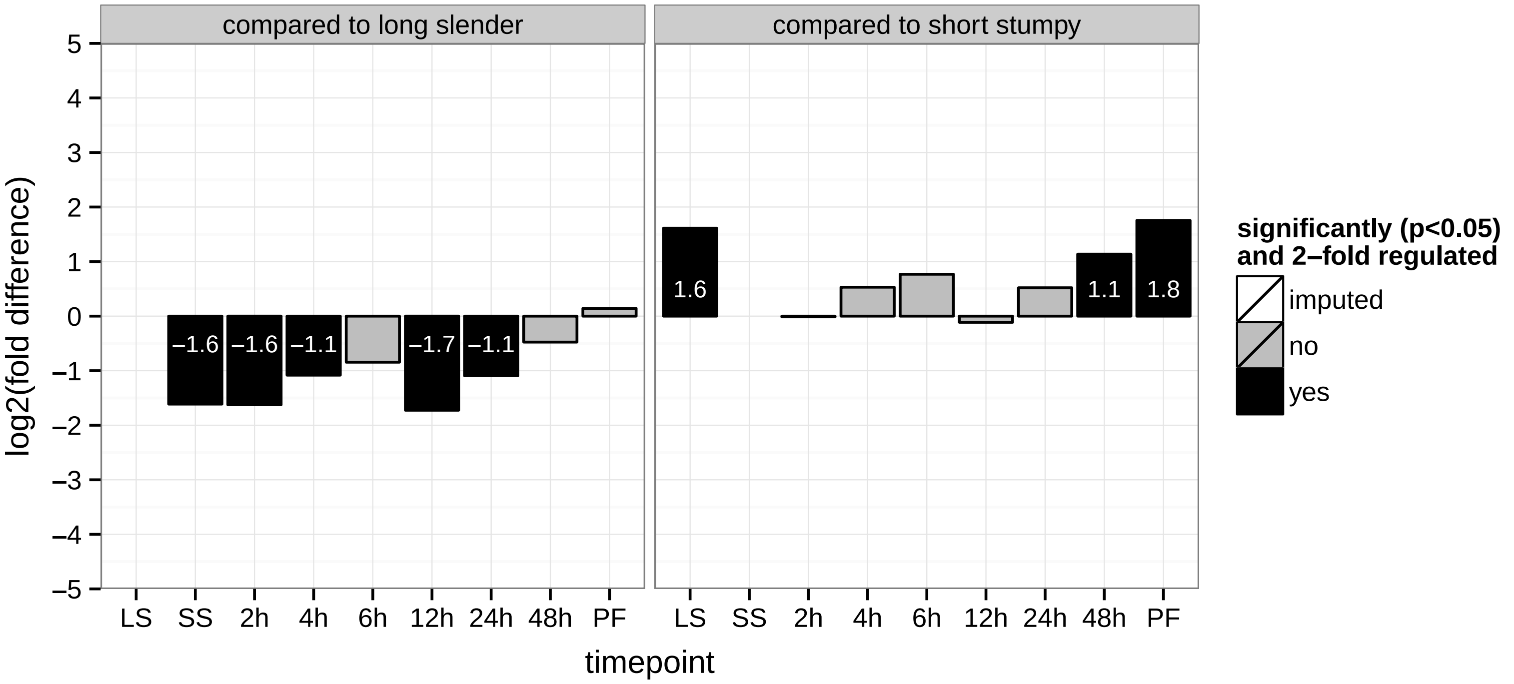
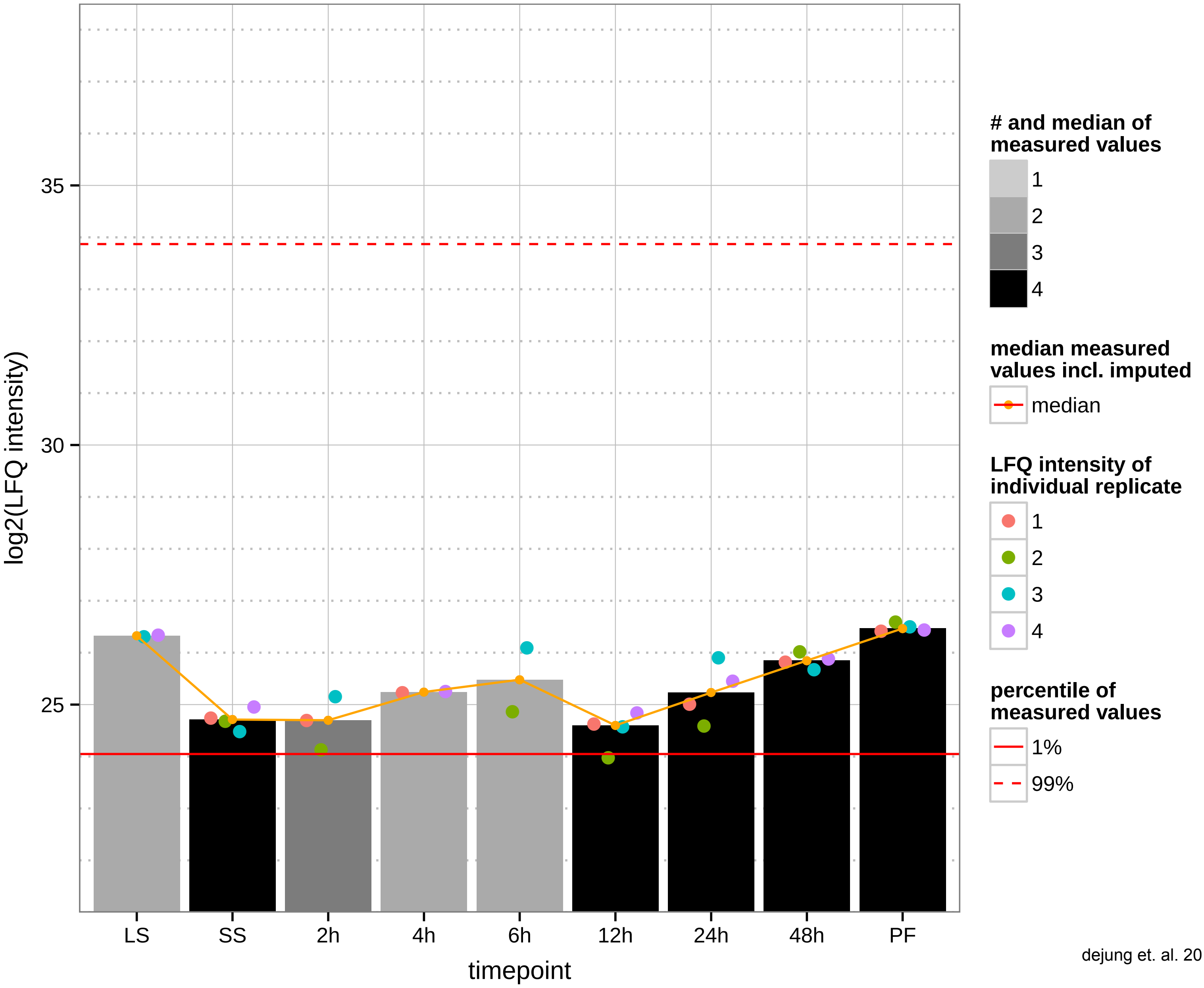
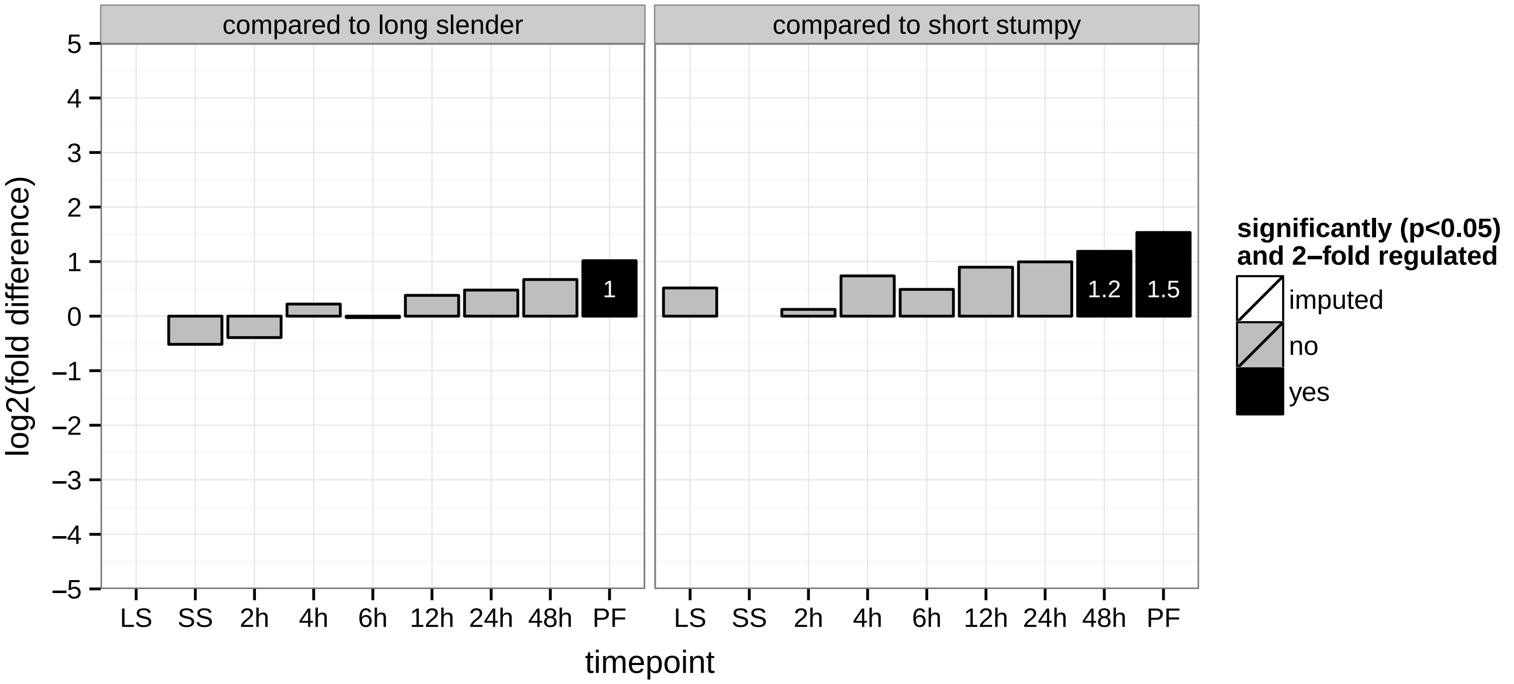
pumilio/PUF RNA binding protein 2 (PUF2)
Tb927.10.12660
AGOF: RNA binding
AGOC: cytoplasm
AGOP: mRNA metabolic process
PGOF: RNA binding, binding
PGOC: null
PGOP: null

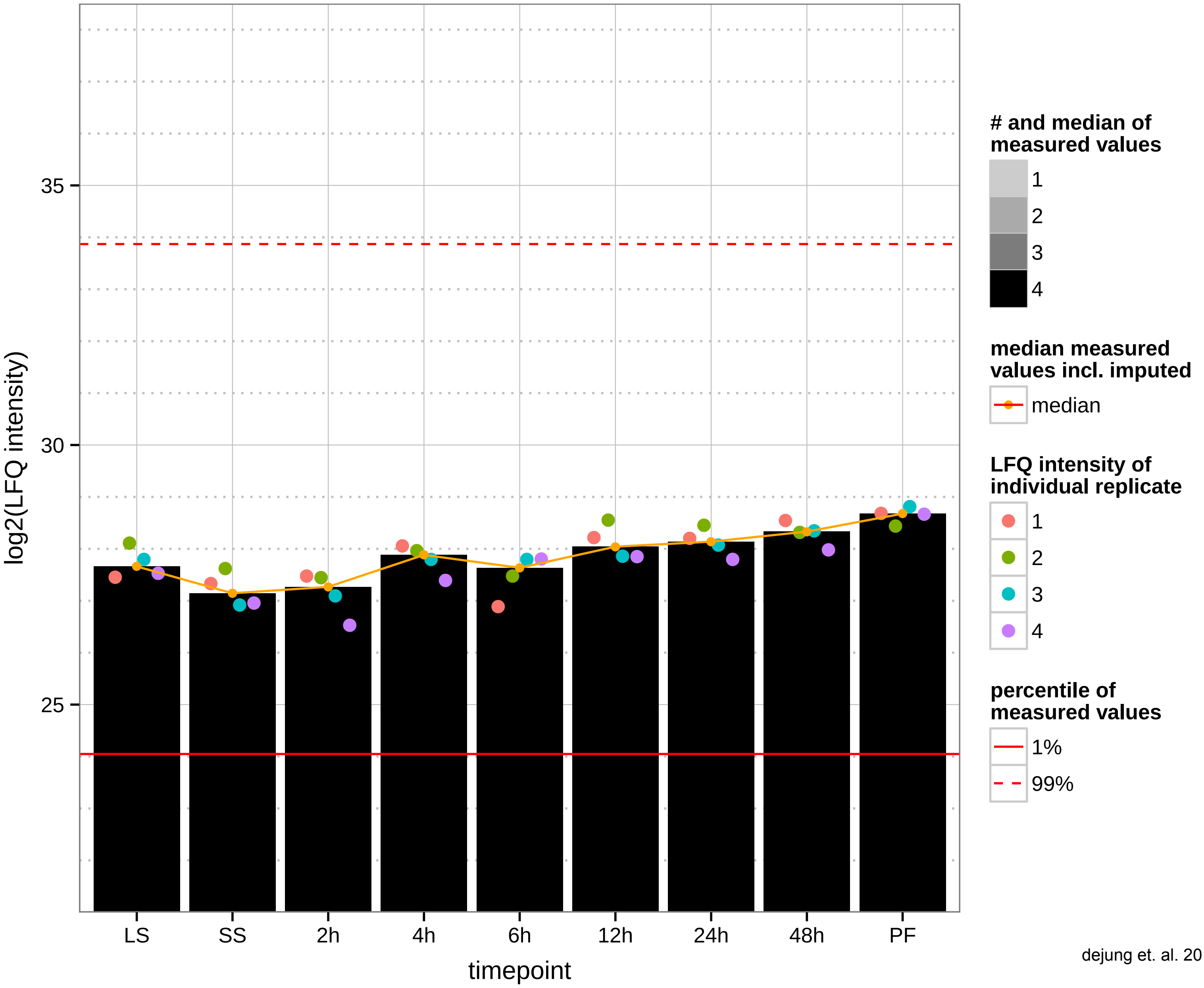




dejung et. al. 2015

tubulin–specific chaperone, putative
Tb927.10.13950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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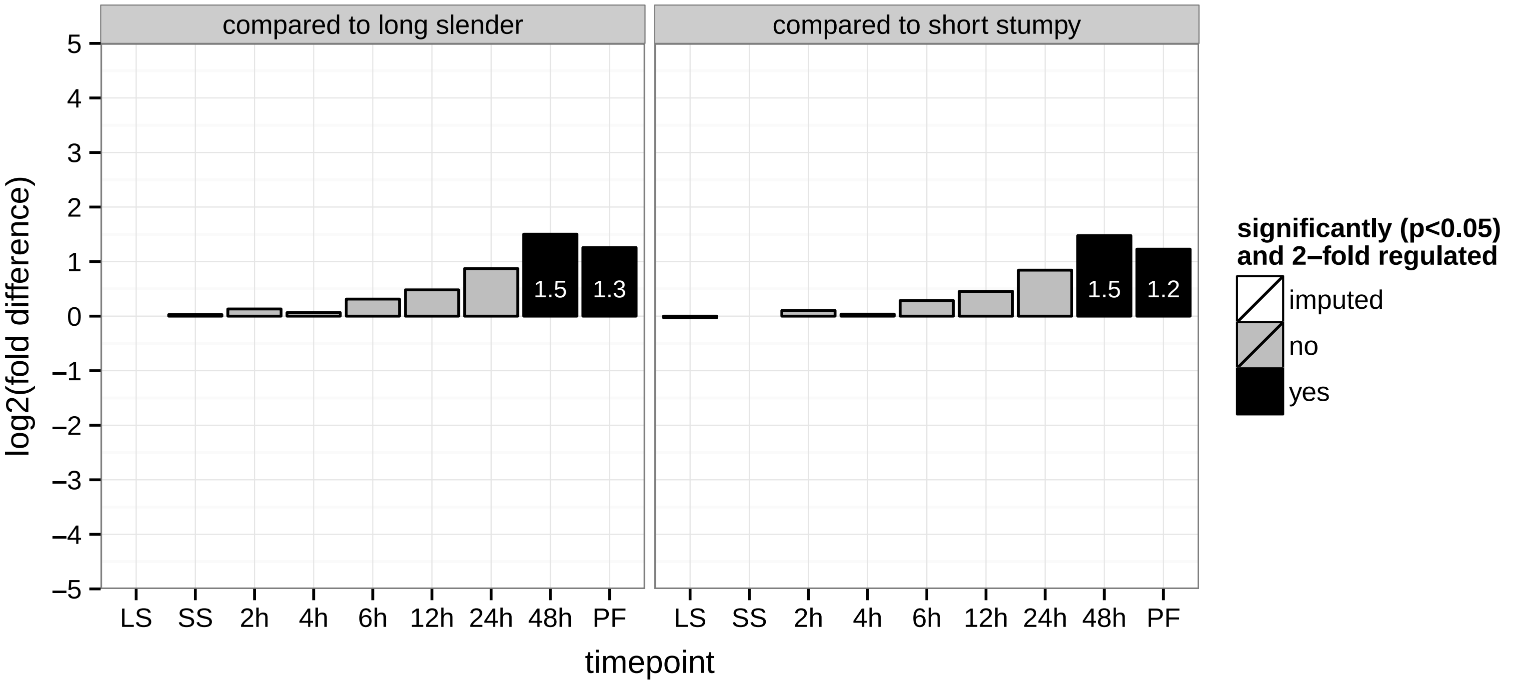
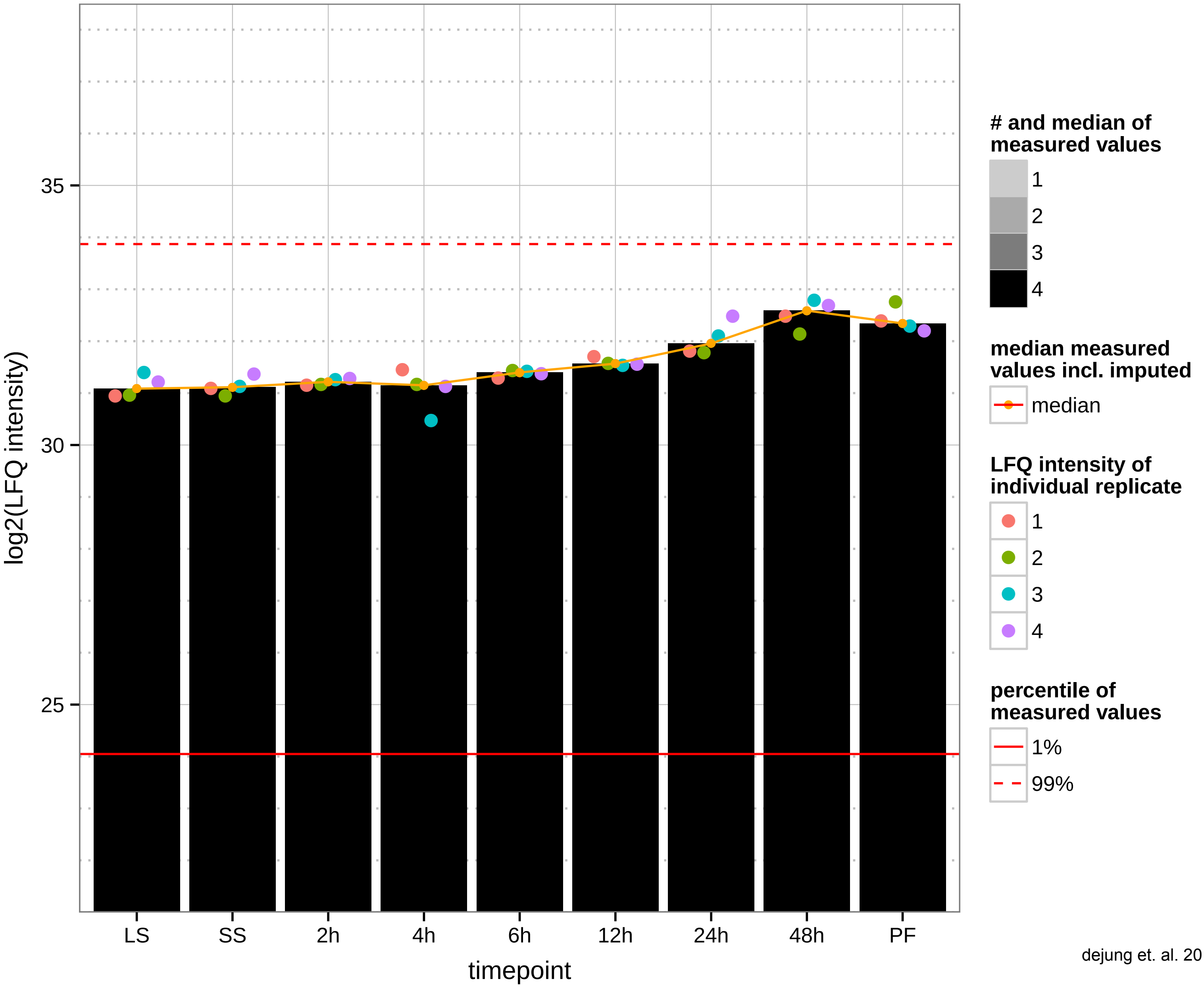
60S ribosomal protein L17, putative
Tb927.11.4820;Tb927.10.14580
AGOF: structural constituent of ribosome
AGOC: intracellular, large ribosomal subunit, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, large ribosomal subunit, ribosome
PGOP: translation





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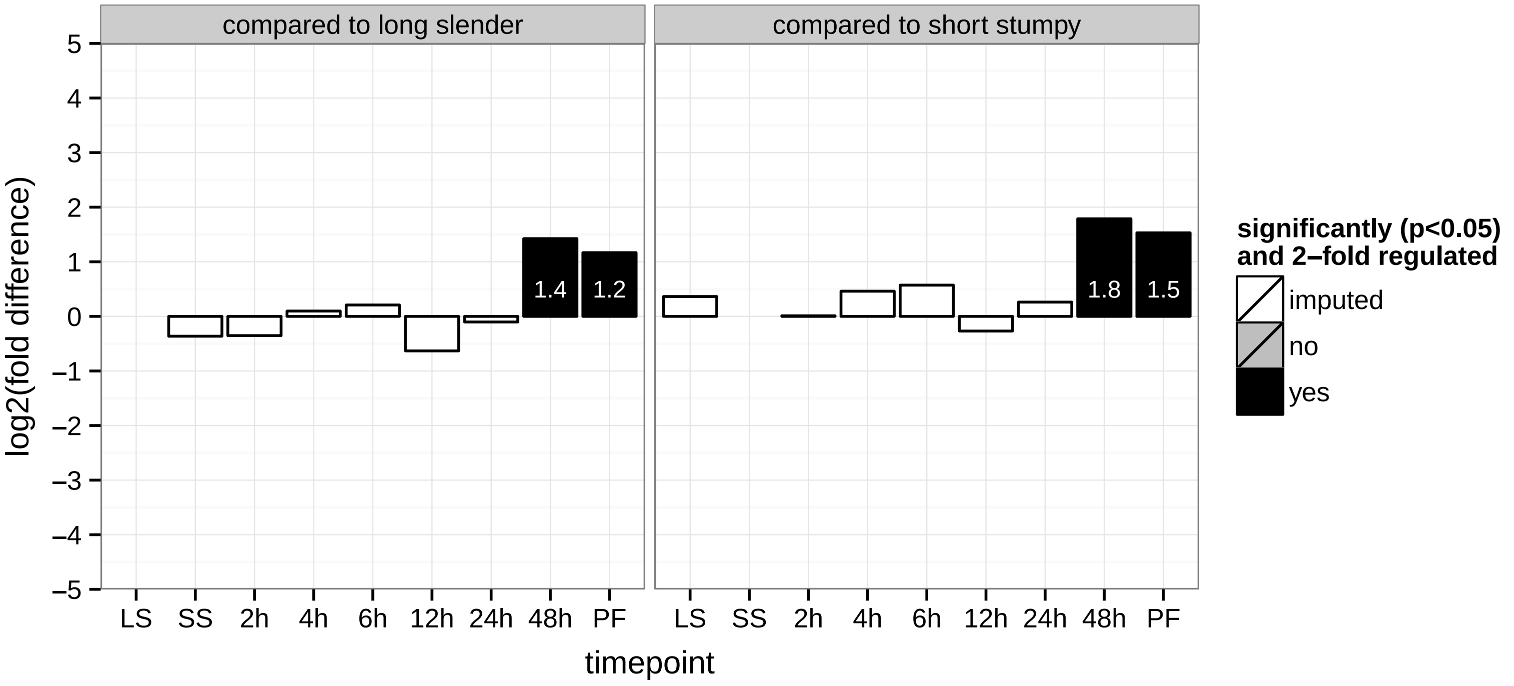
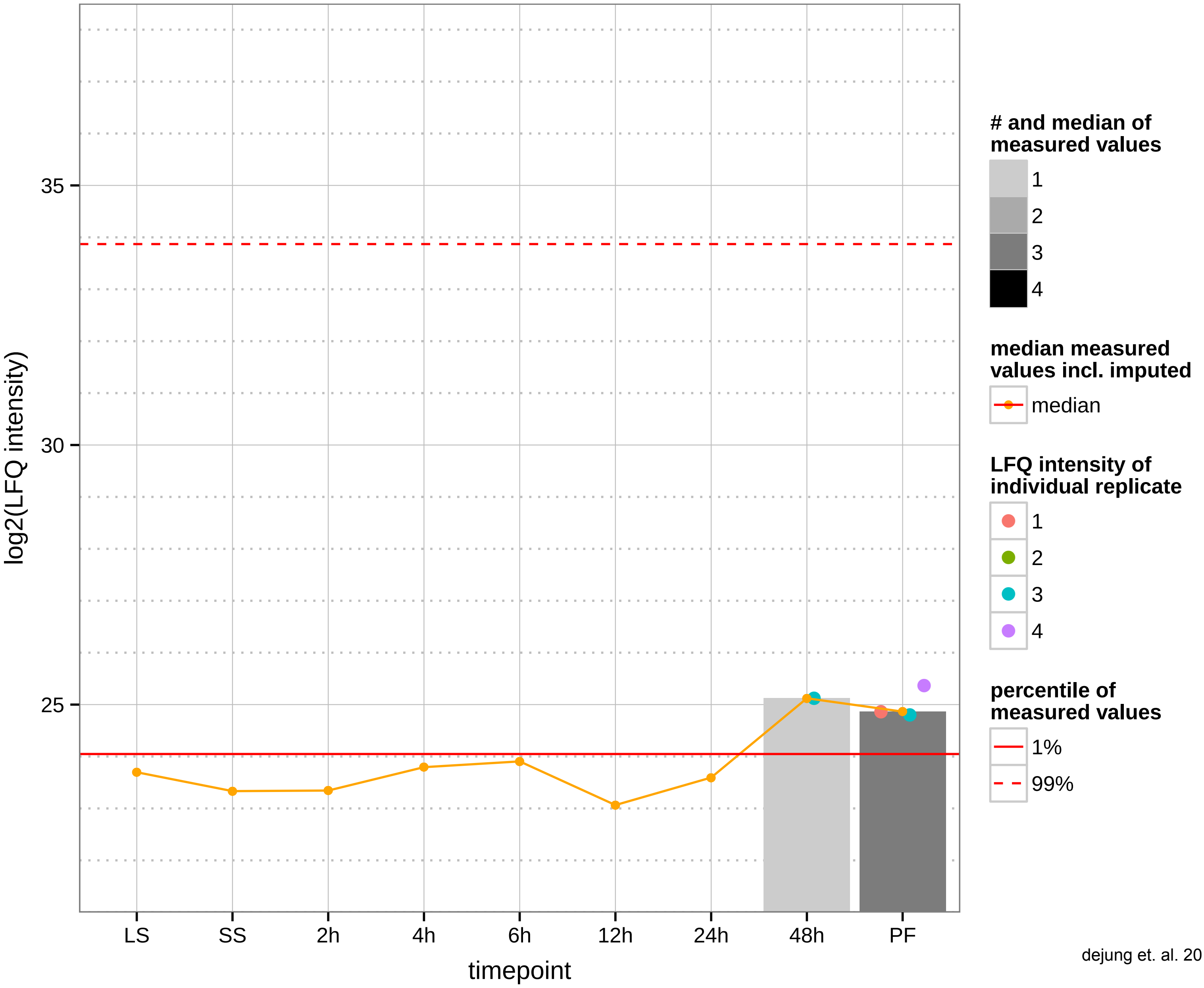
hypothetical protein, conserved
Tb927.10.15220
AGOF: null
AGOC: endoplasmic reticulum
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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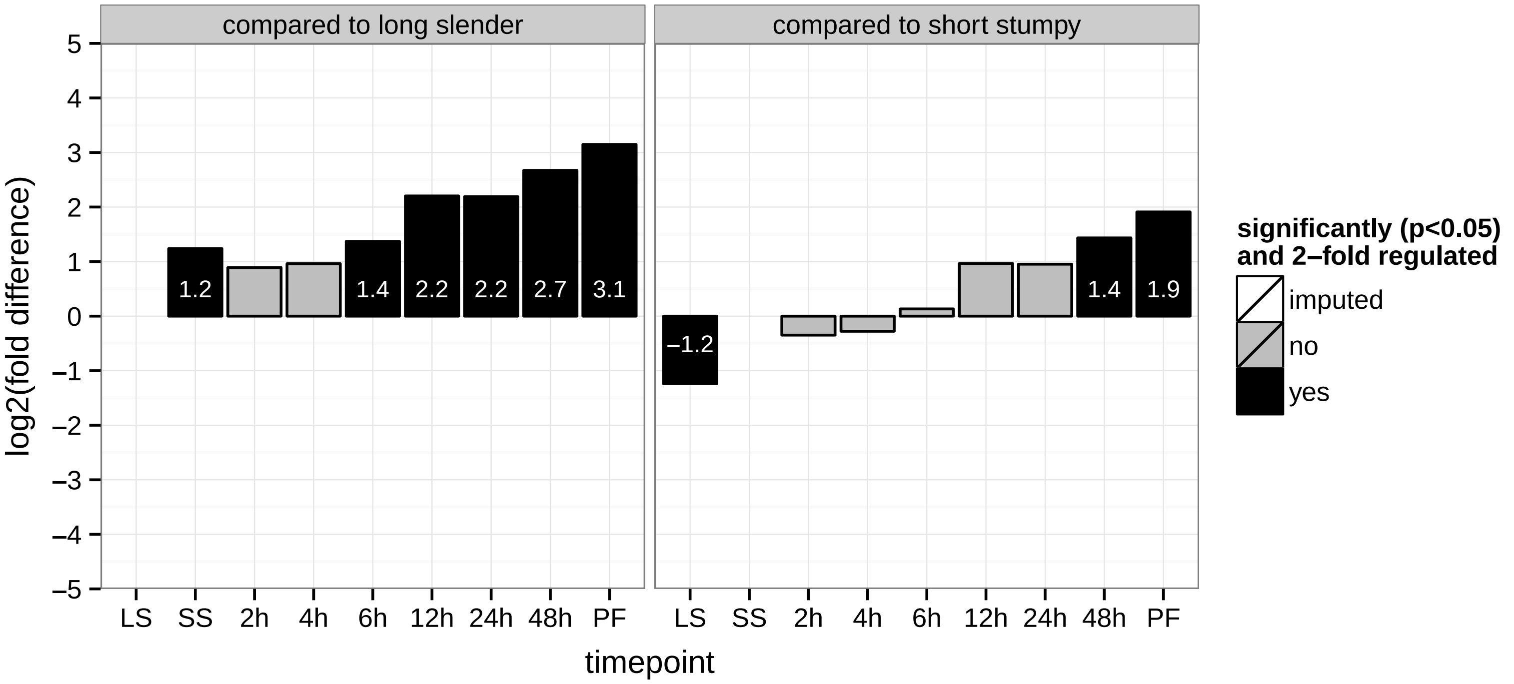
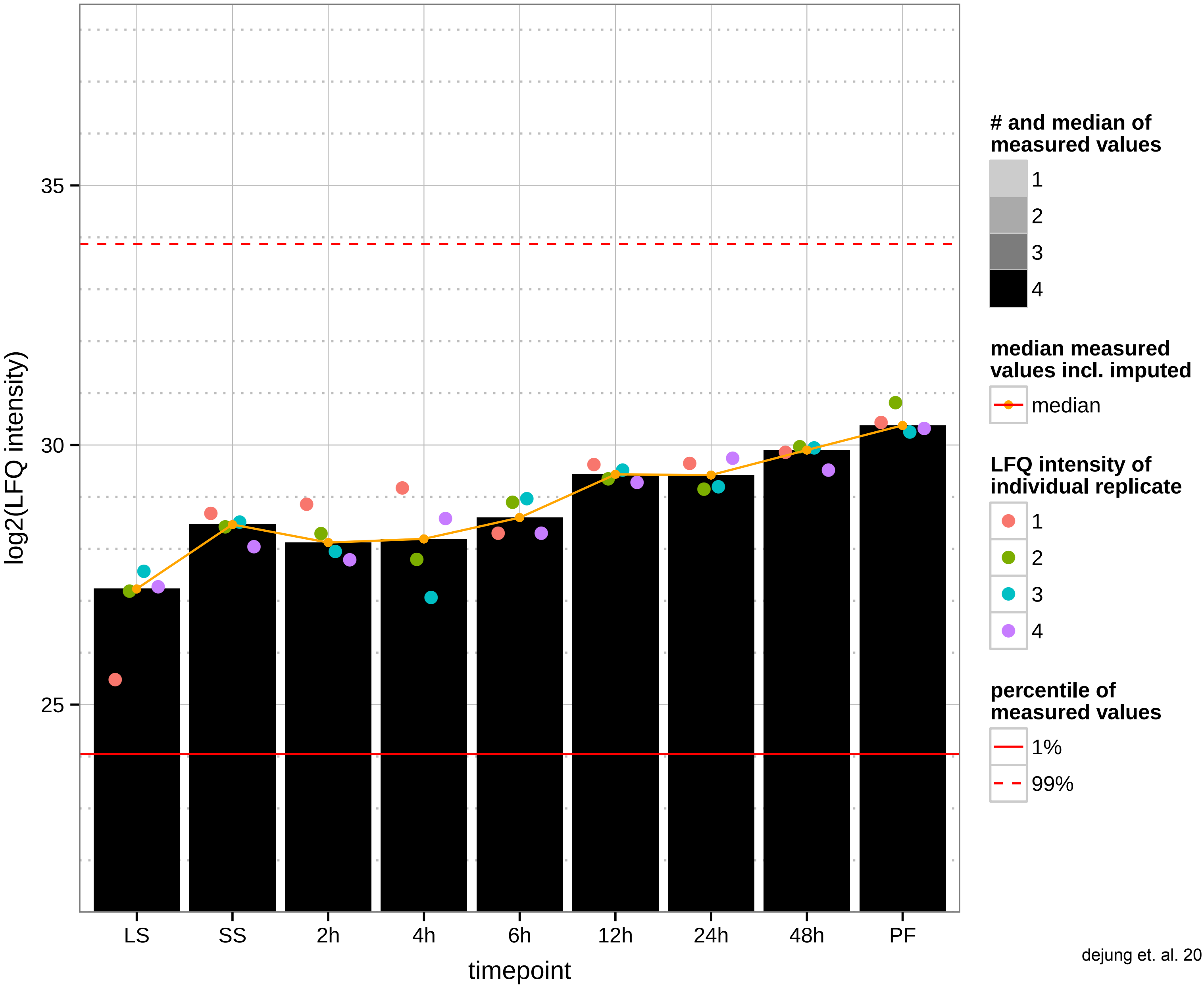
ABC transporter, putative, ABC transport system ATP−binding protein
Tb927.10.15530;Tb11.v5.0748
AGOF: null, ATP binding, ATPase activity, uncoupled
AGOC: null, integral to membrane, internal side of plasma membrane
AGOP: null, regulation of ribosome biogenesis, ribosomal small subunit export from nucleus, transport
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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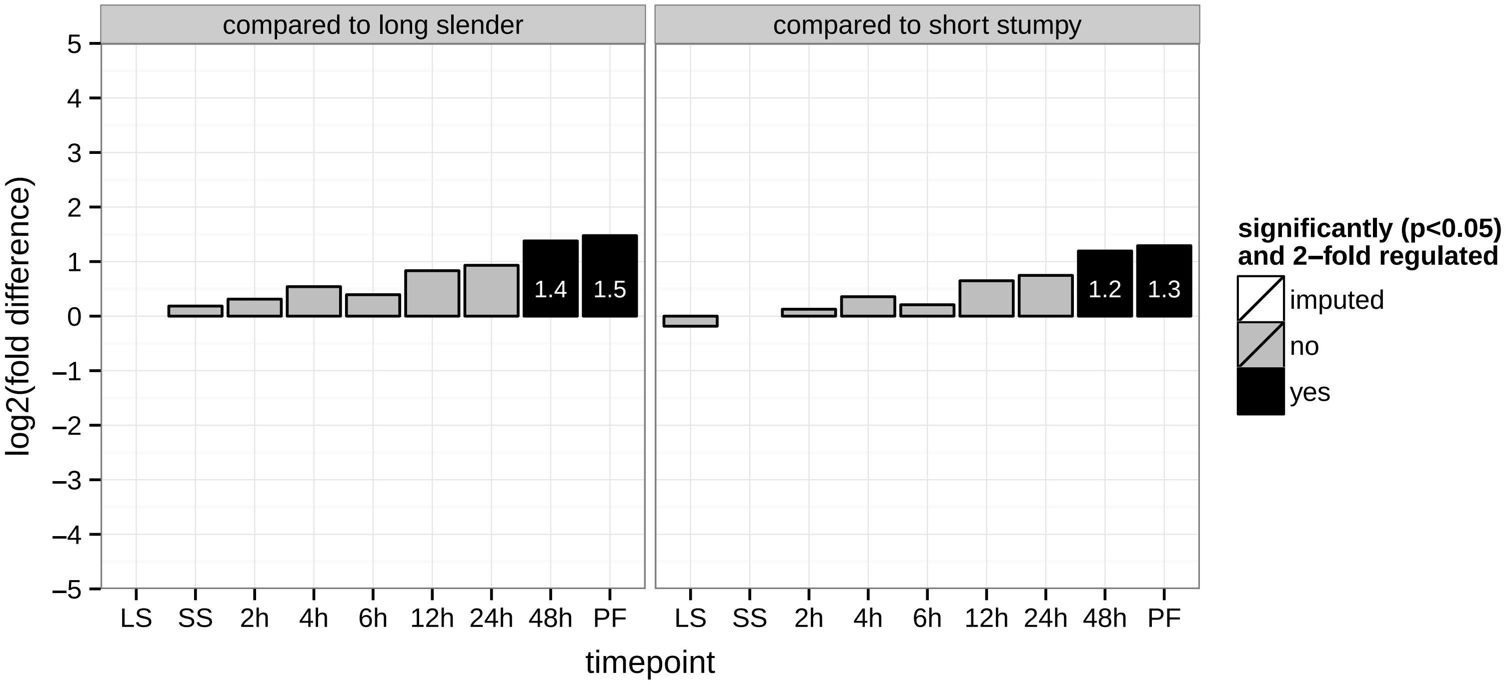
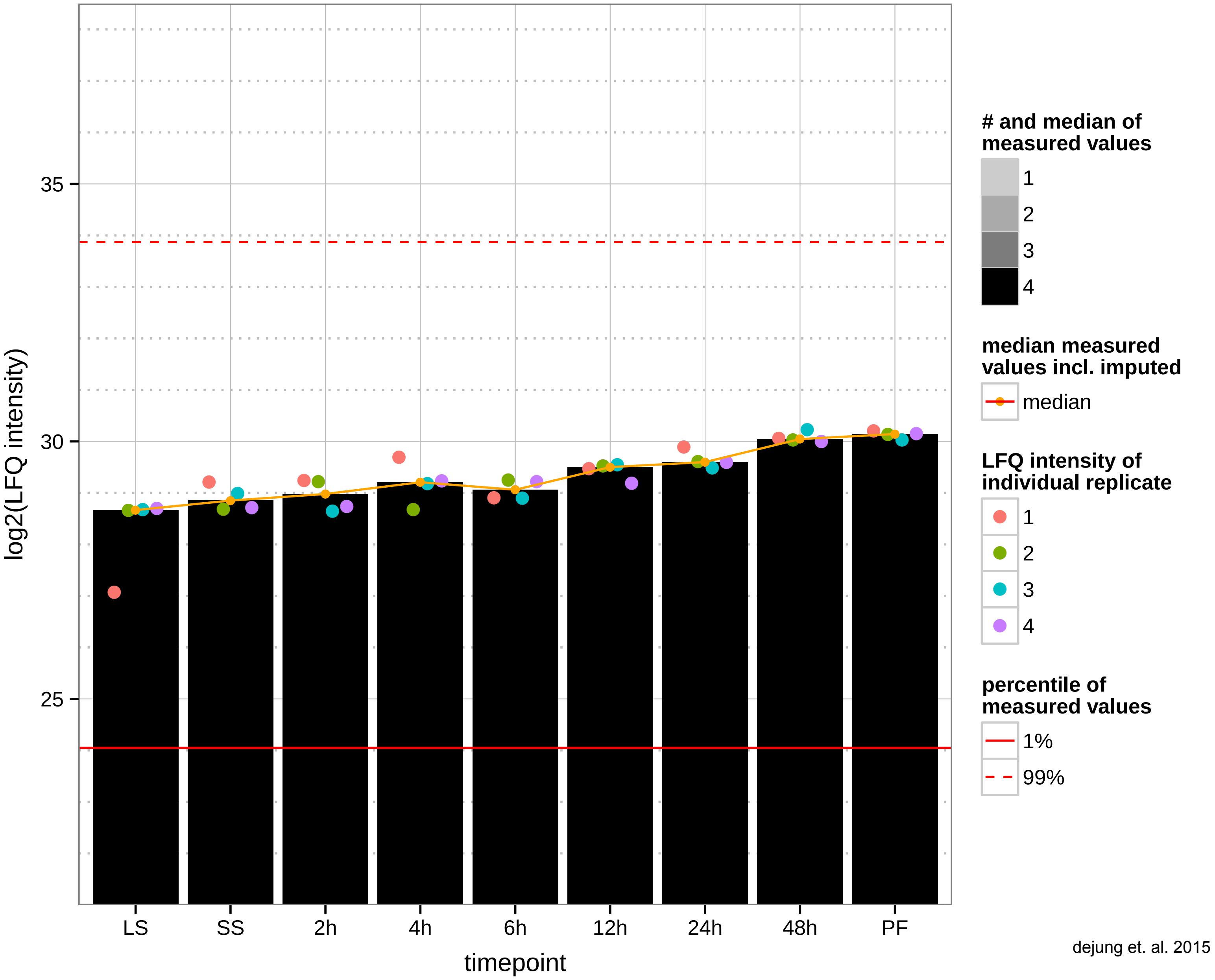
glucose–6–phosphate 1–dehydrogenase (G6PD)
Tb927.10.2490
AGOF: glucose–6–phosphate dehydrogenase activity
AGOC: cytoplasm, glycosome
AGOP: cell proliferation, oxidation–reduction process, pentose–phosphate shunt, oxidative branch, response to drug, respons
PGOF: NADP binding, glucose–6–phosphate dehydrogenase activity
PGOC: null
PGOP: glucose metabolic process, oxidation–reduction process





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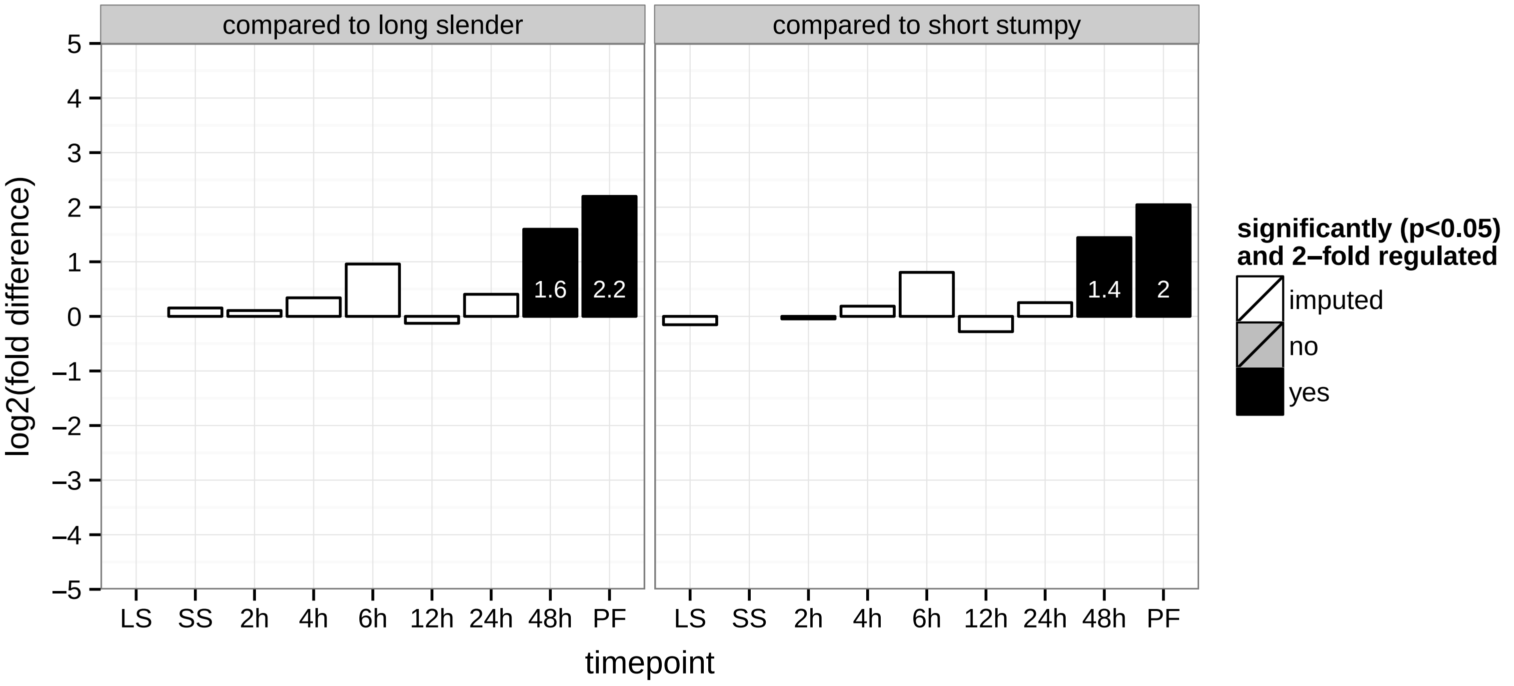
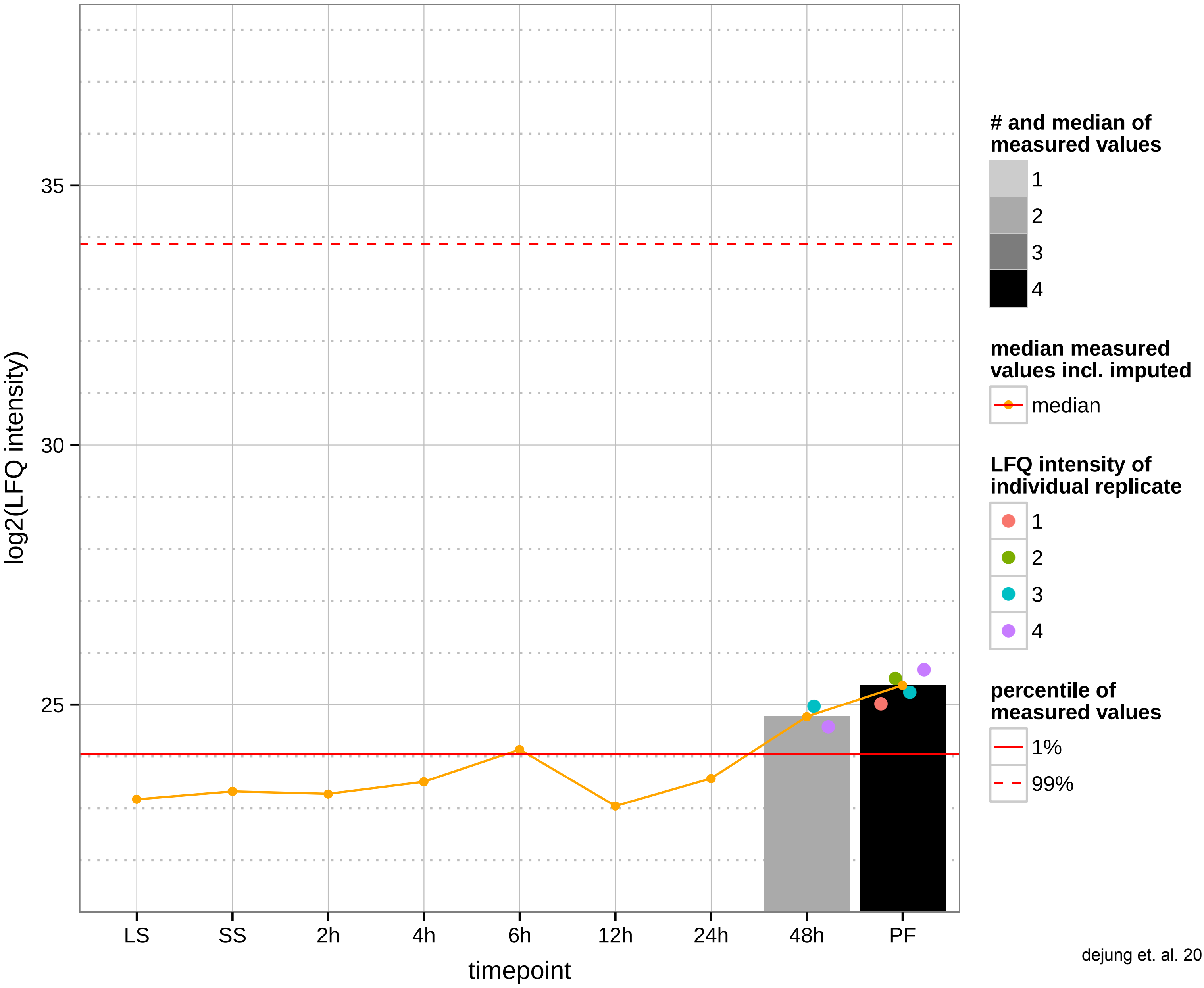
DNA primase large subunit, putative (pril)
Tb927.10.3110
AGOF: DNA primase activity
AGOC: alpha DNA polymerase:primase complex
AGOP: DNA replication, synthesis of RNA primer
PGOF: DNA primase activity, nucleotidyltransferase activity
PGOC: null
PGOP: DNA replication, synthesis of RNA primer





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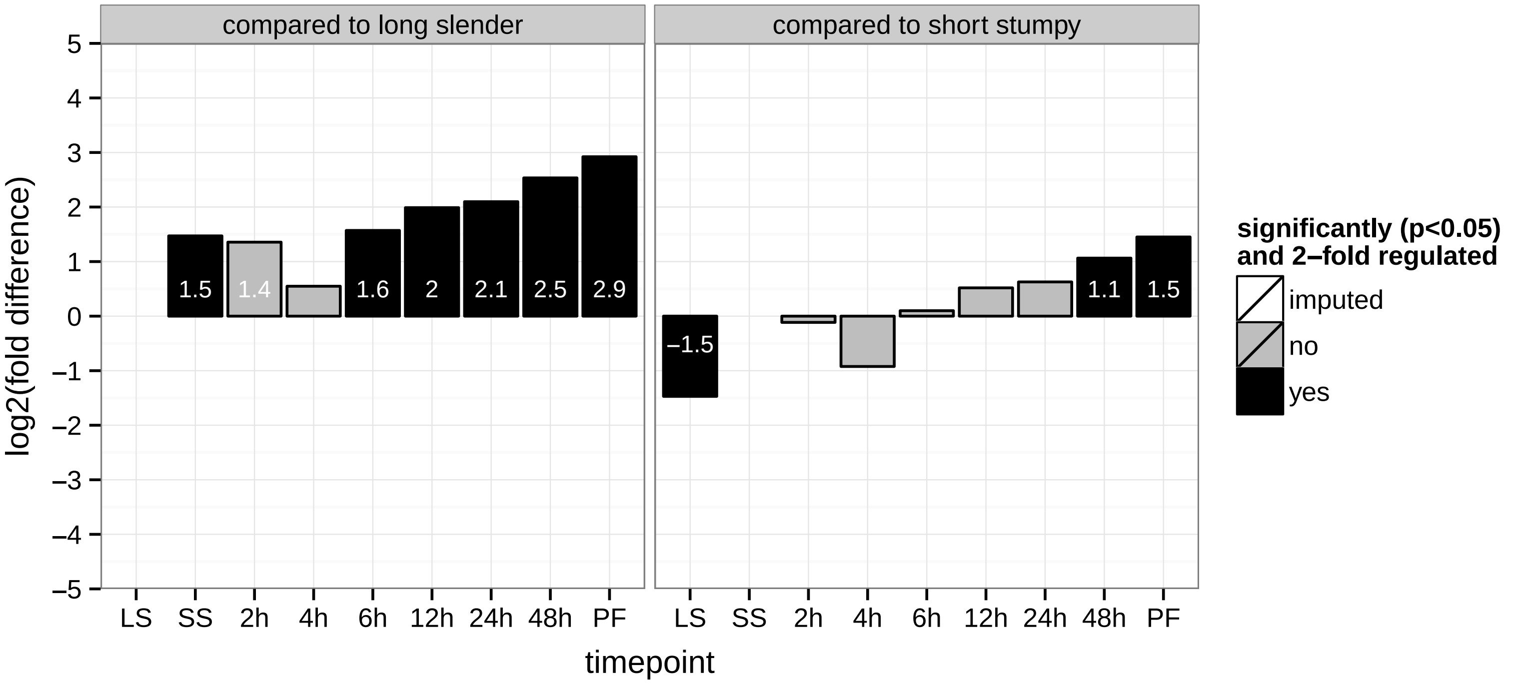
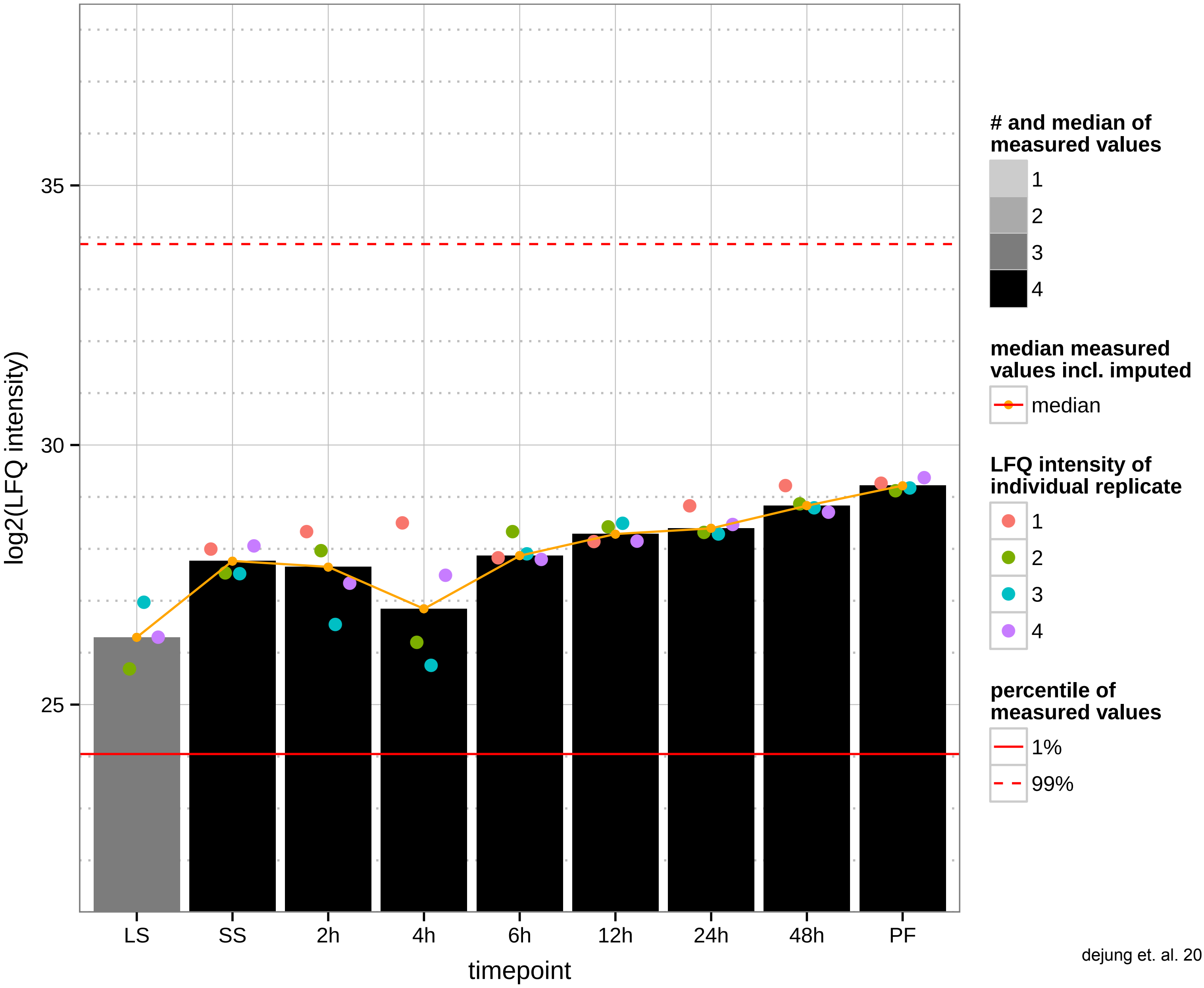
ABC transporter, putative
Tb927.10.3170;Tb11.v5.0791
AGOF: null, ATP binding, ATPase activity, coupled to transmembrane movement of substances
AGOC: null, integral to membrane, internal side of plasma membrane
AGOP: null, transport
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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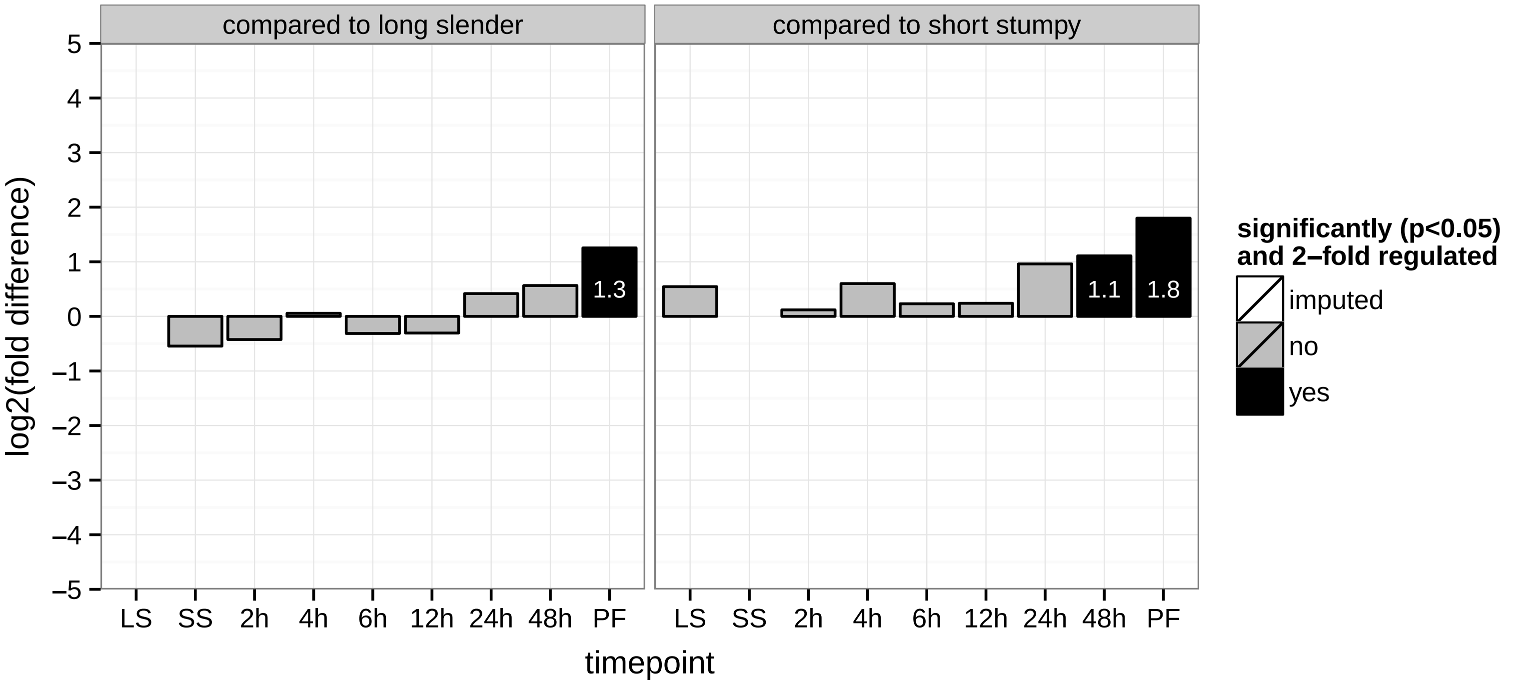
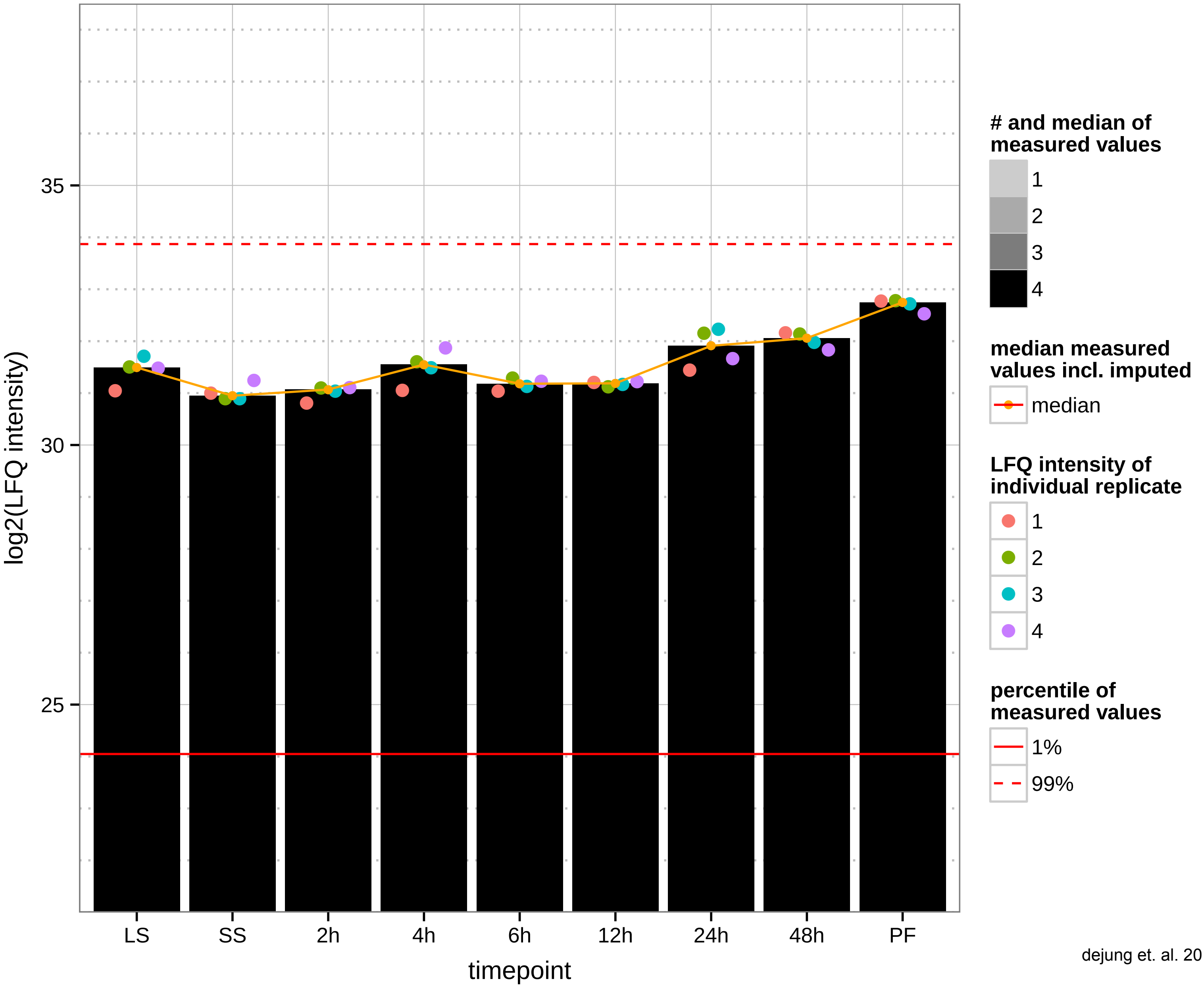
40S ribosomal protein S10, putative
Tb927.10.5370;Tb927.10.5360
AGOF: RNA binding
AGOC: cytoplasm
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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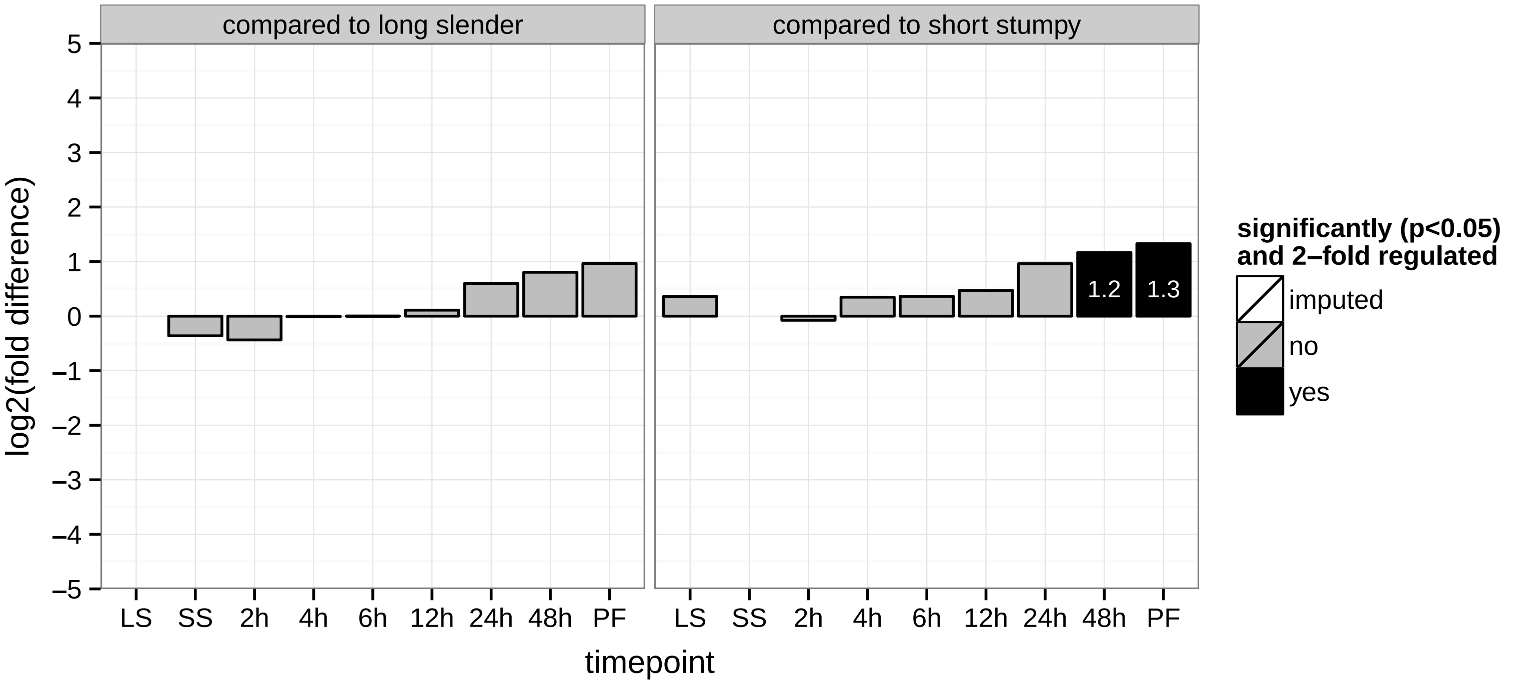
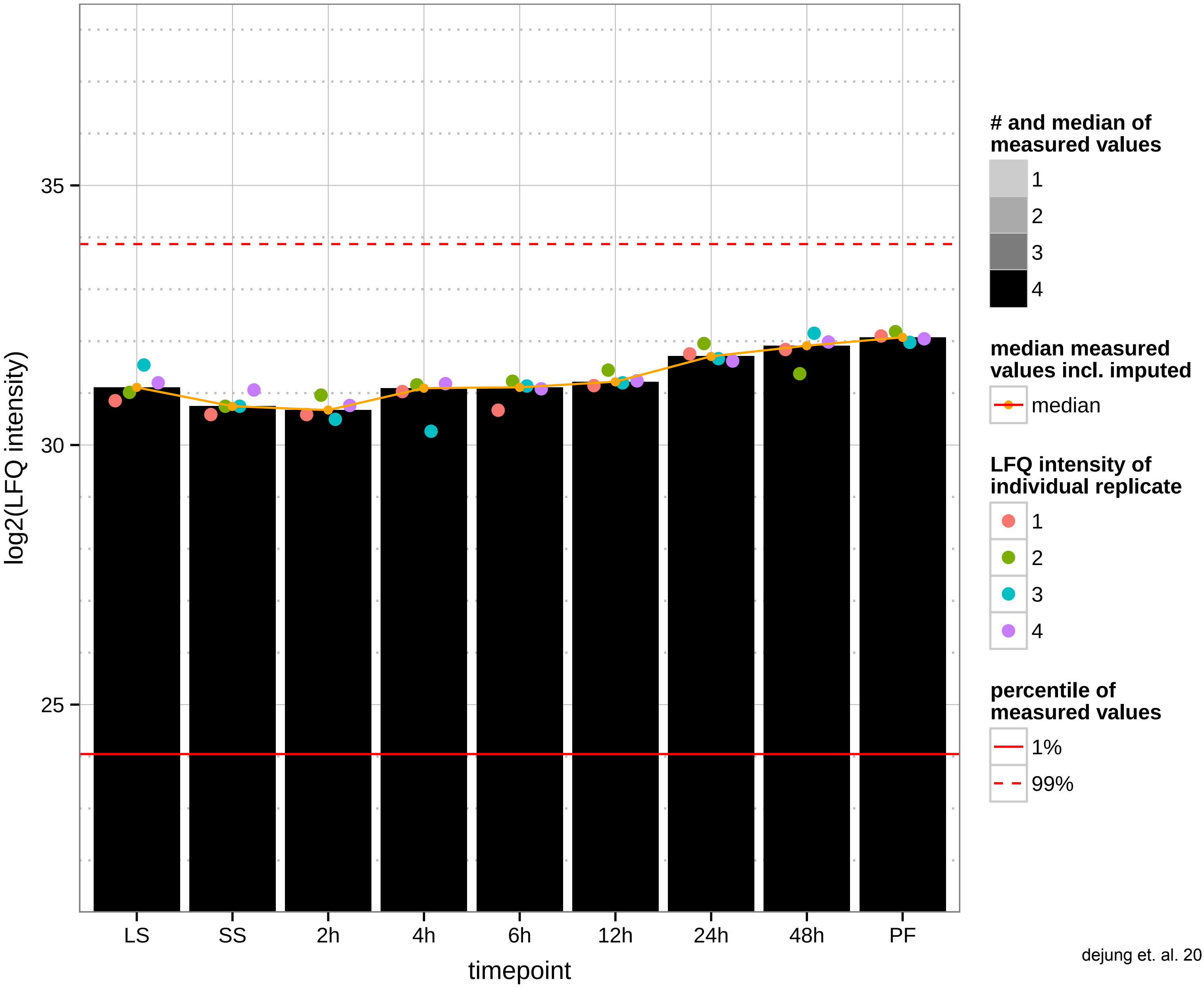
60S ribosomal protein L24, putative
Tb927.10.5480;Tb927.10.5460
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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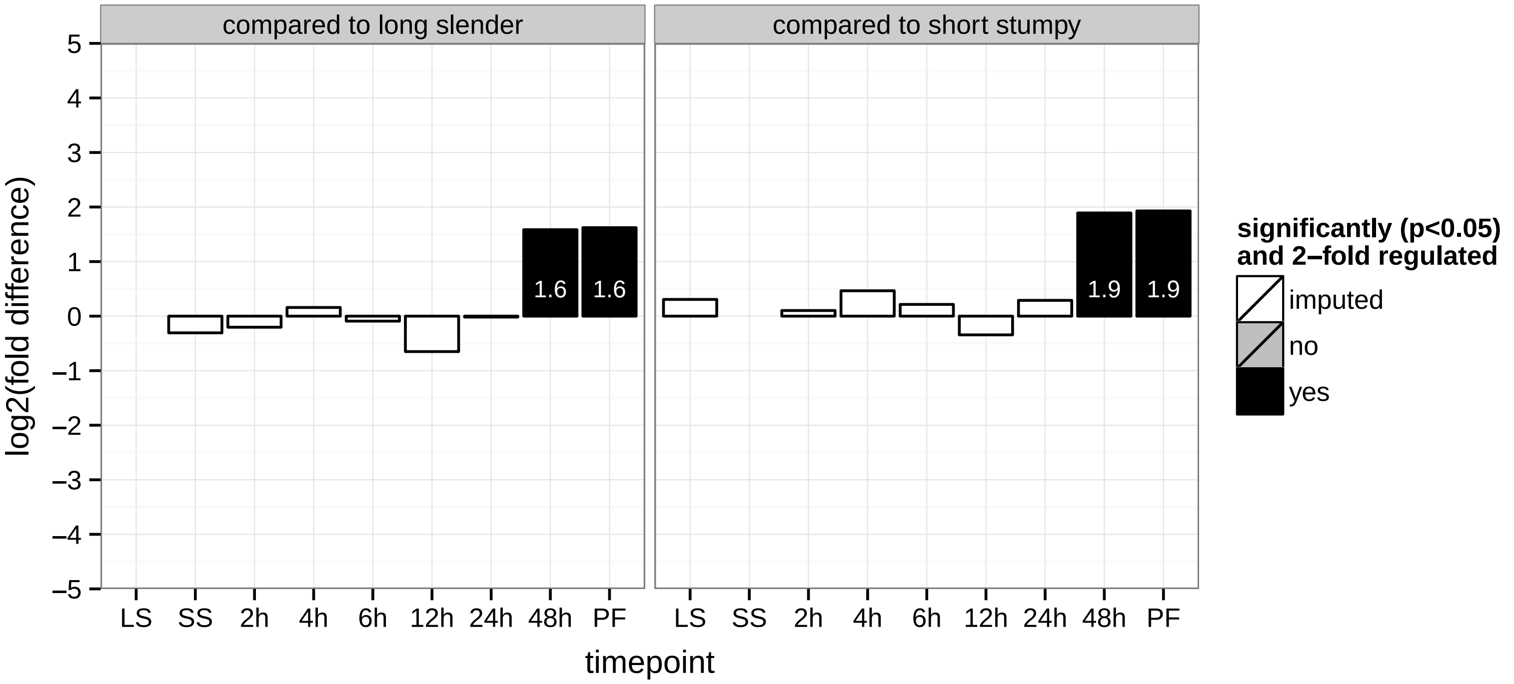
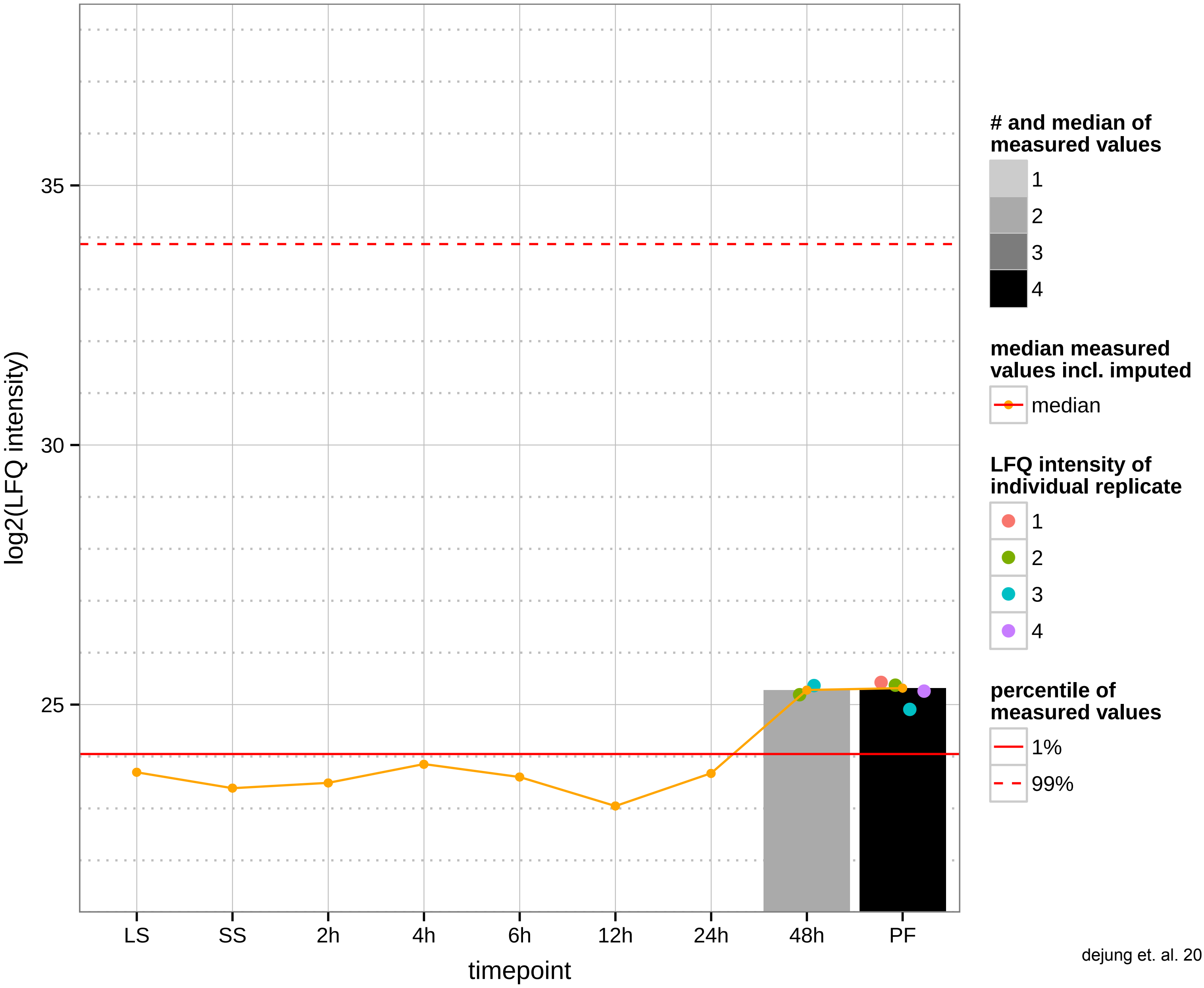
structural maintenance of chromosome 4, putative, dual specificity protein phosphatase, putative (SMC4)
Tb927.10.740
AGOF: null, ATP binding
AGOC: null, chromosome, condensin complex, nucleus
AGOP: null, chromosome organization, chromosome segregation, mitosis
PGOF: null, ATP binding, protein binding
PGOC: null, chromosome
PGOP: null, chromosome organization, DNA recombination, DNA repair, chromosome condensation, chromosome organizati





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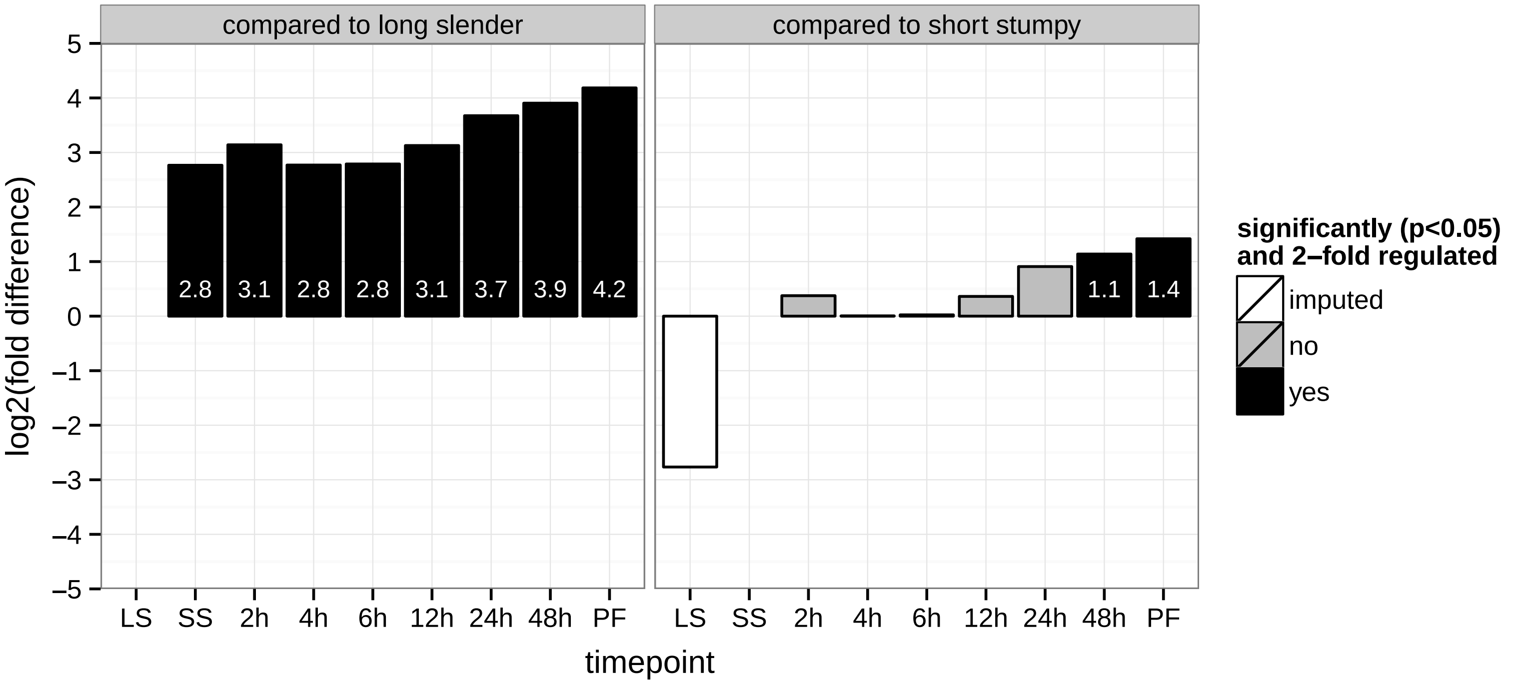
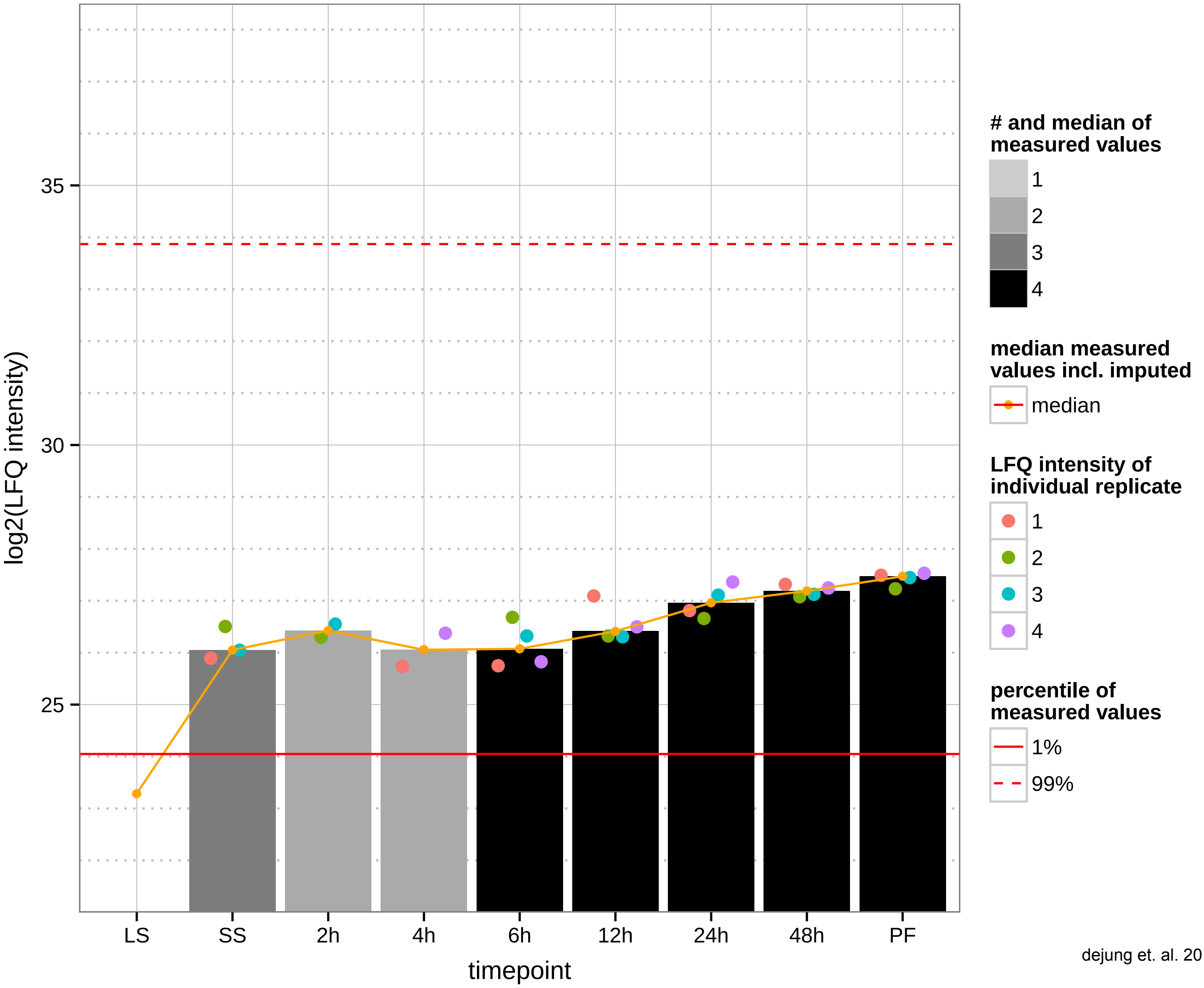
hypothetical protein, conserved
Tb927.10.770
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: translation release factor activity
PGOC: null
PGOP: translational termination





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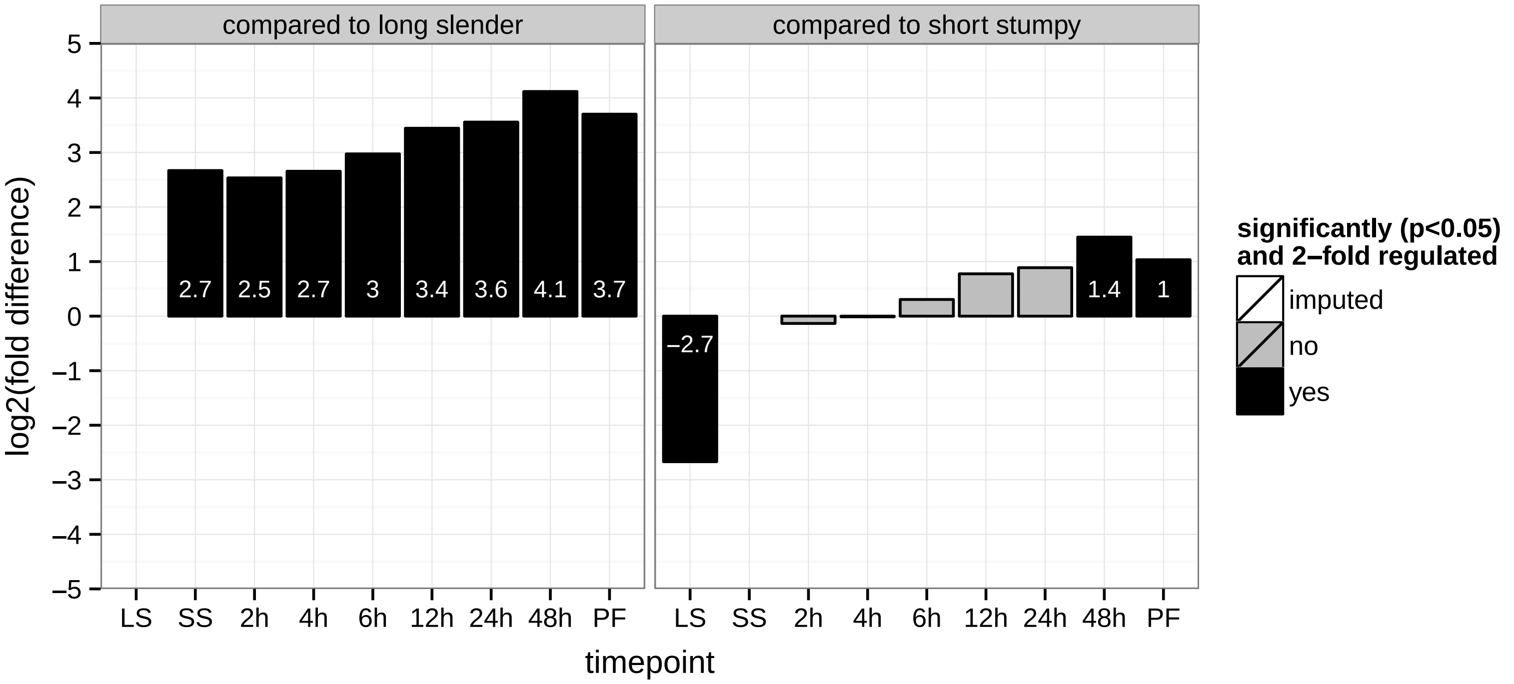
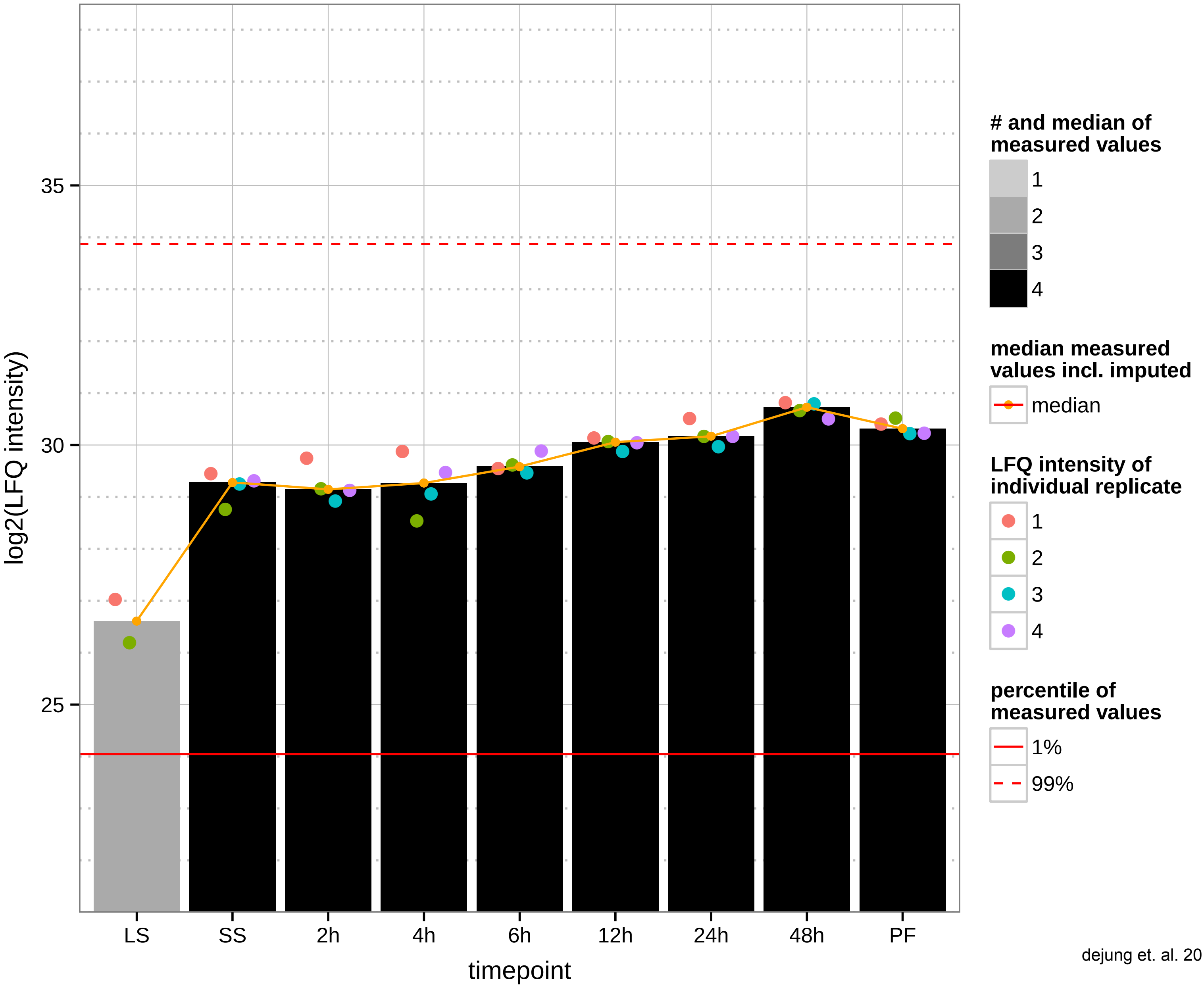
ABC transporter, putative
Tb927.10.7700
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances
AGOC: integral to membrane, internal side of plasma membrane, membrane
AGOP: transport
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: membrane
PGOP: null





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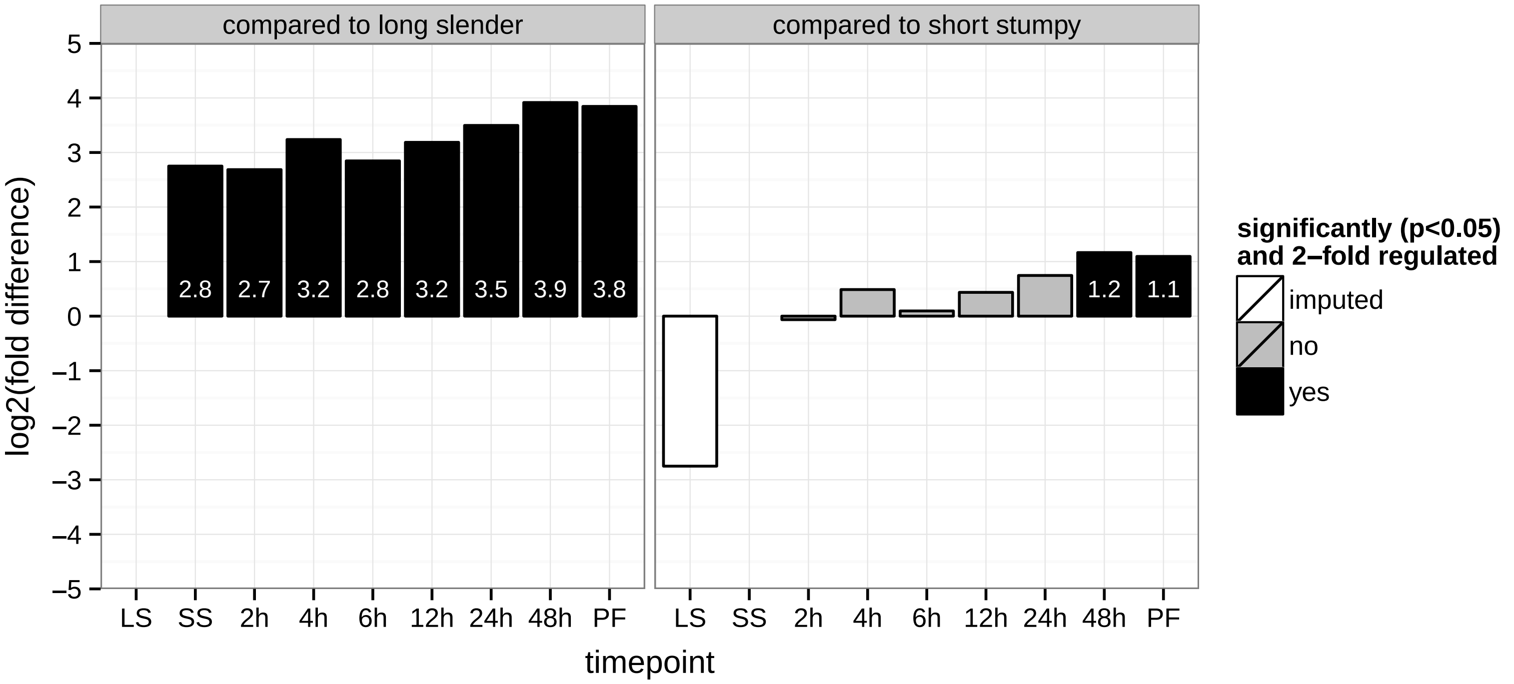
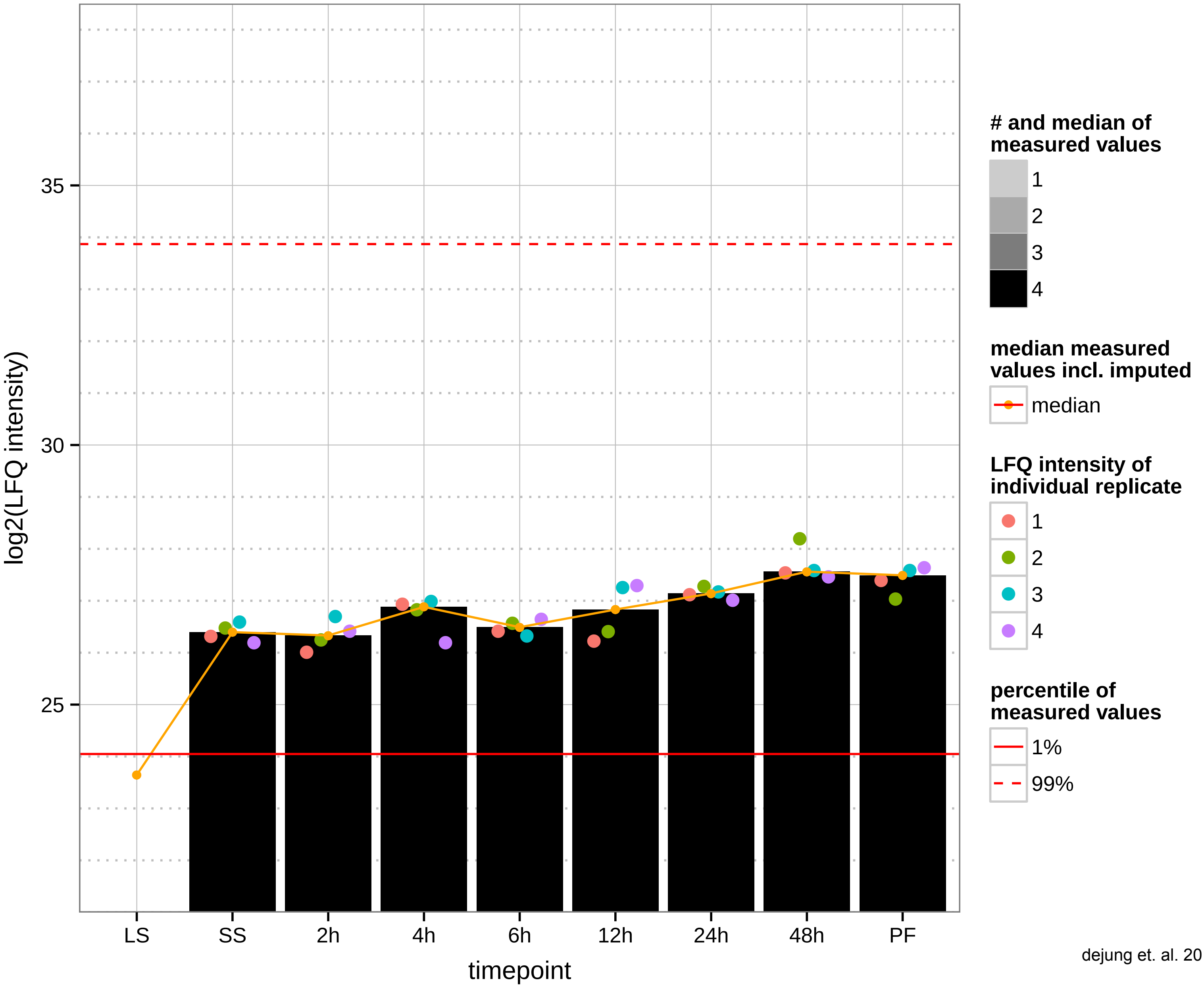
hypothetical protein, conserved
Tb927.10.8630
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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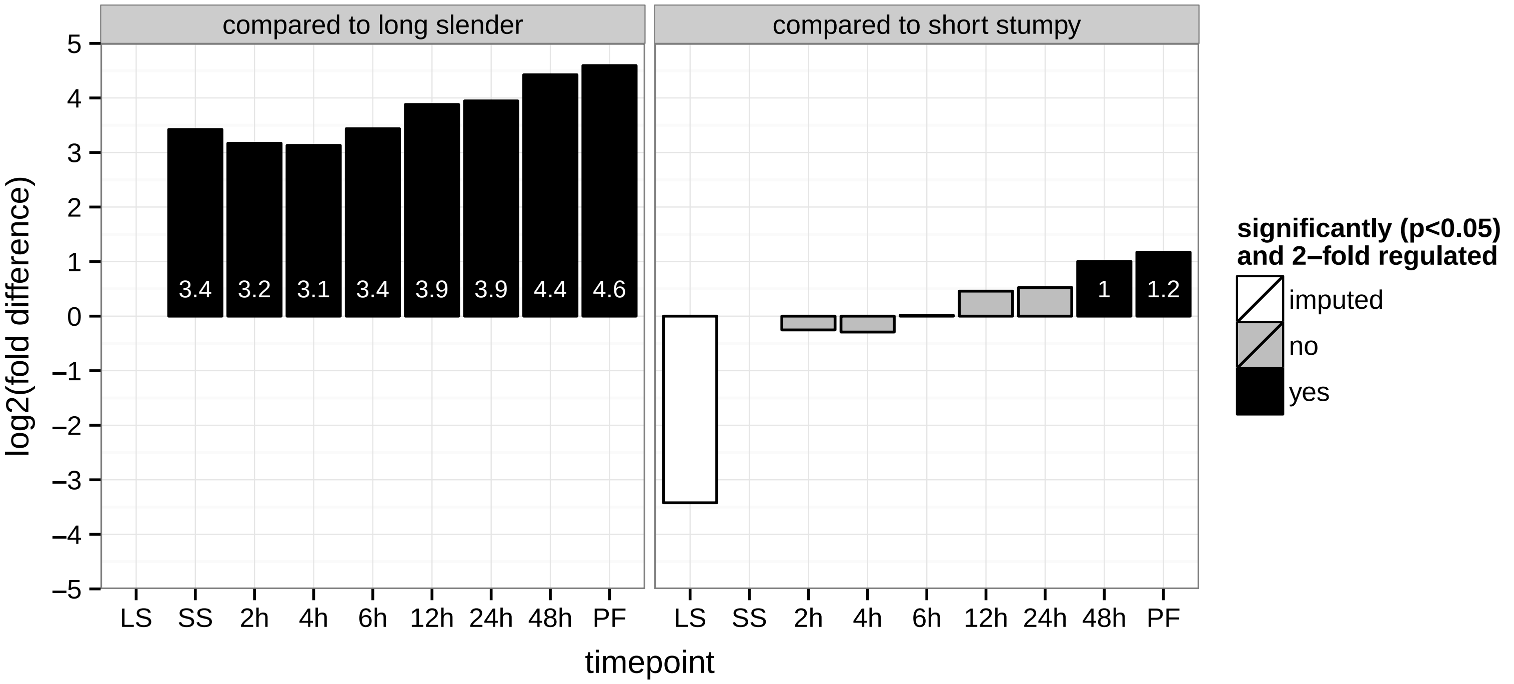
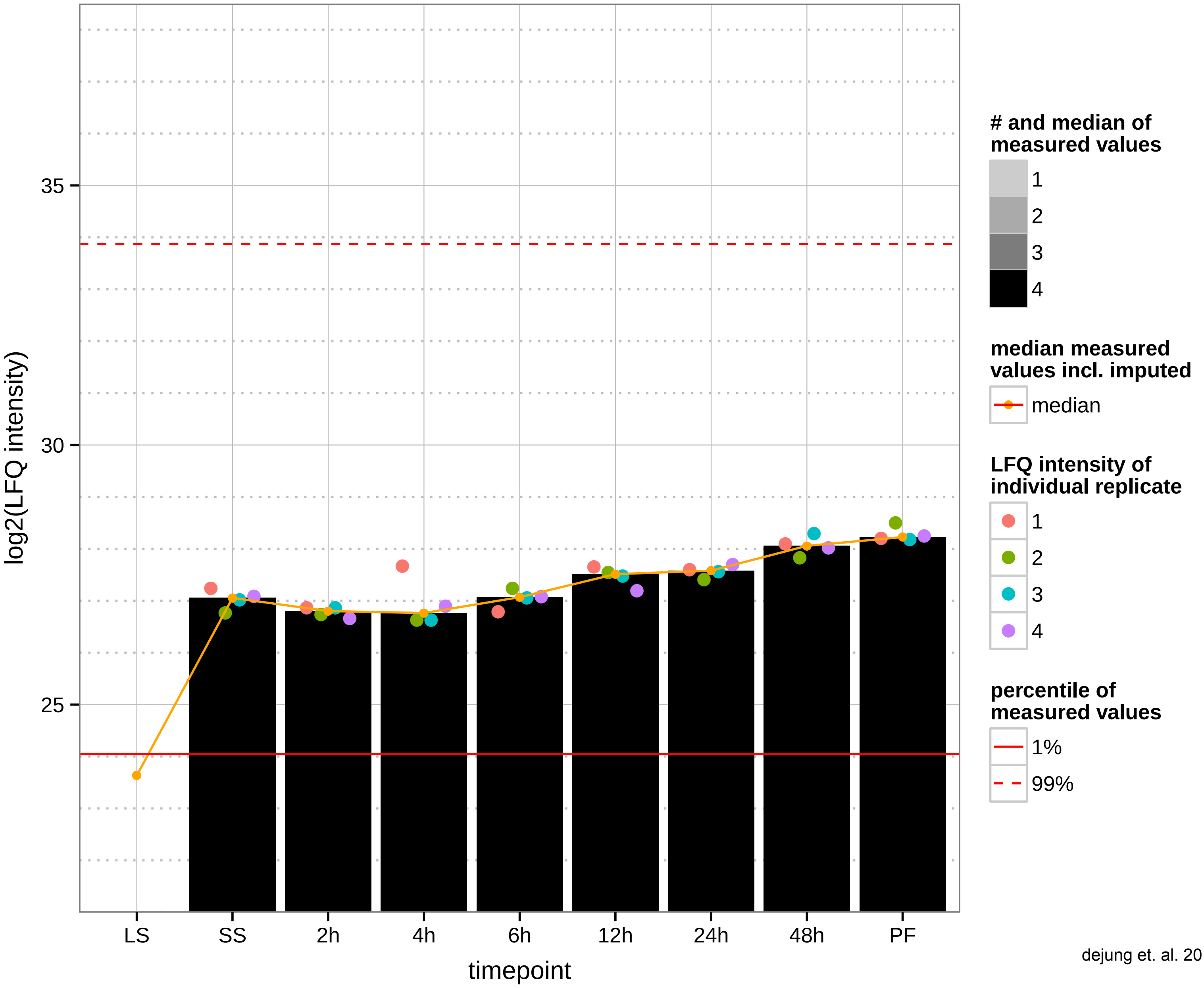
hypothetical protein, conserved
Tb927.10.8730
AGOF: ATP binding, protein kinase activity
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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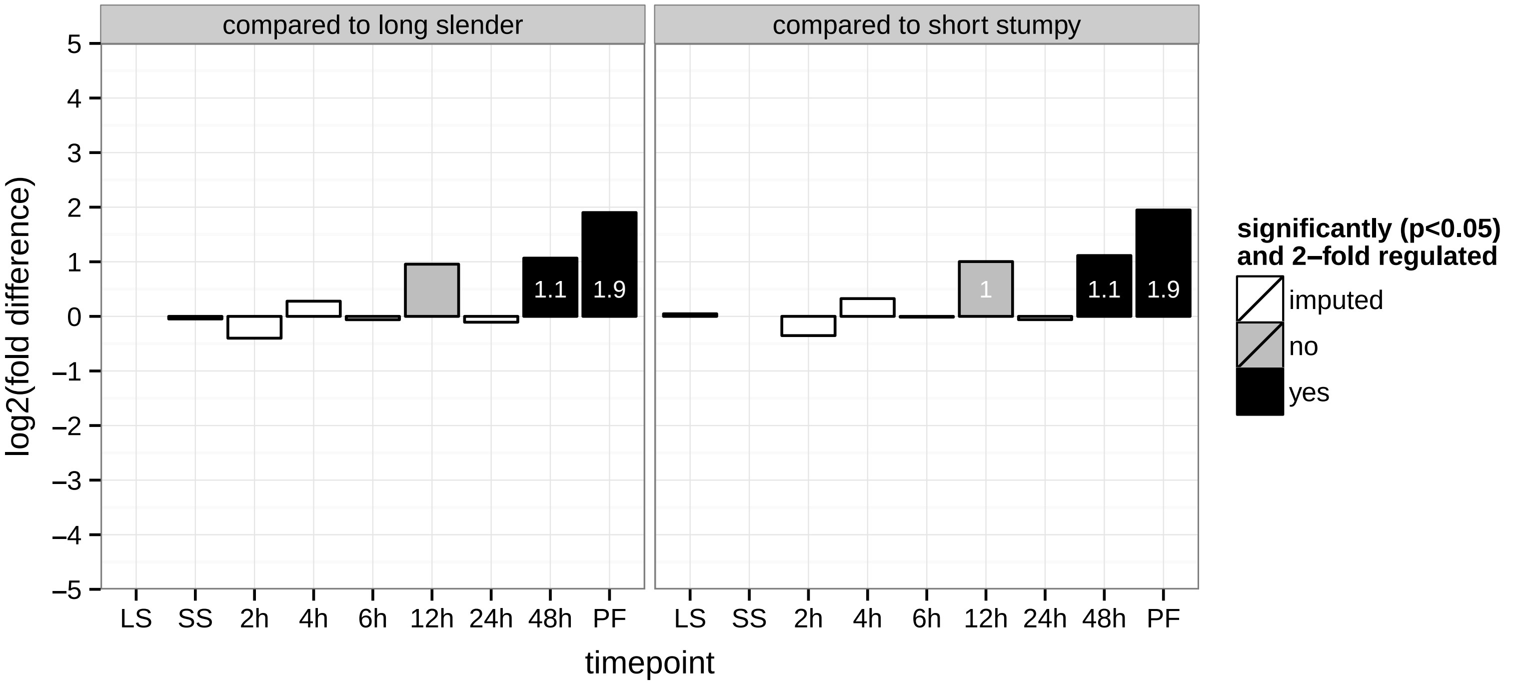
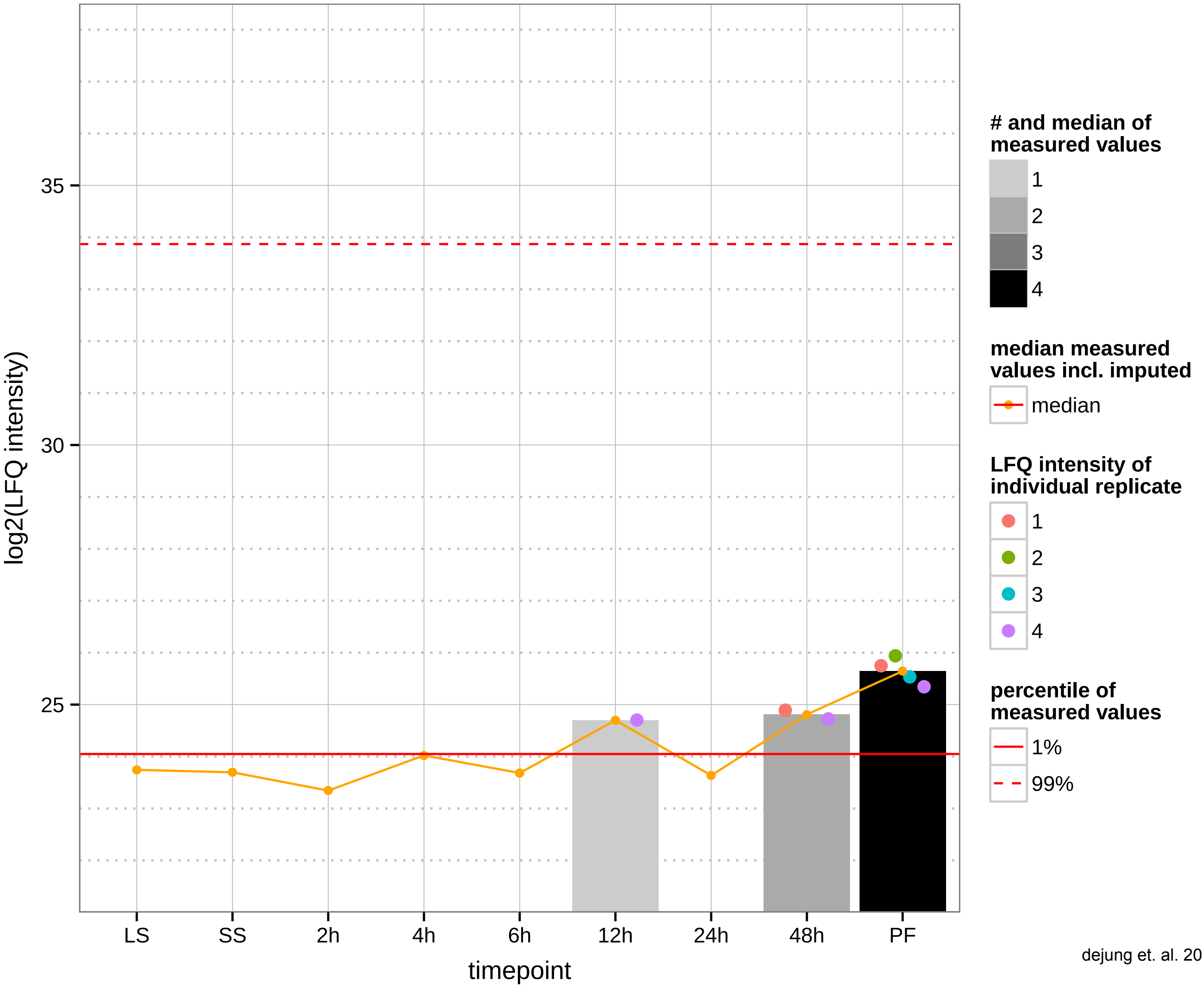
hypothetical protein, conserved
Tb927.11.10320
AGOF: endodeoxyribonuclease activity, producing 5'−phosphomonoesters
AGOC: null
AGOP: null
PGOF: endodeoxyribonuclease activity, producing 5'−phosphomonoesters
PGOC: null
PGOP: null





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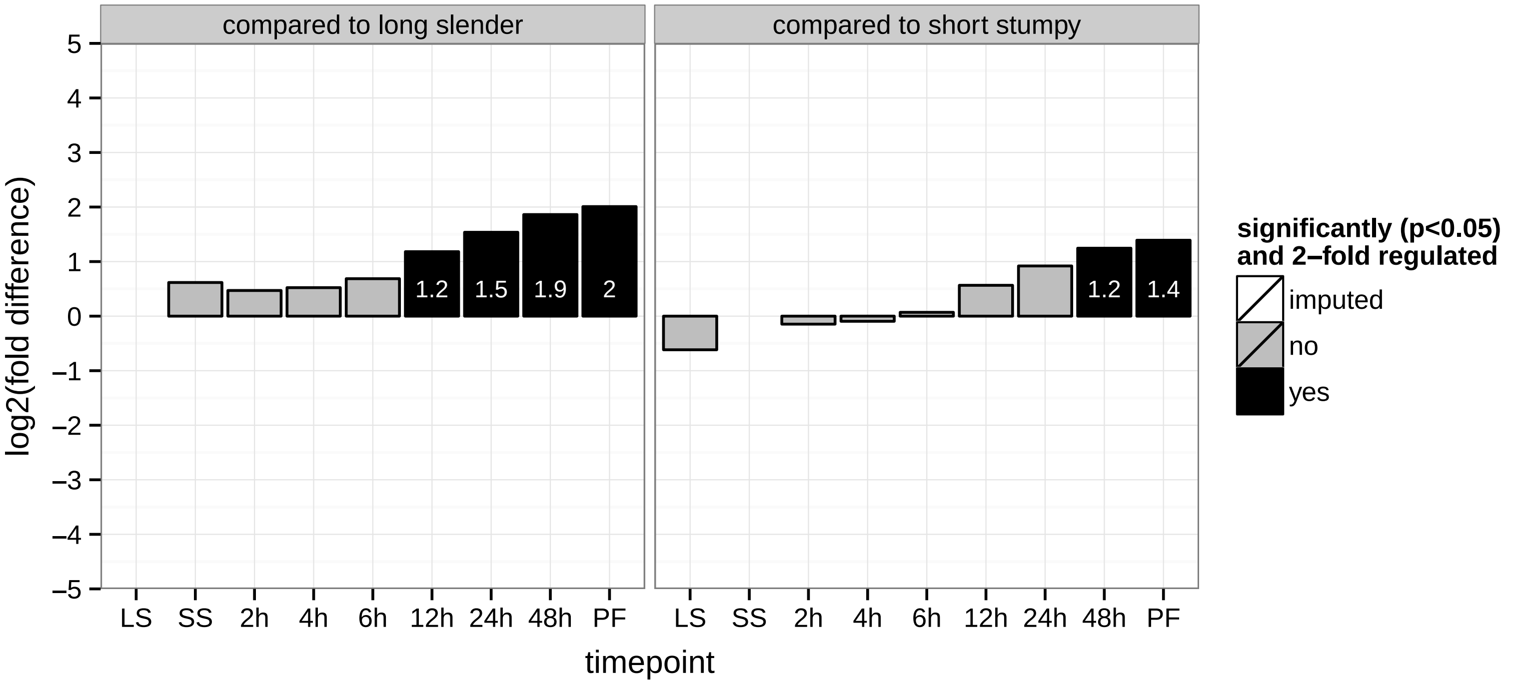
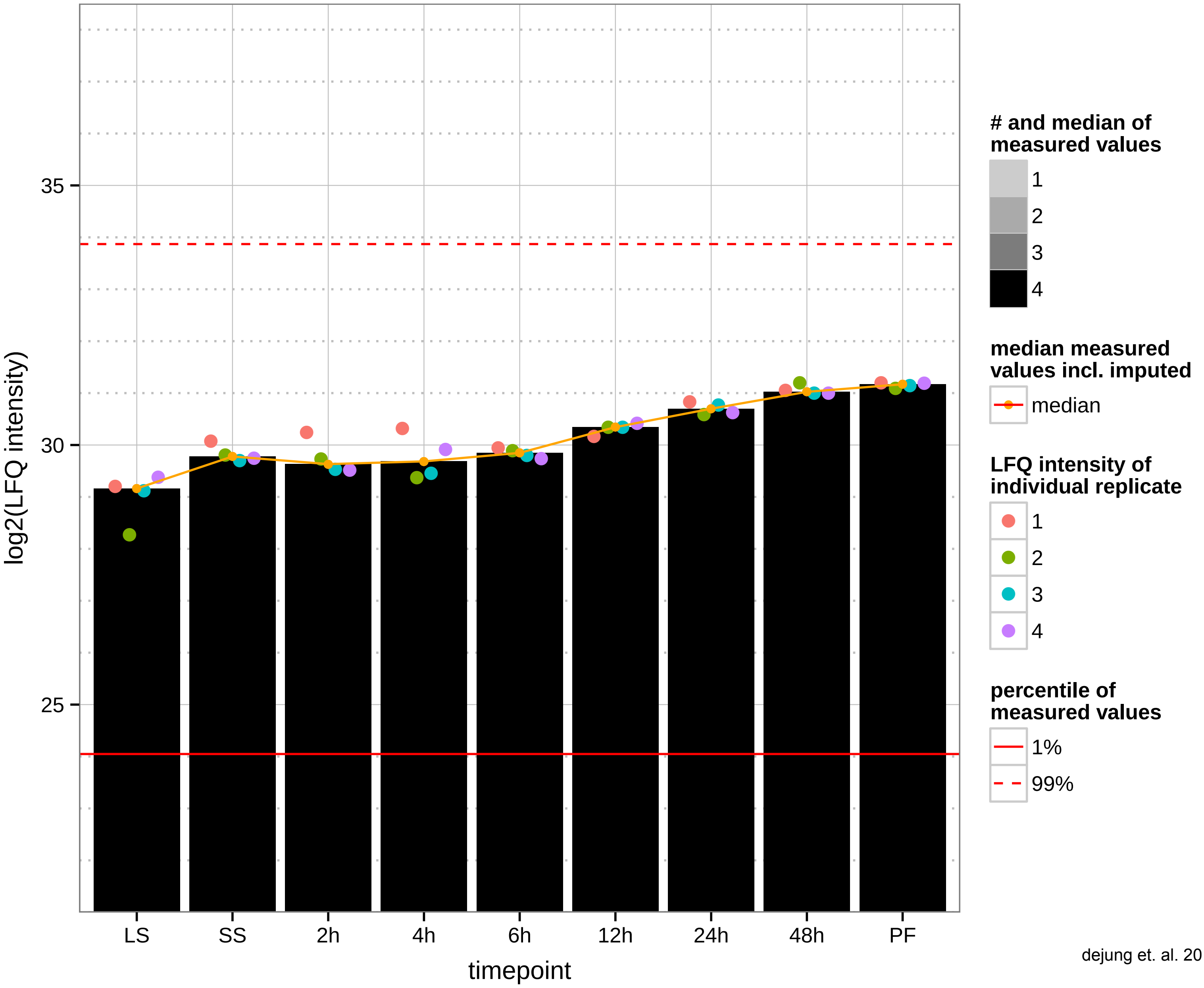
hypothetical protein, conserved
Tb927.11.11460
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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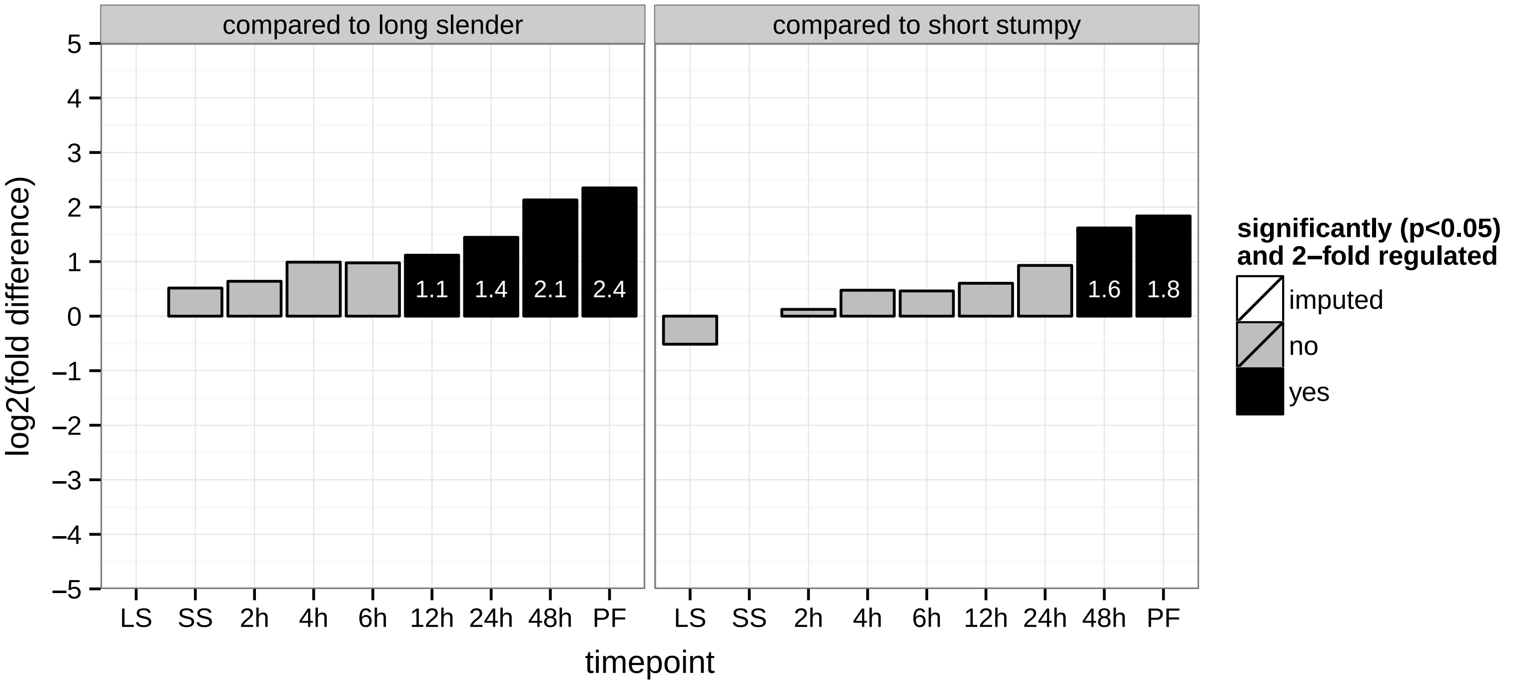
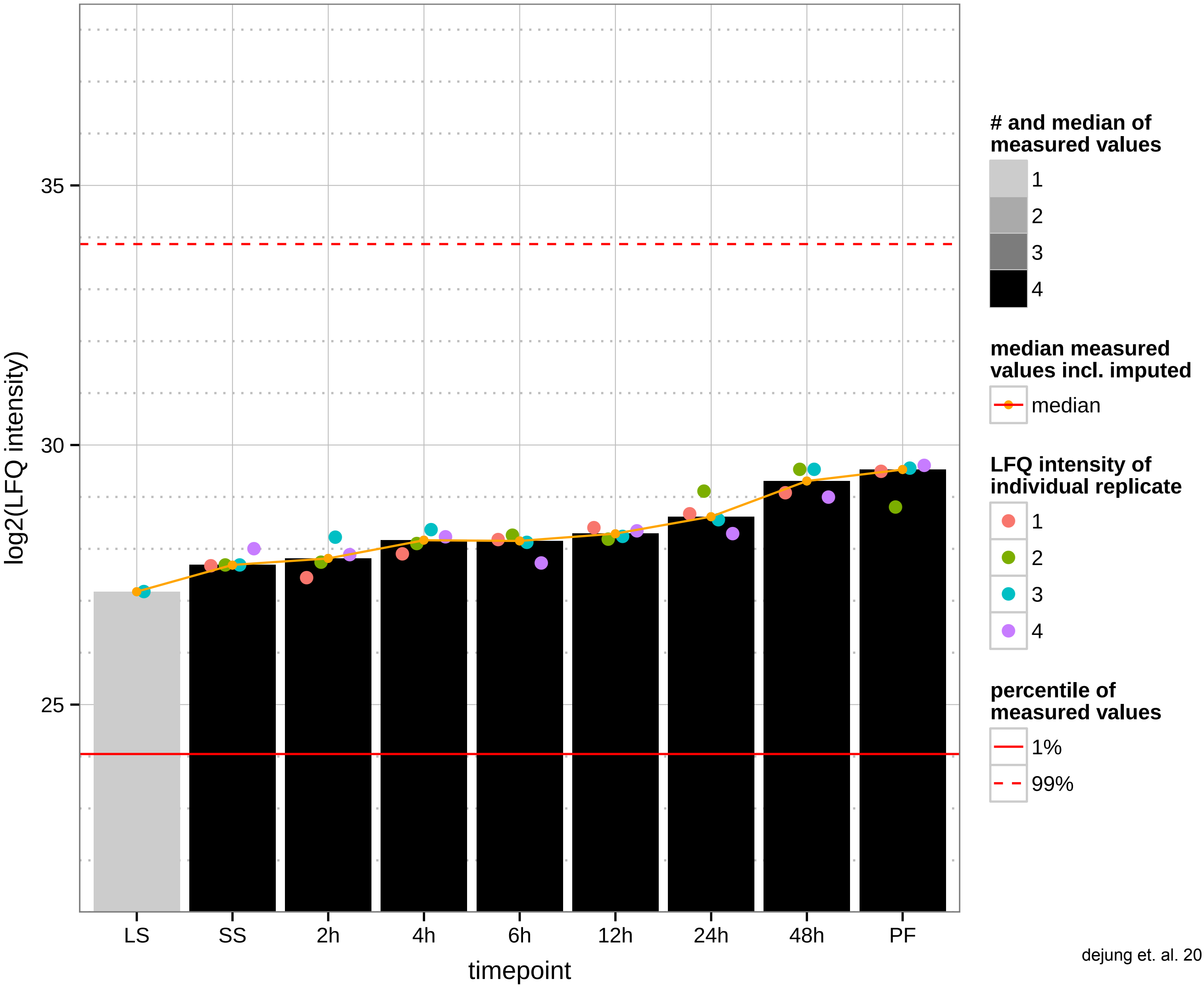
glutaredoxin, putative
Tb927.11.1370
AGOF: disulfide oxidoreductase activity, electron carrier activity, protein disulfide isomerase activity, protein disulfide oxidoredu
AGOC: mitochondrion
AGOP: cell redox homeostasis, oxidation–reduction process
PGOF: electron carrier activity, protein disulfide oxidoreductase activity
PGOC: null
PGOP: cell redox homeostasis





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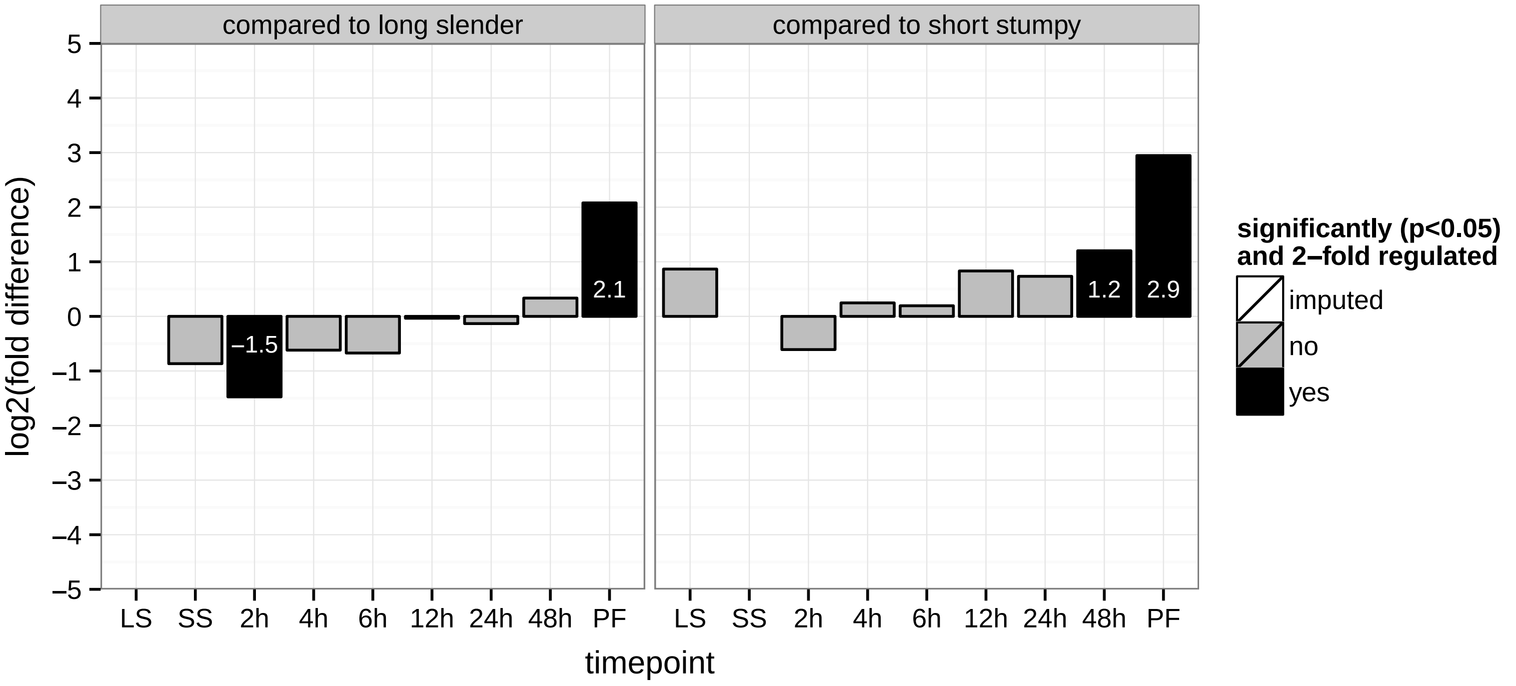
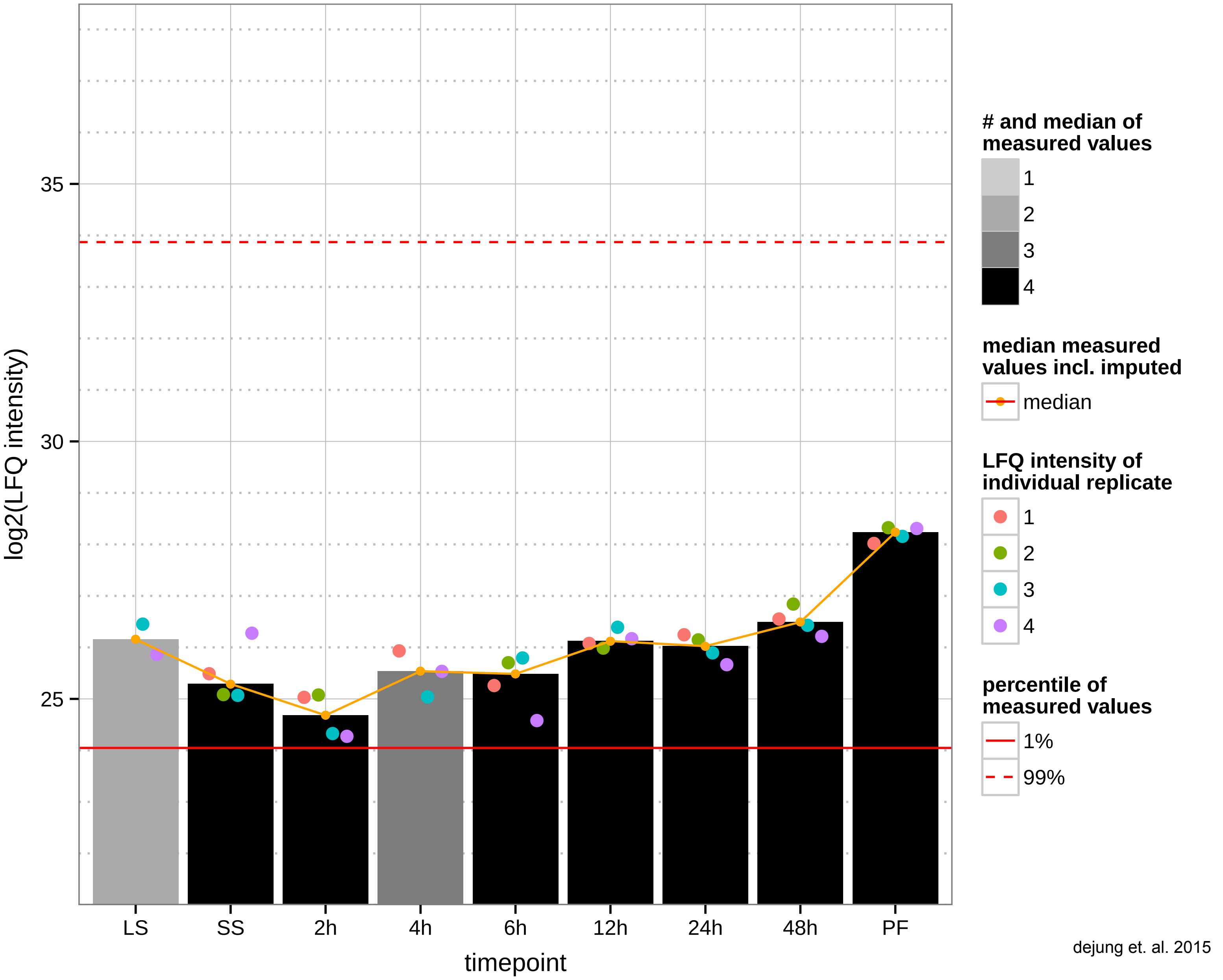
hypothetical protein, conserved
Tb927.11.14170
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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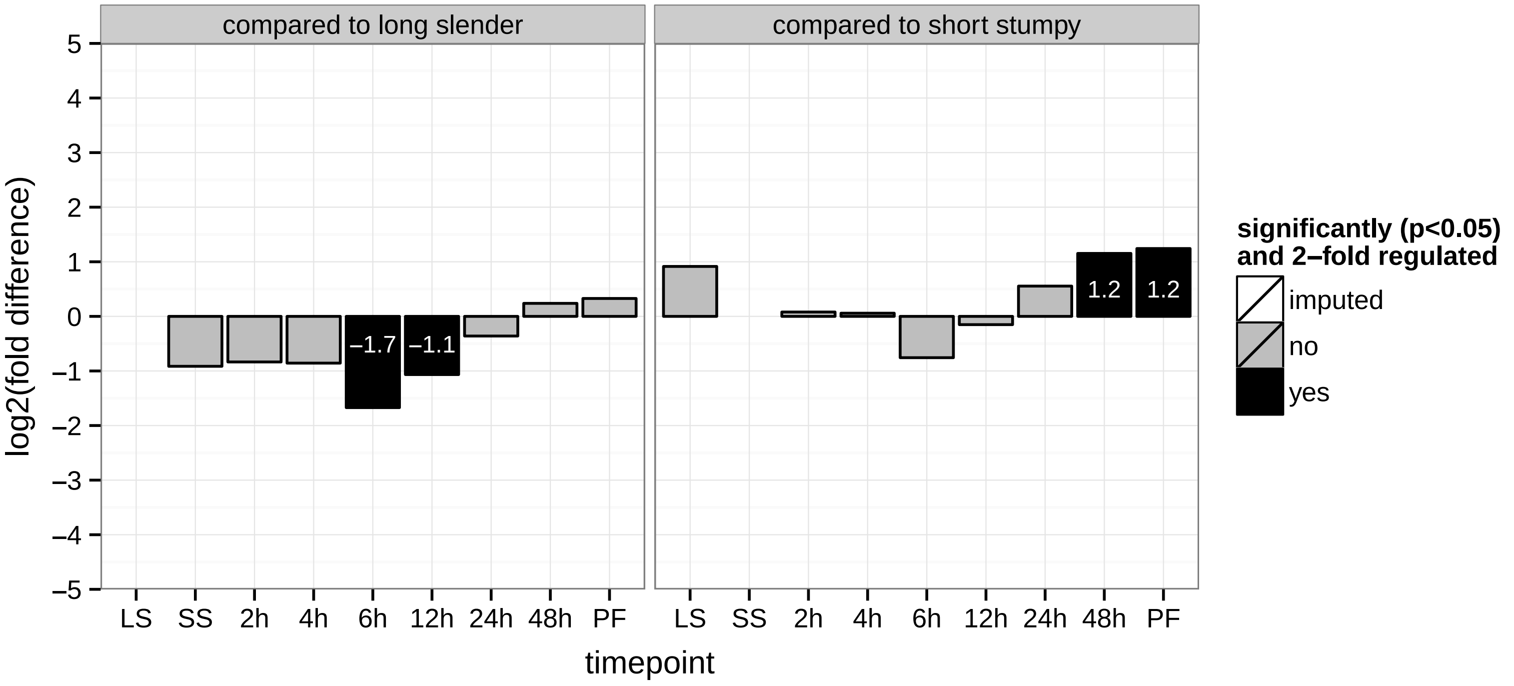
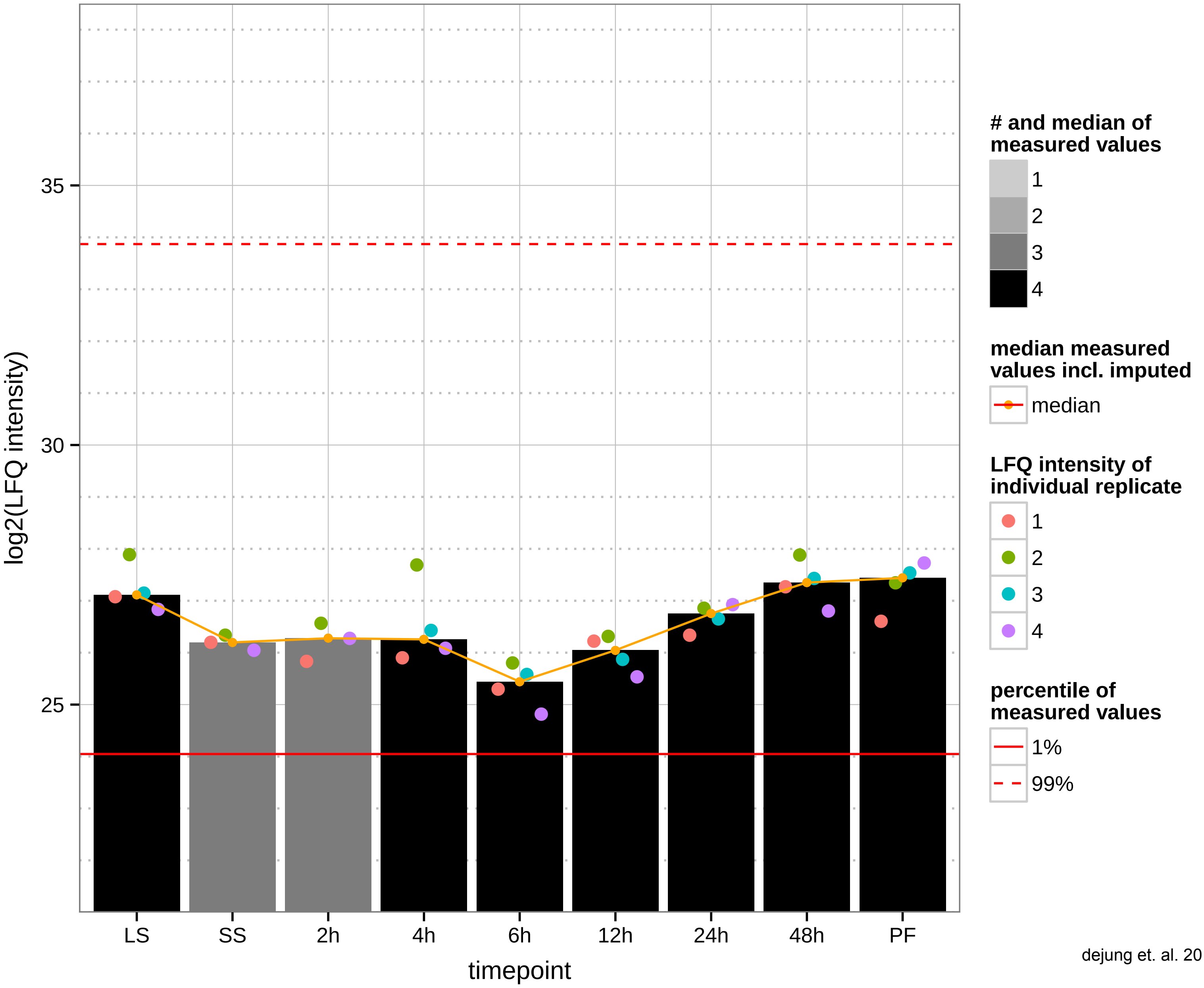
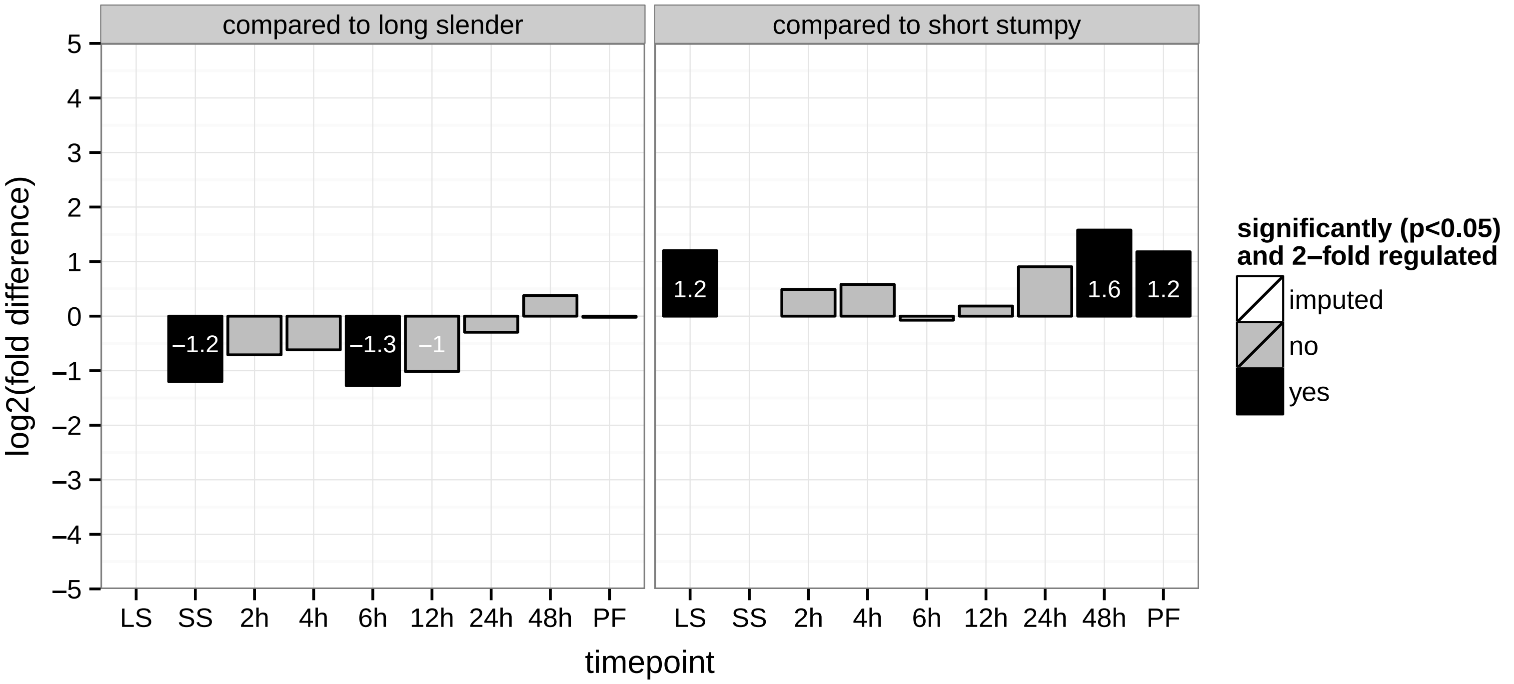
ubiquitin–conjugating enzyme E2, putative, ubiquitin carrier protein, ubiquitin–protein ligase
Tb927.11.14200
AGOF: ubiquitin–protein ligase activity
AGOC: null
AGOP: cellular protein modification process, post–translational protein modification, regulation of protein metabolic process
PGOF: acid–amino acid ligase activity
PGOC: null
PGOP: null

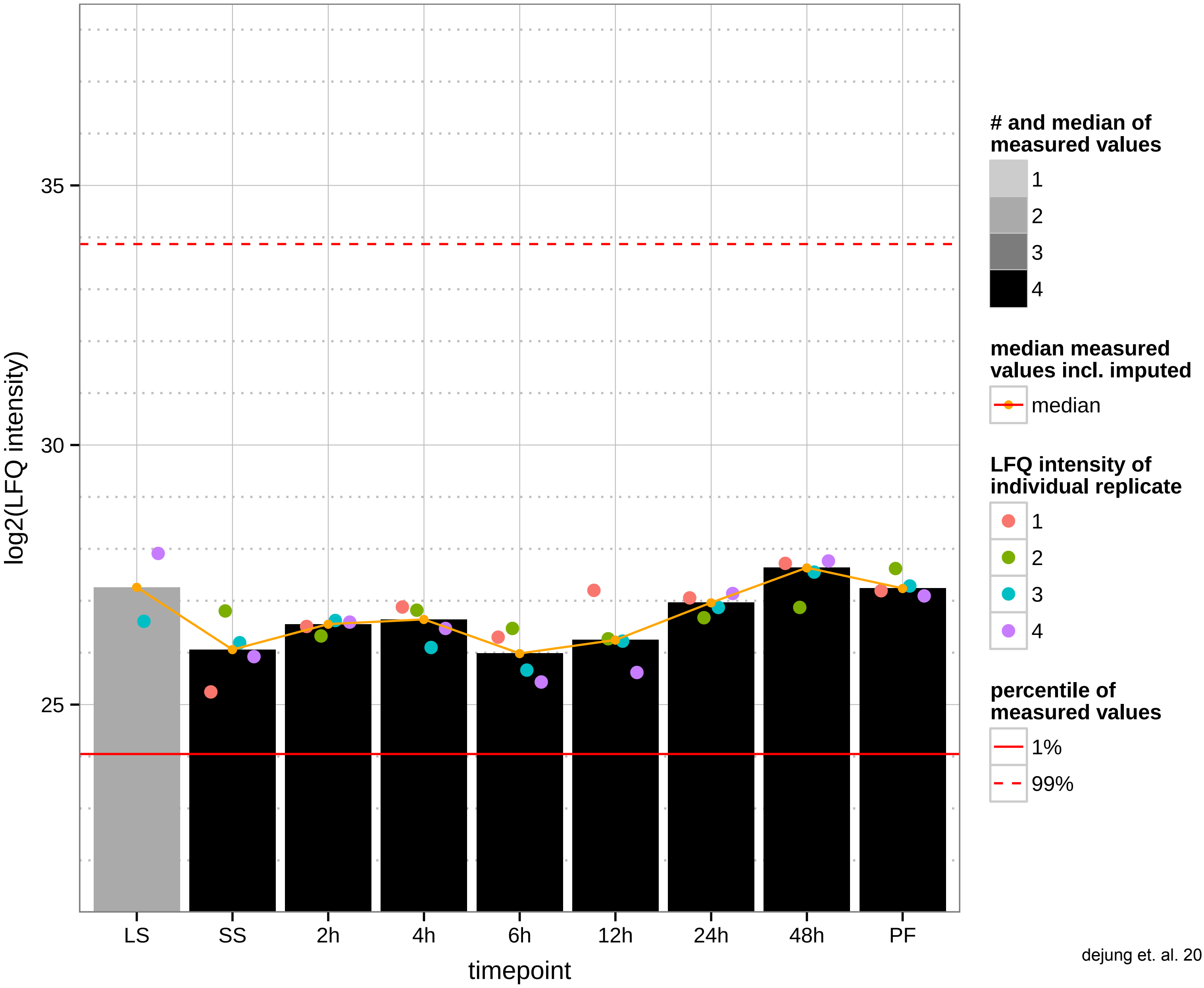




dejung et. al. 2015

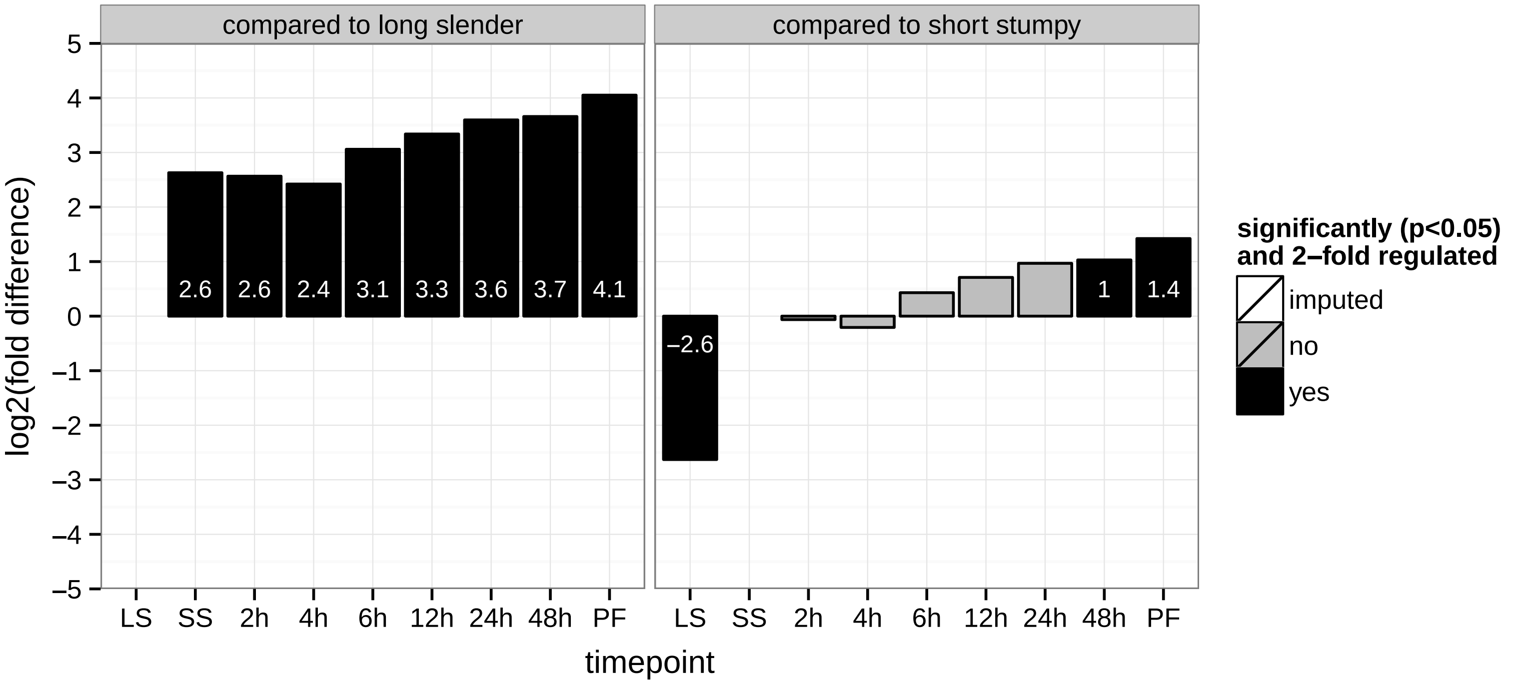
hypothetical protein, conserved
Tb927.11.14980
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

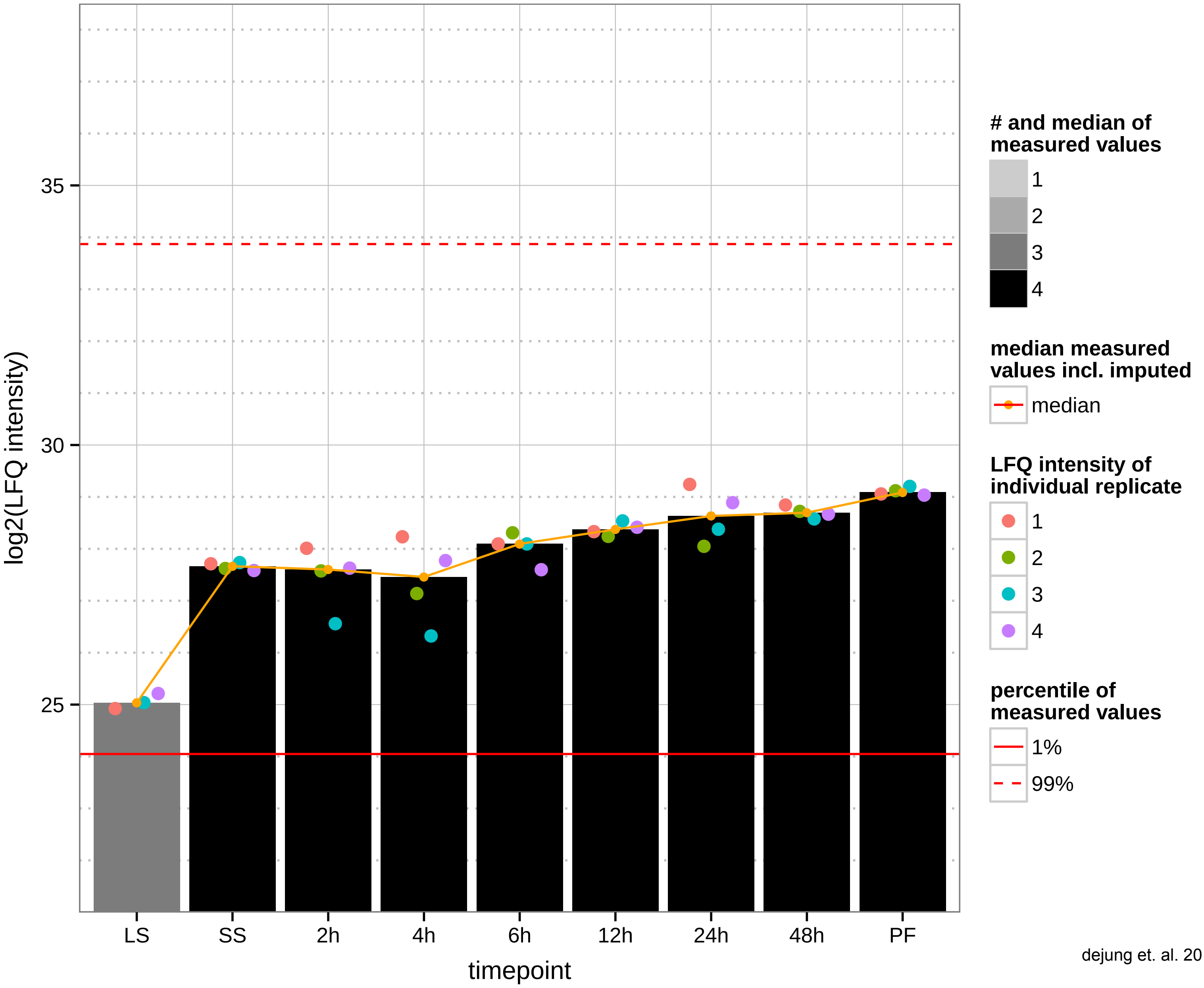




dejung et. al. 2015

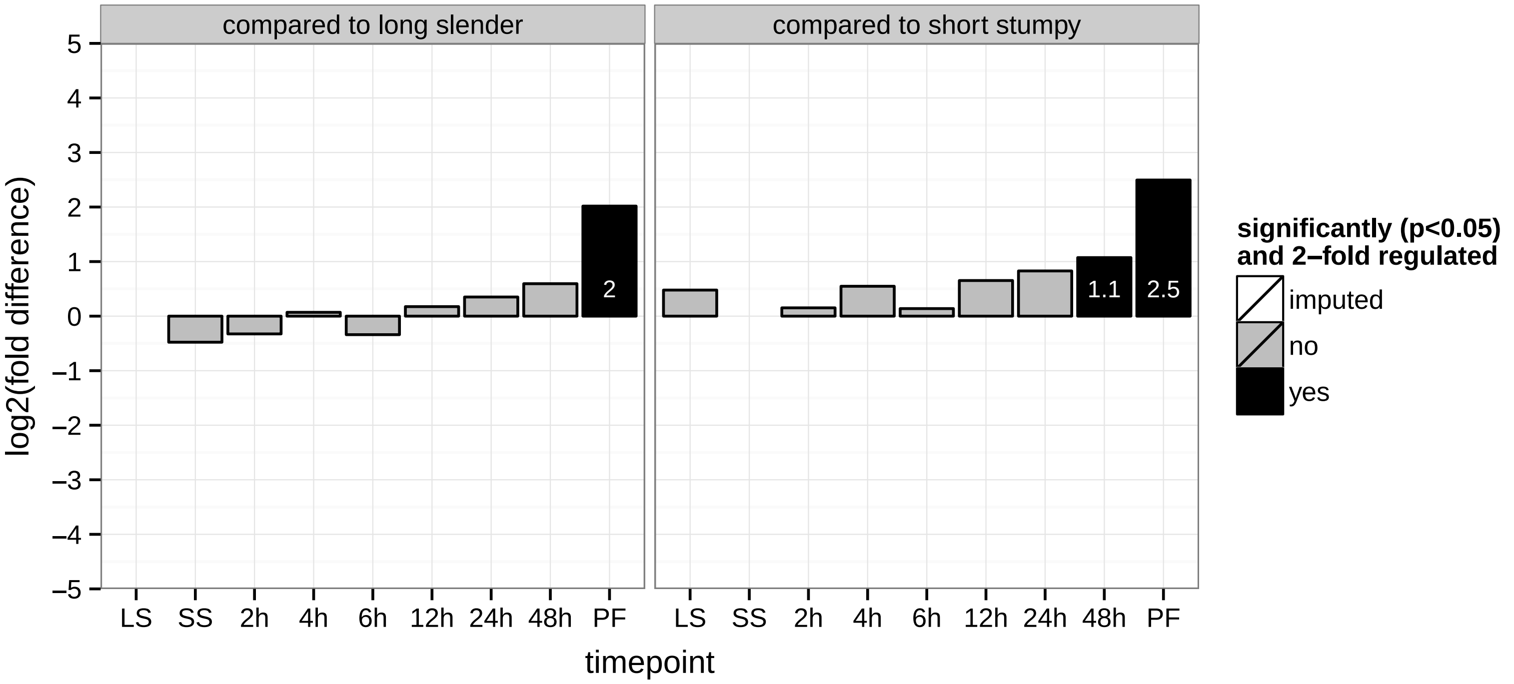
hypothetical protein, conserved
Tb927.11.2120
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

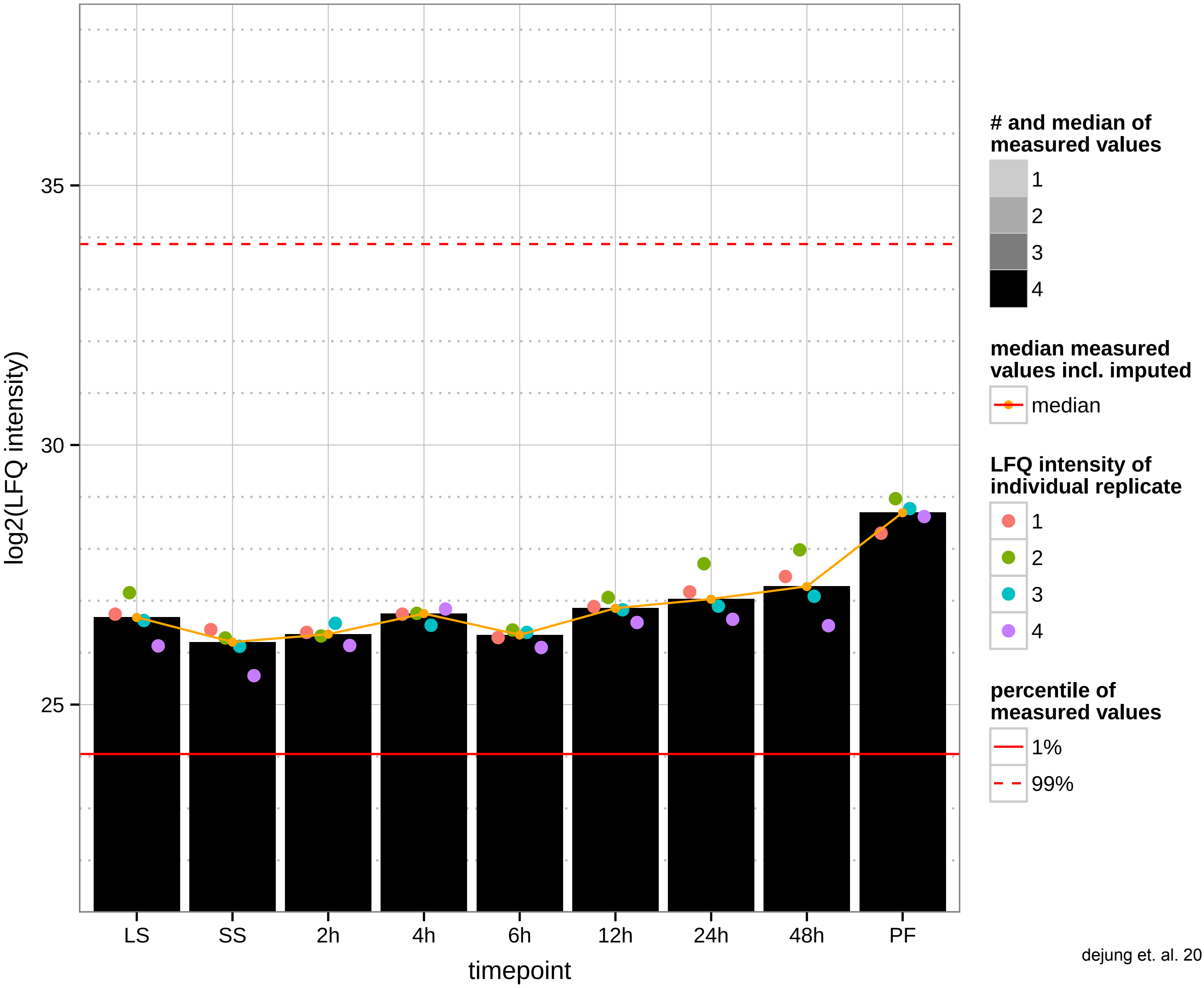




dejung et. al. 2015

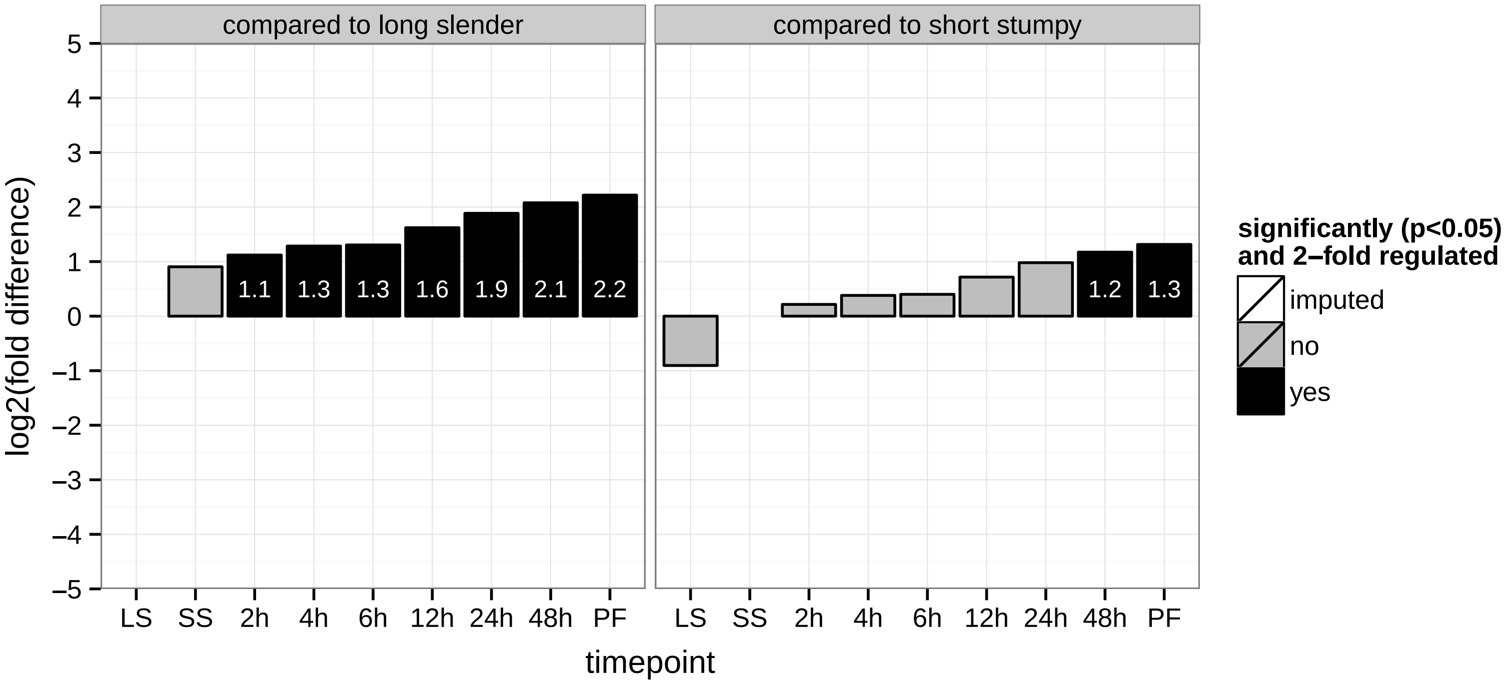
hypothetical protein, conserved
Tb927.11.2840
AGOF: null
AGOC: null
AGOP: null
PGOF: phosphatase activity
PGOC: null
PGOP: null

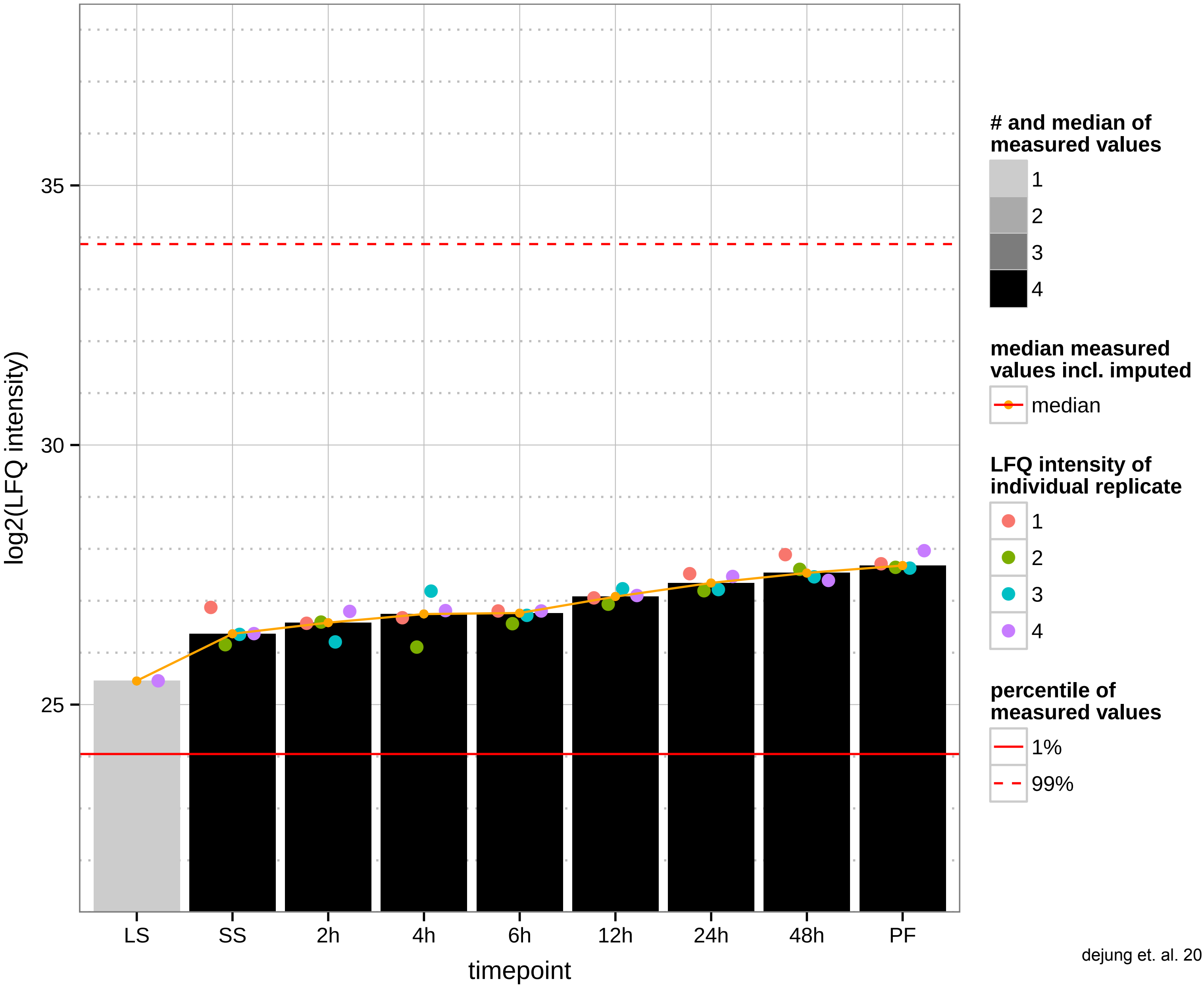




dejung et. al. 2015

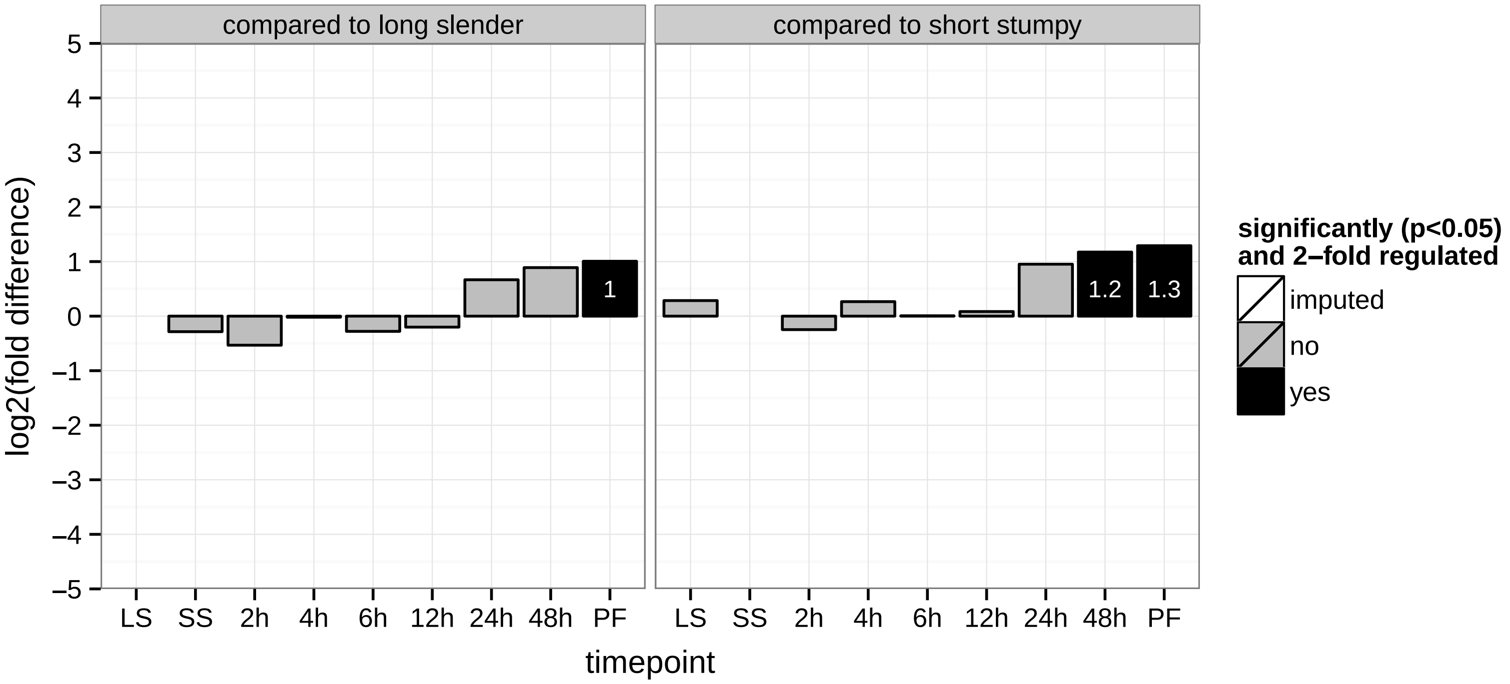
Ribosome assembly protein rrb1, putative
Tb927.11.3070
AGOF: null
AGOC: nucleolus
AGOP: ribosome biogenesis
PGOF: protein binding
PGOC: null
PGOP: null

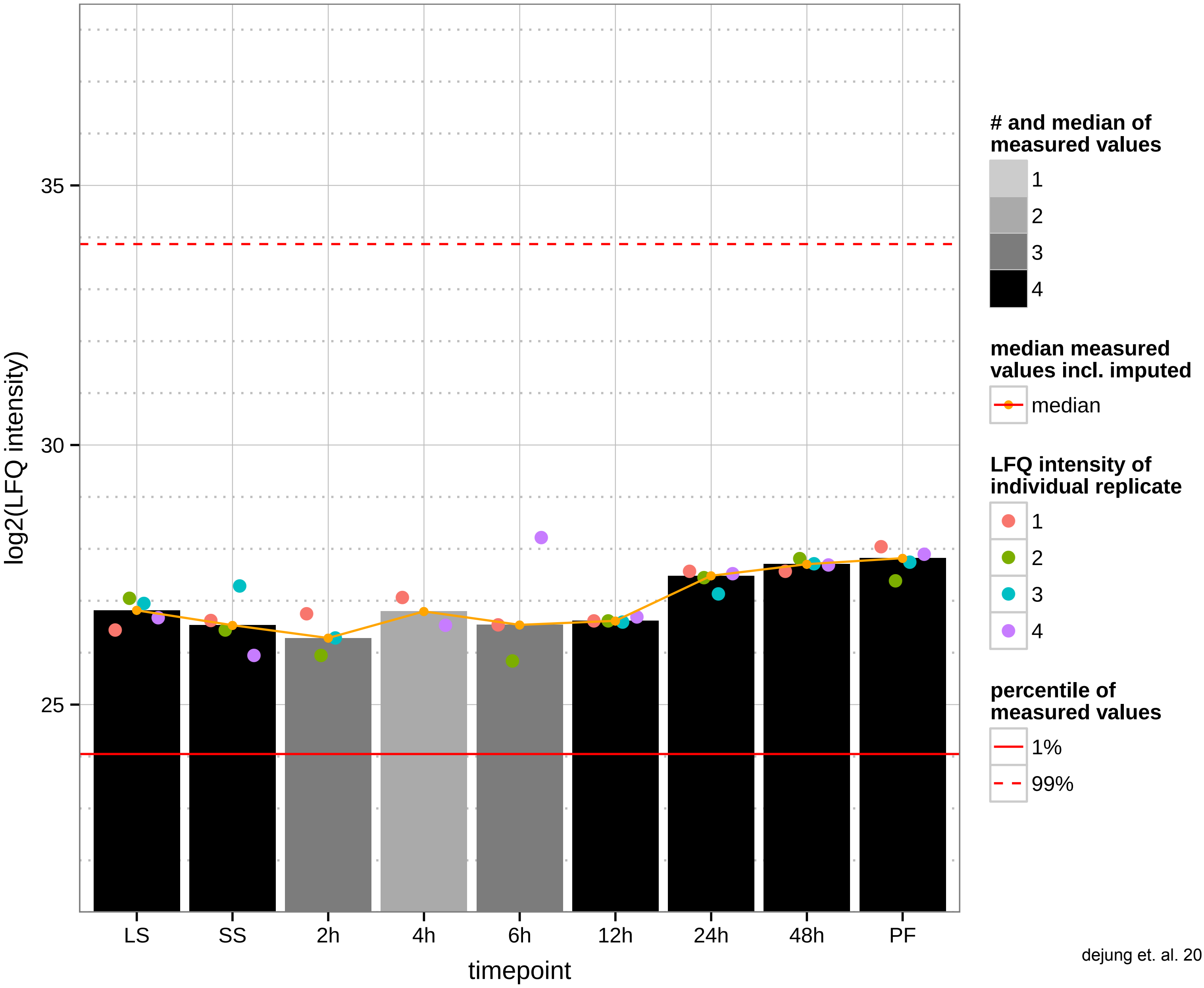




dejung et. al. 2015

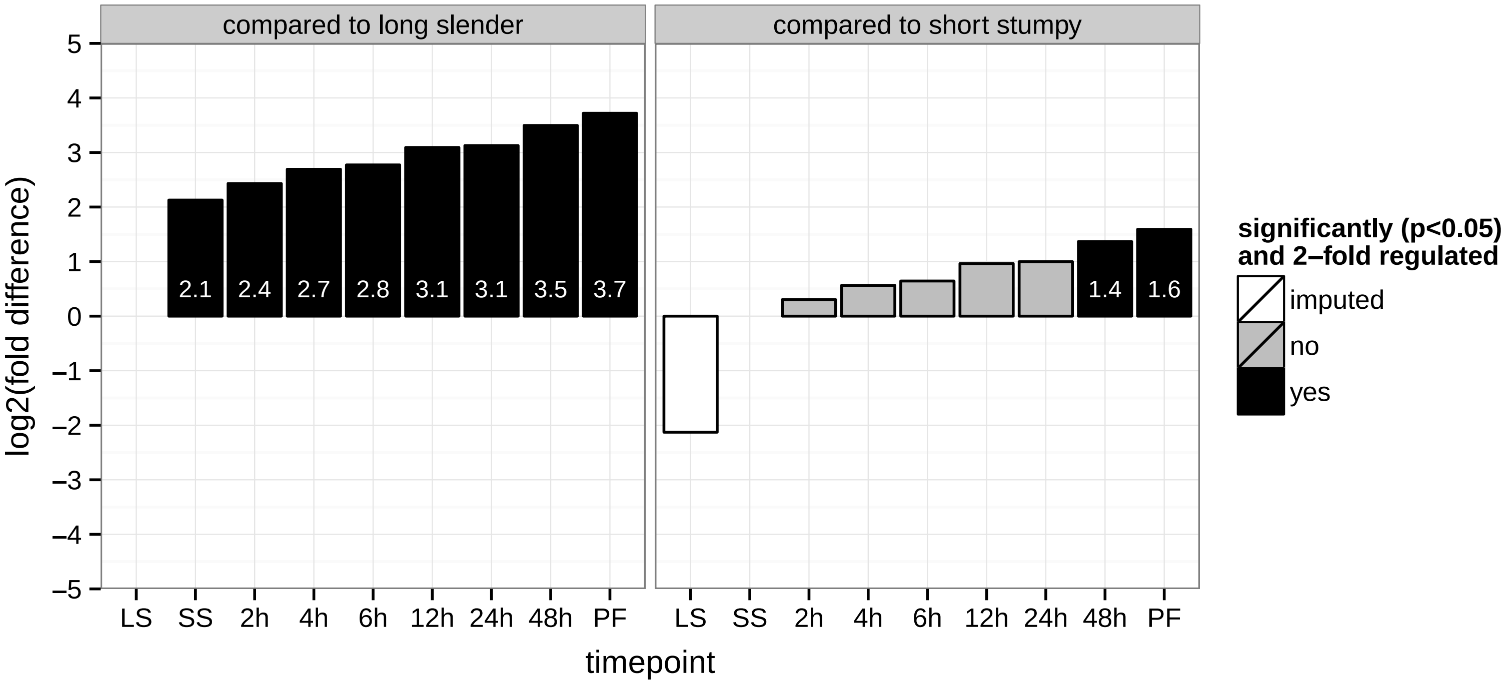
hypothetical protein, conserved
Tb927.11.4420
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

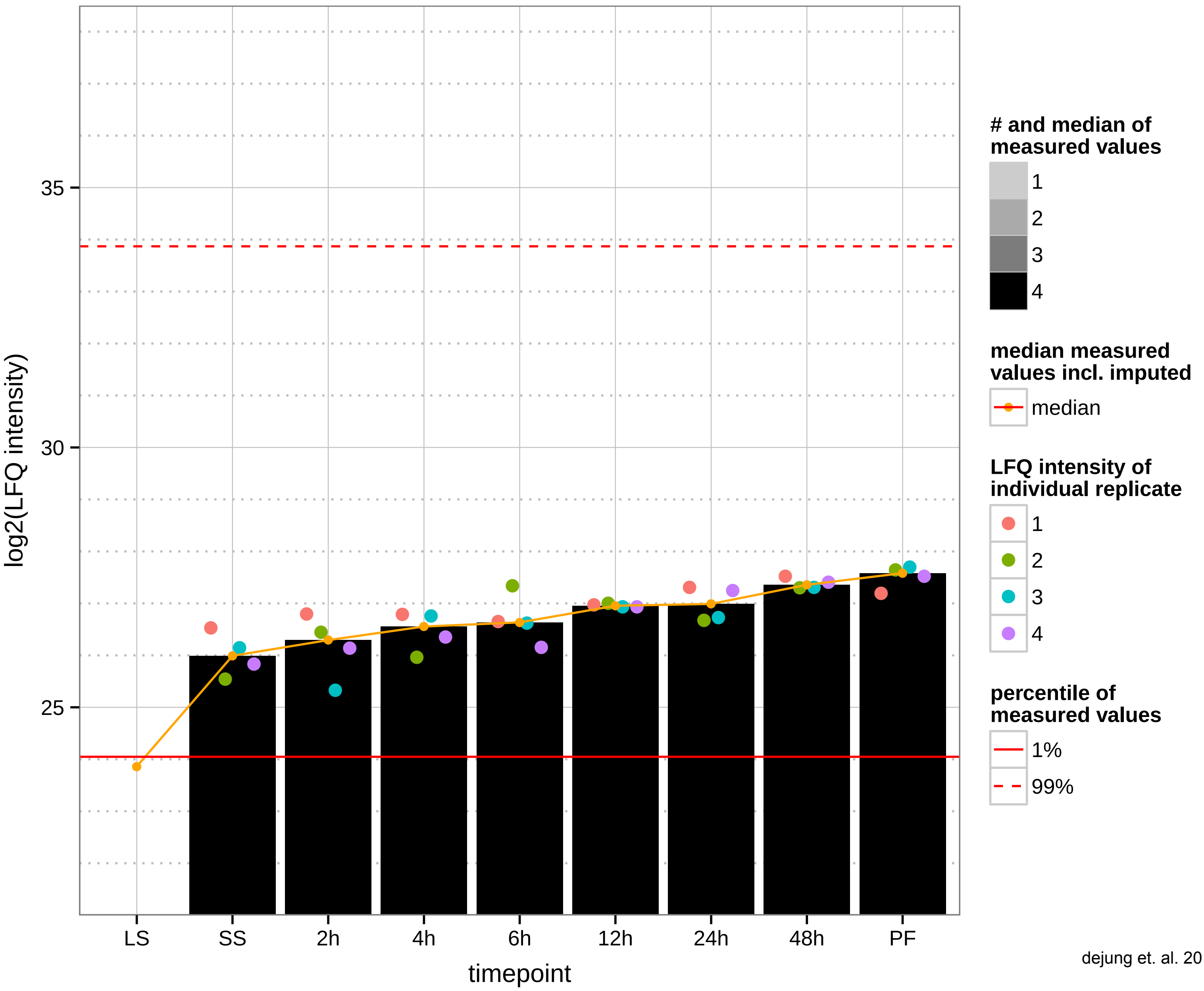




dejung et. al. 2015

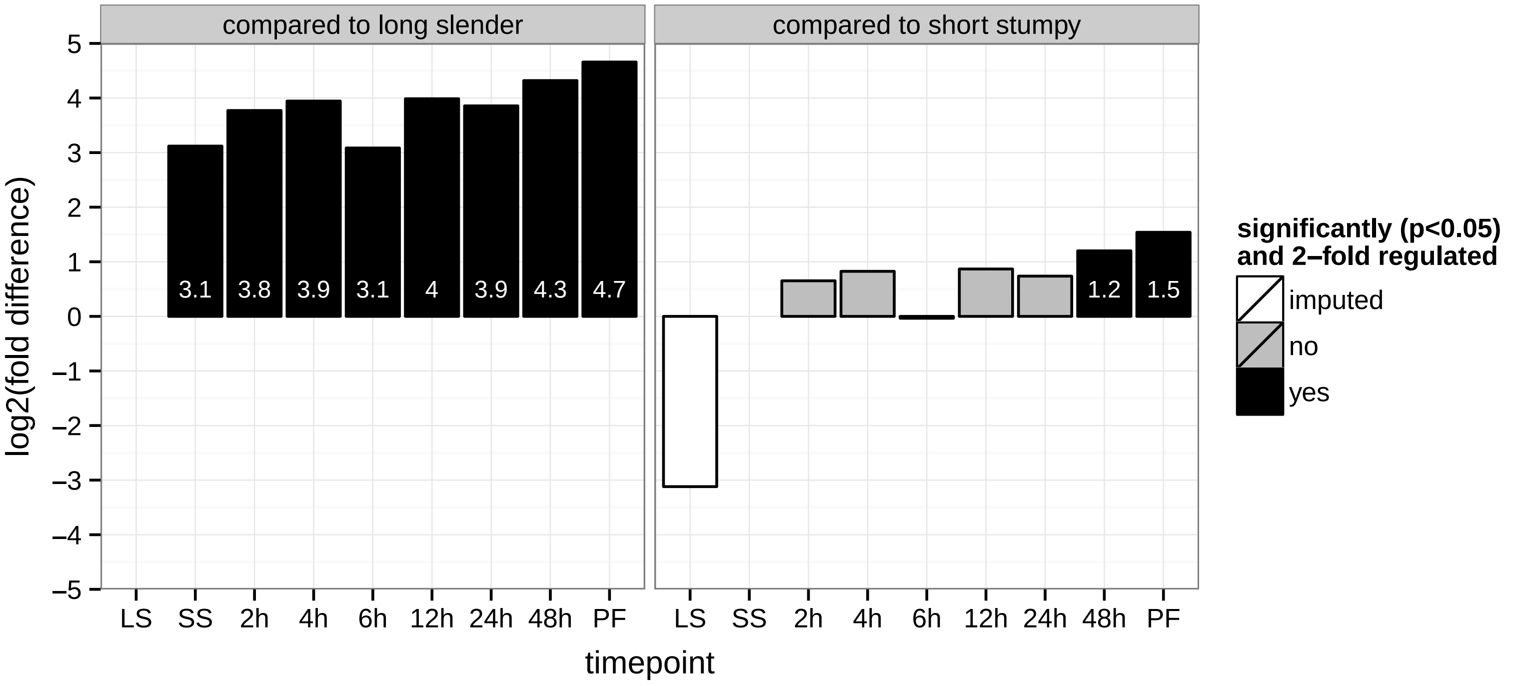
pyruvate dehydrogenase (lipoamide) kinase, putative
Tb927.11.4780
AGOF: ATP binding, pyruvate dehydrogenase (acetyl–transferring) kinase activity
AGOC: mitochondrion
AGOP: null
PGOF: ATP binding
PGOC: null
PGOP: null

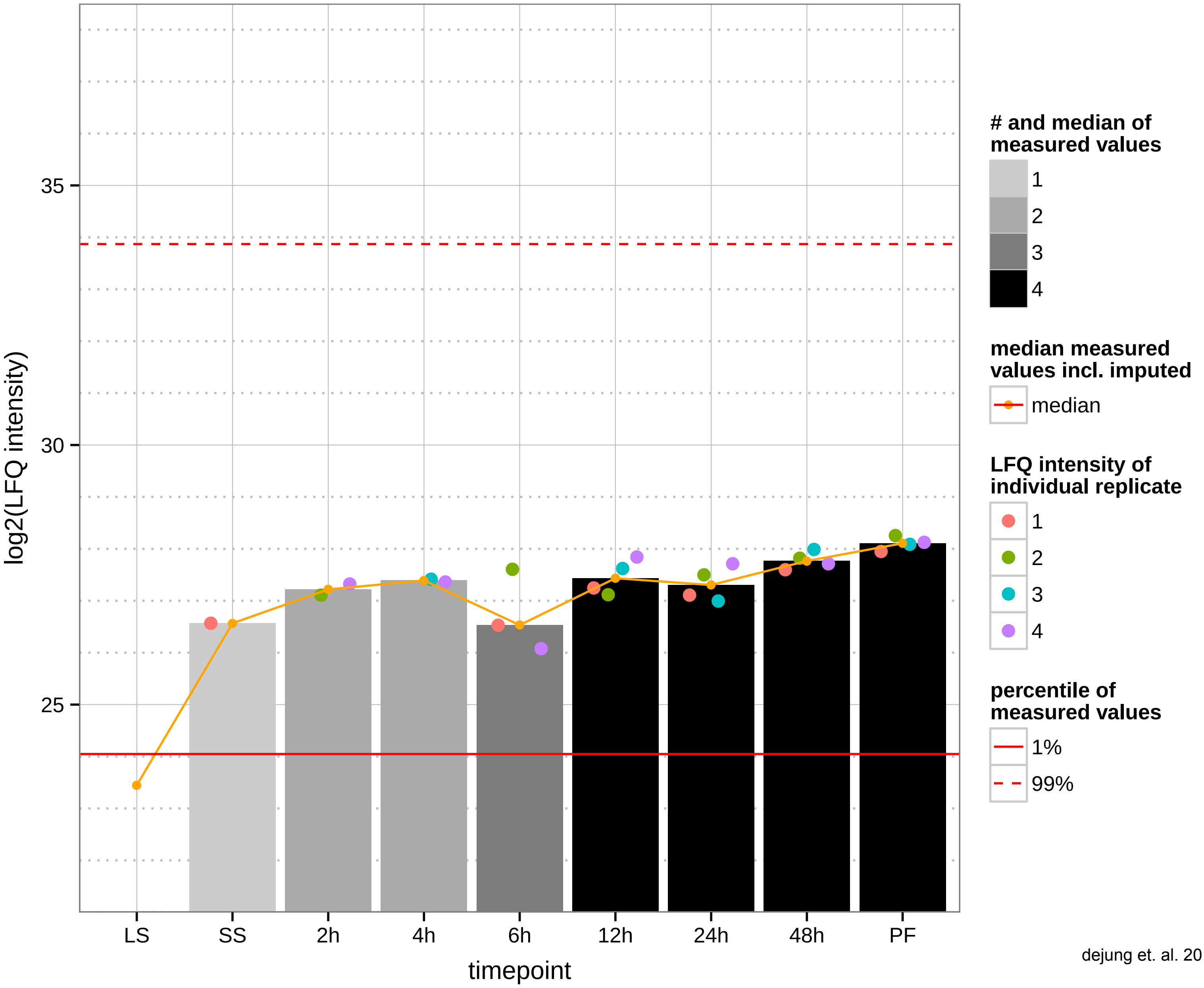




dejung et. al. 2015

chaperone protein DNAj, putative
Tb927.11.5220
AGOF: heat shock protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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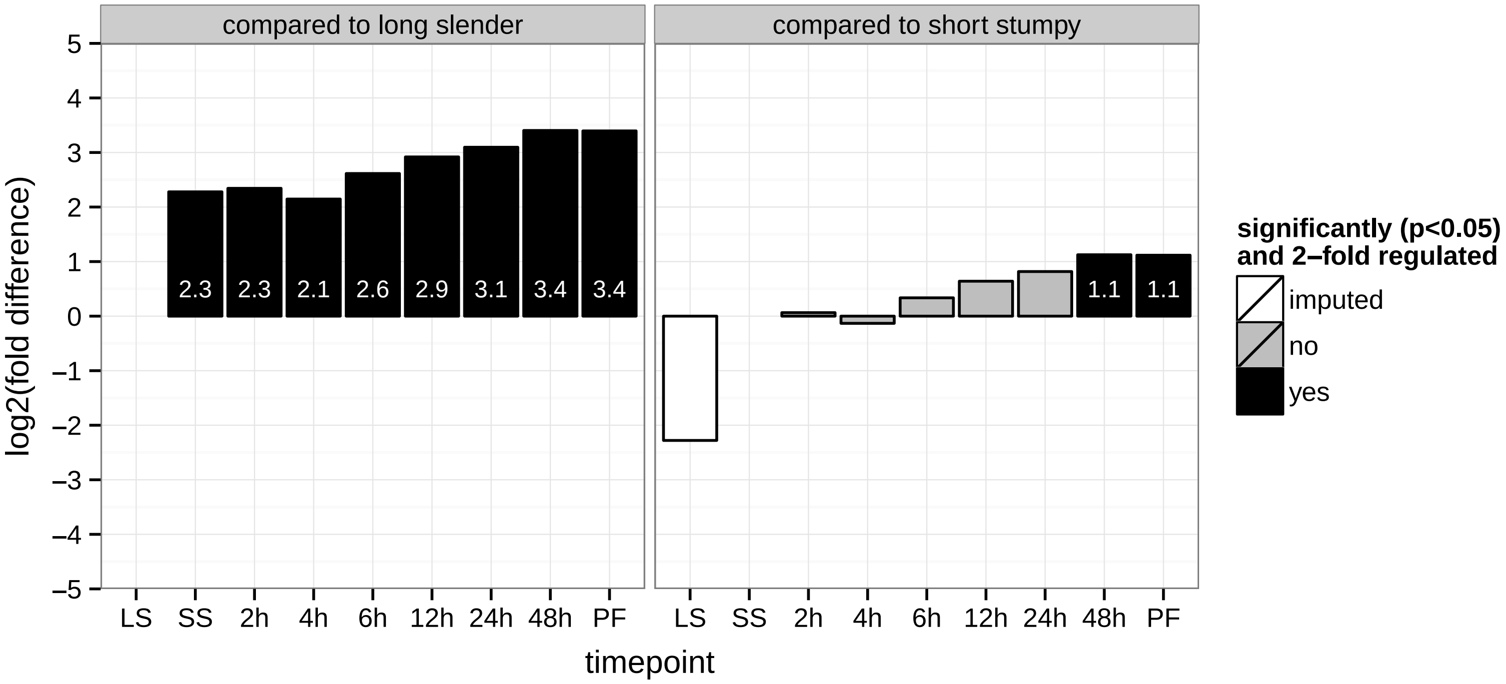
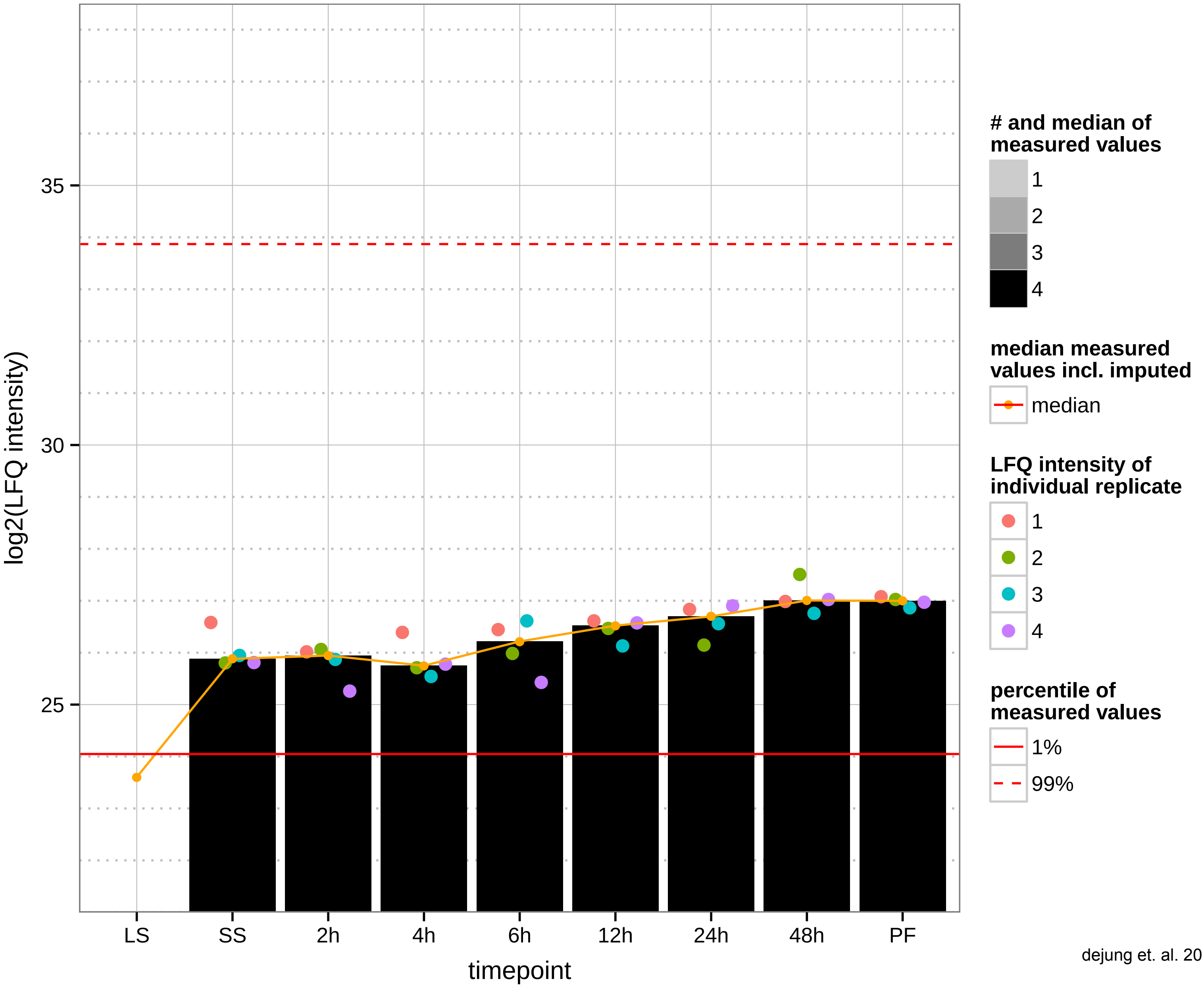
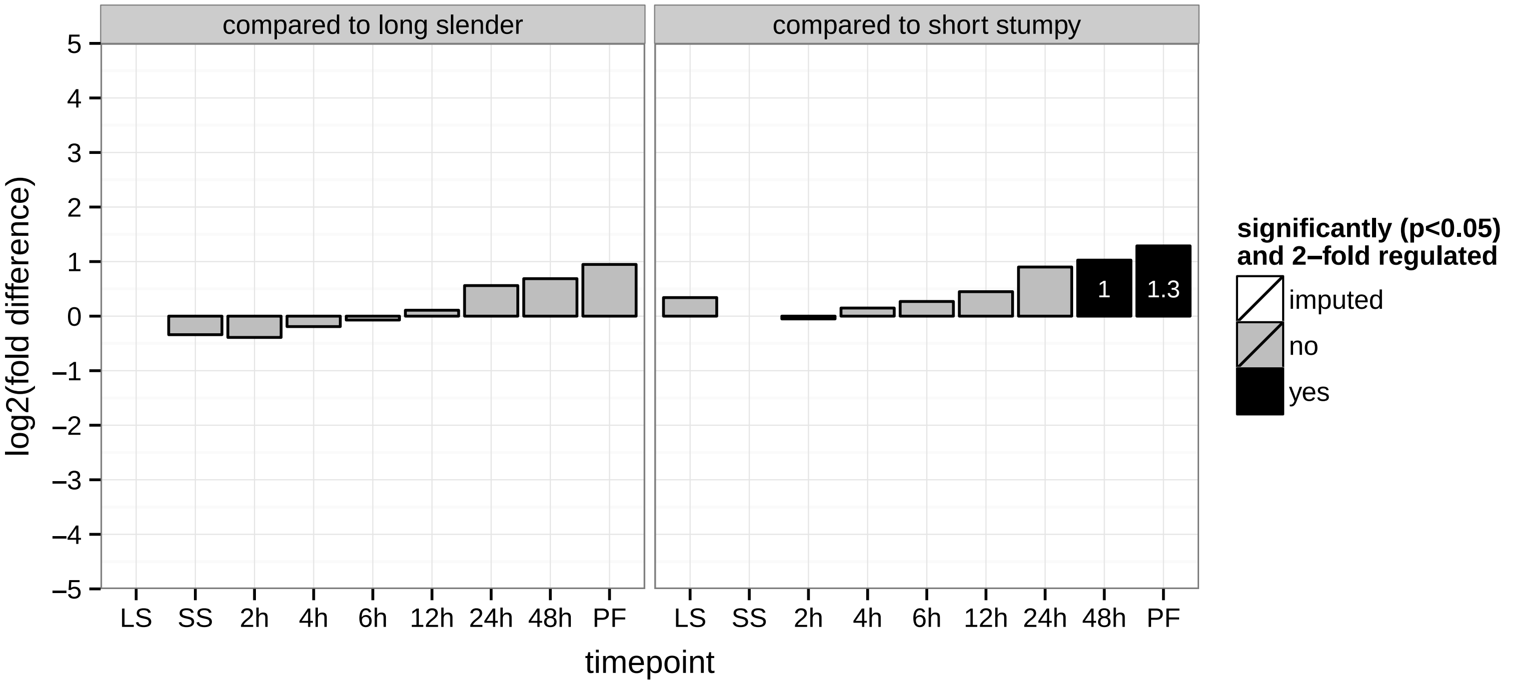
hypothetical protein, conserved
Tb927.11.6000
AGOF: structural constituent of ribosome
AGOC: intracellular, mitochondrion, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: ribosome
PGOP: translation

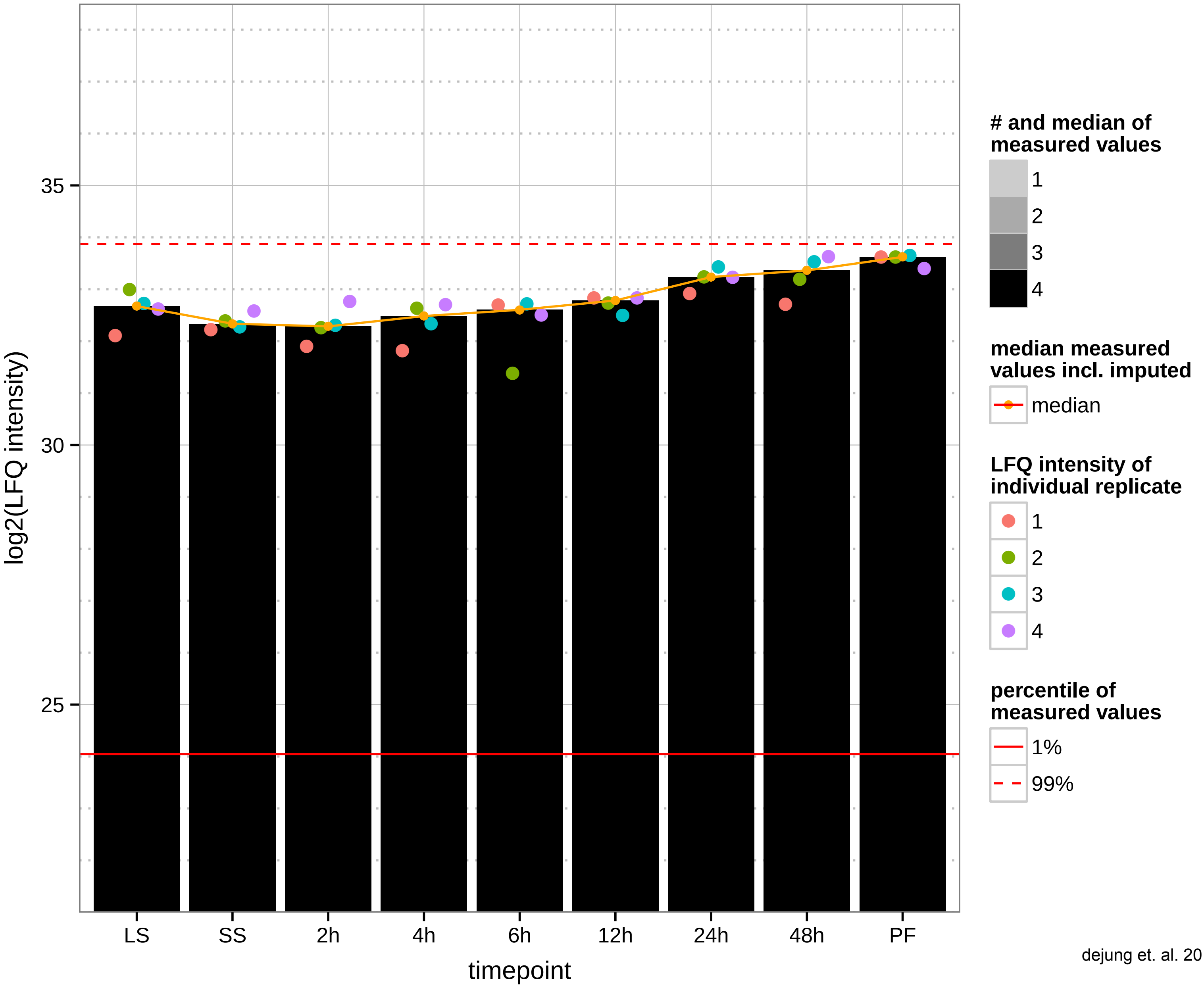




dejung et. al. 2015

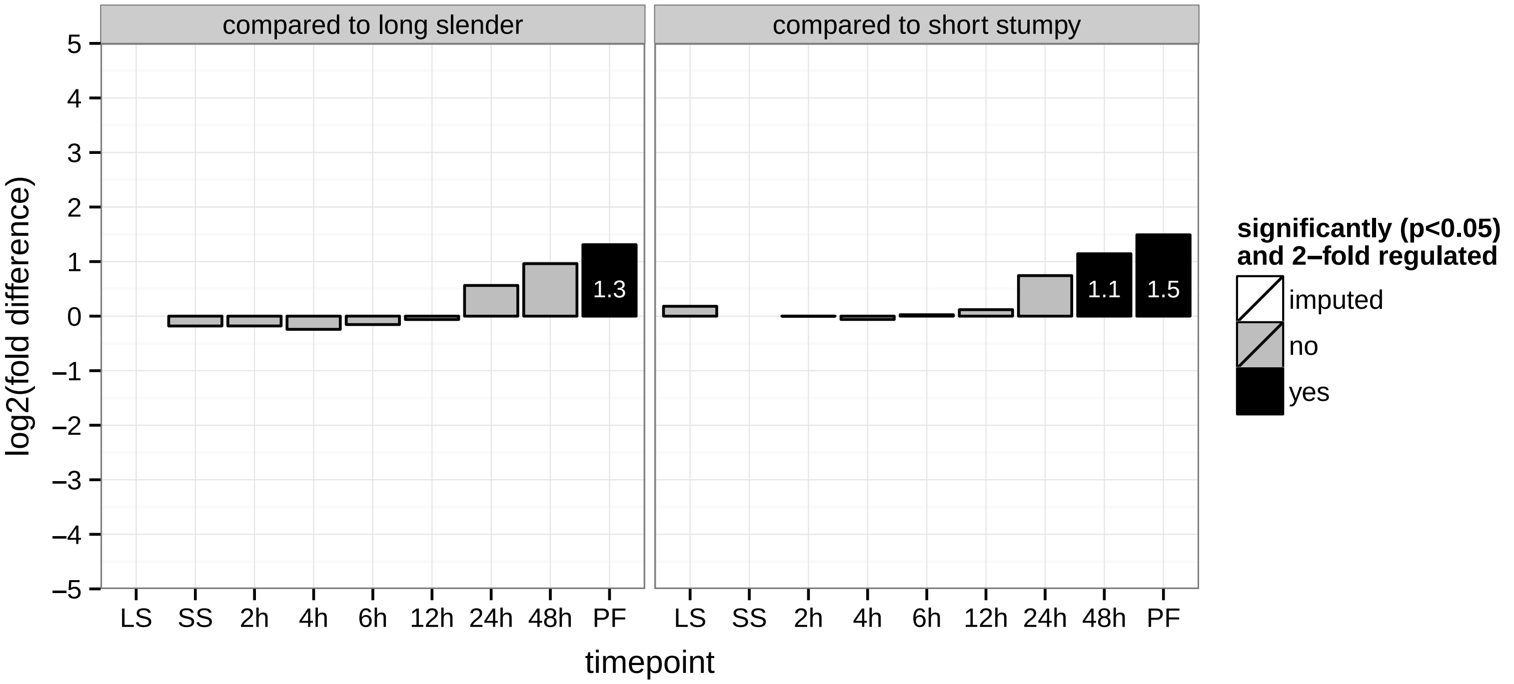
40S ribosomal protein S5, putative
Tb927.11.6300
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome, small ribosomal subunit
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome, small ribosomal subunit
PGOP: translation

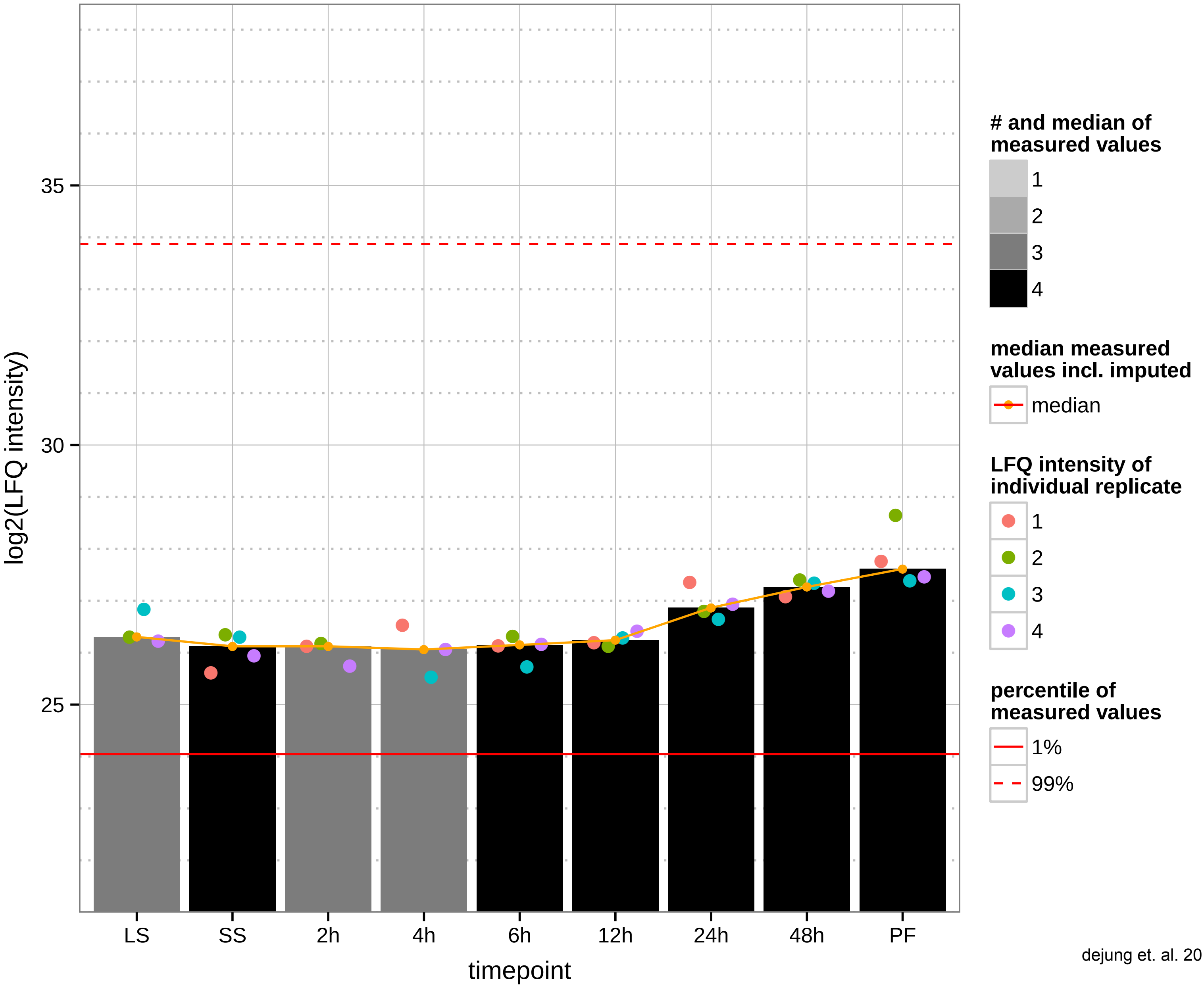




dejung et. al. 2015

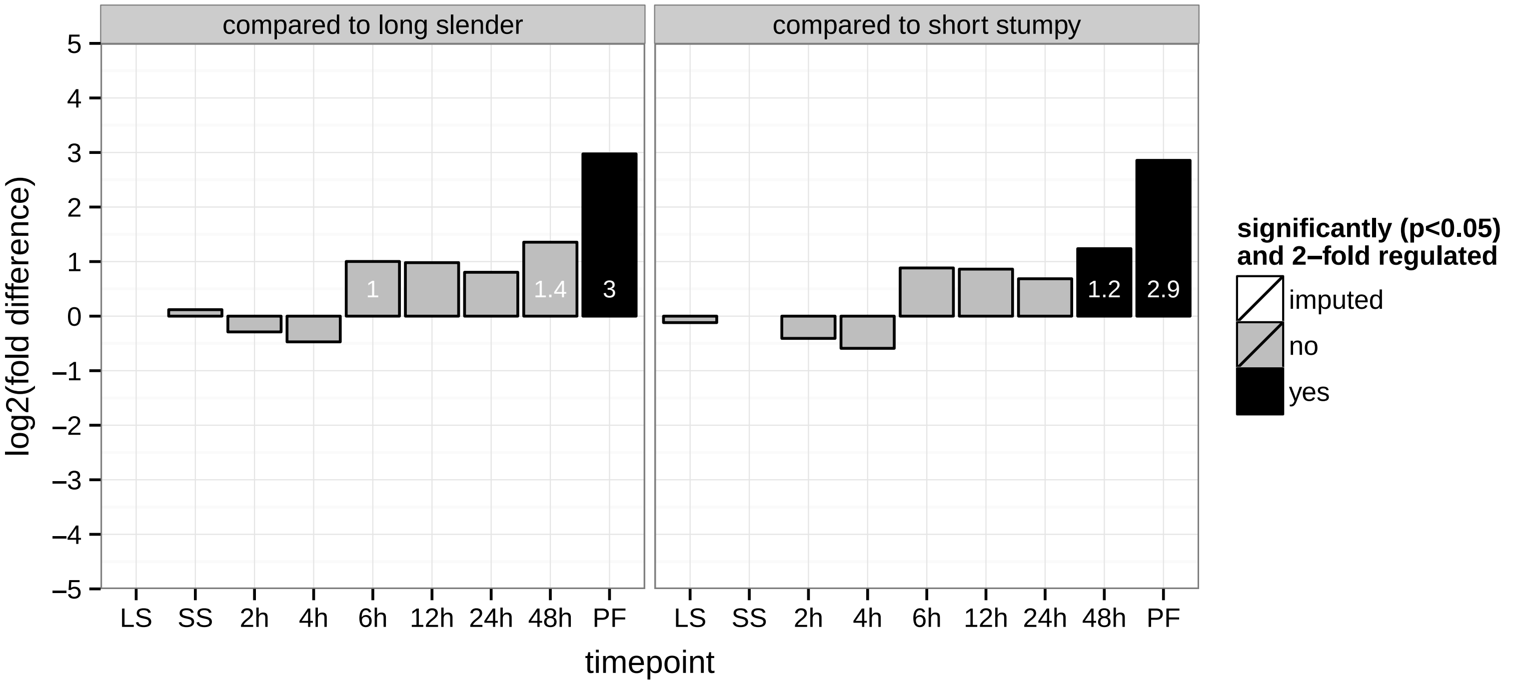
hypothetical protein, conserved
Tb927.11.6420
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

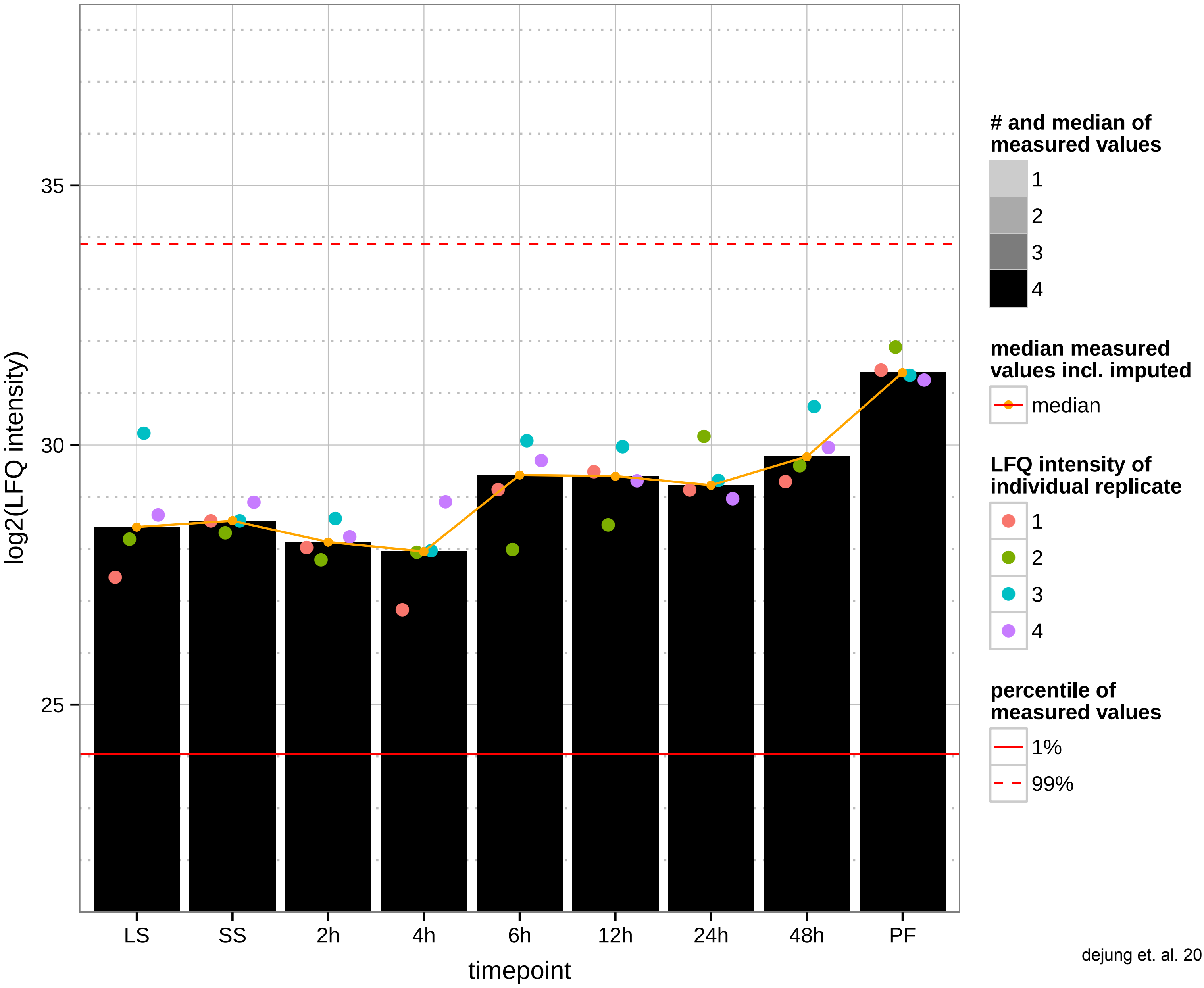




dejung et. al. 2015

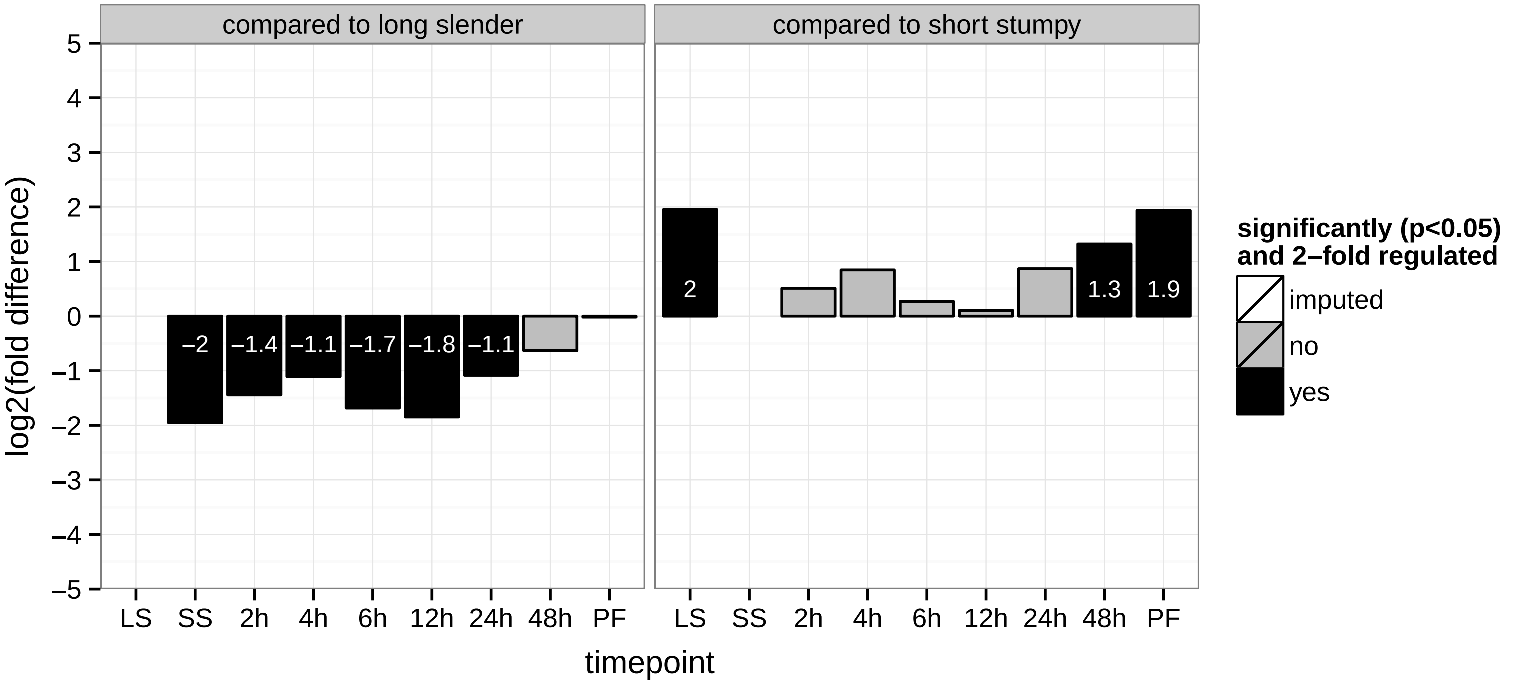
40S ribosomal protein S21, putative
Tb927.11.6510;Tb927.11.6500
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation

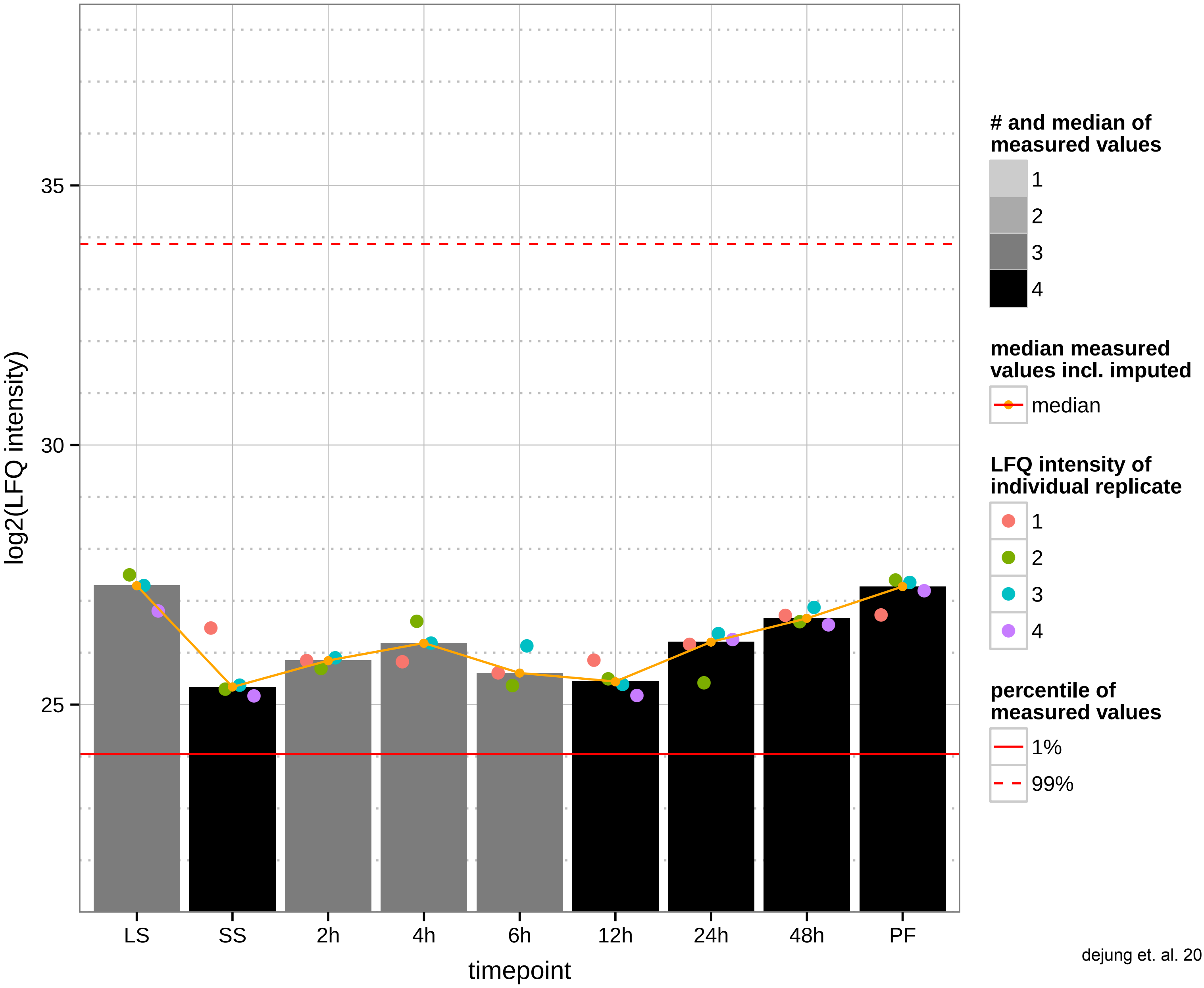




dejung et. al. 2015

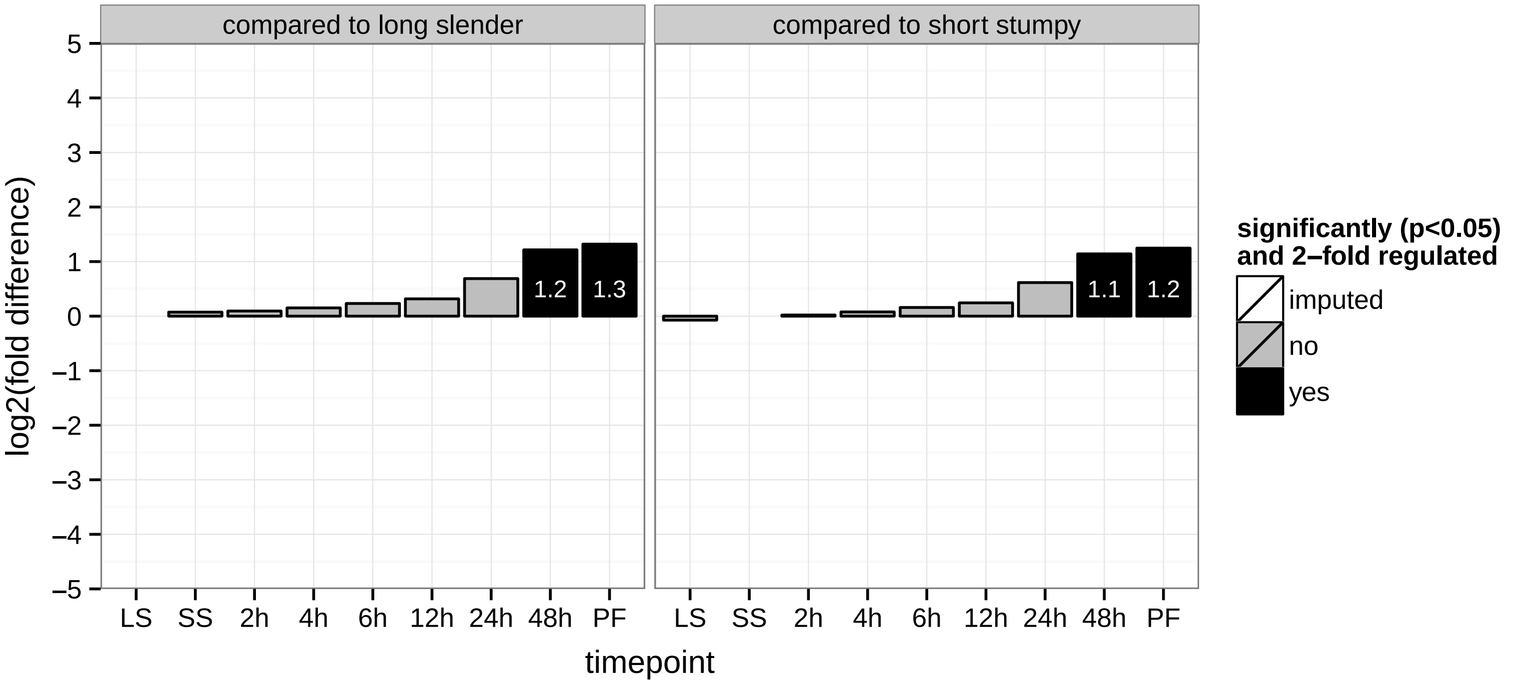
tubulin−tyrsoine ligase−like protein, putative, putative (TTL)
Tb927.11.6810
AGOF: null, tubulin−tyrosine ligase activity
AGOC: null
AGOP: null, cellular protein modification process
PGOF: null, tubulin−tyrosine ligase activity
PGOC: null
PGOP: null, cellular protein modification process

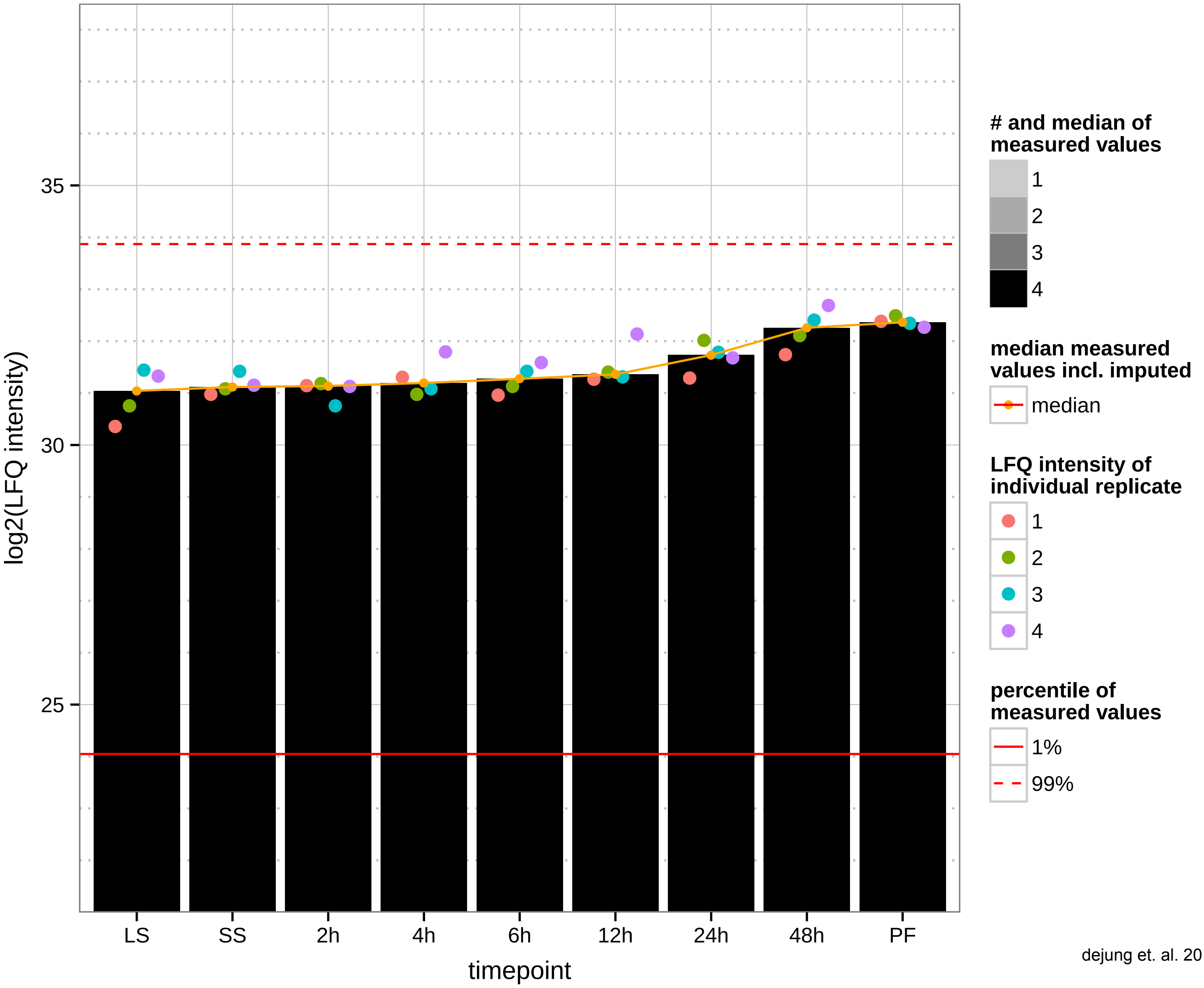




dejung et. al. 2015

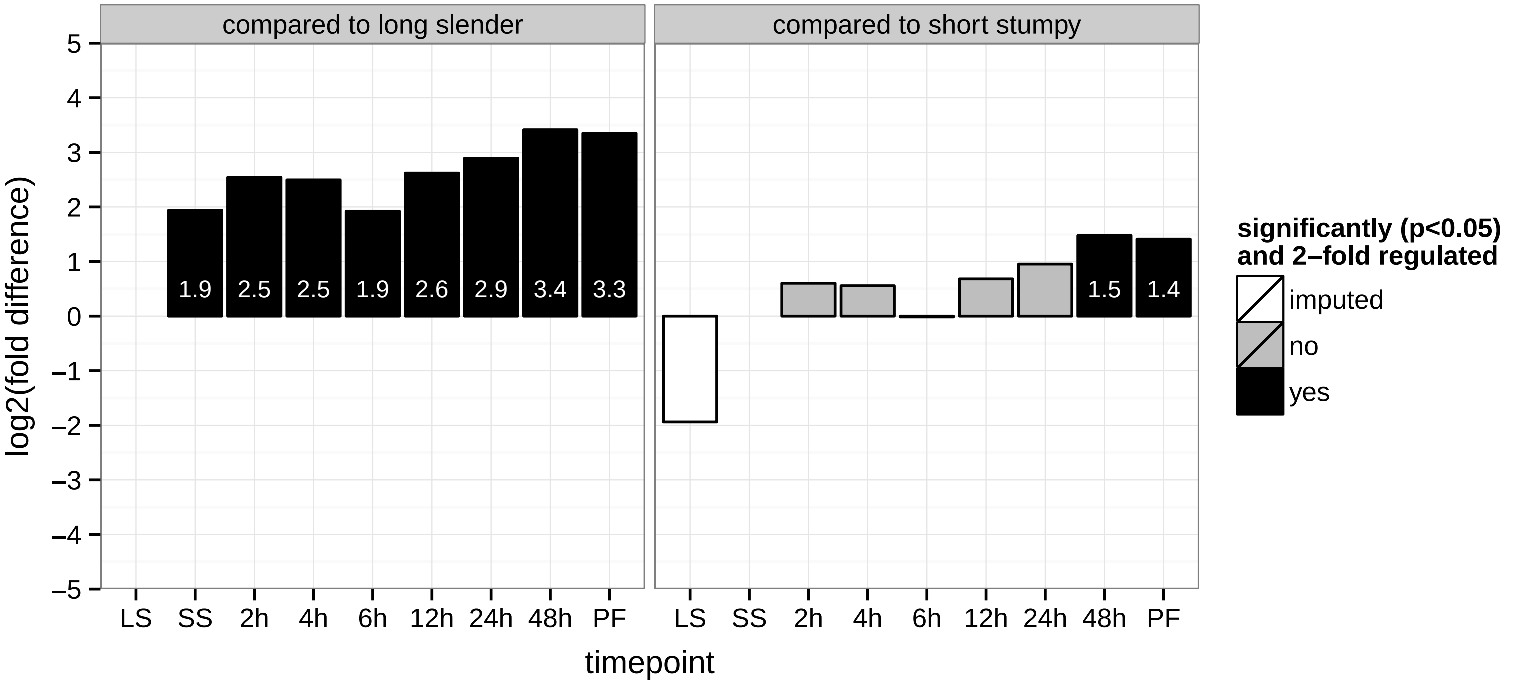
ribosomal protein S26, putative
Tb927.11.8200
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation

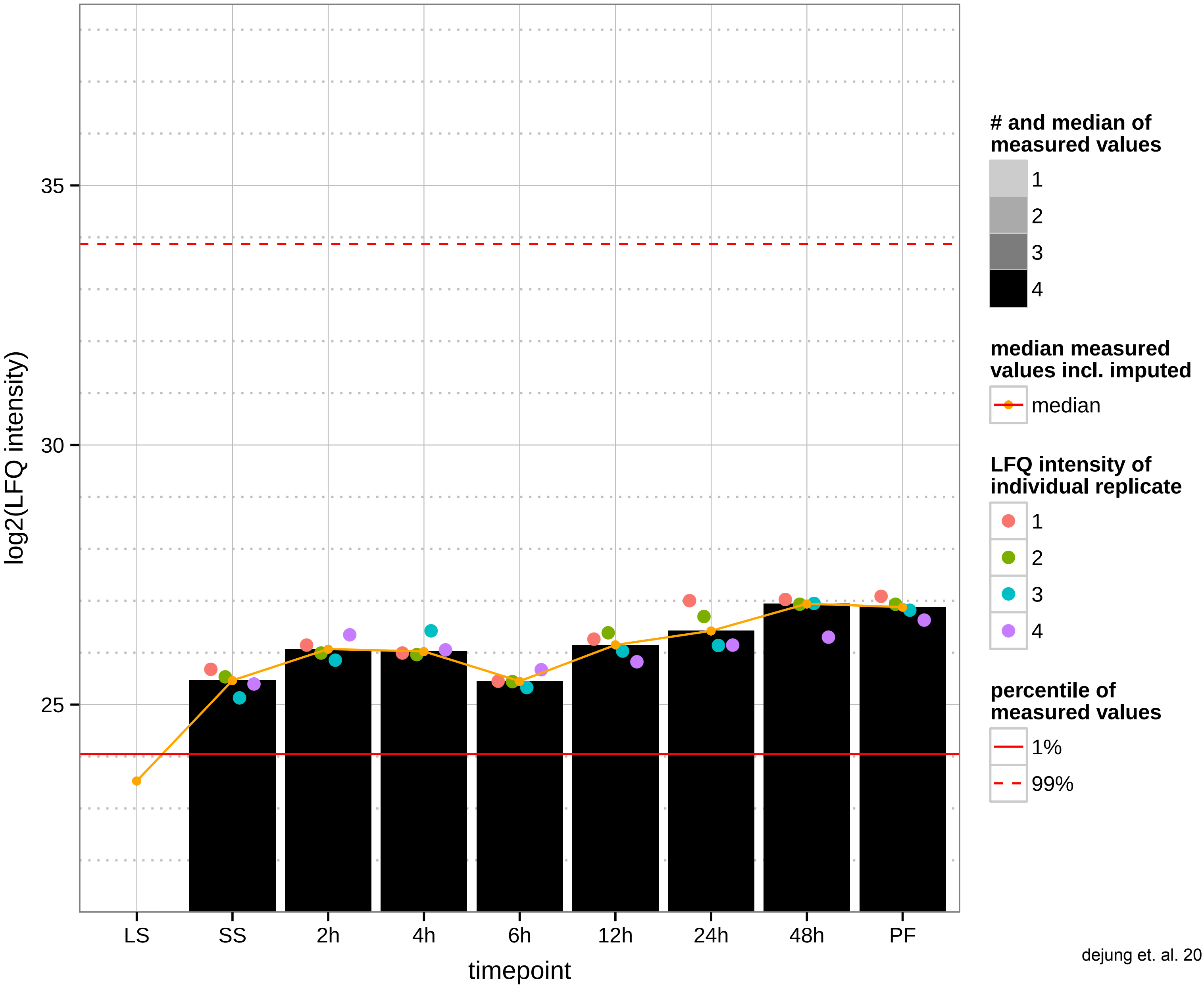




dejung et. al. 2015

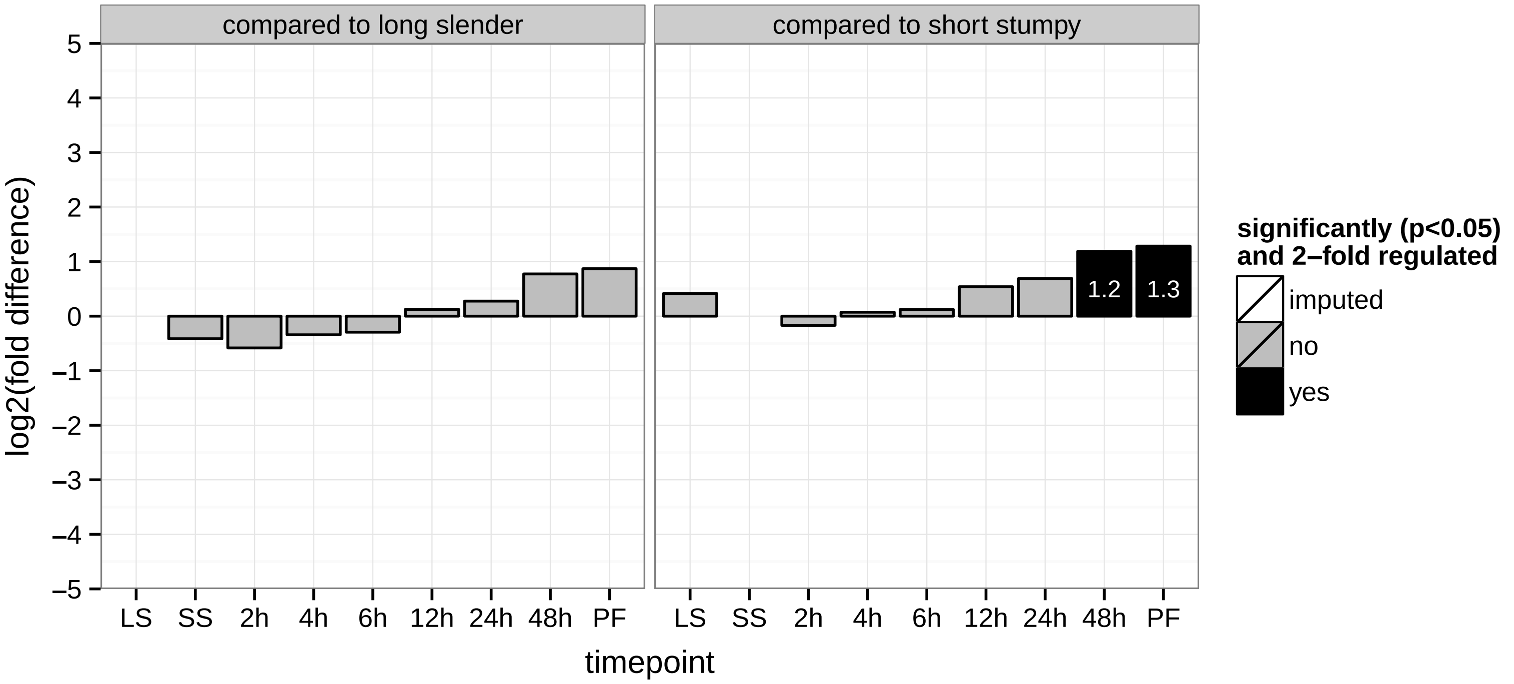
hypothetical protein, conserved
Tb927.11.870
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation

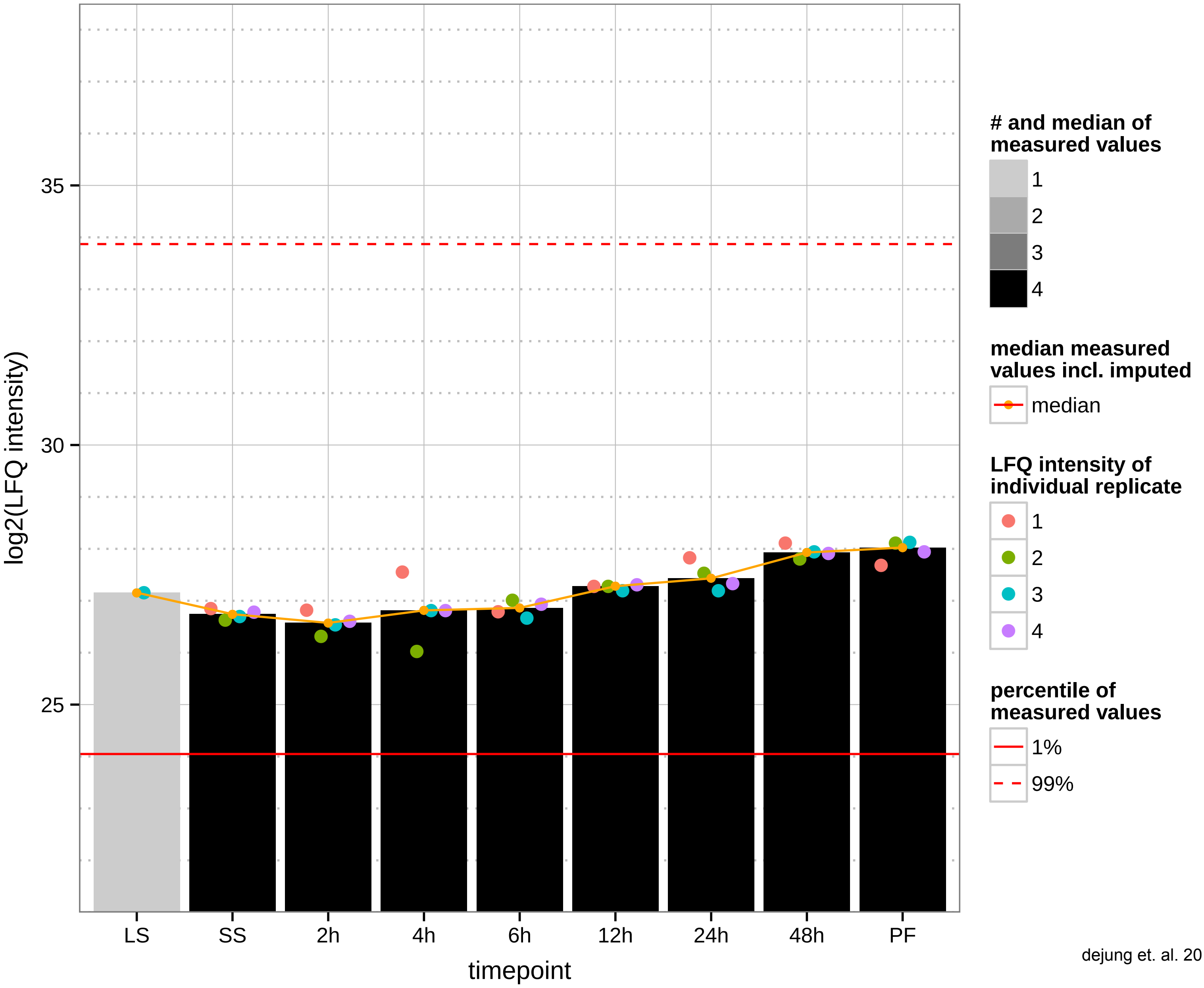




dejung et. al. 2015

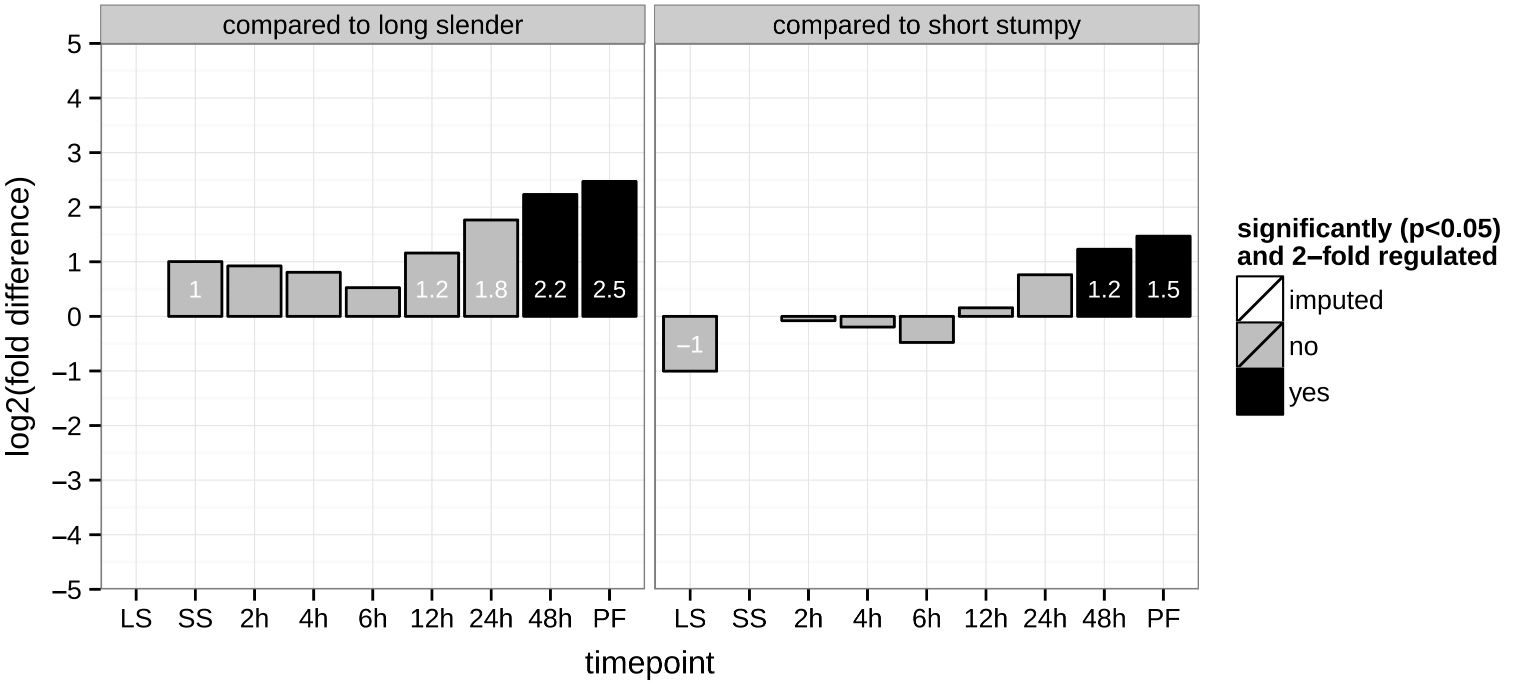
hypothetical protein, conserved
Tb927.11.8880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

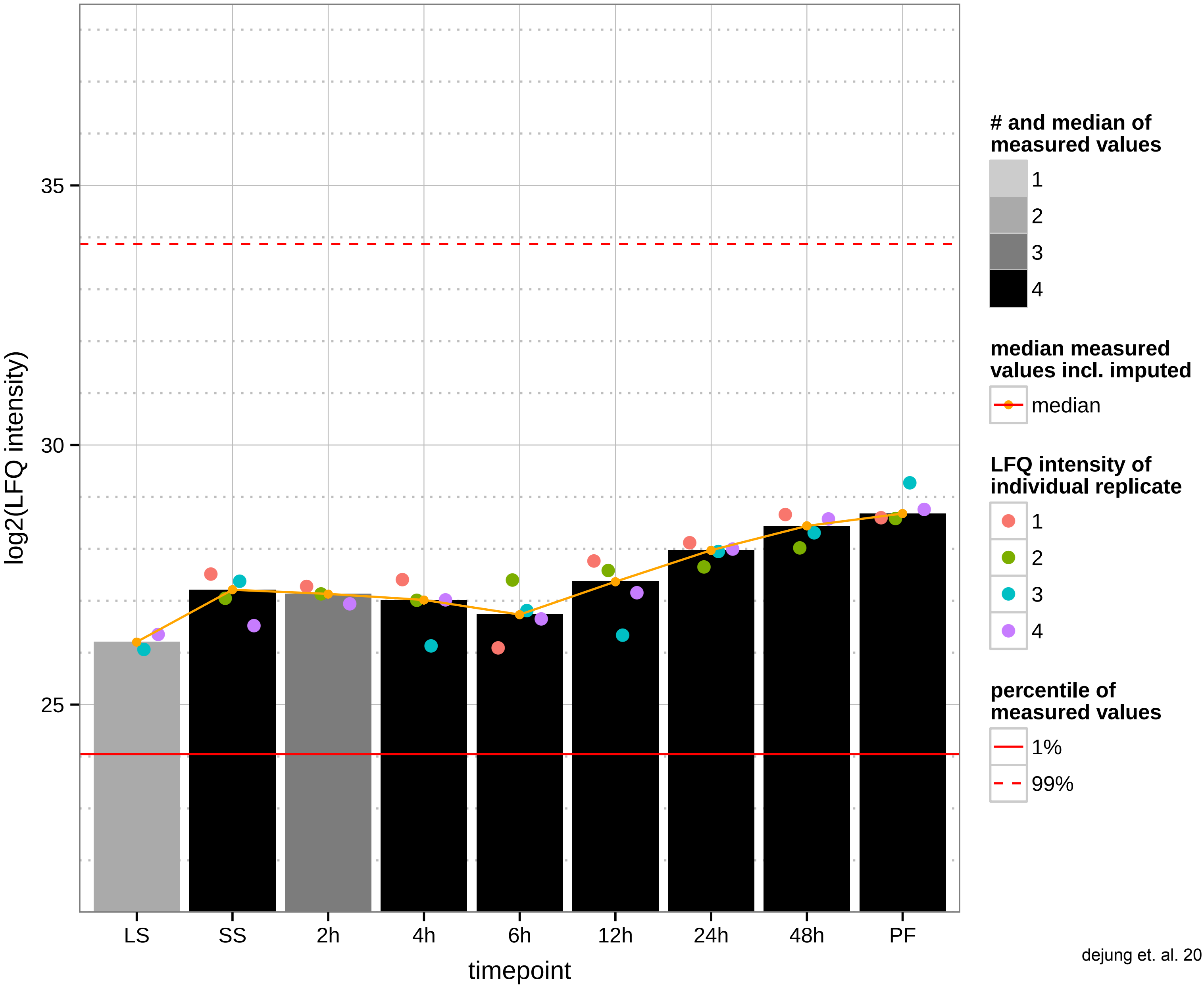




dejung et. al. 2015

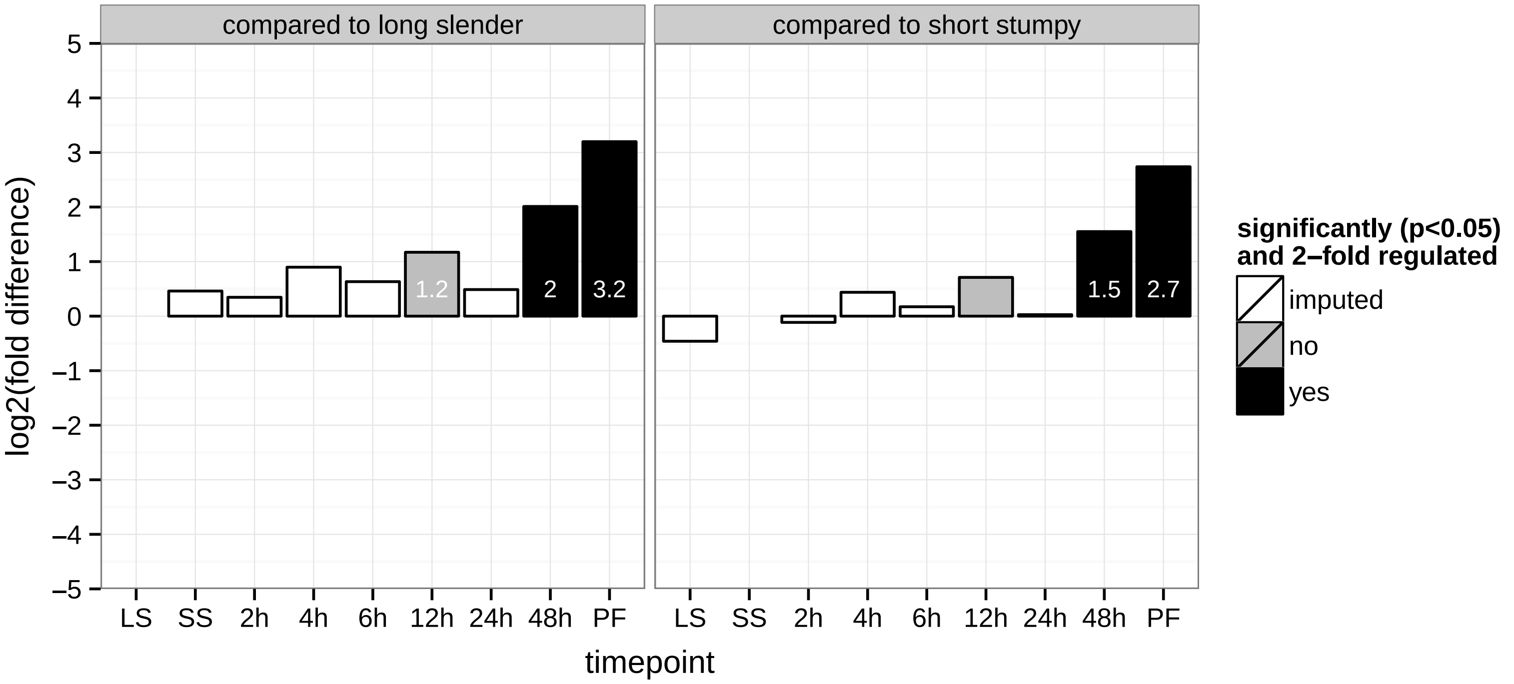
glycine synthase, putative (GCVT1)
Tb927.11.9670
AGOF: aminomethyltransferase activity
AGOC: cytoplasm, mitochondrion
AGOP: glycine decarboxylation via glycine cleavage system
PGOF: aminomethyltransferase activity
PGOC: cytoplasm
PGOP: glycine catabolic process

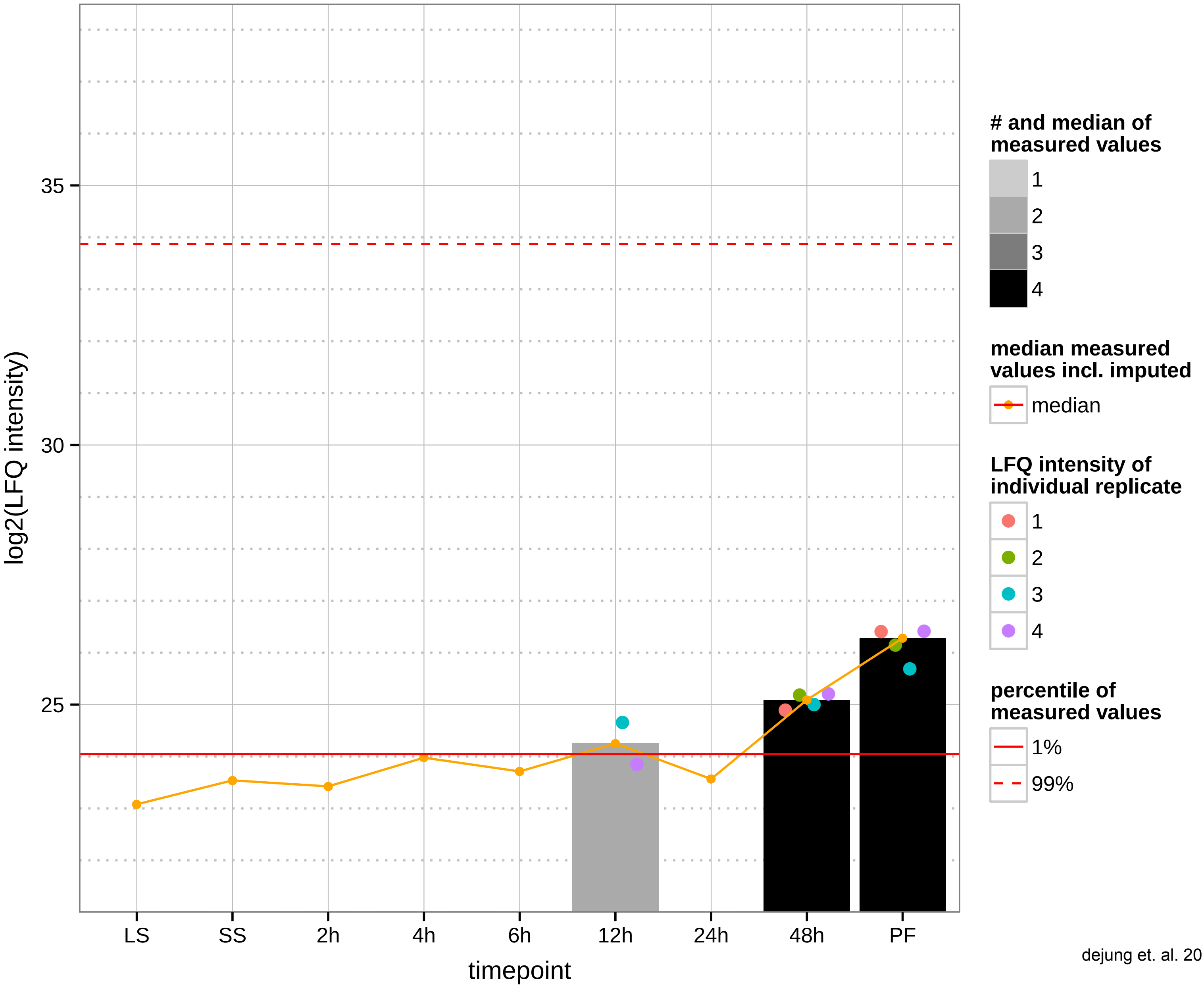




dejung et. al. 2015

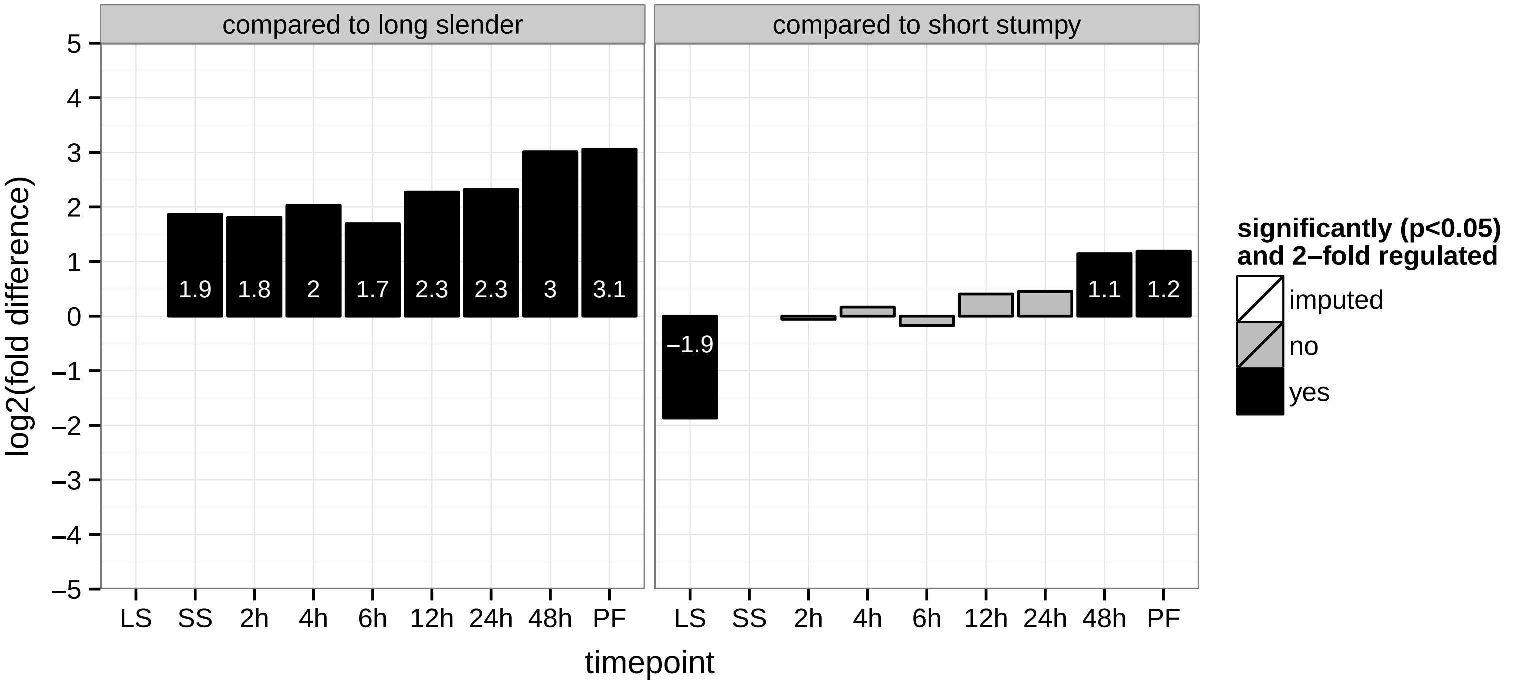
hypothetical protein, conserved
Tb927.11.9820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

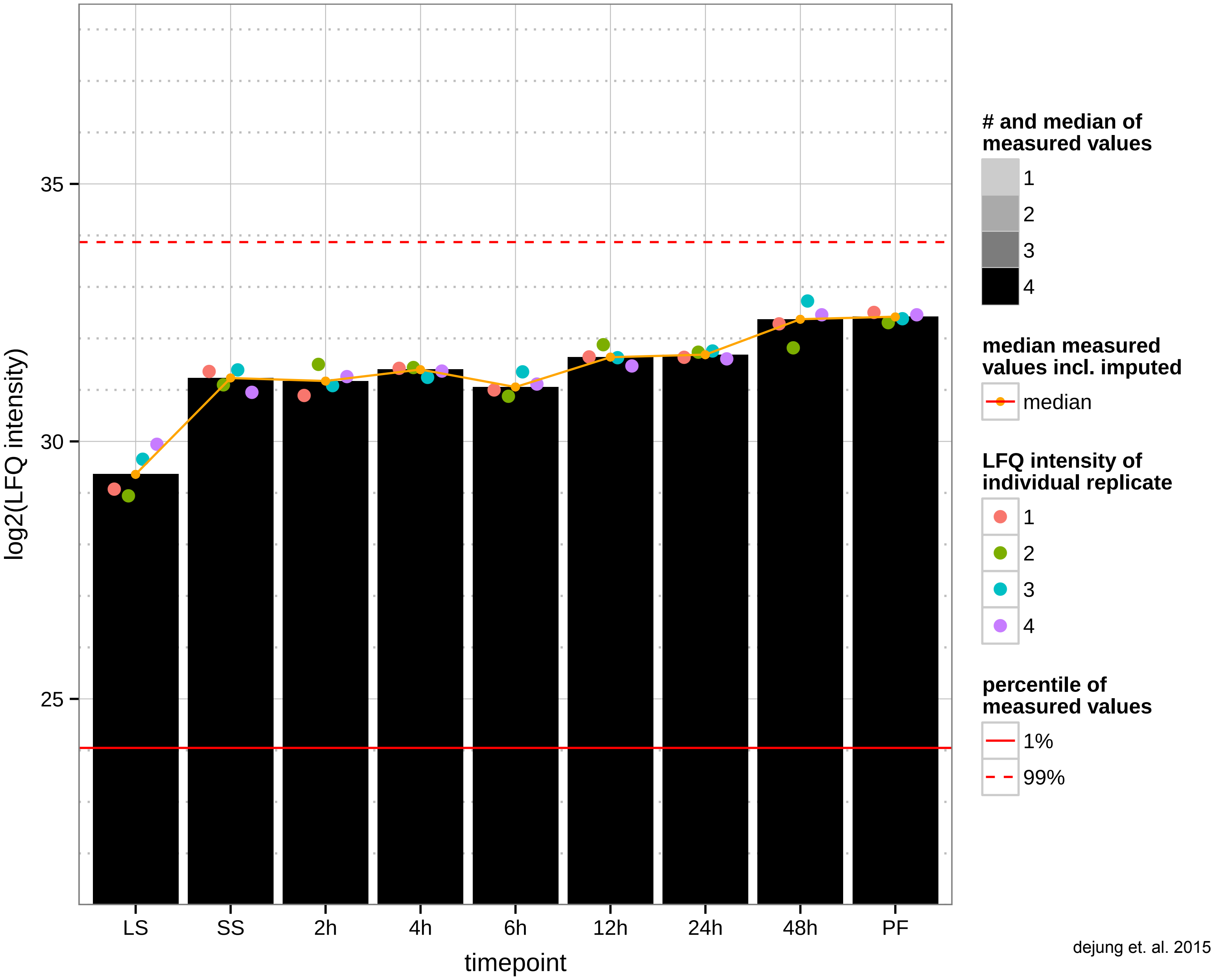




dejung et. al. 2015

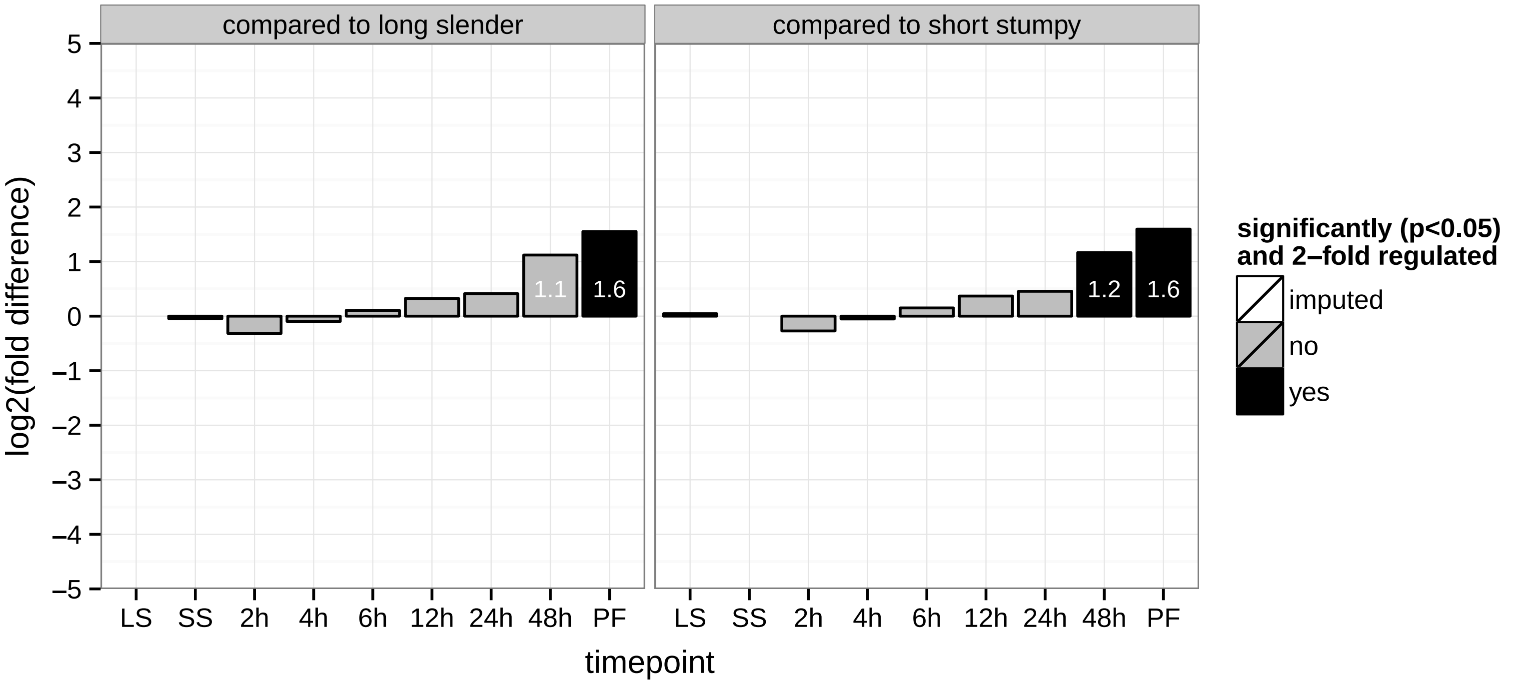
voltage−dependent anion−selective channel (VDAC), voltage−dependent anion−selective channel
Tb927.2.2520;Tb927.2.2510
AGOF: porin activity, voltage−gated anion channel activity, null
AGOC: eukaryotic translation initiation factor 4F complex, mitochondrial outer membrane, pore complex, integral to mitochond
AGOP: ion transport, mitochondrial transport
PGOF: null
PGOC: null
PGOP: null

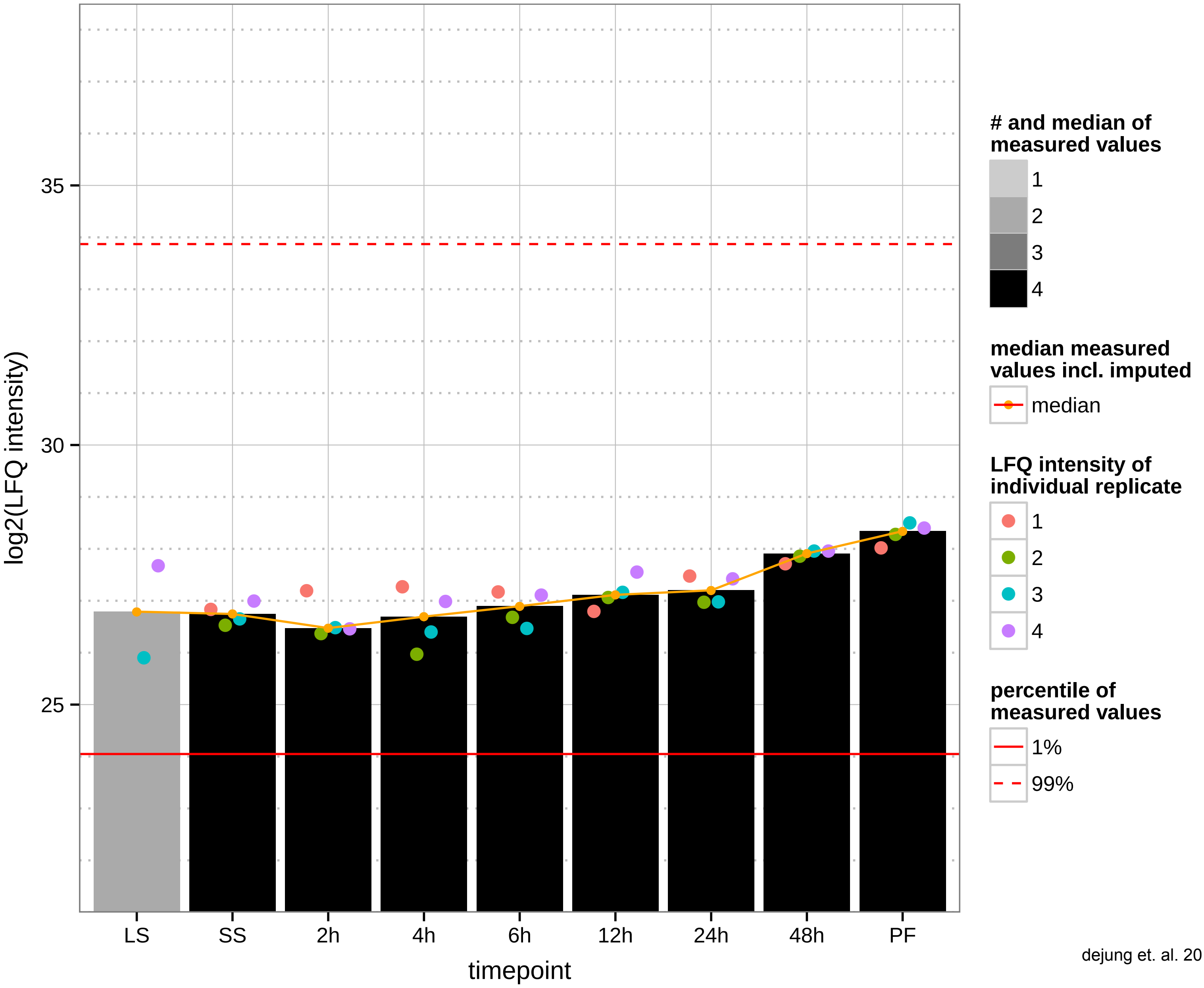




dejung et. al. 2015

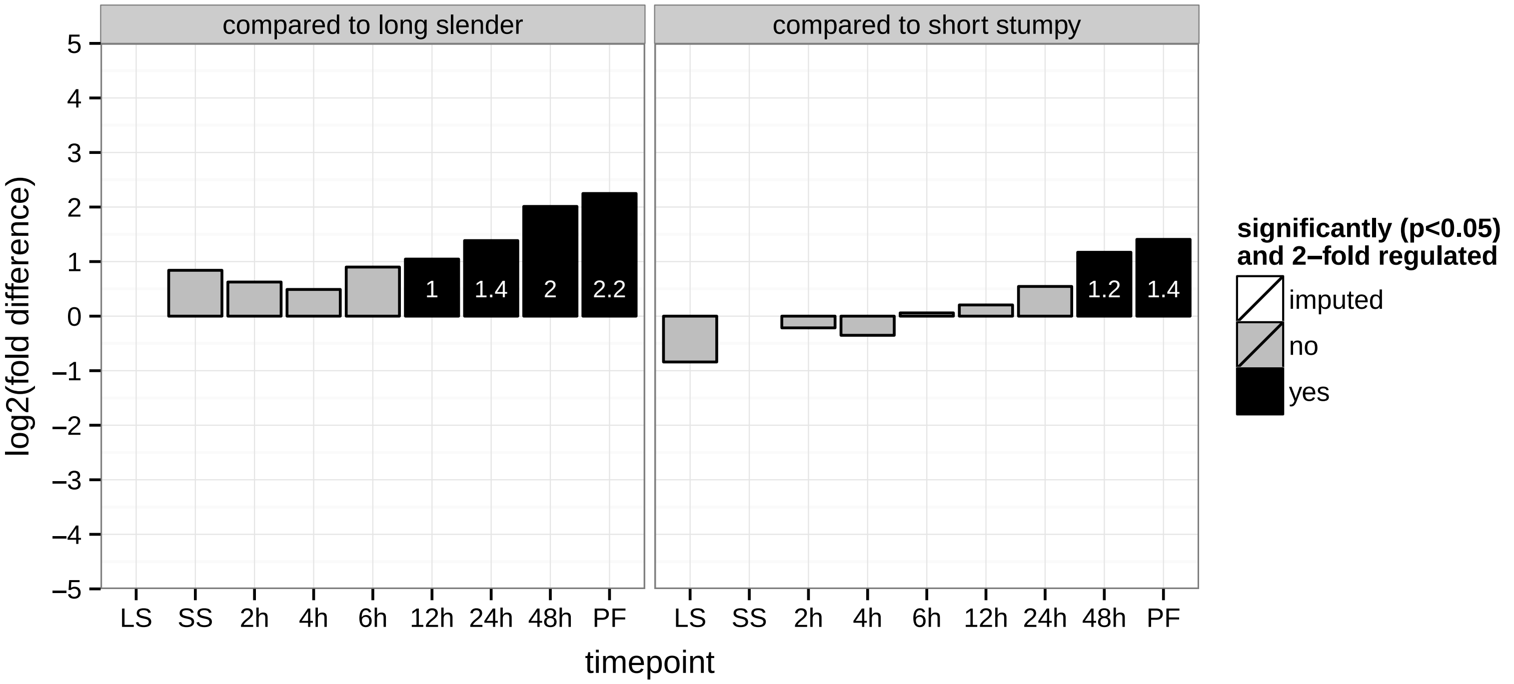
enoyl–CoA hydratase/Enoyl–CoA isomerase/3–hydroxyacyl–CoA dehydrogenase, putative
Tb927.2.4130
AGOF: isomerase activity, oxidoreductase activity
AGOC: mitochondrion
AGOP: fatty acid metabolic process, metabolic process
PGOF: 3–hydroxyacyl–CoA dehydrogenase activity, catalytic activity, oxidoreductase activity
PGOC: null
PGOP: fatty acid metabolic process, metabolic process, oxidation–reduction process

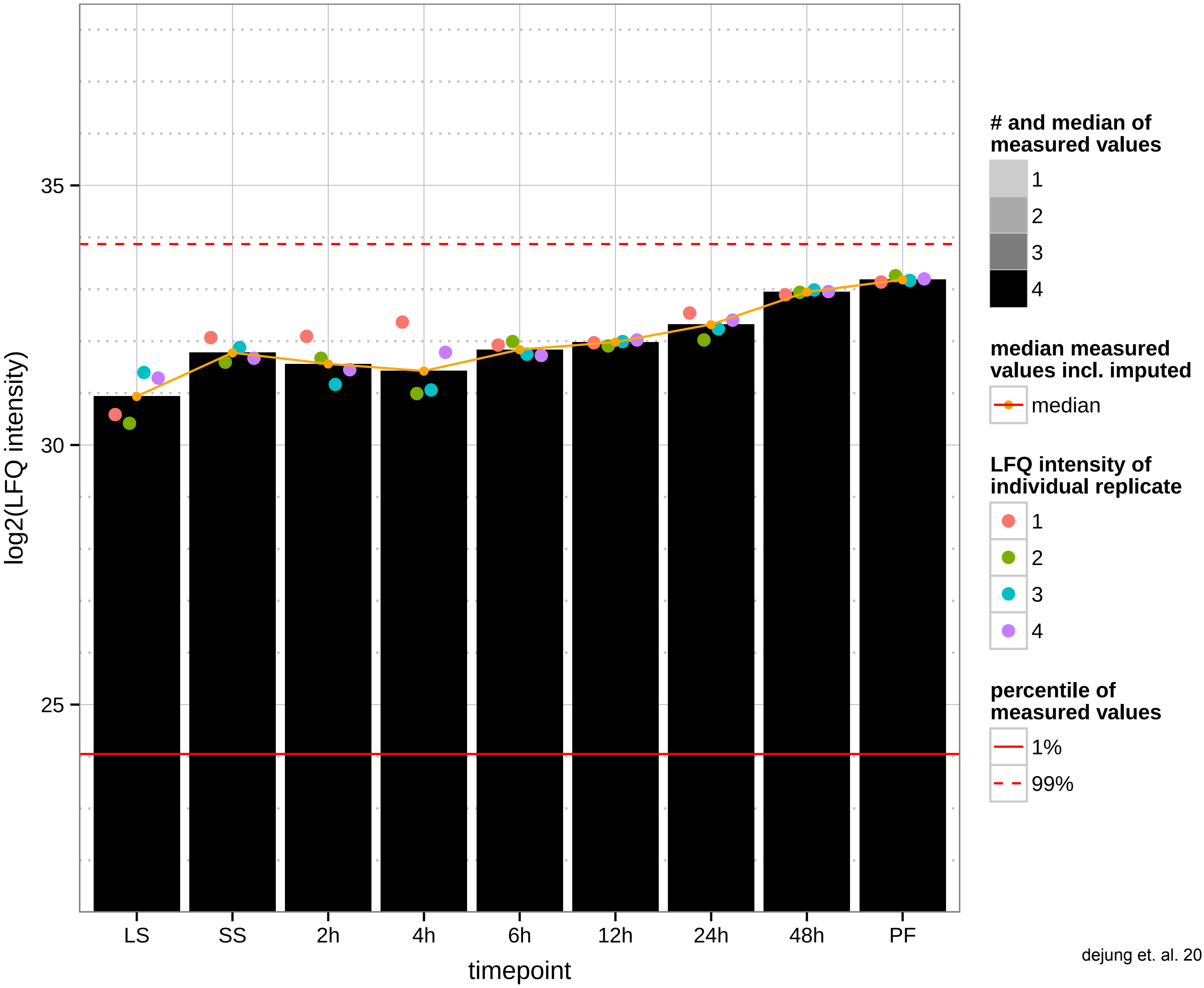




dejung et. al. 2015

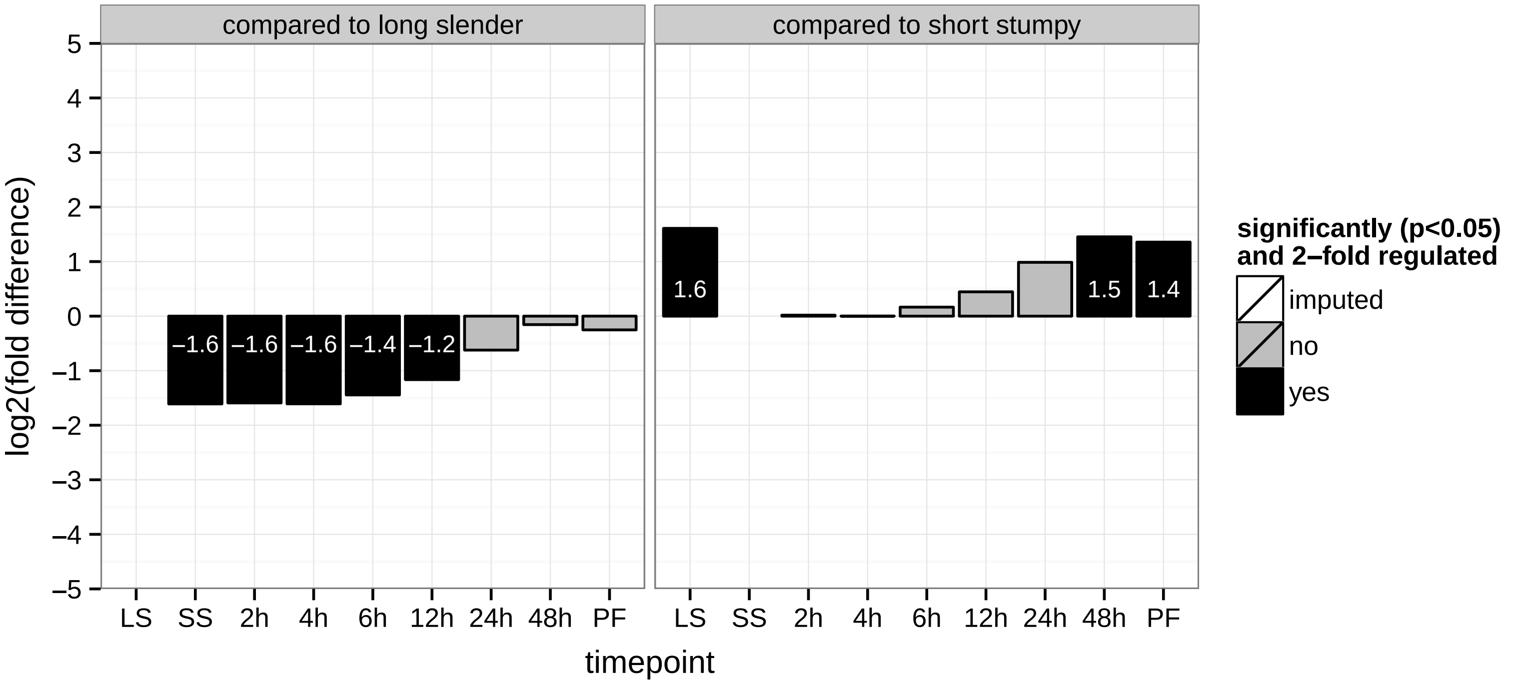
ATP−dependent DEAD/H RNA helicase, putative
Tb927.3.2600
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: null
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null

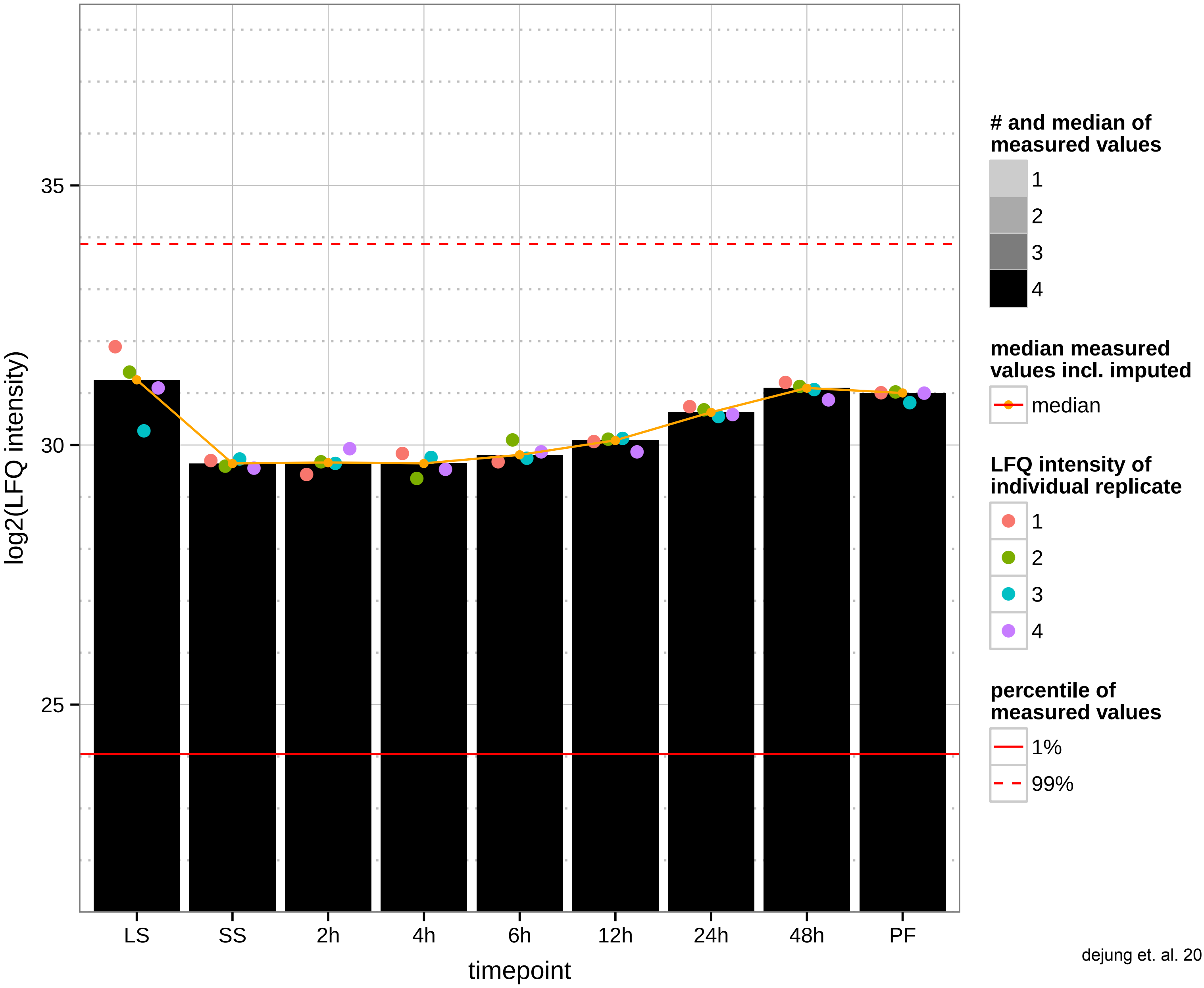




dejung et. al. 2015

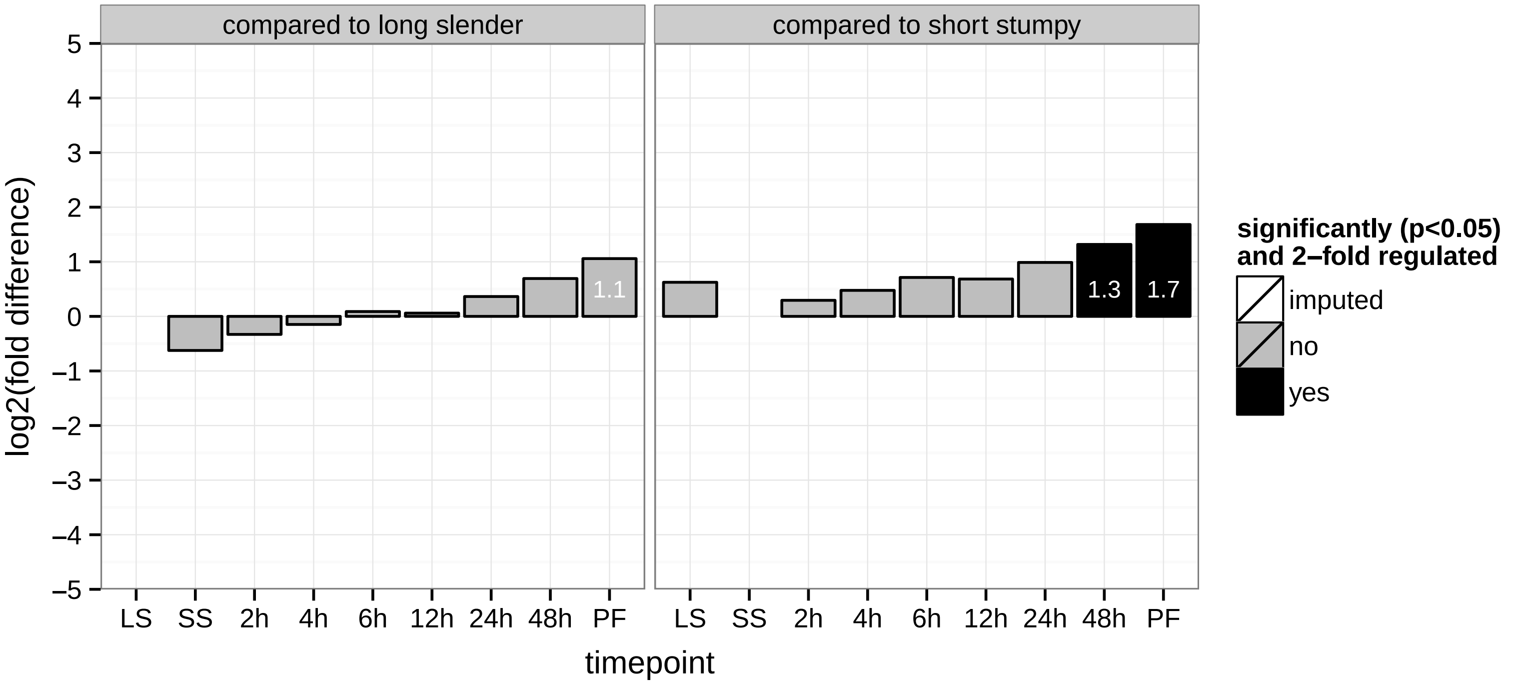
hypothetical protein, conserved
Tb927.3.3130
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

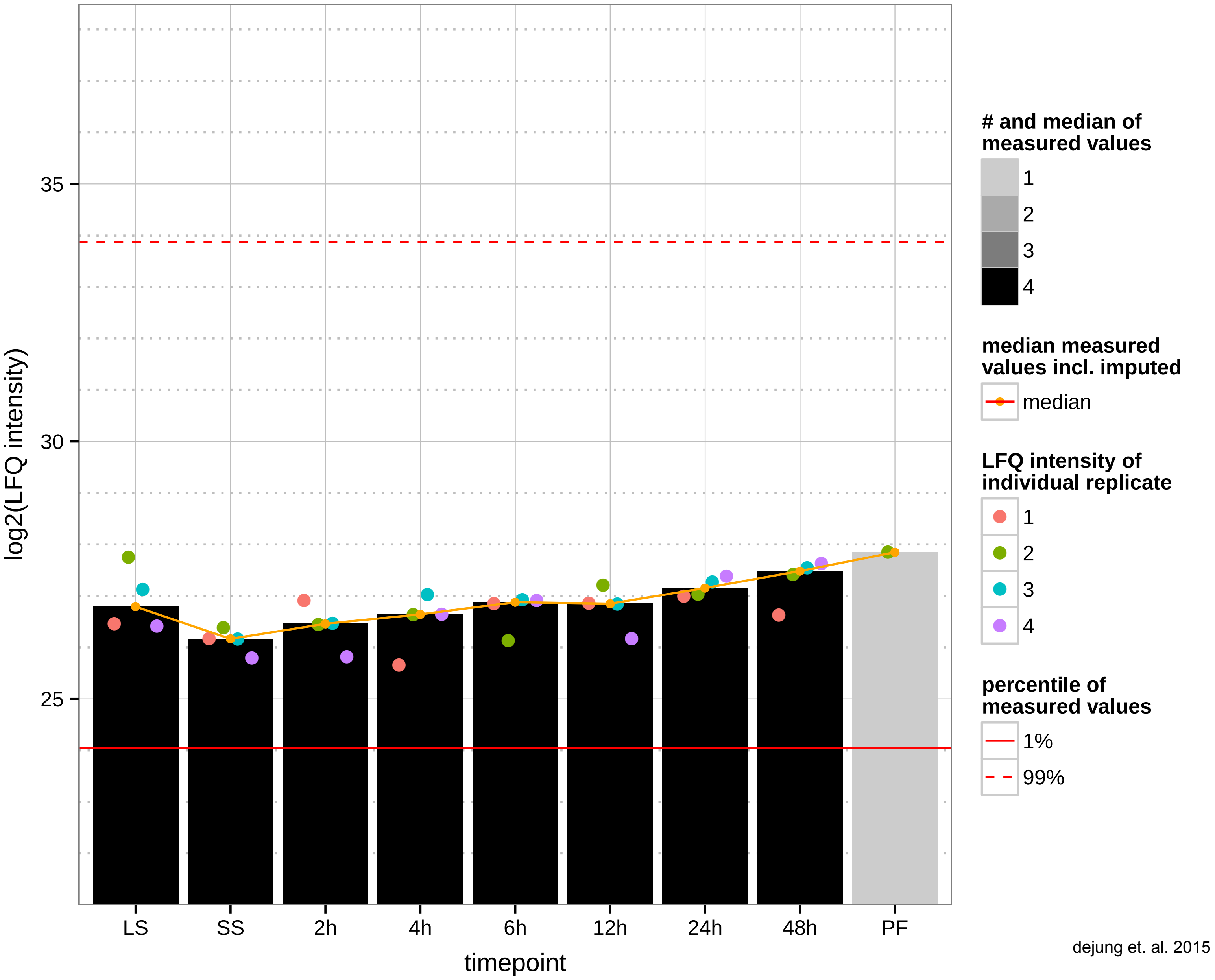




dejung et. al. 2015

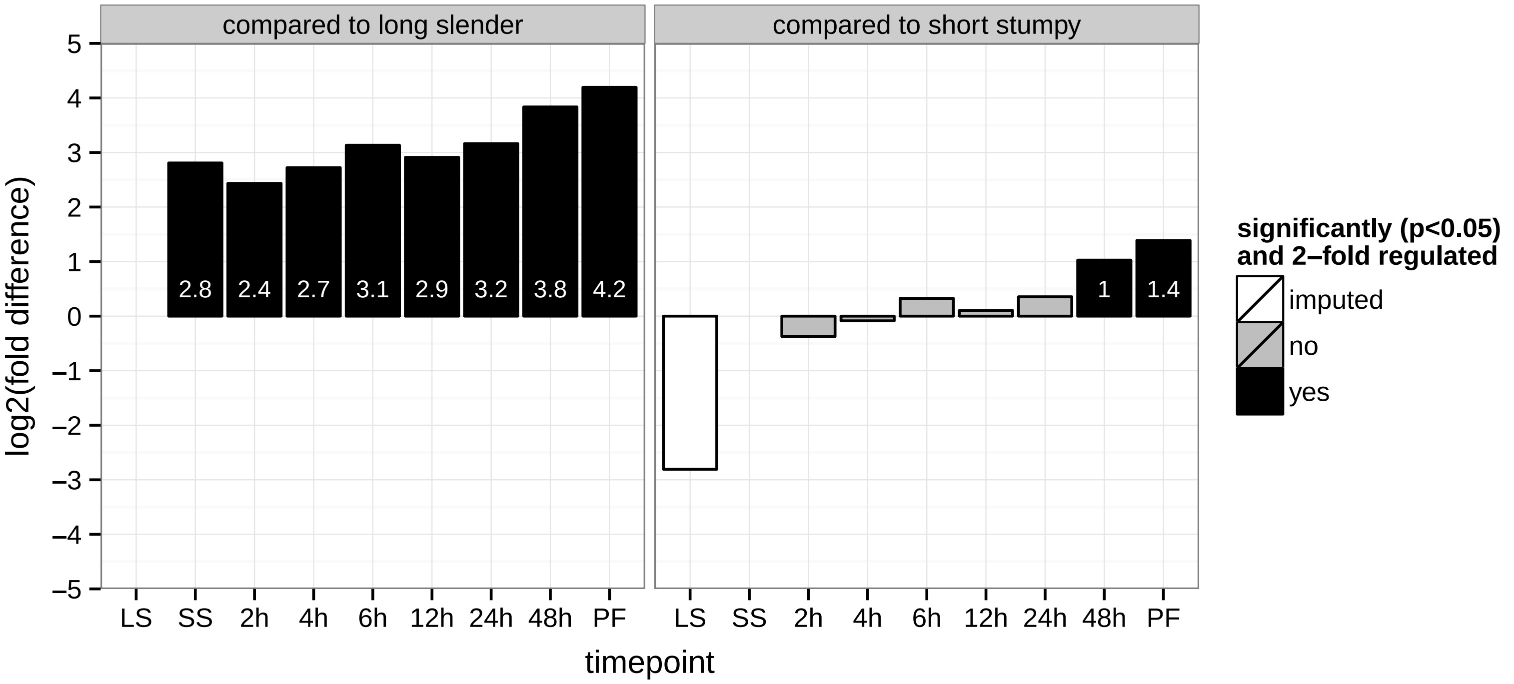
hypothetical protein, conserved (pseudogene), conserved, frameshift
Tb927.3.4980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

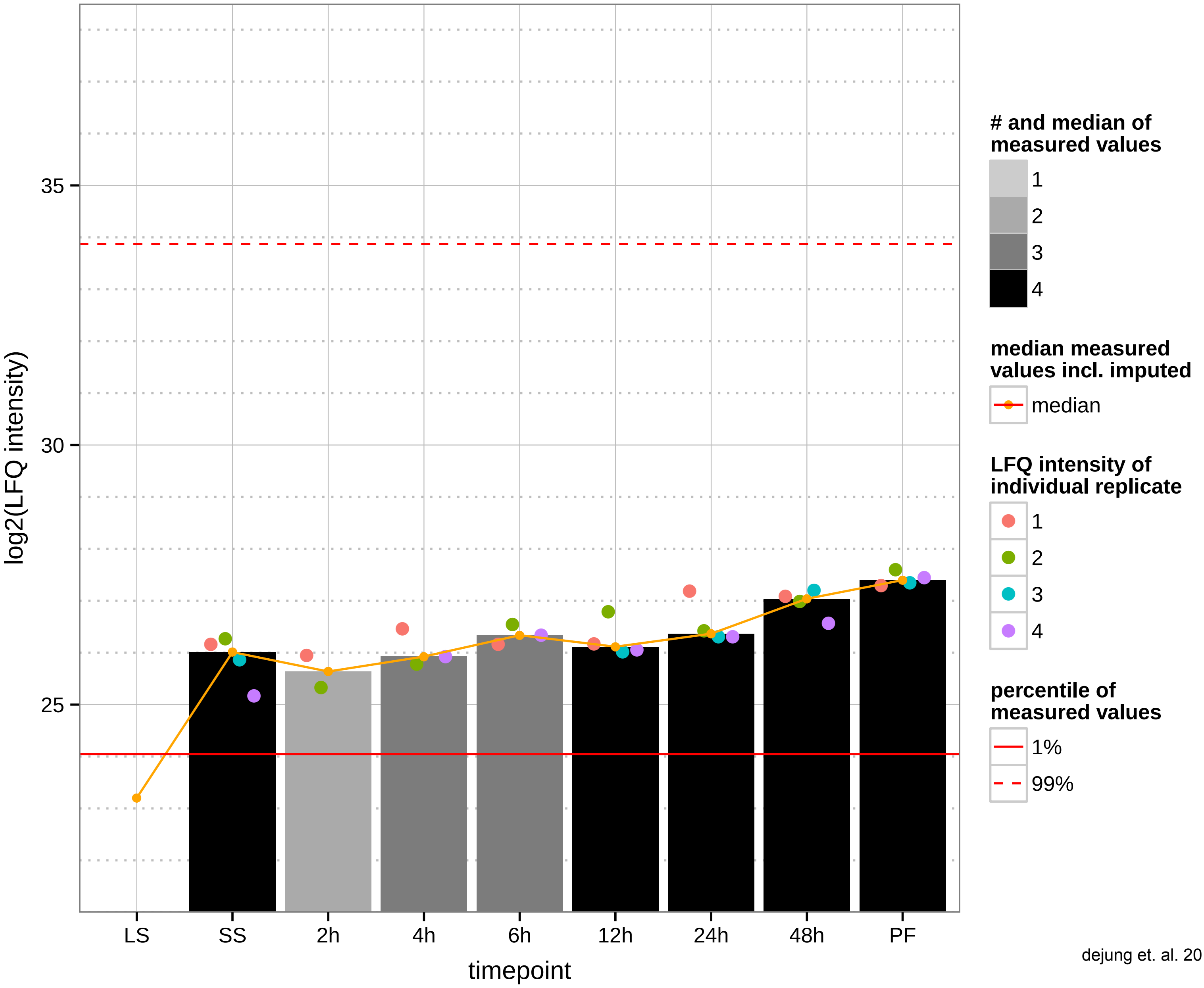




dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.5130
AGOF: exonuclease activity, nucleic acid binding
AGOC: intracellular
AGOP: null
PGOF: exonuclease activity, nucleic acid binding
PGOC: intracellular
PGOP: null





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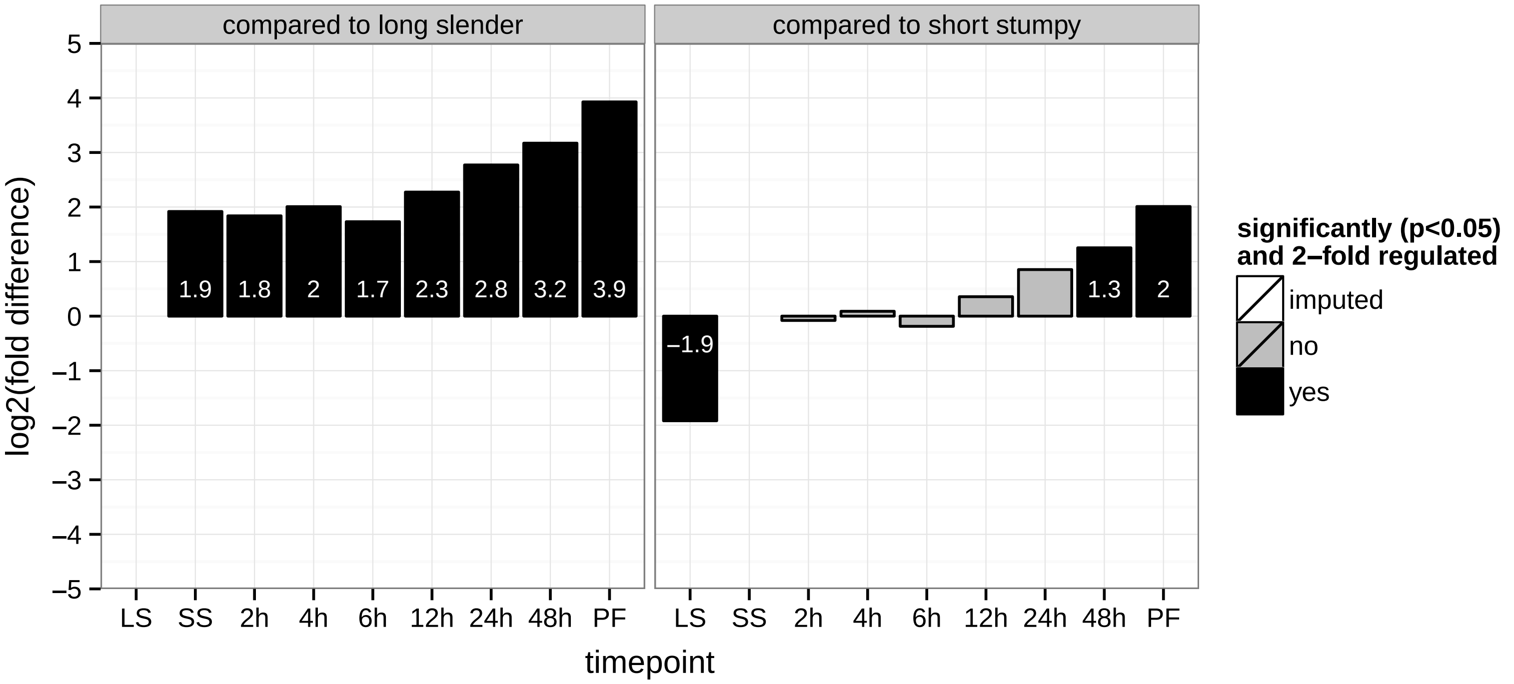
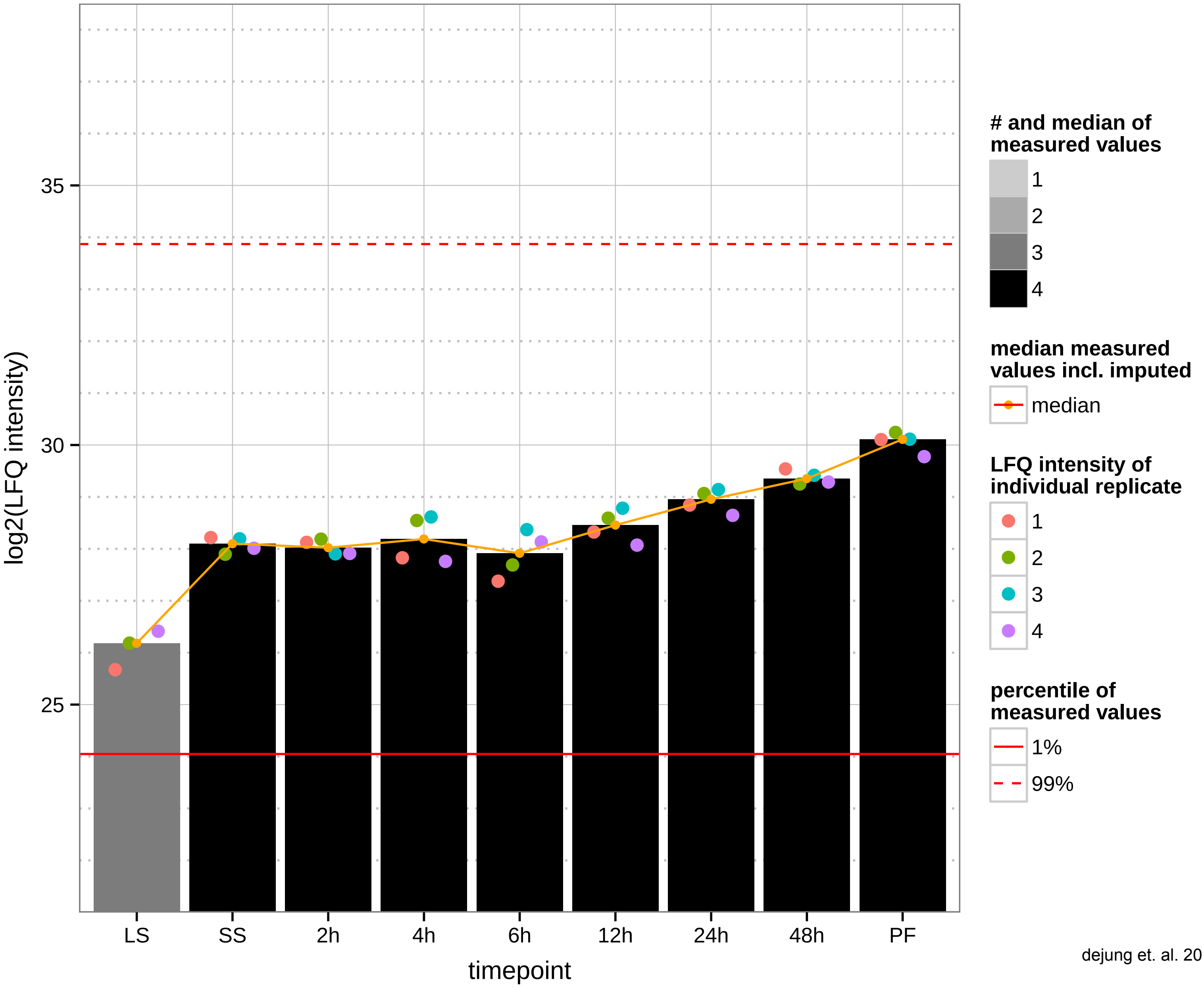
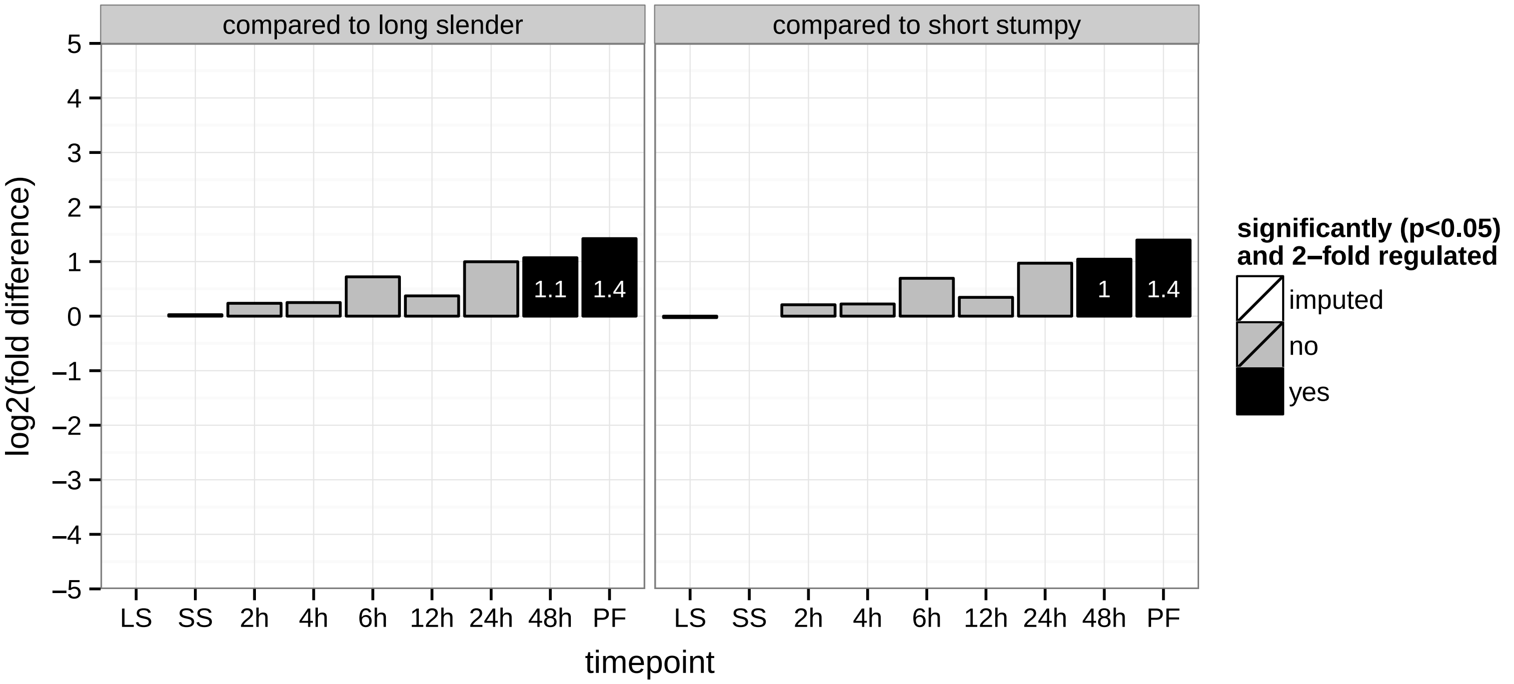
hypothetical protein, conserved
Tb927.4.1360
AGOF: carbohydrate binding, isomerase activity
AGOC: null
AGOP: carbohydrate metabolic process
PGOF: carbohydrate binding, catalytic activity, isomerase activity
PGOC: null
PGOP: carbohydrate metabolic process

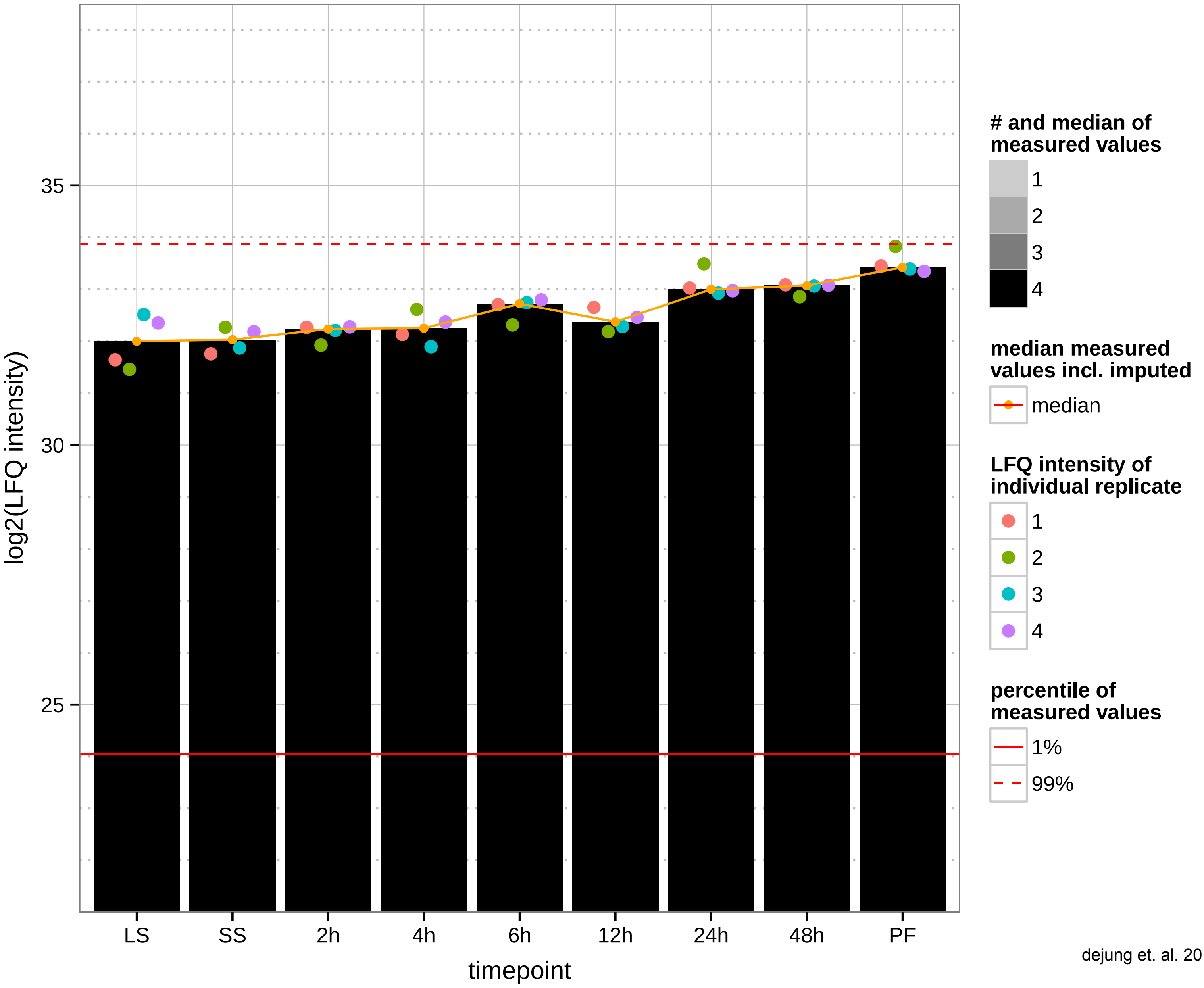




dejung et. al. 2015

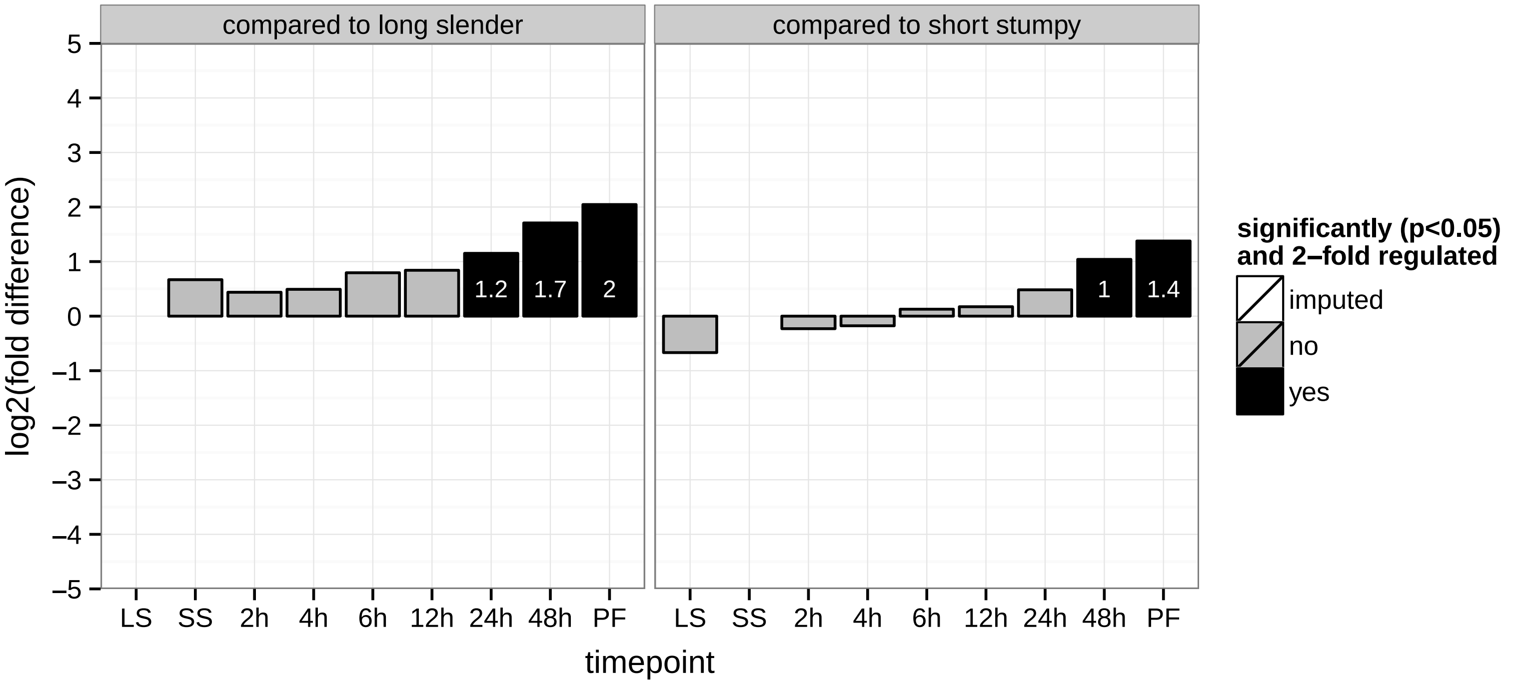
60S ribosomal protein L35a, putative
Tb927.4.2180
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation

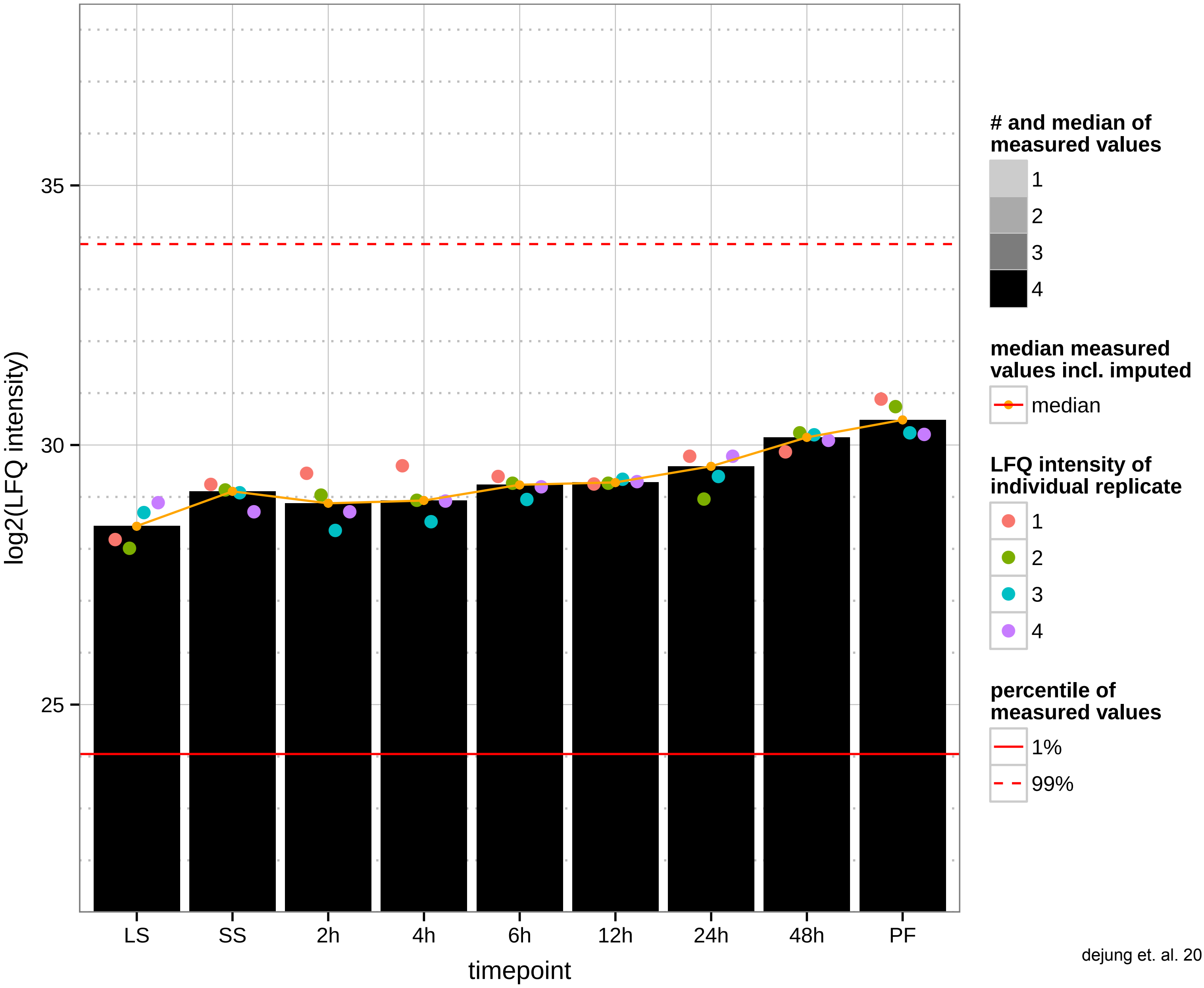




dejung et. al. 2015

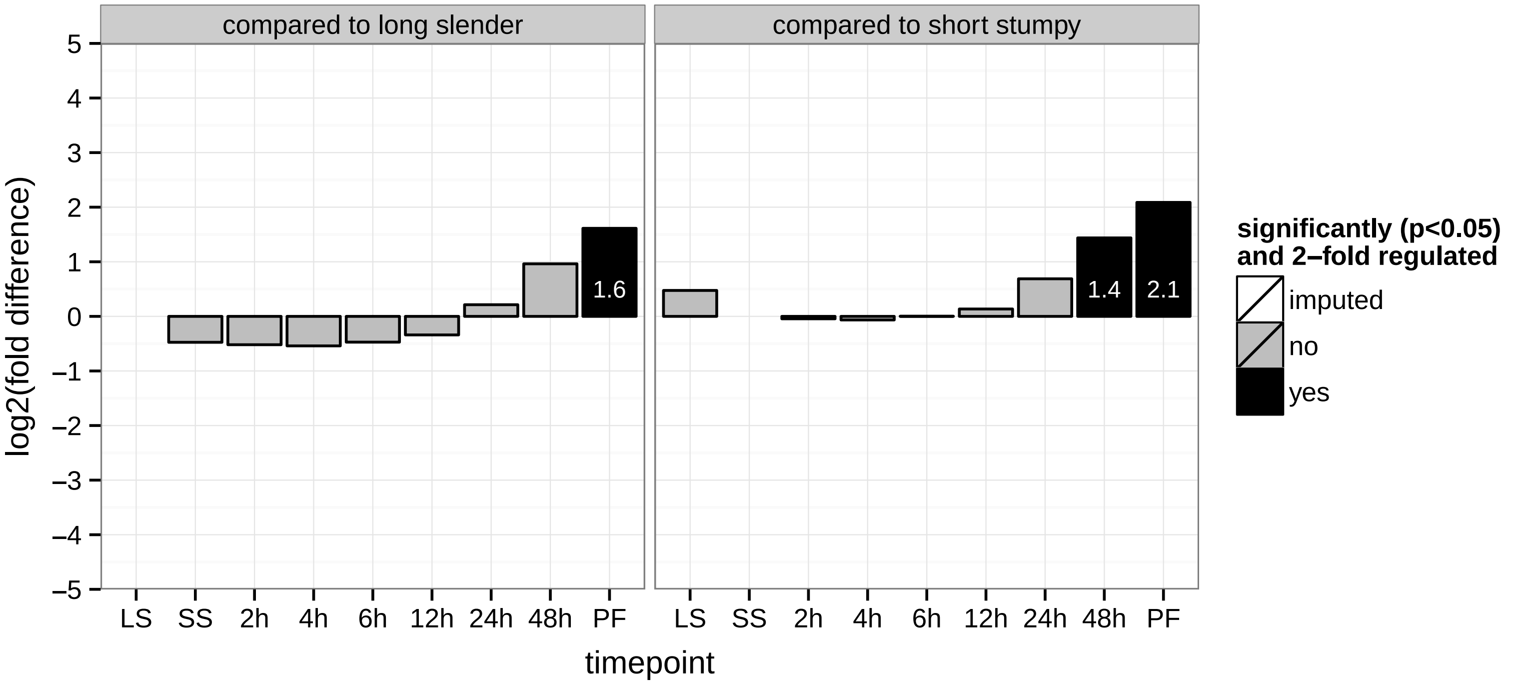
ATP−dependent RNA helicase, putative
Tb927.4.3890
AGOF: ATP binding, helicase activity, nucleic acid binding
AGOC: null
AGOP: null
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null

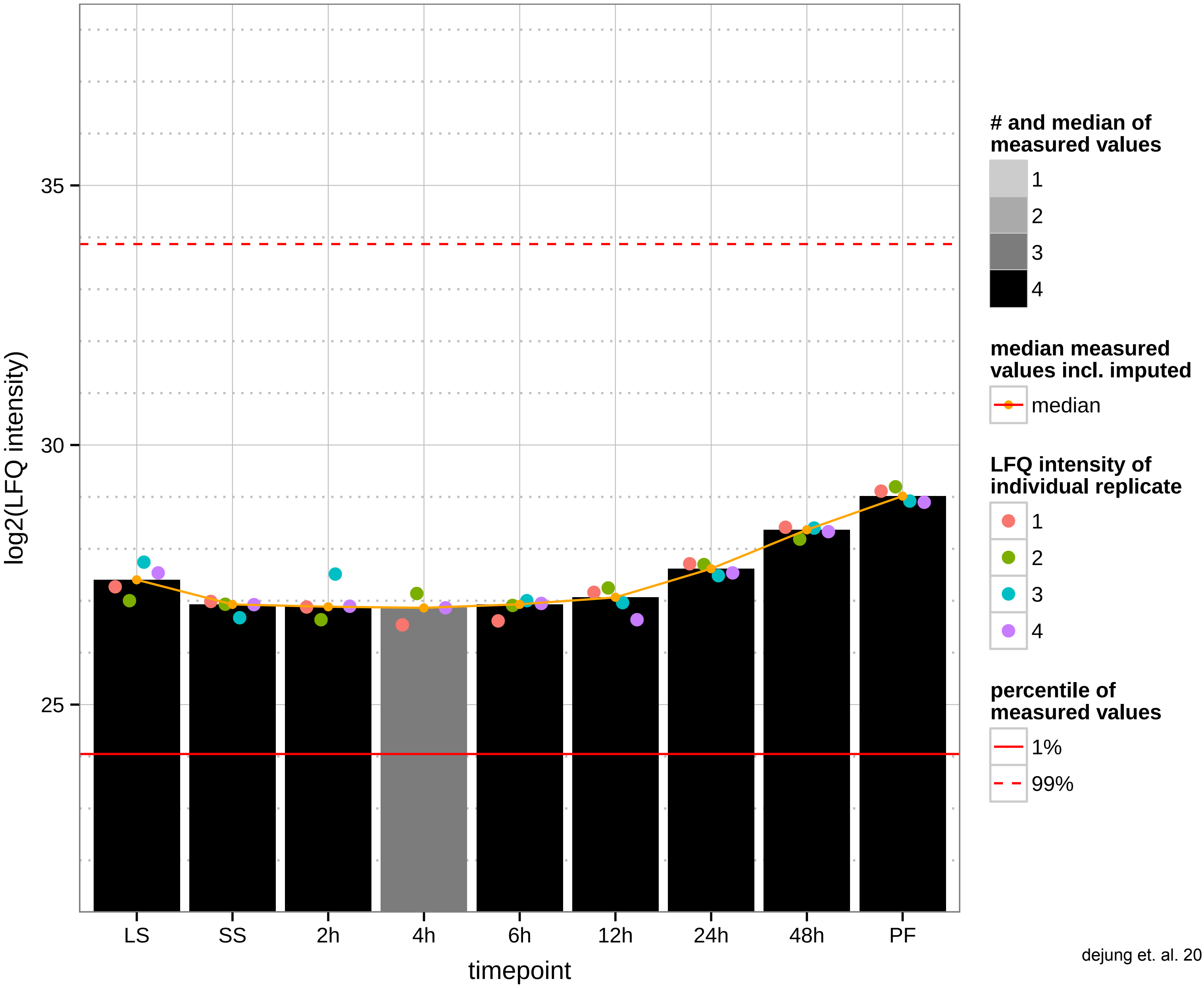




dejung et. al. 2015

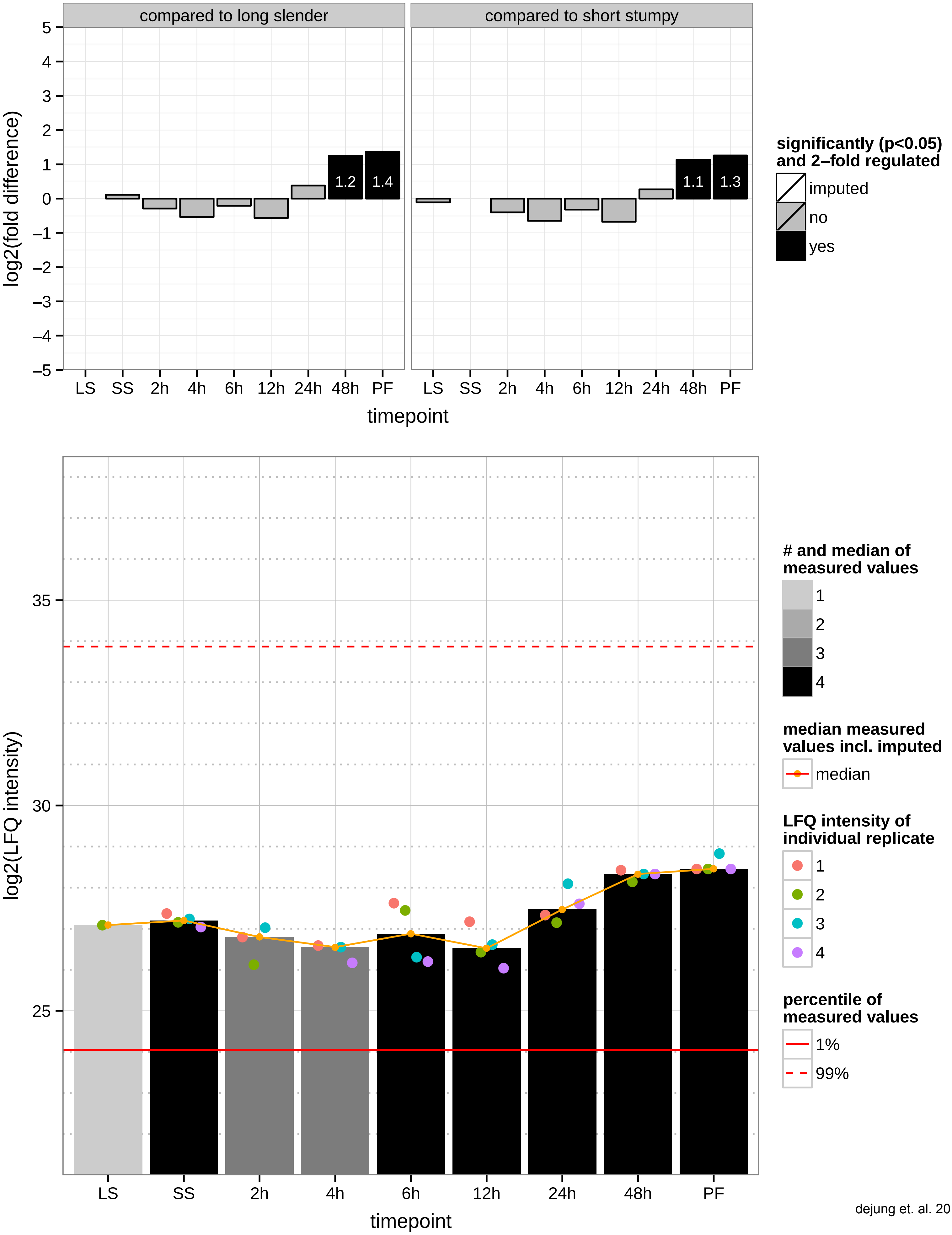
hypothetical protein, conserved
Tb927.4.4040
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





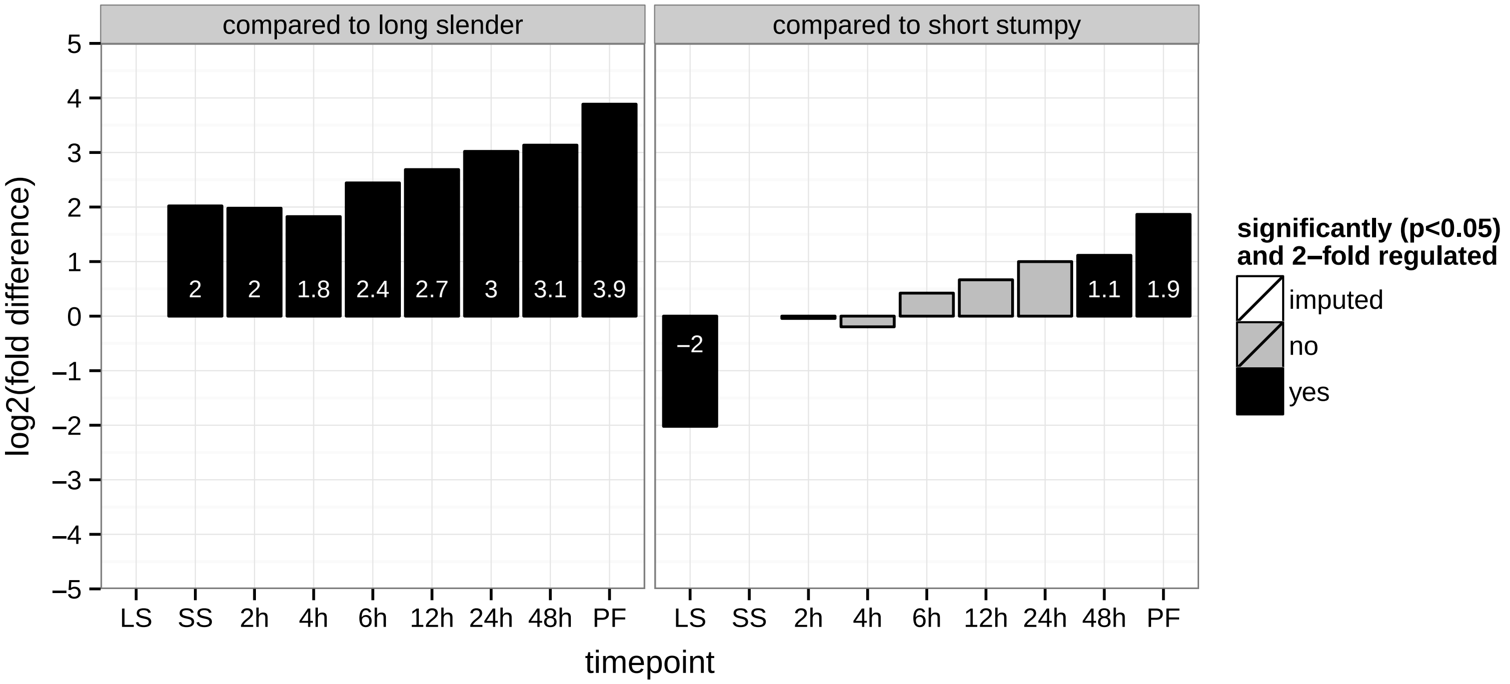
dejung et. al. 2015

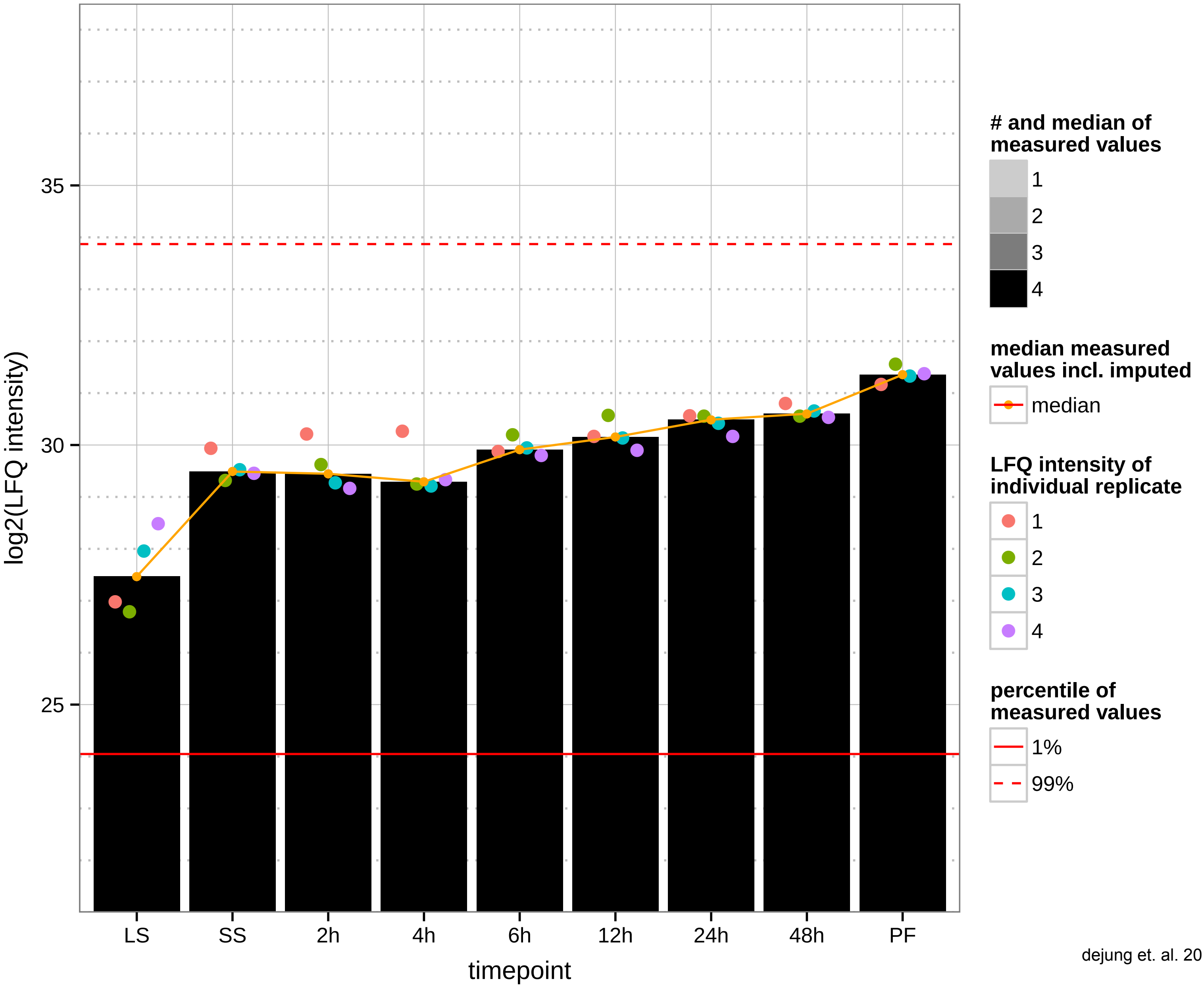
ATP−dependent zinc metallopeptidase, putative, metallo−peptidase, Clan MA(E) Family M41
Tb927.4.4210
AGOF: ATP binding, metalloendopeptidase activity, nucleoside−triphosphatase activity, zinc ion binding
AGOC: integral to membrane, mitochondrial inner membrane
AGOP: proteolysis
PGOF: ATP binding, metalloendopeptidase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: proteolysis



dejung et. al. 2015

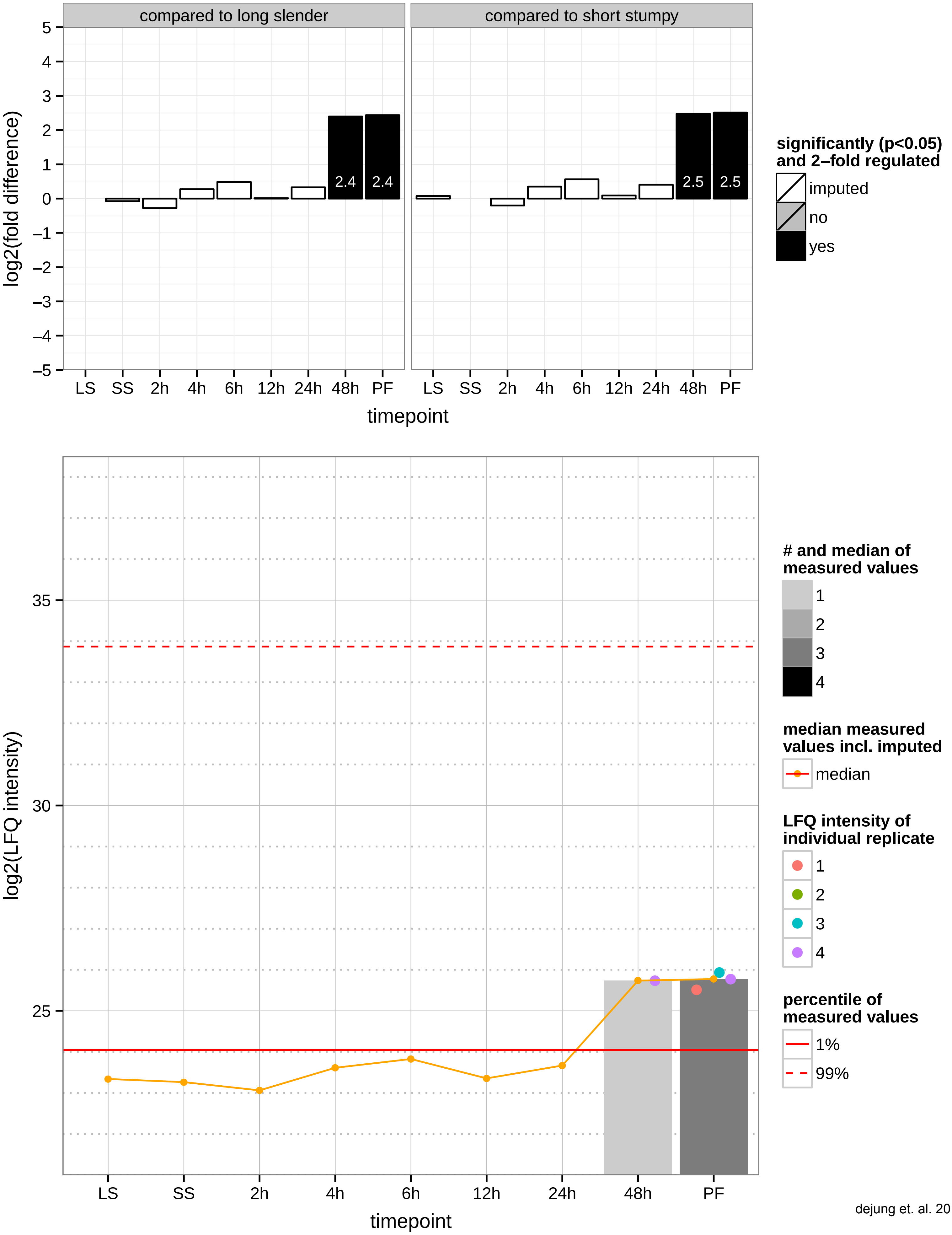
short–chain dehydrogenase, putative
Tb927.5.1210
AGOF: oxidoreductase activity
AGOC: mitochondrial inner membrane
AGOP: metabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process





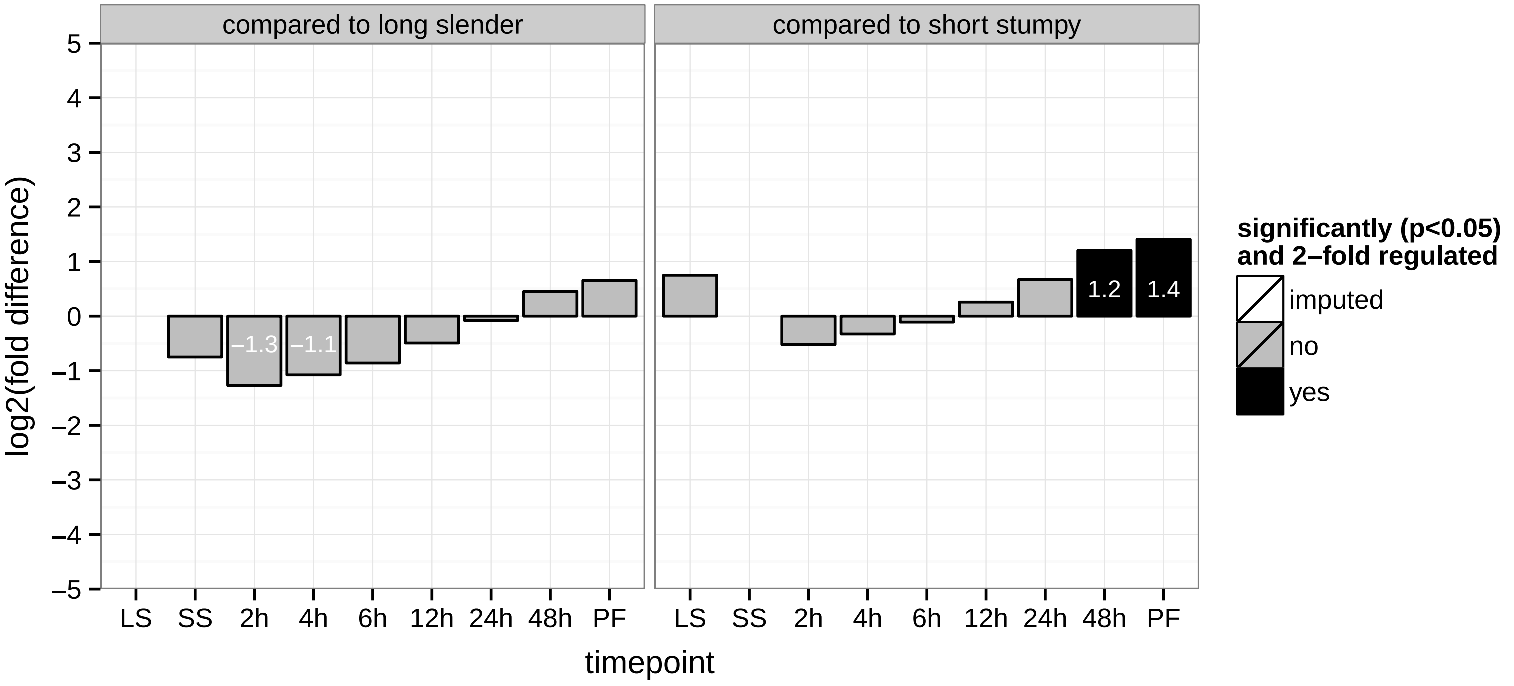
dejung et. al. 2015

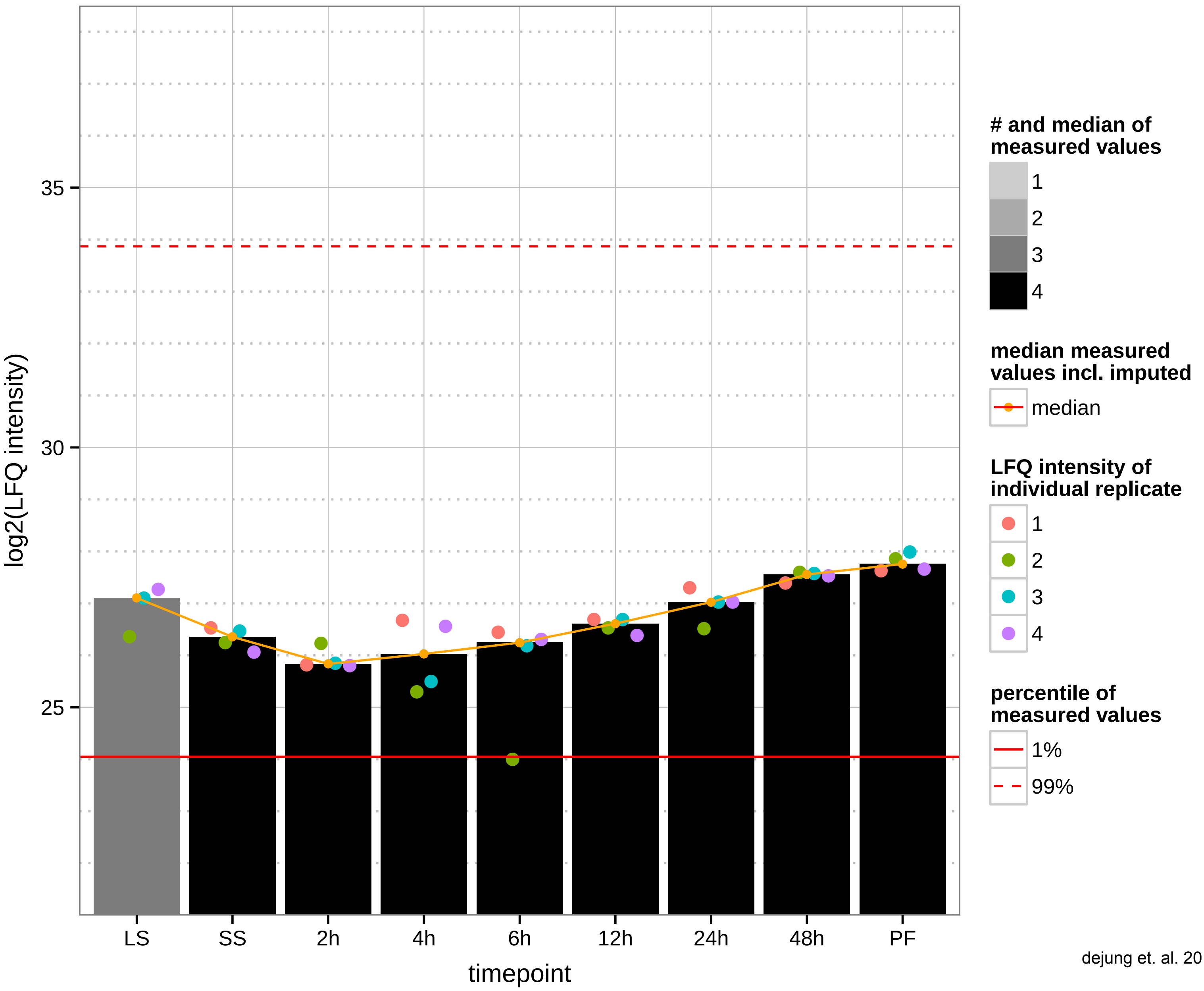
hypothetical protein, conserved
Tb927.5.1790
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015

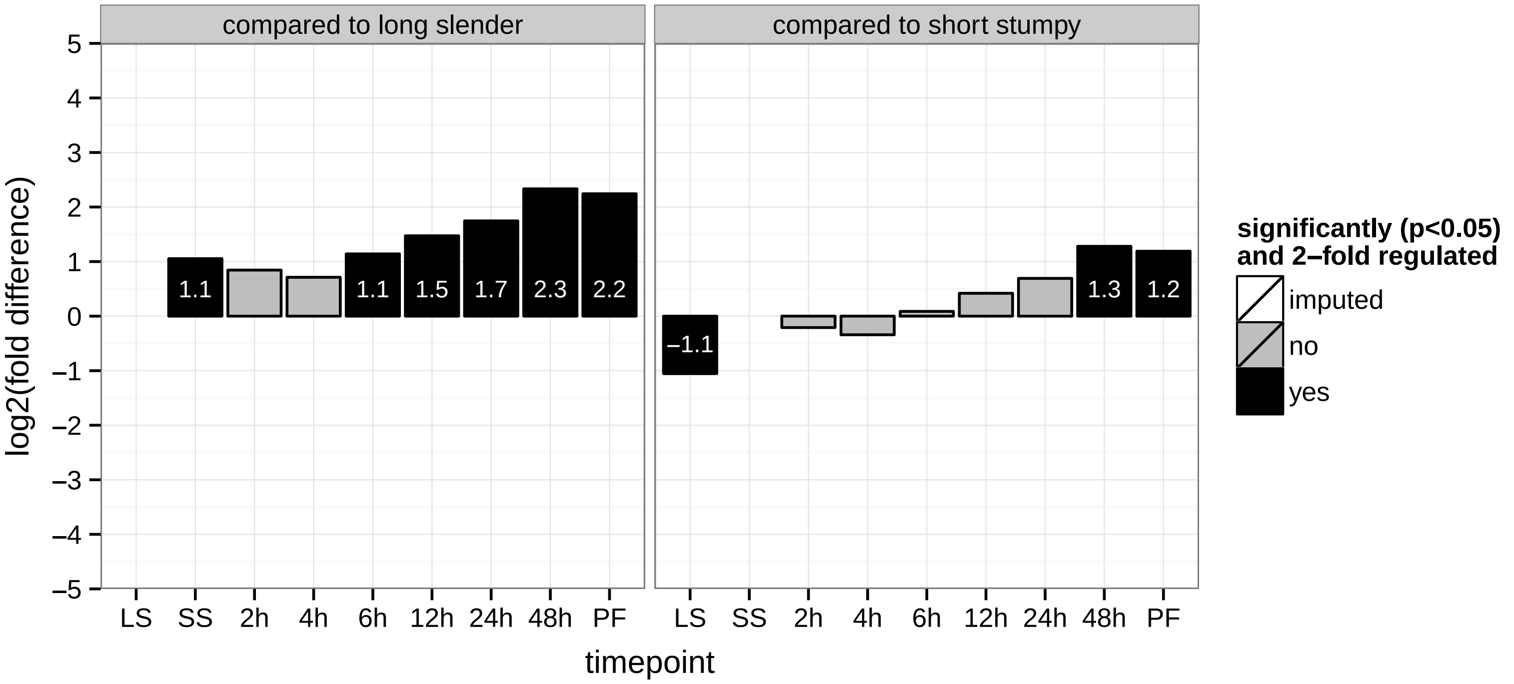
regulator of nonsense transcripts UPF1 (upf1)
Tb927.5.2140
AGOF: ATP binding, DNA binding, helicase activity, nucleoside–triphosphatase activity, zinc ion binding
AGOC: cytoplasm
AGOP: nuclear–transcribed mRNA catabolic process, nonsense–mediated decay
PGOF: ATP binding, DNA binding, helicase activity, nucleoside–triphosphatase activity, nucleotide binding, zinc ion binding
PGOC: cytoplasm
PGOP: nuclear–transcribed mRNA catabolic process, nonsense–mediated decay

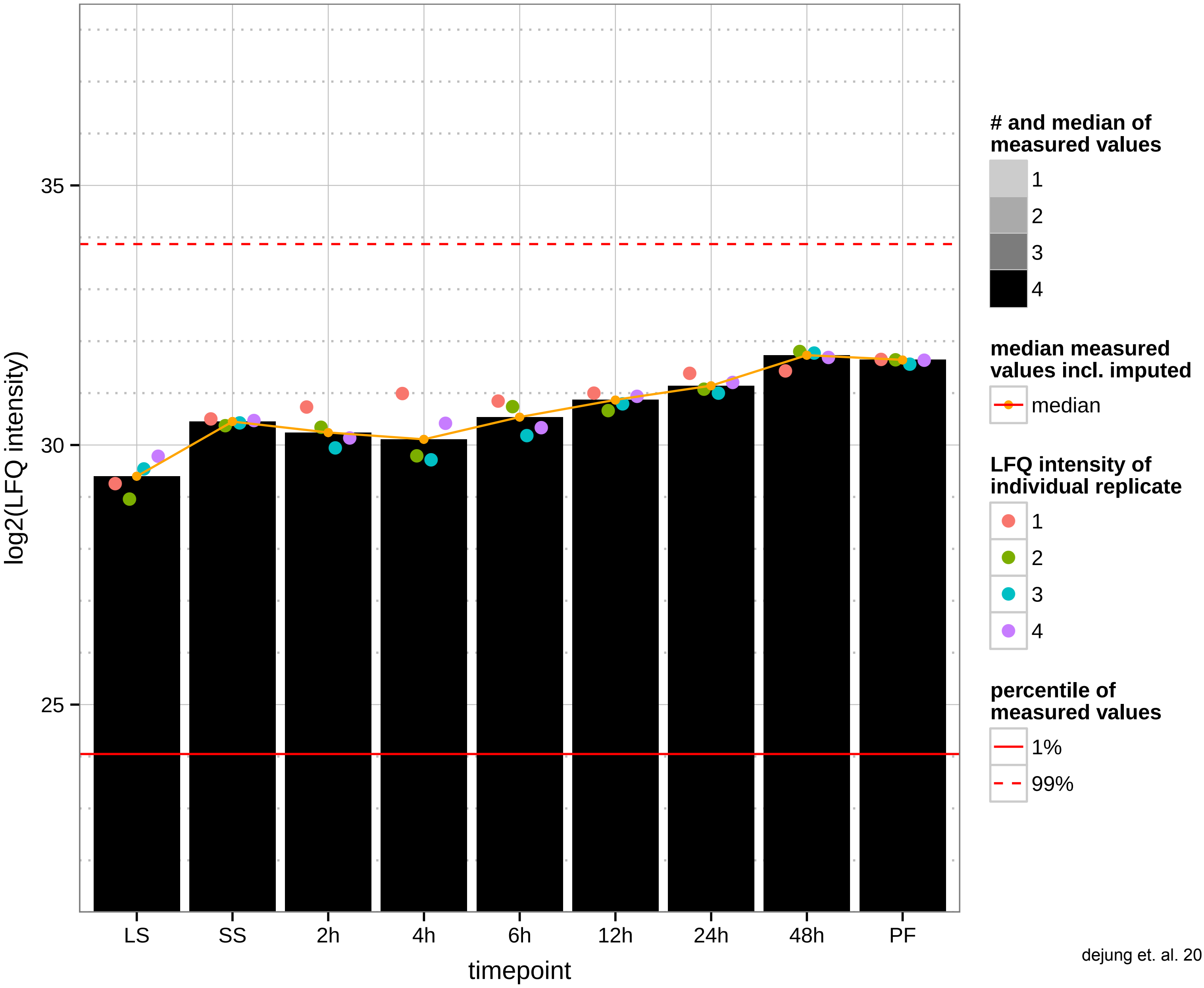




dejung et. al. 2015

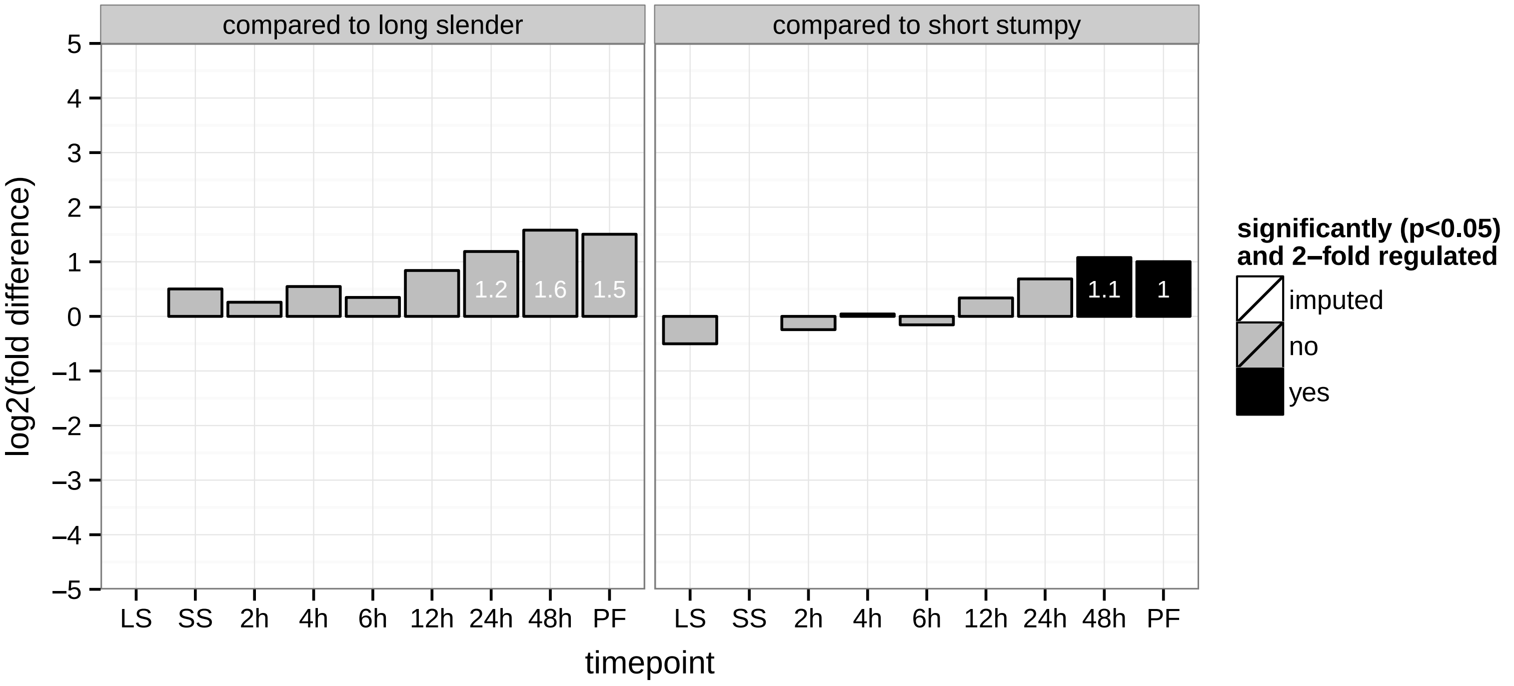
hypothetical protein, conserved
Tb927.5.2320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

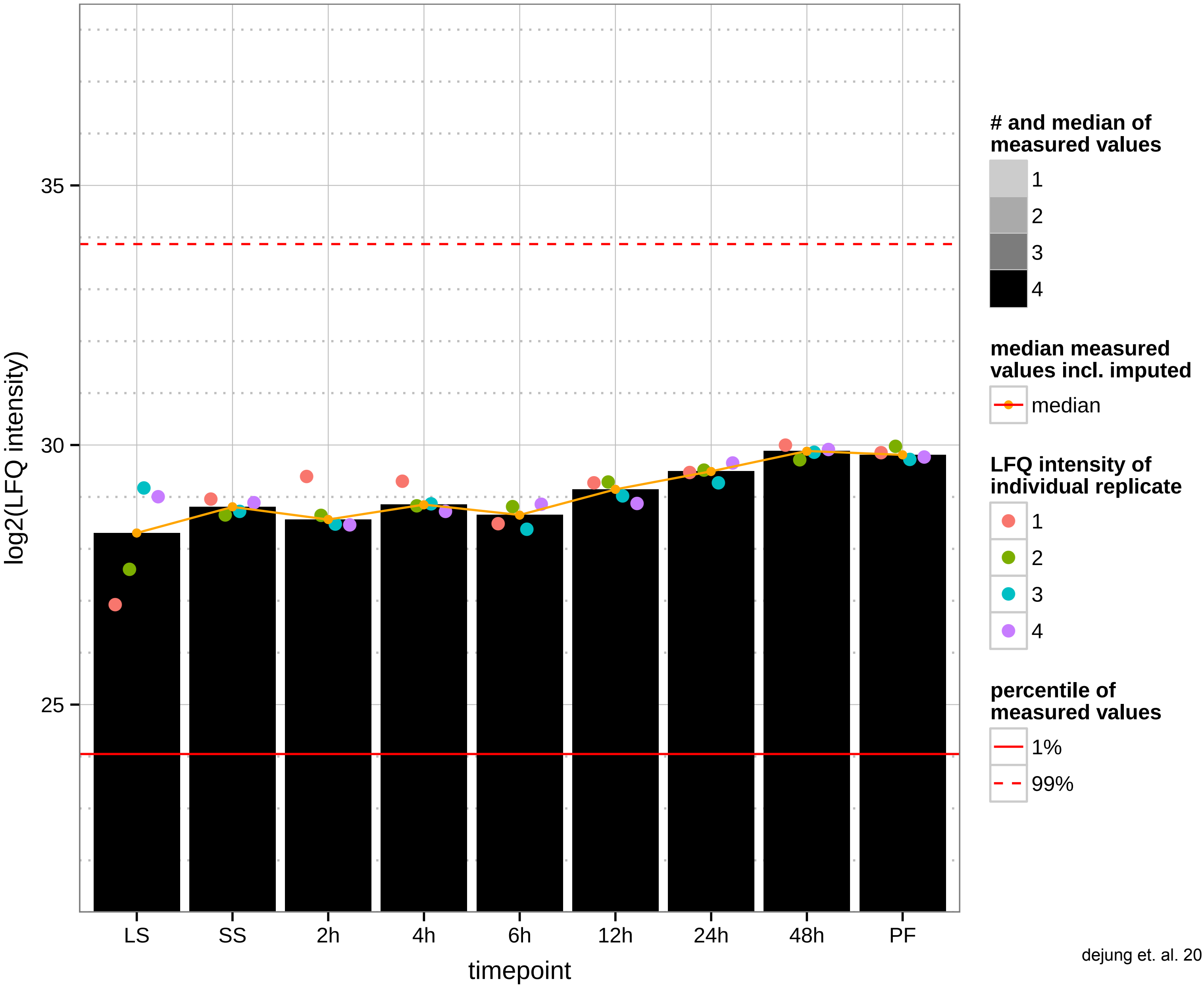




dejung et. al. 2015

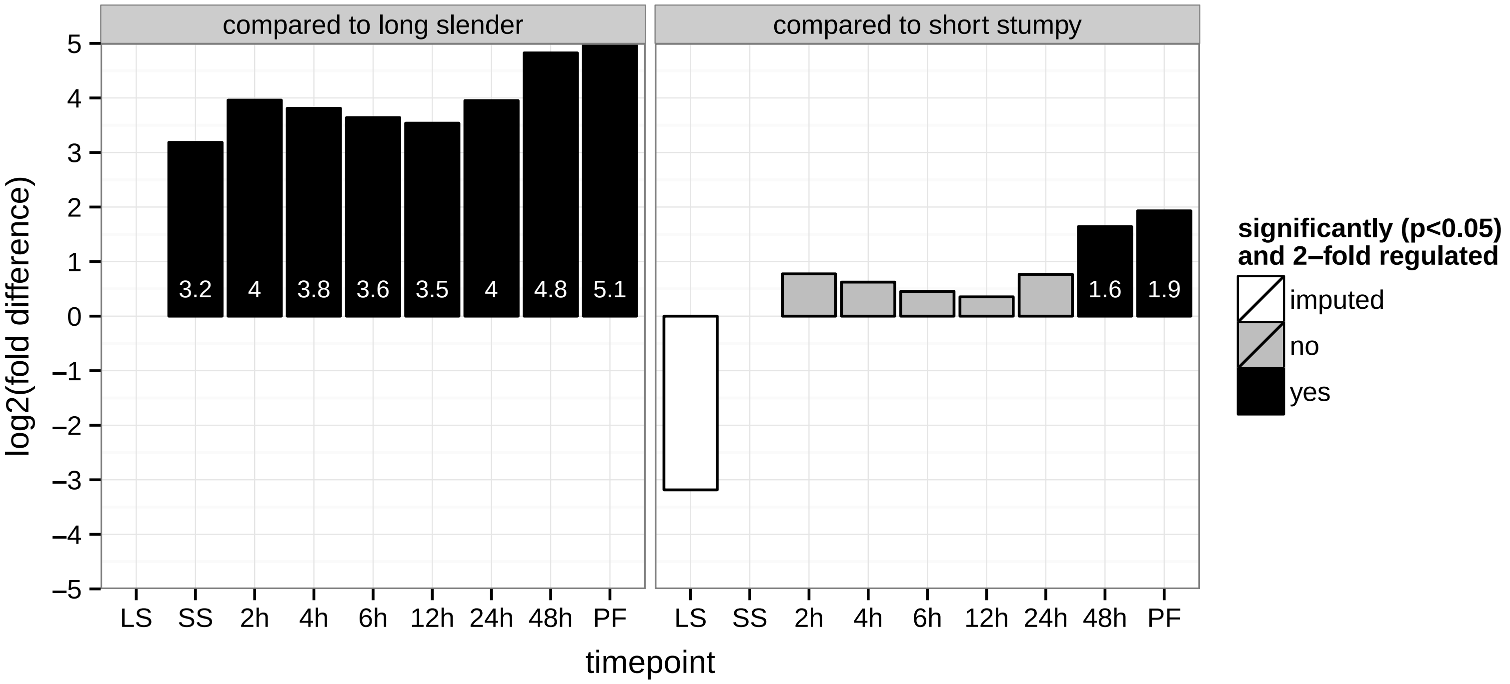
mitochondrial DNA polymerase beta
Tb927.5.2780
AGOF: DNA binding, DNA–directed DNA polymerase activity, catalytic activity
AGOC: mitochondrion
AGOP: DNA repair, DNA replication
PGOF: DNA binding, DNA–directed DNA polymerase activity, catalytic activity, nucleotidyltransferase activity
PGOC: null
PGOP: null

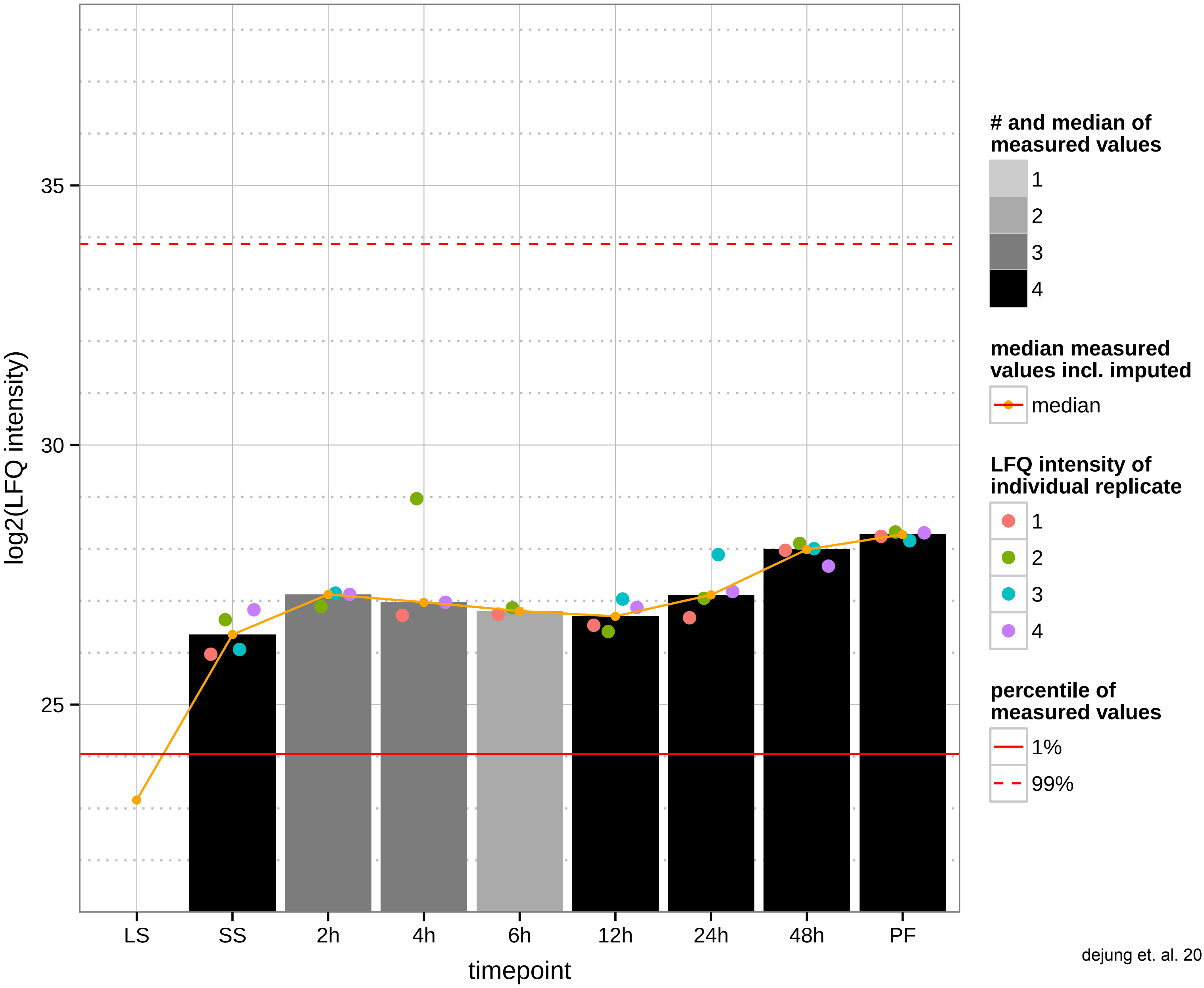




dejung et. al. 2015

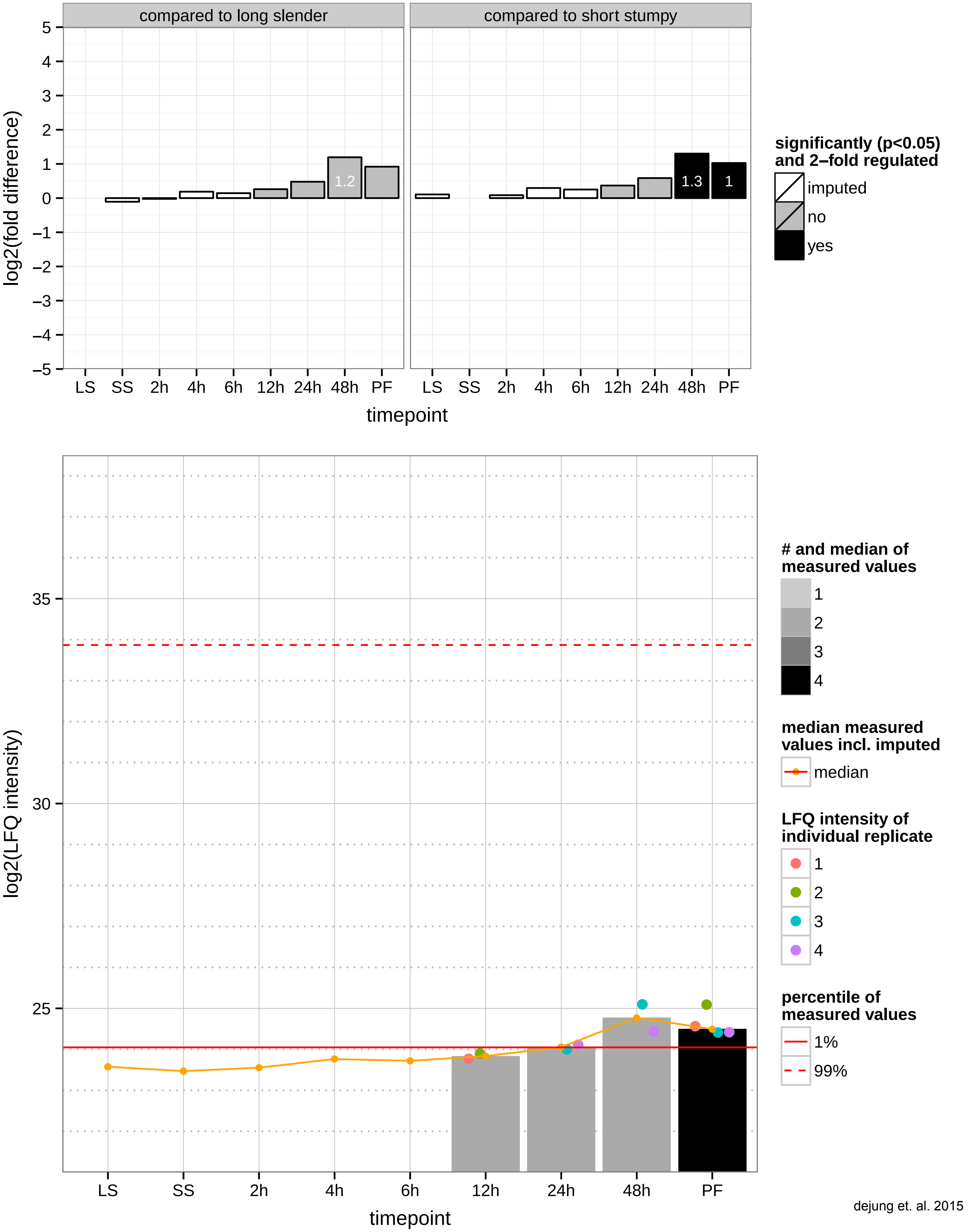
mitochondrial DNA polymerase beta–PAK (Pol beta–PAK)
Tb927.5.2790
AGOF: DNA binding, DNA–directed DNA polymerase activity, catalytic activity
AGOC: kinetoplast
AGOP: DNA replication
PGOF: DNA binding, DNA–directed DNA polymerase activity, catalytic activity, nucleotidyltransferase activity
PGOC: null
PGOP: null





dejung et. al. 2015

hypothetical protein, conserved
Tb927.5.3680
AGOF: null
AGOC: null
AGOP: null
PGOF: phosphatidylinositol N–acetylglucosaminyltransferase activity
PGOC: null
PGOP: null



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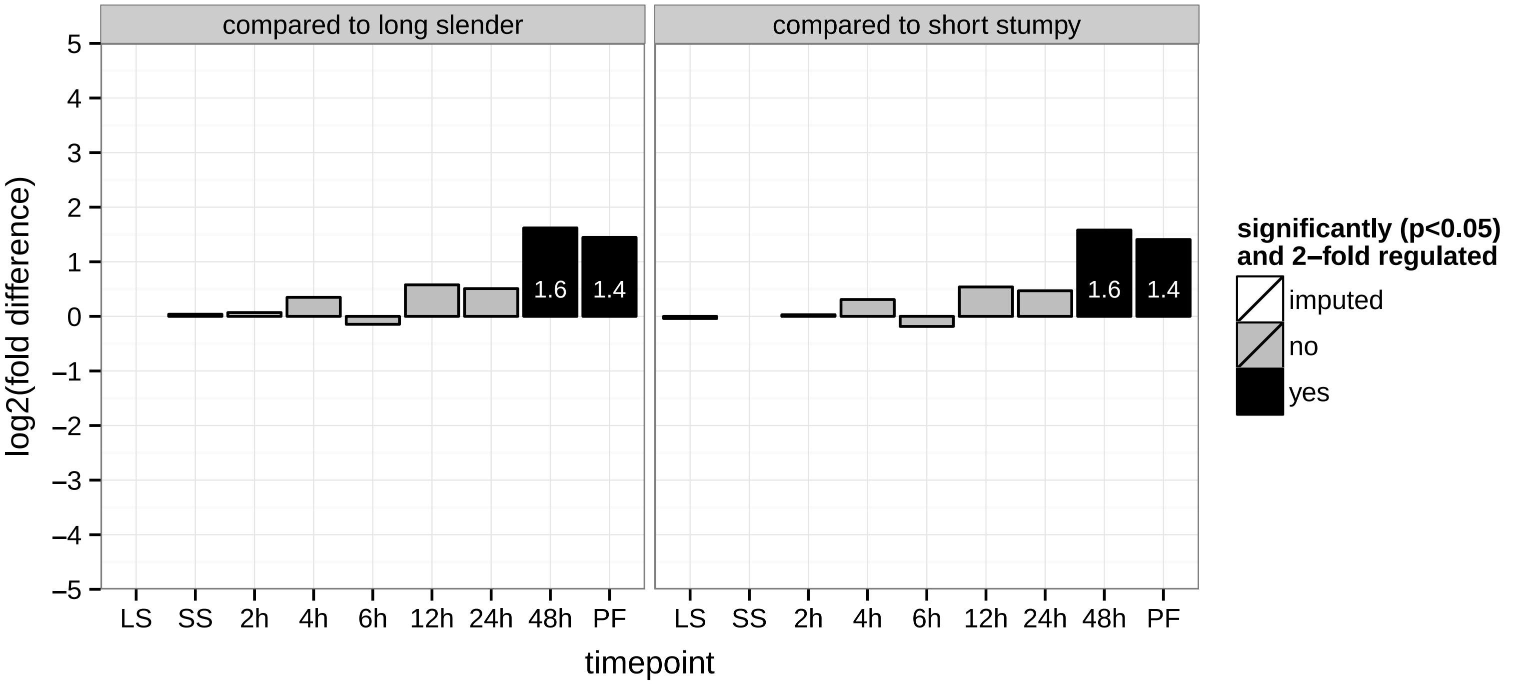
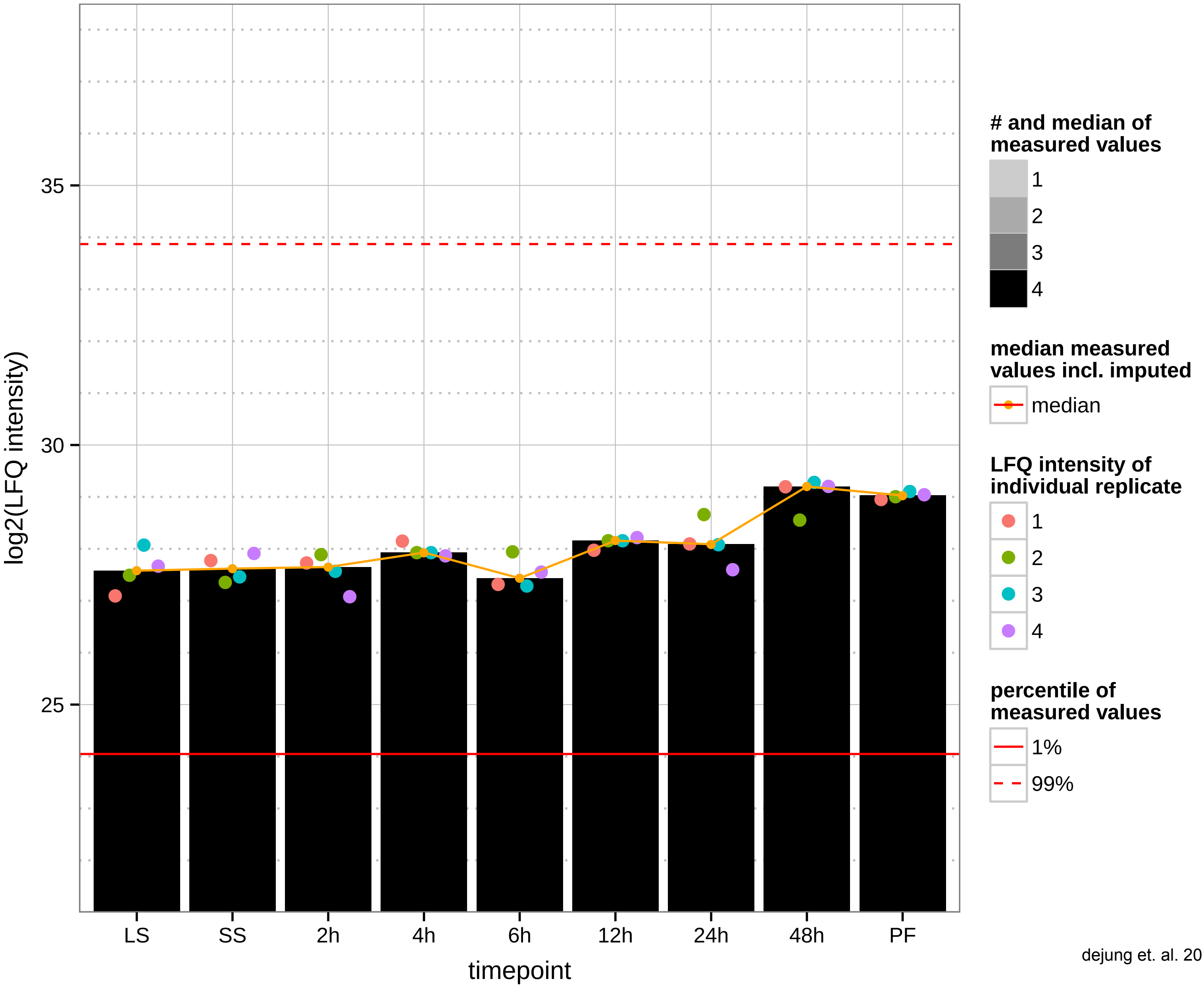
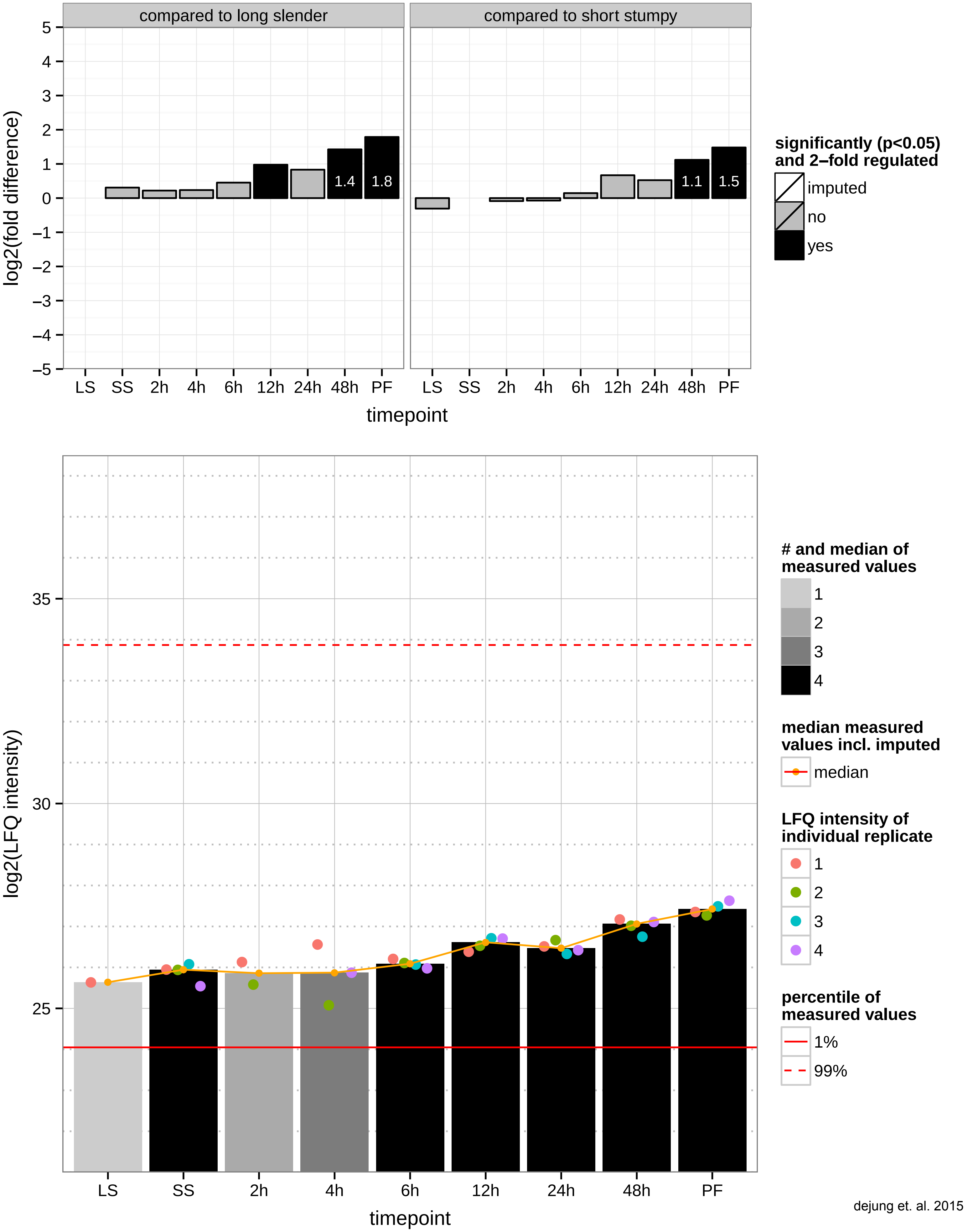
monothiol glutaredoxin, putative
Tb927.5.950
AGOF: electron carrier activity, glutathione−disulfide reductase activity, protein disulfide oxidoreductase activity
AGOC: null
AGOP: cell redox homeostasis, oxidation−reduction process
PGOF: electron carrier activity, protein disulfide oxidoreductase activity
PGOC: null
PGOP: cell redox homeostasis





dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.1430
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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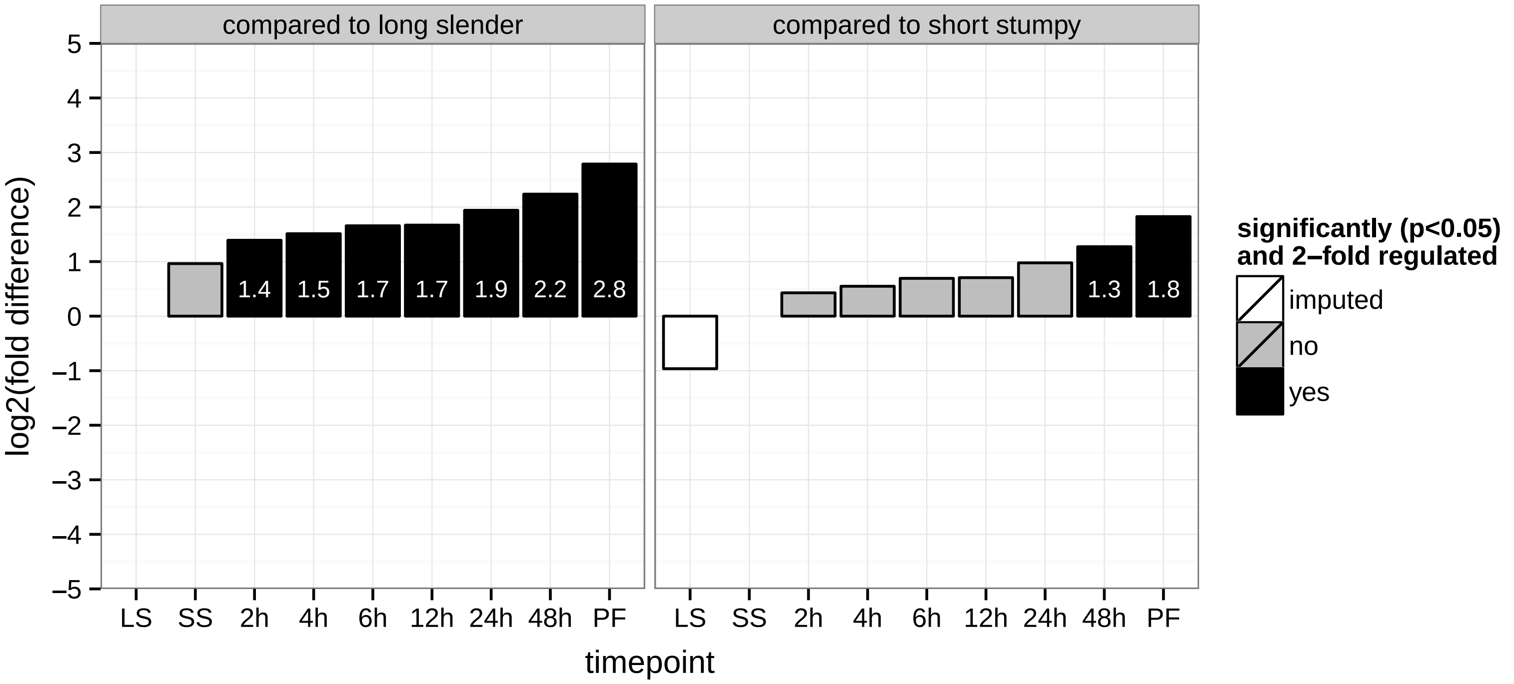
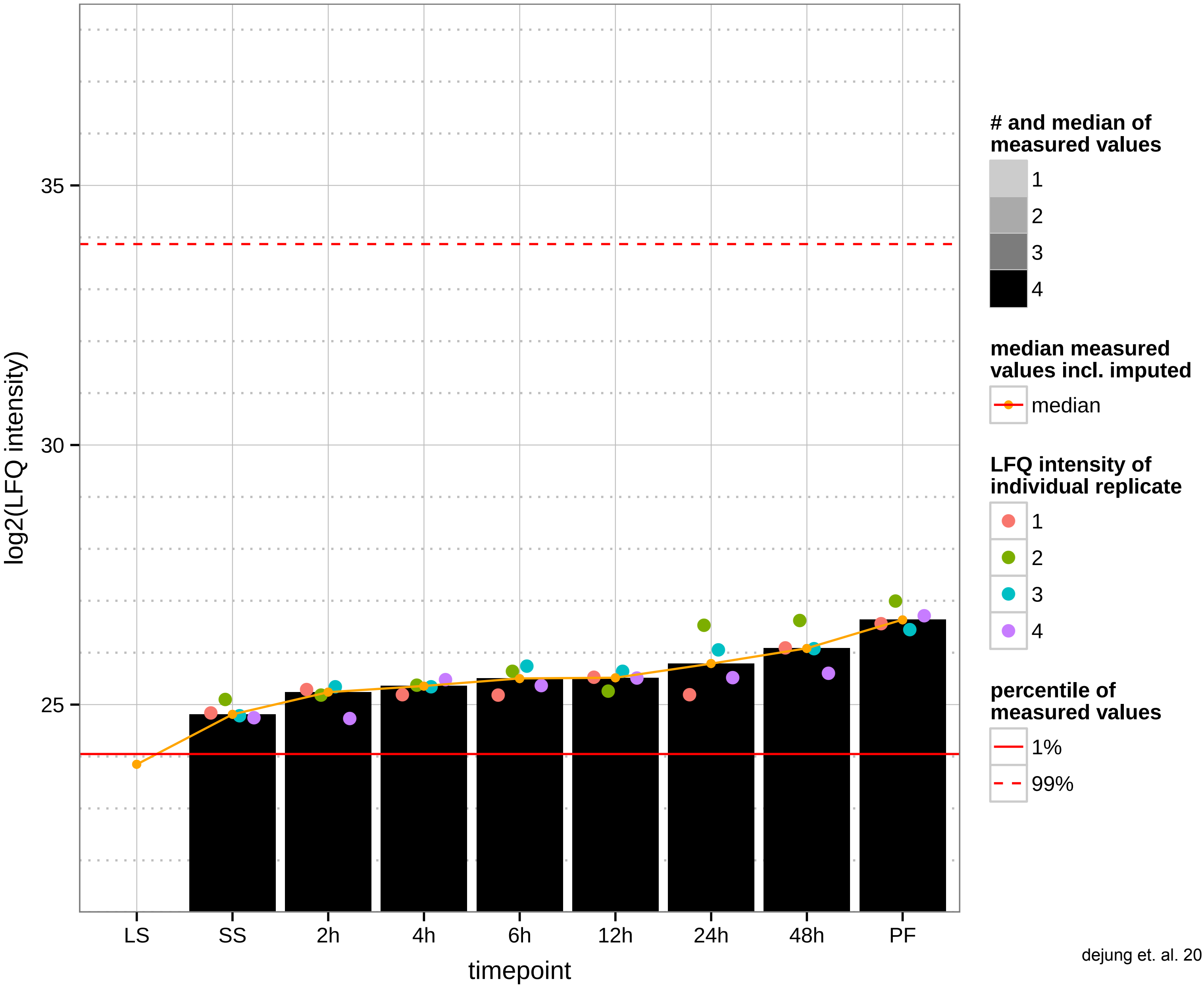
hypothetical protein, conserved
Tb927.6.1440
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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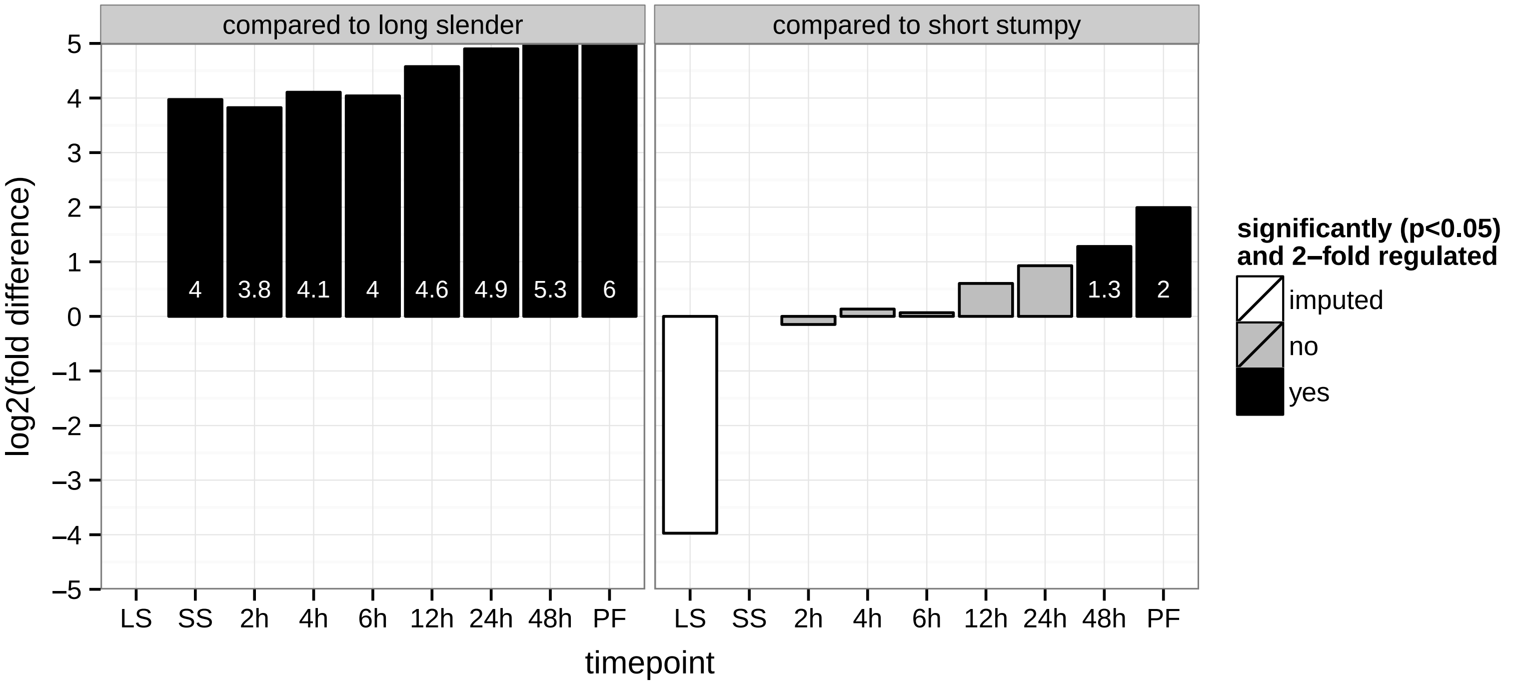
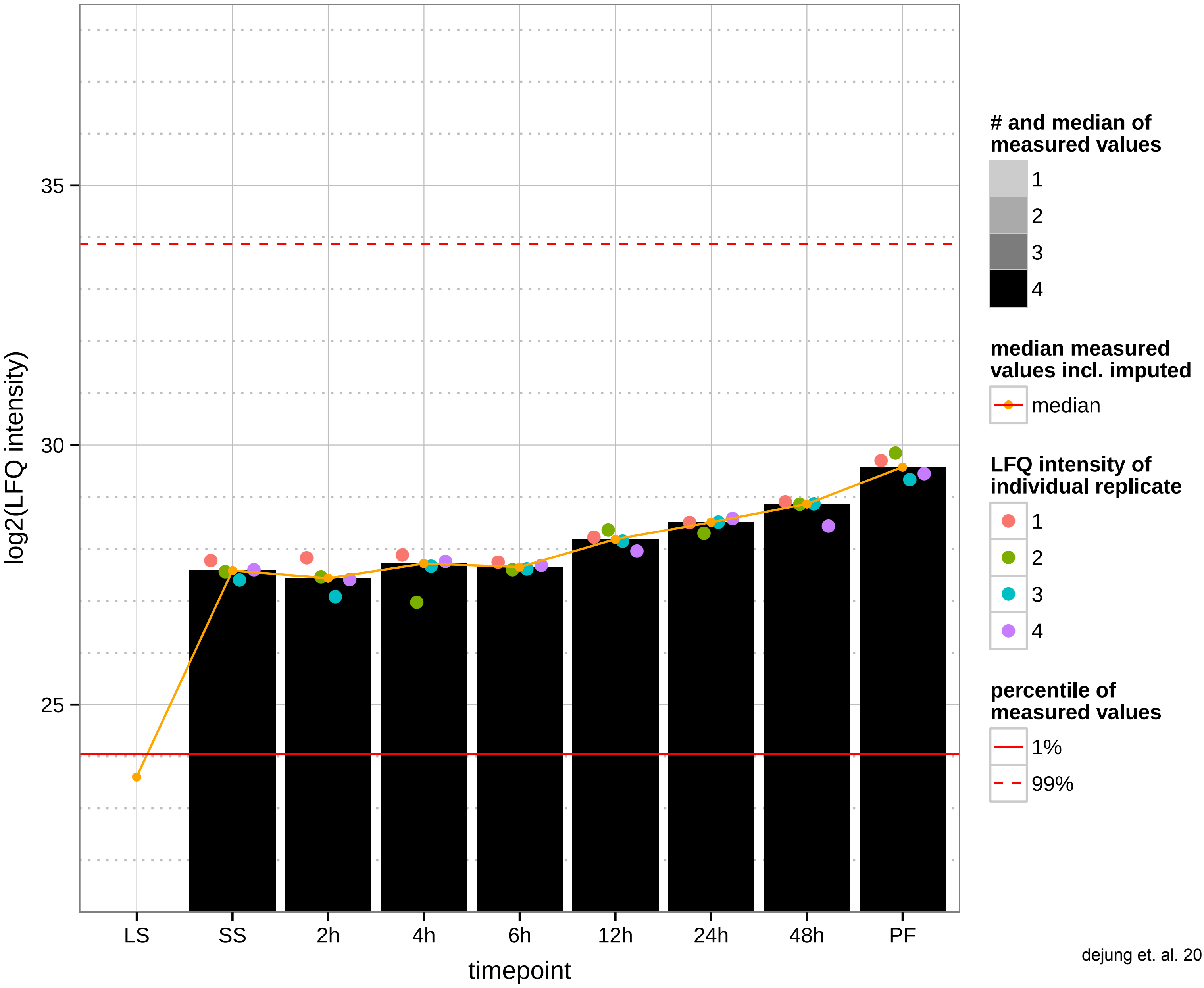
hypothetical protein, conserved
Tb927.6.2010
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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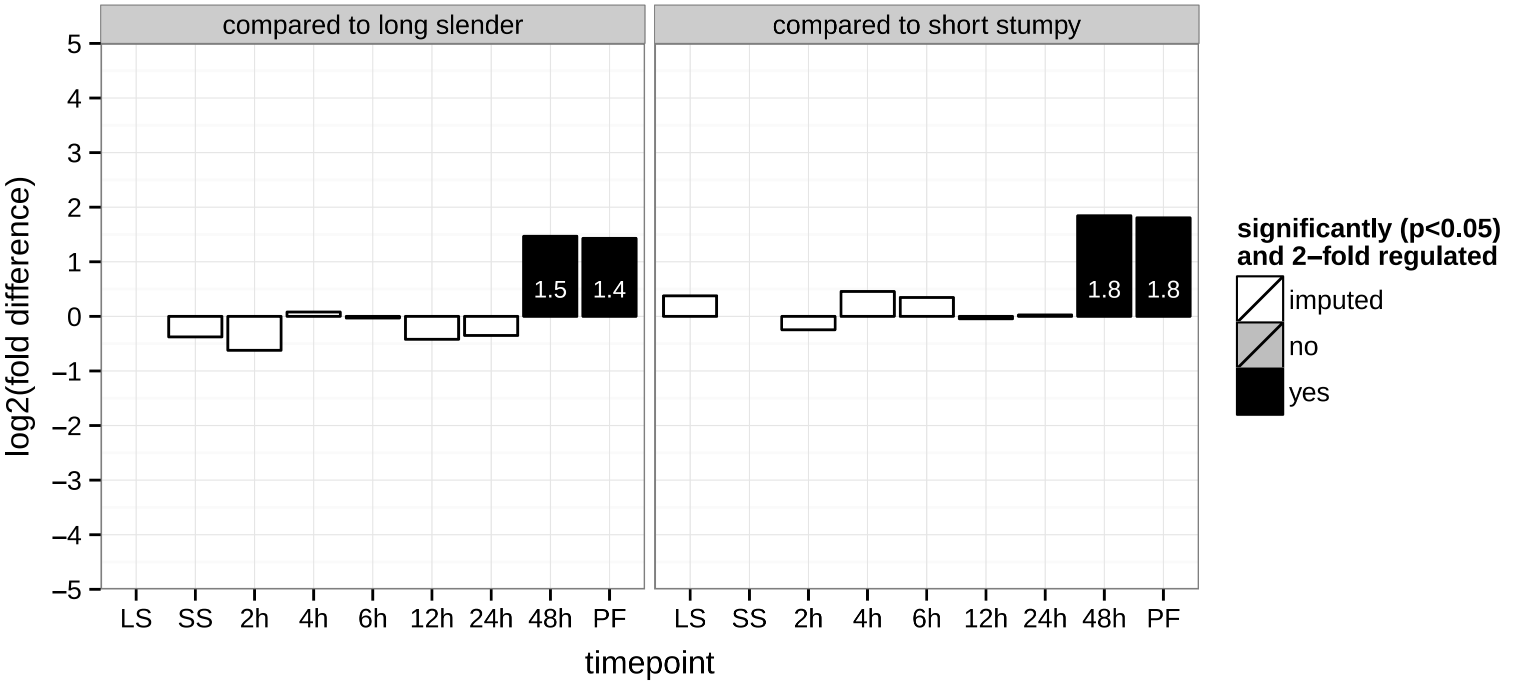
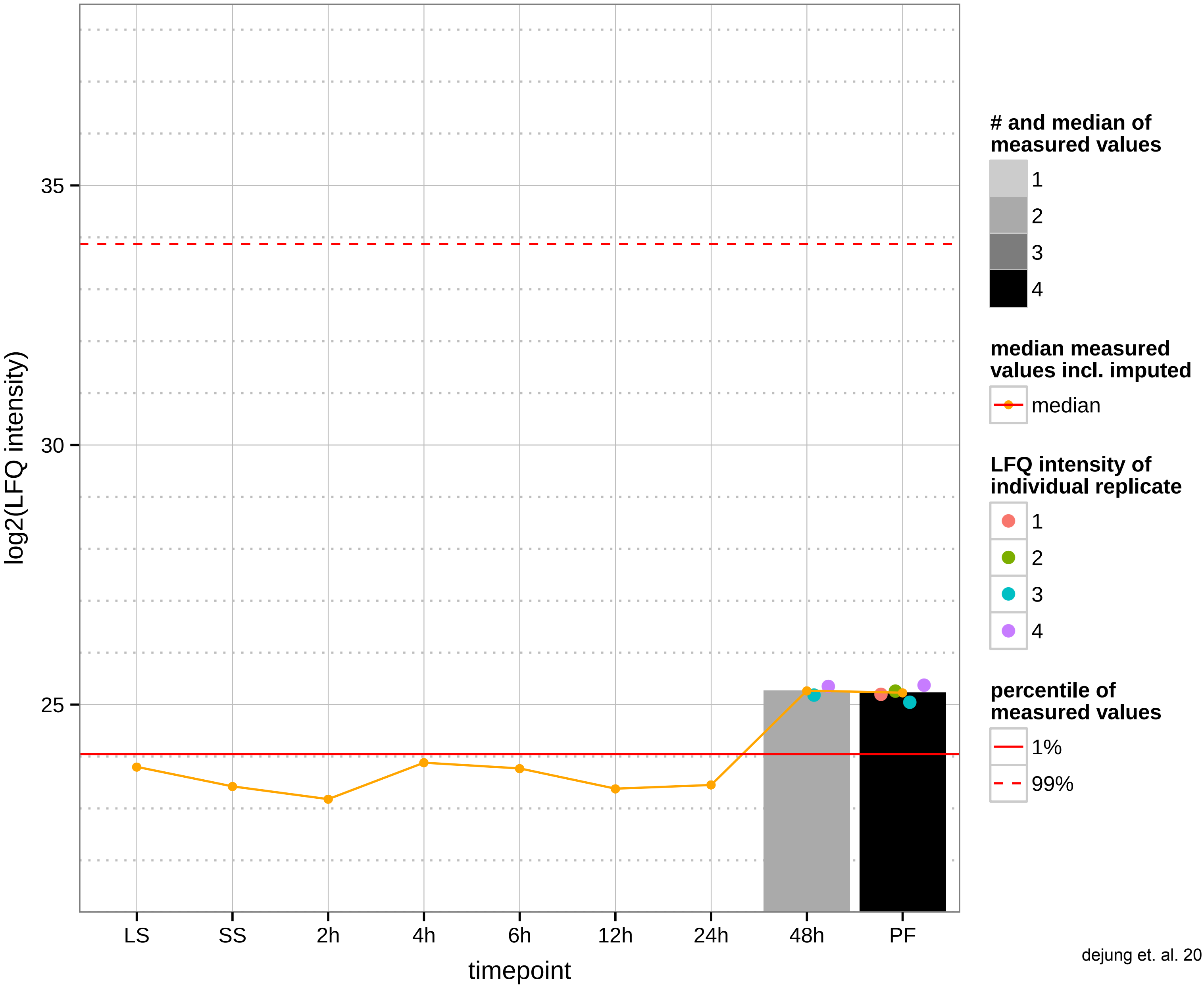
hypothetical protein, conserved
Tb927.6.3220;Tb11.v5.0720
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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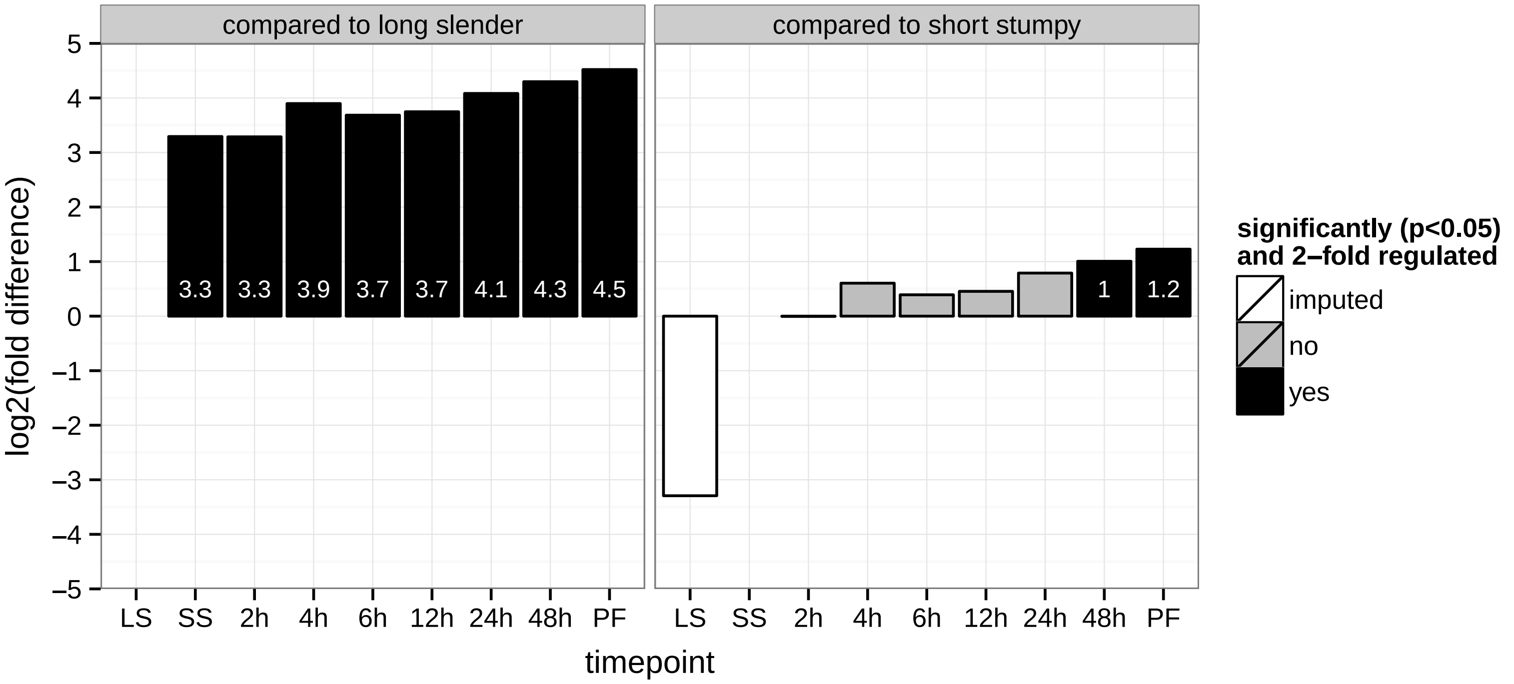
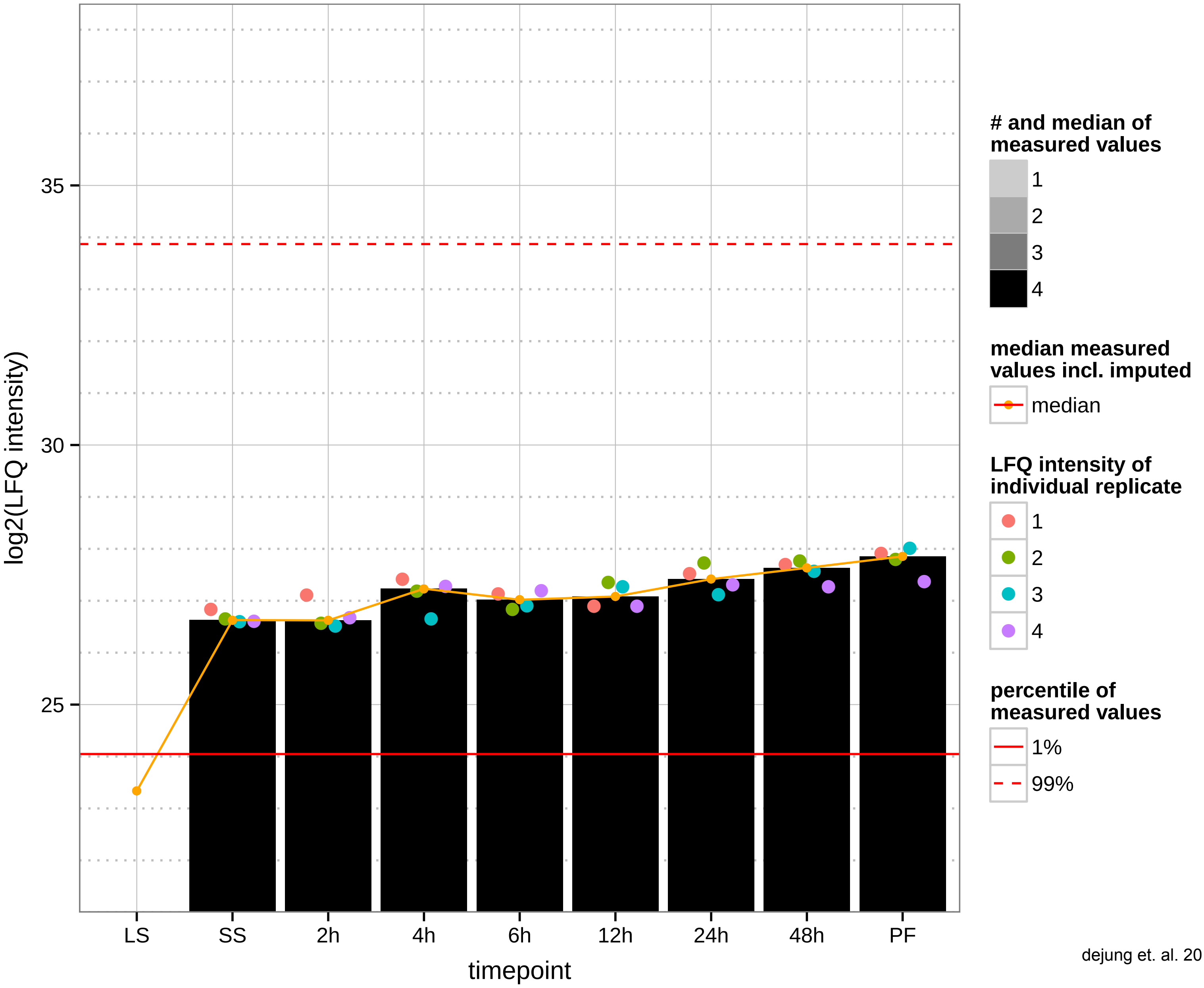
hypothetical protein, conserved
Tb927.6.3930
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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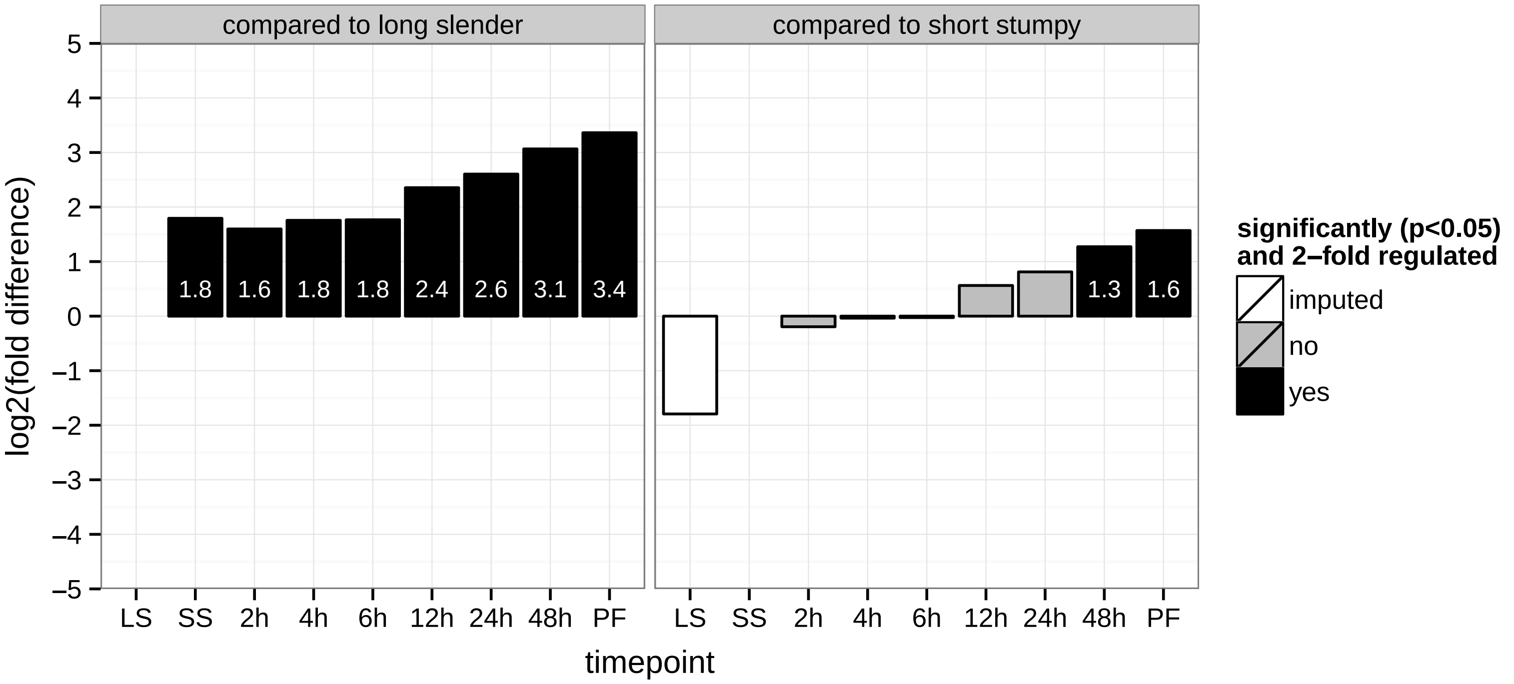
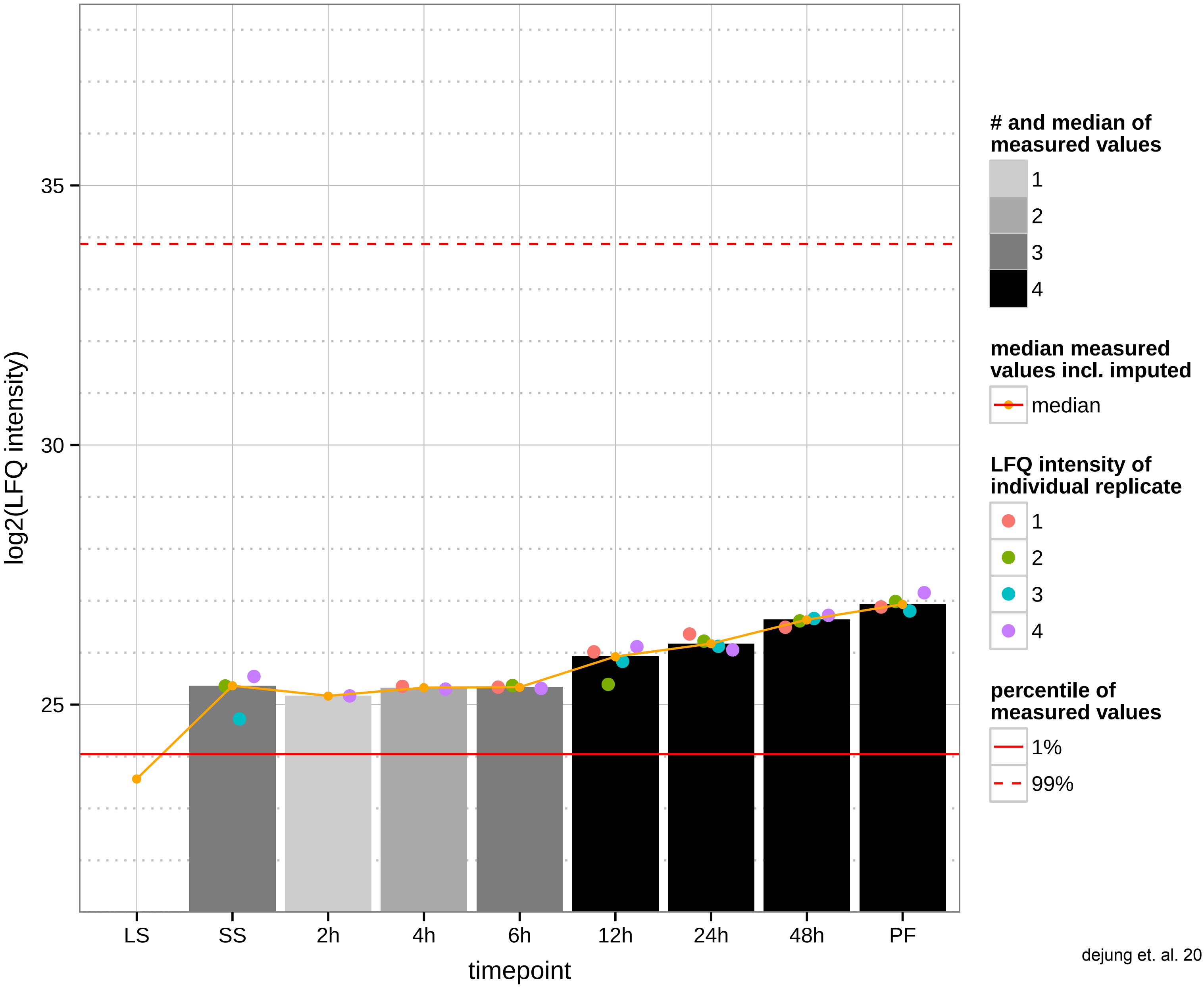
hypothetical protein, conserved
Tb927.6.4200
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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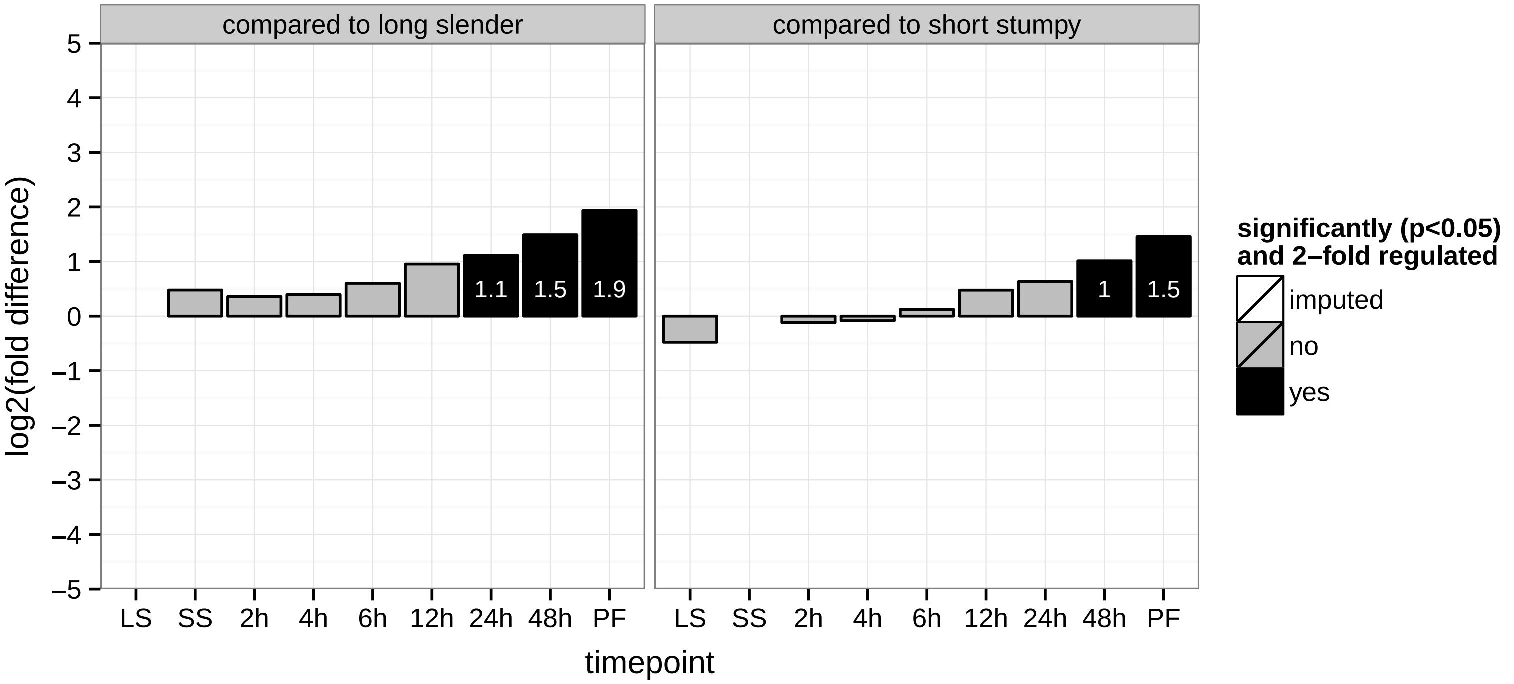
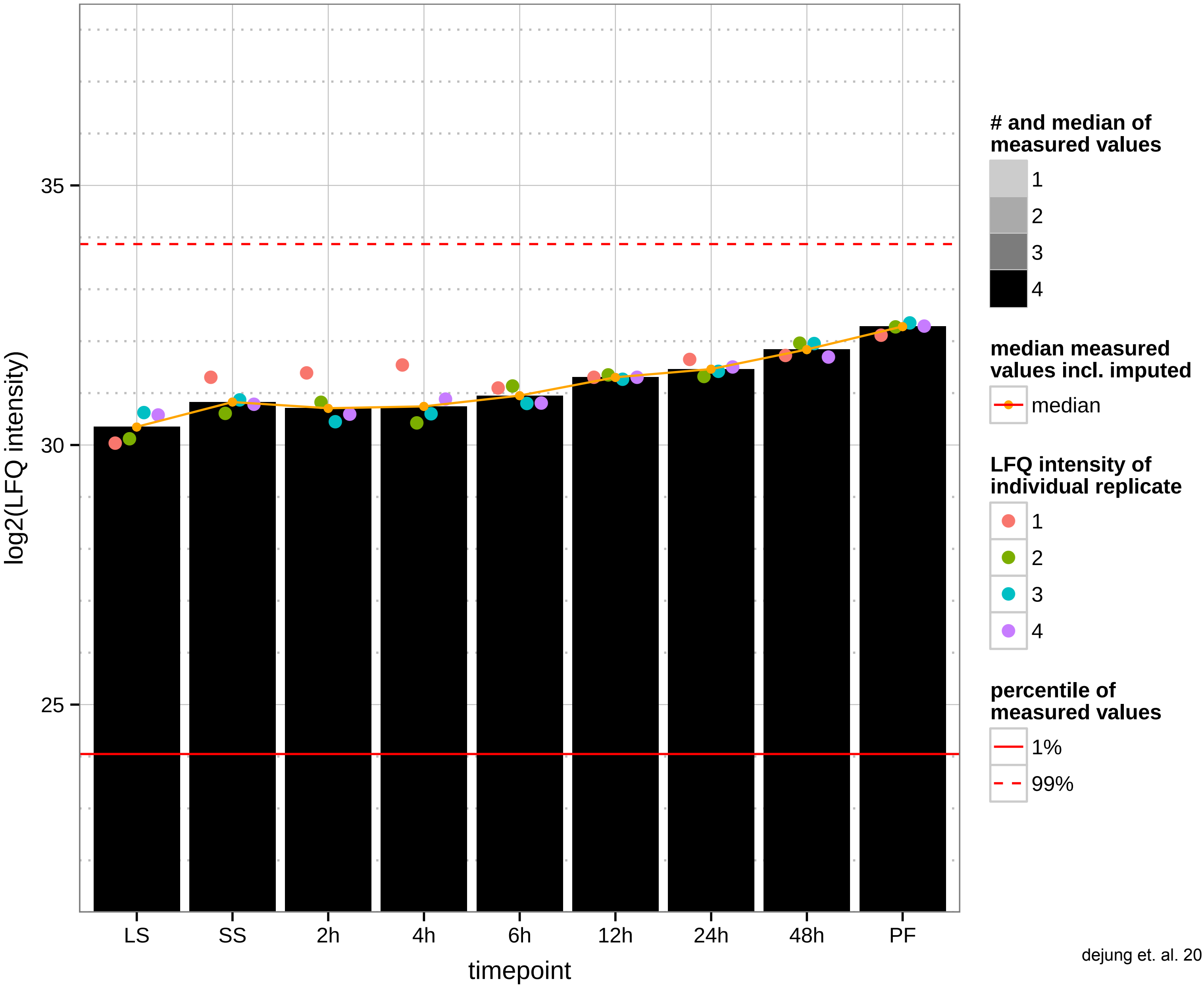
valyl–tRNA synthetase, putative (ValRS)
Tb927.6.4480
AGOF: ATP binding, valine–tRNA ligase activity
AGOC: cytoplasm
AGOP: translation, valyl–tRNA aminoacylation
PGOF: ATP binding, aminoacyl–tRNA editing activity, aminoacyl–tRNA ligase activity, nucleotide binding, valine–tRNA ligase a
PGOC: cytoplasm
PGOP: tRNA aminoacylation for protein translation, valyl–tRNA aminoacylation





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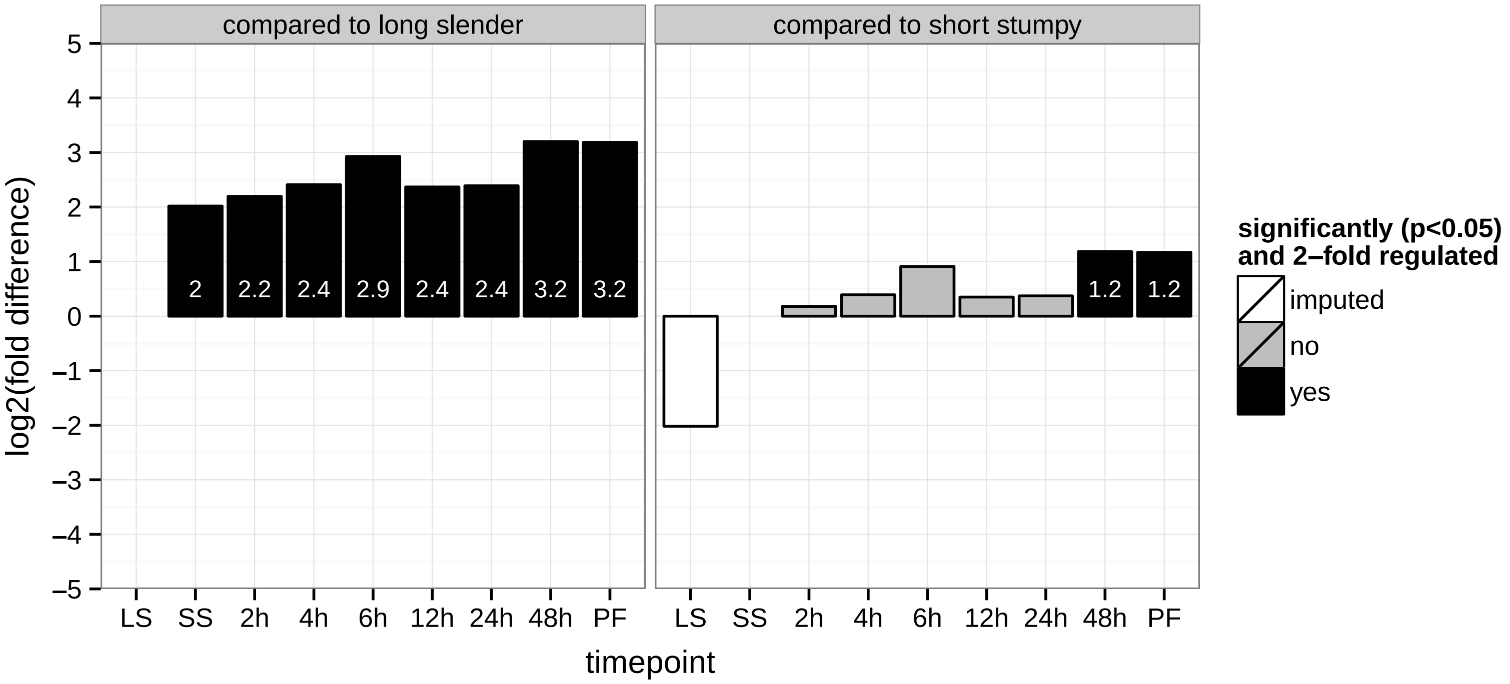
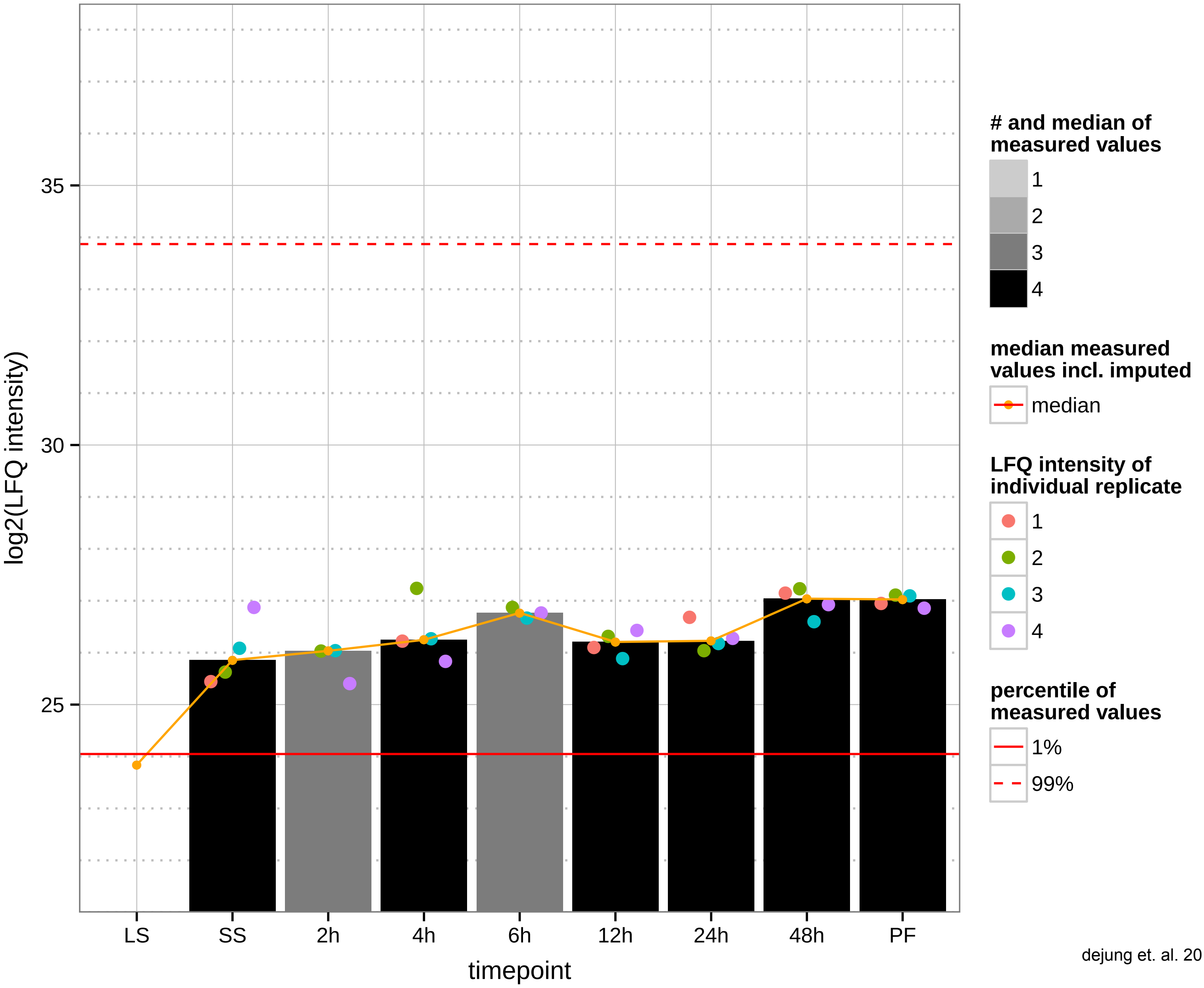
hypothetical protein, conserved
Tb927.6.4750
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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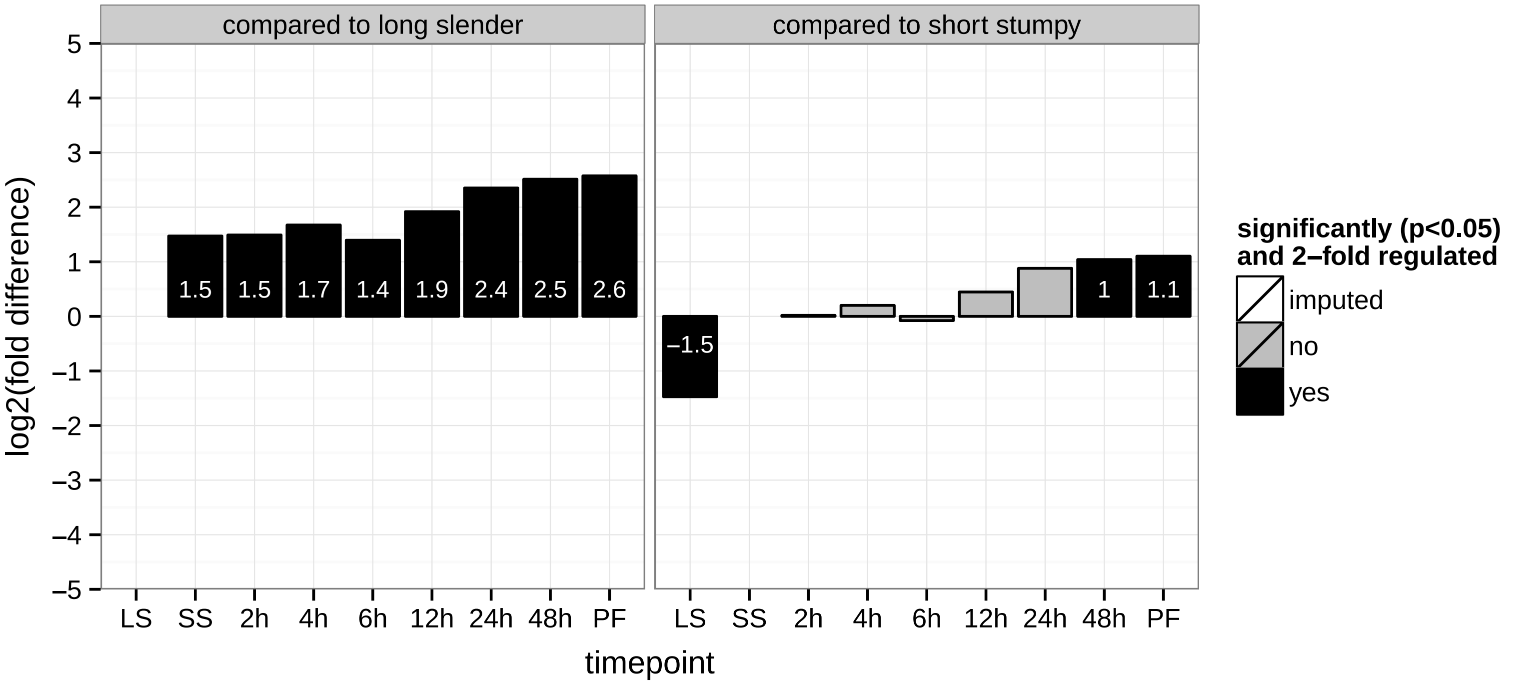
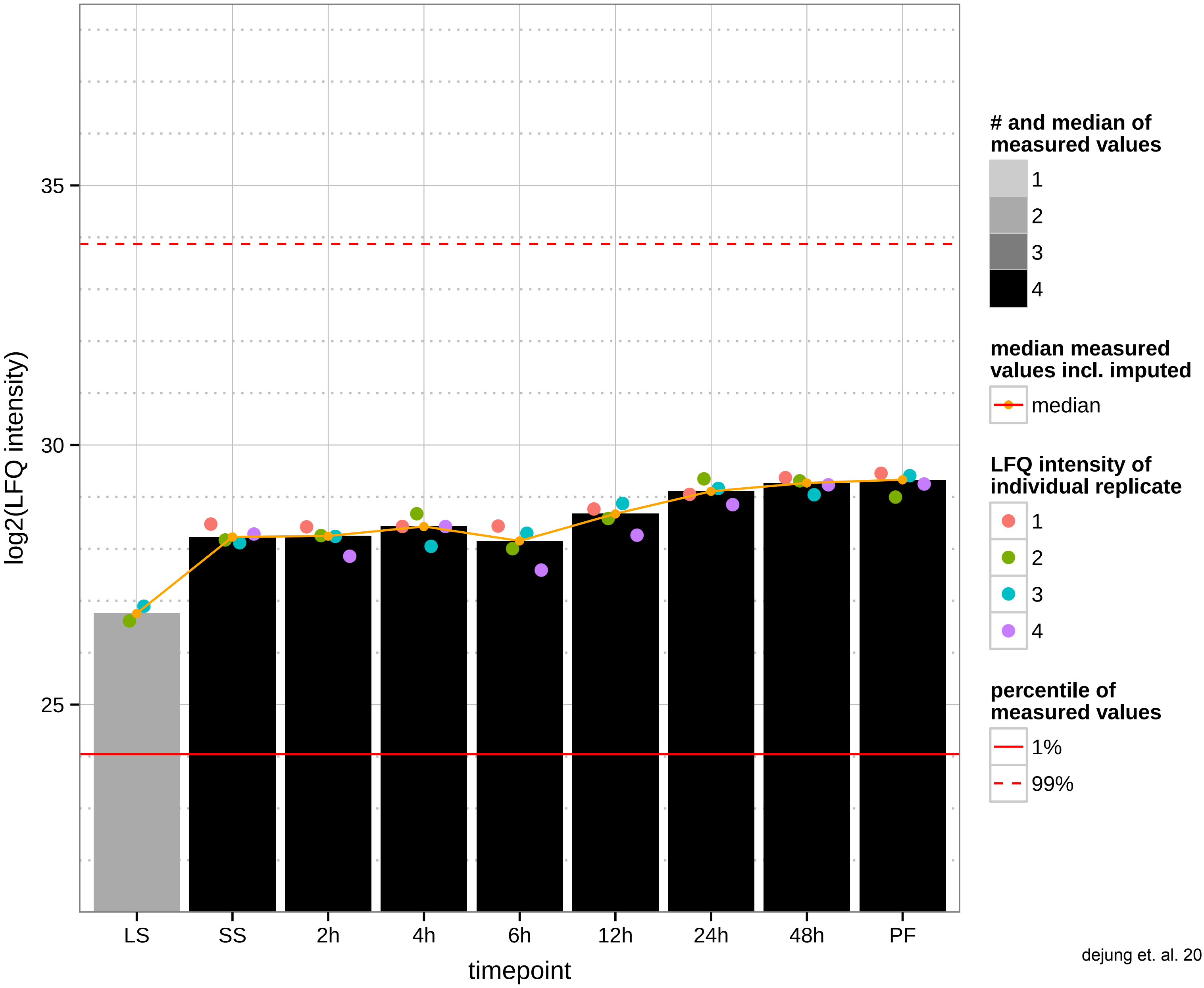
N–acetyltransferase, putative
Tb927.7.2360
AGOF: N–acetyltransferase activity
AGOC: null
AGOP: metabolic process
PGOF: N–acetyltransferase activity
PGOC: null
PGOP: null





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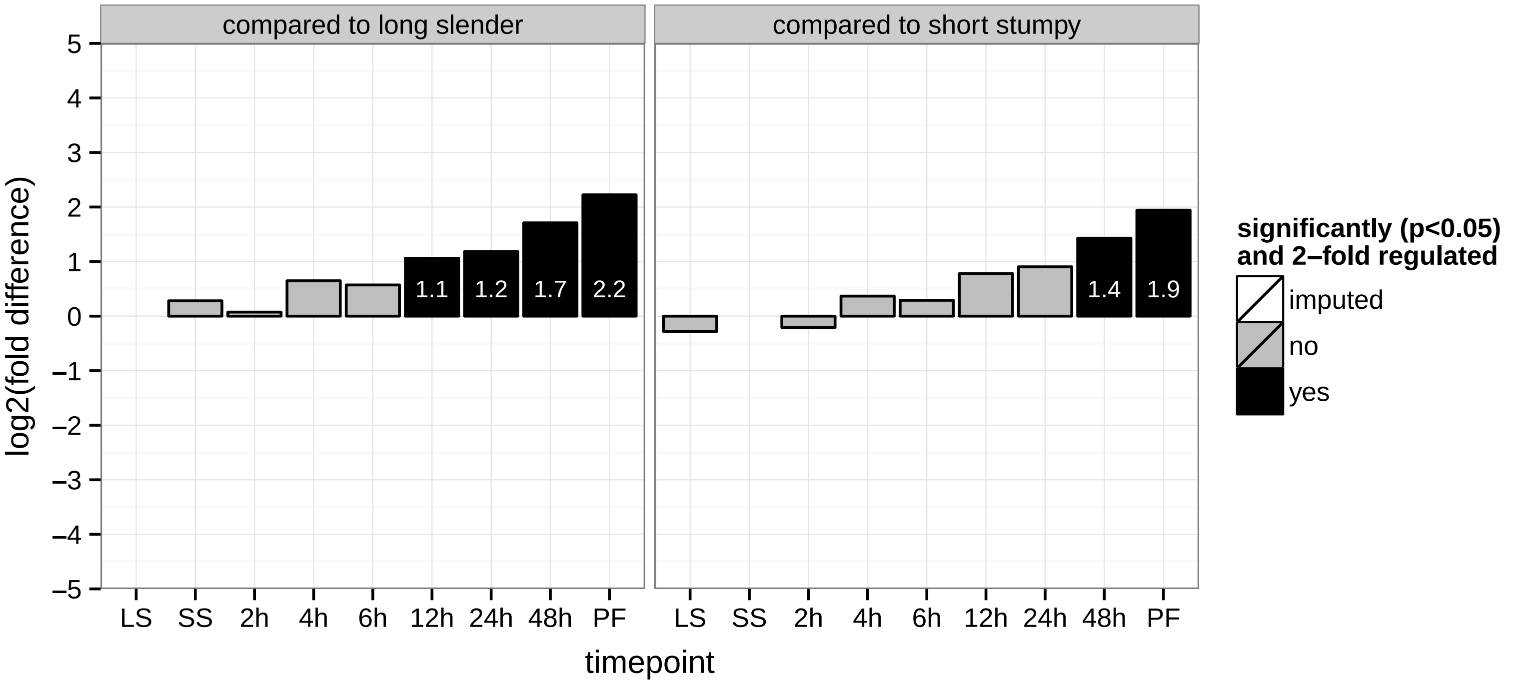
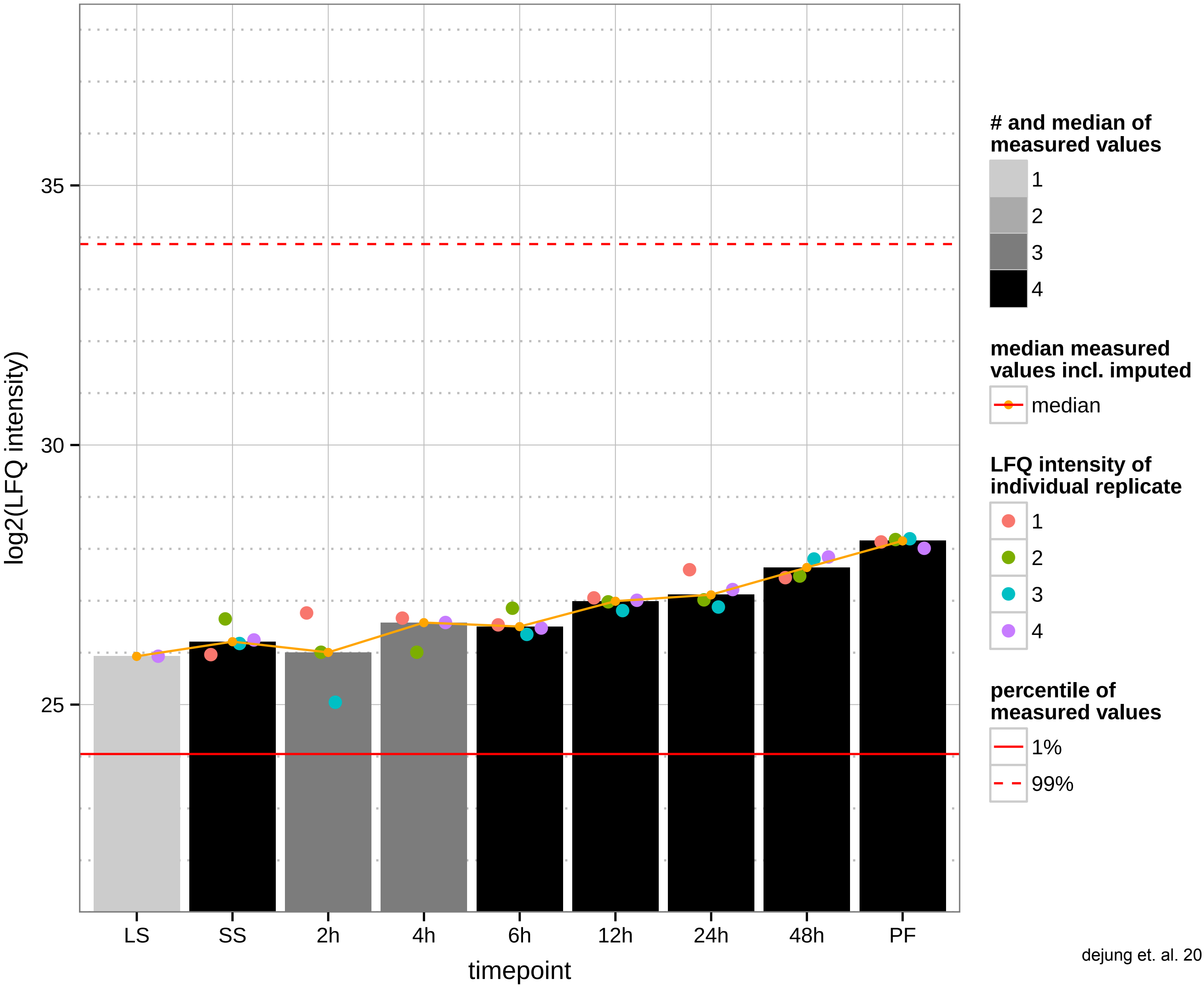
hypothetical protein, conserved
Tb927.7.2410
AGOF: GTP binding
AGOC: intracellular, mitochondrion
AGOP: null
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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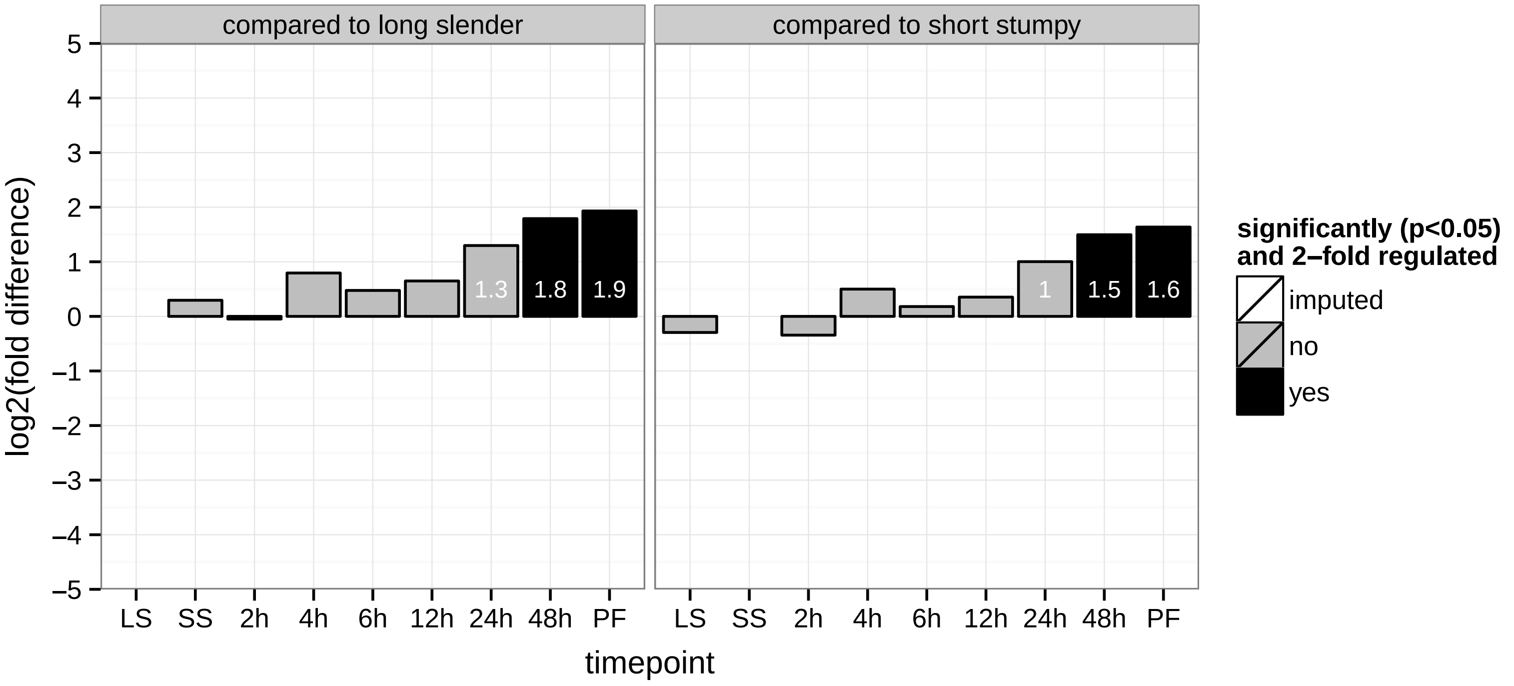
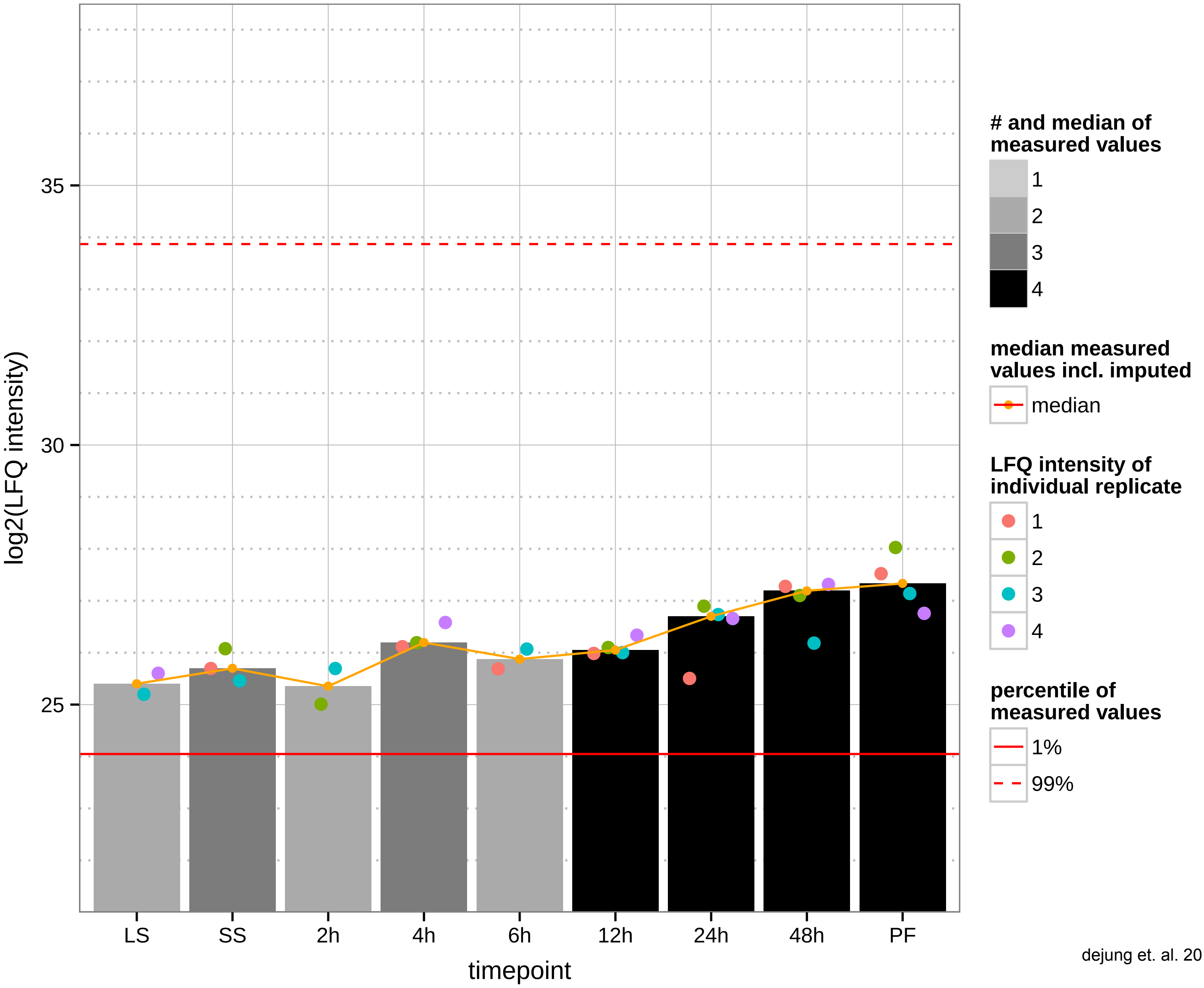
hypothetical protein, conserved
Tb927.7.3030;Tb927.7.2990
AGOF: null
AGOC: mitochondrion, null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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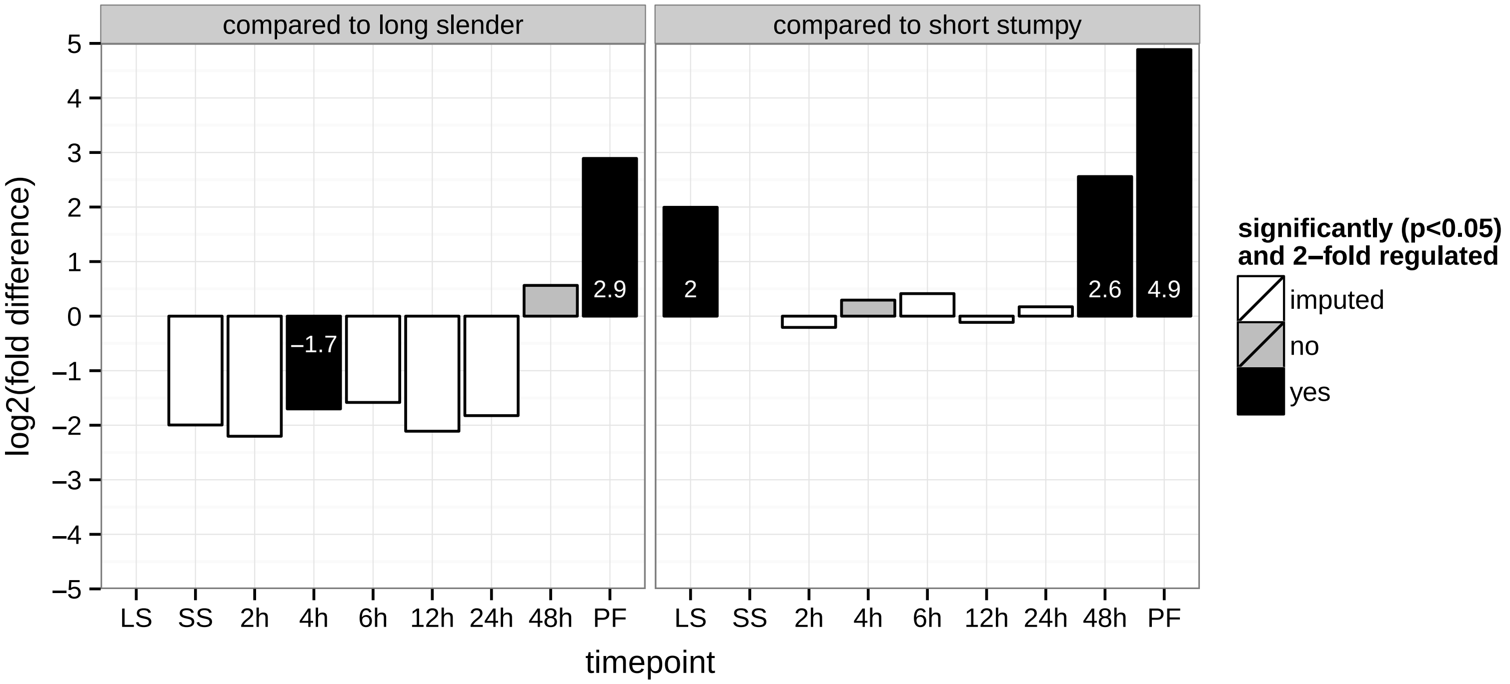
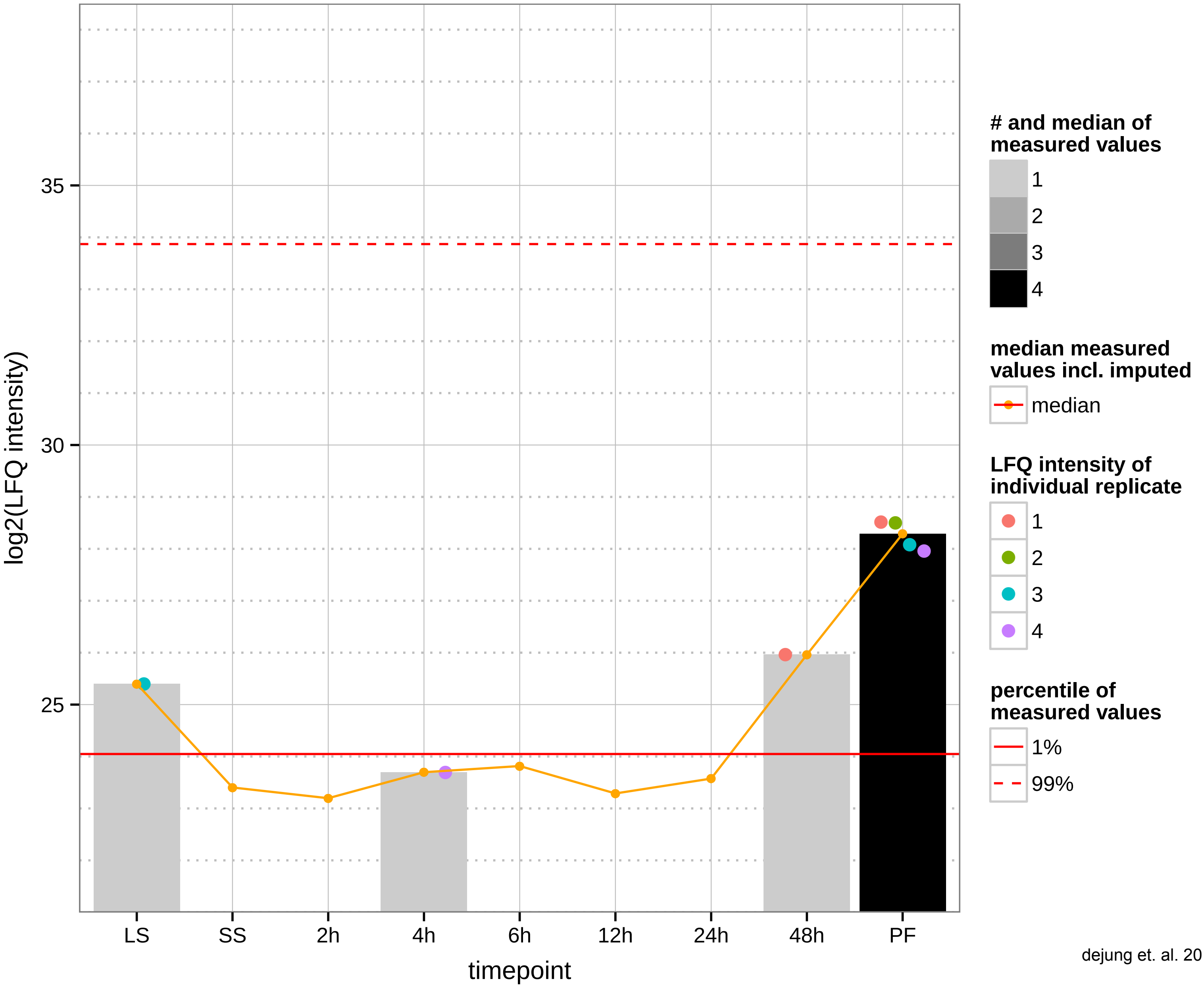
hypothetical protein, conserved
Tb927.7.4880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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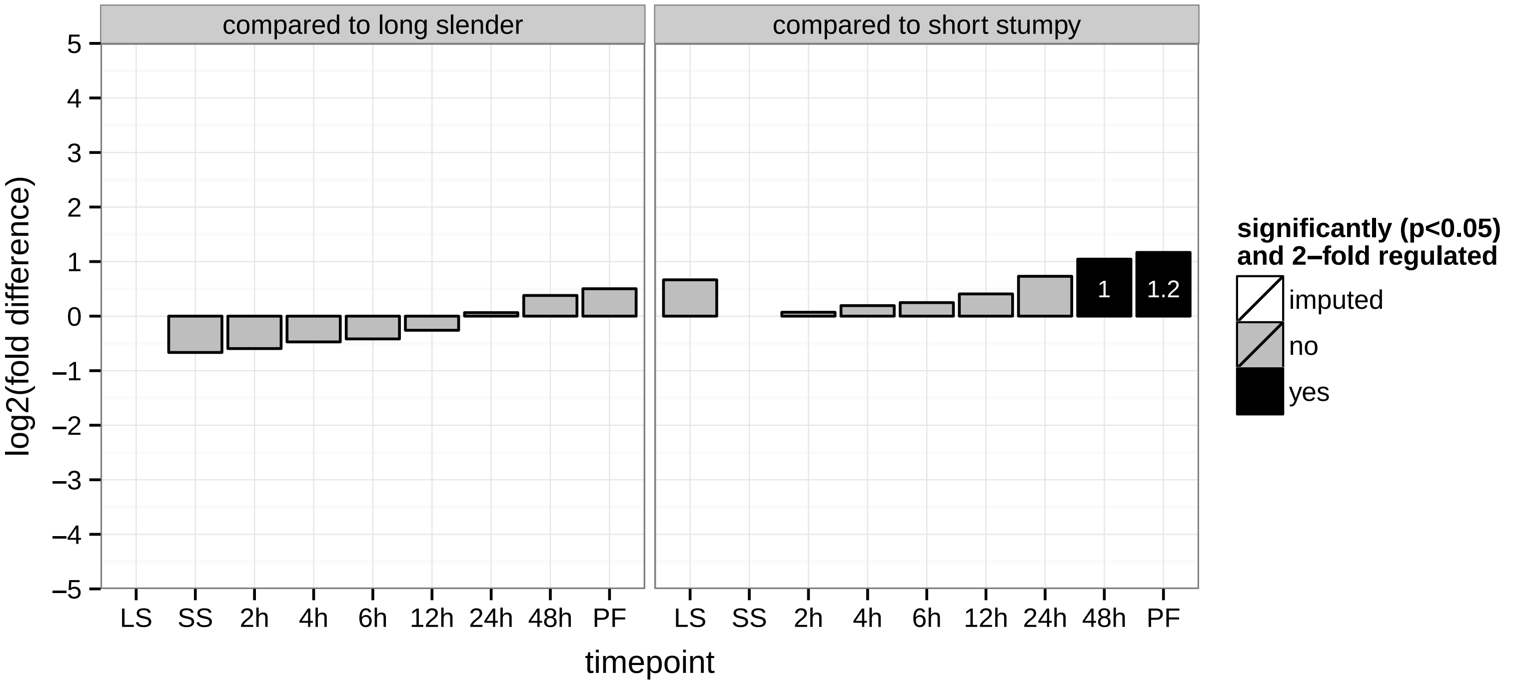
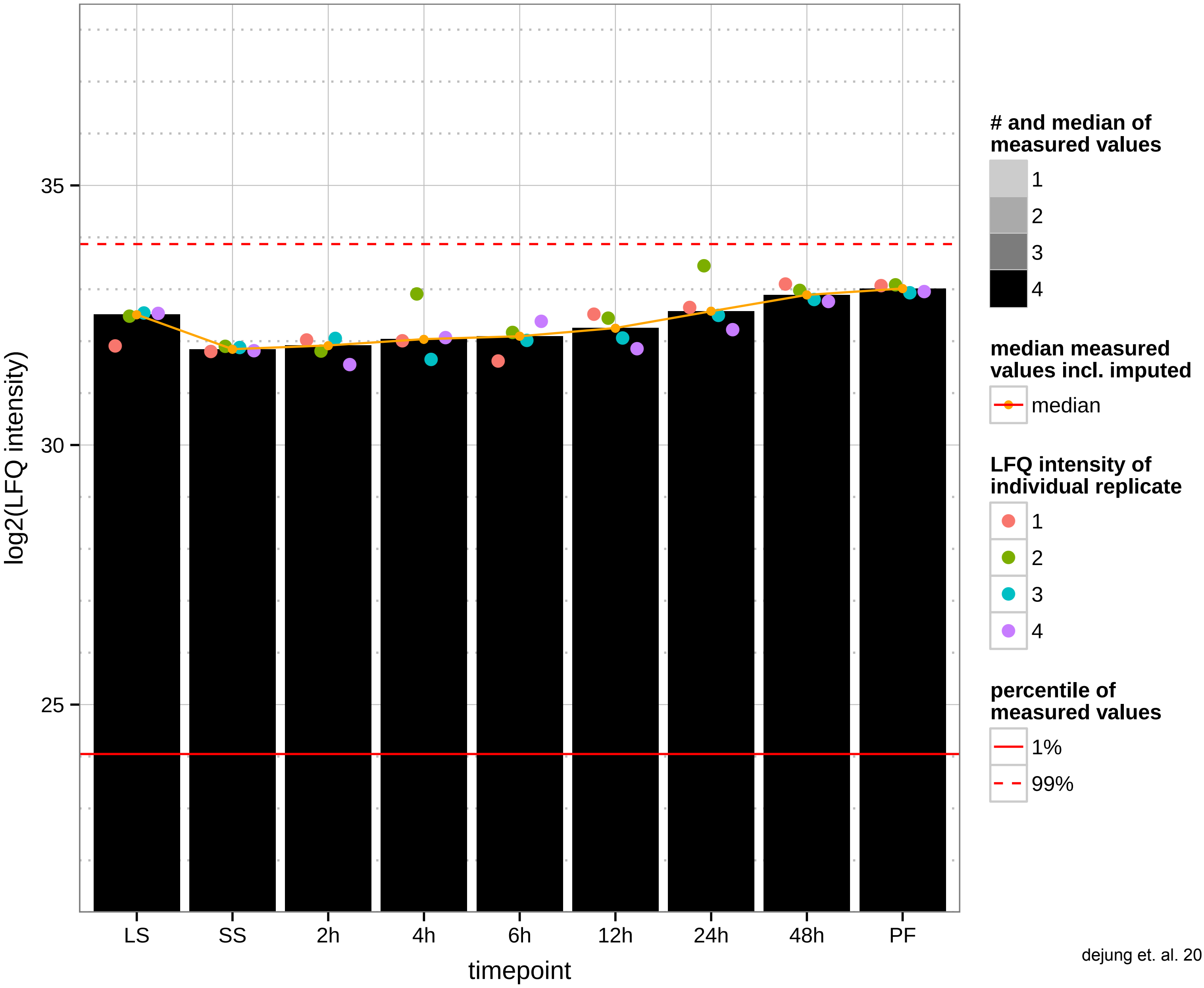
60S ribosomal protein L23a, 60S ribosomal protein L25, putative
Tb927.7.5180;Tb927.7.5170
AGOF: RNA binding, structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: ribosome biogenesis, translation
PGOF: structural constituent of ribosome, null
PGOC: intracellular, ribosome, null
PGOP: translation, null





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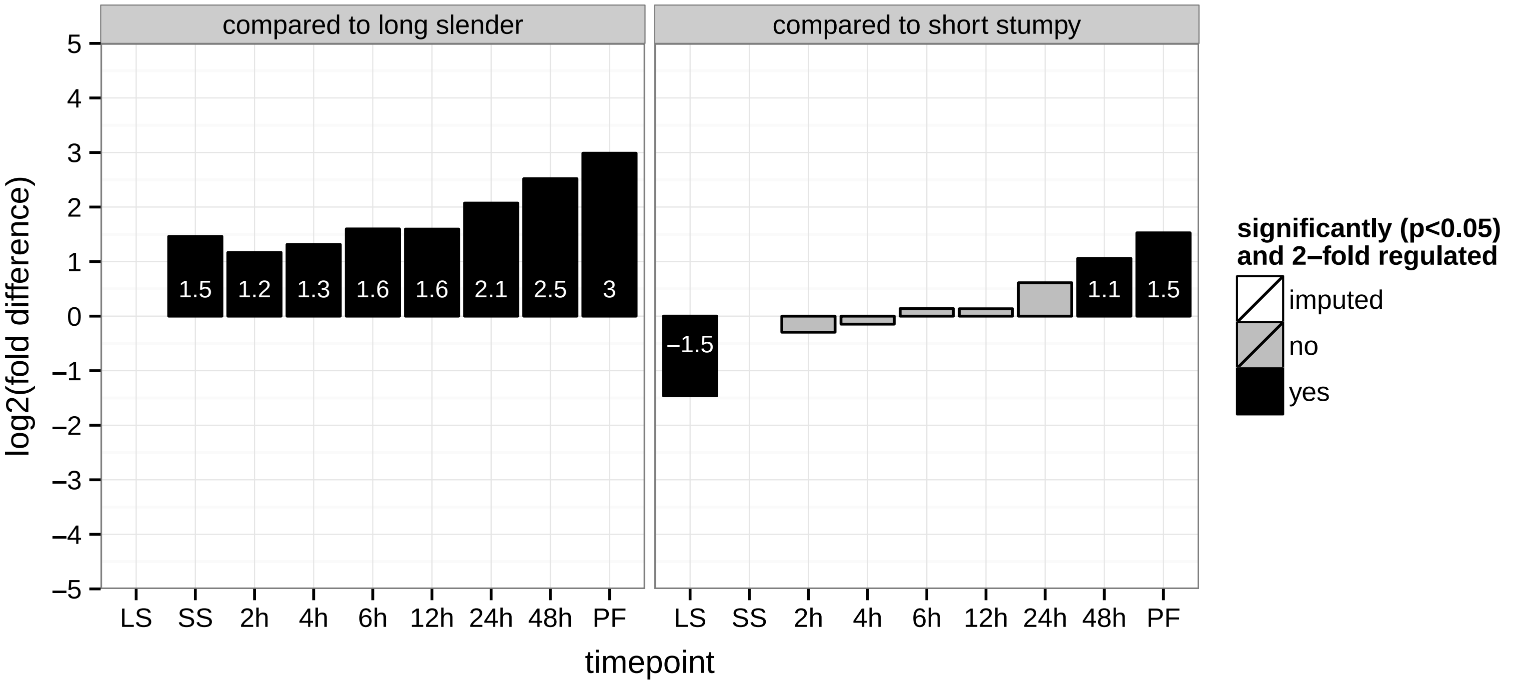
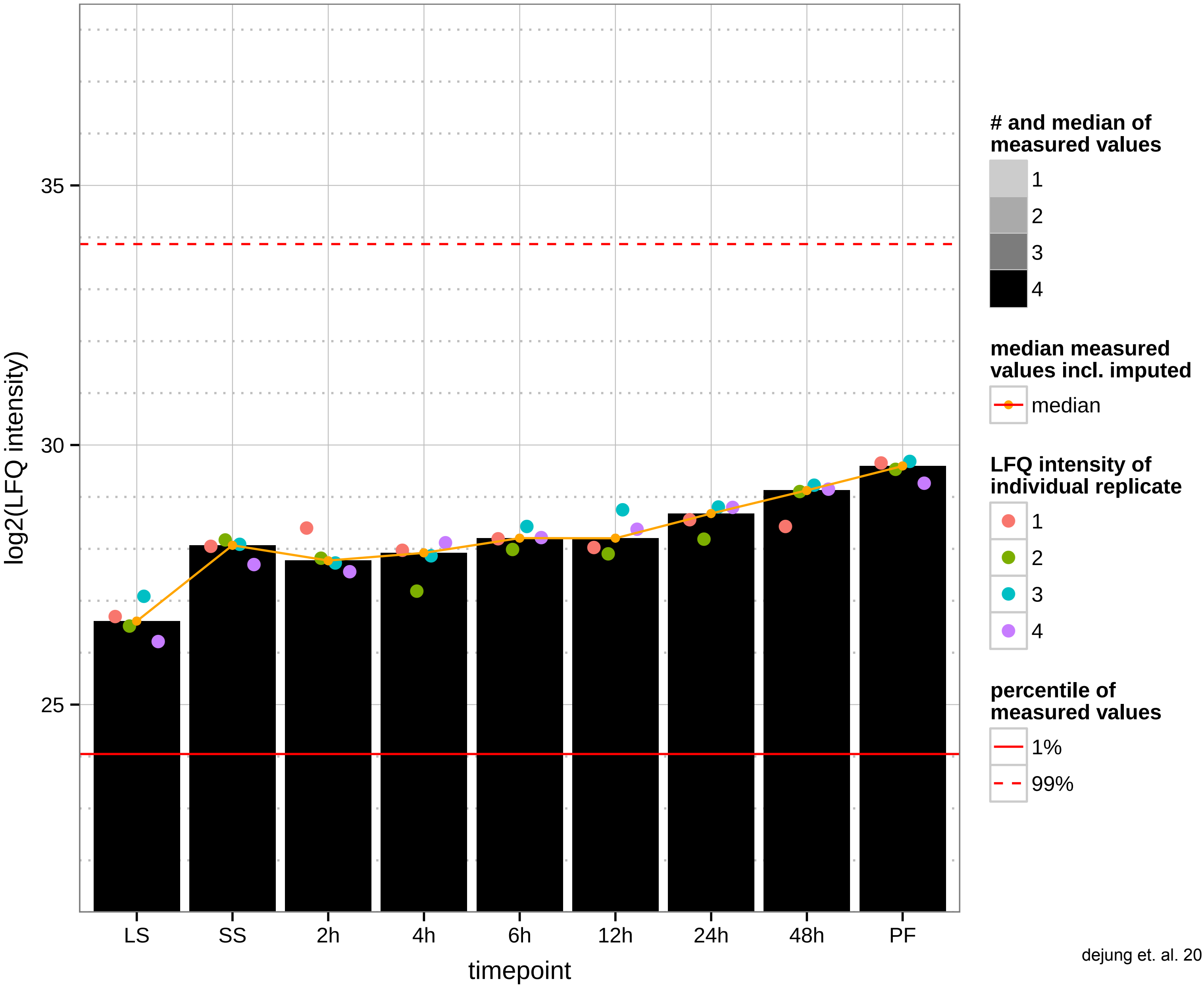
hypothetical protein, conserved
Tb927.7.5210
AGOF: phosphatase activity
AGOC: null
AGOP: null
PGOF: phosphatase activity
PGOC: null
PGOP: null





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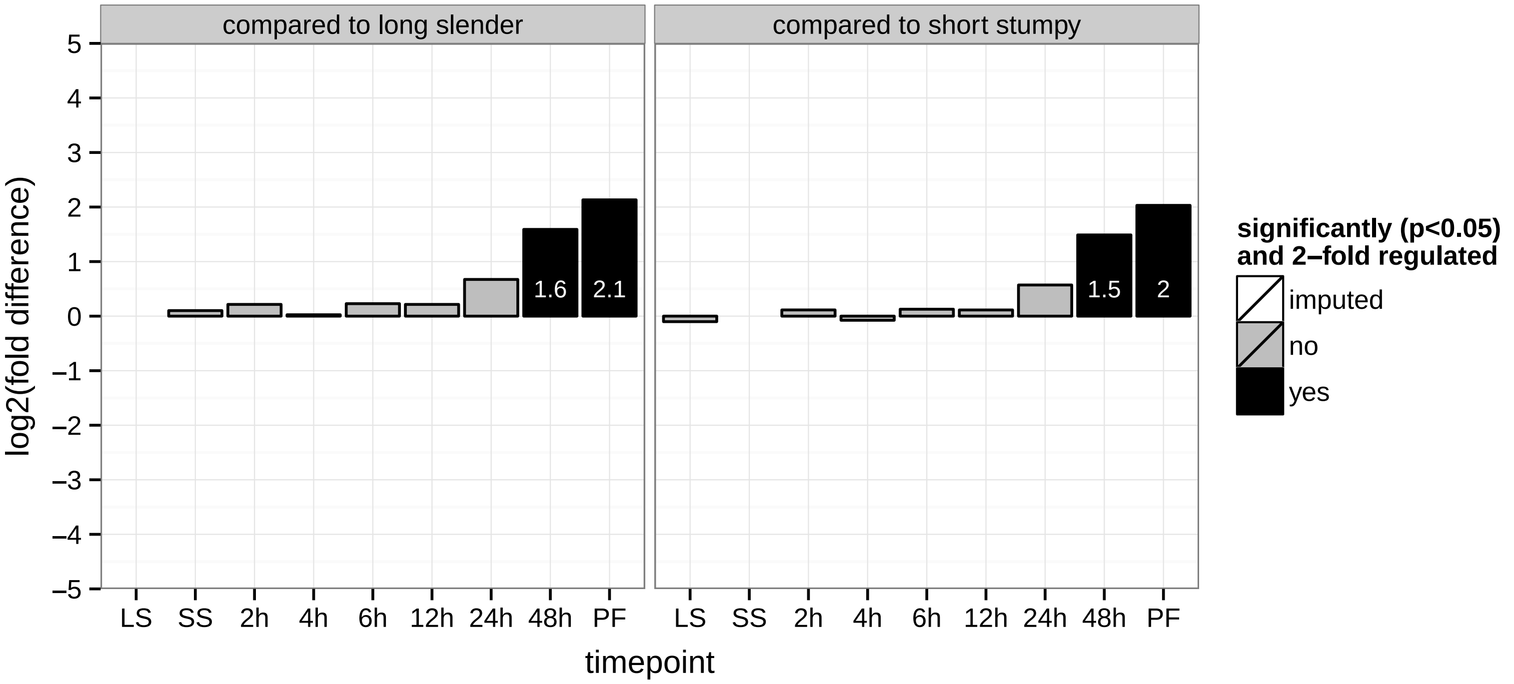
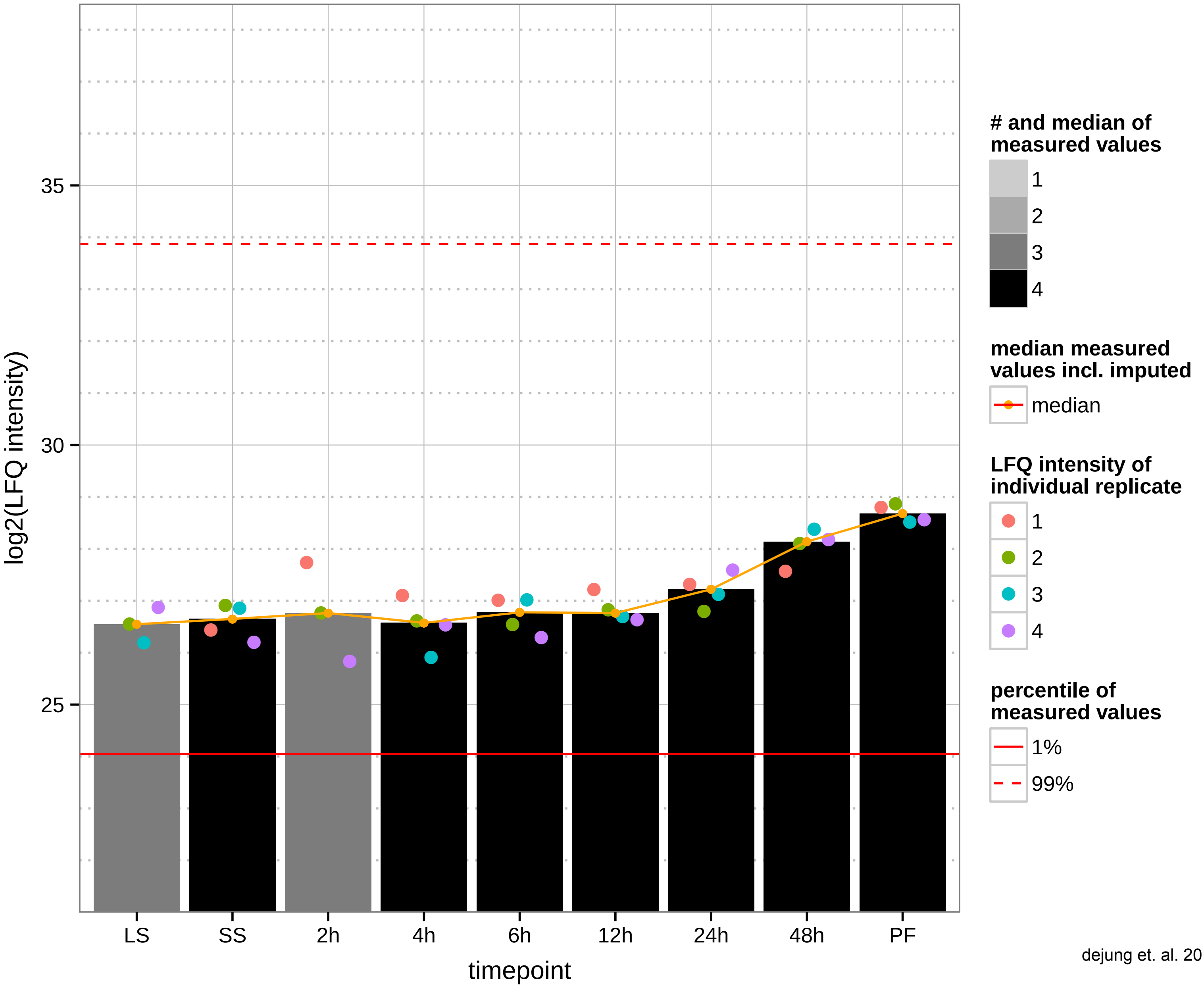
dihydrofolate reductase–thymidylate synthase (DHFR–TS)
Tb927.7.5480
AGOF: dihydrofolate reductase activity, thymidylate synthase activity
AGOC: null
AGOP: dTMP biosynthetic process, glycine biosynthetic process, nucleotide biosynthetic process, one–carbon metabolic proc
PGOF: dihydrofolate reductase activity, thymidylate synthase activity
PGOC: null
PGOP: dTMP biosynthetic process, glycine biosynthetic process, nucleotide biosynthetic process, one–carbon metabolic proc





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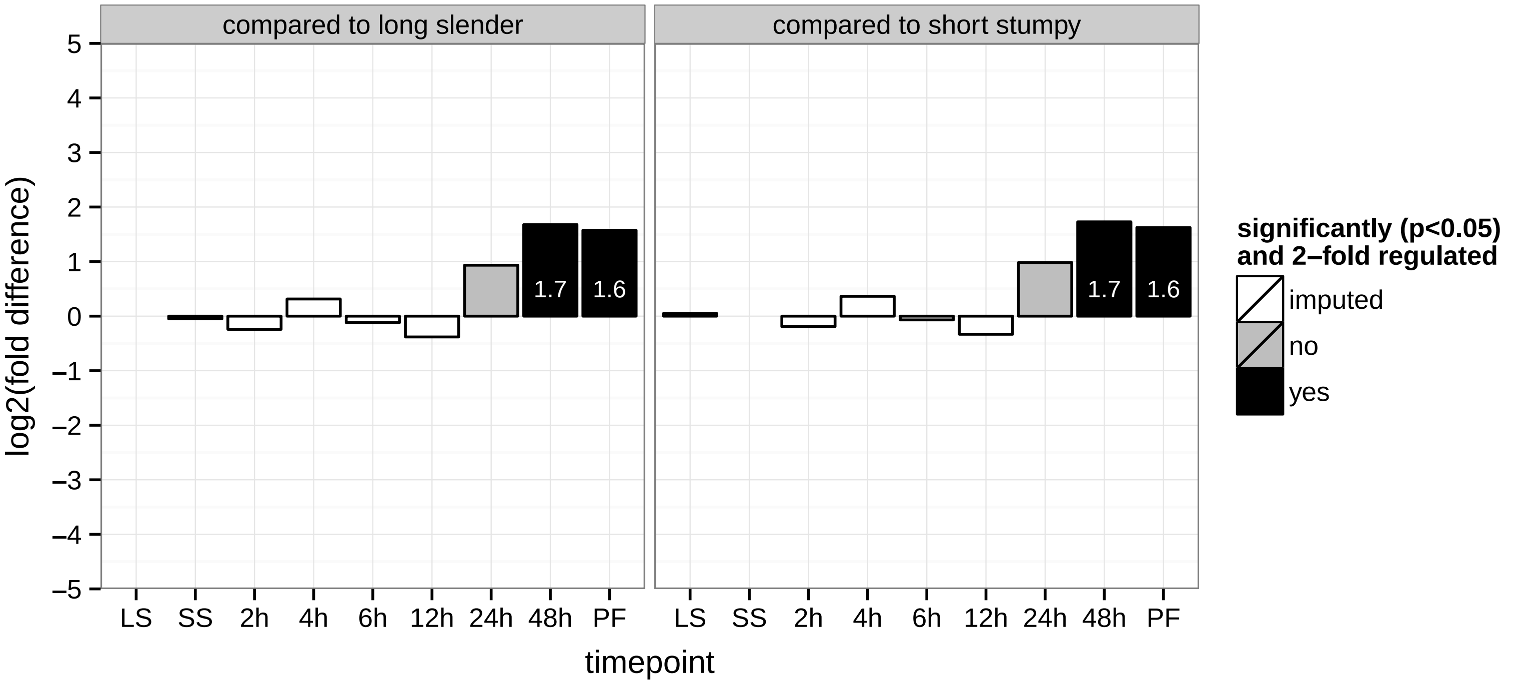
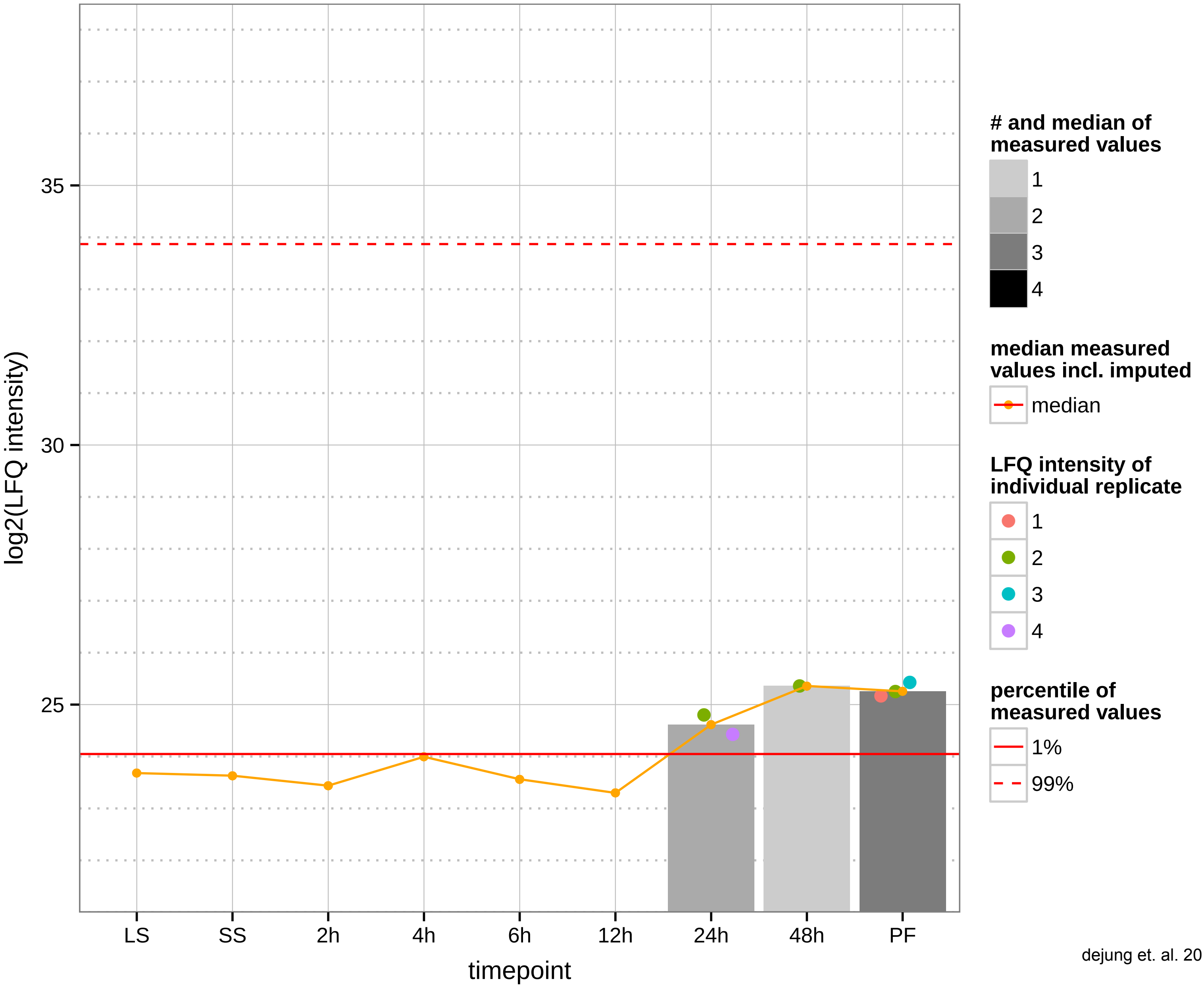
hypothetical protein, conserved
Tb927.7.5670
AGOF: null
AGOC: null
AGOP: null
PGOF: oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular o
PGOC: null
PGOP: oxidation–reduction process





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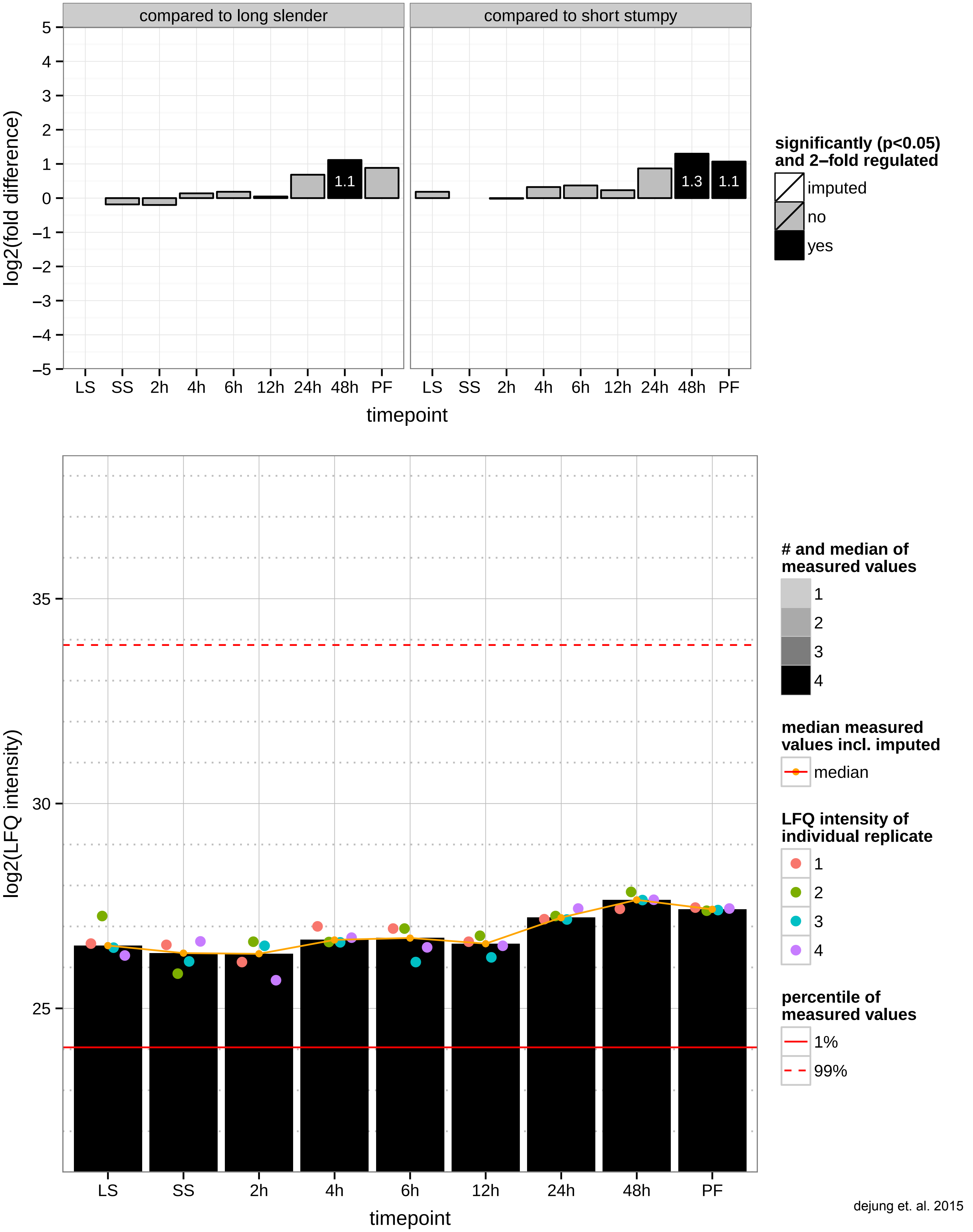
hypothetical protein, conserved
Tb927.7.6620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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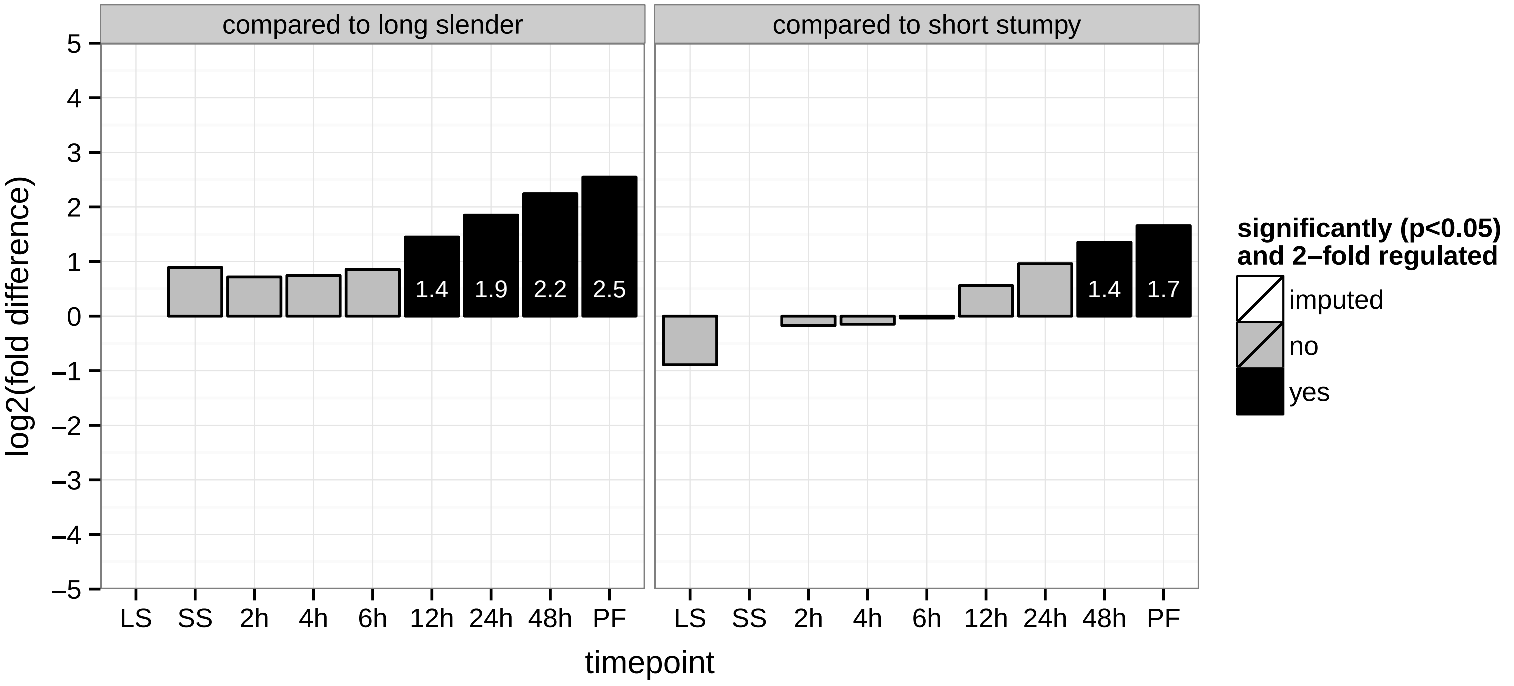
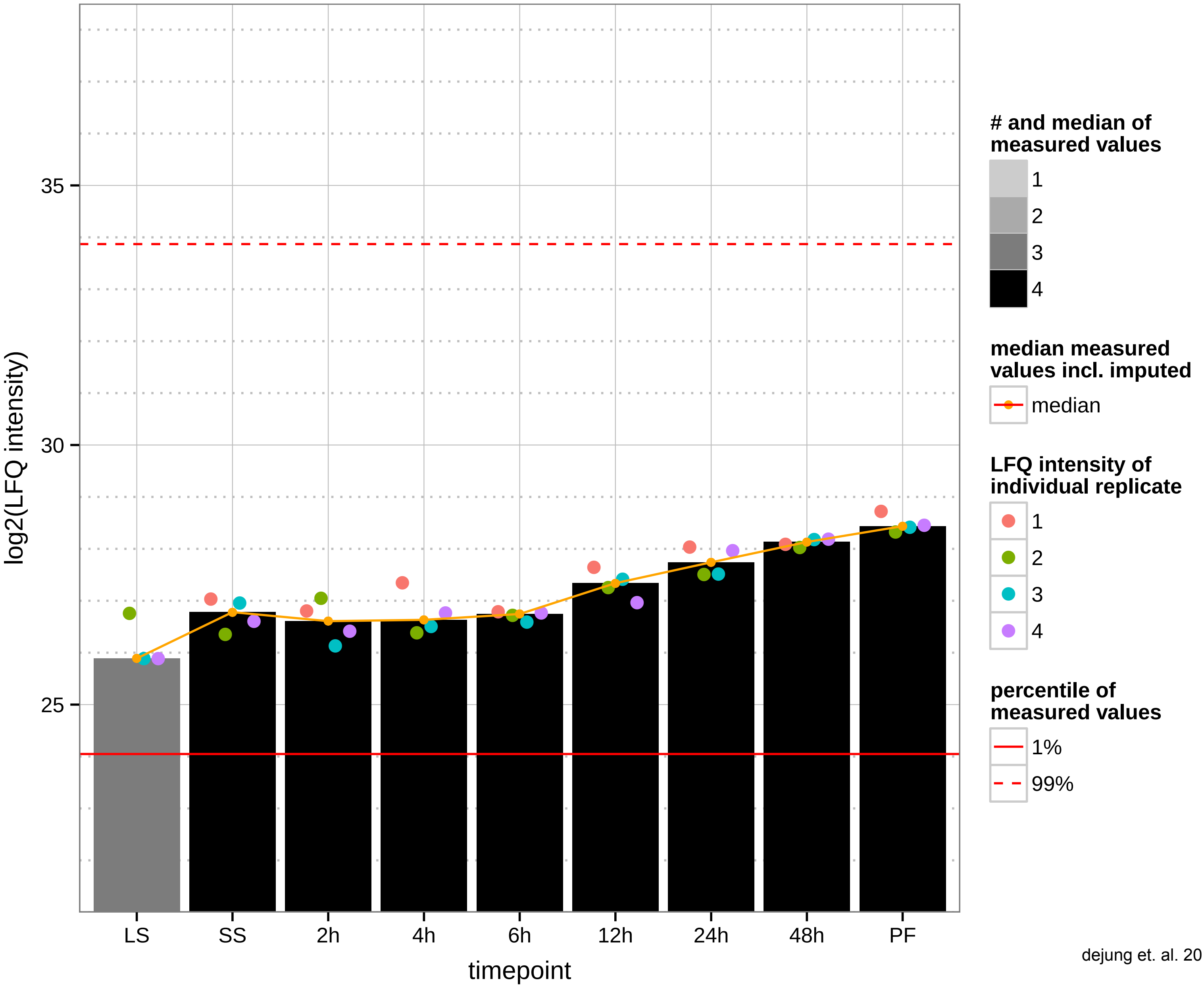
hypothetical protein, conserved
Tb927.7.7050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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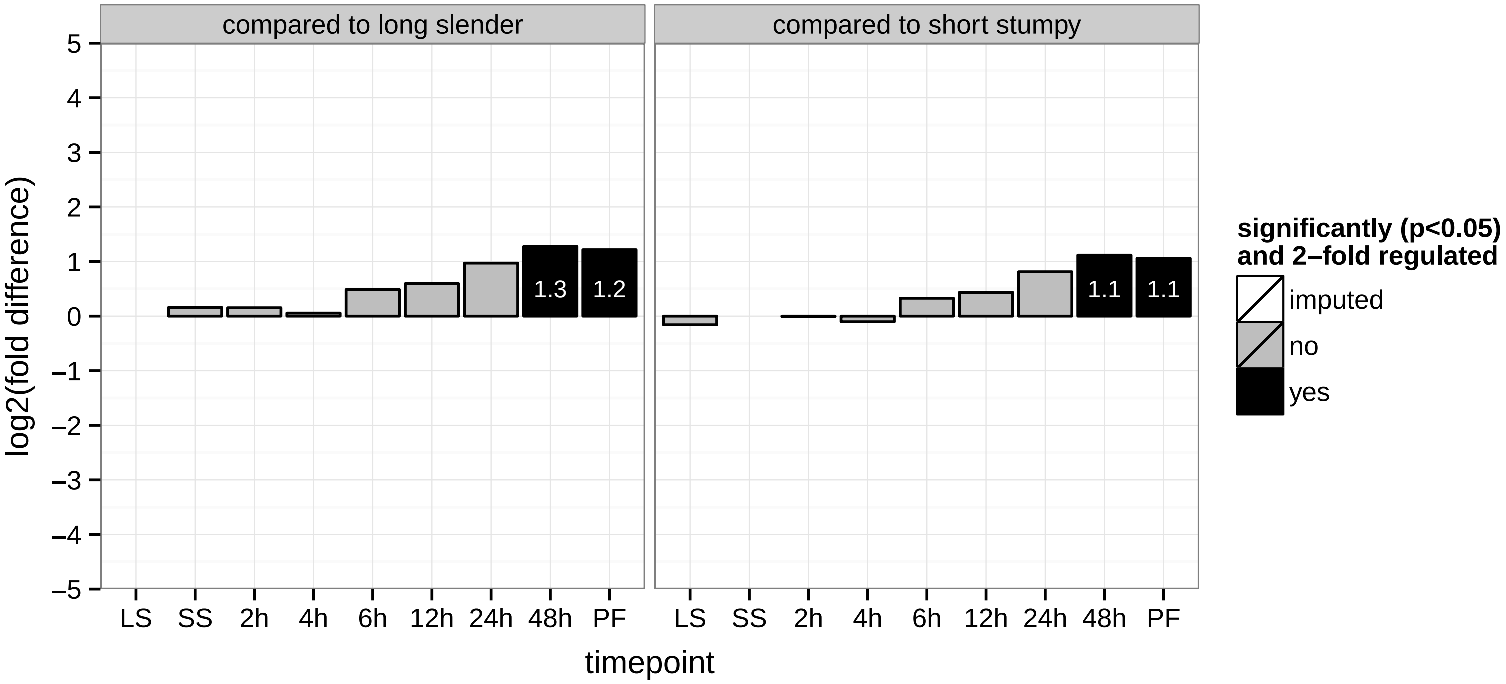
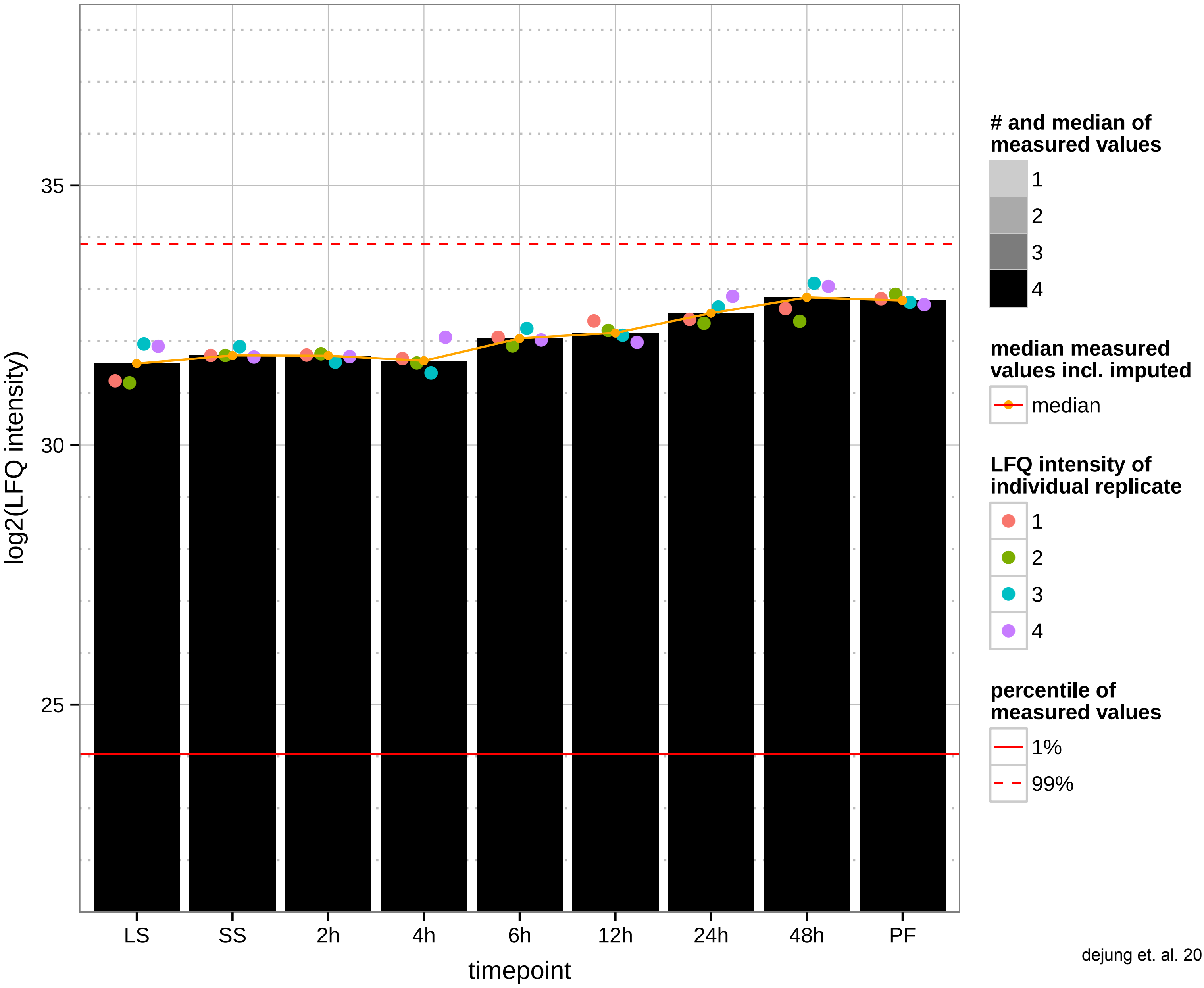
60S ribosomal protein L7a, putative
Tb927.8.1340;Tb927.8.1330
AGOF: structural constituent of ribosome
AGOC: ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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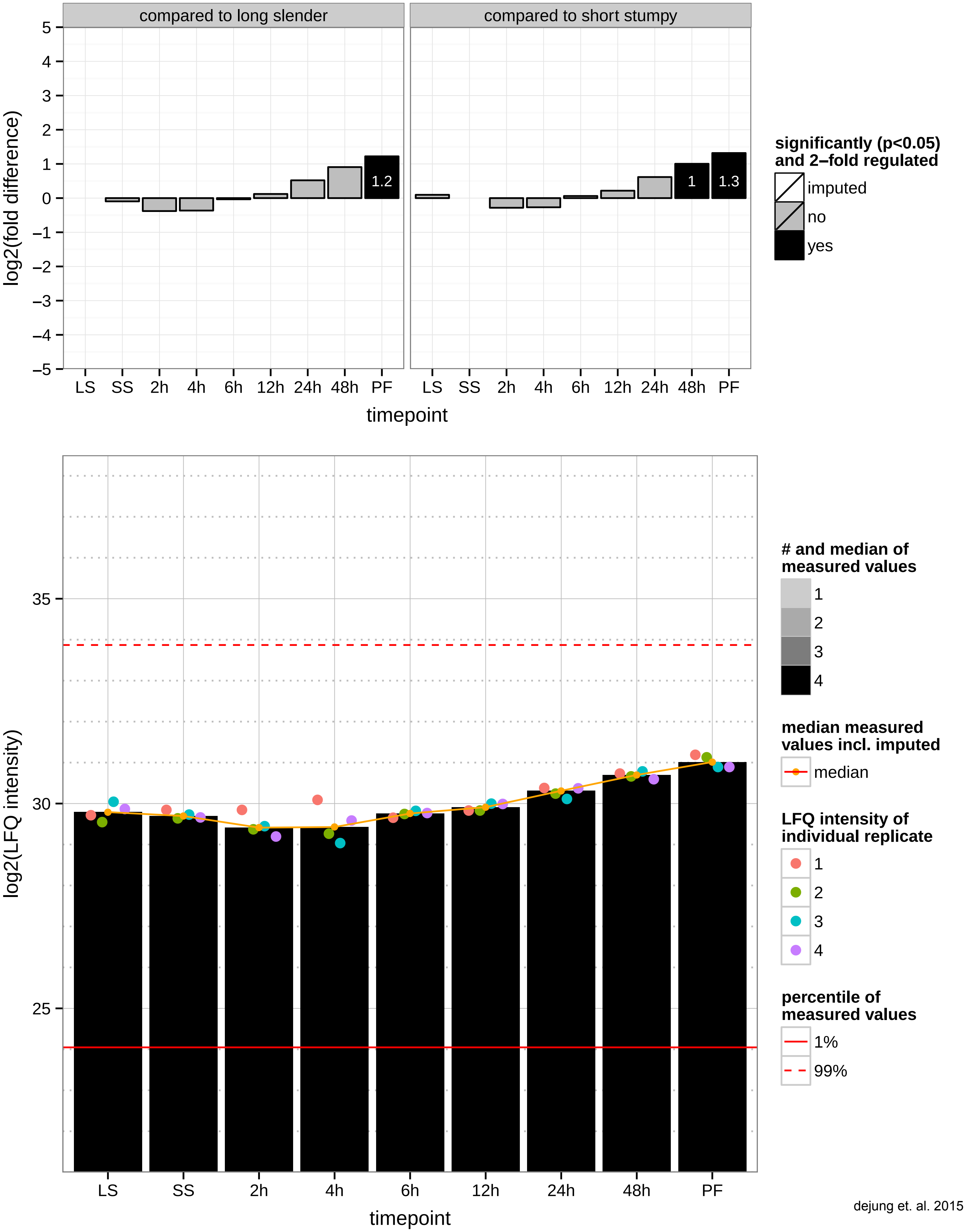
ATP−dependent DEAD/H RNA helicase, putative (DBP2.1)
Tb927.8.1510
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null



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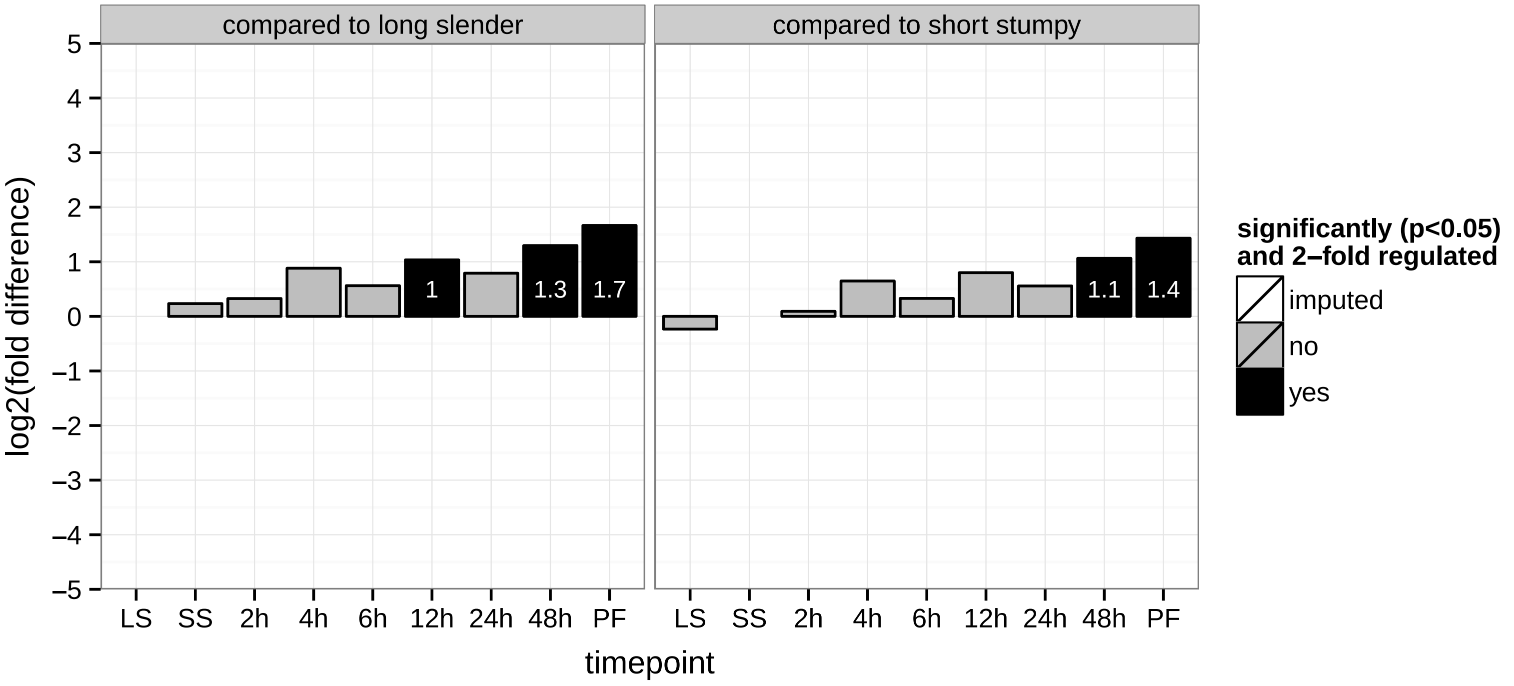
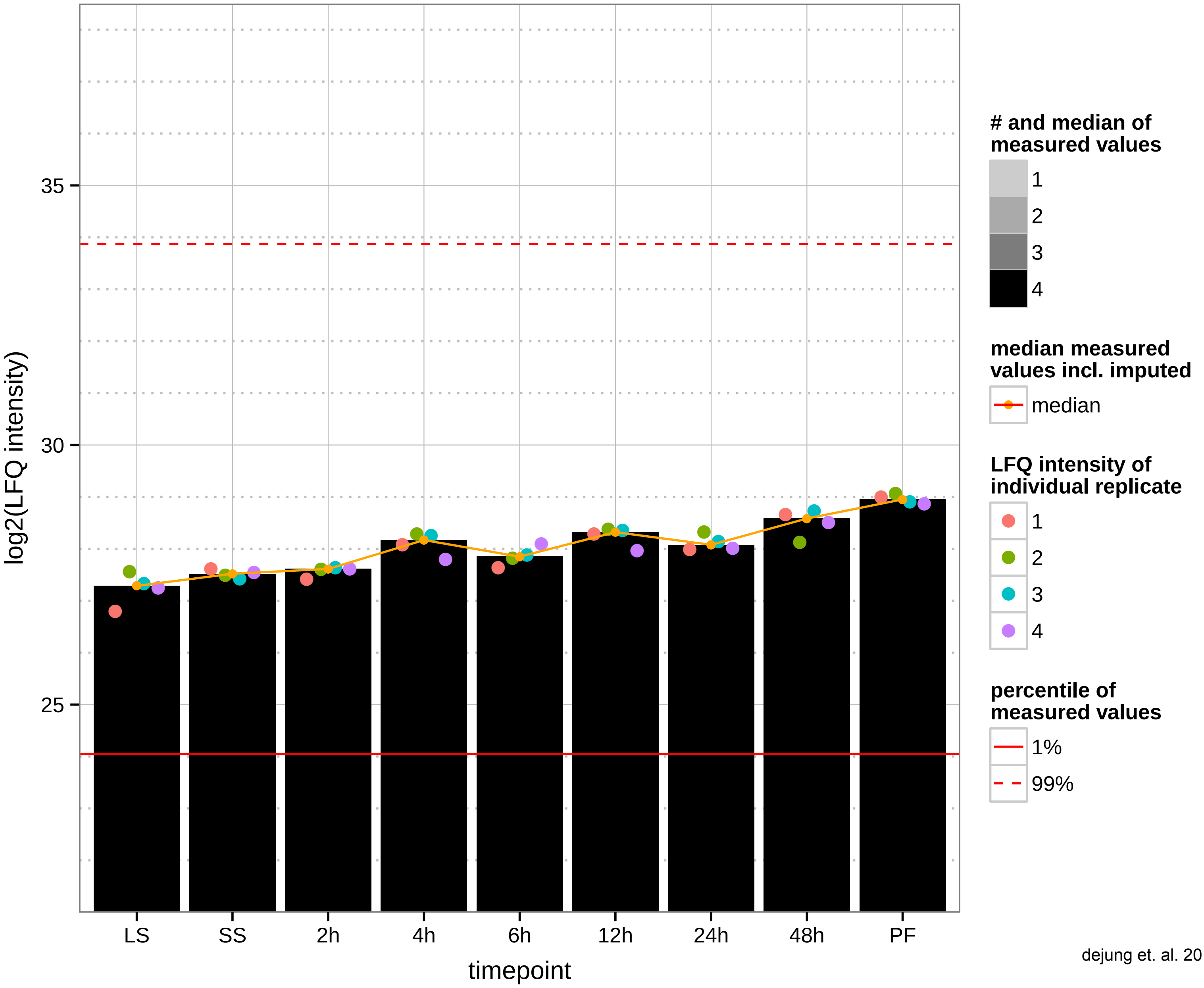
hypothetical protein, conserved
Tb927.8.1570
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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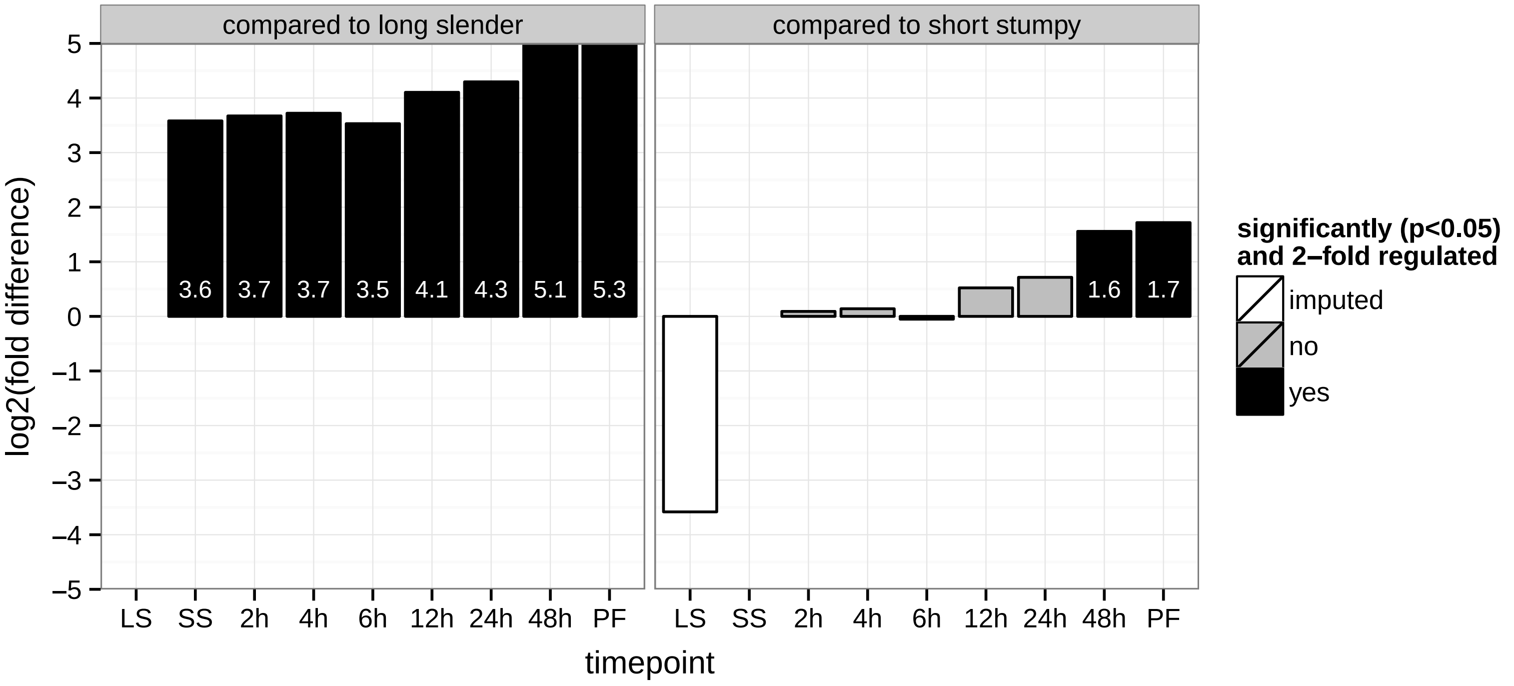
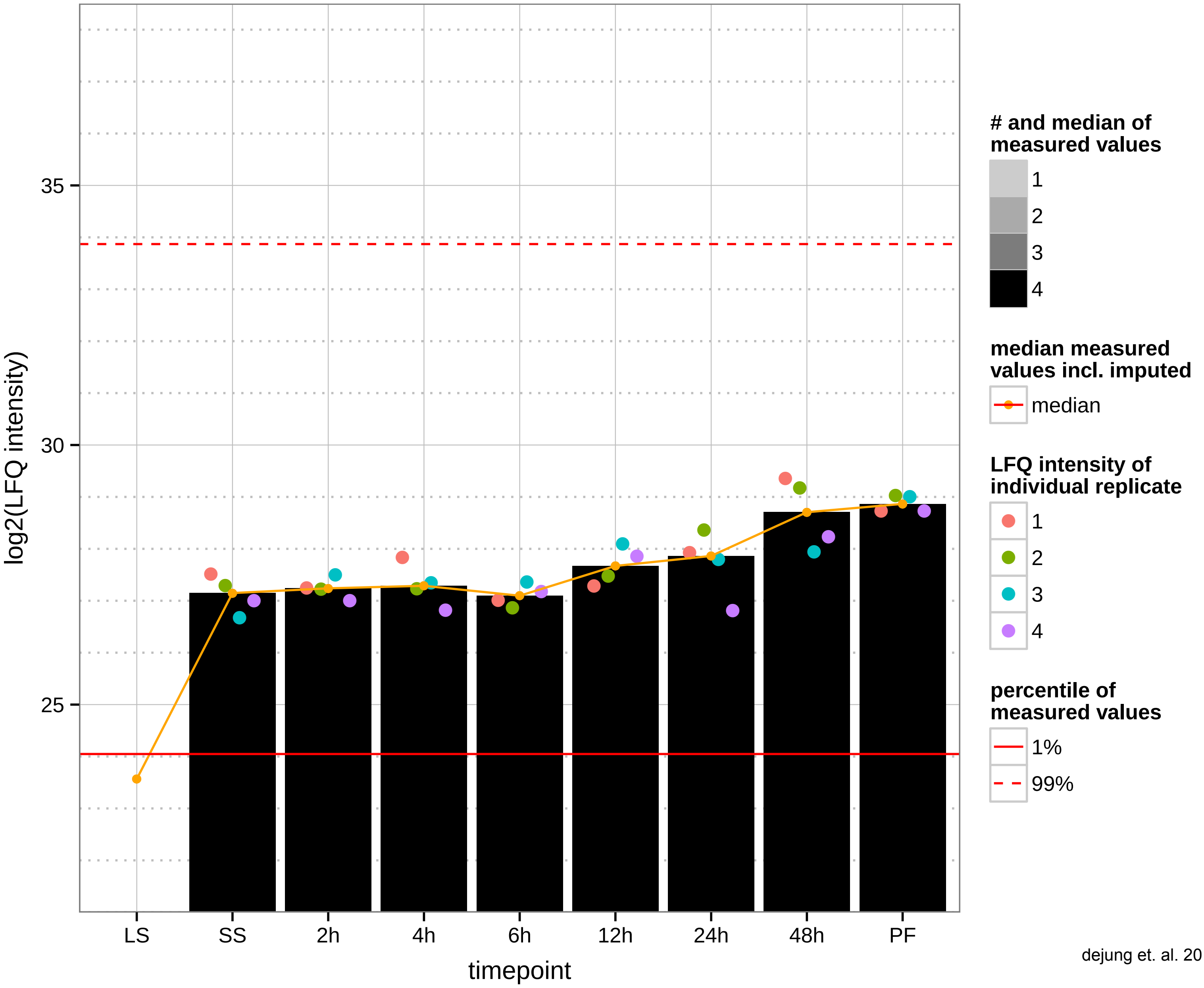
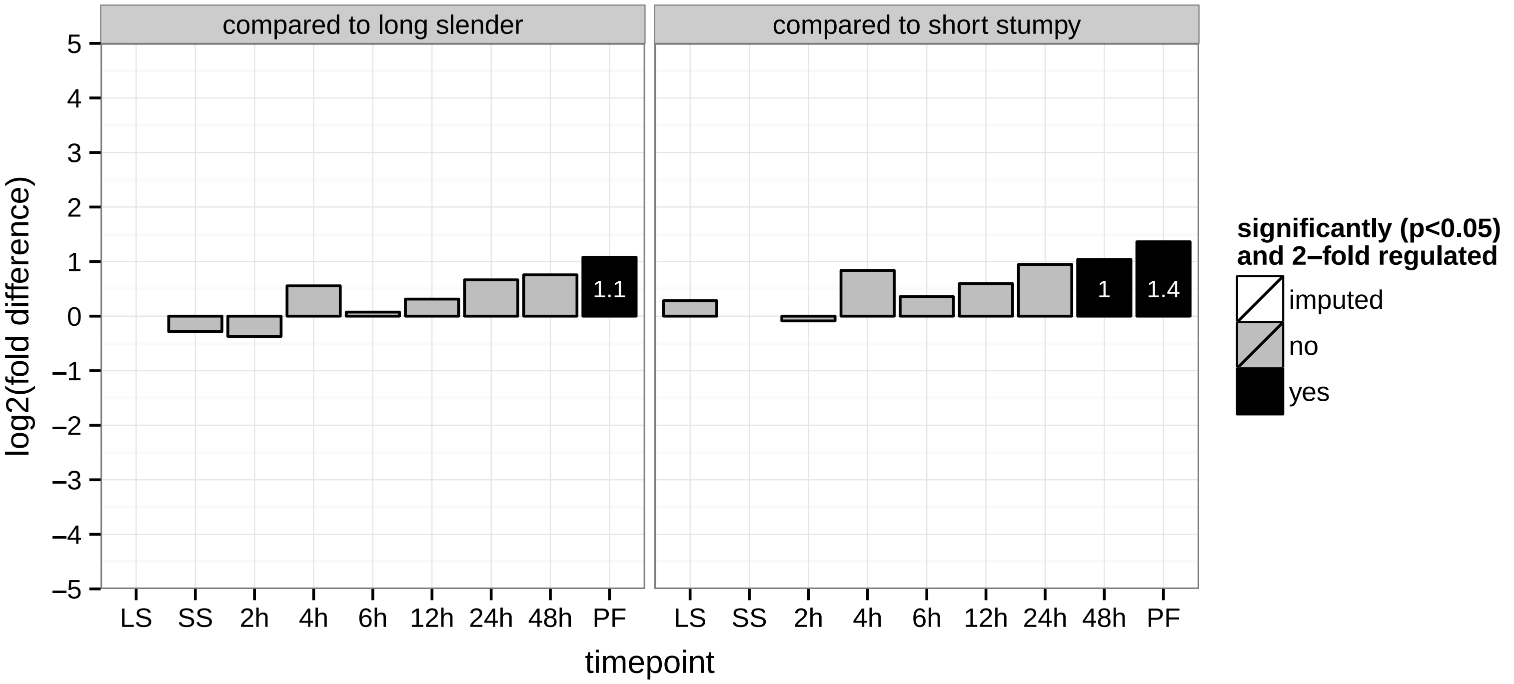
electron transfer protein, putative
Tb927.8.3380
AGOF: electron carrier activity, iron–sulfur cluster binding, oxidoreductase activity
AGOC: null
AGOP: oxidation–reduction process, tricarboxylic acid cycle
PGOF: electron carrier activity, iron–sulfur cluster binding, oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process, tricarboxylic acid cycle

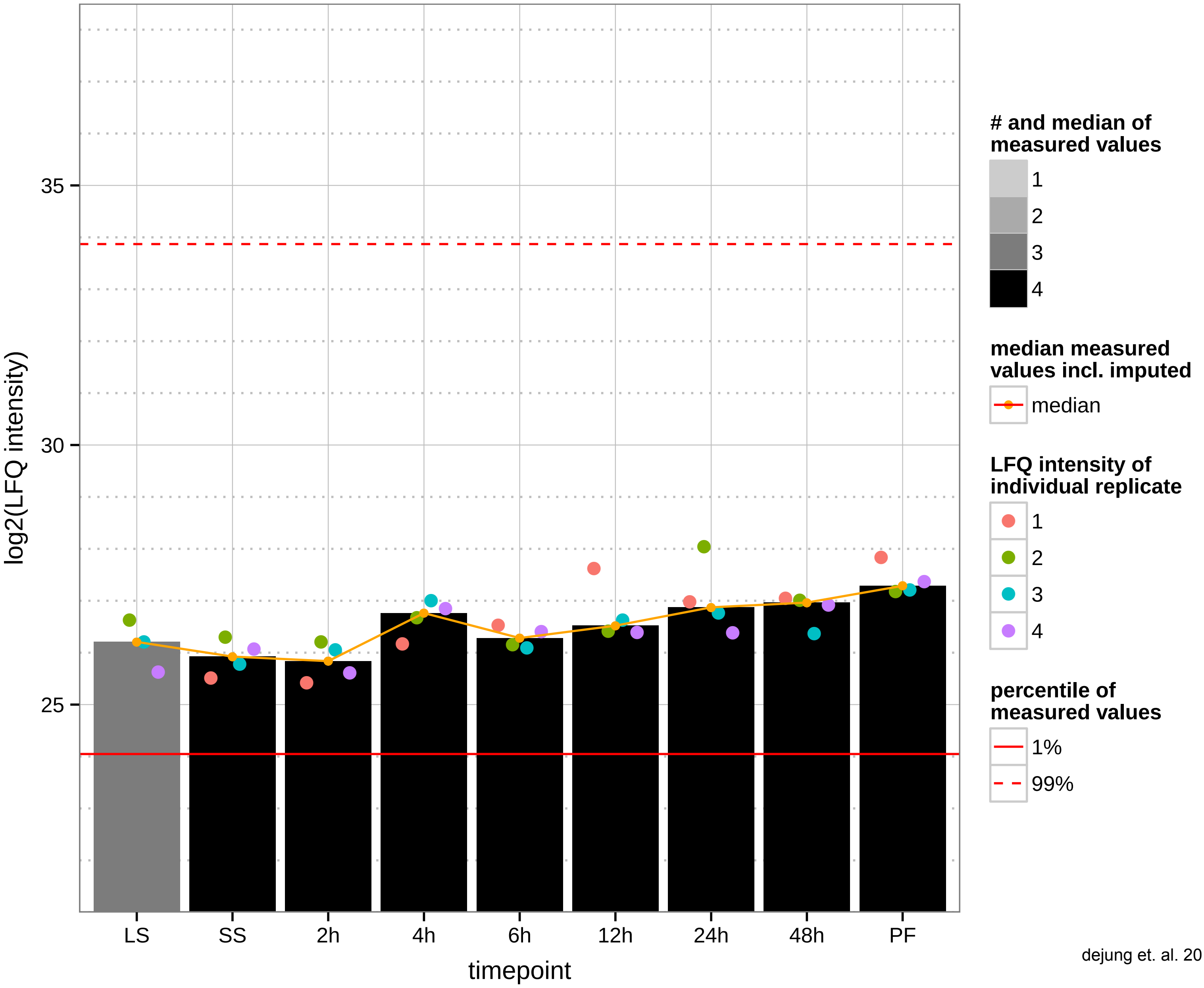




dejung et. al. 2015

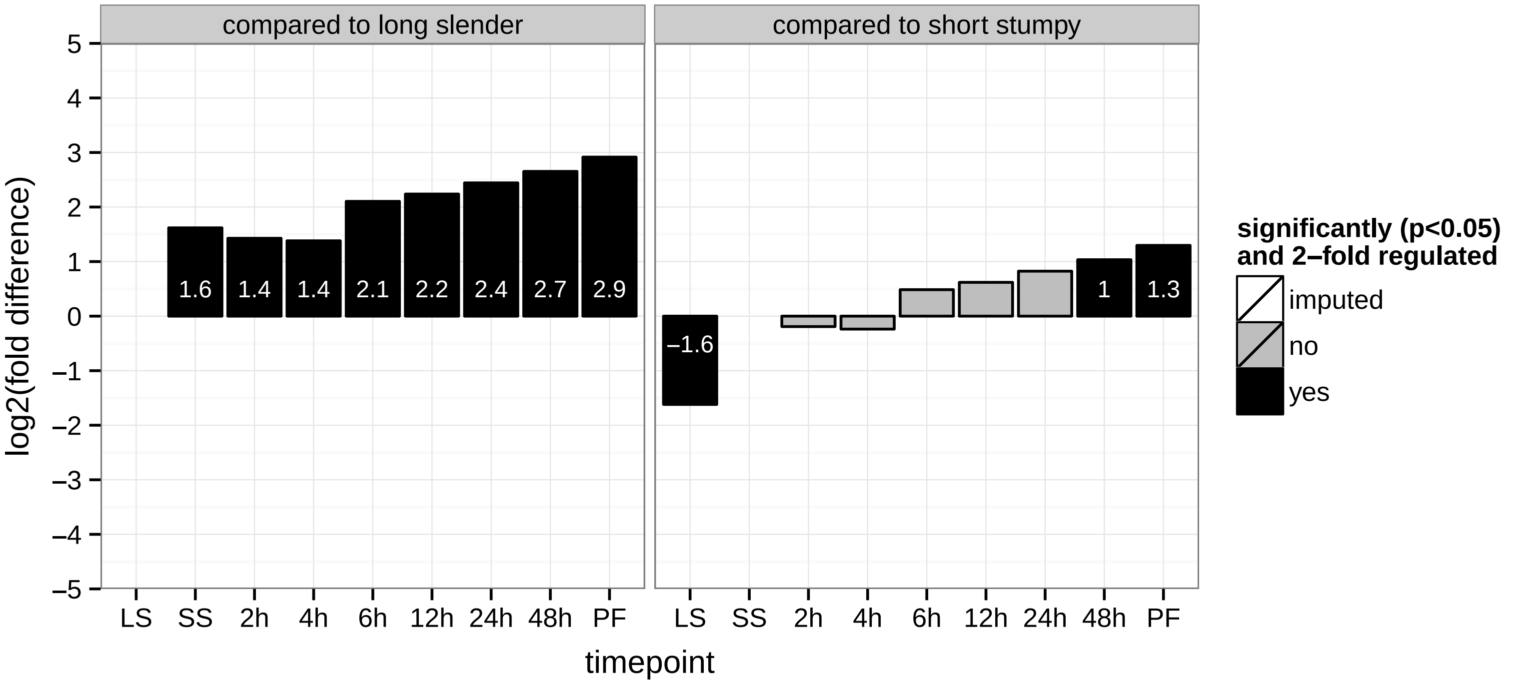
hypothetical protein, conserved
Tb927.8.4290
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

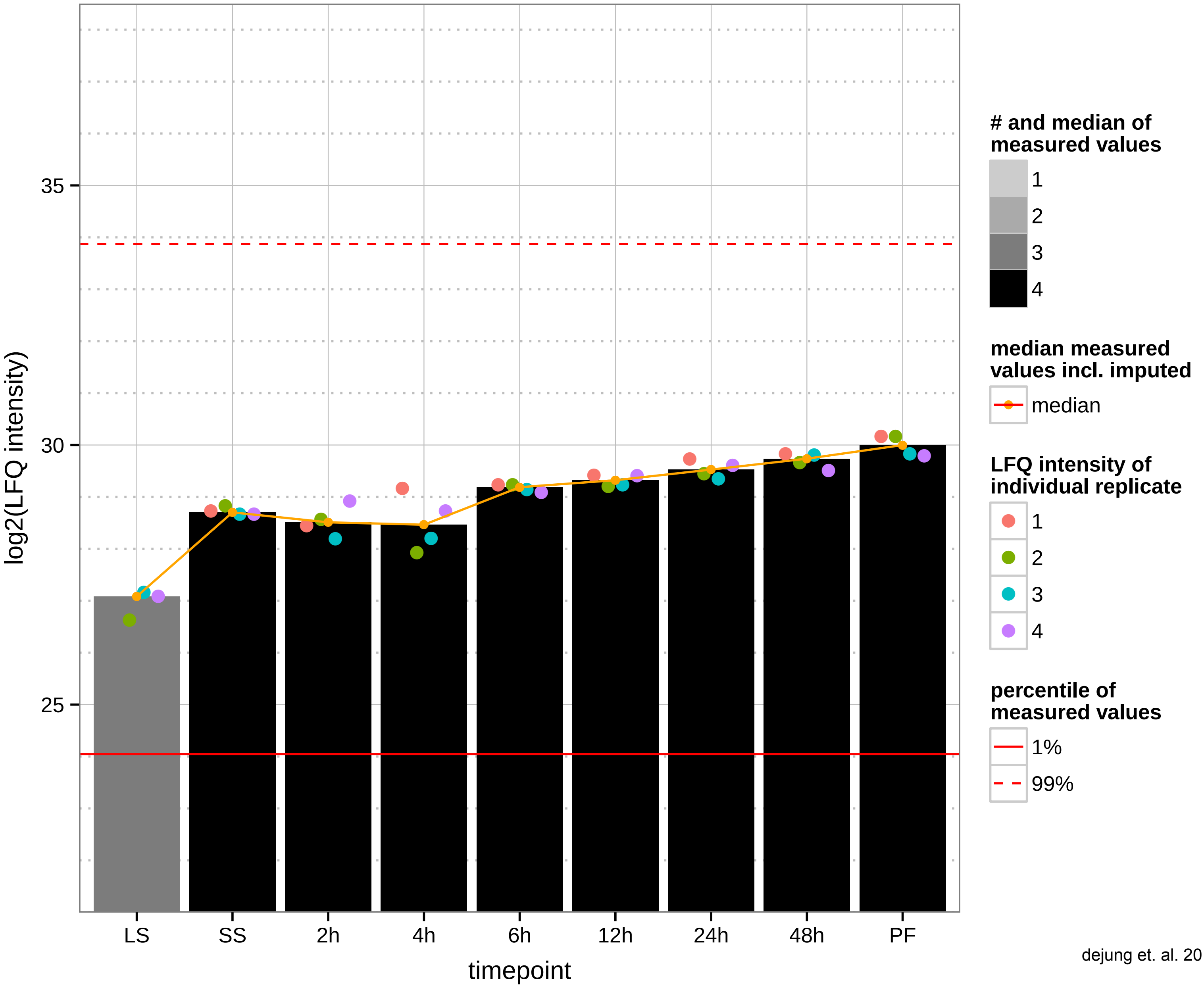




dejung et. al. 2015

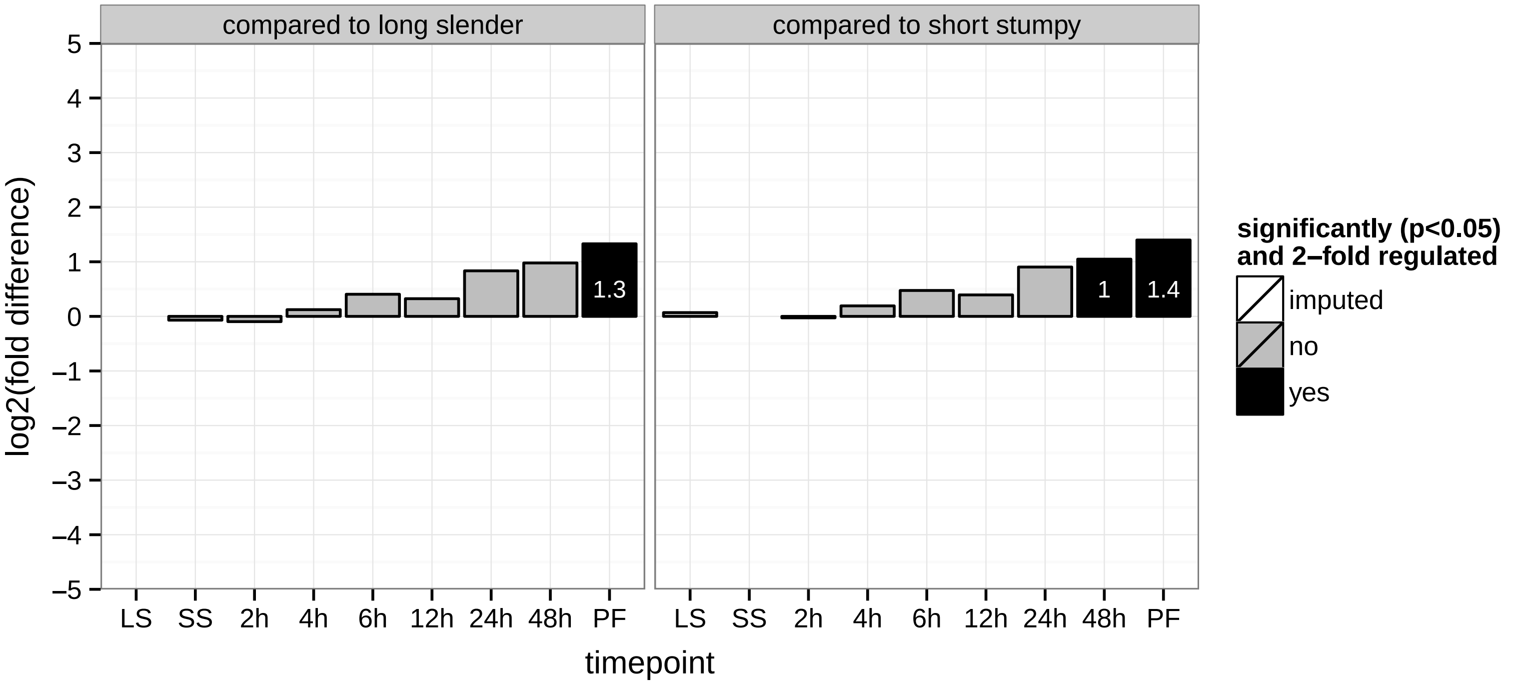
RNA–binding protein, putative (RBP11)
Tb927.8.4450
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null

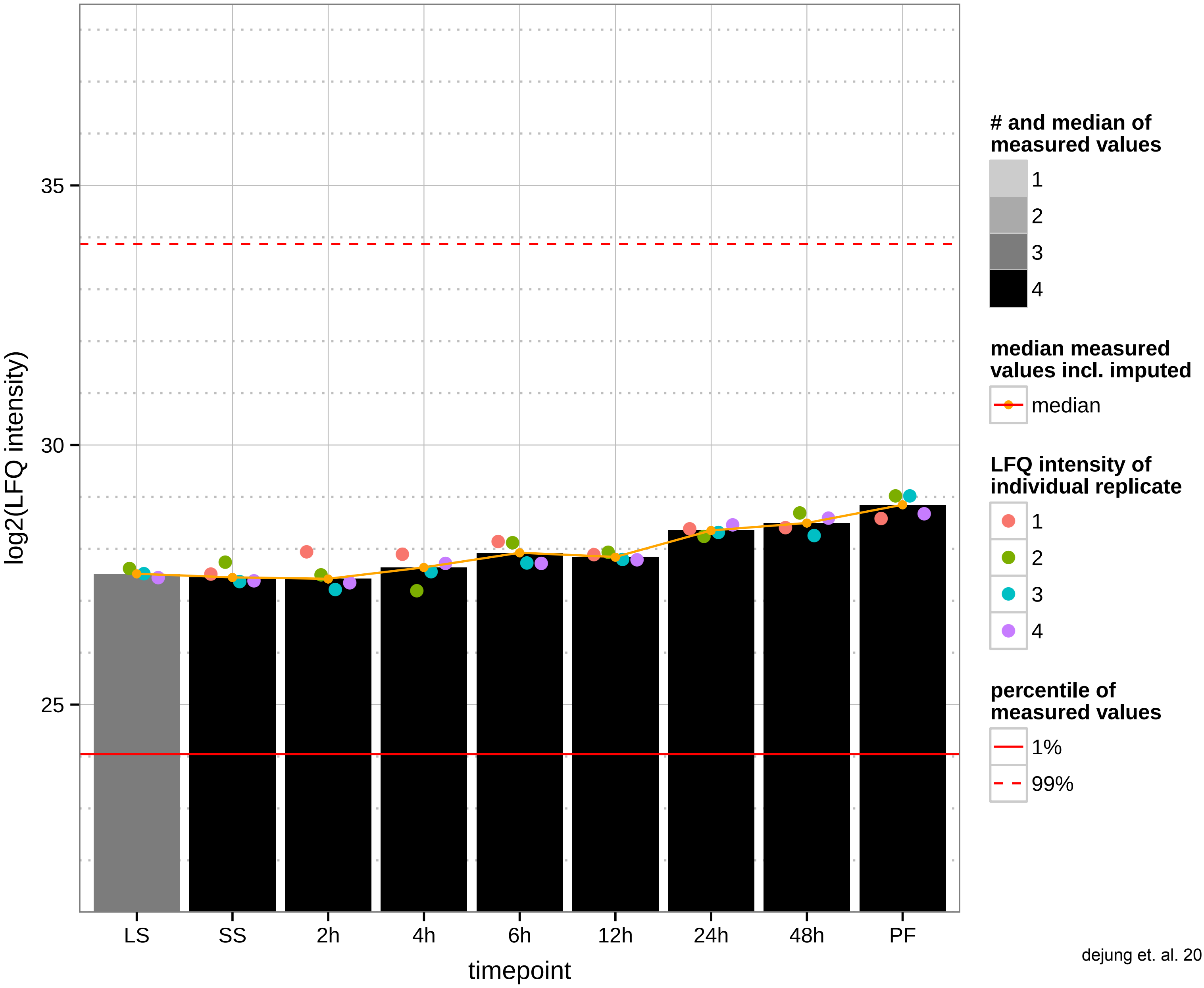




dejung et. al. 2015

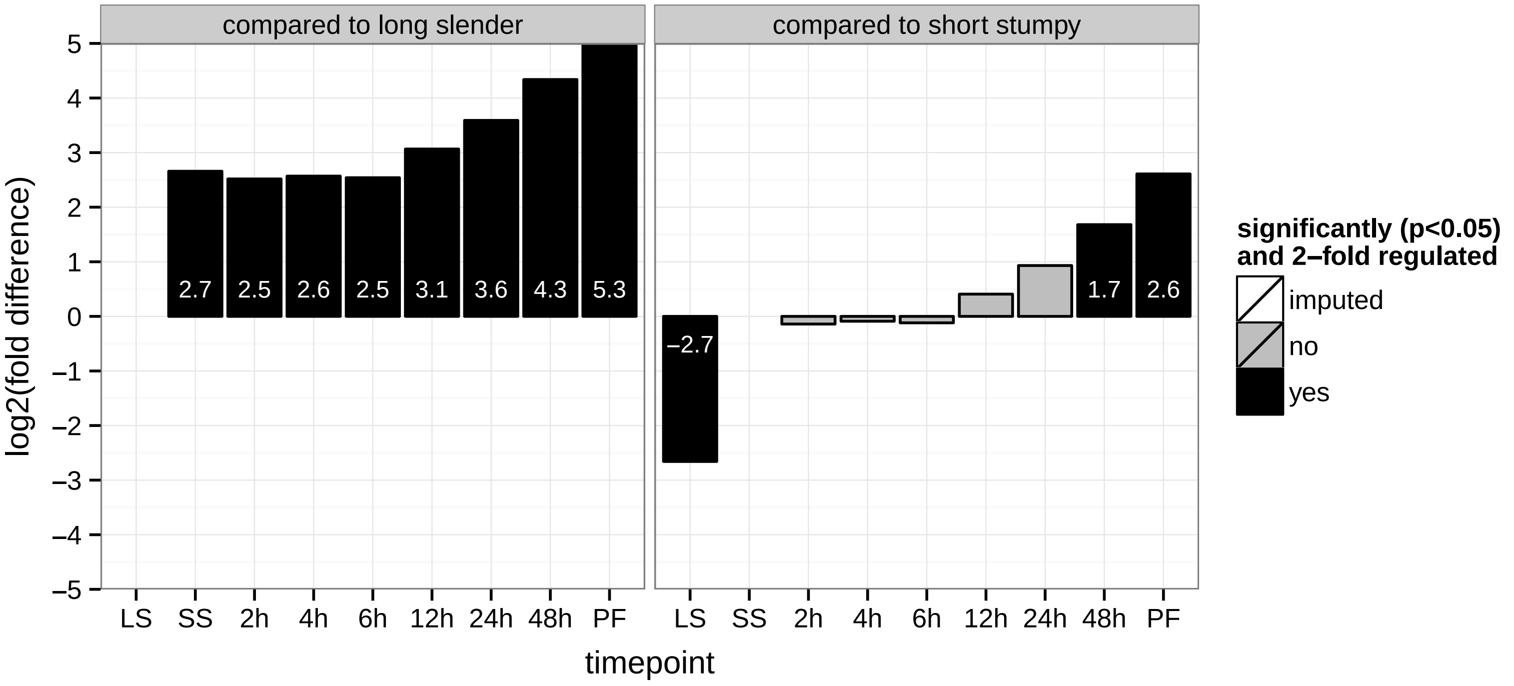
phosphatase of regenerating liver–type phosphatase, putative
Tb927.8.5780
AGOF: phosphoprotein phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: phosphatase activity, protein tyrosine/serine/threonine phosphatase activity
PGOC: null
PGOP: dephosphorylation, protein dephosphorylation

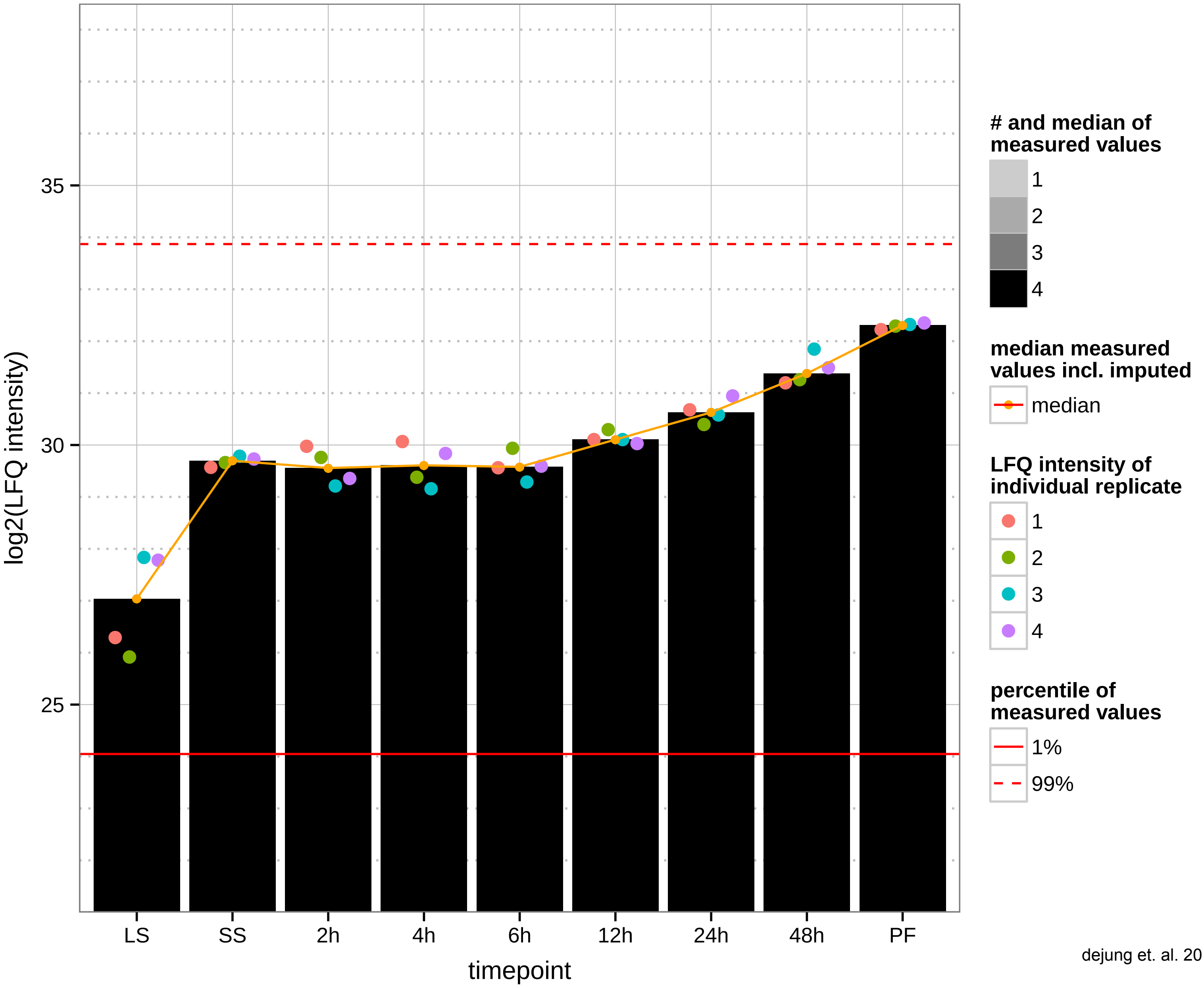




dejung et. al. 2015

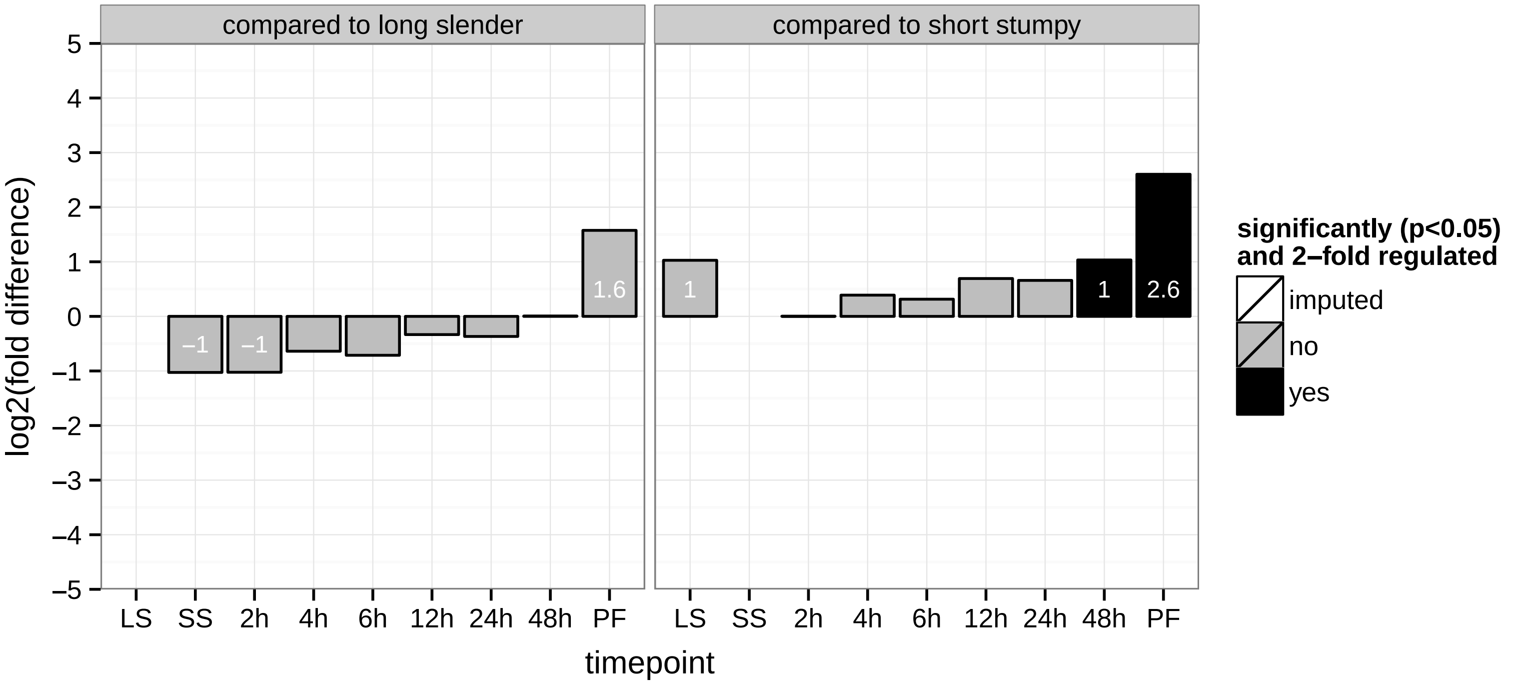
3–hydroxy–3–methylglutaryl–CoA synthase, putative (HMGS)
Tb927.8.6110
AGOF: hydroxymethylglutaryl–CoA synthase activity
AGOC: null
AGOP: ergosterol biosynthetic process
PGOF: catalytic activity, hydroxymethylglutaryl–CoA synthase activity
PGOC: null
PGOP: isoprenoid biosynthetic process, metabolic process

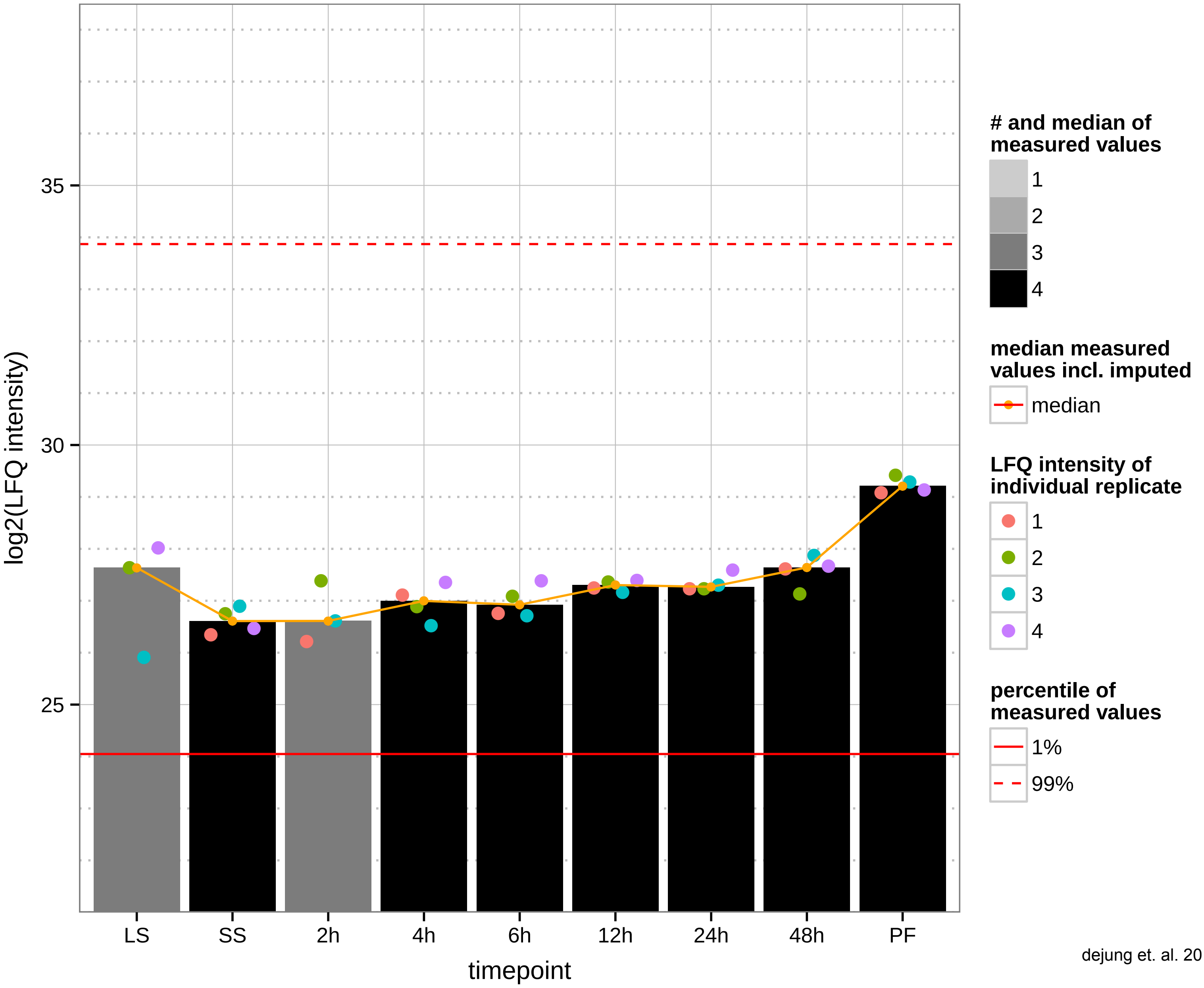




dejung et. al. 2015

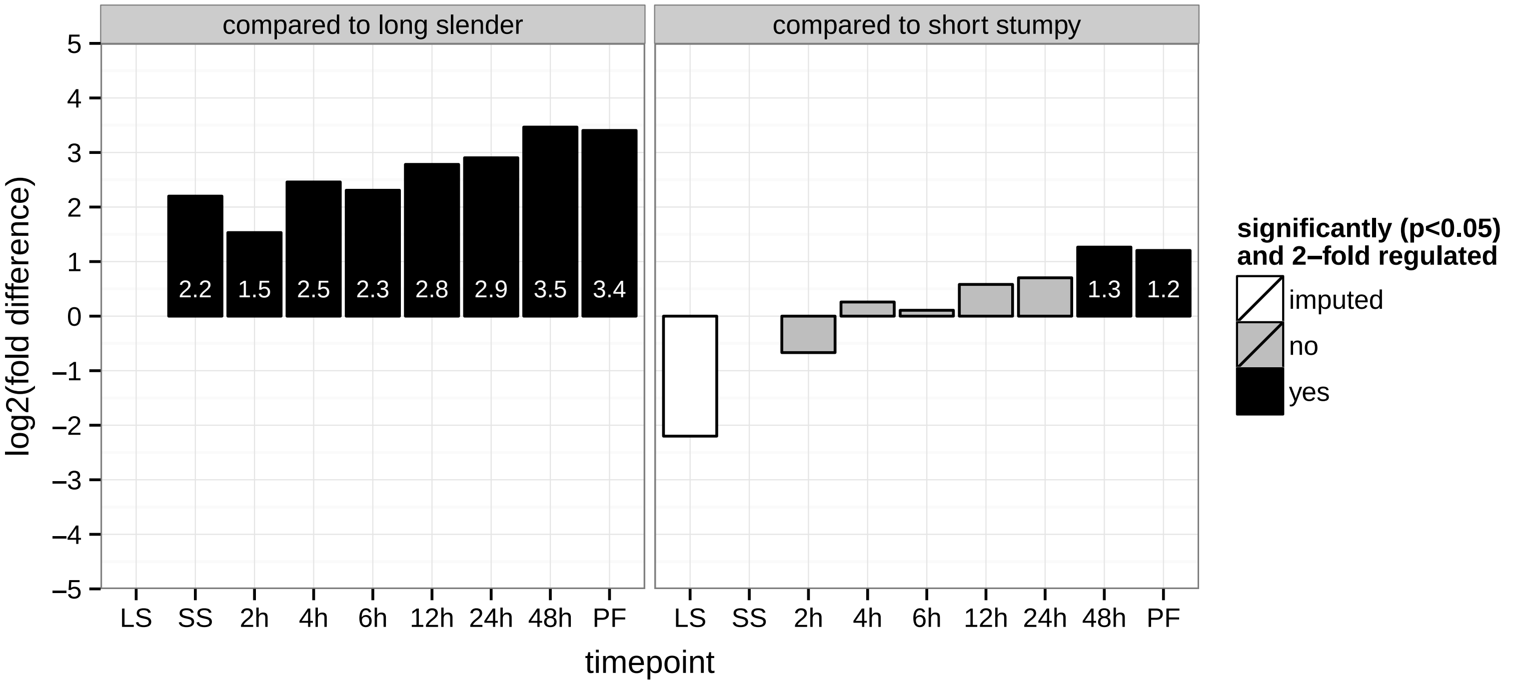
hypothetical protein, conserved
Tb927.8.6330
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

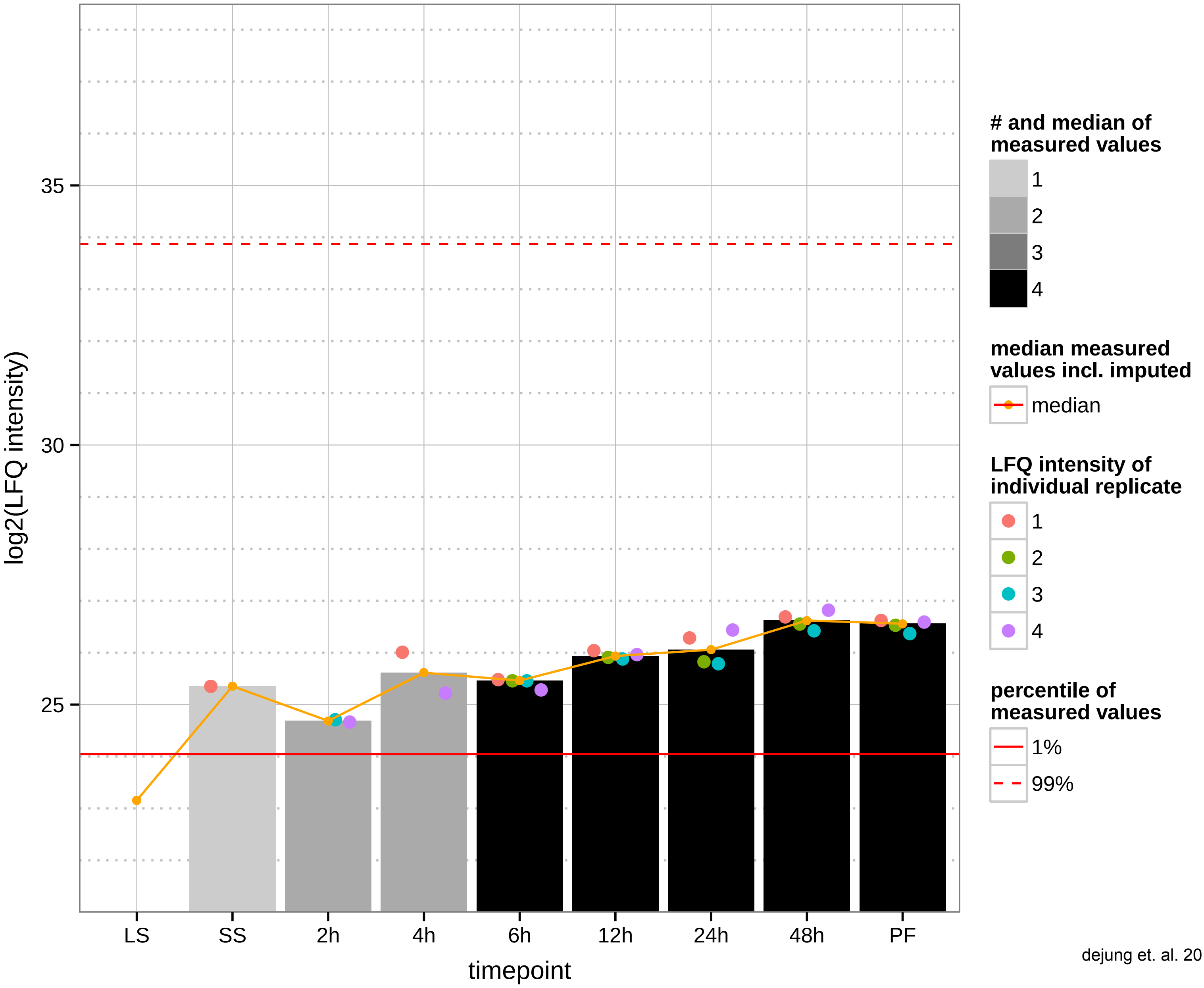




dejung et. al. 2015

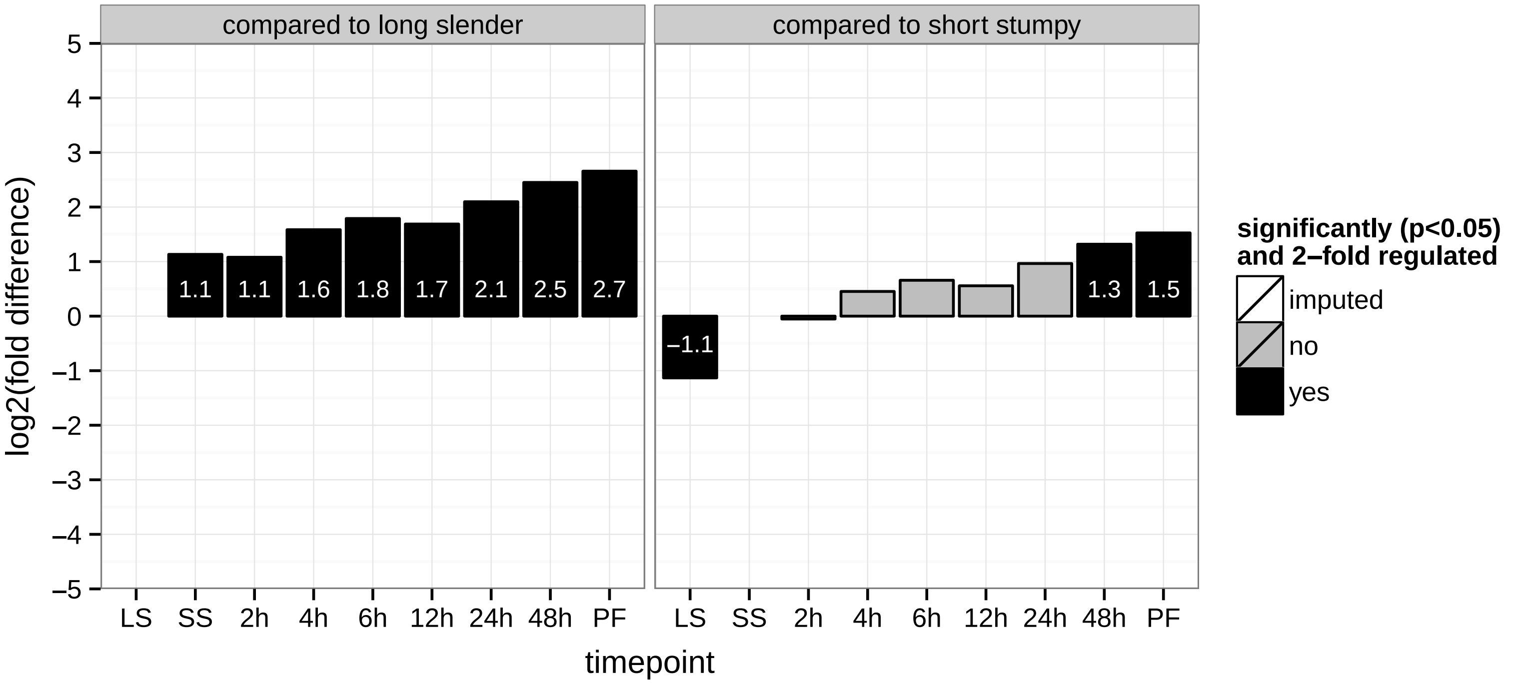
3–methylcrotonyl–CoA carboxylase alpha subunit, putative
Tb927.8.6970
AGOF: ATP binding, biotin binding, methylcrotonoyl–CoA carboxylase activity
AGOC: mitochondrion
AGOP: pyrimidine nucleobase biosynthetic process, urea cycle
PGOF: ATP binding, biotin carboxylase activity, catalytic activity, ligase activity, metal ion binding
PGOC: null
PGOP: metabolic process

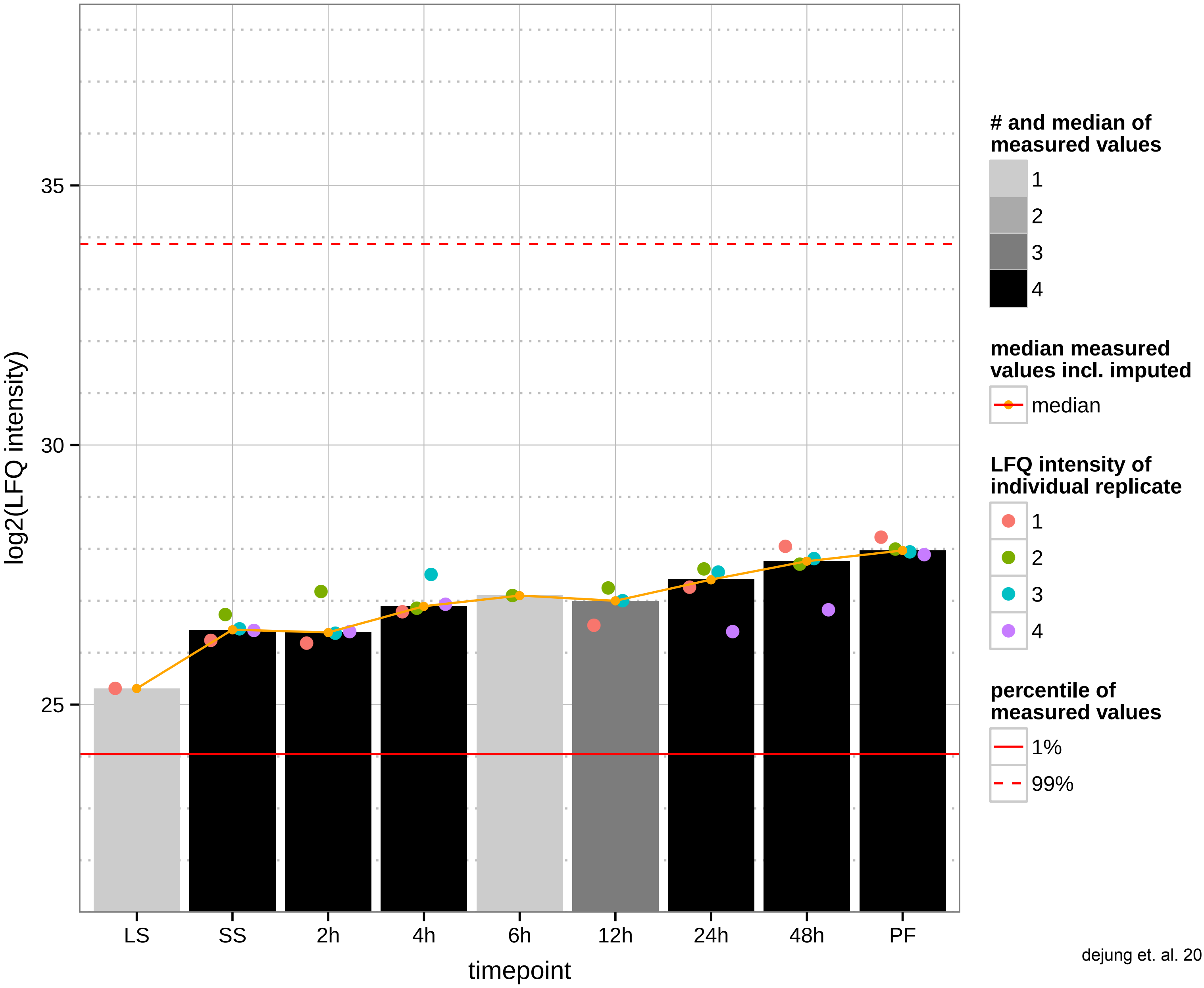




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.7040
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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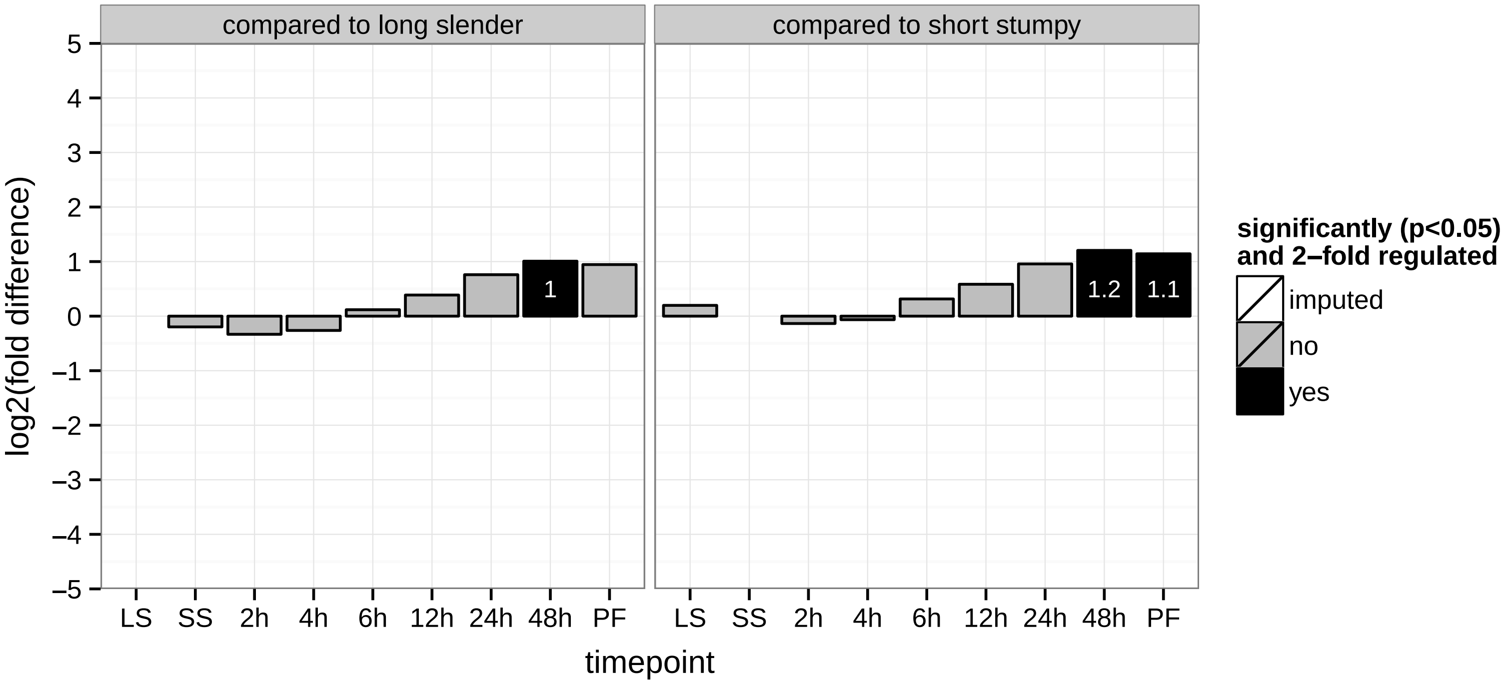
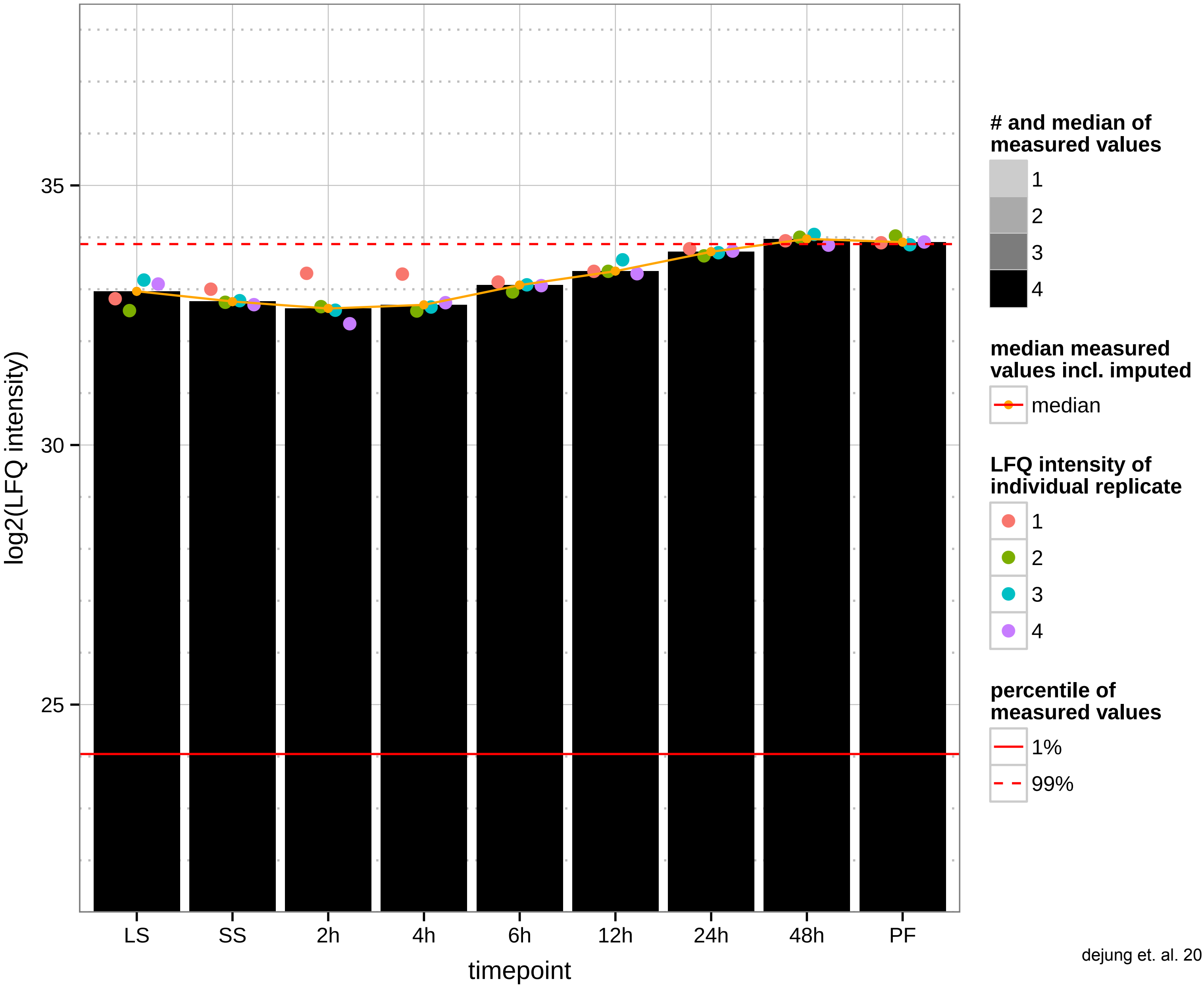
Polyadenylate–binding protein 2 (Poly(A)–binding protein 2) (Poly(A)–binding protein II) (PABII) (Polyadenylate–binding nuclea
Tb927.9.10770
AGOF: RNA binding, poly(A) RNA binding
AGOC: null
AGOP: RNA processing
PGOF: RNA binding, nucleic acid binding
PGOC: null
PGOP: null





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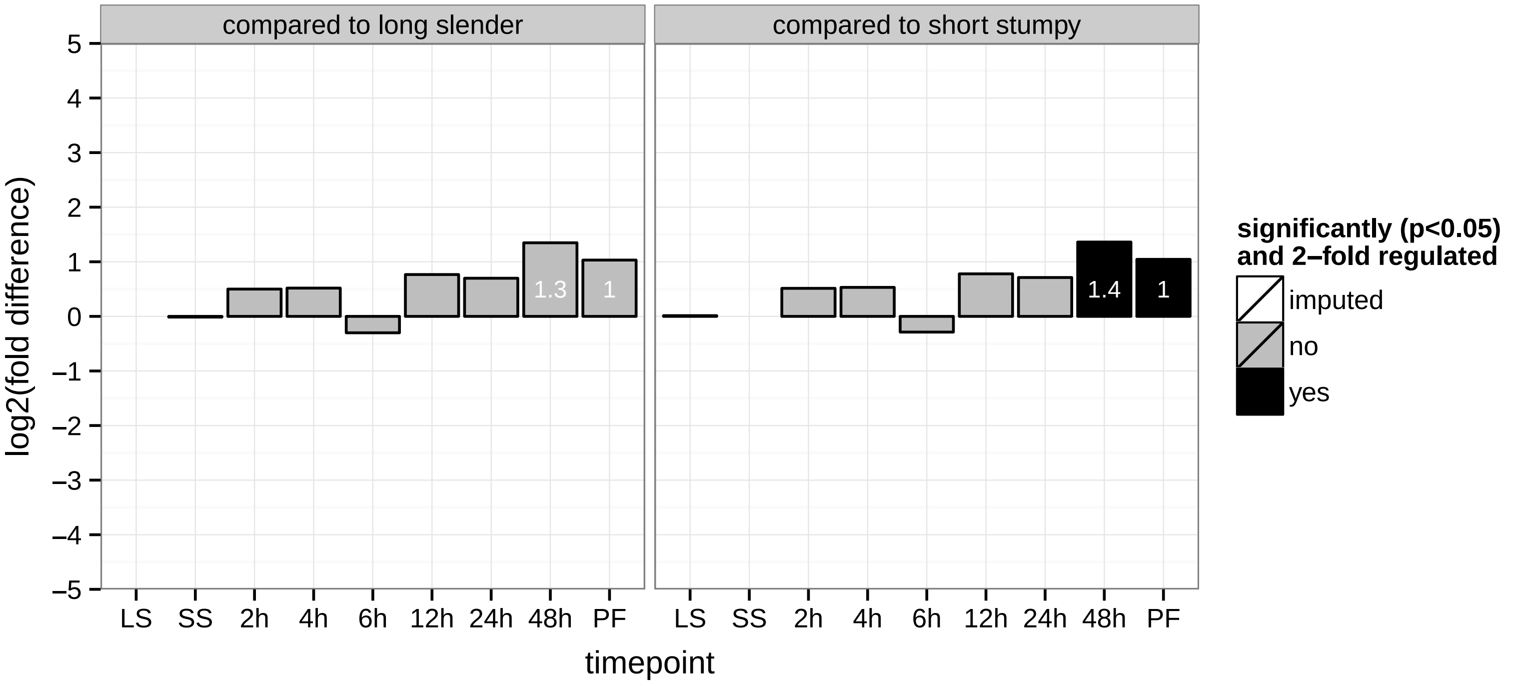
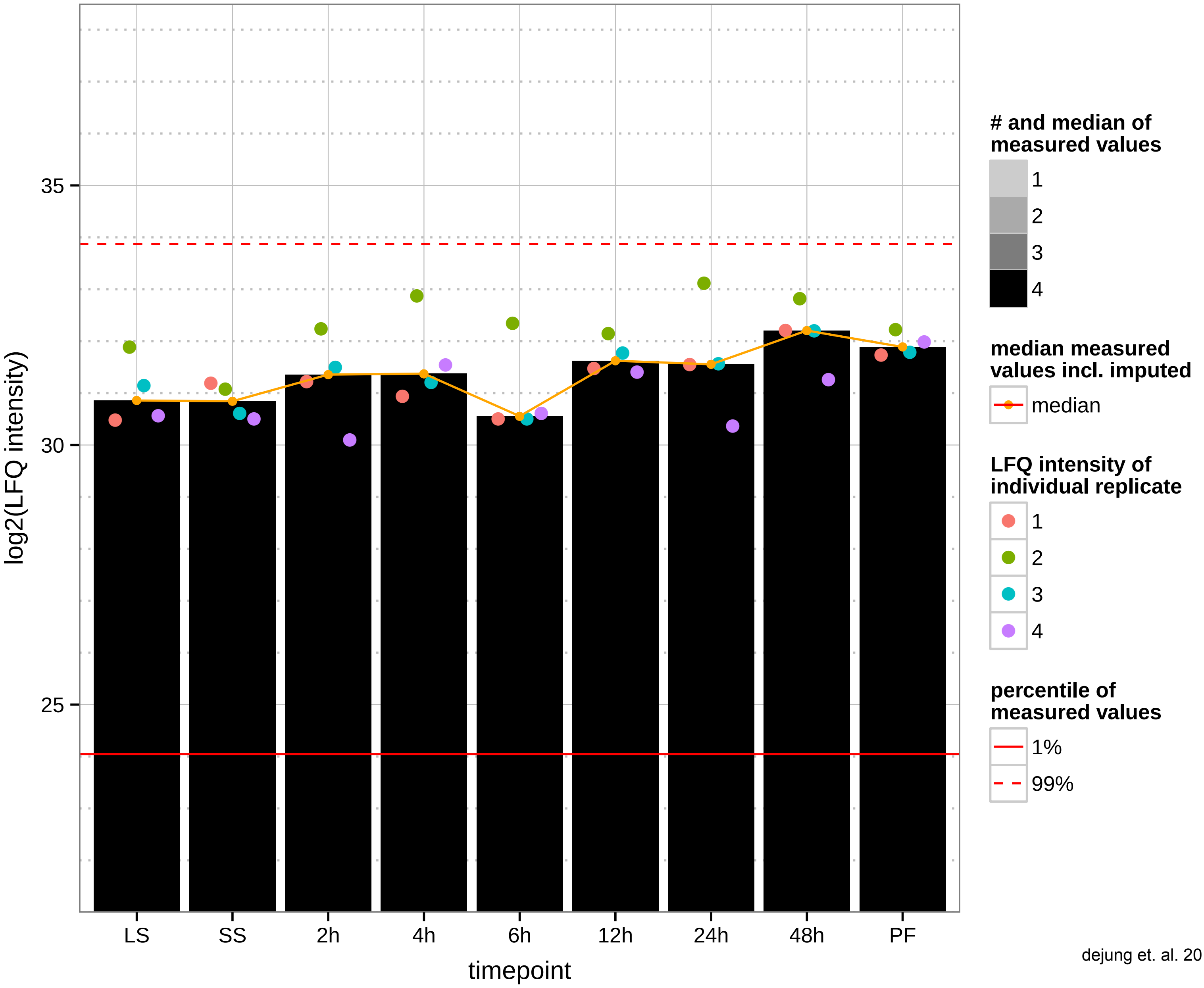
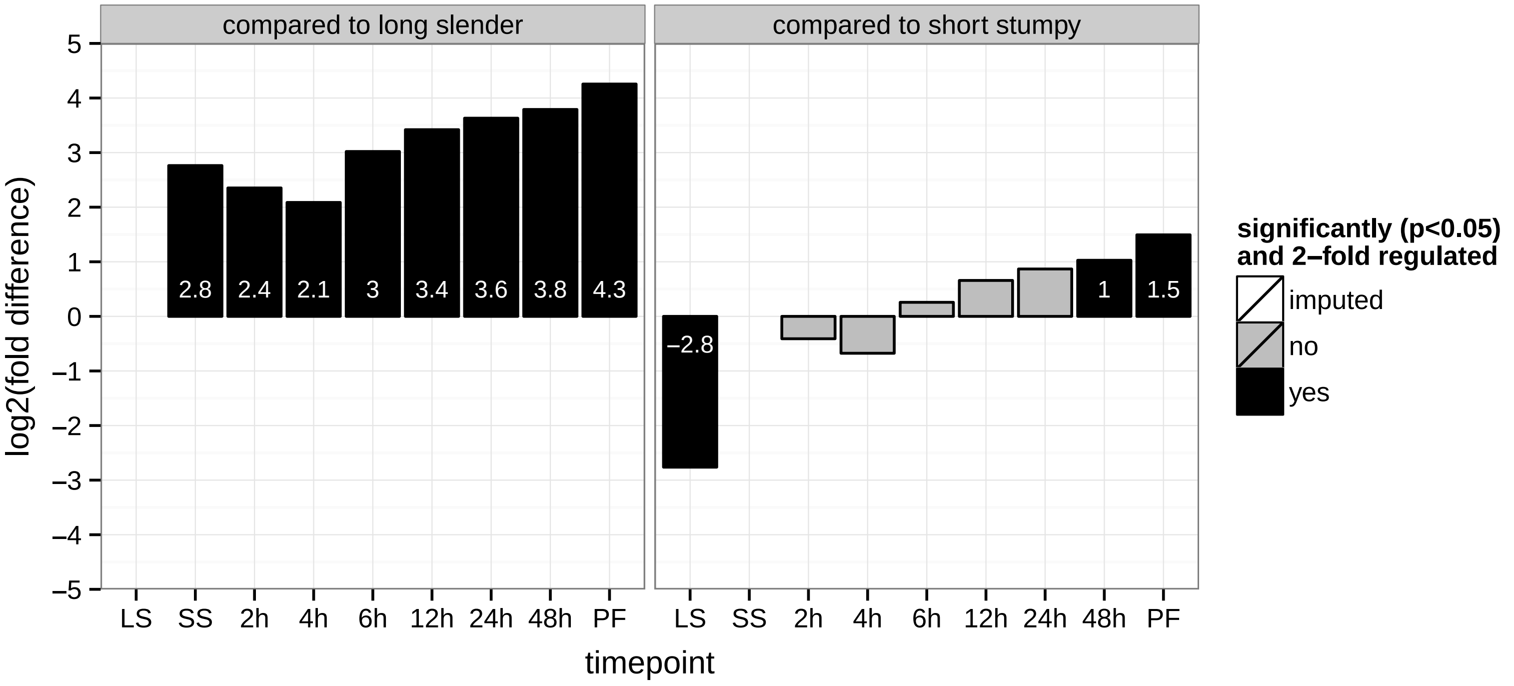
kinetoplastid membrane protein KMP−11, unspecified product, kinetoplastid membrane protein KMP−11 (KMP−11)
Tb927.9.13920;Tb927.9.13880;Tb927.9.13820
AGOF: null
AGOC: mitochondrion, null
AGOP: defense response, positive regulation of cell proliferation, null
PGOF: null
PGOC: null
PGOP: defense response, positive regulation of cell proliferation, null

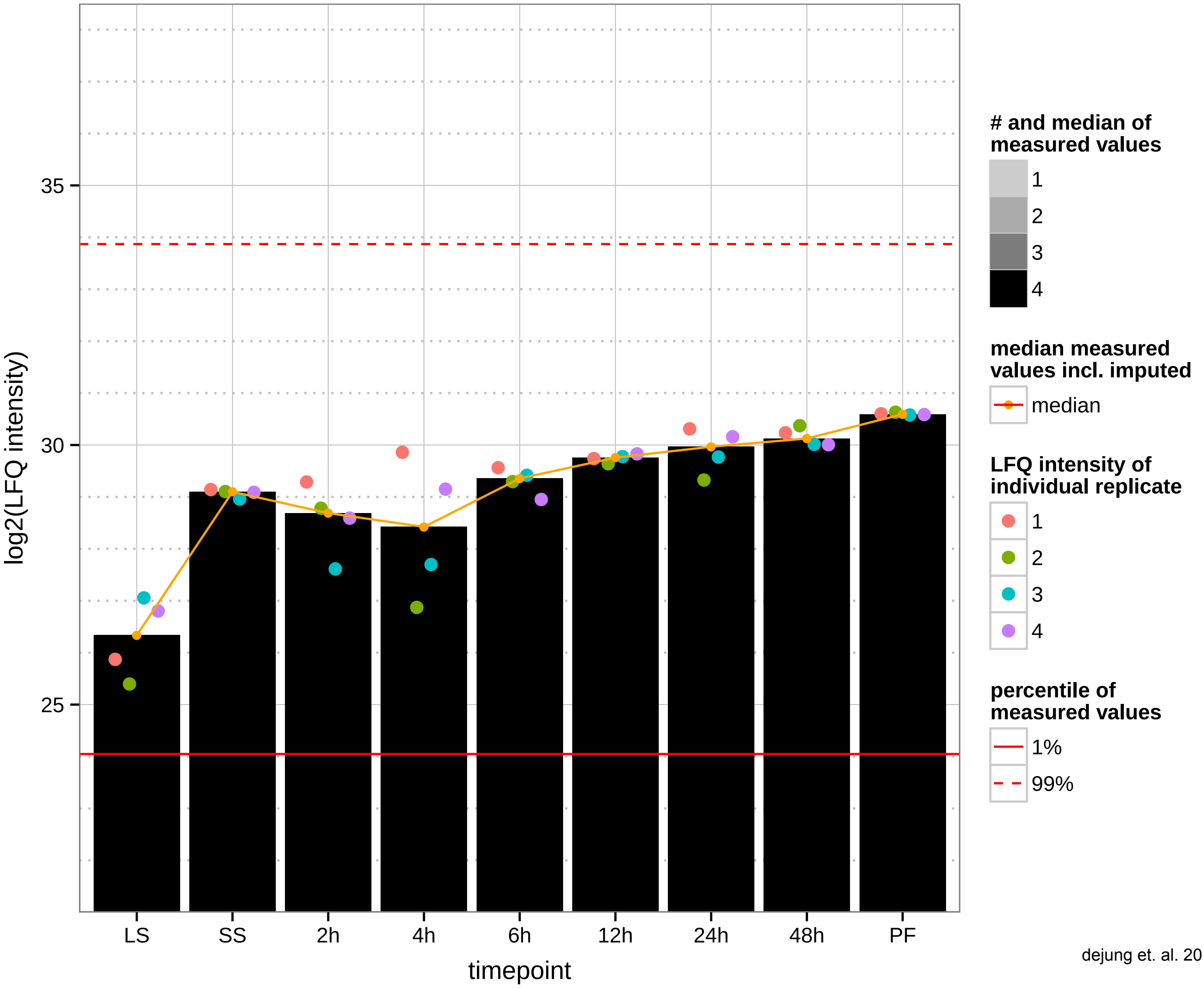




dejung et. al. 2015

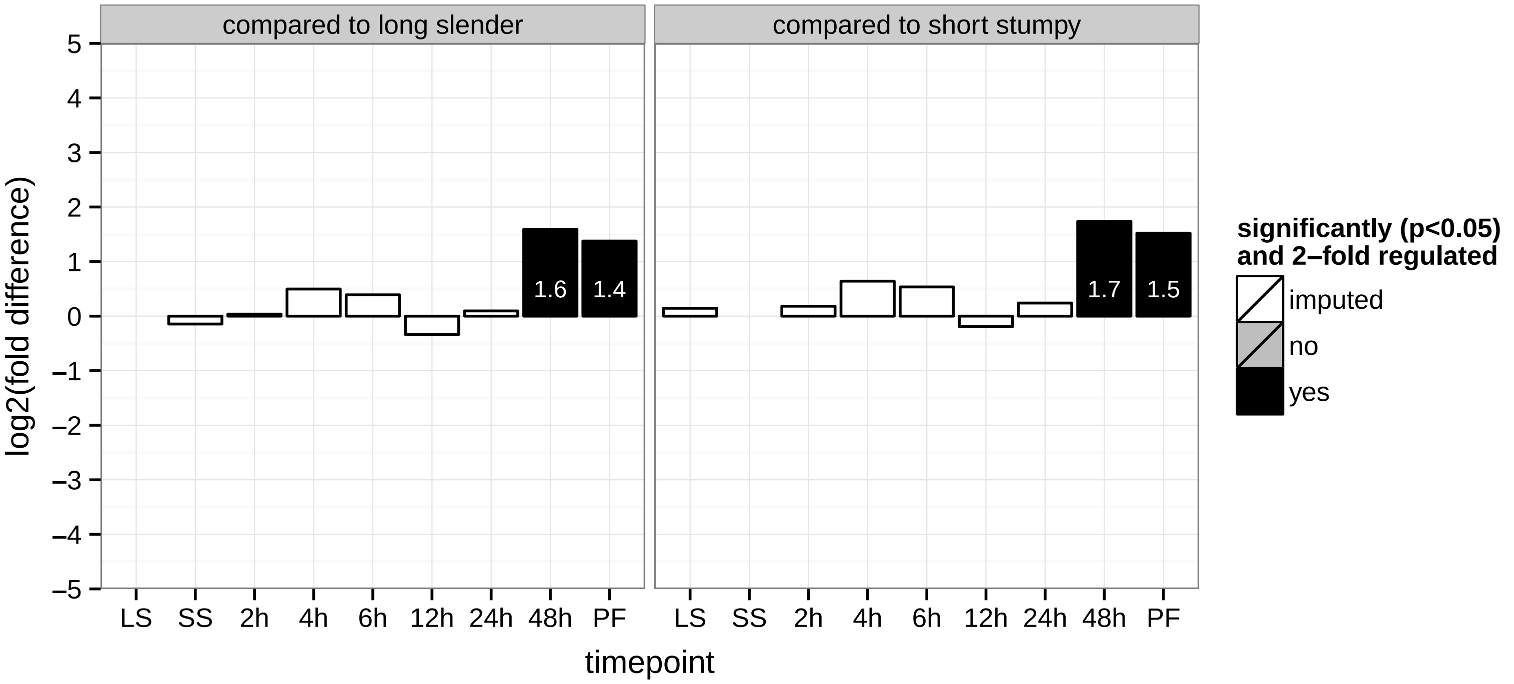
hypothetical protein, conserved
Tb927.9.2900
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

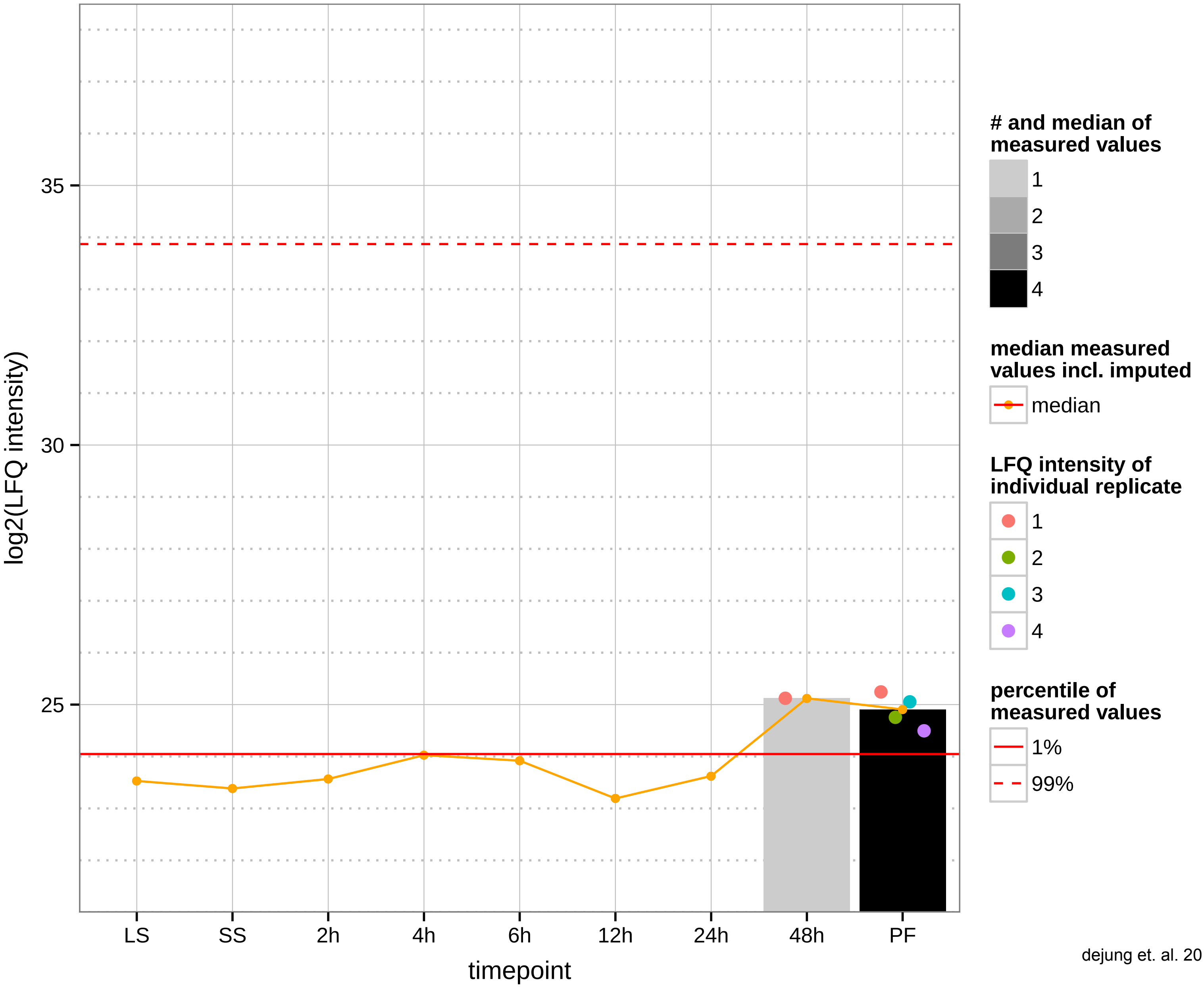




dejung et. al. 2015

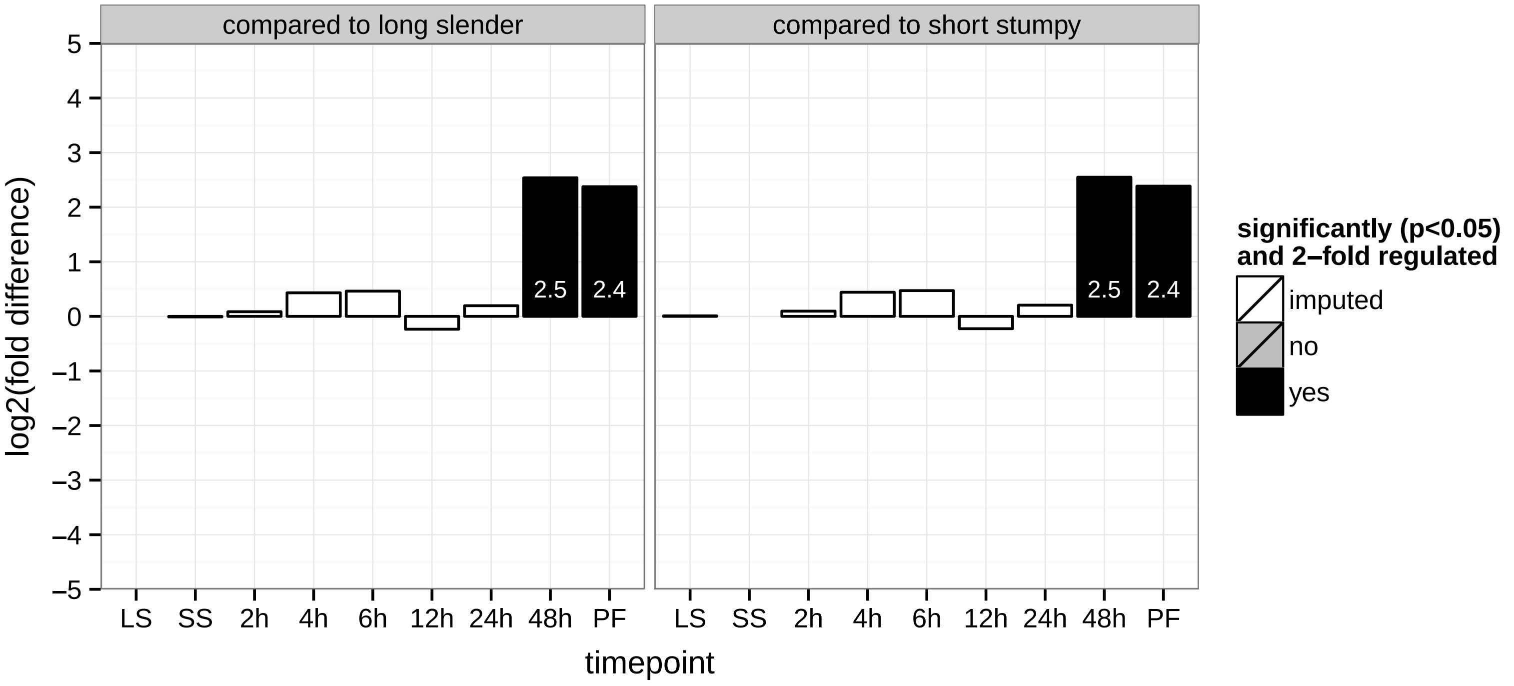
kinesin (Kif–13–1)
Tb927.9.3650
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: microtubule associated complex, nucleus
AGOP: microtubule–based movement, mitotic spindle organization, regulation of chromosome segregation
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement

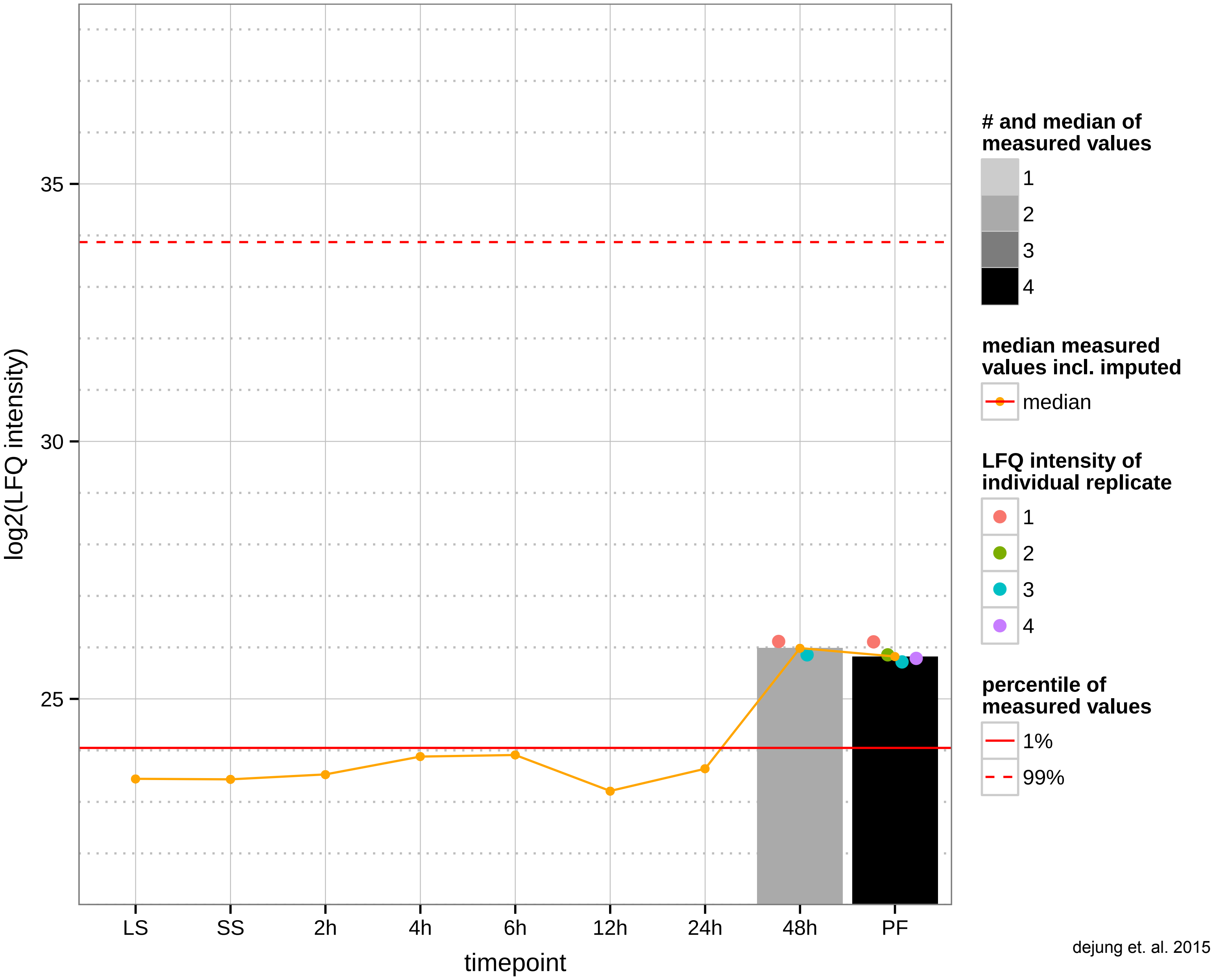




dejung et. al. 2015

condensin subunit 1, putative
Tb927.9.4900
AGOF: null
AGOC: condensin complex
AGOP: mitotic chromosome condensation
PGOF: binding
PGOC: null
PGOP: null





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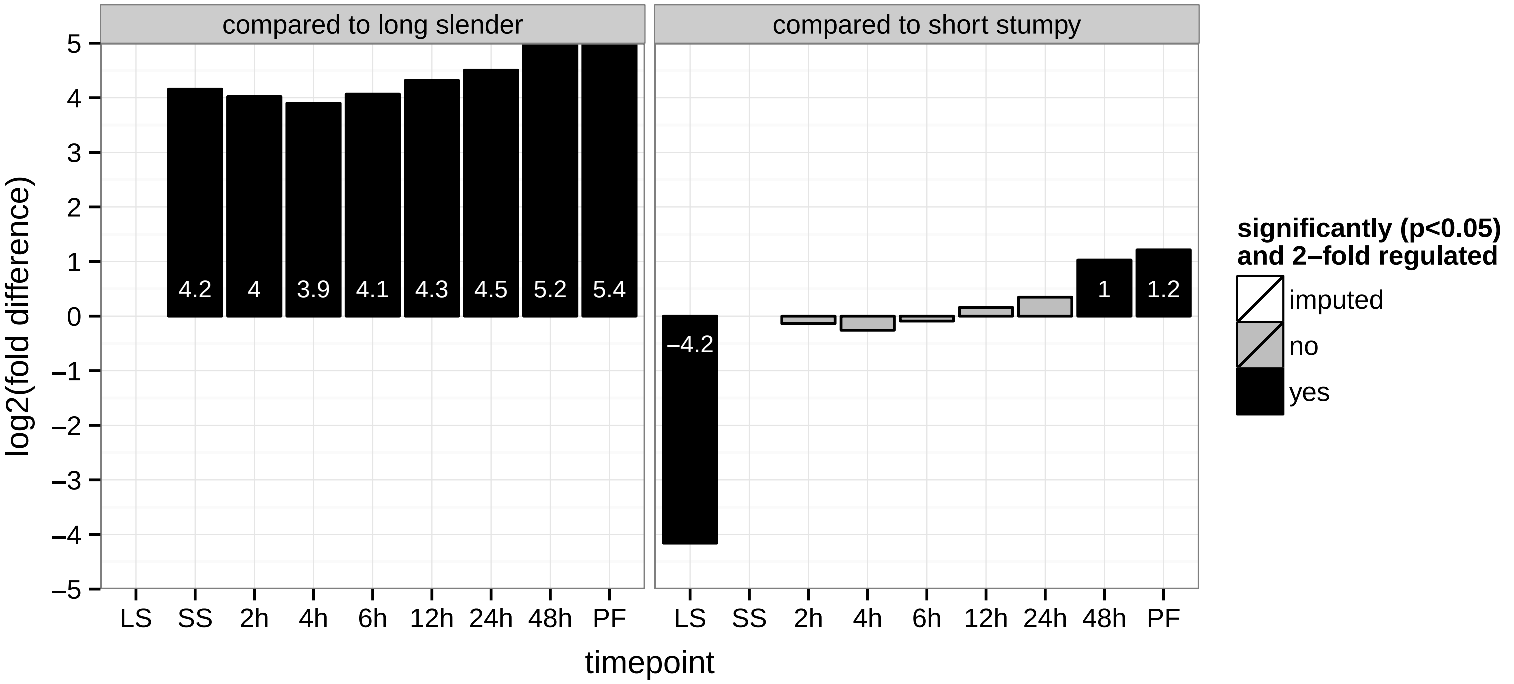
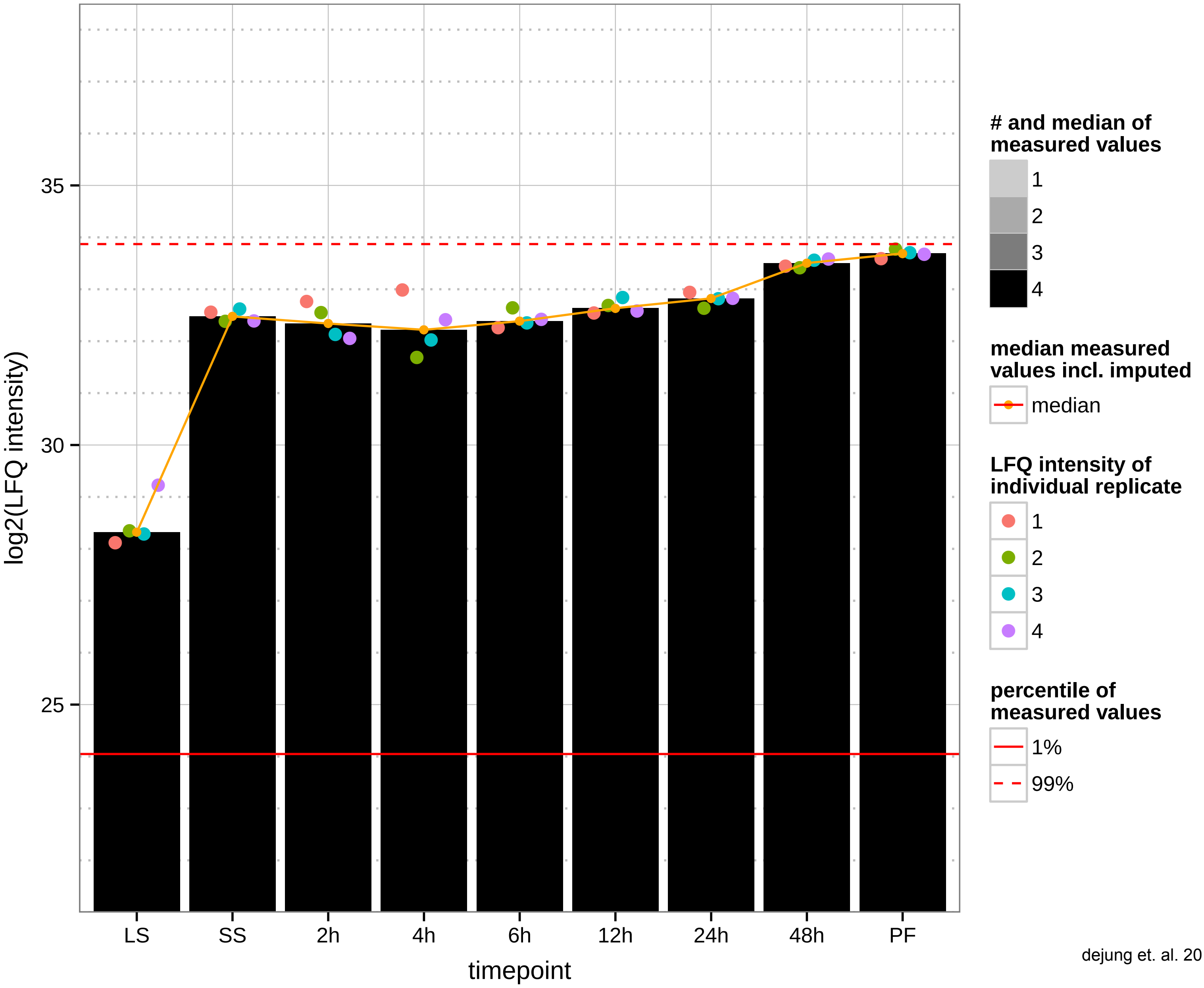
glutamate dehydrogenase (GDH)
Tb927.9.5900
AGOF: glutamate dehydrogenase (NAD+) activity, oxidoreductase activity
AGOC: mitochondrion
AGOP: cellular amino acid metabolic process, glutamate catabolic process to 2–oxoglutarate, oxidation–reduction process
PGOF: glutamate dehydrogenase (NAD+) activity, oxidoreductase activity
PGOC: null
PGOP: cellular amino acid metabolic process, glutamate catabolic process to 2–oxoglutarate, oxidation–reduction process





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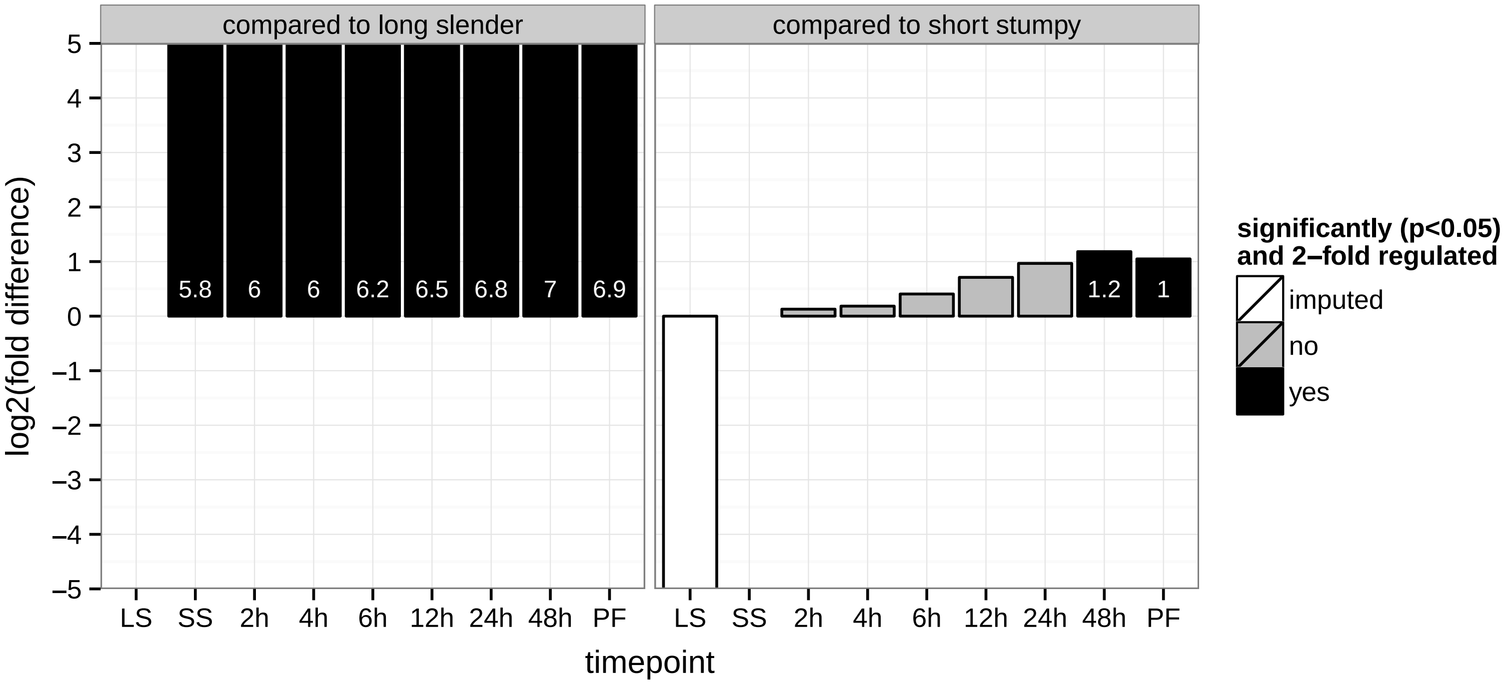
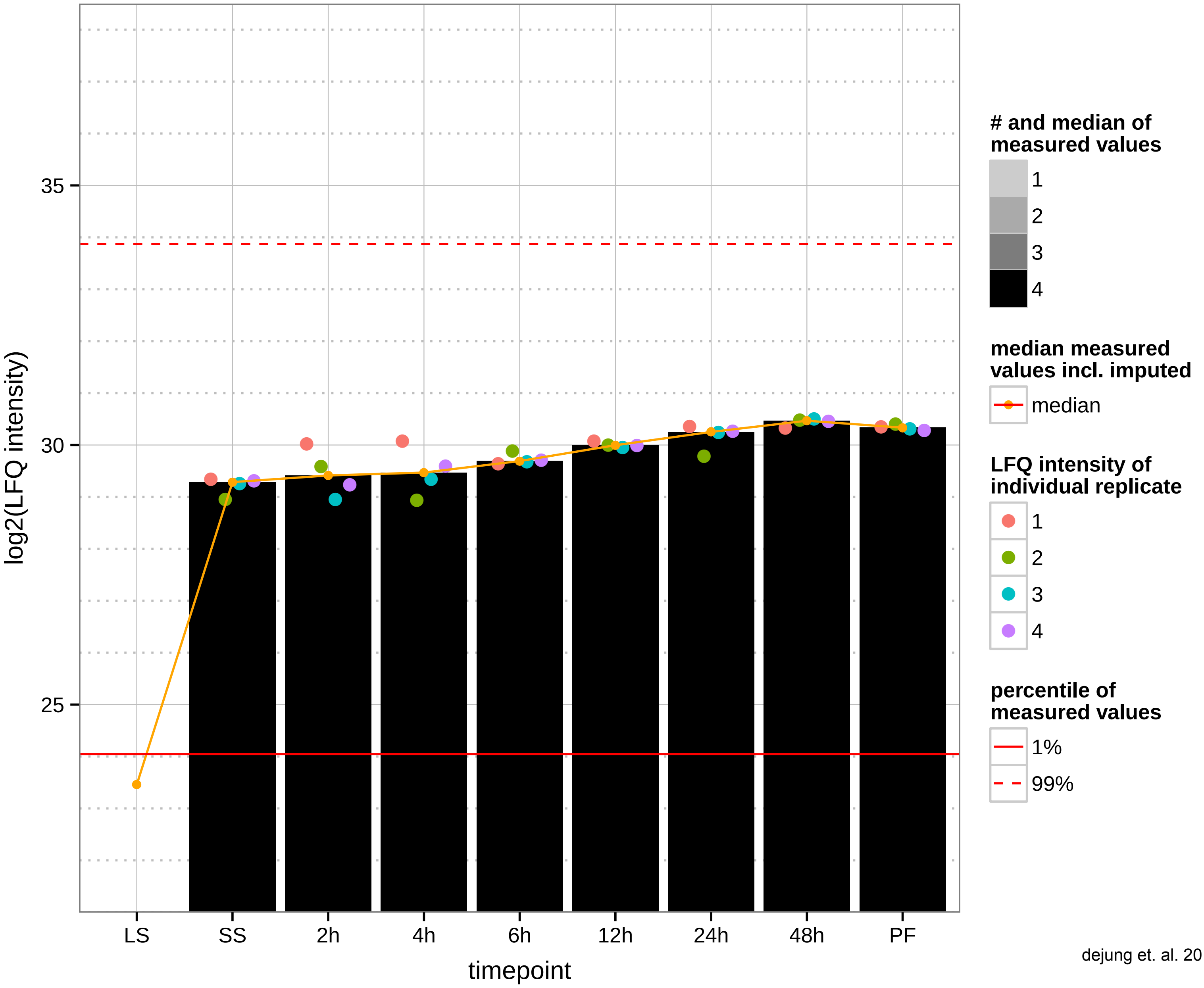
ABC transporter, putative
Tb927.9.6310
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances
AGOC: integral to membrane, internal side of plasma membrane, membrane
AGOP: transport
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: membrane
PGOP: null





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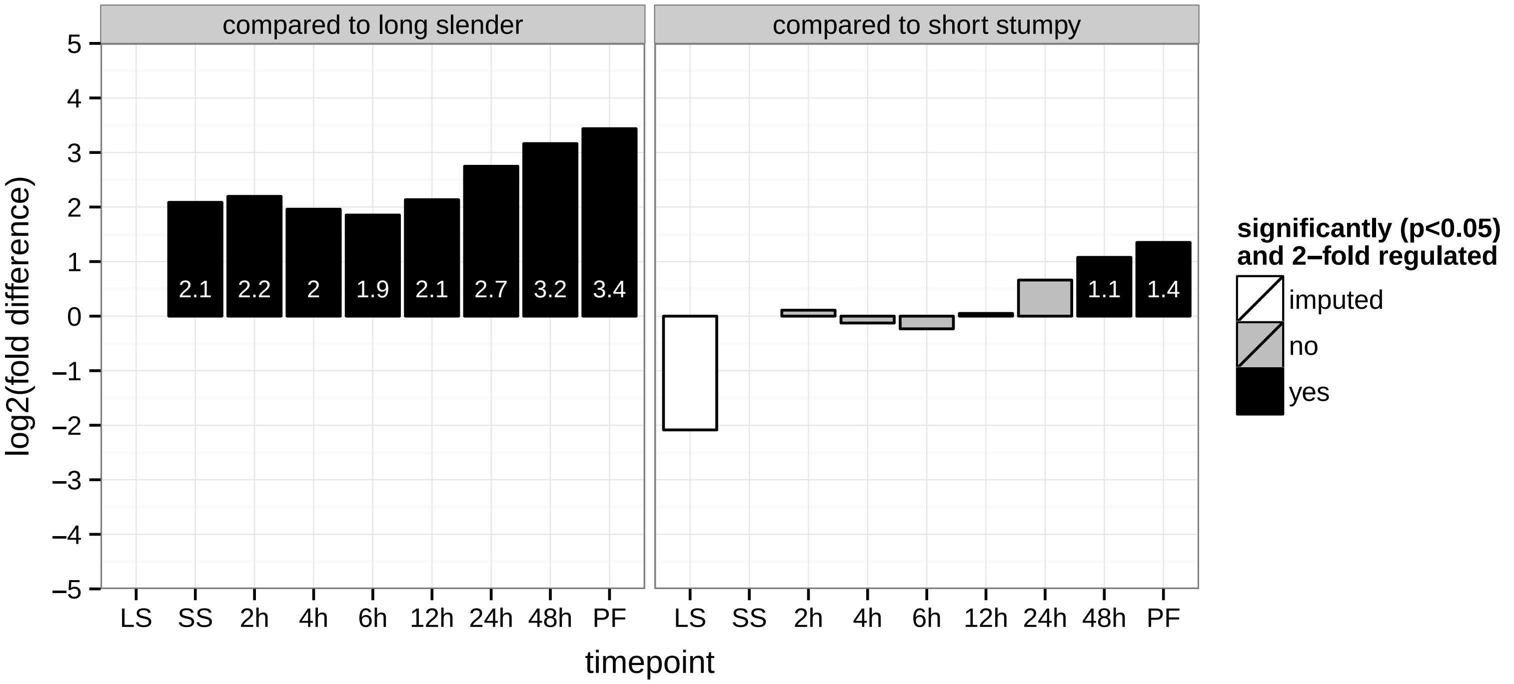
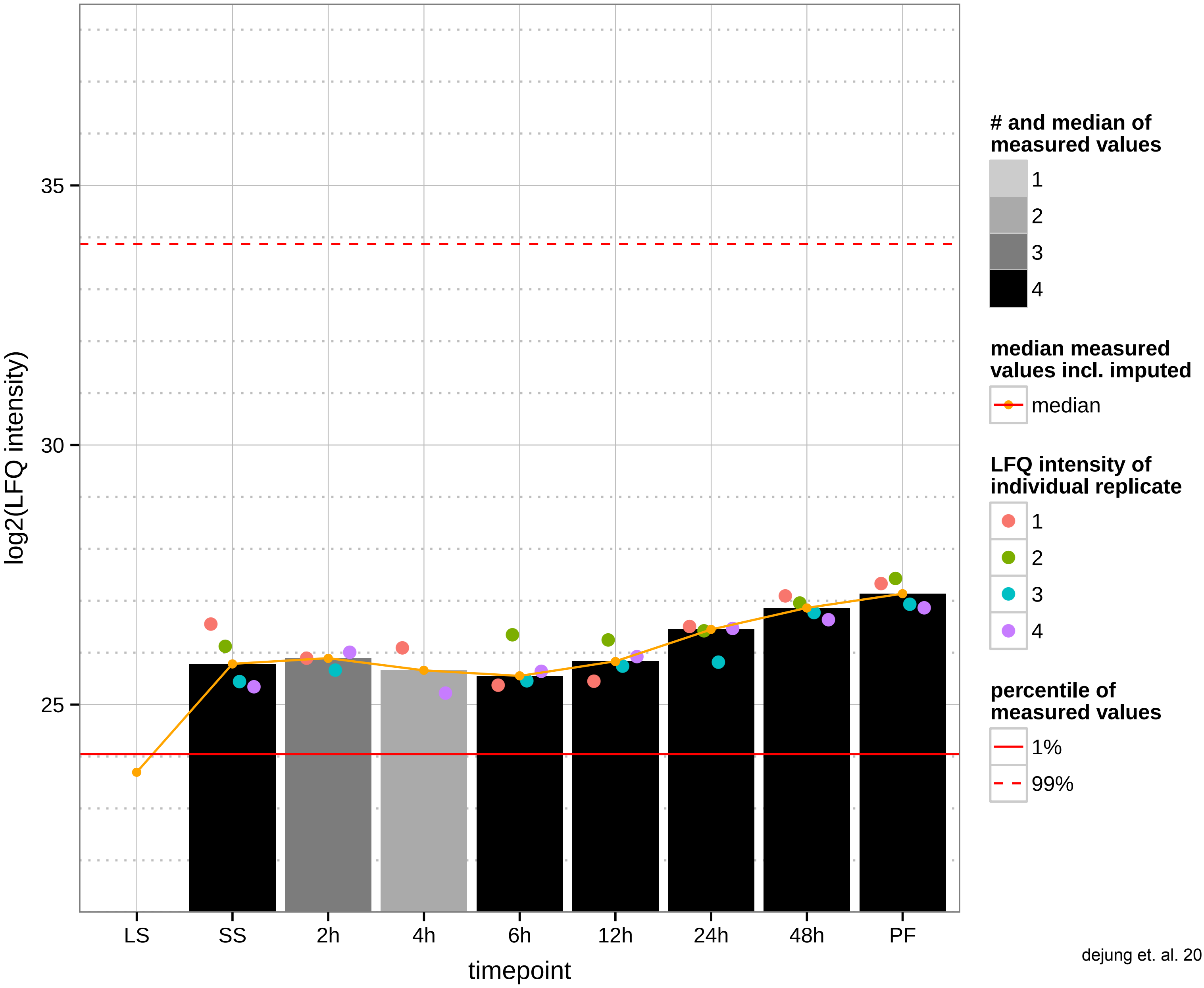
oxidoreductase, putative
Tb927.9.7190
AGOF: alcohol dehydrogenase activity, zinc−dependent, oxidoreductase activity, zinc ion binding
AGOC: mitochondrion
AGOP: metabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation−reduction process





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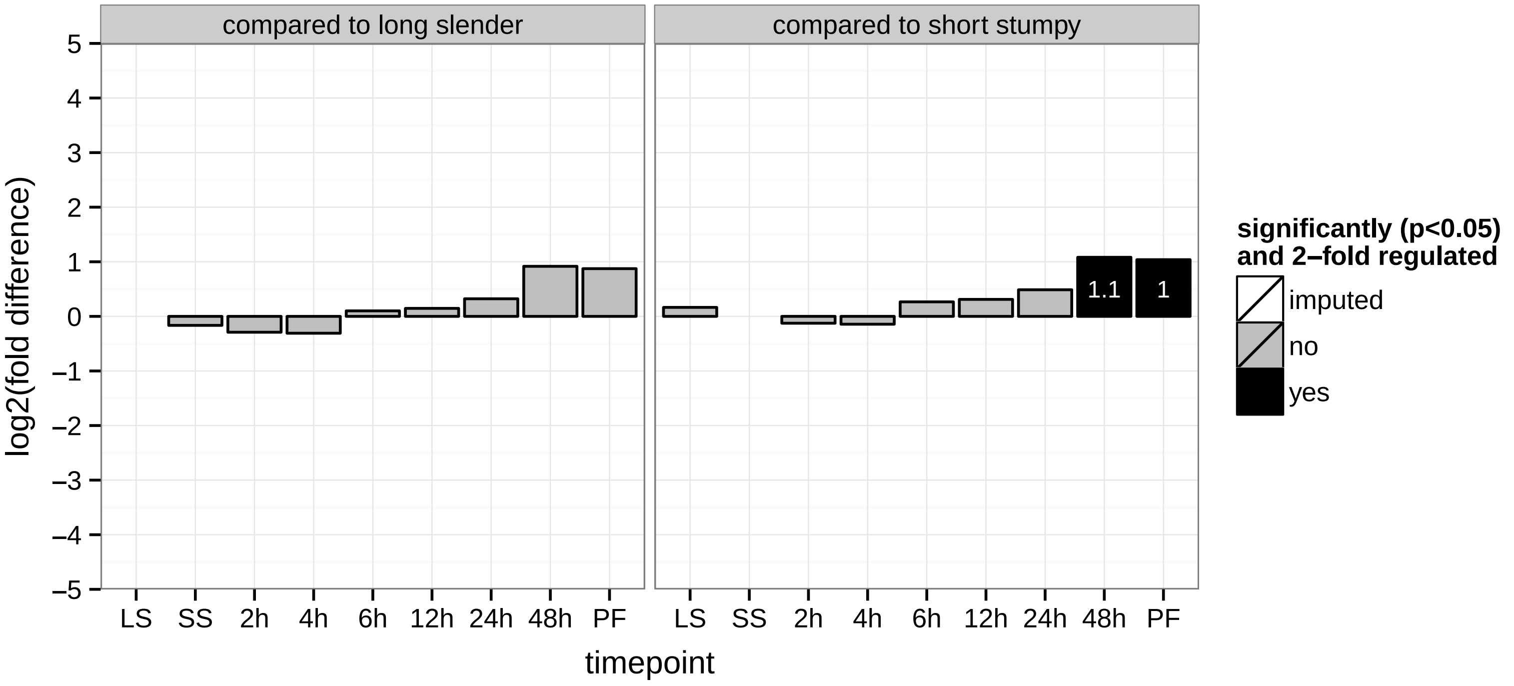
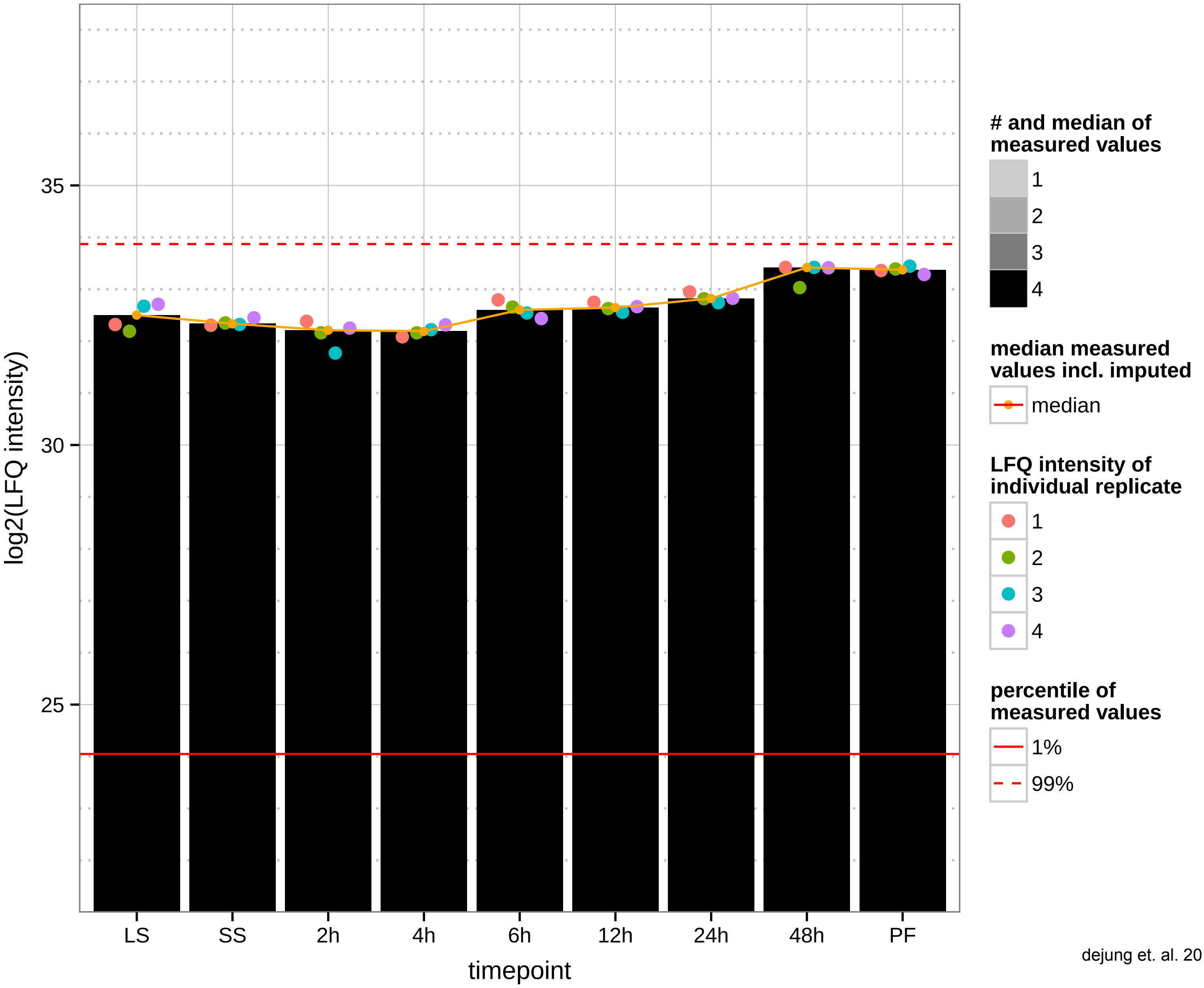
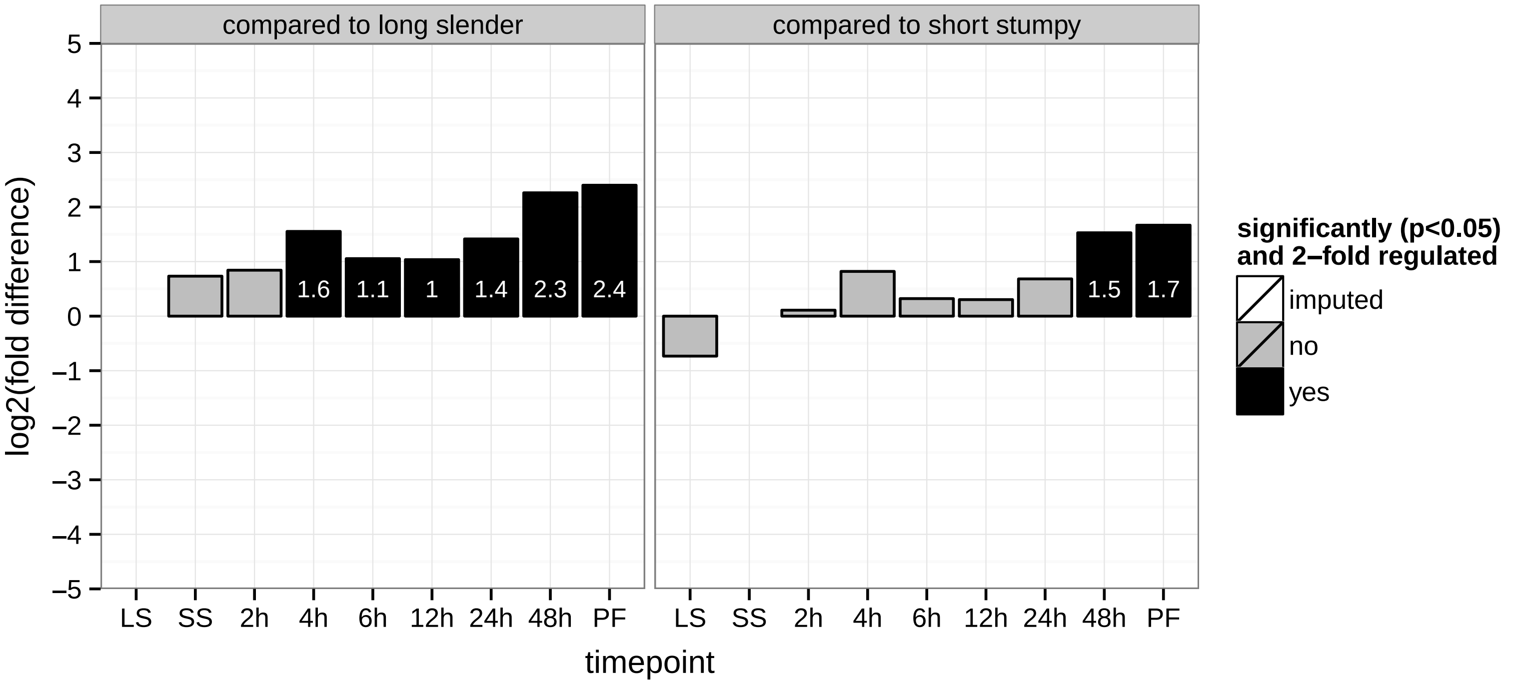
60S ribosomal protein L10, putative, QM–like protein (QM), QM–like protein
Tb927.9.8420;Tb927.9.8070
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation

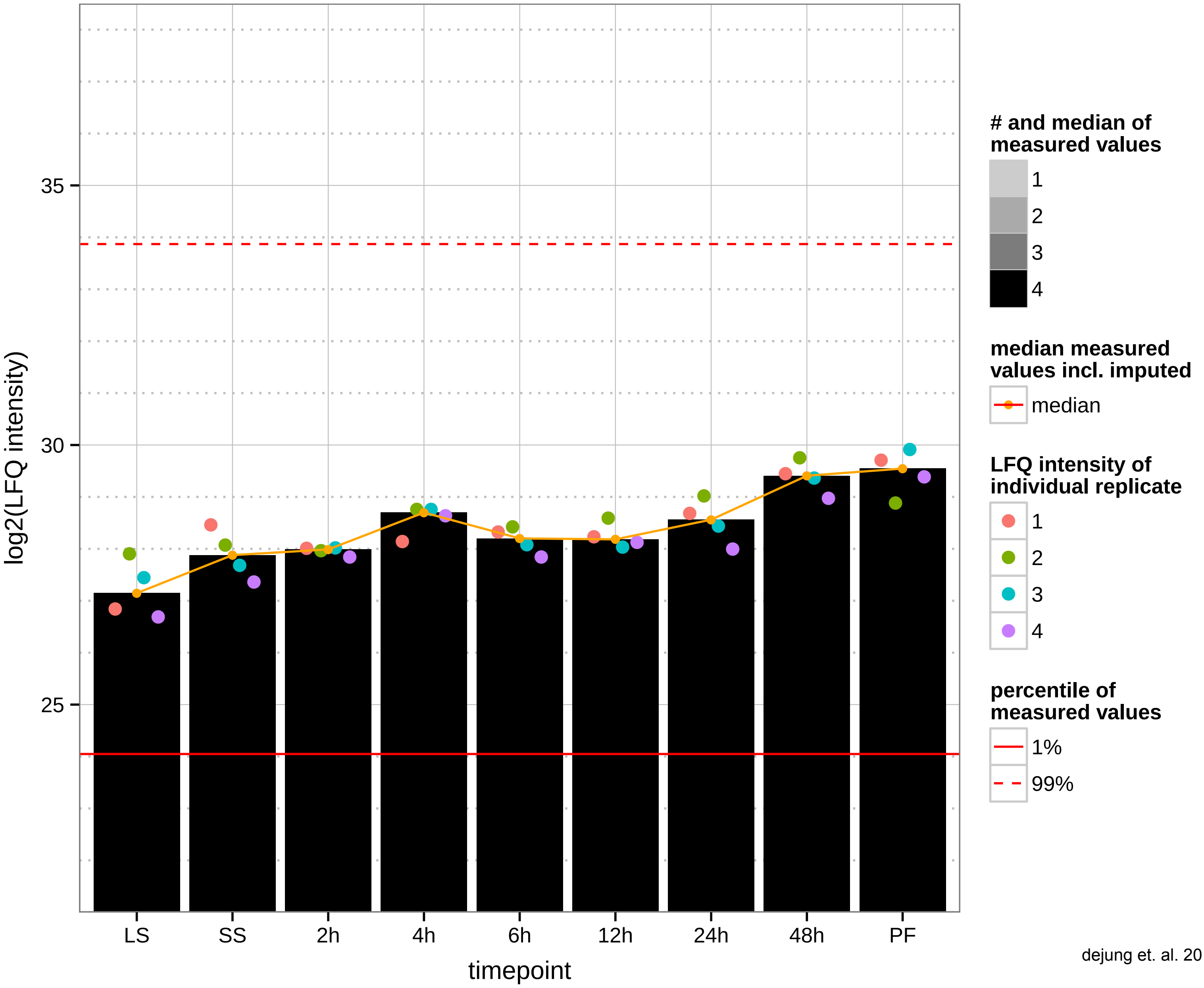




dejung et. al. 2015

adenylate kinase (ADKG)
Tb927.9.8450
AGOF: ATP binding, adenylate kinase activity, cytidylate kinase activity, uridylate kinase activity
AGOC: null
AGOP: nucleobase–containing compound metabolic process, nucleobase–containing small molecule interconversion
PGOF: ATP binding, nucleobase–containing compound kinase activity
PGOC: null
PGOP: nucleobase–containing compound metabolic process





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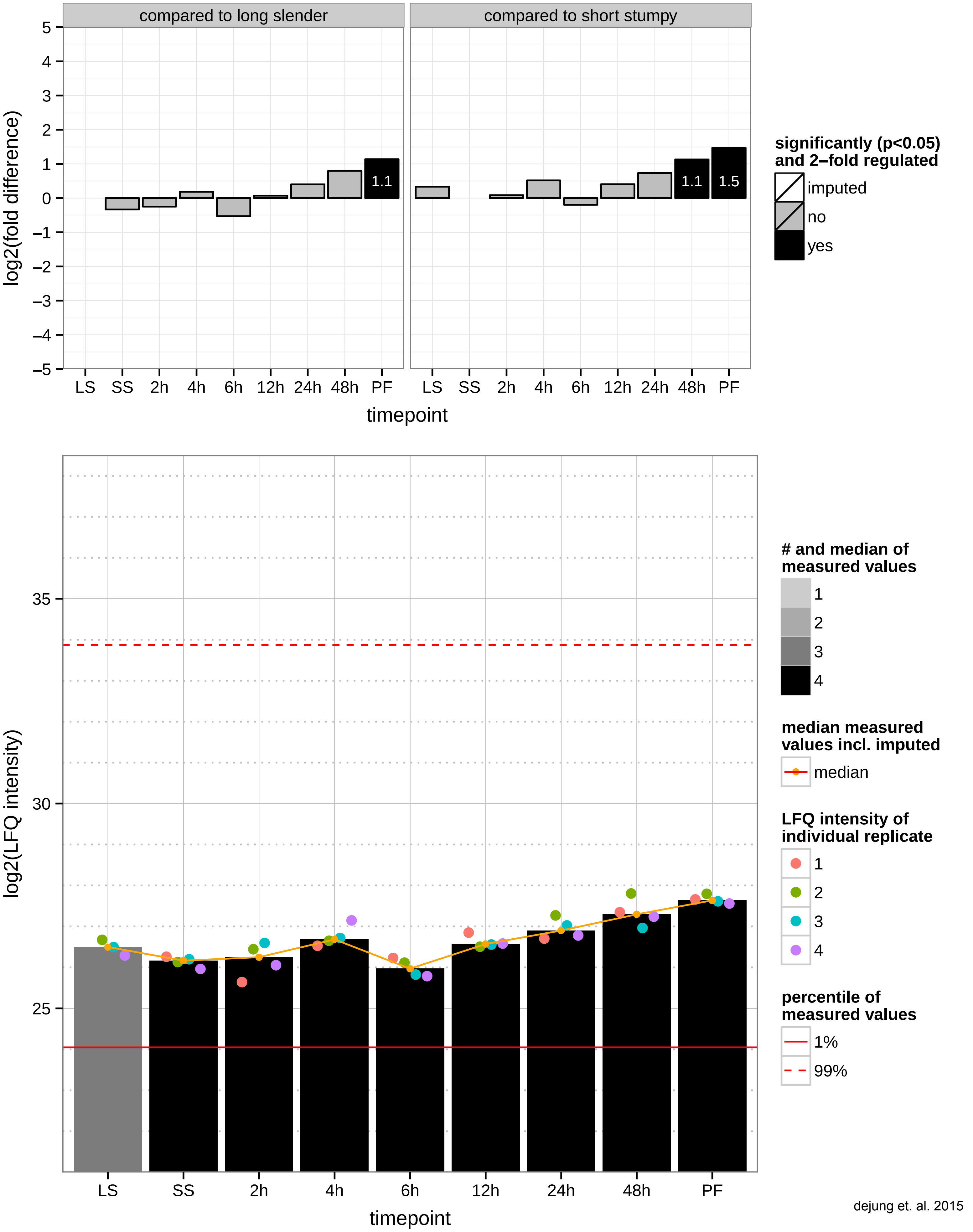
hypothetical protein, conserved
Tb927.9.8520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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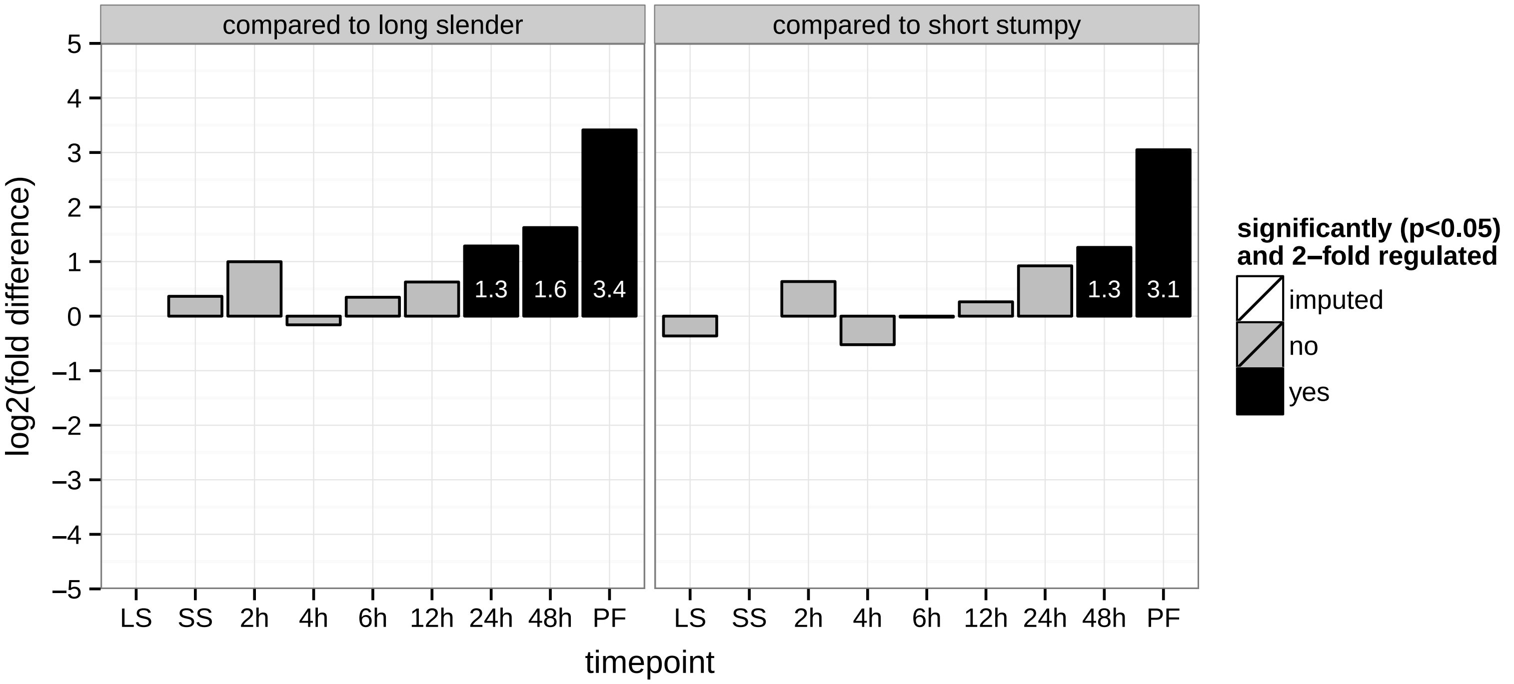
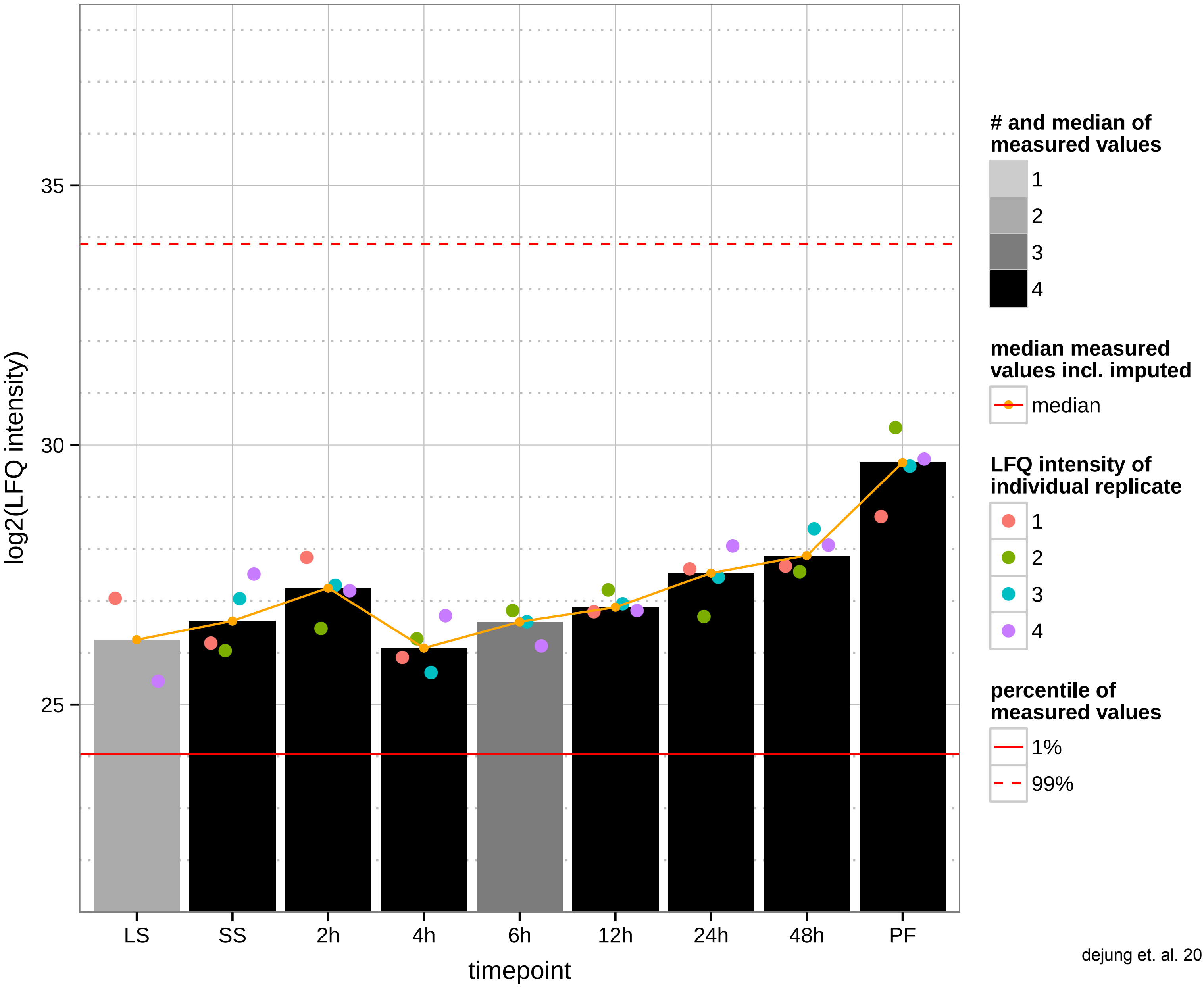
isopentenyl–diphosphate delta–isomerase (type II) (idi1)
Tb927.9.9000
AGOF: FMN binding, oxidoreductase activity
AGOC: cytoplasm
AGOP: isoprenoid biosynthetic process
PGOF: FMN binding, isopentenyl–diphosphate delta–isomerase activity, oxidoreductase activity
PGOC: cytoplasm
PGOP: isoprenoid biosynthetic process





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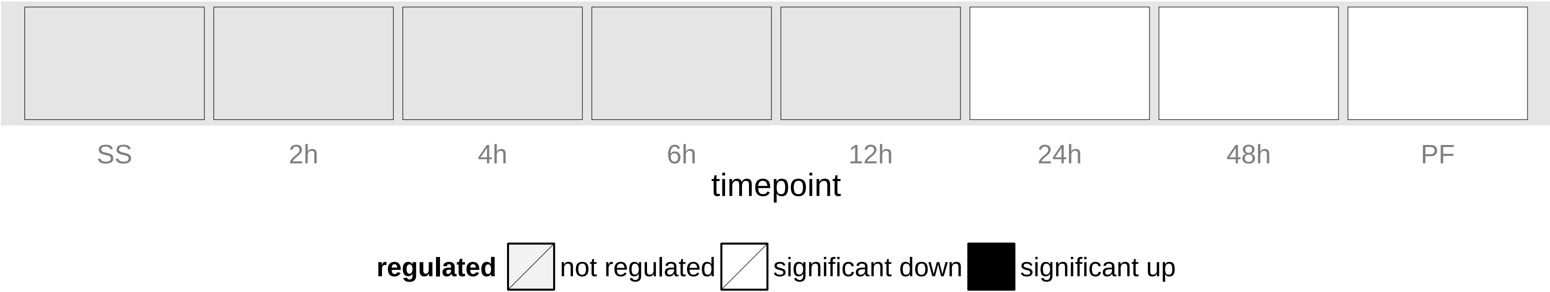

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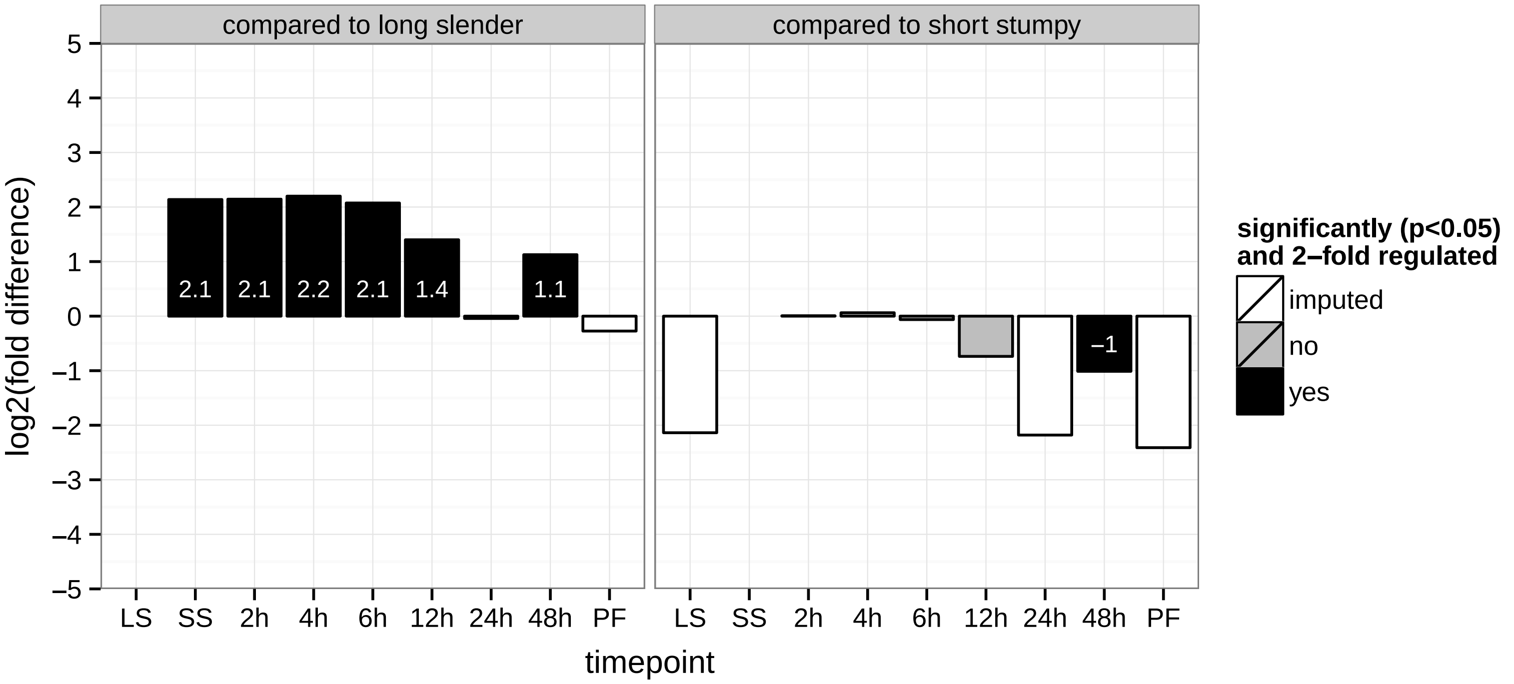
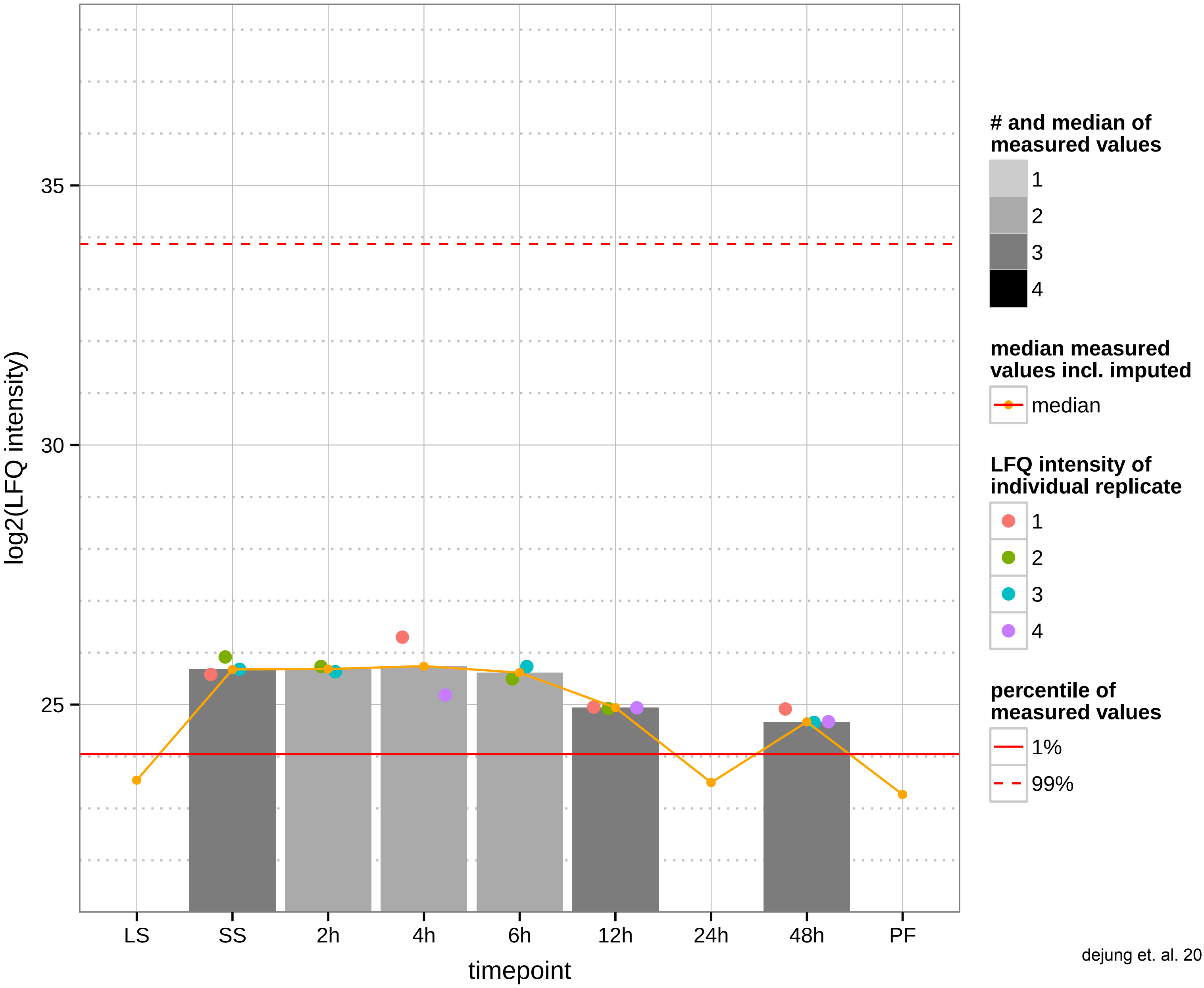
expression site‒ associated gene (ESAG) protein, putative, expression site associated gene 5 (ESAG5) protein, chrIX additior
Tb927.9.15890;Tb11.v5.0463;Tb09.v4.0016
AGOF: lipid binding, null
AGOC: null, plasma membrane
AGOP: null
PGOF: lipid binding
PGOC: null
PGOP: null





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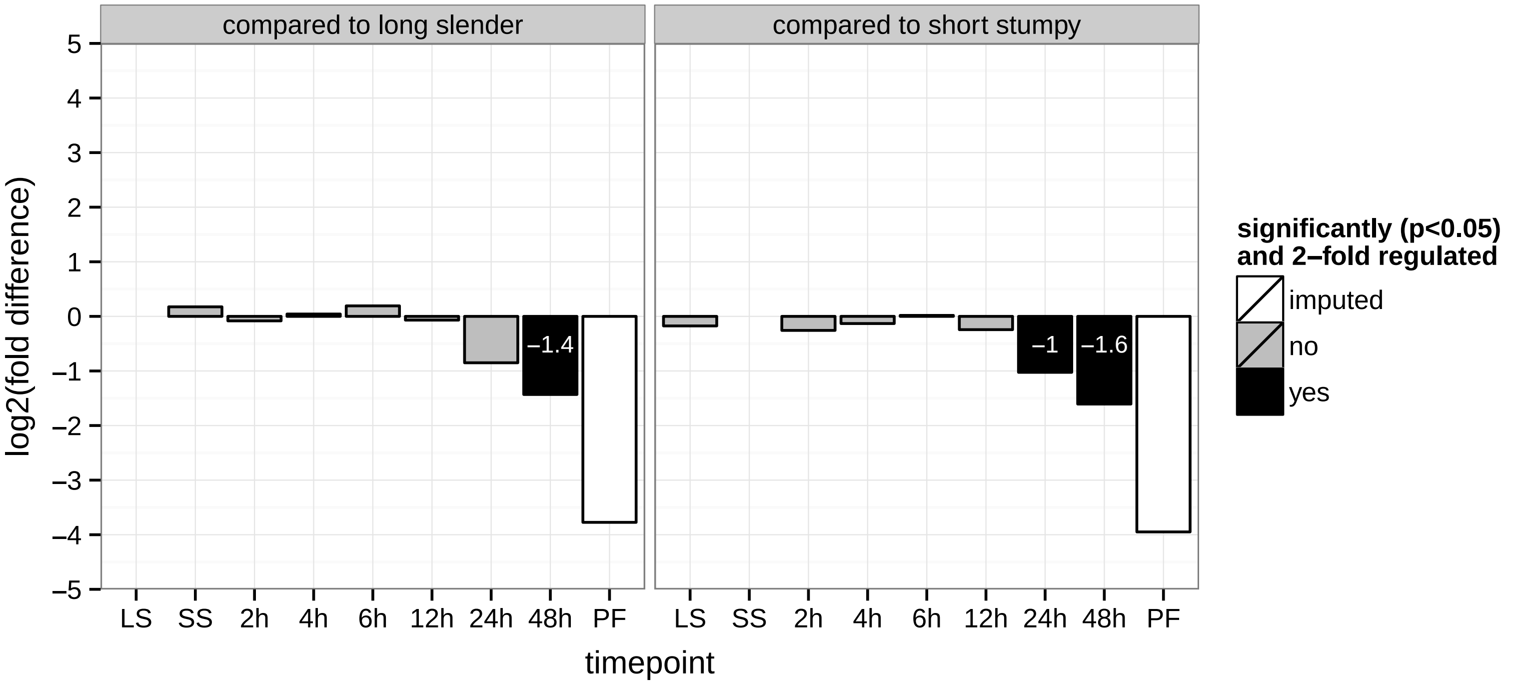
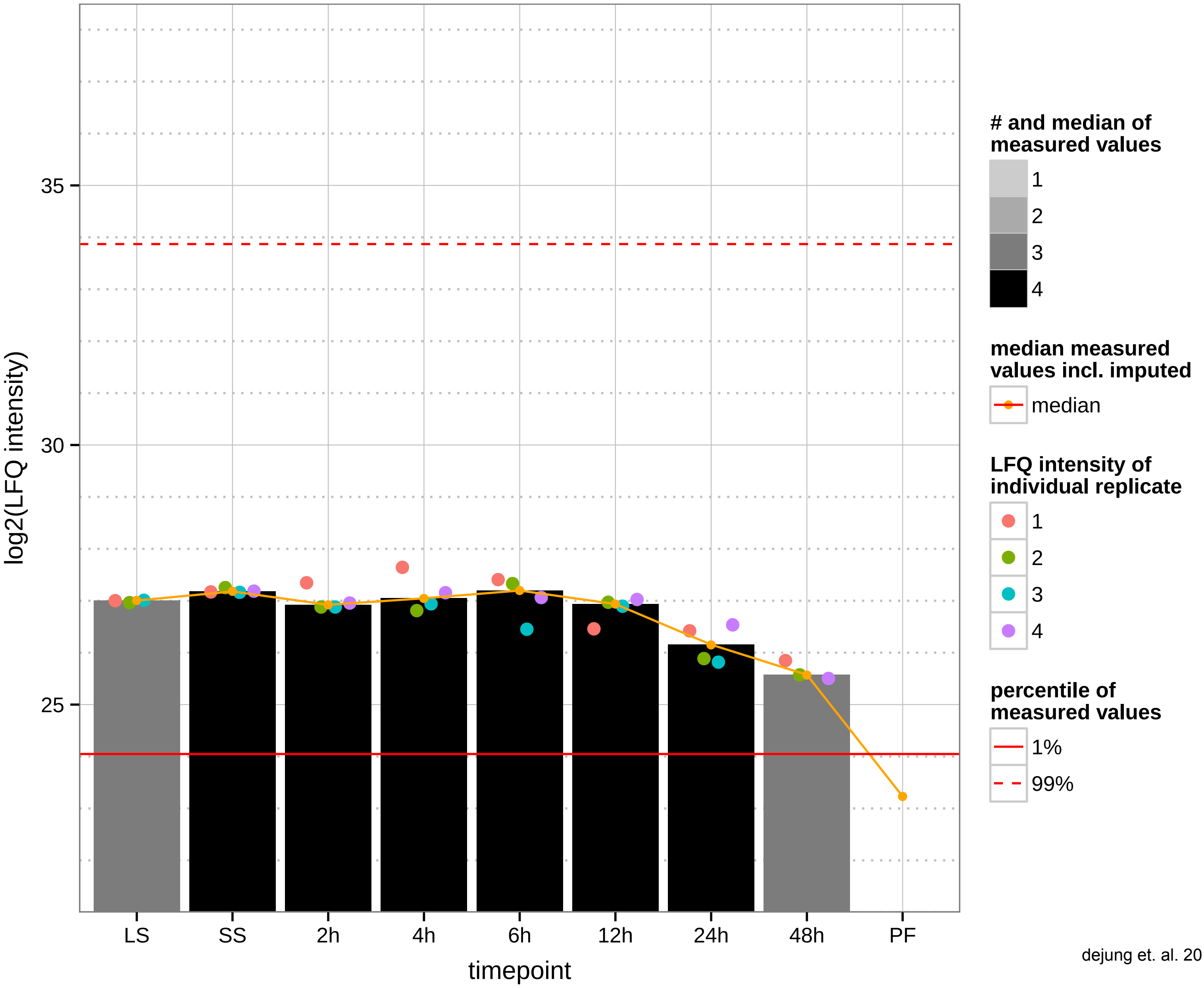
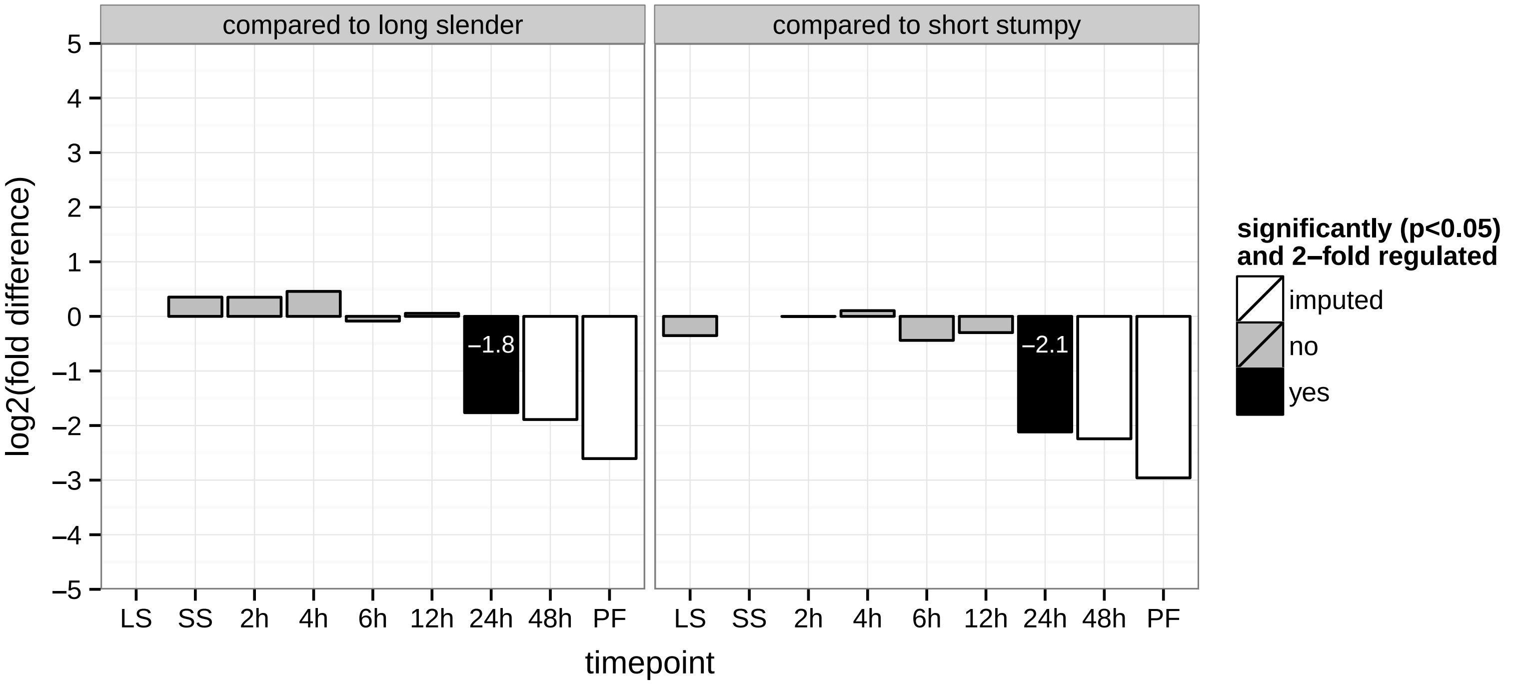
cell–division control protein 2 homolog 6, putative, protein kinase, cdc2–related kinase, putative (CRK6)
Tb927.11.1180;Tb11.v5.0387
AGOF: null, ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null, growth, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

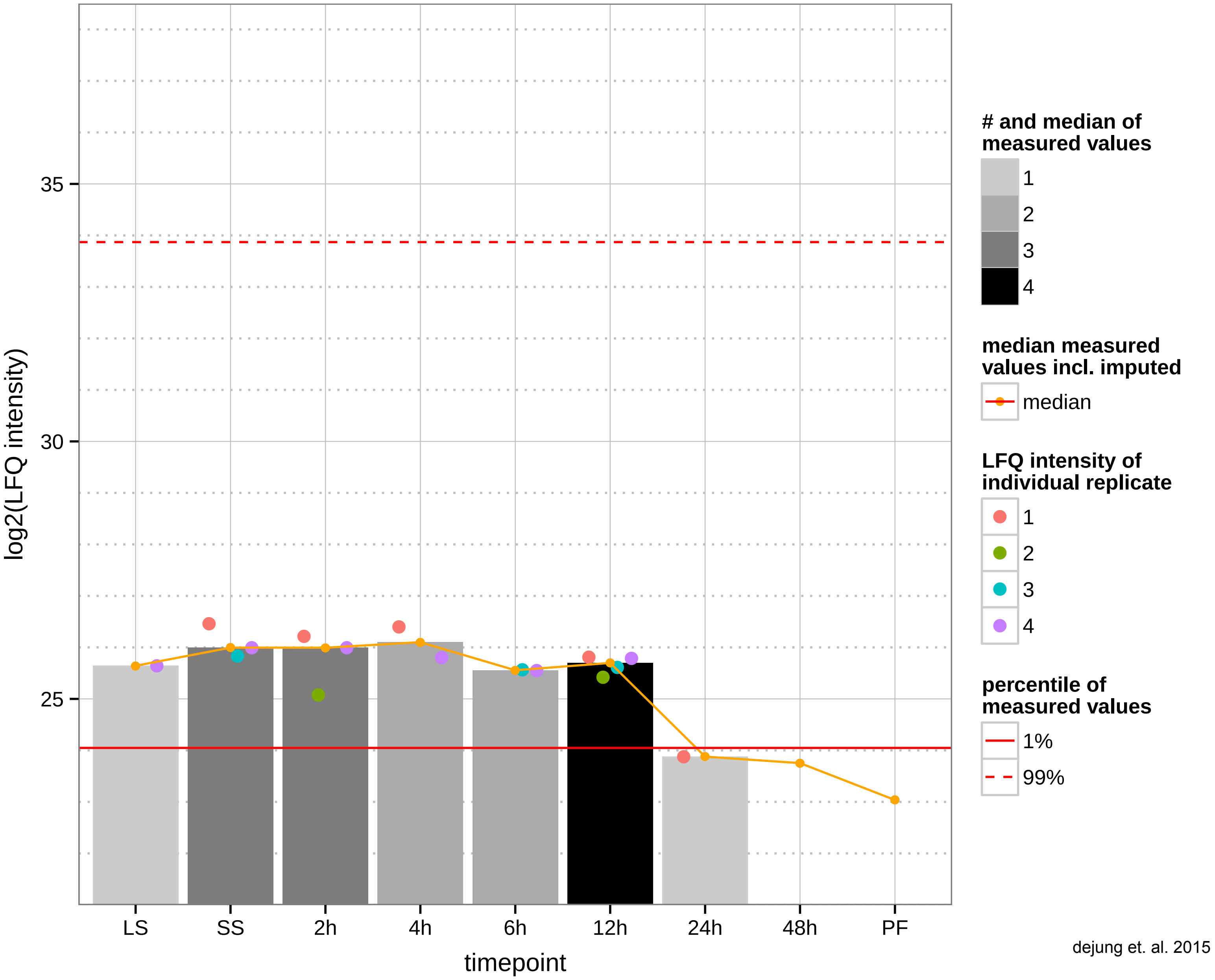




dejung et. al. 2015

glycerol uptake protein, putative
Tb927.10.15910;Tb11.v5.0406
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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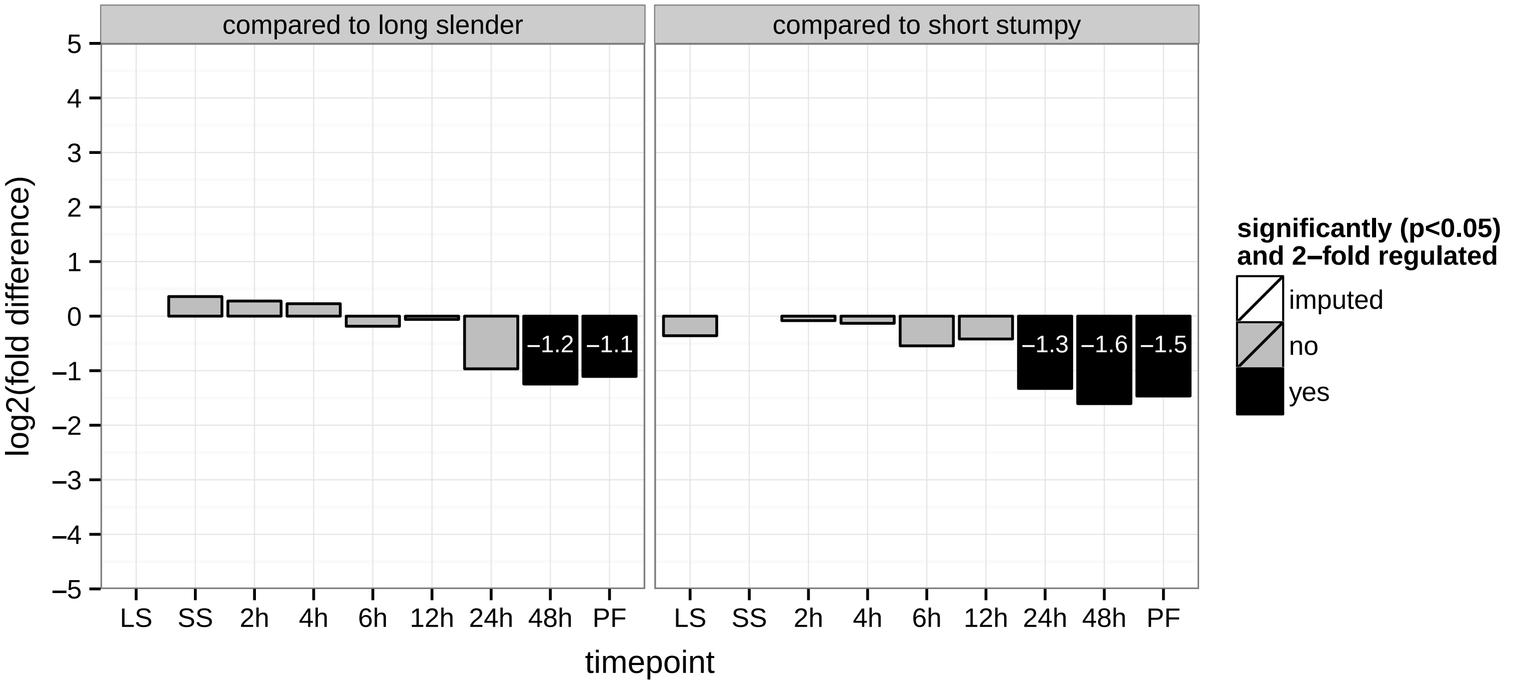
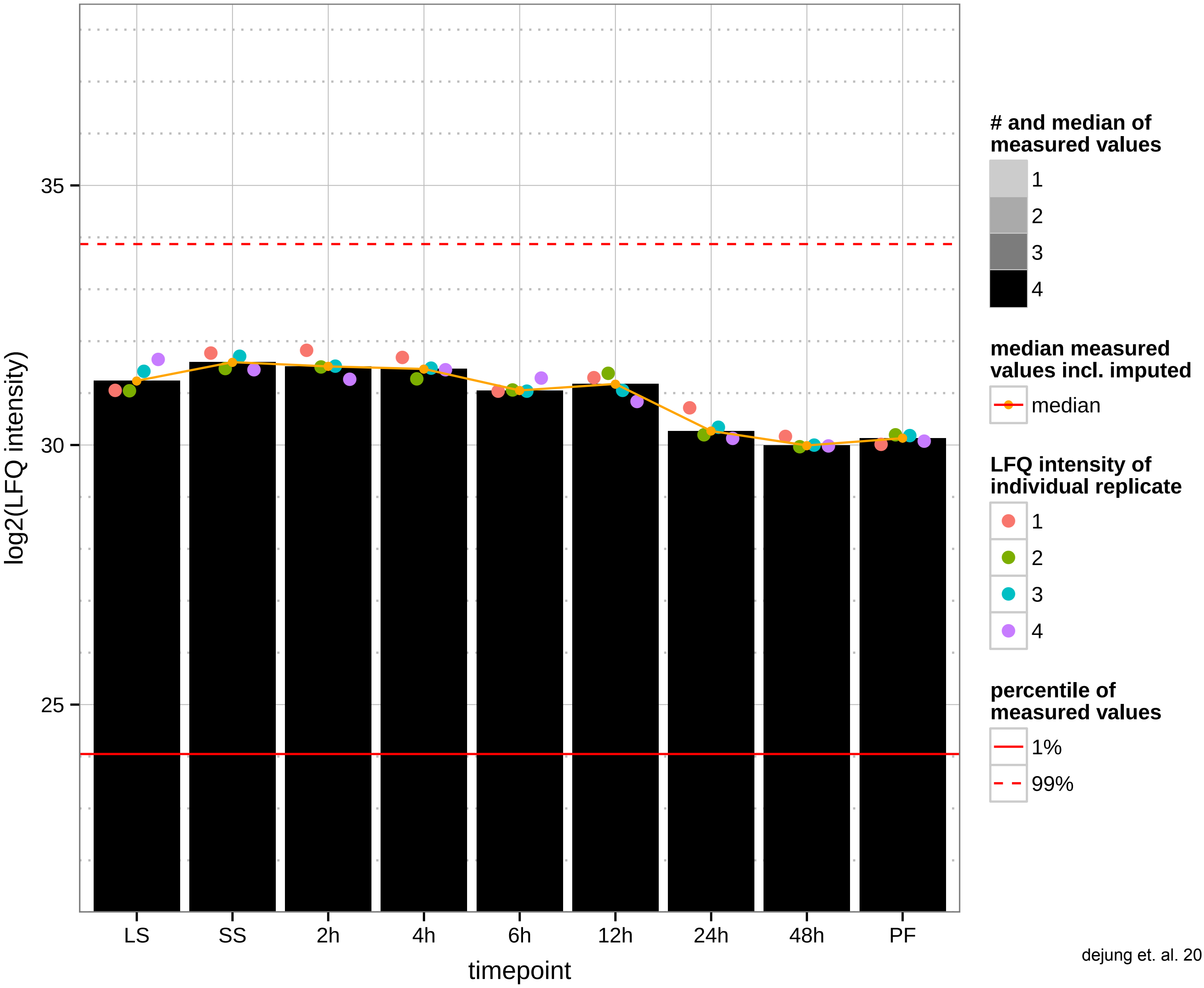
protein kinase A regulatory subunit, putative, protein kinase A regulatory subunit (PKA–R)
Tb927.11.4610;Tb11.v5.0587
AGOF: null, cAMP–dependent protein kinase regulator activity
AGOC: null, cAMP–dependent protein kinase complex
AGOP: null, intracellular signal transduction, modulation of development of symbiont involved in interaction with host, protein p
PGOF: null
PGOC: null
PGOP: null





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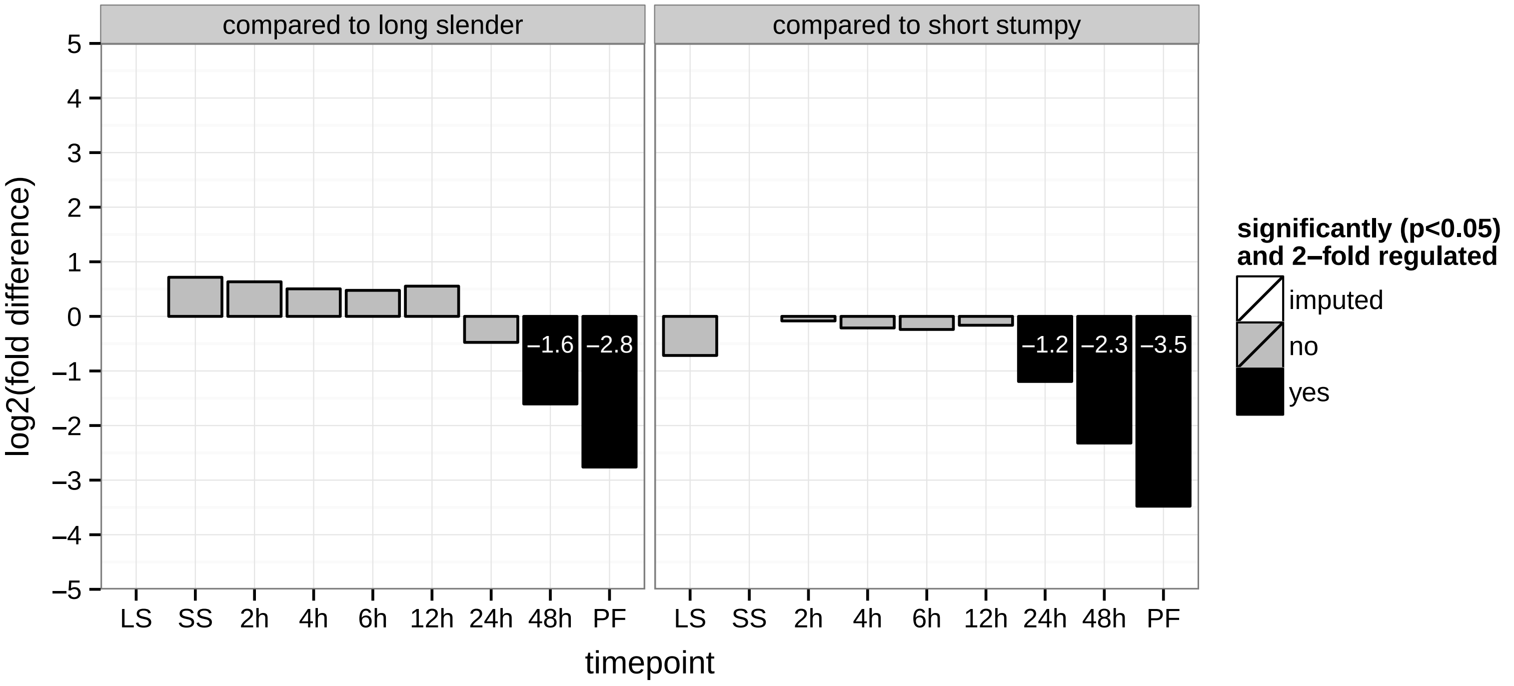
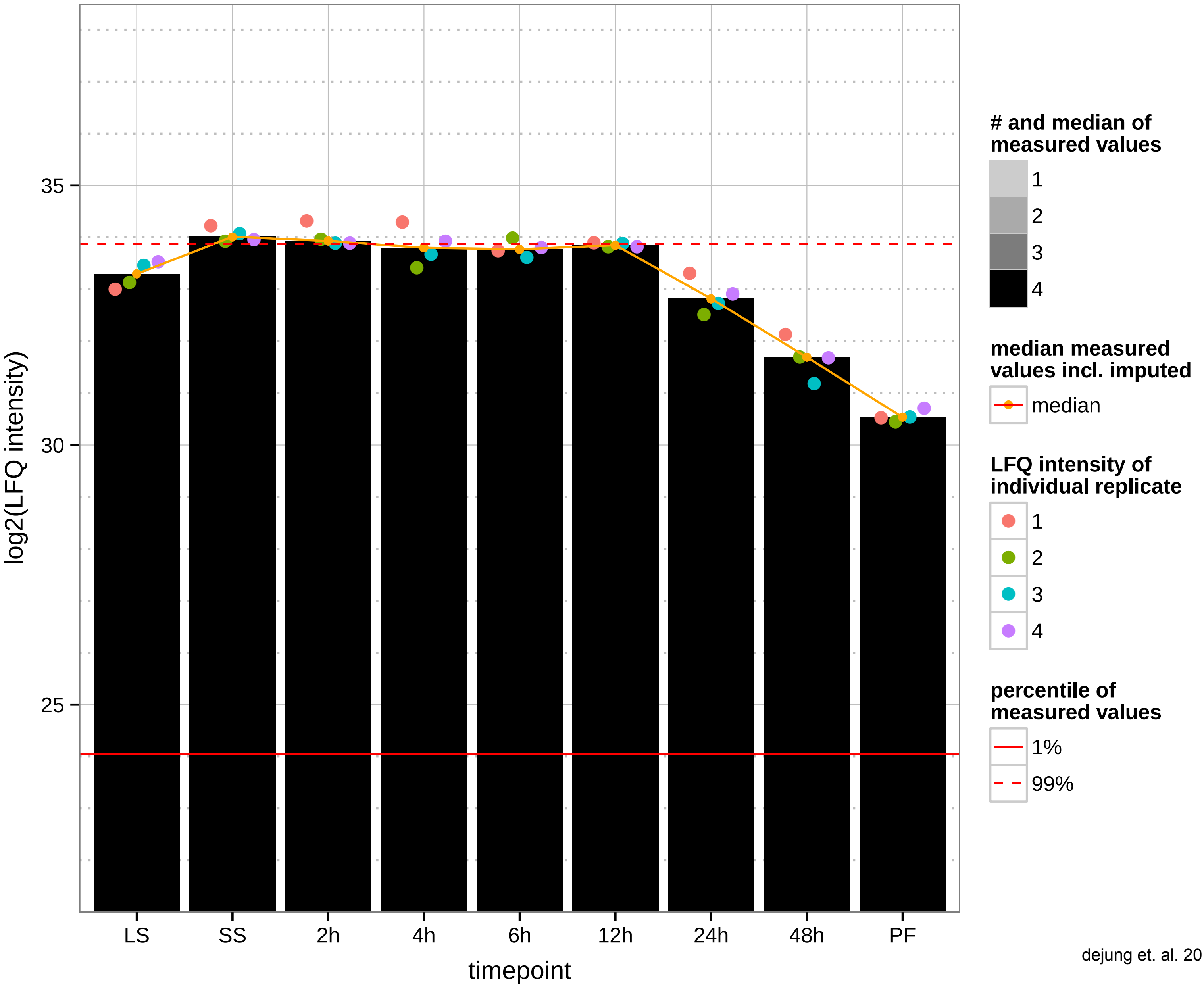
kinesin, putative, C–terminal motor kinesin, putative (TBKIFC1)
Tb927.10.14890;Tb11.v5.0636
AGOF: null, ATP binding, microtubule motor activity, motor activity
AGOC: null, cytoplasm, cytoplasmic microtubule, kinesin complex, kinesin complex, microtubule associated complex
AGOP: null, intracellular protein transport, microtubule–based movement, microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement, intracellular protein transport, microtubule–based movement





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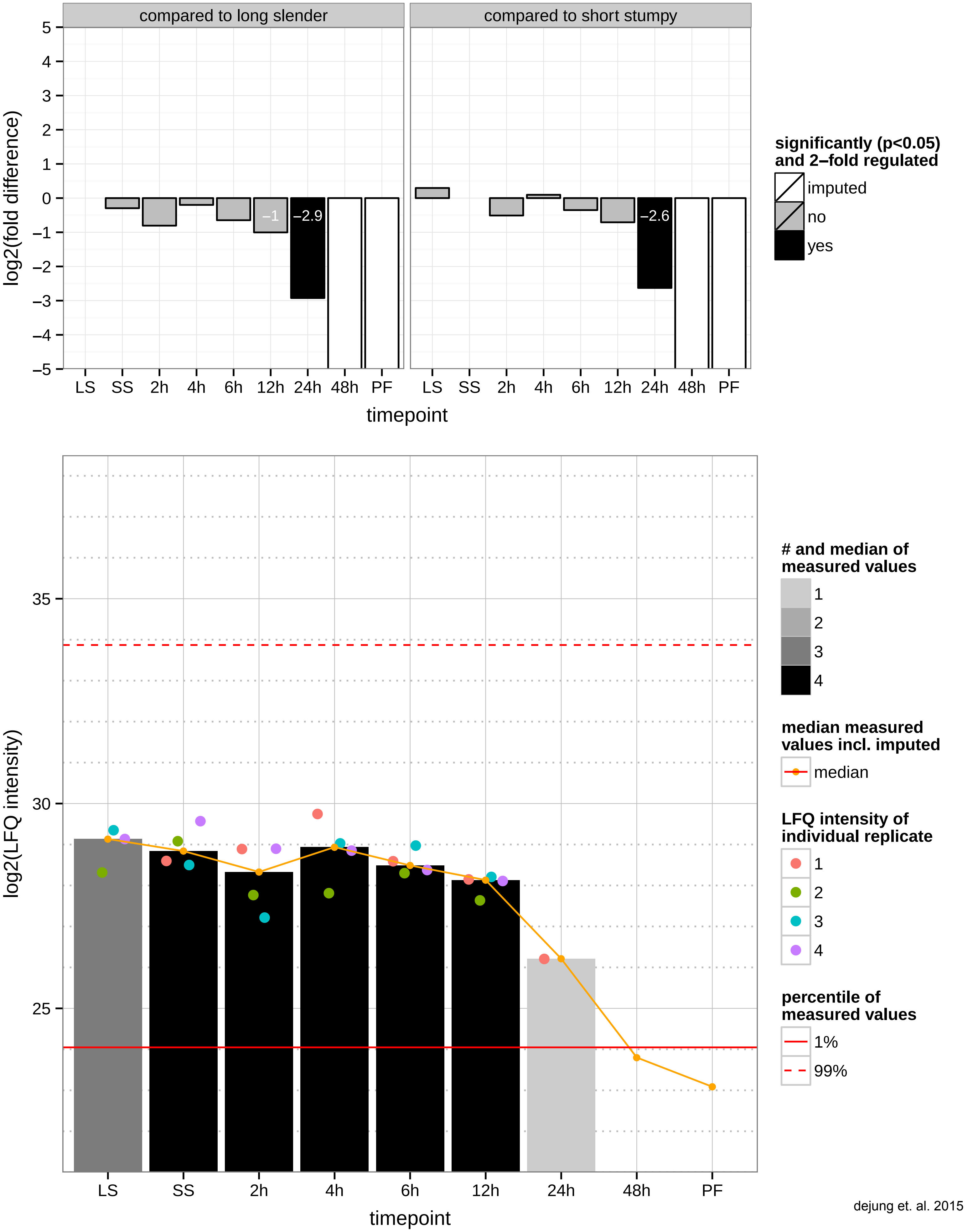
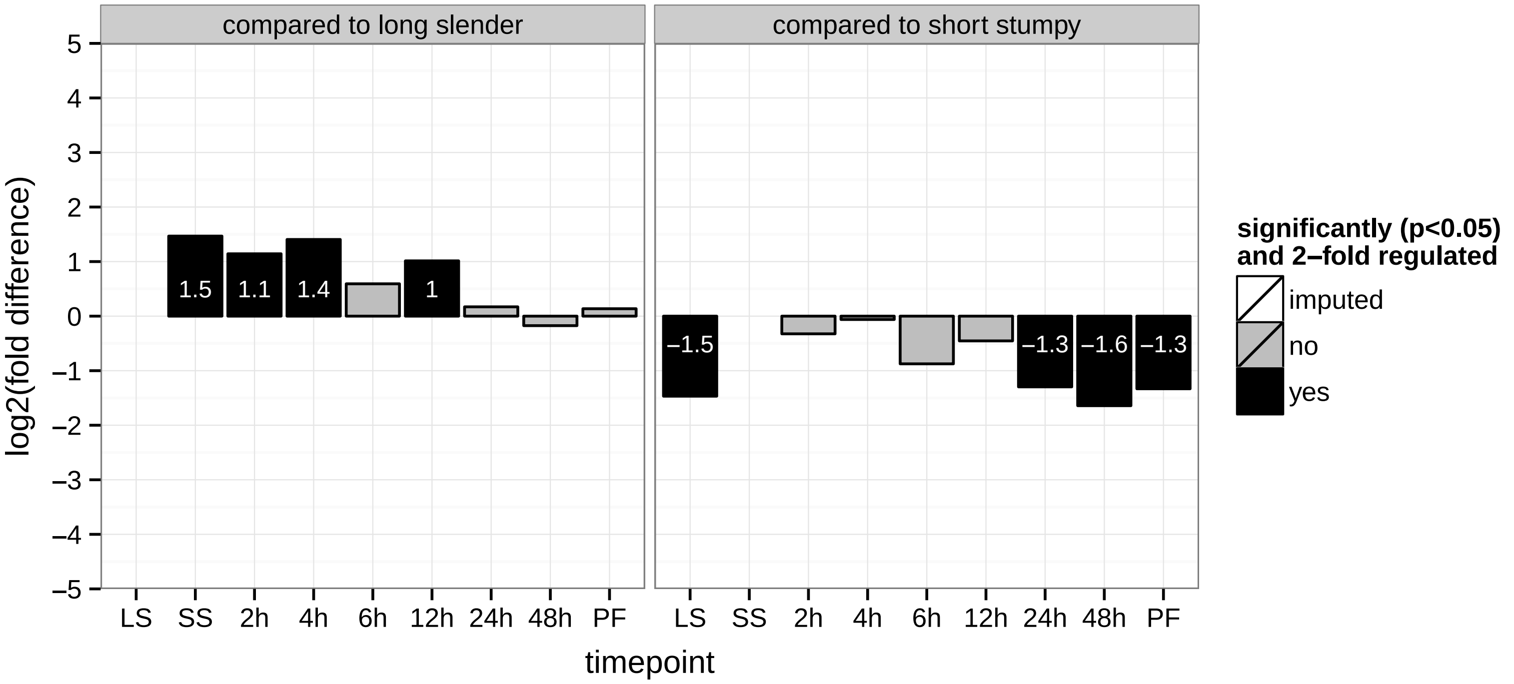
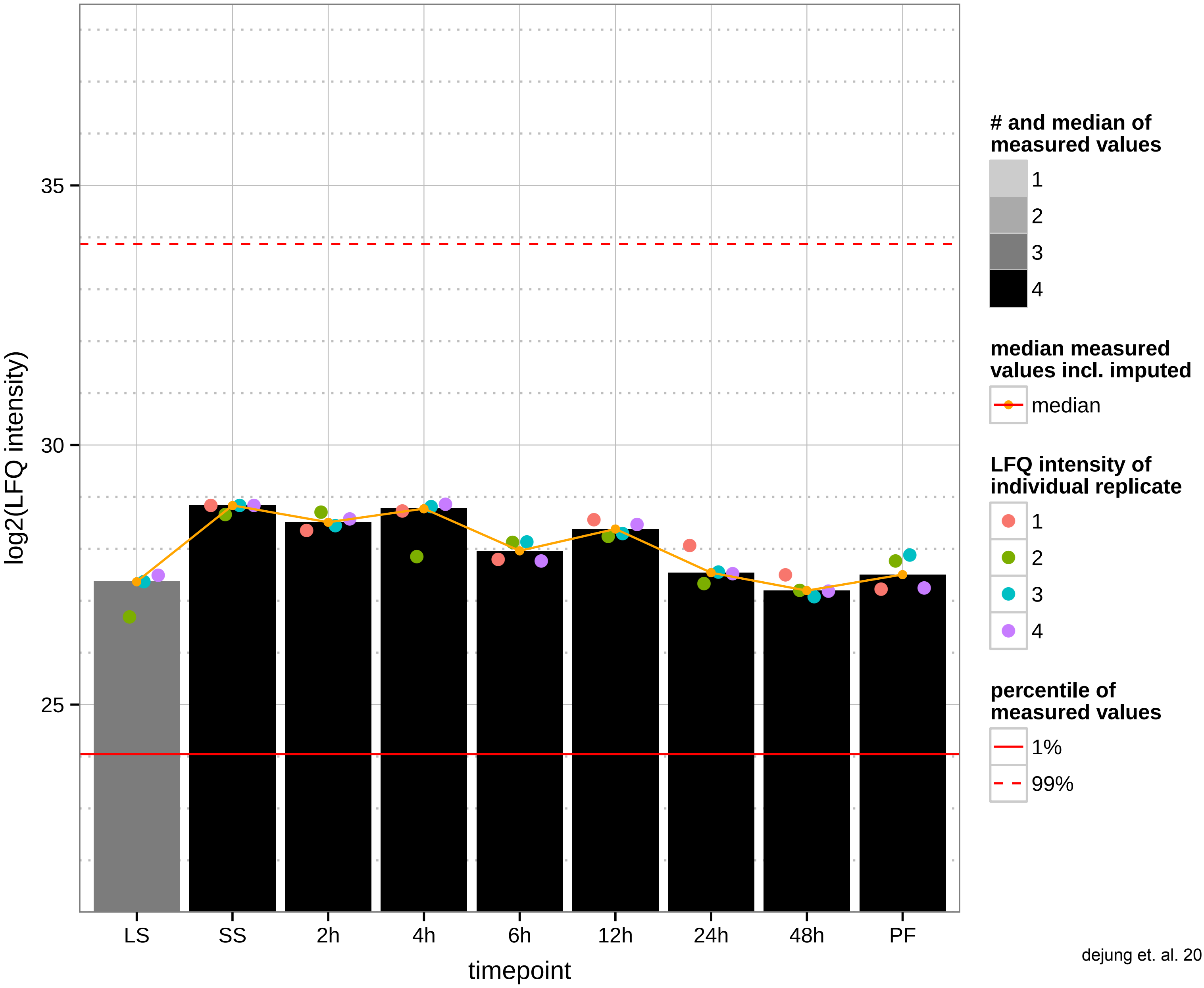
expression site–associated gene (ESAG) protein, putative, expression site–associated gene 5 (ESAG5) protein
Tb11.v5.0826;Tb927.7.6860
AGOF: null, lipid binding
AGOC: null
AGOP: null
PGOF: lipid binding
PGOC: null
PGOP: null



dejung et. al. 2015

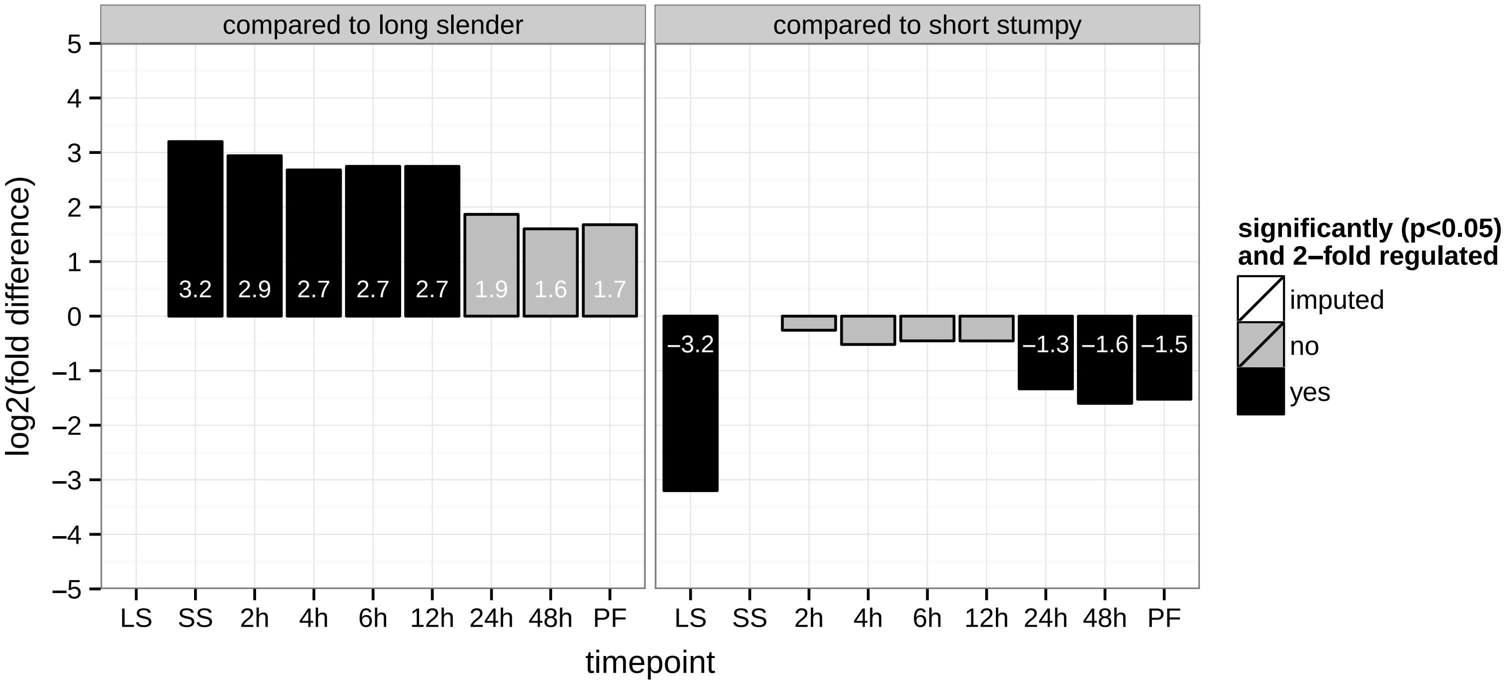
aminoacylase, putative, N–acyl–L–amino acid amidohydrolase
Tb927.1.3000
AGOF: hydrolase activity, metallopeptidase activity, protein dimerization activity
AGOC: null
AGOP: proteolysis
PGOF: hydrolase activity
PGOC: null
PGOP: metabolic process

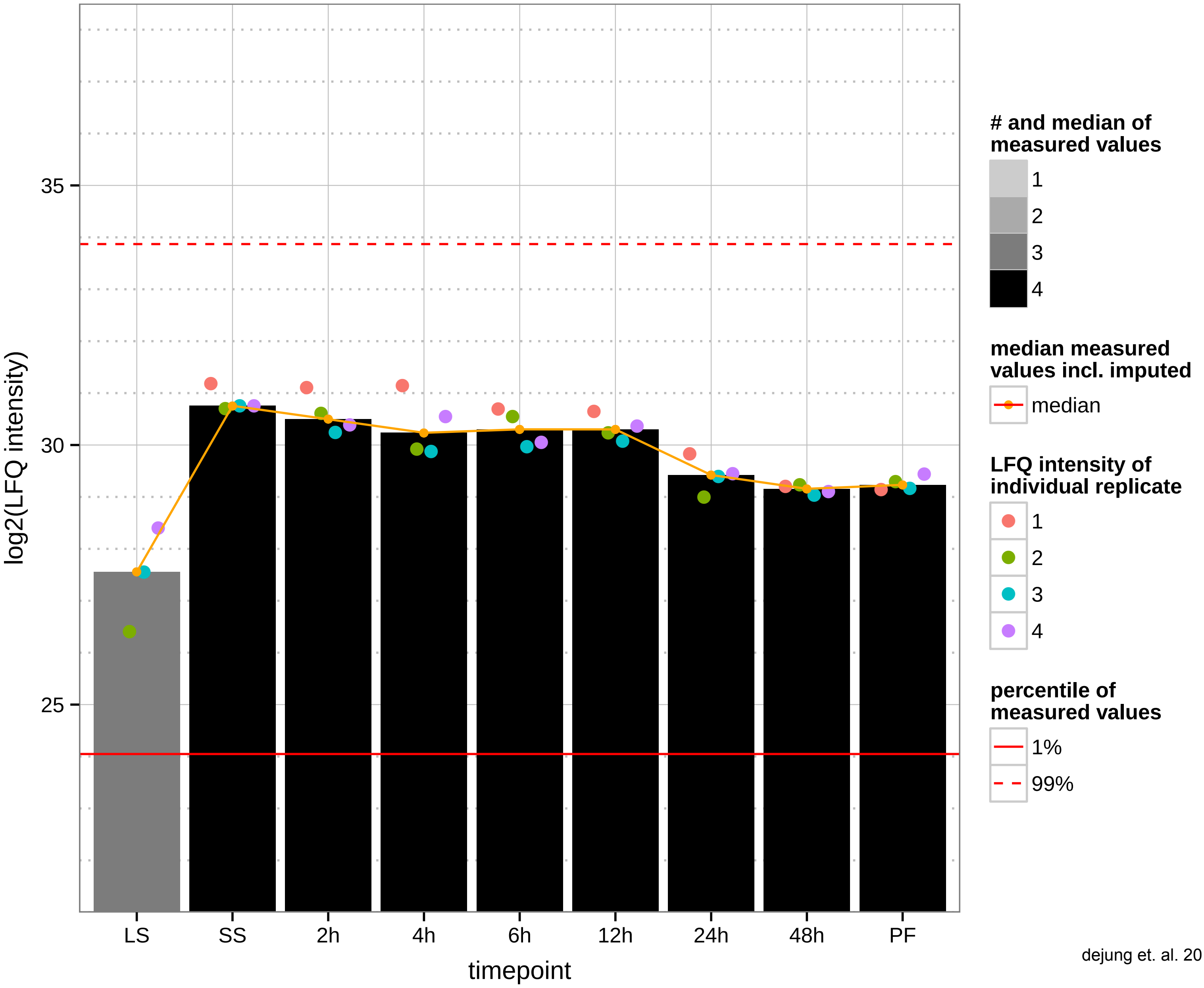




dejung et. al. 2015

hypothetical protein, conserved
Tb927.1.3260
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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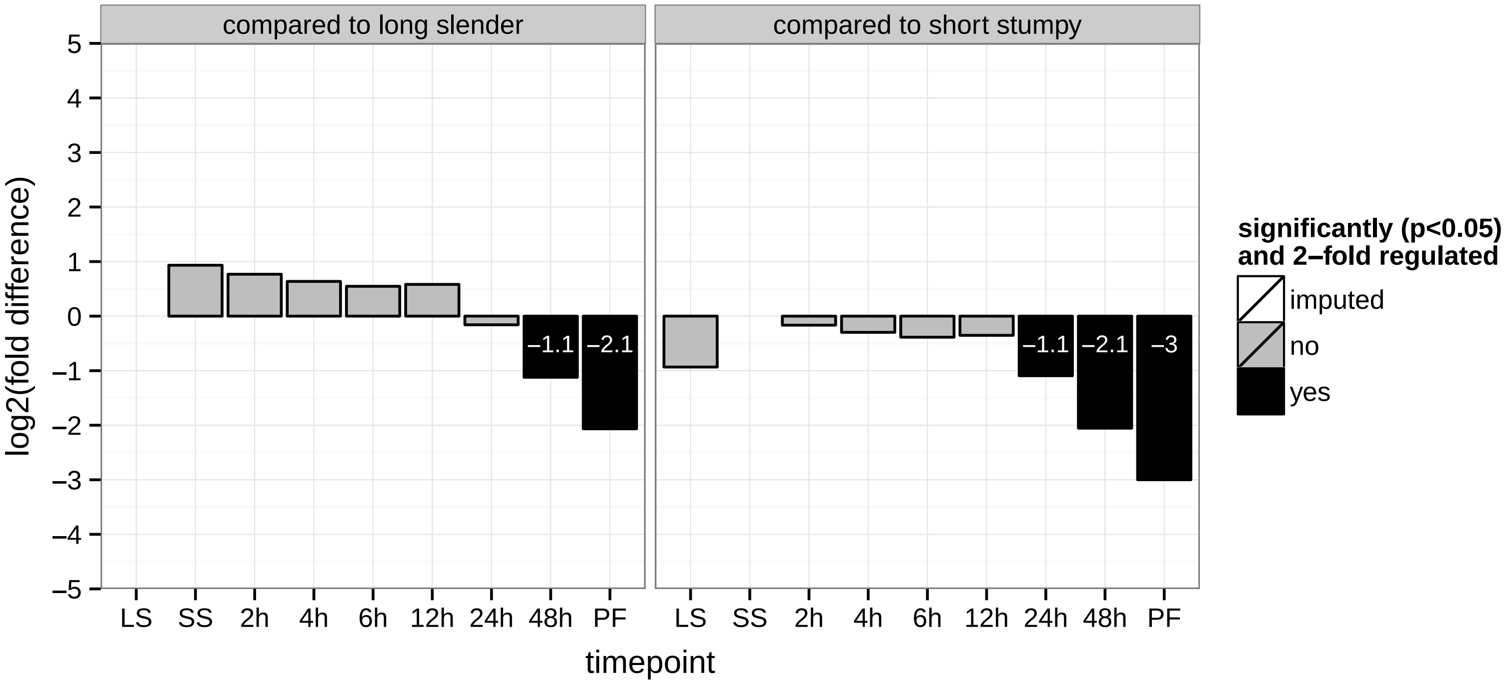
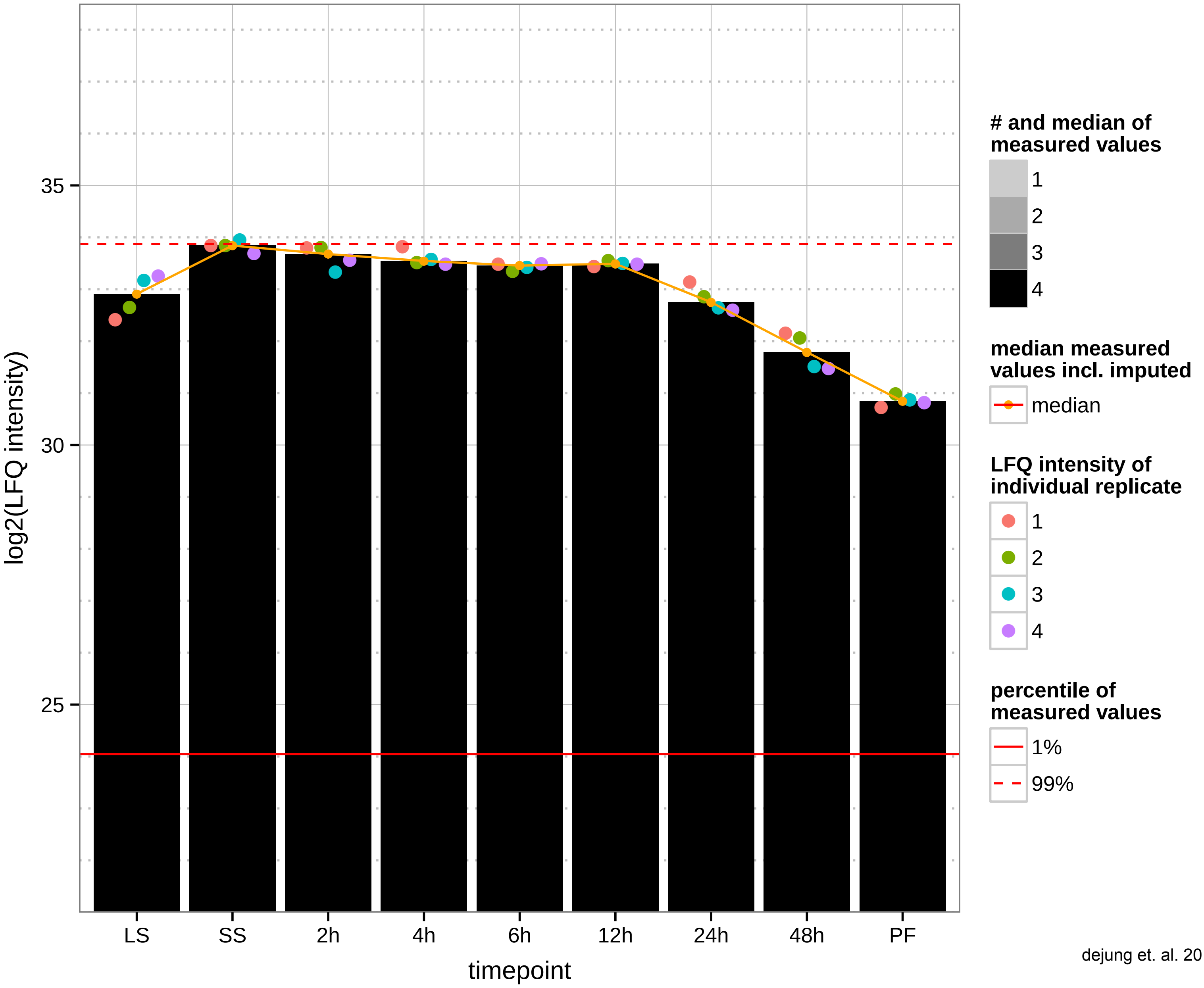
glucose–6–phosphate isomerase, glycosomal (PGI)
Tb927.1.3830
AGOF: glucose–6–phosphate isomerase activity
AGOC: glycosome
AGOP: gluconeogenesis, glycolysis
PGOF: glucose–6–phosphate isomerase activity
PGOC: null
PGOP: gluconeogenesis, glycolysis





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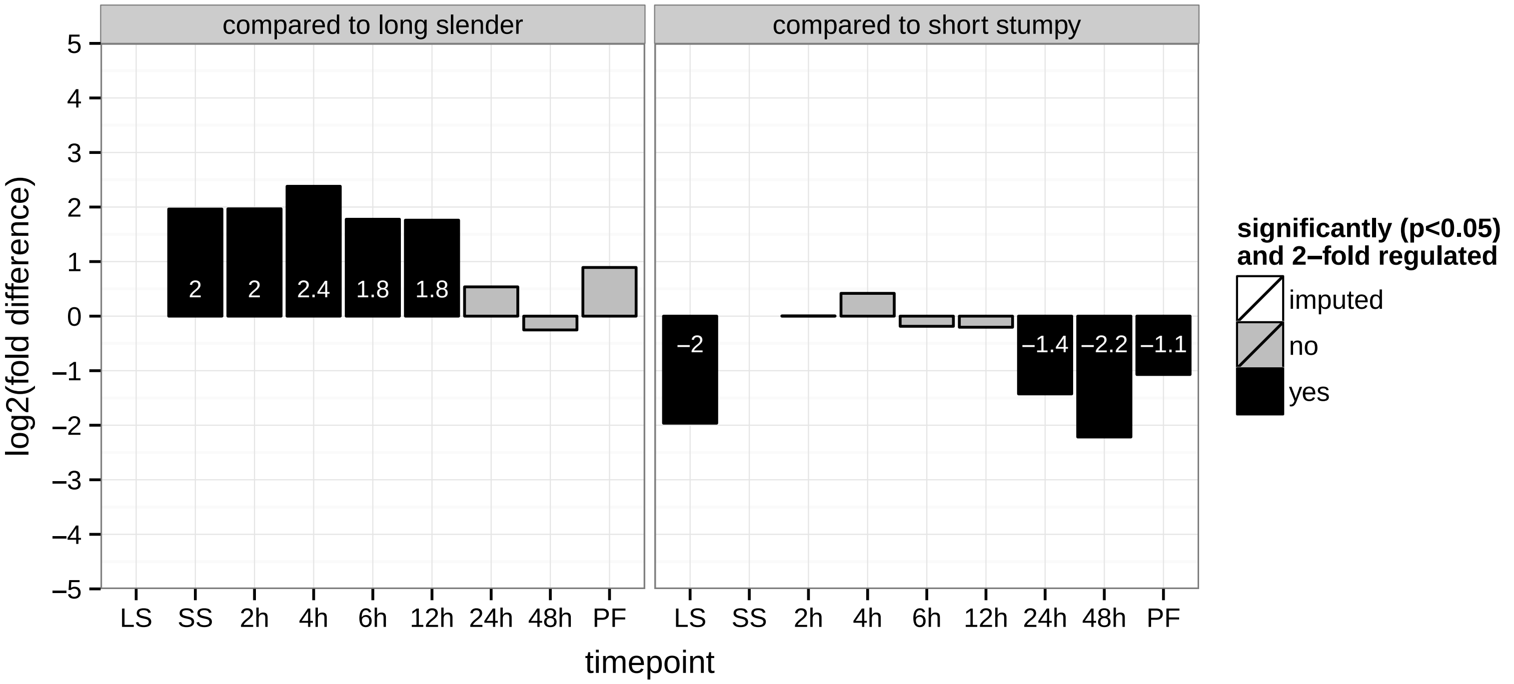
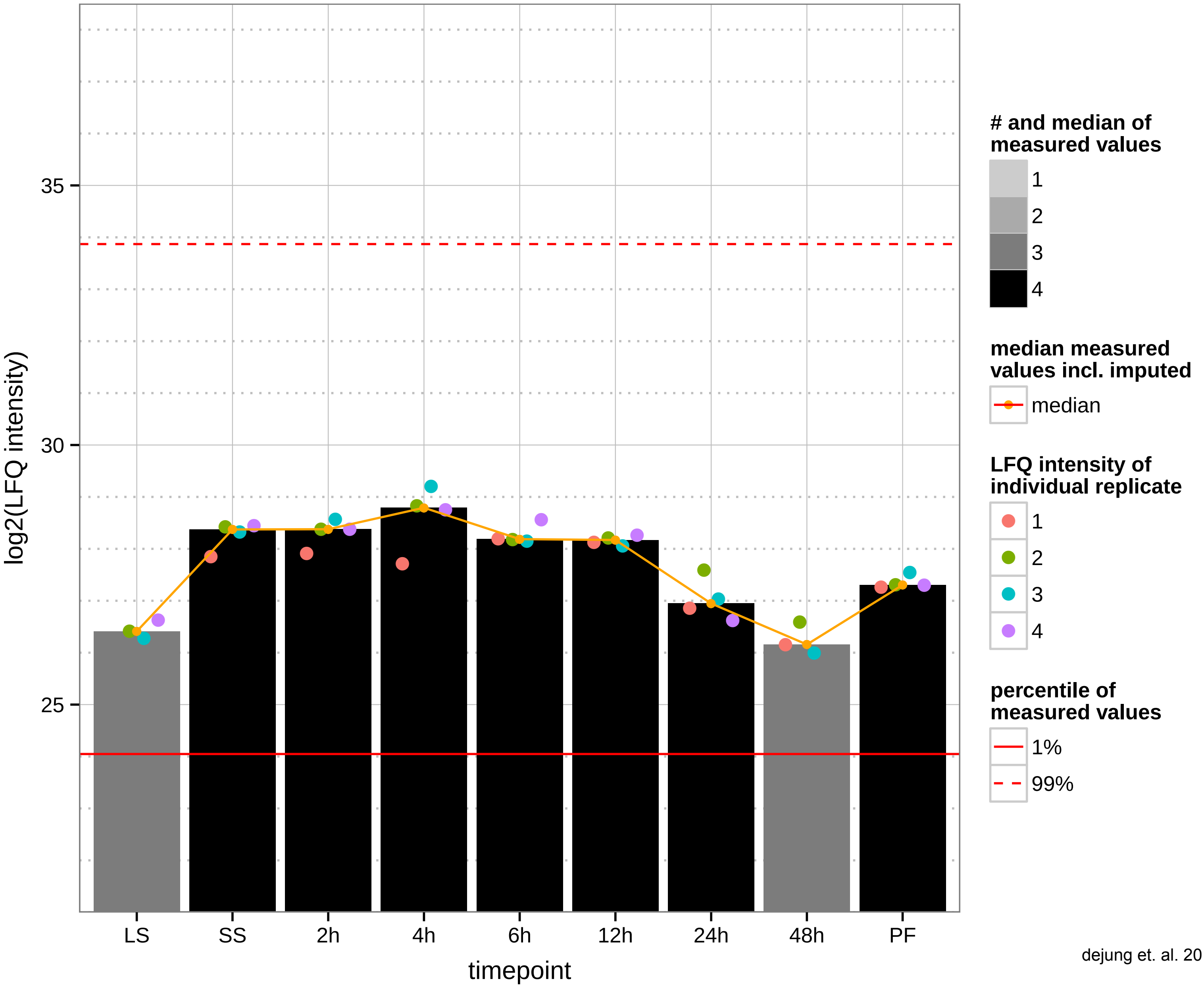
RNA–binding protein, putative (RBP7A)
Tb927.10.12090
AGOF: RNA binding
AGOC: null
AGOP: RNA processing, modulation of development of symbiont involved in interaction with host, quorum sensing involved in
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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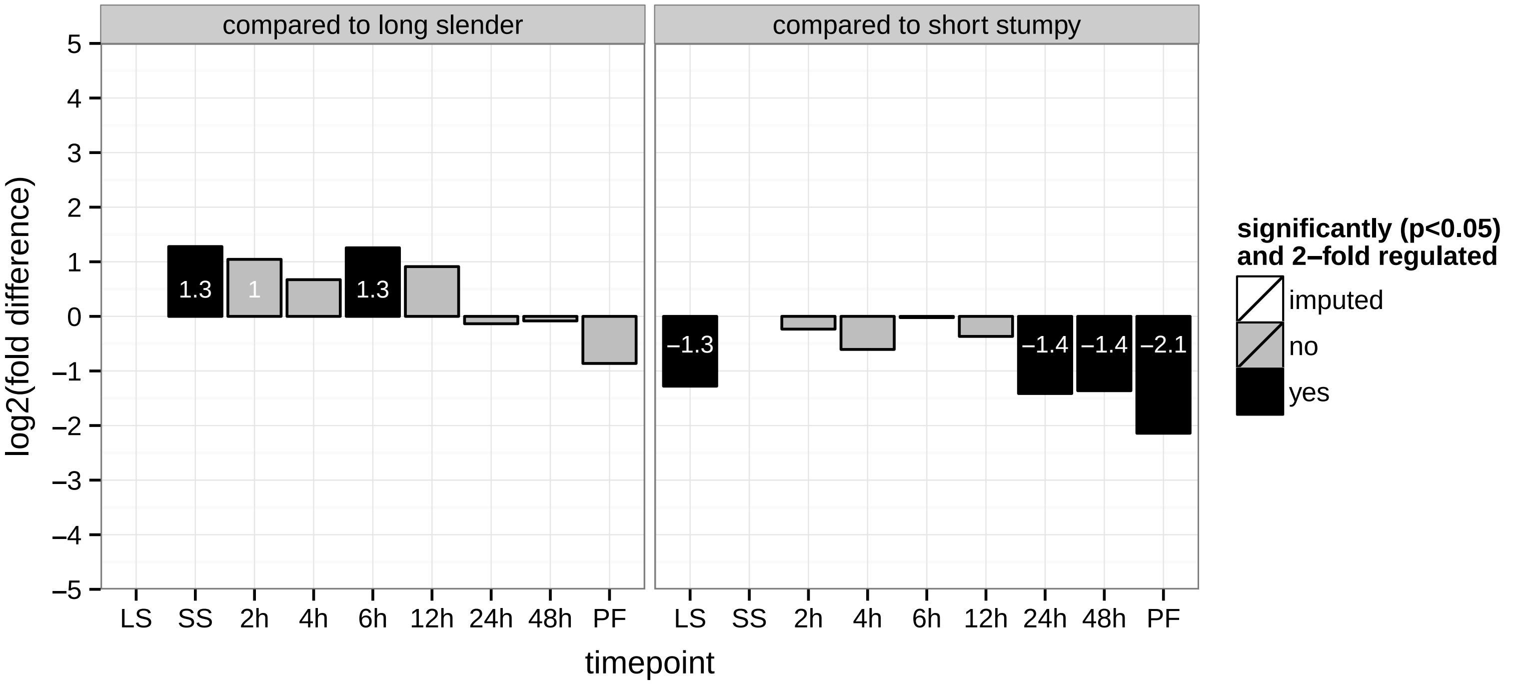
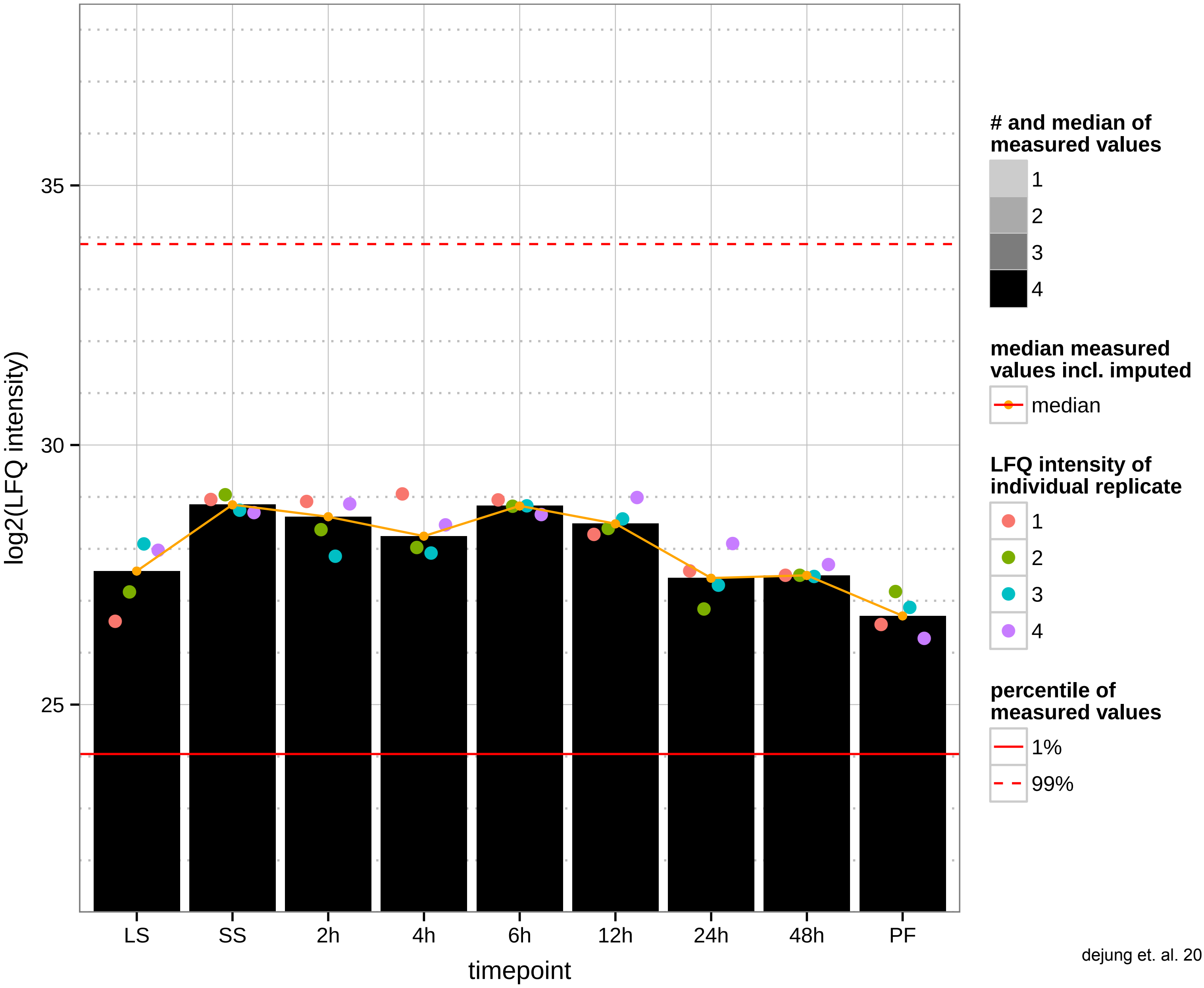
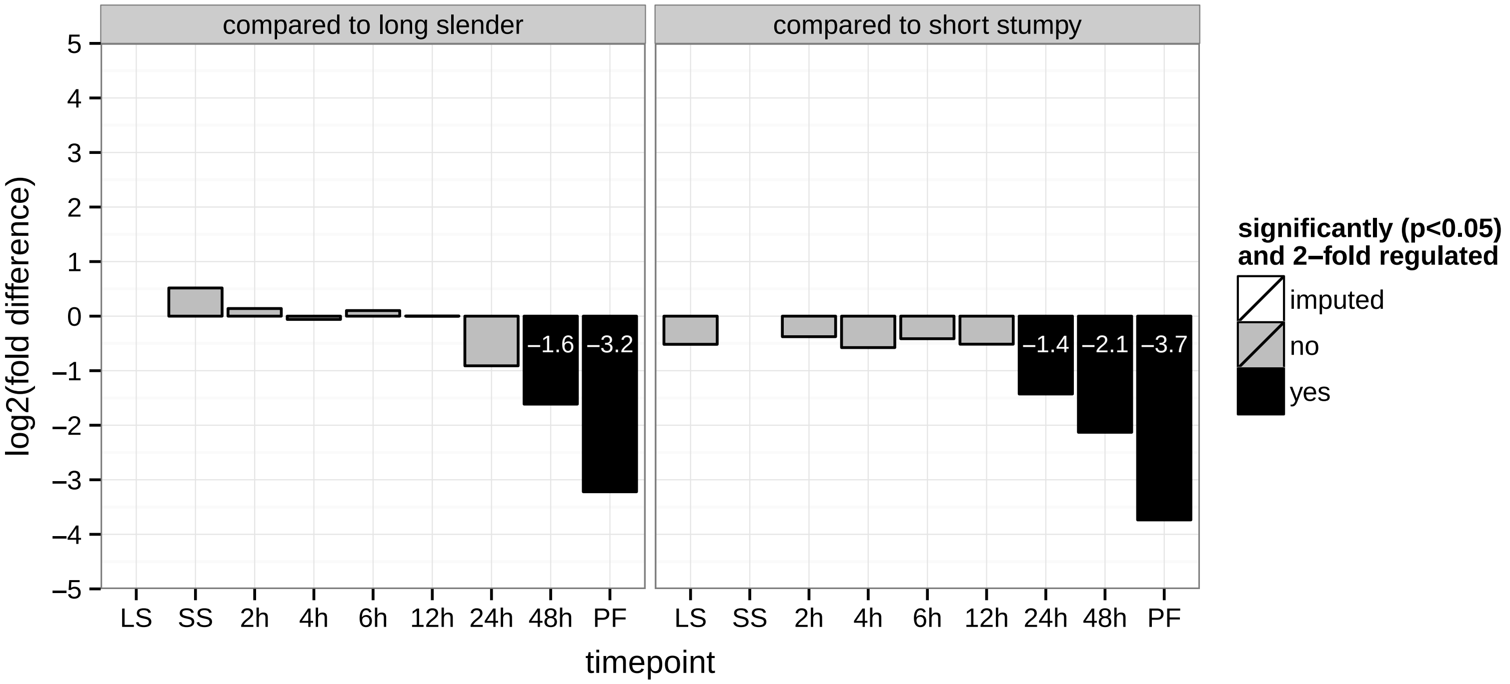
hypothetical protein, conserved
Tb927.10.12590
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

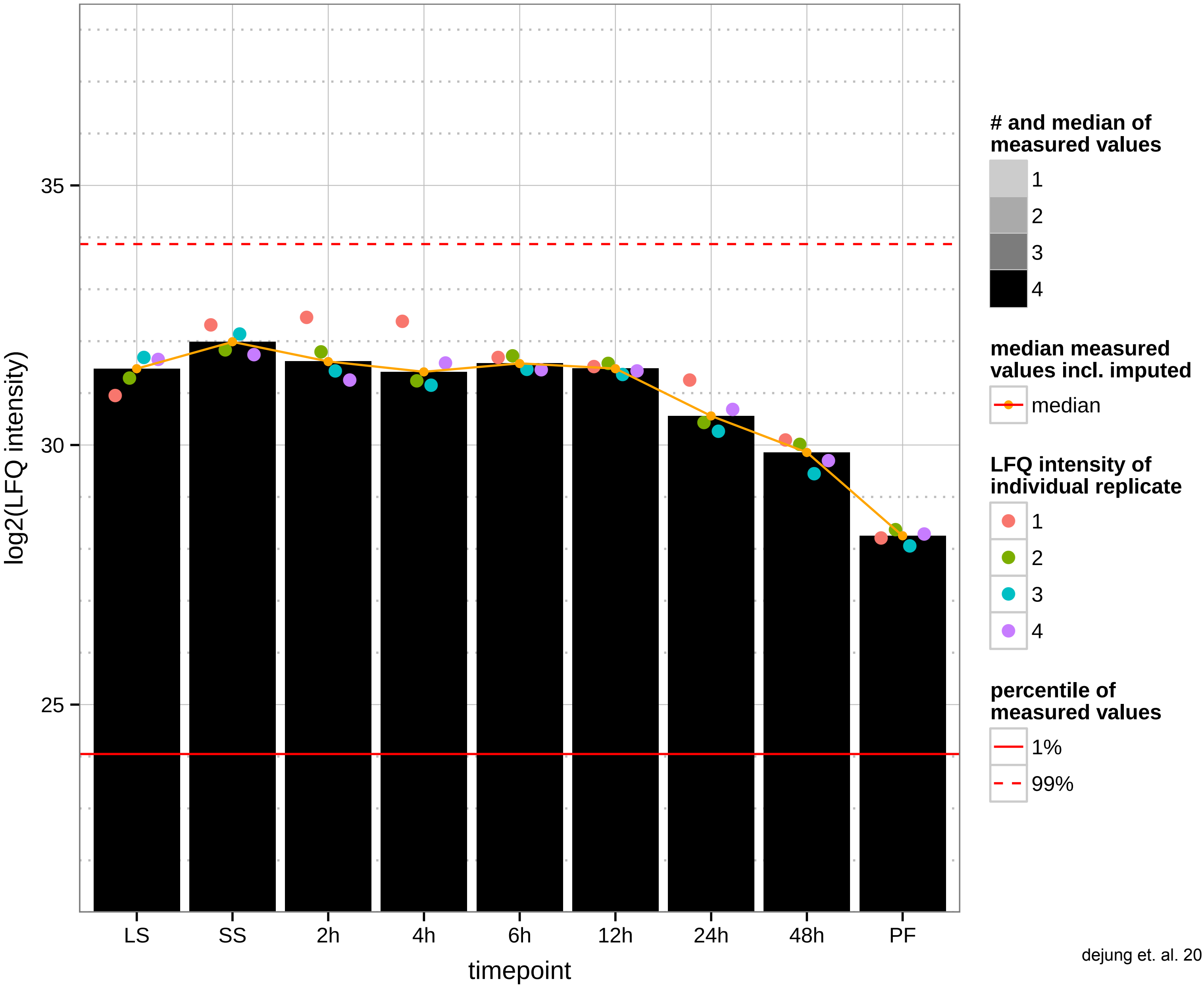




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.12820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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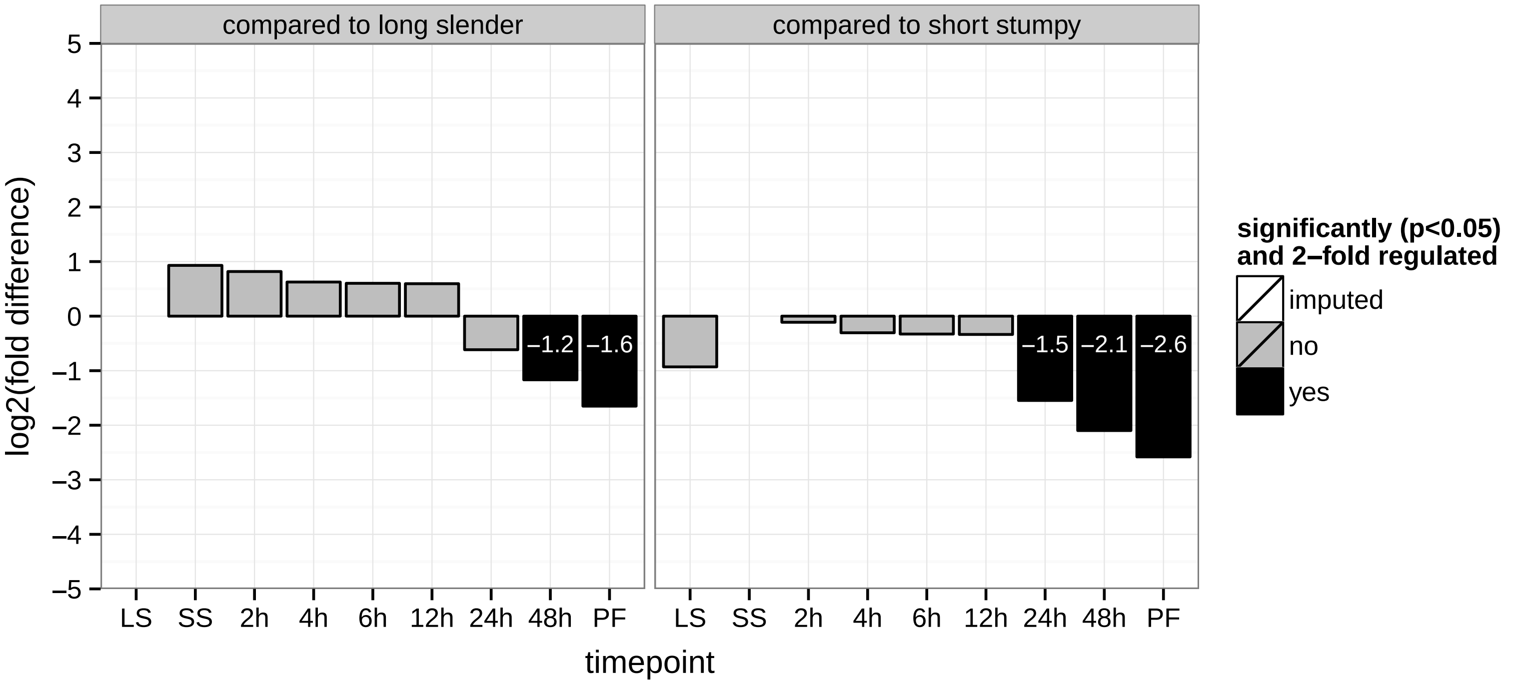
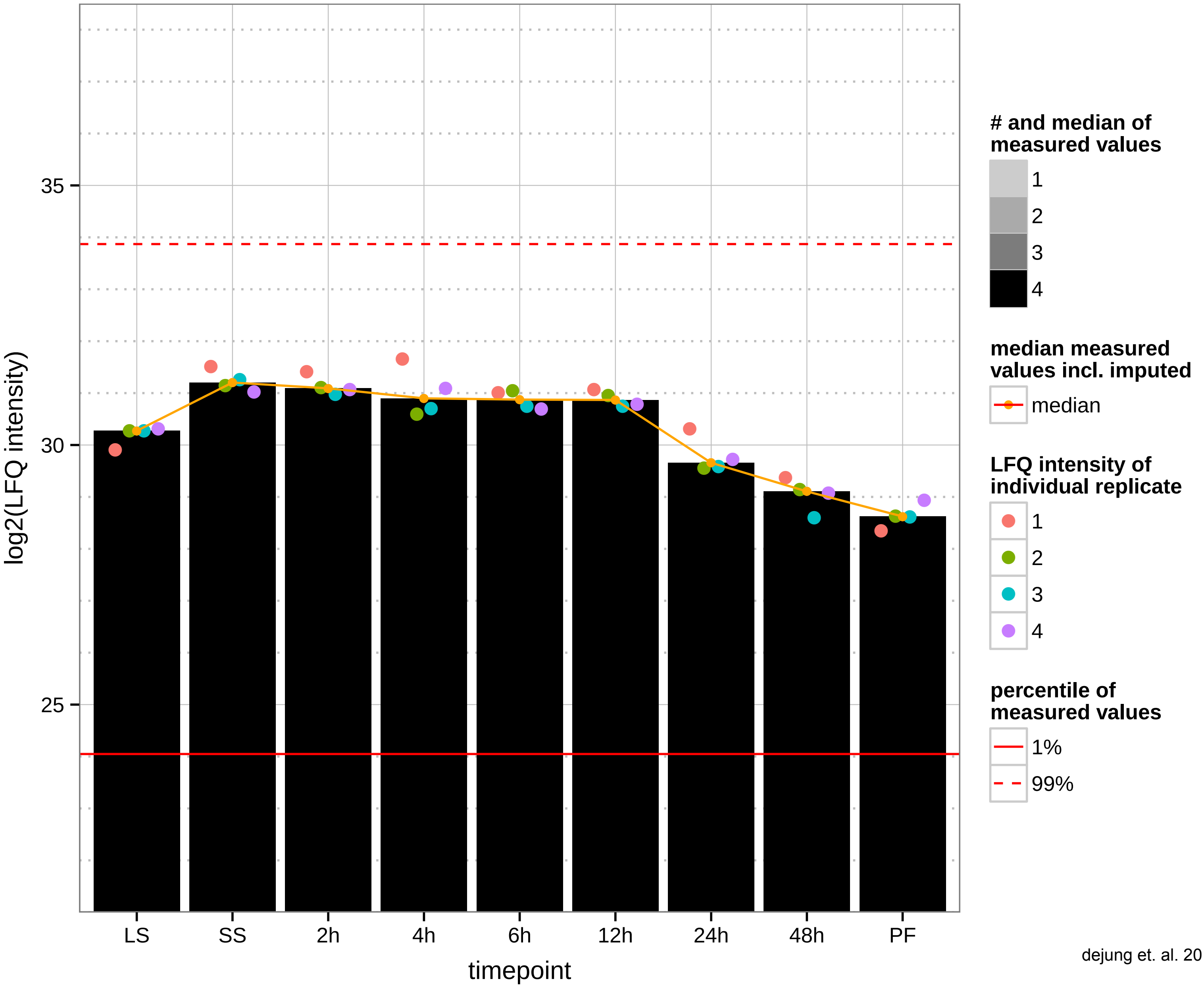
hypothetical protein, conserved
Tb927.10.13790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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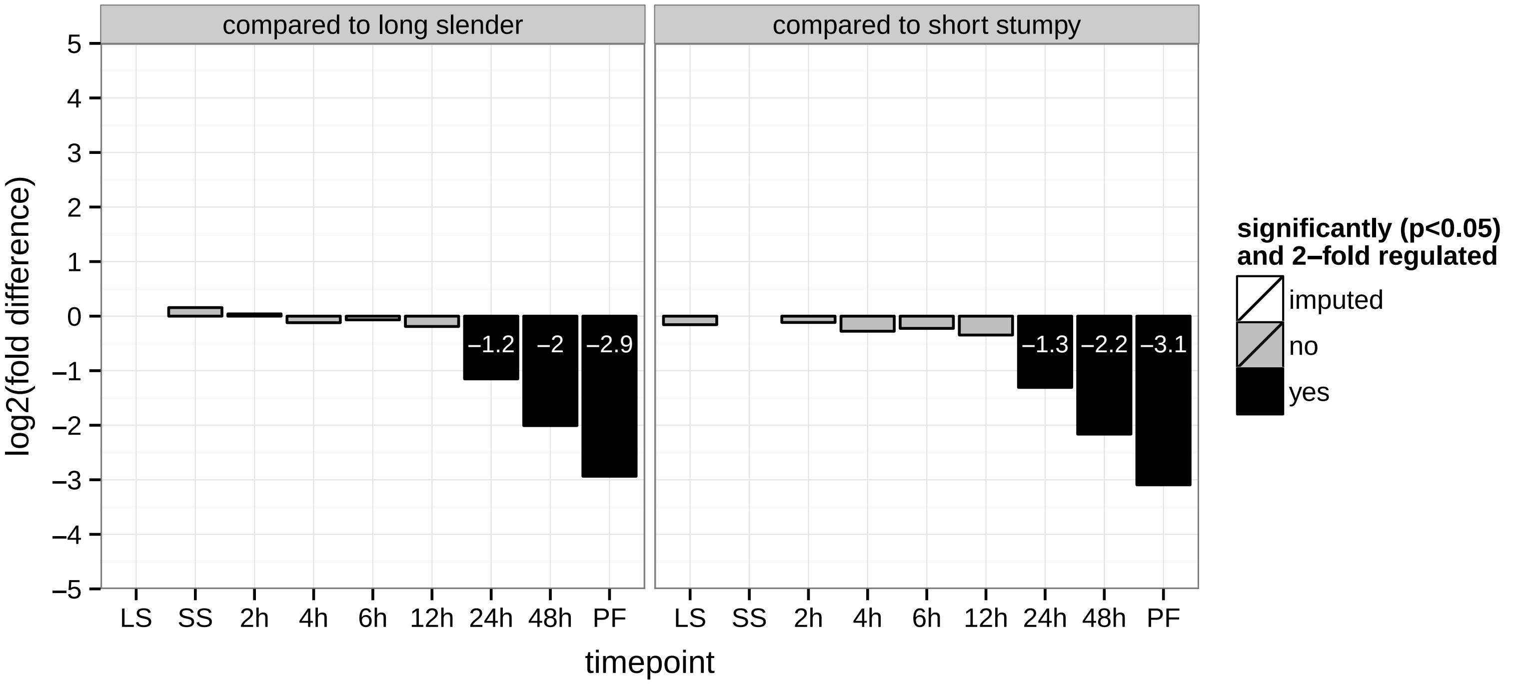
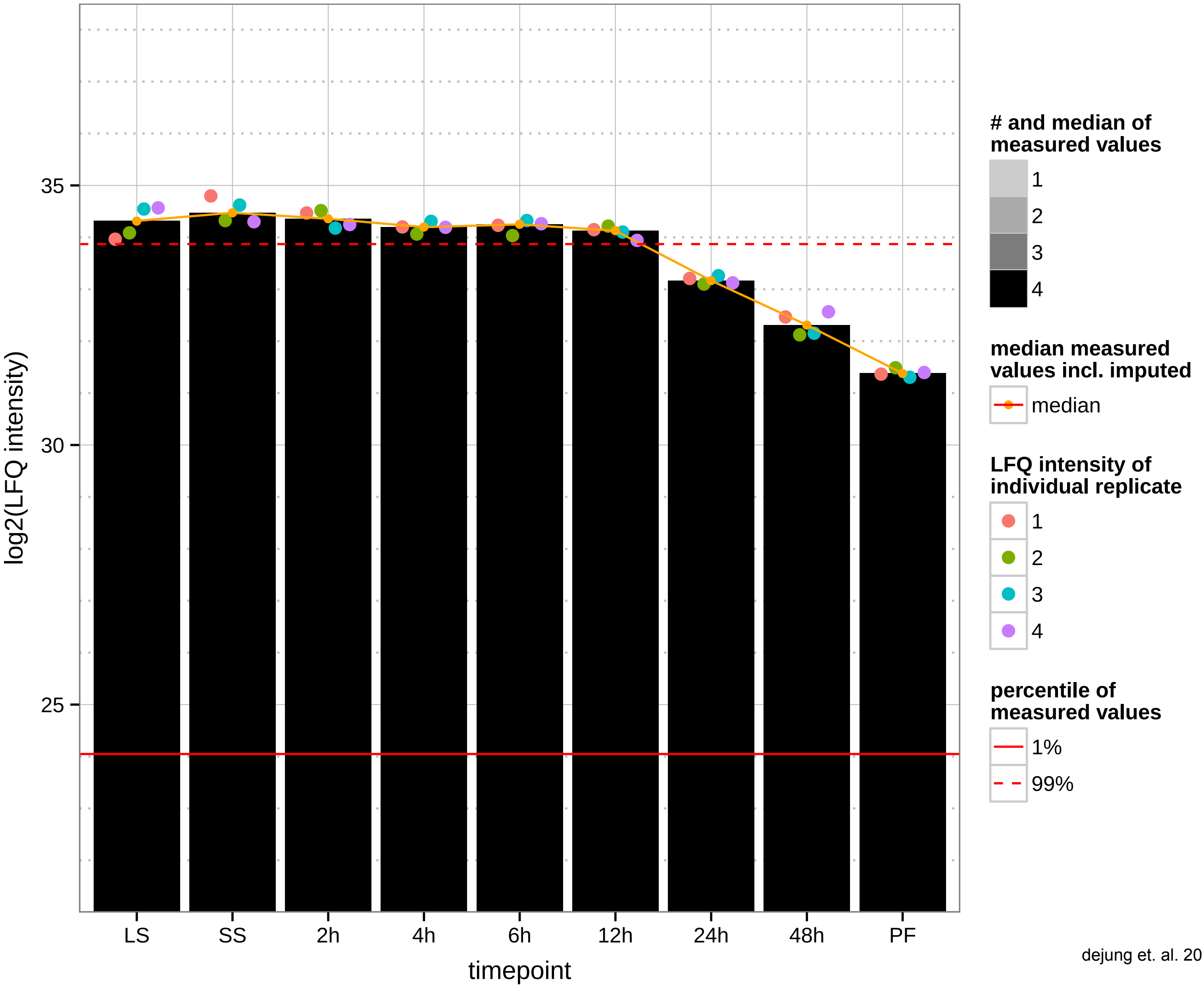
pyruvate kinase 1, putative, pyruvate kinase 1 (PYK1)
Tb927.10.14140;Tb11.v5.0605
AGOF: null, magnesium ion binding, potassium ion binding, pyruvate kinase activity
AGOC: null, cytoplasm
AGOP: null, glycolysis
PGOF: catalytic activity, magnesium ion binding, potassium ion binding, pyruvate kinase activity
PGOC: null
PGOP: glycolysis





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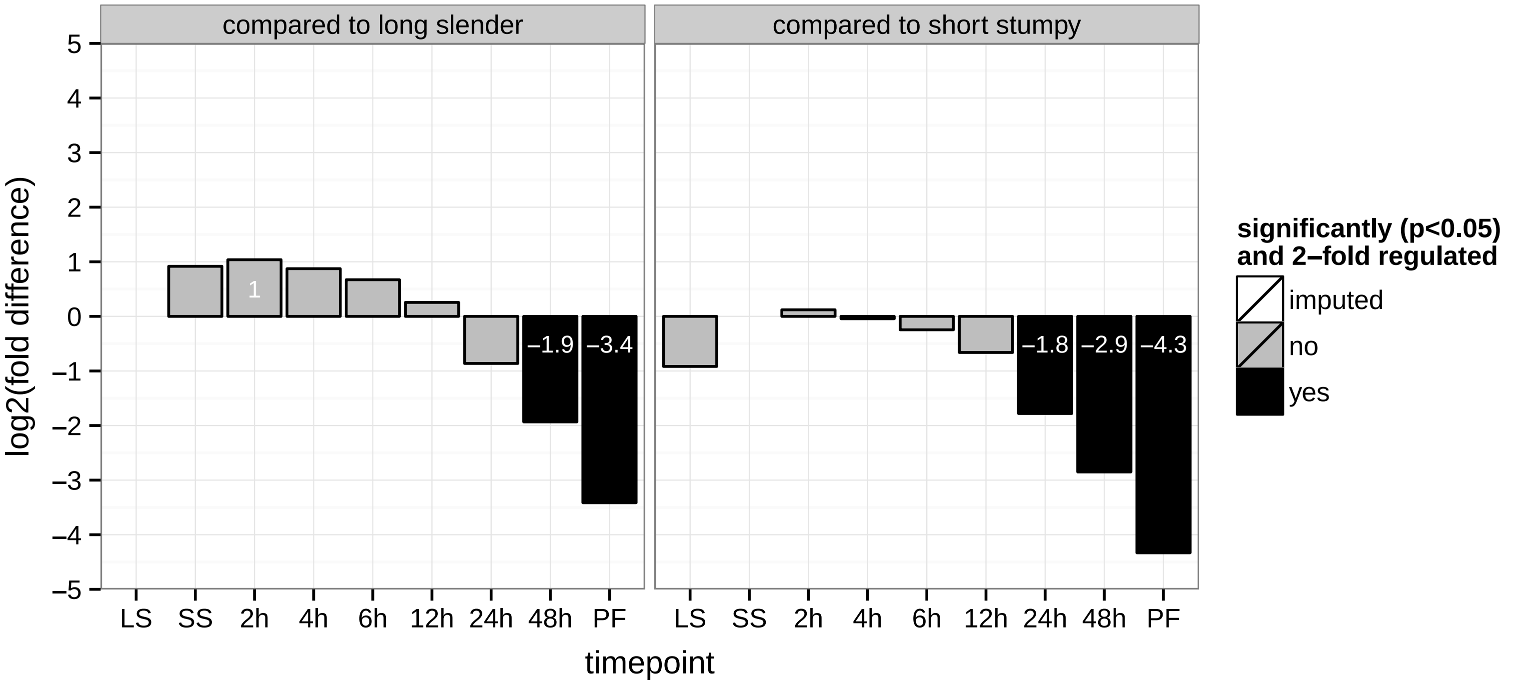
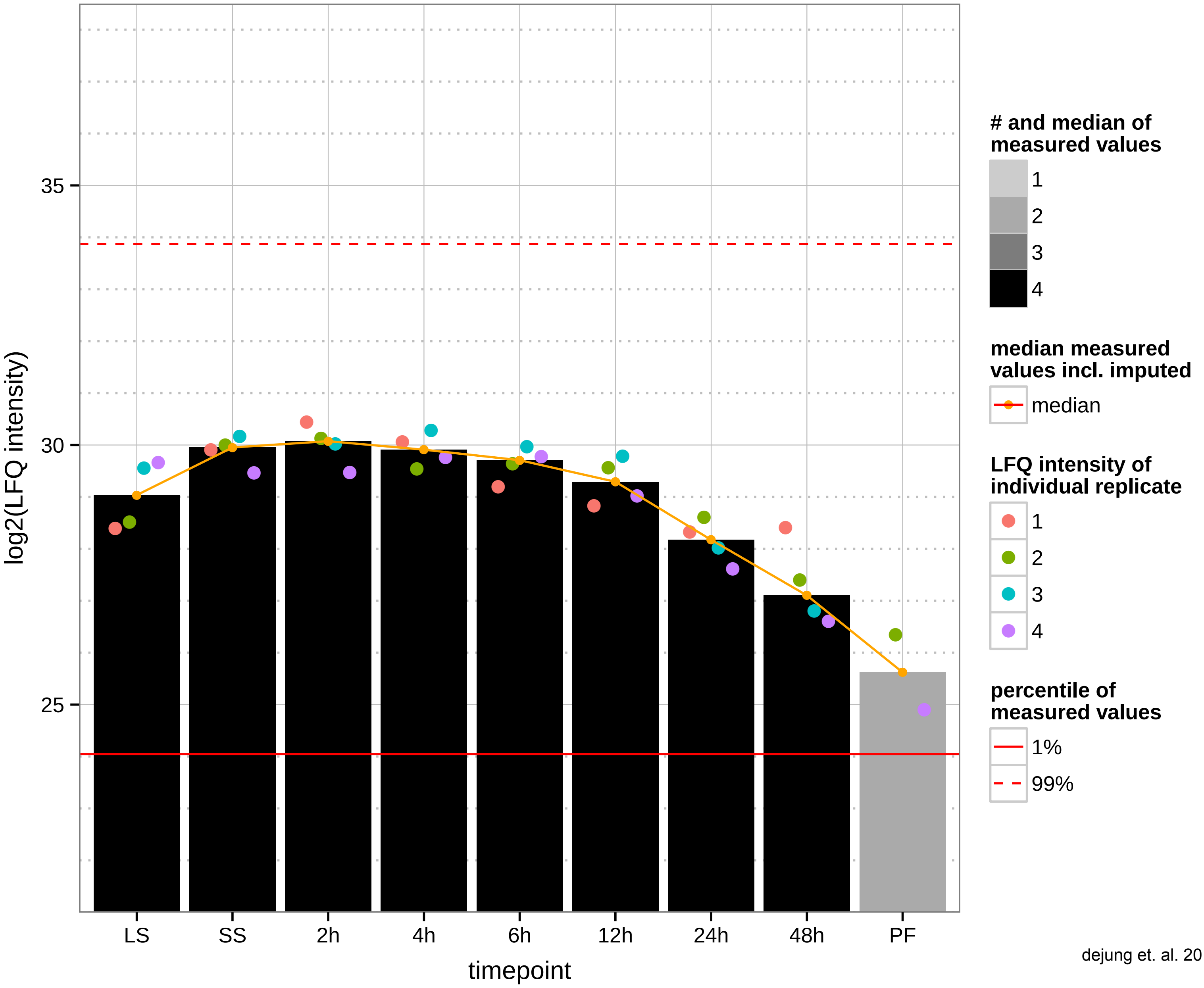
Aquaglyceroporin 3 (AQP3)
Tb927.10.14160
AGOF: glycerol channel activity, water channel activity
AGOC: plasma membrane
AGOP: glycerol transport
PGOF: transporter activity
PGOC: integral to membrane, membrane
PGOP: transmembrane transport, transport, water transport





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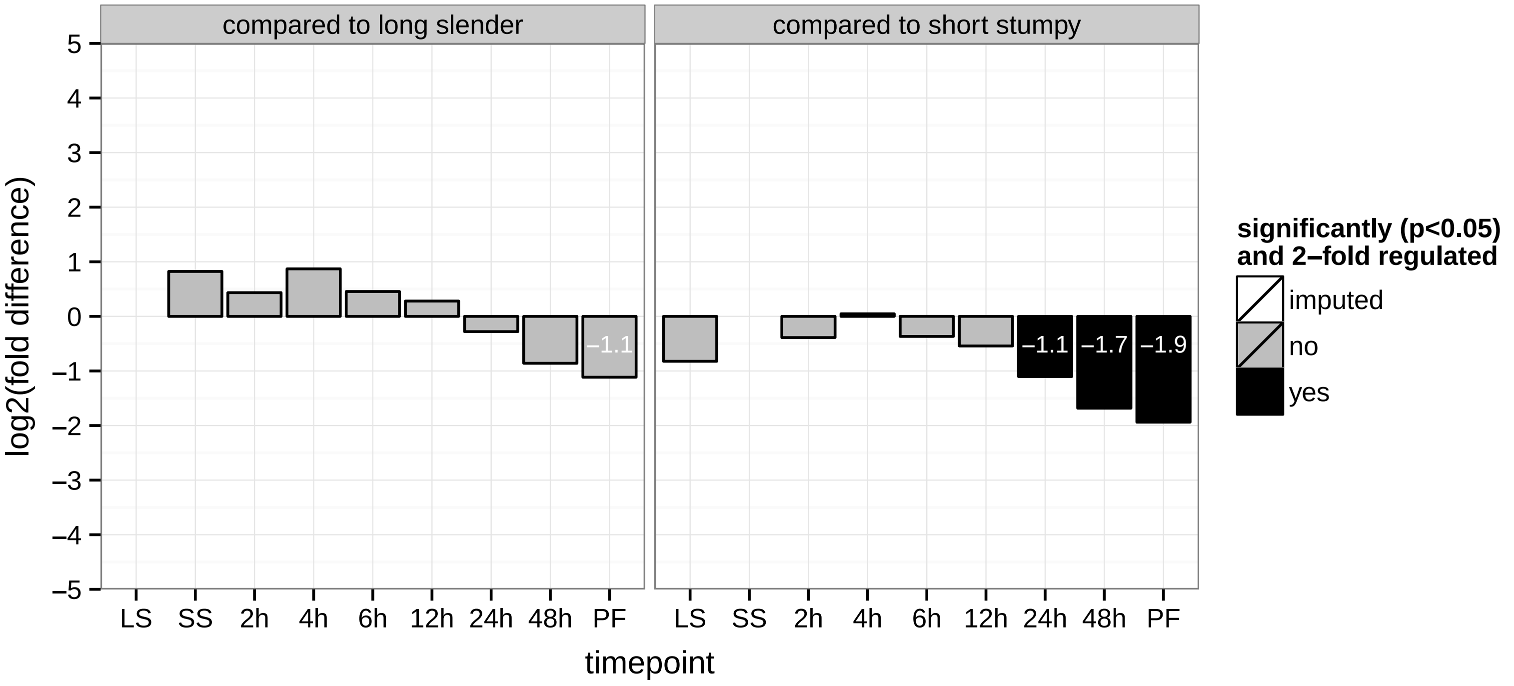
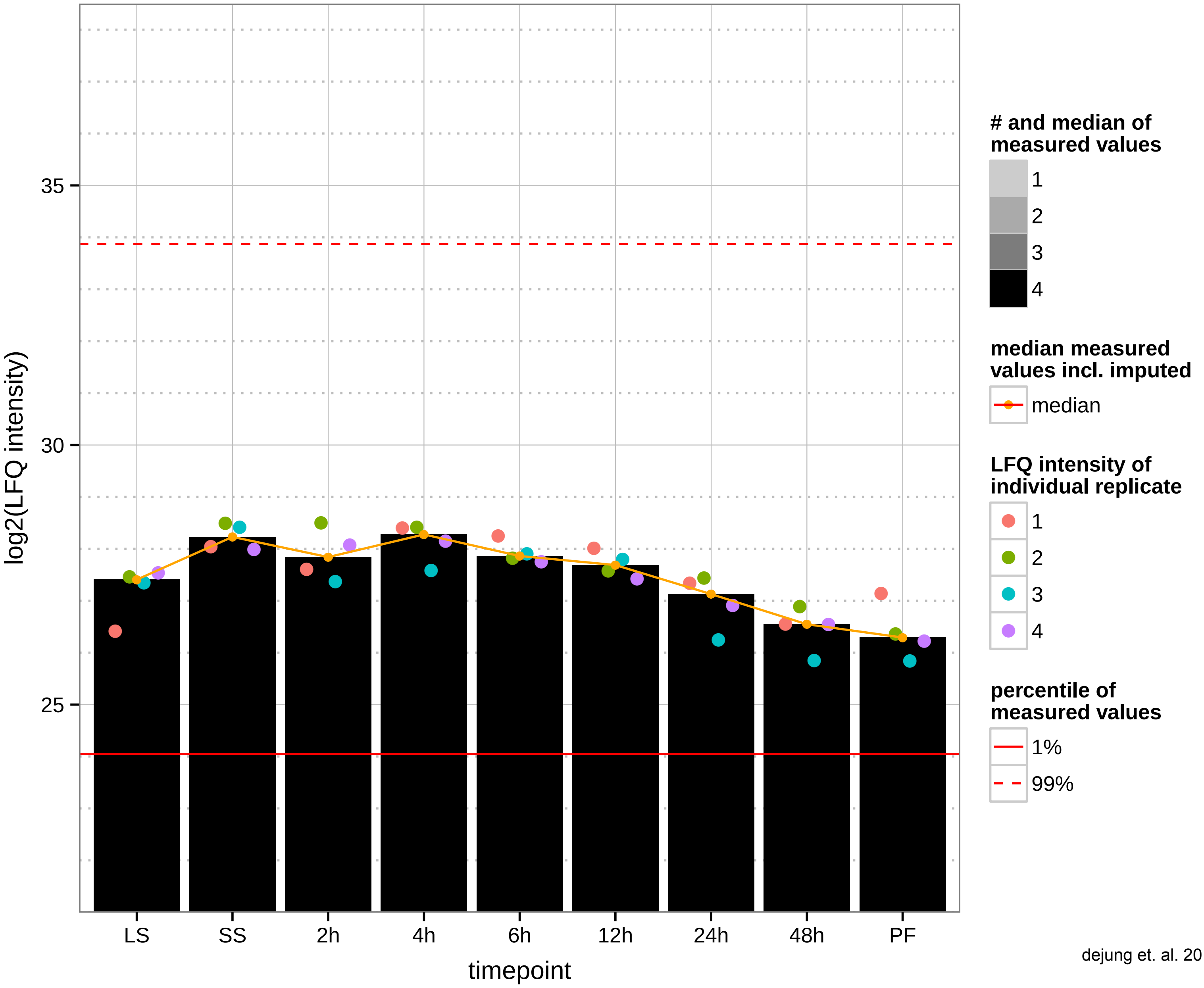
hypothetical protein, conserved
Tb927.10.15440
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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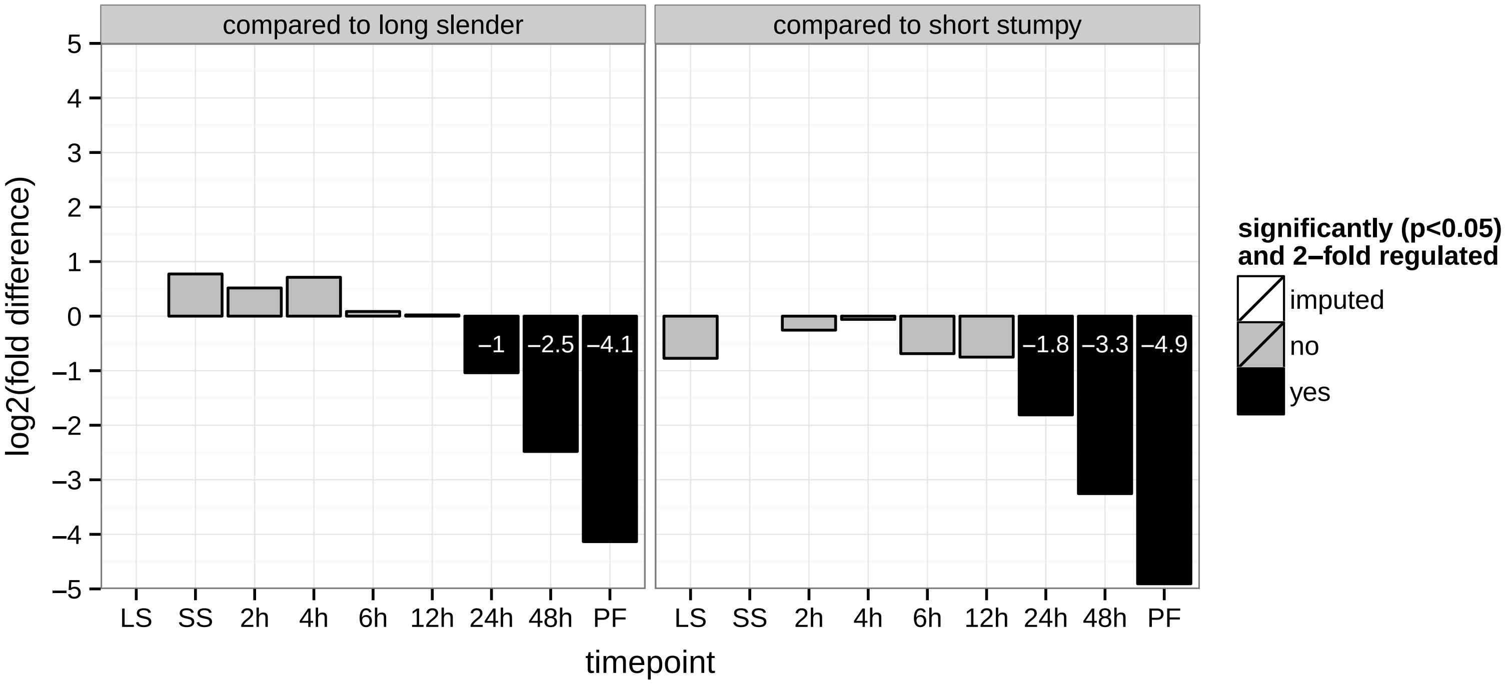
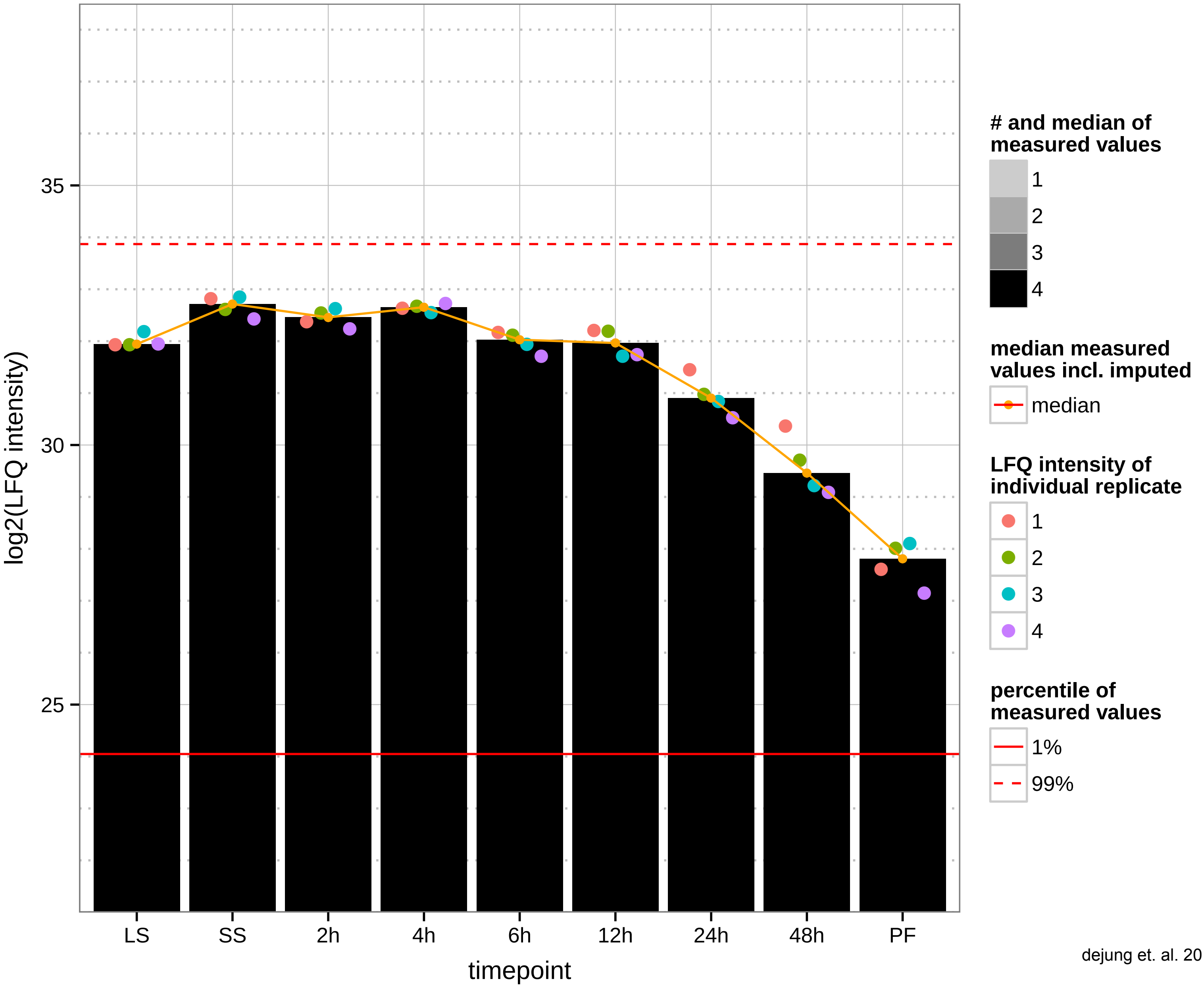
Metacaspase−4 (MCA4)
Tb927.10.2440
AGOF: cysteine−type endopeptidase activity, peptidase activity
AGOC: nucleus
AGOP: aerobic respiration, proteolysis
PGOF: cysteine−type endopeptidase activity
PGOC: null
PGOP: proteolysis





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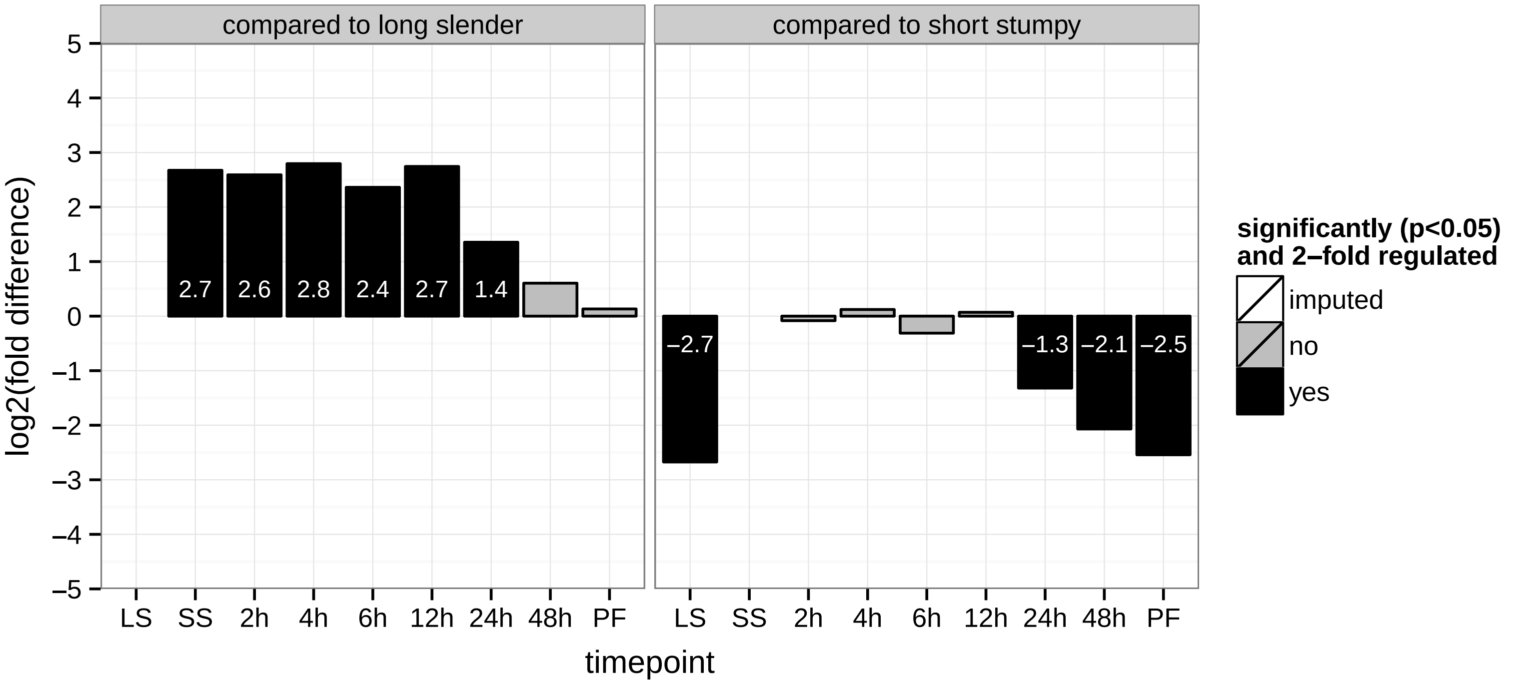
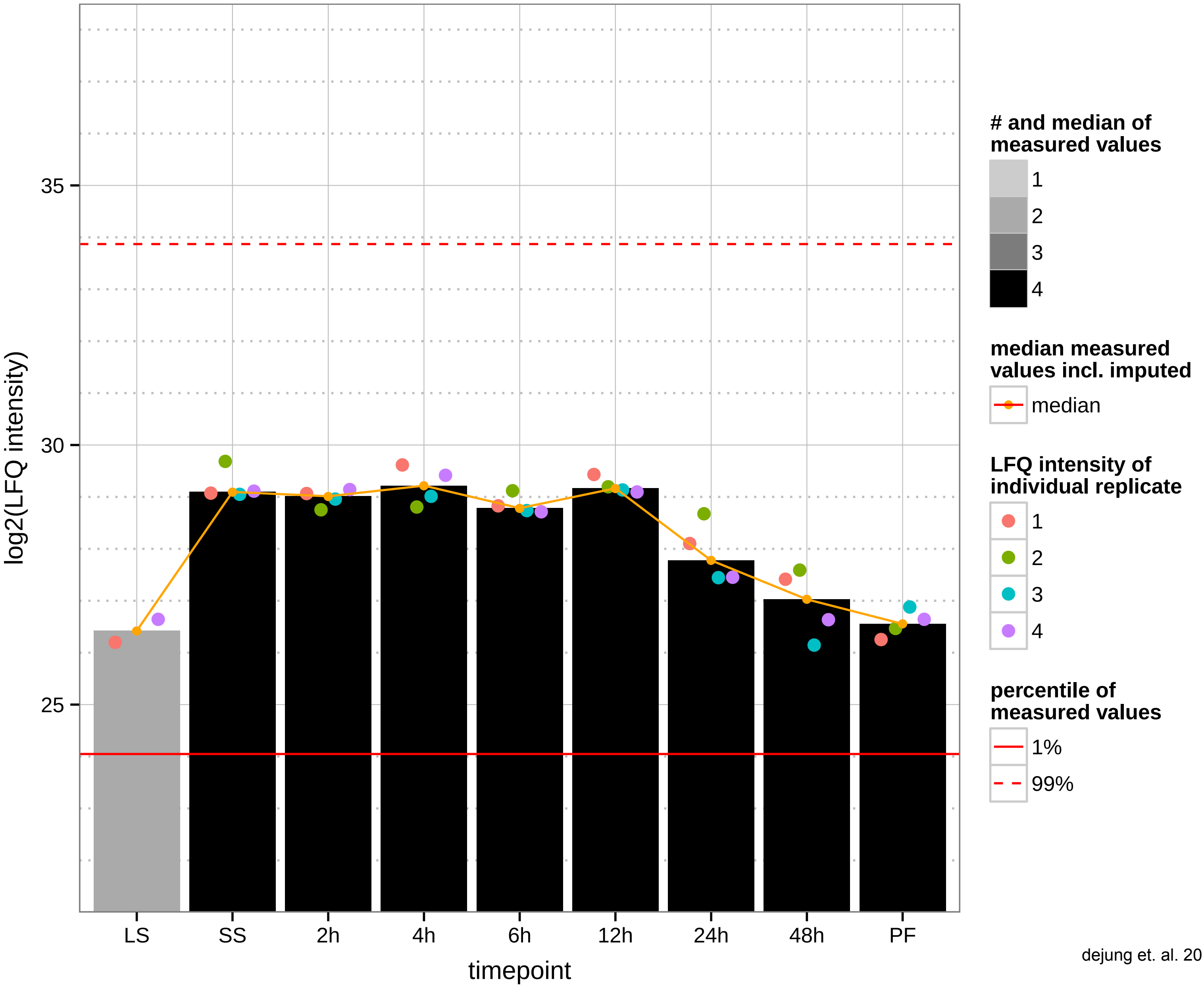
lysosomal alpha–mannosidase precursor, putative
Tb927.10.2570;Tb11.v5.0498
AGOF: null, alpha–mannosidase activity, carbohydrate binding, zinc ion binding
AGOC: null, lysosome
AGOP: null, carbohydrate metabolic process, mannose metabolic process
PGOF: carbohydrate binding, catalytic activity, hydrolase activity, hydrolyzing O–glycosyl compounds, mannosidase activity, zi
PGOC: null
PGOP: carbohydrate metabolic process, mannose metabolic process





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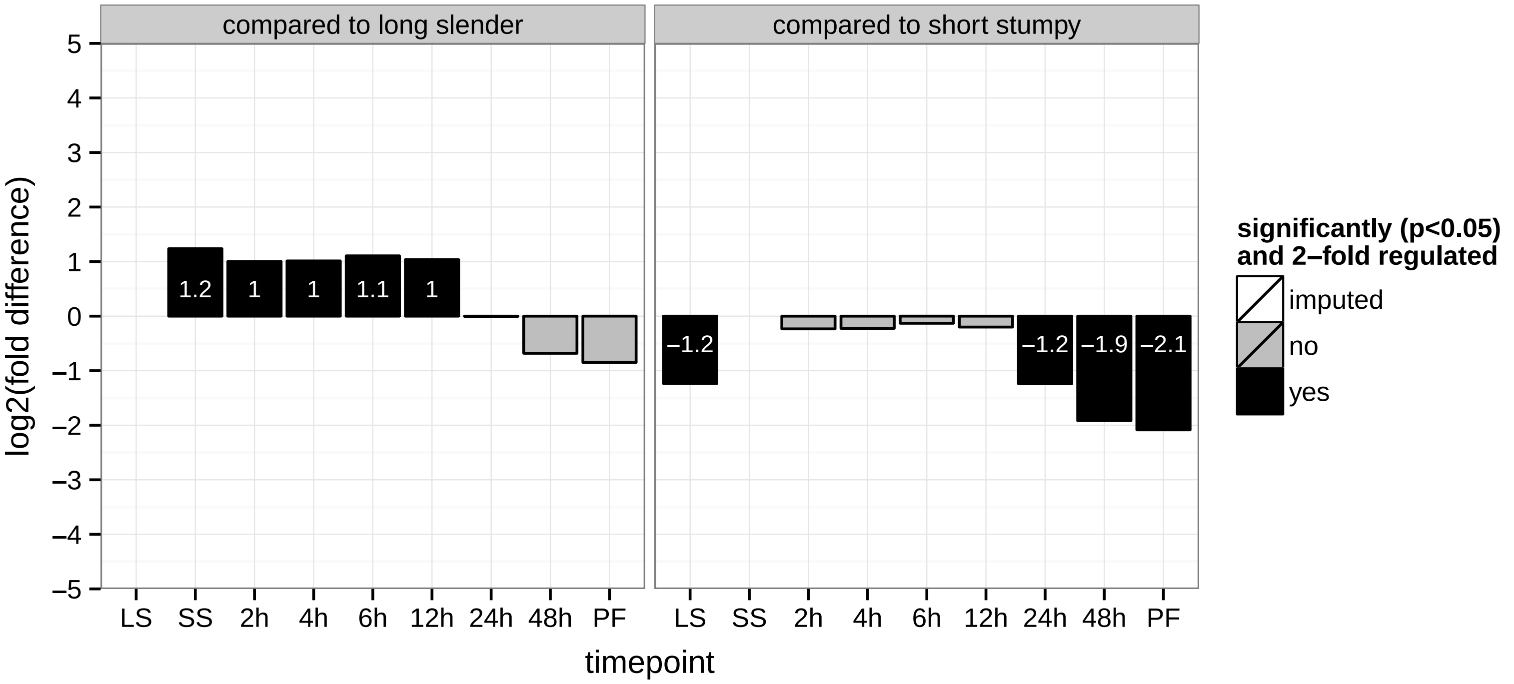
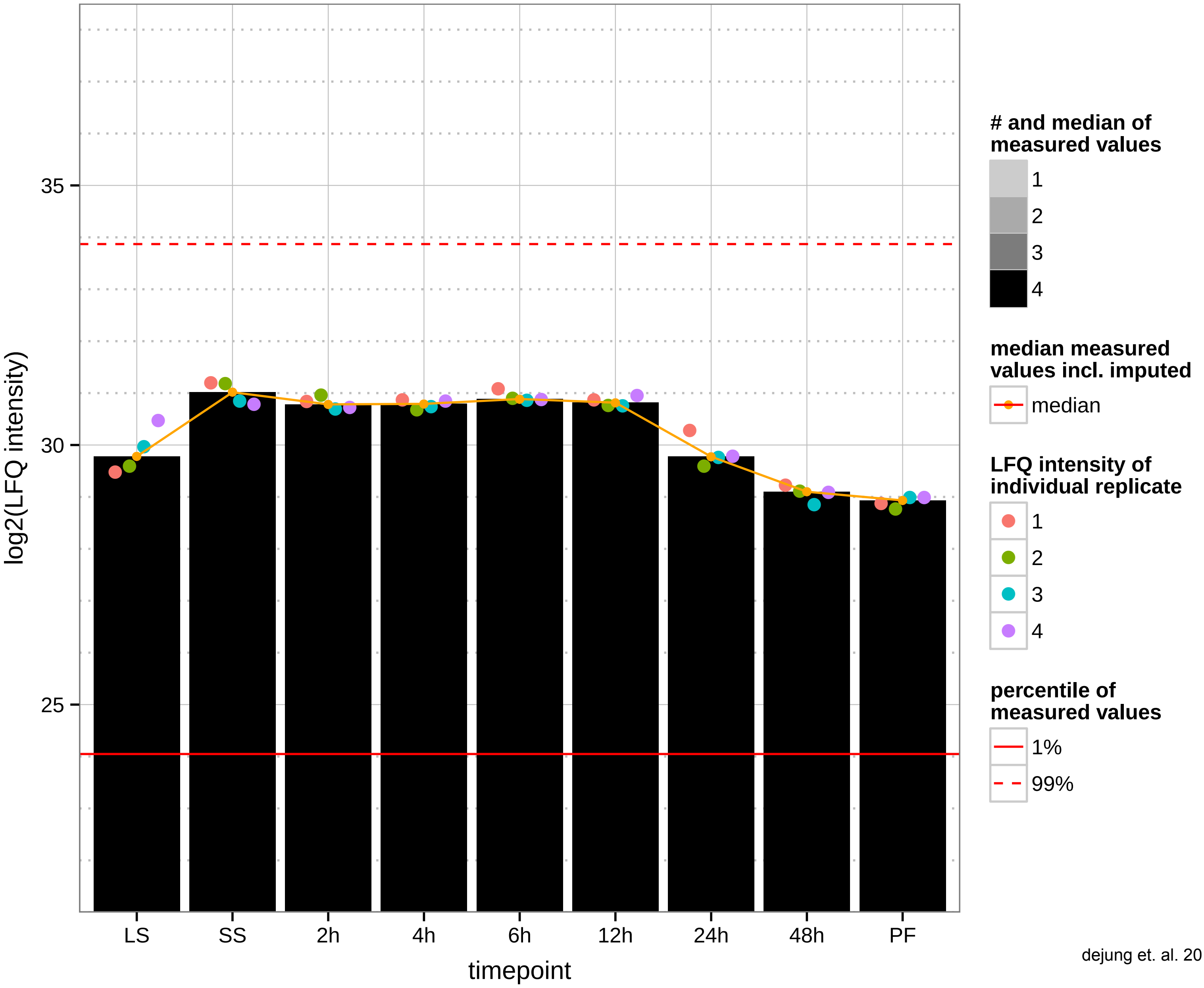
TFIIF–stimulated CTD phosphatase, putative
Tb927.10.4180
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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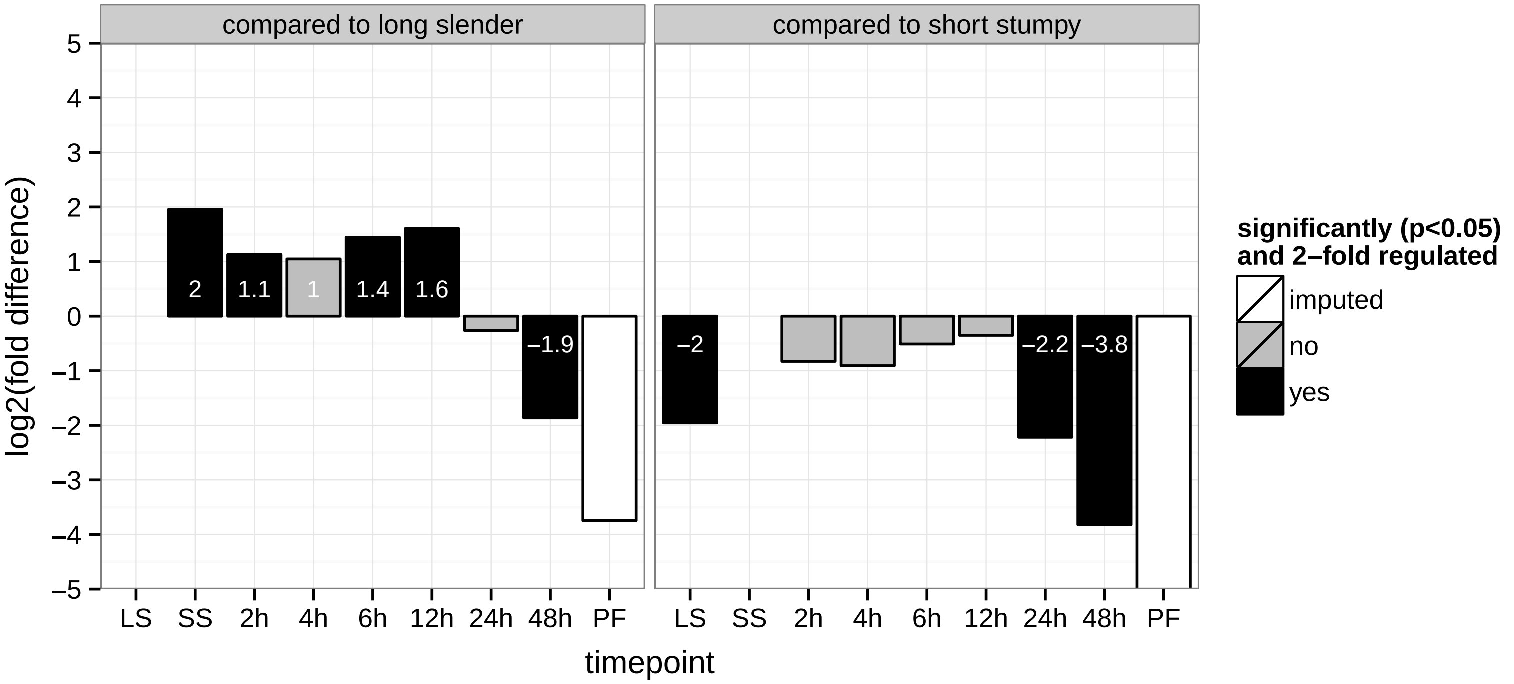
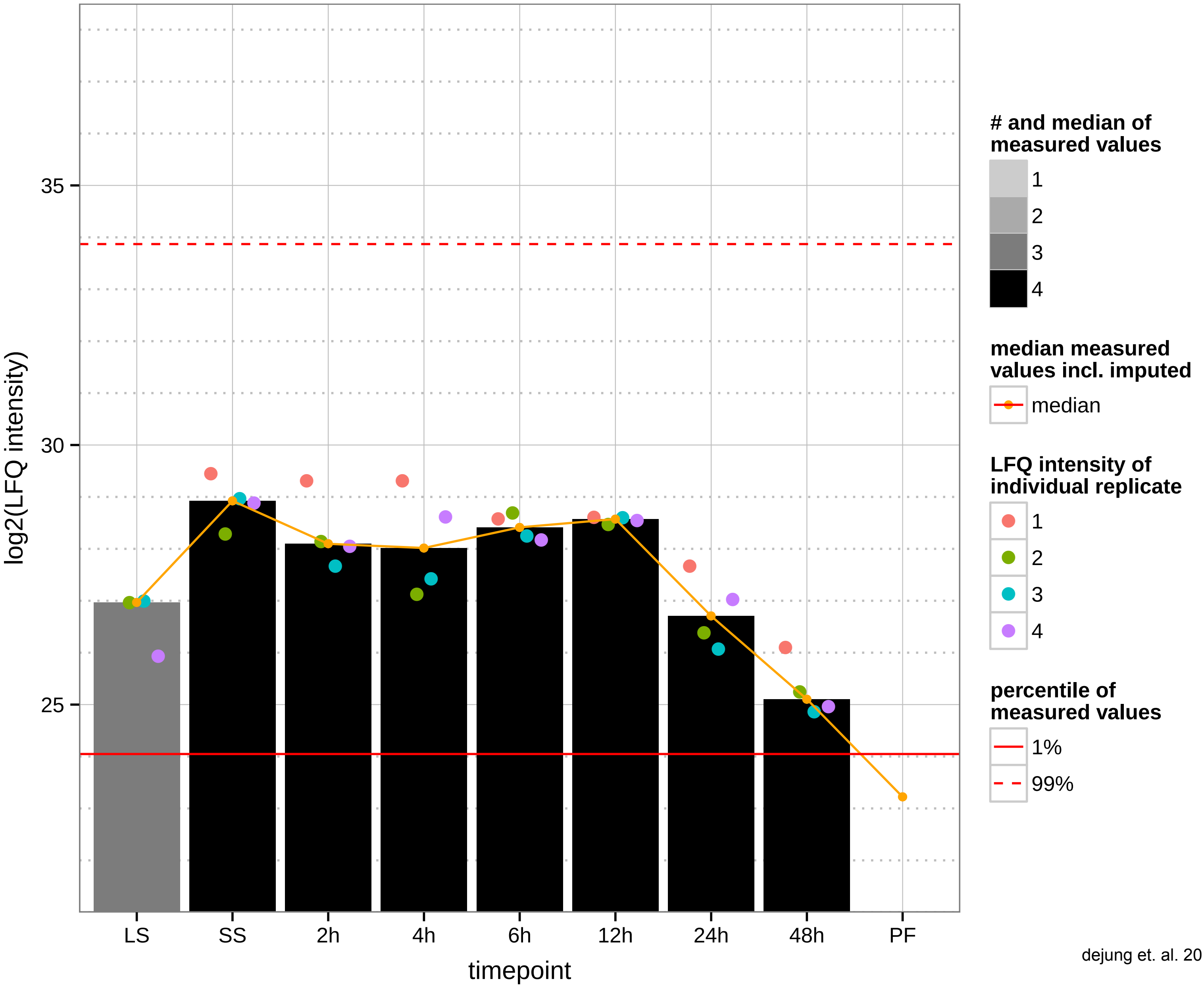
hypothetical protein, conserved, zinc finger protein family member, putative (ZC3H32)
Tb927.10.5250;Tb11.v5.0232
AGOF: null, RNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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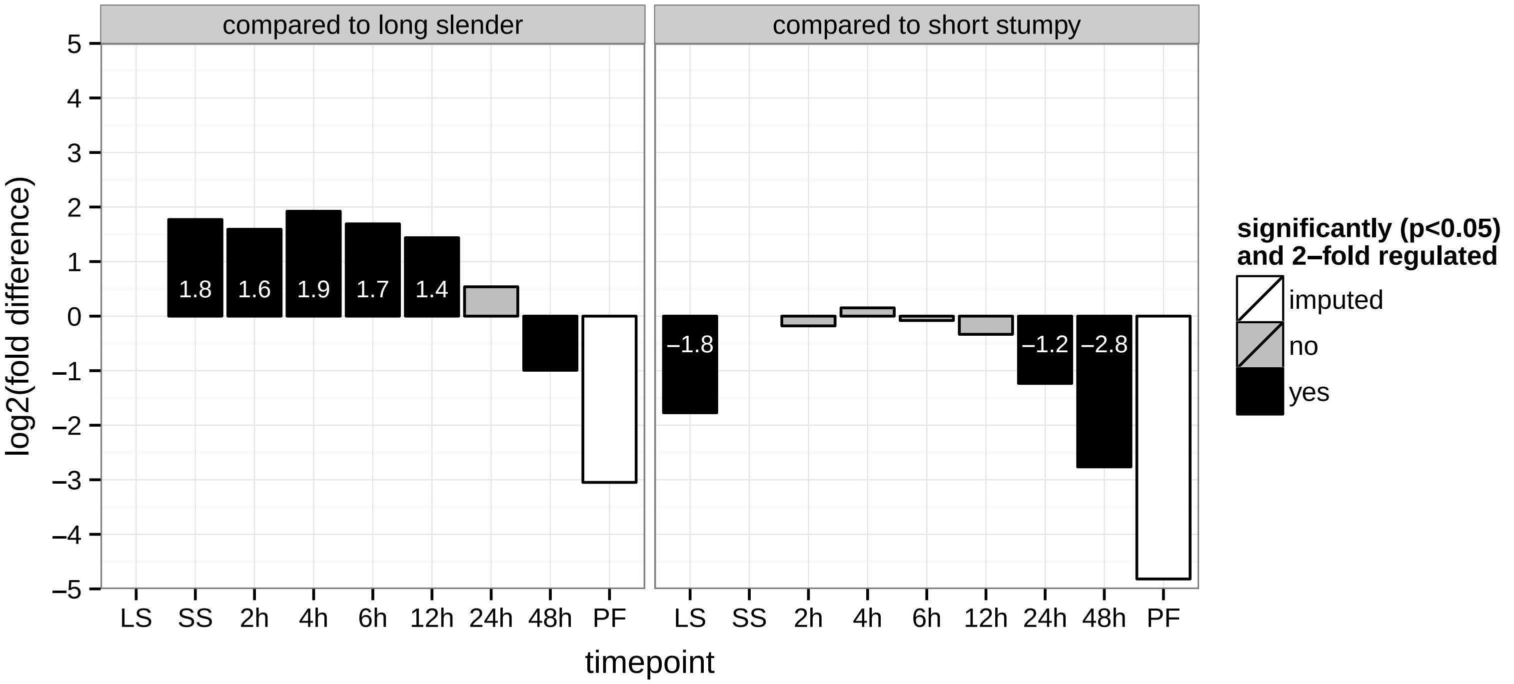
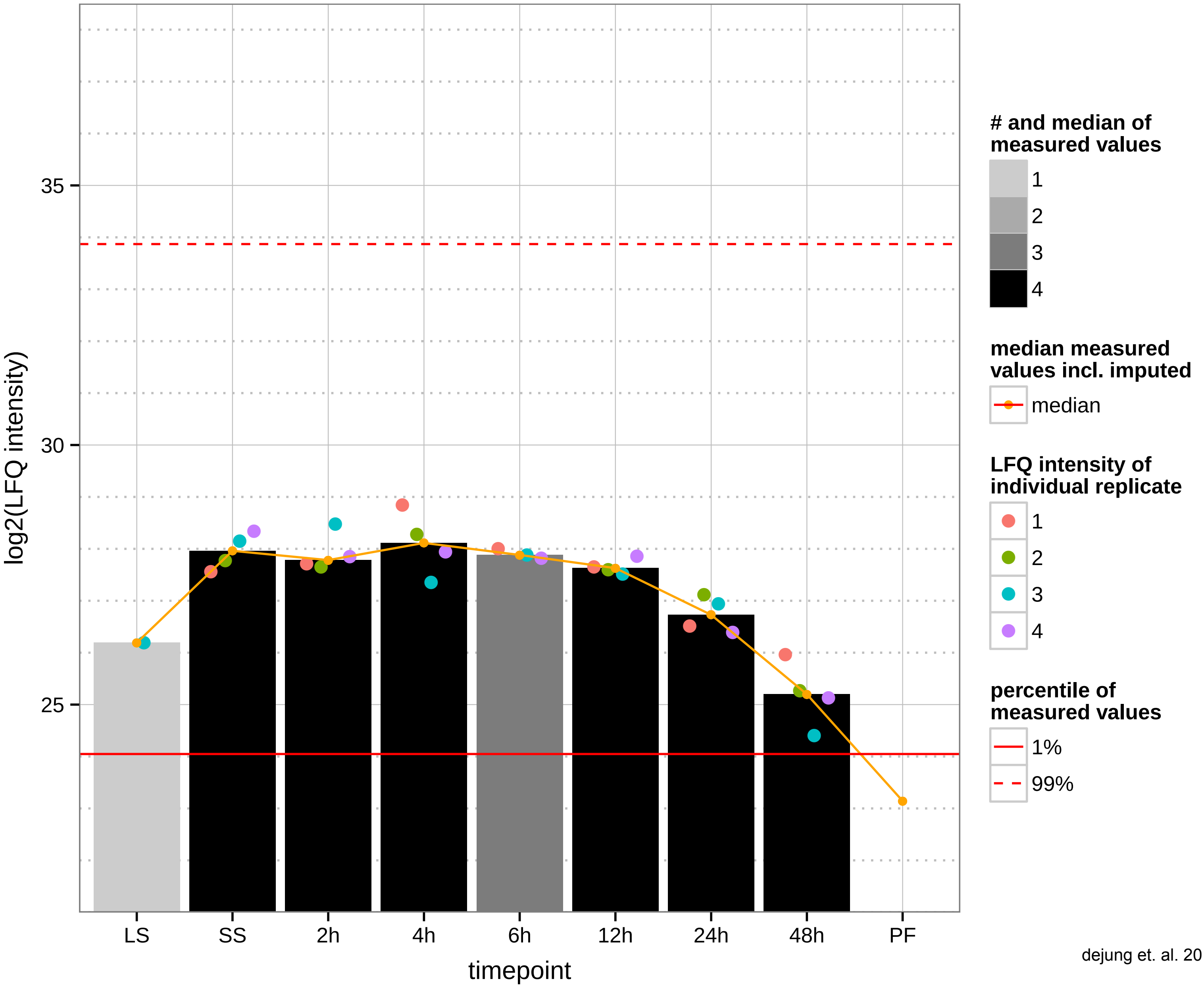
hypothetical protein, conserved
Tb927.10.6750;Tb927.10.6760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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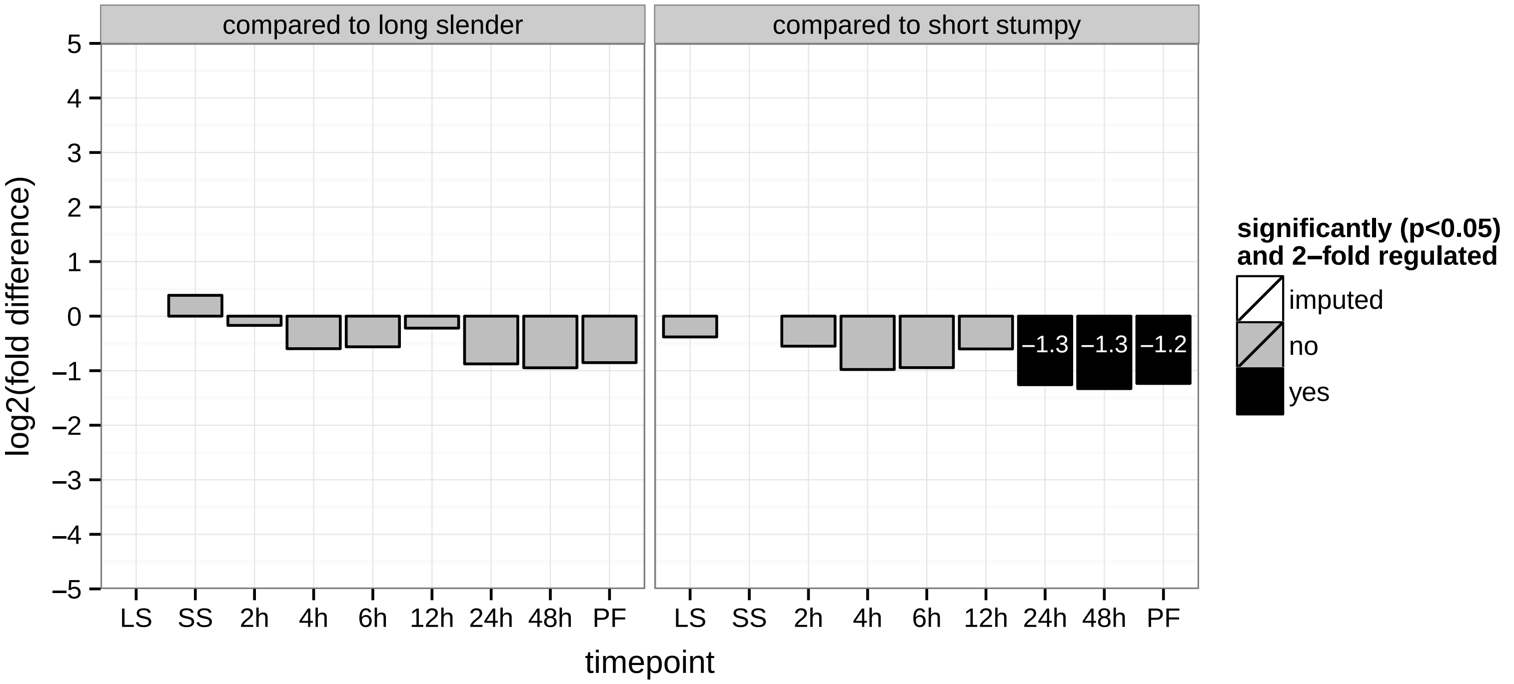
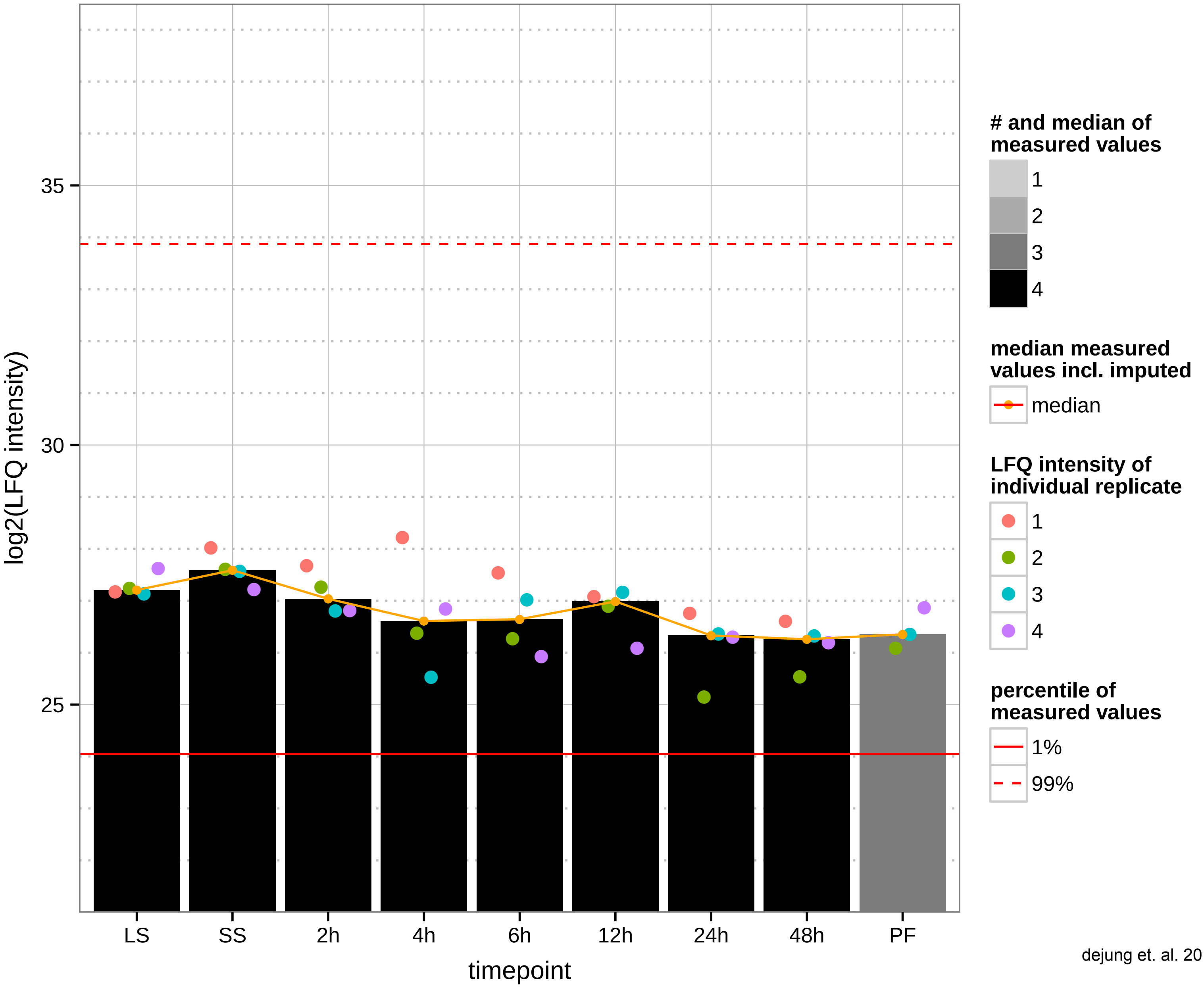
hypothetical protein, conserved
Tb927.10.840;Tb11.v5.0753
AGOF: null
AGOC: null
AGOP: null
PGOF: null, protein binding
PGOC: null
PGOP: null





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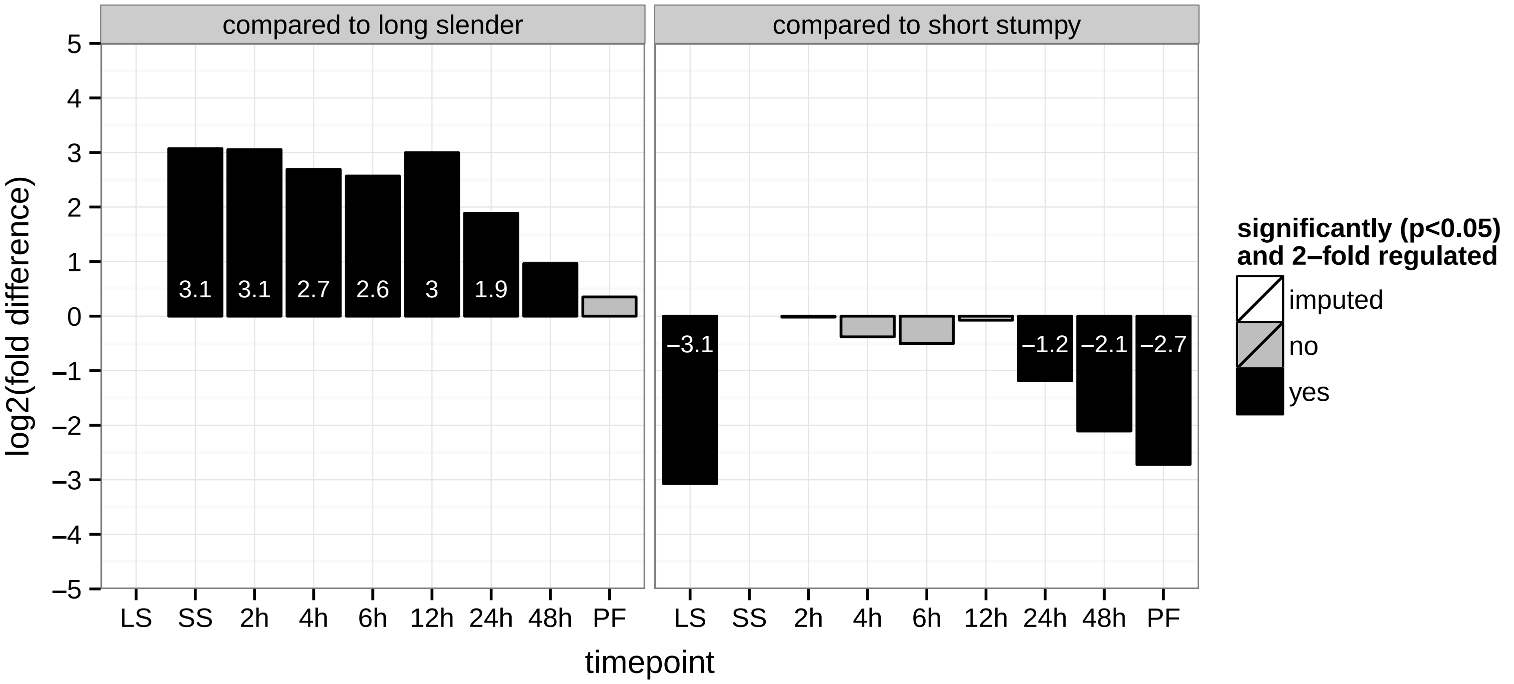
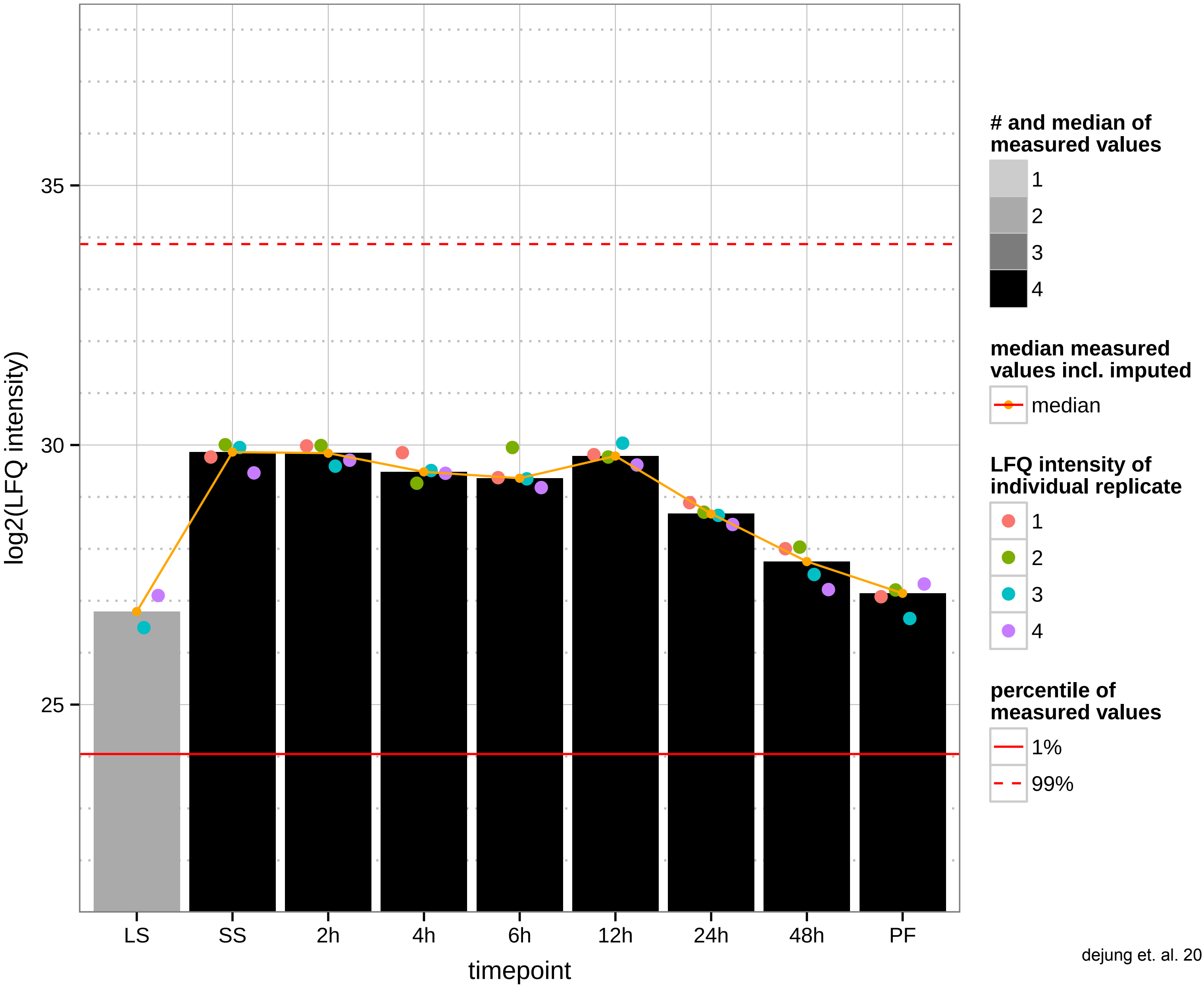
hypothetical protein, conserved
Tb927.10.9360
AGOF: oxidoreductase activity
AGOC: null
AGOP: null
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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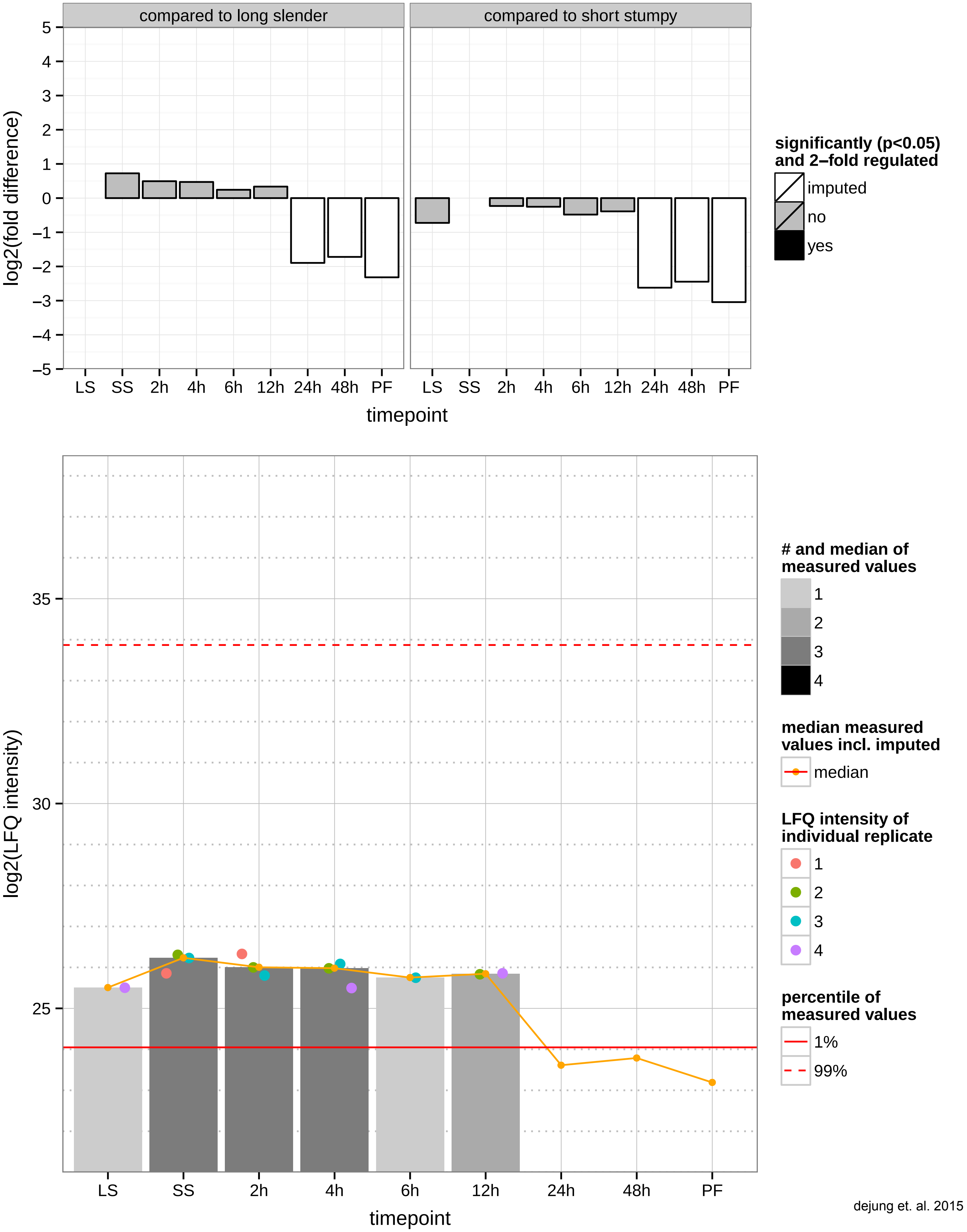
hypothetical protein, conserved
Tb927.11.11710
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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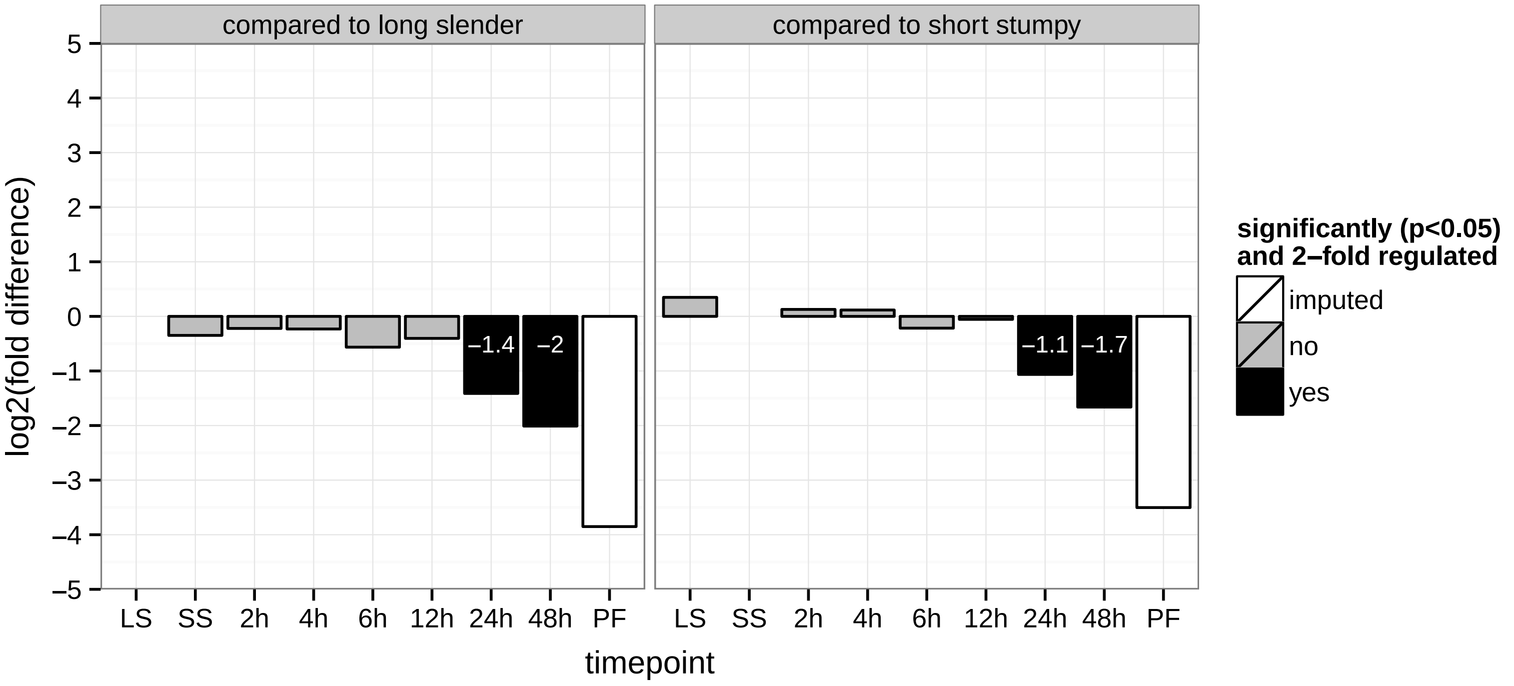
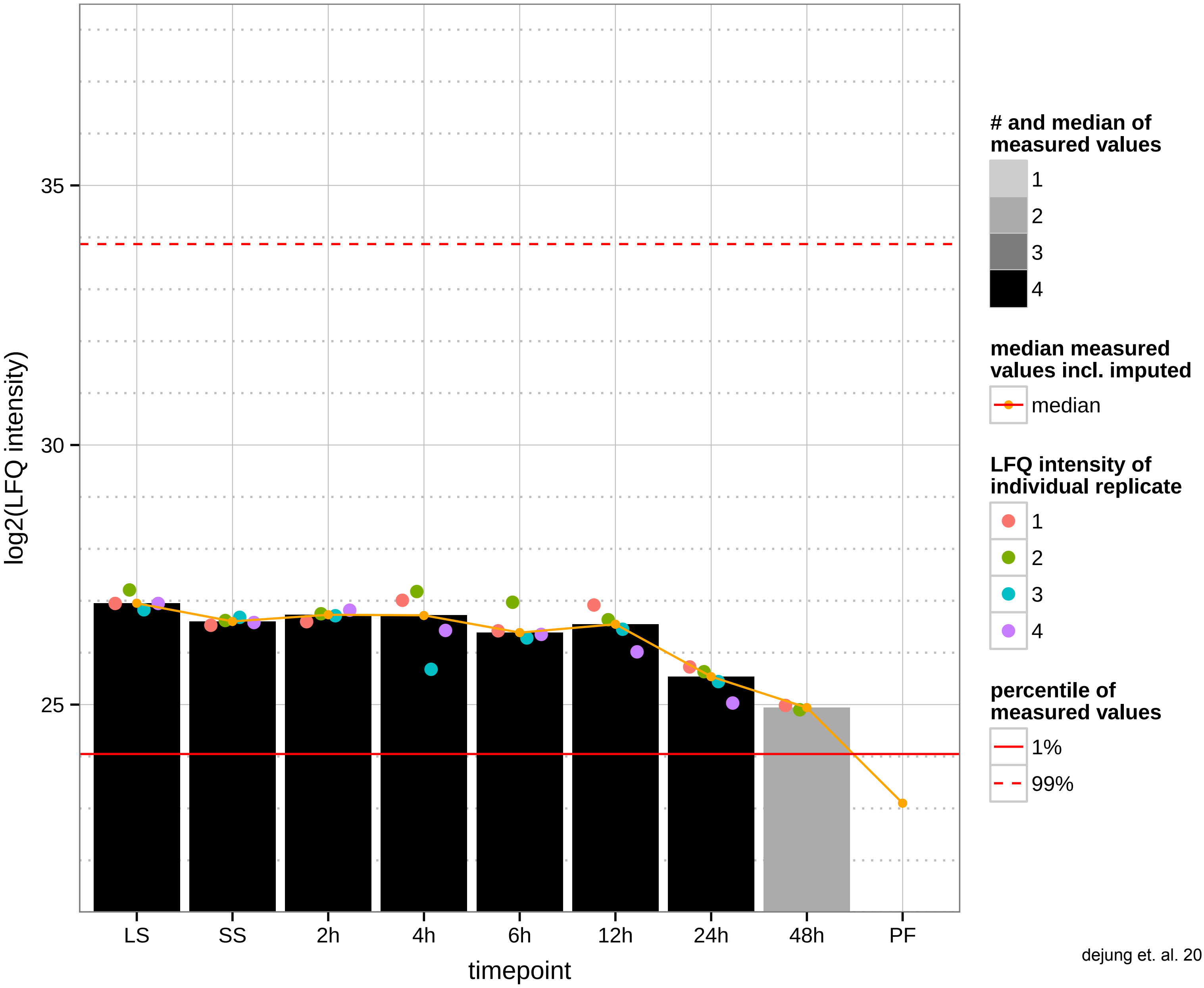
hypothetical protein, conserved
Tb927.11.1230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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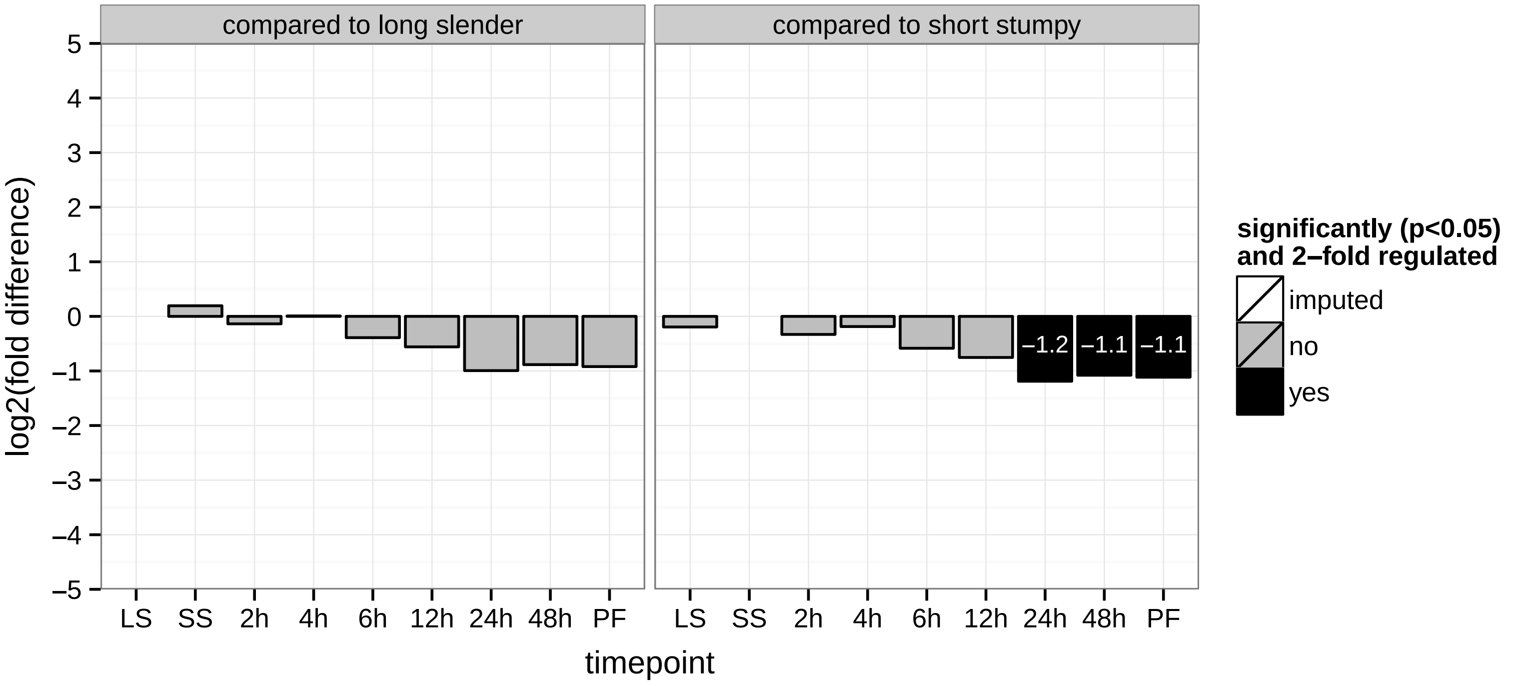
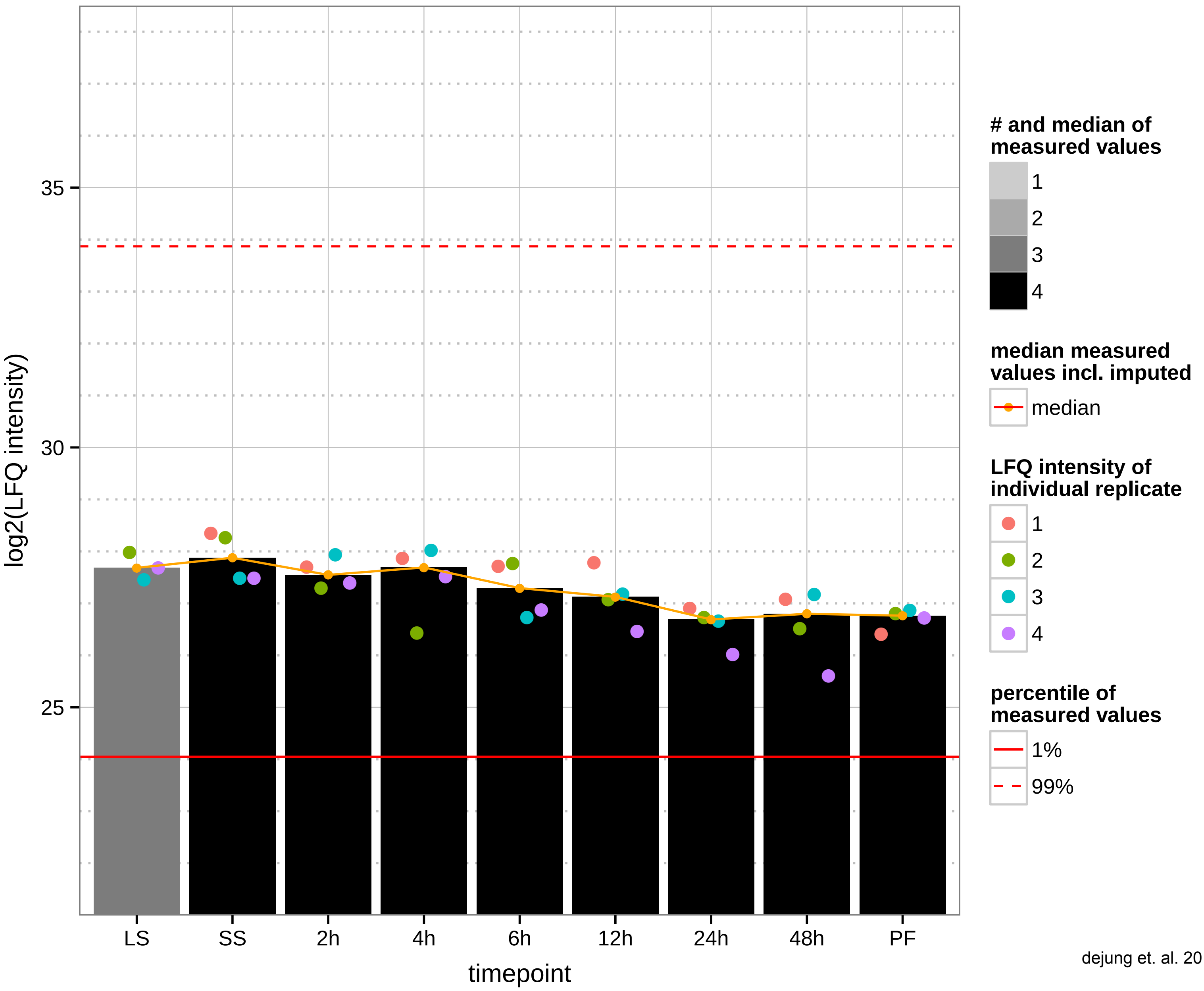
membrane–bound acid phosphatase 1 precursor (MBAP1)
Tb927.11.13130
AGOF: null
AGOC: integral to membrane, lysosomal membrane
AGOP: null
PGOF: acid phosphatase activity
PGOC: null
PGOP: null





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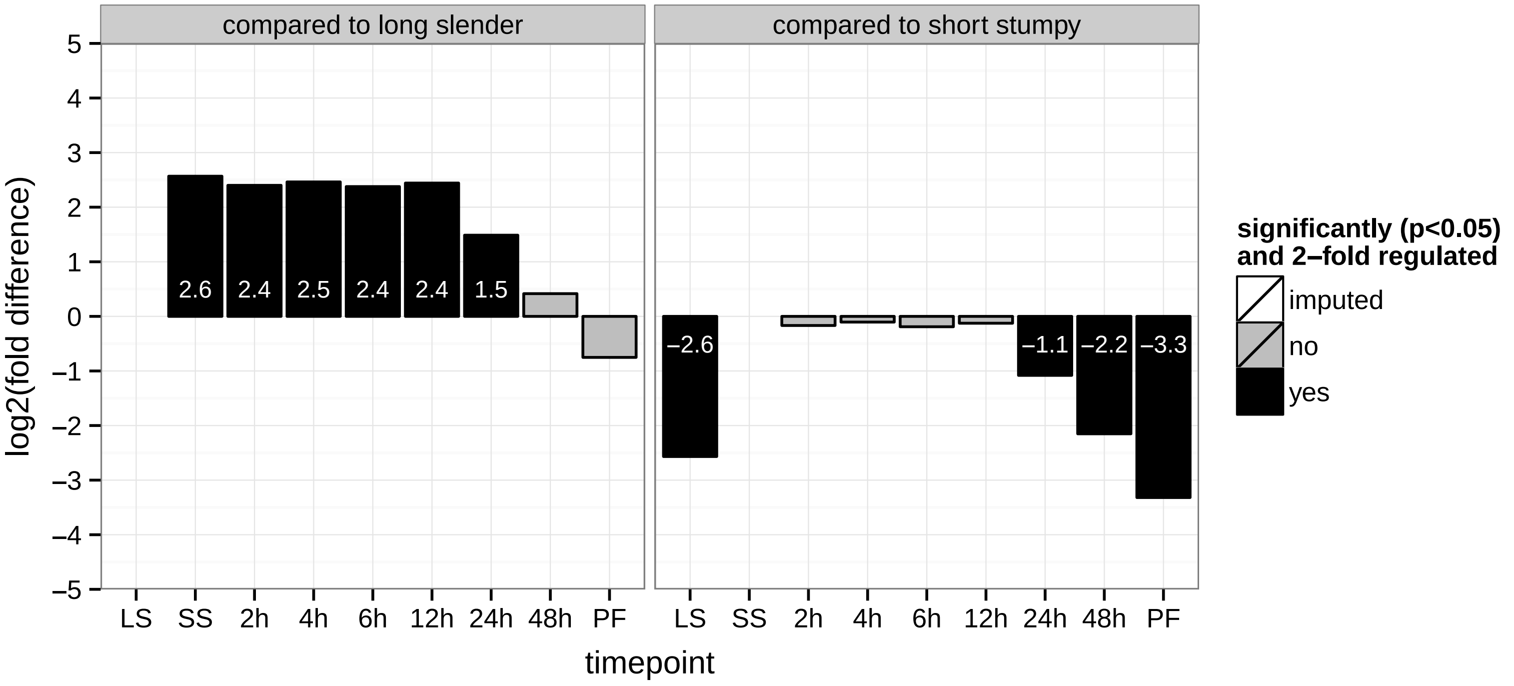
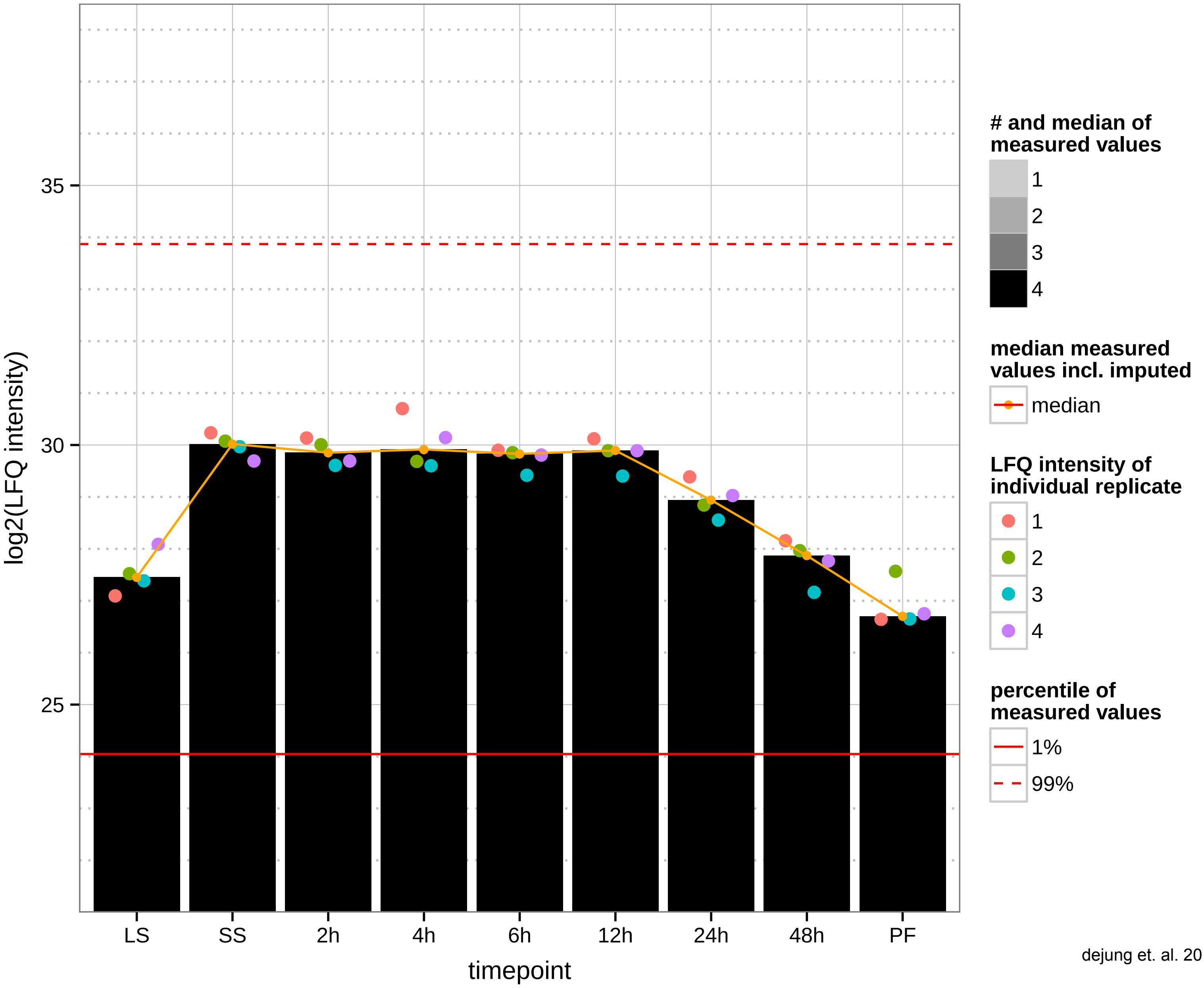
hypothetical protein, conserved
Tb927.11.15870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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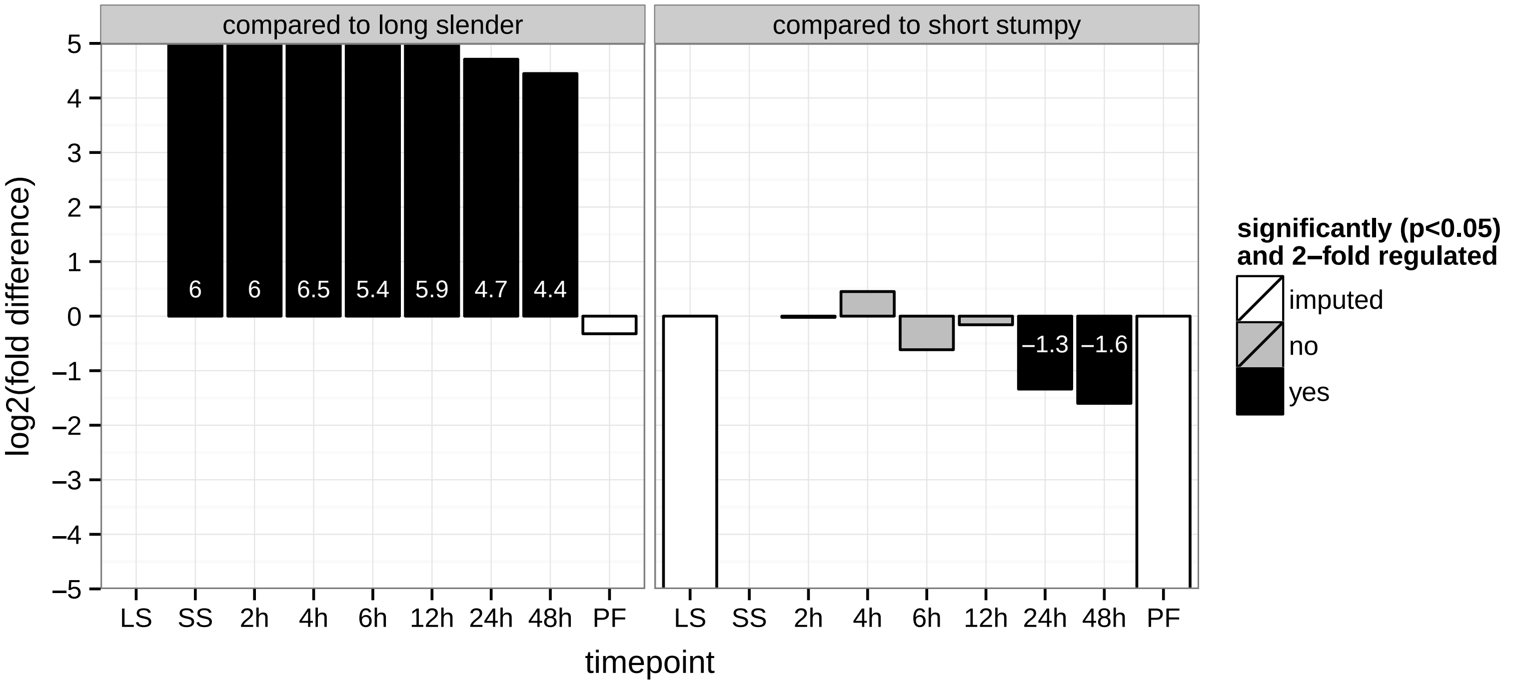
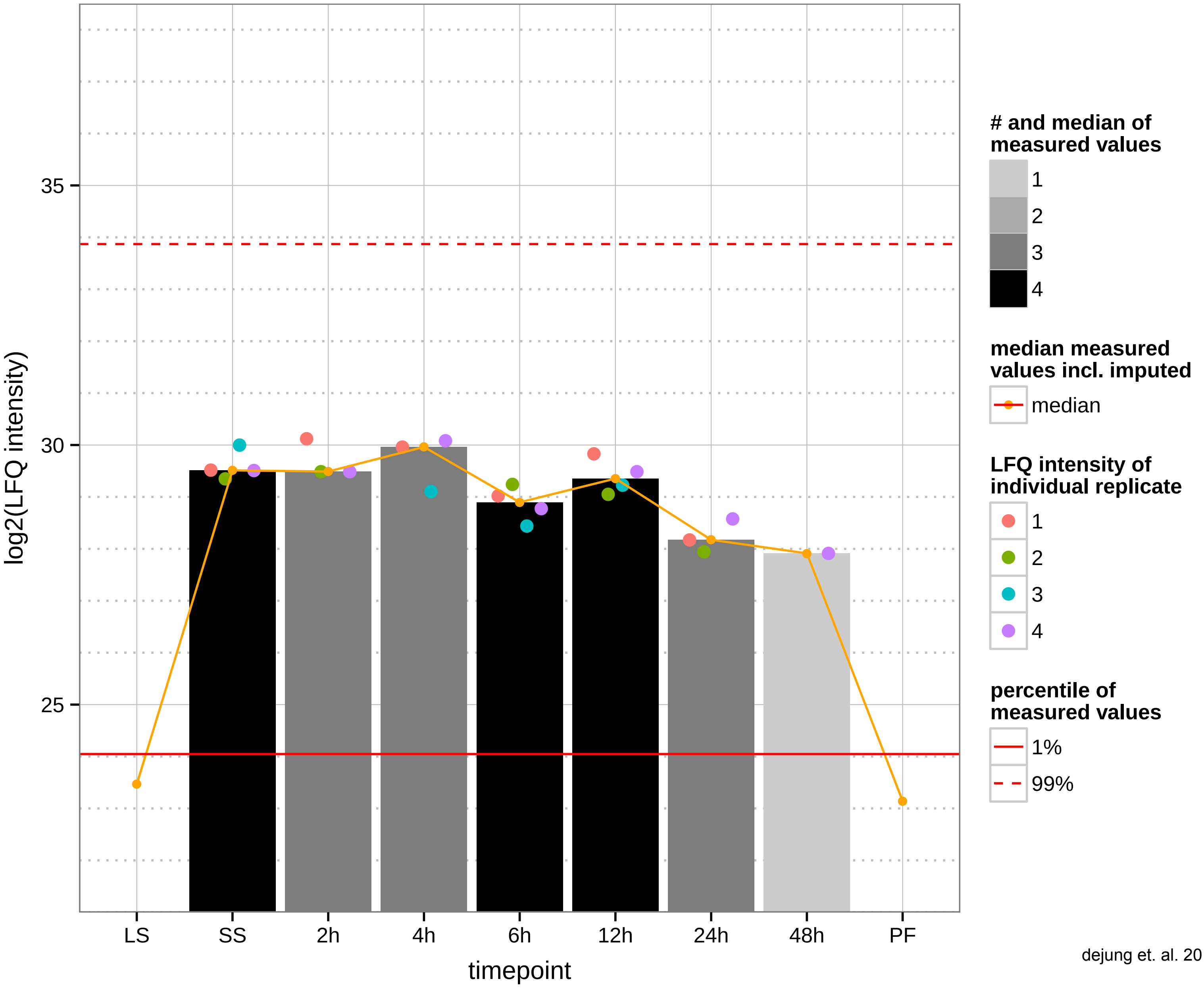
diacylglycerol acyltransferase, putative
Tb927.11.2210
AGOF: diacylglycerol O−acyltransferase activity
AGOC: integral to membrane
AGOP: triglyceride biosynthetic process
PGOF: transferase activity, transferring acyl groups other than amino−acyl groups
PGOC: null
PGOP: null





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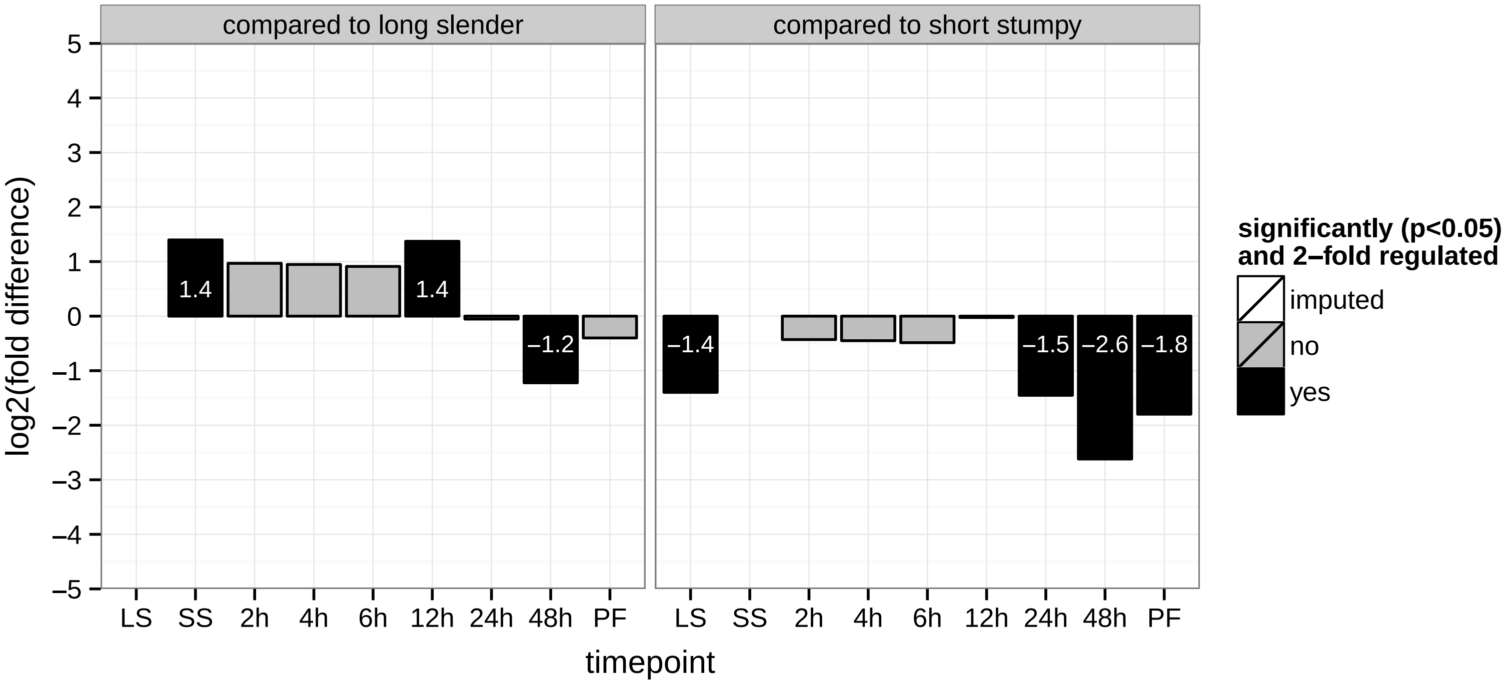
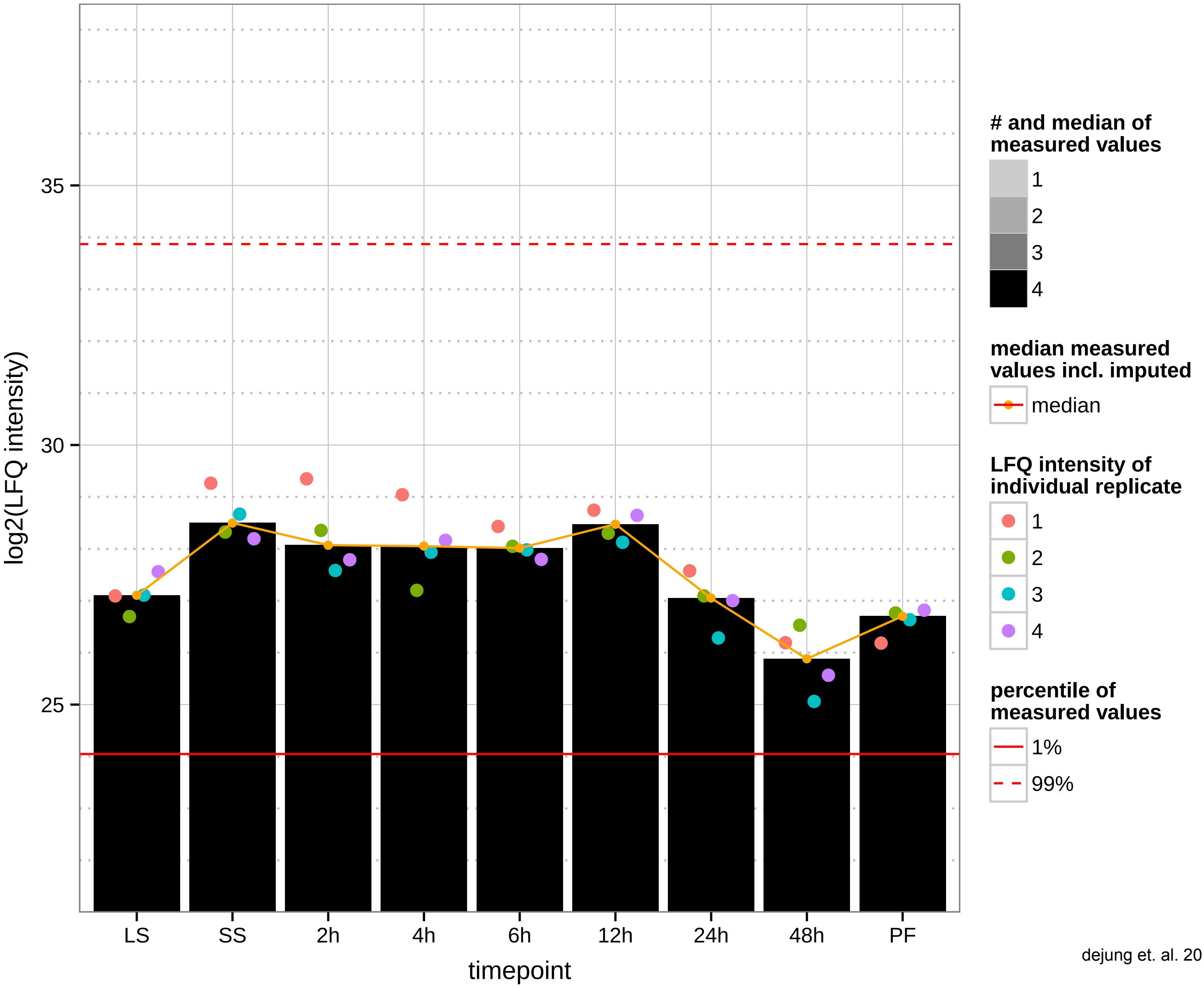
Unc104–like kinesin, putative
Tb927.11.2490
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: kinesin complex, microtubule associated complex
AGOP: microtubule–based movement, vesicle transport along microtubule
PGOF: ATP binding, microtubule motor activity, protein binding
PGOC: null
PGOP: microtubule–based movement





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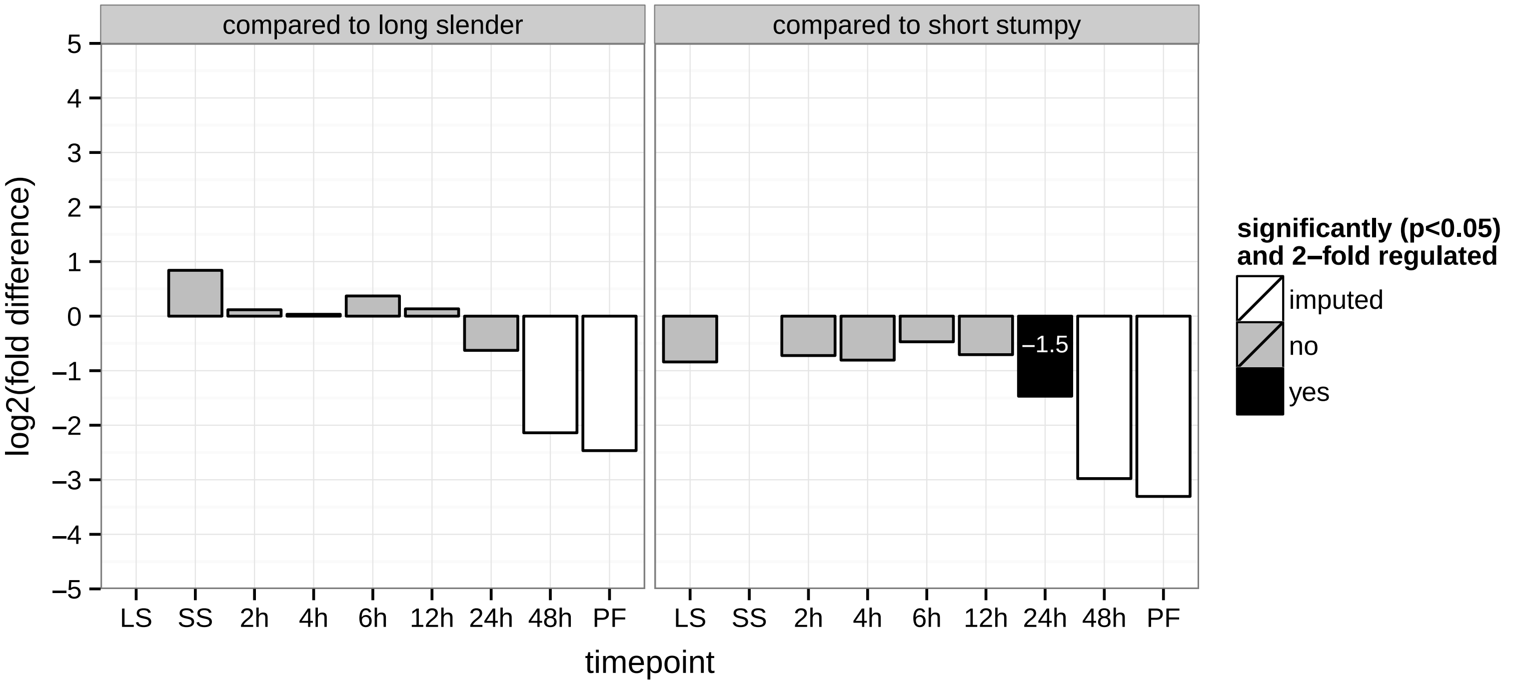
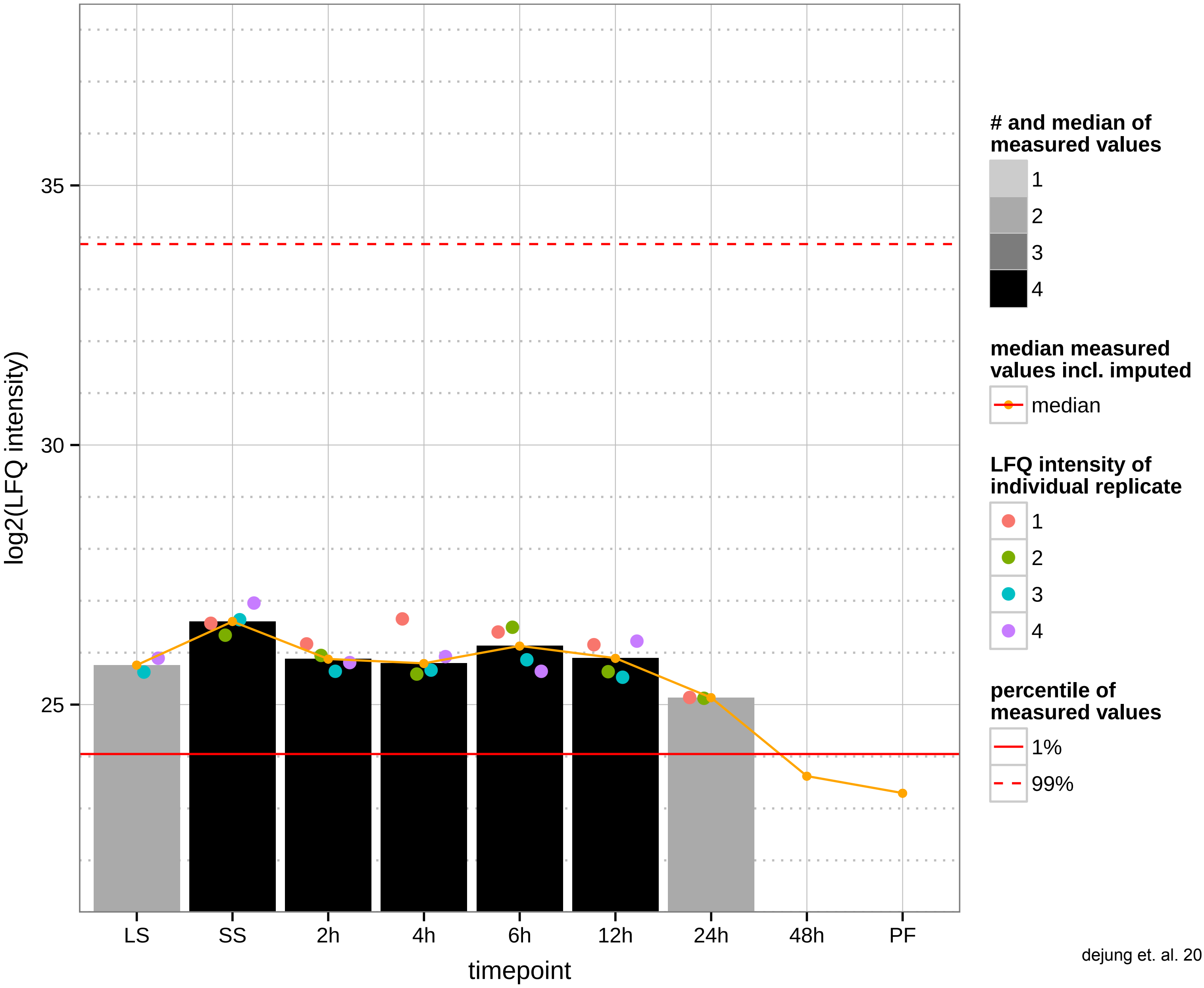
hypothetical protein, conserved
Tb927.11.2860
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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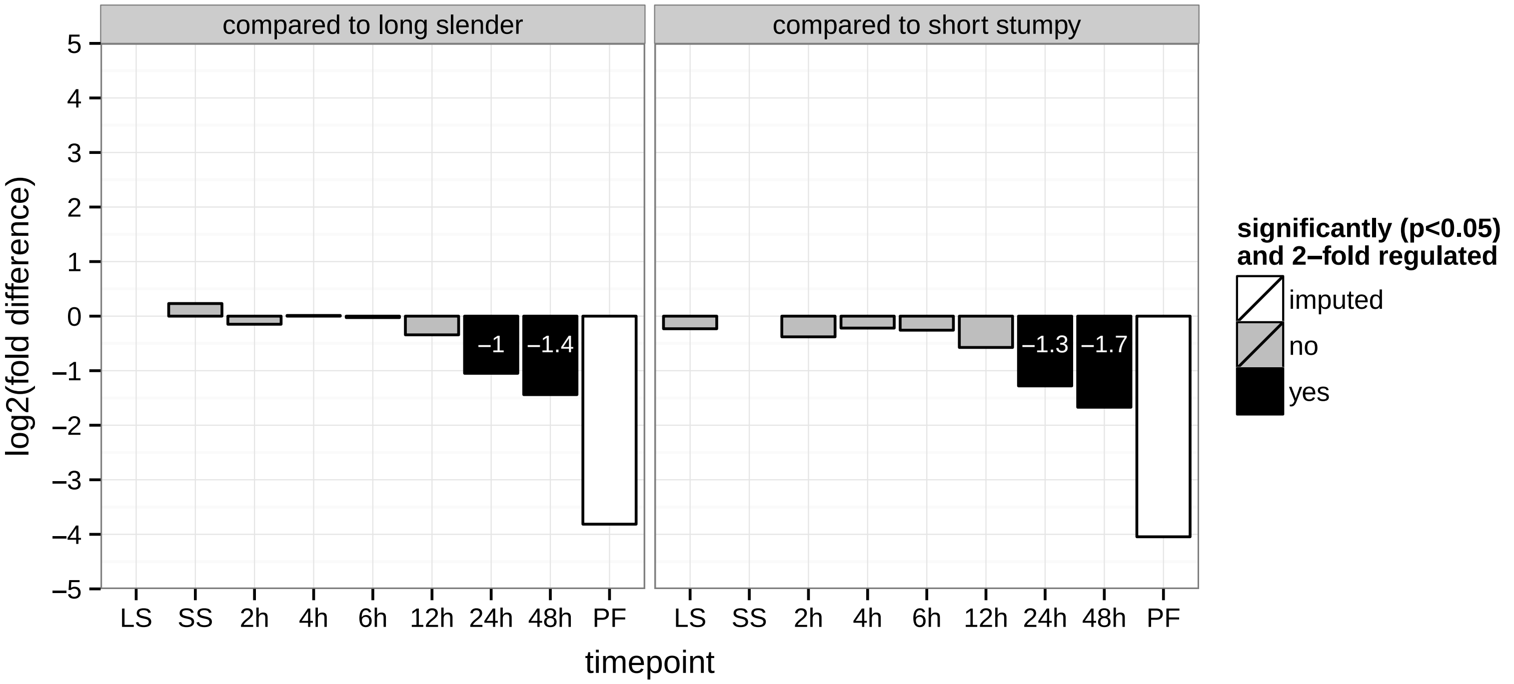
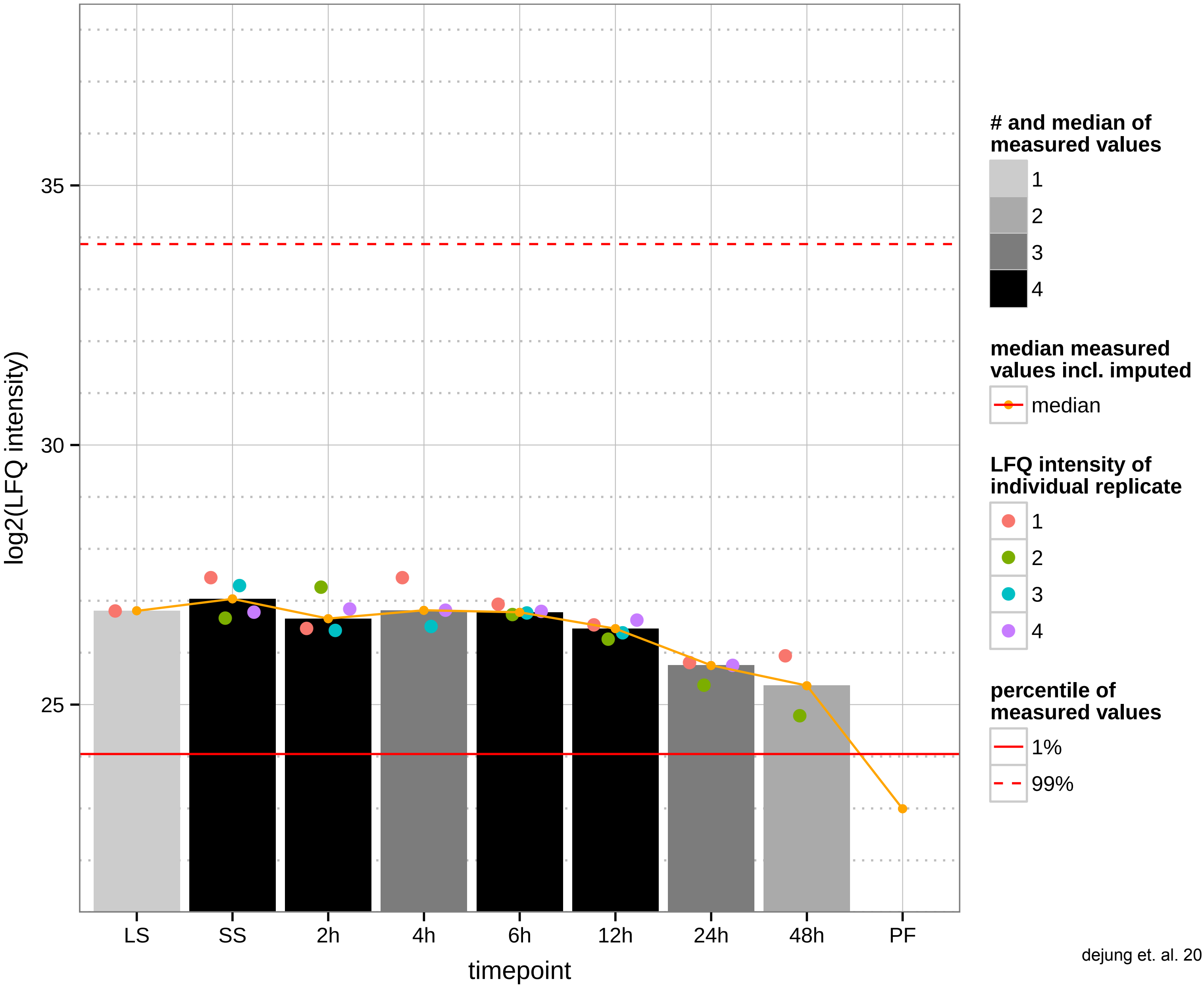
phosphatase and tensin homologue, putative
Tb927.11.290
AGOF: protein tyrosine/serine/threonine phosphatase activity
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, protein dephosphorylation, quorum sensing i
PGOF: phosphatase activity, protein tyrosine/serine/threonine phosphatase activity
PGOC: null
PGOP: dephosphorylation, protein dephosphorylation





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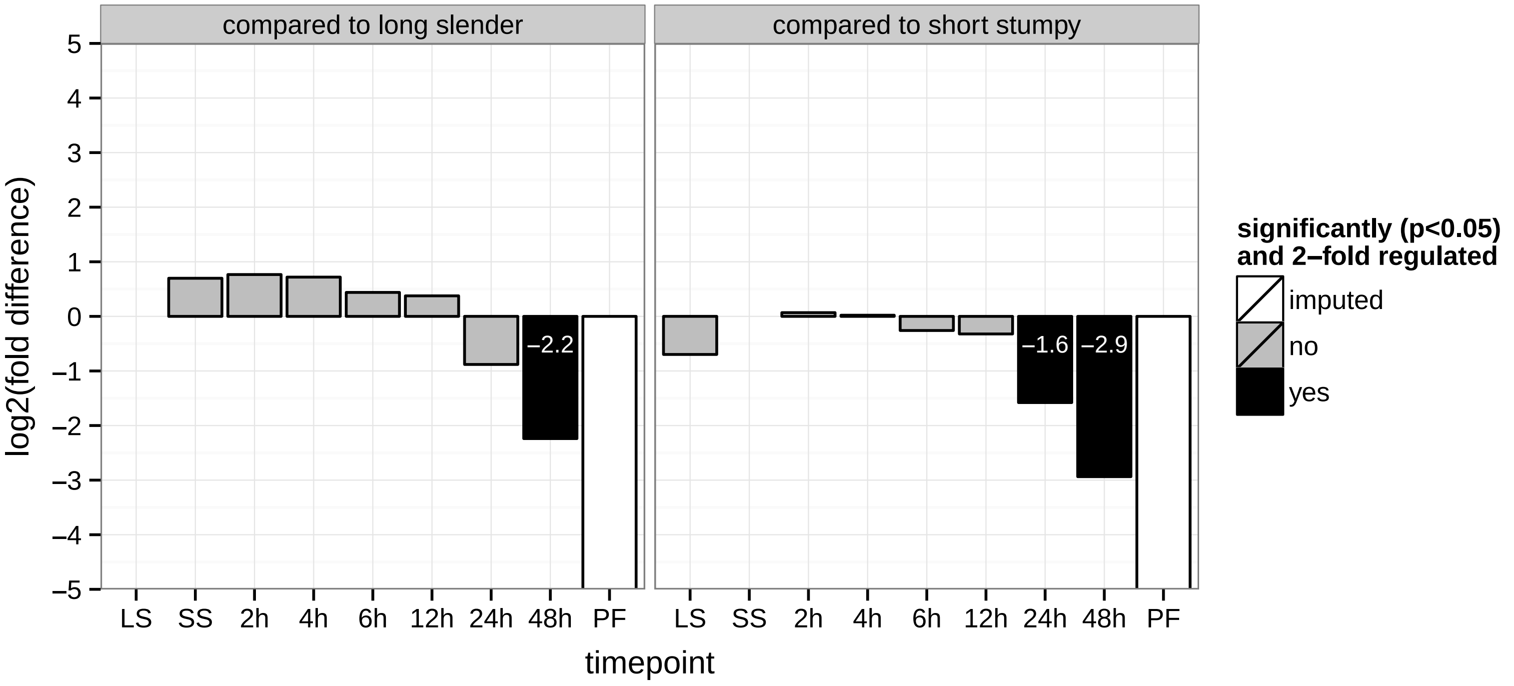
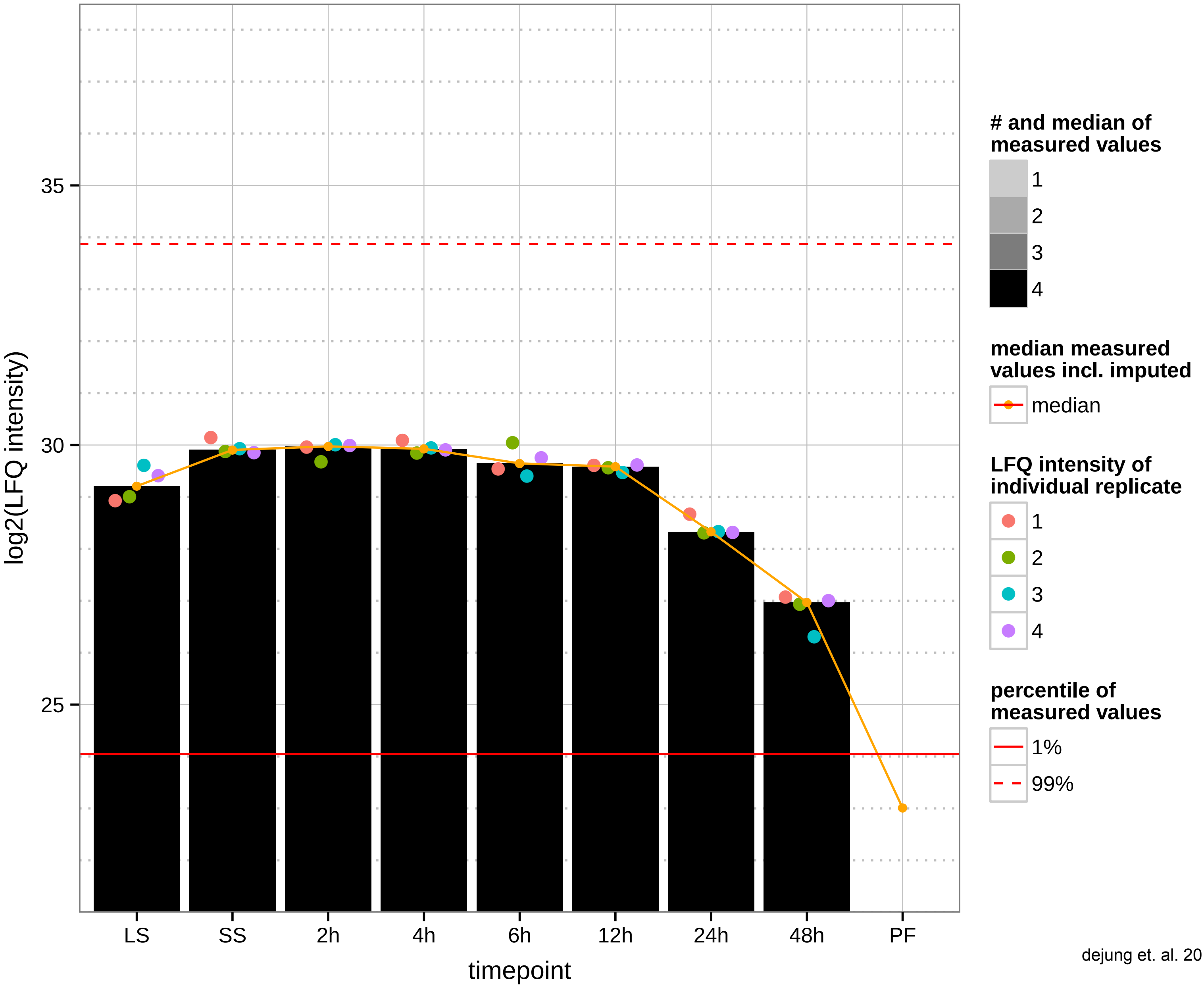
metacaspase, cysteine peptidase, Clan CD, family C13 (mca1)
Tb927.11.3220
AGOF: cysteine–type endopeptidase activity
AGOC: mitochondrion
AGOP: mitochondrion organization, proteolysis
PGOF: cysteine–type endopeptidase activity
PGOC: null
PGOP: proteolysis





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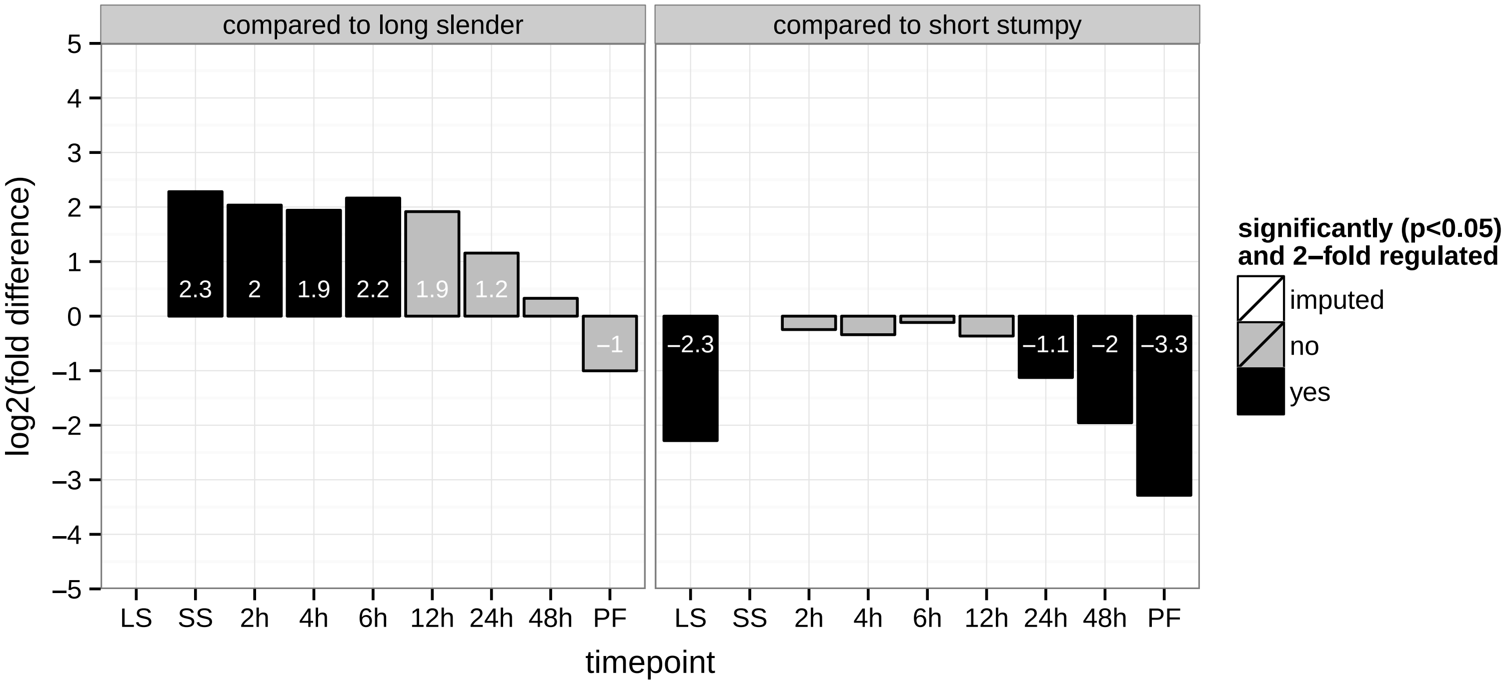
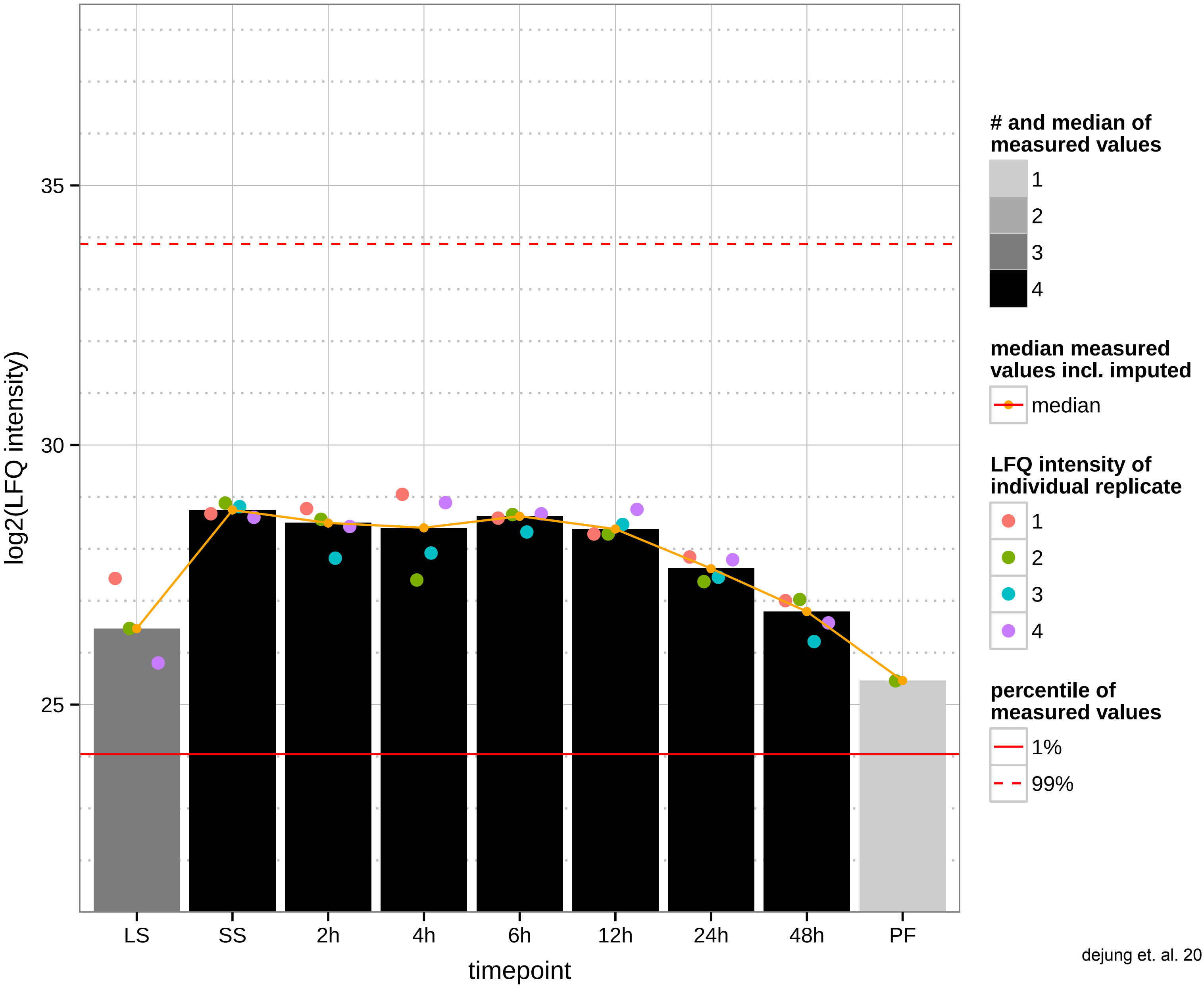
AMP deaminase, putative
Tb927.11.3850
AGOF: deaminase activity
AGOC: null
AGOP: purine ribonucleoside monophosphate biosynthetic process
PGOF: deaminase activity
PGOC: null
PGOP: purine ribonucleoside monophosphate biosynthetic process





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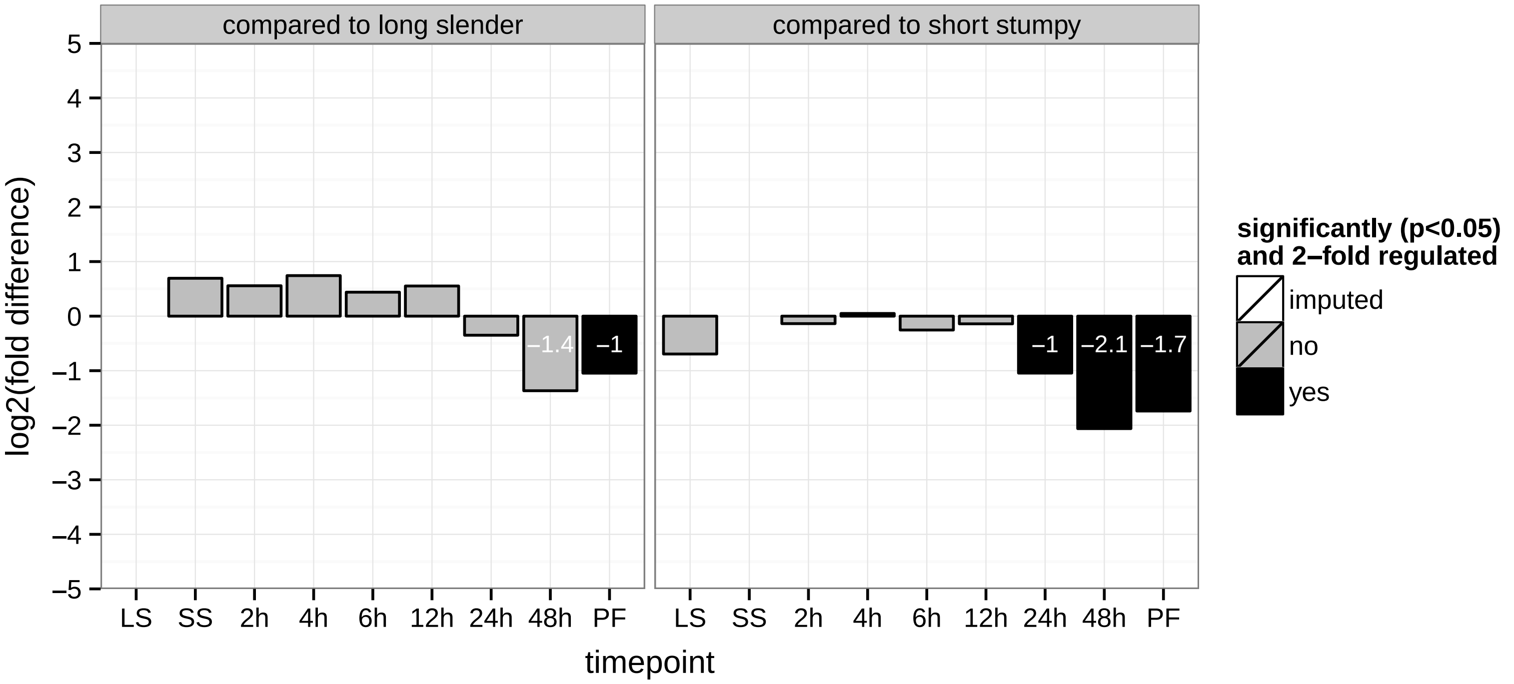
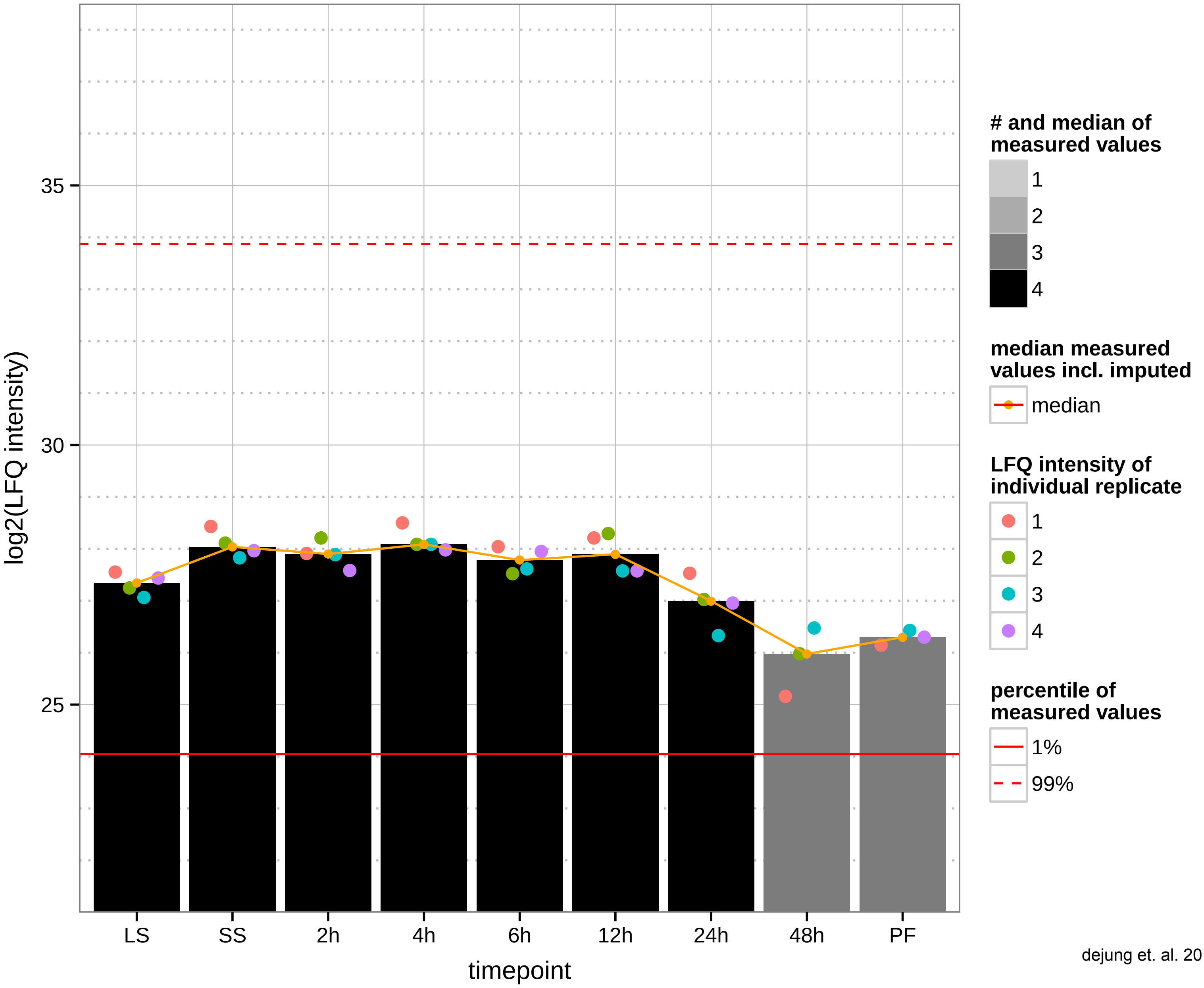
clathrin coat assembly protein, putative
Tb927.11.4800
AGOF: clathrin binding, phospholipid binding
AGOC: clathrin coat of coated pit, contractile vacuole
AGOP: receptor–mediated endocytosis
PGOF: phospholipid binding
PGOC: null
PGOP: null





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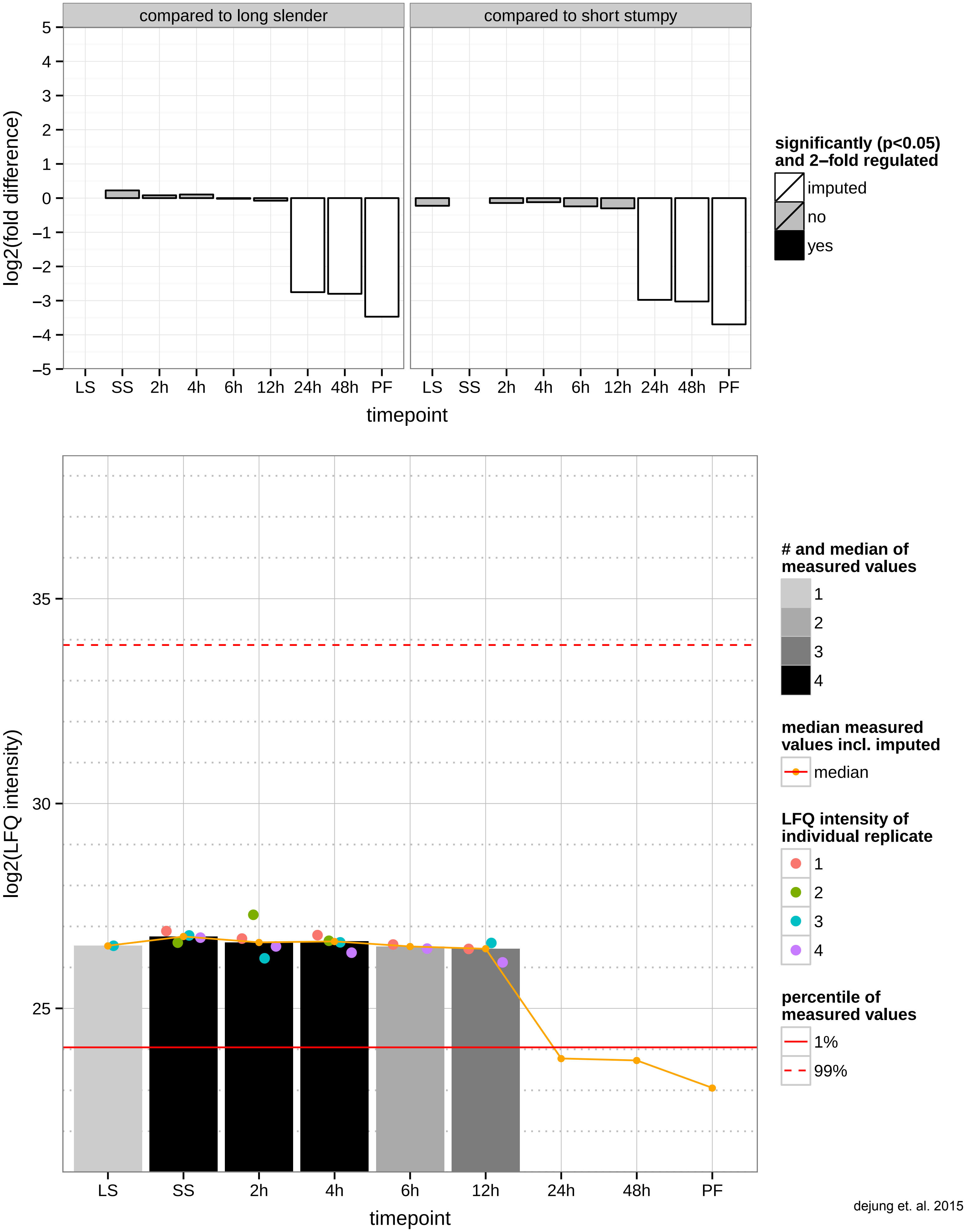
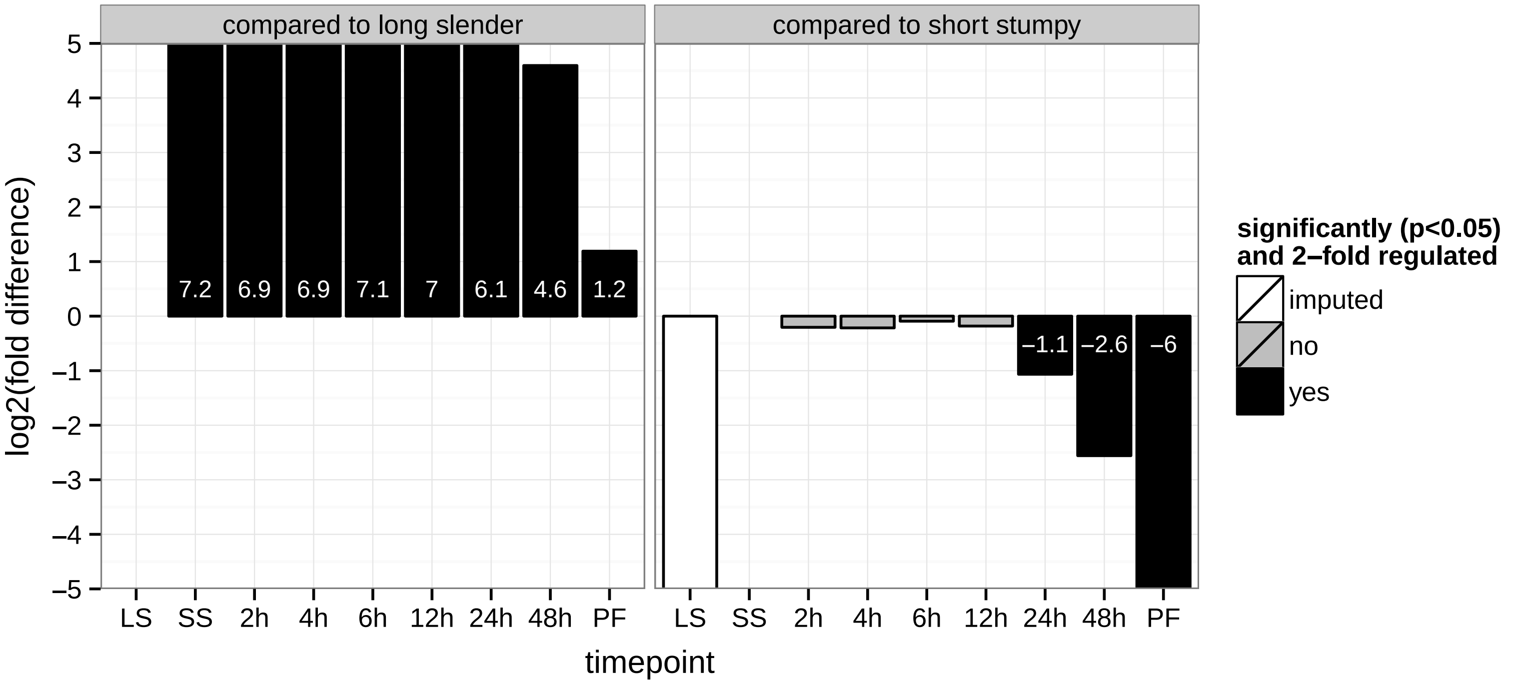
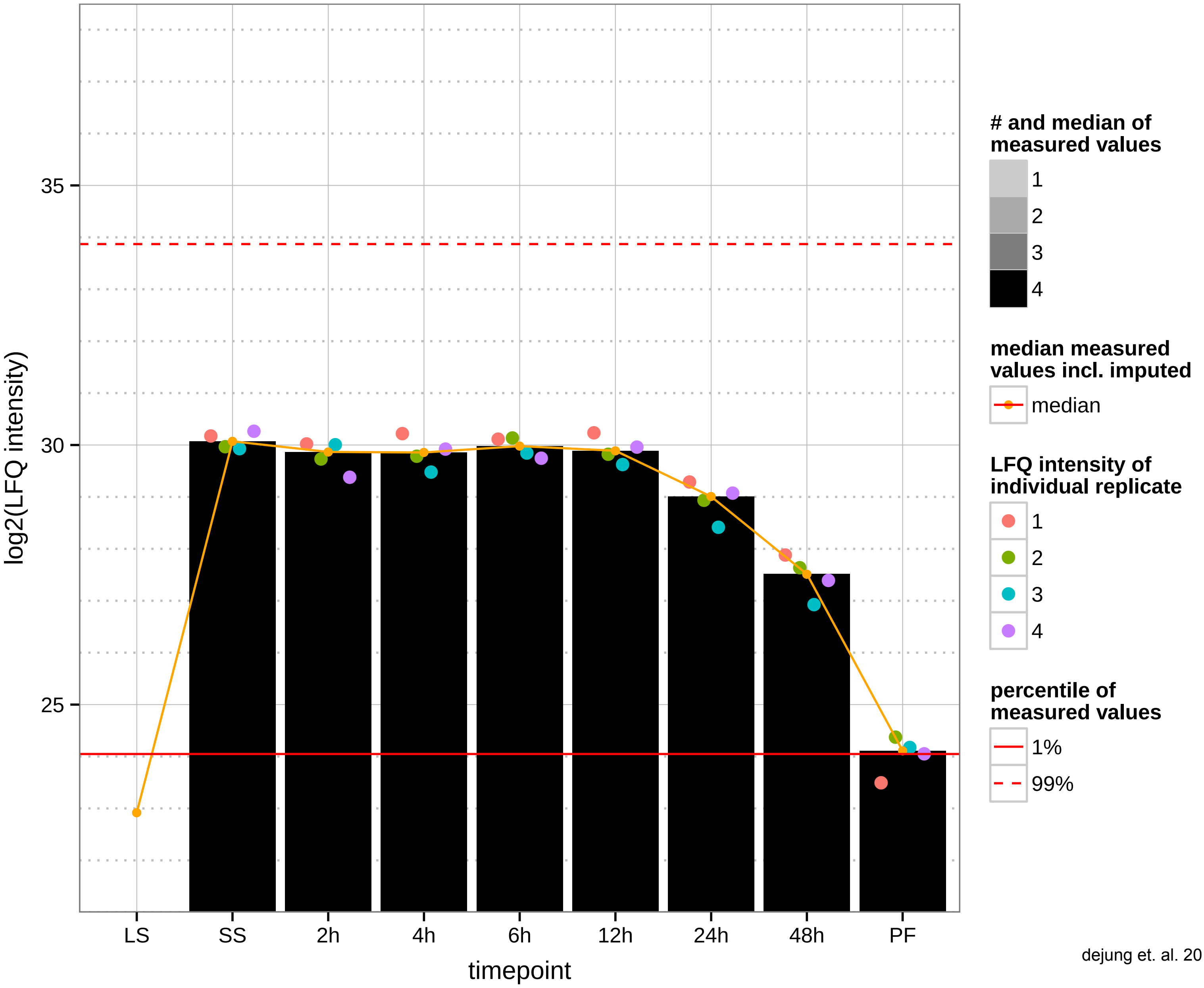
hypothetical protein, conserved
Tb927.11.5370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015

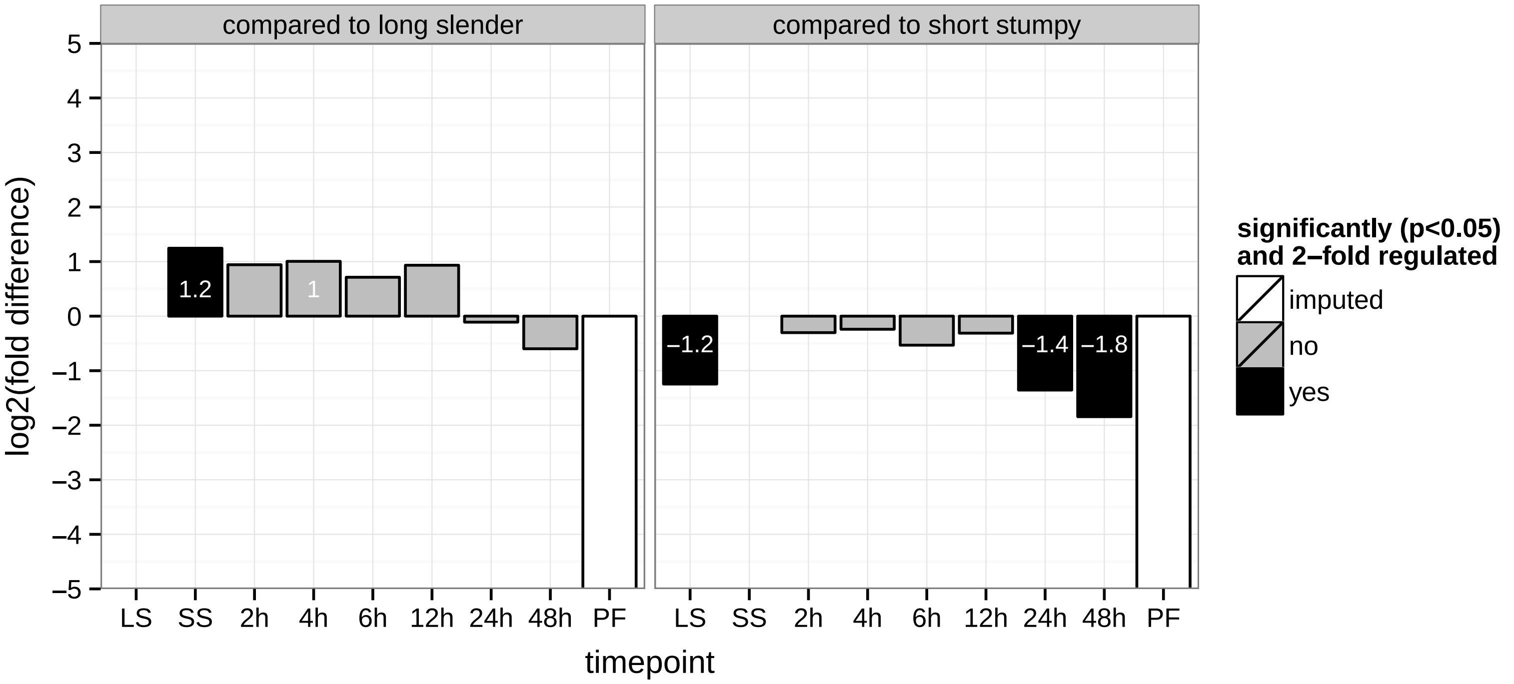
protein kinase, putative
Tb927.11.5860
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

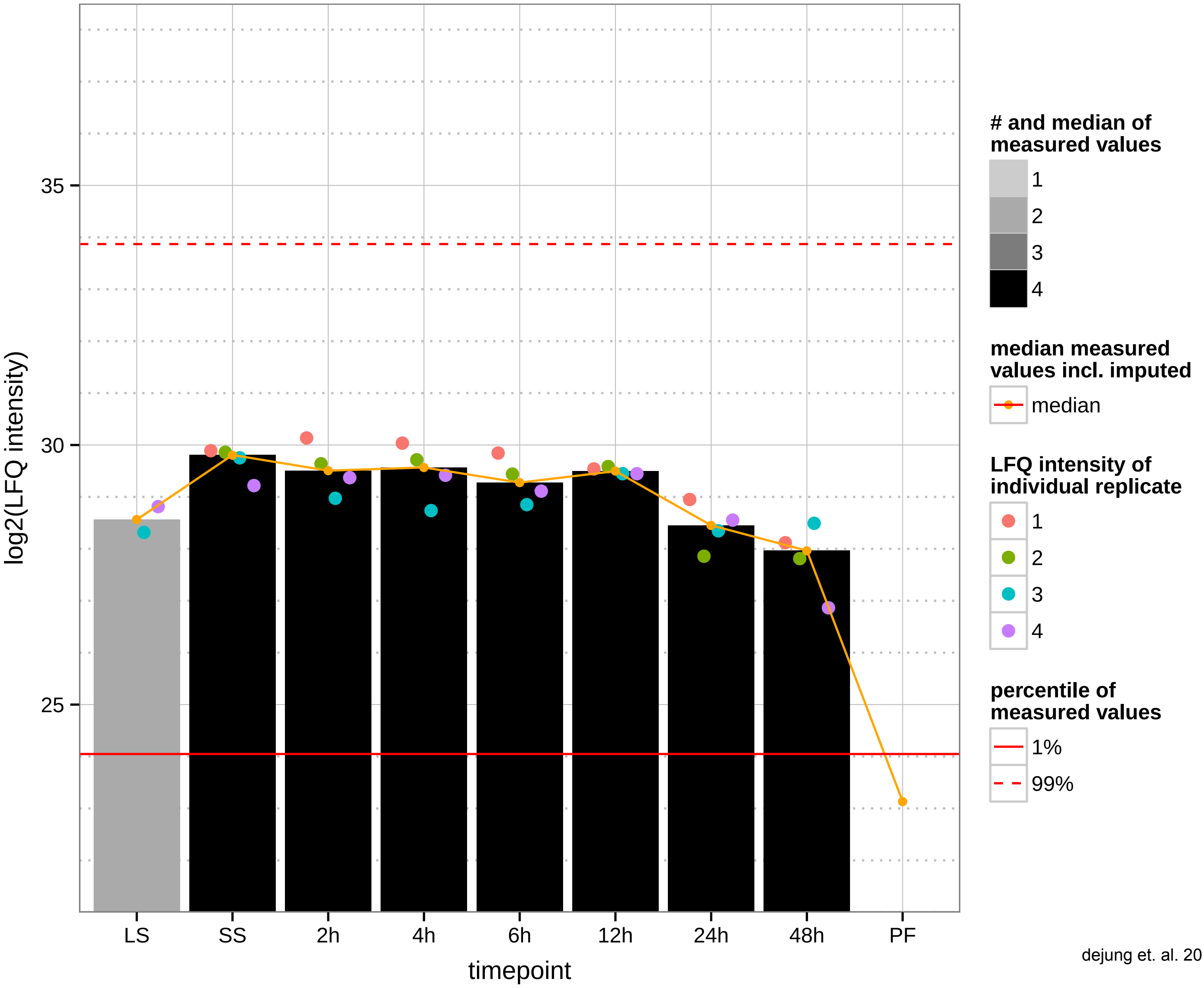




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.5910
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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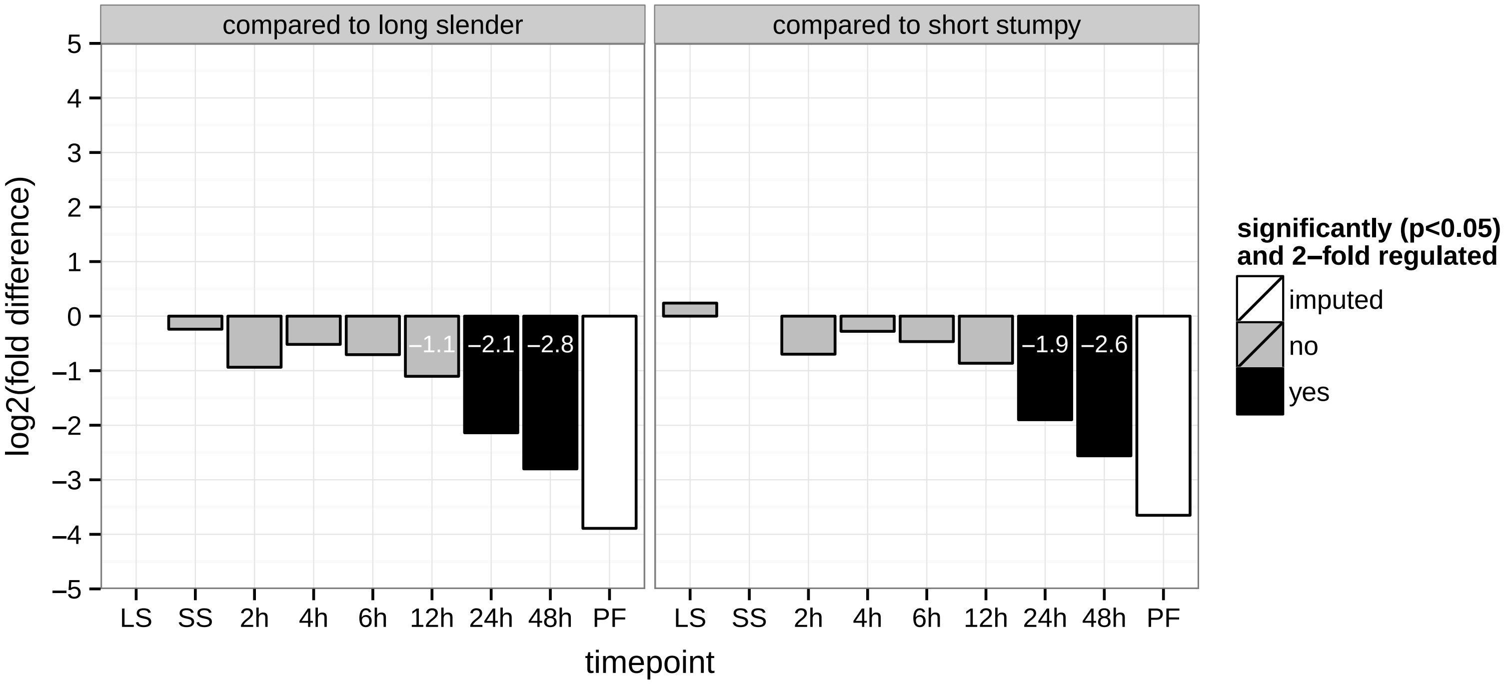
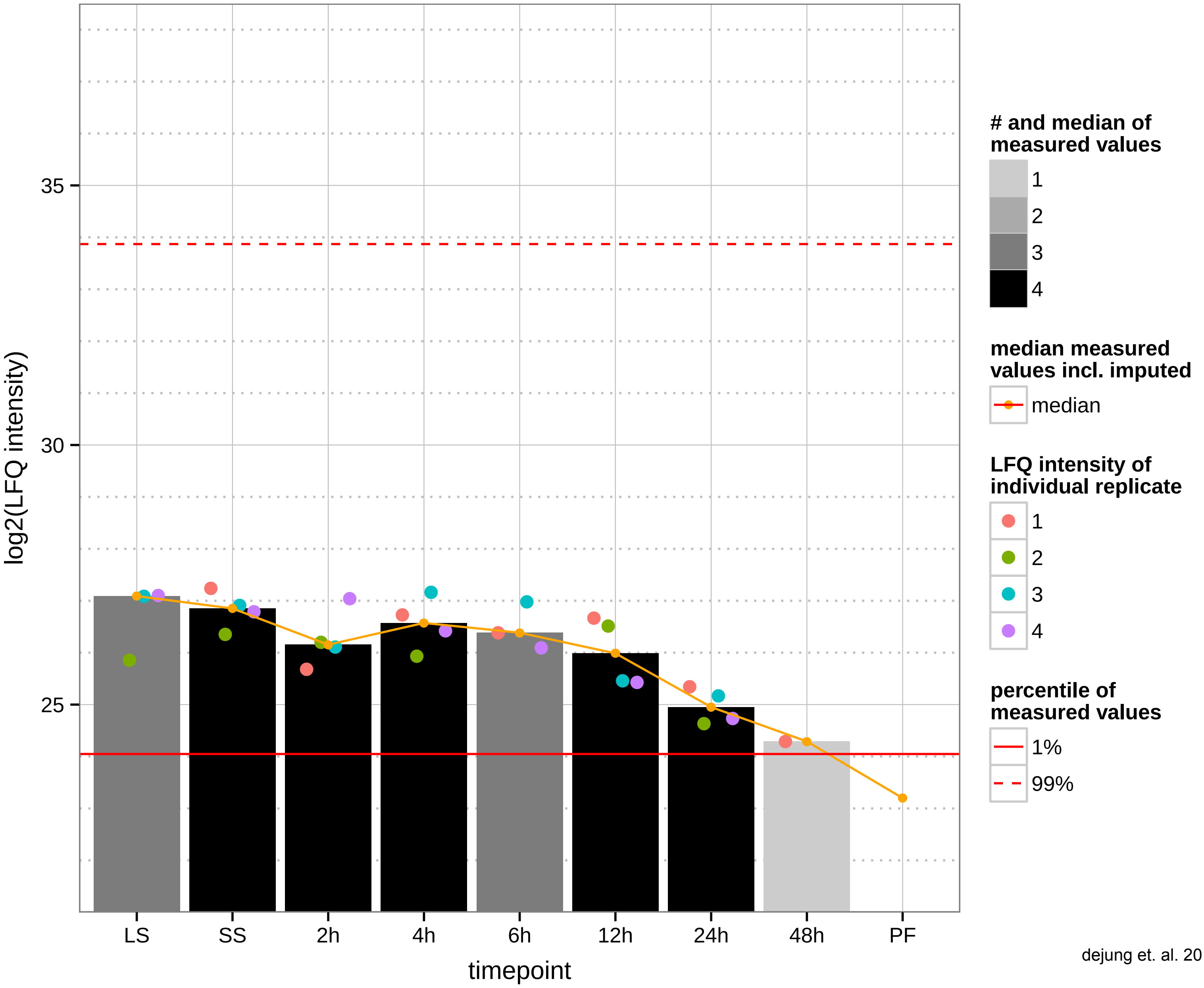
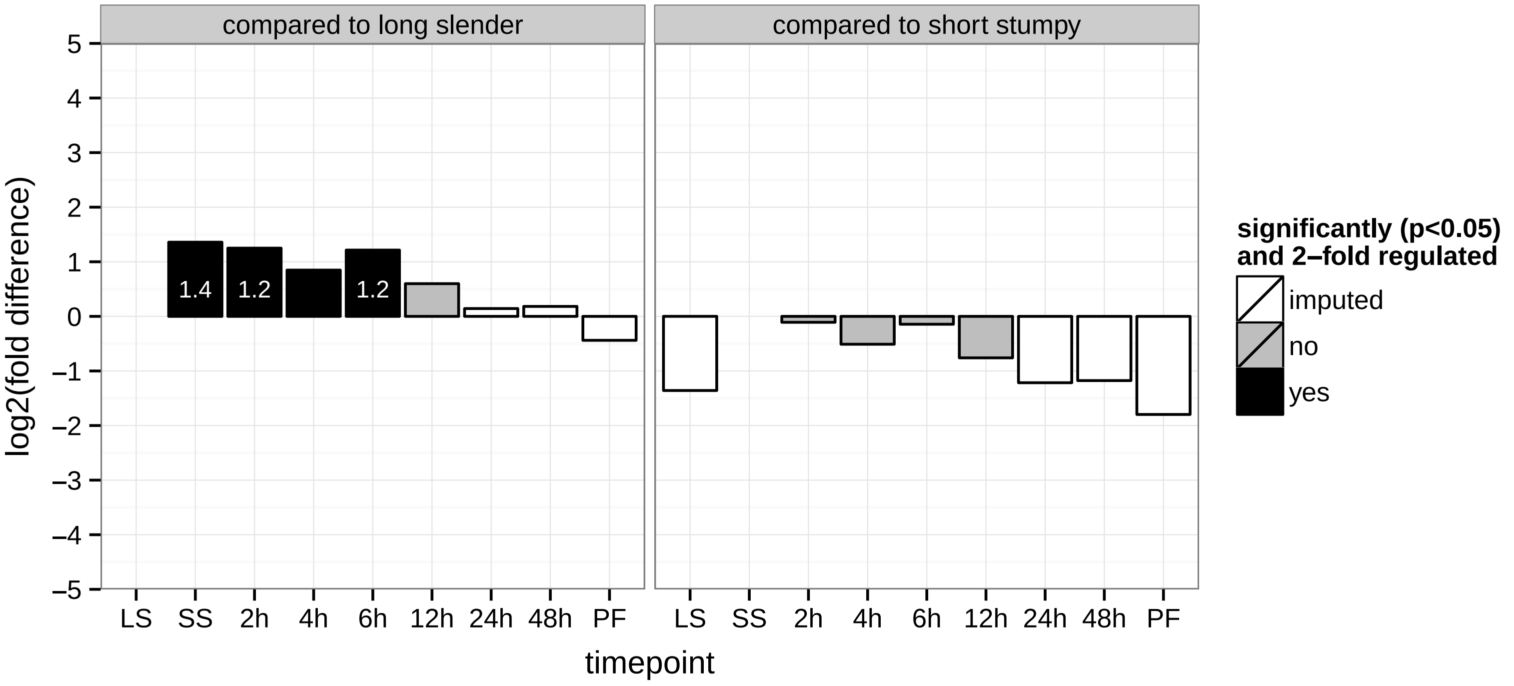
acidocalcisomal pyrophosphatase
Tb927.11.7080
AGOF: calcium ion binding, inorganic diphosphatase activity, magnesium ion binding, pyrophosphatase activity, zinc ion bindi
AGOC: acidocalcisome, cytoplasm
AGOP: phosphate–containing compound metabolic process
PGOF: inorganic diphosphatase activity, magnesium ion binding
PGOC: cytoplasm
PGOP: phosphate–containing compound metabolic process

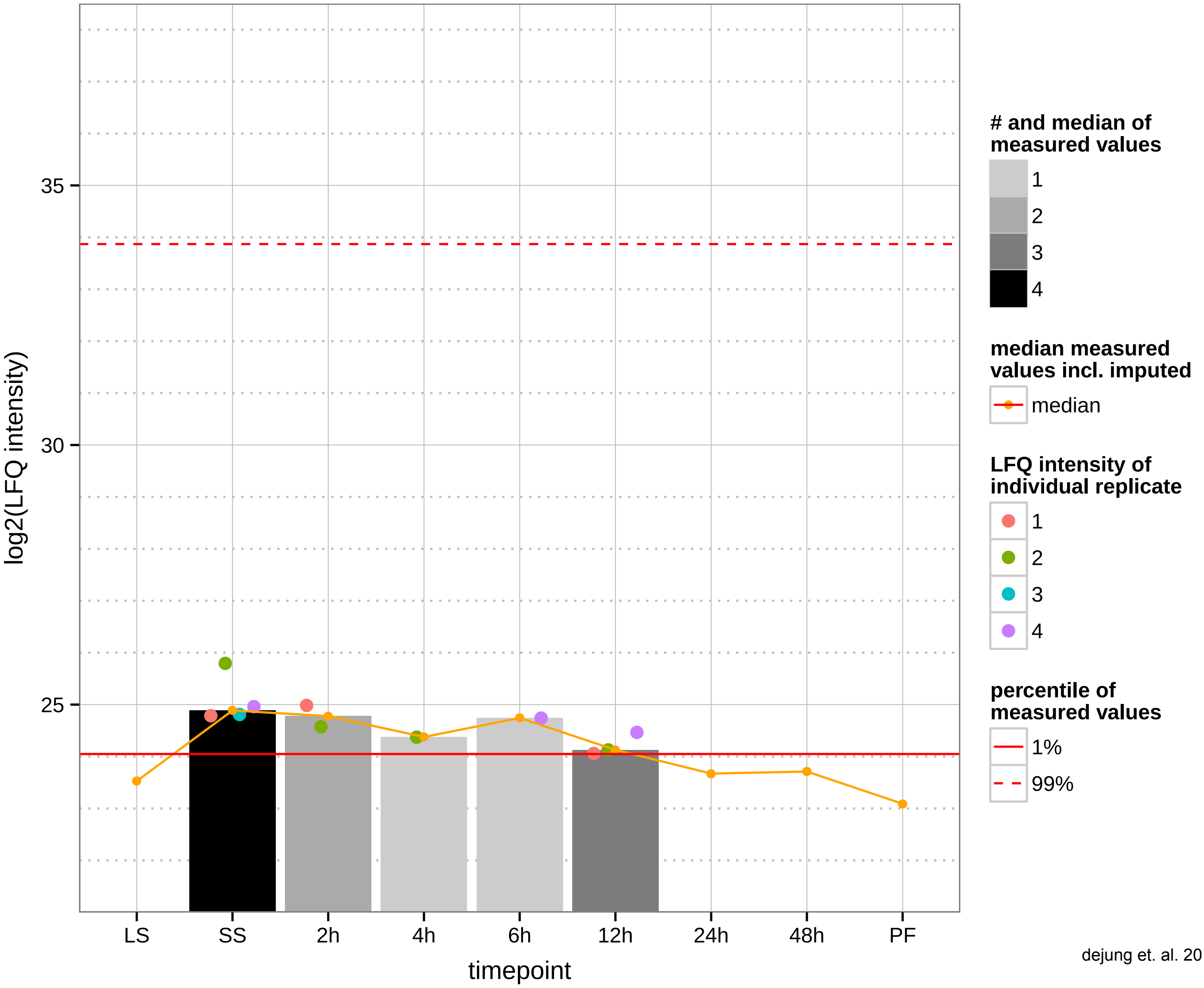




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.7120
AGOF: null
AGOC: exocyst
AGOP: vesicle docking involved in exocytosis
PGOF: null
PGOC: null
PGOP: null





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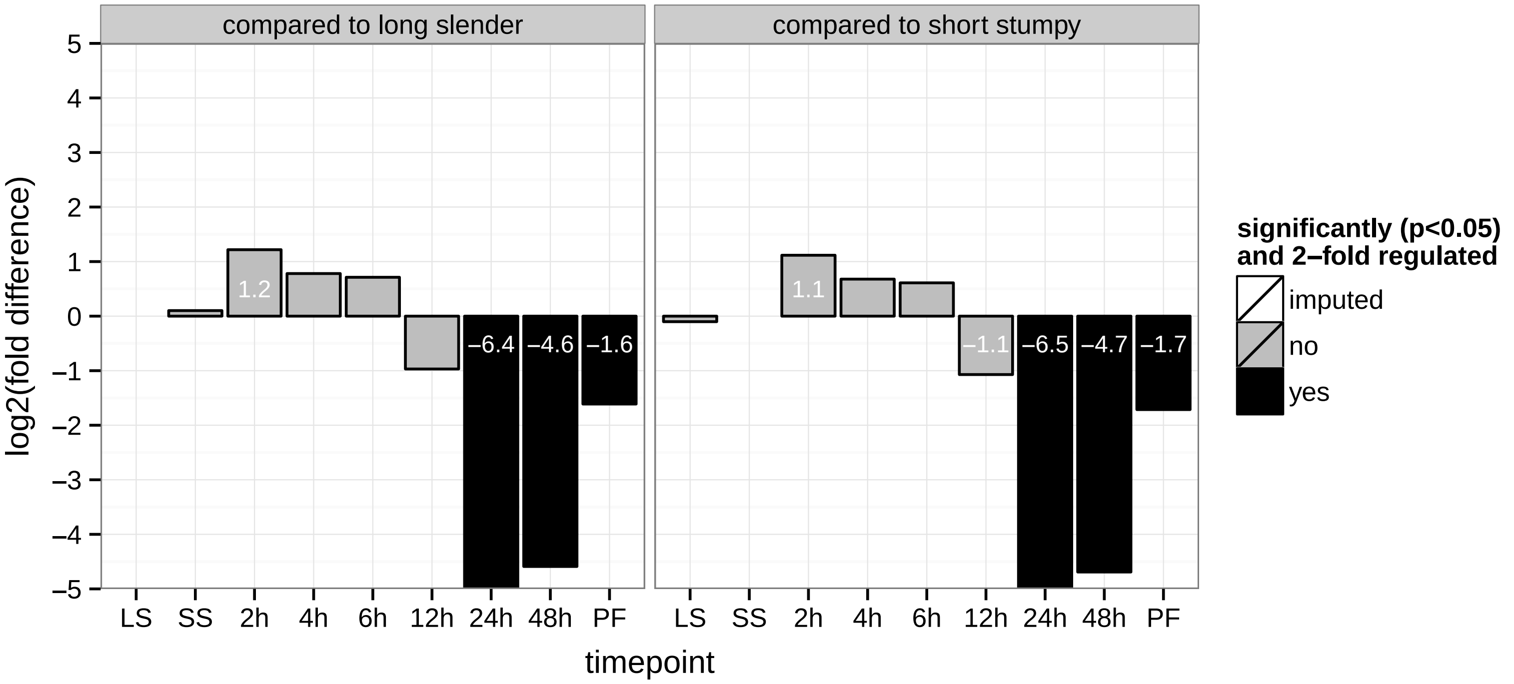
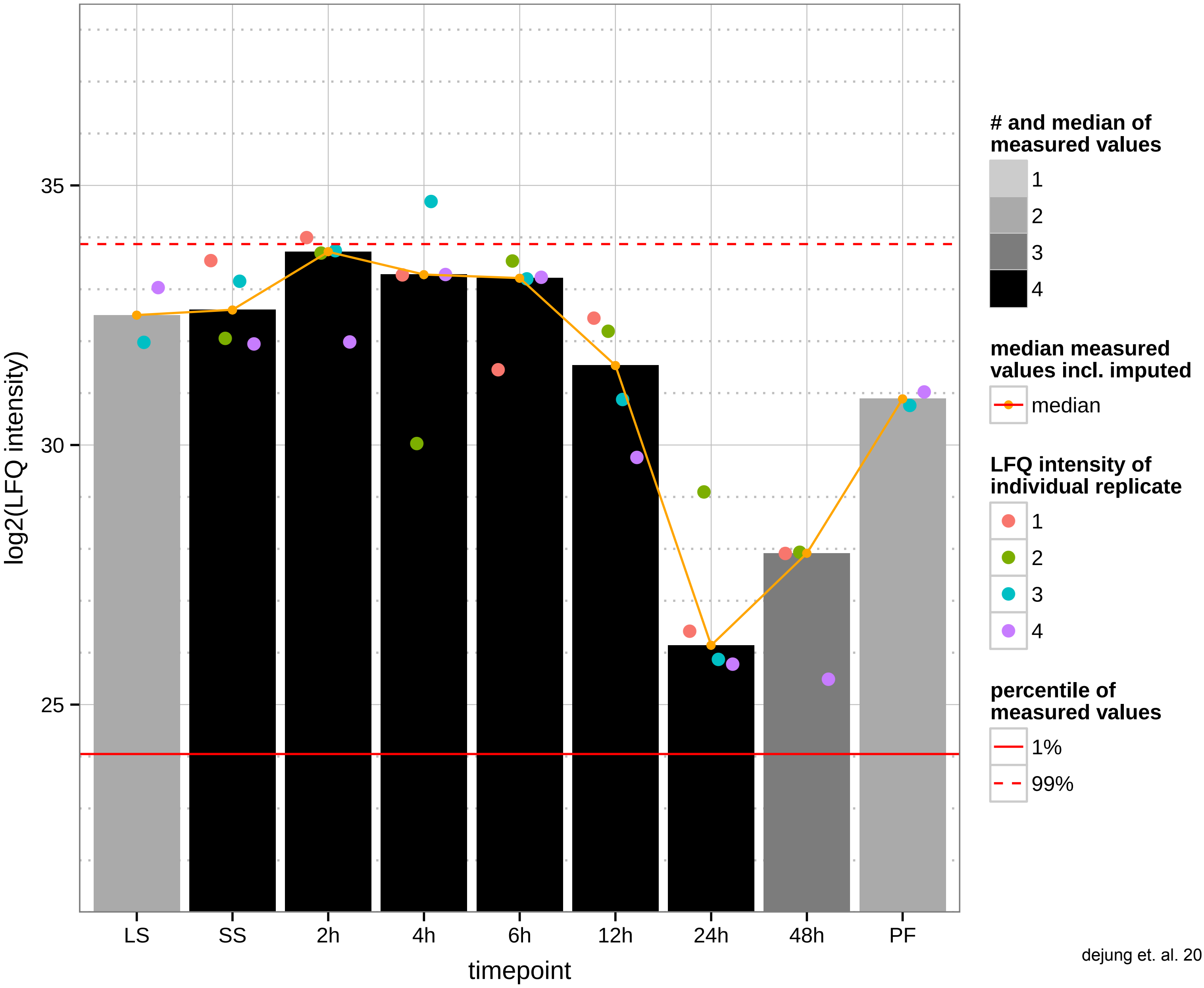
palmitoyl acyltransferase 9, putative
Tb927.11.7360
AGOF: zinc ion binding
AGOC: integral to membrane
AGOP: endocytosis, protein palmitoylation, transport
PGOF: zinc ion binding
PGOC: null
PGOP: null





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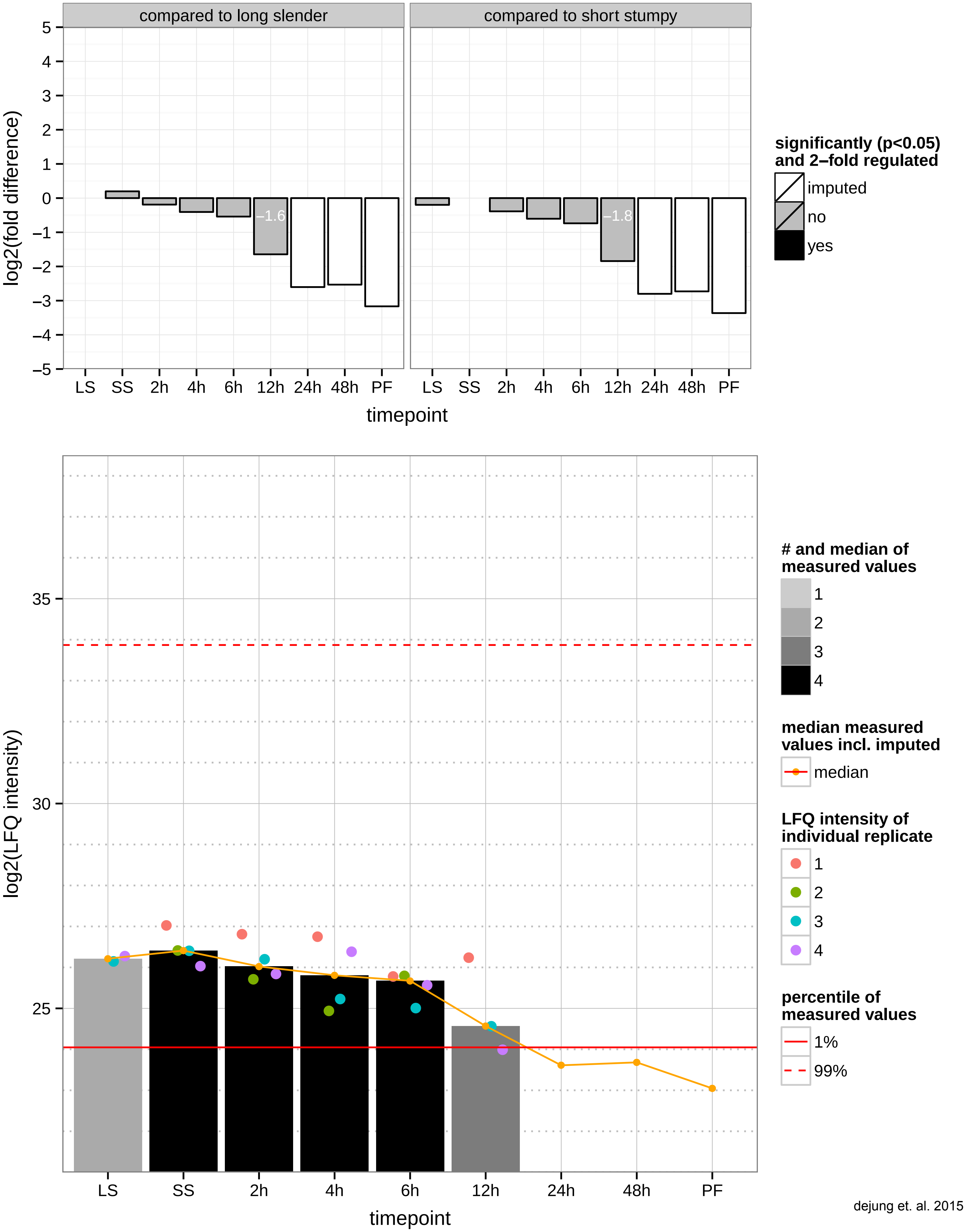
MSP−A, putative, chrXI additional, unordered contigs, Gp63−3 surface protease homolog, Gp63−1 surface protease homolog
Tb927.11.7710;Tb11.0380
AGOF: metalloendopeptidase activity, zinc ion binding, null
AGOC: membrane, null
AGOP: cell adhesion, proteolysis, null
PGOF: metalloendopeptidase activity, zinc ion binding
PGOC: membrane
PGOP: cell adhesion, proteolysis



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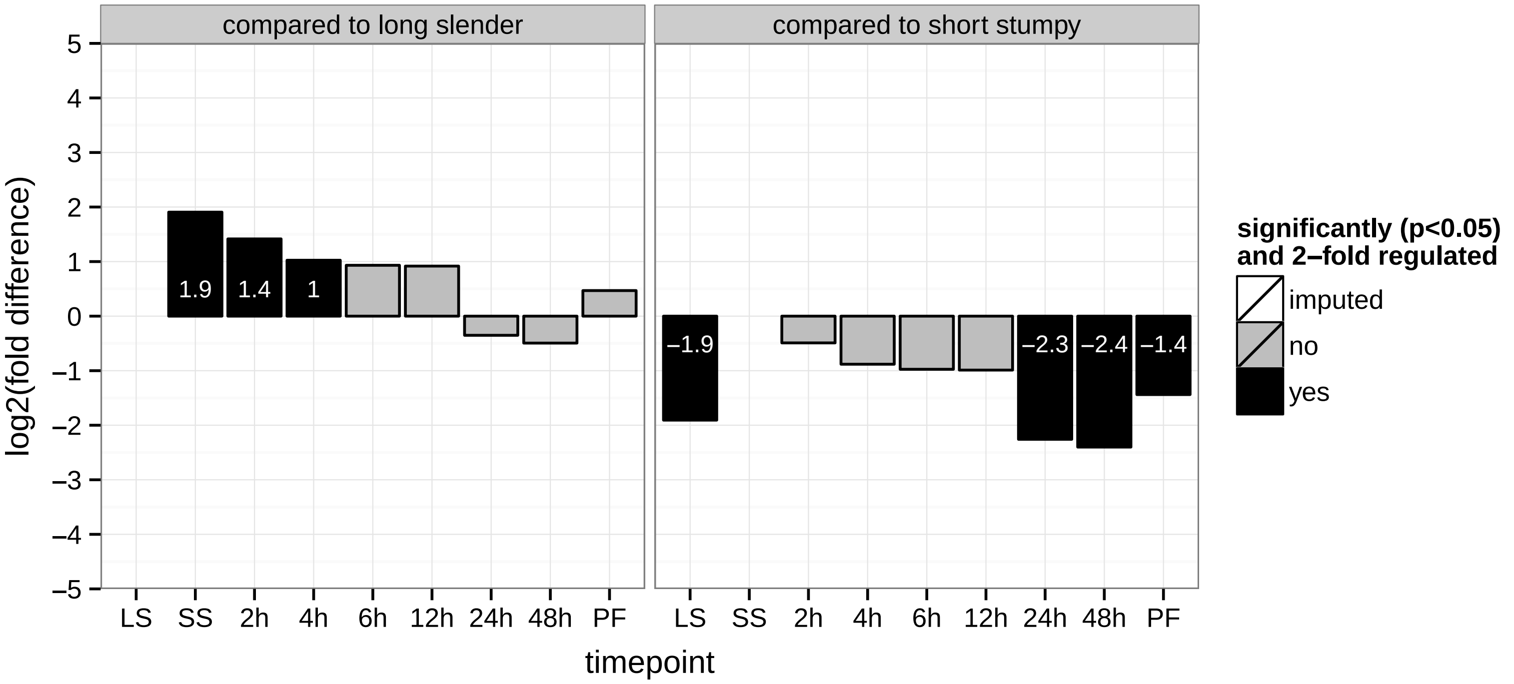
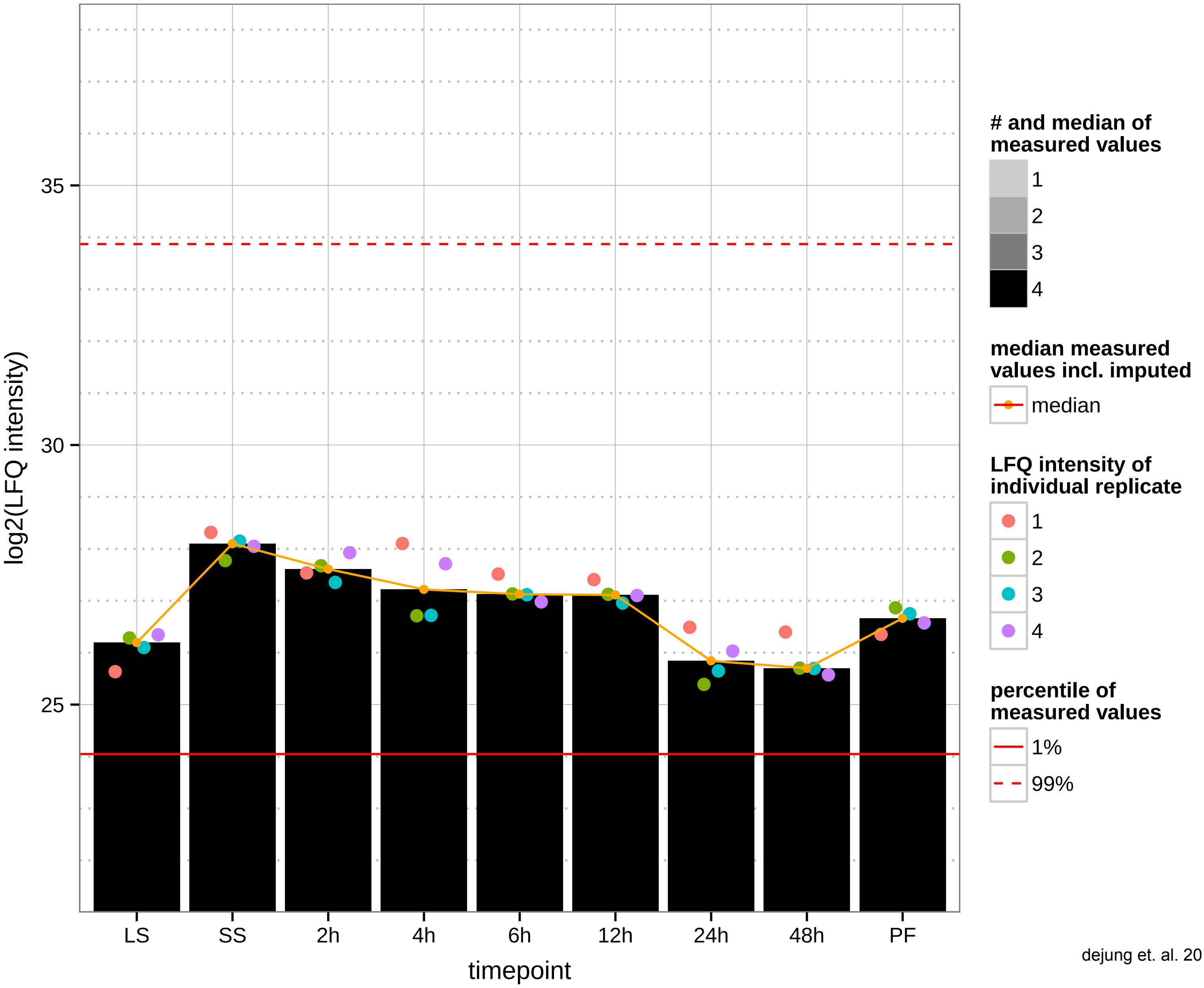
hypothetical protein, conserved
Tb927.11.810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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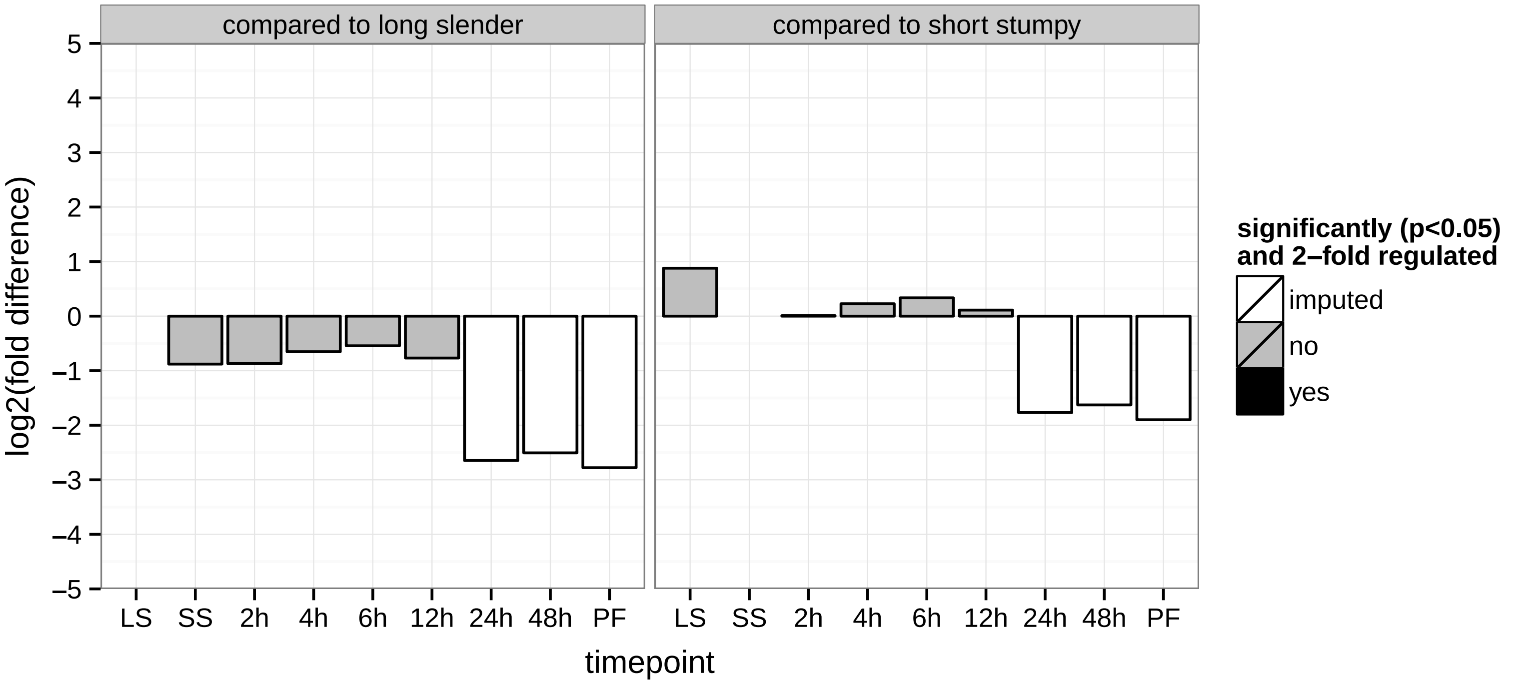
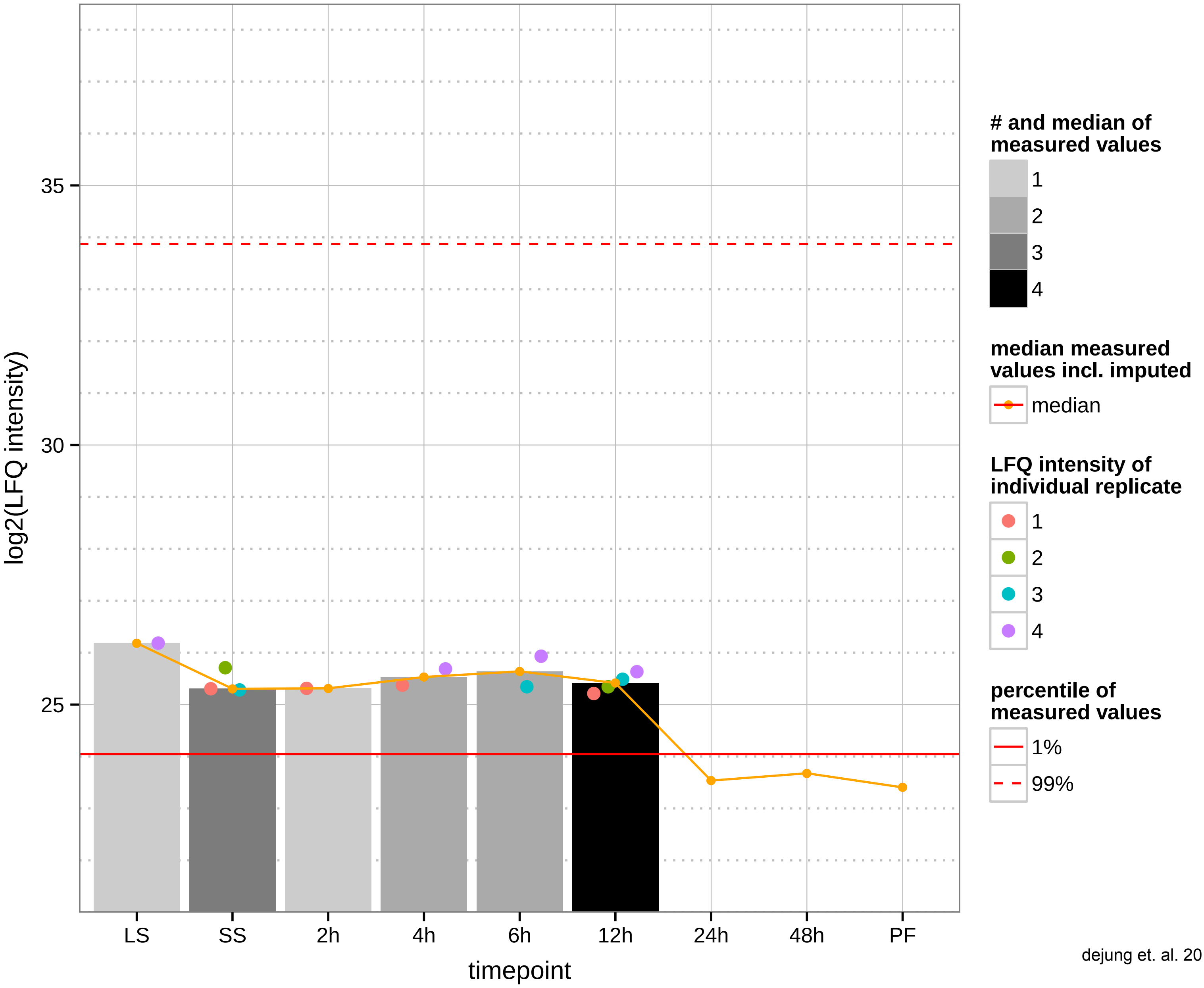
phosphonopyruvate decarboxylase–like protein, putative
Tb927.11.9350
AGOF: carboxy–lyase activity, thiamine pyrophosphate binding
AGOC: null
AGOP: null
PGOF: catalytic activity, thiamine pyrophosphate binding
PGOC: null
PGOP: null





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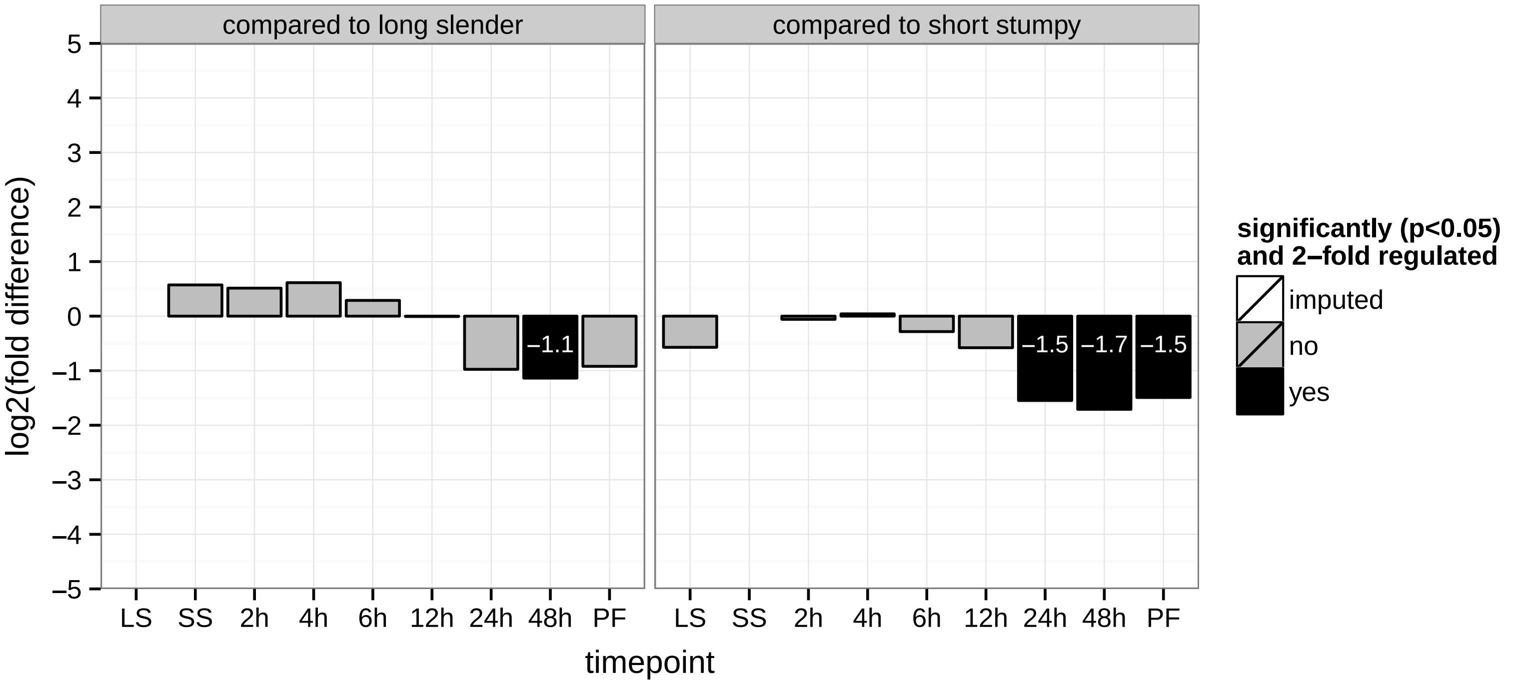
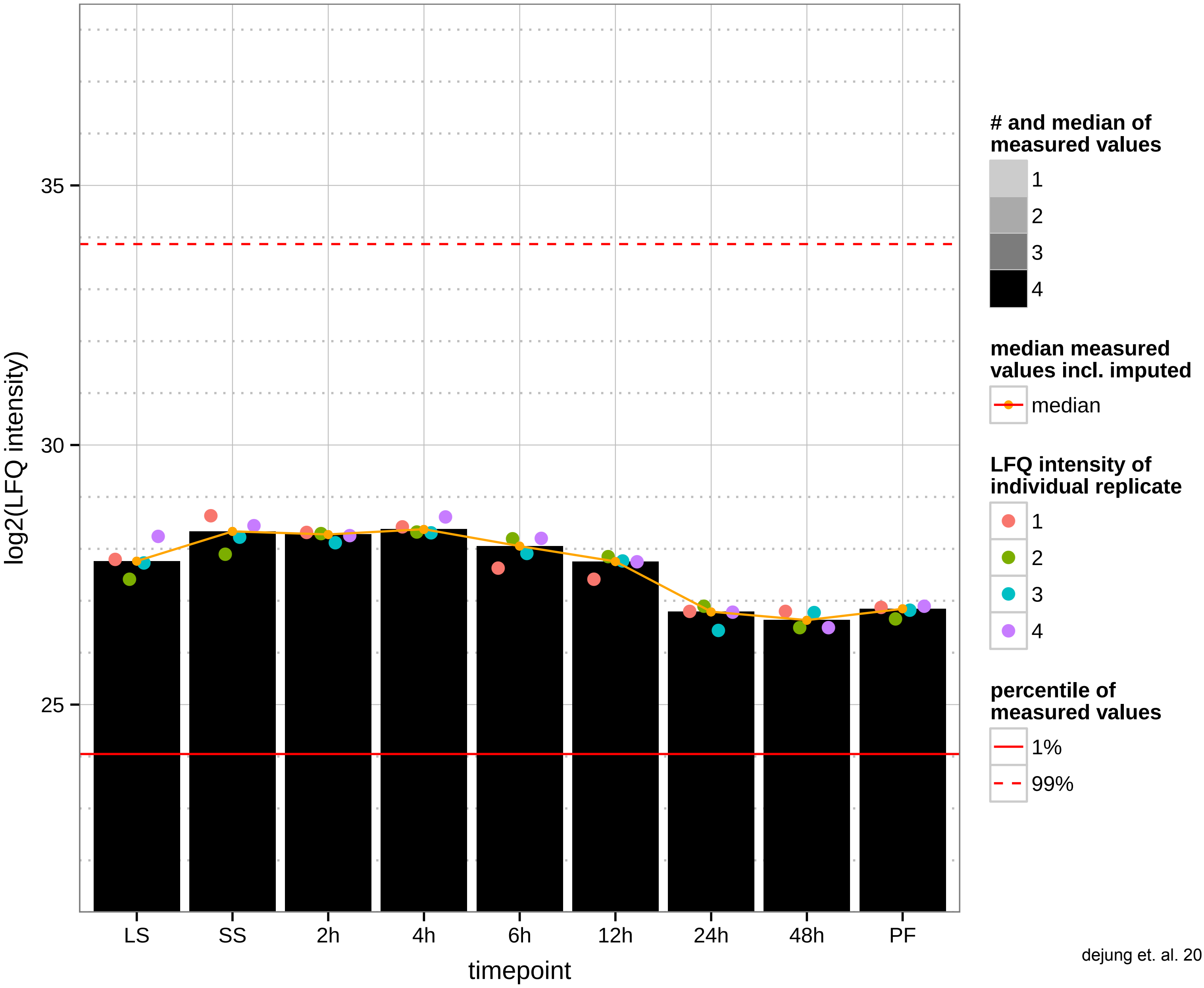
ADP–ribosylation factor GTPase activating protein, putative
Tb927.11.9470
AGOF: ARF GTPase activator activity, DNA binding, zinc ion binding
AGOC: nucleus
AGOP: regulation of ARF GTPase activity
PGOF: ARF GTPase activator activity, zinc ion binding
PGOC: null
PGOP: regulation of ARF GTPase activity





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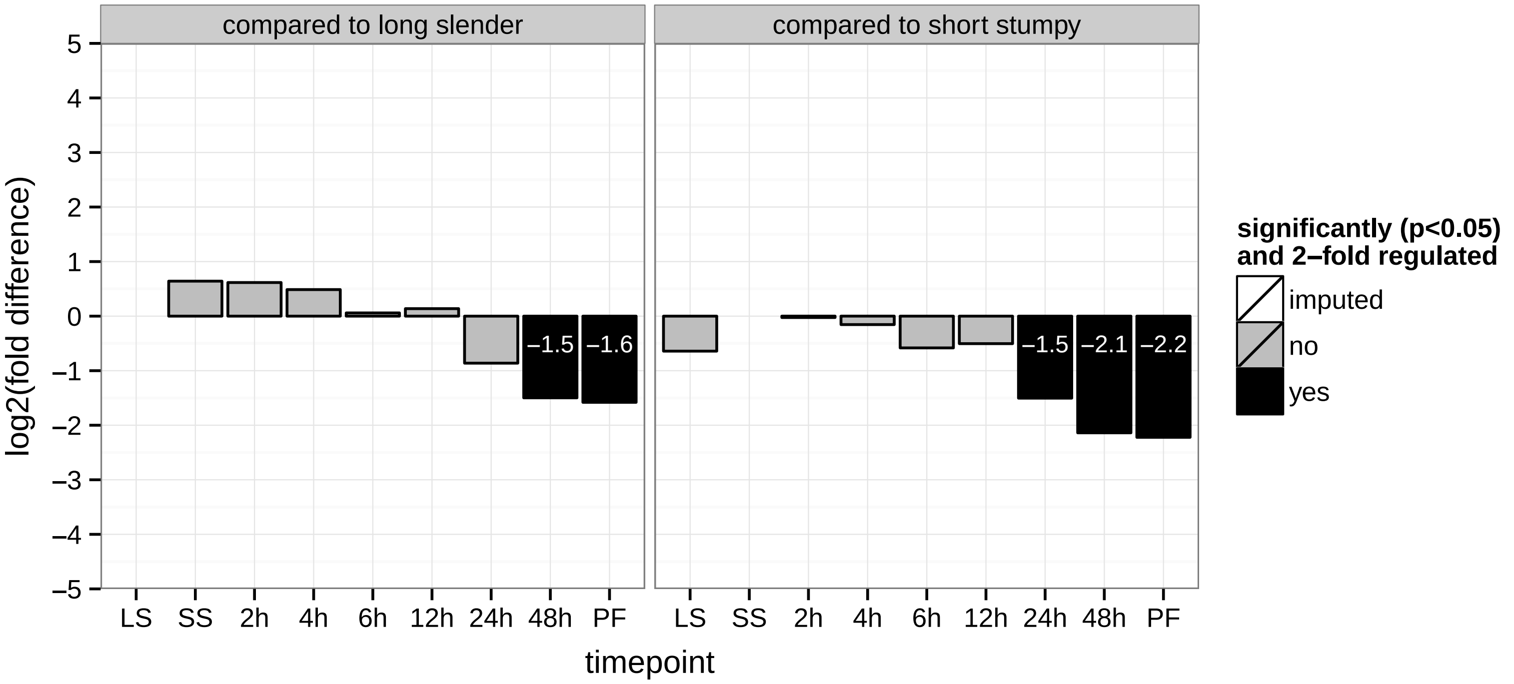
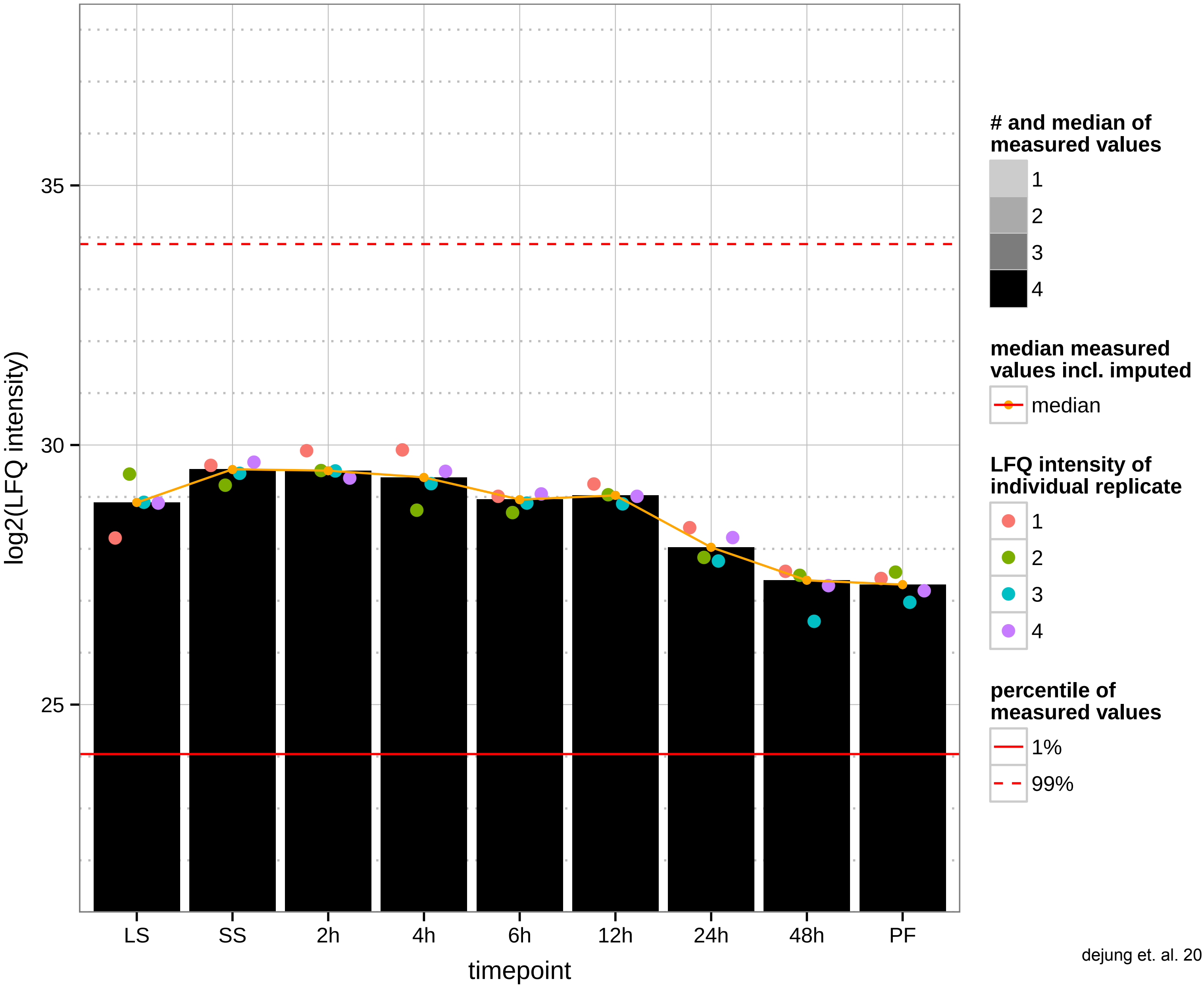
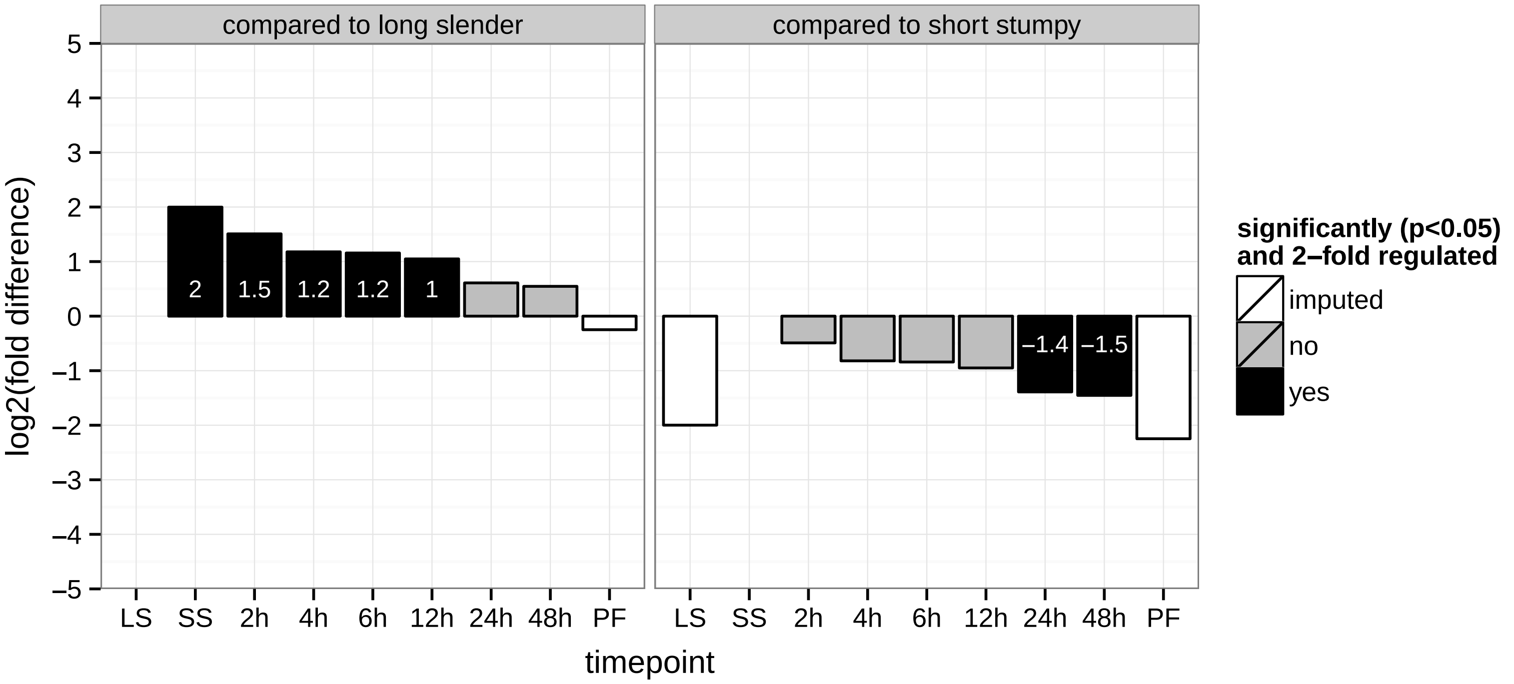
protein kinase, putative, NIMA/Nek Serine/threonine–protein kinase family
Tb927.2.2120
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

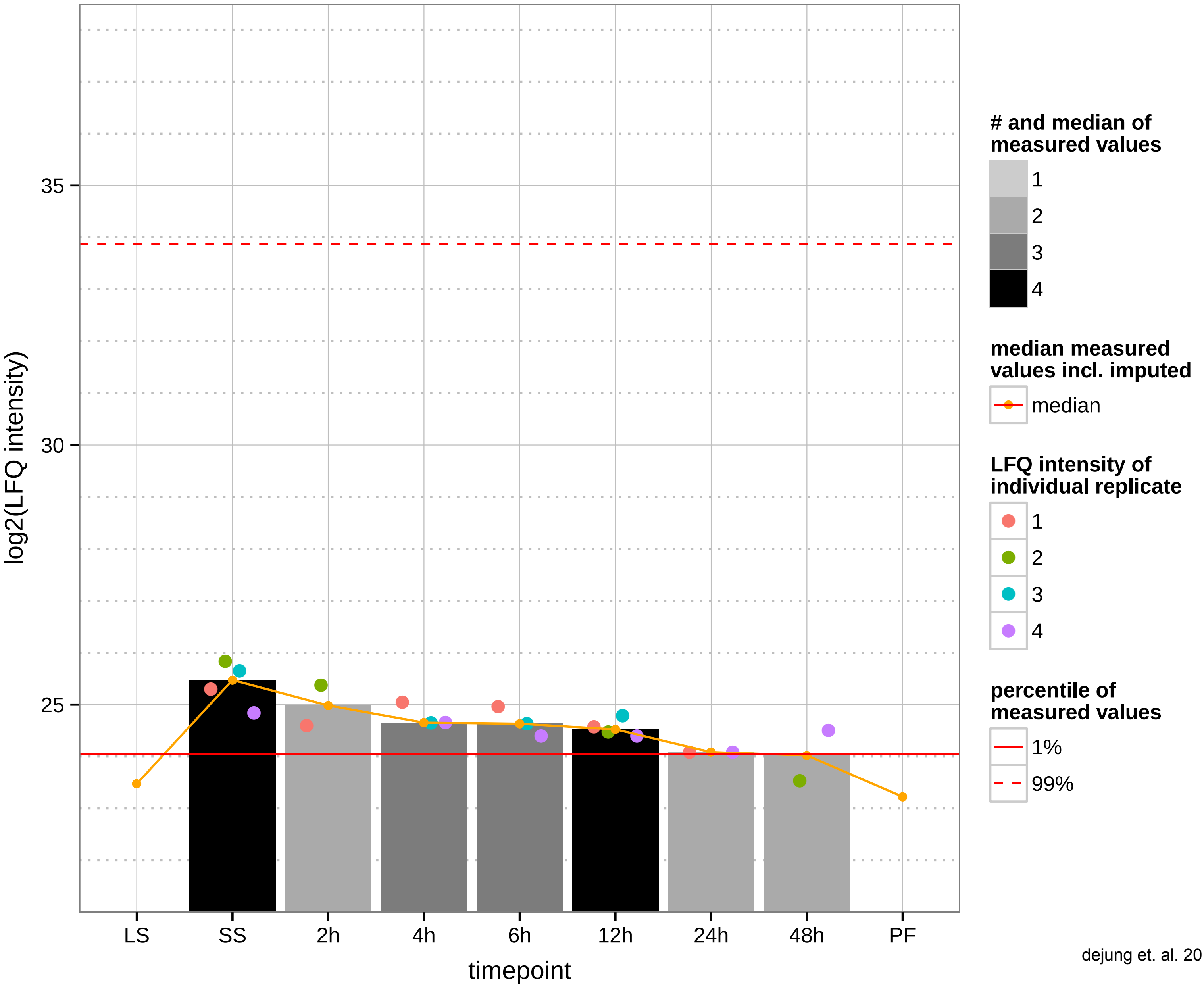




dejung et. al. 2015

hypothetical protein, conserved
Tb927.2.5010
AGOF: null
AGOC: null
AGOP: null
PGOF: phospholipid binding, protein binding
PGOC: cell cortex
PGOP: cortical protein anchoring





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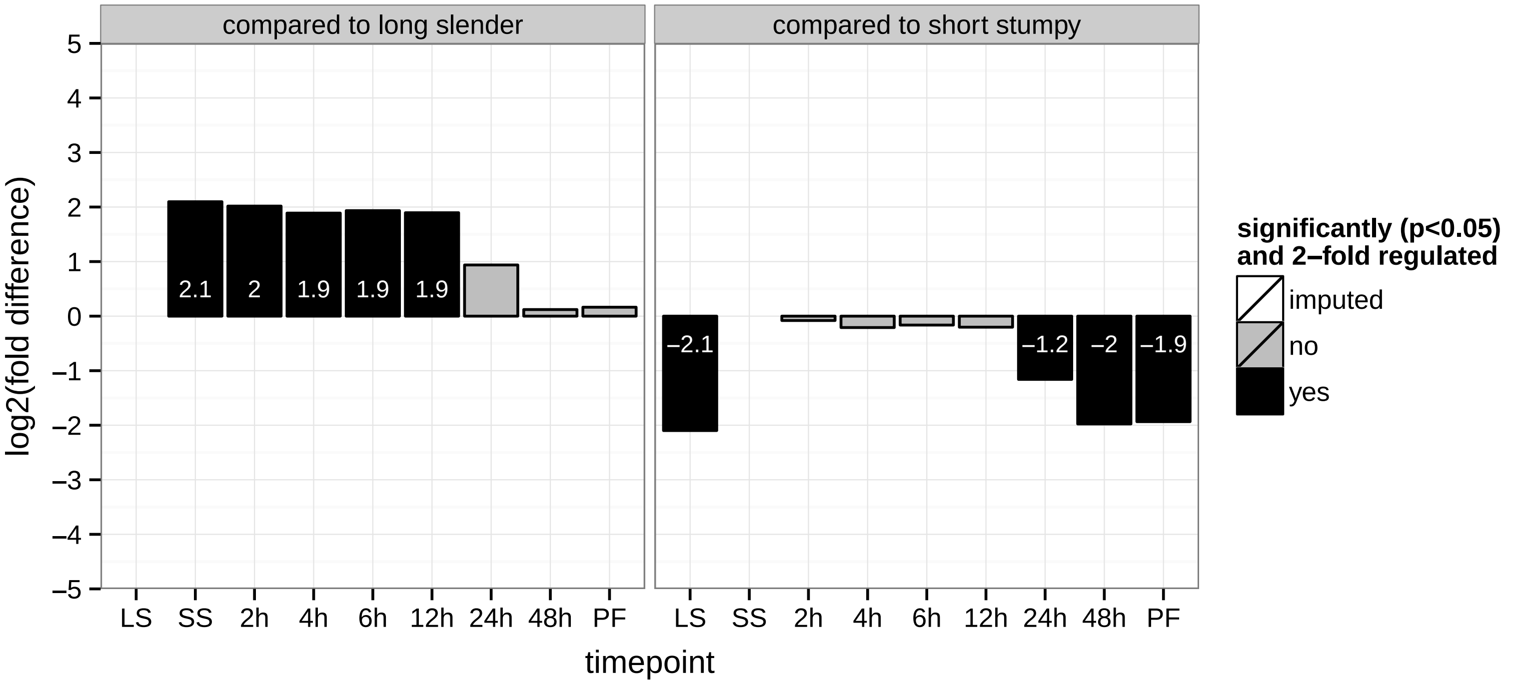
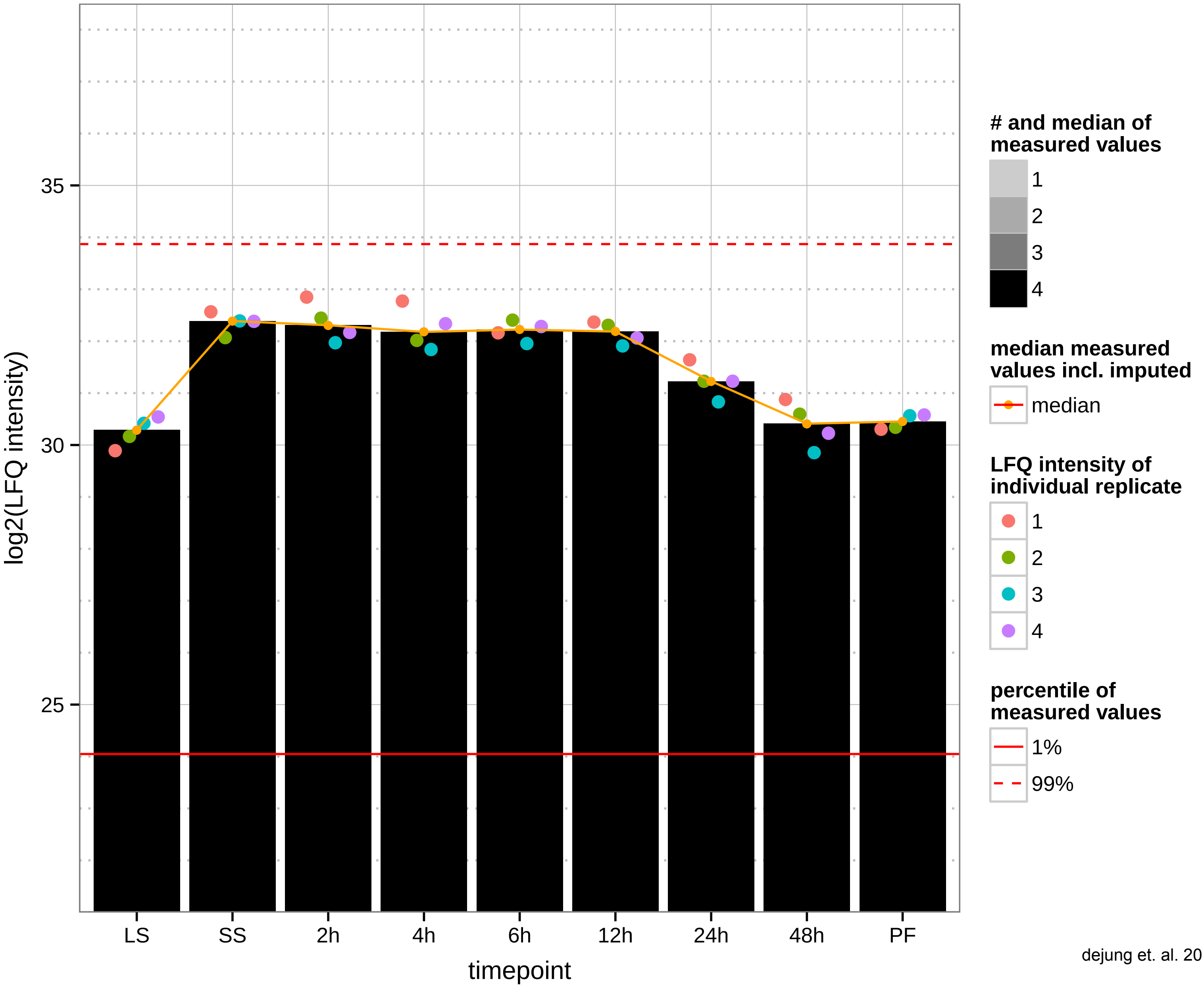
ATP−dependent Clp protease subunit, heat shock protein 104 (HSP104), putative, atp−dependent chaperone (HSP104)
Tb927.2.5980
AGOF: ATP binding, ATPase activity
AGOC: null
AGOP: protein metabolic process
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: protein metabolic process





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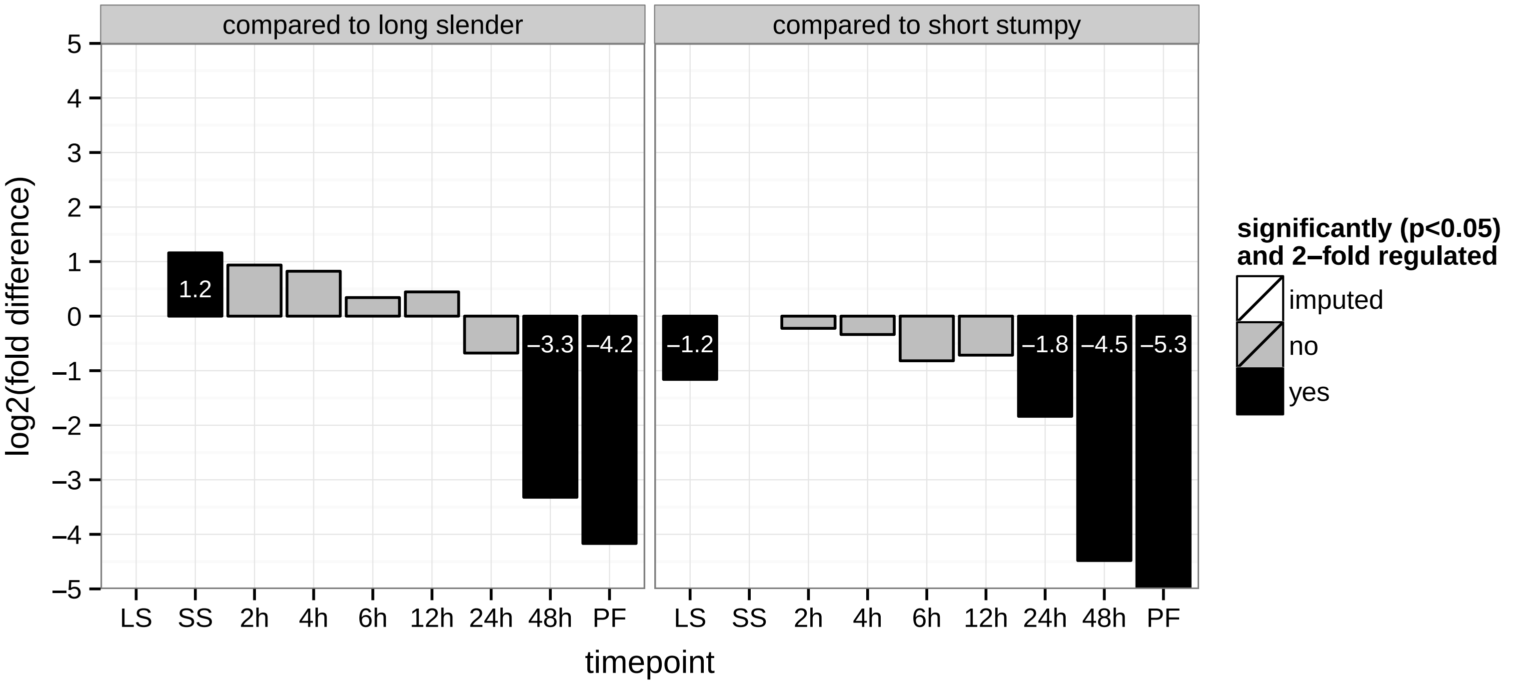
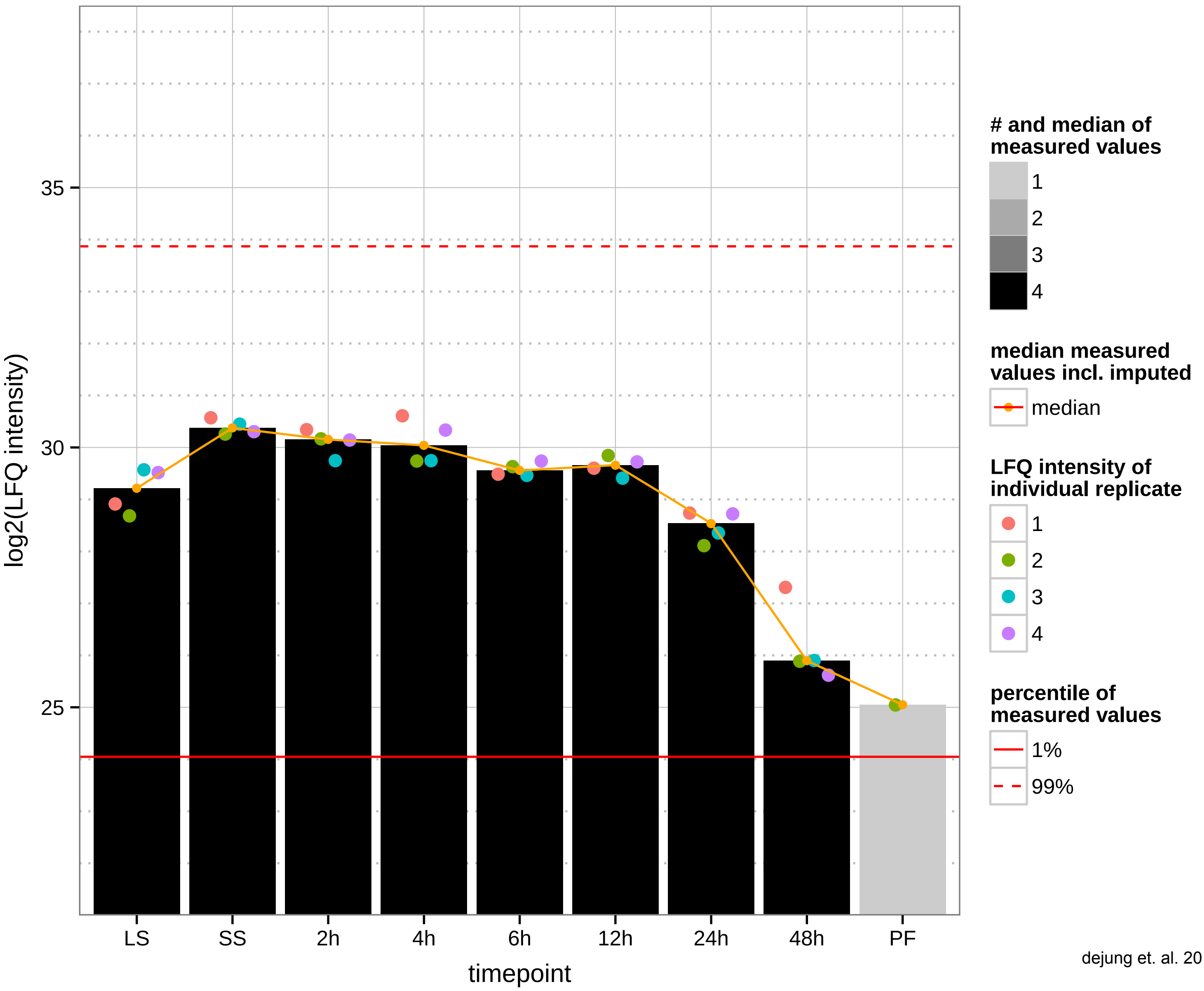
glycosylphosphatidylinositol–specific phospholipase C, VSG lipase (GPI–PLC)
Tb927.2.6000
AGOF: glycosylphosphatidylinositol diacylglycerol–lyase activity, phospholipase C activity
AGOC: plasma membrane
AGOP: GPI anchor release, glycerophospholipid metabolic process, intracellular signal transduction, lipid metabolic process
PGOF: glycosylphosphatidylinositol diacylglycerol–lyase activity, phospholipase C activity, phosphoric diester hydrolase activit
PGOC: null
PGOP: glycerophospholipid metabolic process, intracellular signal transduction, lipid metabolic process





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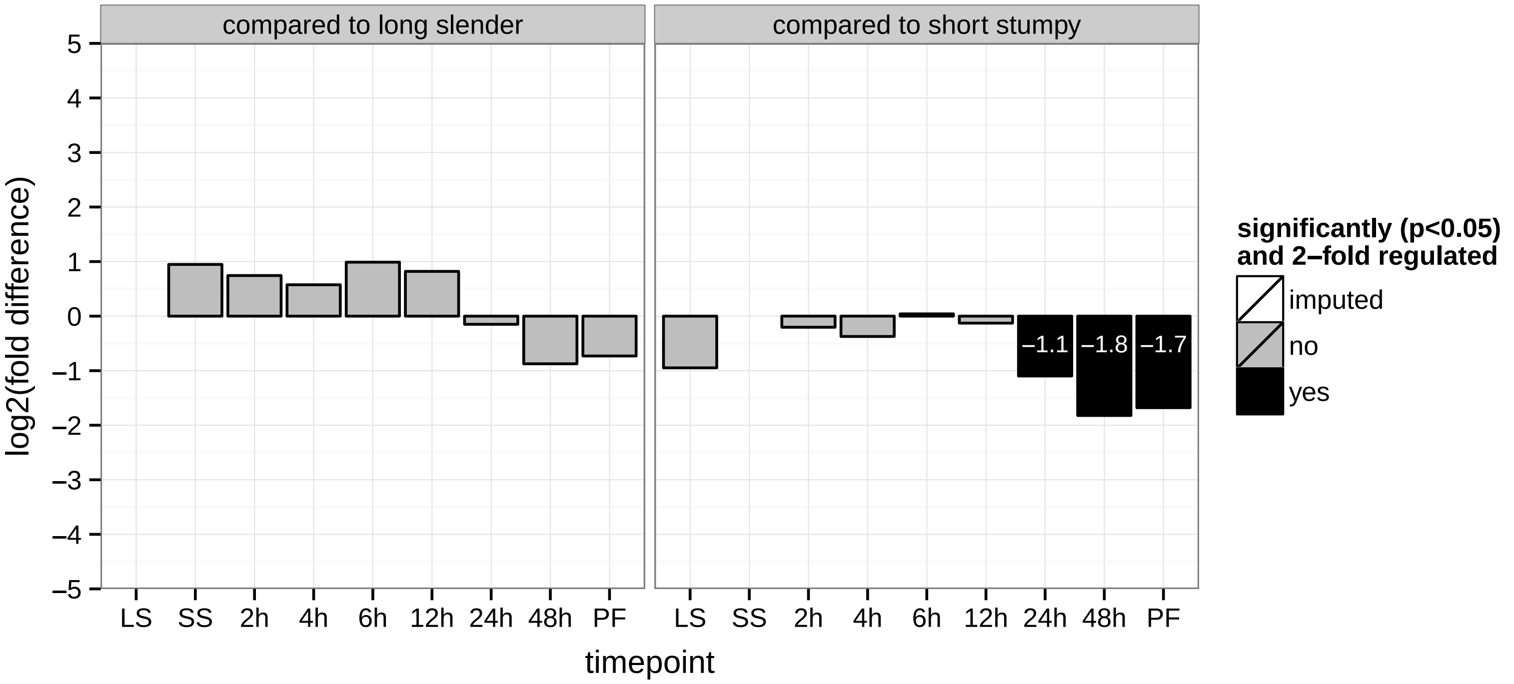
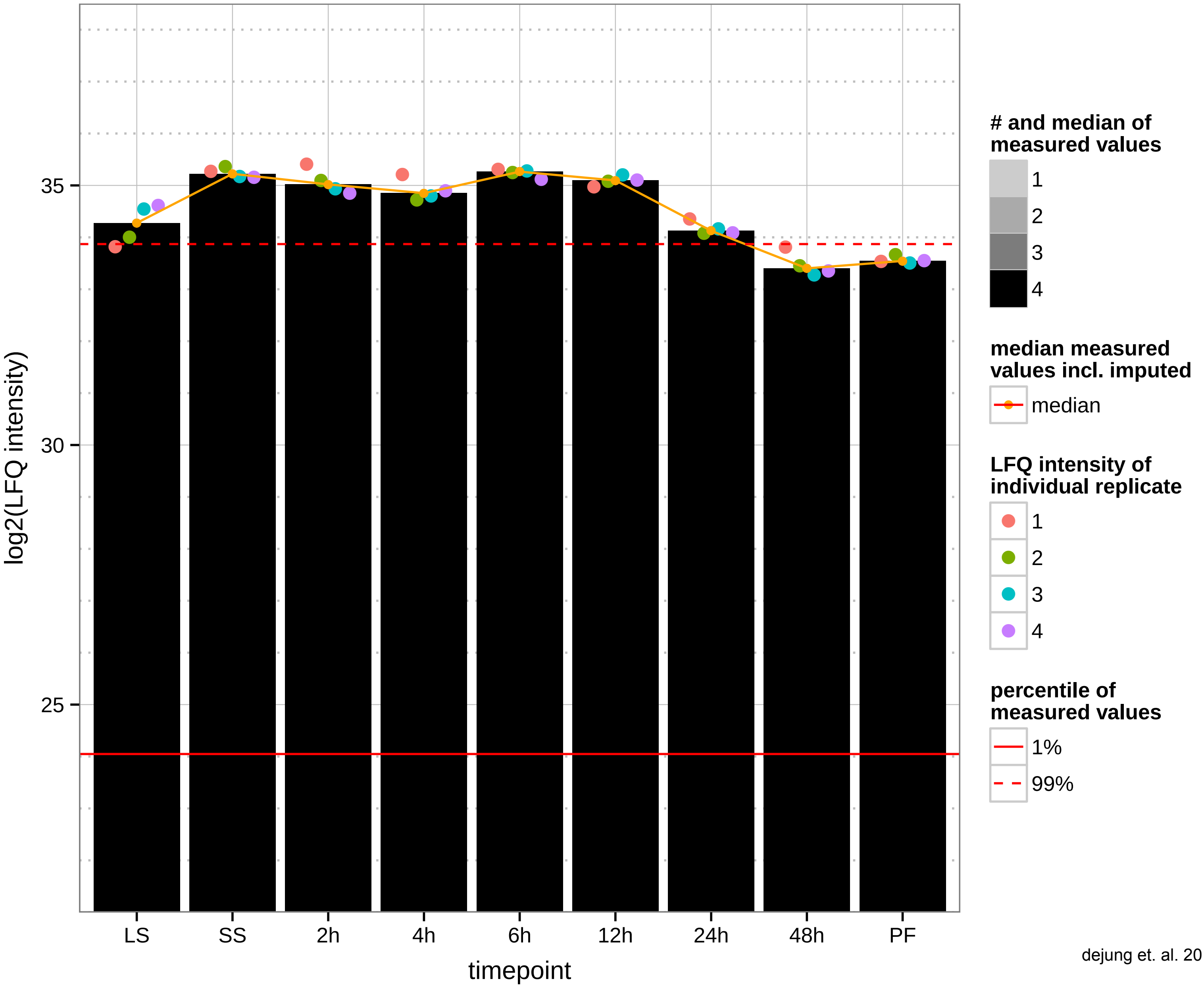
ATP−dependent phosphofructokinase (PFK)
Tb927.3.3270
AGOF: 6−phosphofructokinase activity, ATP binding
AGOC: 6−phosphofructokinase complex, glycosome
AGOP: glycolysis
PGOF: 6−phosphofructokinase activity, ATP binding
PGOC: 6−phosphofructokinase complex
PGOP: glycolysis





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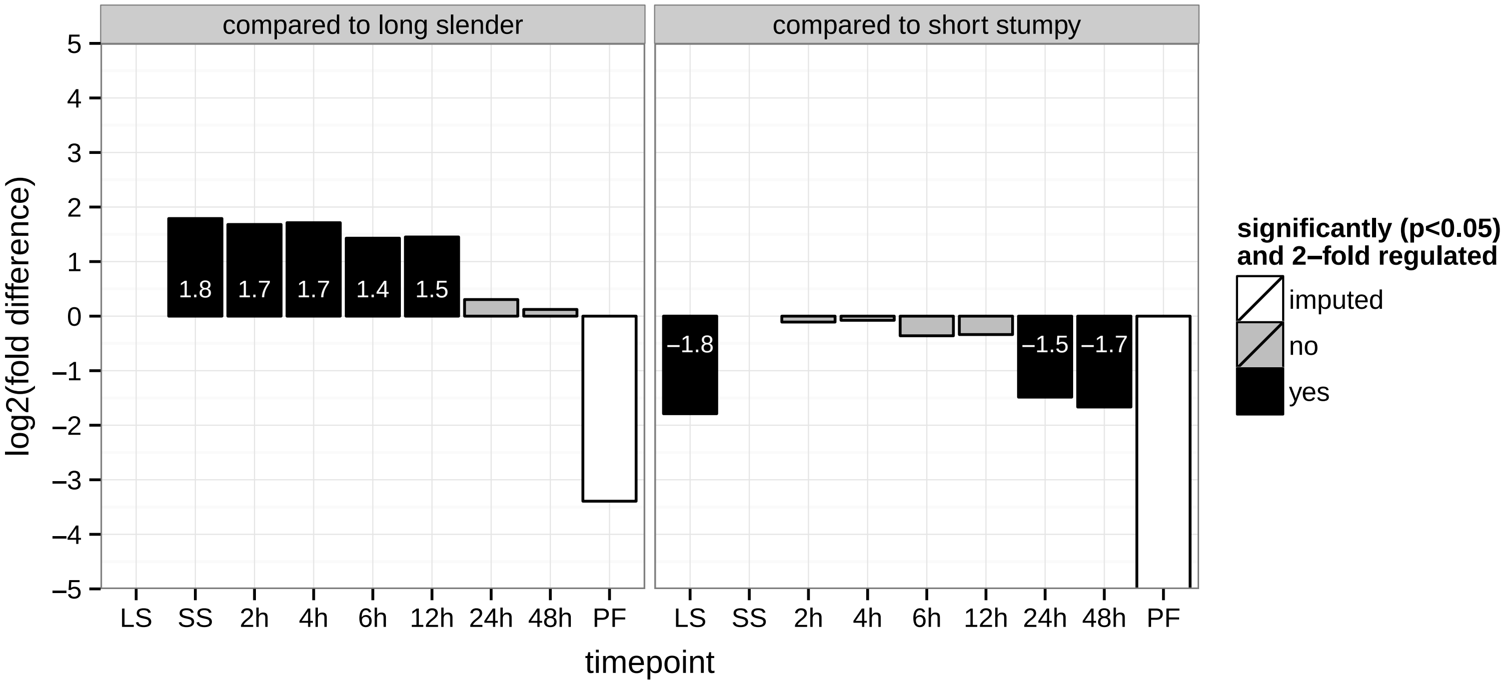
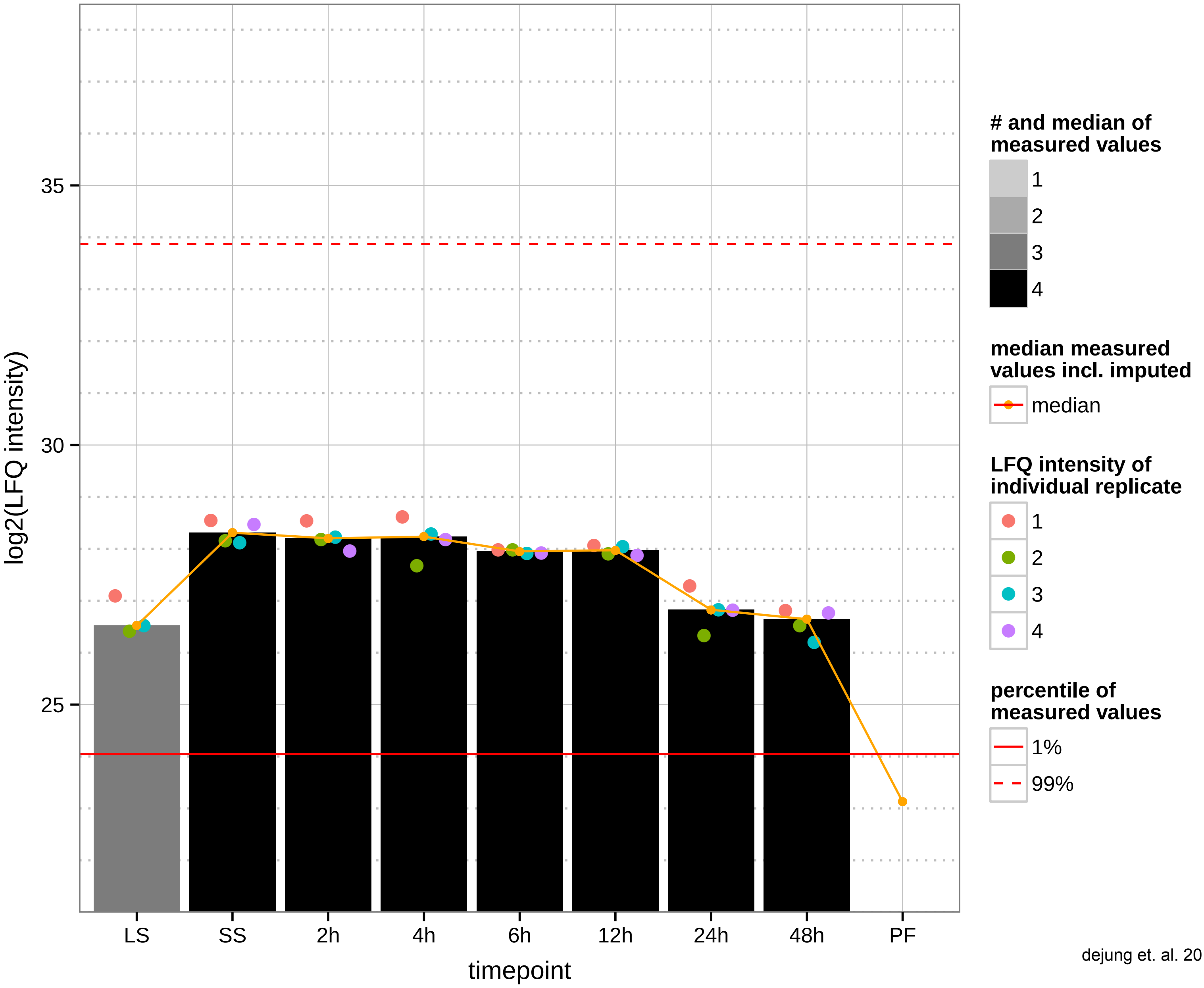
hypothetical protein, conserved
Tb927.3.4660
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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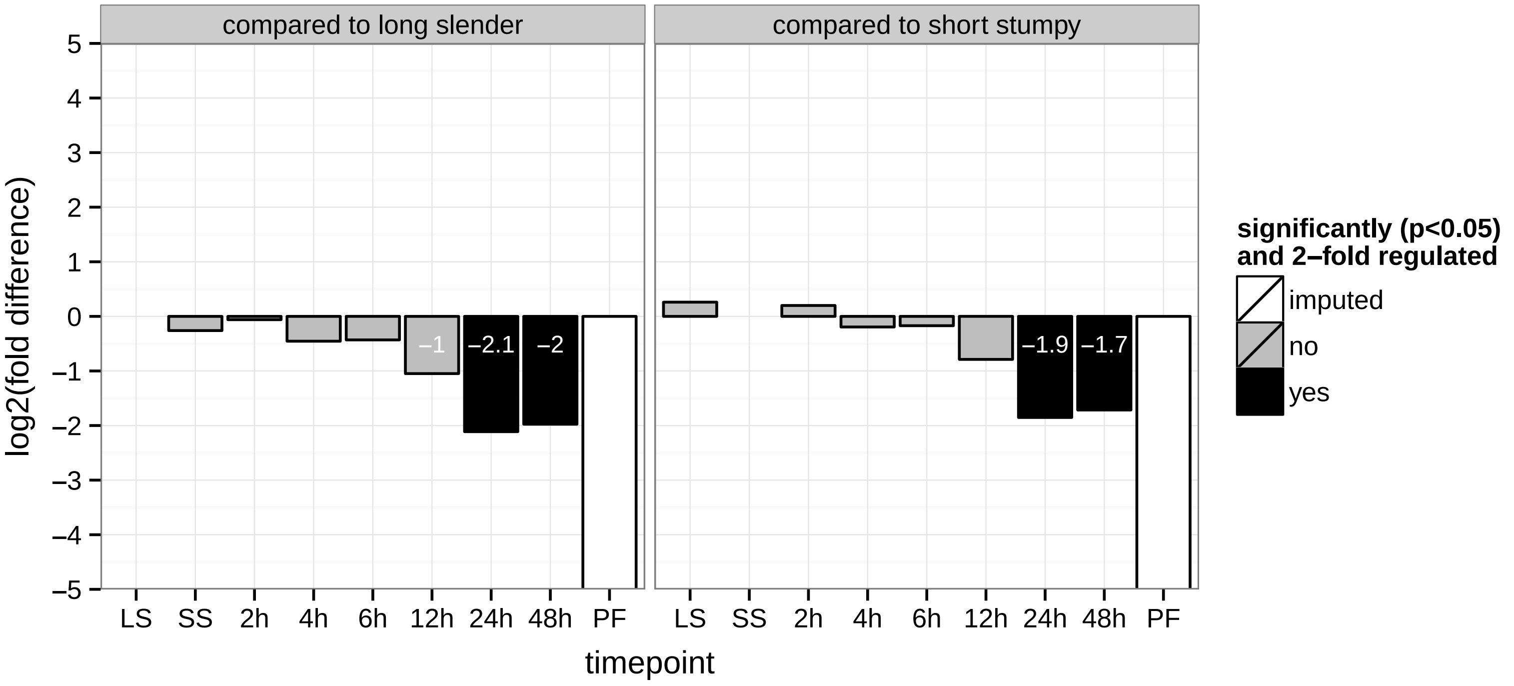
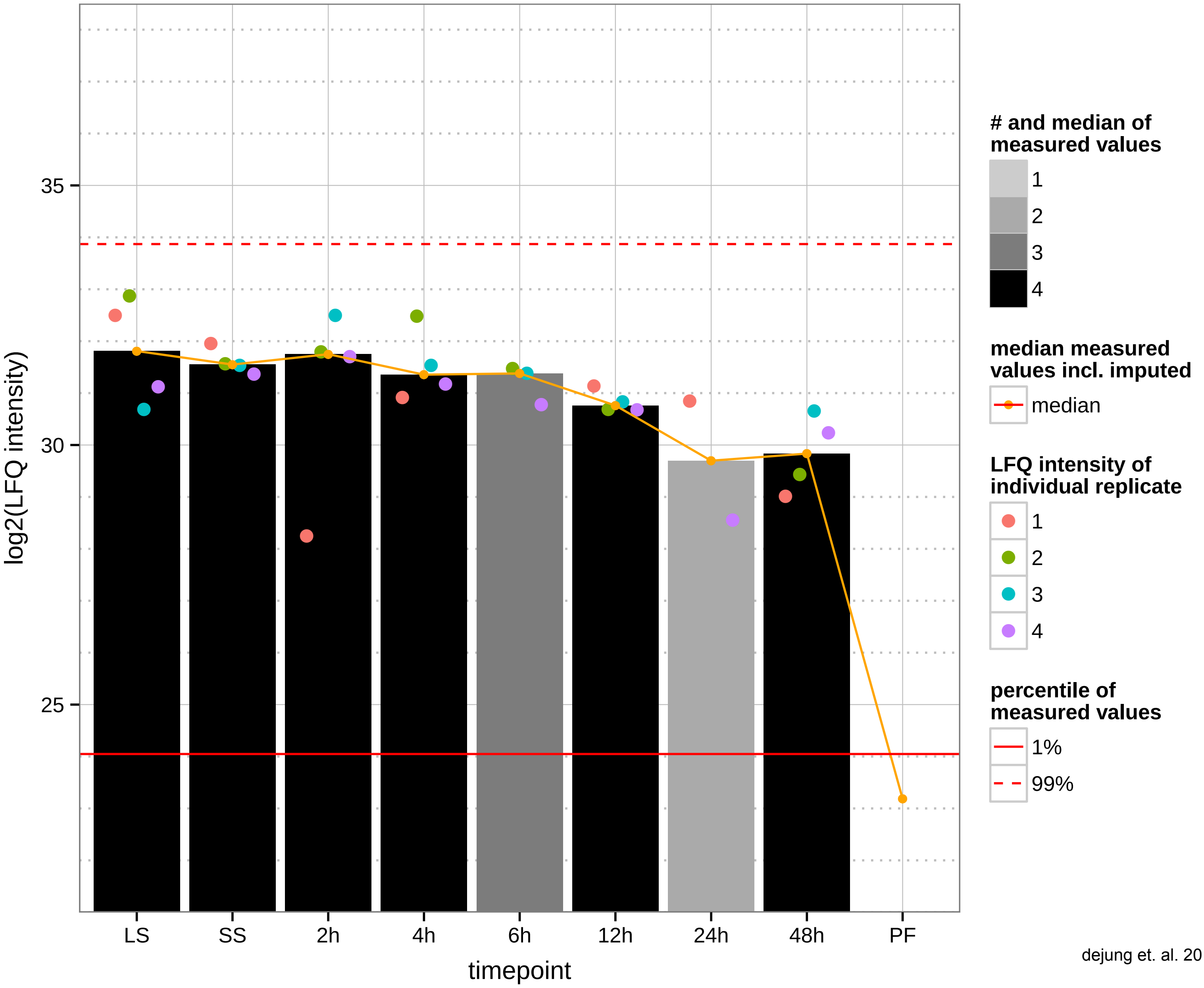
hypothetical protein, conserved
Tb927.3.4710
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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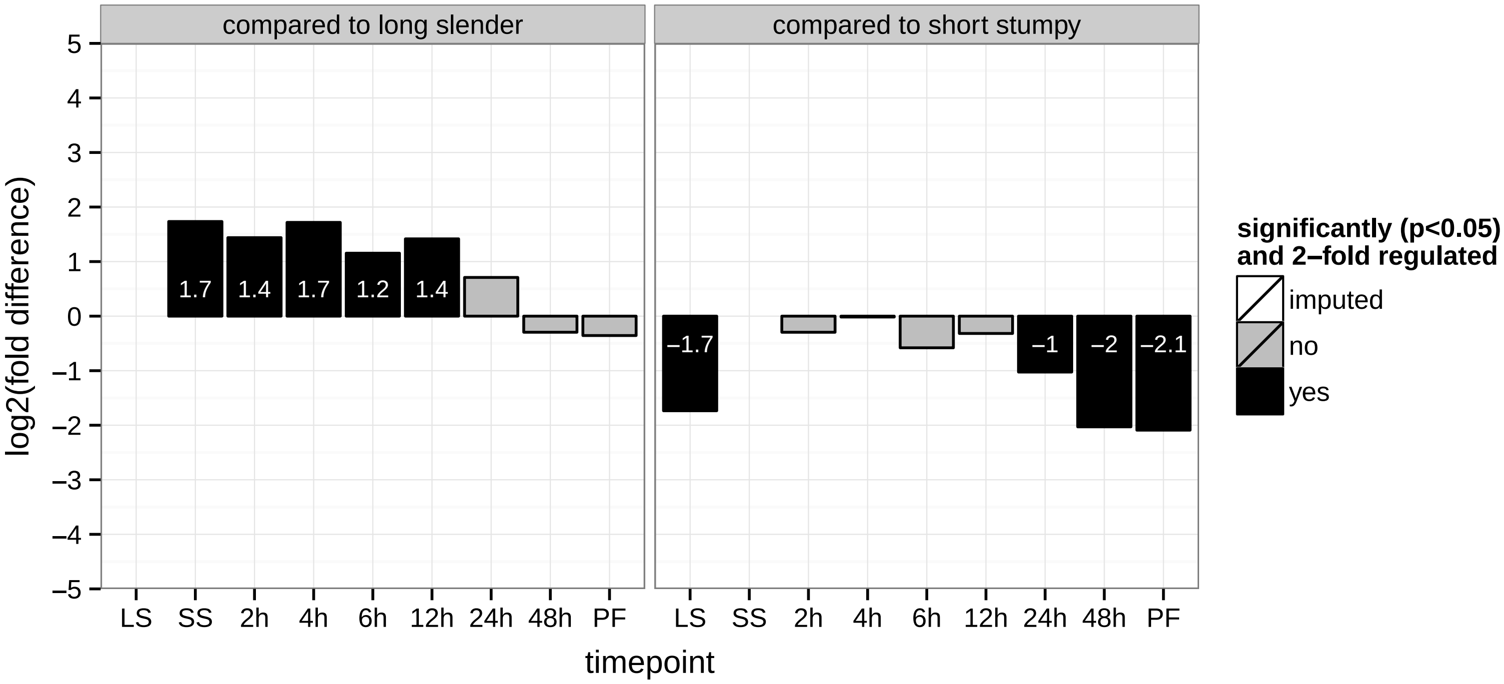
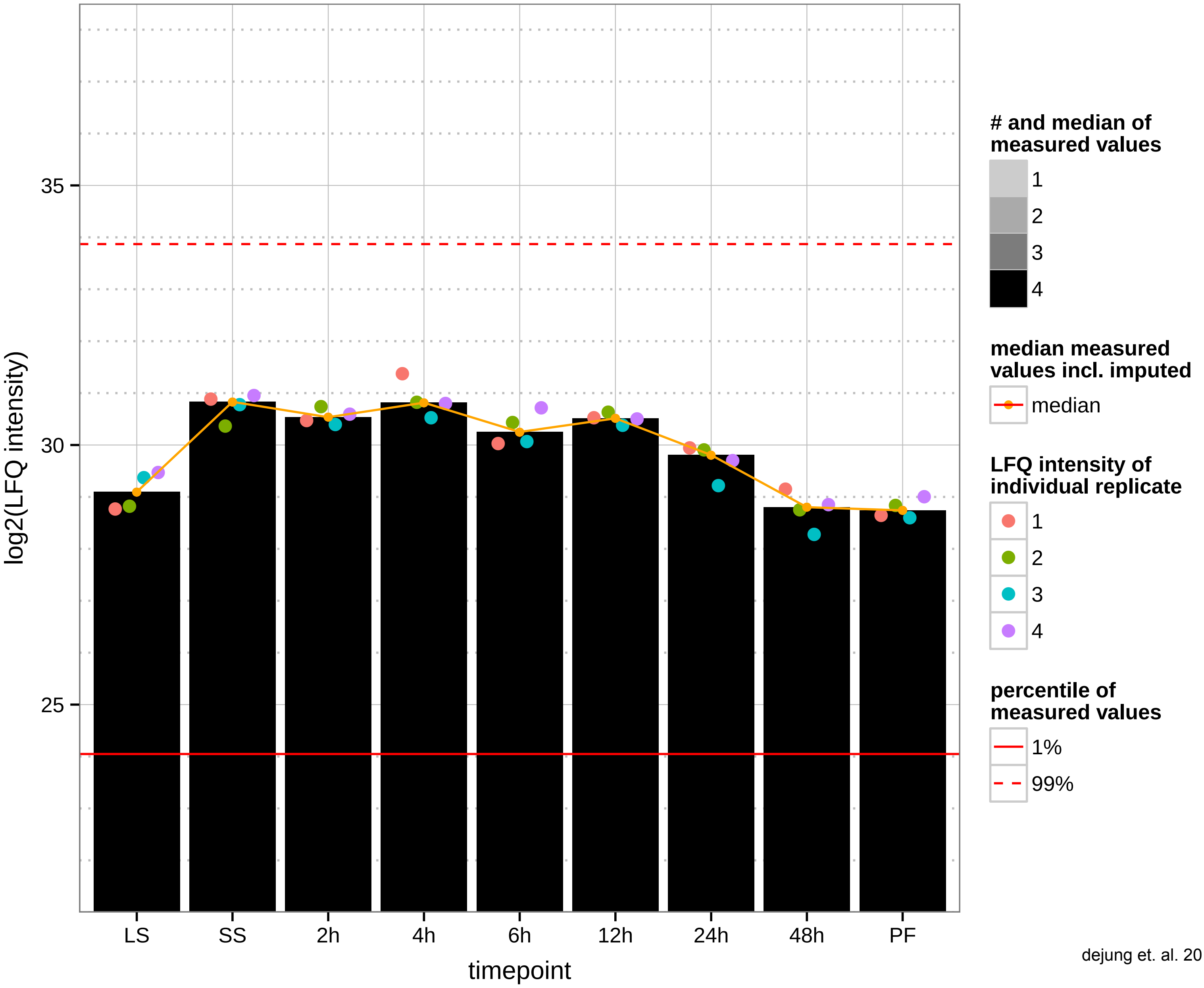
tryparedoxin 2, putative (TXN2)
Tb927.3.5090
AGOF: antioxidant activity, oxidoreductase activity
AGOC: null
AGOP: cell redox homeostasis
PGOF: null
PGOC: null
PGOP: null





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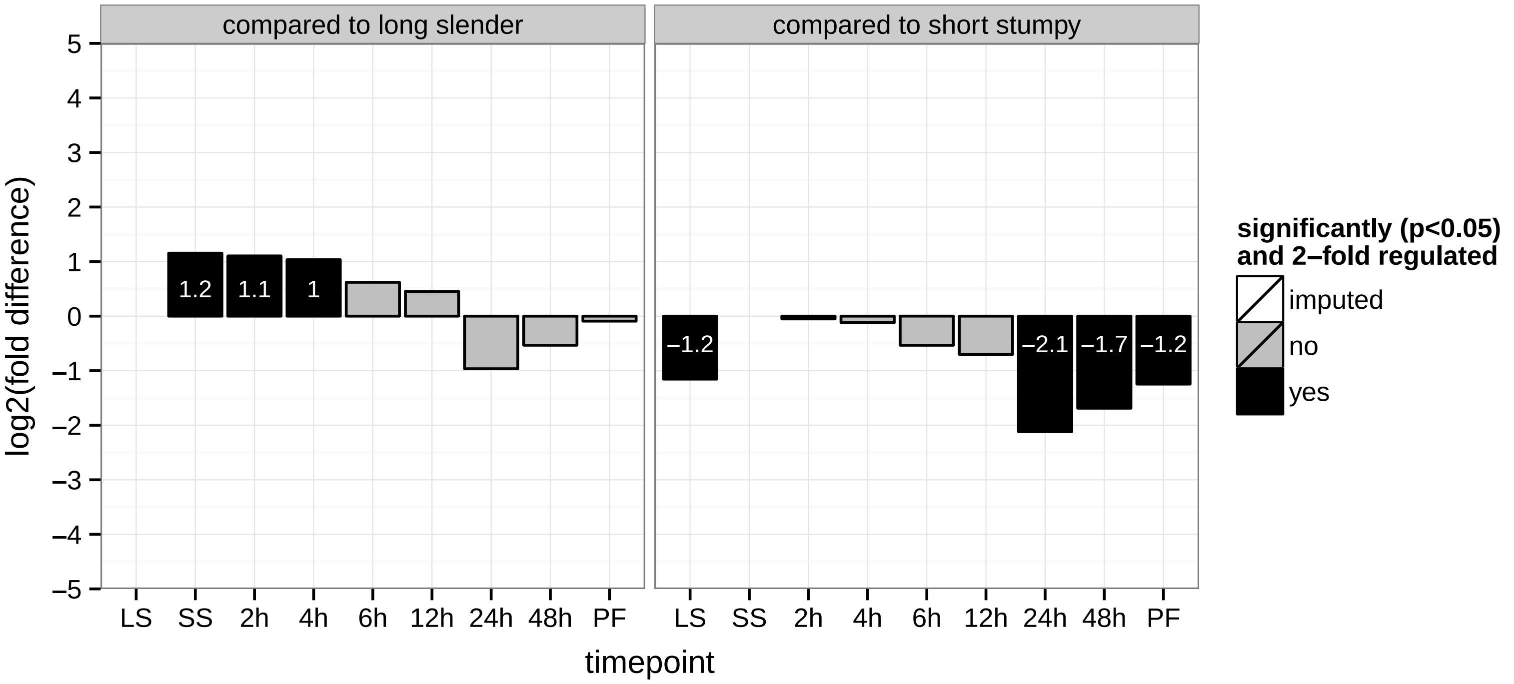
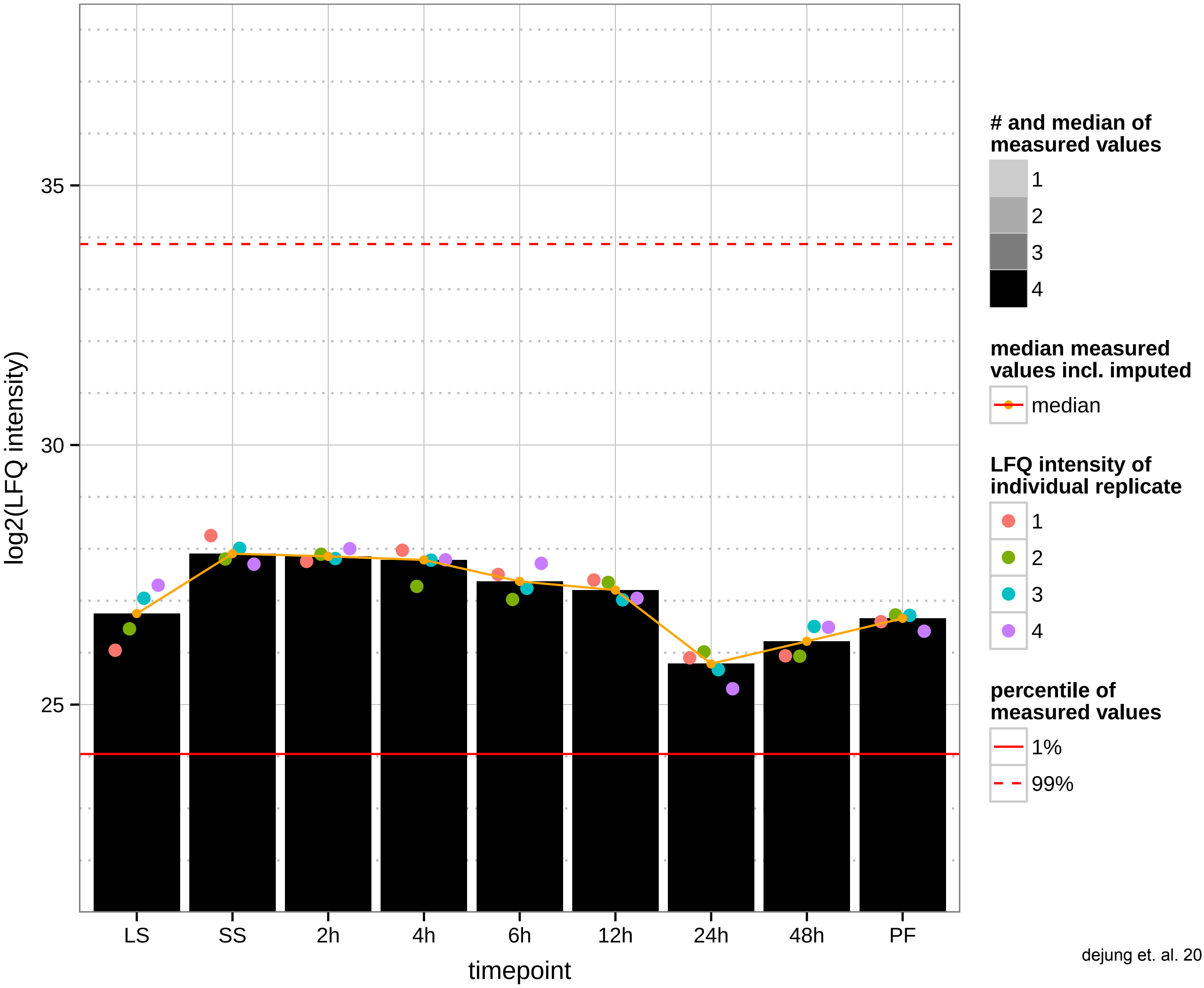
leucine–rich repeat protein (LRRP), putative
Tb927.4.1220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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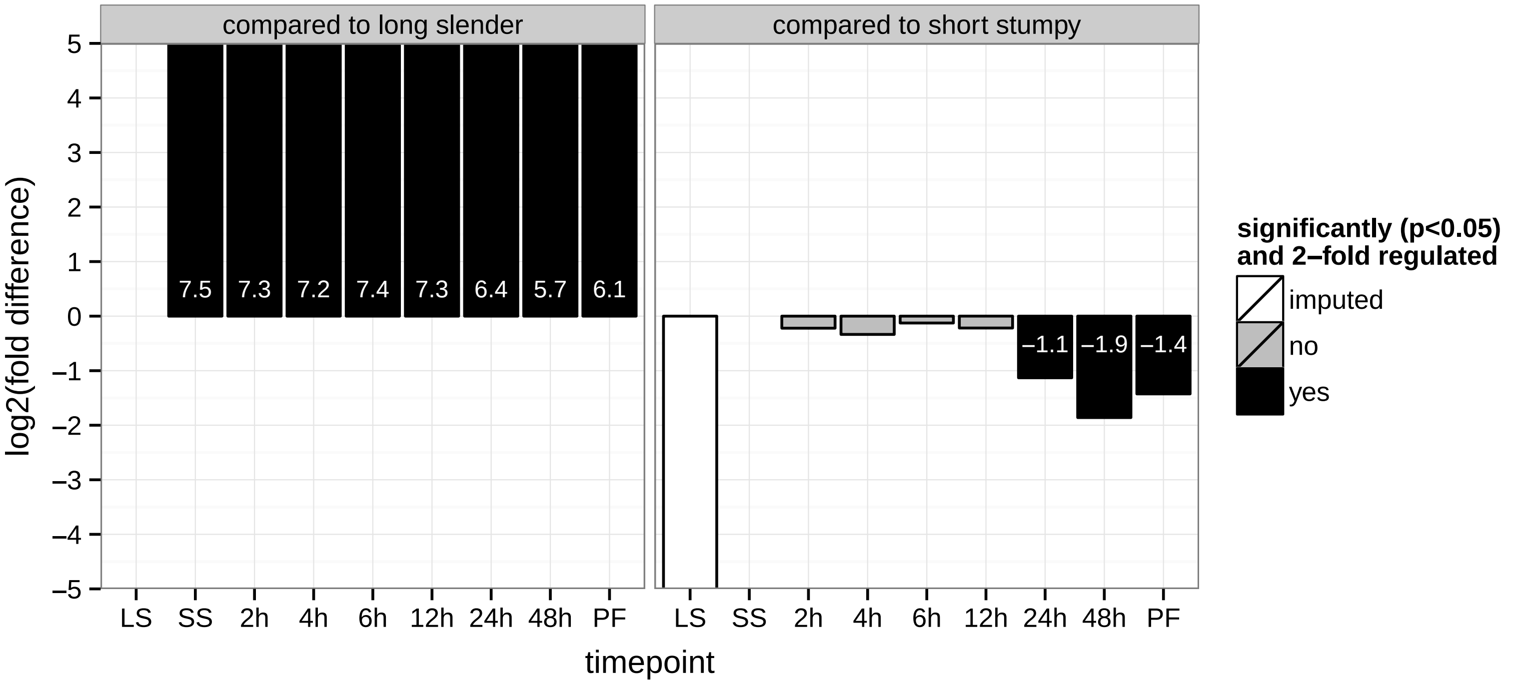
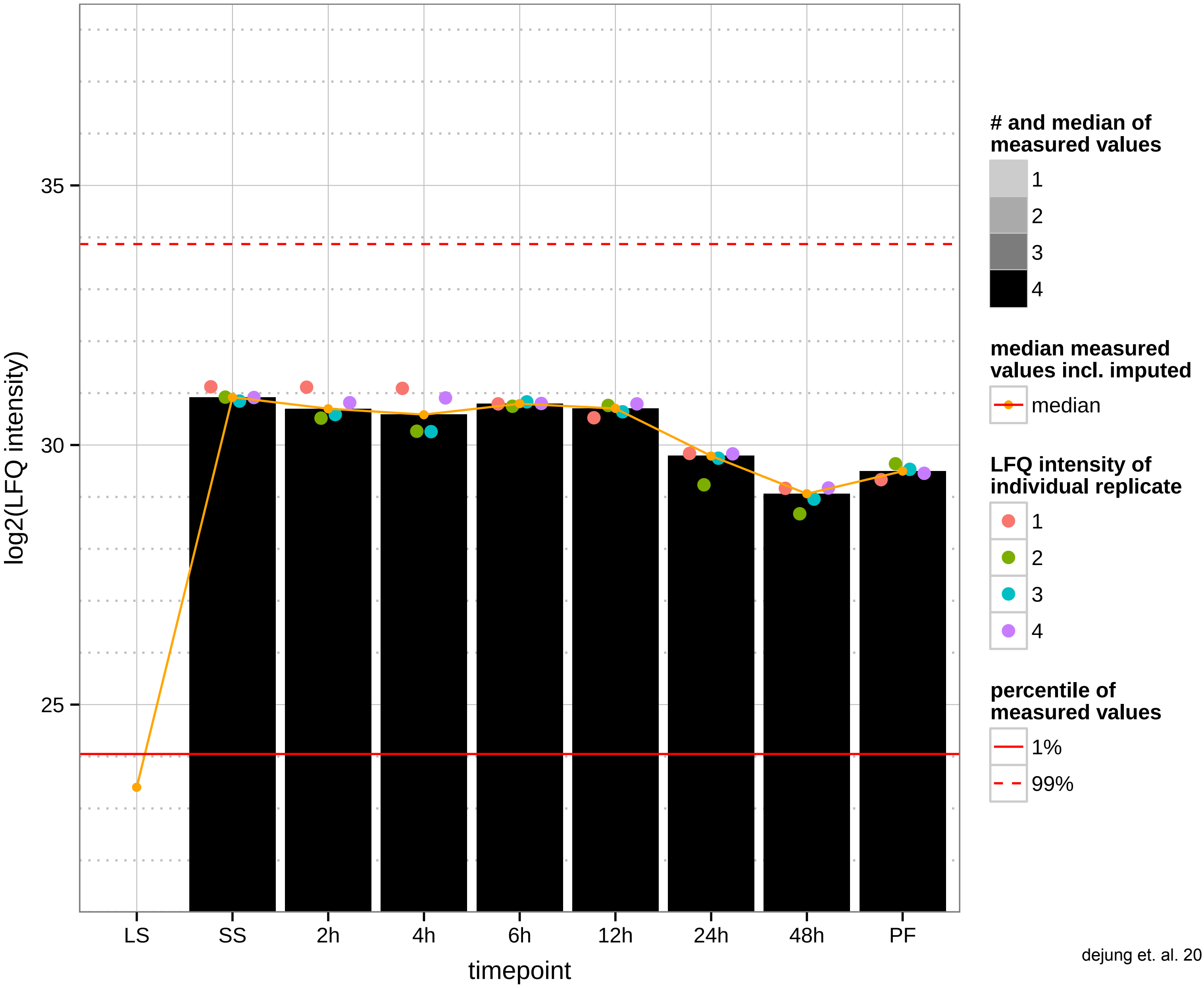
hypothetical protein, conserved
Tb927.4.2240
AGOF: catalytic activity
AGOC: null
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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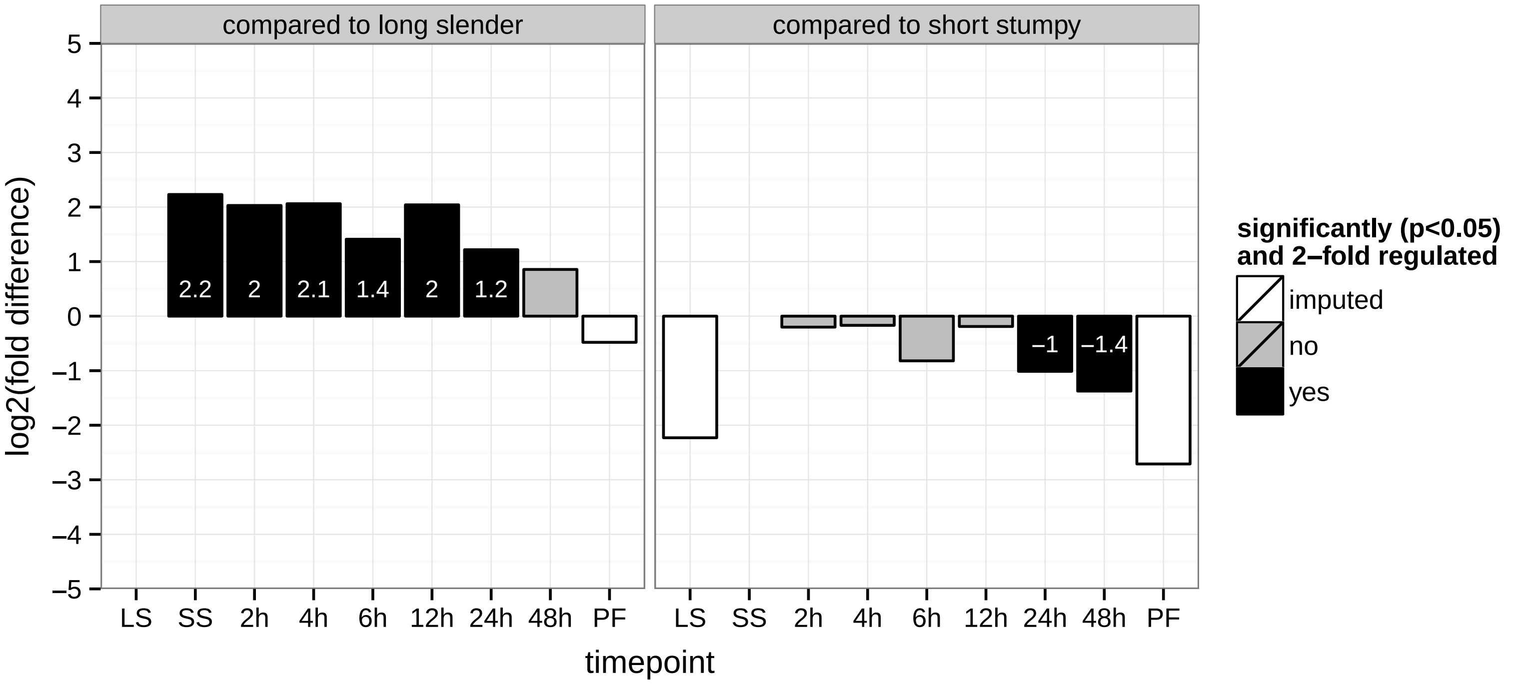
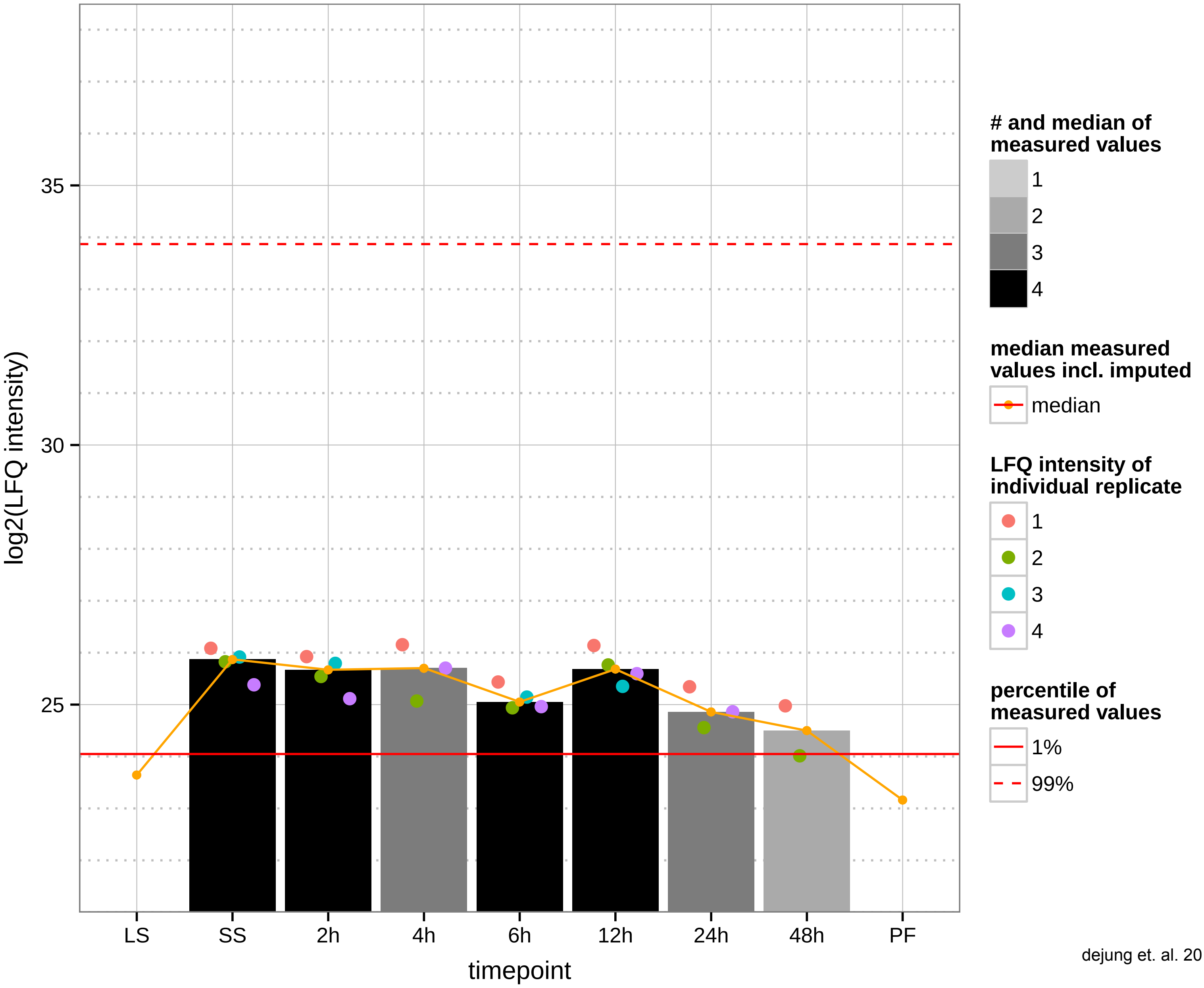
hypothetical protein, conserved
Tb927.4.2370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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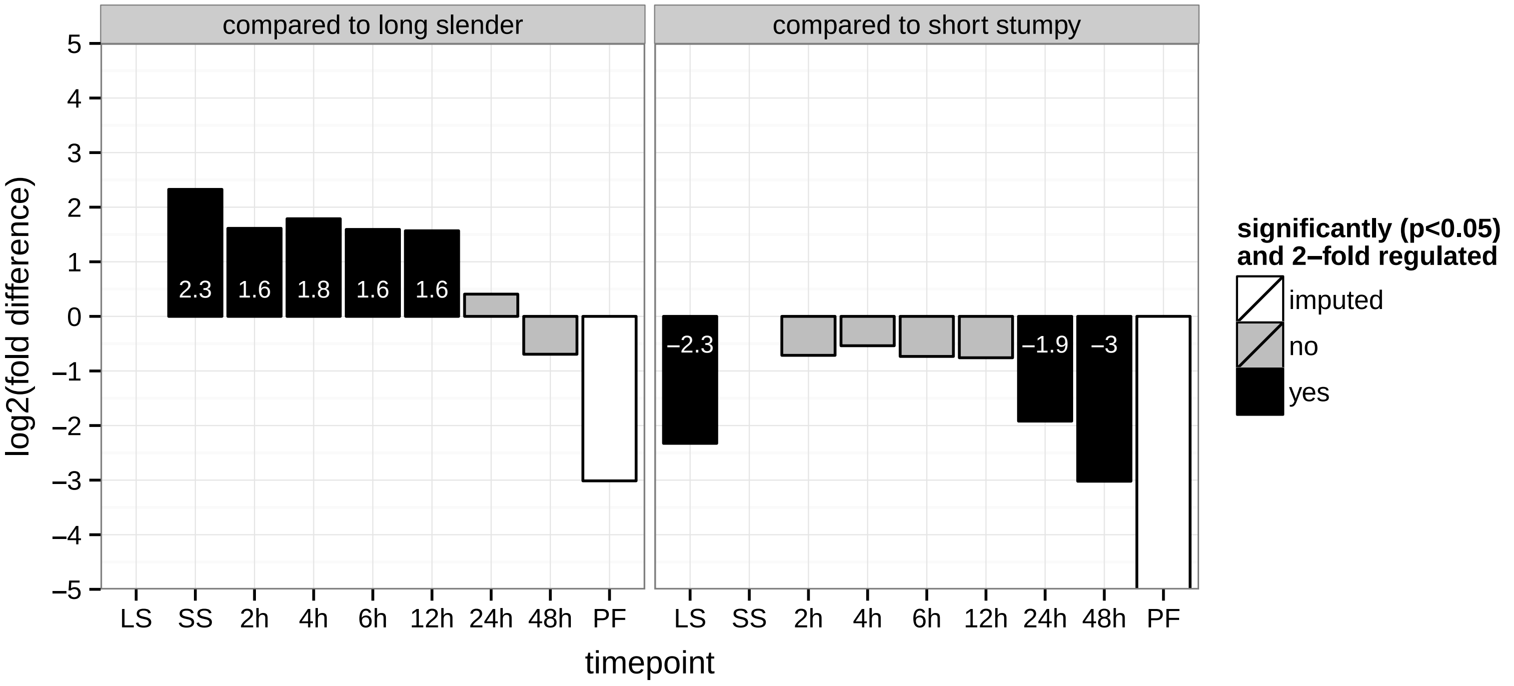
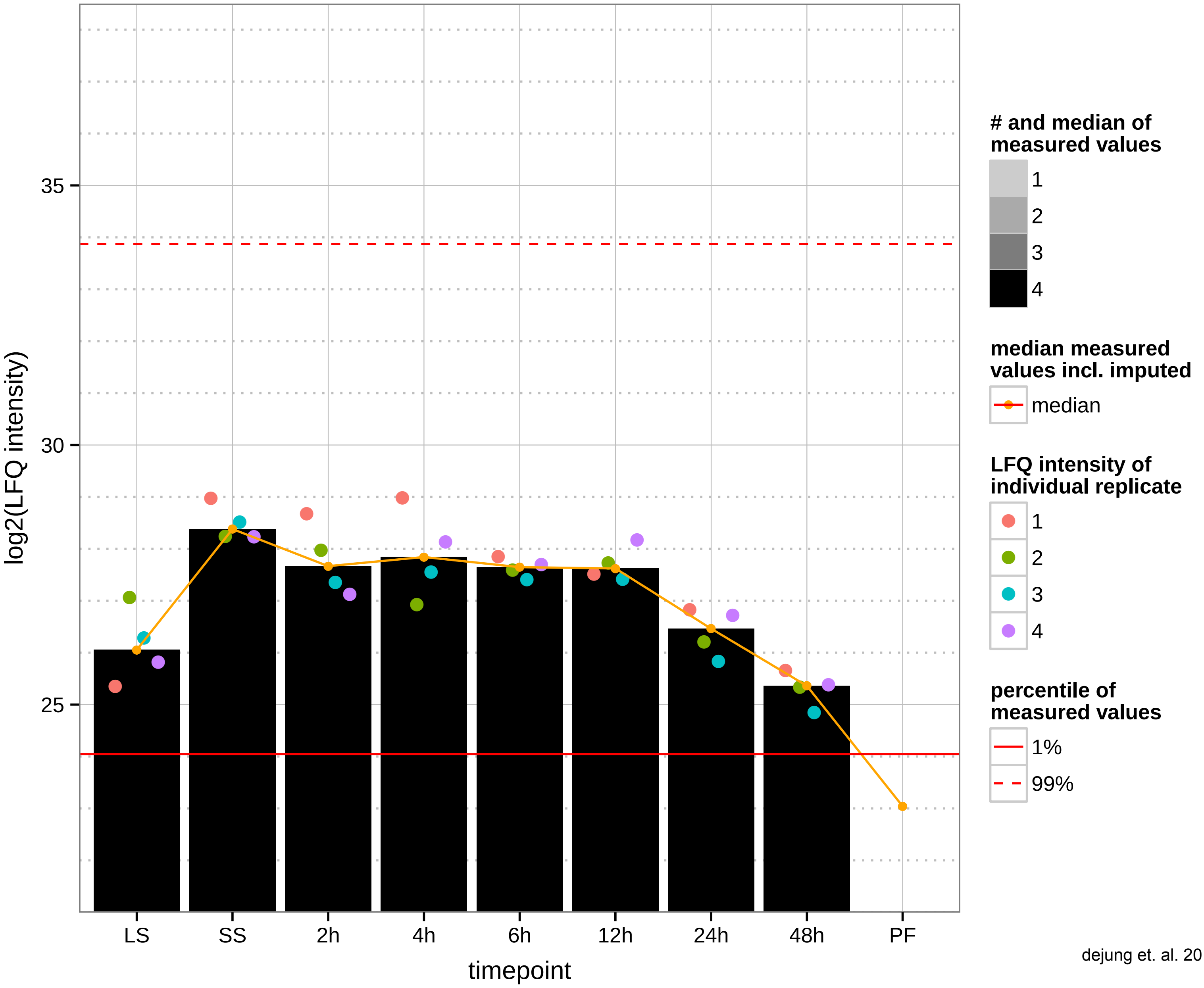
sarcoplasmic reticulum glycoprotein, putative
Tb927.4.2380
AGOF: GTP binding, calcium ion binding
AGOC: intracellular, sarcoplasmic reticulum
AGOP: calcium ion transport
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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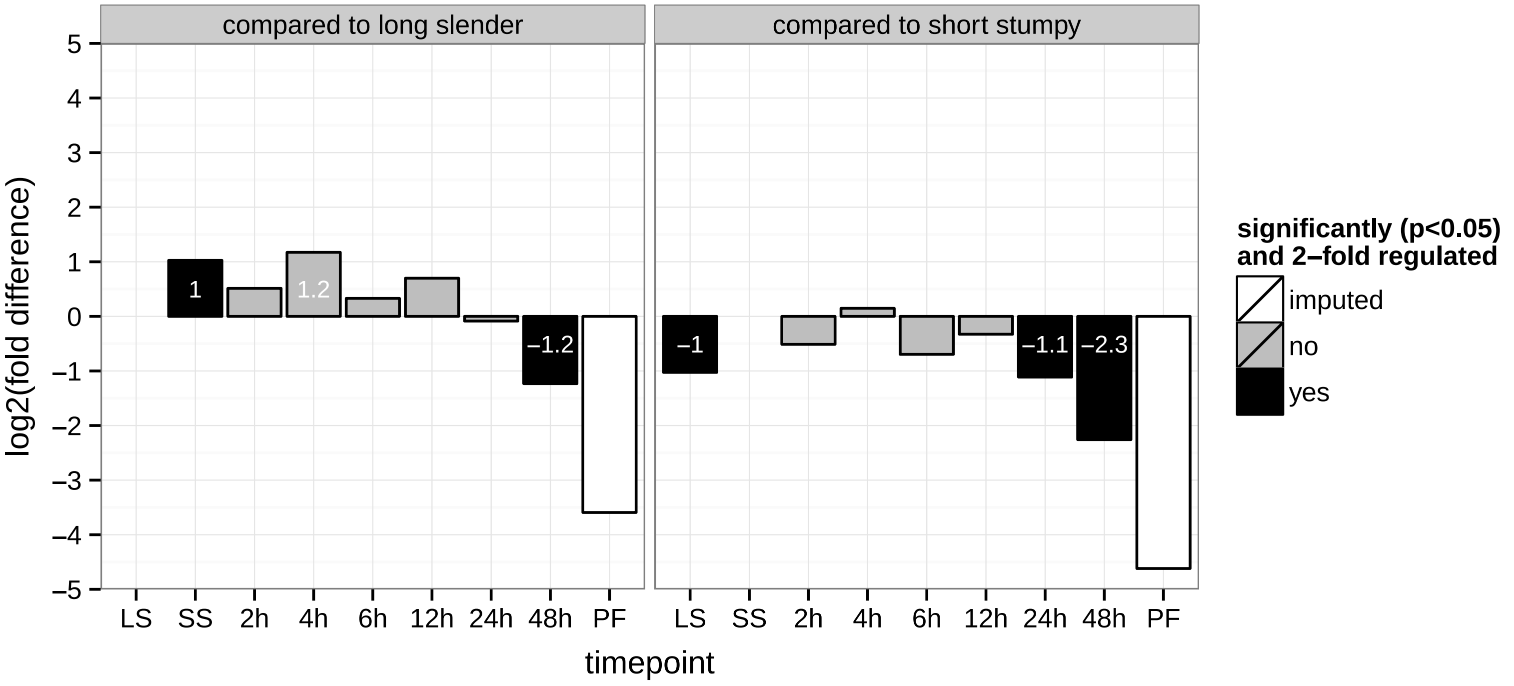
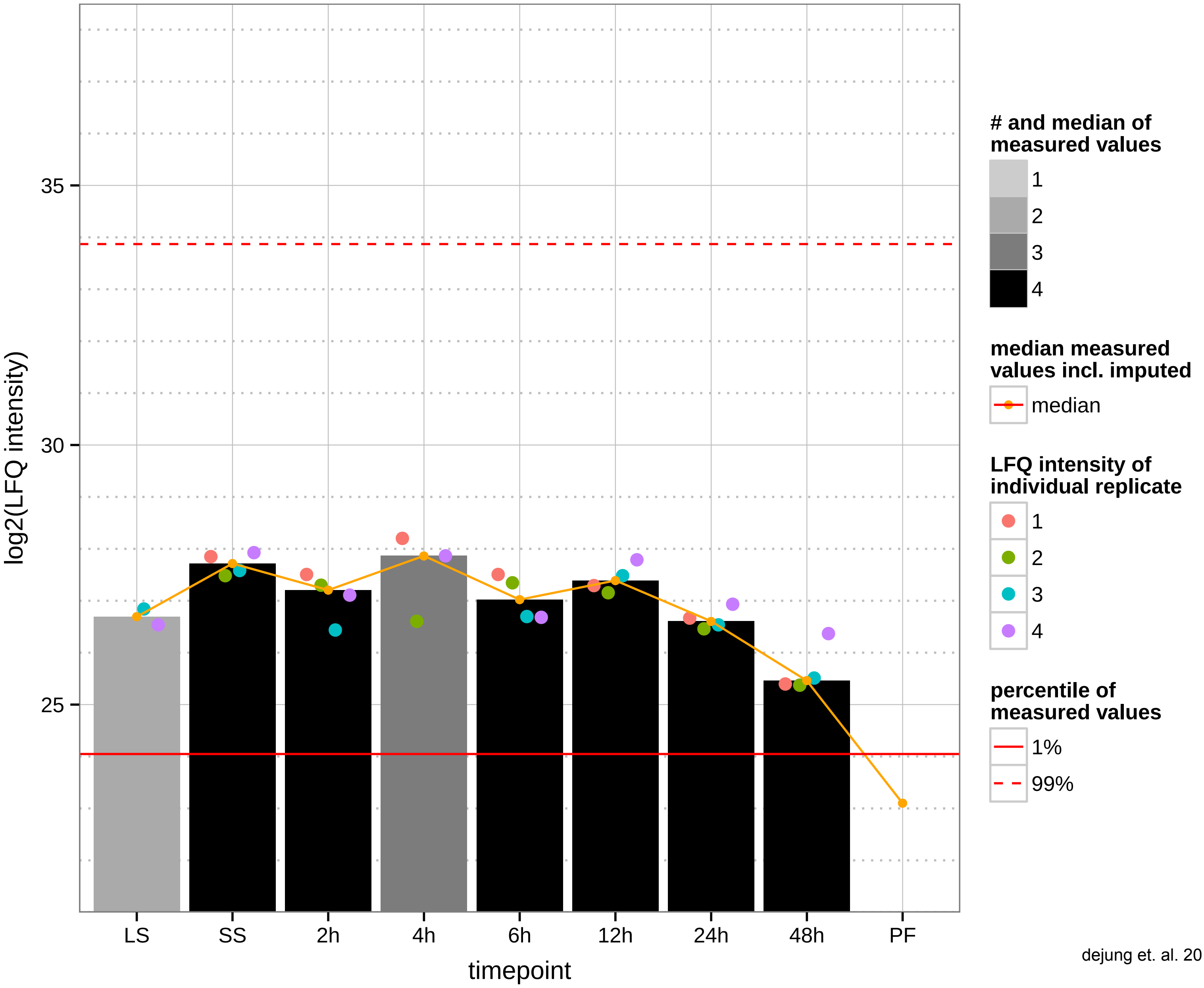
myosin IB heavy chain, putative
Tb927.4.3380
AGOF: ATP binding, motor activity, zinc ion binding
AGOC: myosin complex
AGOP: null
PGOF: ATP binding, motor activity, protein binding
PGOC: myosin complex
PGOP: null





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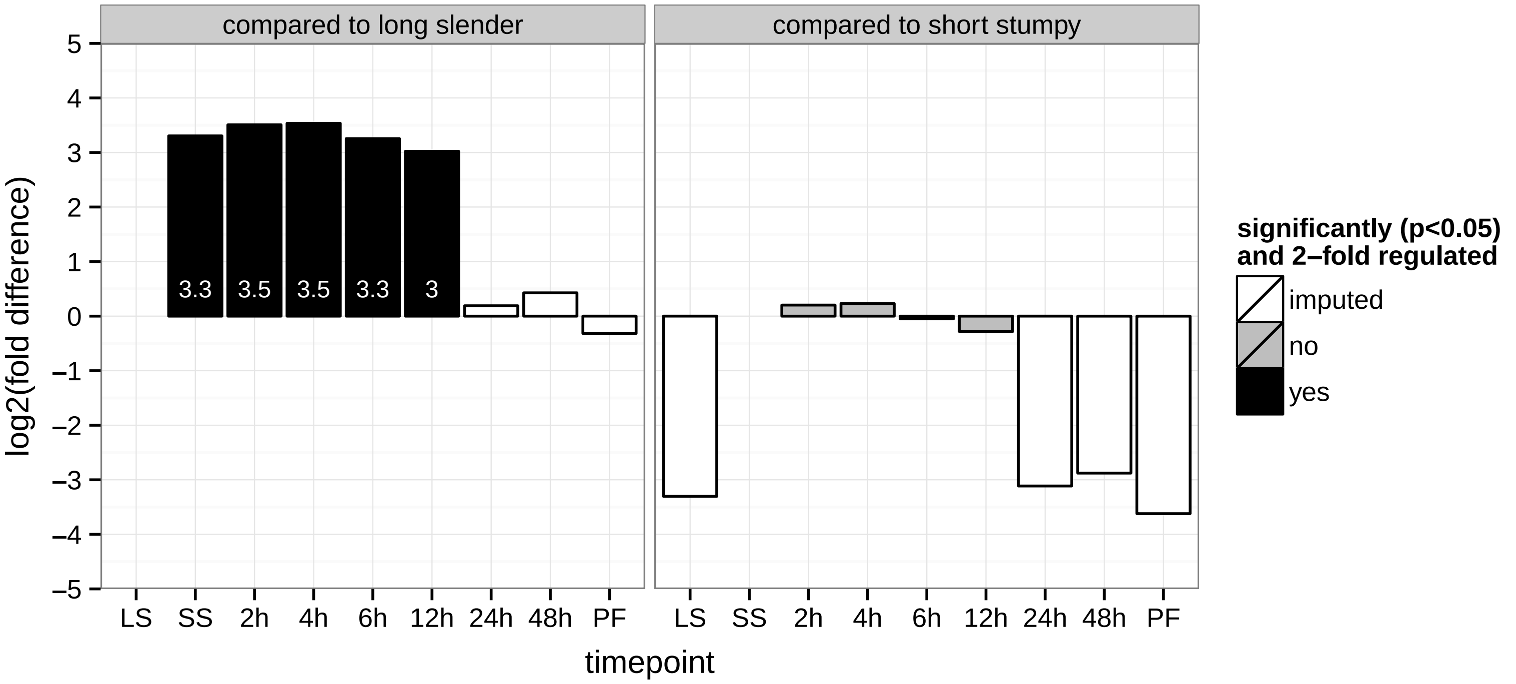
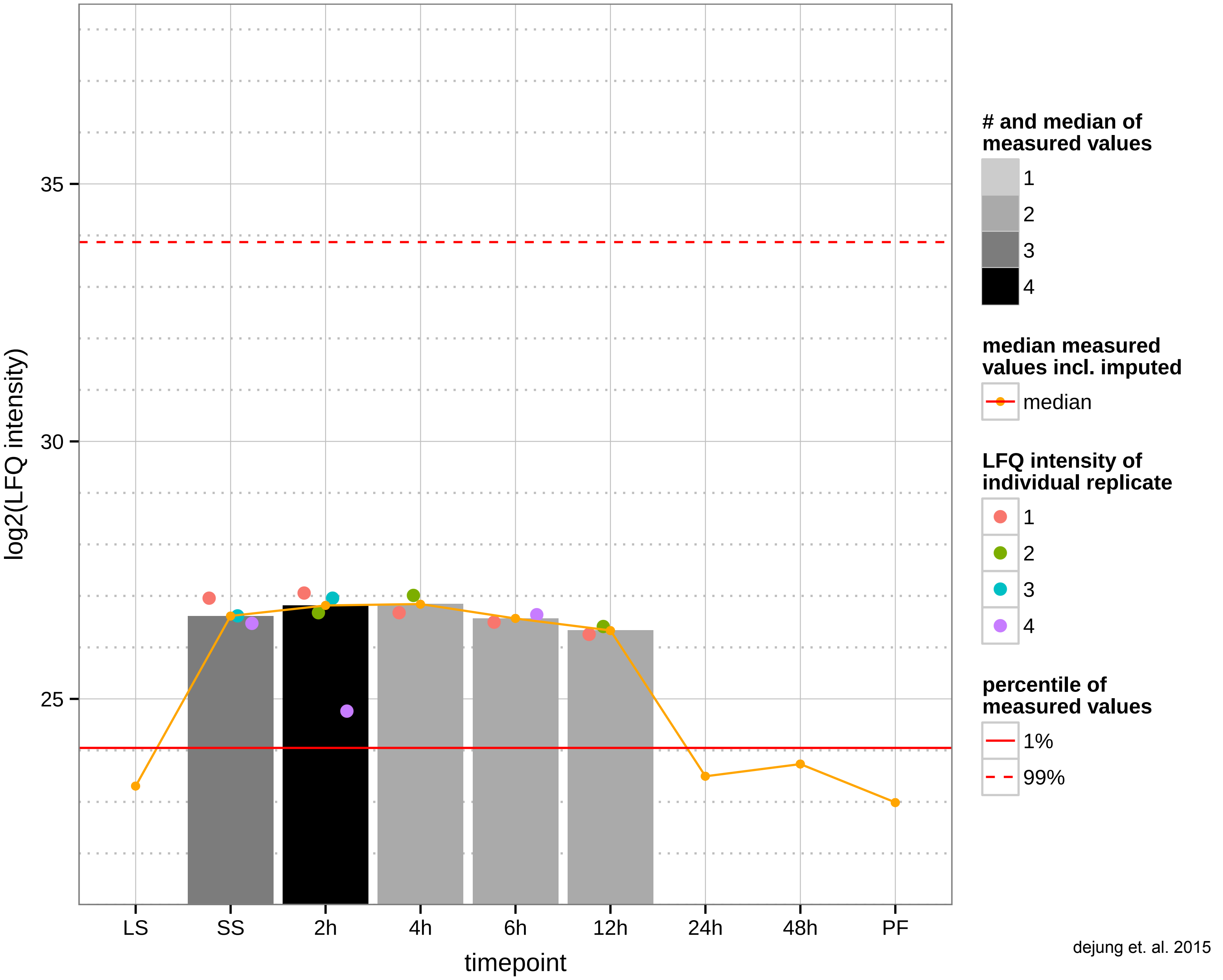
hypothetical protein
Tb927.4.3480
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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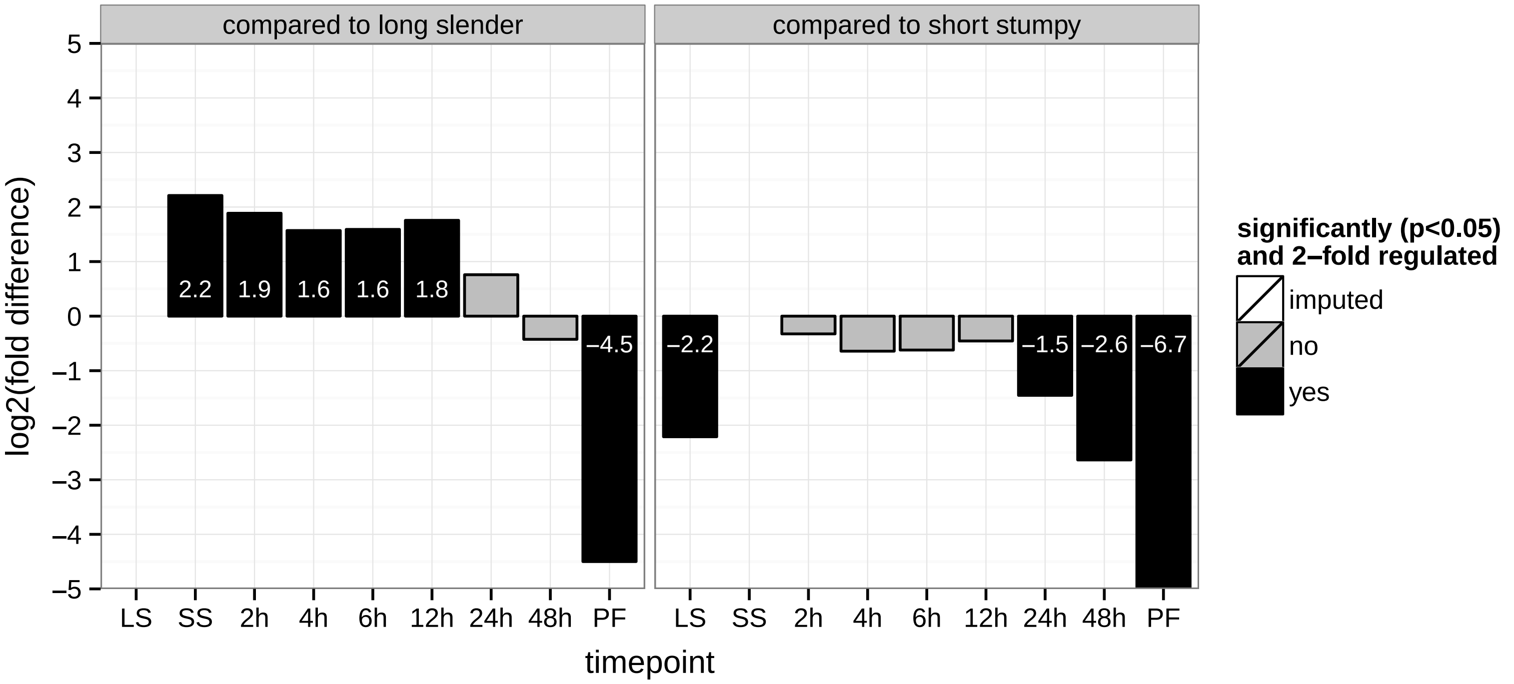
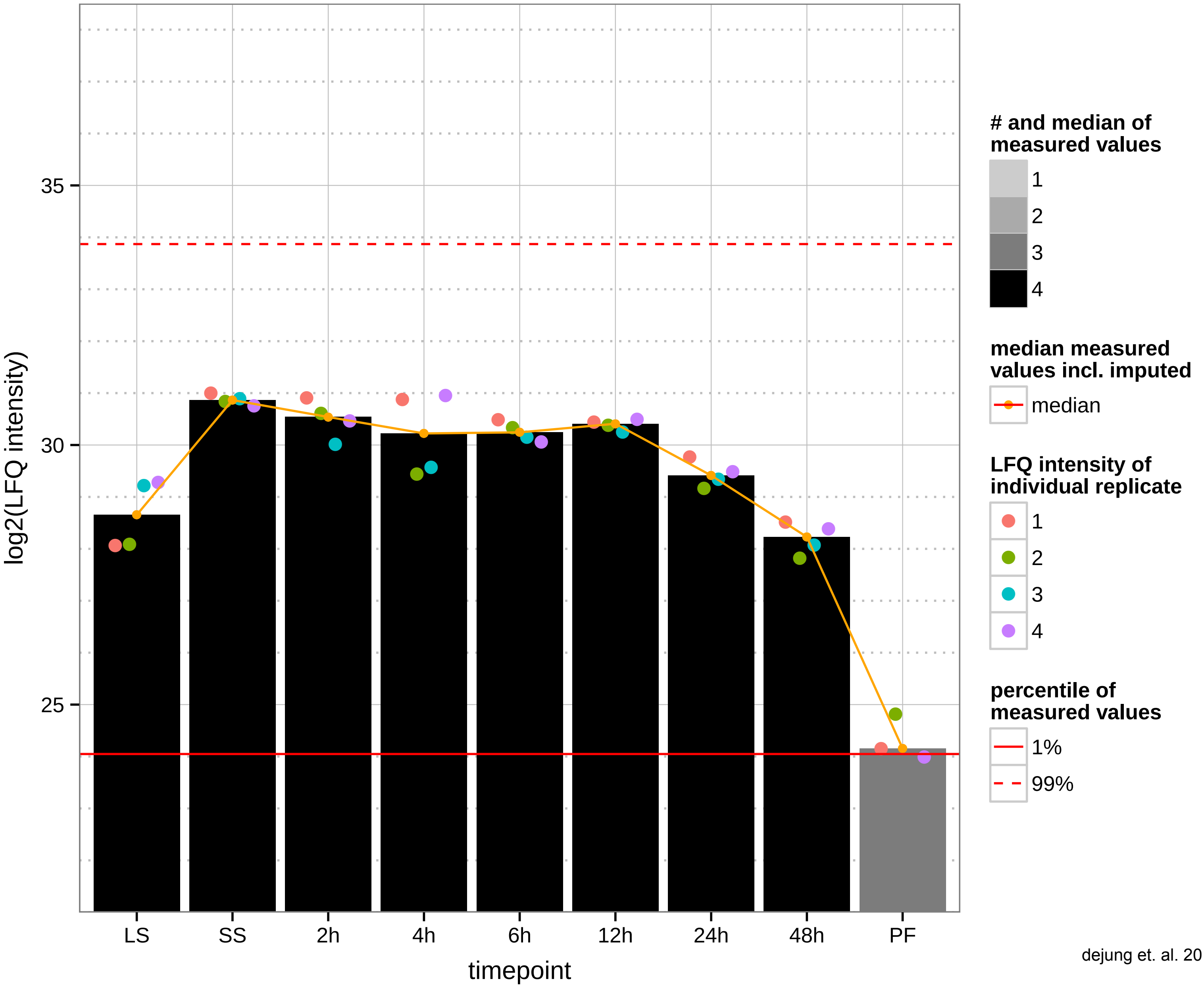
Repressor of differentiation kinase 2 (RDK2), serine/threonine−protein kinase a, putative, protein kinase
Tb927.4.5310
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, protein phosphorylation, protein phosphorylat
PGOF: ATP binding, phospholipid binding, protein binding, protein kinase activity, transferase activity, transferring phosphorus
PGOC: null
PGOP: protein phosphorylation





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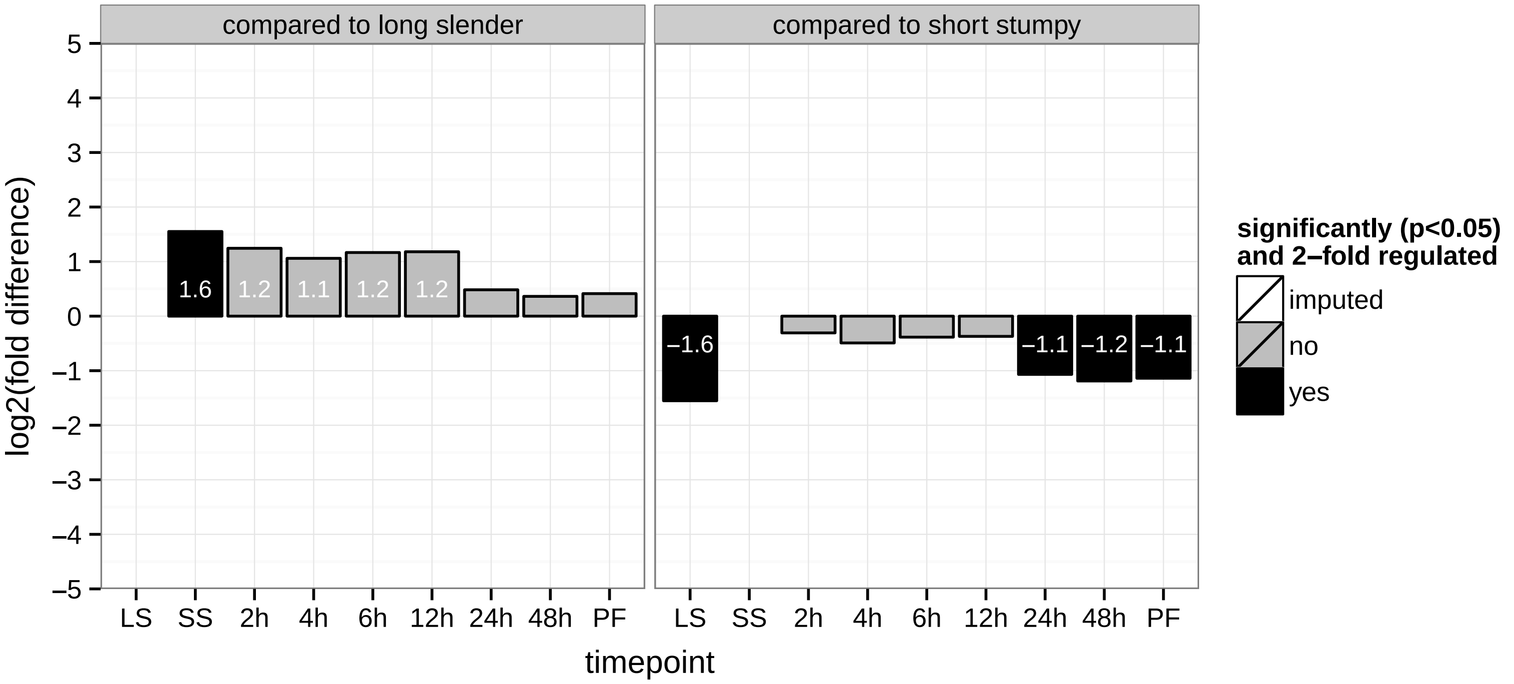
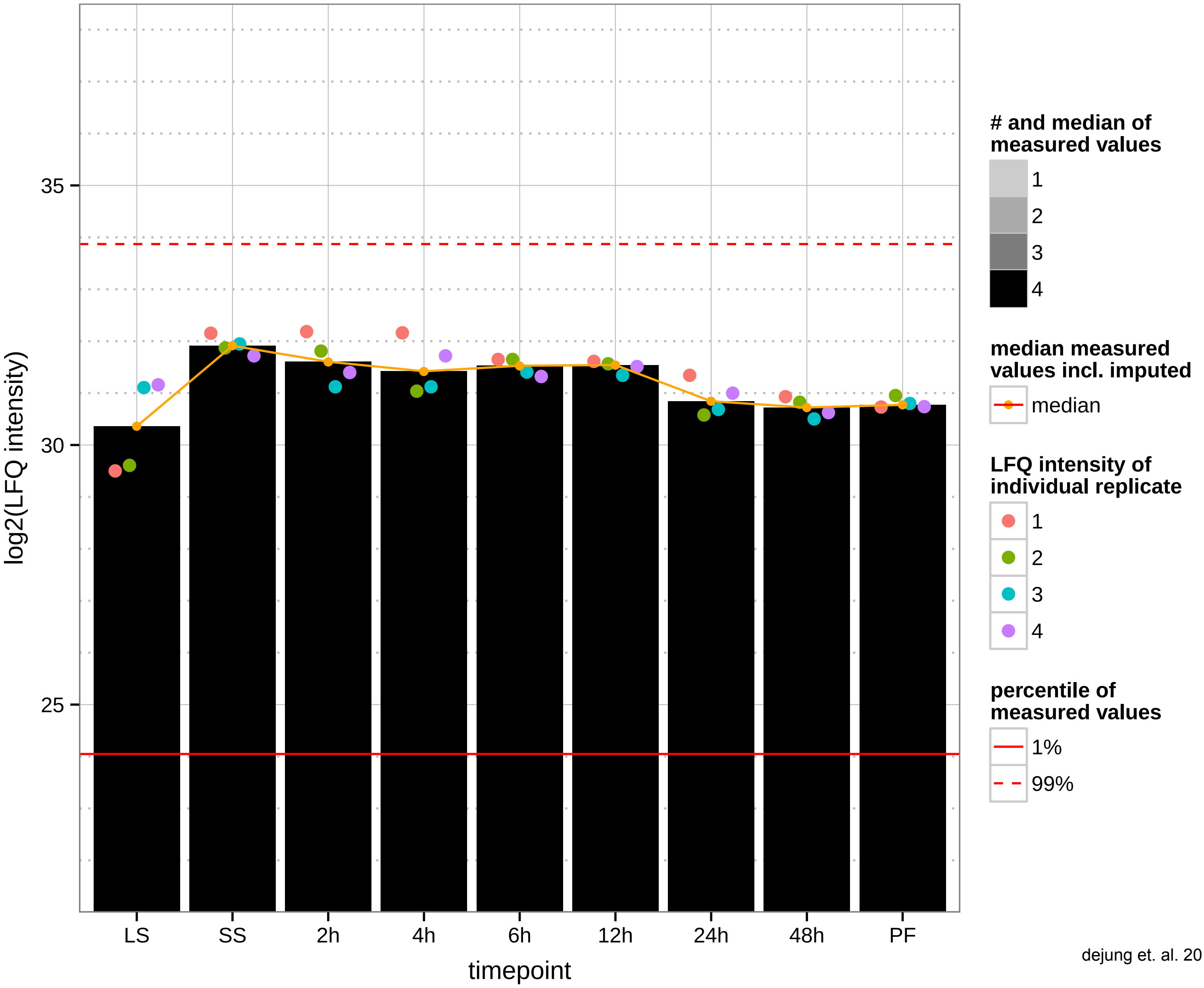
Cytoplasmic dynein 2 heavy chain (DYNC2H1), putative
Tb927.4.560
AGOF: ATP binding, ATPase activity, microtubule motor activity
AGOC: dynein complex
AGOP: chromosome segregation, microtubule–based movement, minus–end–directed vesicle transport along microtubule, m
PGOF: ATP binding, ATPase activity, microtubule motor activity, nucleoside–triphosphatase activity, nucleotide binding
PGOC: dynein complex
PGOP: microtubule–based movement





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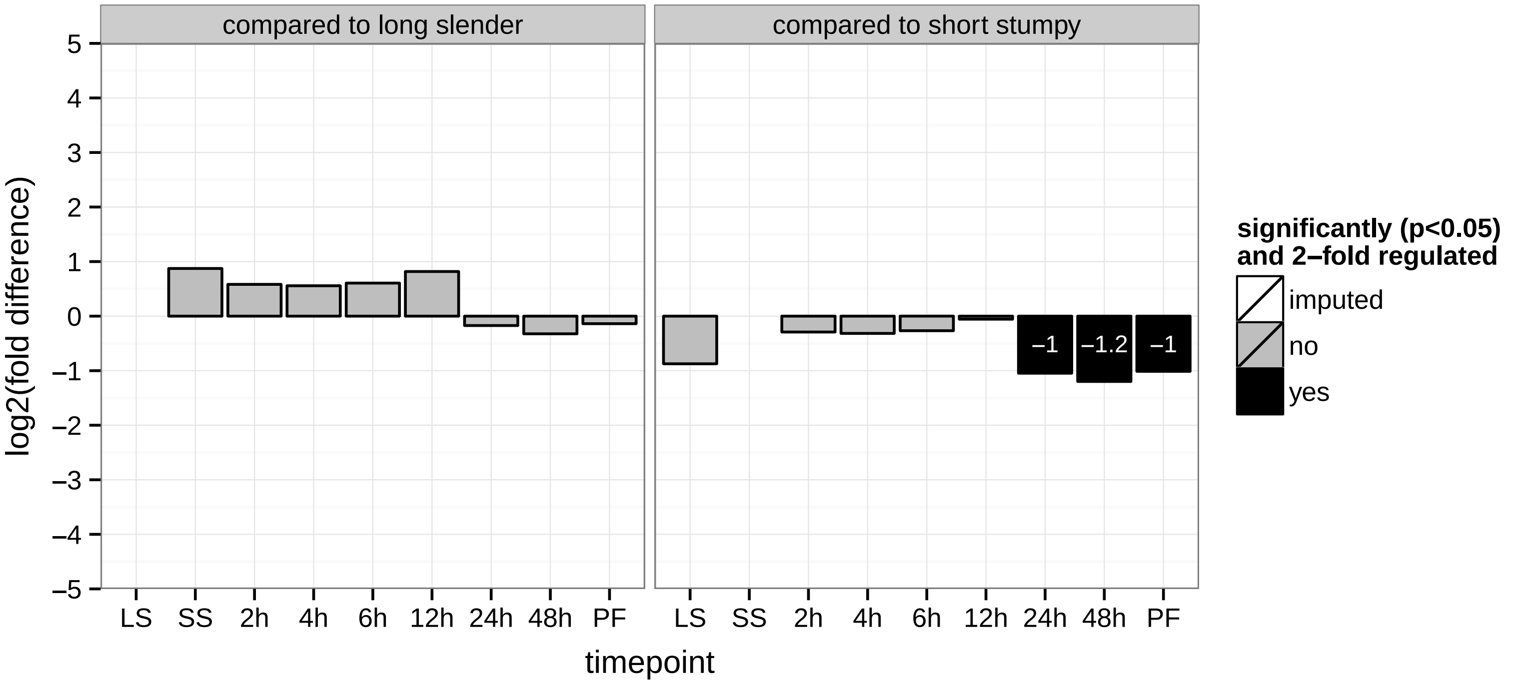
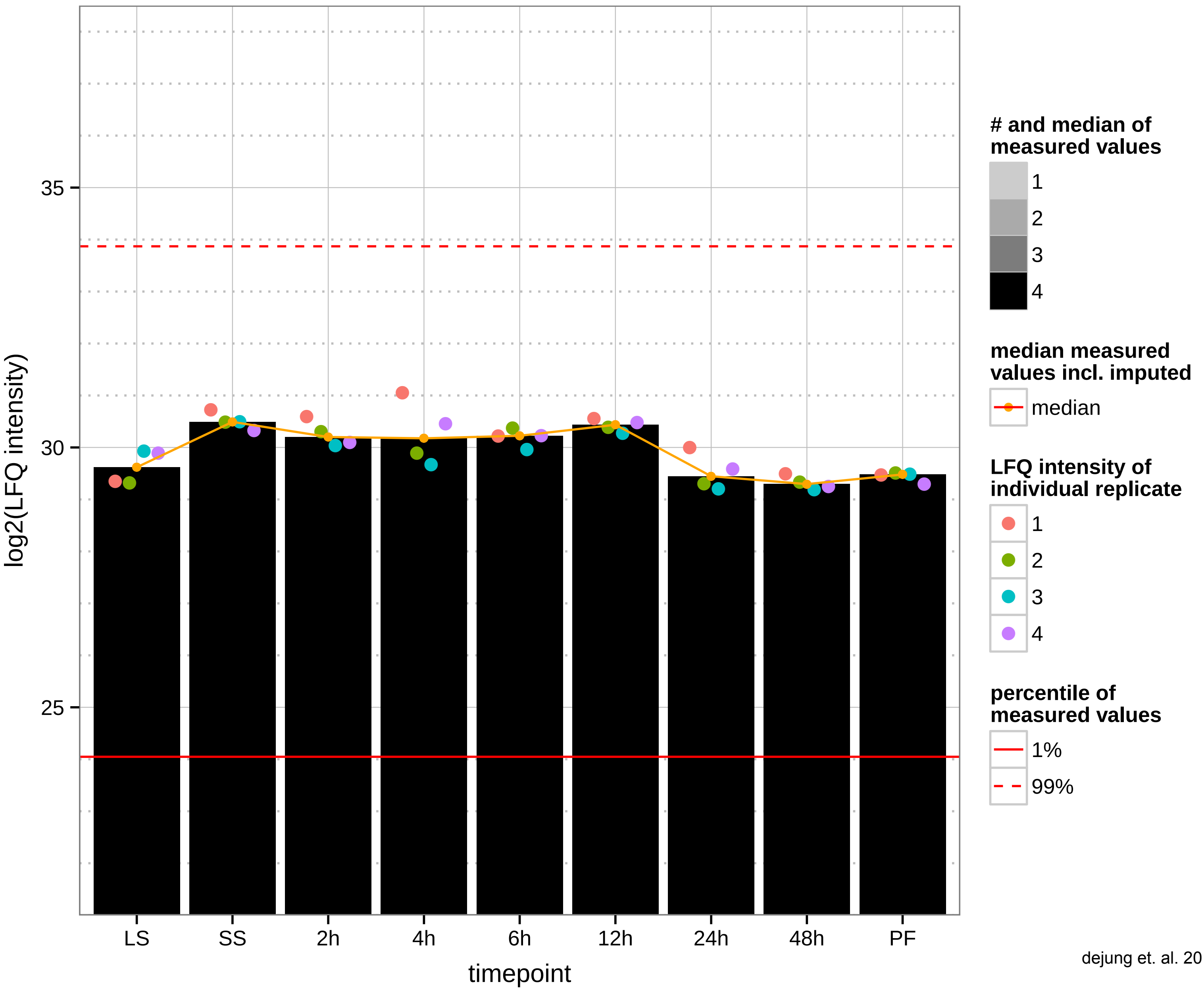
gamma–adaptin 1, putative, AP–1 adapter complex gamma subunit
Tb927.4.760
AGOF: protein transporter activity
AGOC: Golgi apparatus, Golgi apparatus part, clathrin adaptor complex, membrane coat
AGOP: intracellular protein transport, vesicle–mediated transport
PGOF: binding, protein transporter activity
PGOC: Golgi apparatus, Golgi apparatus part, clathrin adaptor complex, membrane coat
PGOP: intracellular protein transport, protein transport, vesicle–mediated transport





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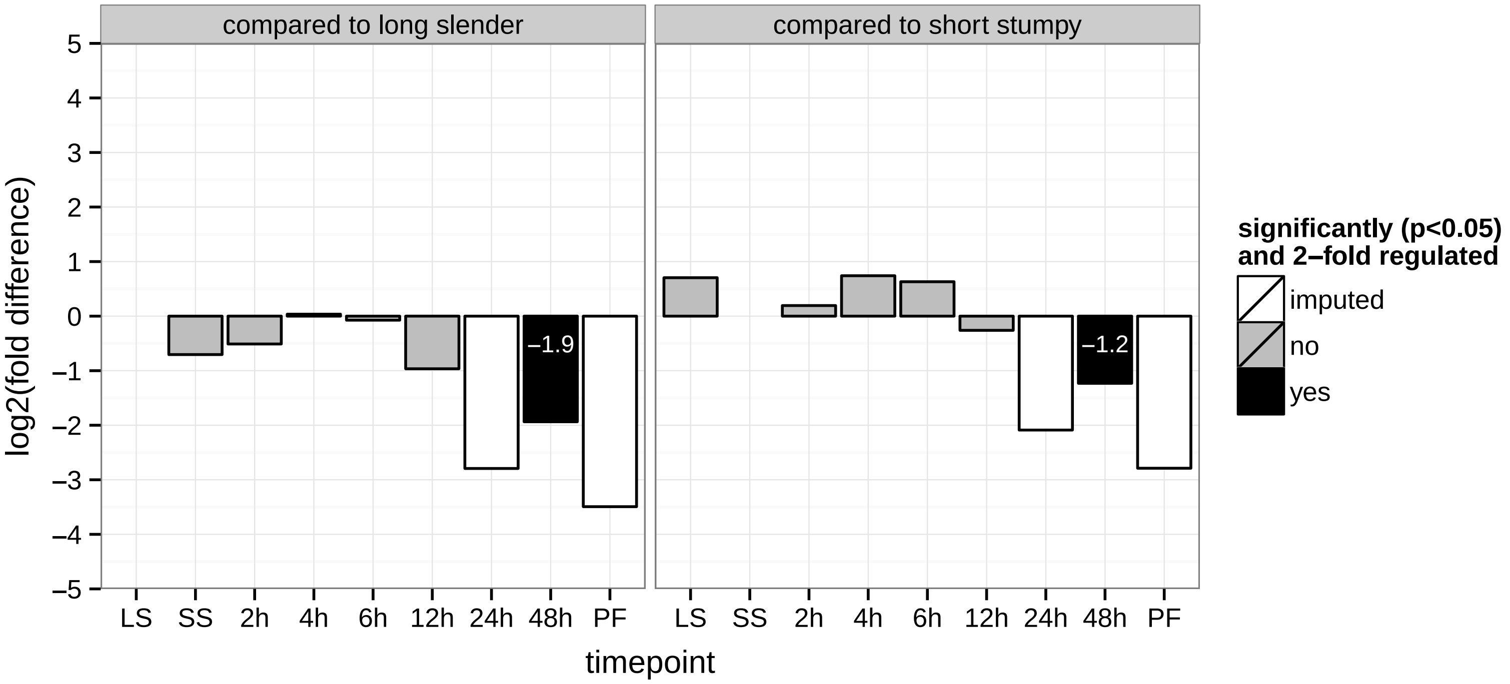
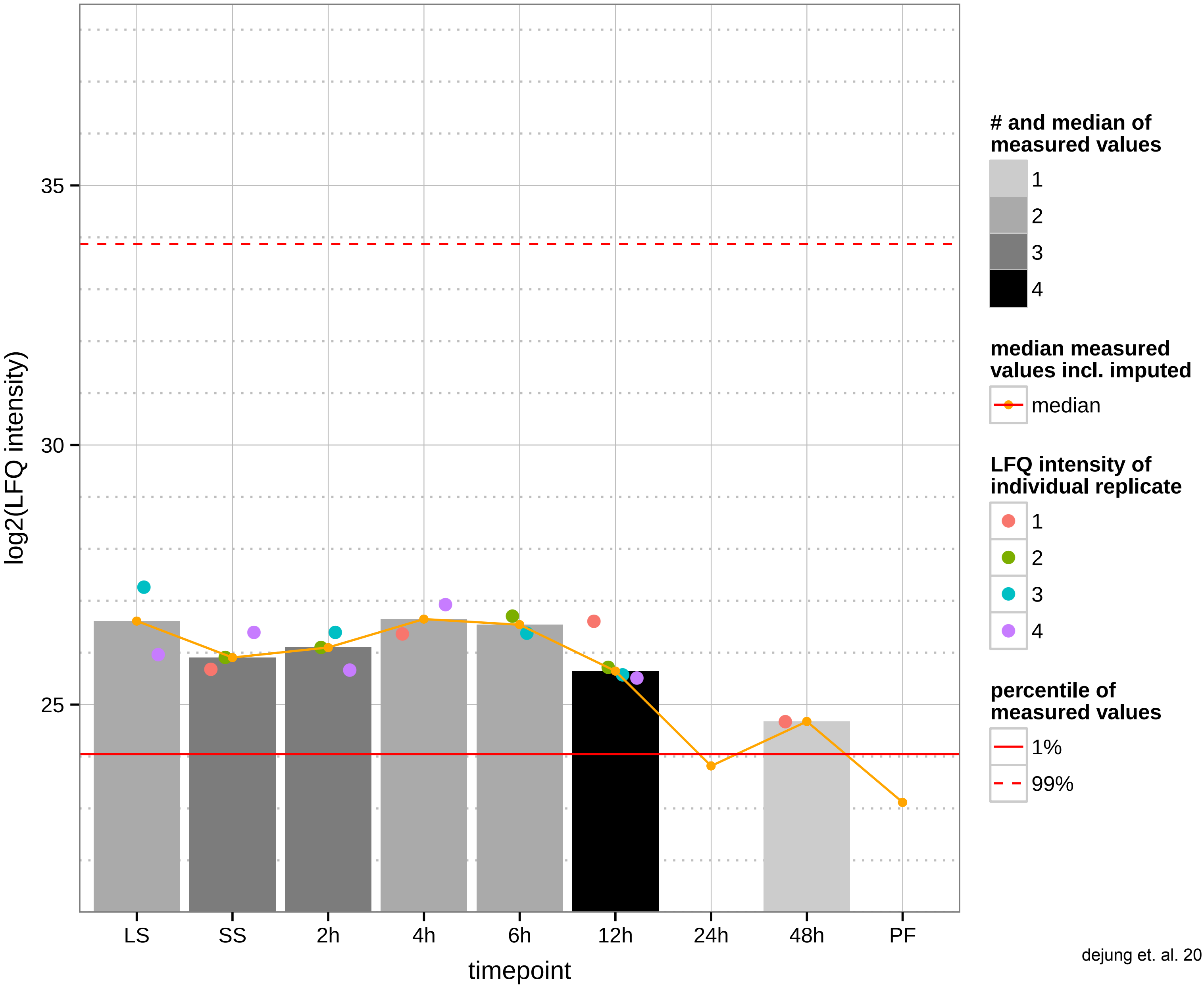
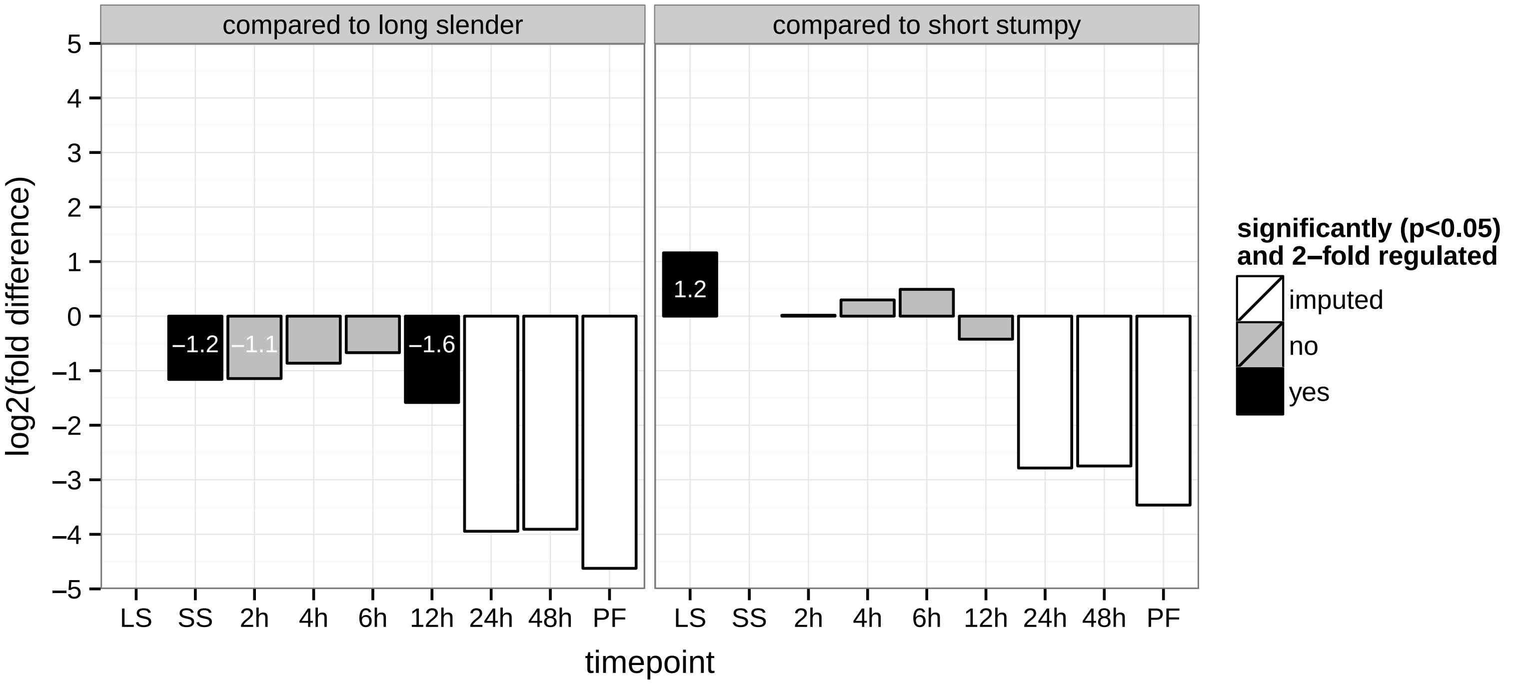
expression site−associated gene (ESAG) protein, putative, expression site−associated gene 5 (ESAG5) protein
Tb927.4.810
AGOF: lipid binding
AGOC: null
AGOP: null
PGOF: lipid binding
PGOC: null
PGOP: null

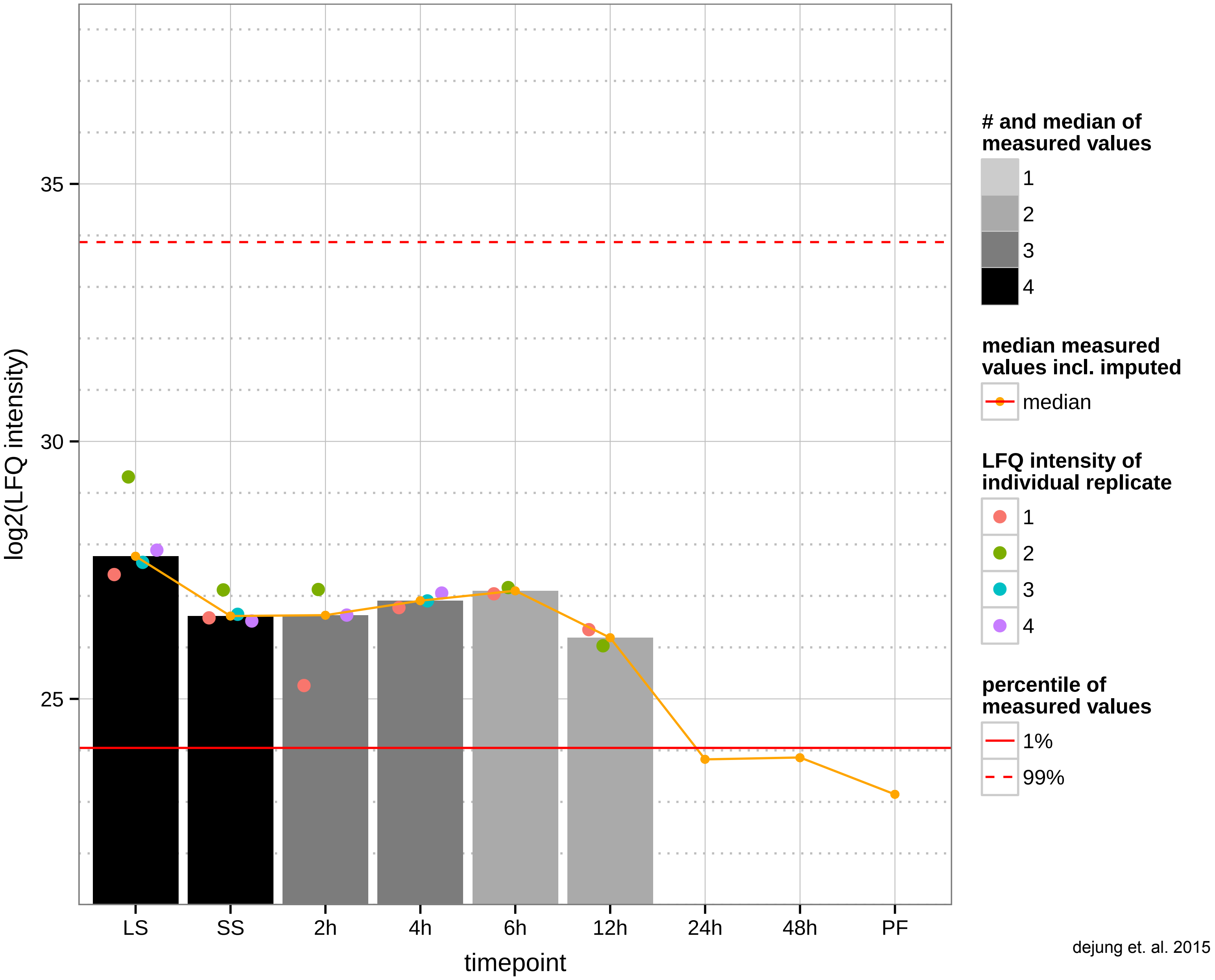




dejung et. al. 2015

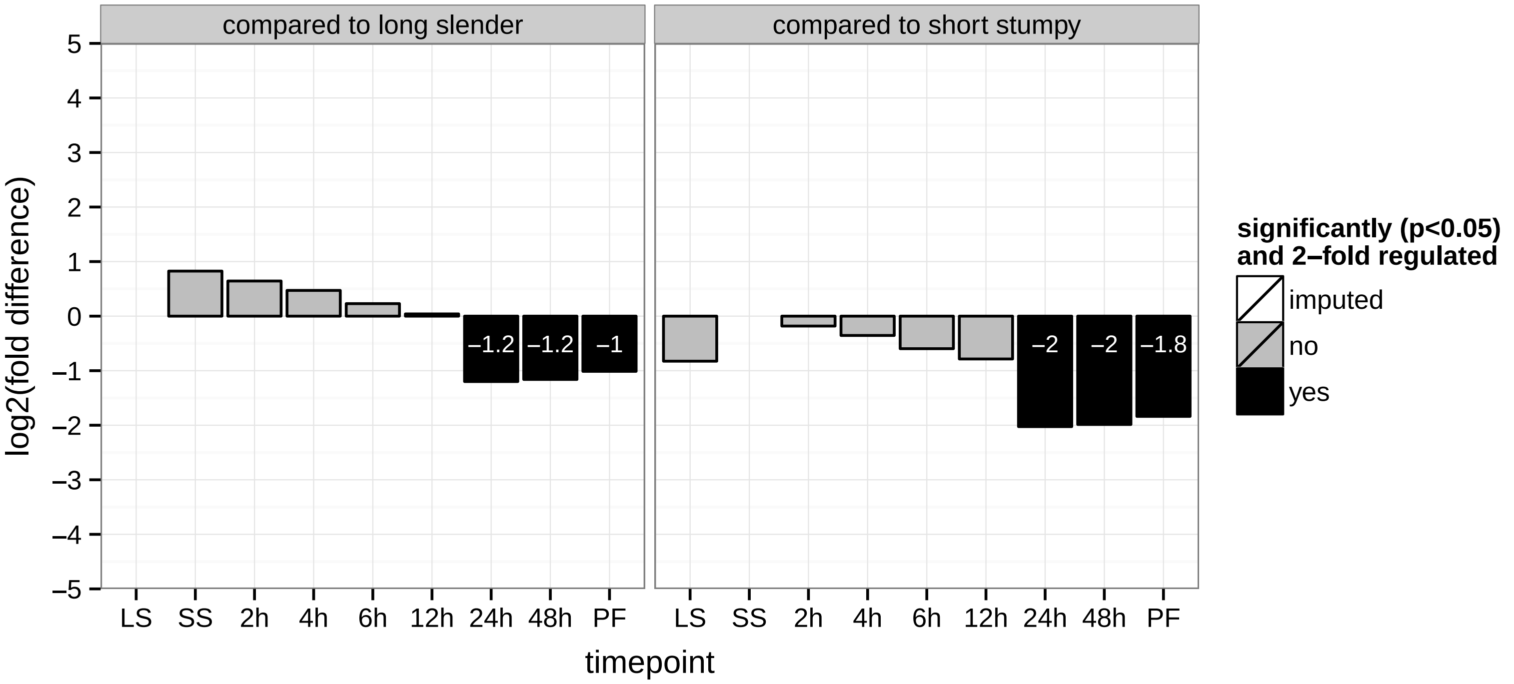
64 kDa invariant surface glycoprotein (ISG64)
Tb927.5.1410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

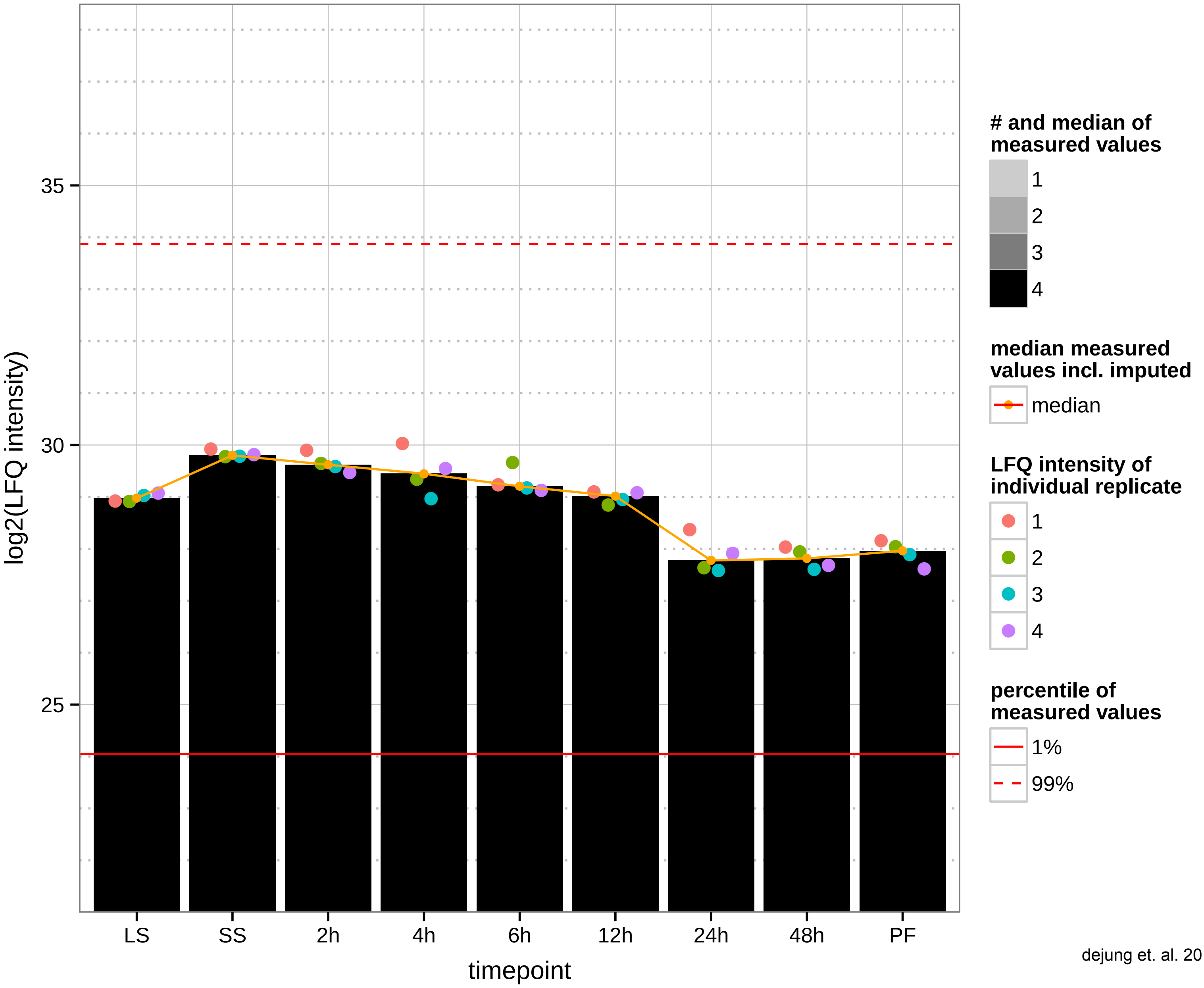




dejung et. al. 2015

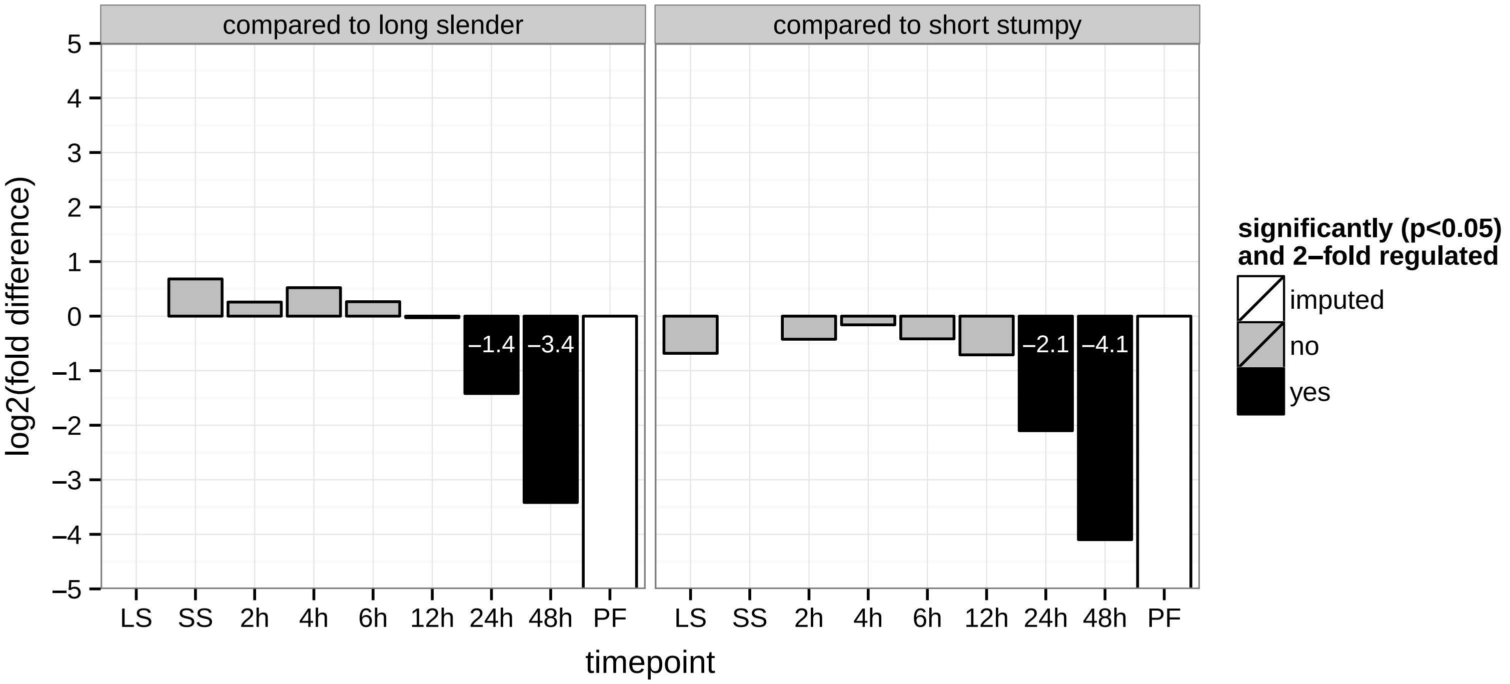
kinesin, putative
Tb927.5.2090
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: microtubule associated complex, kinesin complex, microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement

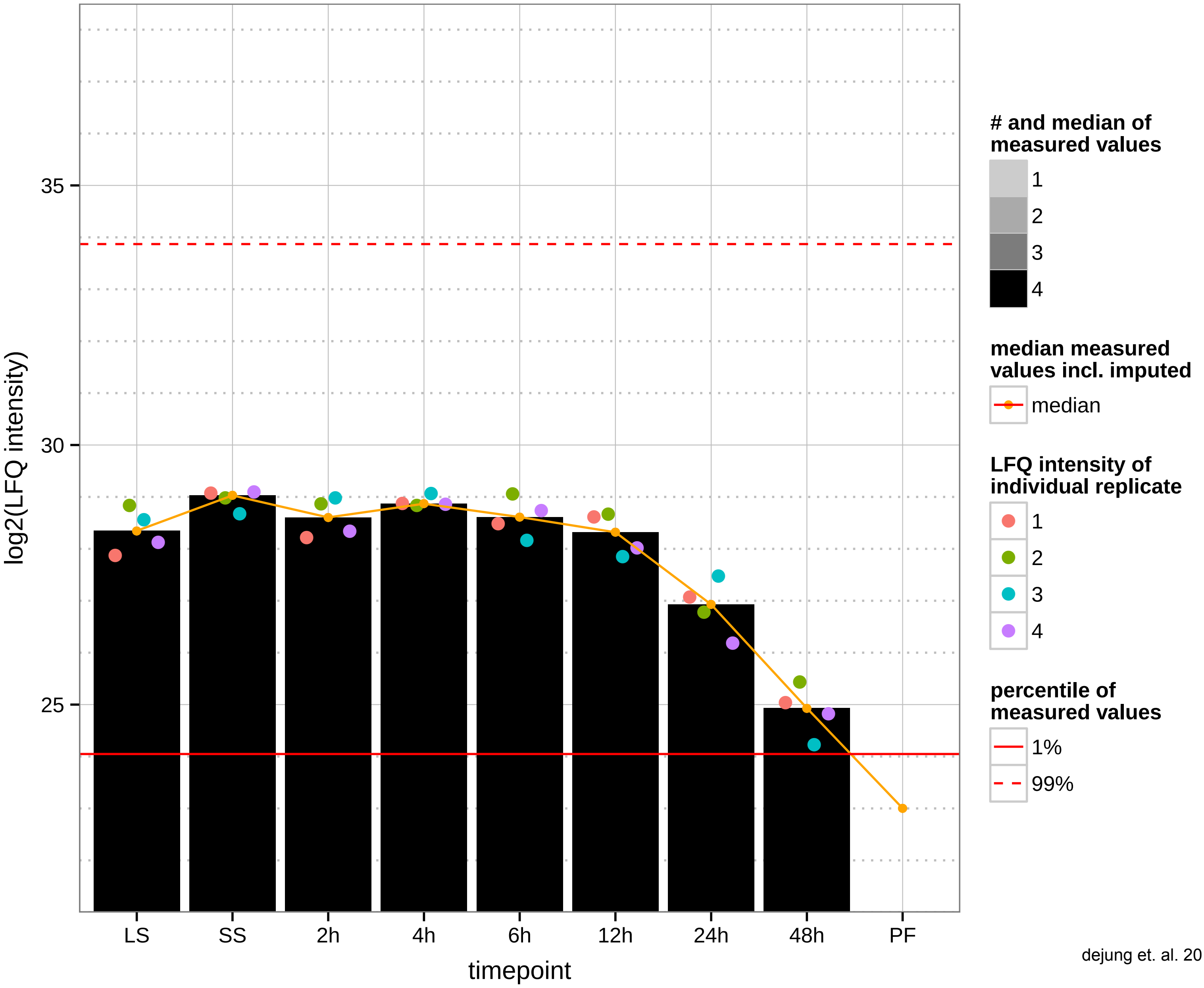




dejung et. al. 2015

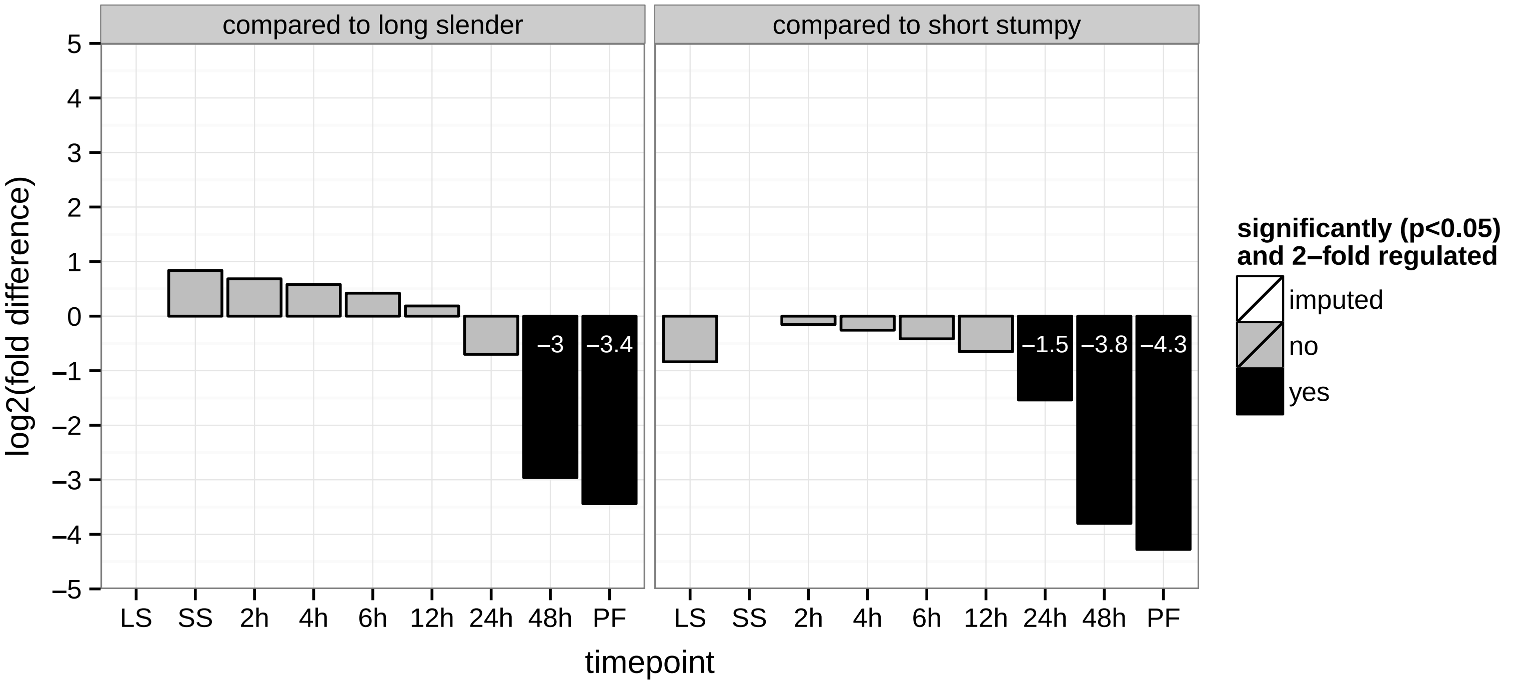
hypothetical protein, conserved
Tb927.5.310;Tb11.v5.0208
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

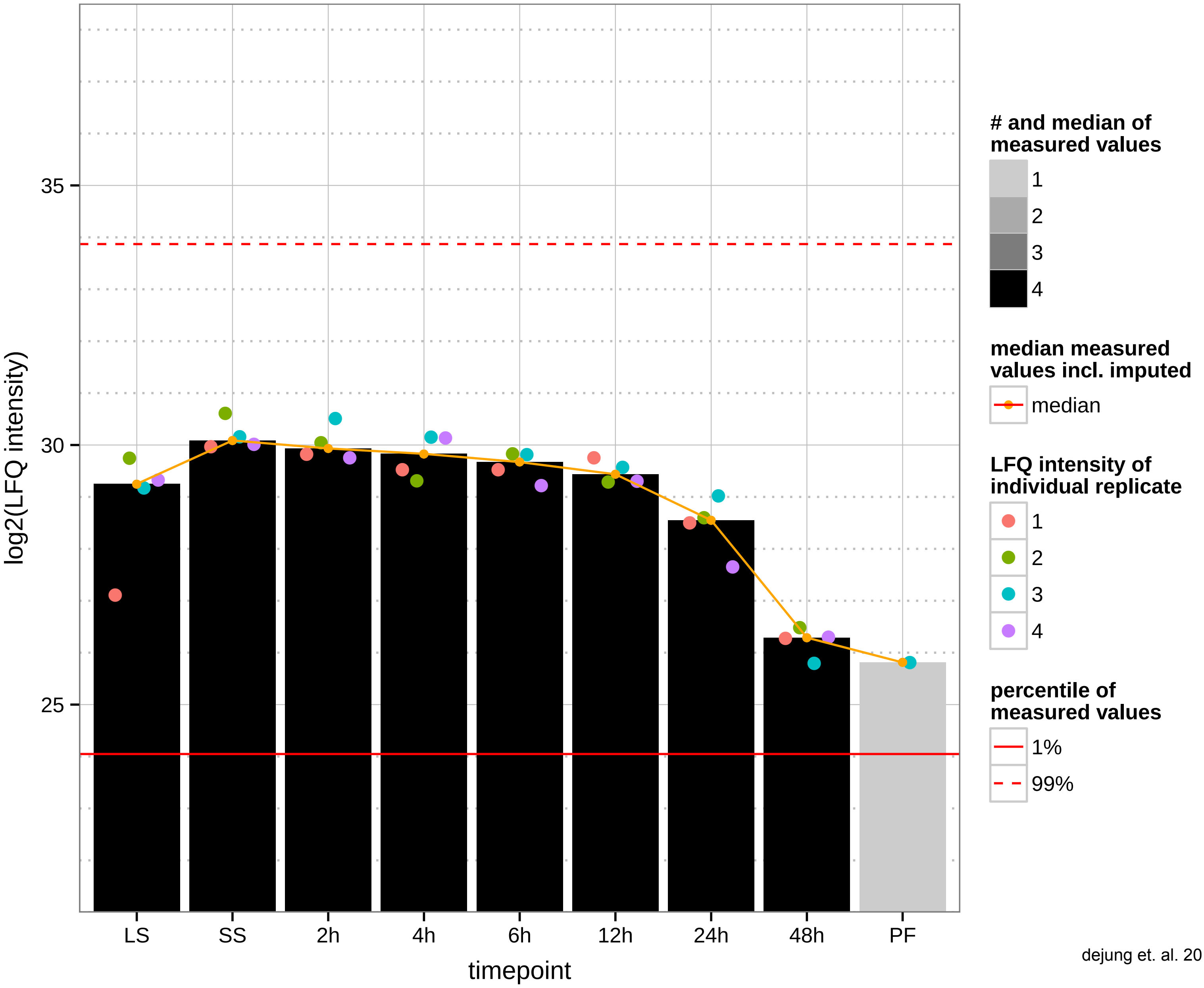




dejung et. al. 2015

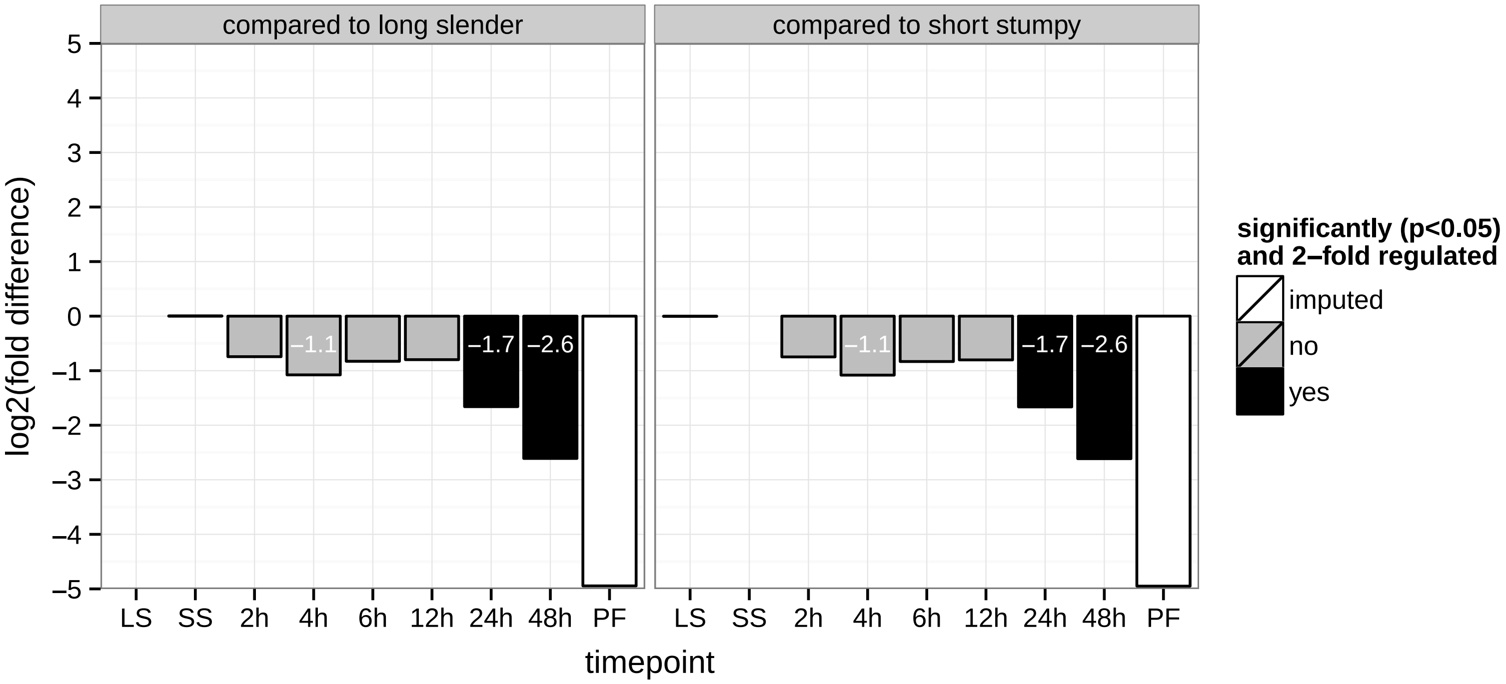
hypothetical protein, conserved, acidic phosphatase, putative
Tb927.5.630
AGOF: null
AGOC: null
AGOP: null
PGOF: nucleic acid binding, null
PGOC: null
PGOP: null

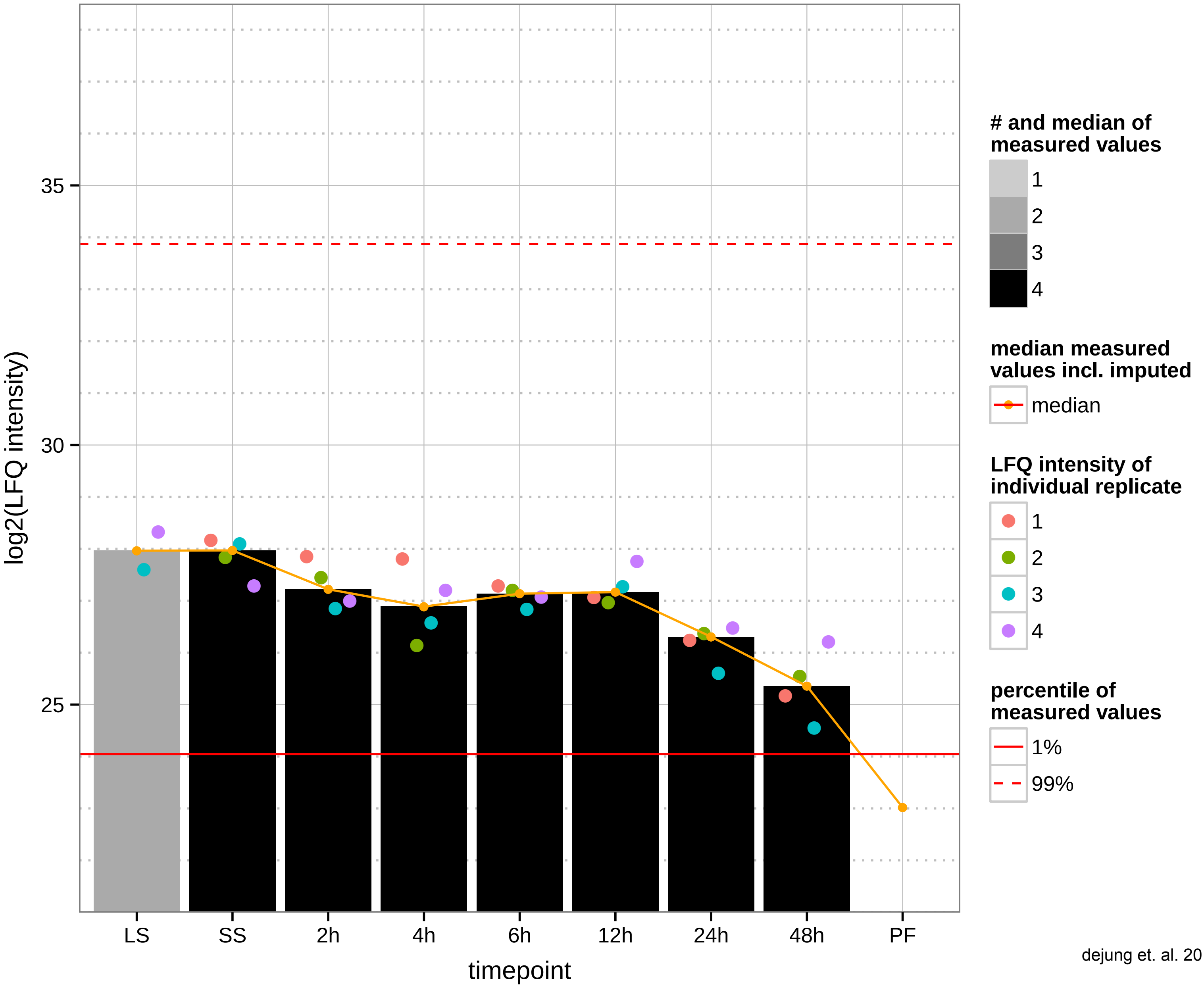




dejung et. al. 2015

hypothetical protein, conserved, oligosaccharyl transferase subunit, putative
Tb927.5.890
AGOF: oligosaccharyl transferase activity
AGOC: membrane
AGOP: protein glycosylation, protein mannosylation
PGOF: oligosaccharyl transferase activity
PGOC: membrane
PGOP: protein glycosylation





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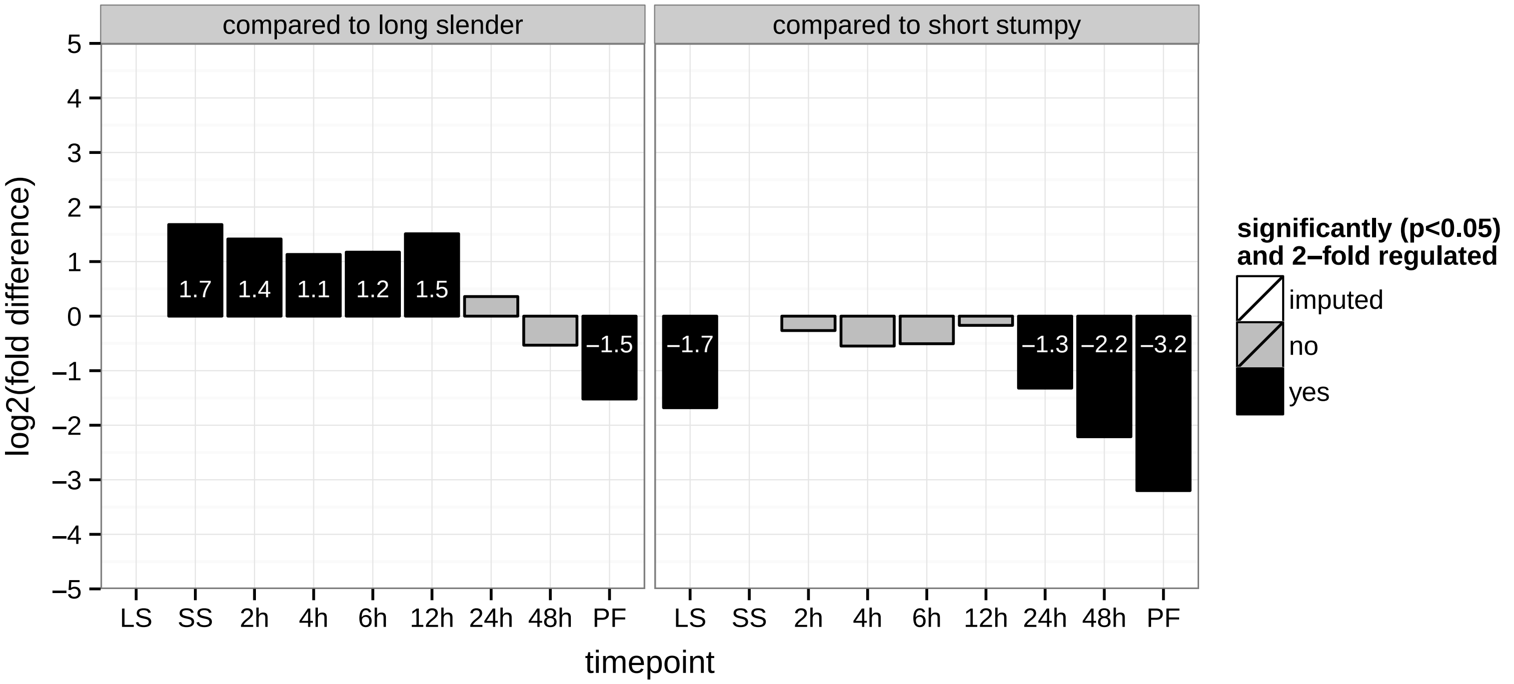
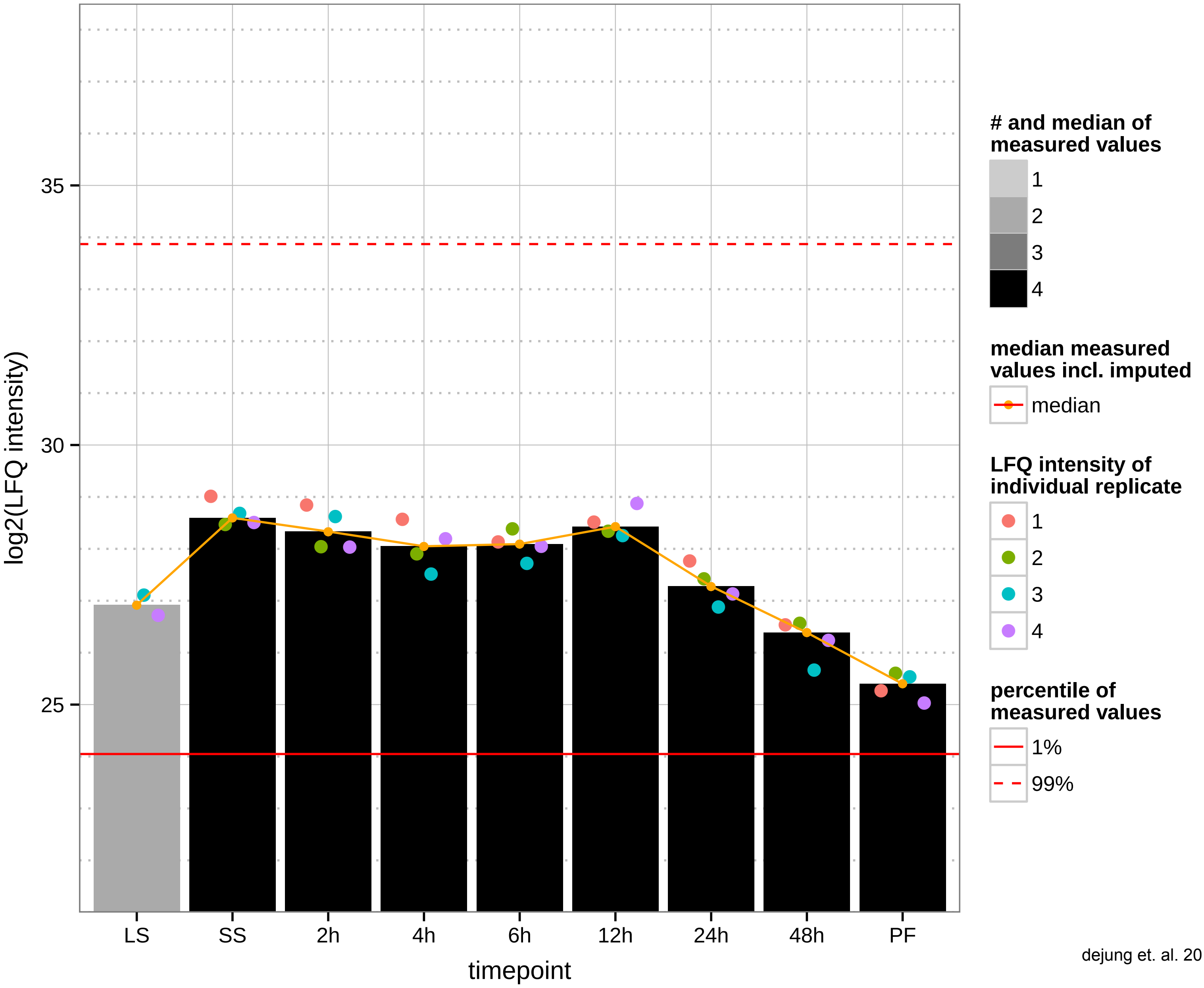
hypothetical protein, conserved
Tb927.6.1730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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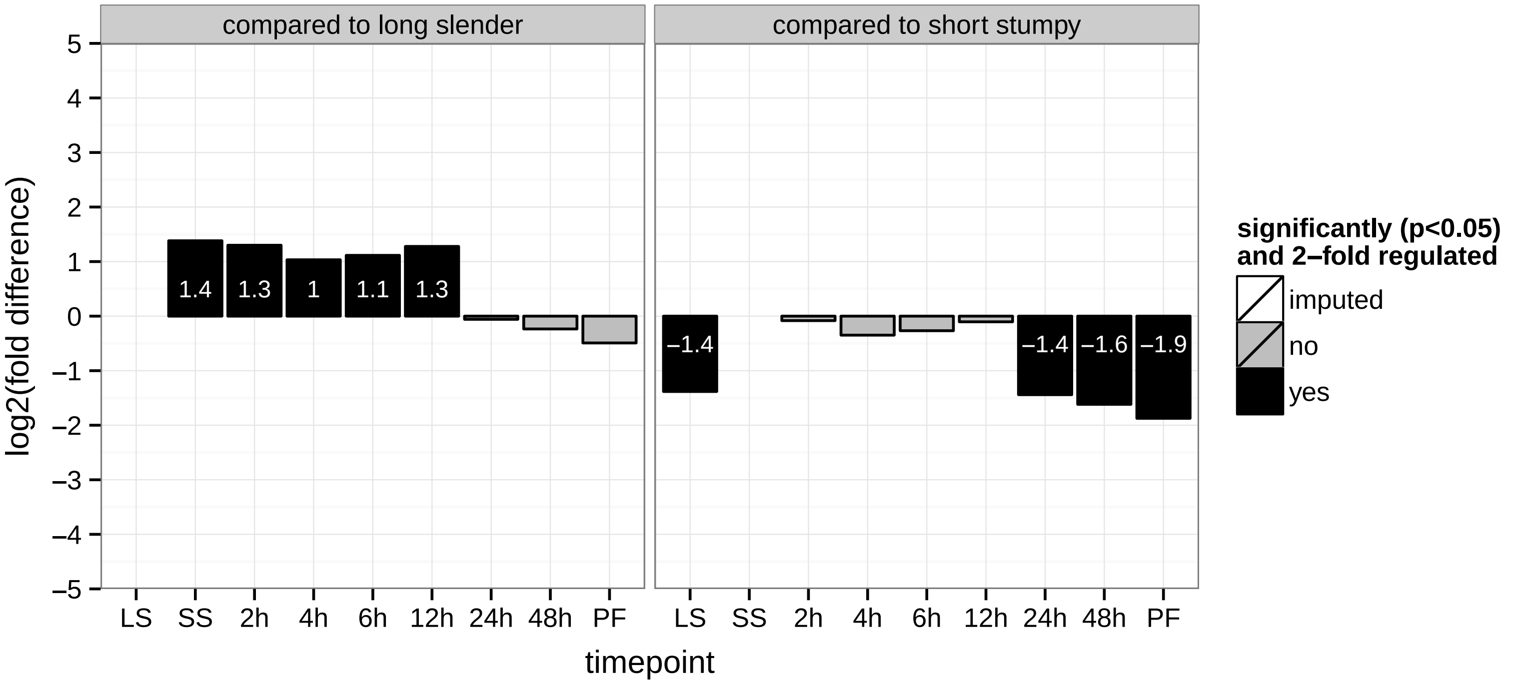
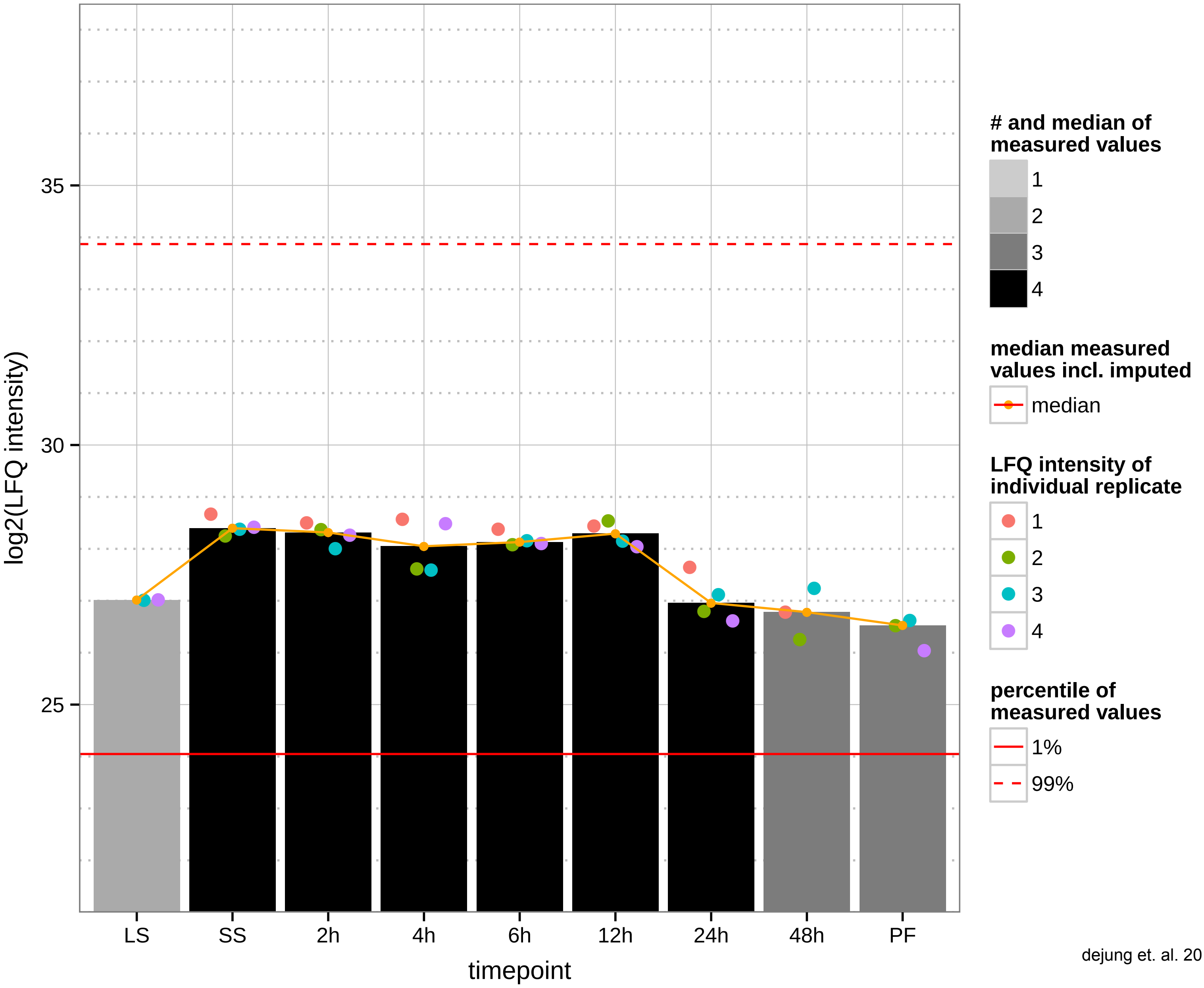
rac serine–threonine kinase, putative, protein kinase
Tb927.6.2250
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, phospholipid binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, tran
PGOC: null
PGOP: protein phosphorylation





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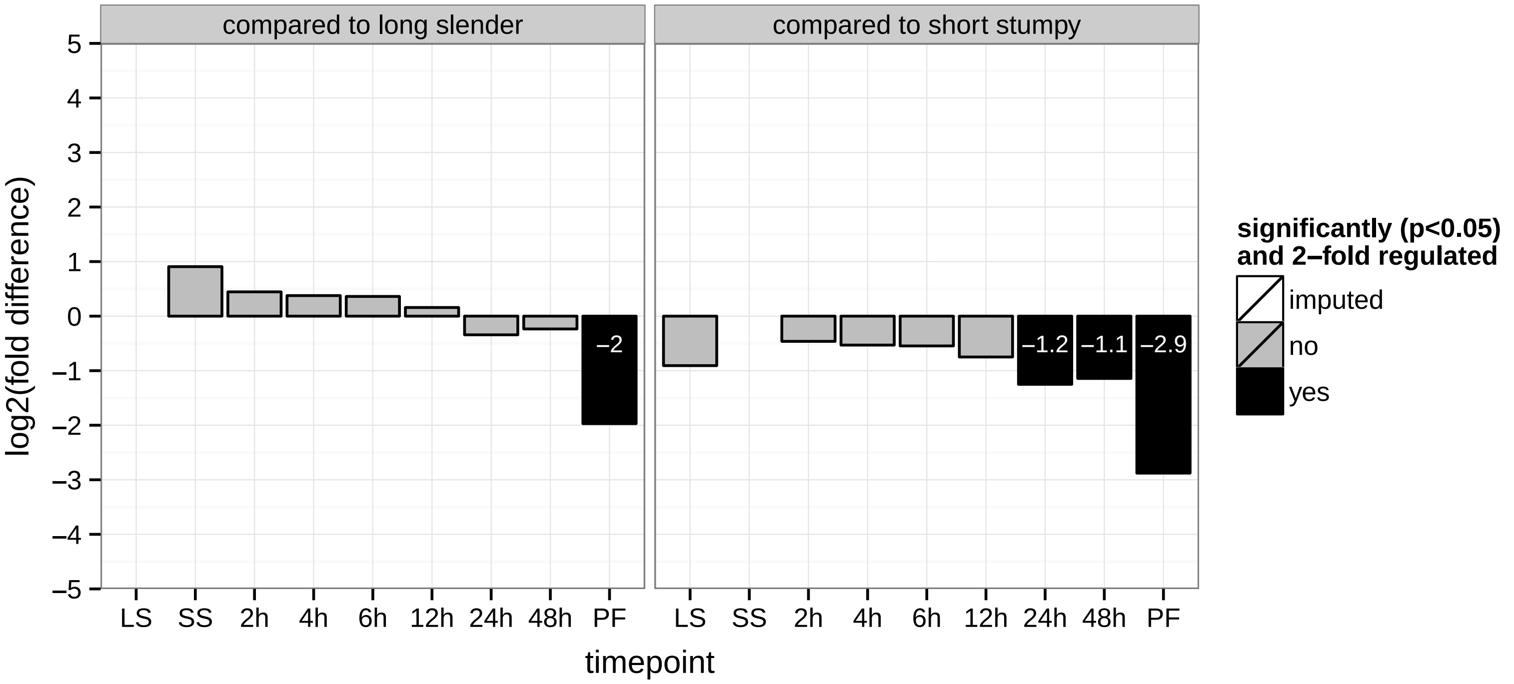
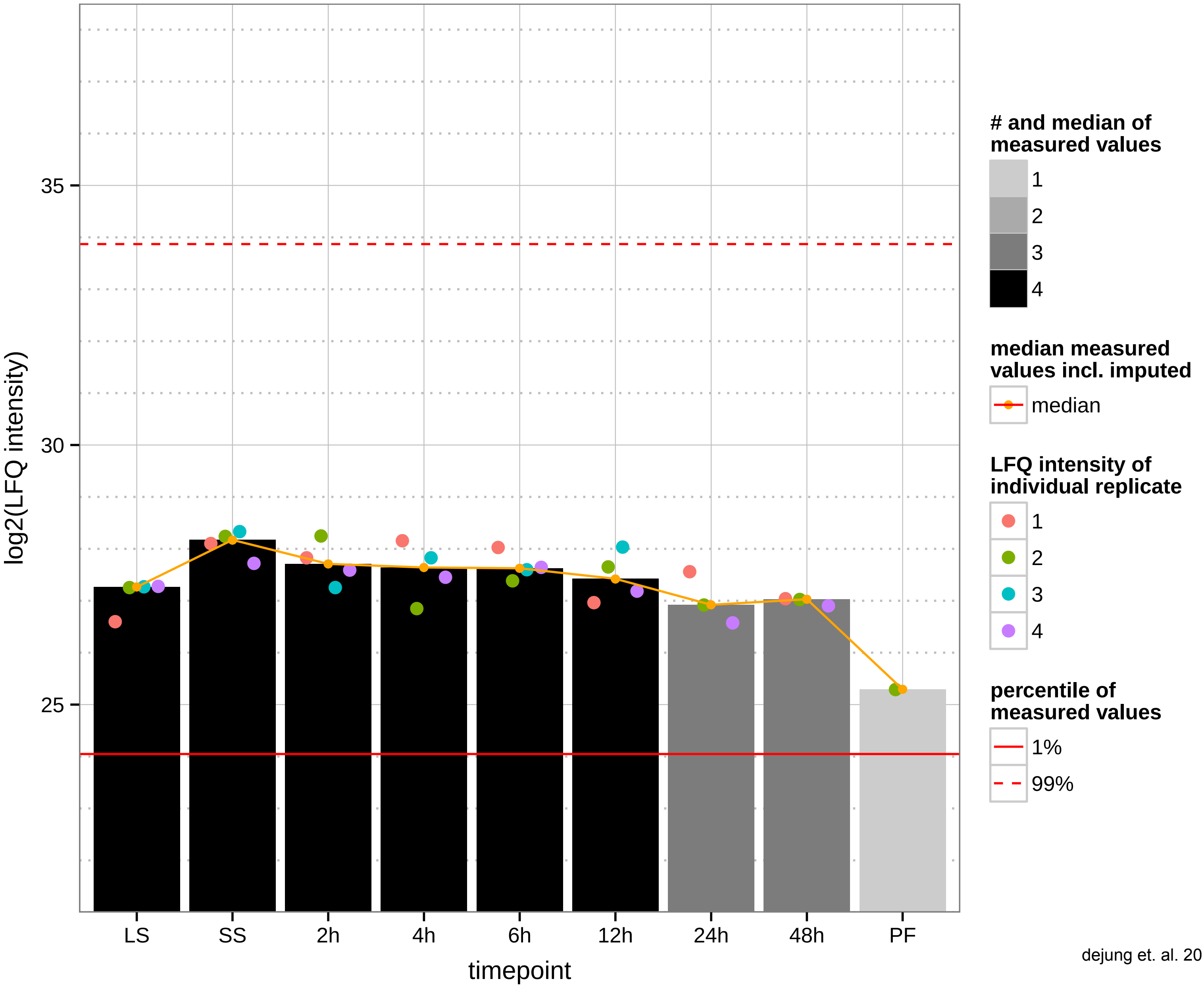
hypothetical protein, conserved
Tb927.6.3640
AGOF: zinc ion binding
AGOC: intracellular
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: intracellular
PGOP: null





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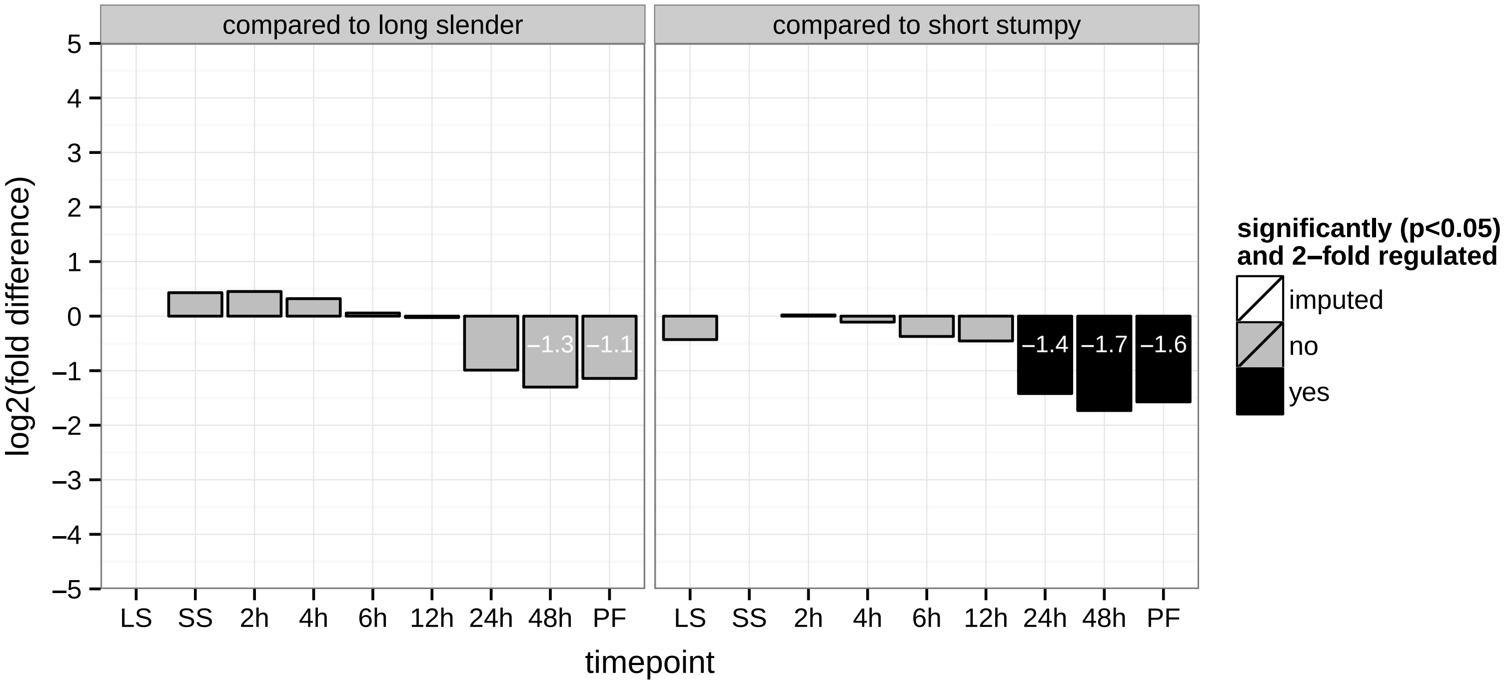
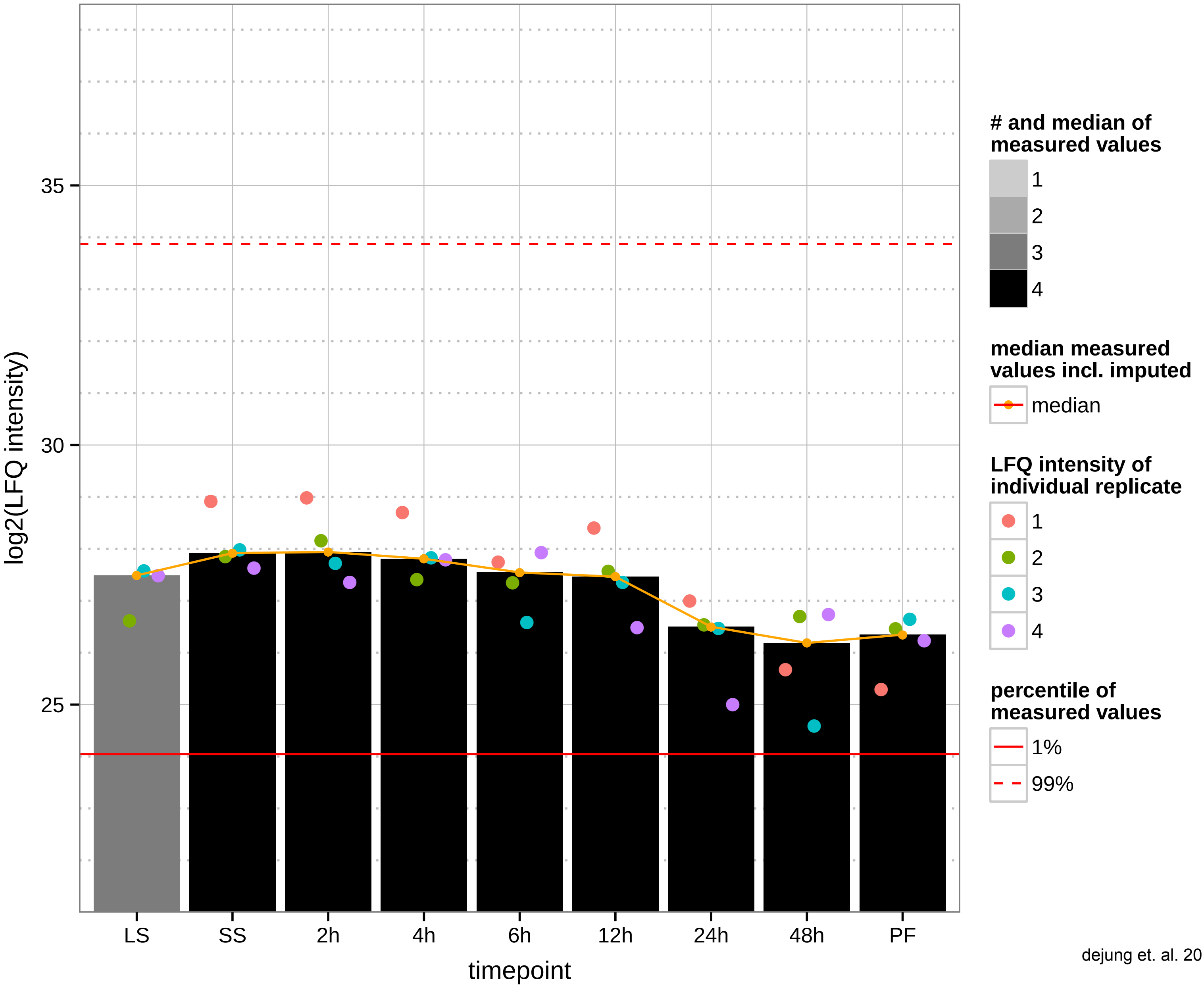
kinesin, putative
Tb927.6.4390
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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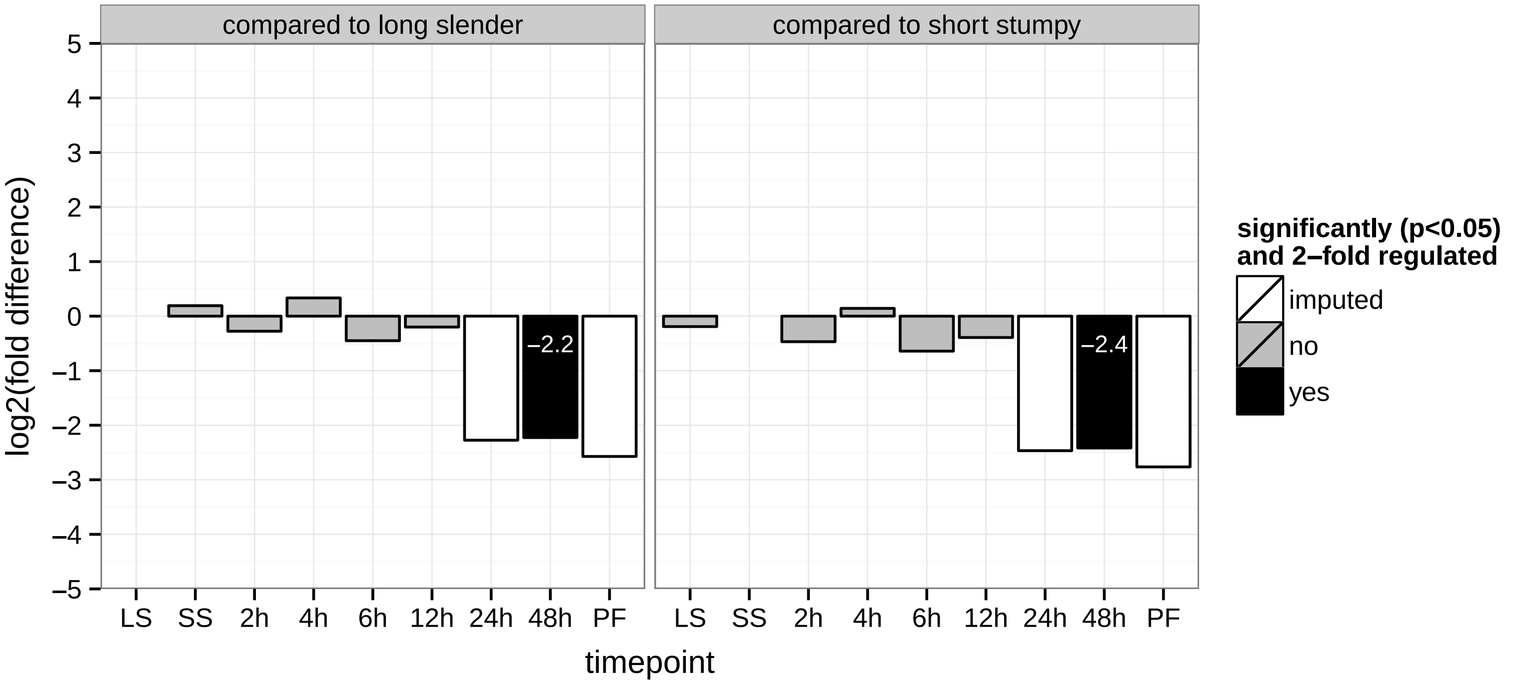
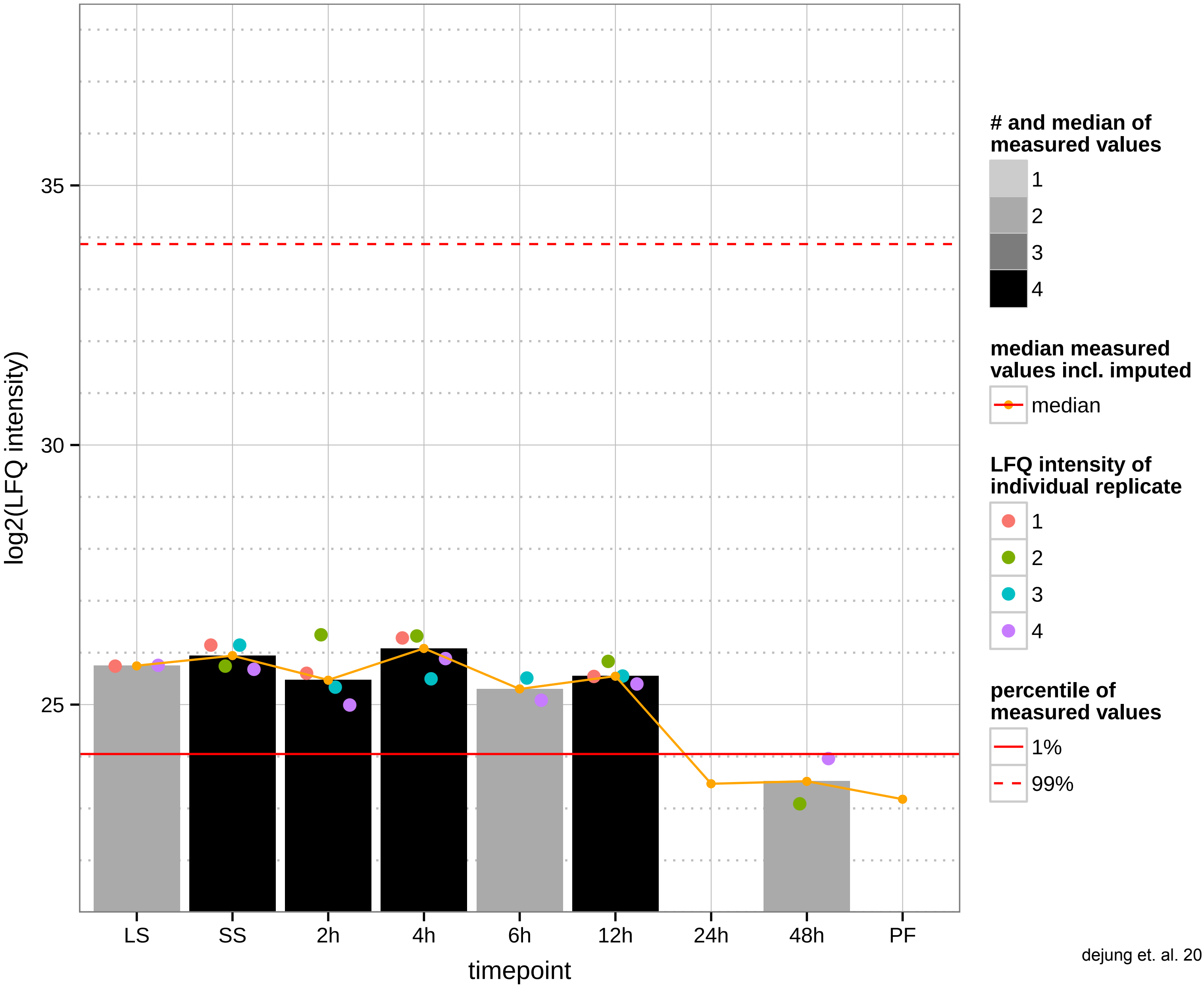
metacaspase MCA3, cysteine peptidase, Clan CD, family C13, putative (TbMCA4), metacaspase MCA2 (MCA2)
Tb927.6.940;Tb927.6.930
AGOF: cysteine–type endopeptidase activity, peptidase activity, cysteine–type peptidase activity
AGOC: nucleus
AGOP: aerobic respiration, proteolysis, proteolysis
PGOF: cysteine–type endopeptidase activity
PGOC: null
PGOP: proteolysis





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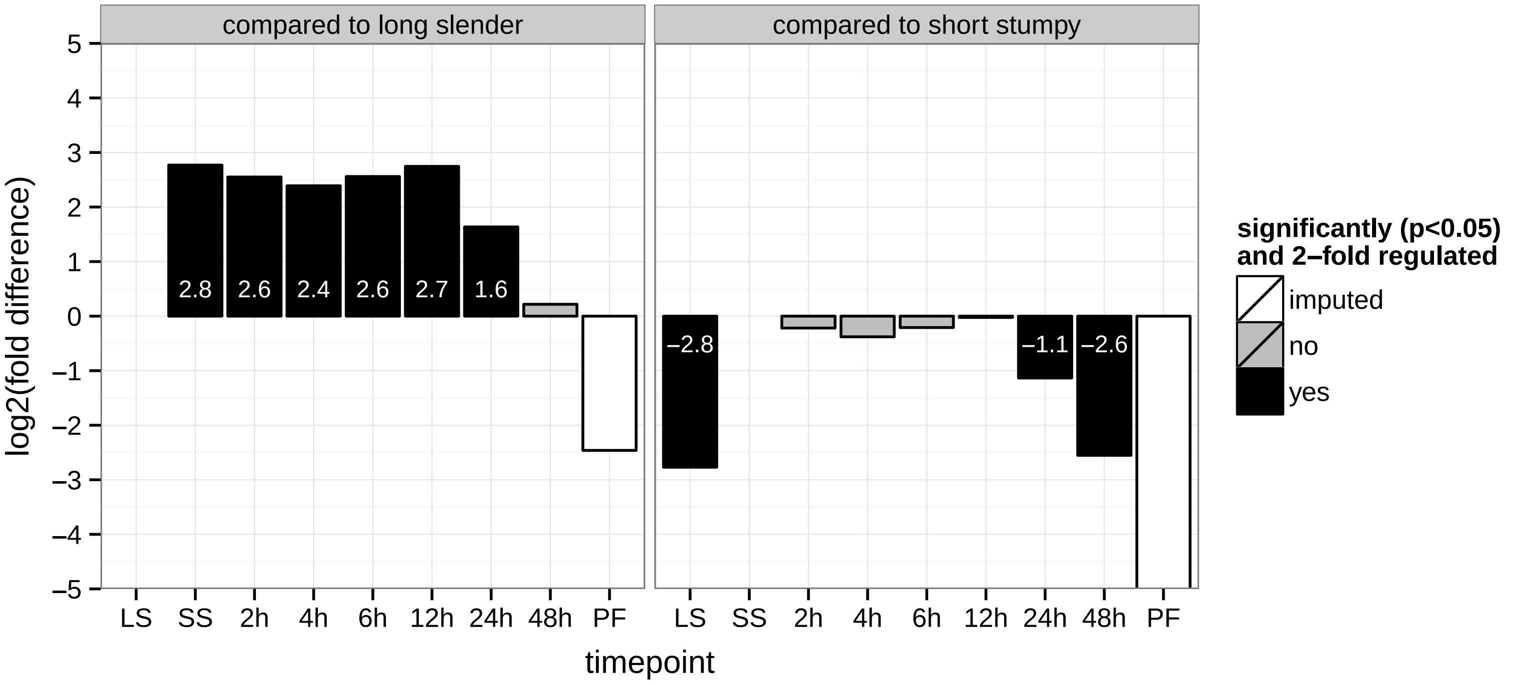
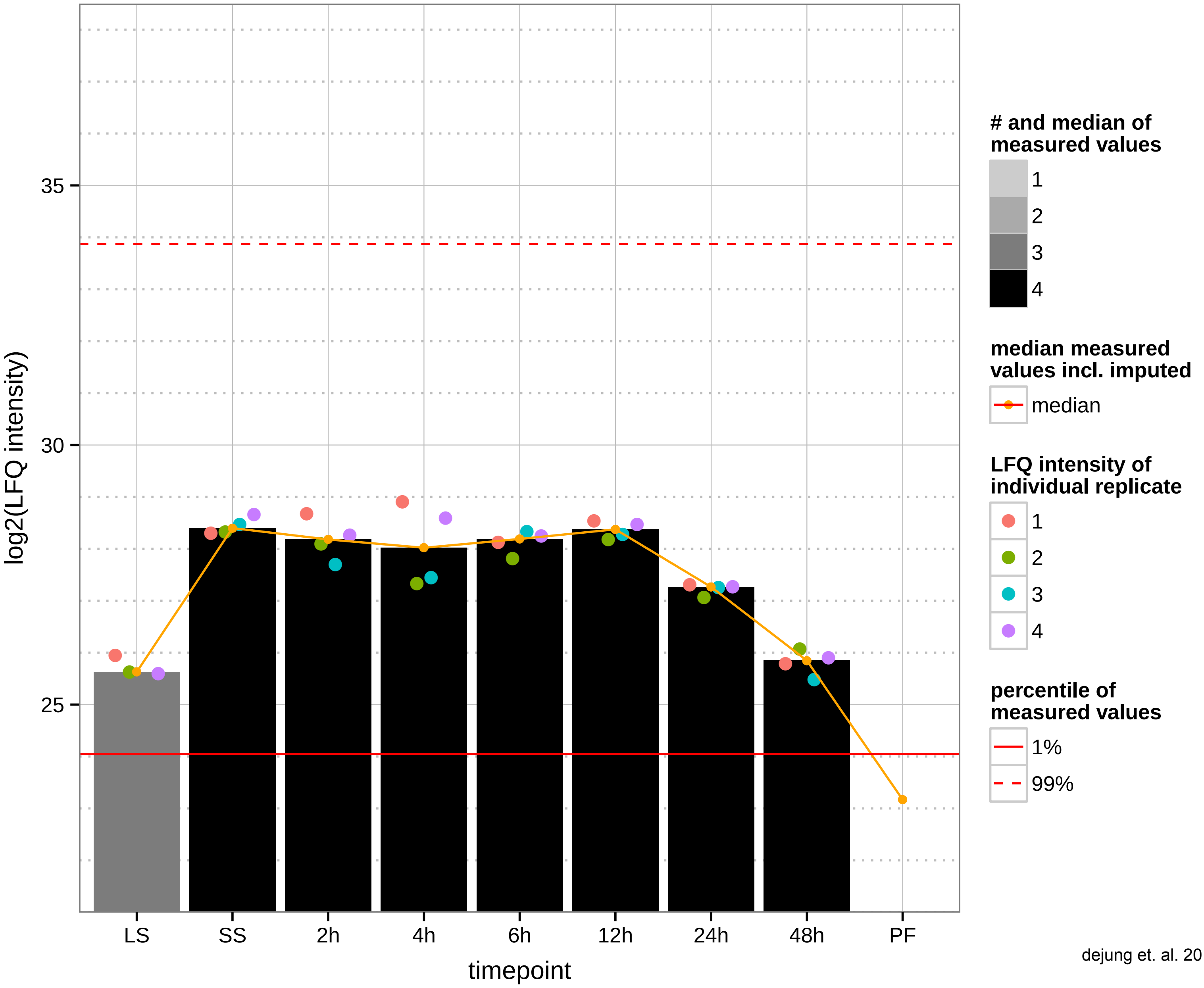
synaptojanin (N−terminal domain), putative
Tb927.7.3490
AGOF: inositol−polyphosphate 5−phosphatase activity
AGOC: null
AGOP: endocytosis
PGOF: phosphoric ester hydrolase activity
PGOC: null
PGOP: null





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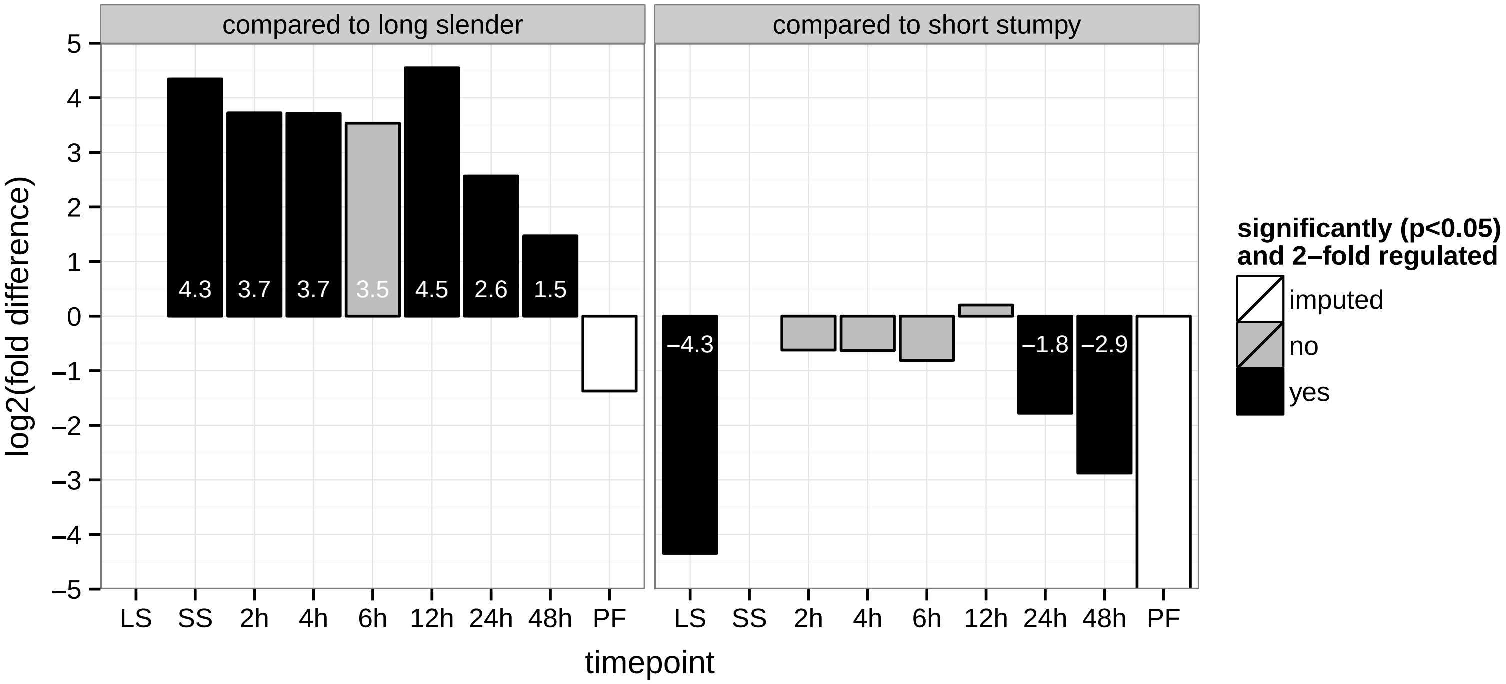
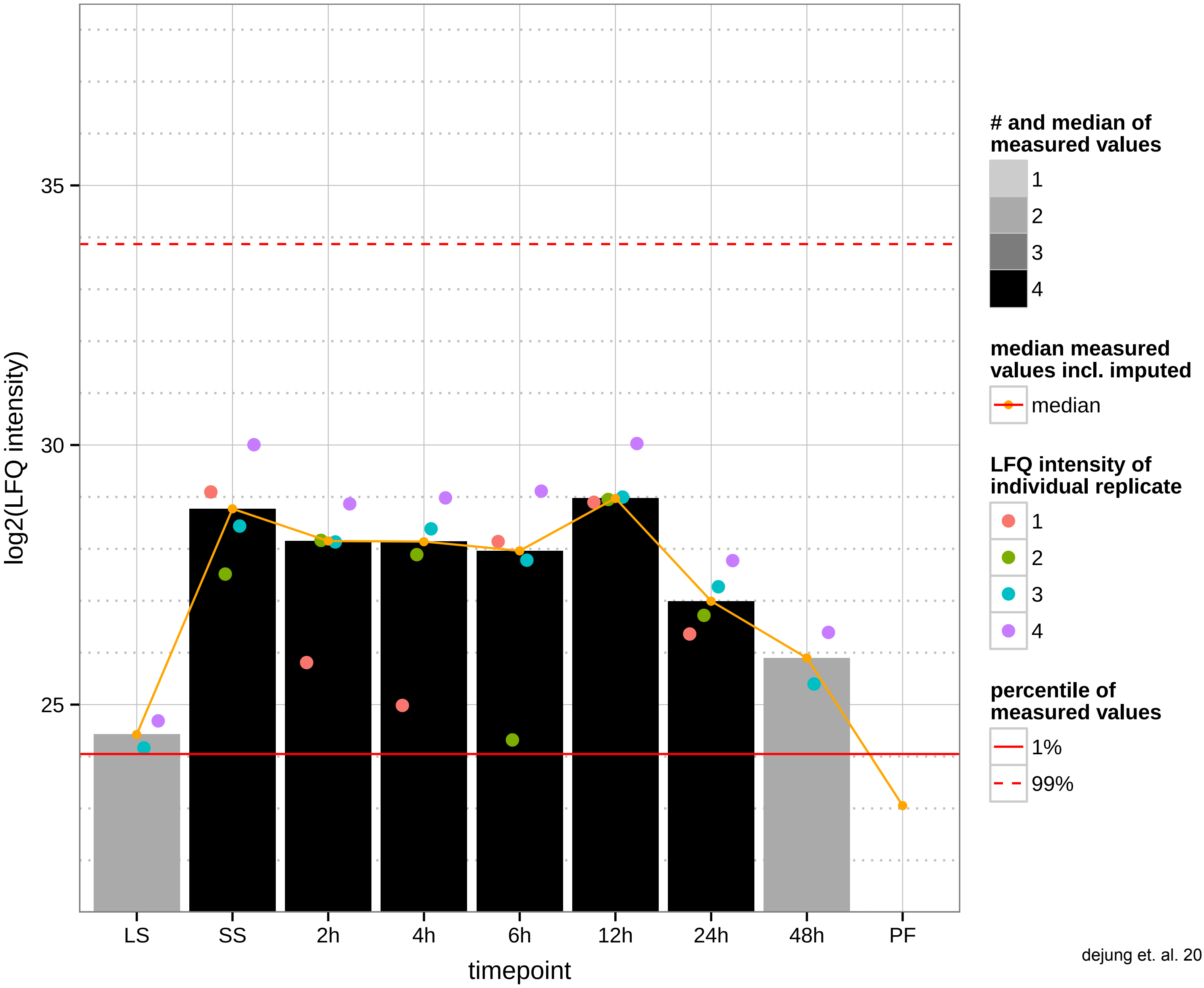
Protein Associated with Differentiation (PAD1)
Tb927.7.5930
AGOF: null
AGOC: cell surface, plasma membrane
AGOP: citrate transport, regulation of developmental process, response to temperature stimulus
PGOF: null
PGOC: integral to membrane
PGOP: transmembrane transport





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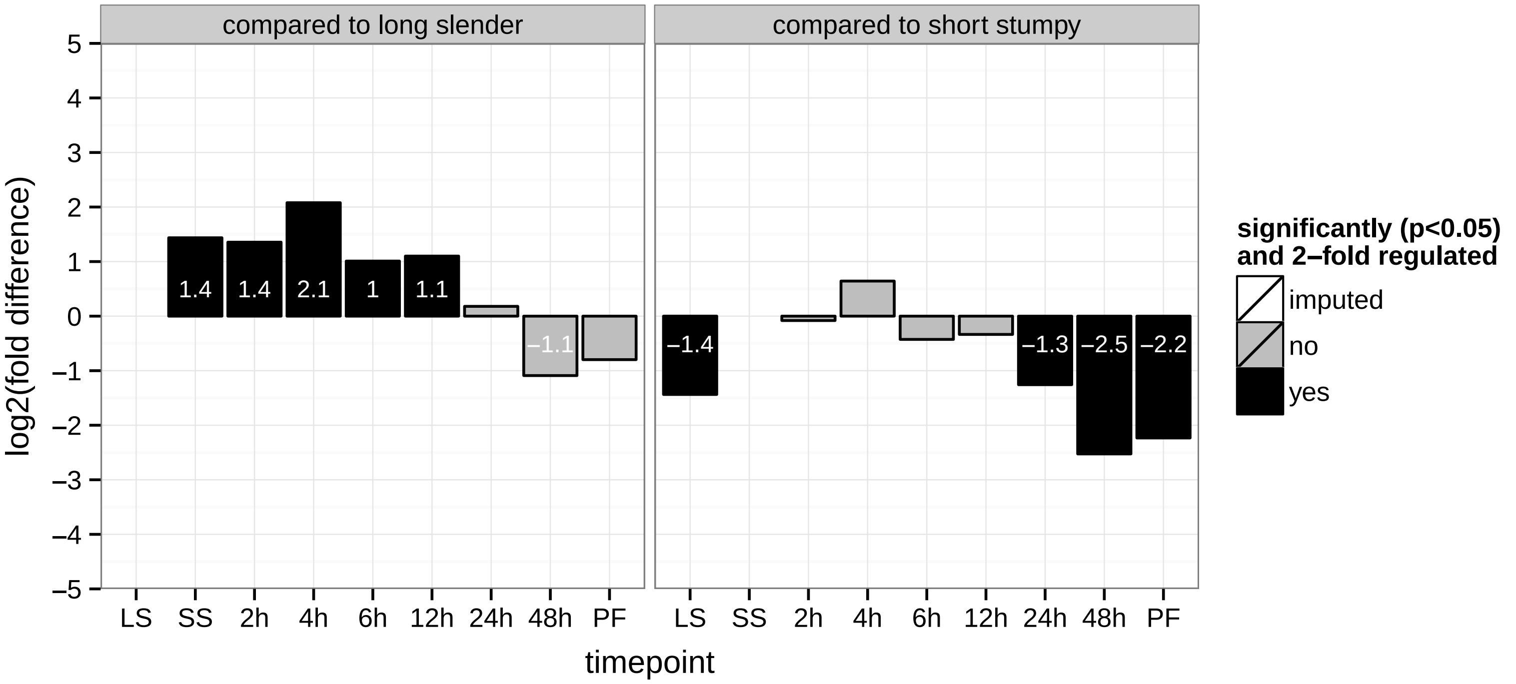
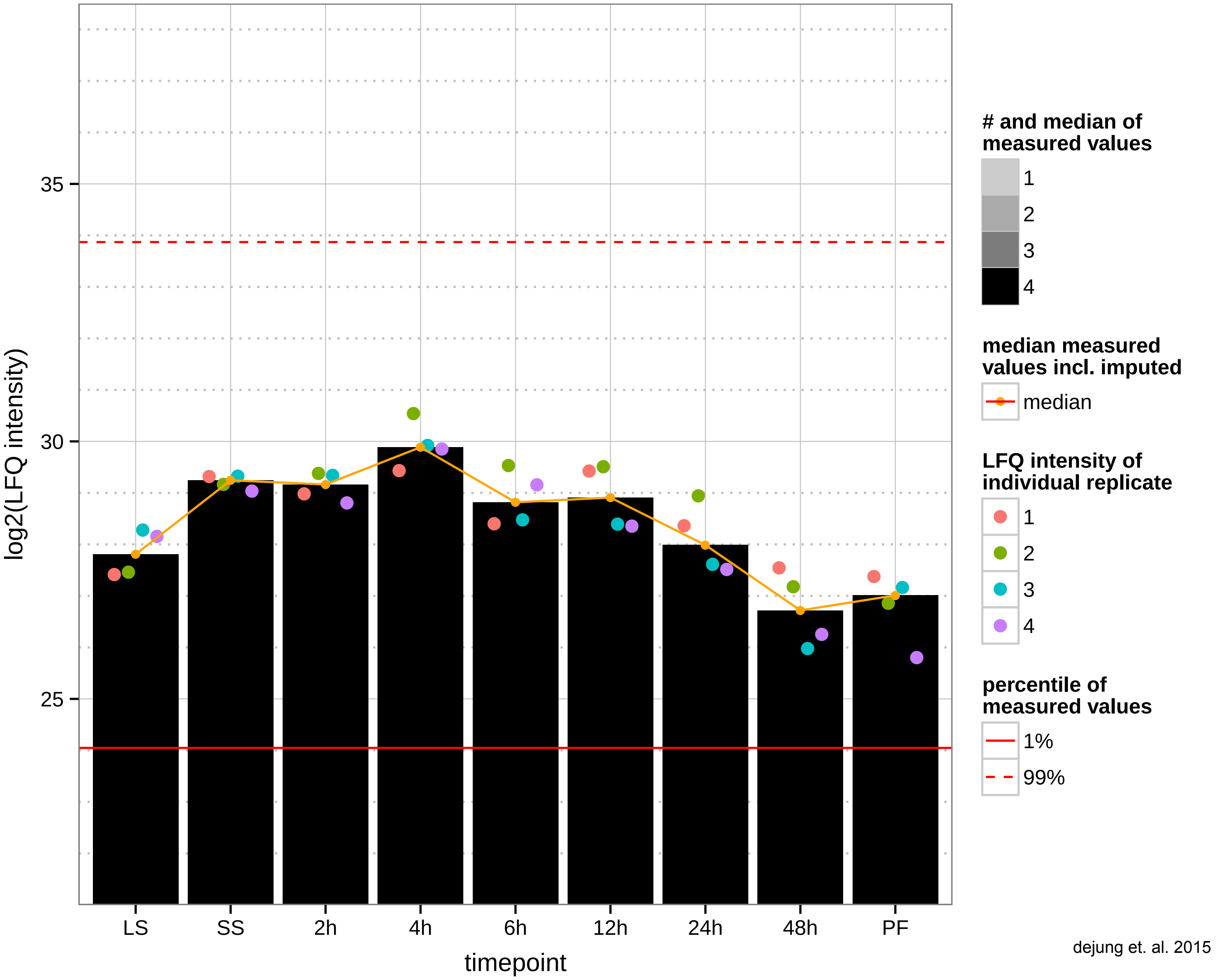
vesicle transport v–SNARE protein, putative
Tb927.7.6440
AGOF: SNAP receptor activity
AGOC: SNARE complex
AGOP: intracellular protein transport
PGOF: null
PGOC: null
PGOP: null





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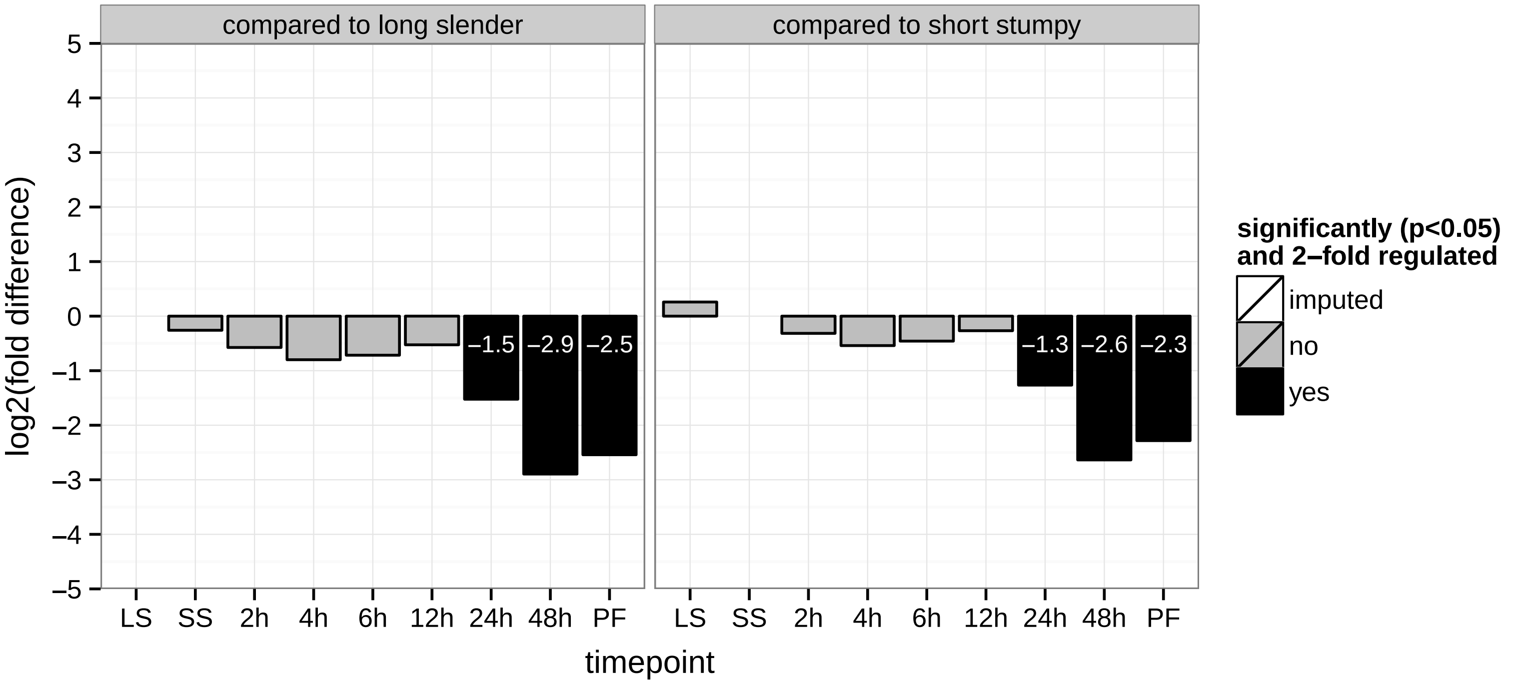
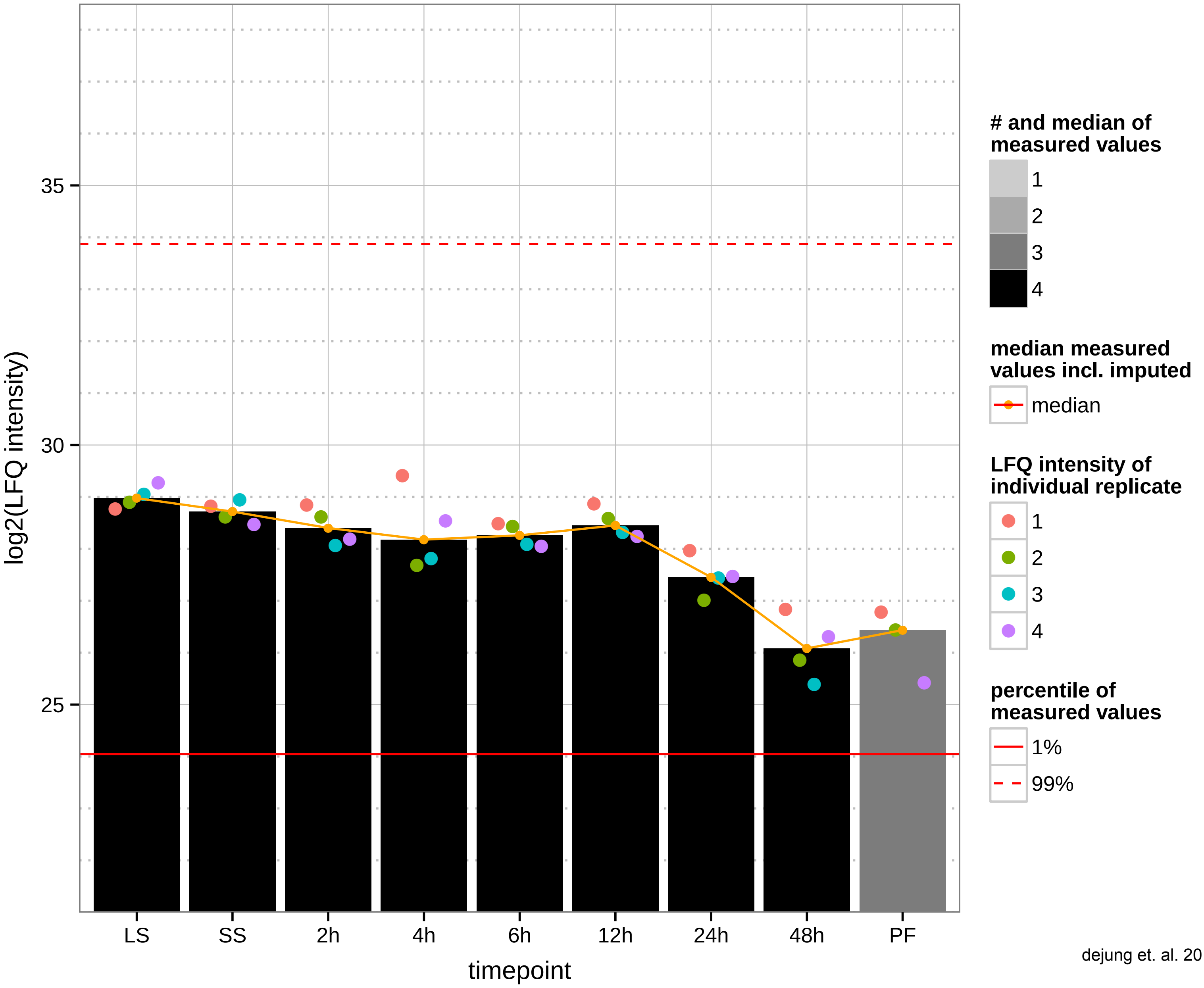
receptor–type adenylate cyclase GRESAG 4, putative
Tb927.7.7530;Tb927.7.7520
AGOF: phosphorus–oxygen lyase activity, adenylate cyclase activity
AGOC: integral to membrane
AGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction
PGOF: phosphorus–oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction





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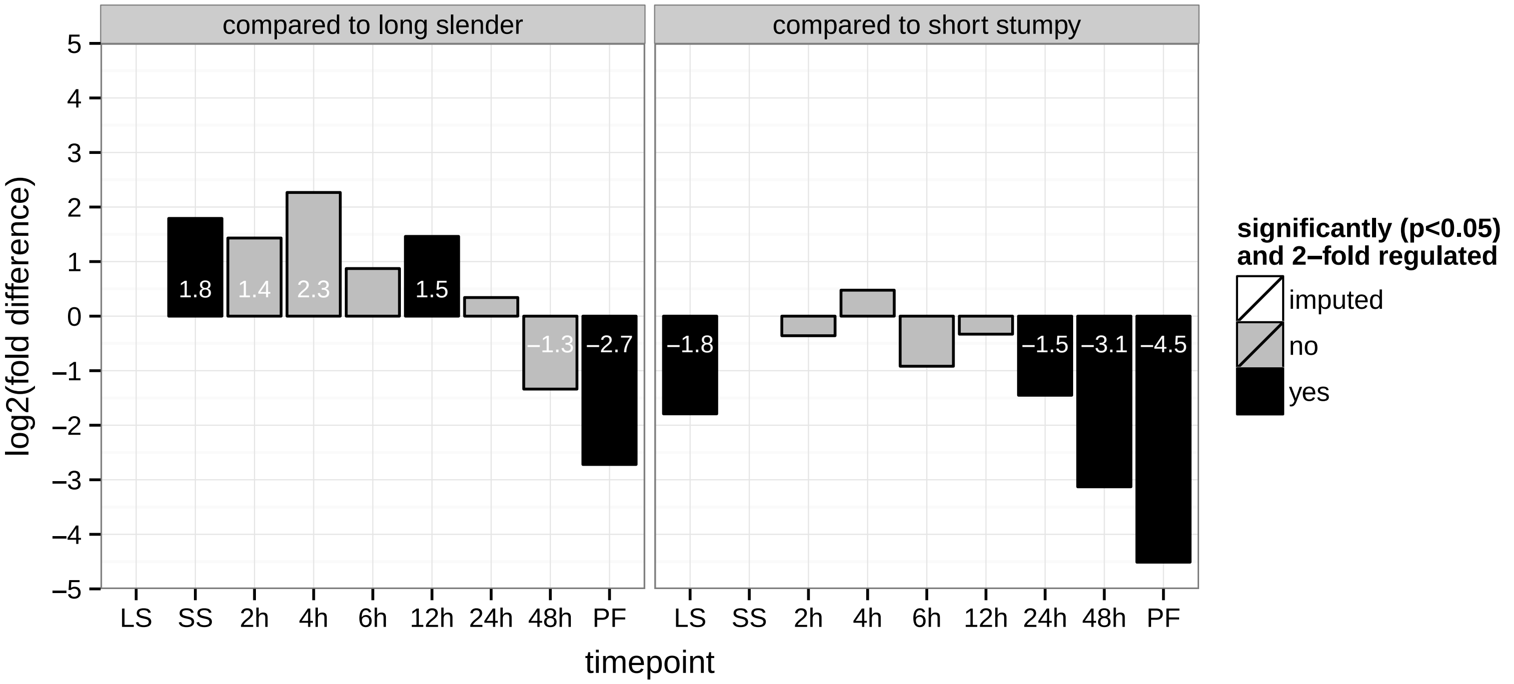
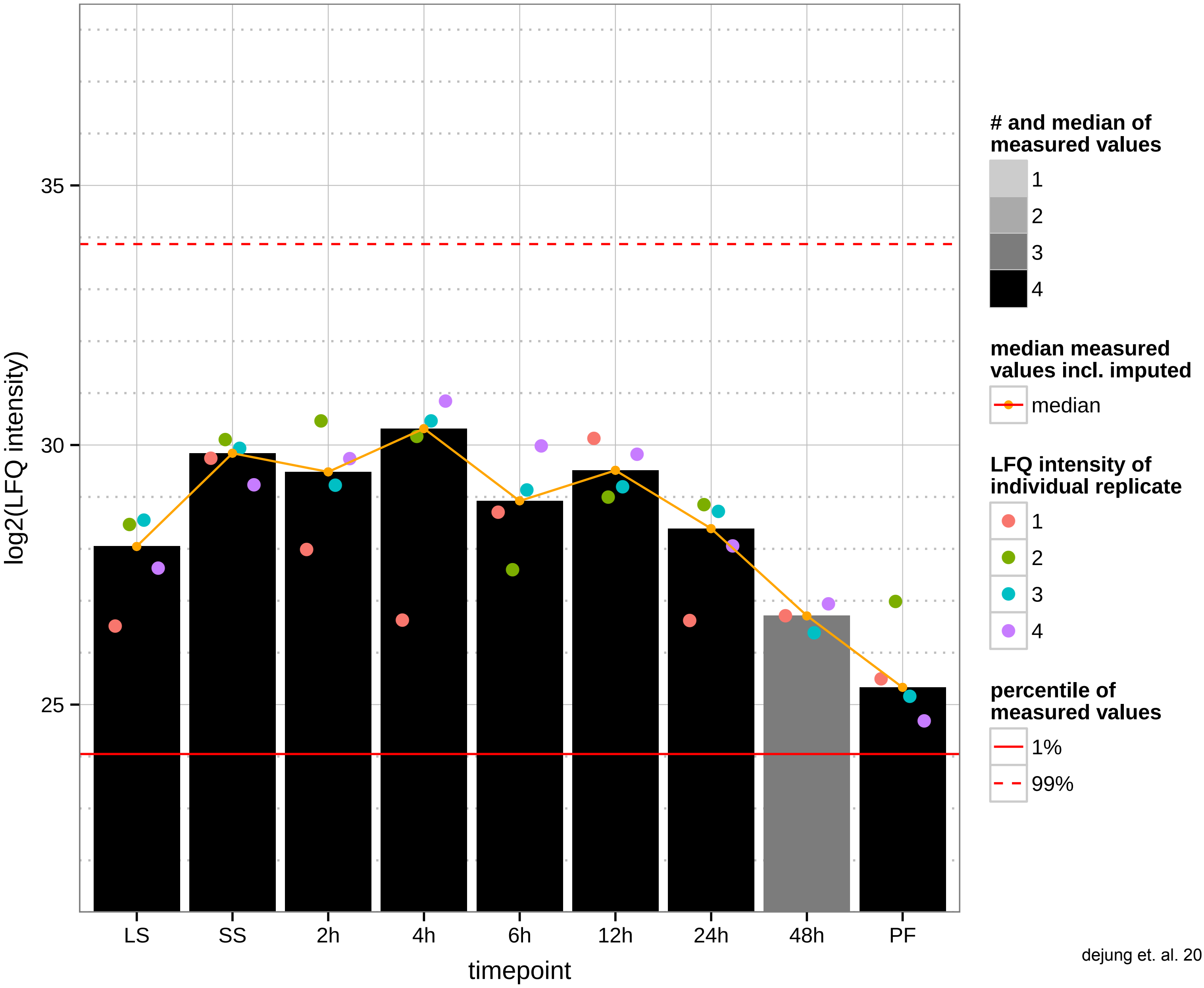
hypothetical protein, conserved
Tb927.8.2070;Tb927.8.2270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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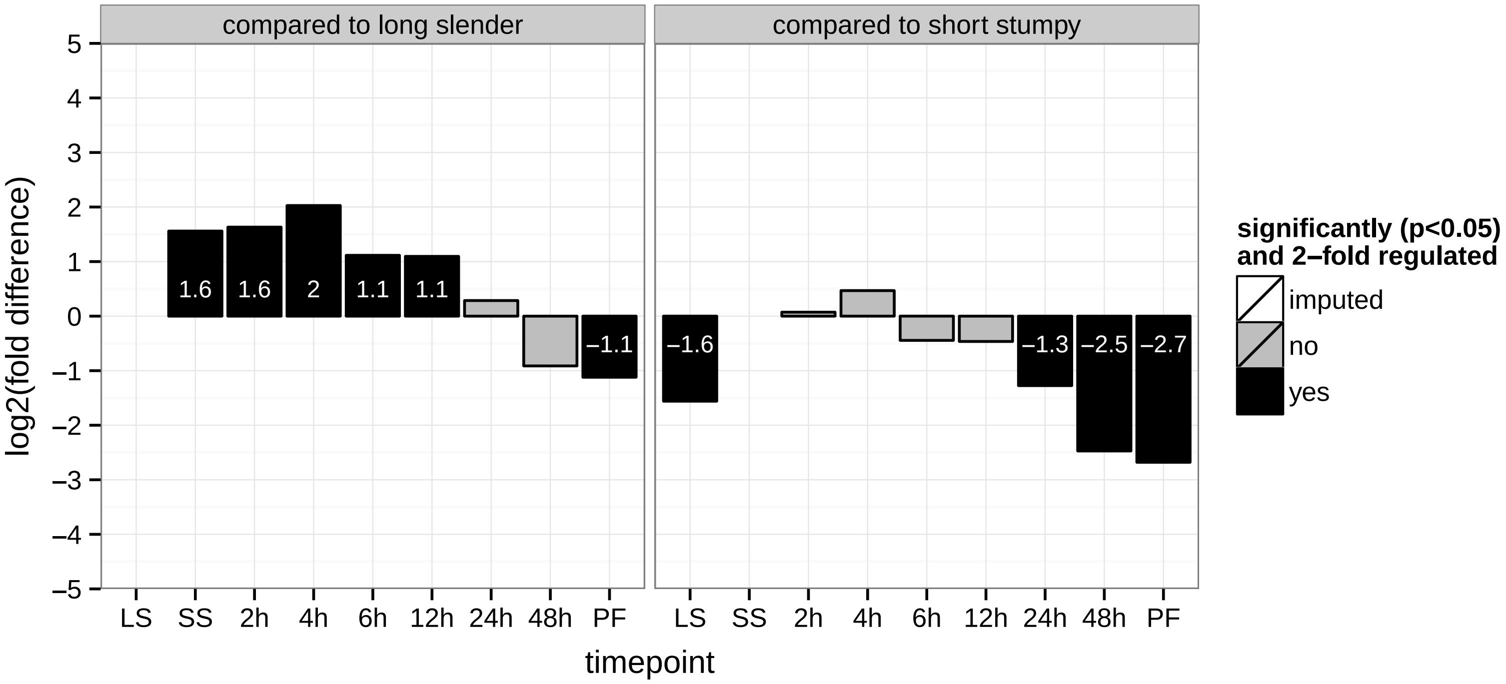
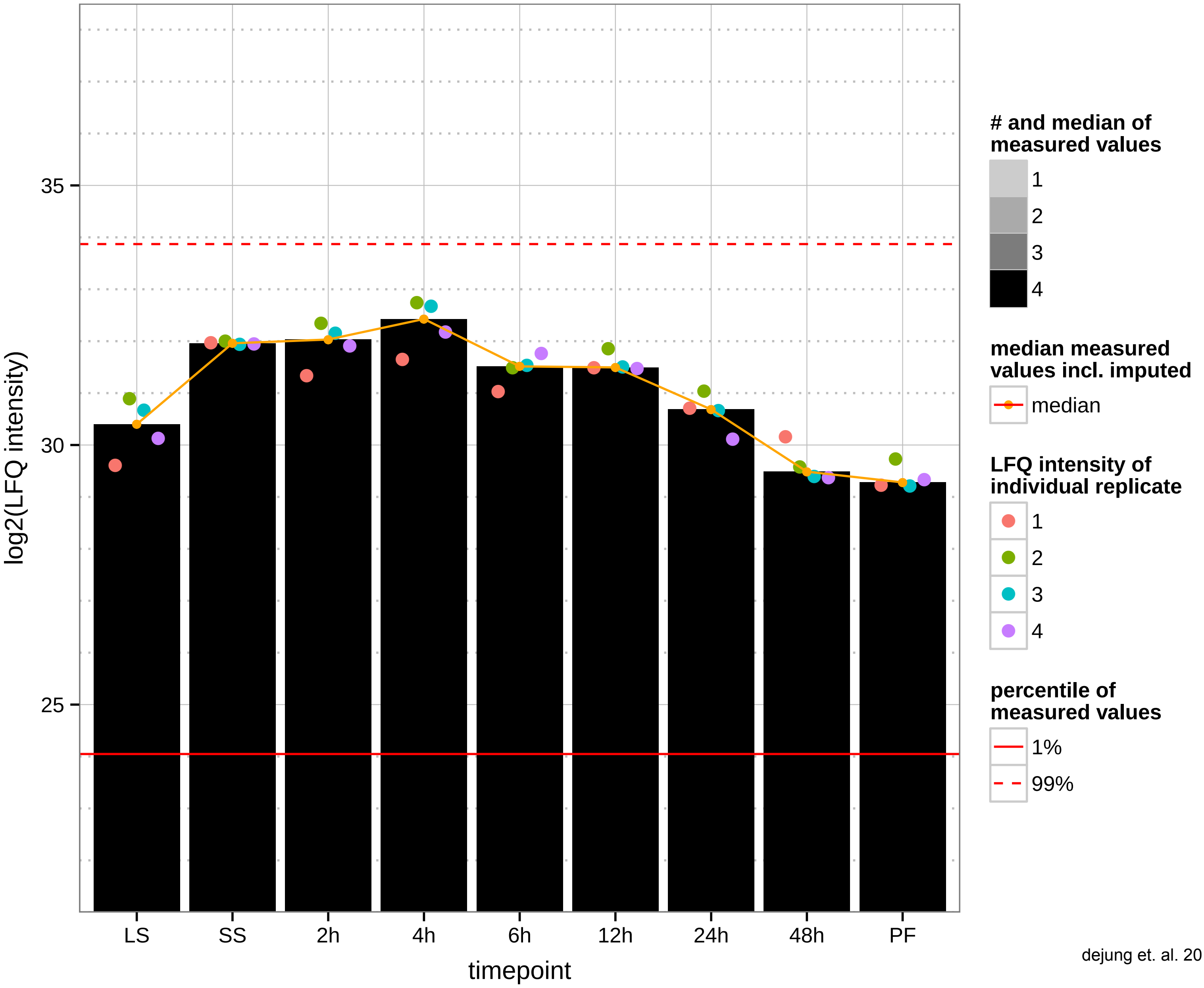
hypothetical protein, conserved
Tb927.8.2280;Tb927.8.2260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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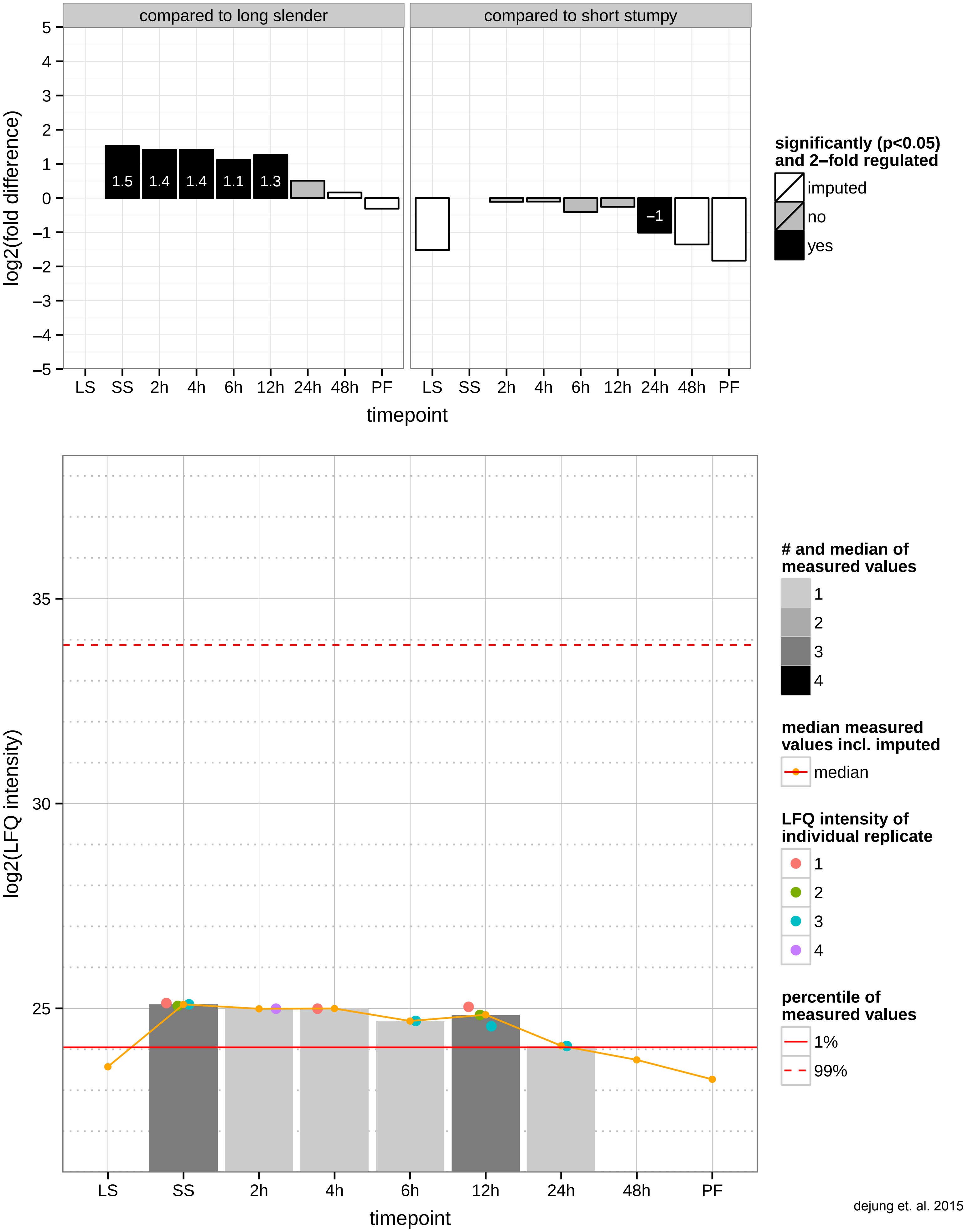
hypothetical protein, conserved
Tb927.8.2720
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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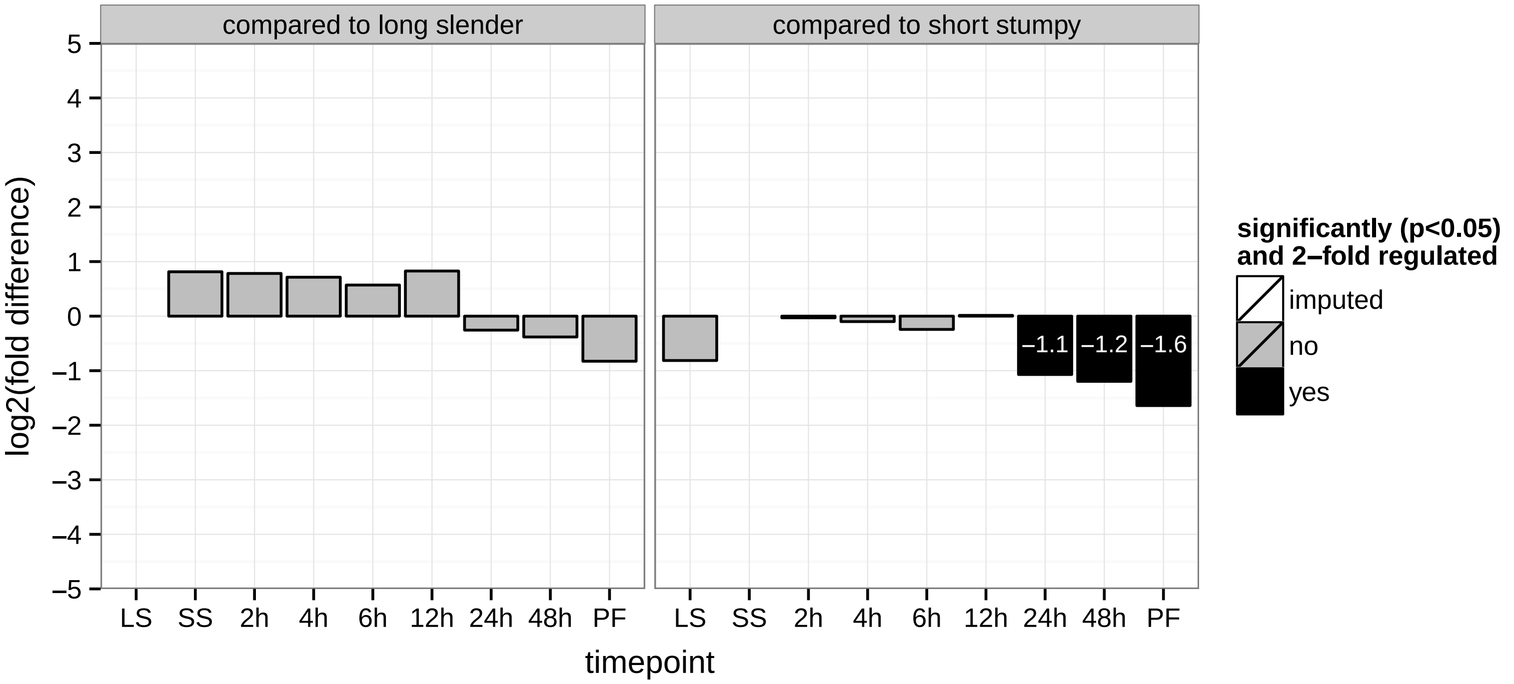
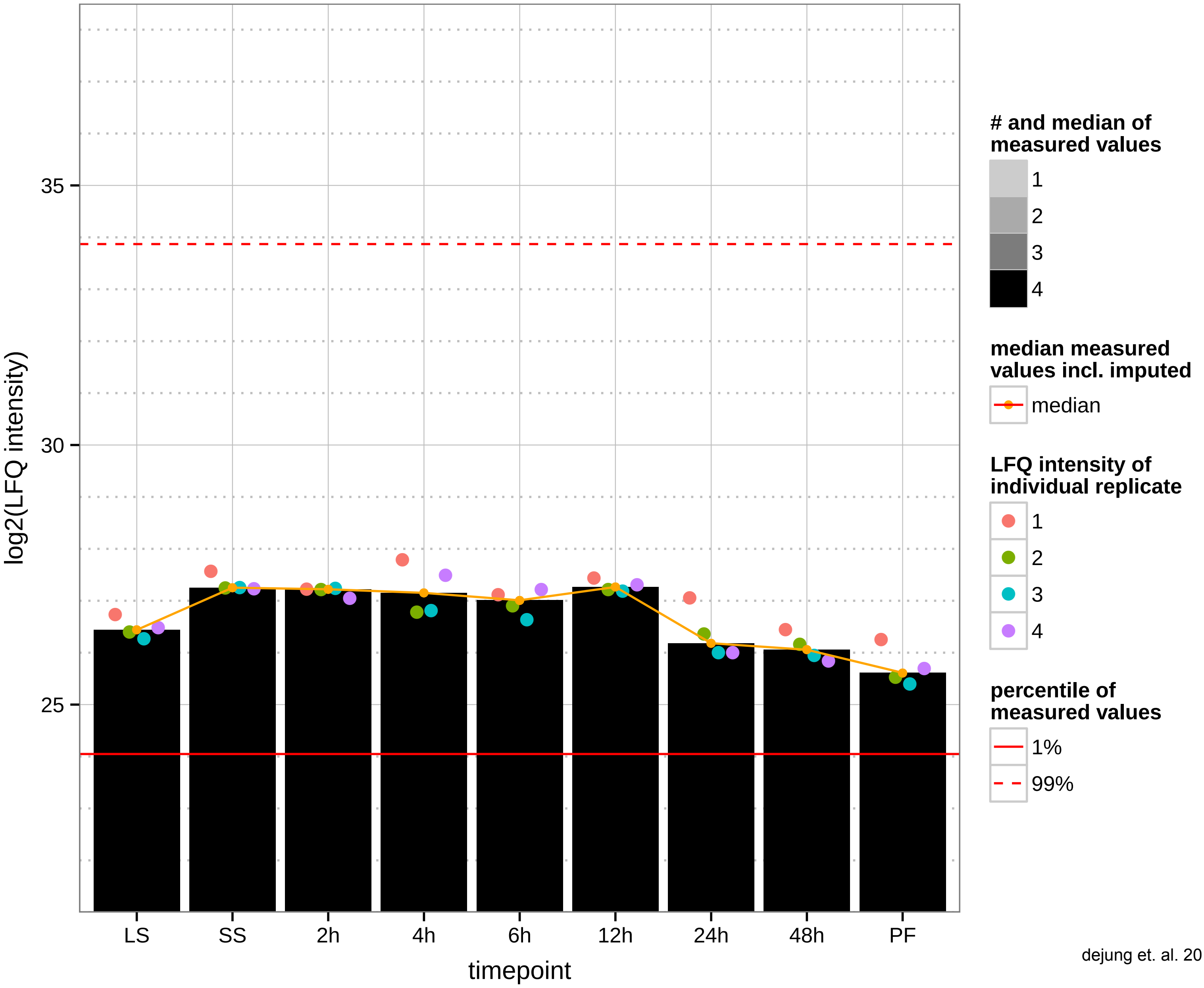
hypothetical protein, conserved
Tb927.8.2860
AGOF: null
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, quorum sensing involved in interaction with h
PGOF: null
PGOC: null
PGOP: null





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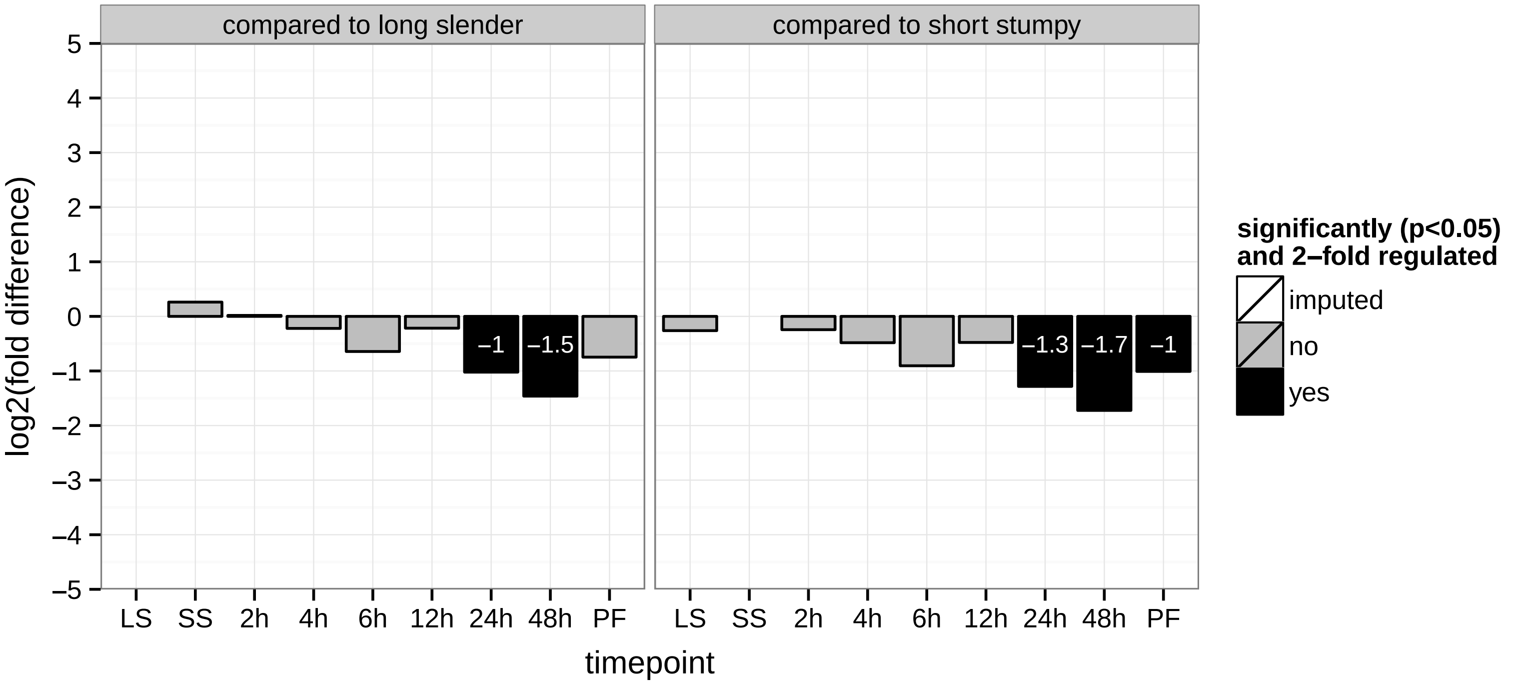
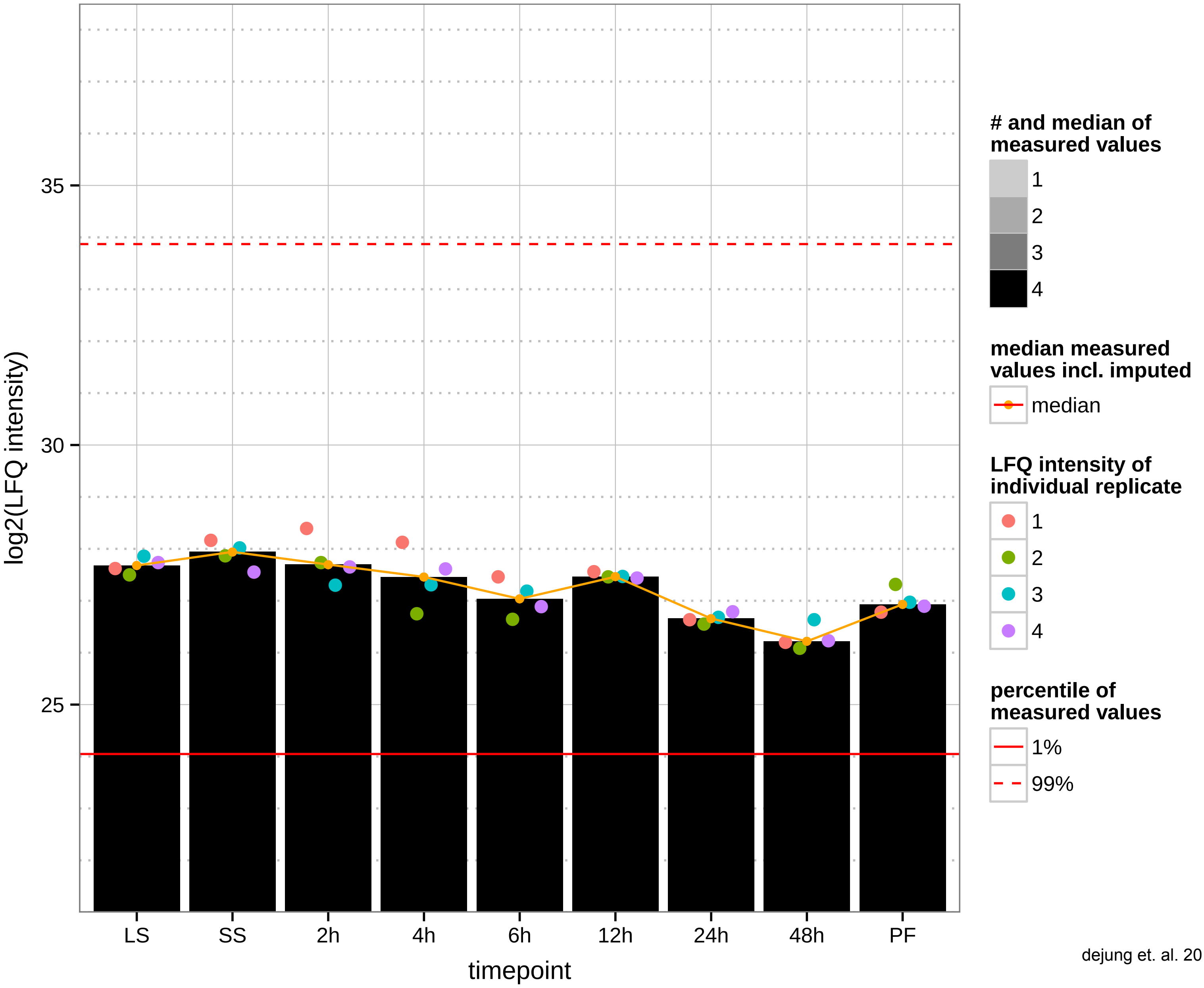
mitogen–activated protein kinase 3, putative
Tb927.8.3550
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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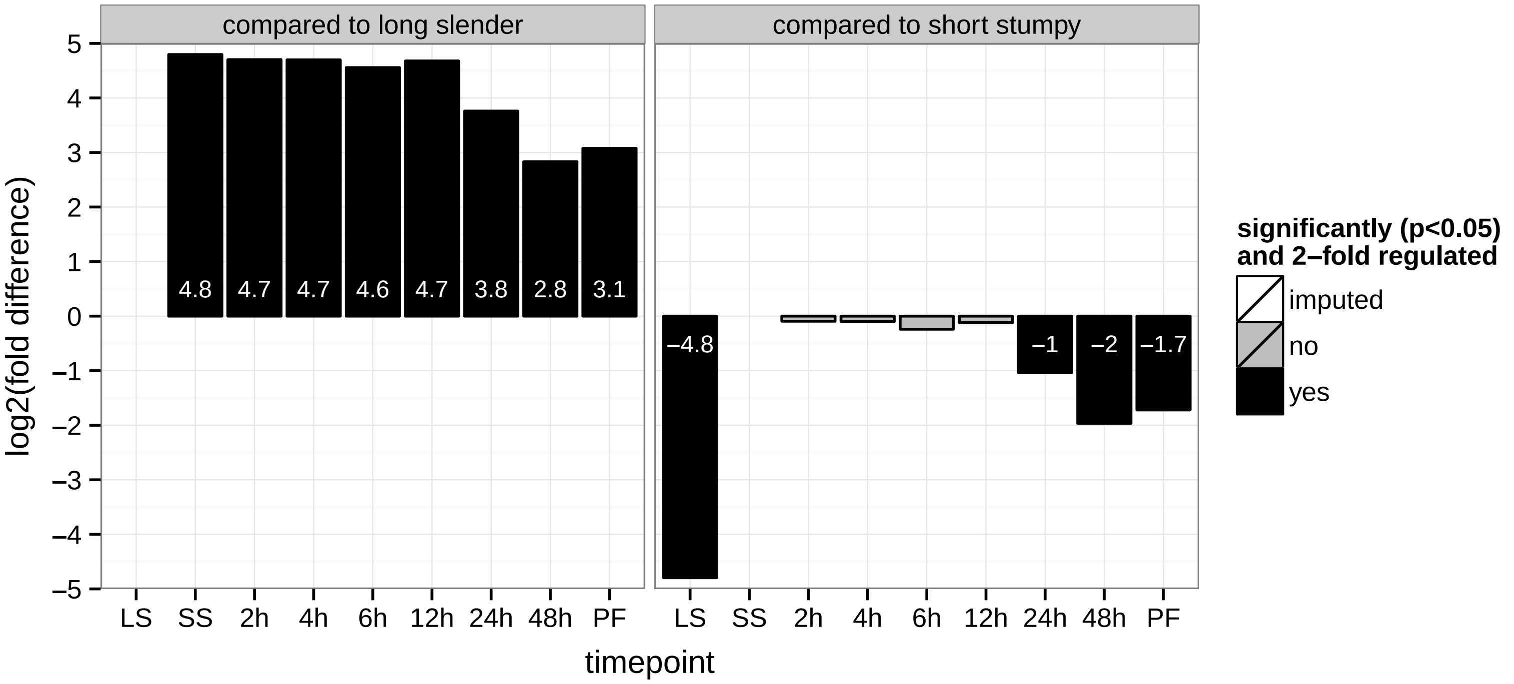
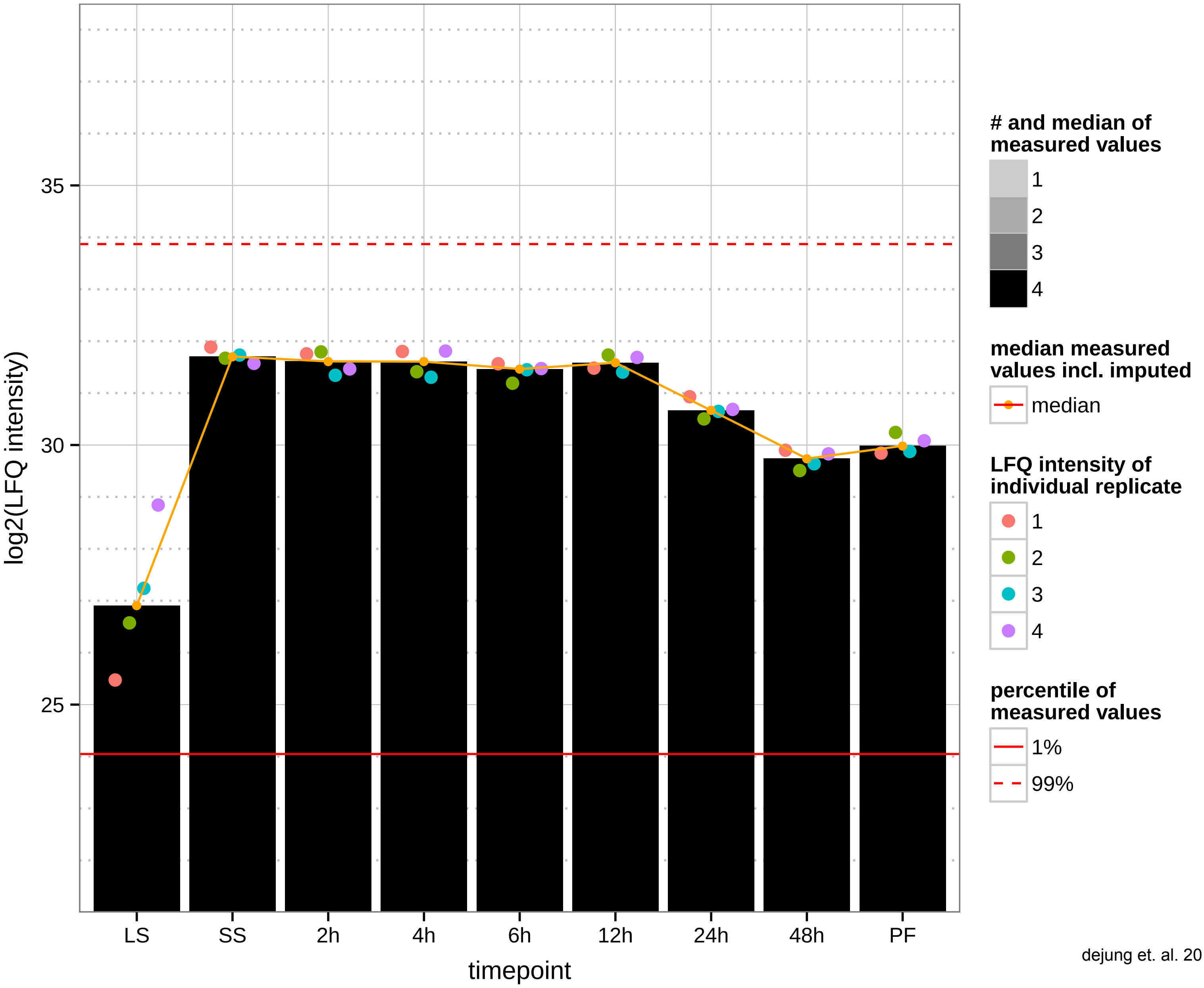
mitogen–activated protein kinase, putative (MPK10)
Tb927.8.3770
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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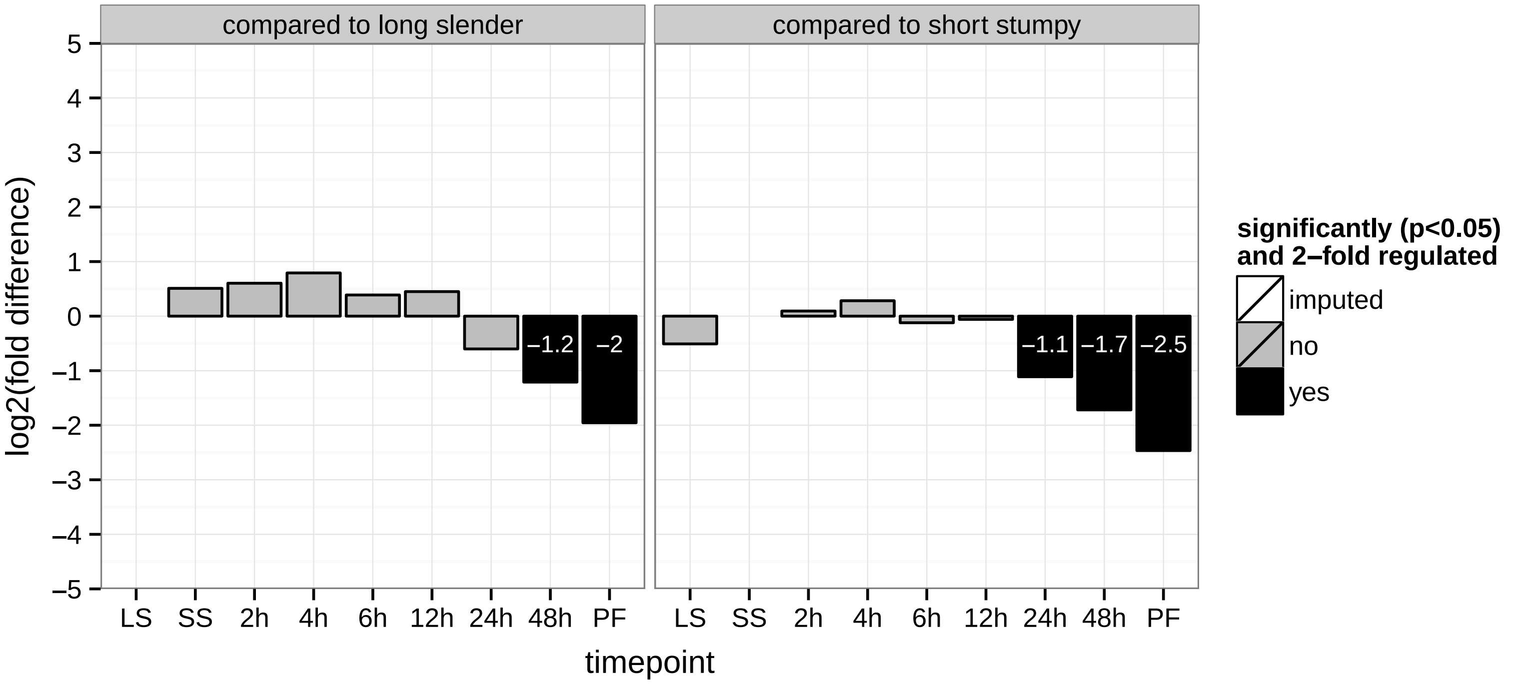
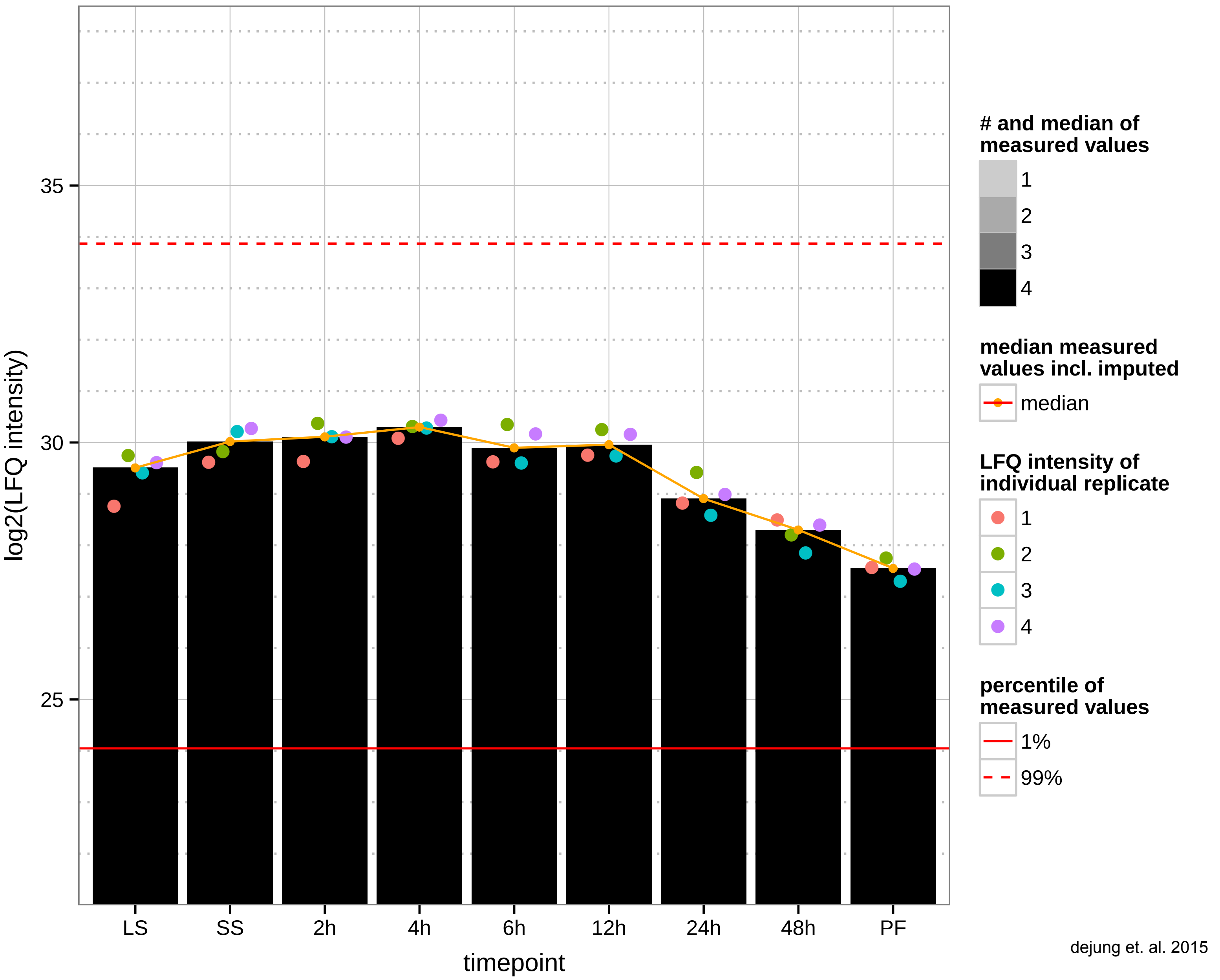
endoplasmic reticulum oxidoreductin, putative, pol–associated gene 1
Tb927.8.4890
AGOF: disulfide oxidoreductase activity, electron carrier activity, flavin adenine dinucleotide binding, oxidoreductase activity, a
AGOC: endoplasmic reticulum membrane, integral to membrane
AGOP: oxidation–reduction process, protein thiol–disulfide exchange
PGOF: flavin adenine dinucleotide binding, oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor
PGOC: endoplasmic reticulum membrane
PGOP: oxidation–reduction process, protein thiol–disulfide exchange





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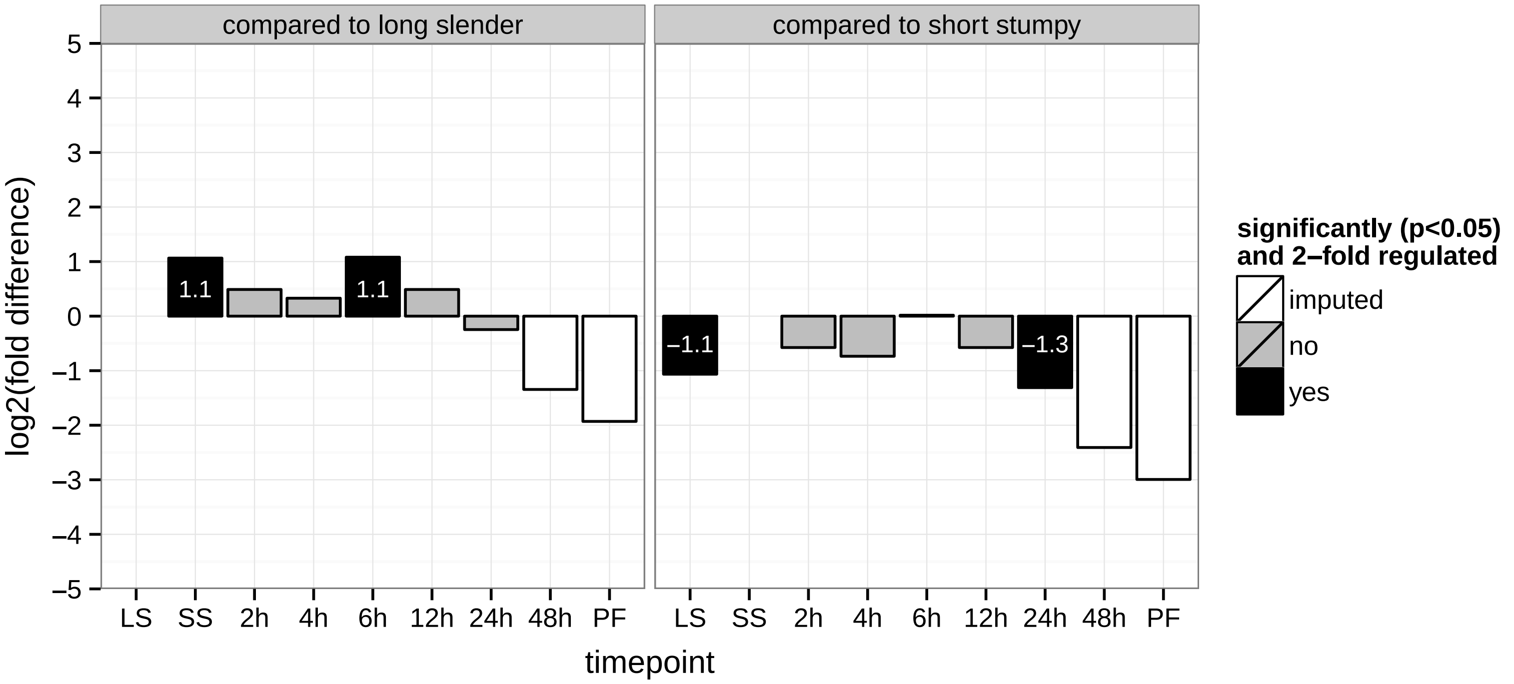
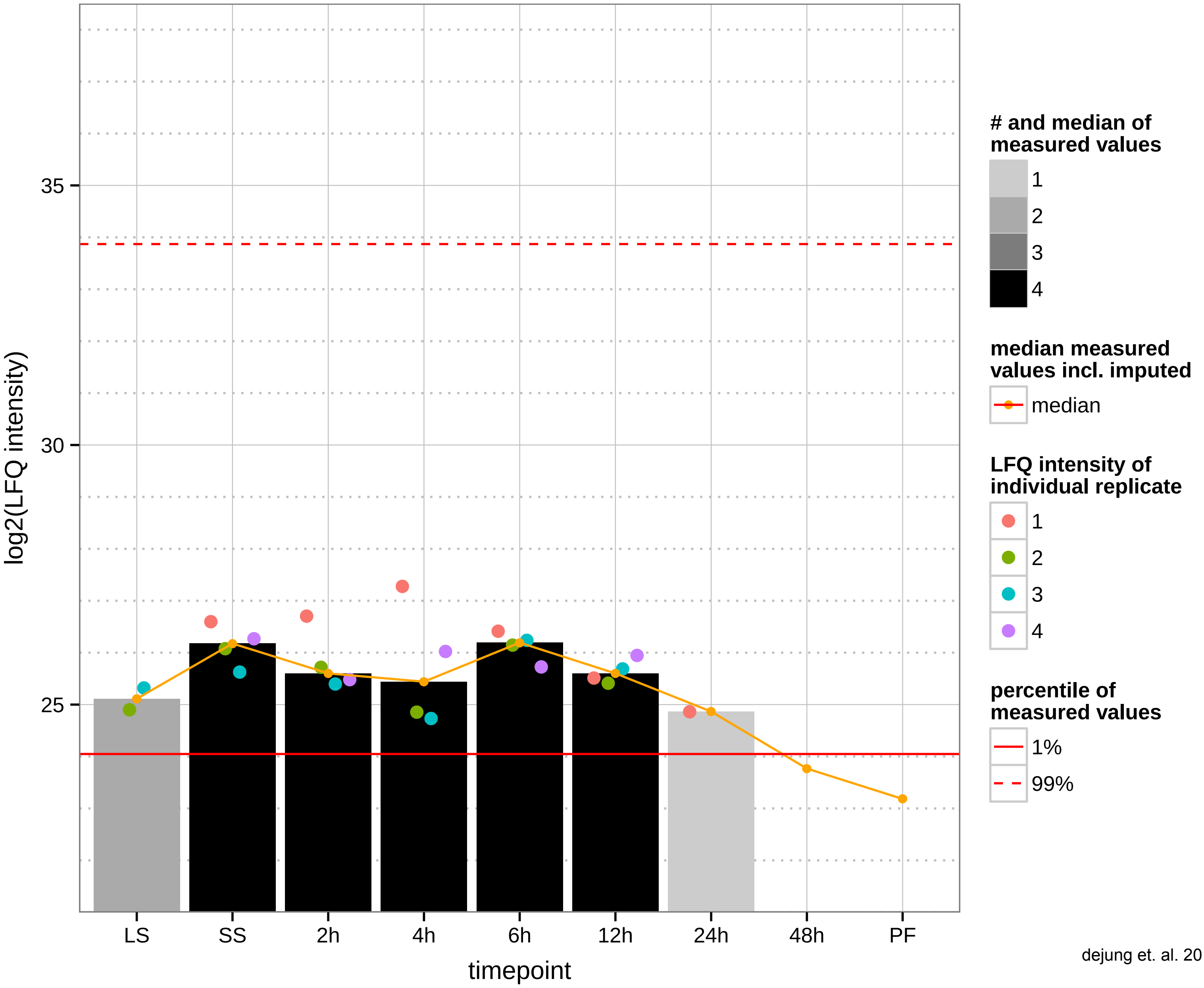
hypothetical protein, conserved
Tb927.8.5050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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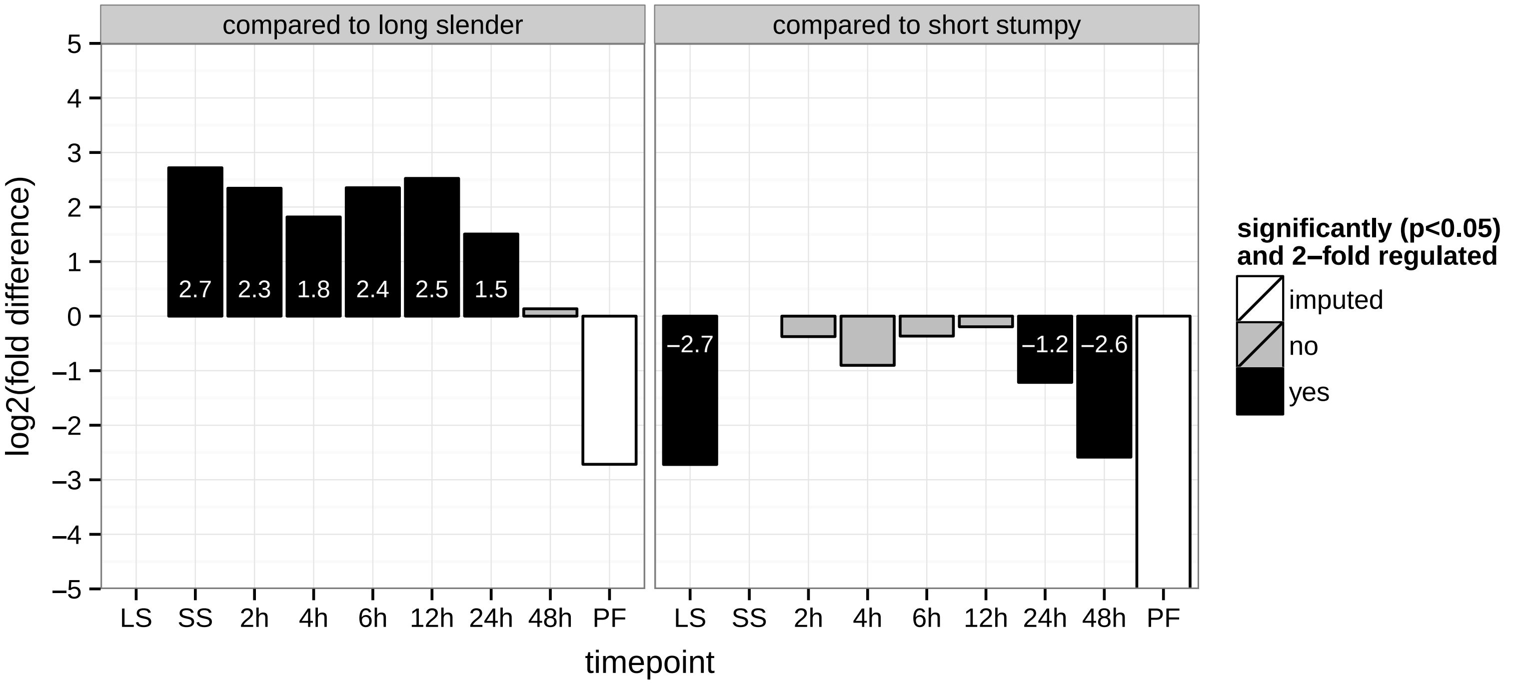
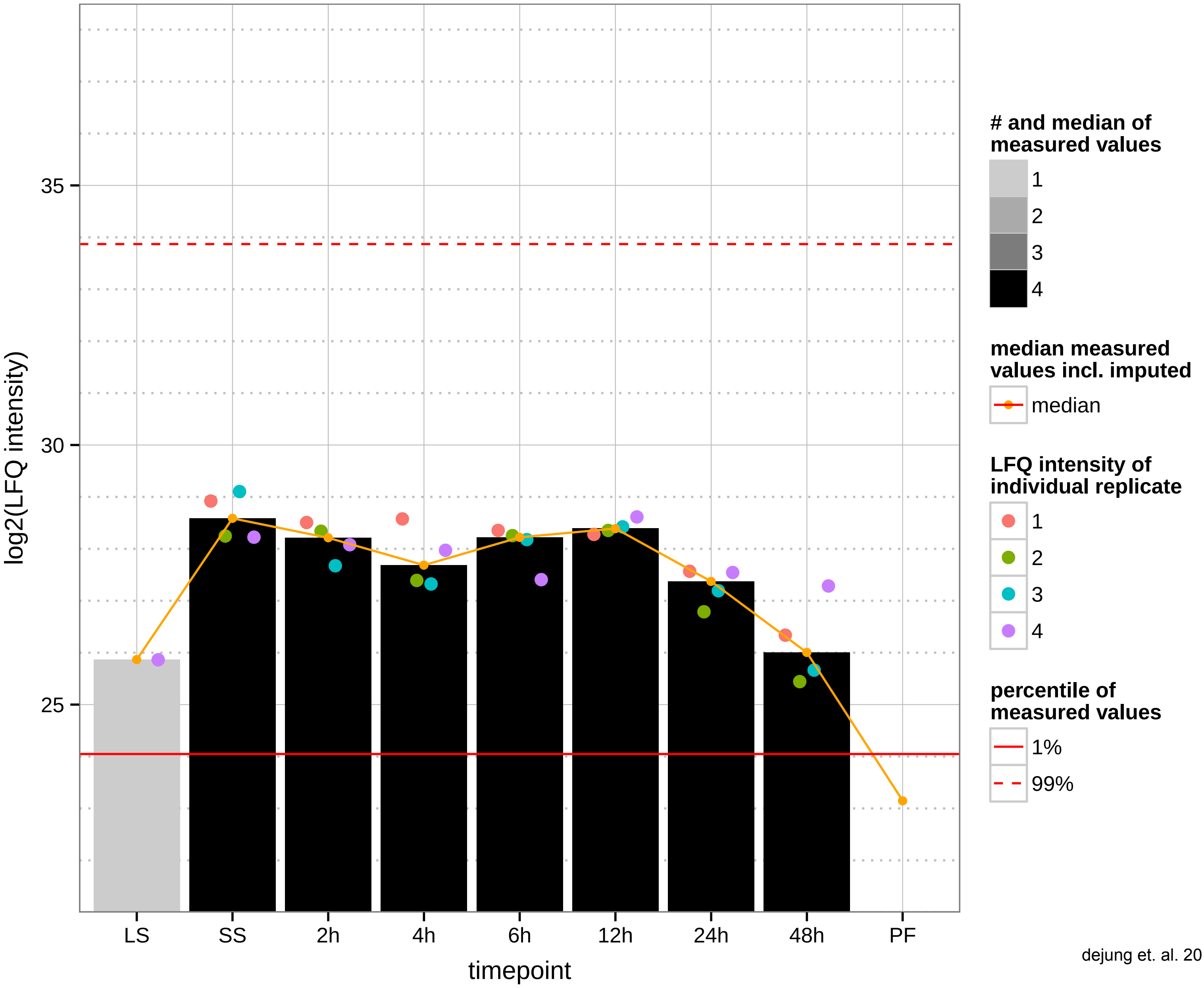
hypothetical protein, conserved
Tb927.8.5080
AGOF: carbon−nitrogen ligase activity, with glutamine as amido−N−donor
AGOC: null
AGOP: null
PGOF: carbon−nitrogen ligase activity, with glutamine as amido−N−donor
PGOC: null
PGOP: null





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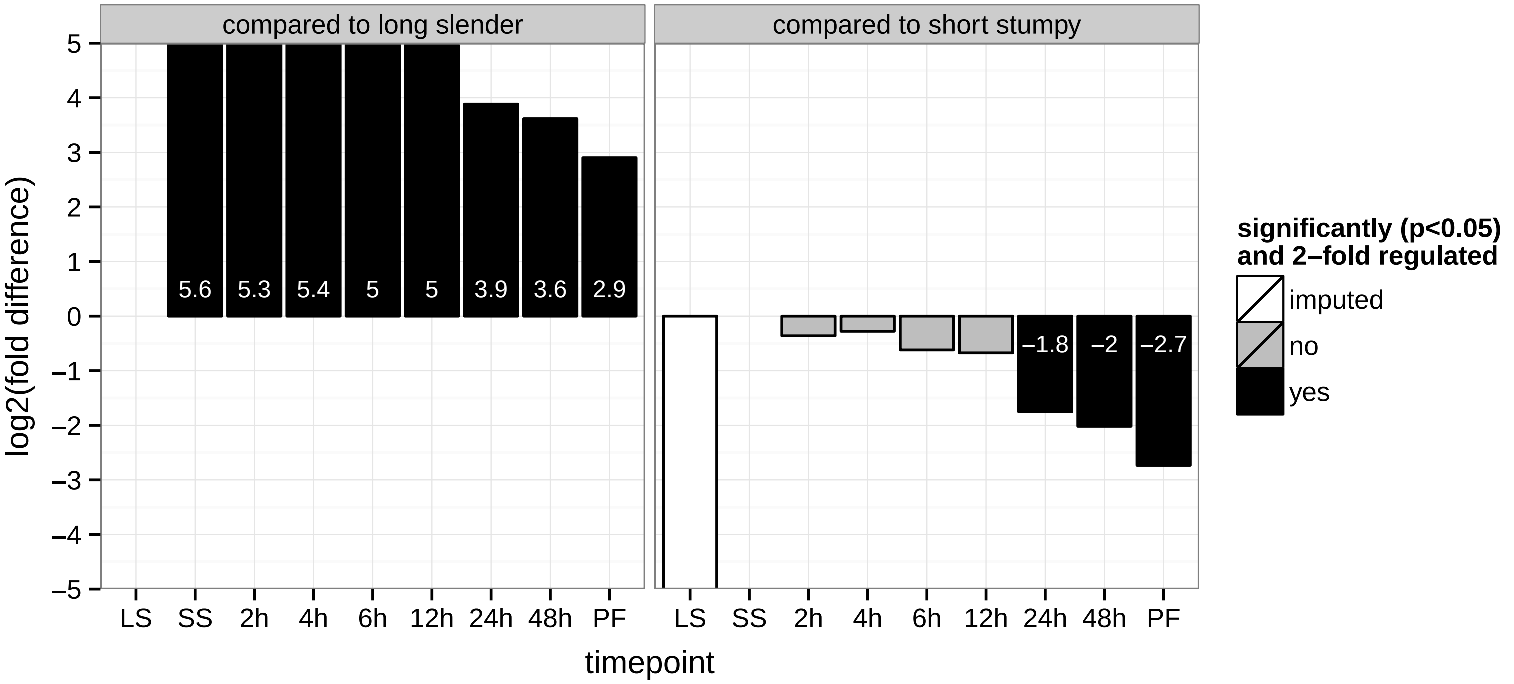
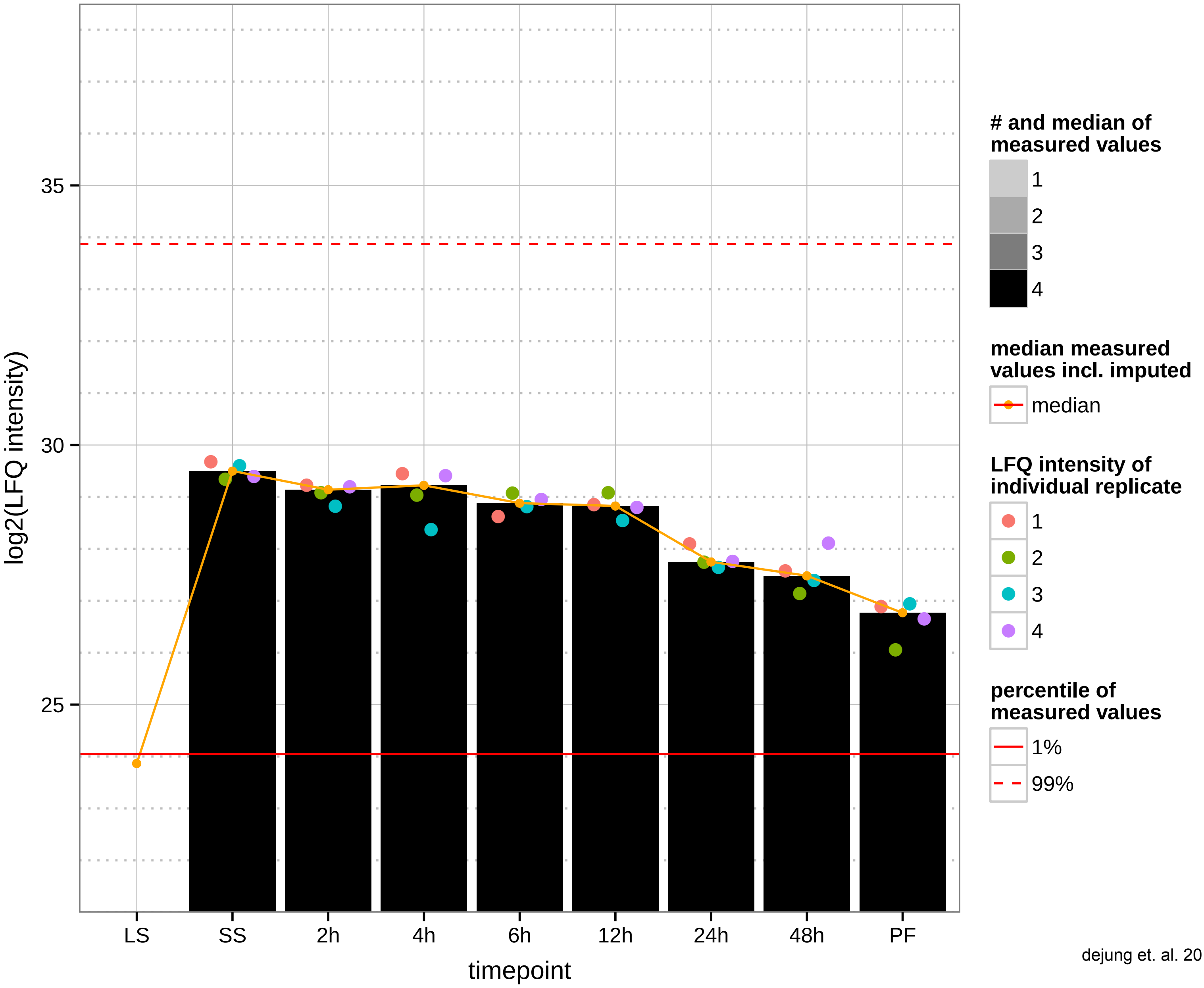
serine/threonine–protein kinase NrkA (NRKB)
Tb927.8.6930
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, phospholipid binding, protein binding, protein kinase activity, transferase activity, transferring phosphorus
PGOC: null
PGOP: protein phosphorylation





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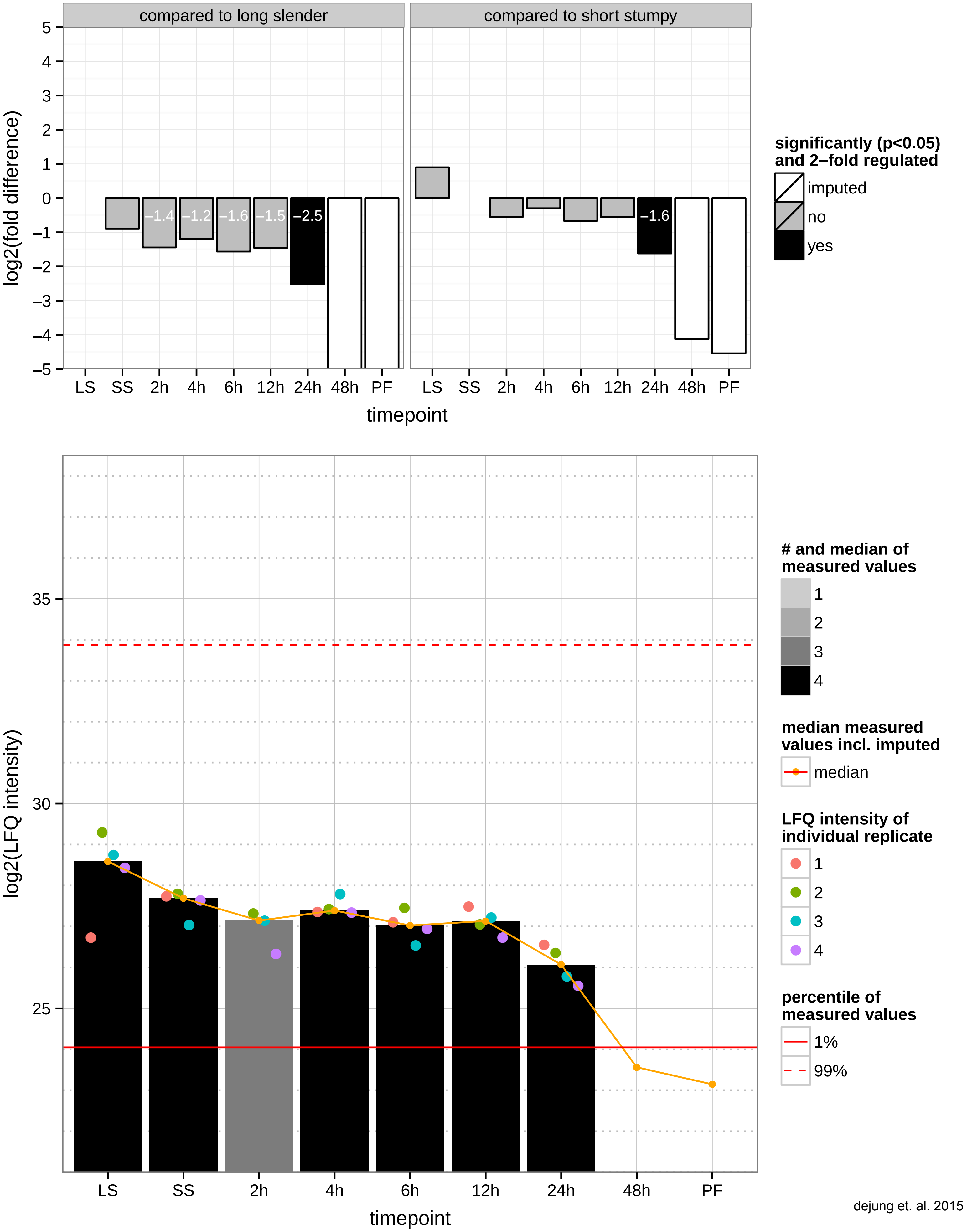
hypothetical protein
Tb927.8.7970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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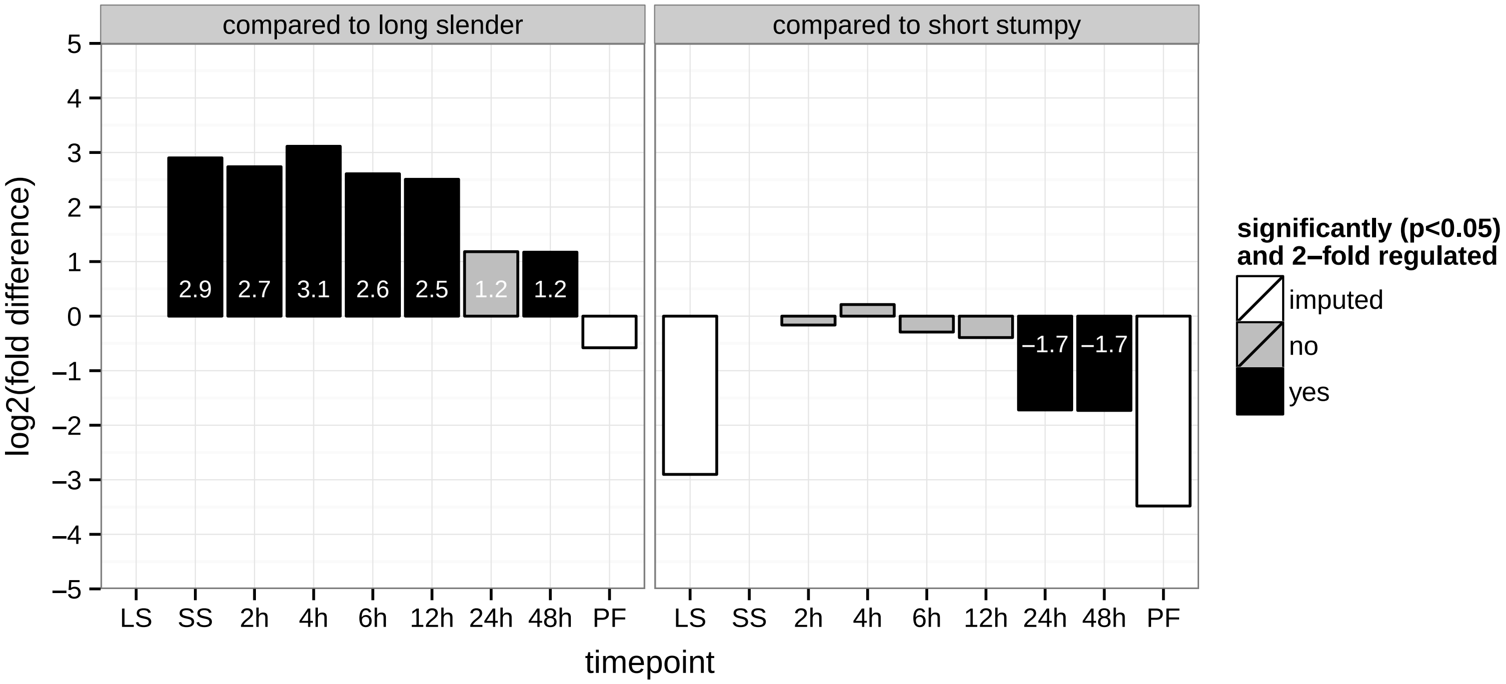
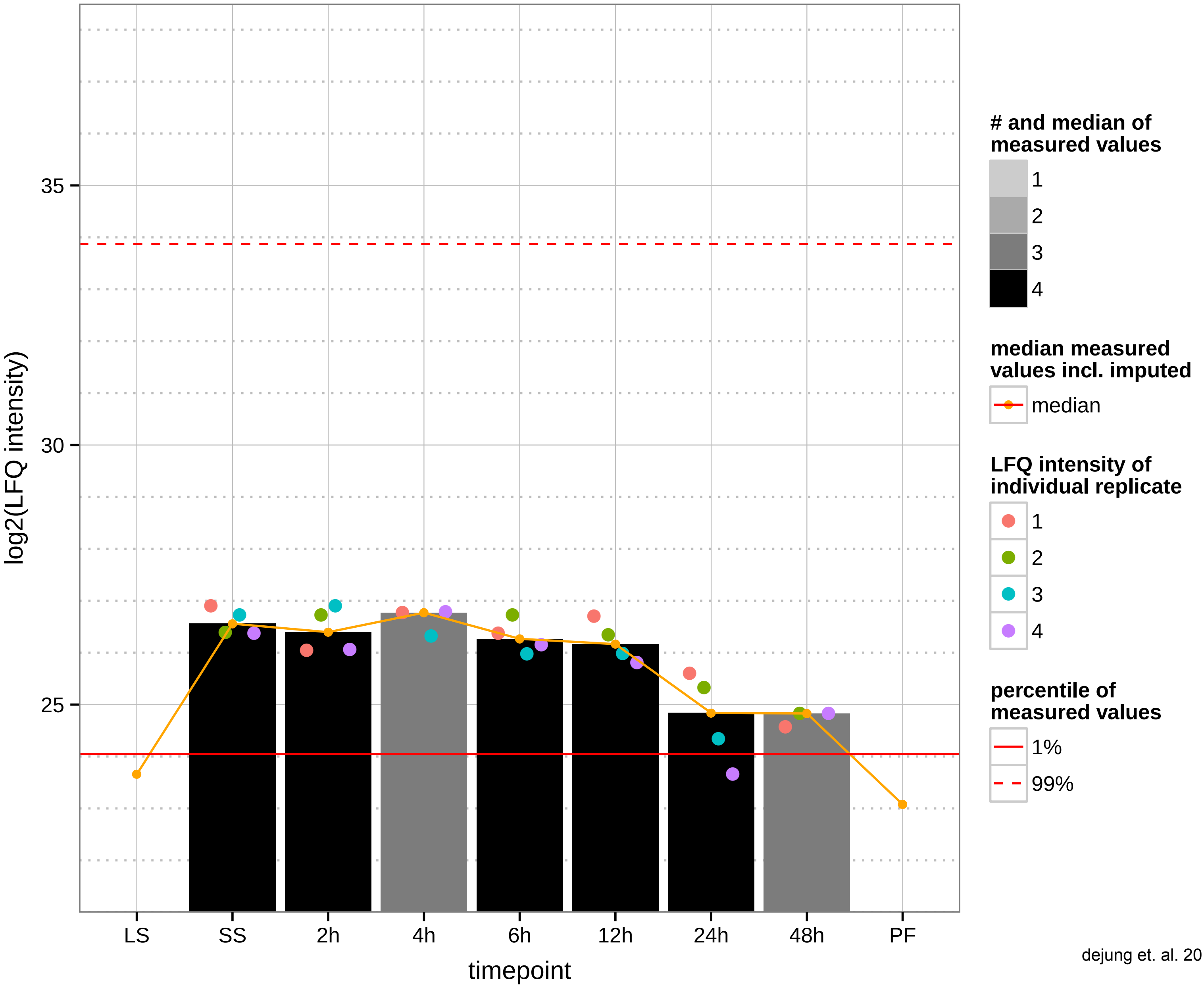
small GTP–binding rab protein, putative
Tb927.8.8140
AGOF: GTP binding
AGOC: intracellular
AGOP: protein transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, protein transport, signal transduction, small GTPase mediated signal transduction





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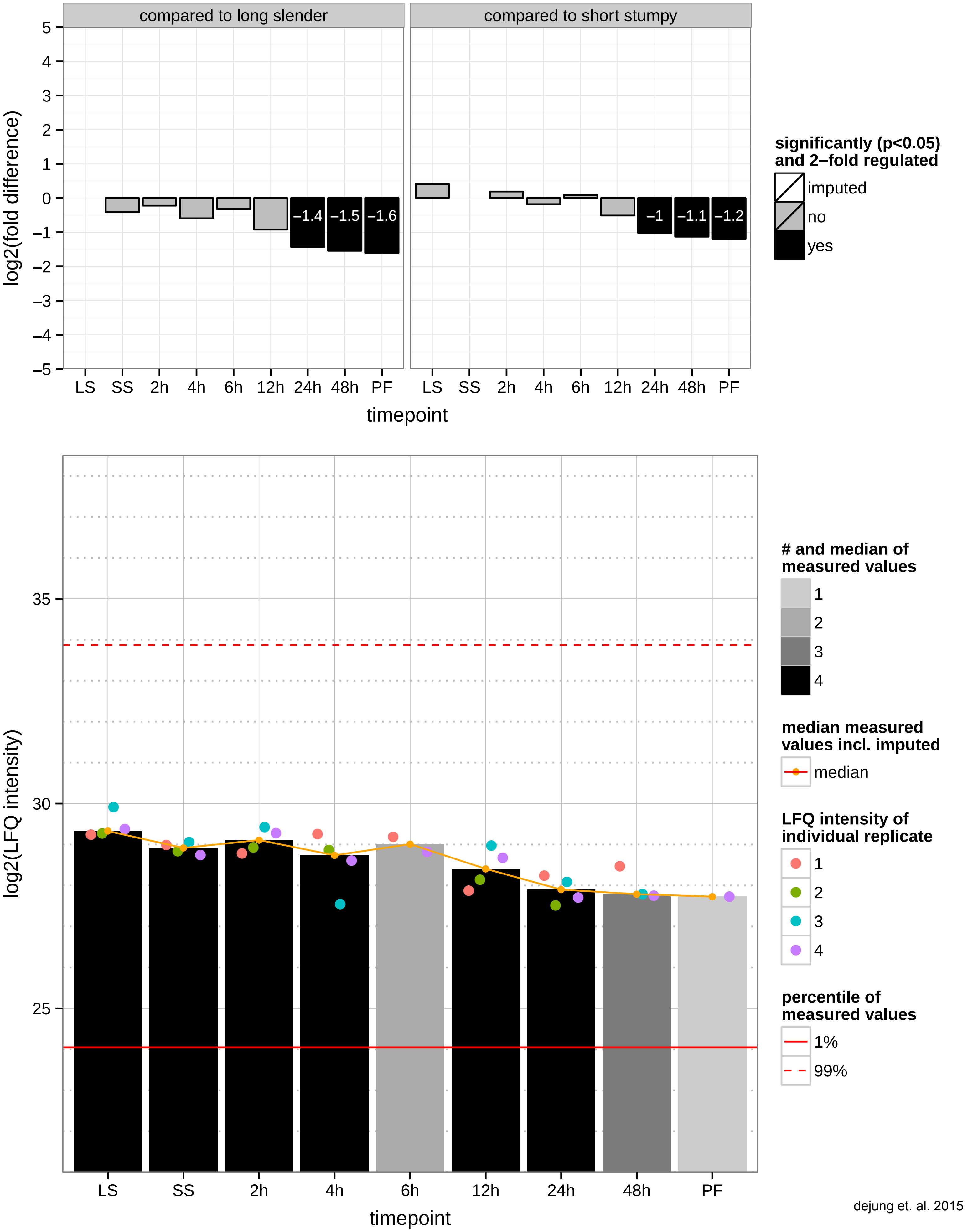
hypothetical protein, conserved
Tb927.8.8150
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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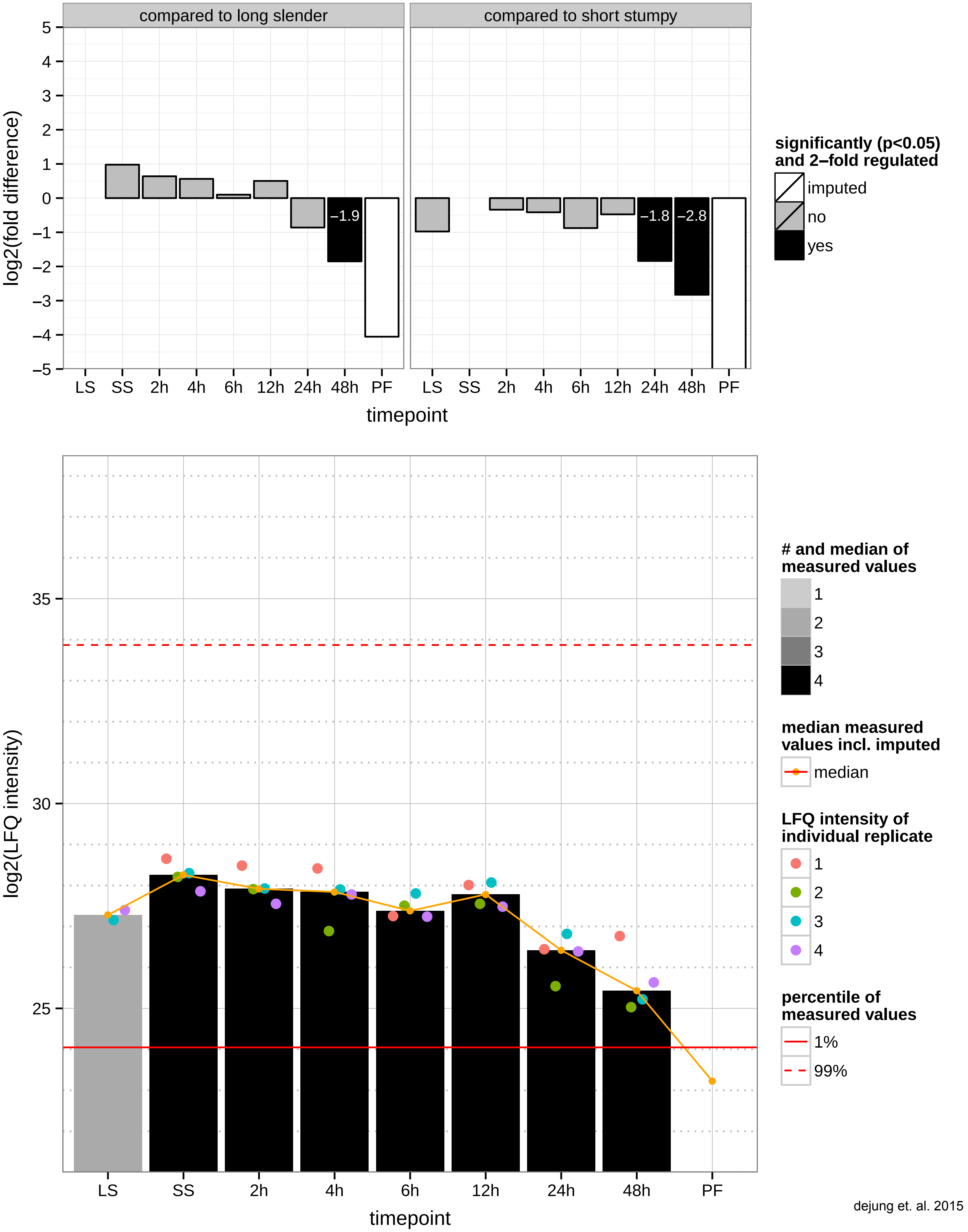
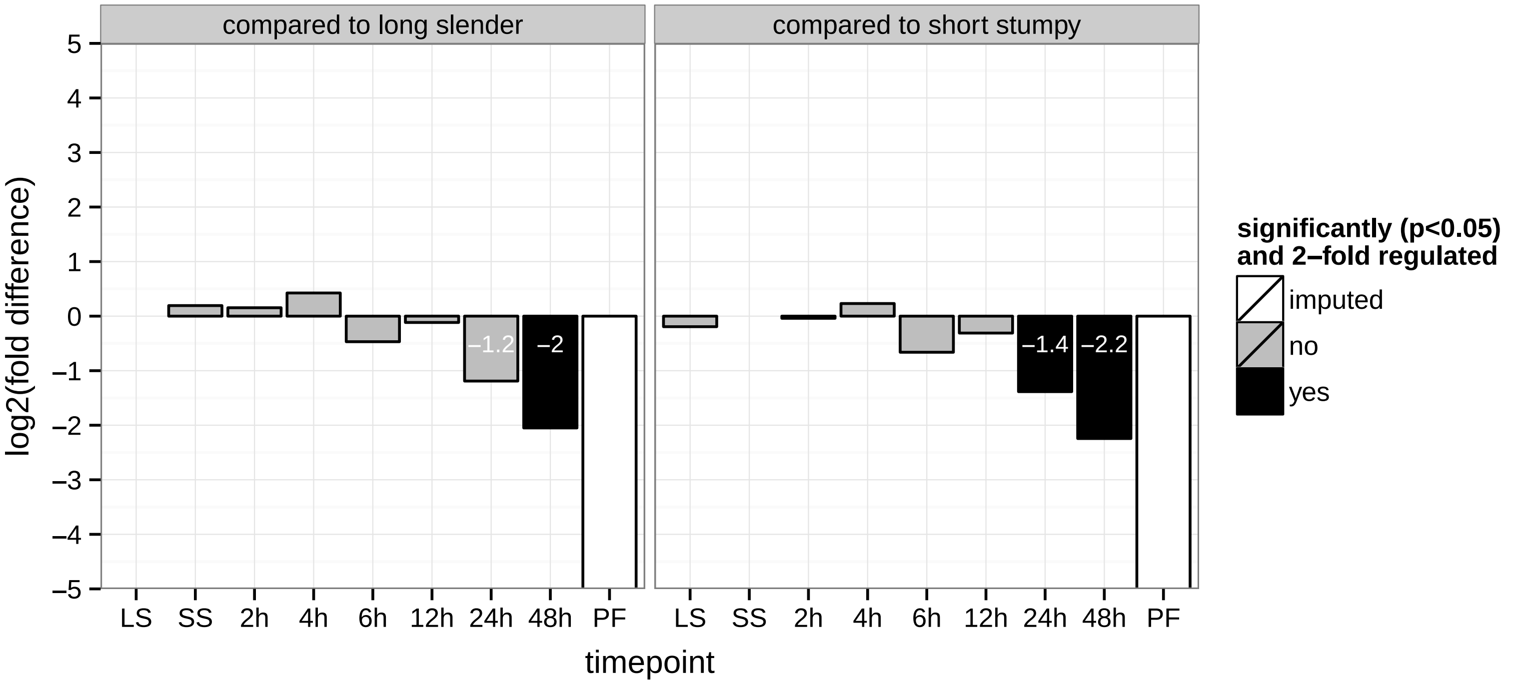
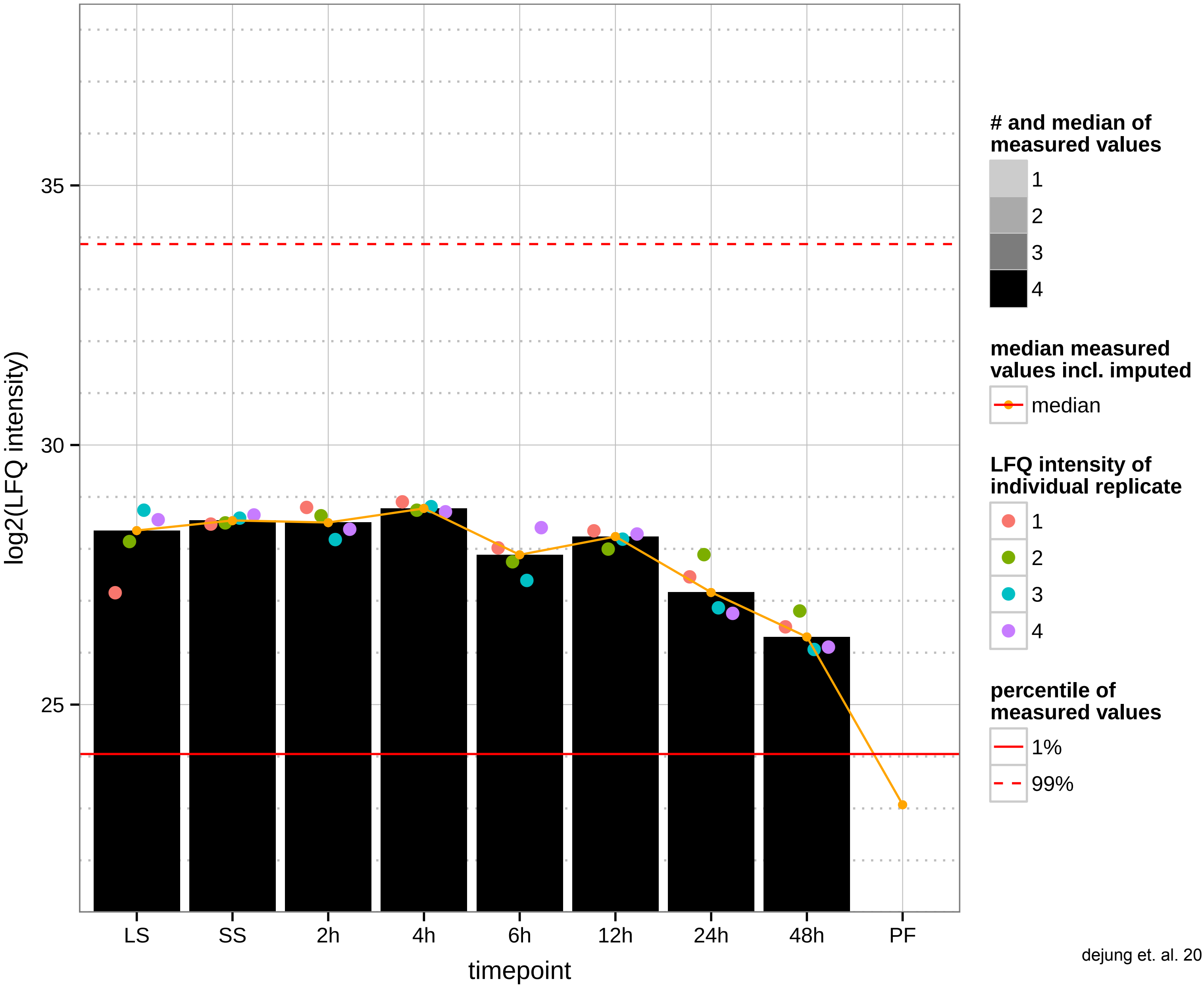
amino acid transporter, putative
Tb927.8.8230
AGOF: amine transmembrane transporter activity
AGOC: integral to membrane
AGOP: amino acid transport
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.8280
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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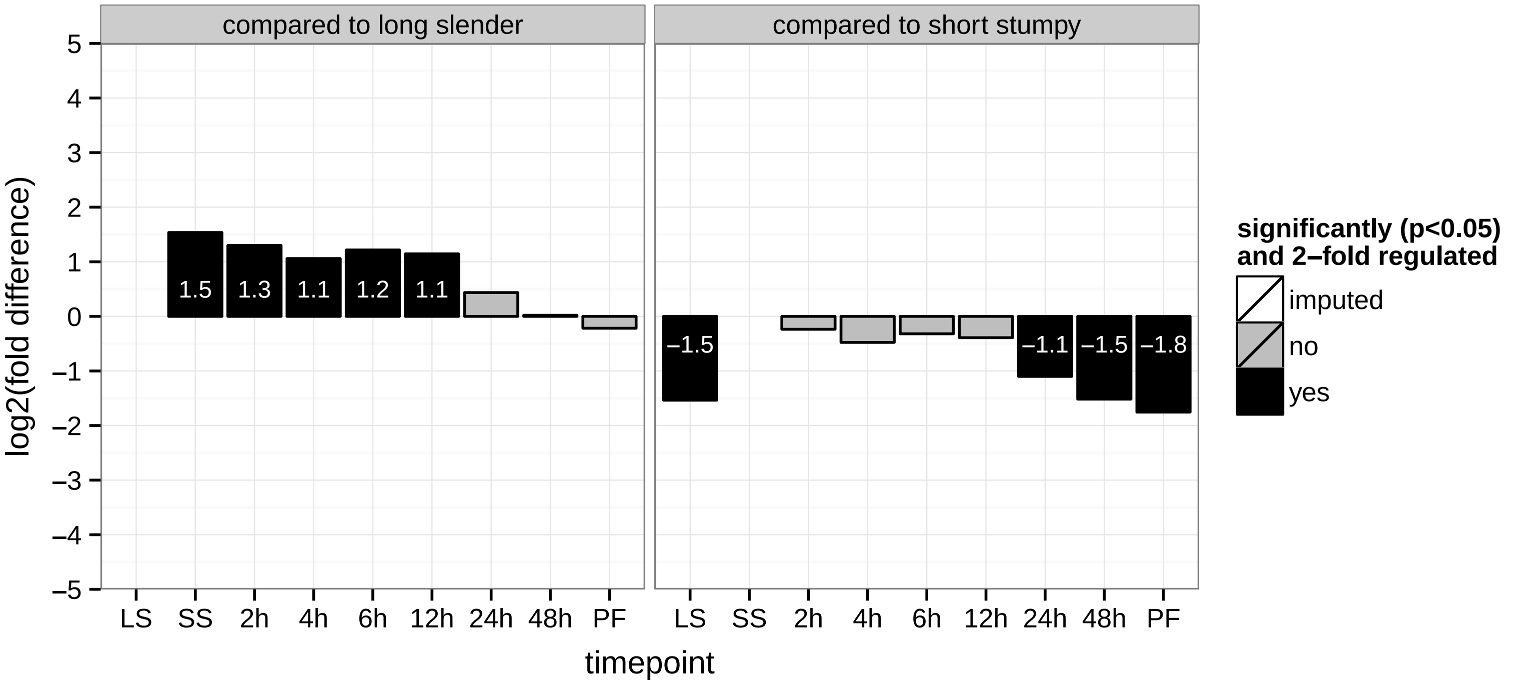
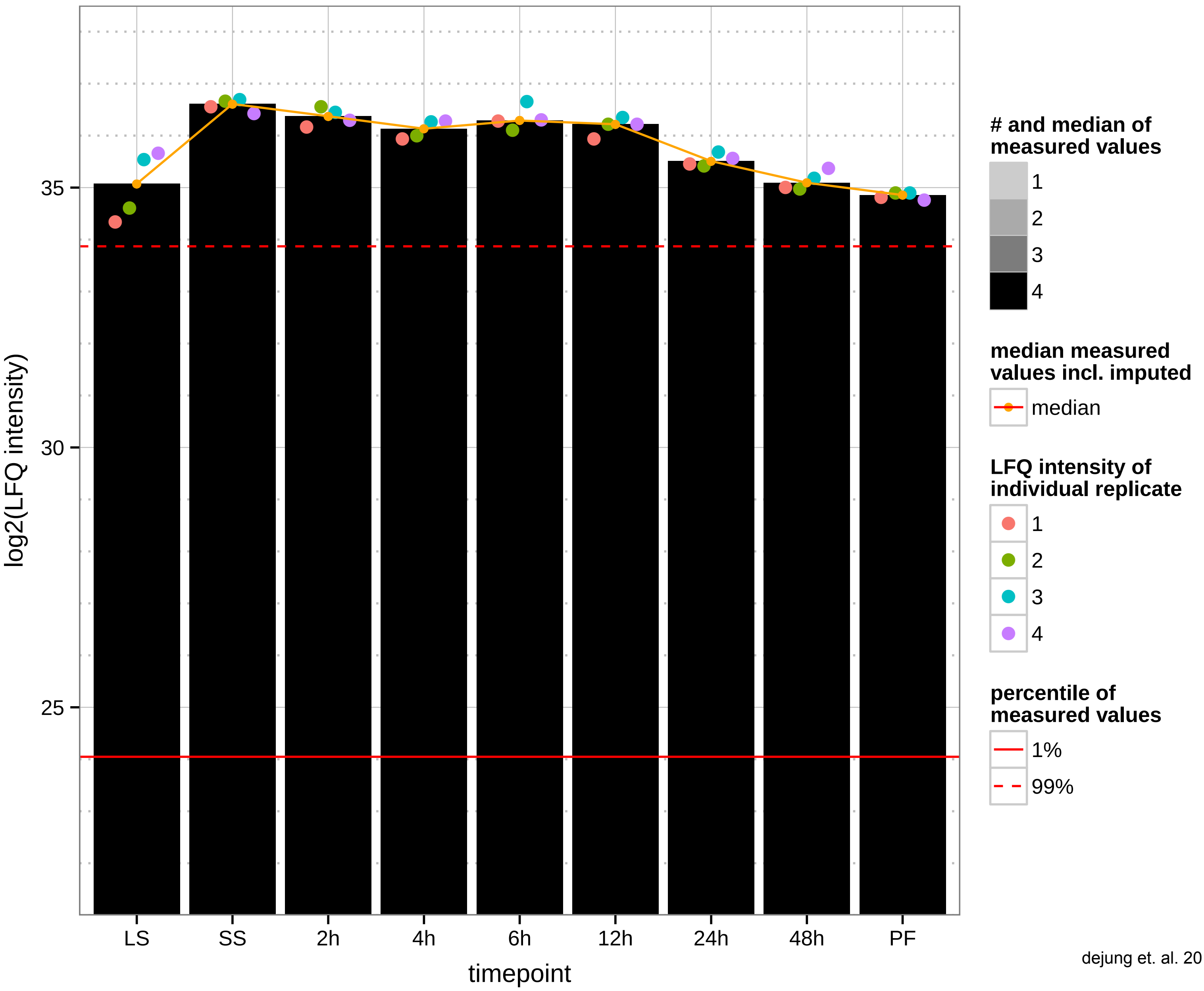
glycerol kinase, glycosomal (glk1)
Tb927.9.12630;Tb927.9.12590;Tb927.9.12570;Tb927.9.12550;Tb927.9.12610
AGOF: ATP binding, glycerol kinase activity
AGOC: glycosome
AGOP: carbohydrate metabolic process, glycerol–3–phosphate metabolic process
PGOF: glycerol kinase activity, phosphotransferase activity, alcohol group as acceptor
PGOC: null
PGOP: carbohydrate metabolic process, glycerol–3–phosphate metabolic process





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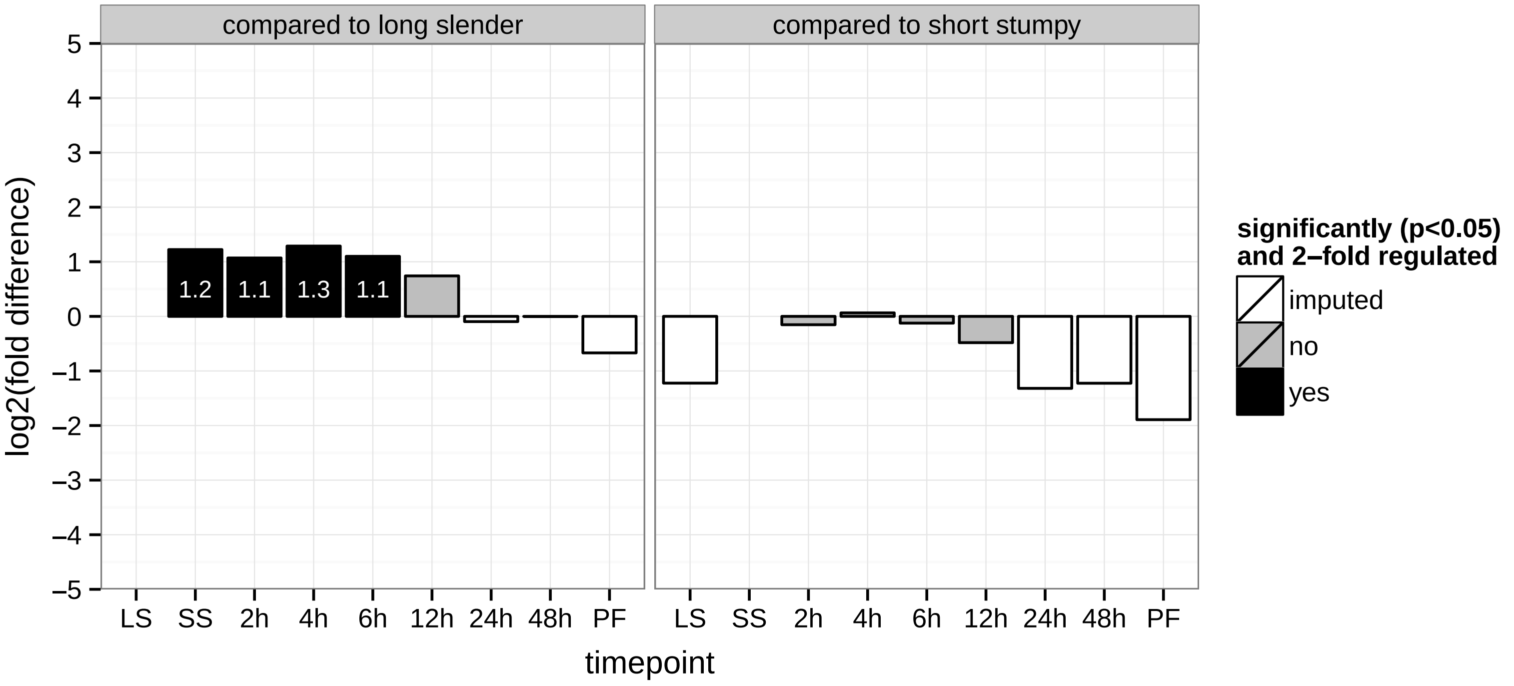
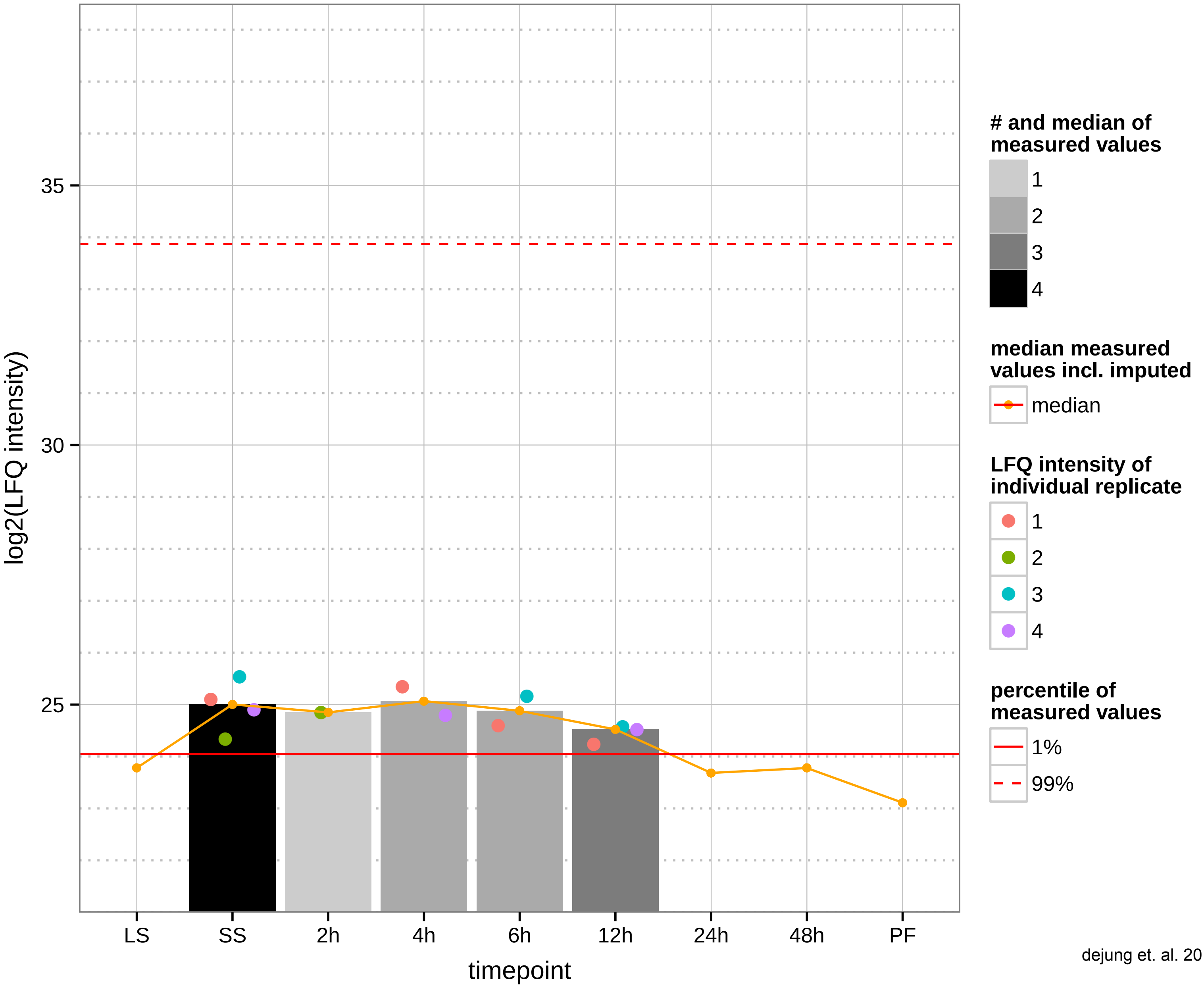
hypothetical protein, conserved
Tb927.9.13620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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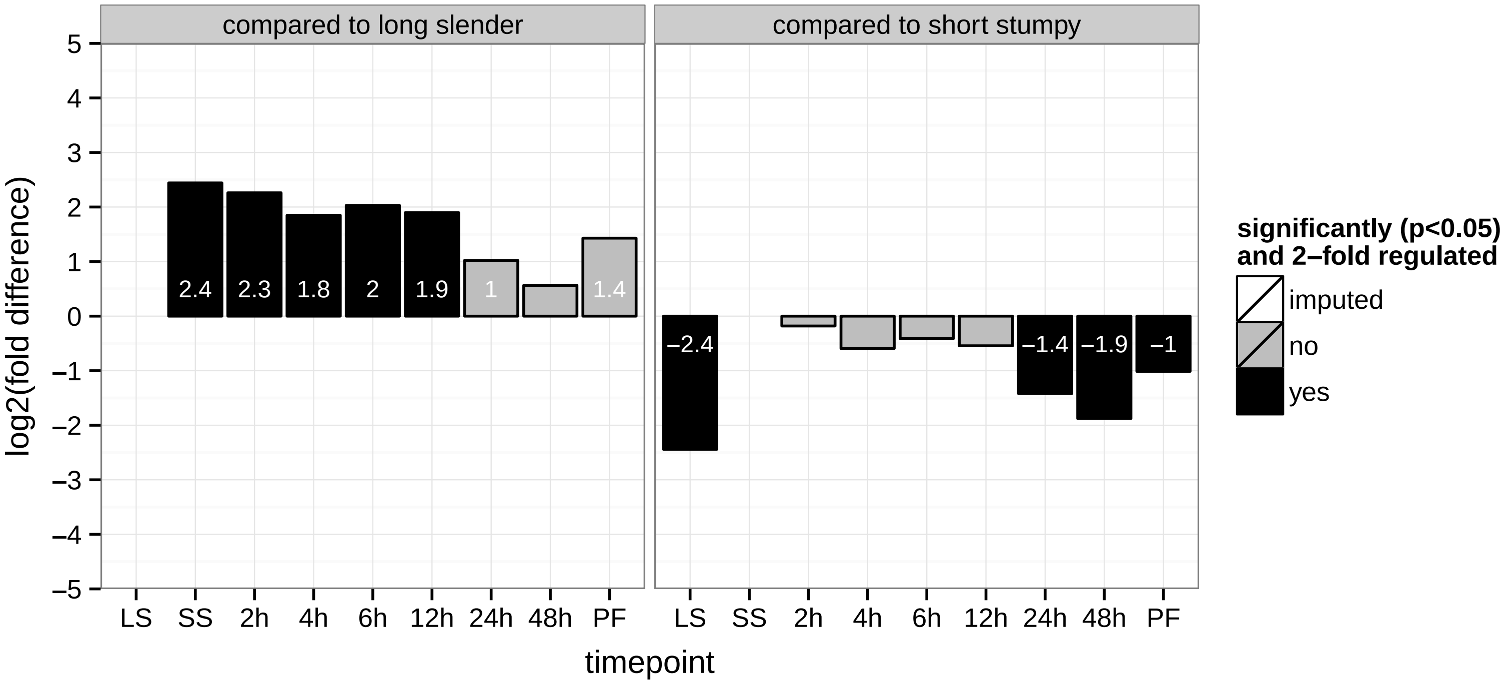
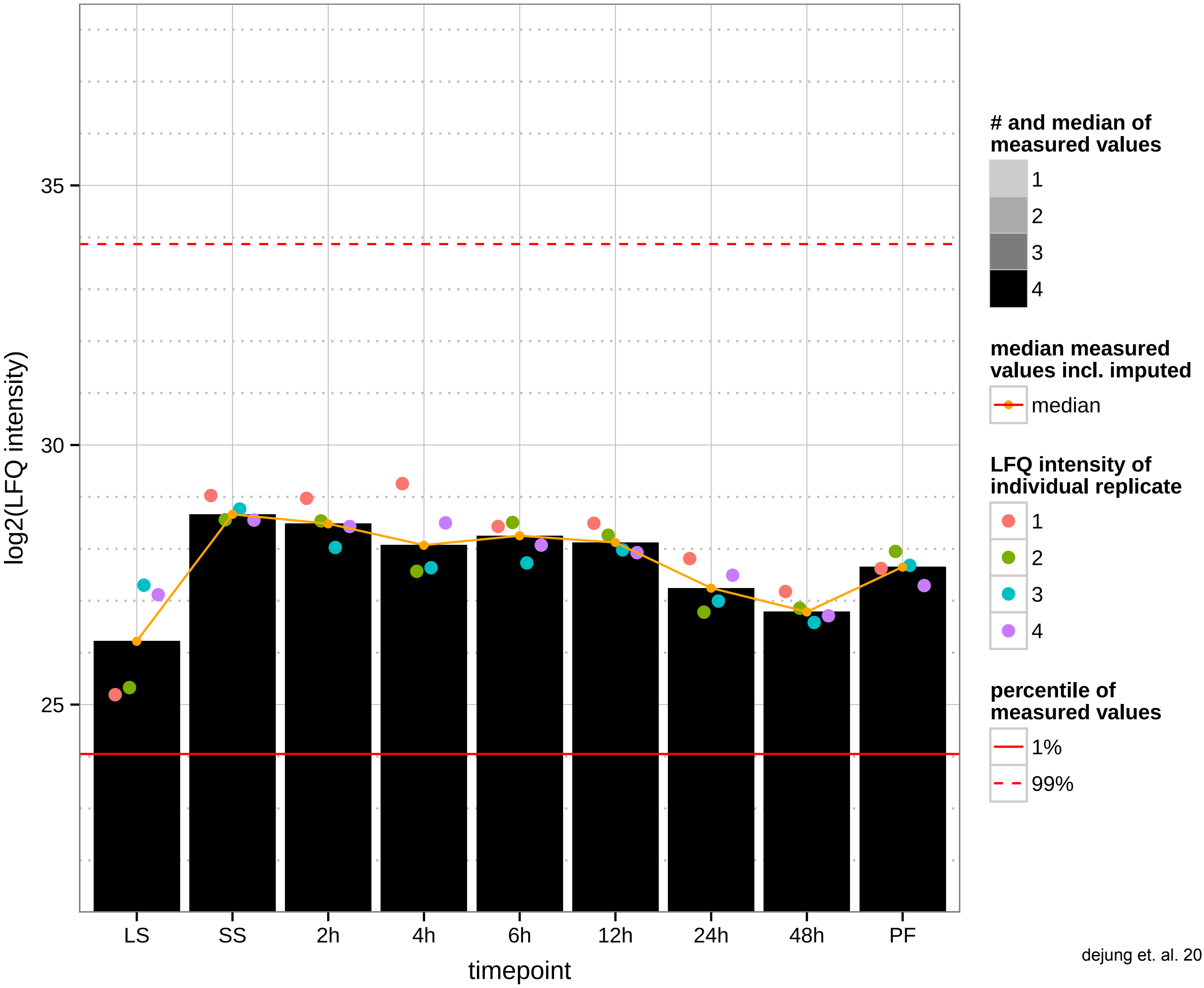
ubiquitin carboxyl–terminal hydrolase, putative, cysteine peptidase, Clan CA, family C19
Tb927.9.14470
AGOF: cysteine–type endopeptidase activity, ubiquitin thiolesterase activity
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ubiquitin thiolesterase activity
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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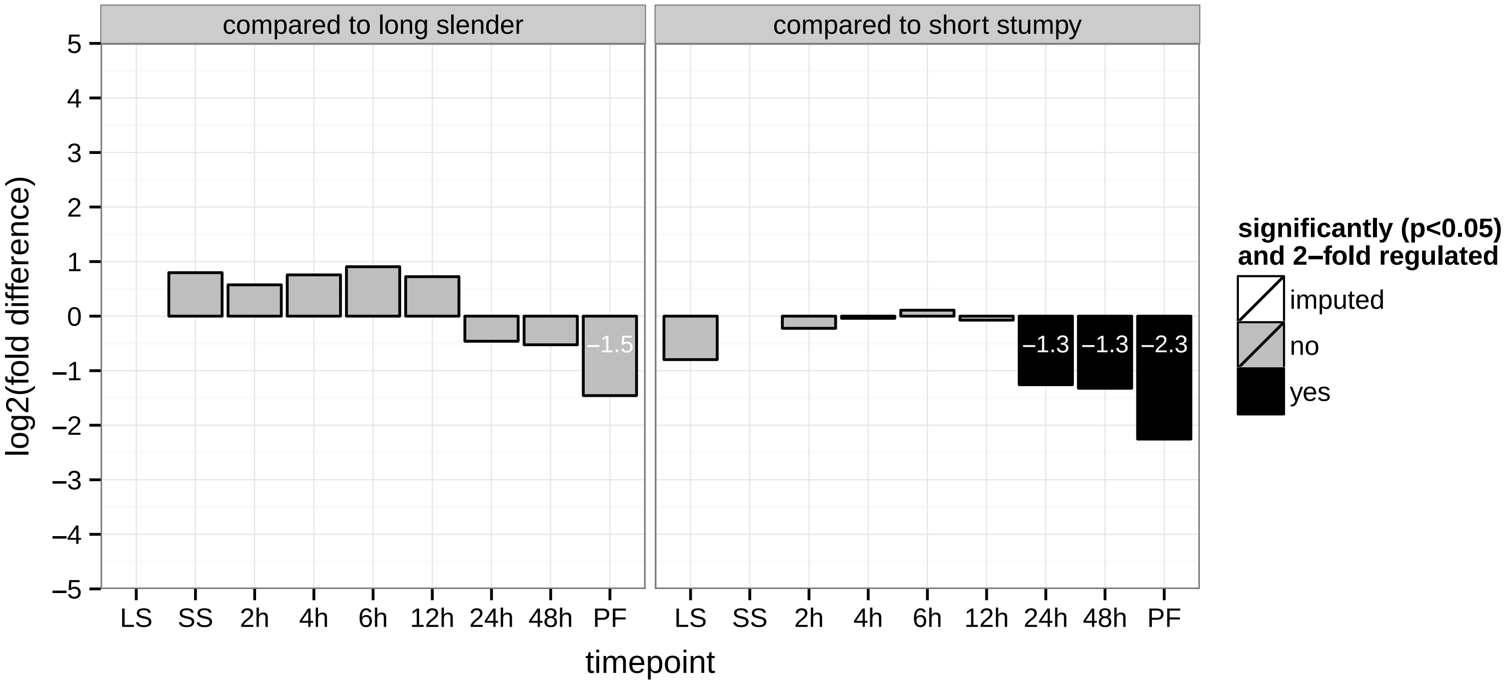
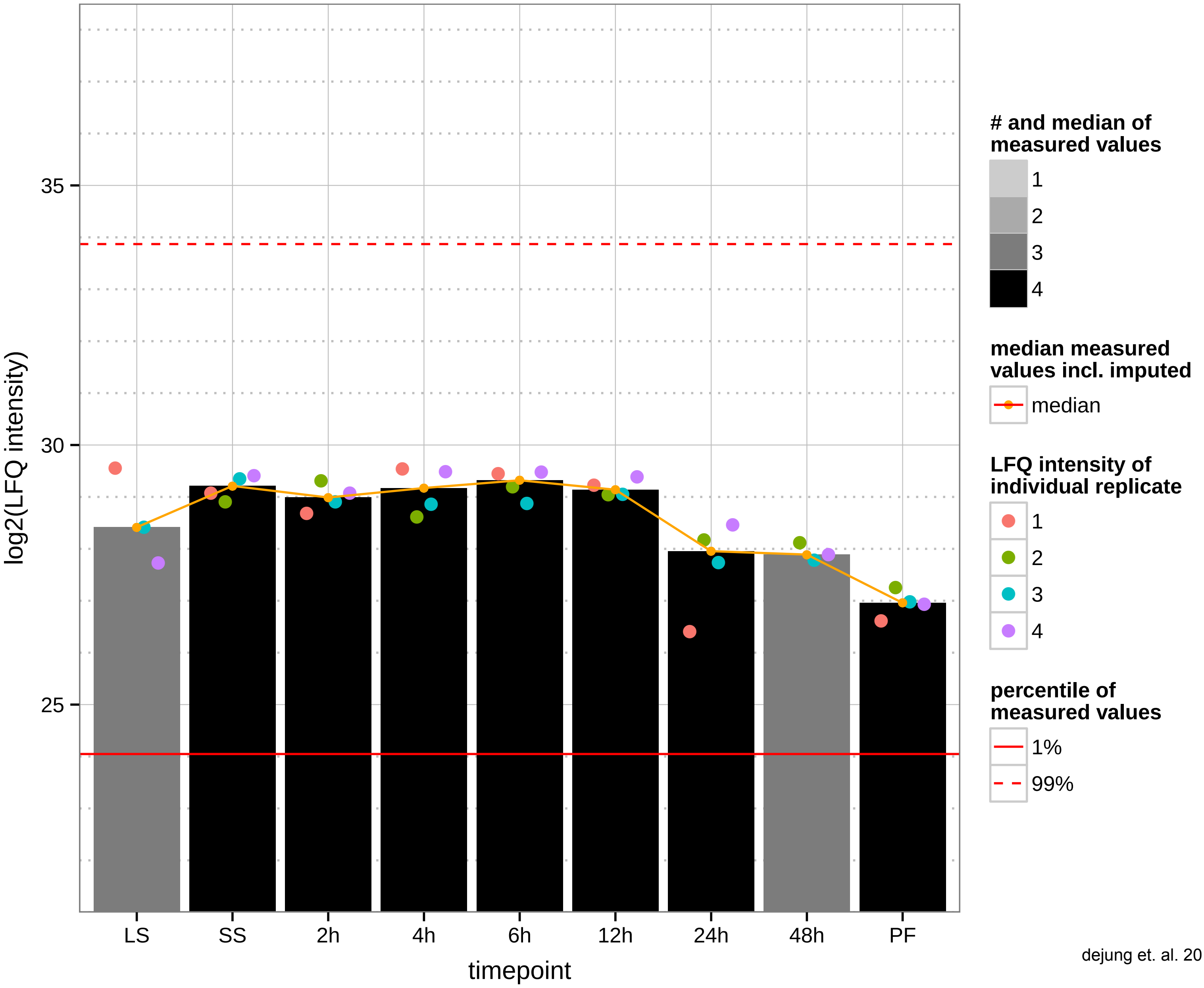
hypothetical protein, conserved
Tb927.9.1600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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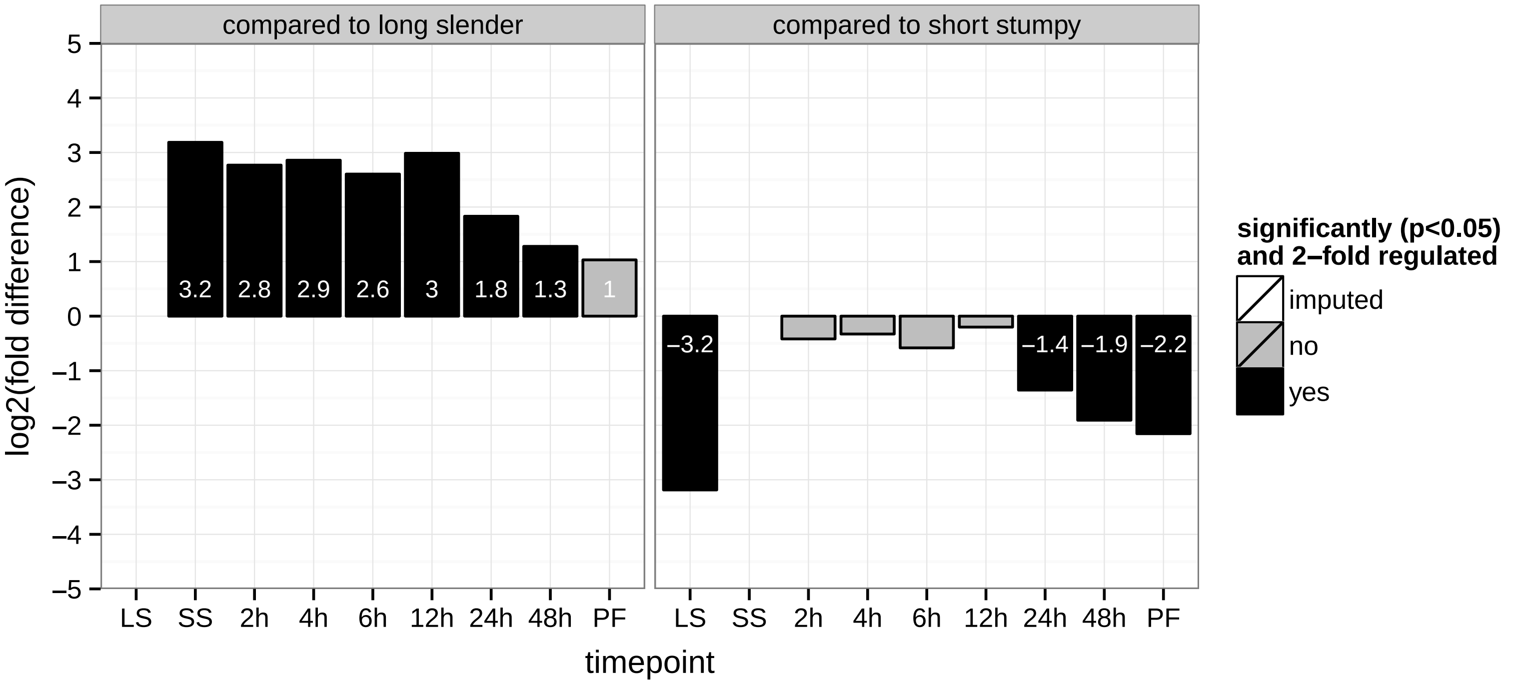
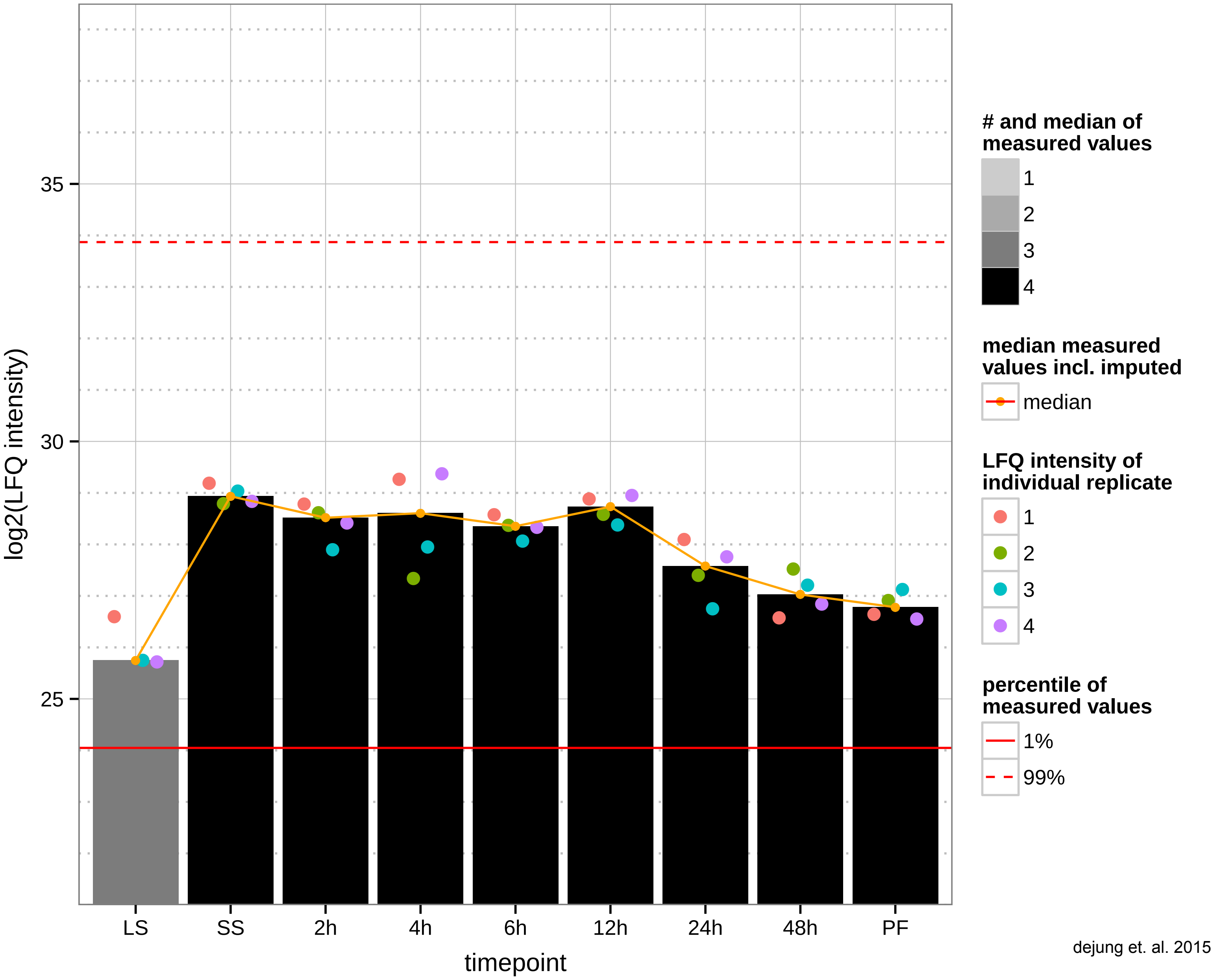
syntaxin binding protein 1, putative
Tb927.9.1970
AGOF: SNARE binding, protein transporter activity
AGOC: null
AGOP: vesicle docking involved in exocytosis, vesicle–mediated transport
PGOF: null
PGOC: null
PGOP: vesicle docking involved in exocytosis, vesicle–mediated transport





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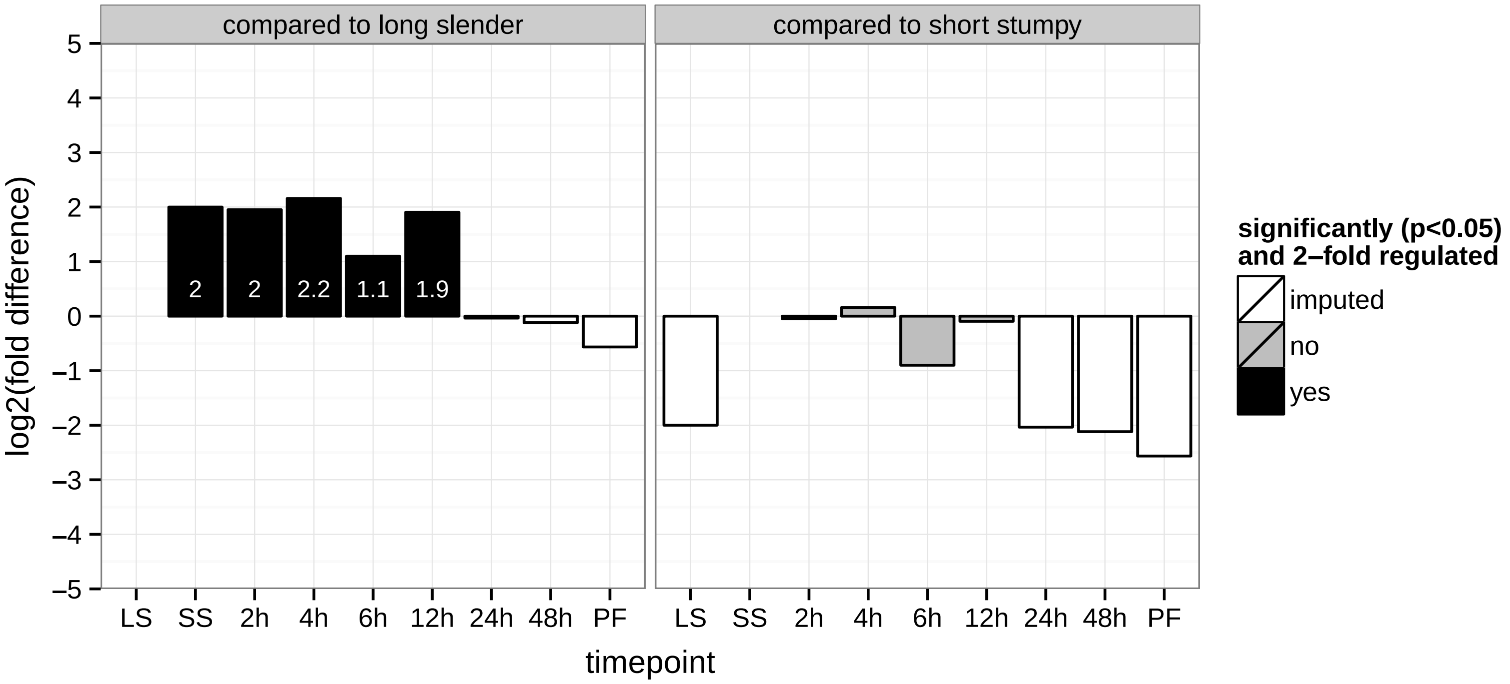
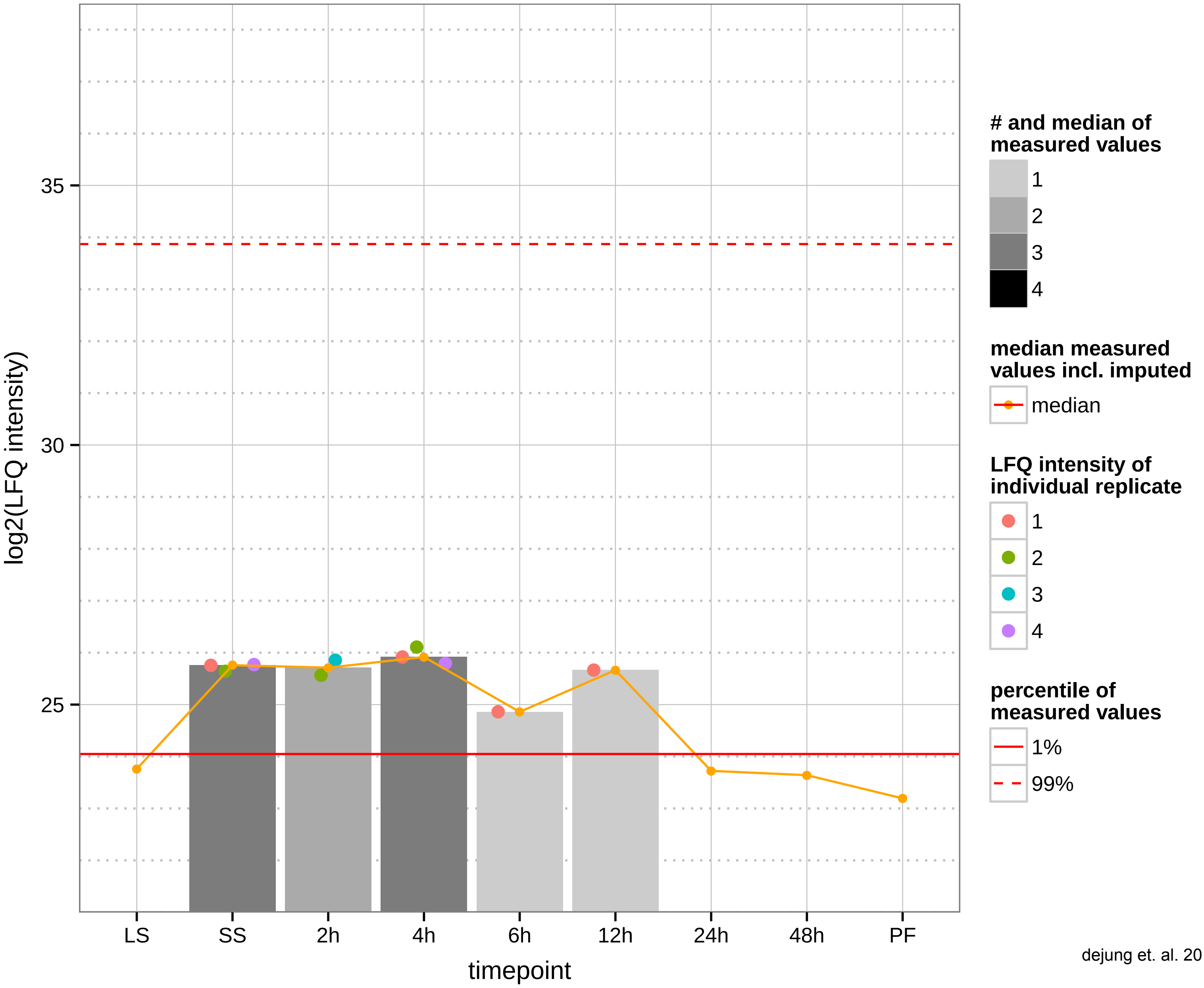
hypothetical protein, conserved
Tb927.9.2290
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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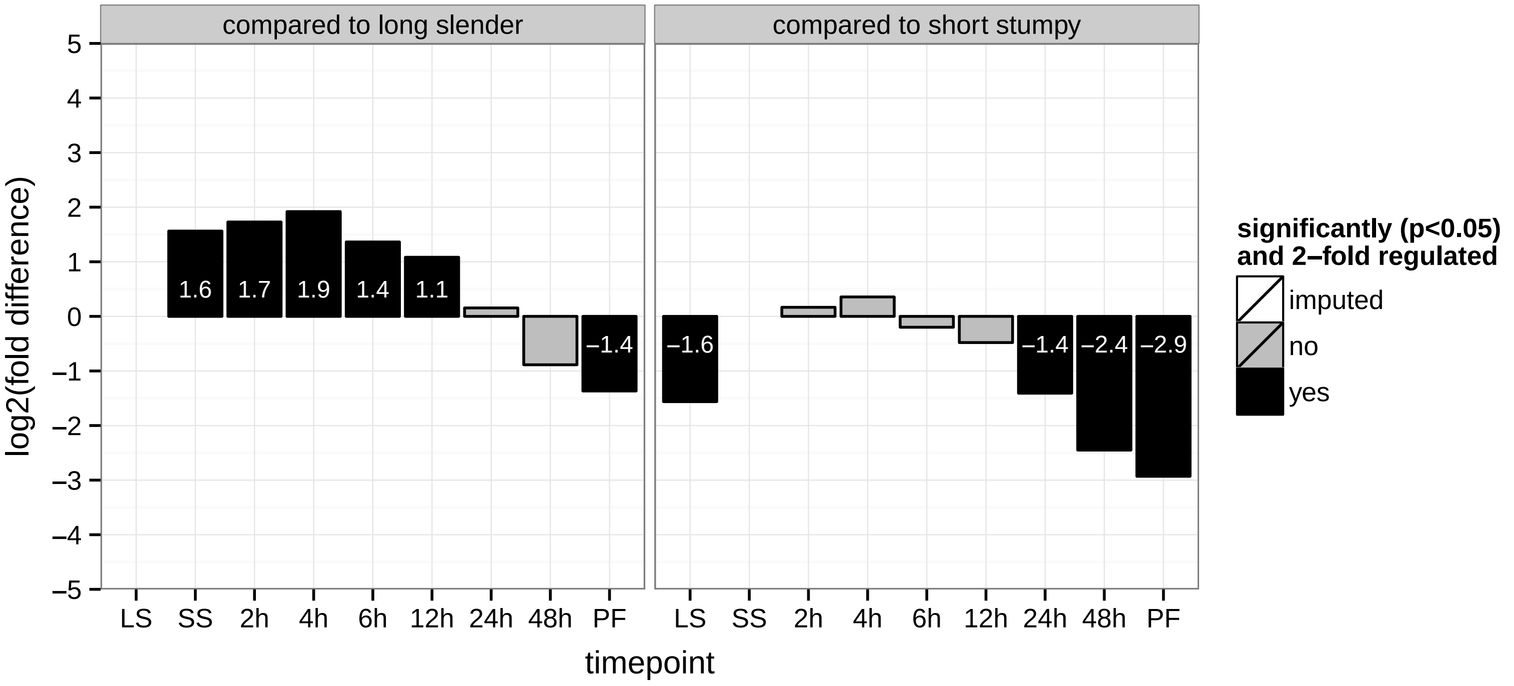
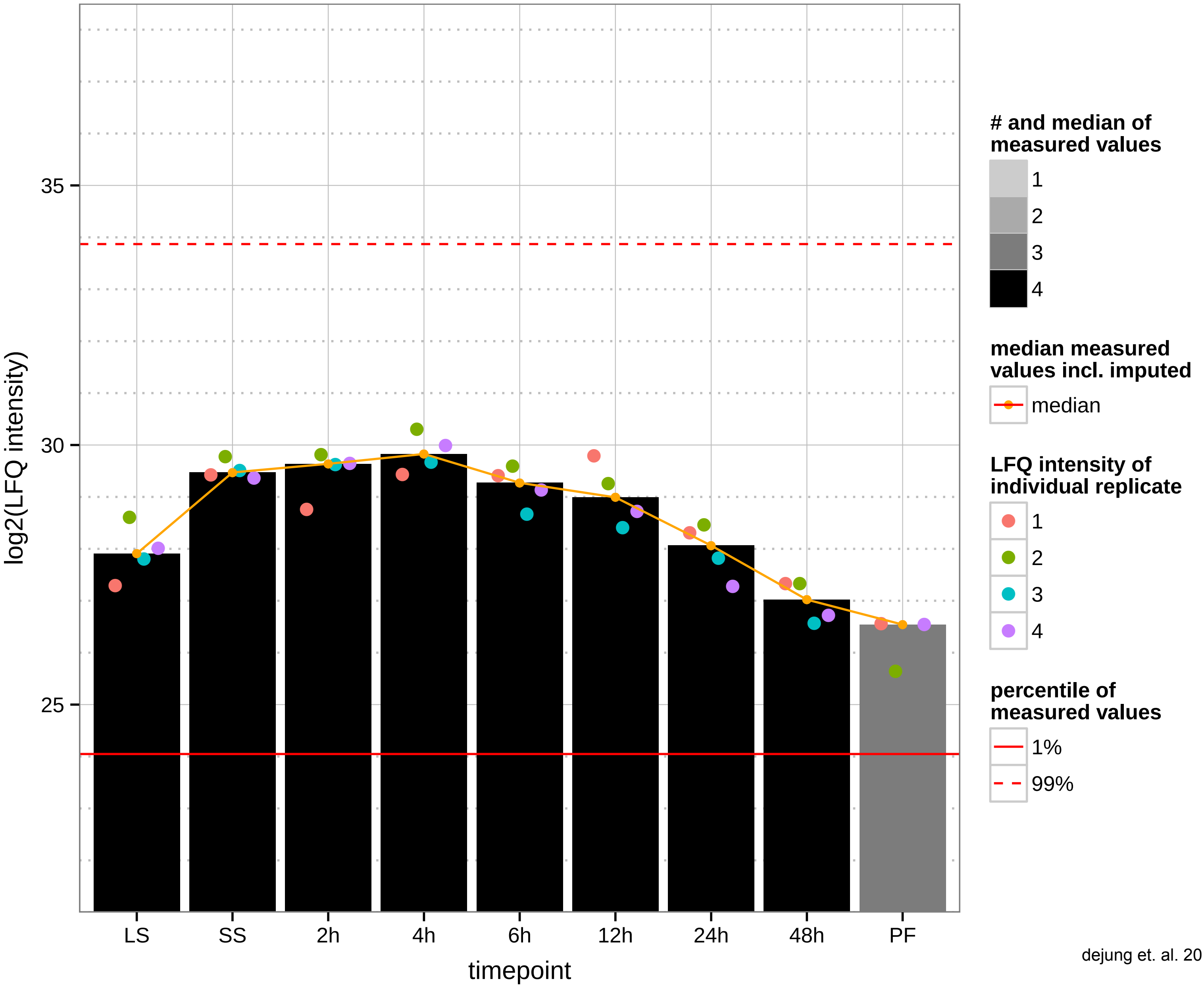
syntaxin, putative
Tb927.9.3820
AGOF: transporter activity
AGOC: membrane
AGOP: vesicle−mediated transport
PGOF: protein binding
PGOC: null
PGOP: null





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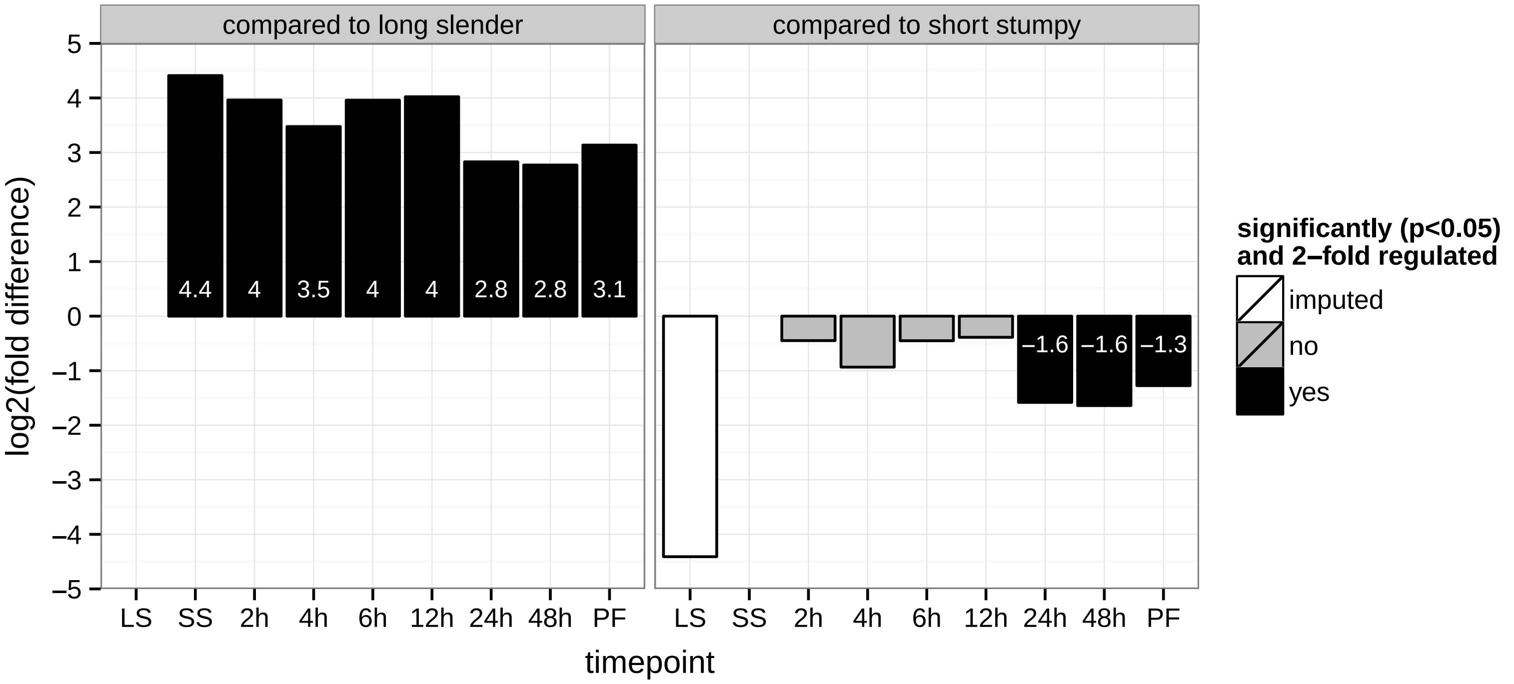
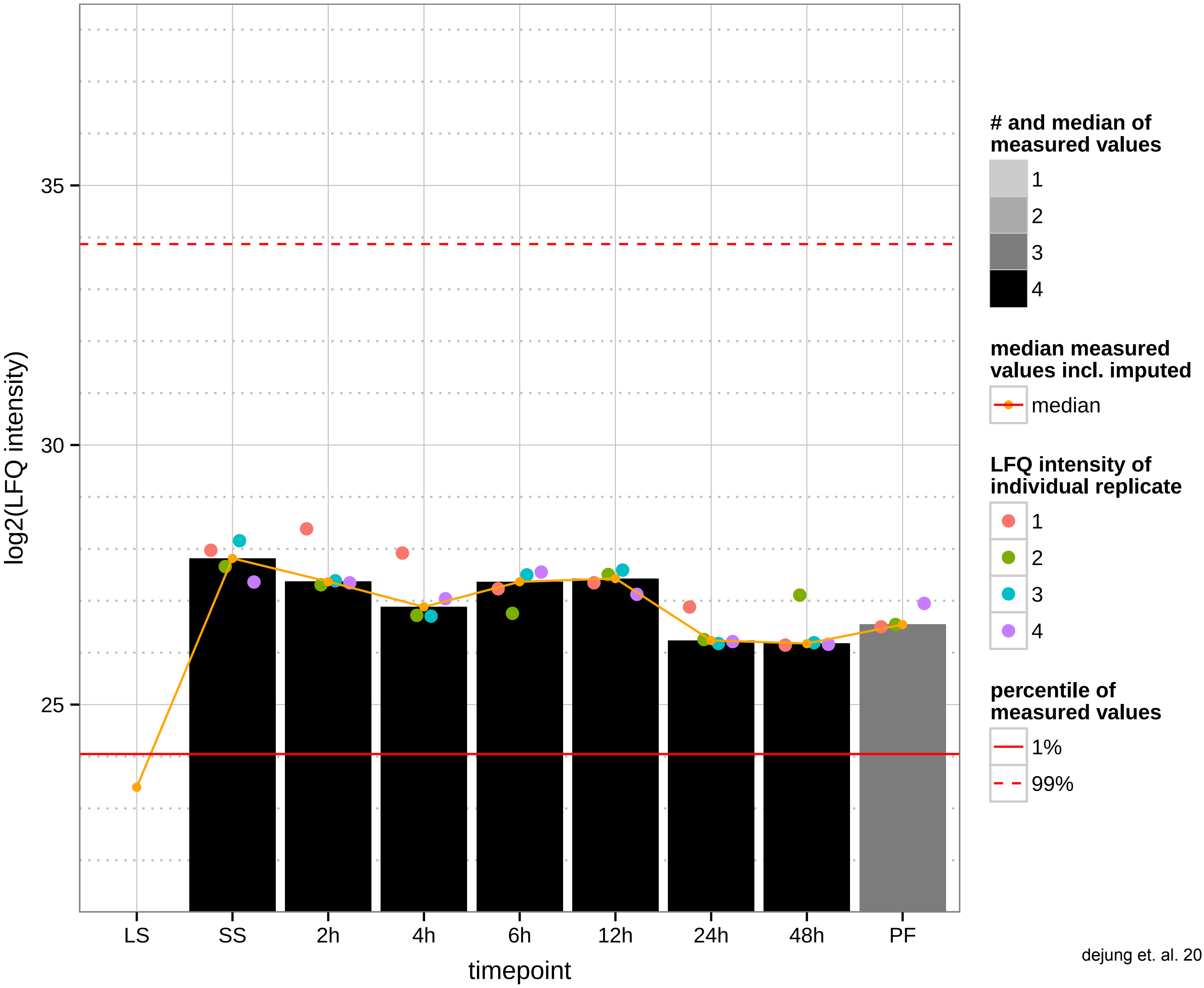
hypothetical protein, conserved
Tb927.9.7760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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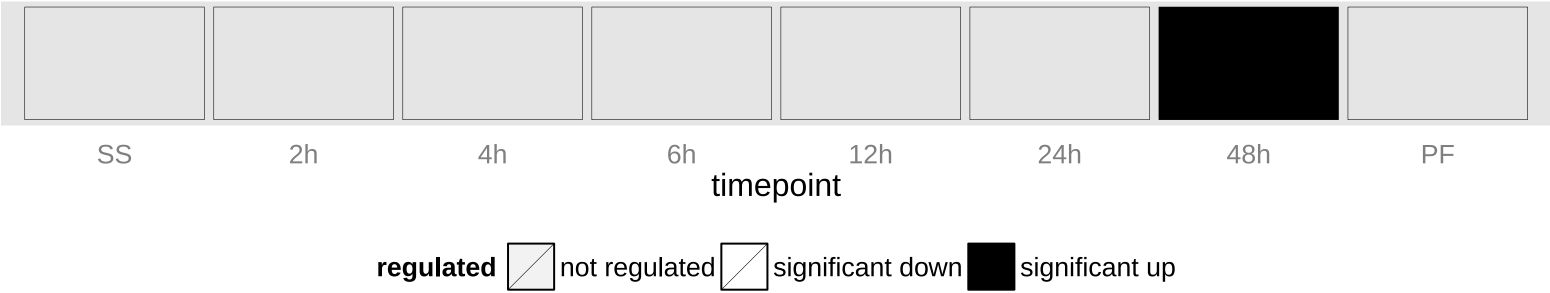

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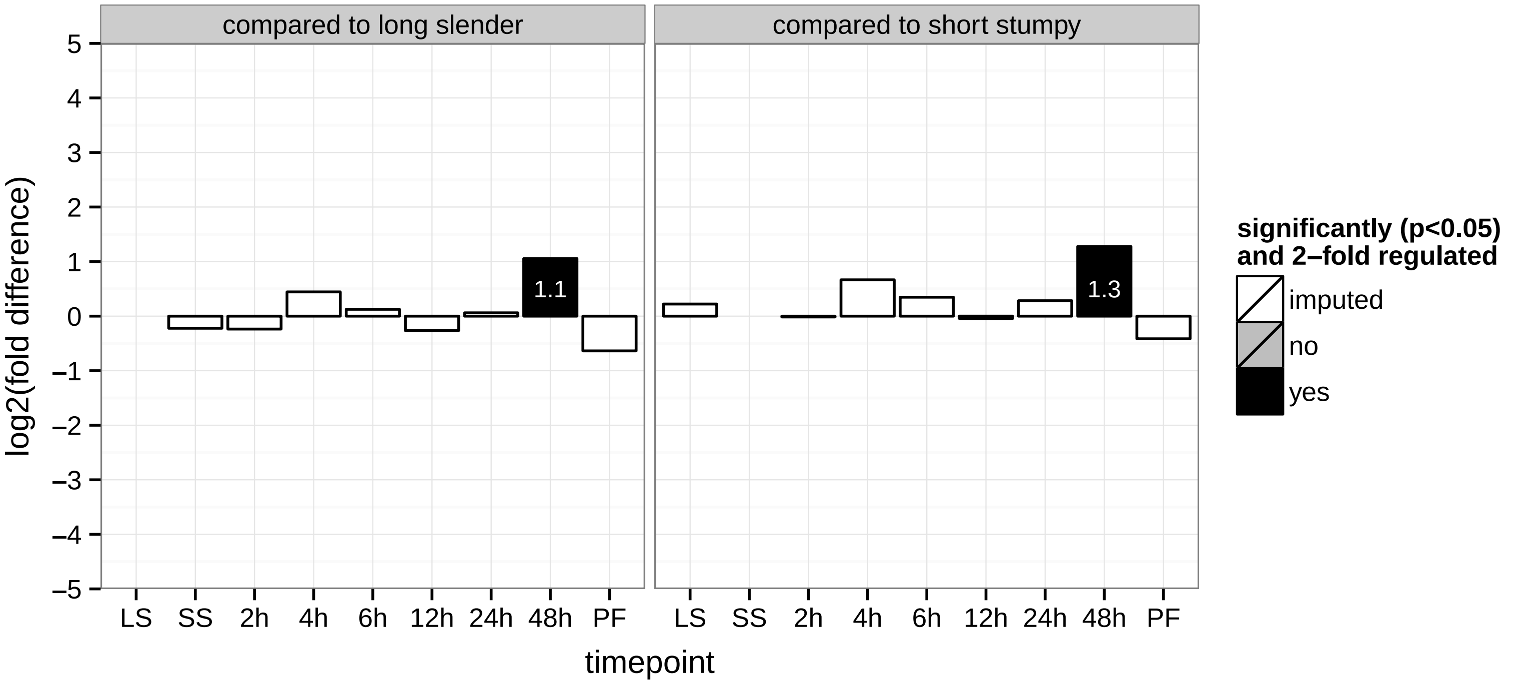
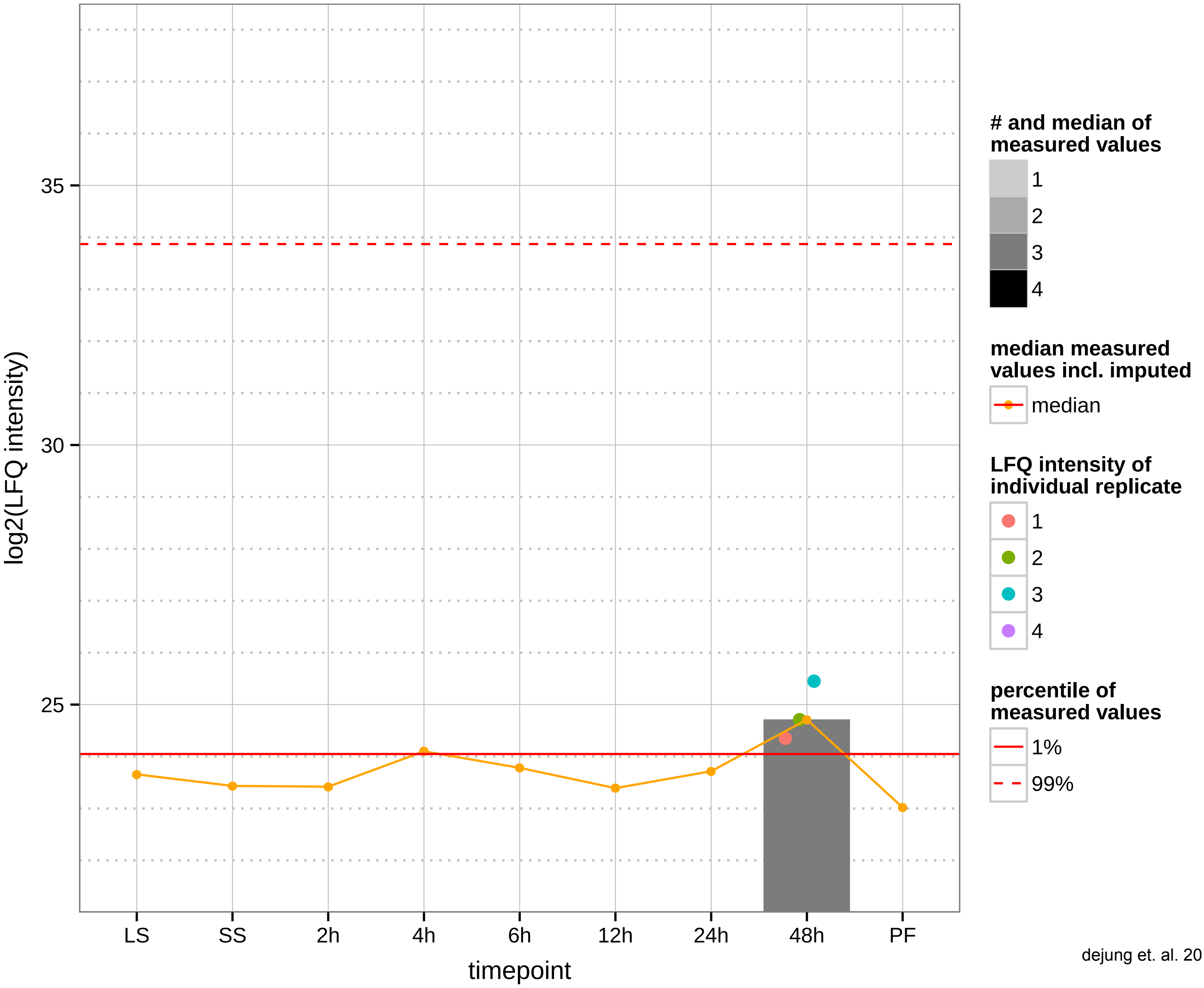
hypothetical protein, conserved
Tb11.02.5430b;Tb11.02.5430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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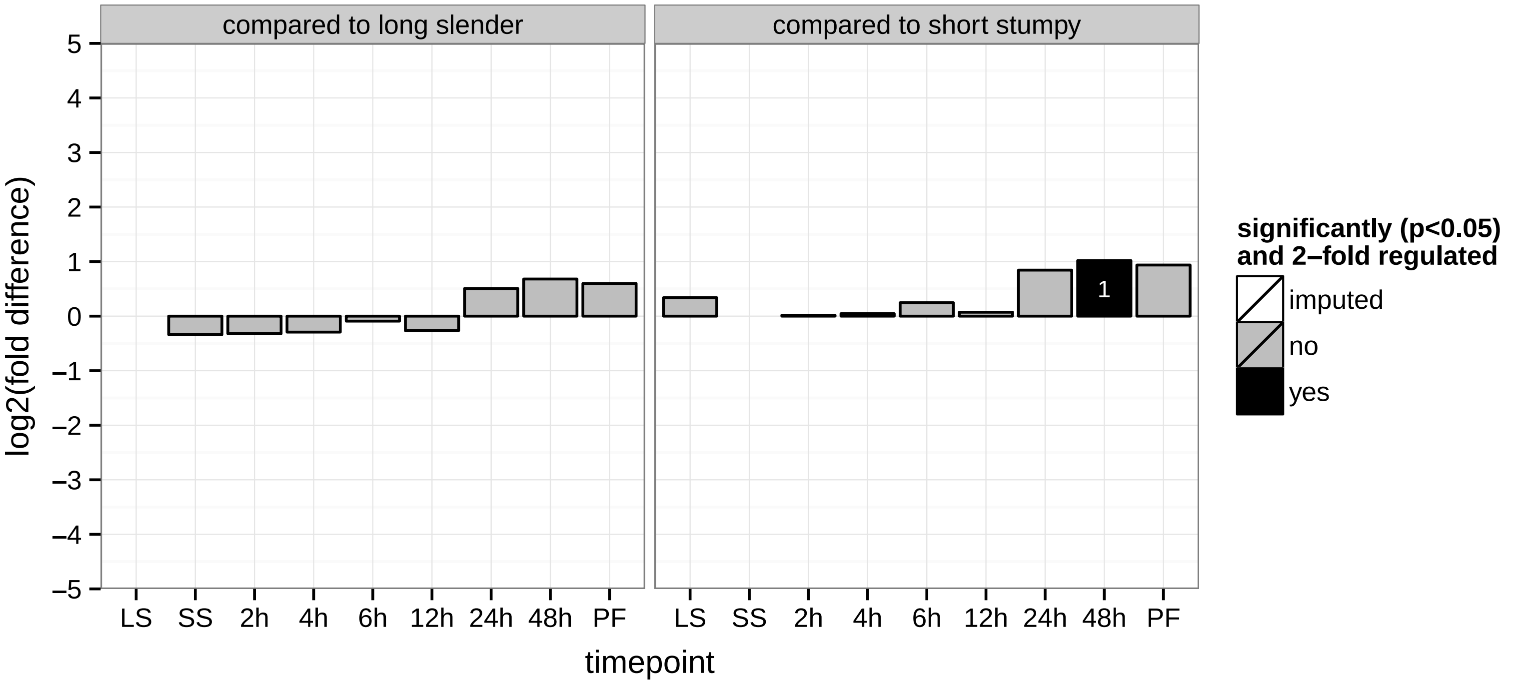
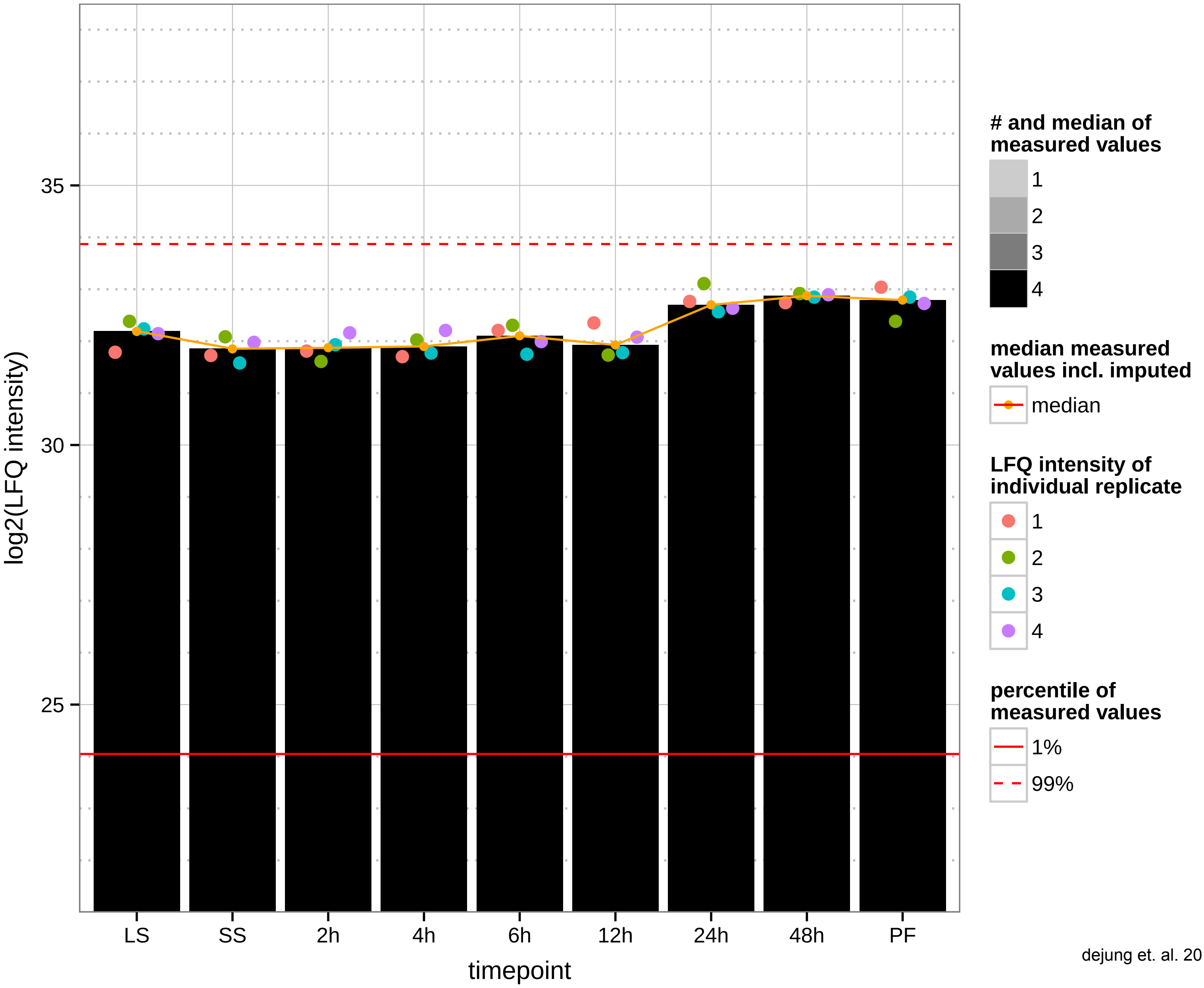
60S ribosomal protein L19, putative
Tb927.7.5020;Tb927.7.5000;Tb11.v5.0182;Tb11.v5.0181
AGOF: null, structural constituent of ribosome
AGOC: null, intracellular, ribosome
AGOP: null, ribosome biogenesis, translation
PGOF: null, structural constituent of ribosome
PGOC: null, intracellular, ribosome
PGOP: null, translation





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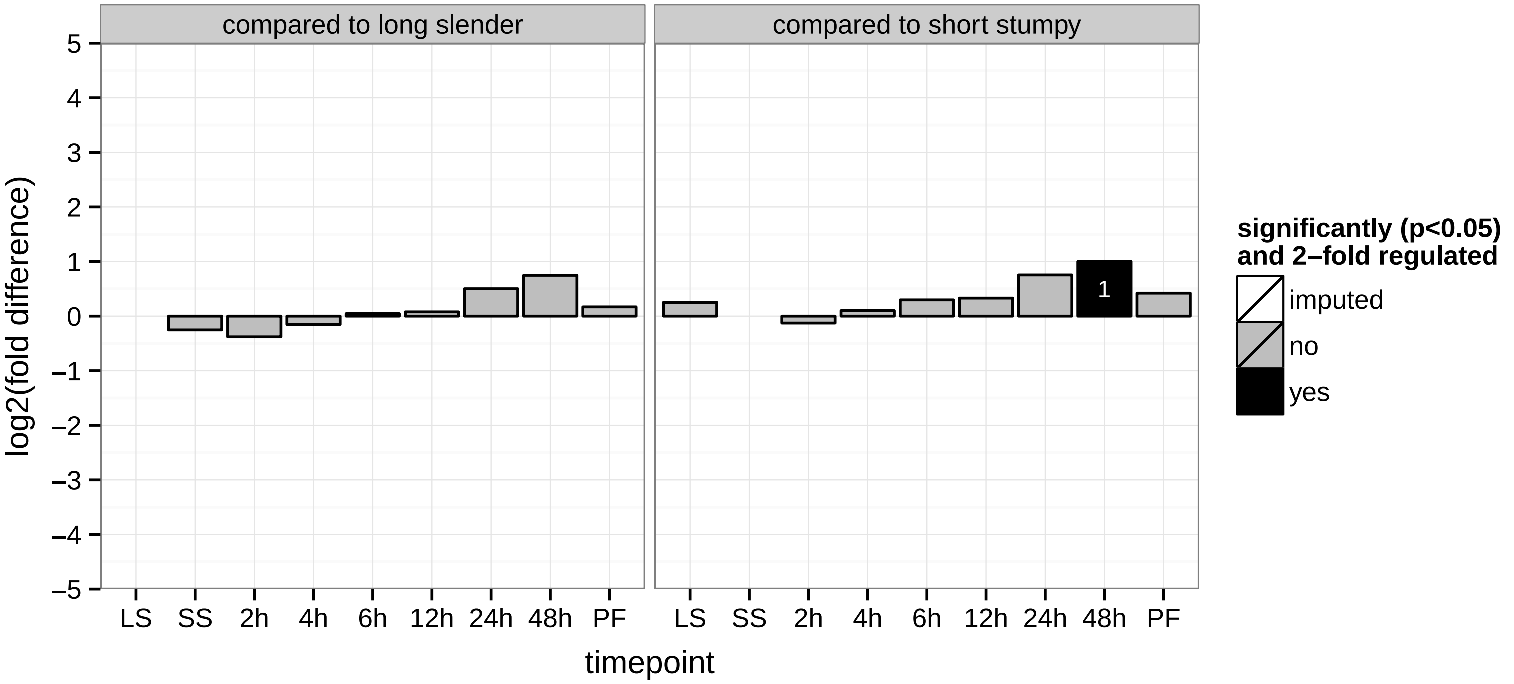
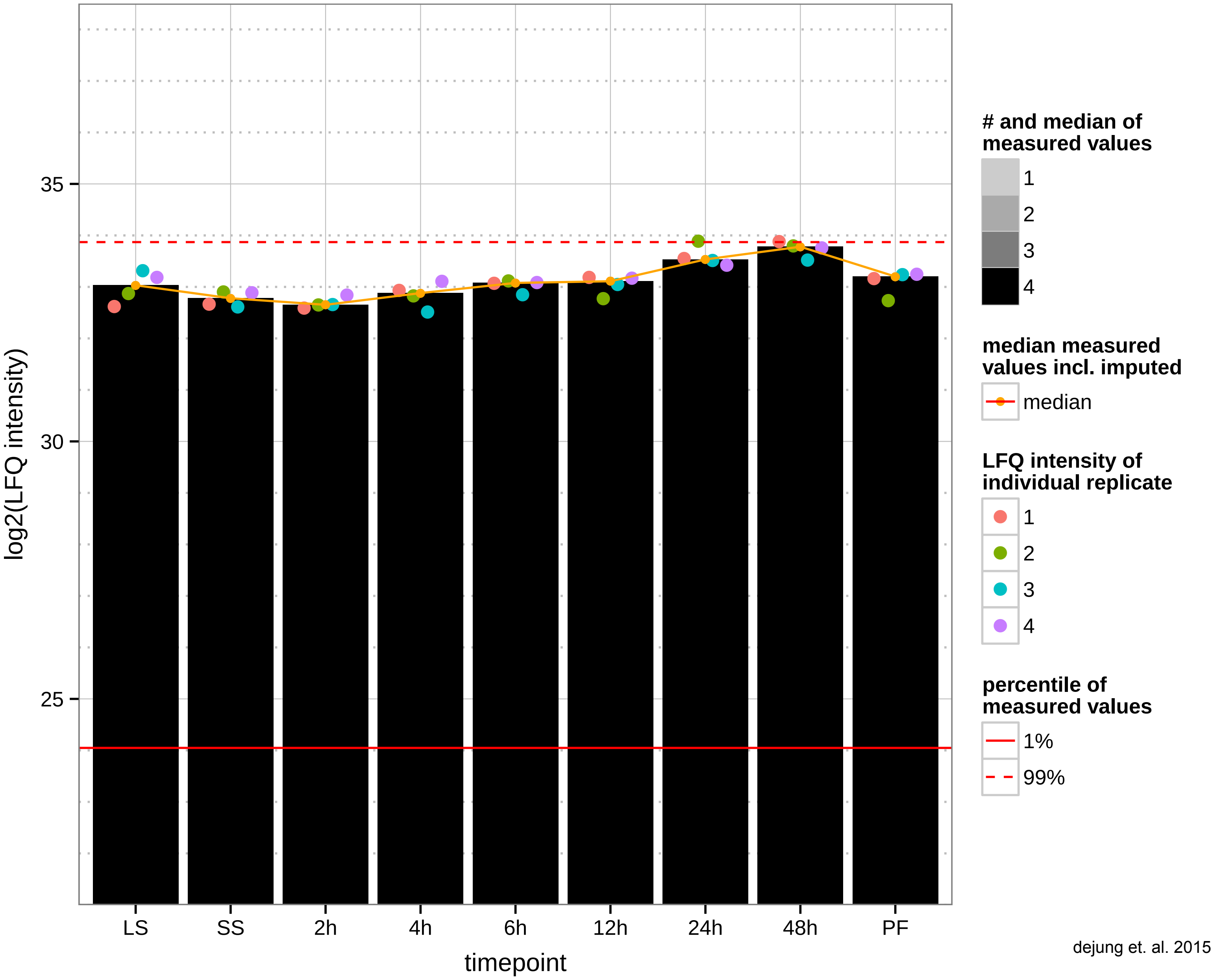
40S ribosomal protein S18, putative, variant surface glycoprotein (VSG), putative (RPS18)
Tb927.10.5340;Tb927.10.5330;Tb11.v5.1060;Tb11.v5.0243
AGOF: null, RNA binding, structural constituent of ribosome
AGOC: null, intracellular, organellar small ribosomal subunit, ribosome
AGOP: null, translation
PGOF: null, RNA binding, nucleic acid binding, structural constituent of ribosome
PGOC: null, intracellular, ribosome
PGOP: null, translation





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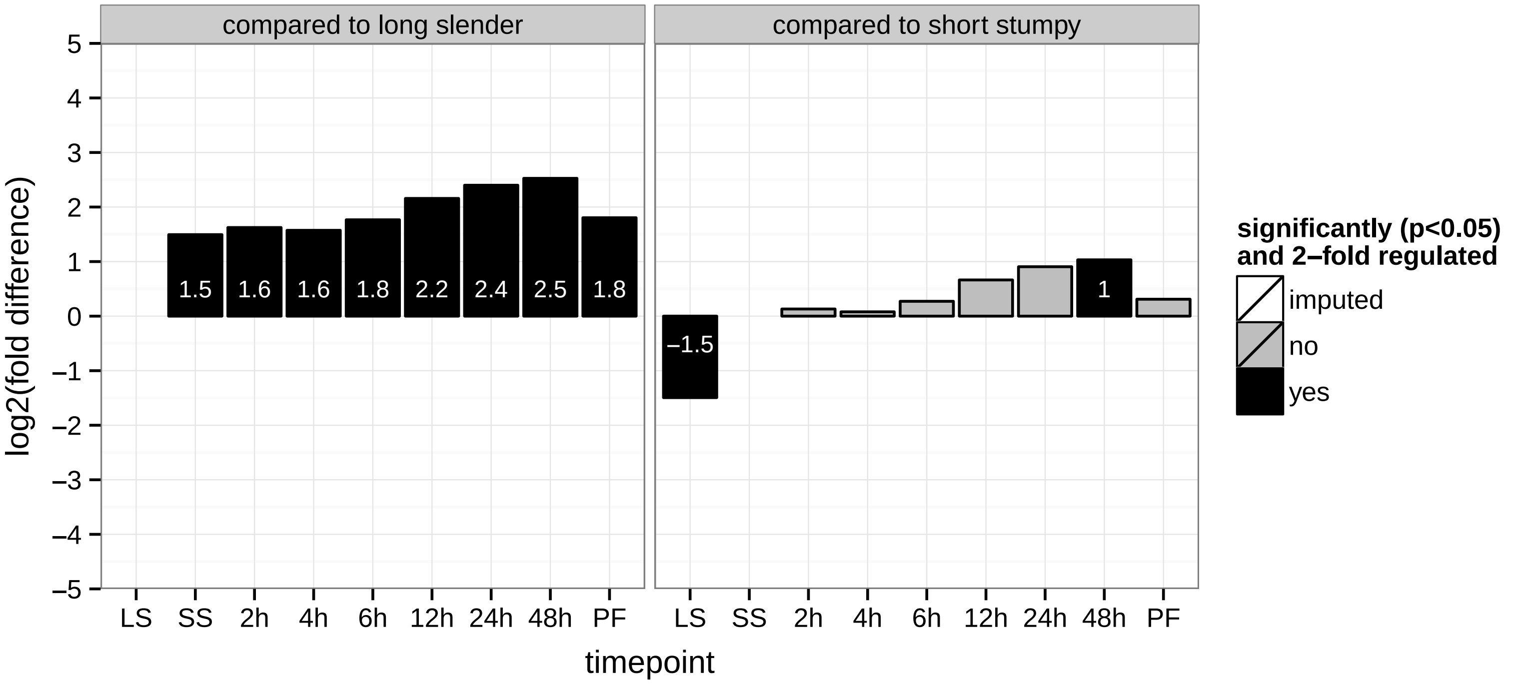
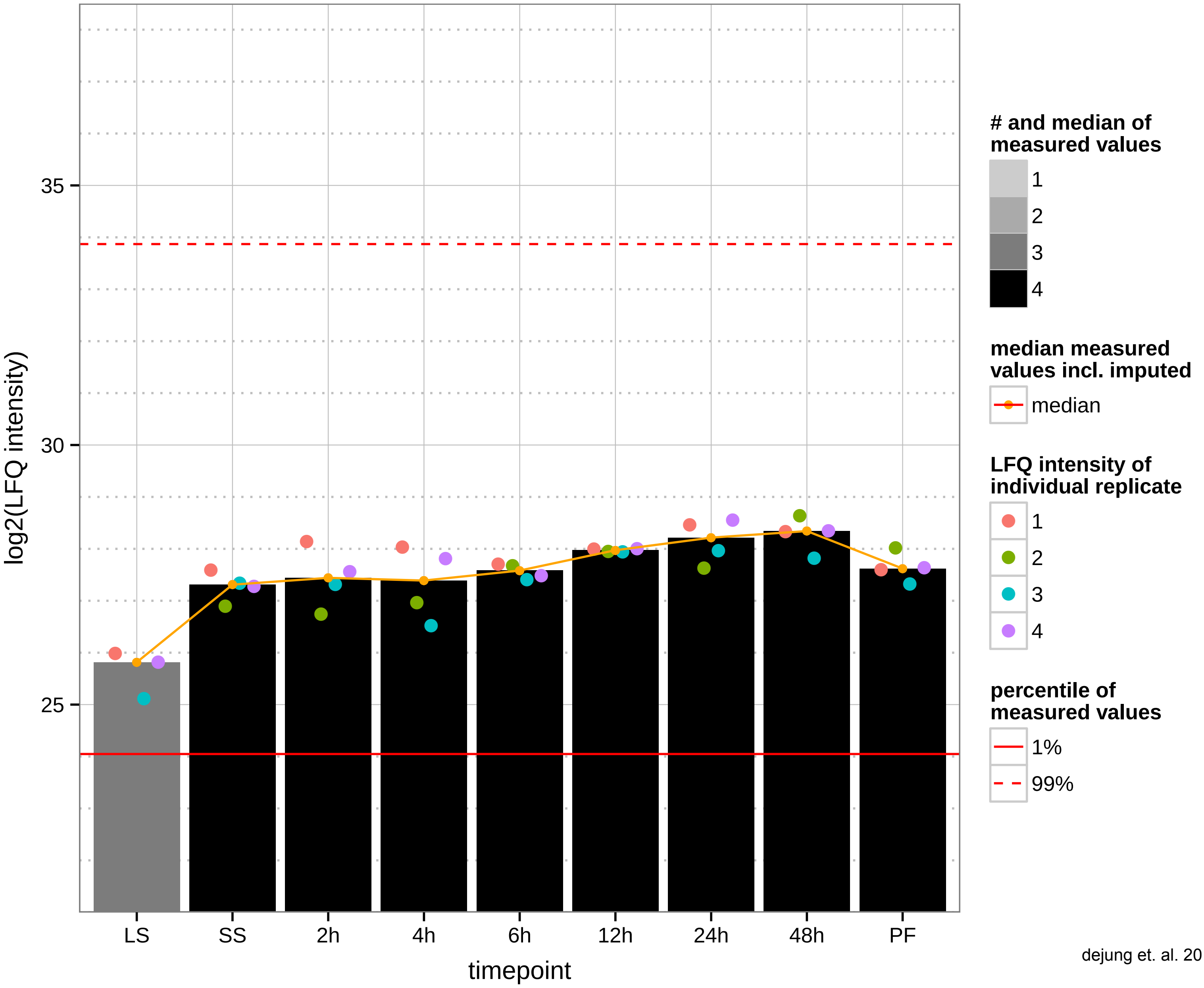
periodic tryptophan protein 2, putative, Periodic tryptophan protein 2 homolog
Tb927.10.13270;Tb11.v5.0563
AGOF: null, snoRNA binding
AGOC: null, Pwp2p–containing subcomplex of 90S preribosome, small–subunit processome
AGOP: null, cytokinesis, completion of separation
PGOF: protein binding
PGOC: null
PGOP: null





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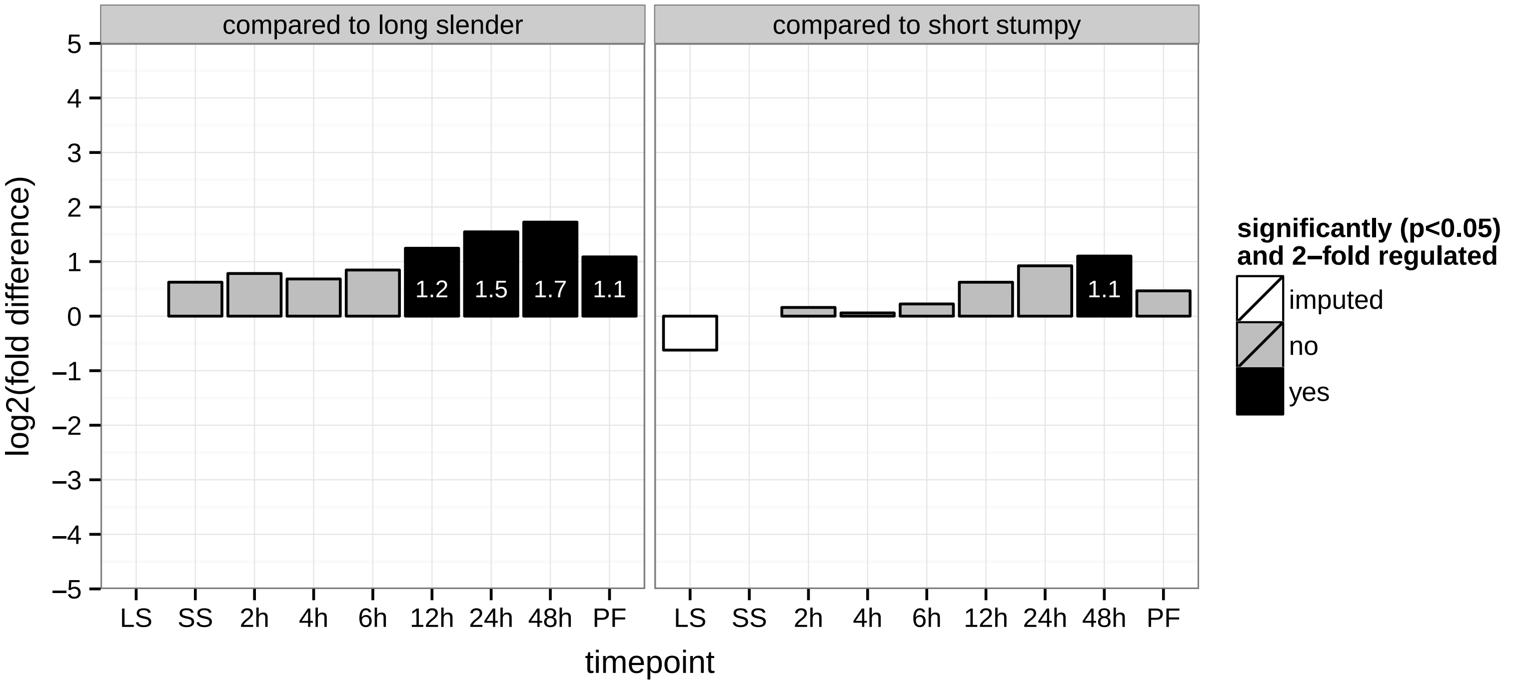
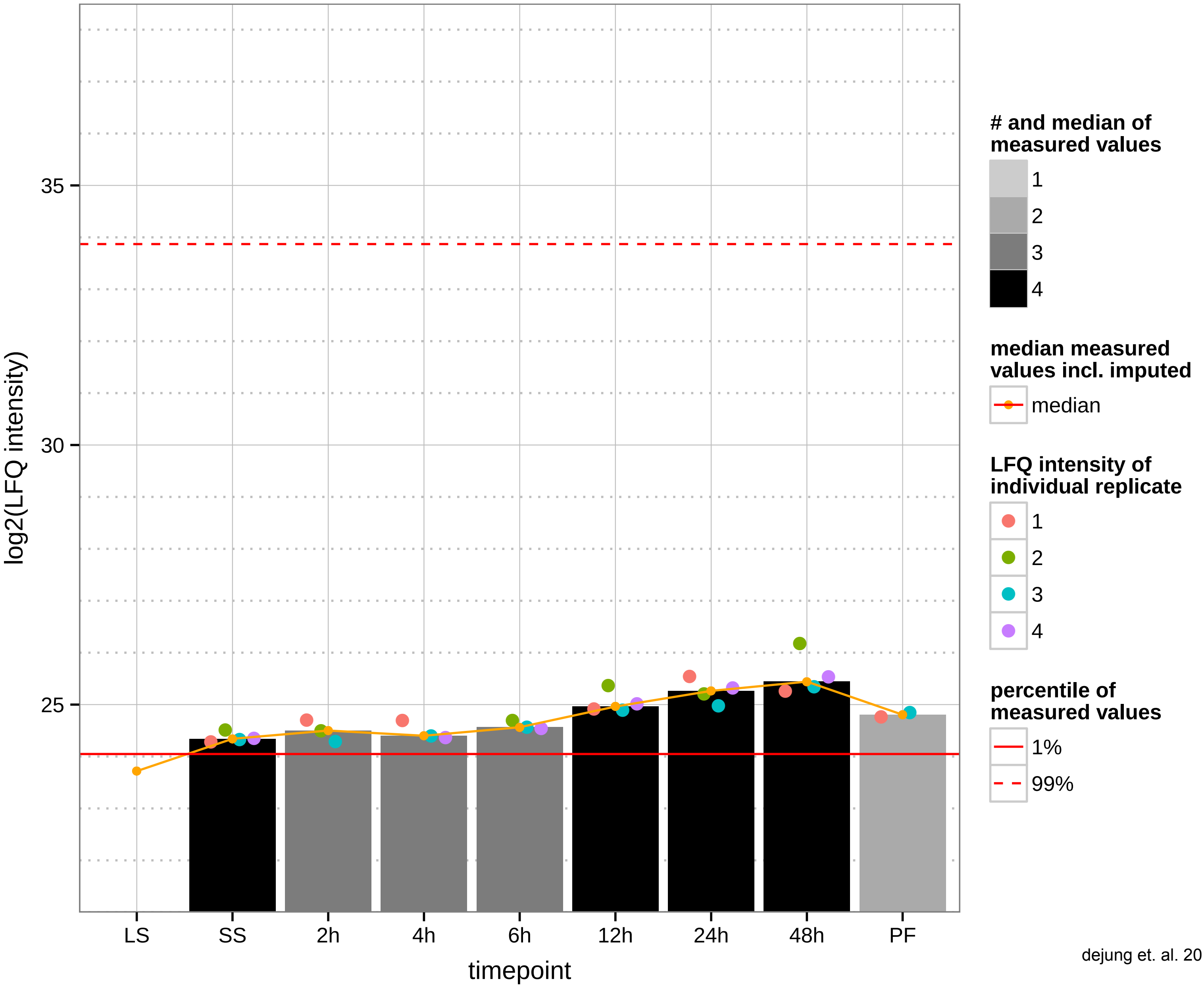
hypothetical protein, conserved, NADH−ubiquinone oxidoreductase complex I subunit, putative, NDUFA9 subunit
Tb927.9.15380;Tb11.v5.0686
AGOF: null, catalytic activity
AGOC: null, mitochondrion, respiratory chain complex I
AGOP: null, metabolic process
PGOF: null
PGOC: null
PGOP: null





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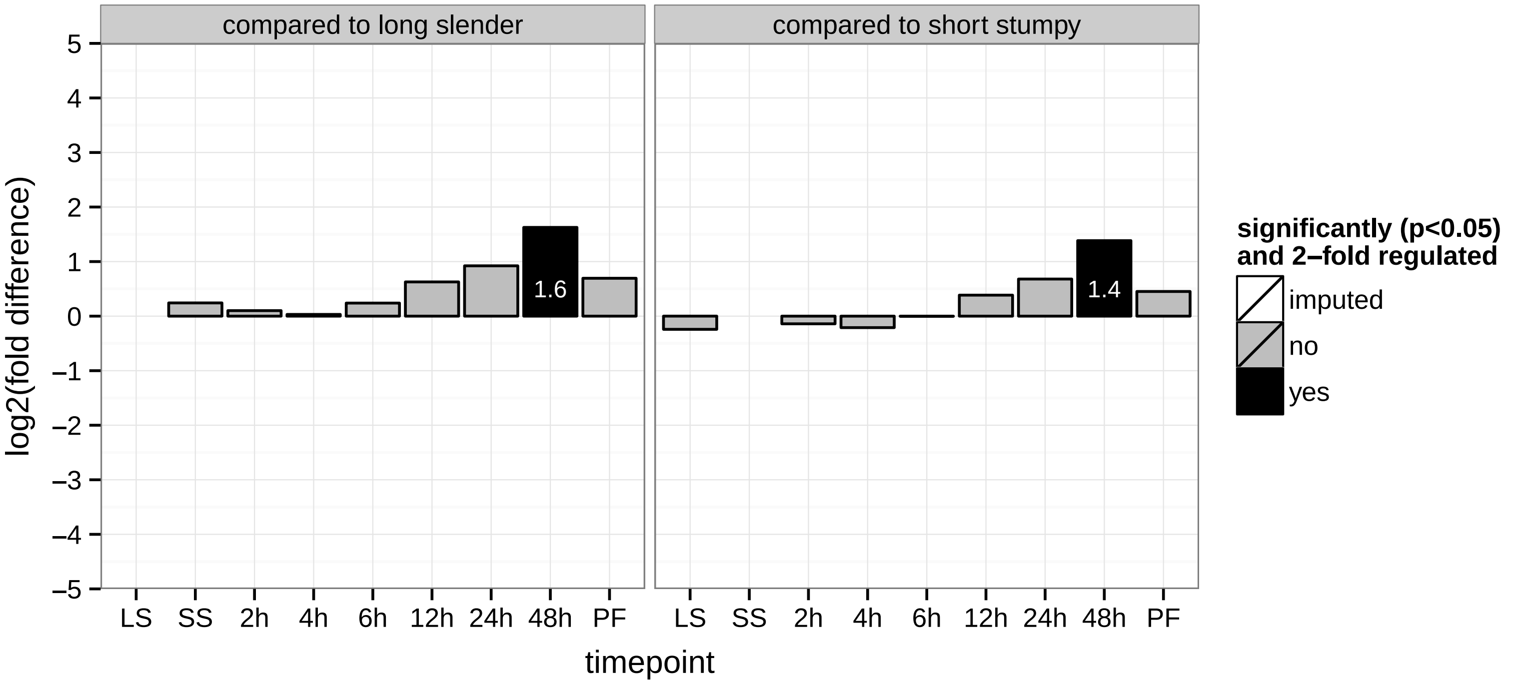
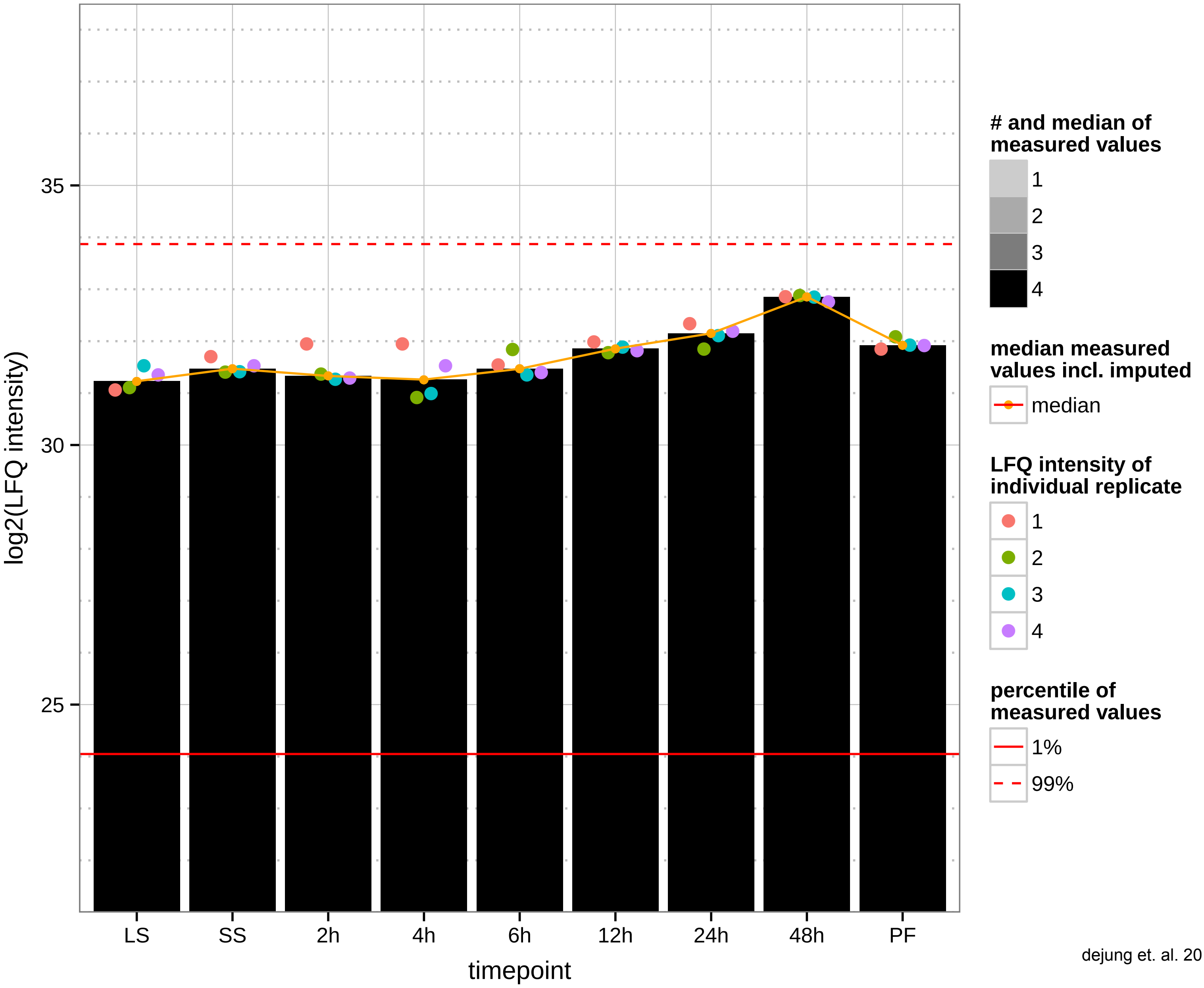
retrotransposon hot spot (RHS) protein, putative
Tb11.v5.0713
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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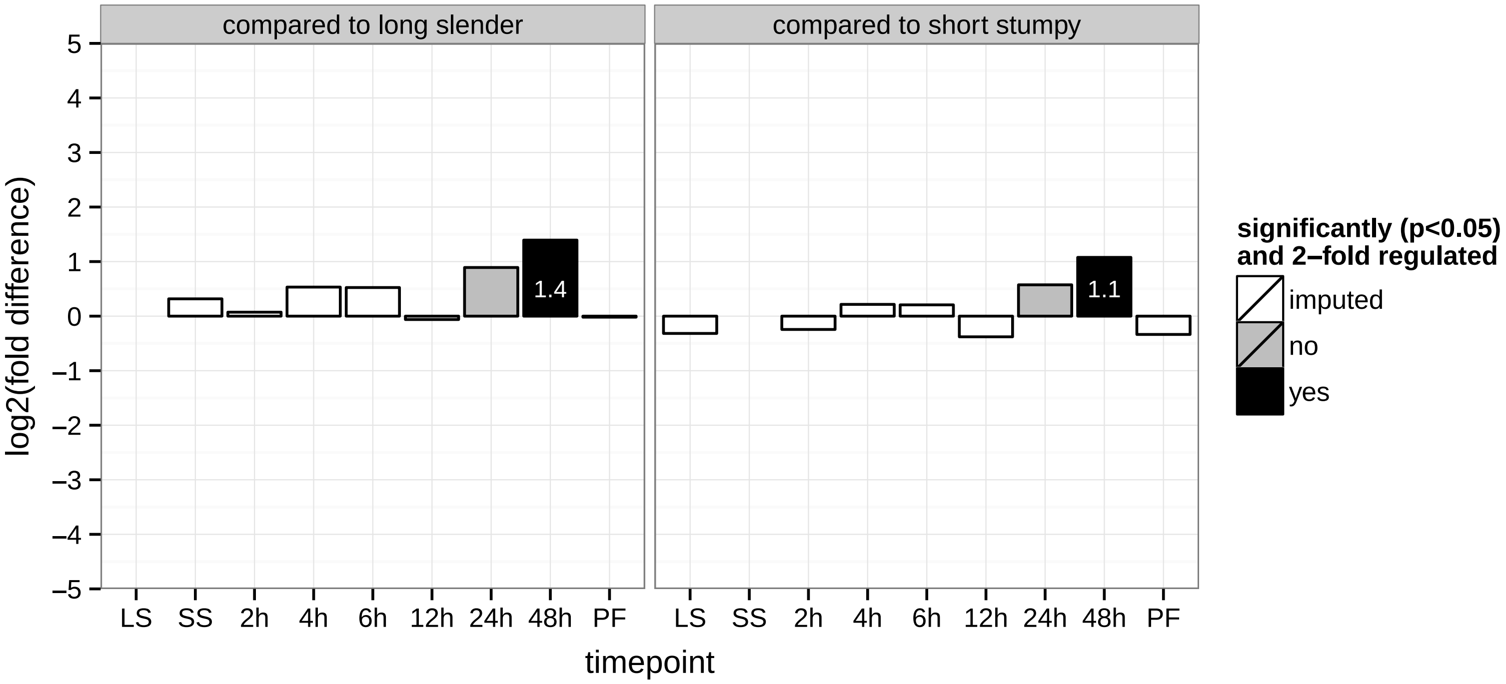
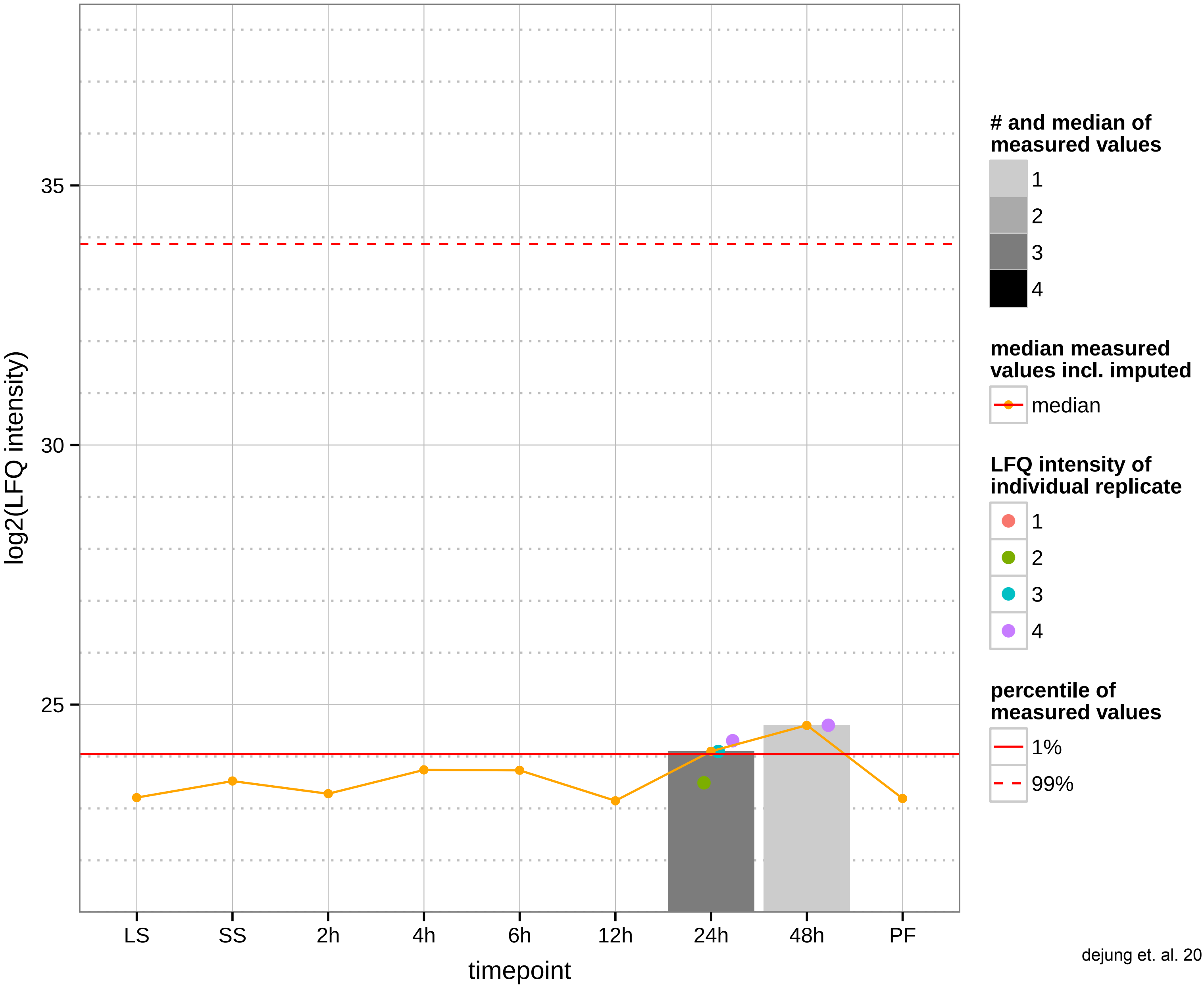
hypothetical protein, conserved, ATP dependent DEAD−box helicase (RH)
Tb11.v5.0842;Tb927.4.2720
AGOF: null, ATP binding, helicase activity, nucleic acid binding, ribosome binding
AGOC: null, mitochondrial ribosome, mitochondrion
AGOP: null
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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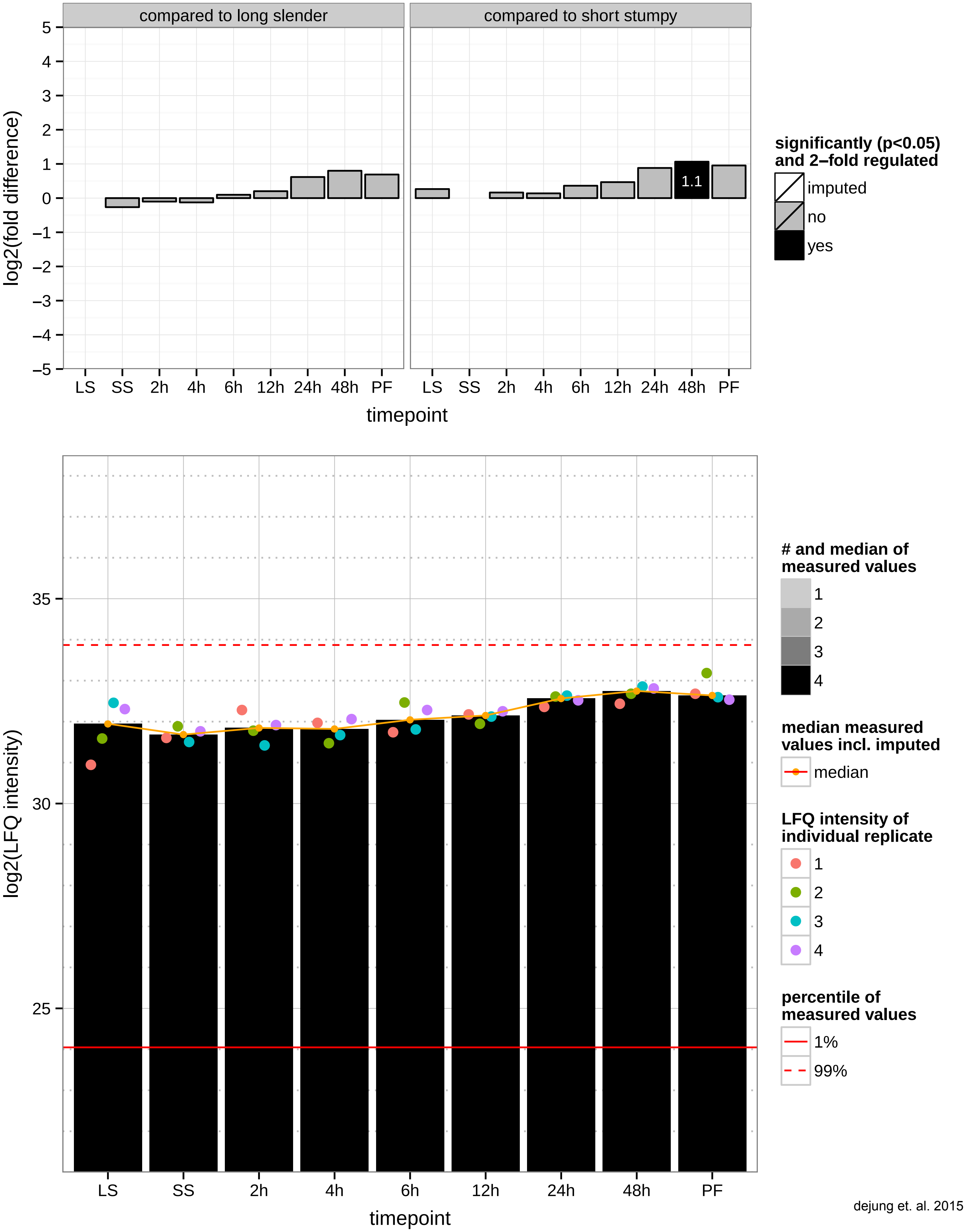
40S ribosomal protein S11, putative
Tb927.1.3180
AGOF: null
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation



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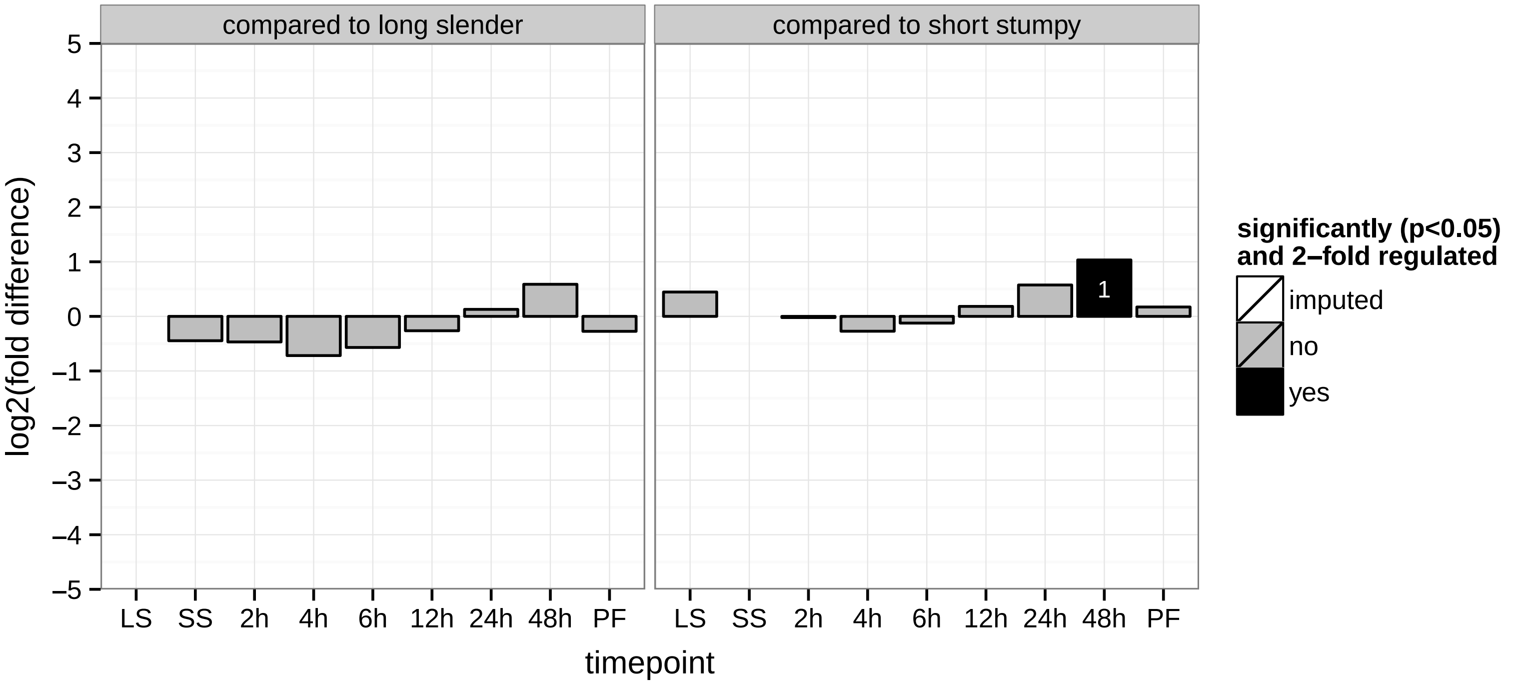
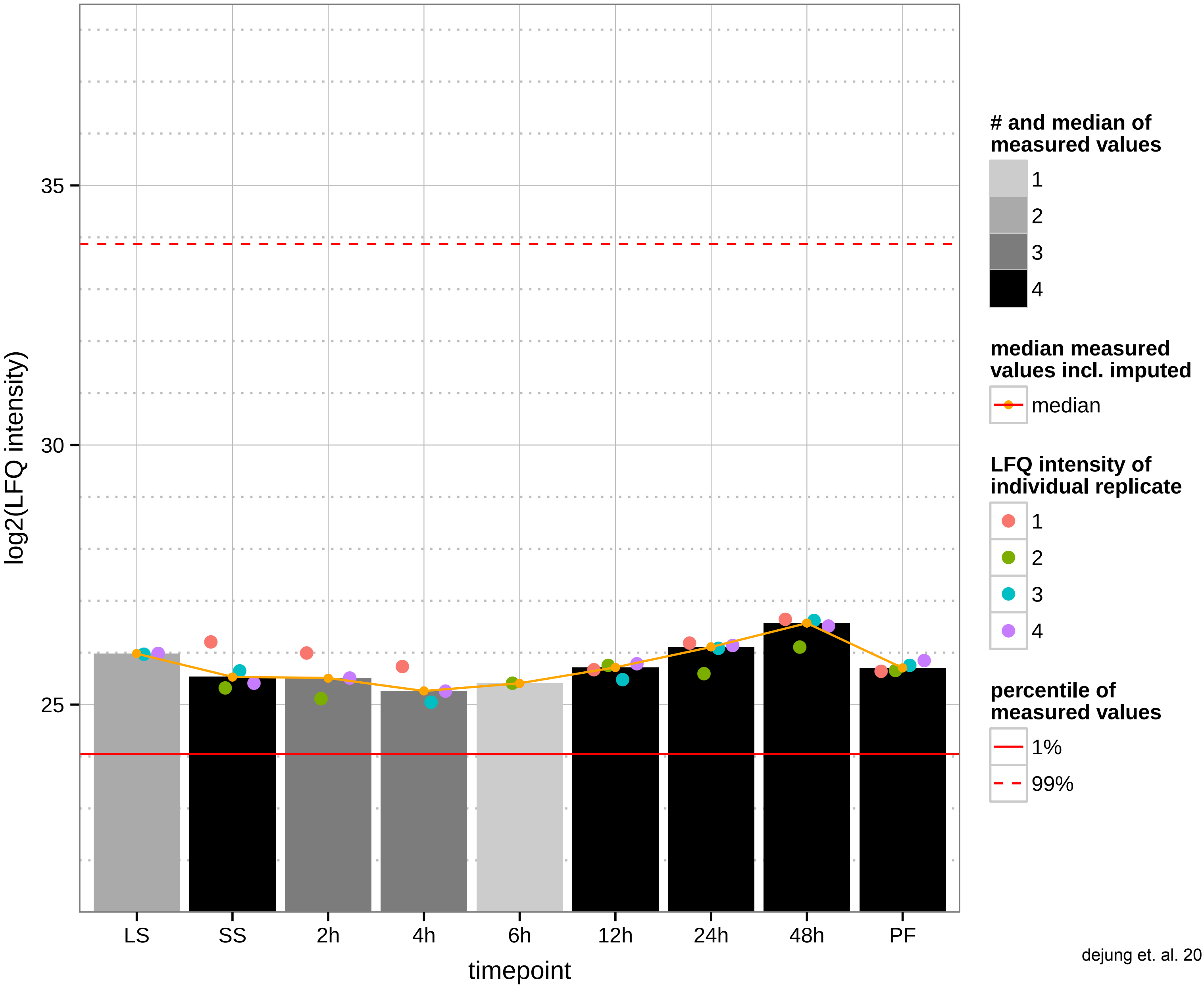
hypothetical protein, conserved
Tb927.1.3910
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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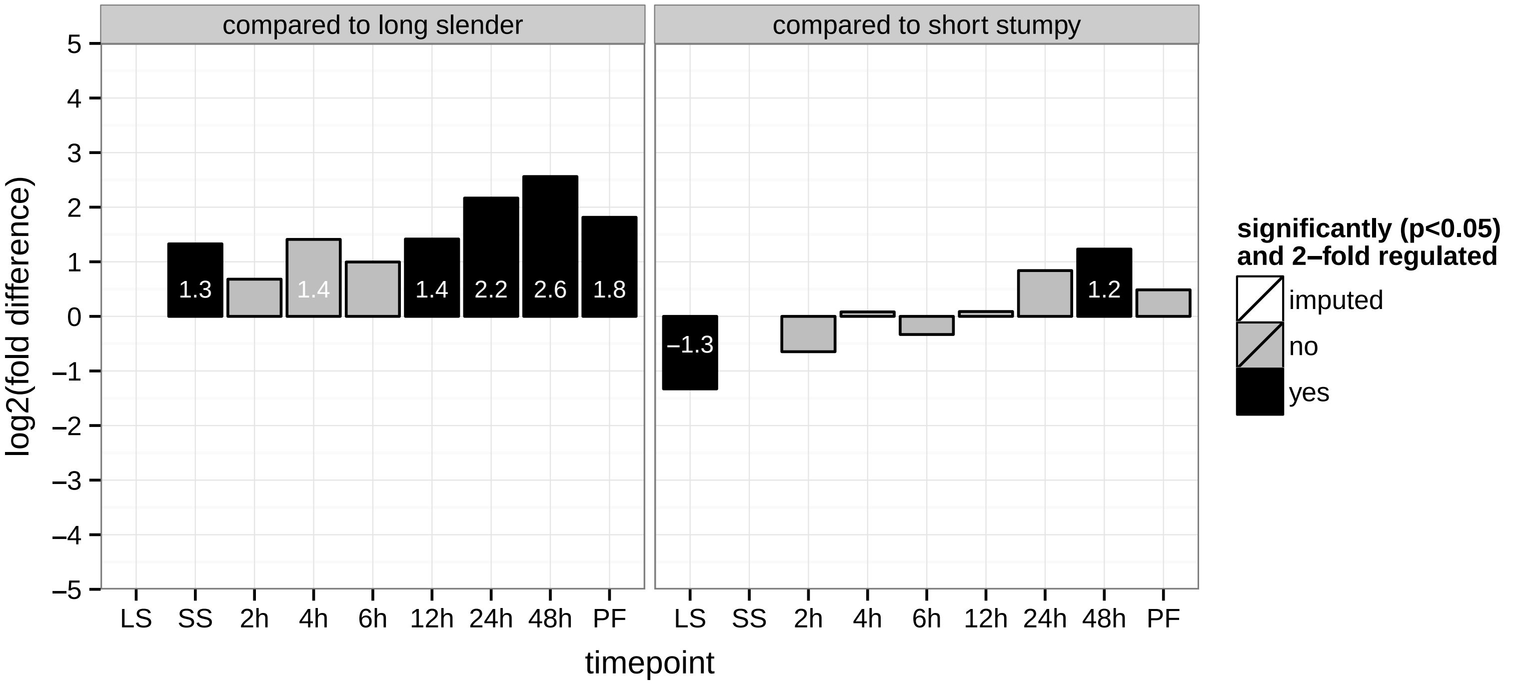
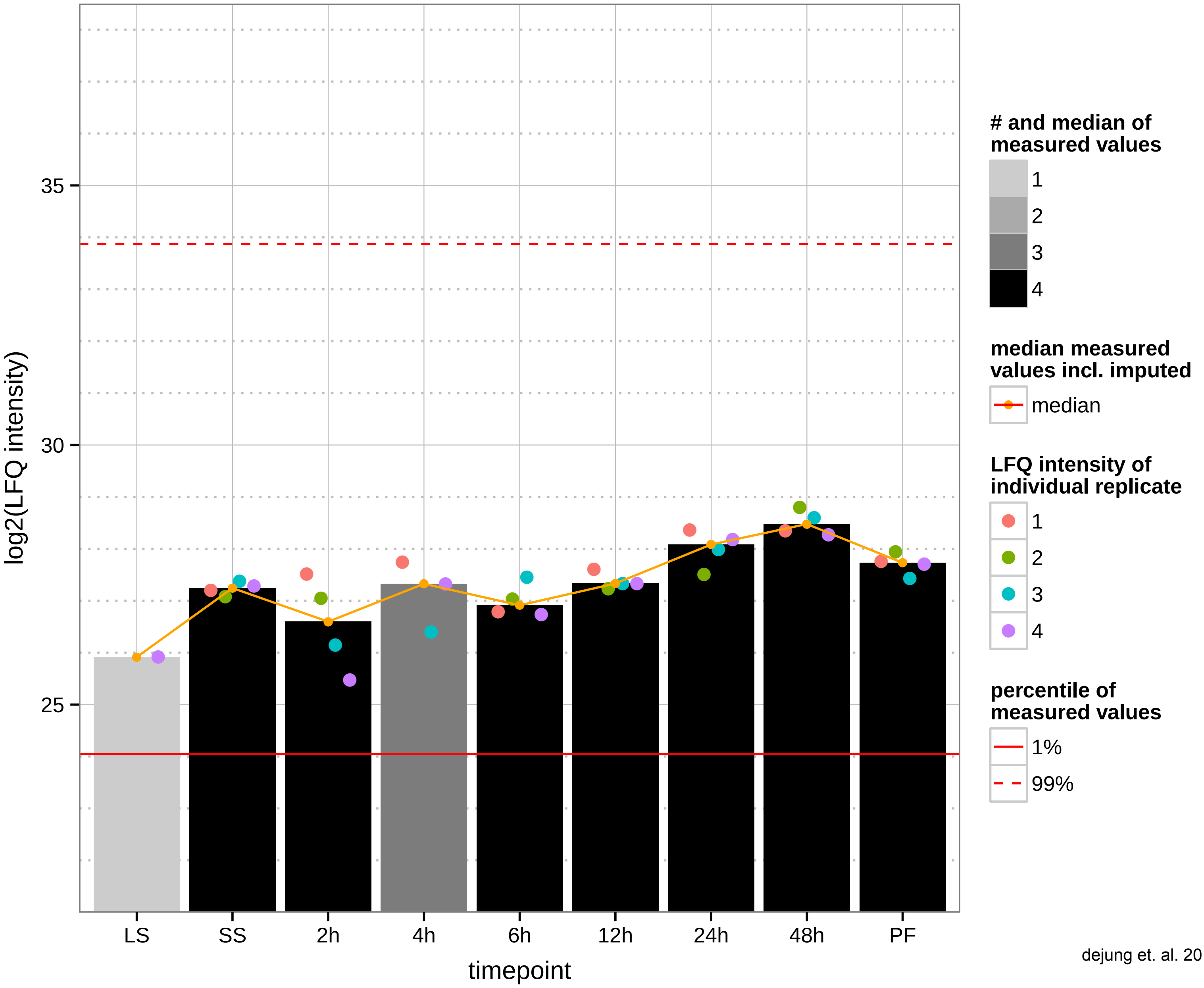
ABC transporter, putative
Tb927.1.4420
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances
AGOC: ATP−binding cassette (ABC) transporter complex
AGOP: transport
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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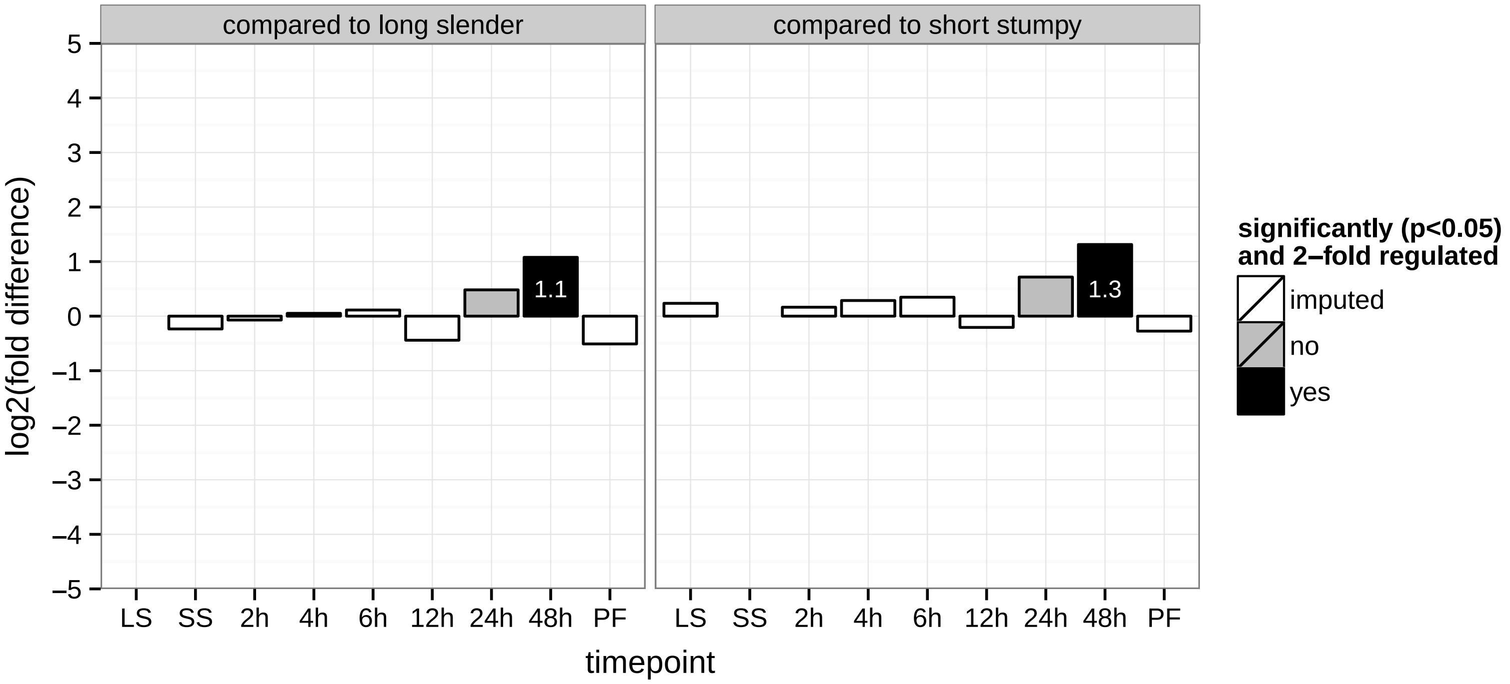
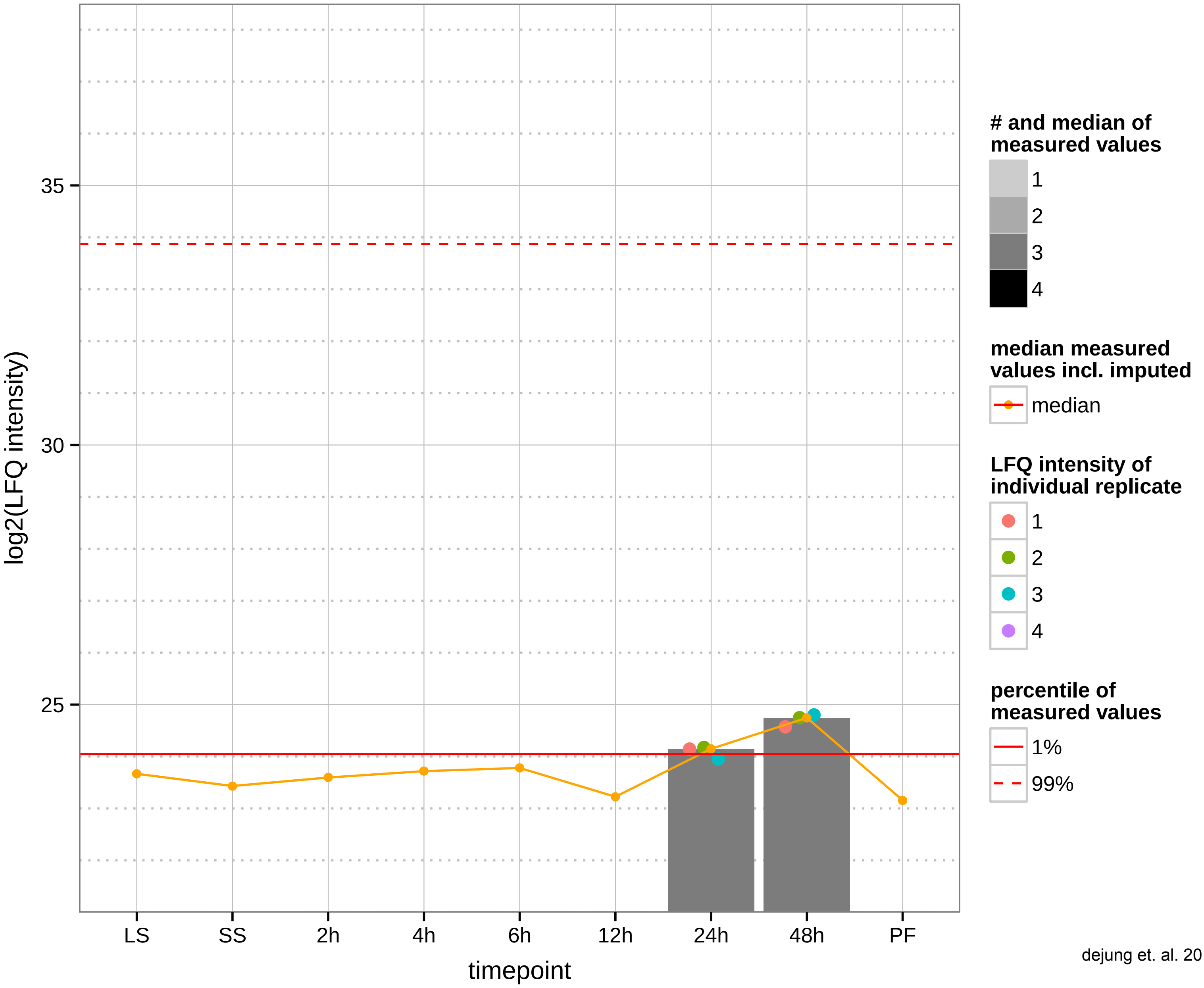
hypothetical protein, conserved
Tb927.1.4480
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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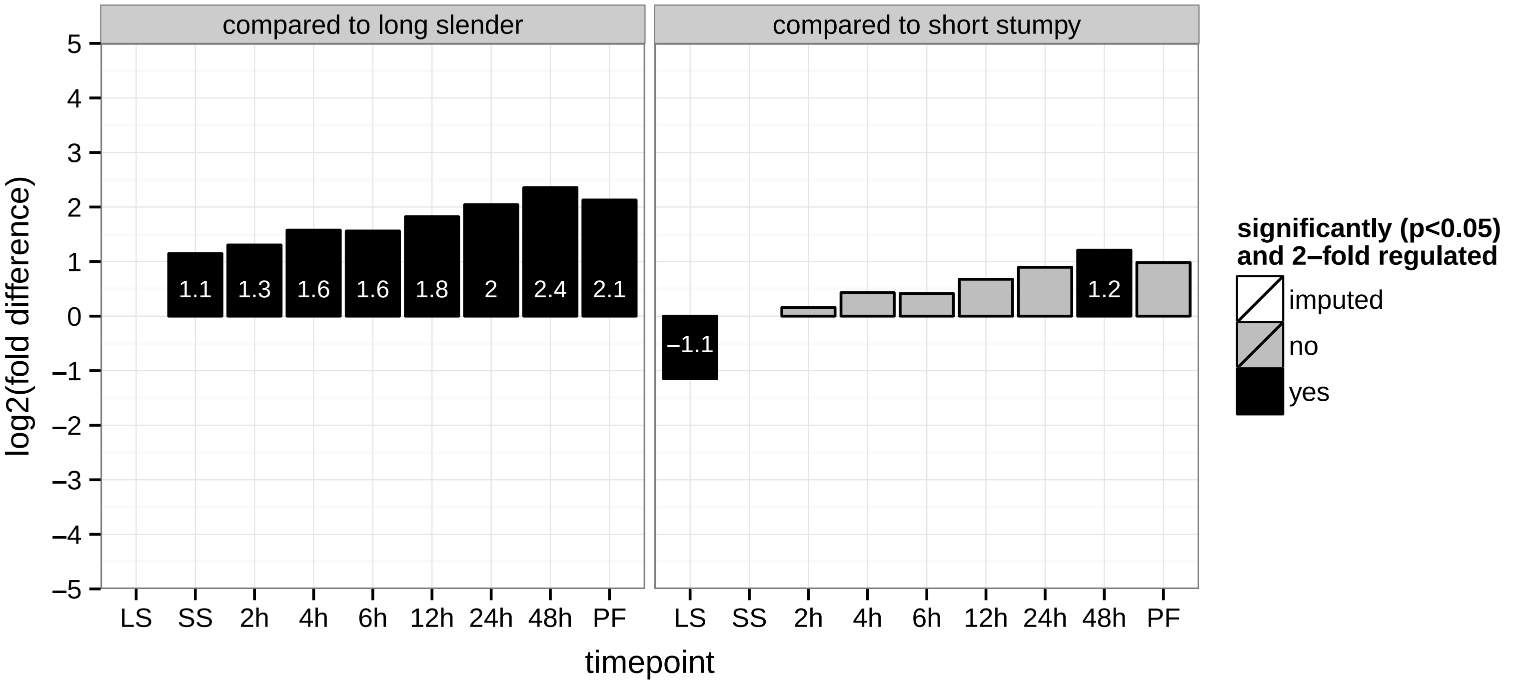
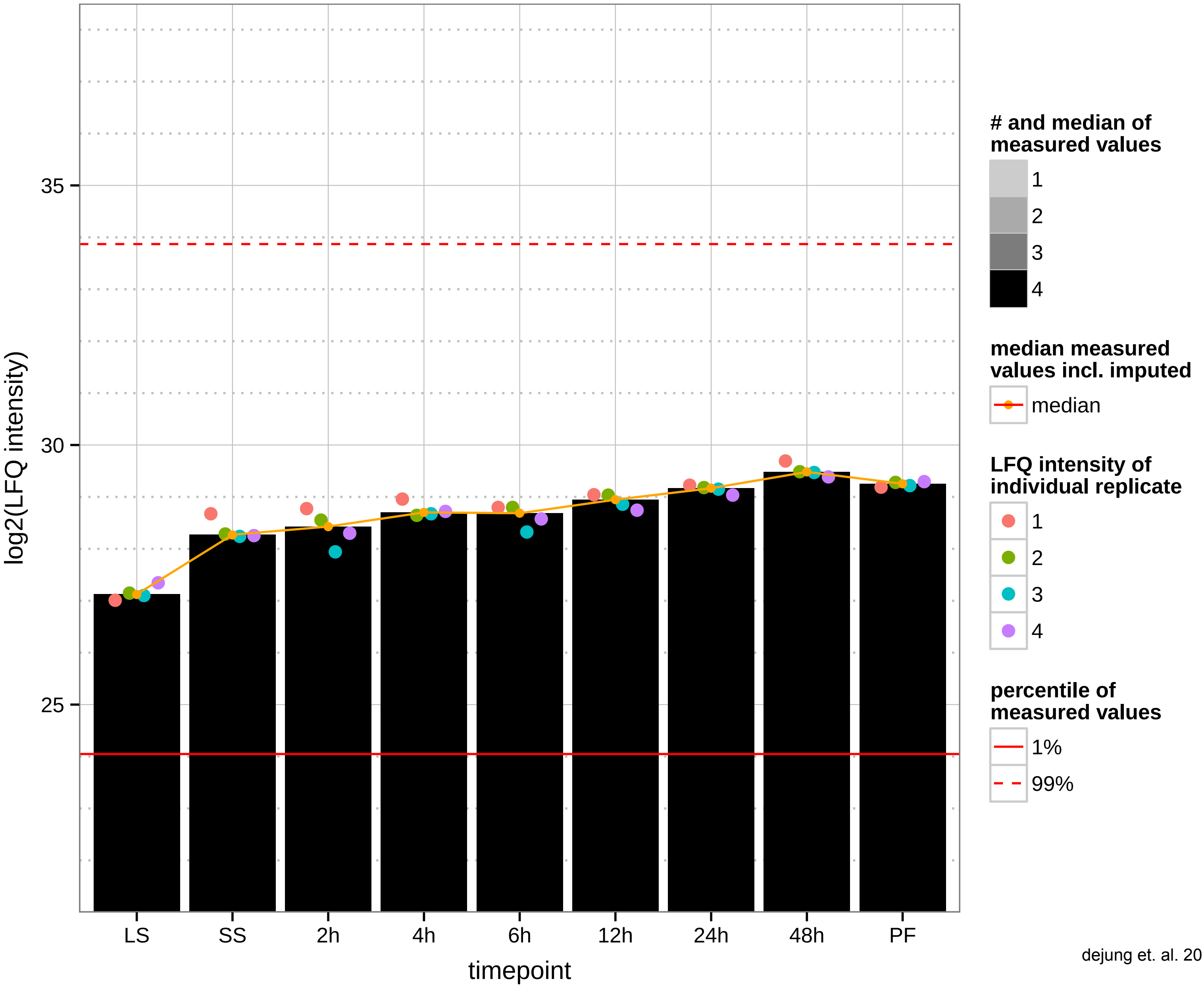
arginine N−methyltransferase (PRMT1)
Tb927.1.4690
AGOF: arginine N−methyltransferase activity, protein−arginine N−methyltransferase activity
AGOC: null
AGOP: peptidyl−arginine methylation, to asymmetrical−dimethyl arginine, protein methylation
PGOF: null
PGOC: null
PGOP: null





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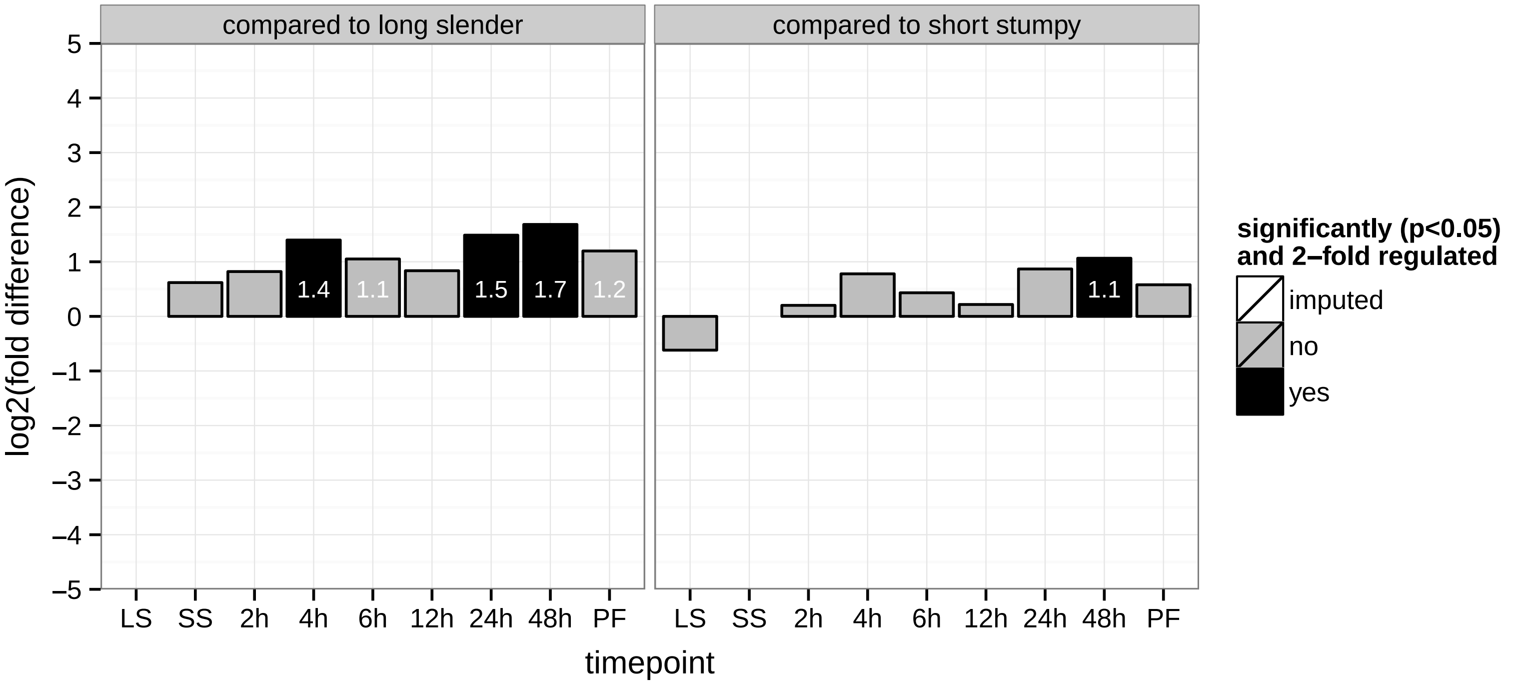
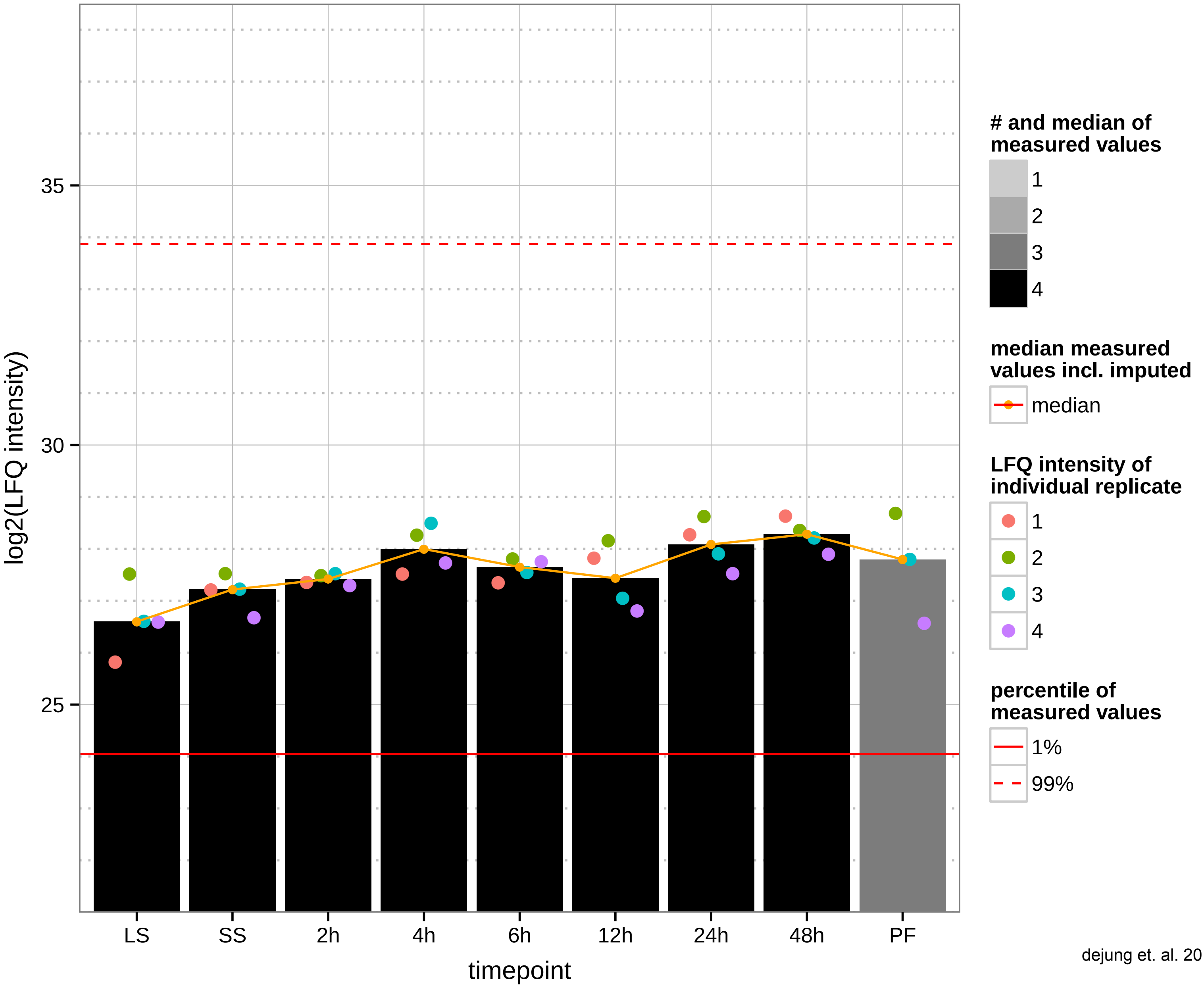
hypothetical protein, conserved
Tb927.1.5000
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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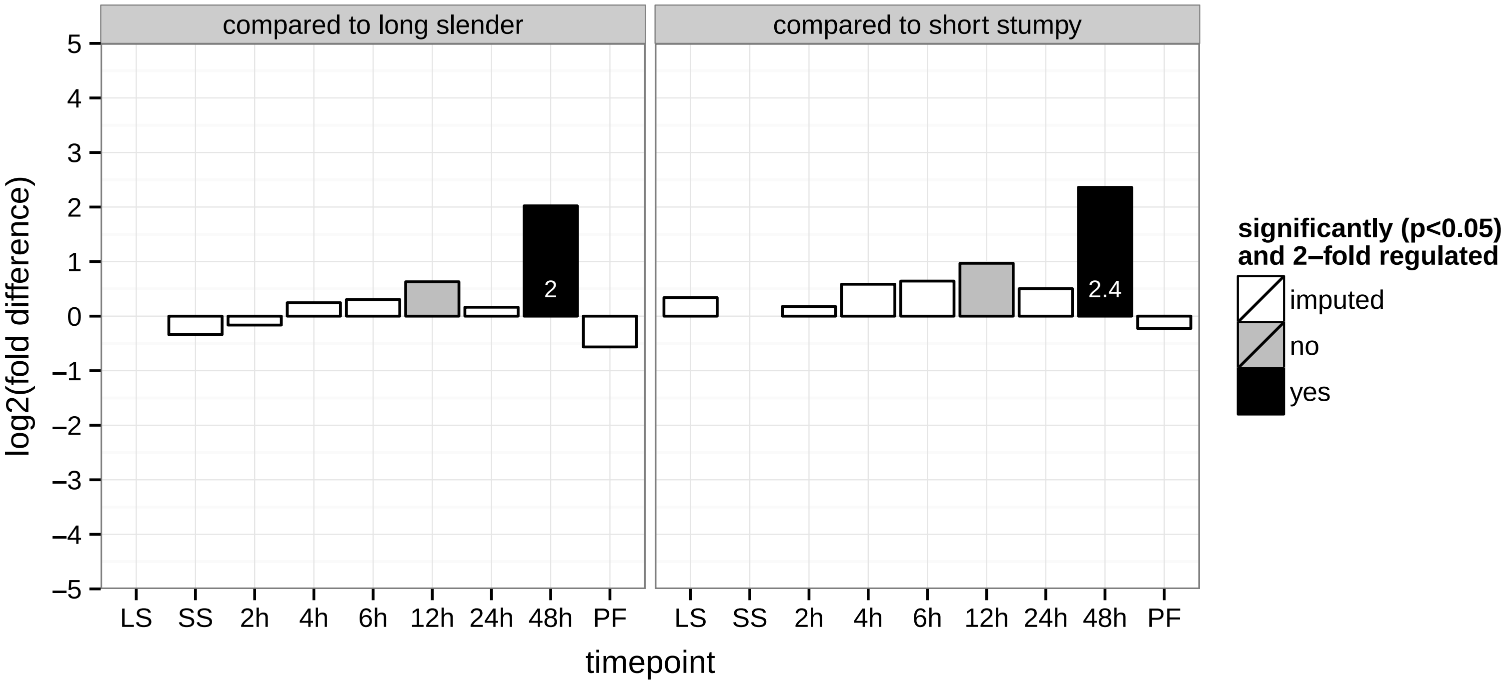
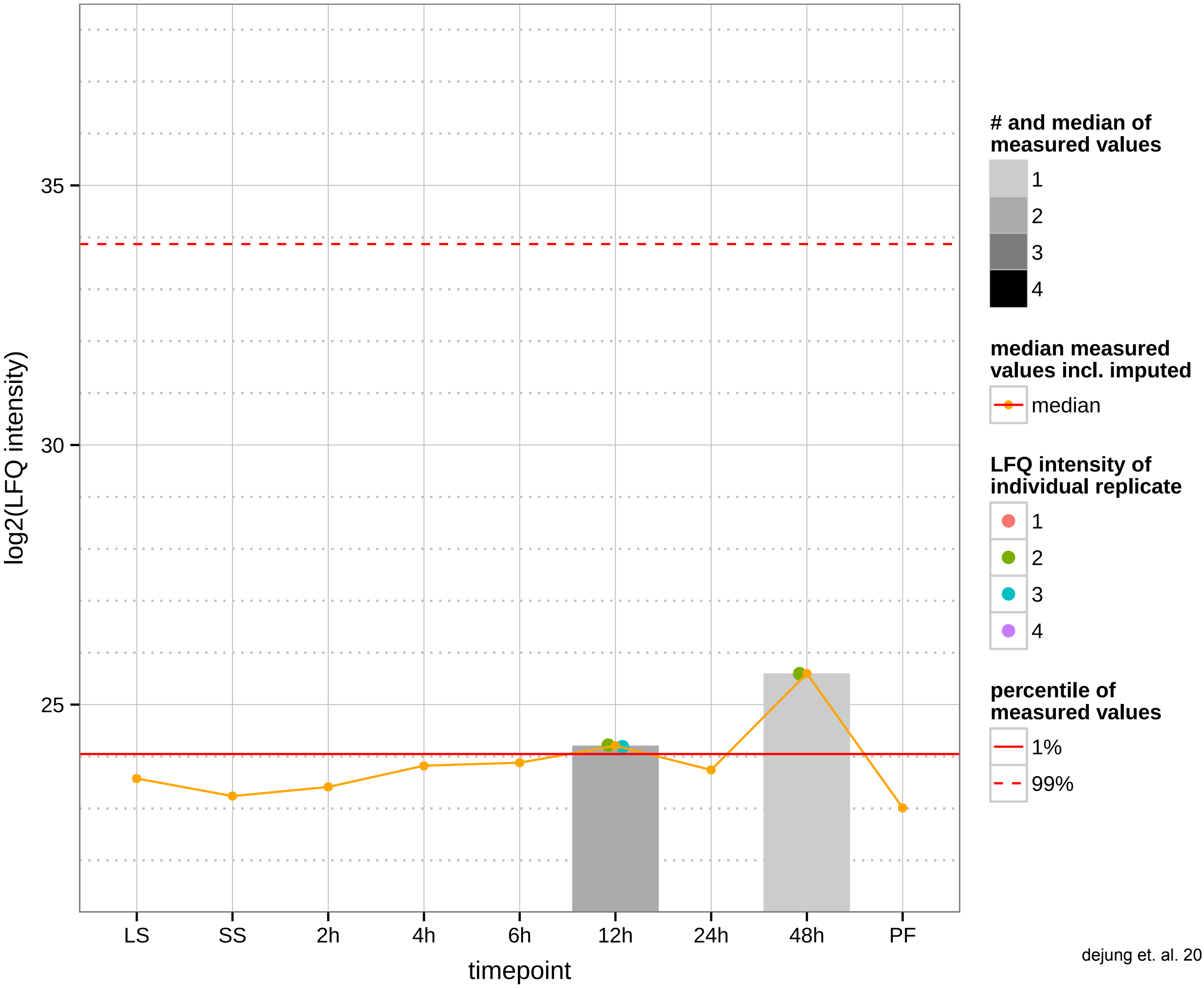
phosphate–repressible phosphate permease, putative
Tb927.1.600
AGOF: inorganic phosphate transmembrane transporter activity, phosphate ion transmembrane transporter activity
AGOC: membrane
AGOP: null
PGOF: inorganic phosphate transmembrane transporter activity
PGOC: membrane
PGOP: phosphate ion transport





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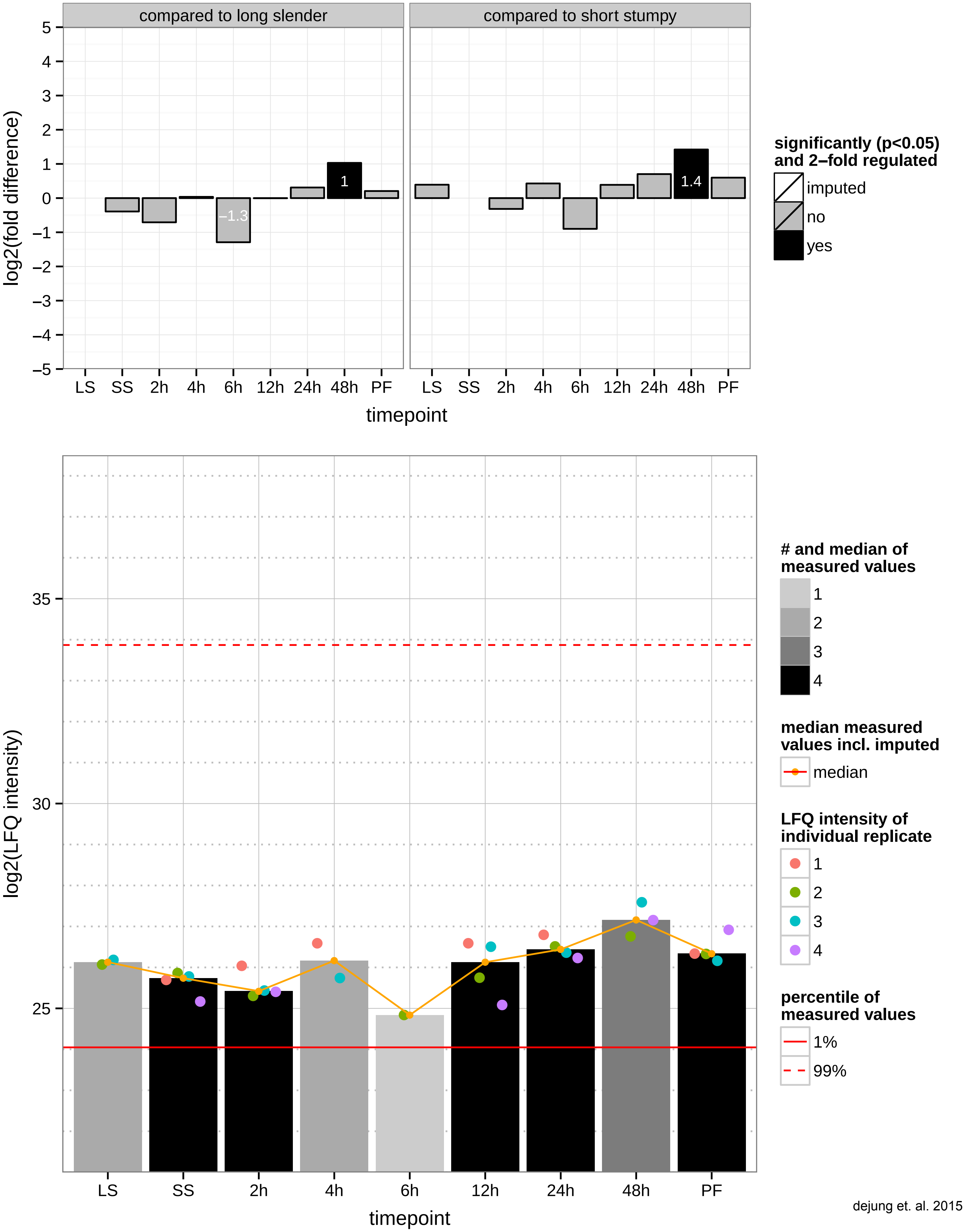
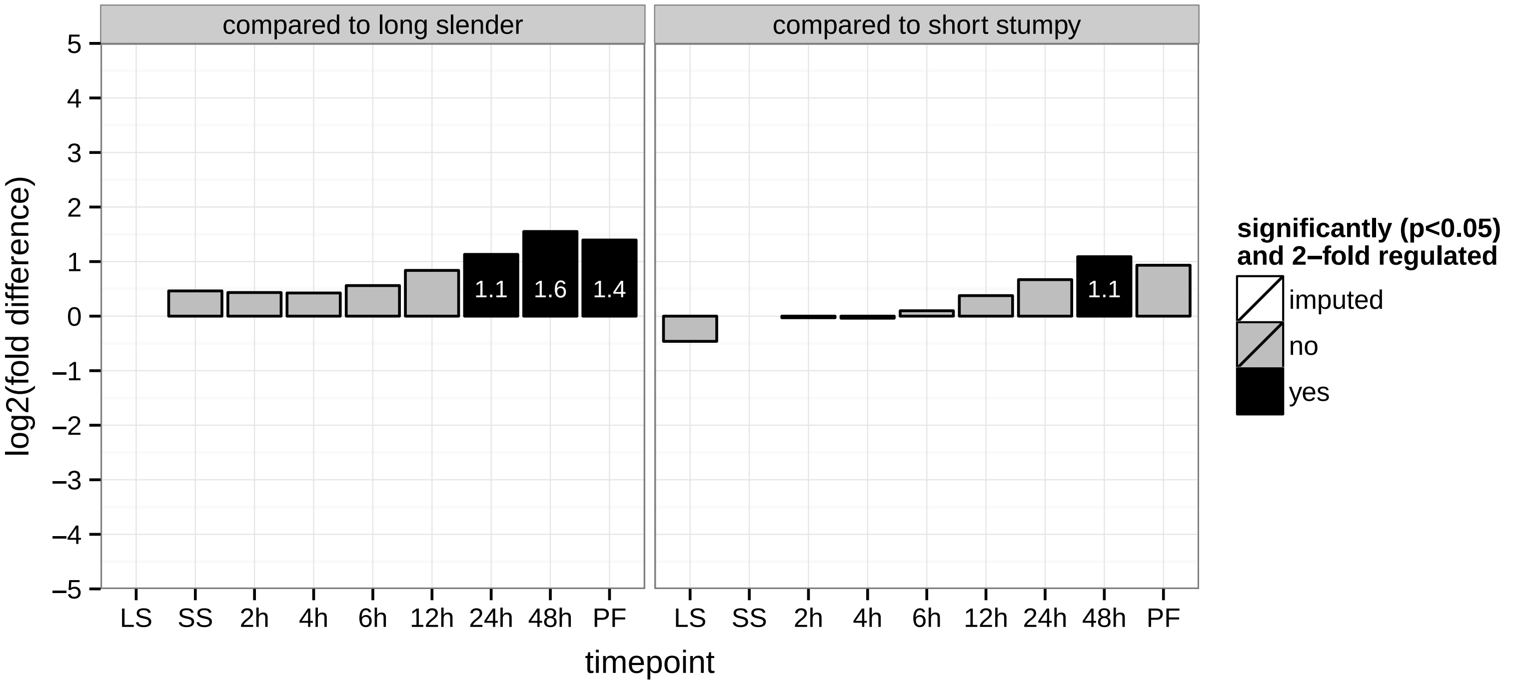
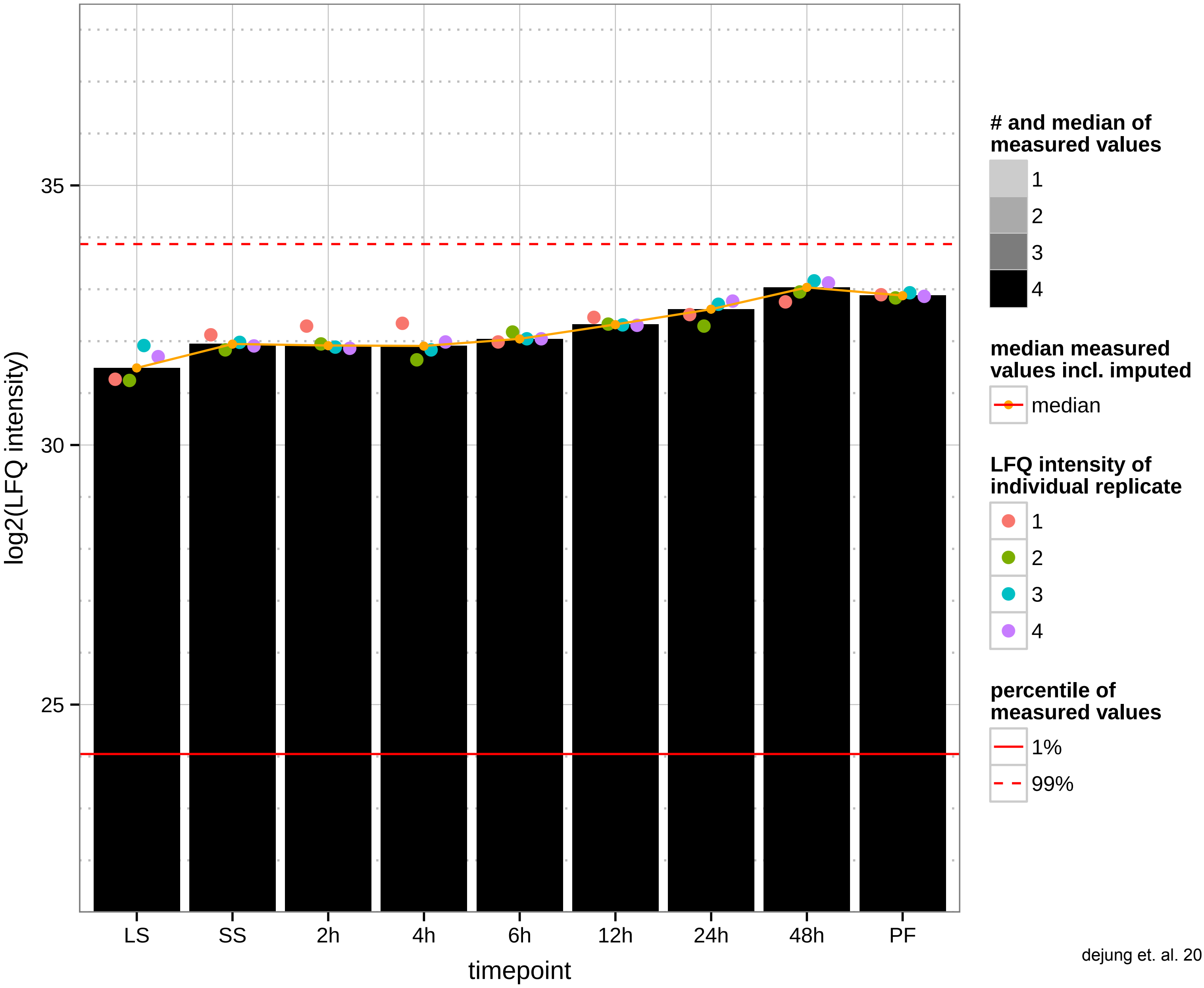
Metal–binding domain–containing protein
Tb927.1.750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



T–complex protein 1, delta subunit, putative (TCP–1–delta)
Tb927.10.1060
AGOF: ATP binding, unfolded protein binding
AGOC: chaperonin–containing T–complex
AGOP: protein folding, regulation of cell cycle
PGOF: ATP binding, unfolded protein binding
PGOC: null
PGOP: cellular protein metabolic process, protein folding





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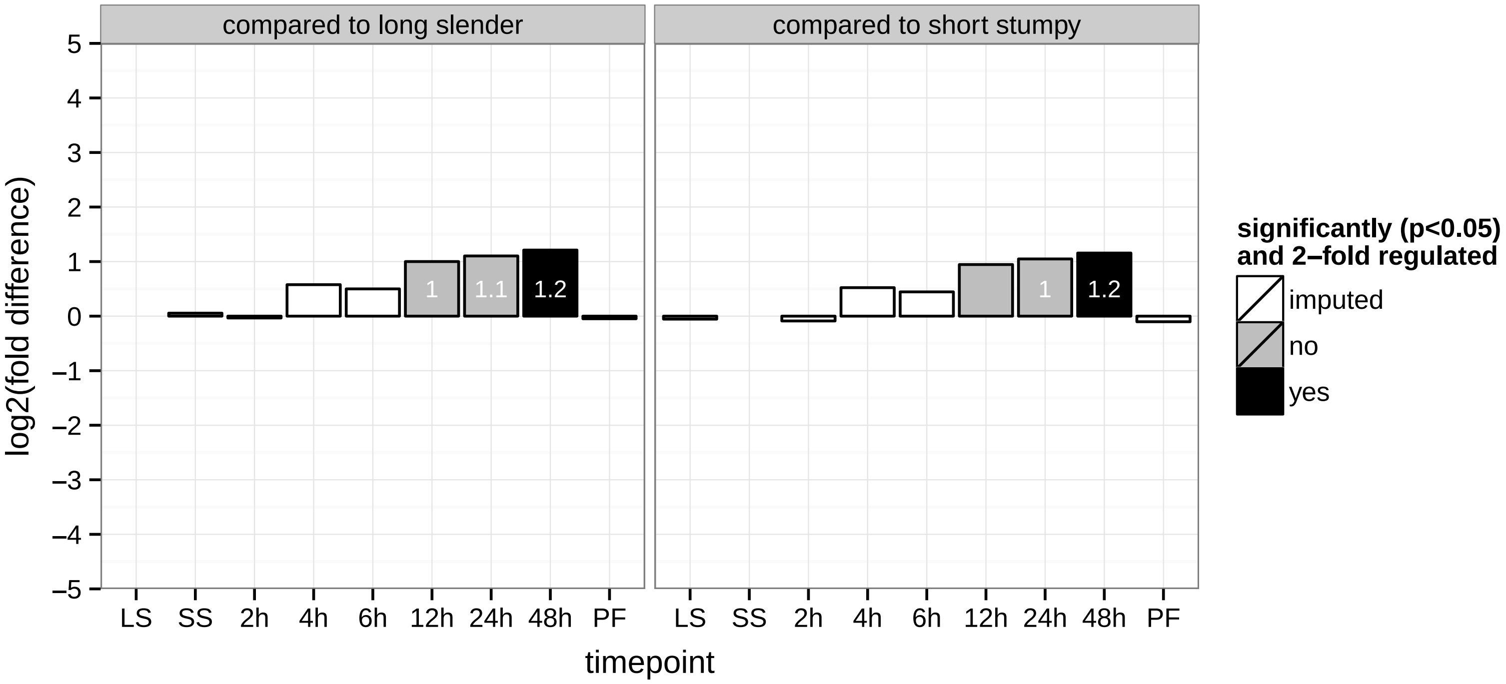
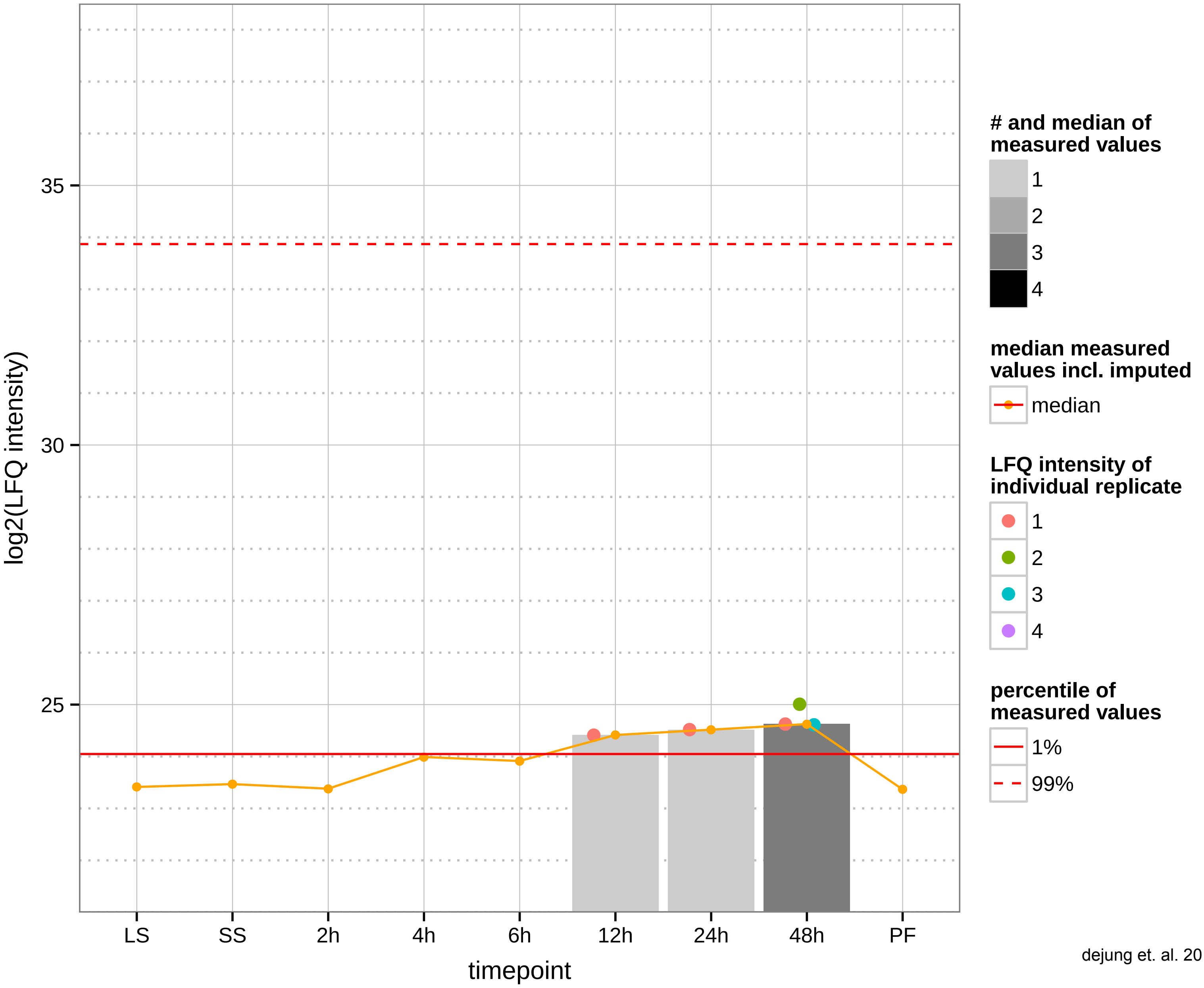
hypothetical protein, conserved
Tb927.10.11050
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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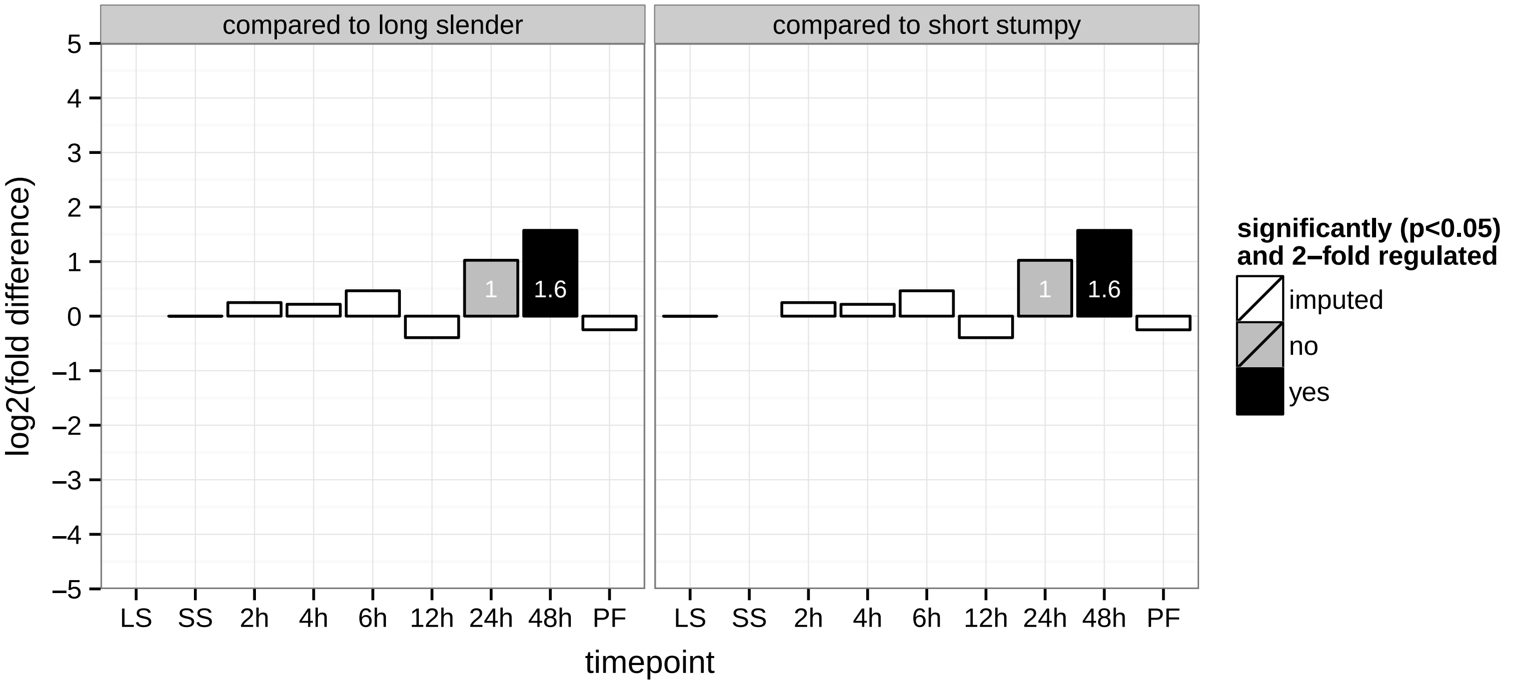
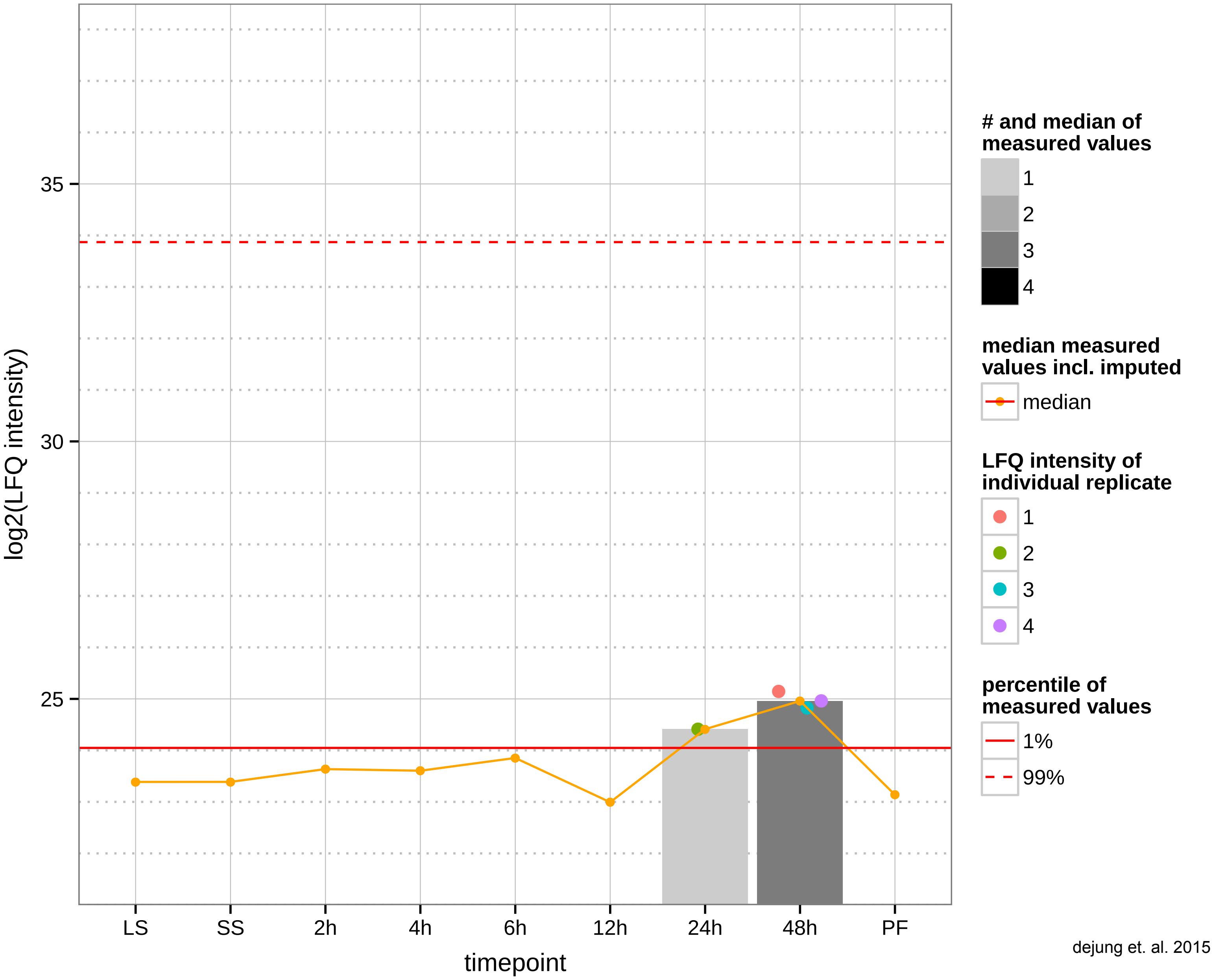
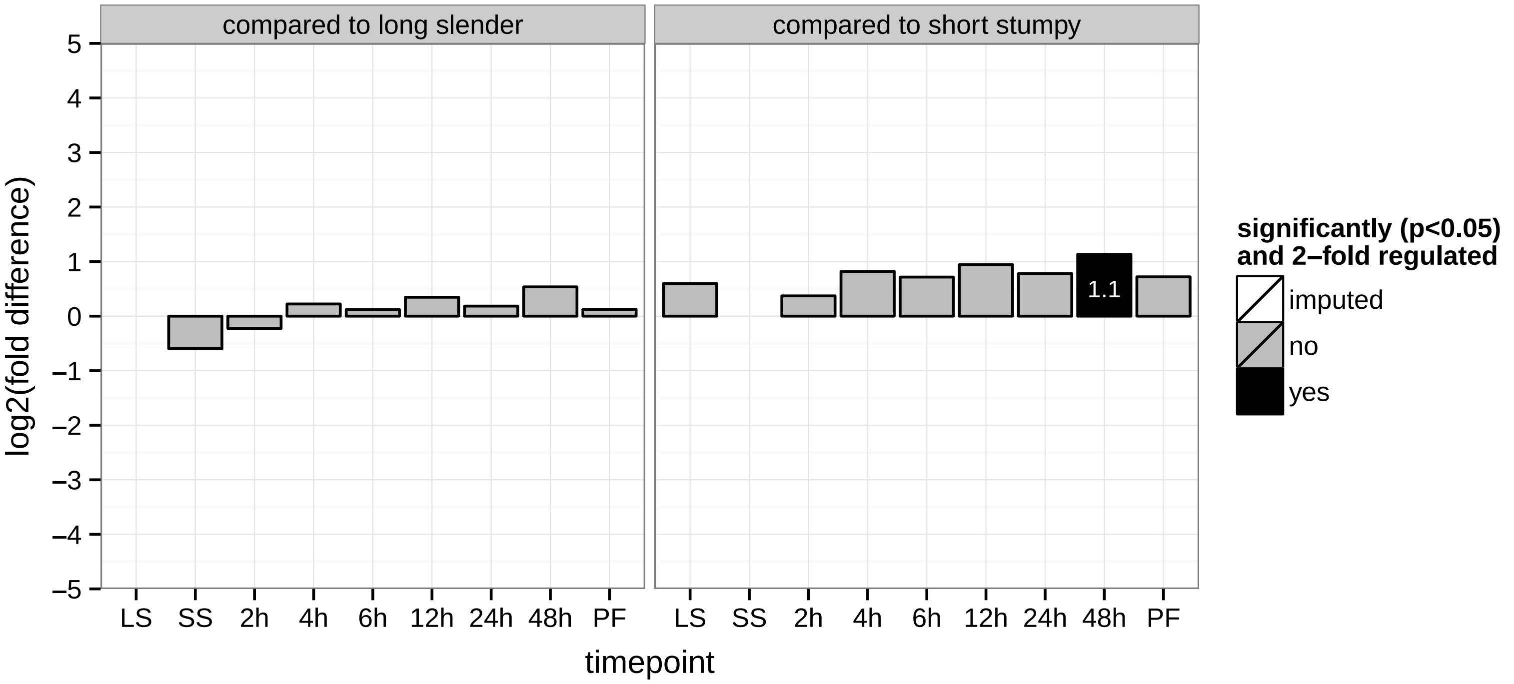
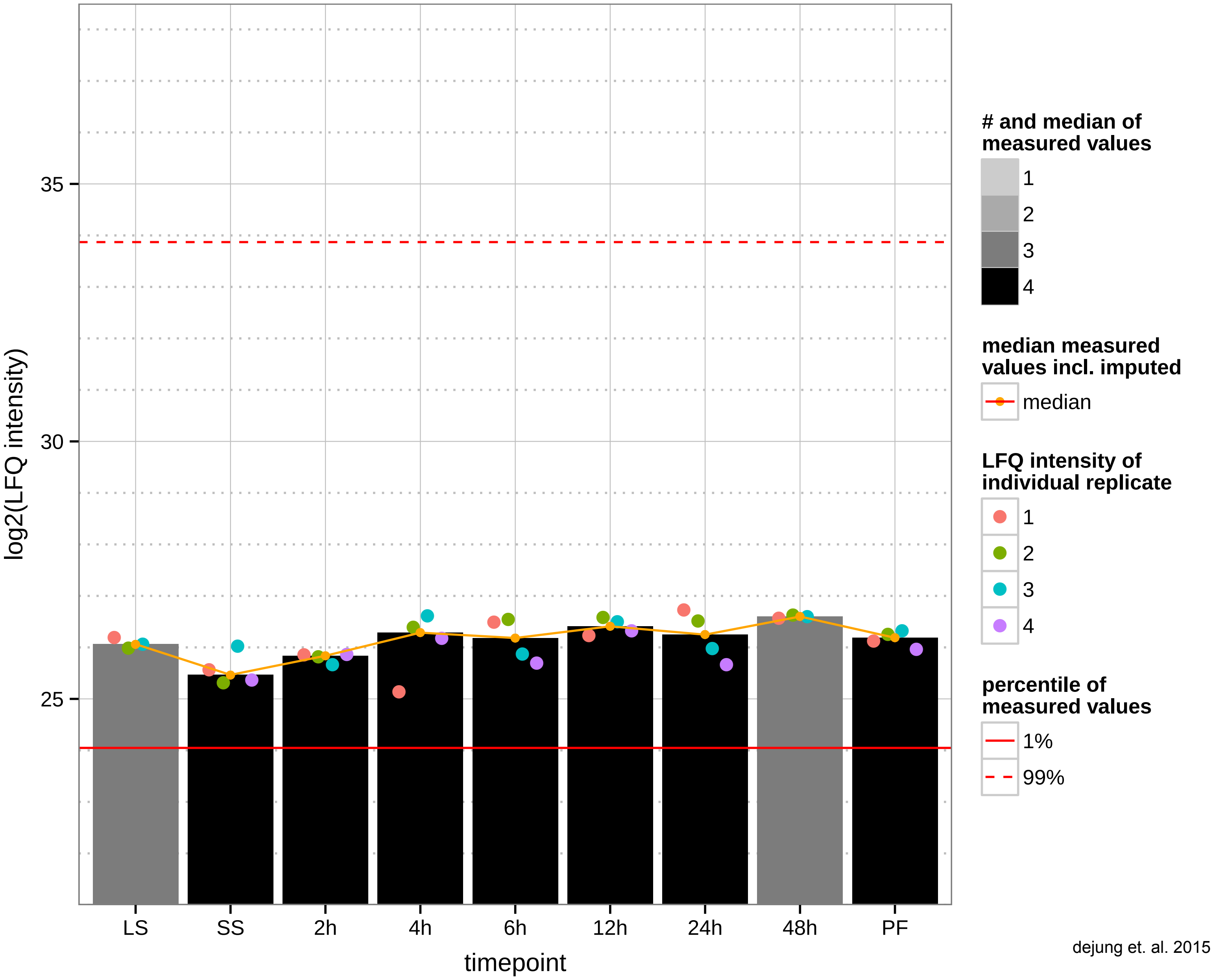
hypothetical protein, conserved
Tb927.10.11120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





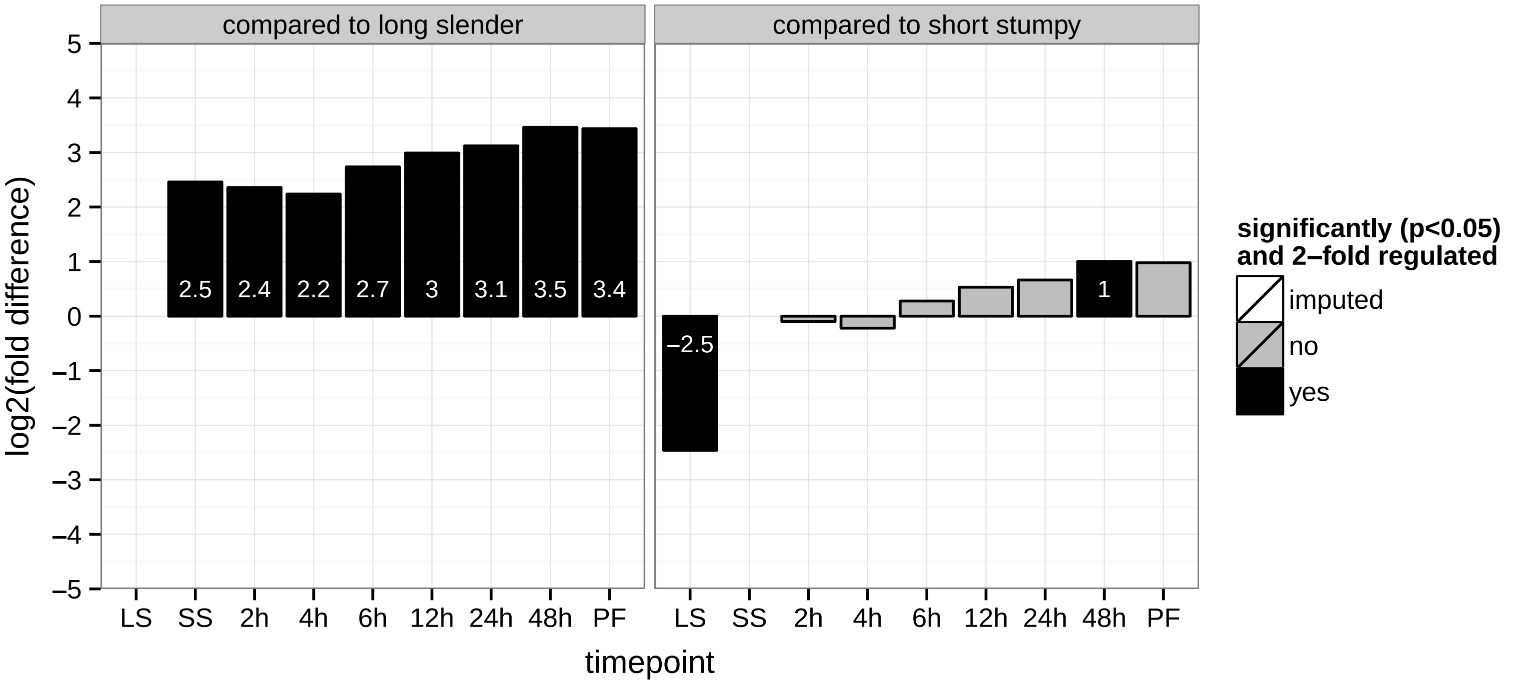
hypothetical protein, conserved
Tb927.10.14130
AGOF: 7S RNA binding
AGOC: signal recognition particle
AGOP: SRP–dependent cotranslational protein targeting to membrane
PGOF: 7S RNA binding
PGOC: signal recognition particle
PGOP: SRP–dependent cotranslational protein targeting to membrane

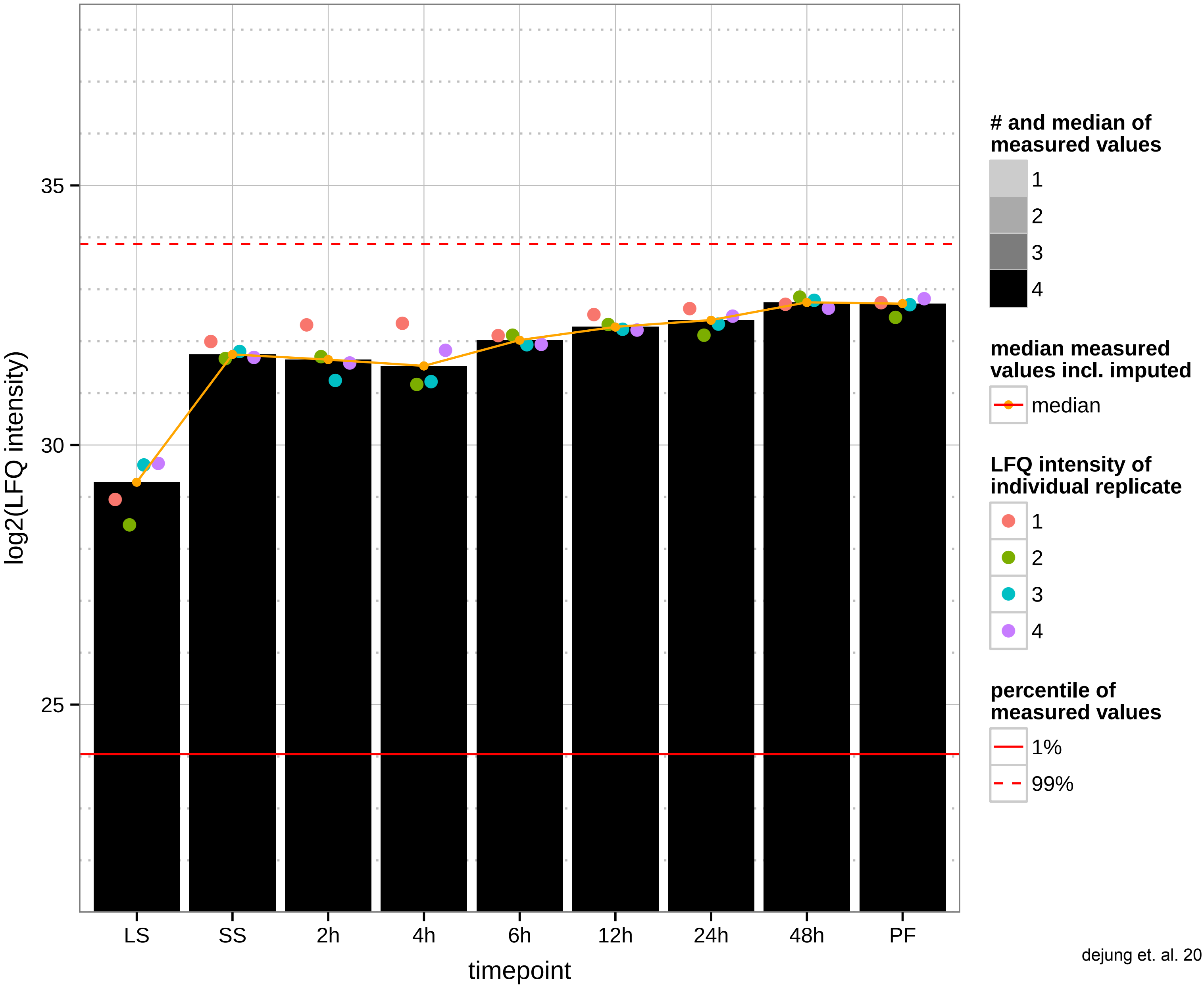




dejung et. al. 2015

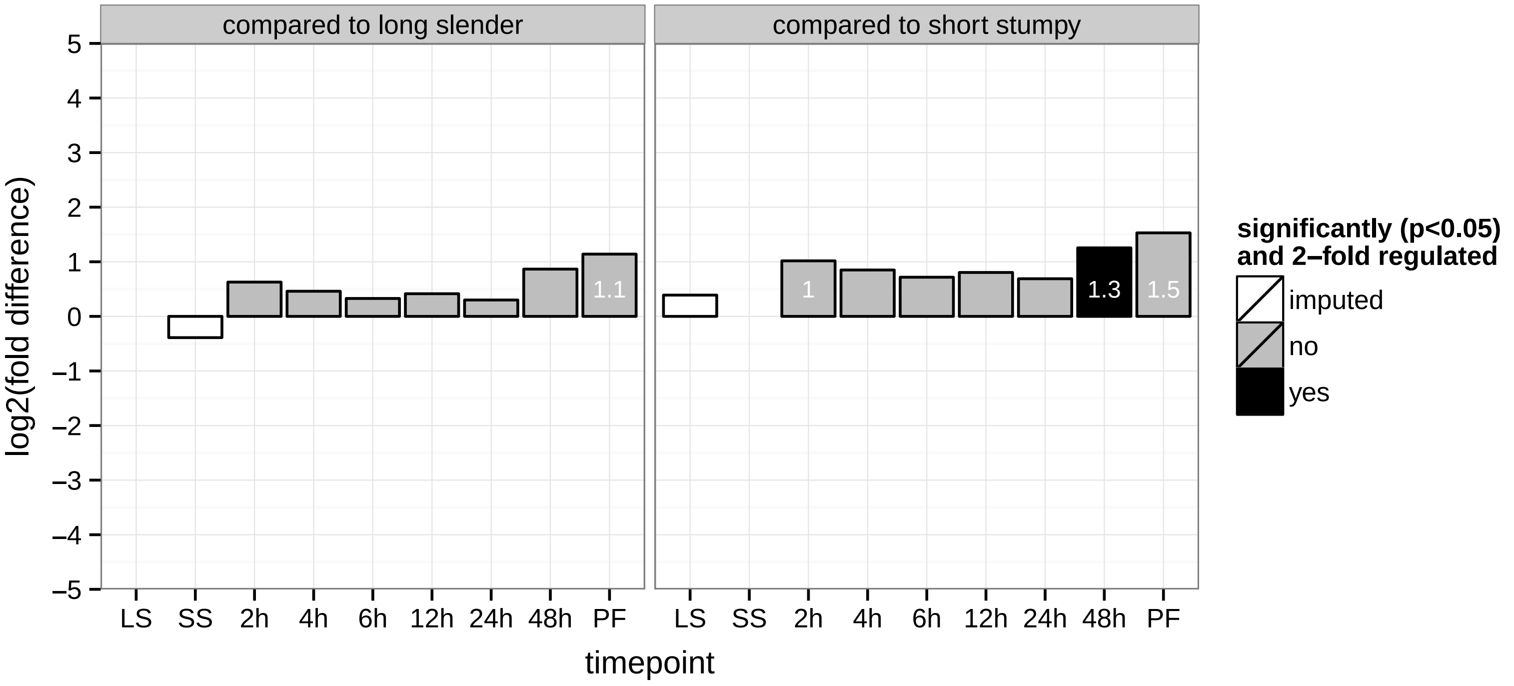
NA, ATP–dependent DEAD/H RNA helicase, putative
Tb927.10.14550
AGOF: NA, ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
AGOC: NA, null
AGOP: NA, nucleobase–containing compound metabolic process
PGOF: NA, ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
PGOC: NA, null
PGOP: NA, null

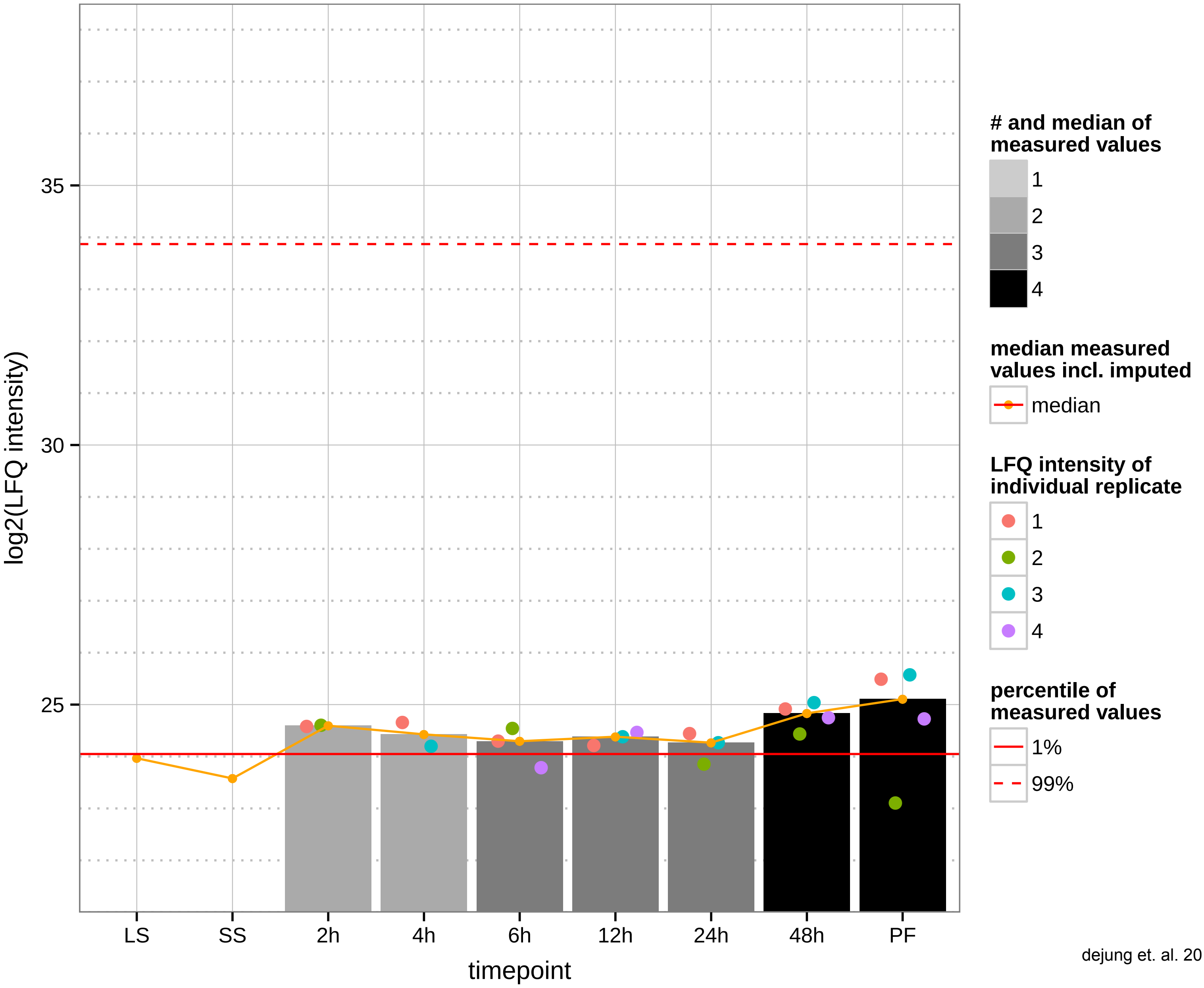




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.14560;Tb11.v5.0477
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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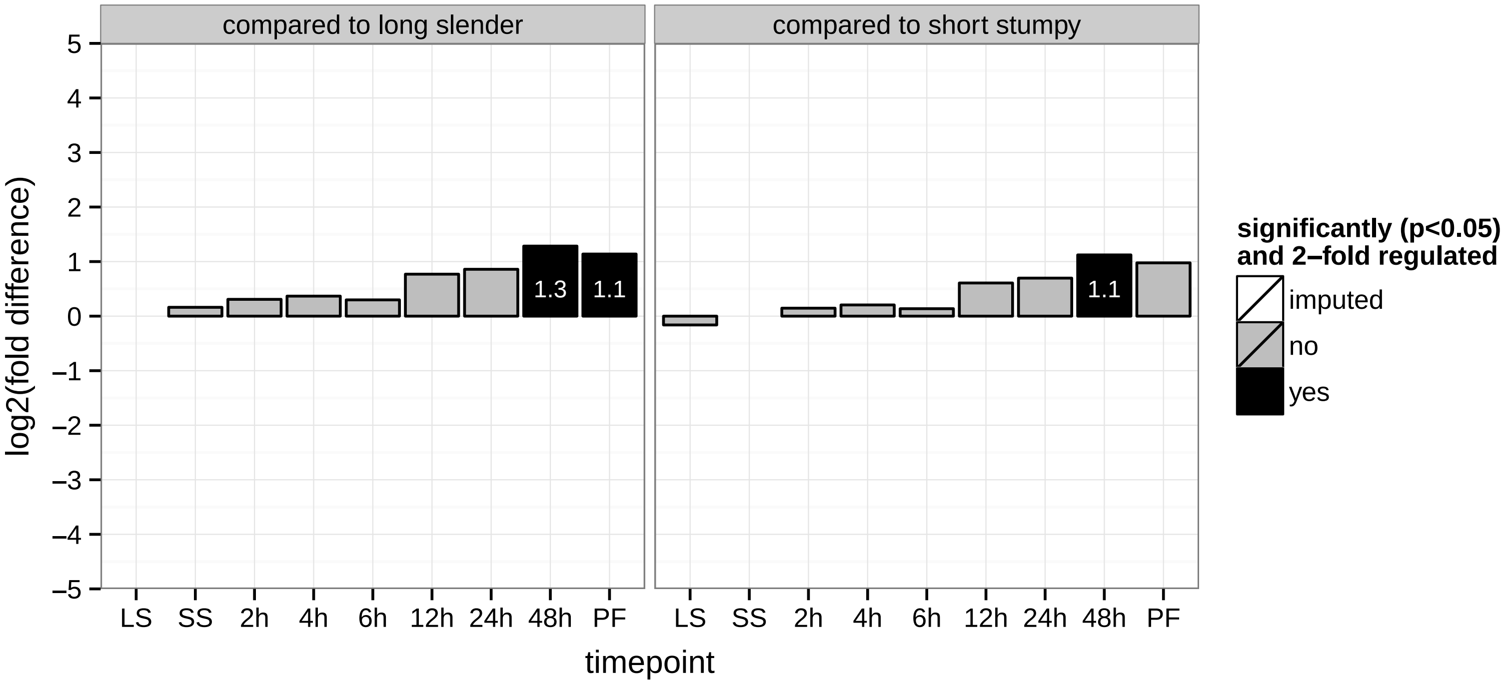
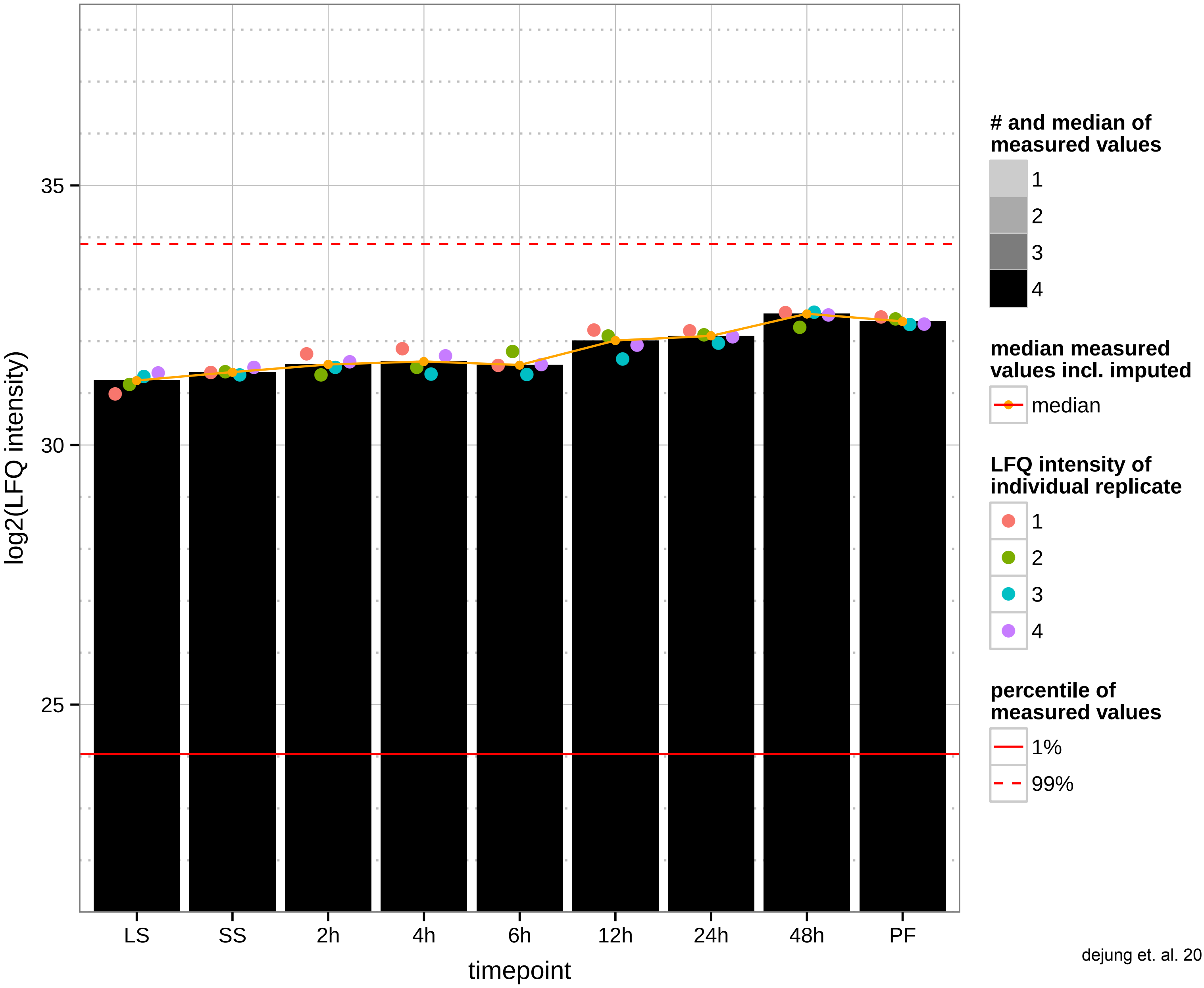
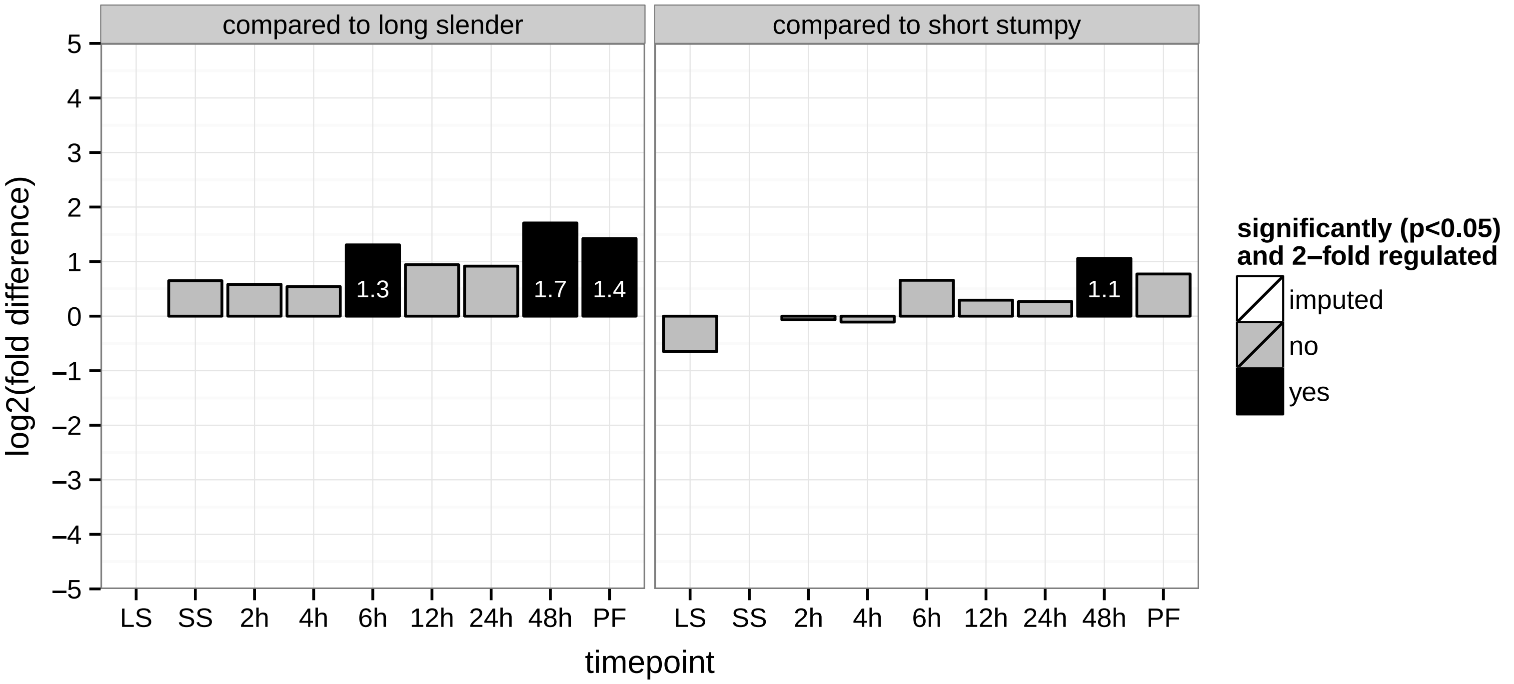
metallo–peptidase, Clan MG, Family M24, aminopeptidase, putative
Tb927.10.14790
AGOF: null
AGOC: null
AGOP: cellular process
PGOF: null
PGOC: null
PGOP: cellular process

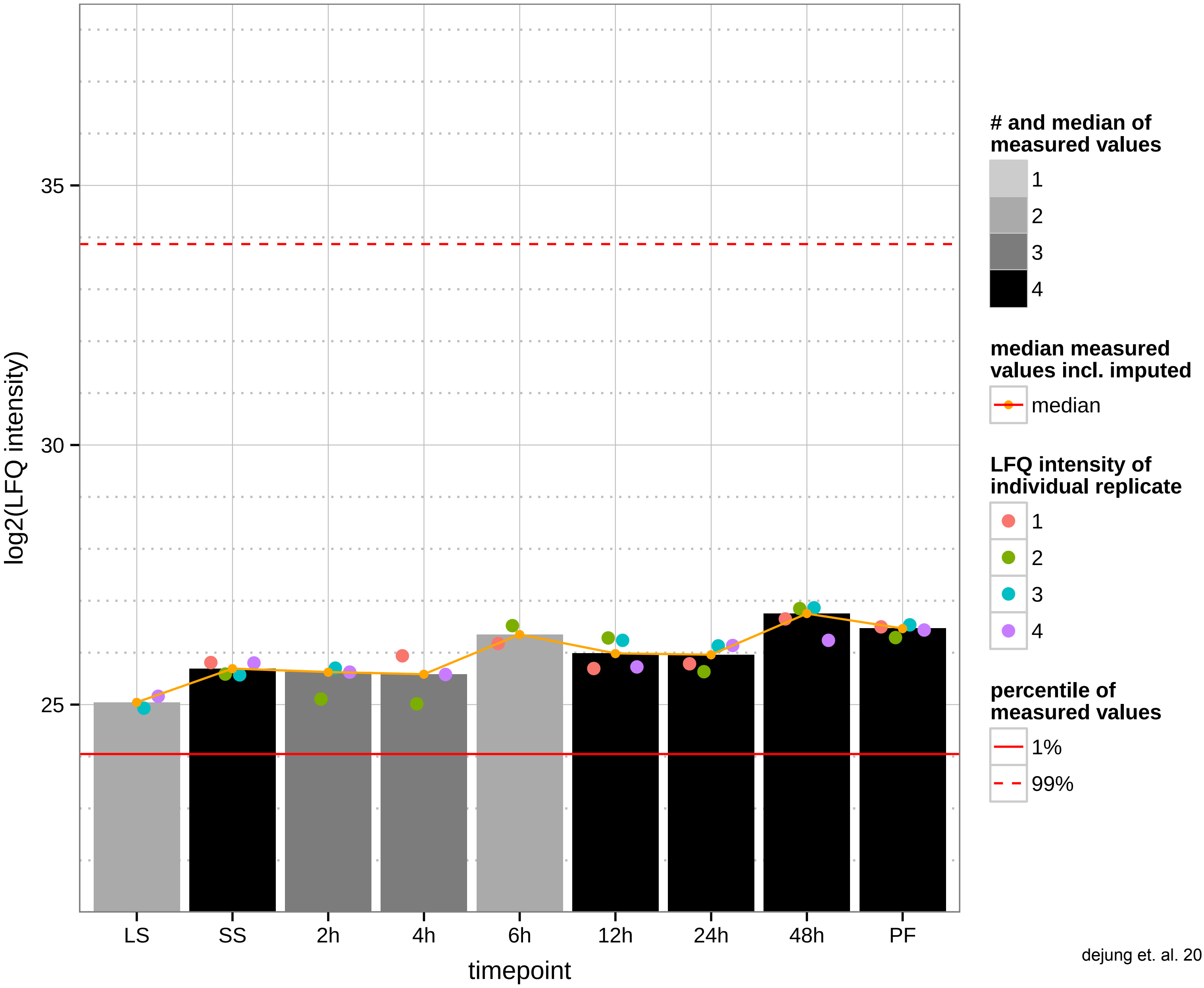




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.1730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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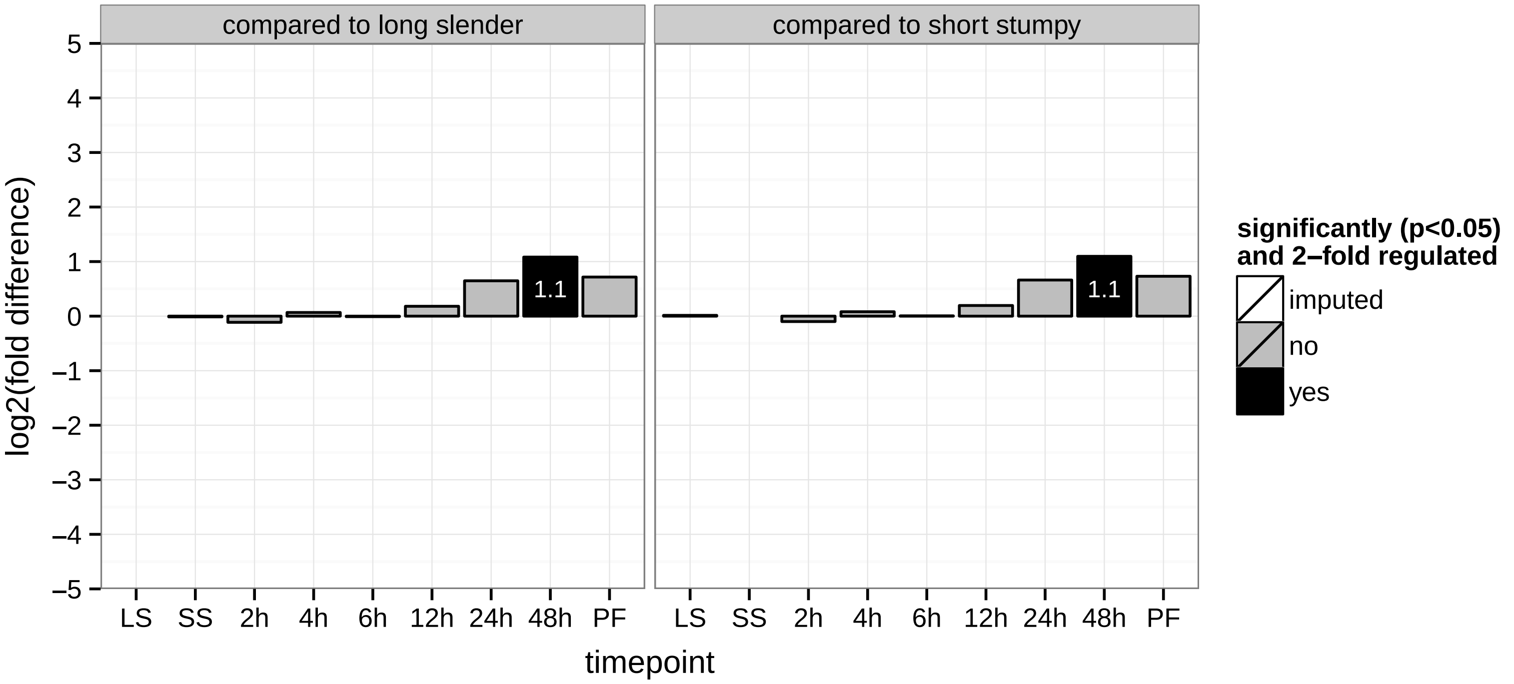
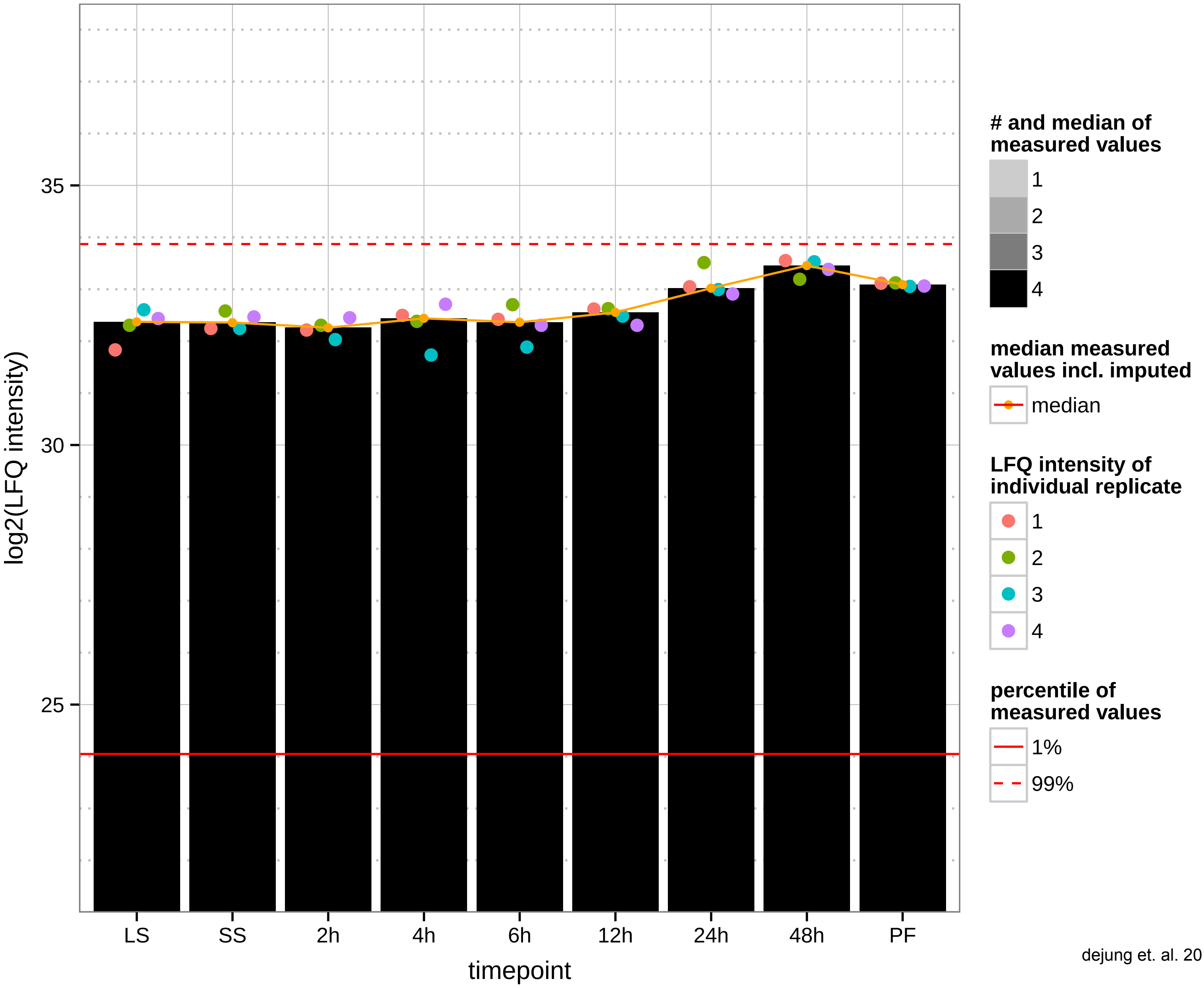
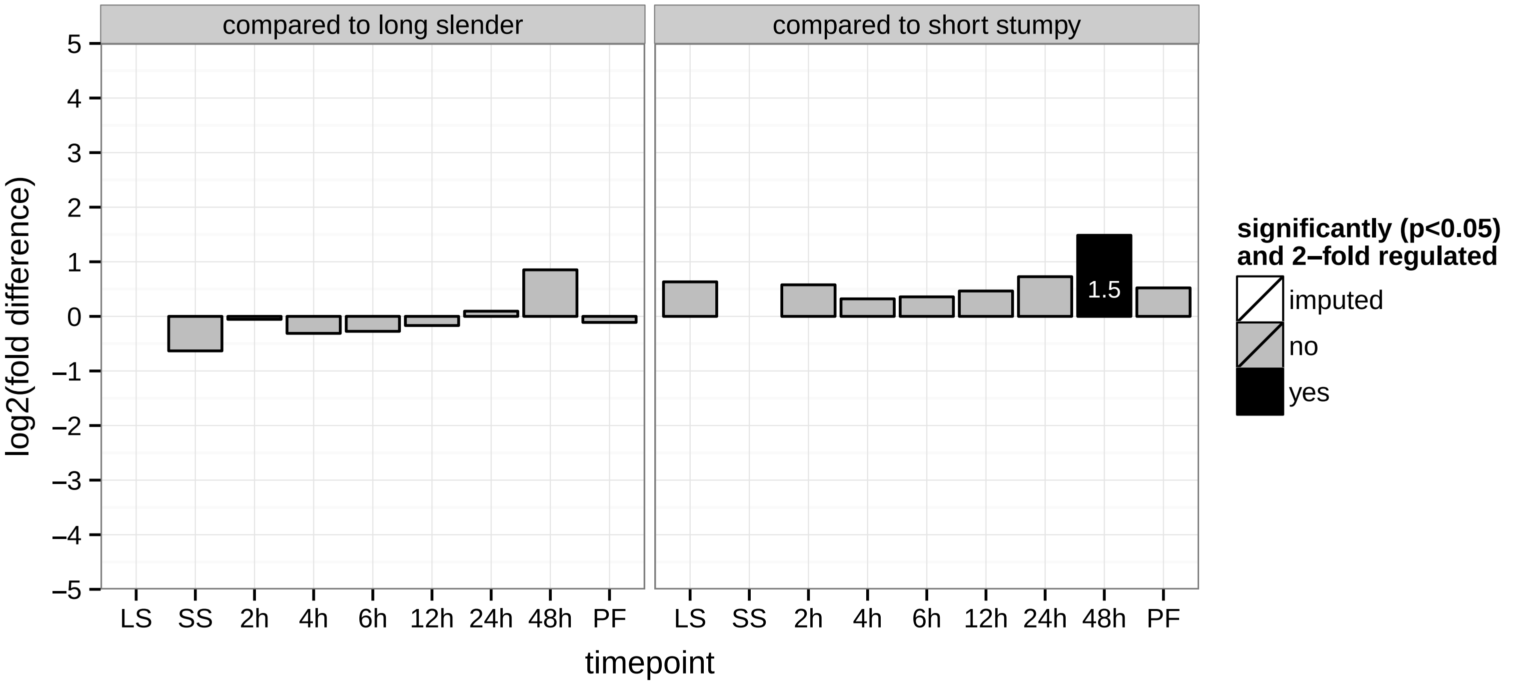
40S ribosomal protein S9, putative
Tb927.8.1110;Tb927.10.5610
AGOF: RNA binding, rRNA binding, structural constituent of ribosome, rRNA binding
AGOC: intracellular, ribosome, small ribosomal subunit
AGOP: translation
PGOF: RNA binding, rRNA binding, structural constituent of ribosome
PGOC: intracellular, small ribosomal subunit
PGOP: translation

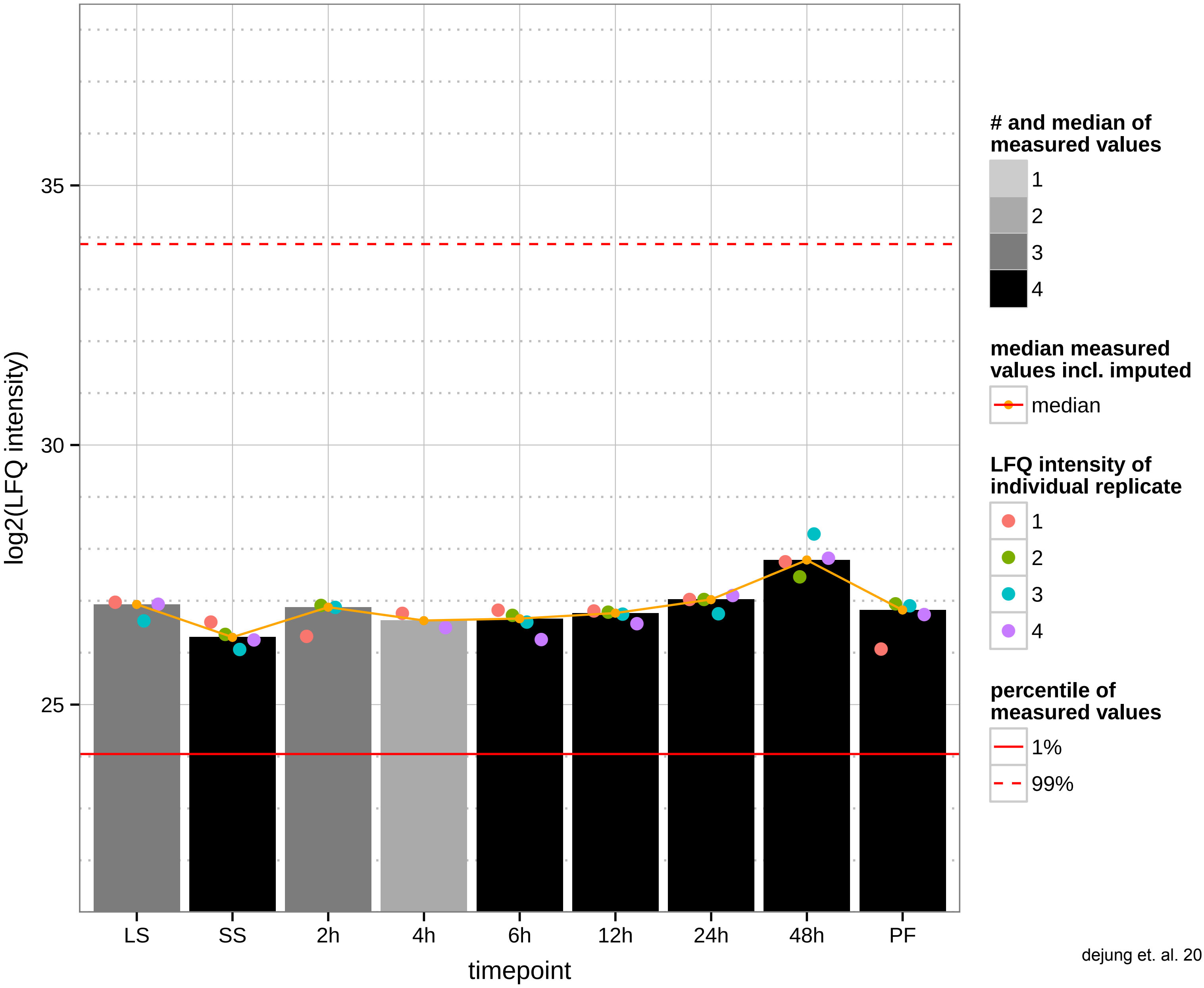




dejung et. al. 2015

Proteophosphoglycan, putative
Tb927.10.5880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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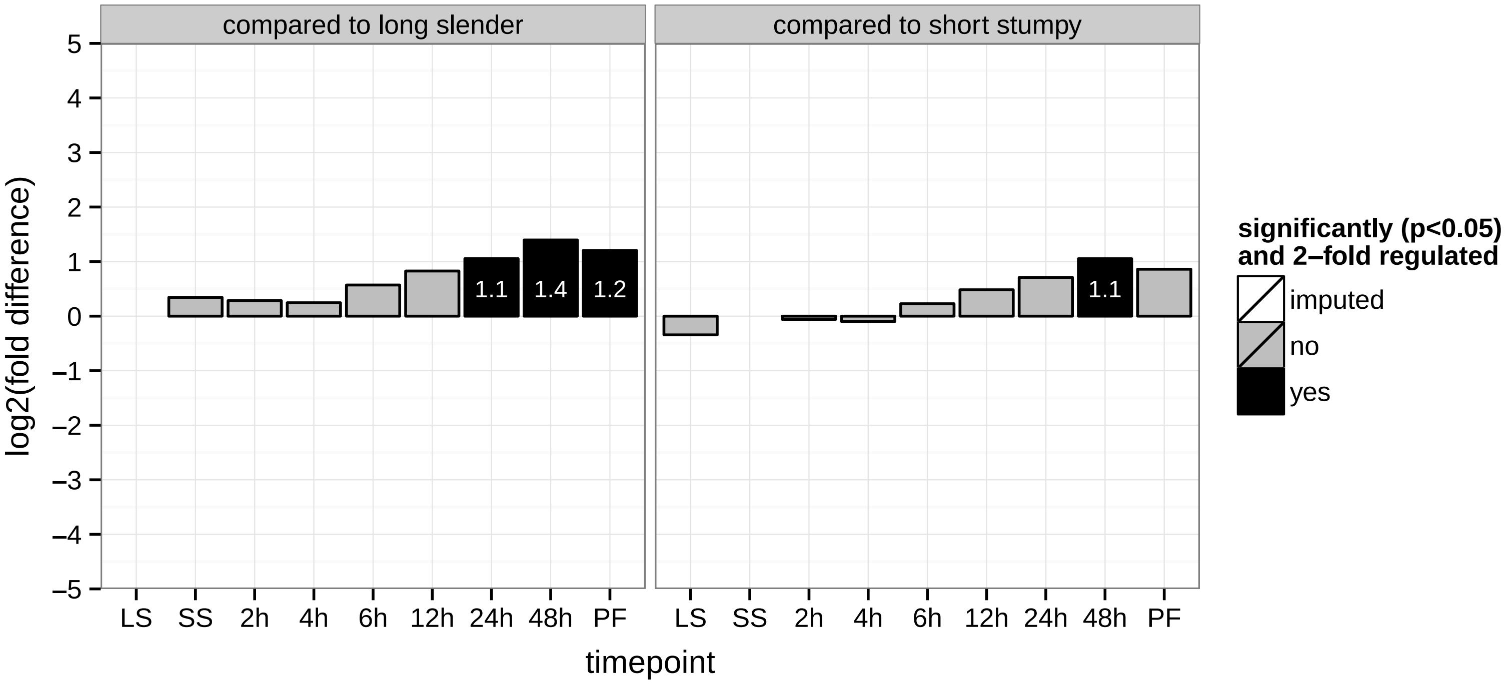
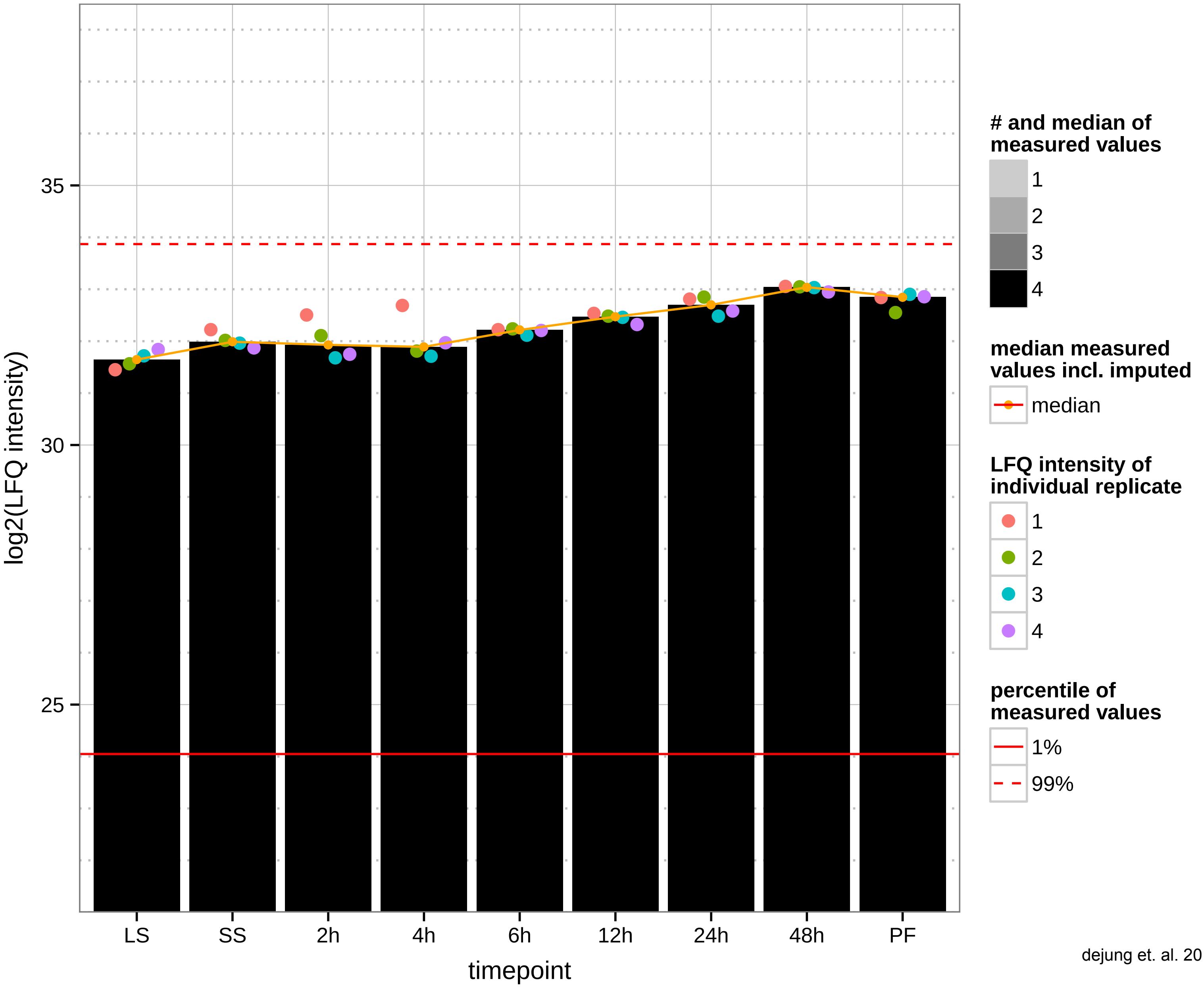
T−complex protein 1, theta subunit, putative, CCT−theta, putative (TCP−1−theta)
Tb927.10.8190
AGOF: ATP binding, unfolded protein binding
AGOC: chaperonin−containing T−complex
AGOP: protein folding, regulation of cell cycle
PGOF: ATP binding, unfolded protein binding
PGOC: null
PGOP: cellular protein metabolic process, protein folding





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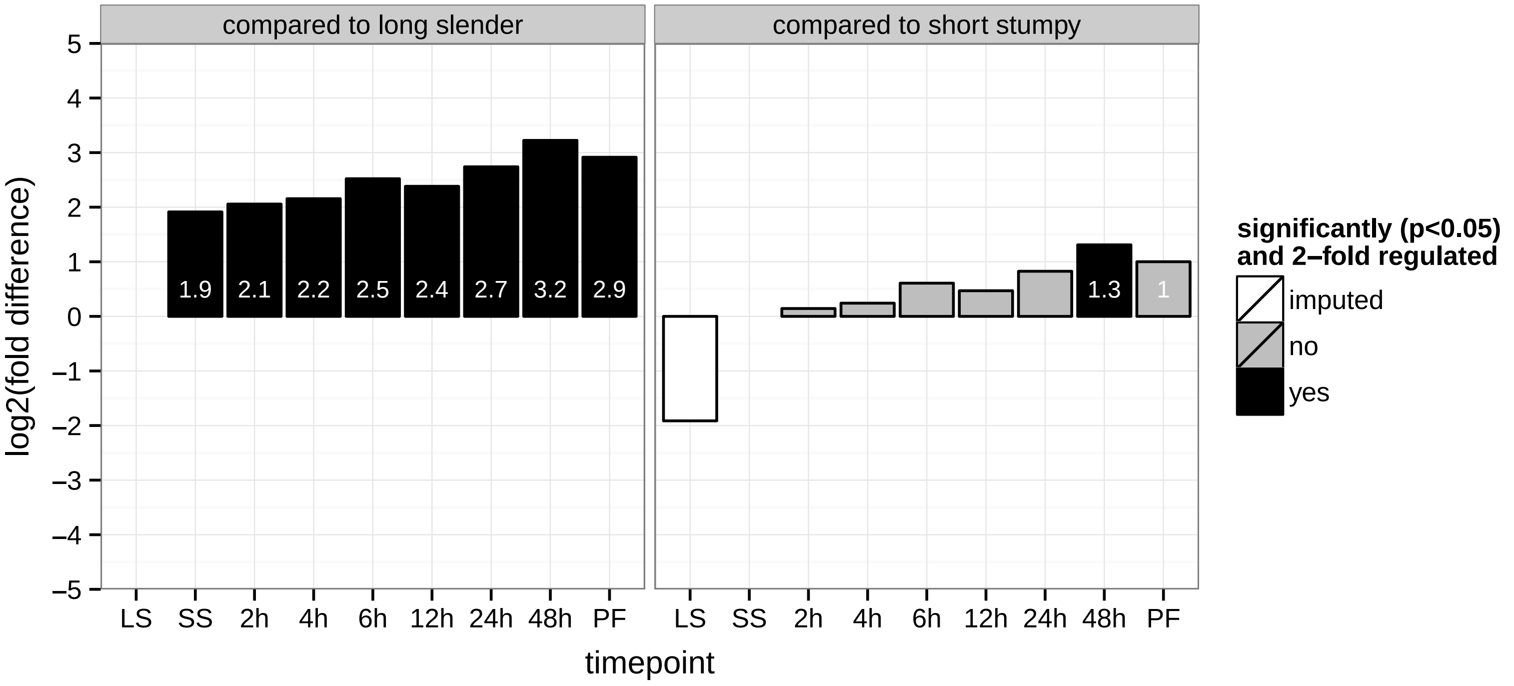
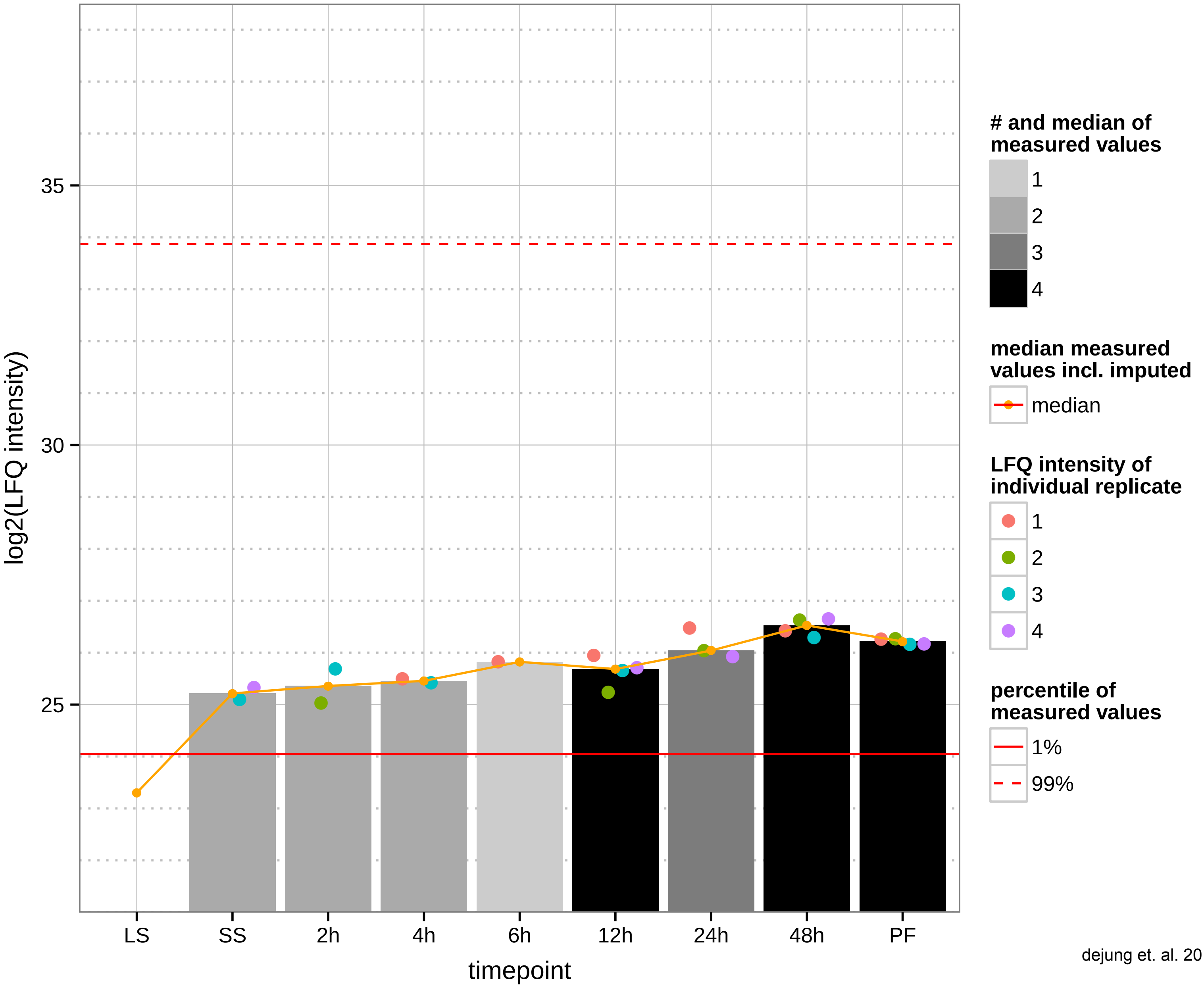
hypothetical protein, conserved
Tb927.10.820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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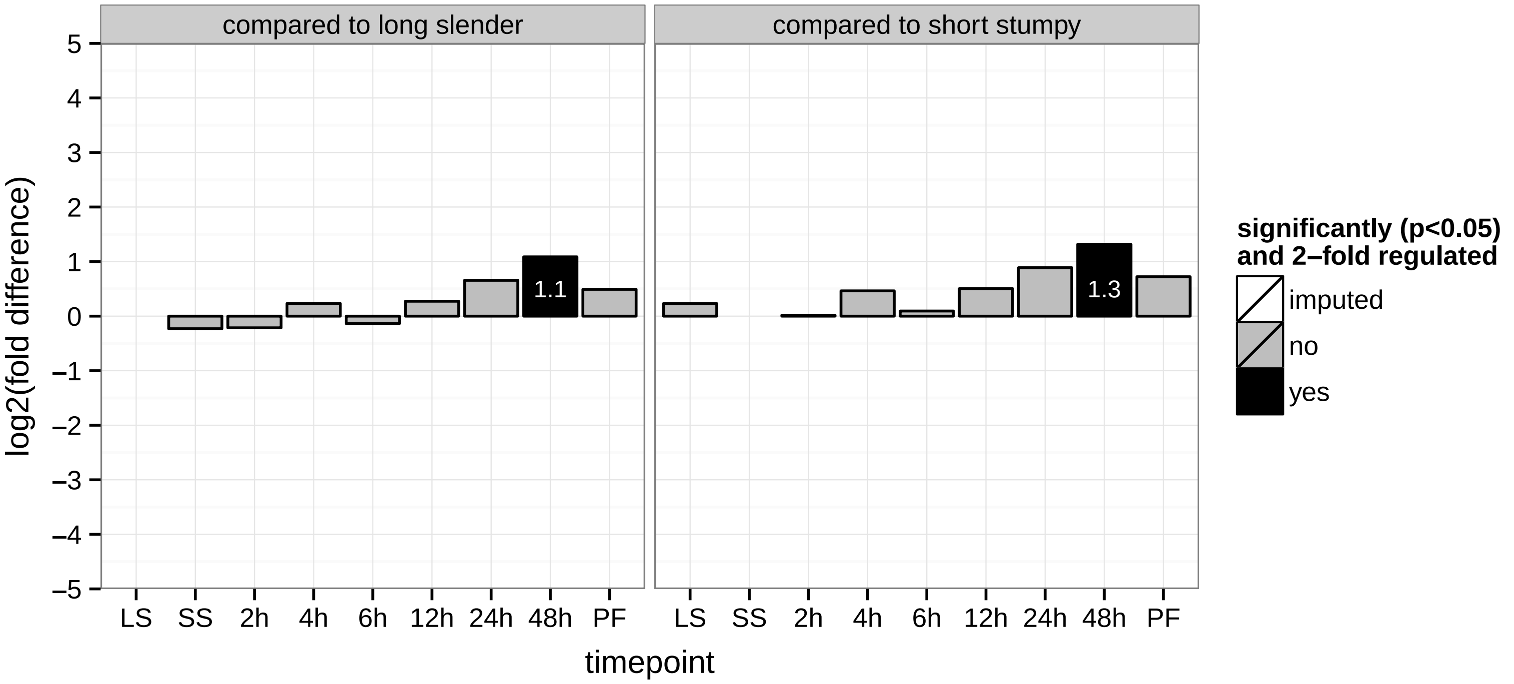
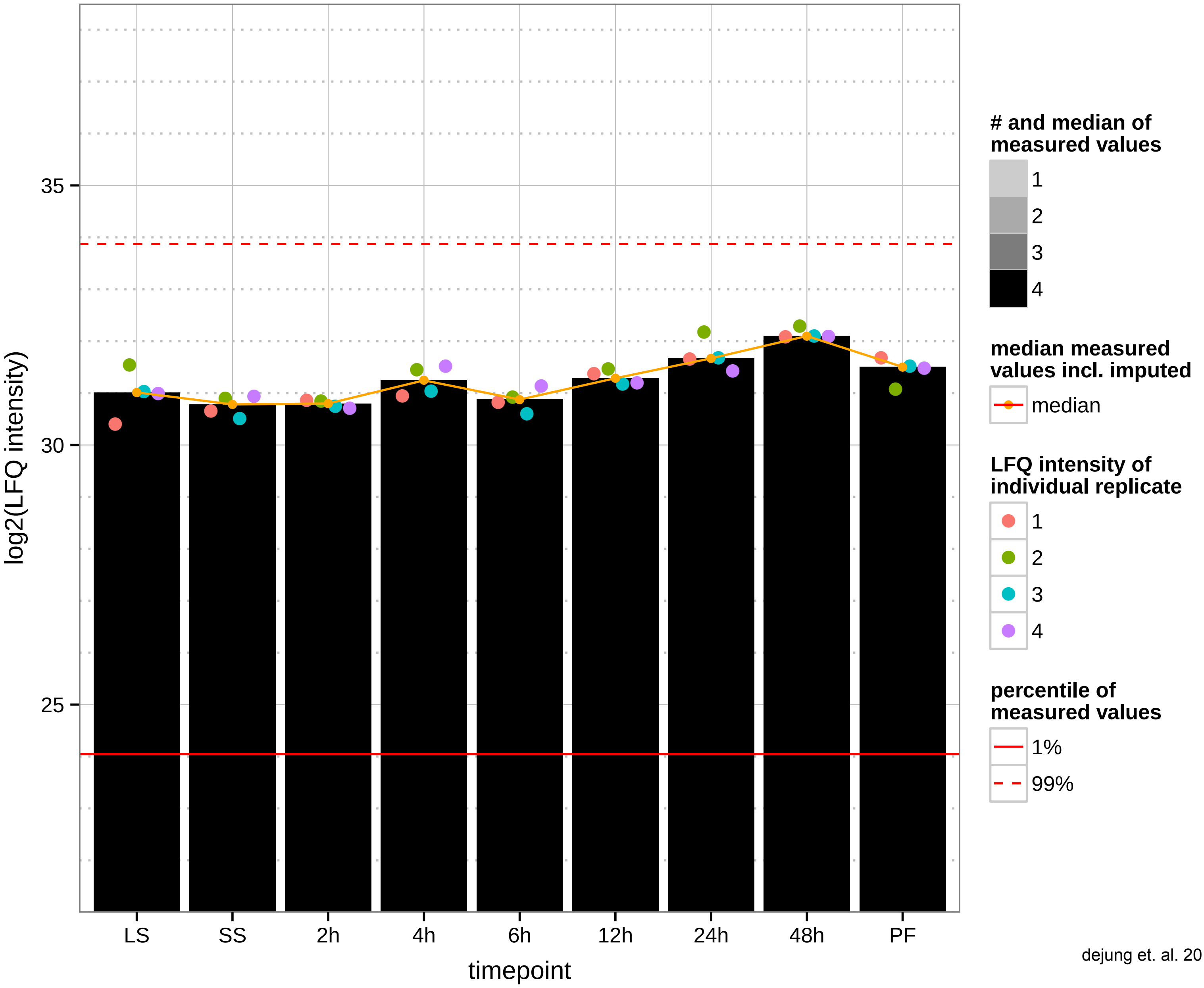
40S ribosomal protein S12, putative
Tb927.10.8430
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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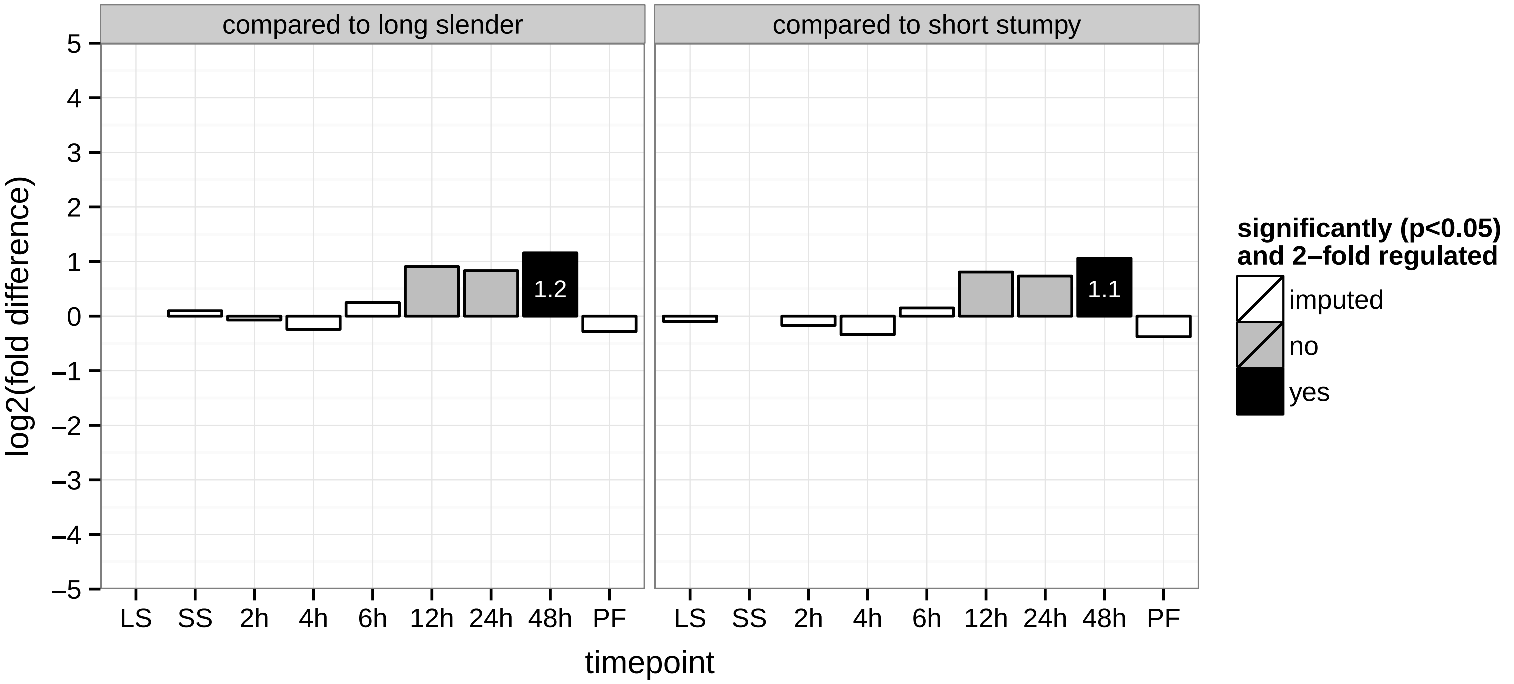
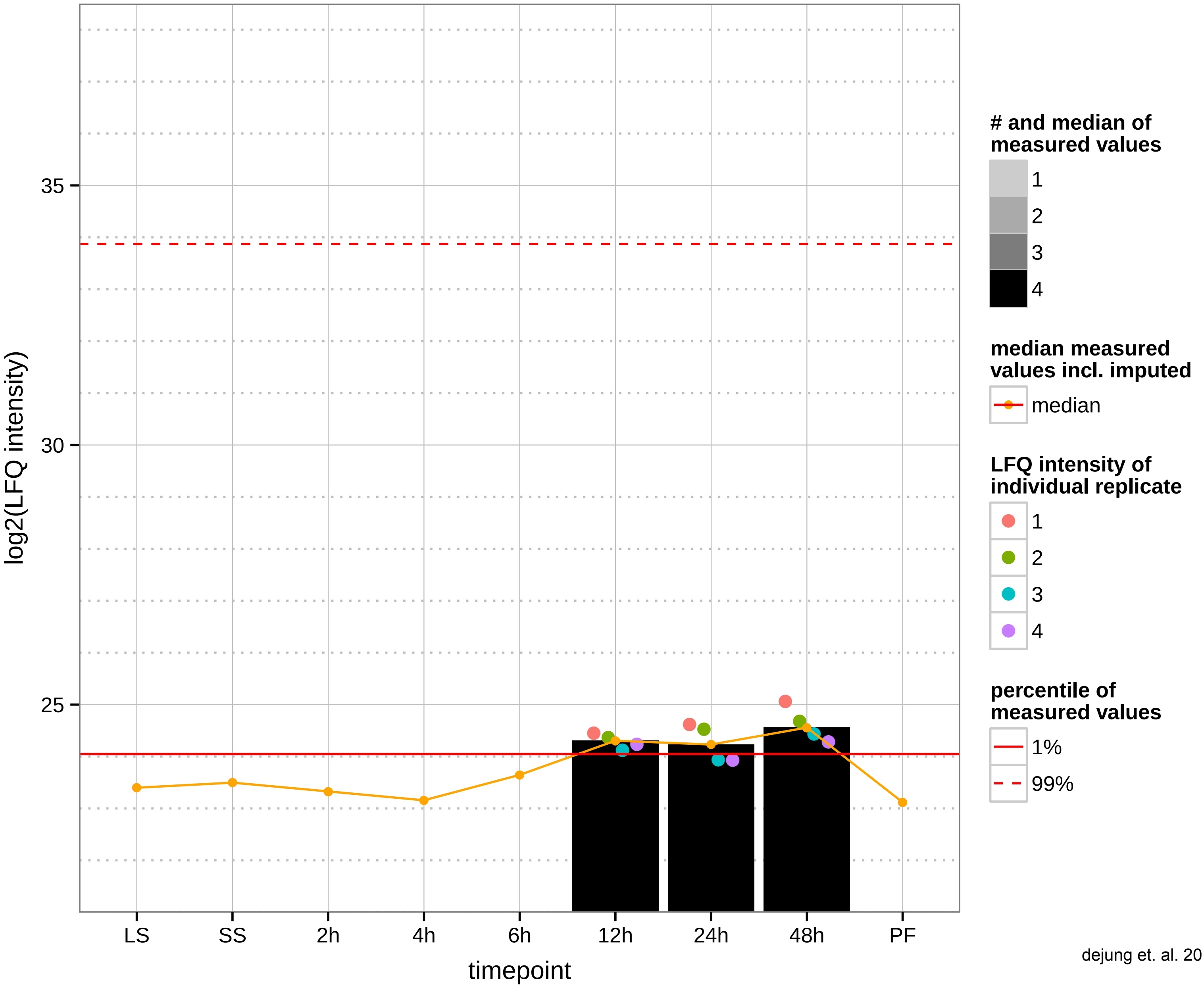
hypothetical protein, conserved
Tb927.10.9200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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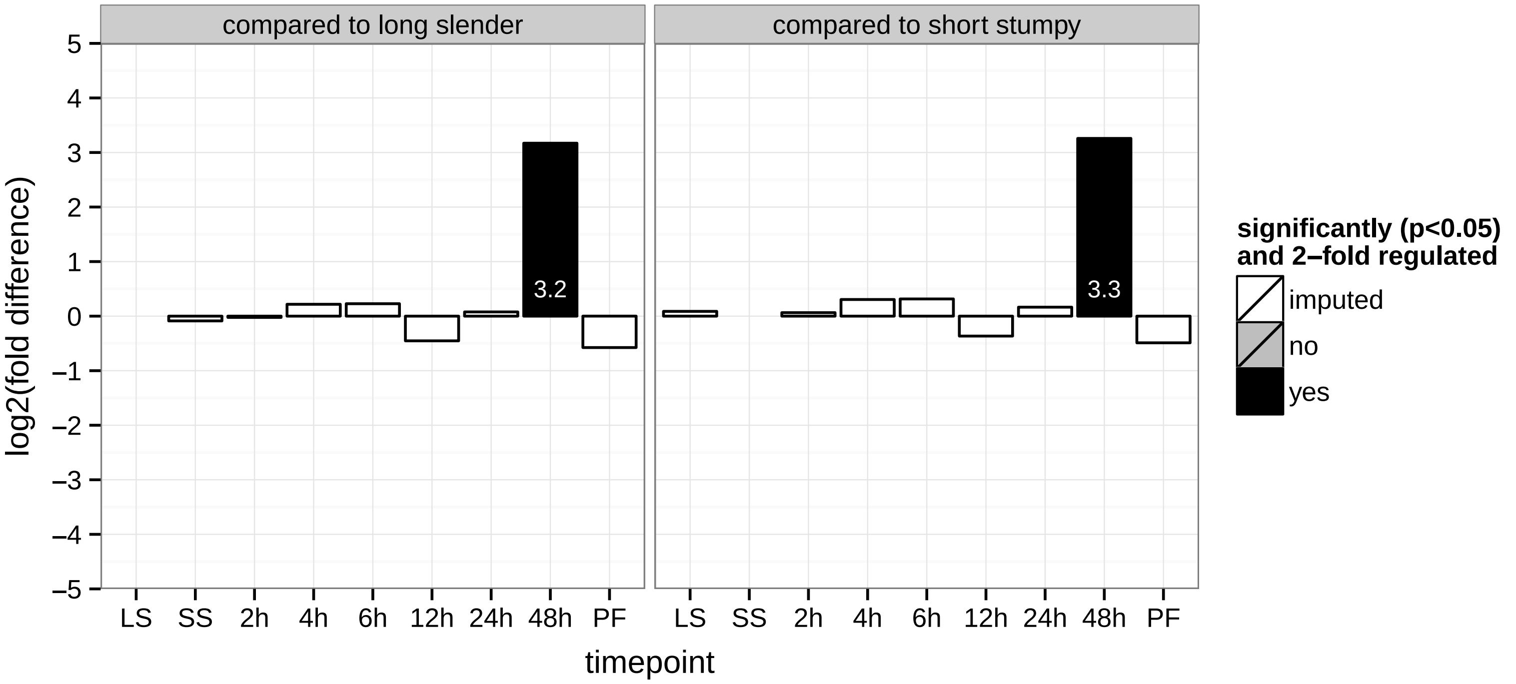
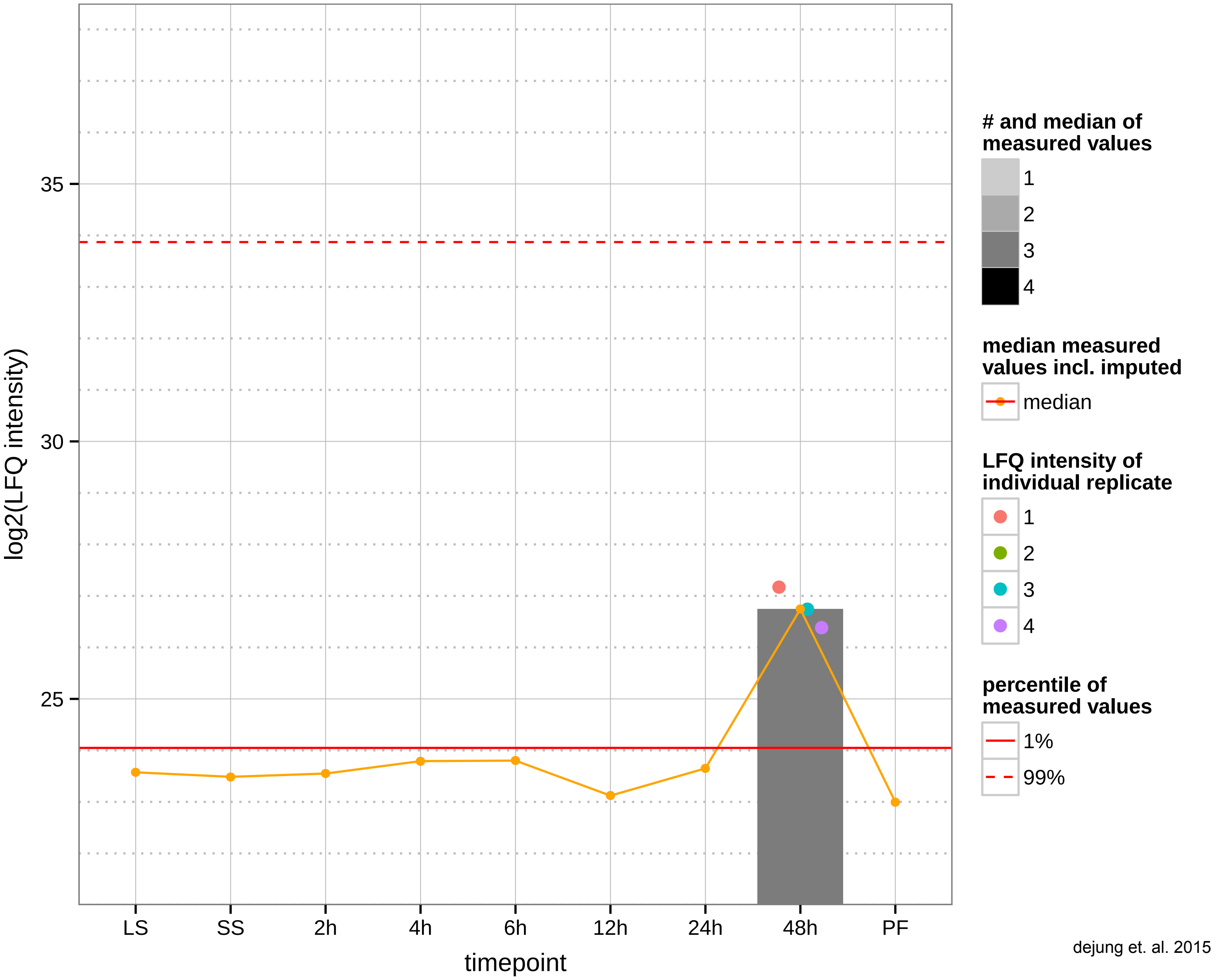
RNA–editing–associated protein 1, RNA–binding protein, oligo (U) binding protein, RNA editing complex protein (REAP–1)
Tb927.10.9720
AGOF: null
AGOC: mitochondrial mRNA editing complex
AGOP: RNA modification
PGOF: null
PGOC: null
PGOP: null





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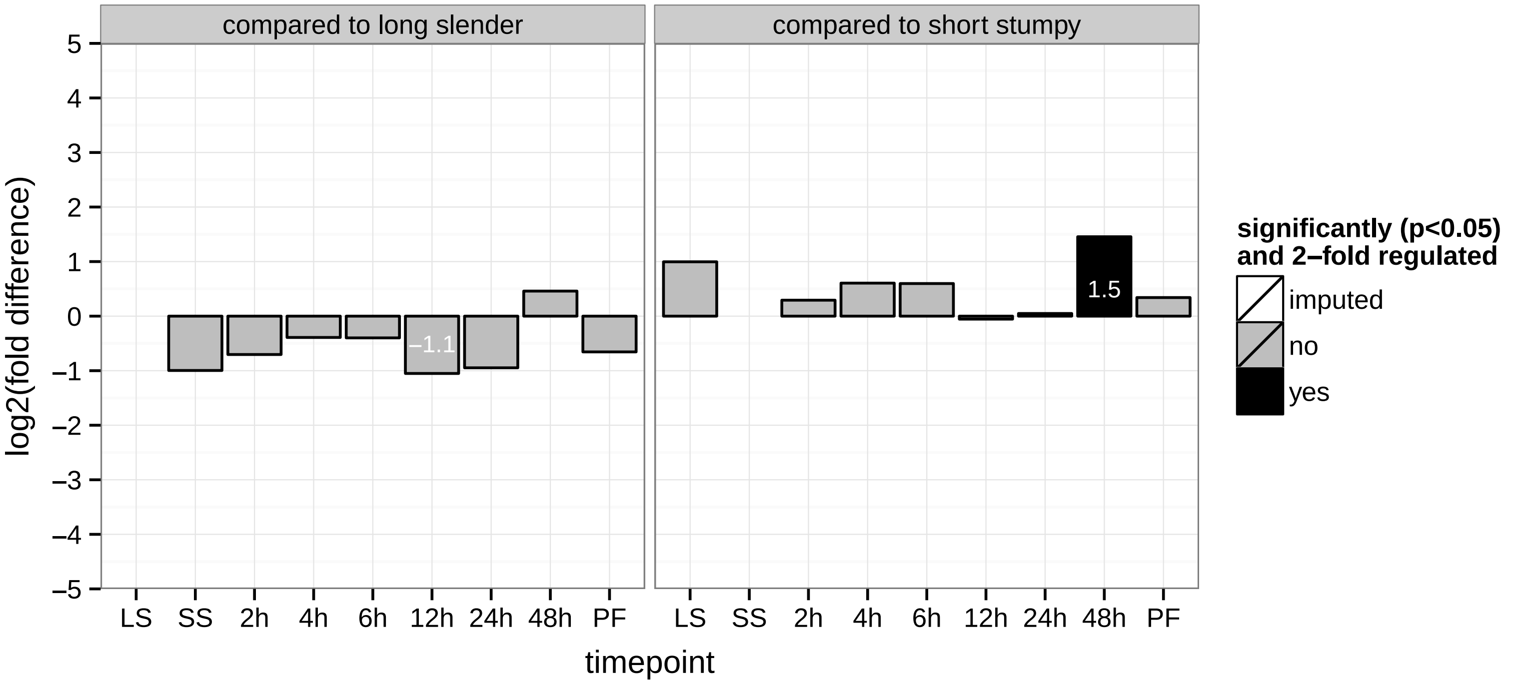
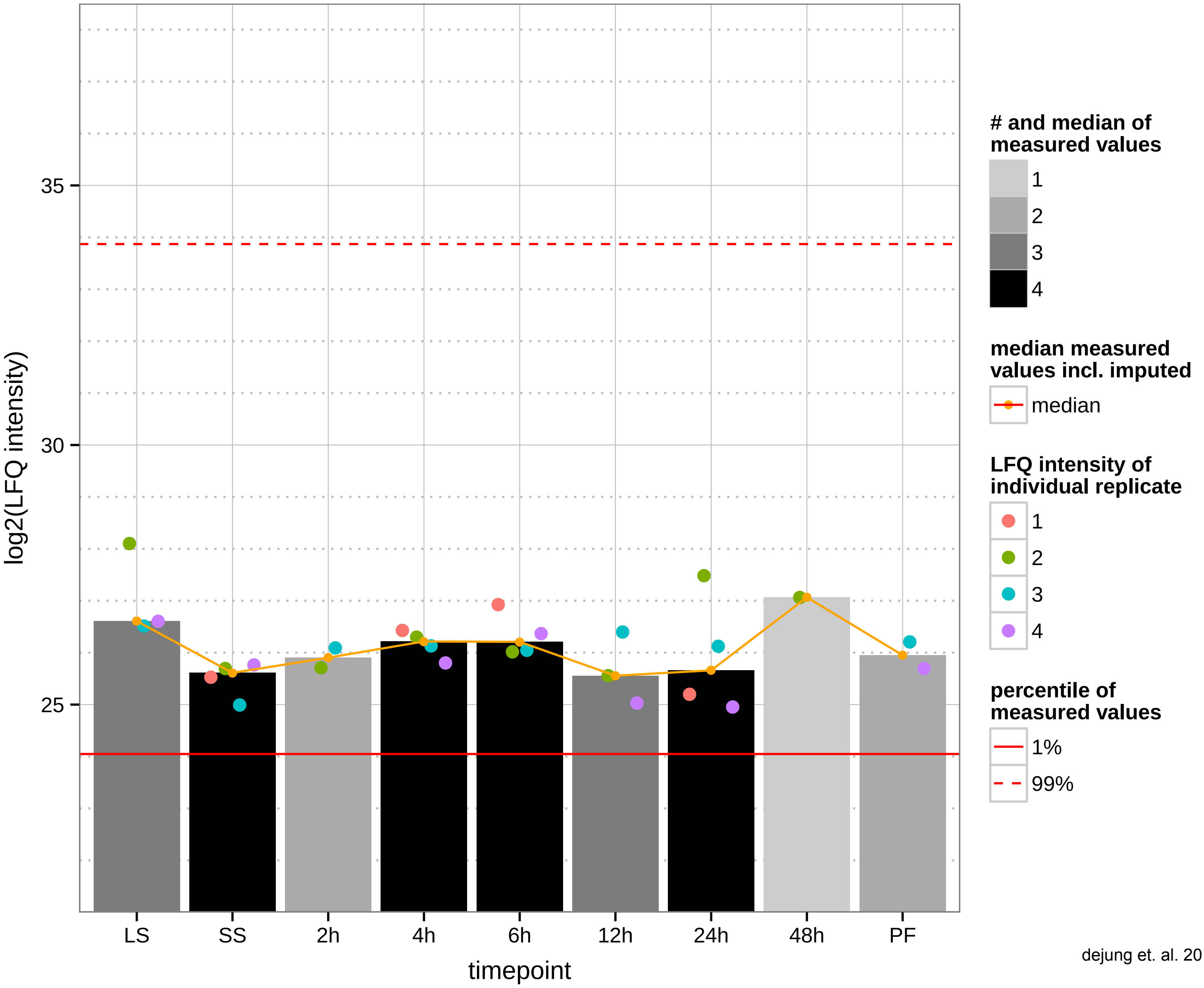
hypothetical protein, conserved
Tb927.11.10220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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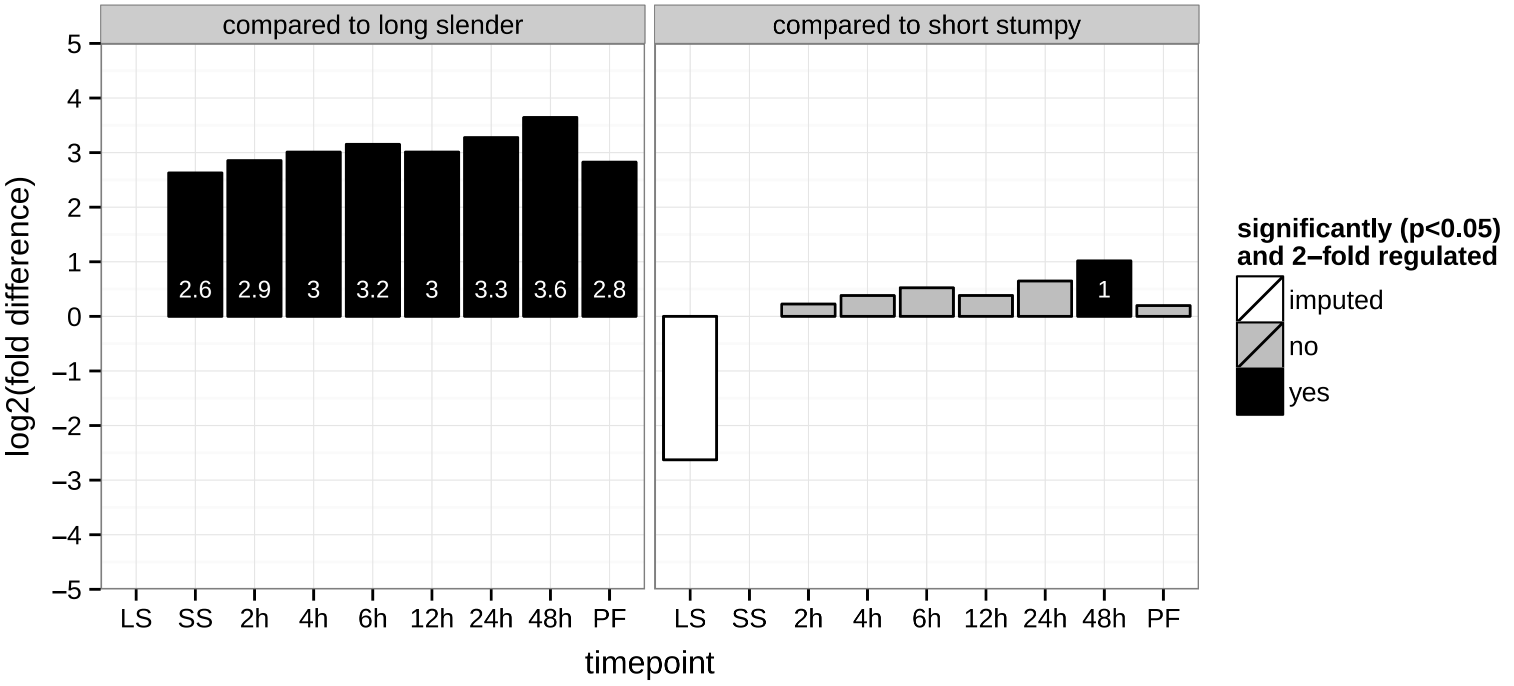
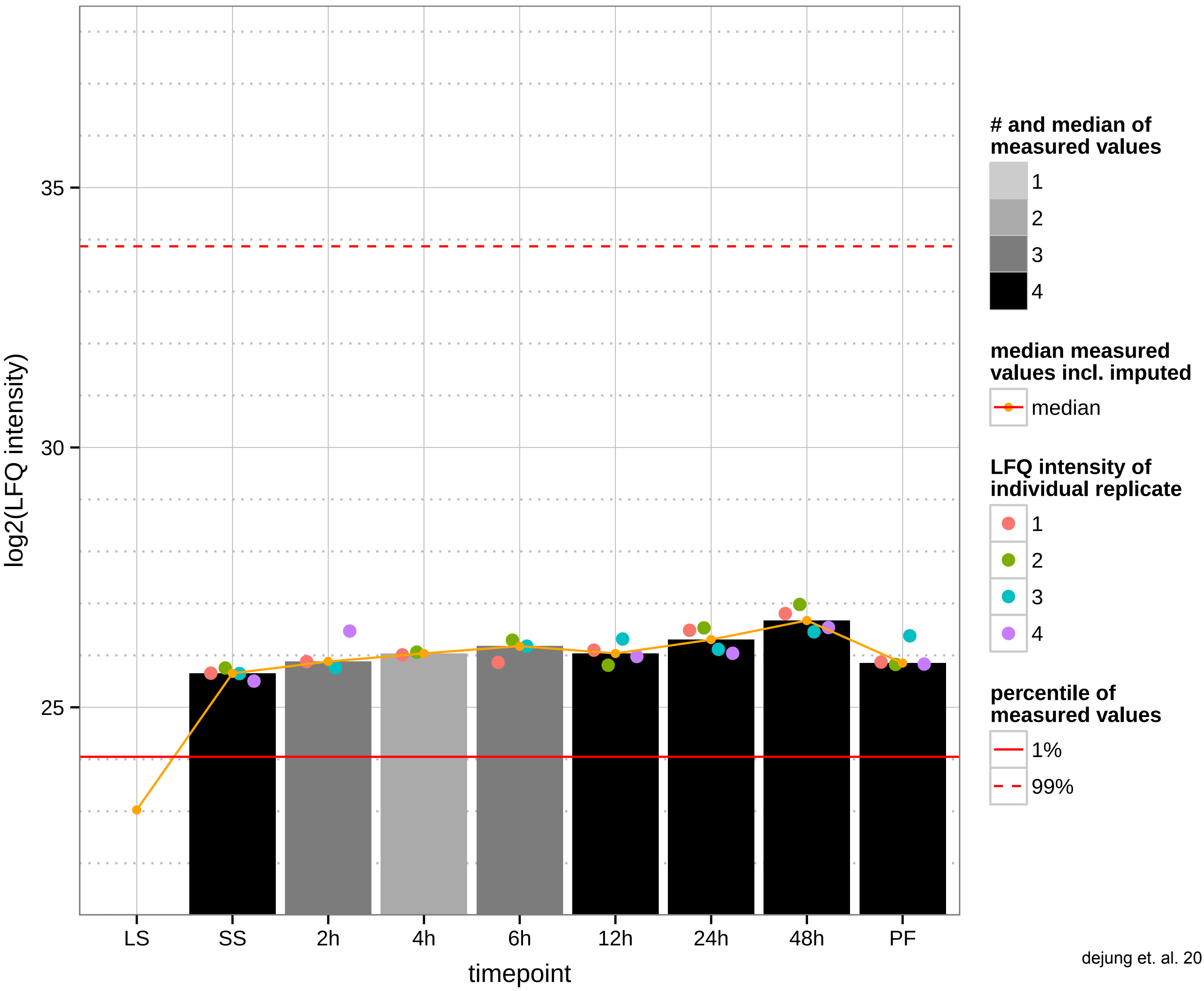
hypothetical protein, conserved
Tb927.11.10300
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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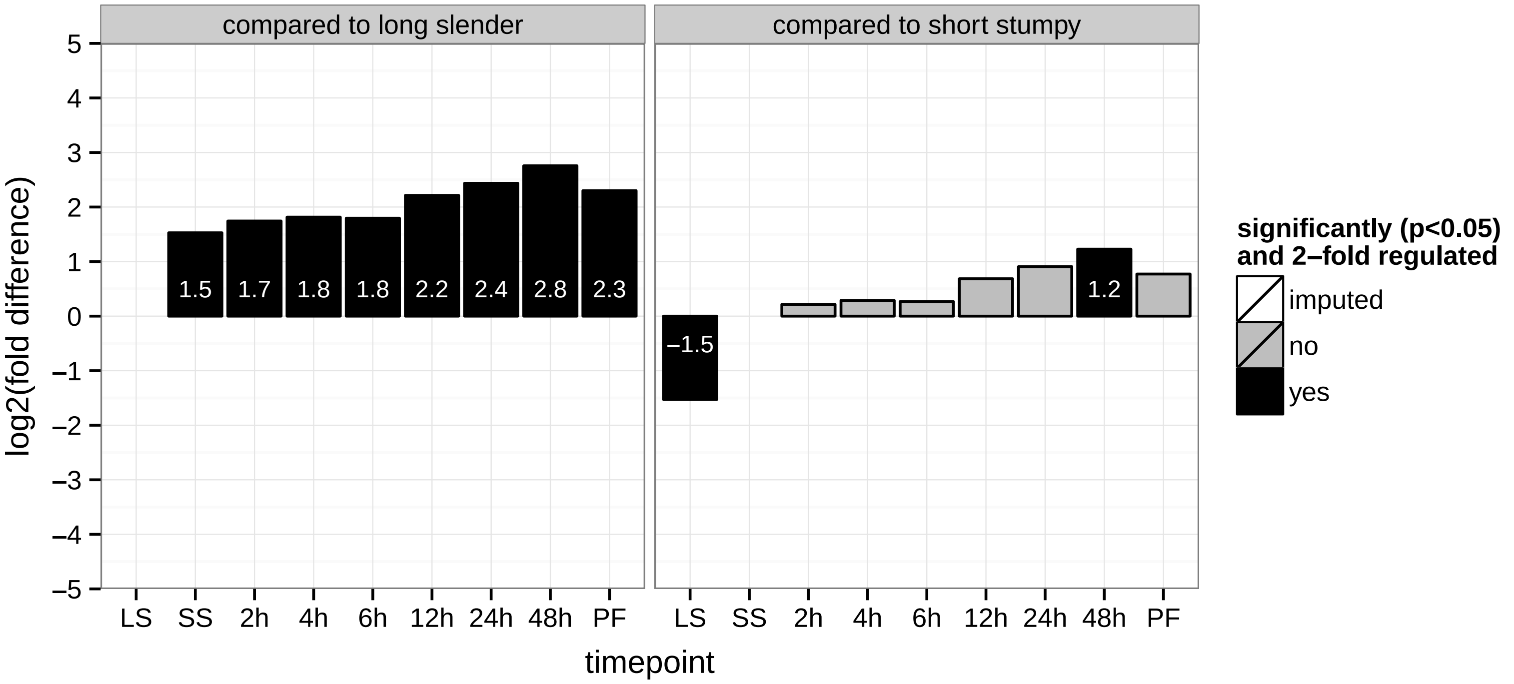
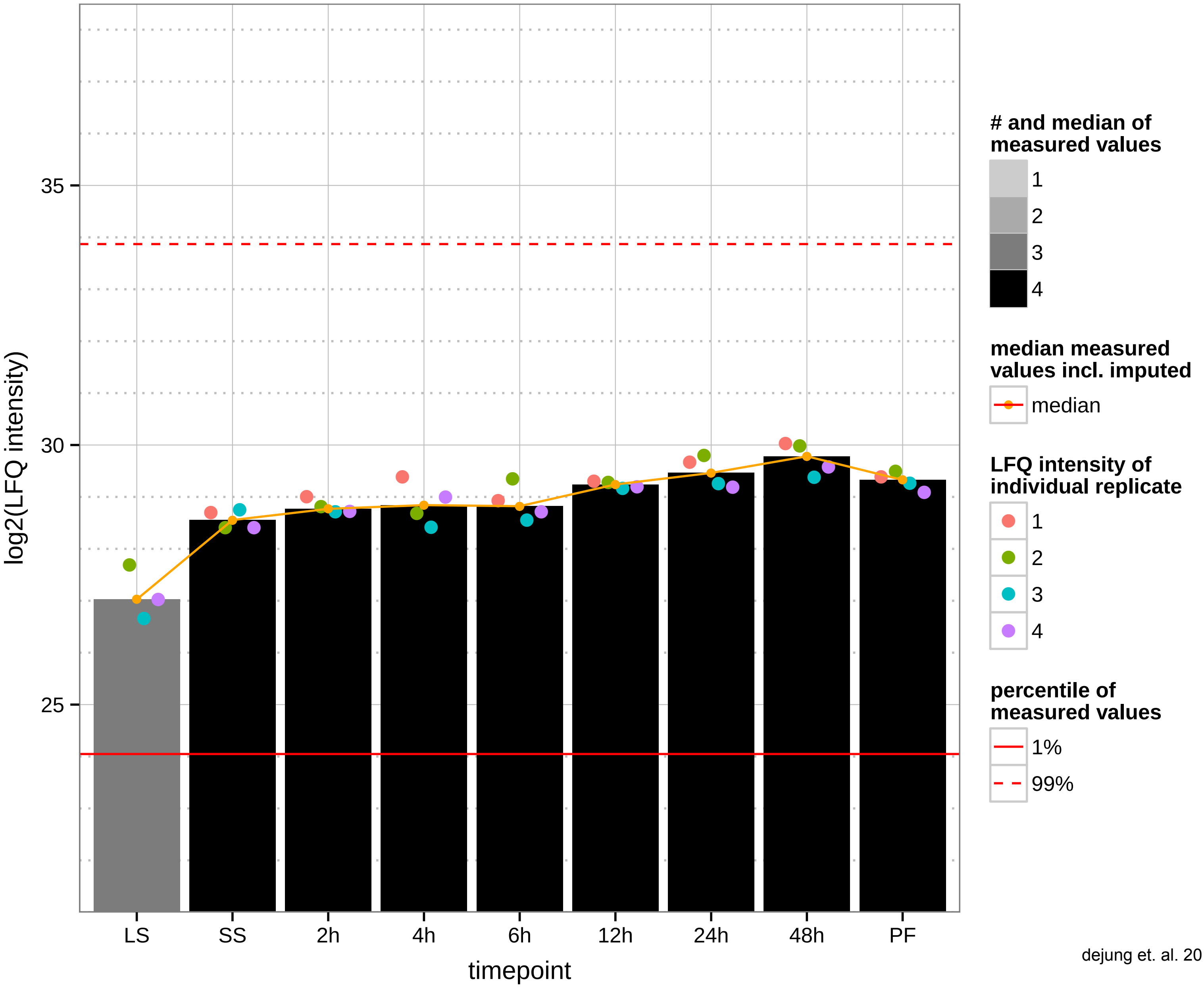
heat shock protein HslVU, ATPase subunit HslU, putative, ATP−dependent hsl protease ATP−binding subunit hslU
Tb927.11.12230
AGOF: ATP binding, ATP−dependent peptidase activity, ATPase activity, peptidase activity, acting on L−amino acid peptides
AGOC: HslUV protease complex
AGOP: null
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding, peptidase activity, acting on L−an
PGOC: HslUV protease complex, cytoplasm
PGOP: null





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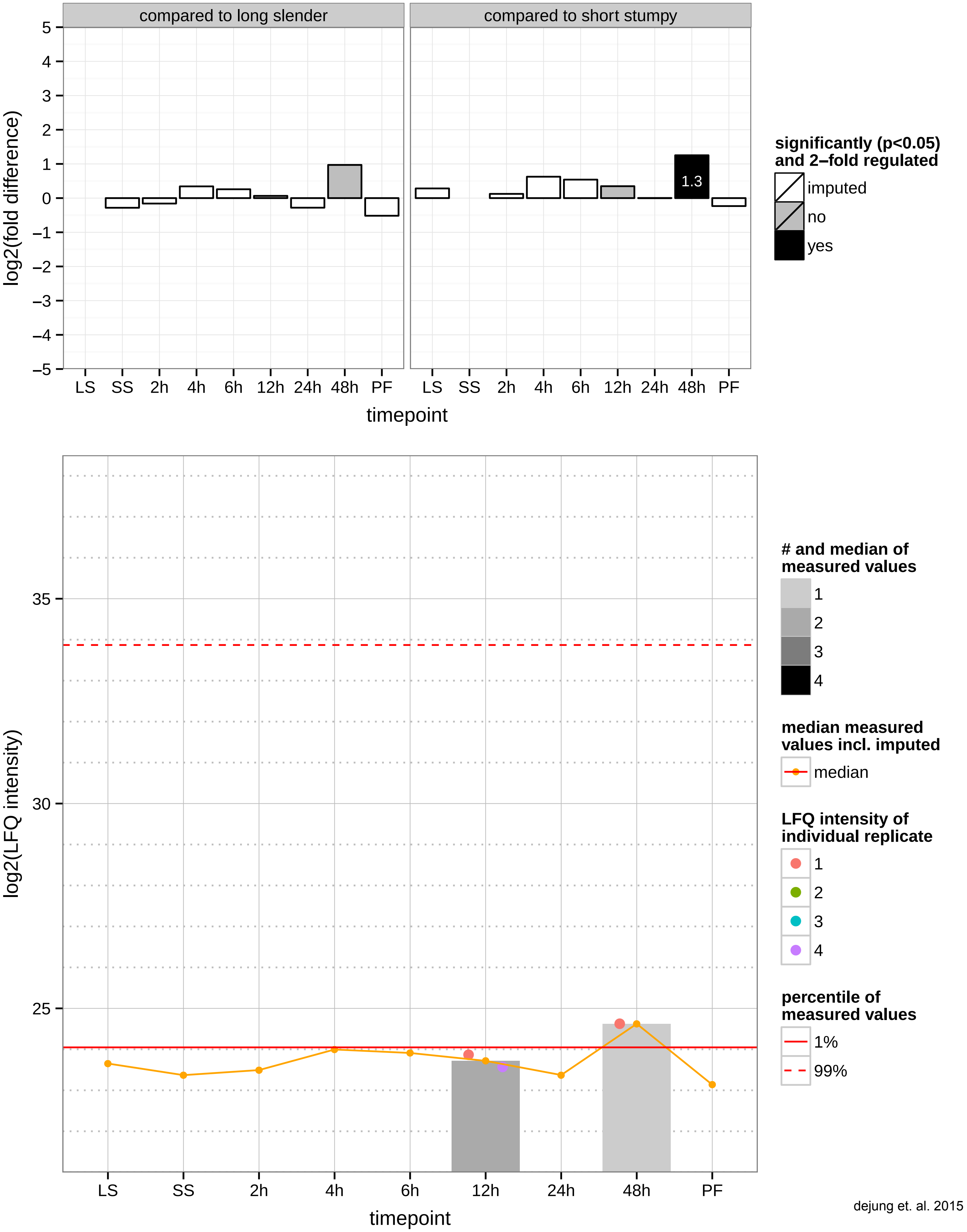
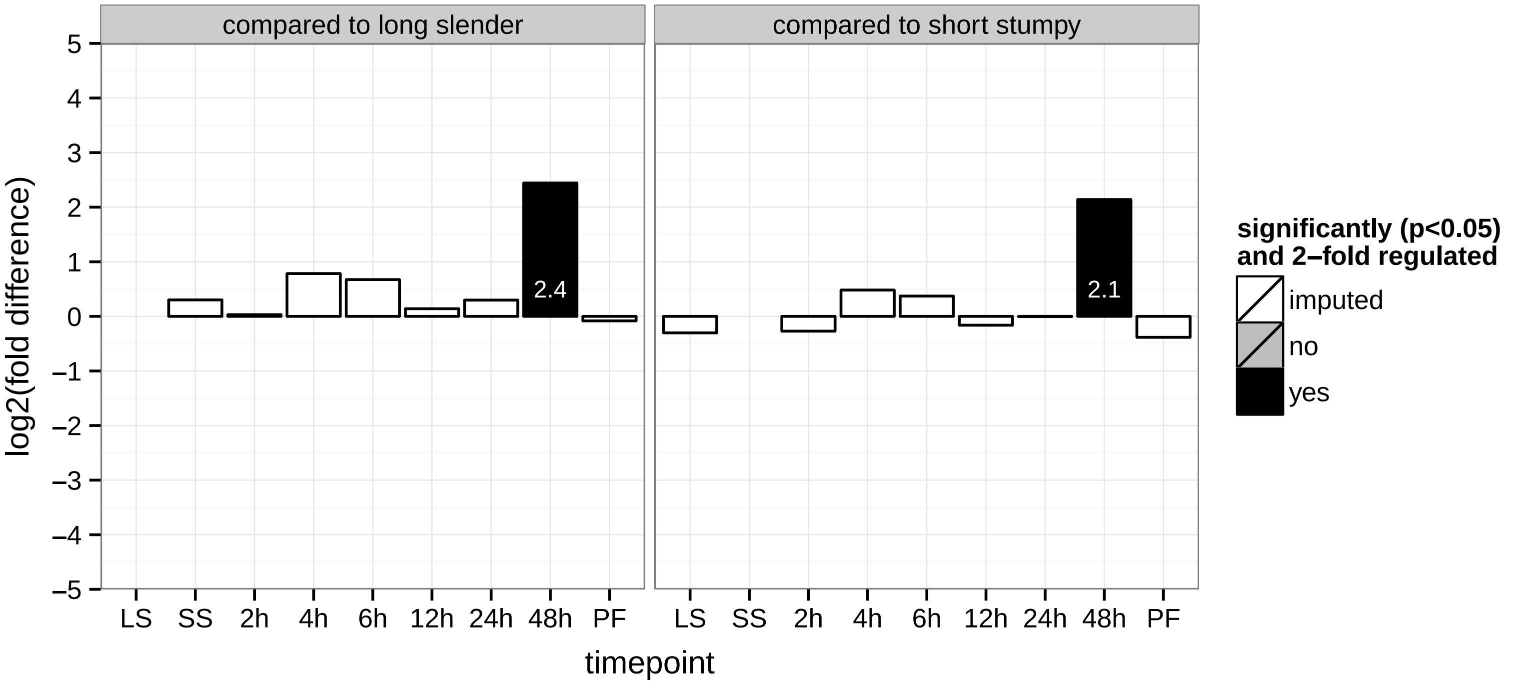
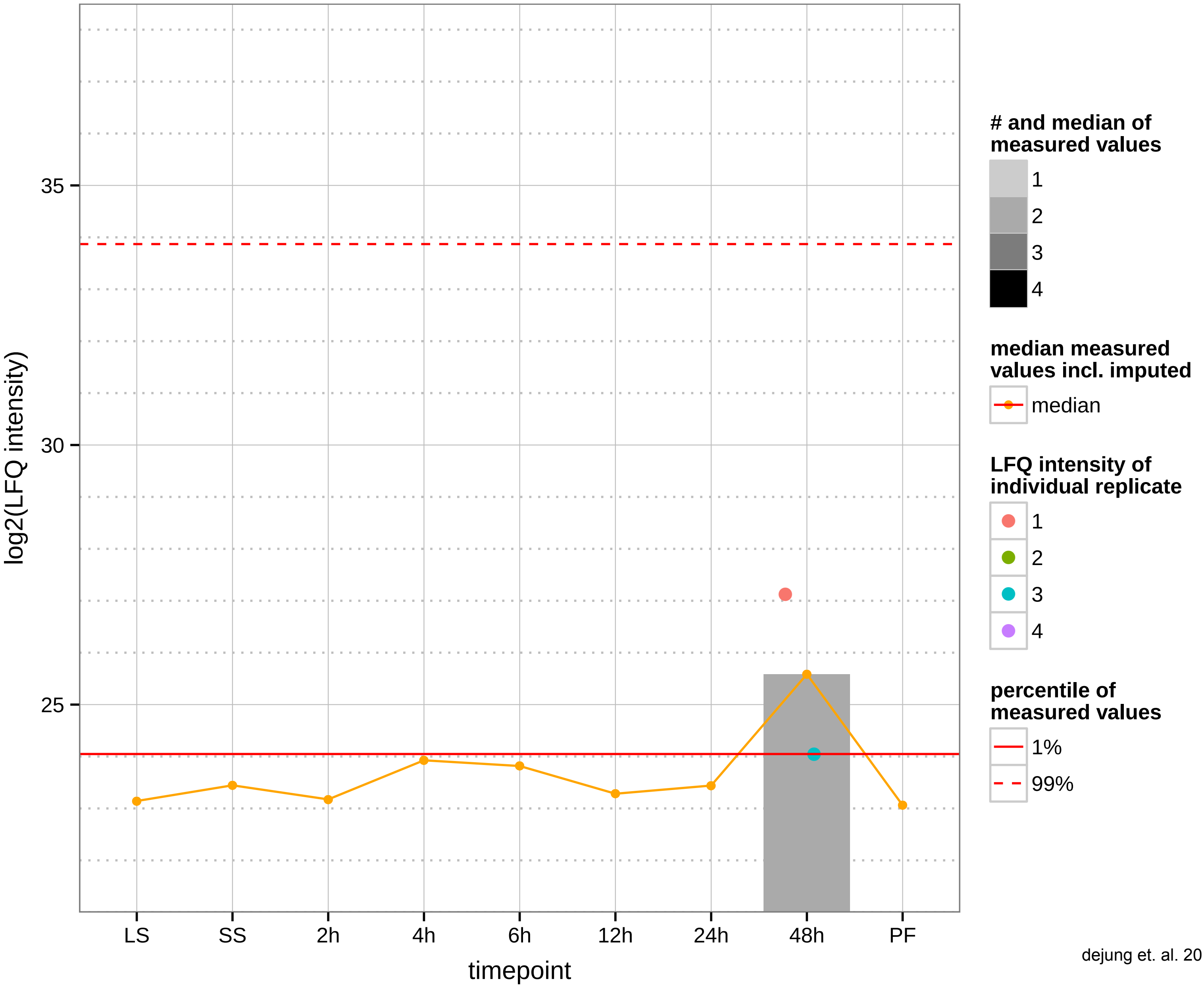
hypothetical protein, conserved
Tb927.11.13340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



phosphatidylinositol 3−related kinase, putative (ATR)
Tb927.11.14680
AGOF: 1−phosphatidylinositol−3−kinase activity, phosphotransferase activity, alcohol group as acceptor
AGOC: null
AGOP: cytokinesis checkpoint, growth
PGOF: phosphotransferase activity, alcohol group as acceptor, protein binding, transferase activity, transferring phosphorus−c
PGOC: null
PGOP: null





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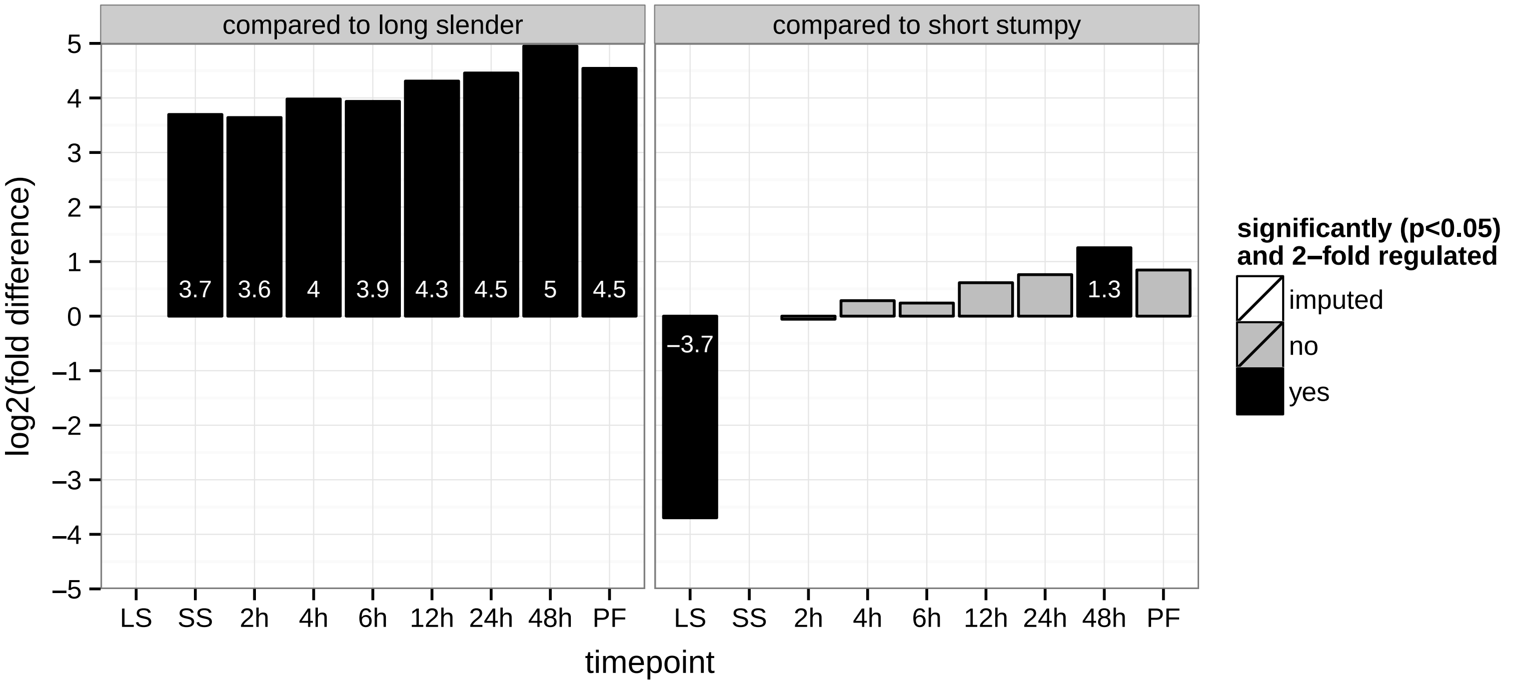
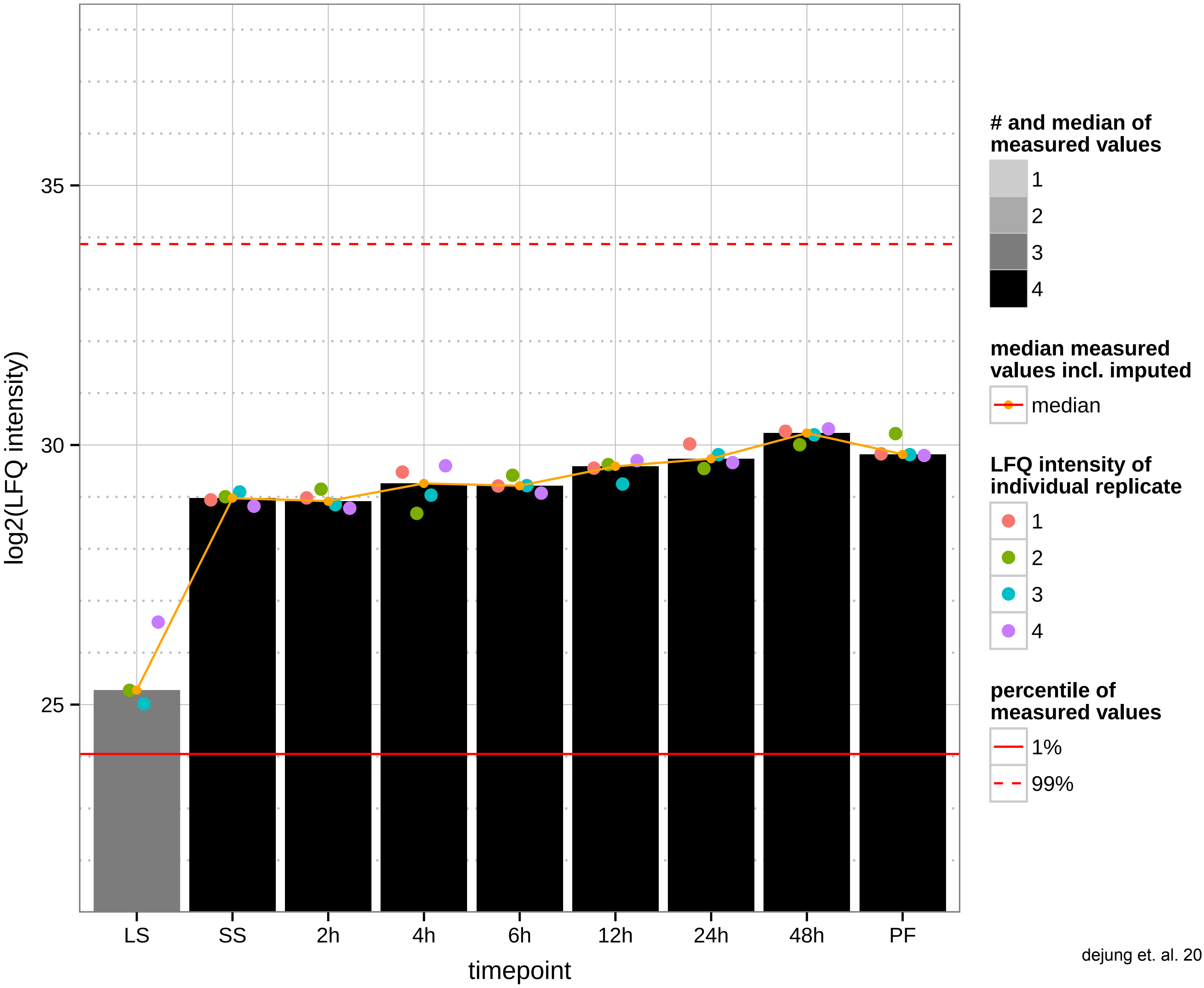
metalloprotease, putative, cell division protein FtsH homologue
Tb927.11.14730
AGOF: ATP binding, ATPase activity, metalloendopeptidase activity, zinc ion binding
AGOC: integral to membrane, mitochondrial inner membrane
AGOP: proteolysis
PGOF: ATP binding, metalloendopeptidase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: proteolysis





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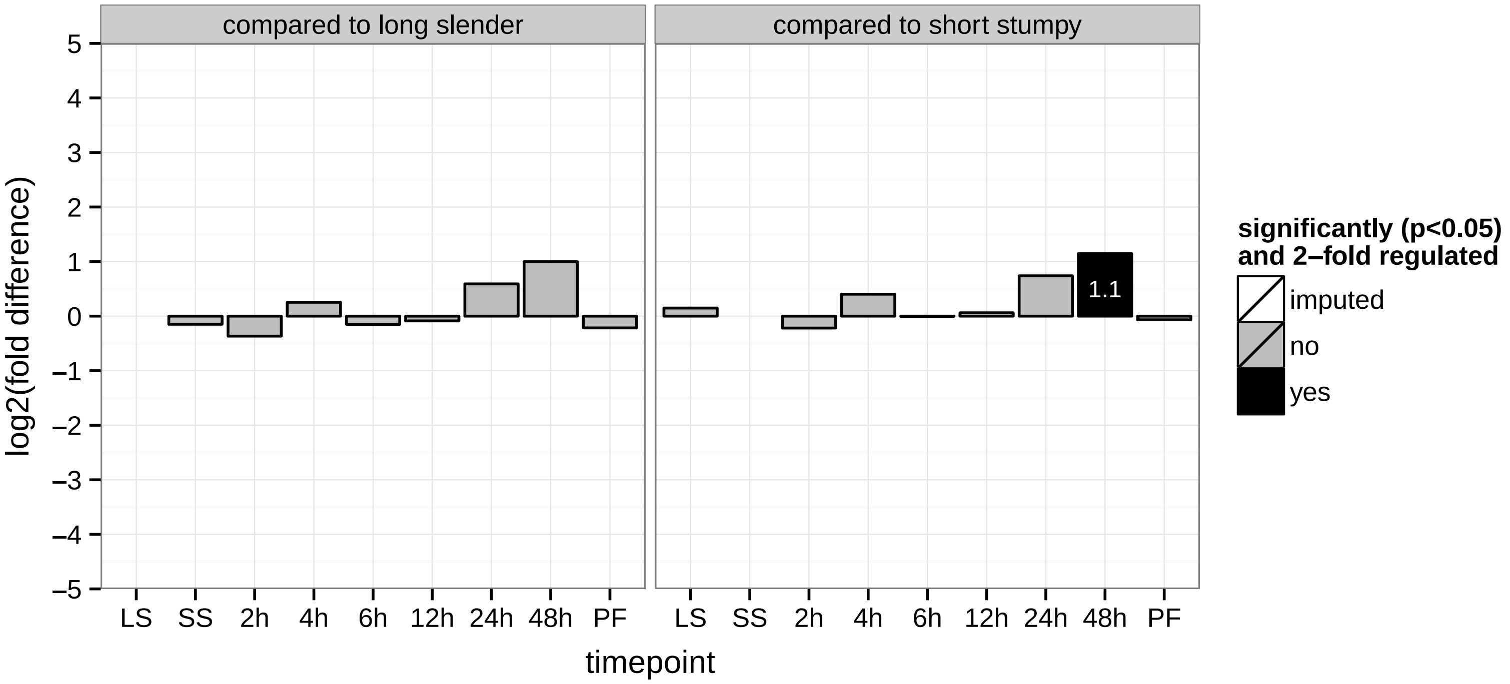
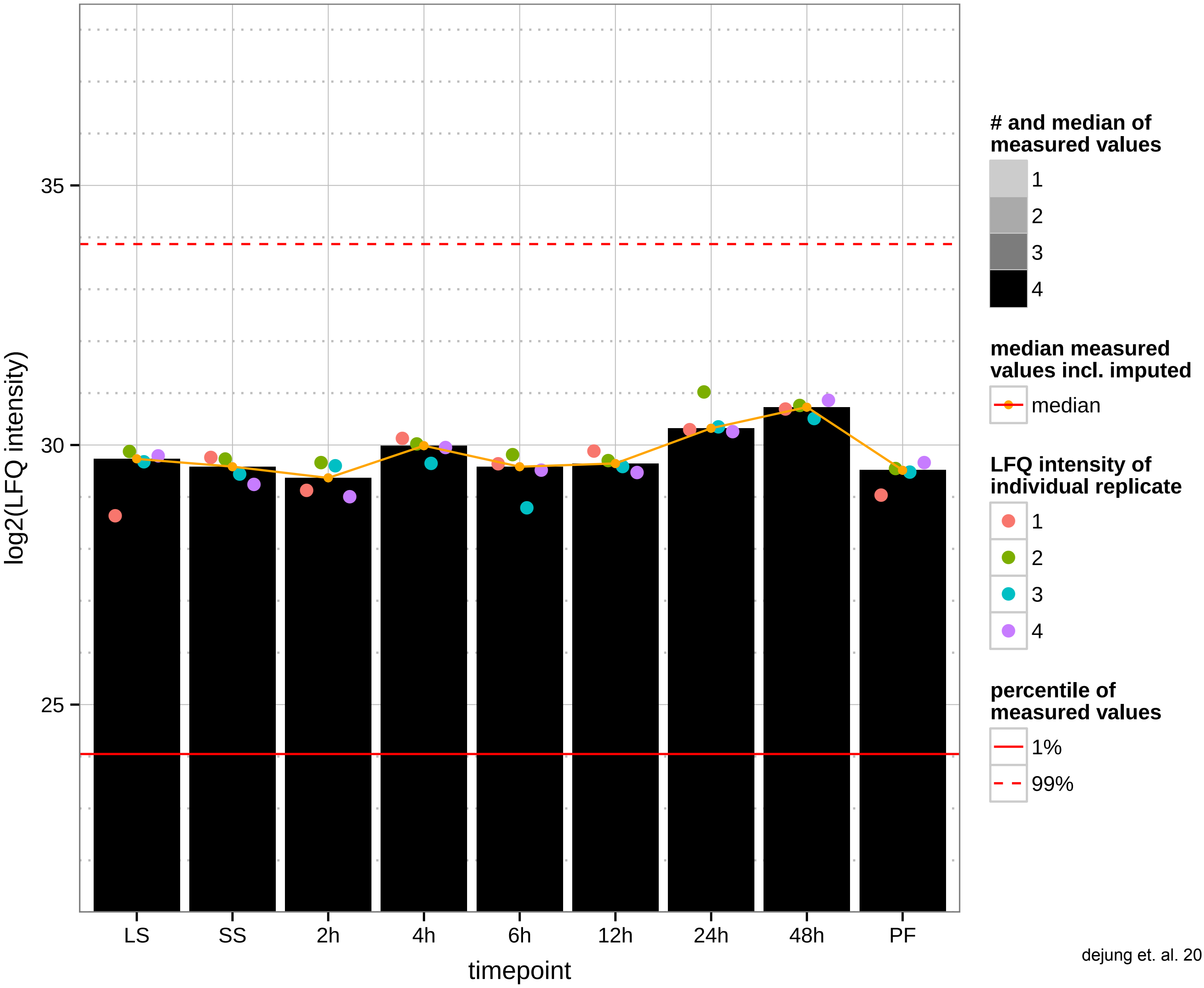
iron superoxide dismutase
Tb927.11.15910
AGOF: metal ion binding, superoxide dismutase activity
AGOC: null
AGOP: oxidation–reduction process, superoxide metabolic process
PGOF: metal ion binding, superoxide dismutase activity
PGOC: null
PGOP: oxidation–reduction process, superoxide metabolic process





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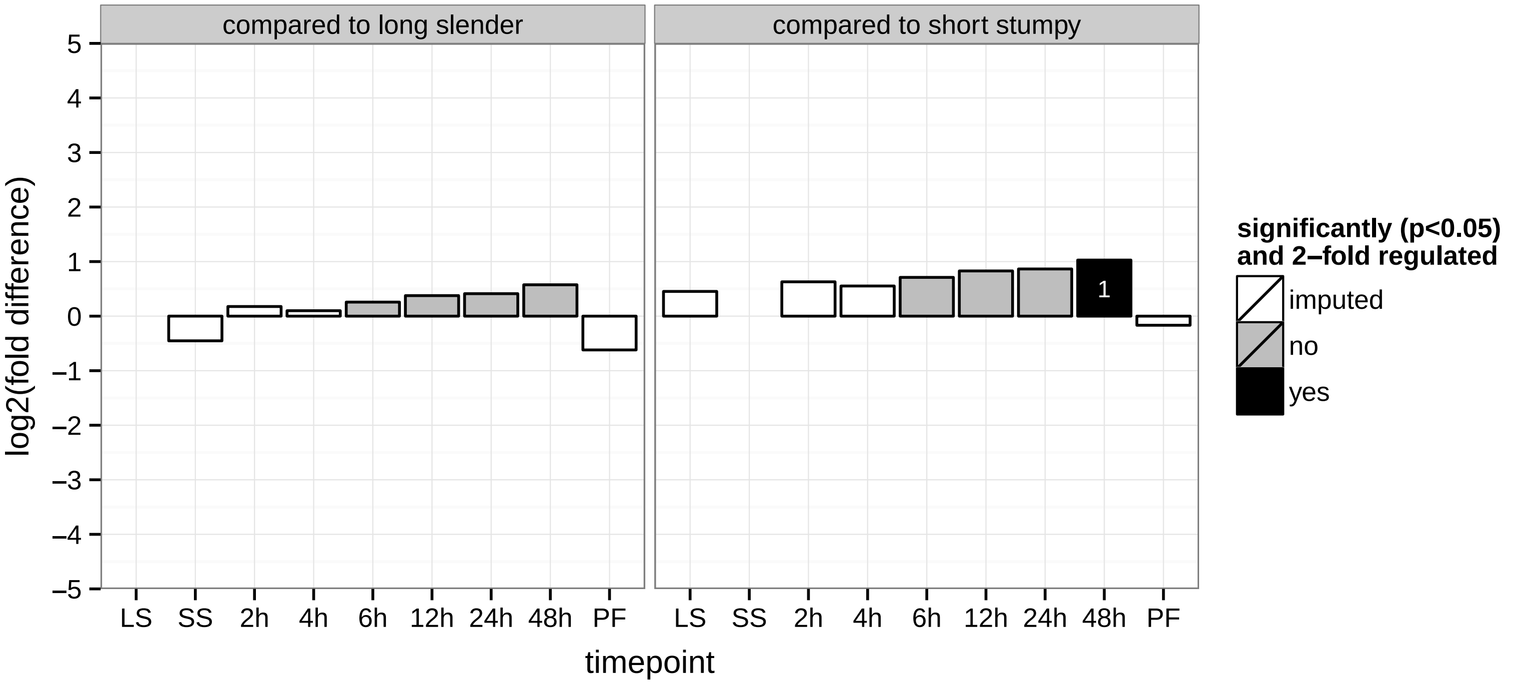
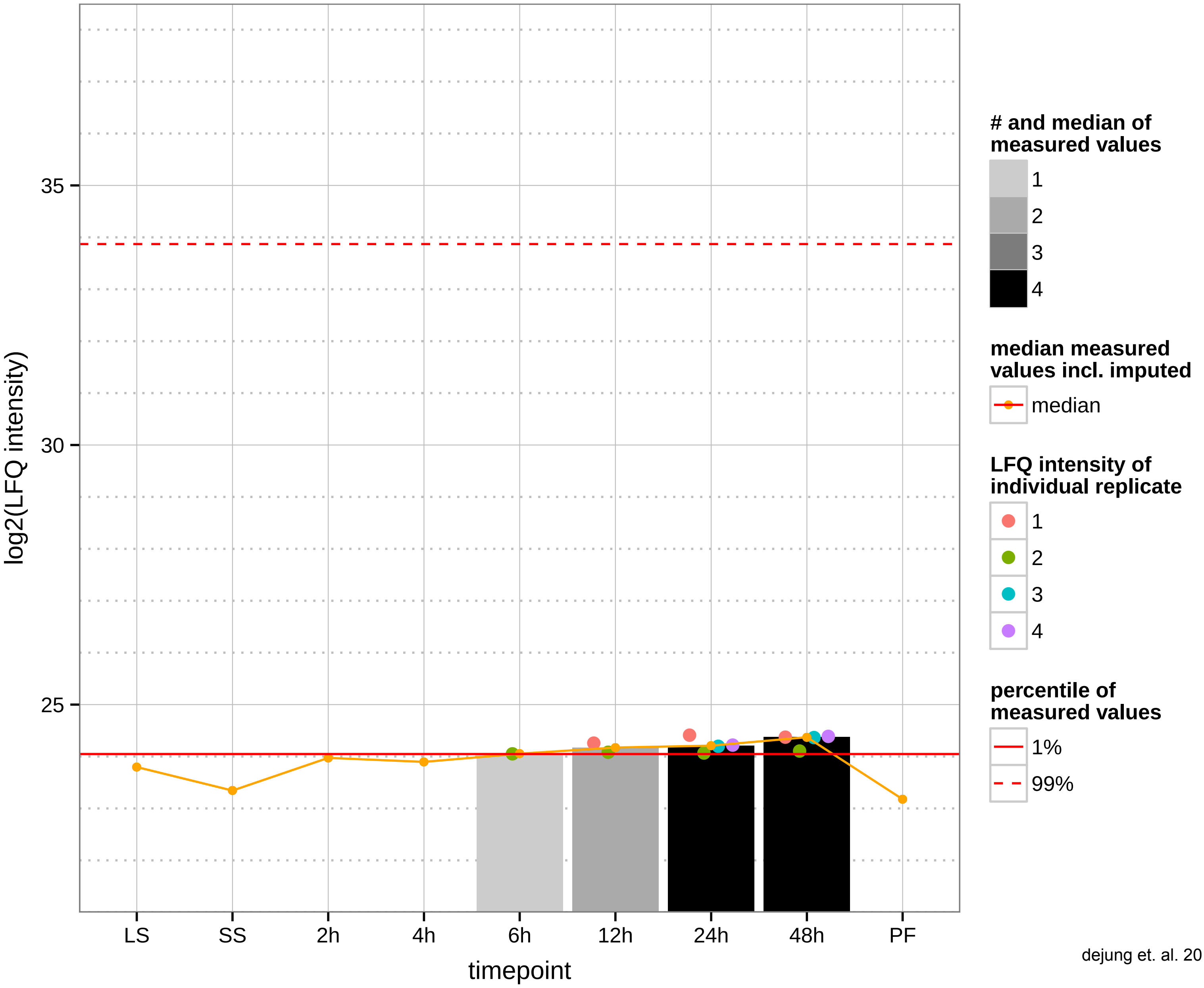
hypothetical protein, conserved
Tb927.11.1950
AGOF: RNA binding, ribonuclease III activity
AGOC: mitochondrion
AGOP: RNA processing
PGOF: RNA binding, ribonuclease III activity
PGOC: null
PGOP: RNA processing





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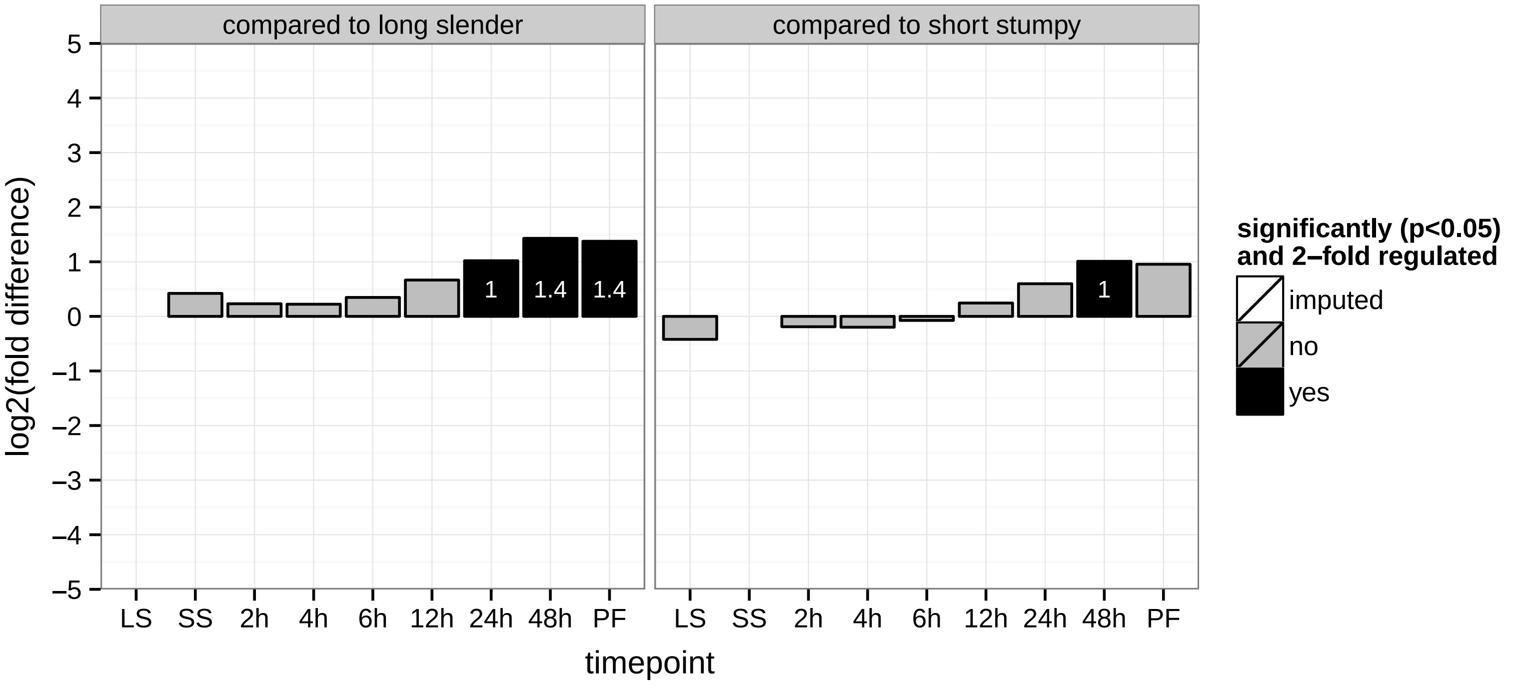
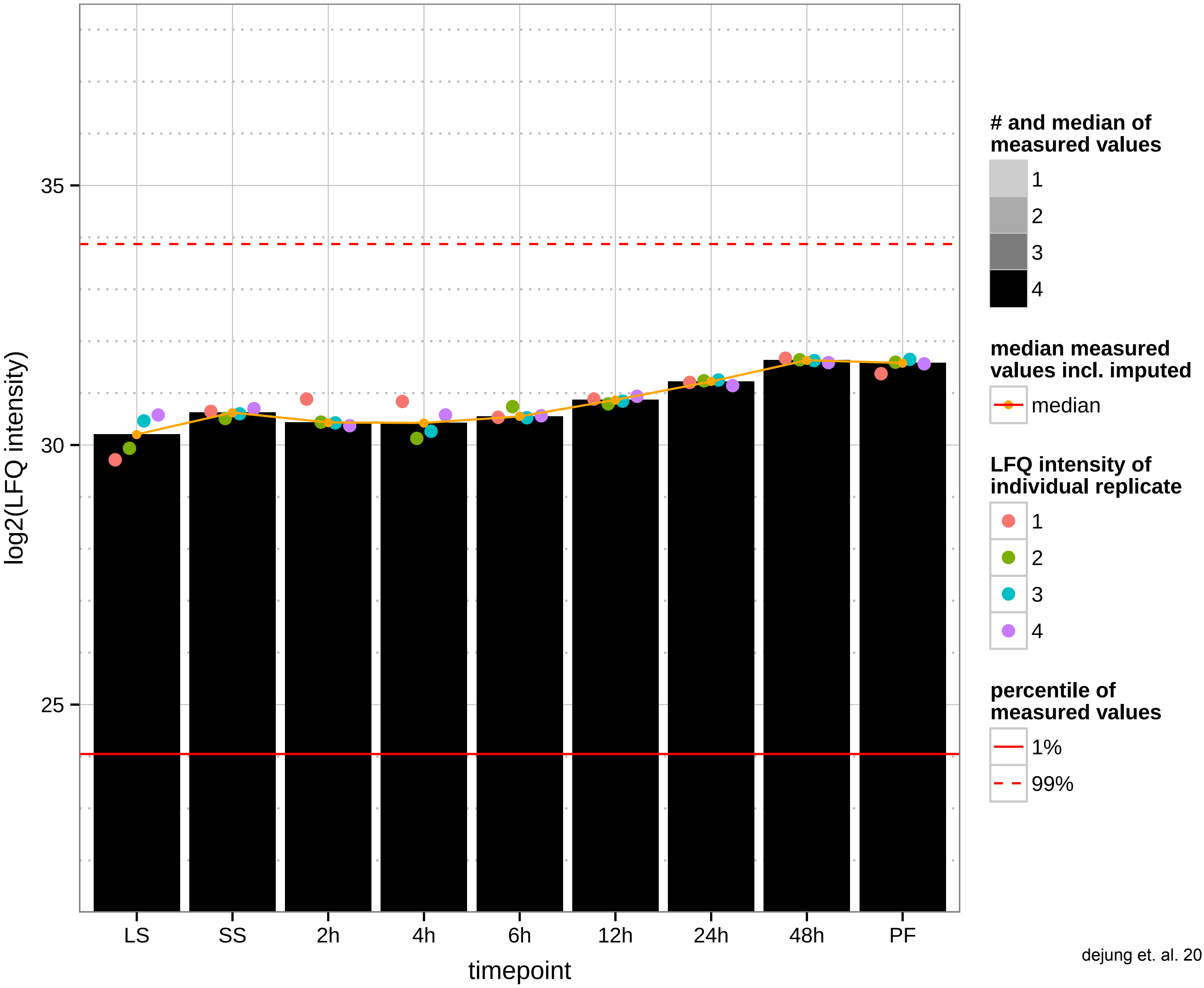
arginyl–tRNA synthetase, putative
Tb927.11.1990
AGOF: ATP binding, arginine–tRNA ligase activity
AGOC: cytoplasm
AGOP: arginyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, arginine–tRNA ligase activity, nucleotide binding
PGOC: cytoplasm
PGOP: arginyl–tRNA aminoacylation, tRNA aminoacylation for protein translation





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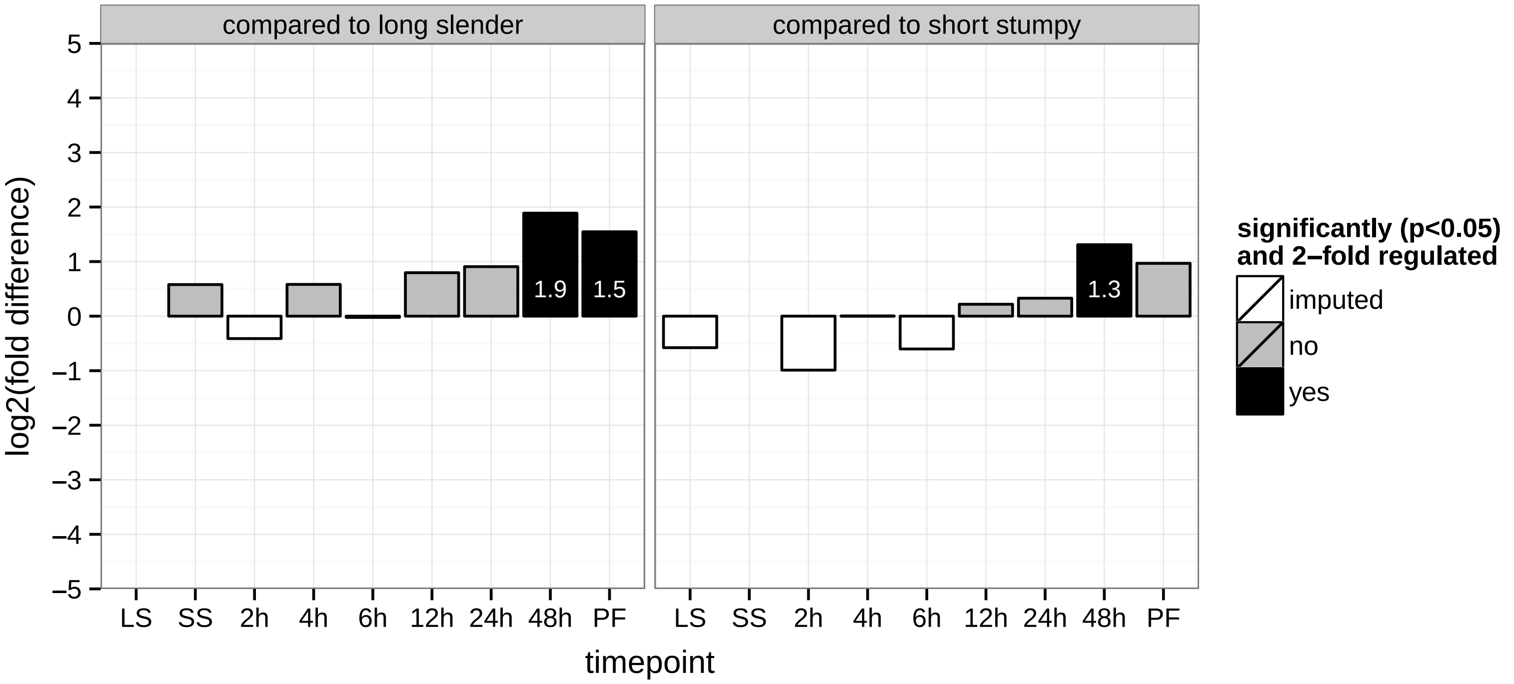
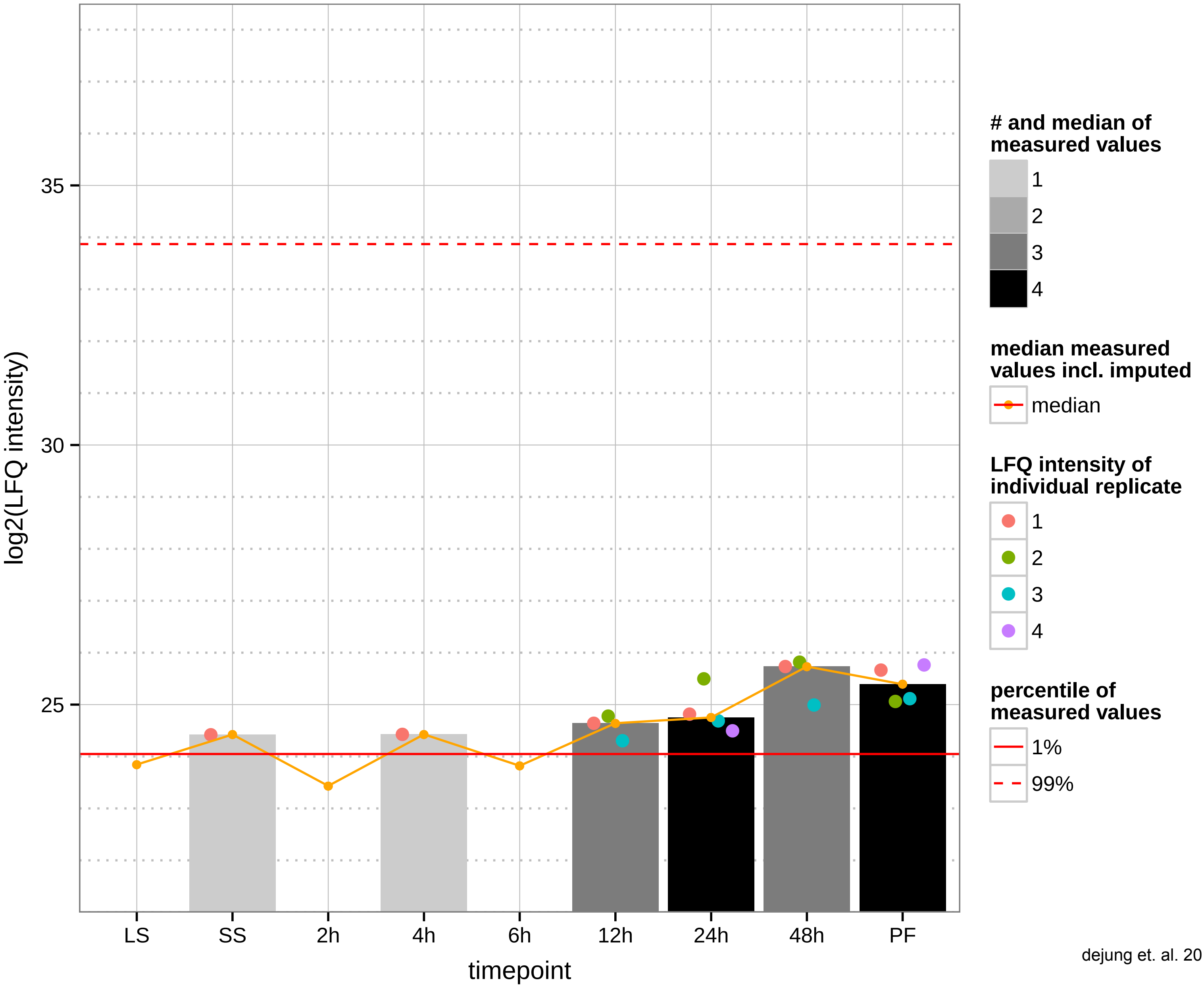
hypothetical protein, conserved
Tb927.11.4330
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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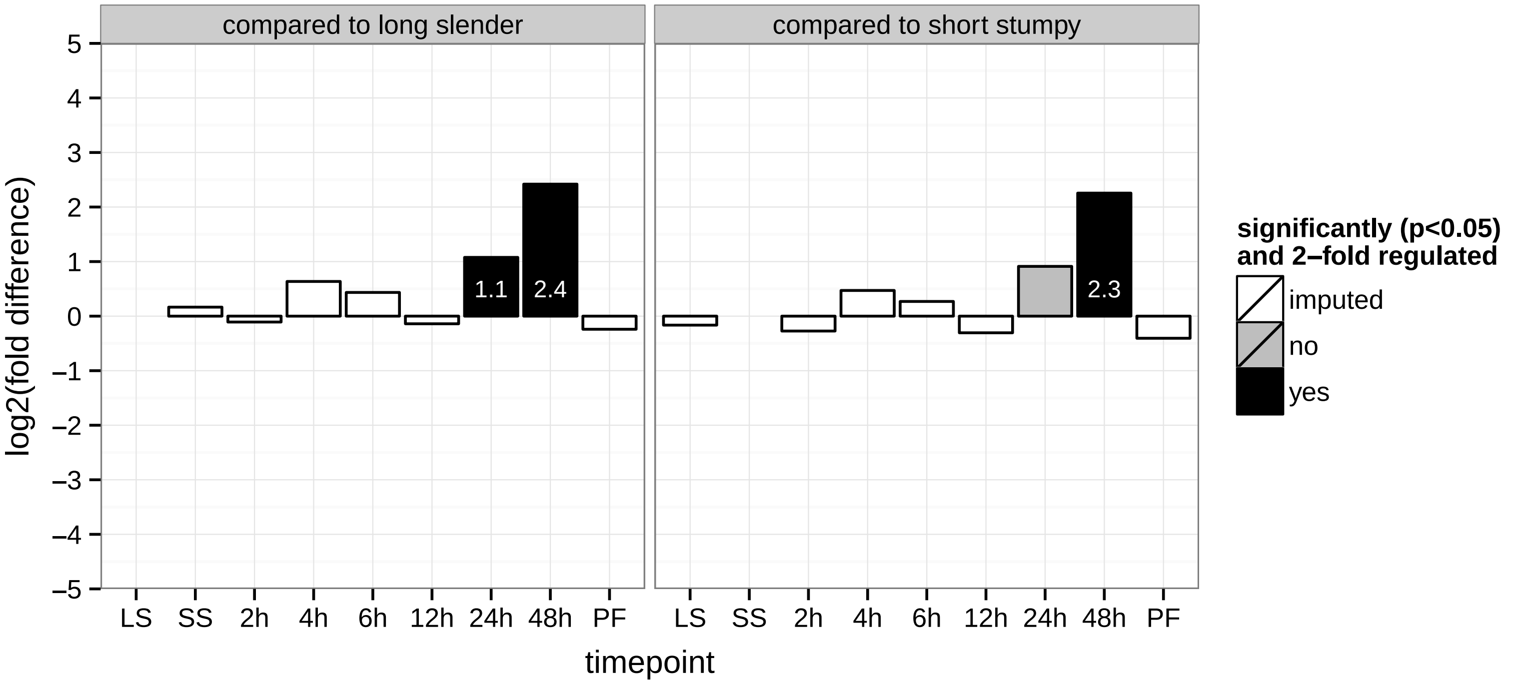
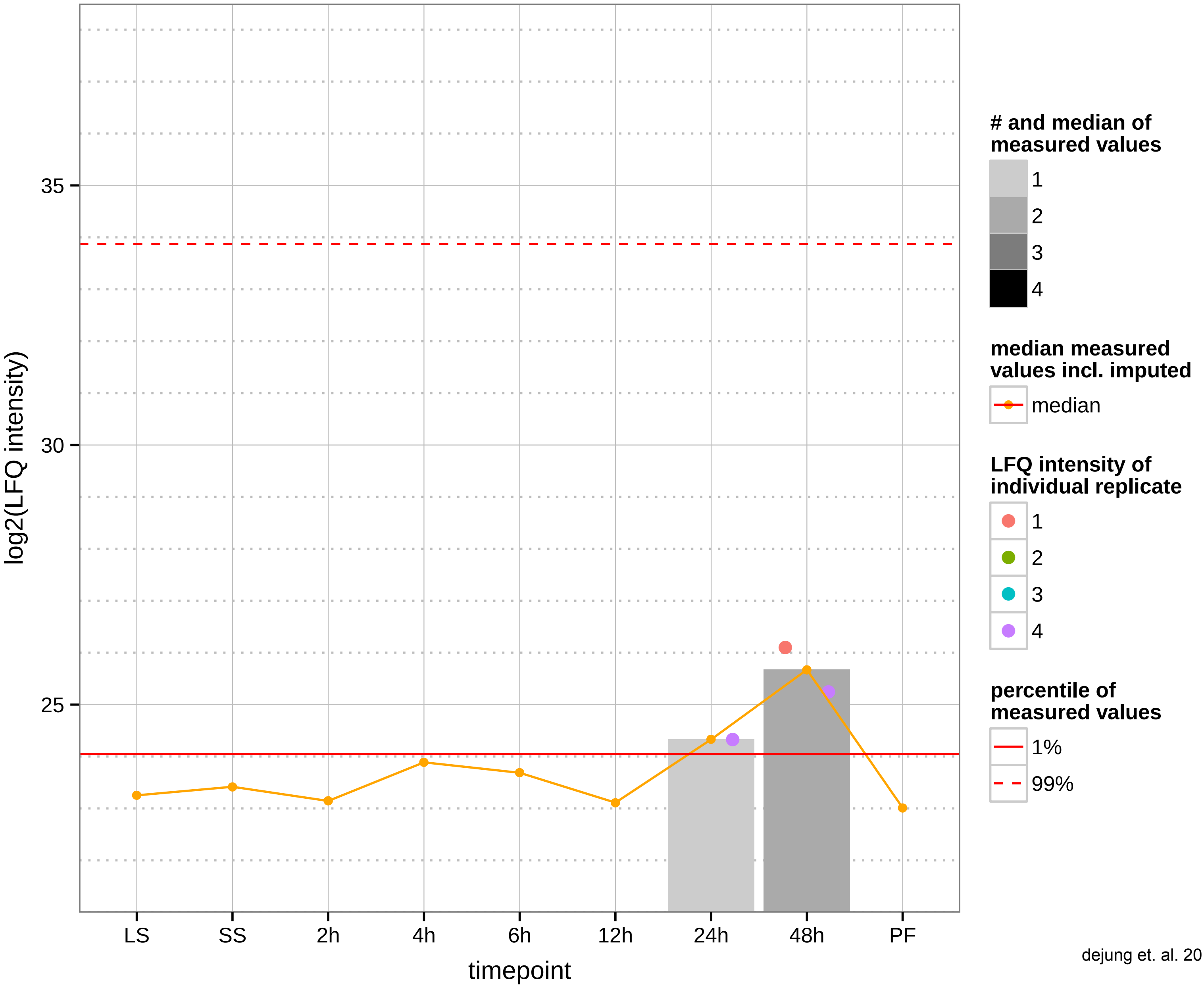
aspartate aminotransferase, mitochondrial
Tb927.11.5090
AGOF: L−alanine:2−oxoglutarate aminotransferase activity, pyridoxal phosphate binding, transaminase activity
AGOC: mitochondrion
AGOP: L−methionine salvage from methylthioadenosine, biosynthetic process
PGOF: pyridoxal phosphate binding, transferase activity
PGOC: null
PGOP: biosynthetic process





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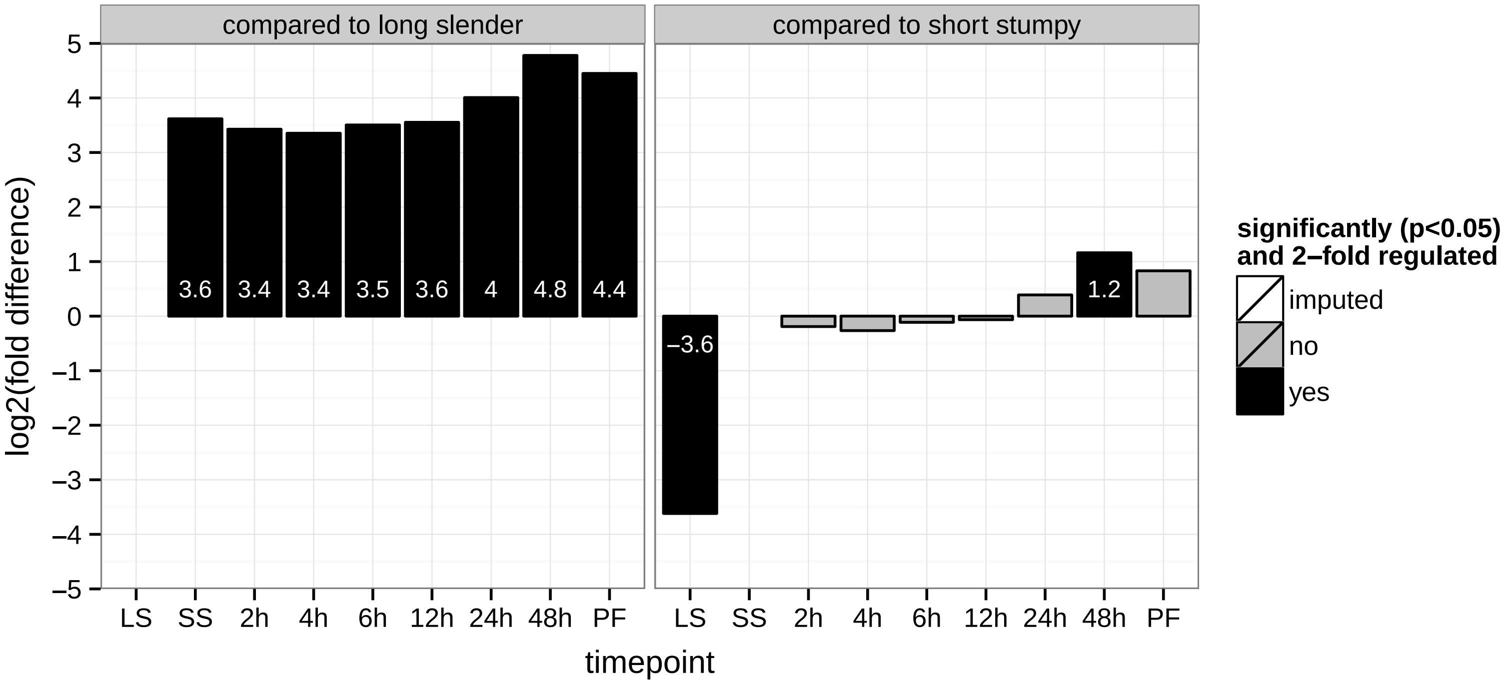
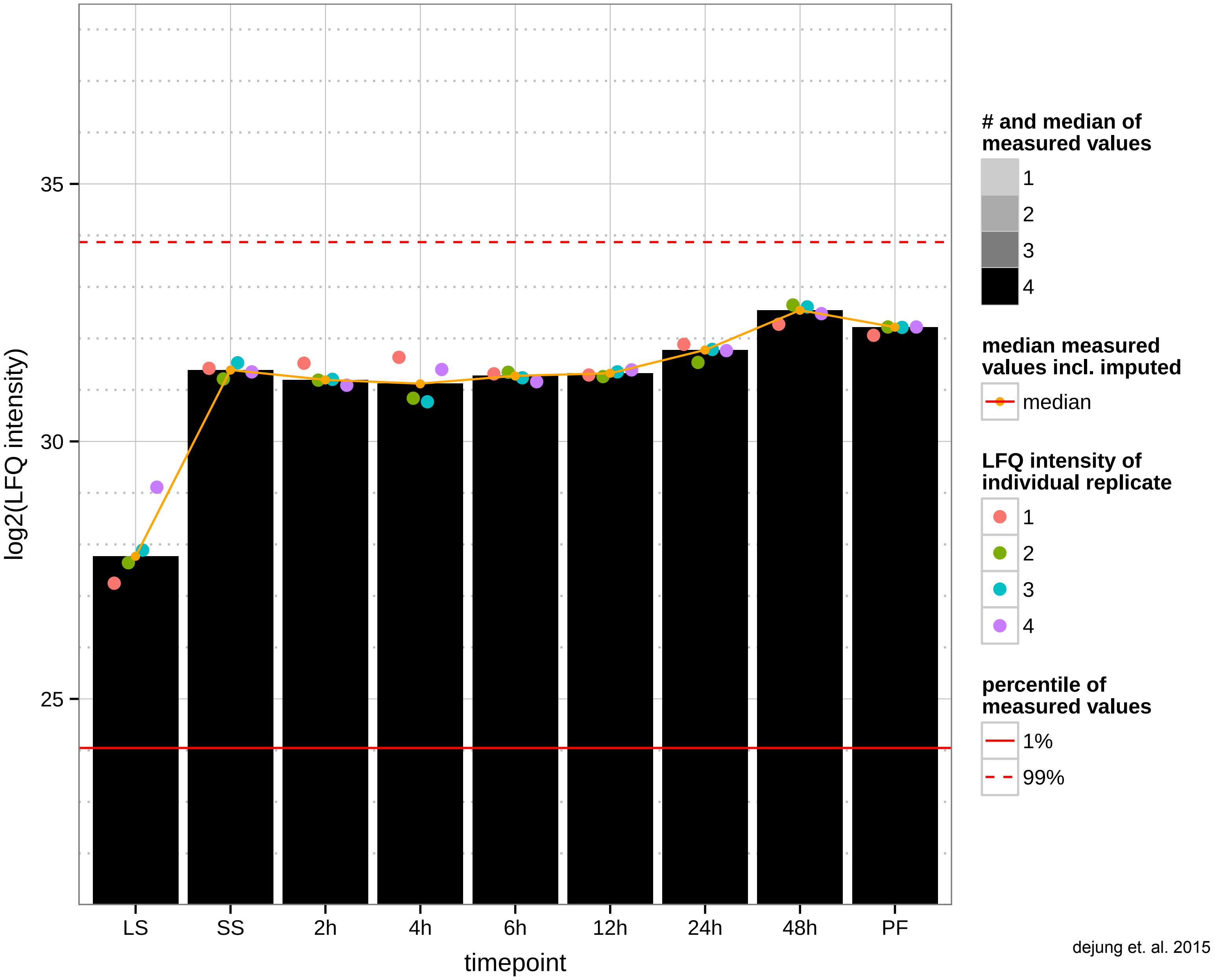
malic enzyme
Tb927.11.5440
AGOF: NAD binding, malic enzyme activity, oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP as
AGOC: cytosol
AGOP: malate metabolic process
PGOF: NAD binding, malate dehydrogenase (oxaloacetate−decarboxylating) activity, malic enzyme activity, oxidoreductase ac
PGOC: null
PGOP: malate metabolic process, oxidation−reduction process





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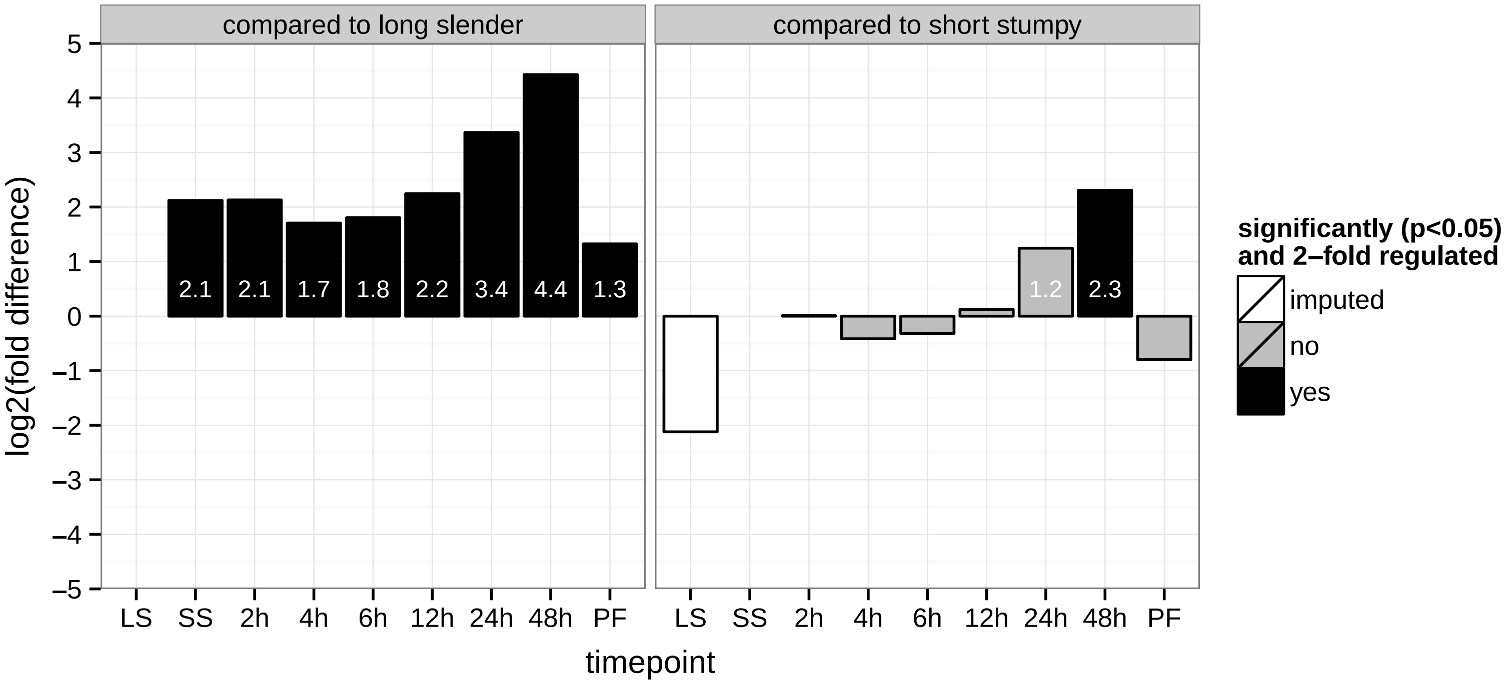
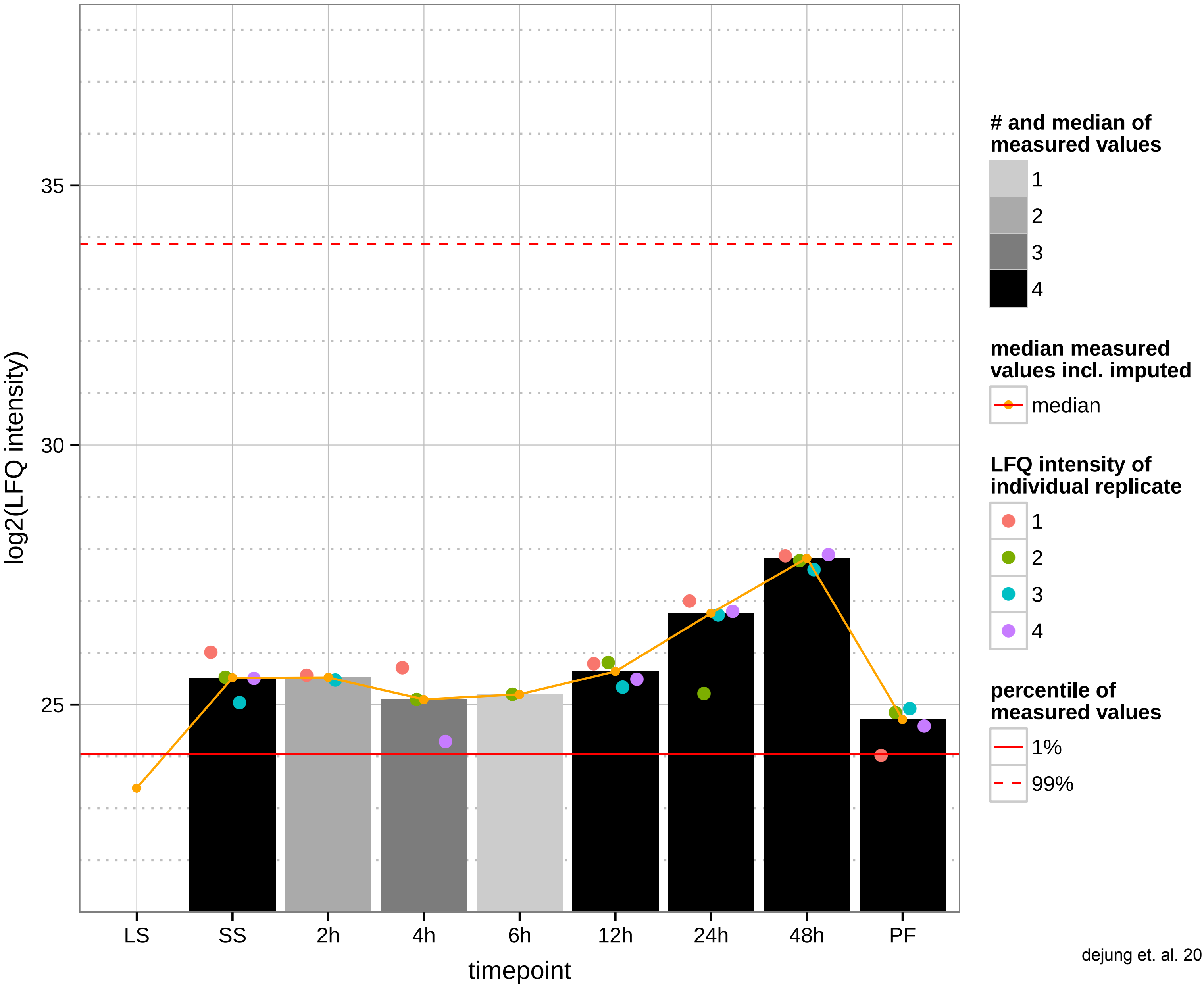
hypothetical protein, conserved
Tb927.11.6040
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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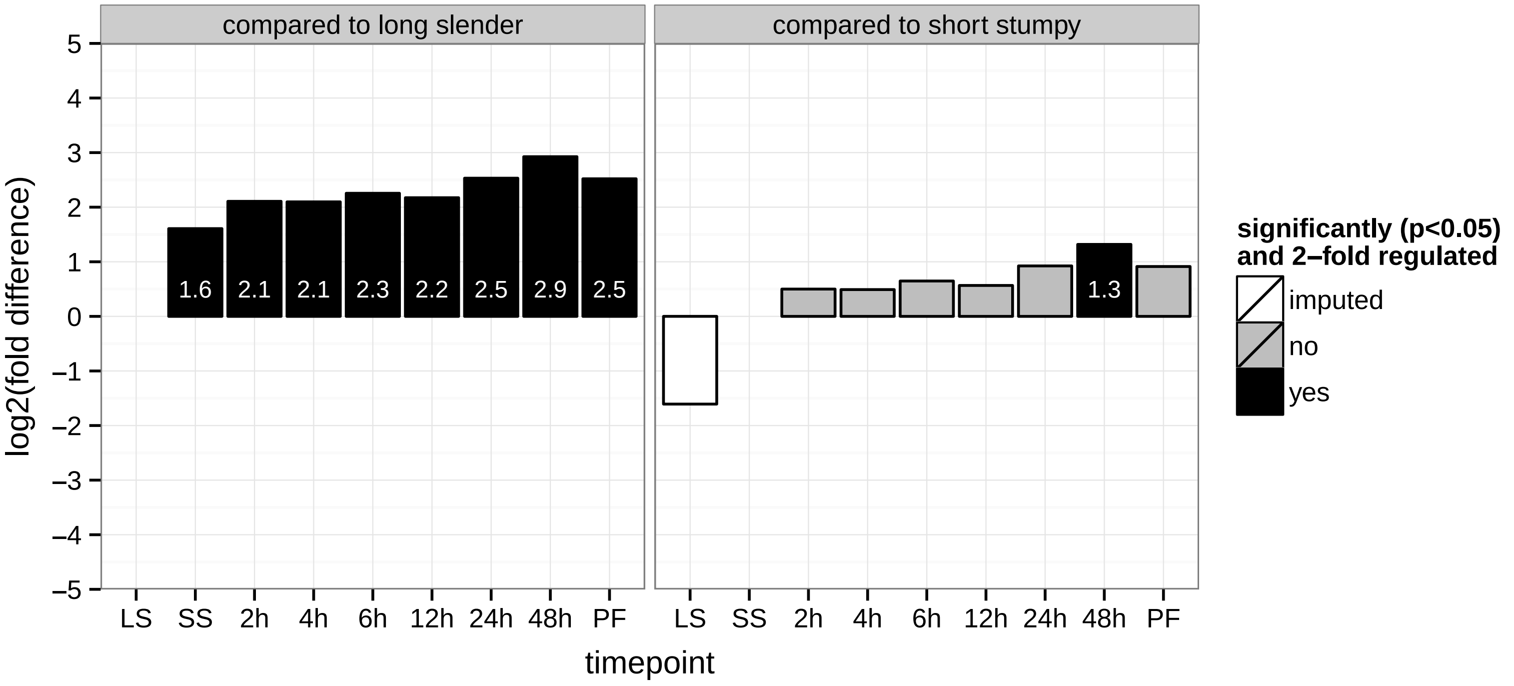
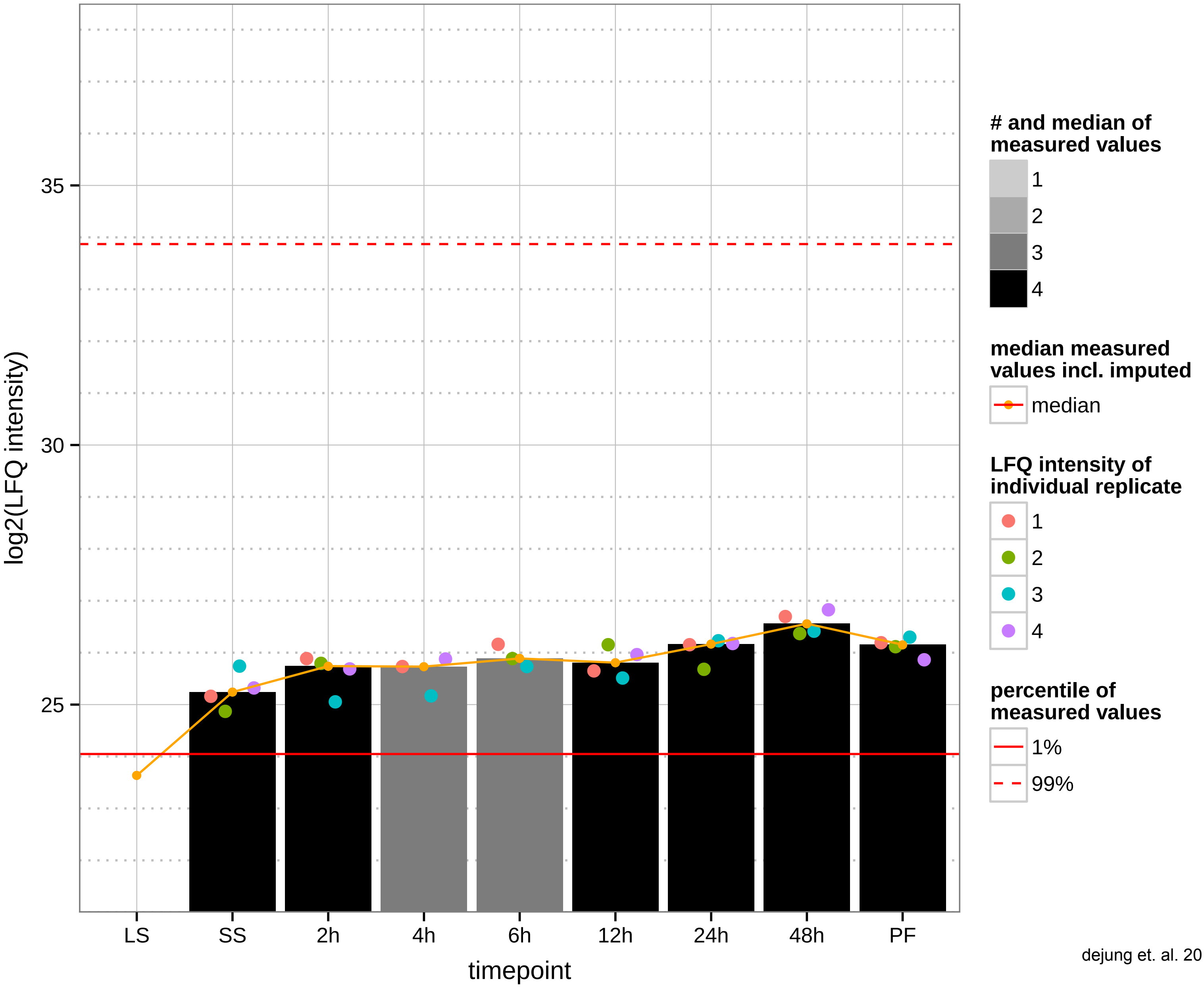
hypothetical protein, conserved
Tb927.11.6570
AGOF: calcium ion binding
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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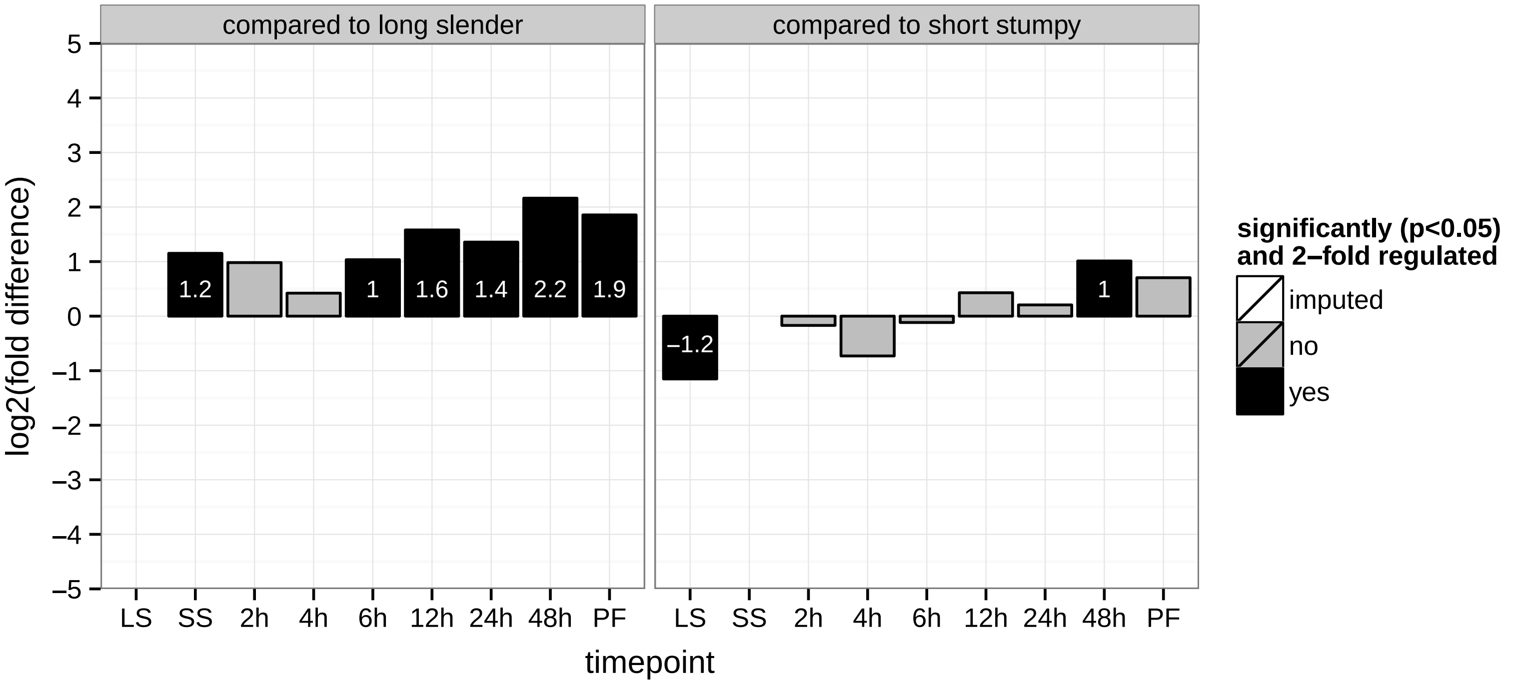
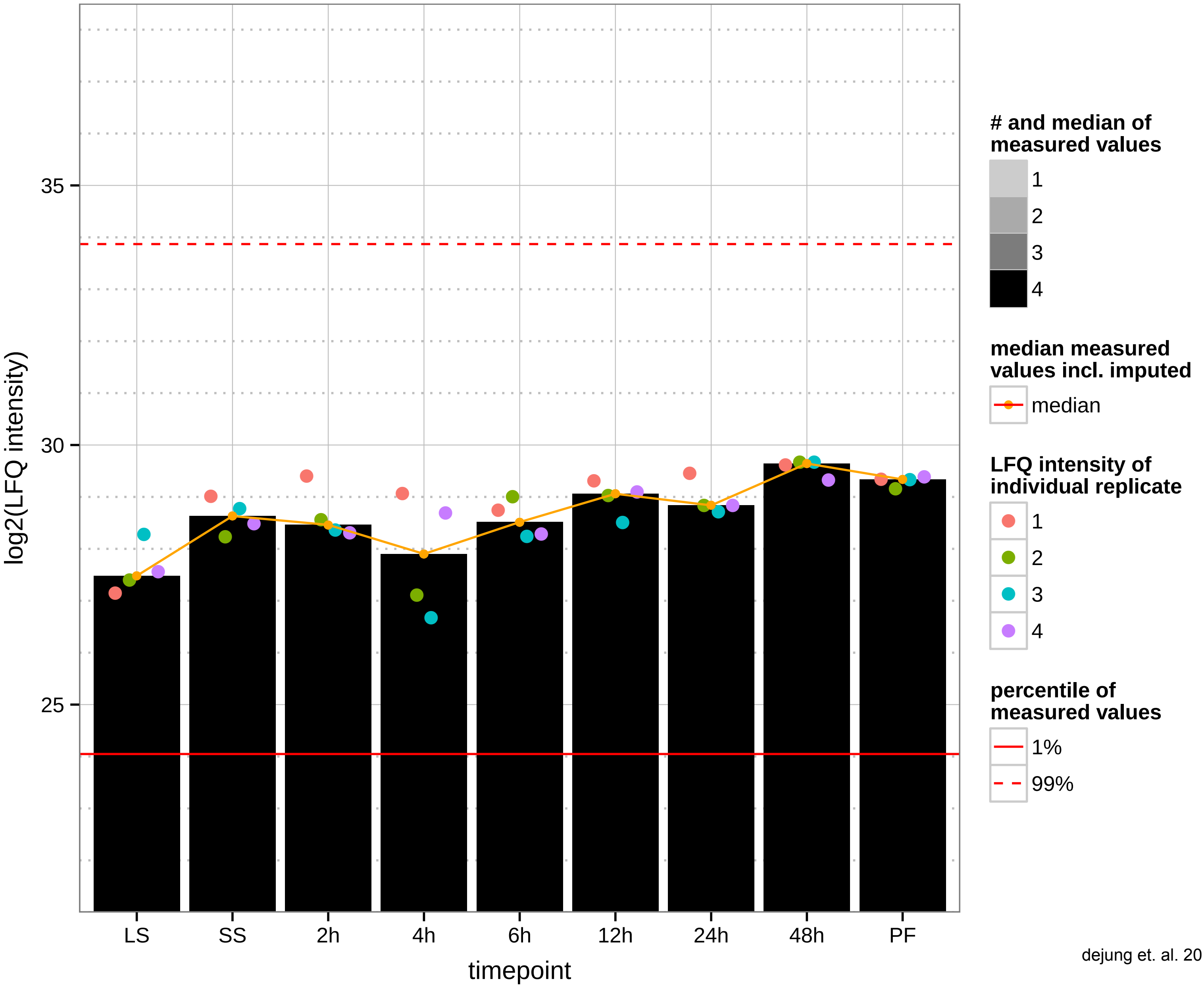
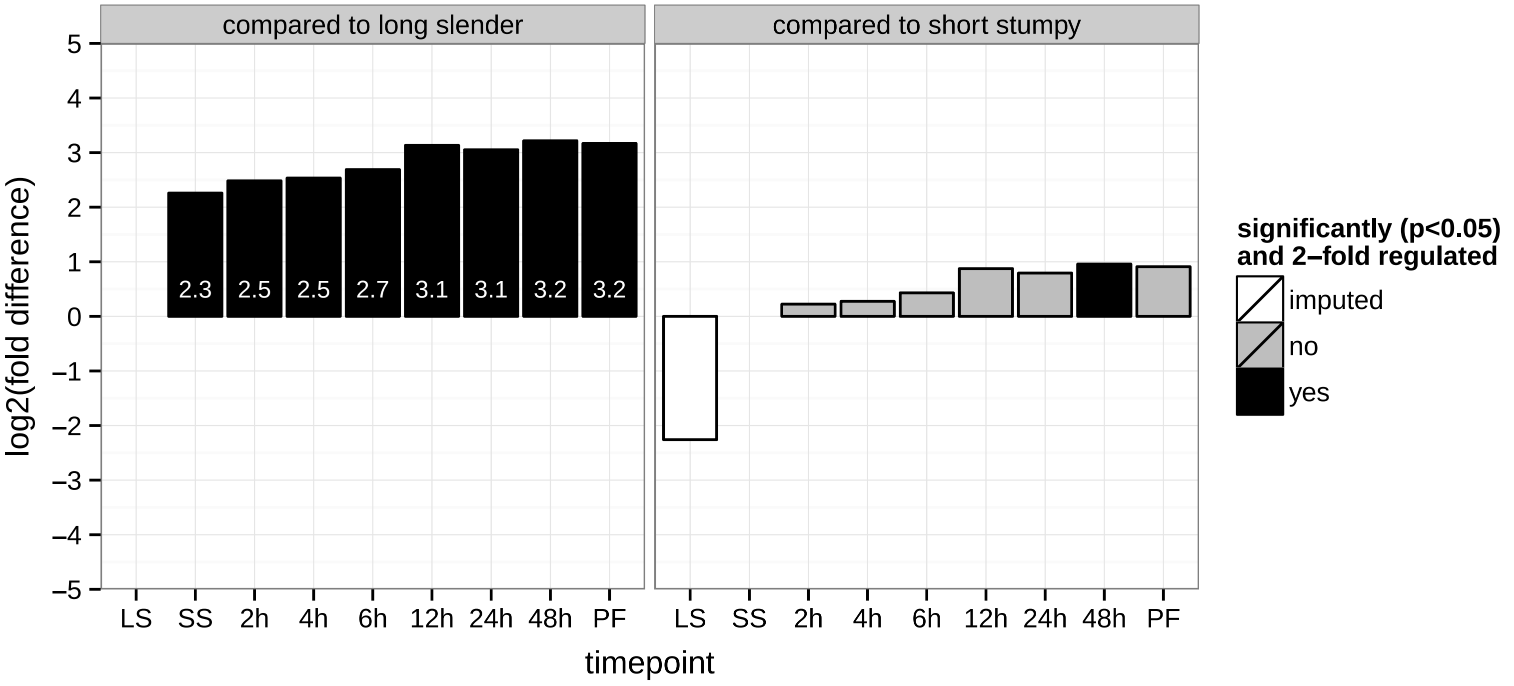
replication factor A, 51kDa subunit, putative
Tb927.11.9130
AGOF: DNA binding
AGOC: nucleus
AGOP: DNA replication
PGOF: DNA binding, nucleic acid binding
PGOC: nucleus
PGOP: DNA replication

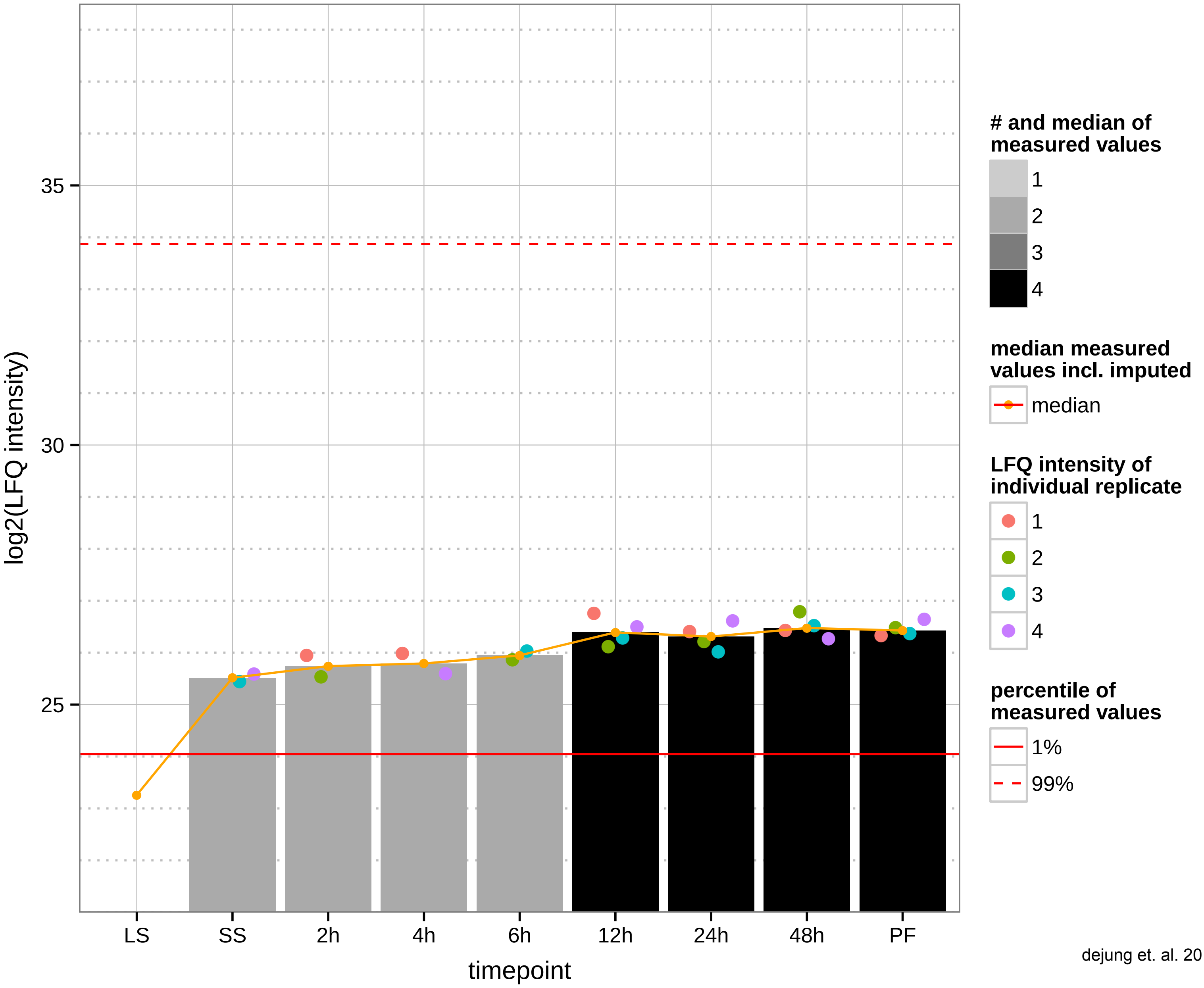




dejung et. al. 2015

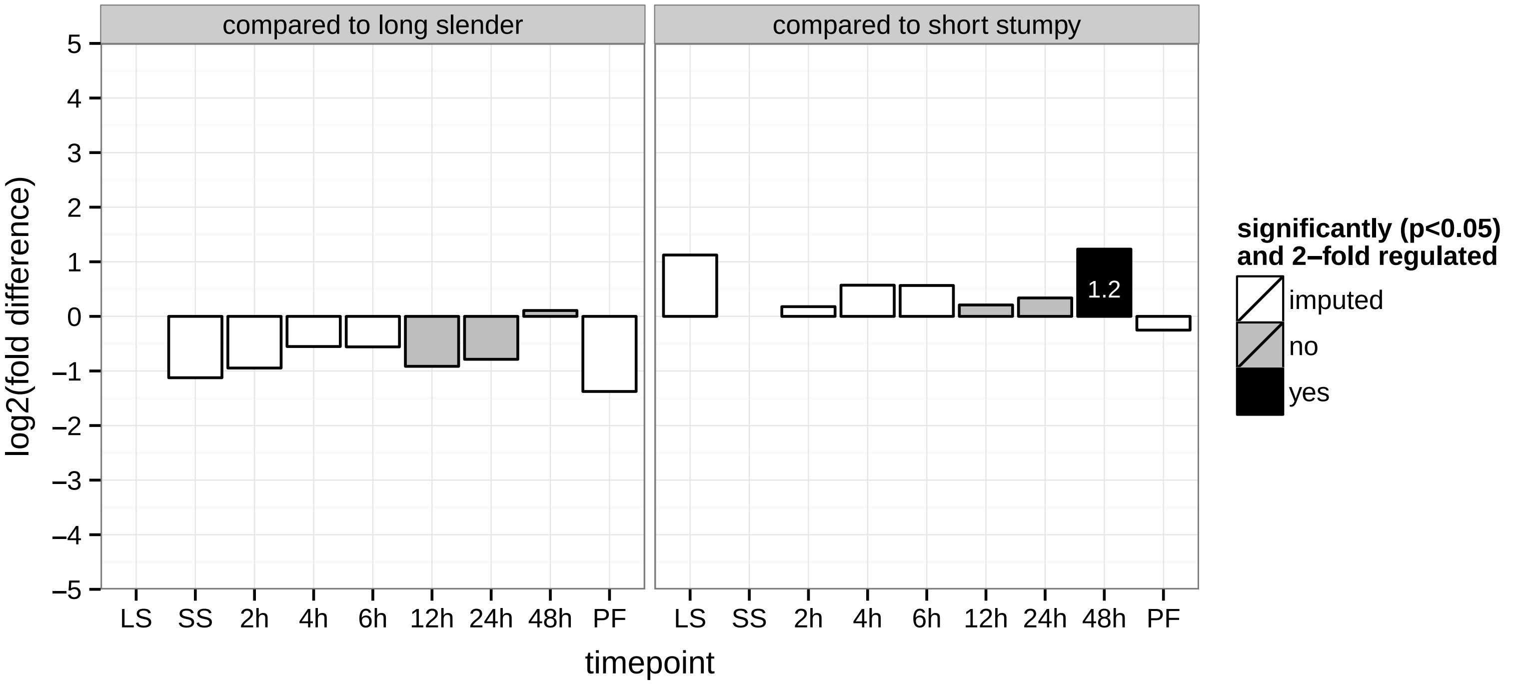
hypothetical protein, conserved
Tb927.11.9210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

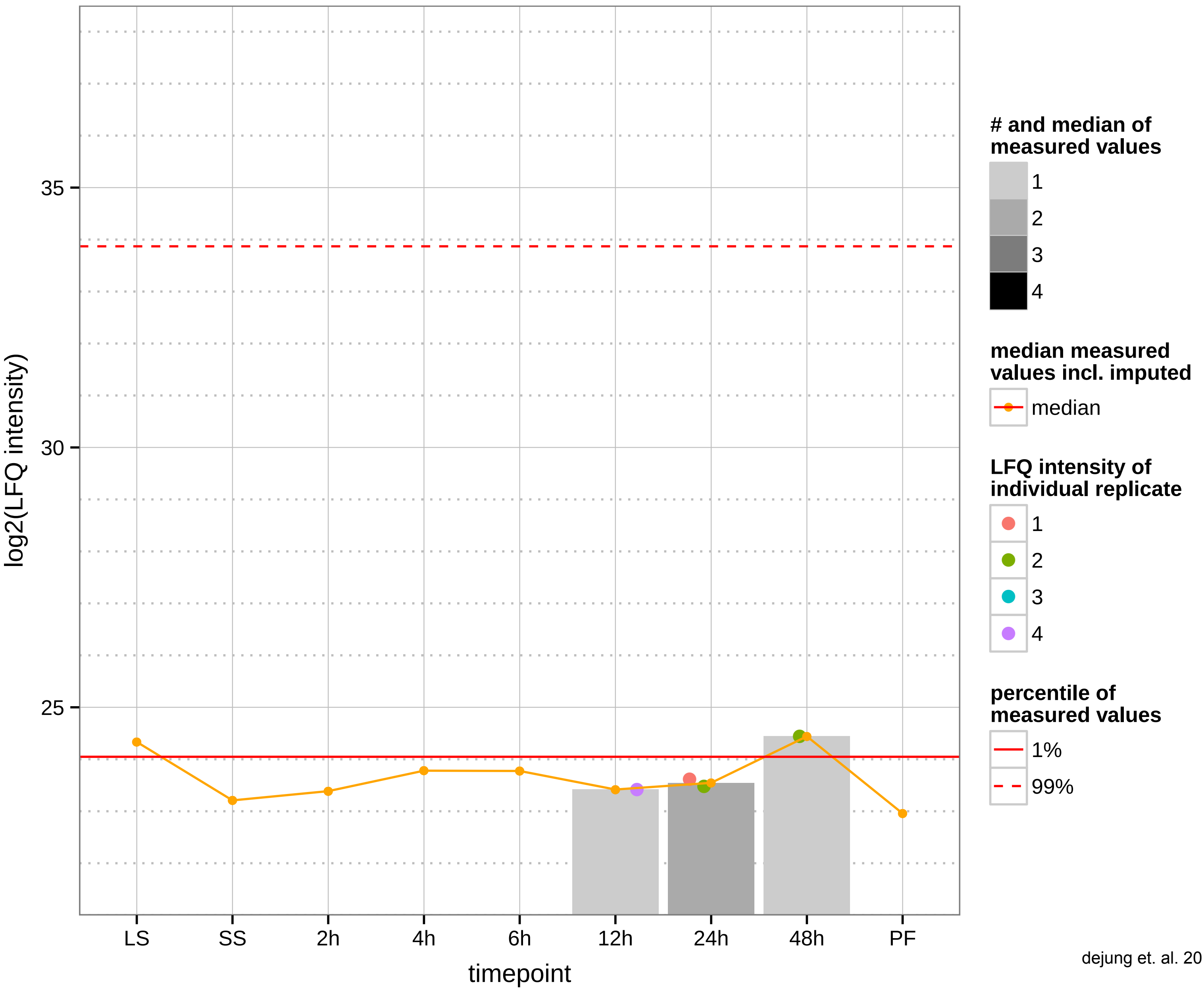




dejung et. al. 2015

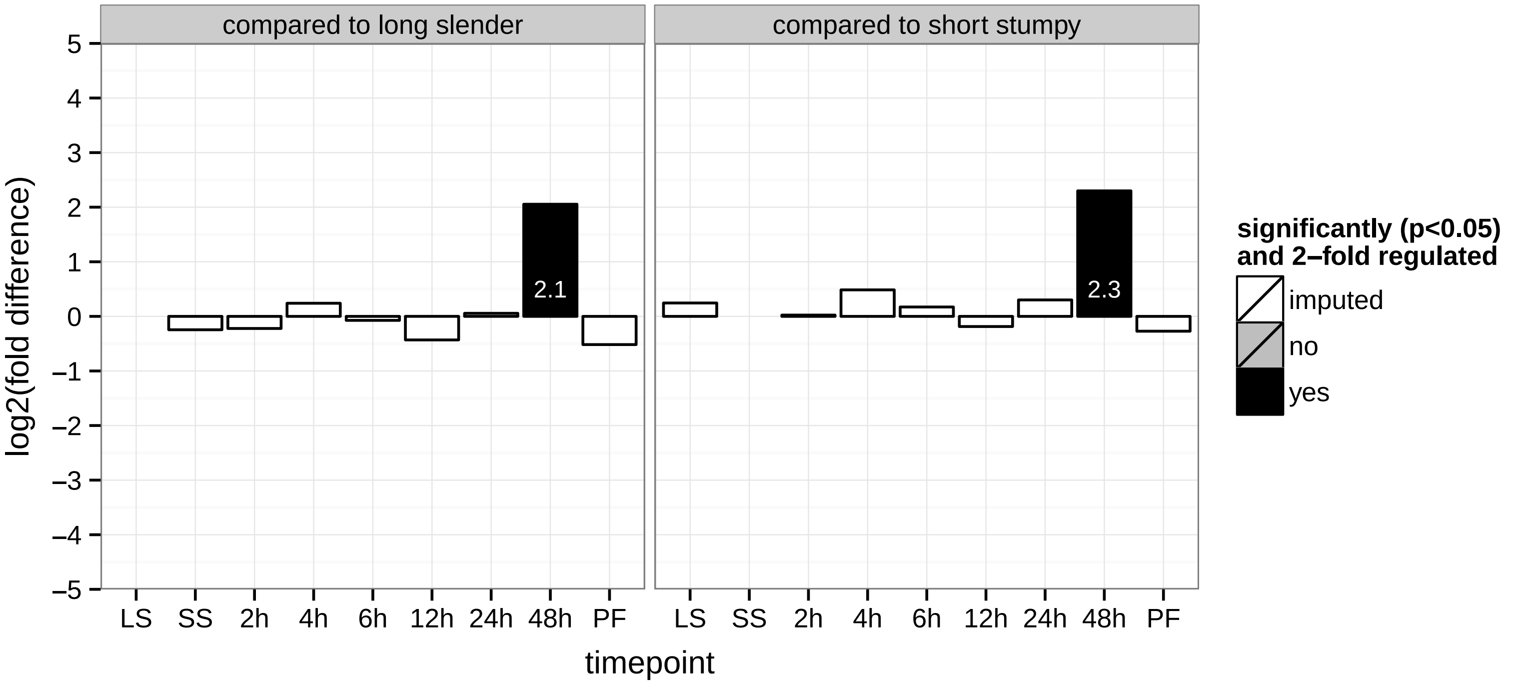
hypothetical protein, conserved
Tb927.11.9230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

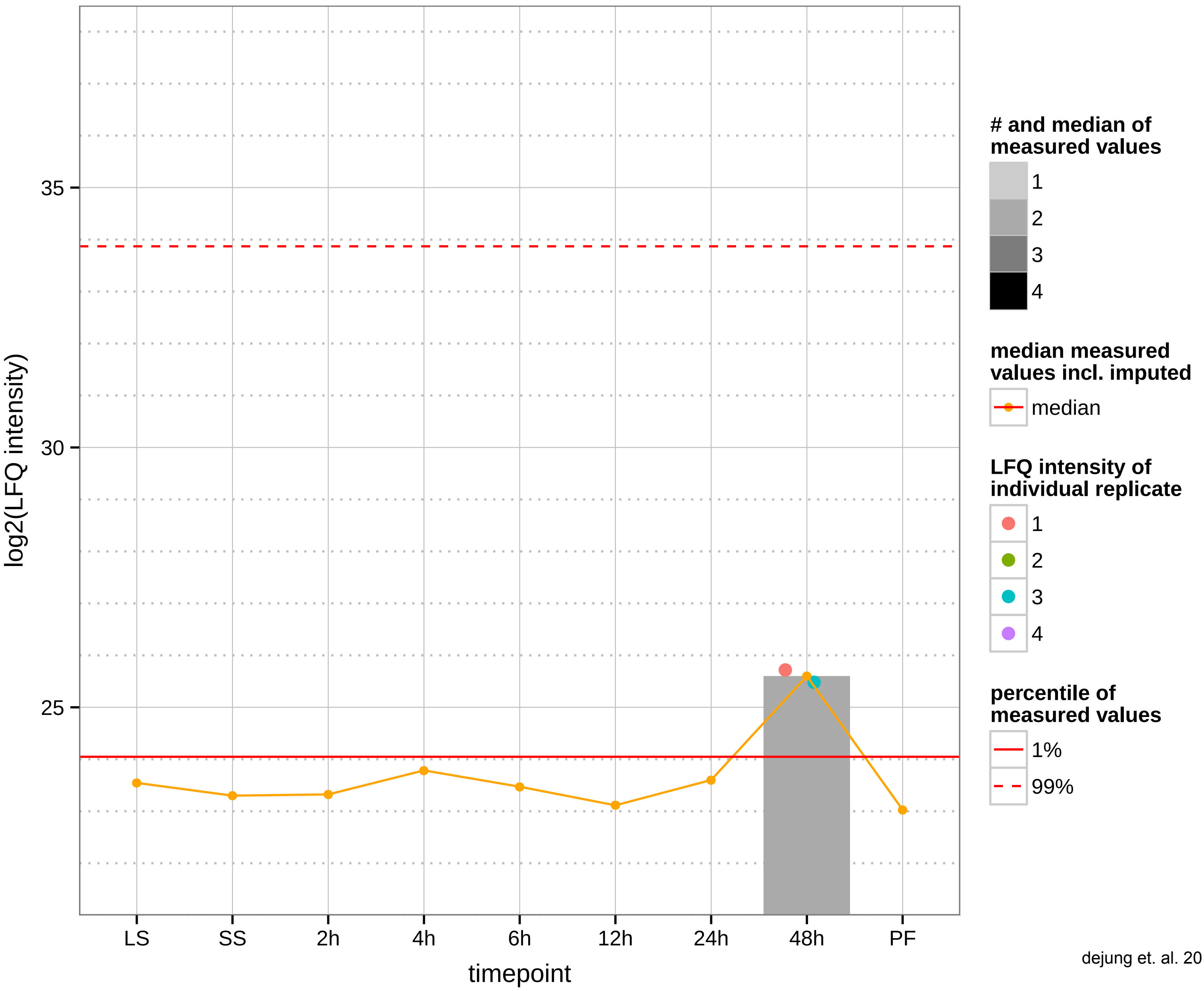




dejung et. al. 2015

calmodulin, putative
Tb927.11.9790
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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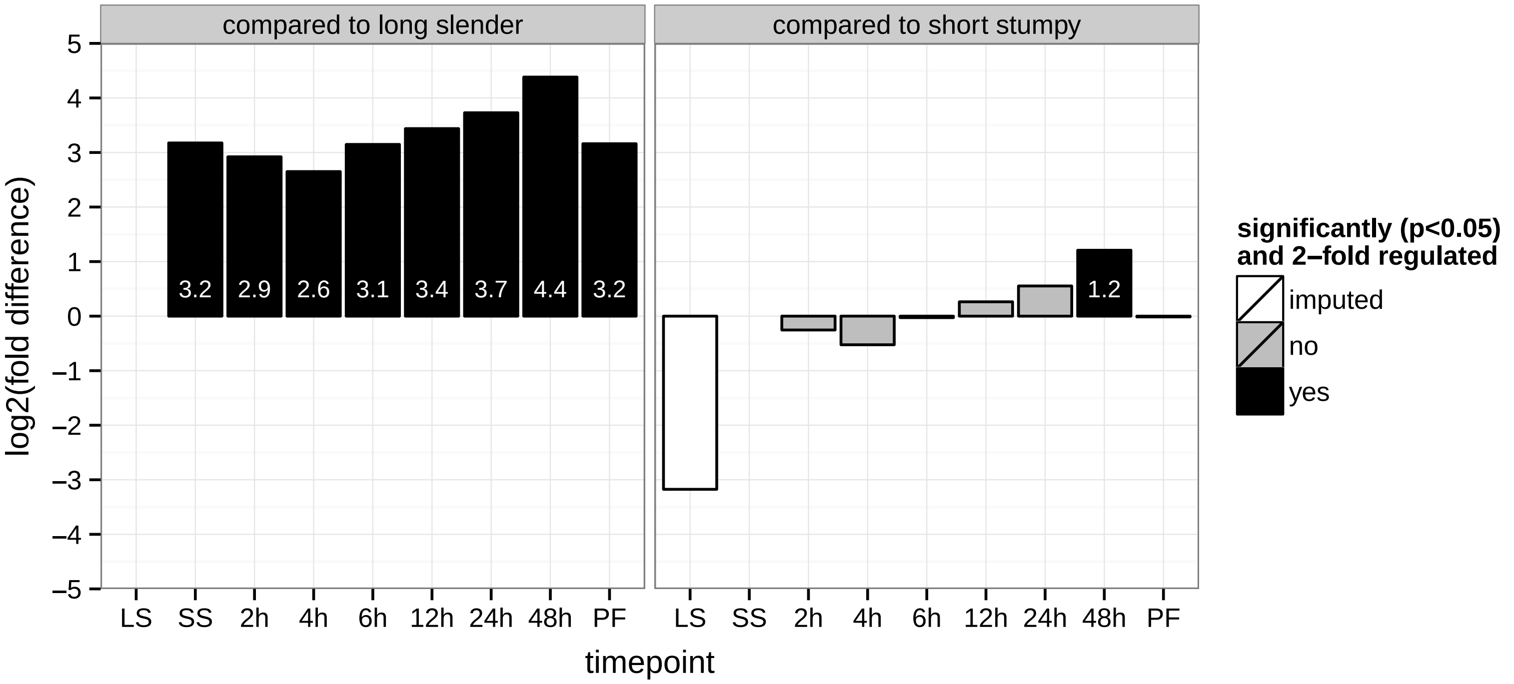
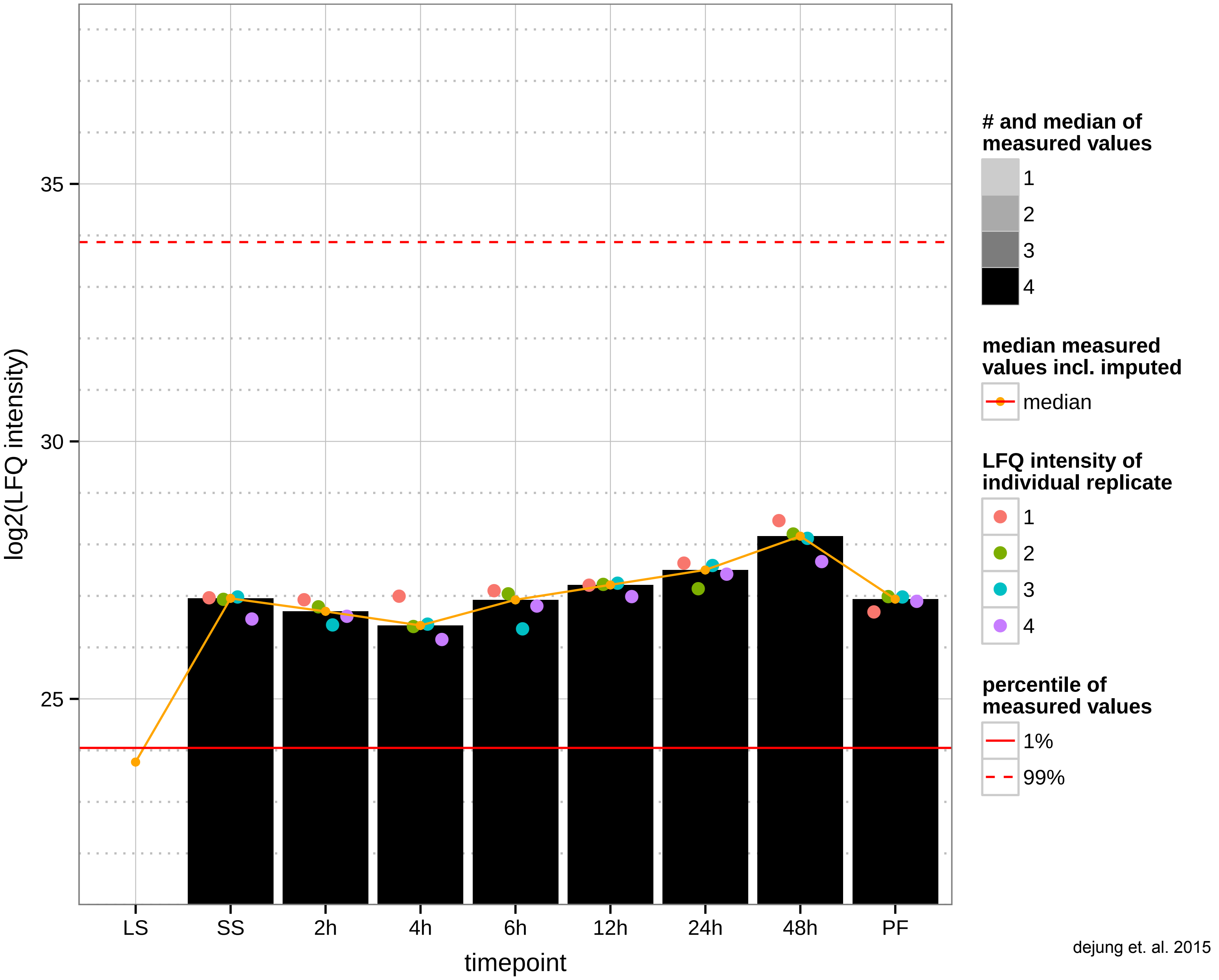
protein kinase, putative
Tb927.2.1820
AGOF: ATP binding, calcium ion binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinas
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, calcium ion binding, protein kinase activity, transferase activity, transferring phosphorus–containing grou
PGOC: null
PGOP: protein phosphorylation





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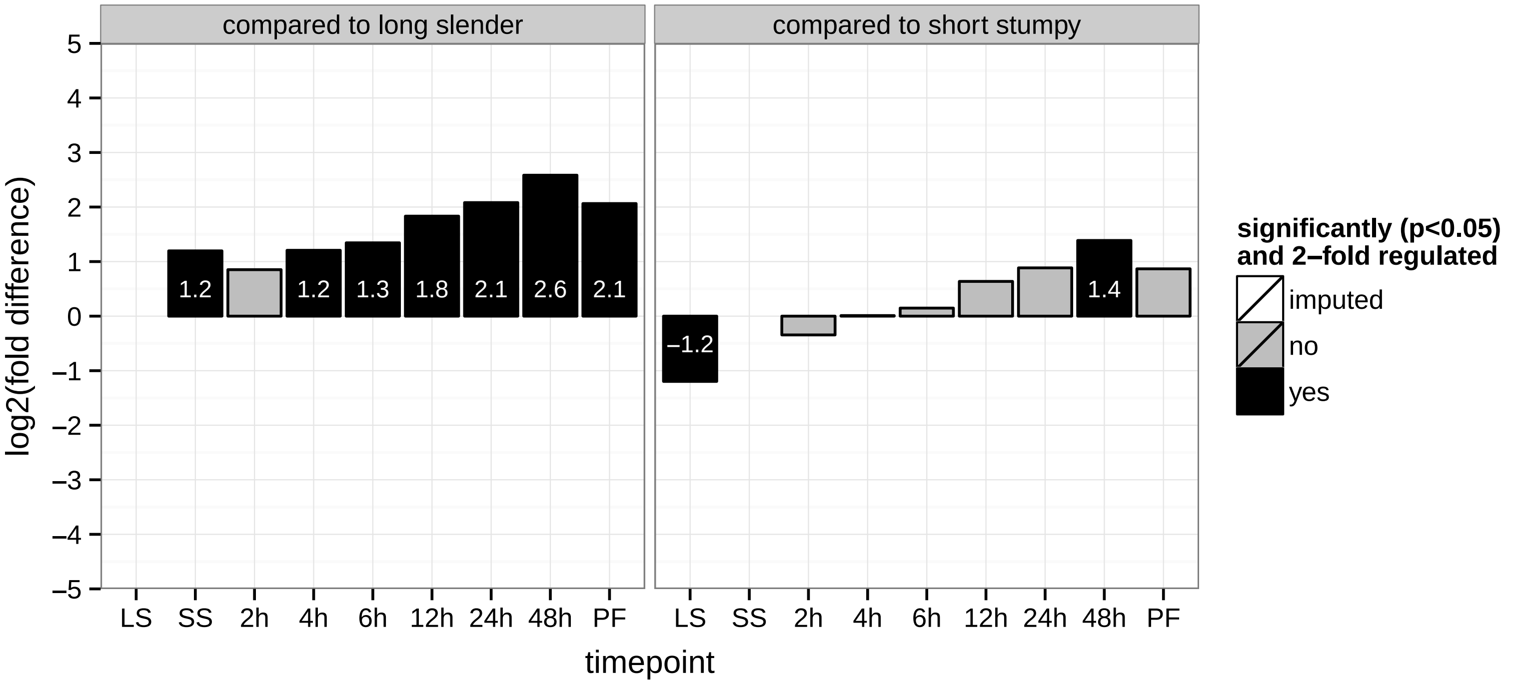
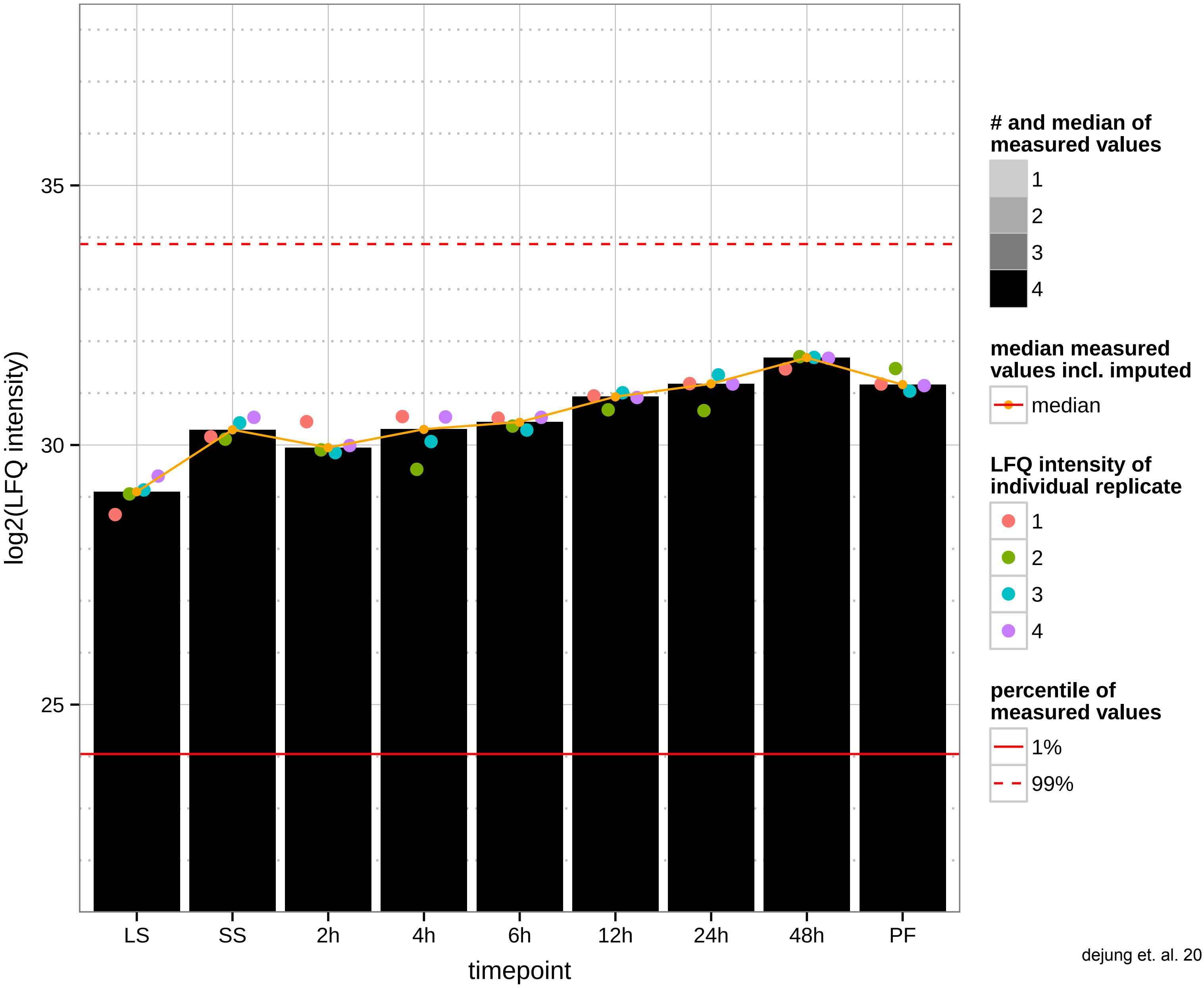
retrotransposon hot spot protein 5 (RHS5), putative, retrotransposon hot spot protein (RHS, pseudogene), degenerate
Tb927.2.240
AGOF: null
AGOC: nucleus, null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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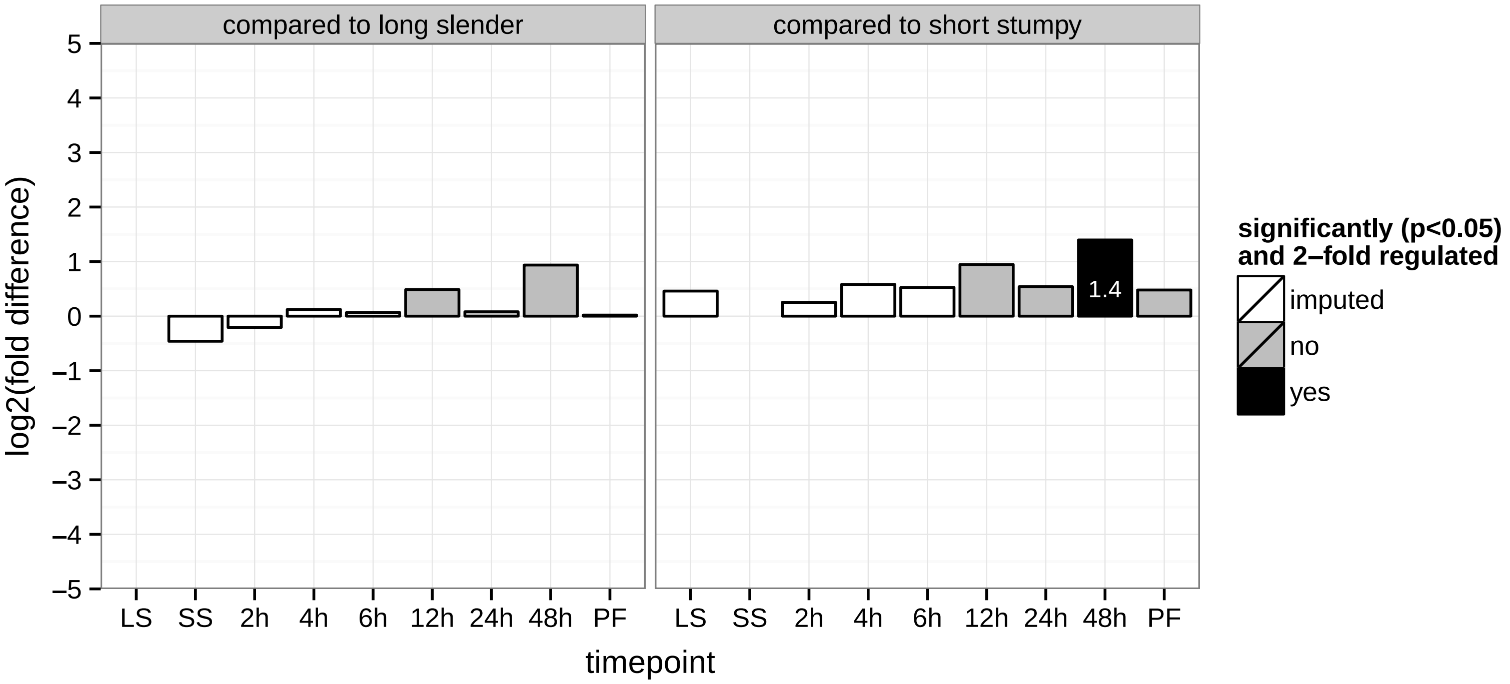
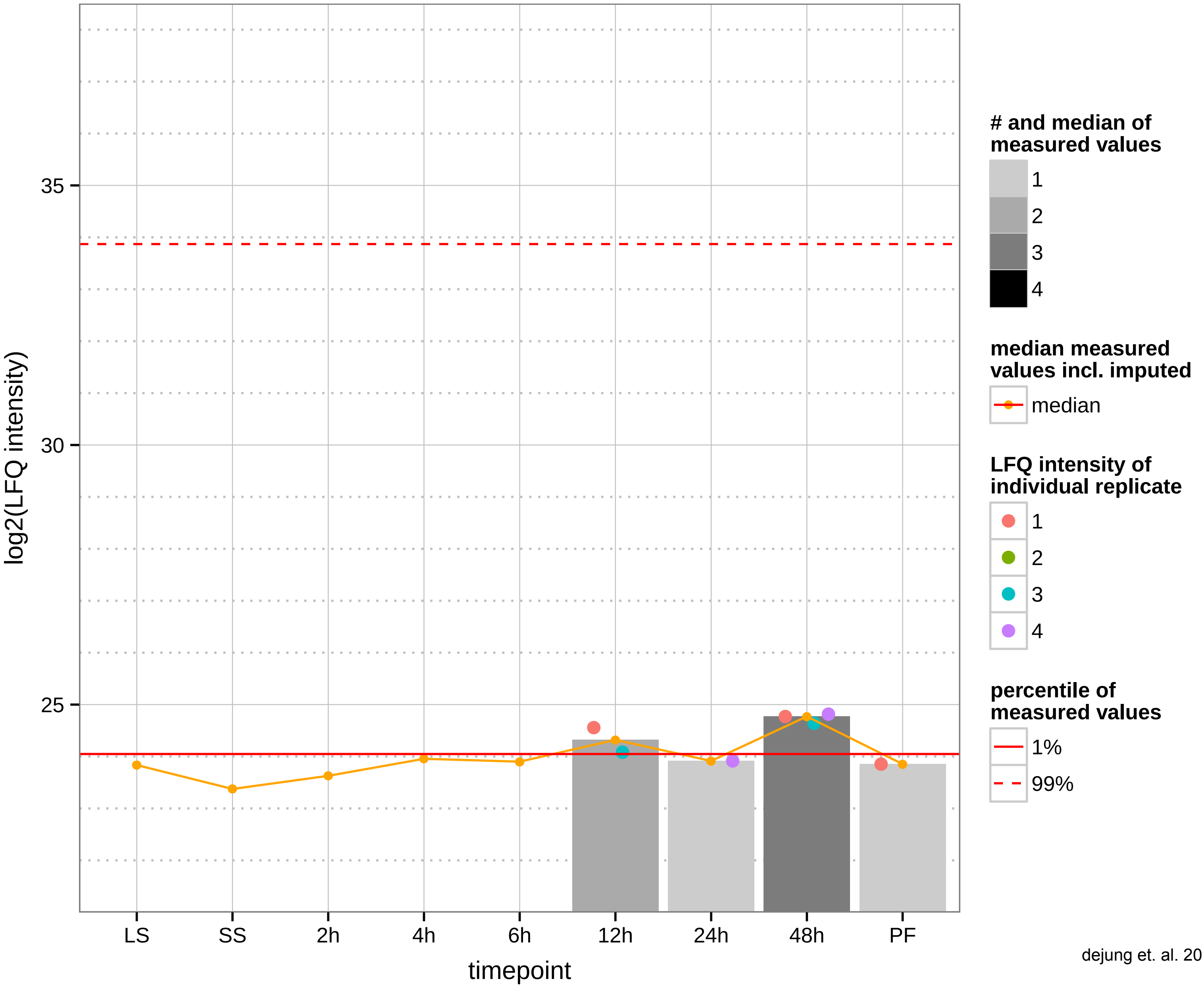
RNA–editing complex protein, KREPA1, RNA–editing complex protein (KREPA1)
Tb927.2.2470
AGOF: alpha–catenin binding, zinc ion binding
AGOC: intracellular, mitochondrial mRNA editing complex, mitochondrion
AGOP: RNA nucleotide deletion, RNA nucleotide insertion
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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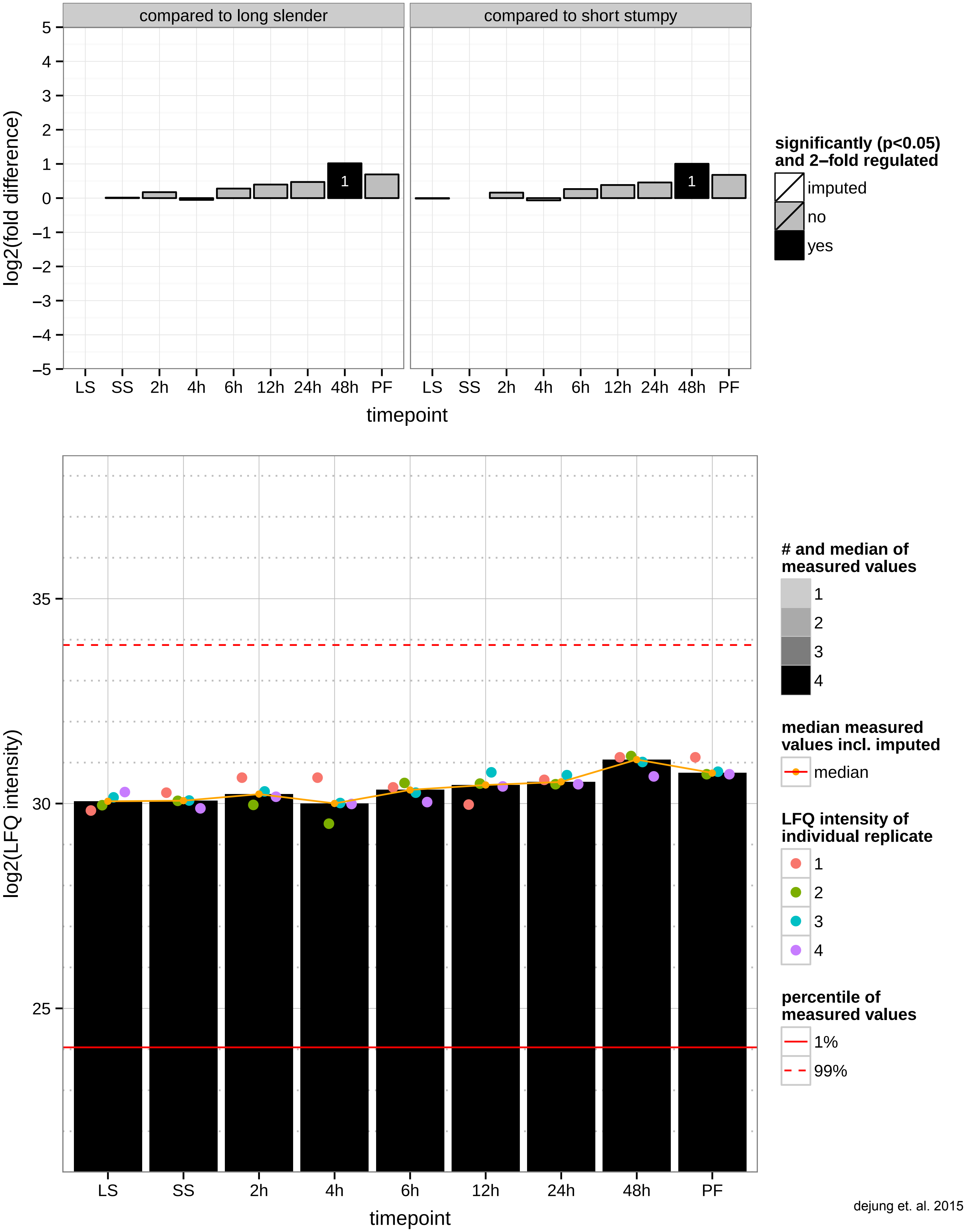
NUP−1 protein, putative
Tb927.2.4230
AGOF: null
AGOC: null, nuclear lamina
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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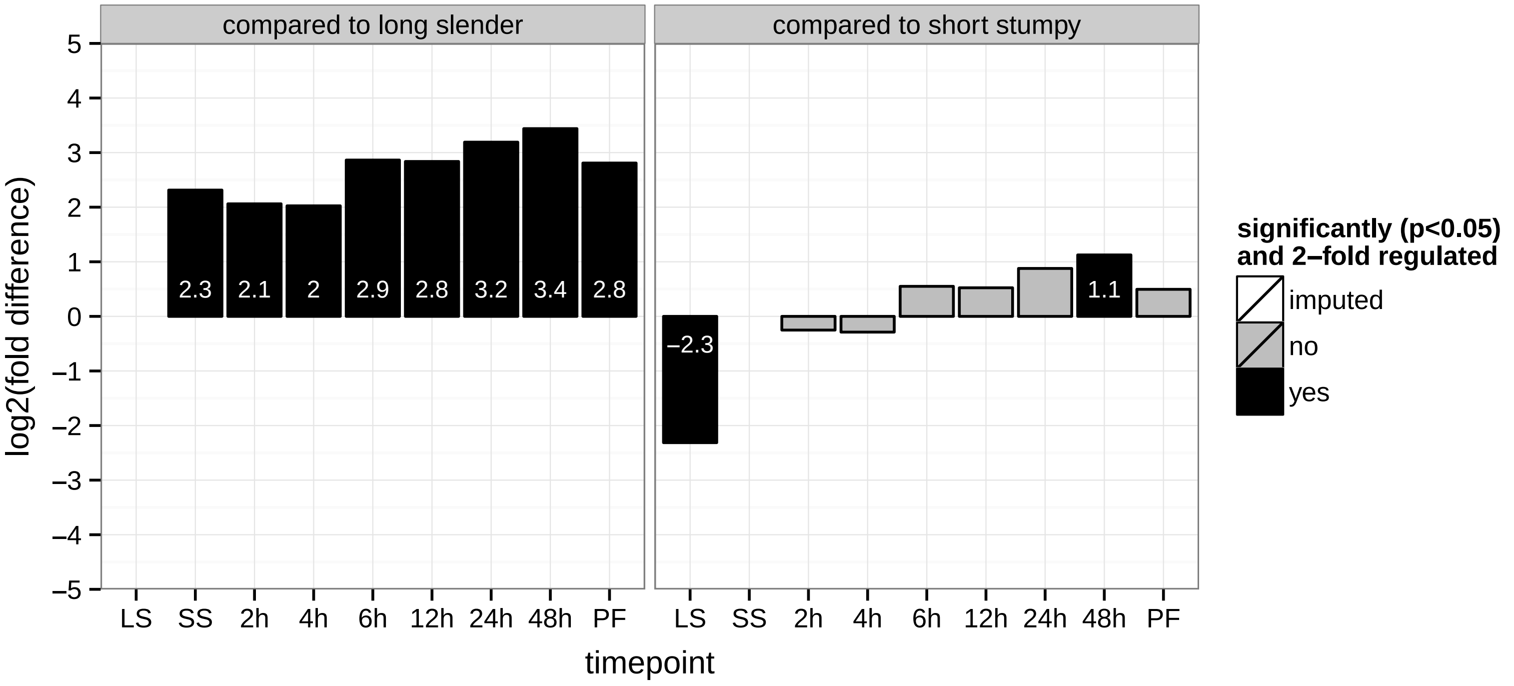
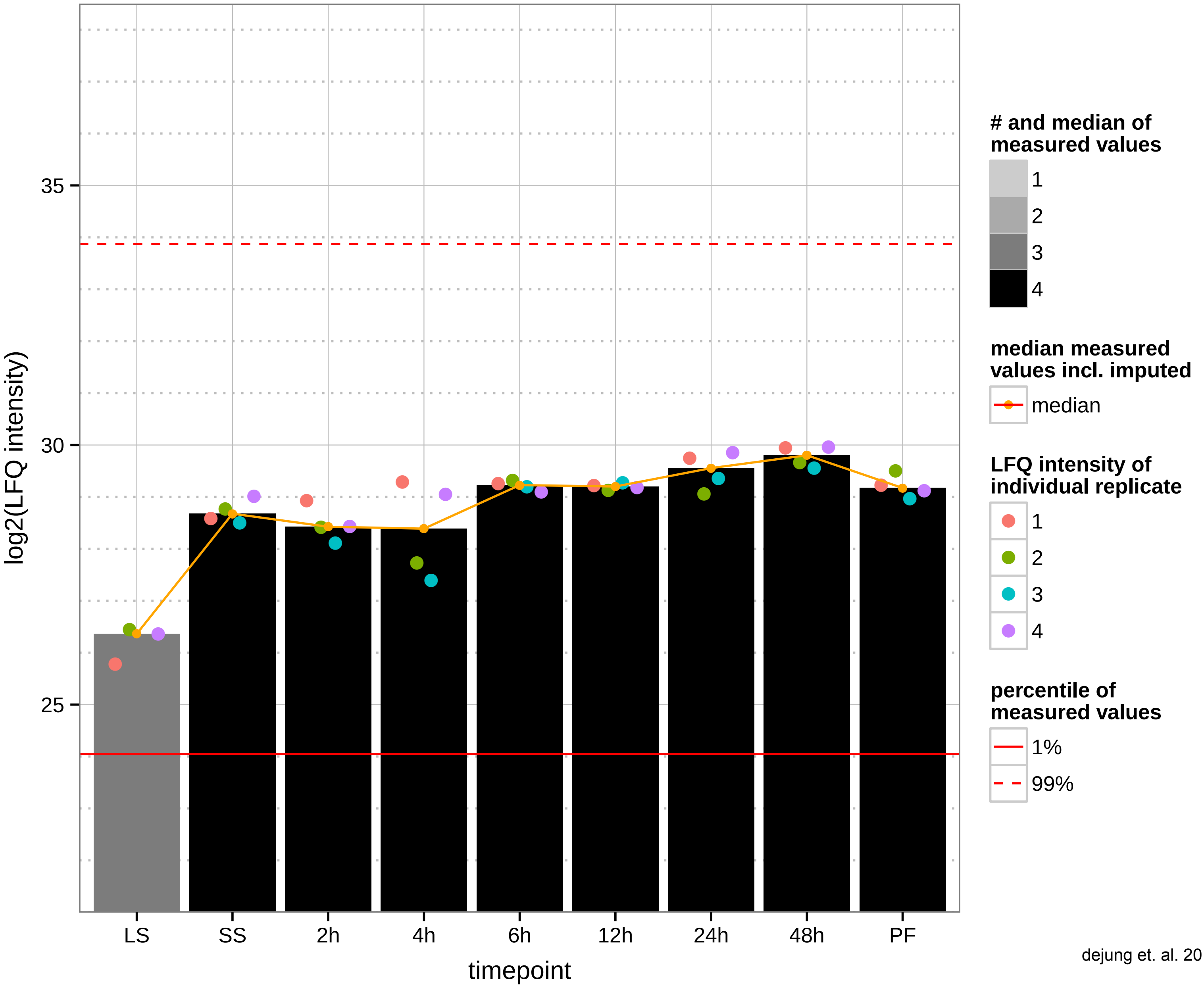
FtsJ cell division protein, putative
Tb927.2.4550
AGOF: methyltransferase activity, nucleic acid binding
AGOC: nucleus
AGOP: rRNA methylation
PGOF: methyltransferase activity, nucleic acid binding
PGOC: nucleus
PGOP: methylation, rRNA processing





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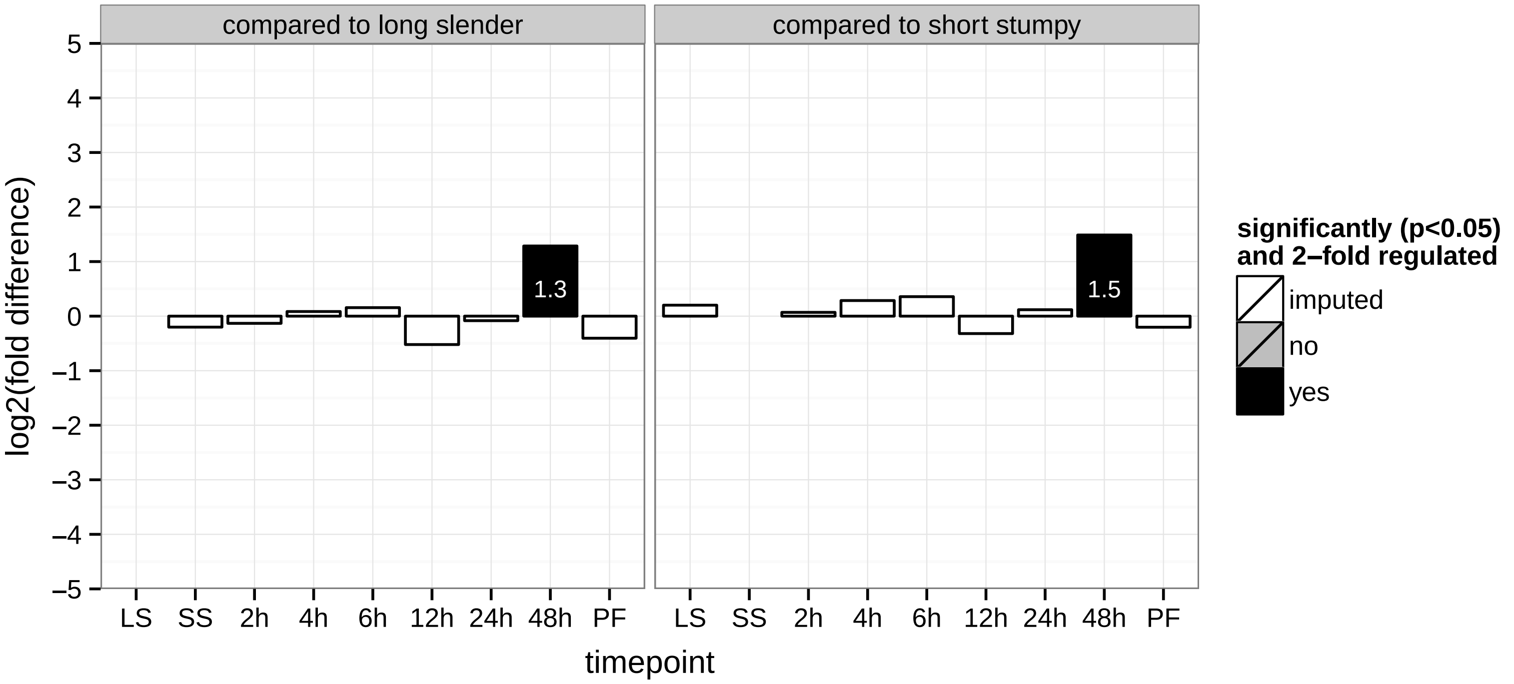
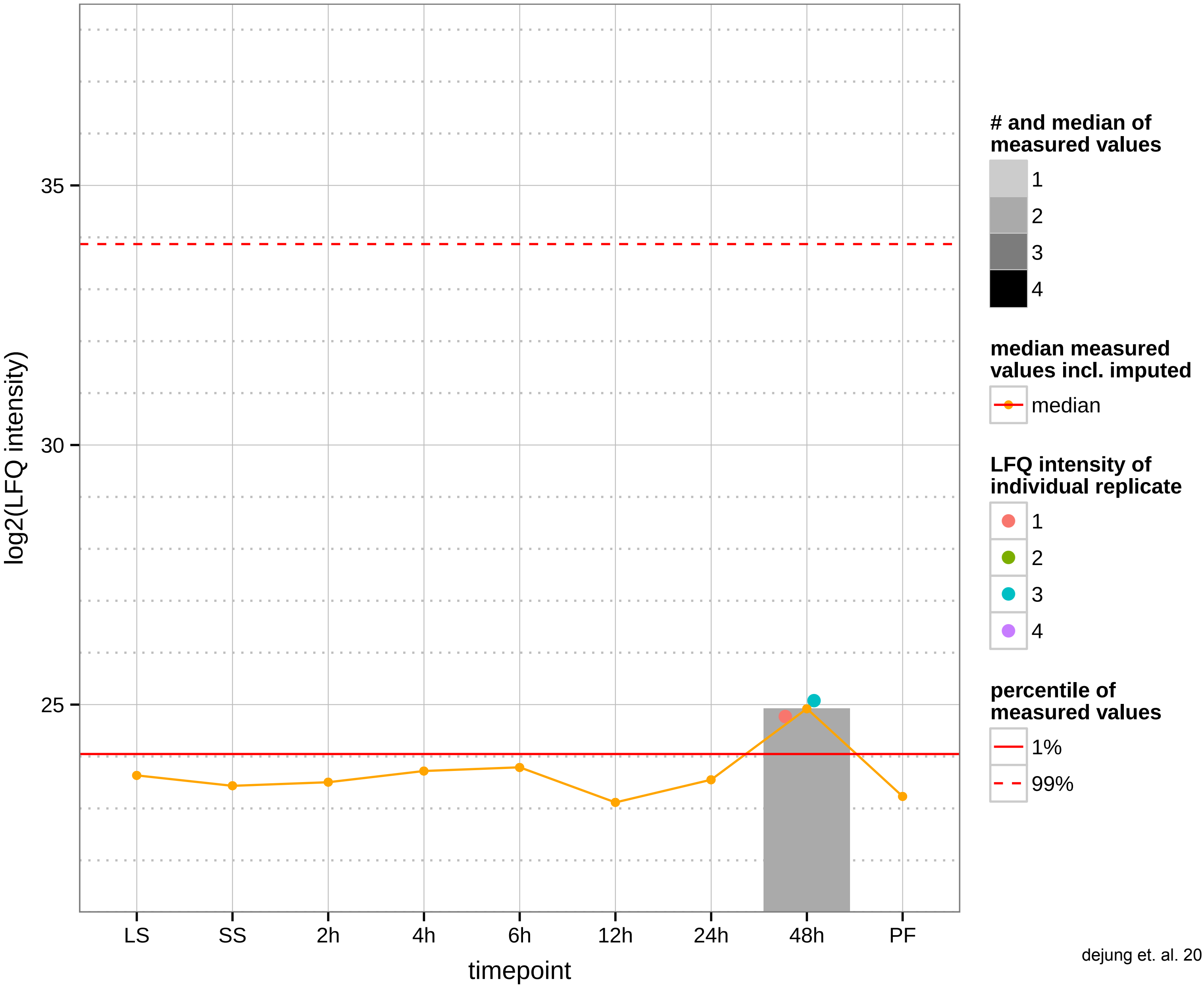
U6 snRNA–associated Sm–like protein LSm8p (TbLSm8)
Tb927.3.1780
AGOF: U6 snRNA 3'–end binding
AGOC: U4/U6 x U5 tri–snRNP complex, nucleus
AGOP: assembly of spliceosomal tri–snRNP, nuclear mRNA splicing, via spliceosome
PGOF: null
PGOC: null
PGOP: null





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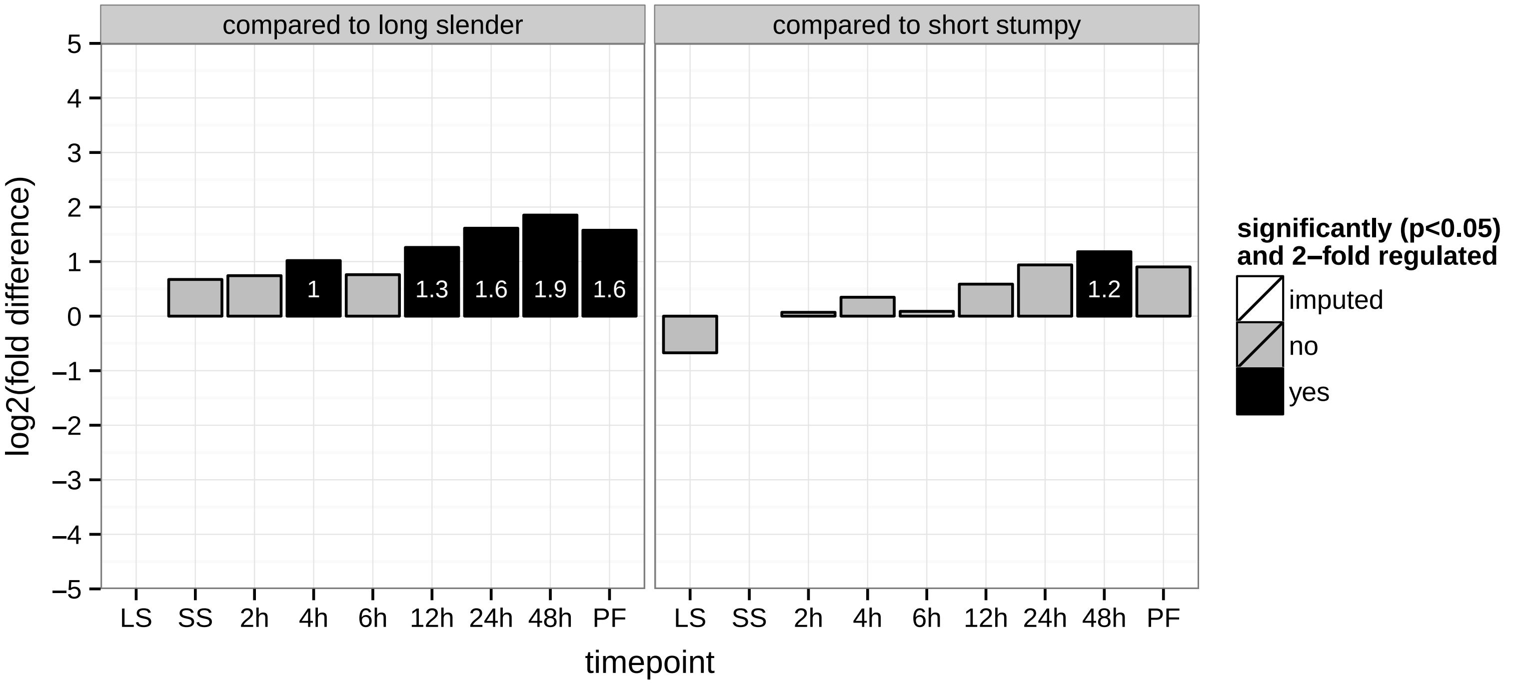
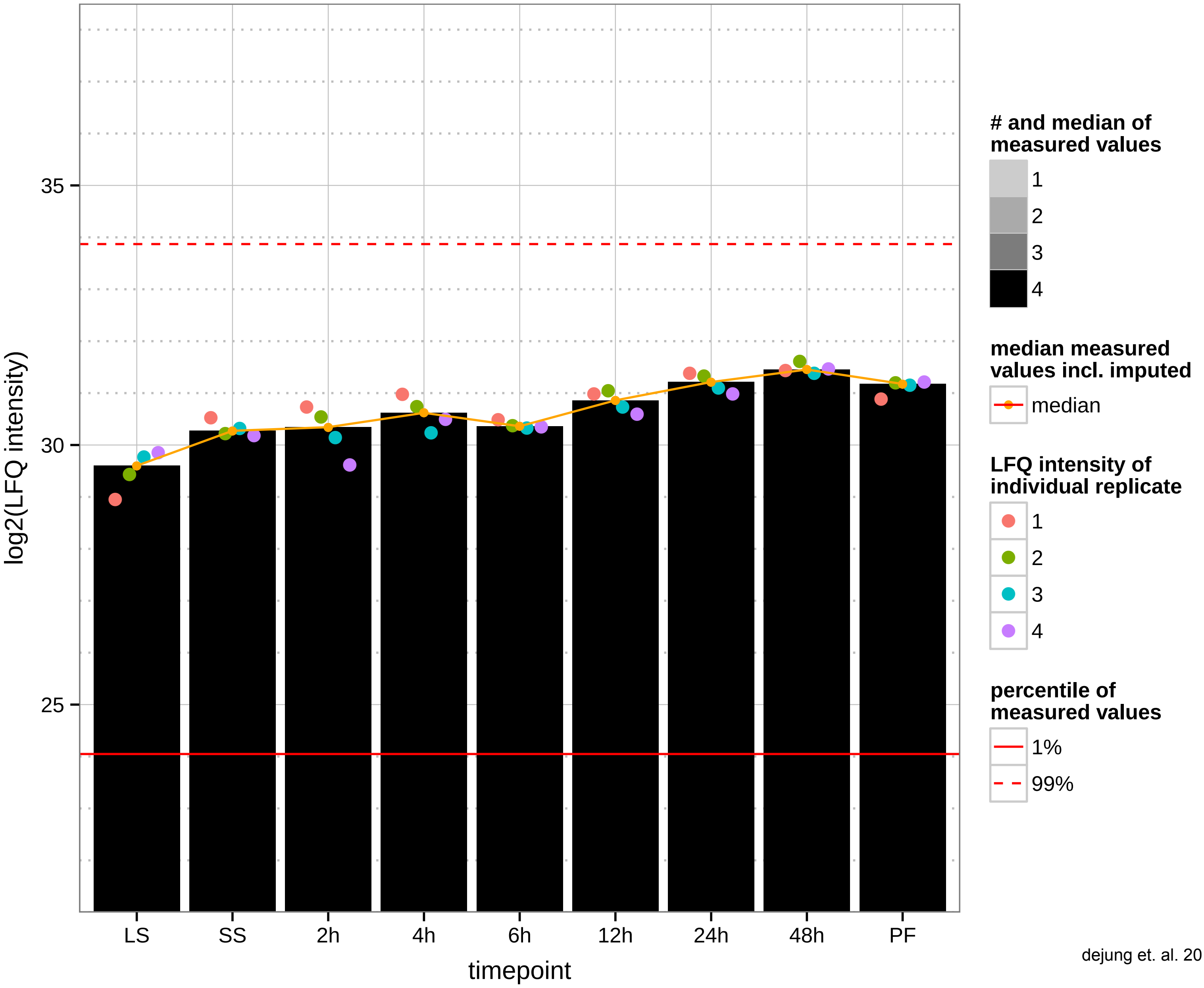
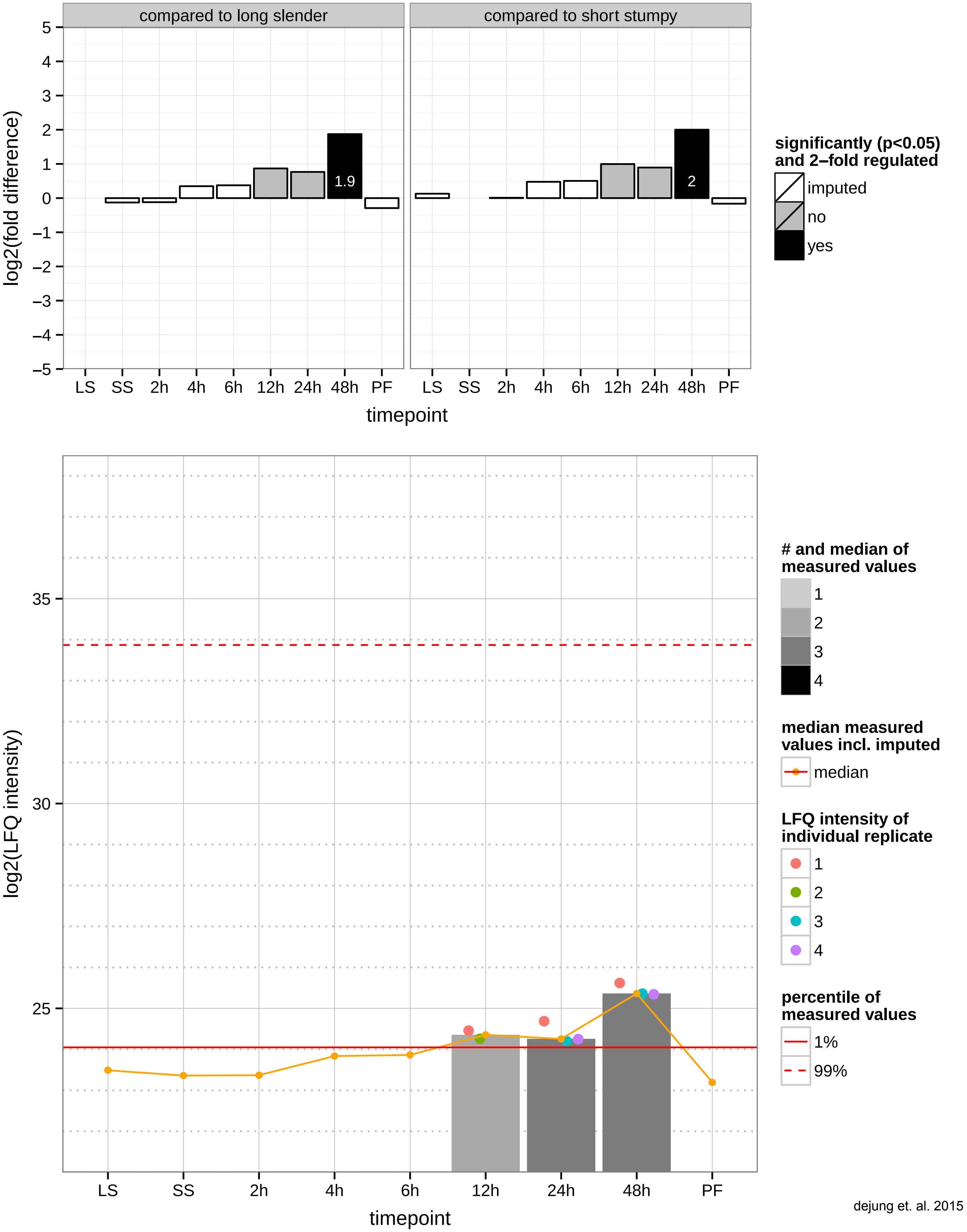
hypothetical protein, conserved
Tb927.3.2100
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.2660
AGOF: endodeoxyribonuclease activity, producing 5'−phosphomonoesters
AGOC: null
AGOP: null
PGOF: endodeoxyribonuclease activity, producing 5'−phosphomonoesters
PGOC: null
PGOP: null



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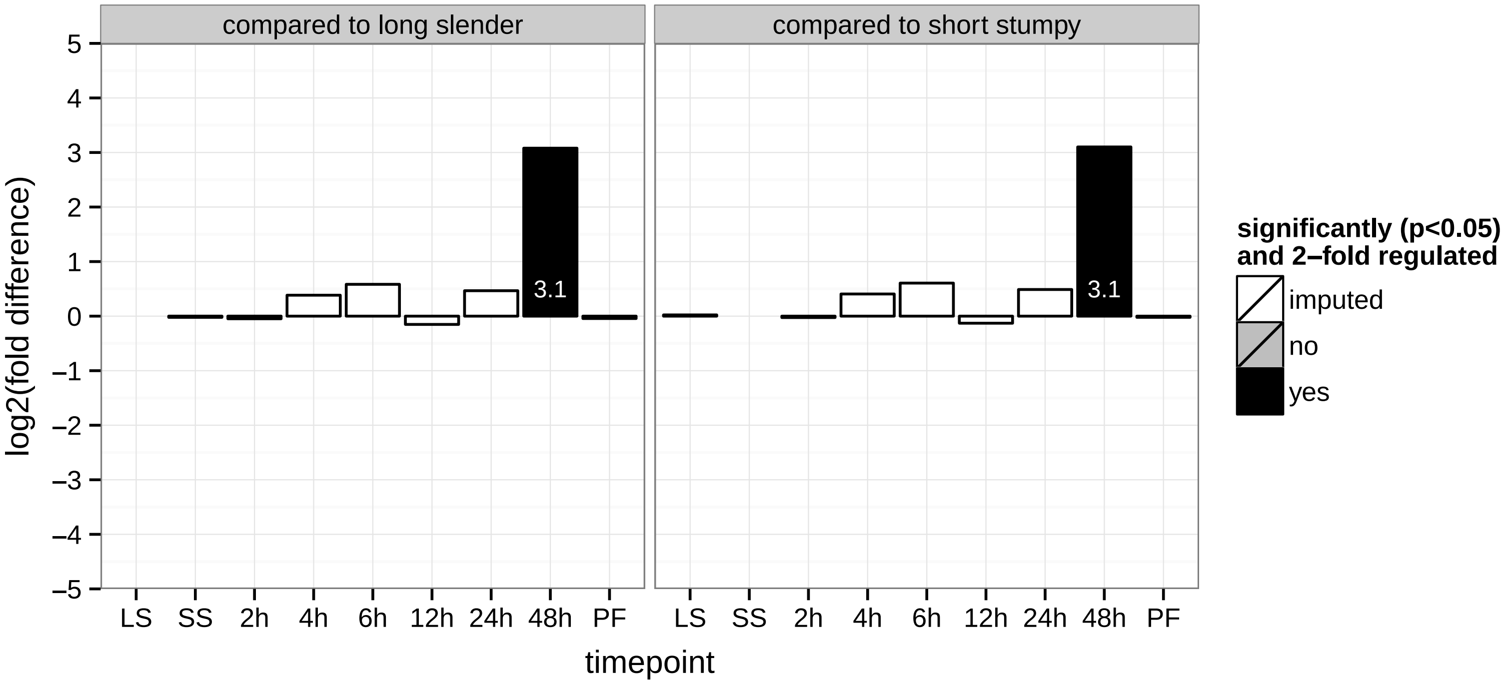
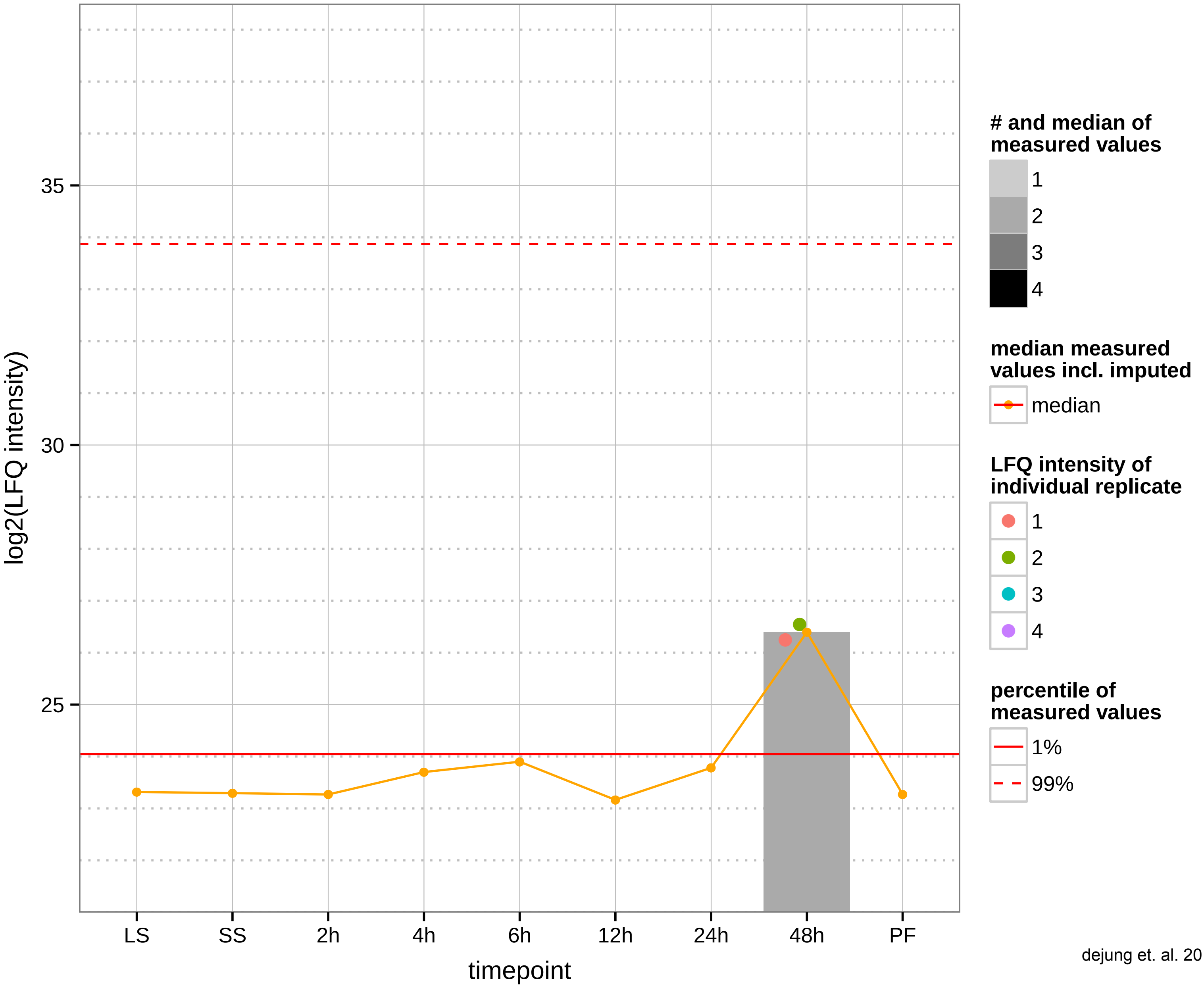
hypothetical protein, conserved
Tb927.3.3150;Tb11.v5.0796
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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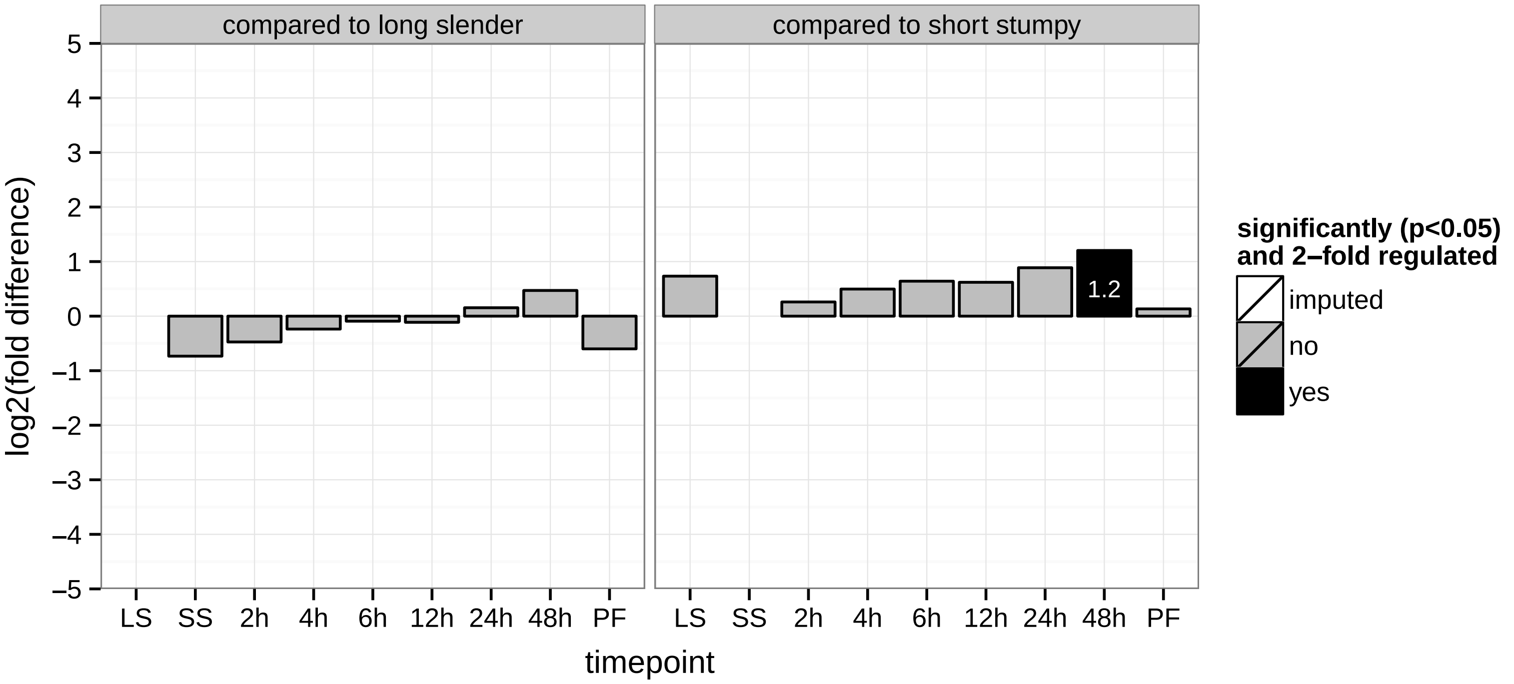
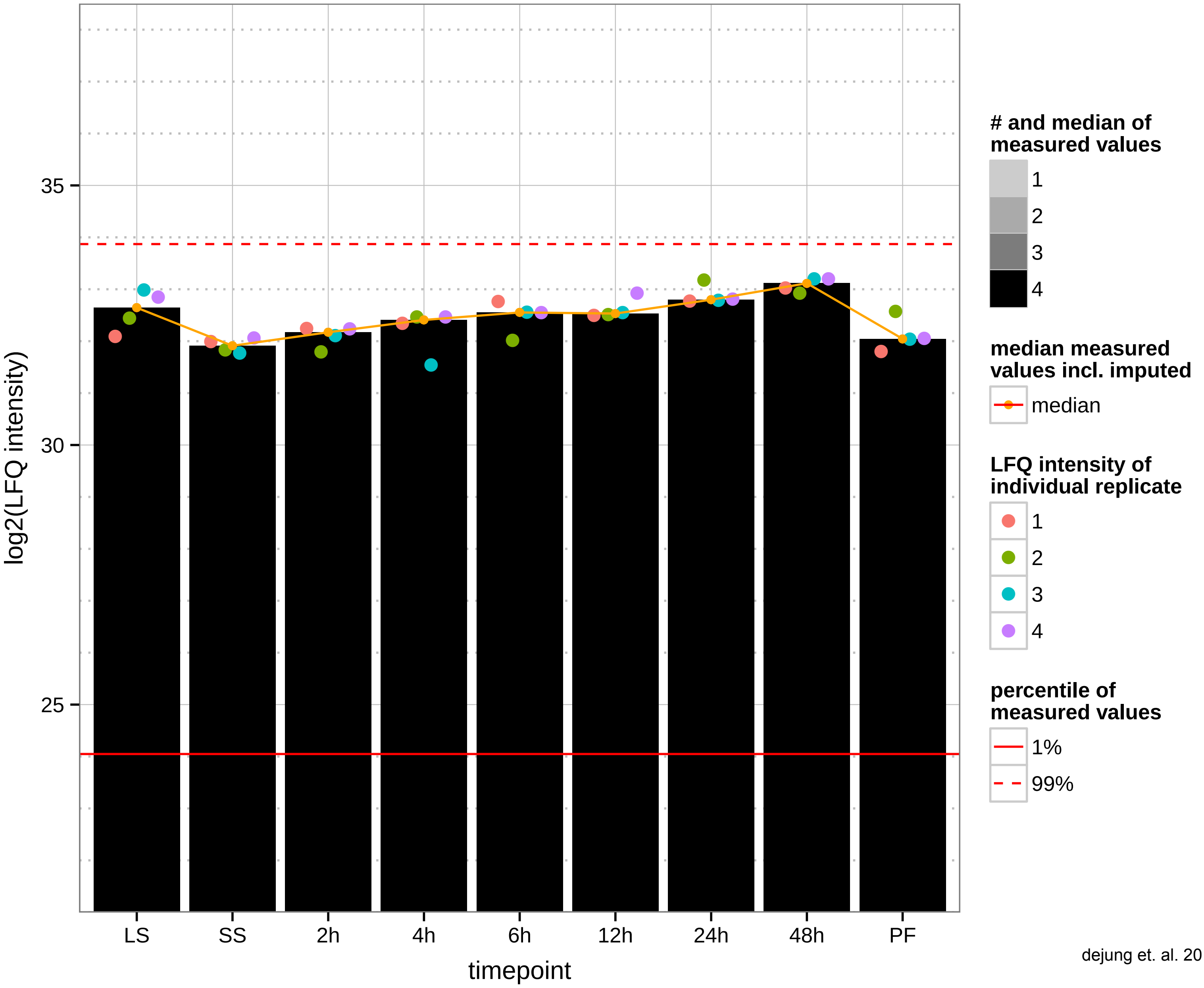
60S ribosomal protein L13, putative
Tb927.3.3320;Tb927.3.3310
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: null
PGOF: structural constituent of ribosome, null
PGOC: intracellular, ribosome, null
PGOP: translation, null





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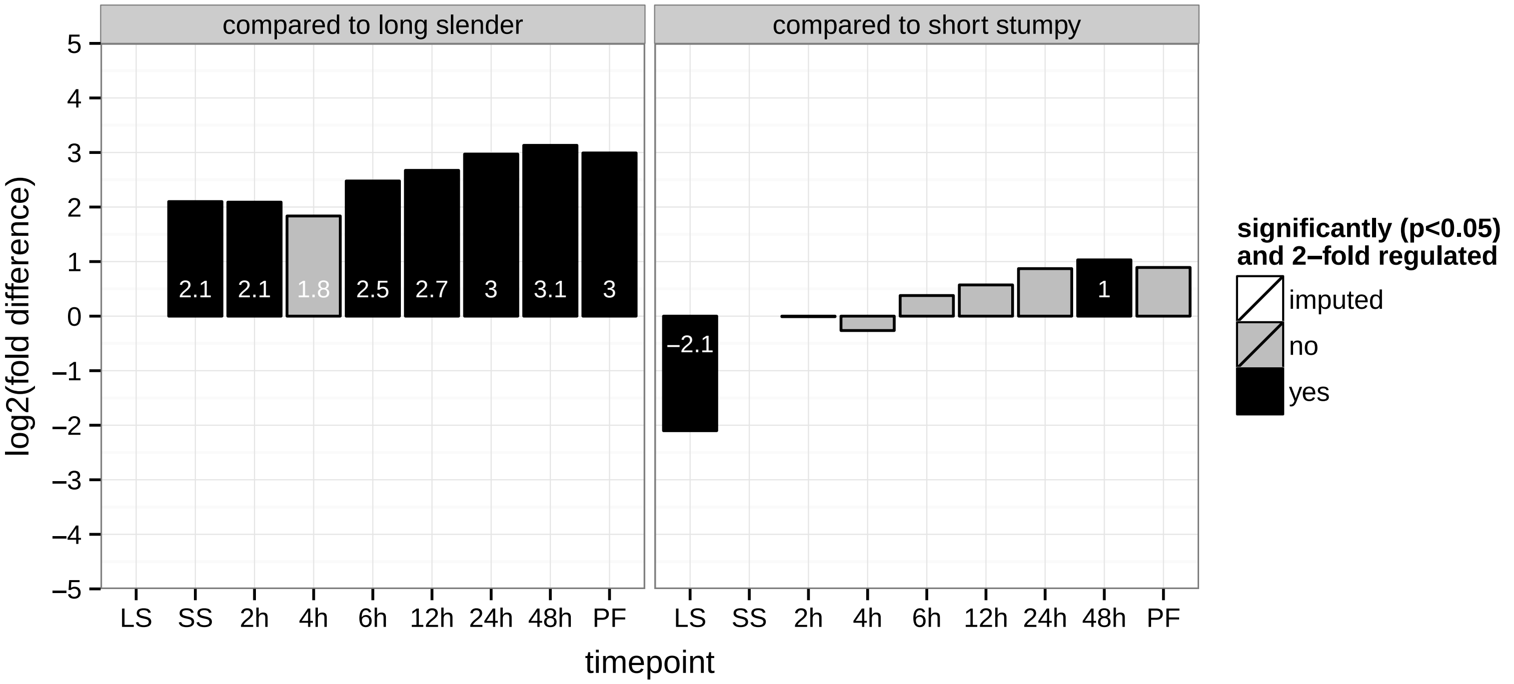
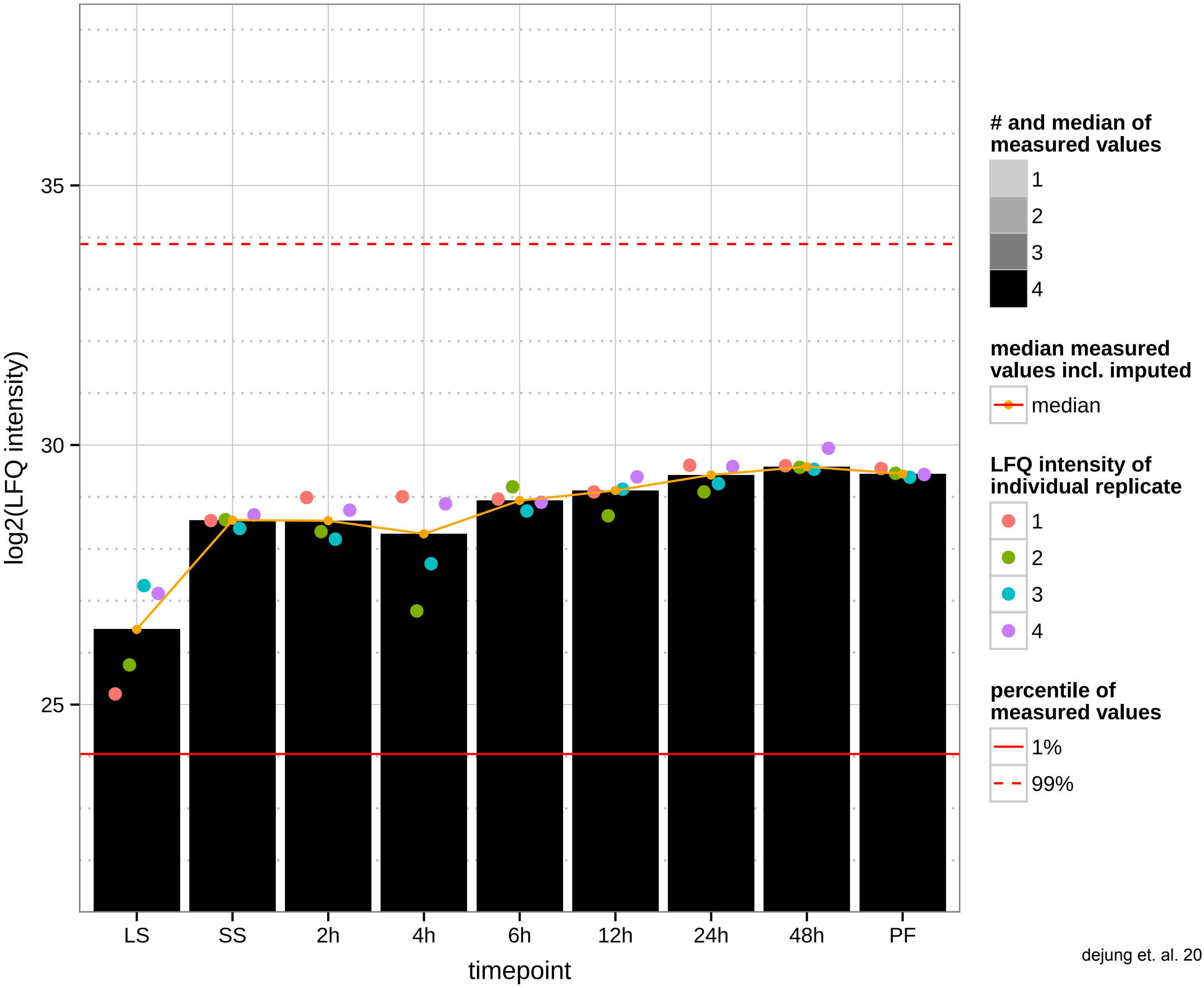
RNA–binding protein, putative (TRRM3)
Tb927.3.3670
AGOF: RNA binding
AGOC: nucleus
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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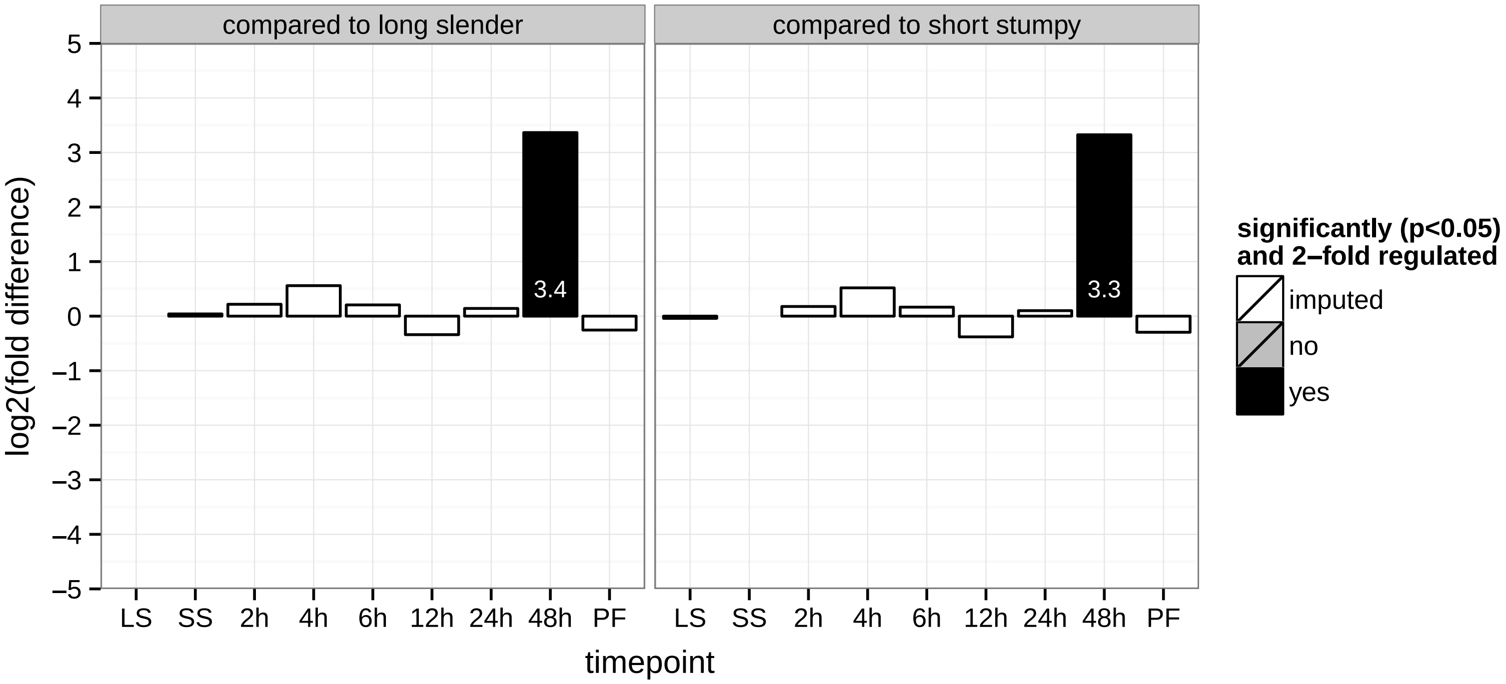
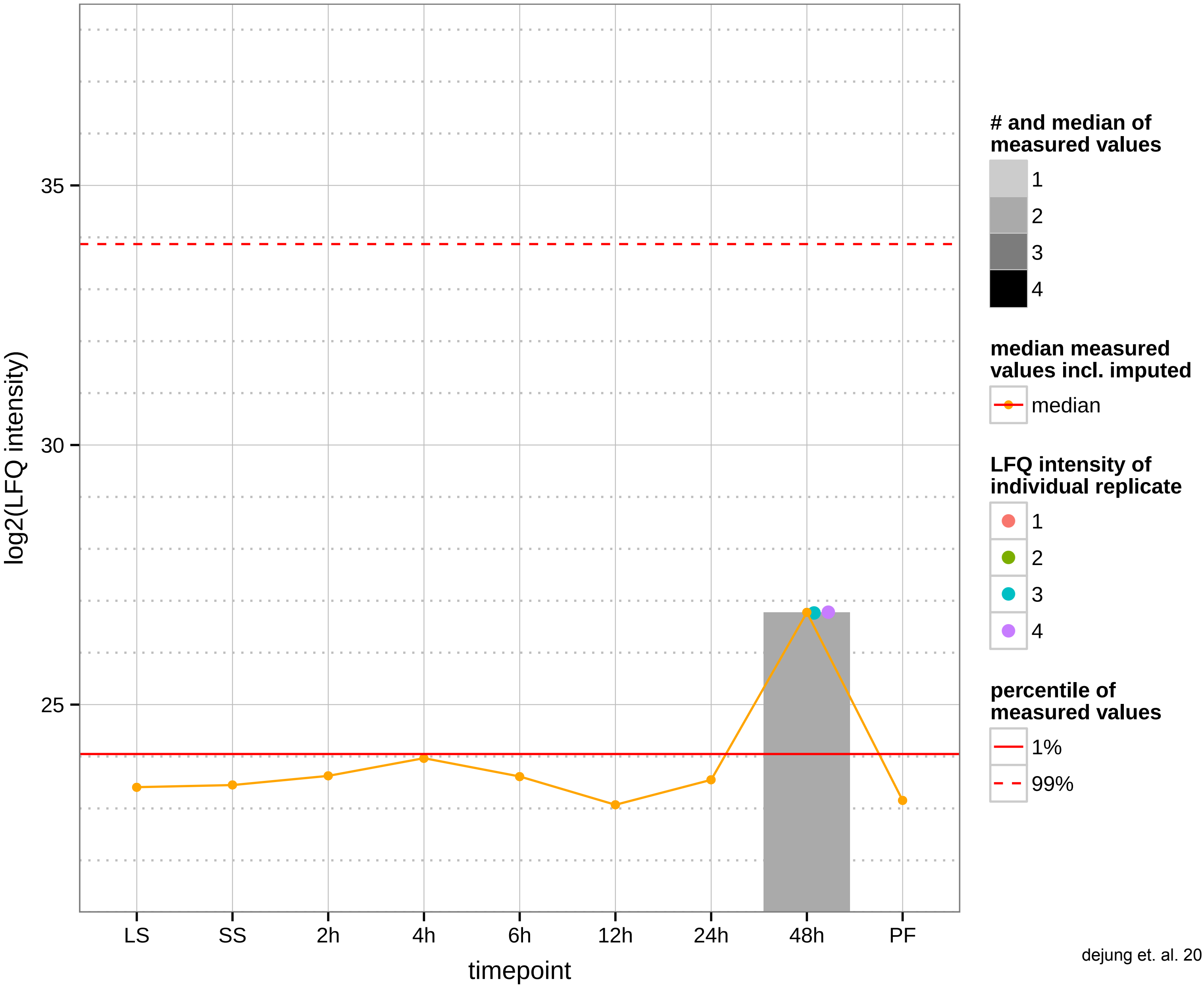
hypothetical protein, conserved
Tb927.3.3740
AGOF: zinc ion binding
AGOC: intracellular
AGOP: null
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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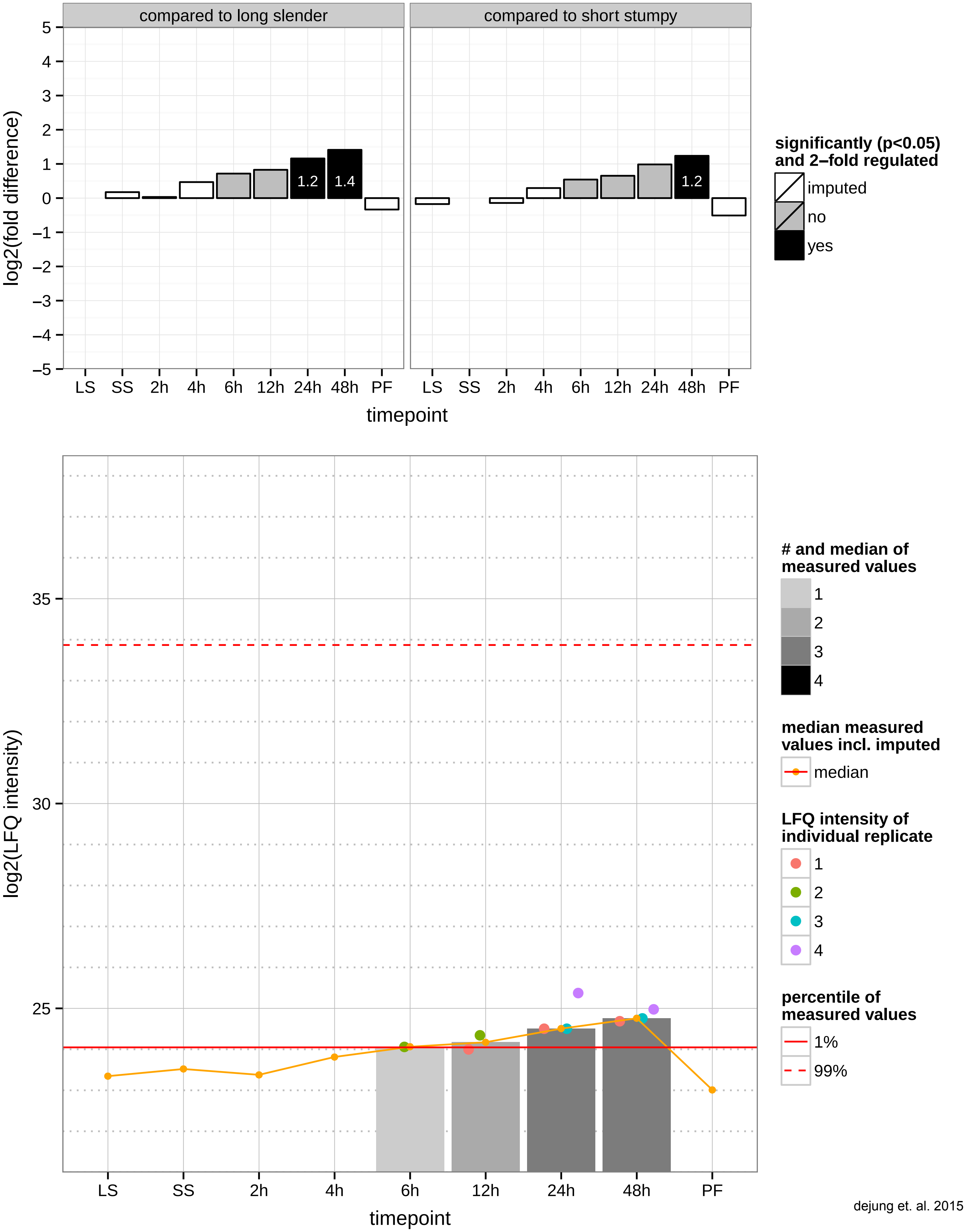
hypothetical protein, conserved
Tb927.3.4620
AGOF: nucleic acid binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null



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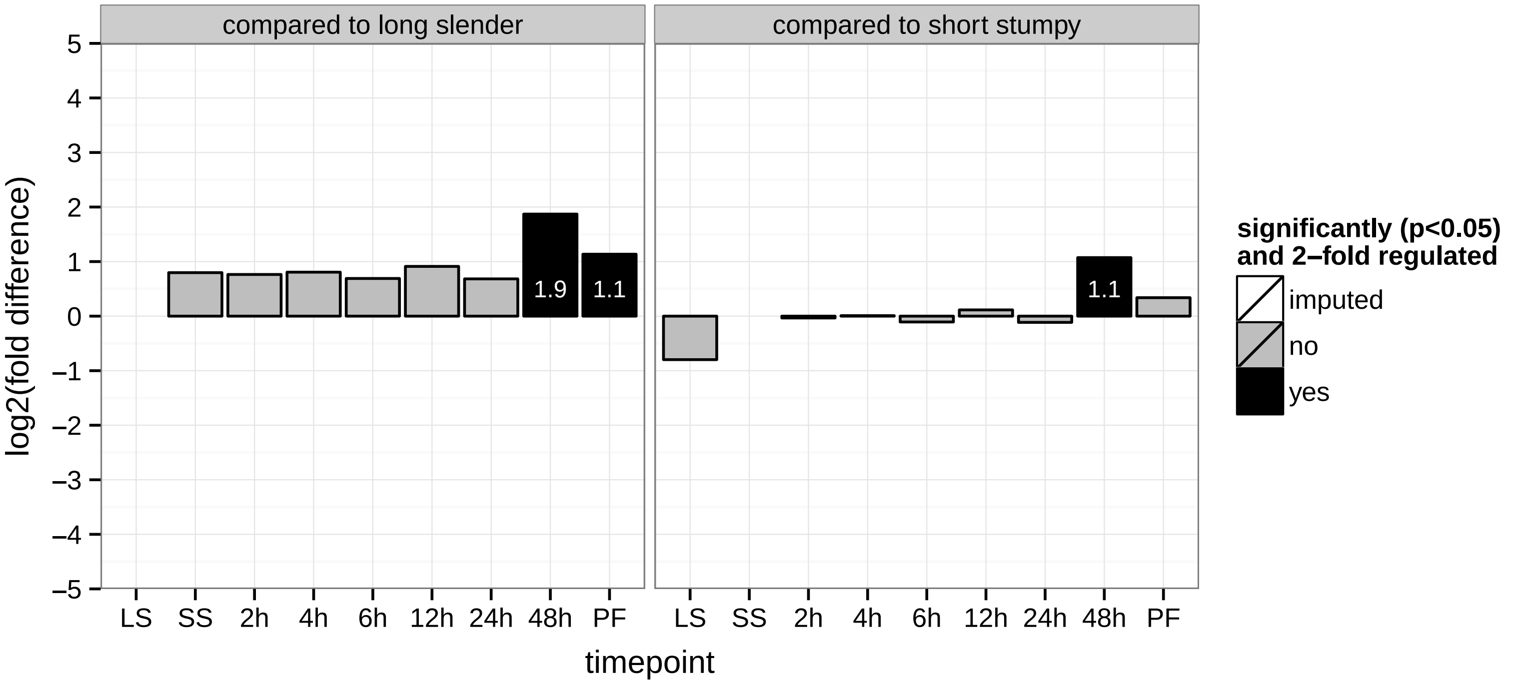
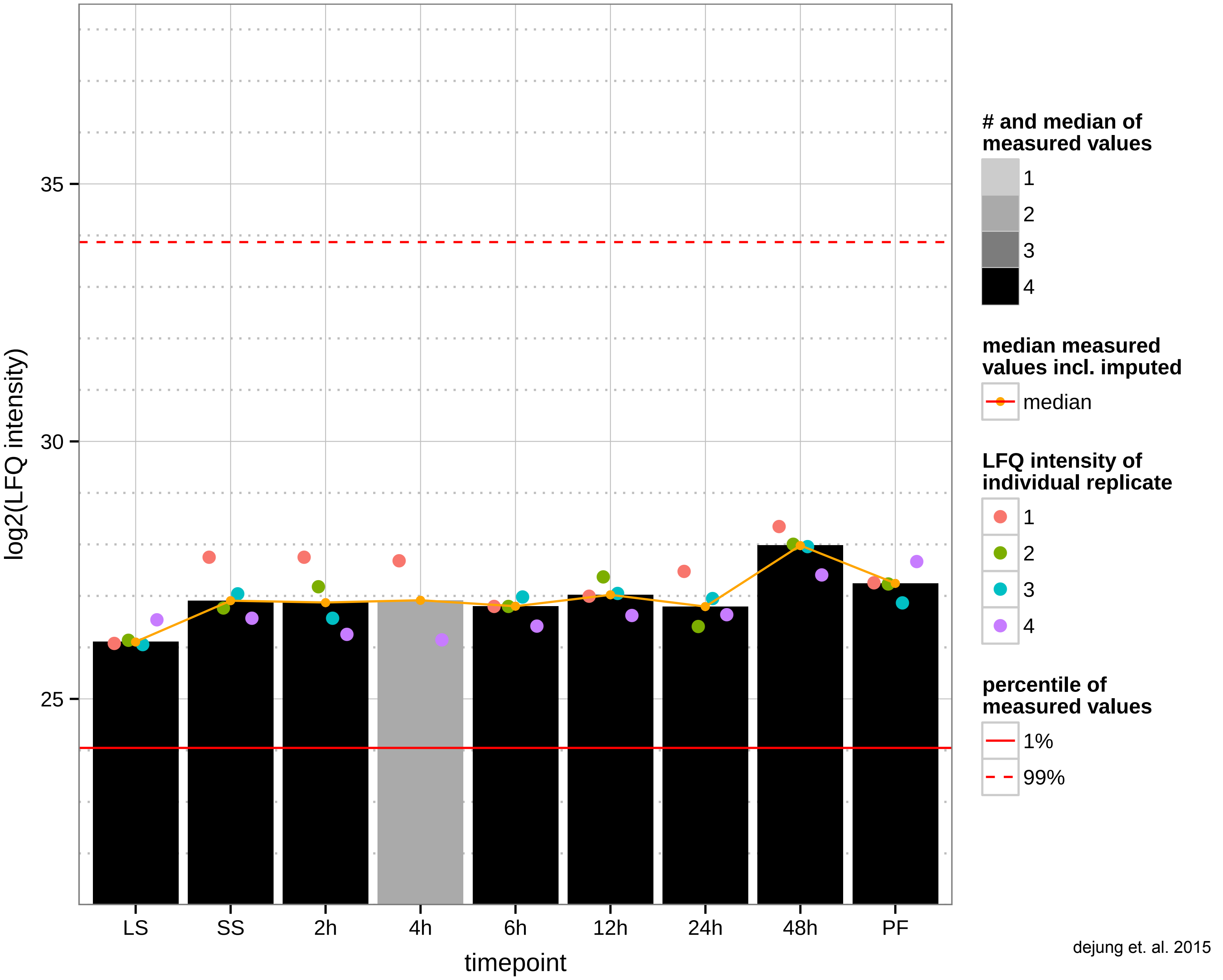
paraflagellar rod protein, I2 antigen
Tb927.3.5310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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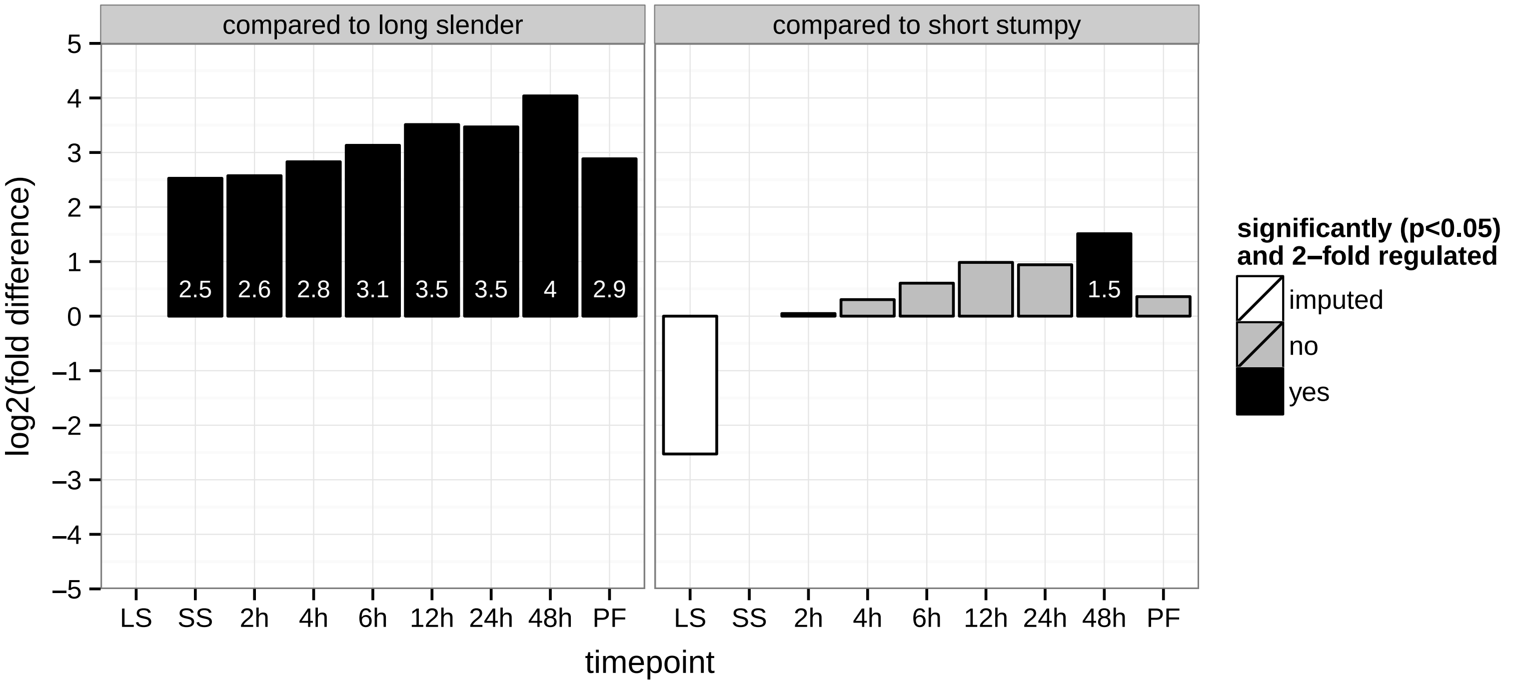
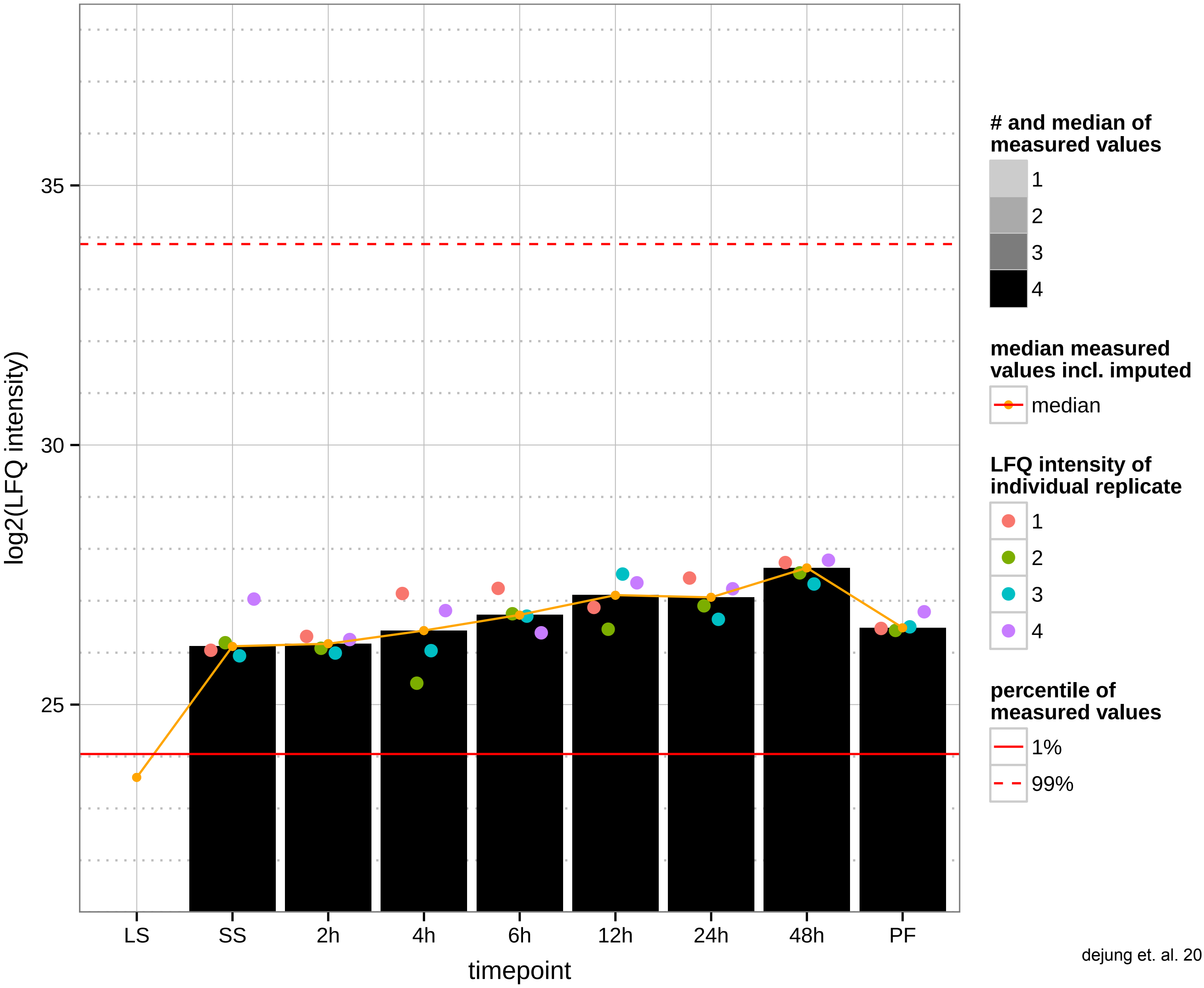
hypothetical protein, conserved
Tb927.3.5400
AGOF: ATP binding, protein serine/threonine kinase activity
AGOC: null
AGOP: growth
PGOF: ATP binding, catalytic activity, protein serine/threonine kinase activity, transferase activity, transferring phosphorus–co
PGOC: null
PGOP: null





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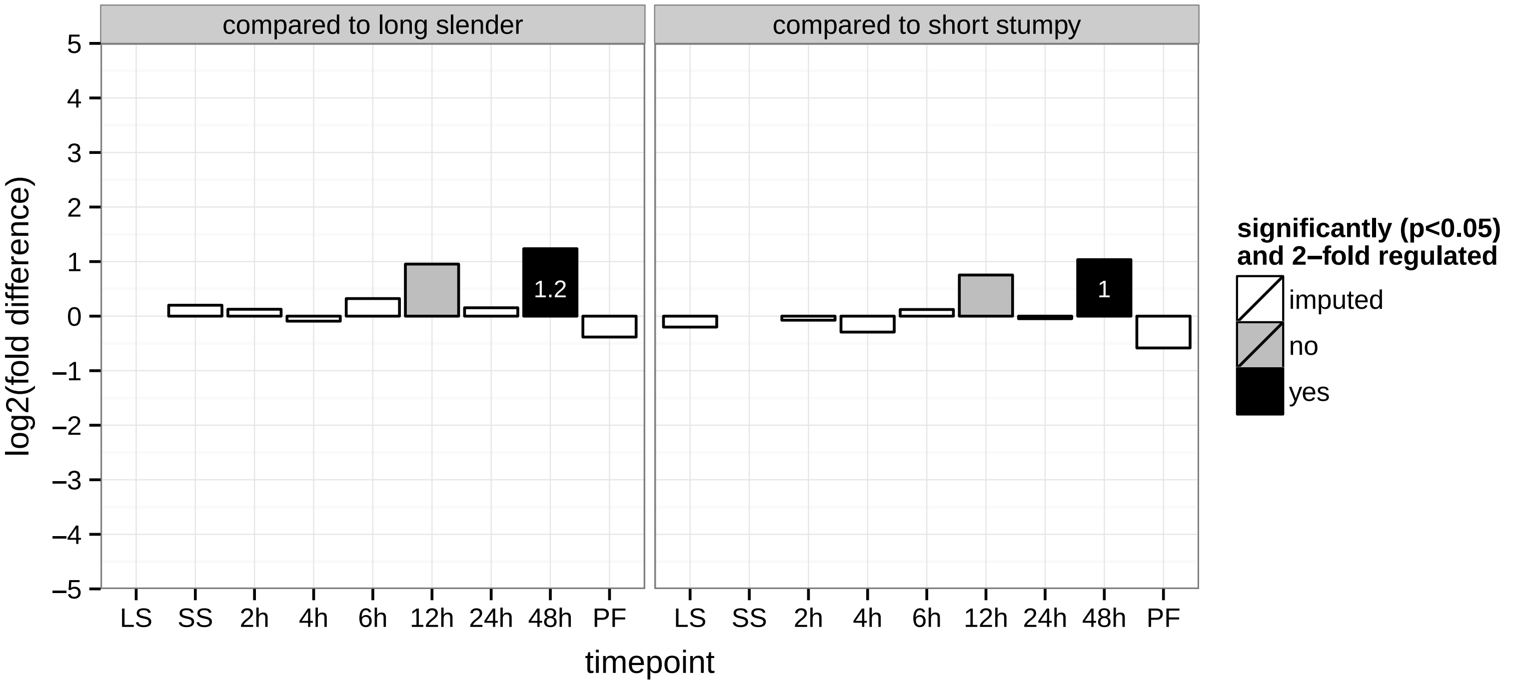
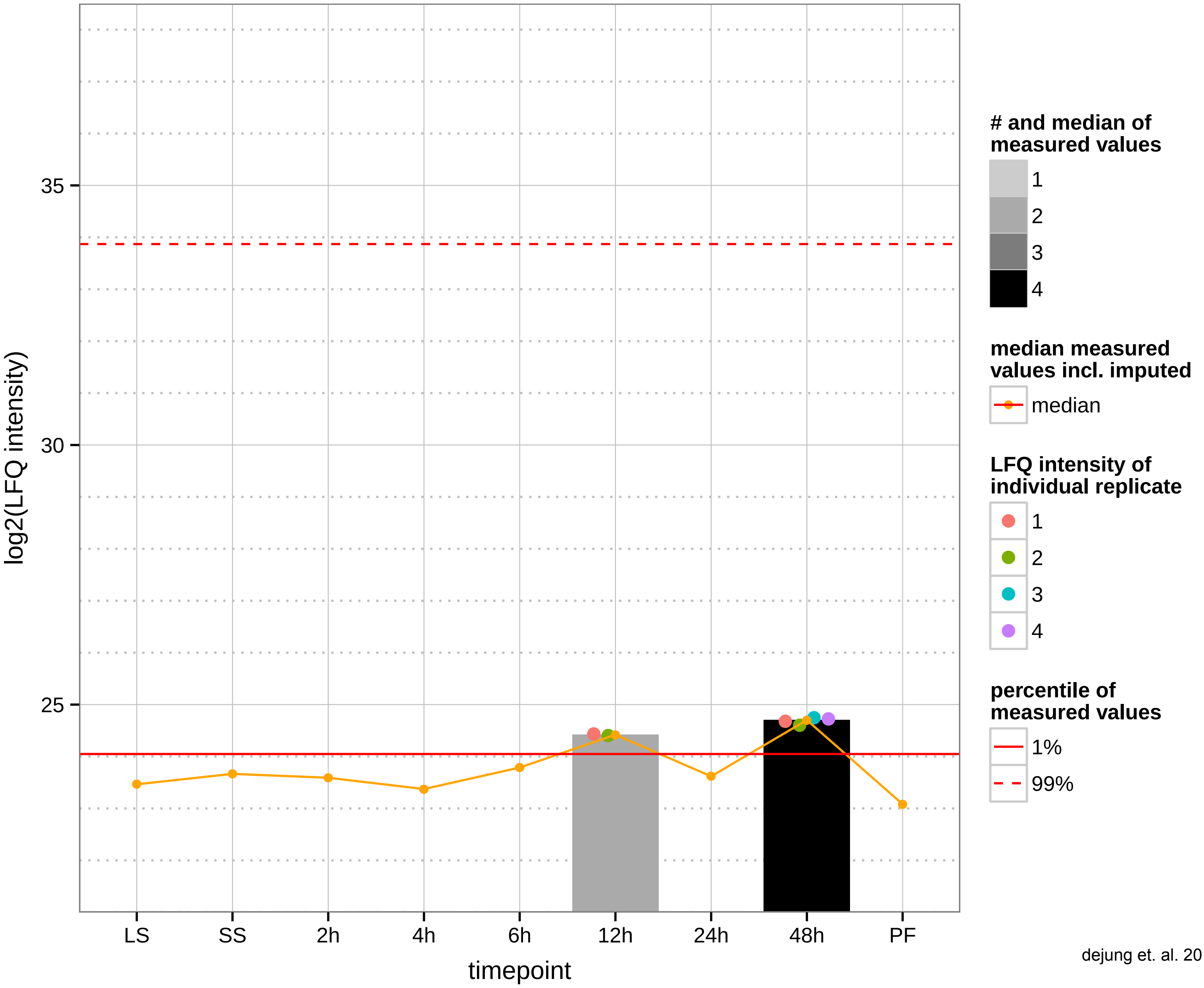
hypothetical protein, conserved
Tb927.4.1520
AGOF: null
AGOC: null
AGOP: viral protein processing, viral reproduction
PGOF: null
PGOC: null
PGOP: viral protein processing, viral reproduction





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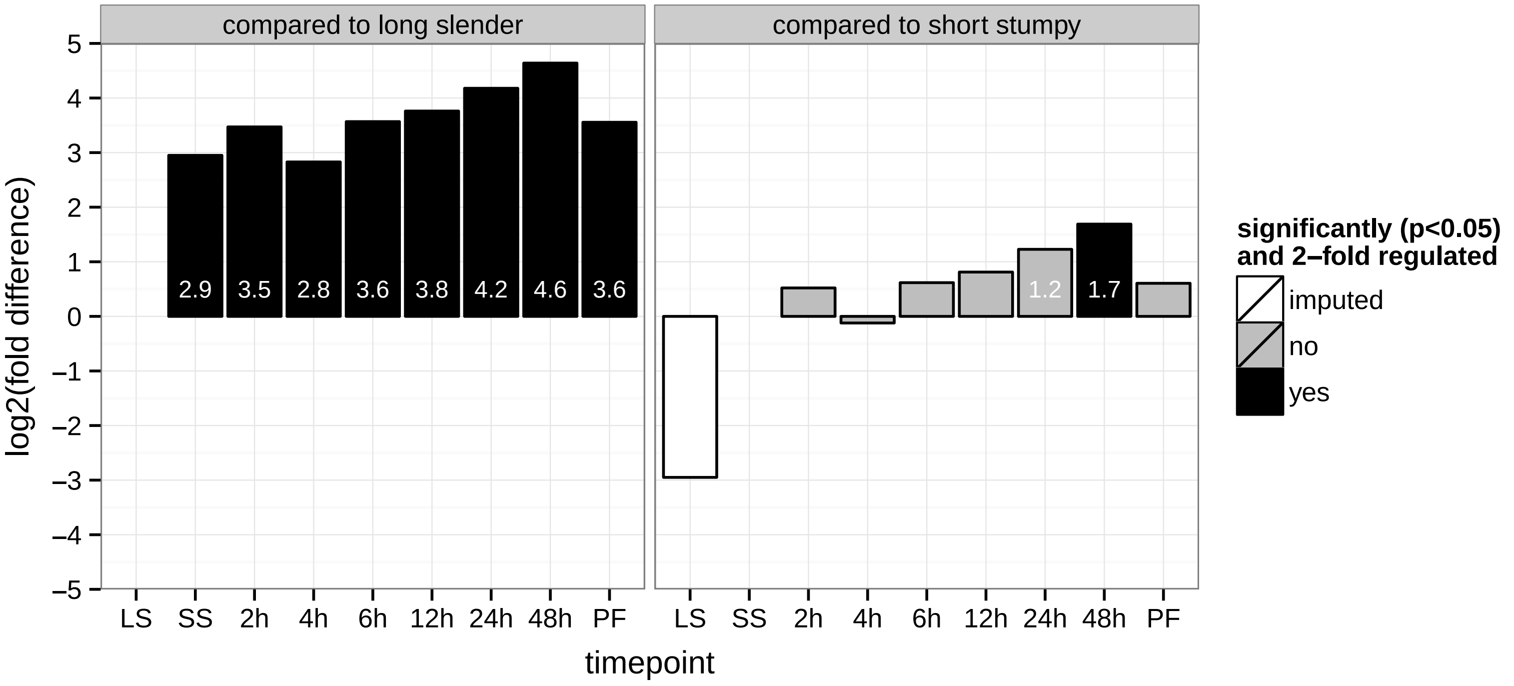
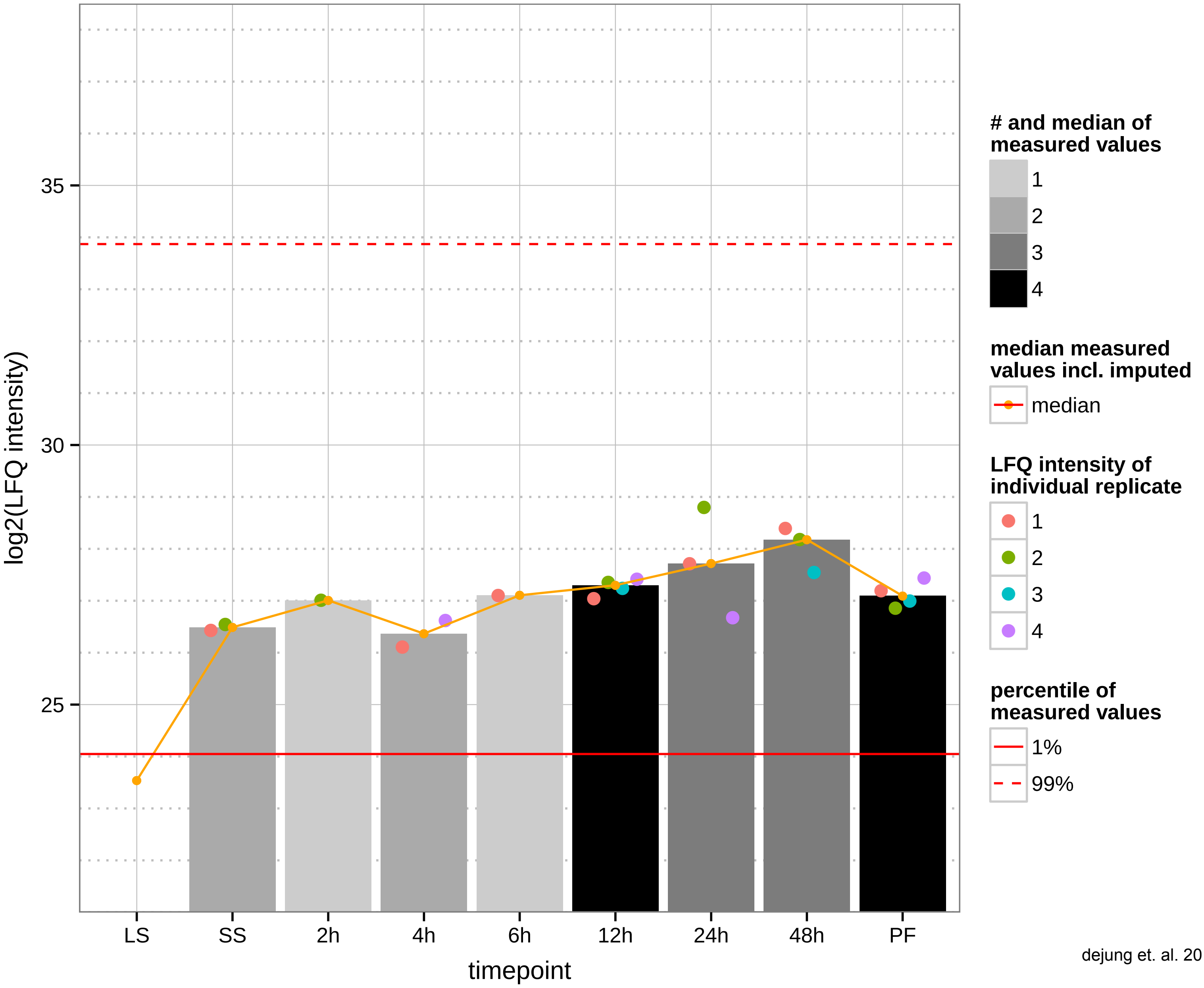
hypothetical protein, conserved
Tb927.4.720
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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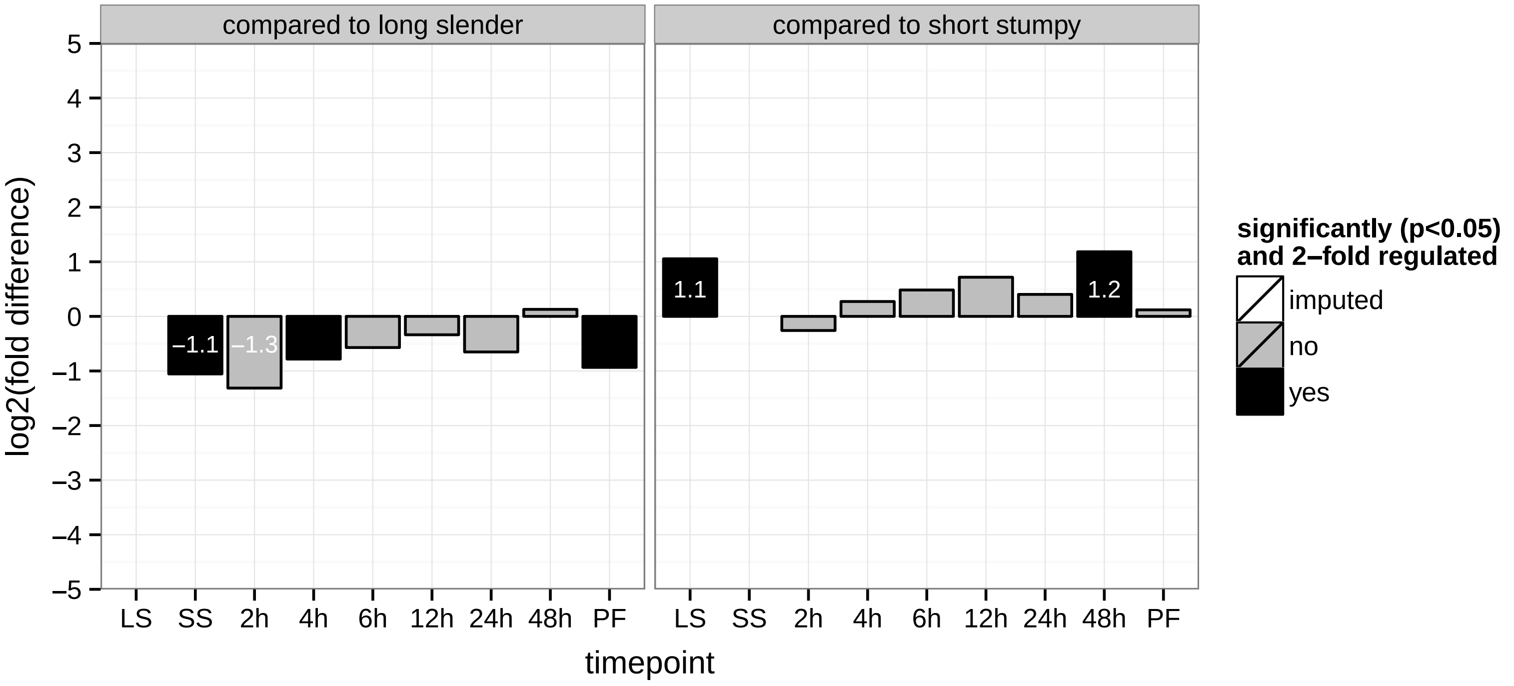
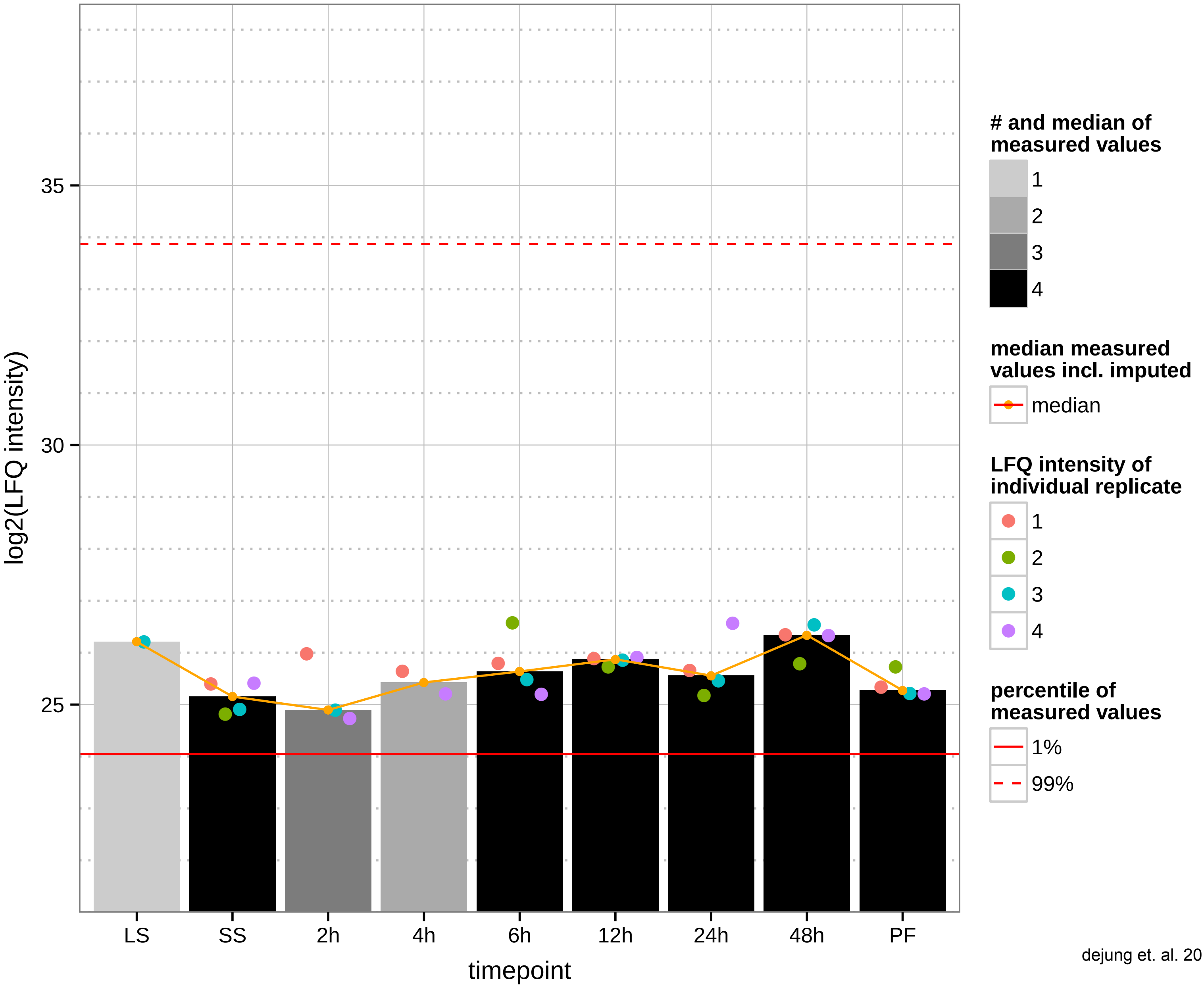
ubiquitin–protein ligase, putative (upl3)
Tb927.4.770
AGOF: acid–amino acid ligase activity
AGOC: intracellular
AGOP: cellular protein modification process
PGOF: acid–amino acid ligase activity
PGOC: intracellular
PGOP: cellular protein modification process





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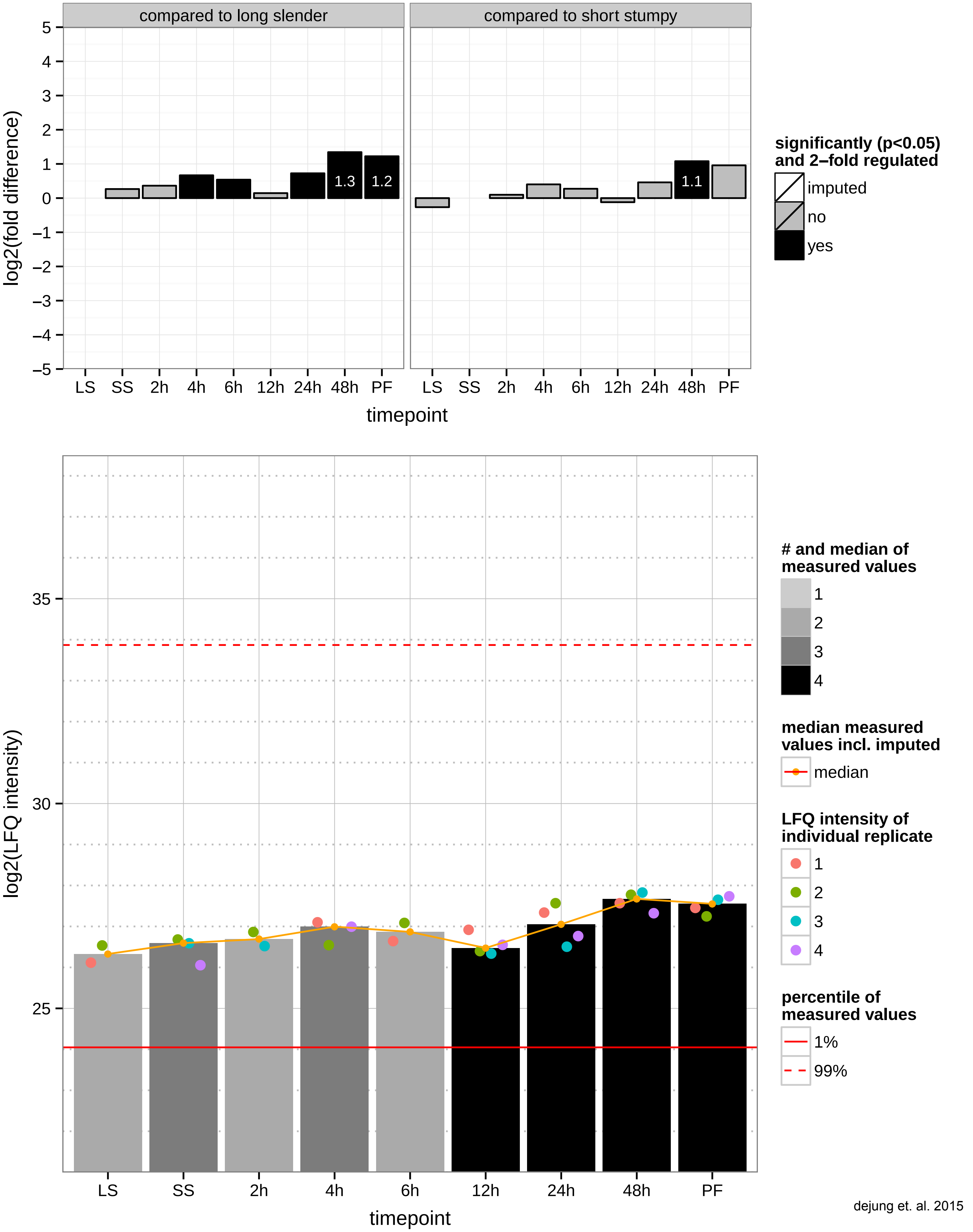
ADG1, pseudogene
Tb927.5.3390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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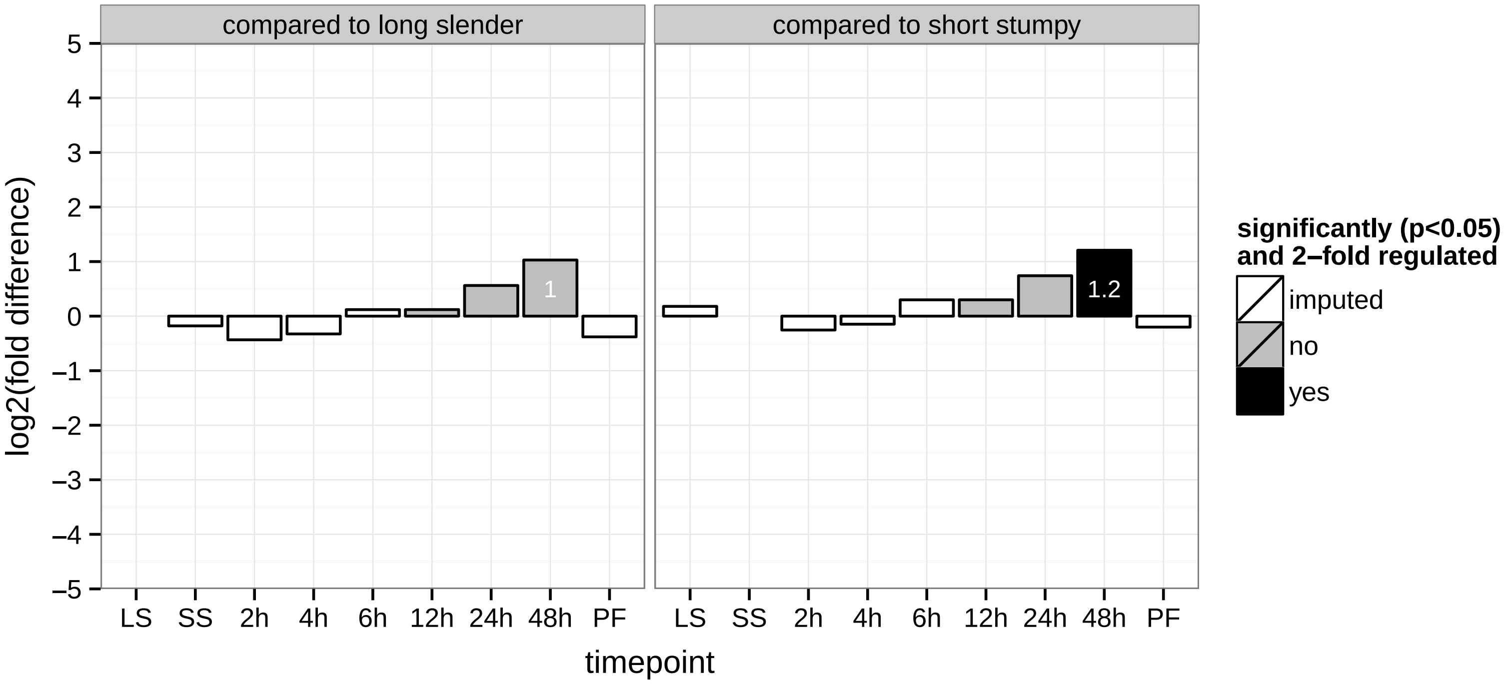
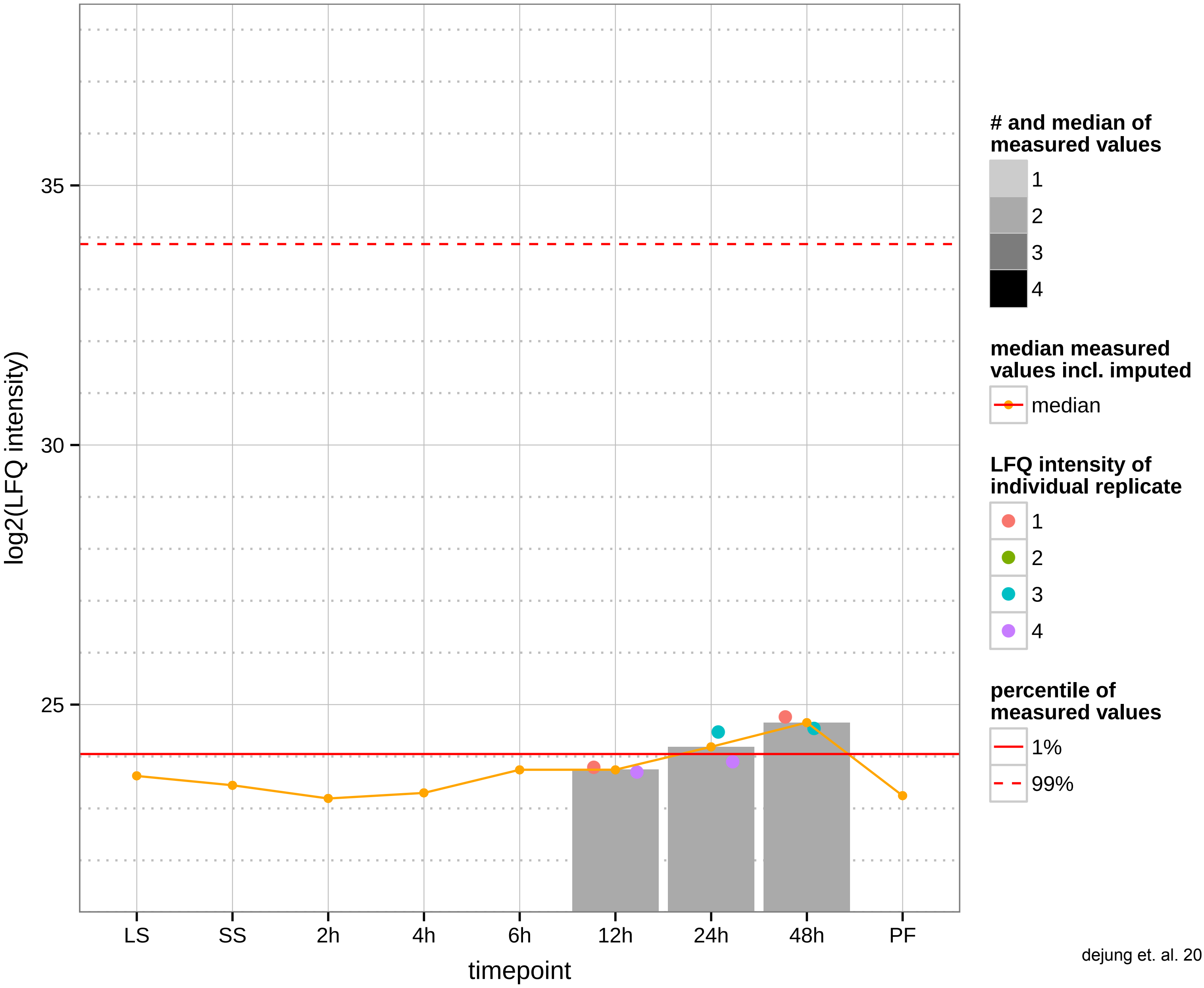
hypothetical protein, conserved
Tb927.5.770
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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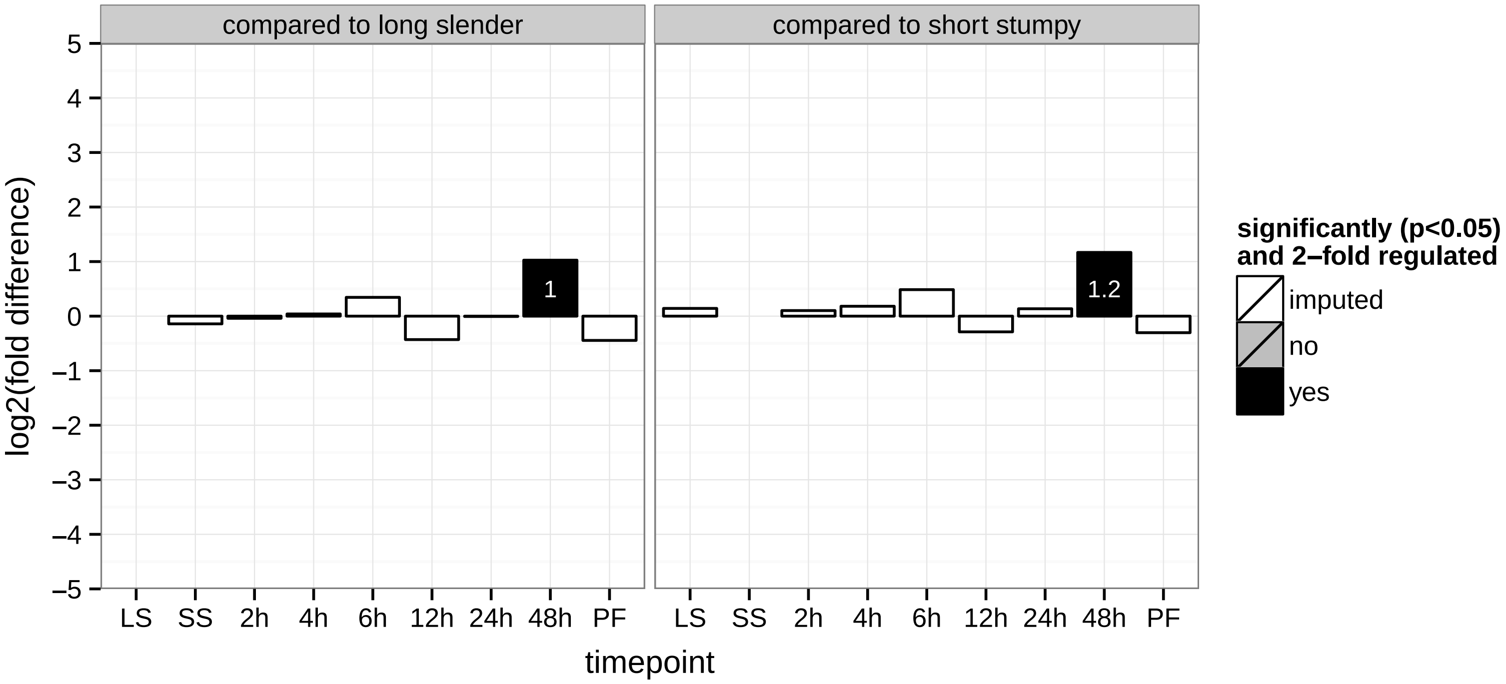
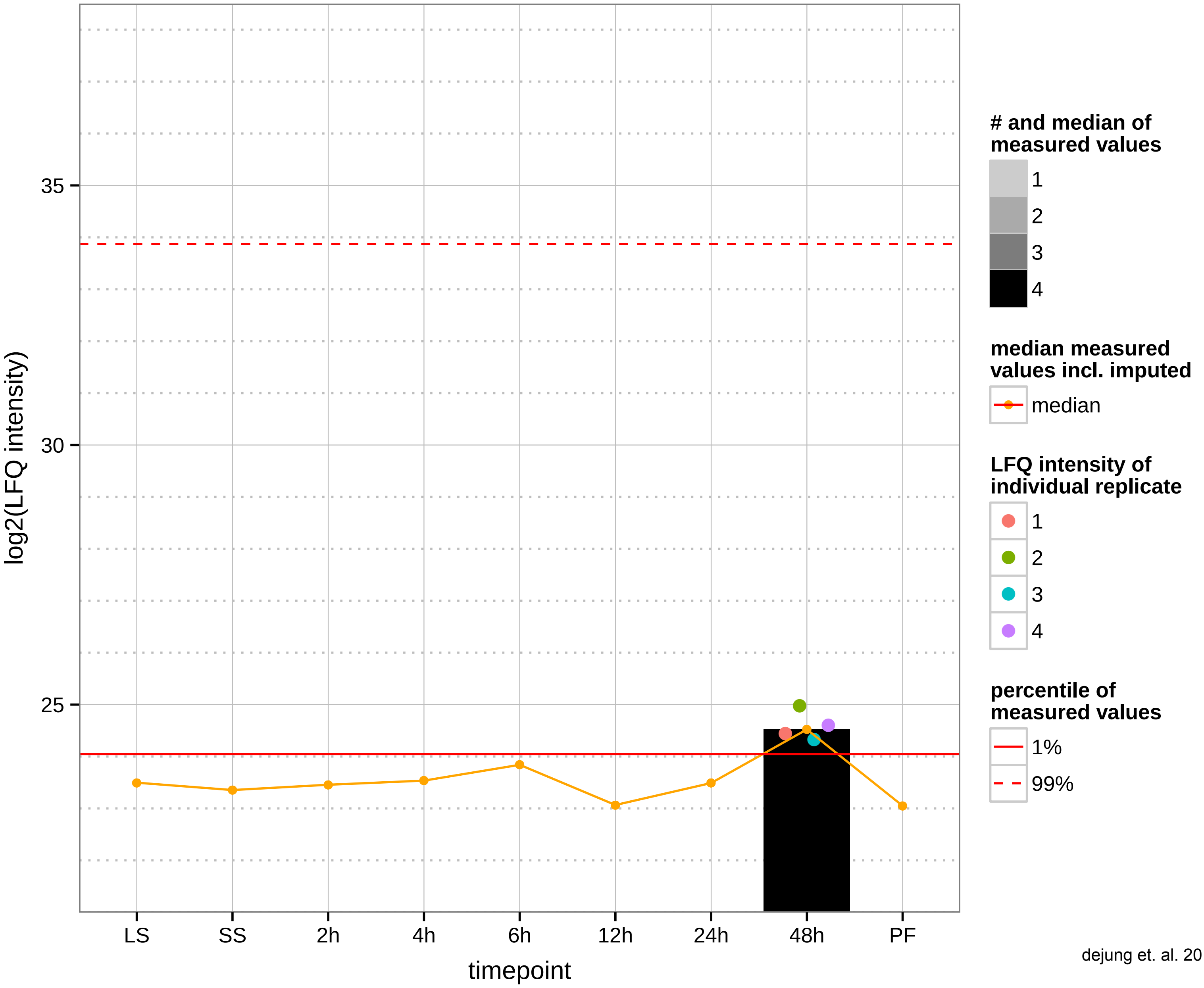
ubiquitin carboxyl–terminal hydrolase, putative, cysteine peptidase, Clan CA, family C19
Tb927.6.1110
AGOF: ubiquitin thiolesterase activity
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ubiquitin thiolesterase activity
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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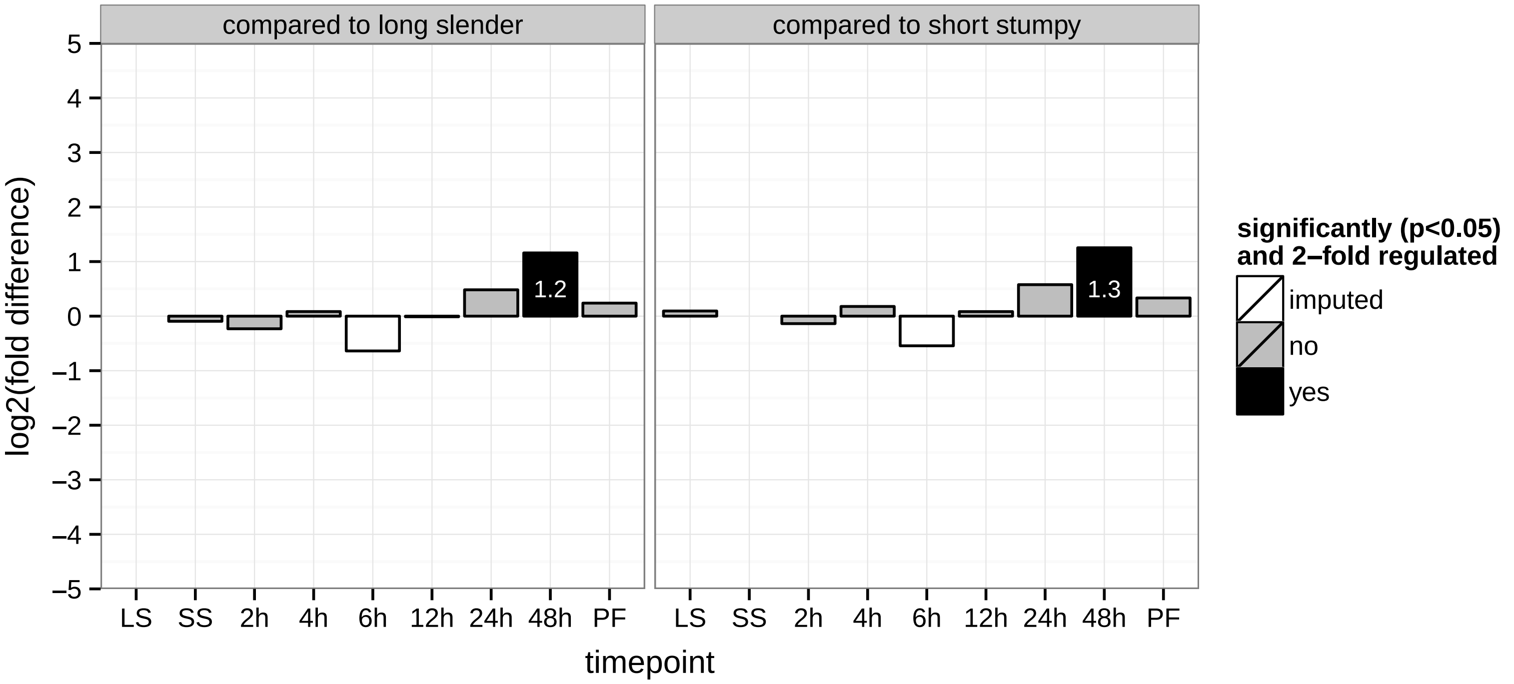
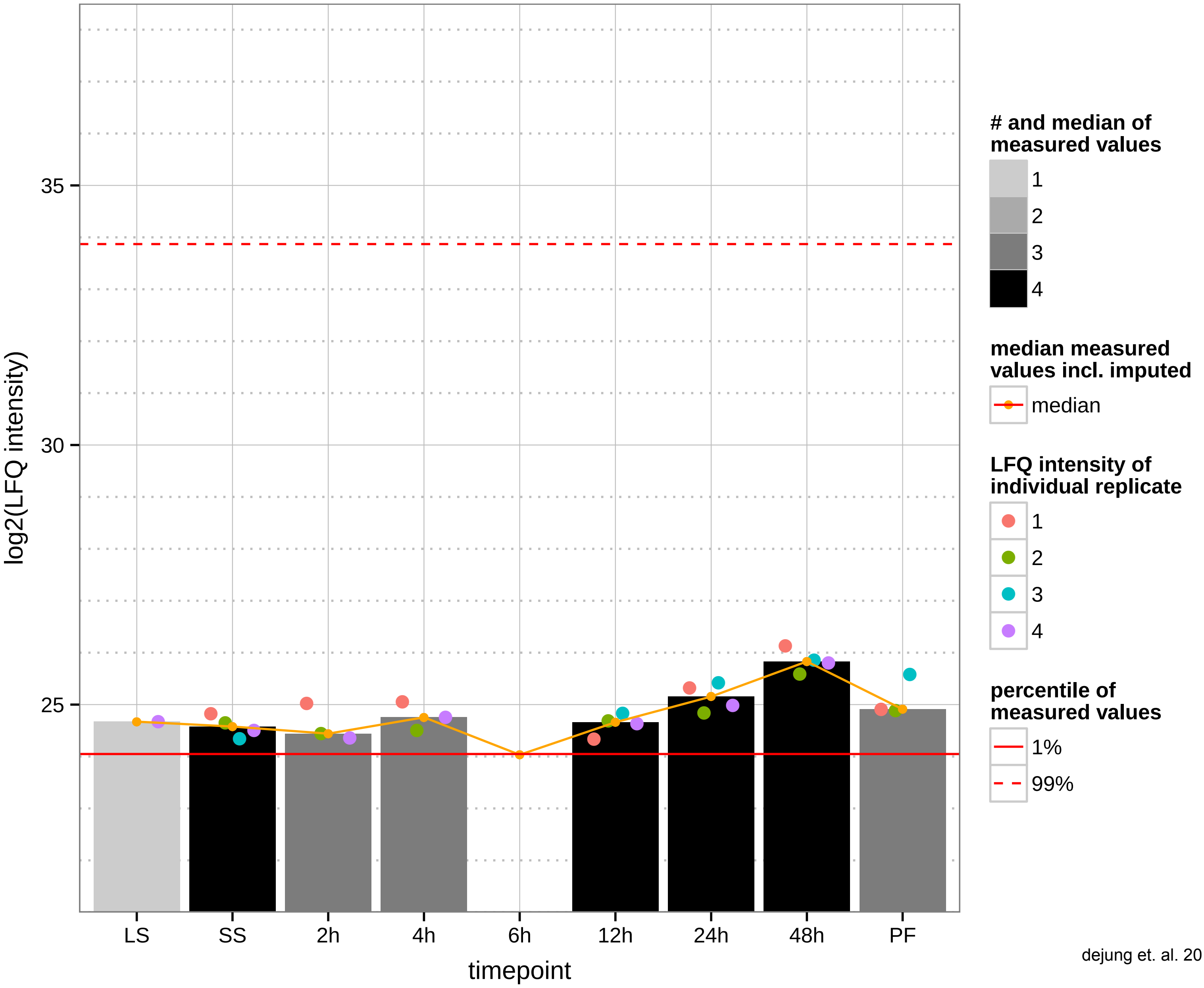
cell division cycle protein 16 homolog, putative
Tb927.6.2150
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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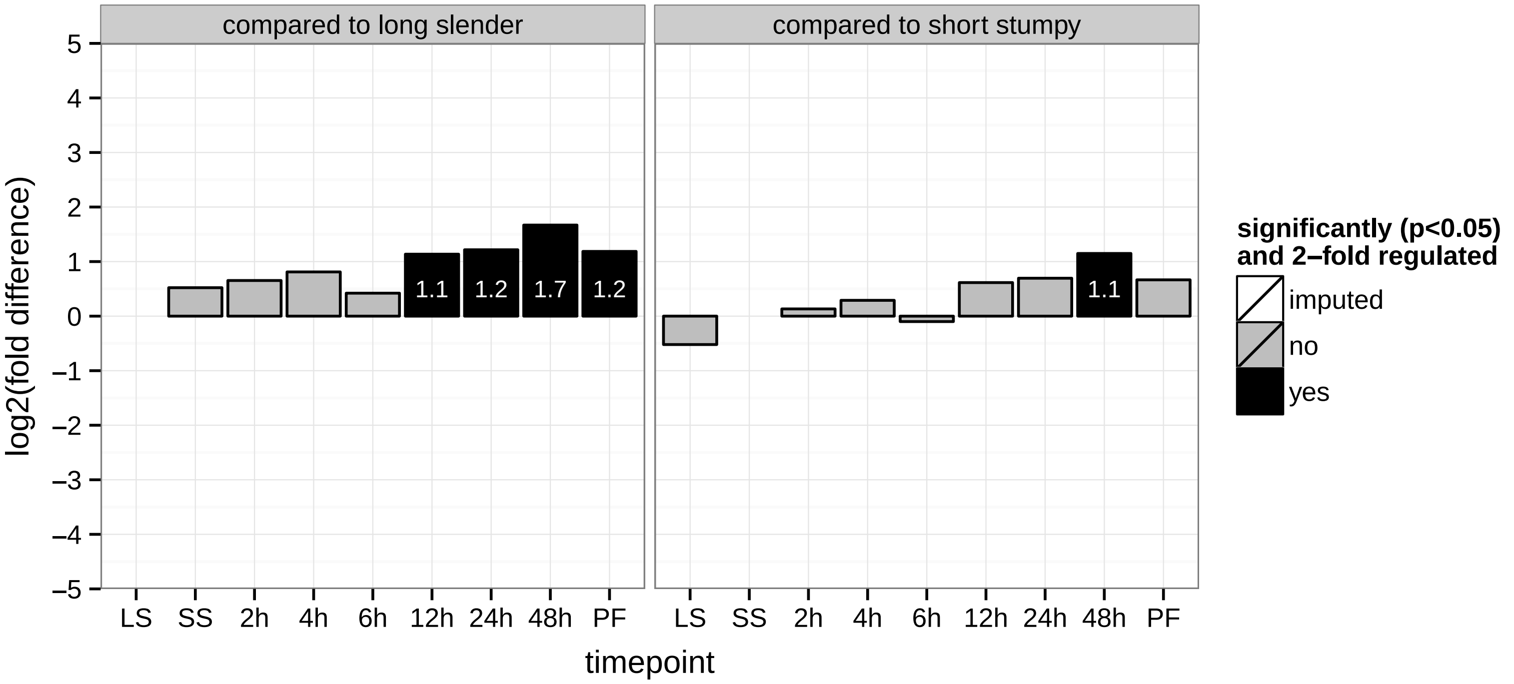
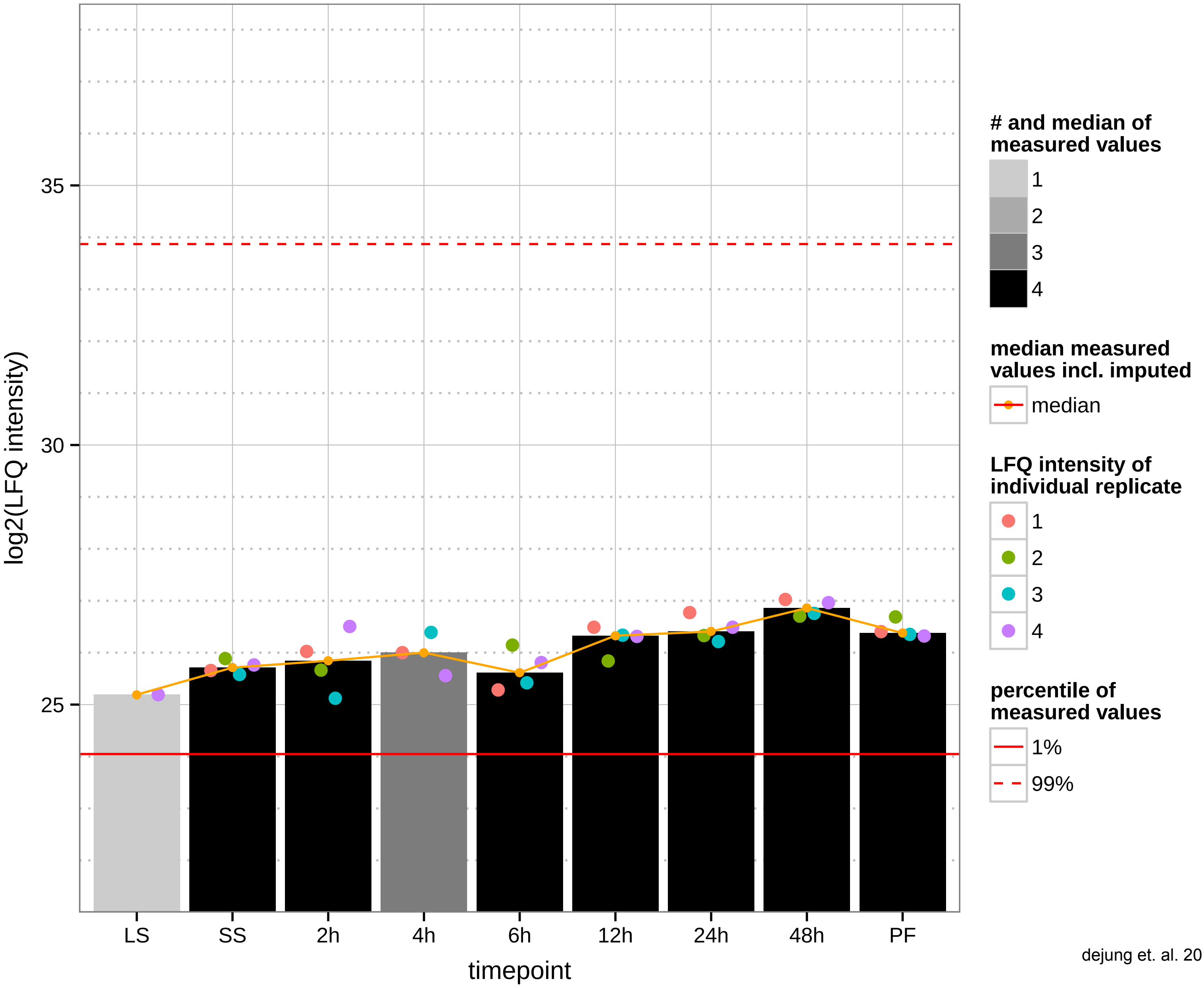
hypothetical protein, conserved
Tb927.6.2710
AGOF: zinc ion binding
AGOC: integral to membrane, intracellular
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: intracellular
PGOP: null





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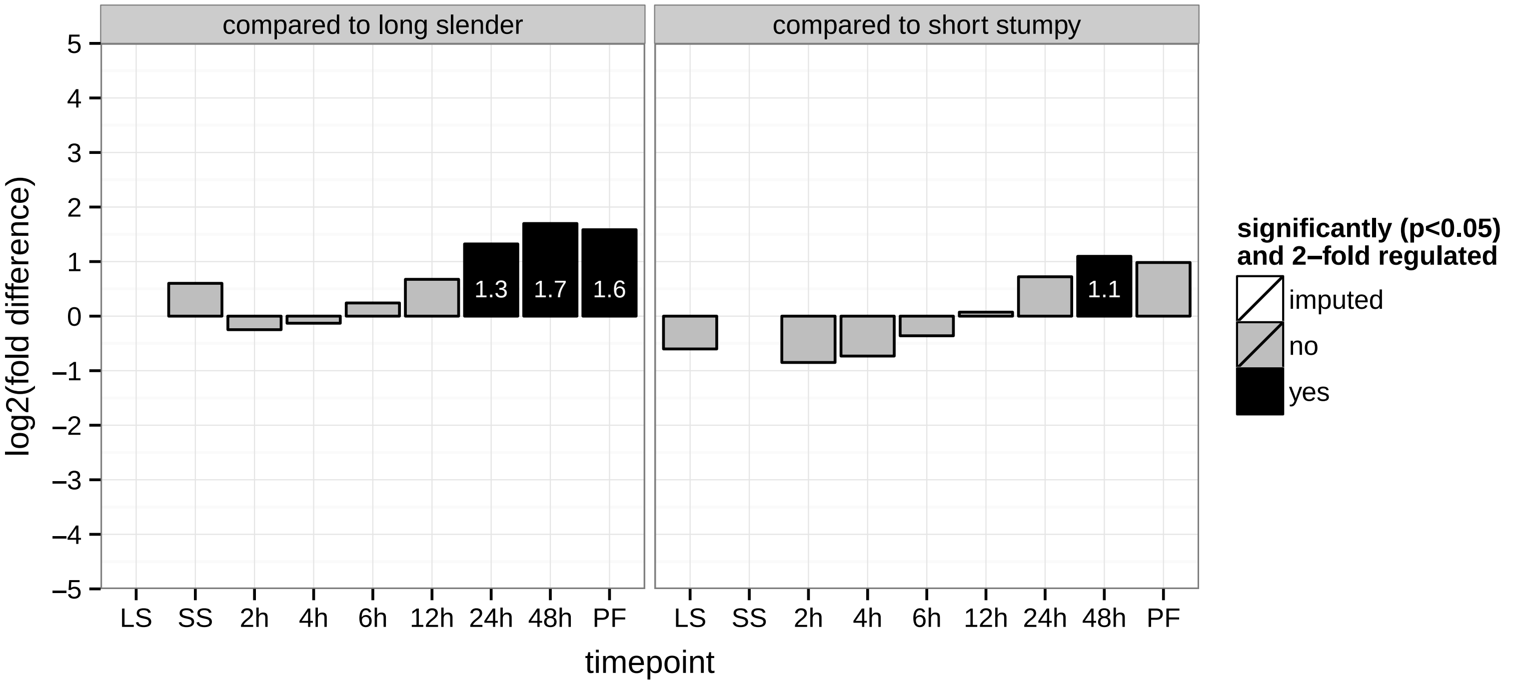
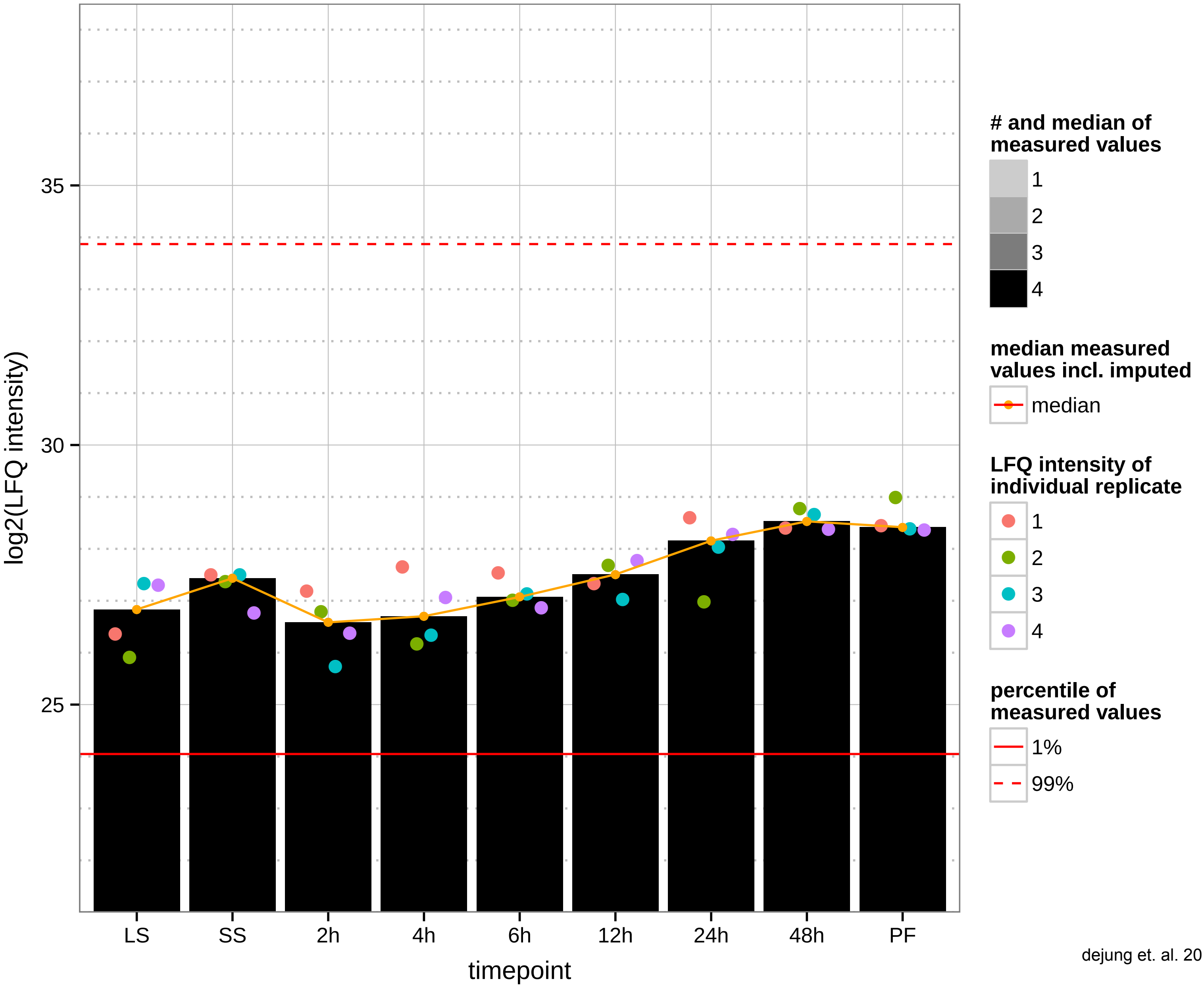
serine/arginine–rich protein specific kinase SRPK, putative, protein kinase
Tb927.6.4970
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: growth, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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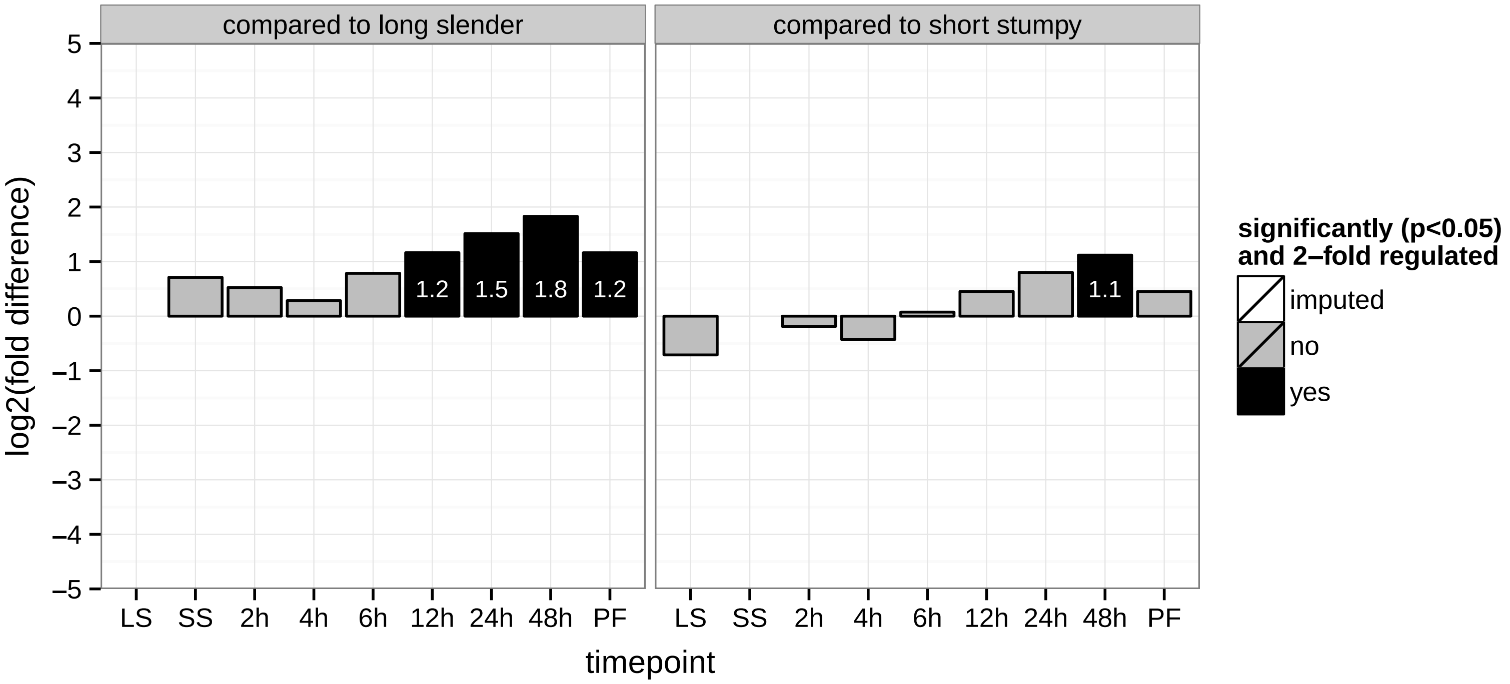
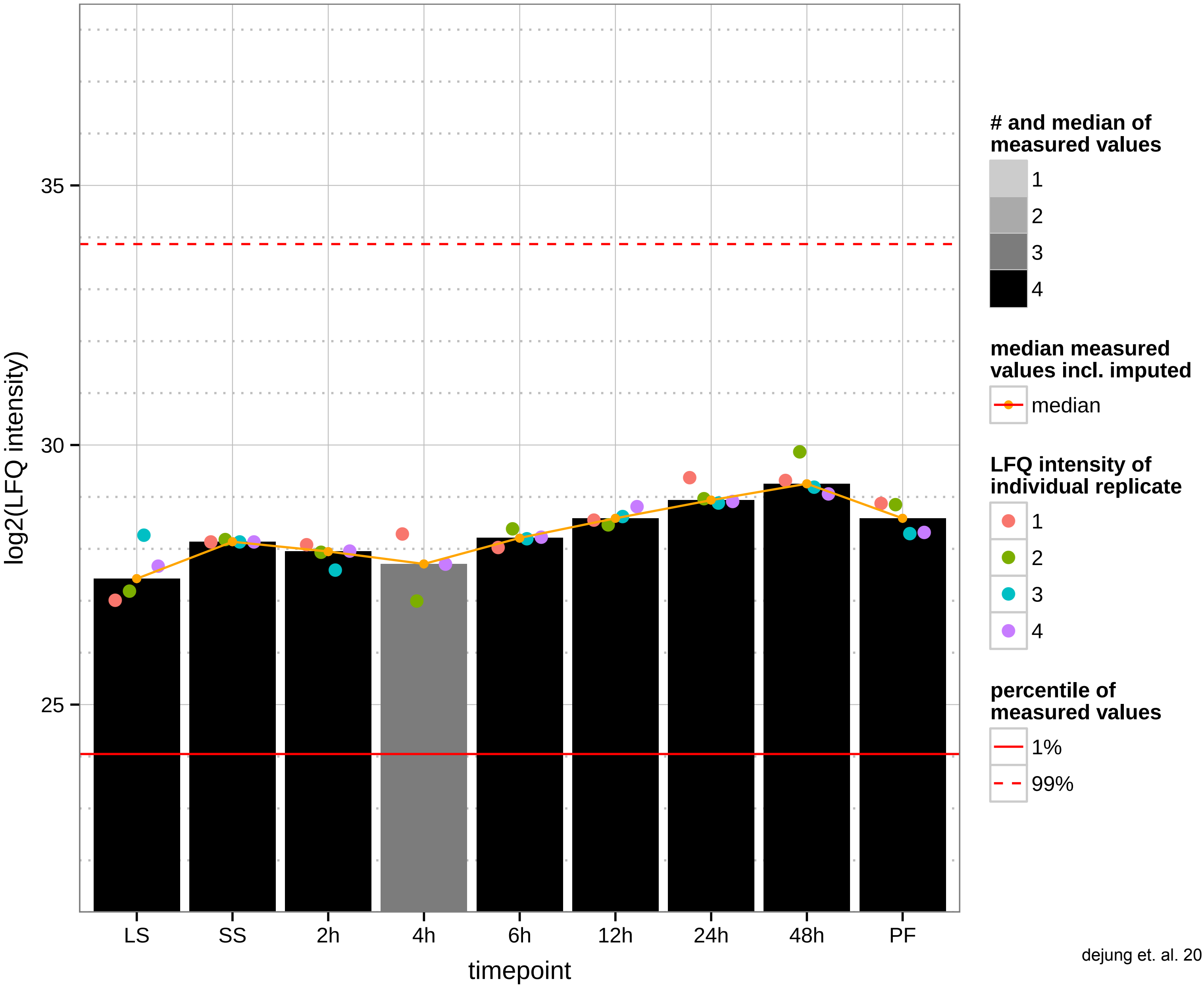
hypothetical protein, conserved
Tb927.7.2390
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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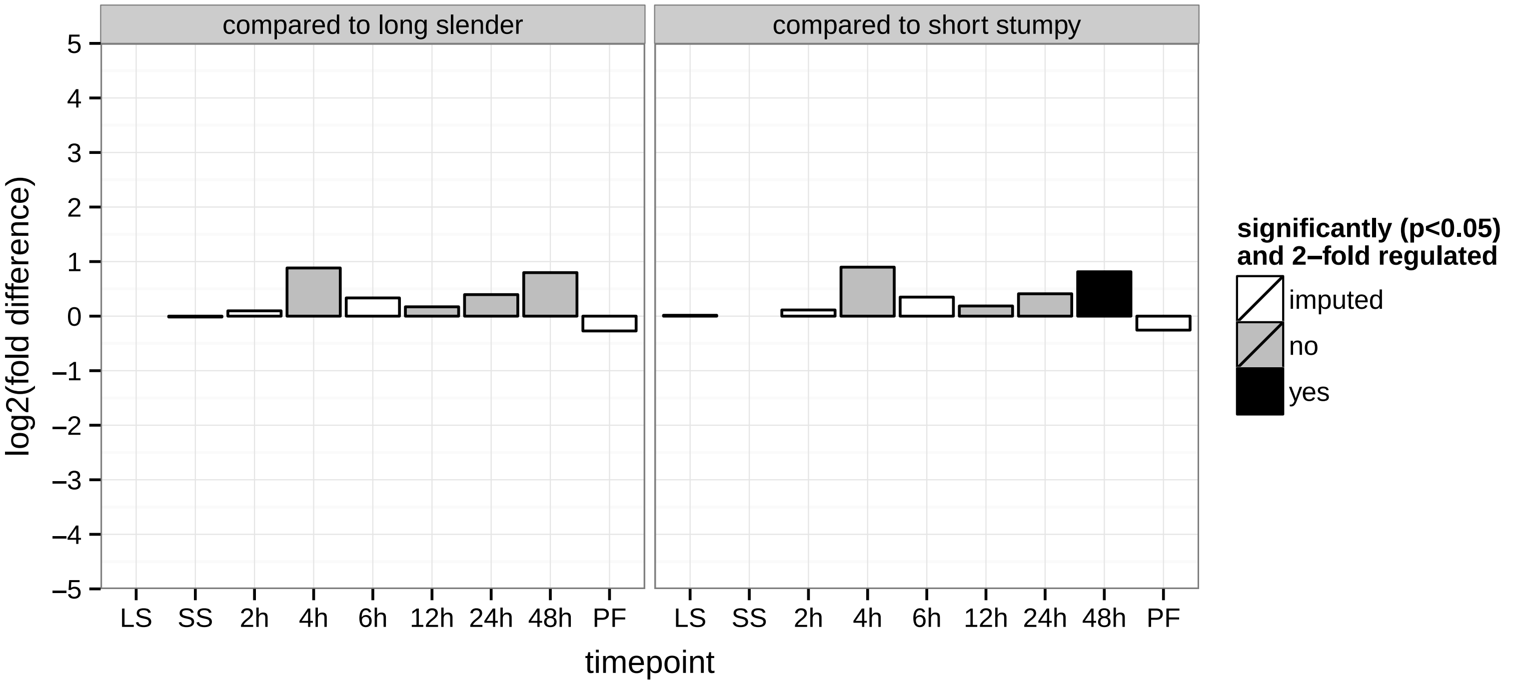
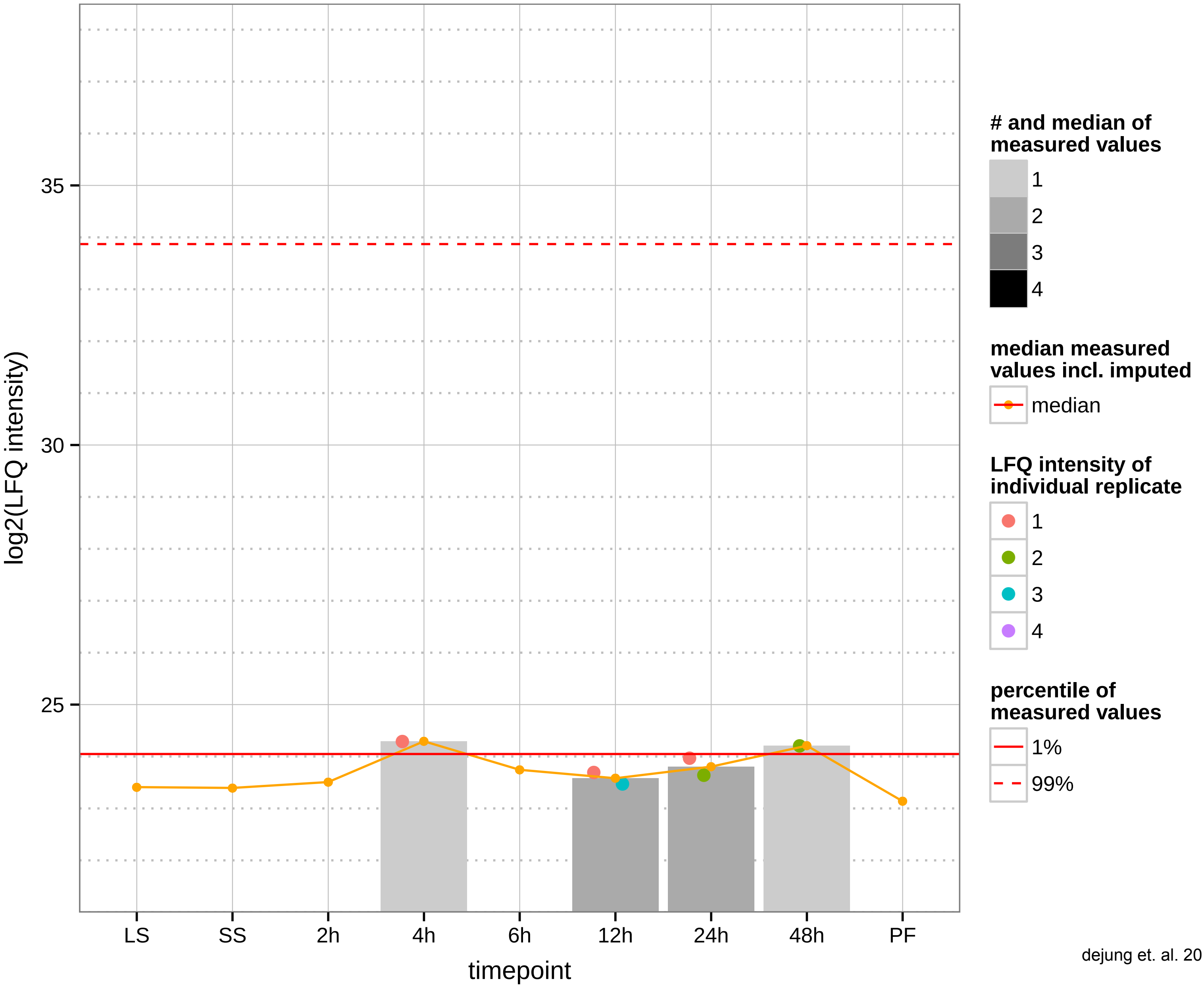
peptidyl–prolyl cis–trans isomerase, putative, parvulin (PAR45)
Tb927.7.2480
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: nucleus
AGOP: null
PGOF: isomerase activity, protein binding
PGOC: null
PGOP: null





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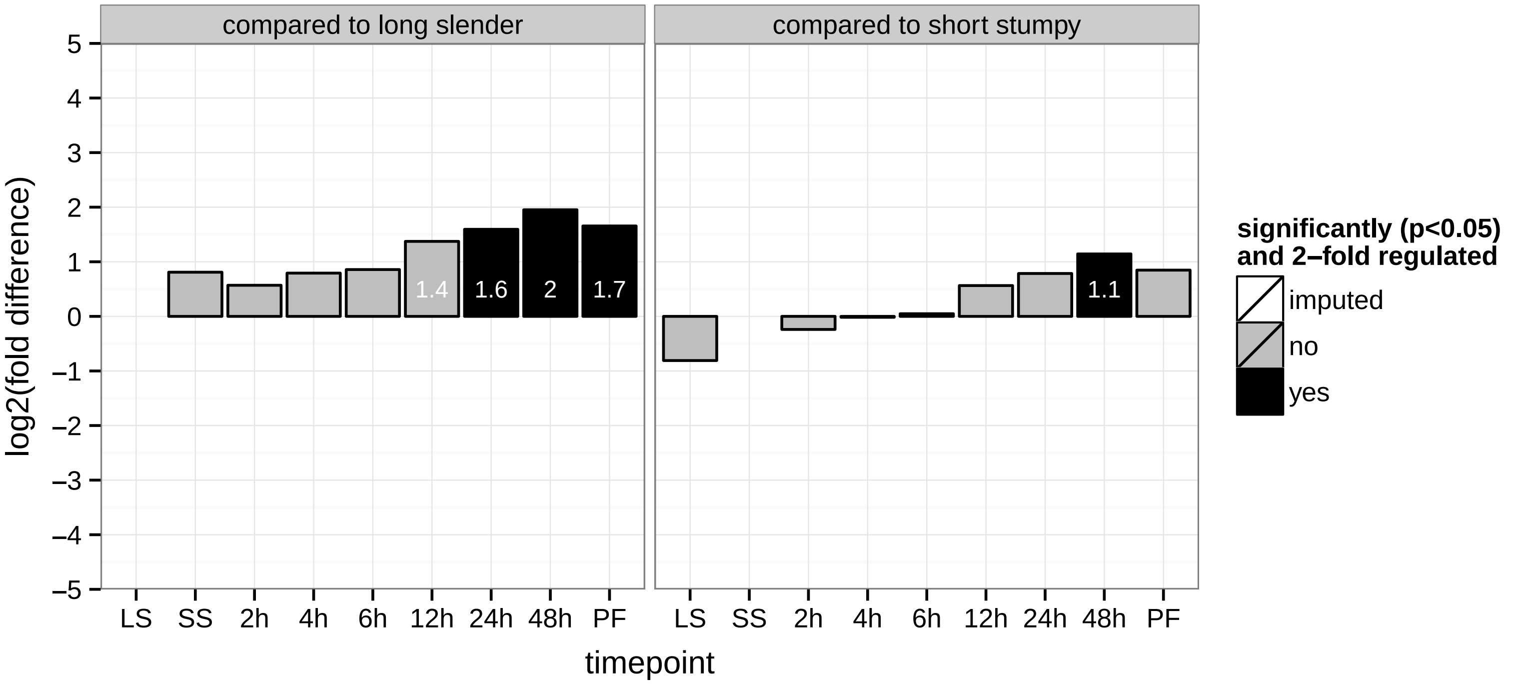
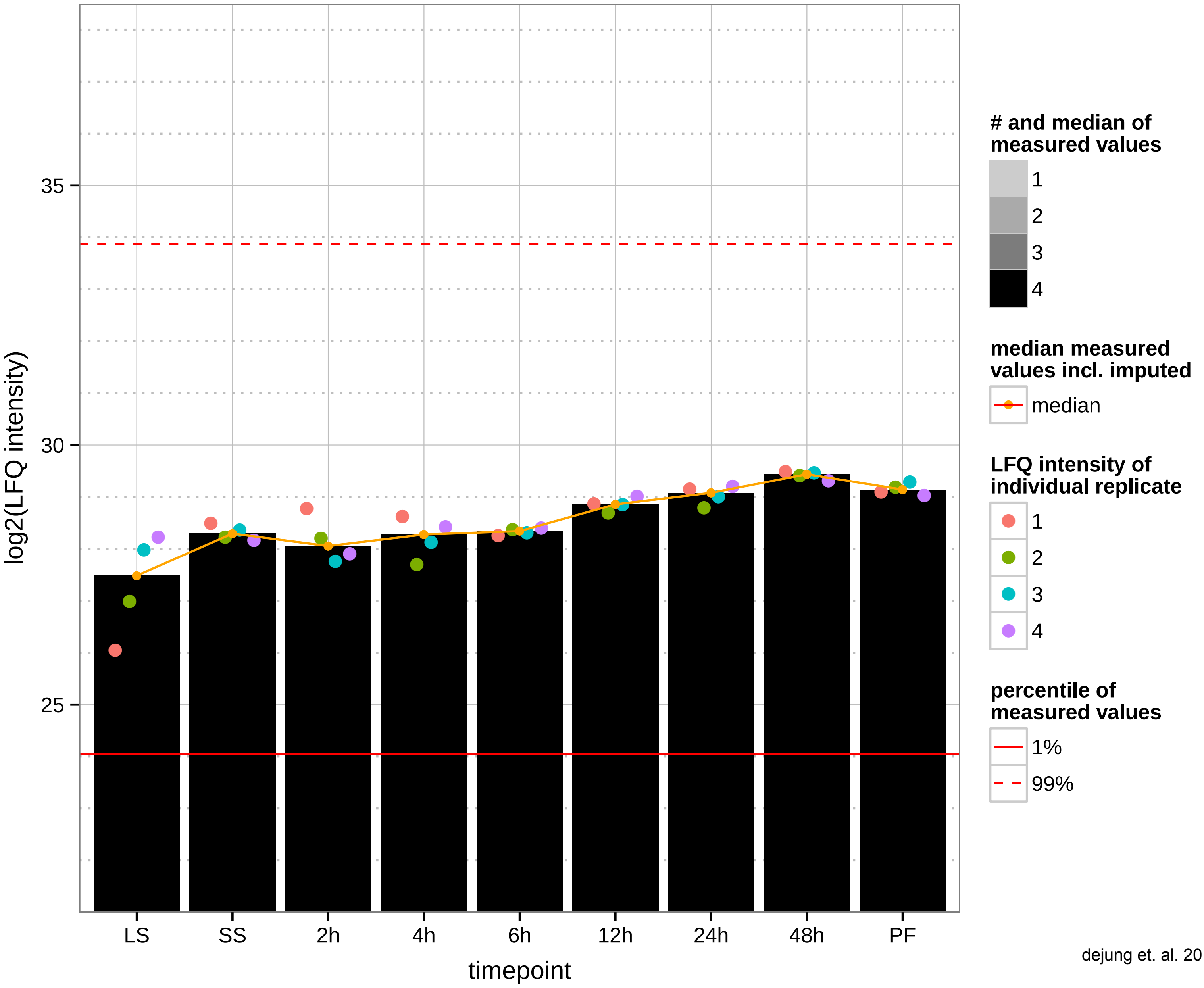
hypothetical protein, conserved
Tb927.7.3040
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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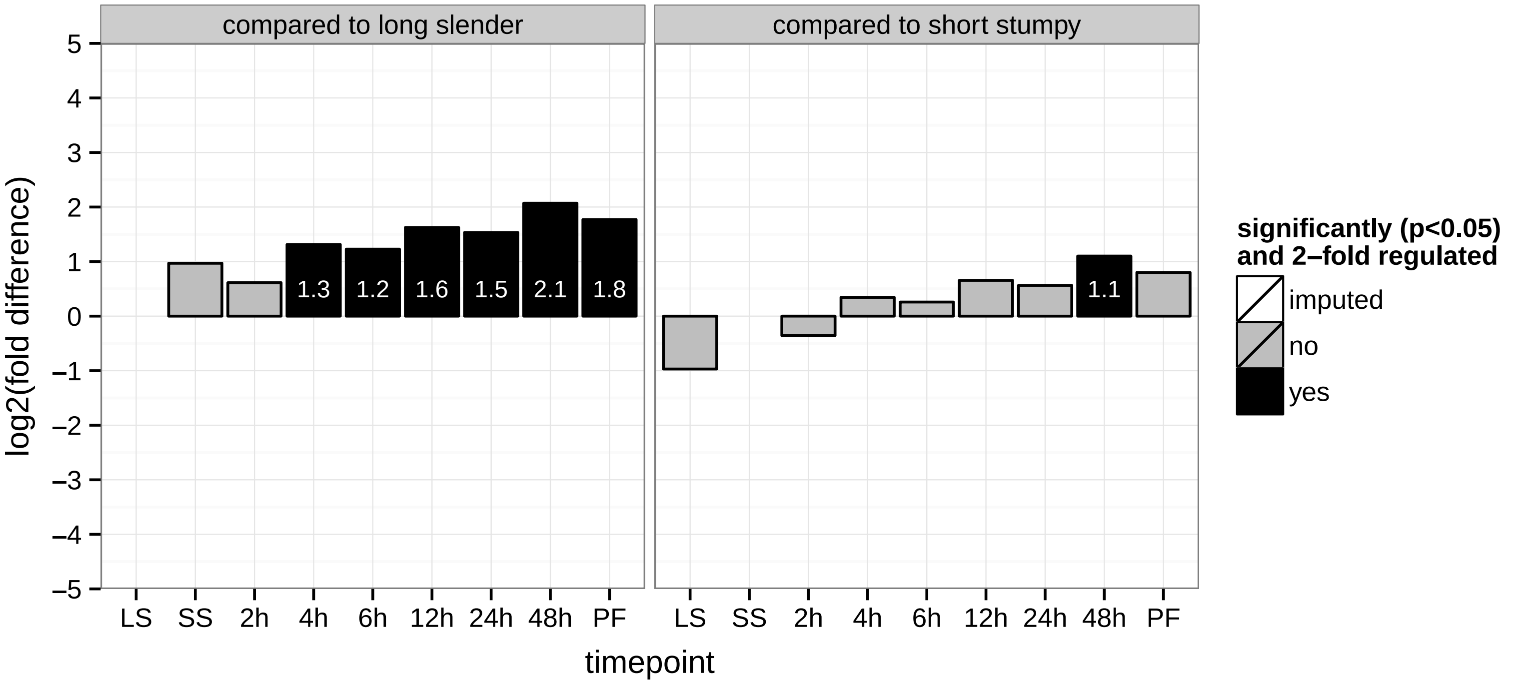
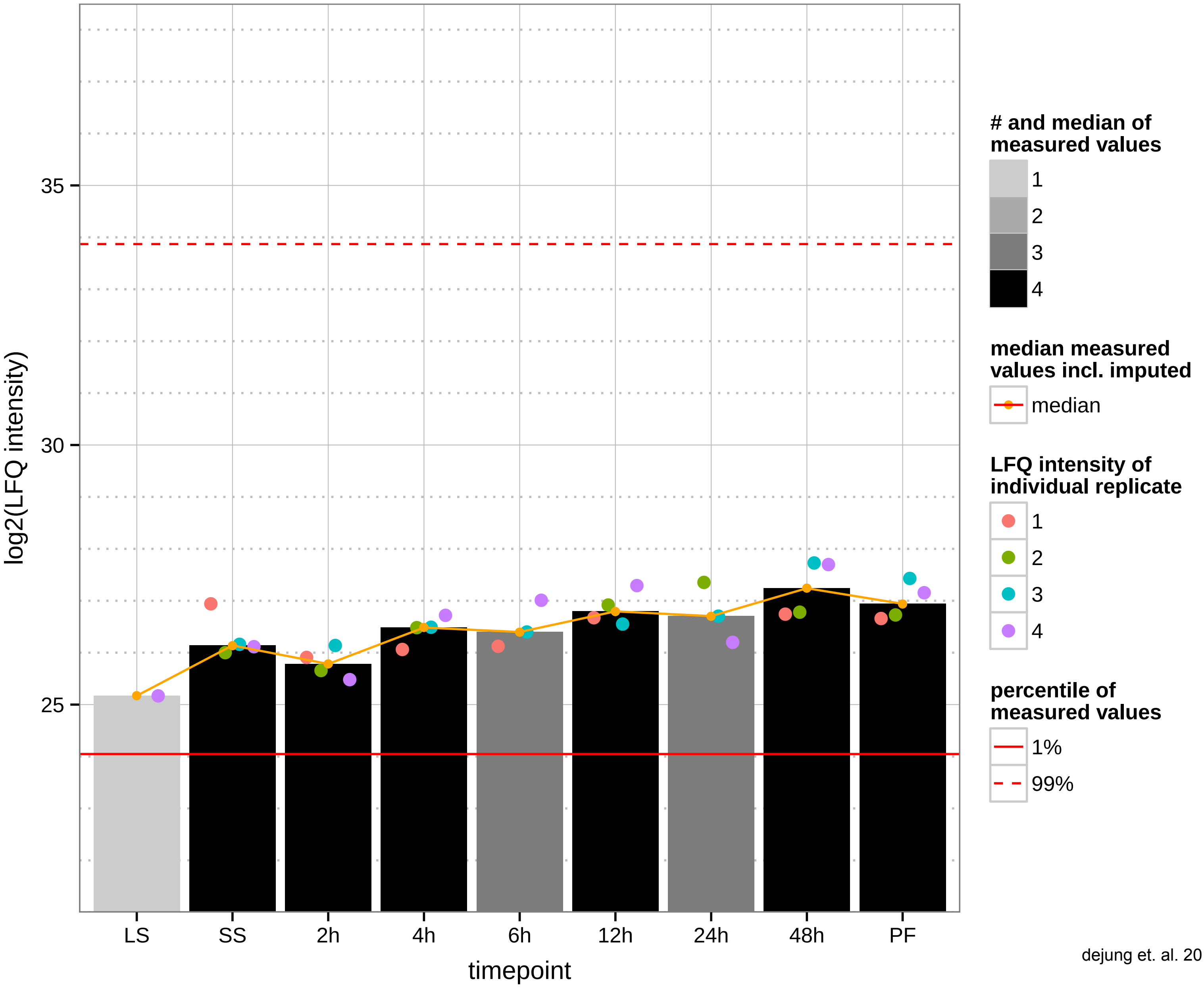
farnesyl pyrophosphate synthase (FPPS)
Tb927.7.3360
AGOF: dimethylallyltranstransferase activity, geranyltranstransferase activity
AGOC: cytosol, endoplasmic reticulum
AGOP: cholesterol biosynthetic process, farnesyl diphosphate biosynthetic process
PGOF: null
PGOC: null
PGOP: isoprenoid biosynthetic process





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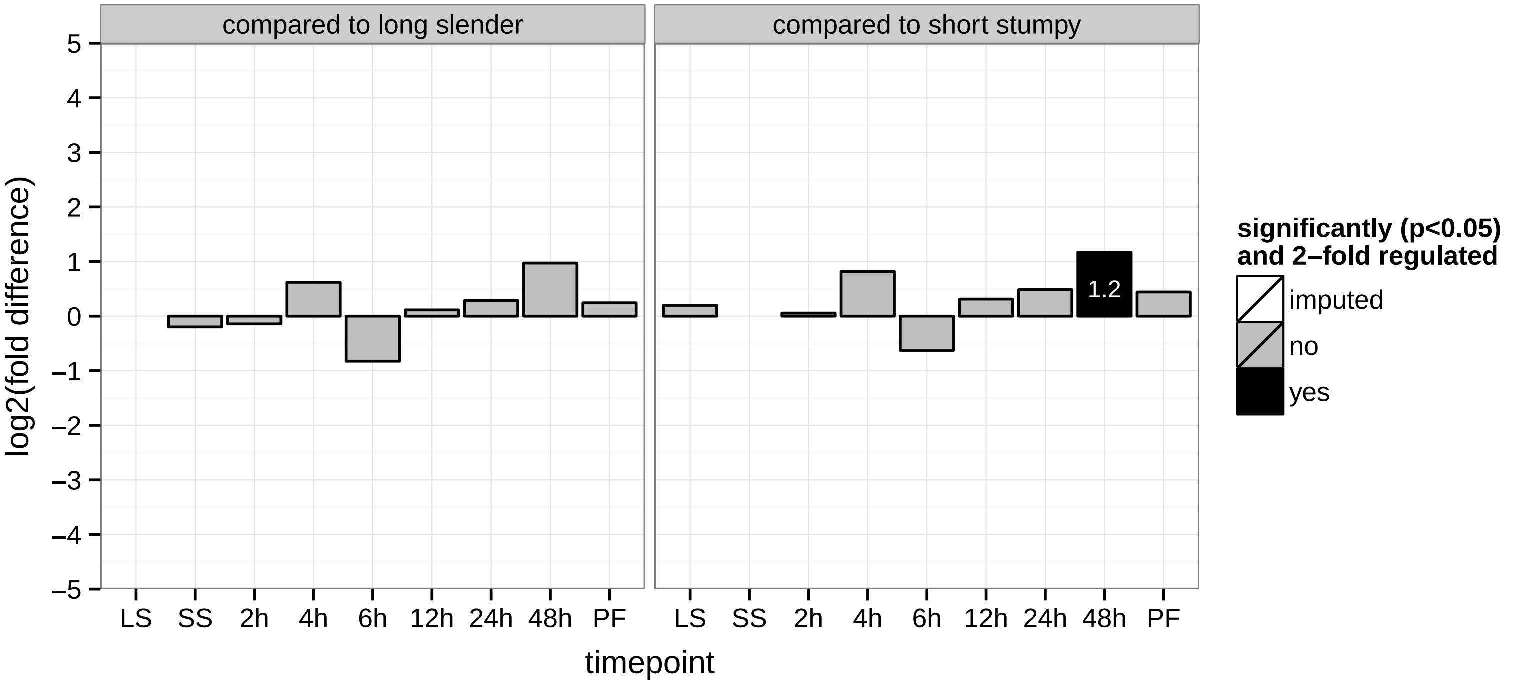
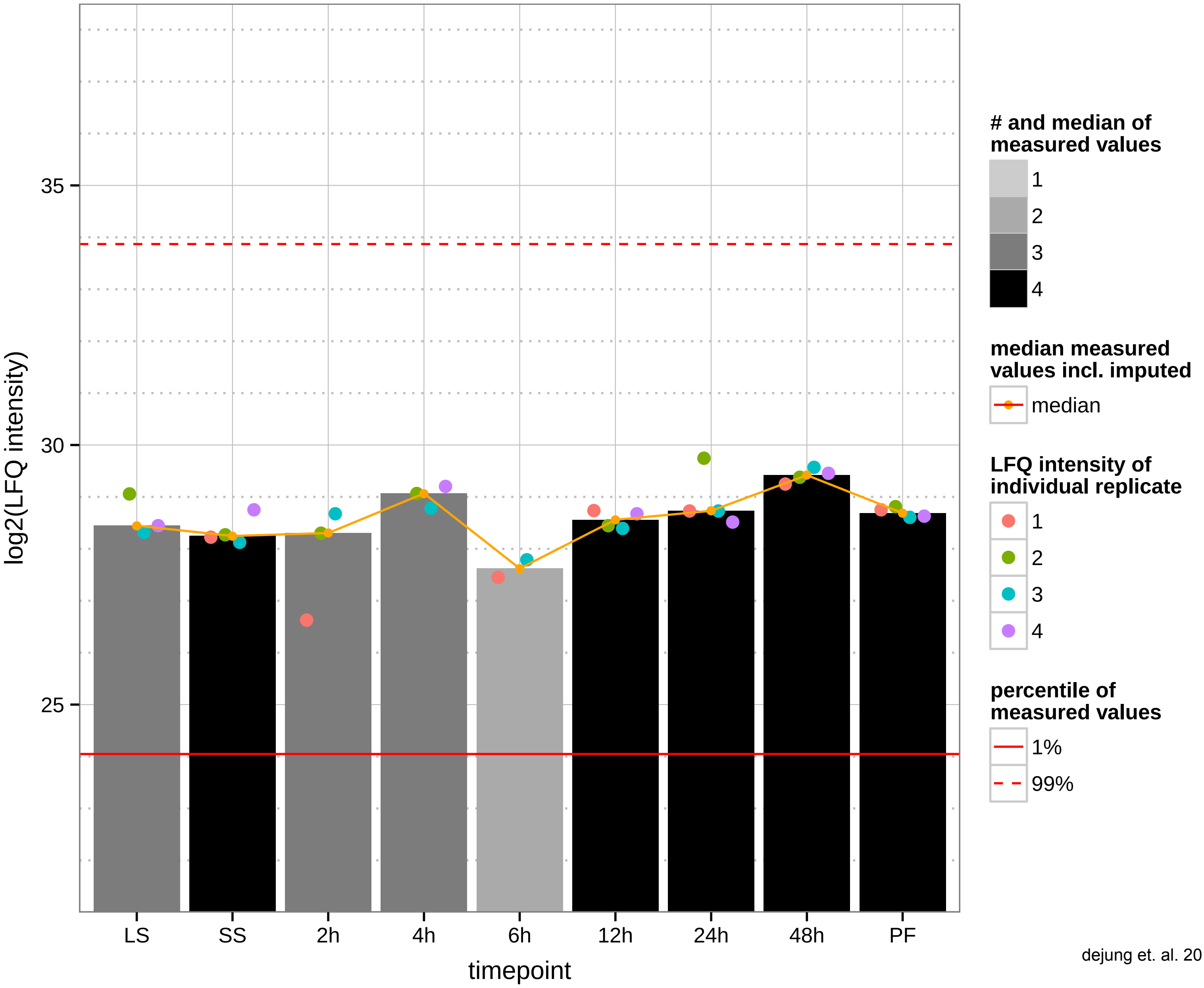
calpain–like cysteine peptidase, putative, cysteine peptidase, Clan CA, family C2
Tb927.7.4060
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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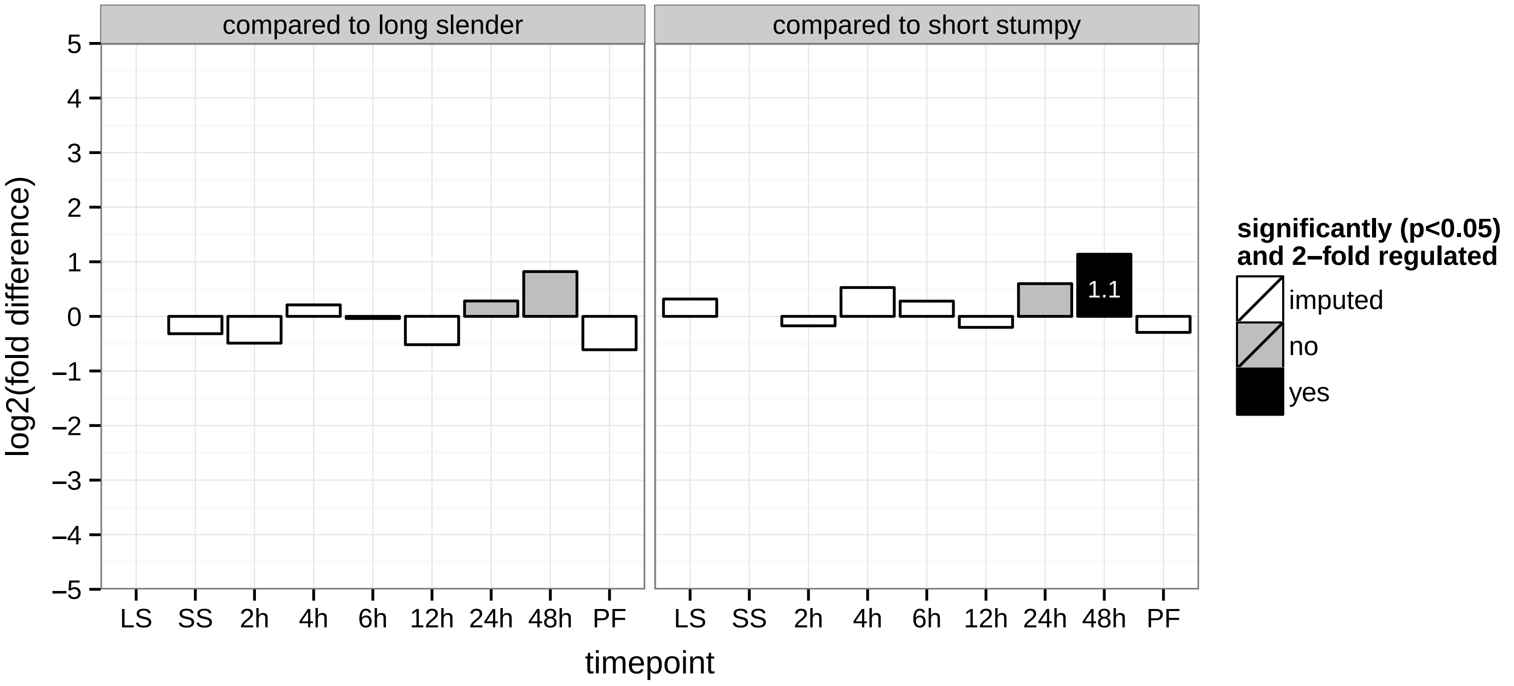
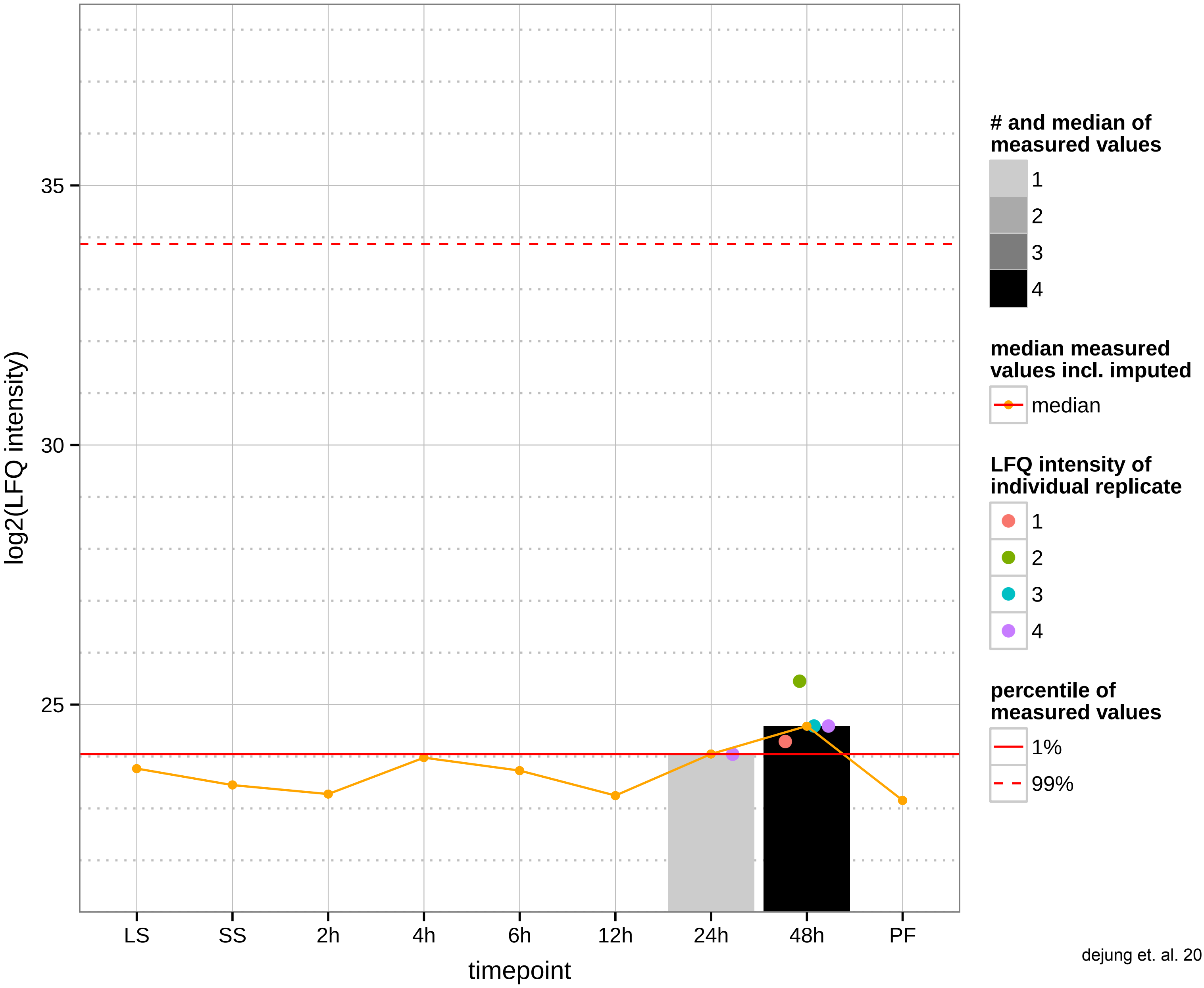
leucine–rich repeat protein (LRRP), putative
Tb927.7.5600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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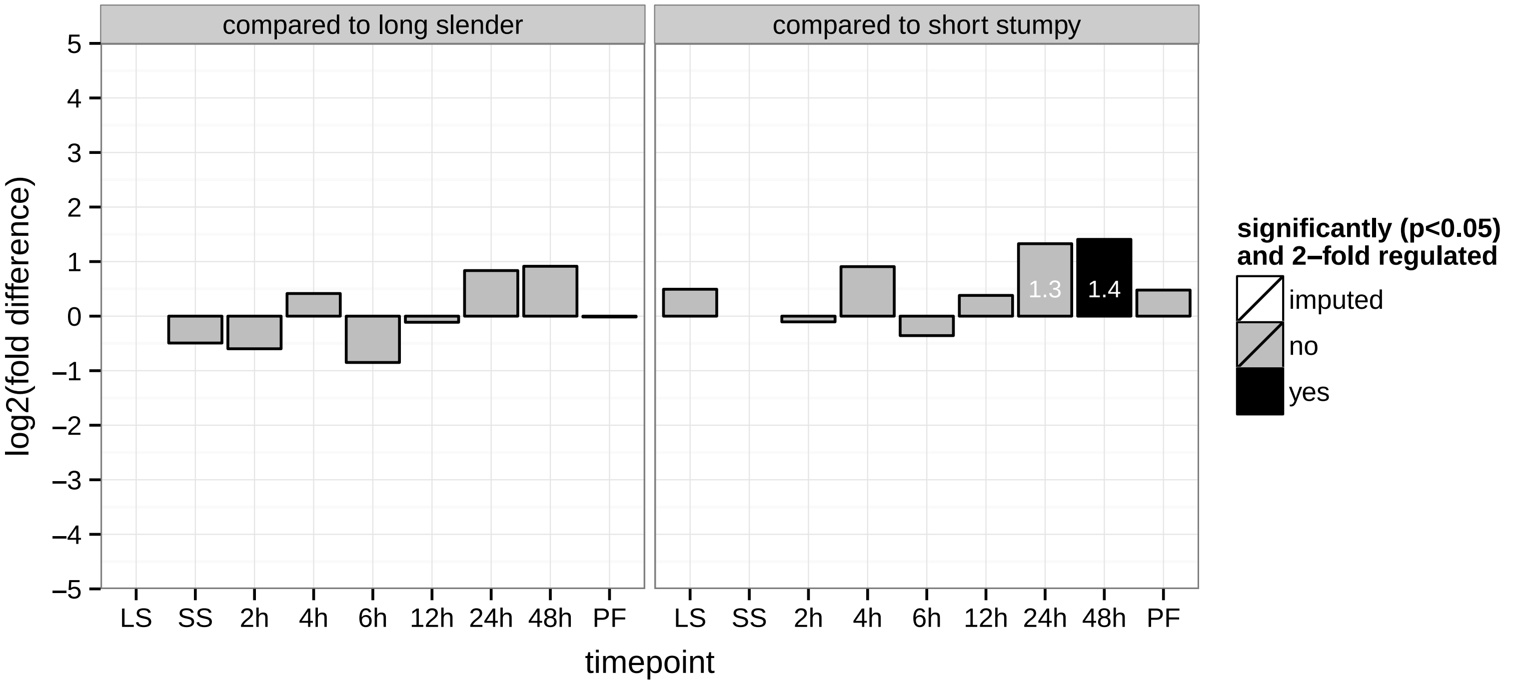
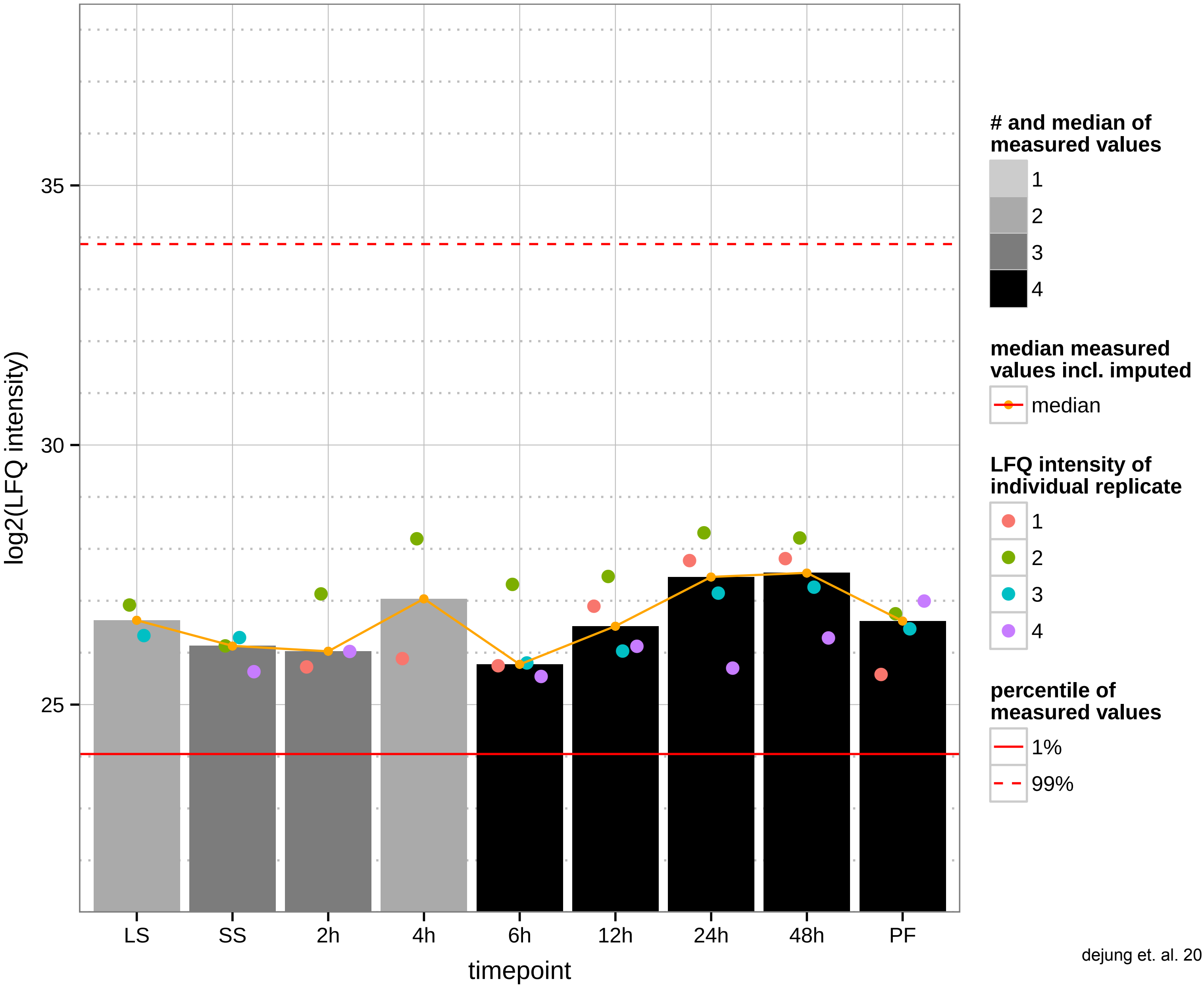
hypothetical protein, conserved
Tb927.7.6770
AGOF: fatty–acyl–CoA binding
AGOC: null
AGOP: null
PGOF: fatty–acyl–CoA binding
PGOC: null
PGOP: null





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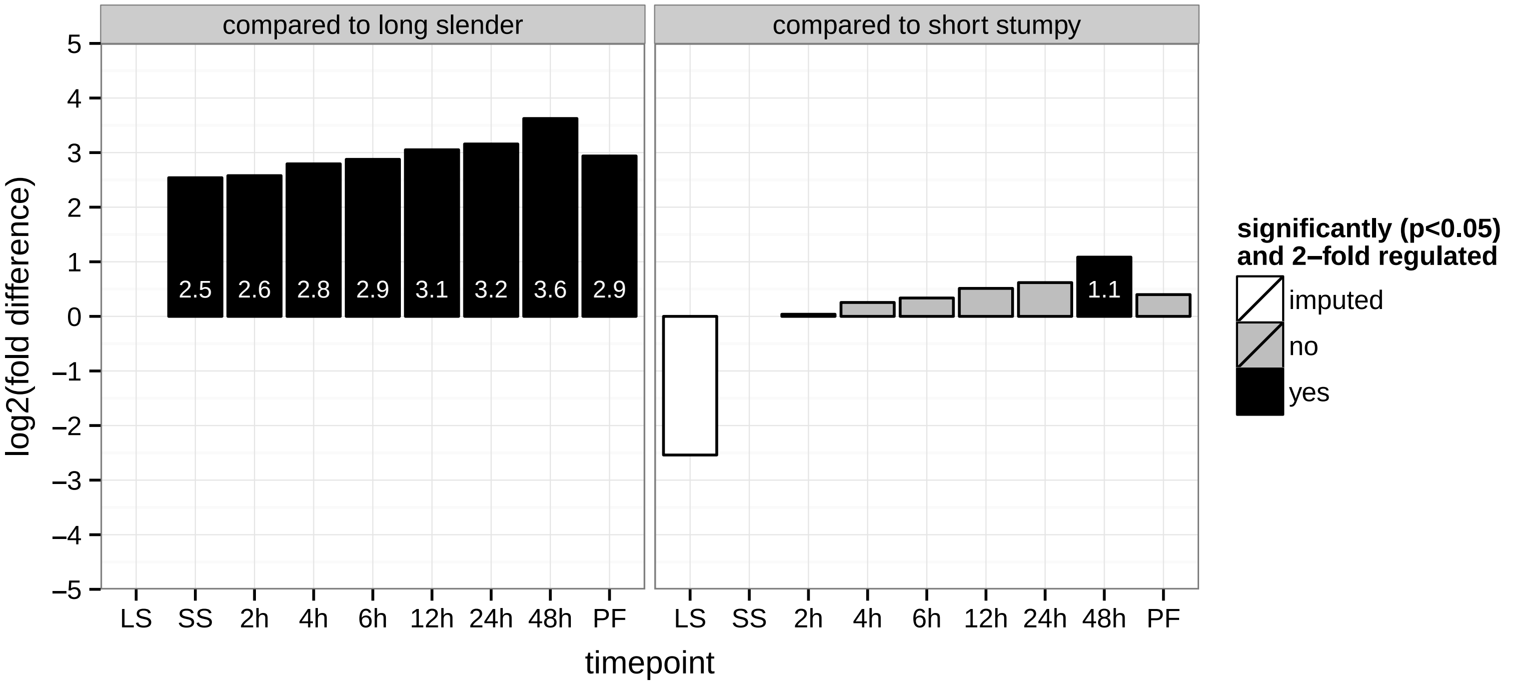
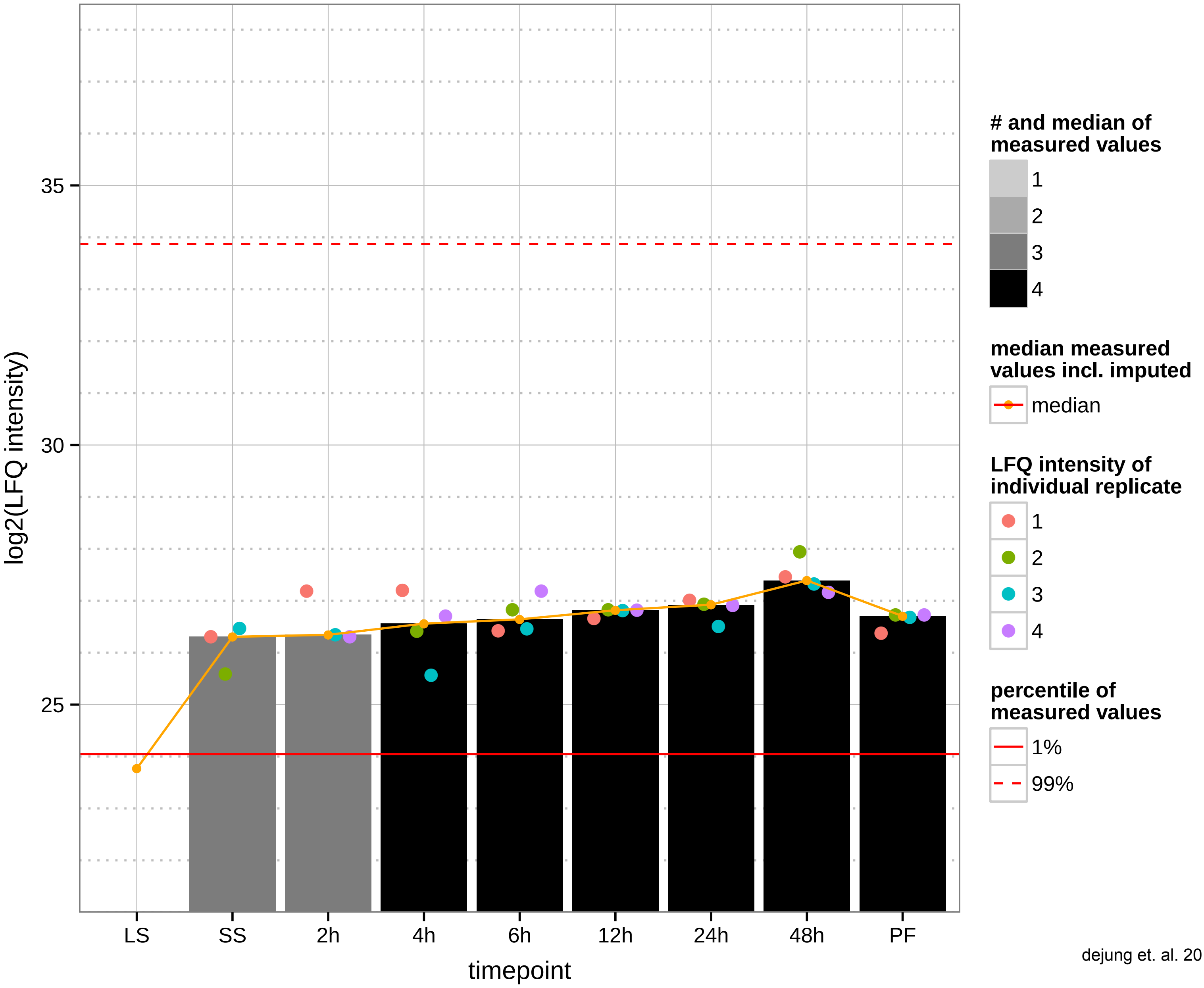
hypothetical protein, conserved
Tb927.7.7210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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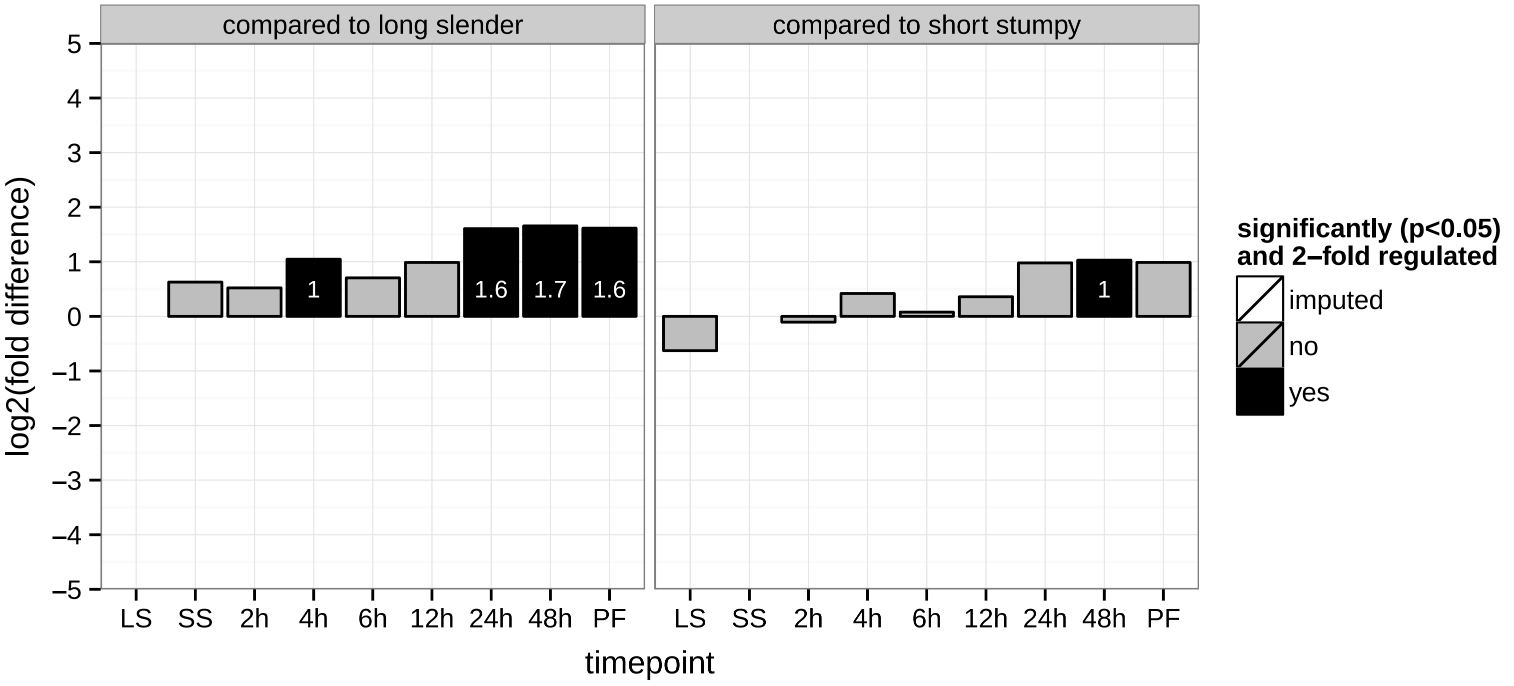
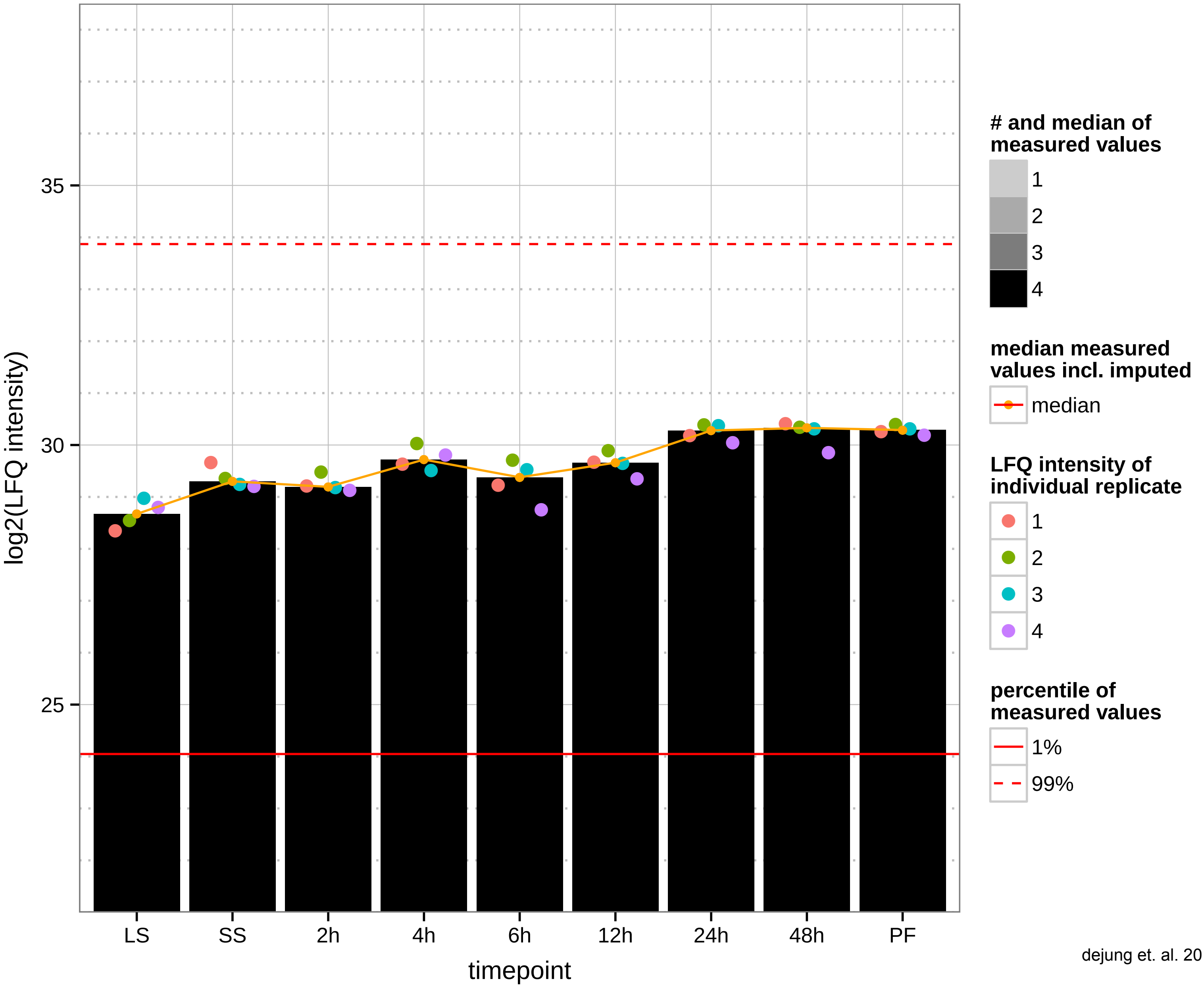
mitochondrial RNA binding protein (TbRBP38)
Tb927.8.2740
AGOF: RNA binding
AGOC: mitochondrion
AGOP: mRNA stabilization
PGOF: null
PGOC: null
PGOP: null





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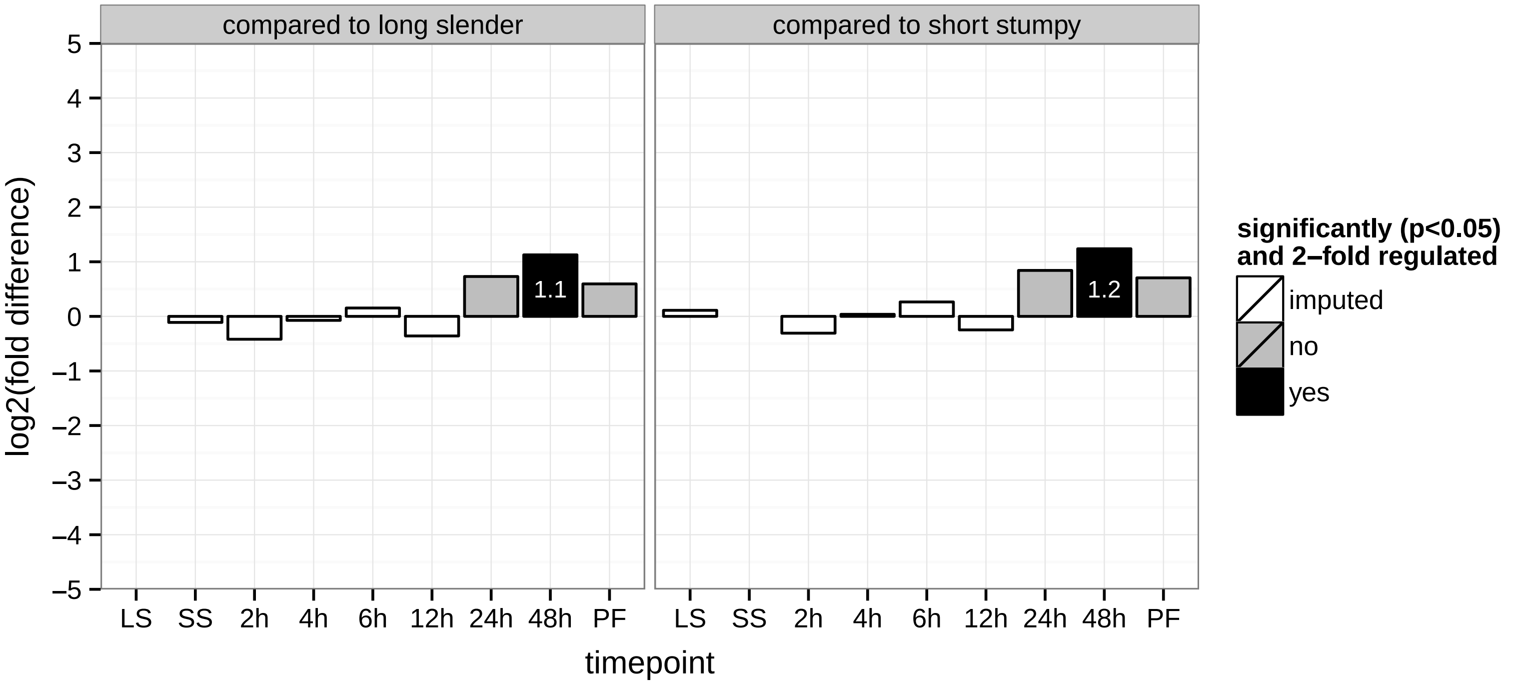
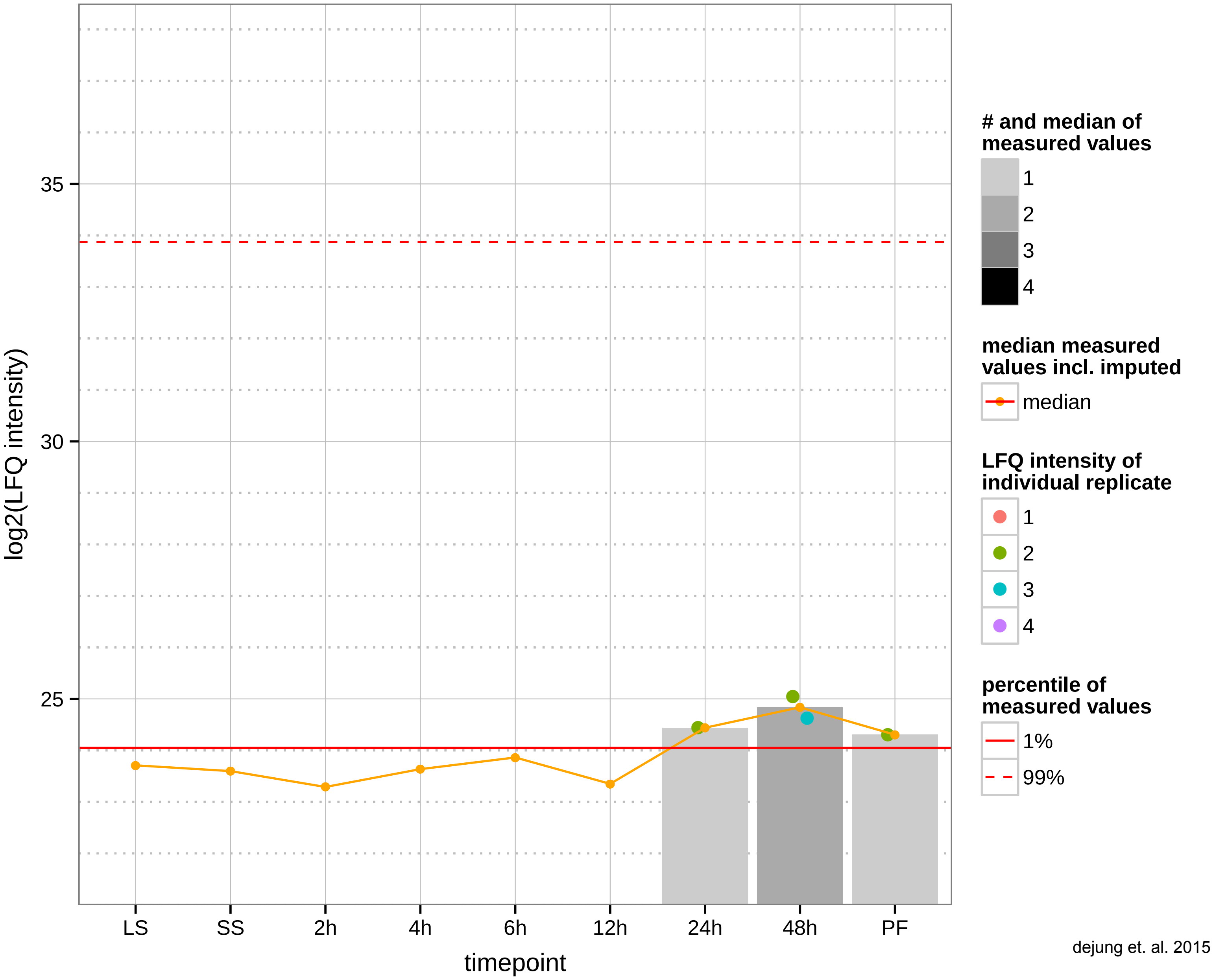
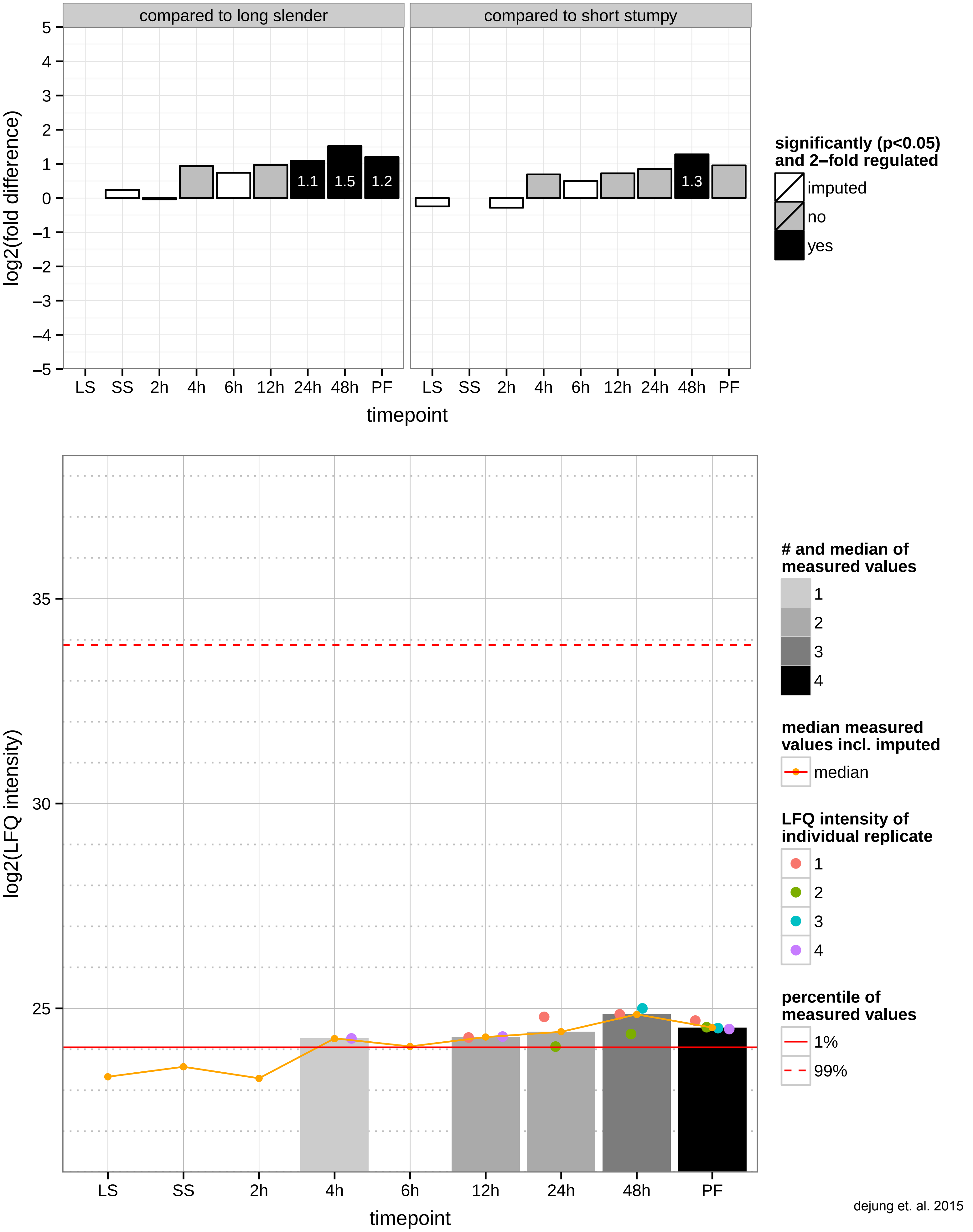
hypothetical protein, conserved
Tb927.8.3260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





hypothetical protein, conserved
Tb927.8.5610
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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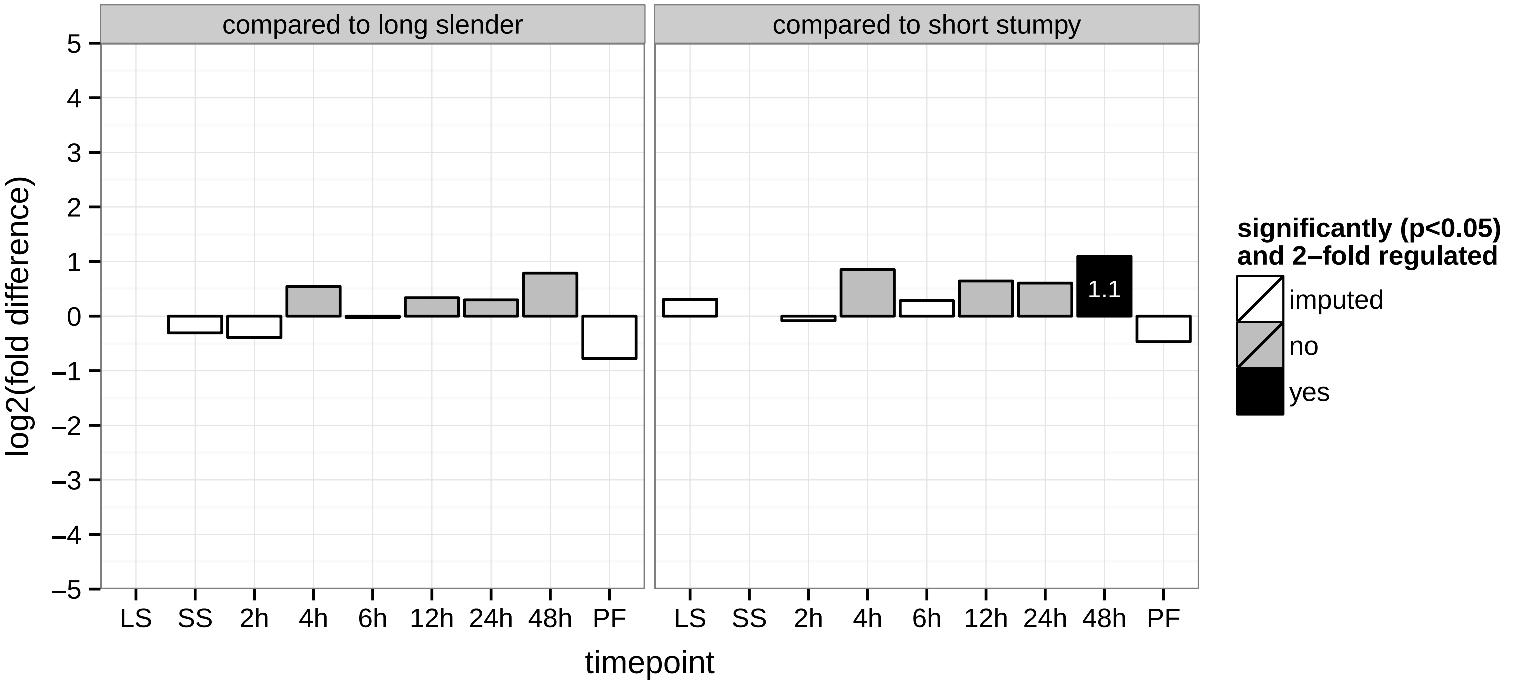
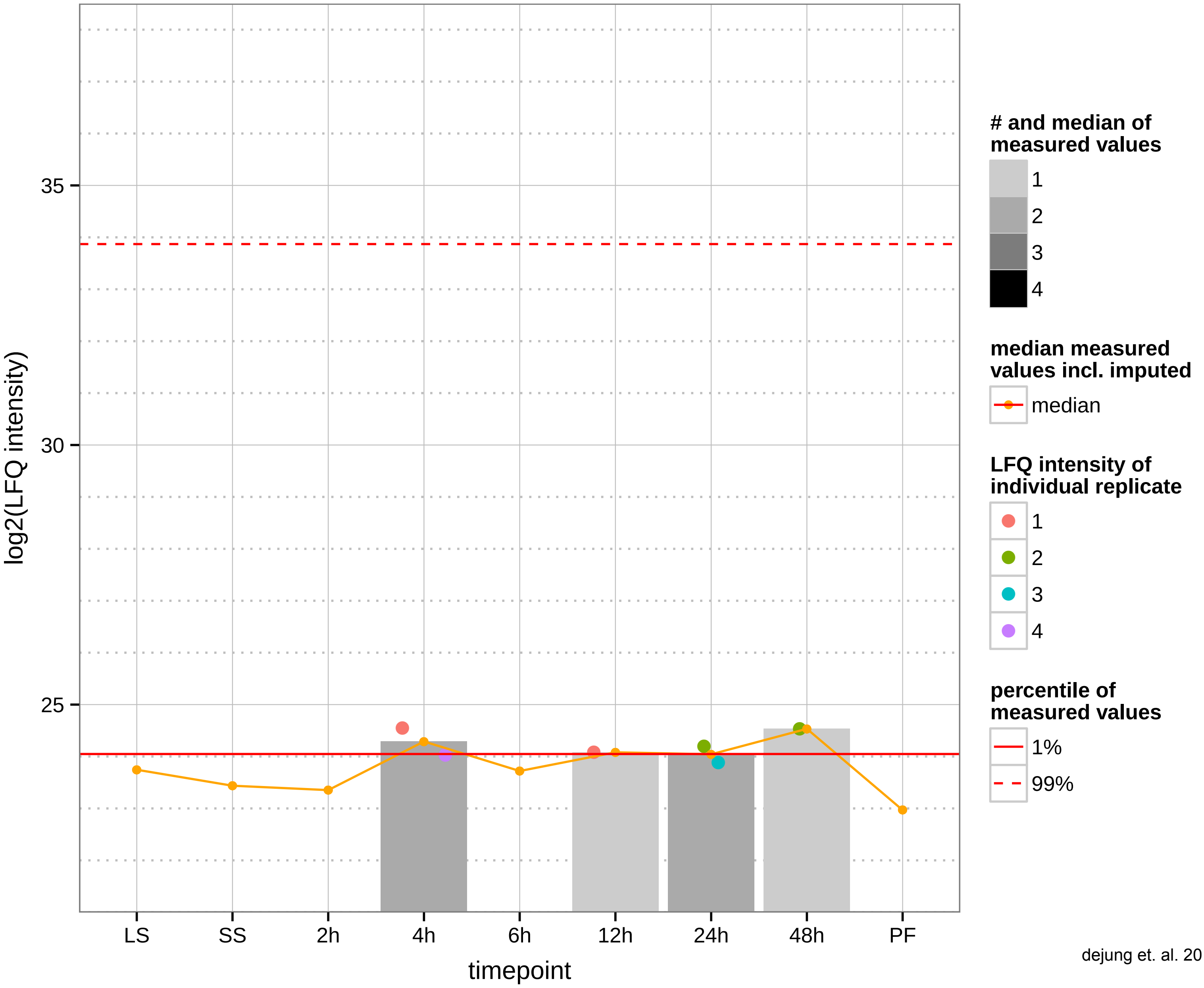
hypothetical protein, conserved
Tb927.8.6280
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: null
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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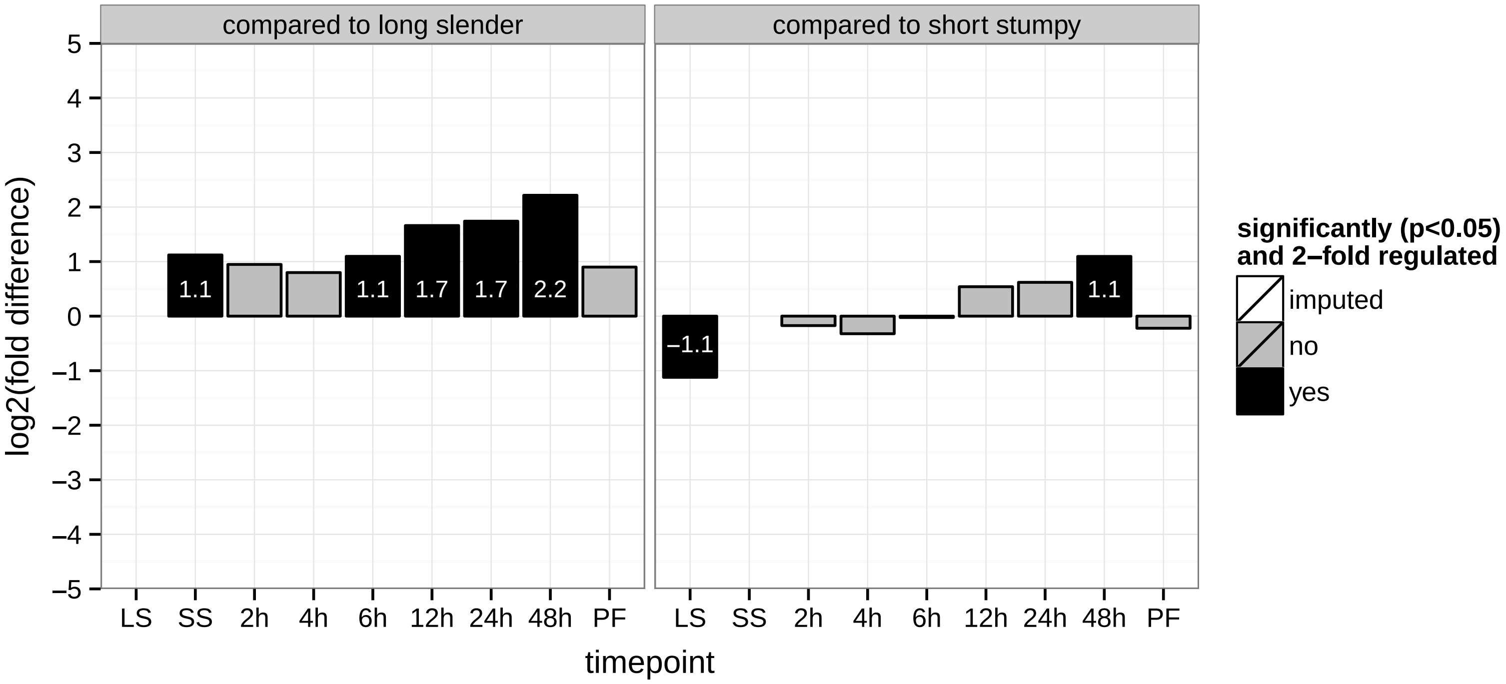
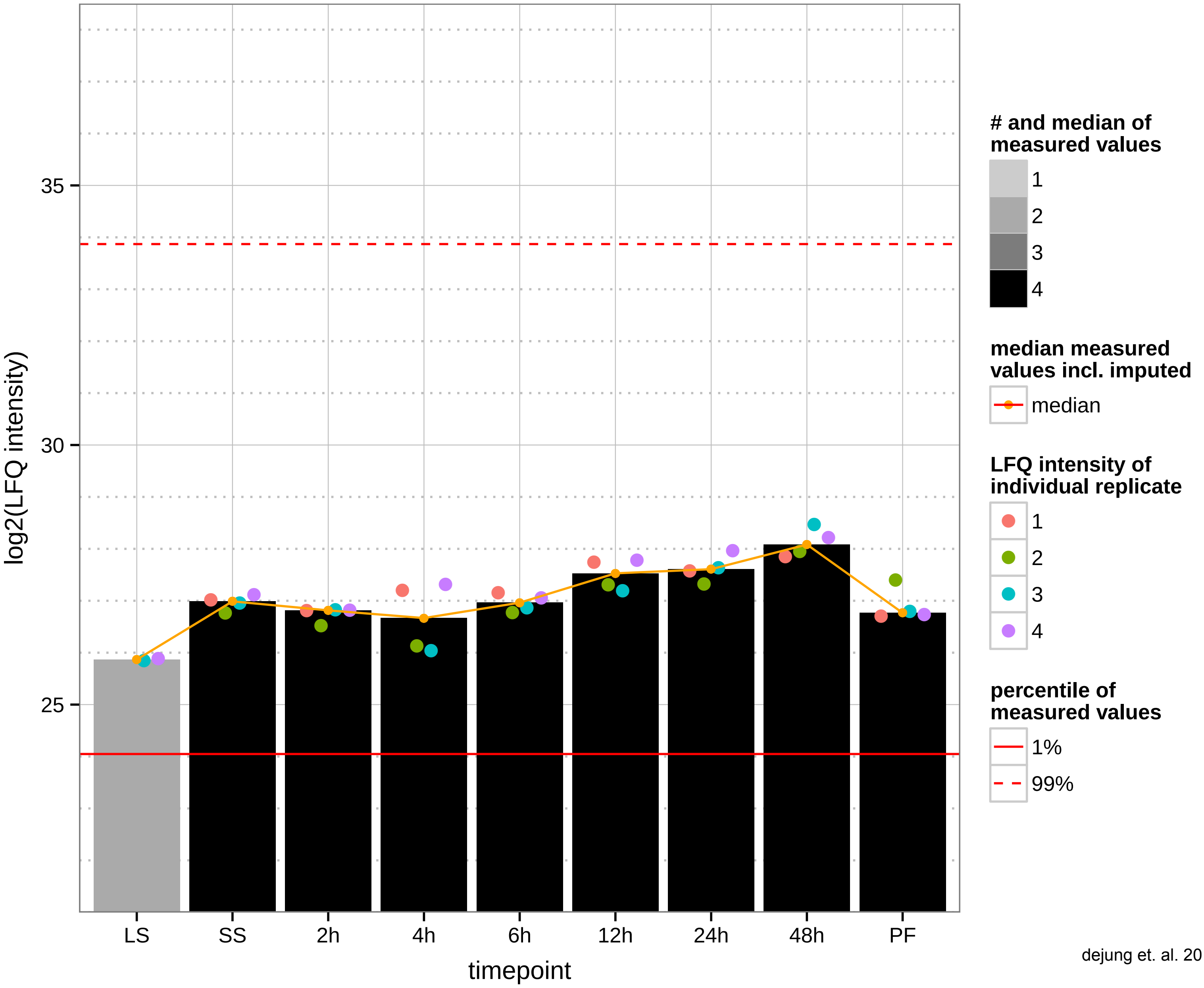
mitochondrial RNA binding complex 1 subunit (MRB8180)
Tb927.8.8180
AGOF: RNA binding
AGOC: mitochondrion
AGOP: cytidine to uridine editing, mRNA stabilization
PGOF: null
PGOC: null
PGOP: null





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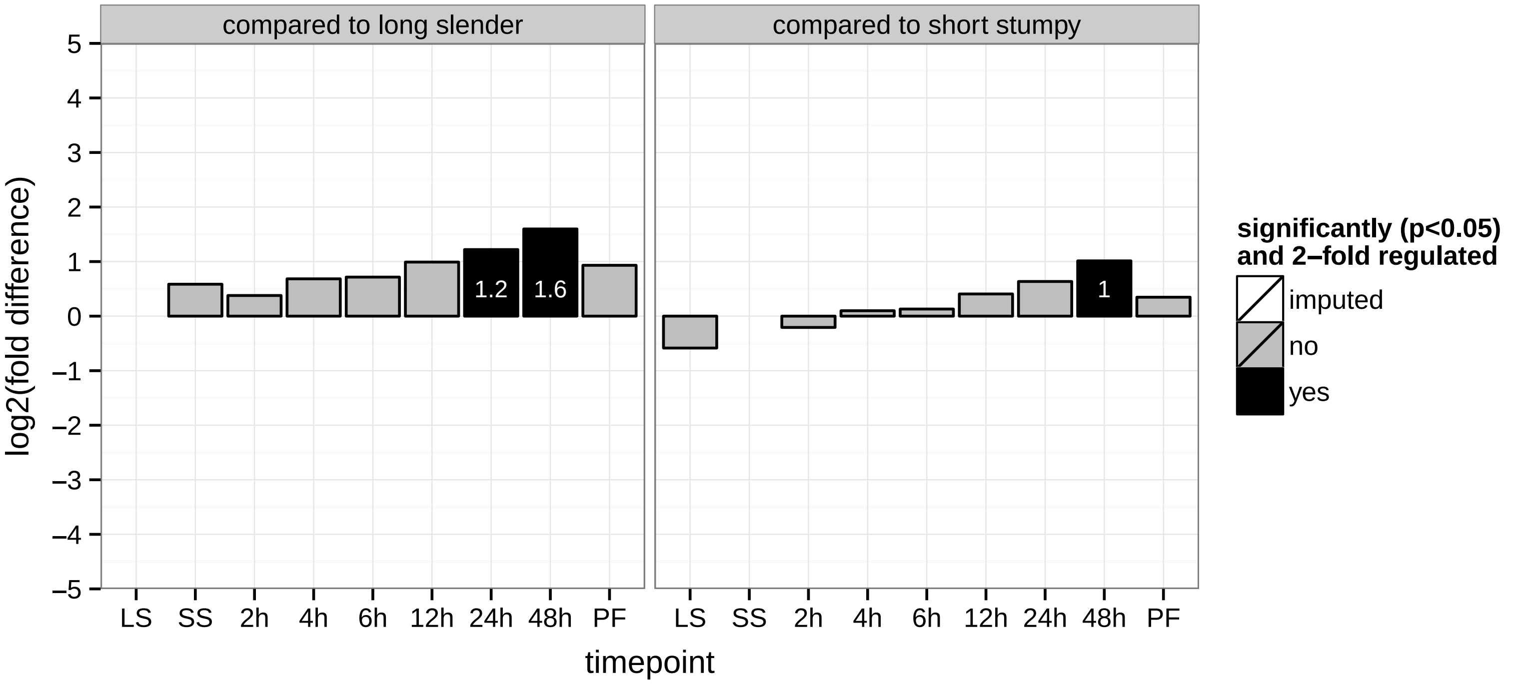
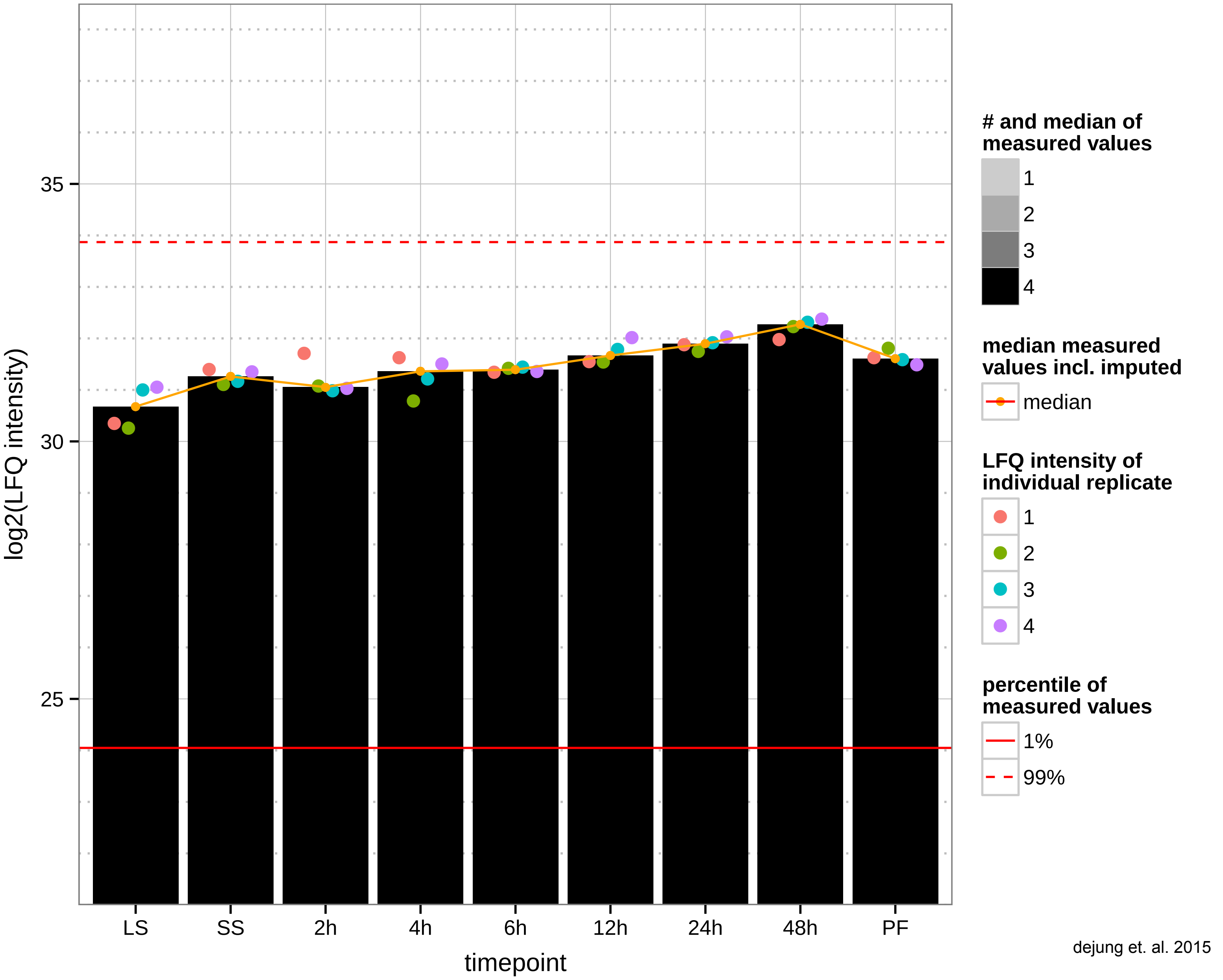
mitochondrial carrier protein, mitochondrial carrier protein (MCP11)
Tb927.9.10310
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrial part
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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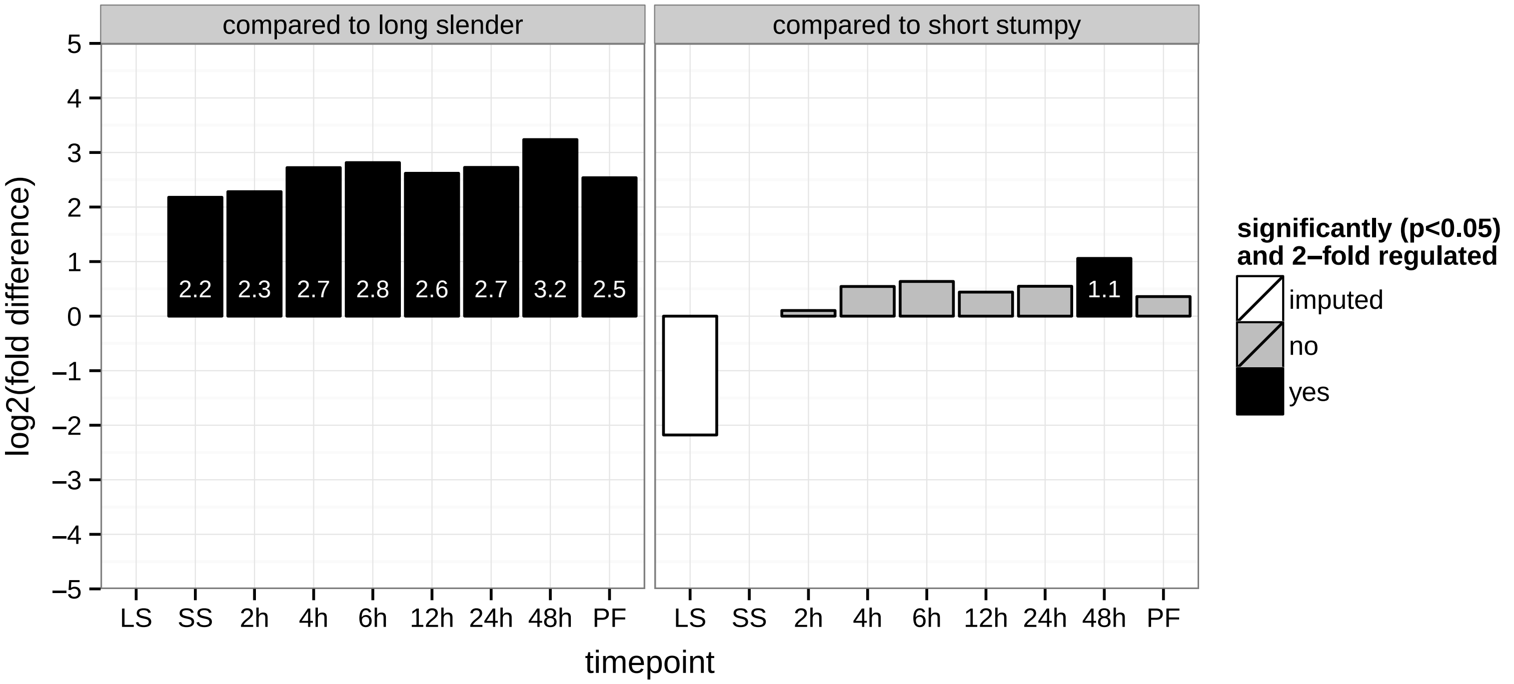
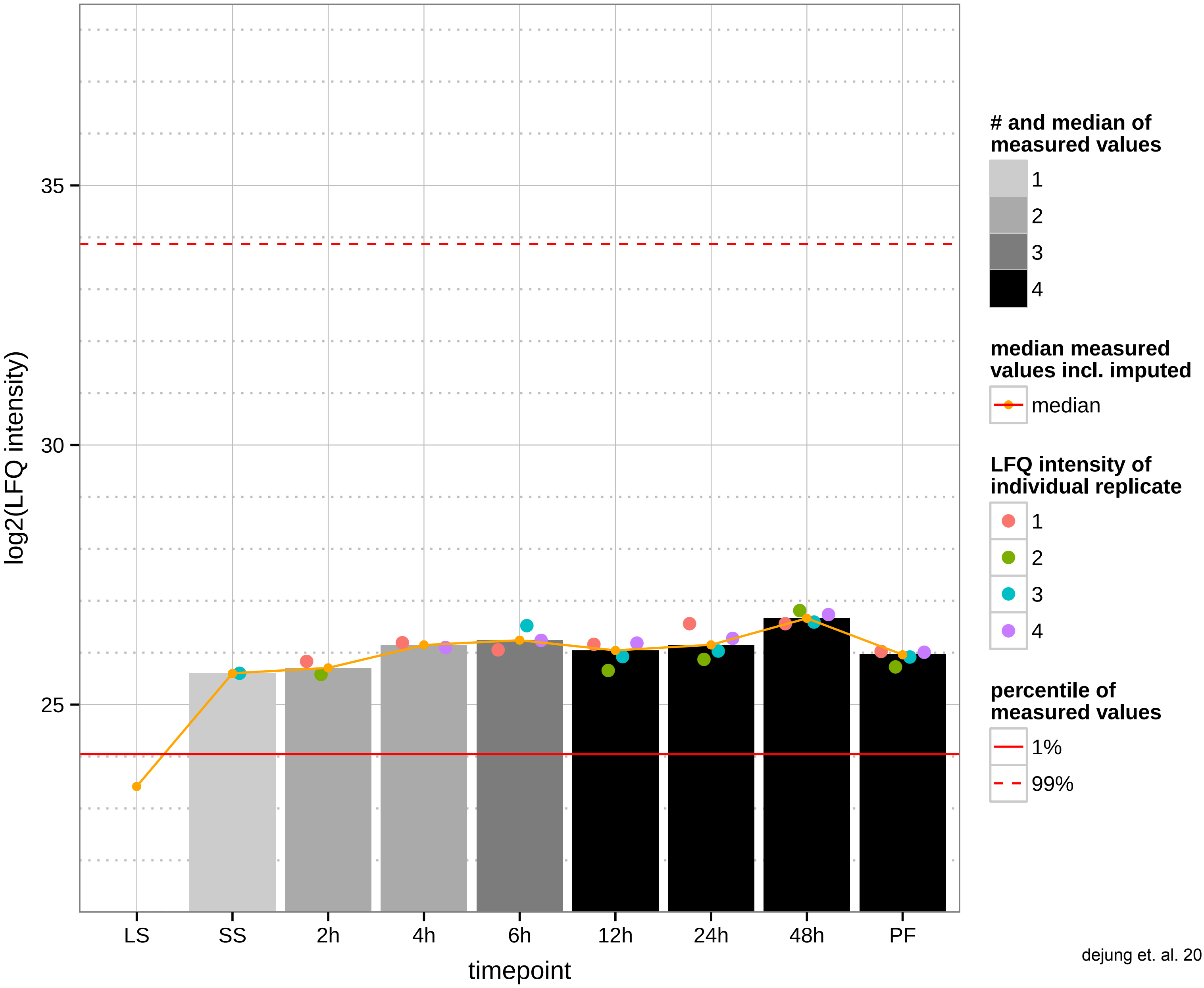
elongation factor 1−alpha, putative, hsp70 subfamily B suppressor 1
Tb927.9.10710
AGOF: GTP binding, GTPase activity, translation elongation factor activity
AGOC: eukaryotic translation elongation factor 1 complex
AGOP: translational elongation
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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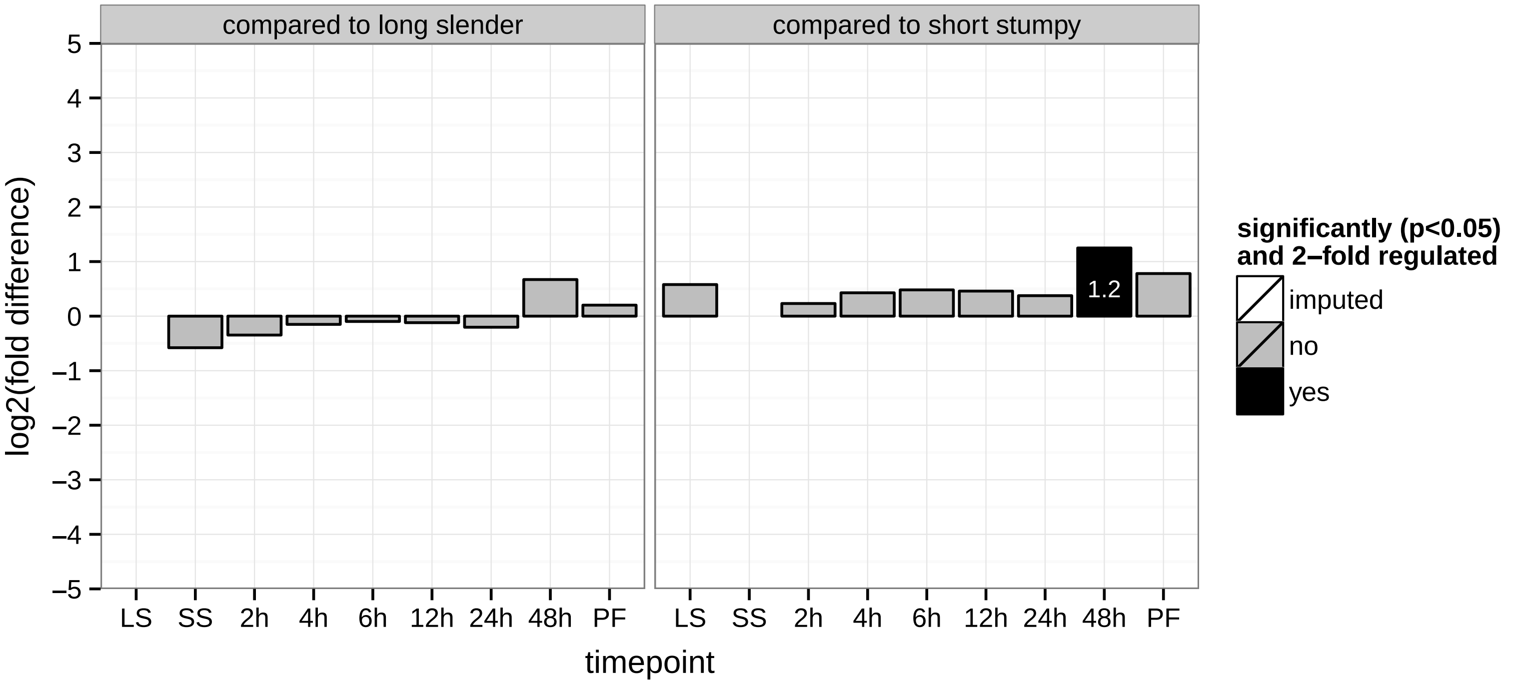
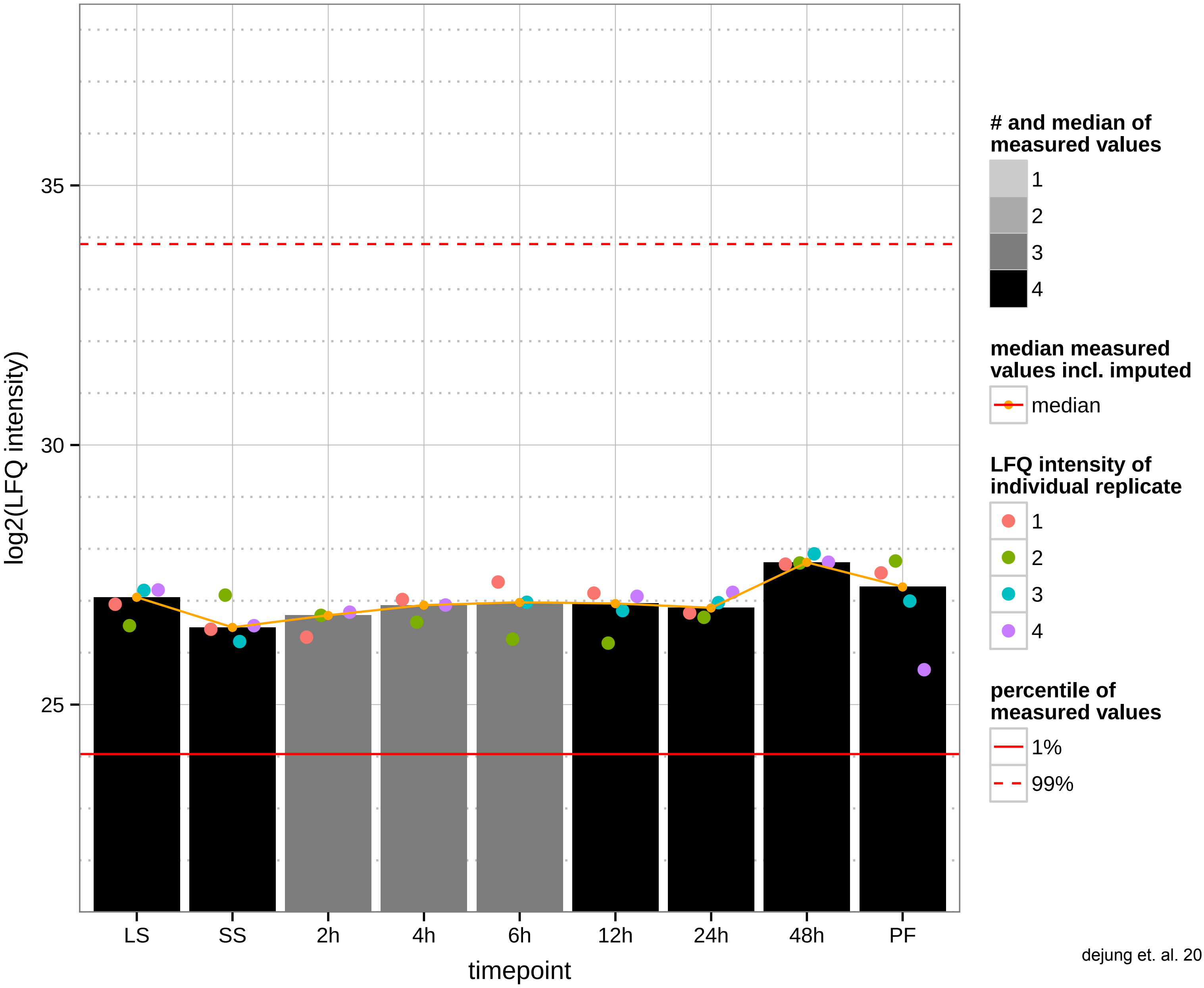
hypothetical protein
Tb927.9.10790
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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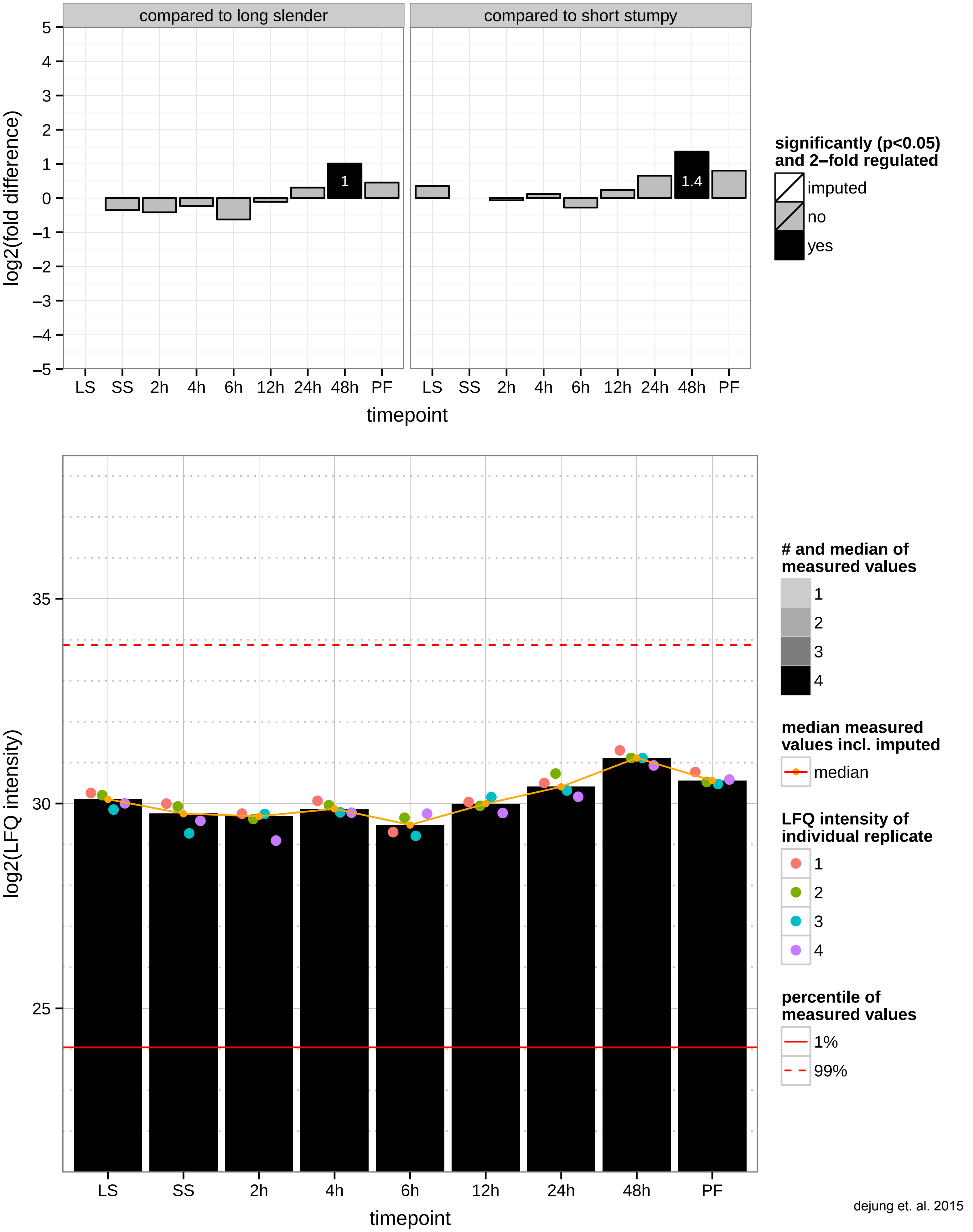
hypothetical protein, conserved
Tb927.9.11540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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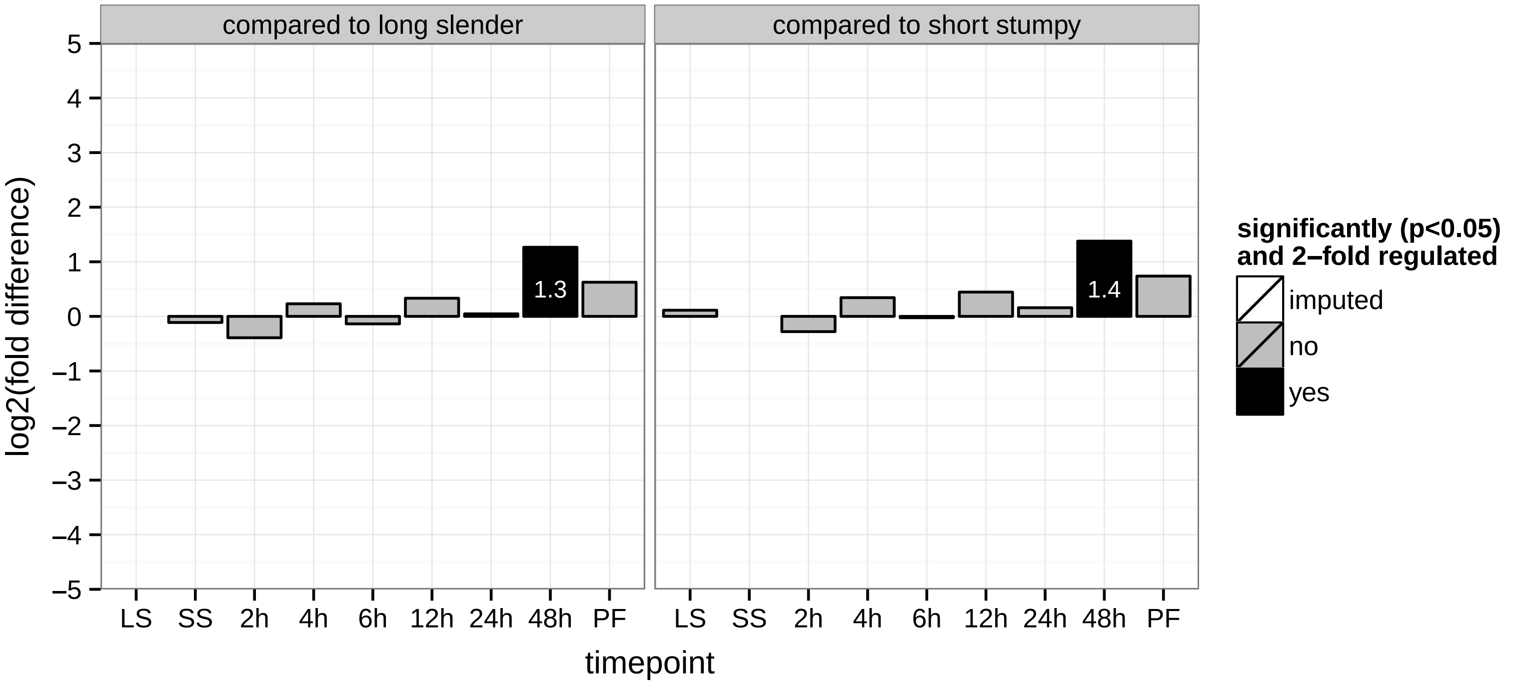
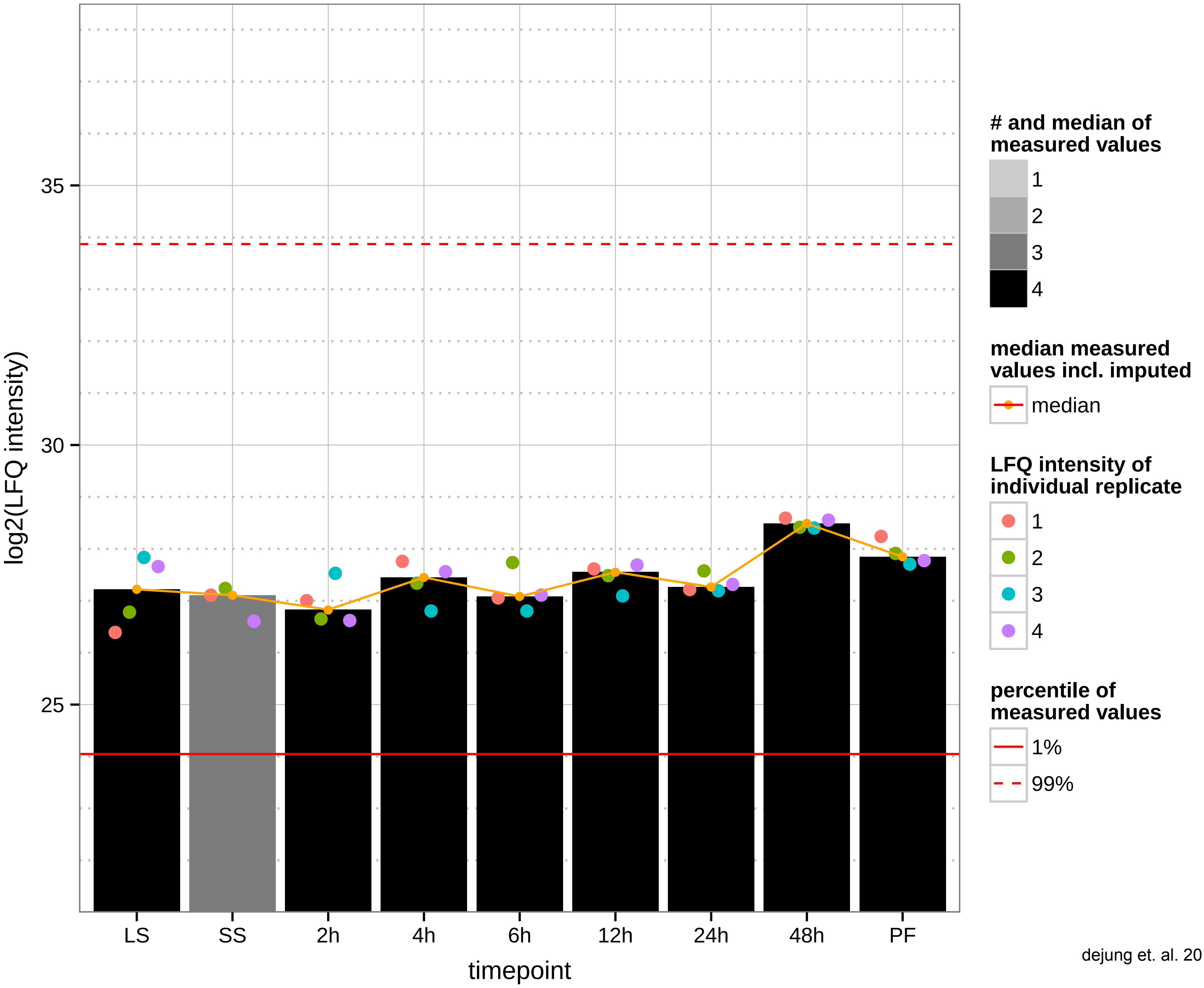
leucine–rich repeat protein (LRRP), putative
Tb927.9.12170
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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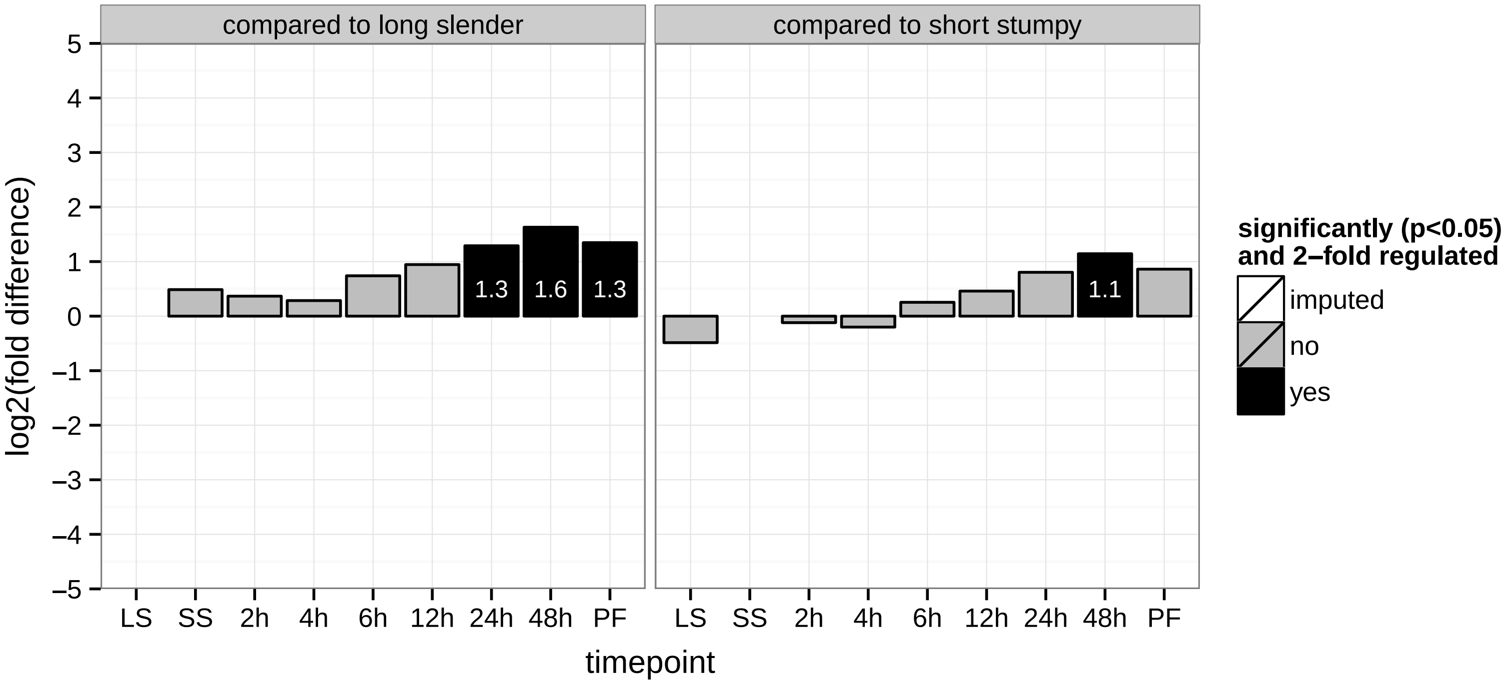
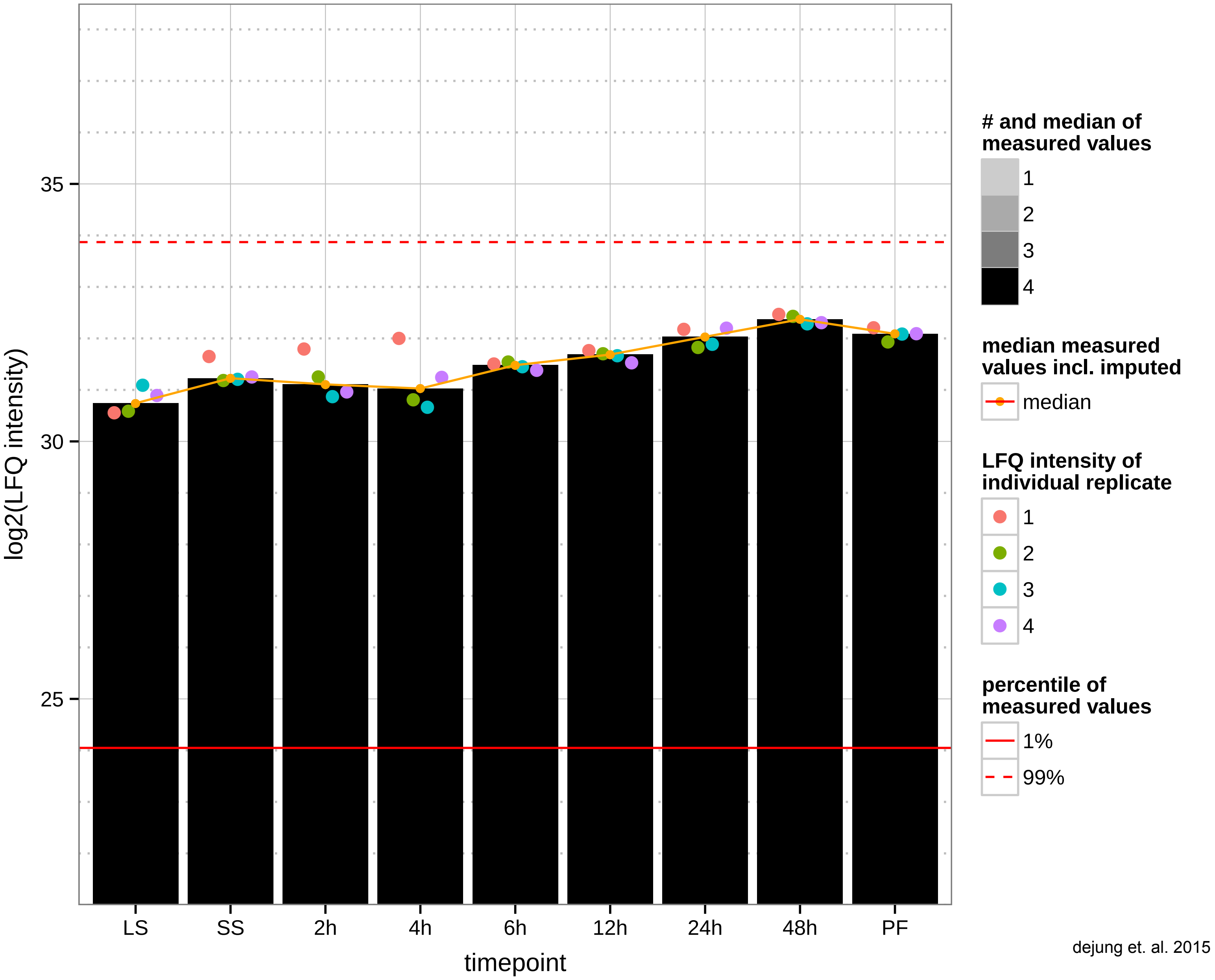
ATP−dependent DEAD/H RNA helicase, putative (DED1)
Tb927.9.12510
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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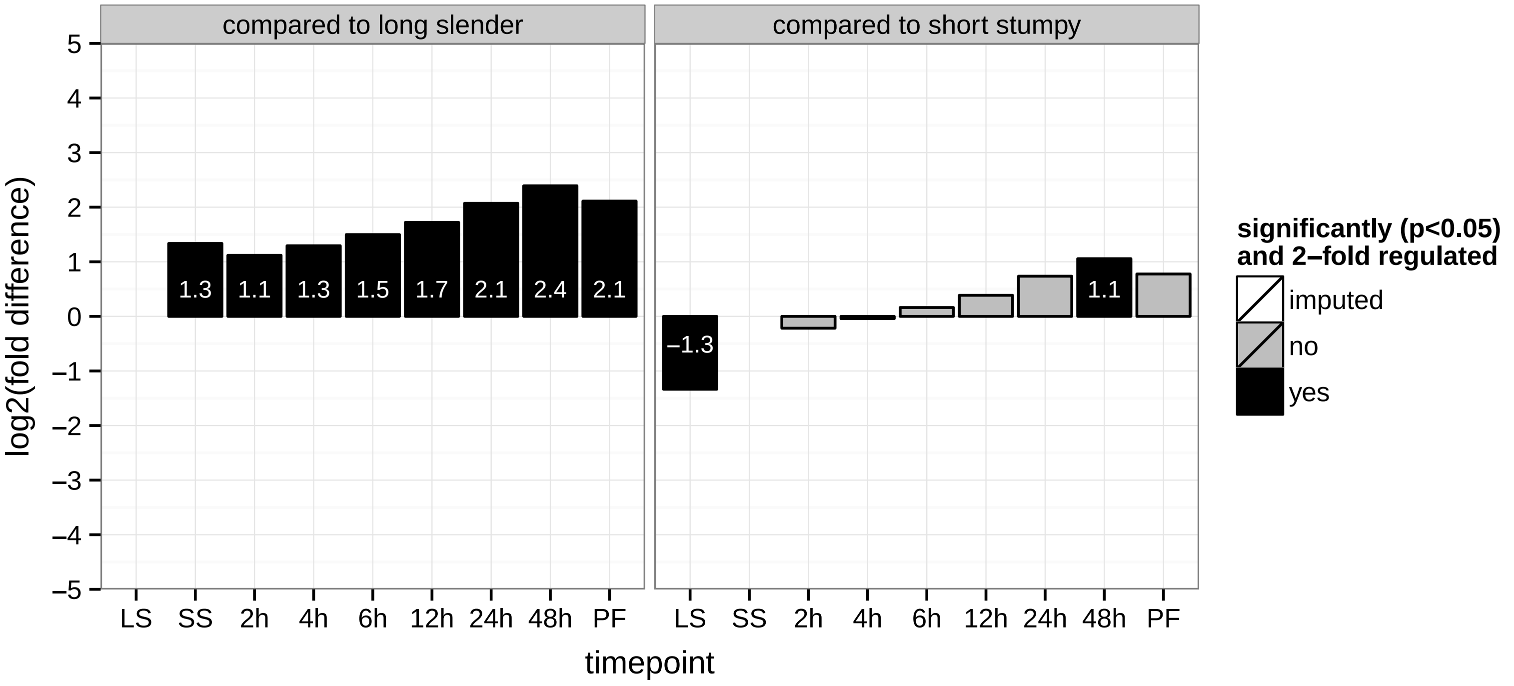
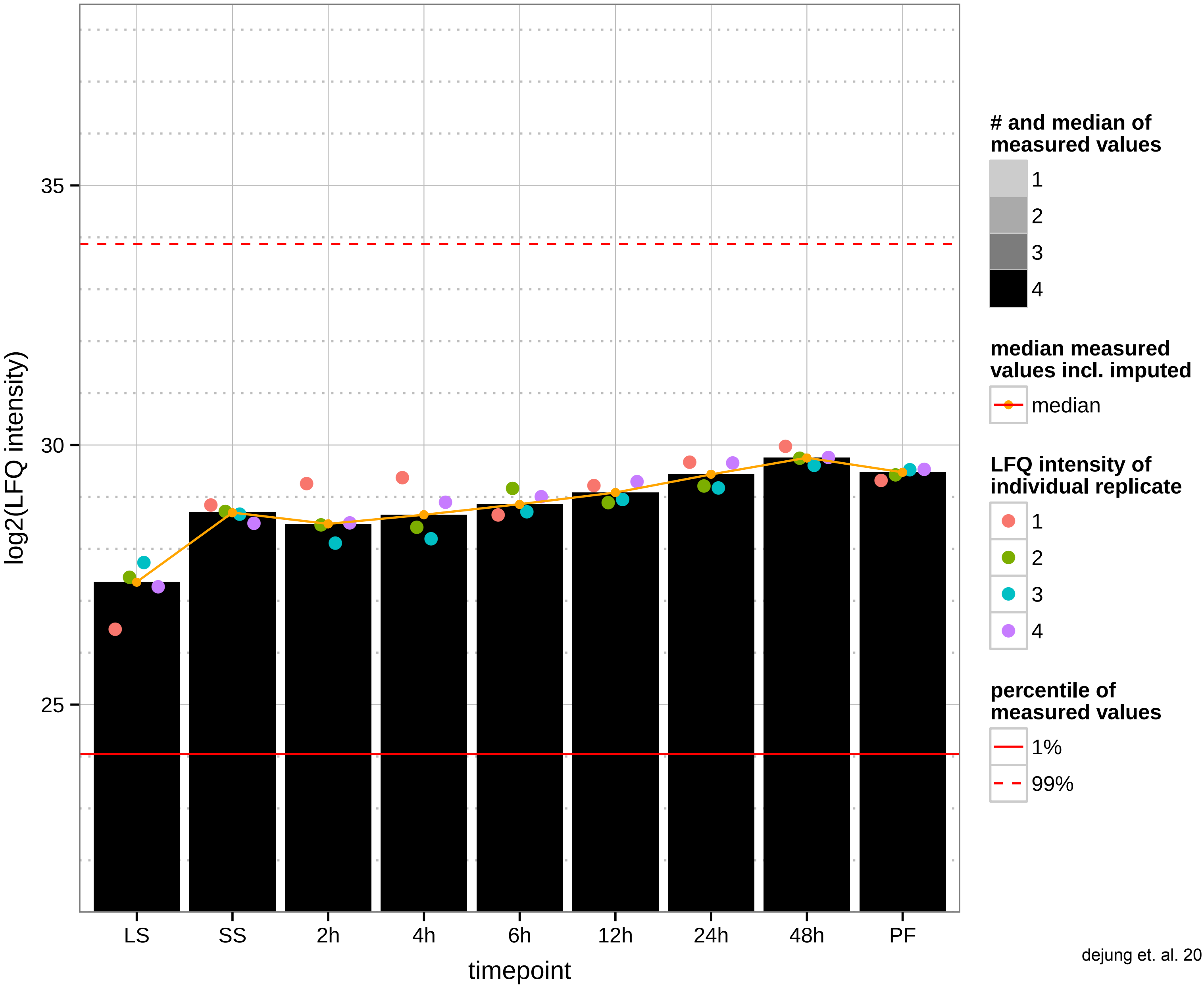
hypothetical protein, conserved
Tb927.9.13520
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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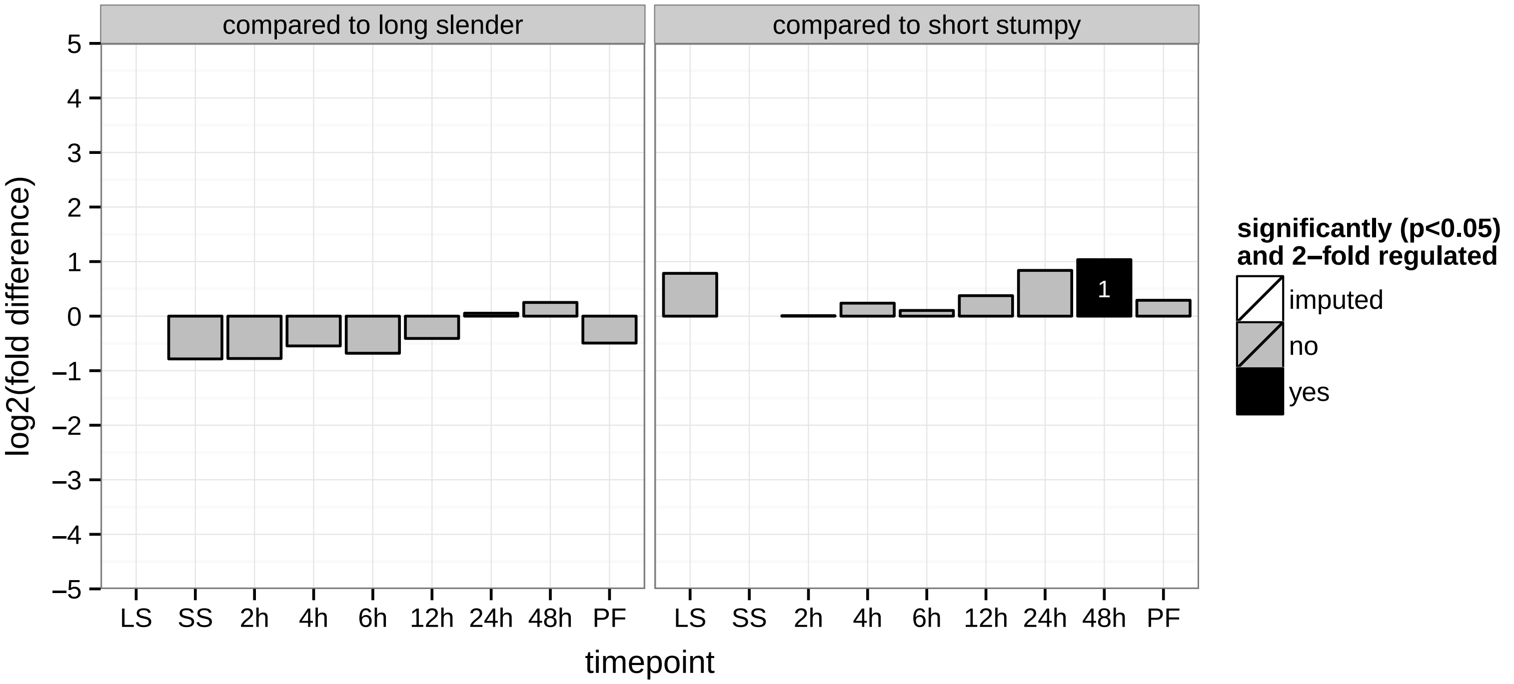
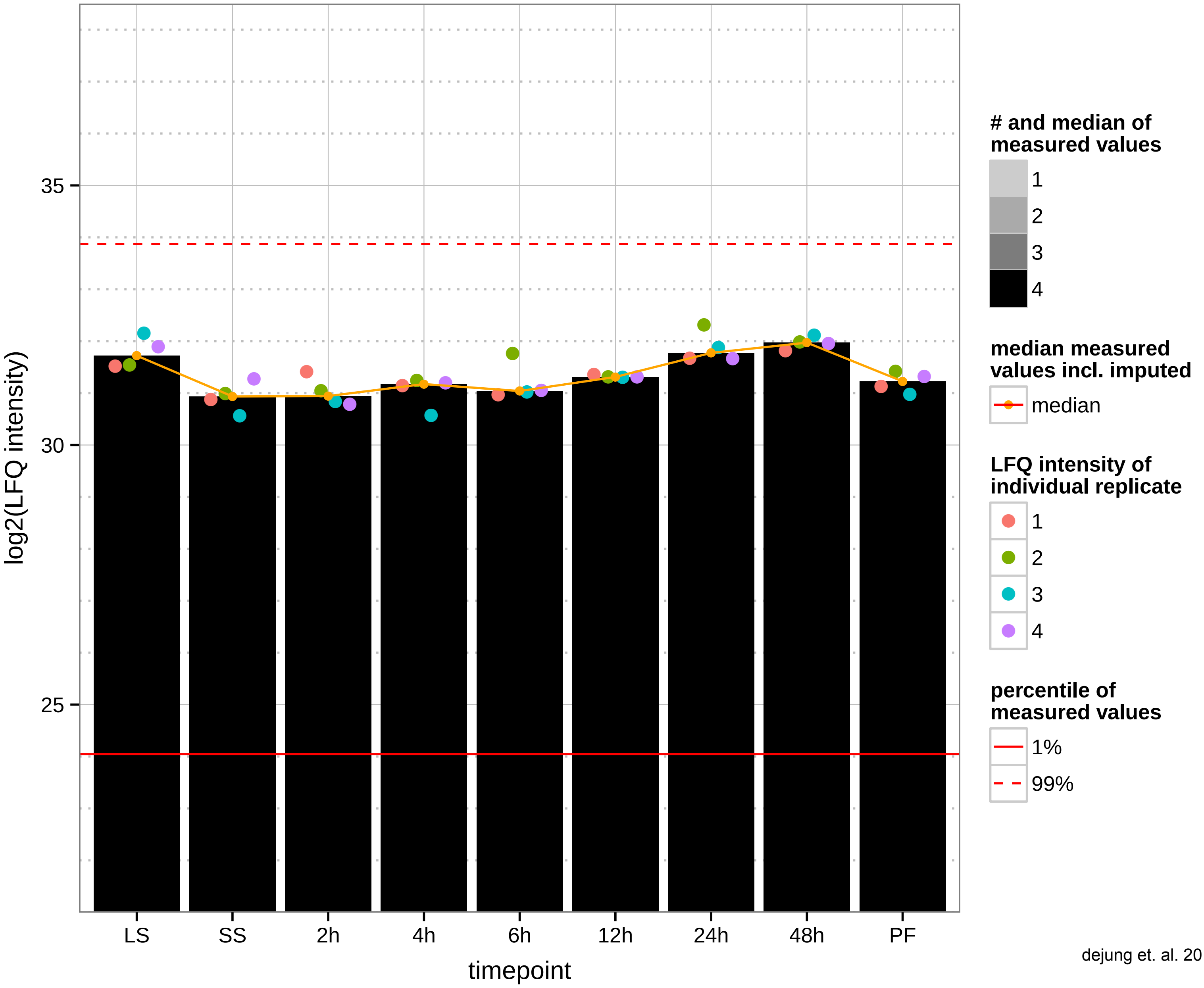
ribosomal protein L15, putative
Tb927.9.15190
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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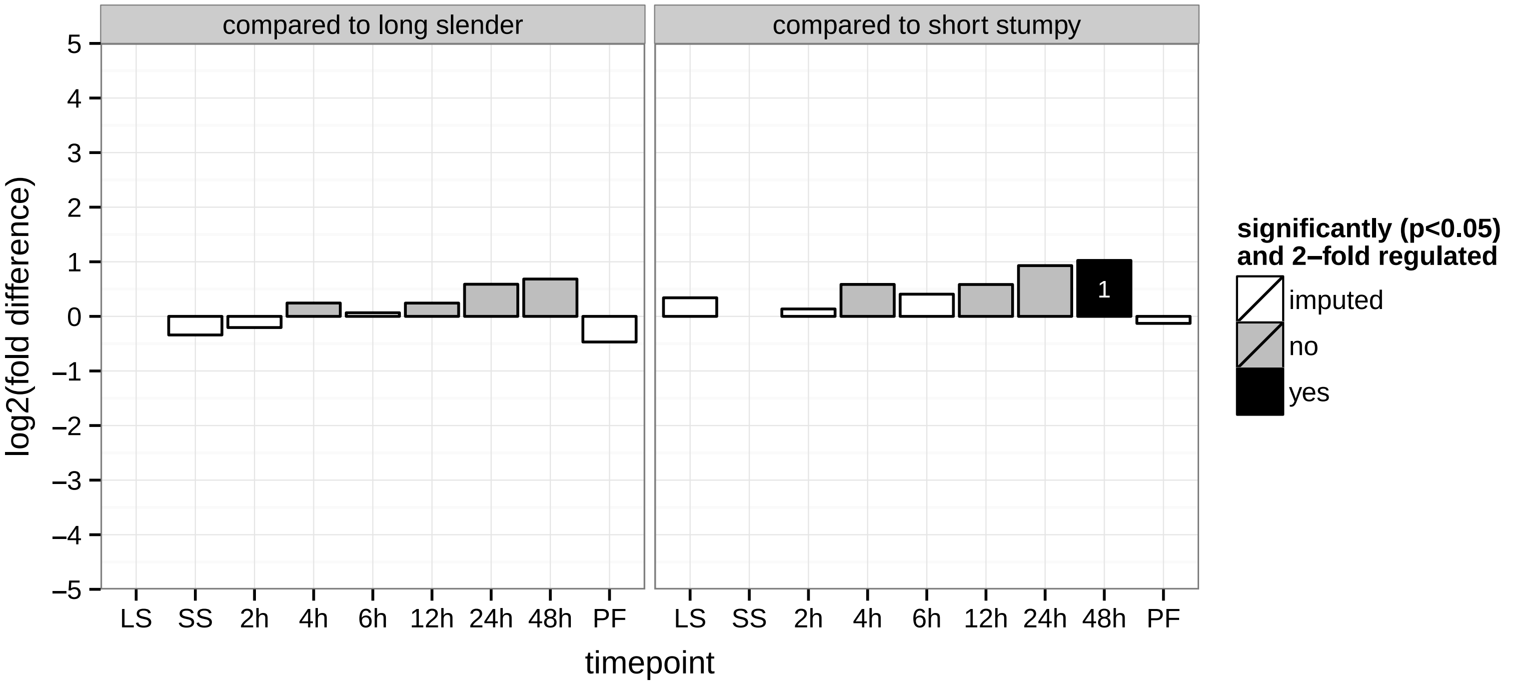
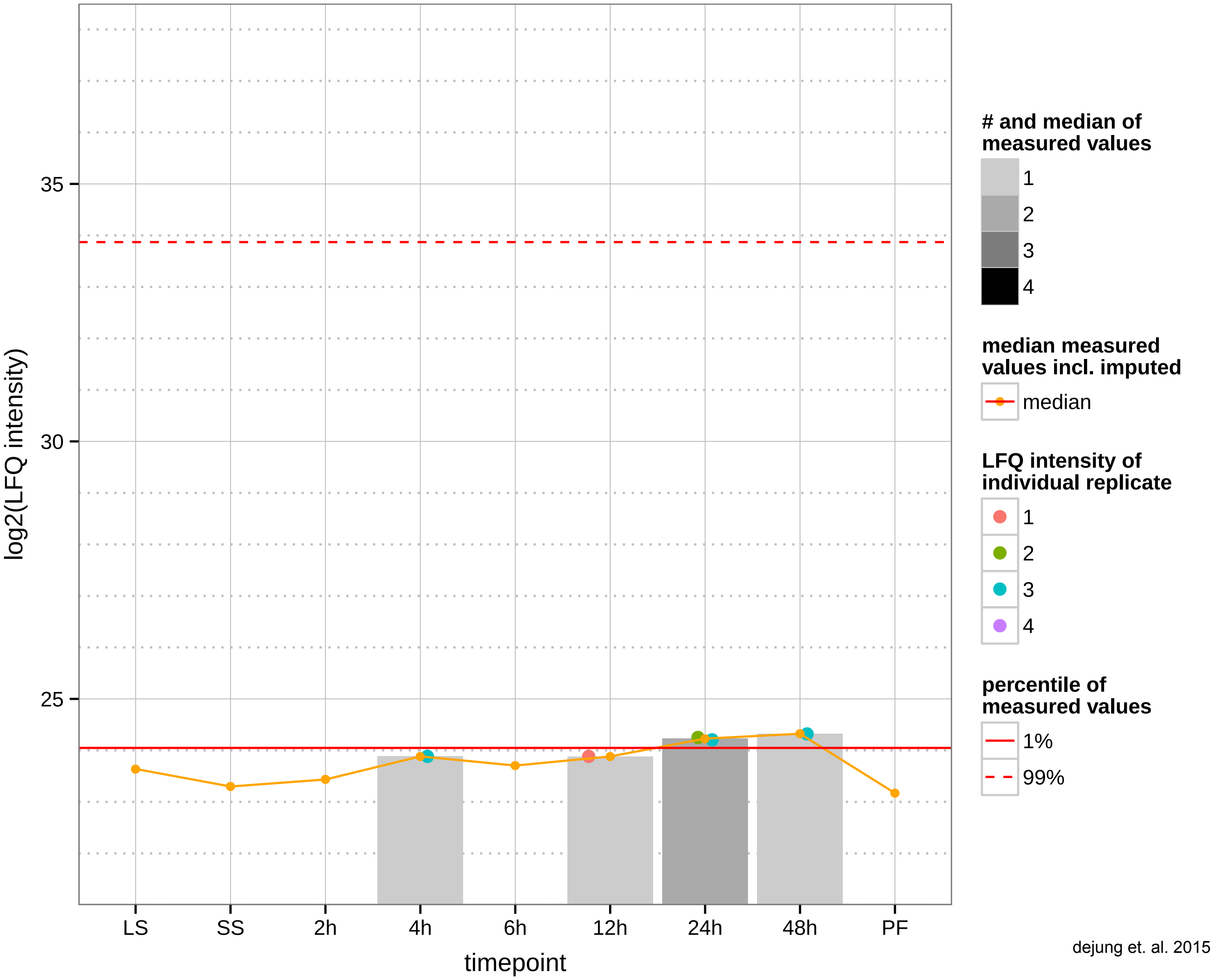
hypothetical protein, conserved
Tb927.9.1590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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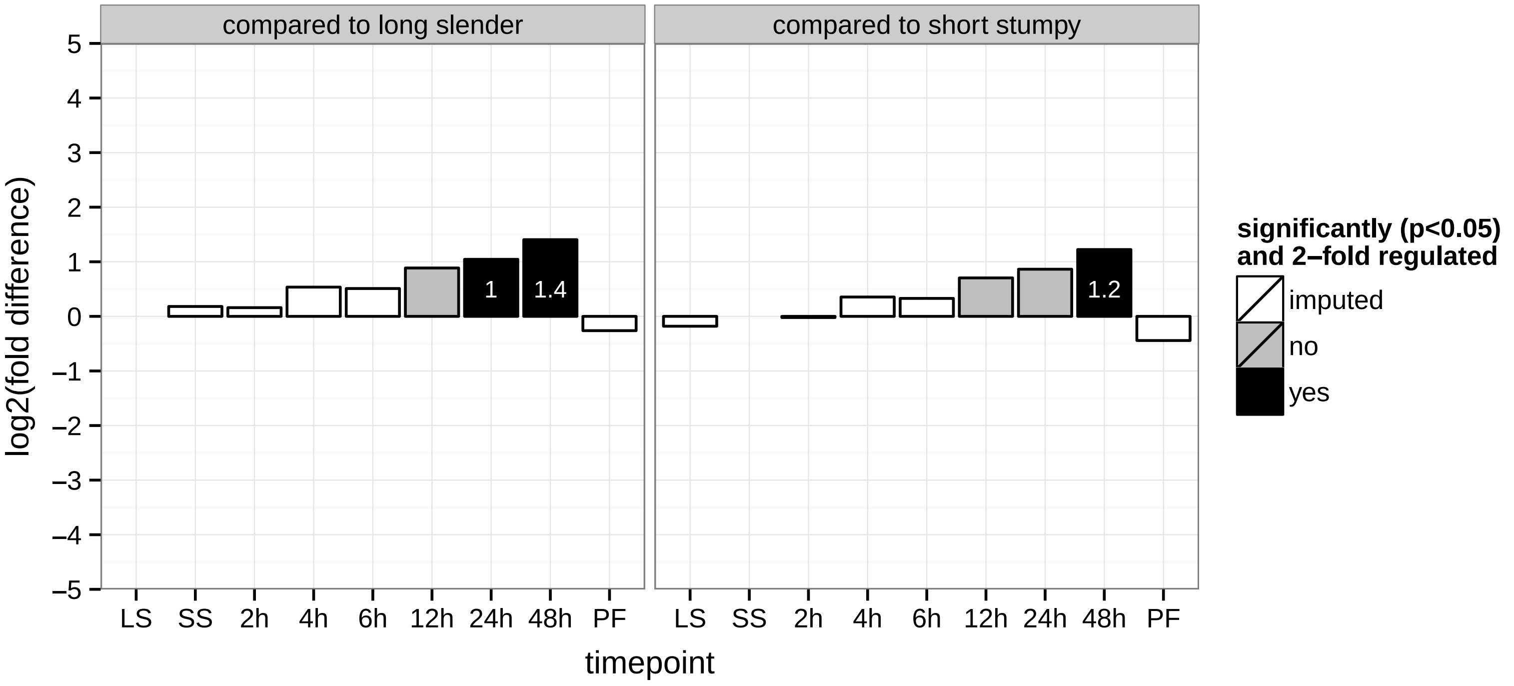
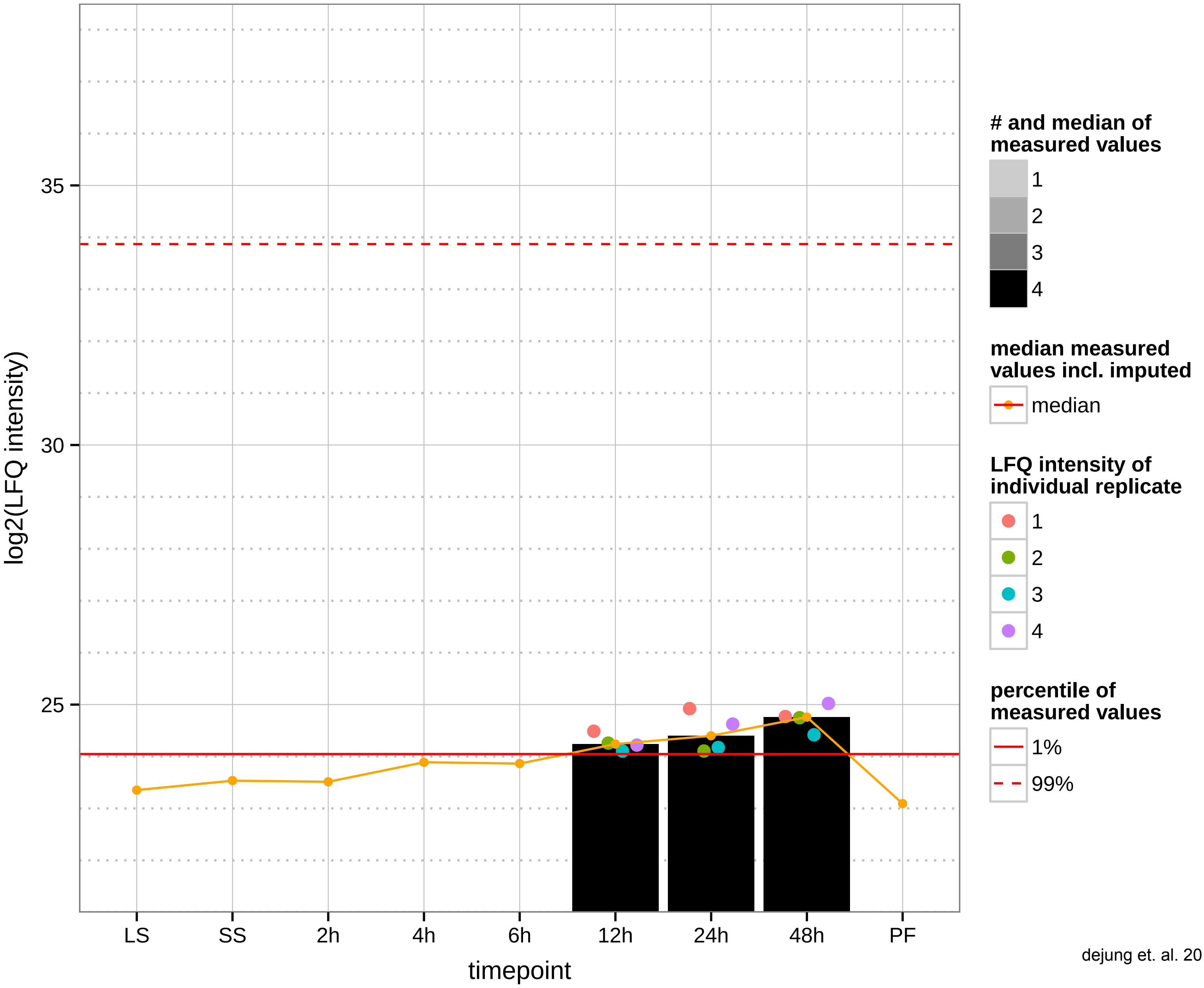
hypothetical protein, conserved
Tb927.9.2620
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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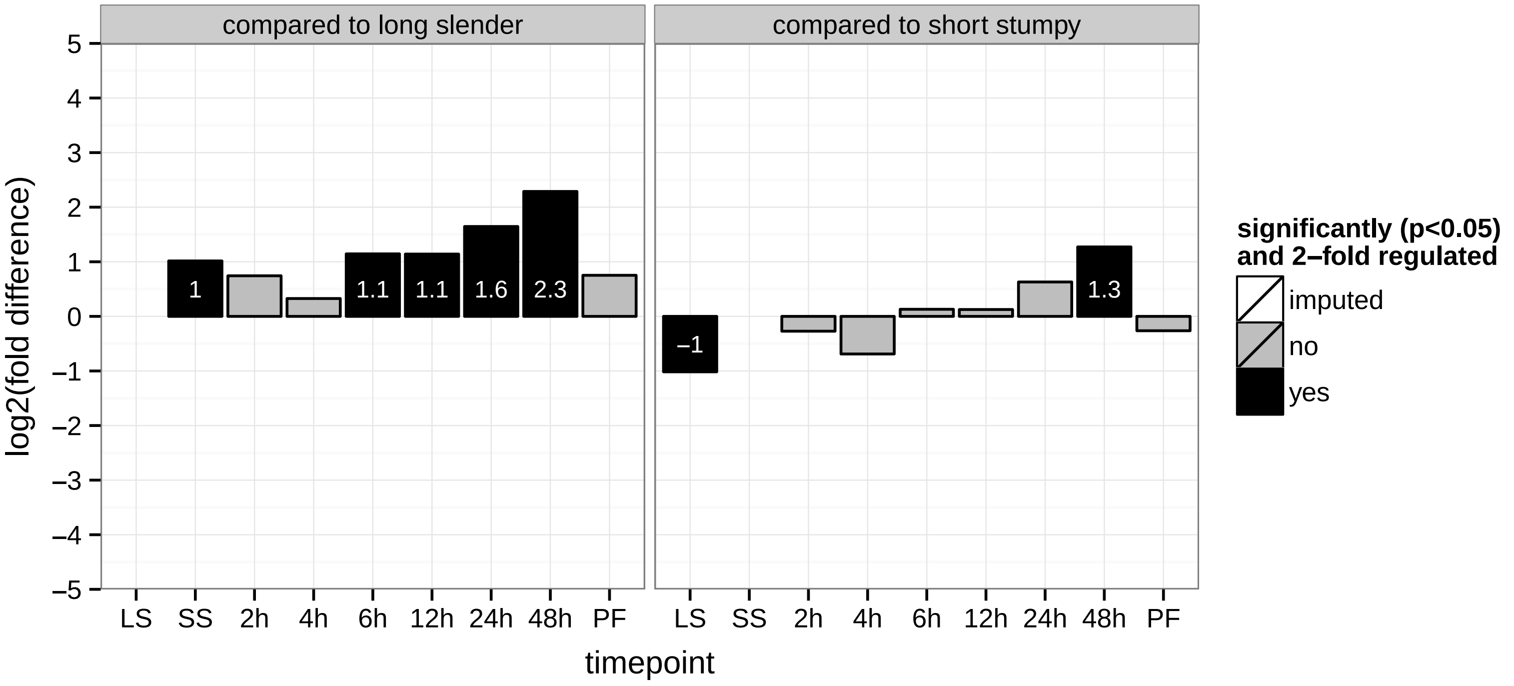
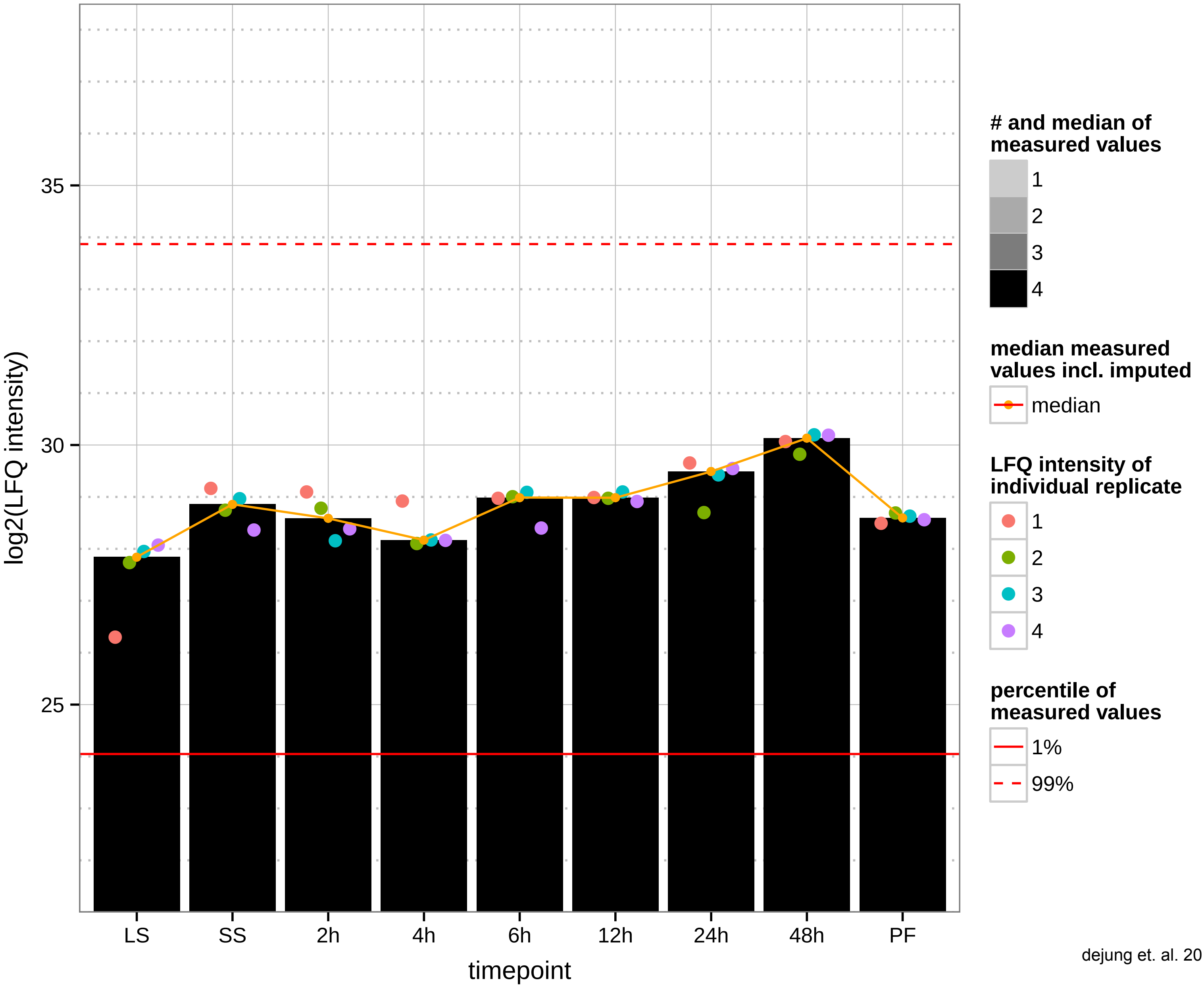
cAMP–specific phosphodiesterase (PDEB1)
Tb927.9.5040
AGOF: 3', 5'–cyclic–nucleotide phosphodiesterase activity
AGOC: cytoplasm
AGOP: cell proliferation, signal transduction
PGOF: 3', 5'–cyclic–nucleotide phosphodiesterase activity, catalytic activity, protein binding
PGOC: null
PGOP: signal transduction





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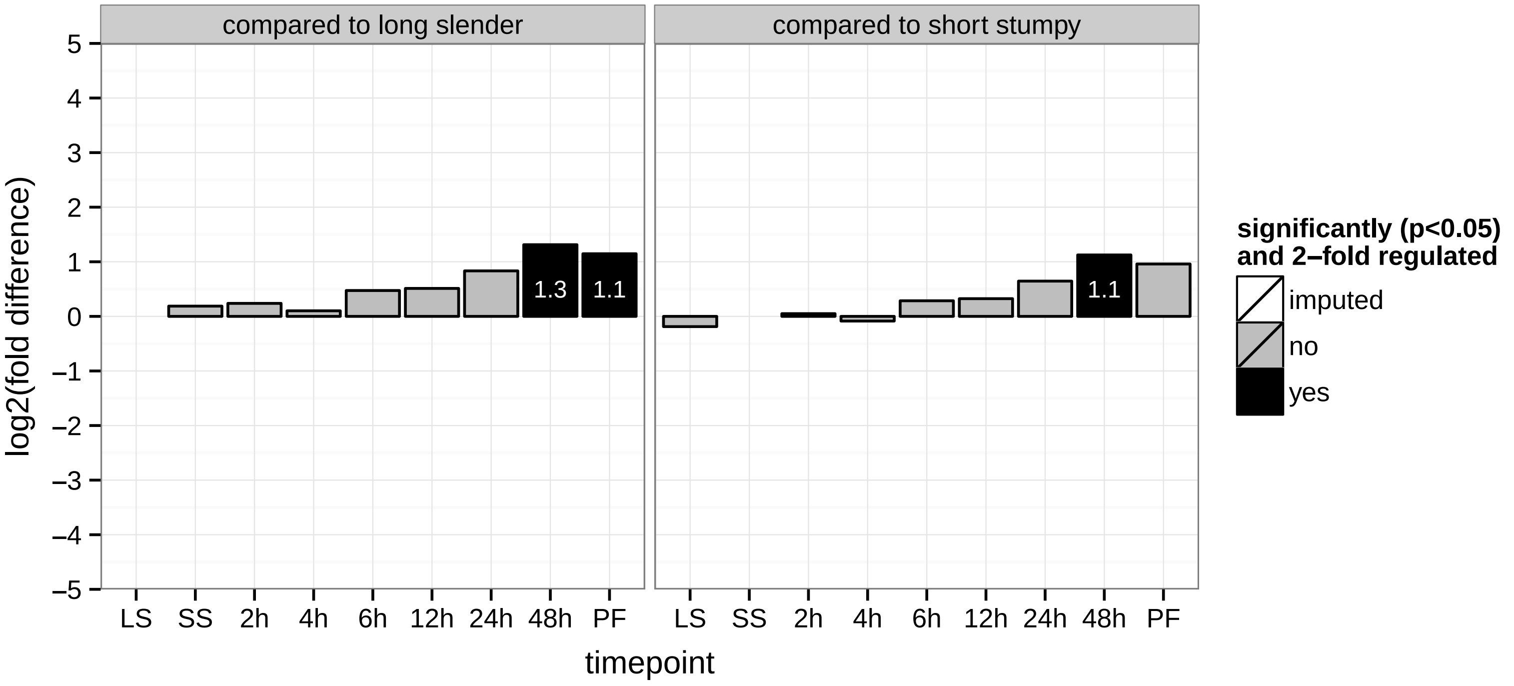
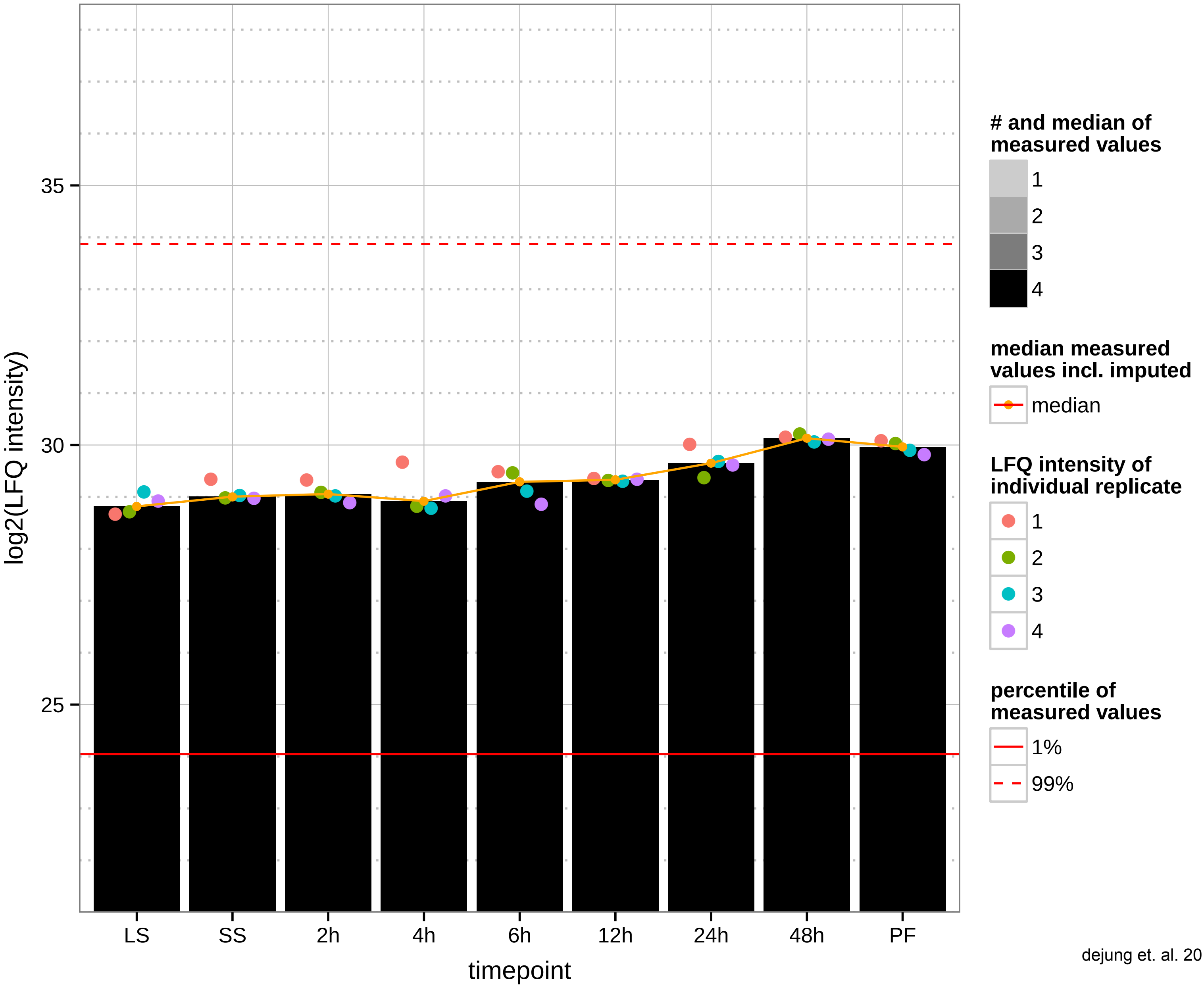
adenylosuccinate lyase, putative (ADSL)
Tb927.9.7550
AGOF: N6−(1, 2−dicarboxyethyl)AMP AMP−lyase (fumarate−forming) activity
AGOC: null
AGOP: IMP biosynthetic process, purine nucleobase metabolic process, purine ribonucleotide biosynthetic process
PGOF: N6−(1, 2−dicarboxyethyl)AMP AMP−lyase (fumarate−forming) activity, catalytic activity
PGOC: null
PGOP: IMP biosynthetic process, purine ribonucleotide biosynthetic process





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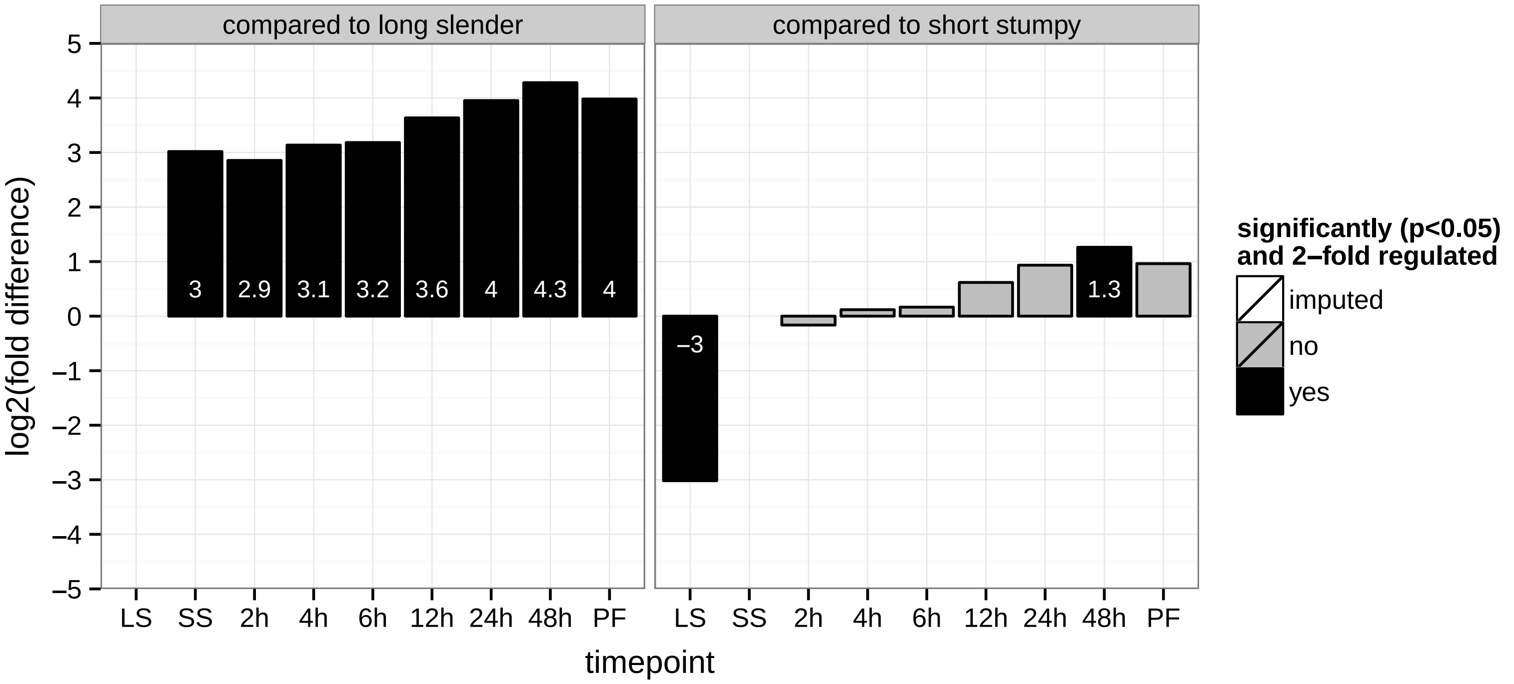
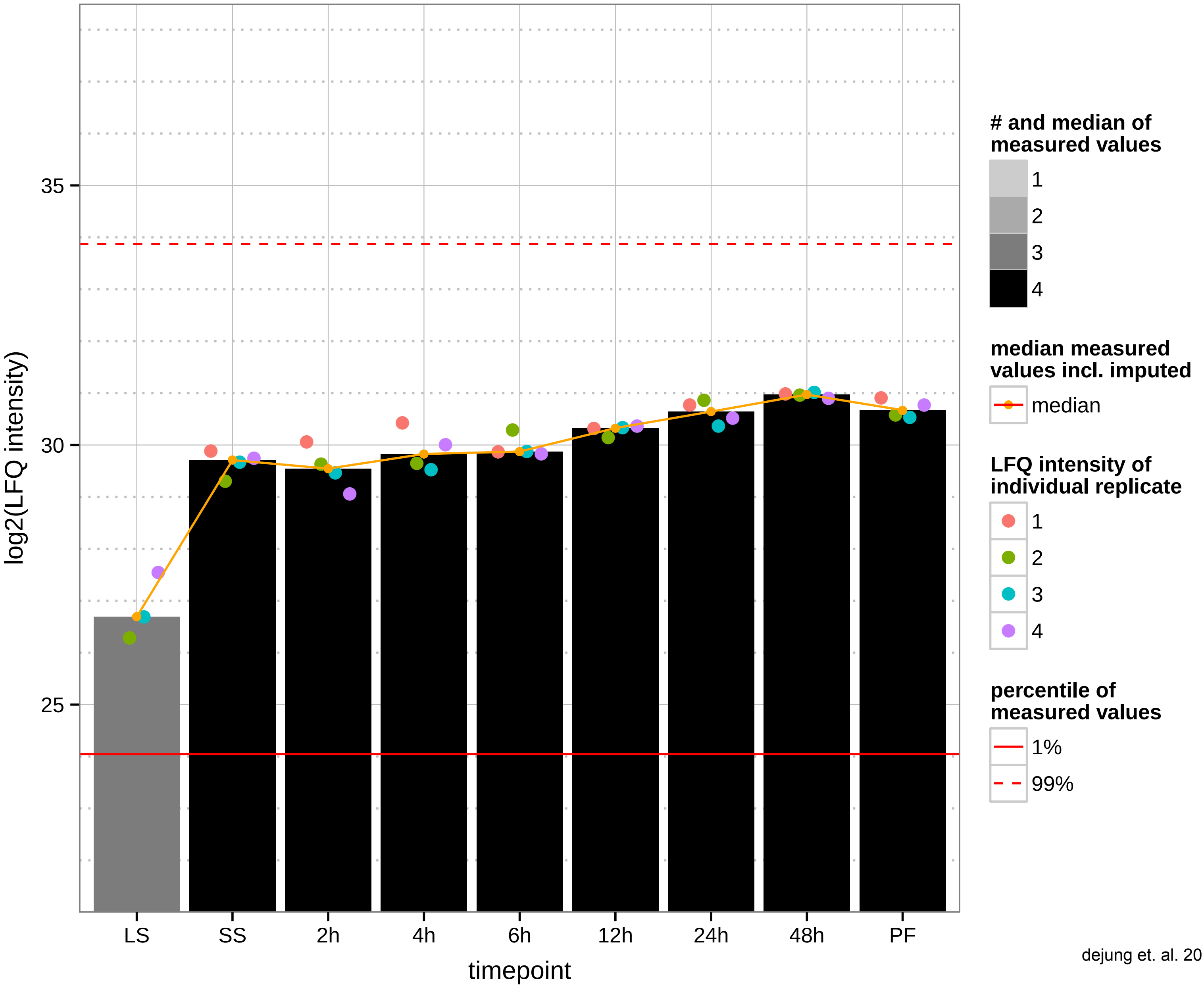
hypothetical protein, conserved
Tb927.9.9660
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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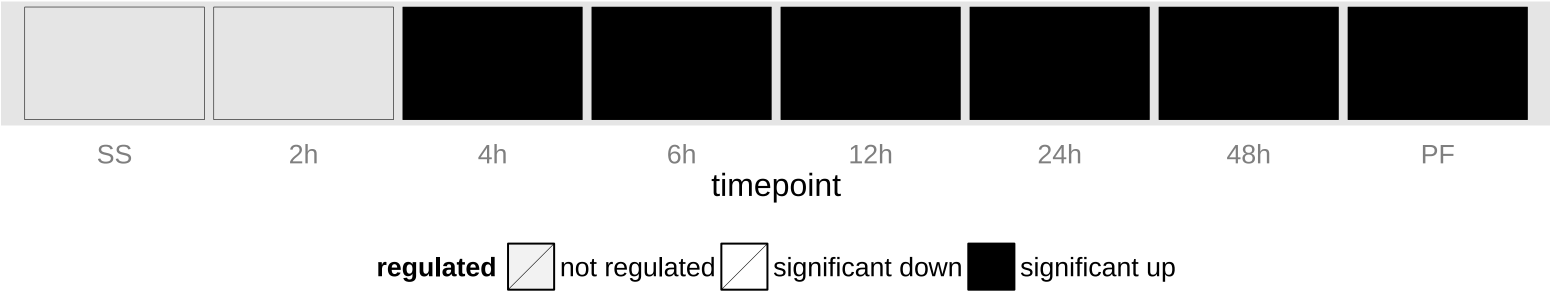

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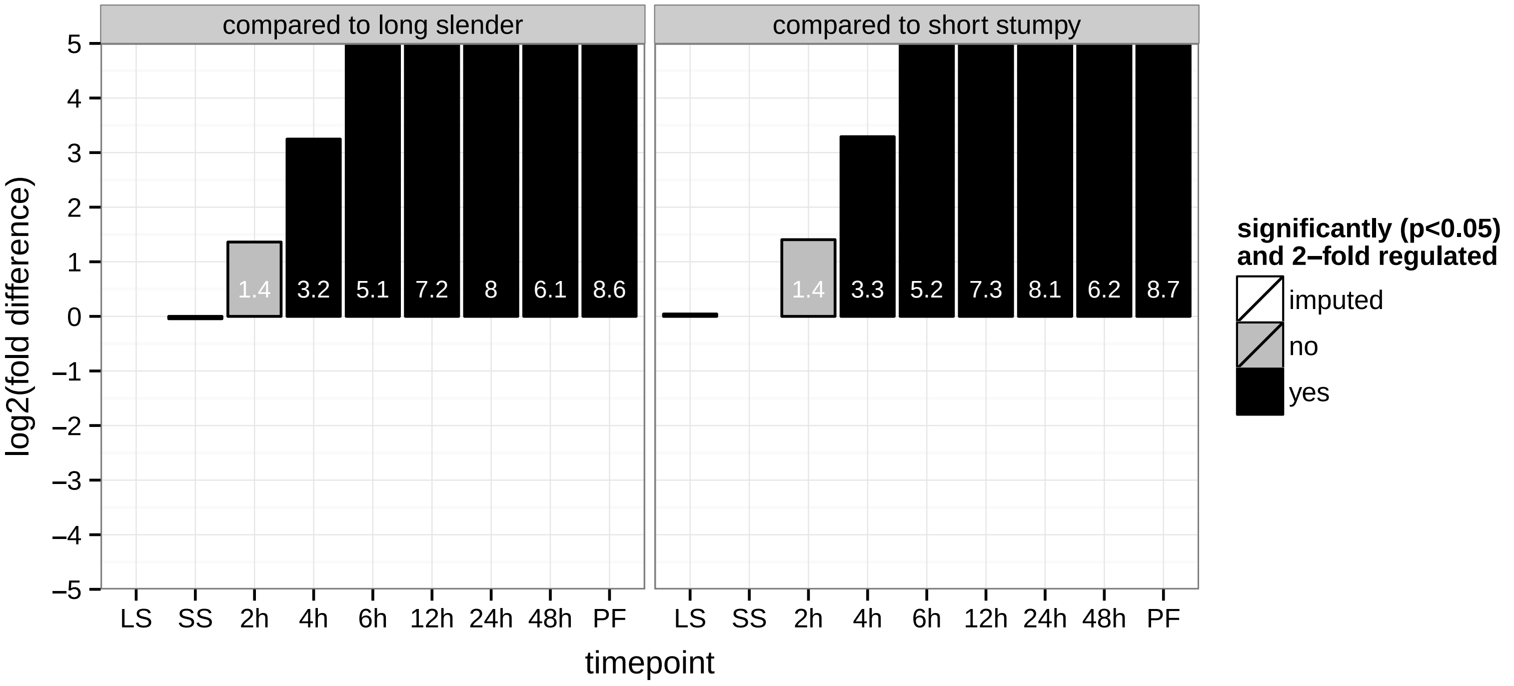
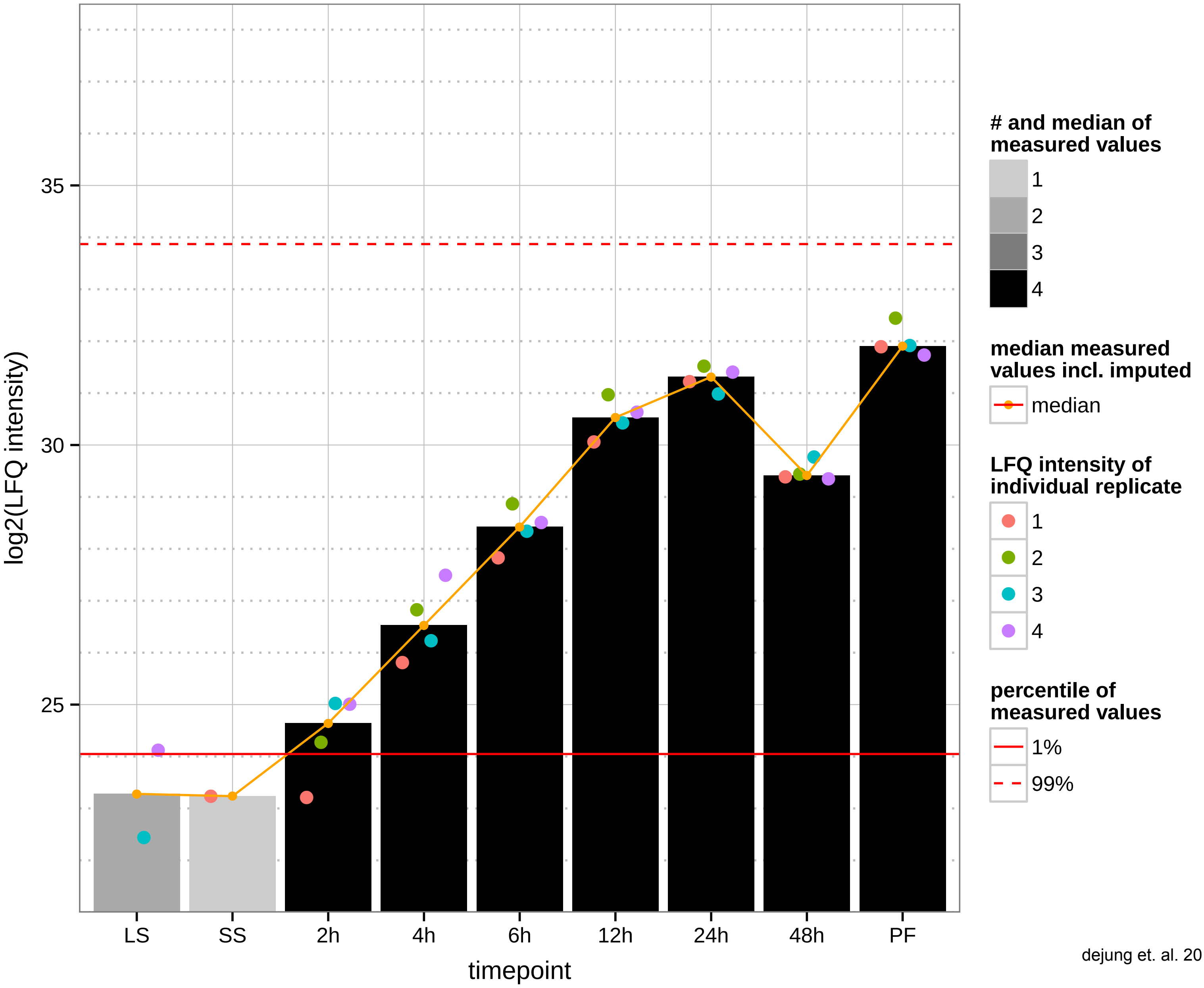
hypothetical protein, conserved, trans–sialidase, putative
Tb927.5.440;Tb11.v5.0223
AGOF: null, exo–alpha–sialidase activity
AGOC: null
AGOP: null, pathogenesis
PGOF: null
PGOC: null
PGOP: null





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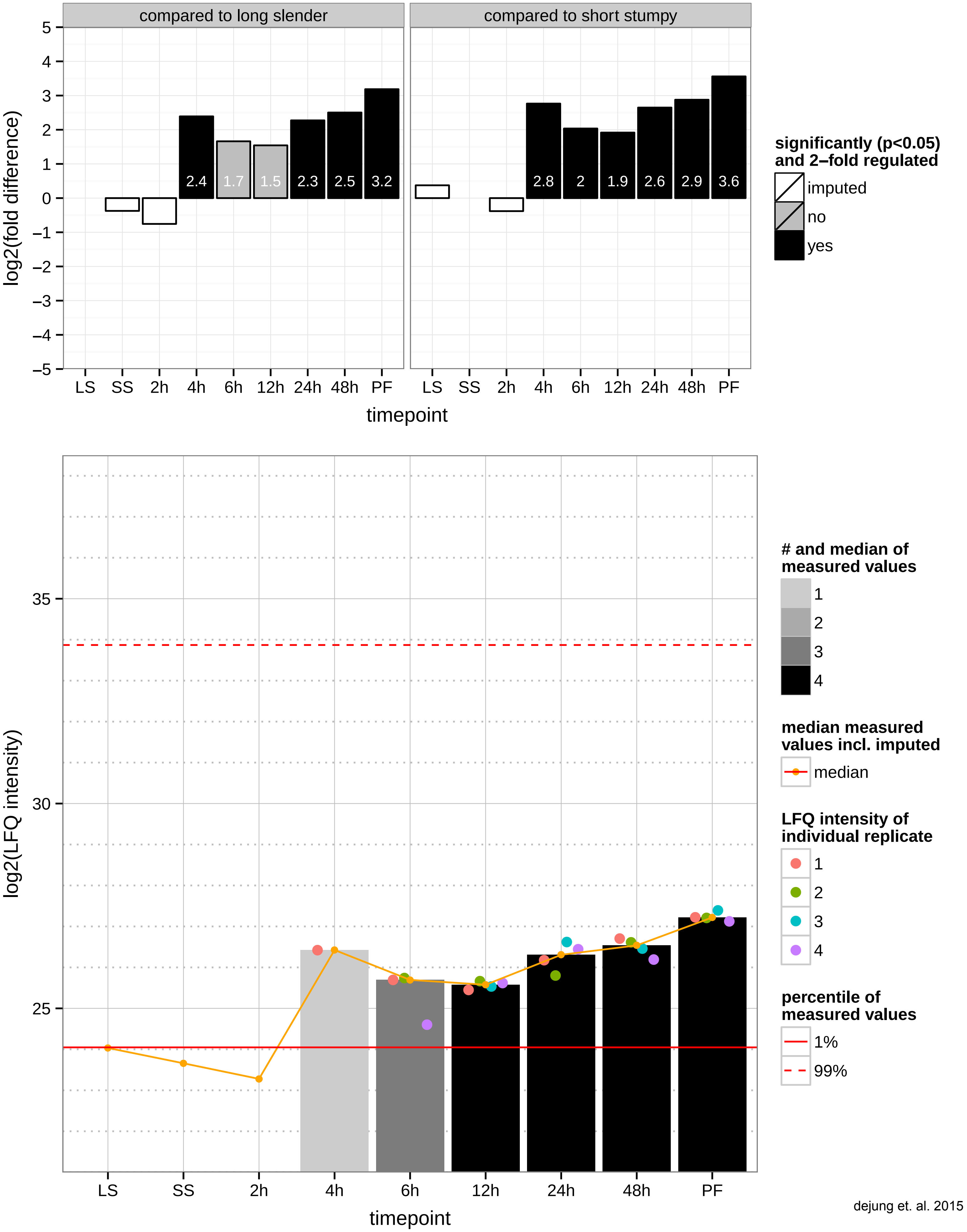
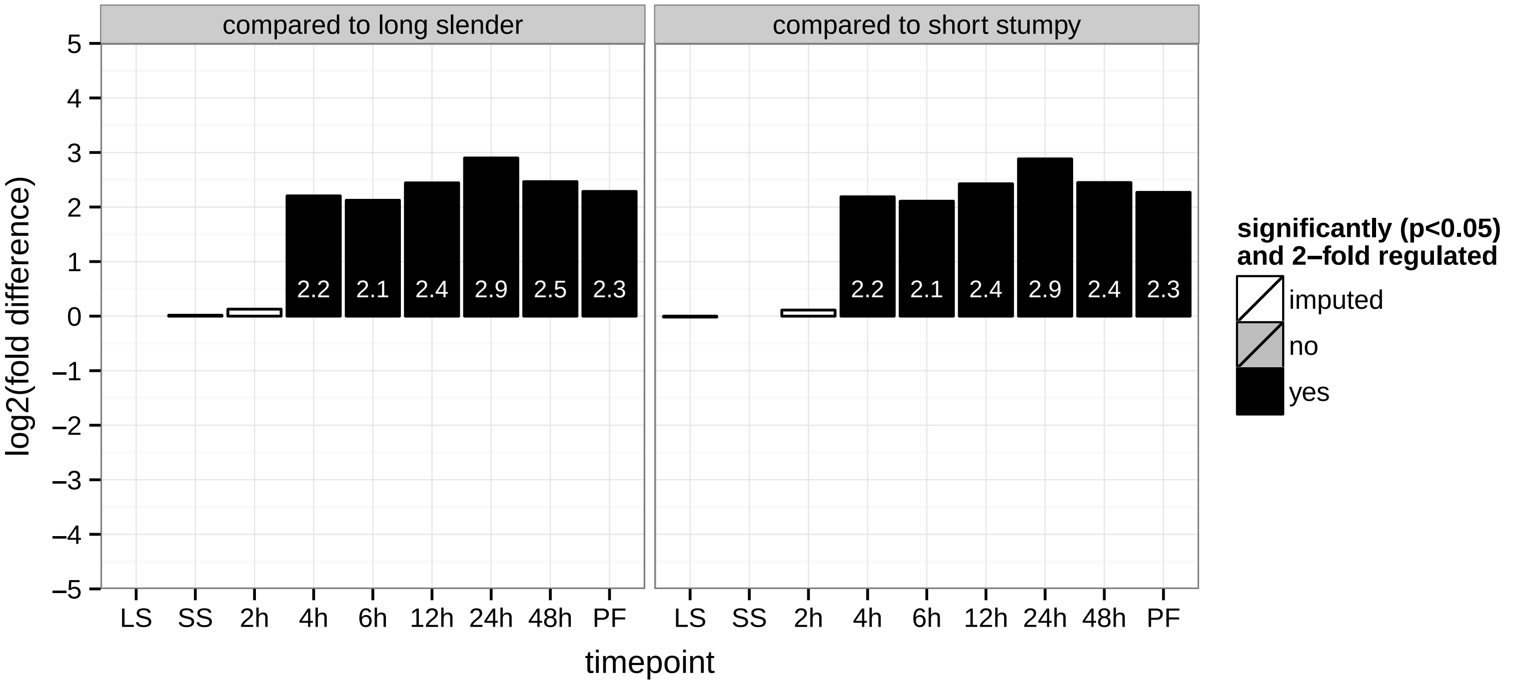
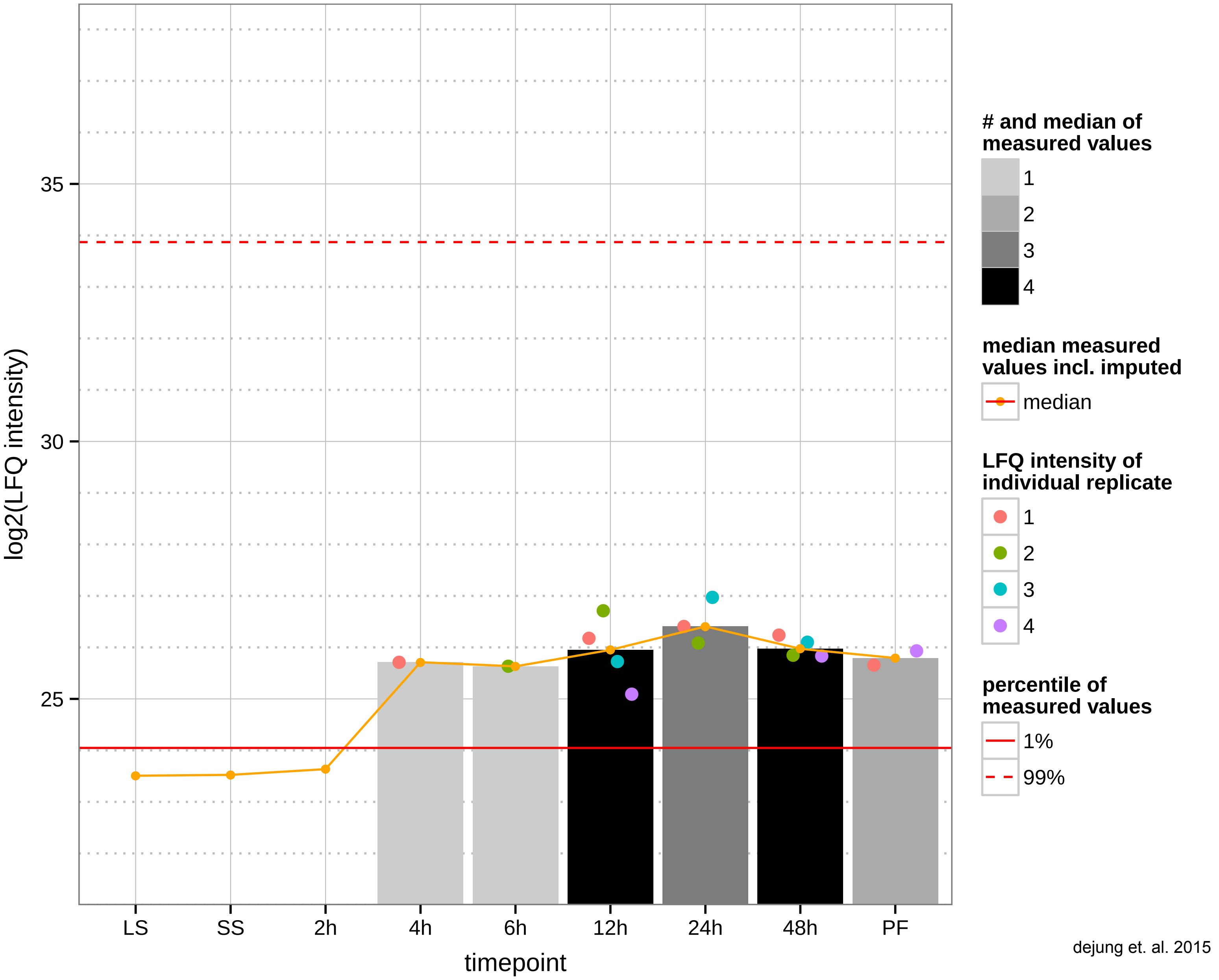
hypothetical protein, conserved, mitochondrial RNA binding complex 1 subunit (PPR5)
Tb927.10.380;Tb11.v5.0637
AGOF: null, RNA binding
AGOC: null, mitochondrion
AGOP: null, RNA polyadenylation
PGOF: null
PGOC: null
PGOP: null



hypothetical protein, conserved
Tb11.v5.0775;Tb927.10.7560
AGOF: null, methyltransferase activity
AGOC: null
AGOP: null, metabolic process
PGOF: methyltransferase activity
PGOC: null
PGOP: metabolic process





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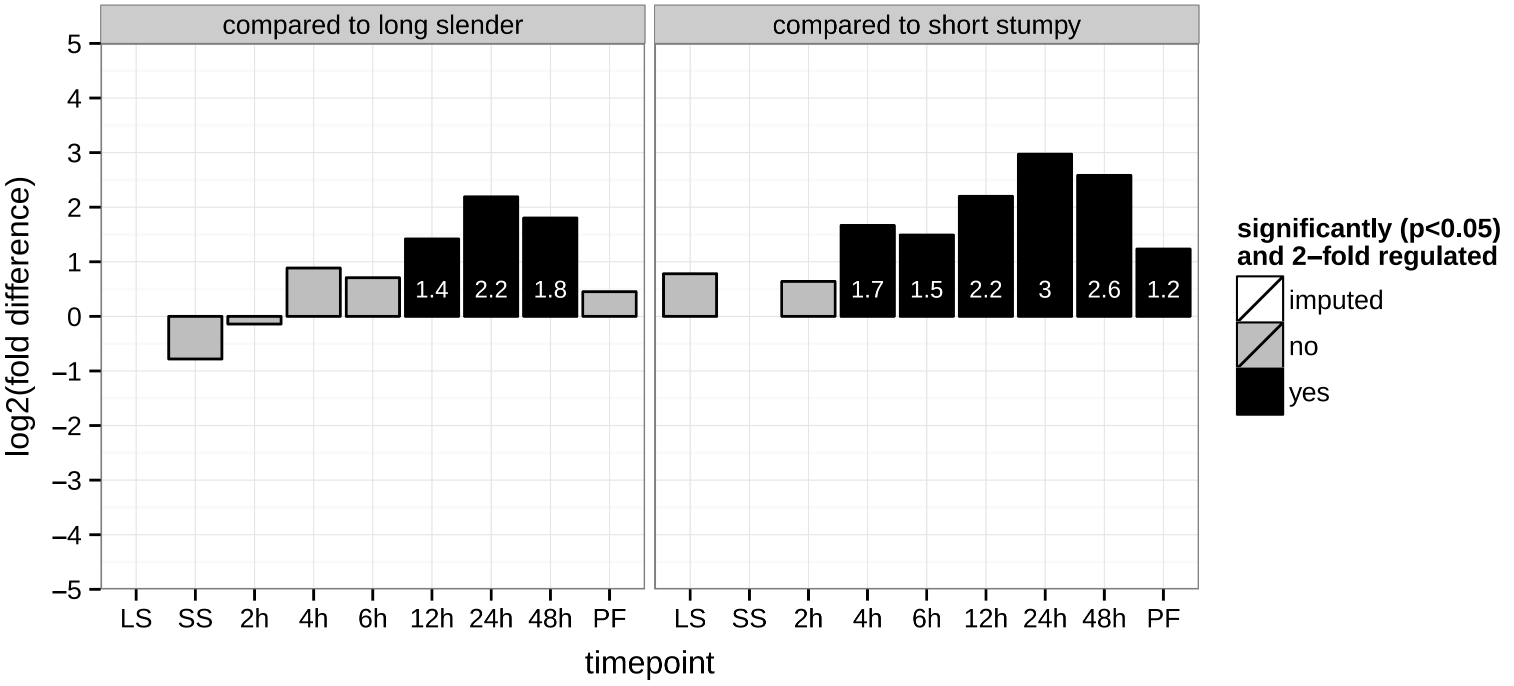
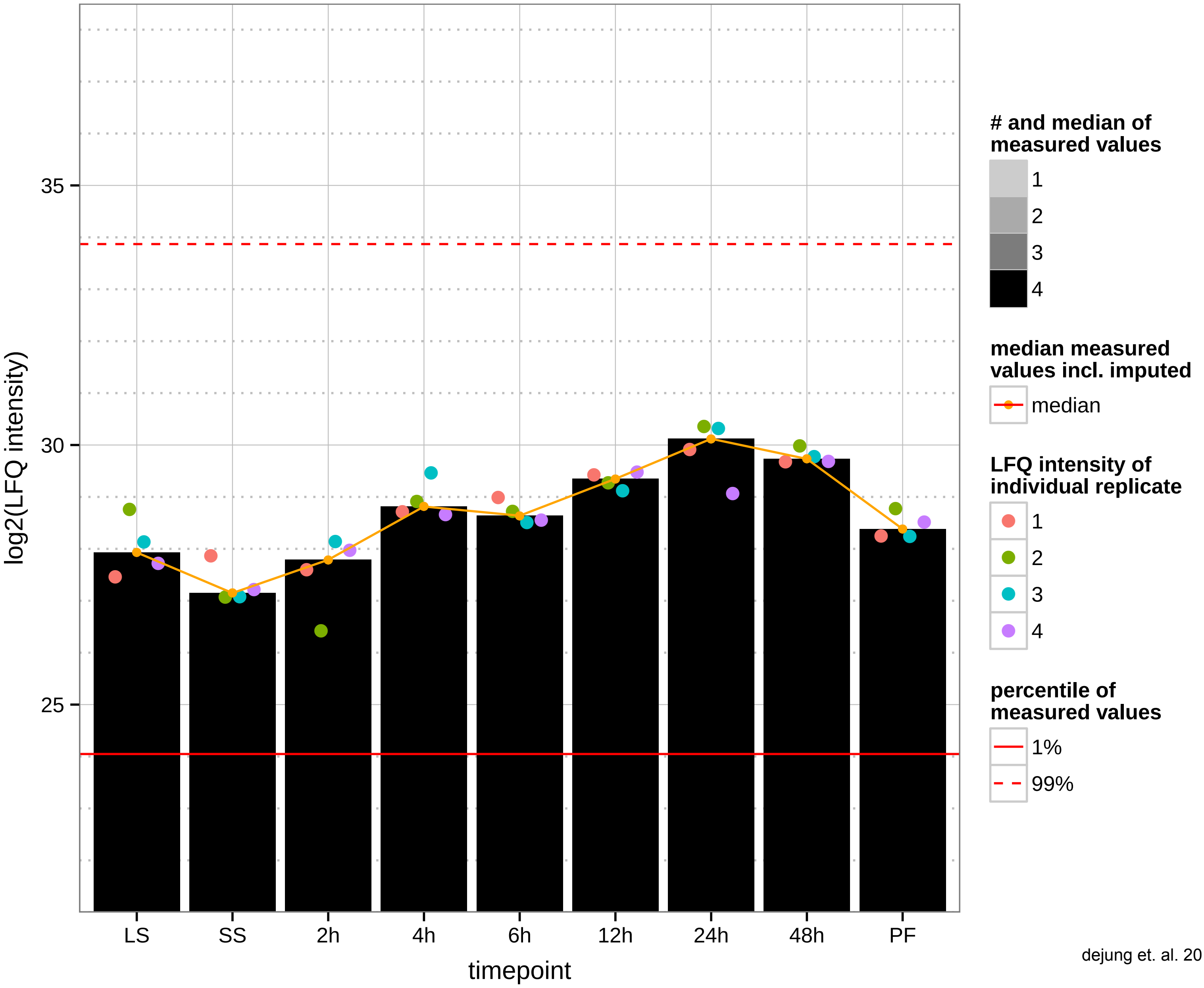
hypothetical protein, conserved
Tb927.1.2210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: nucleus
PGOP: nucleosome assembly





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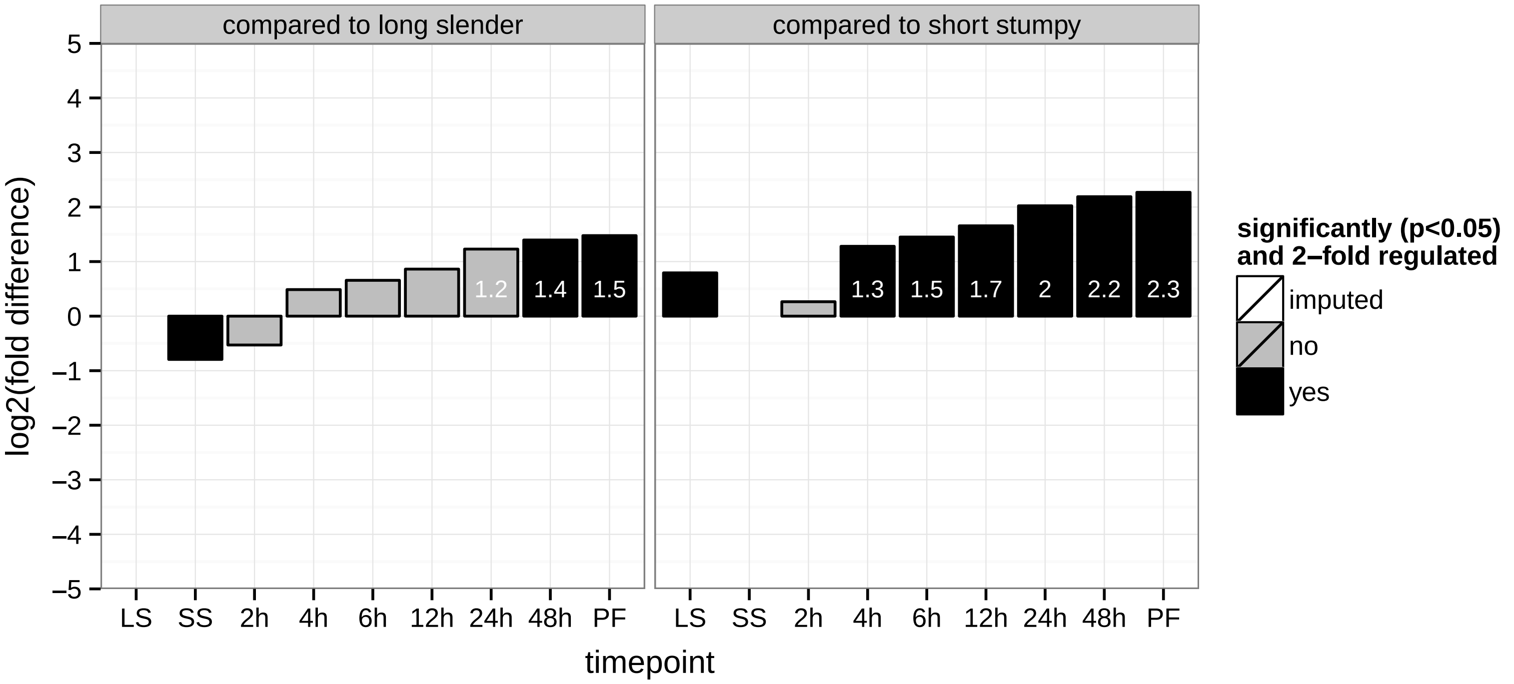
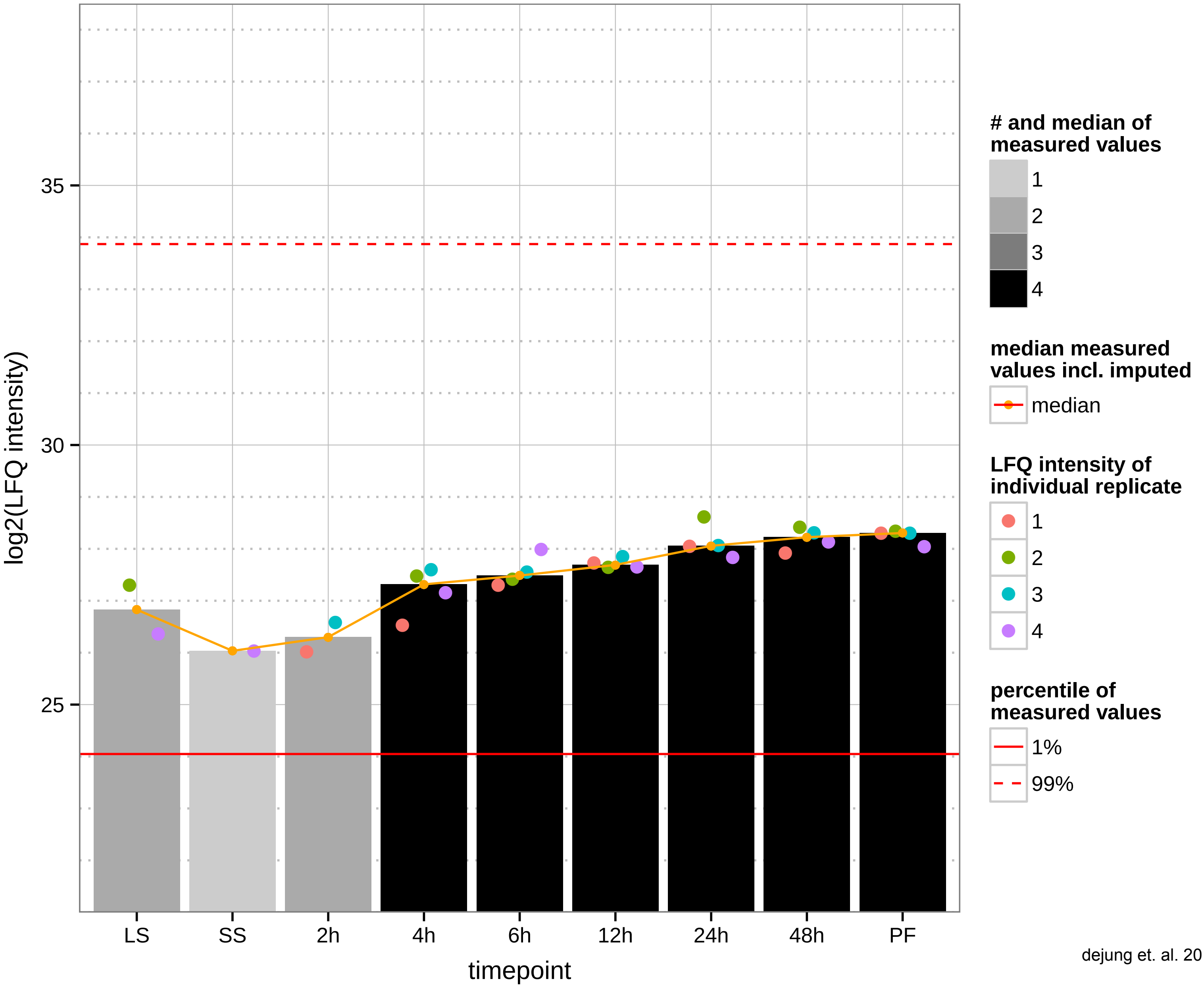
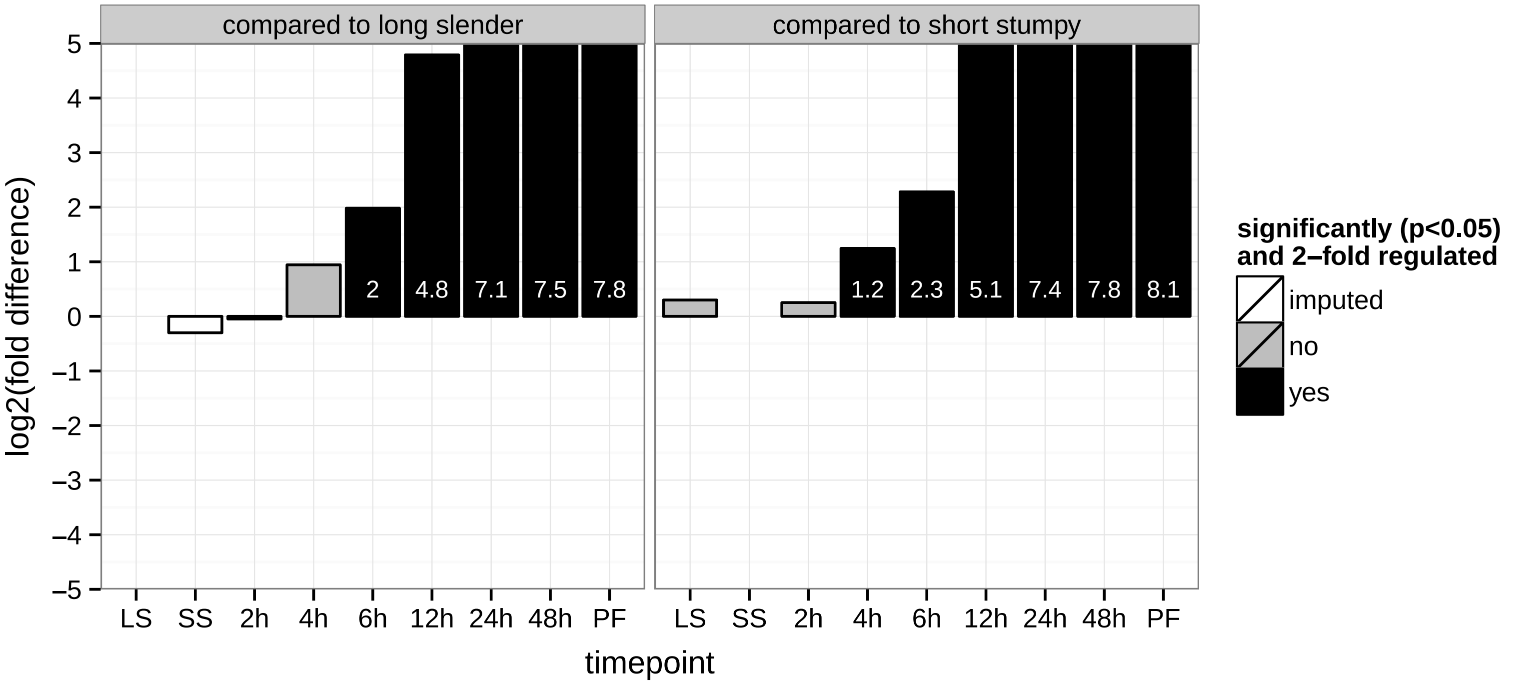
hypothetical protein, conserved
Tb927.1.3070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

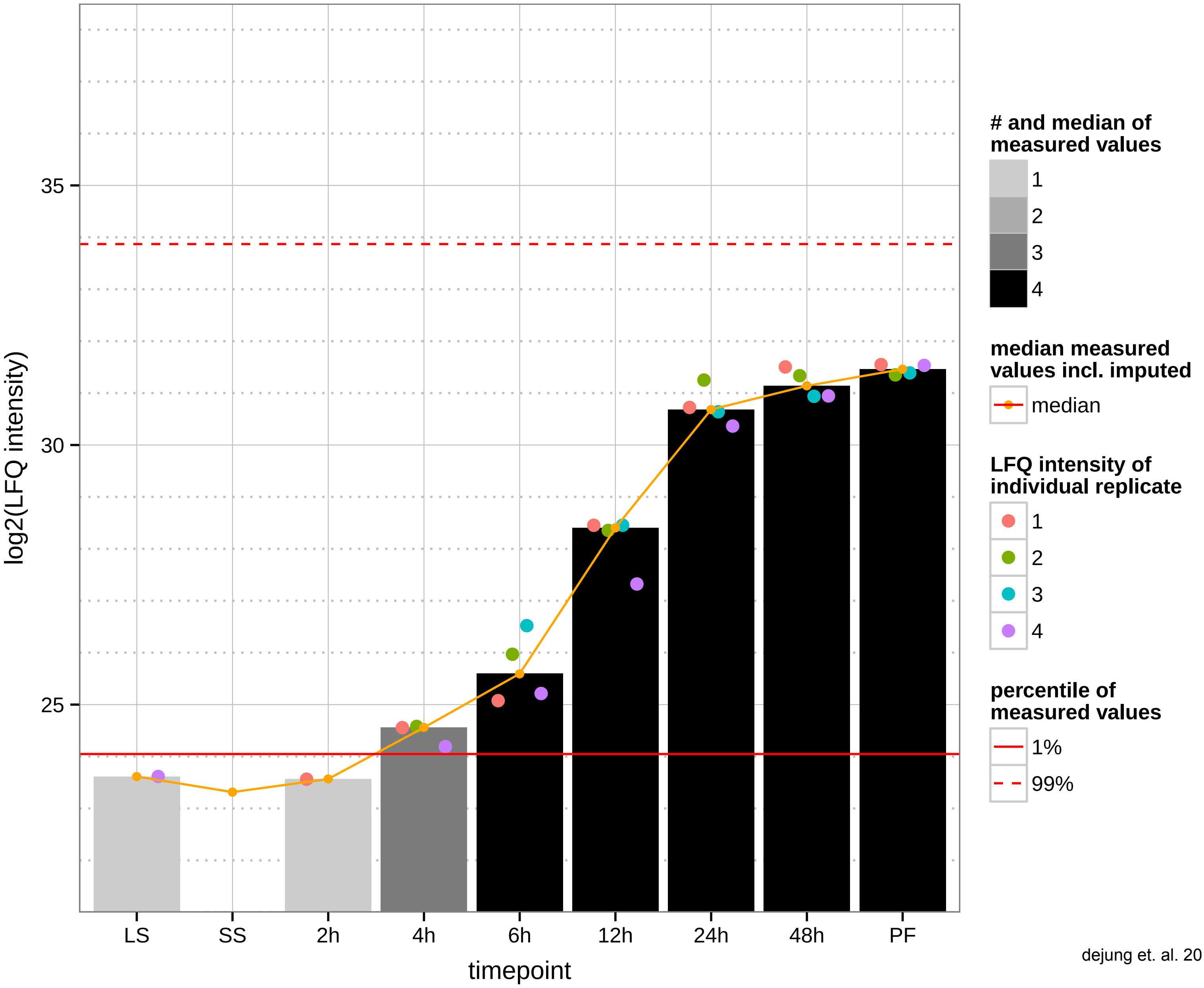




dejung et. al. 2015

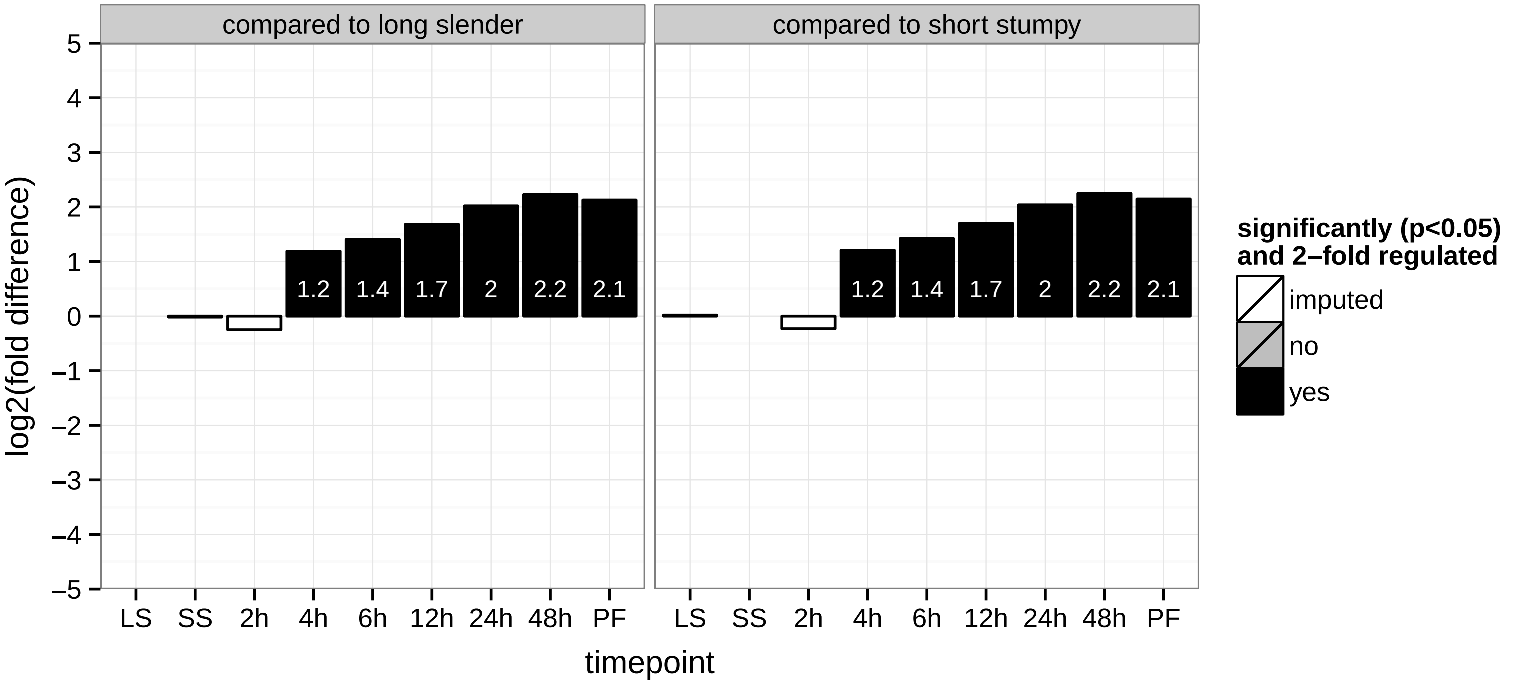
cytochrome oxidase subunit IV (COXIV)
Tb927.1.4100
AGOF: cytochrome−c oxidase activity
AGOC: mitochondrial respiratory chain complex IV, mitochondrion
AGOP: oxidation−reduction process
PGOF: null
PGOC: null
PGOP: null

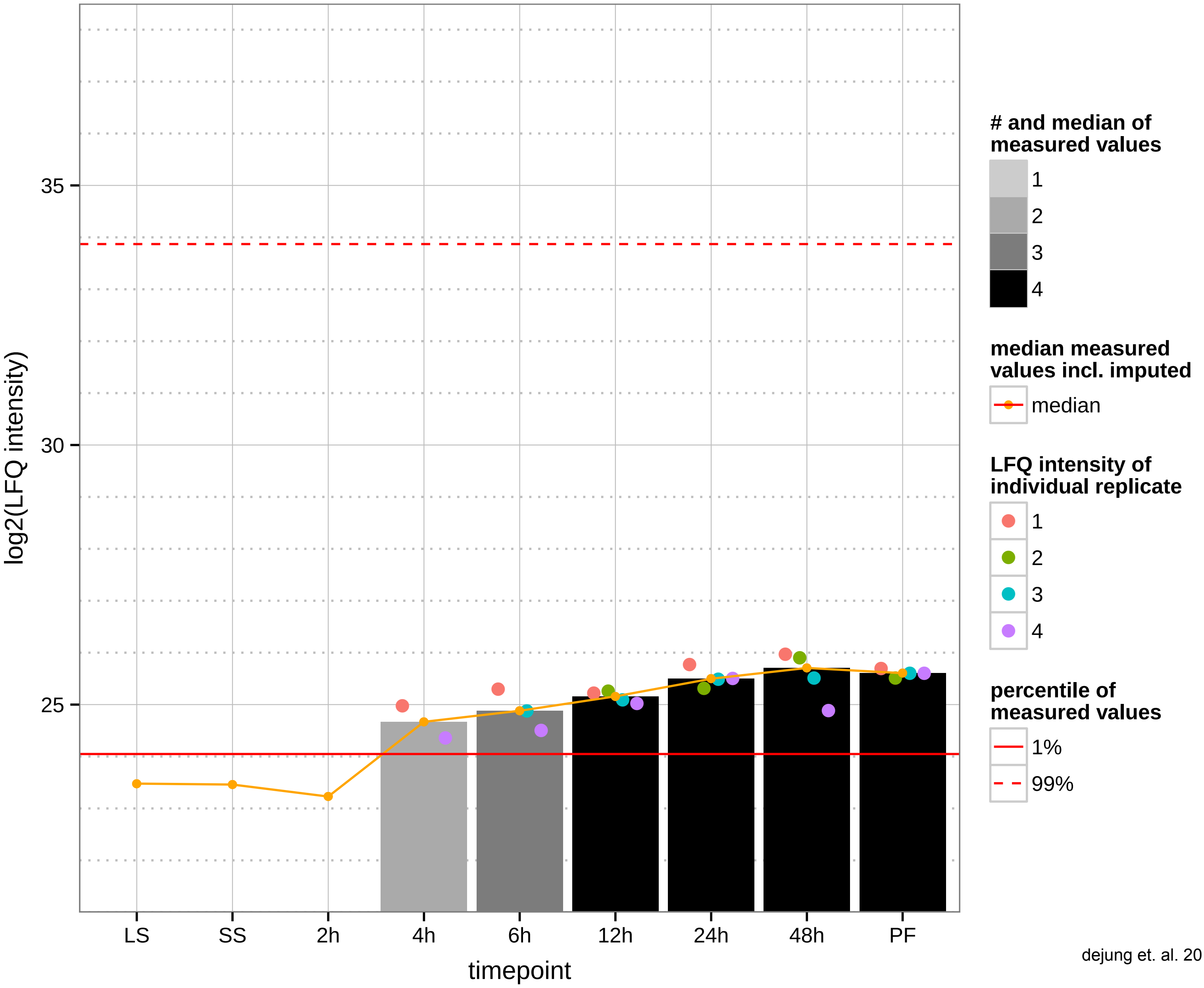




dejung et. al. 2015

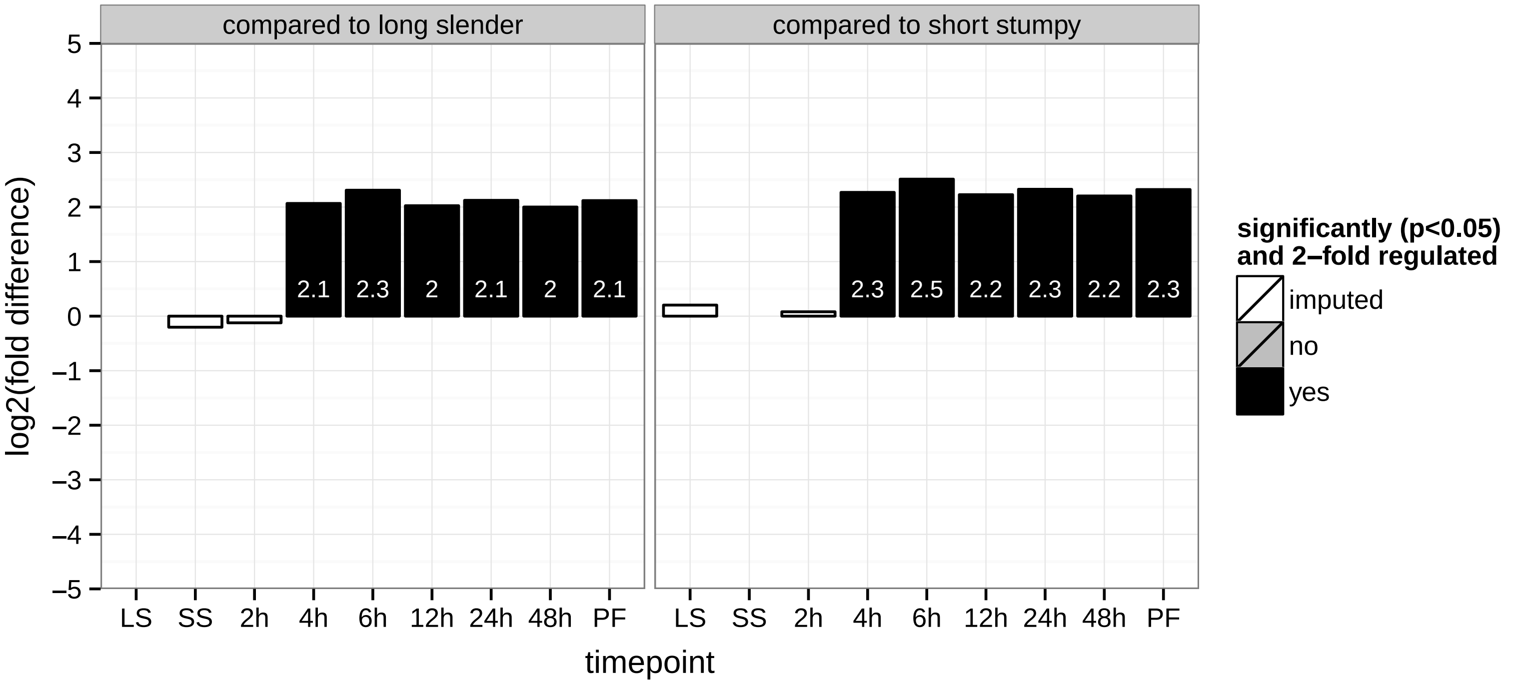
hypothetical protein, conserved
Tb927.1.560
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

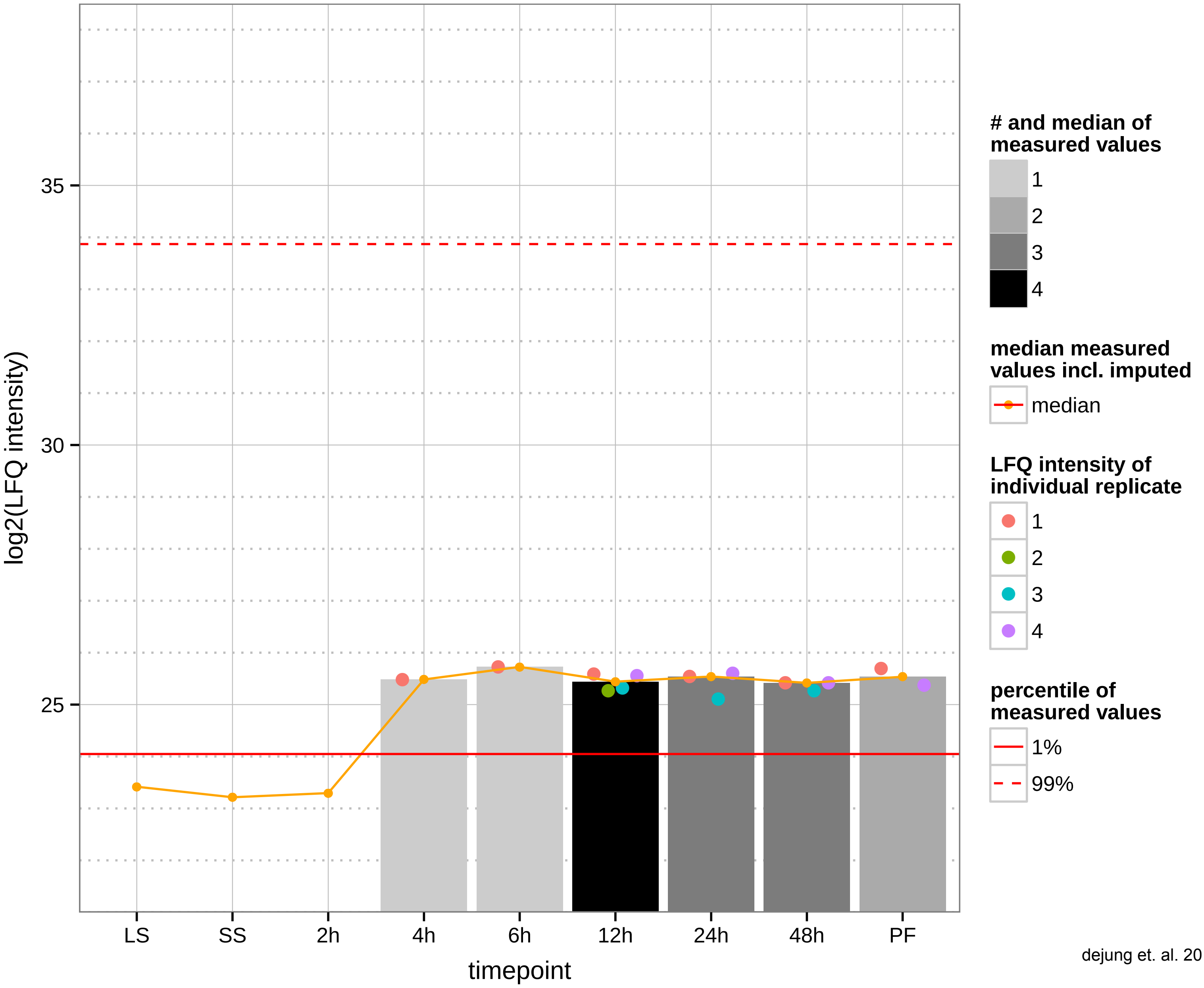




dejung et. al. 2015

splicing factor Prp31
Tb927.10.10700
AGOF: RNA binding
AGOC: nucleus
AGOP: RNA splicing
PGOF: null
PGOC: null
PGOP: null





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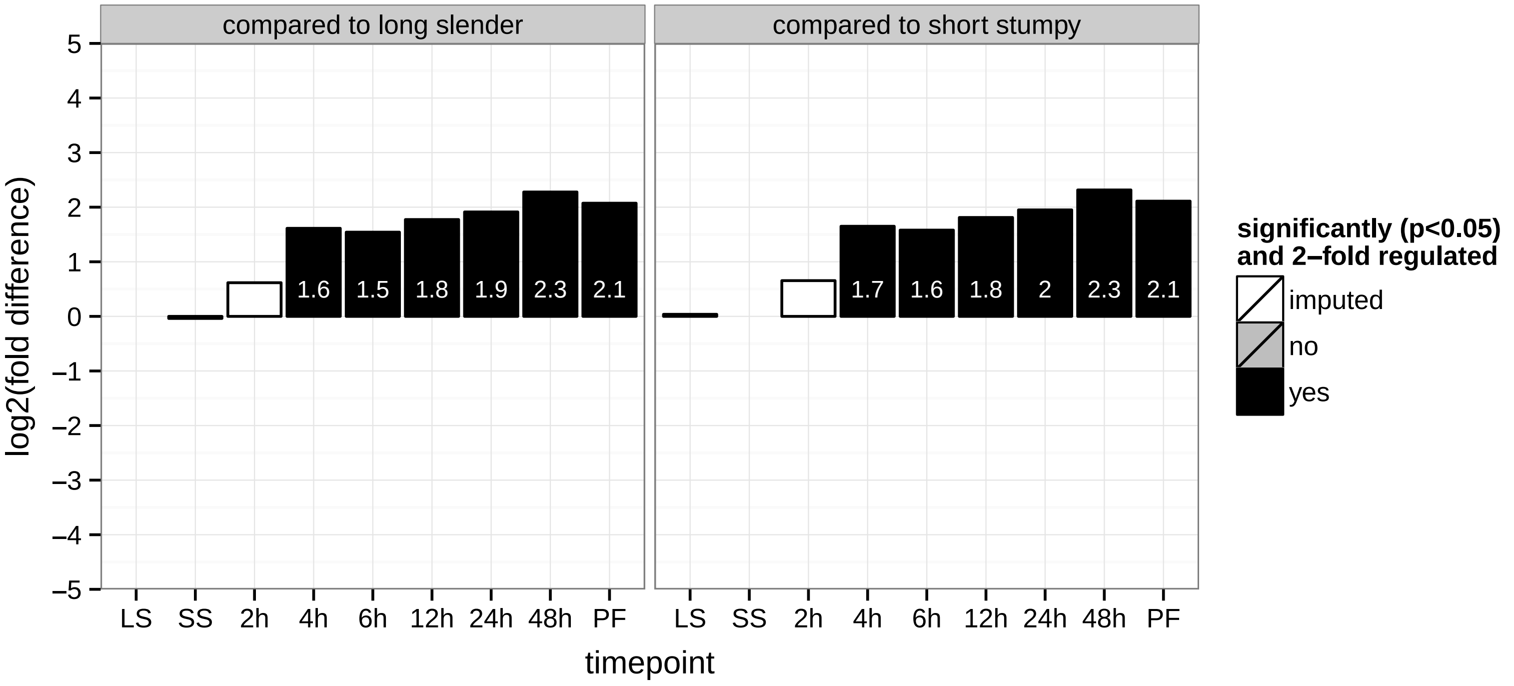
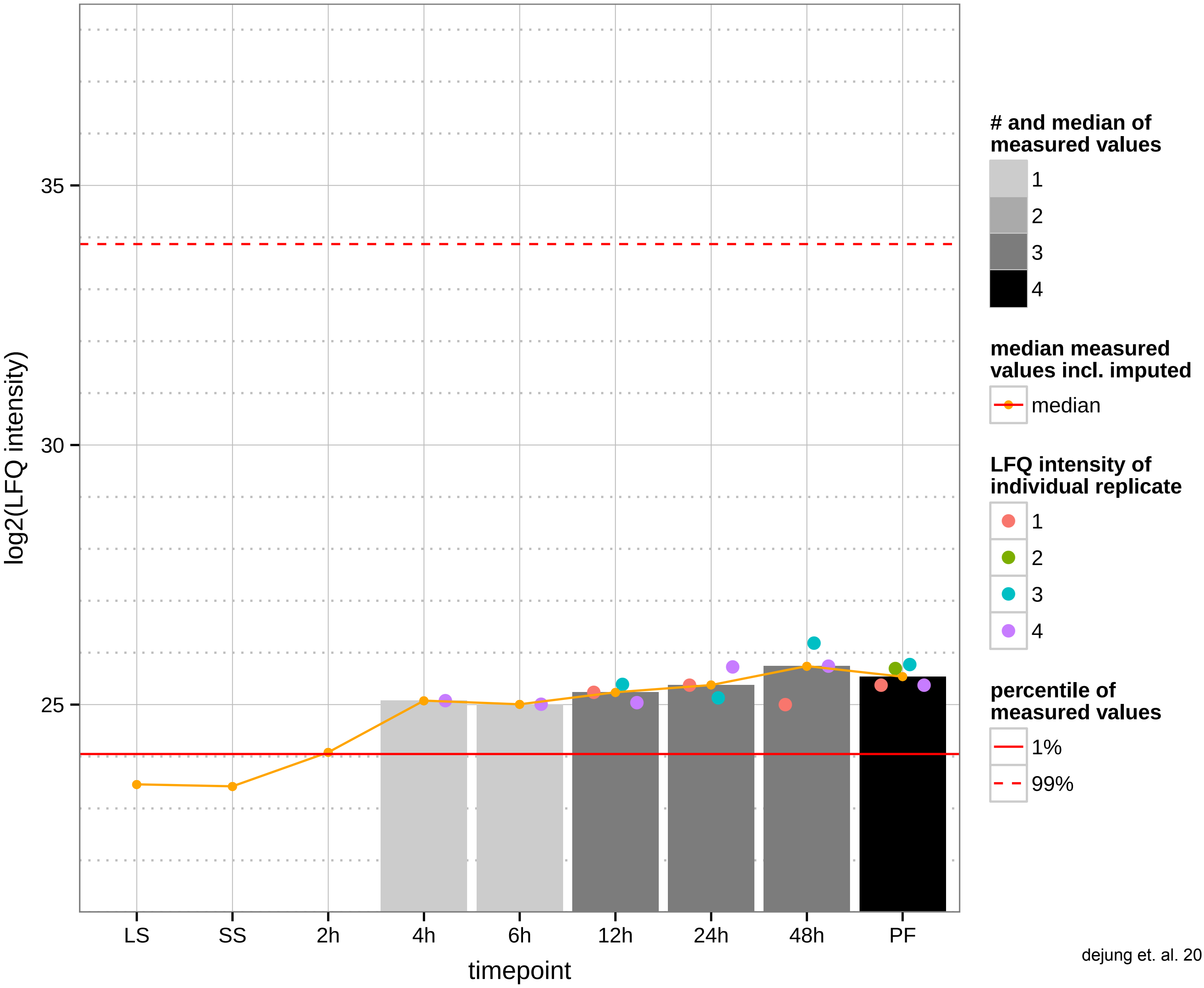
Ubiquitin–like modifier–activating enzyme ATG7, putative, Autophagy–related protein 7 (ATG7)
Tb927.10.11180
AGOF: catalytic activity
AGOC: null
AGOP: autophagy, protein targeting to vacuole
PGOF: catalytic activity
PGOC: null
PGOP: null





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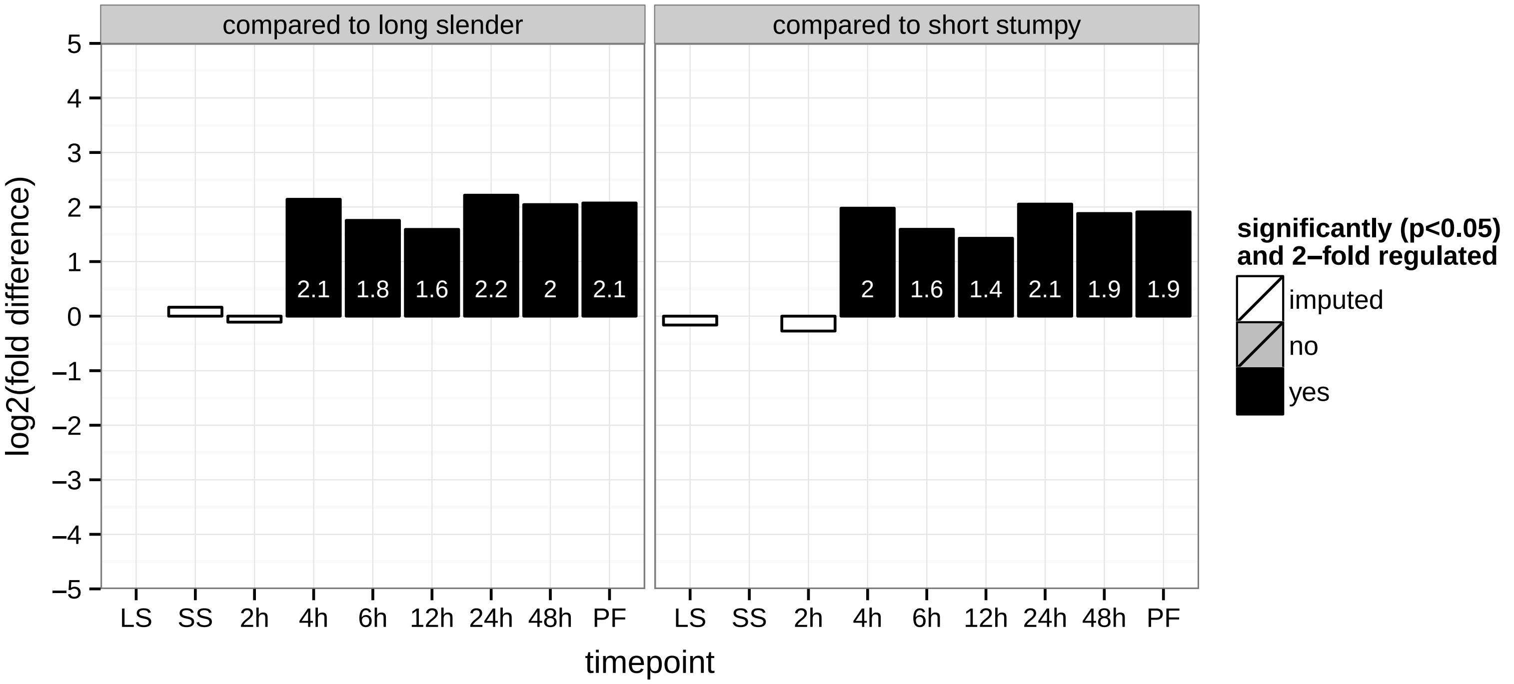
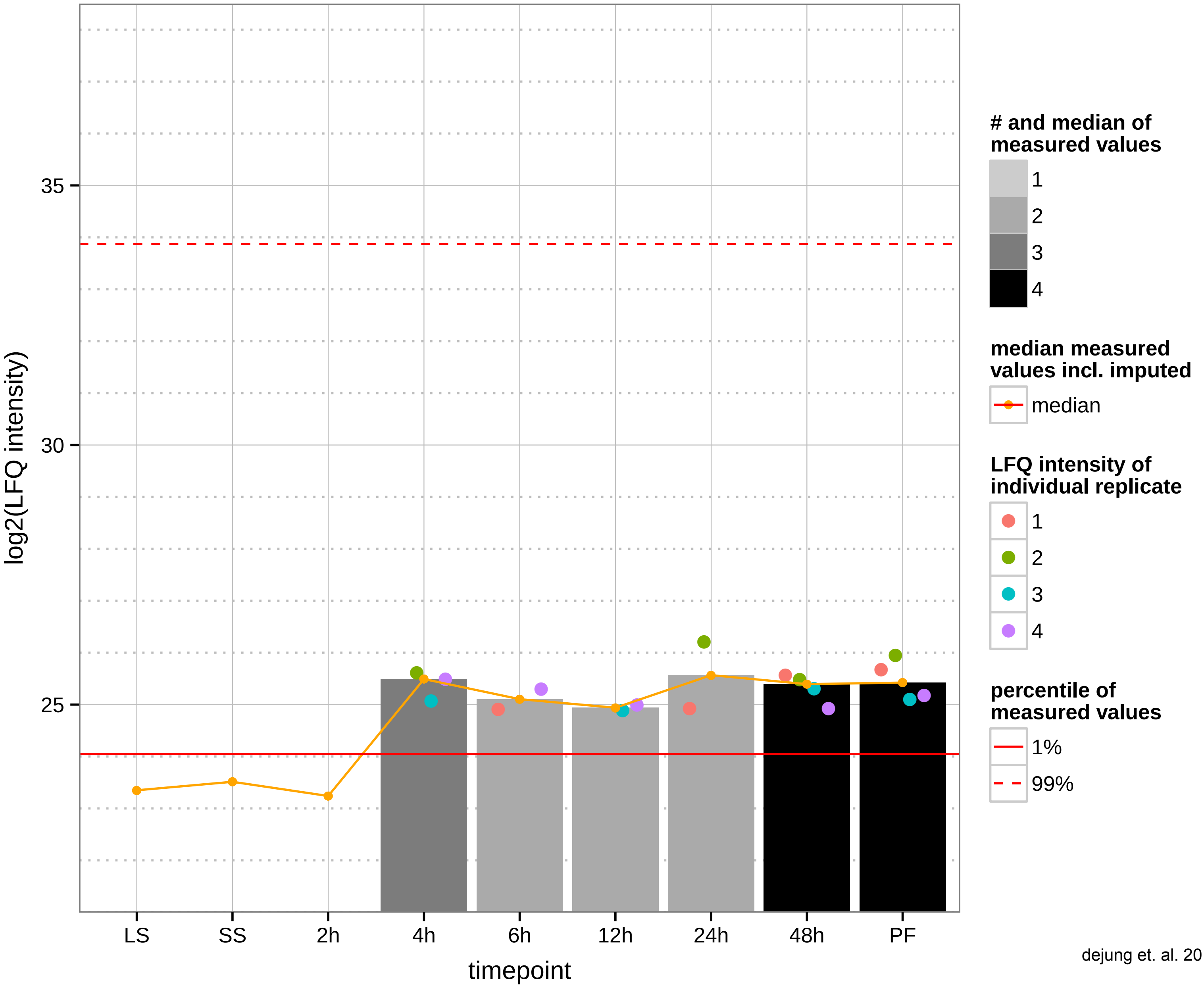
hypothetical protein, conserved
Tb927.10.11370
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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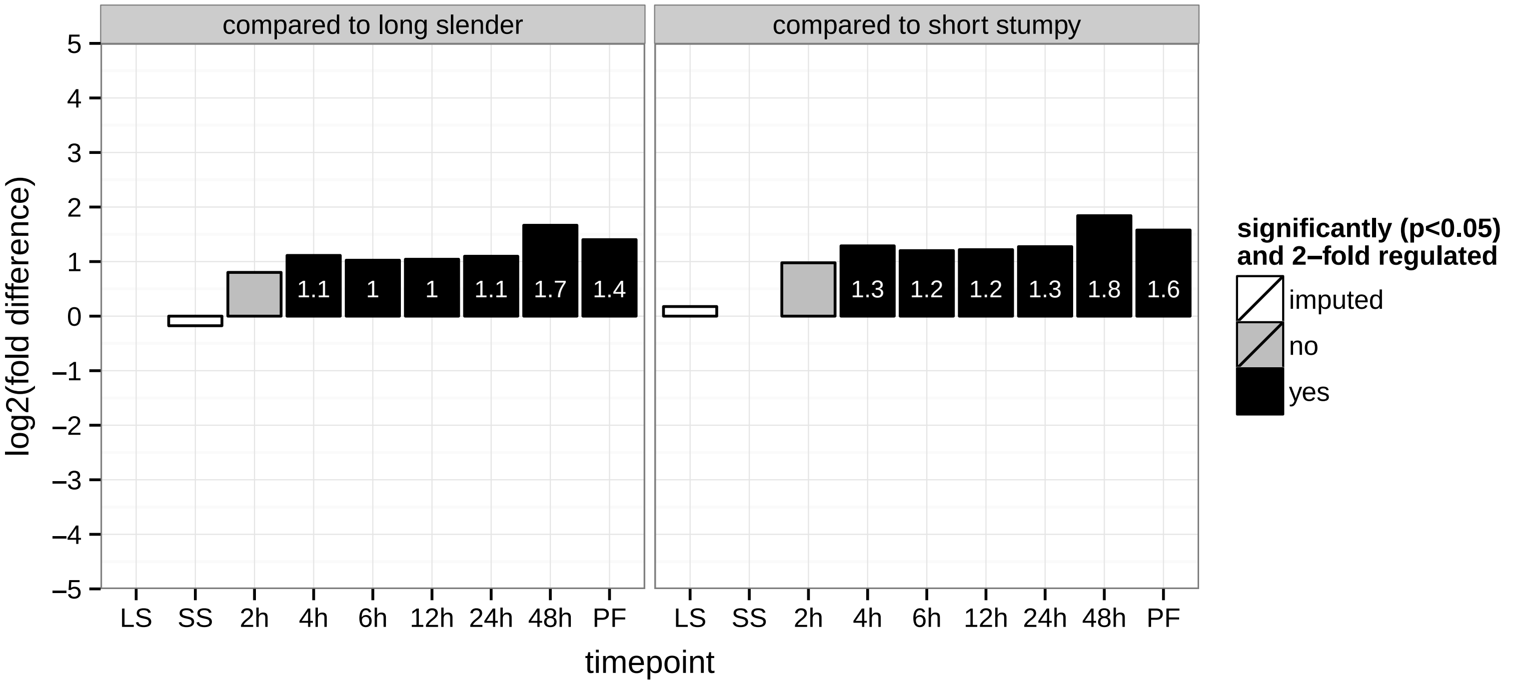
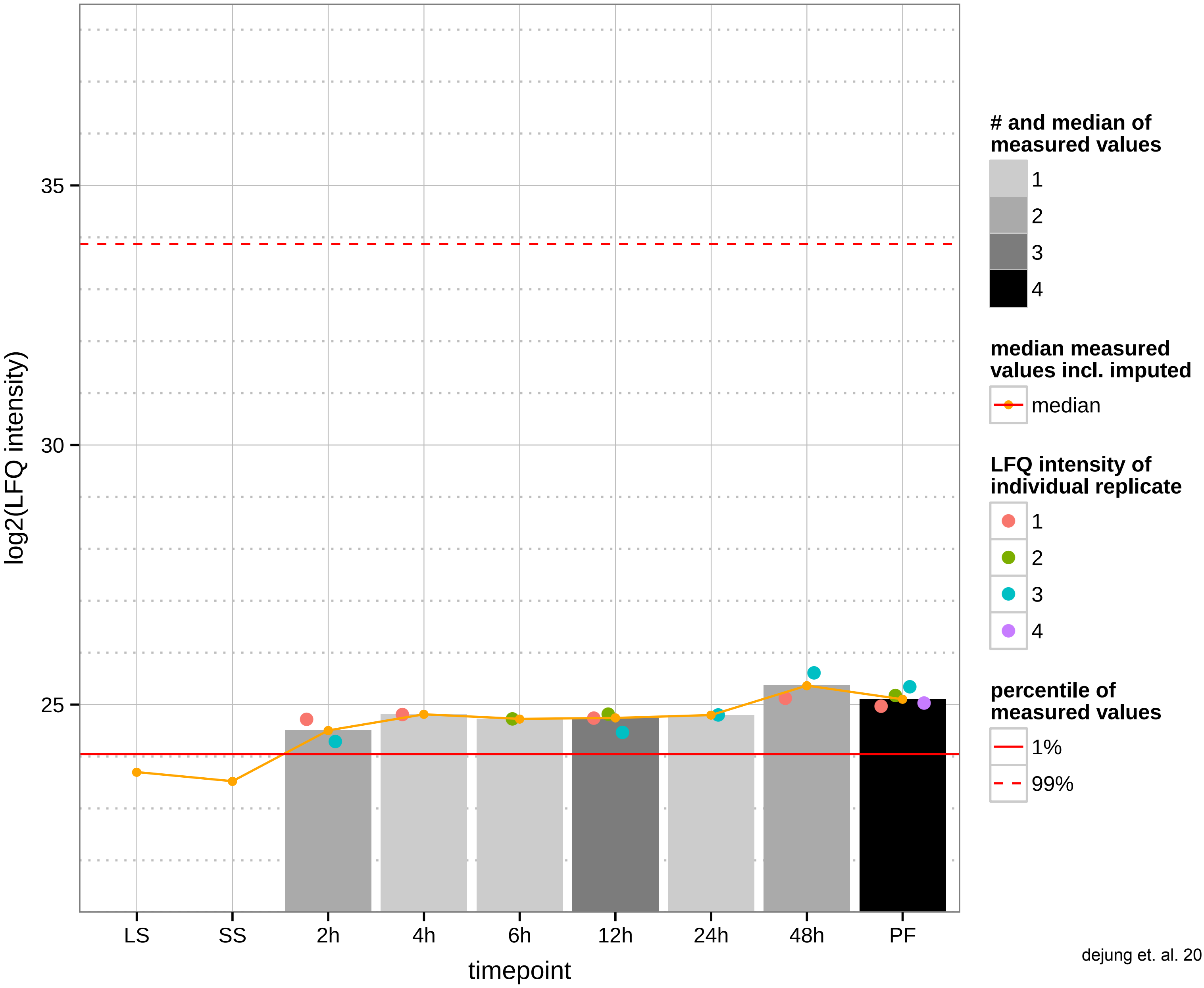
hypothetical protein, conserved
Tb927.10.1310
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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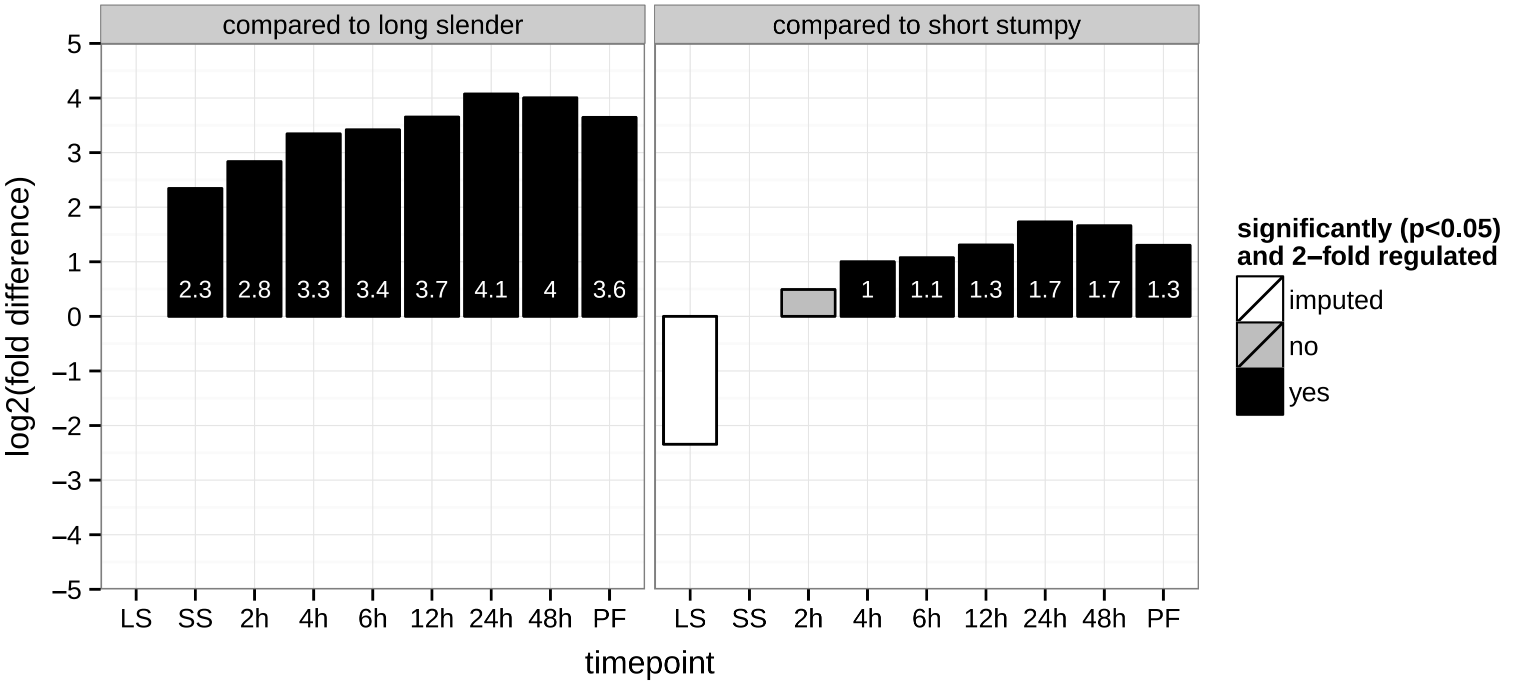
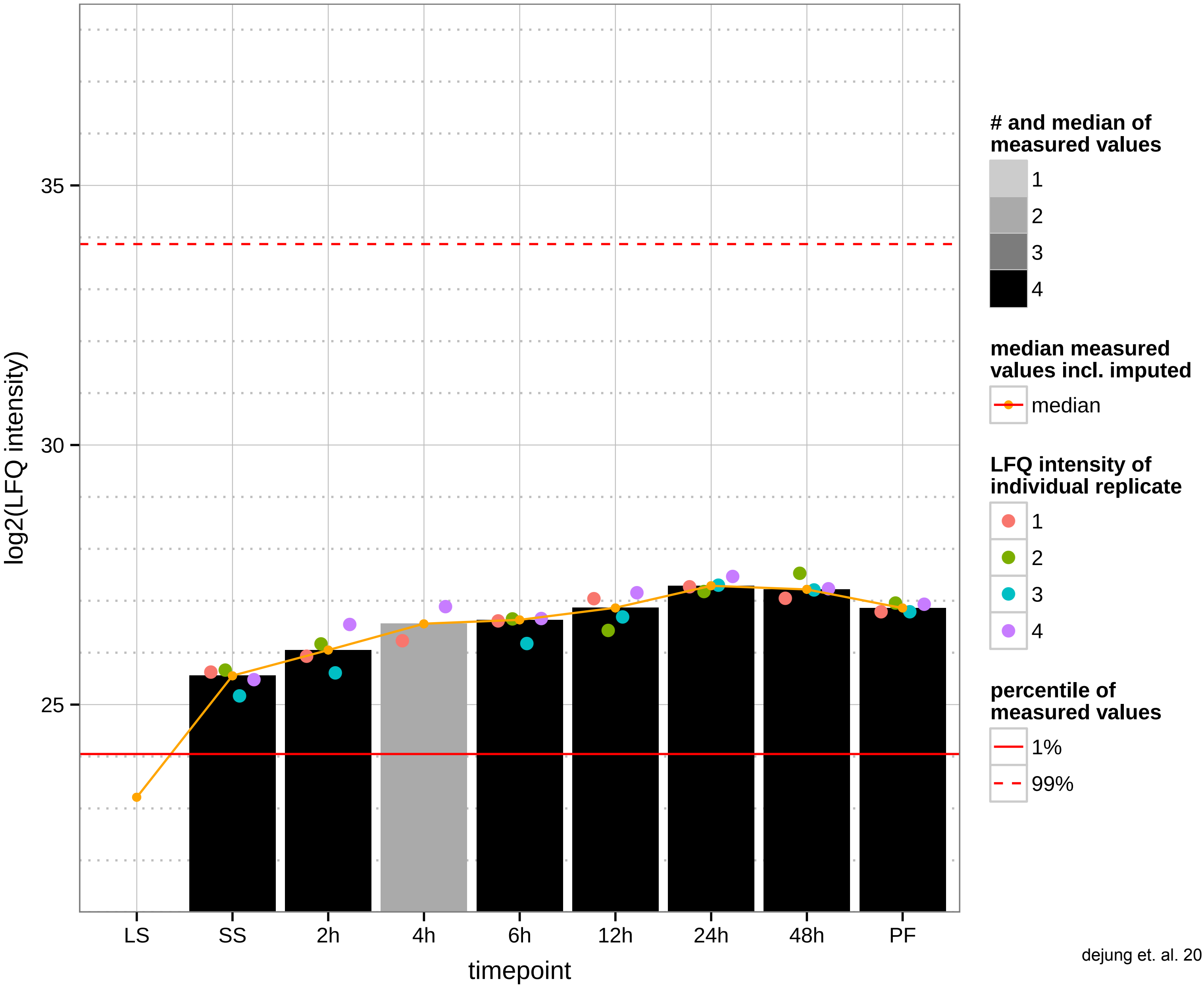
hypothetical protein, conserved
Tb927.10.14330
AGOF: null
AGOC: small–subunit processome
AGOP: rRNA processing
PGOF: null
PGOC: small–subunit processome
PGOP: rRNA processing





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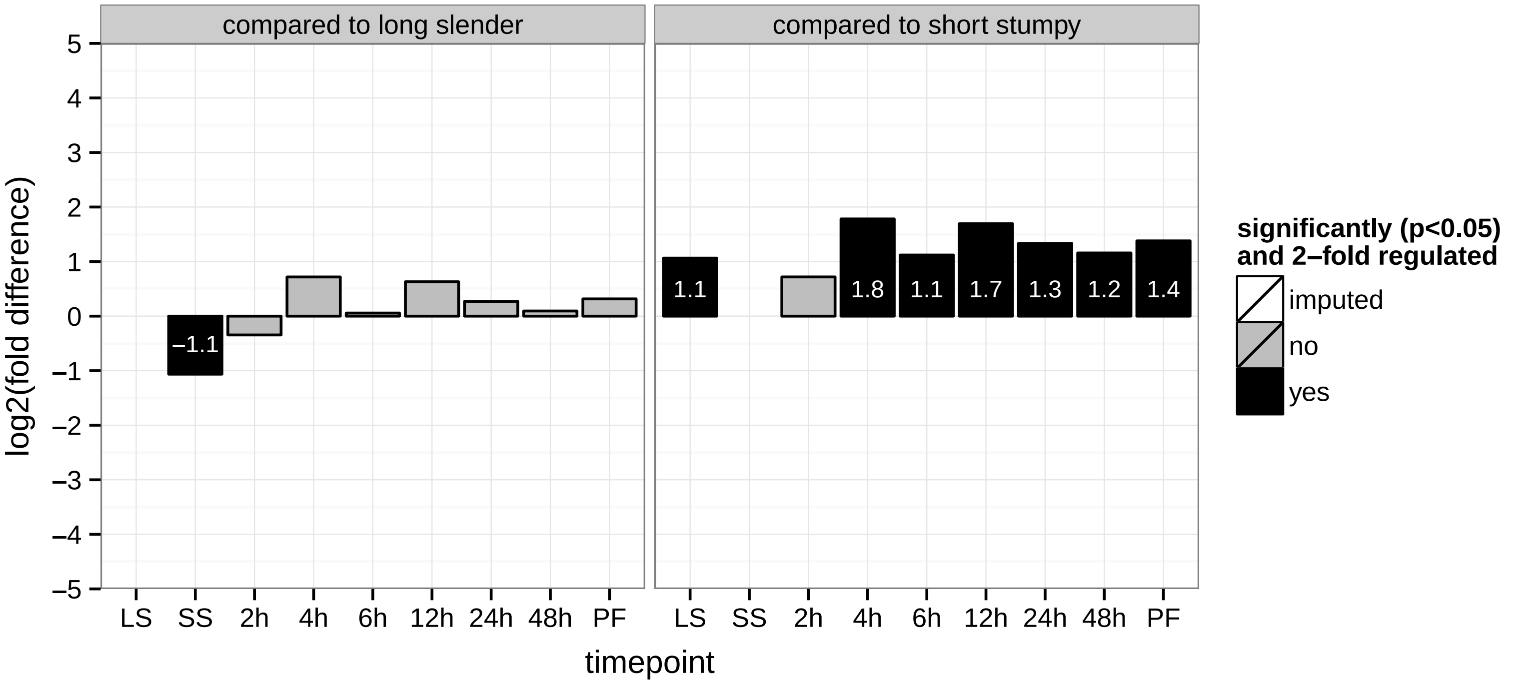
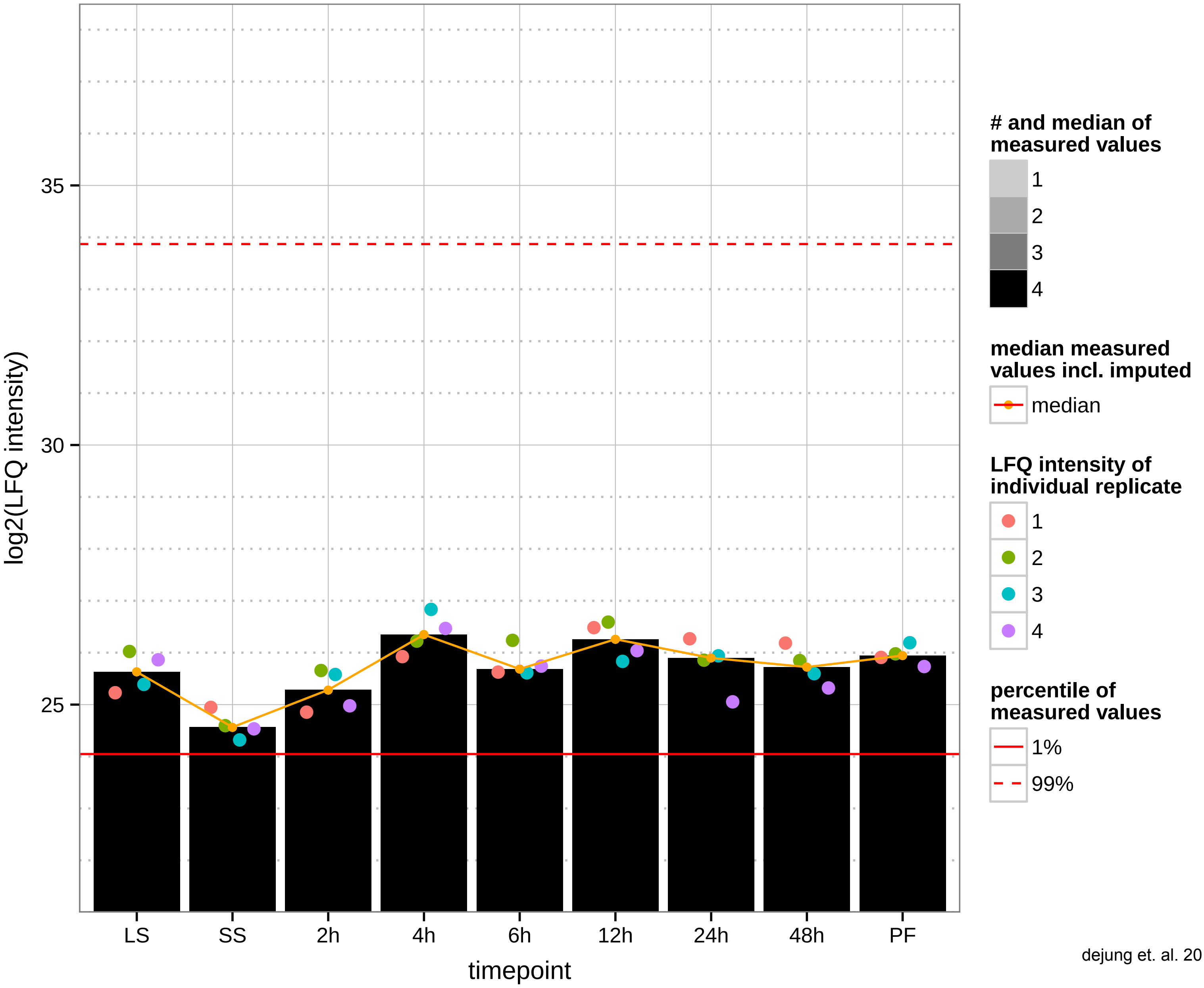
chaperone protein DNAj, putative, variant surface glycoprotein (VSG)
Tb927.10.14730;Tb11.v5.1062
AGOF: null, heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: null, protein folding
PGOF: heat shock protein binding, null
PGOC: null
PGOP: null





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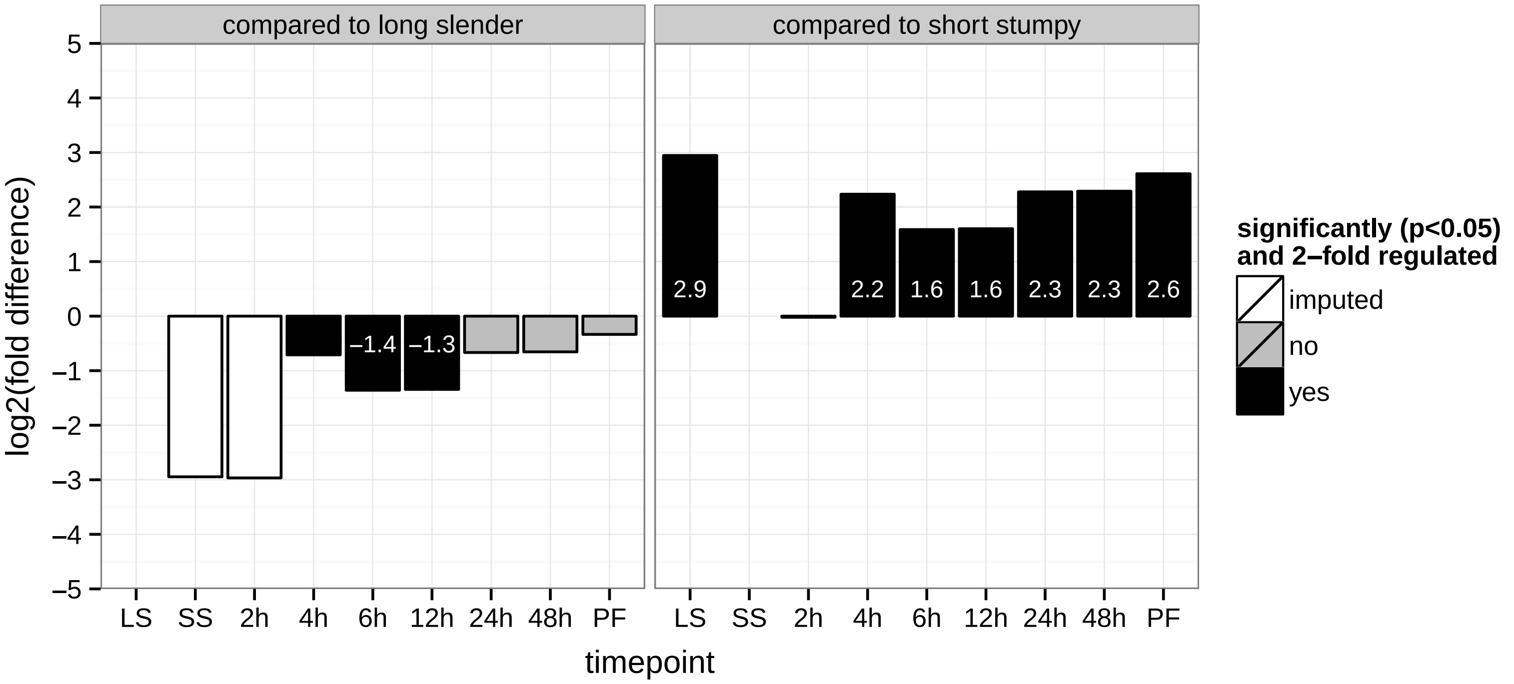
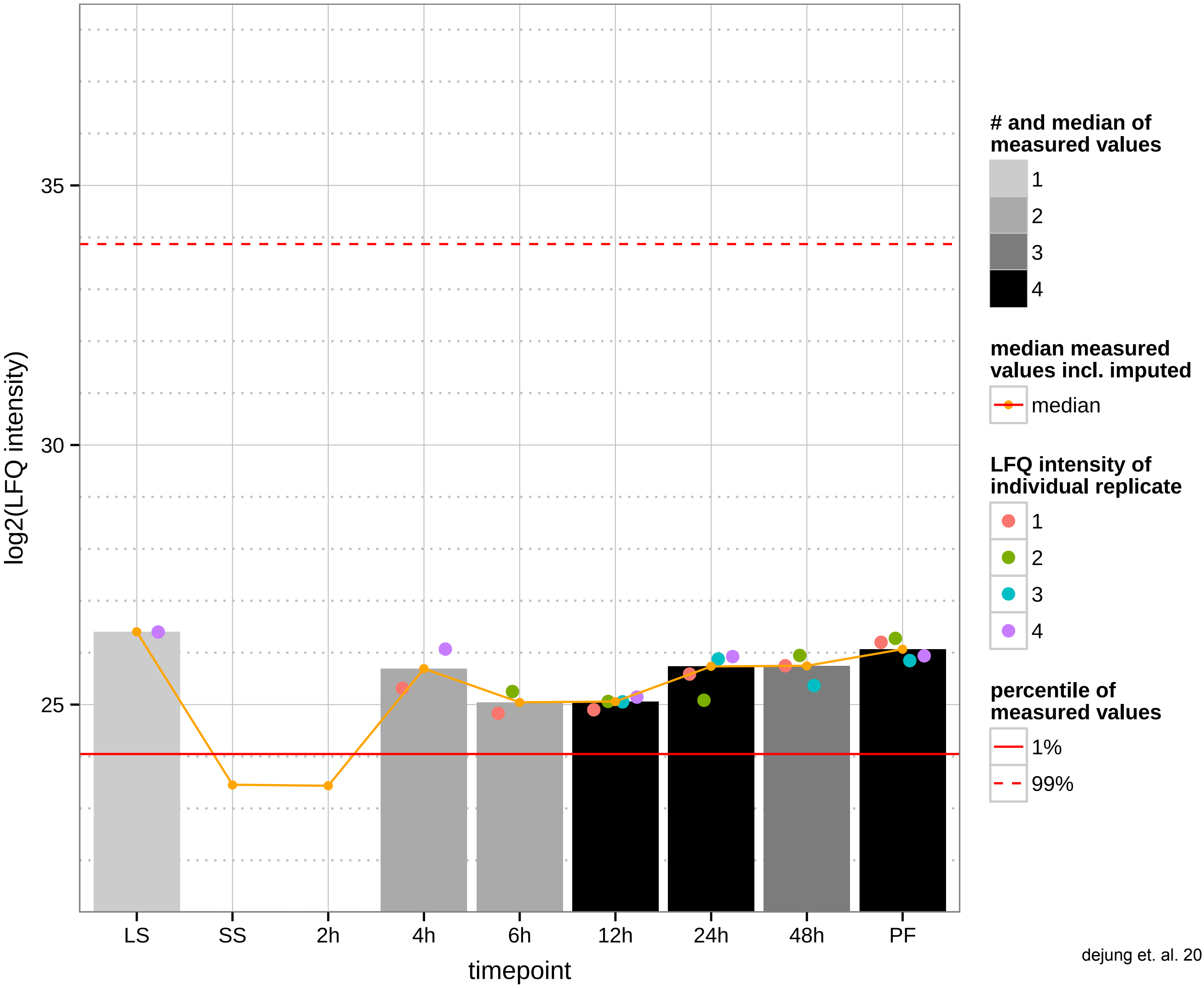
dual specificity protein phosphatase, putative, phosphoserine/threonine/tyrosine−binding protein
Tb927.10.1620;Tb11.v5.0643
AGOF: null, protein tyrosine/serine/threonine phosphatase activity
AGOC: null
AGOP: null, protein dephosphorylation
PGOF: phosphatase activity, protein tyrosine/serine/threonine phosphatase activity
PGOC: null
PGOP: dephosphorylation, protein dephosphorylation





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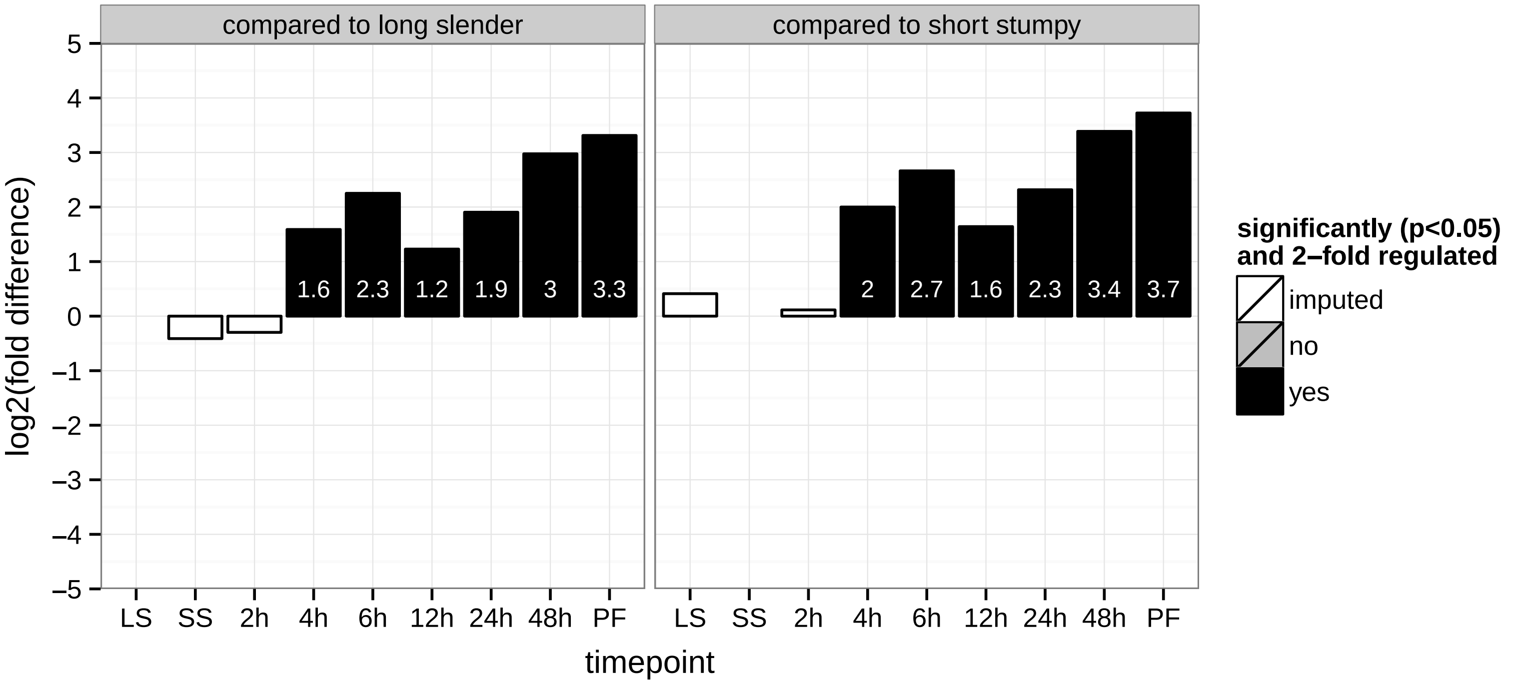
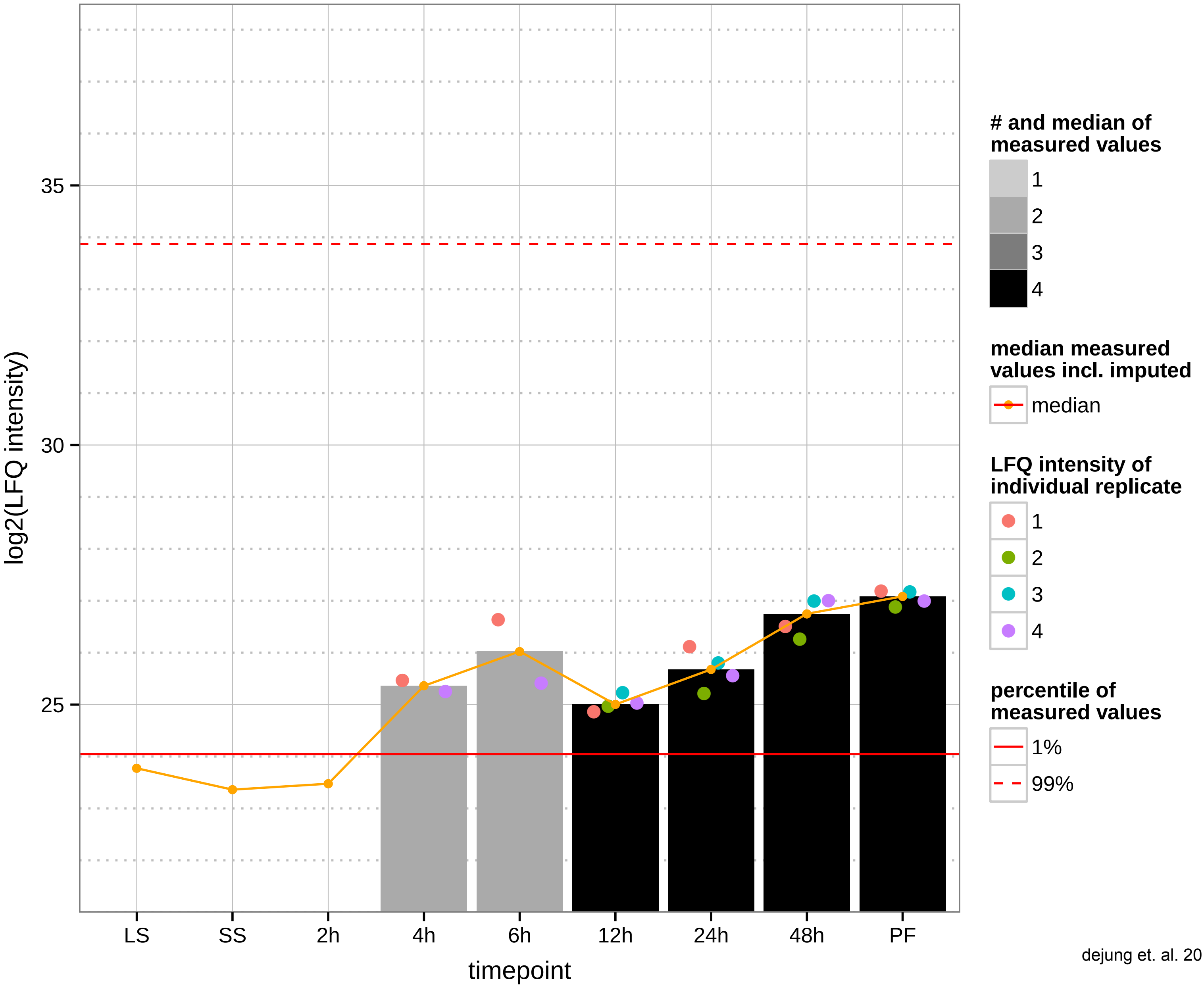
malate dehydrogenase–related
Tb927.10.2550
AGOF: L–malate dehydrogenase activity
AGOC: mitochondrion
AGOP: glycolysis, malate metabolic process, oxidation–reduction process
PGOF: catalytic activity, oxidoreductase activity, acting on the CH–OH group of donors, NAD or NADP as acceptor
PGOC: null
PGOP: carbohydrate metabolic process, cellular carbohydrate metabolic process, oxidation–reduction process





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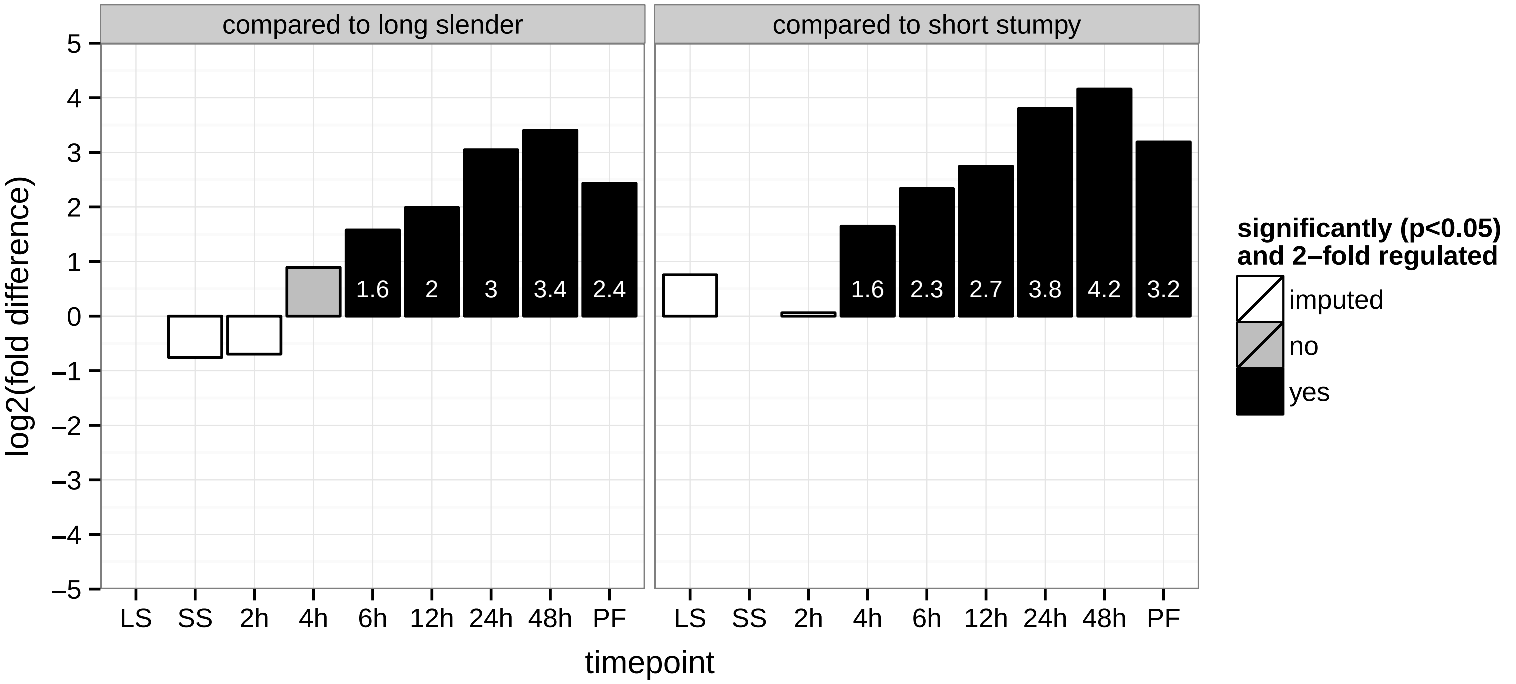
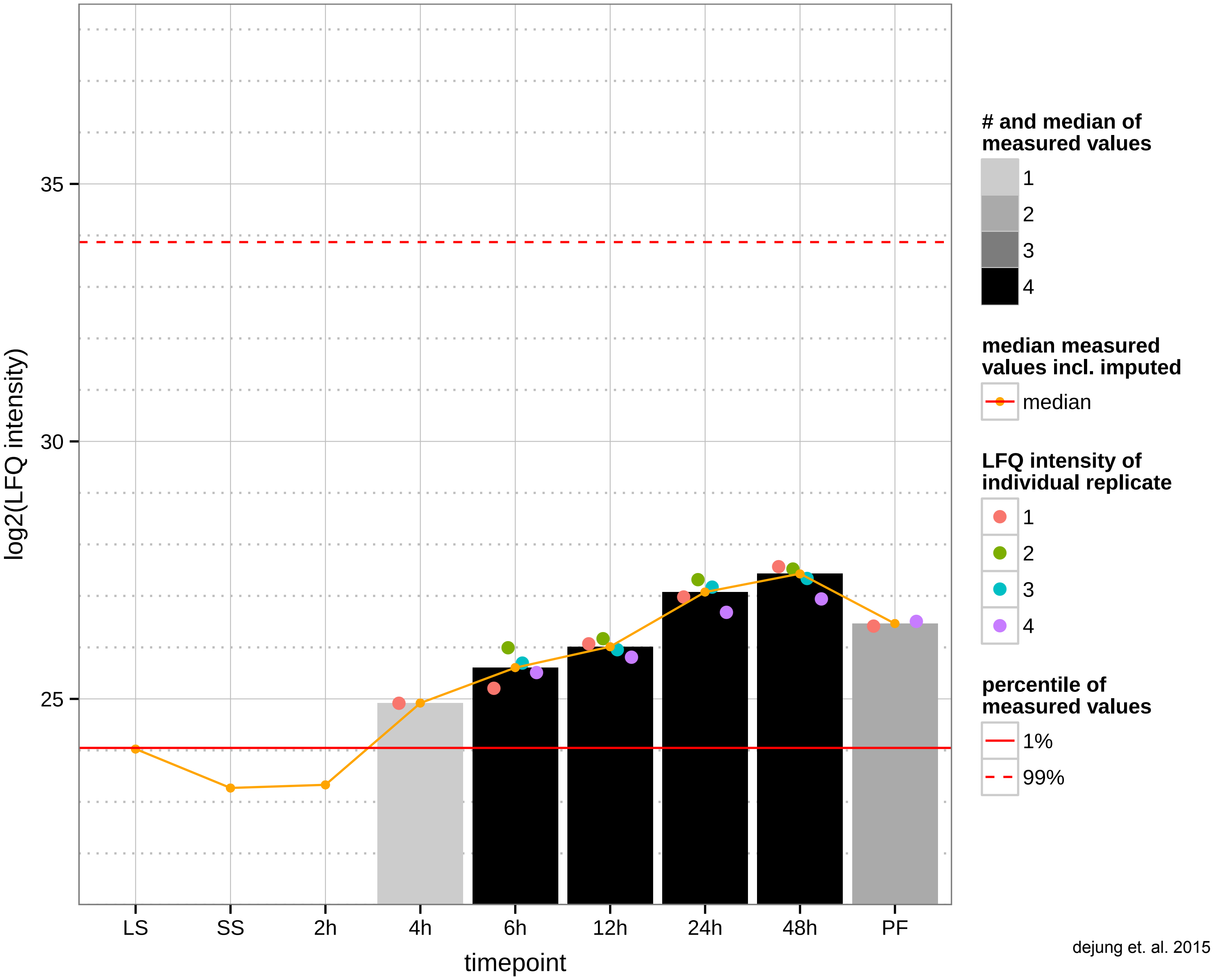
NDUFA5/B13 subunit, putative
Tb927.10.4130
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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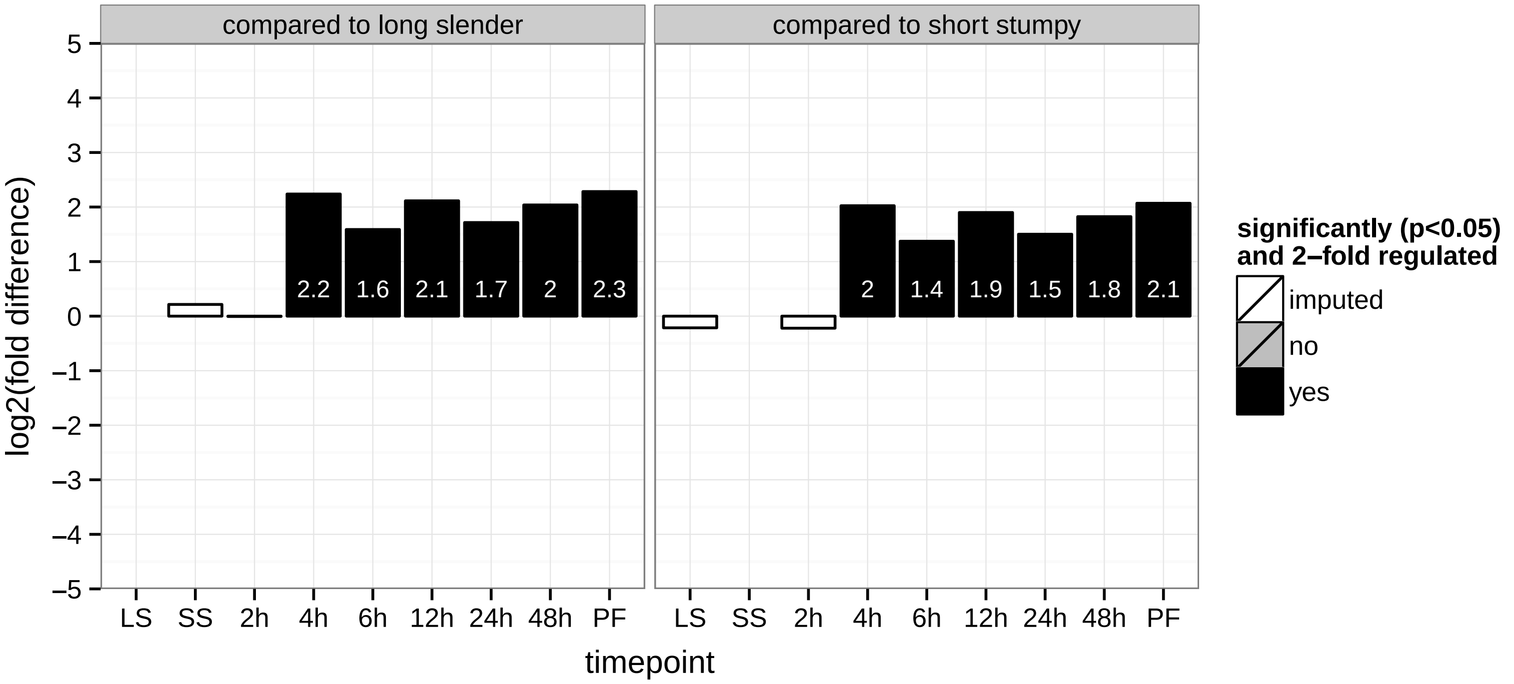
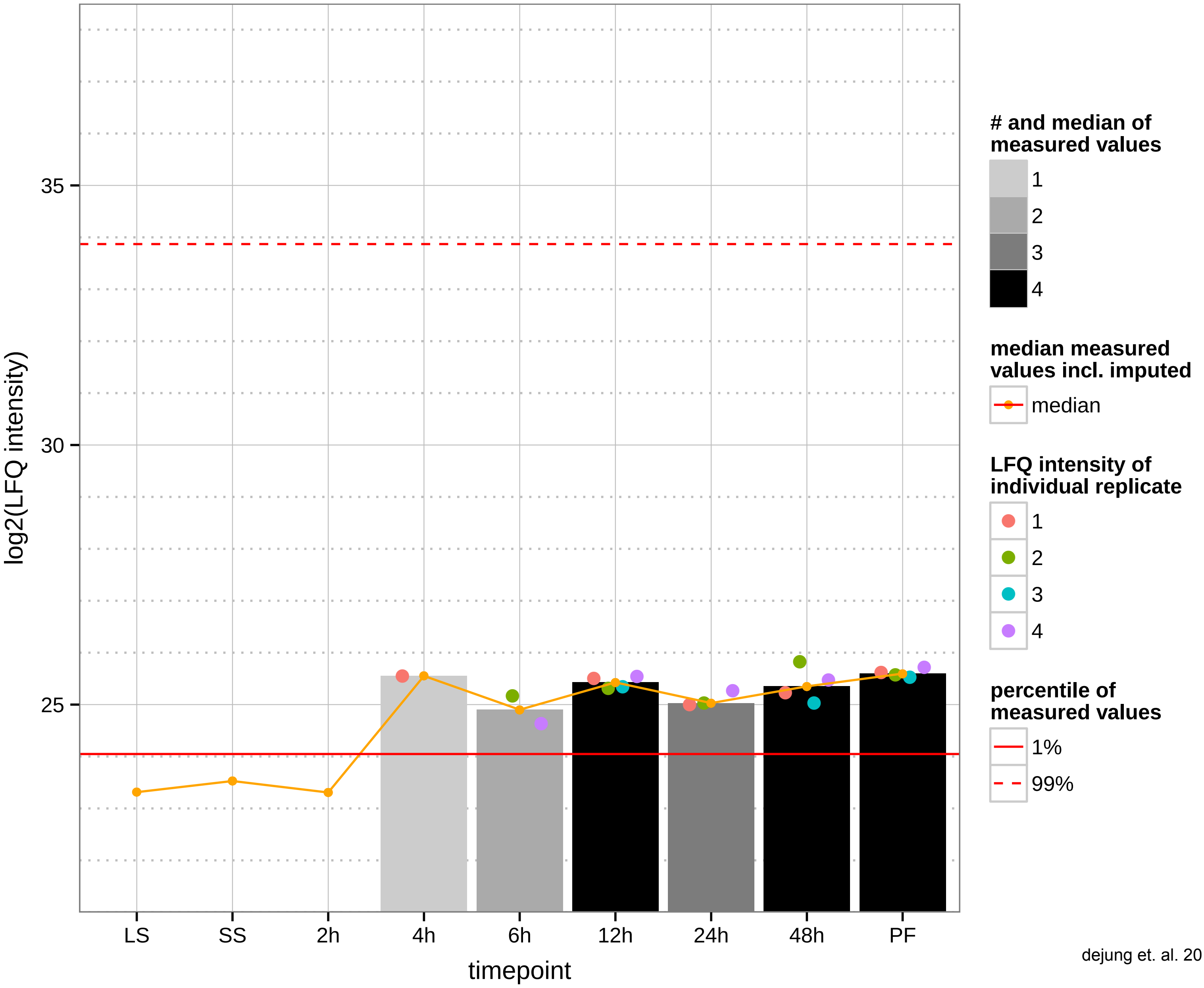
protein phosphatase 2C, putative
Tb927.10.5590
AGOF: catalytic activity, phosphatase activity
AGOC: mitochondrion
AGOP: dephosphorylation
PGOF: catalytic activity
PGOC: null
PGOP: null





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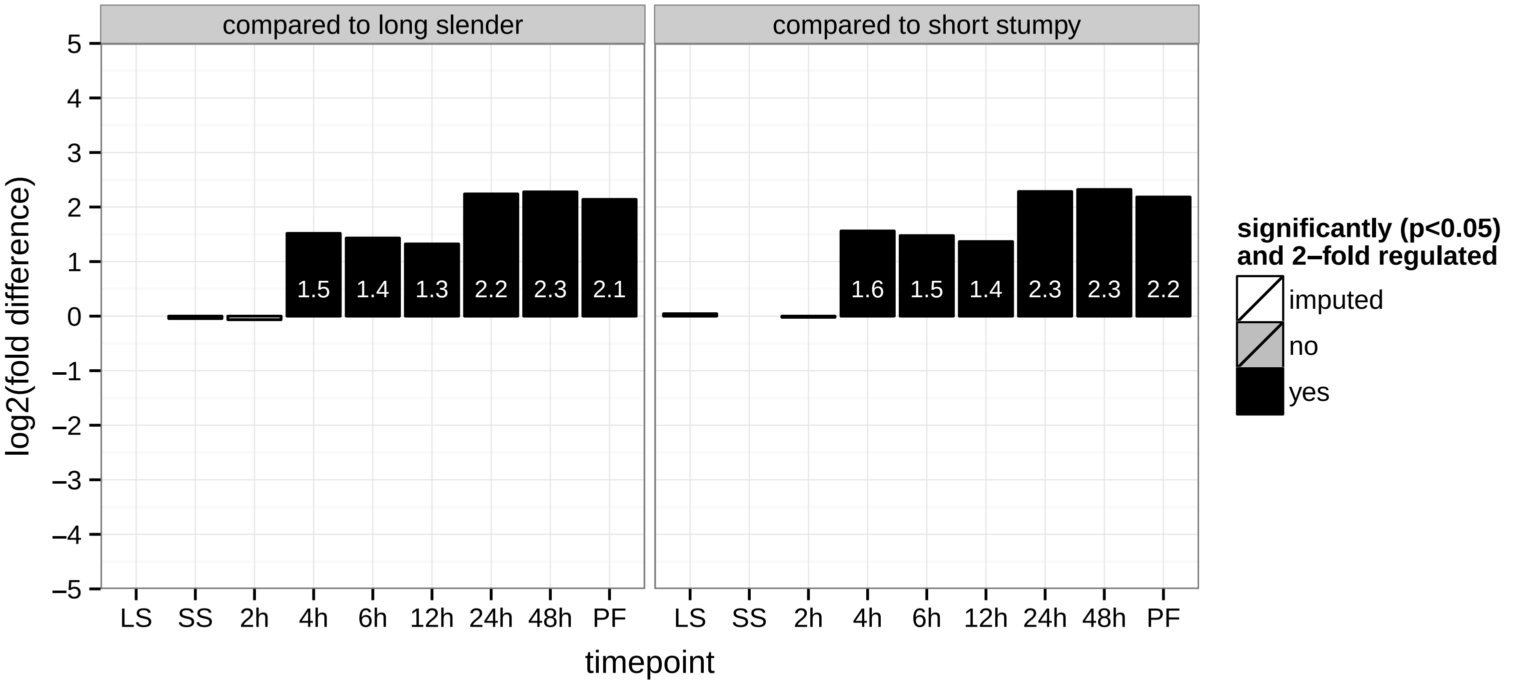
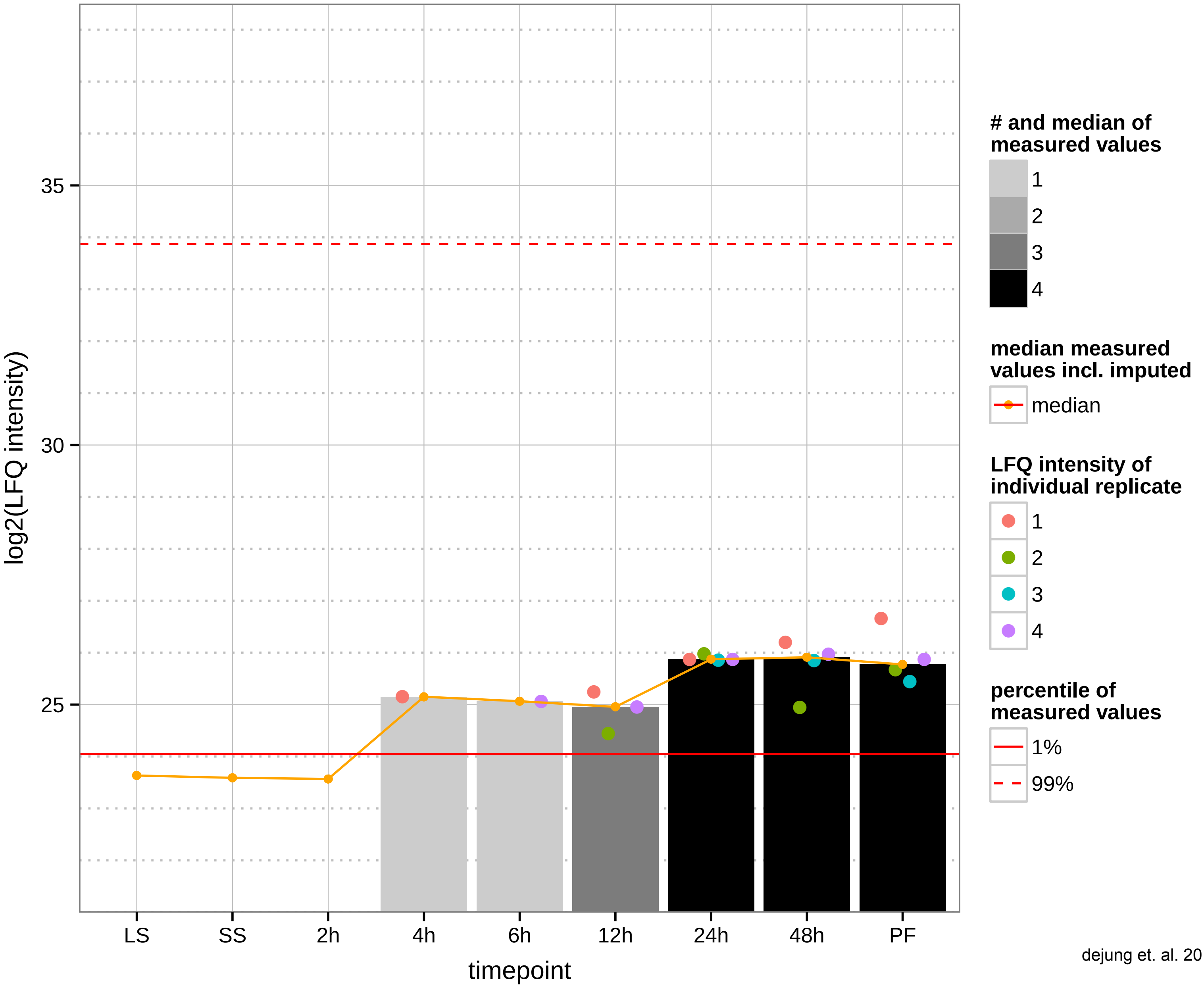
mitochondrial RNA binding complex 1 subunit, mitochondrial edited mRNA stability factor 1 subunit, kinteoplast poly(A) polym
Tb927.10.6850
AGOF: RNA binding, structural constituent of ribosome
AGOC: intracellular, mitochondrion, ribosome
AGOP: RNA polyadenylation, mRNA stabilization, translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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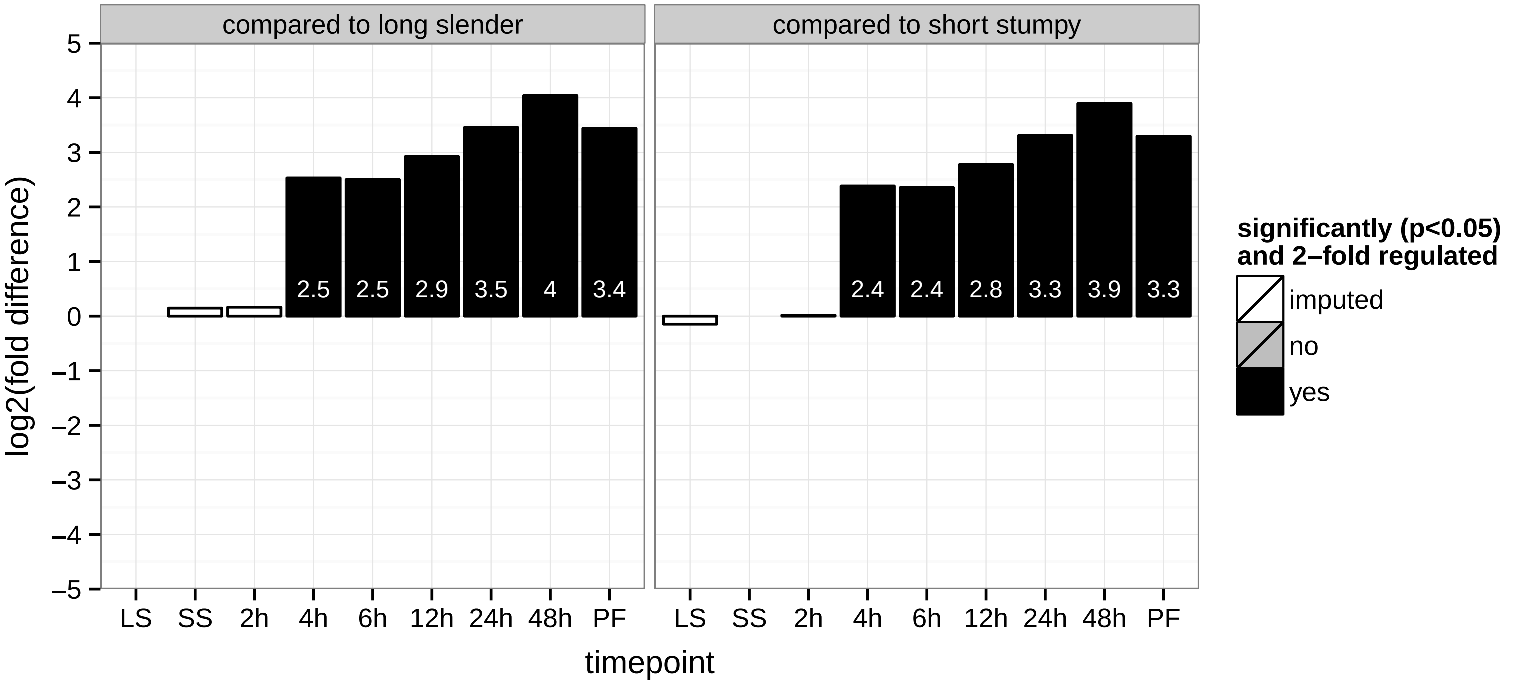
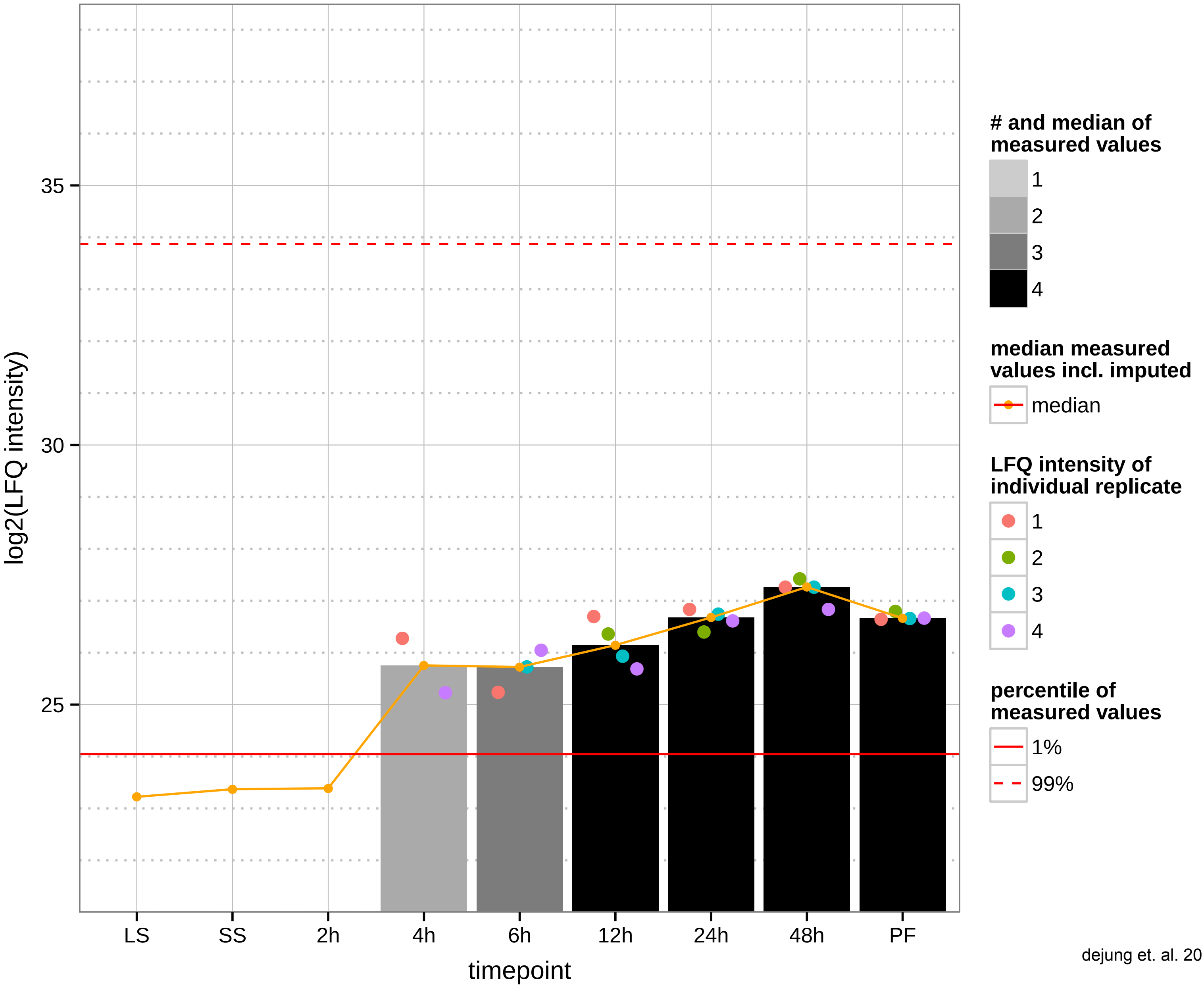
mitochondrial ATP−dependent zinc metallopeptidase, putative, metallo−peptidase, Clan MA(E) Family M41
Tb927.10.7620
AGOF: ATP binding, metalloendopeptidase activity, nucleoside−triphosphatase activity, unfolded protein binding
AGOC: membrane, mitochondrion
AGOP: cell cycle, protein catabolic process, proteolysis
PGOF: ATP binding, metalloendopeptidase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: membrane
PGOP: protein catabolic process, proteolysis





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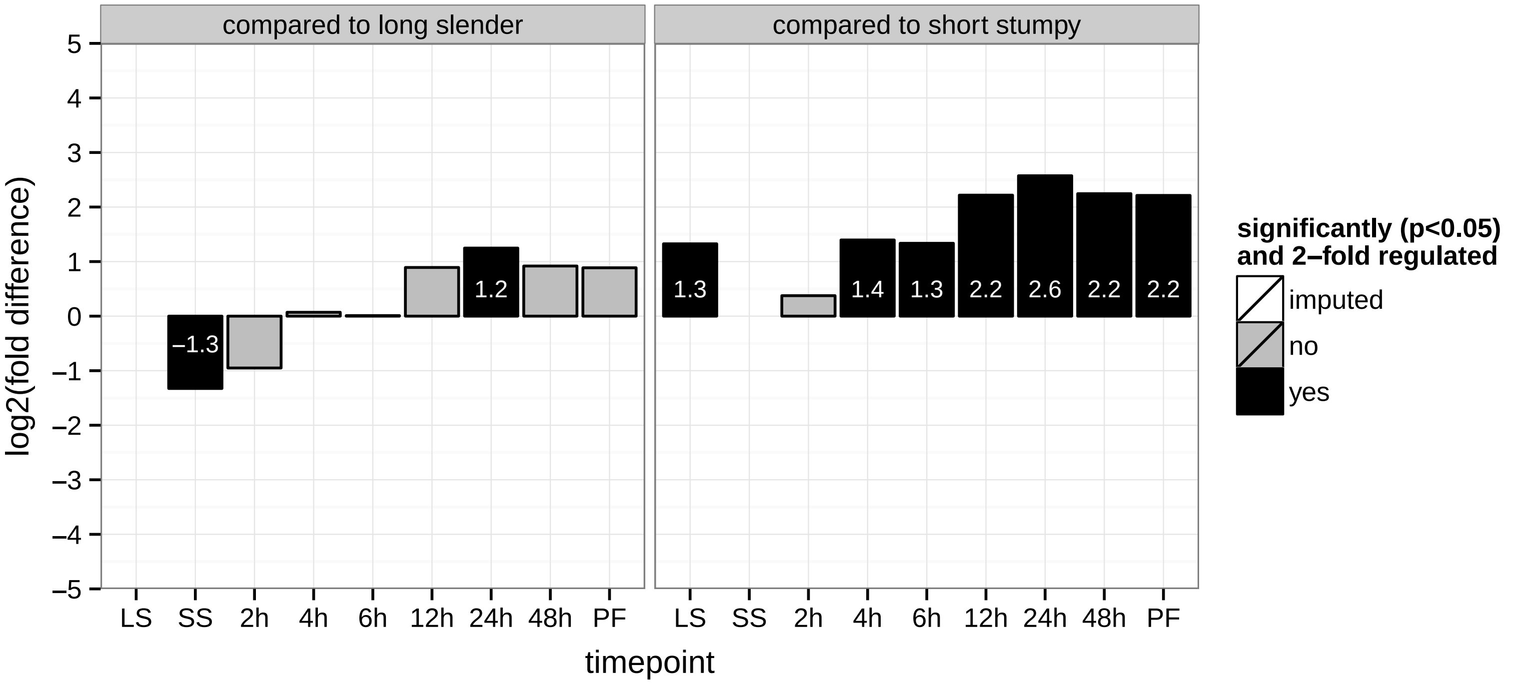
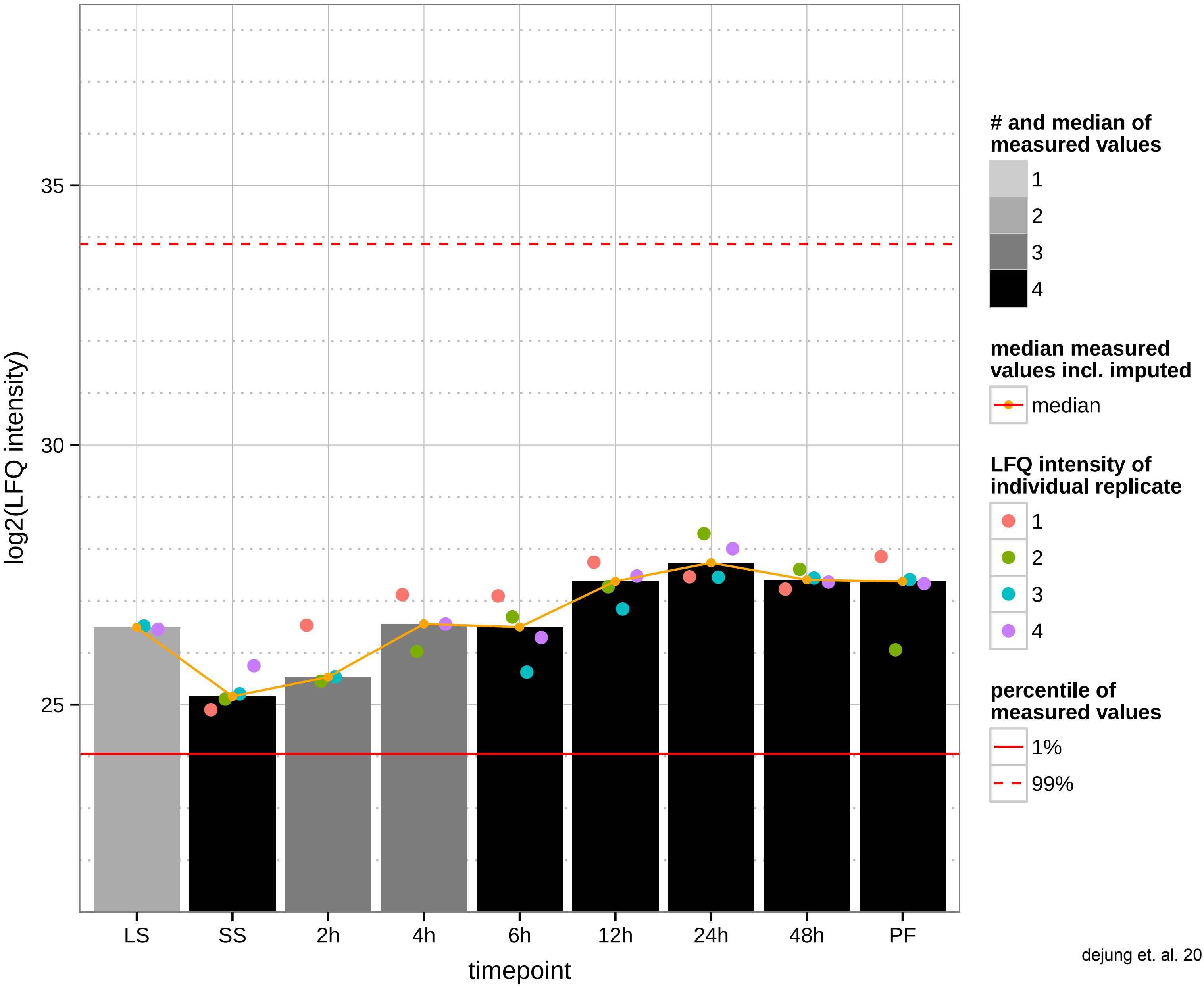
40S ribosomal protein S8, putative
Tb927.10.7710
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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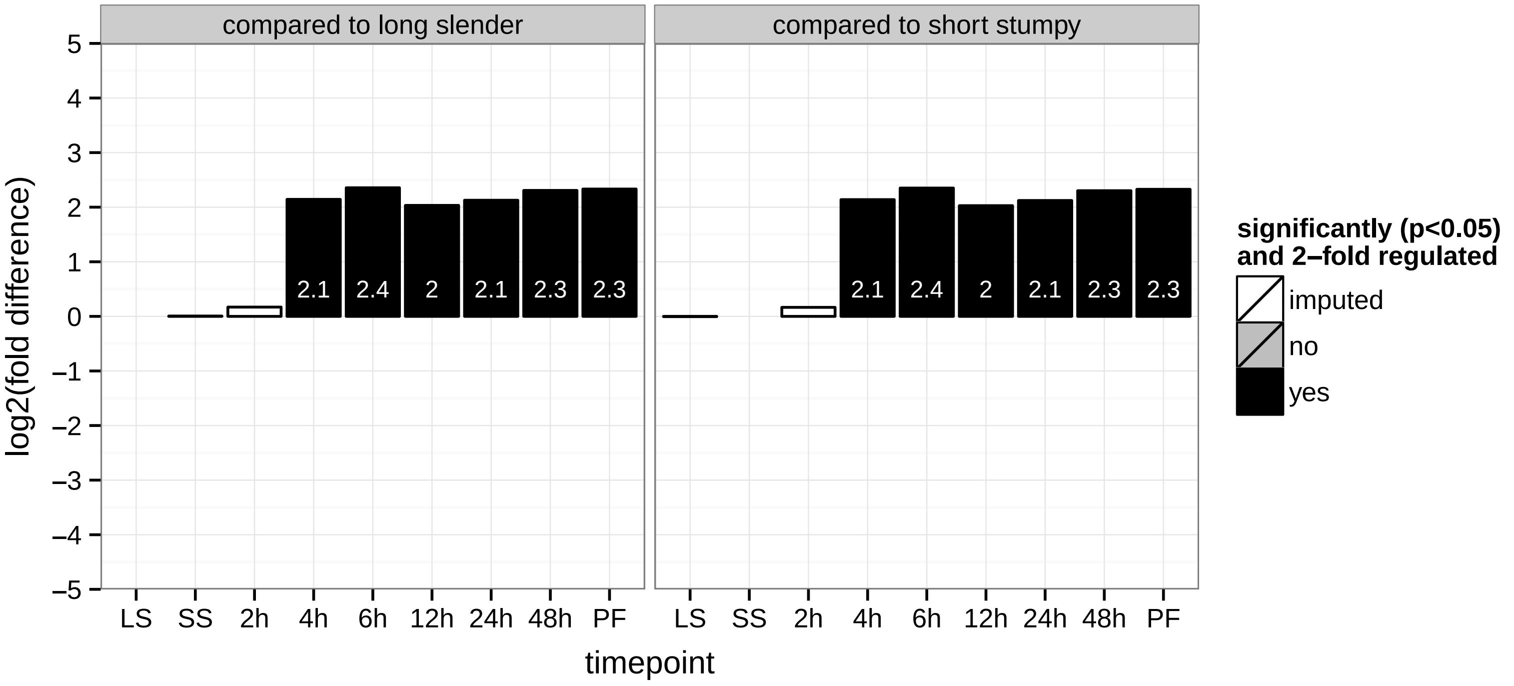
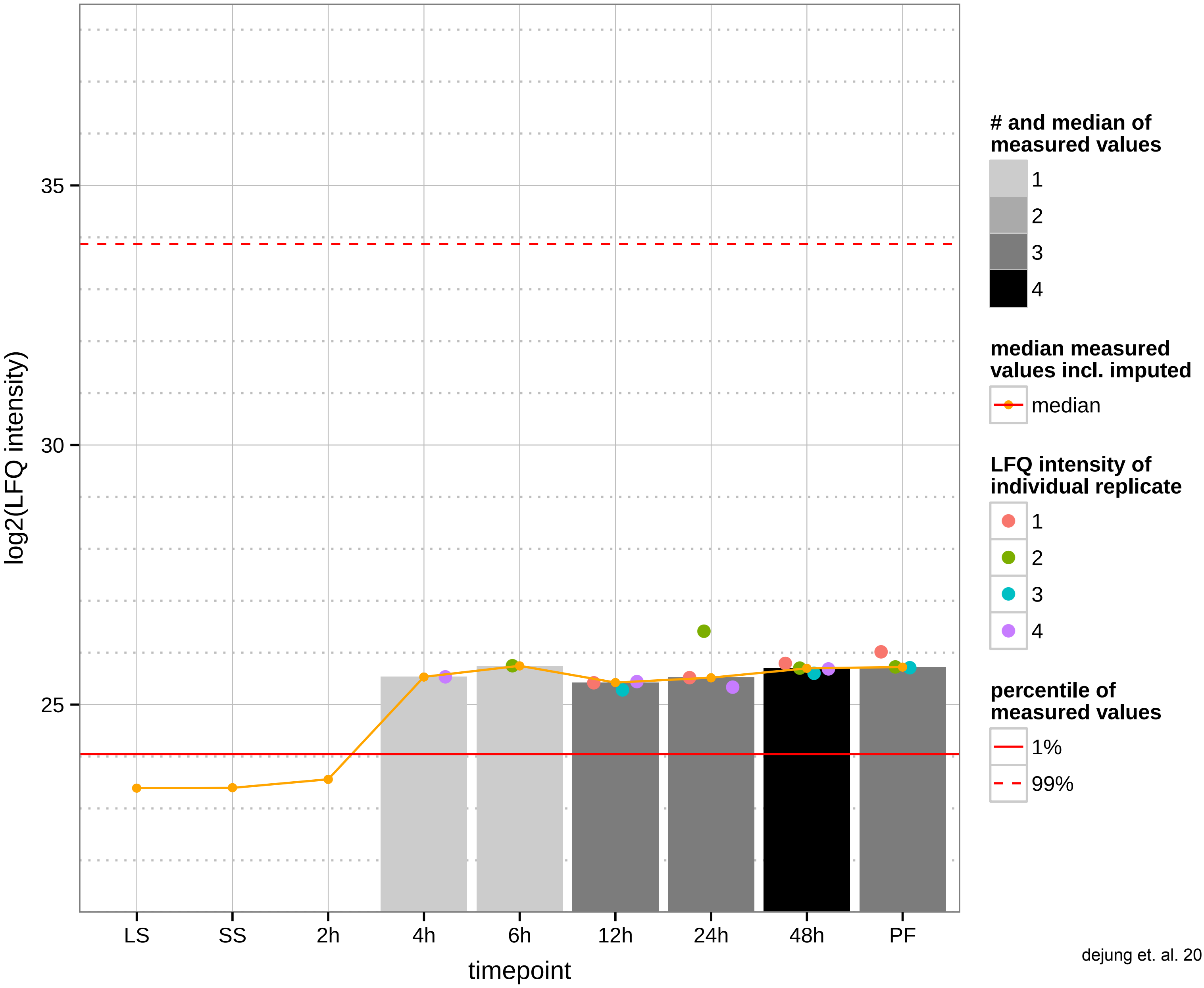
hypothetical protein, conserved
Tb927.11.13710
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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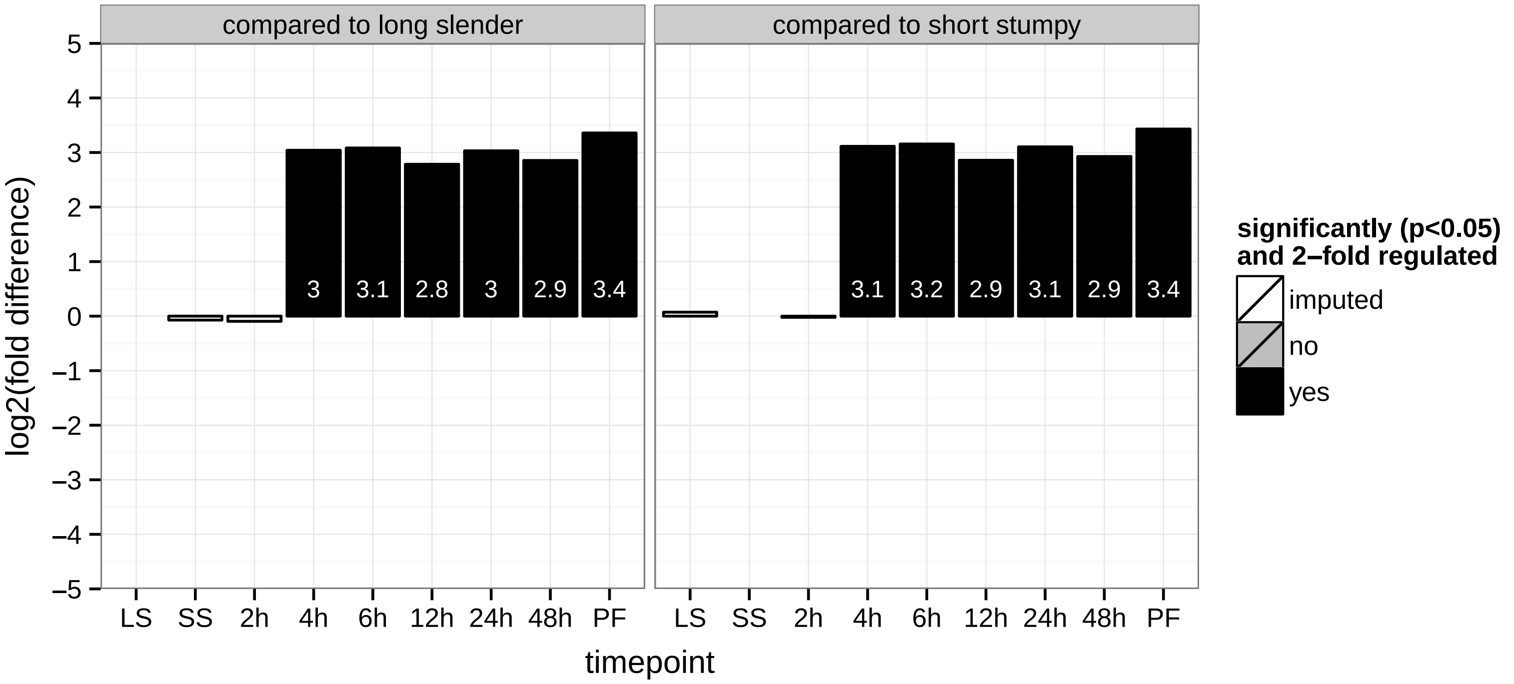
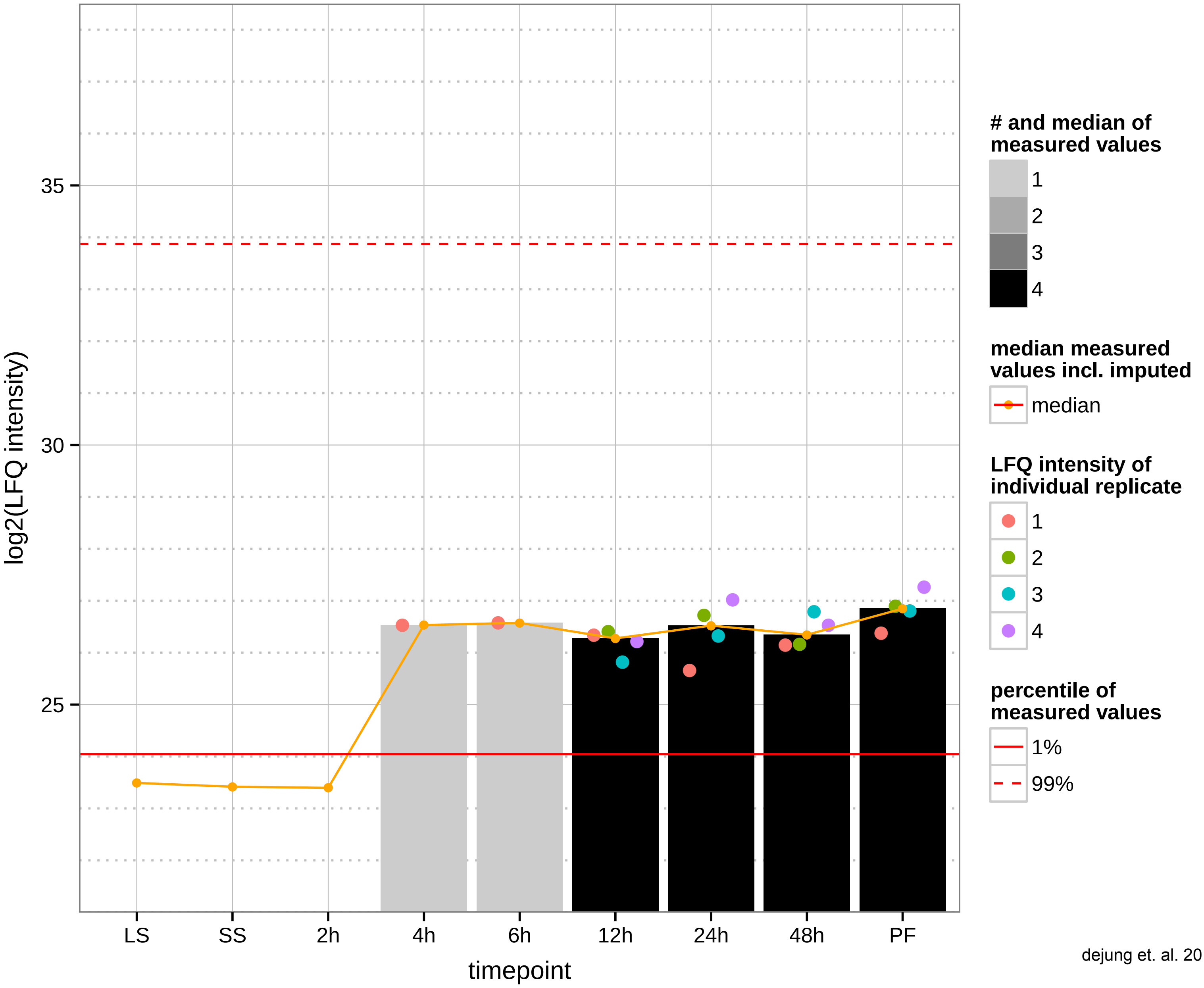
hypothetical protein, conserved
Tb927.11.14390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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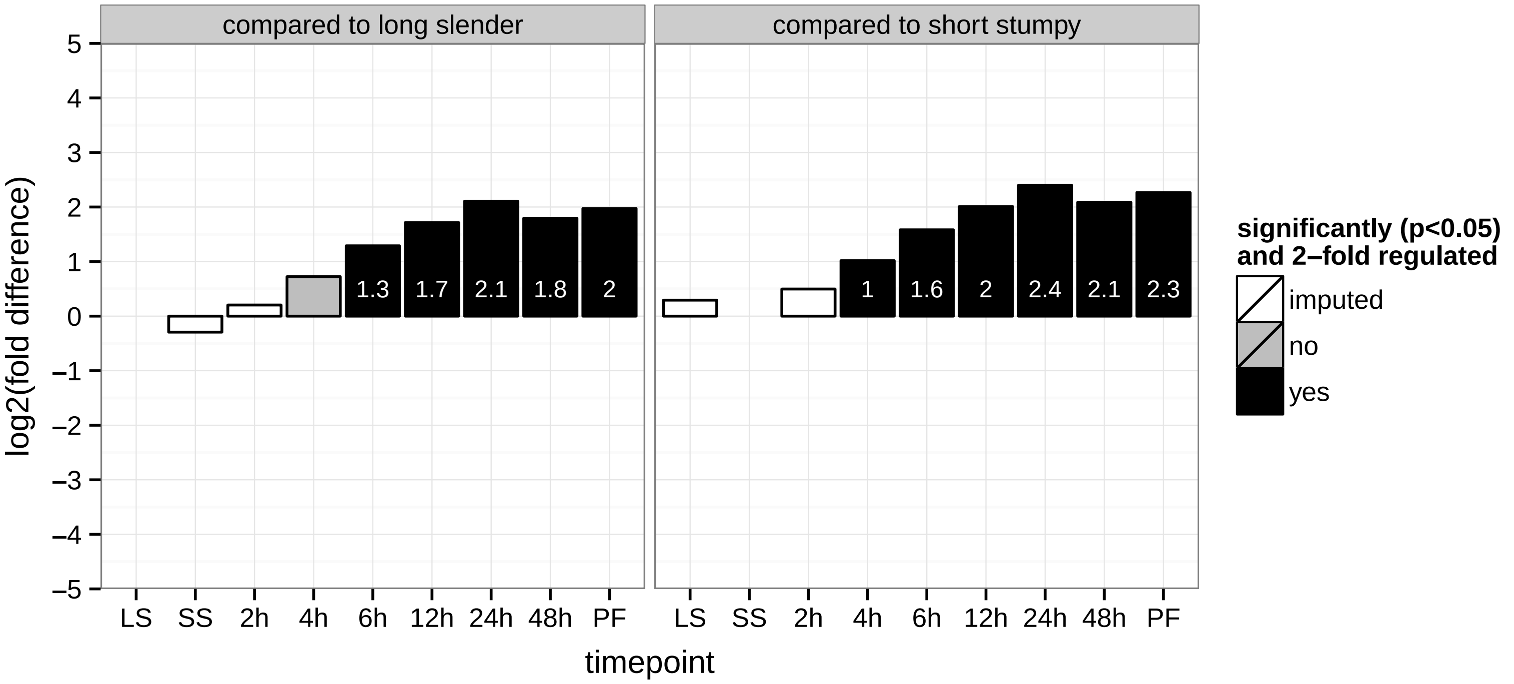
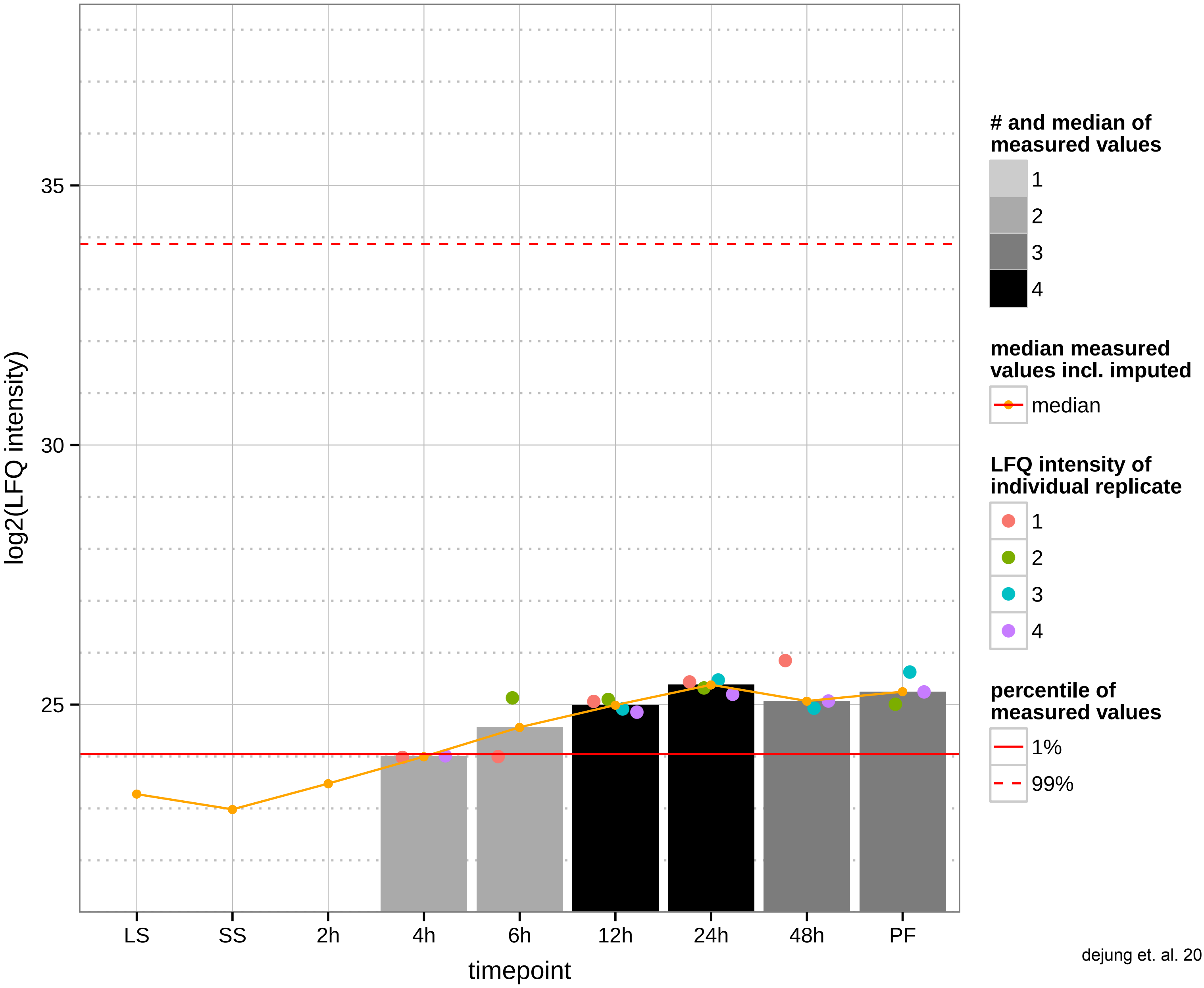
hypothetical protein, conserved
Tb927.11.15590
AGOF: catalytic activity
AGOC: null
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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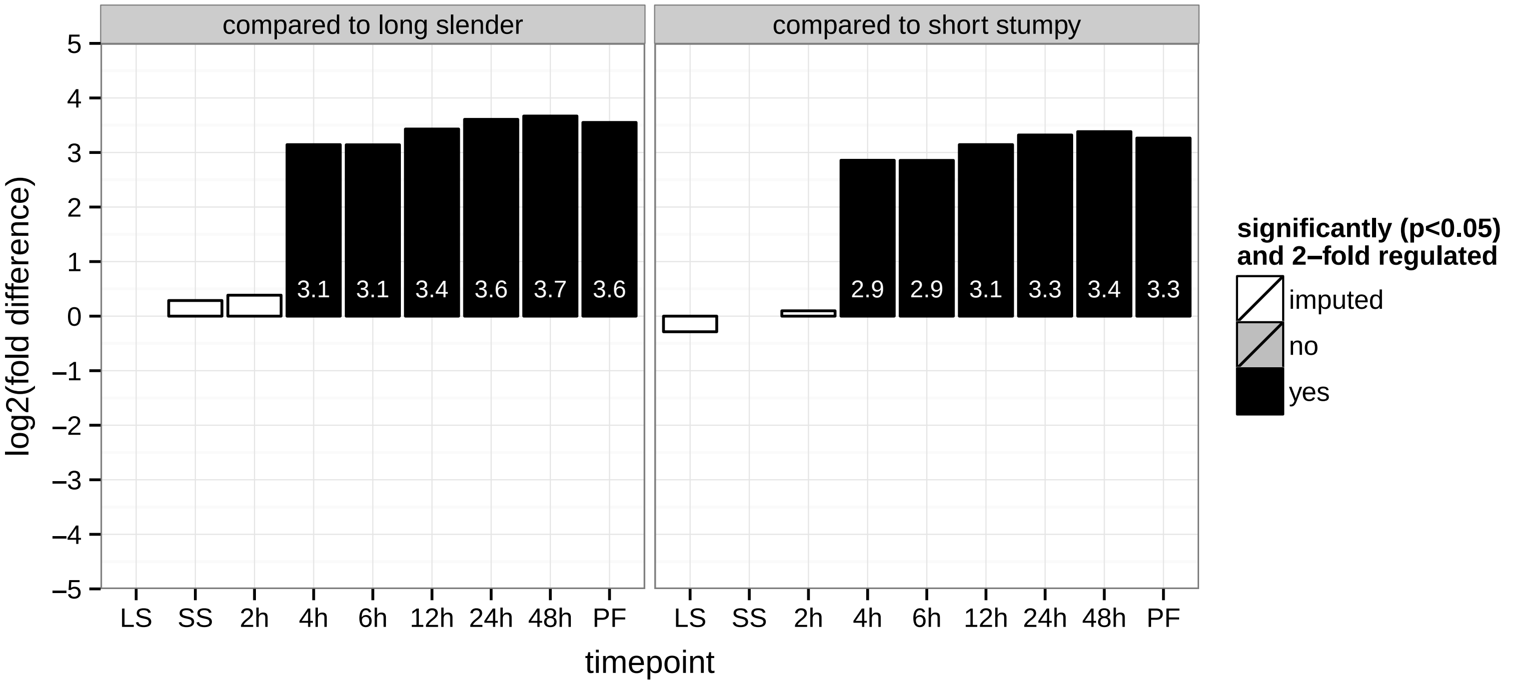
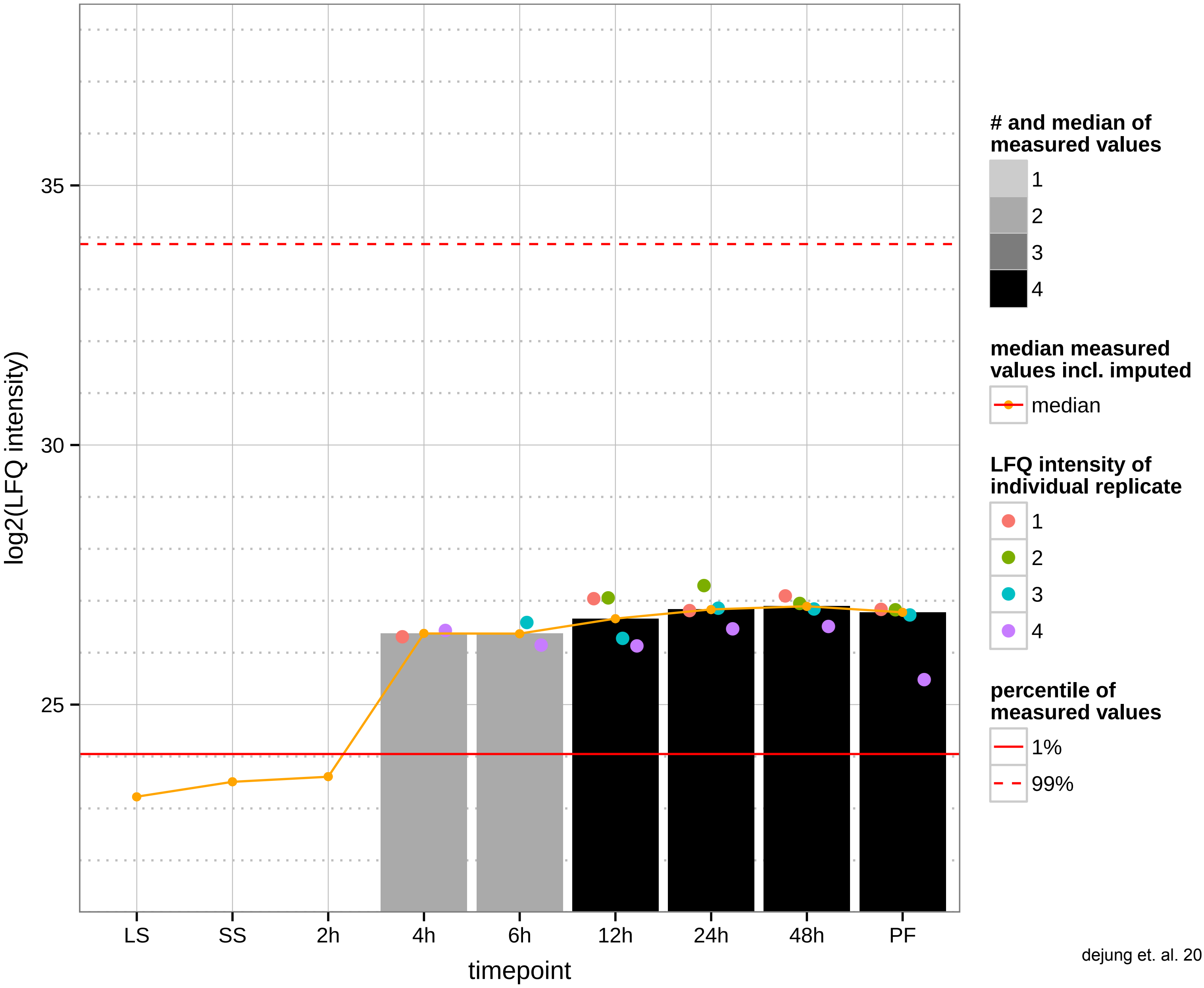
hypothetical protein, conserved
Tb927.11.16750
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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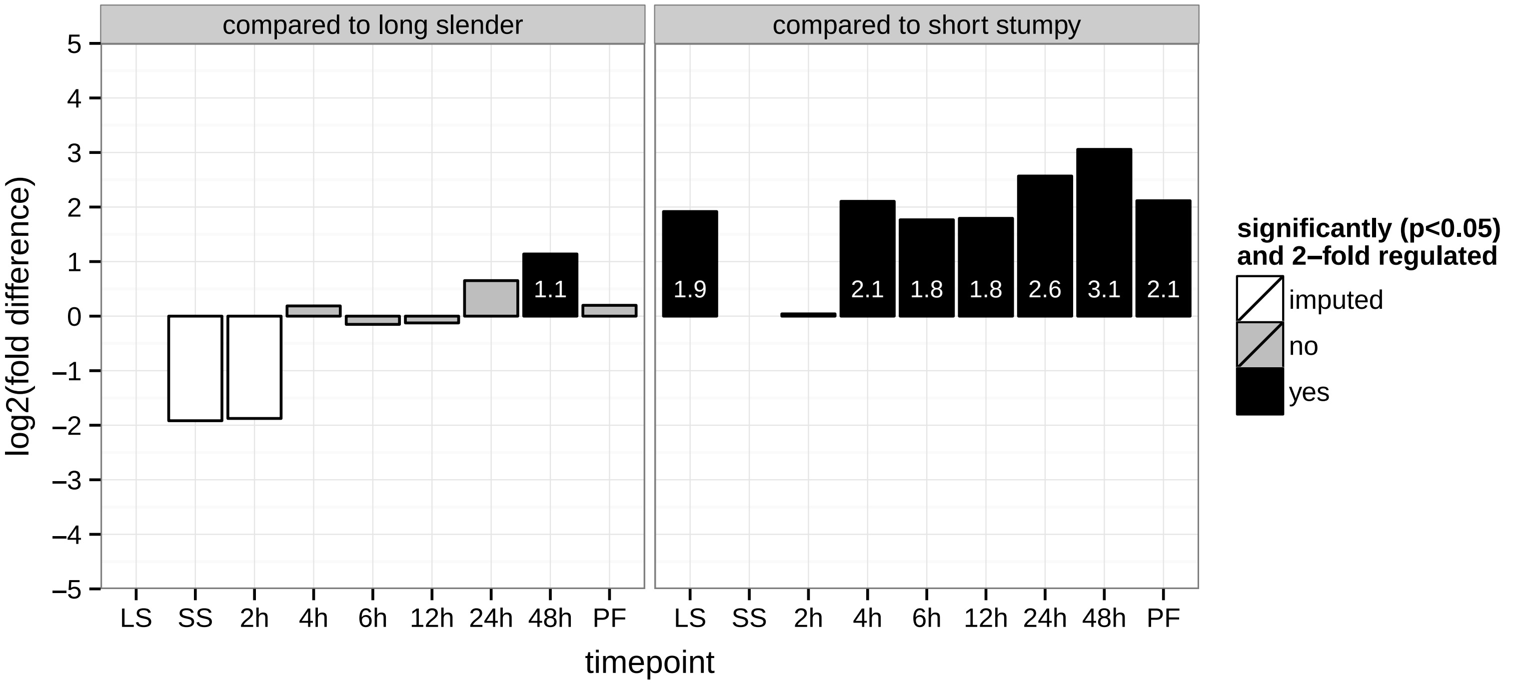
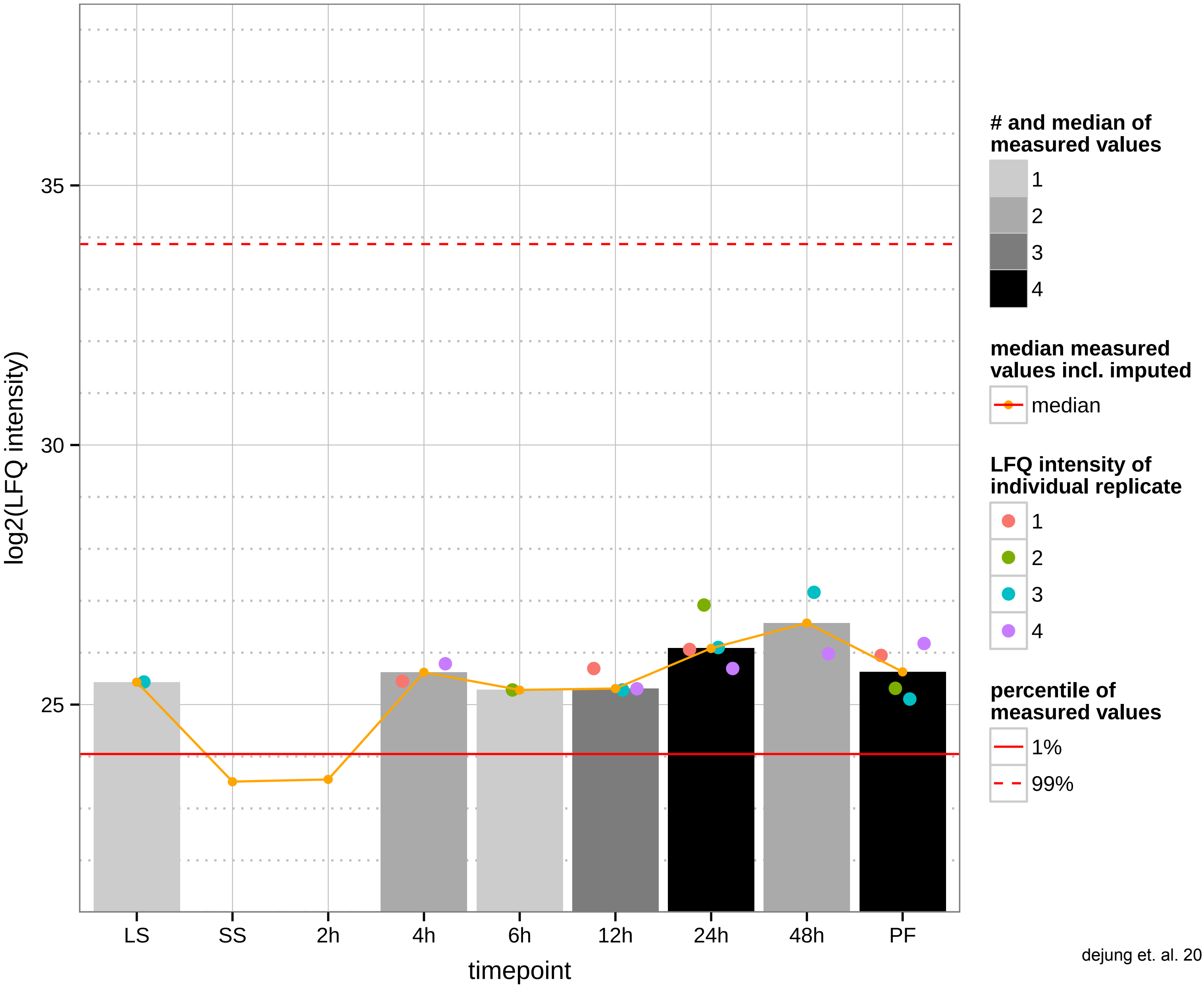
hypothetical protein, conserved
Tb927.11.1720
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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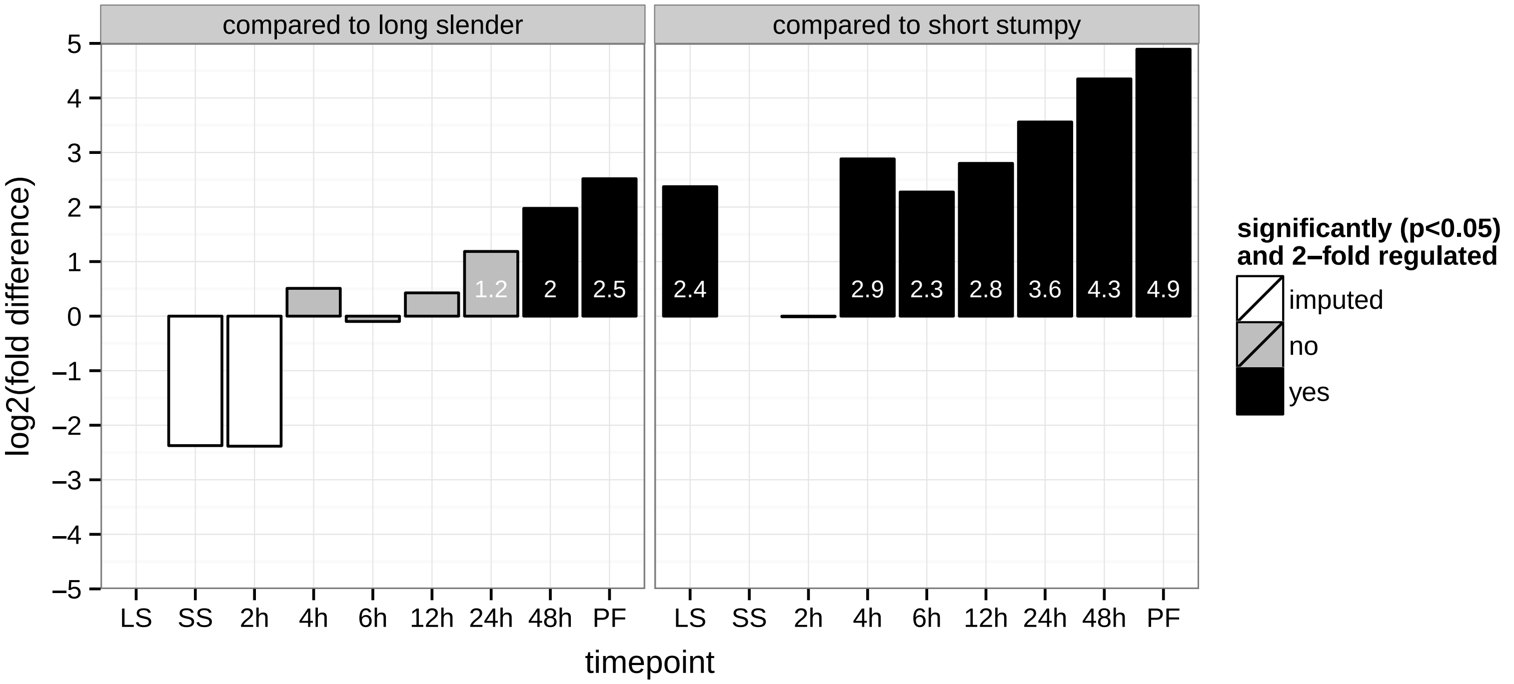
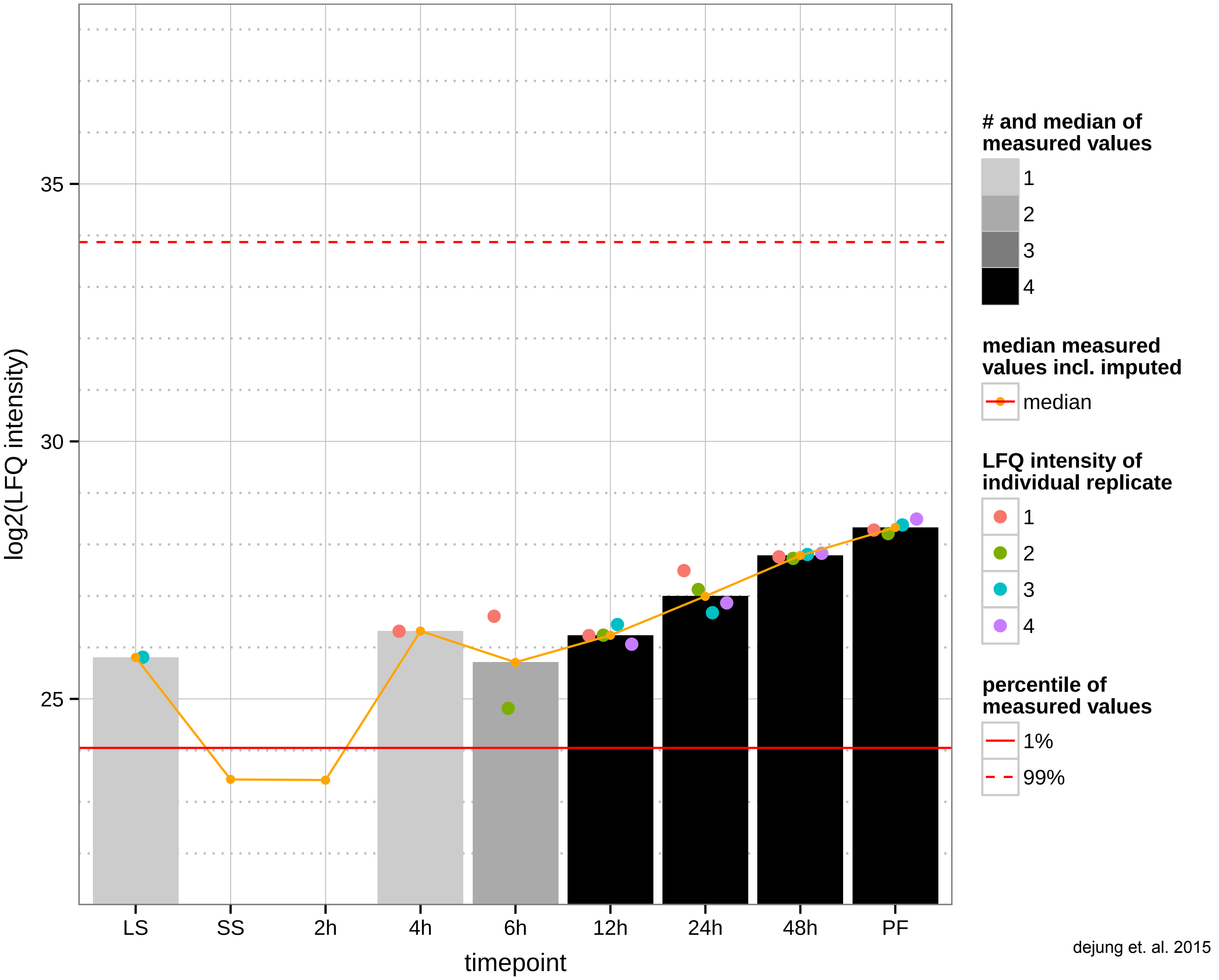
hypothetical protein, conserved
Tb927.11.2420
AGOF: tubulin−tyrosine ligase activity
AGOC: null
AGOP: cellular protein modification process
PGOF: tubulin−tyrosine ligase activity
PGOC: null
PGOP: cellular protein modification process





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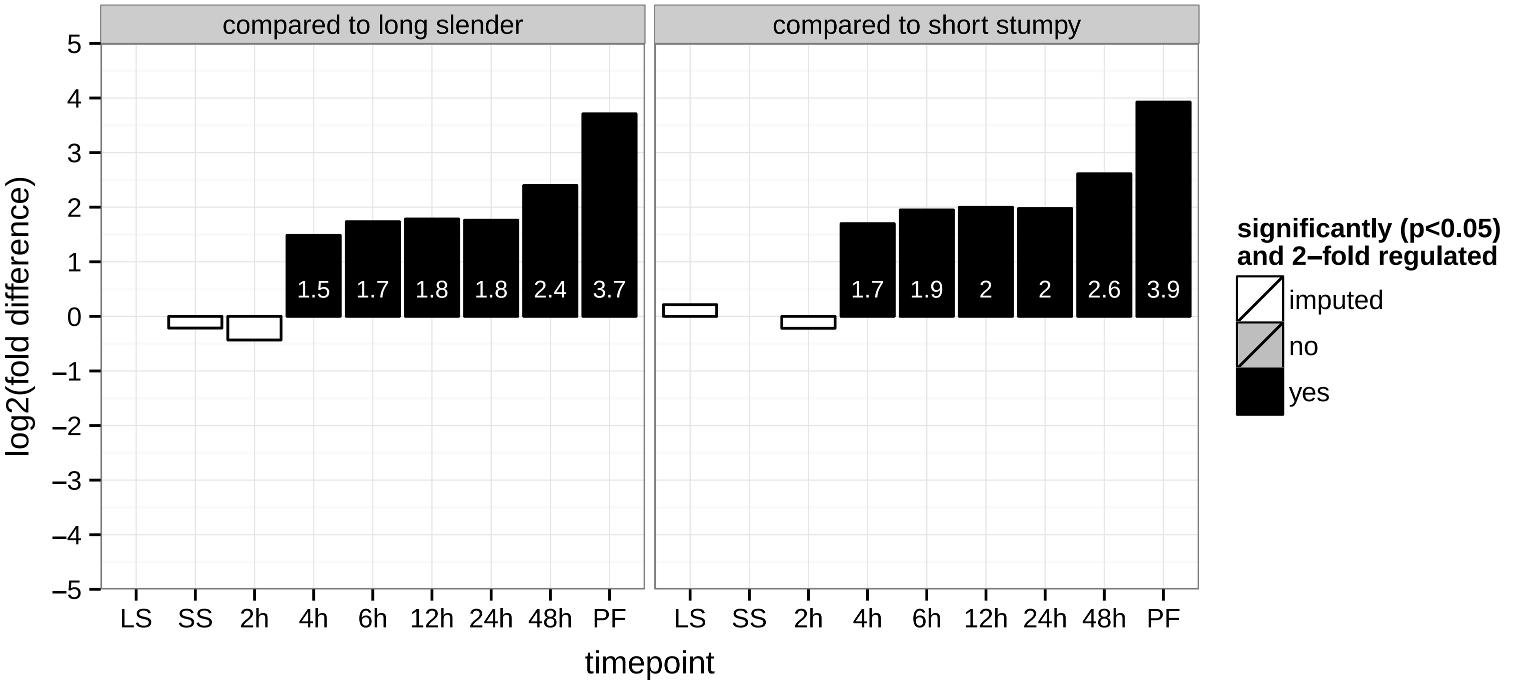
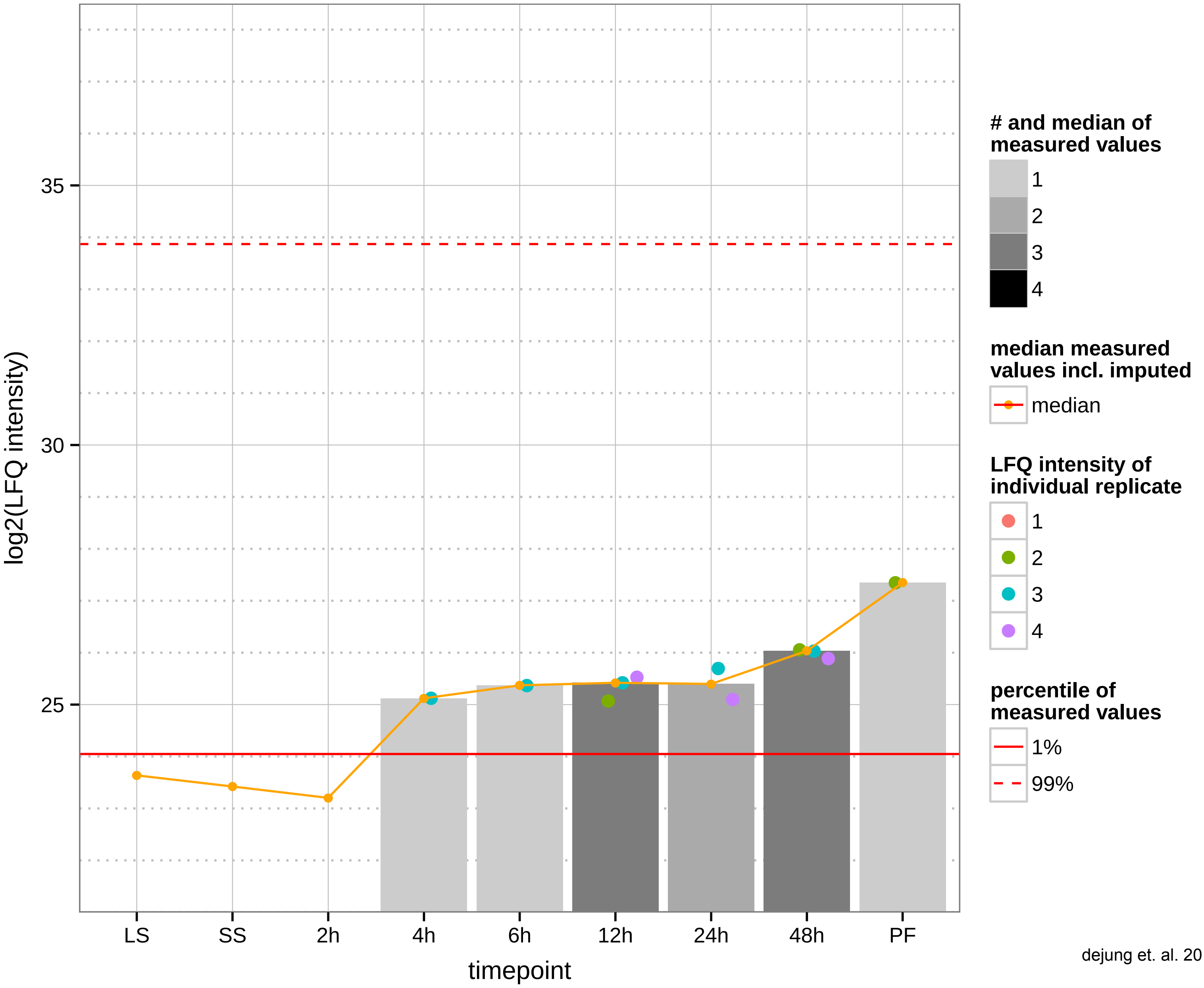
hypothetical protein, conserved
Tb927.11.3100
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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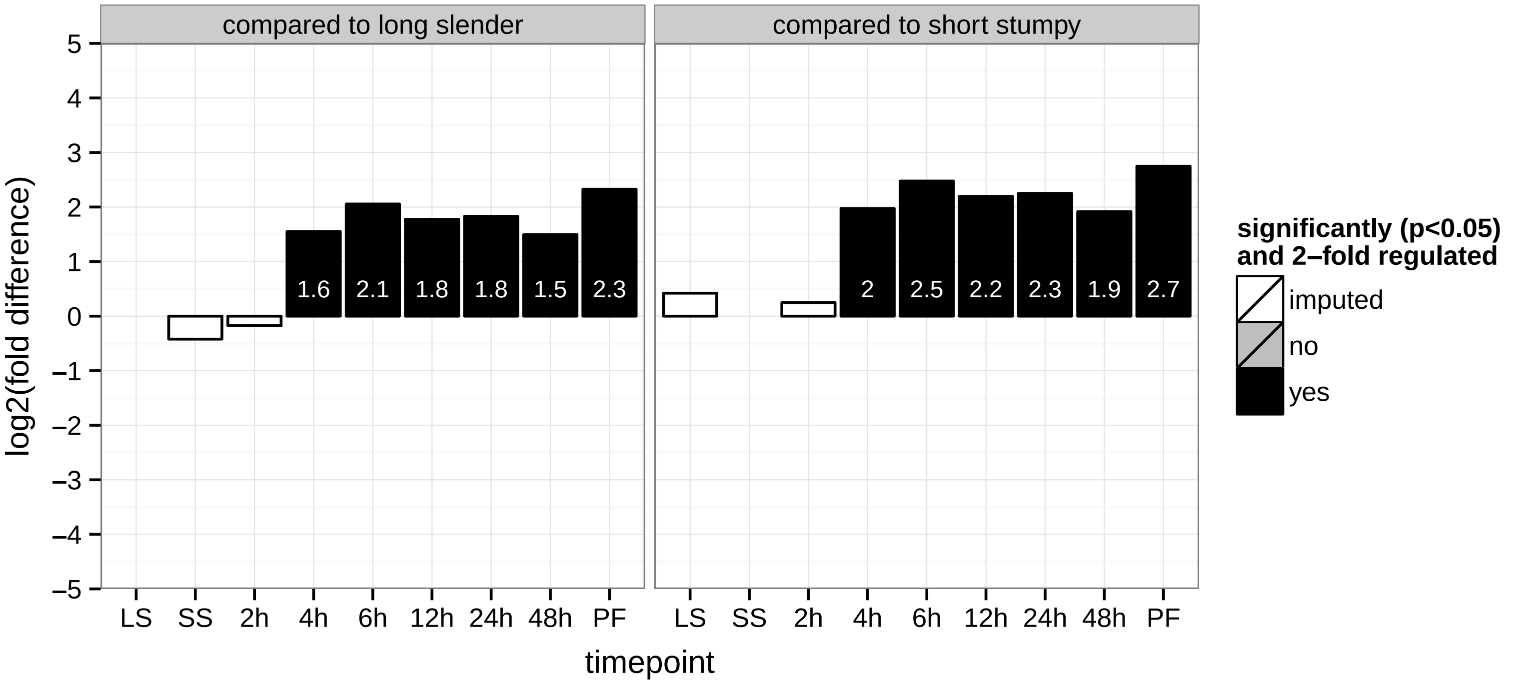
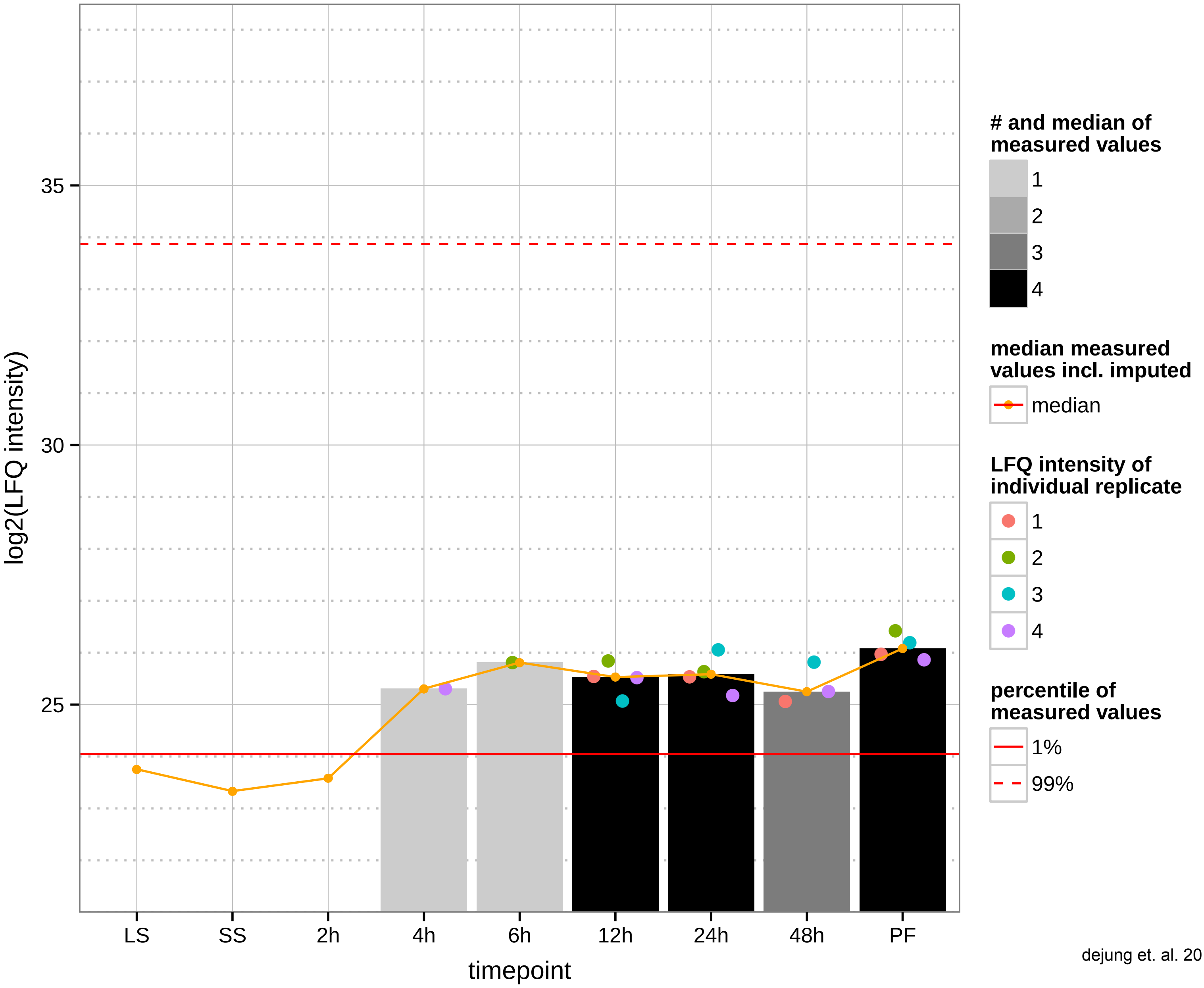
RNA–binding protein, putative (RBP34)
Tb927.11.3340
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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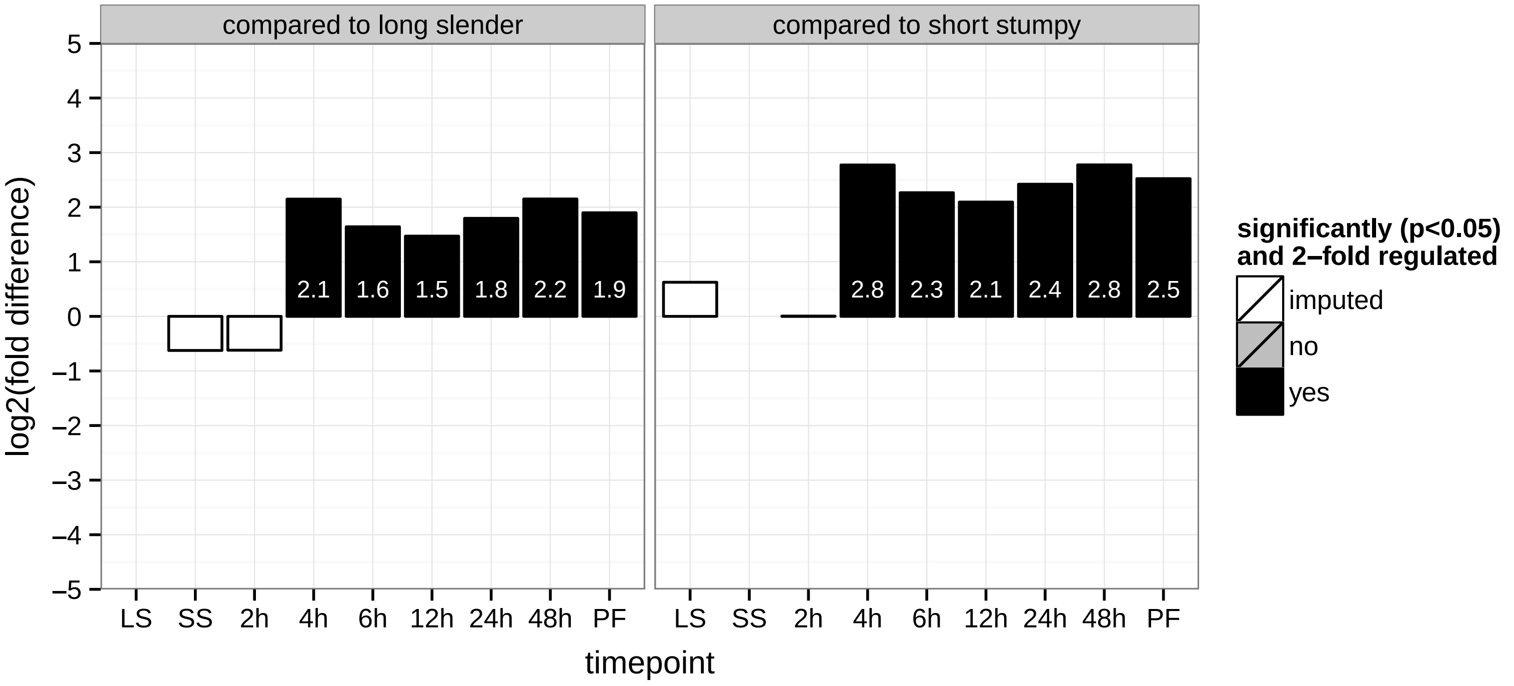
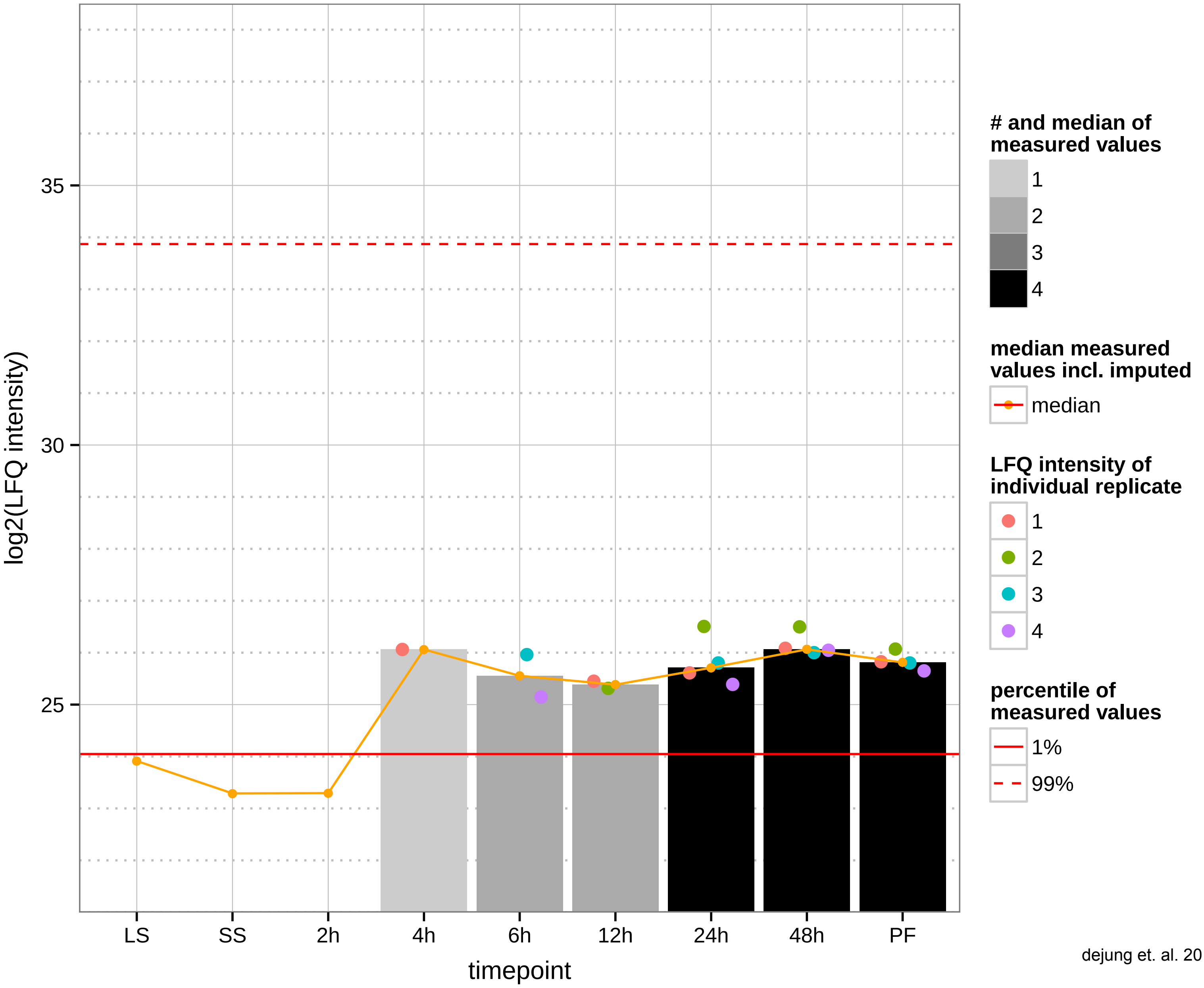
hypothetical protein, conserved
Tb927.11.3640
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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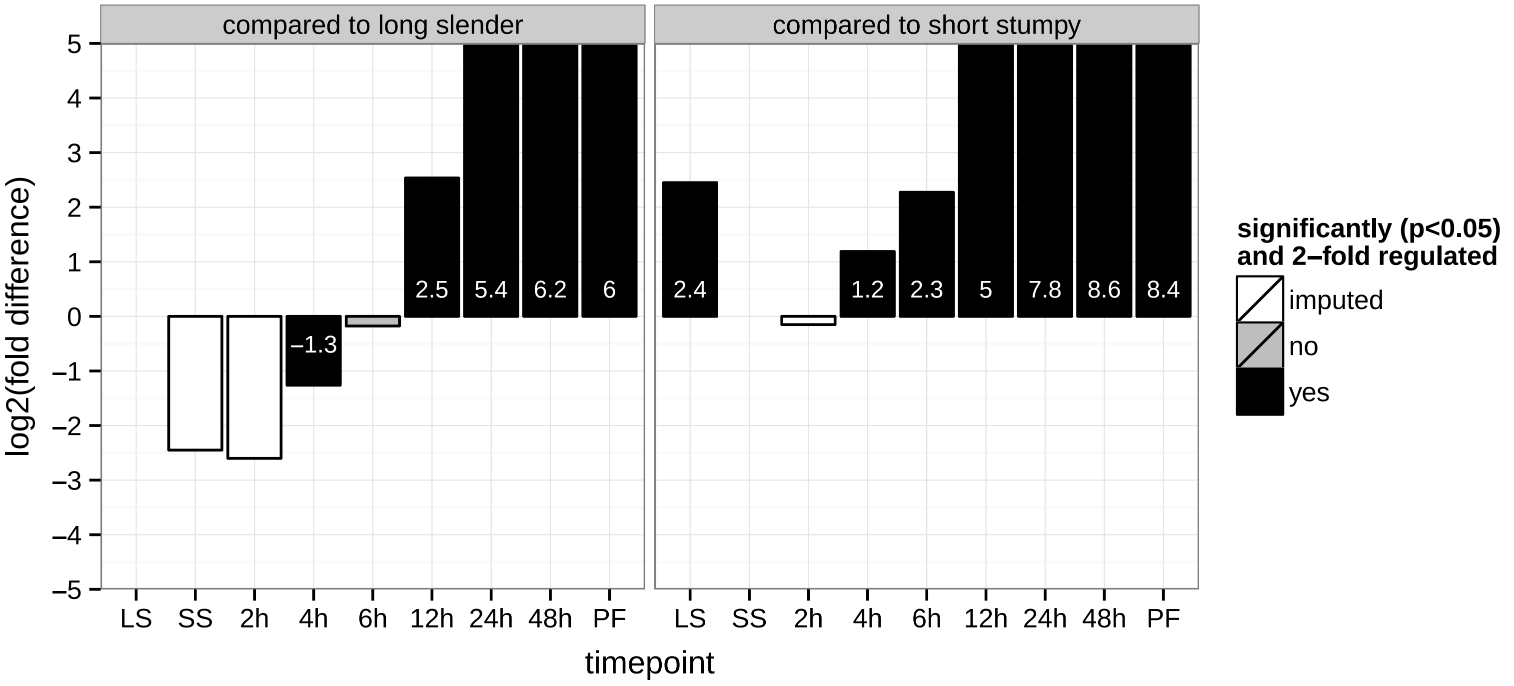
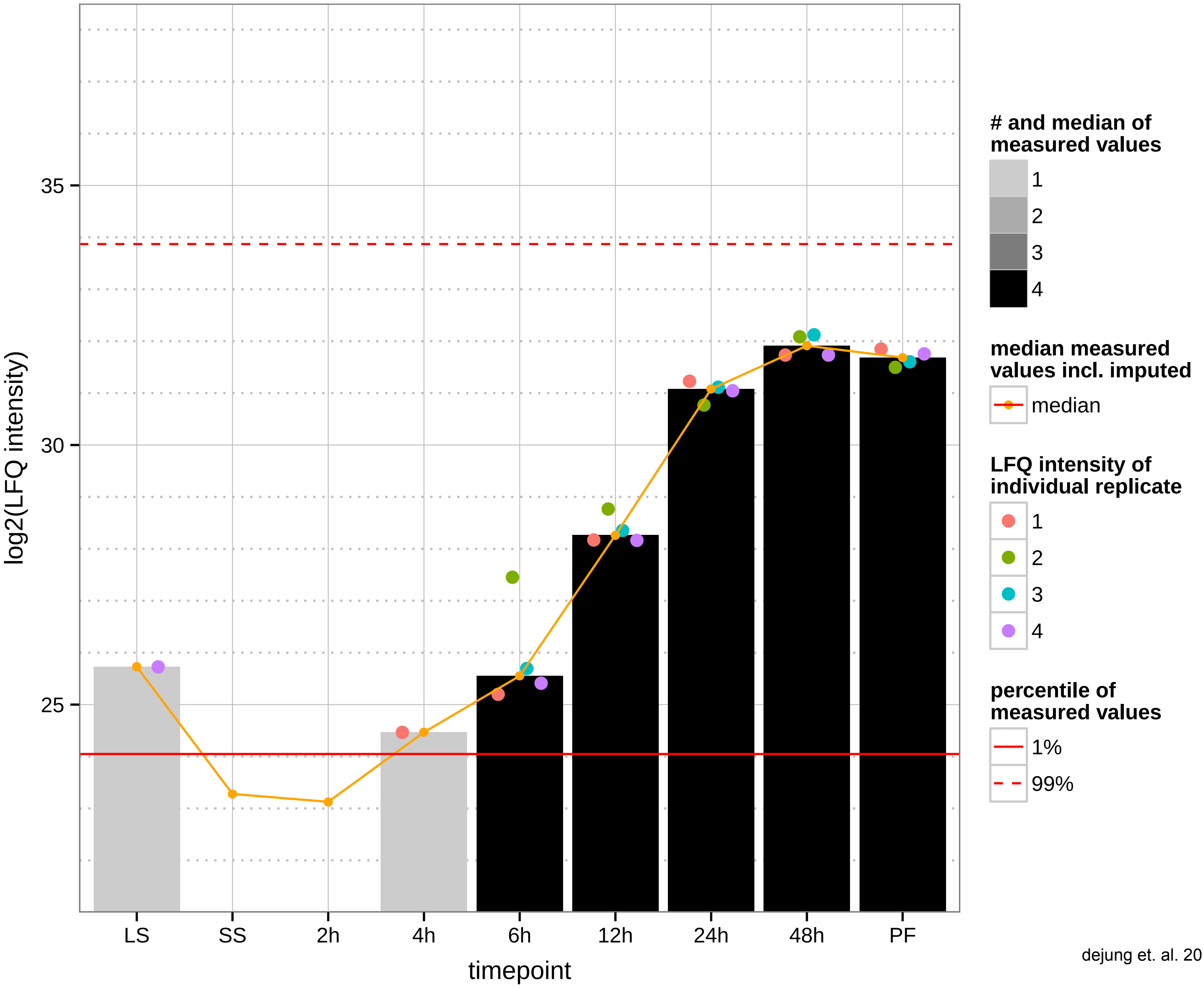
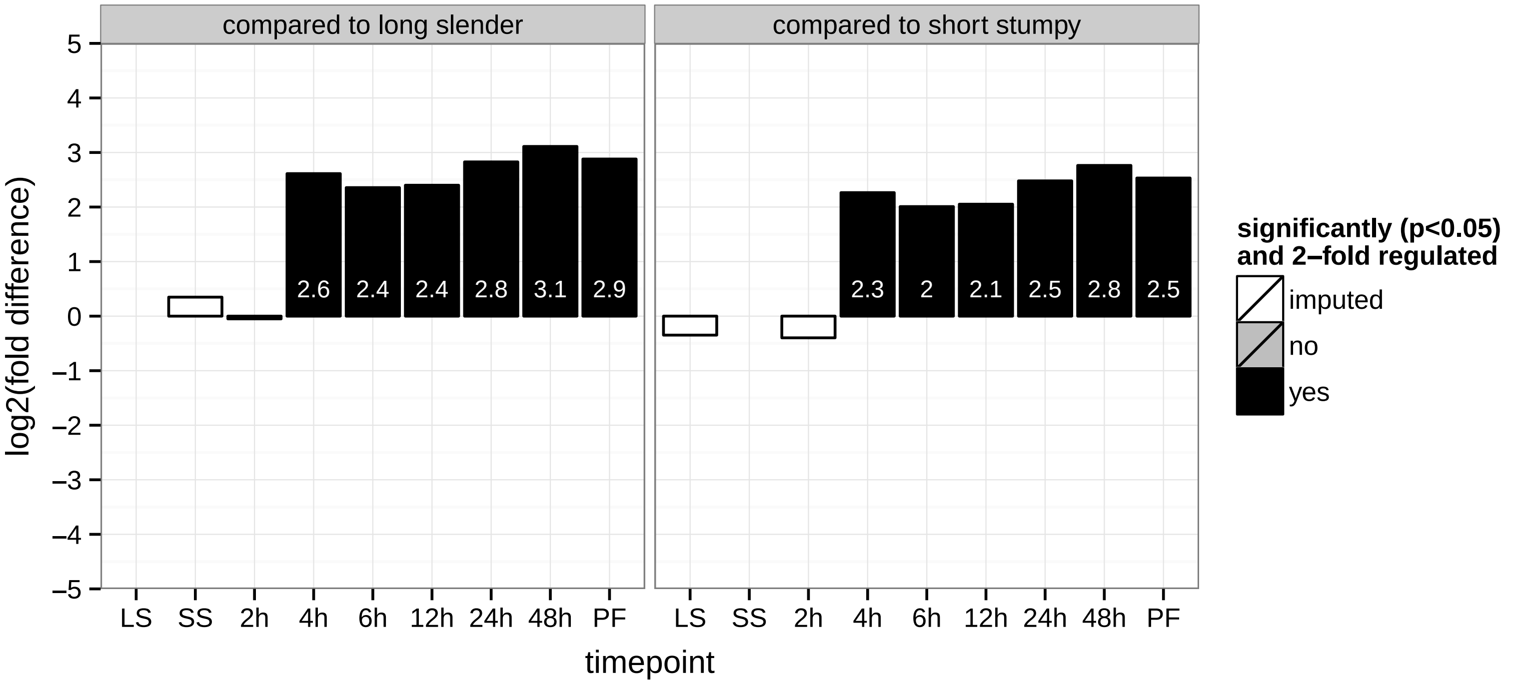
mitochondrial processing peptidase alpha subunit, putative, metallo–peptidase, Clan ME, Family M16
Tb927.11.3980
AGOF: catalytic activity, metalloendopeptidase activity, zinc ion binding
AGOC: mitochondrion
AGOP: proteolysis
PGOF: catalytic activity, metal ion binding, metalloendopeptidase activity, zinc ion binding
PGOC: null
PGOP: proteolysis

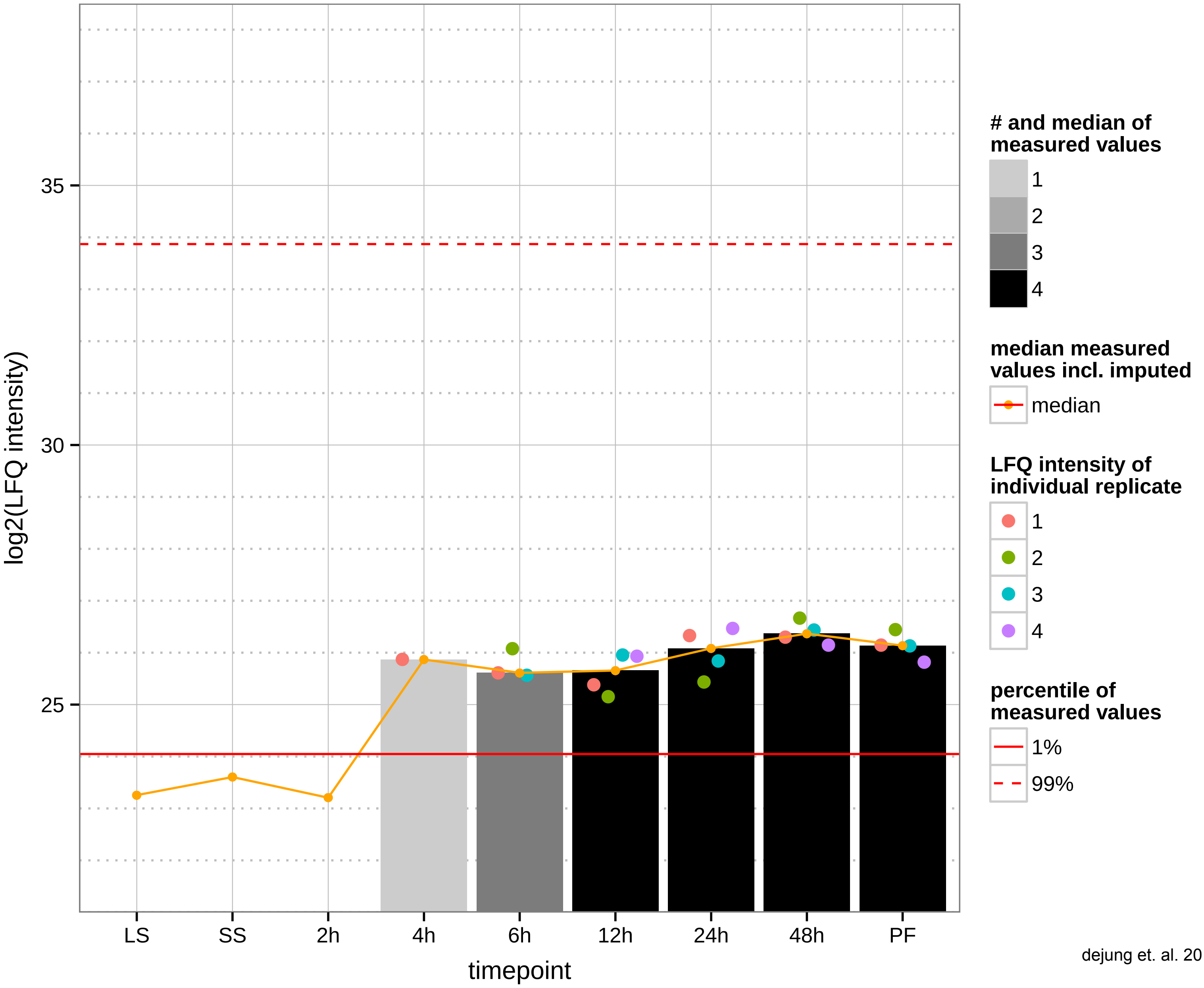




dejung et. al. 2015

ATP–dependent RNA helicase, putative
Tb927.11.4380
AGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: null
PGOF: ATP binding, ATP–dependent helicase activity, helicase activity, nucleic acid binding, nucleoside–triphosphatase activi
PGOC: null
PGOP: null





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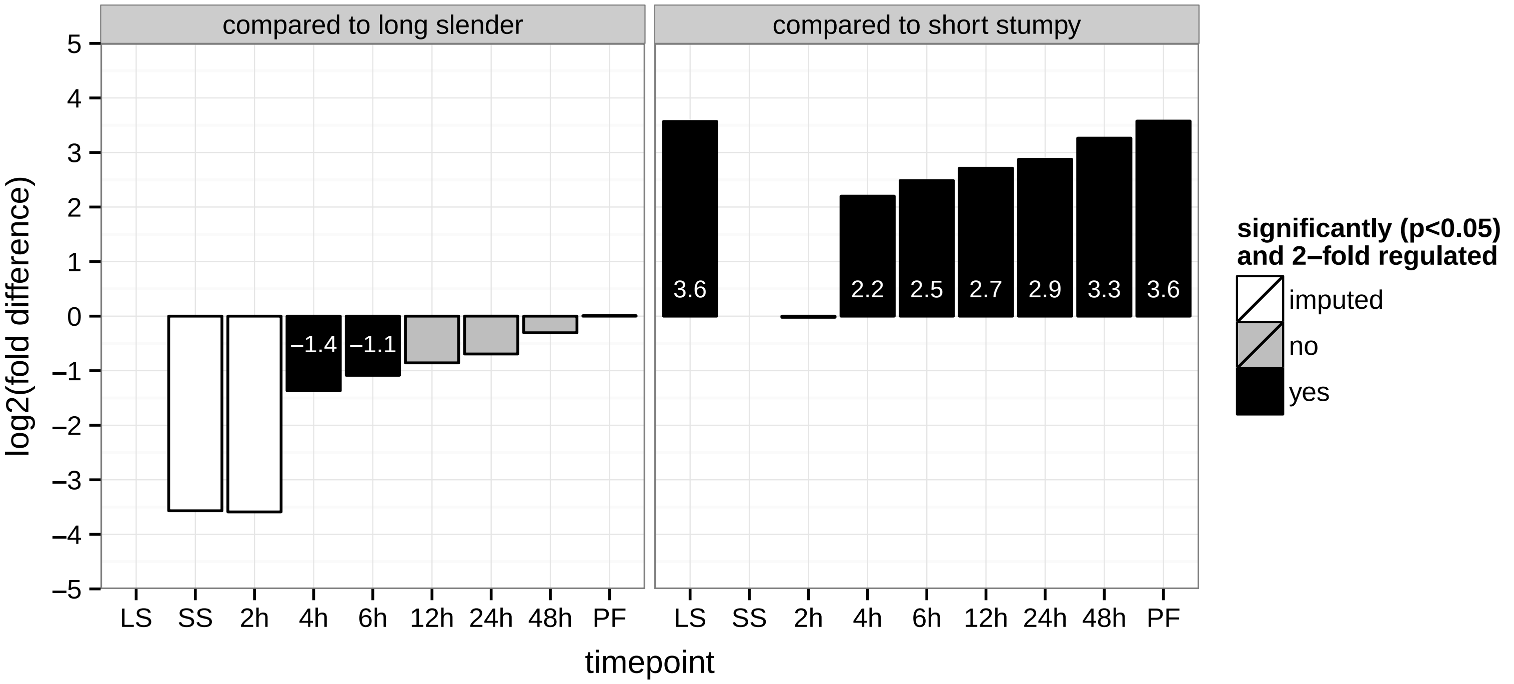
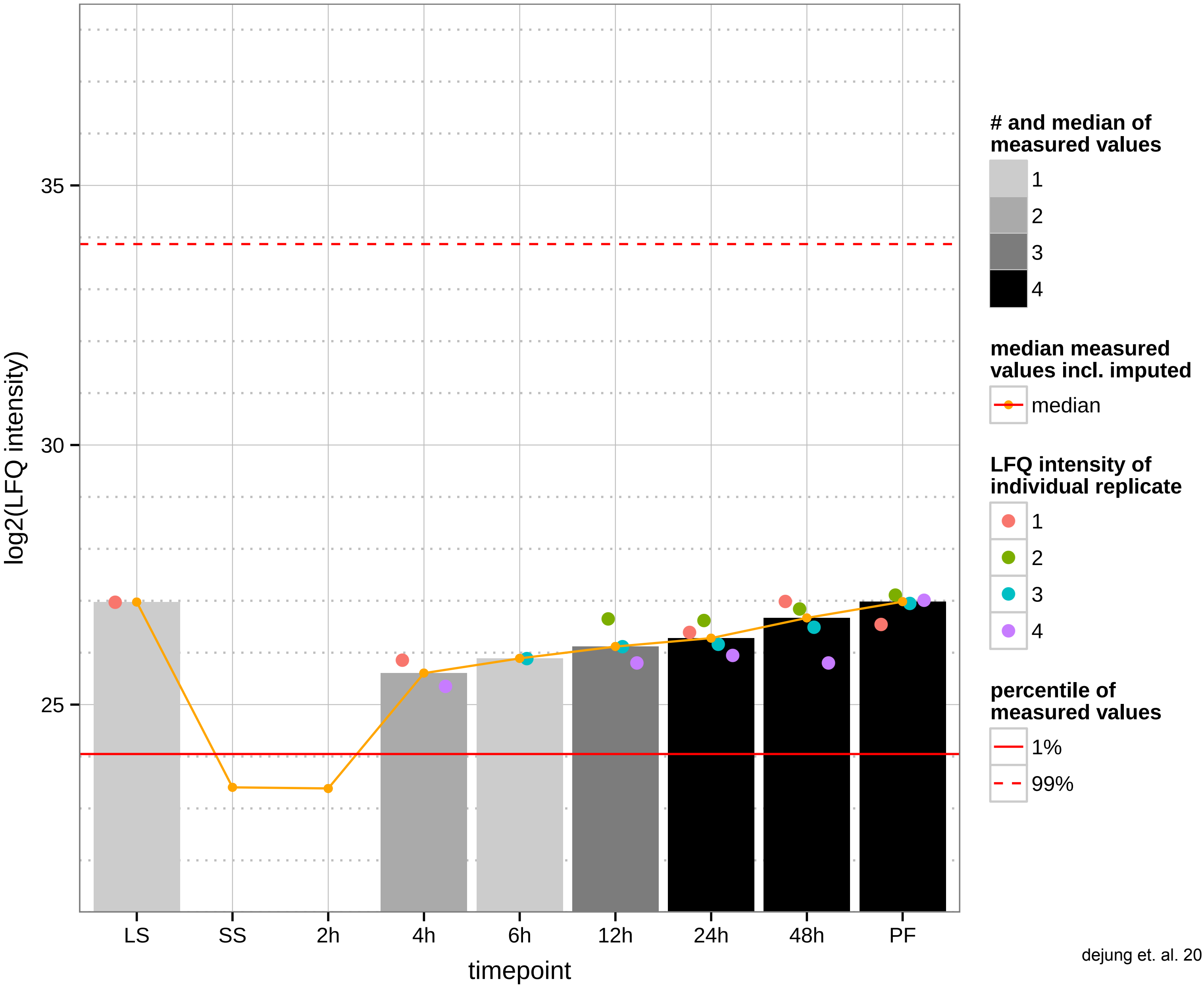
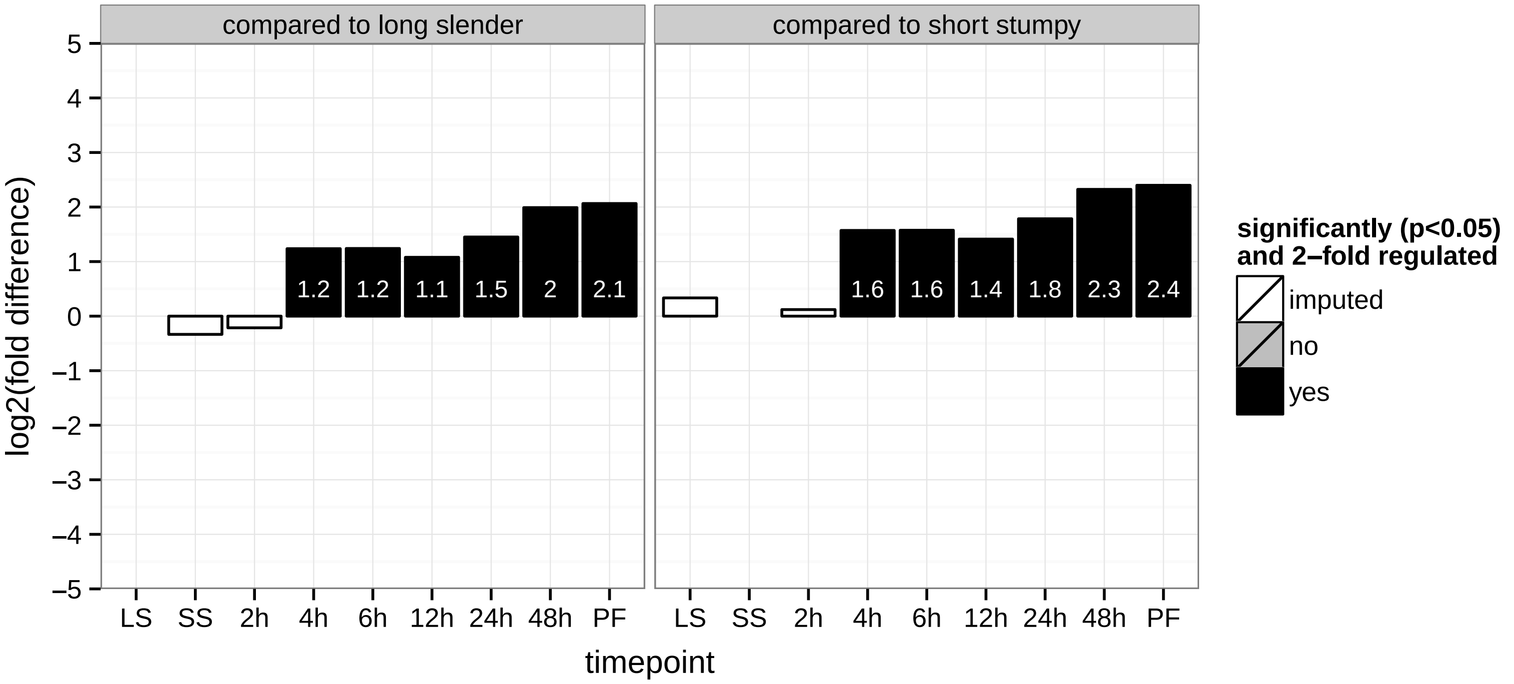
hypothetical protein, conserved
Tb927.11.4650
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

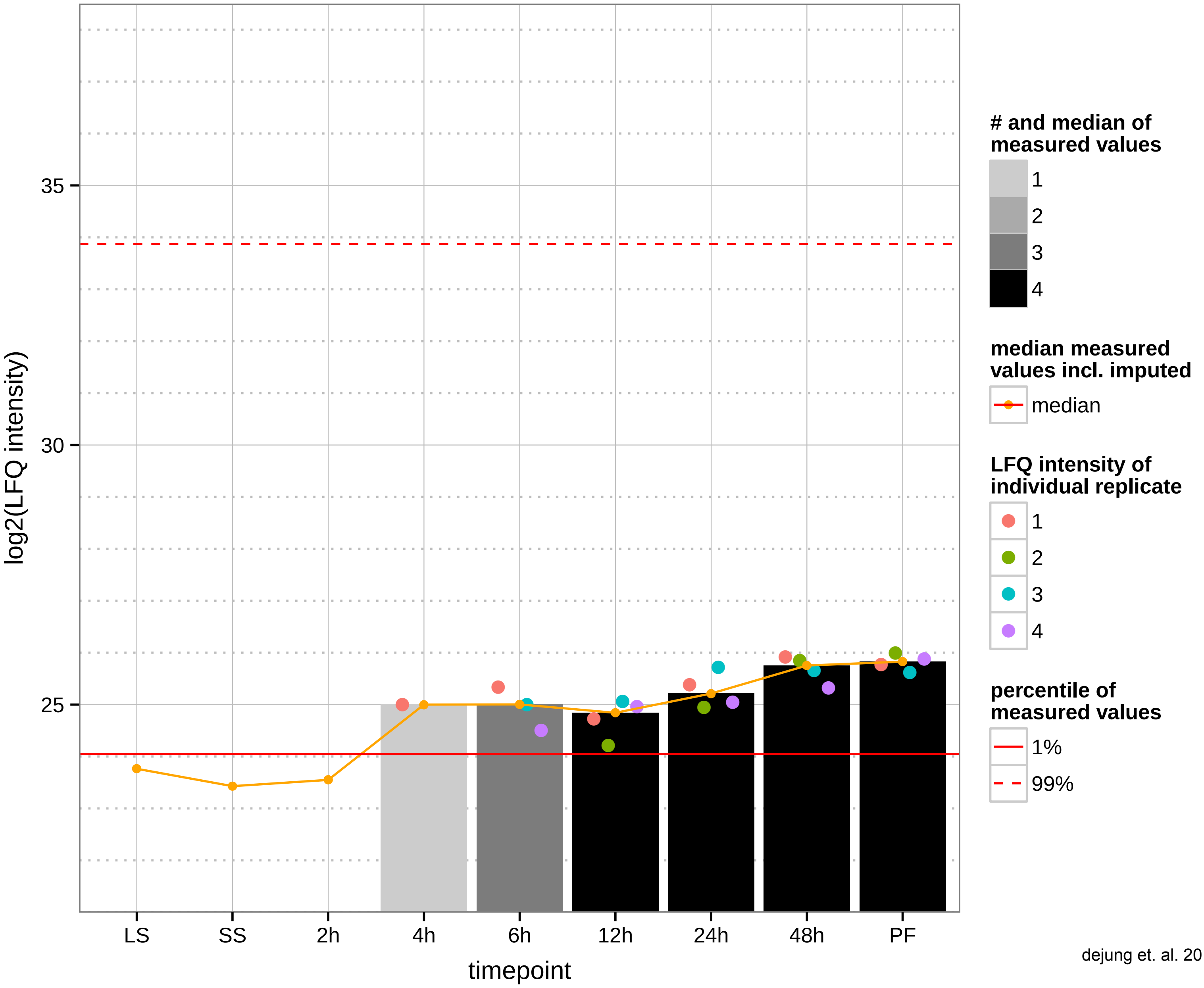




dejung et. al. 2015

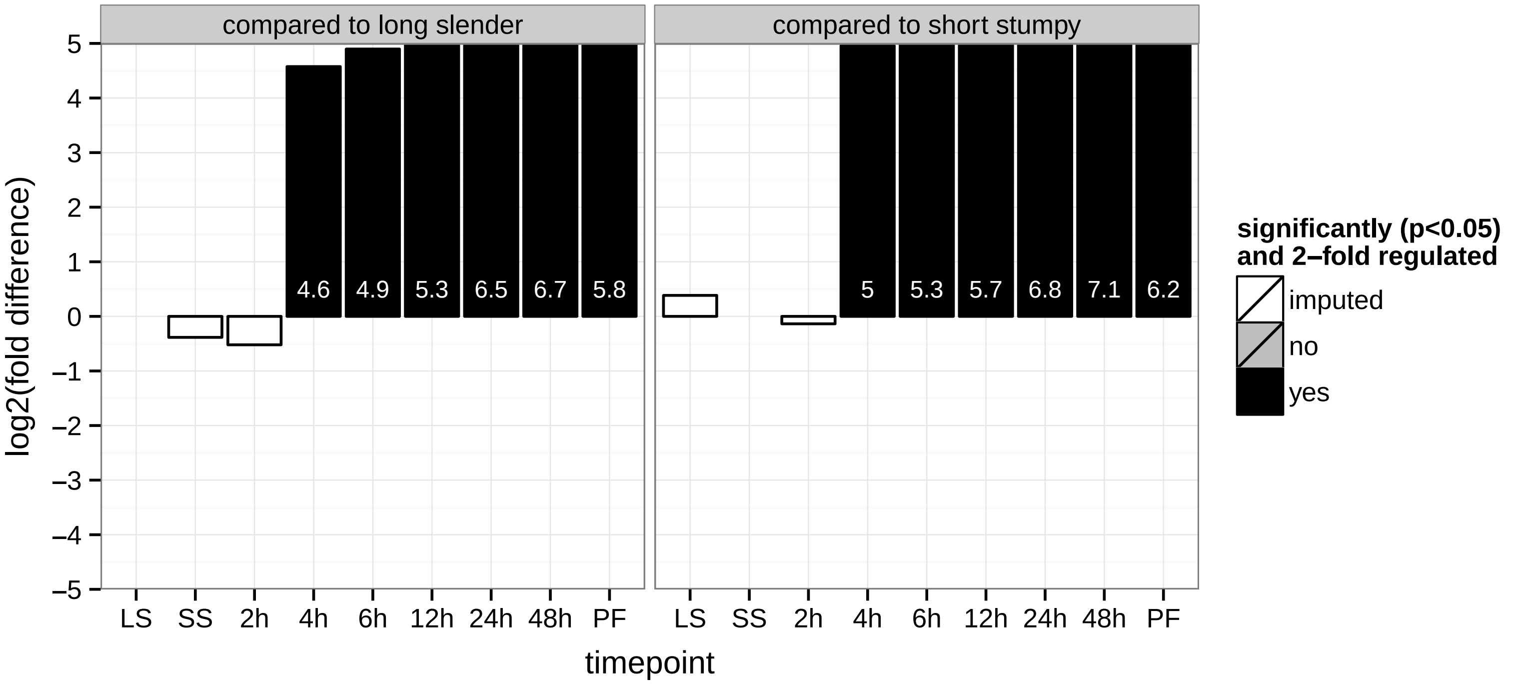
hypothetical protein, conserved
Tb927.11.5880
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

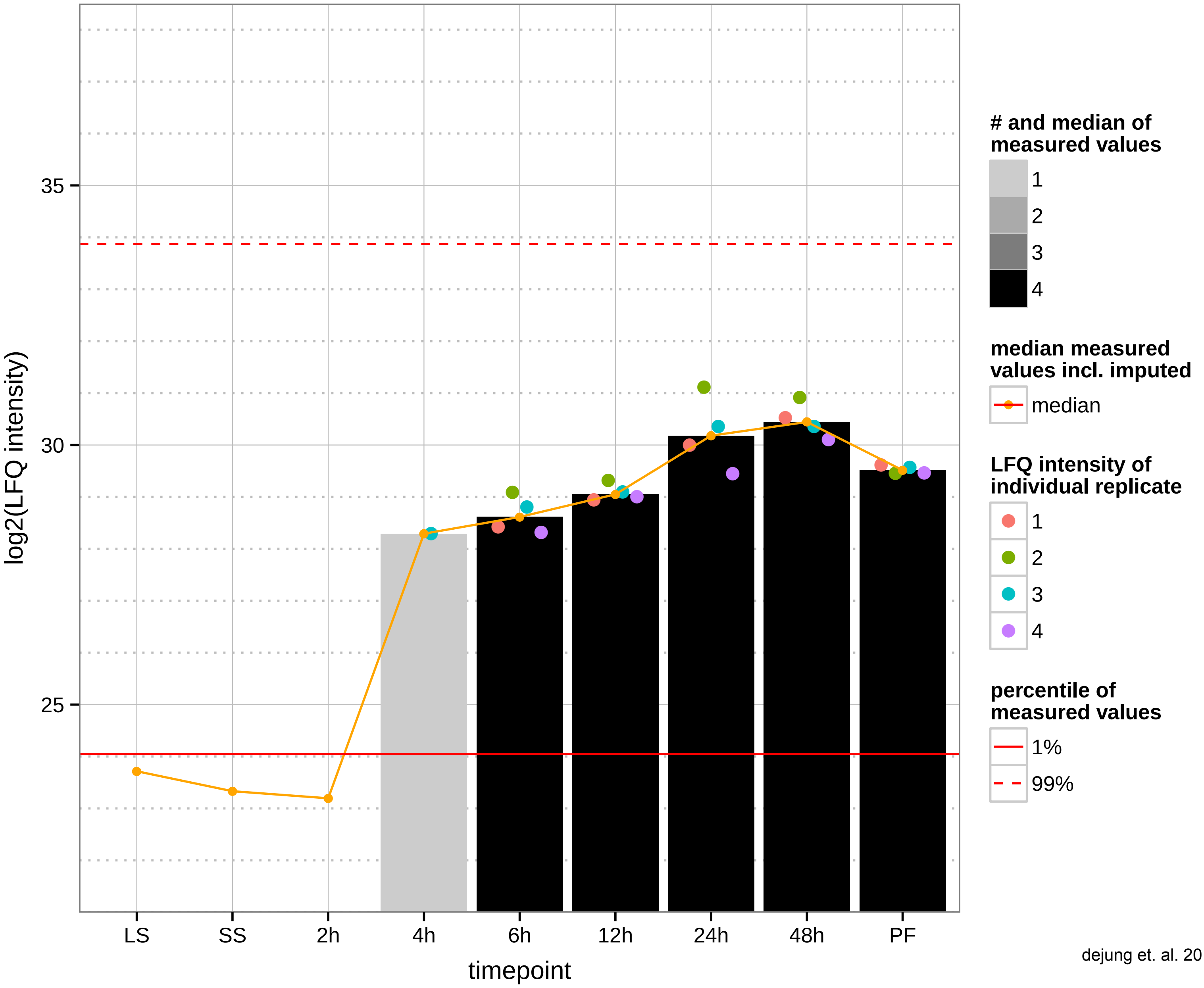




dejung et. al. 2015

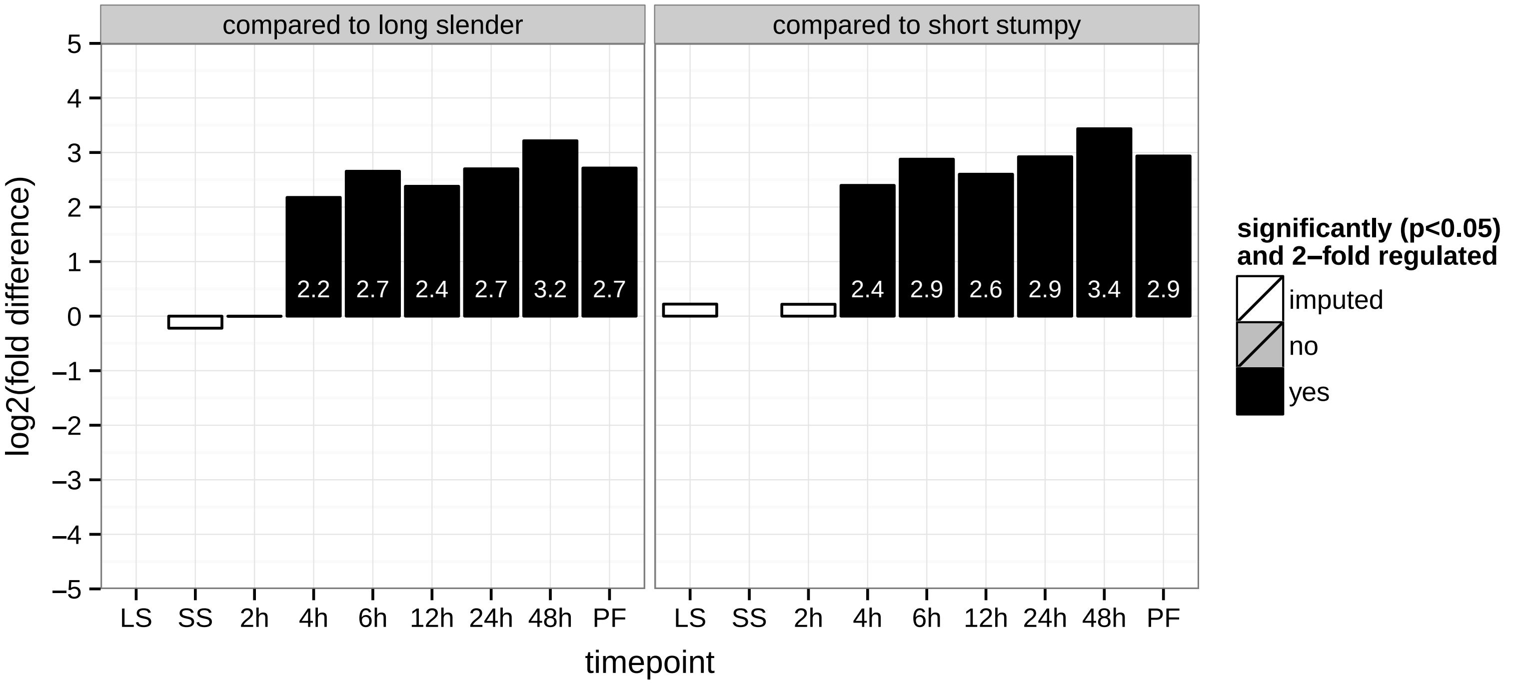
hypothetical protein, conserved
Tb927.11.600
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

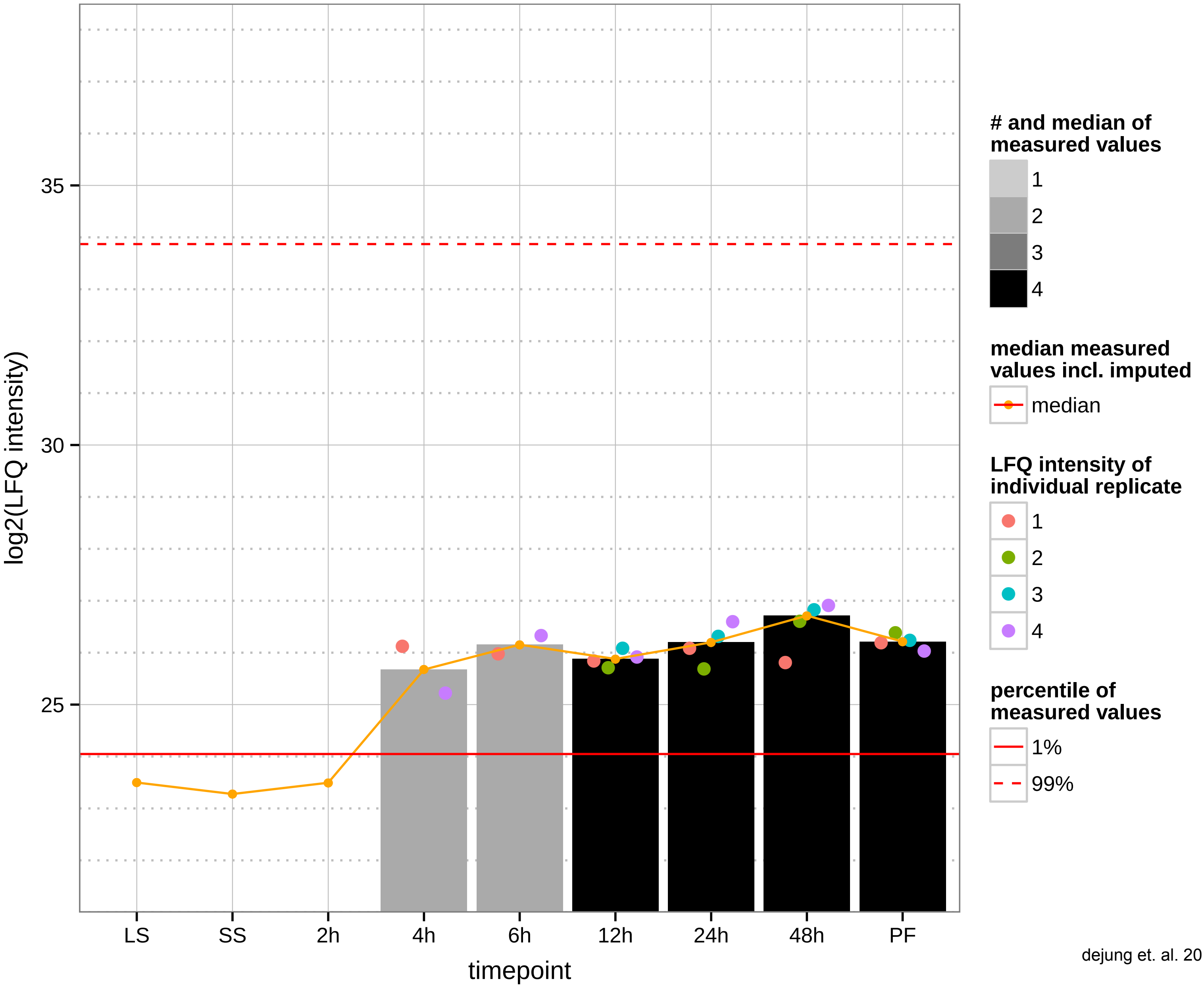




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.6430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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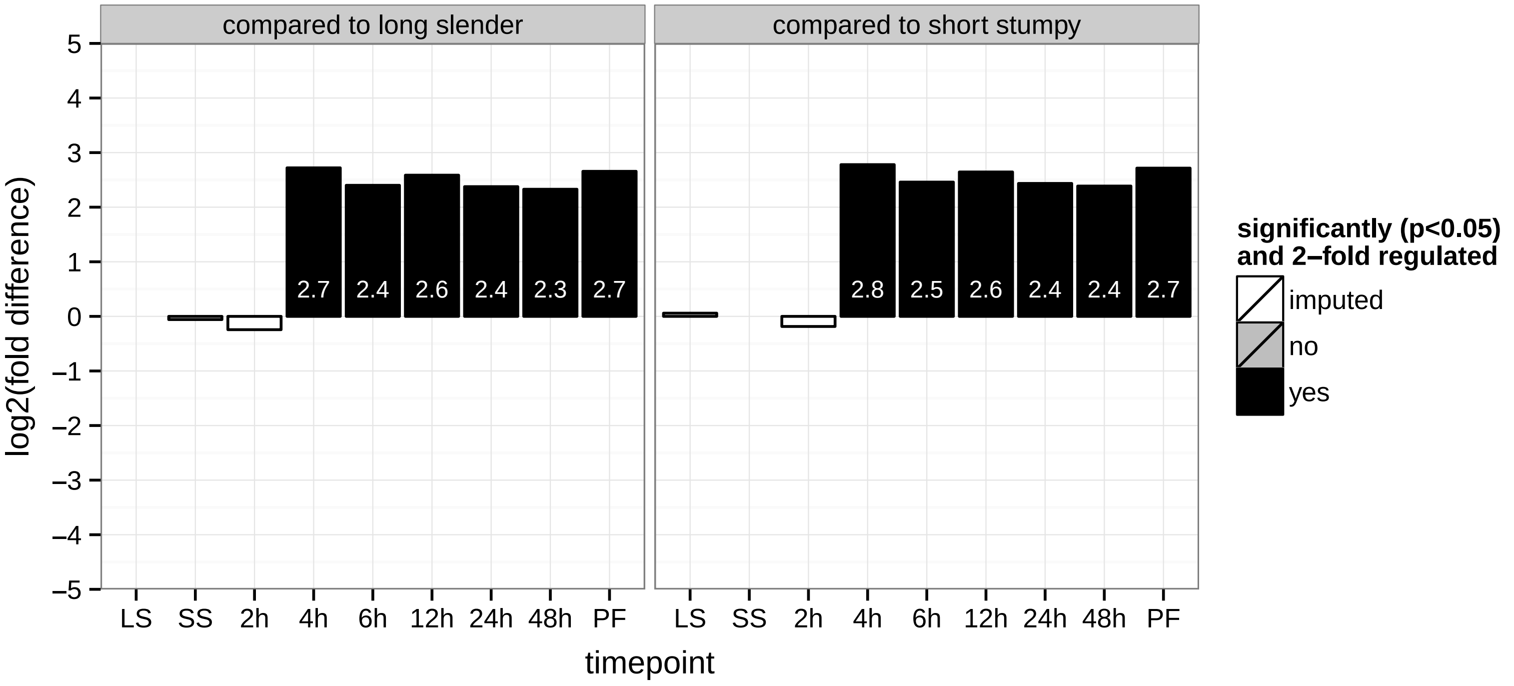
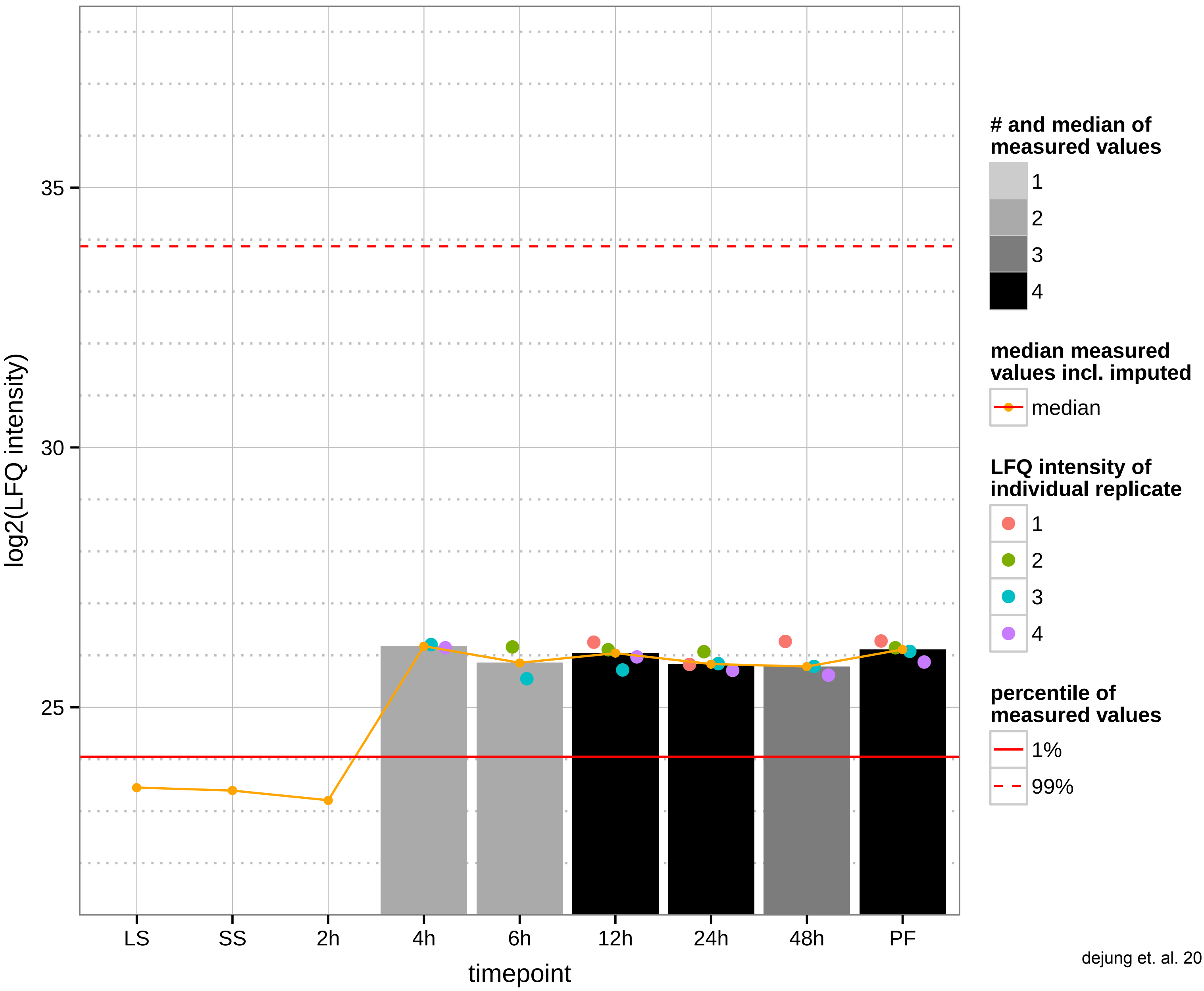
hypothetical protein, conserved
Tb927.11.8180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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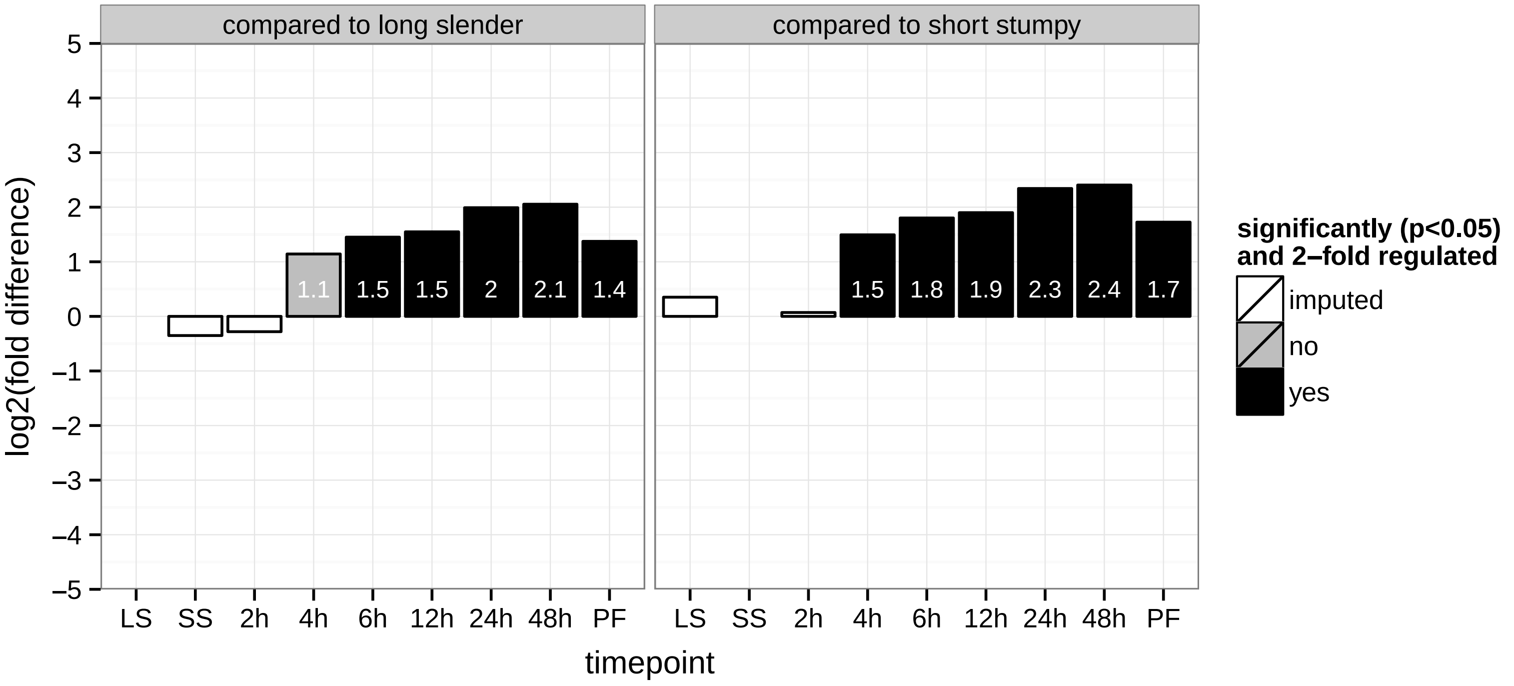
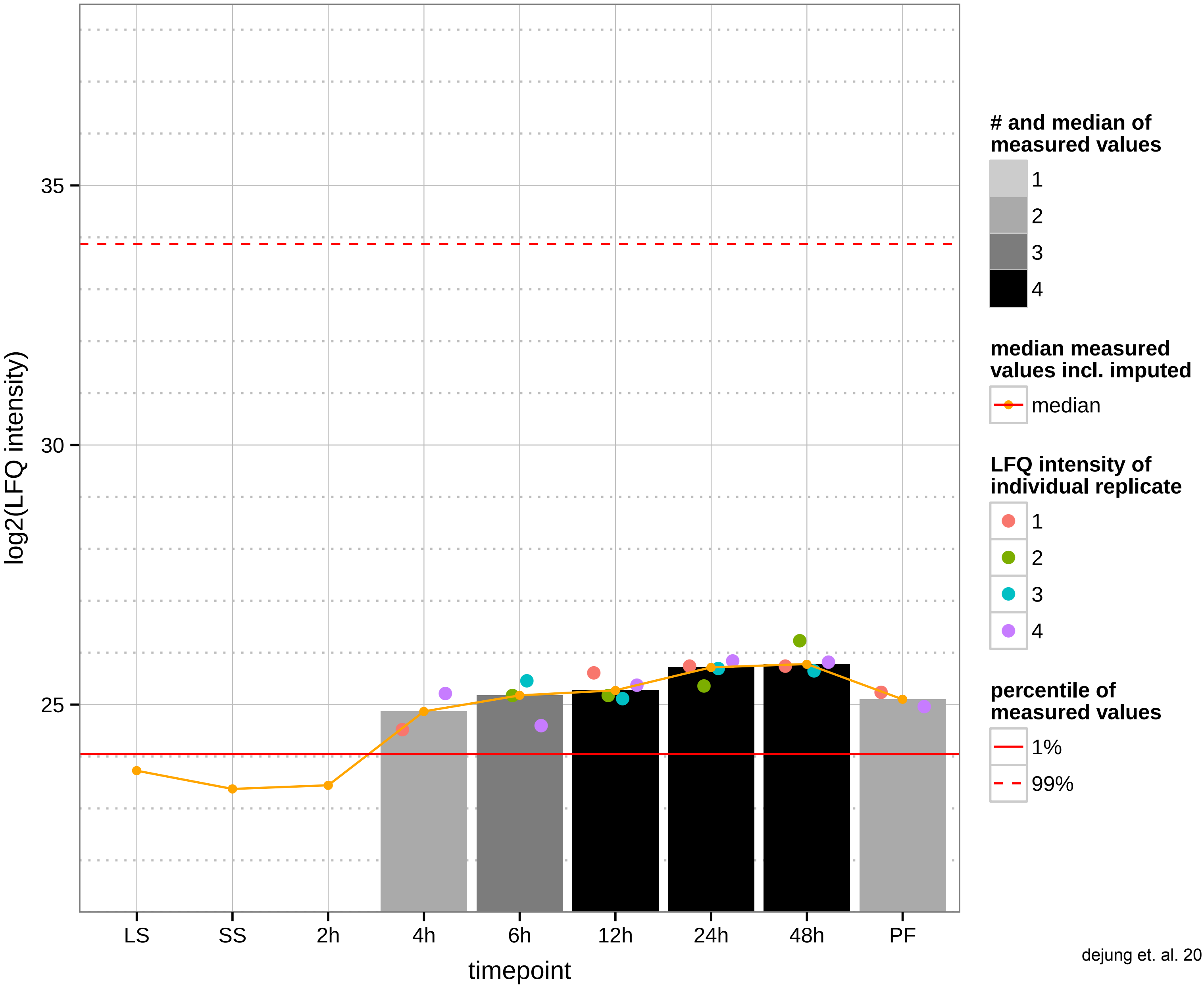
nucleic acid binding protein, putative
Tb927.11.9510
AGOF: nucleic acid binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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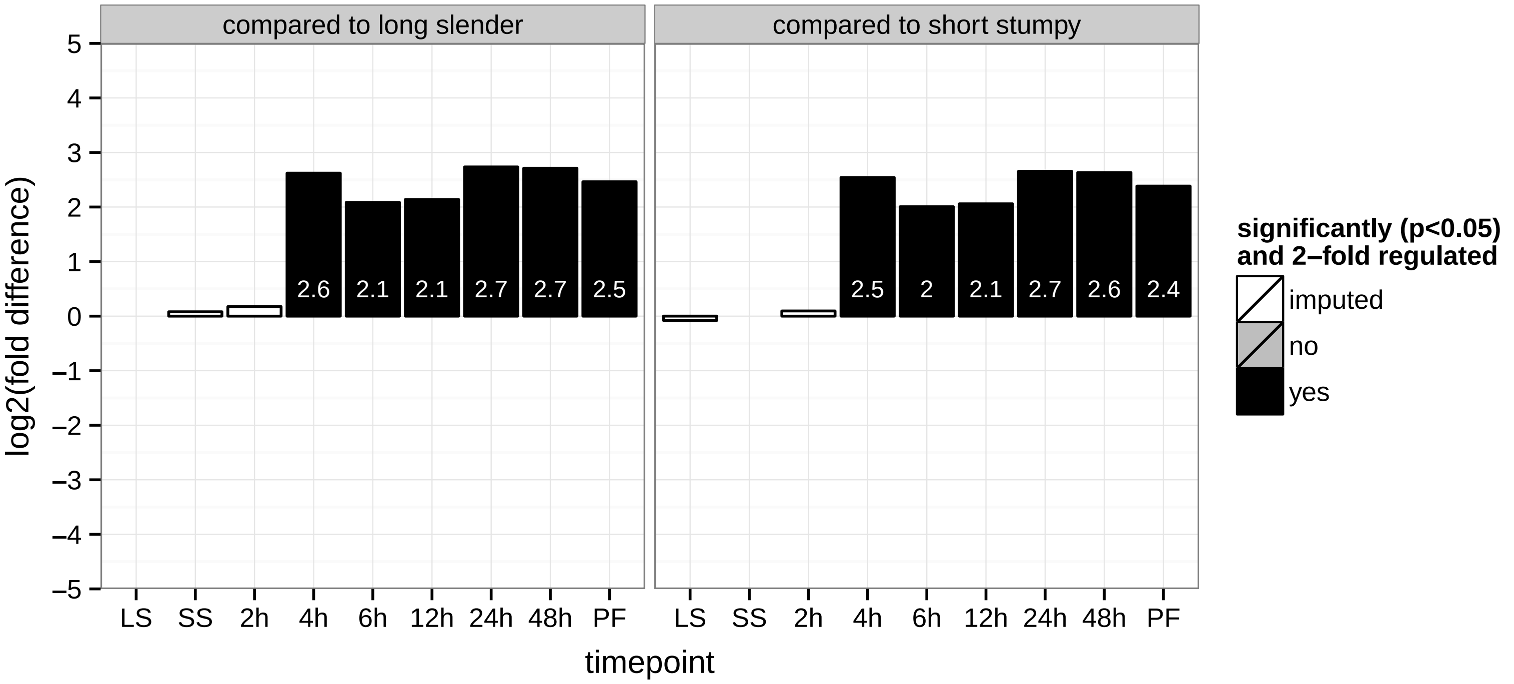
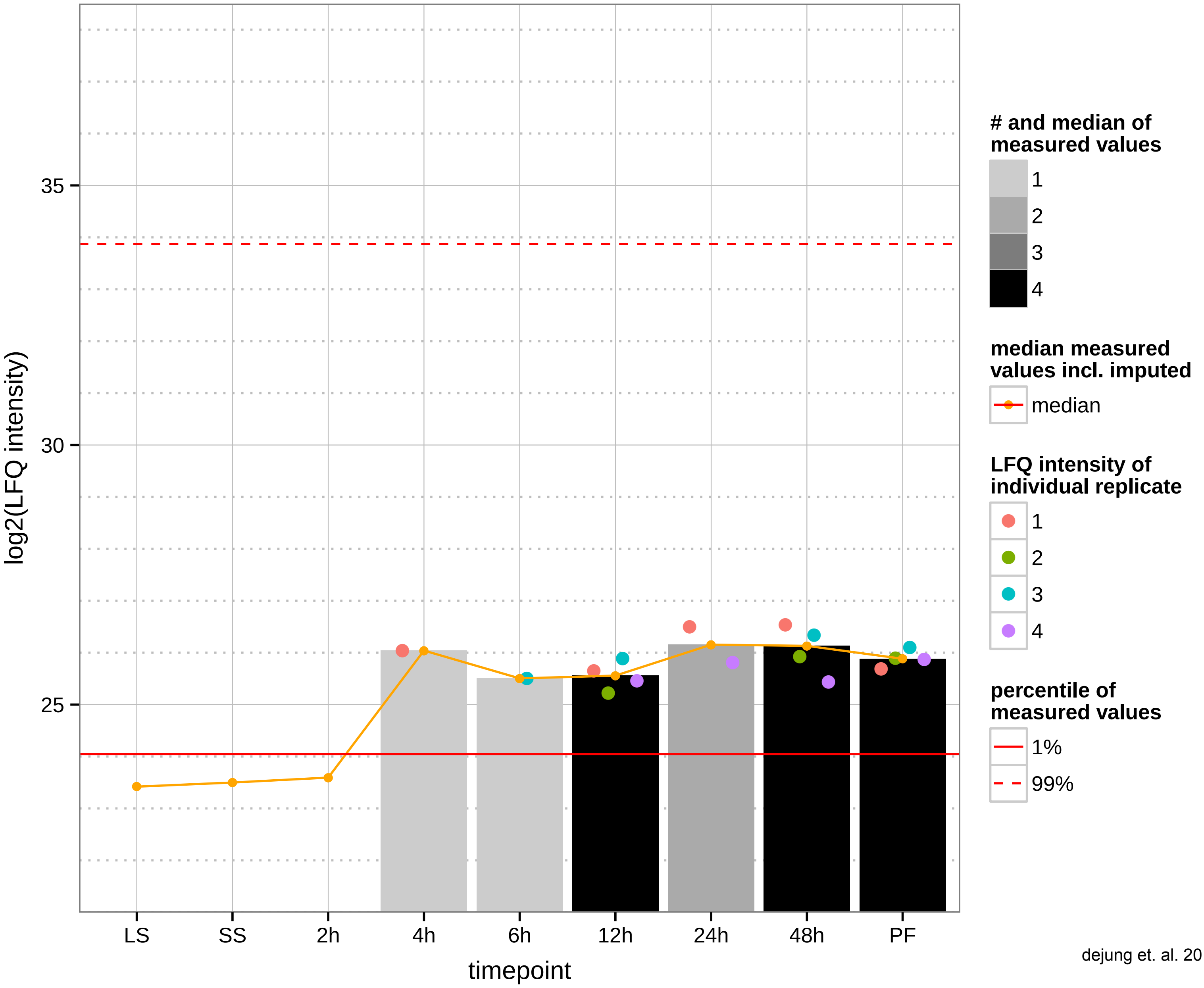
retrotransposon hot spot protein (RHS, pseudogene), putative, retrotransposon hot spot protein 3 (RHS3), interrupted
Tb927.2.1140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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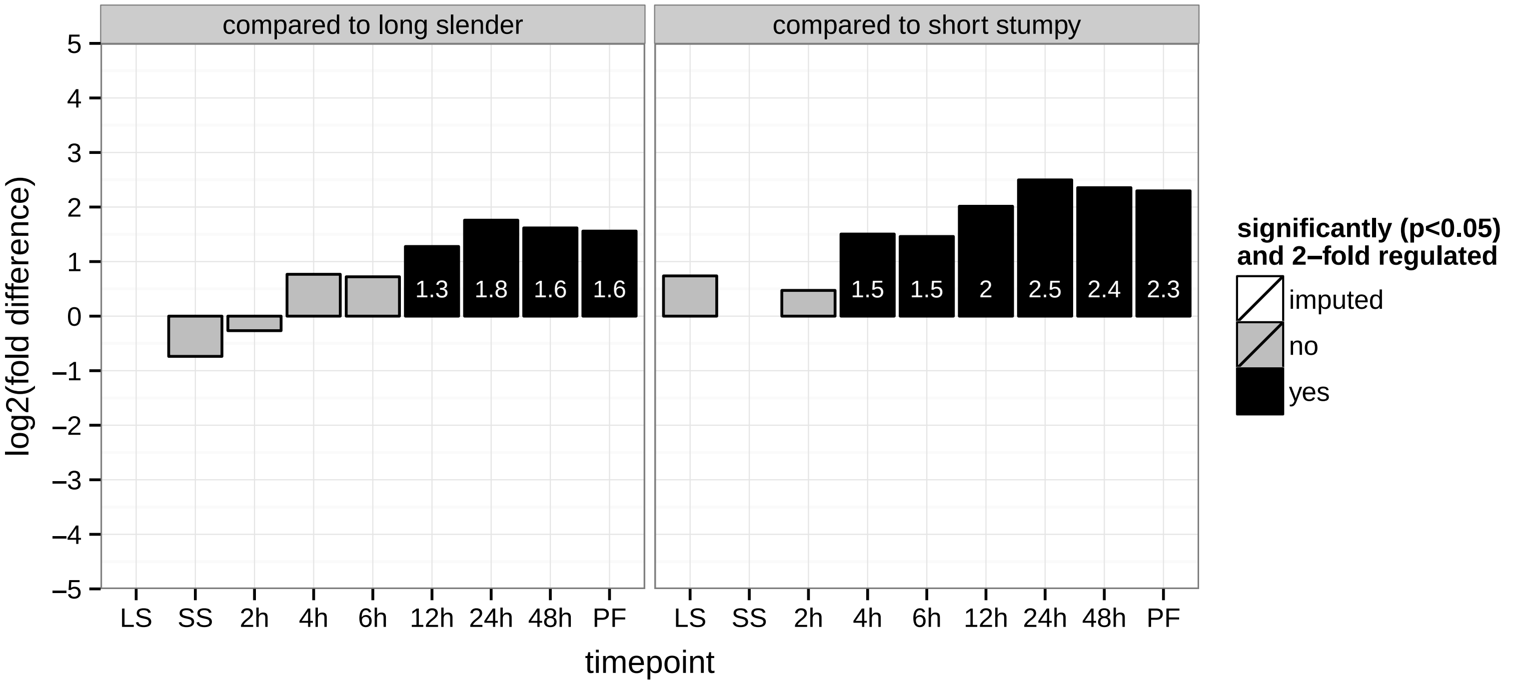
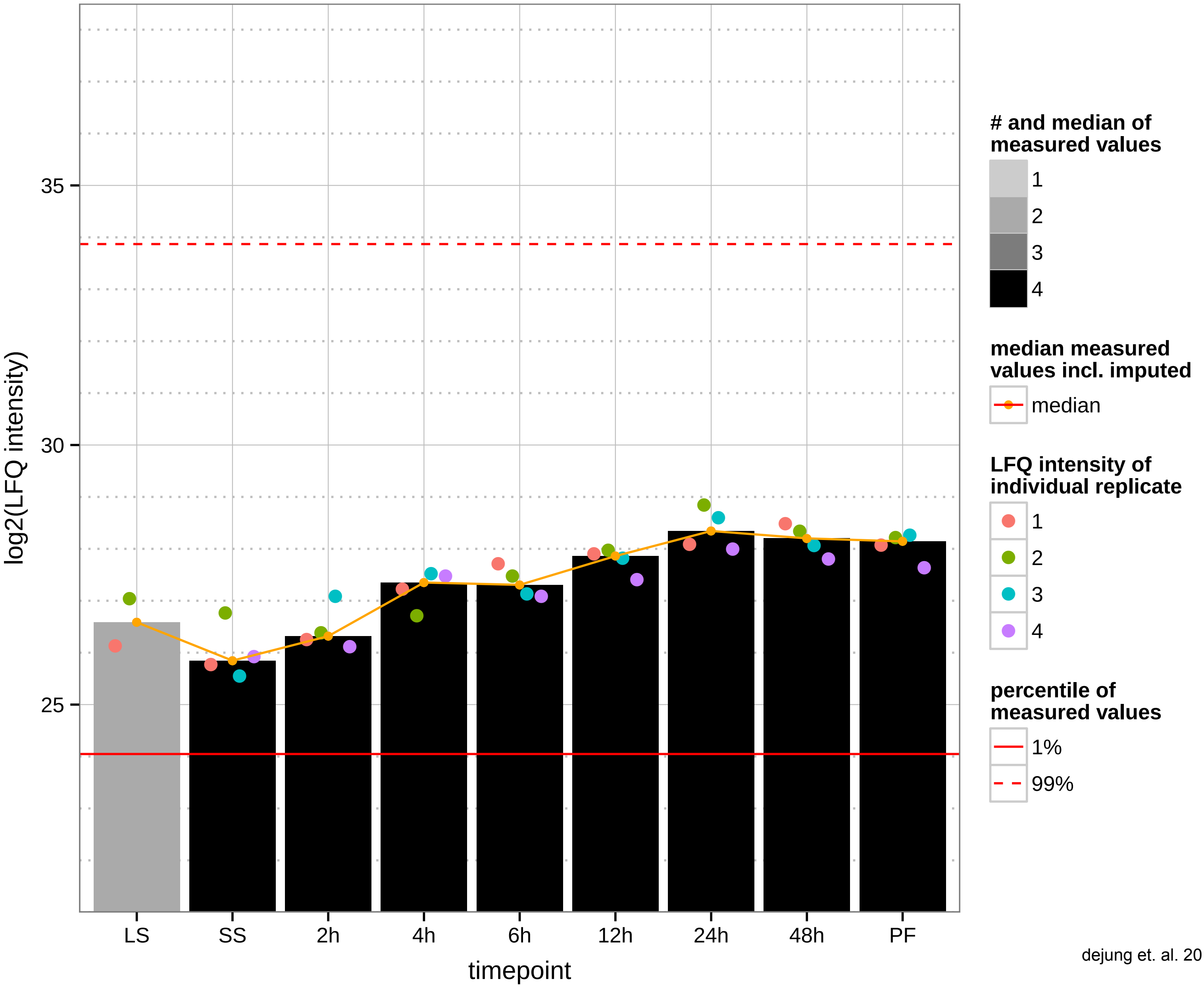
hypothetical protein, conserved
Tb927.3.4160
AGOF: damaged DNA binding
AGOC: null
AGOP: nucleotide–excision repair, proteasomal ubiquitin–dependent protein catabolic process
PGOF: damaged DNA binding, protein binding
PGOC: null
PGOP: nucleotide–excision repair, proteasomal ubiquitin–dependent protein catabolic process





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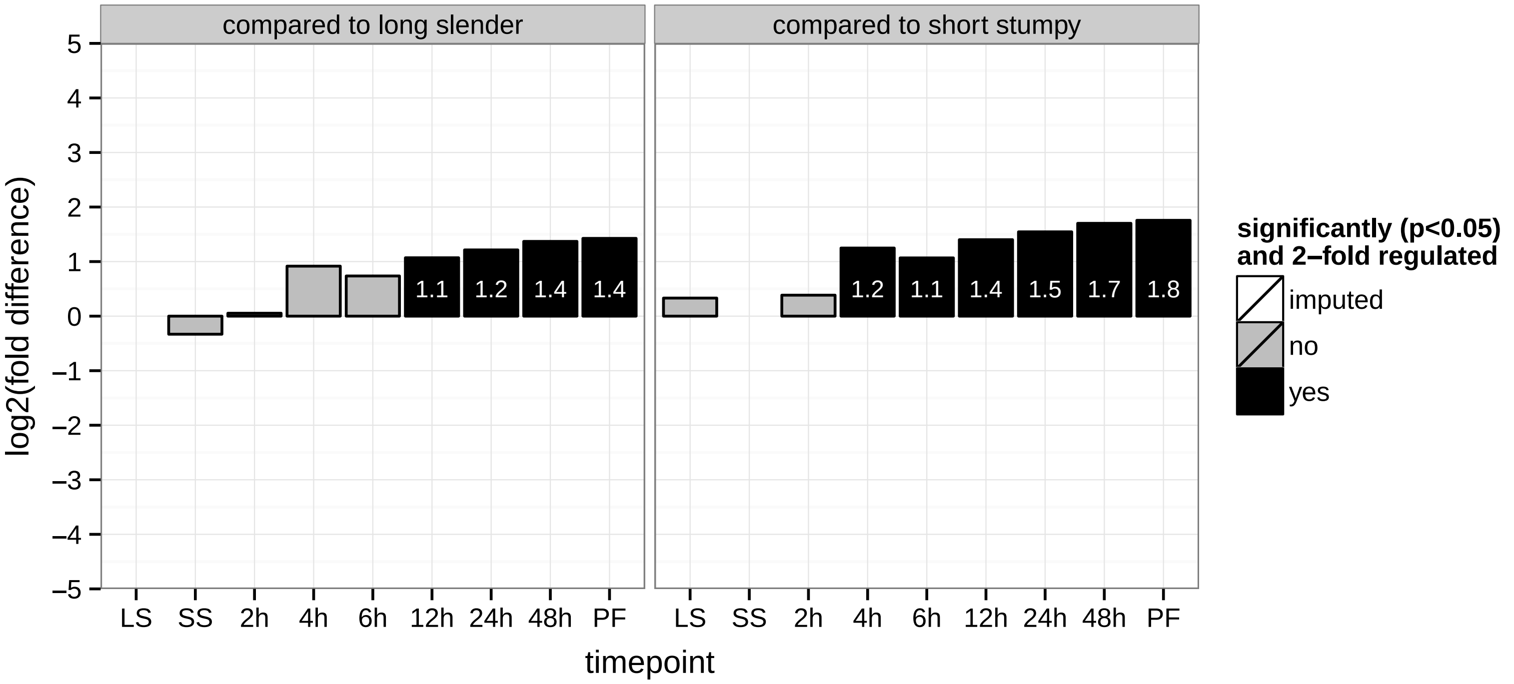
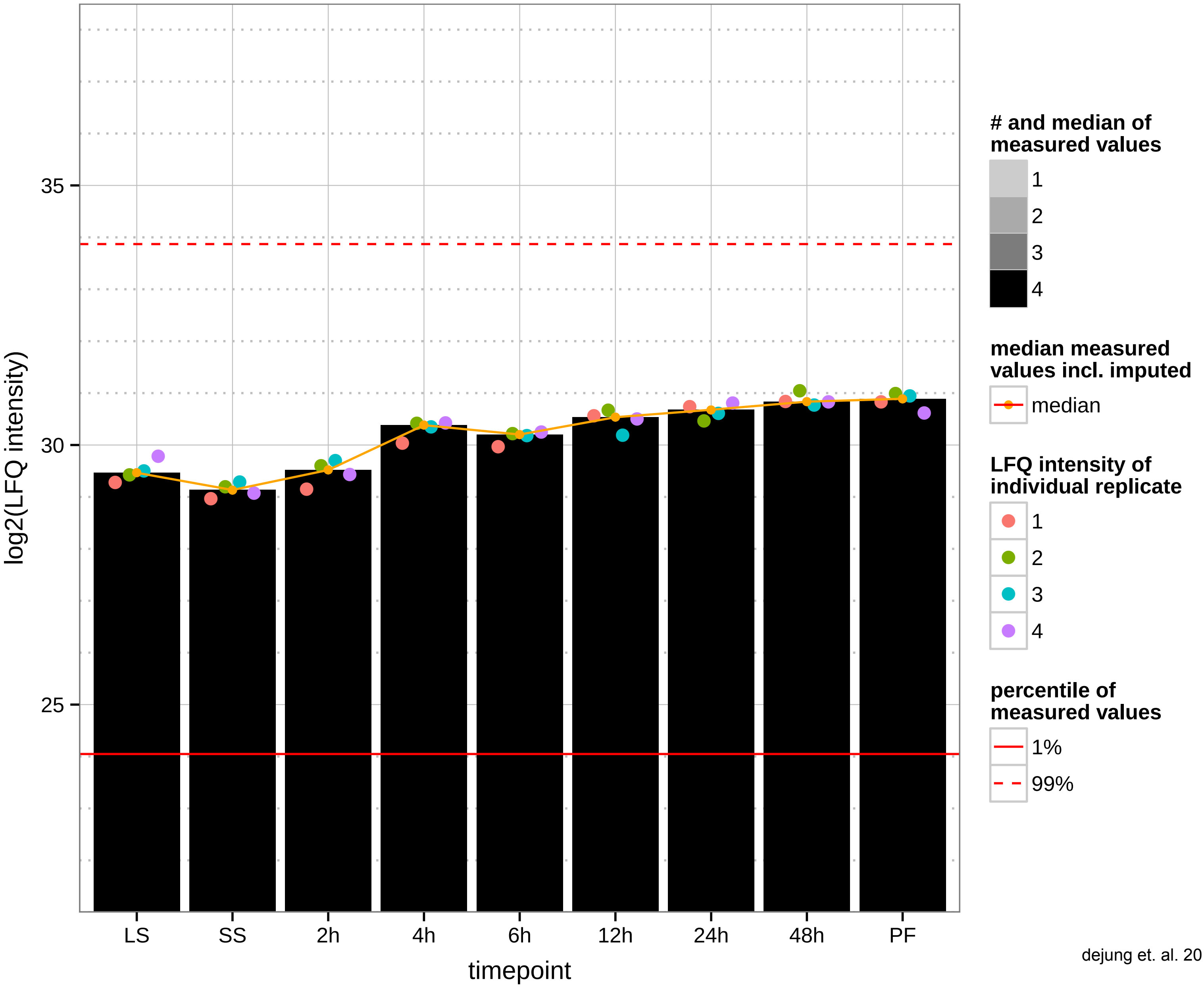
uracil phosphoribosyltransferase, putative
Tb927.4.3320
AGOF: null
AGOC: null
AGOP: nucleoside metabolic process
PGOF: null
PGOC: null
PGOP: nucleoside metabolic process





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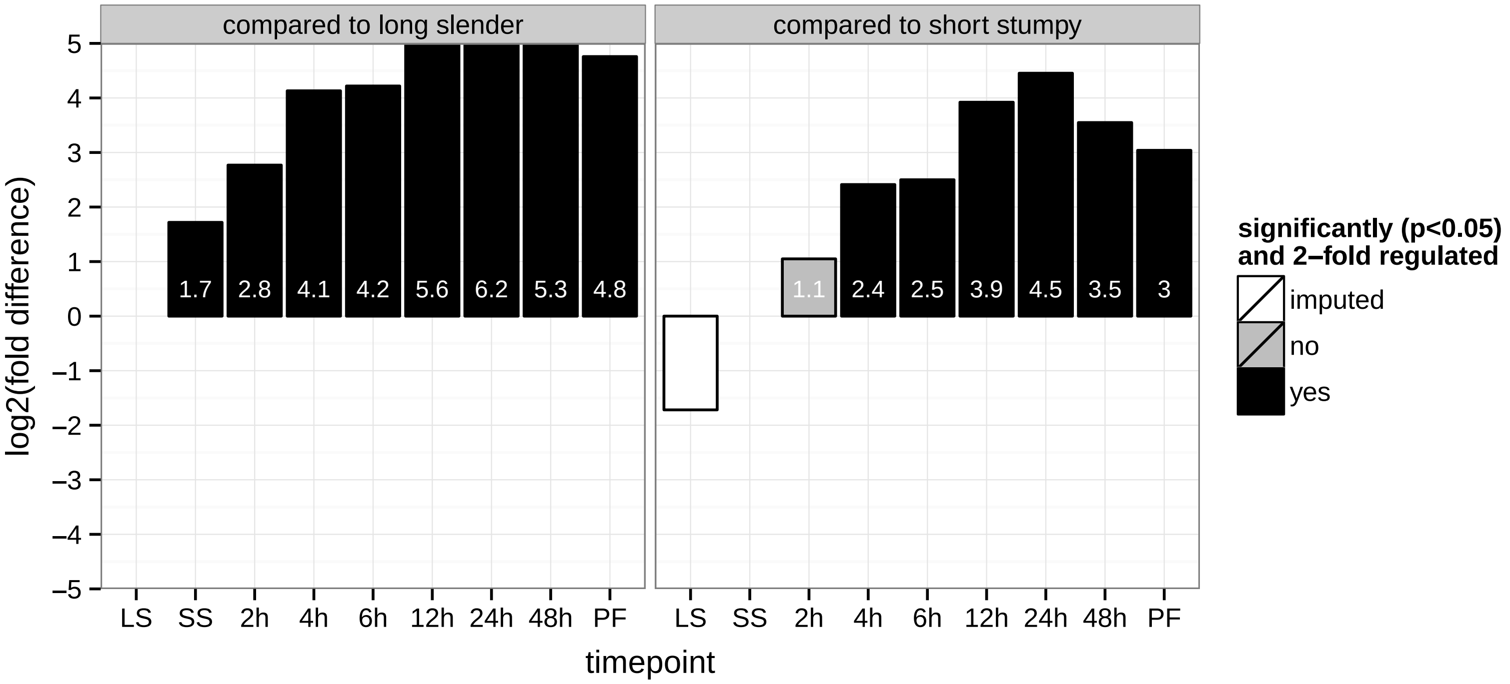
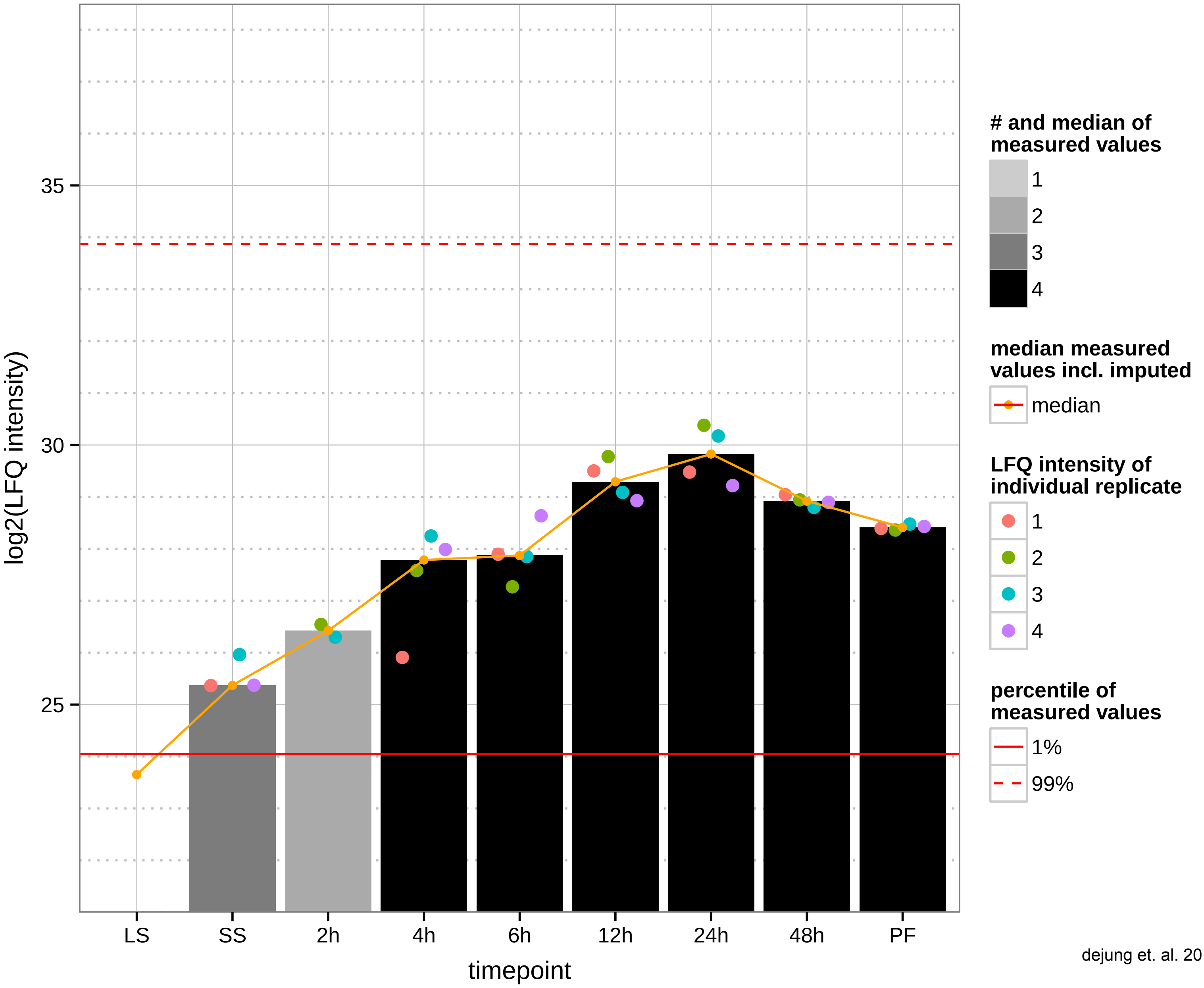
hypothetical protein, conserved
Tb927.4.3500
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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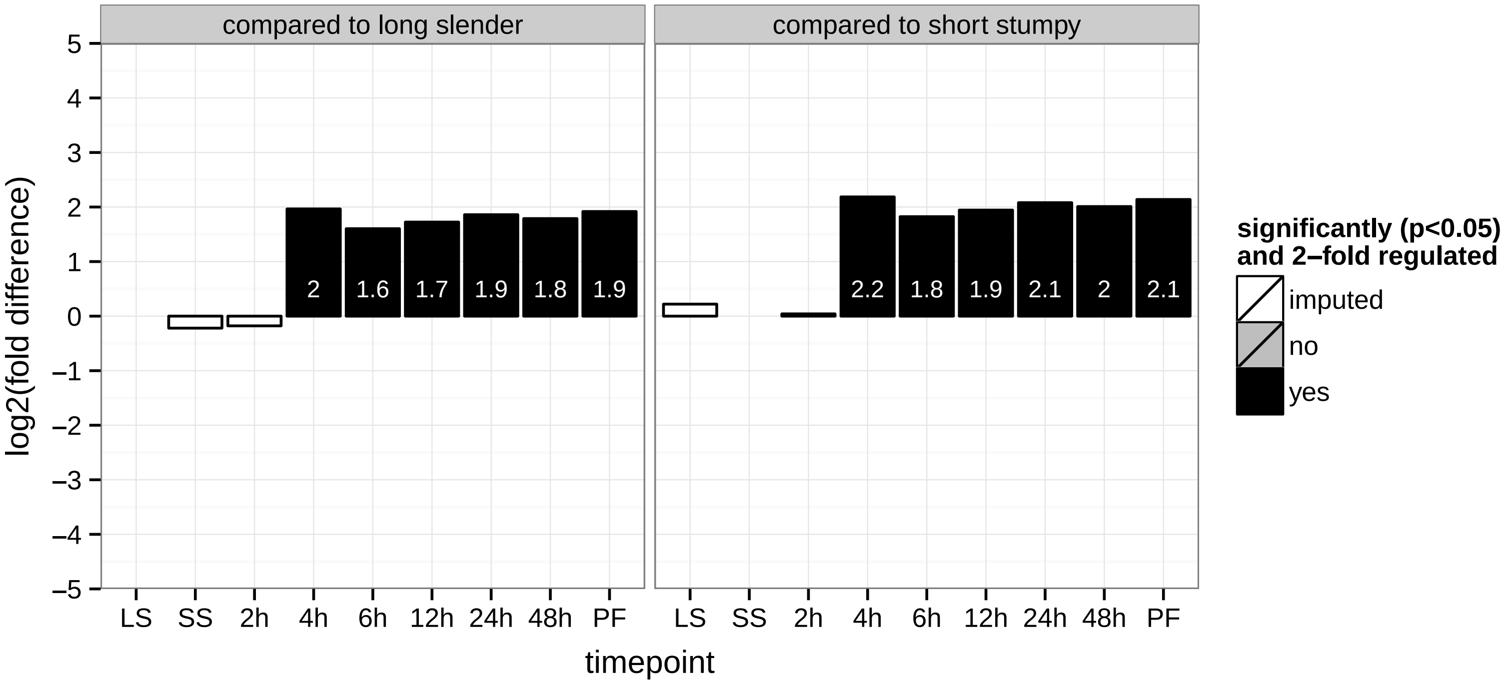
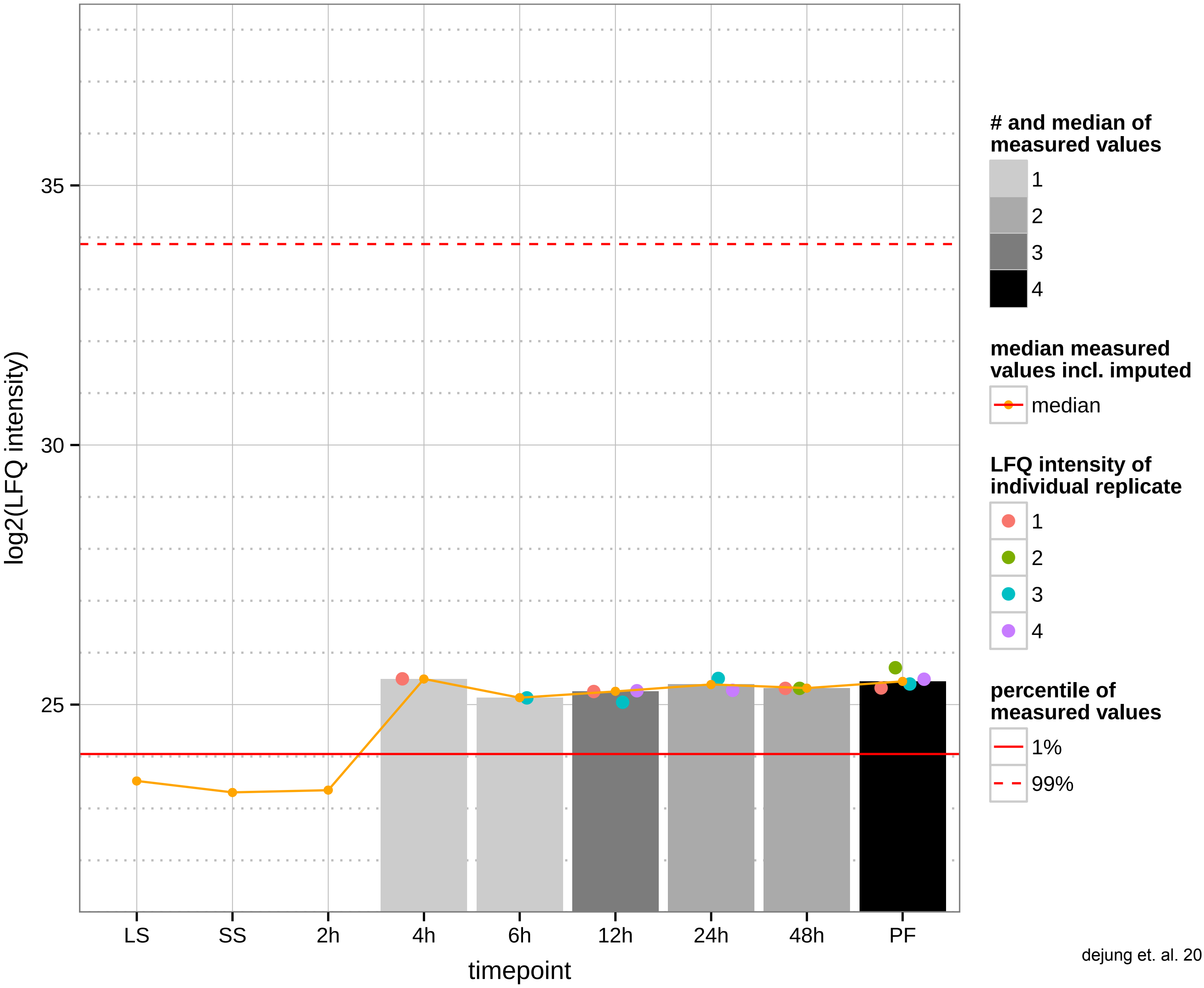
hypothetical protein, conserved
Tb927.4.3900
AGOF: zinc ion binding
AGOC: intracellular
AGOP: null
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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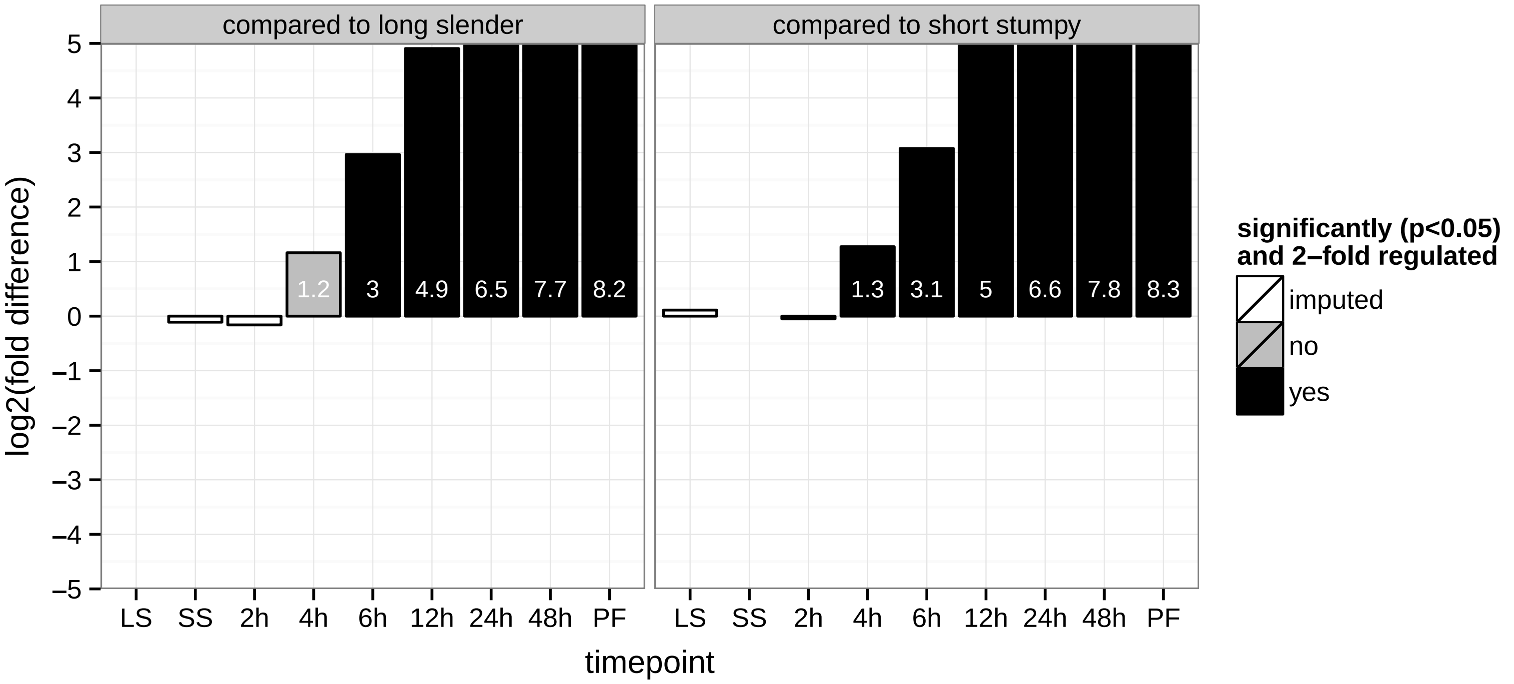
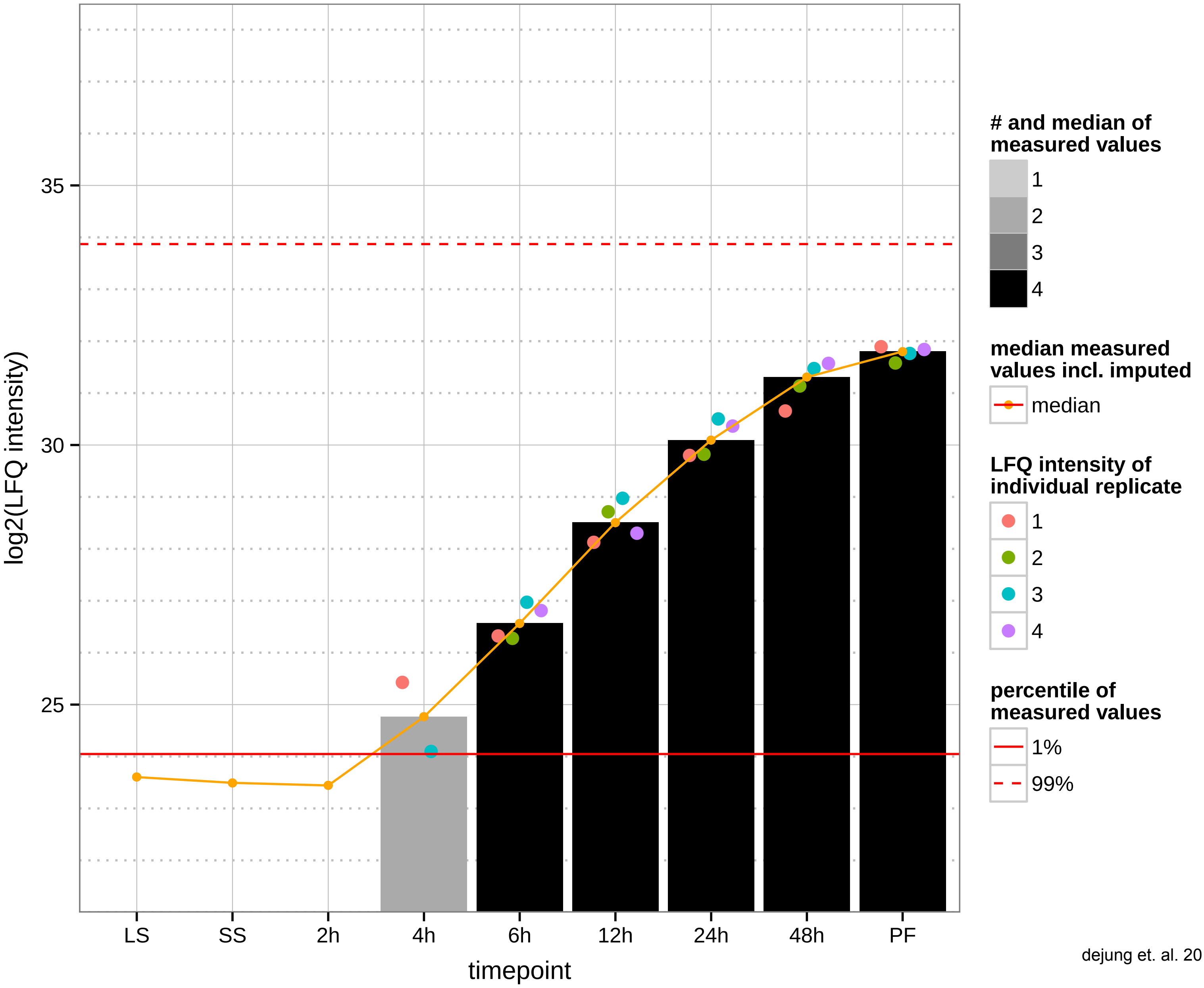
cytoskeleton–associated protein CAP5.5, putative, cysteine peptidase, Clan CA, family C2, putative (CAP5.5)
Tb927.4.3950
AGOF: calcium–dependent cysteine–type endopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: calcium–dependent cysteine–type endopeptidase activity
PGOC: intracellular
PGOP: proteolysis





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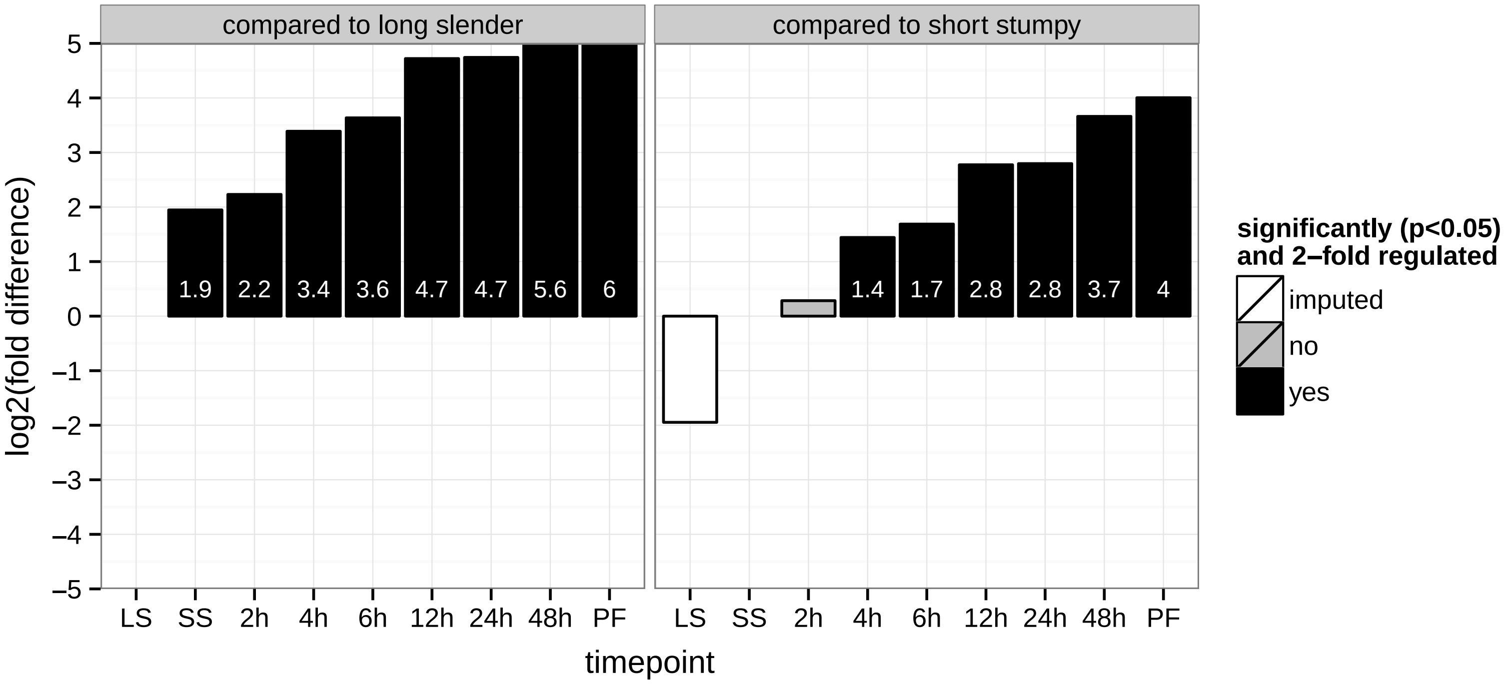
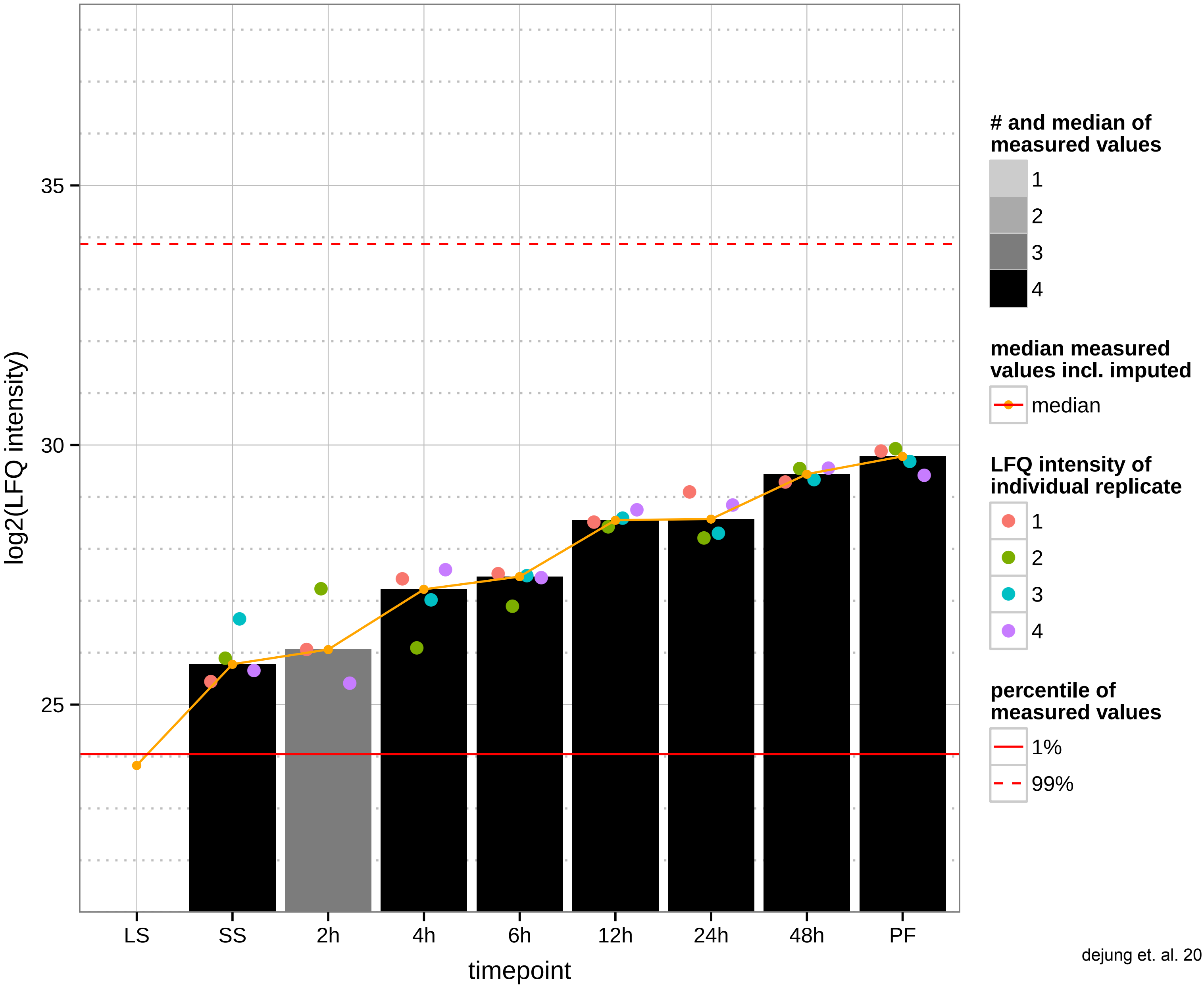
mevalonate kinase, putative
Tb927.4.4070
AGOF: ATP binding, mevalonate kinase activity
AGOC: cytoplasm
AGOP: isoprenoid biosynthetic process, phosphorylation
PGOF: ATP binding, mevalonate kinase activity
PGOC: cytoplasm
PGOP: isoprenoid biosynthetic process





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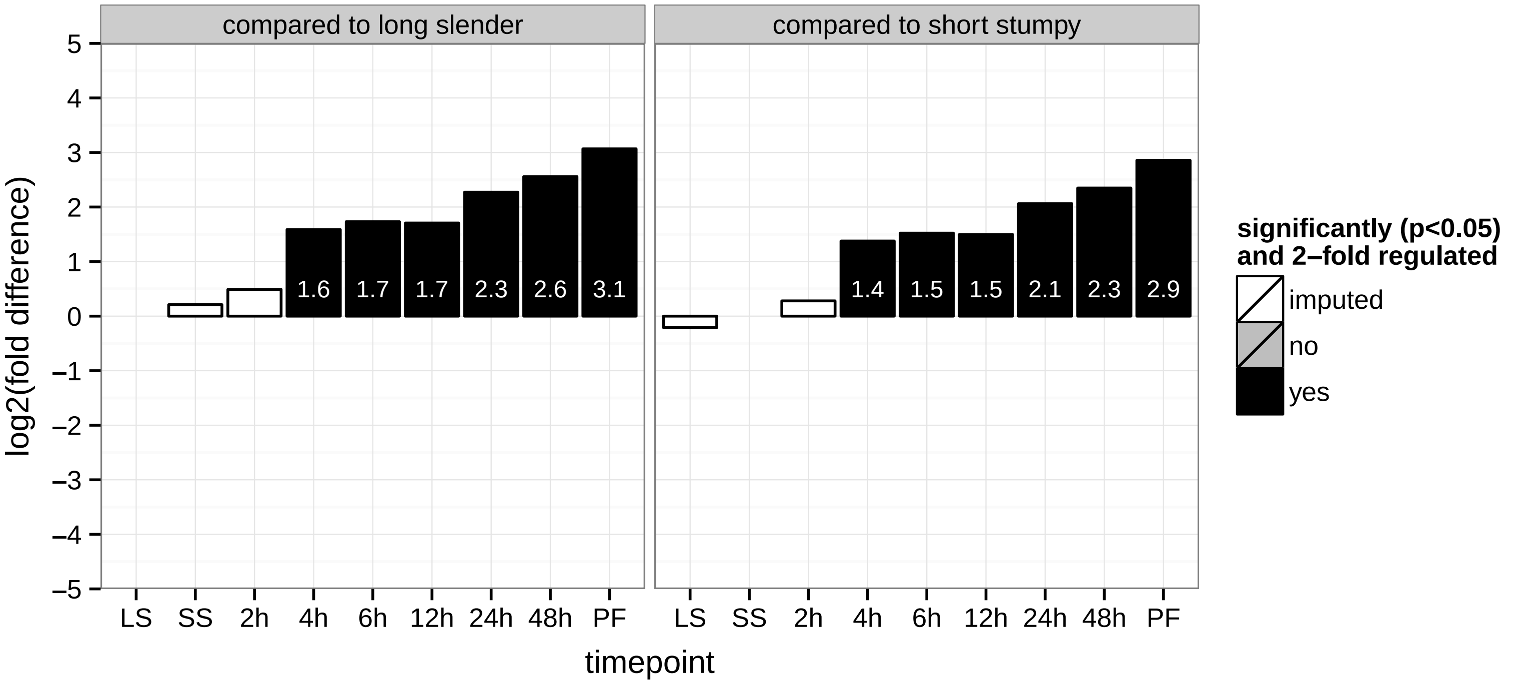
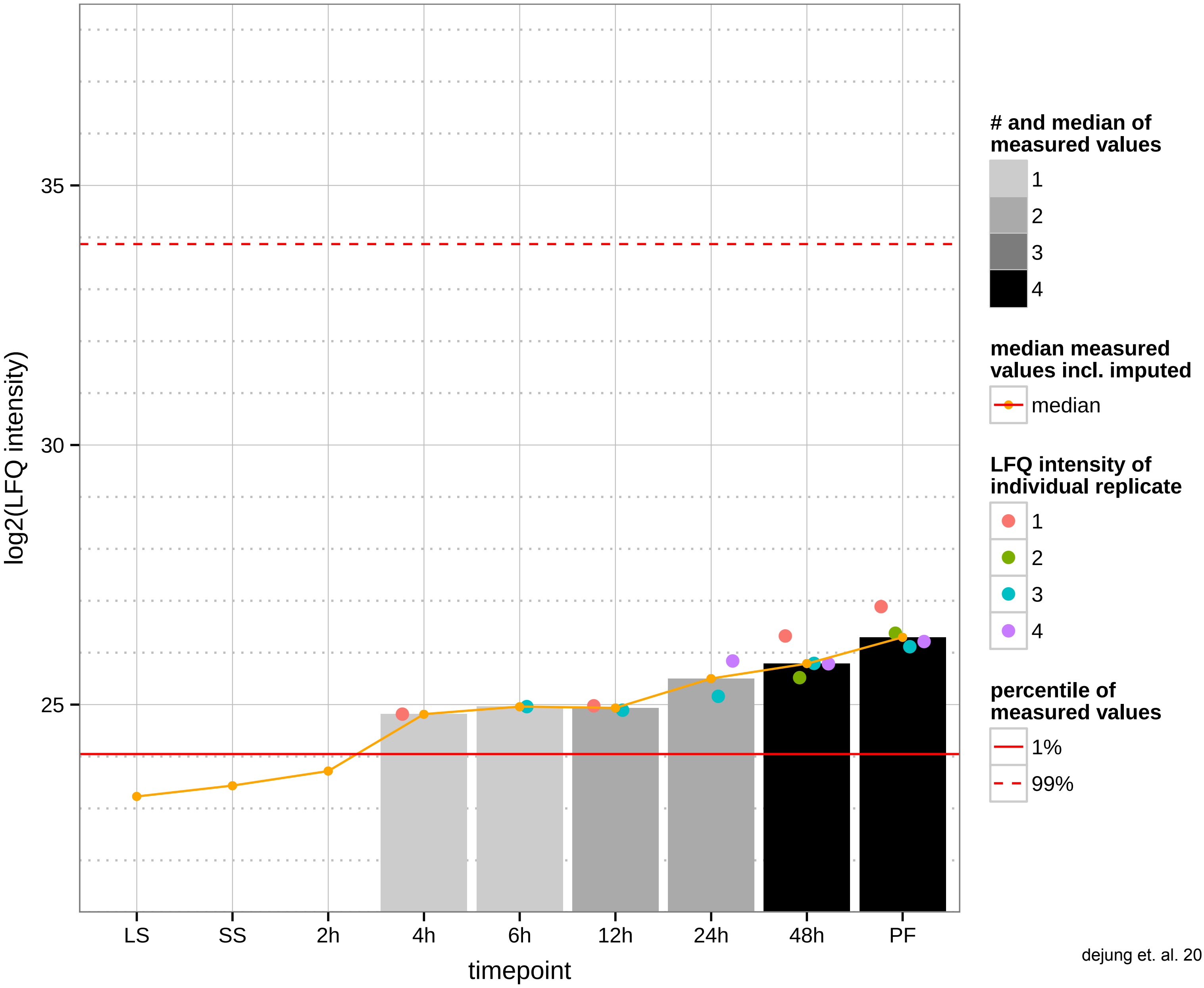
hypothetical protein, conserved
Tb927.6.1250
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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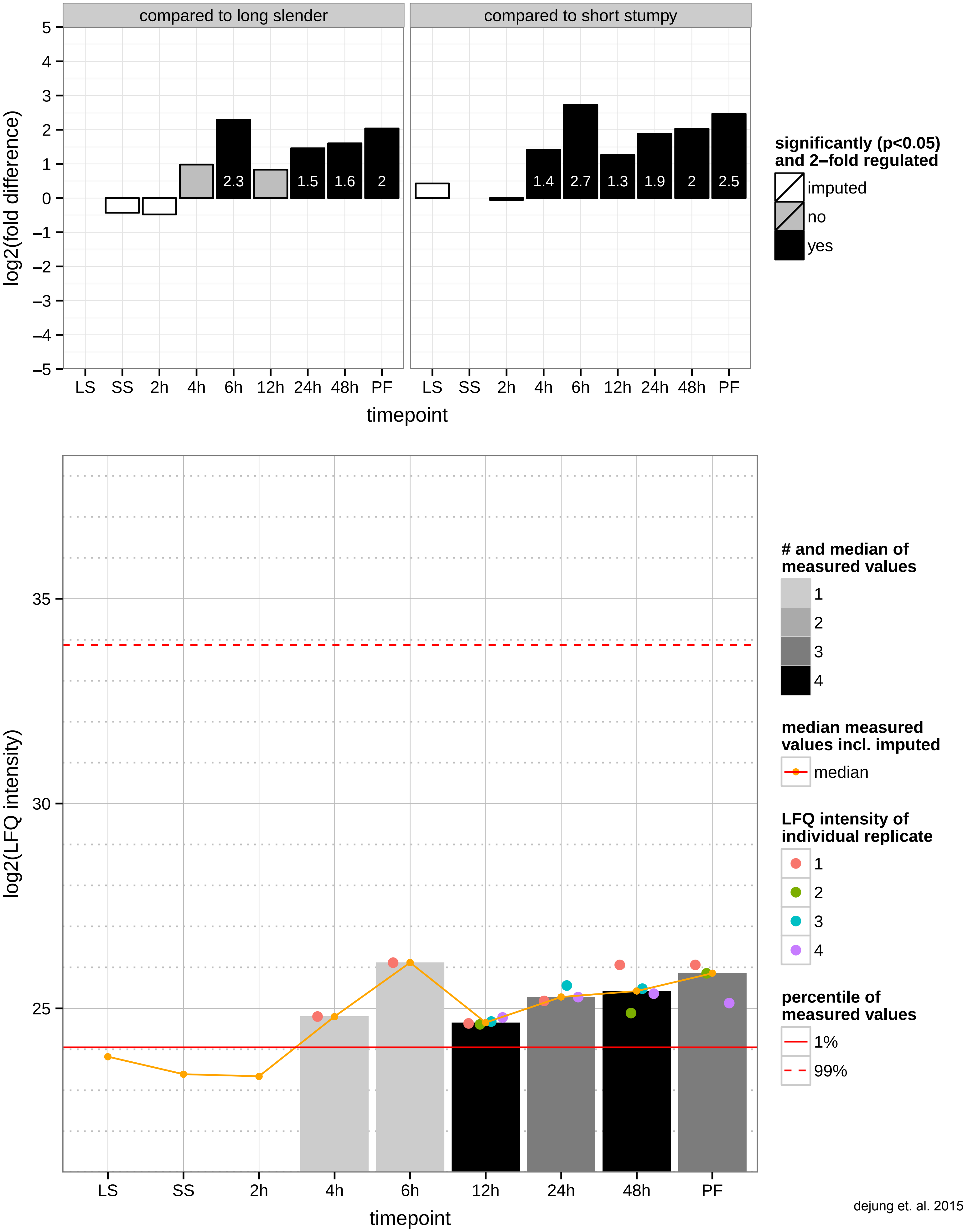
hypothetical protein, conserved
Tb927.6.2380
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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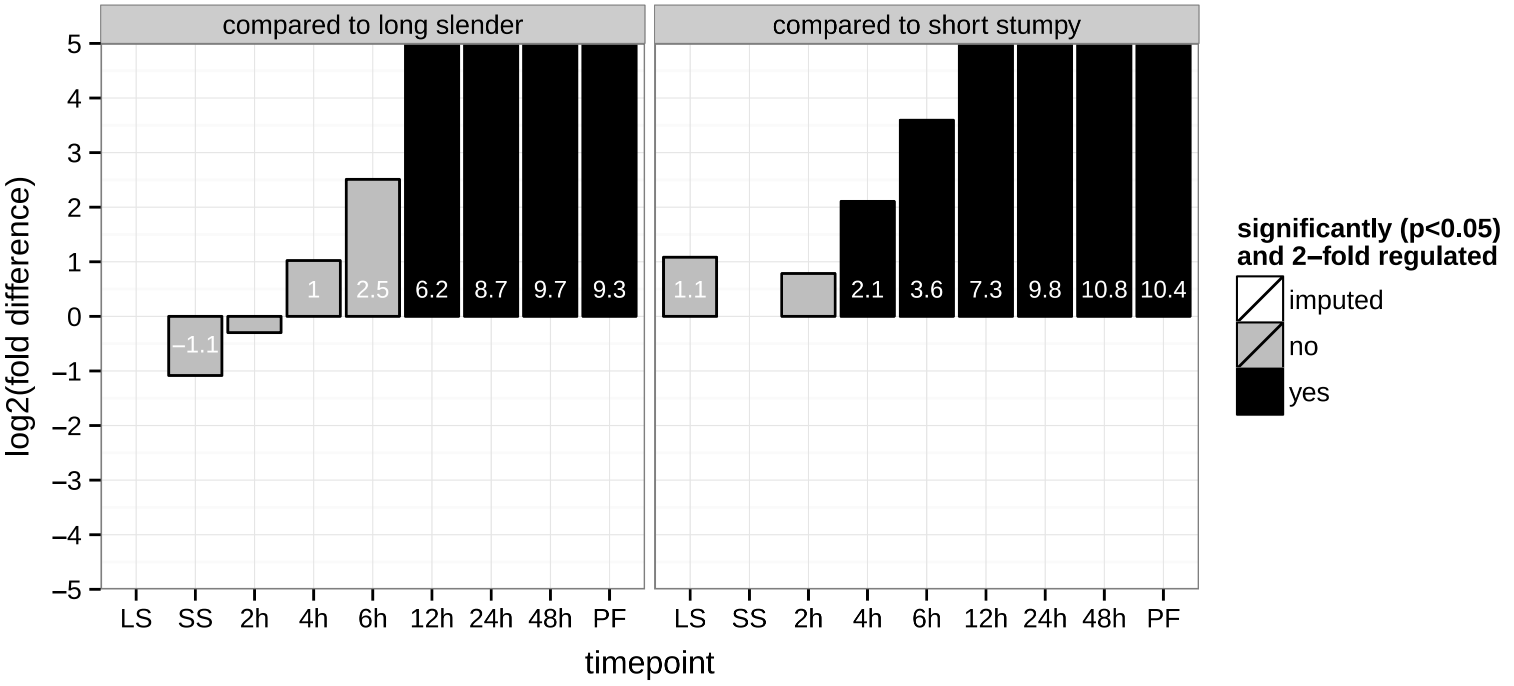
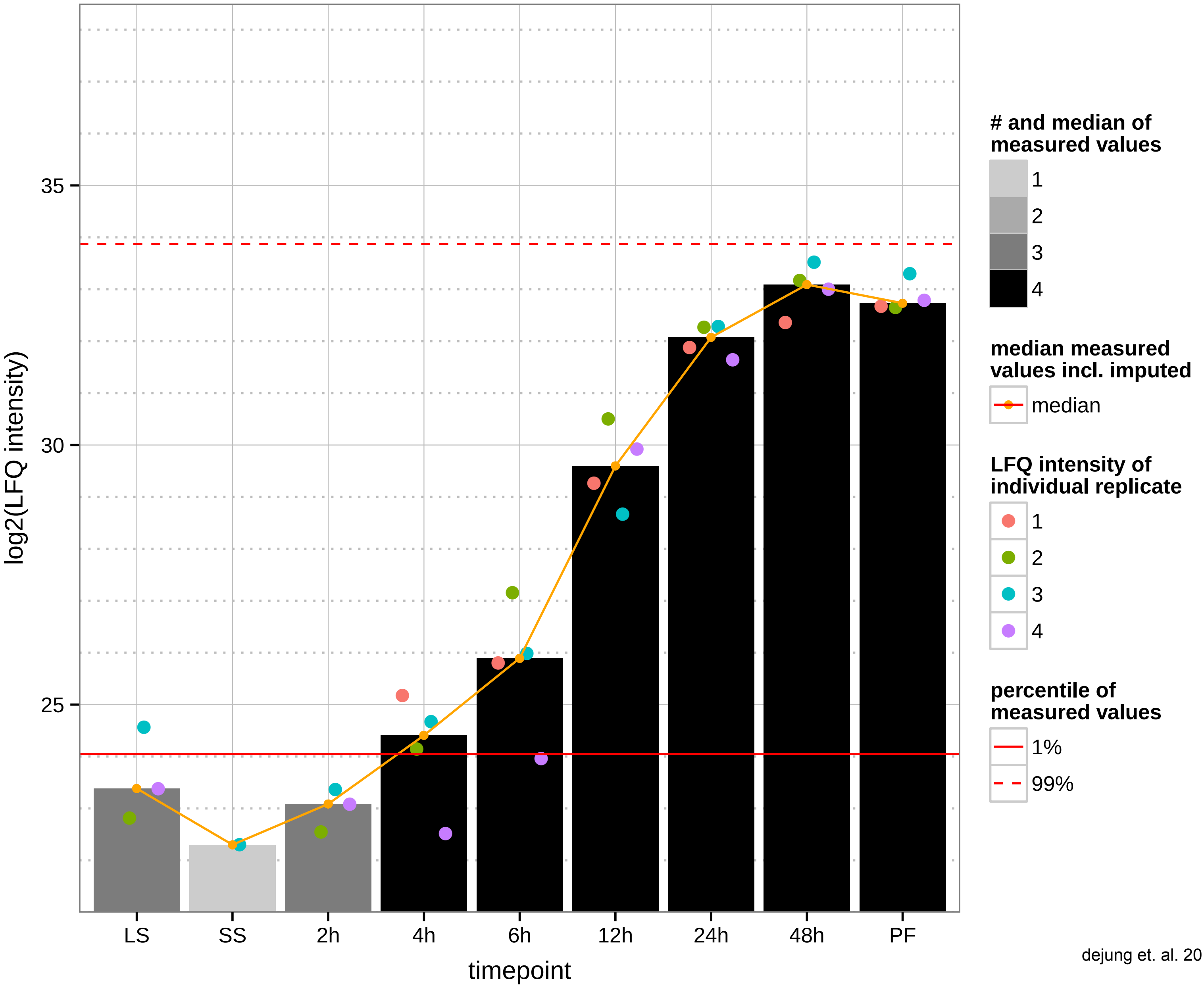
hypothetical protein, conserved
Tb927.7.2980;Tb927.7.3020
AGOF: oxidoreductase activity
AGOC: null
AGOP: null
PGOF: oxidoreductase activity
PGOC: null
PGOP: null





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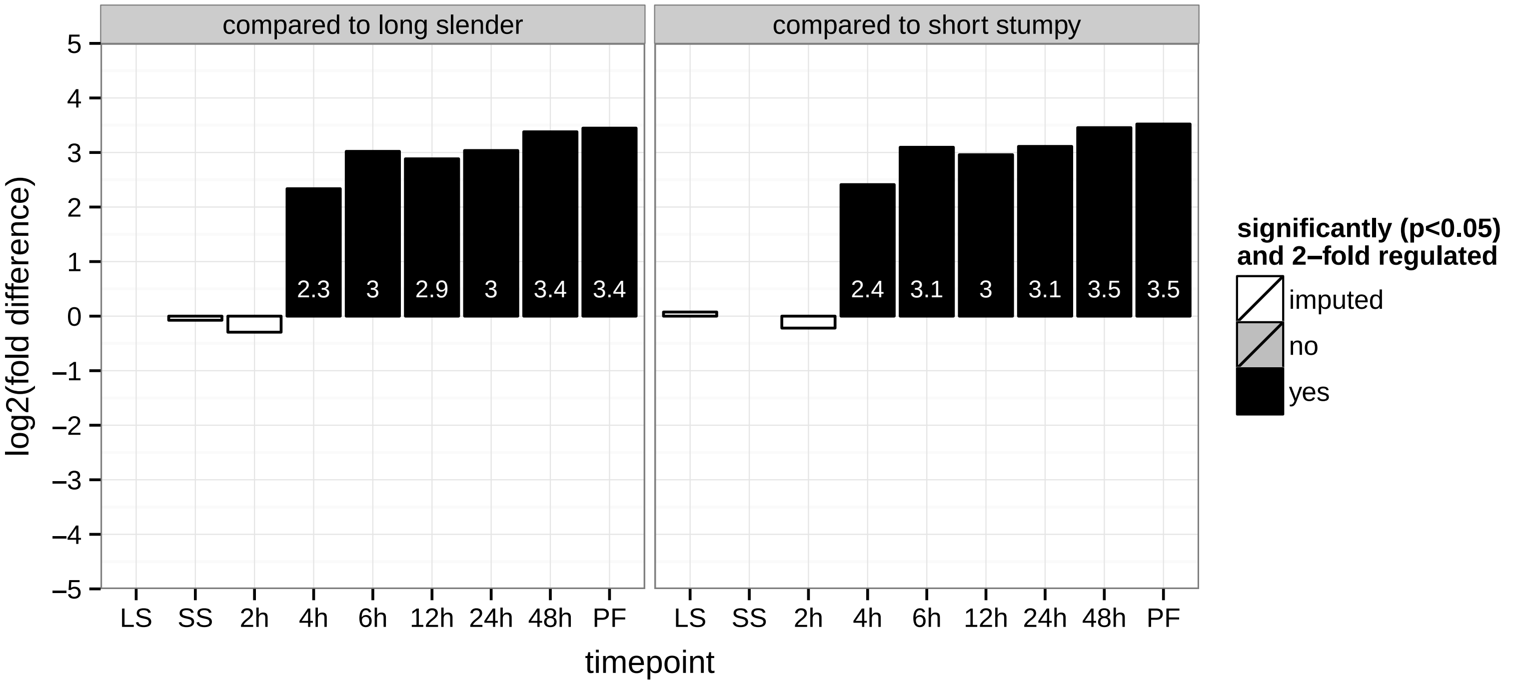
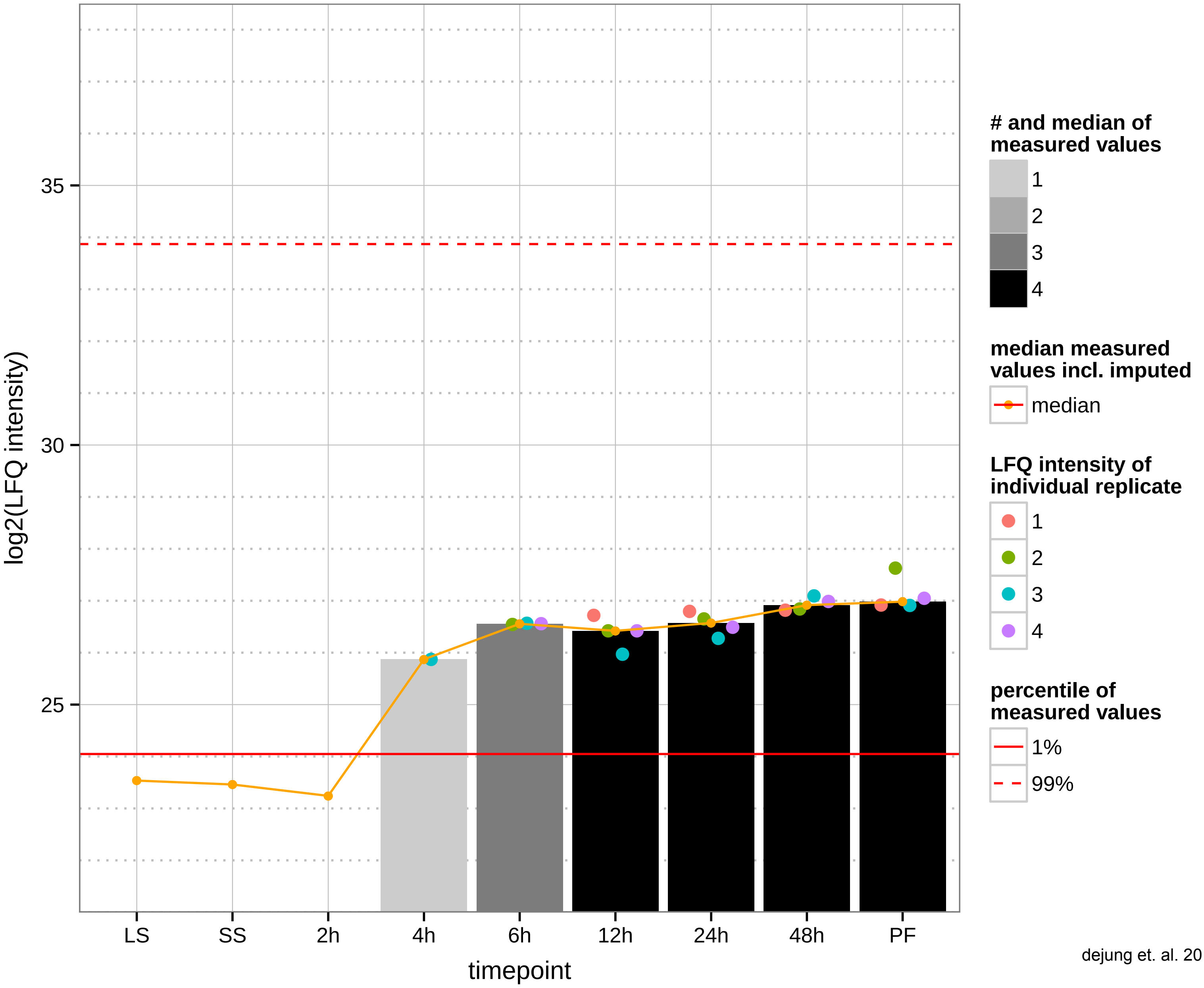
hypothetical protein, conserved
Tb927.7.3810
AGOF: DNA binding
AGOC: mitochondrion
AGOP: regulation of transcription, DNA–dependent
PGOF: DNA binding
PGOC: null
PGOP: regulation of transcription, DNA–dependent





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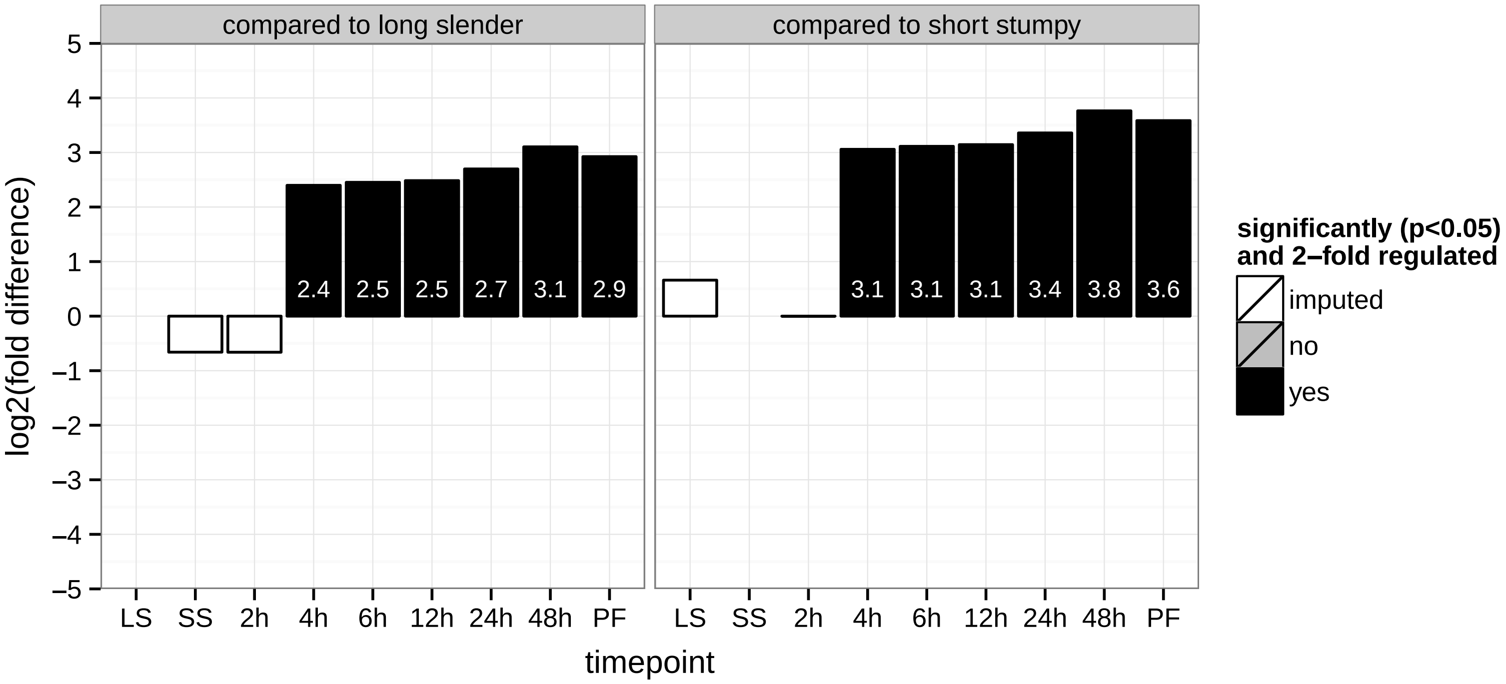
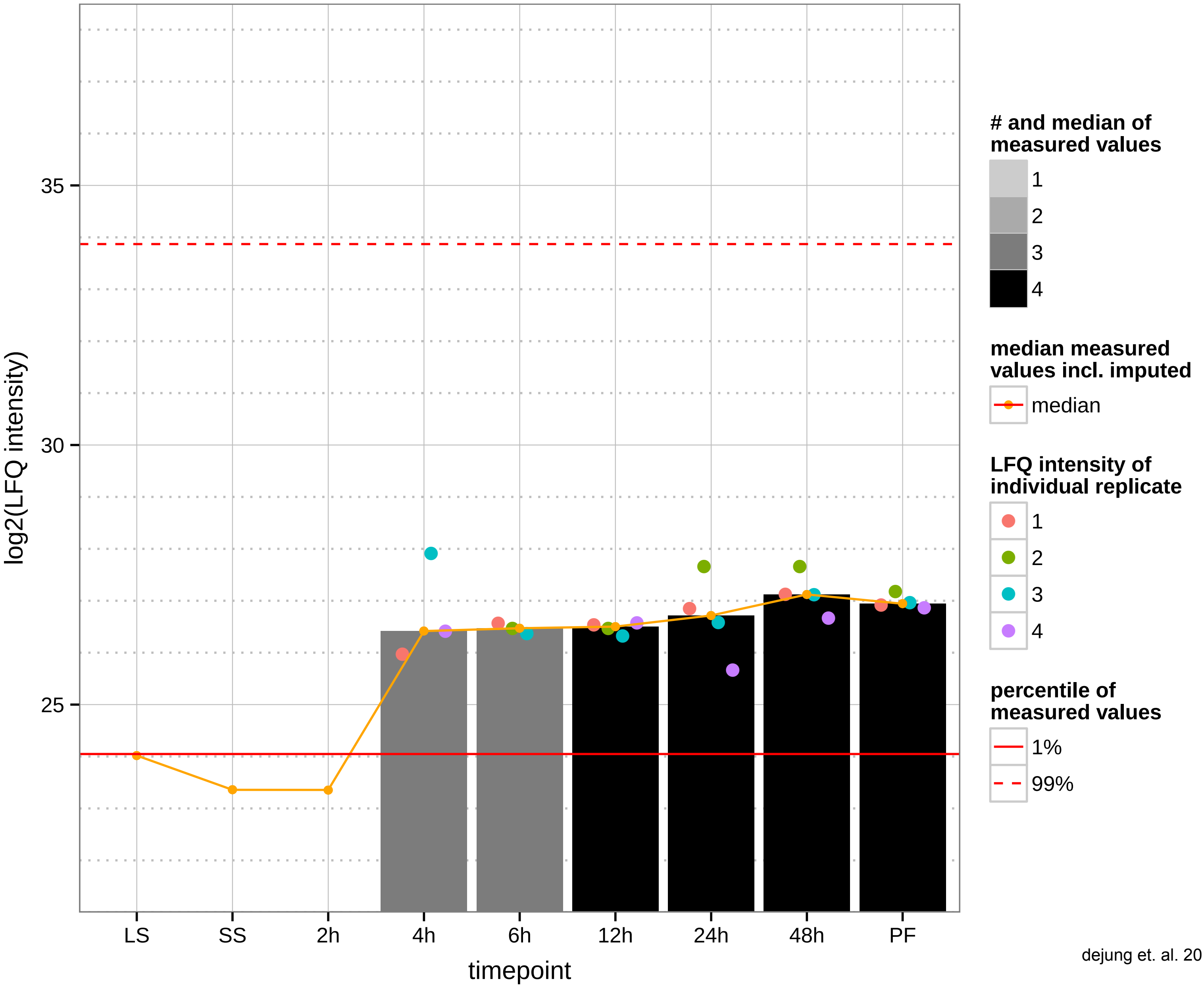
hypothetical protein, conserved
Tb927.7.4270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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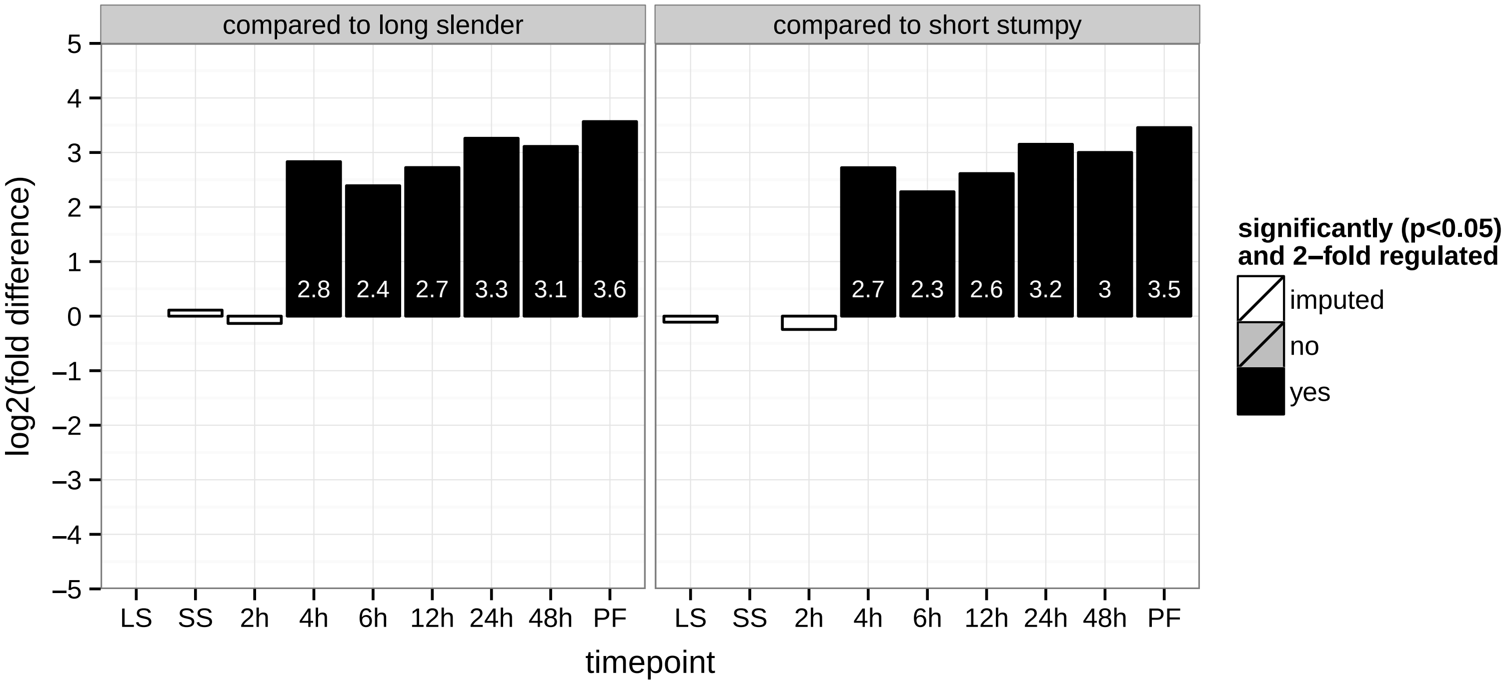
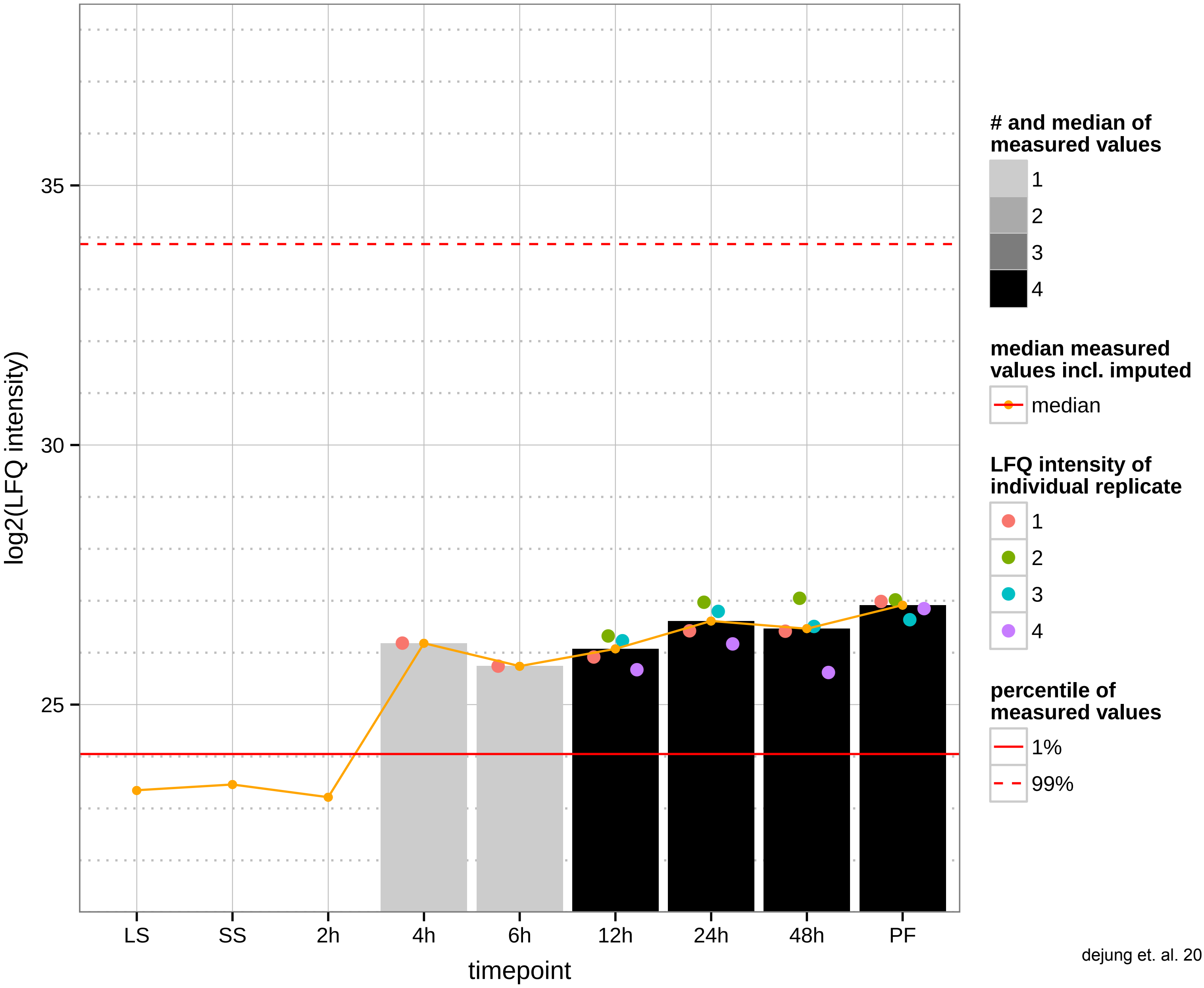
hypothetical protein, conserved
Tb927.7.6820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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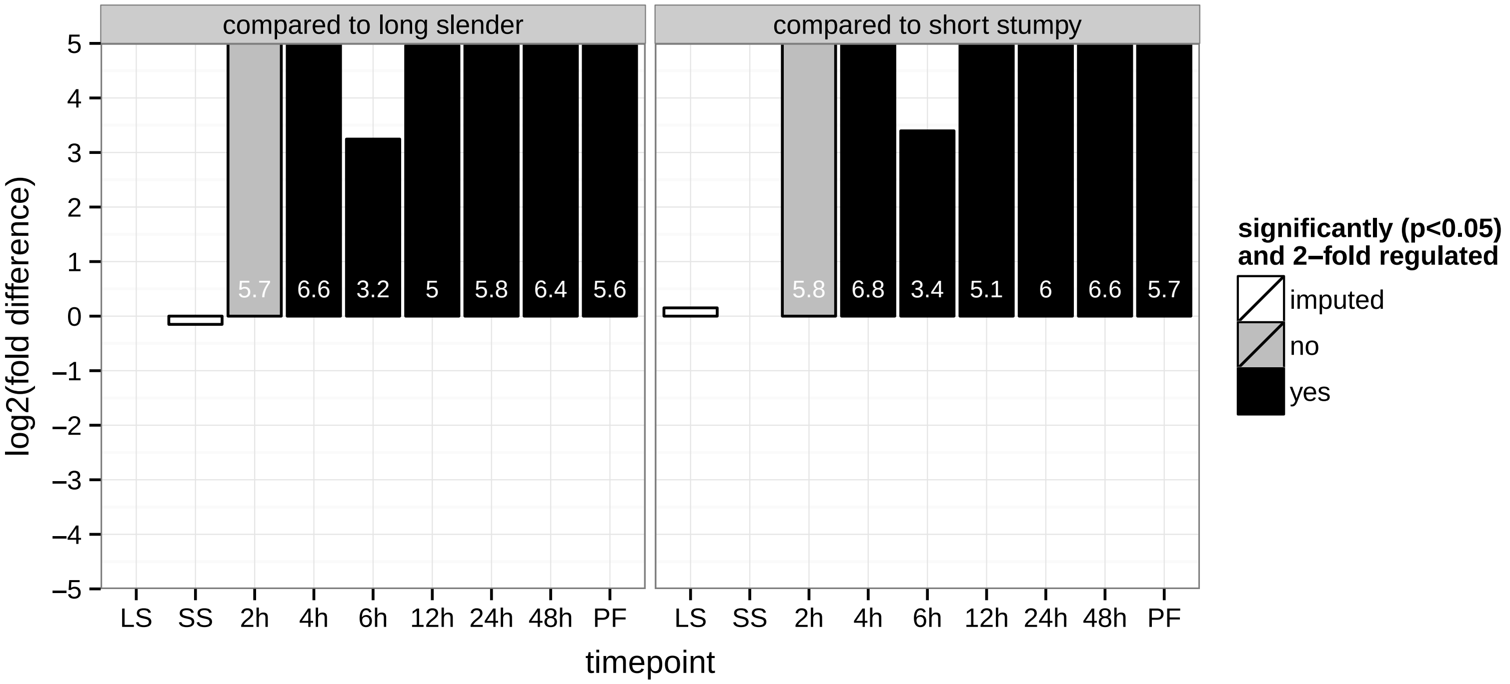
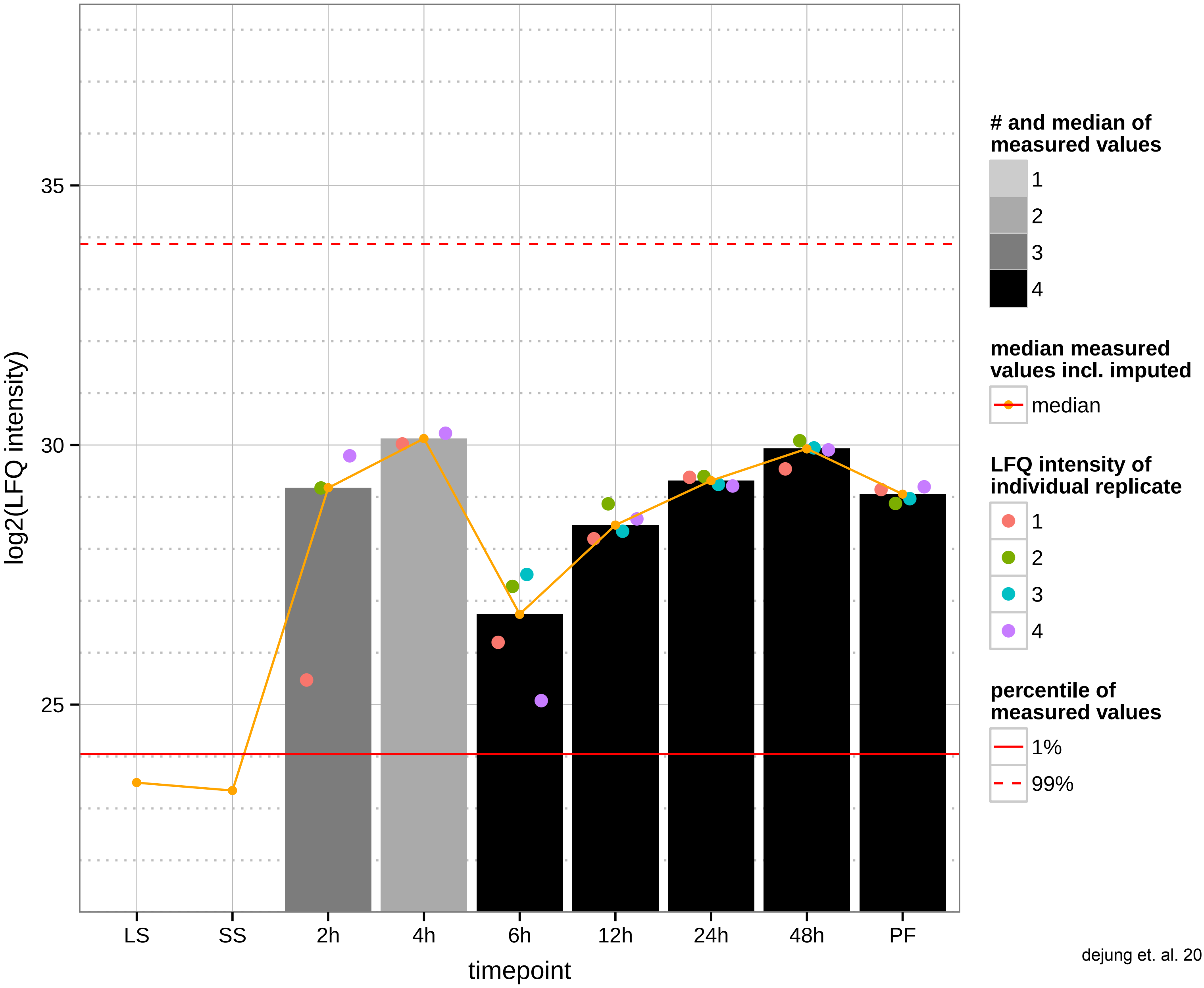
receptor–type adenylate cyclase GRESAG 4, putative, adenylyl cyclase, ATP pyrophosphate–lyase, BAC from homologous re
Tb927.7.7470
AGOF: phosphorus–oxygen lyase activity, null, adenylate cyclase activity
AGOC: null, integral to membrane
AGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction, null
PGOF: phosphorus–oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction





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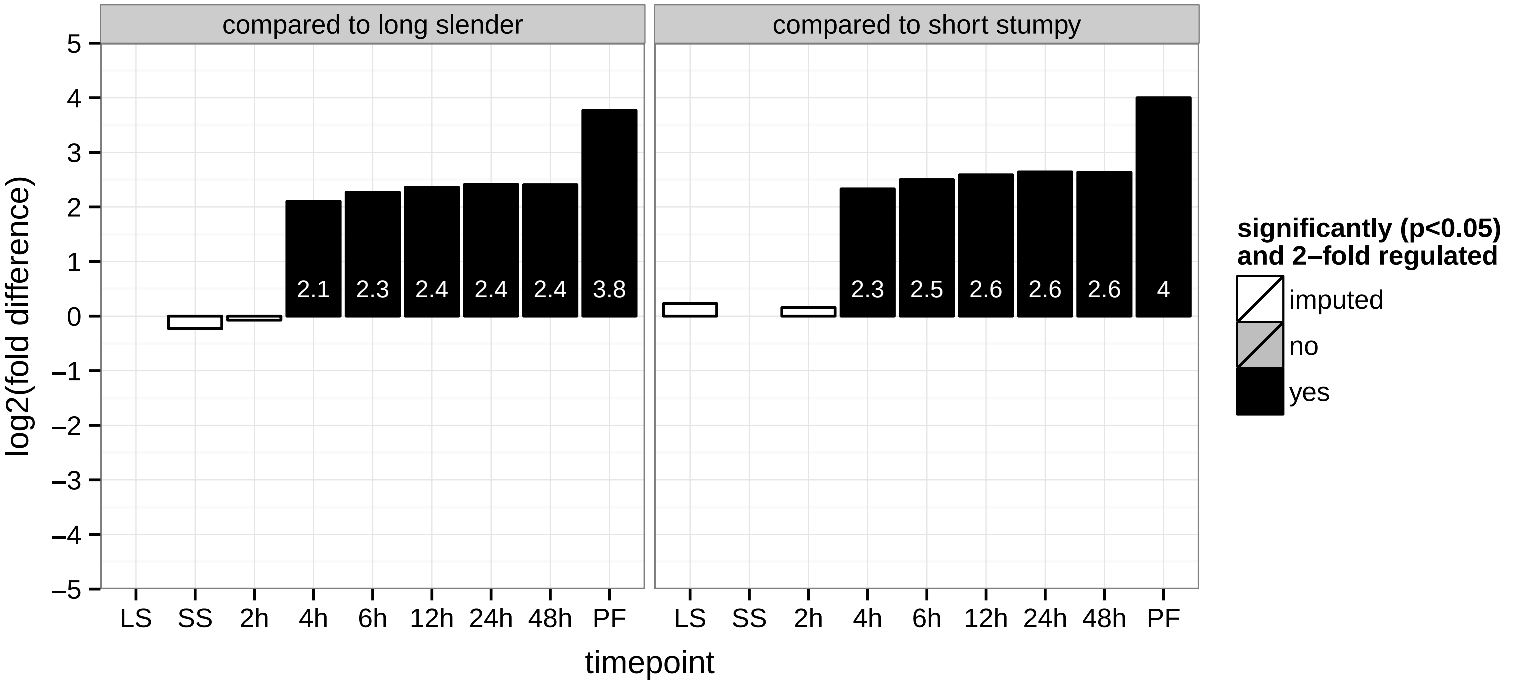
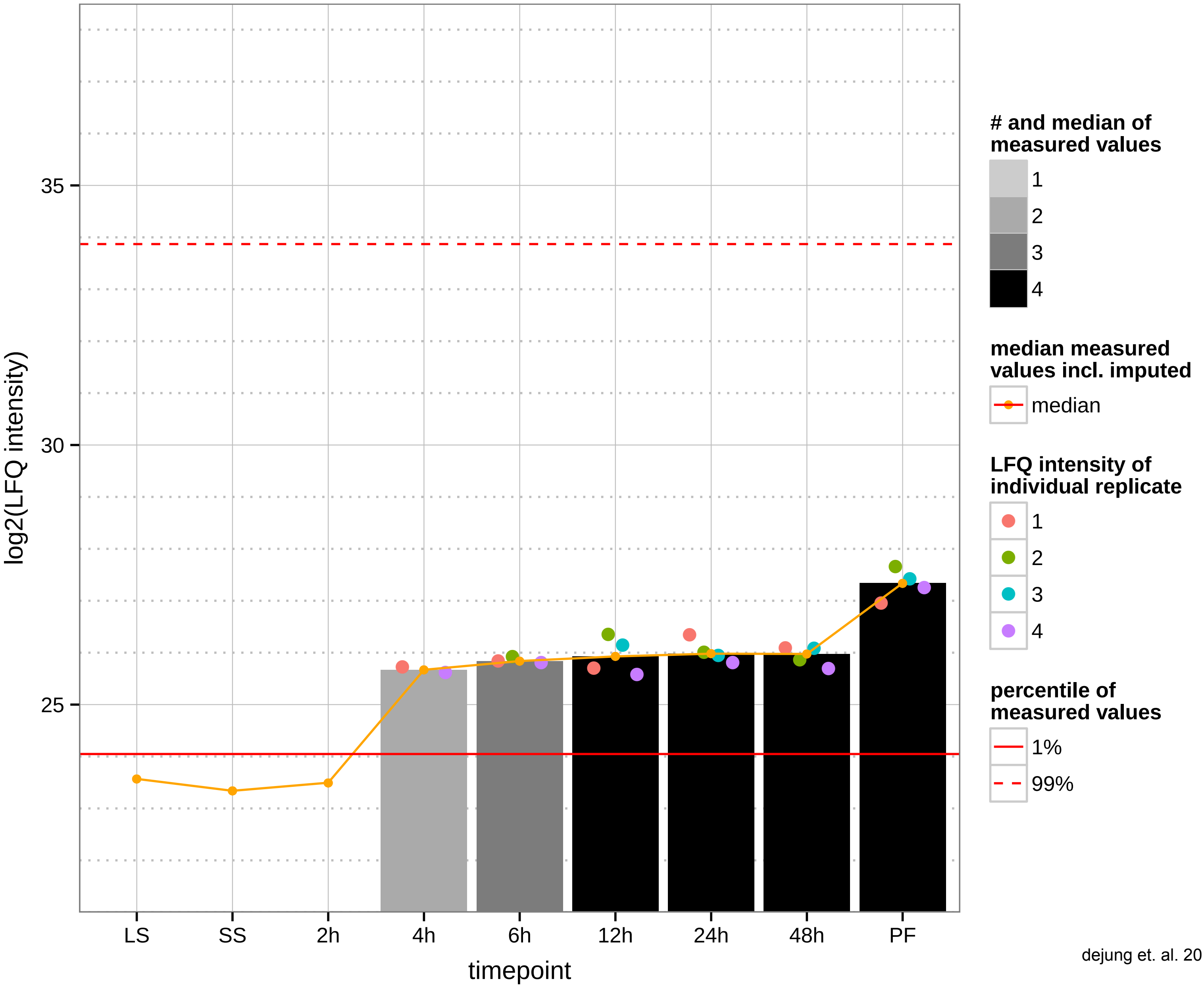
phosphatidylglycerolphosphate synthase, mitochondrial (pgps)
Tb927.8.1720
AGOF: CDP−diacylglycerol−glycerol−3−phosphate 3−phosphatidyltransferase activity
AGOC: membrane, mitochondrion
AGOP: cardiolipin biosynthetic process, glycerophospholipid biosynthetic process, inner mitochondrial membrane organizatio
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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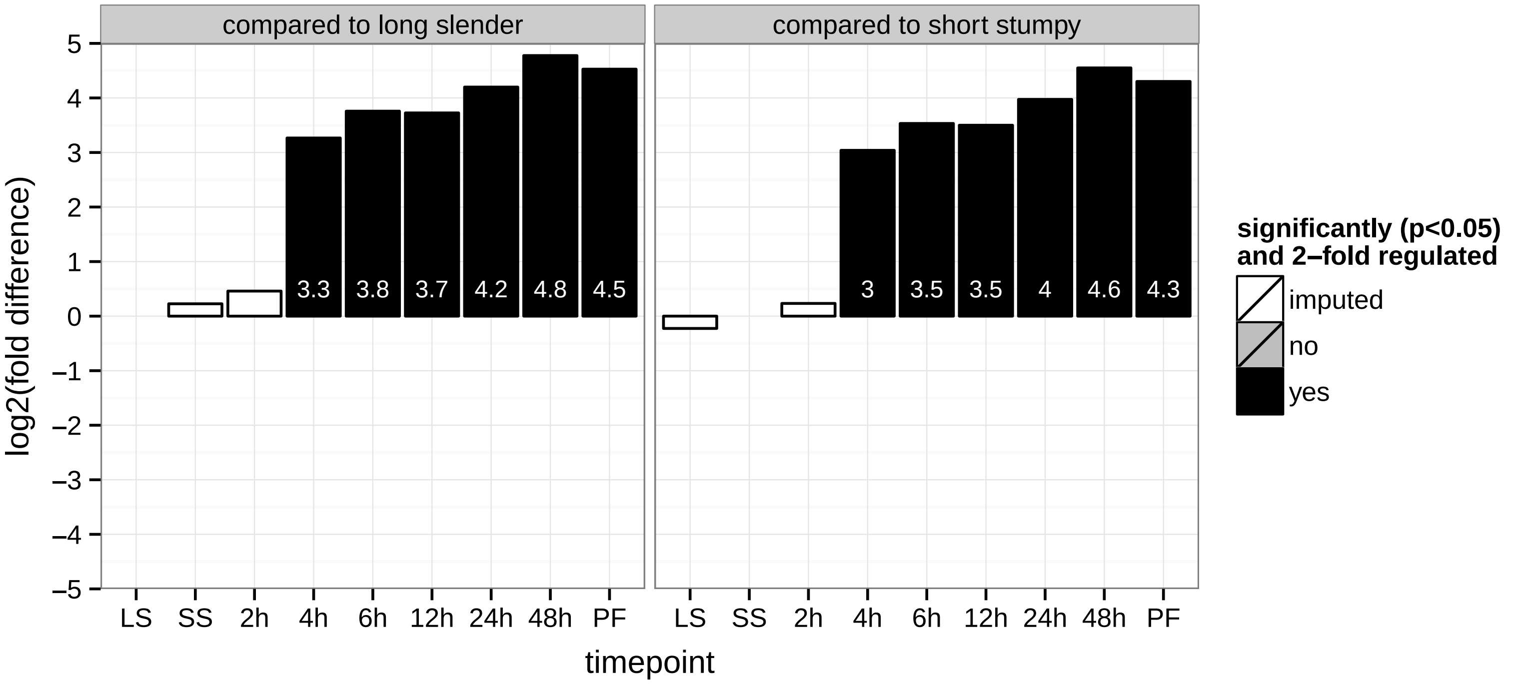
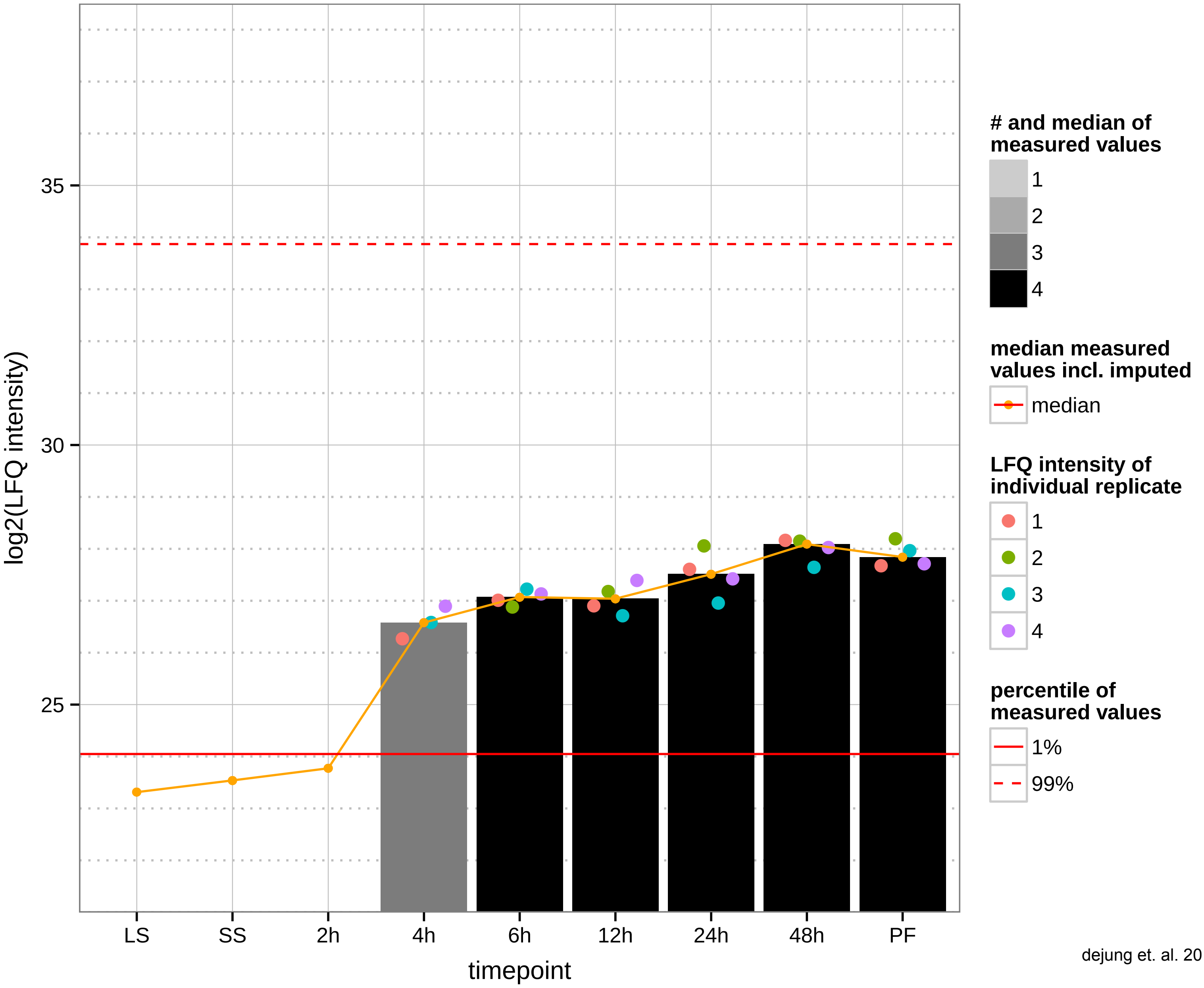
hypothetical protein, conserved
Tb927.8.2330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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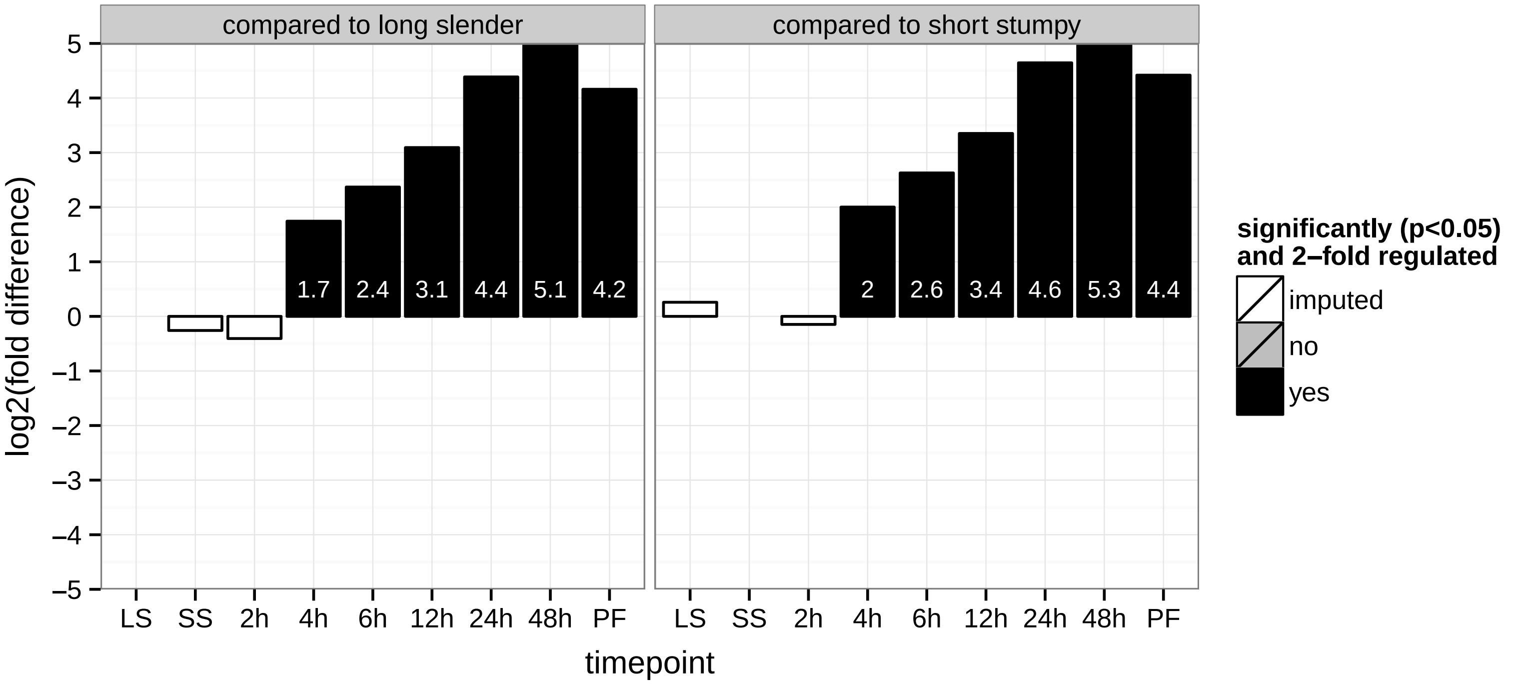
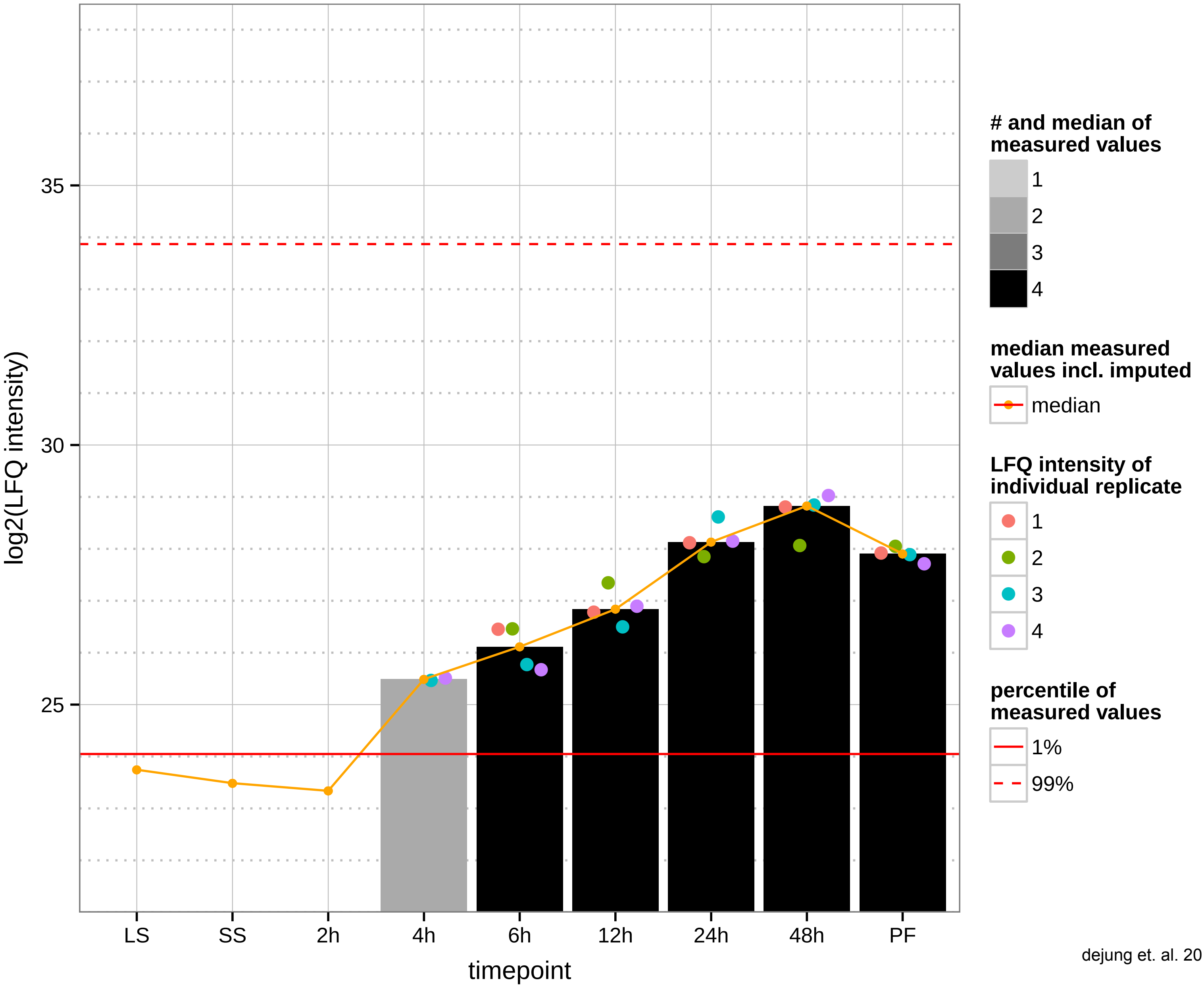
flagellum–adhesion glycoprotein (fla1)
Tb927.8.4010
AGOF: null
AGOC: cilium, flagellar pocket, integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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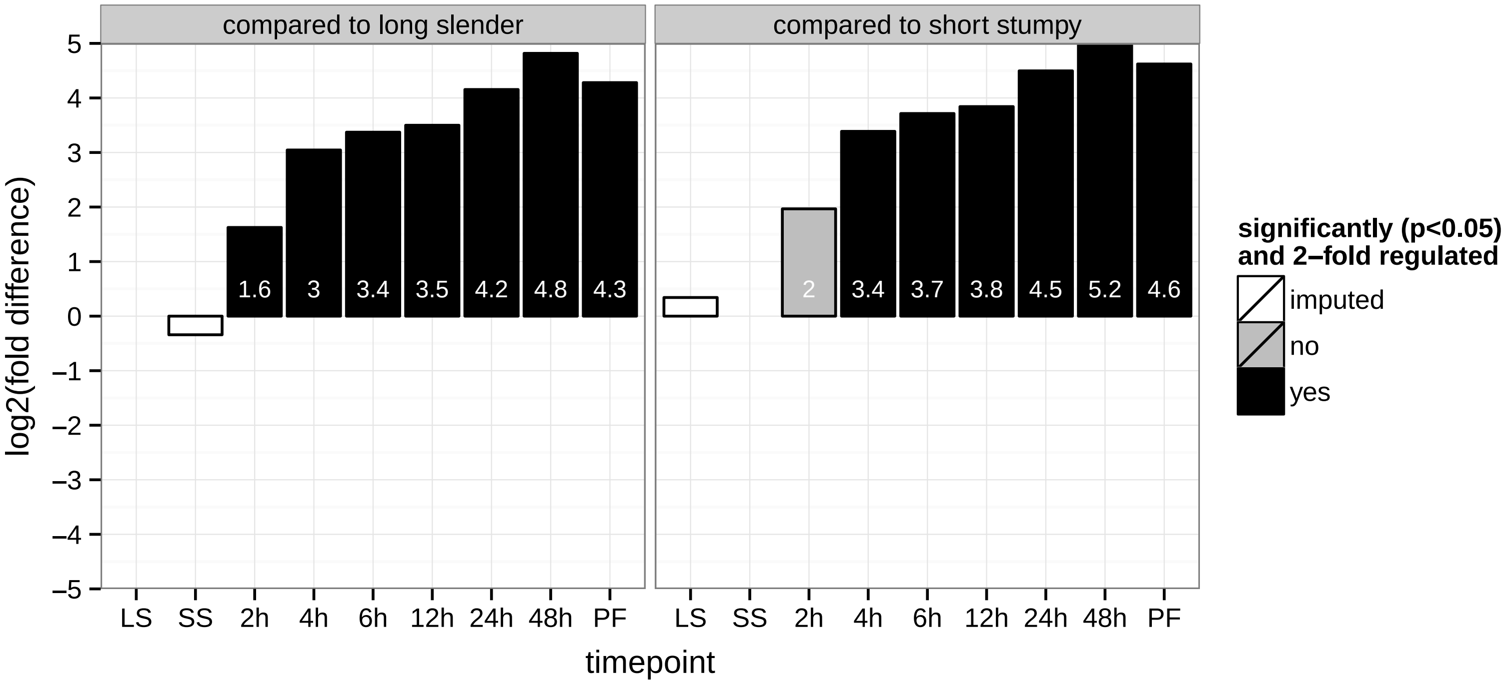
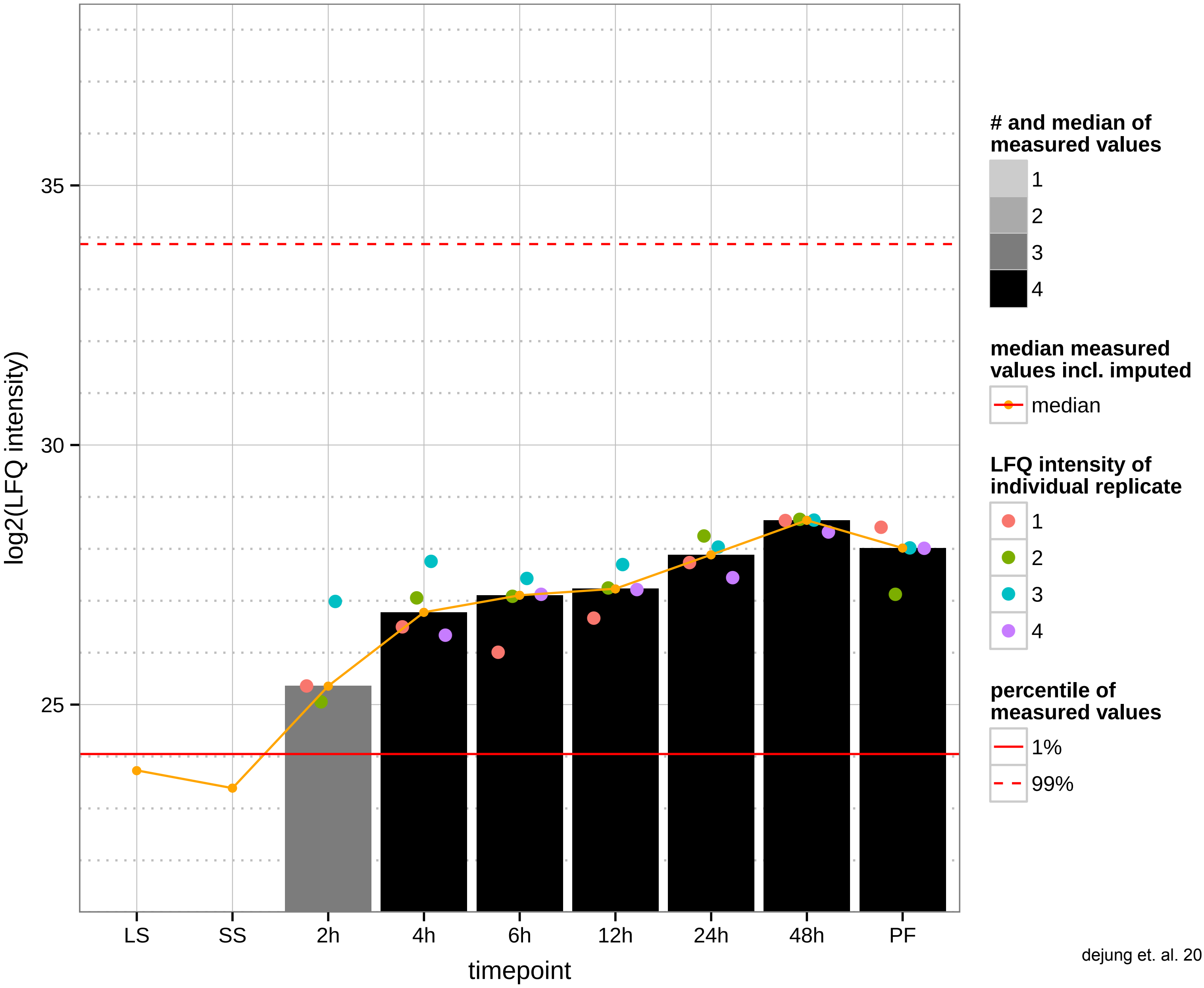
hypothetical protein, conserved
Tb927.8.4100;Tb927.8.4050
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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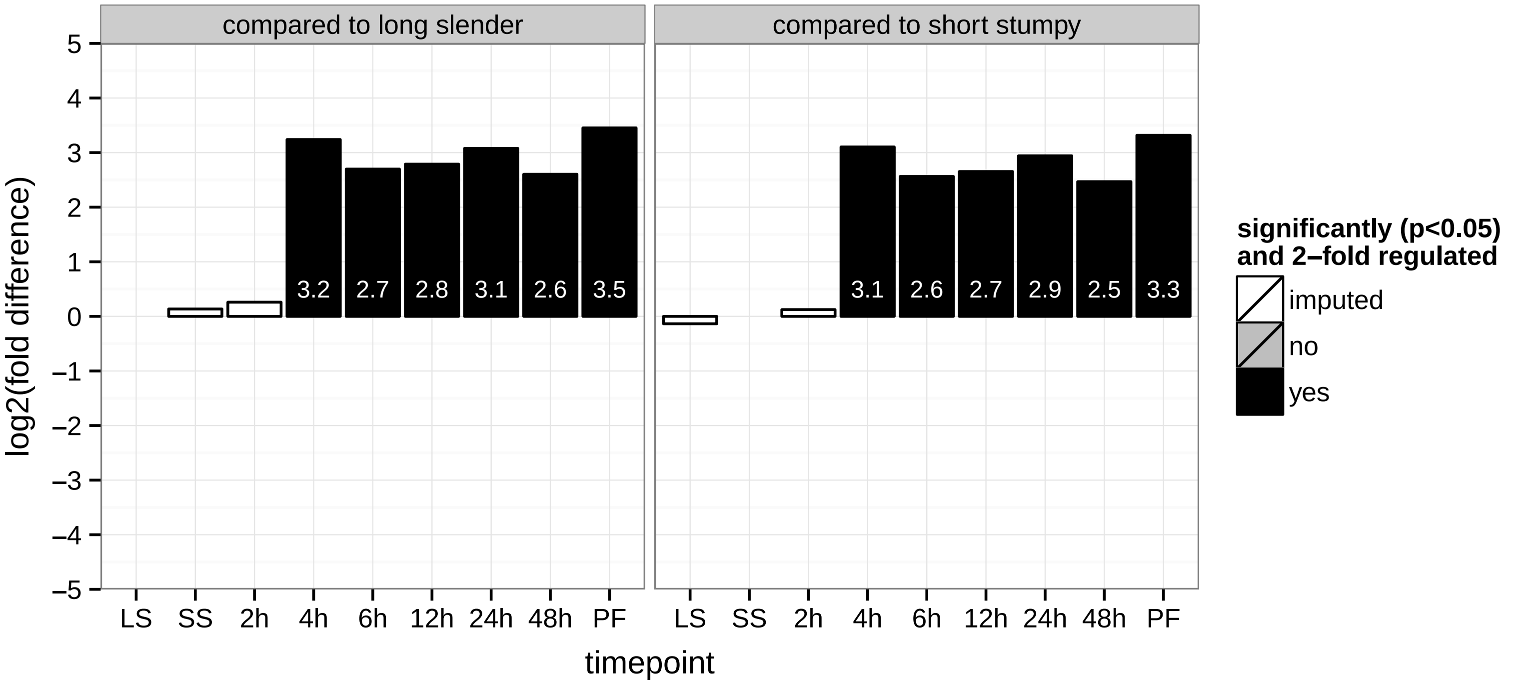
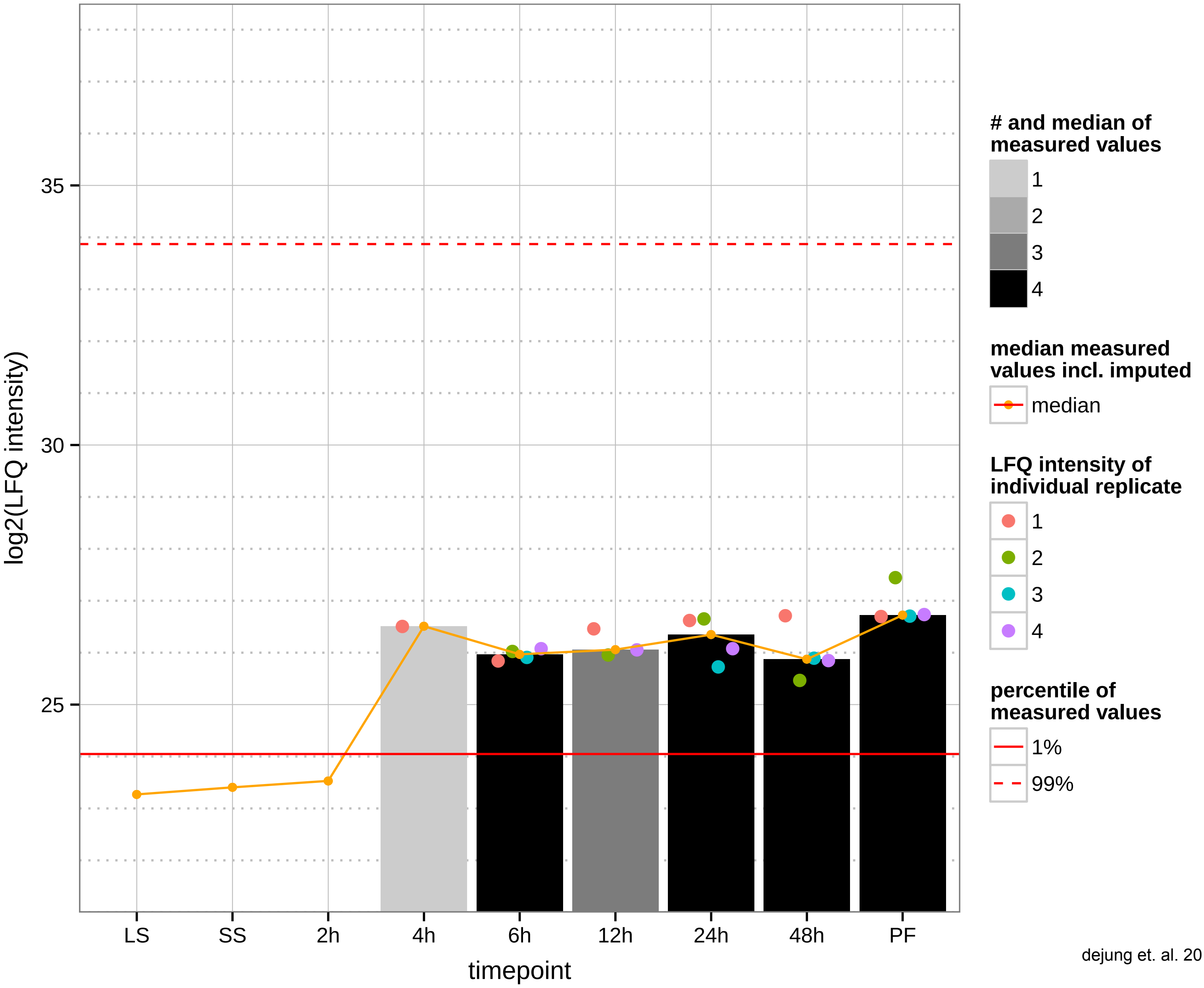
hypothetical protein, conserved
Tb927.8.4150
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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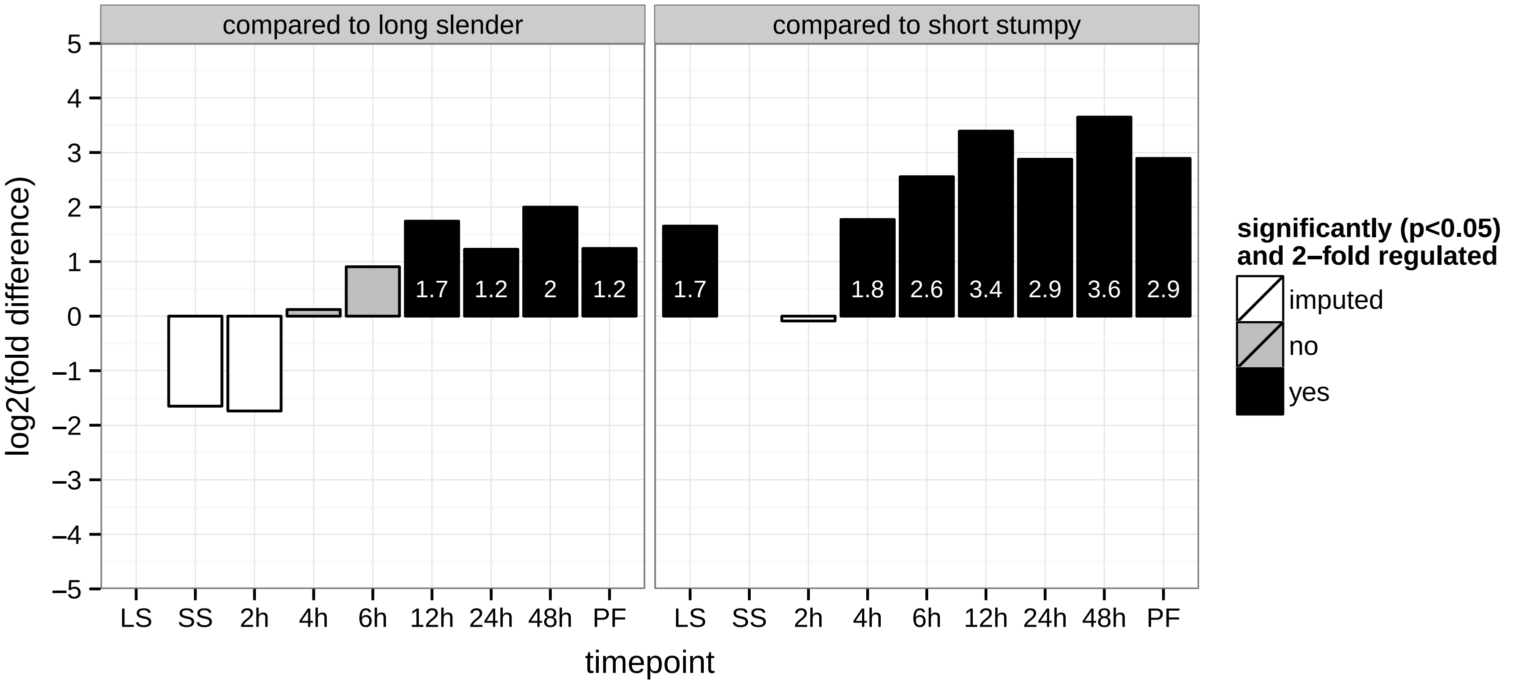
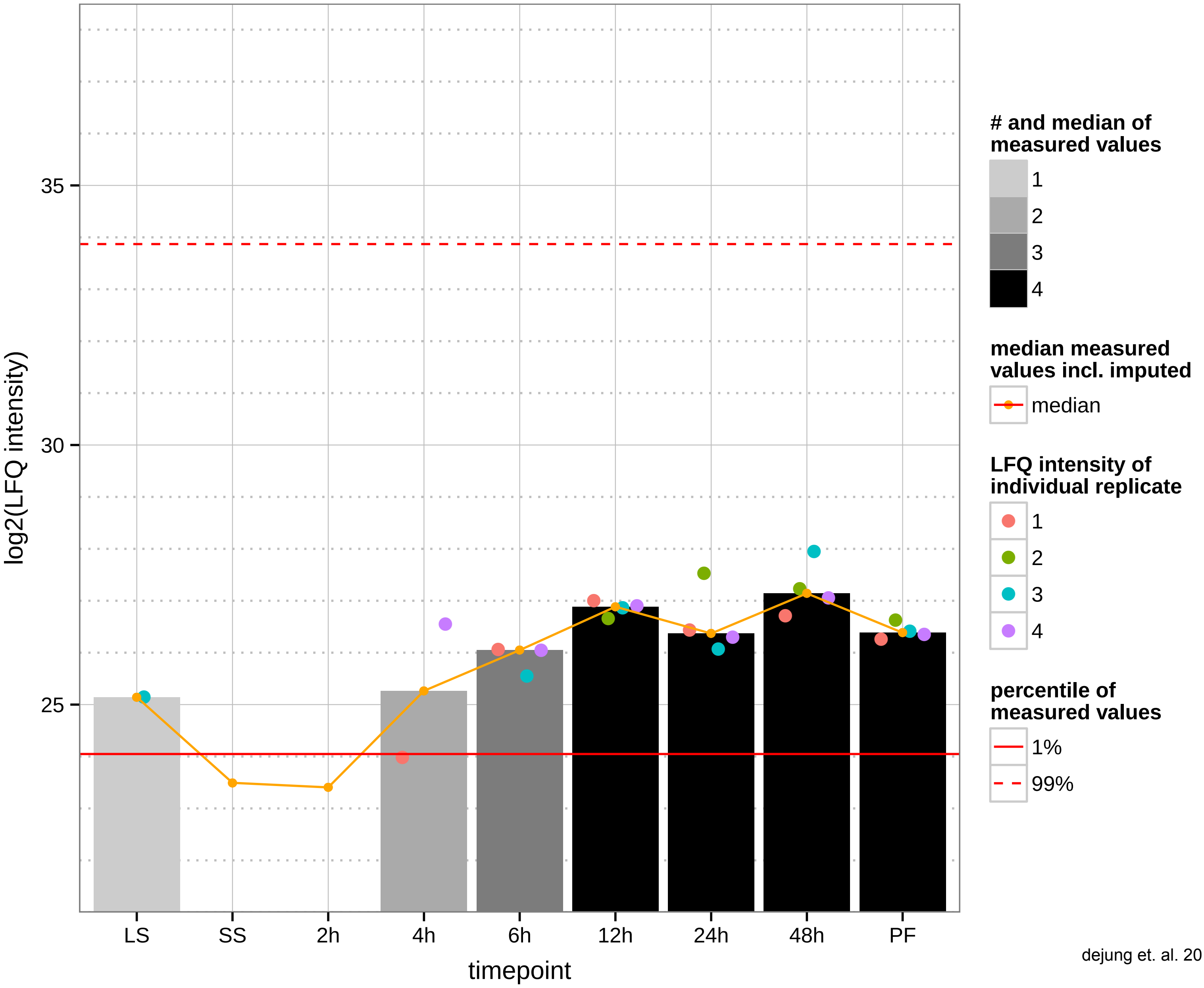
hypothetical protein, conserved
Tb927.8.4190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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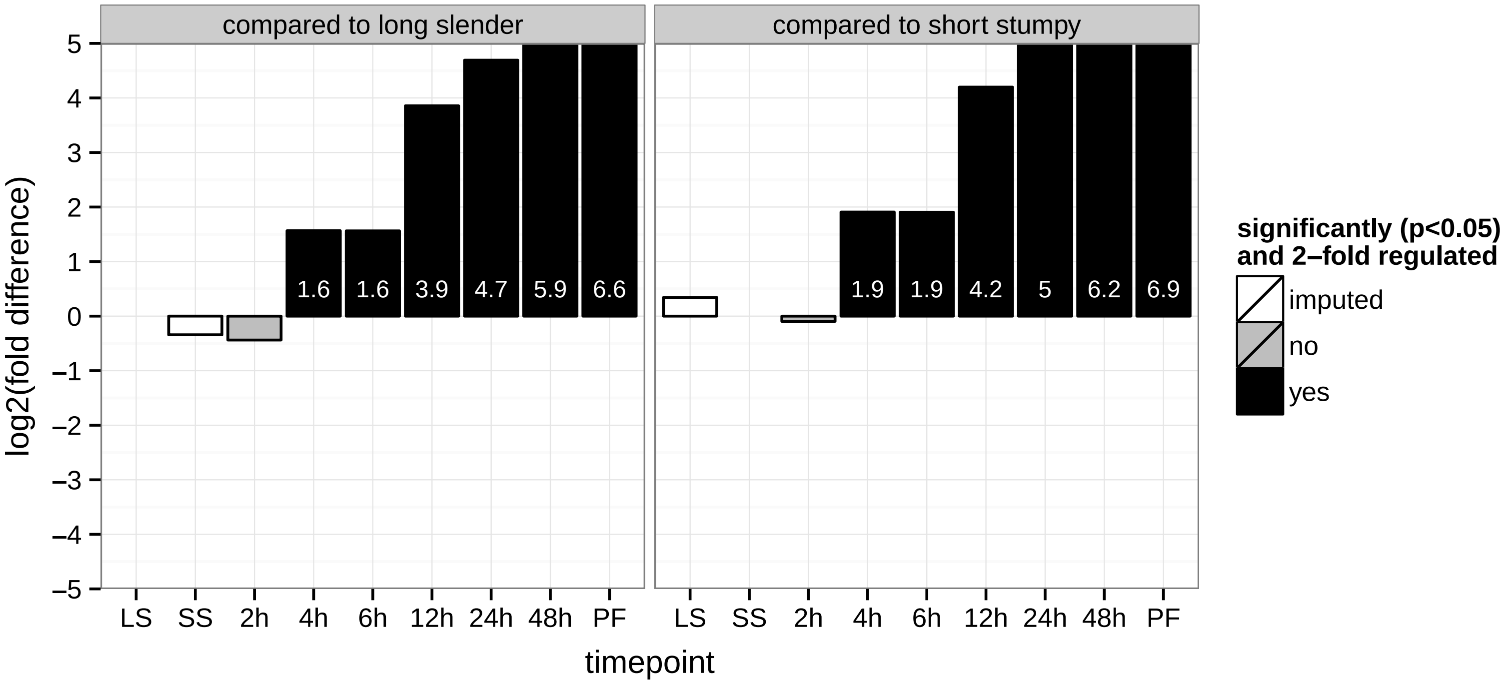
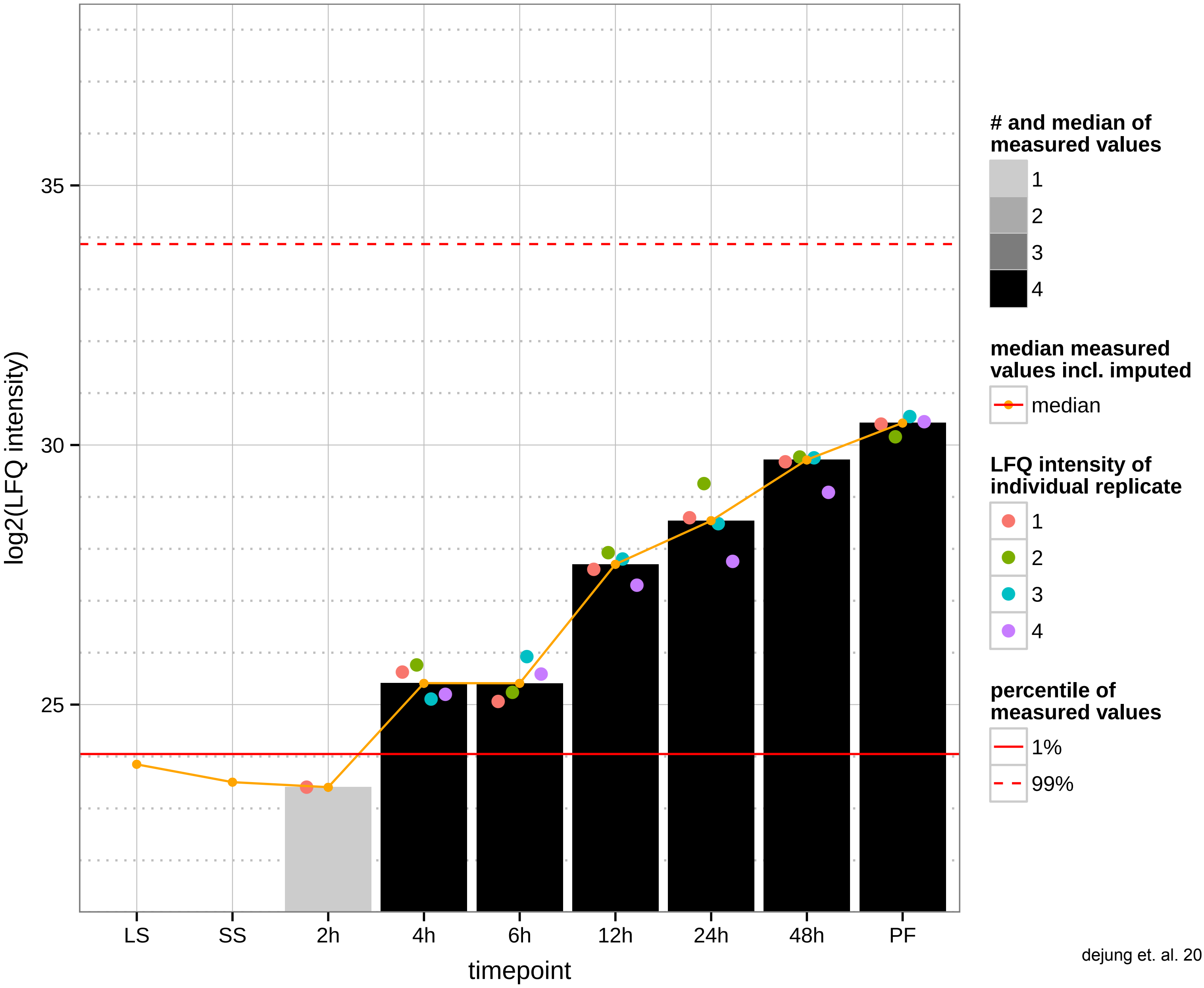
cytochrome c
Tb927.8.5120
AGOF: electron carrier activity, heme binding, iron ion binding
AGOC: mitochondrion
AGOP: aerobic respiration
PGOF: electron carrier activity, heme binding, iron ion binding
PGOC: null
PGOP: null





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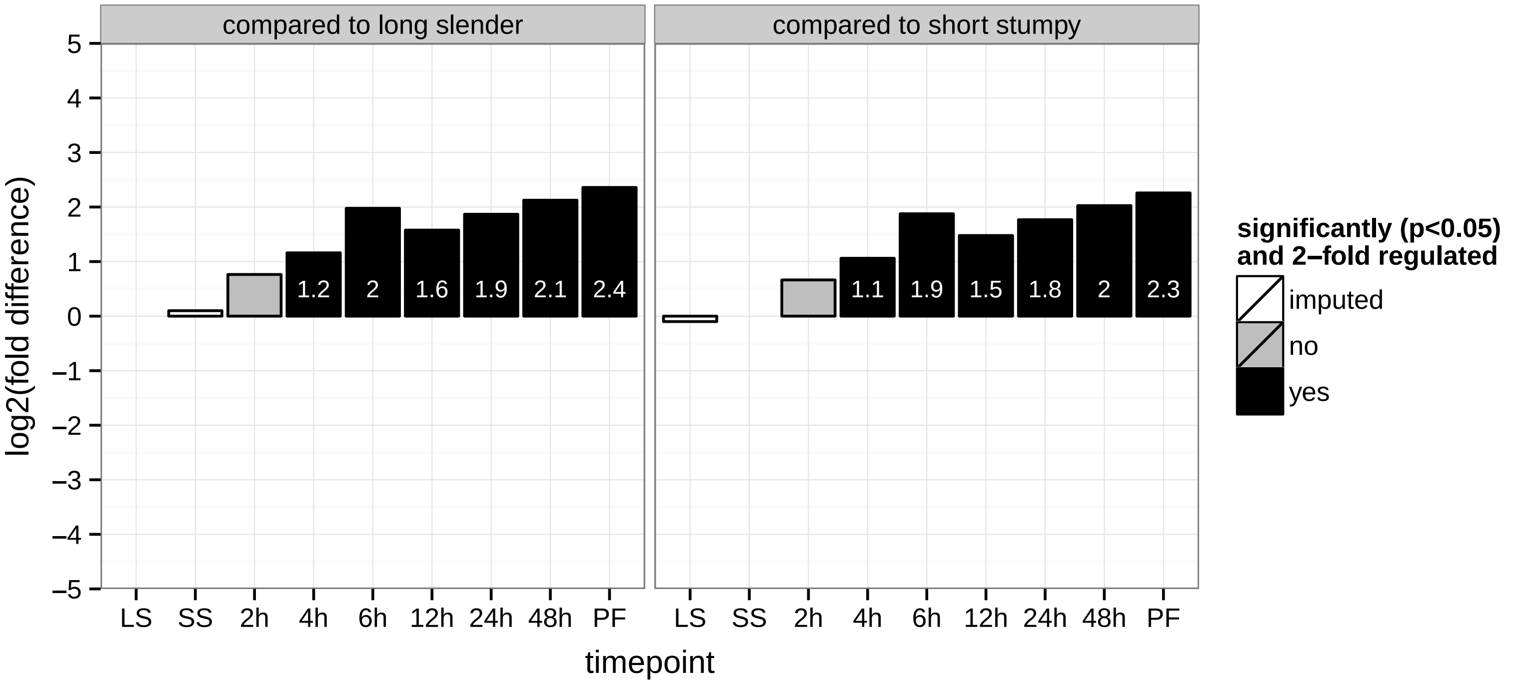
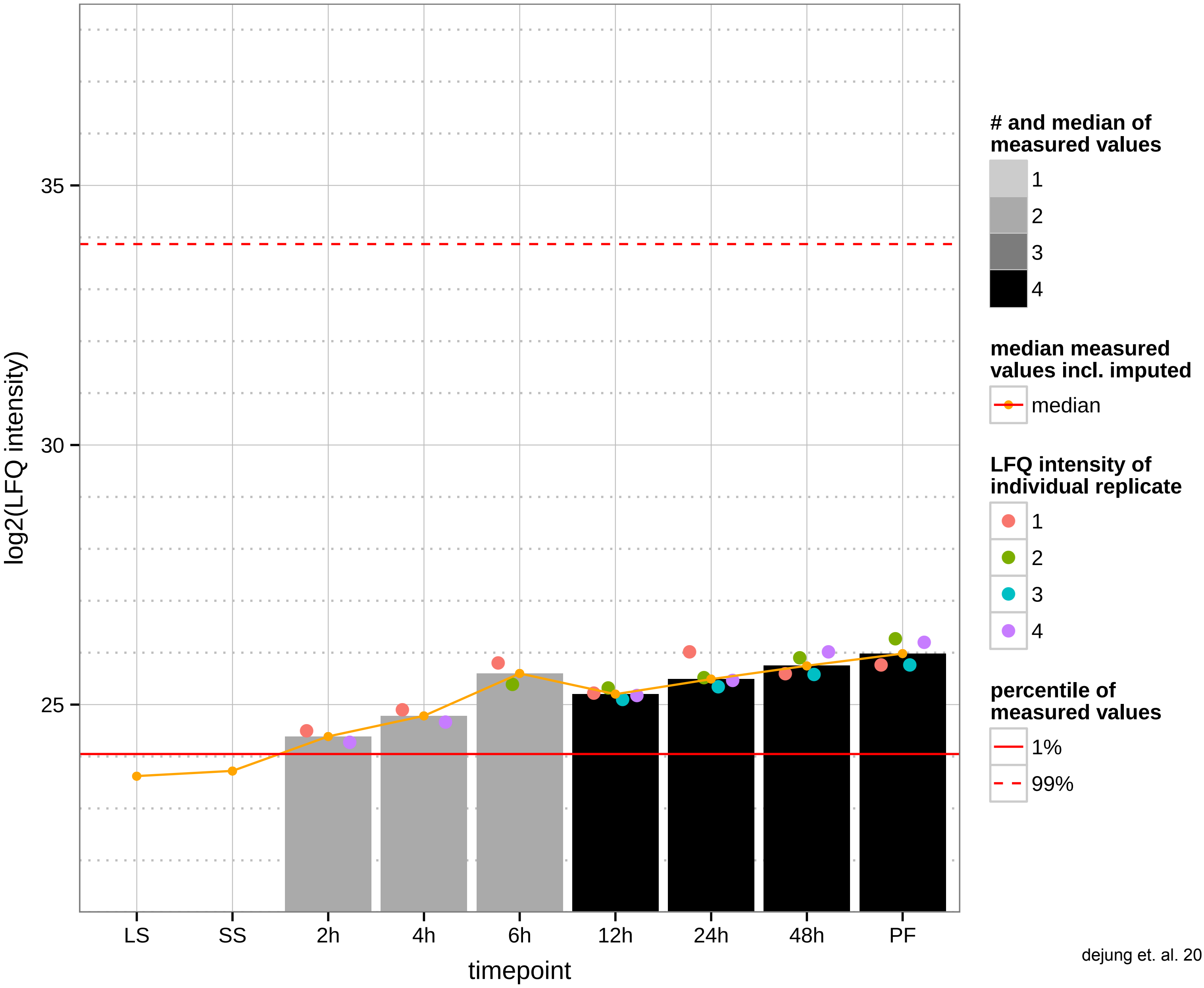
hypothetical protein, conserved
Tb927.8.5560
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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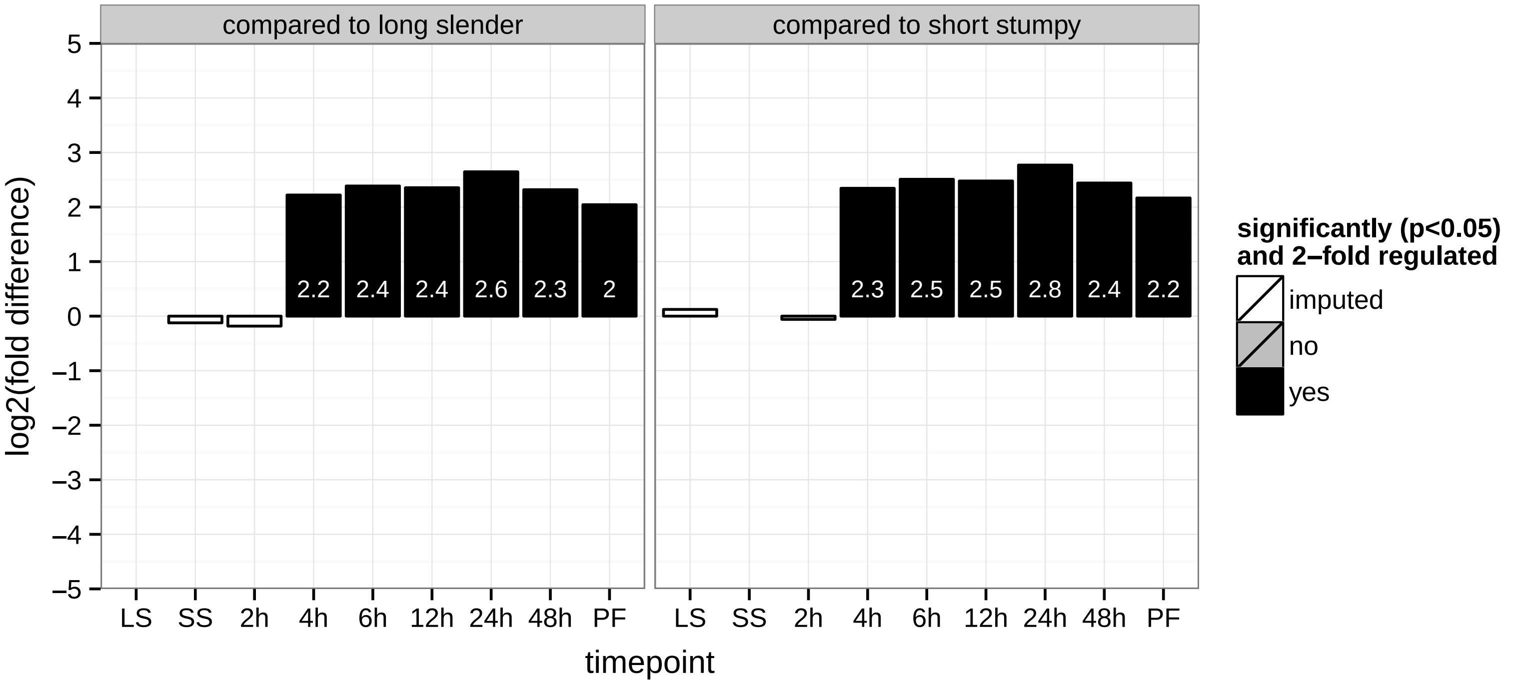
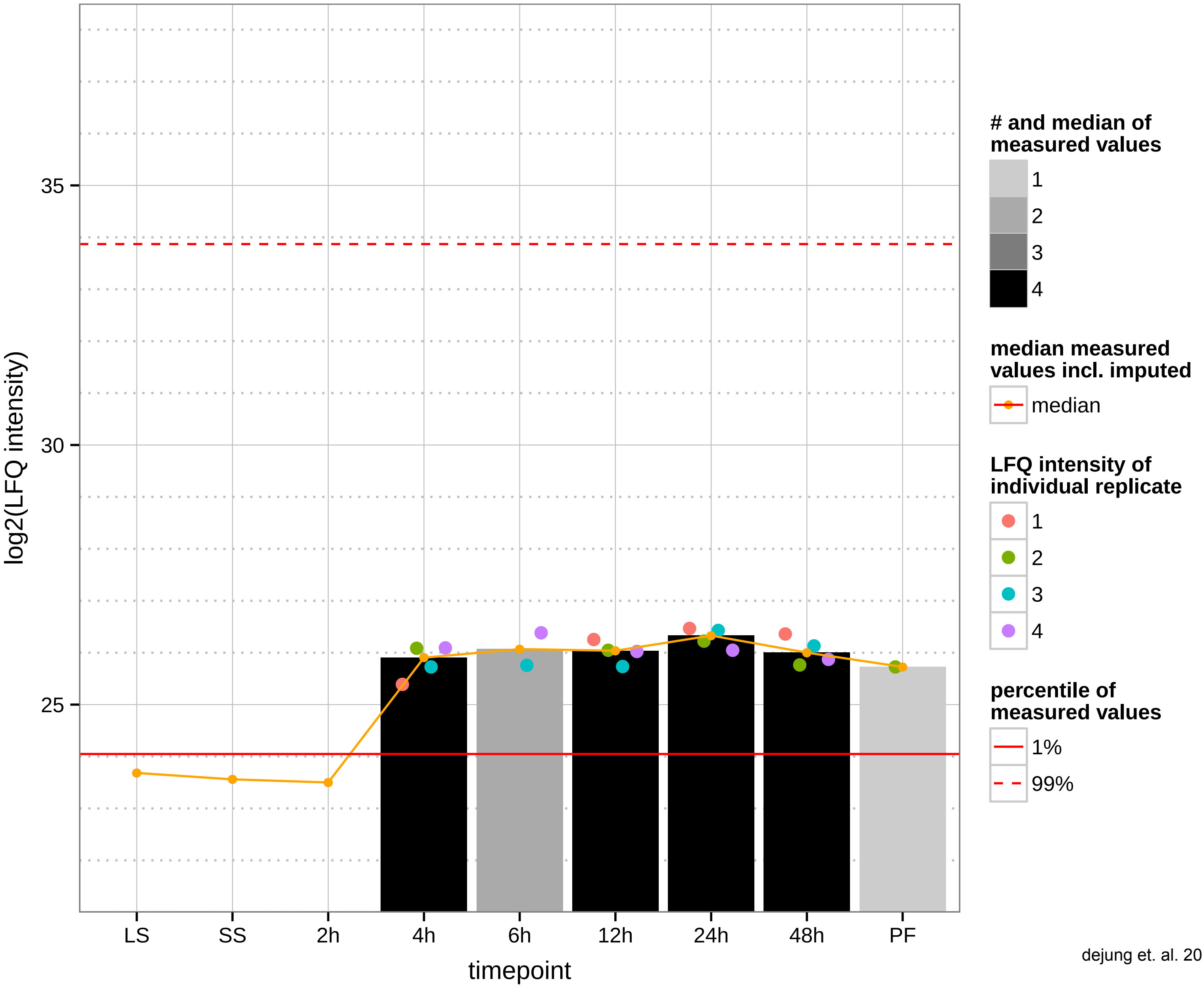
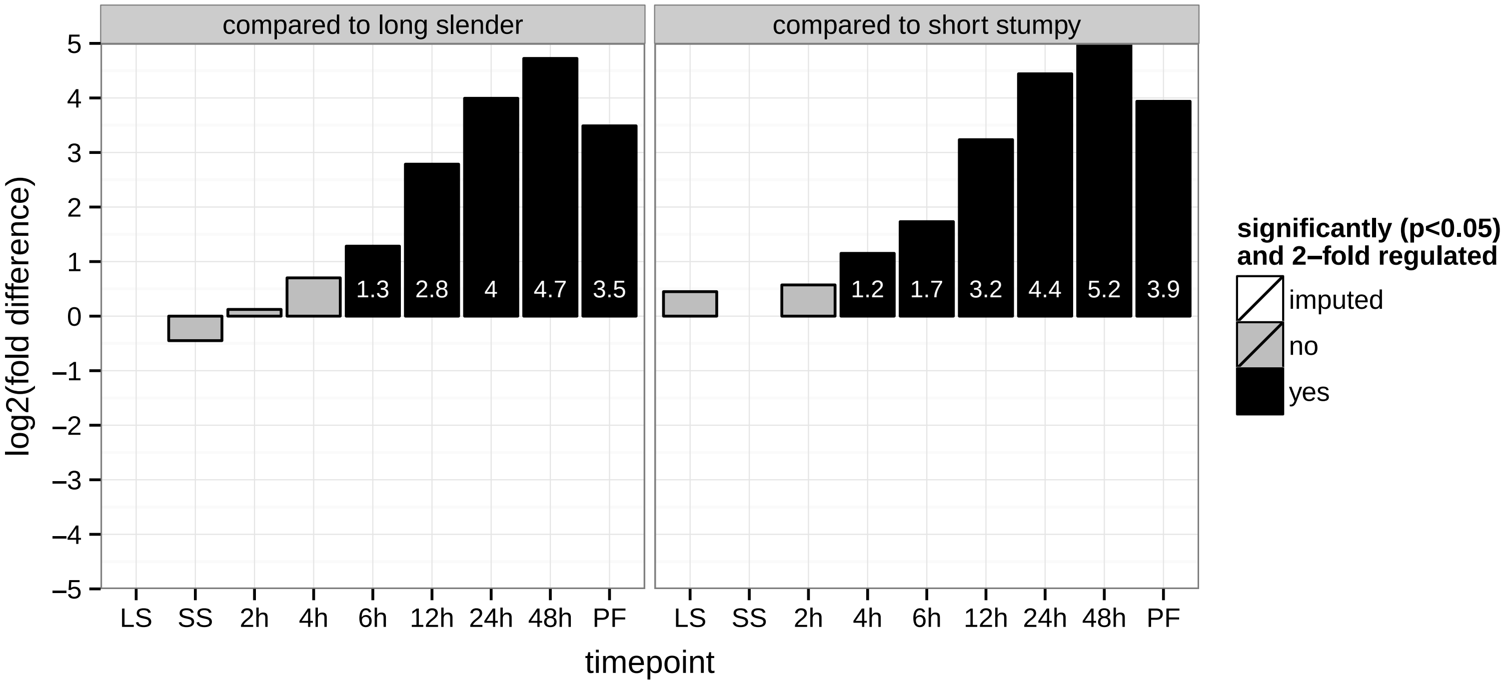
proteasome 26S non–ATPase subunit 9, putative
Tb927.8.5740
AGOF: endopeptidase activity
AGOC: proteasome regulatory particle
AGOP: proteasomal ubiquitin–dependent protein catabolic process
PGOF: protein binding
PGOC: null
PGOP: null

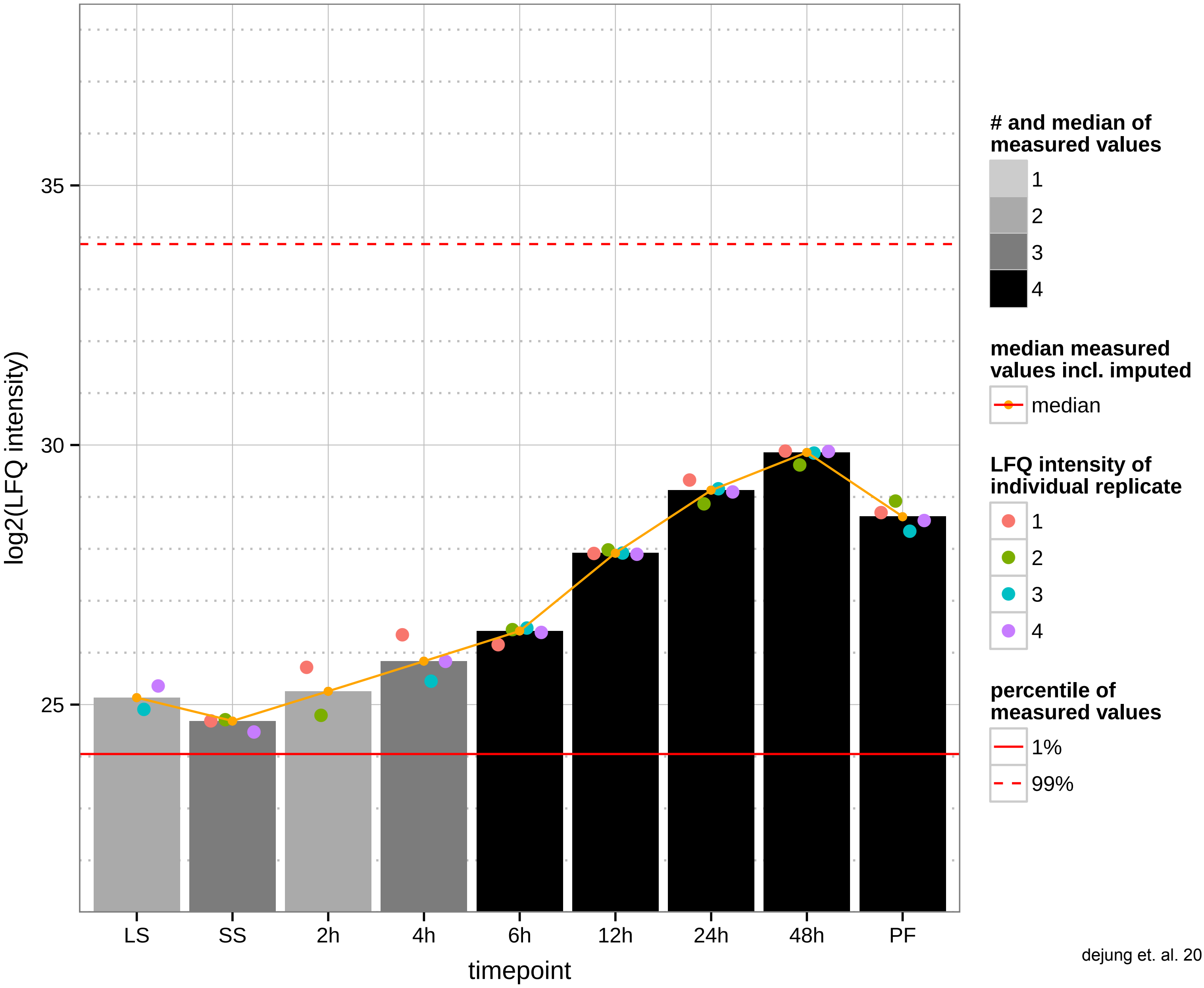




dejung et. al. 2015

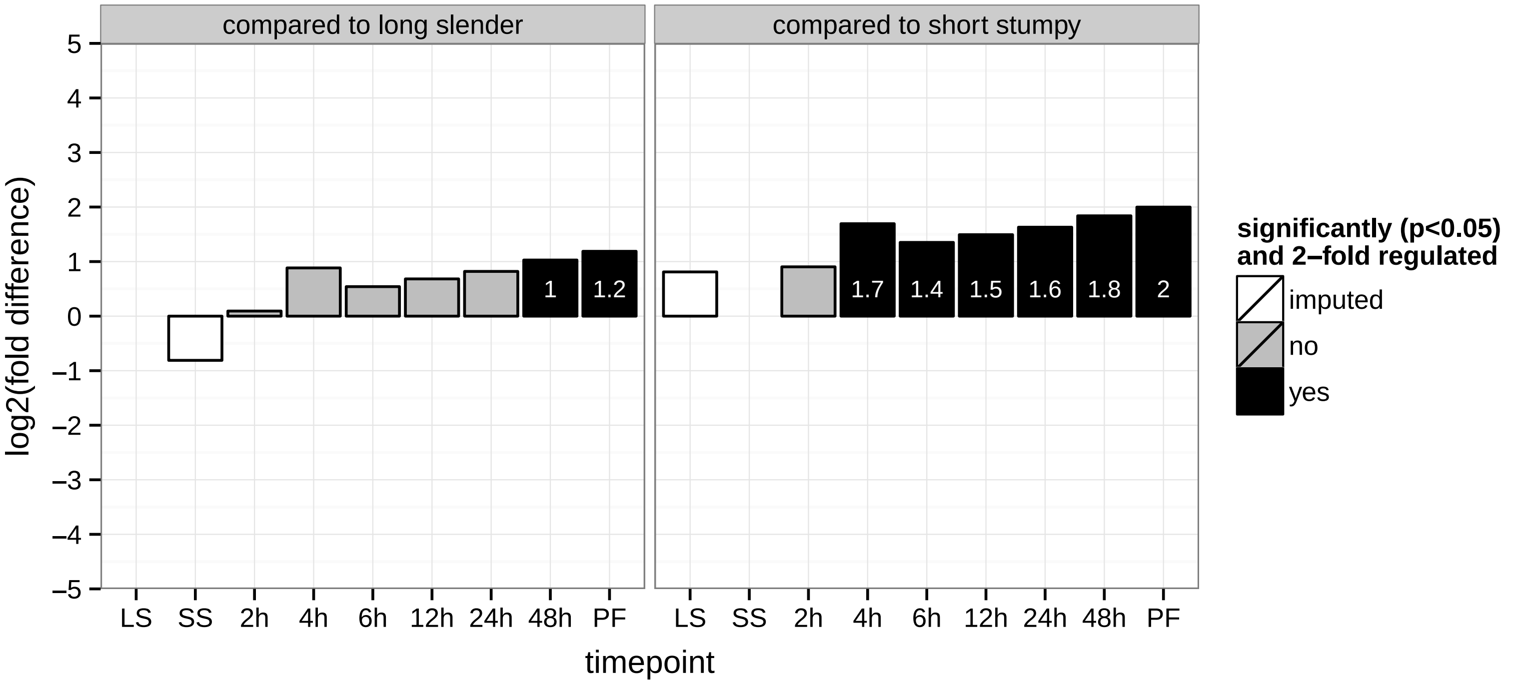
hypothetical protein, conserved
Tb927.8.6640
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
PGOC: null
PGOP: oxidation–reduction process

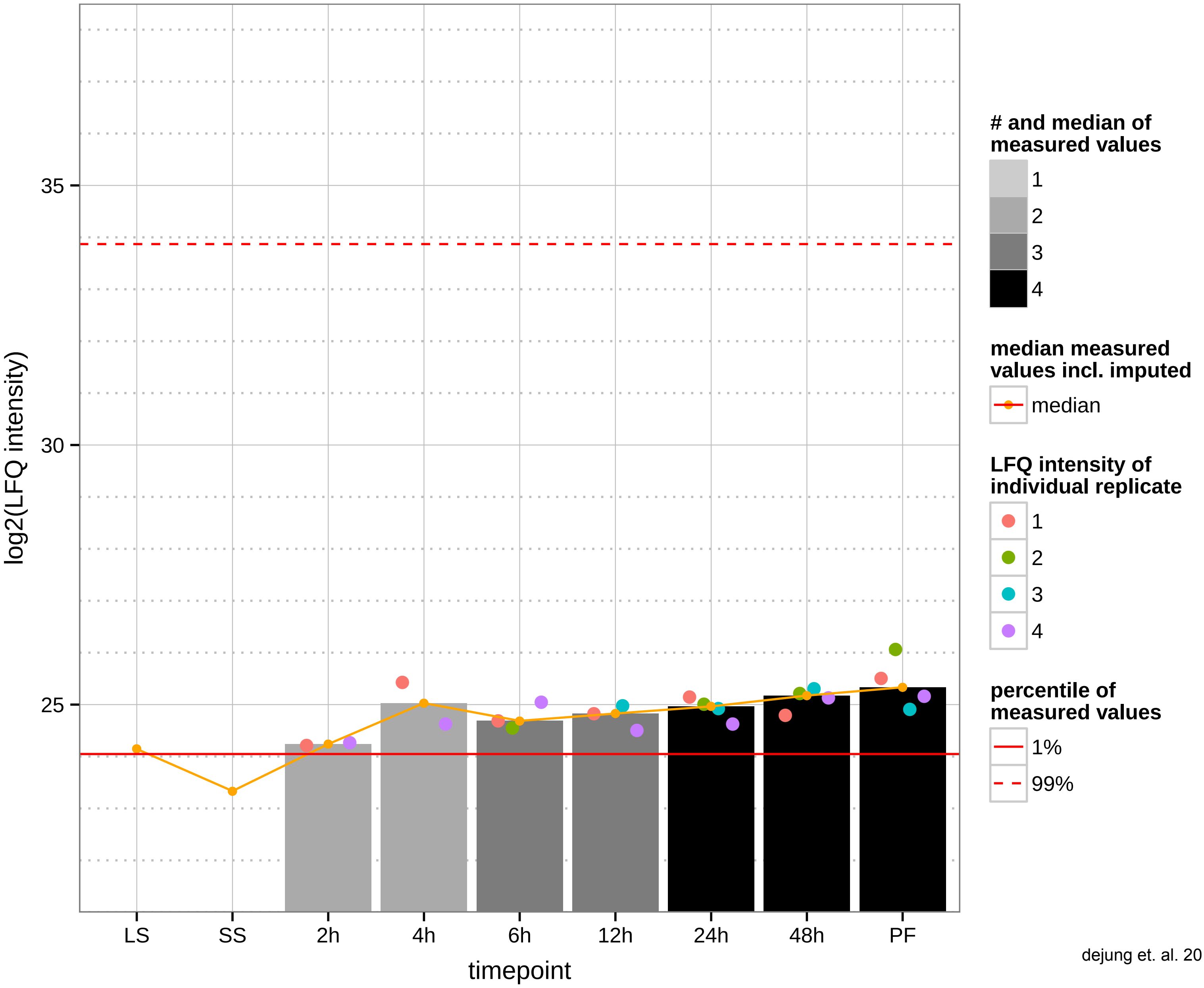




dejung et. al. 2015

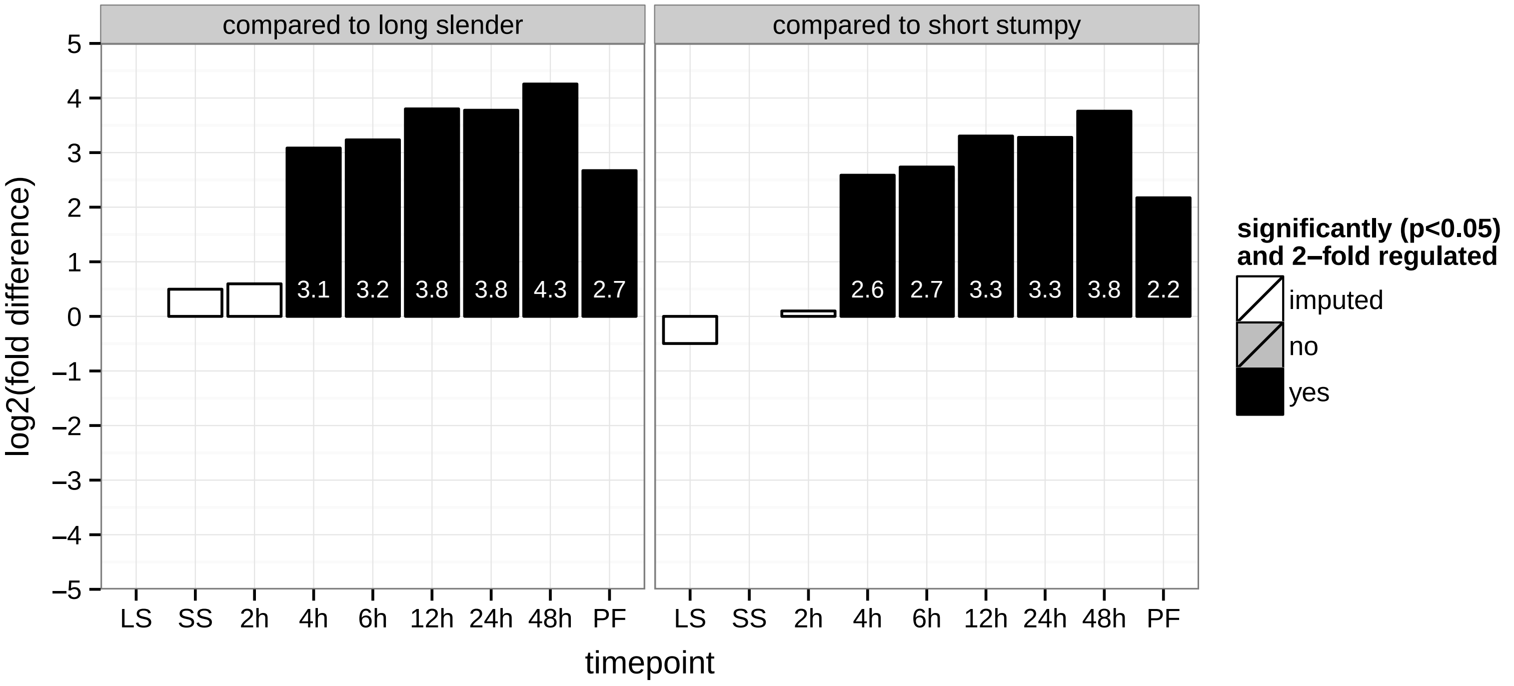
hypothetical protein, conserved
Tb927.8.6860
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

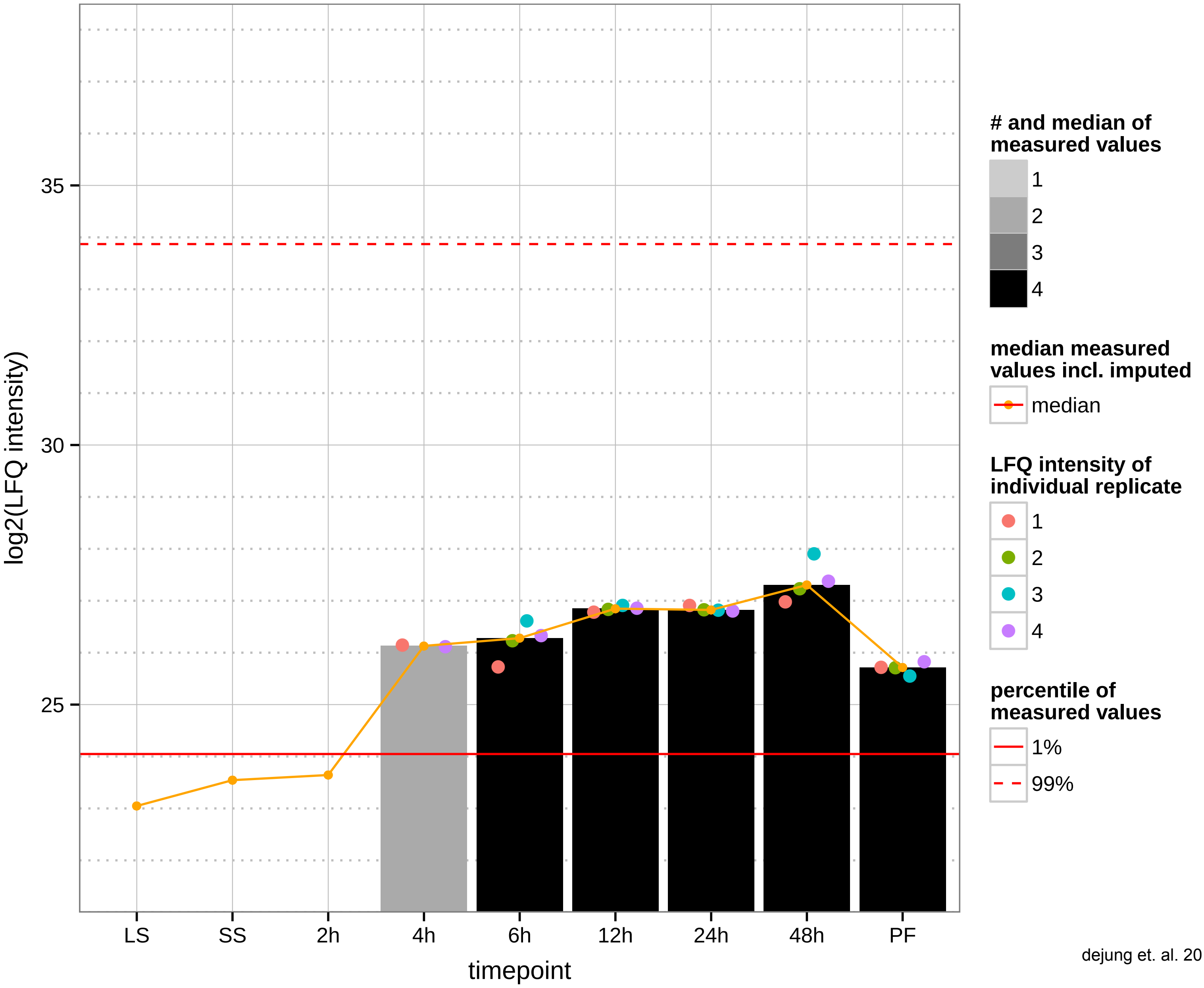




dejung et. al. 2015

squalene synthase, putative
Tb927.8.7120
AGOF: farnesyl–diphosphate farnesyltransferase activity, oxidoreductase activity
AGOC: endoplasmic reticulum membrane, integral to membrane, mitochondrial outer membrane
AGOP: cholesterol biosynthetic process, ergosterol biosynthetic process, isoprenoid biosynthetic process, oxidation–reductio
PGOF: transferase activity
PGOC: null
PGOP: biosynthetic process





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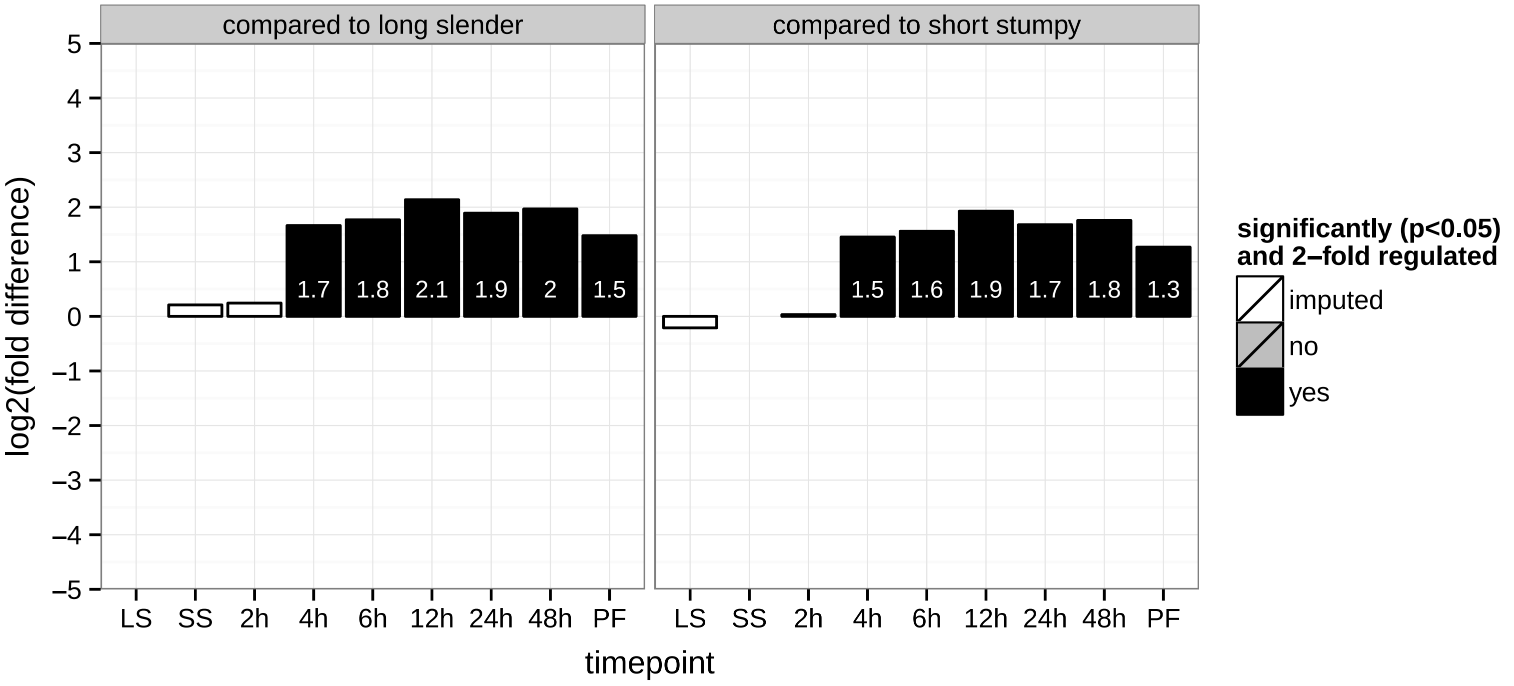
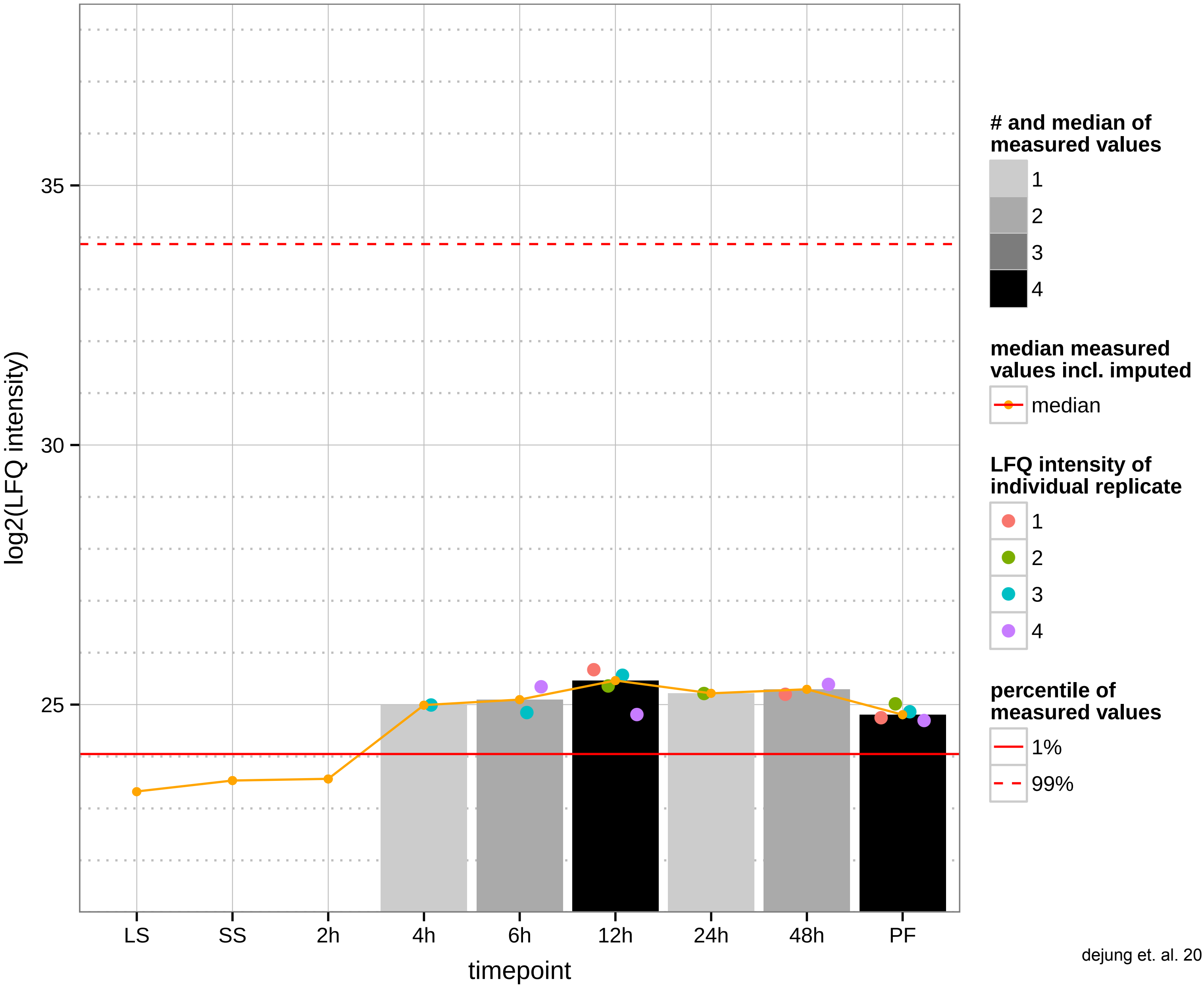
zinc finger protein, putative, predicted zinc finger protein
Tb927.9.11870
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: metal ion binding
PGOC: null
PGOP: null





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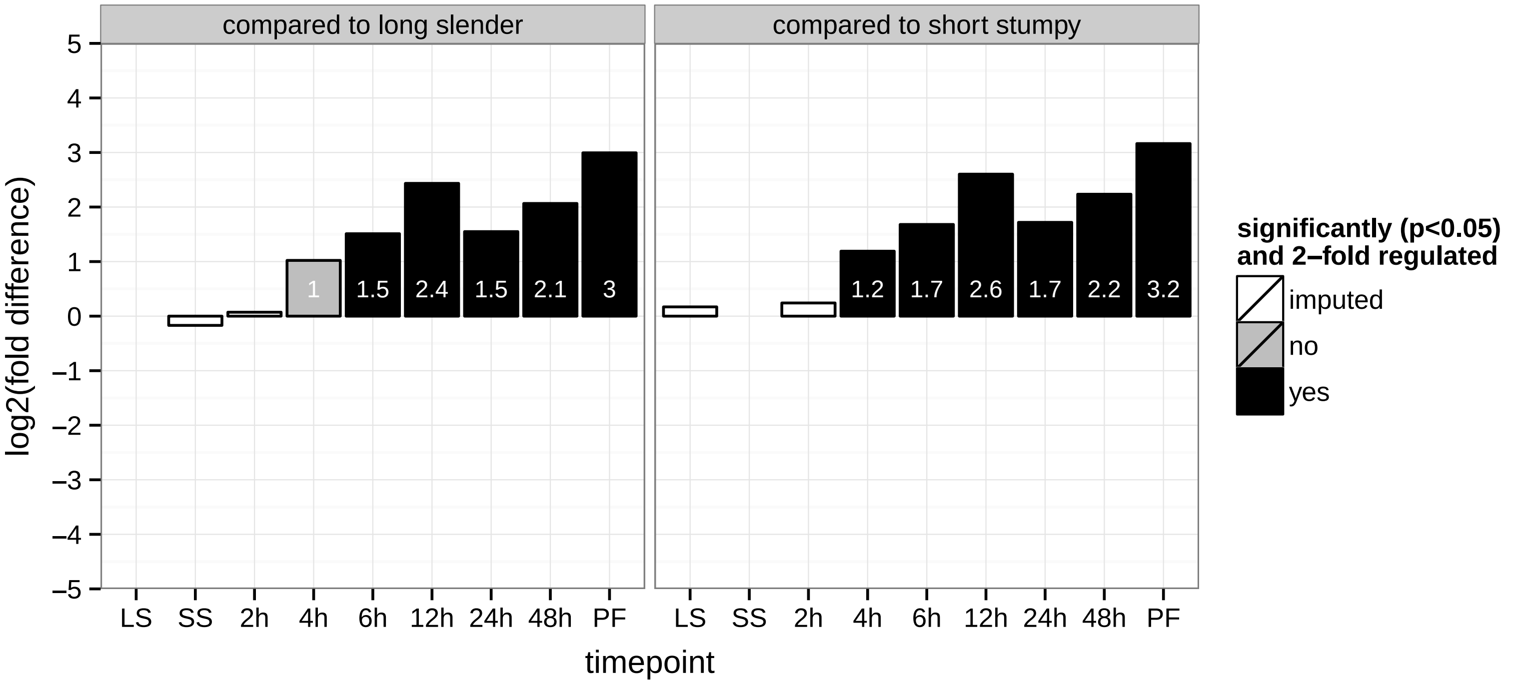
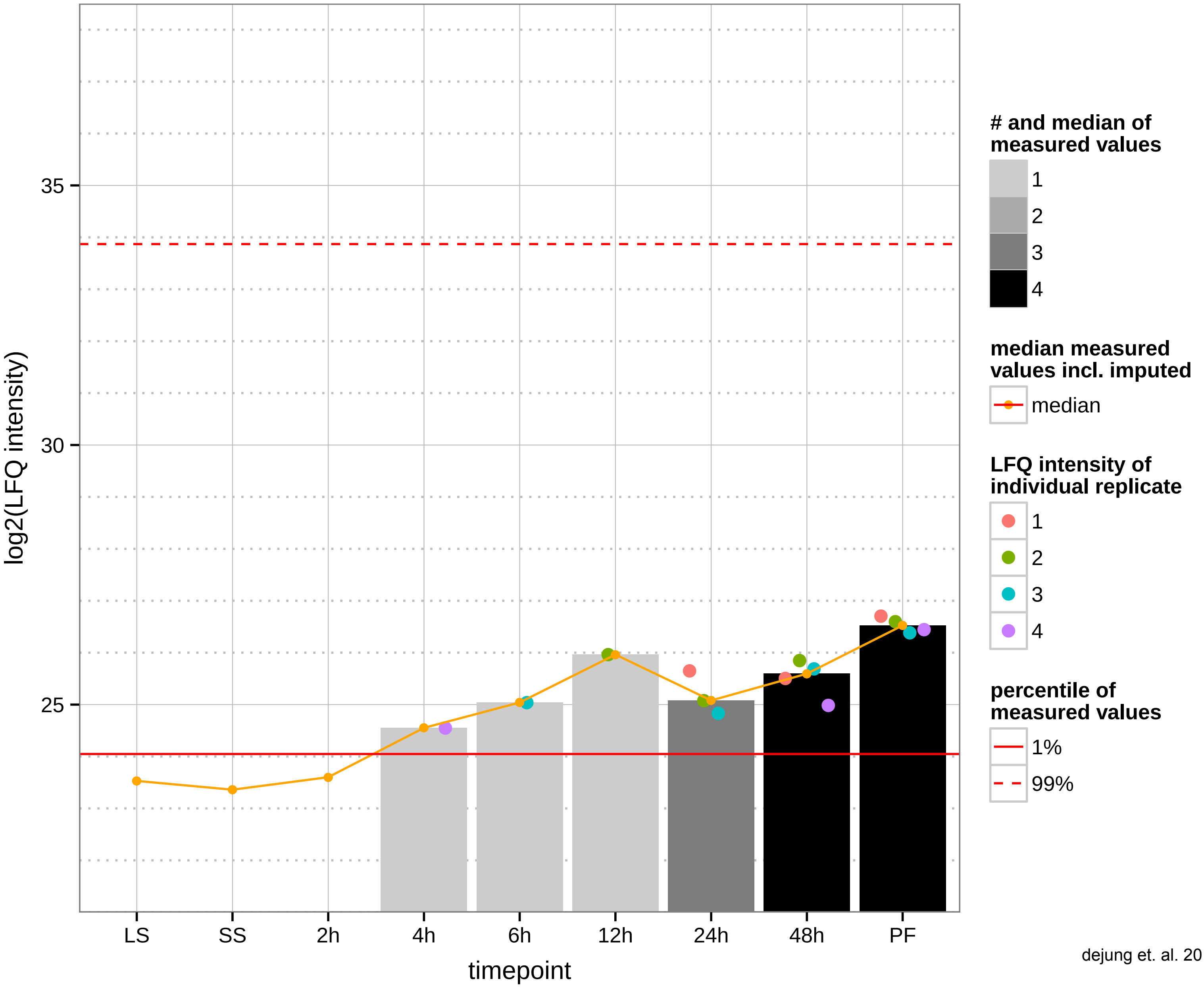
hypothetical protein, conserved
Tb927.9.11910
AGOF: heme binding, peroxidase activity
AGOC: mitochondrion
AGOP: oxidation−reduction process, response to oxidative stress
PGOF: heme binding, peroxidase activity
PGOC: null
PGOP: oxidation−reduction process, response to oxidative stress





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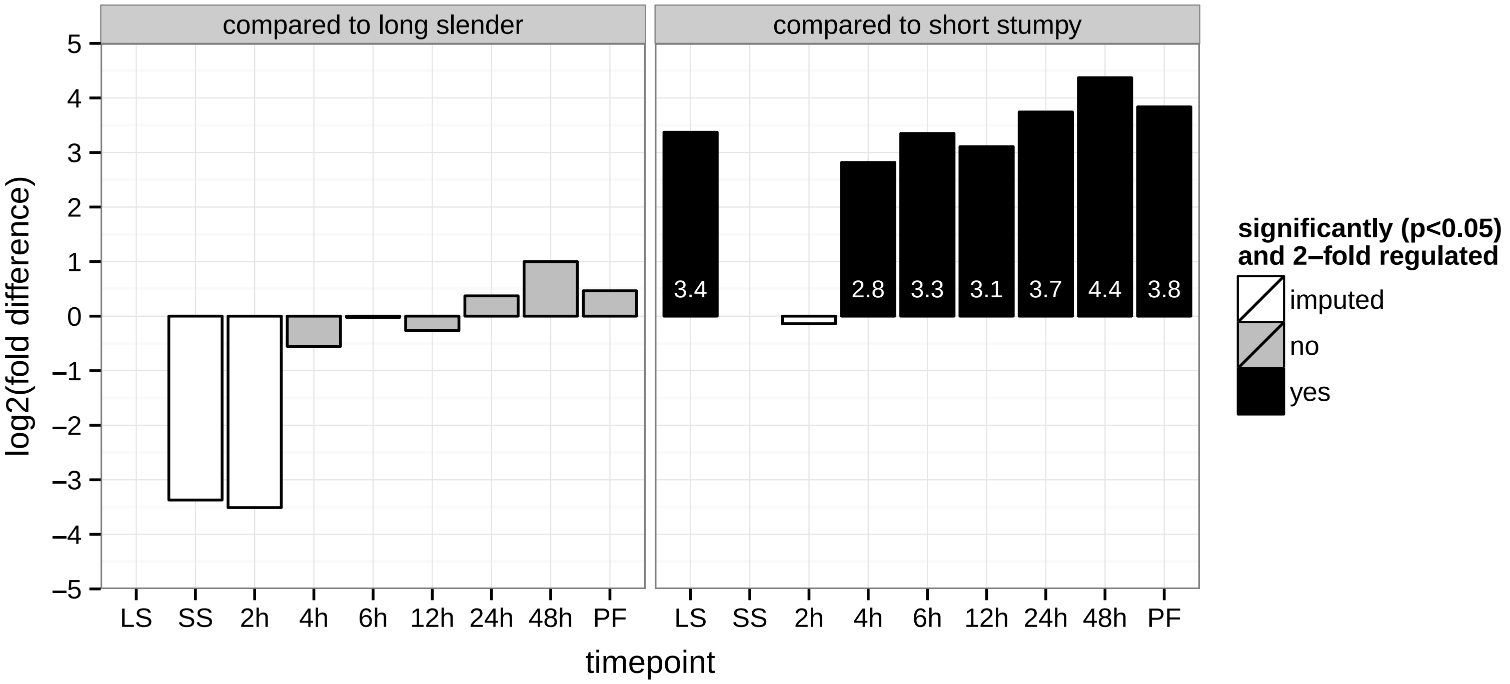
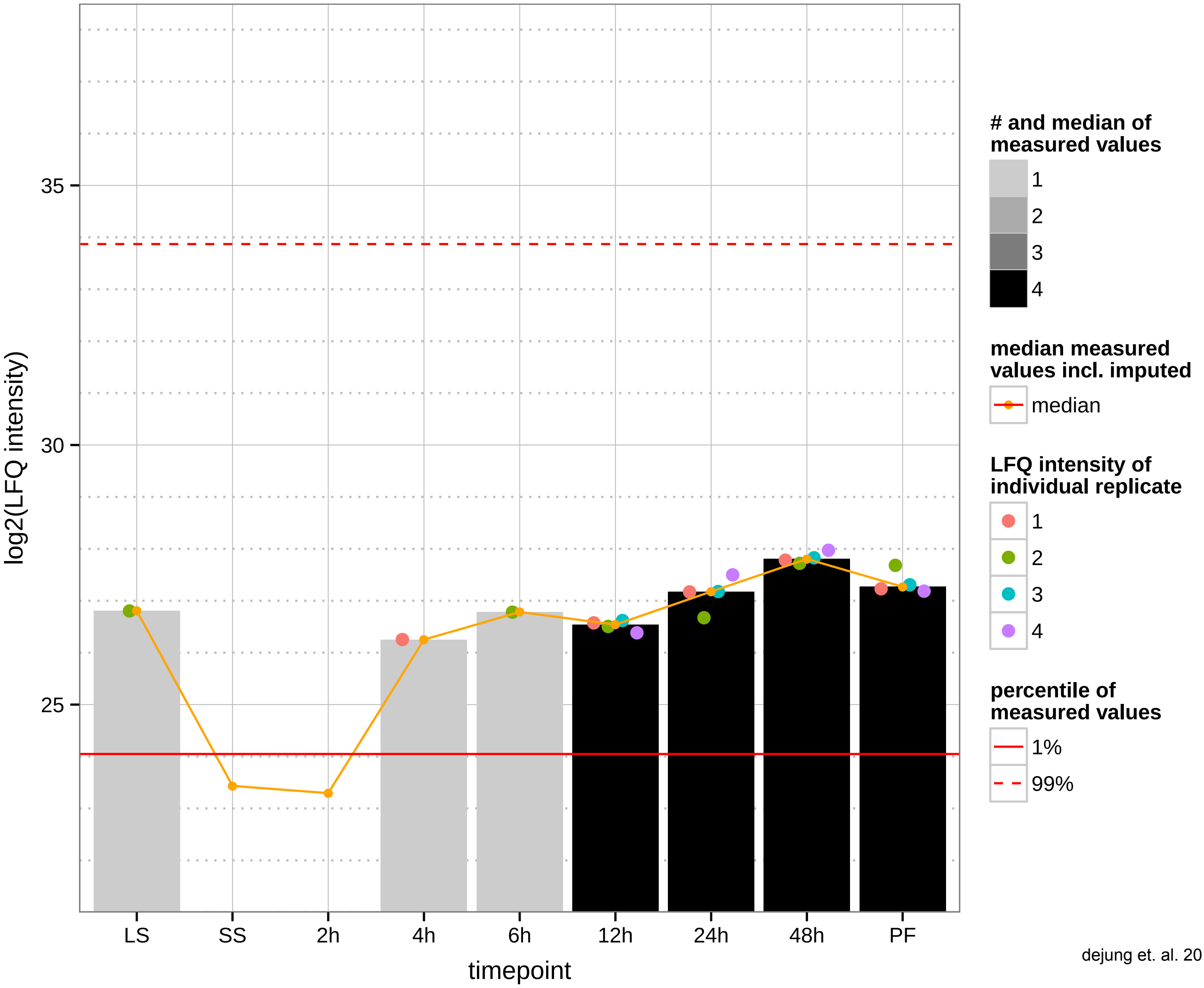
hypothetical protein, conserved
Tb927.9.1710
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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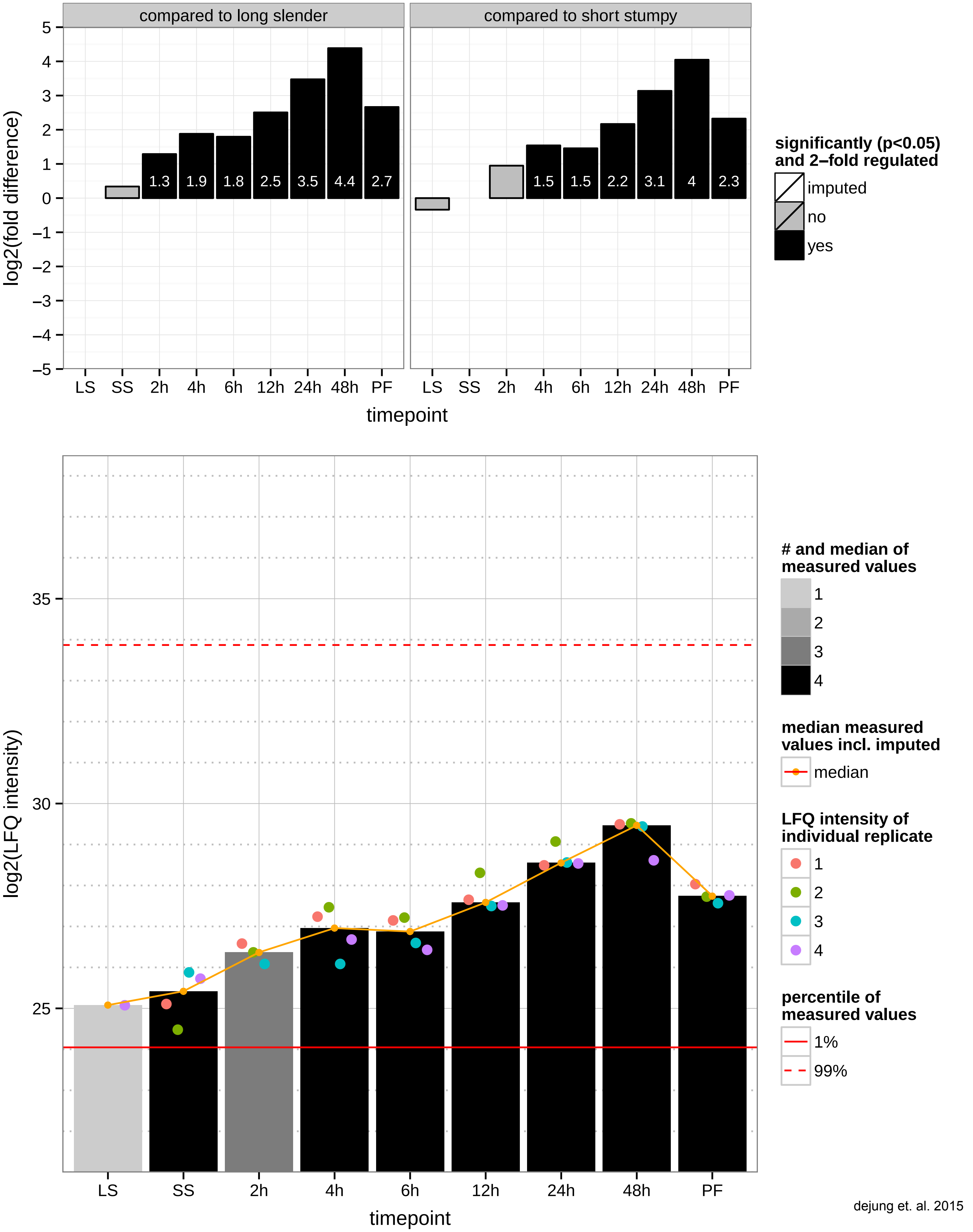
hypothetical protein, conserved
Tb927.9.2390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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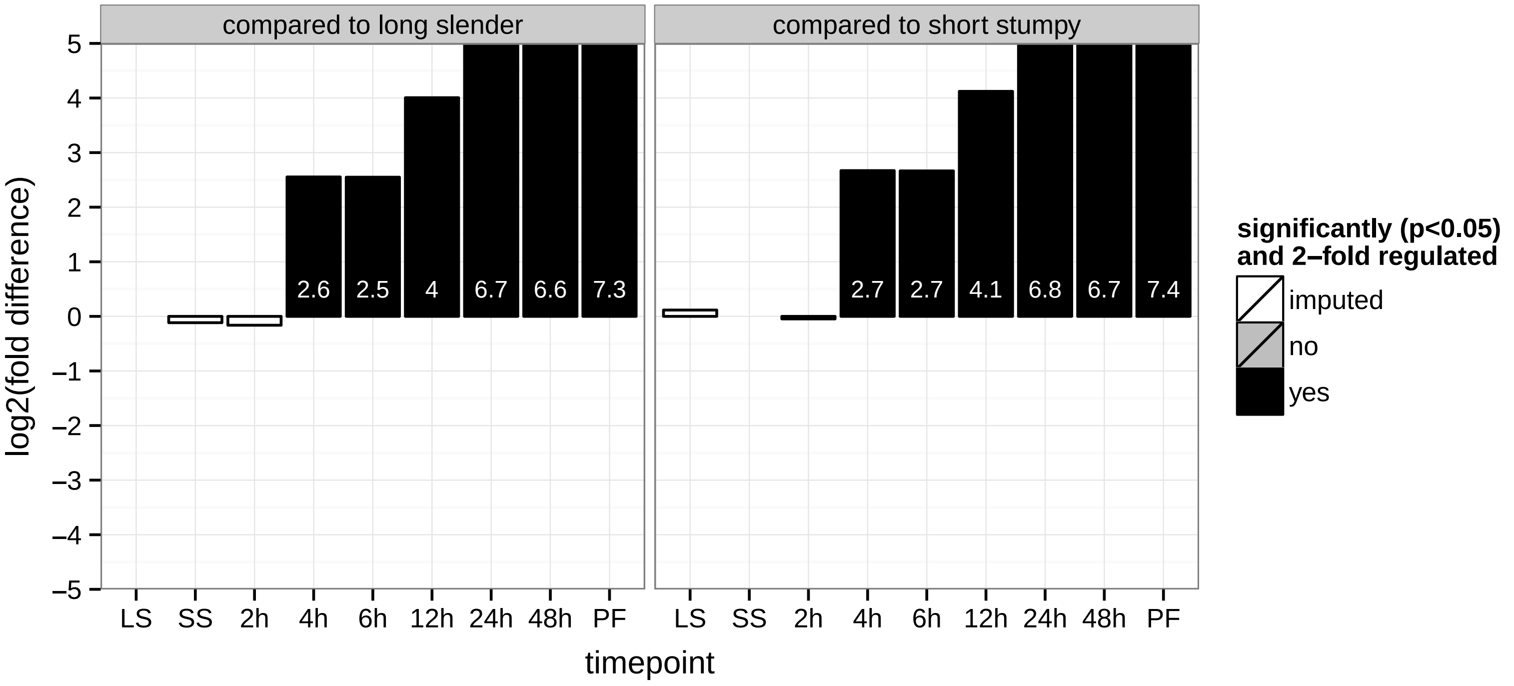
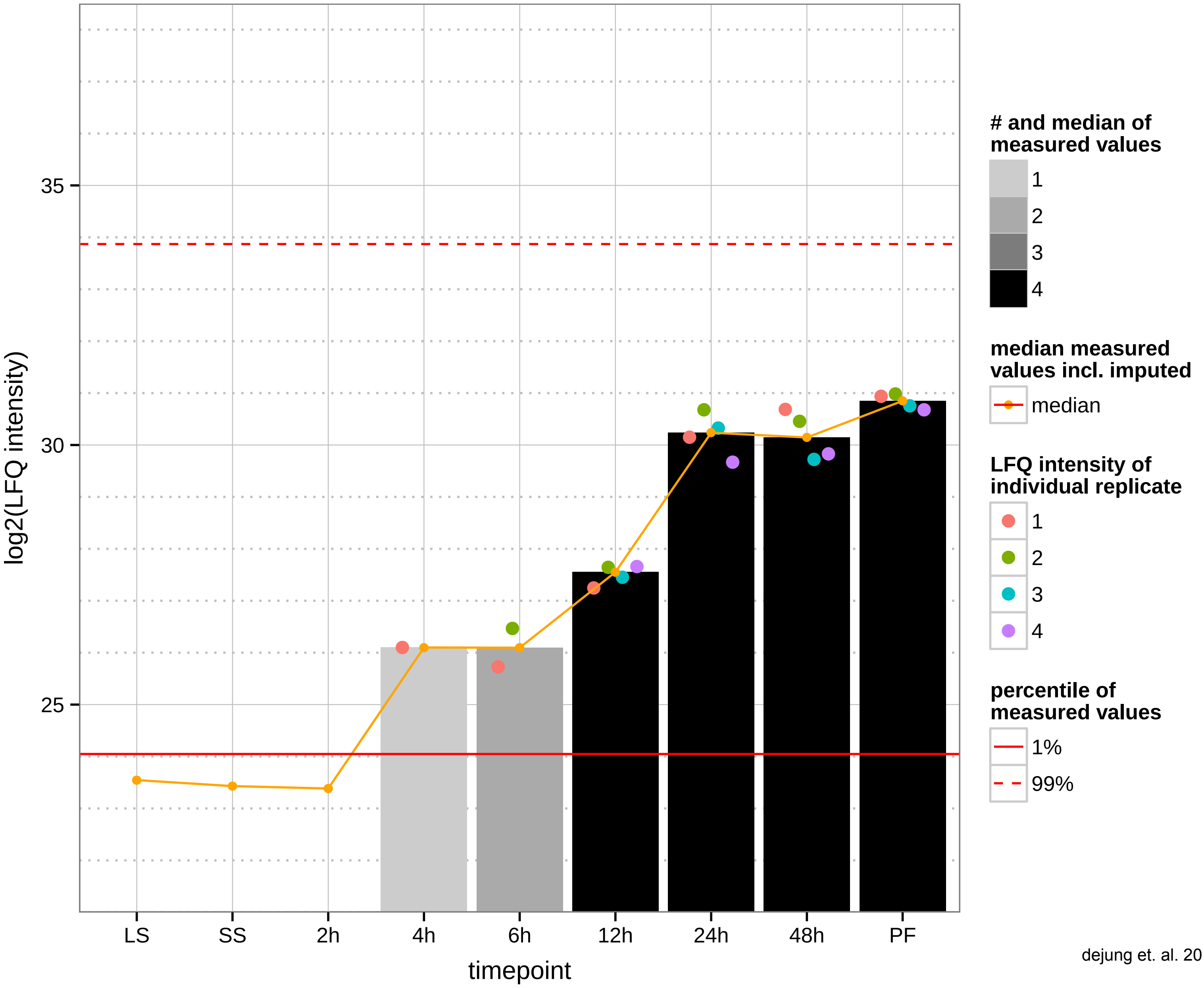
cytochrome oxidase subunit V (COXV)
Tb927.9.3170
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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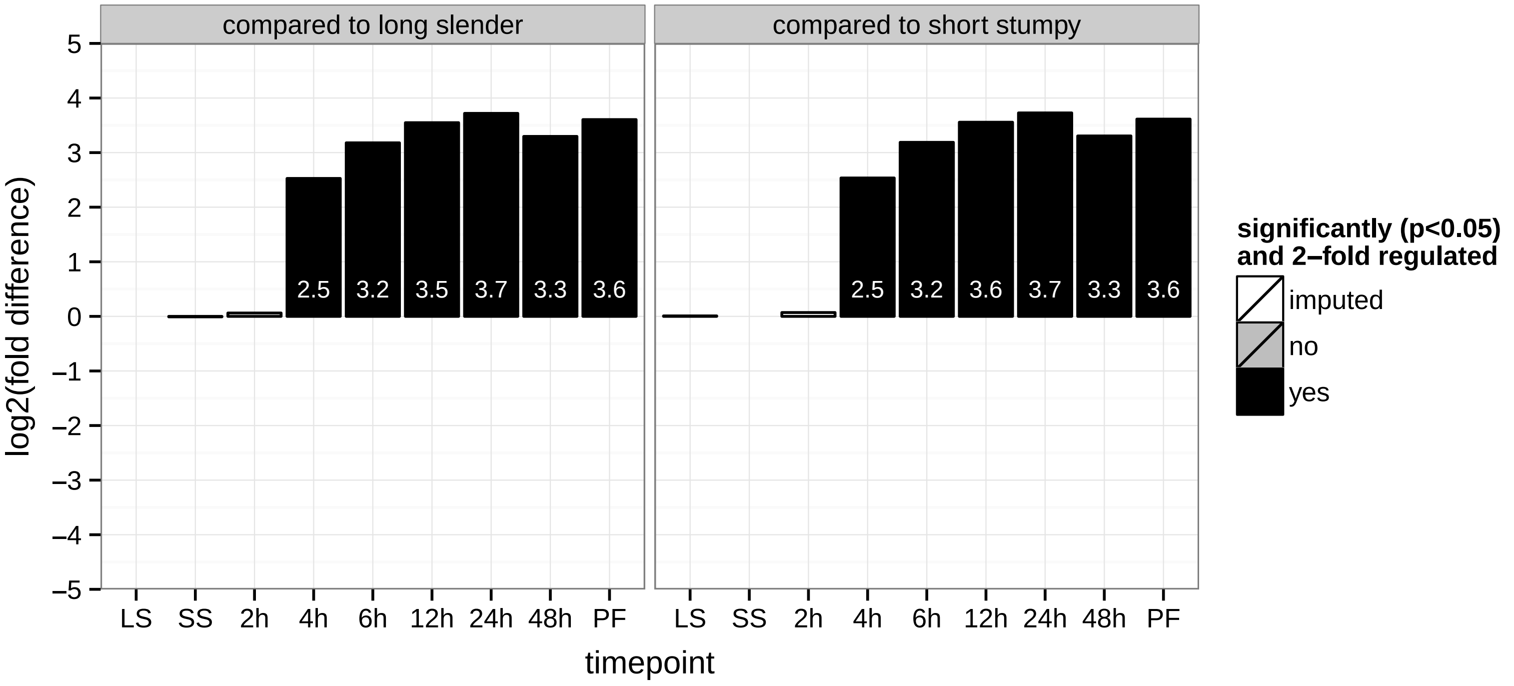
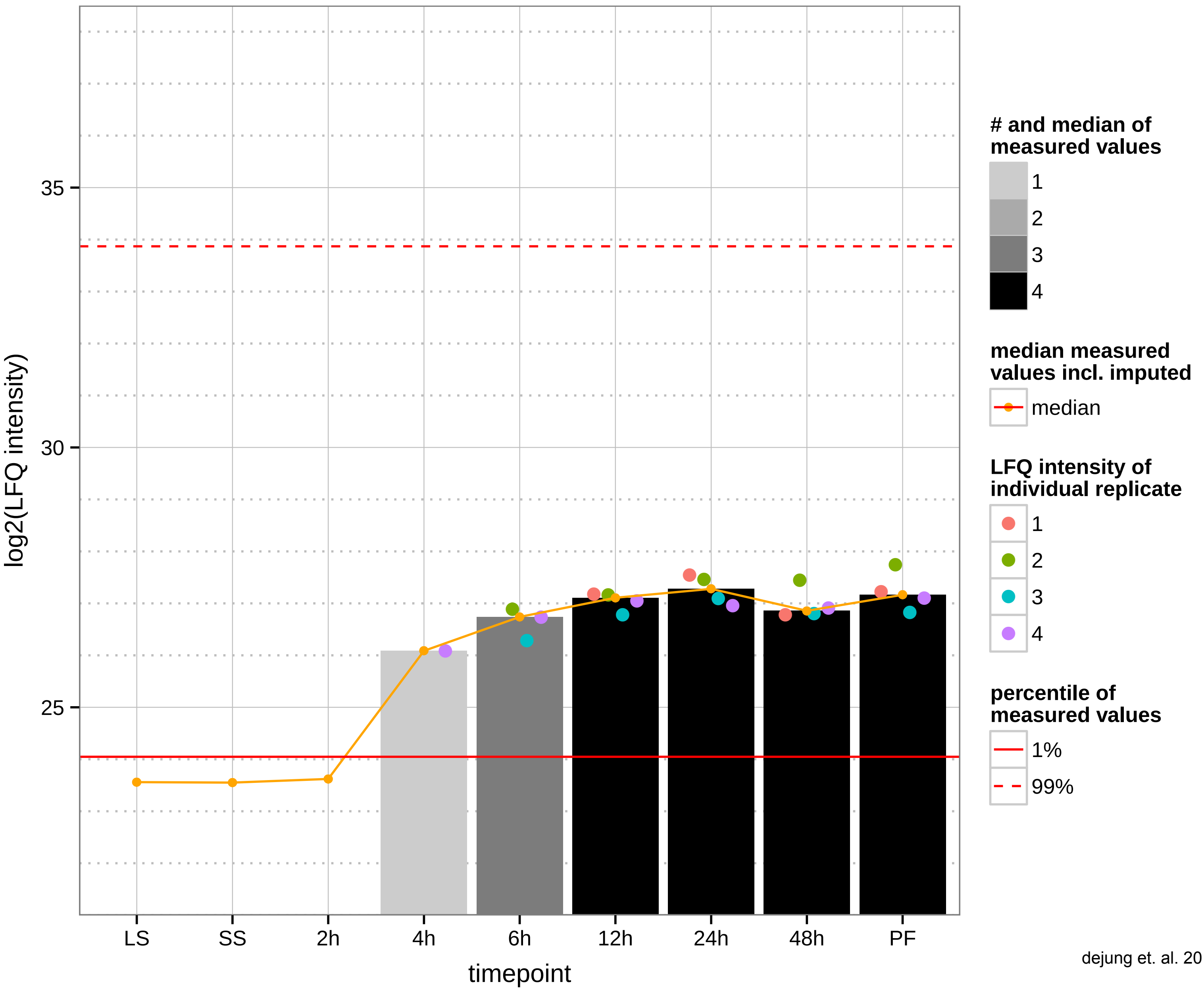
2Fe–2S iron–sulfur cluster binding domain containing protein, putative
Tb927.9.6060
AGOF: thiol oxidase activity
AGOC: mitochondrial intermembrane space, mitochondrion
AGOP: oxidation–reduction process, protein import into mitochondrial intermembrane space
PGOF: thiol oxidase activity
PGOC: null
PGOP: oxidation–reduction process





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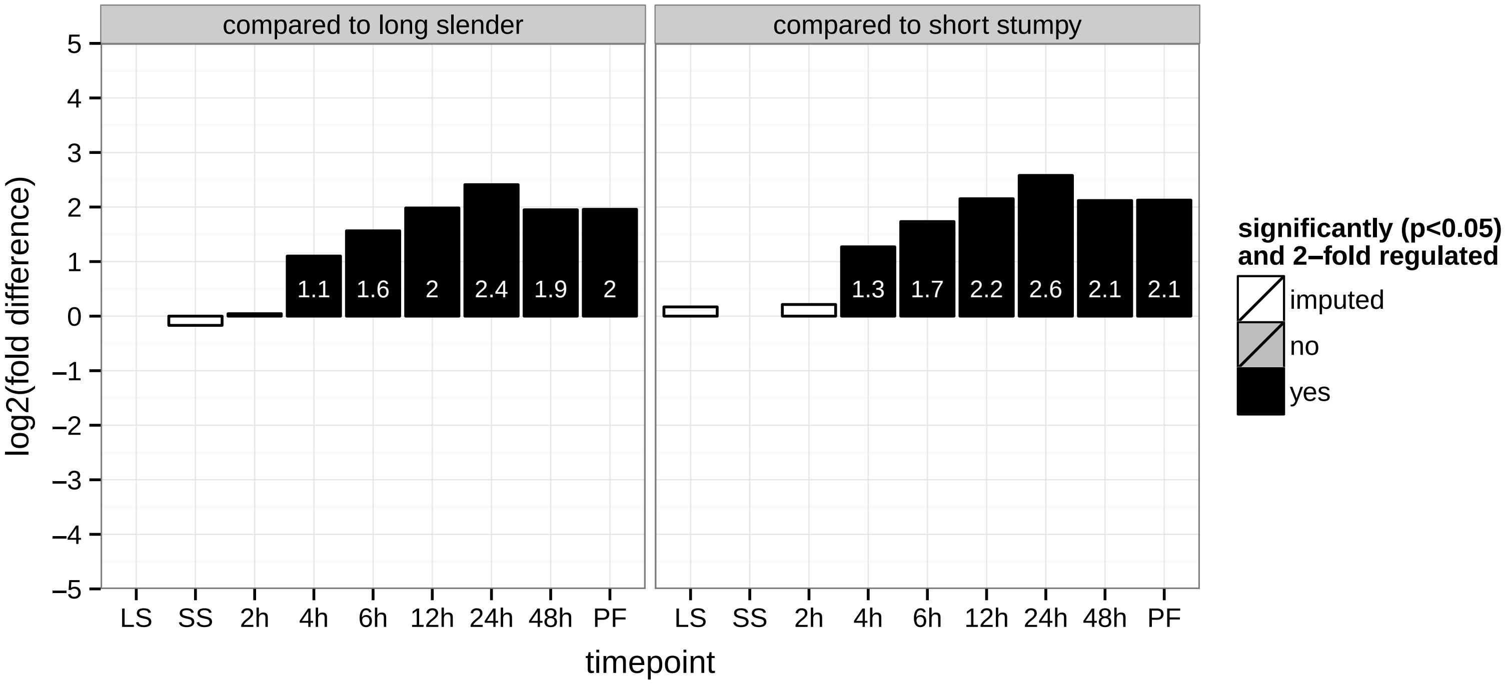
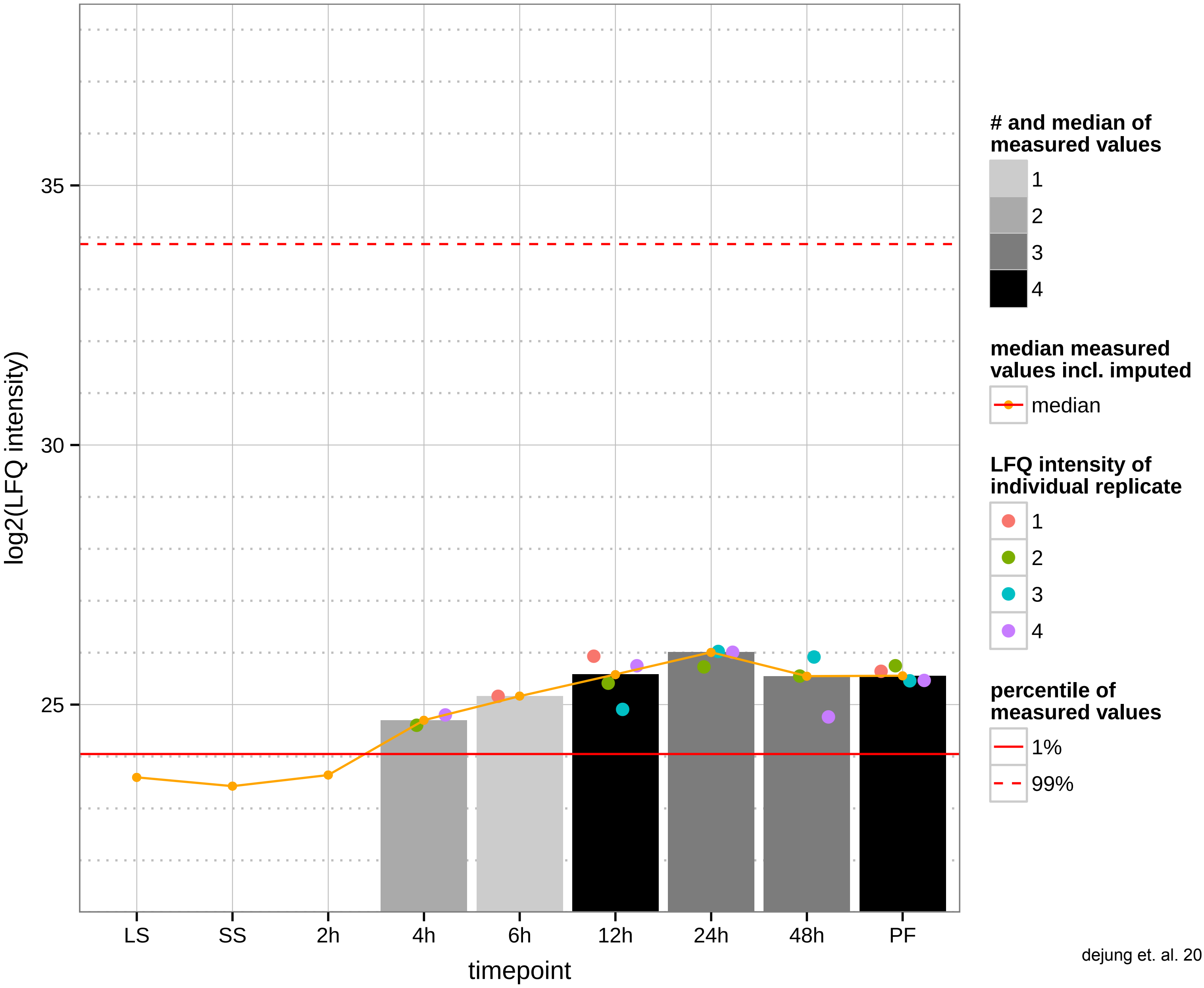
hypothetical protein, conserved
Tb927.9.6620
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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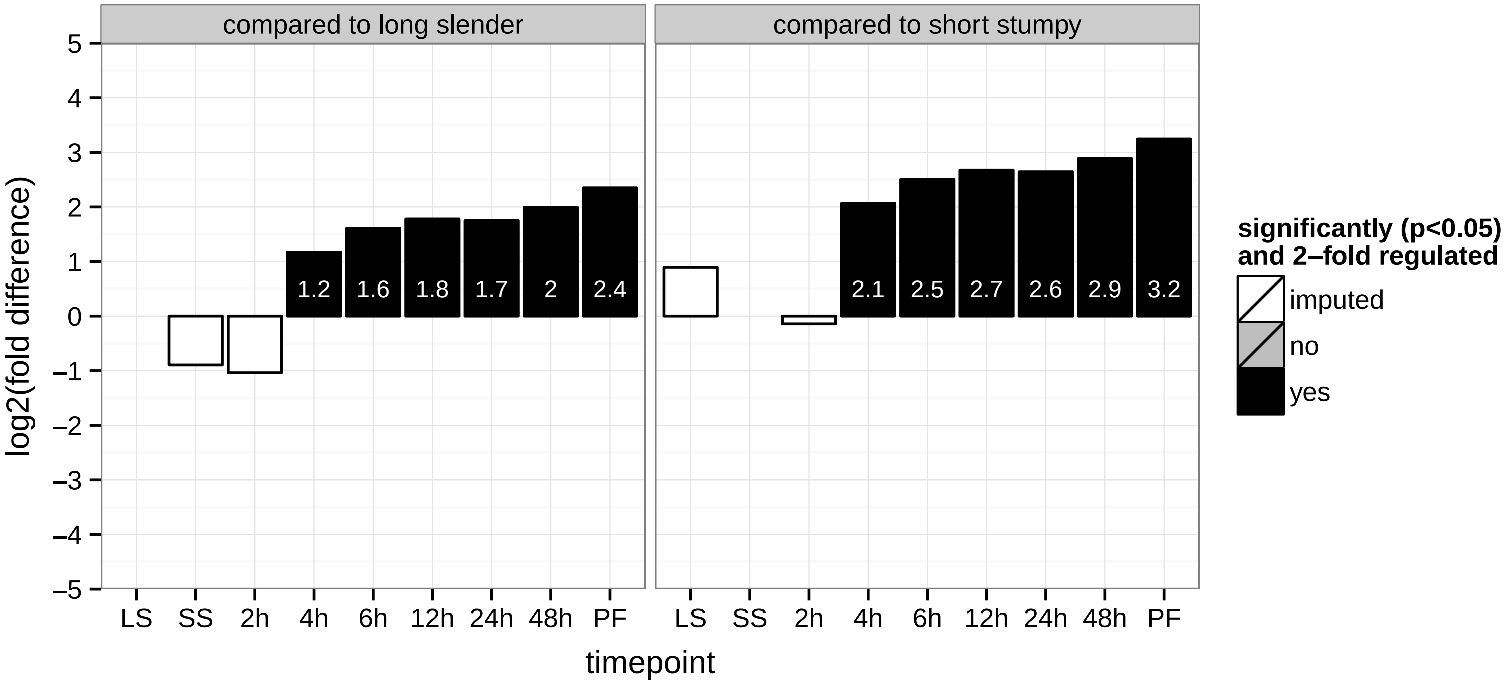
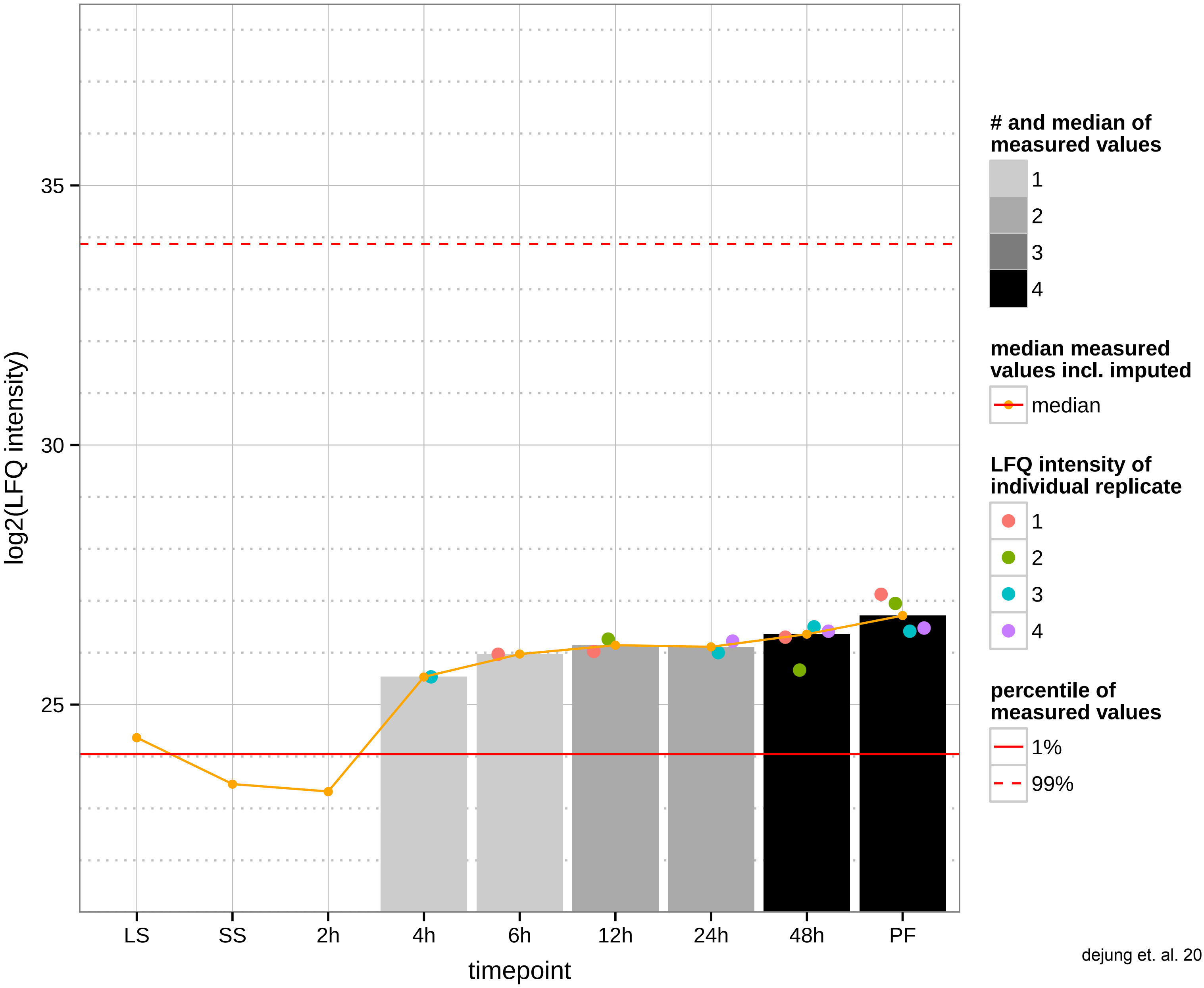
hypothetical protein, conserved
Tb927.9.7170
AGOF: structural constituent of ribosome
AGOC: mitochondrial ribosome, mitochondrion
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: mitochondrial ribosome
PGOP: translation





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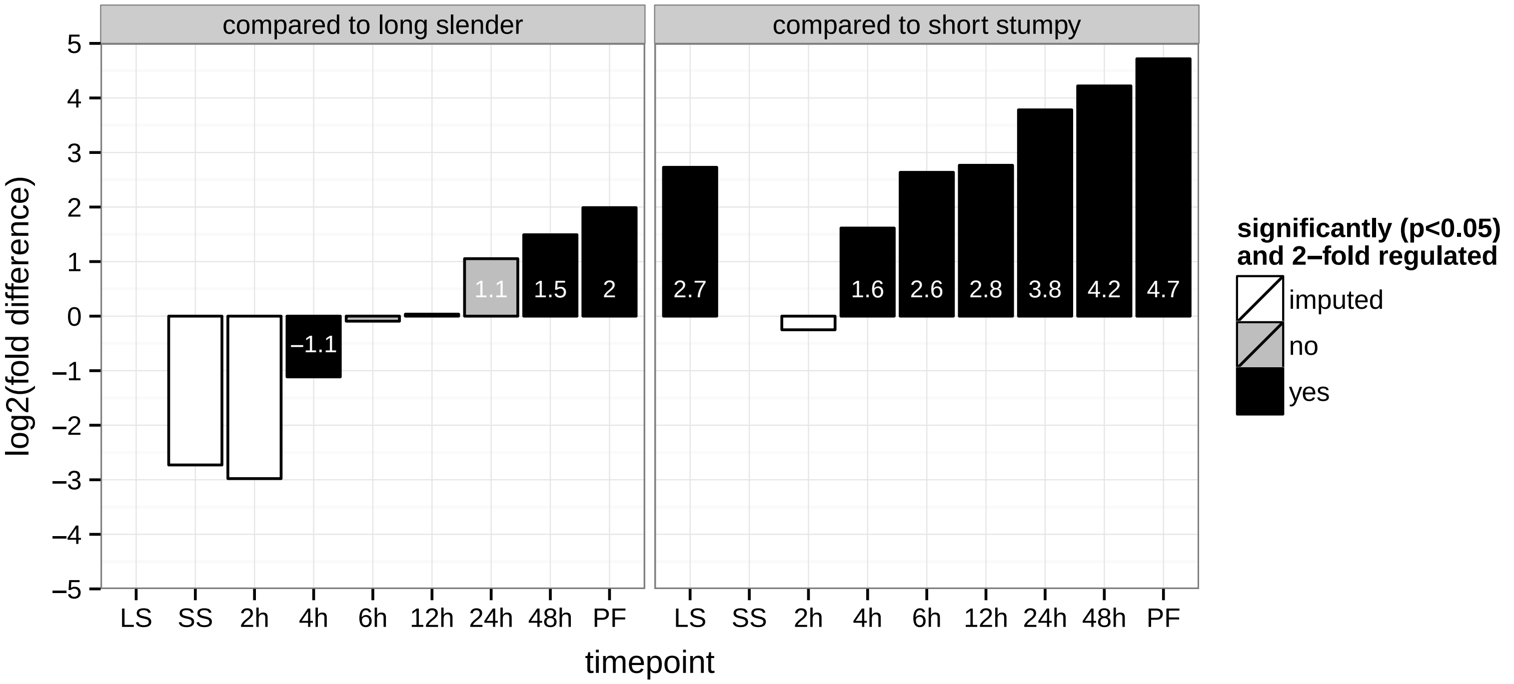
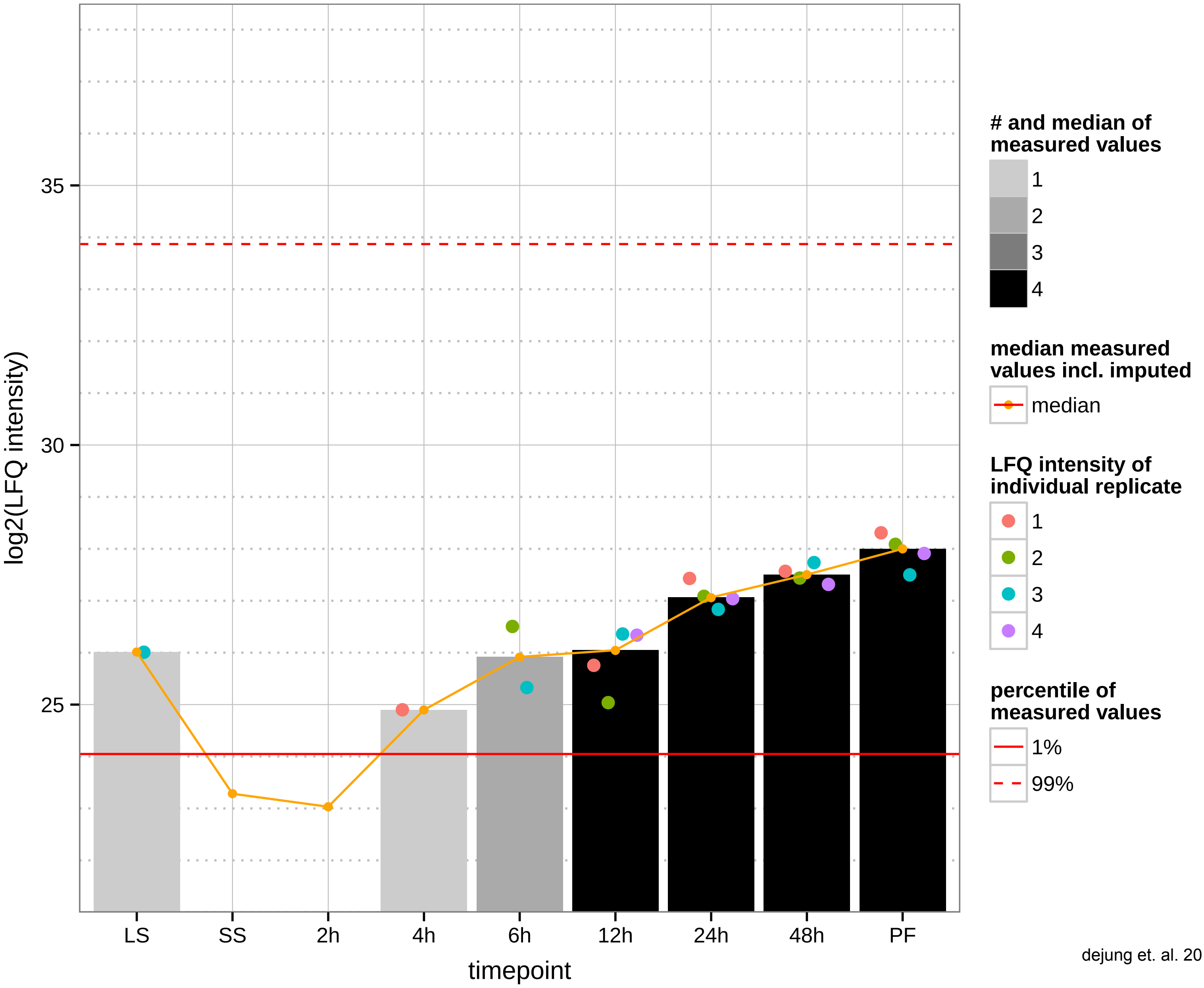
hypothetical protein, conserved
Tb927.9.8820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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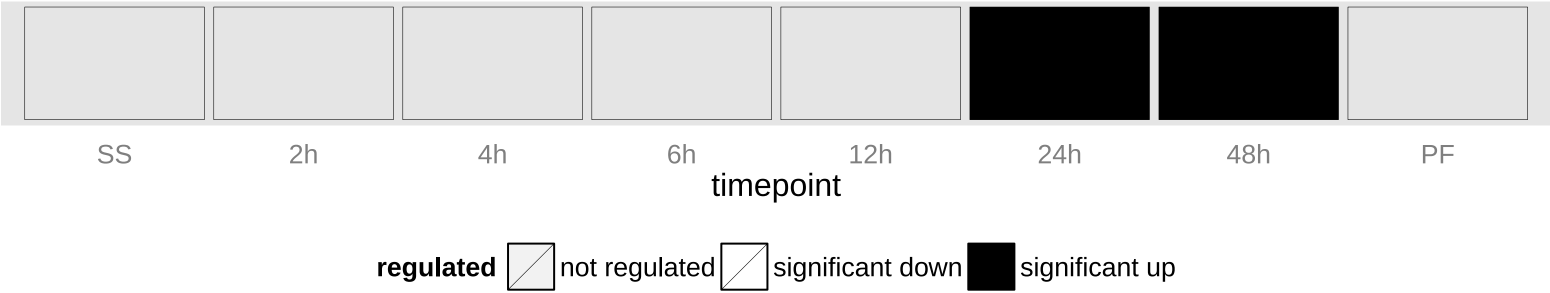

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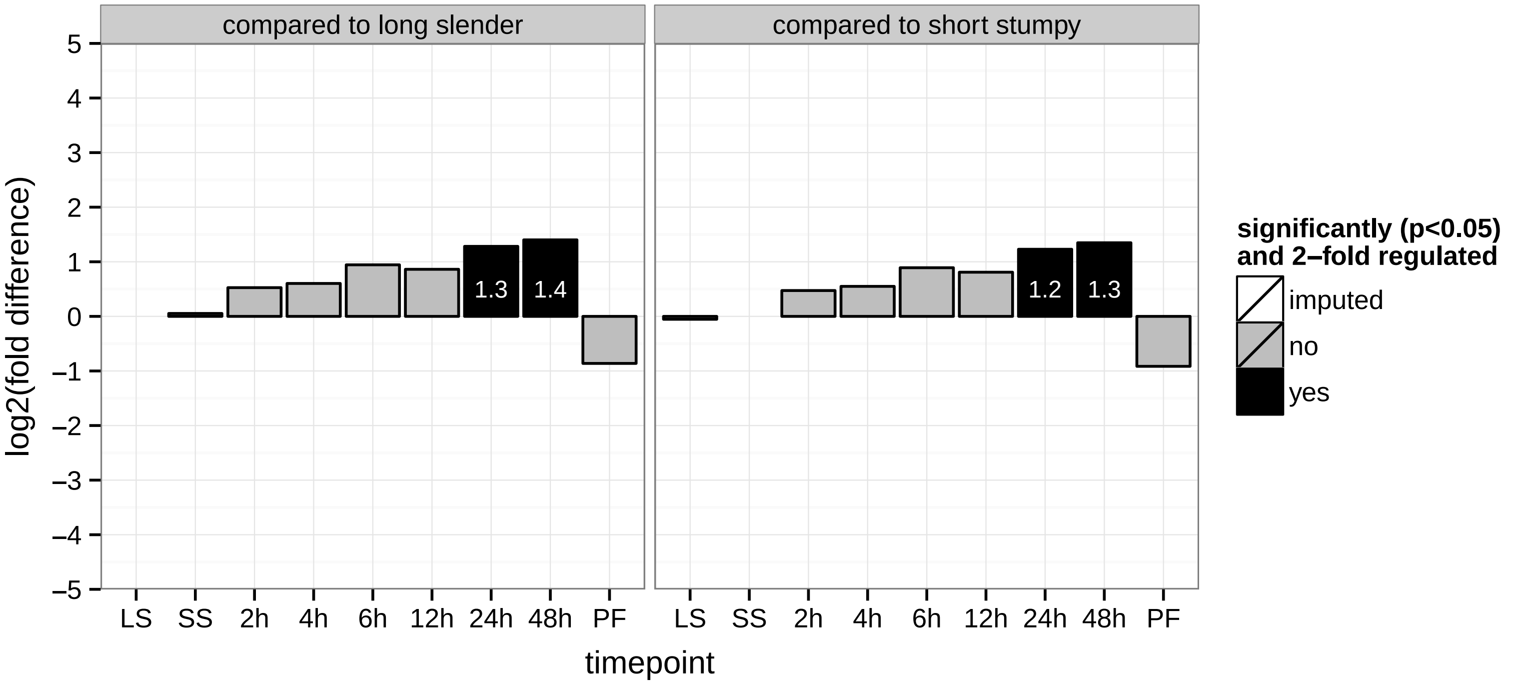
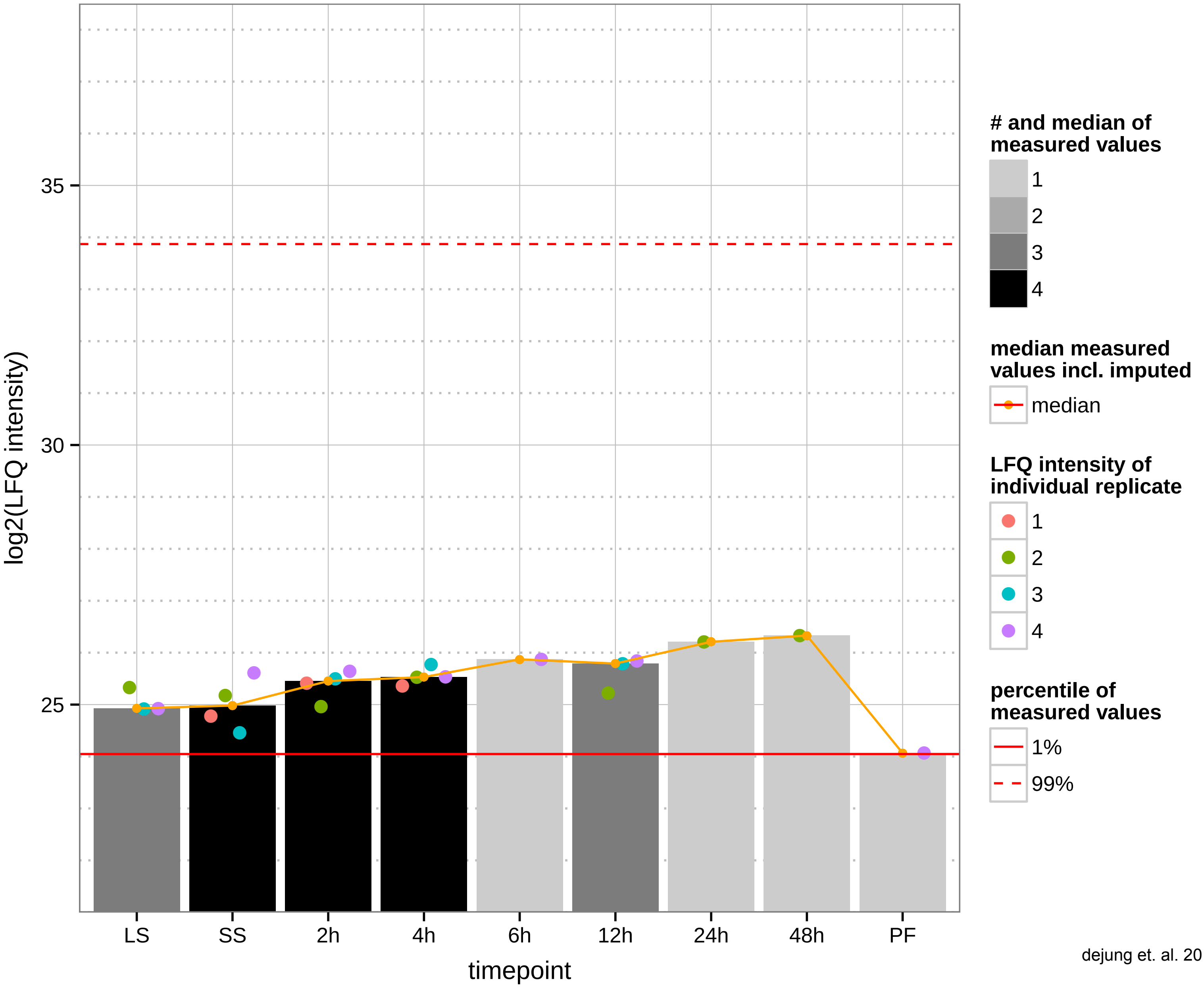
hypothetical protein, conserved, chrX additional, unordered contigs
Tb10.v4.0041;Tb927.10.4510
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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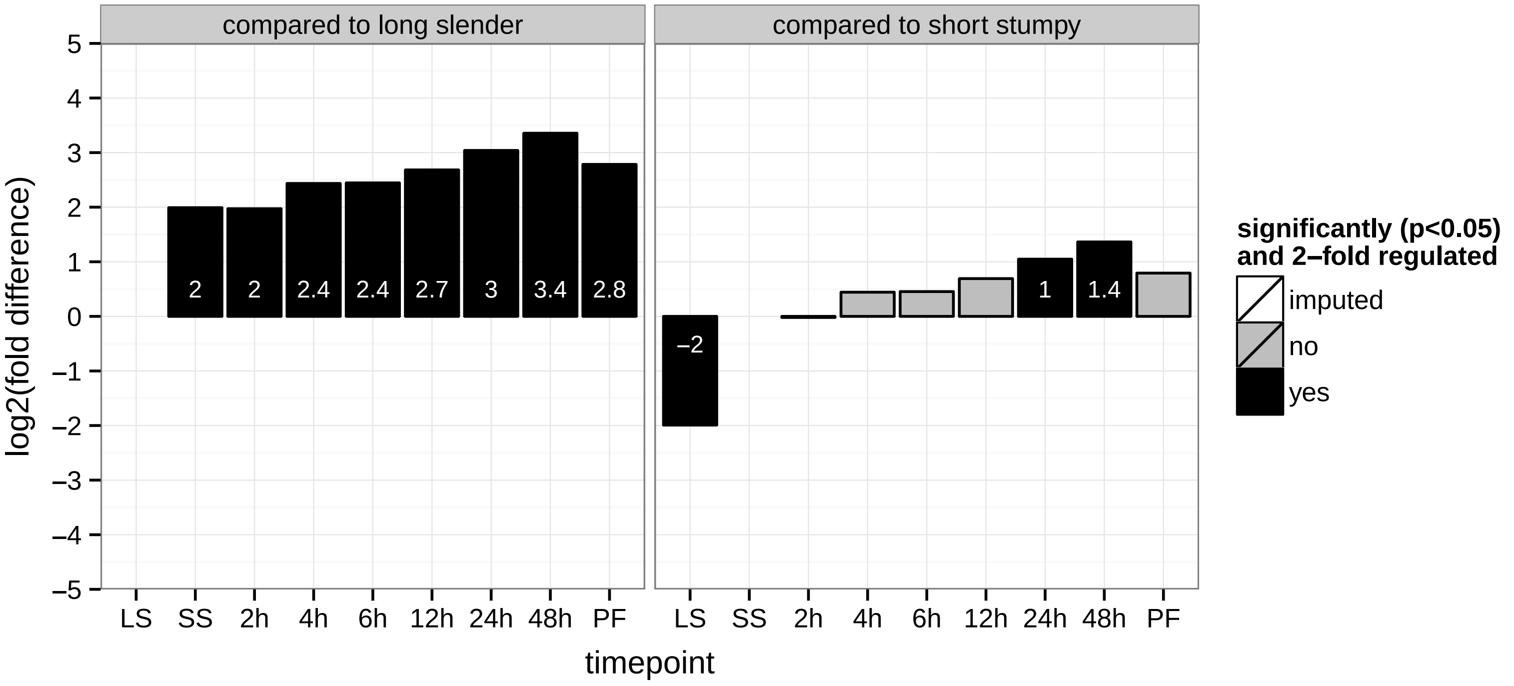
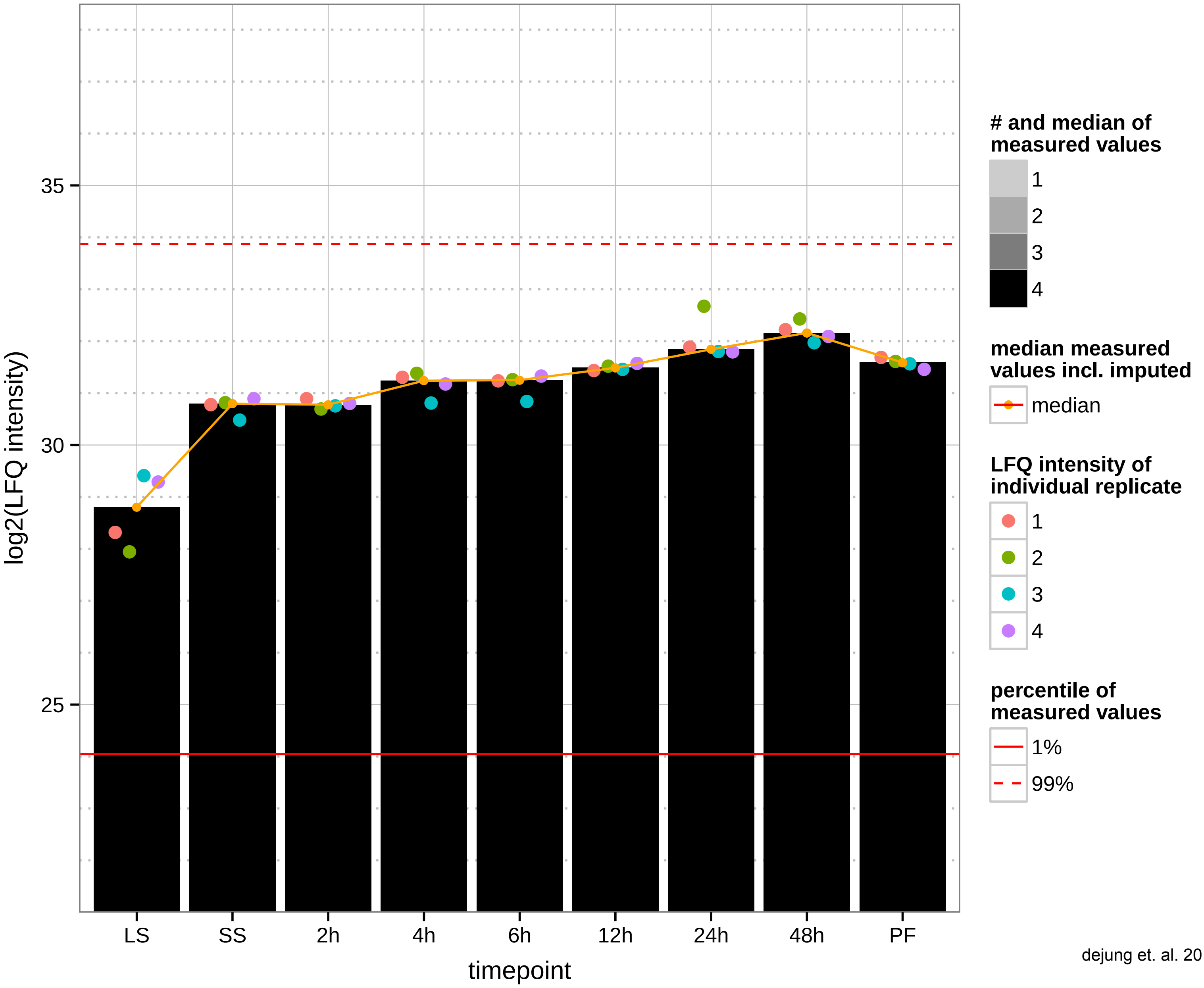
prohibitin, putative, chrX additional, unordered contigs, prohibitin 2, putative (PHB2)
Tb927.10.4310;Tb10.v4.0045
AGOF: null
AGOC: mitochondrial inner membrane, membrane, mitochondrion
AGOP: null, proteolysis, regulation of mitochondrial translation, replicative cell aging
PGOF: null
PGOC: null
PGOP: null





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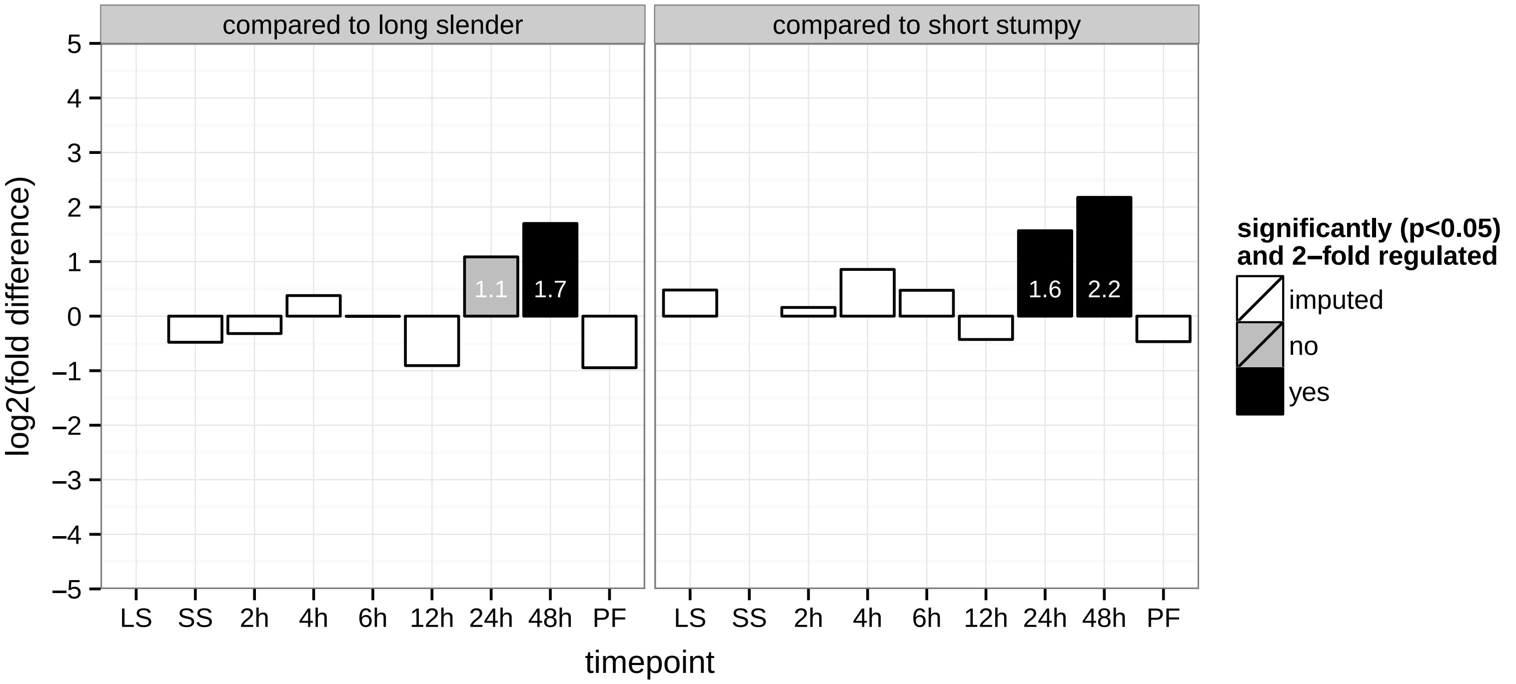
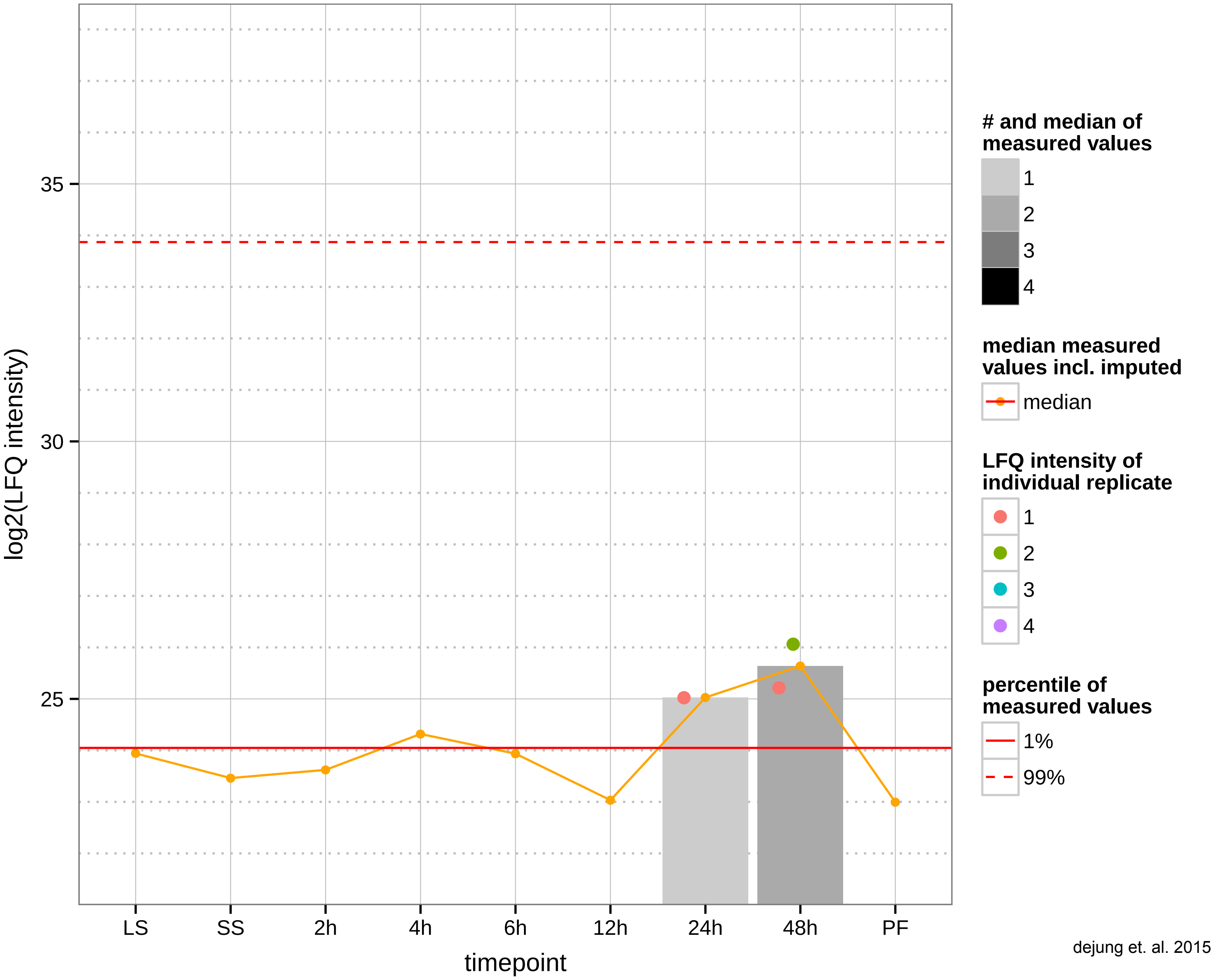
hypothetical protein, conserved
Tb11.02.5070b;Tb927.11.7212
AGOF: transferase activity
AGOC: null
AGOP: null
PGOF: transferase activity
PGOC: null
PGOP: null





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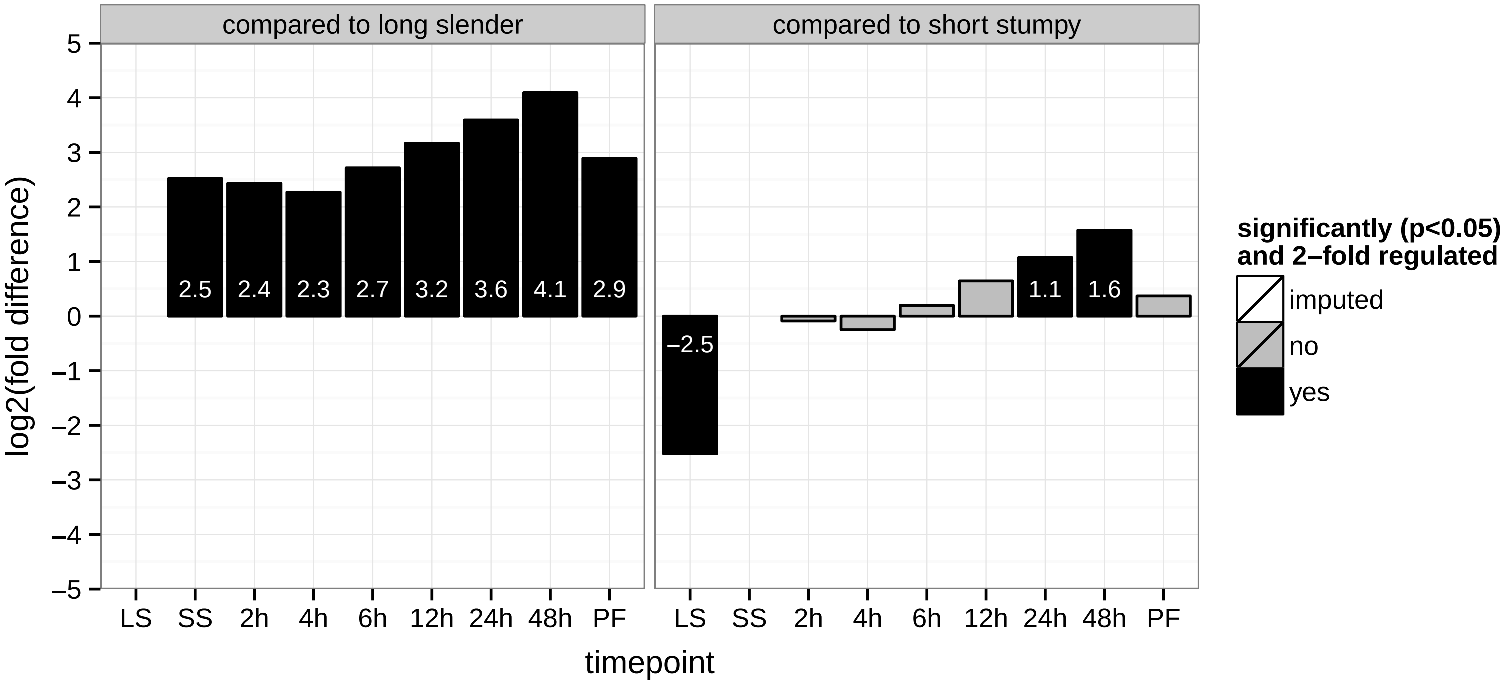
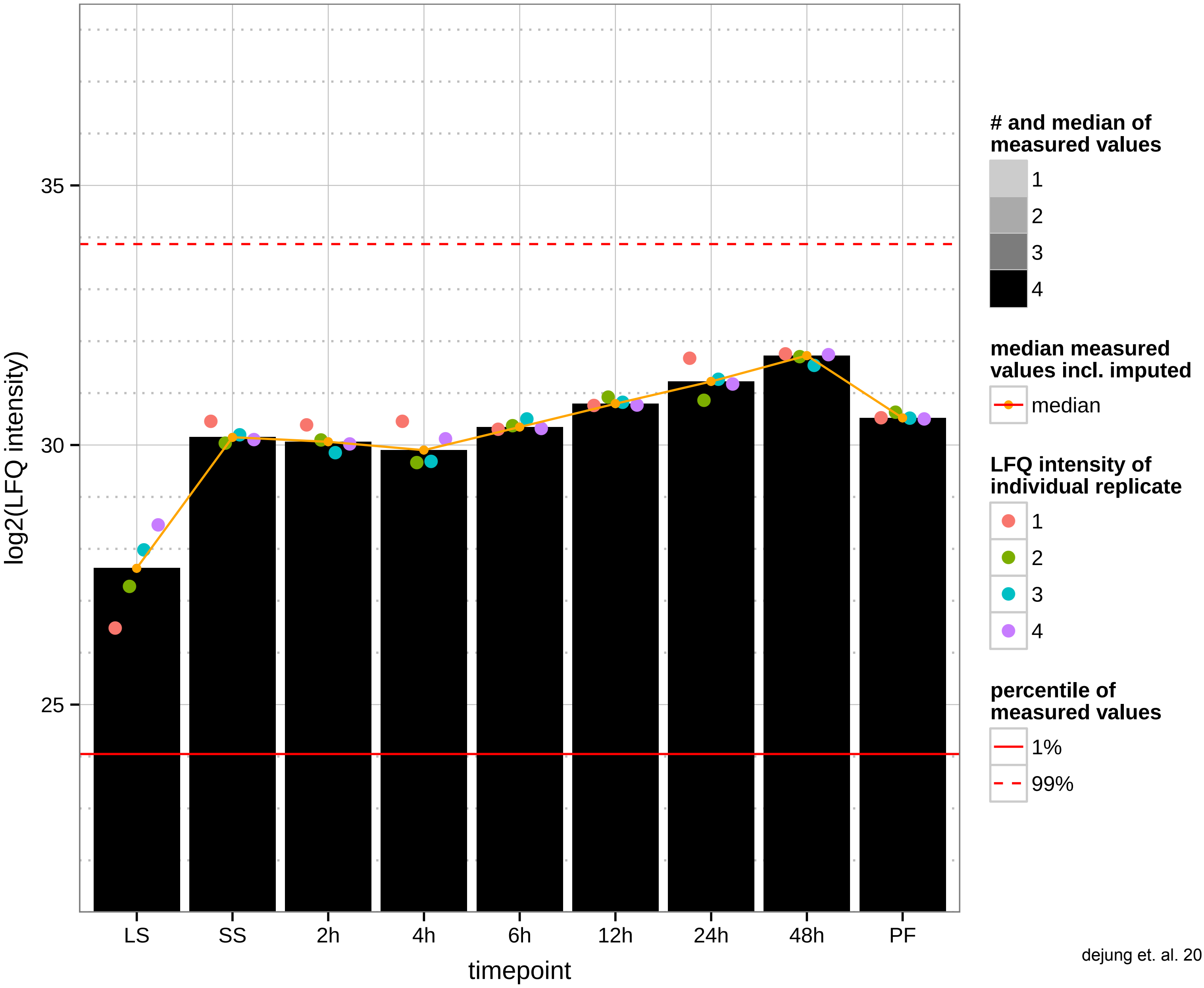
retrotransposon hot spot (RHS) protein, putative, retrotransposon hotspot (RHS) protein 1
Tb927.5.295b;Tb11.v5.0214
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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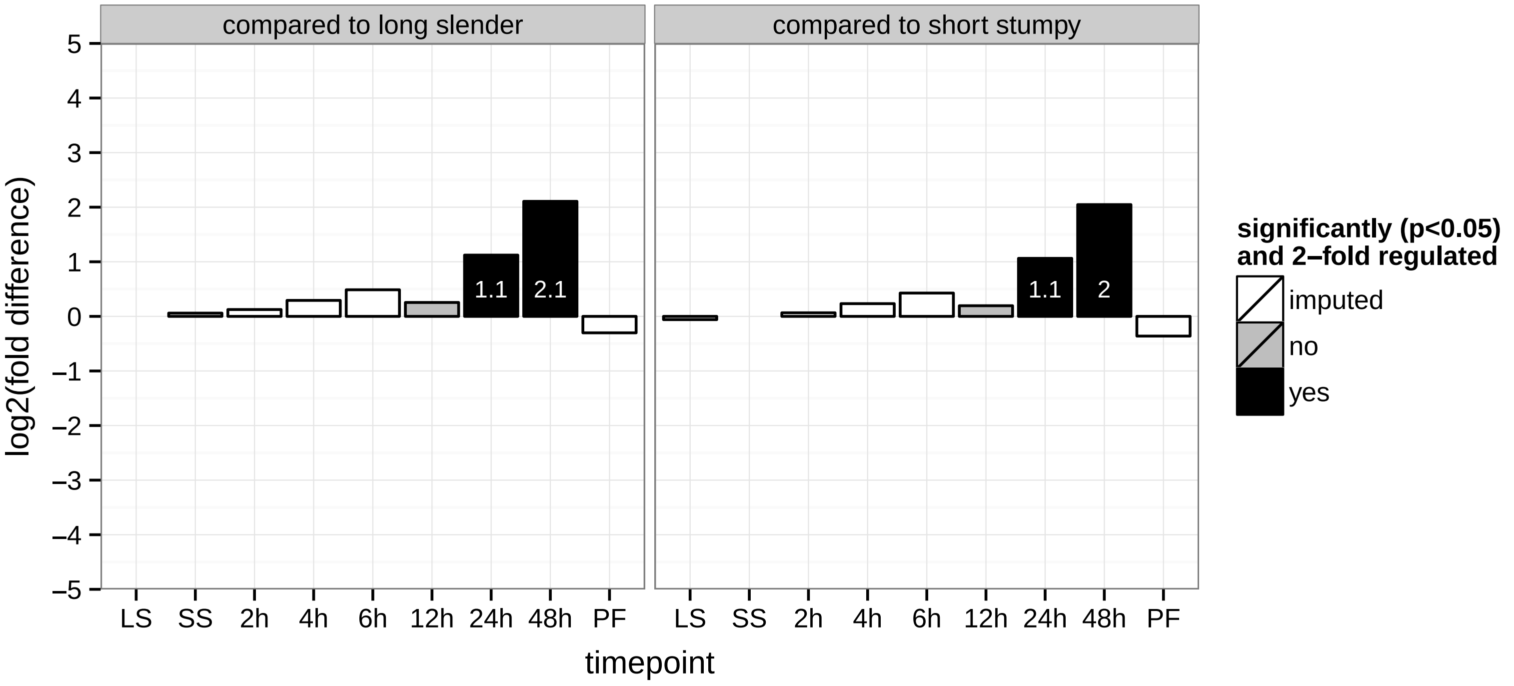
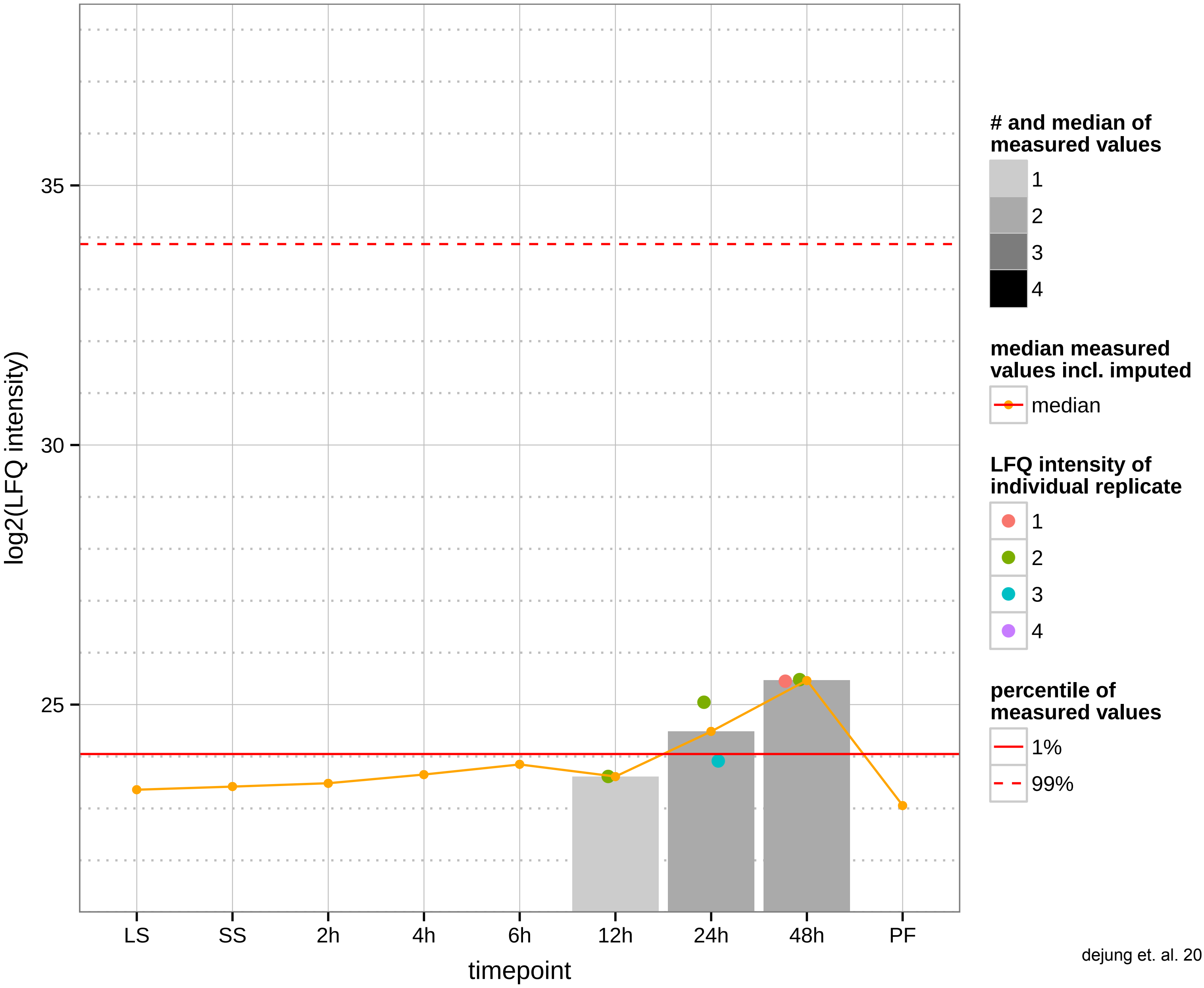
hypothetical protein, conserved
Tb927.8.2470;Tb11.v5.0799
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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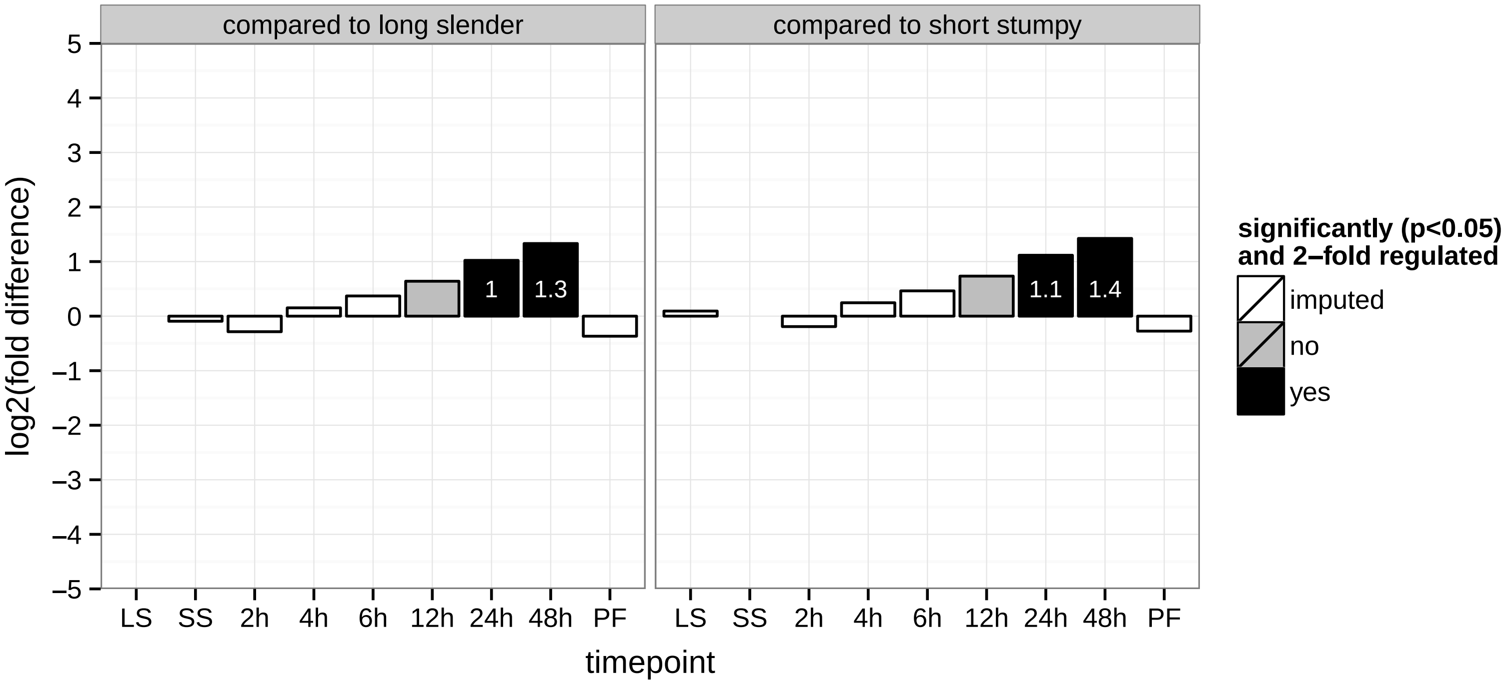
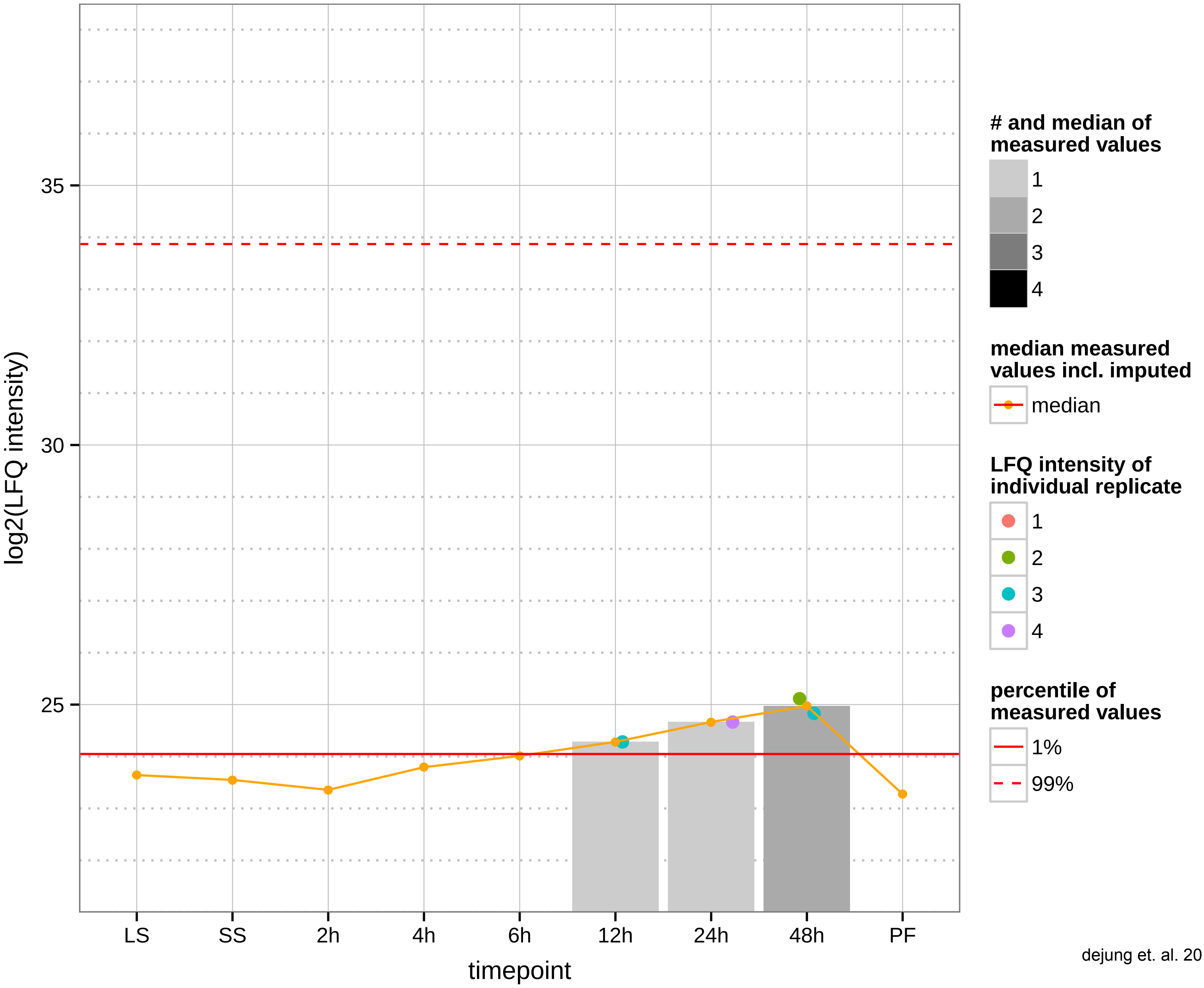
hypothetical protein, conserved
Tb927.1.3250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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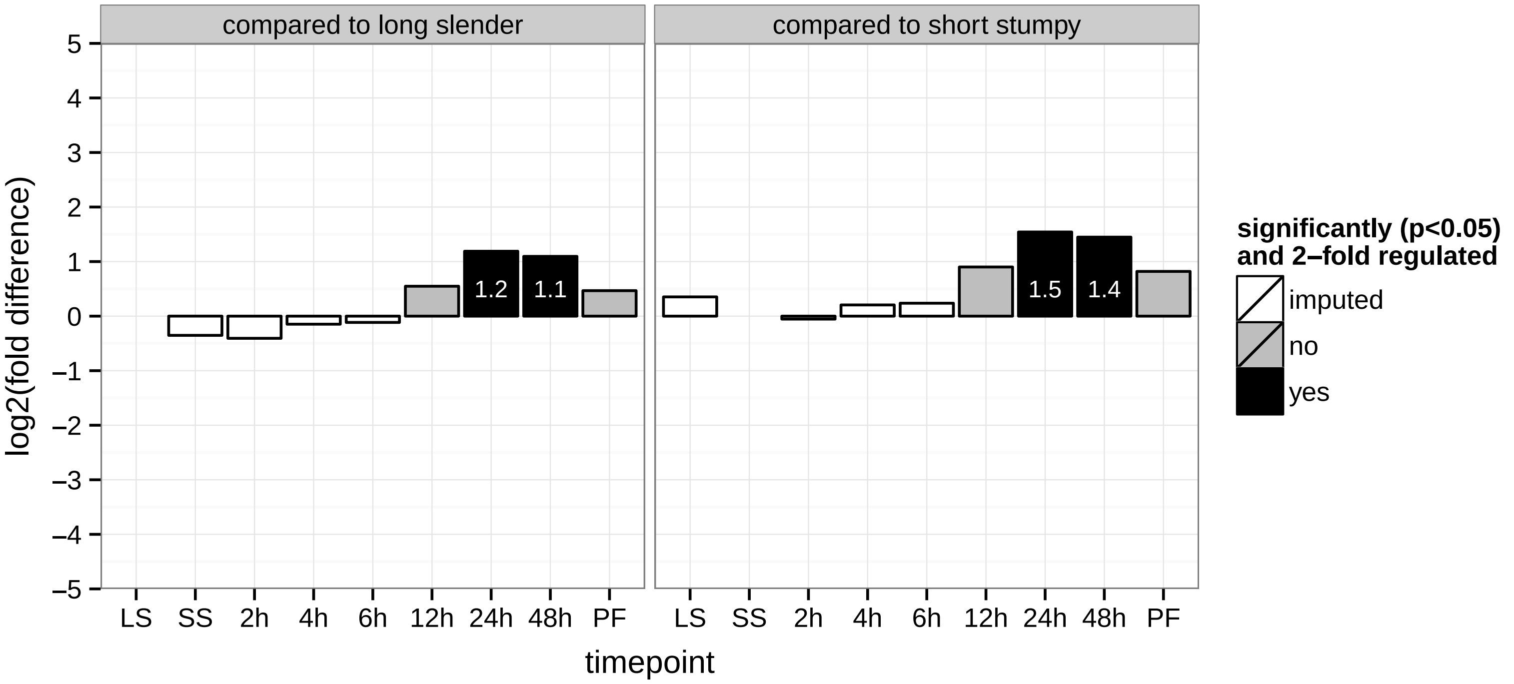
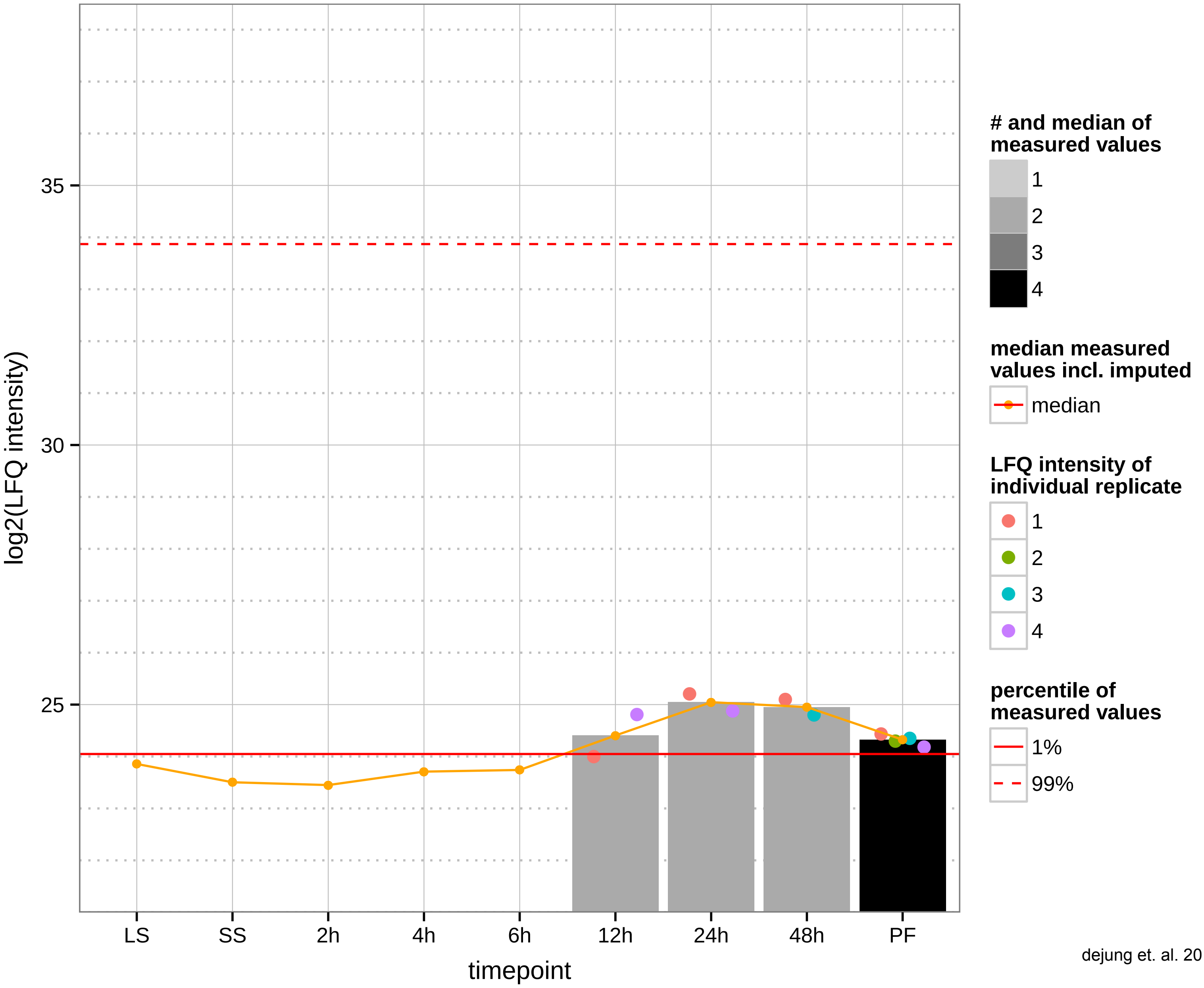
minichromosome maintenance (MCM) complex subunit, putative, DNA replication licensing factor MCM8
Tb927.10.10410;Tb11.v5.0535
AGOF: null, ATP binding, DNA binding
AGOC: null
AGOP: null, DNA replication, DNA–dependent DNA replication initiation
PGOF: ATP binding, DNA binding
PGOC: null
PGOP: DNA replication





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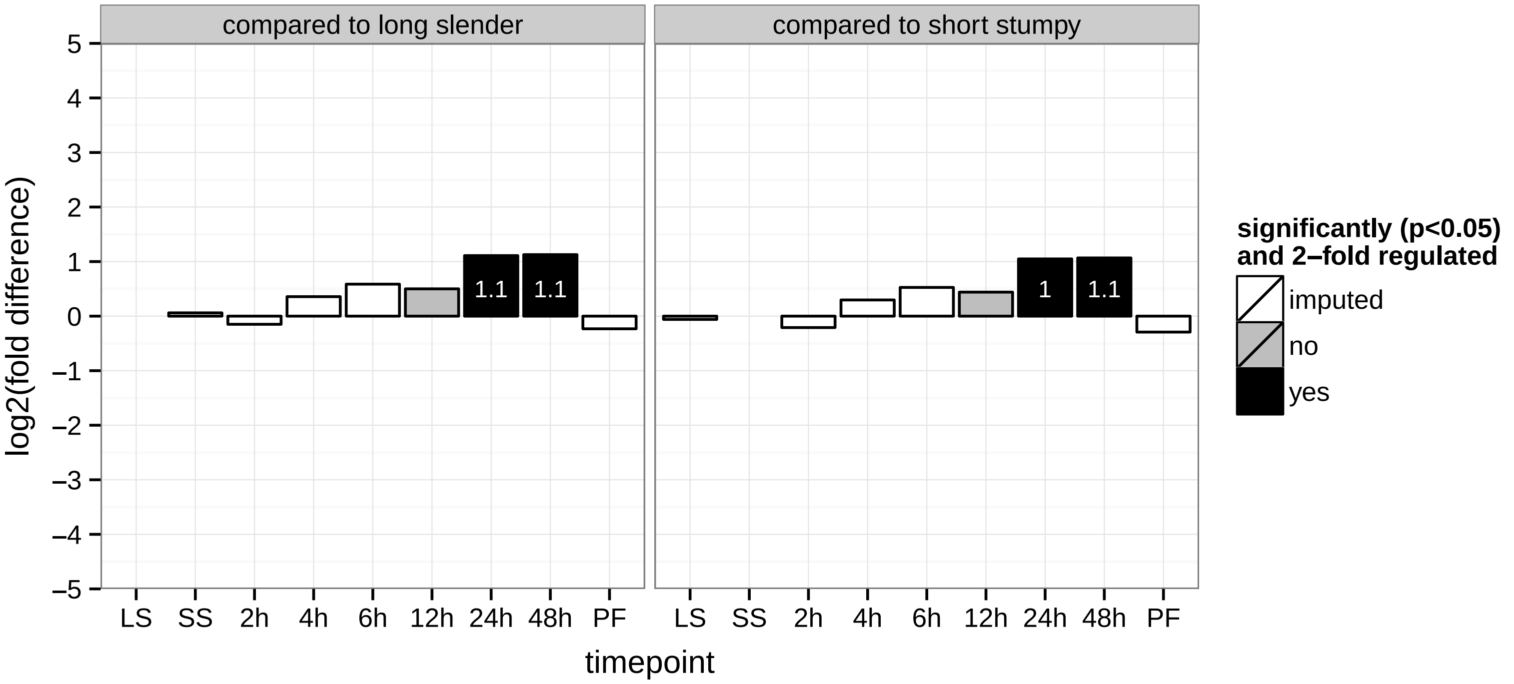
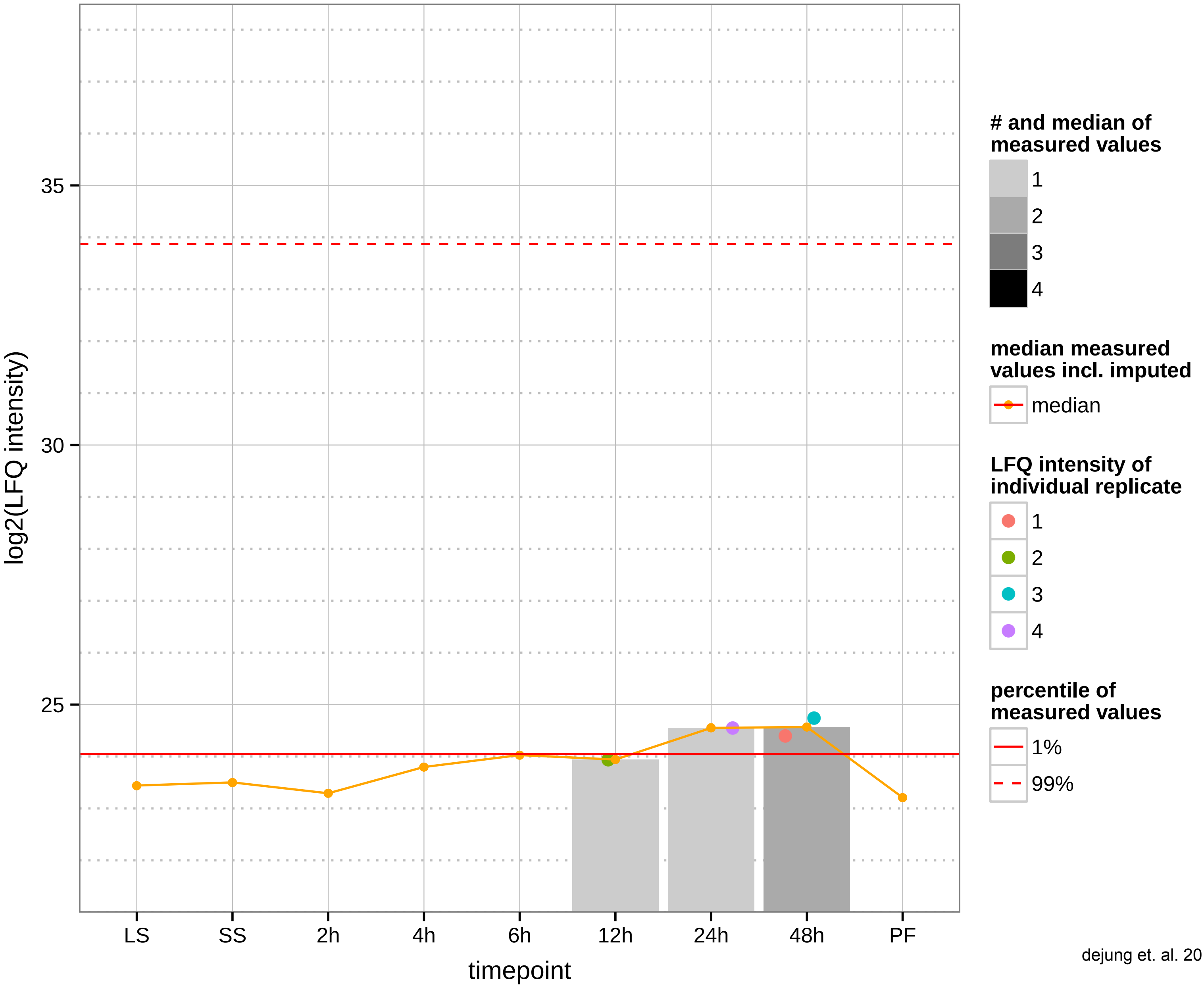
cAMP phosphodiesterase A, putative, 3', 5'−cyclic nucleotide phosphodiesterase, phosphodiesterase, putative (PDEA)
Tb927.10.13000
AGOF: 3', 5'−cyclic−AMP phosphodiesterase activity, 3', 5'−cyclic−nucleotide phosphodiesterase activity
AGOC: cytosol
AGOP: negative regulation of reactive oxygen species metabolic process, signal transduction
PGOF: 3', 5'−cyclic−nucleotide phosphodiesterase activity, catalytic activity
PGOC: null
PGOP: signal transduction





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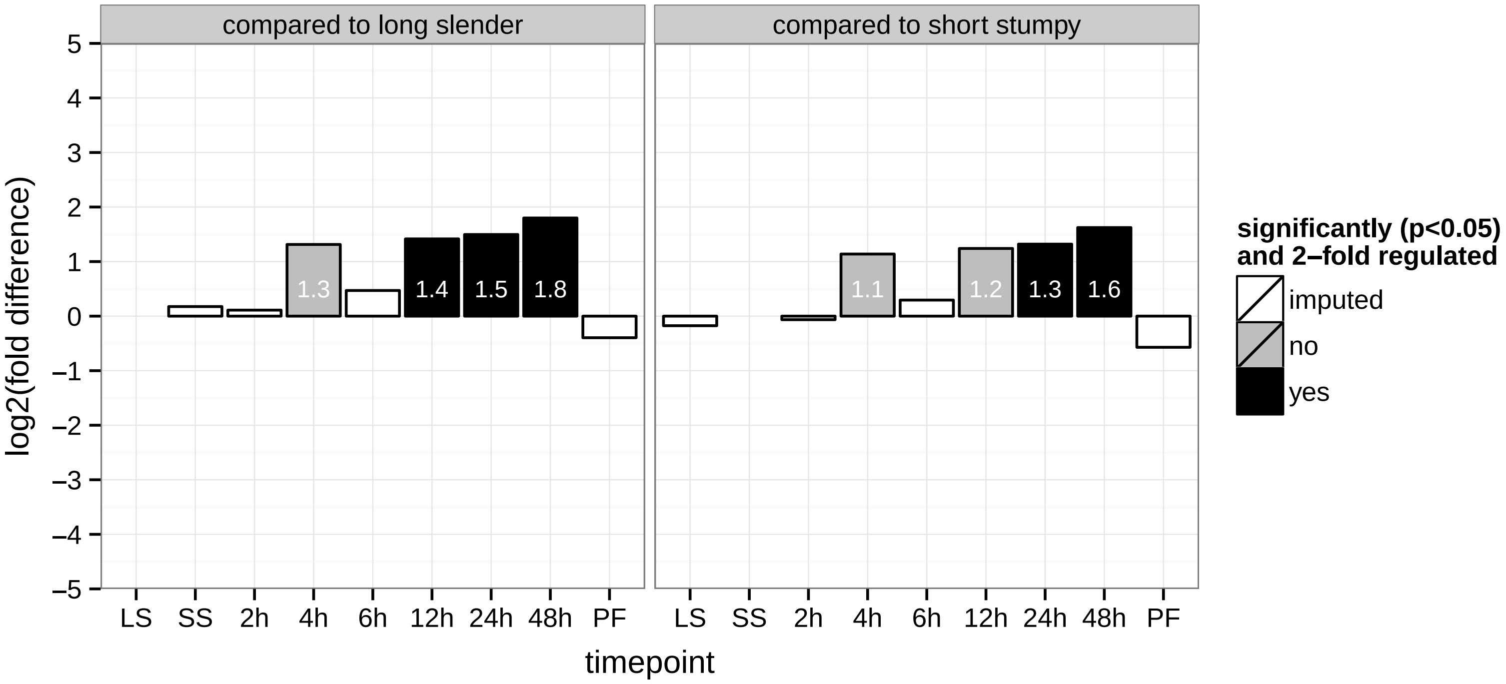
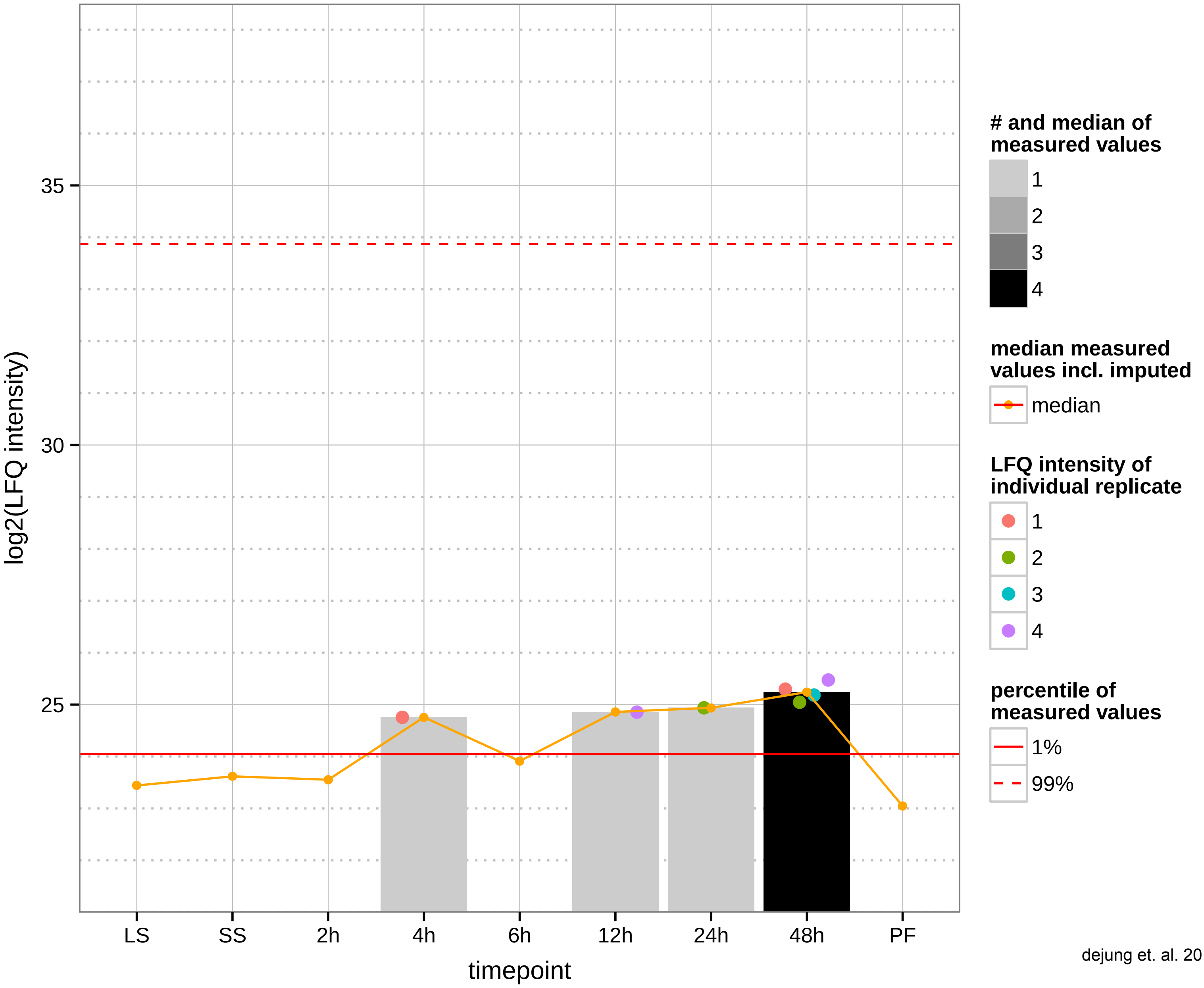
30S ribosomal protein S8, putative
Tb927.10.13300
AGOF: structural constituent of ribosome
AGOC: intracellular, mitochondrion, organellar small ribosomal subunit, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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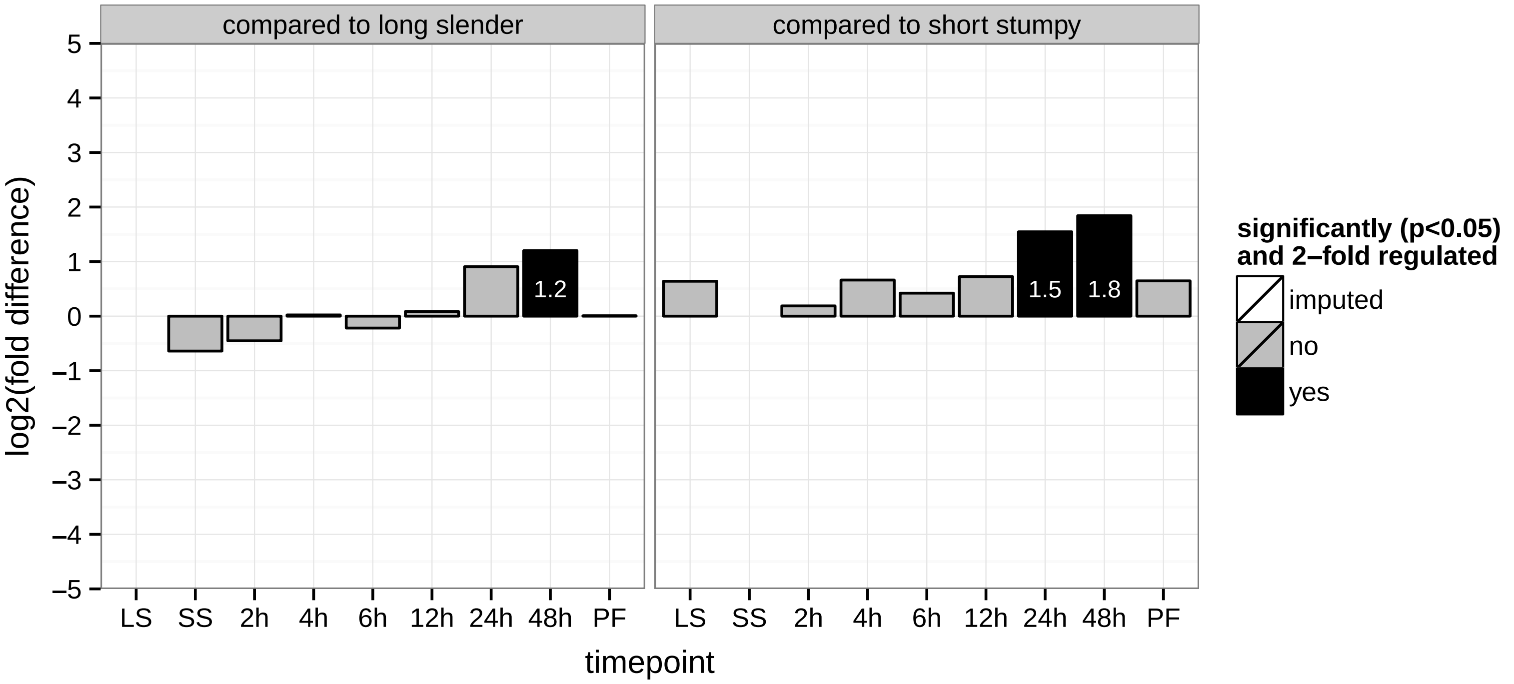
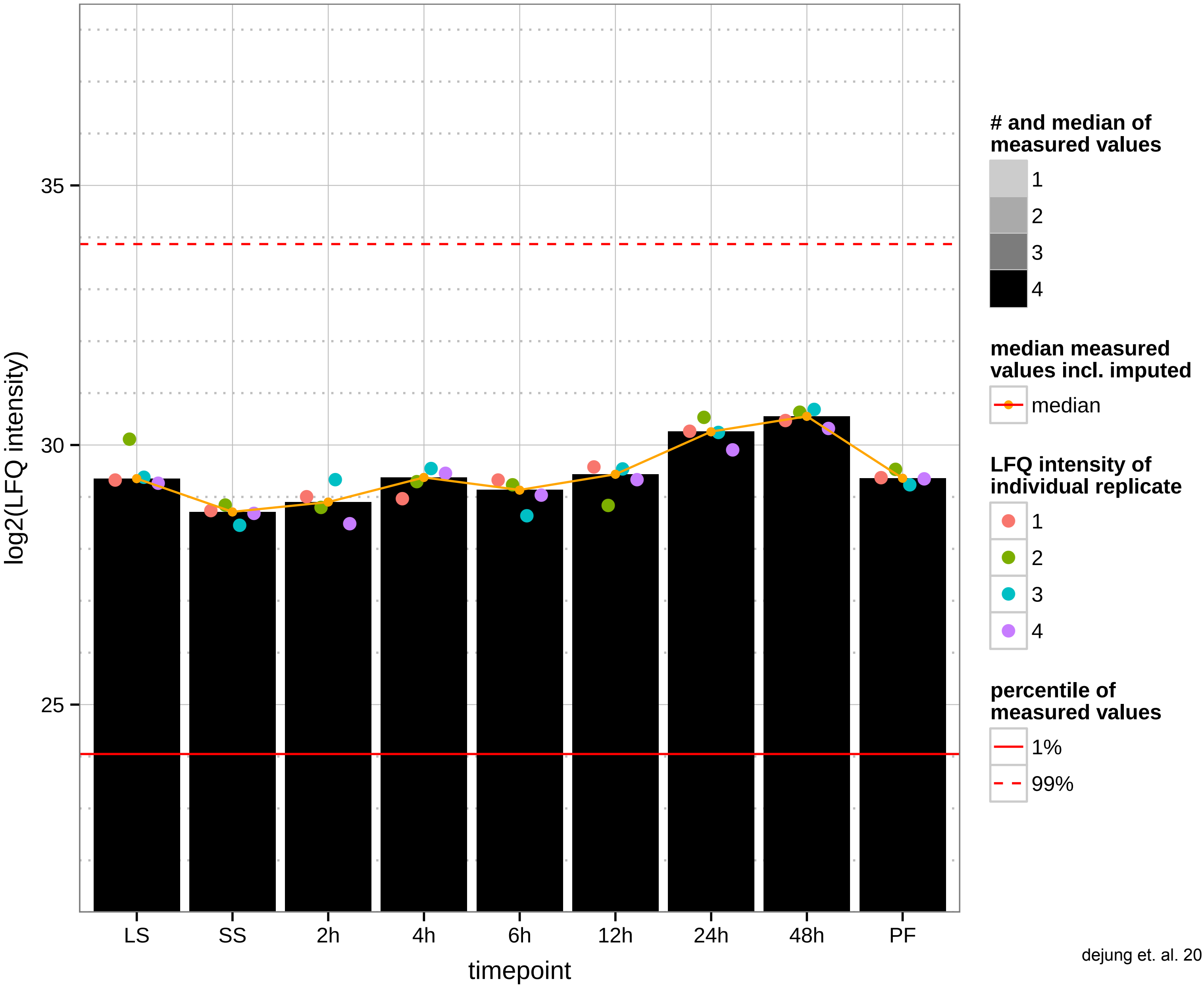
hypothetical protein, conserved
Tb927.10.14700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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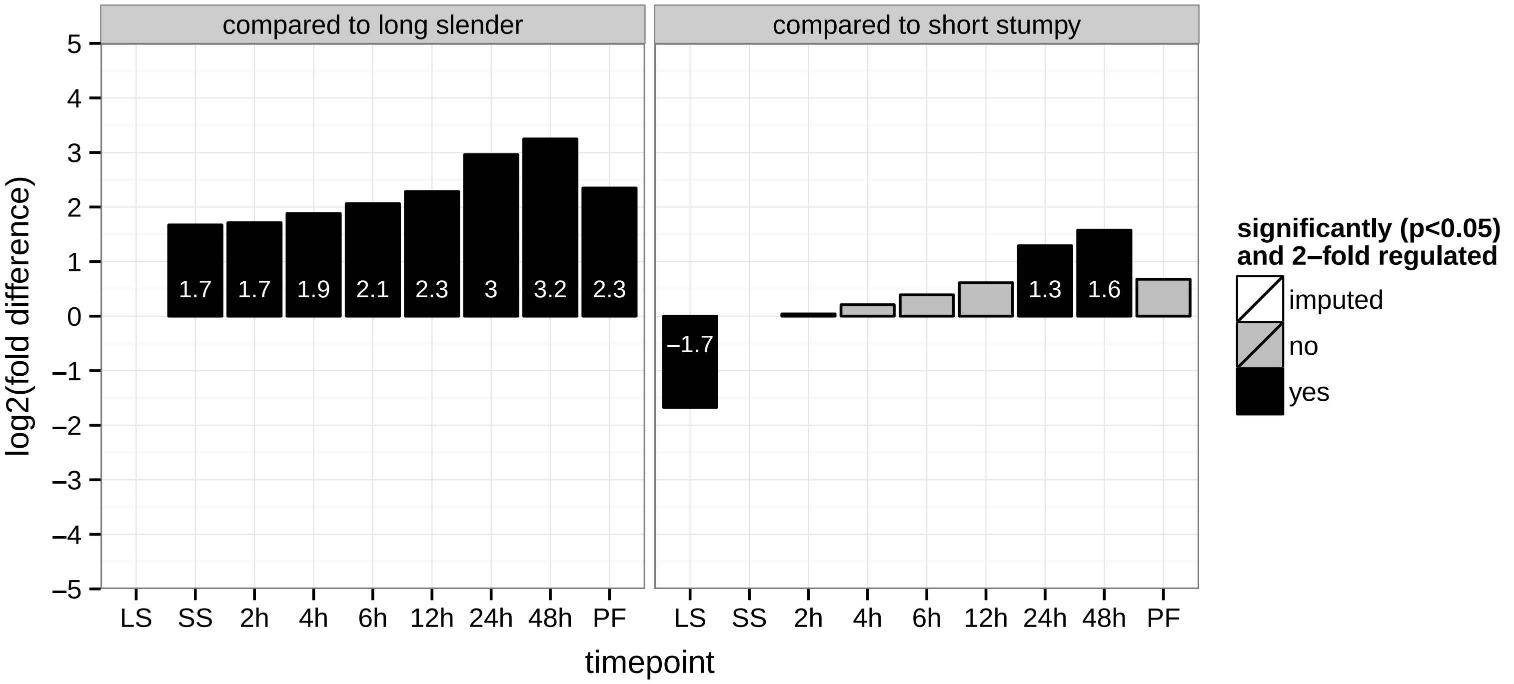
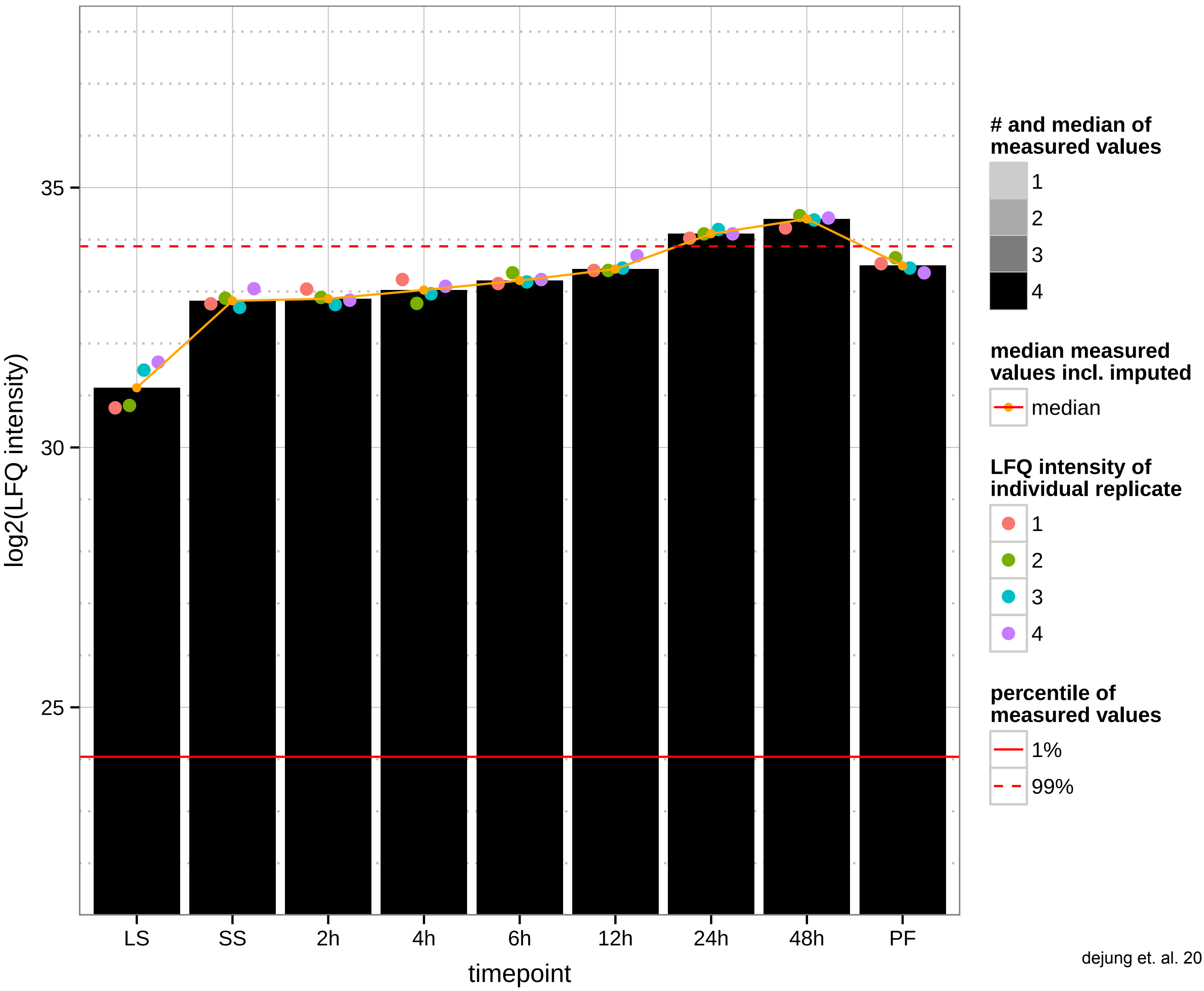
Mitochondrial ADP/ATP carrier protein 5c (MCP5c), Mitochondrial ADP/ATP carrier protein 5b, putative (MCP5b), Mitochondri
Tb927.10.14840;Tb927.10.14830;Tb927.10.14820
AGOF: transporter activity
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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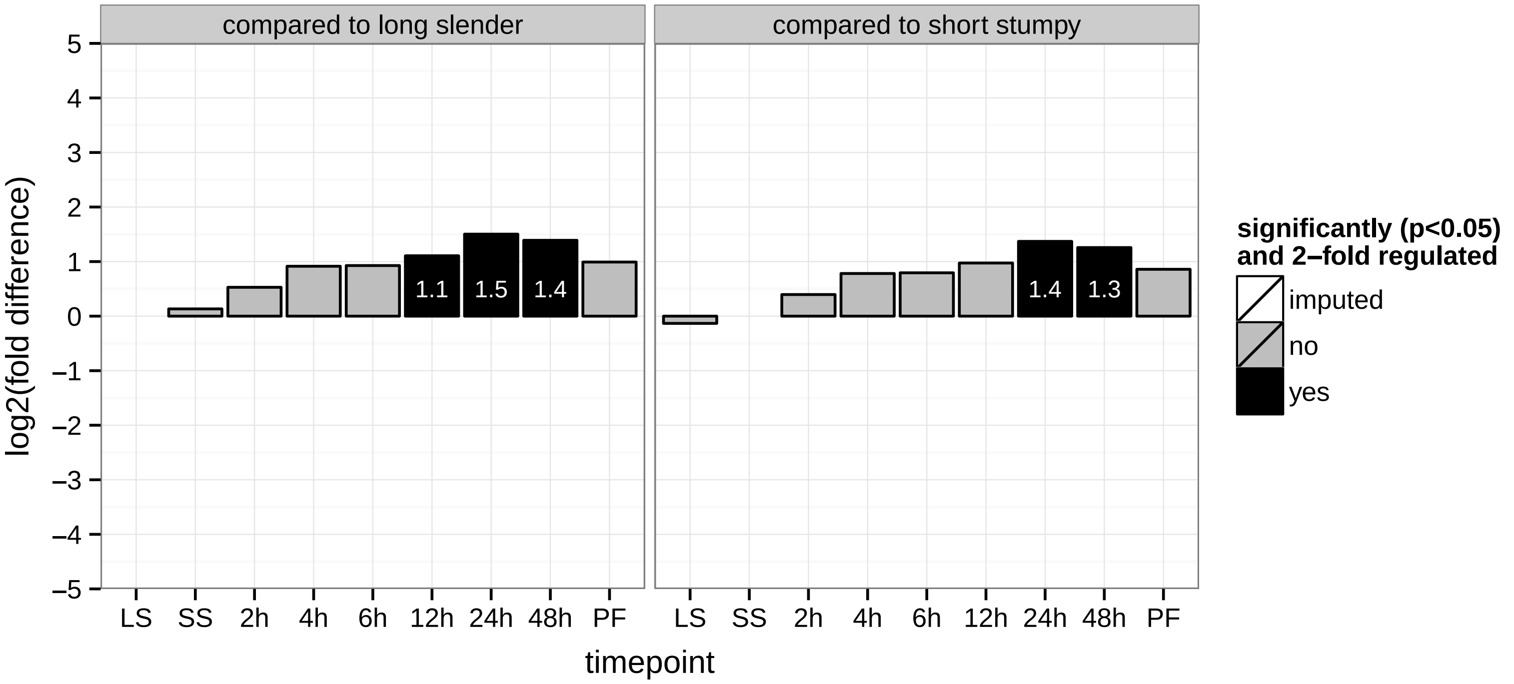
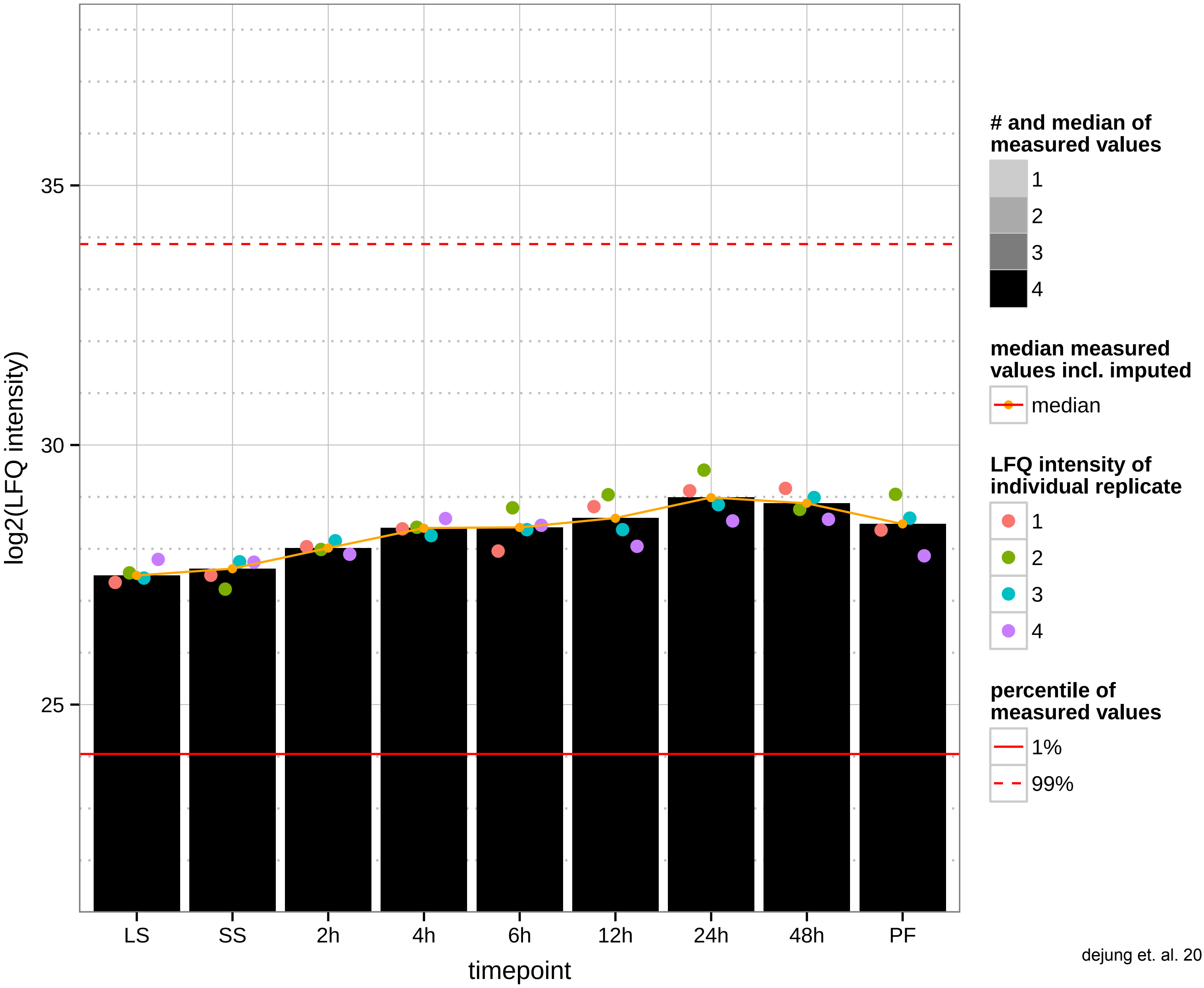
hypothetical protein, conserved
Tb927.10.2620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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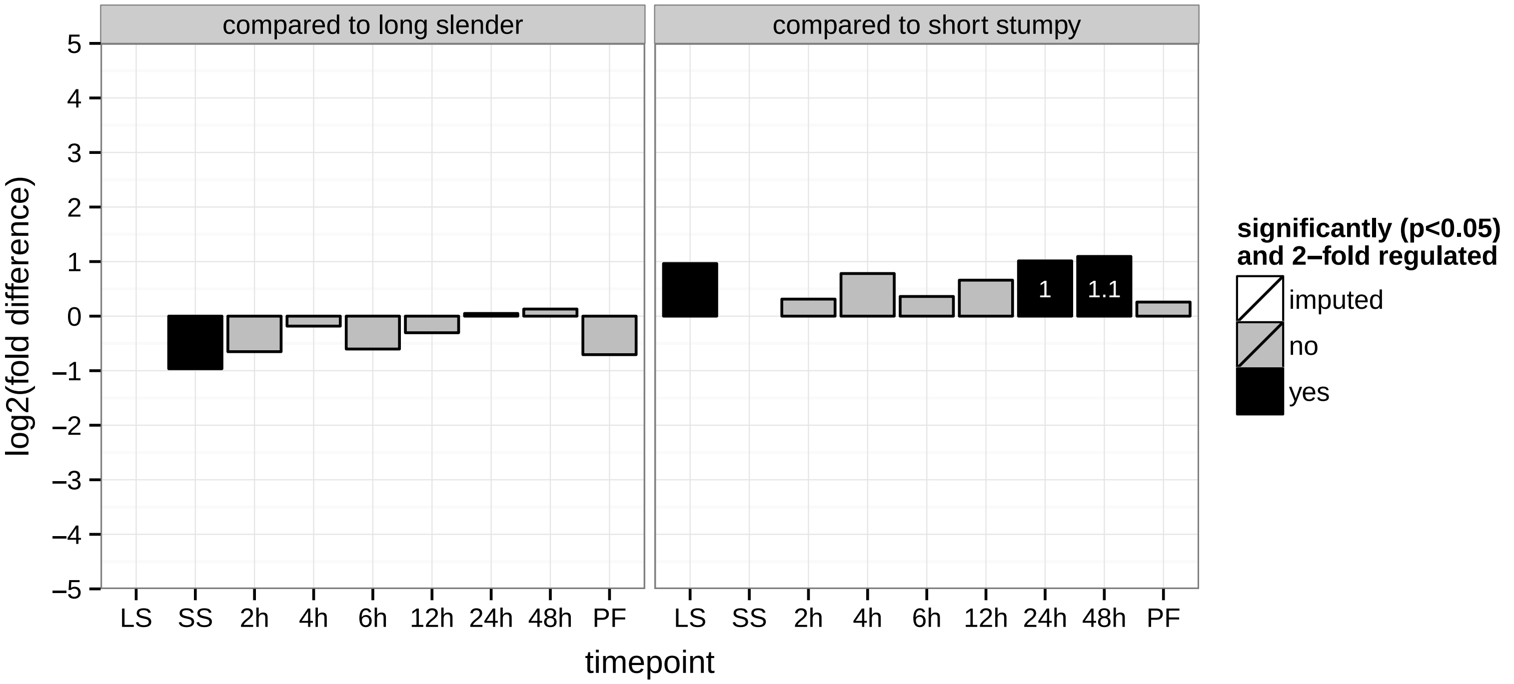
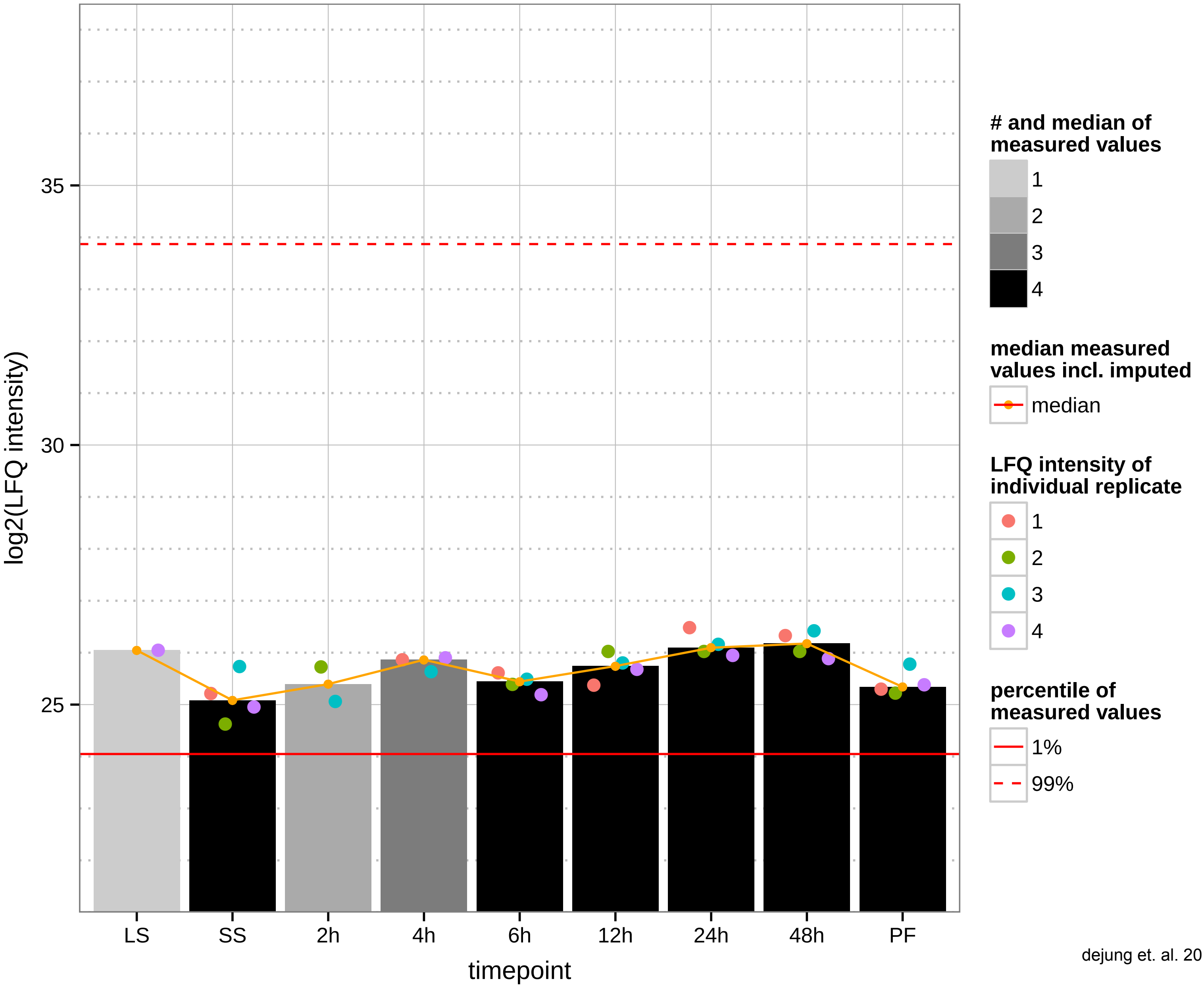
hypothetical protein, conserved
Tb927.10.9330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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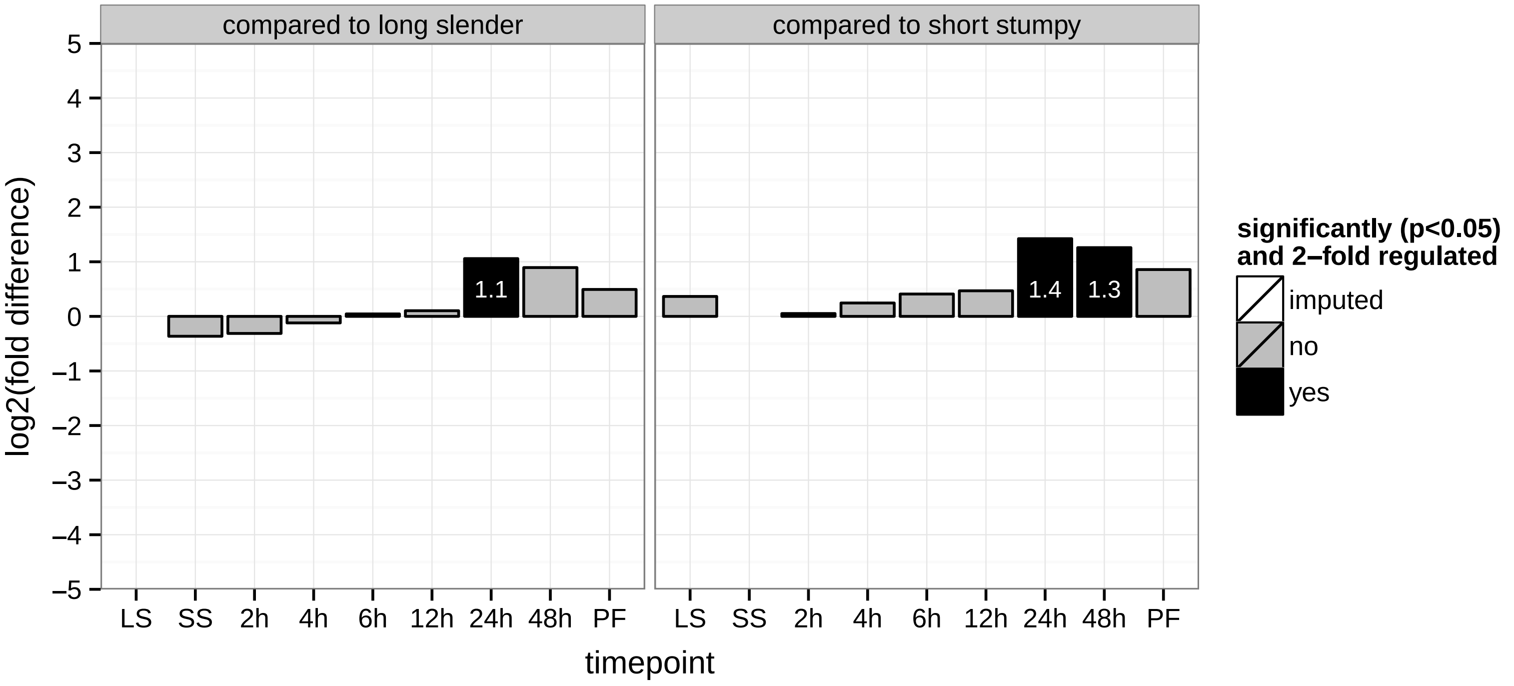
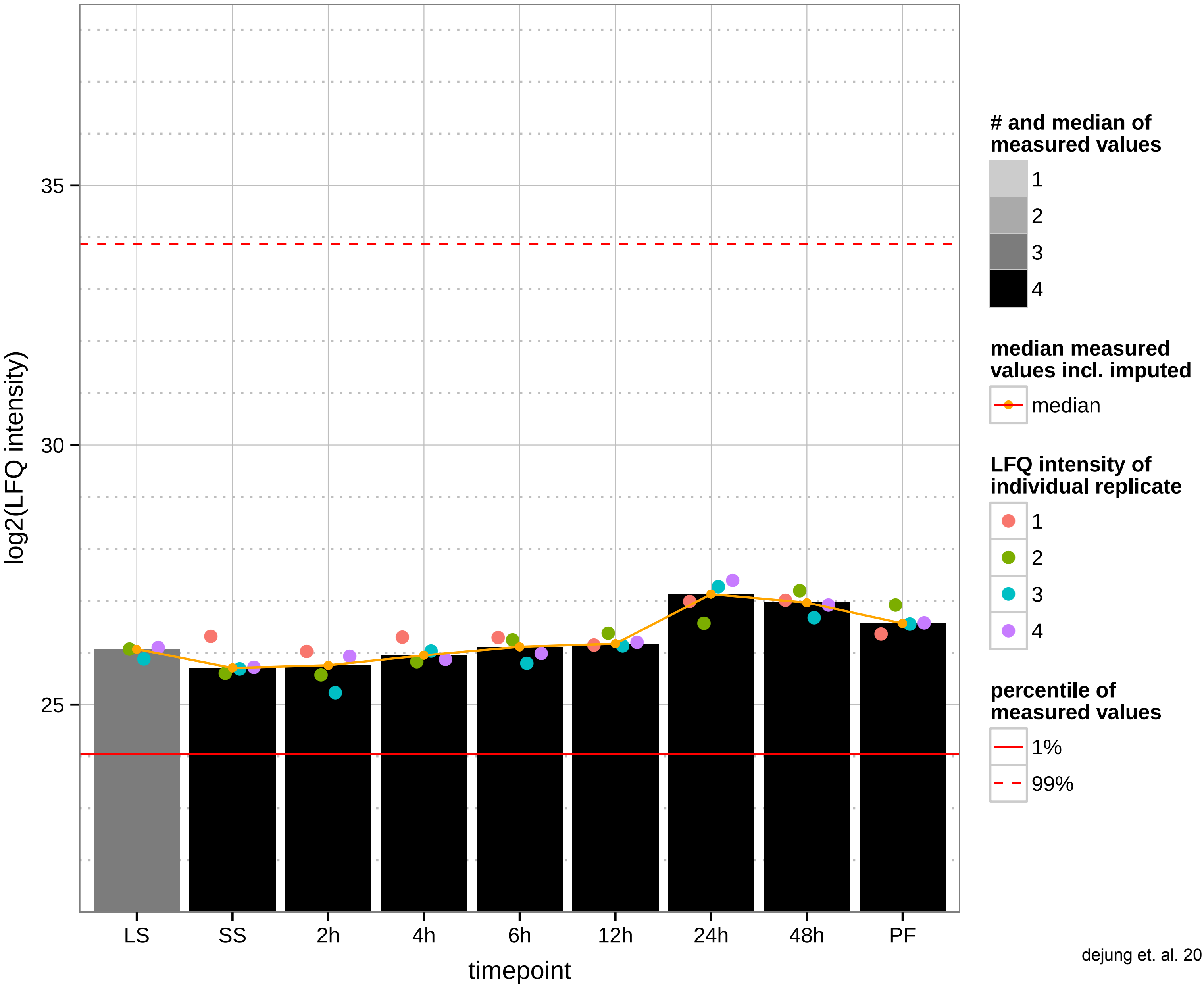
hypothetical protein, conserved
Tb927.11.10260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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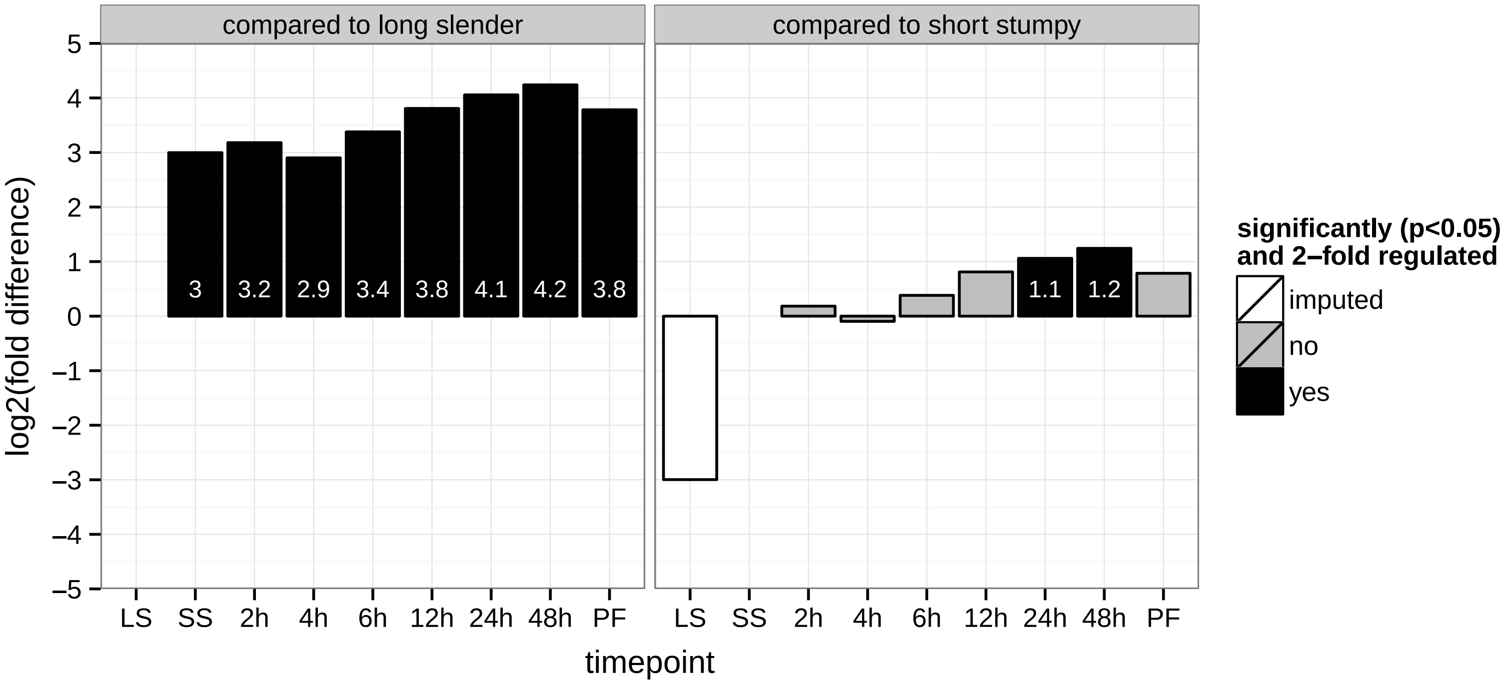
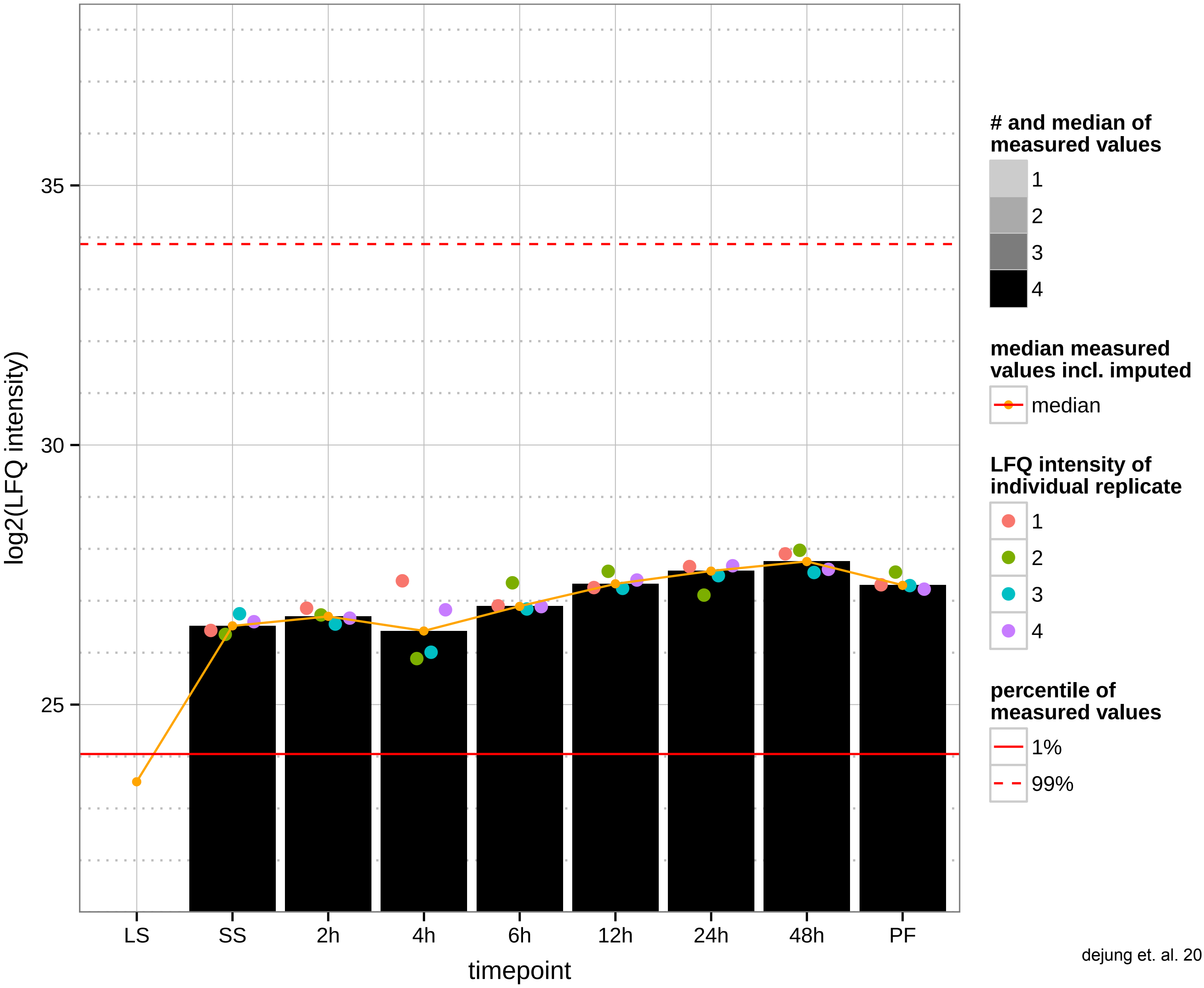
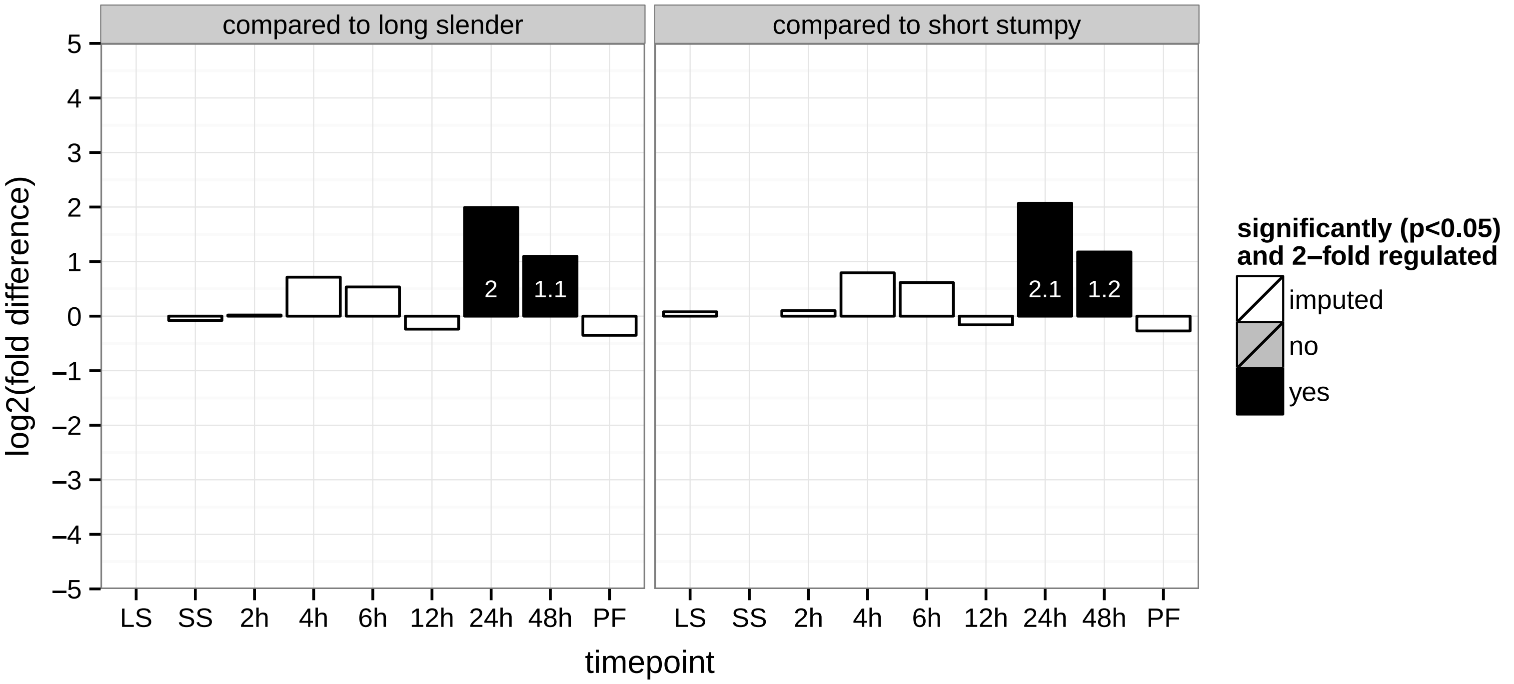
hypothetical protein, conserved
Tb927.11.10960
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular o
PGOC: null
PGOP: oxidation–reduction process

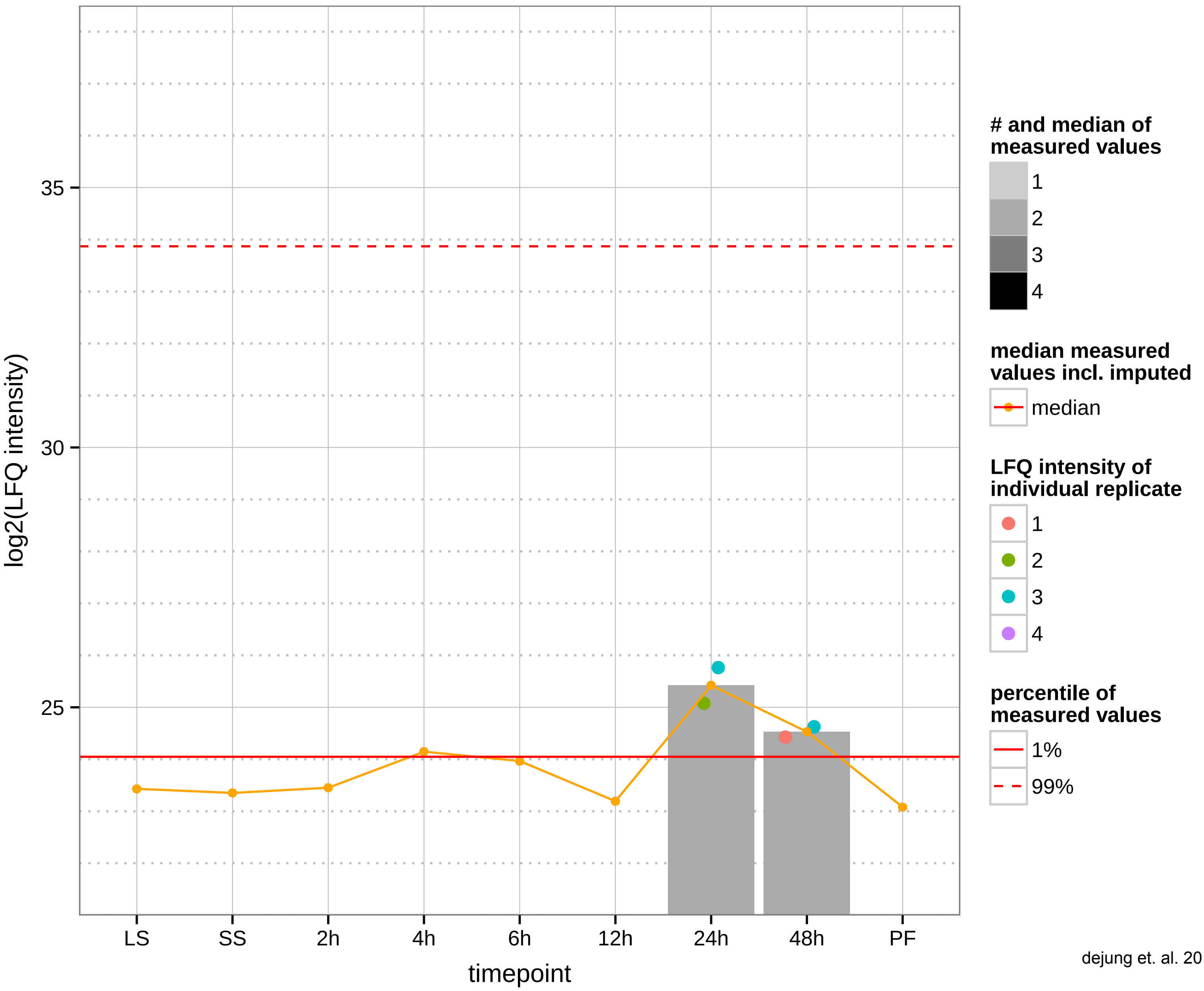




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.11760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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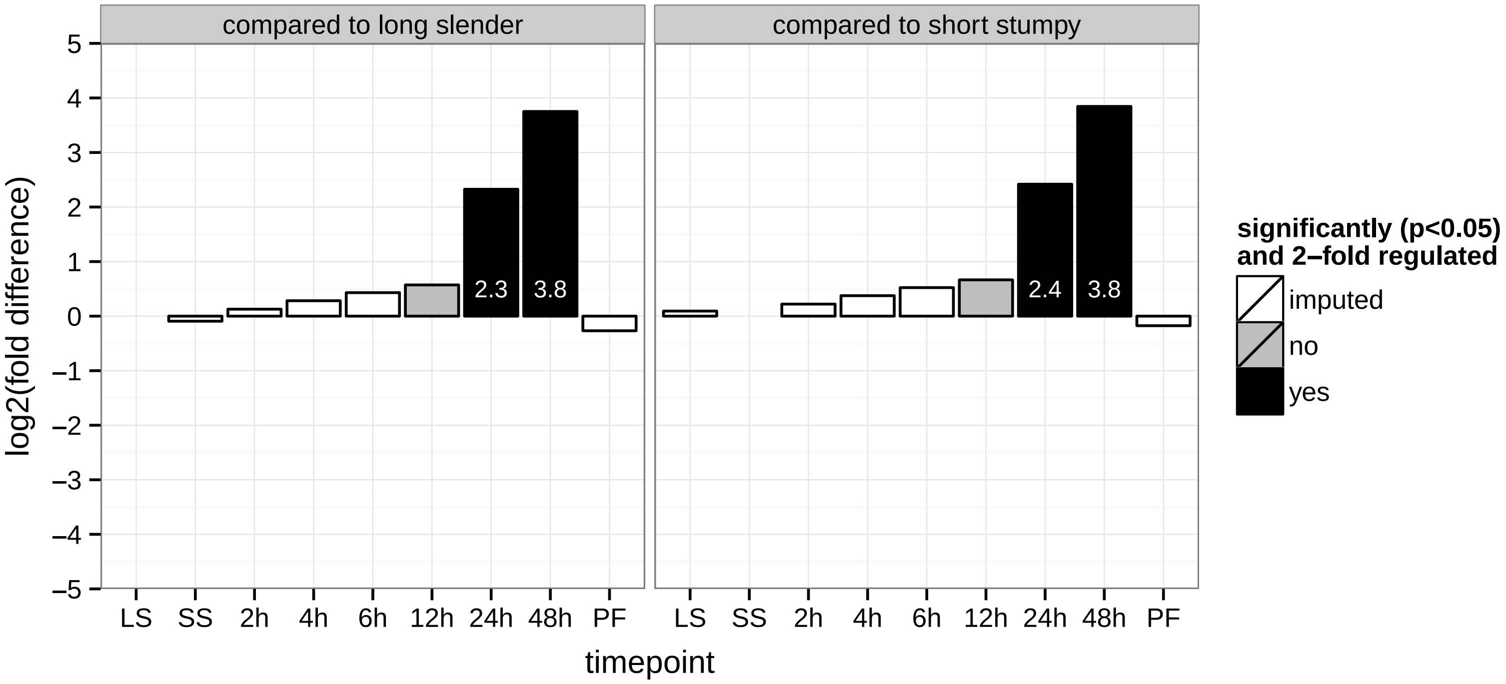
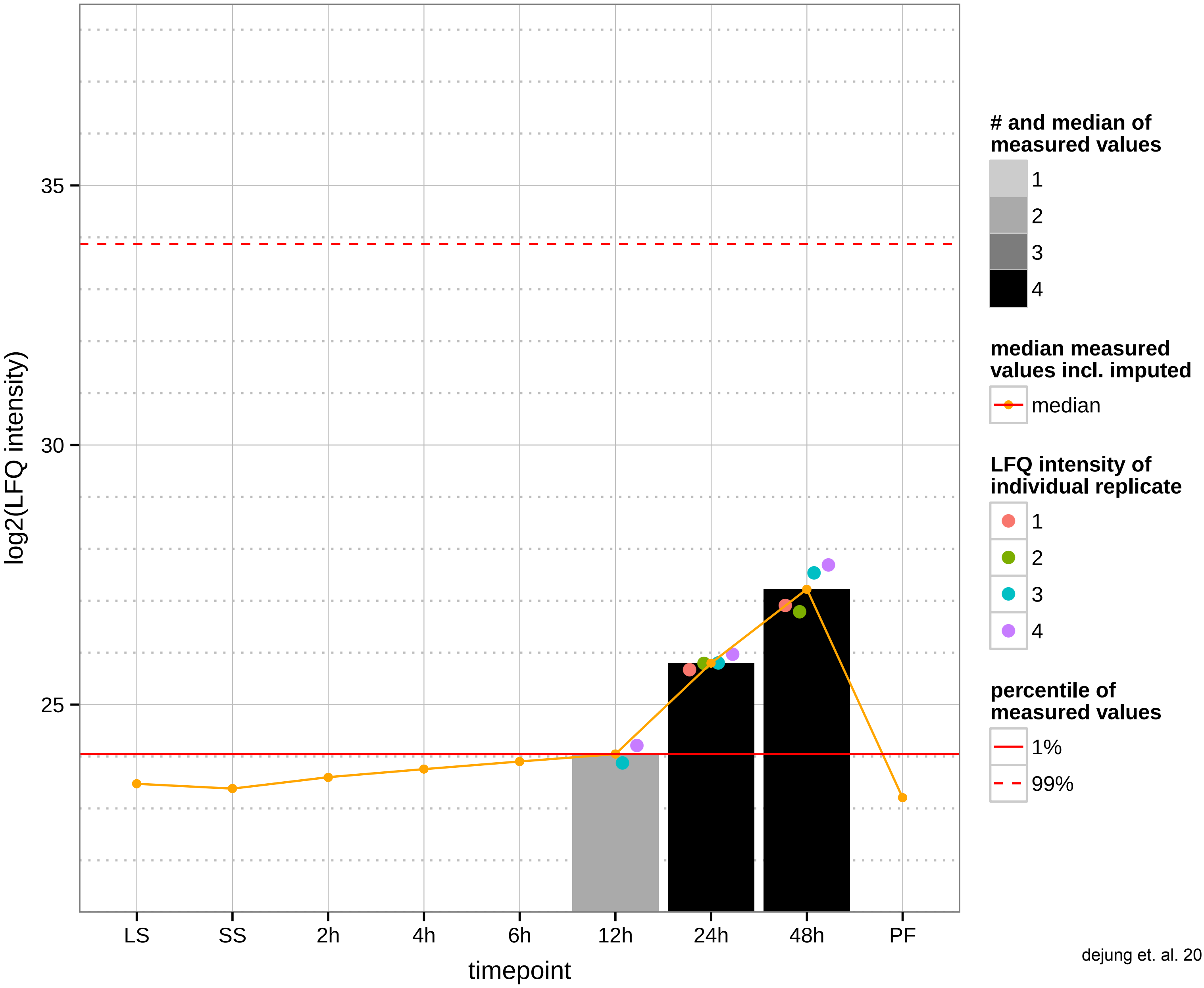
cytochrome oxidase assembly protein, putative
Tb927.11.11950
AGOF: null
AGOC: mitochondrial membrane, mitochondrion
AGOP: protein complex assembly
PGOF: oxidoreductase activity, acting on the CH–CH group of donors
PGOC: membrane
PGOP: heme a biosynthetic process, oxidation–reduction process





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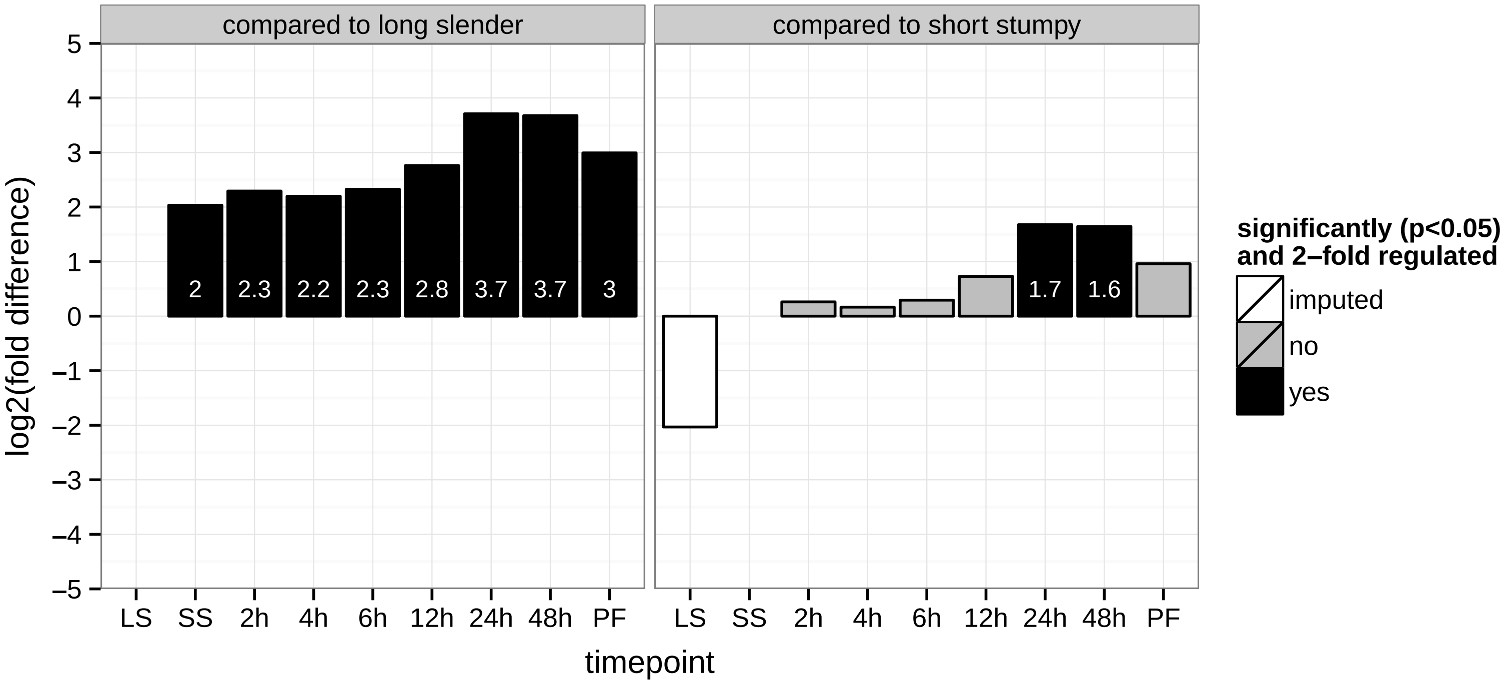
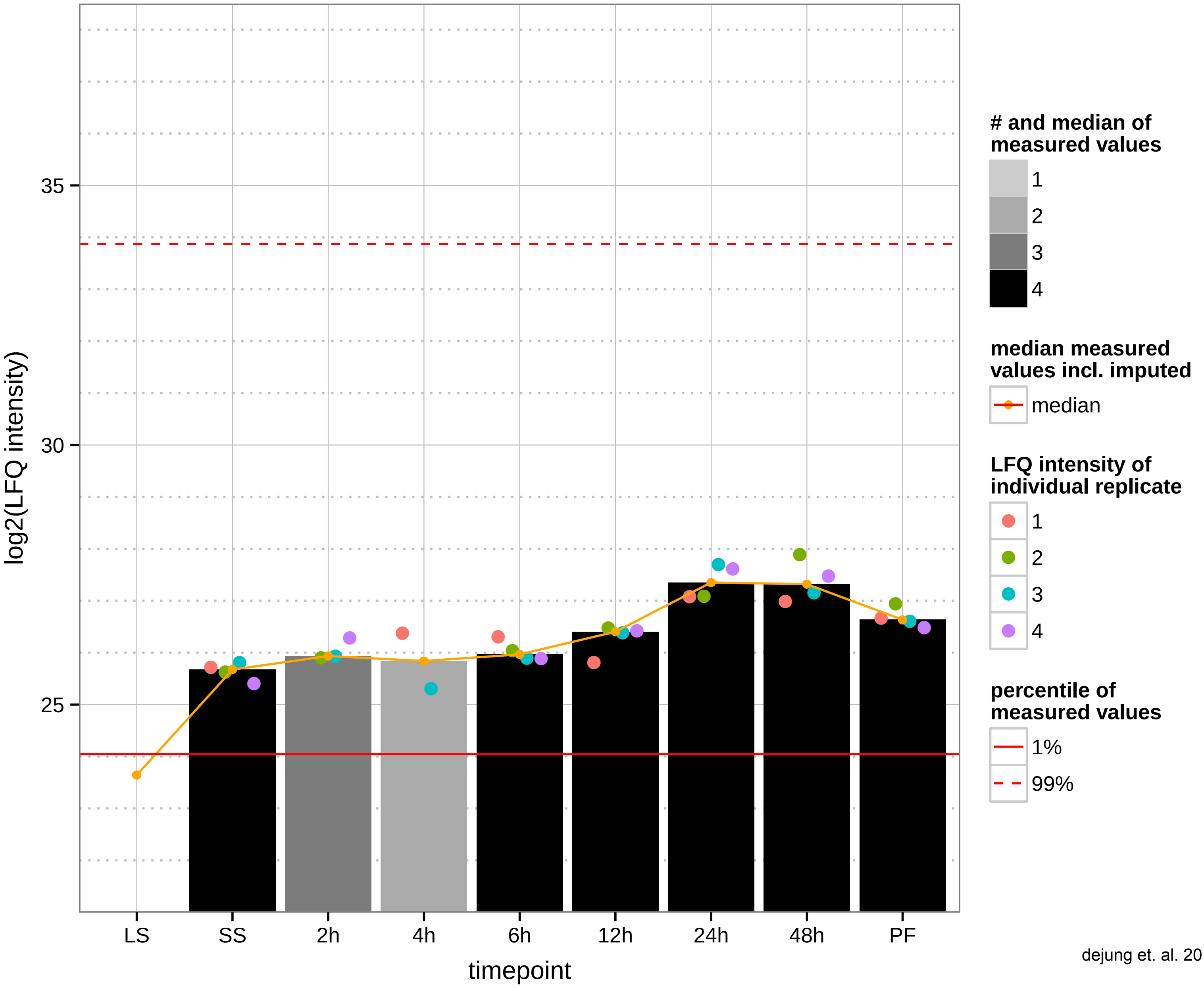
hypothetical protein, conserved
Tb927.11.1290
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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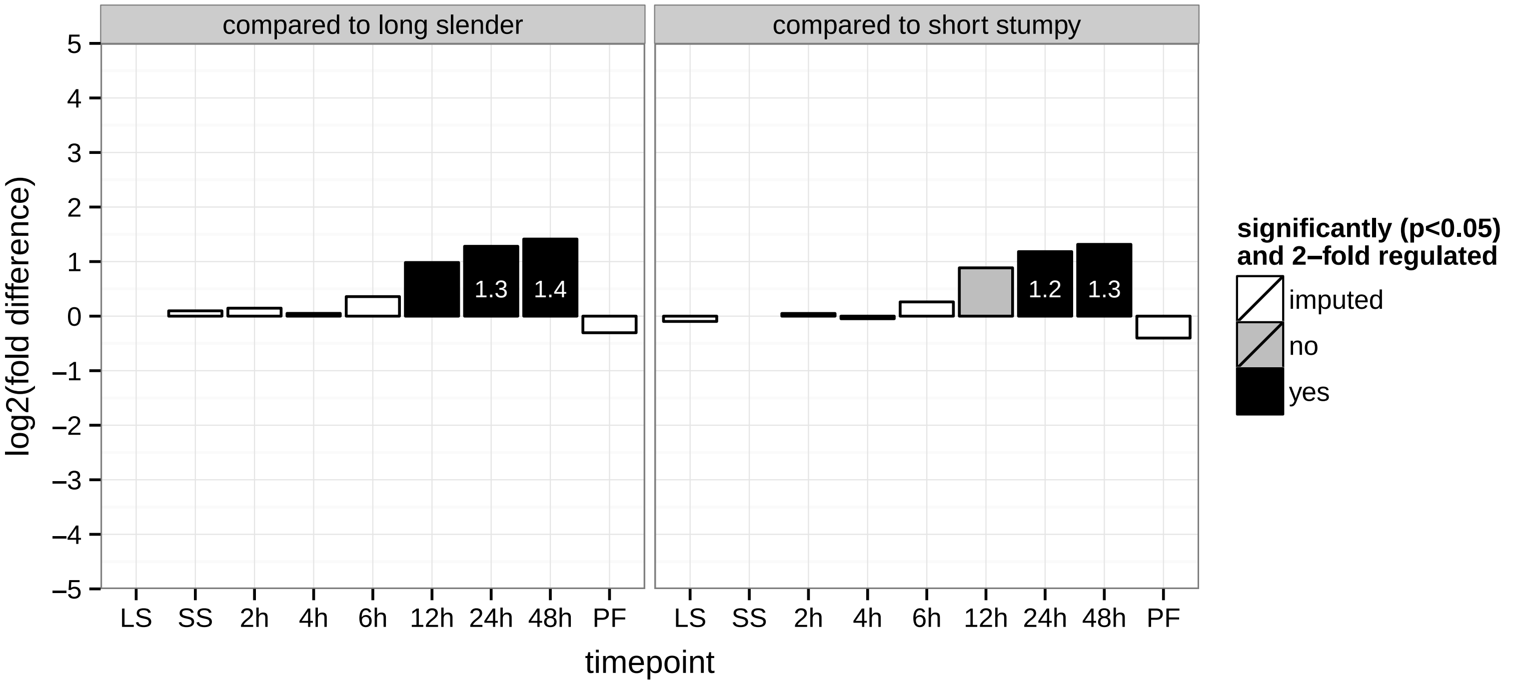
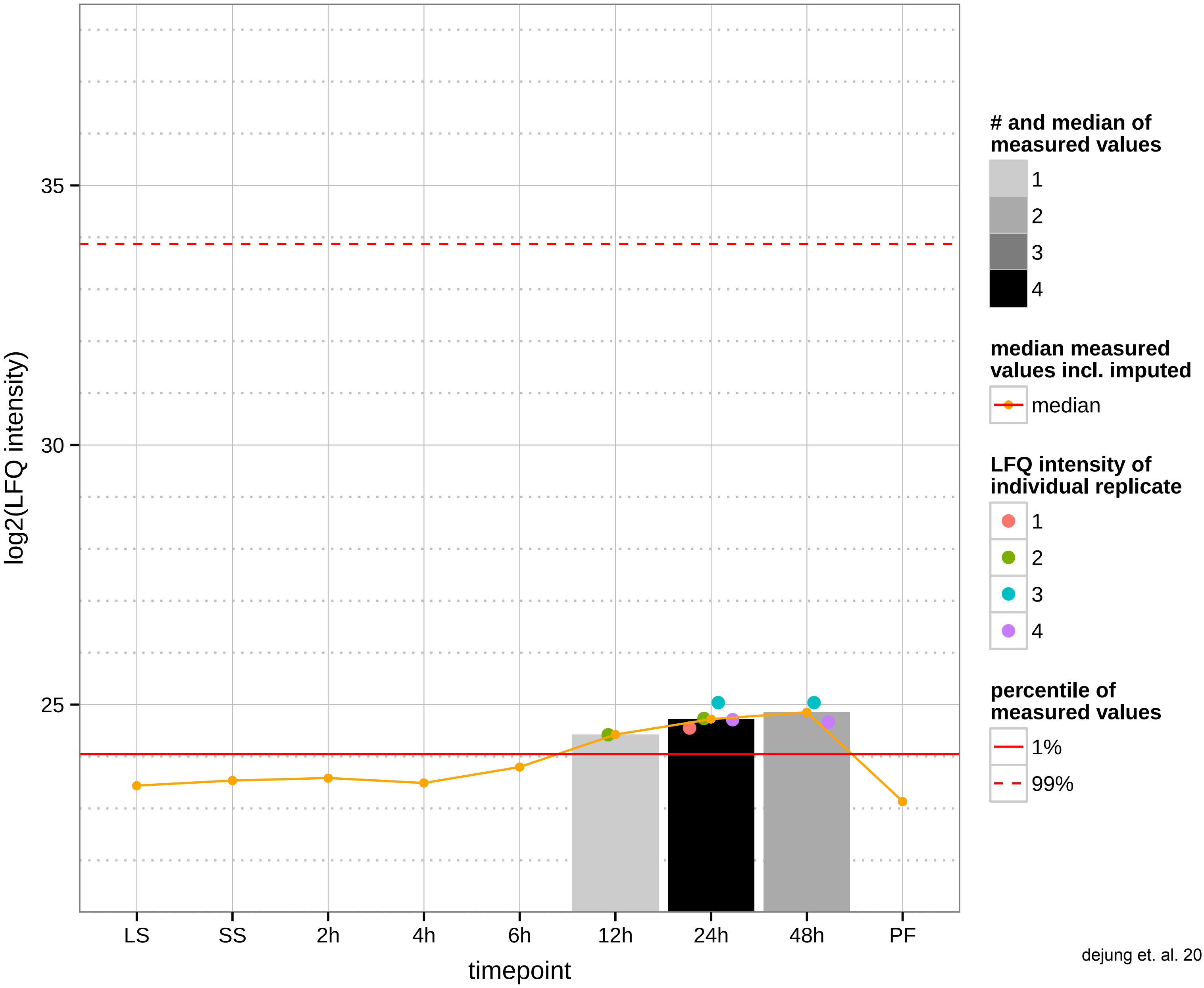
hypothetical protein, conserved
Tb927.11.1550
AGOF: null
AGOC: null
AGOP: null
PGOF: exonuclease activity, nucleic acid binding
PGOC: intracellular
PGOP: null





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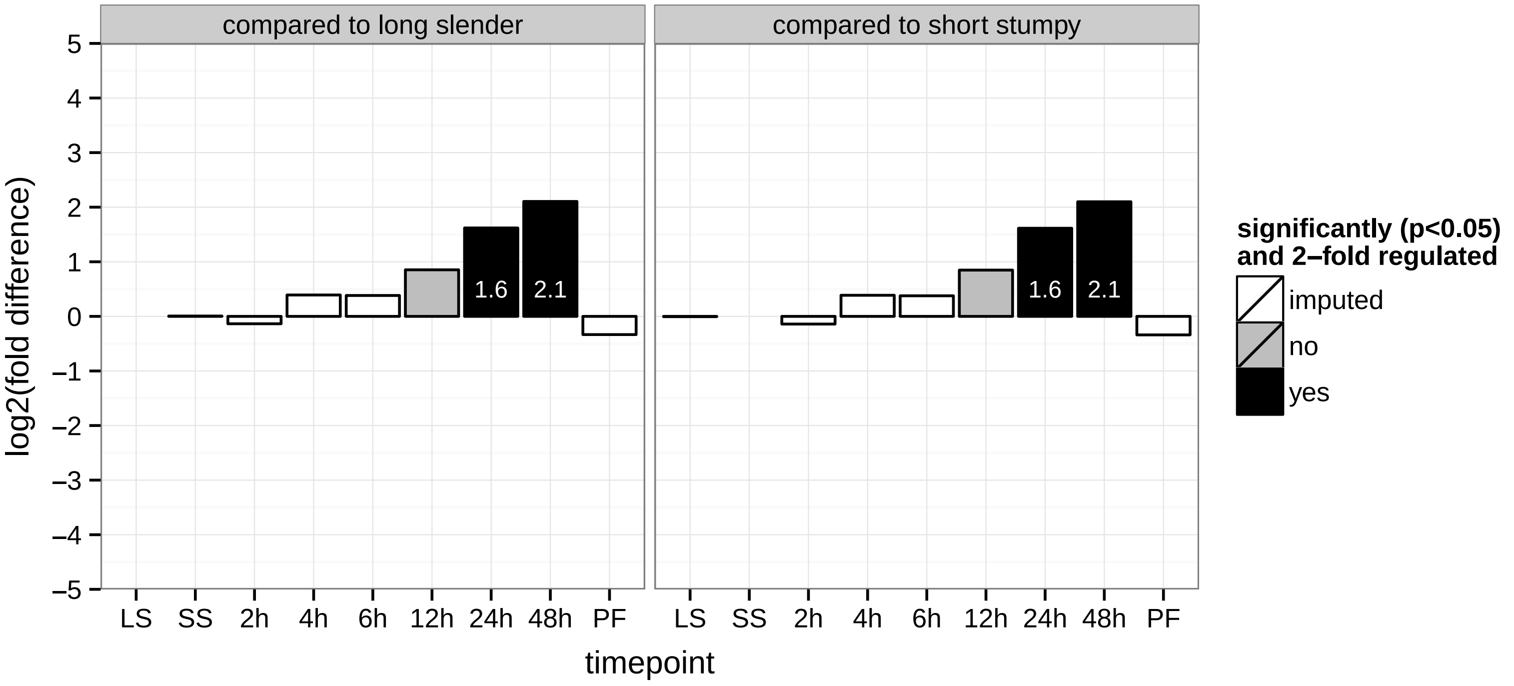
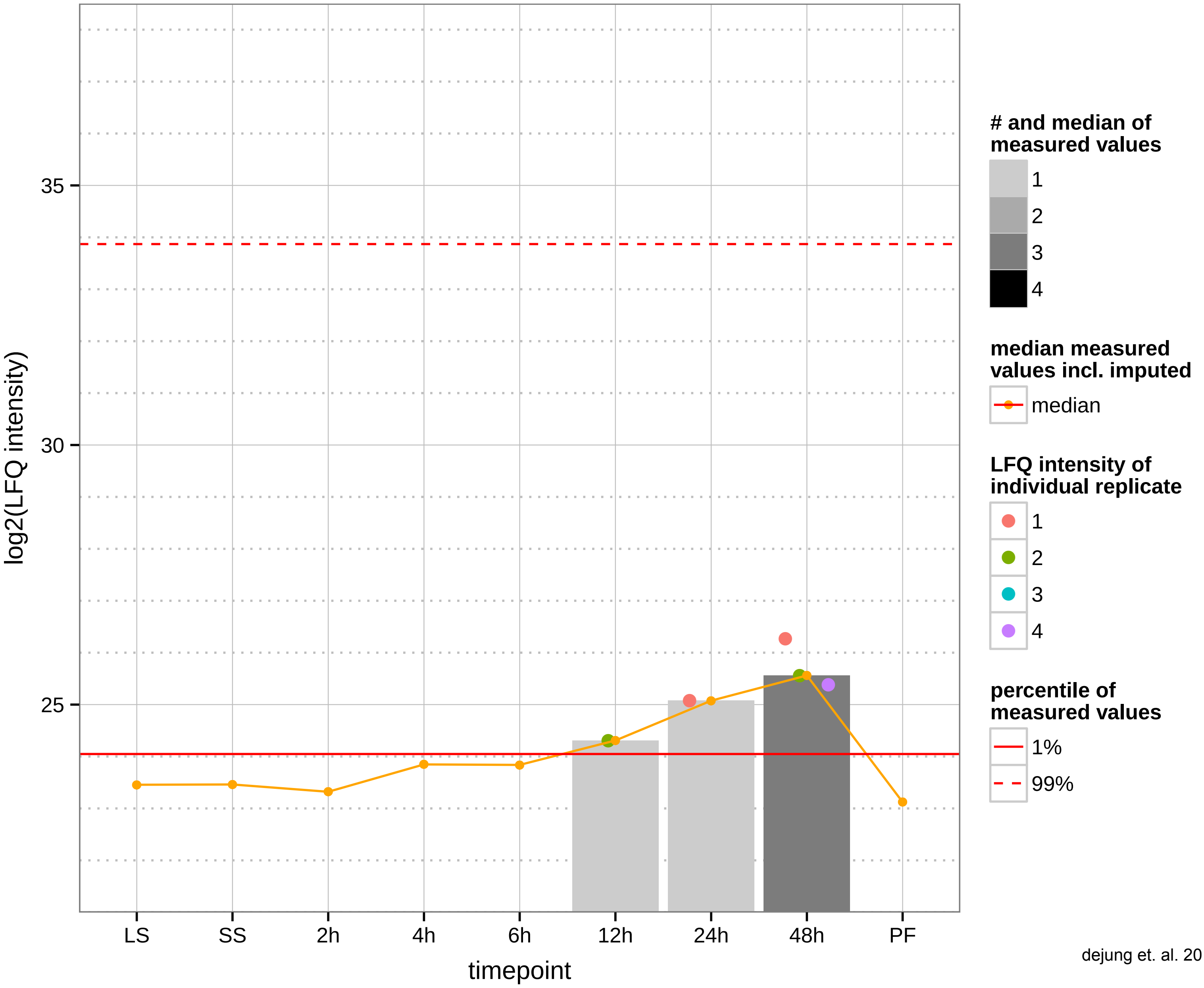
cyclin dependent kinases regulatory subunit, putative (CKS1)
Tb927.11.16390
AGOF: cyclin–dependent protein kinase activity, cyclin–dependent protein kinase regulator activity
AGOC: protein kinase CK2 complex
AGOP: cell cycle
PGOF: cyclin–dependent protein kinase regulator activity
PGOC: null
PGOP: cell cycle





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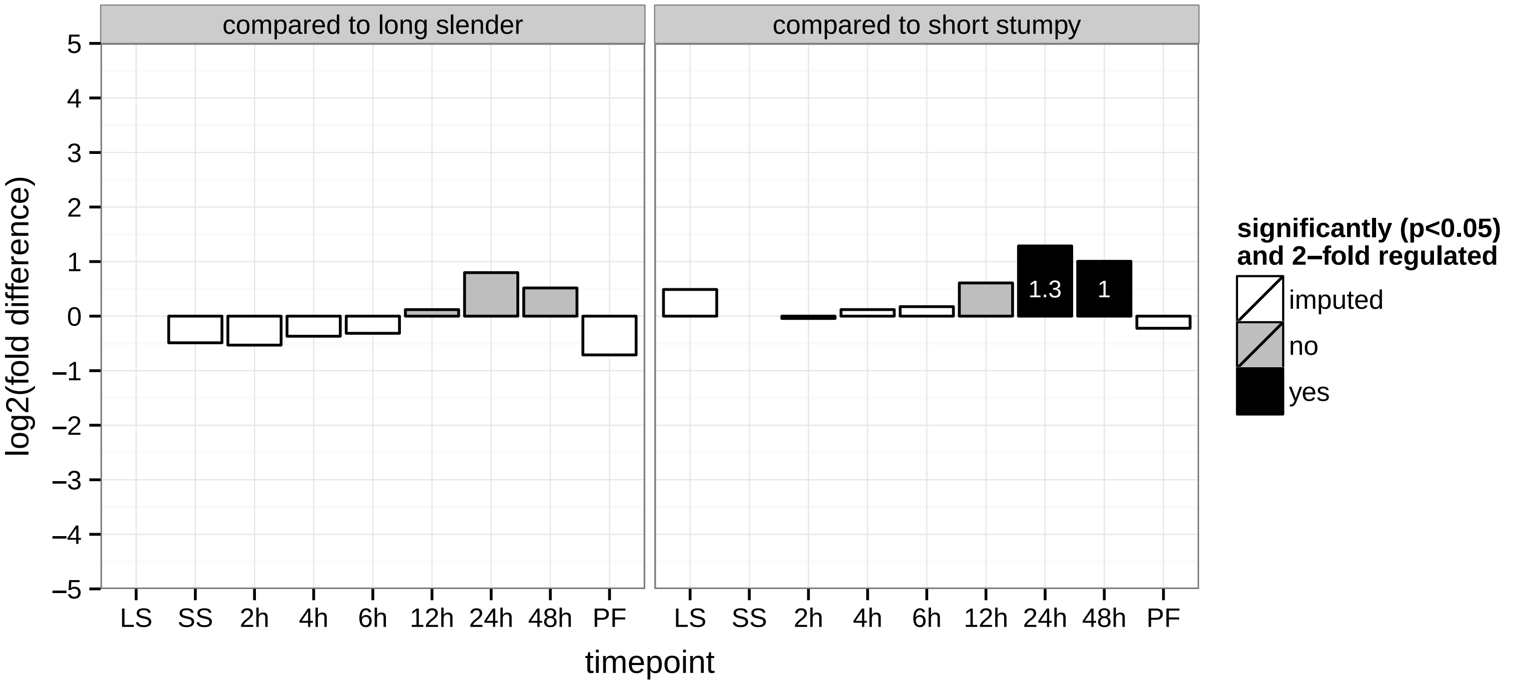
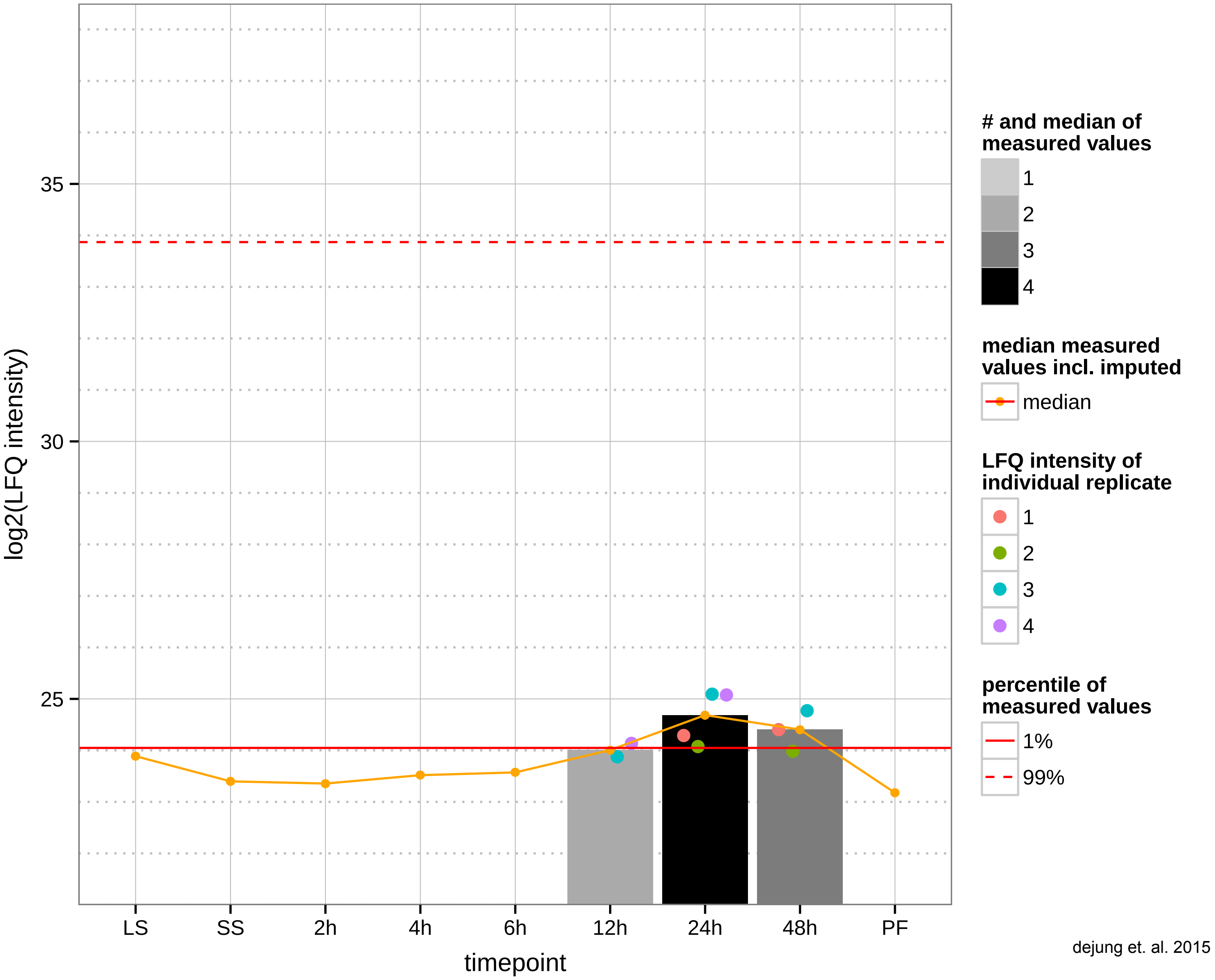
hypothetical protein, conserved
Tb927.11.480
AGOF: GTP binding, RNA binding
AGOC: intracellular, mitochondrion
AGOP: null
PGOF: GTP binding
PGOC: null
PGOP: null





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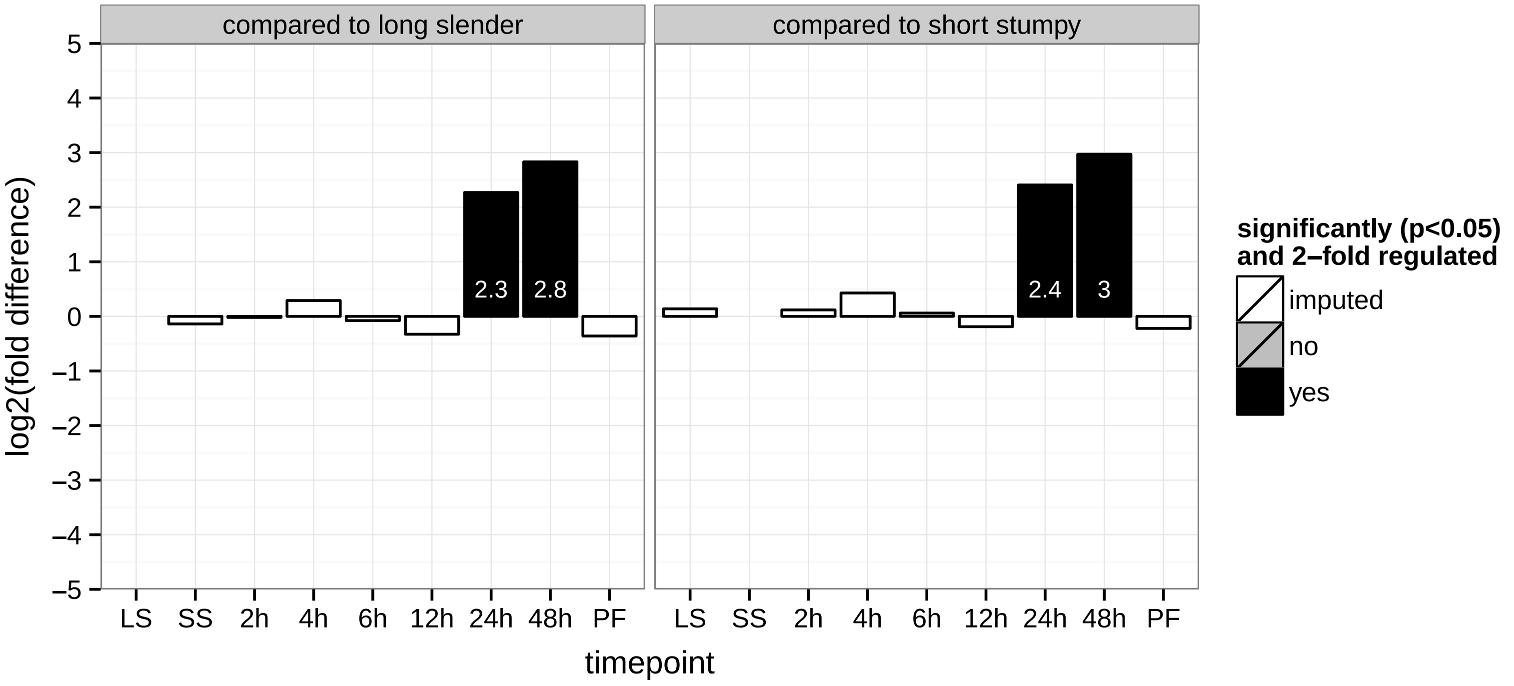
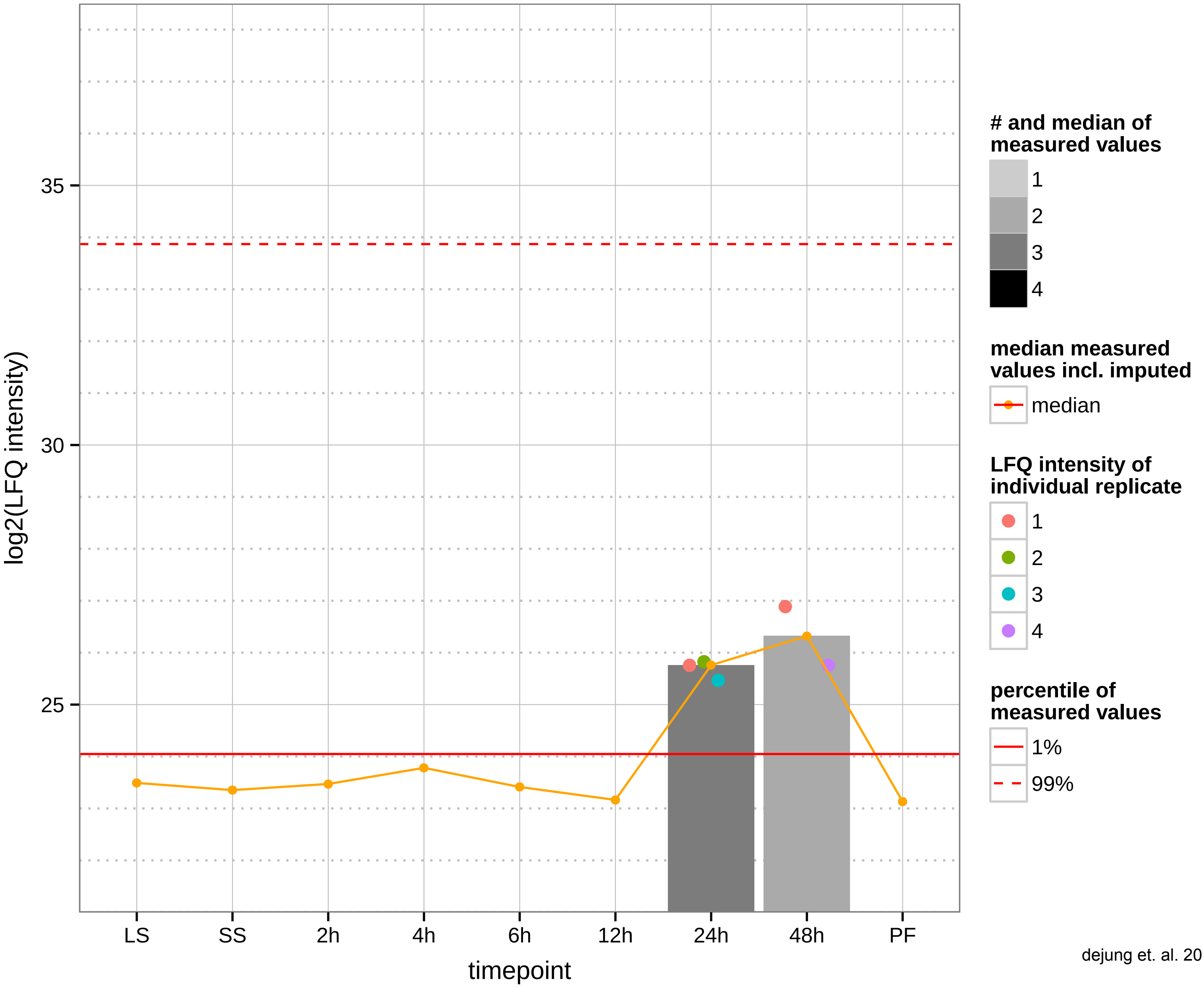
hypothetical protein, conserved
Tb927.11.4840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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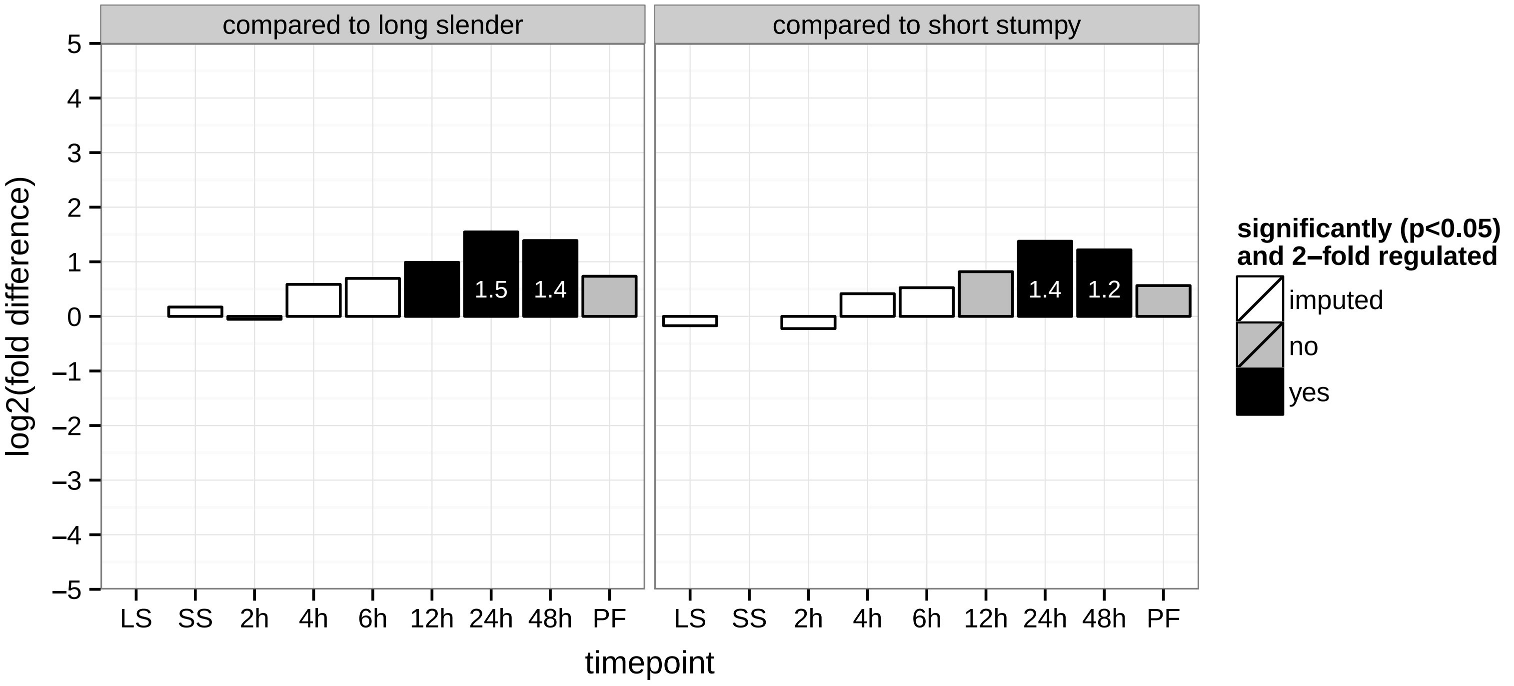
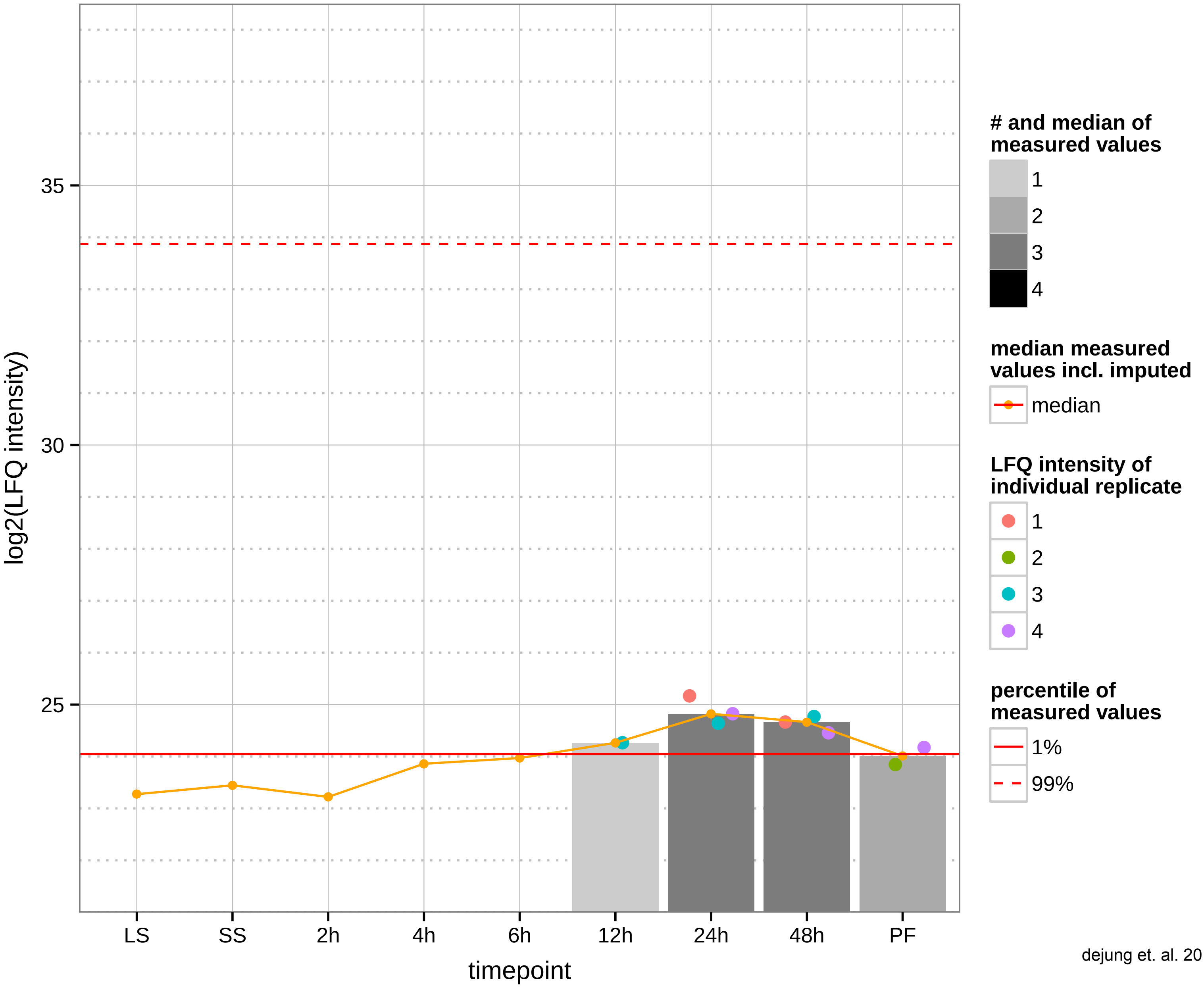
hypothetical protein, conserved
Tb927.11.7340
AGOF: null
AGOC: null
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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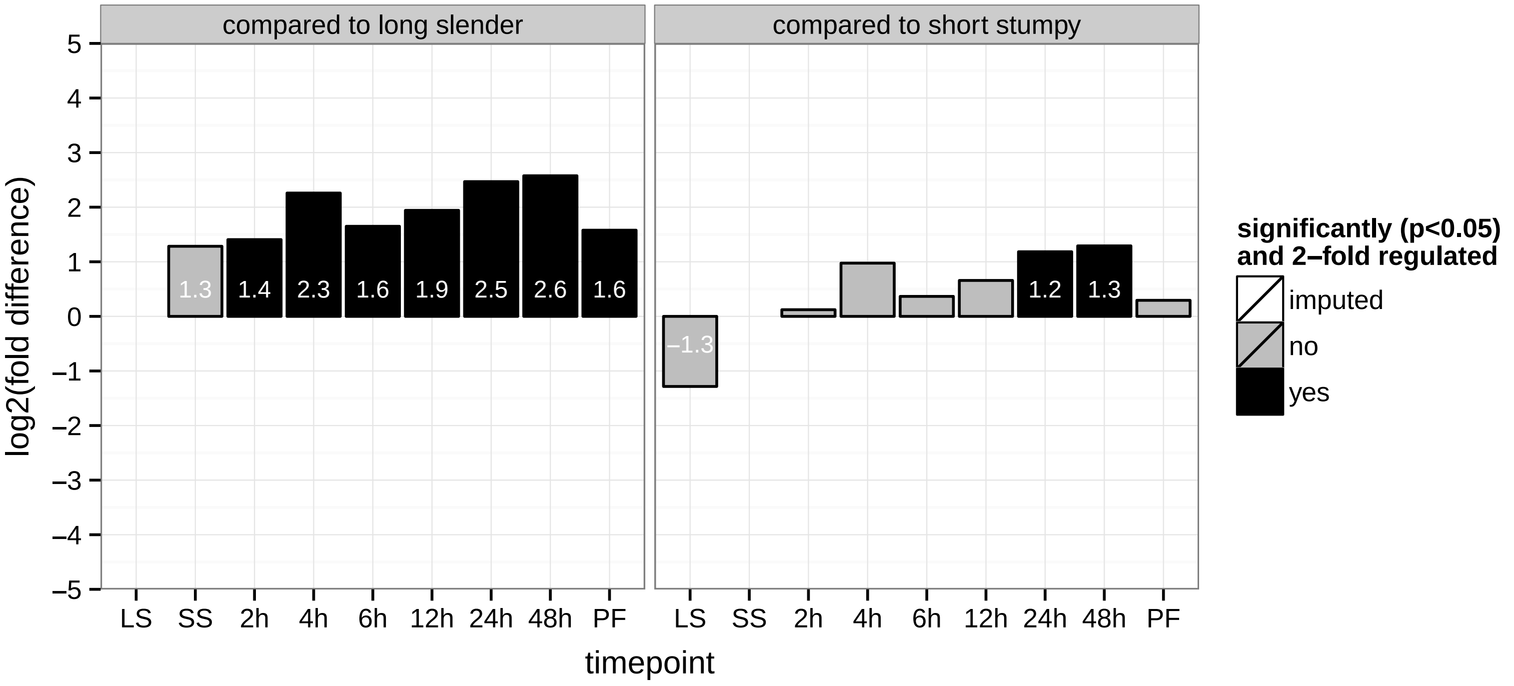
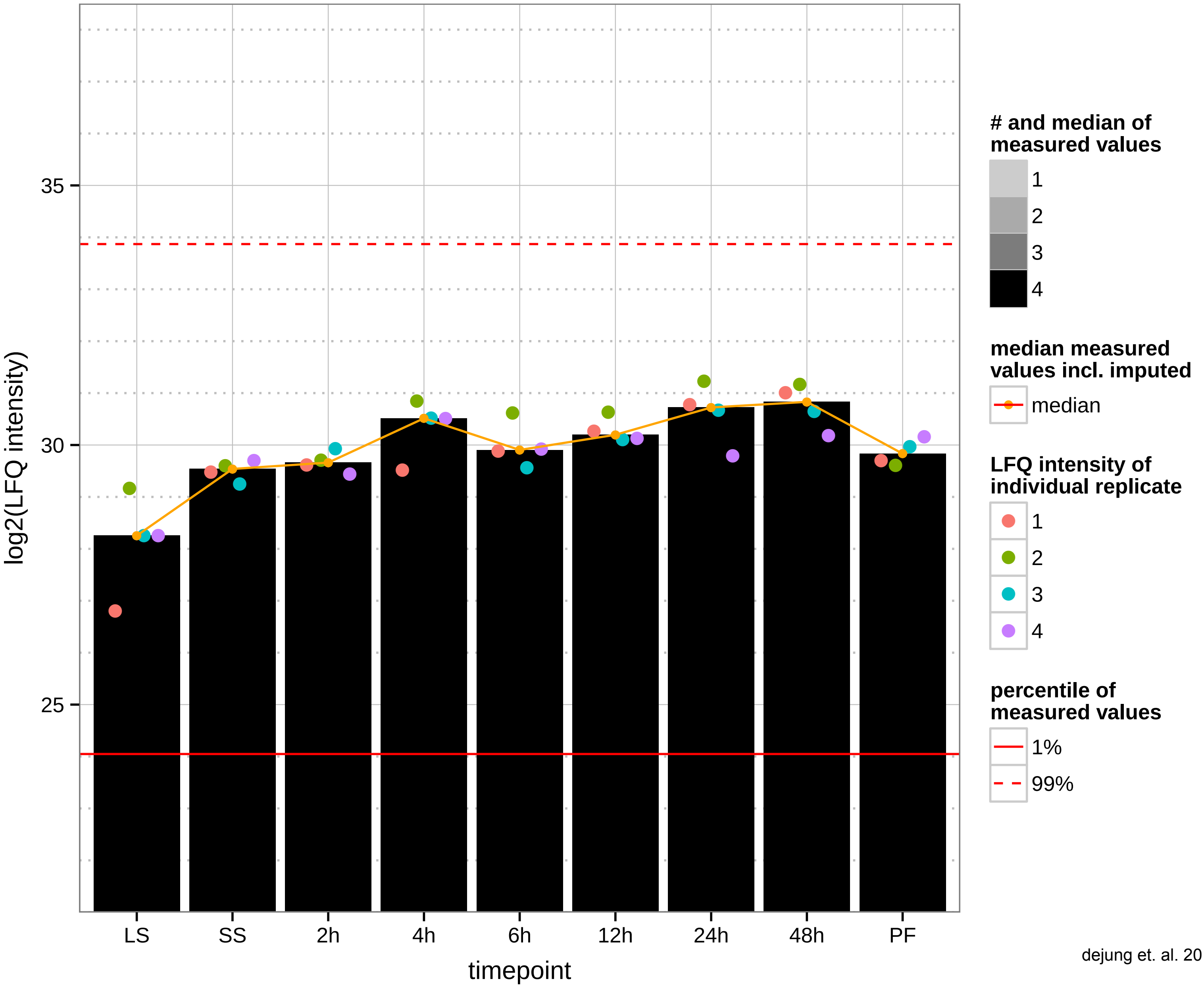
mitochondrial RNA binding protein 16 (RBP16)
Tb927.11.7900
AGOF: DNA binding, RNA binding
AGOC: mitochondrion
AGOP: RNA modification, regulation of transcription, DNA–dependent
PGOF: DNA binding, nucleic acid binding
PGOC: null
PGOP: regulation of transcription, DNA–dependent





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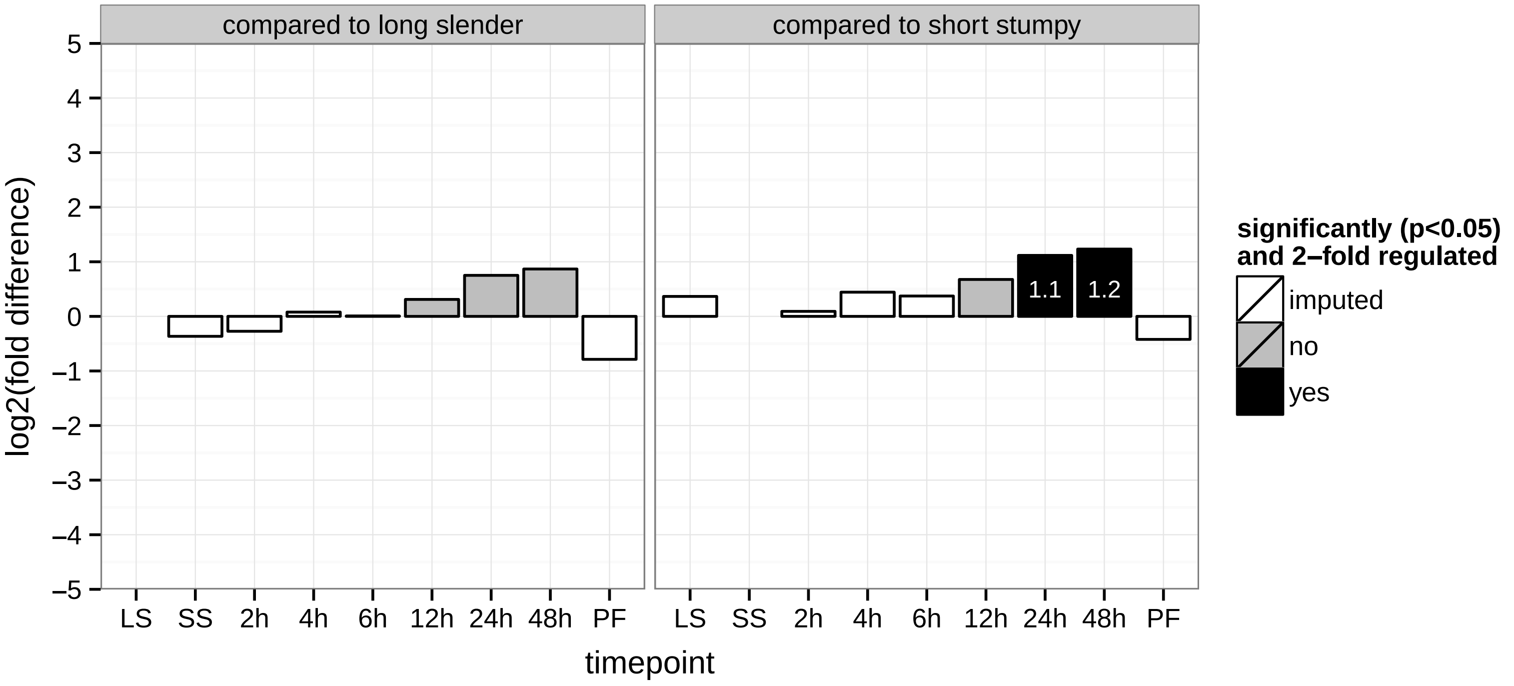
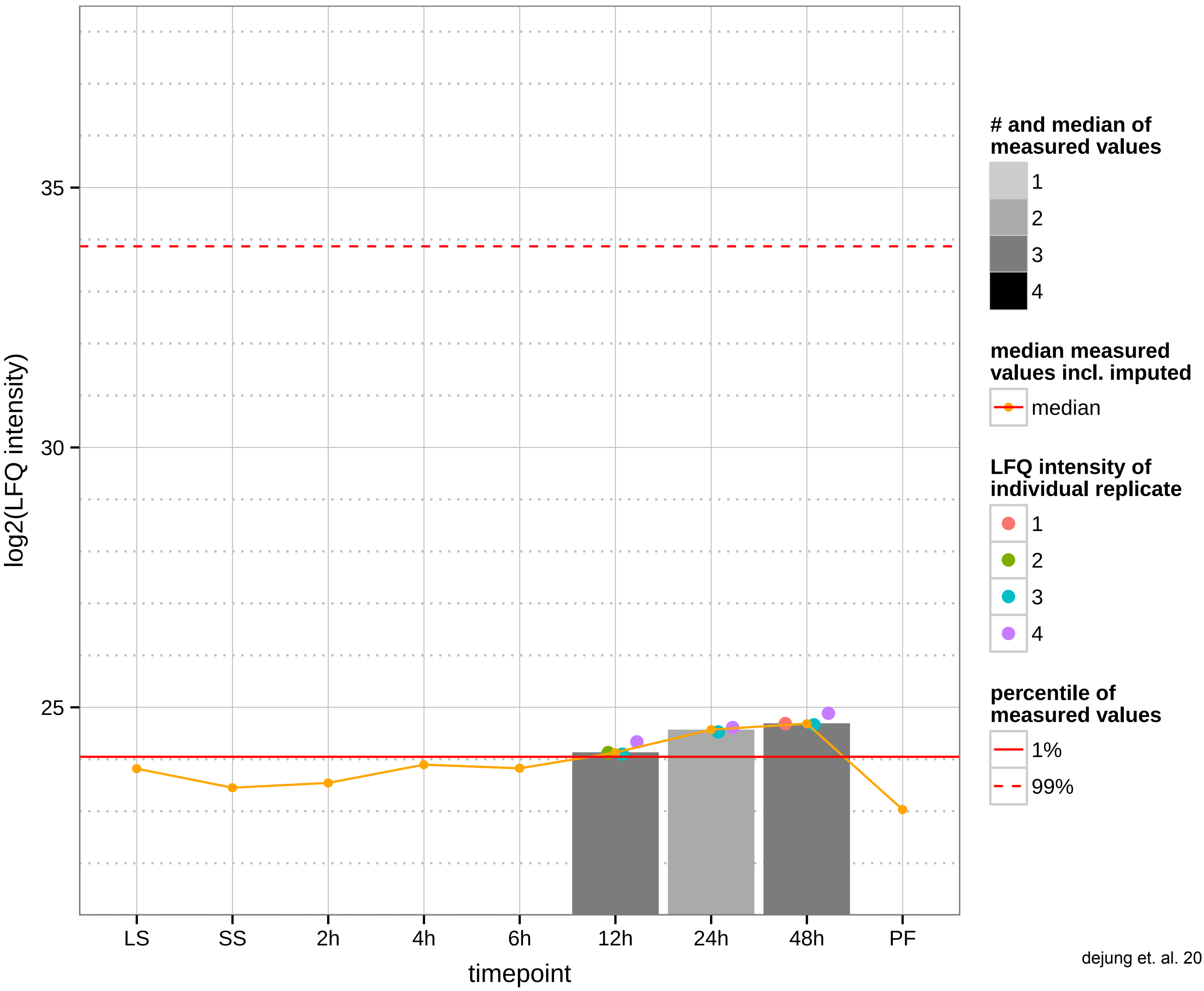
palmitoyl acyltransferase 4, putative
Tb927.11.9070
AGOF: transferase activity, transferring acyl groups, zinc ion binding
AGOC: integral to membrane
AGOP: endocytosis, protein palmitoylation, transport
PGOF: zinc ion binding
PGOC: null
PGOP: null





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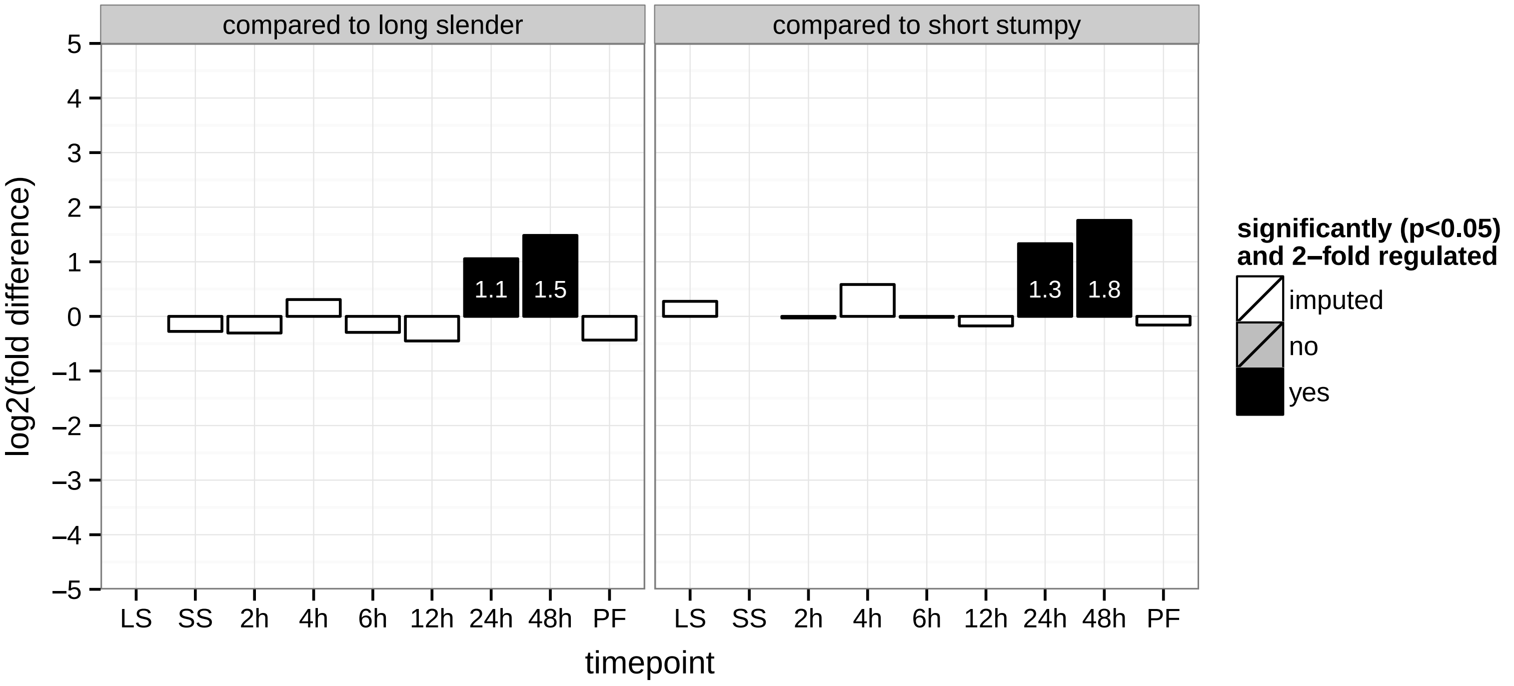
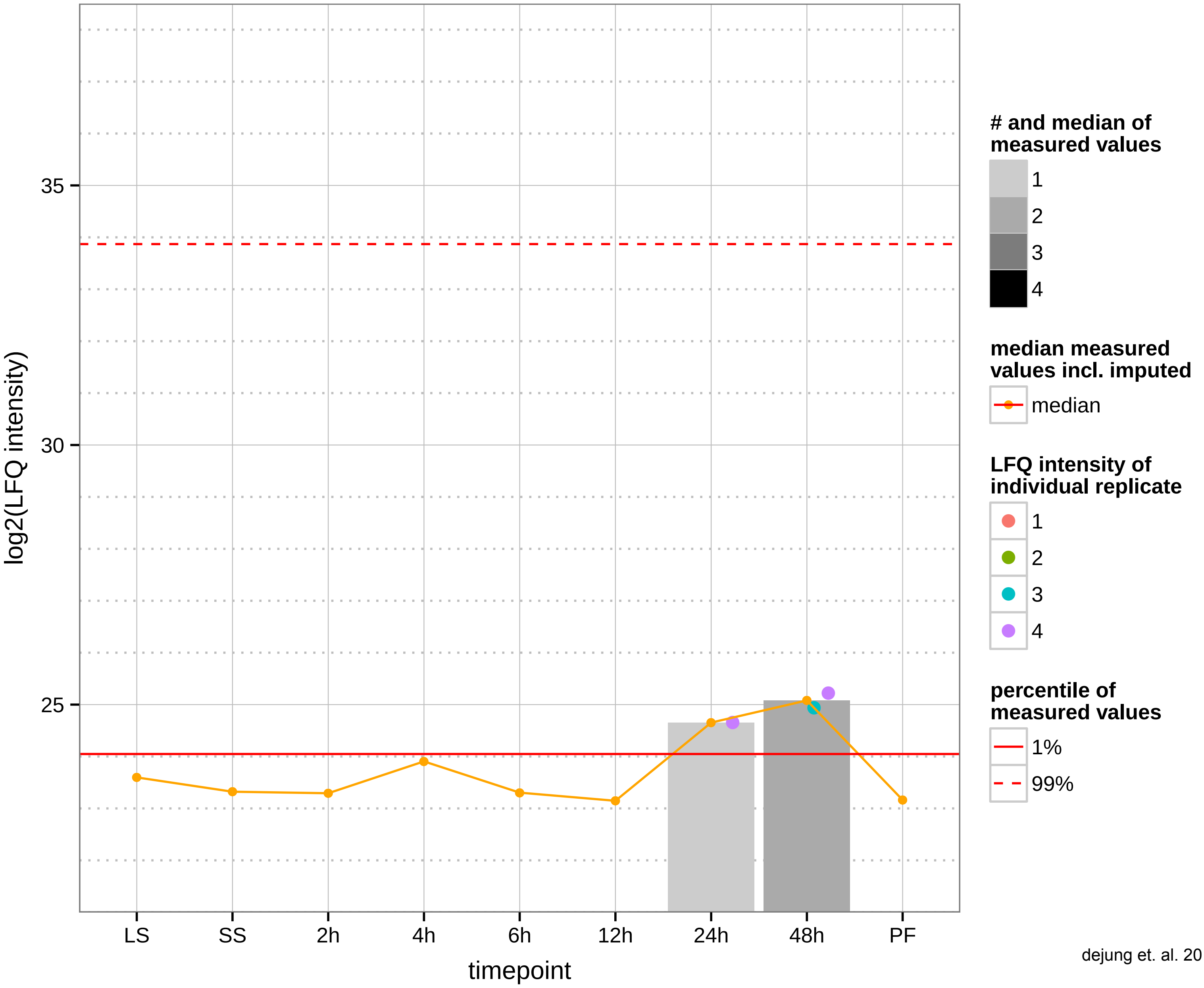
hypothetical protein, conserved
Tb927.11.910
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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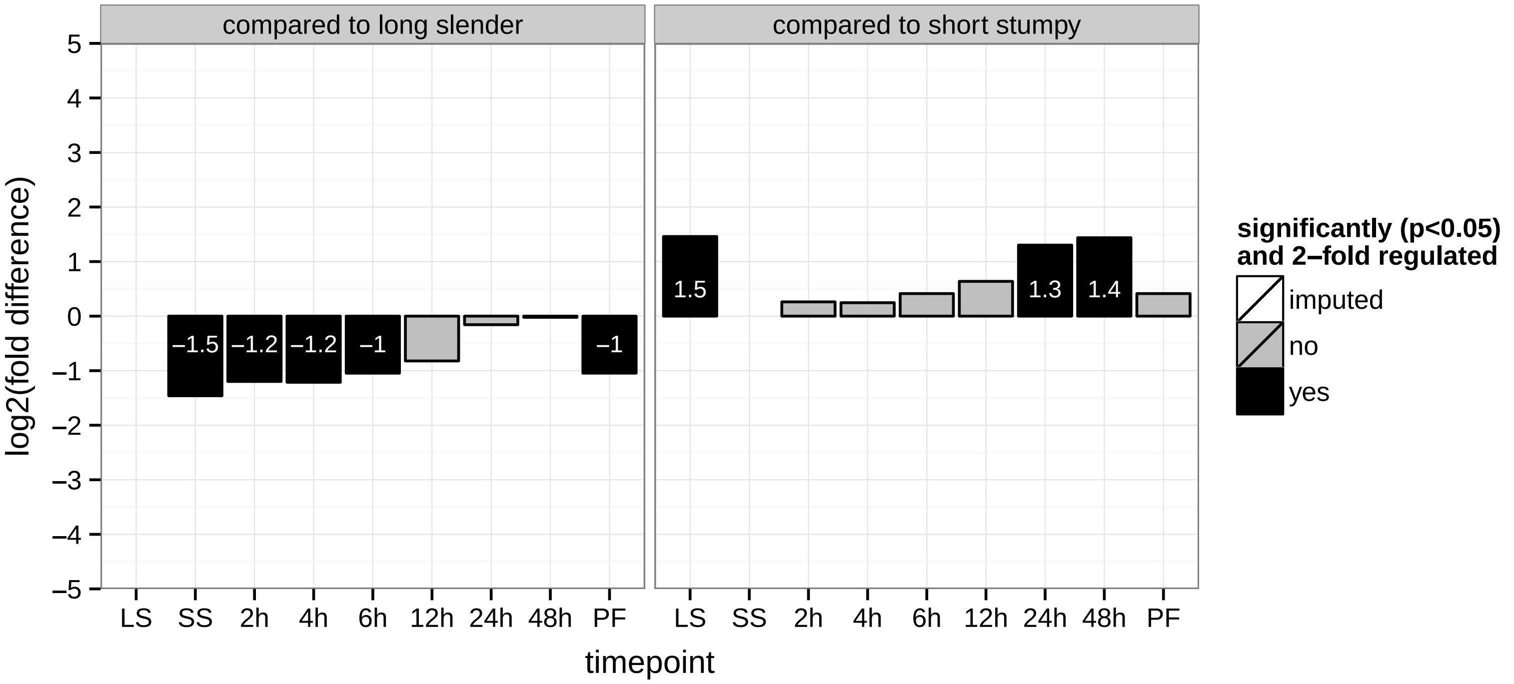
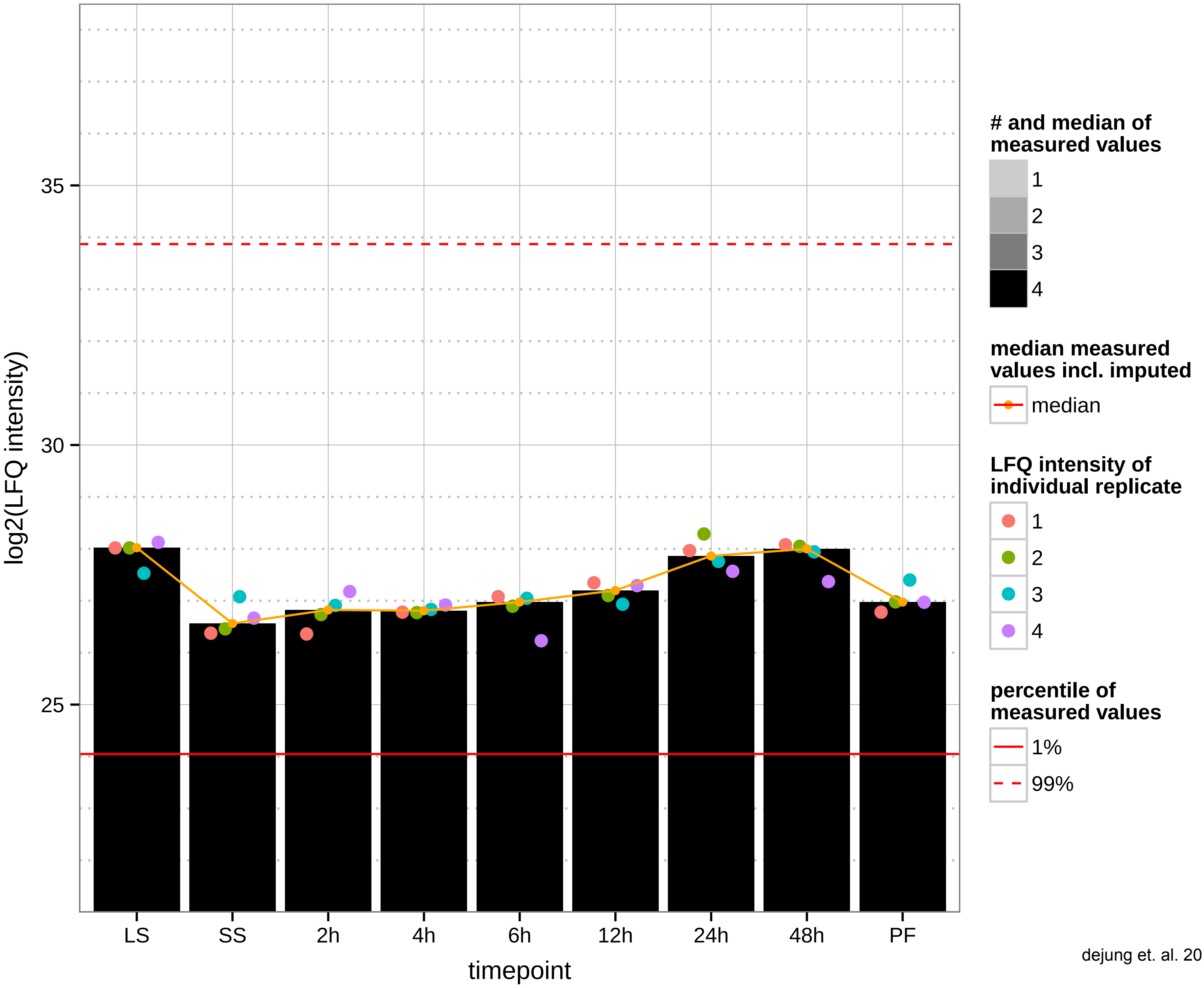
small GTP–binding protein RAB6, putative
Tb927.2.2130
AGOF: GTP binding, GTPase activity
AGOC: intracellular, plasma membrane
AGOP: intracellular protein transport, mitosis, nucleocytoplasmic transport, small GTPase mediated signal transduction, synap
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti





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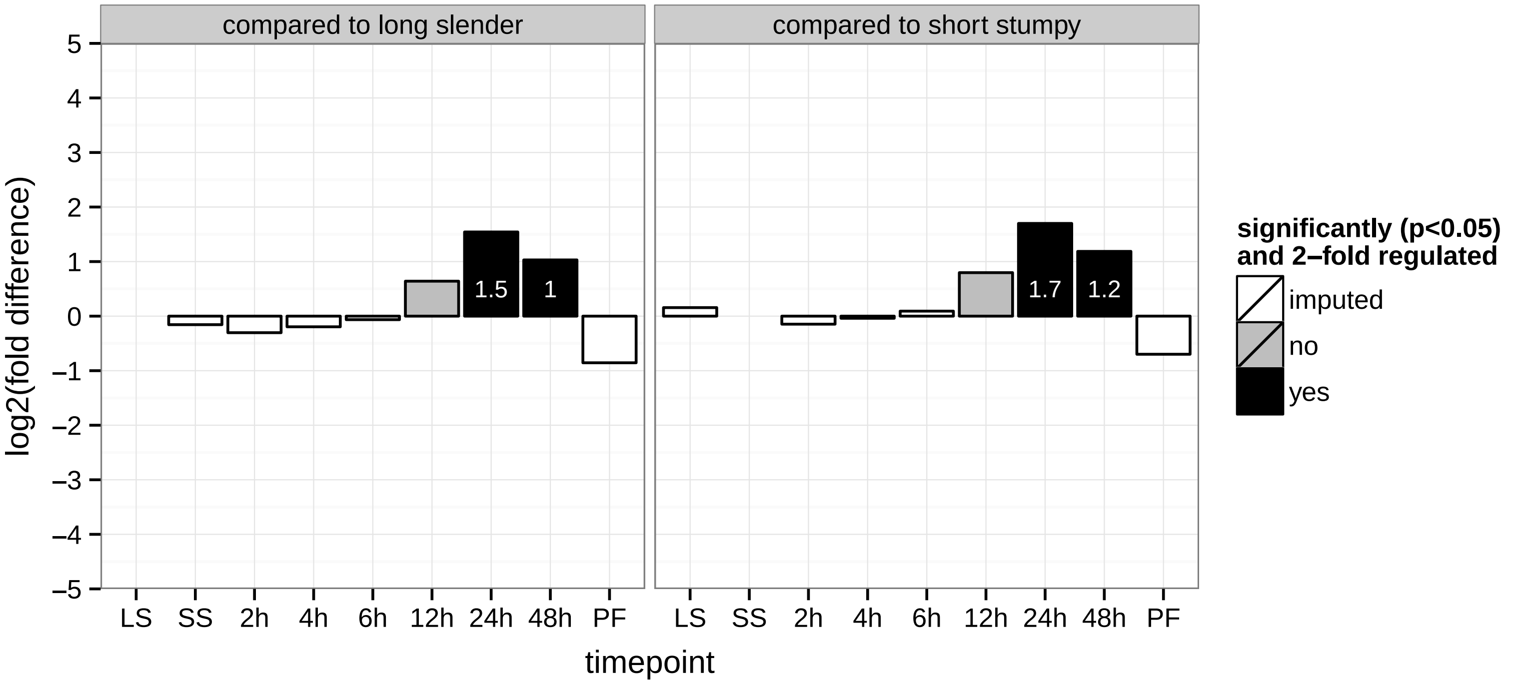
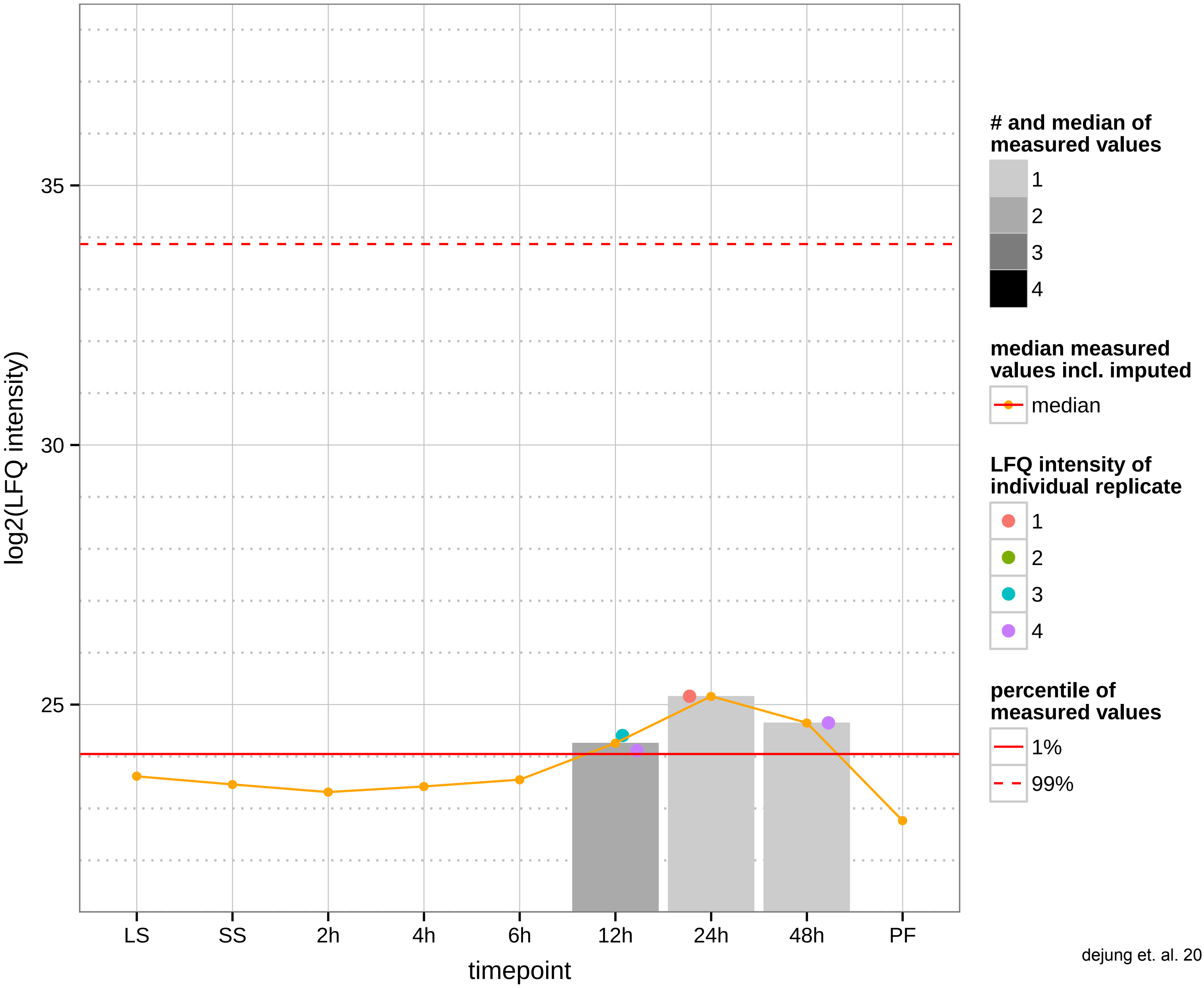
cdc2–related kinase, putative (CRK9)
Tb927.2.4510
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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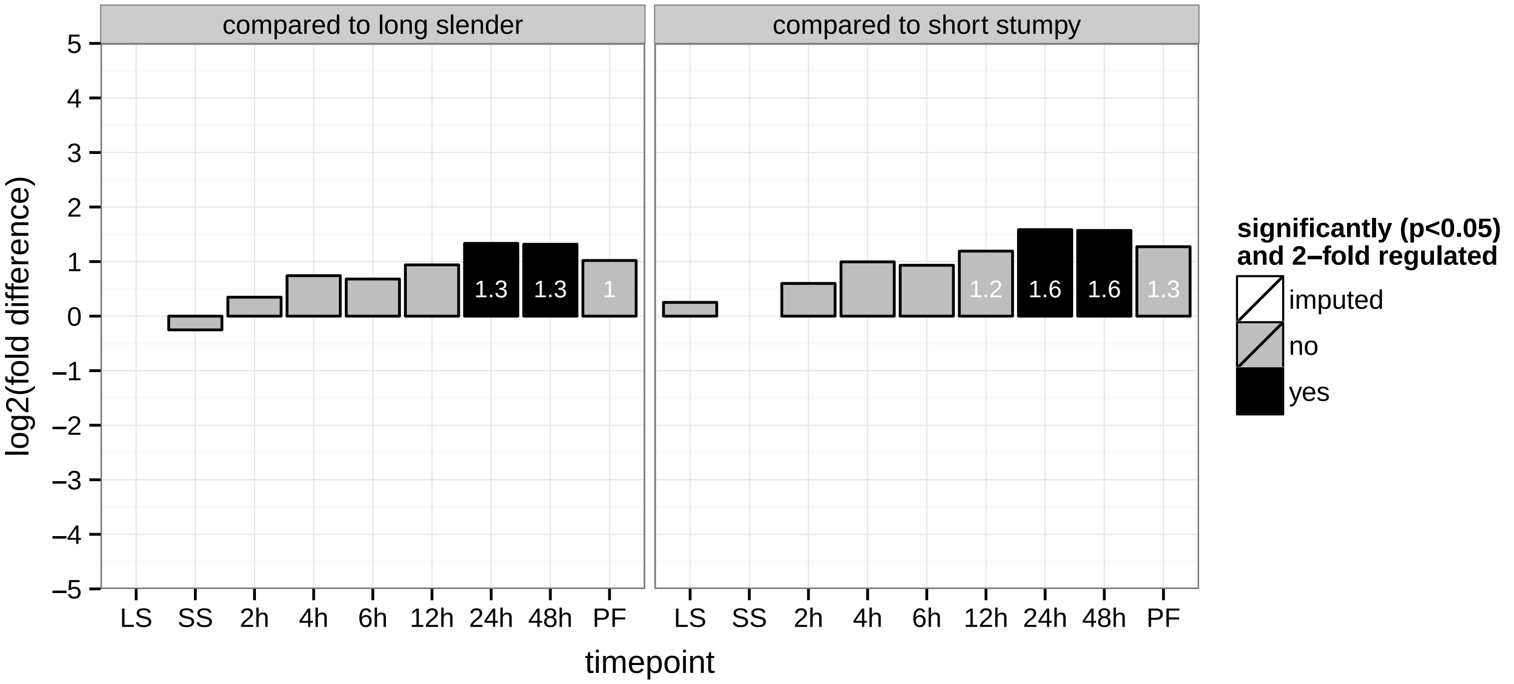
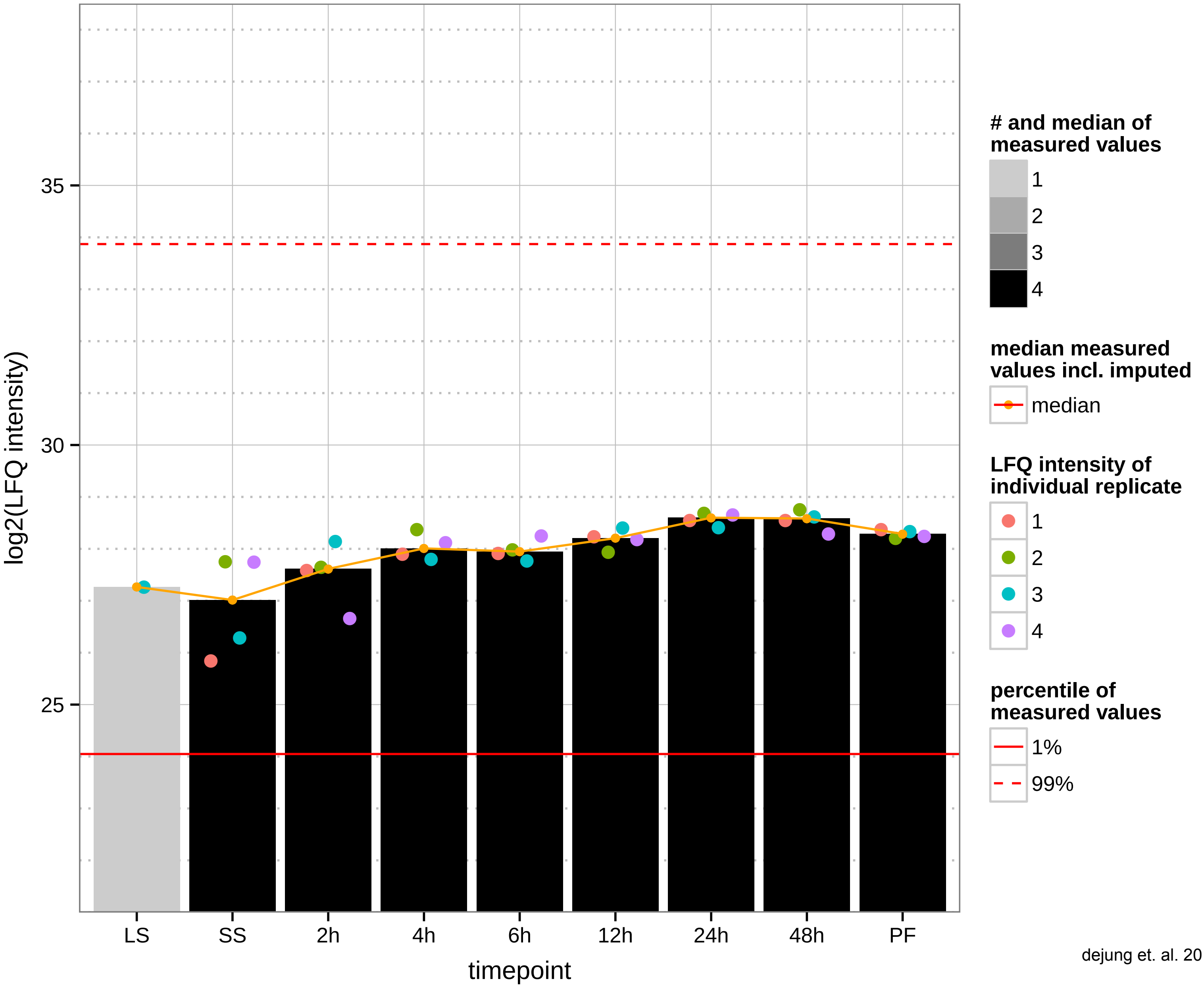
hypothetical protein, conserved
Tb927.3.3030
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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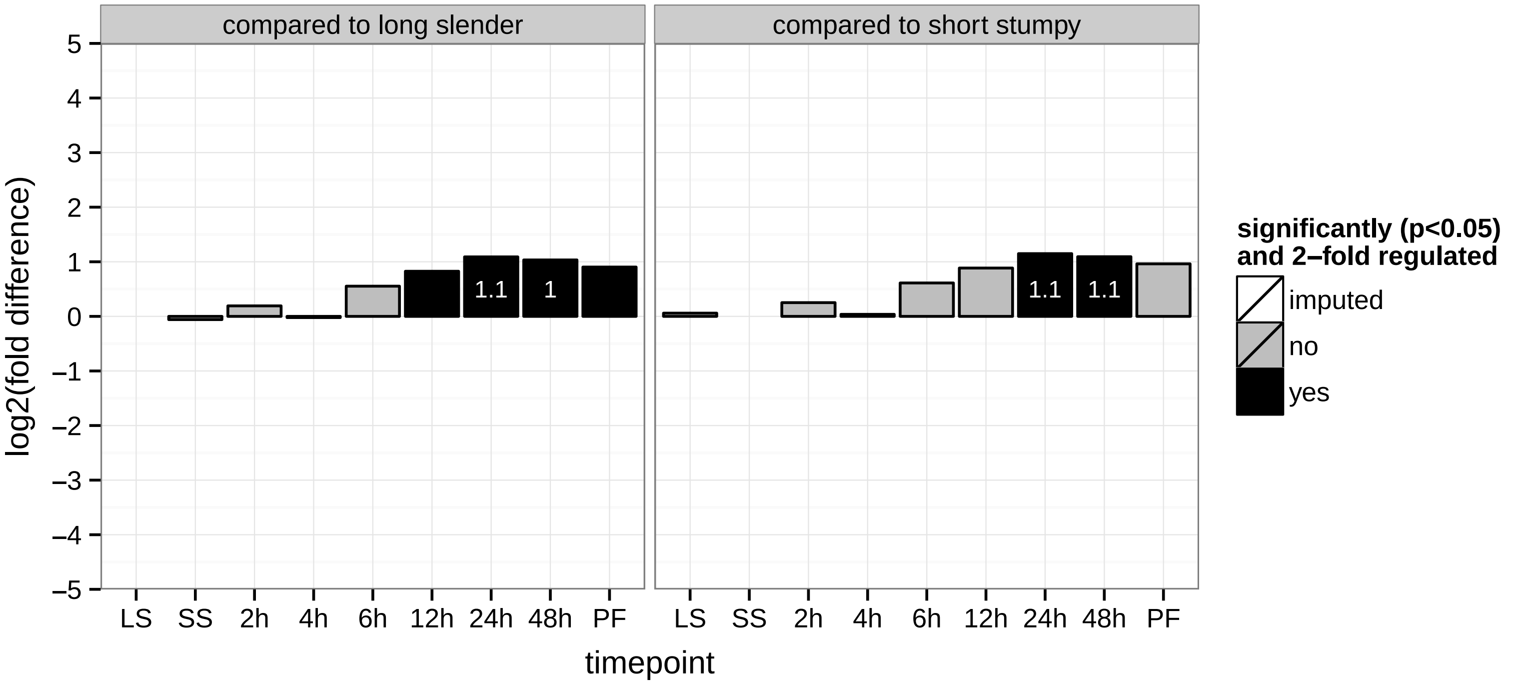
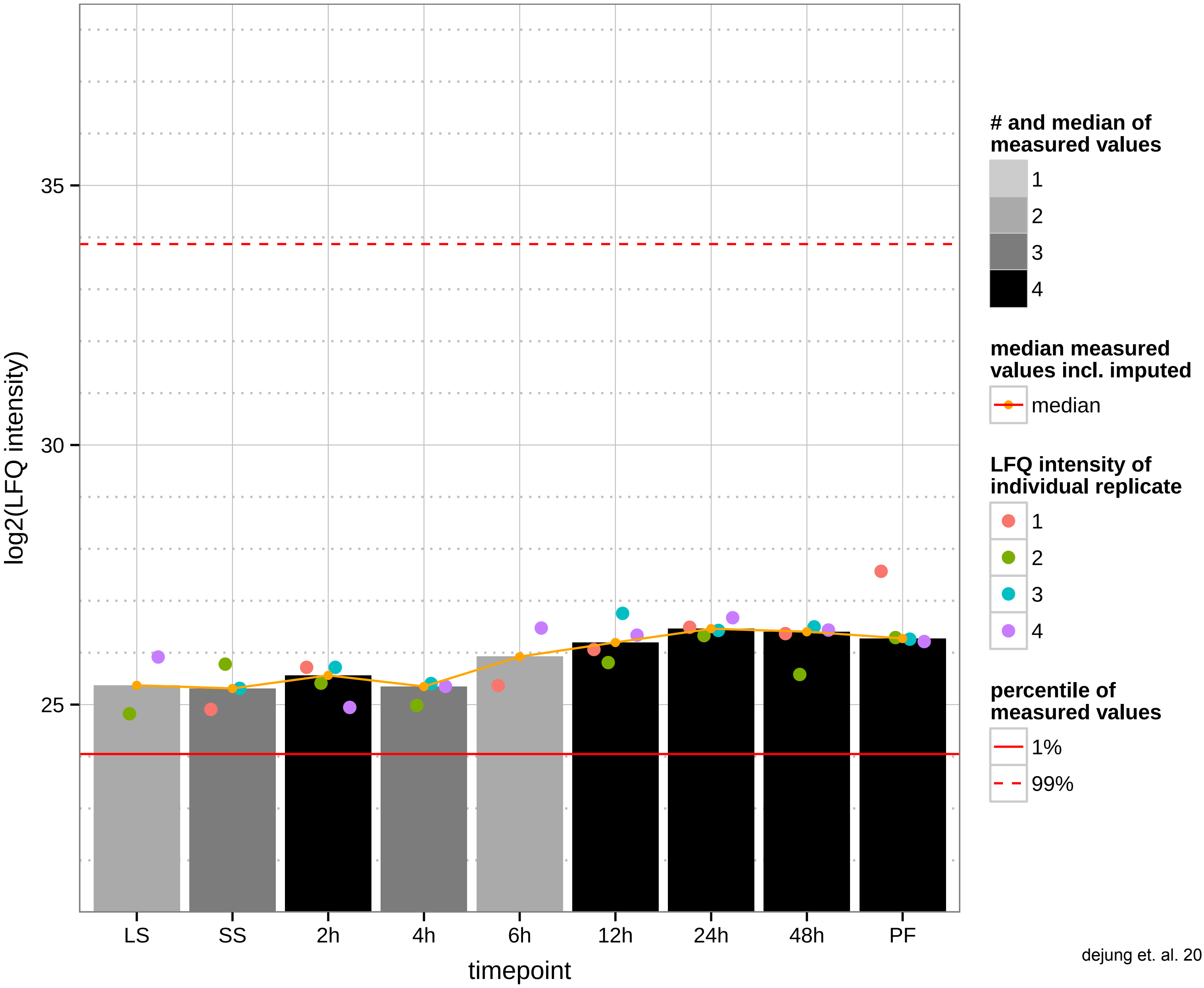
Cell growth–regulating nucleolar protein, putative
Tb927.3.3970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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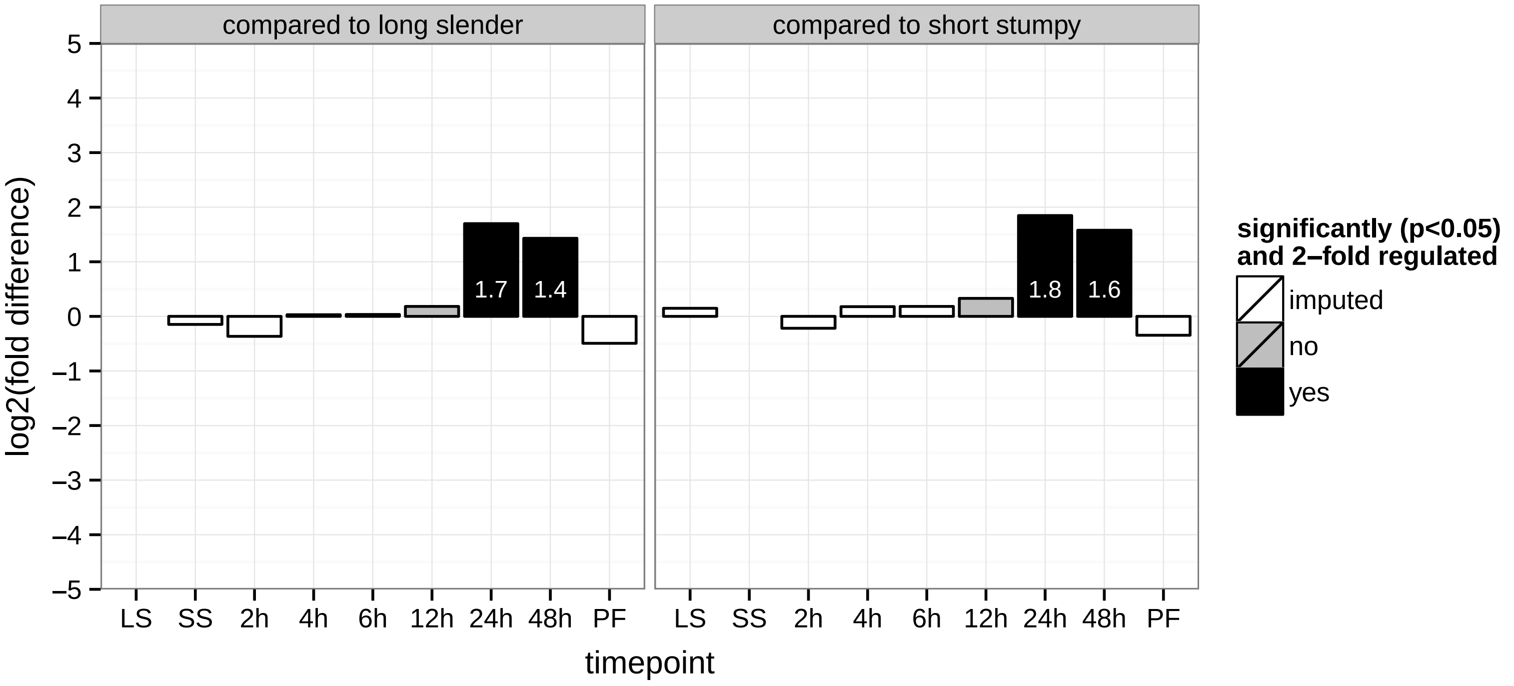
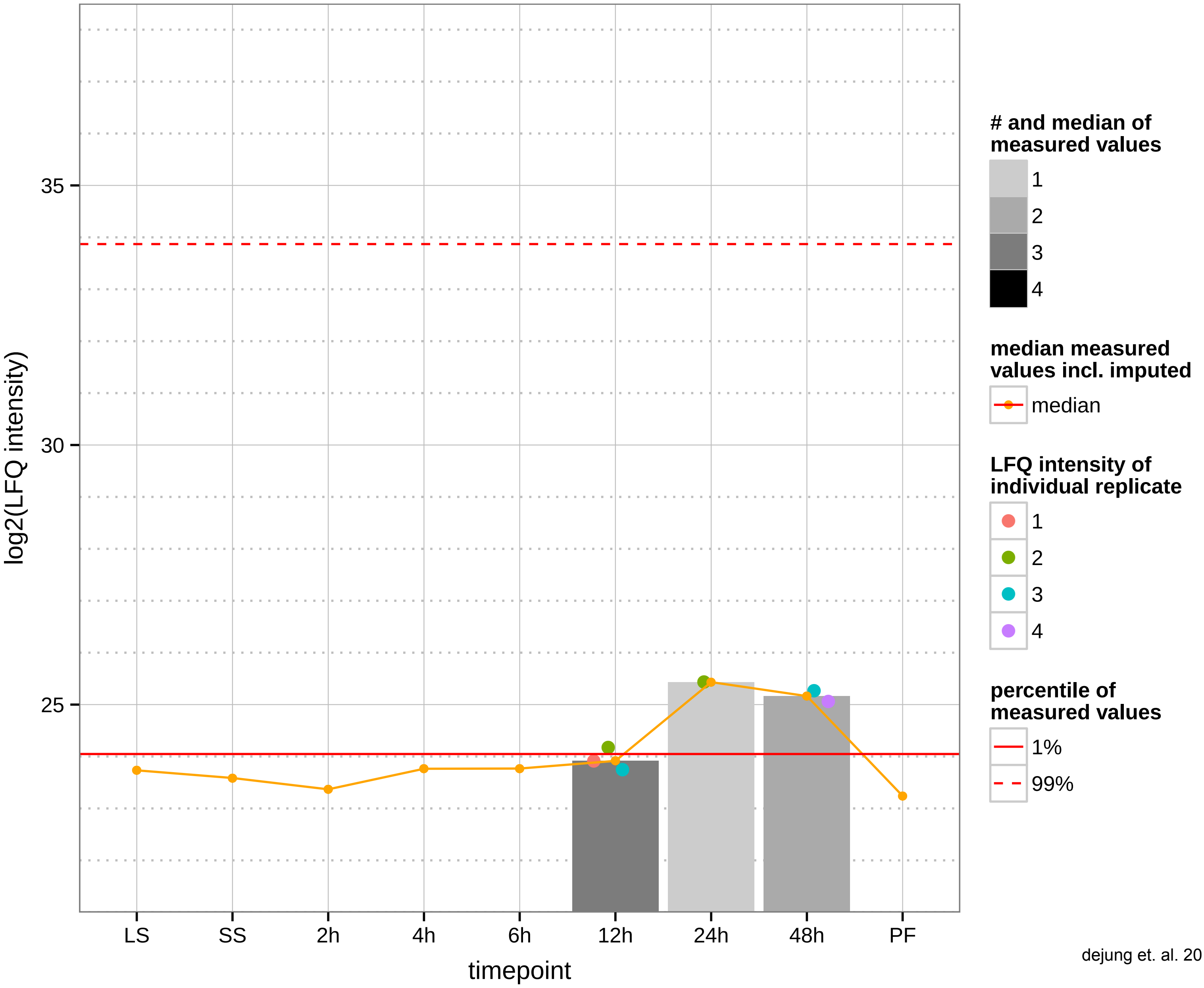
hypothetical protein, conserved
Tb927.3.4250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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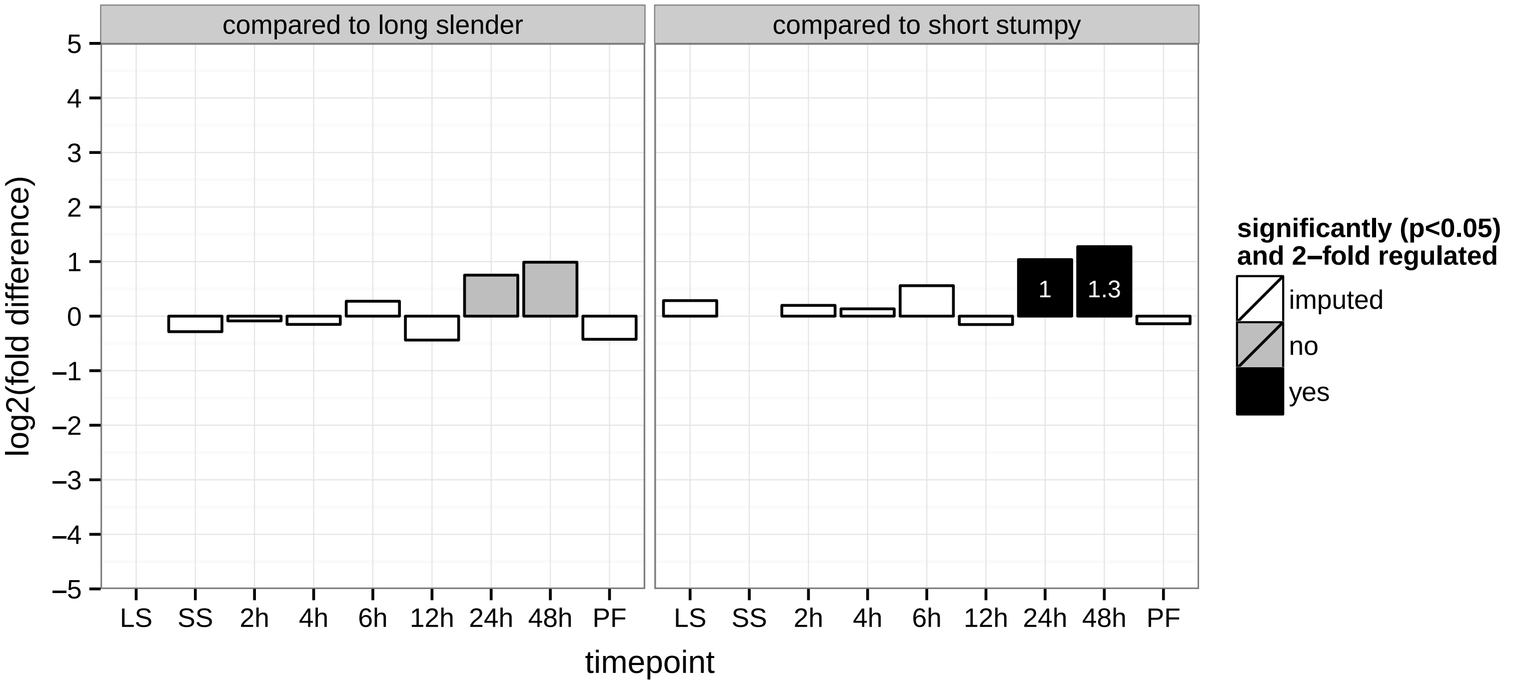
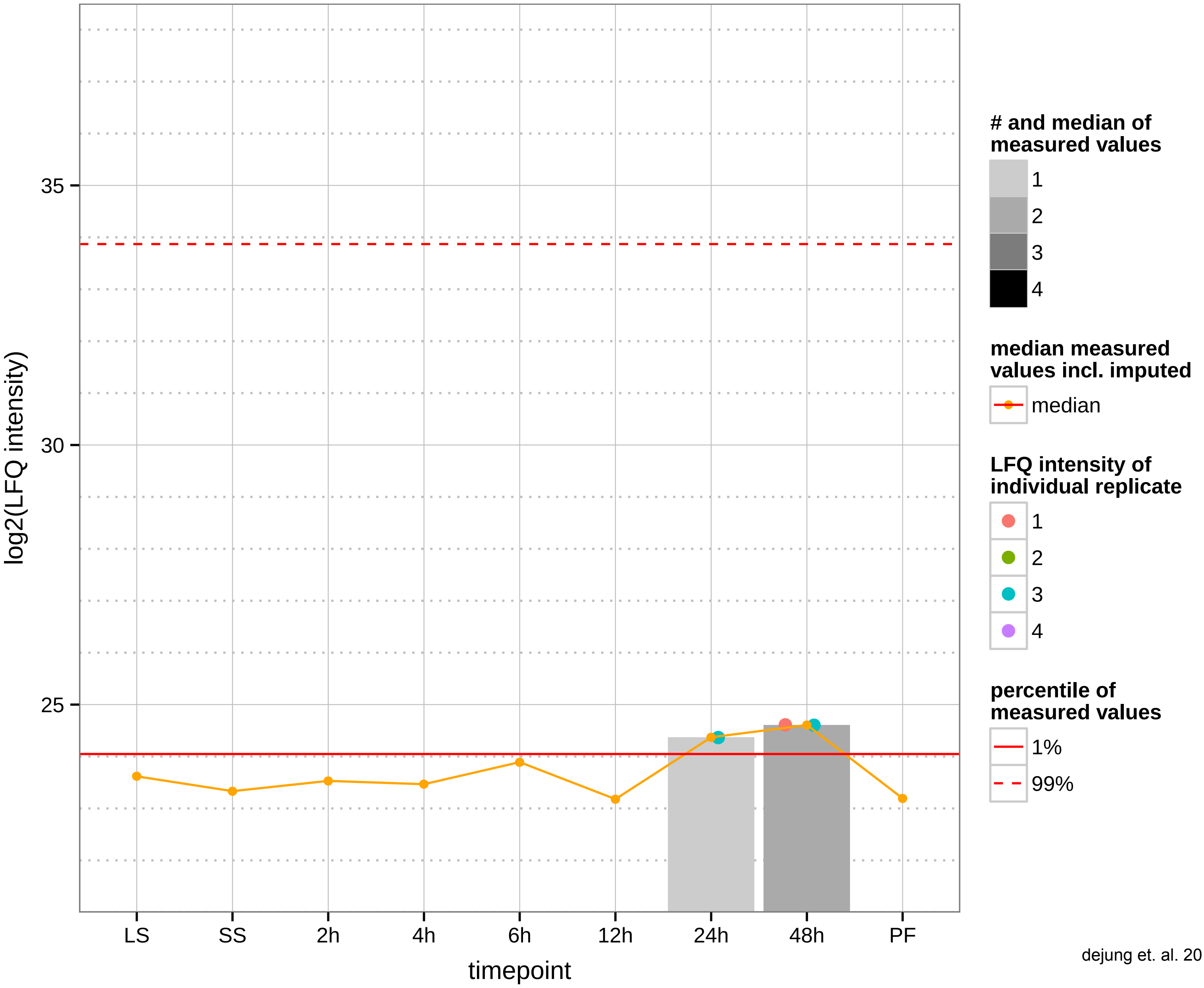
hypothetical protein, conserved
Tb927.3.4780;Tb927.3.4740
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: NAD binding, oxidoreductase activity, acting on the CH–OH group of donors, NAD or NADP as acceptor
PGOC: cytoplasm
PGOP: glycerol–3–phosphate catabolic process, oxidation–reduction process





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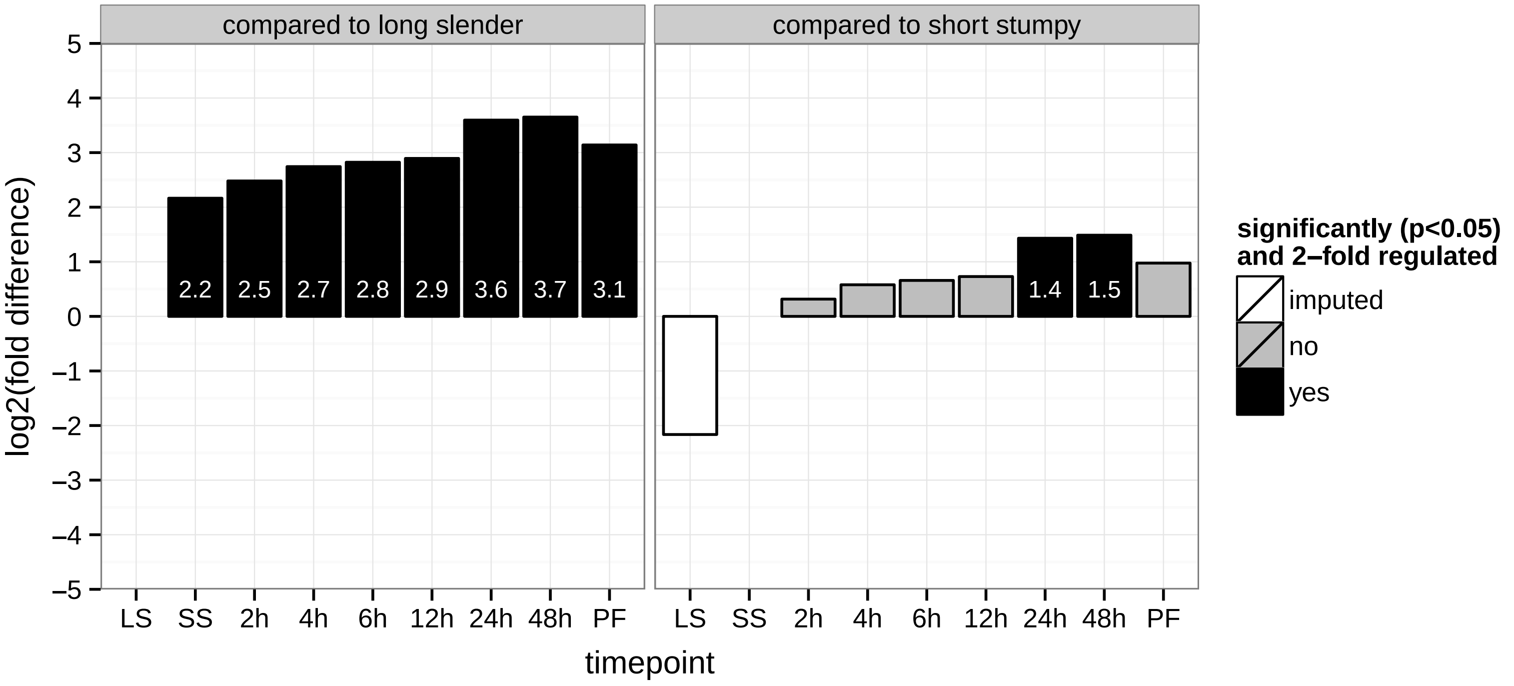
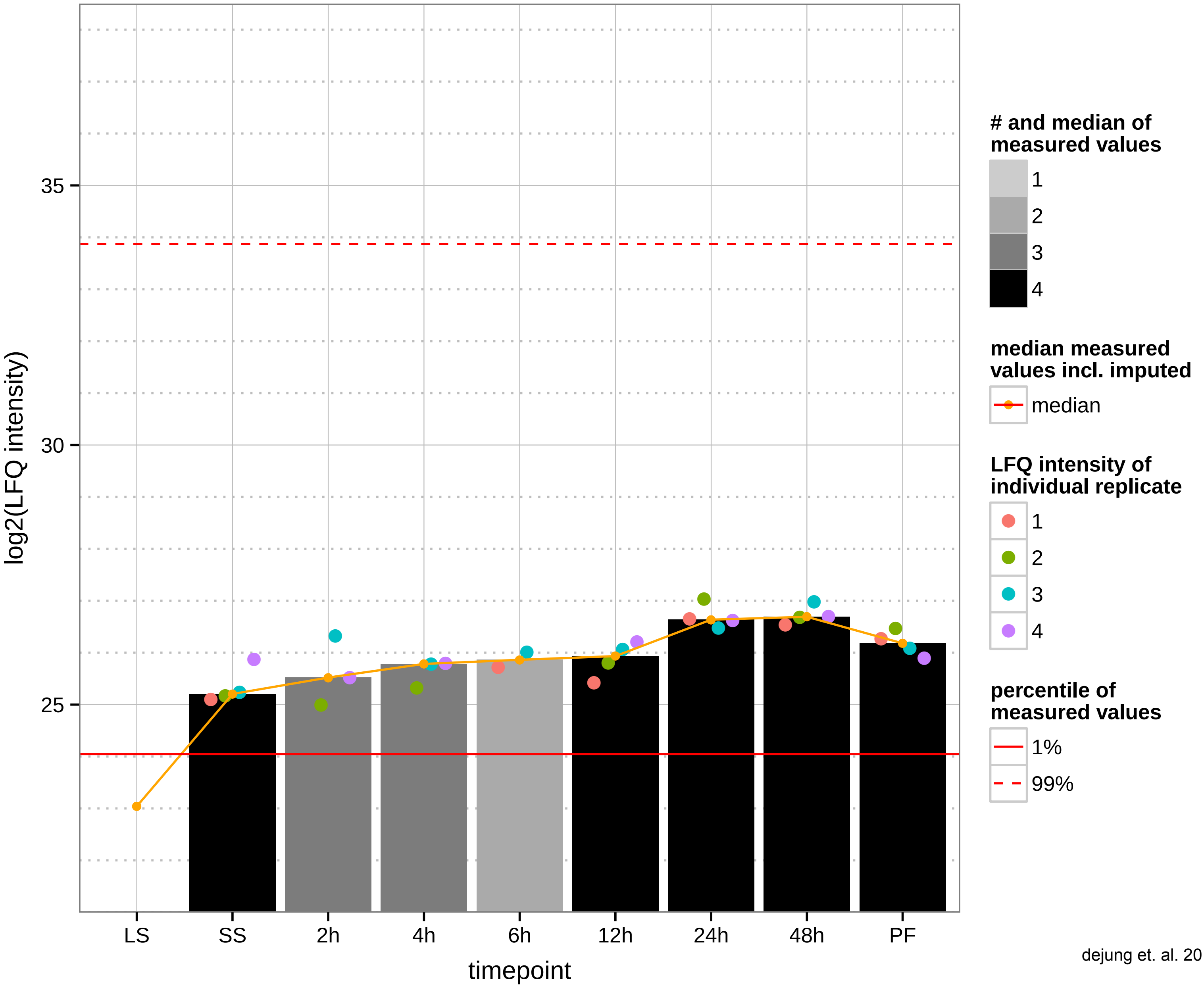
enoyl–CoA hydratase, mitochondrial precursor, putative
Tb927.3.4850
AGOF: catalytic activity
AGOC: null
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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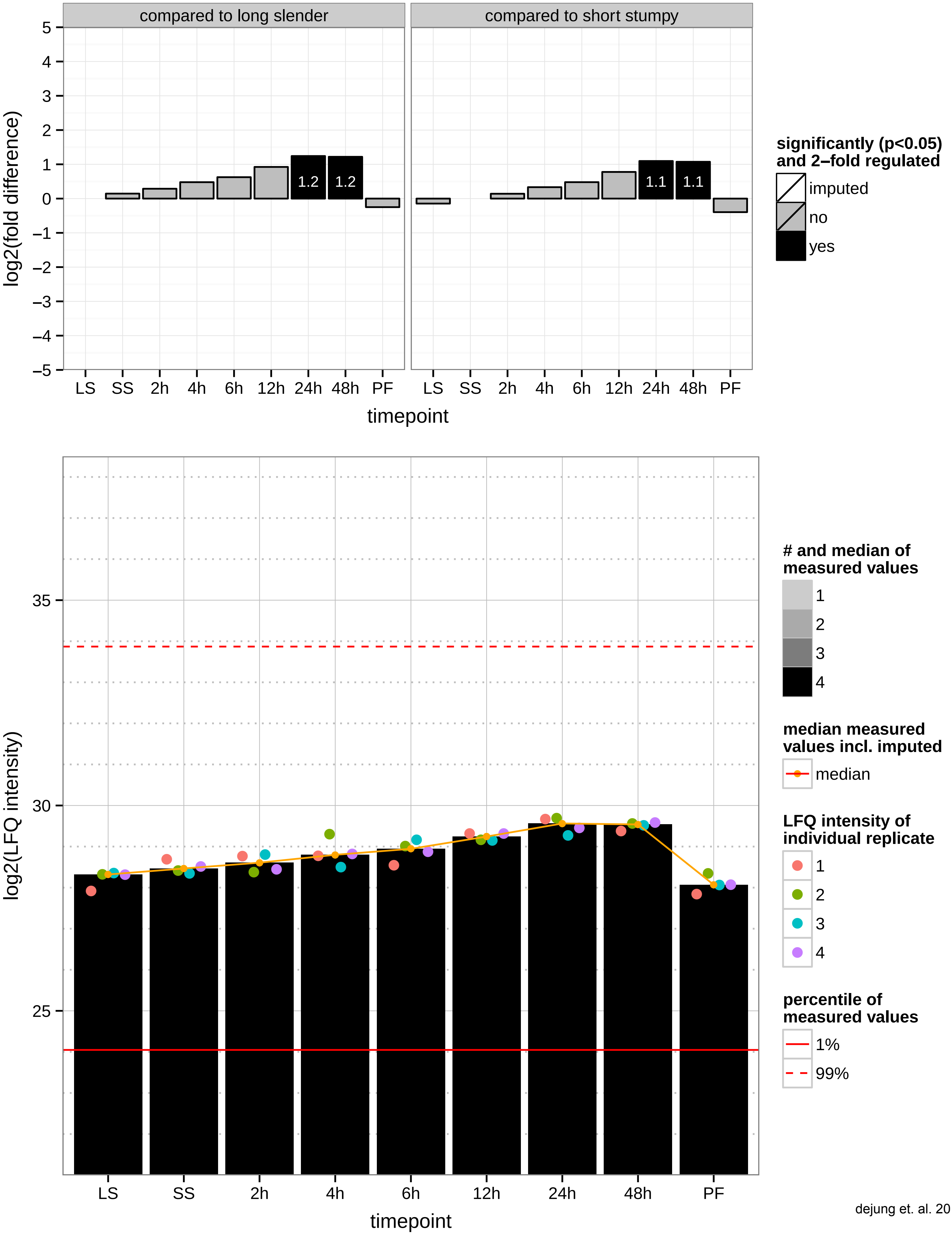
hypothetical protein, conserved
Tb927.3.4880
AGOF: null
AGOC: nucleus
AGOP: nucleosome assembly
PGOF: null
PGOC: nucleus
PGOP: nucleosome assembly



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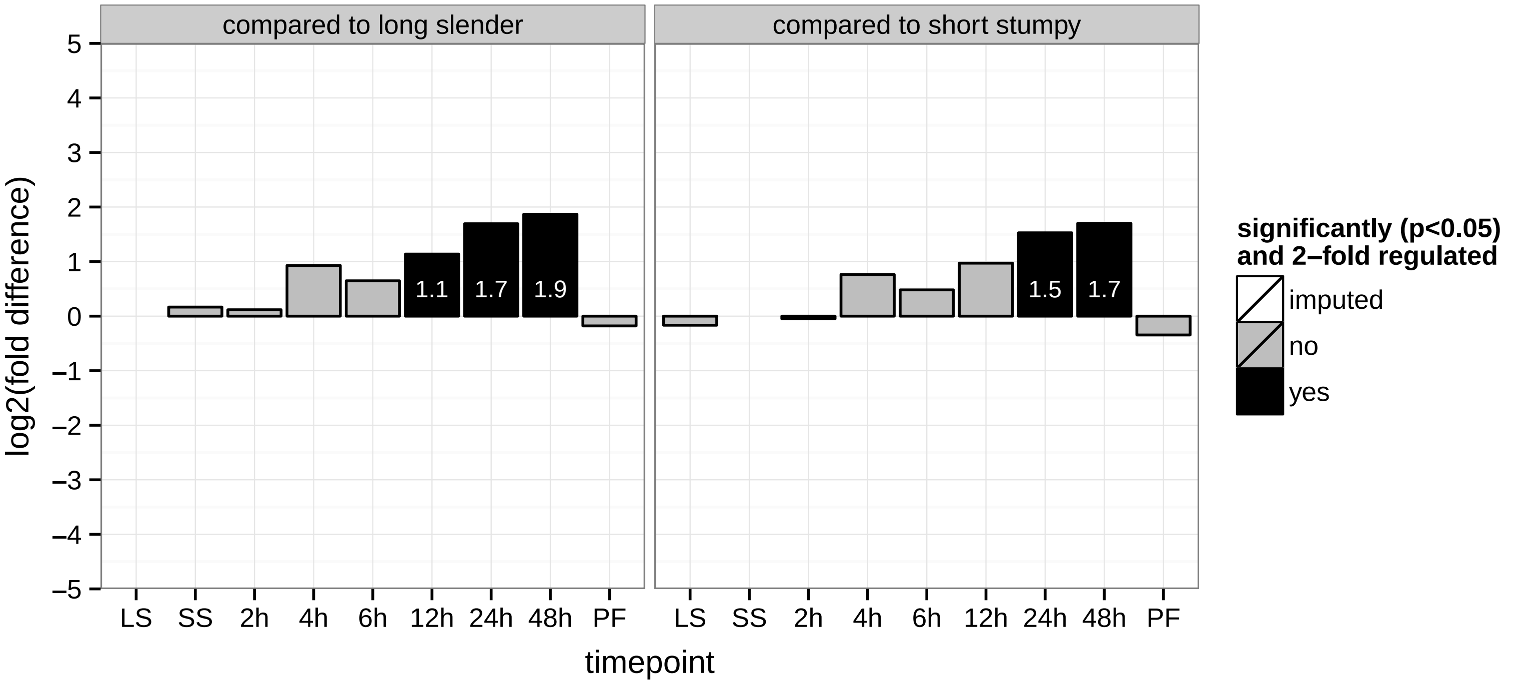
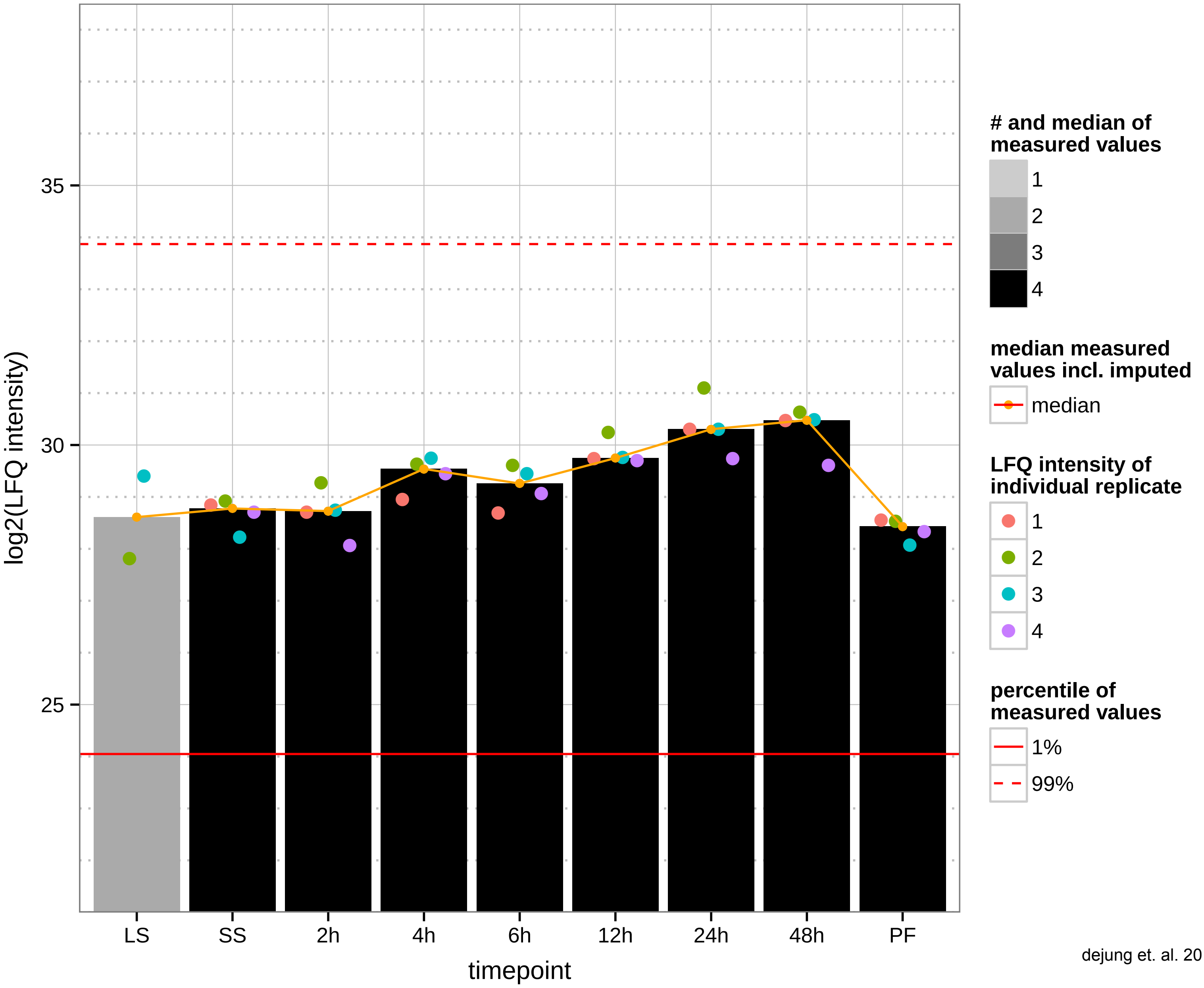
acyl carrier protein, mitochondrial precursor, putative (ACP)
Tb927.3.860
AGOF: ACP phosphopantetheine attachment site binding involved in fatty acid biosynthetic process, cofactor binding
AGOC: mitochondrion
AGOP: fatty acid biosynthetic process
PGOF: null
PGOC: null
PGOP: fatty acid biosynthetic process





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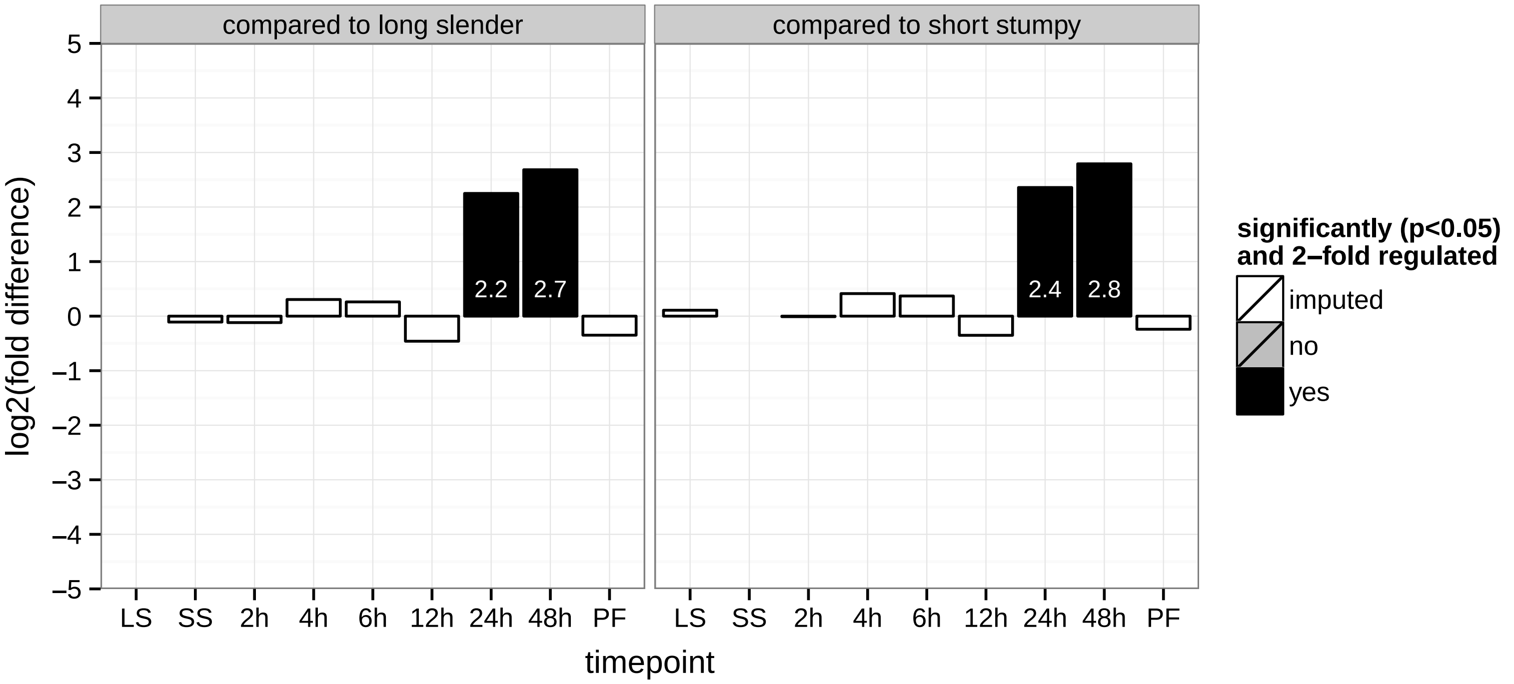
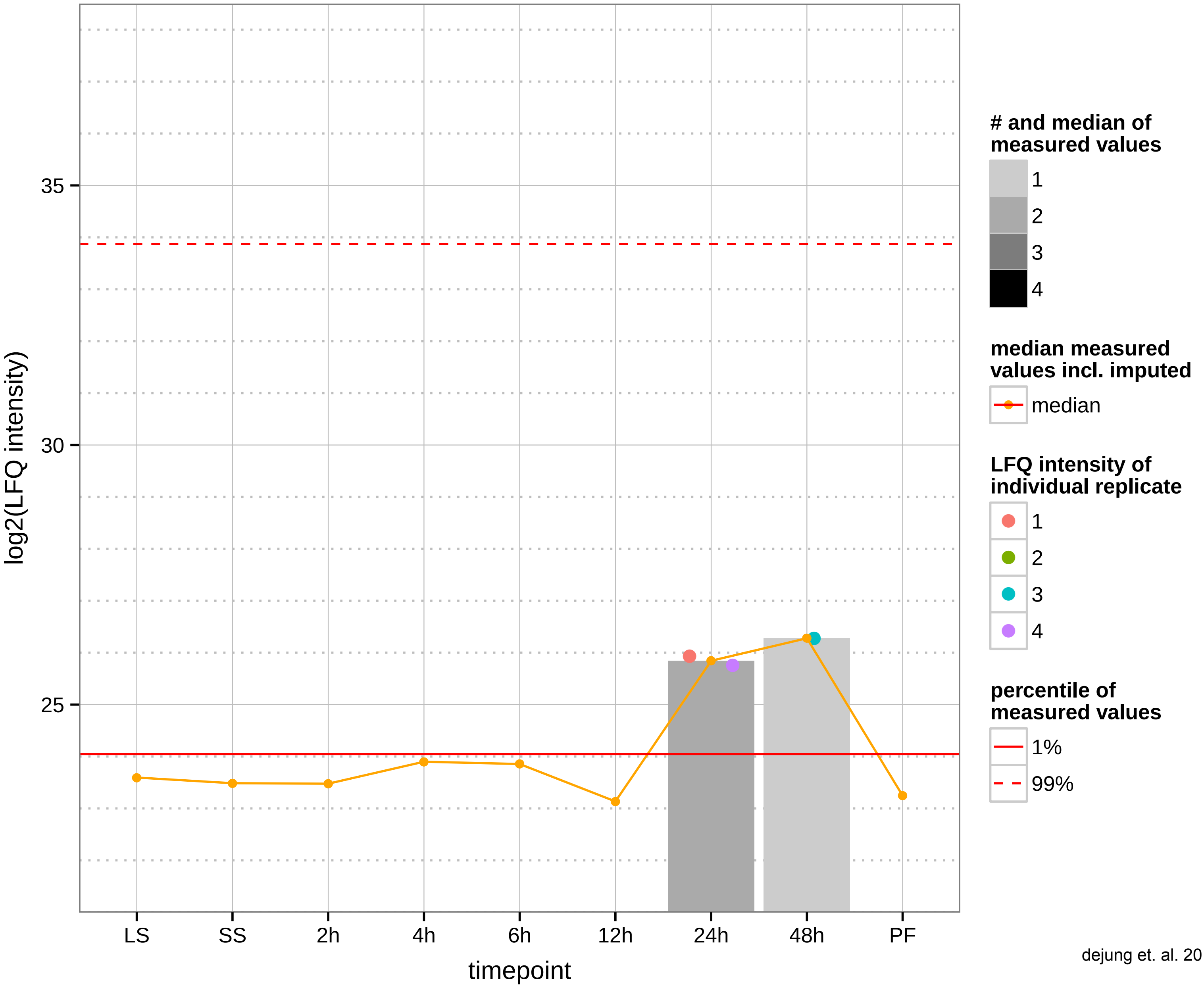
hypothetical protein, conserved
Tb927.3.940
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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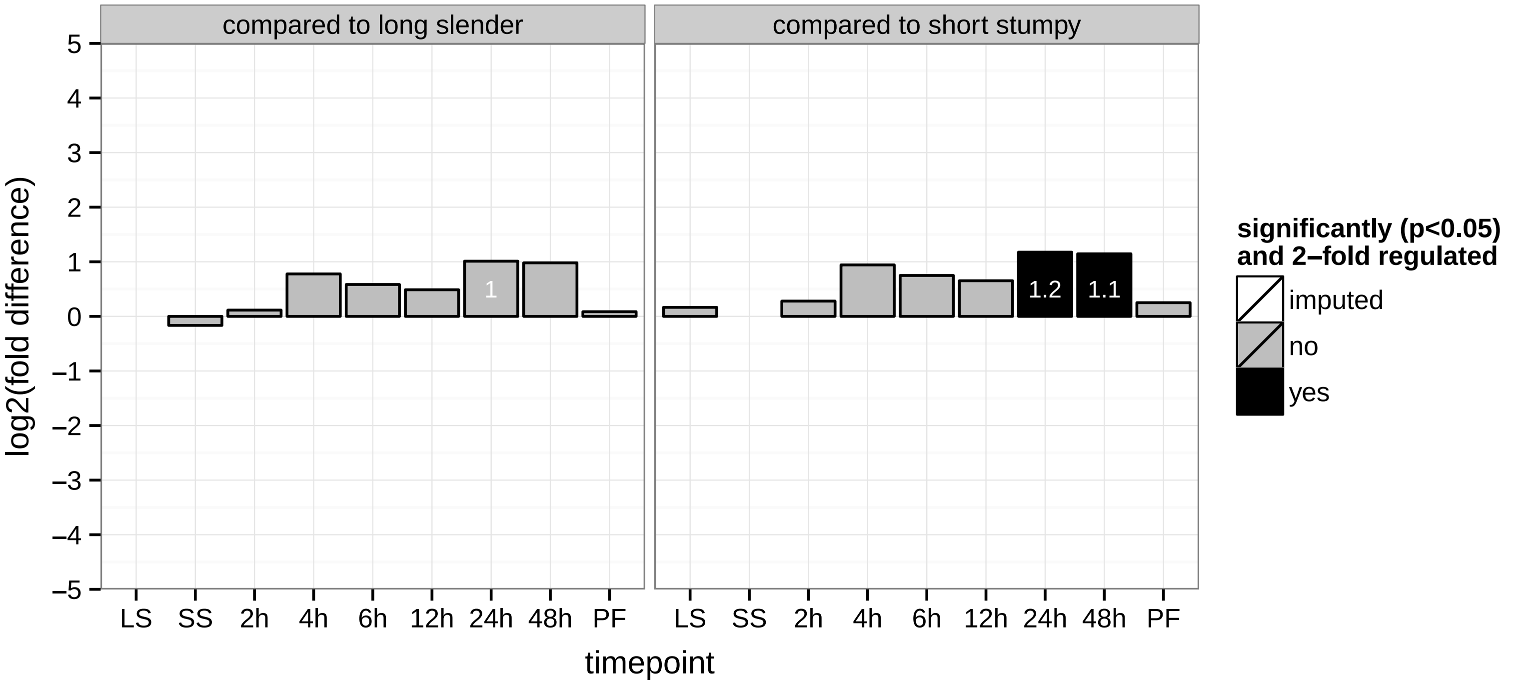
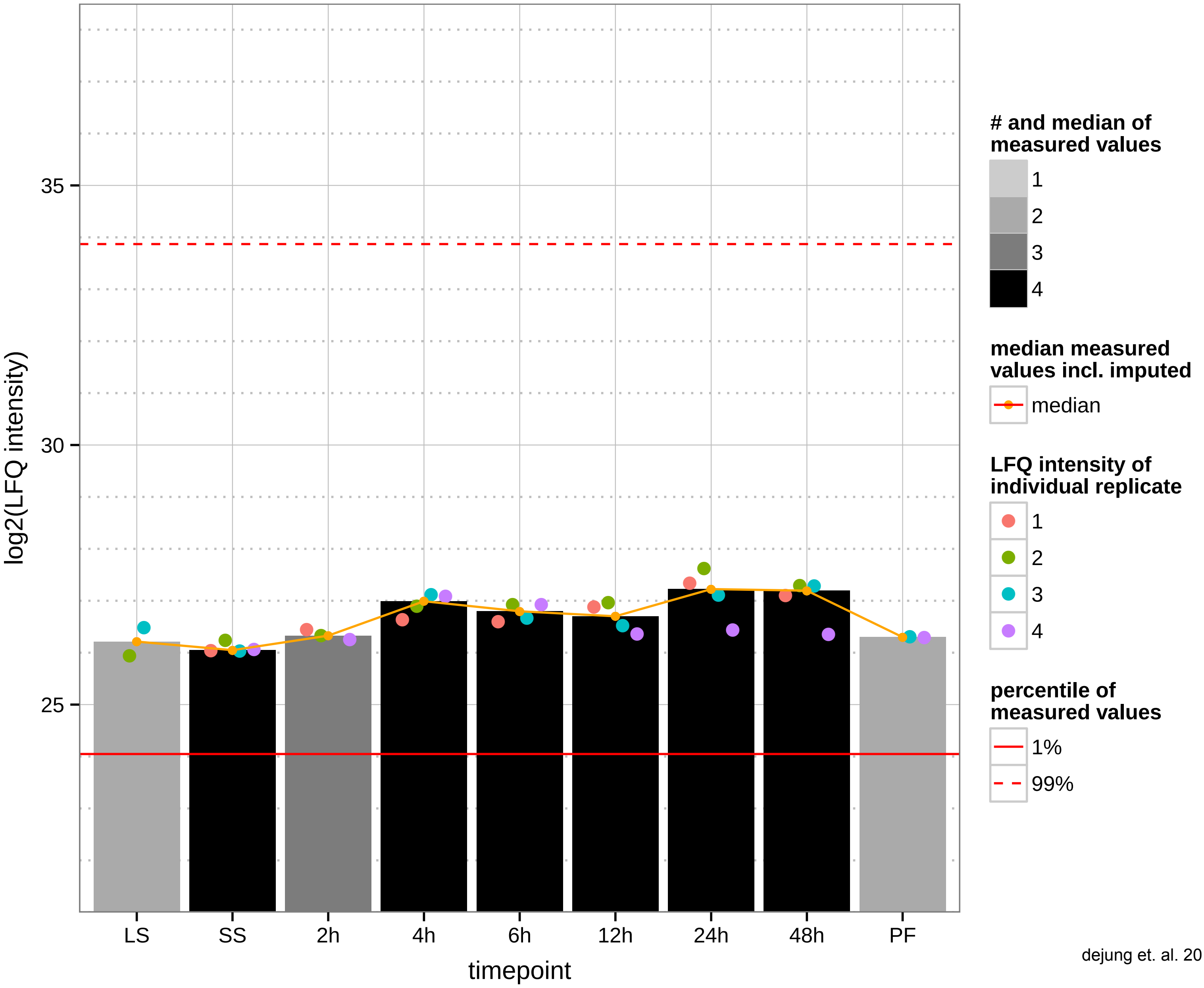
hypothetical protein, conserved
Tb927.4.2320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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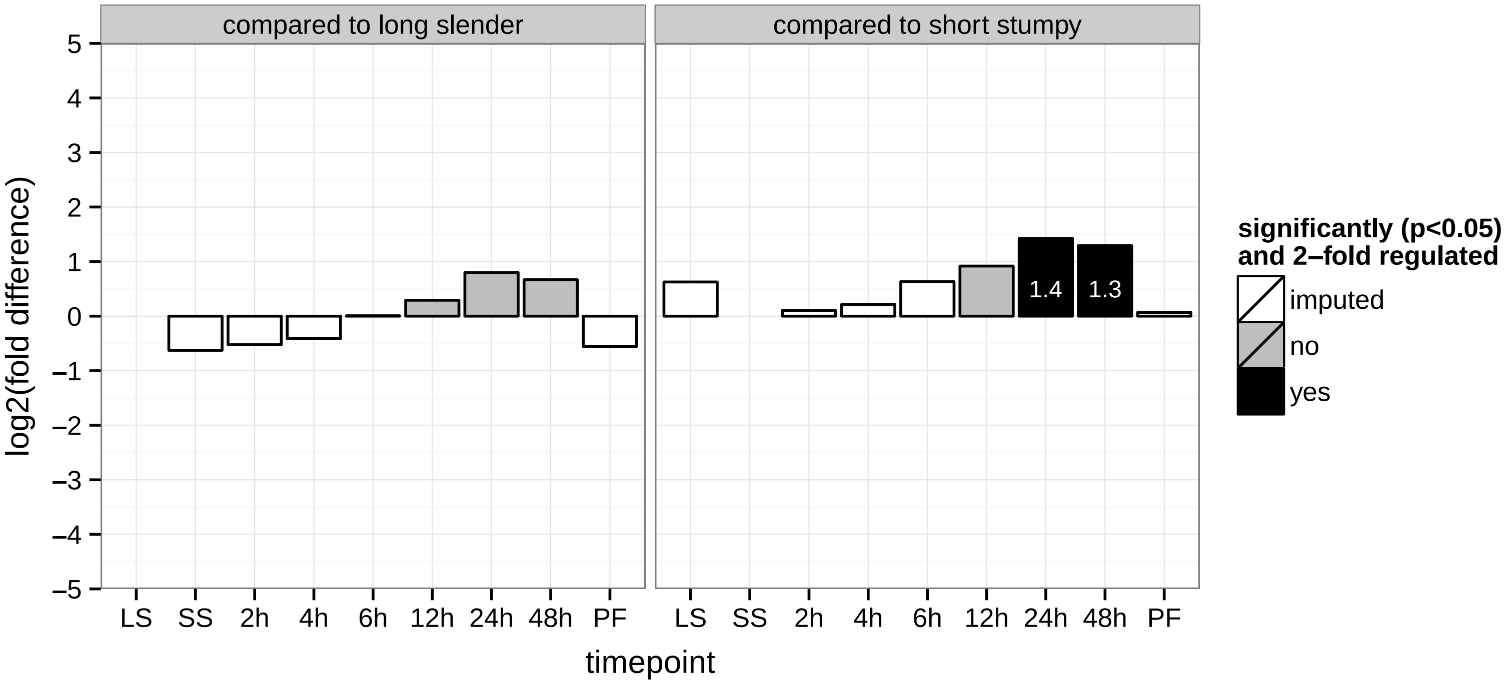
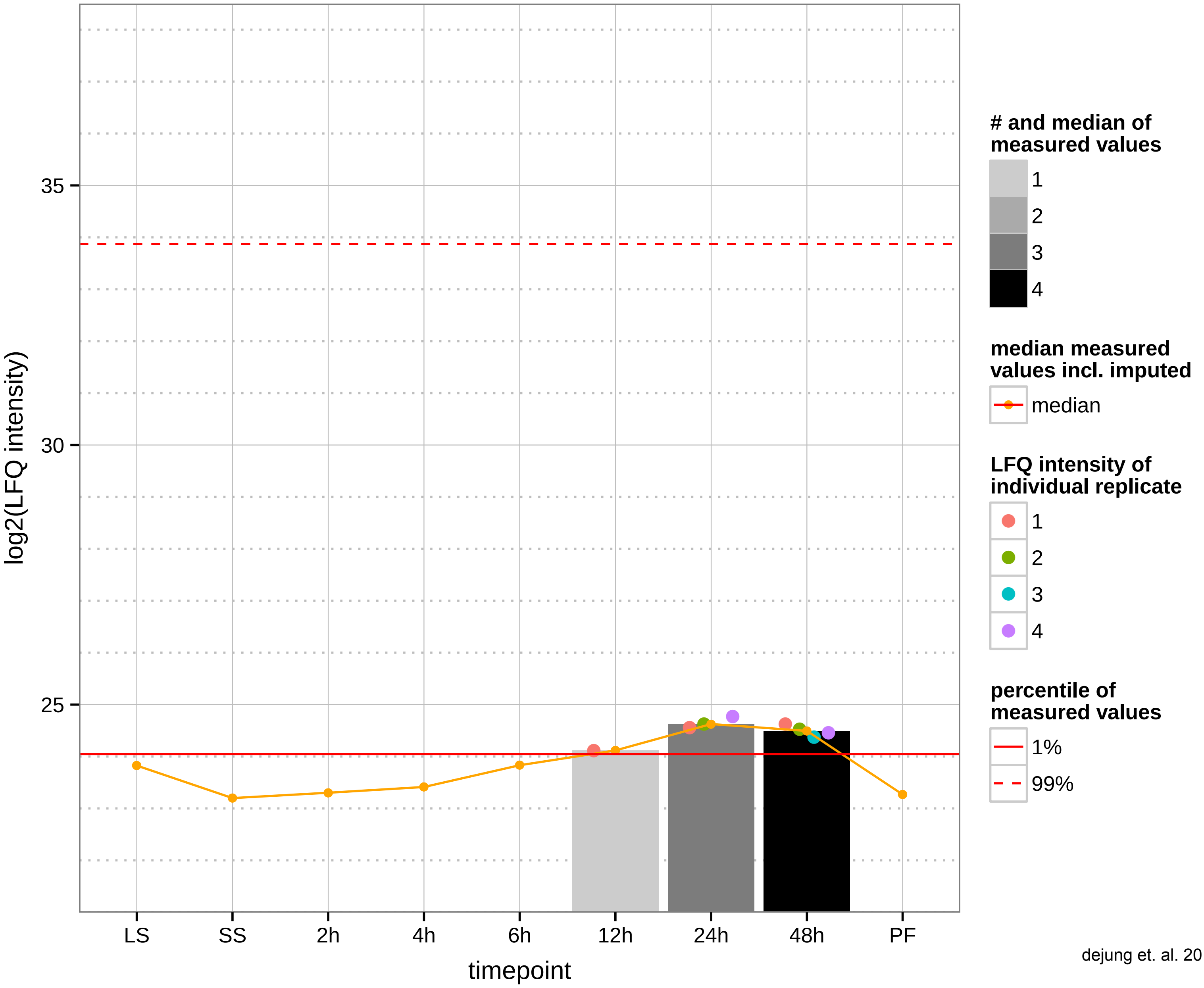
hypothetical protein, conserved
Tb927.4.2400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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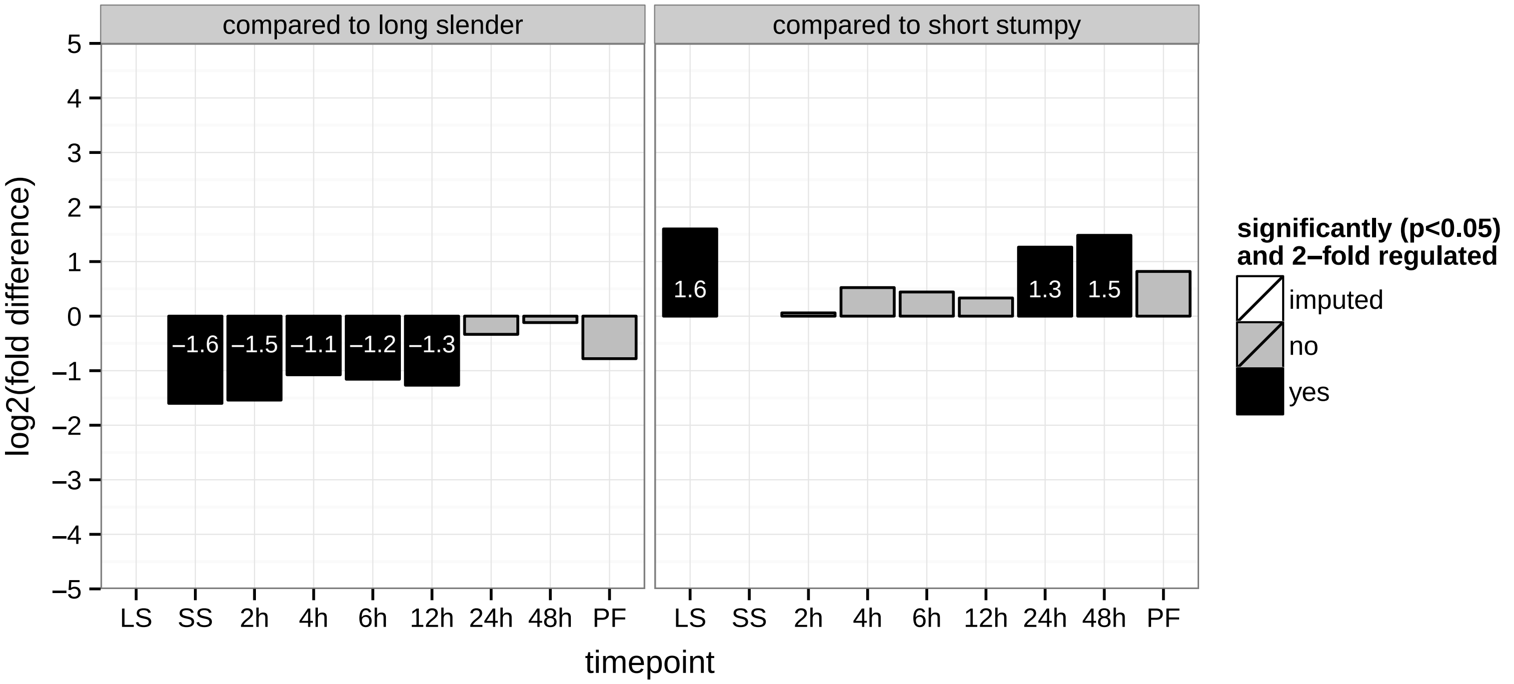
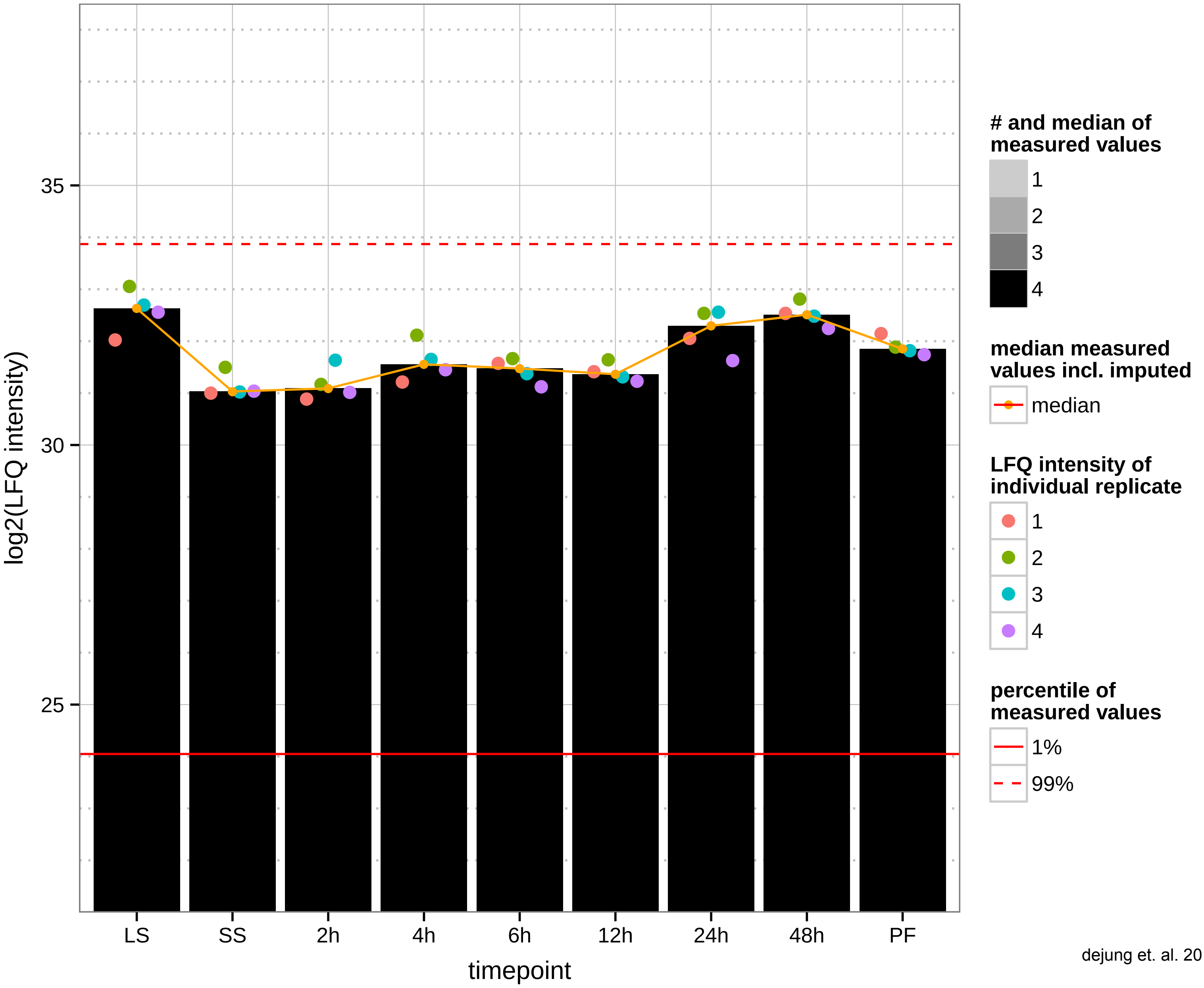
hypothetical protein, conserved
Tb927.4.2740
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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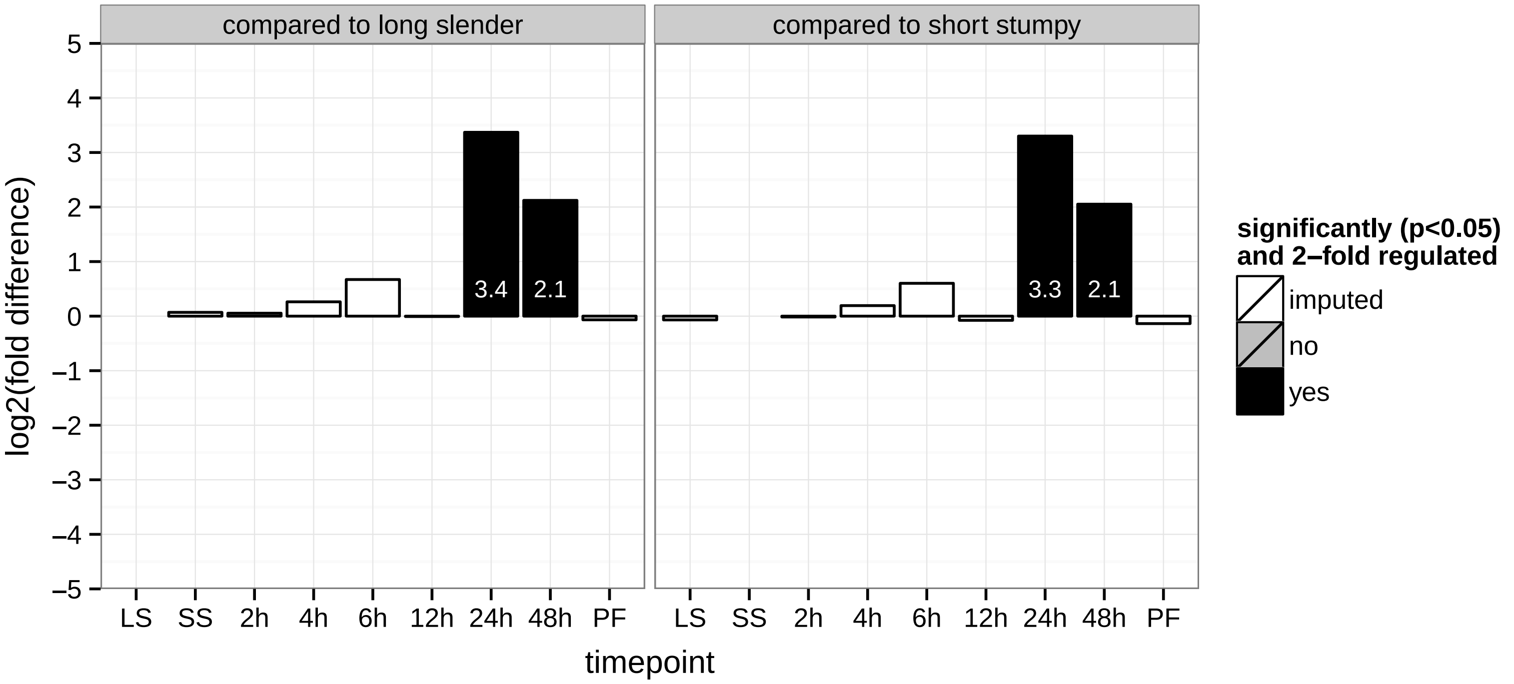
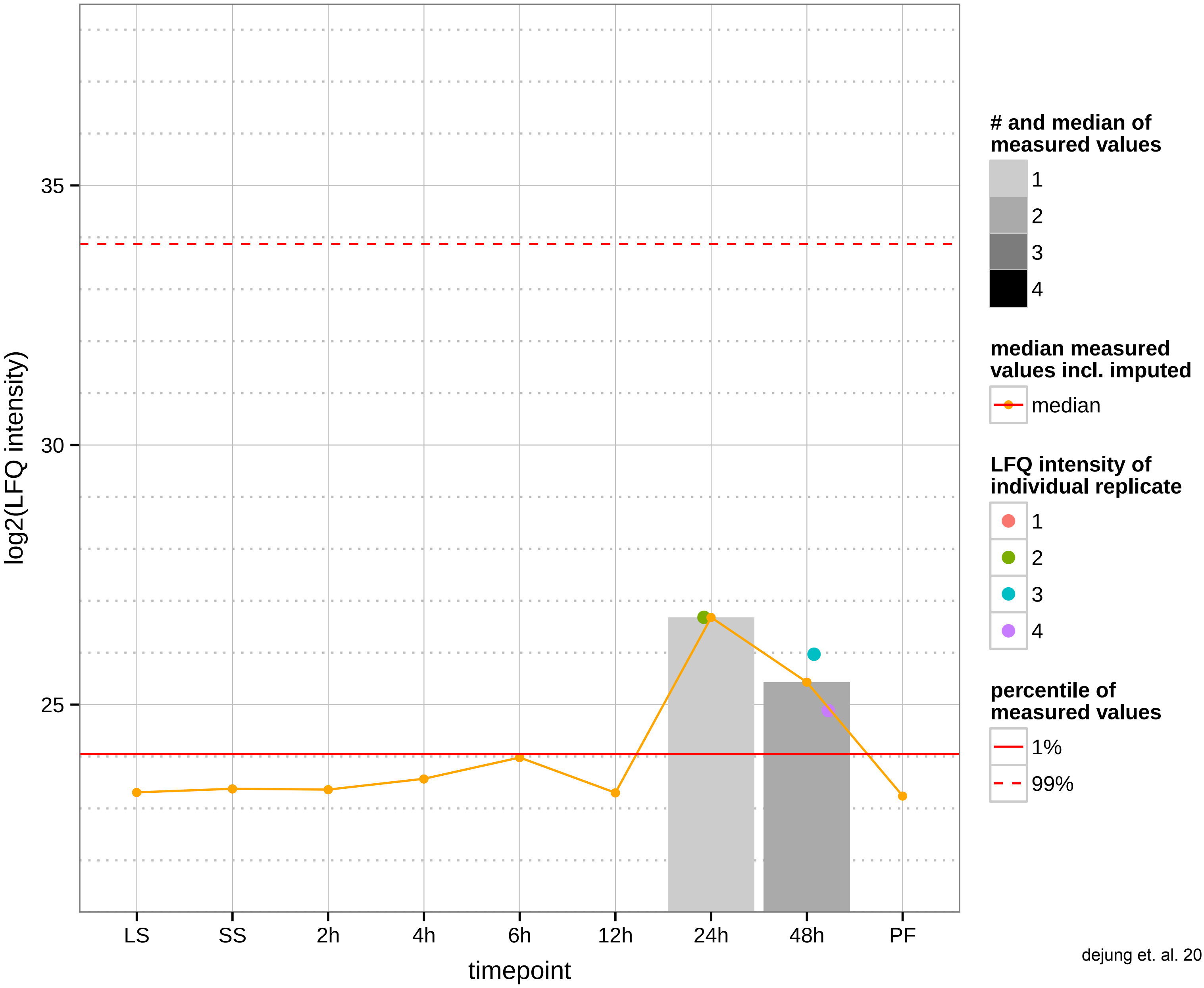
ubiquinol–cytochrome c reductase, putative
Tb927.4.4990;Tb927.8.7430
AGOF: null, ubiquinol–cytochrome–c reductase activity
AGOC: null, mitochondrial respiratory chain complex III
AGOP: null, mitochondrial electron transport, ubiquinol to cytochrome c
PGOF: null
PGOC: null
PGOP: null





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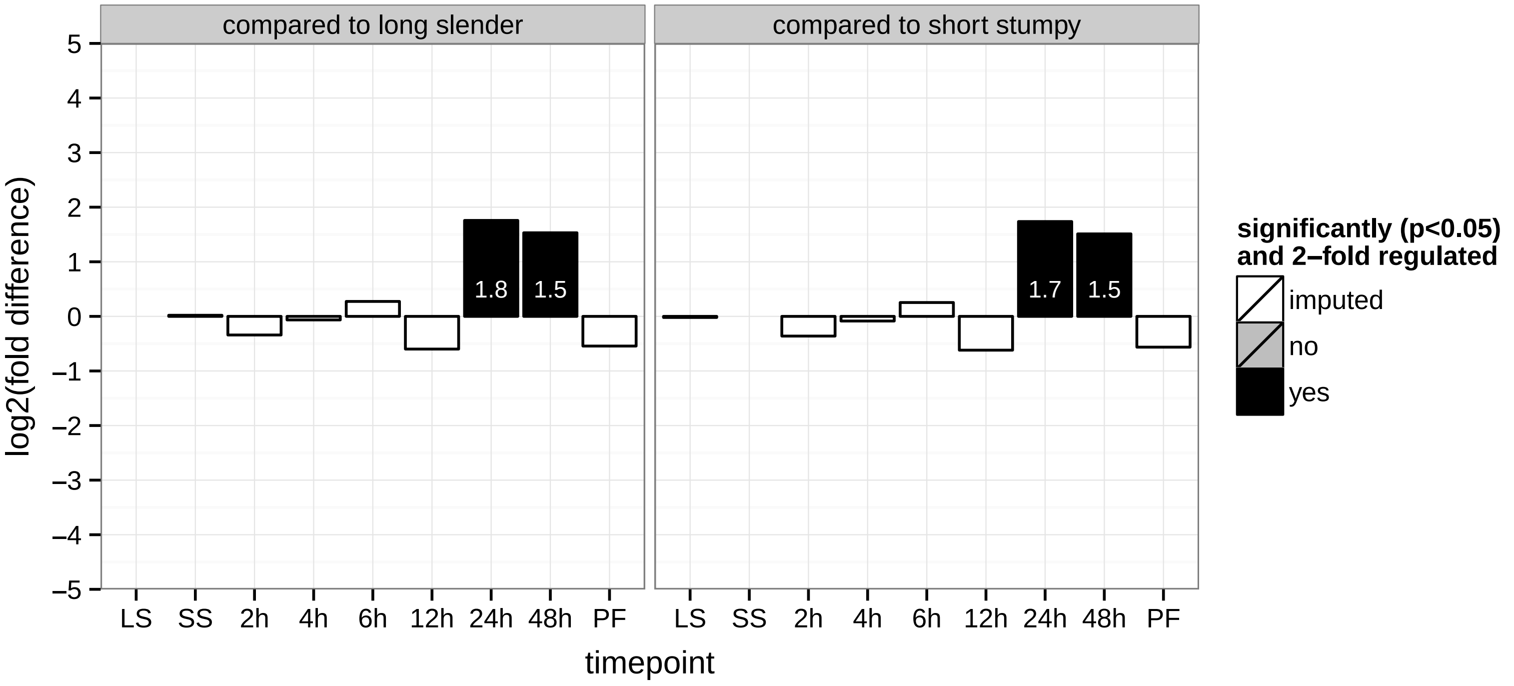
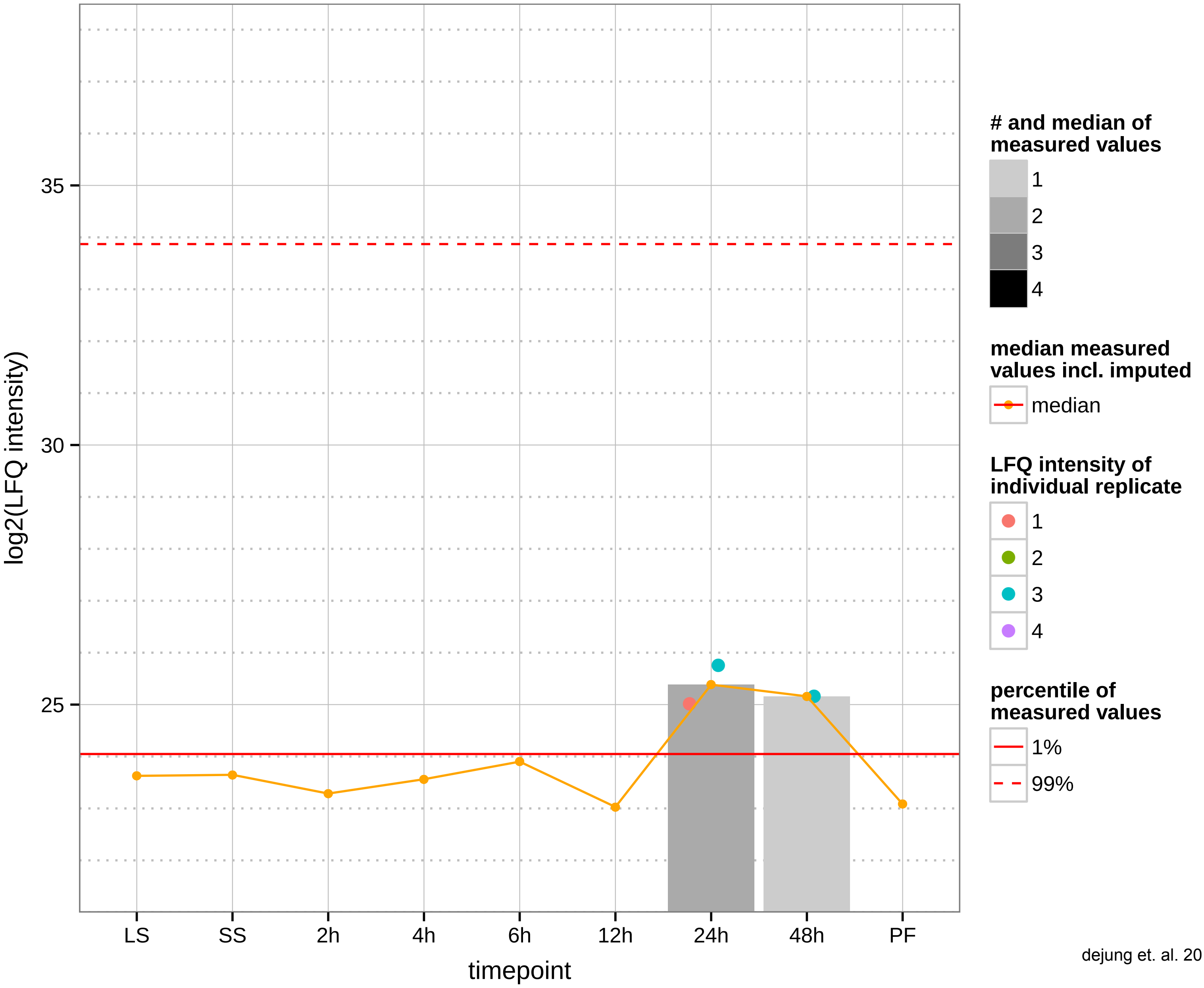
hypothetical protein, conserved
Tb927.4.510
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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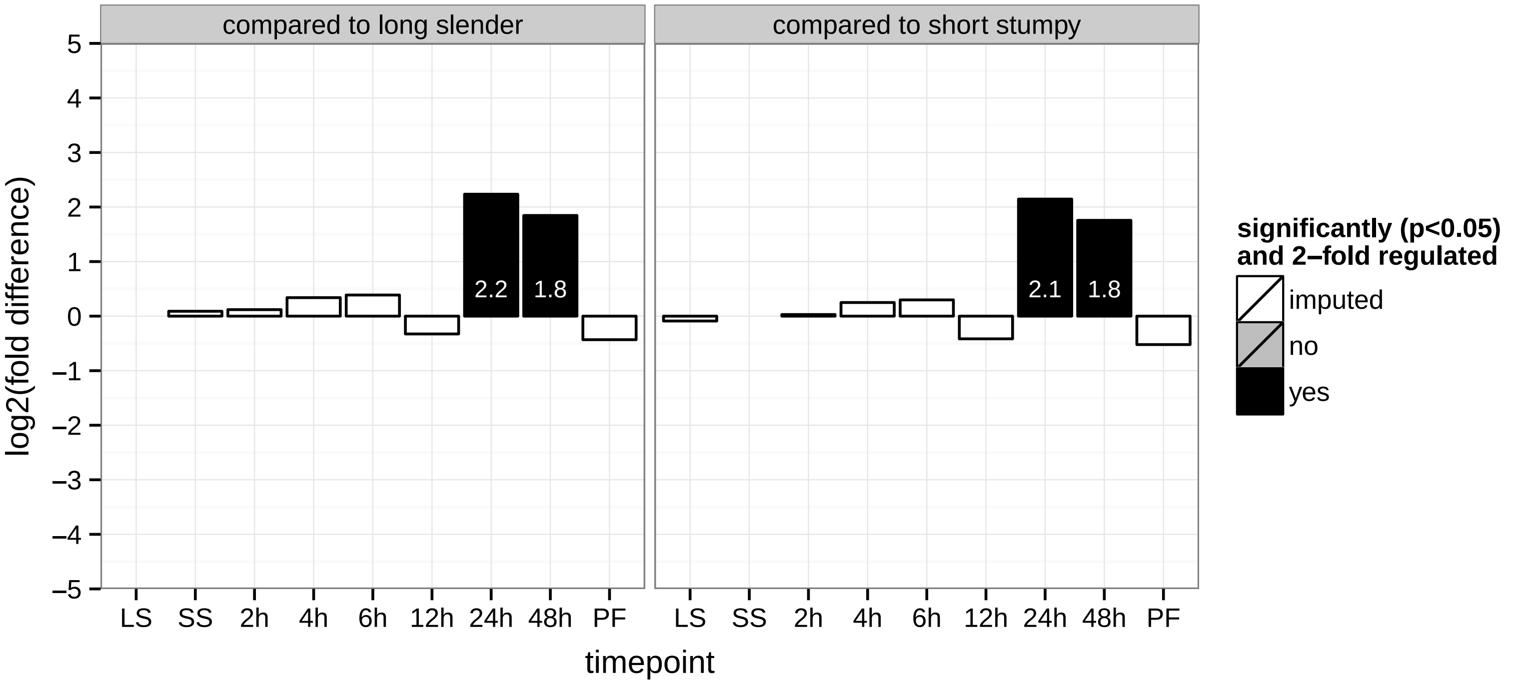
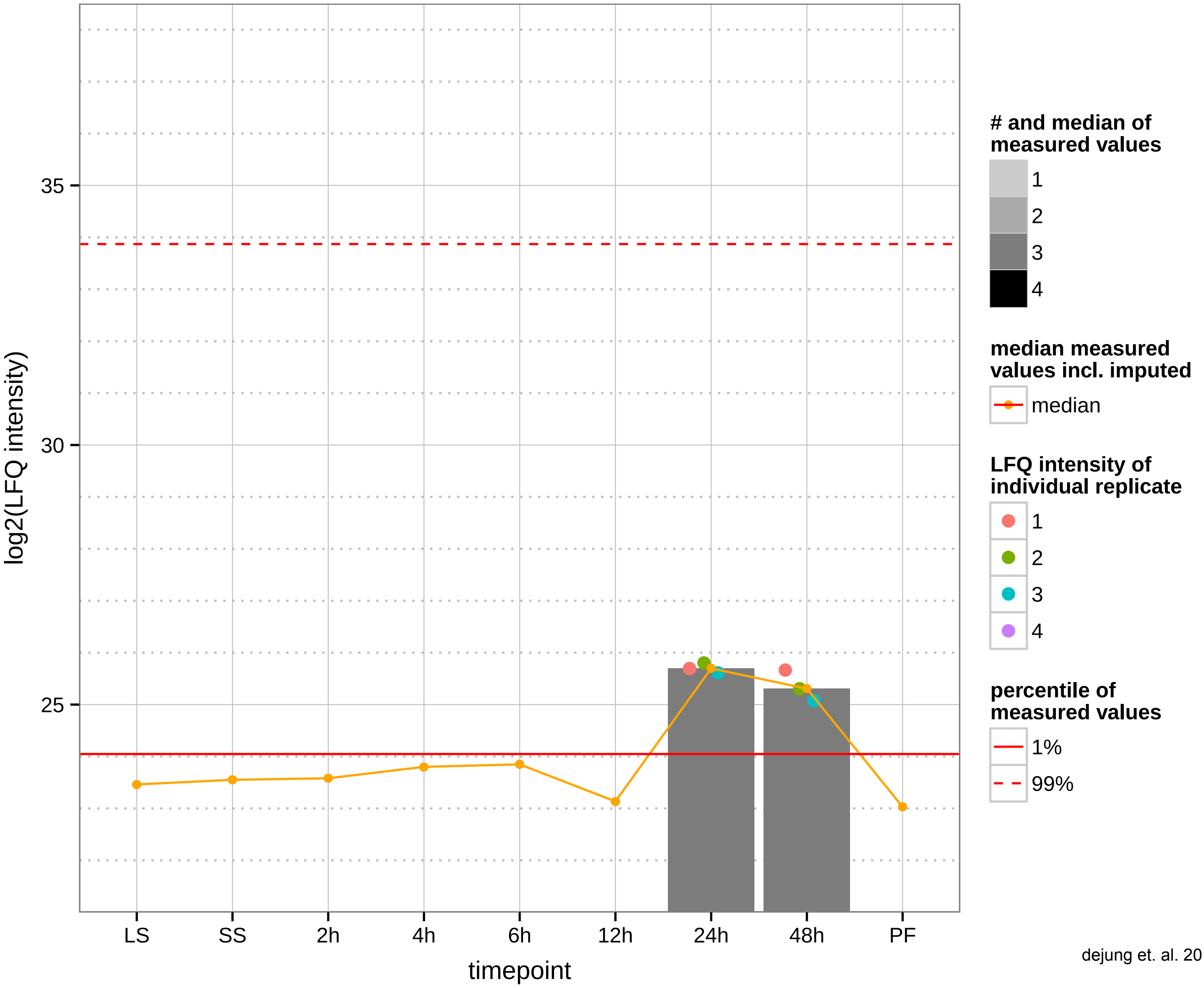
hypothetical protein, conserved
Tb927.5.2580
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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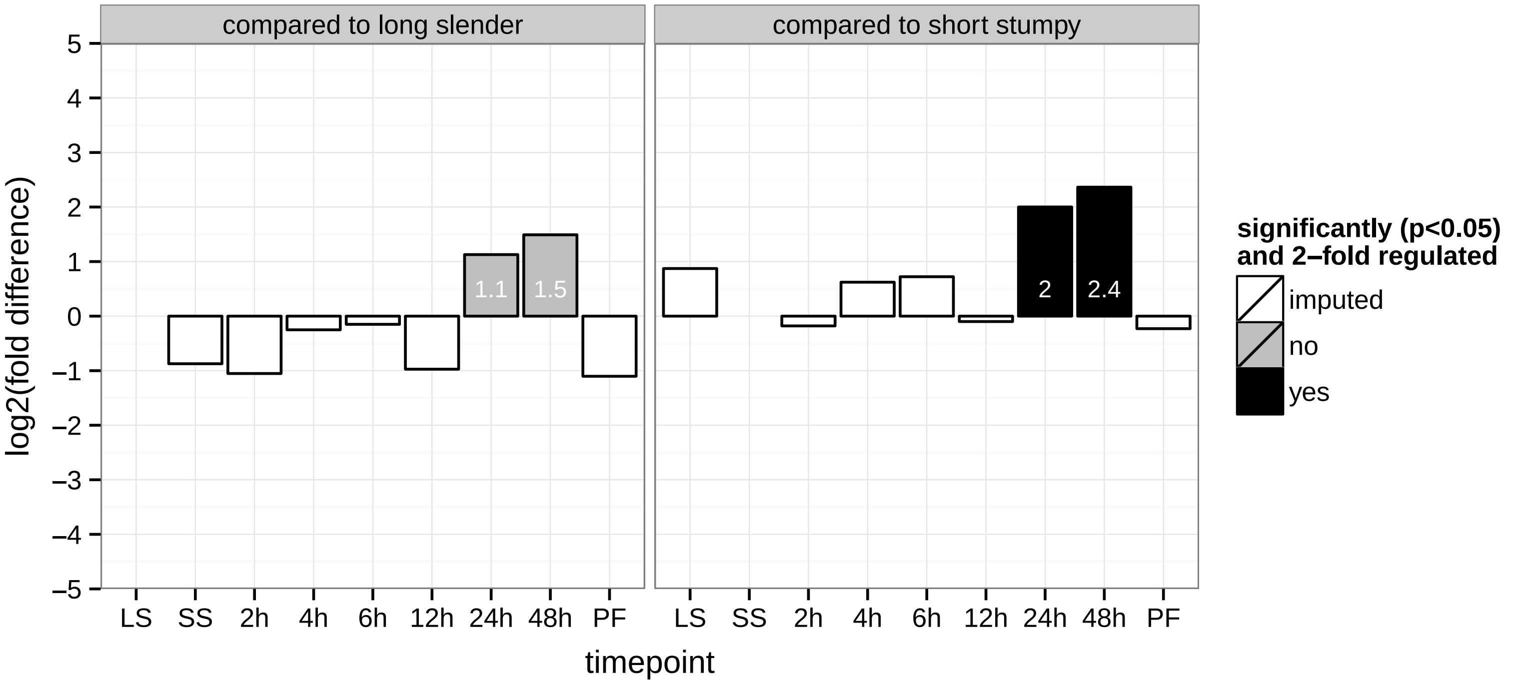
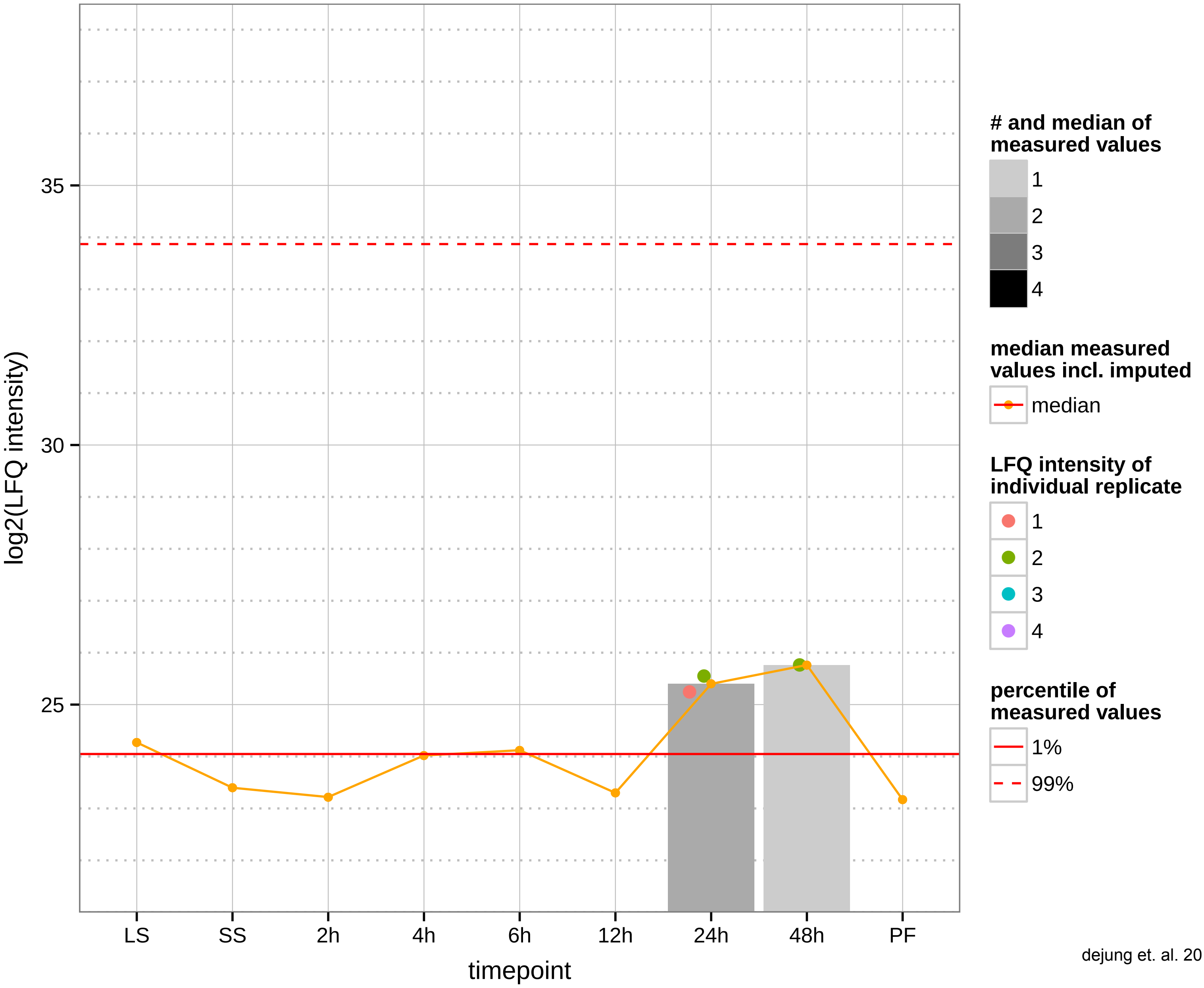
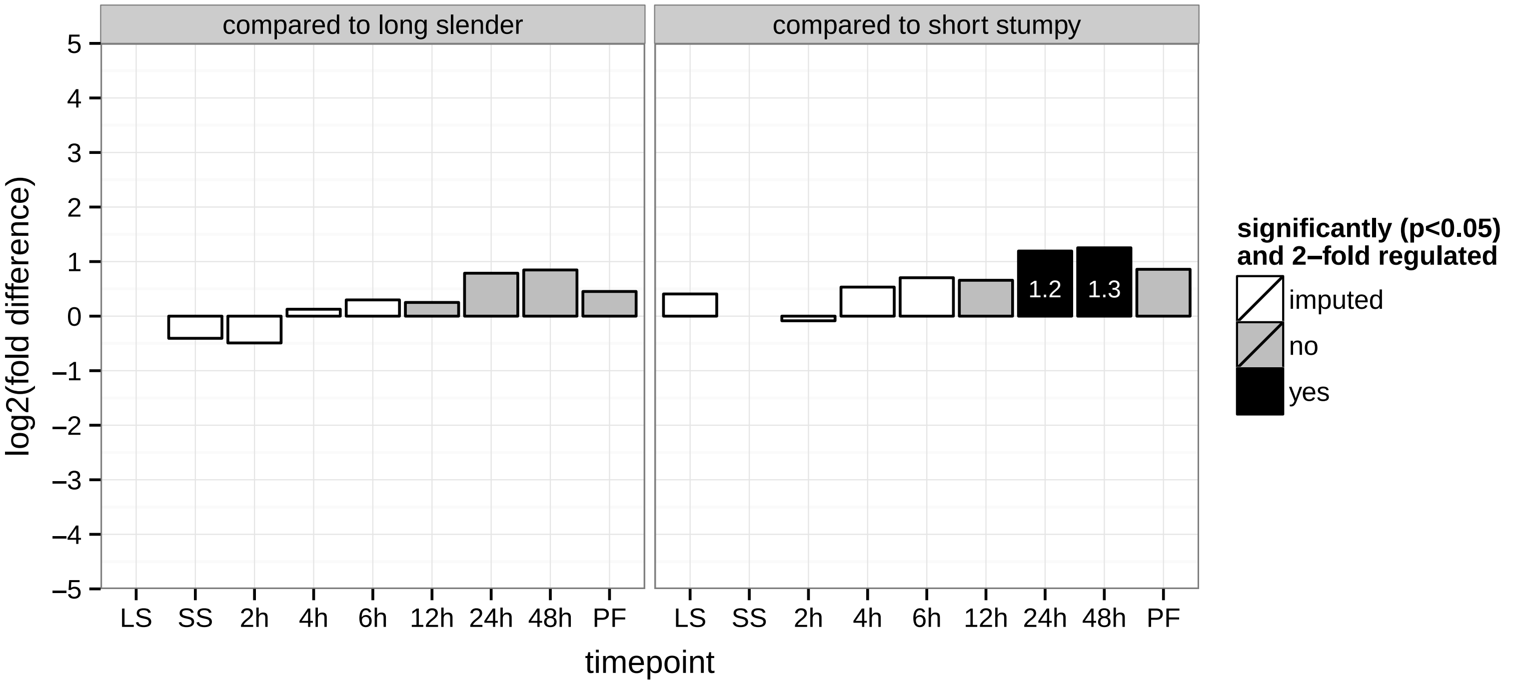
MIX protein
Tb927.5.3040
AGOF: null
AGOC: cytochrome complex, mitochondrial inner membrane, mitochondrion
AGOP: electron transport chain, mitochondrial respiratory chain complex IV assembly
PGOF: null
PGOC: null
PGOP: null

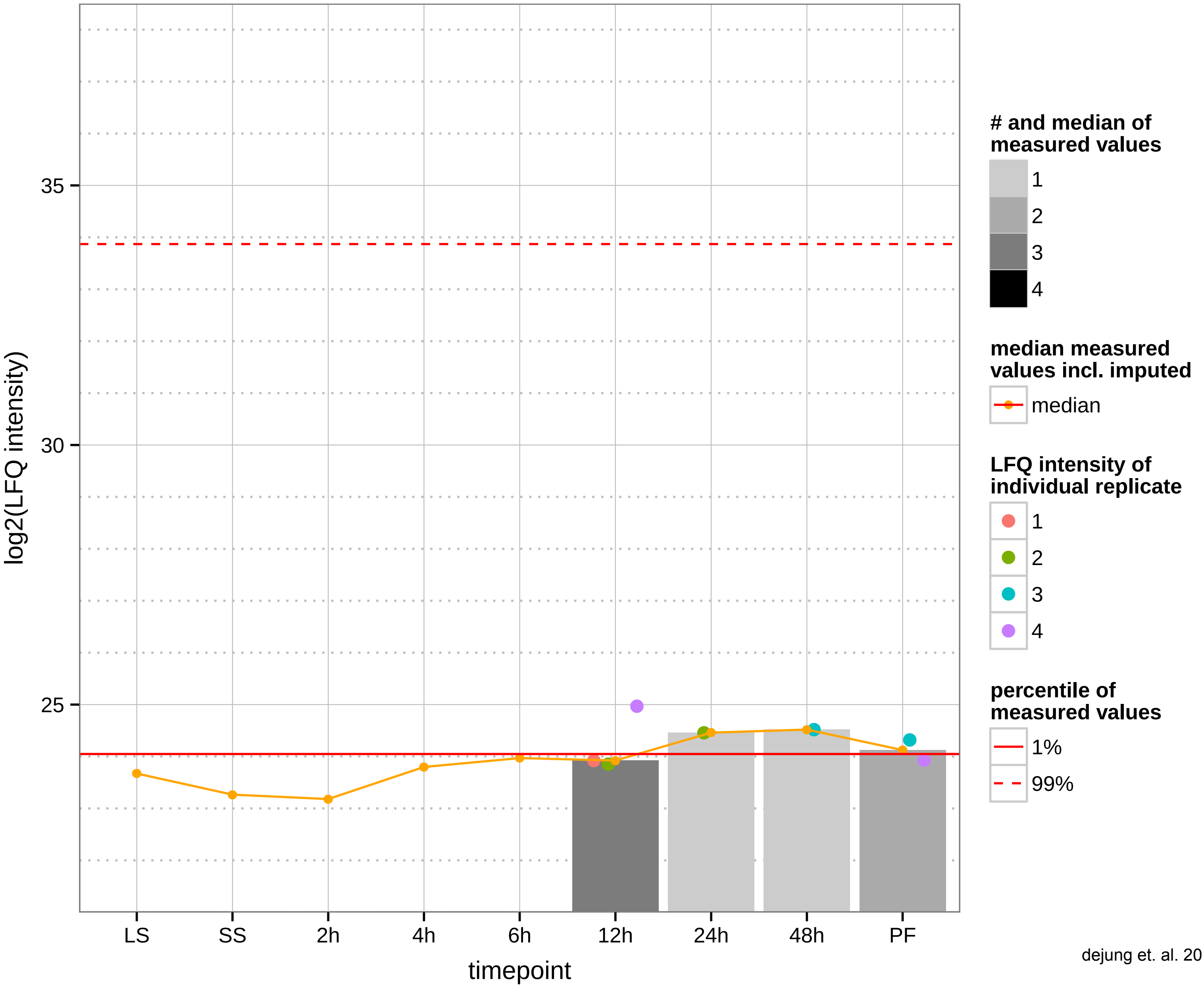




dejung et. al. 2015

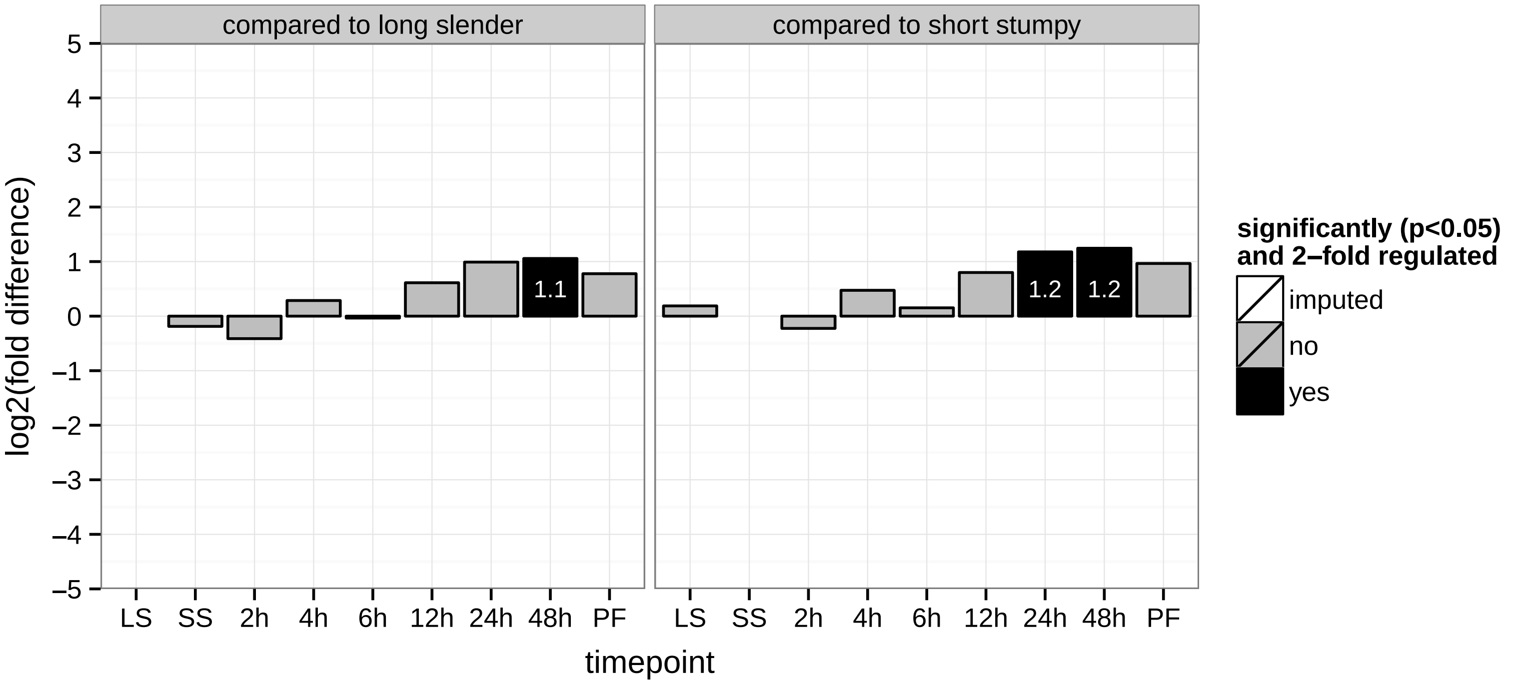
U6 snRNA–associated Sm–like protein LSm7p (TbLSm7)
Tb927.5.4030
AGOF: null
AGOC: U6 snRNP, nucleolus, nucleus
AGOP: maturation of SSU–rRNA, nuclear mRNA splicing, via spliceosome, nuclear–transcribed mRNA catabolic process
PGOF: null
PGOC: null
PGOP: null

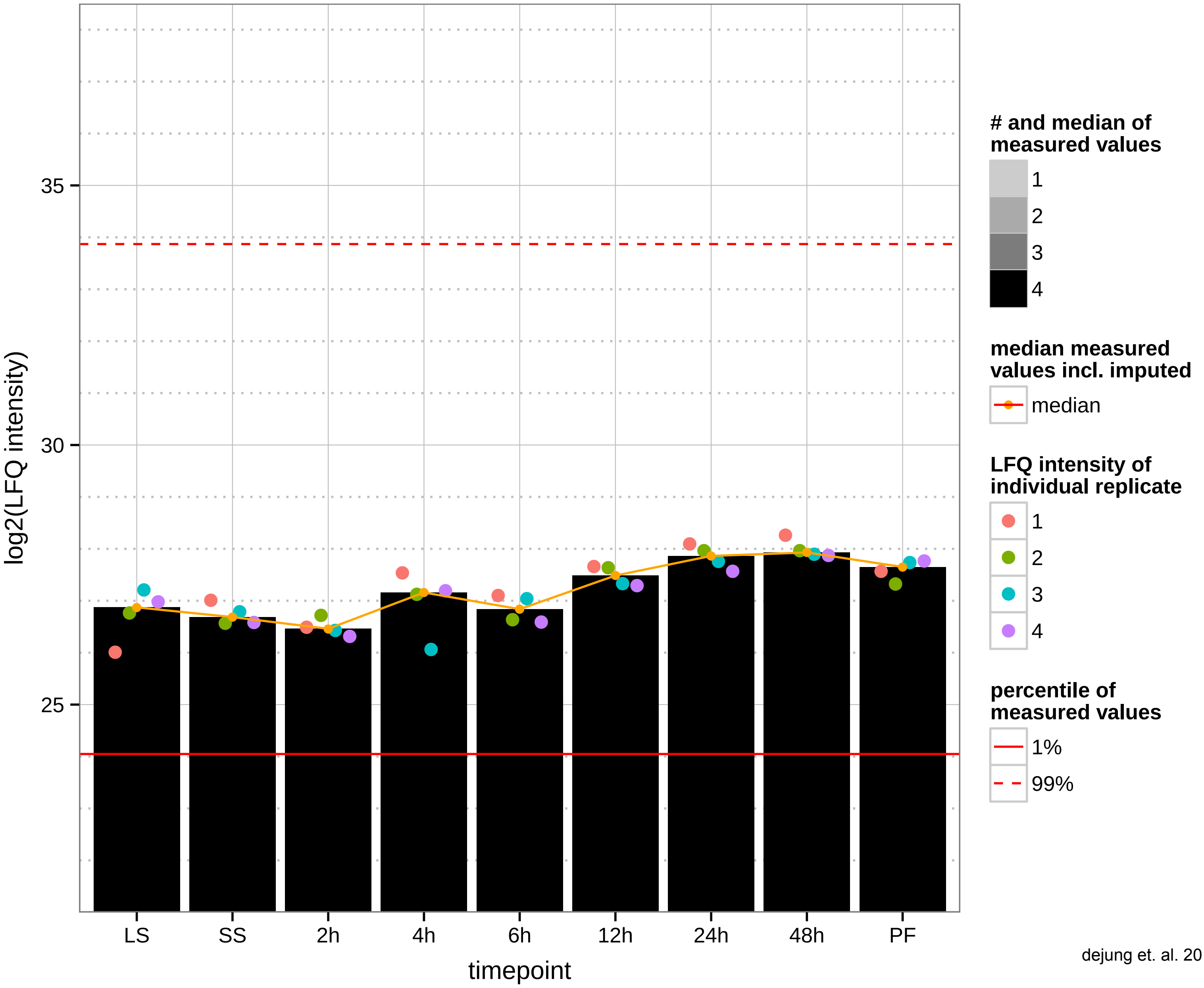




dejung et. al. 2015

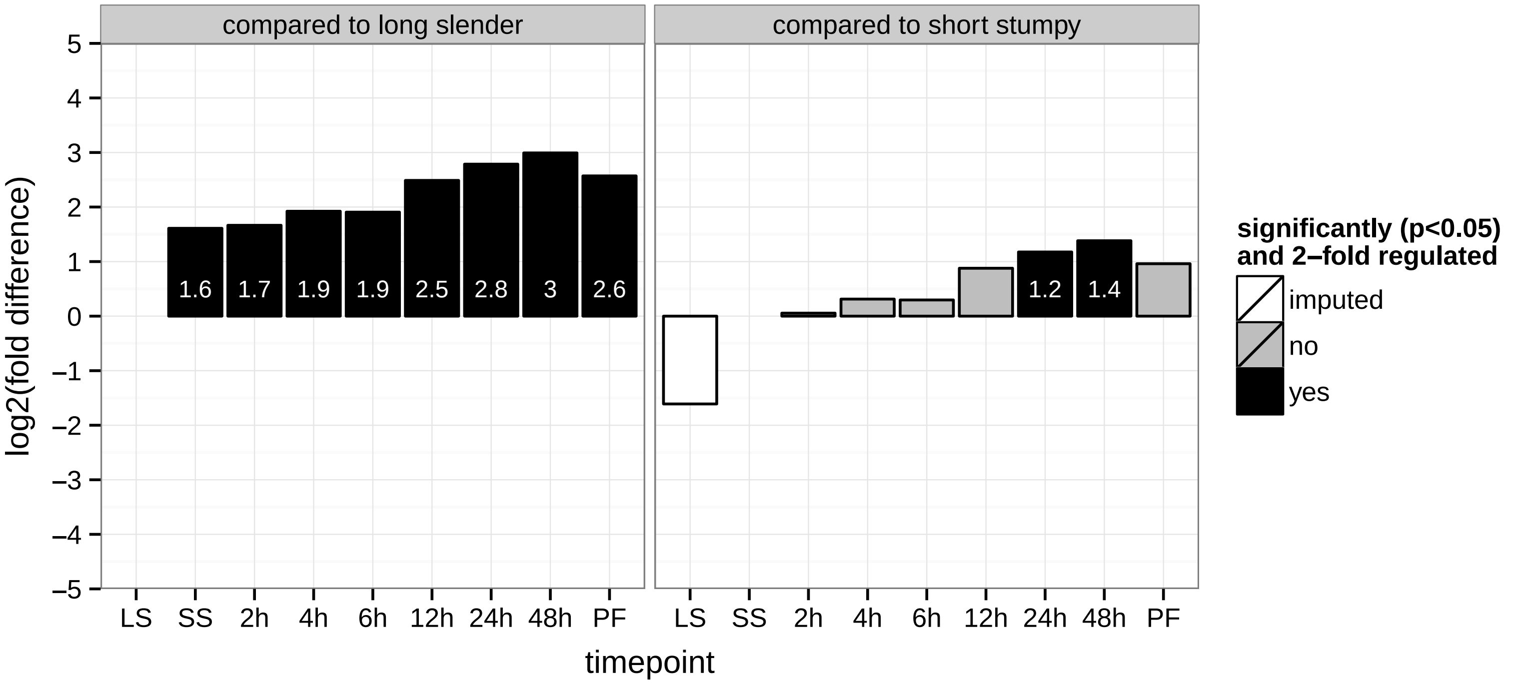
protein phosphatase 1, regulatory subunit, putative
Tb927.5.590
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

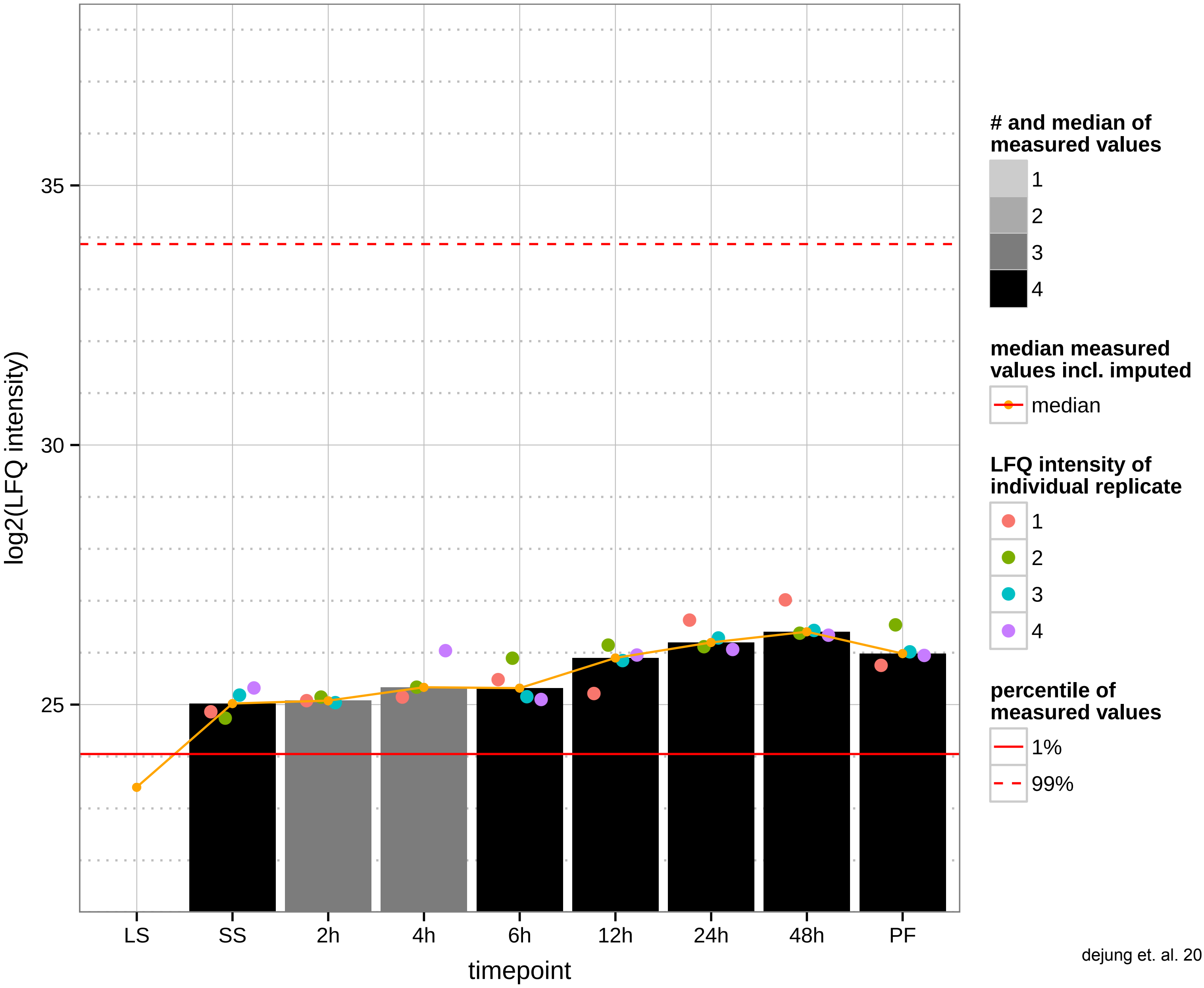




dejung et. al. 2015

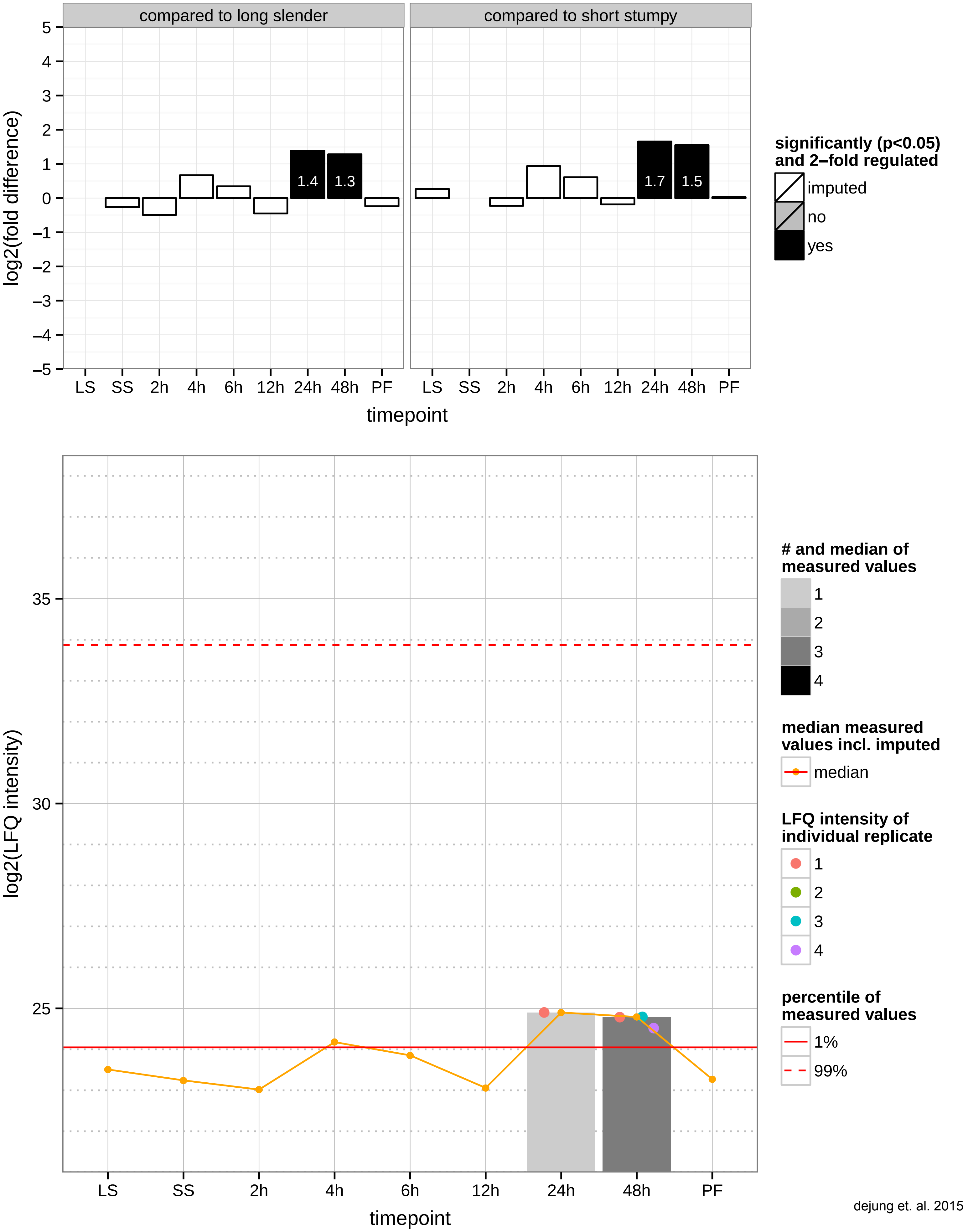
hypothetical protein, conserved
Tb927.5.980
AGOF: oxidoreductase activity
AGOC: null
AGOP: null
PGOF: oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular o
PGOC: null
PGOP: oxidation–reduction process





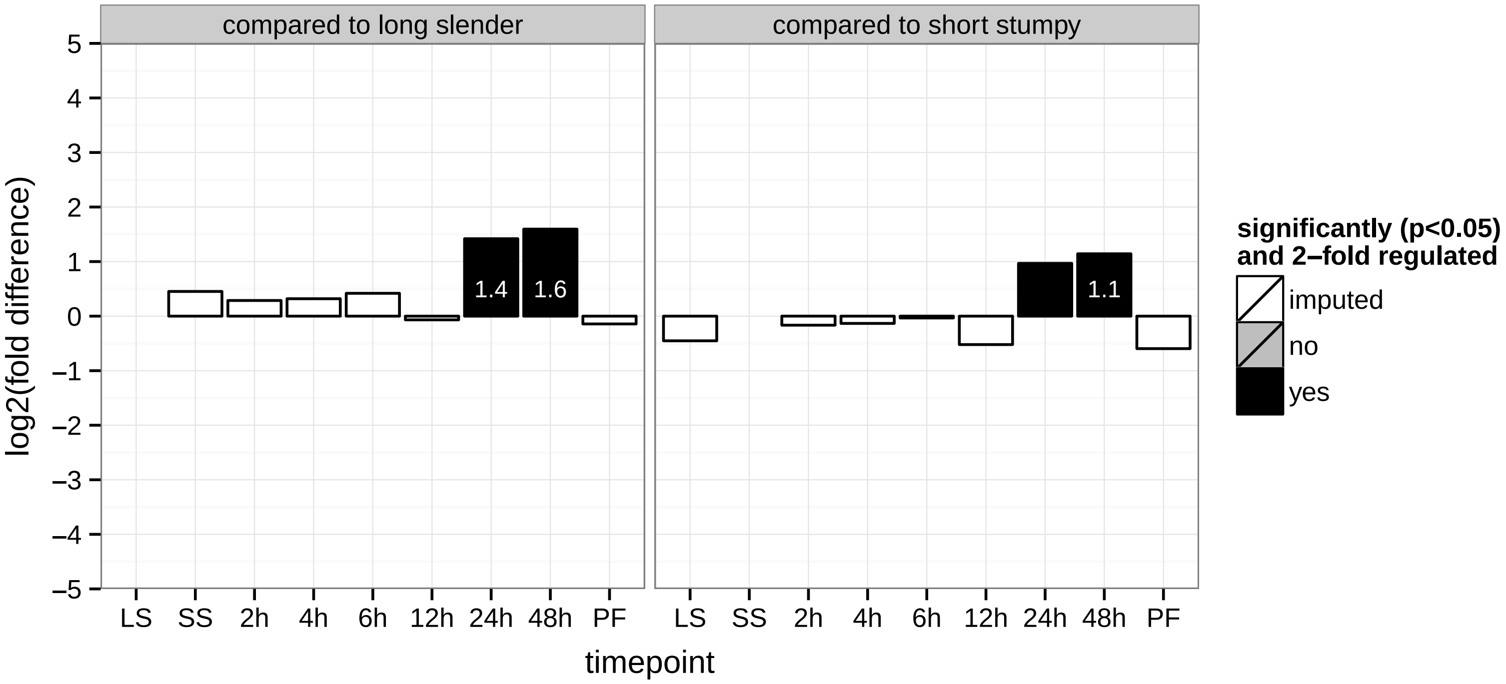
dejung et. al. 2015

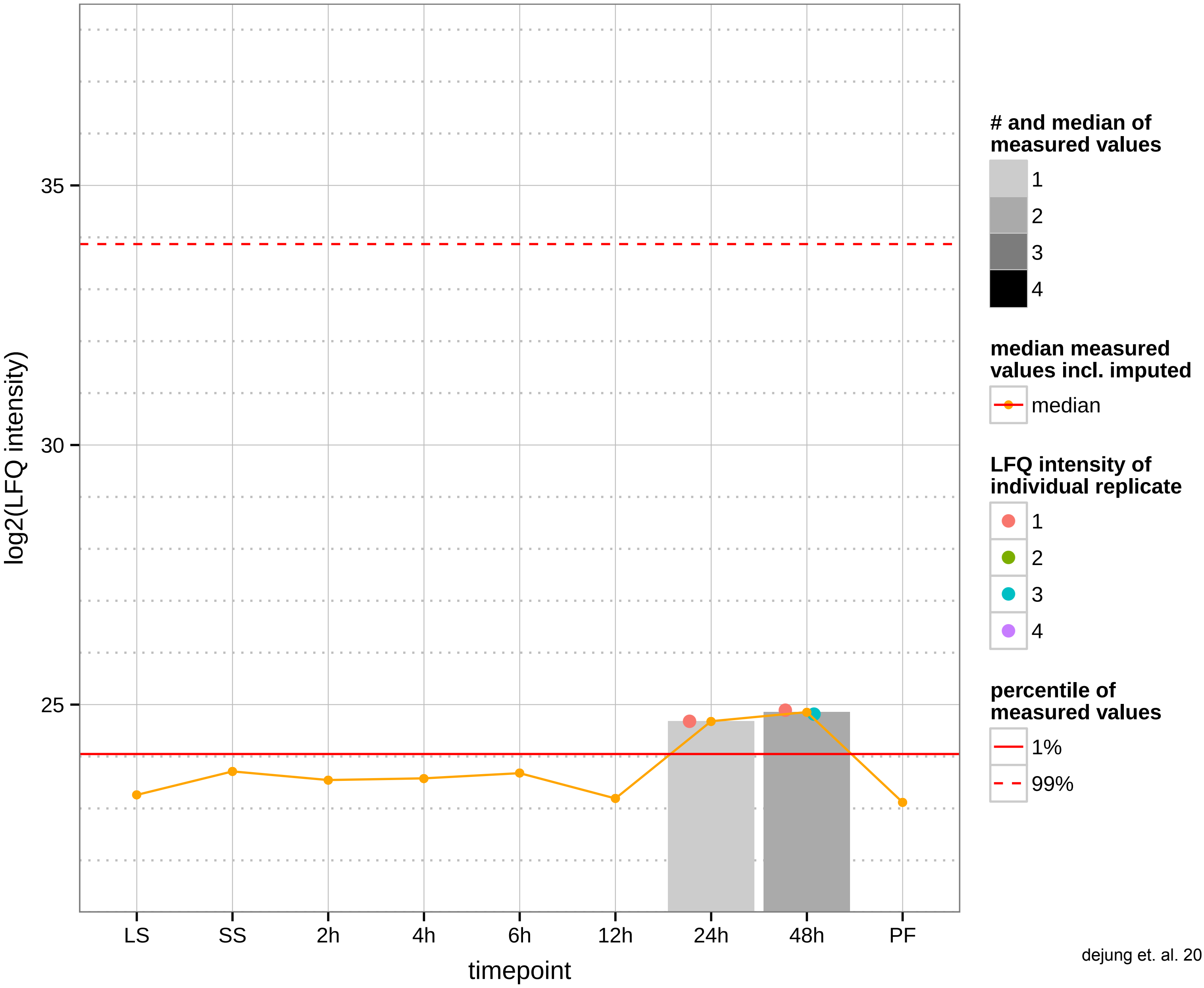
hypothetical protein, conserved
Tb927.6.1910
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015

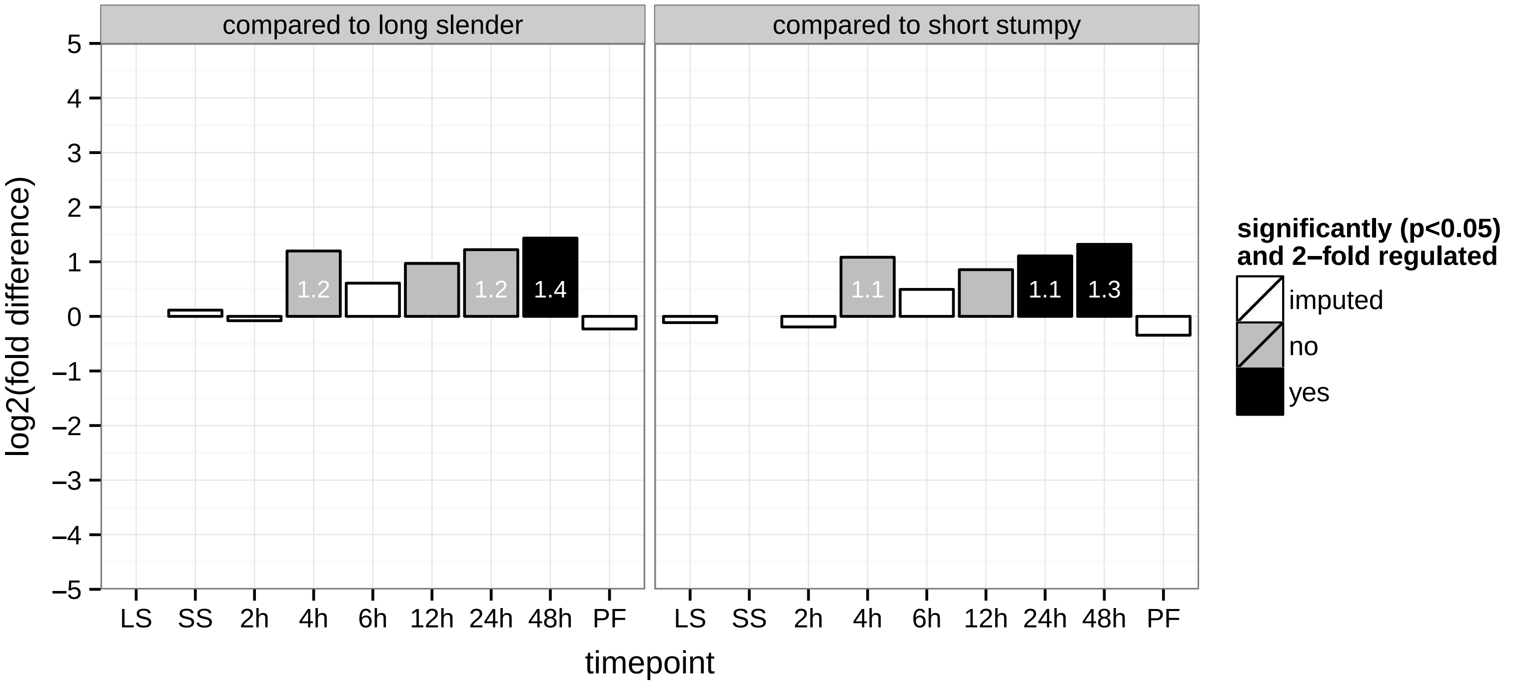
hypothetical protein, conserved
Tb927.6.3530
AGOF: null
AGOC: membrane
AGOP: transport
PGOF: null
PGOC: null
PGOP: null

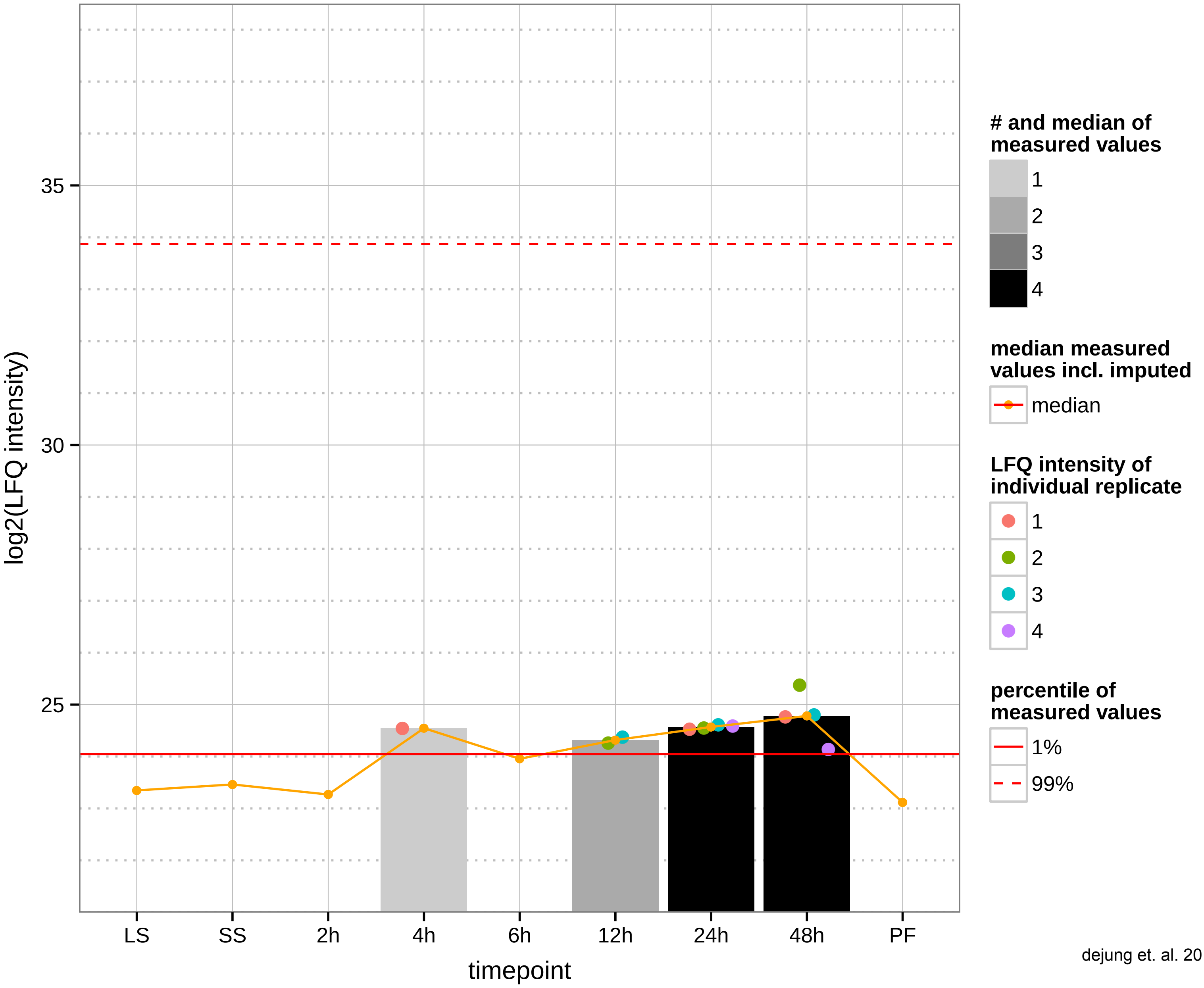




dejung et. al. 2015

tubulin–tyrosine ligase–like protein, conserved
Tb927.6.3570
AGOF: tubulin–tyrosine ligase activity
AGOC: null
AGOP: cellular protein modification process
PGOF: tubulin–tyrosine ligase activity
PGOC: null
PGOP: cellular protein modification process





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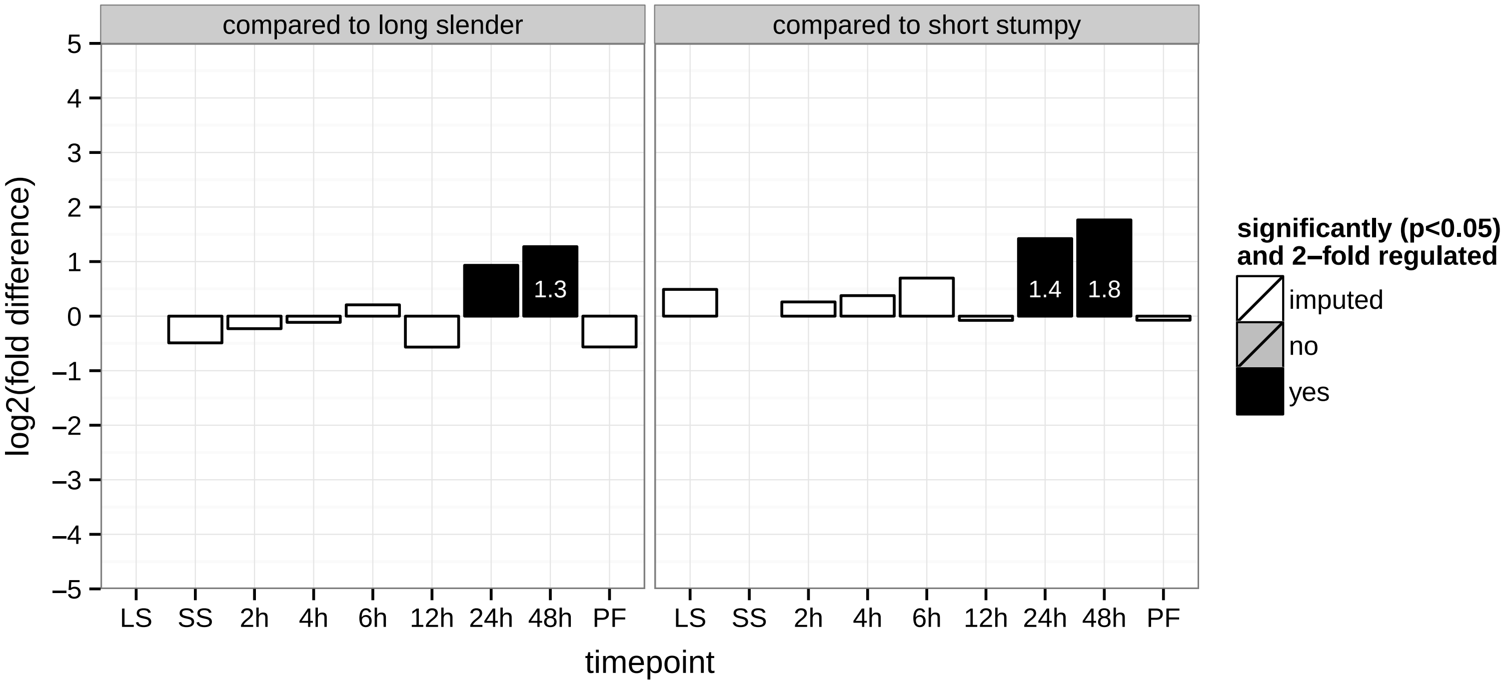
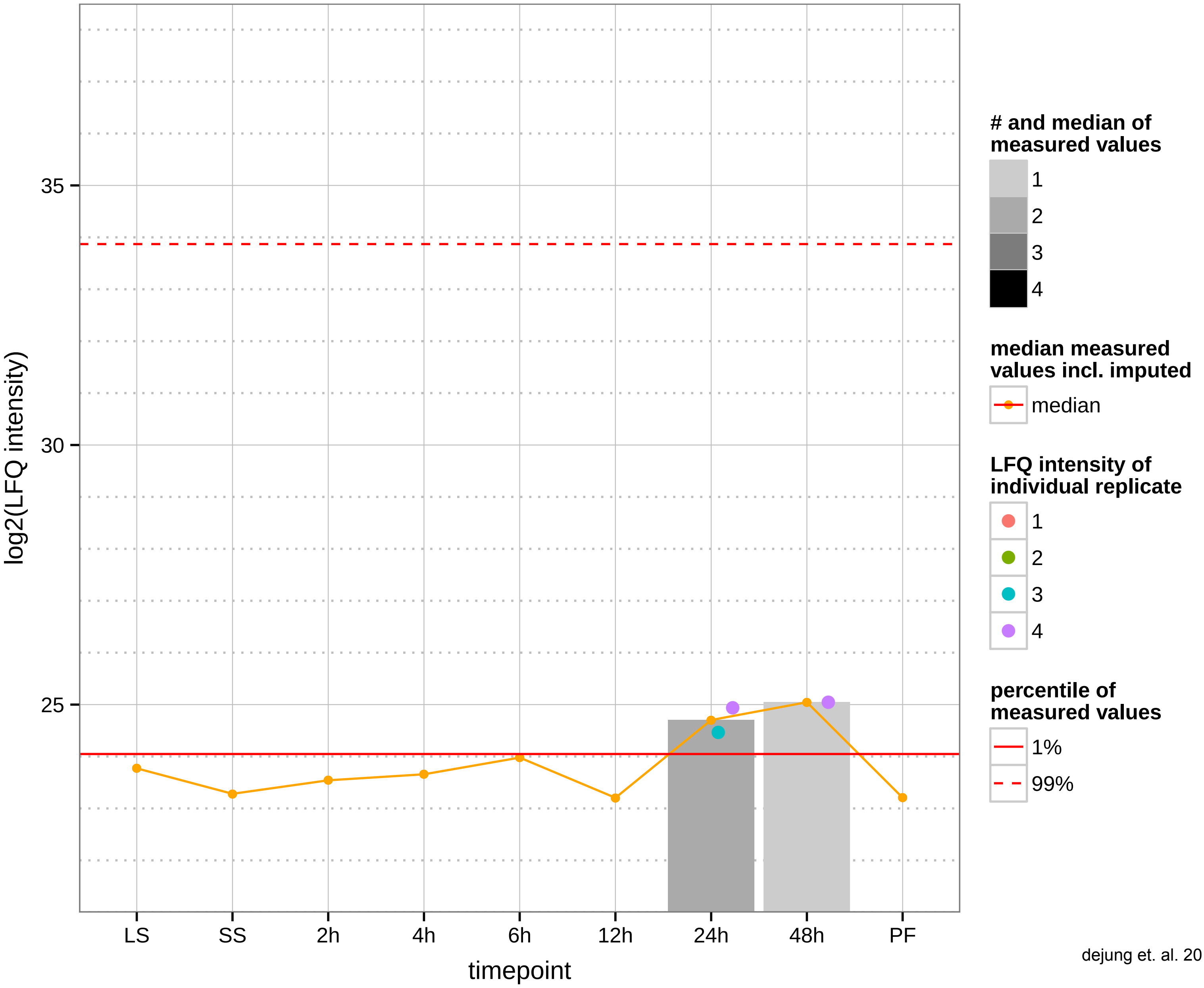
hypothetical protein, conserved
Tb927.6.3600
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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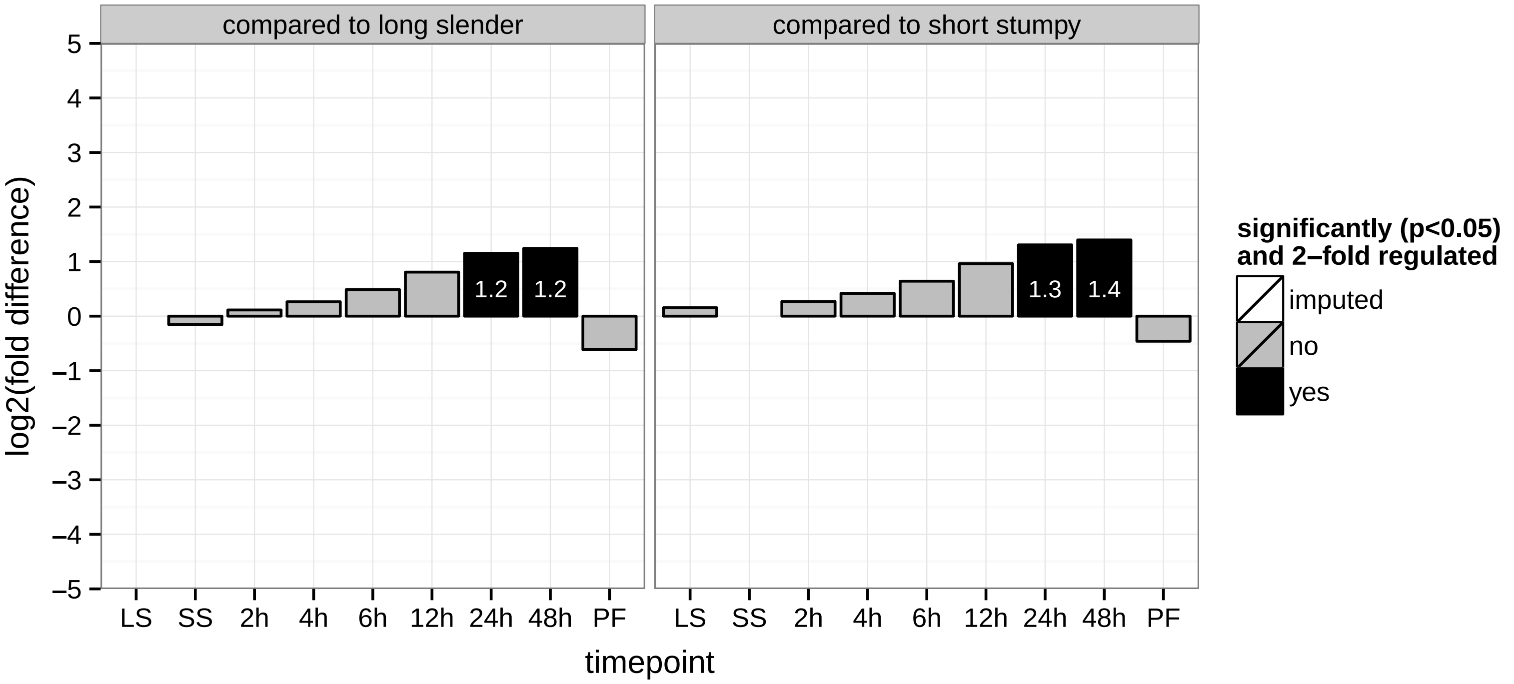
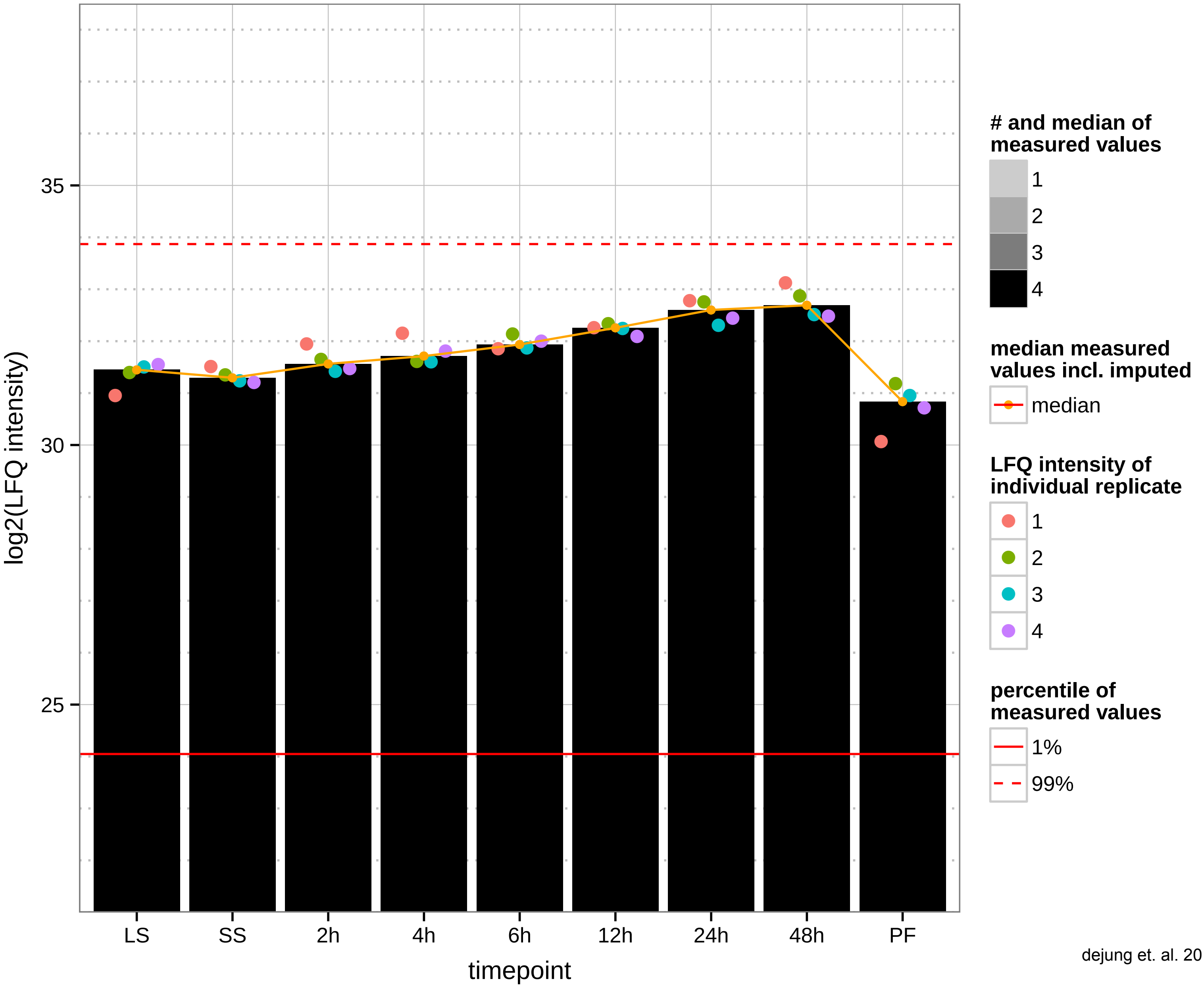
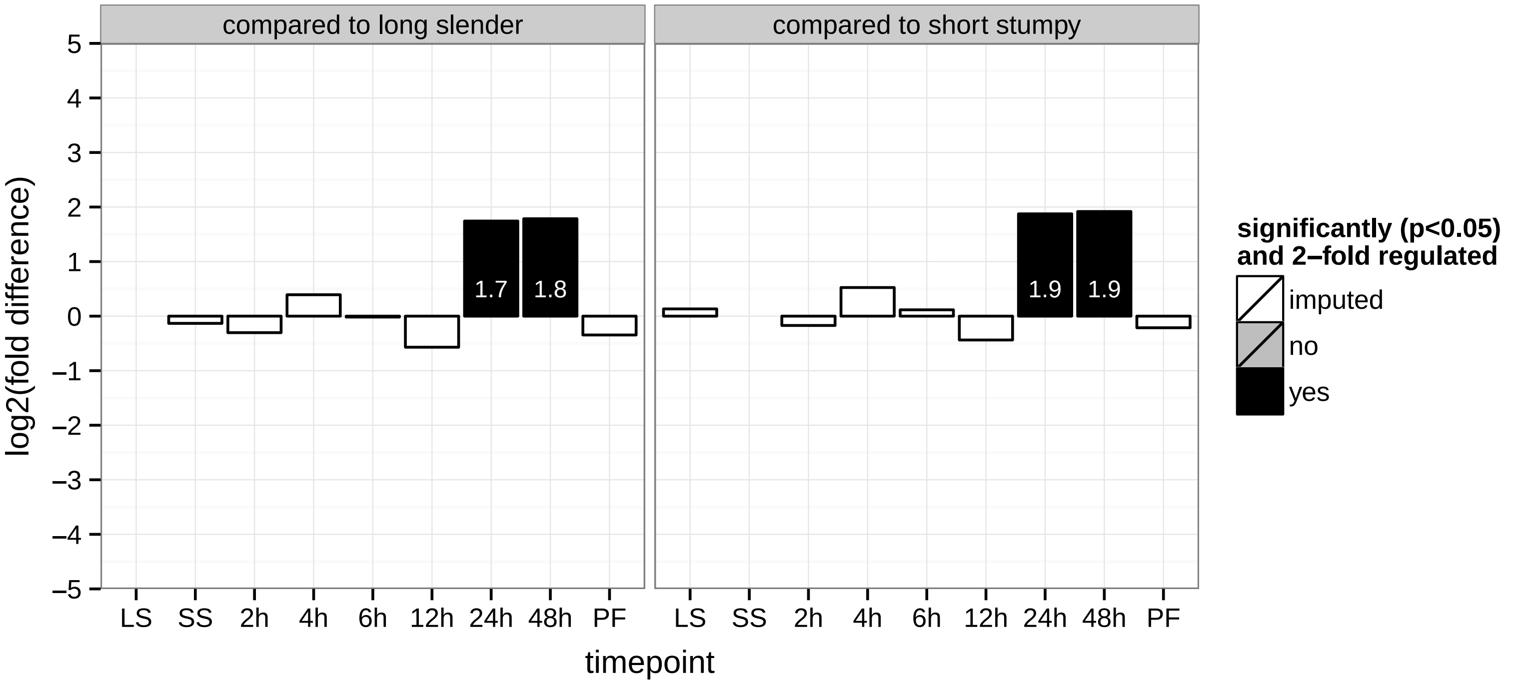
S–adenosylmethionine synthetase, putative (METK1)
Tb927.6.4920;Tb927.6.4910;Tb927.6.4900;Tb927.6.4880;Tb927.6.4860;Tb927.6.4850;Tb927.6.4840;Tb927.6.4890;Tb927.6
AGOF: ATP binding, methionine adenosyltransferase activity
AGOC: null
AGOP: one–carbon metabolic process
PGOF: null, ATP binding, methionine adenosyltransferase activity
PGOC: null
PGOP: null, S–adenosylmethionine biosynthetic process

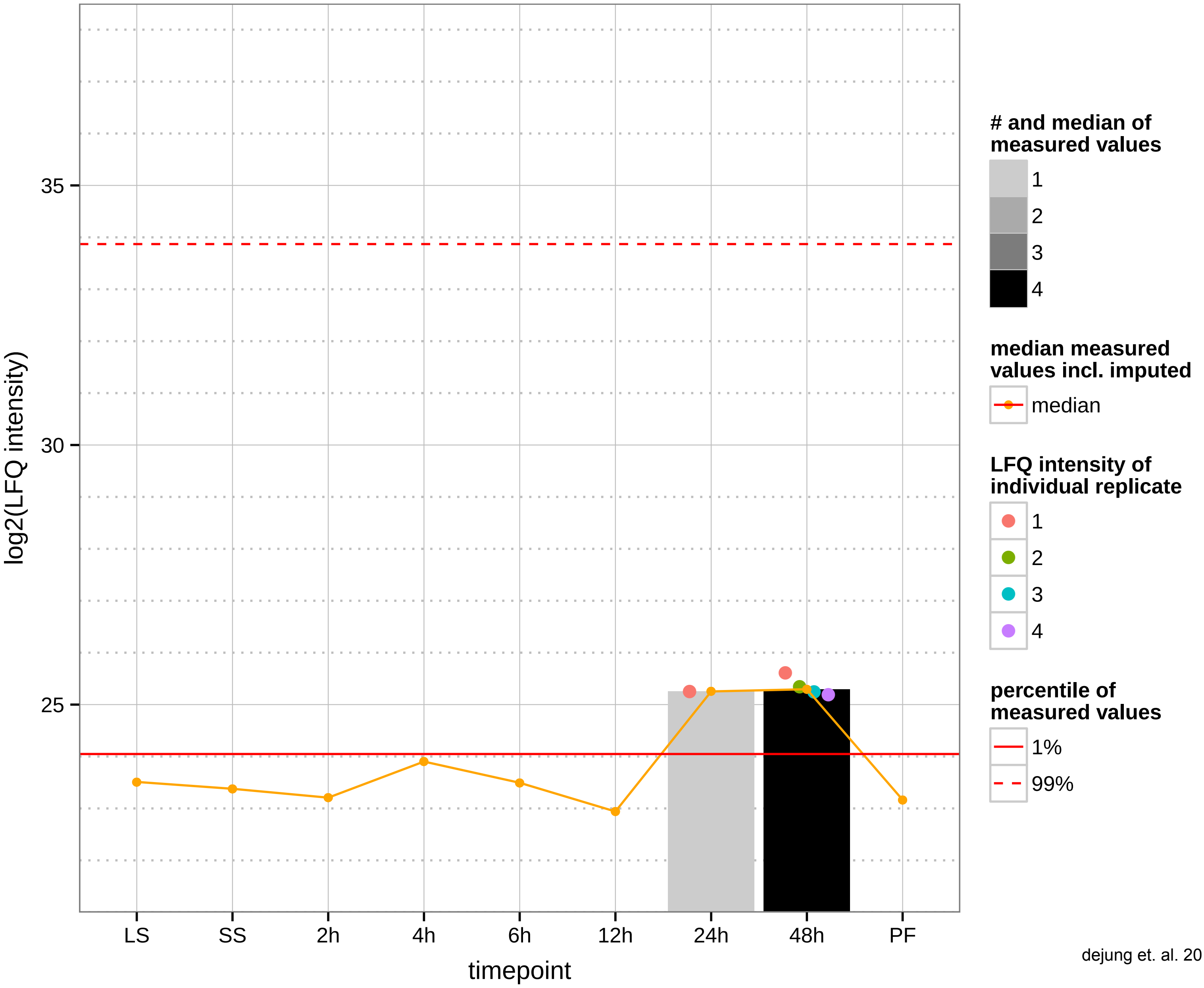




dejung et. al. 2015

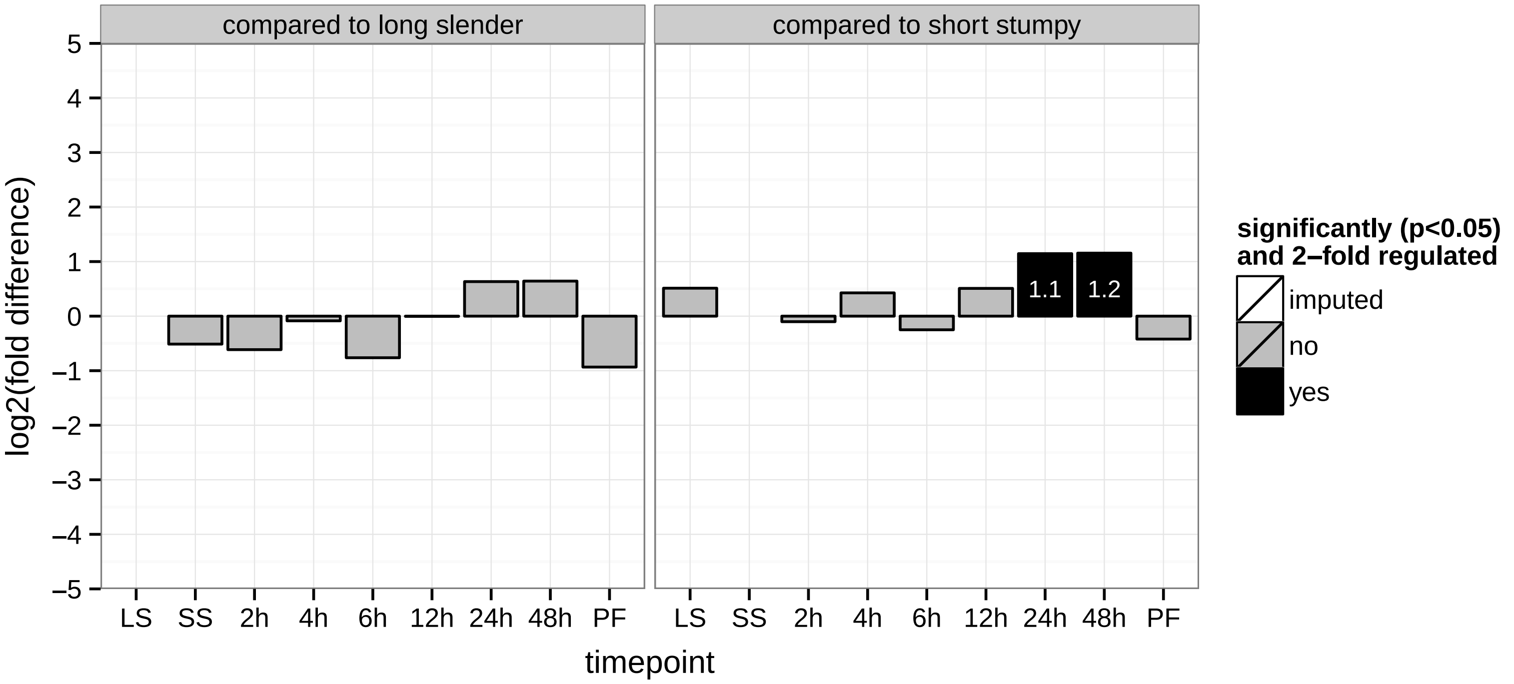
Zinc finger CCCH domain−containing protein 47 (zc3h47)
Tb927.6.4960
AGOF: RNA binding, nucleic acid binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null

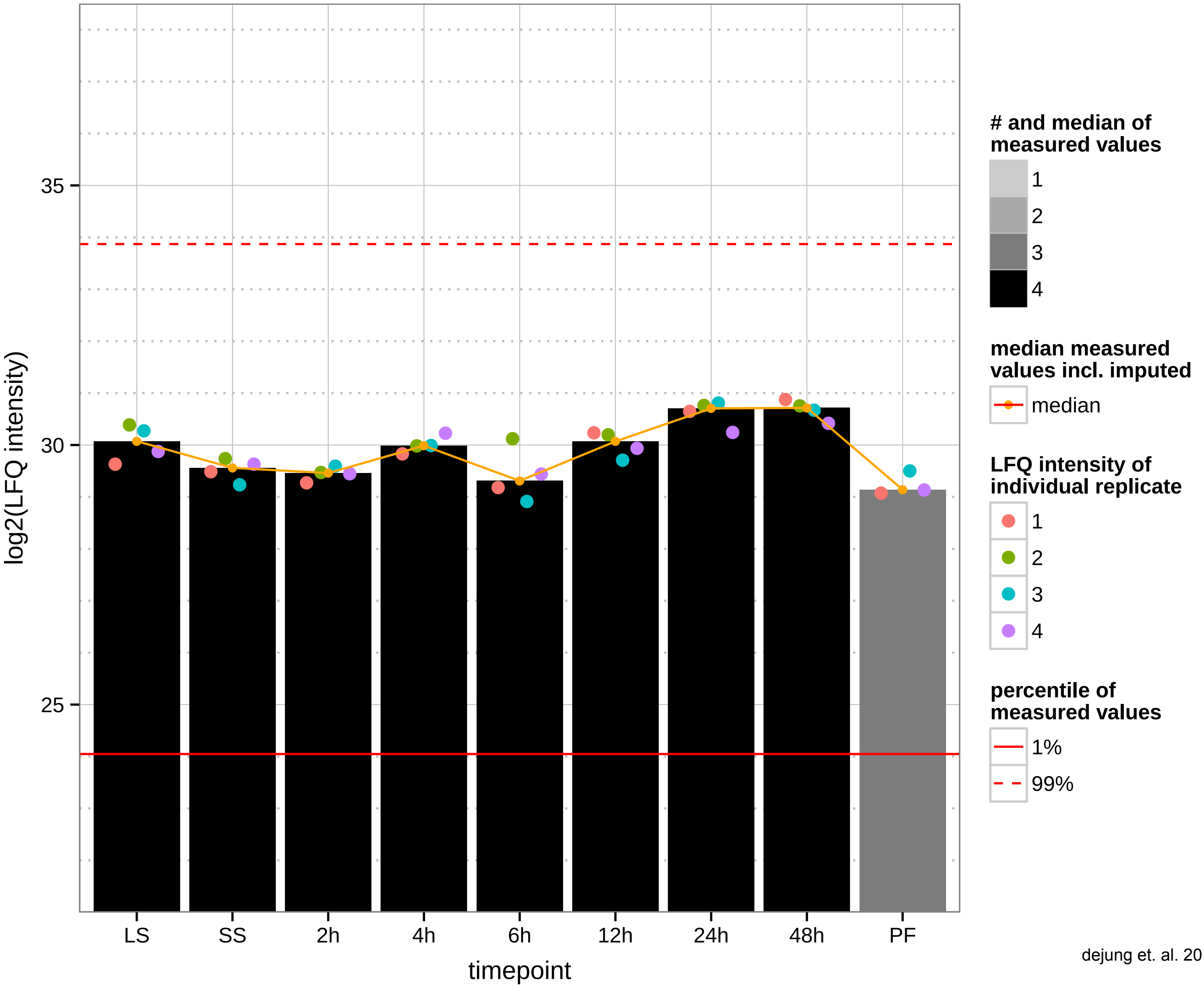




dejung et. al. 2015

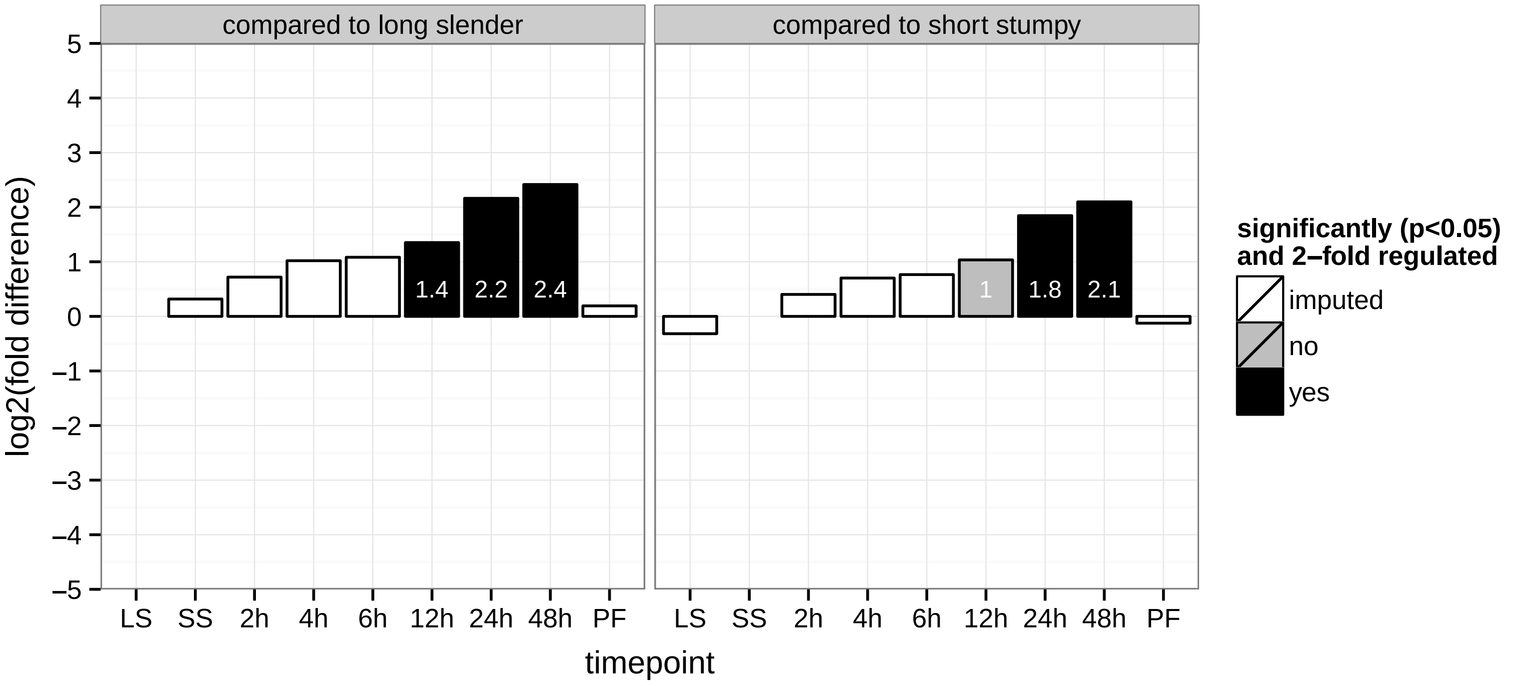
40S ribosomal protein S33, putative
Tb927.7.240;Tb927.7.230
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: null, structural constituent of ribosome
PGOC: null, intracellular, ribosome
PGOP: null, translation

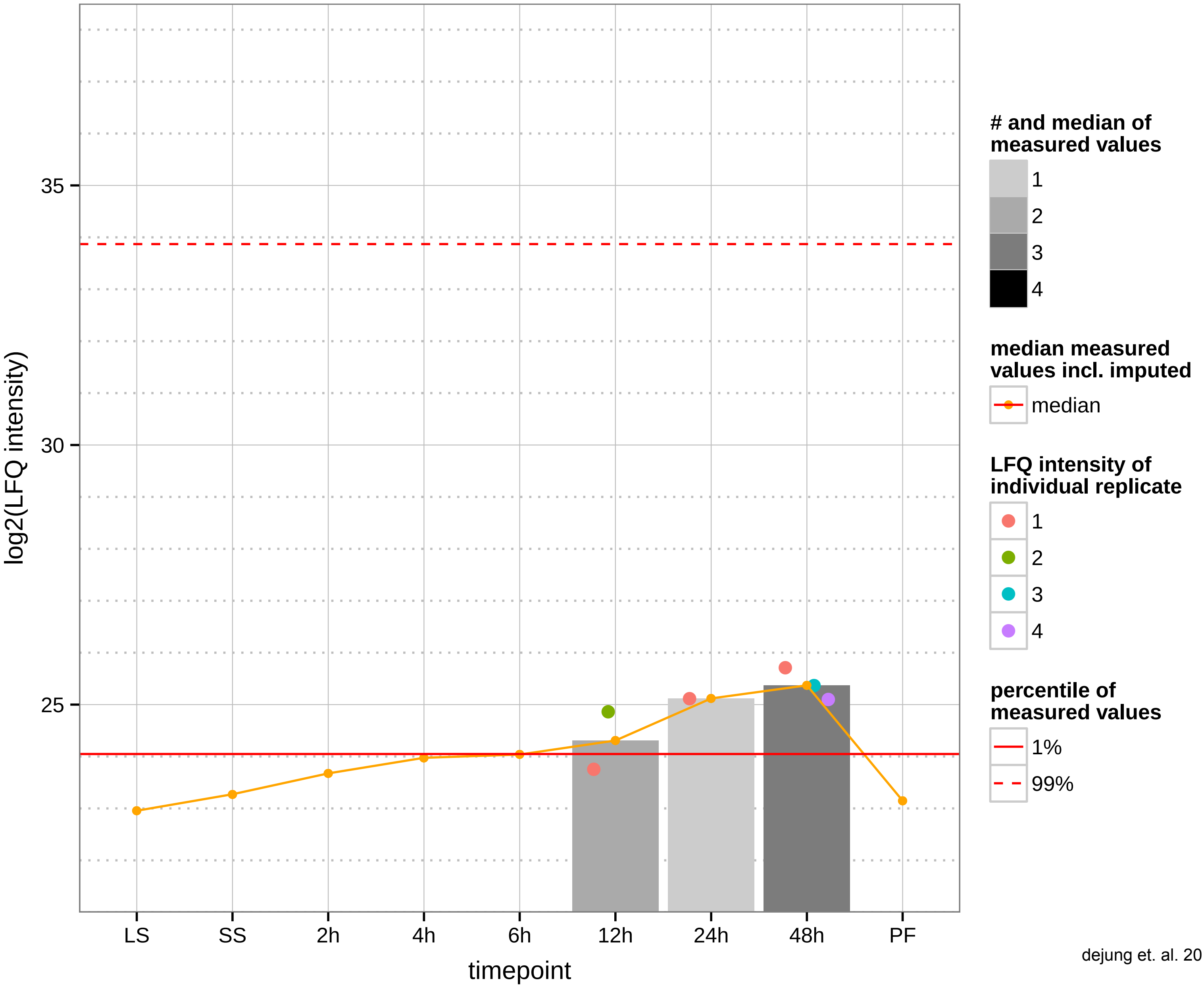




dejung et. al. 2015

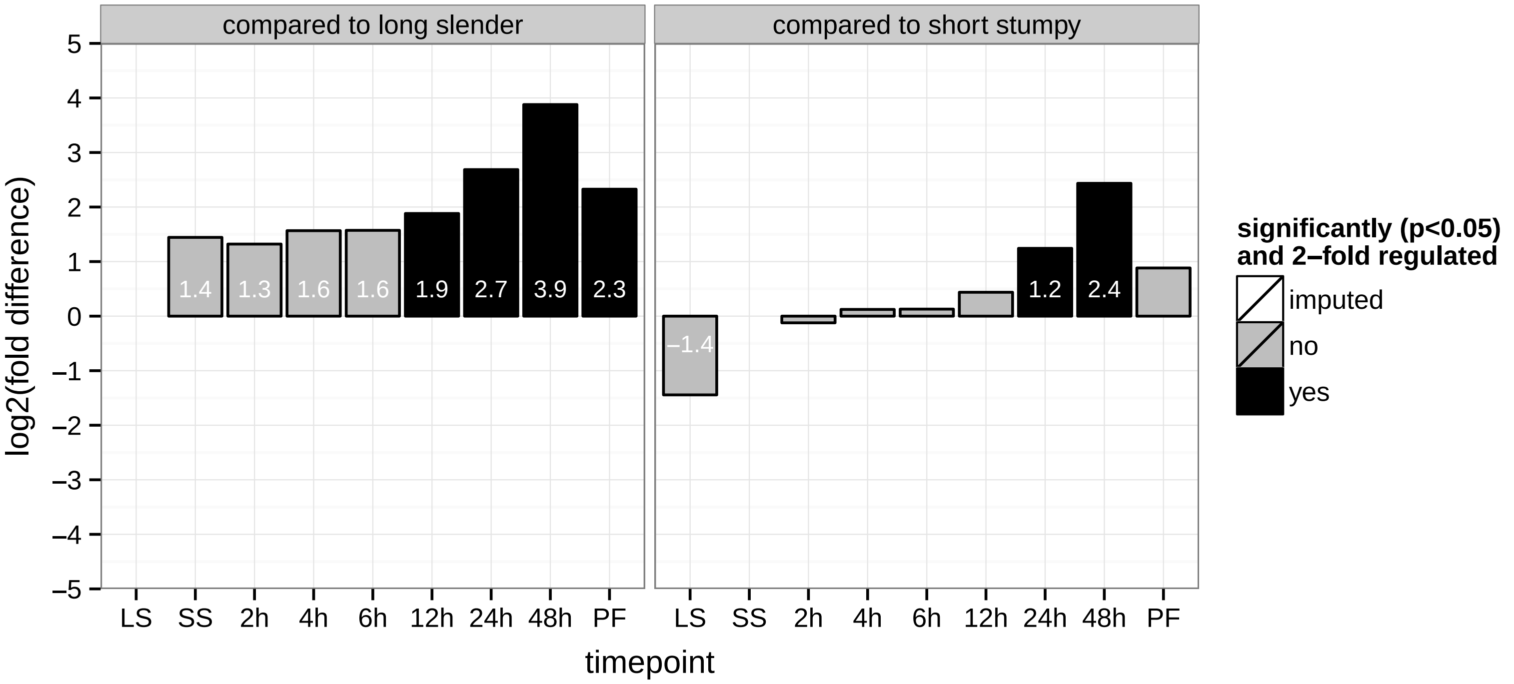
hypothetical protein, conserved
Tb927.7.7130
AGOF: FMN binding, iron–sulfur cluster binding, oxidoreductase activity
AGOC: null
AGOP: null
PGOF: FMN binding, catalytic activity, iron–sulfur cluster binding, oxidoreductase activity
PGOC: null
PGOP: null

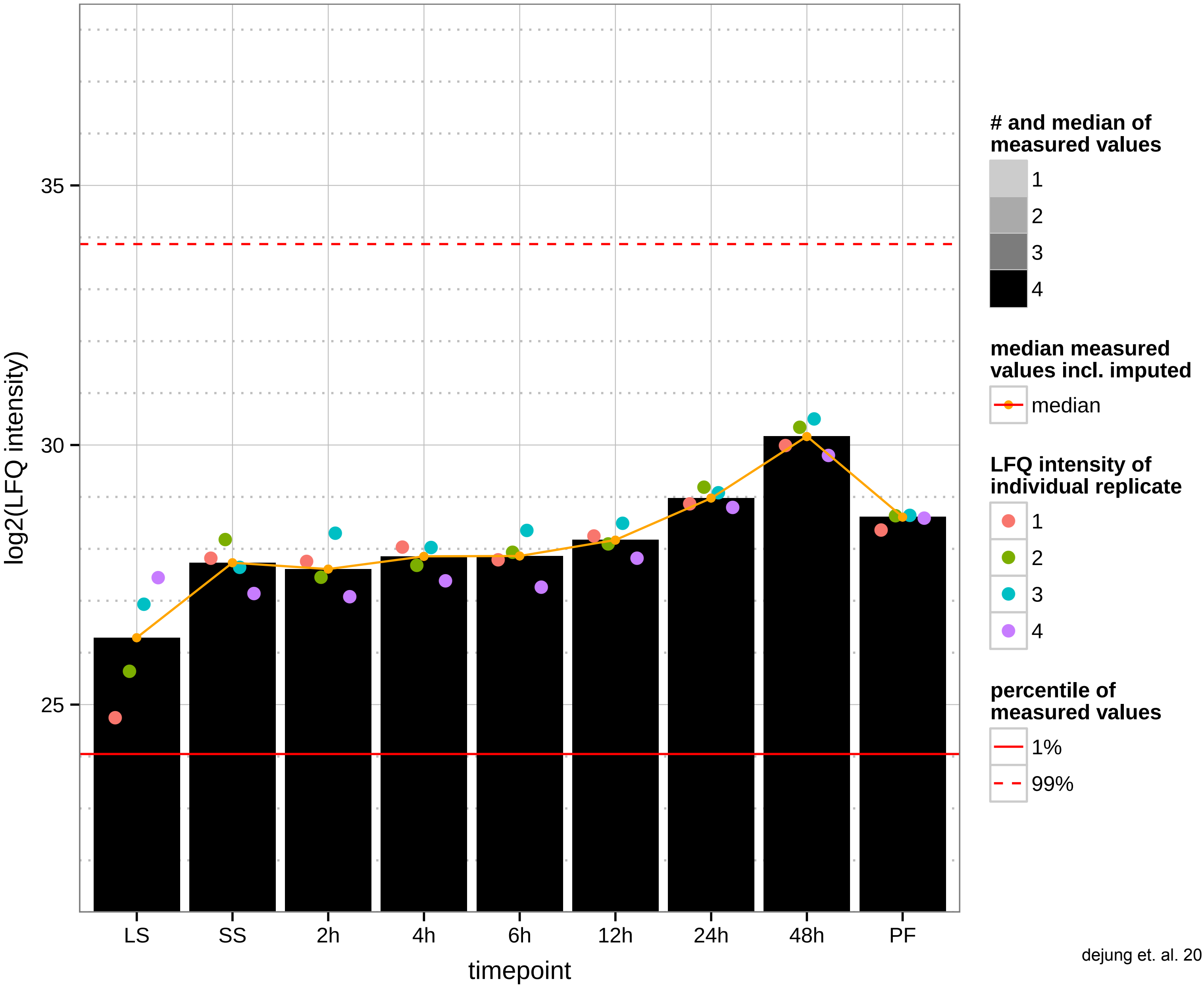




dejung et. al. 2015

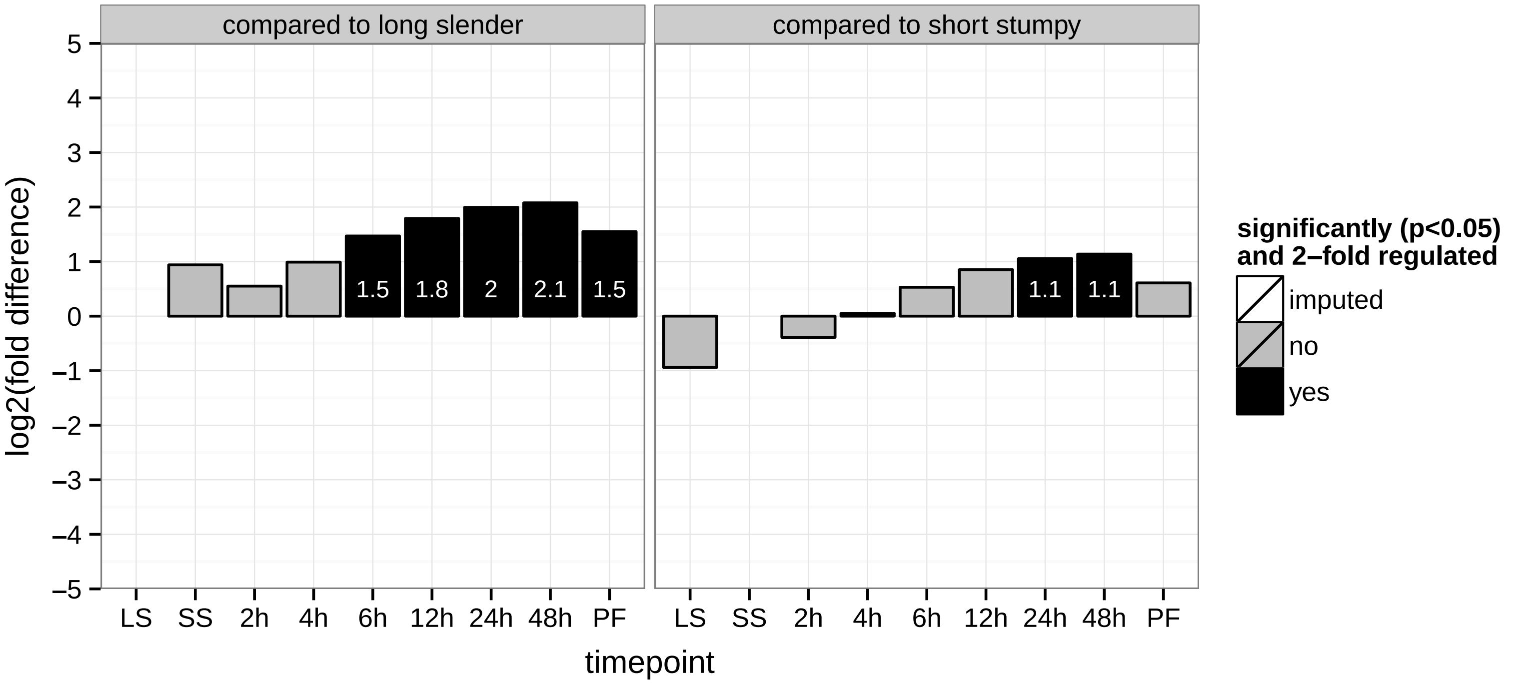
thymine−7−hydroxylase, putative (TLP7)
Tb927.7.7500
AGOF: ferrous iron binding, oxidoreductase activity
AGOC: null
AGOP: metabolic process
PGOF: oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular o
PGOC: null
PGOP: oxidation−reduction process

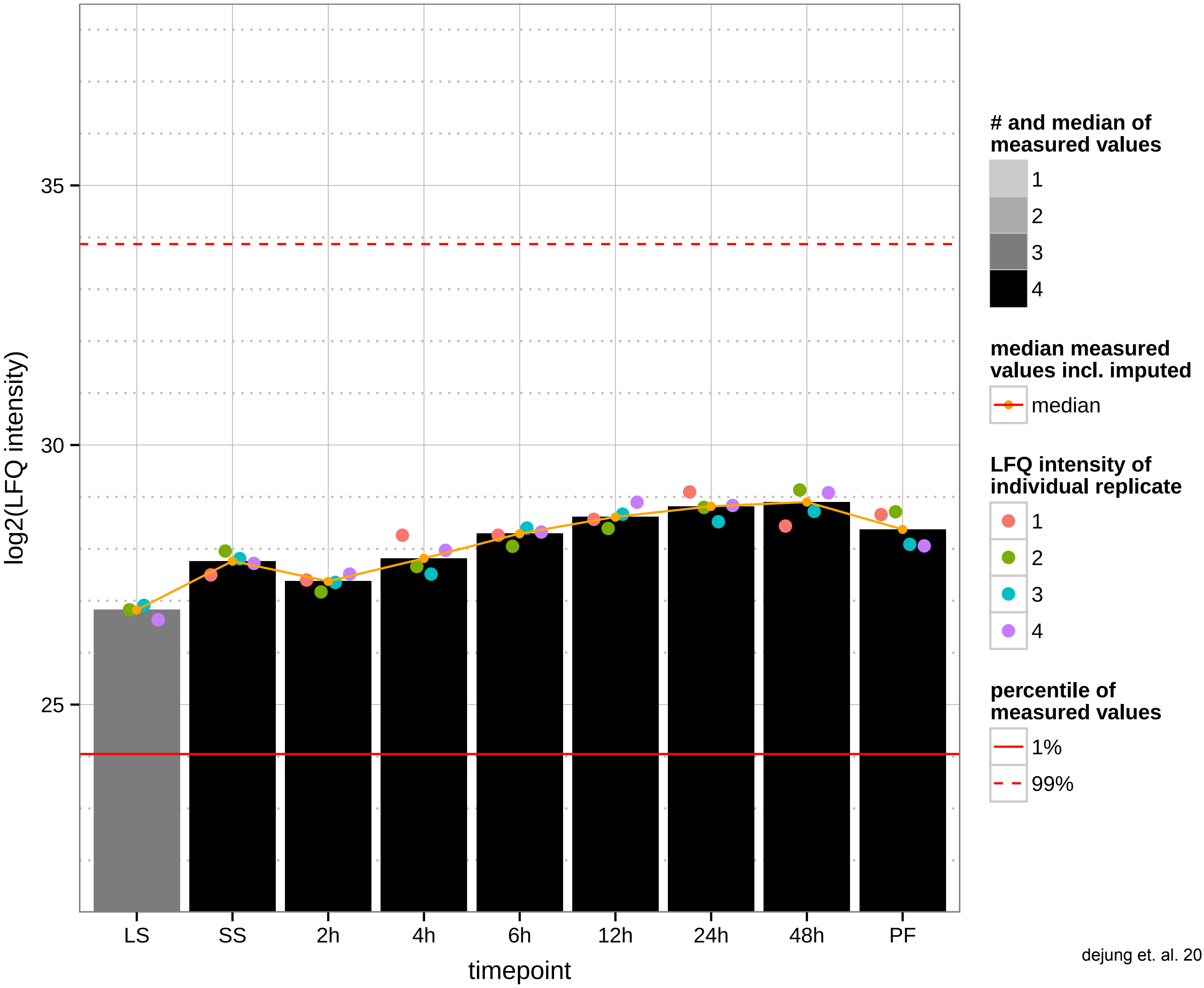




dejung et. al. 2015

conserved protein
Tb927.8.1270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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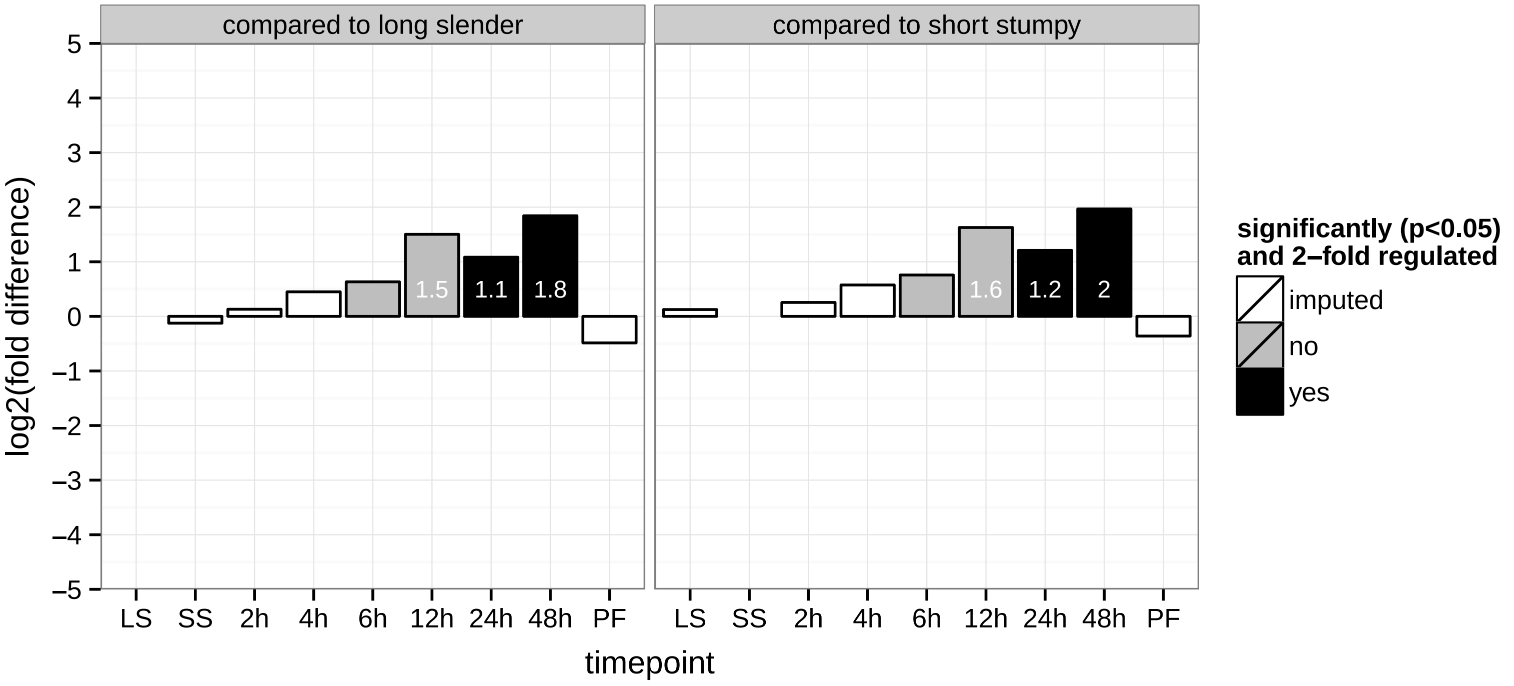
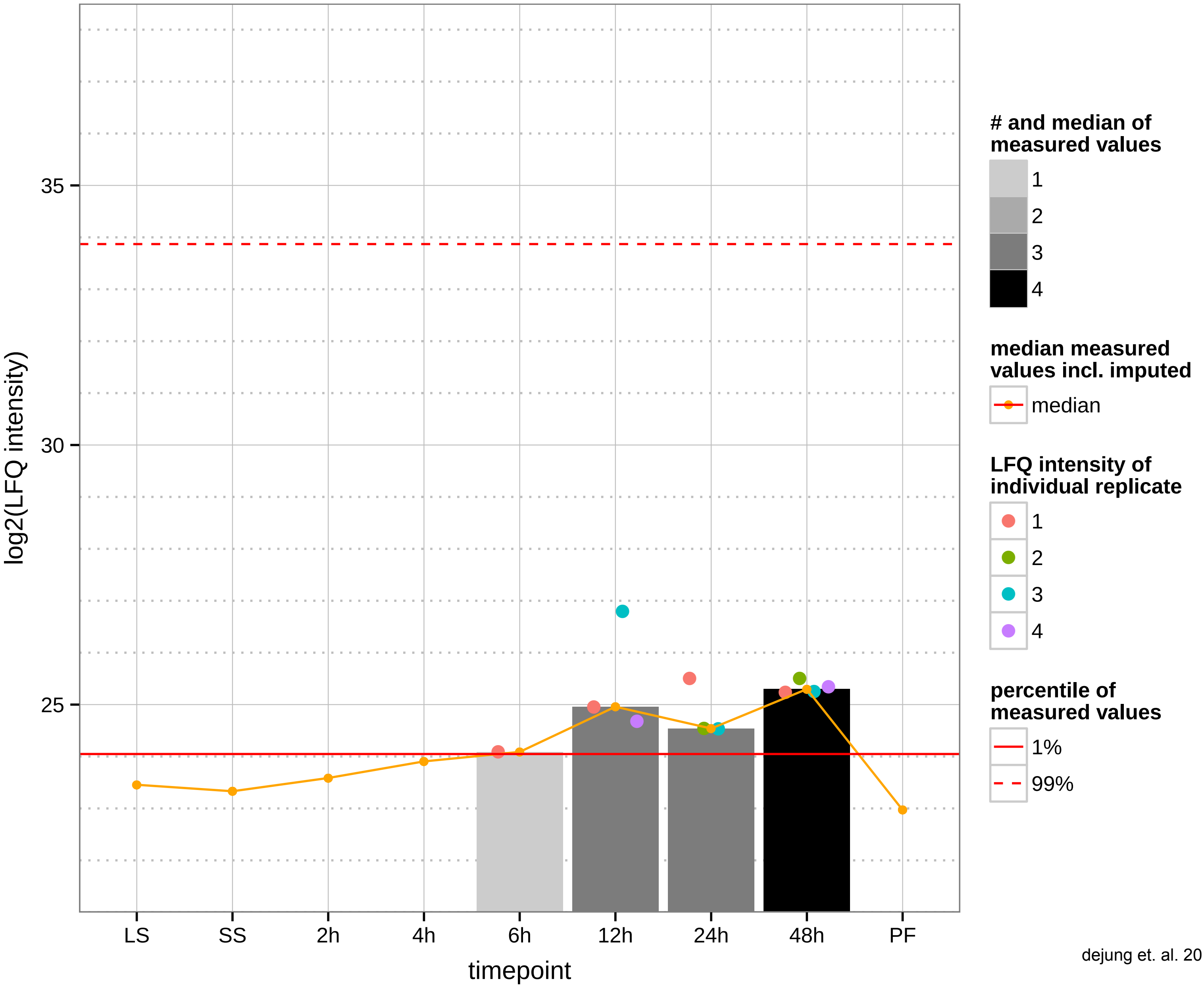
hypothetical protein, conserved
Tb927.8.3050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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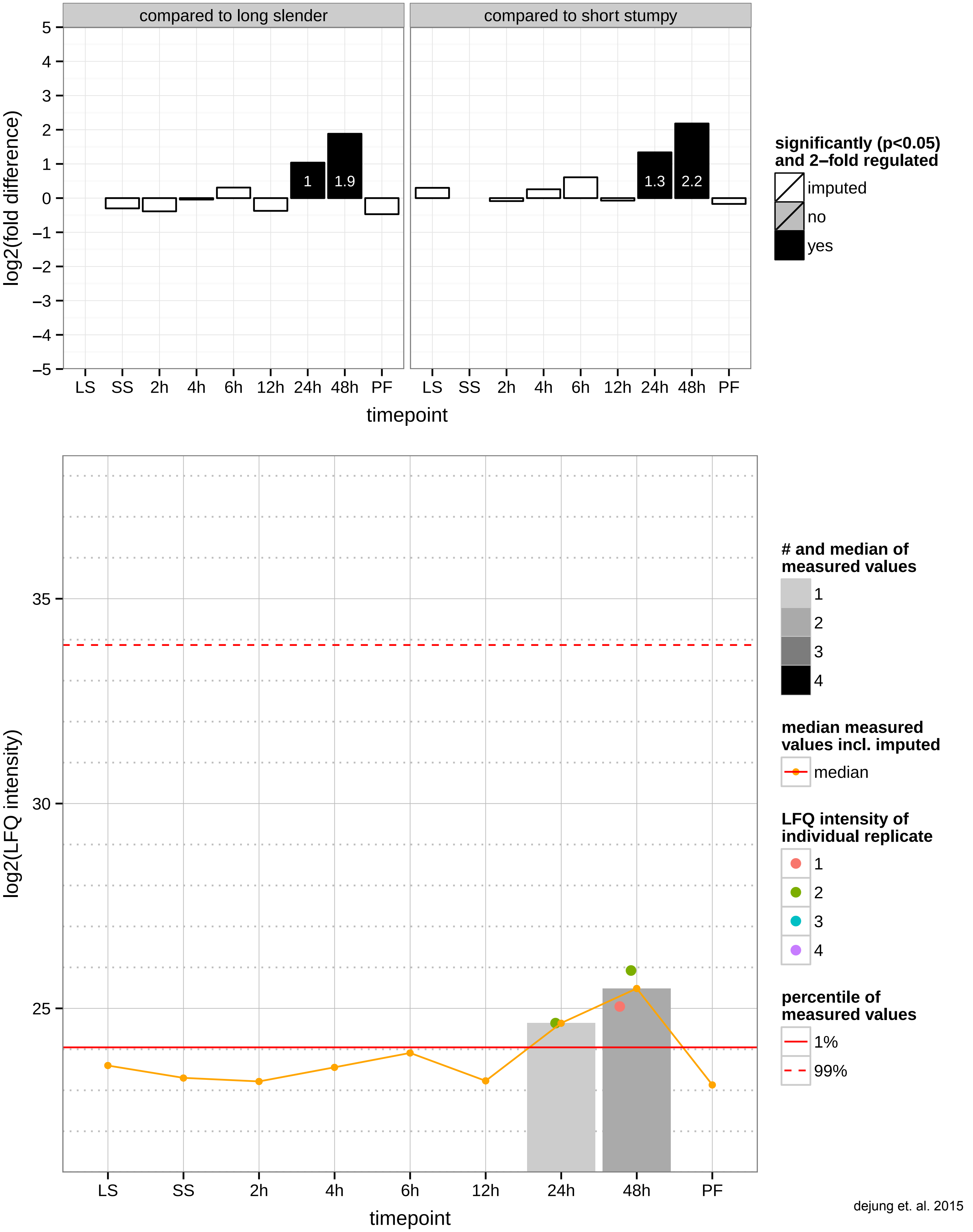
hypothetical protein, conserved
Tb927.8.3540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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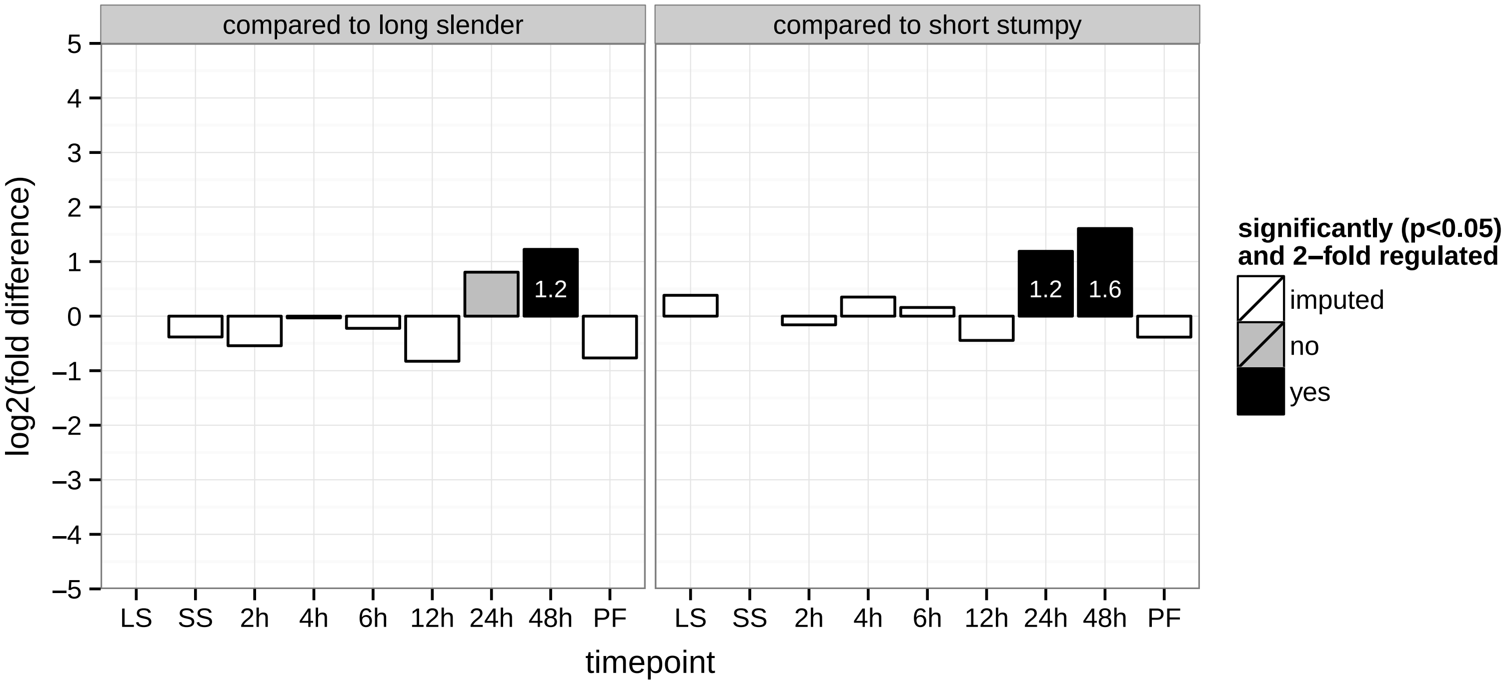
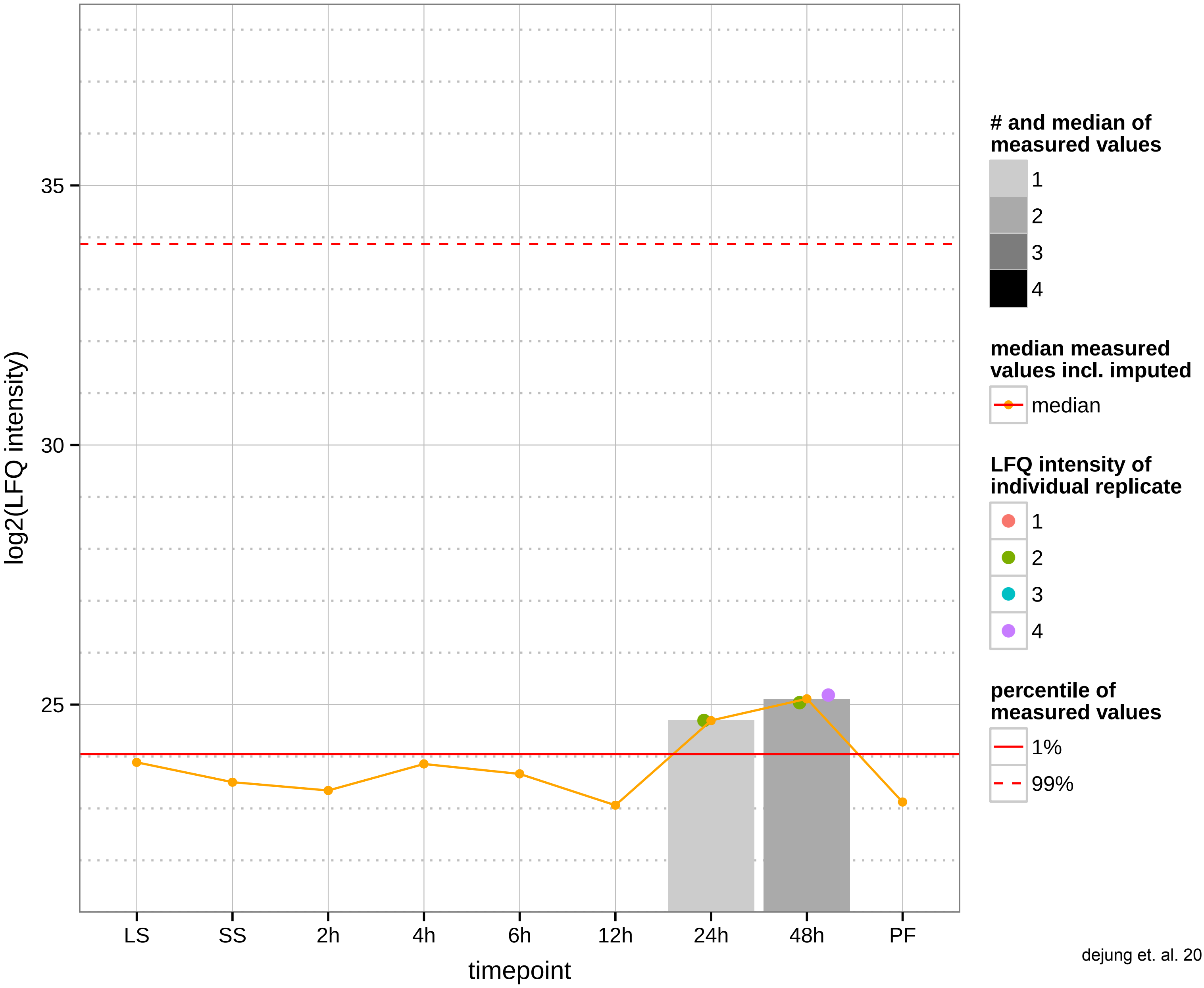
hypothetical protein, conserved
Tb927.8.4550
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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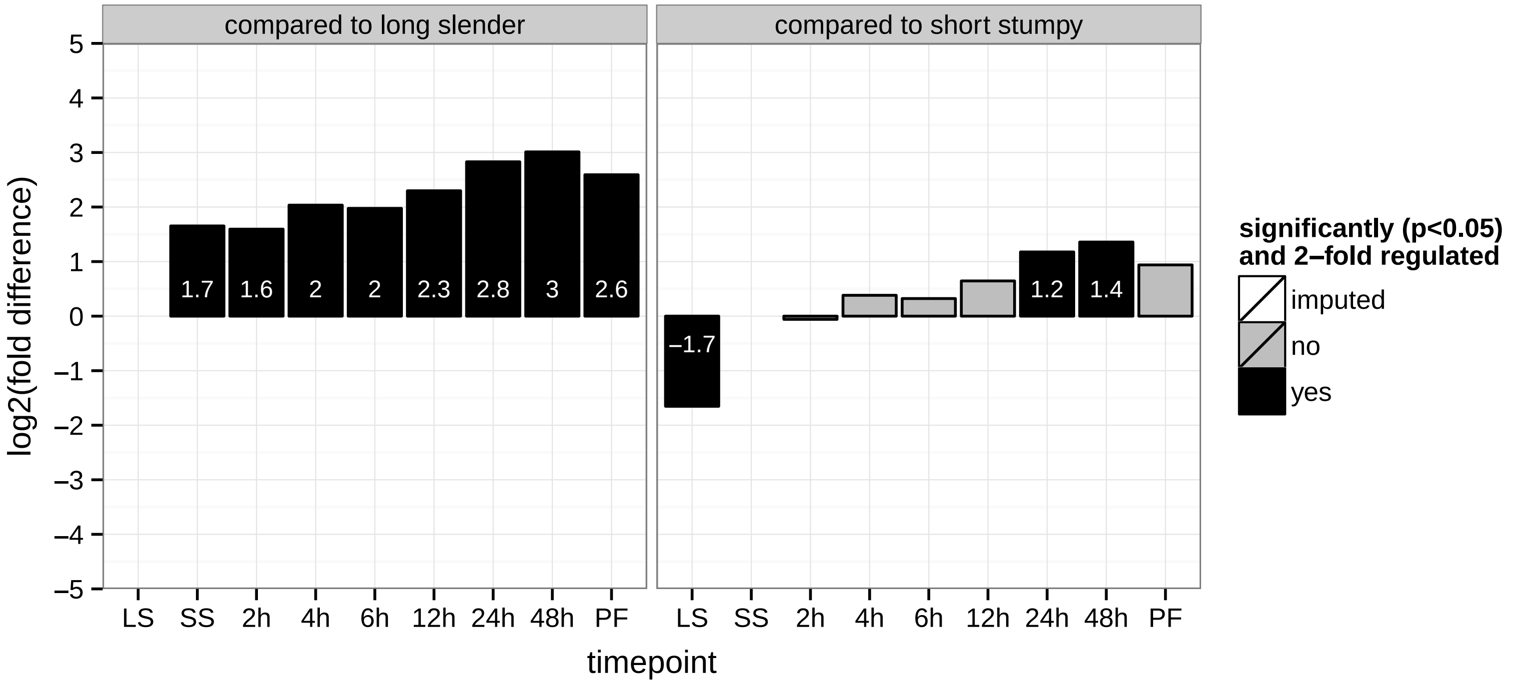
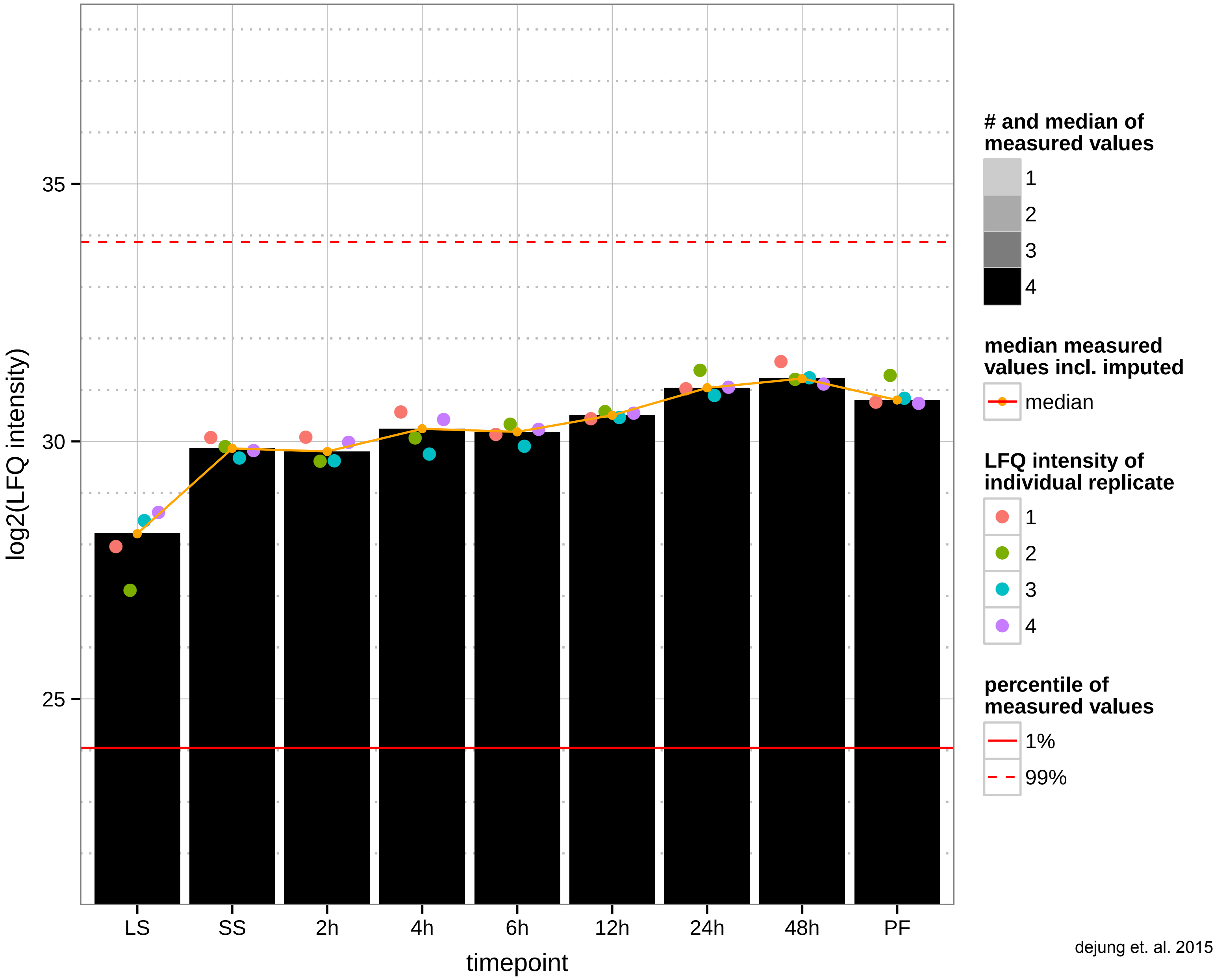
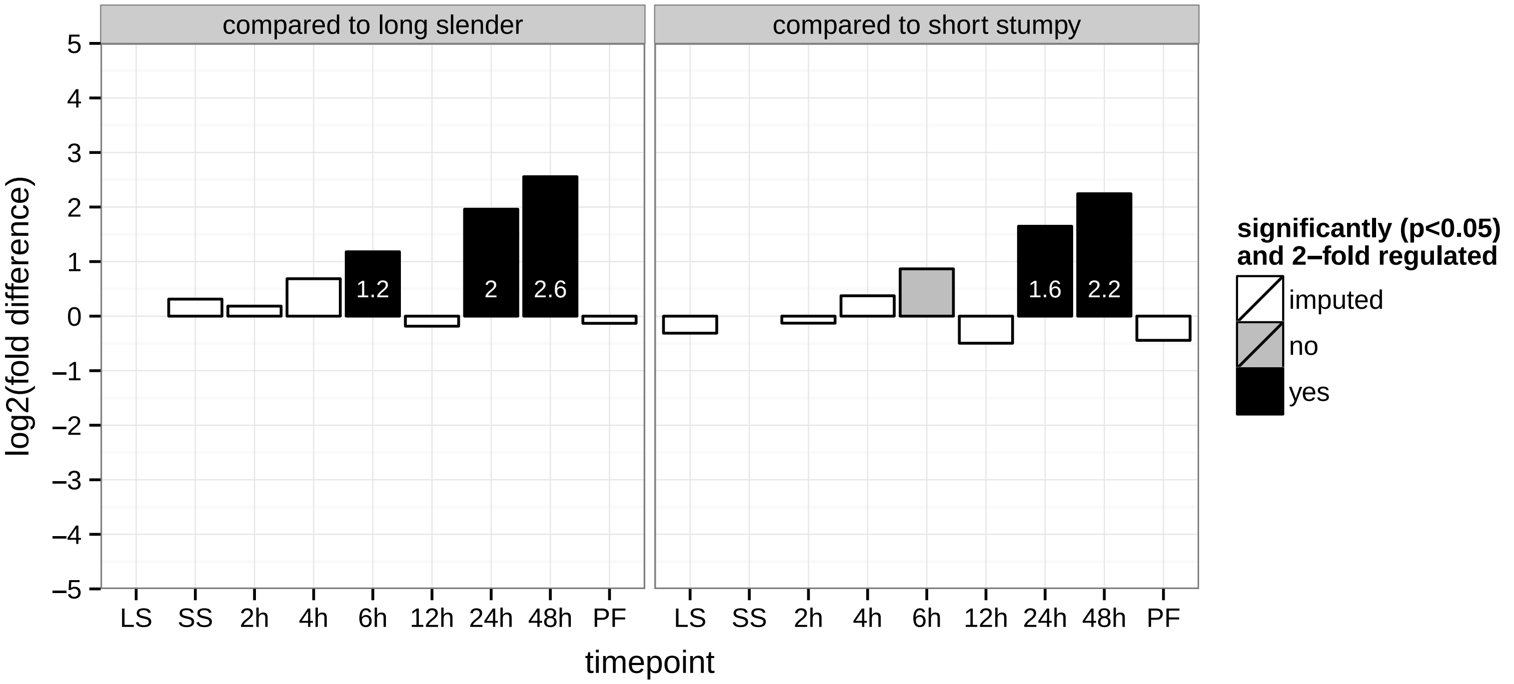
prohibitin 1 (PHB1)
Tb927.8.4810
AGOF: null
AGOC: membrane, mitochondrion
AGOP: mitochondrion organization, regulation of cell cycle, regulation of mitochondrial membrane potential, regulation of mito
PGOF: null
PGOC: null
PGOP: null

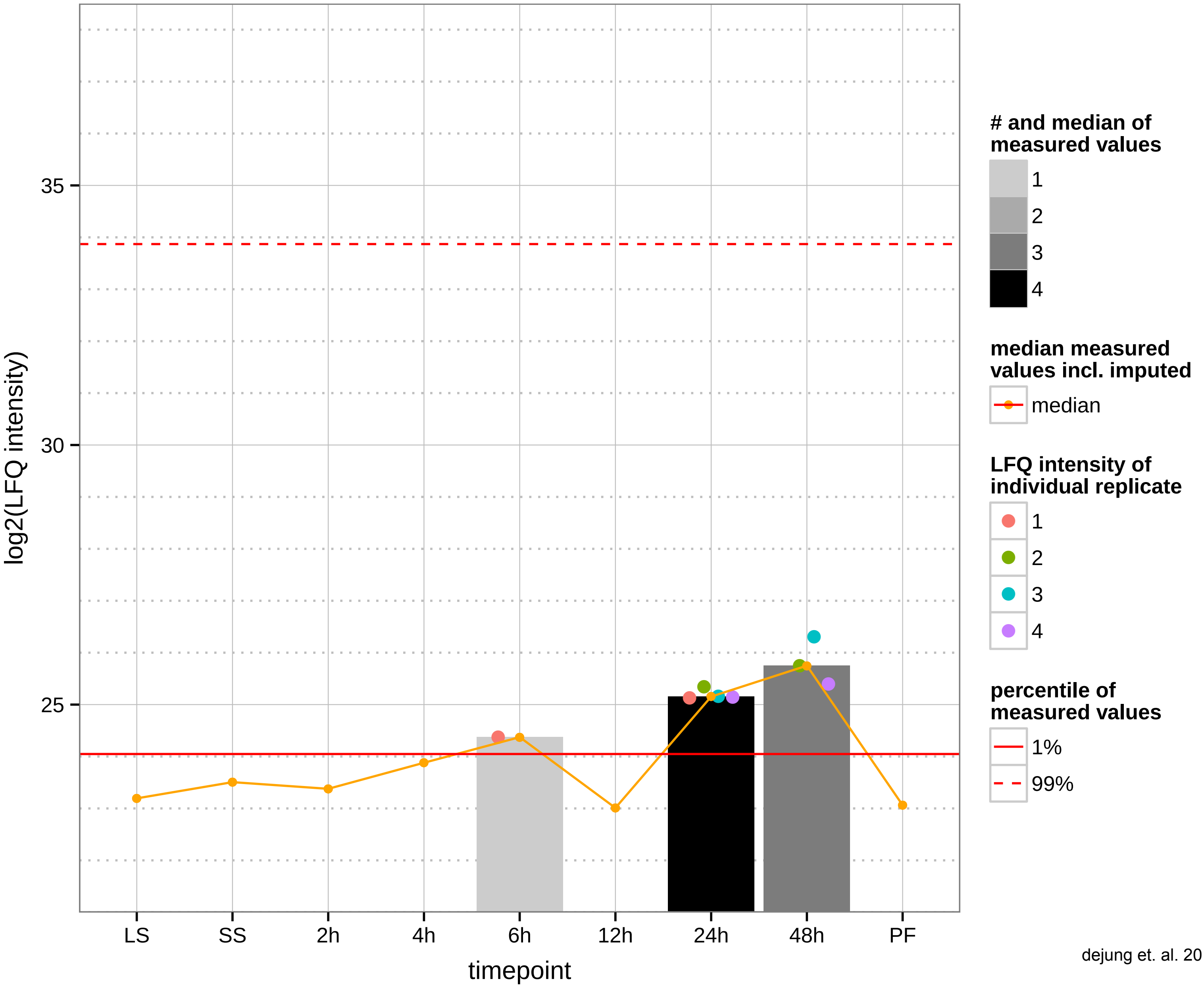




dejung et. al. 2015

50S ribosomal protein L17, putative
Tb927.8.5860
AGOF: structural constituent of ribosome
AGOC: intracellular, mitochondrion, organellar large ribosomal subunit, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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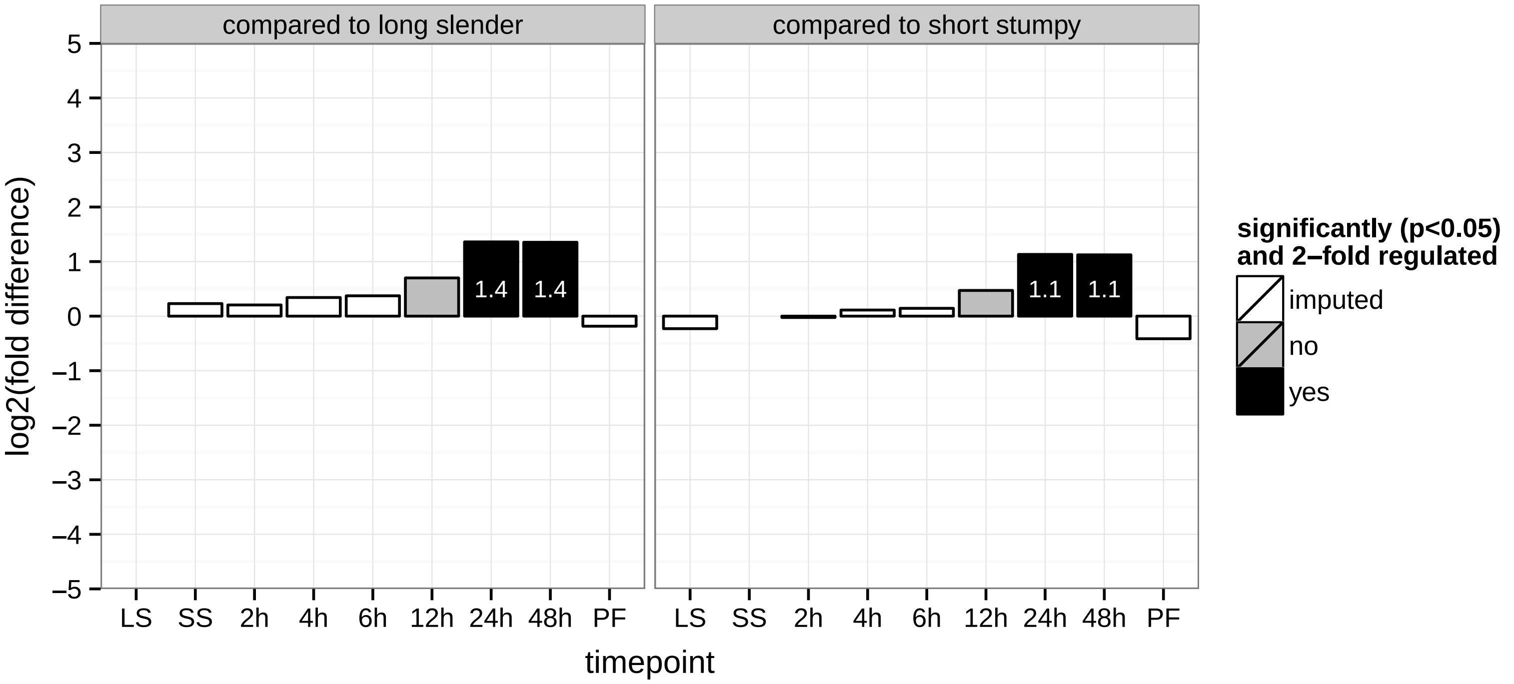
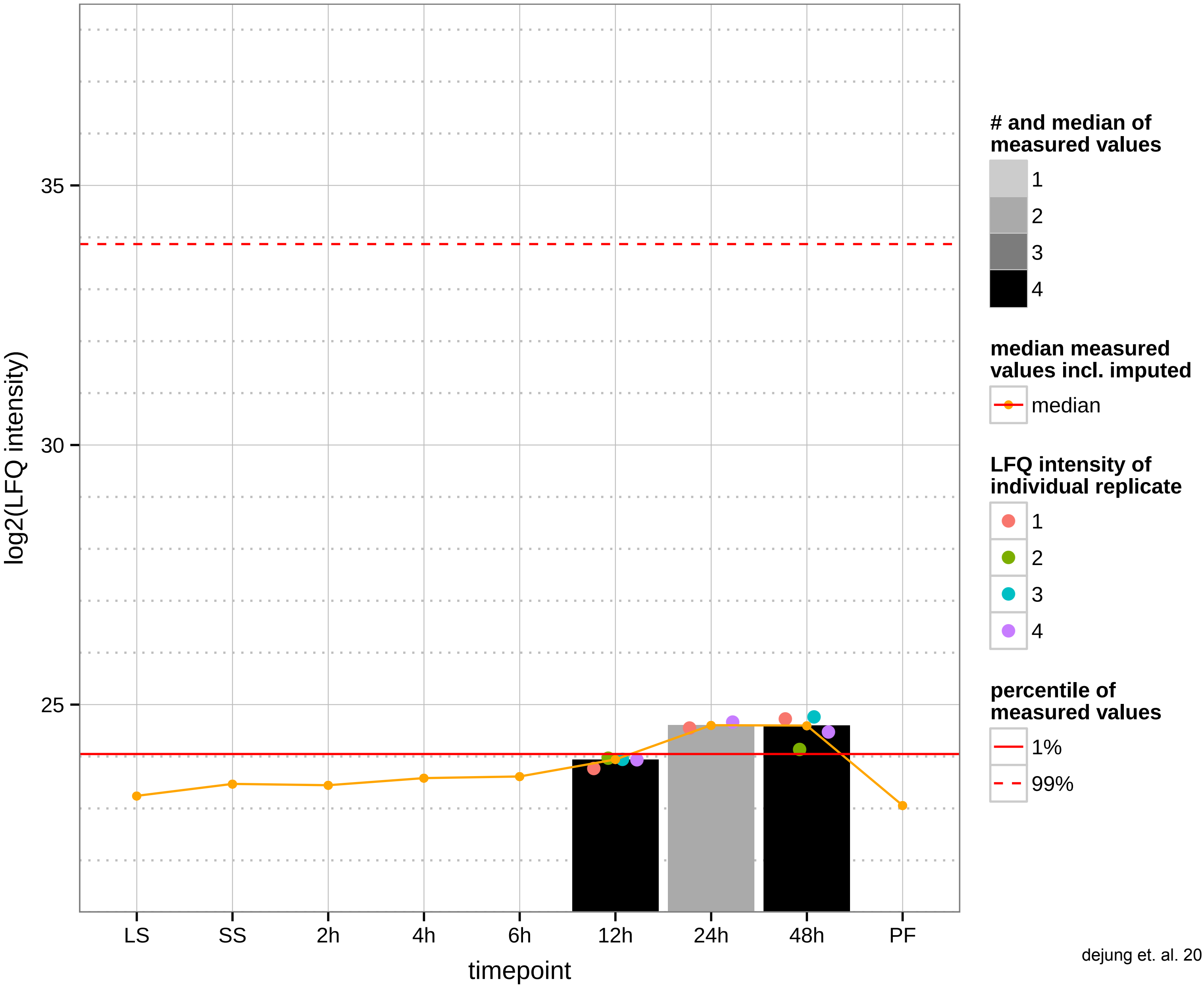
TFIIH basal transcription factor complex helicase subunit, putative, DNA excision repair protein, Transcription factor II H comp
Tb927.8.5980
AGOF: 5'−3' DNA helicase activity, ATP binding, ATP−dependent DNA helicase activity, sequence−specific DNA binding trans
AGOC: holo TFIIH complex
AGOP: DNA repair, mRNA transcription from RNA polymerase II promoter, nucleotide−excision repair
PGOF: ATP binding, ATP−dependent DNA helicase activity, ATP−dependent helicase activity, DNA binding, hydrolase activity,
PGOC: nucleus
PGOP: nucleobase−containing compound metabolic process





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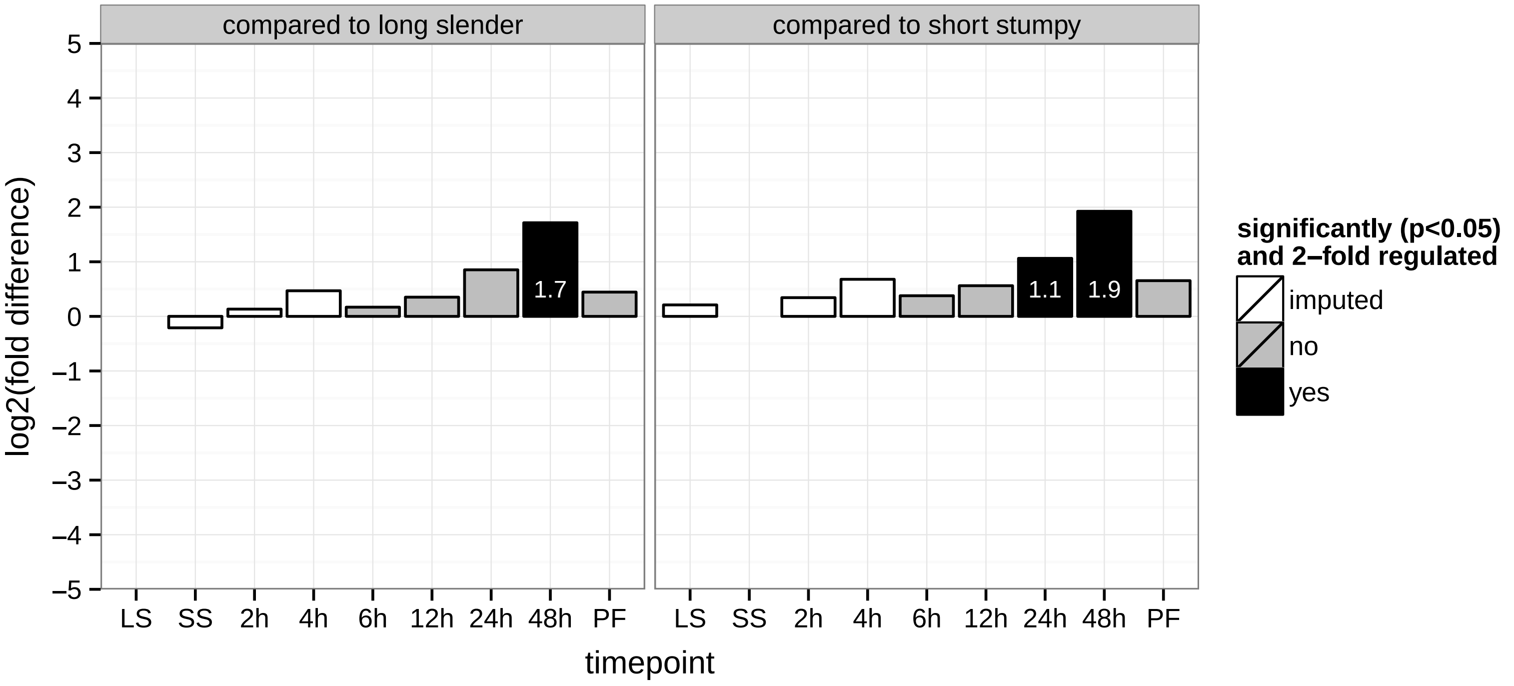
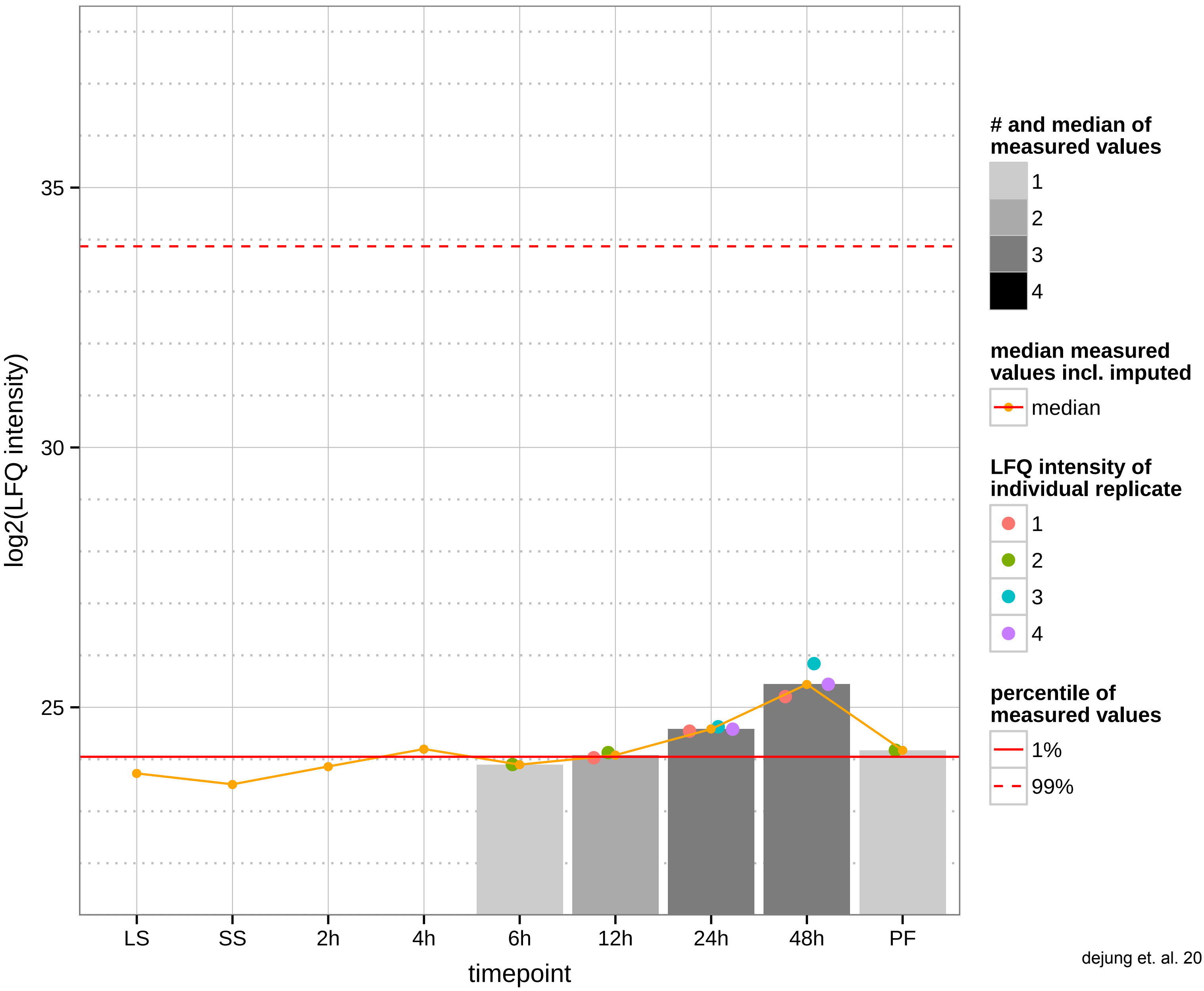
DNA polymerase epsilon catalytic subunit, putative
Tb927.9.10440
AGOF: DNA binding, DNA−directed DNA polymerase activity, nucleotide binding, zinc ion binding
AGOC: nucleus
AGOP: DNA−dependent DNA replication
PGOF: DNA binding, DNA−directed DNA polymerase activity, nucleic acid binding, nucleotide binding, zinc ion binding
PGOC: nucleus
PGOP: DNA replication, nucleobase−containing compound metabolic process





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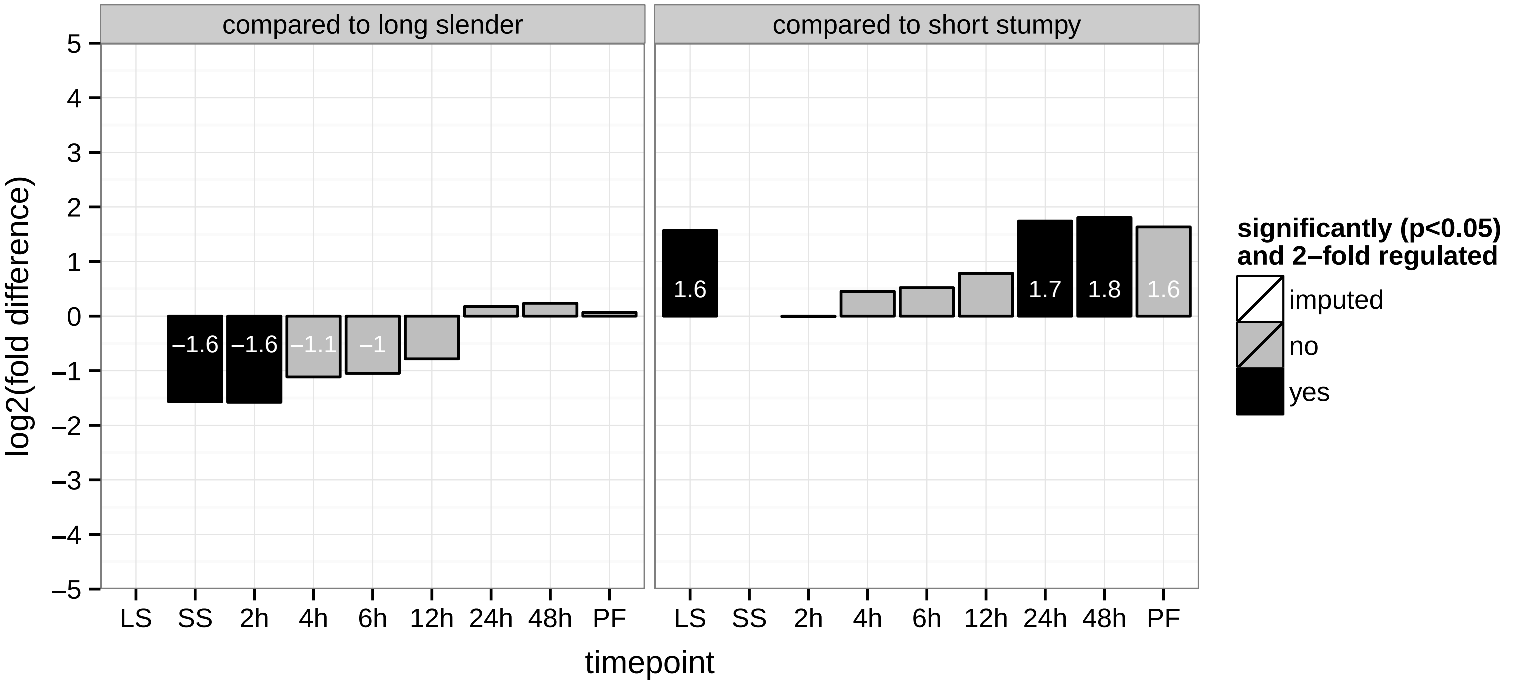
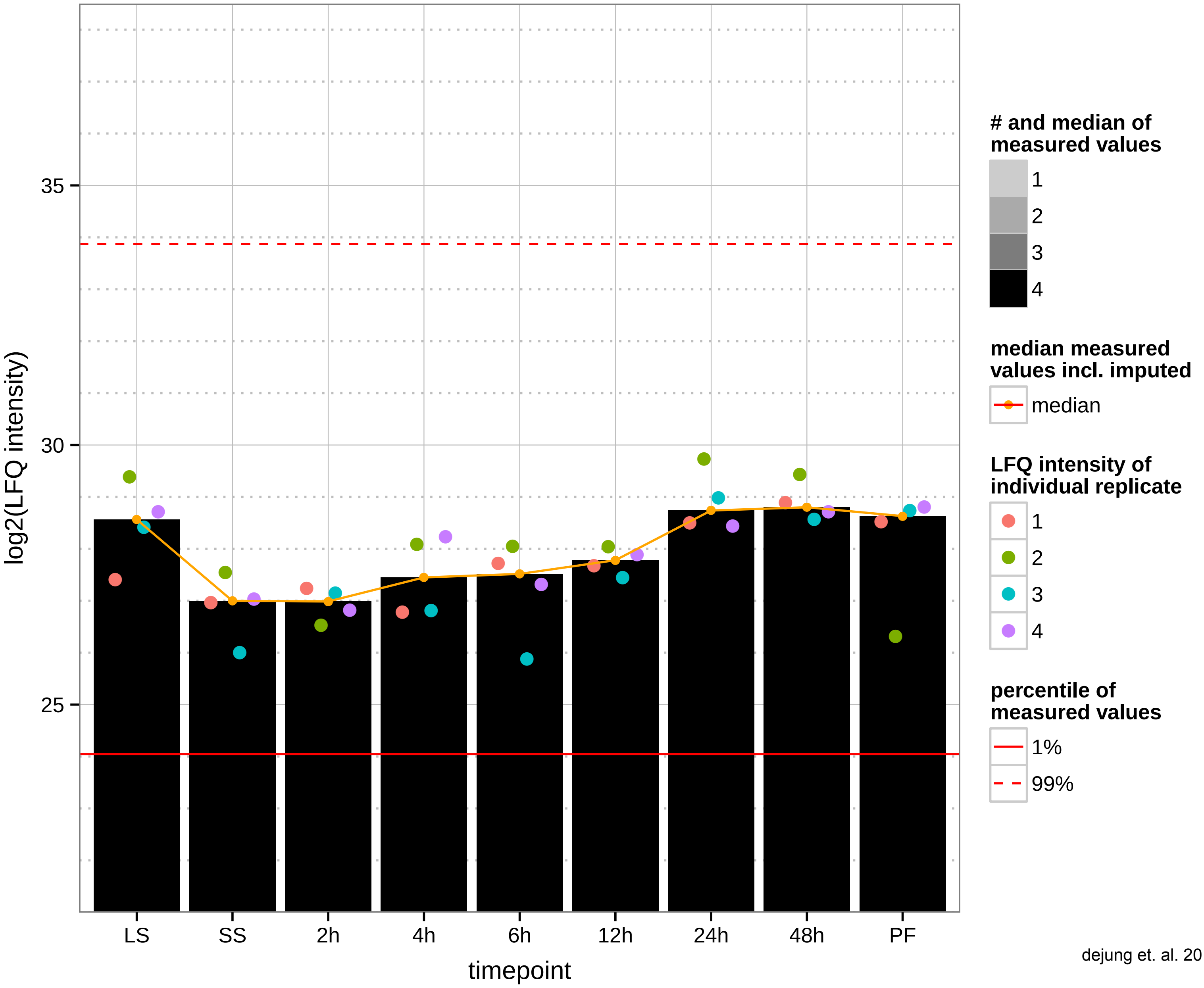
calmodulin–like protein, putative, EF hand containing protein
Tb927.9.11230
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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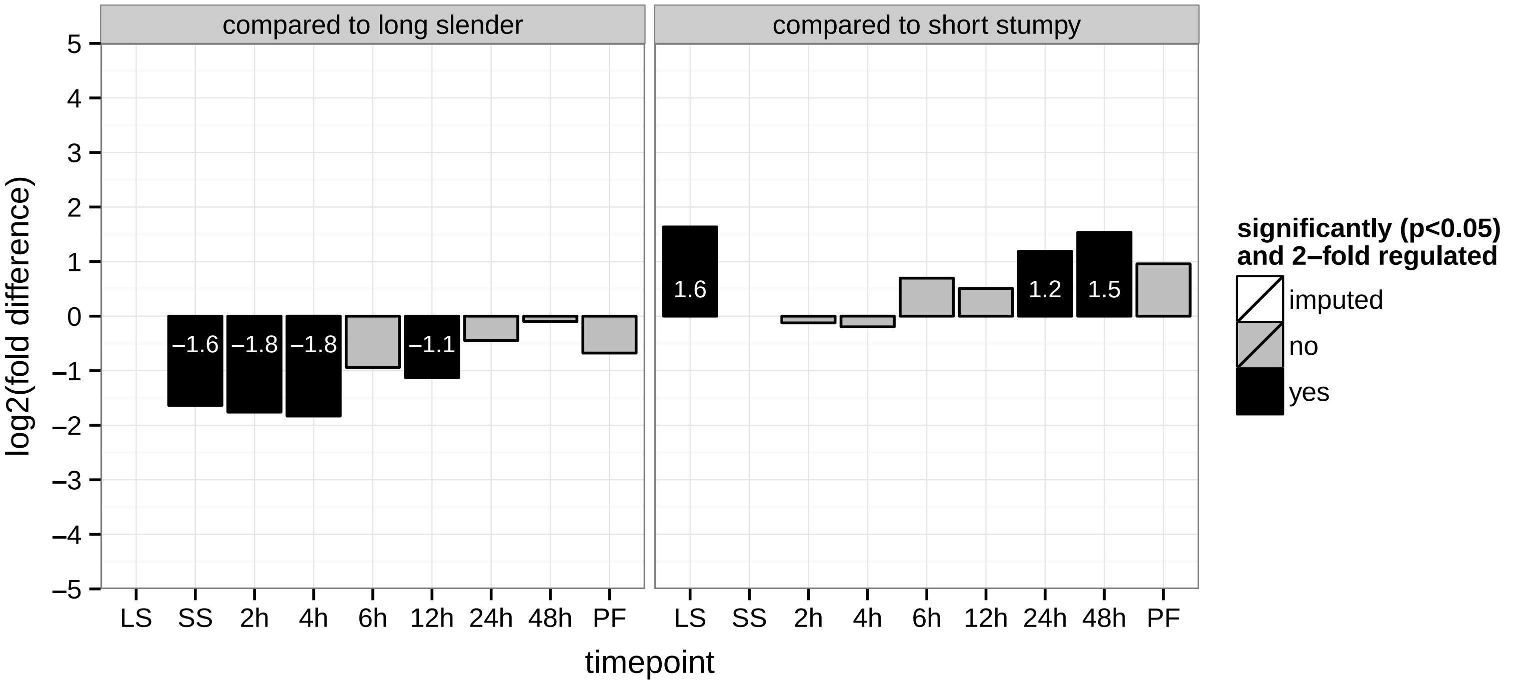
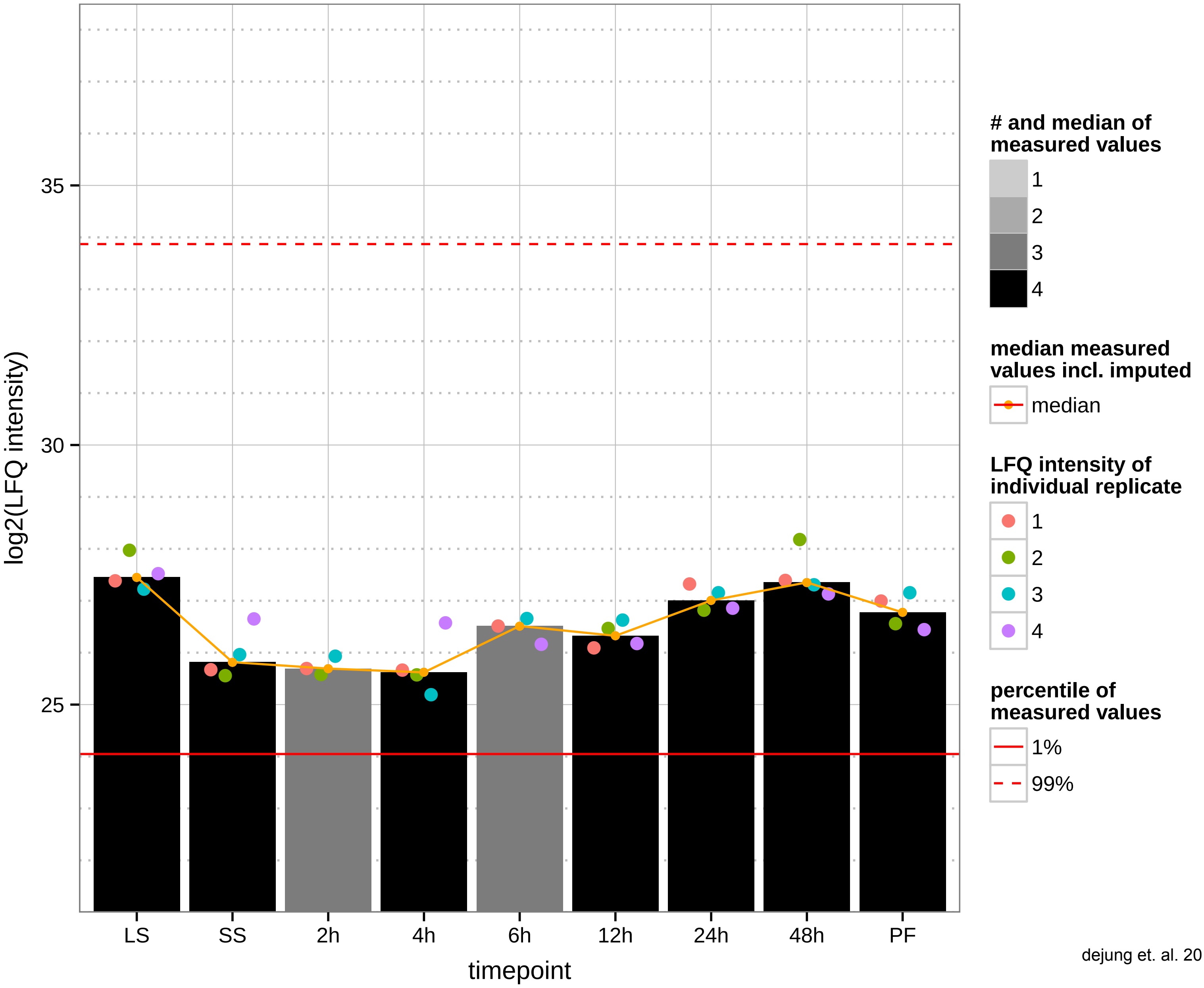
hypothetical protein, conserved
Tb927.9.2760
AGOF: microtubule binding
AGOC: null
AGOP: null
PGOF: microtubule binding, protein binding
PGOC: null
PGOP: null





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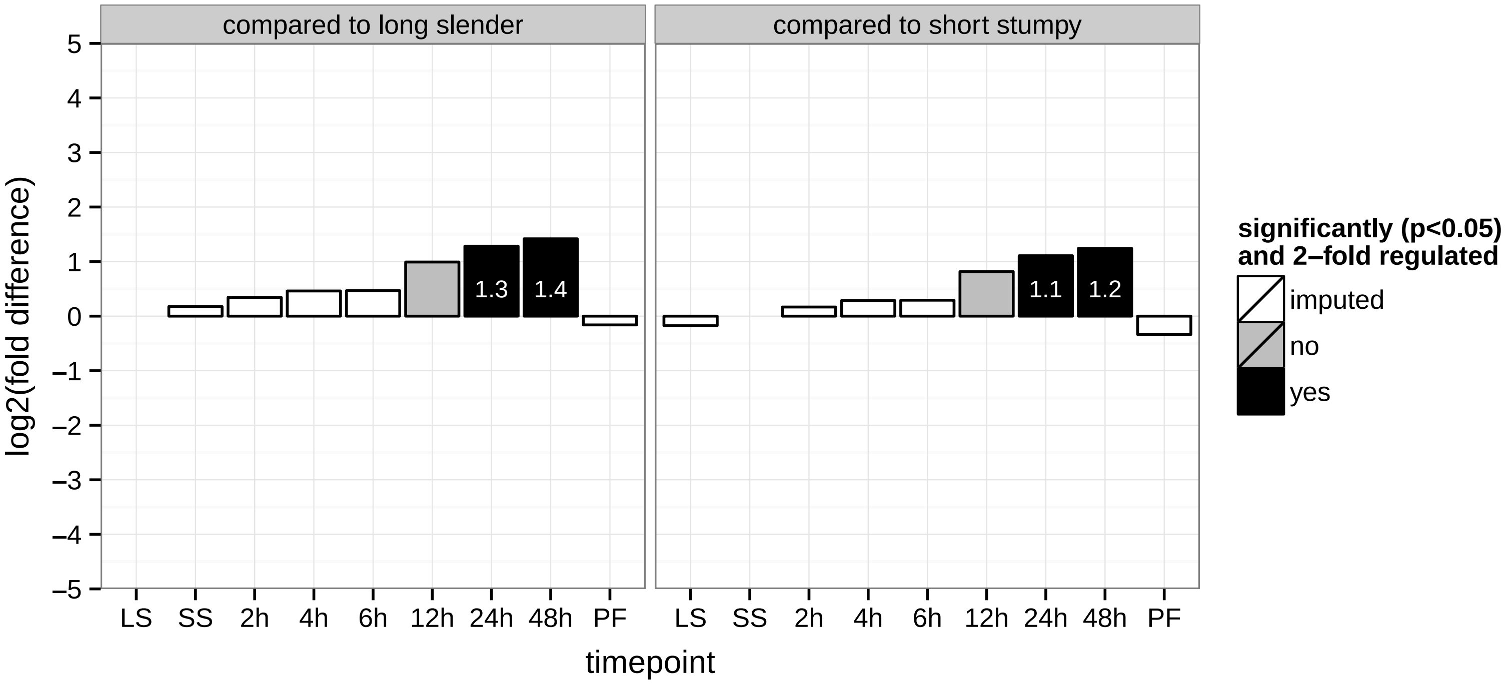
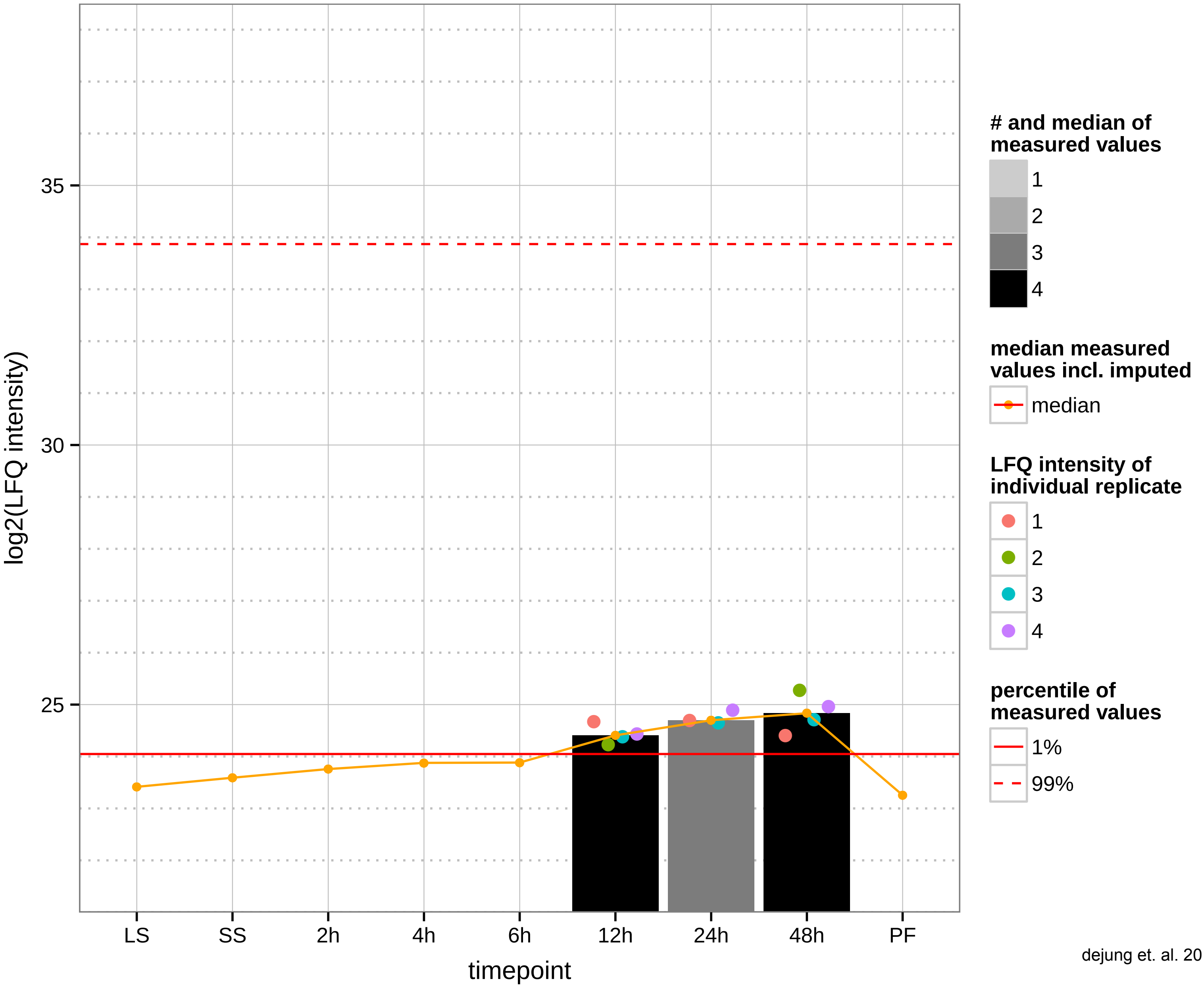
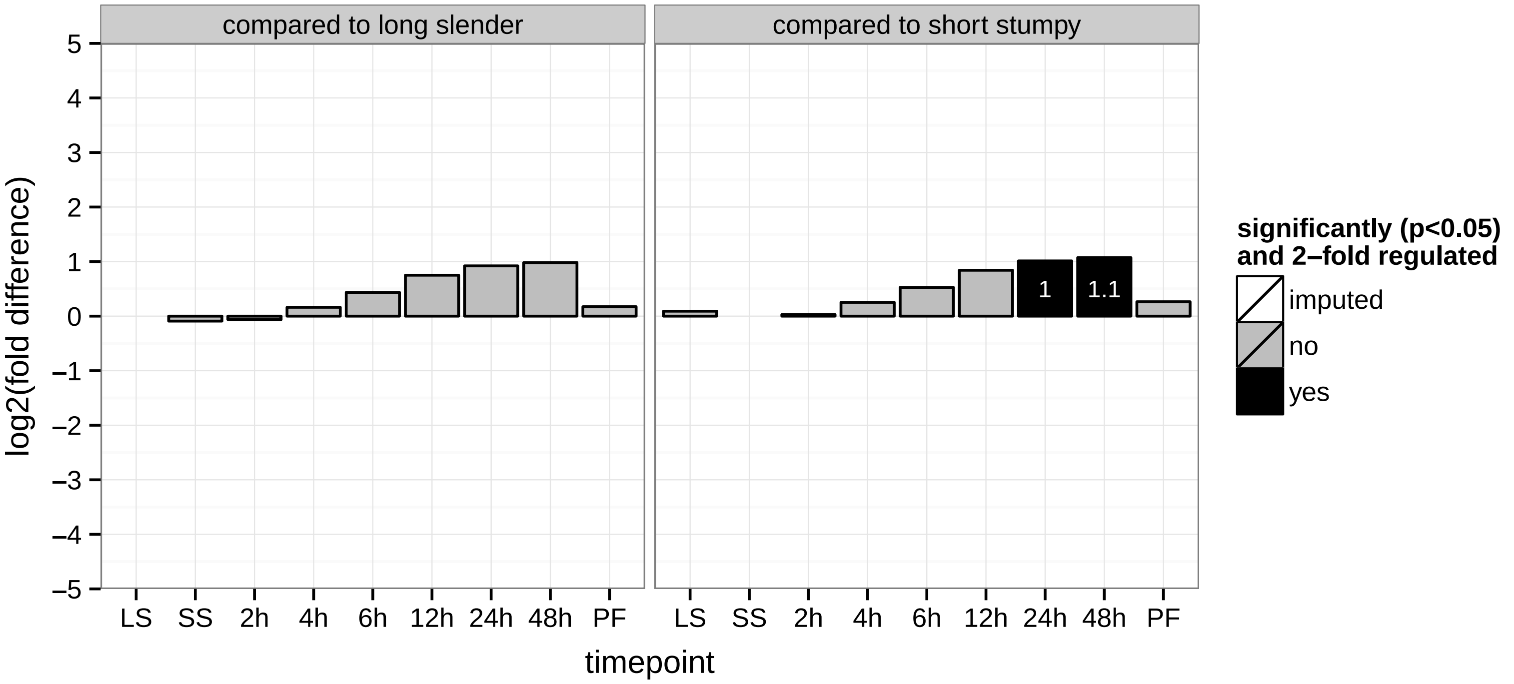
cation transporter, putative
Tb927.9.5490
AGOF: metal ion transmembrane transporter activity
AGOC: membrane
AGOP: metal ion transport
PGOF: metal ion transmembrane transporter activity
PGOC: membrane
PGOP: metal ion transport, transmembrane transport

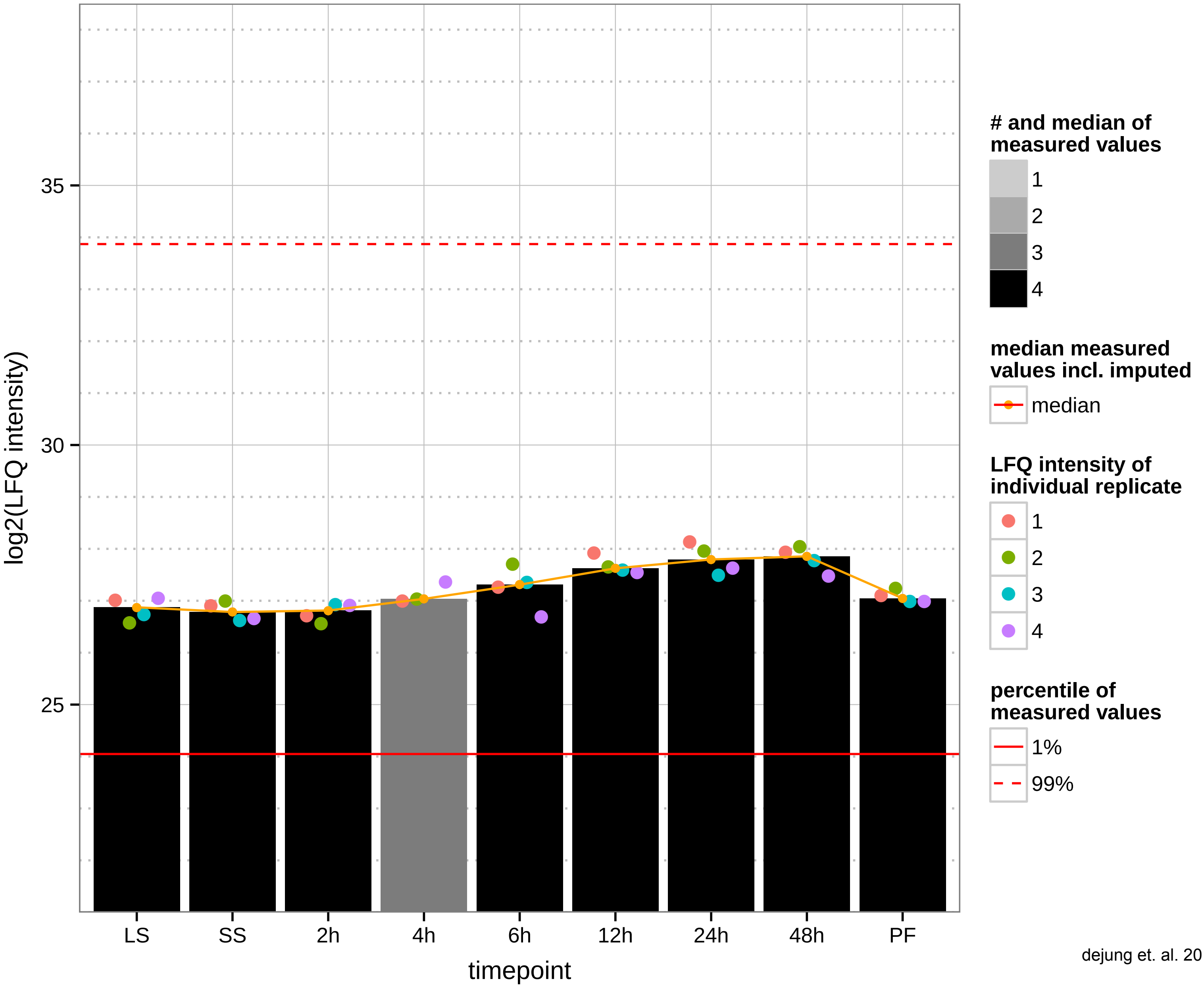




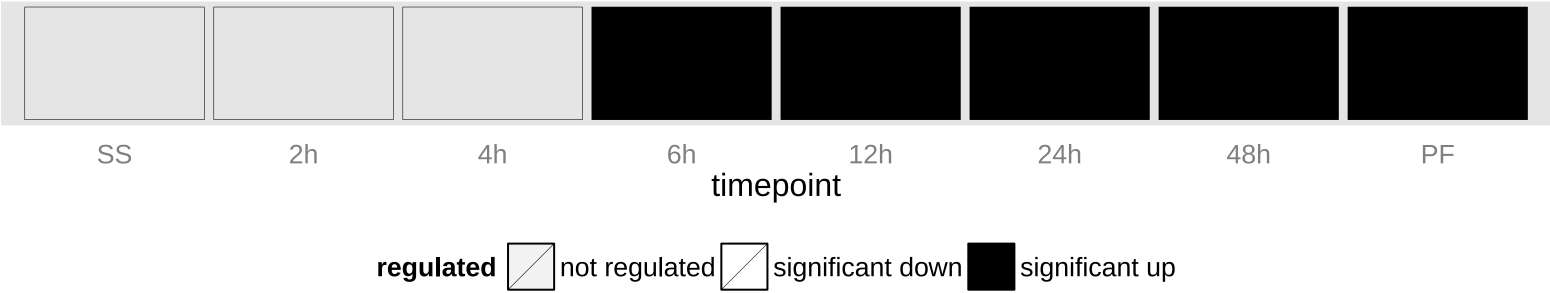
dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.7670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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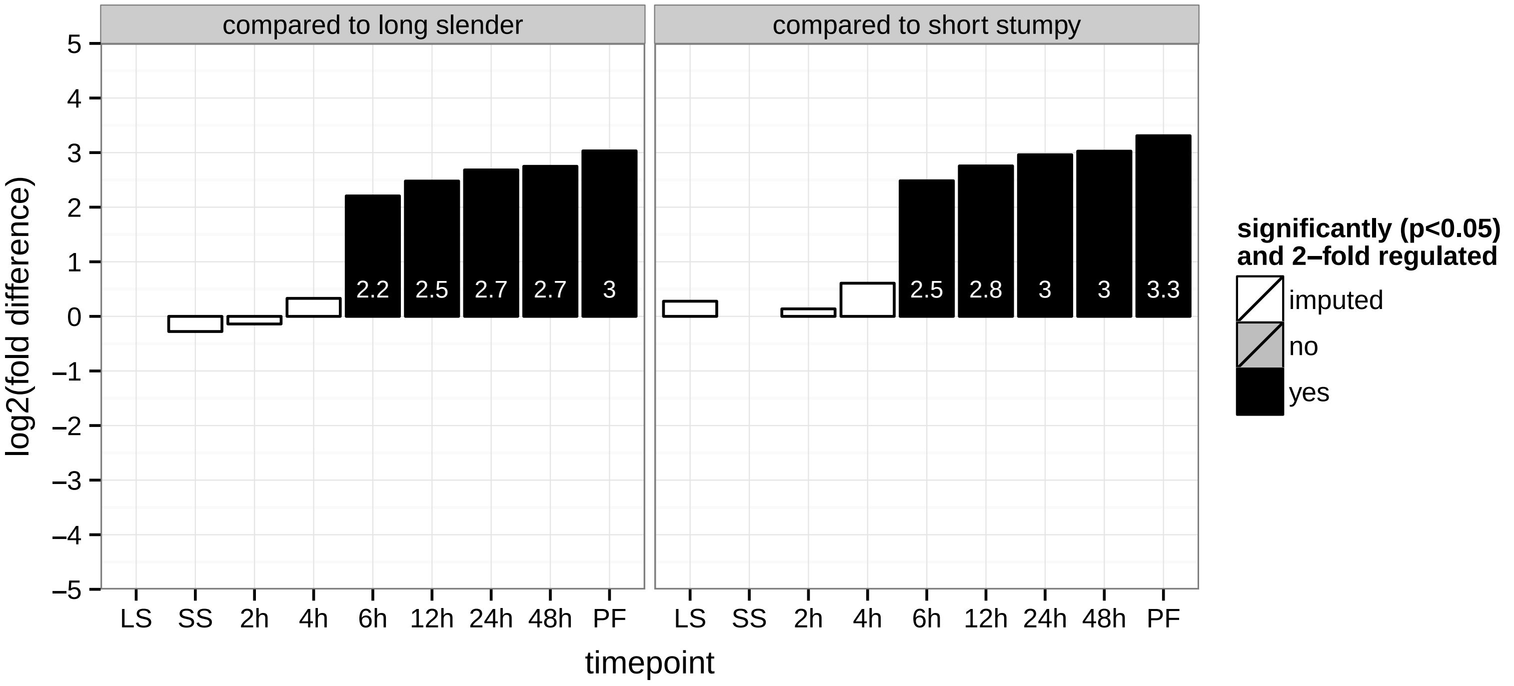
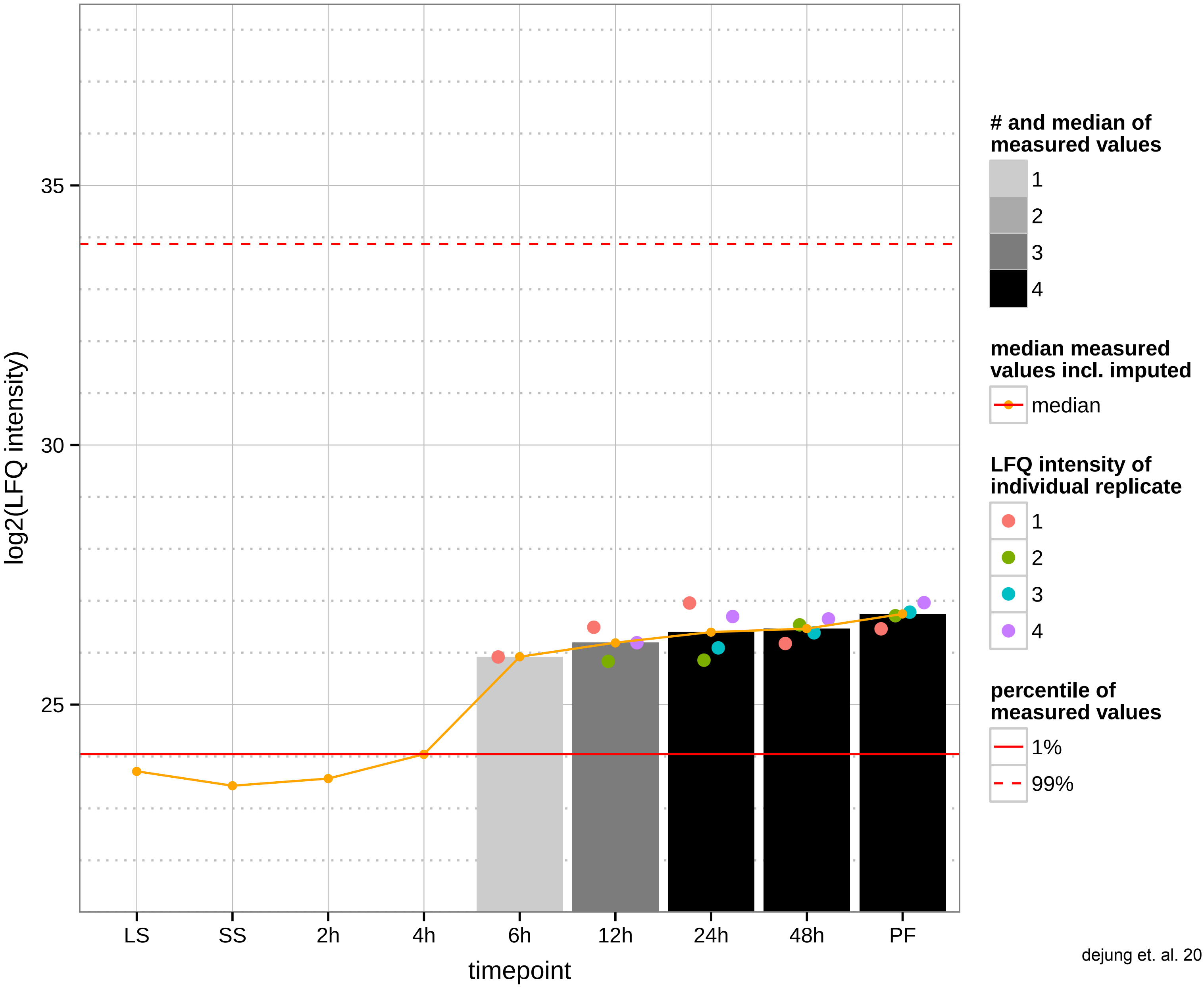
zinc finger protein family member, putative (ZC3H18), hypothetical protein
Tb927.7.2140;Tb07.11L3.90
AGOF: nucleic acid binding, zinc ion binding, RNA binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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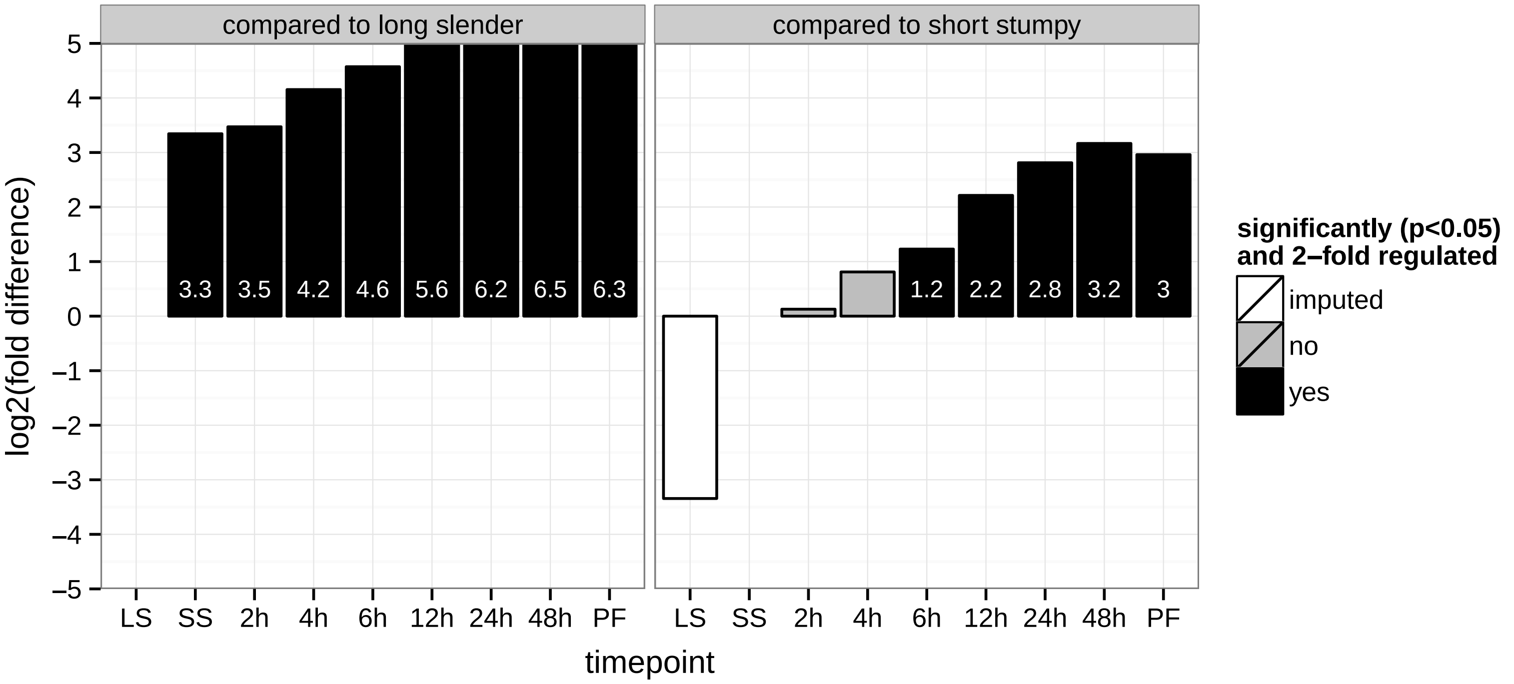
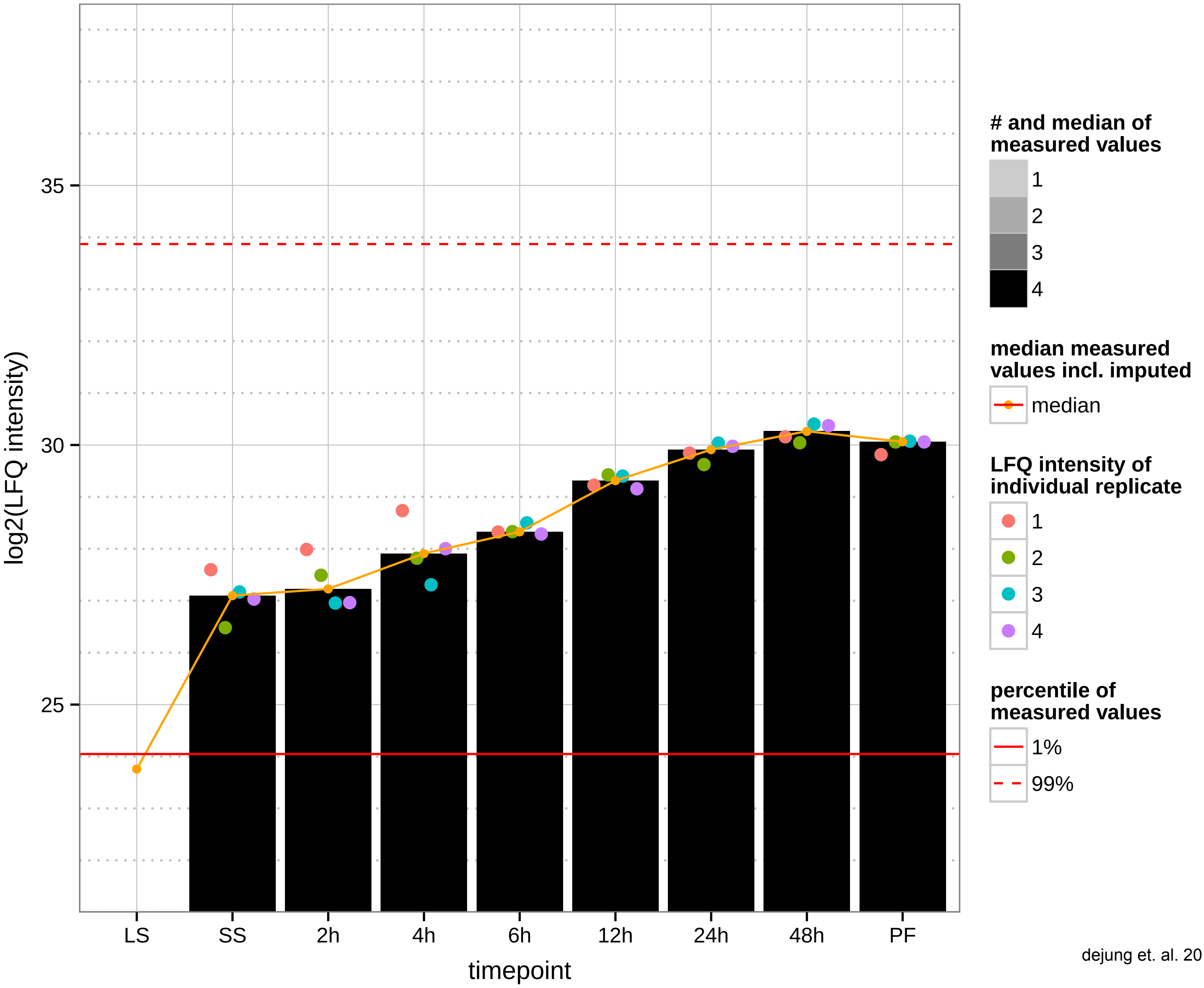
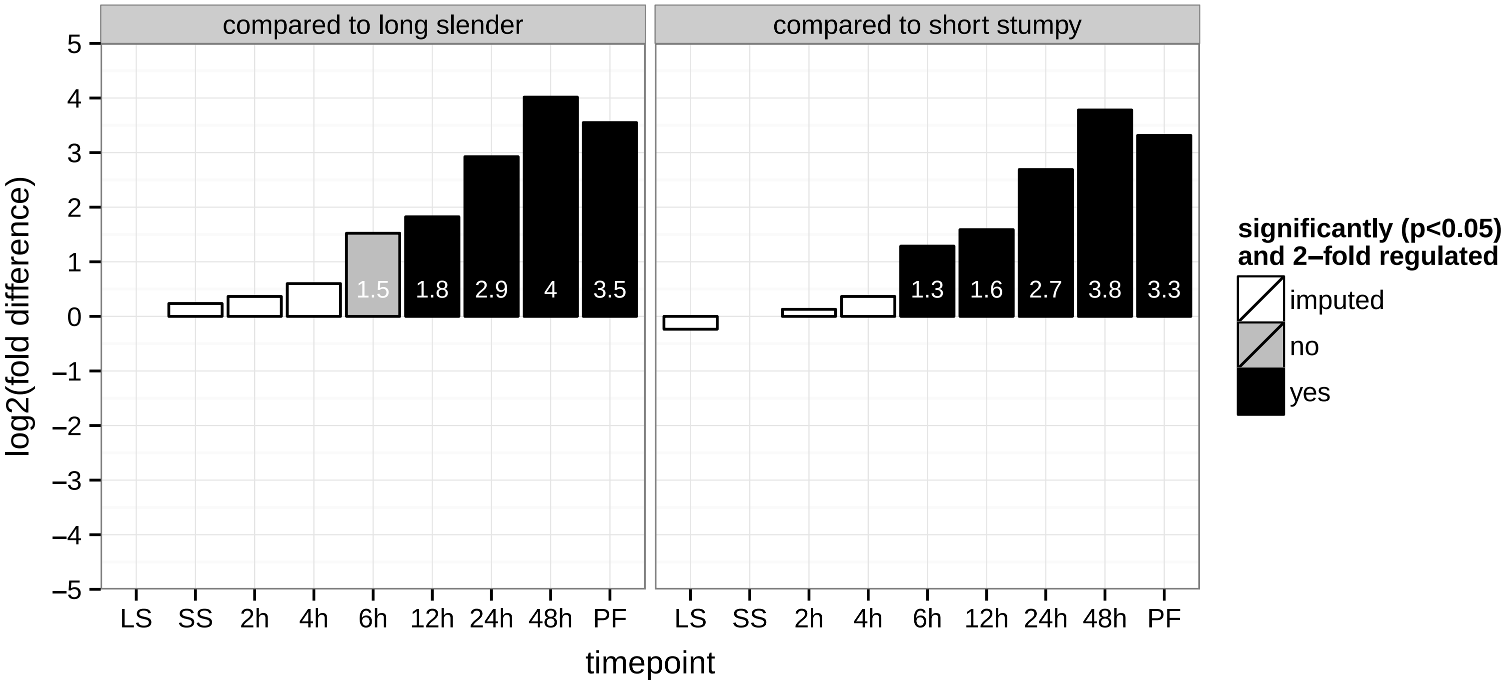
s–adenosyl–L–methionine–c–24–delta–sterol–methyl transferase a, putative, sterol 24–c–methyltransferase, Sterol methyltra
Tb927.10.6950;Tb927.10.6910;Tb11.v5.0496;Tb10.v4.0247
AGOF: methyltransferase activity, null
AGOC: null
AGOP: steroid biosynthetic process, null
PGOF: methyltransferase activity, sterol 24–C–methyltransferase activity
PGOC: null
PGOP: metabolic process, steroid biosynthetic process

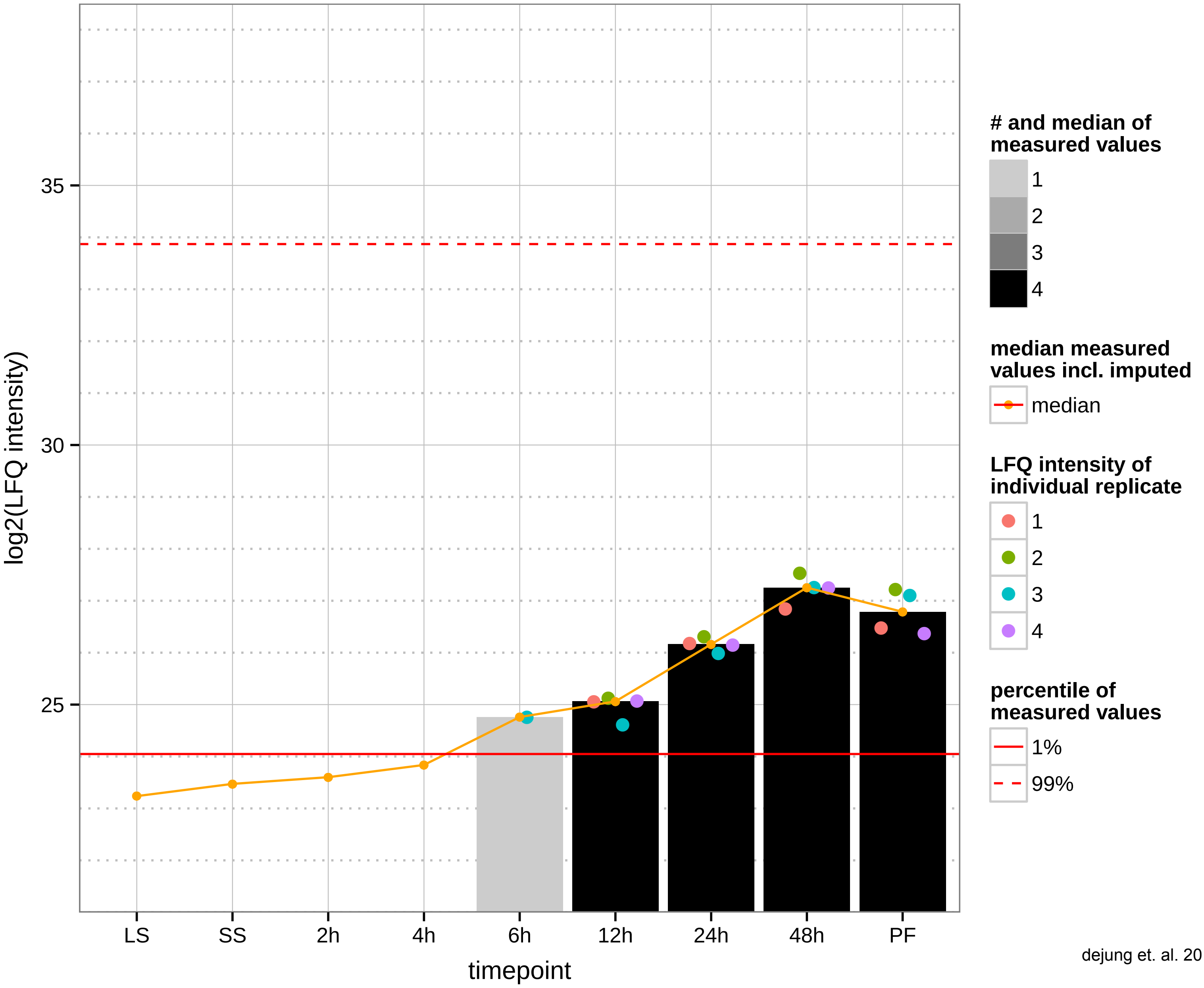




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.5220;Tb11.v5.0235
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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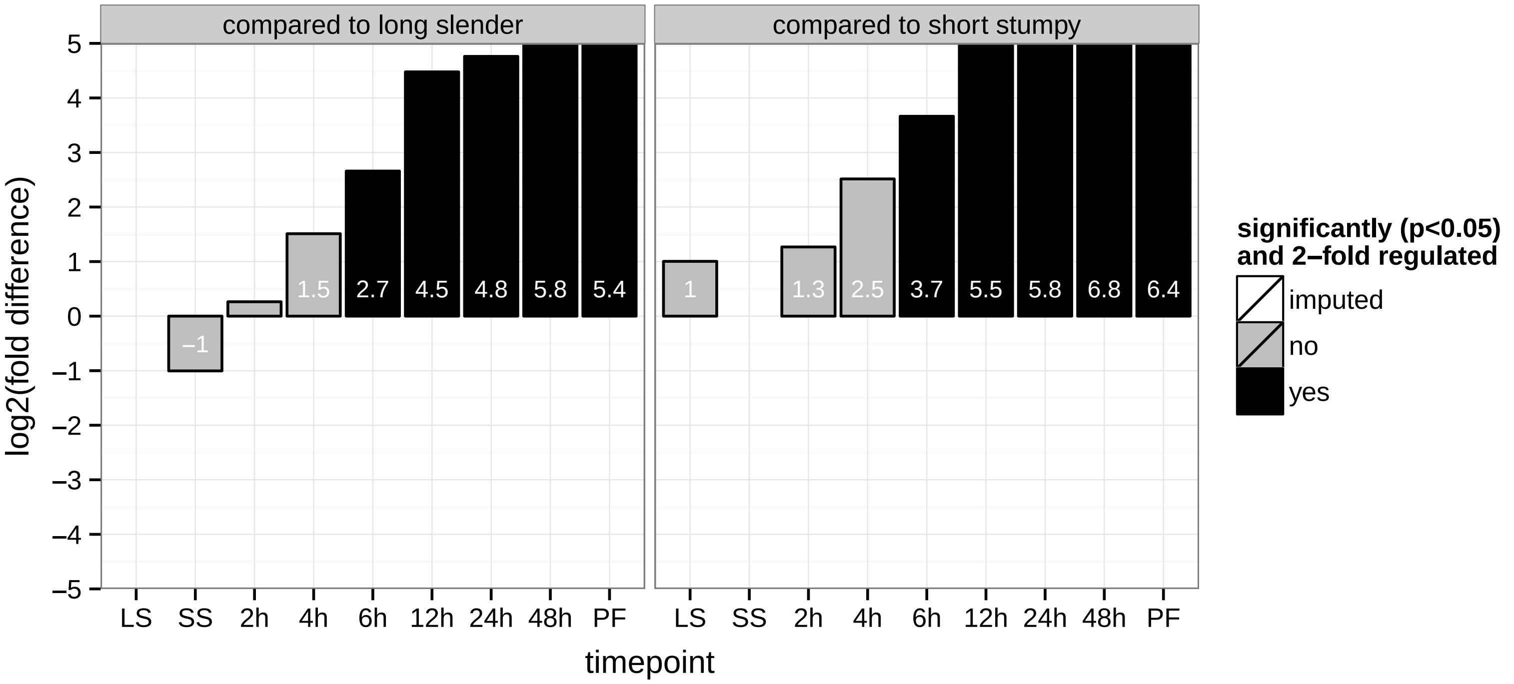
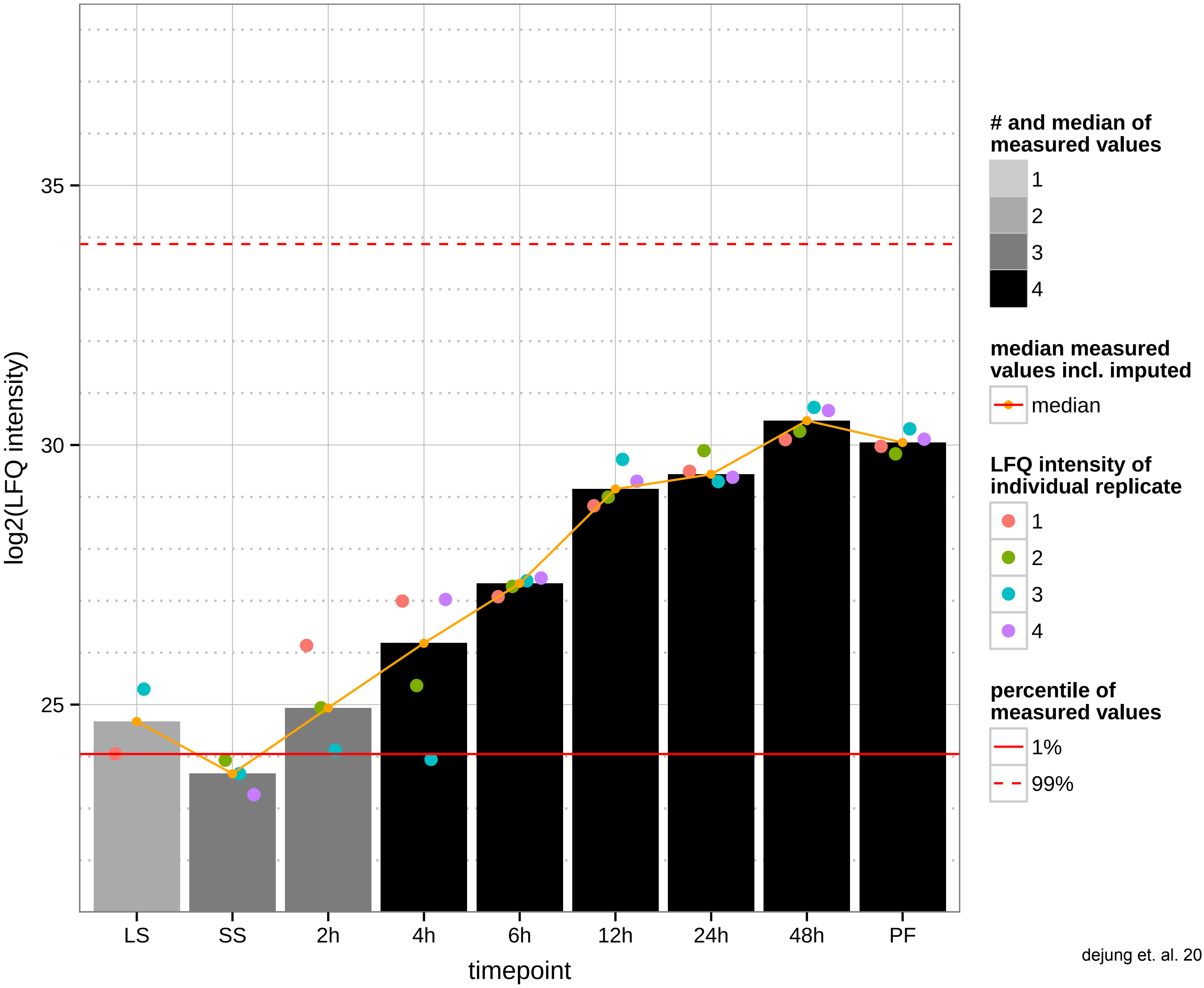
receptor–type adenylate cyclase GRESAG 4, putative, adenylyl cyclase, ATP pyrophosphate–lyase
Tb927.5.330;Tb11.v5.0281
AGOF: null, adenylate cyclase activity
AGOC: null, integral to membrane
AGOP: null, cyclic nucleotide biosynthetic process, intracellular signal transduction
PGOF: phosphorus–oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction





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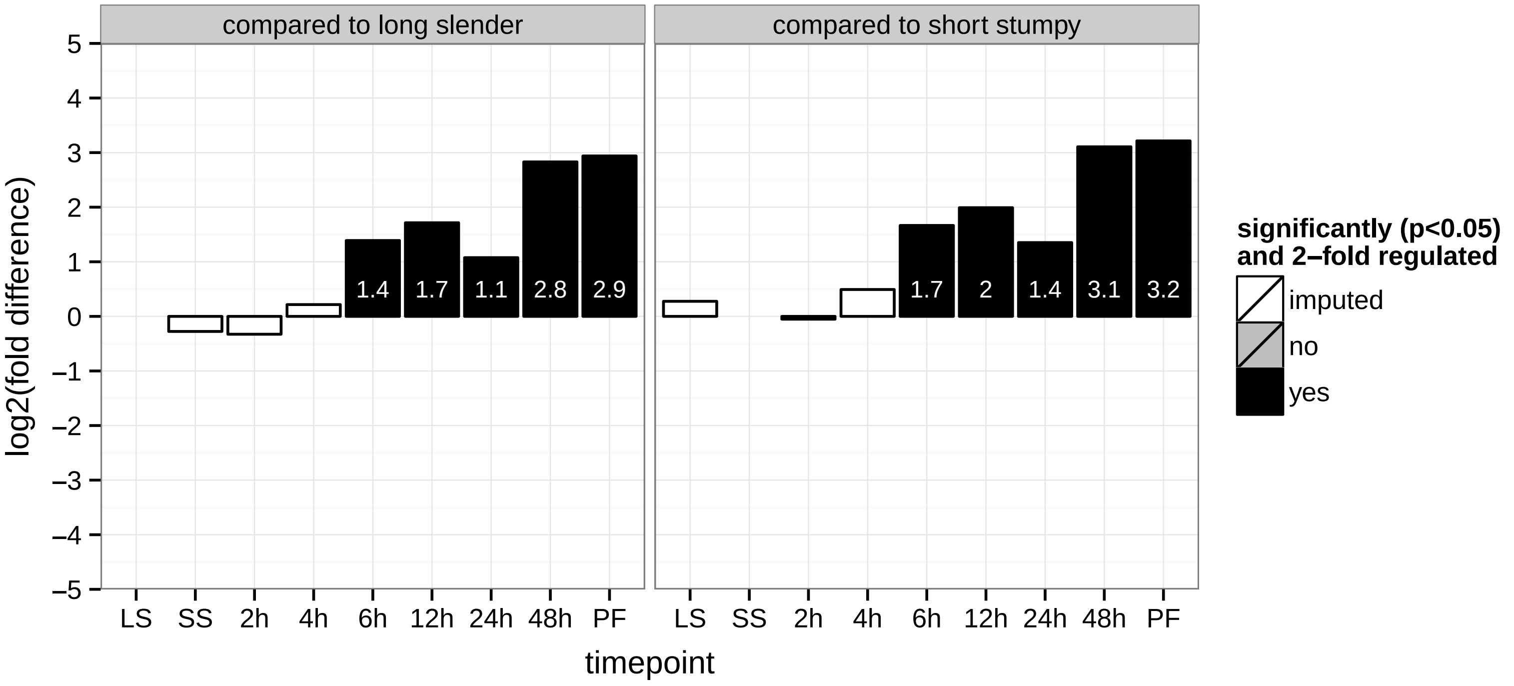
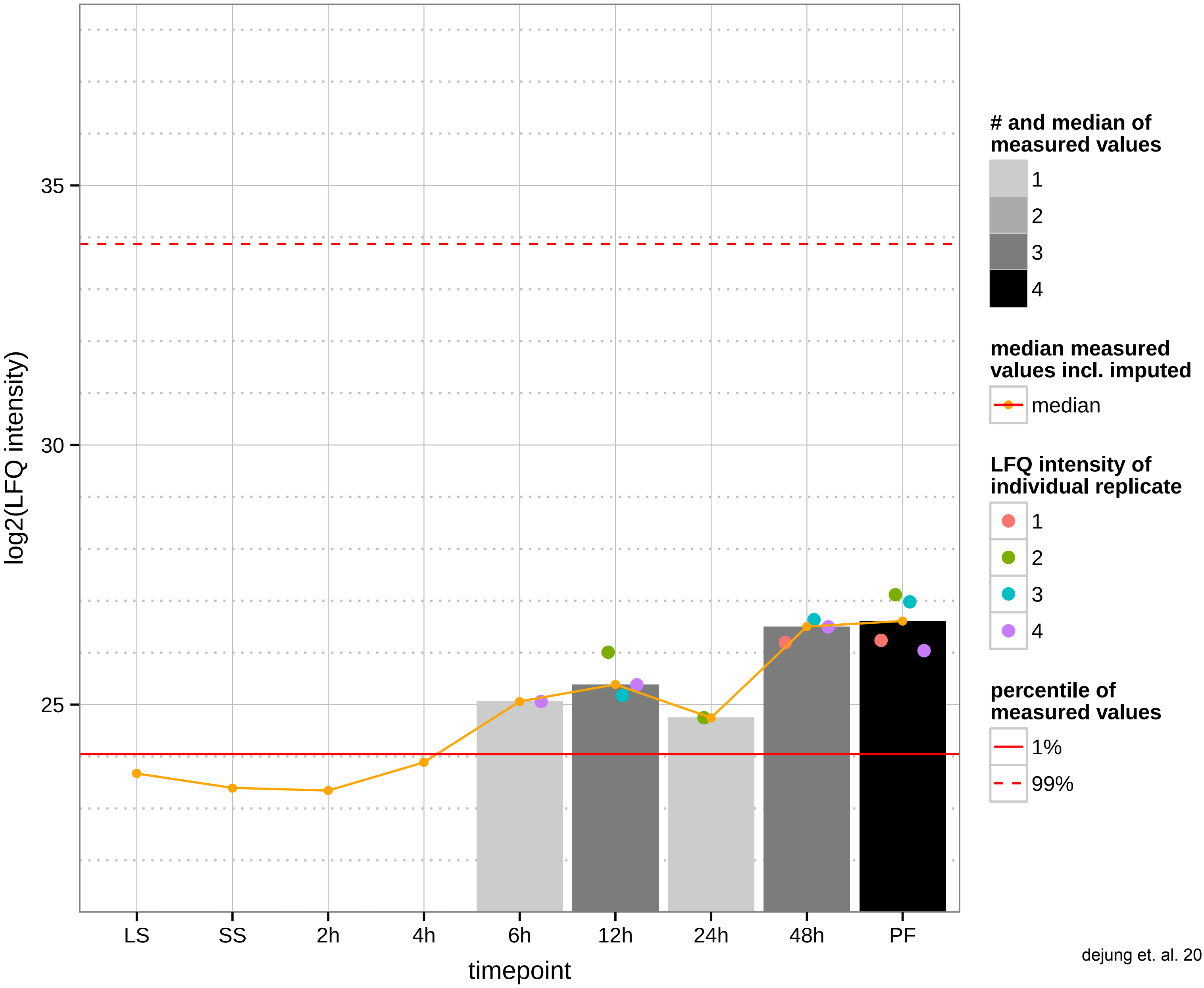
hypothetical protein, conserved, predicted SET domain protein
Tb927.10.4600;Tb11.v5.0422
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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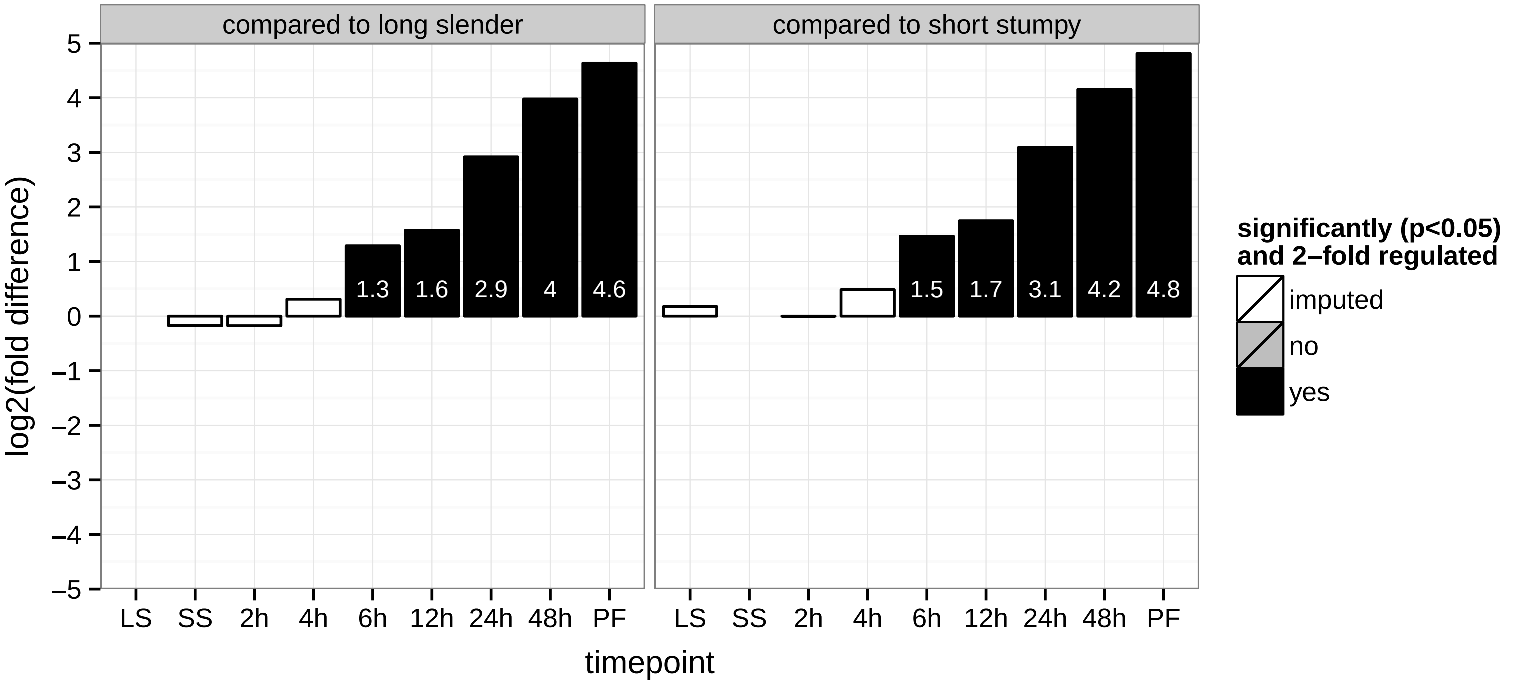
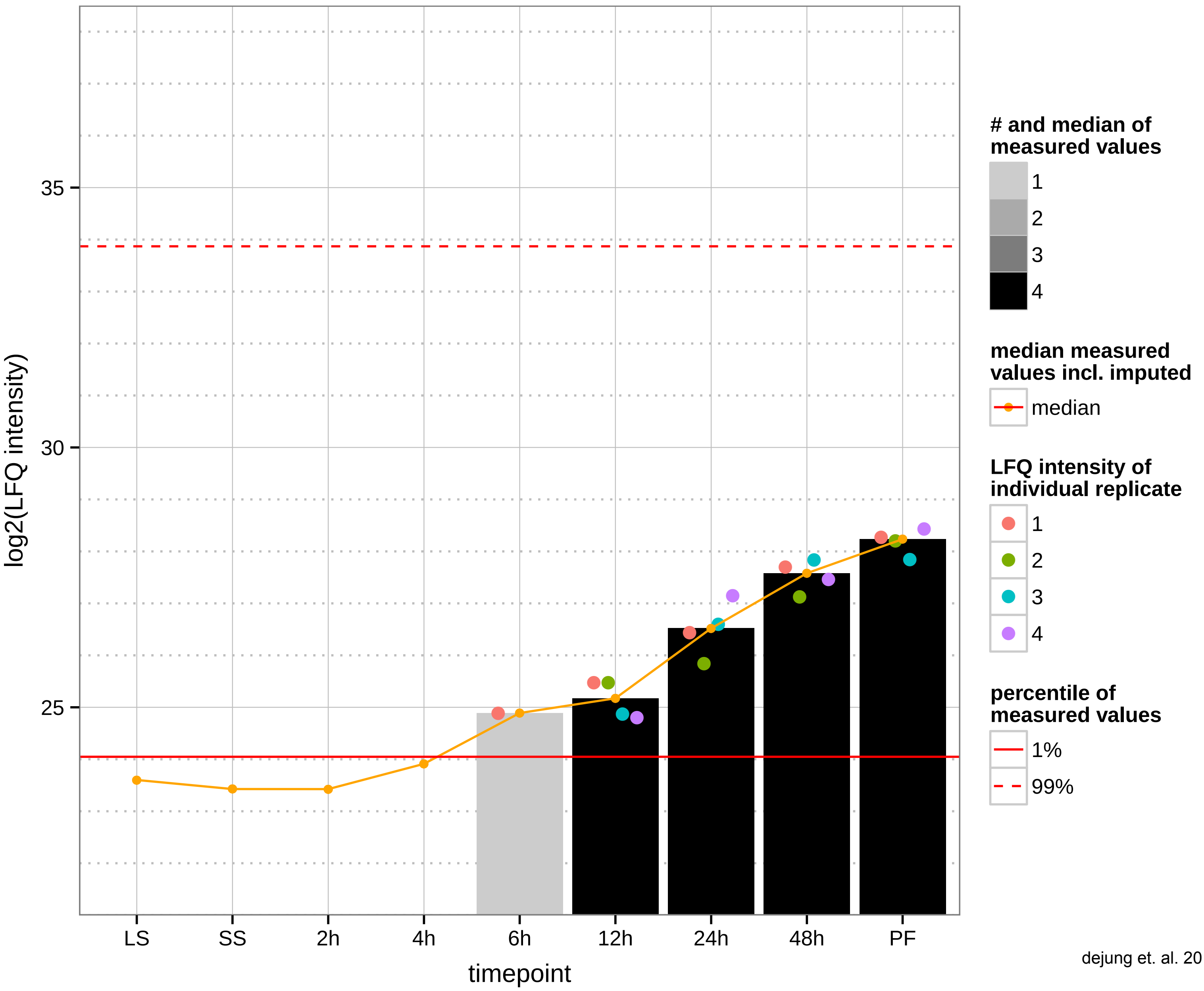
delta−6 fatty acid desaturase, putative, delta−4 fatty acid desaturase
Tb927.10.7100;Tb11.v5.0580
AGOF: null, heme binding, oxidoreductase activity, stearoyl−CoA 9−desaturase activity
AGOC: null
AGOP: null, fatty acid biosynthetic process
PGOF: heme binding
PGOC: null
PGOP: lipid metabolic process





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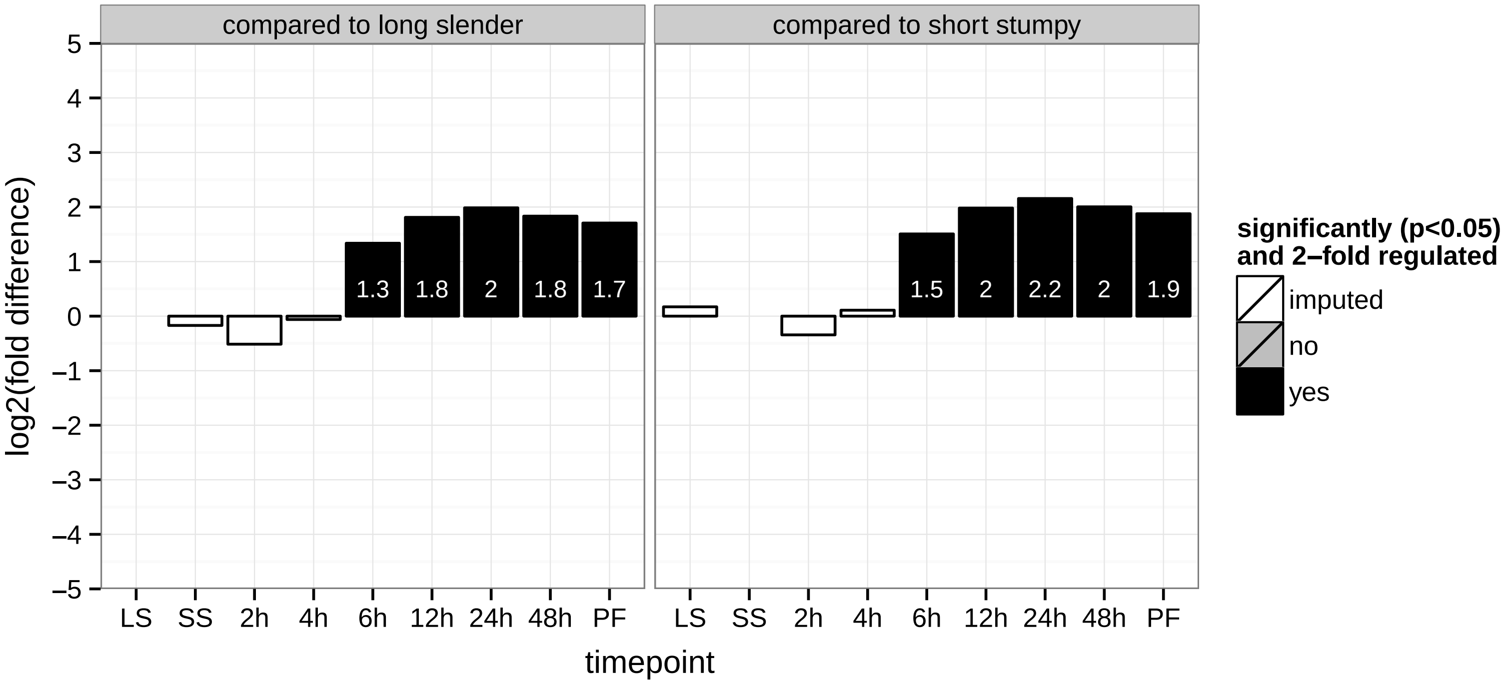
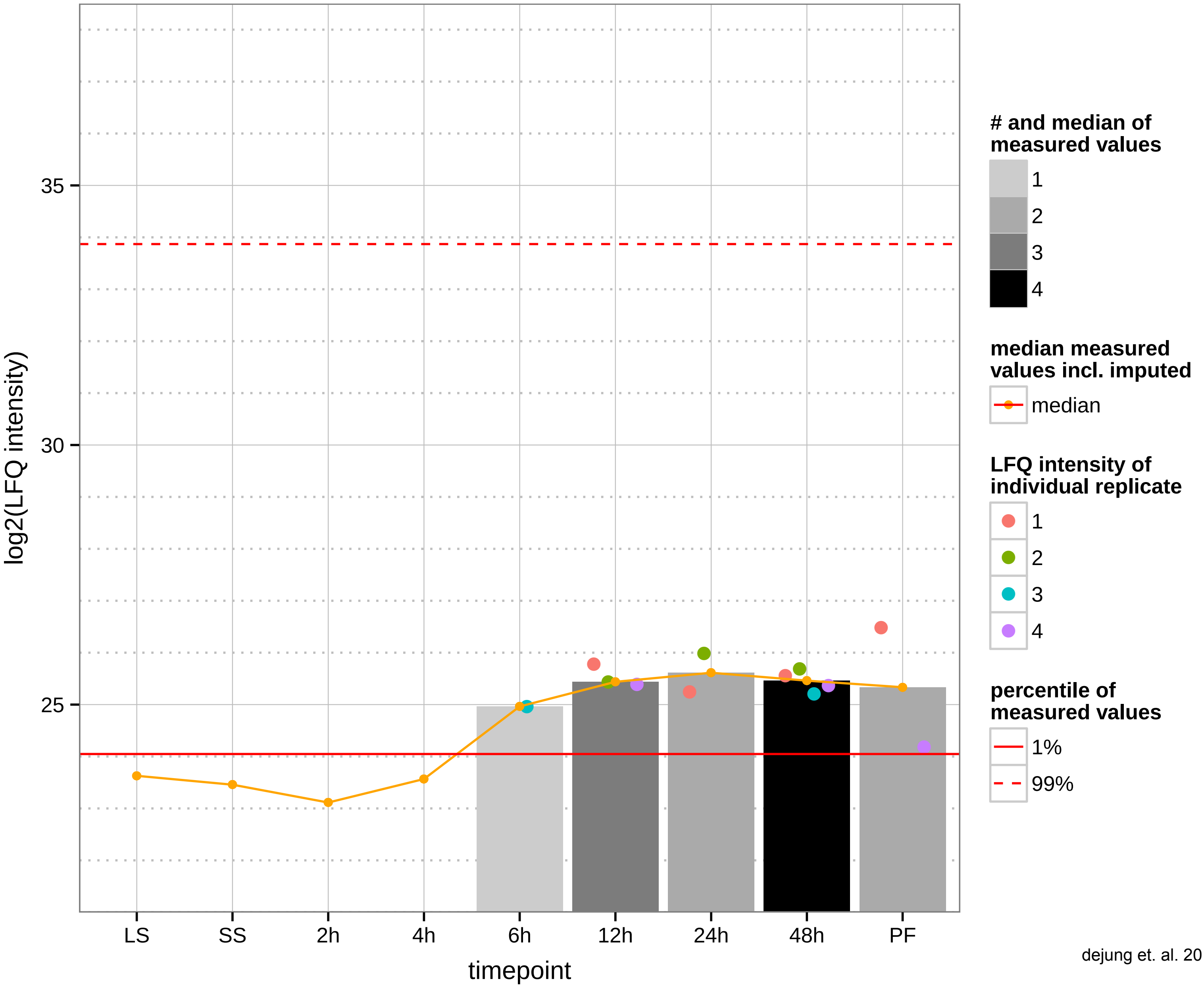
transcription elongation factor 1 homolog (ELOF1)
Tb927.1.1630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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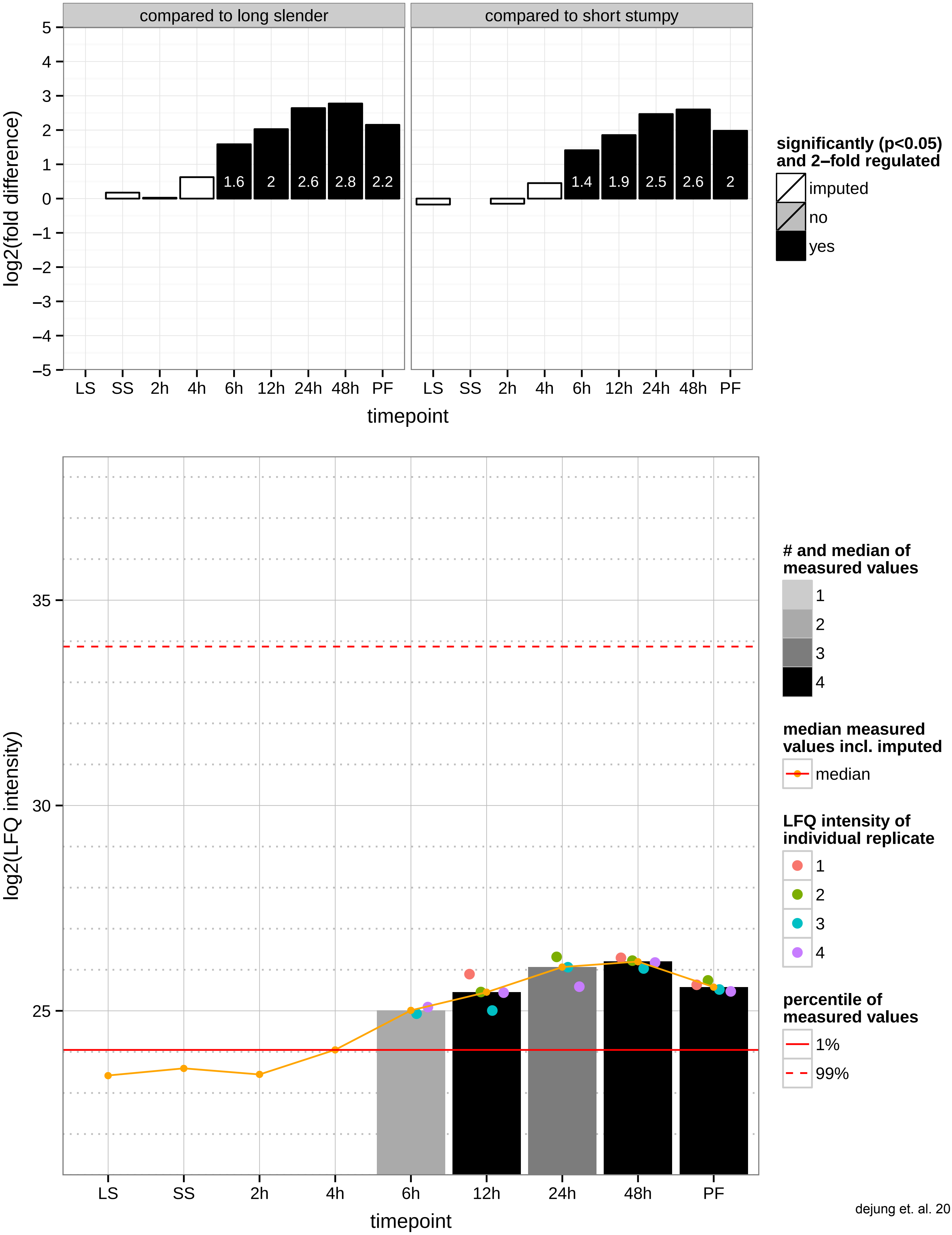
transmembrane protein, putative
Tb927.1.840
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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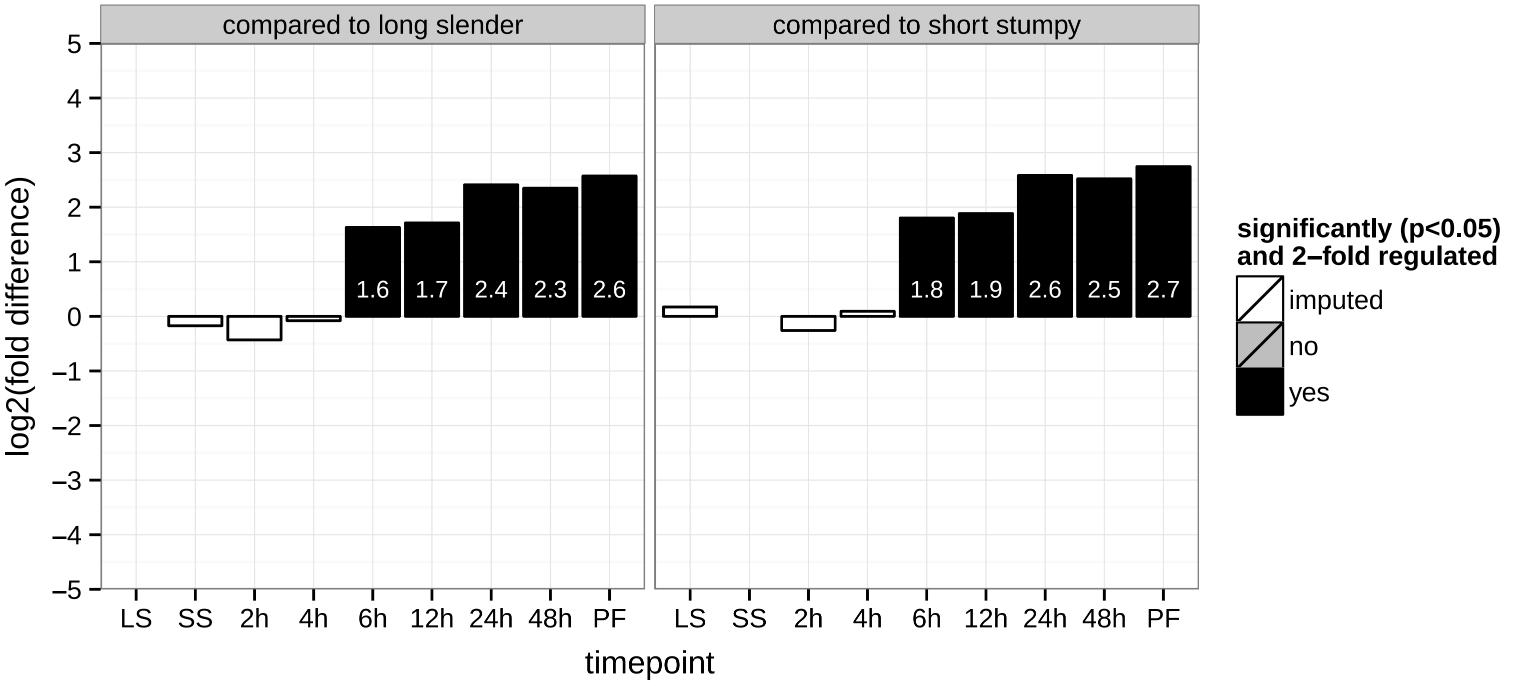
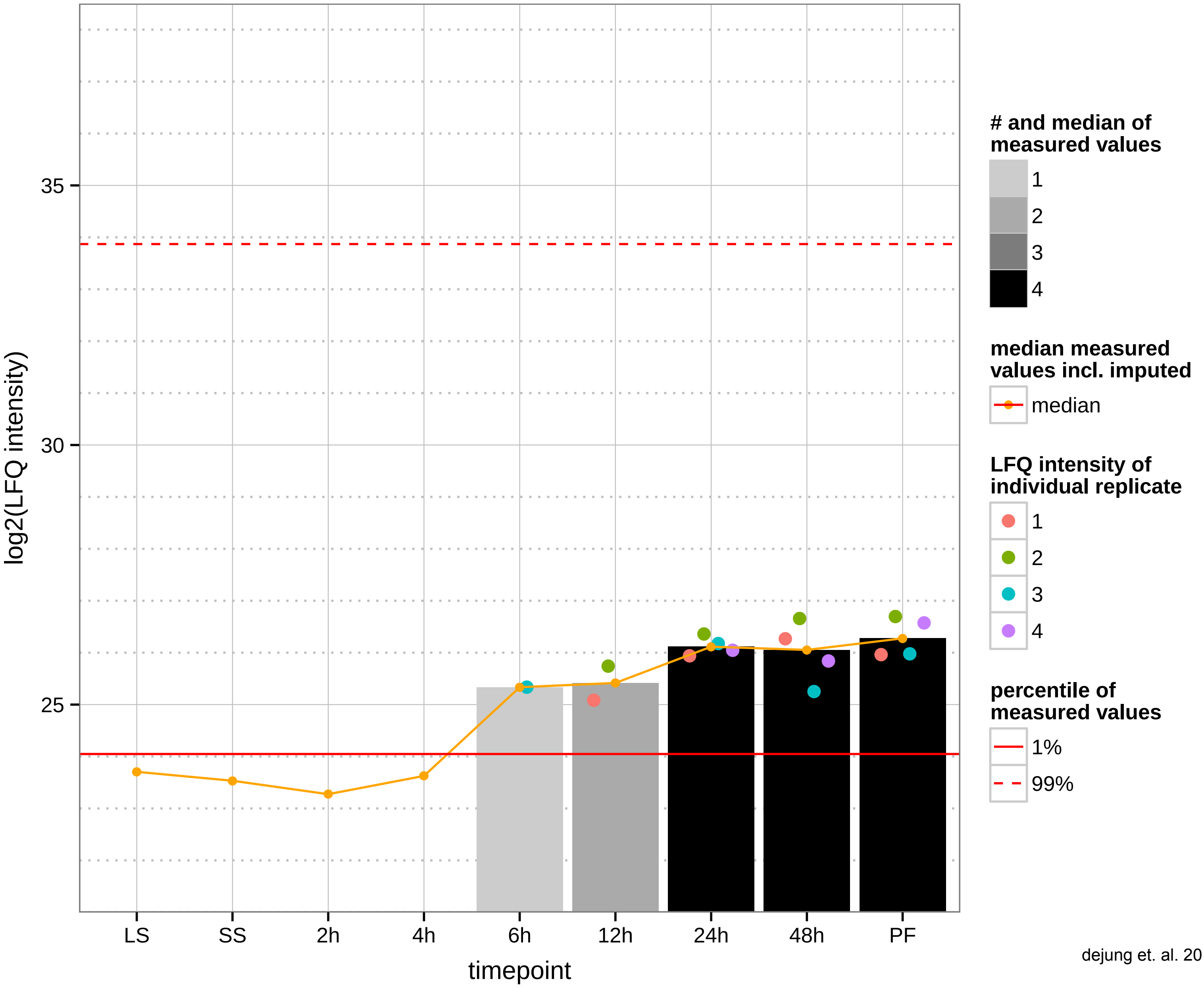
hypothetical protein, conserved
Tb927.10.10120
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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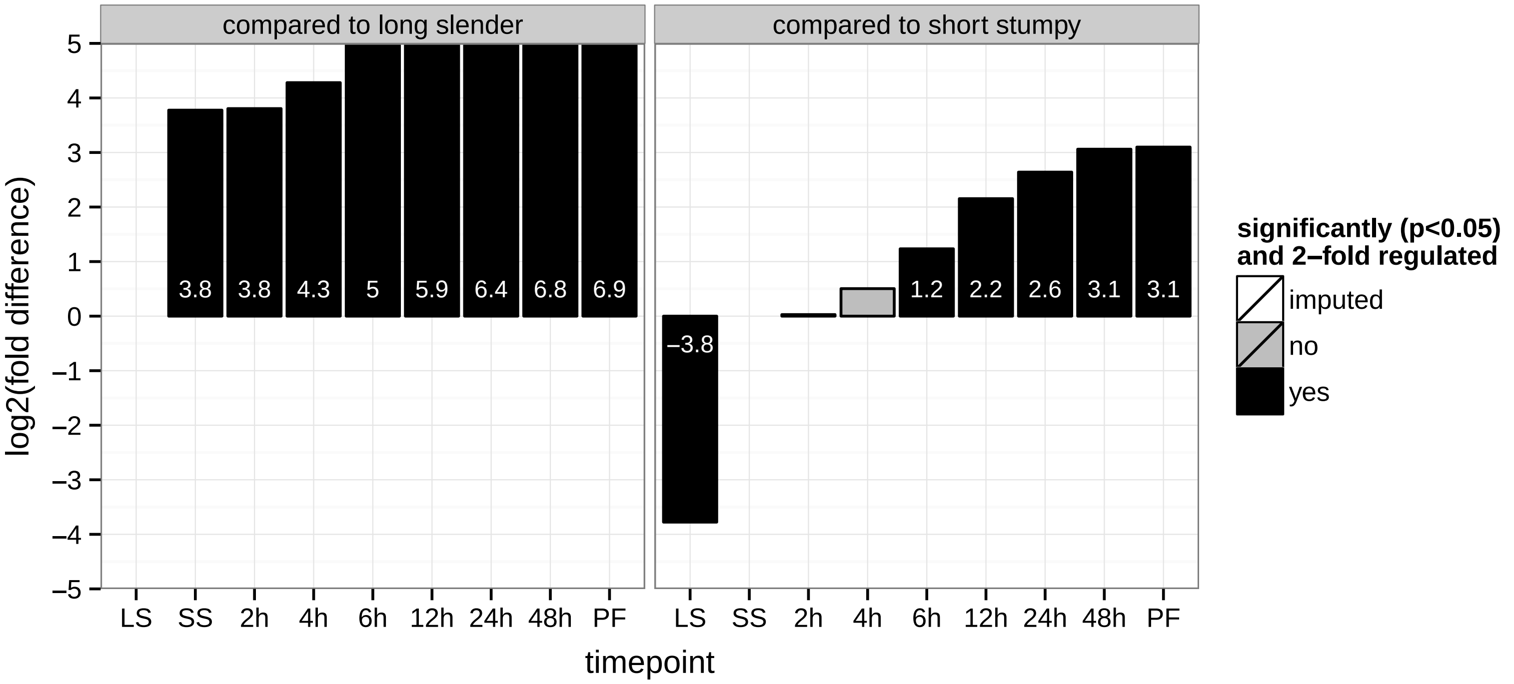
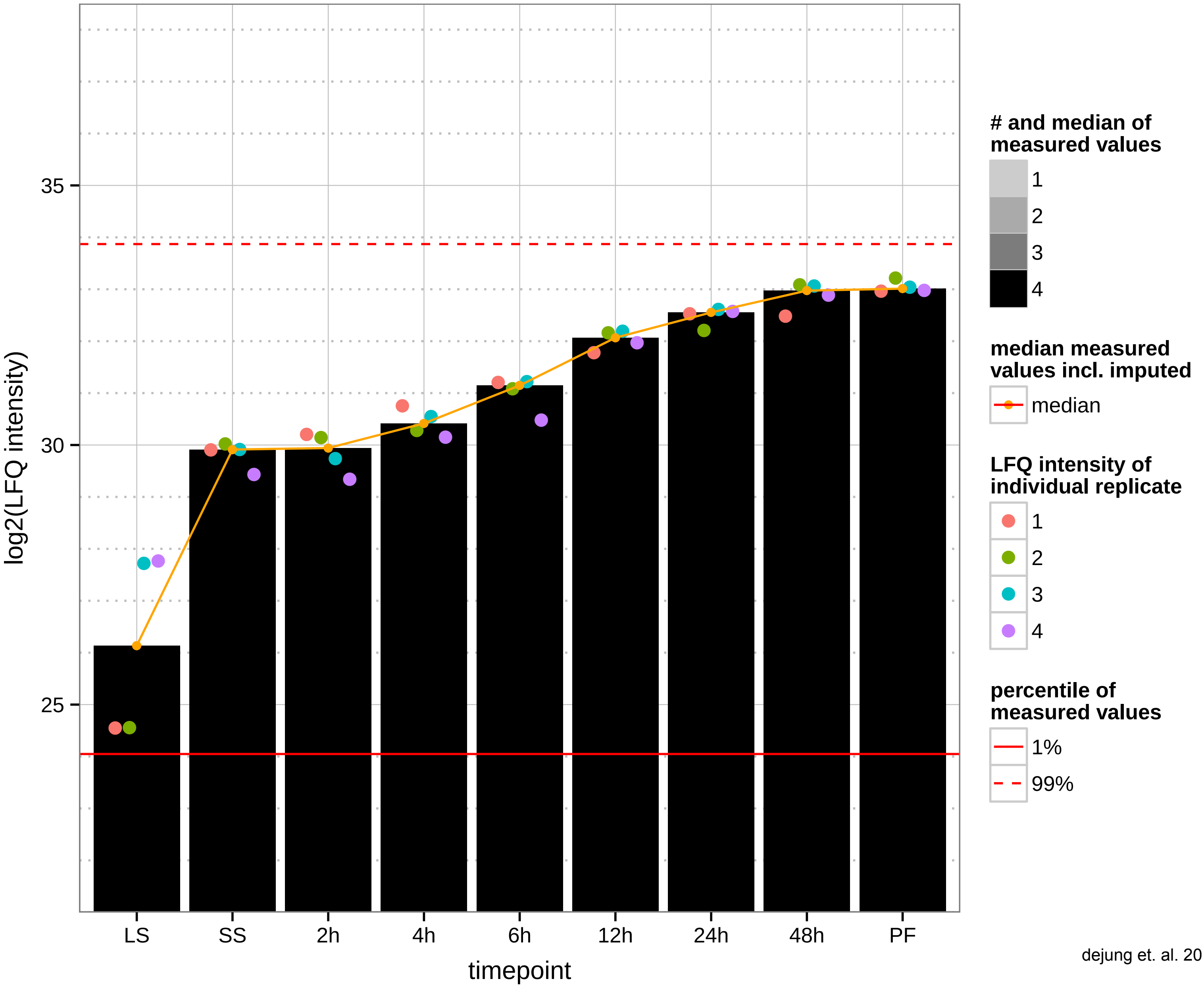
mitochondrial malate dehydrogenase (mMDH)
Tb927.10.2560
AGOF: L–malate dehydrogenase activity, malate dehydrogenase activity, oxidoreductase activity
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: glycolysis, malate metabolic process, oxidation–reduction process, tricarboxylic acid cycle
PGOF: L–malate dehydrogenase activity, catalytic activity, oxidoreductase activity, acting on the CH–OH group of donors, NAI
PGOC: null
PGOP: carbohydrate metabolic process, cellular carbohydrate metabolic process, malate metabolic process, oxidation–reduct





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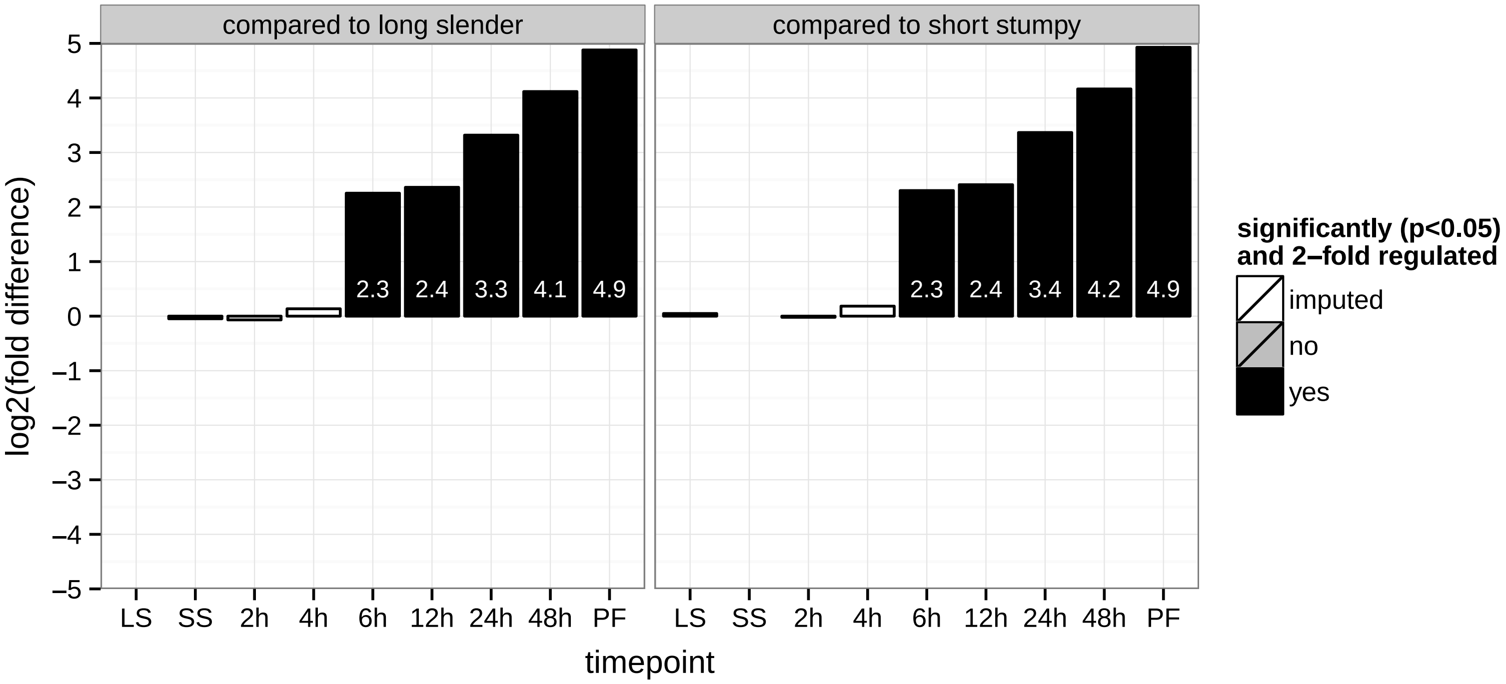
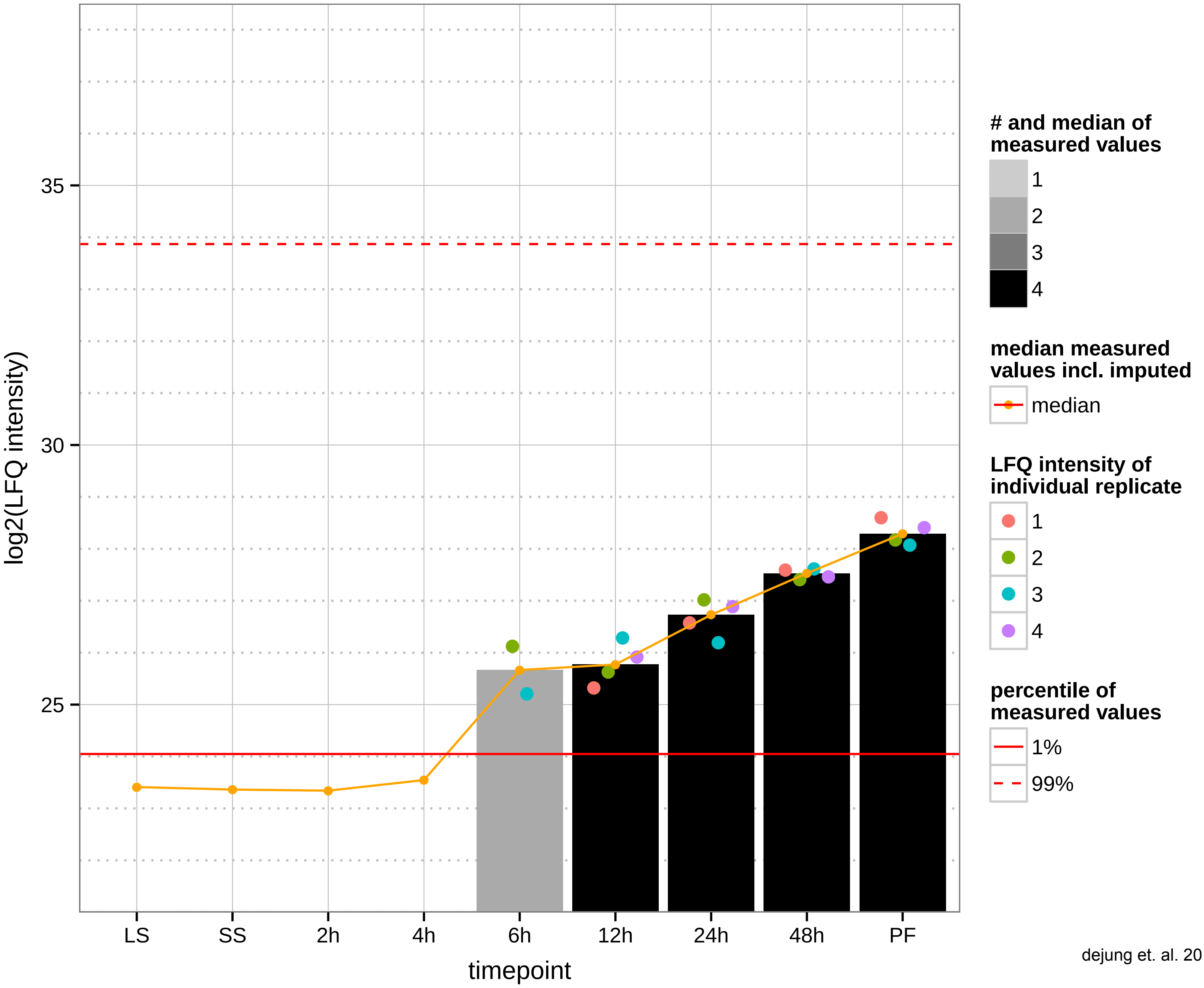
choline dehydrogenase, putative
Tb927.10.470
AGOF: choline dehydrogenase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of mol
AGOC: mitochondrion
AGOP: carotenoid biosynthetic process, glycine betaine biosynthetic process from choline
PGOF: flavin adenine dinucleotide binding, oxidoreductase activity, acting on CH−OH group of donors
PGOC: null
PGOP: oxidation−reduction process





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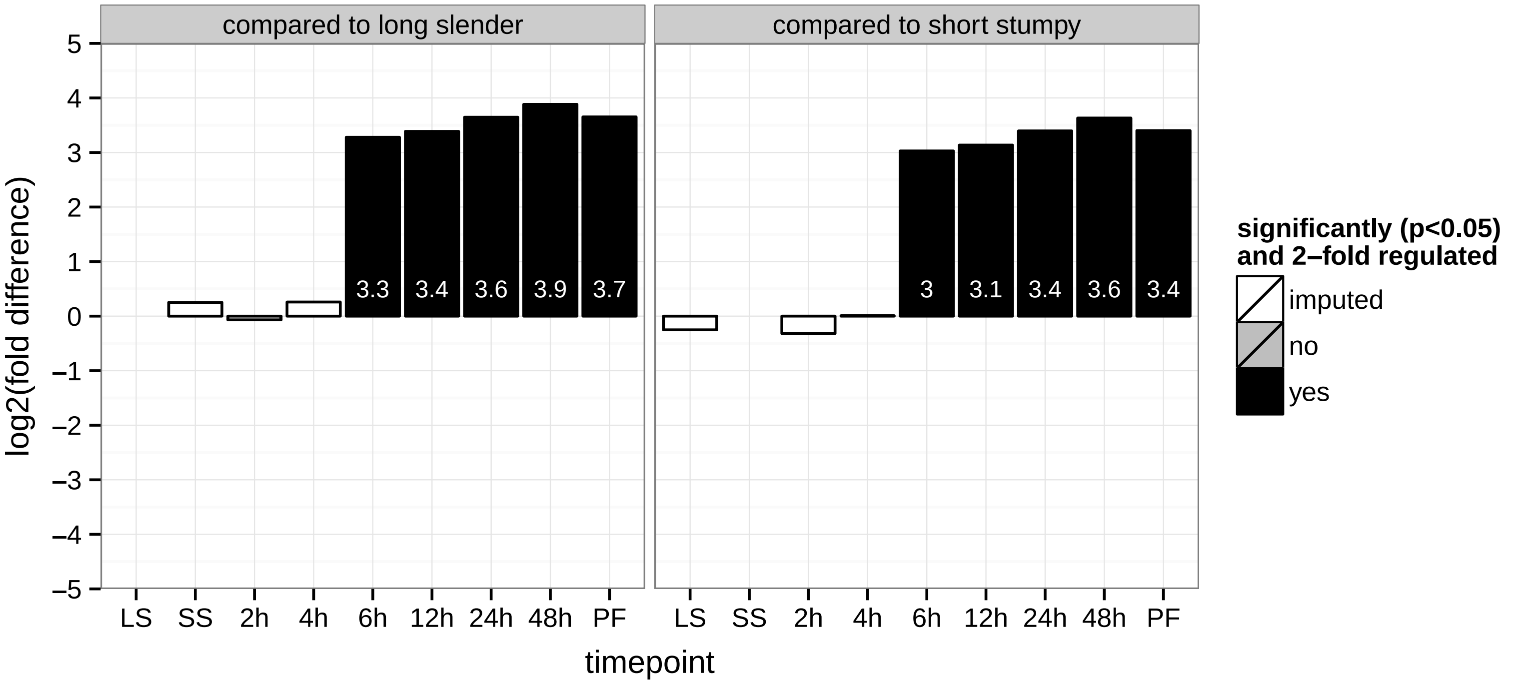
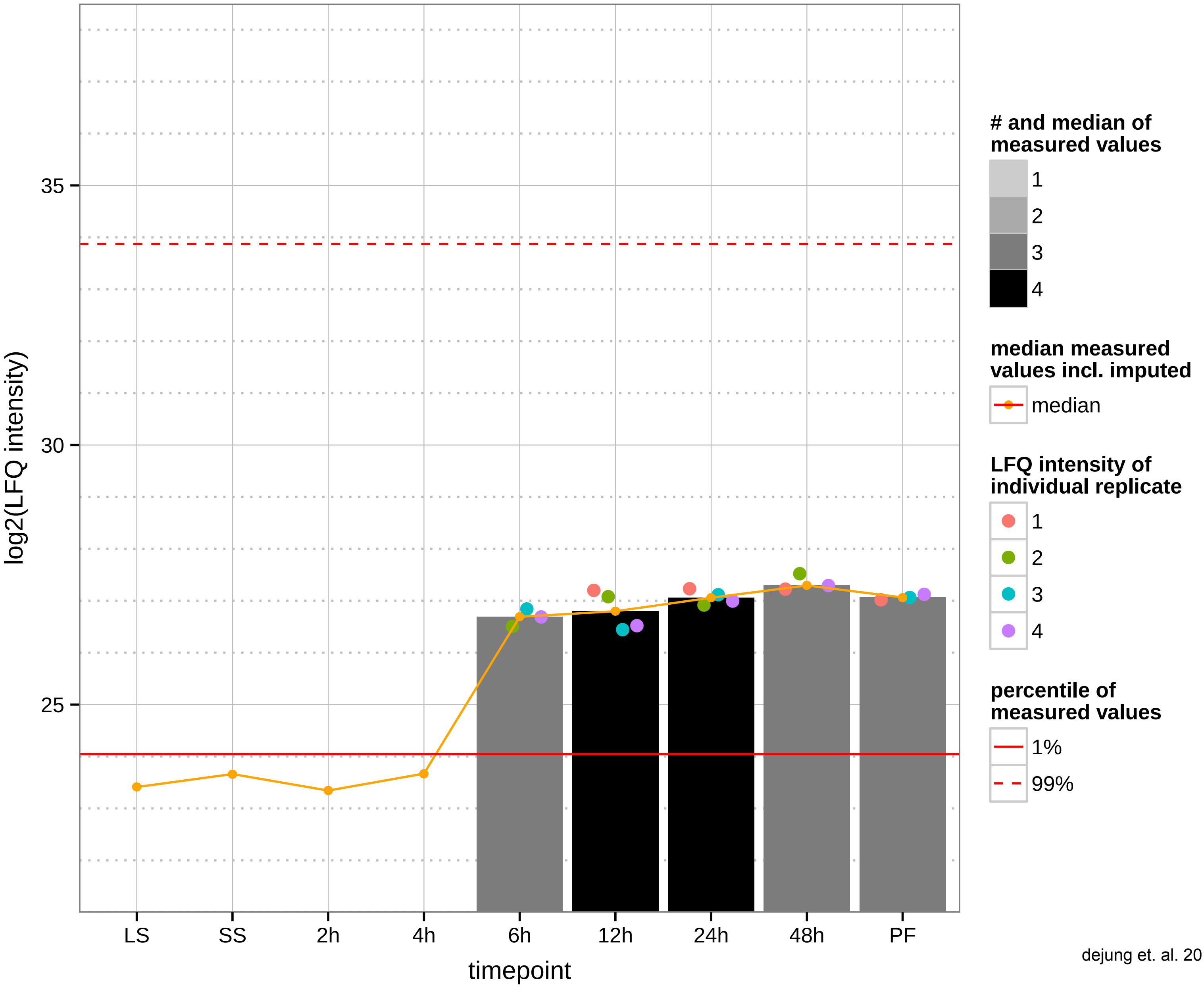
protein kinase, putative, (OTHER) NEK family, HsNEK1–like
Tb927.10.5940;Tb927.10.5930
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, protein phosphorylation, quorum sensing invo
PGOF: ATP binding, phospholipid binding, protein binding, protein kinase activity, transferase activity, transferring phosphorus
PGOC: null
PGOP: protein phosphorylation





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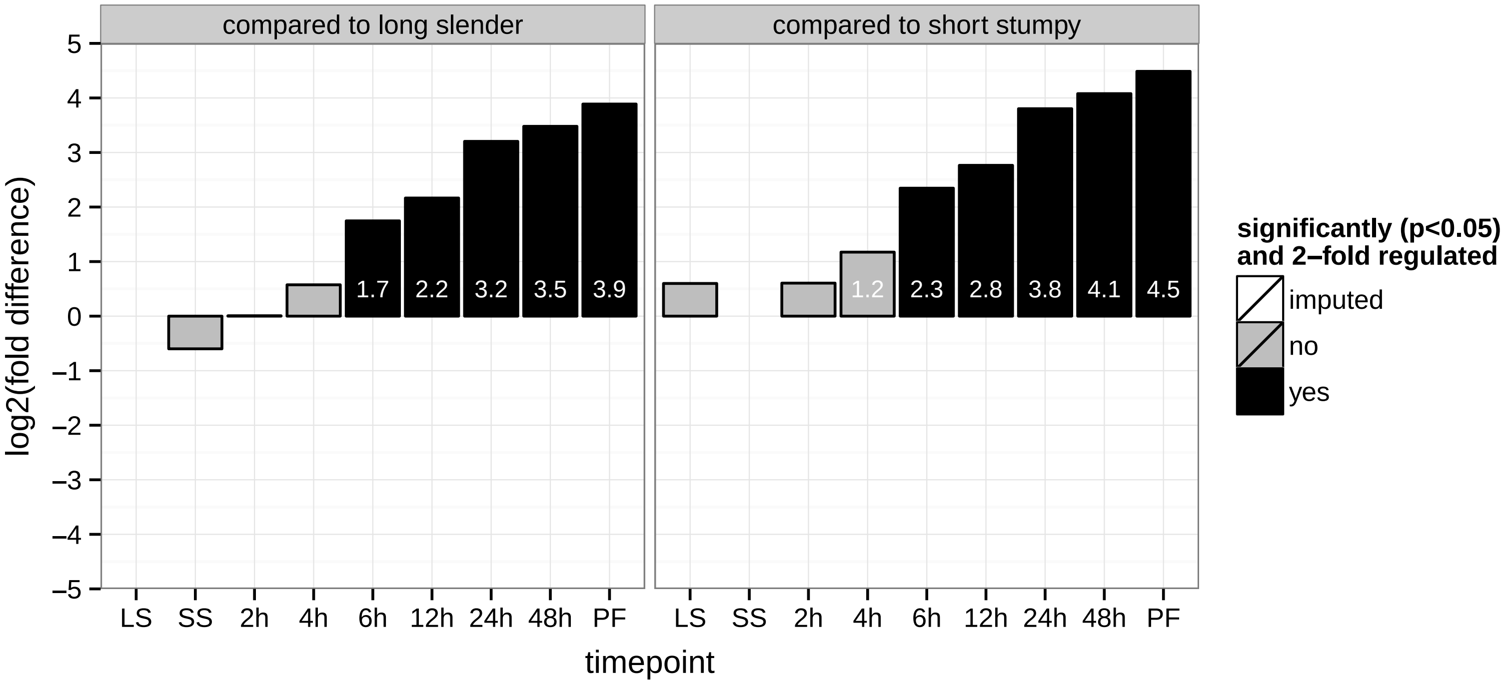
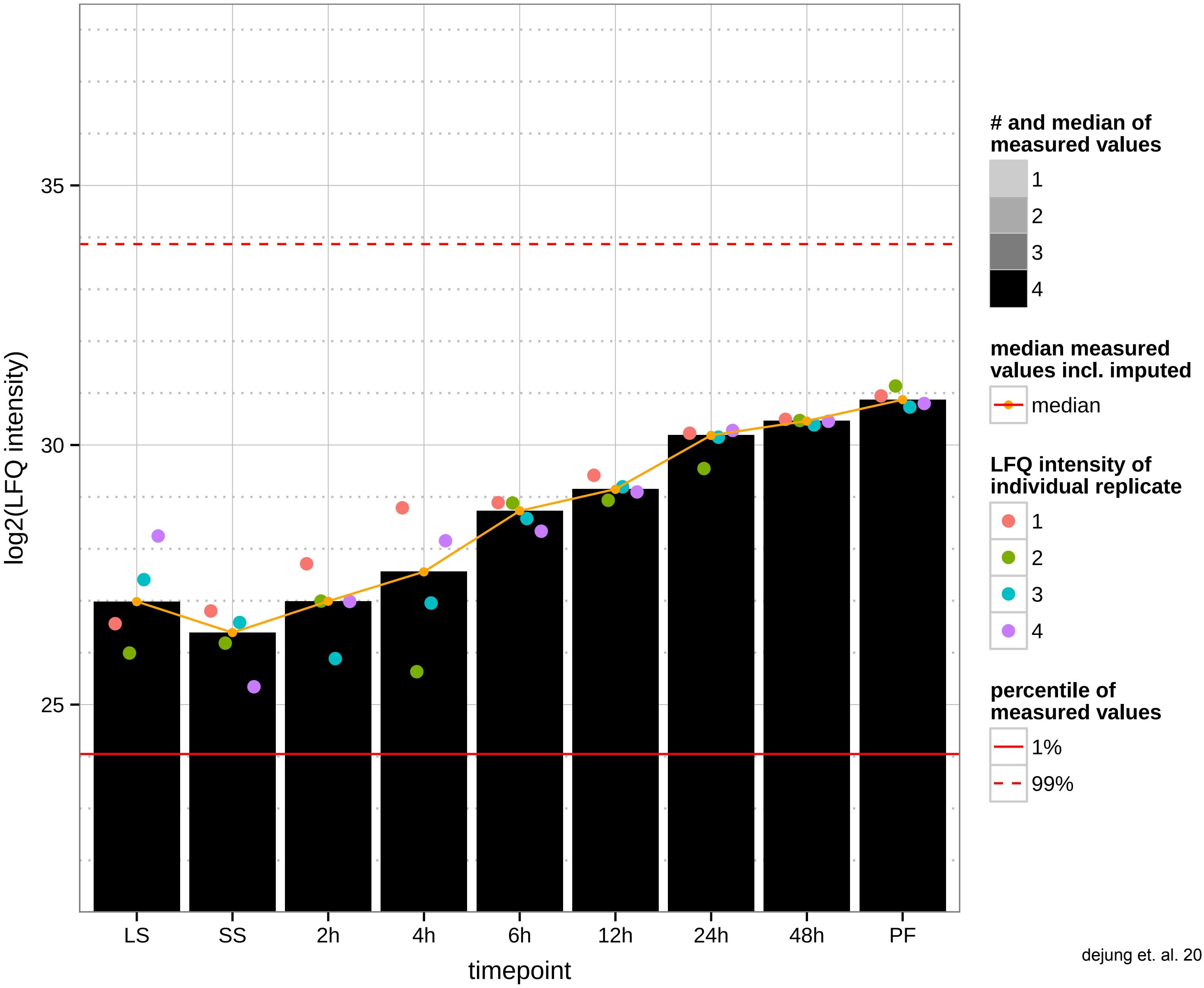
ATP−dependent DEAD/H RNA helicase HEL64, putative (HEL64)
Tb927.10.6630
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: cytosol
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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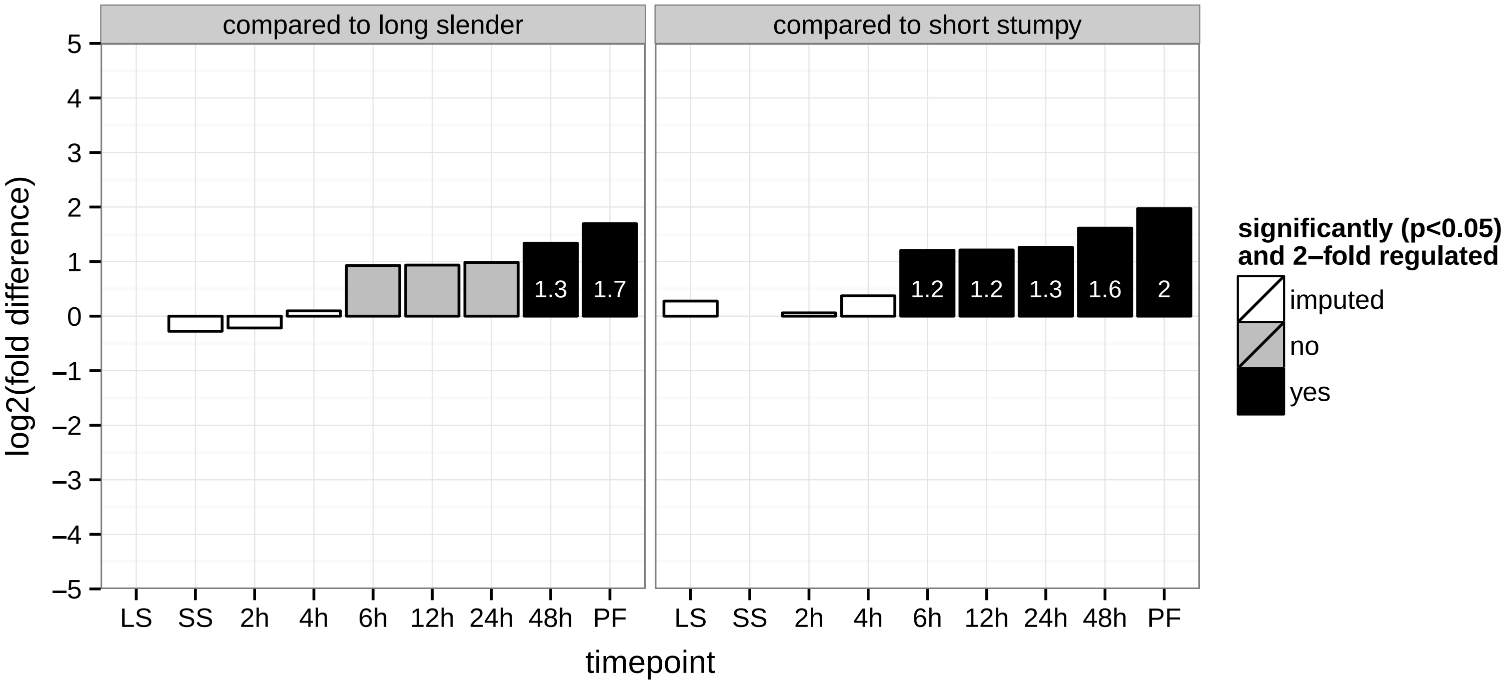
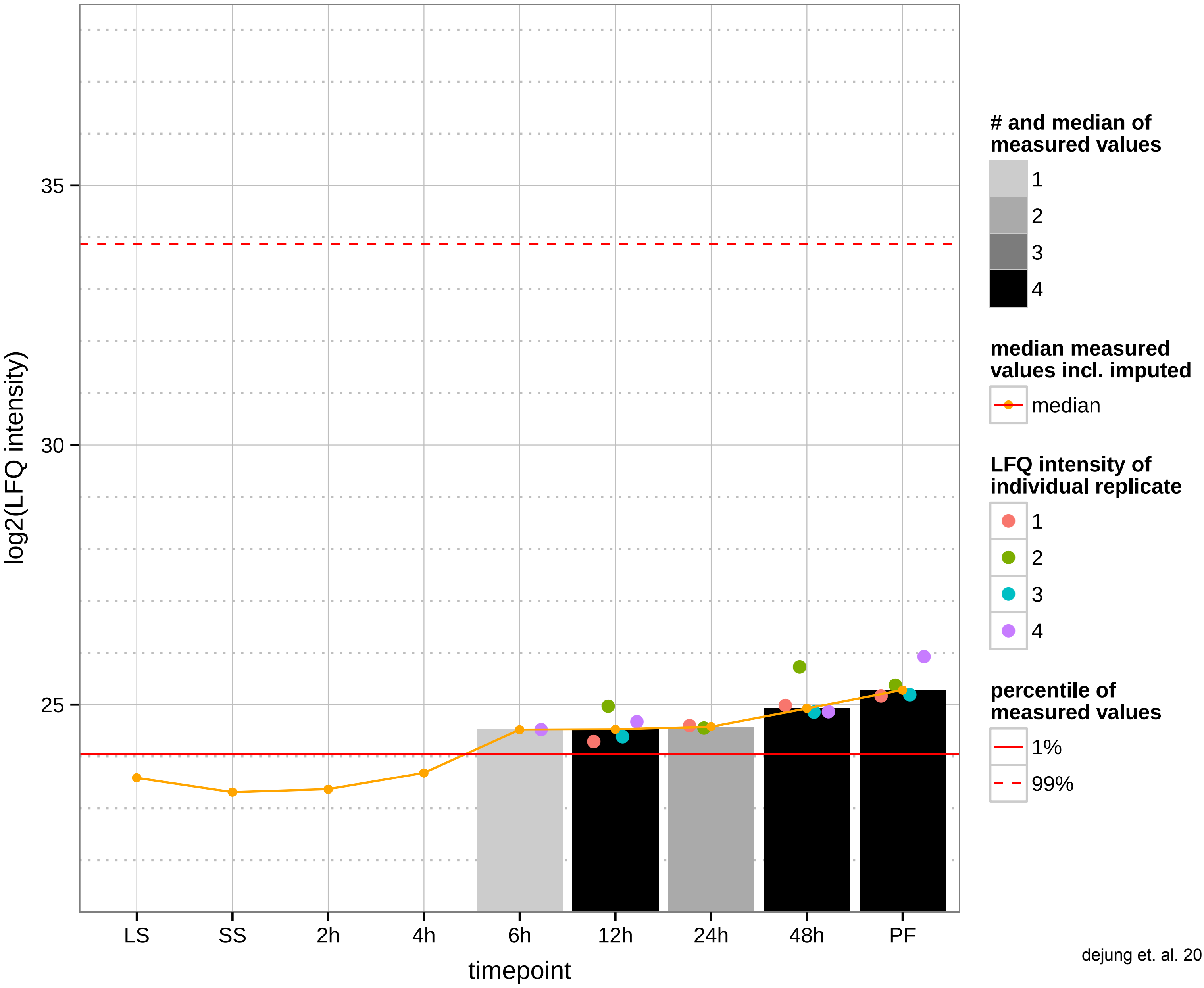
hypothetical protein, conserved
Tb927.10.9000
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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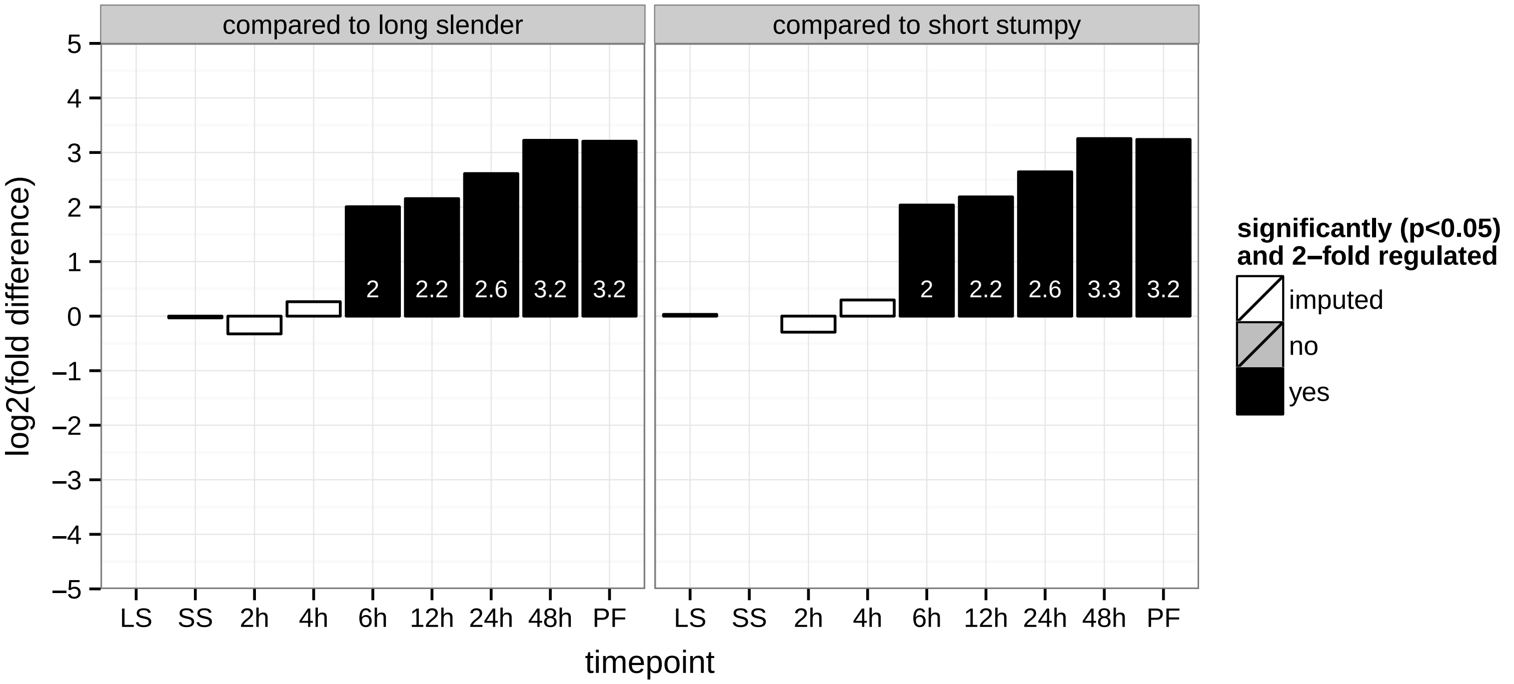
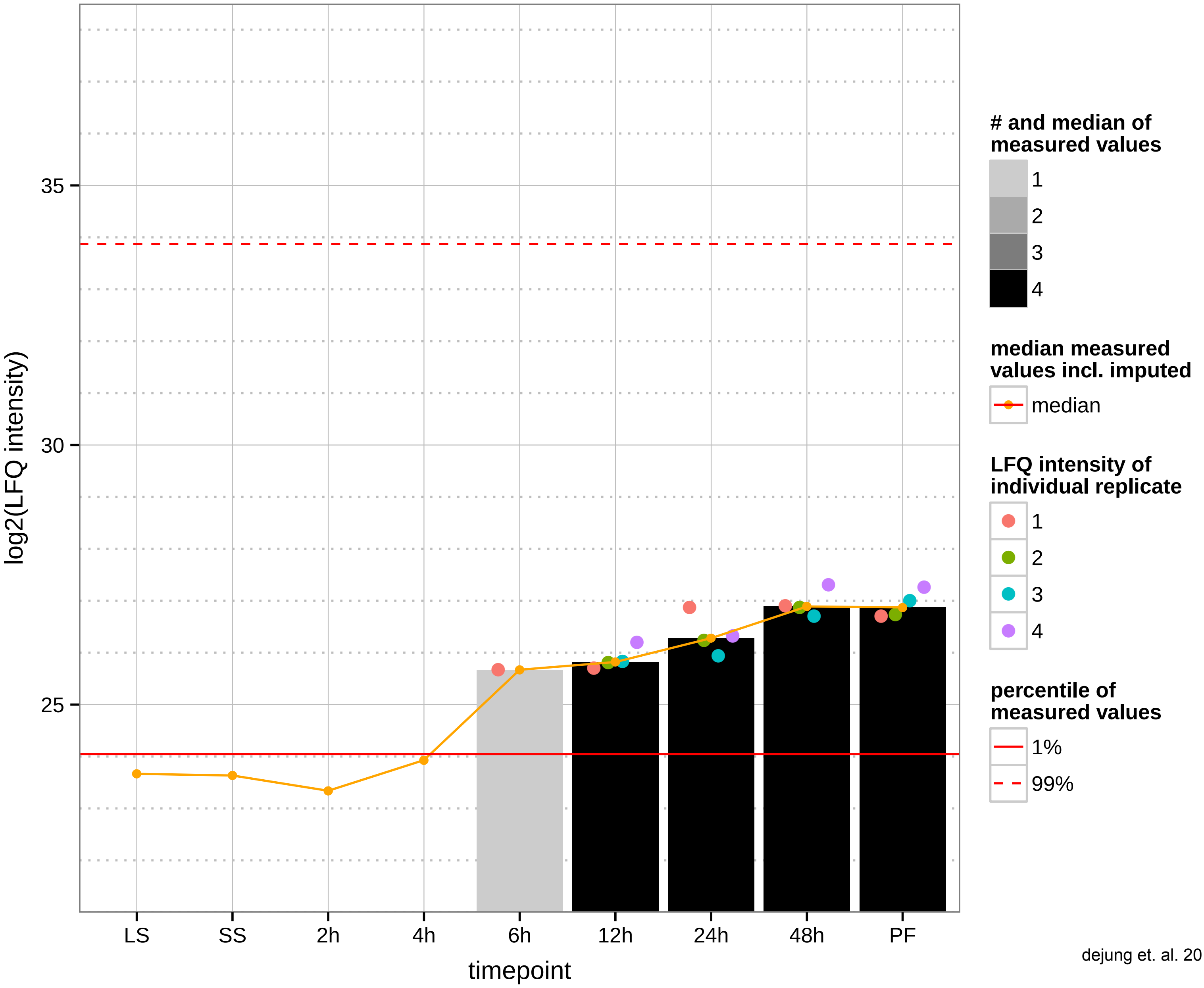
hypothetical protein, conserved
Tb927.11.10150
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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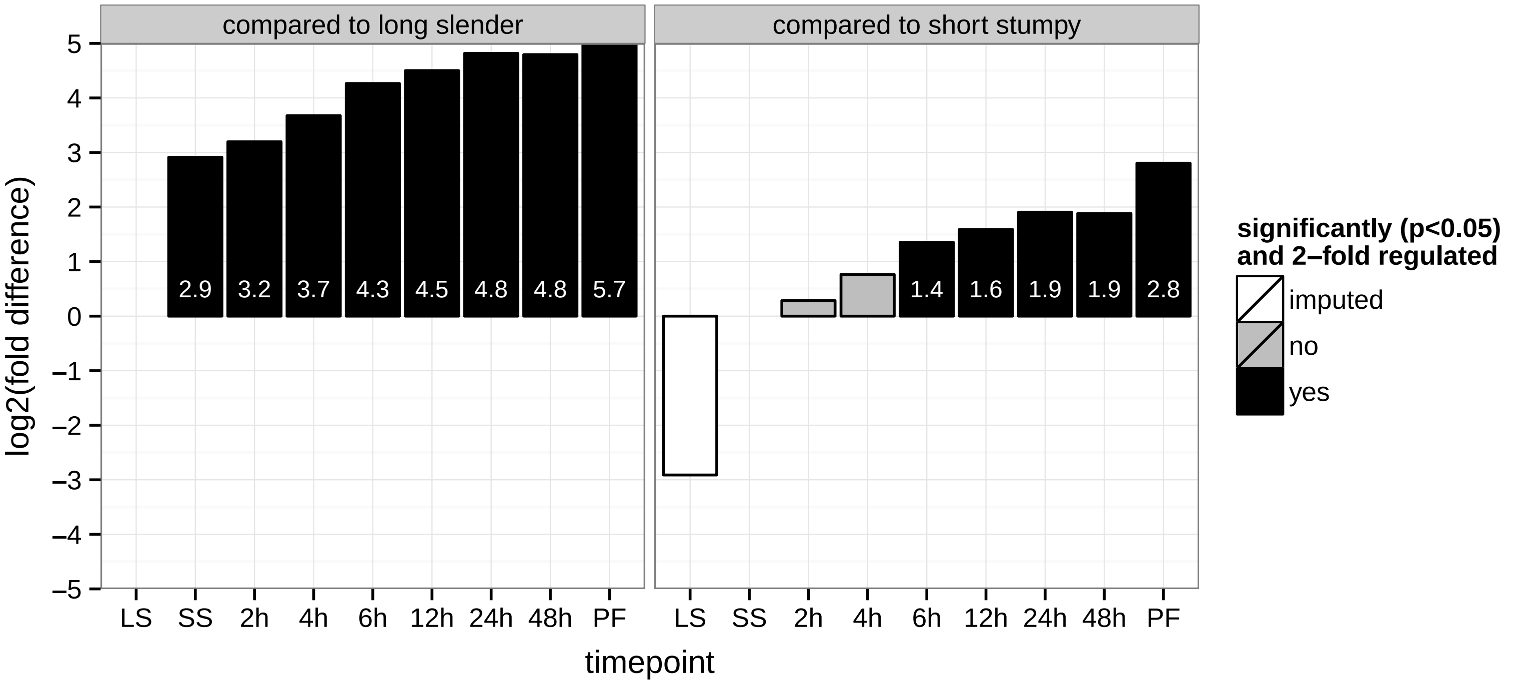
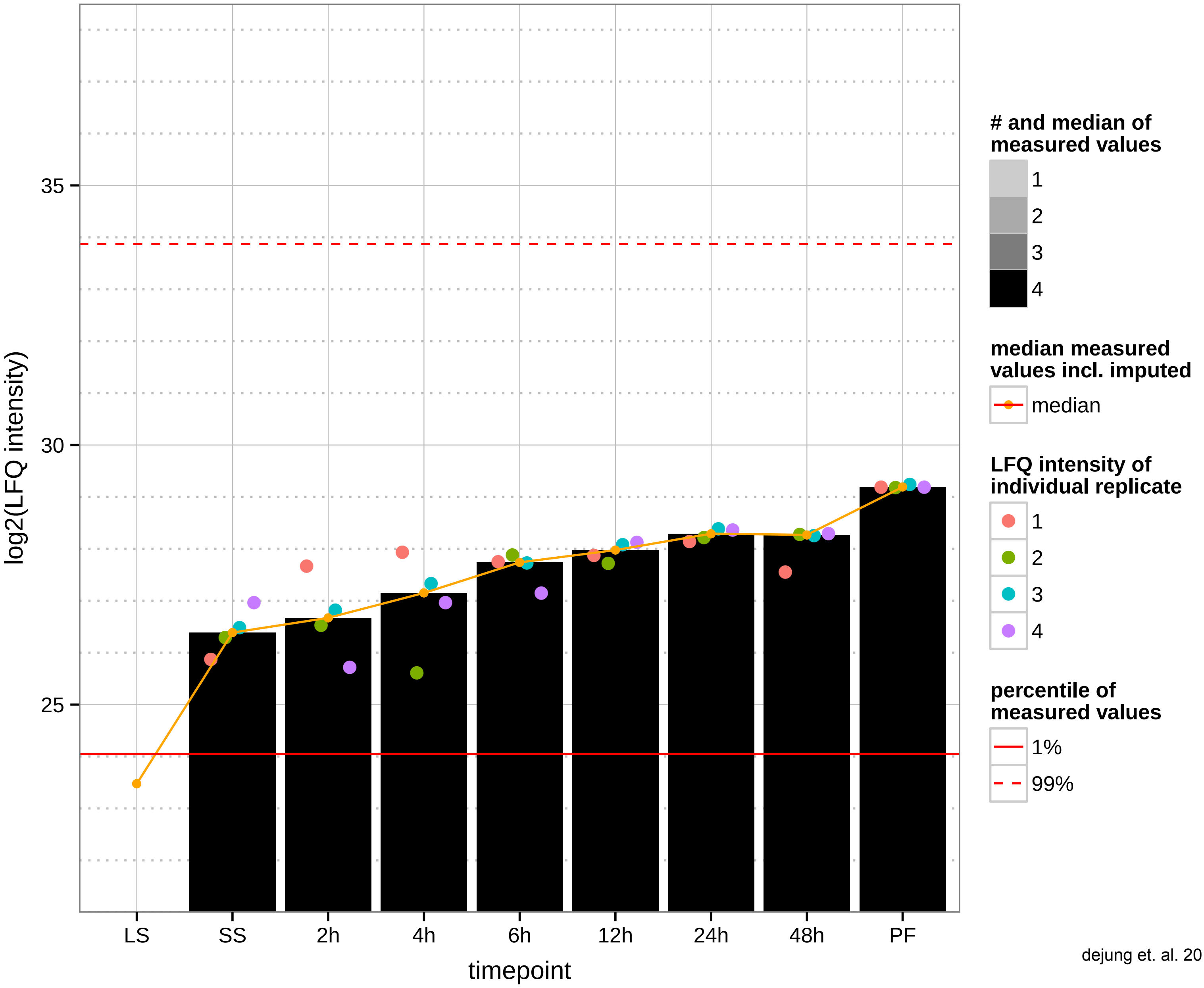
glycosyl hydrolase–like protein
Tb927.11.10370
AGOF: hydrolase activity, hydrolyzing O–glycosyl compounds
AGOC: null
AGOP: carbohydrate metabolic process
PGOF: hydrolase activity, hydrolyzing O–glycosyl compounds
PGOC: null
PGOP: carbohydrate metabolic process





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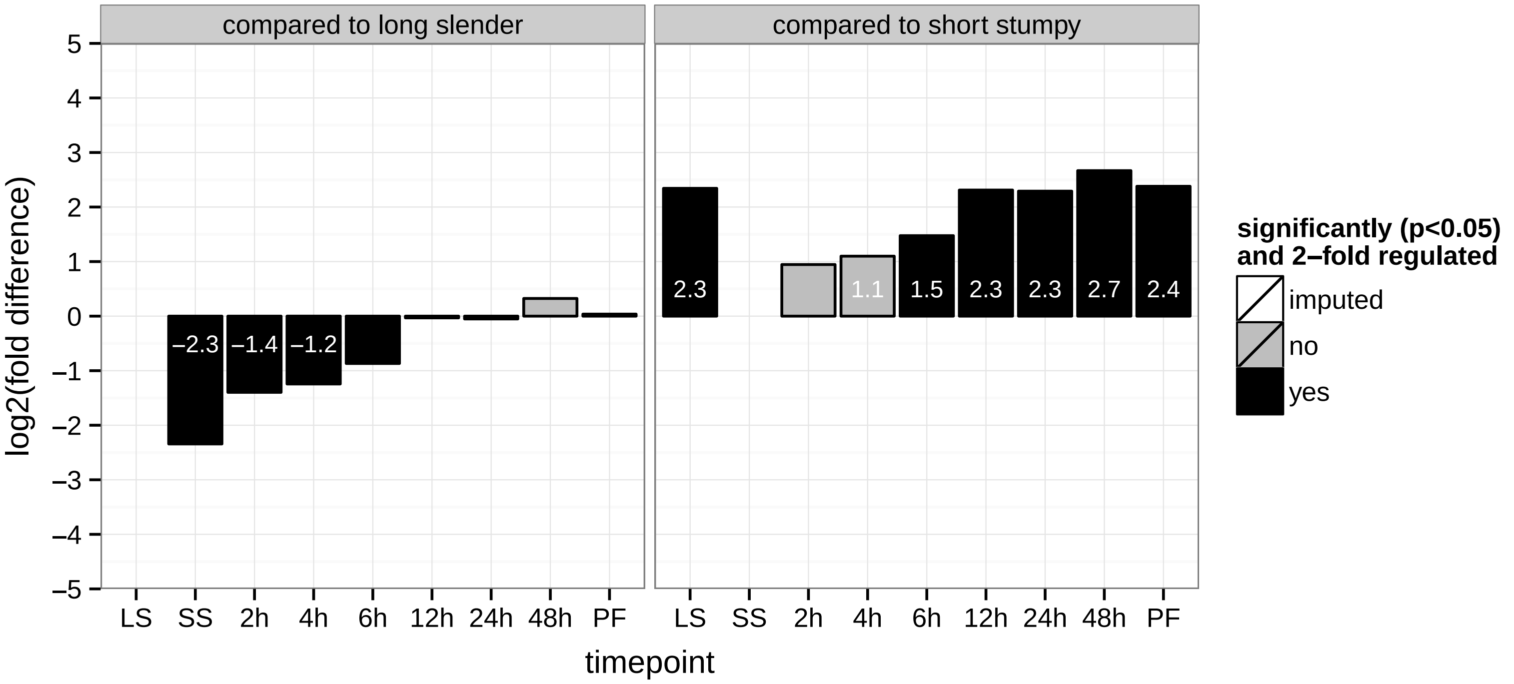
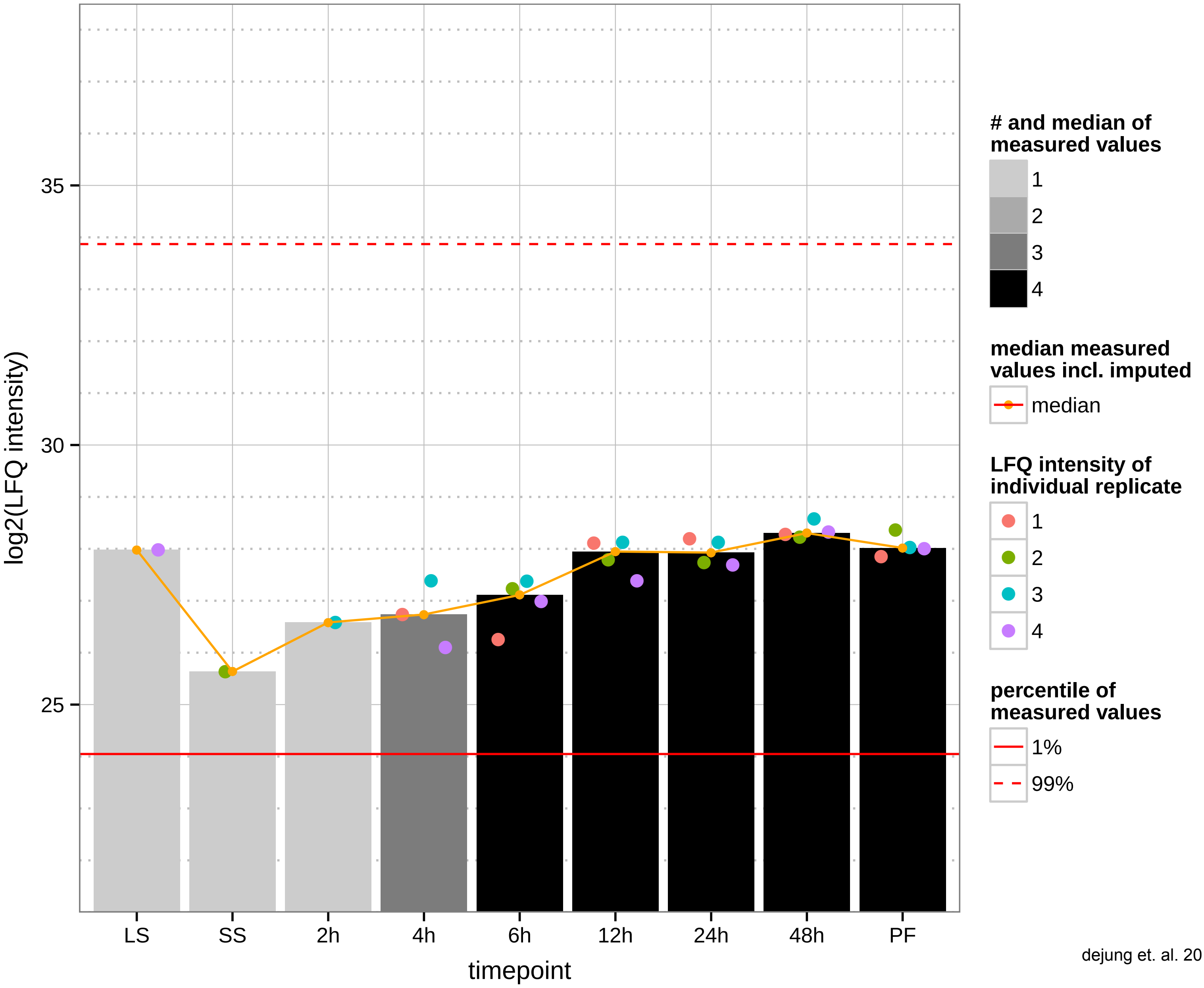
hypothetical protein, conserved
Tb927.11.10770
AGOF: null
AGOC: null
AGOP: intracellular protein transport
PGOF: null
PGOC: null
PGOP: intracellular protein transport





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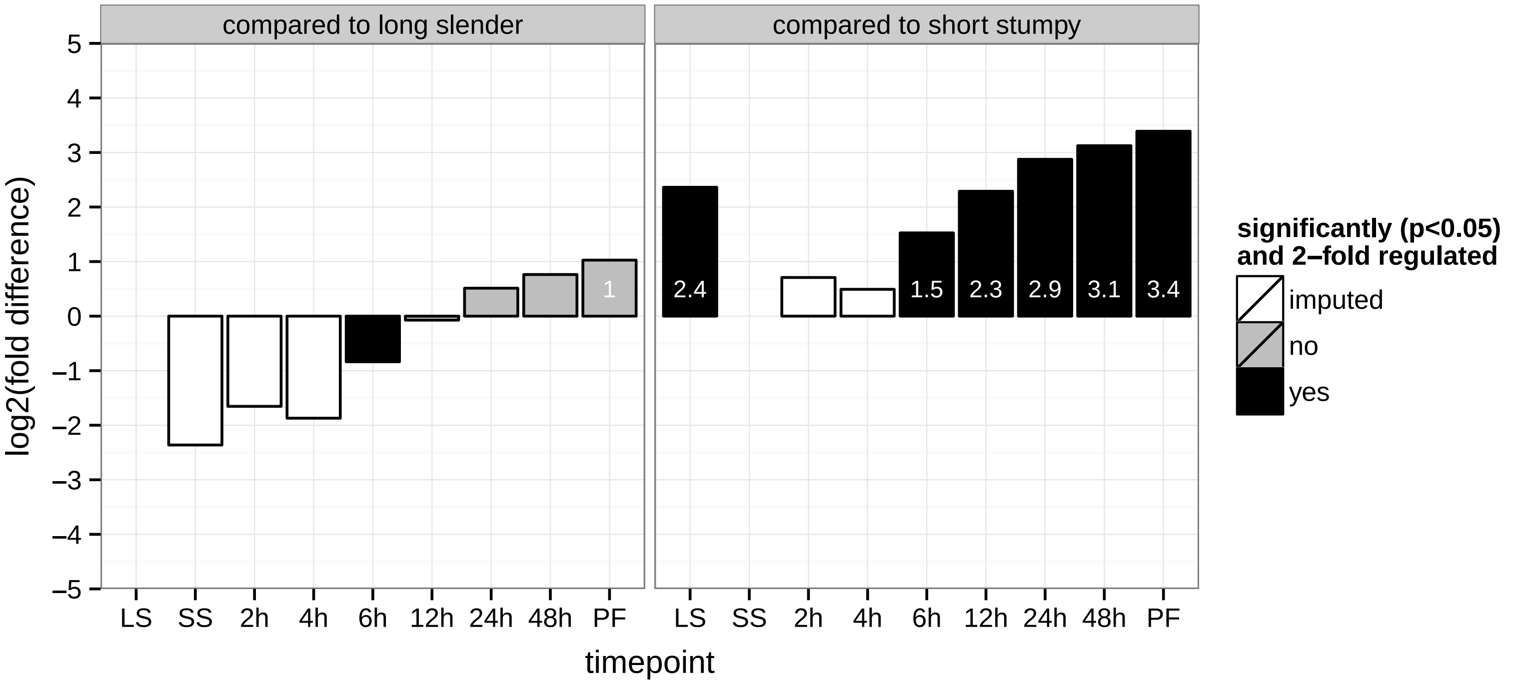
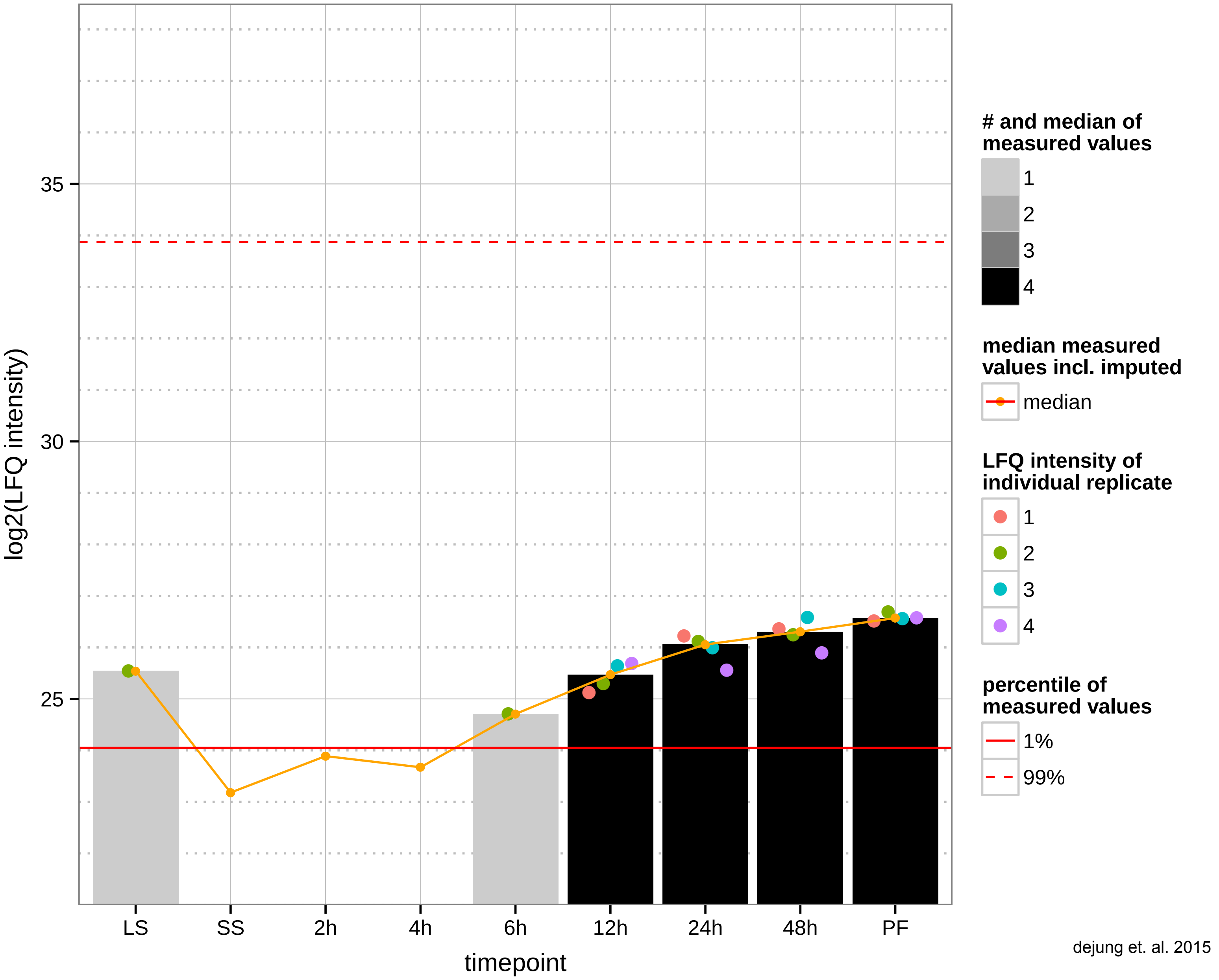
hypothetical protein, conserved
Tb927.11.12440
AGOF: DNA binding, zinc ion binding
AGOC: nucleus
AGOP: DNA–dependent transcription, initiation, histone modification
PGOF: DNA binding, protein binding, zinc ion binding
PGOC: nucleus
PGOP: DNA–dependent transcription, initiation, histone modification





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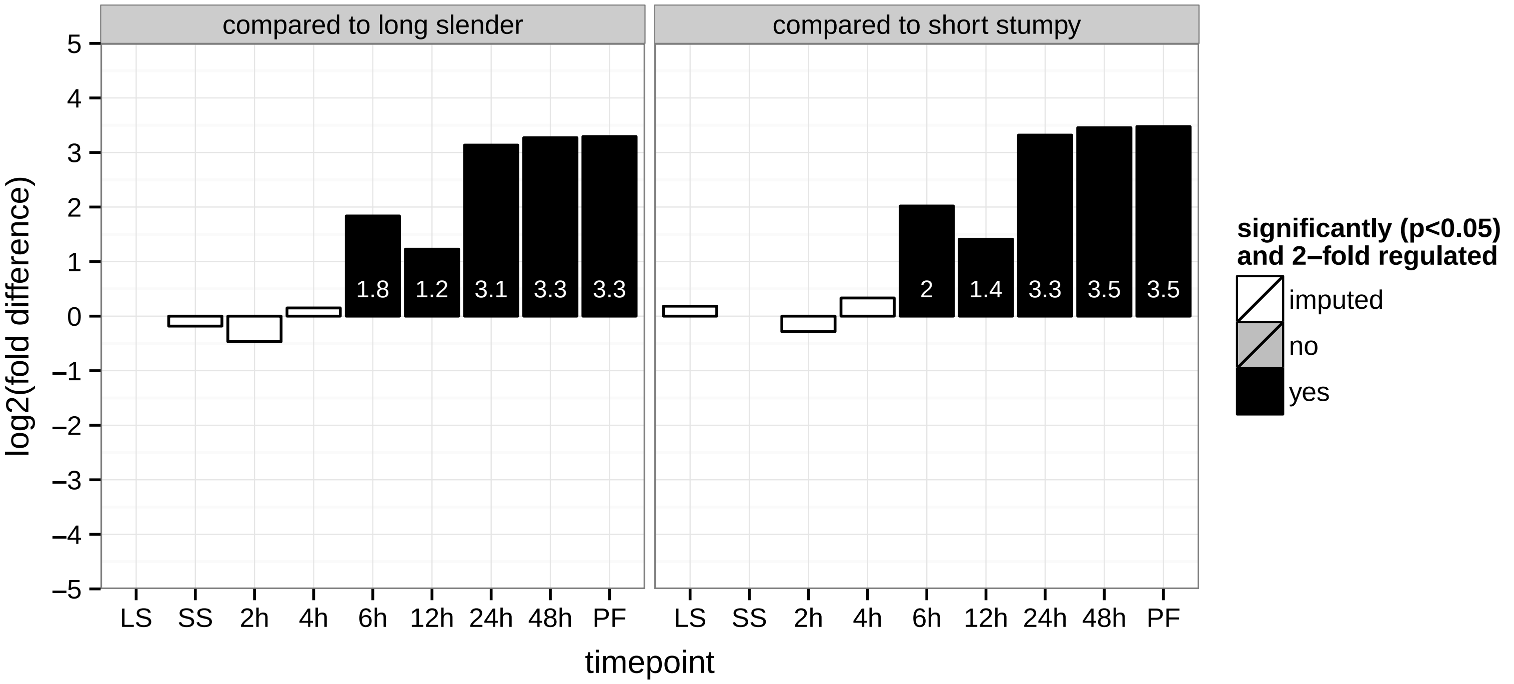
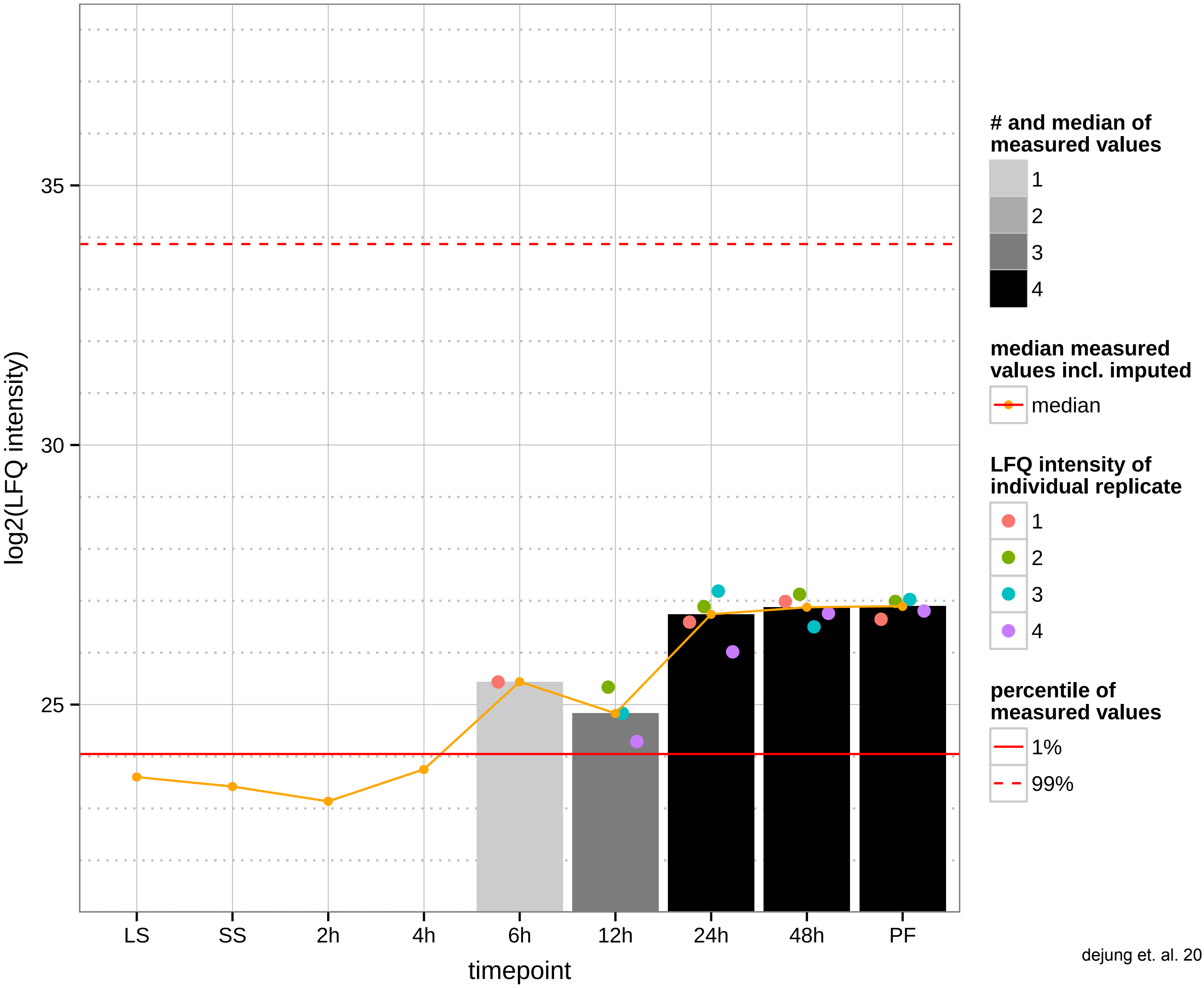
cytochrome b5, putative (CYB5)
Tb927.11.13650
AGOF: glutathione−disulfide reductase activity, heme binding
AGOC: integral to membrane
AGOP: oxidation−reduction process
PGOF: heme binding
PGOC: null
PGOP: null





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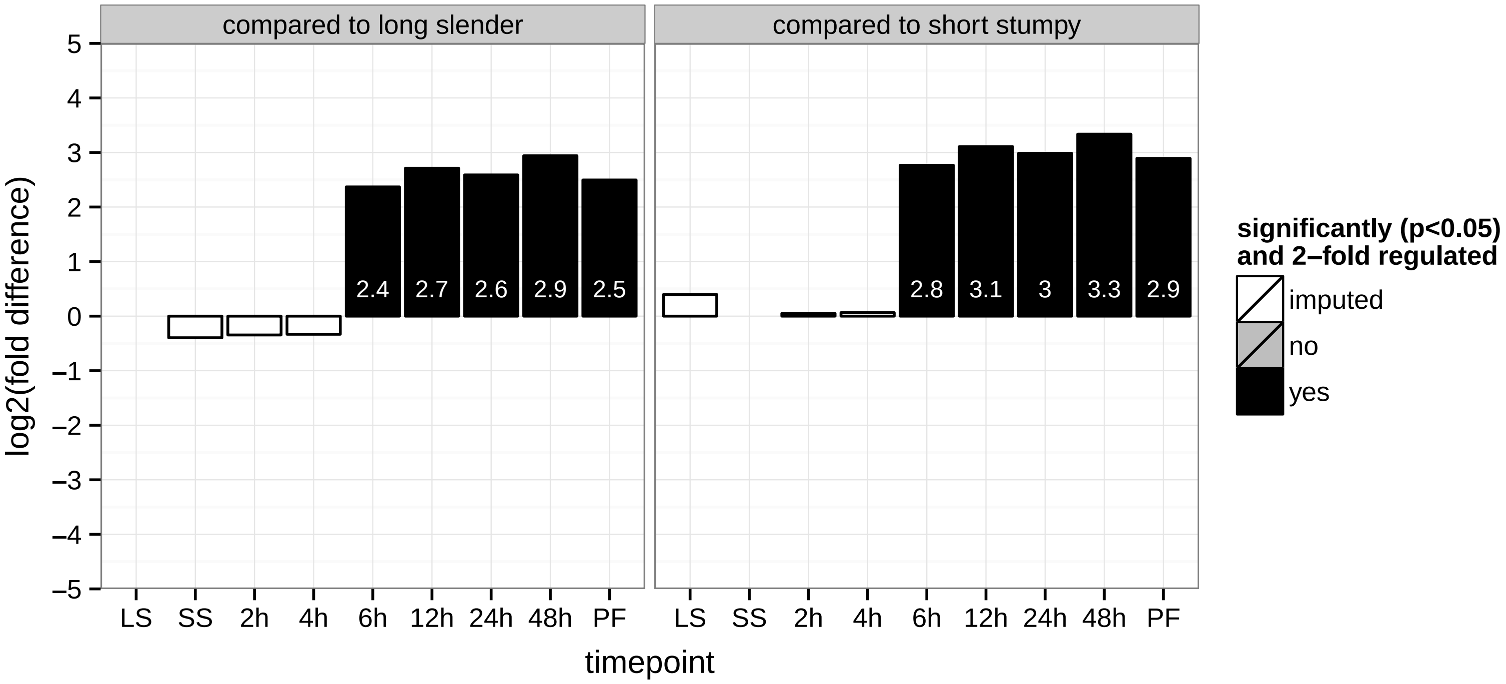
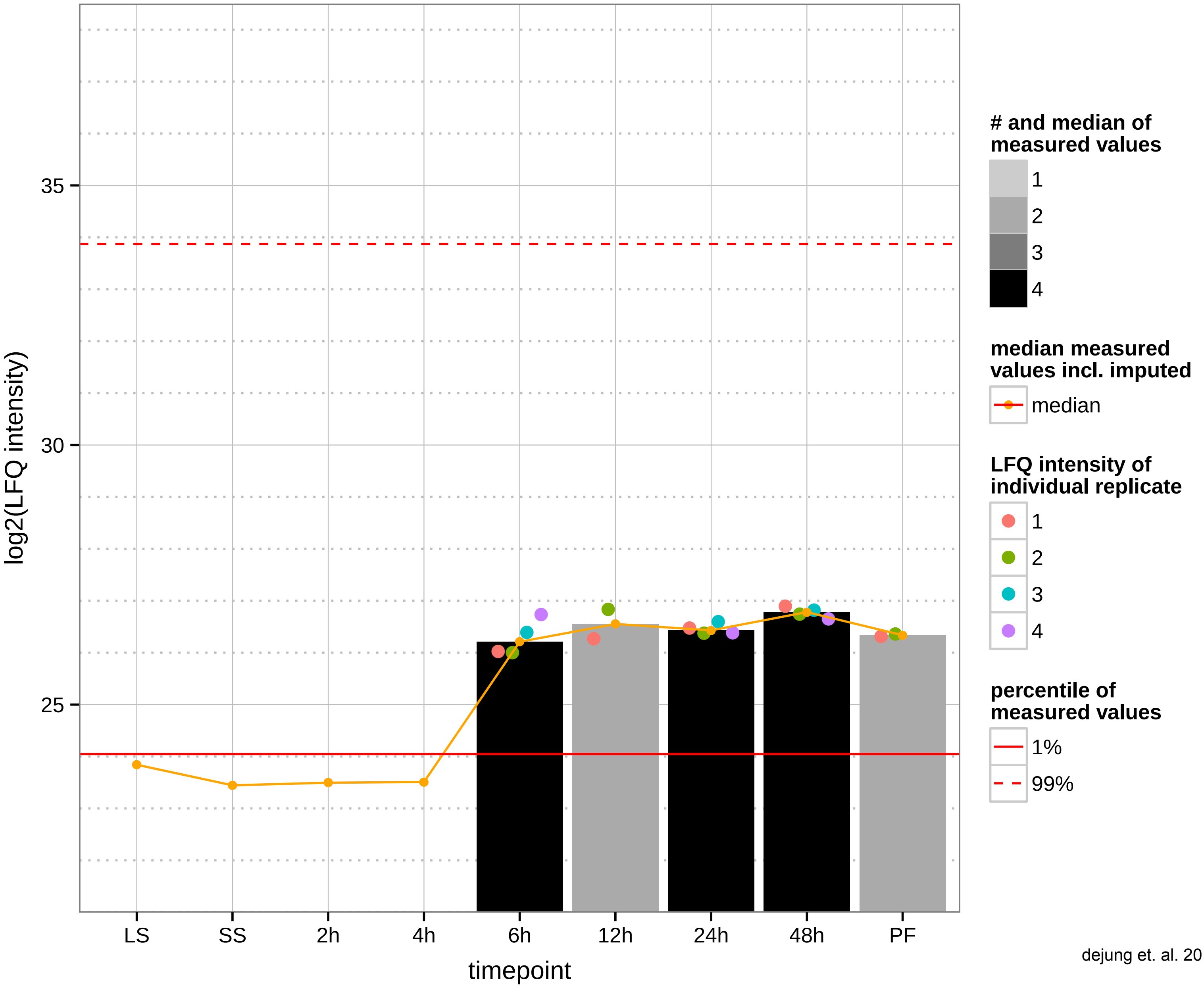
hypothetical protein, conserved
Tb927.11.14160
AGOF: null
AGOC: null
AGOP: null
PGOF: carboxylesterase activity
PGOC: null
PGOP: null





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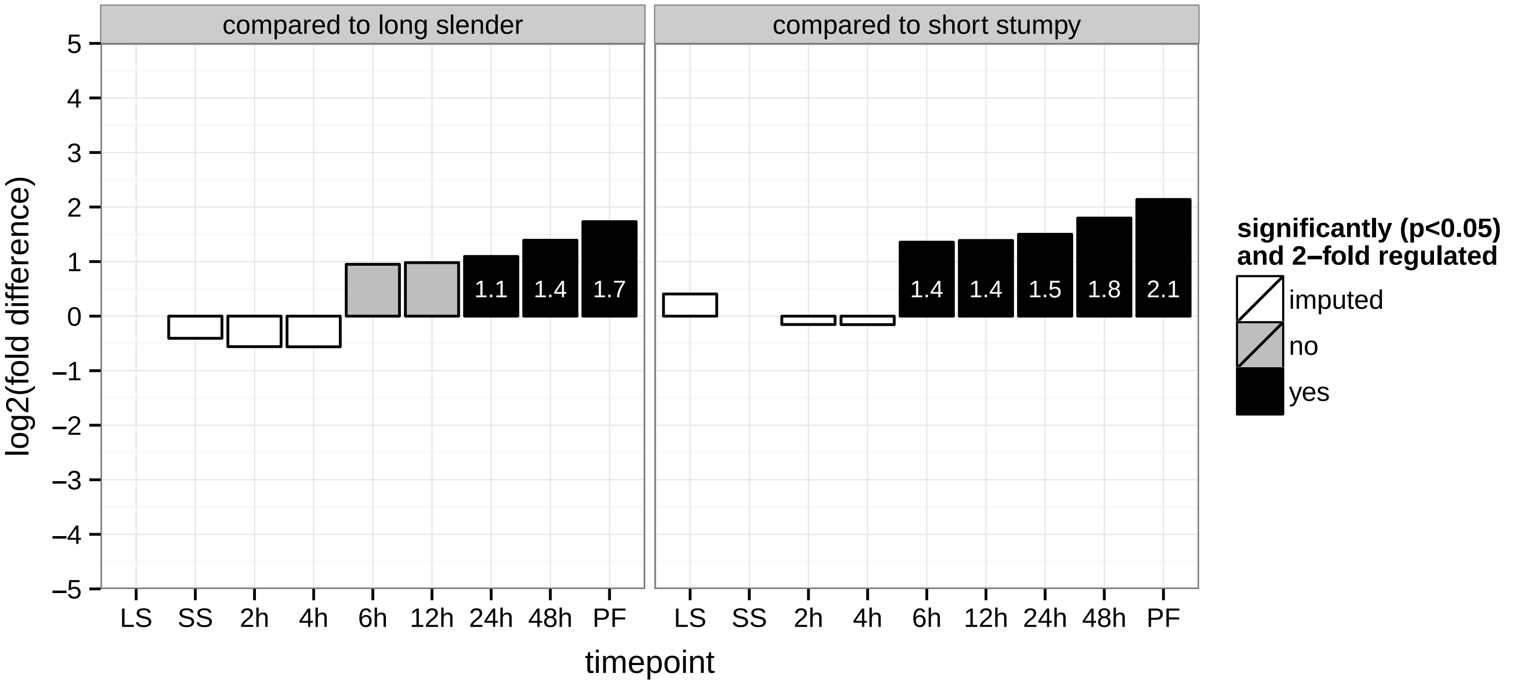
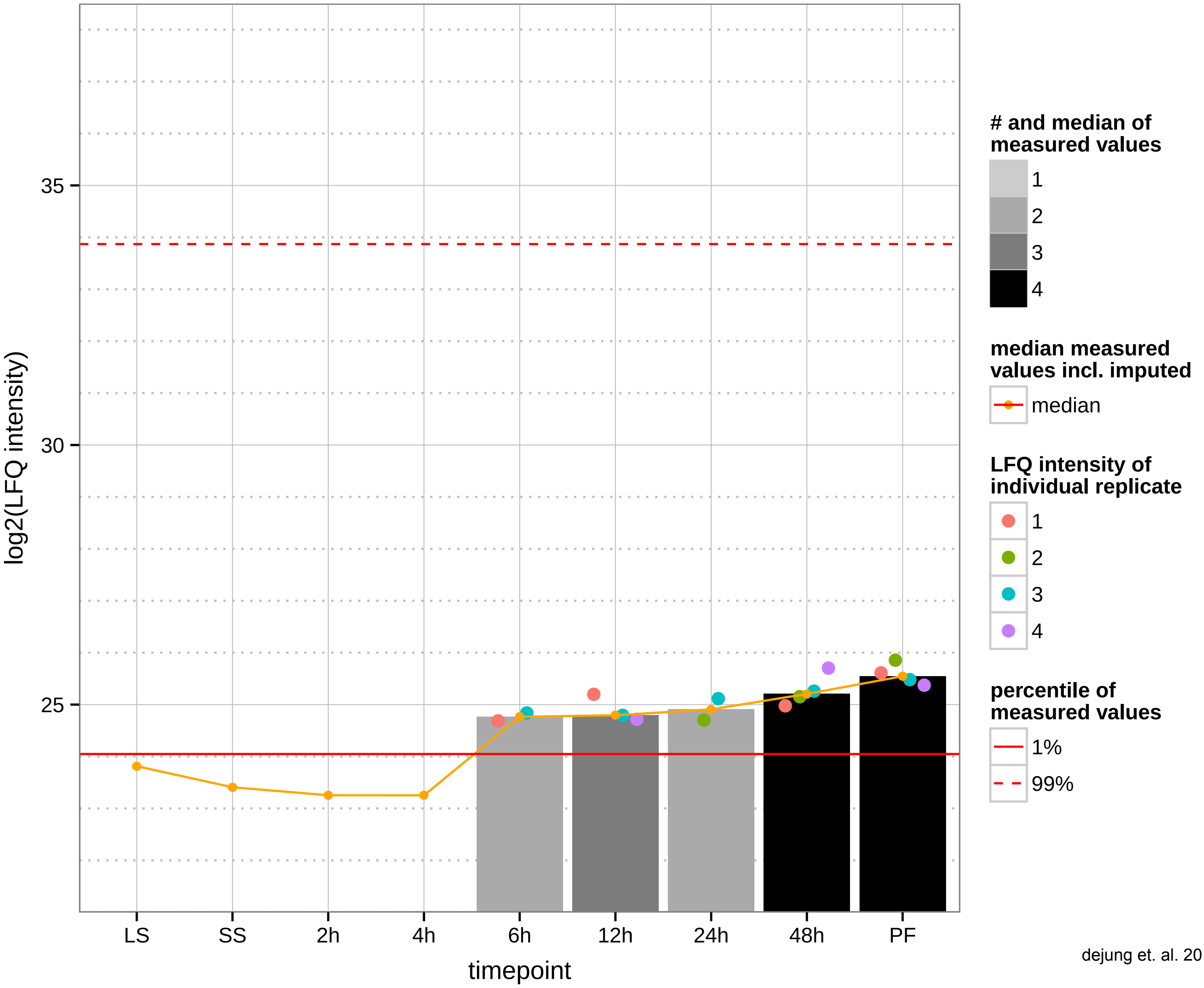
hypothetical protein, conserved
Tb927.11.15630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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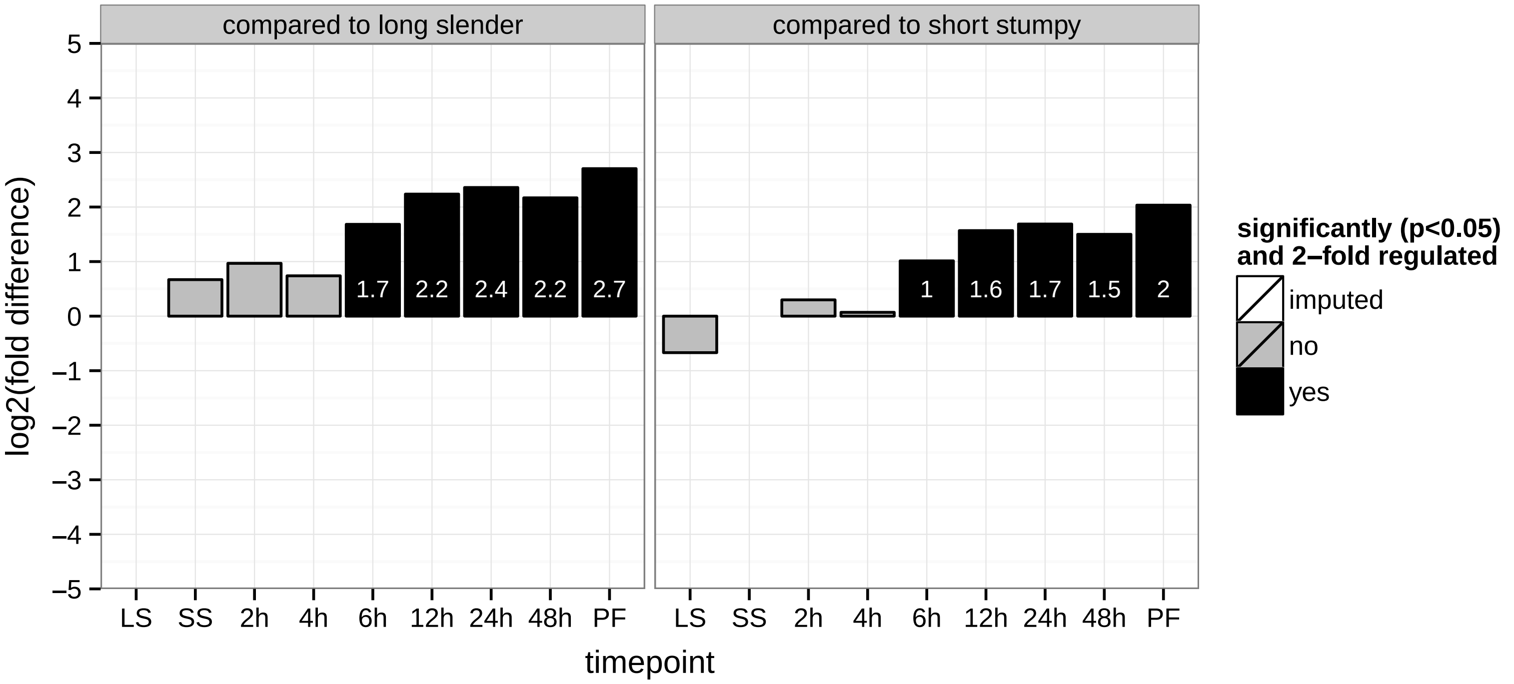
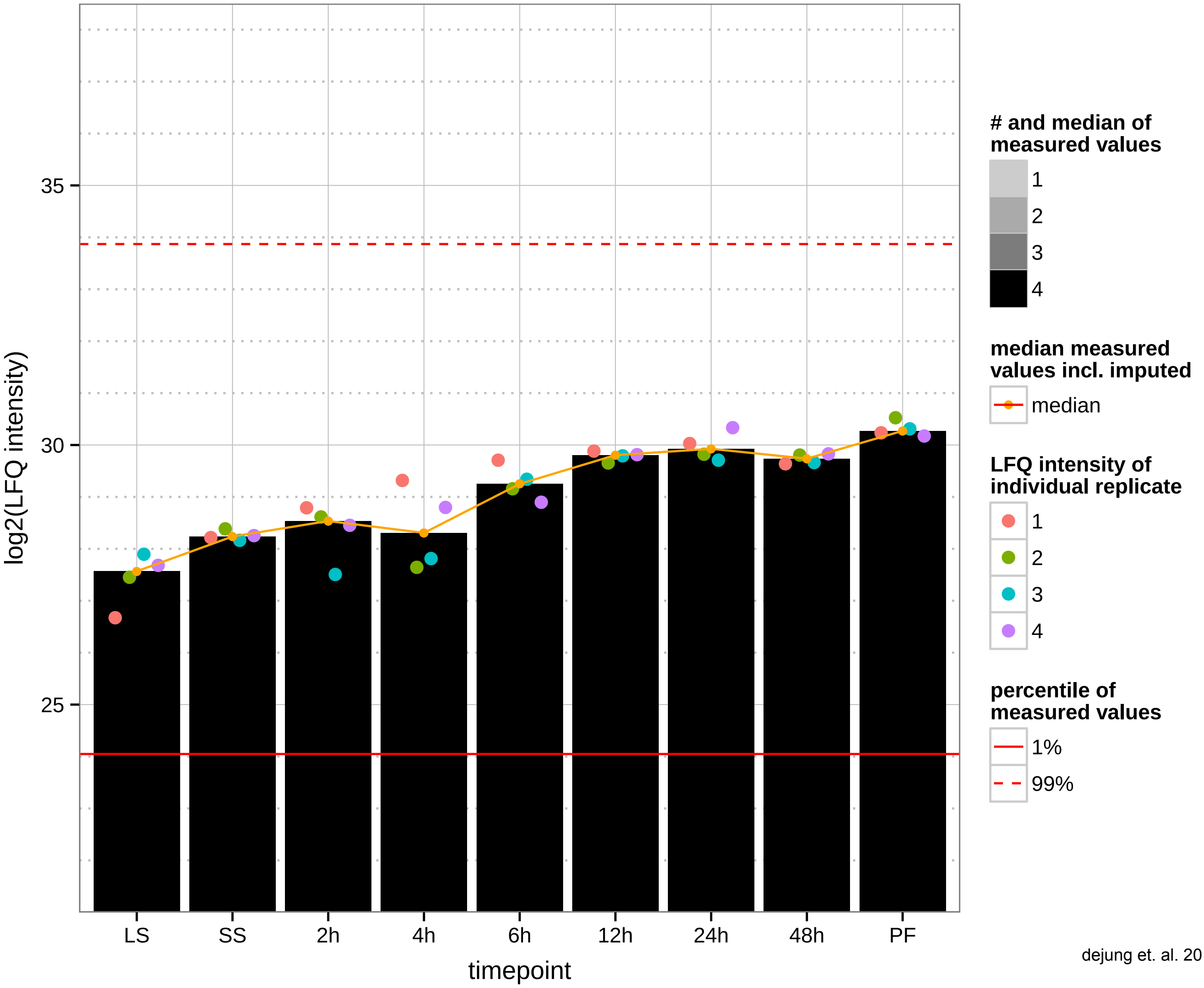
nucleolar GTP−binding protein 1 (NOG1)
Tb927.11.3120
AGOF: GTP binding
AGOC: nucleolus
AGOP: ribosome biogenesis
PGOF: GTP binding
PGOC: nucleolus
PGOP: null





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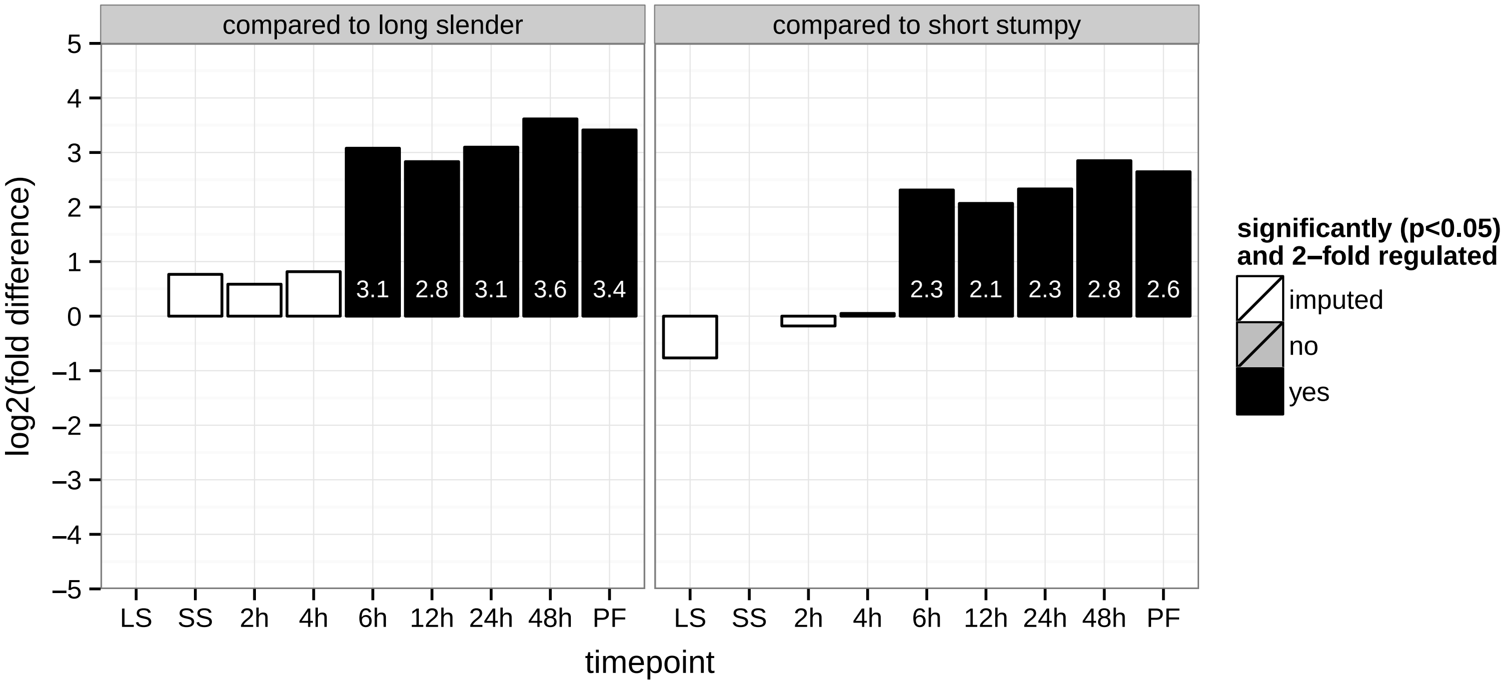
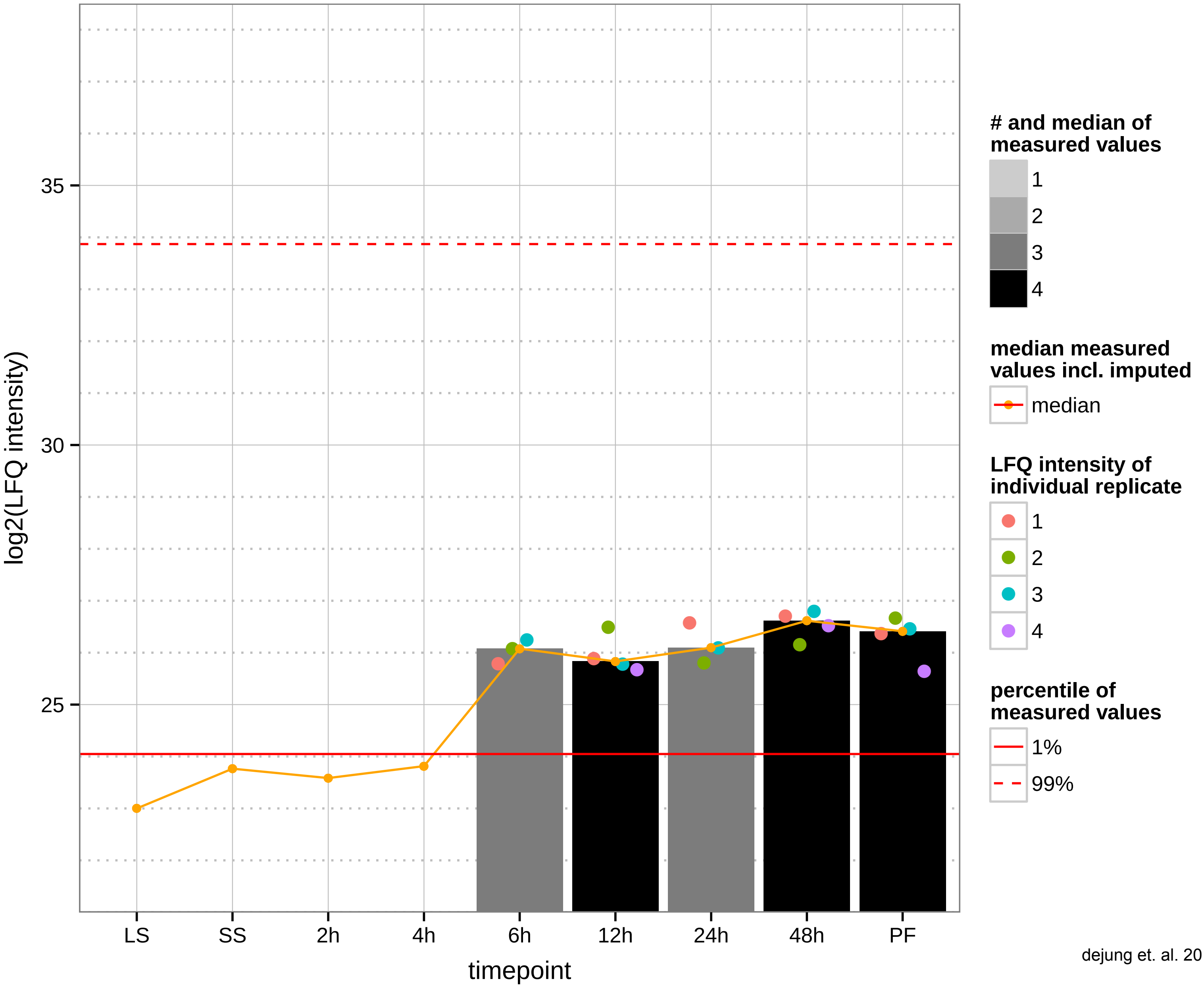
nucleoporin 48 (TbNup48)
Tb927.11.4540
AGOF: null
AGOC: nuclear pore
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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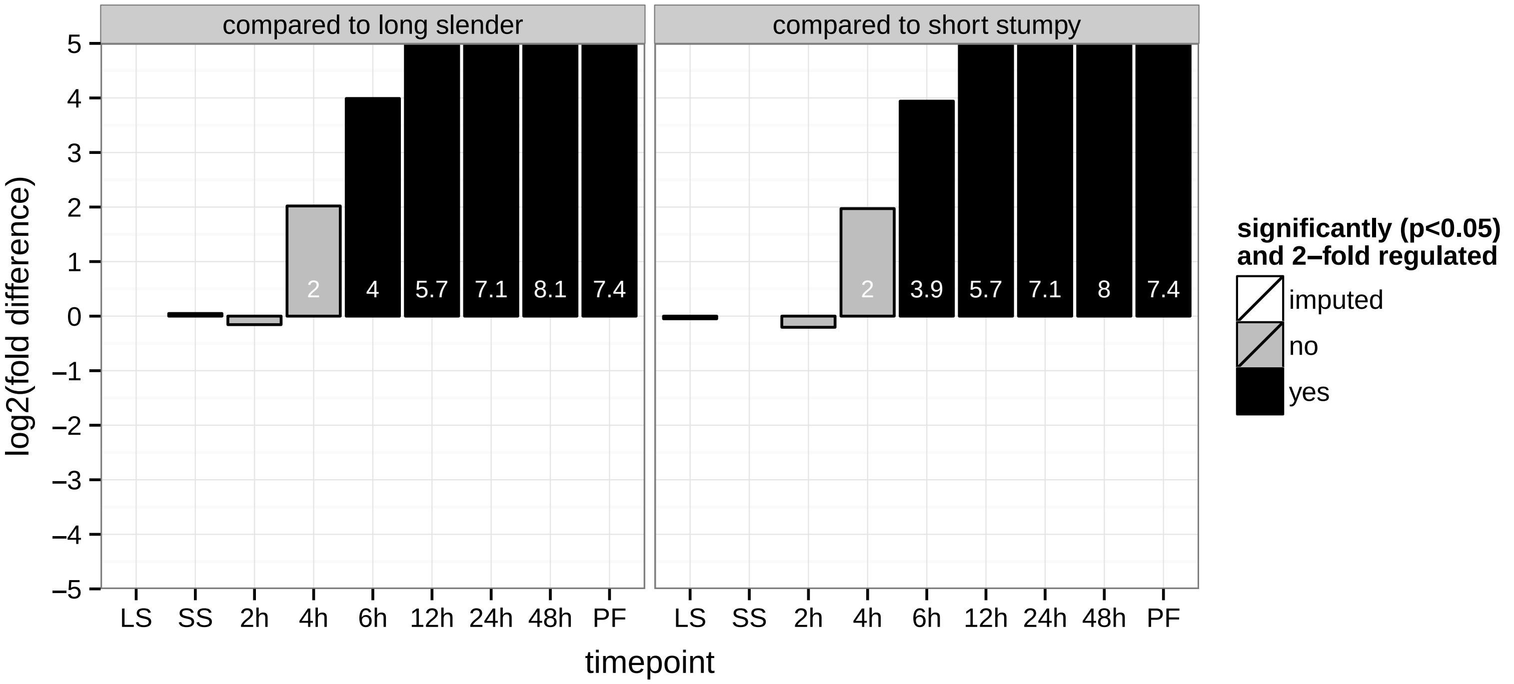
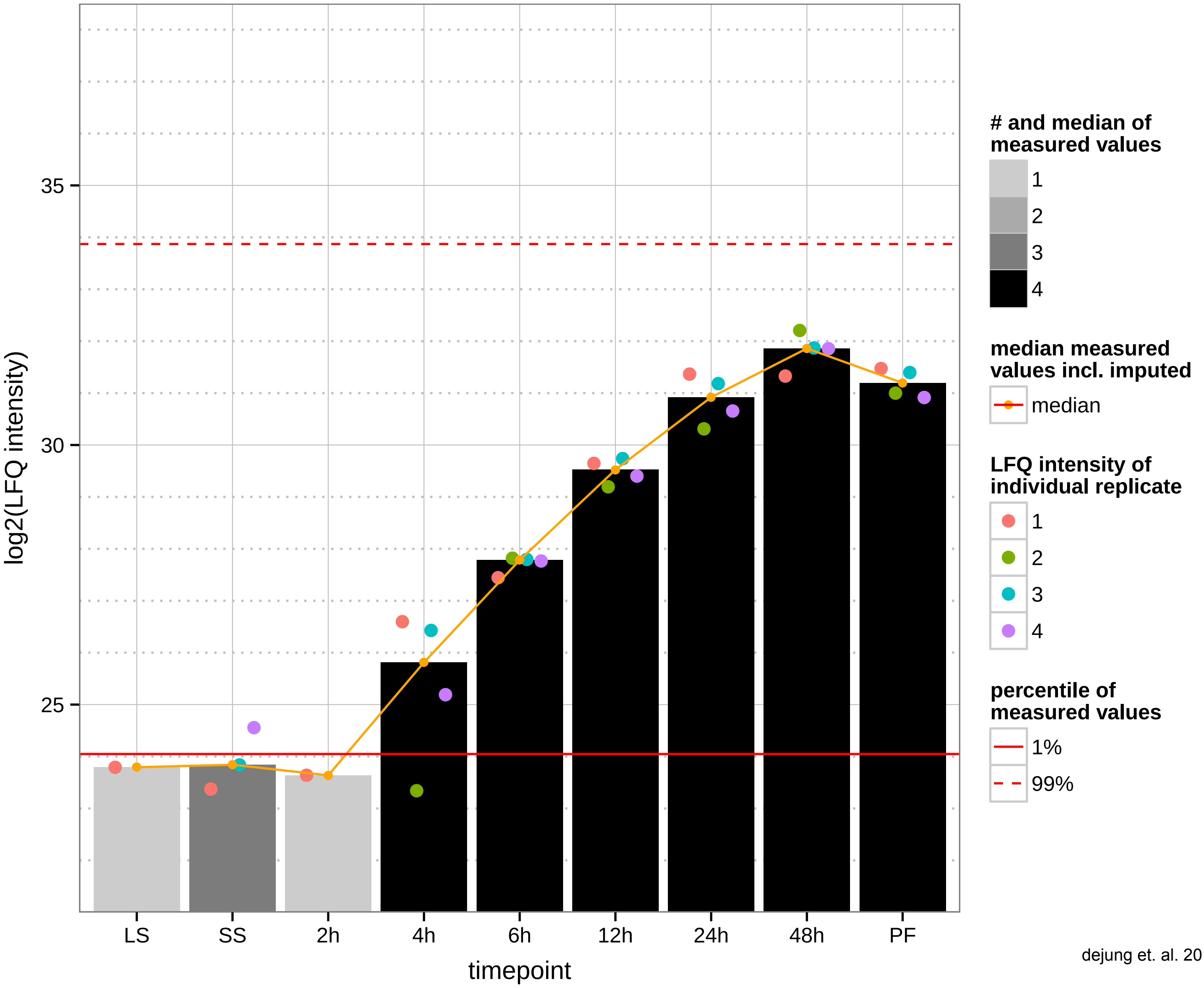
sterol 14–alpha–demethylase, cytochrome P450 51A1, lanosterol 14–alpha–demethylase (CYP51)
Tb927.11.6210
AGOF: electron carrier activity, heme binding, iron ion binding, monooxygenase activity, oxidoreductase activity
AGOC: null
AGOP: metabolic process
PGOF: electron carrier activity, heme binding, iron ion binding, oxidoreductase activity, acting on paired donors, with incorpora
PGOC: null
PGOP: oxidation–reduction process





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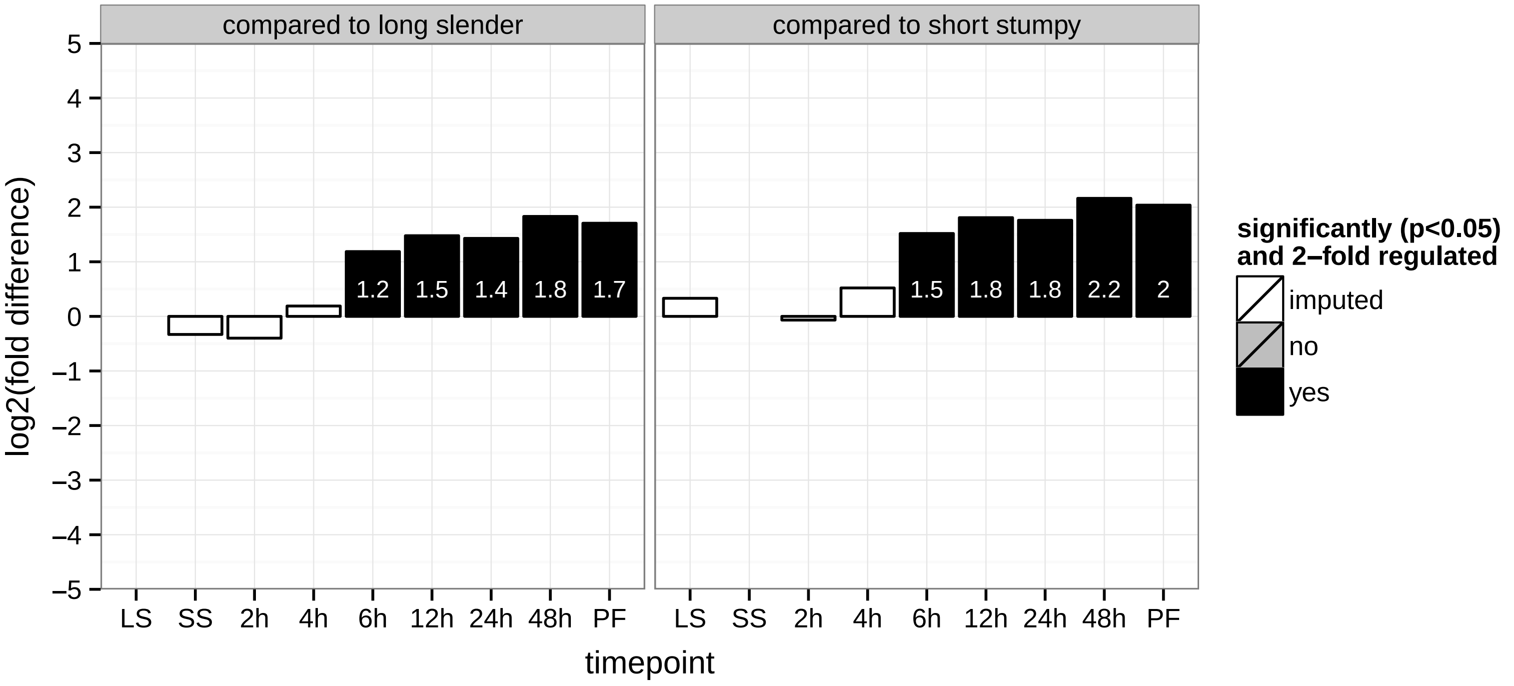
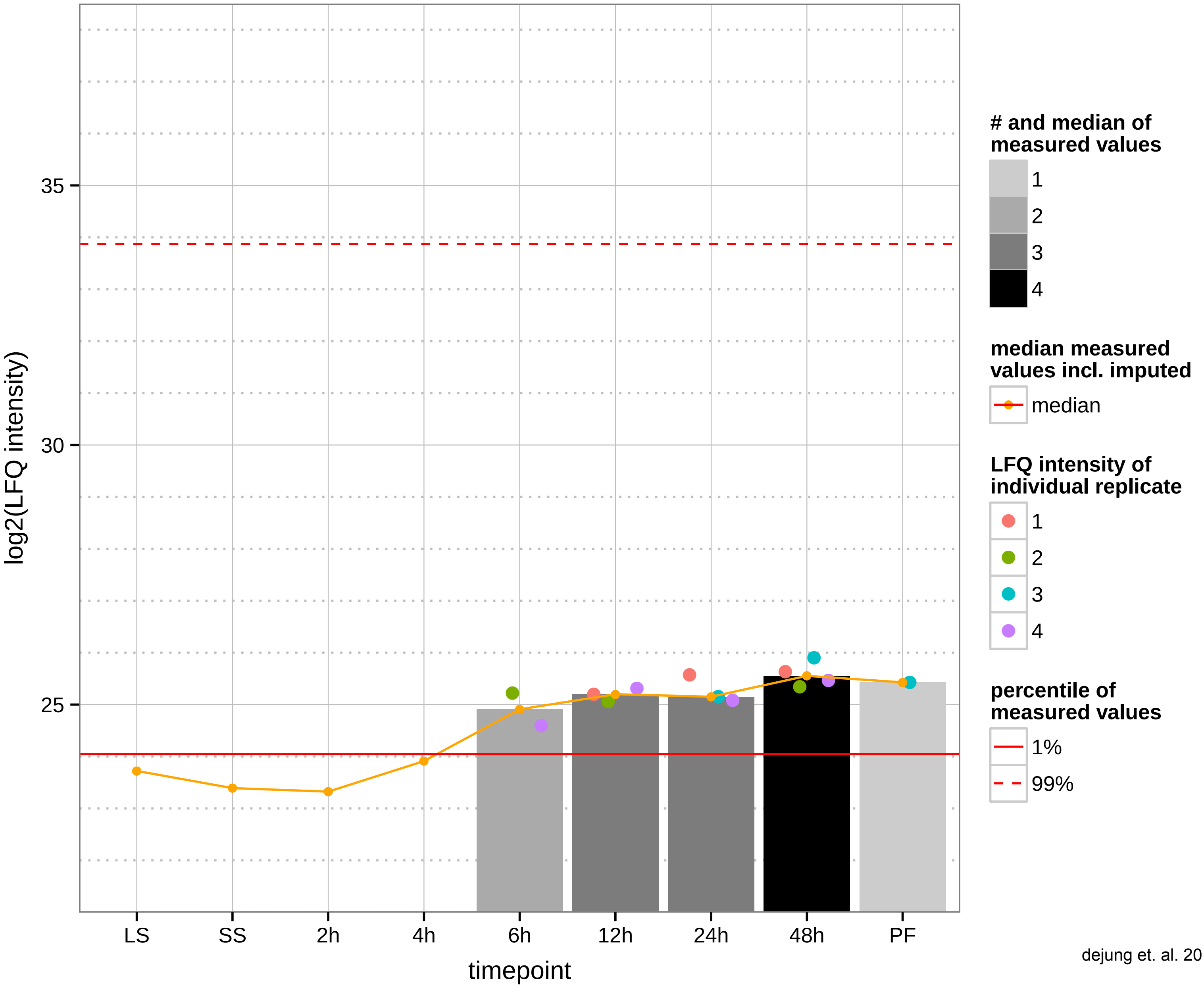
hypothetical protein, conserved
Tb927.11.6670
AGOF: RNA binding, pseudouridine synthase activity
AGOC: null
AGOP: pseudouridine synthesis
PGOF: RNA binding, pseudouridine synthase activity
PGOC: null
PGOP: RNA modification, pseudouridine synthesis





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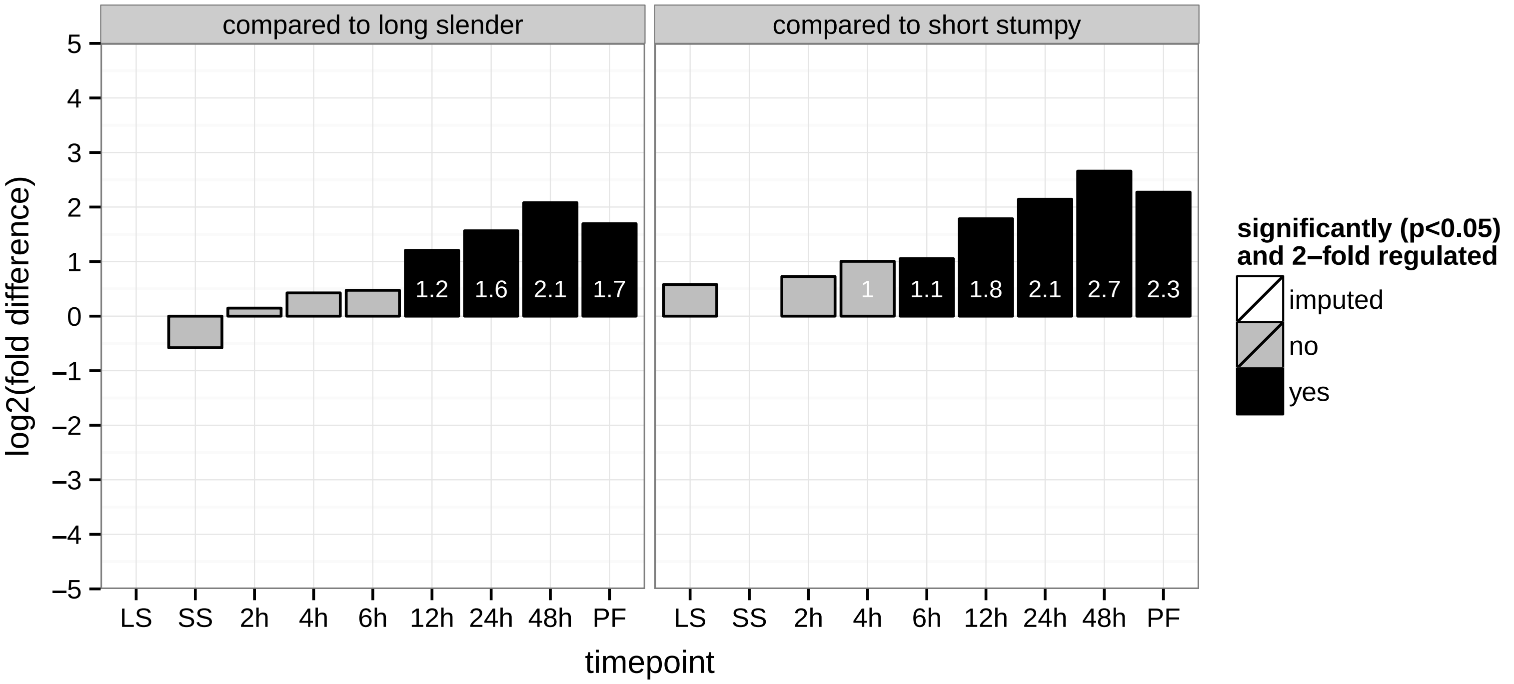
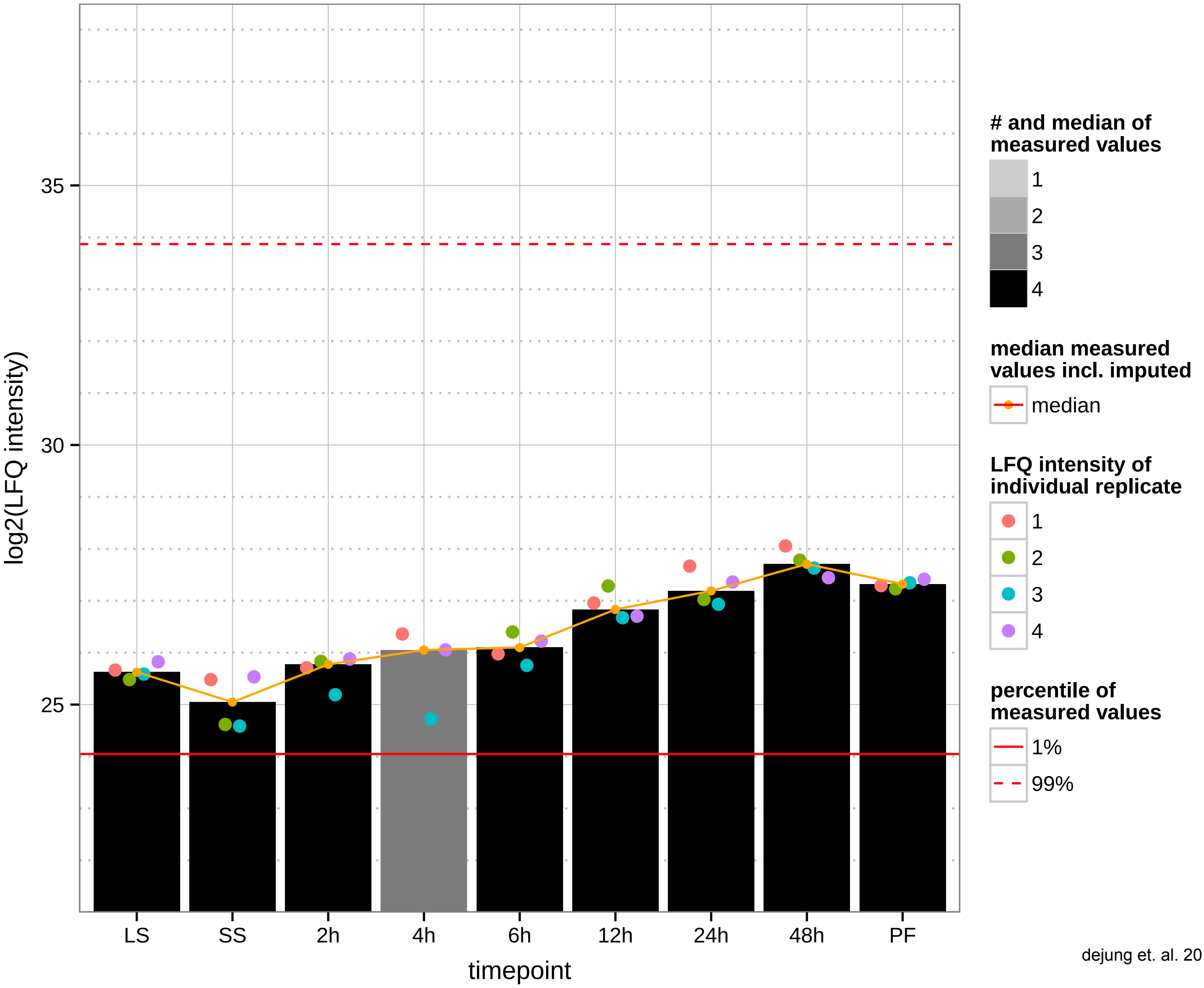
phosphoadenosine phosphosulfate reductase–like protein
Tb927.11.7420
AGOF: transferase activity
AGOC: null
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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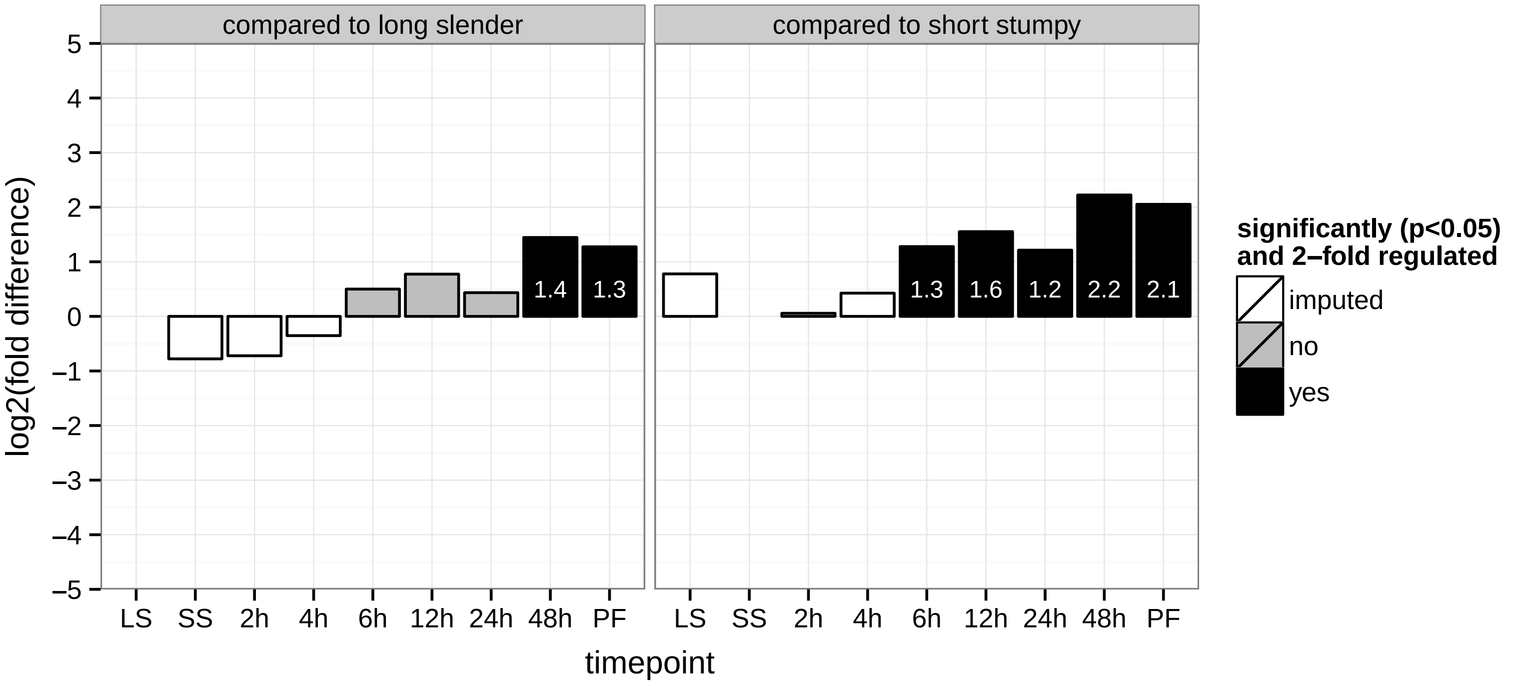
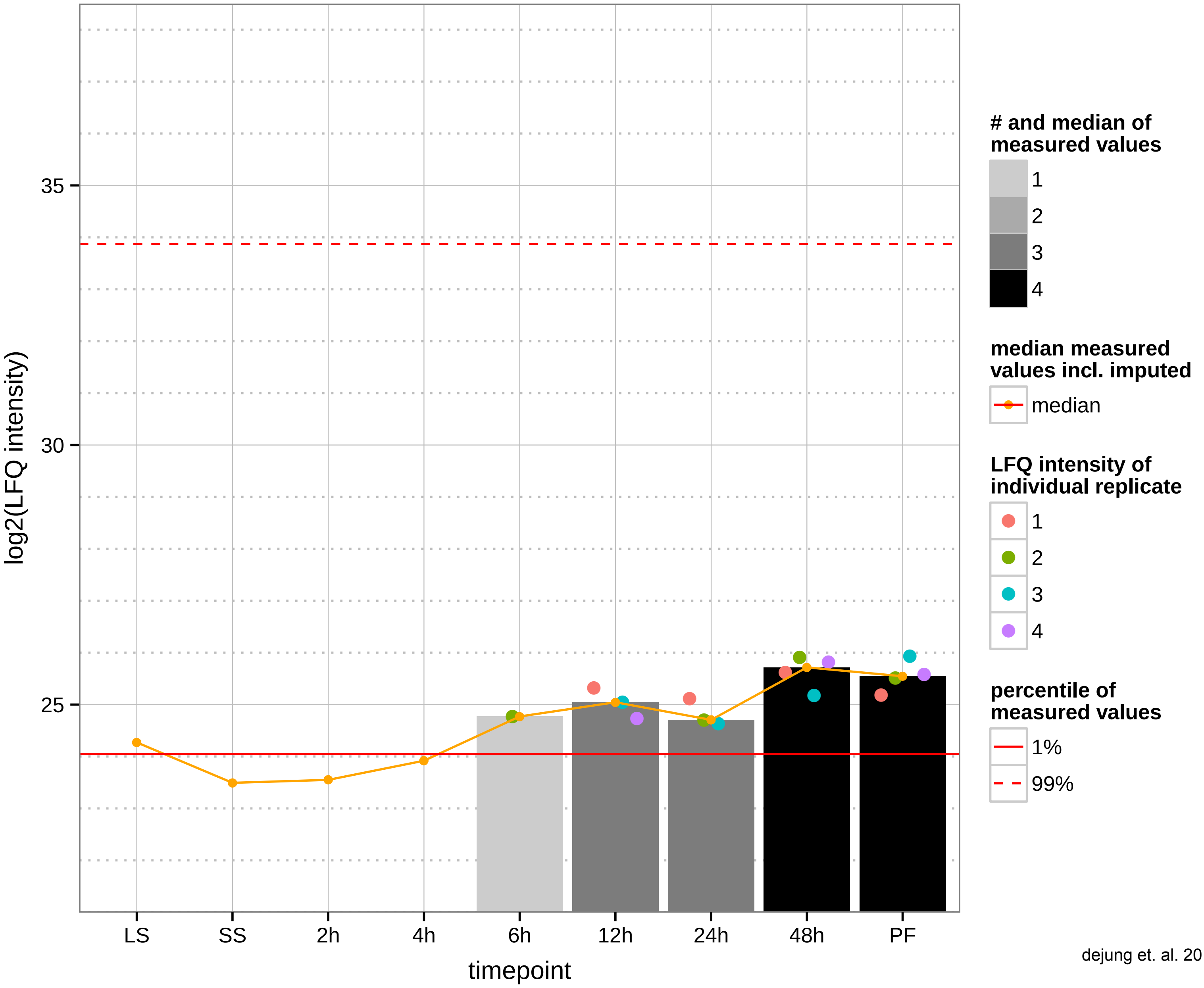
oxidoreductase–like protein
Tb927.11.7770
AGOF: oxidoreductase activity
AGOC: null
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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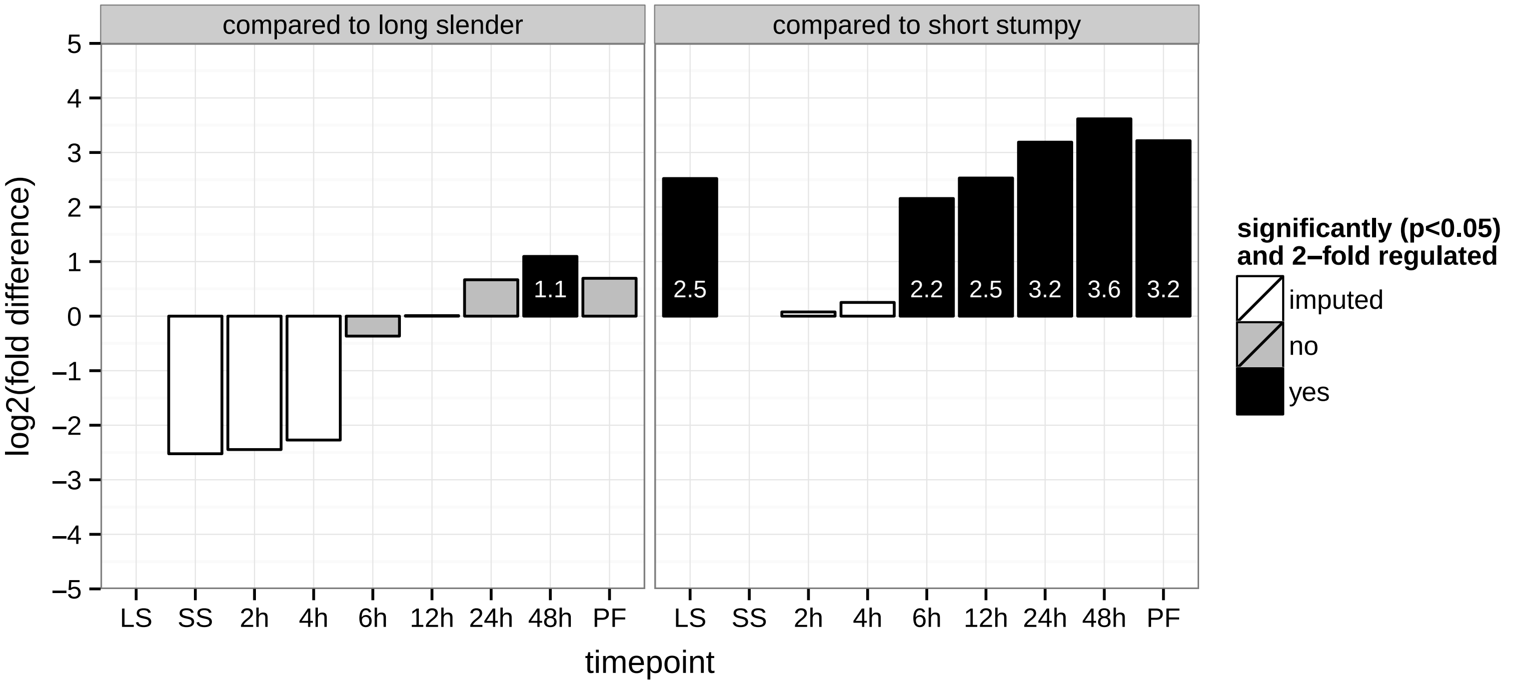
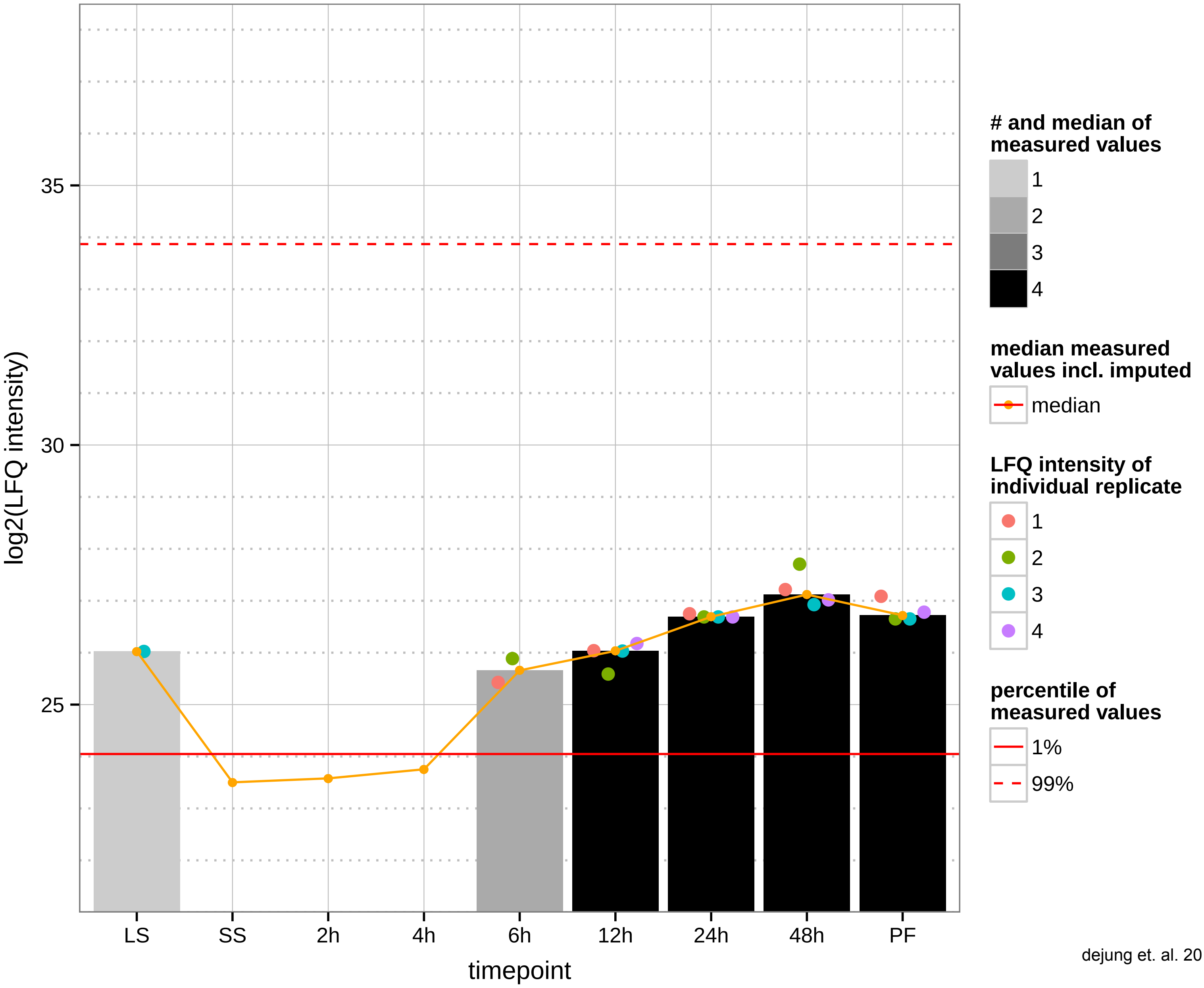
RAD50 DNA repair–like protein, putative
Tb927.11.8210
AGOF: null, ATP binding, double–stranded DNA binding
AGOC: null, chromosome, nucleus
AGOP: null, double–strand break repair via nonhomologous end joining
PGOF: null, ATP binding
PGOC: null, Mre11 complex
PGOP: null, DNA repair





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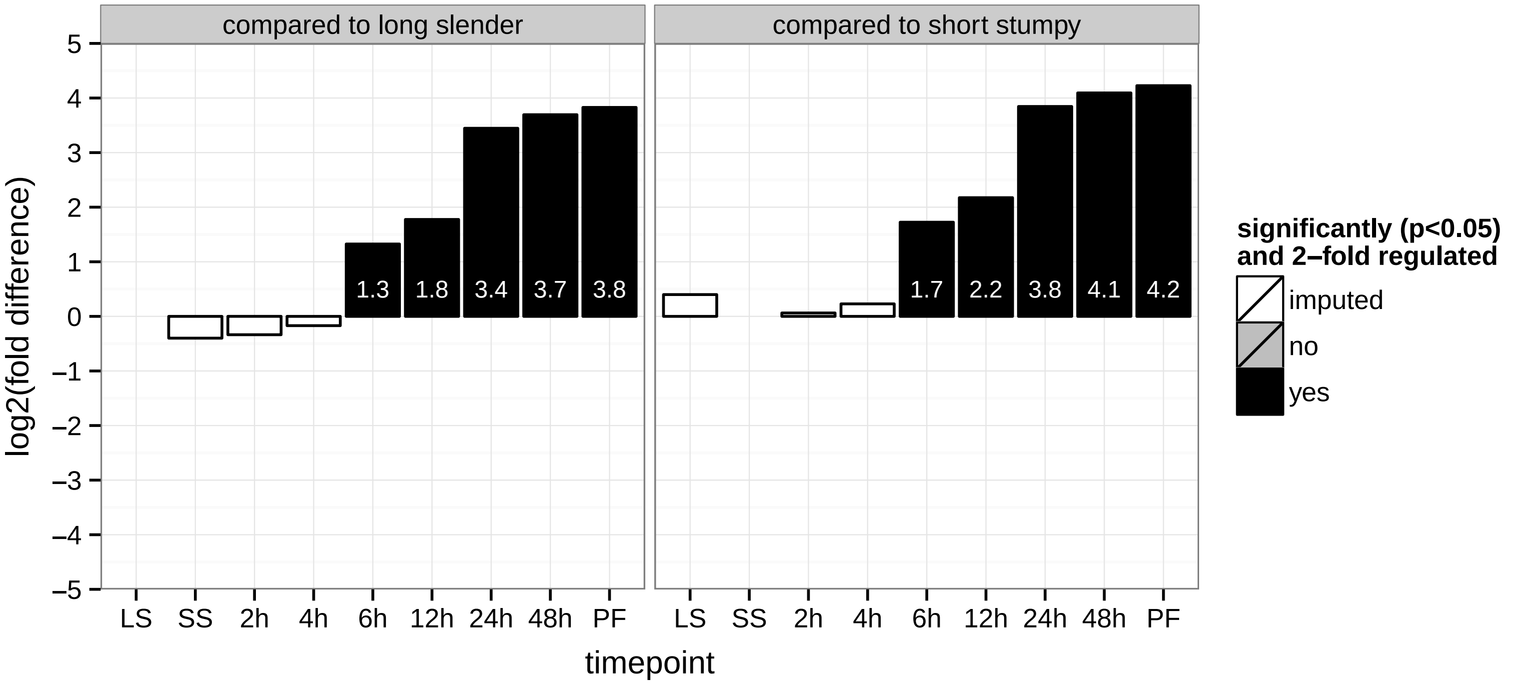
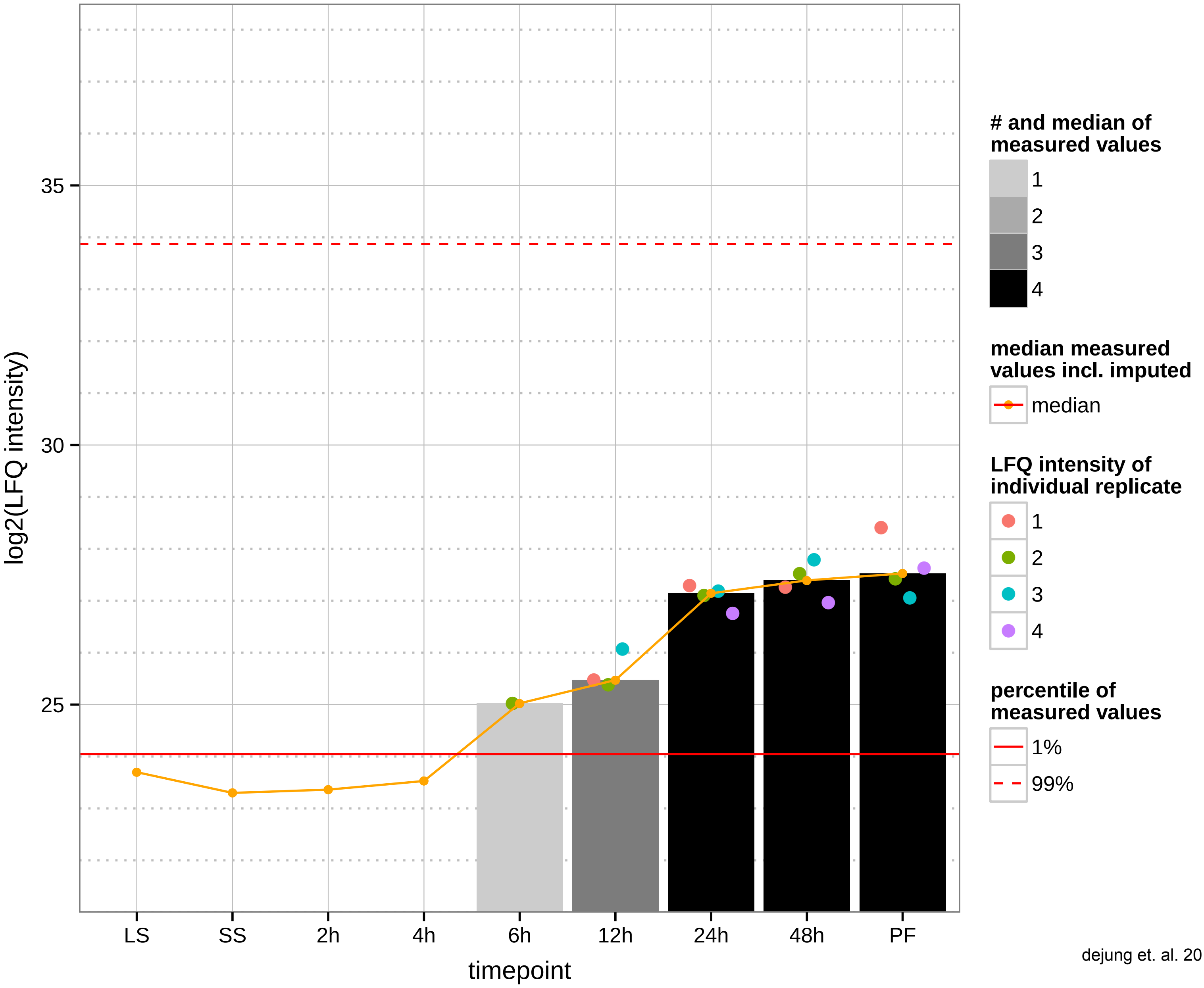
cation transporter, putative
Tb927.11.8990
AGOF: metal ion transmembrane transporter activity
AGOC: mitochondrial membrane
AGOP: metal ion transport
PGOF: metal ion transmembrane transporter activity
PGOC: membrane
PGOP: metal ion transport, transmembrane transport





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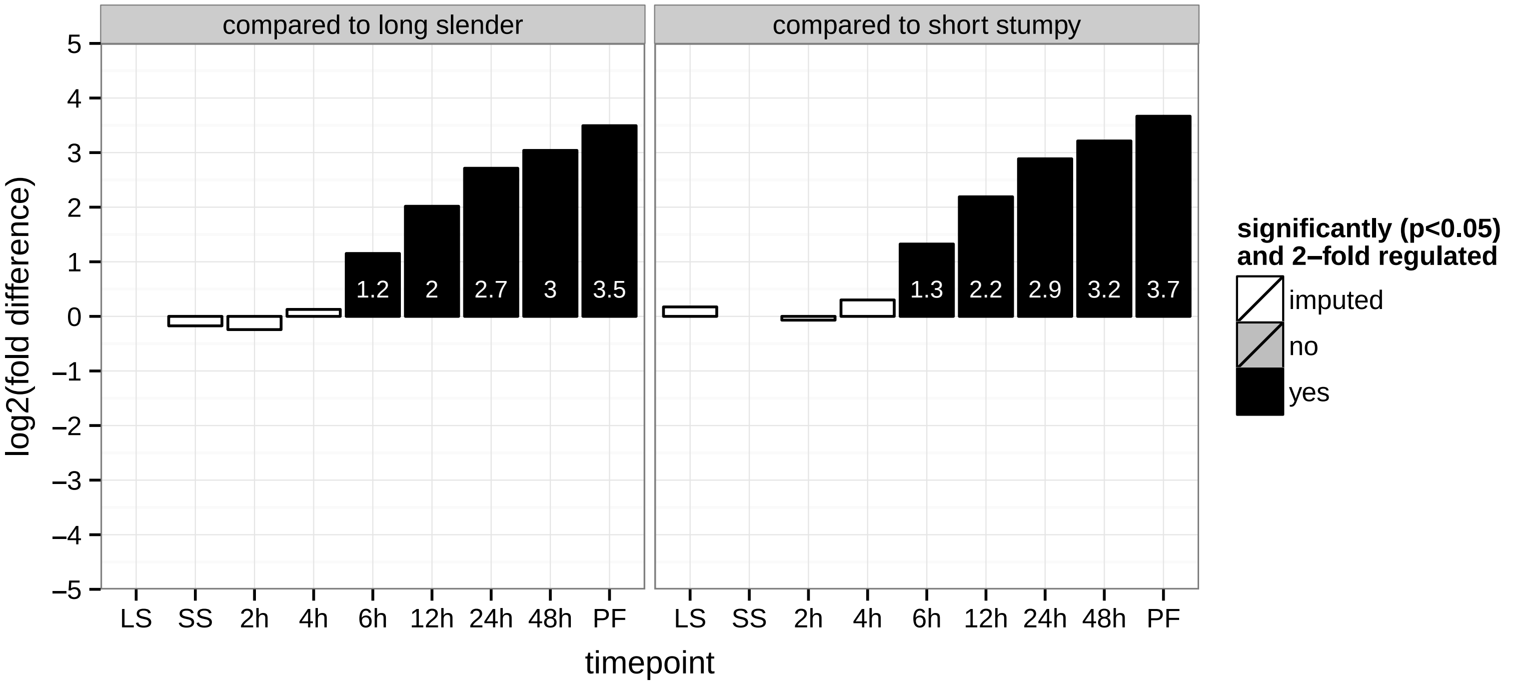
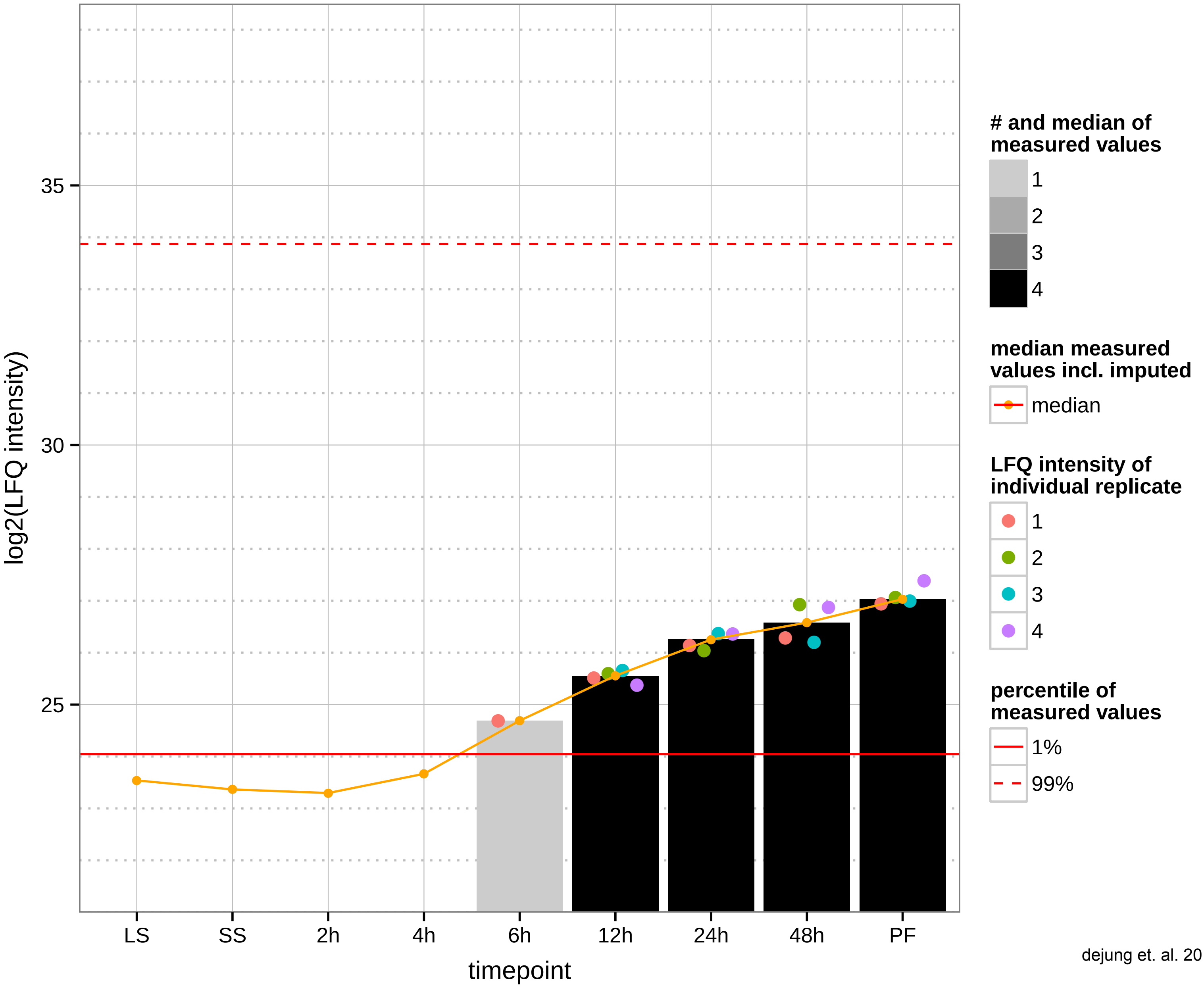
hypothetical protein, conserved
Tb927.3.2680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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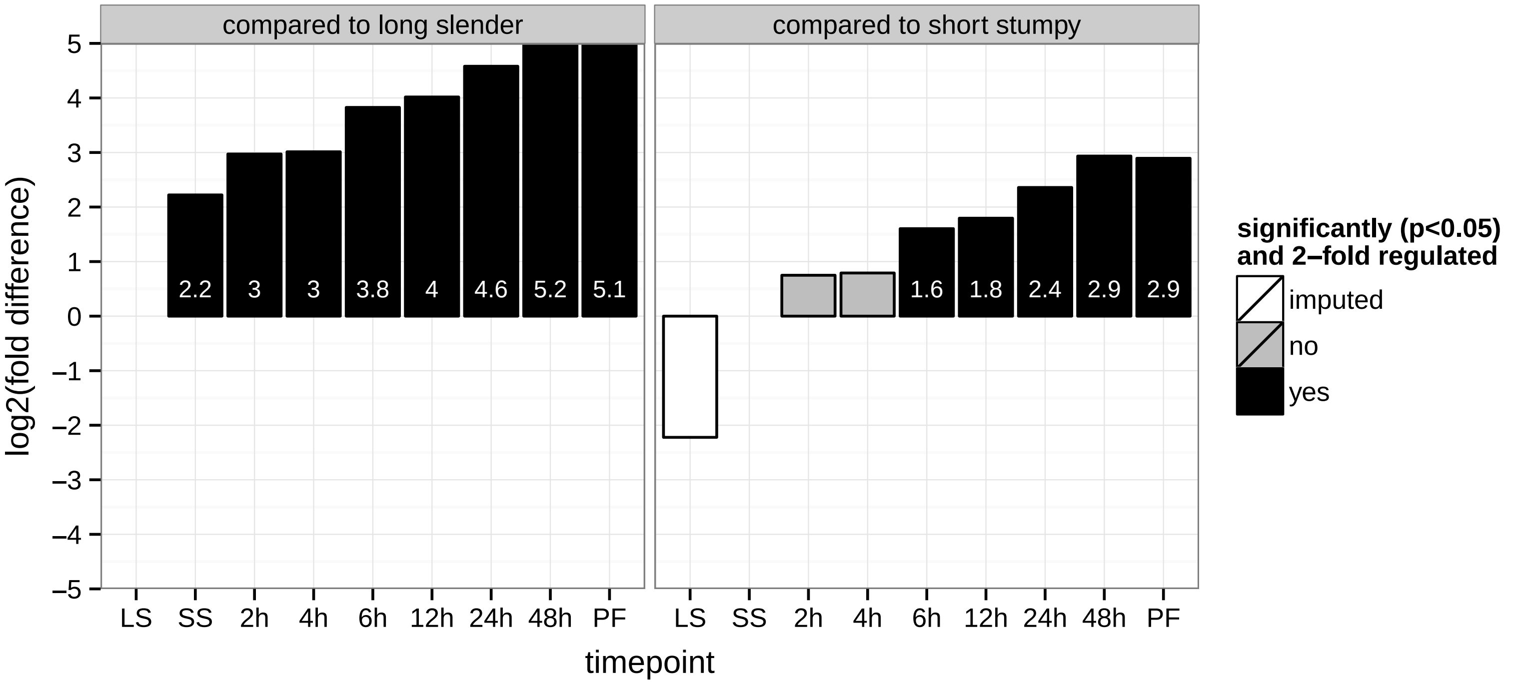
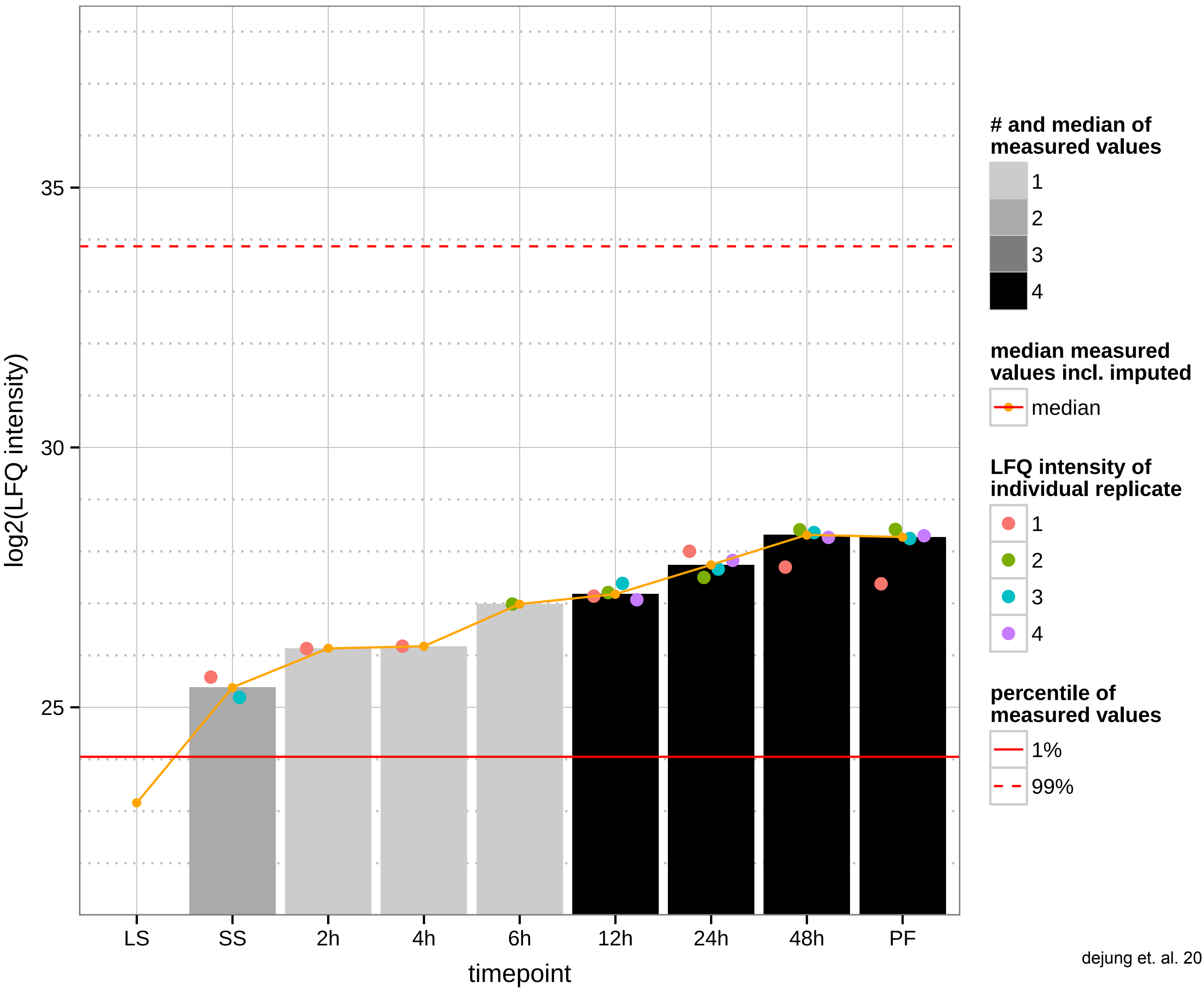
Elongation factor Ts, mitochondrial, putative (EF−Ts)
Tb927.3.3630
AGOF: protein binding, translation elongation factor activity
AGOC: intracellular, mitochondrion
AGOP: growth, oxidative phosphorylation, translational elongation
PGOF: protein binding, translation elongation factor activity
PGOC: intracellular
PGOP: translational elongation





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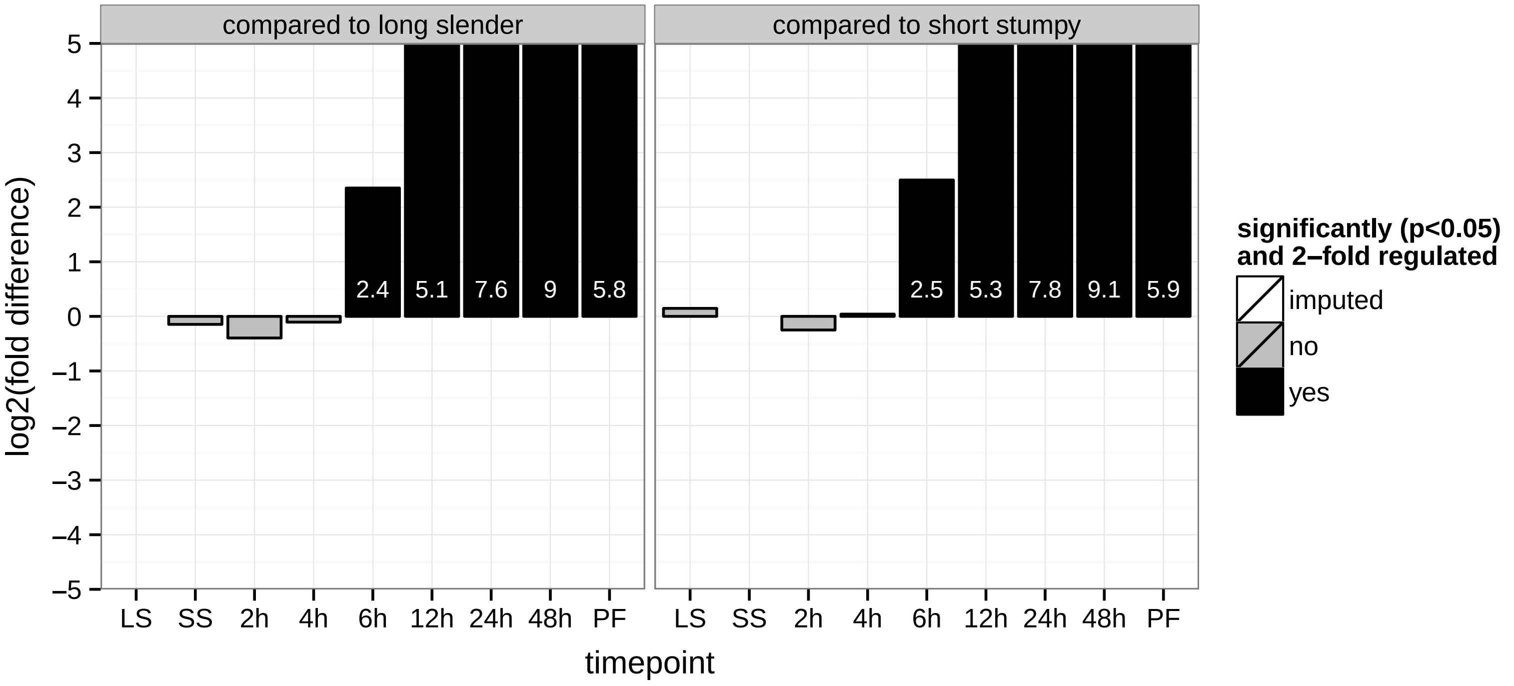
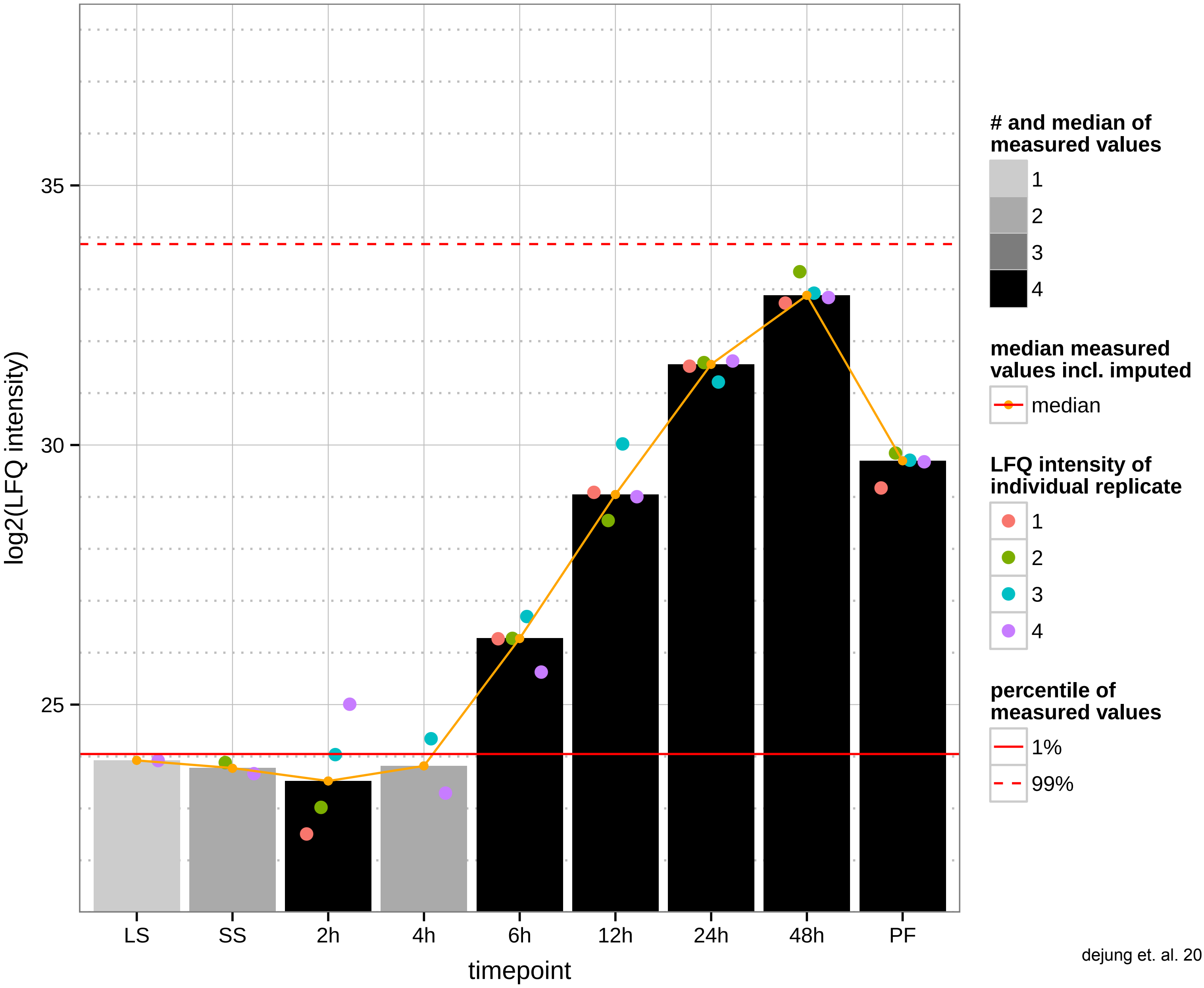
fumarate hydratase, putative, class I (FHc)
Tb927.3.4500;Tb11.v5.0629
AGOF: null, fumarate hydratase activity
AGOC: null, cytosol
AGOP: null, generation of precursor metabolites and energy
PGOF: hydro–lyase activity, lyase activity, fumarate hydratase activity, hydro–lyase activity
PGOC: null
PGOP: null, generation of precursor metabolites and energy





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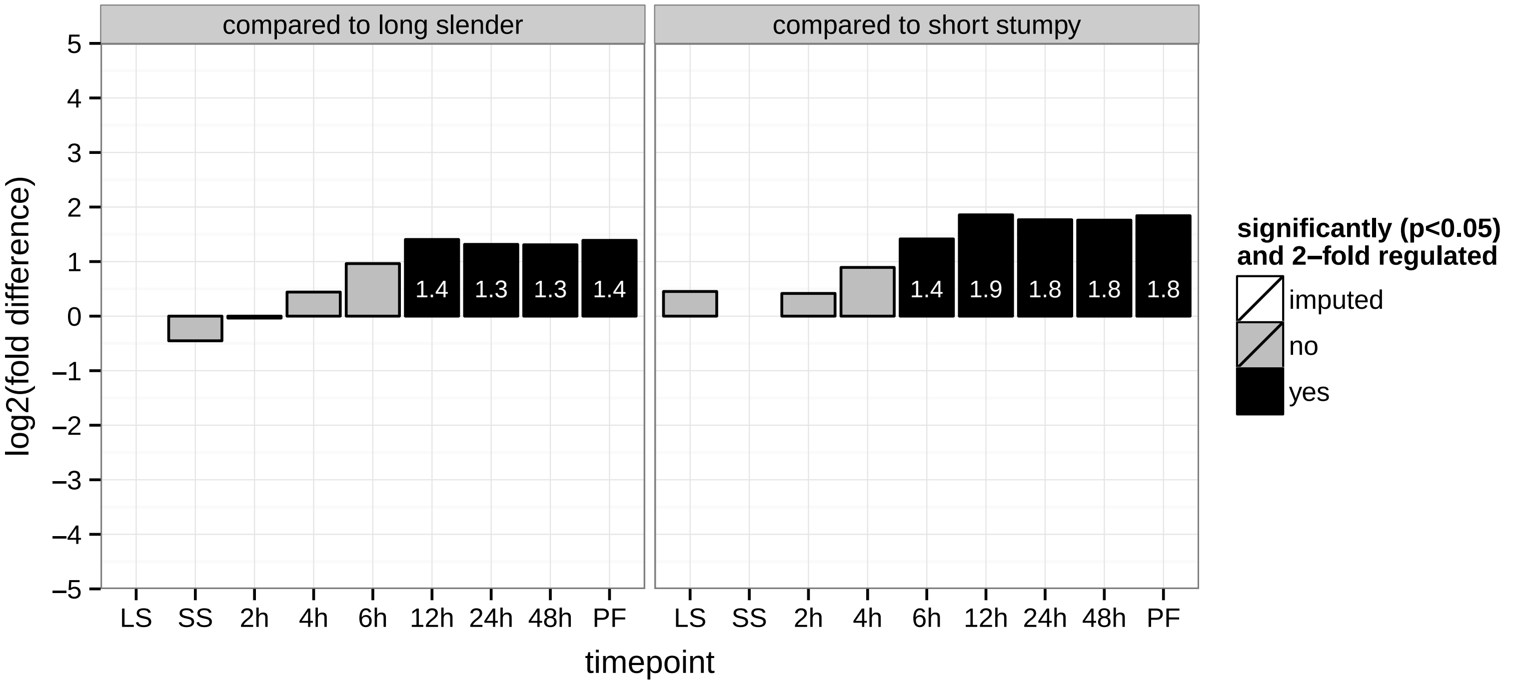
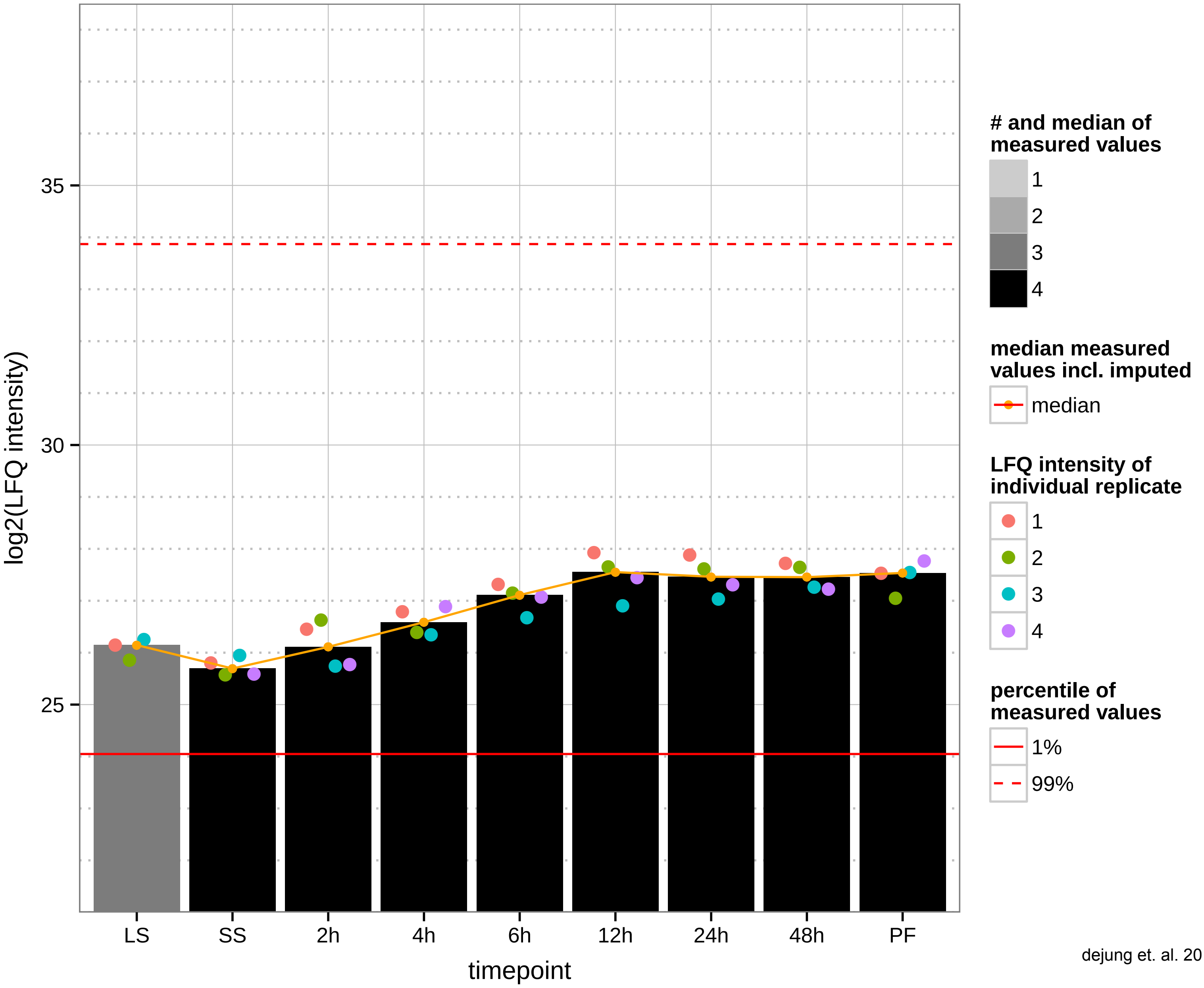
hypothetical protein, conserved
Tb927.3.640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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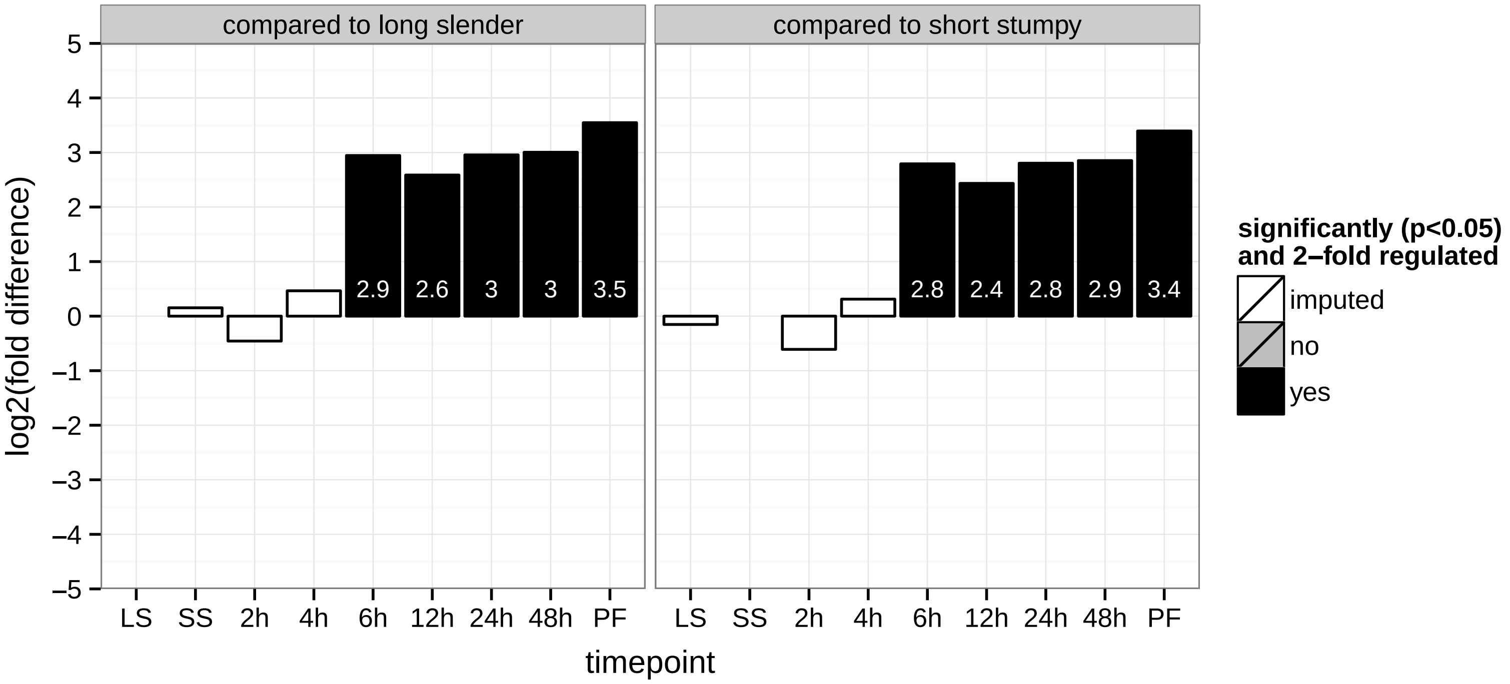
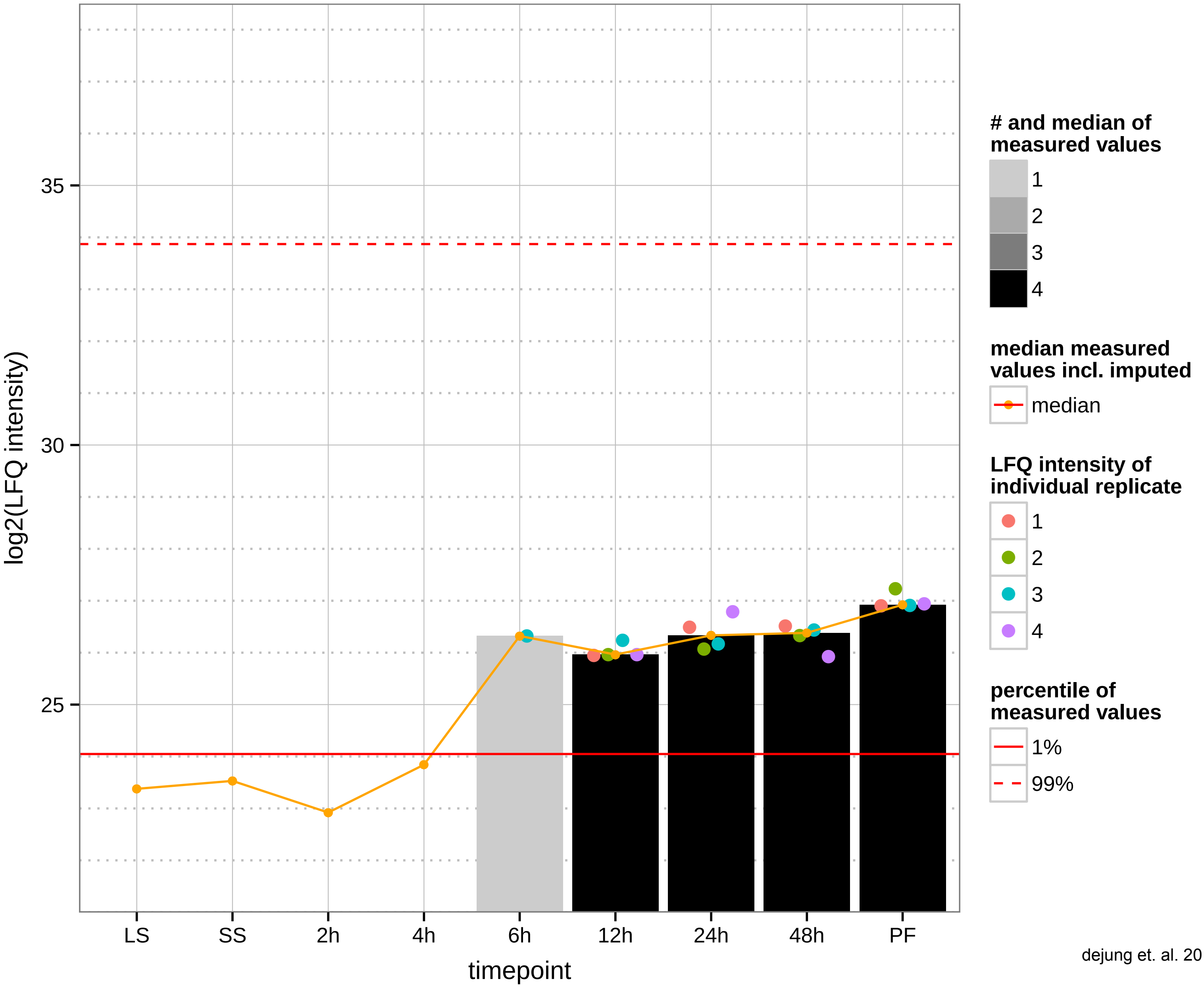
hypothetical protein, conserved
Tb927.4.3670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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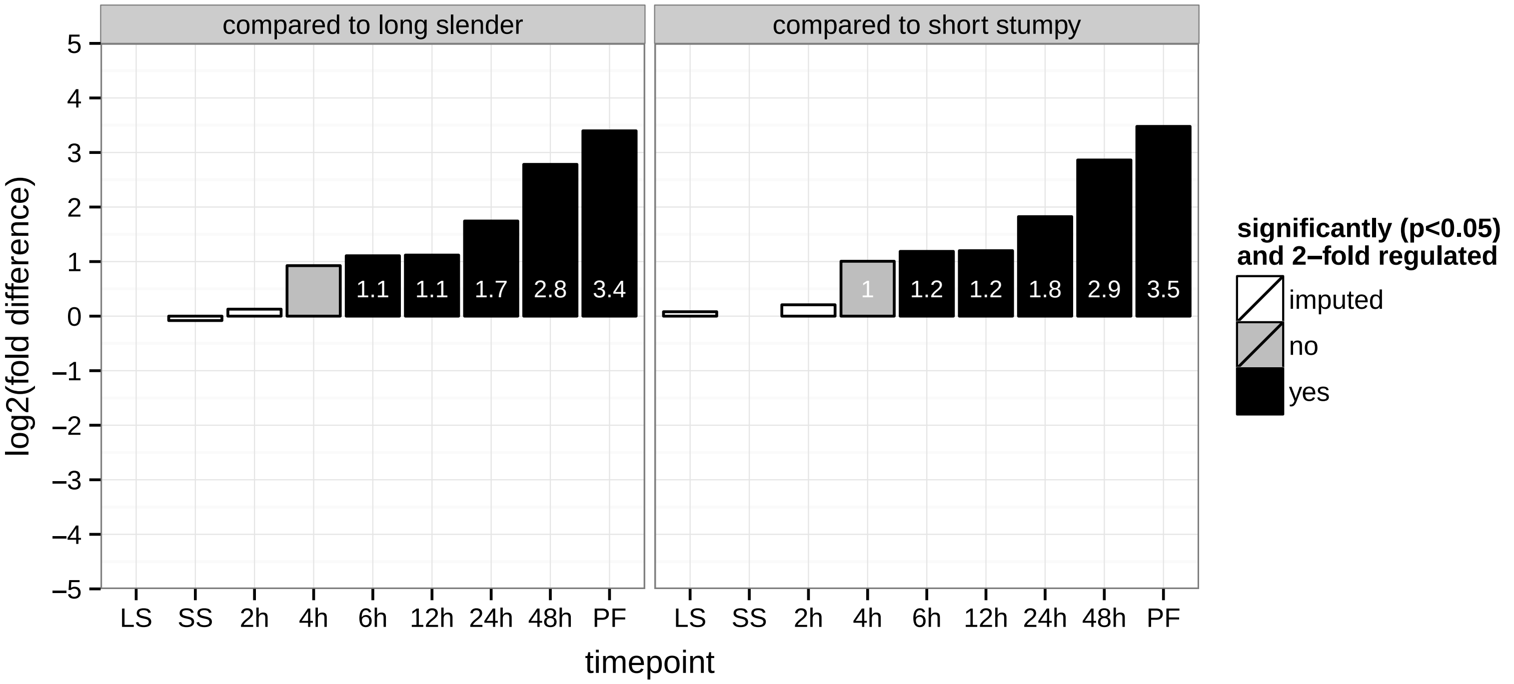
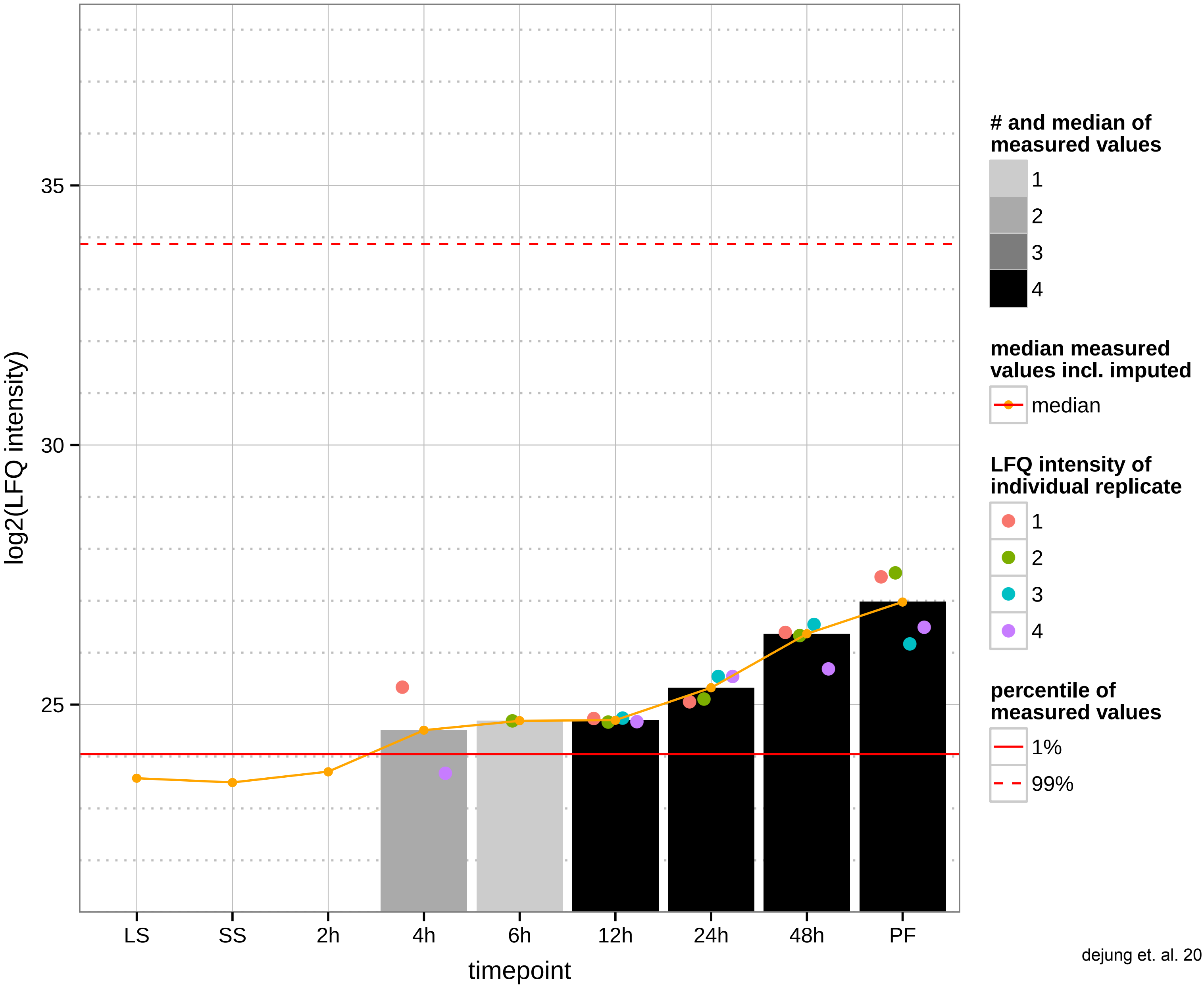
glycosomal transporter (GAT1), ABC transporter, putative (GAT1)
Tb927.4.4050
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances, transporter activity
AGOC: glycosome membrane, integral to membrane
AGOP: fatty acid transport
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances, nucleoside–triphosphatase activity
PGOC: integral to membrane, membrane
PGOP: transmembrane transport, transport





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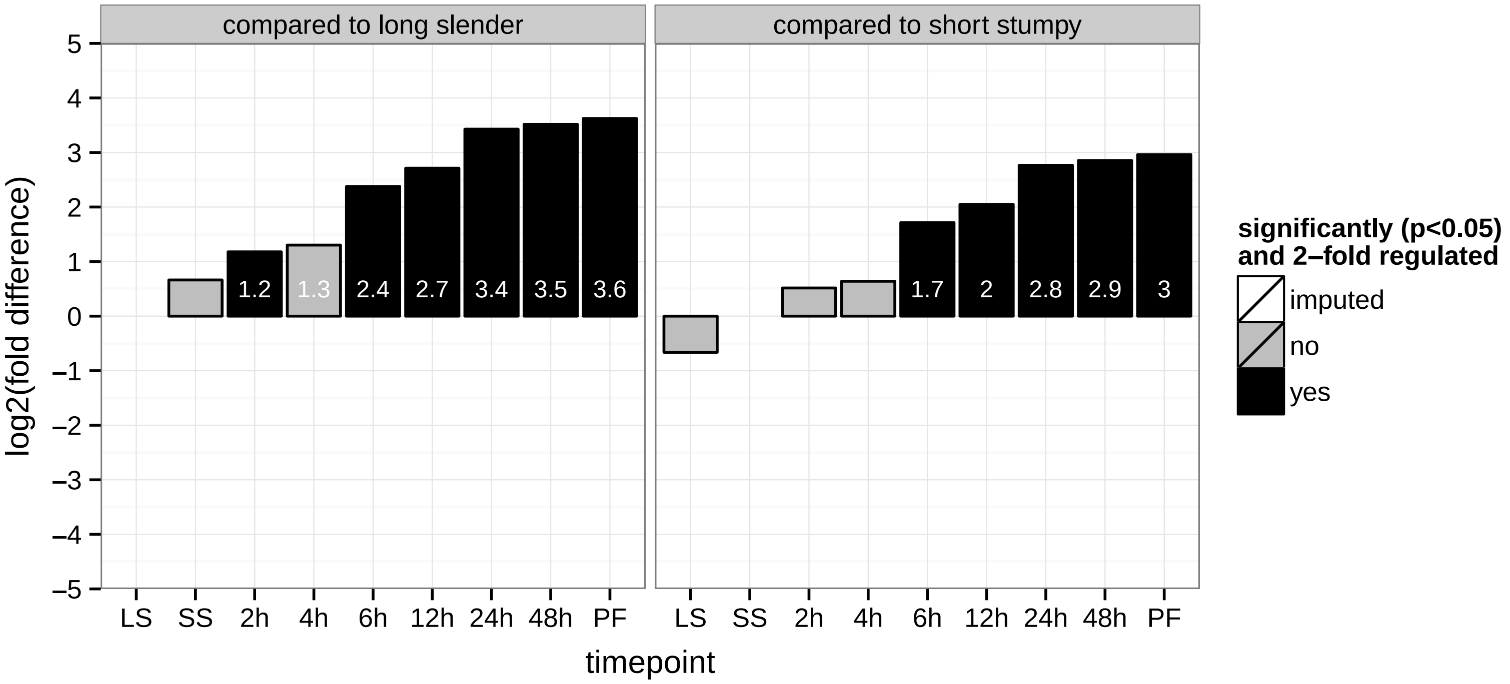
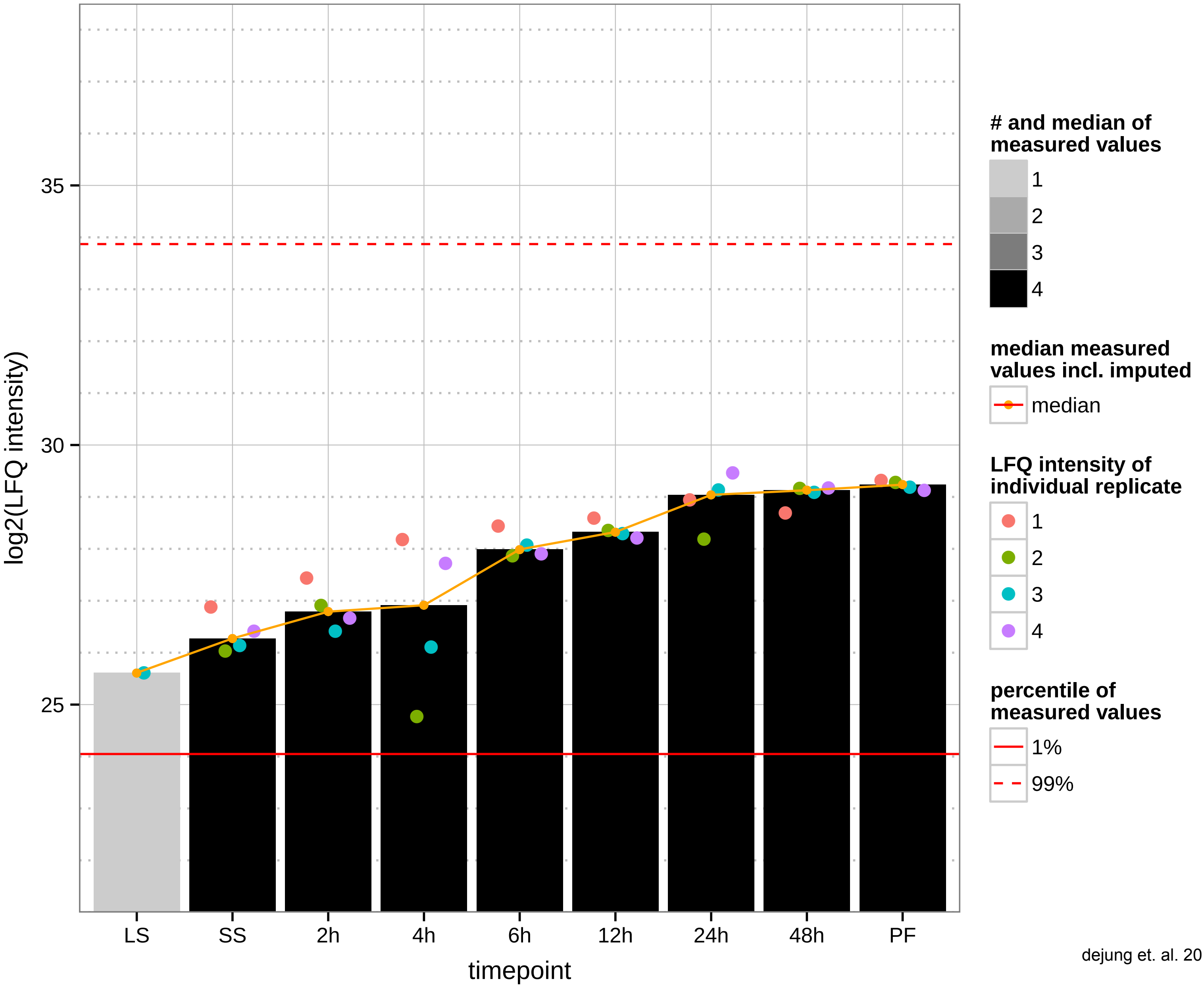
Eukaryotic translation initiation factor 4 gamma type 1 (eif4g1)
Tb927.5.1490
AGOF: protein binding
AGOC: eukaryotic translation initiation factor 4F complex
AGOP: RNA metabolic process
PGOF: DNA binding, RNA binding, binding, protein binding
PGOC: null
PGOP: null





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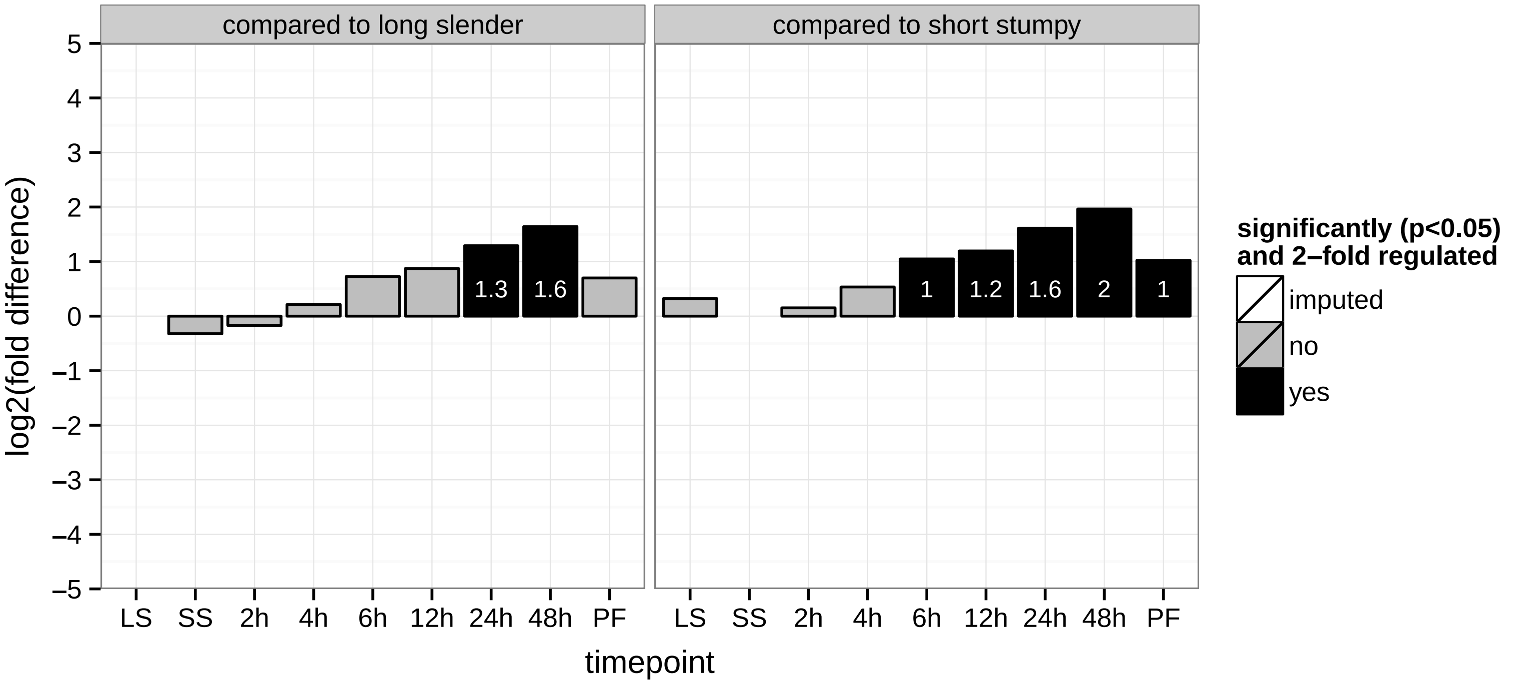
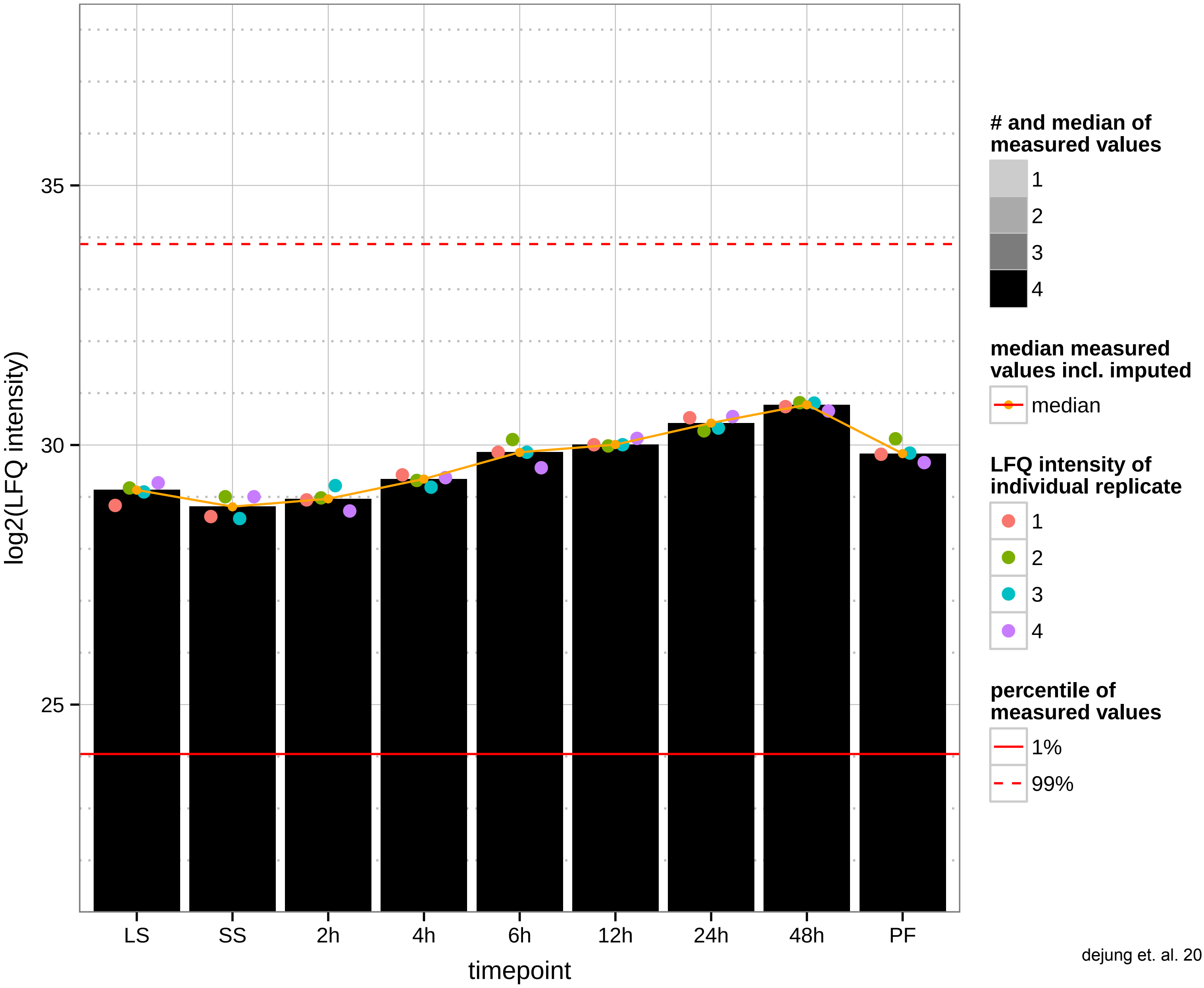
protein phosphatase 2C, putative
Tb927.5.1660
AGOF: phosphatase activity
AGOC: null
AGOP: dephosphorylation
PGOF: catalytic activity
PGOC: null
PGOP: null





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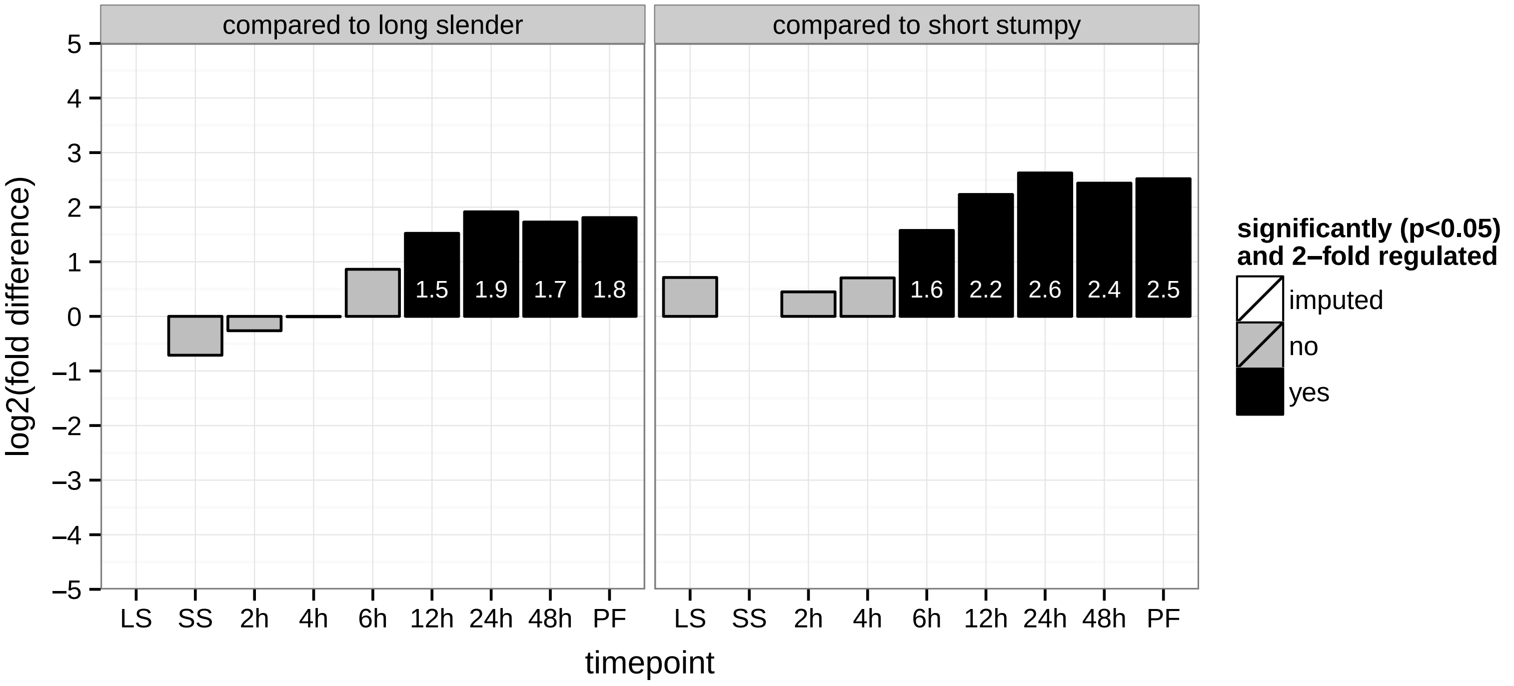
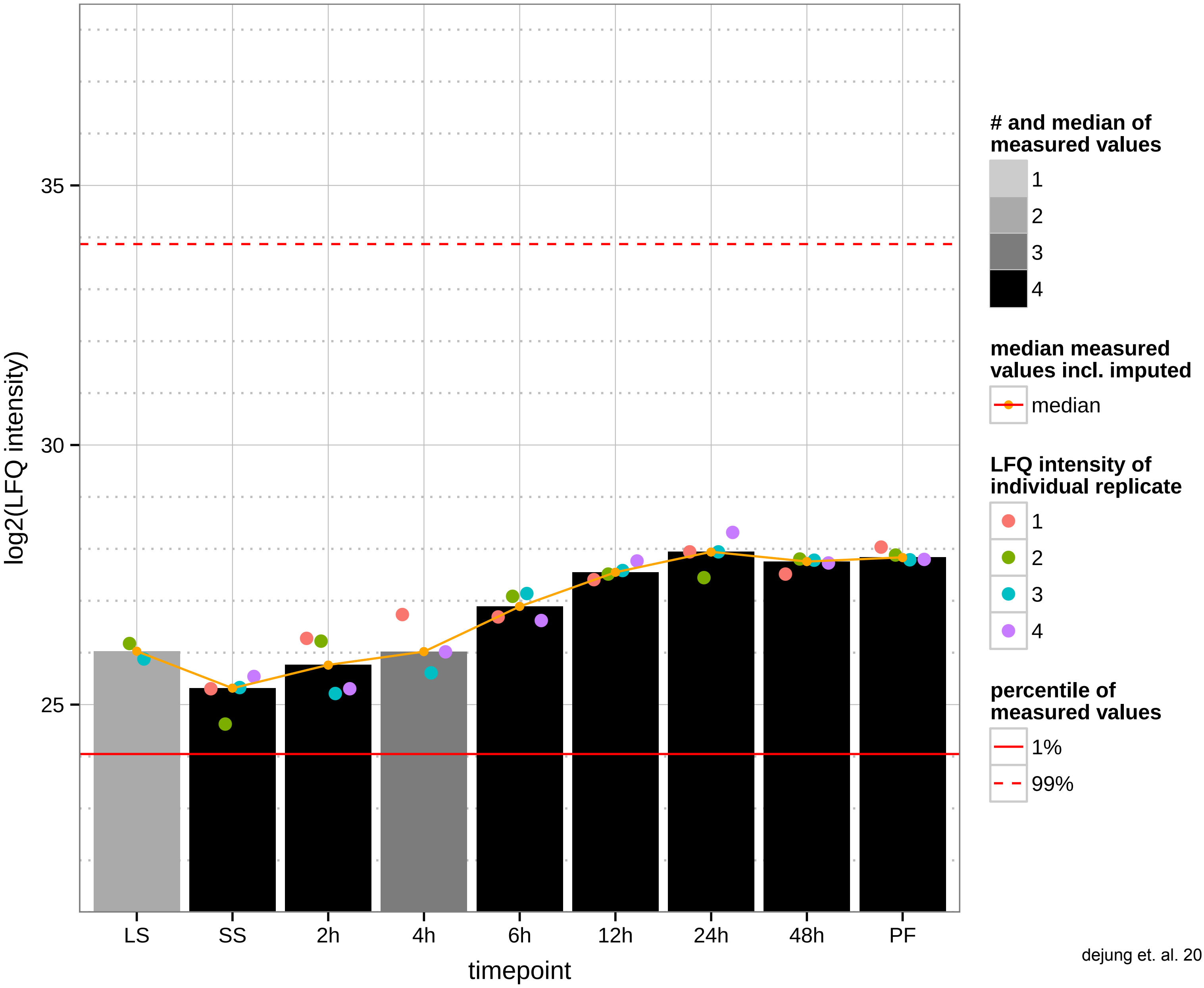
GTP–binding protein, putative
Tb927.5.4310
AGOF: GTP binding
AGOC: intracellular
AGOP: null
PGOF: GTP binding
PGOC: null
PGOP: null





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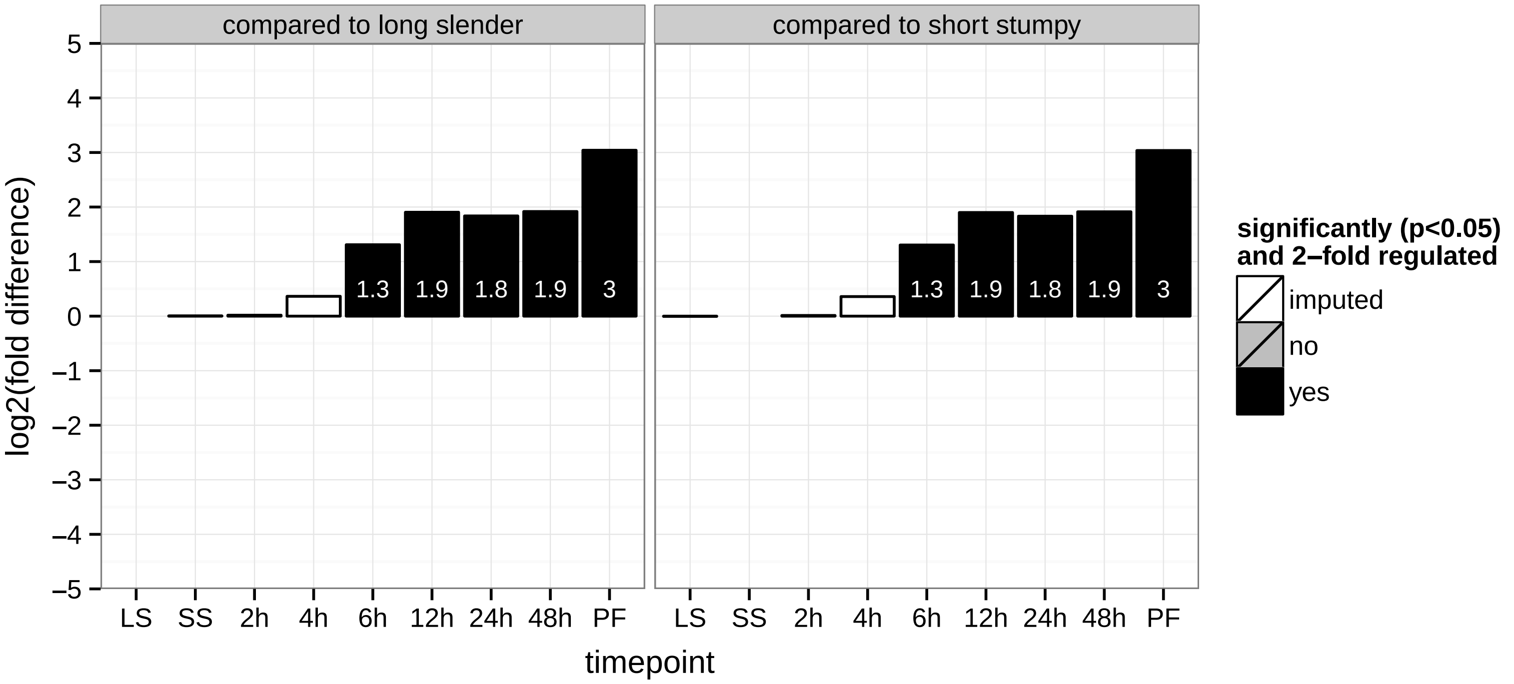
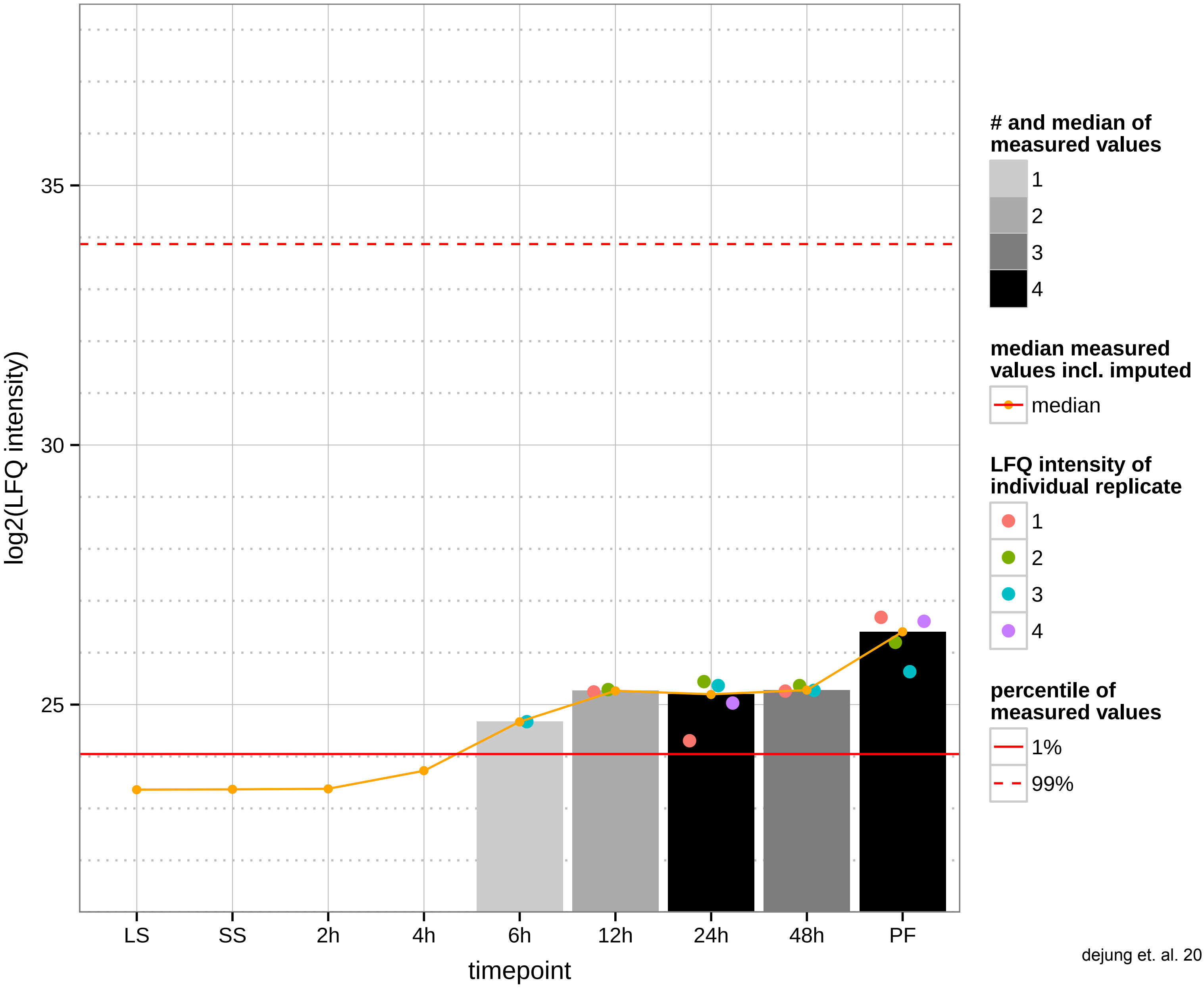
hypothetical protein, conserved
Tb927.6.3030
AGOF: nucleoside−triphosphatase activity, nucleotide binding
AGOC: null
AGOP: null
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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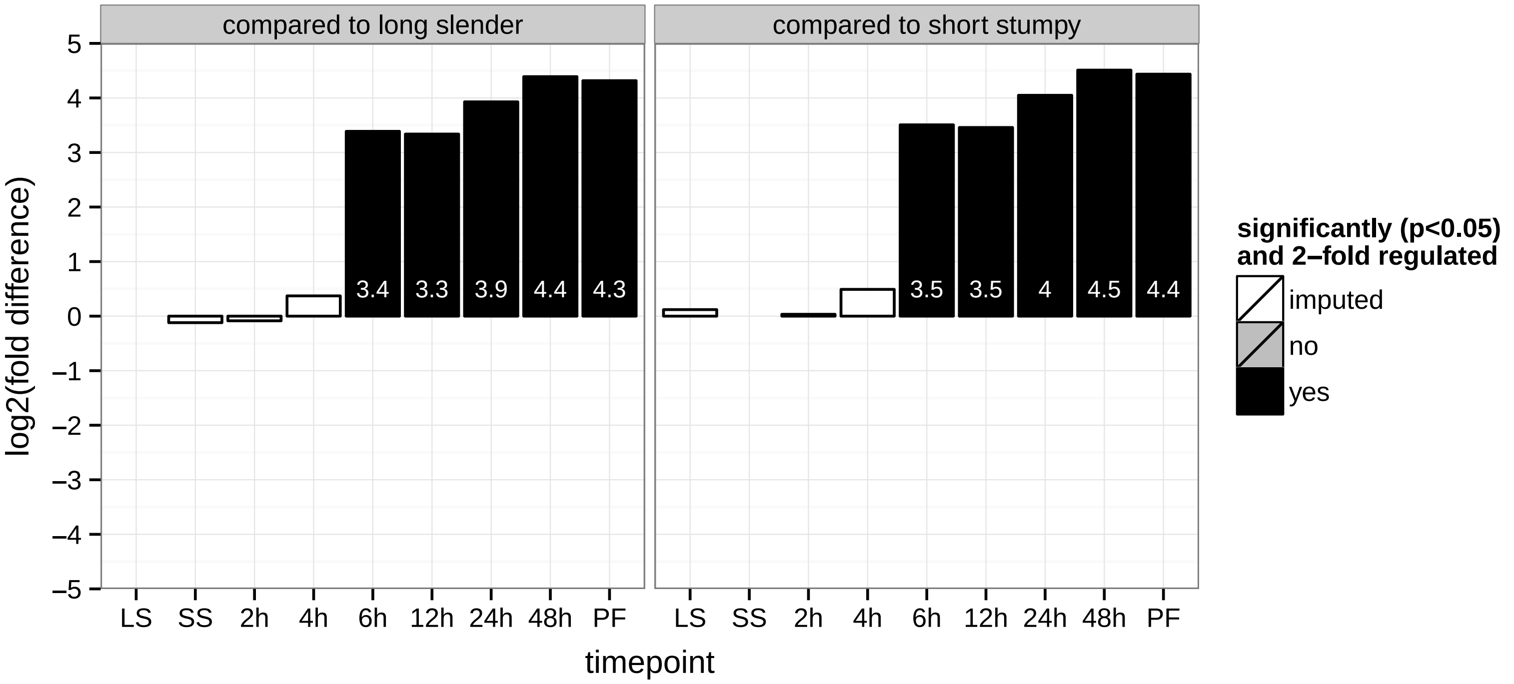
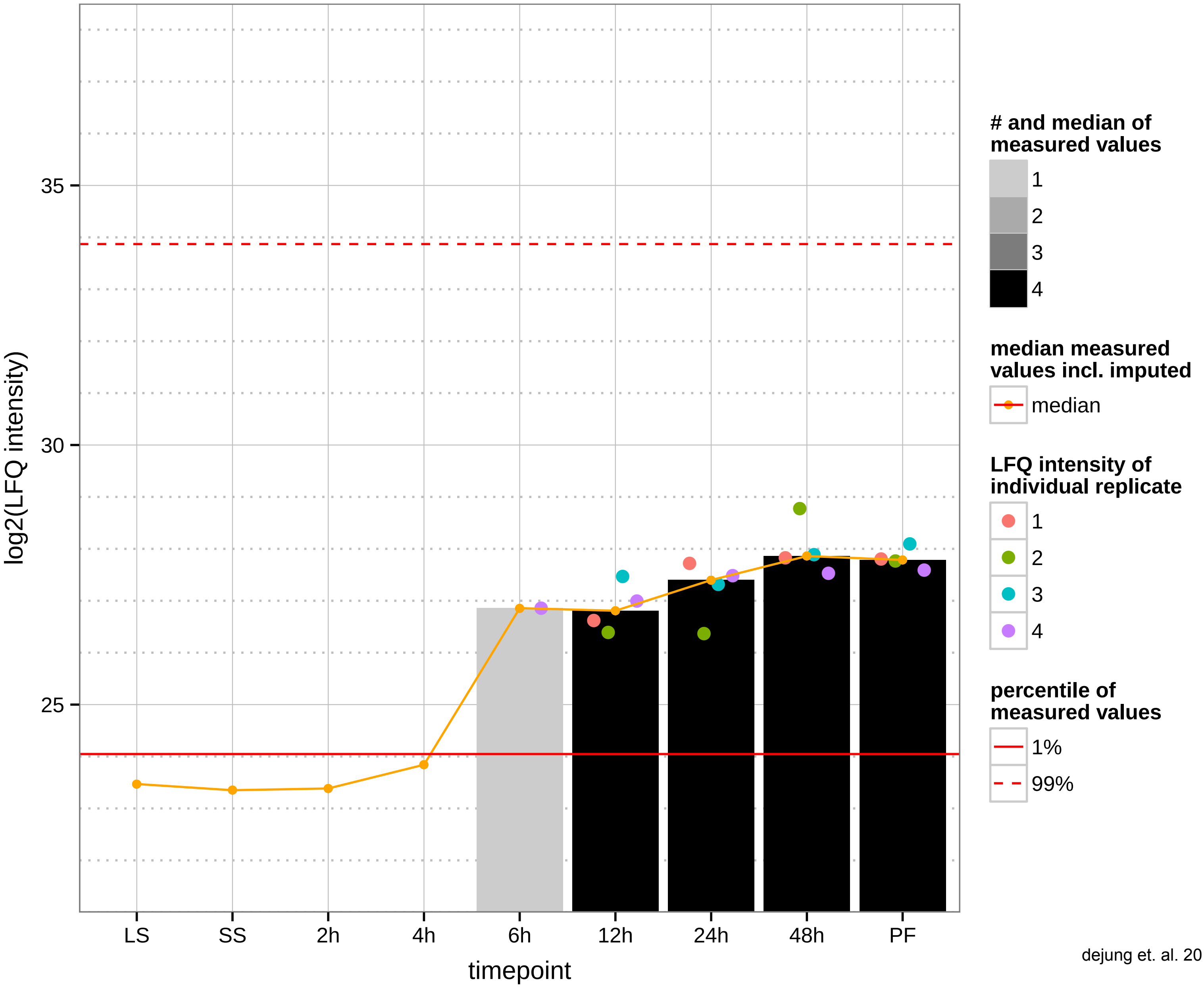
homoserine kinase, putative (HK)
Tb927.6.4430
AGOF: ATP binding, homoserine kinase activity
AGOC: null
AGOP: phosphorylation, threonine metabolic process
PGOF: ATP binding, homoserine kinase activity
PGOC: null
PGOP: threonine metabolic process





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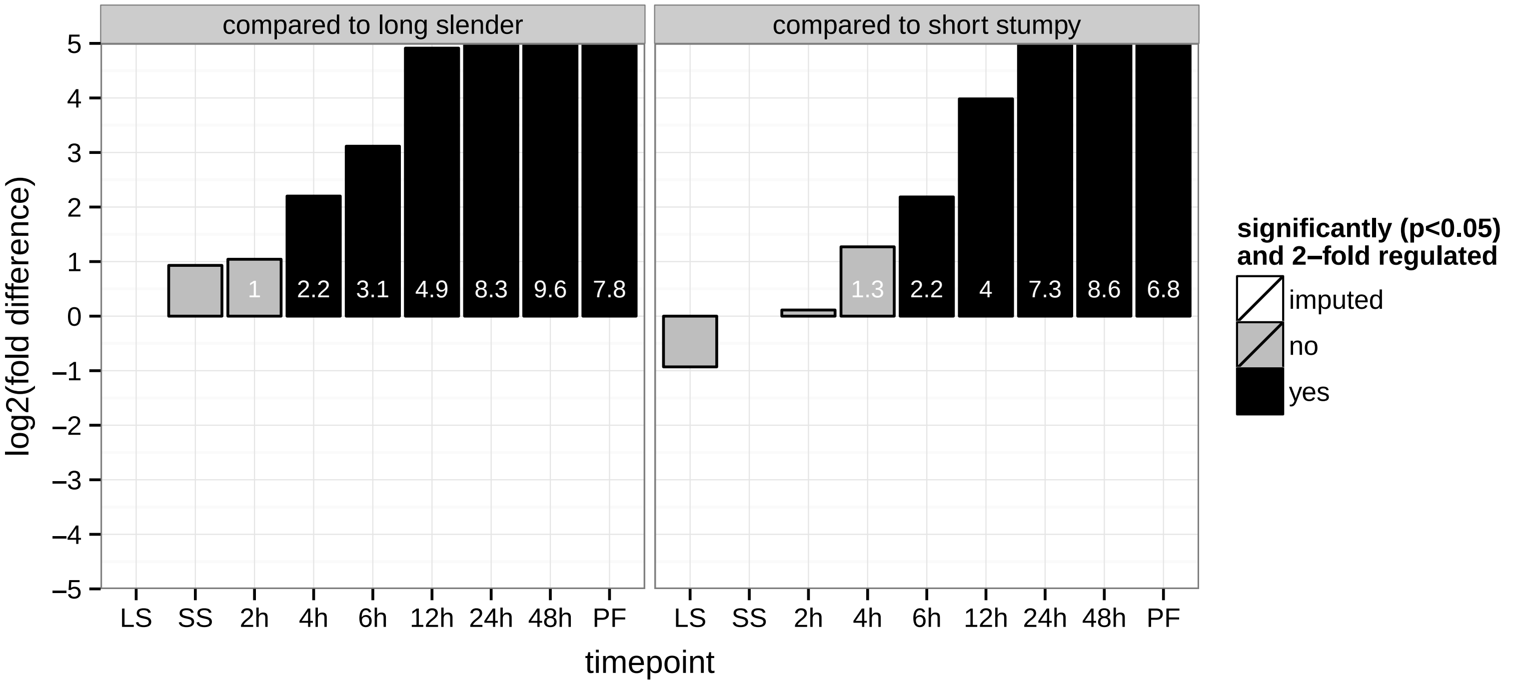
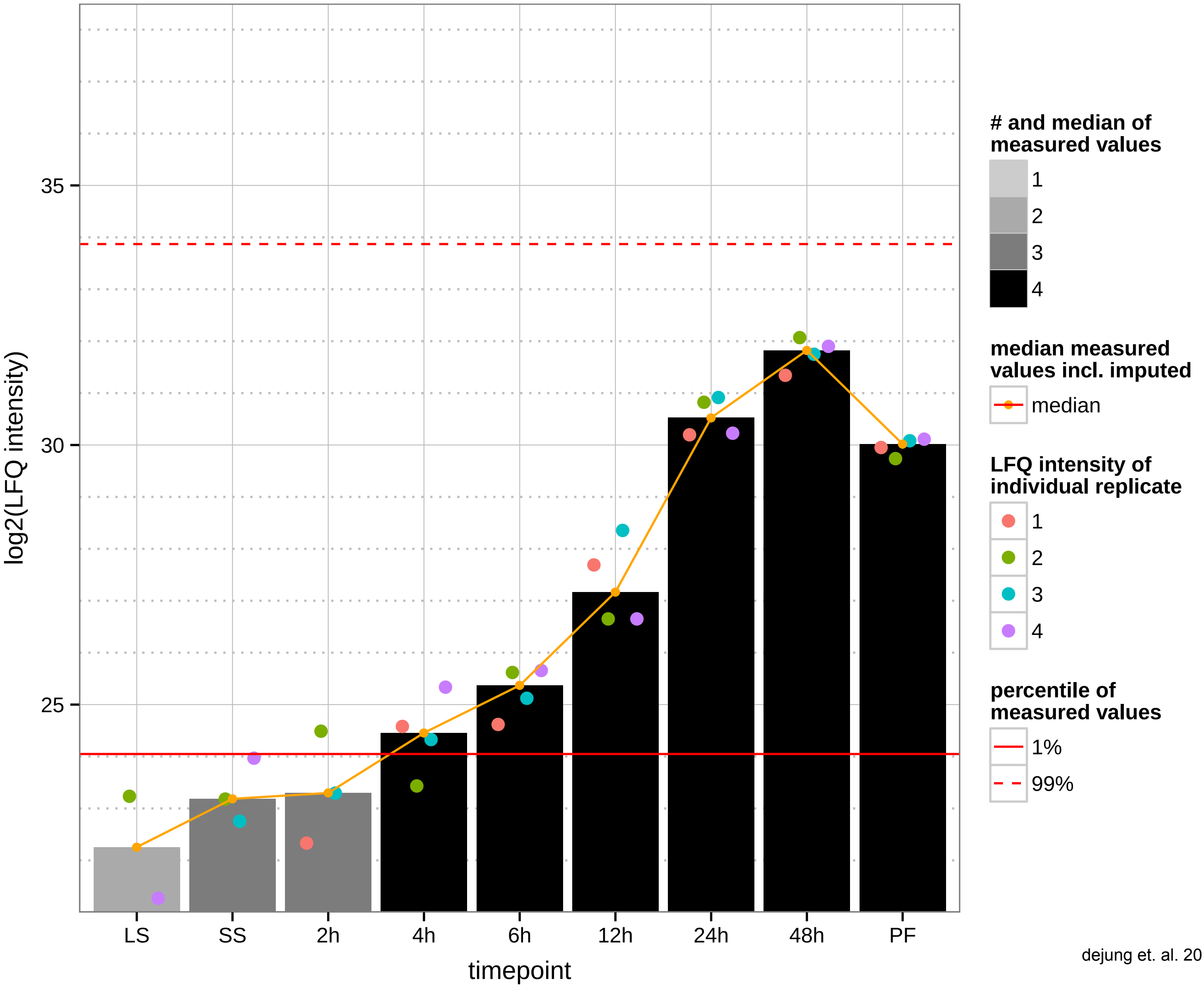
hypothetical protein, conserved
Tb927.7.2640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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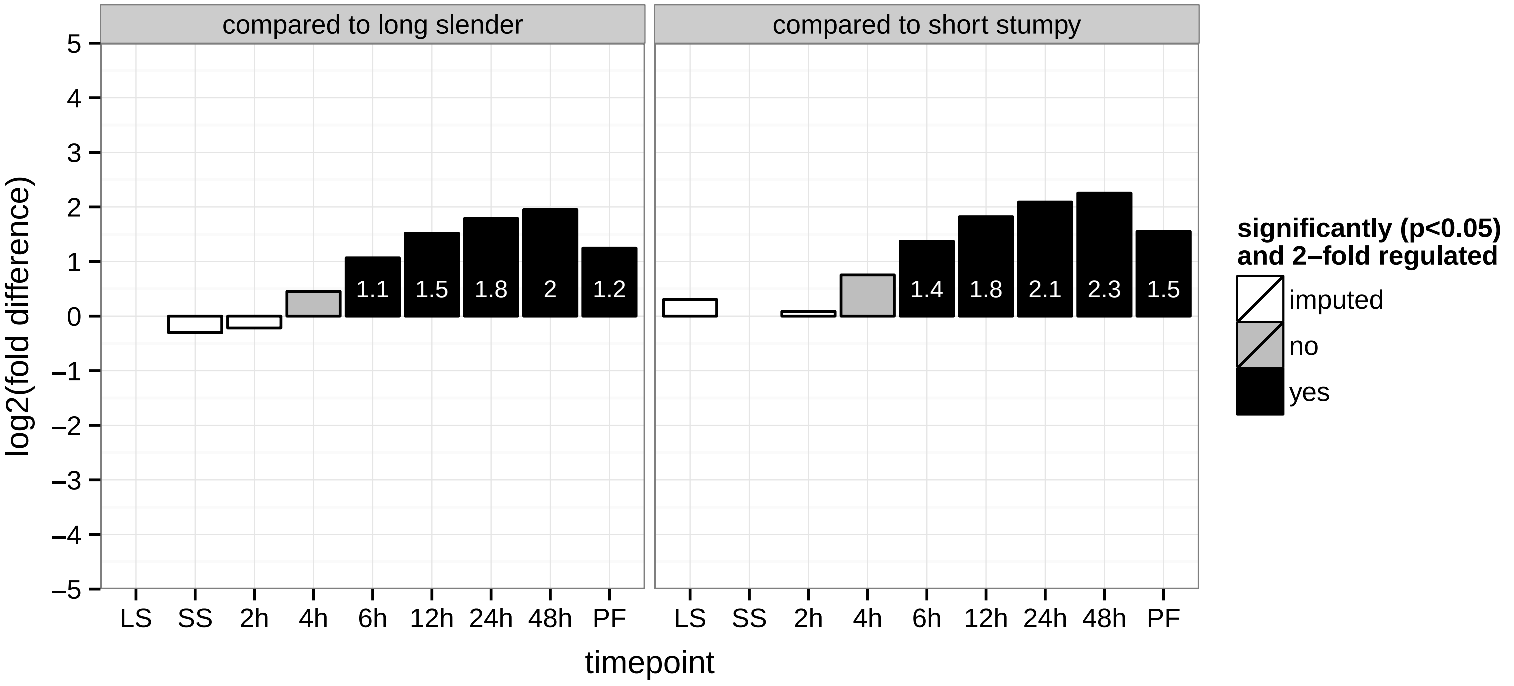
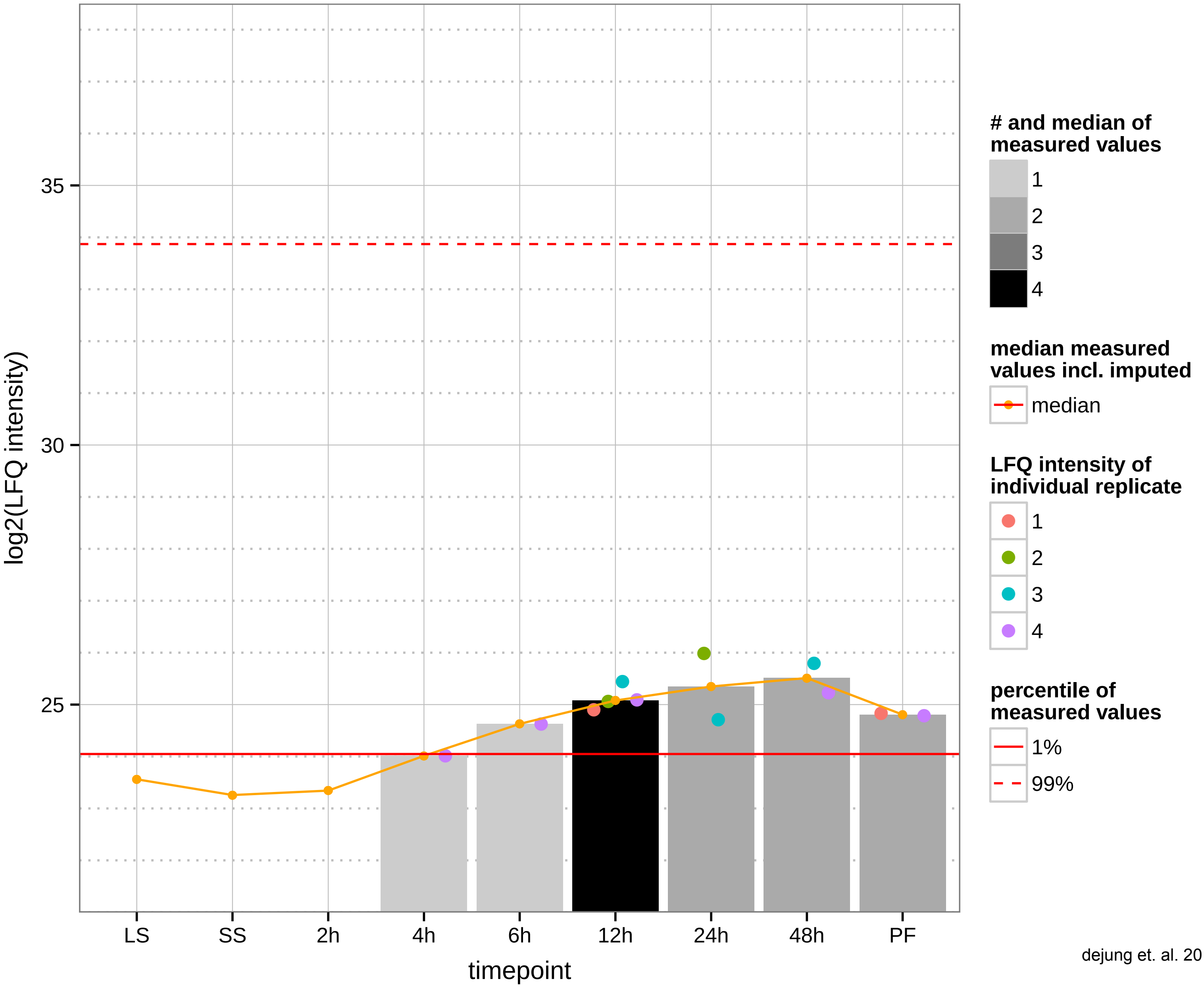
hypothetical protein, conserved
Tb927.7.2740
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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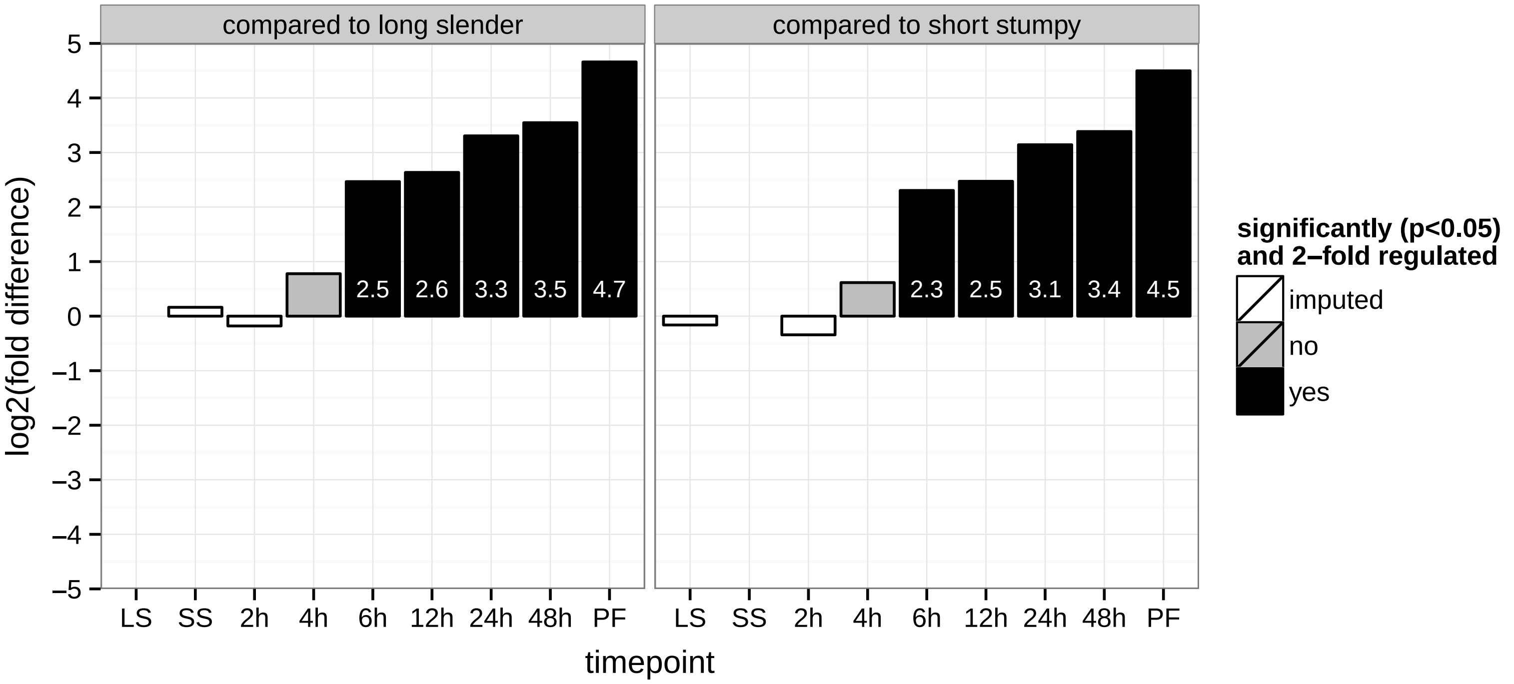
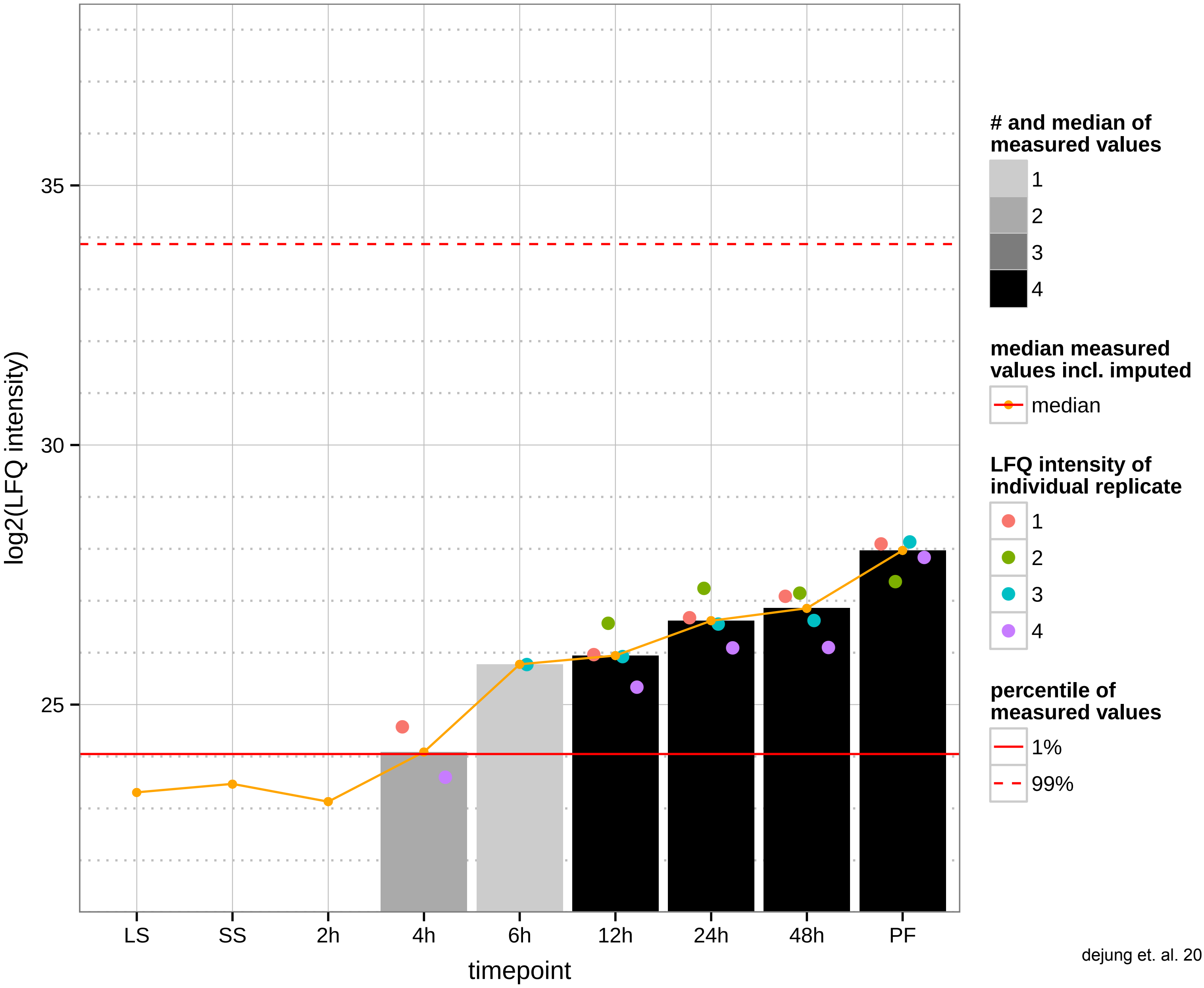
hypothetical protein, conserved (TbRBP8)
Tb927.7.320
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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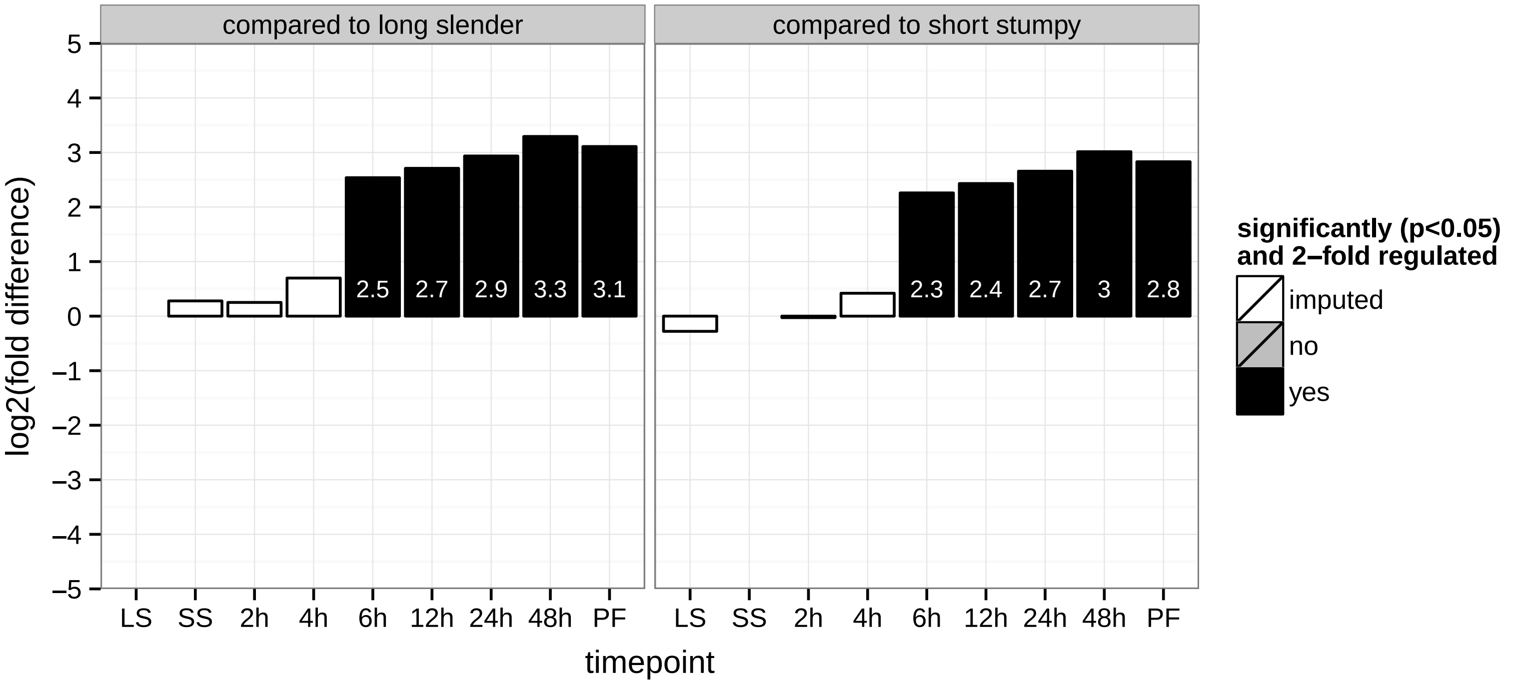
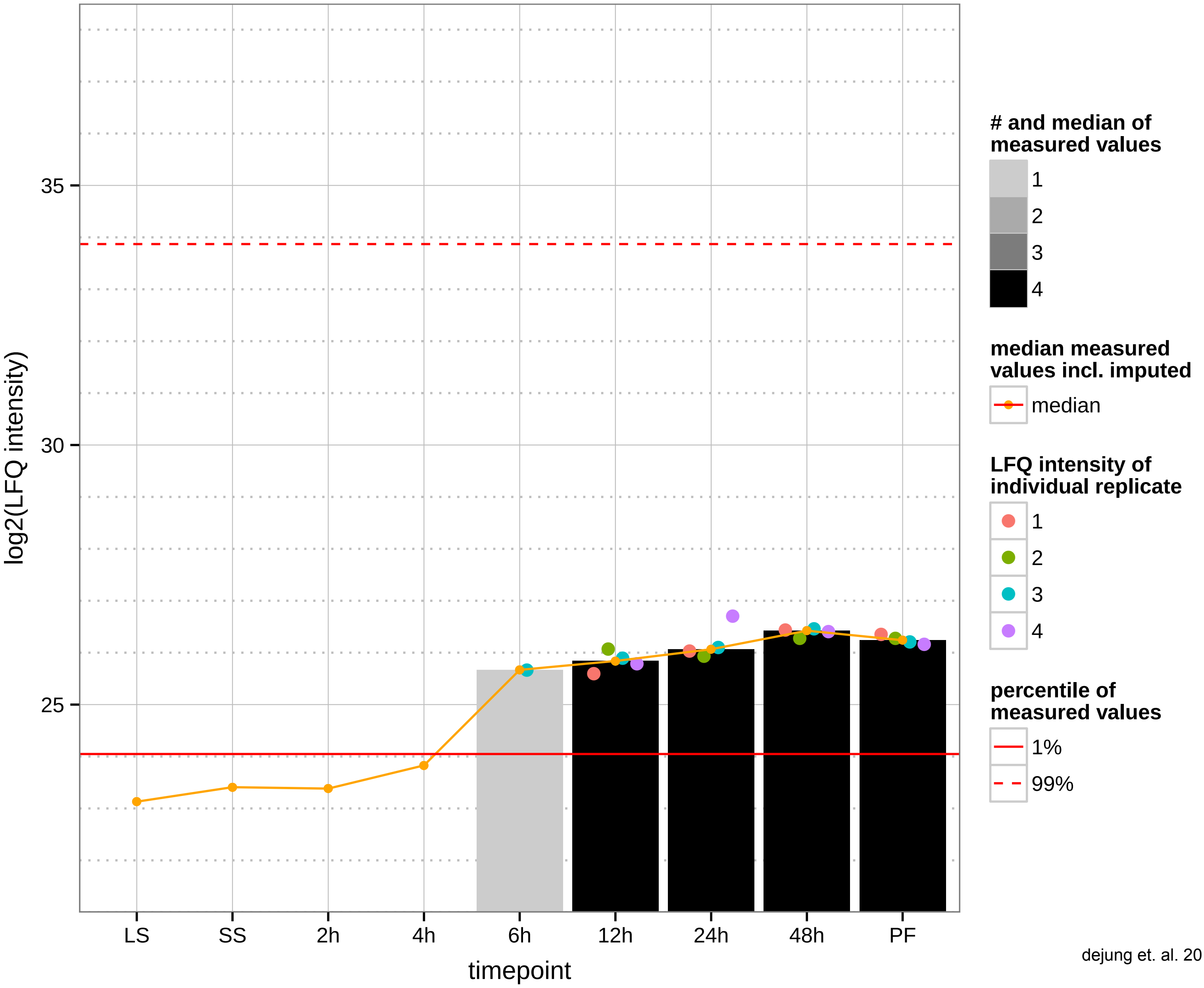
translation initiation factor IF−2, putative
Tb927.7.3280
AGOF: GTP binding, GTPase activity, translation factor activity, nucleic acid binding
AGOC: null
AGOP: translation
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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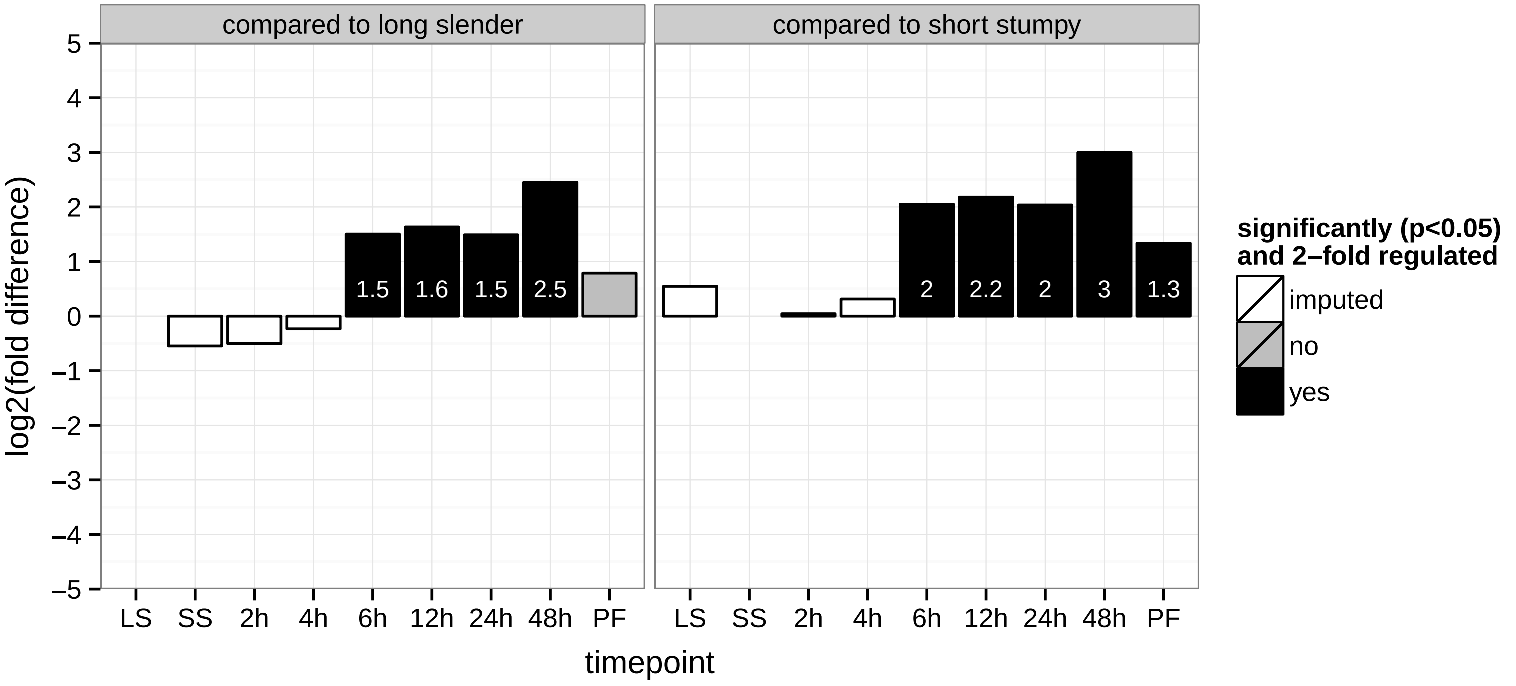
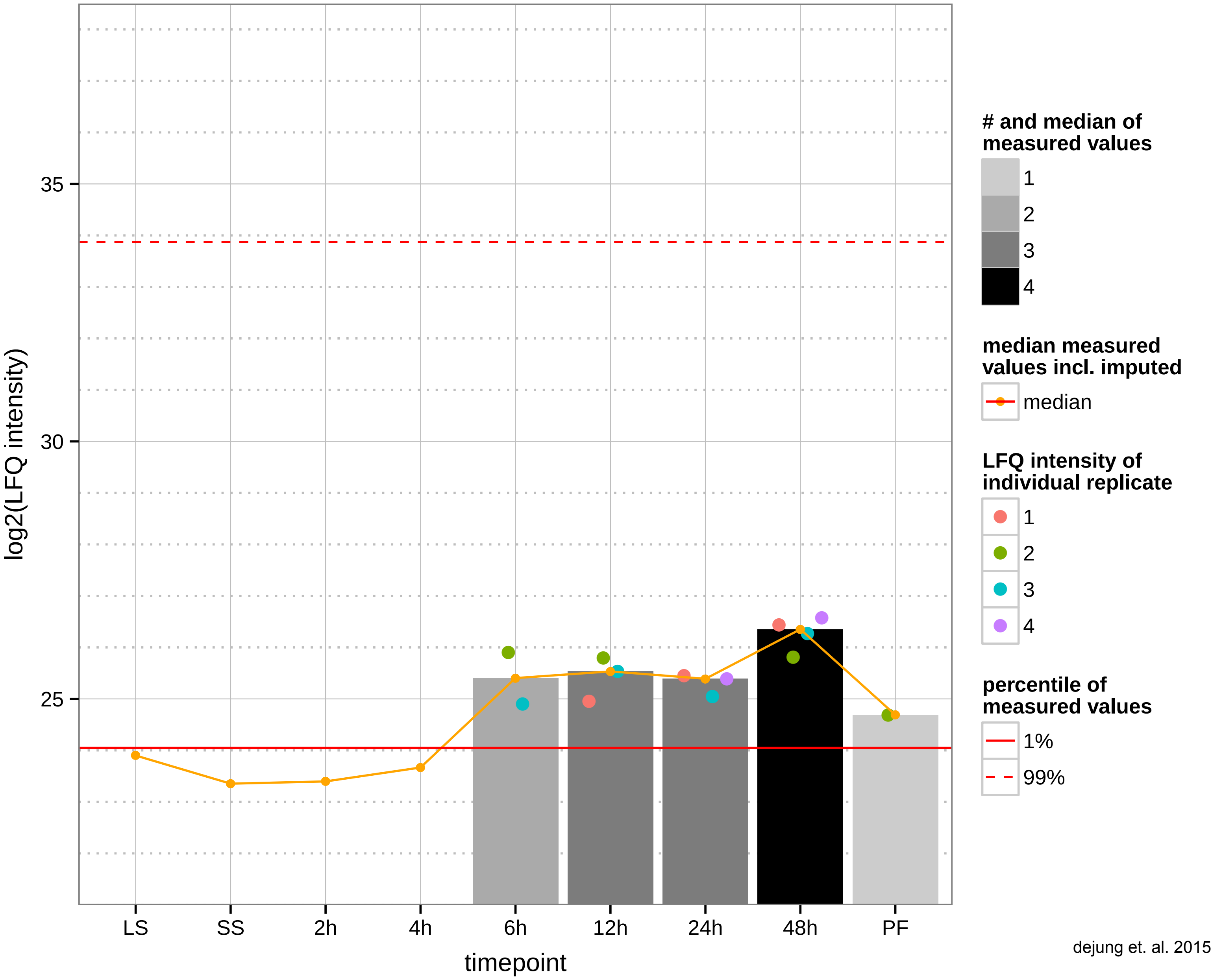
hypothetical protein, conserved
Tb927.7.3890
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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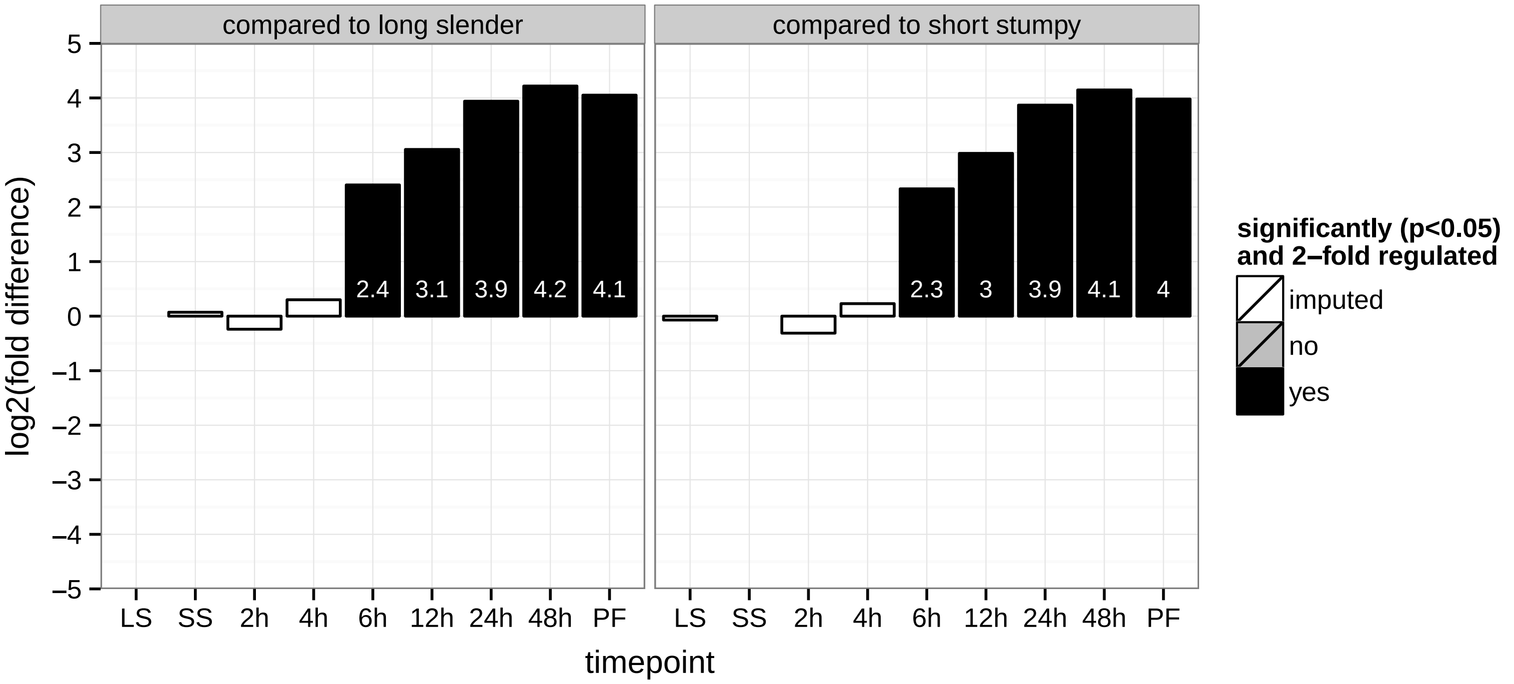
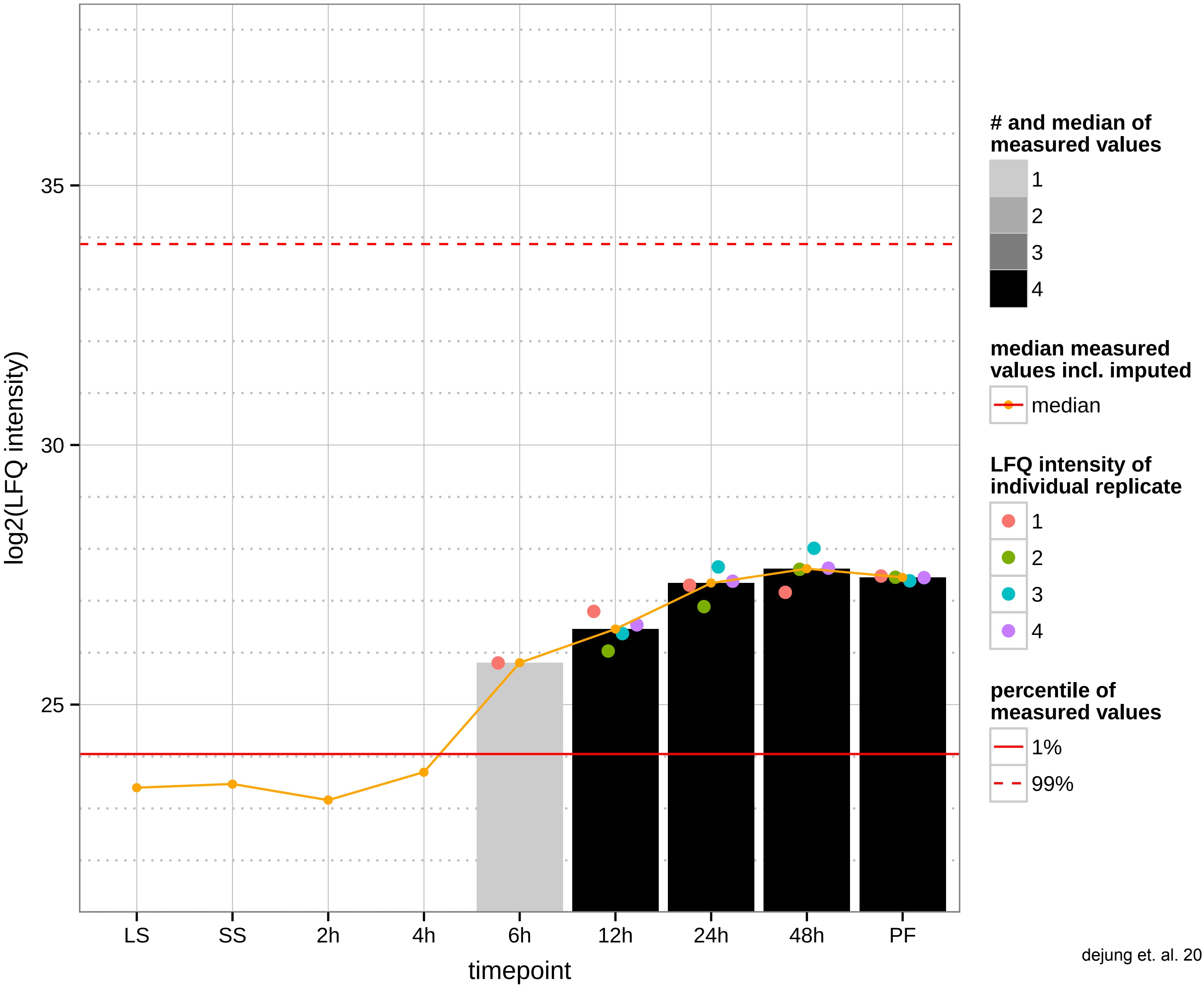
deoxyribose–phosphate aldolase, putative
Tb927.7.5680
AGOF: deoxyribose–phosphate aldolase activity
AGOC: cytoplasm, mitochondrial membrane
AGOP: deoxyribonucleotide catabolic process
PGOF: deoxyribose–phosphate aldolase activity, lyase activity
PGOC: cytoplasm
PGOP: deoxyribonucleotide catabolic process





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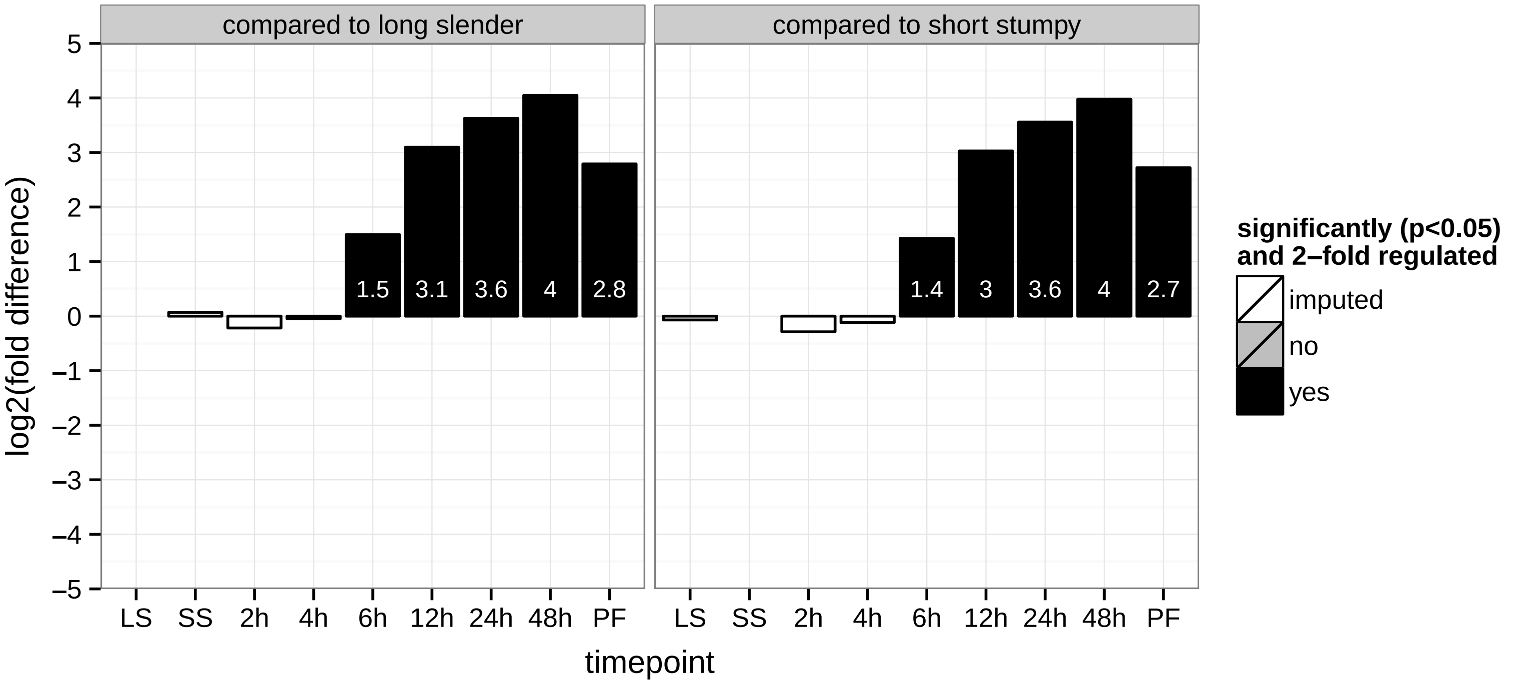
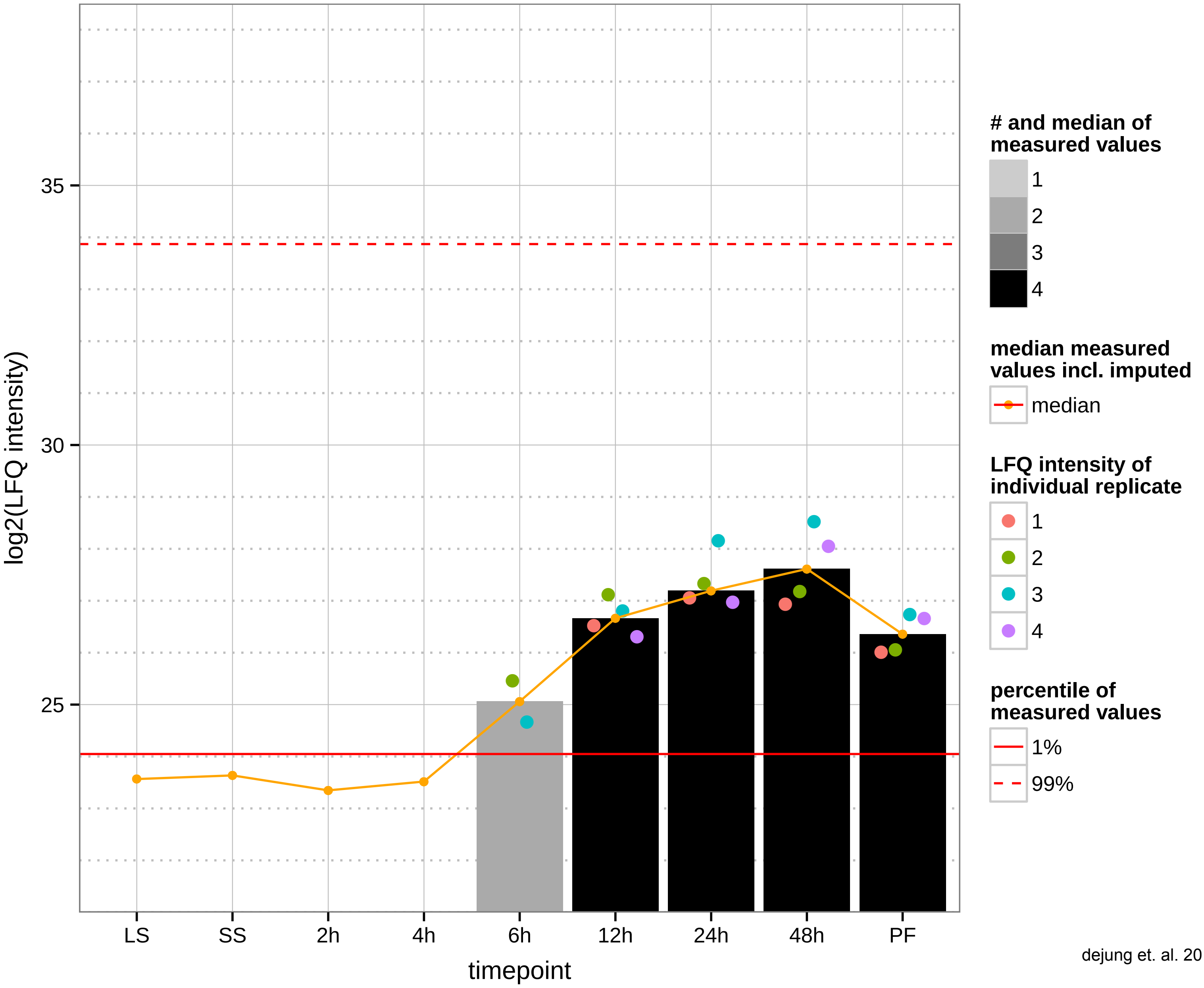
protein associated with differentiation 5, putative (PAD5), protein associated with differentiation 7, putative (PAD7)
Tb927.7.5990;Tb927.7.5970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: integral to membrane
PGOP: transmembrane transport





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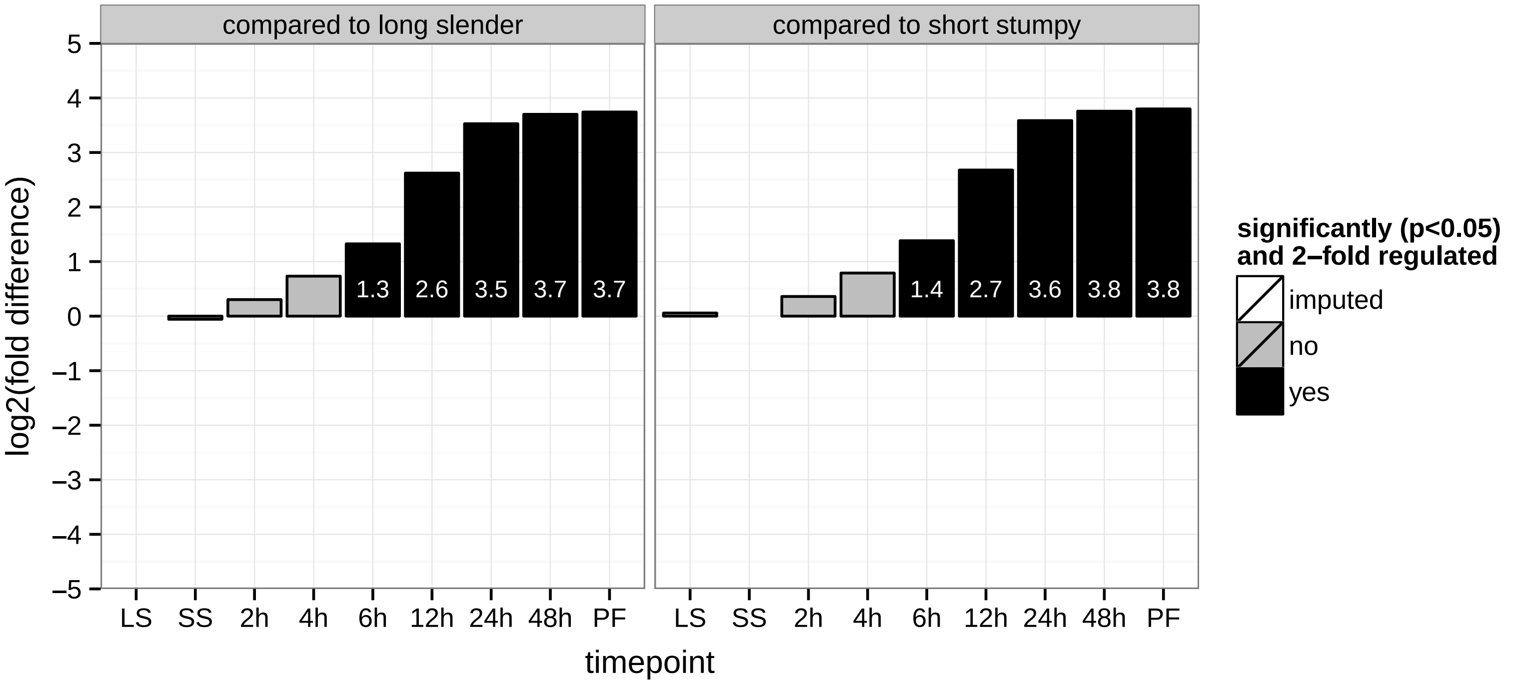
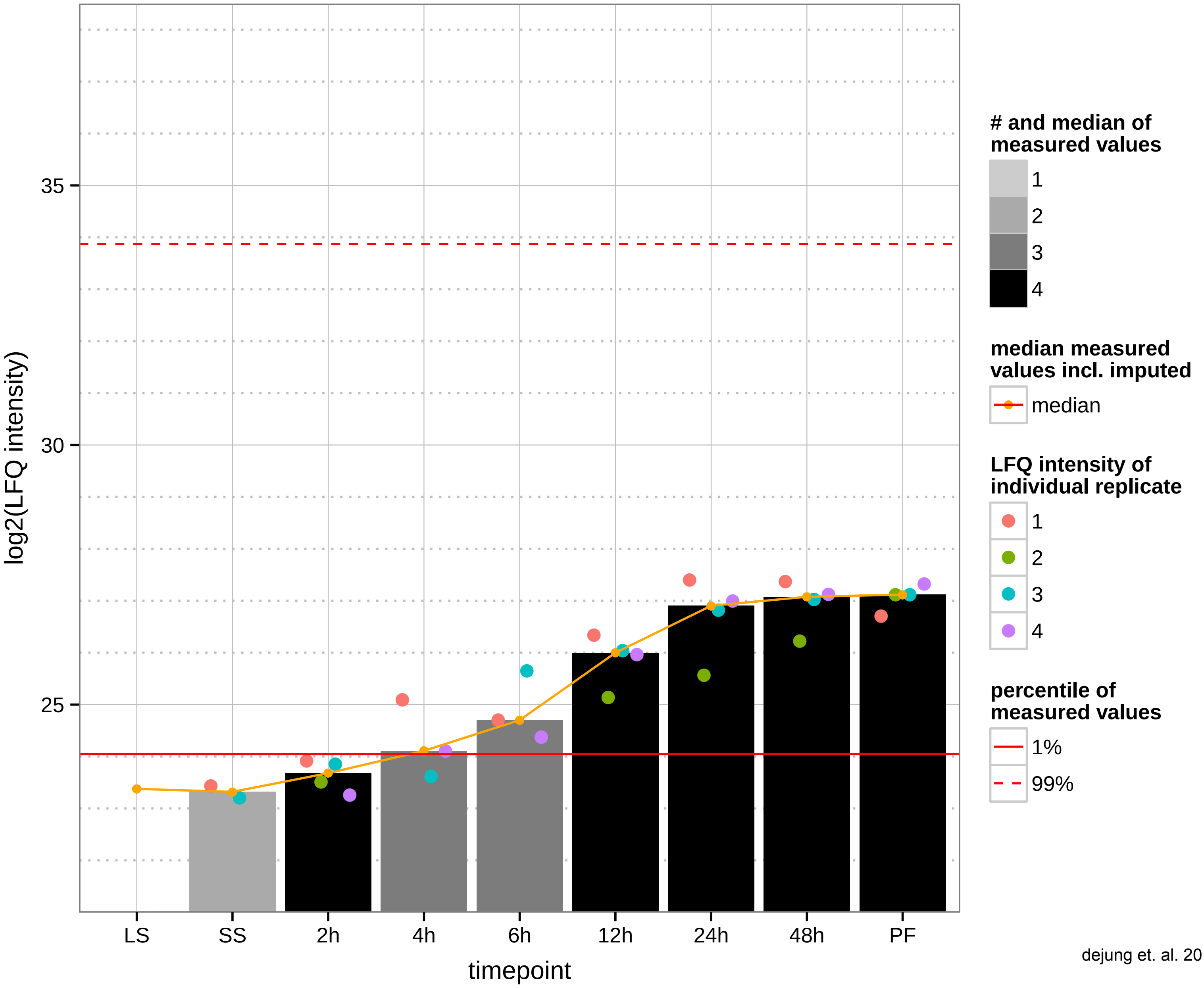
tRNA–dihydrouridine synthase 3, putative
Tb927.7.6450
AGOF: flavin adenine dinucleotide binding, tRNA dihydrouridine synthase activity
AGOC: null
AGOP: oxidation–reduction process, tRNA processing
PGOF: flavin adenine dinucleotide binding, tRNA dihydrouridine synthase activity
PGOC: null
PGOP: oxidation–reduction process, tRNA processing





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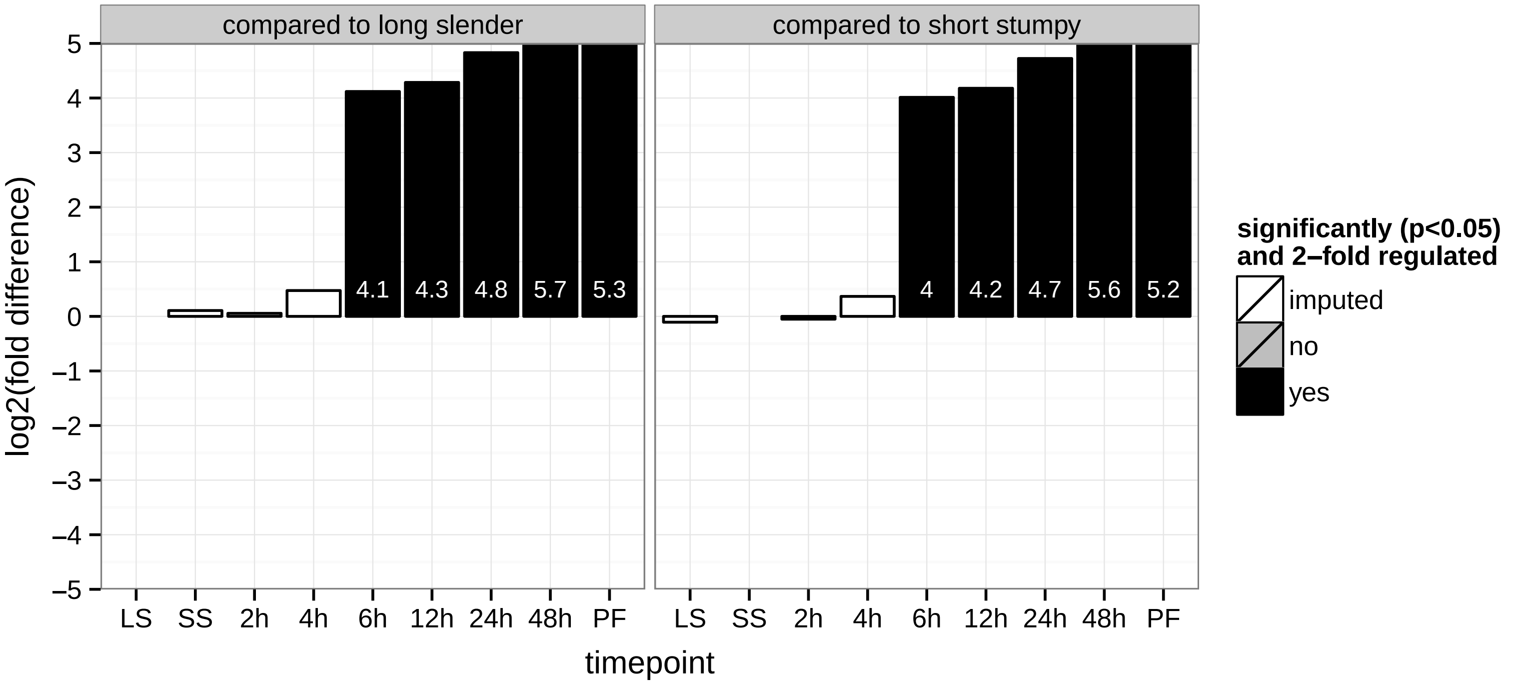
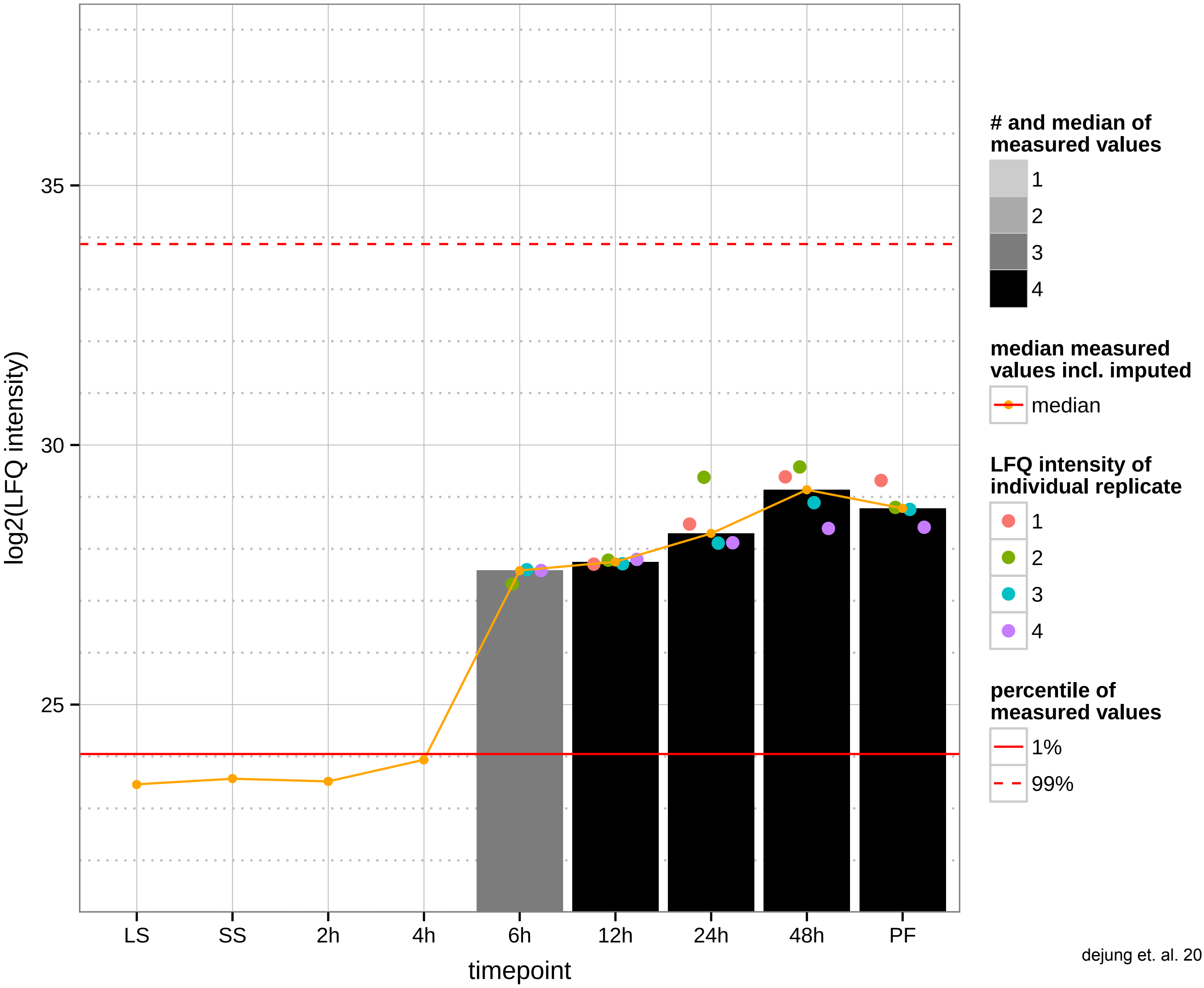
hypothetical protein, conserved
Tb927.7.6990
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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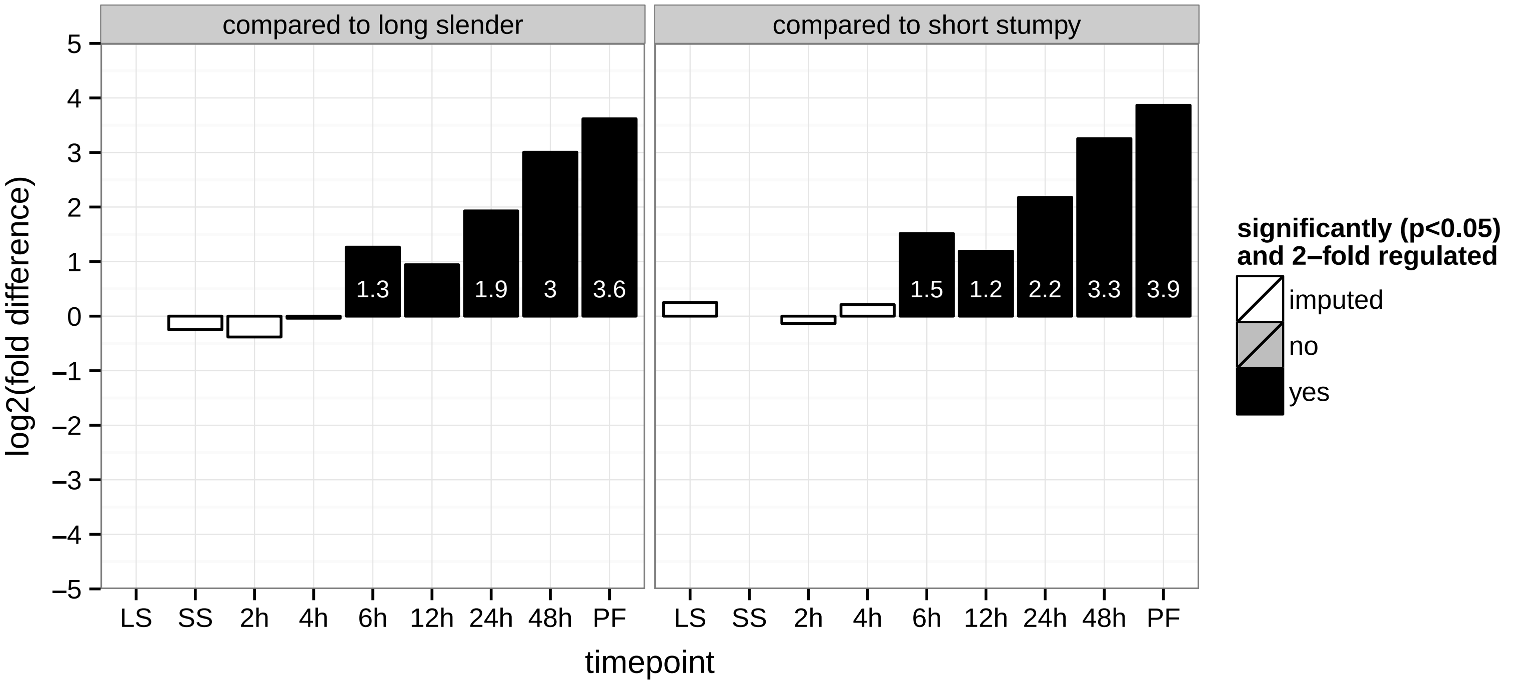
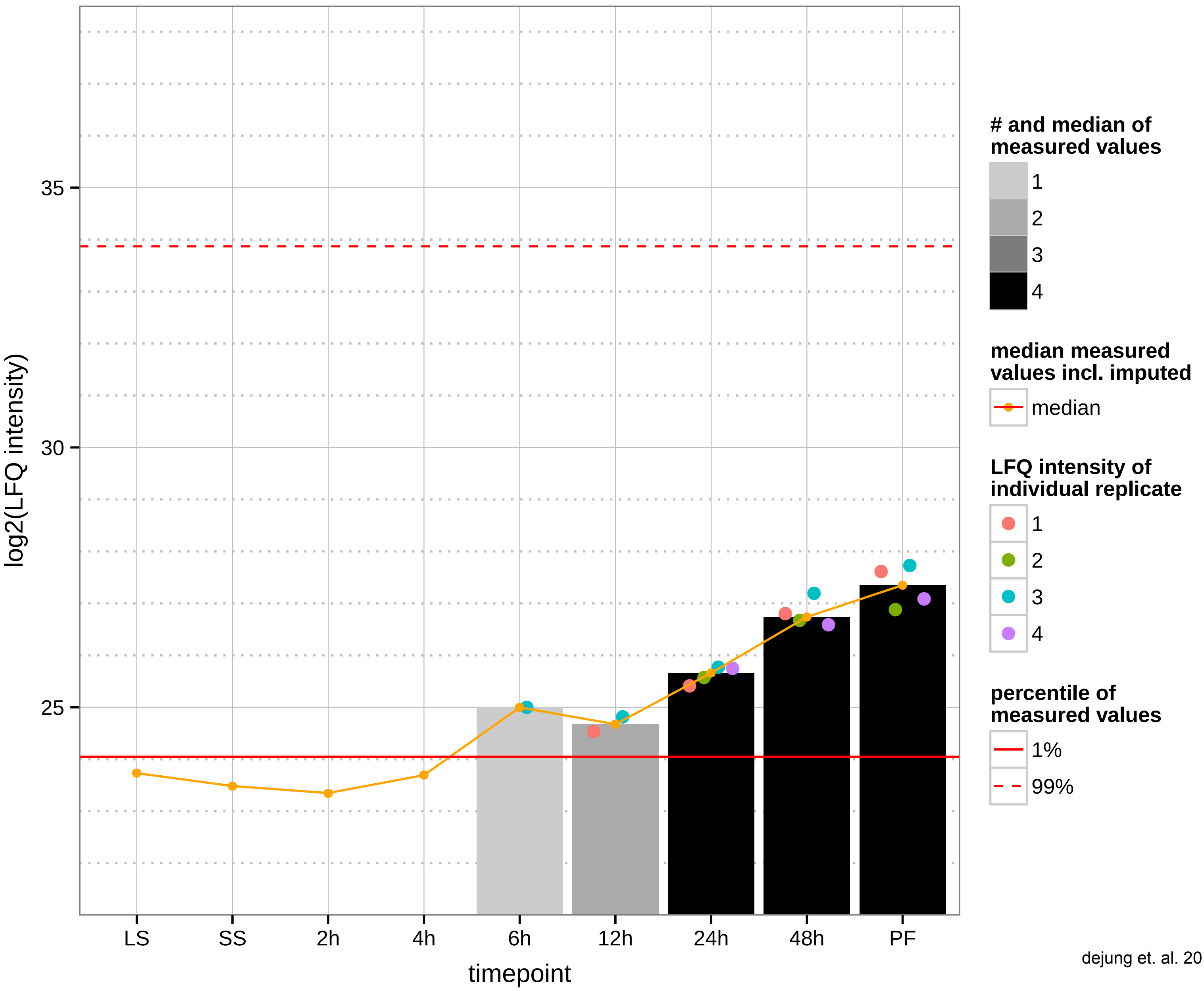
acetylornithine deacetylase, putative, metallo–peptidase, Clan MH, Family M18 (ArgE)
Tb927.8.1910
AGOF: acetylornithine deacetylase activity, cobalt ion binding, metallopeptidase activity, protein dimerization activity, zinc ion b
AGOC: cytoplasm
AGOP: arginine biosynthetic process, proteolysis
PGOF: acetylornithine deacetylase activity, cobalt ion binding, hydrolase activity, zinc ion binding
PGOC: cytoplasm
PGOP: arginine biosynthetic process, metabolic process





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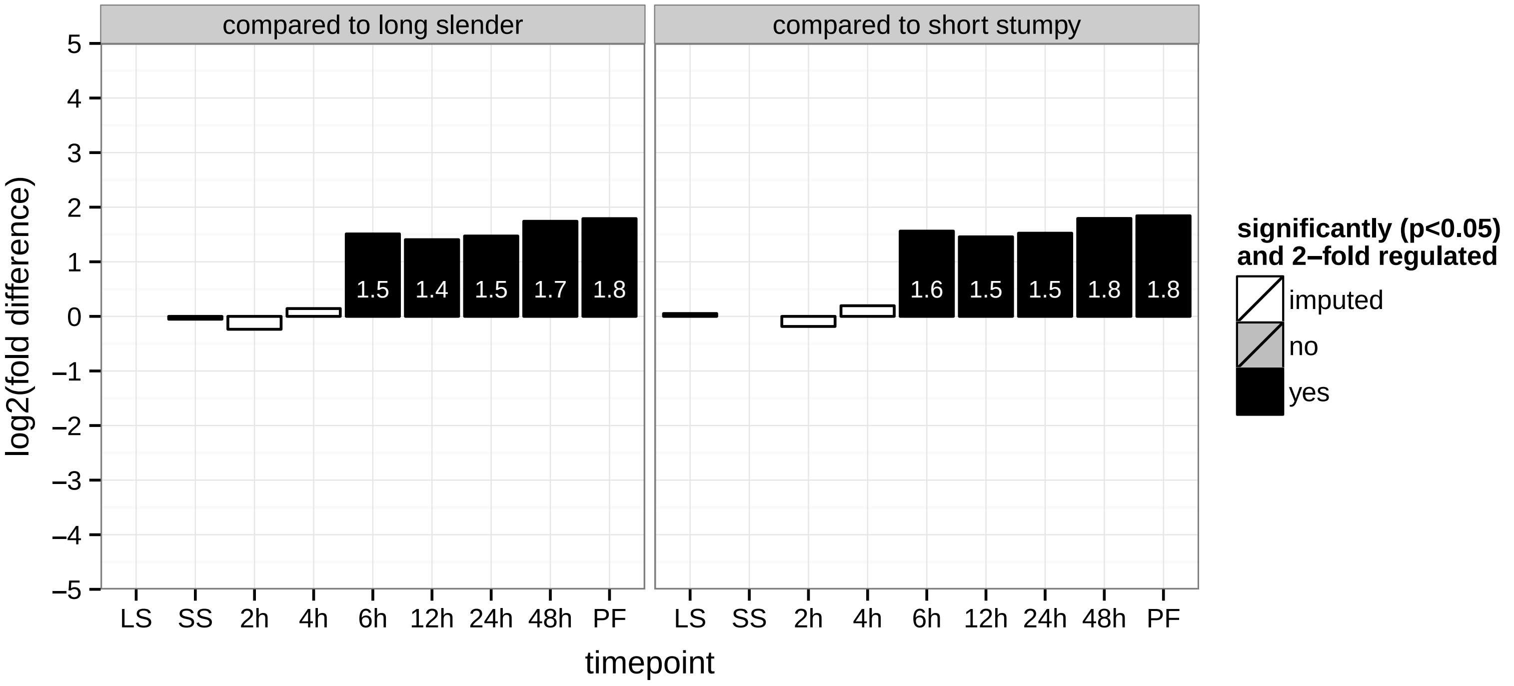
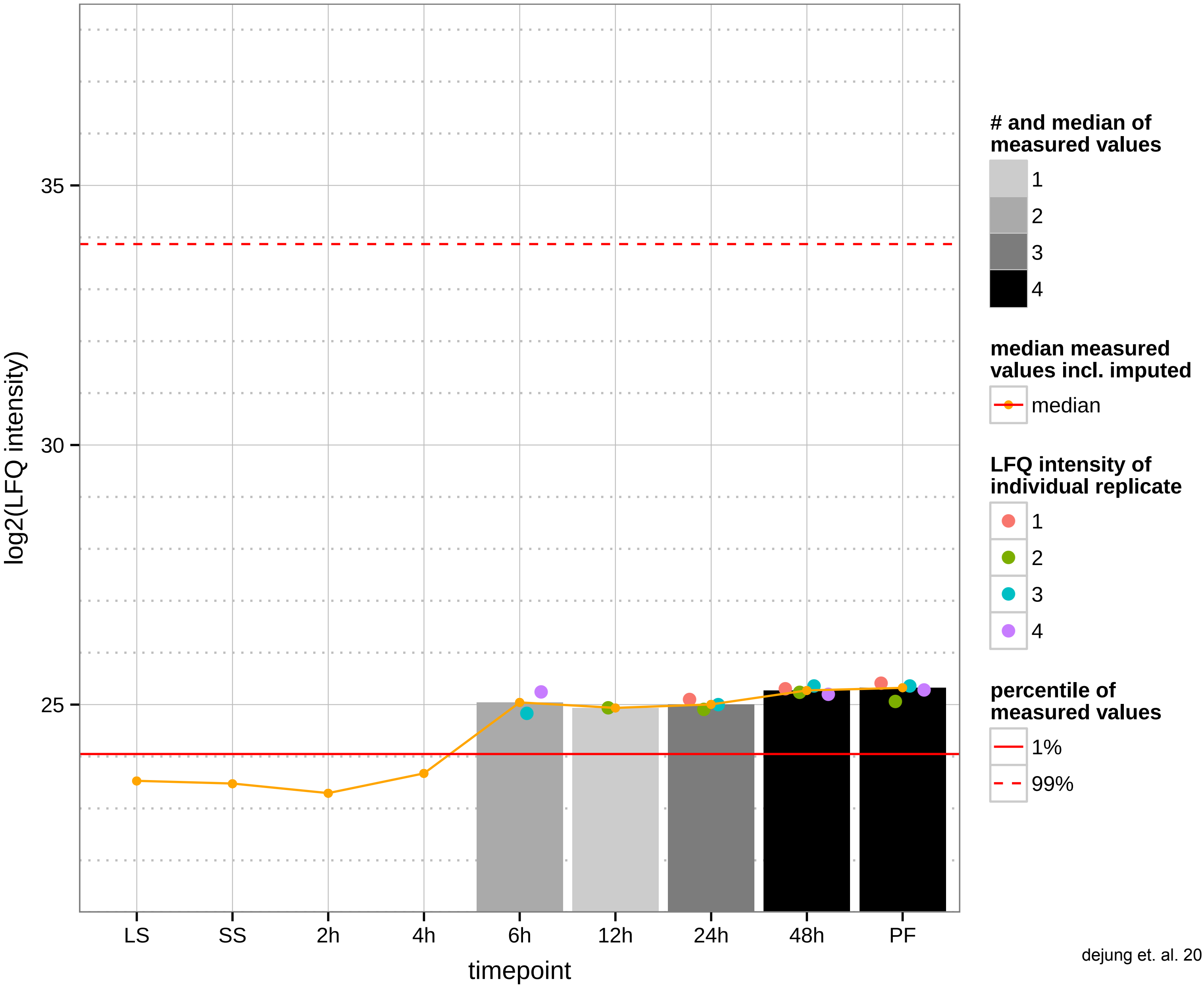
Tryptophanyl–tRNA synthetase 2
Tb927.8.2240
AGOF: ATP binding, aminoacyl–tRNA ligase activity, tryptophan–tRNA ligase activity
AGOC: cytoplasm, mitochondrial part
AGOP: tRNA aminoacylation for protein translation, translation, tryptophanyl–tRNA aminoacylation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, nucleotide binding, tryptophan–tRNA ligase activity
PGOC: cytoplasm
PGOP: tRNA aminoacylation for protein translation, tryptophanyl–tRNA aminoacylation





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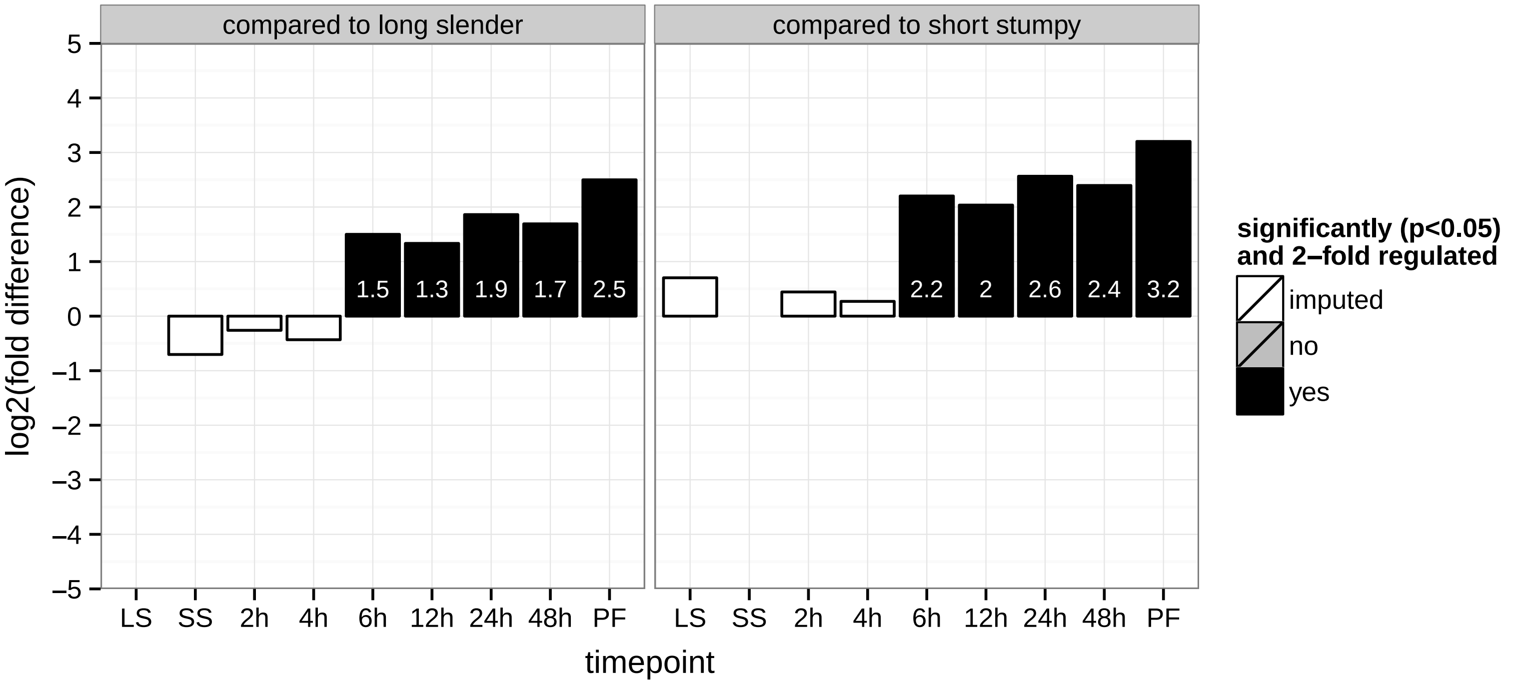
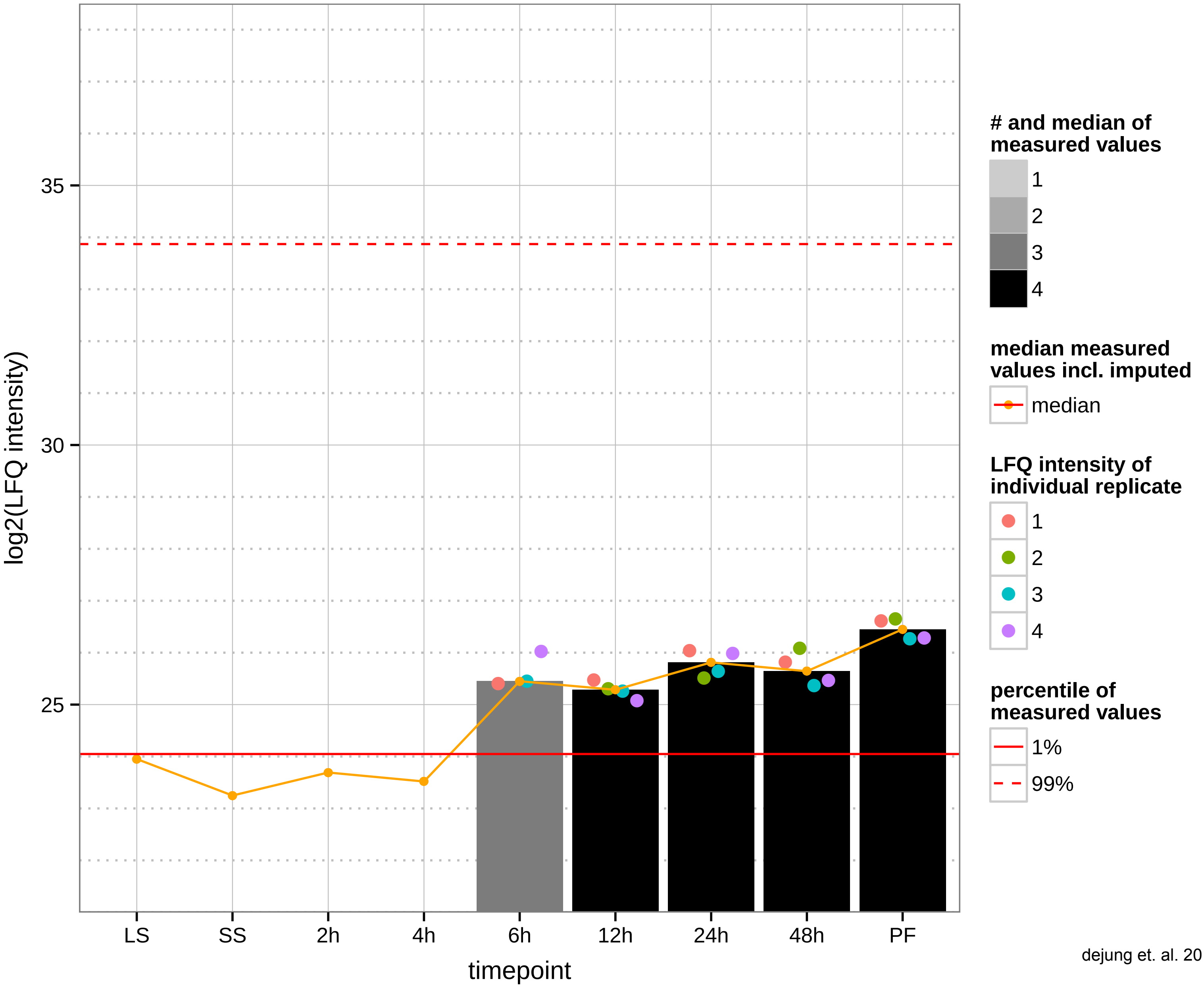
hypothetical protein, conserved
Tb927.8.5990
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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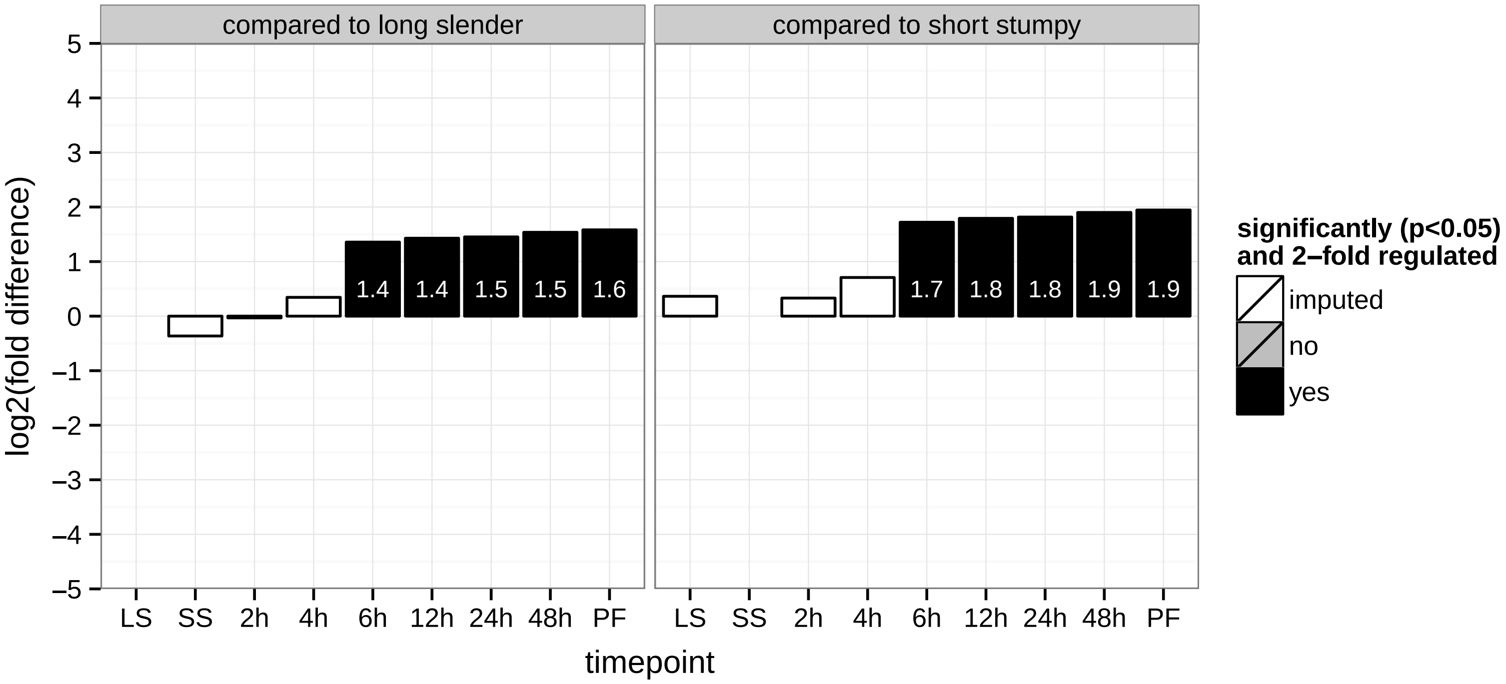
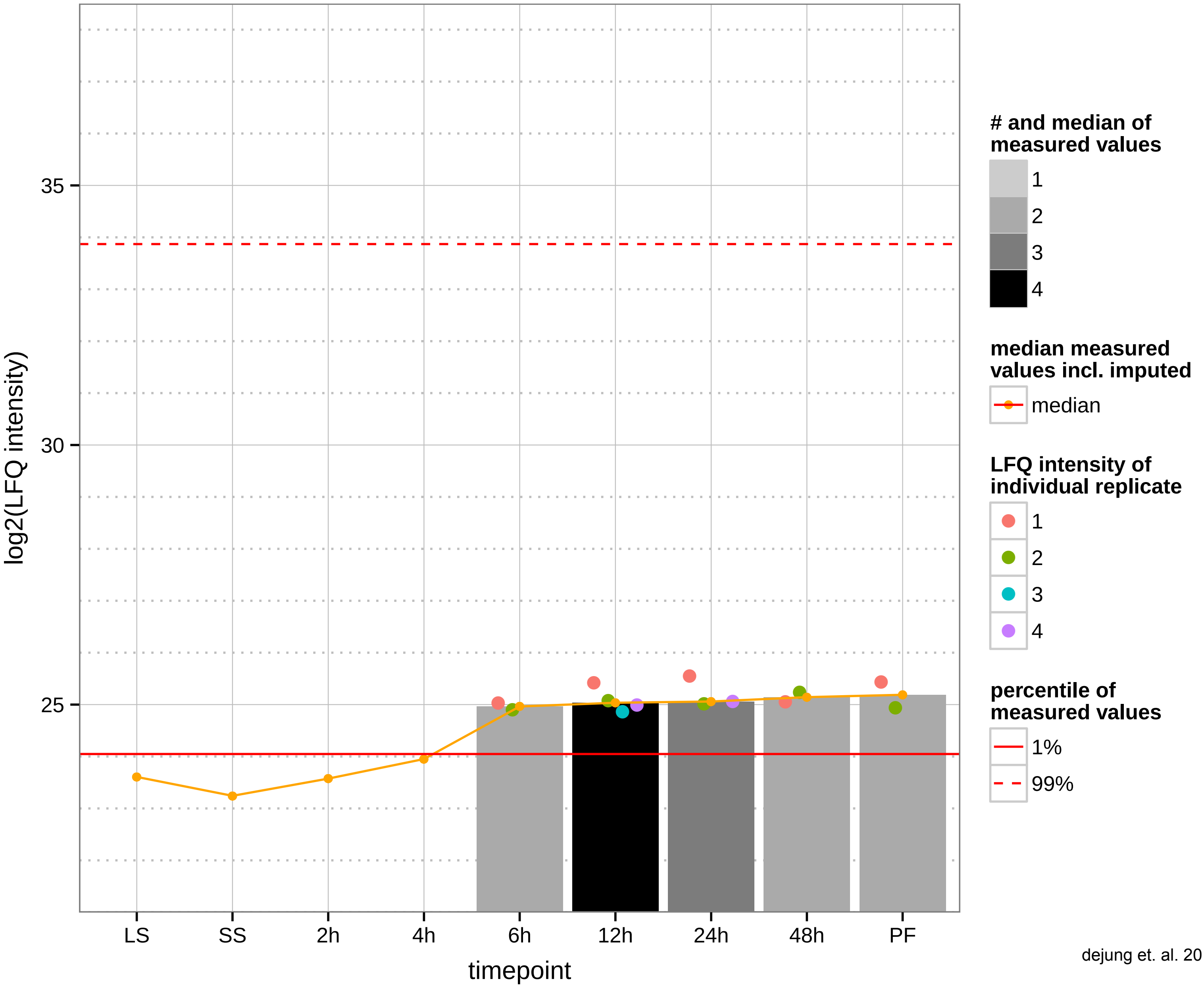
hypothetical protein, conserved
Tb927.8.6130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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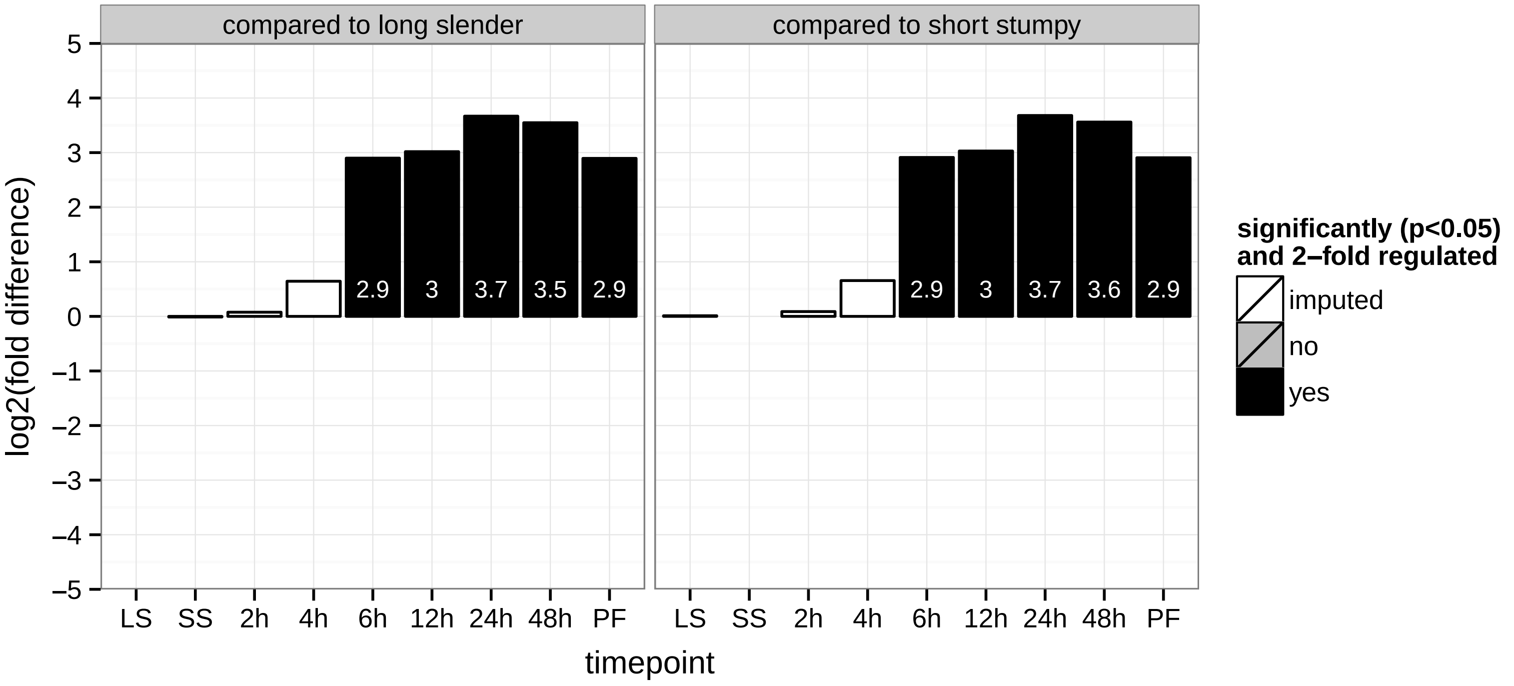
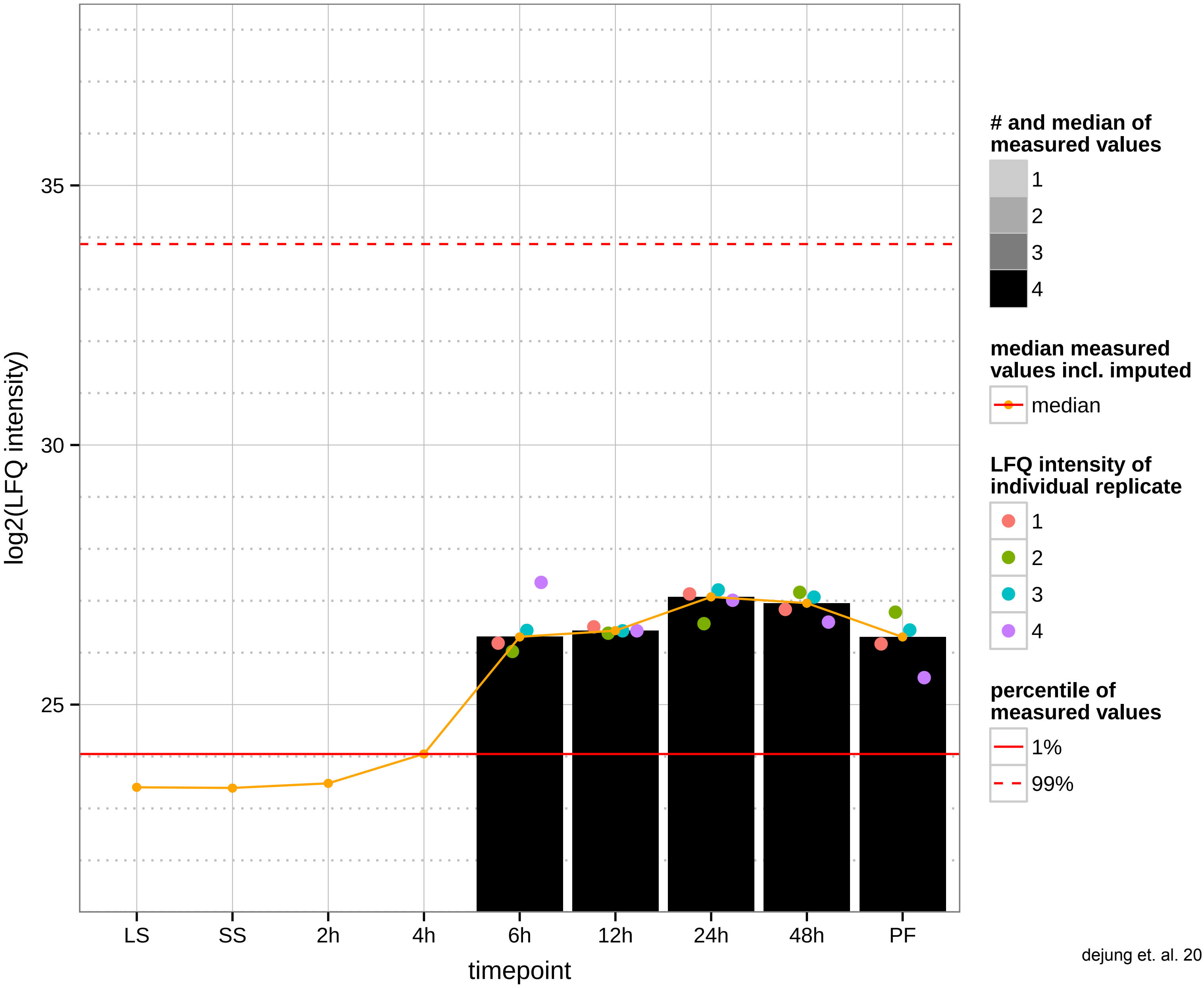
amino acid transporter, putative
Tb927.8.7700;Tb927.8.7680
AGOF: amine transmembrane transporter activity
AGOC: integral to membrane
AGOP: amino acid transport
PGOF: null
PGOC: null
PGOP: null





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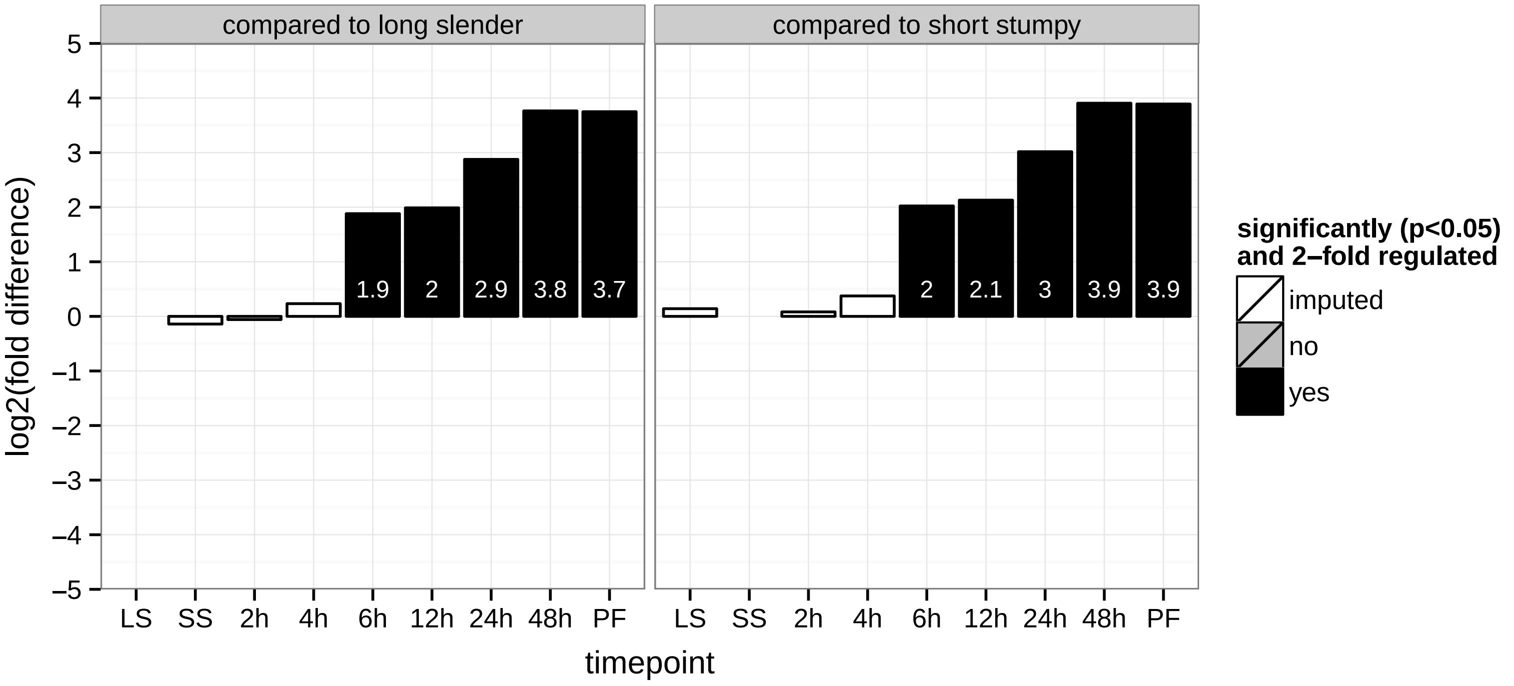
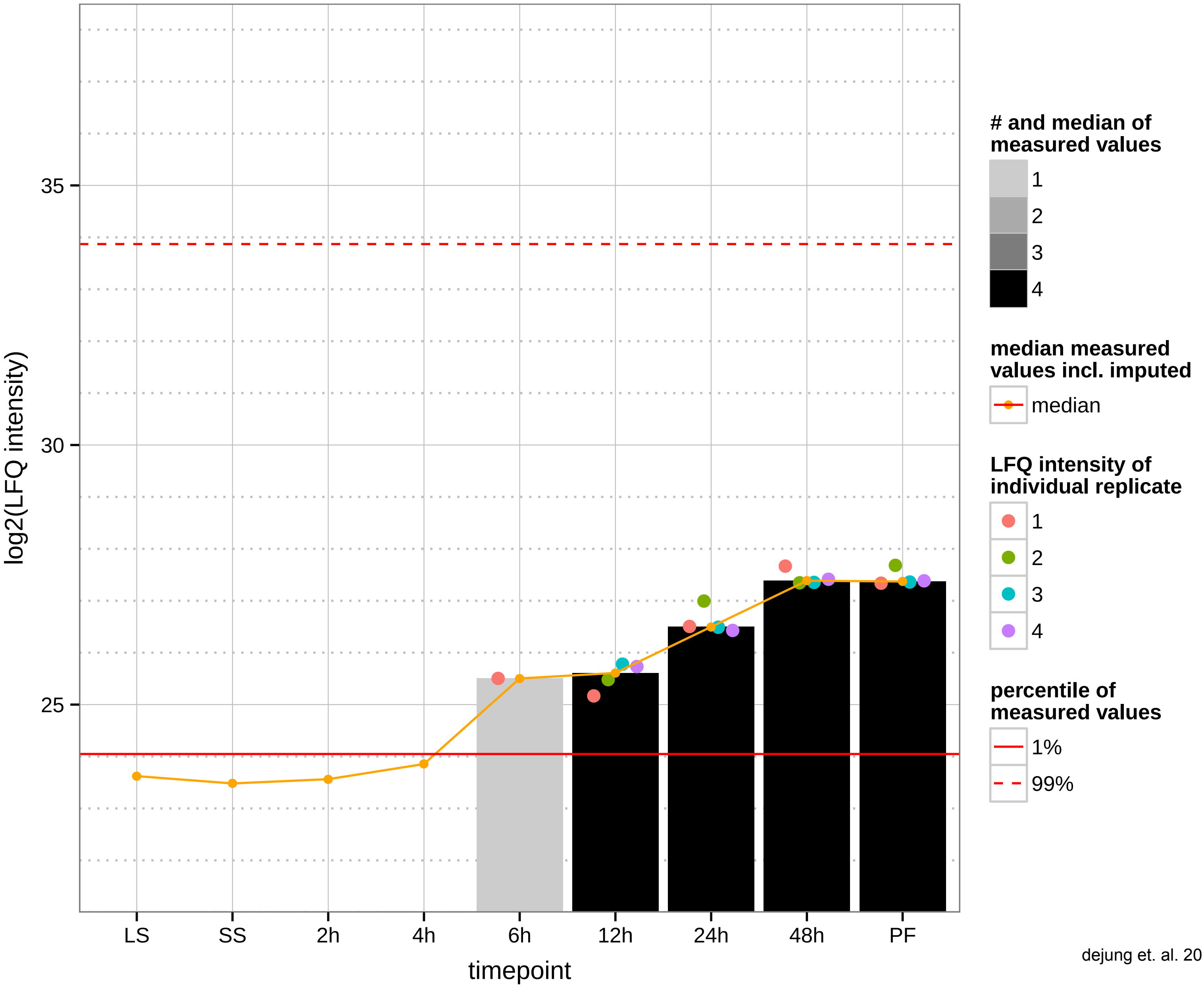
hypothetical protein, conserved
Tb927.9.10520
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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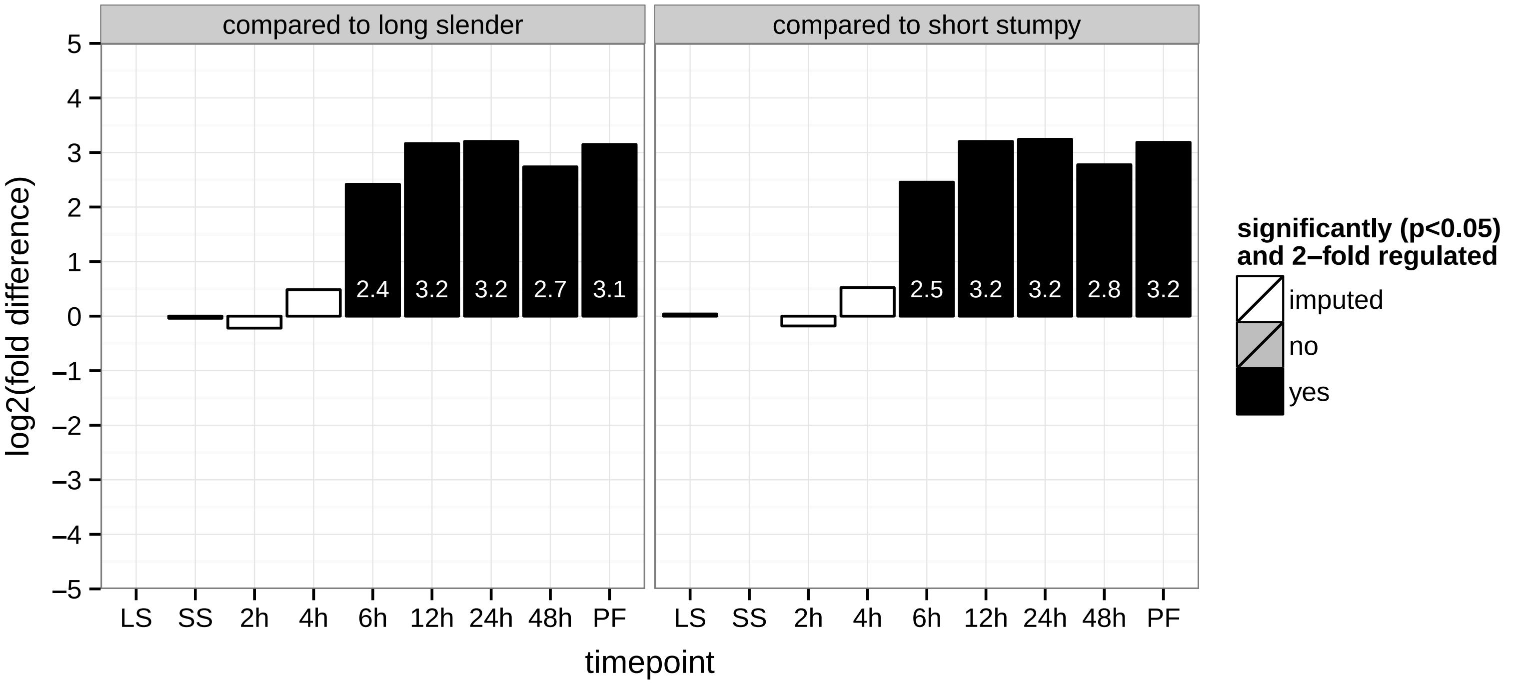
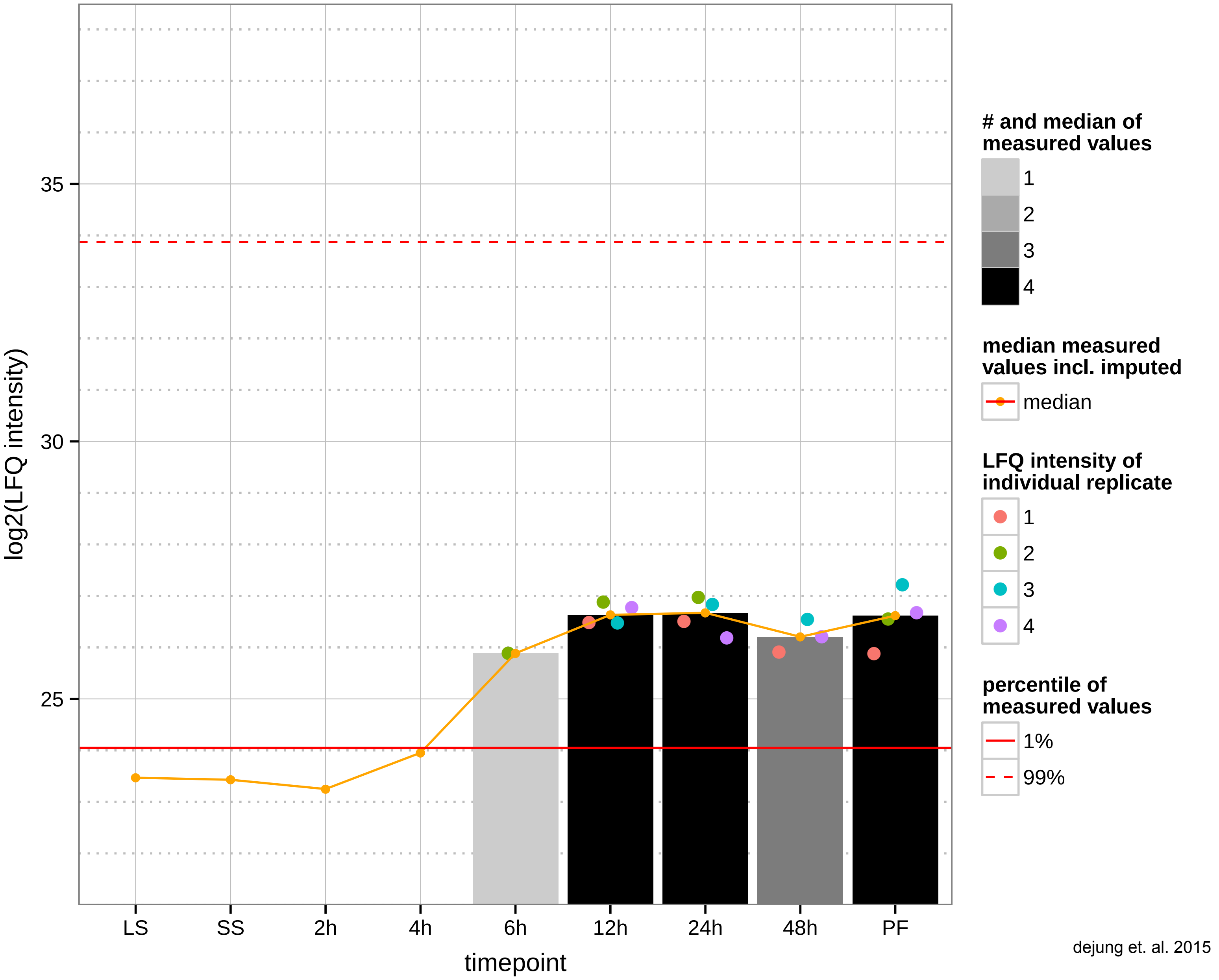
Iron–sulfur cluster assembly protein
Tb927.9.11720
AGOF: iron ion binding, iron–sulfur cluster binding, metallochaperone activity
AGOC: mitochondrion
AGOP: iron–sulfur cluster assembly
PGOF: iron ion binding, iron–sulfur cluster binding
PGOC: null
PGOP: iron–sulfur cluster assembly





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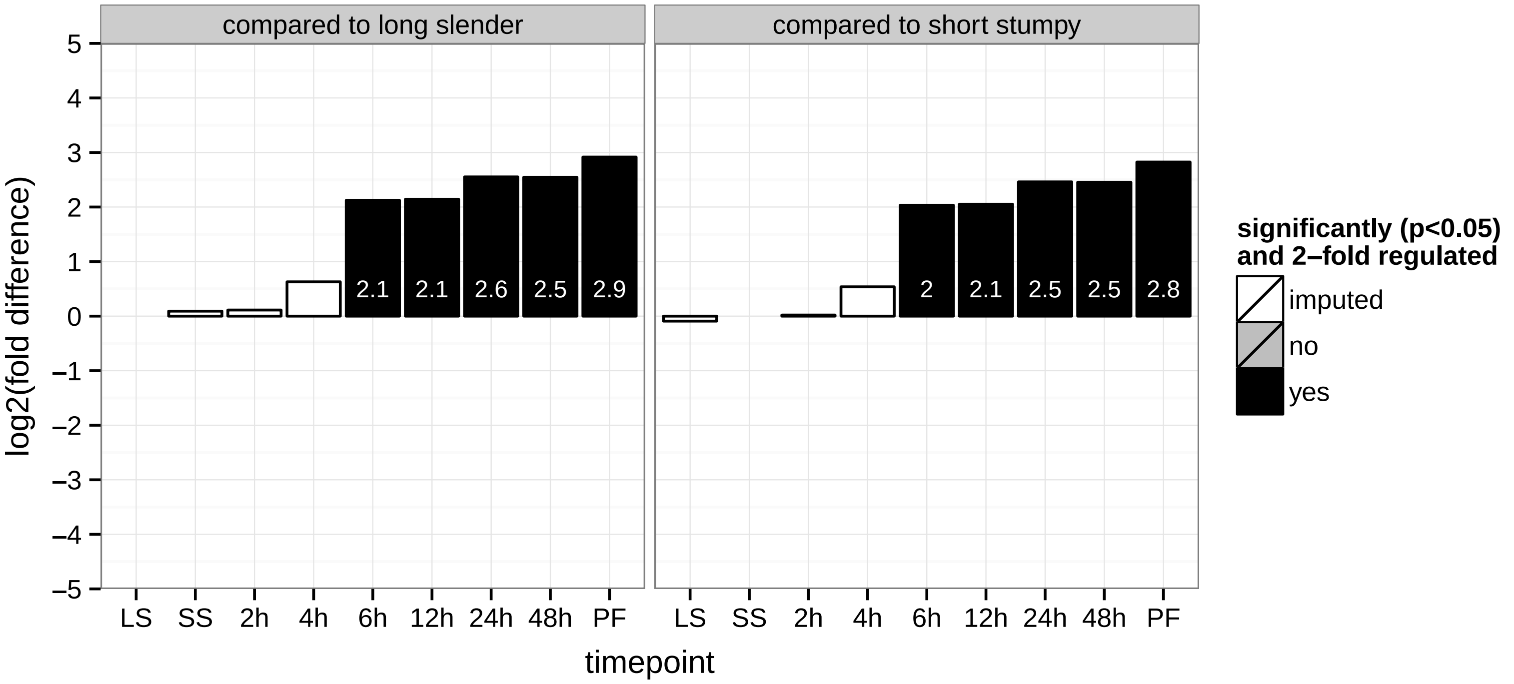
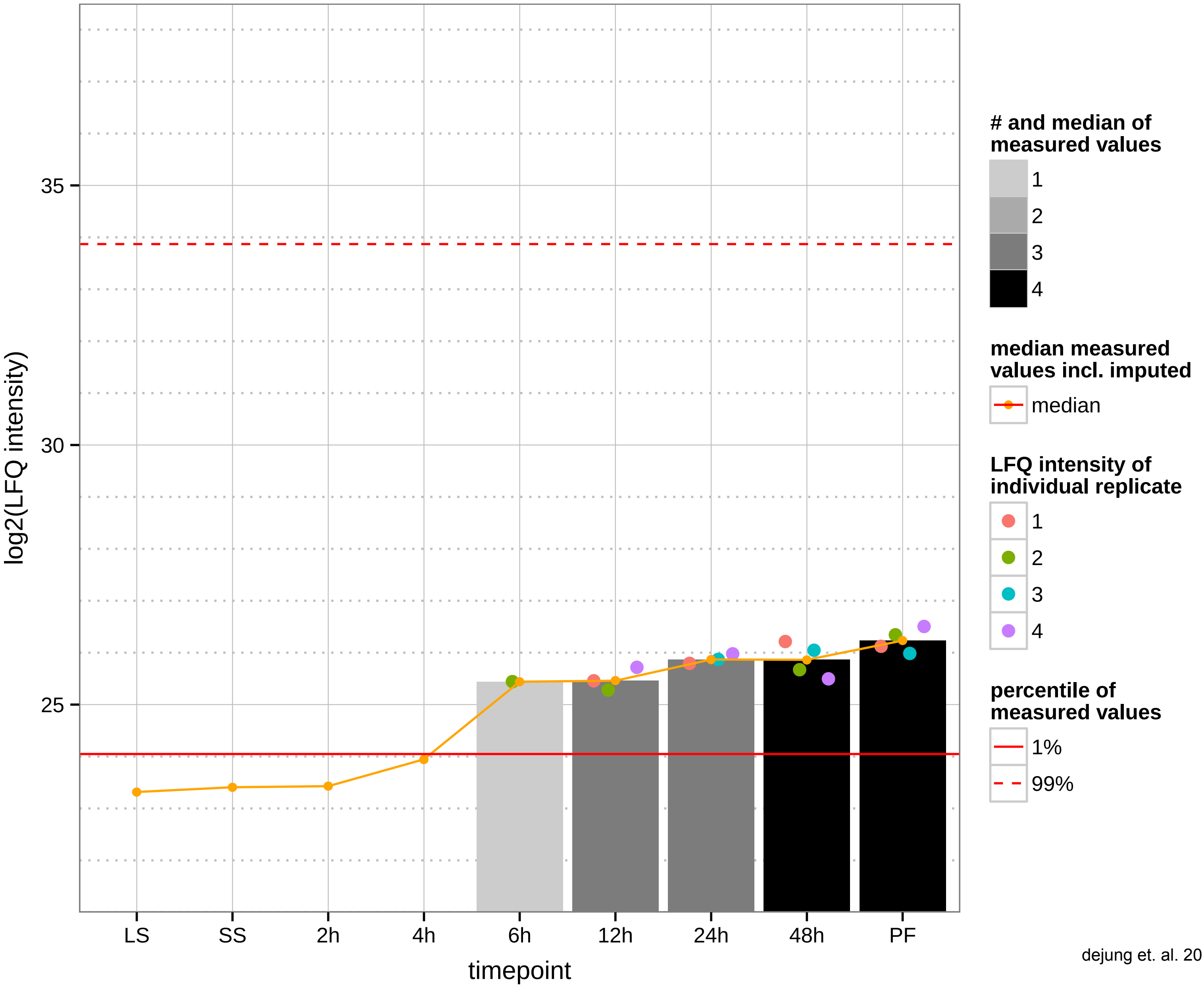
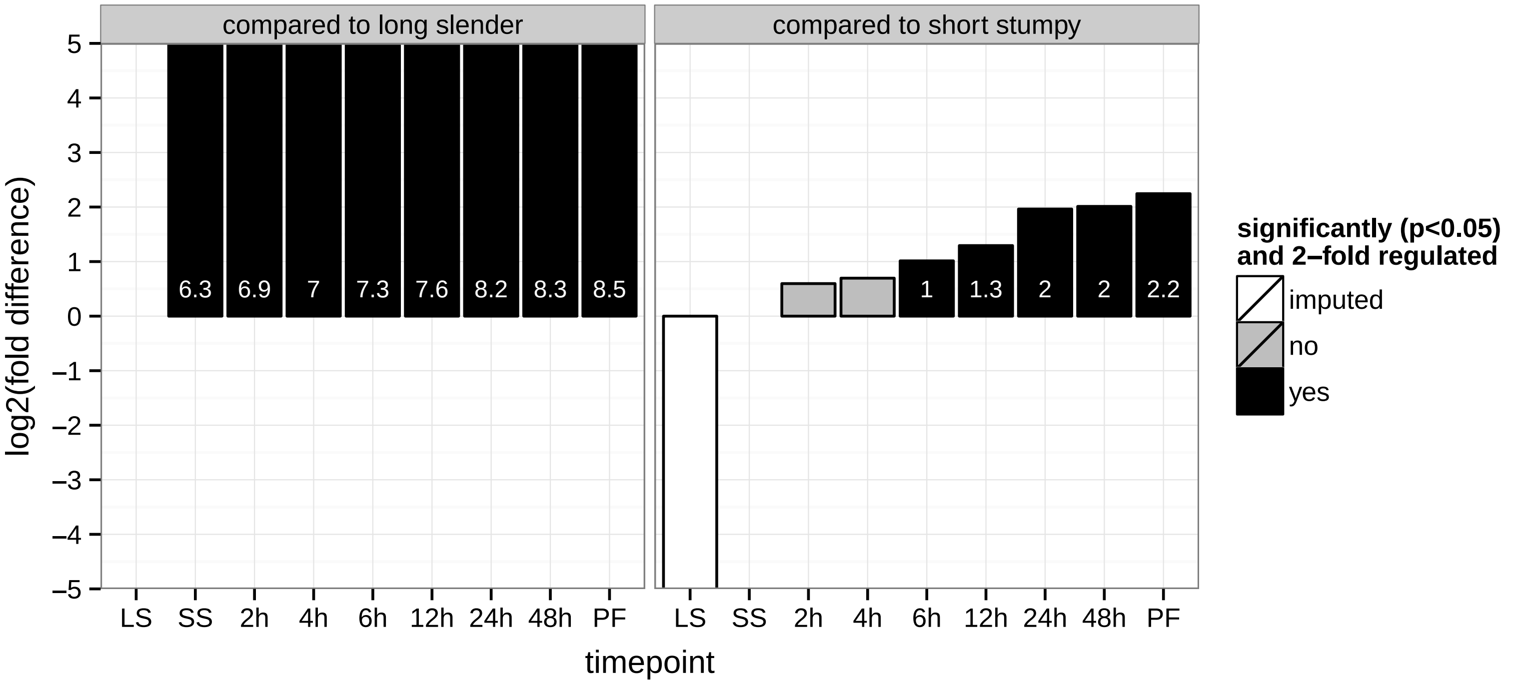
hypothetical protein, conserved
Tb927.9.11880
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

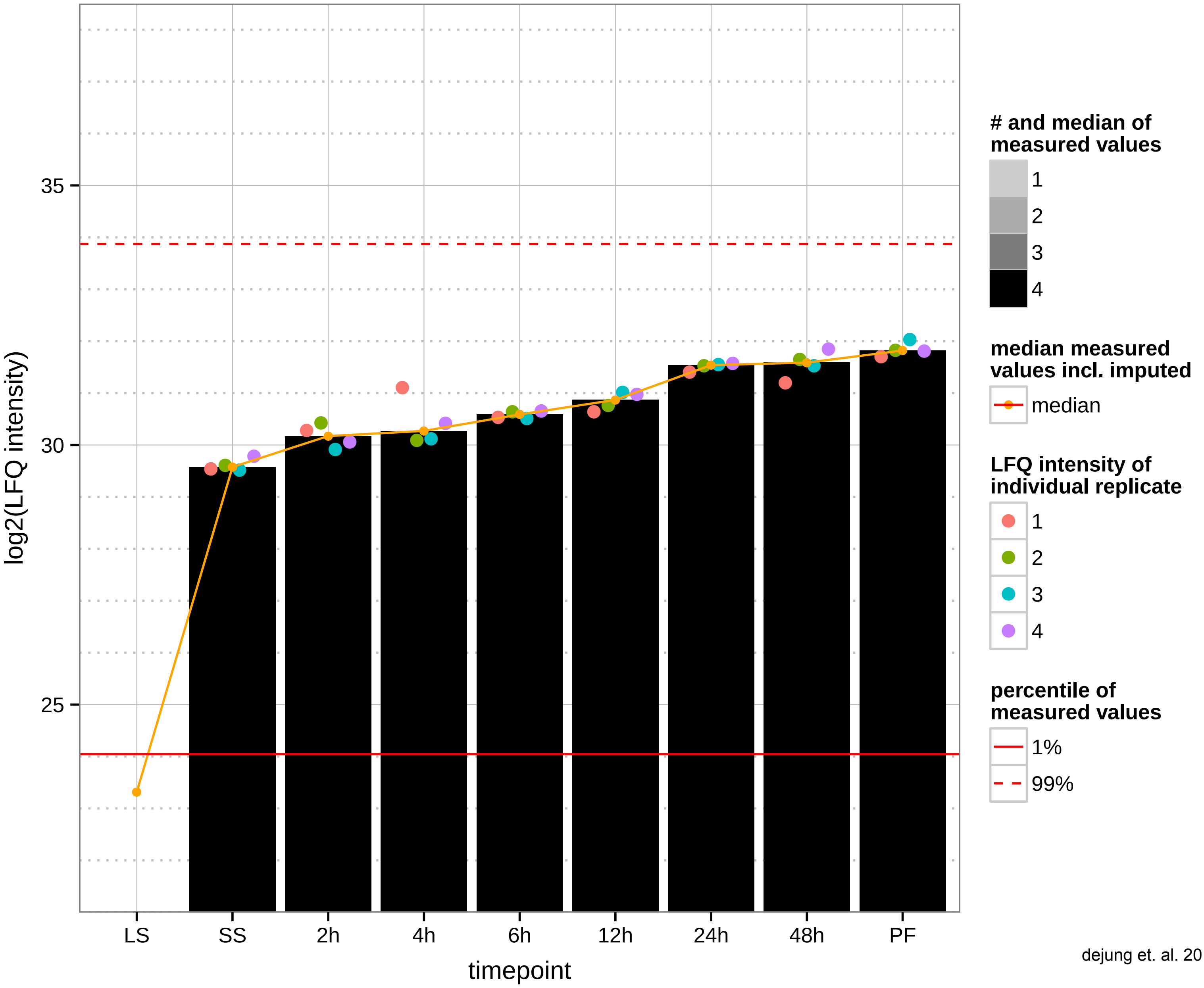




dejung et. al. 2015

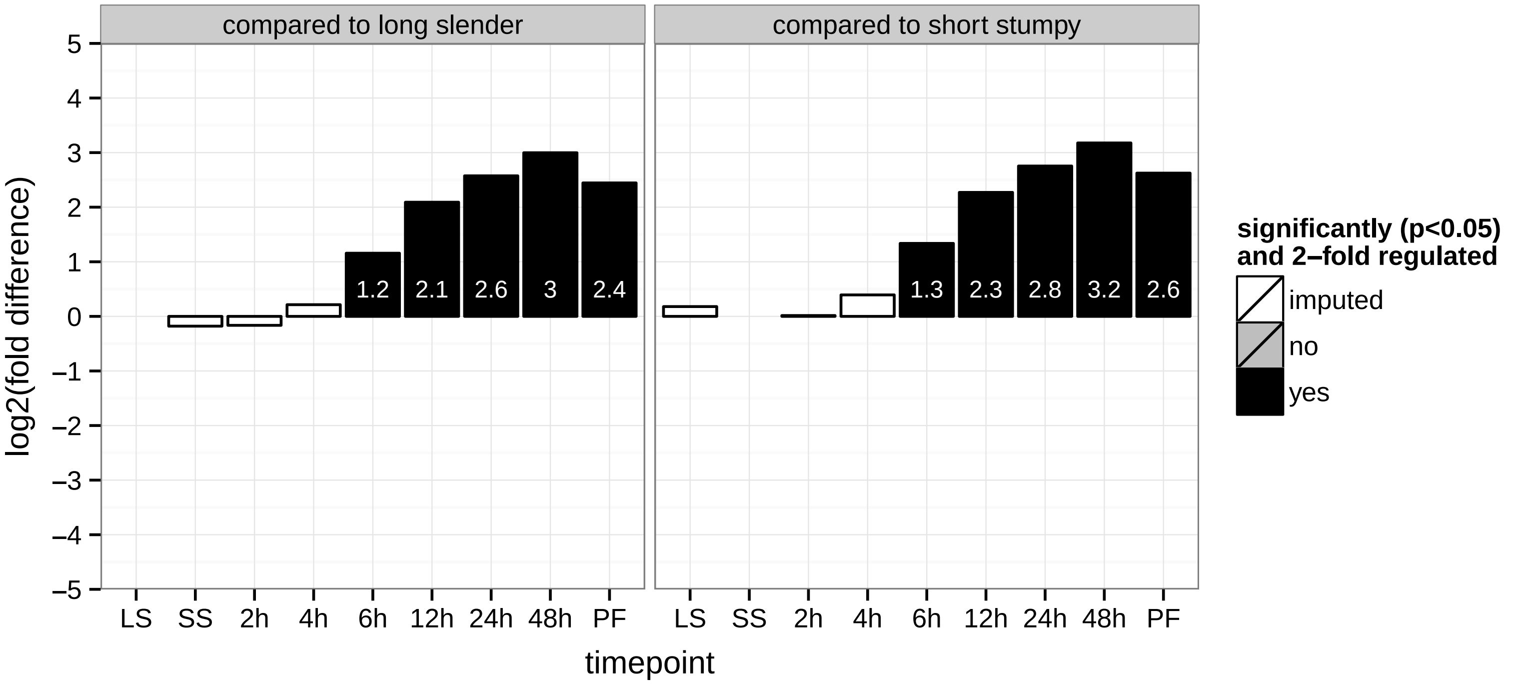
cystathione gamma lyase, putative
Tb927.9.12320
AGOF: null, cystathionine gamma–lyase activity, pyridoxal phosphate binding
AGOC: null
AGOP: null, sulfur amino acid metabolic process
PGOF: pyridoxal phosphate binding
PGOC: null
PGOP: cellular amino acid metabolic process

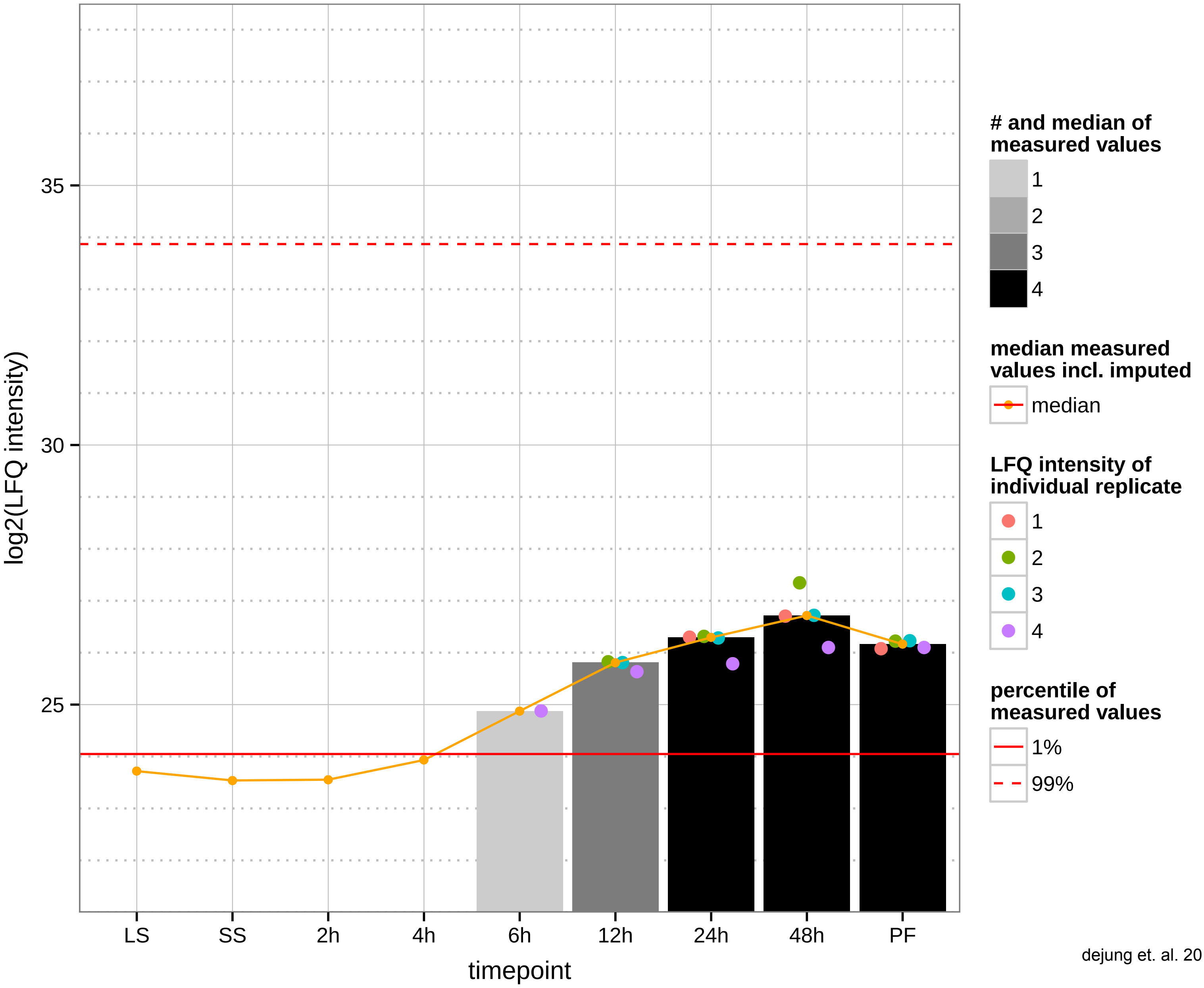




dejung et. al. 2015

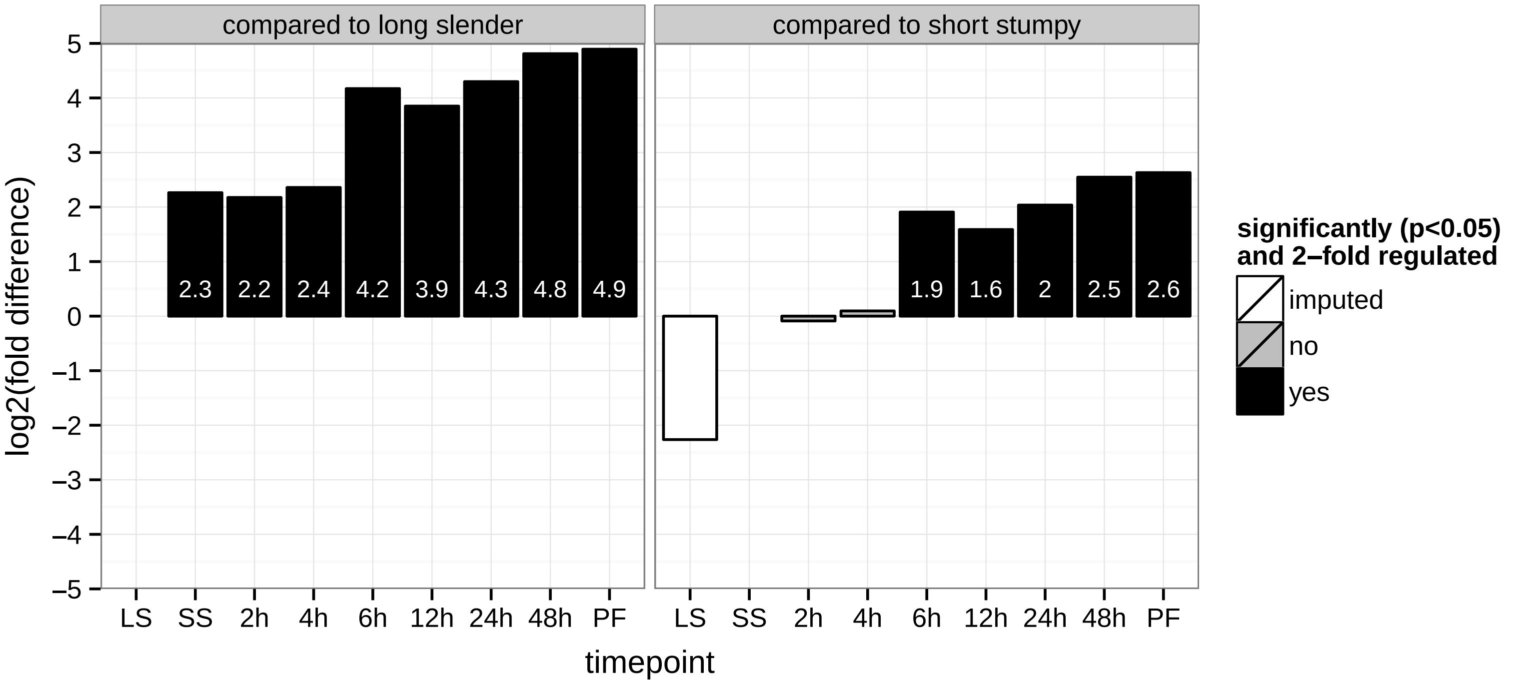
hypothetical protein, conserved
Tb927.9.13780
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

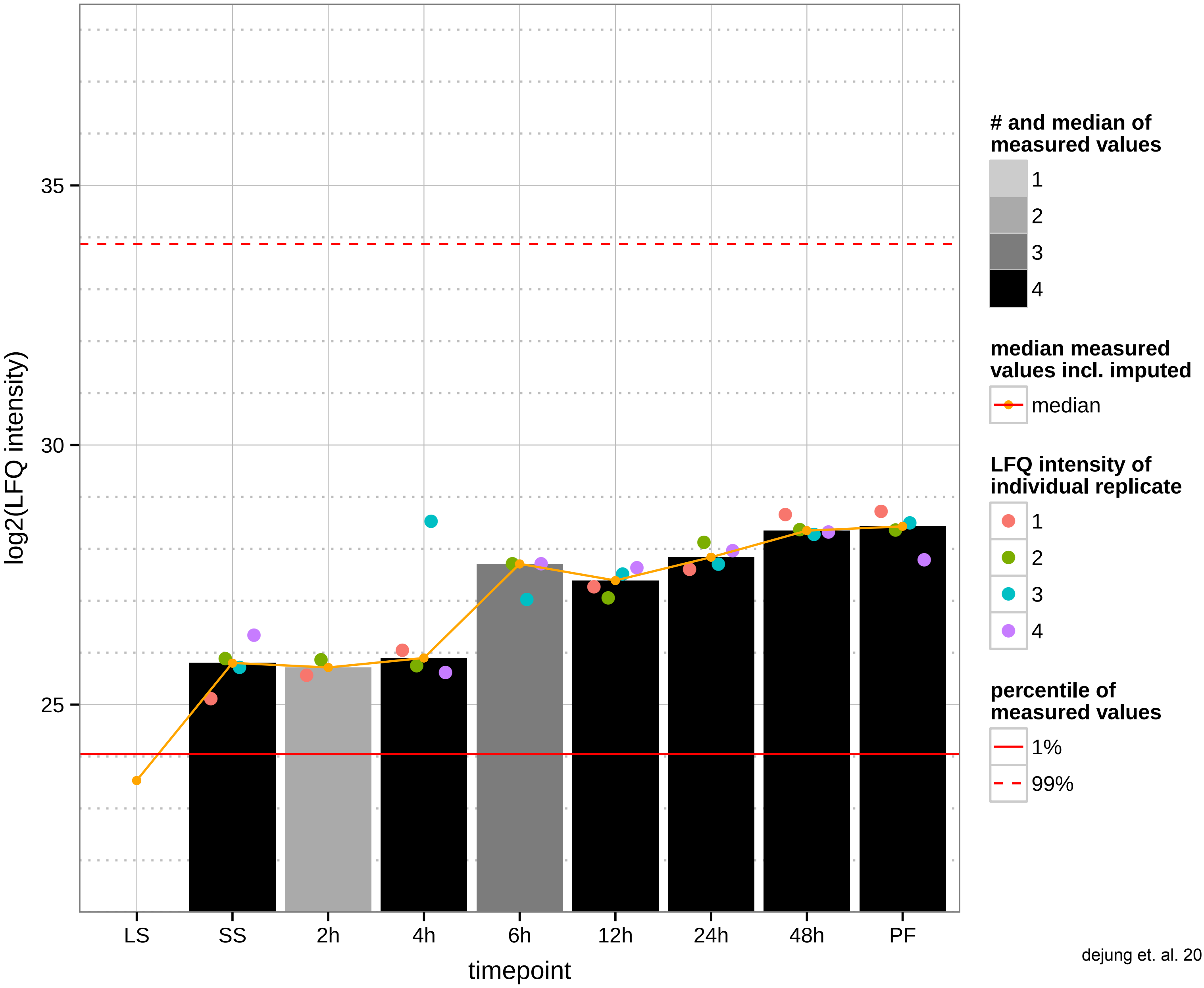




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.15290
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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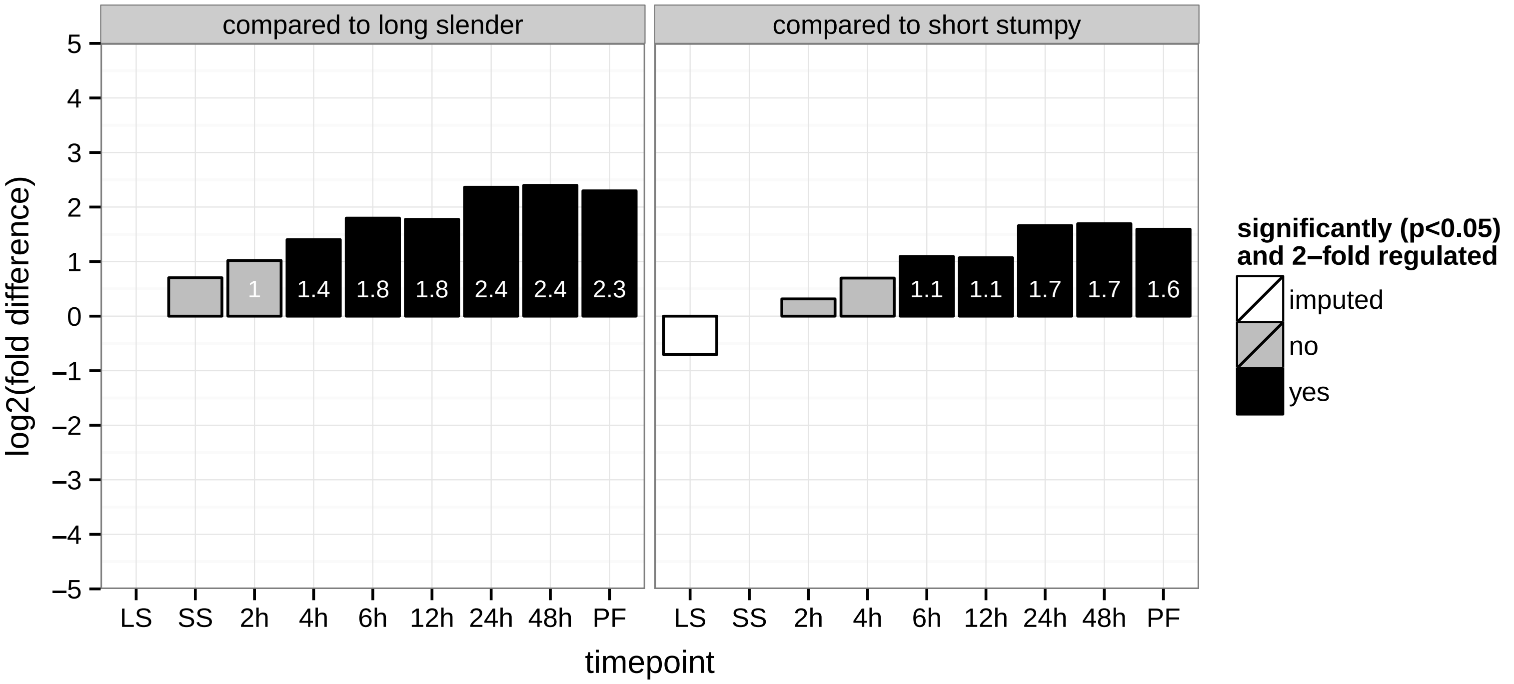
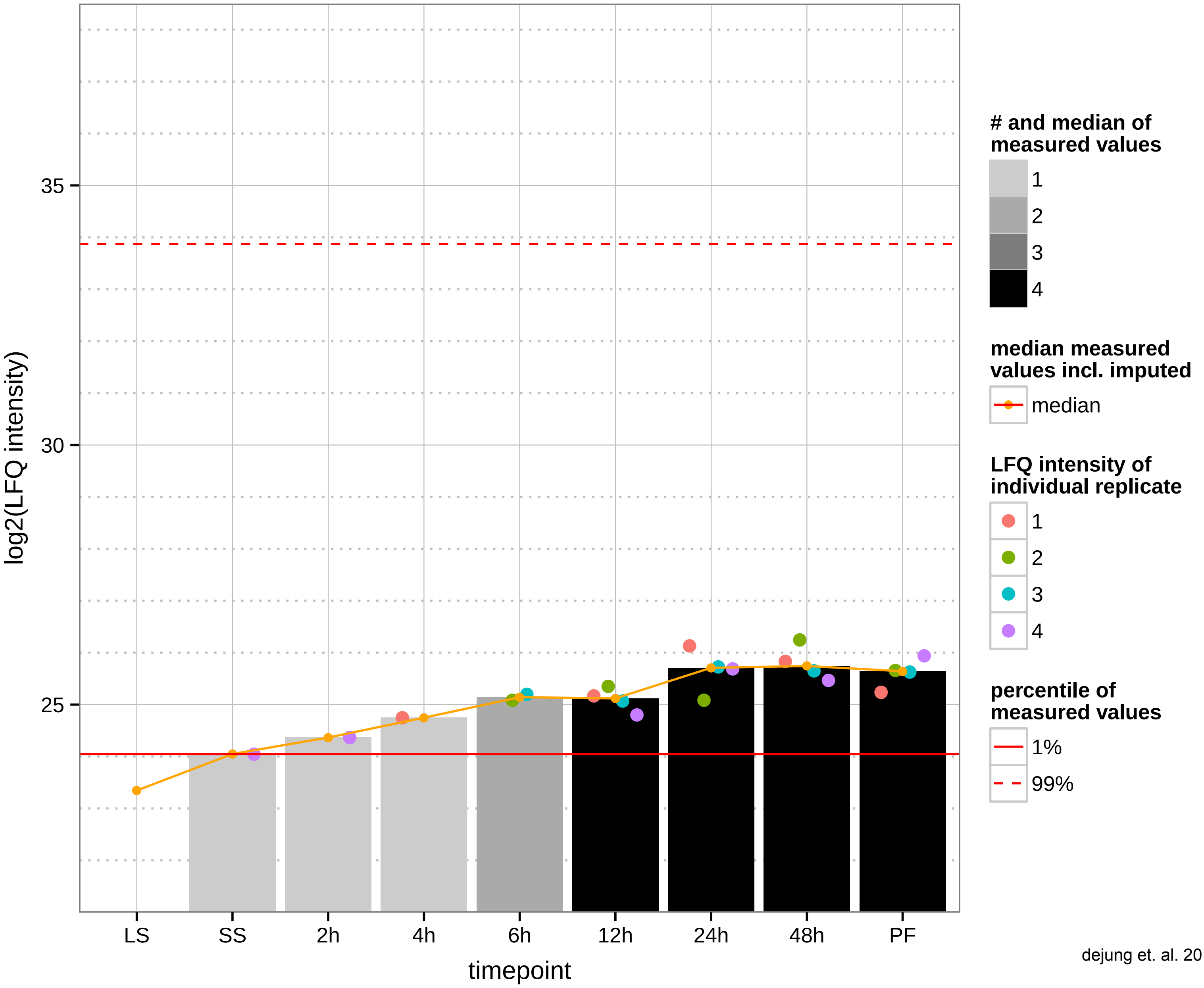
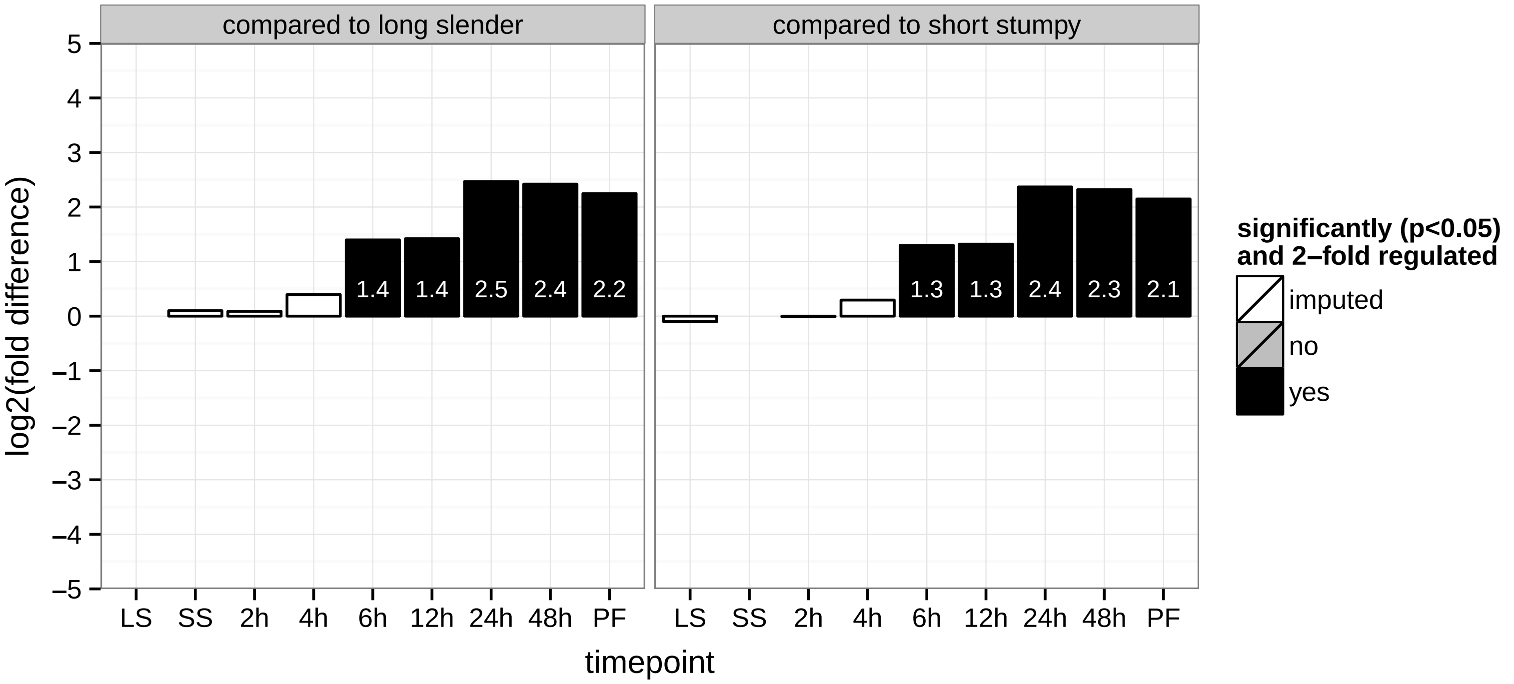
hypothetical protein, conserved
Tb927.9.2270
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

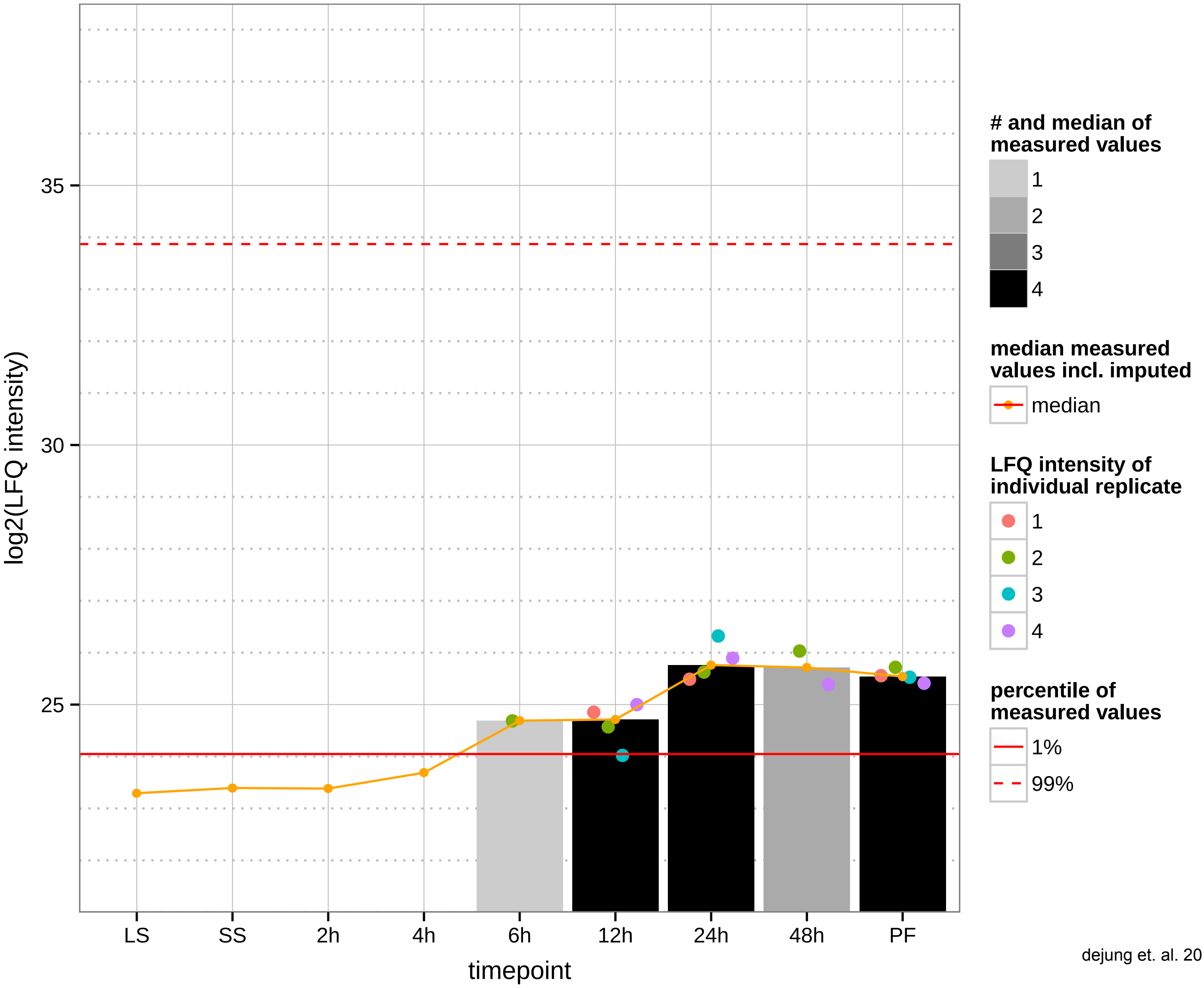




dejung et. al. 2015

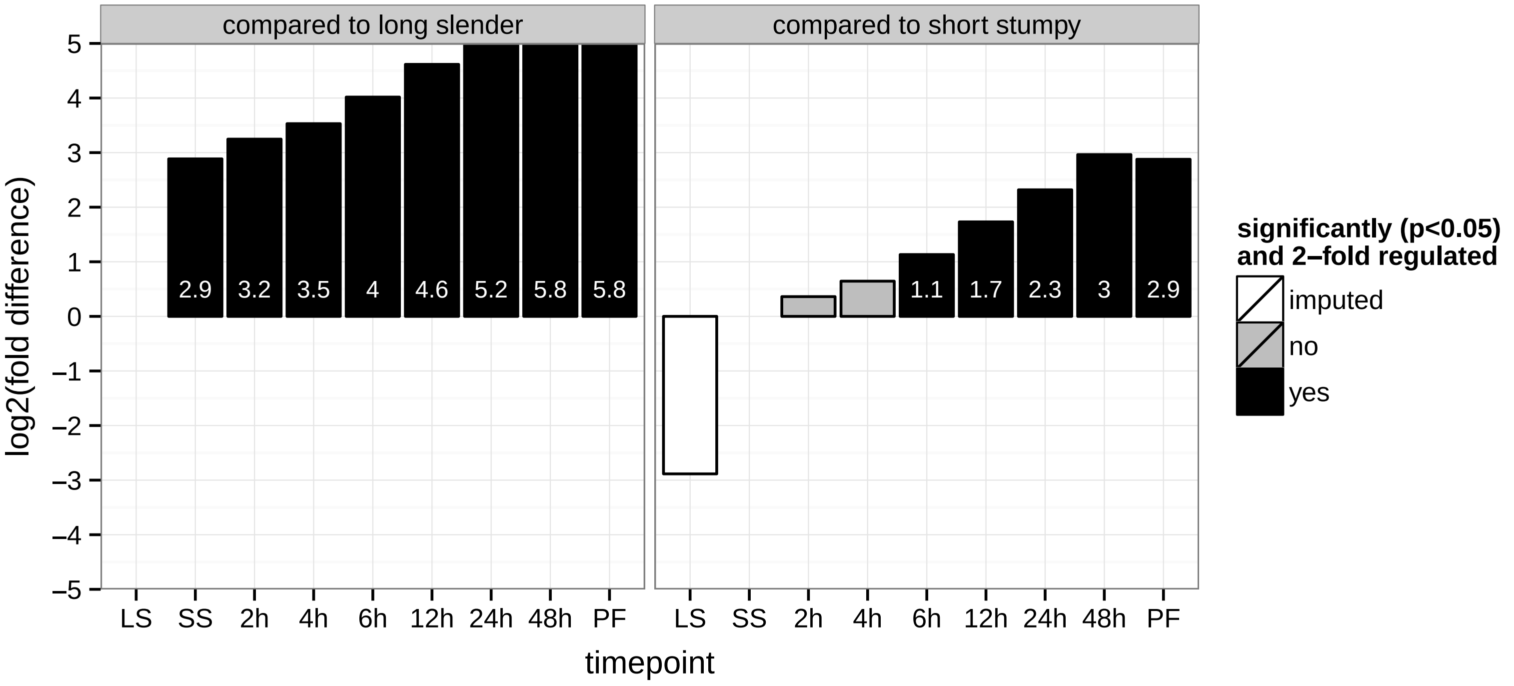
protein kinase, putative
Tb927.9.3120
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: integral to membrane
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

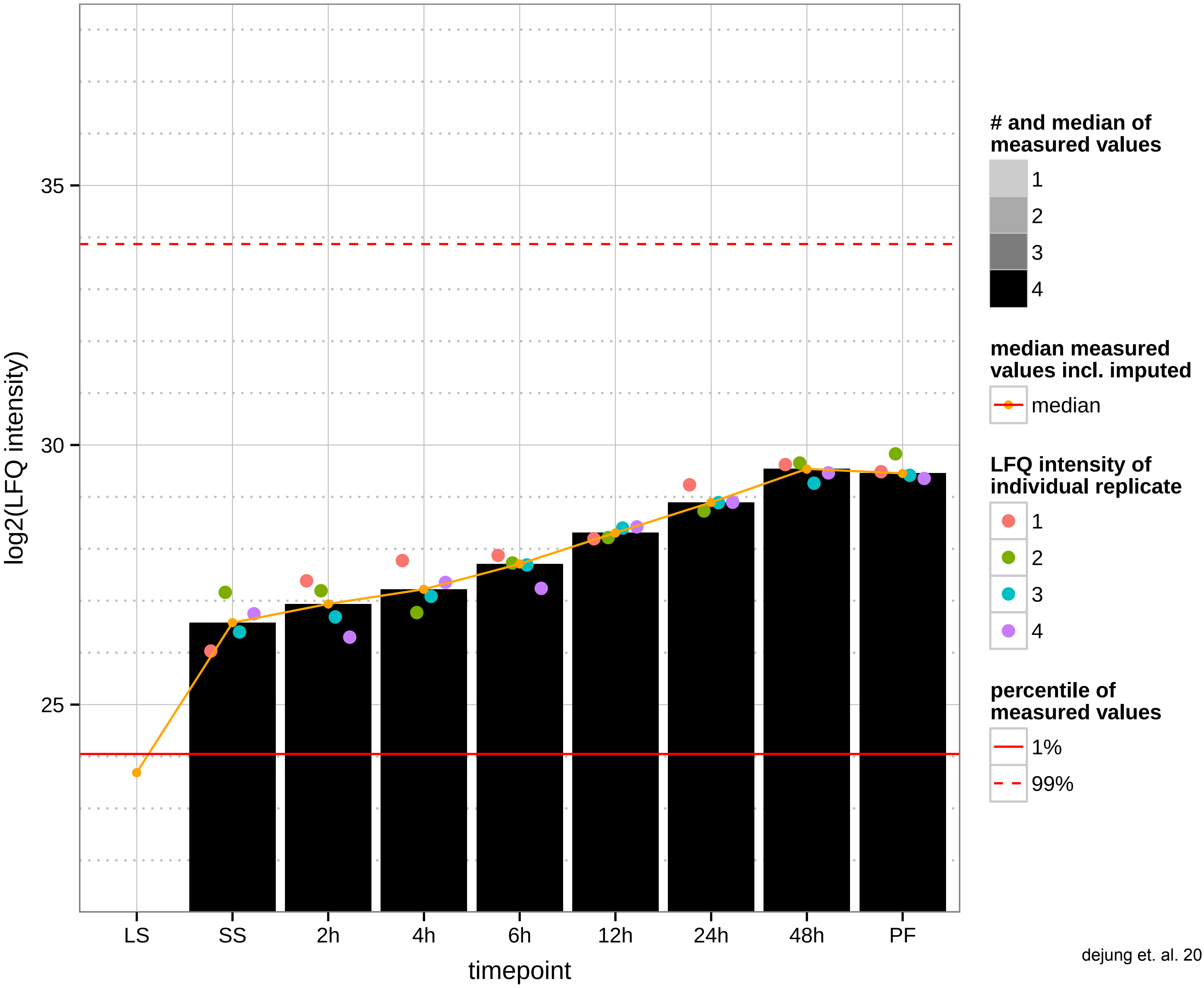




dejung et. al. 2015

tricarboxylate carrier, putative
Tb927.9.4310
AGOF: cation transmembrane transporter activity
AGOC: mitochondrial inner membrane
AGOP: cation transport
PGOF: cation transmembrane transporter activity
PGOC: membrane
PGOP: cation transport, transmembrane transport





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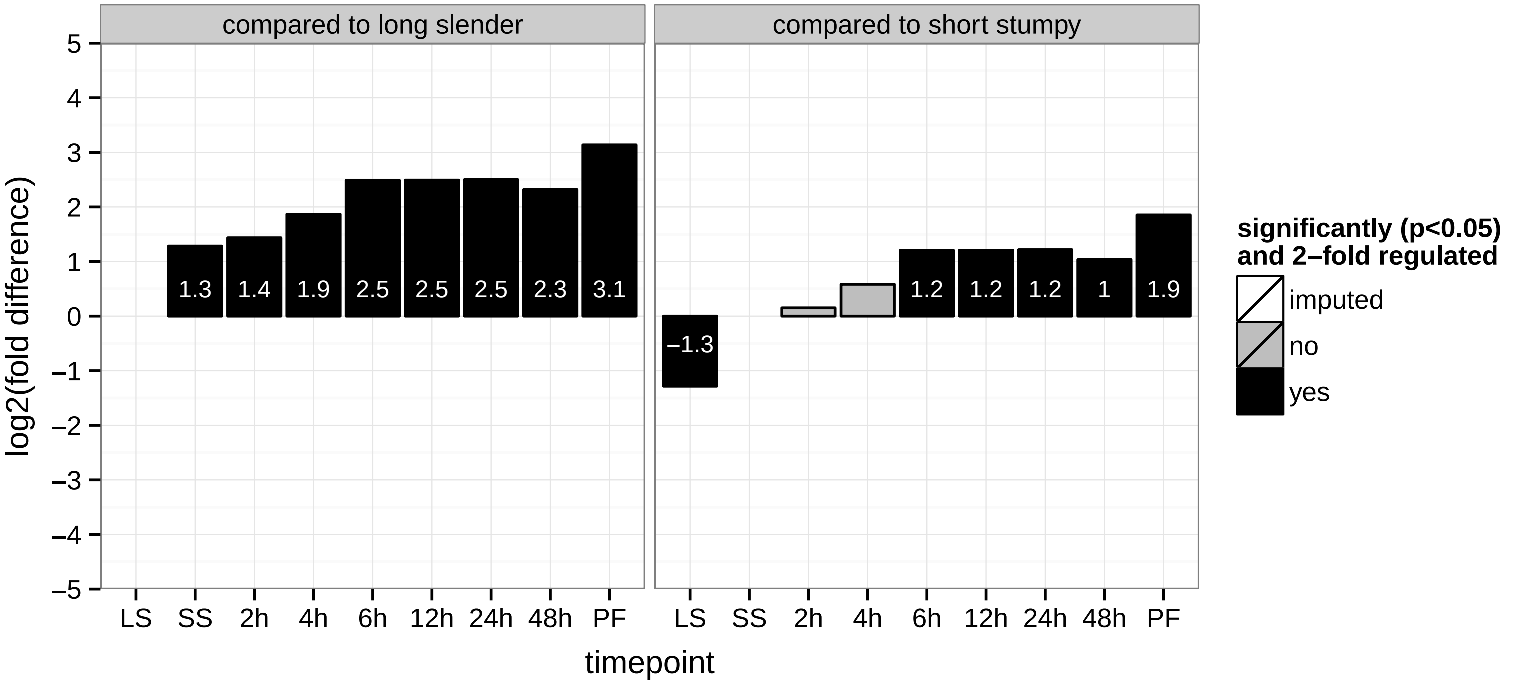
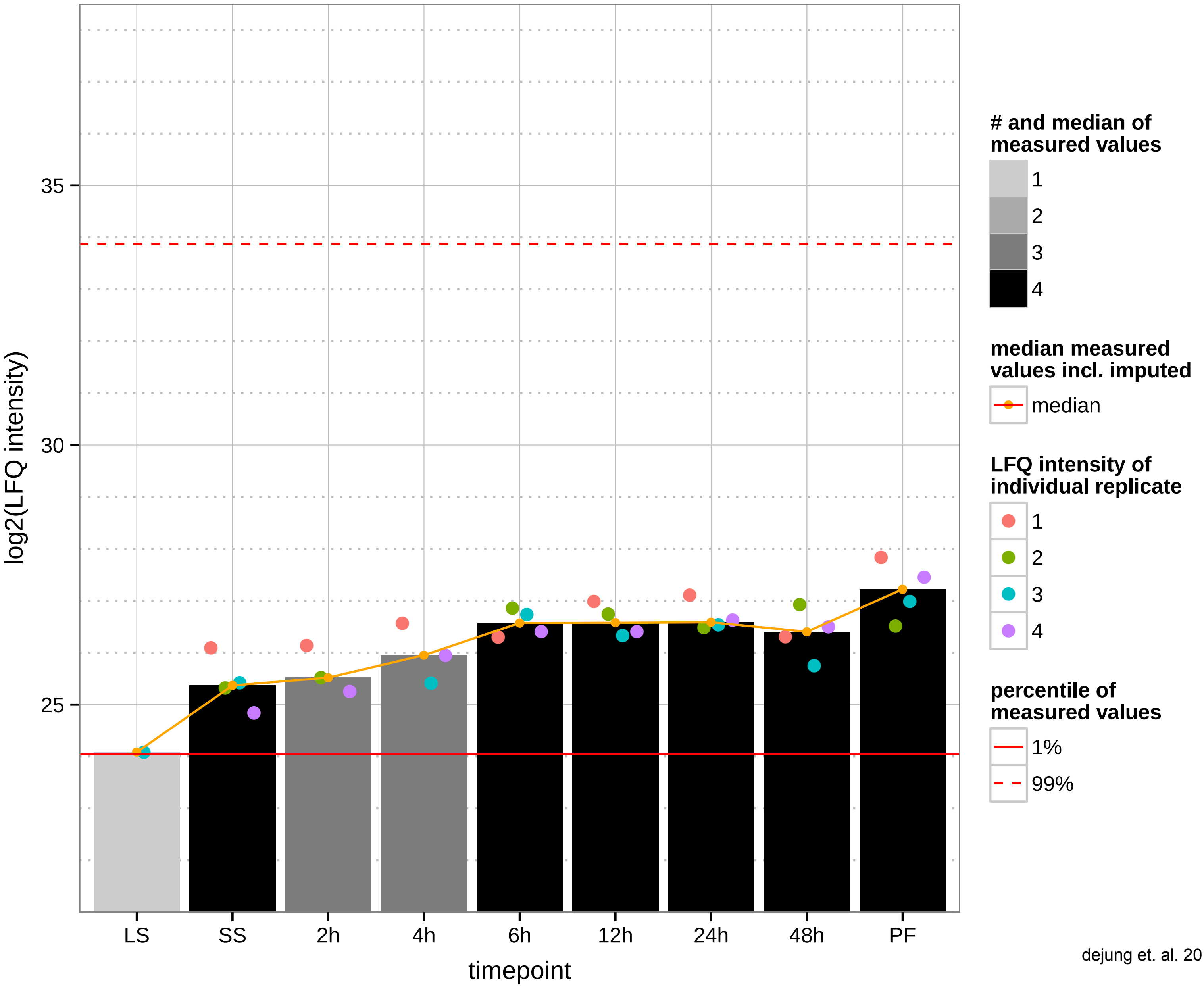
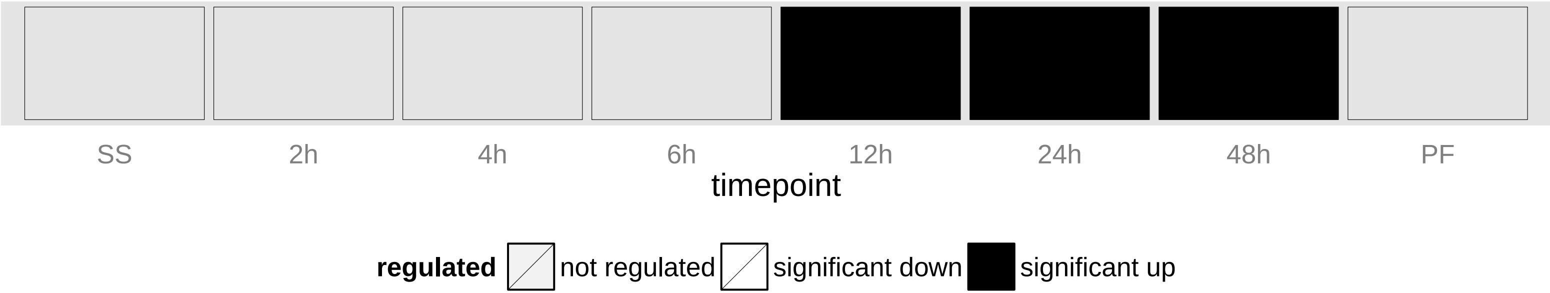
exosome complex exonuclease RRP40 (RRP40)
Tb927.9.7070
AGOF: 3'−5'−exoribonuclease activity
AGOC: null
AGOP: rRNA processing
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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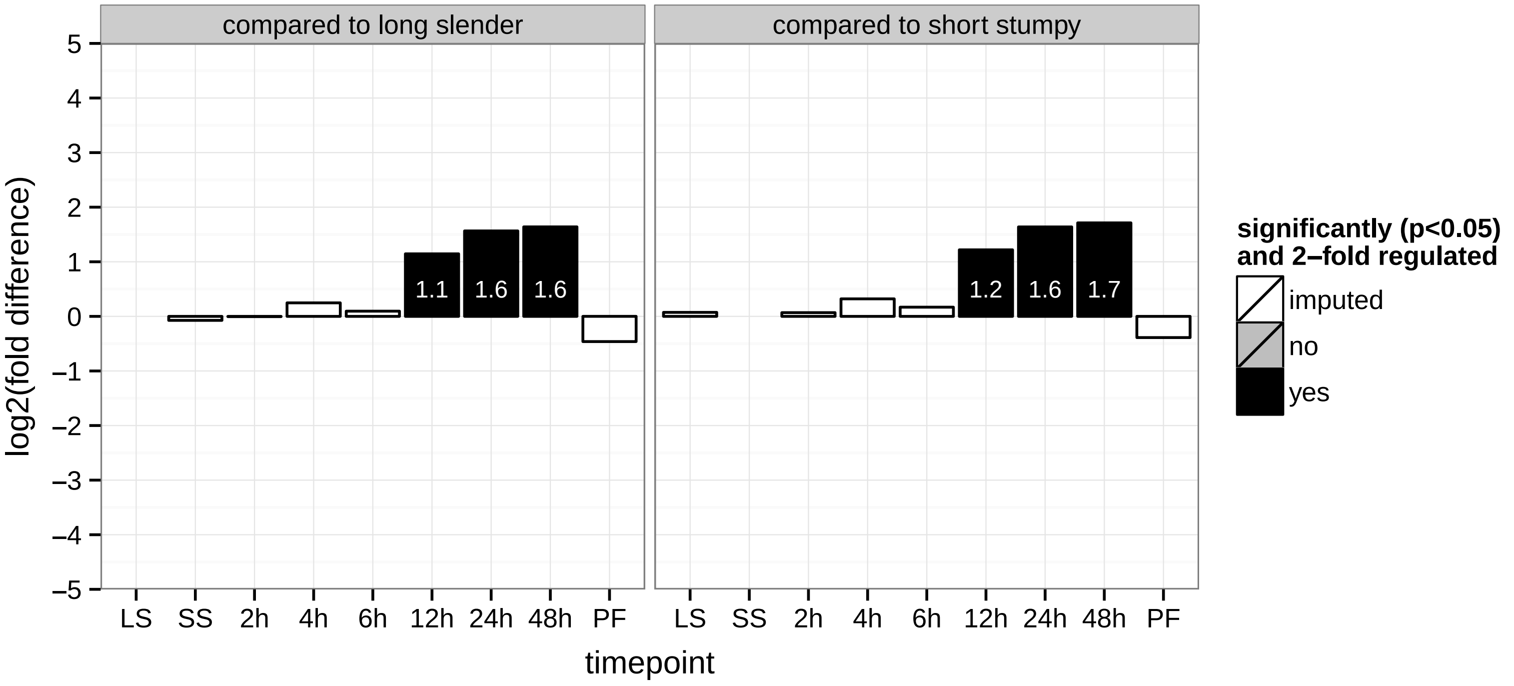
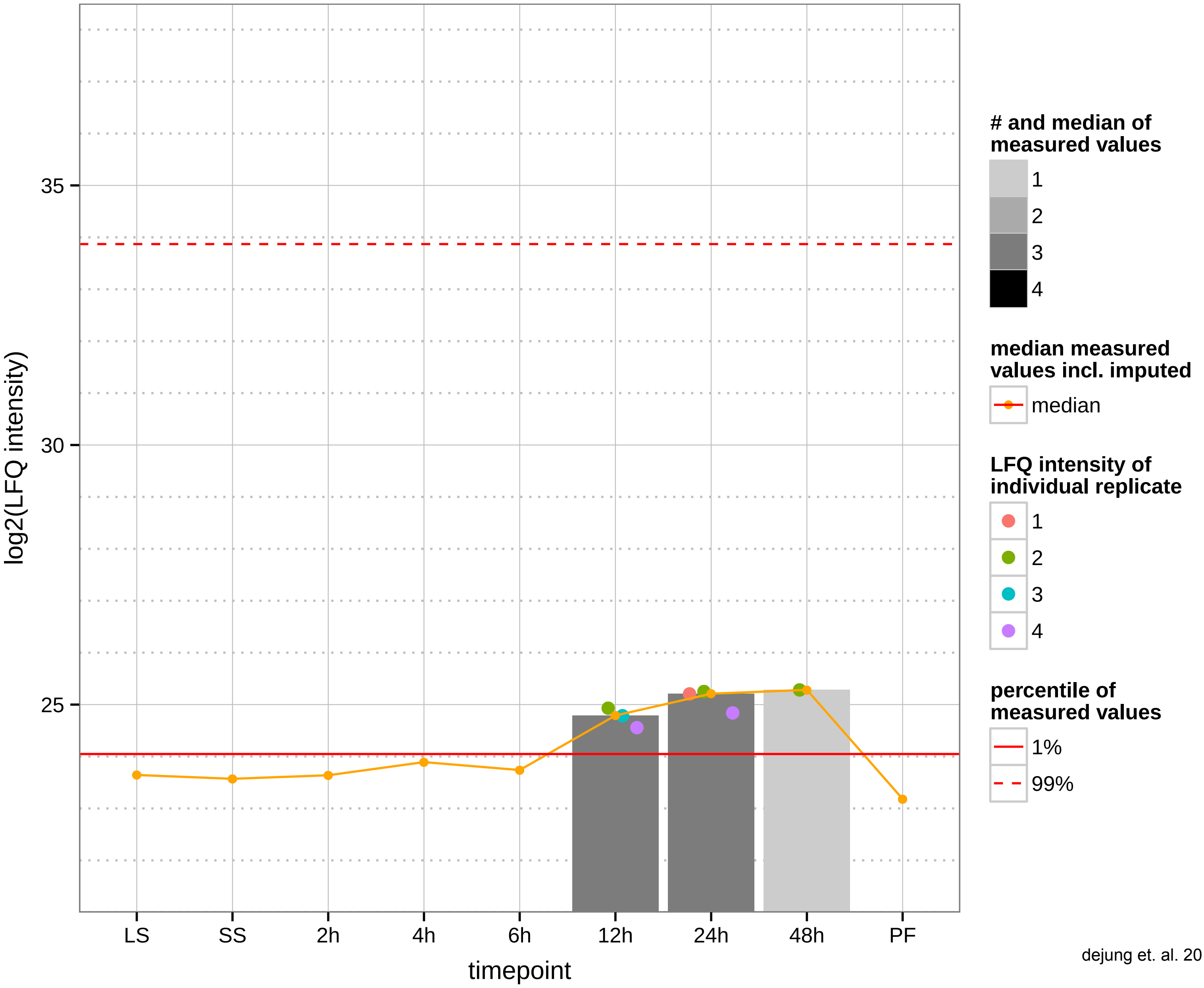
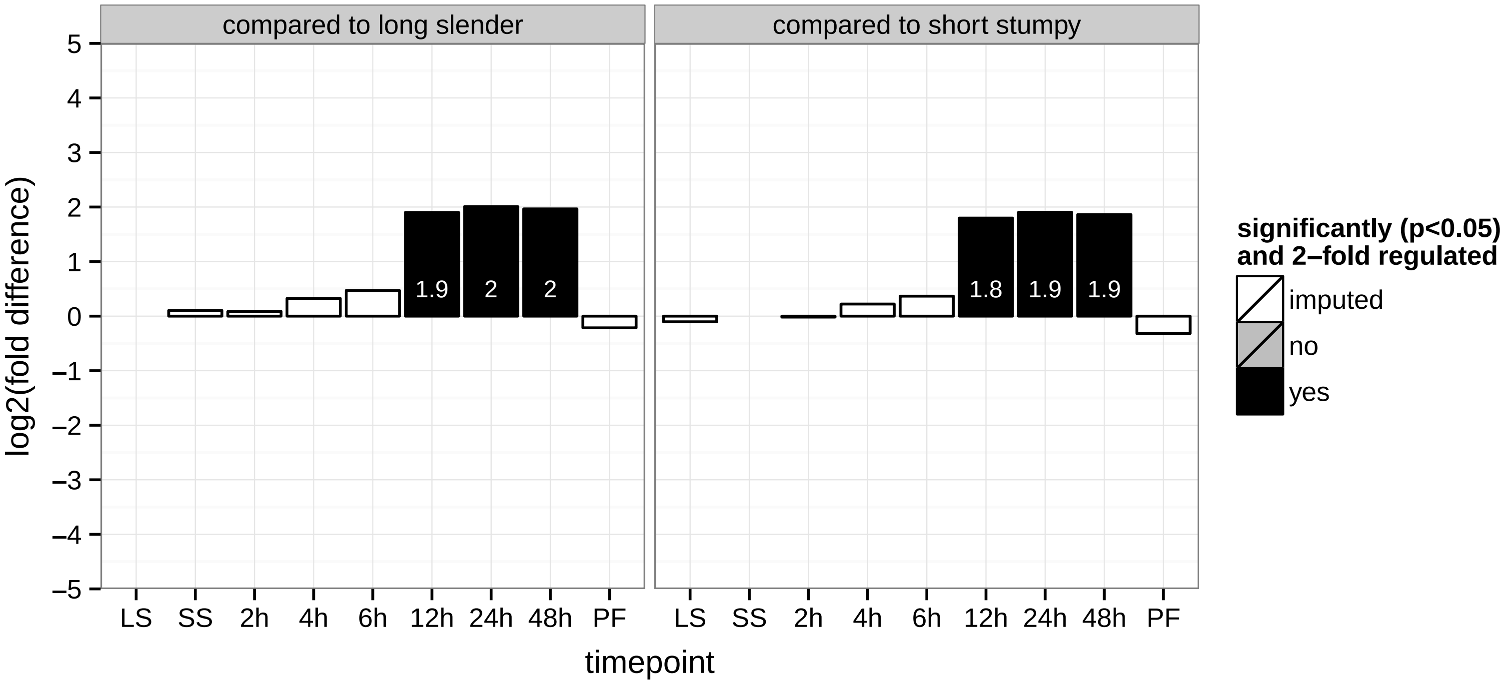
DNA–directed RNA polymerase II, subunit 9, putative, DNA–direcetd RNA polymerase II, putative (RPB9)
Tb927.11.7280;Tb11.v5.0255
AGOF: null, DNA binding, DNA–directed RNA polymerase activity
AGOC: null, nucleus
AGOP: null, transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA–dependent

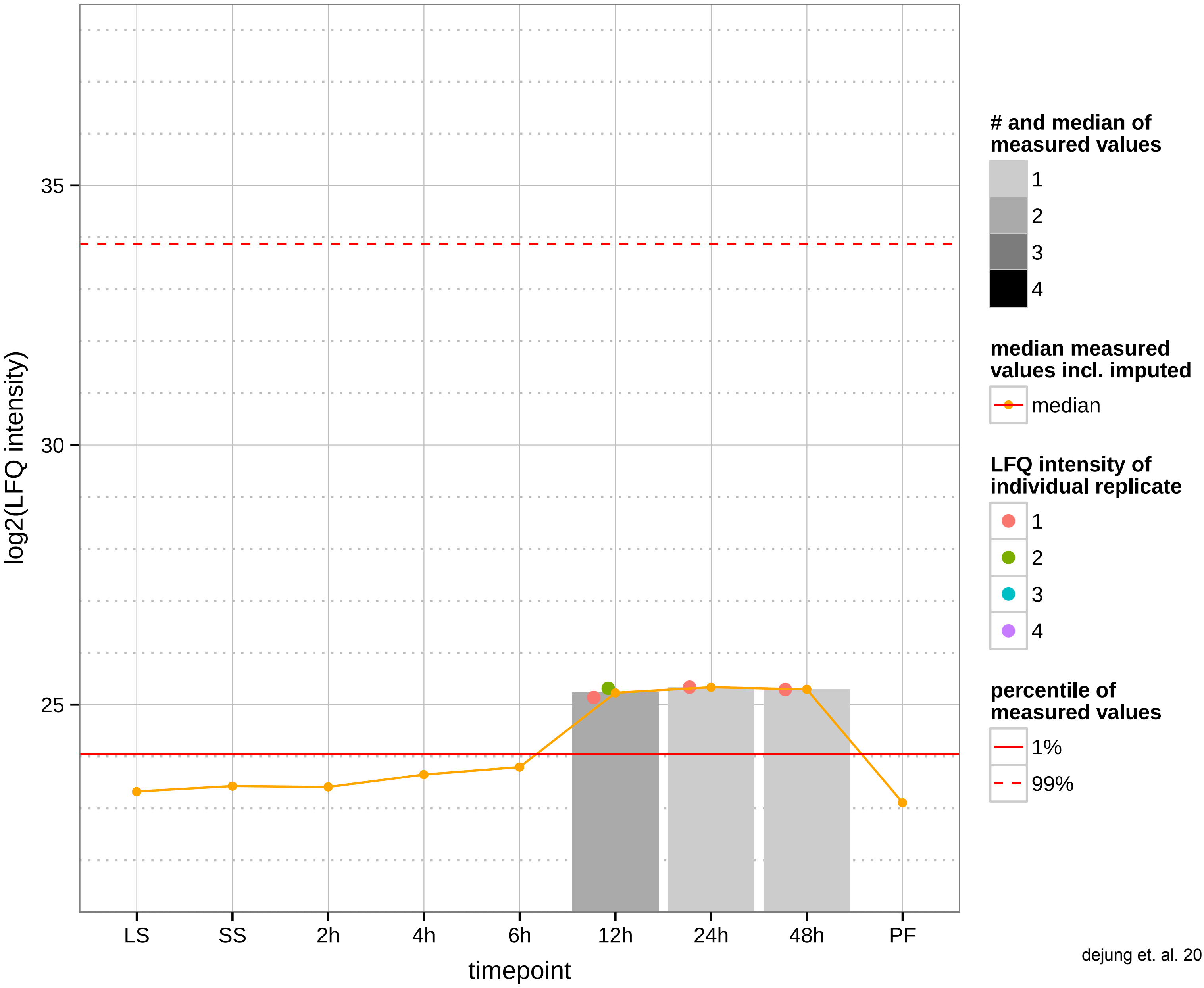




dejung et. al. 2015

conserved protein, unknown function
Tb927.1.1750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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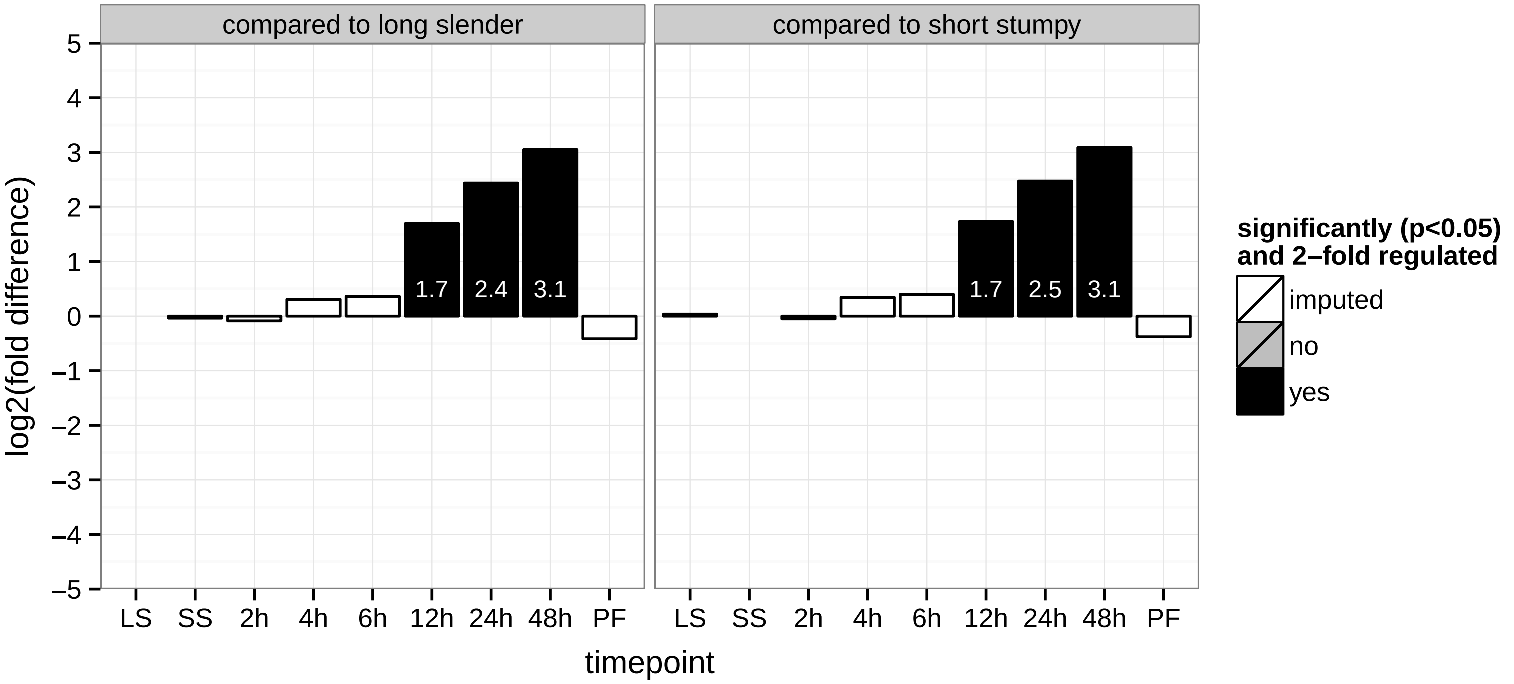
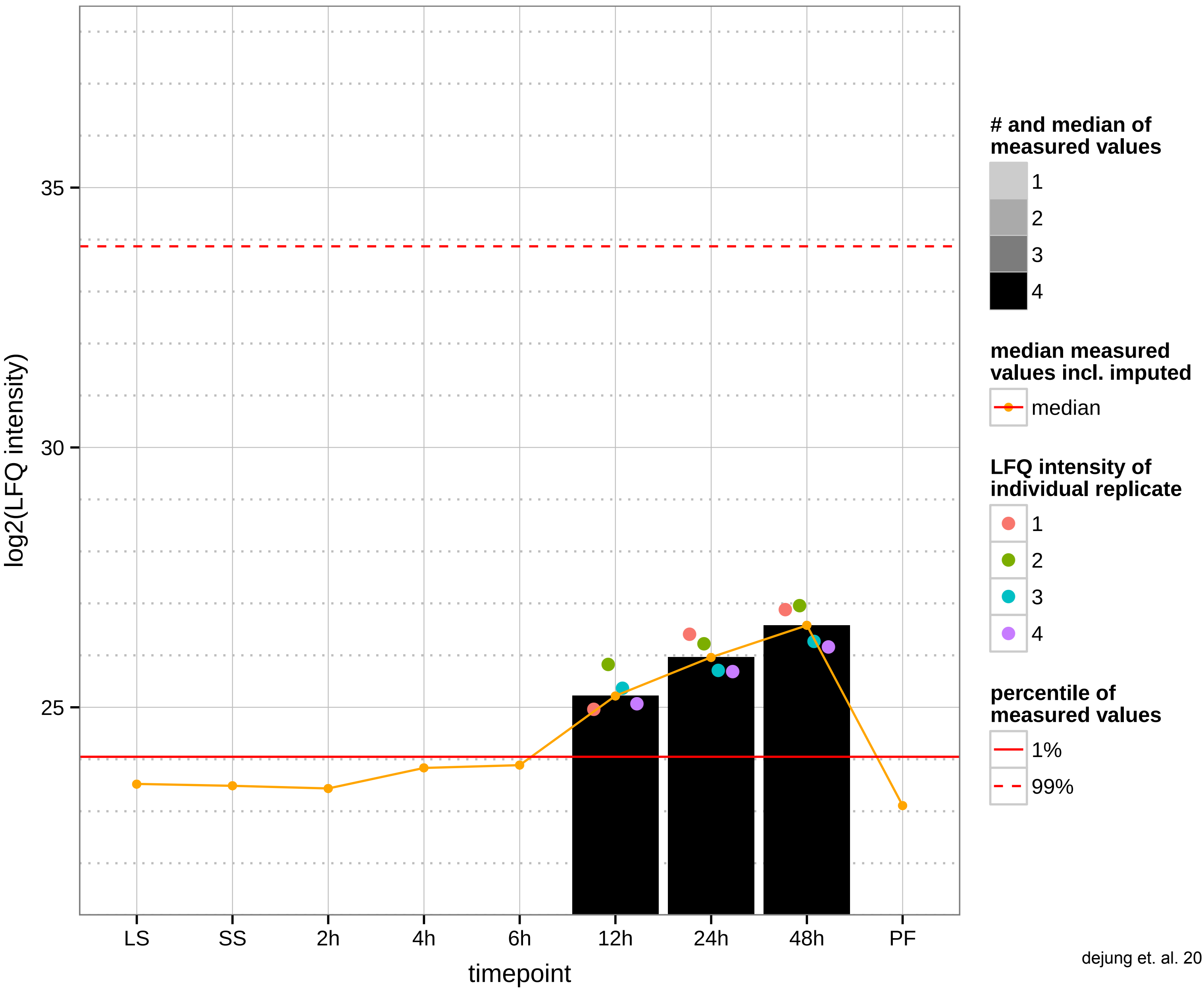
hypothetical protein, conserved
Tb927.1.2730
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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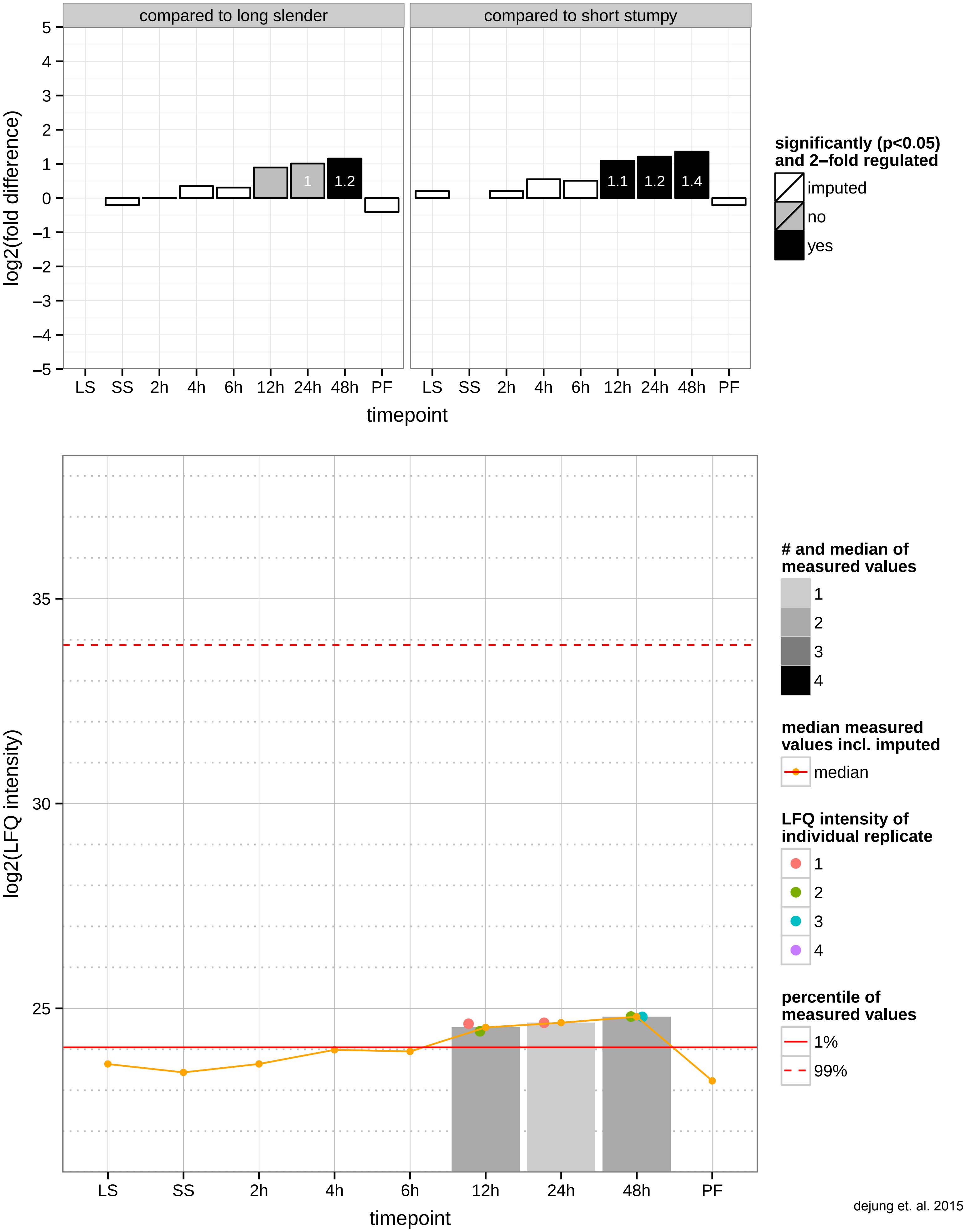
hypothetical protein, conserved
Tb927.1.2990
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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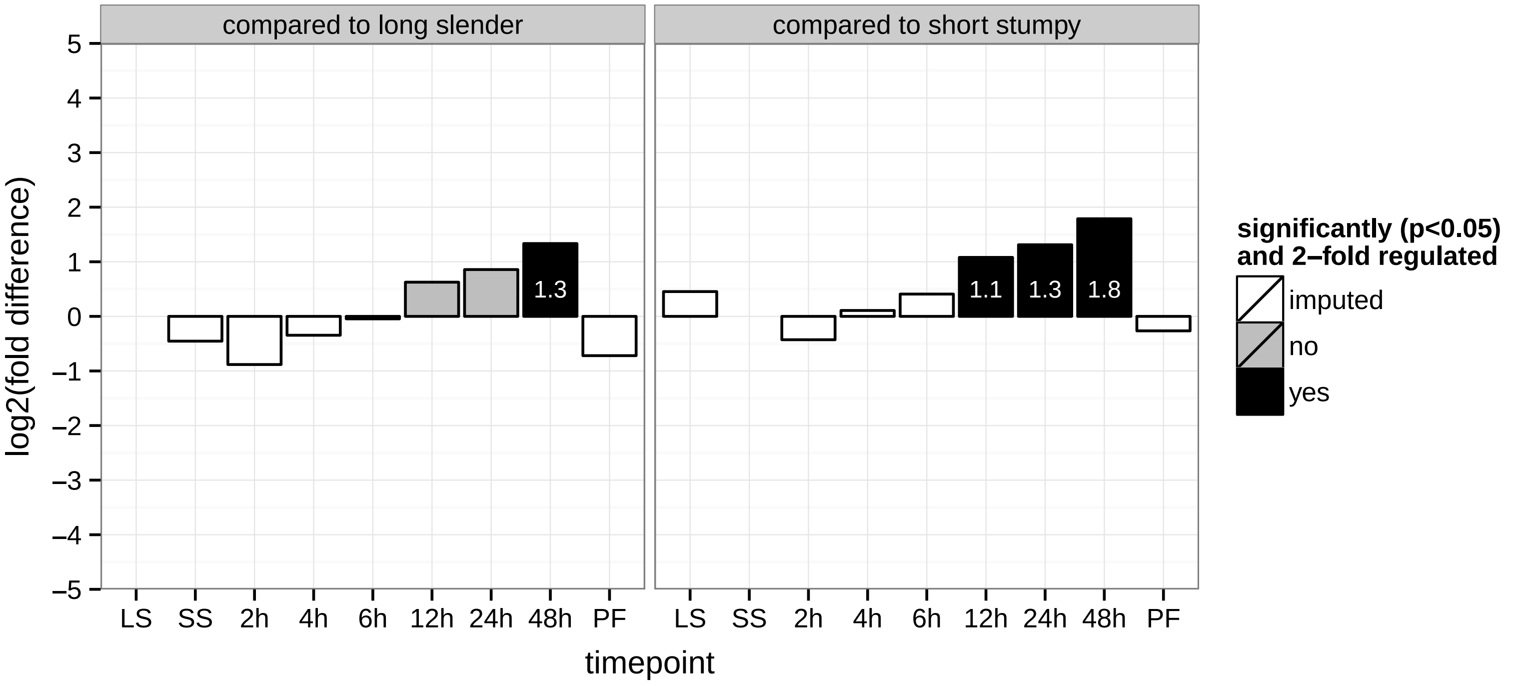
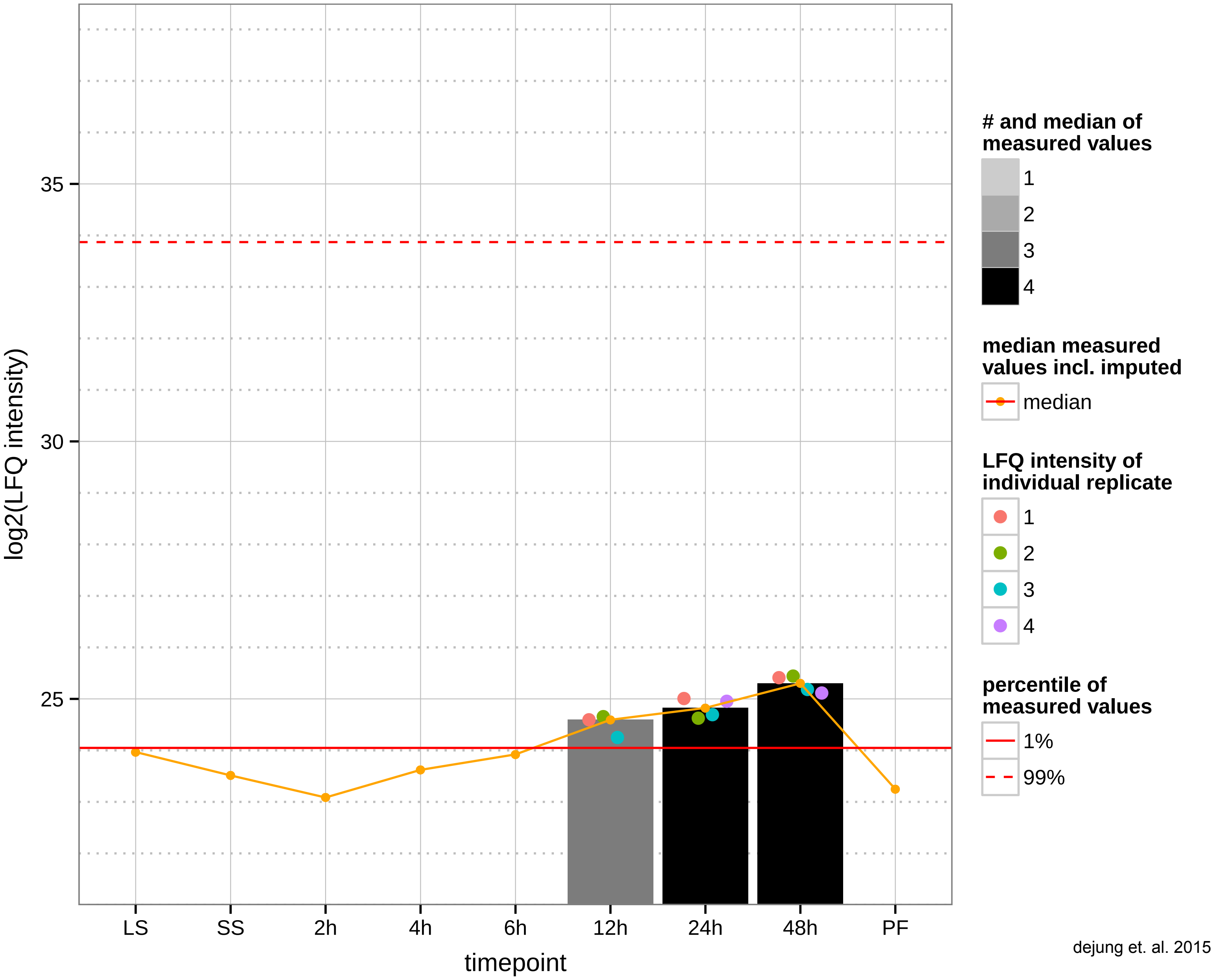
hypothetical protein, conserved
Tb927.10.1930
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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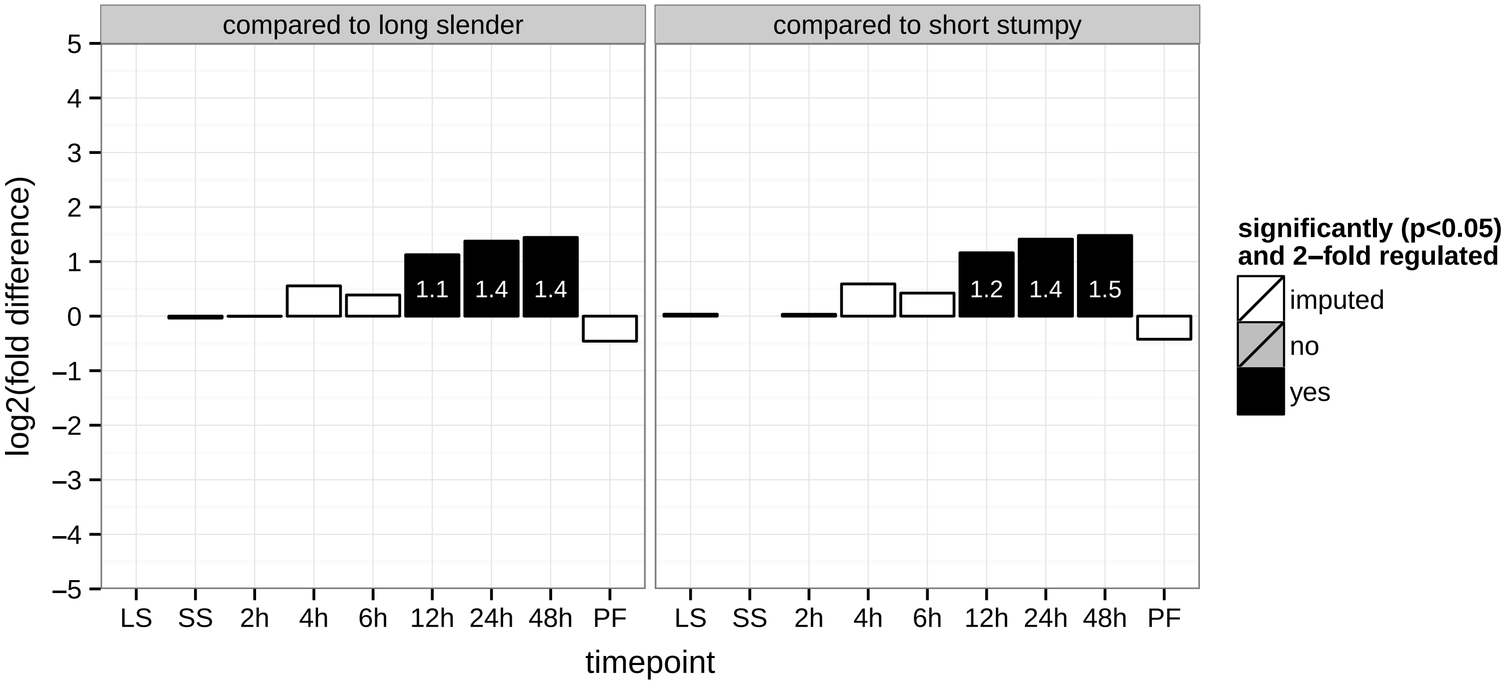
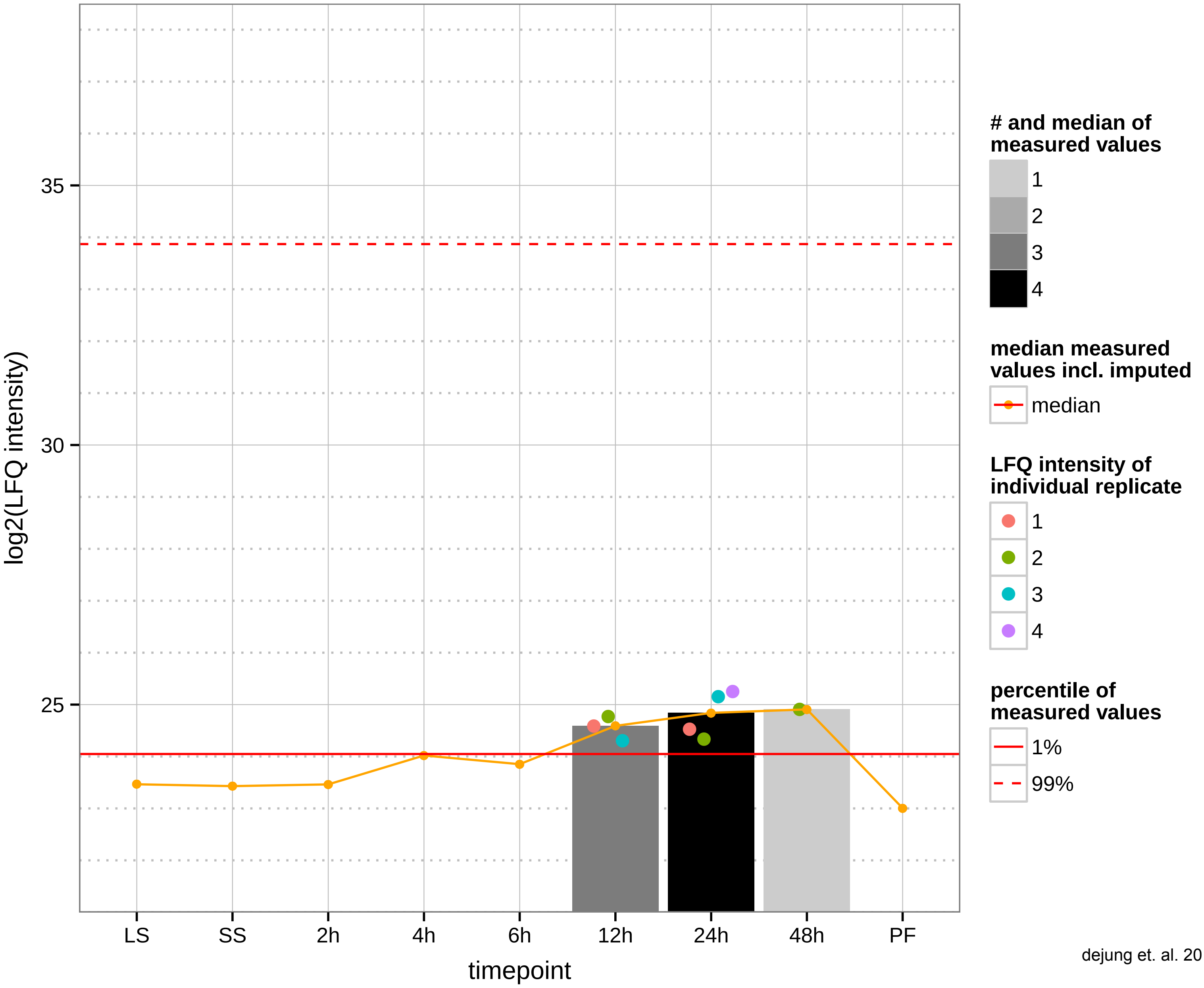
actin–like protein, putative
Tb927.10.2000
AGOF: structural constituent of cytoskeleton
AGOC: mitochondrion
AGOP: cytoskeleton organization
PGOF: null
PGOC: null
PGOP: null





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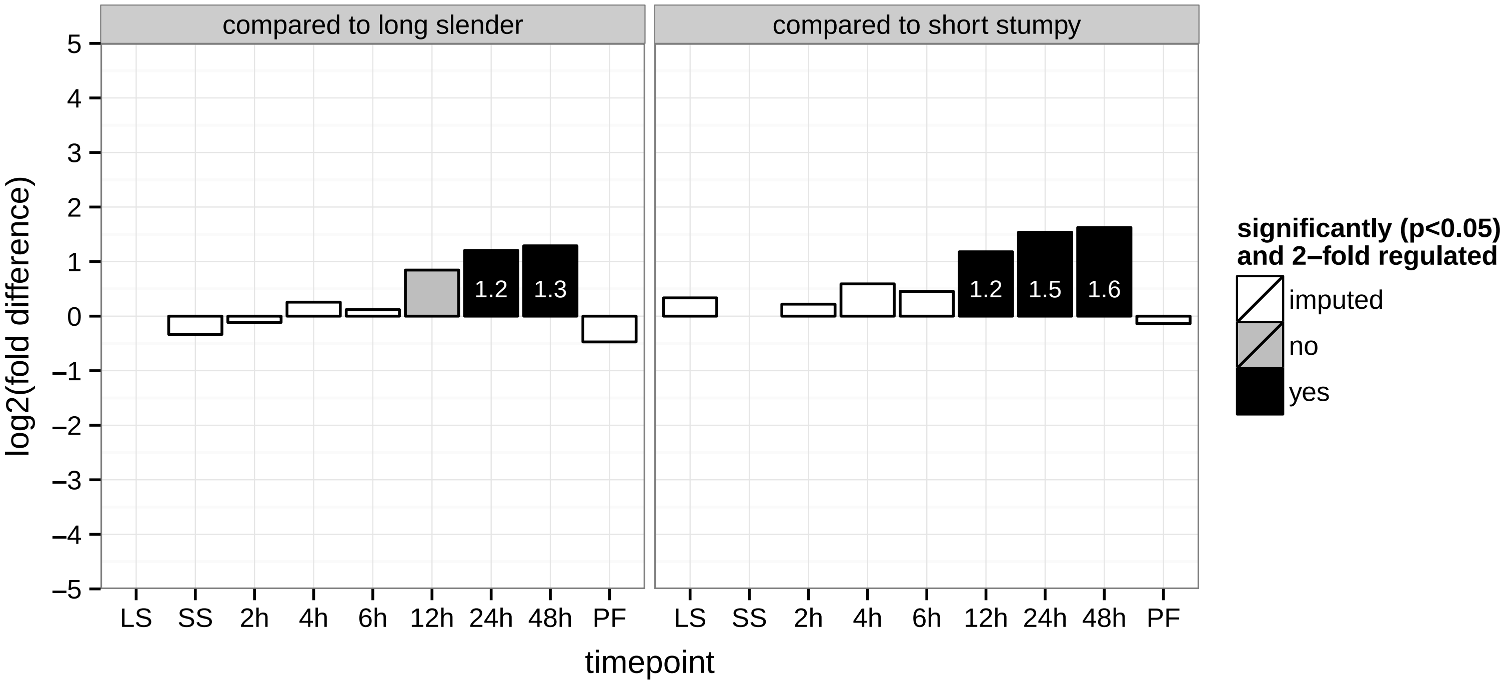
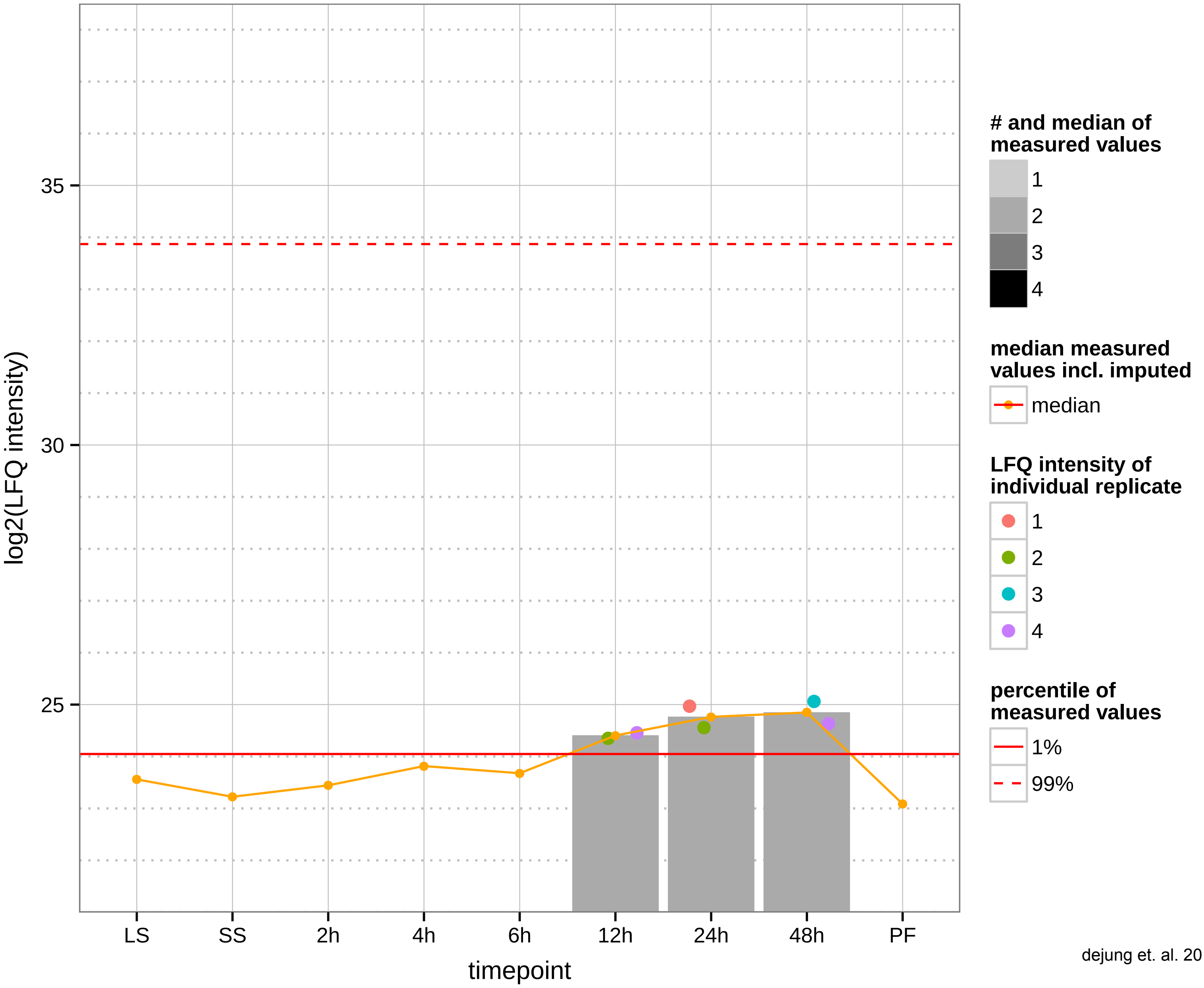
ubiquitin–conjugating enzyme variant Kua homologue, putative
Tb927.10.2250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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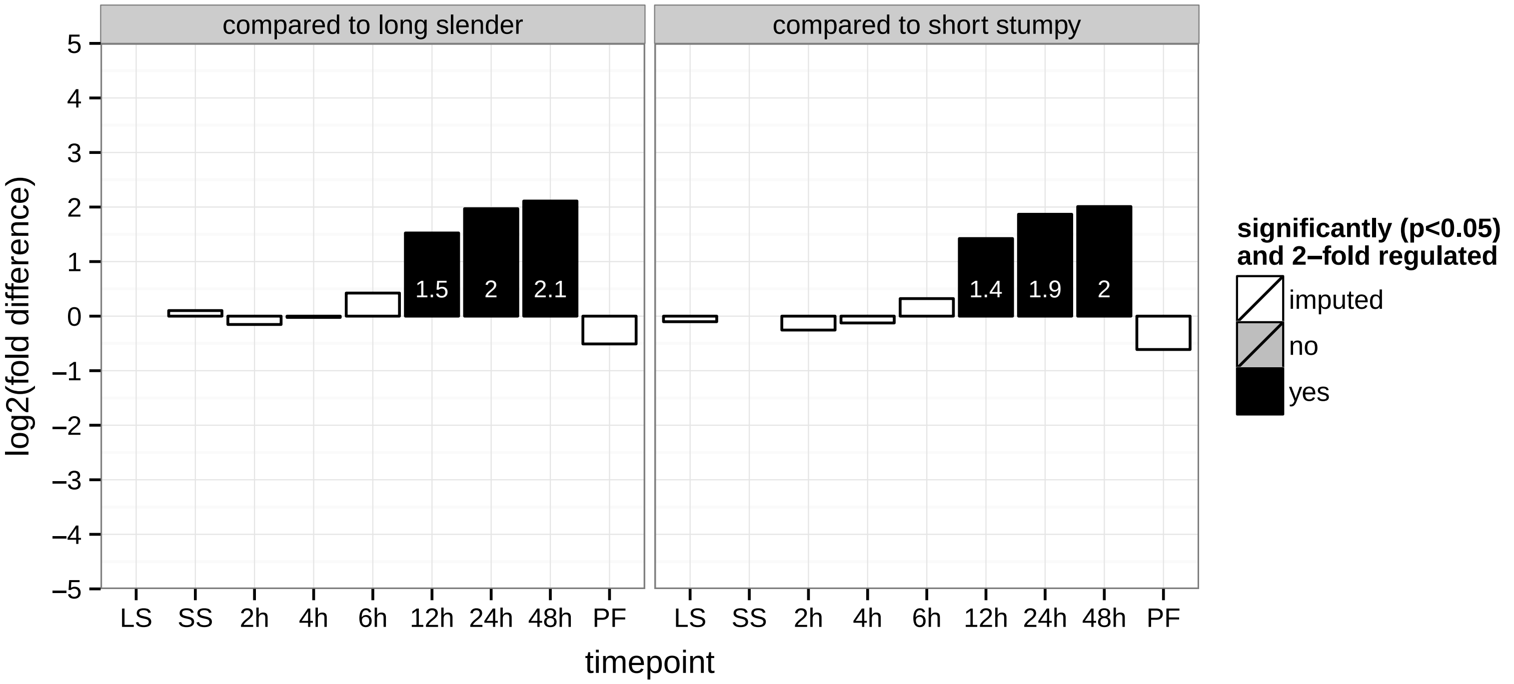
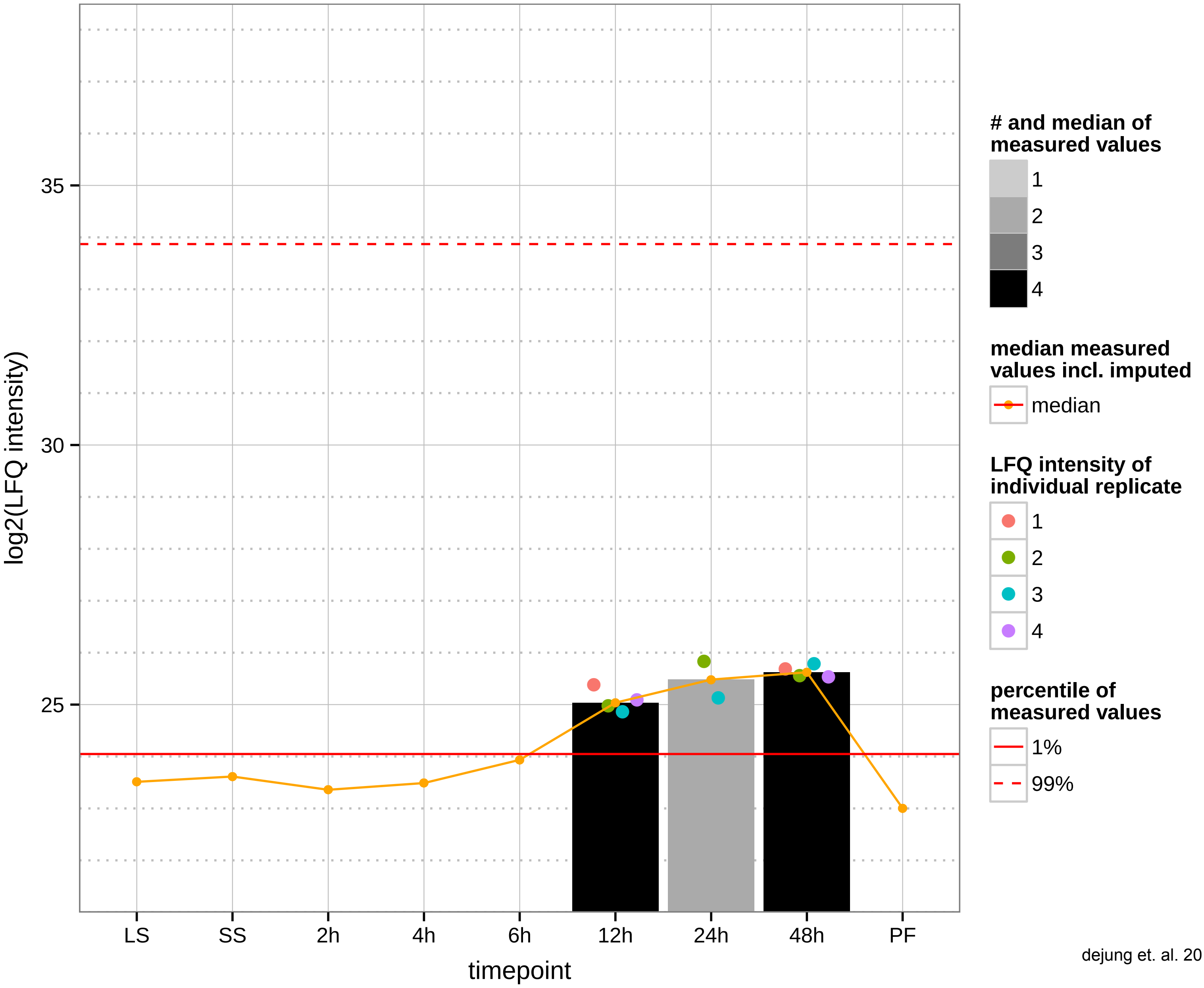
hypothetical protein, conserved
Tb927.10.2260
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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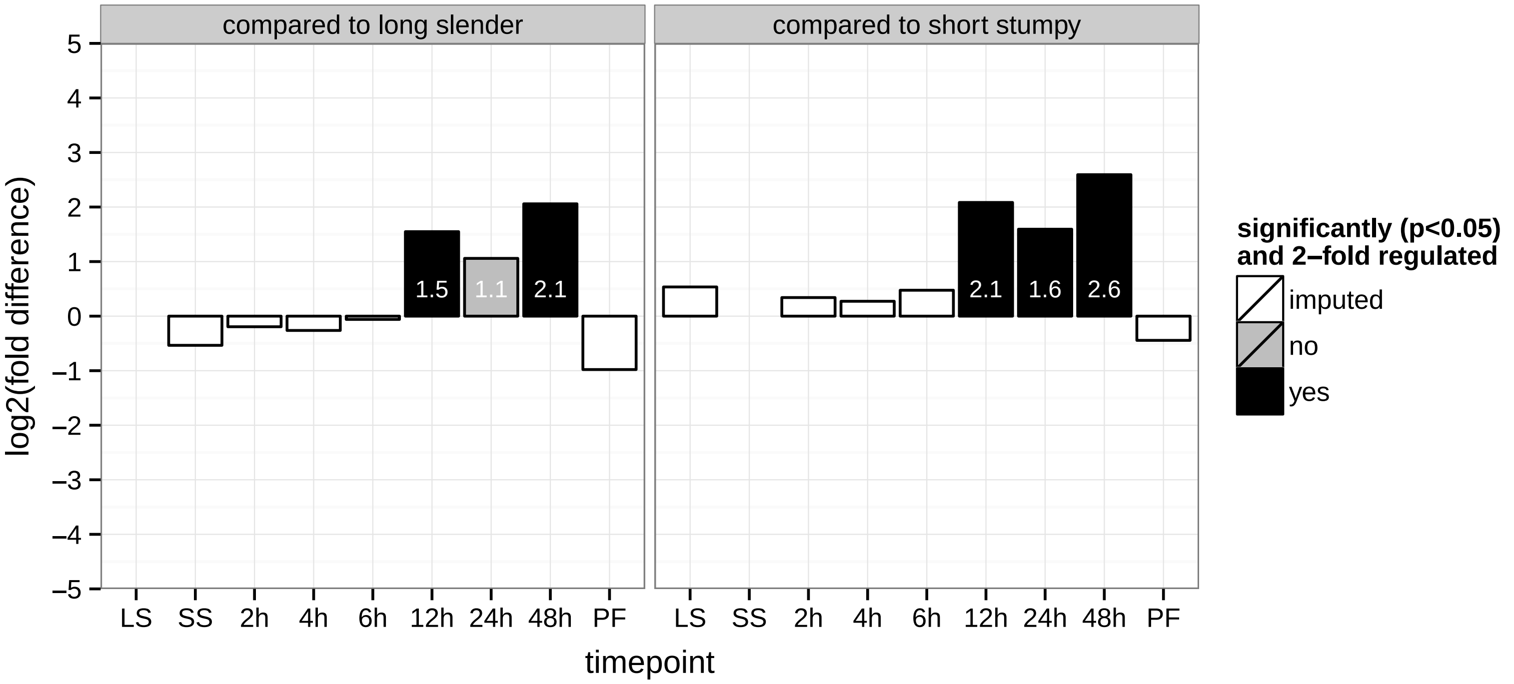
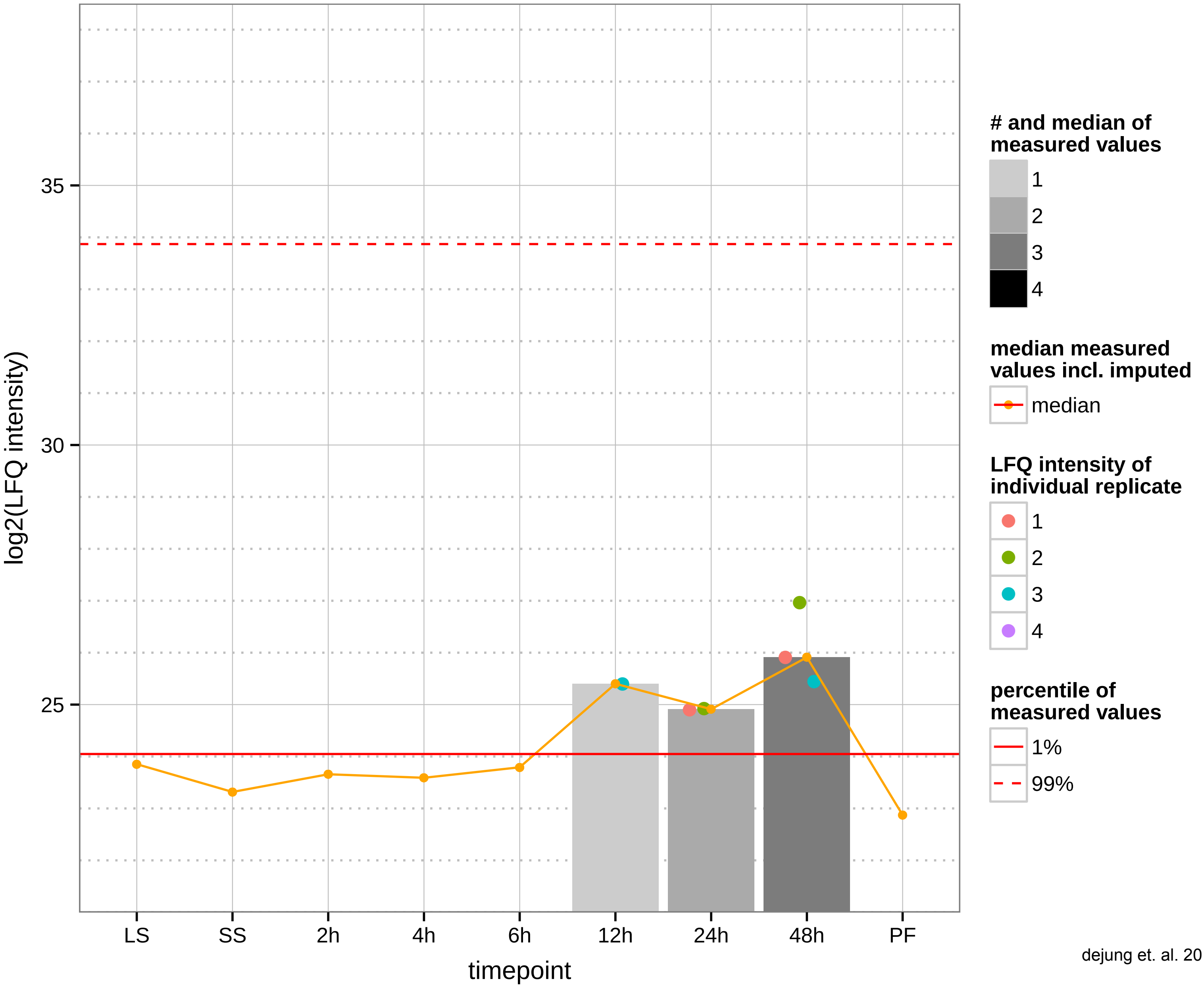
hypothetical protein, conserved
Tb927.10.2970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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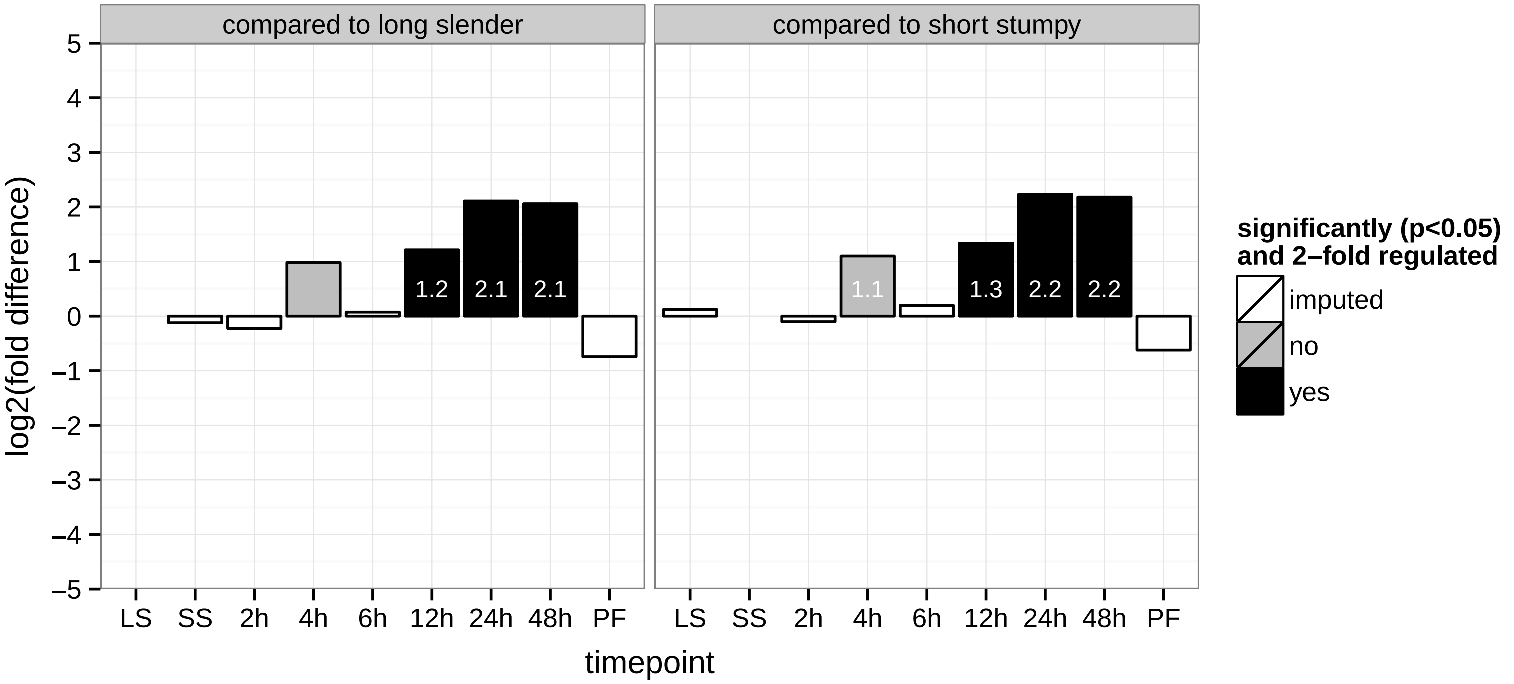
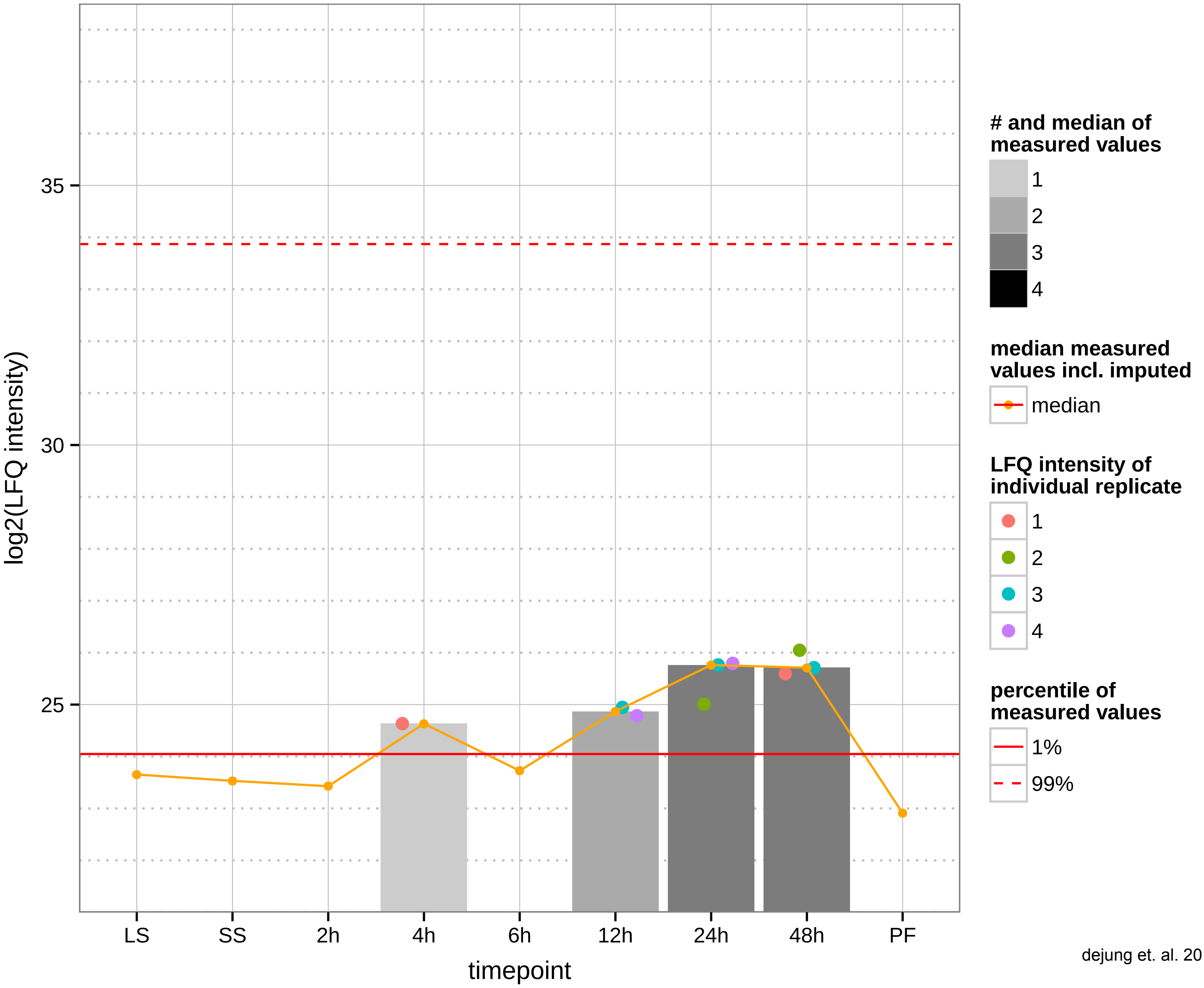
hypothetical protein, conserved
Tb927.10.3630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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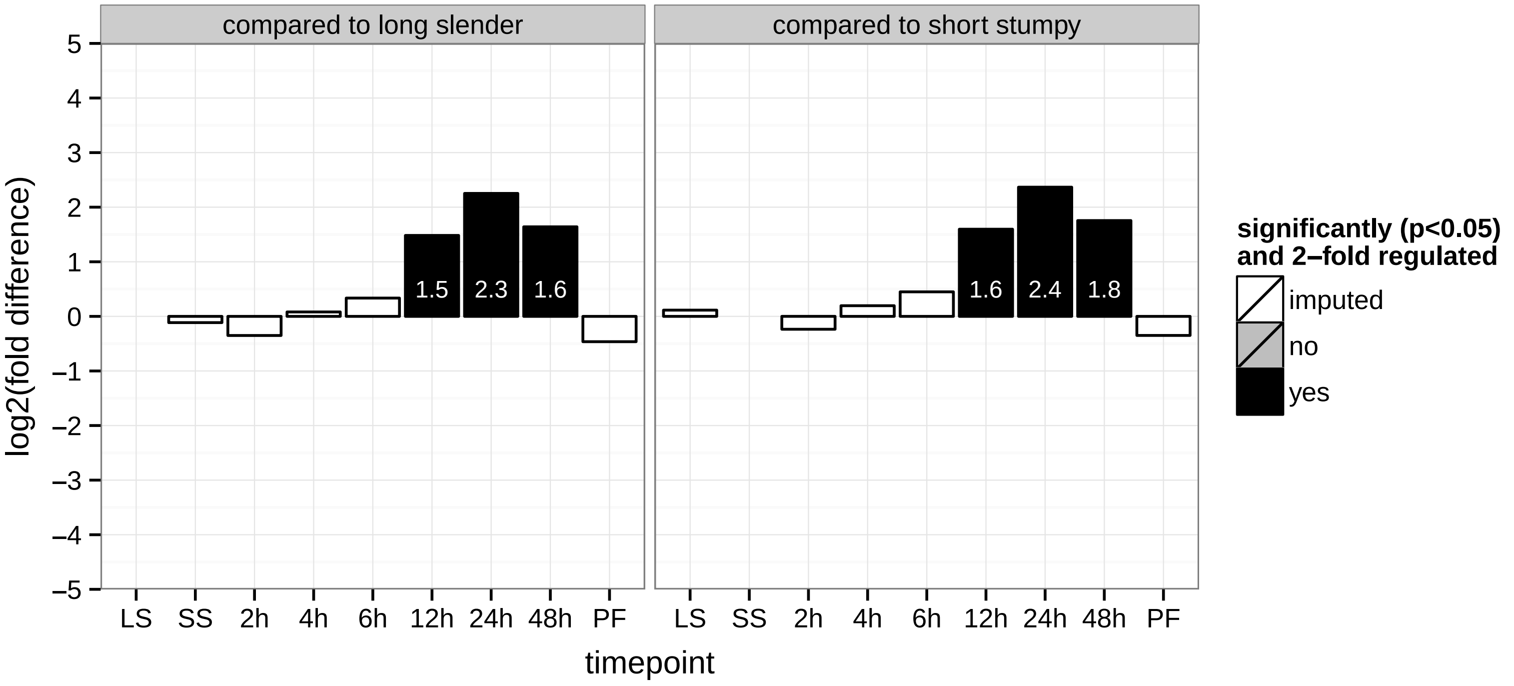
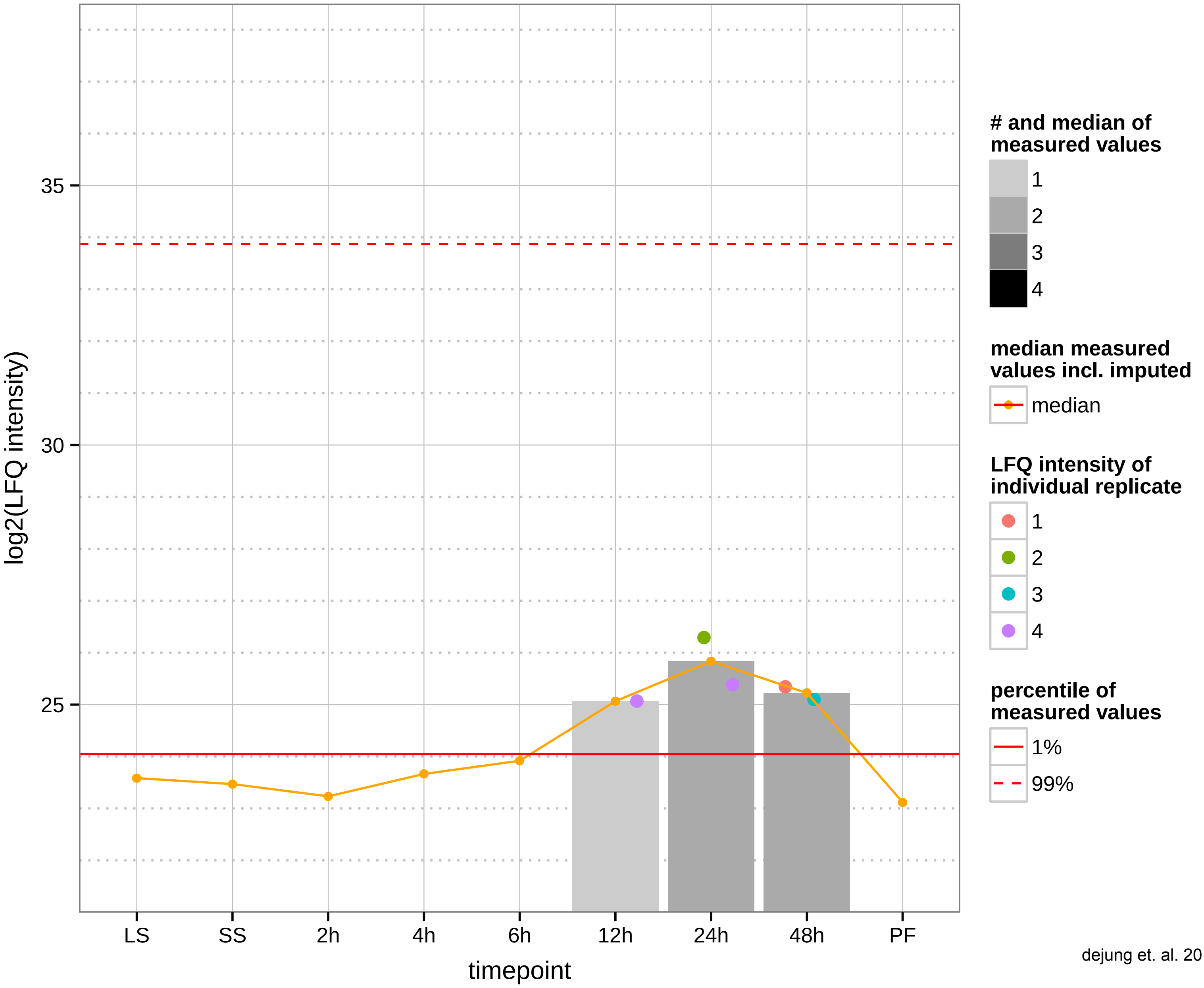
ARP2/3 complex subunit, putative
Tb927.10.4540
AGOF: actin binding
AGOC: Arp2/3 protein complex, cytoskeleton
AGOP: cytoskeleton organization, regulation of actin filament polymerization
PGOF: null
PGOC: cytoskeleton
PGOP: regulation of actin filament polymerization





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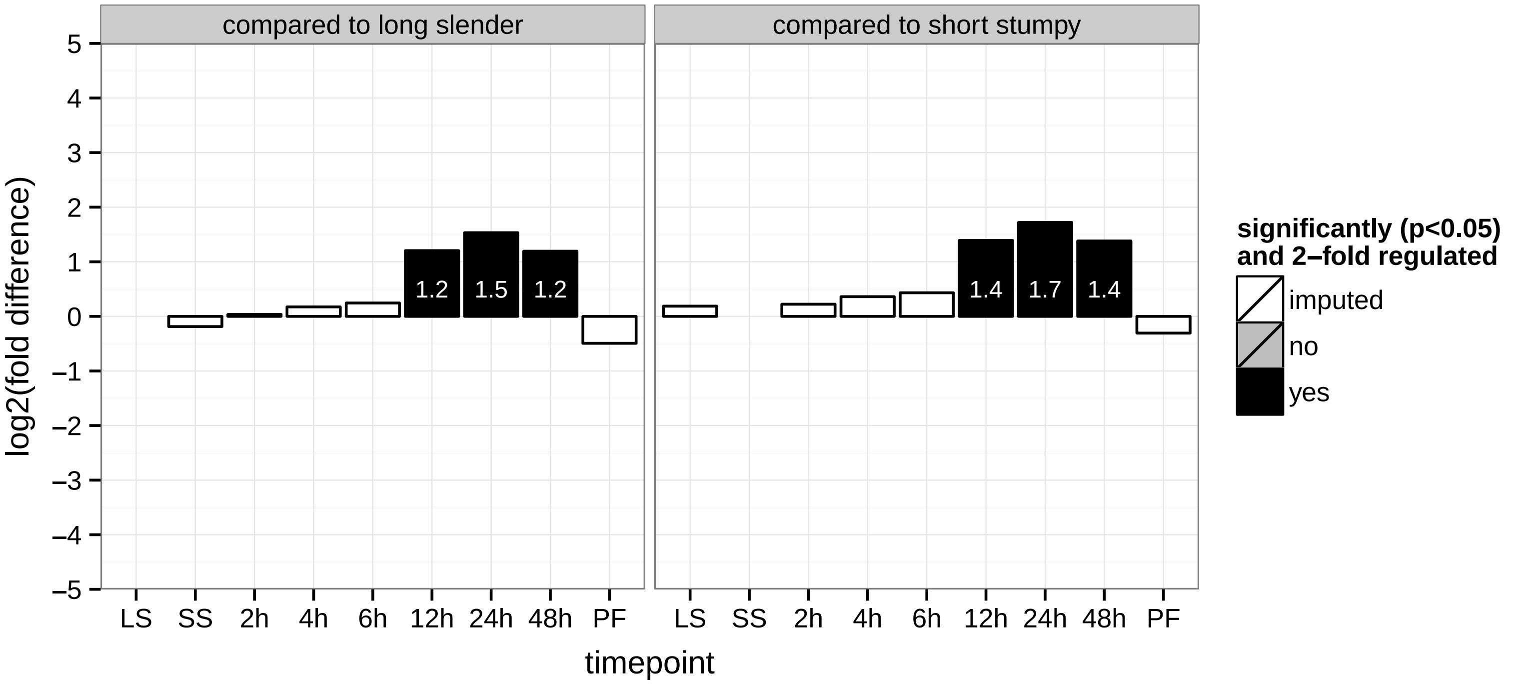
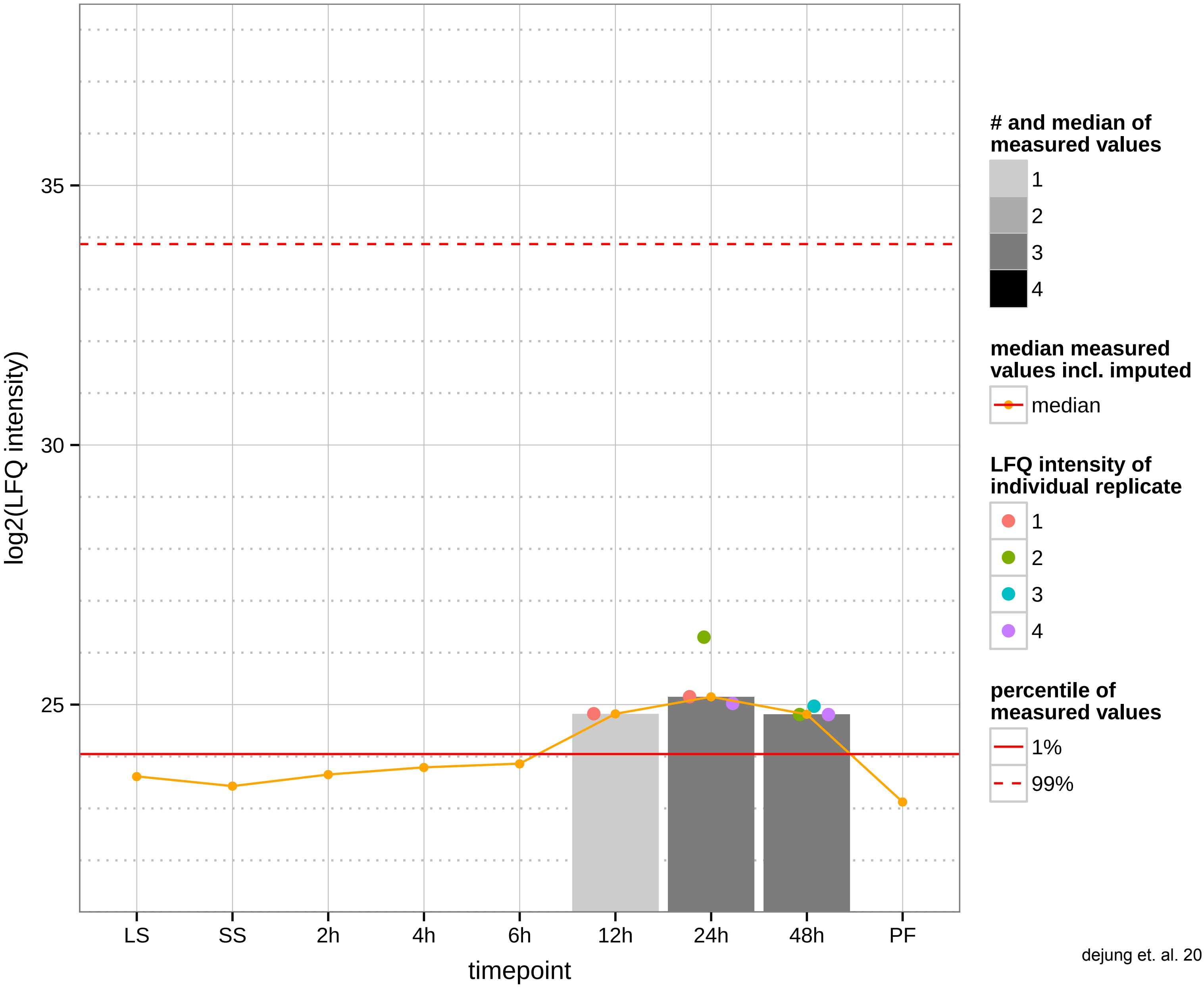
DNA–directed RNA polymerase I subunit, putative (RPA12)
Tb927.11.10420
AGOF: DNA binding, sequence–specific DNA binding transcription factor activity, zinc ion binding
AGOC: null
AGOP: DNA–dependent transcription, elongation, regulation of transcription, DNA–dependent
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: transcription, DNA–dependent





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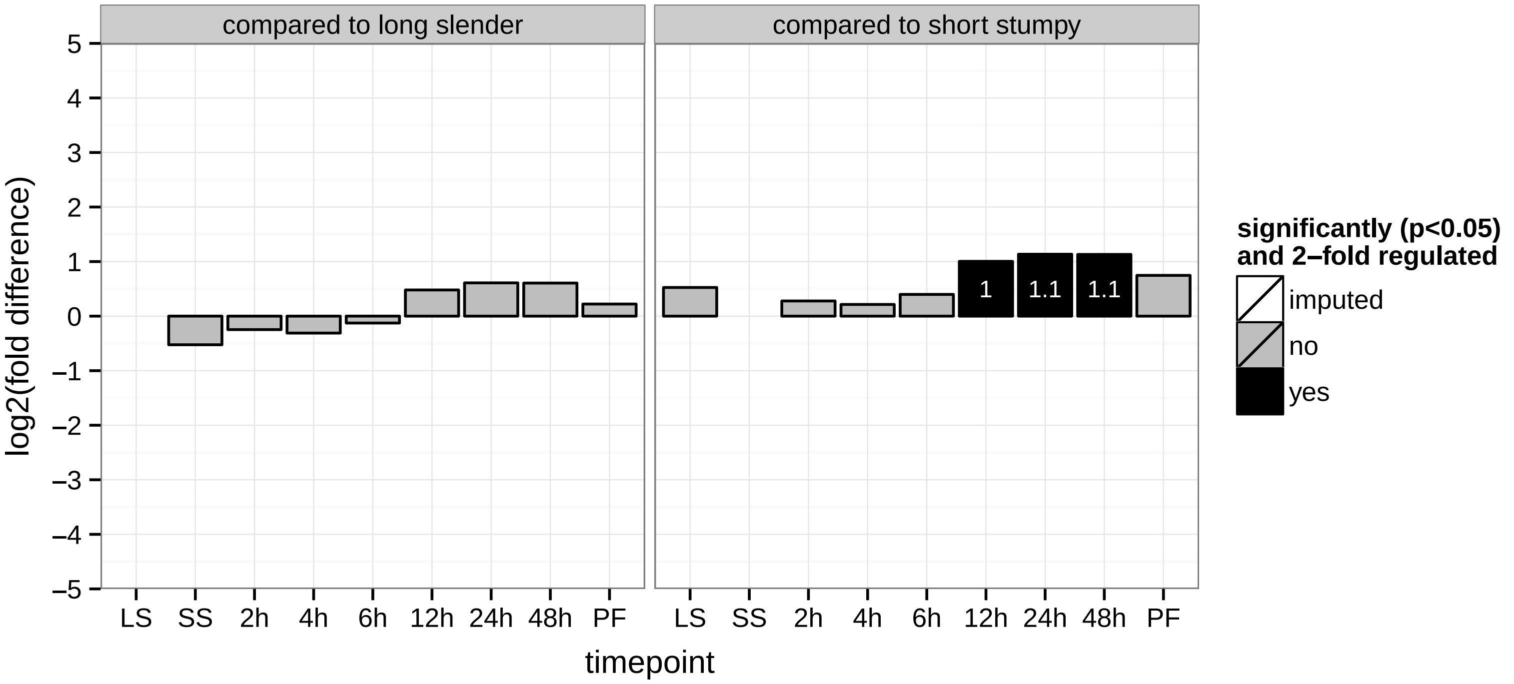
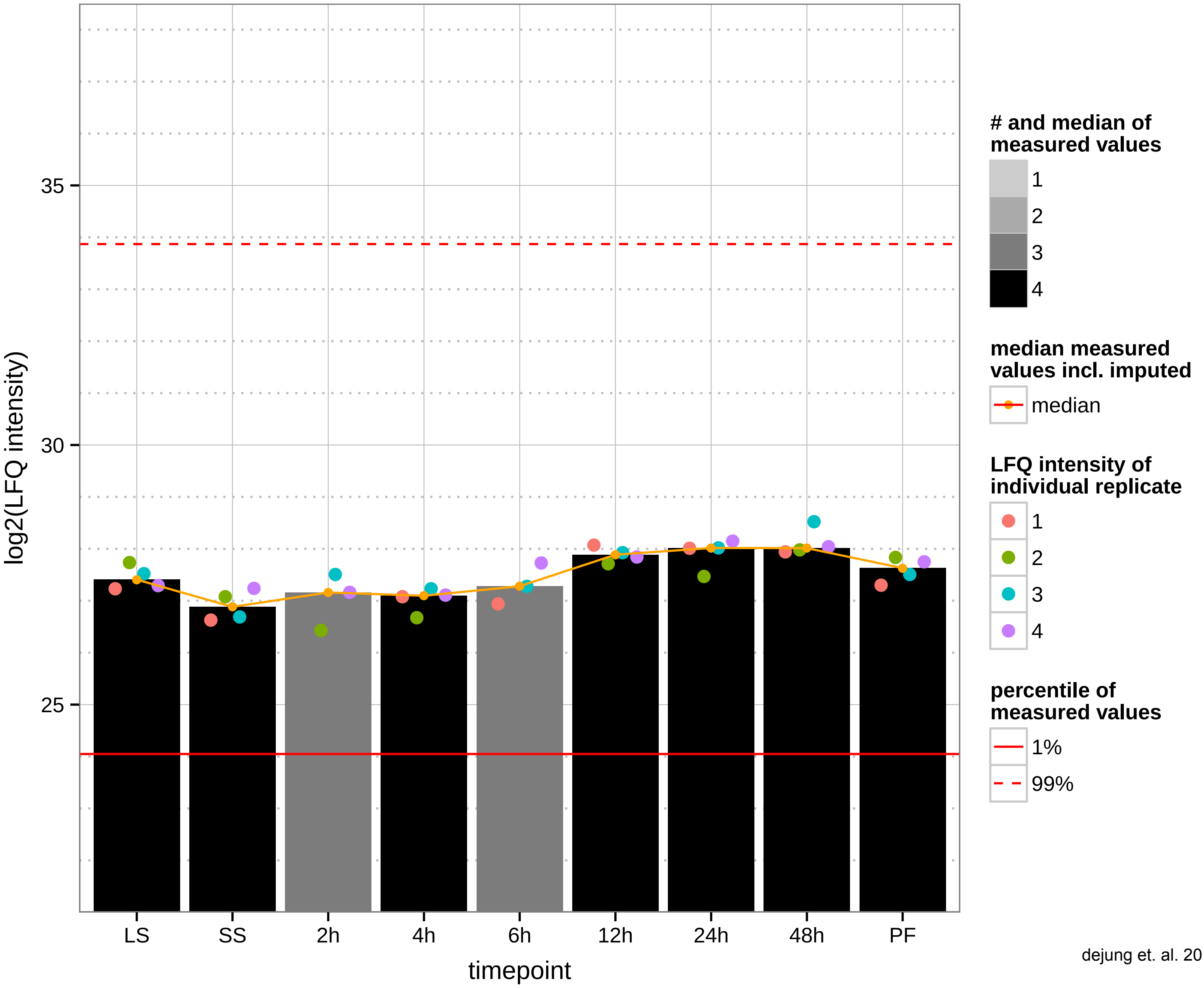
Nucleoporin (TbNup149)
Tb927.11.11080
AGOF: null
AGOC: nuclear pore
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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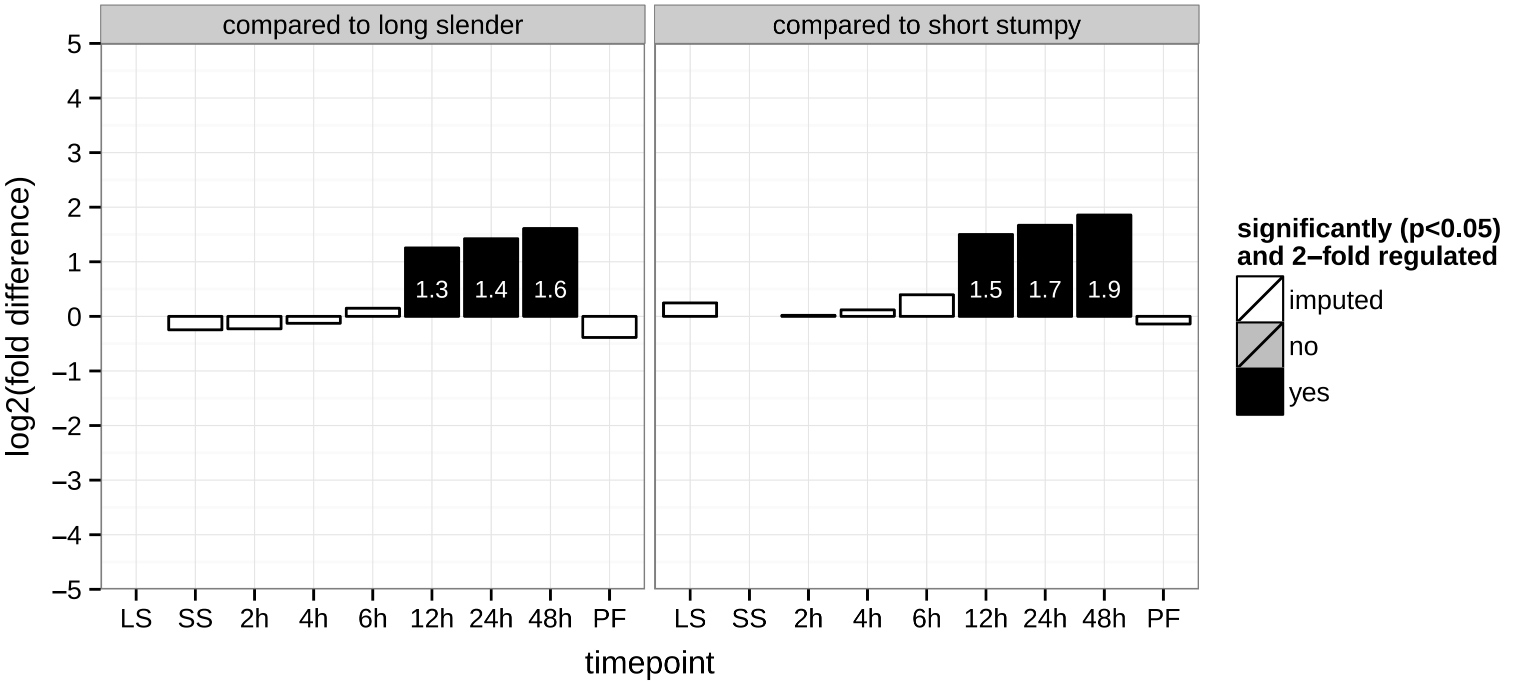
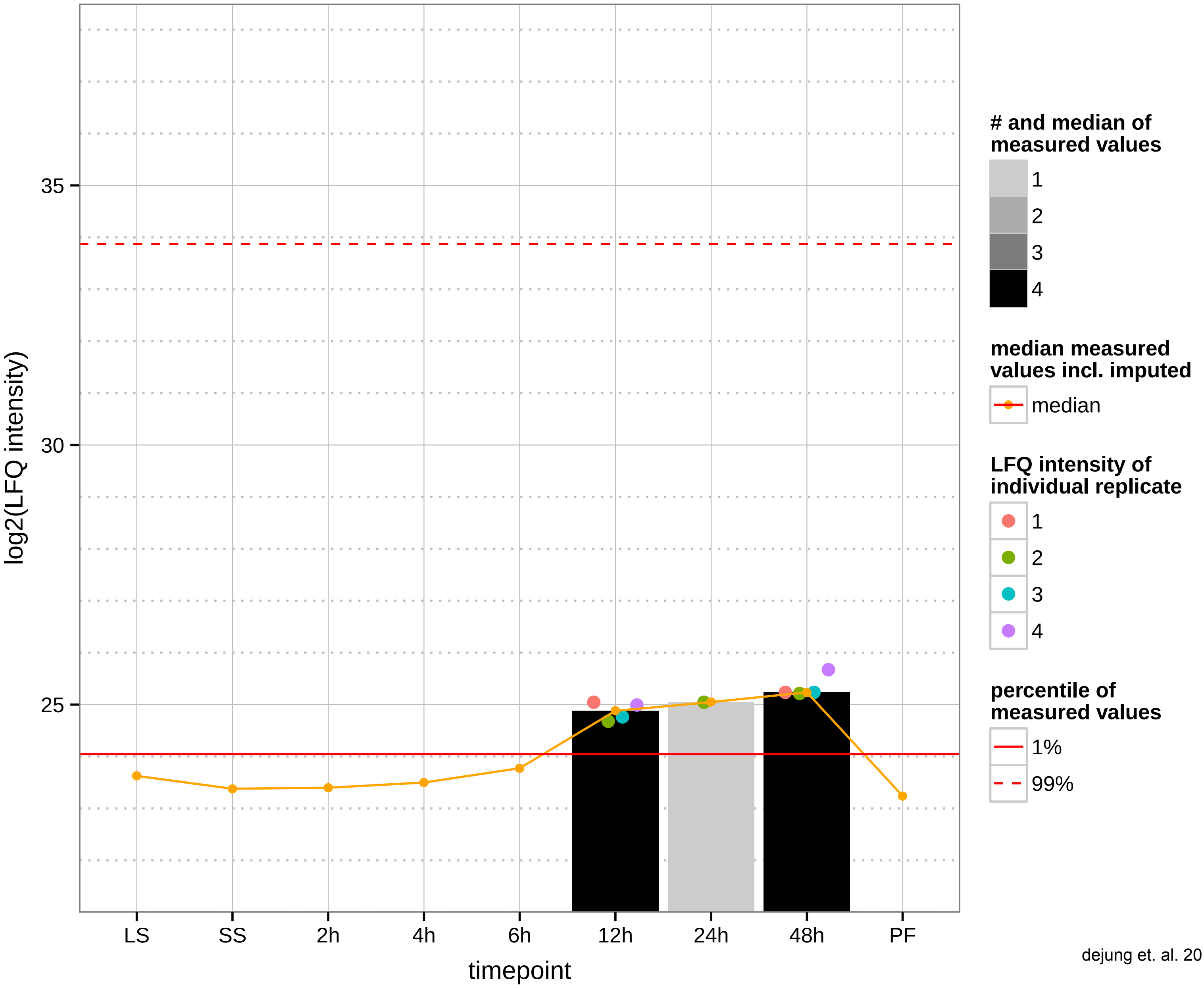
histone acetyltransferase, putative (HAT2)
Tb927.11.11530
AGOF: histone acetyltransferase activity
AGOC: null
AGOP: histone acetylation, regulation of transcription, DNA–dependent
PGOF: transferase activity, transferring acyl groups other than amino–acyl groups
PGOC: nucleus
PGOP: regulation of transcription, DNA–dependent





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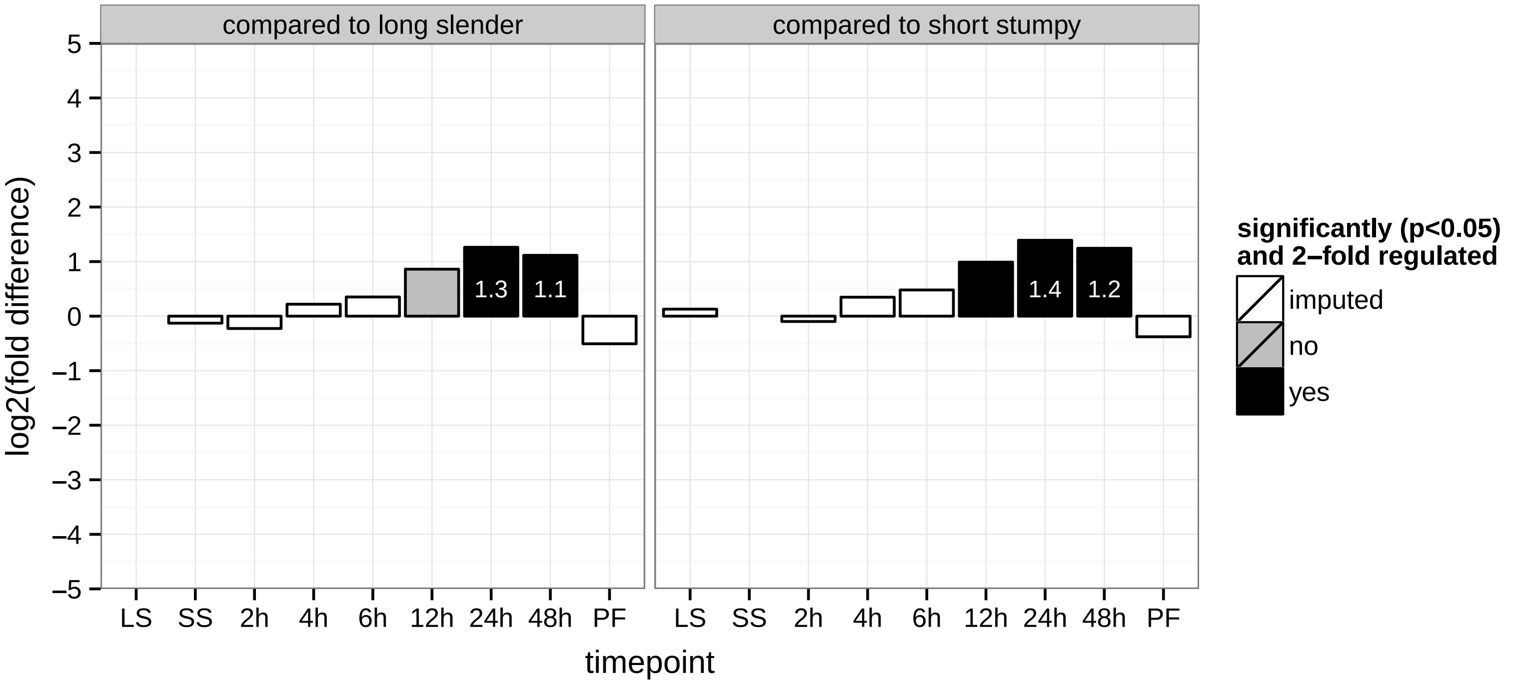
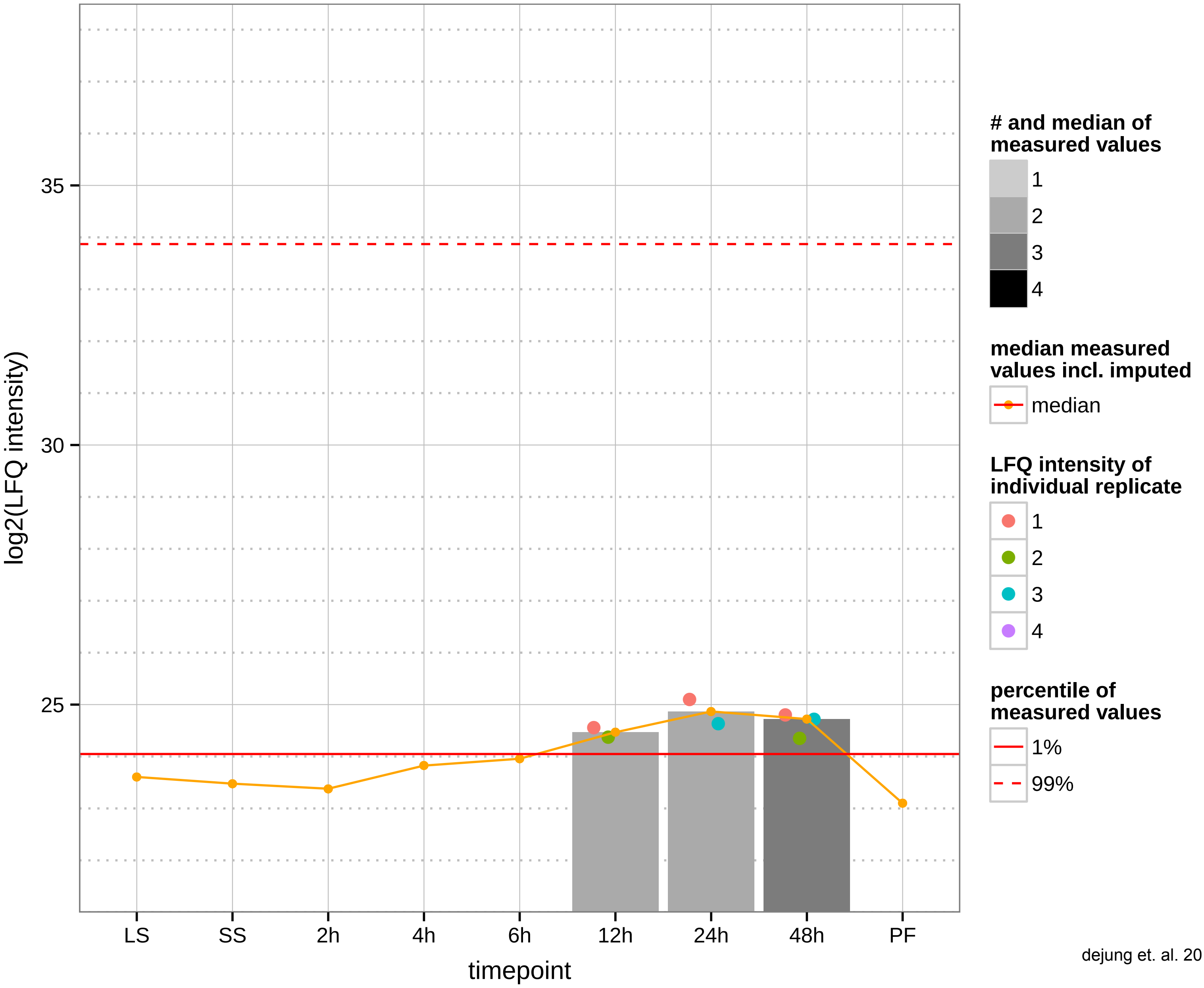
hypothetical protein, conserved
Tb927.11.13600
AGOF: heat shock protein binding
AGOC: integral to membrane
AGOP: null
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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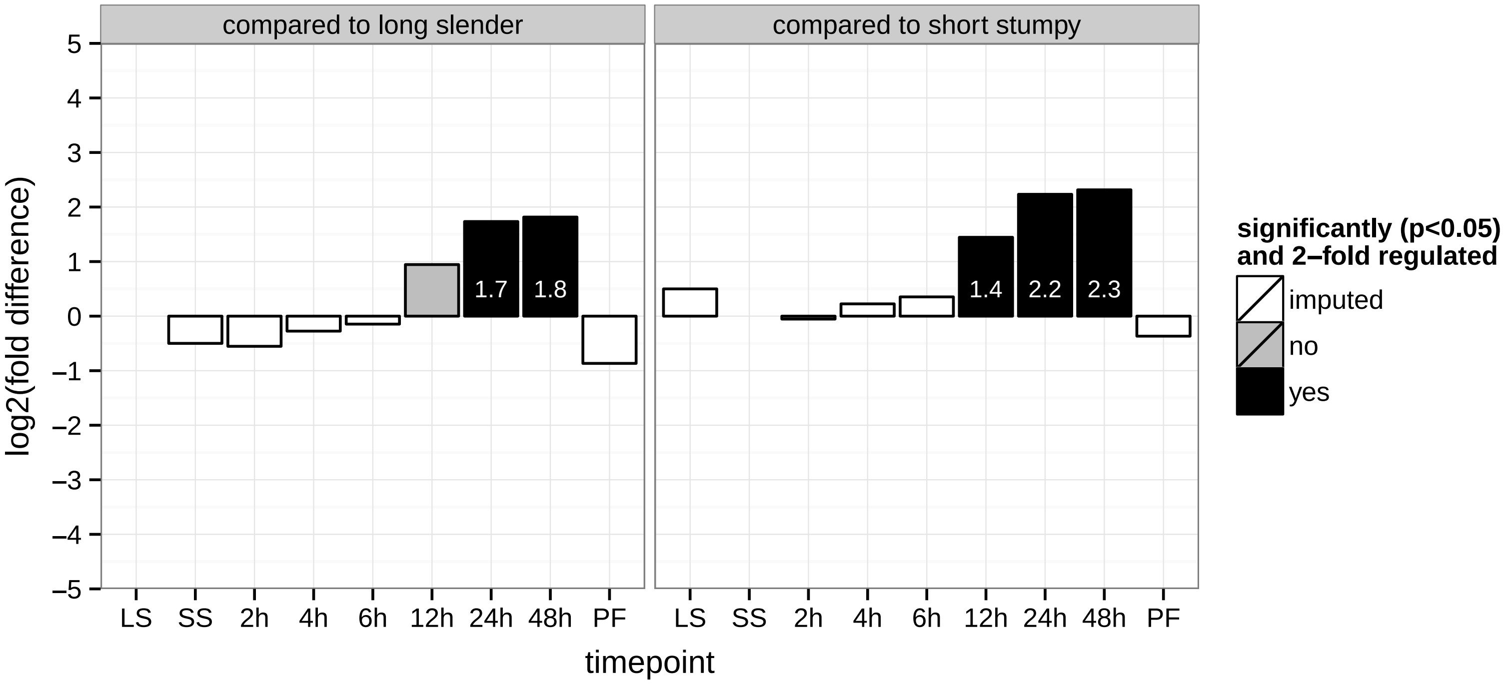
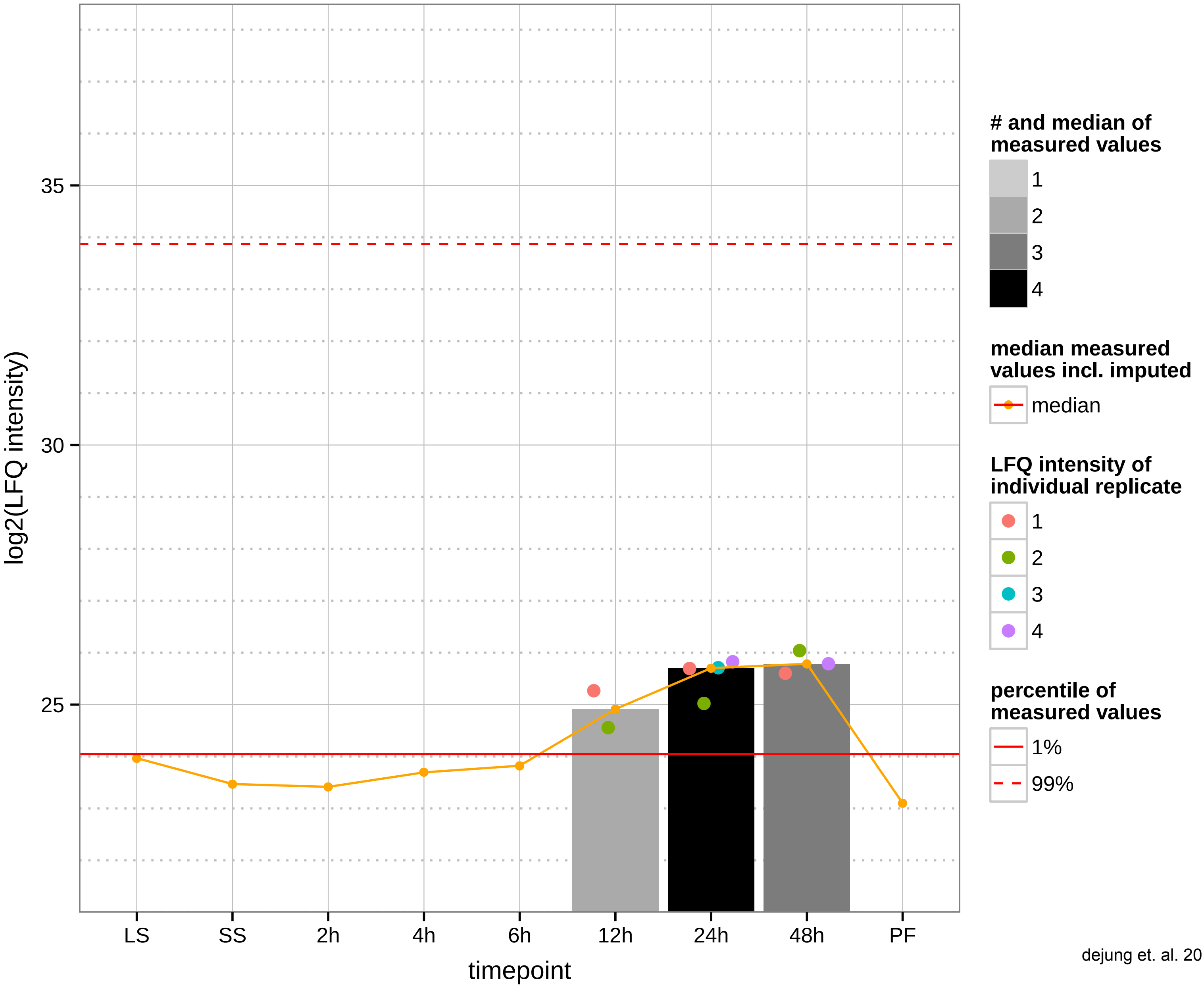
C–14 sterol reductase, putative
Tb927.11.15530
AGOF: delta14–sterol reductase activity
AGOC: integral to membrane, membrane
AGOP: ergosterol biosynthetic process
PGOF: null
PGOC: membrane
PGOP: null





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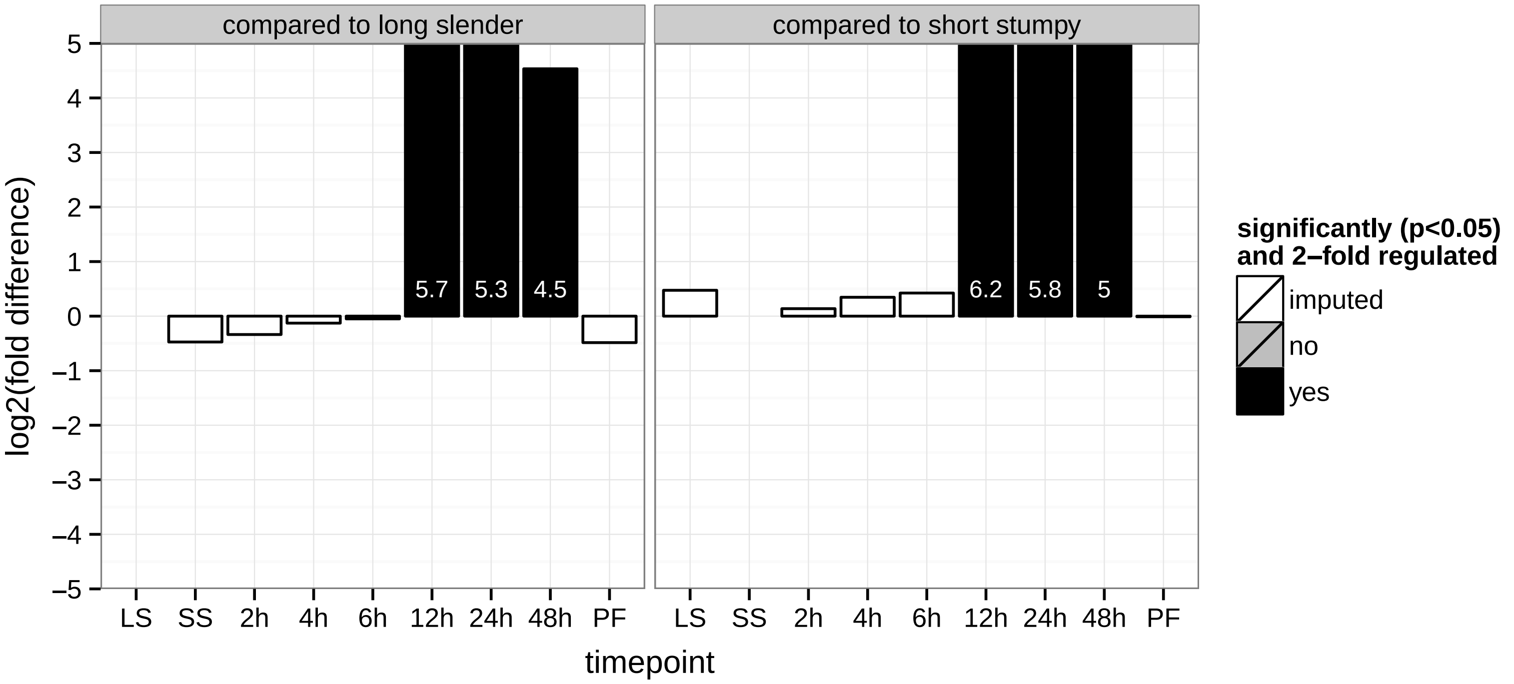
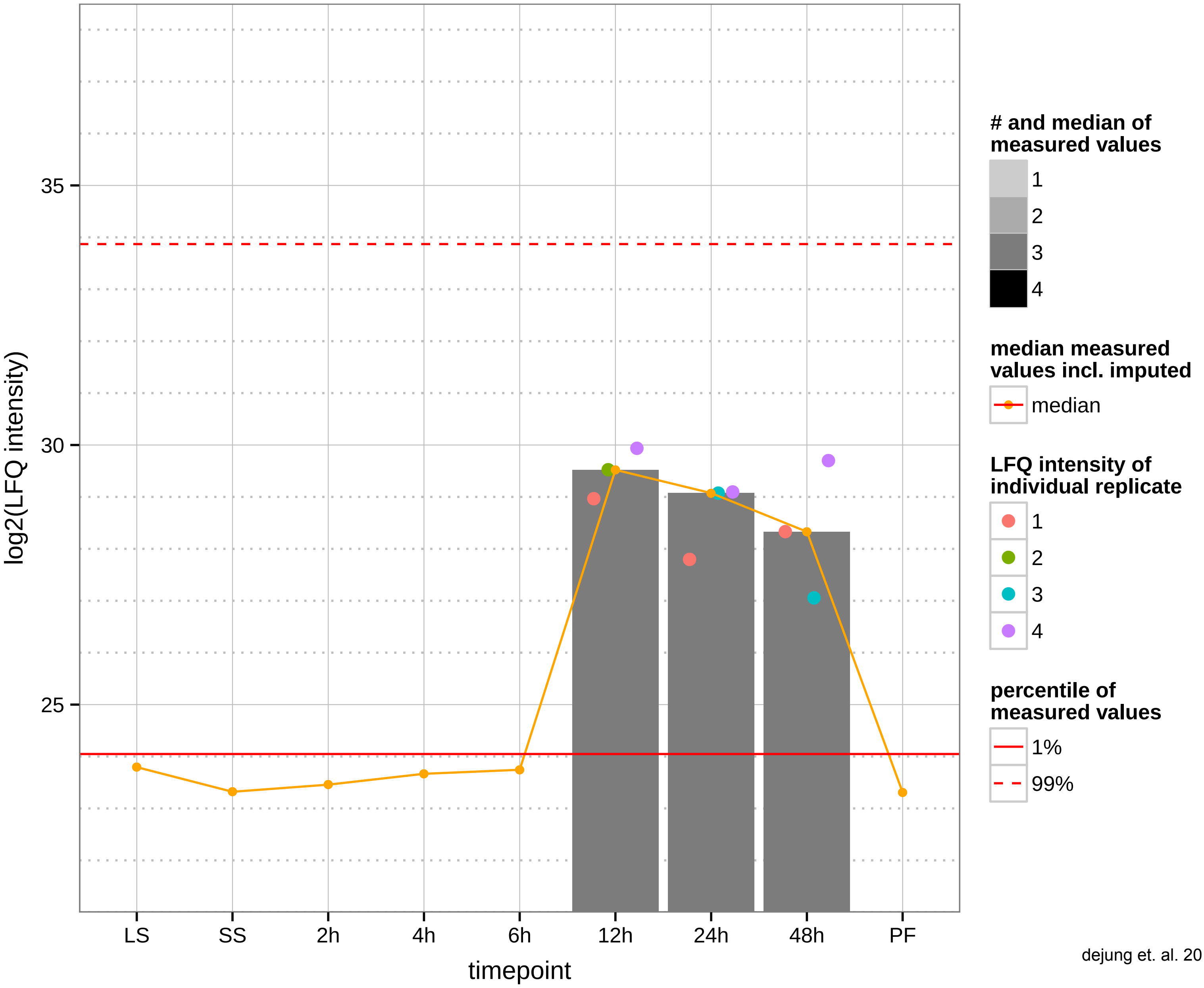
hypothetical protein, conserved
Tb927.11.16010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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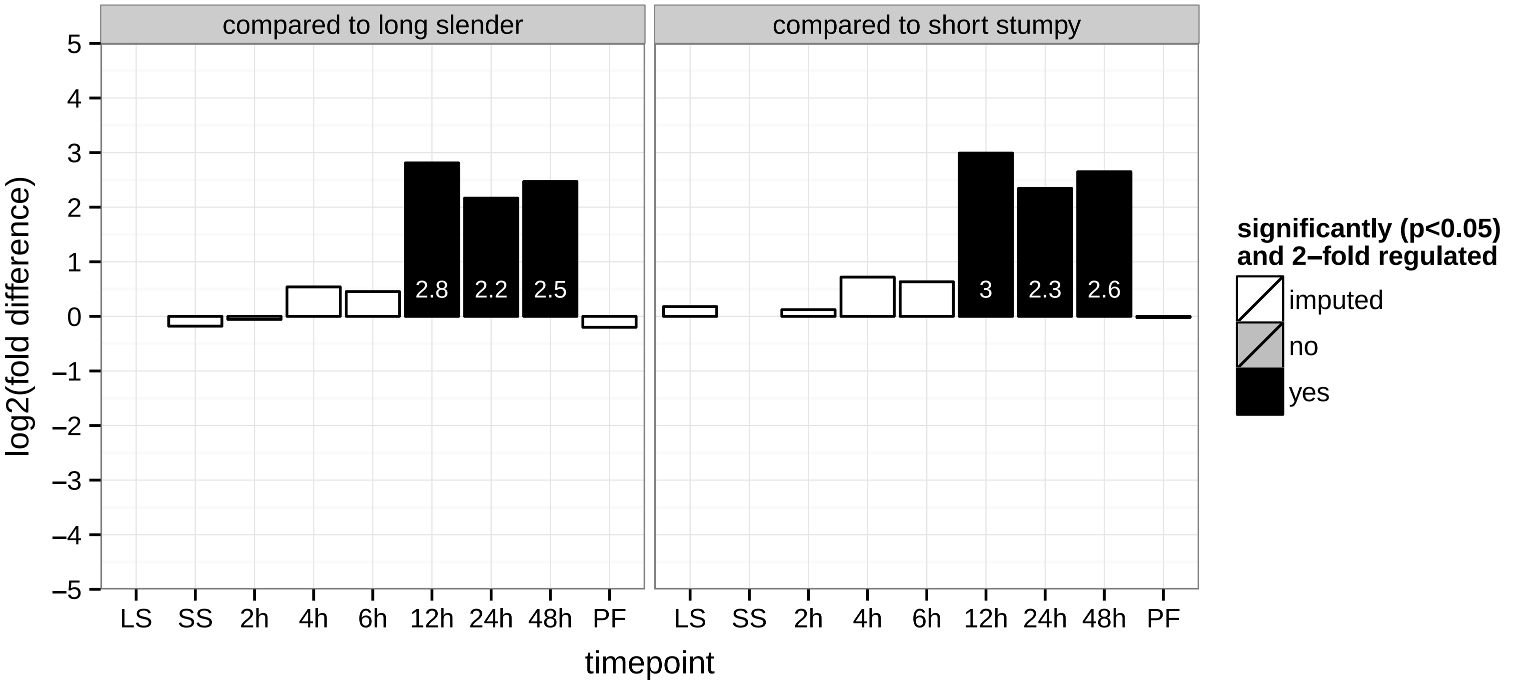
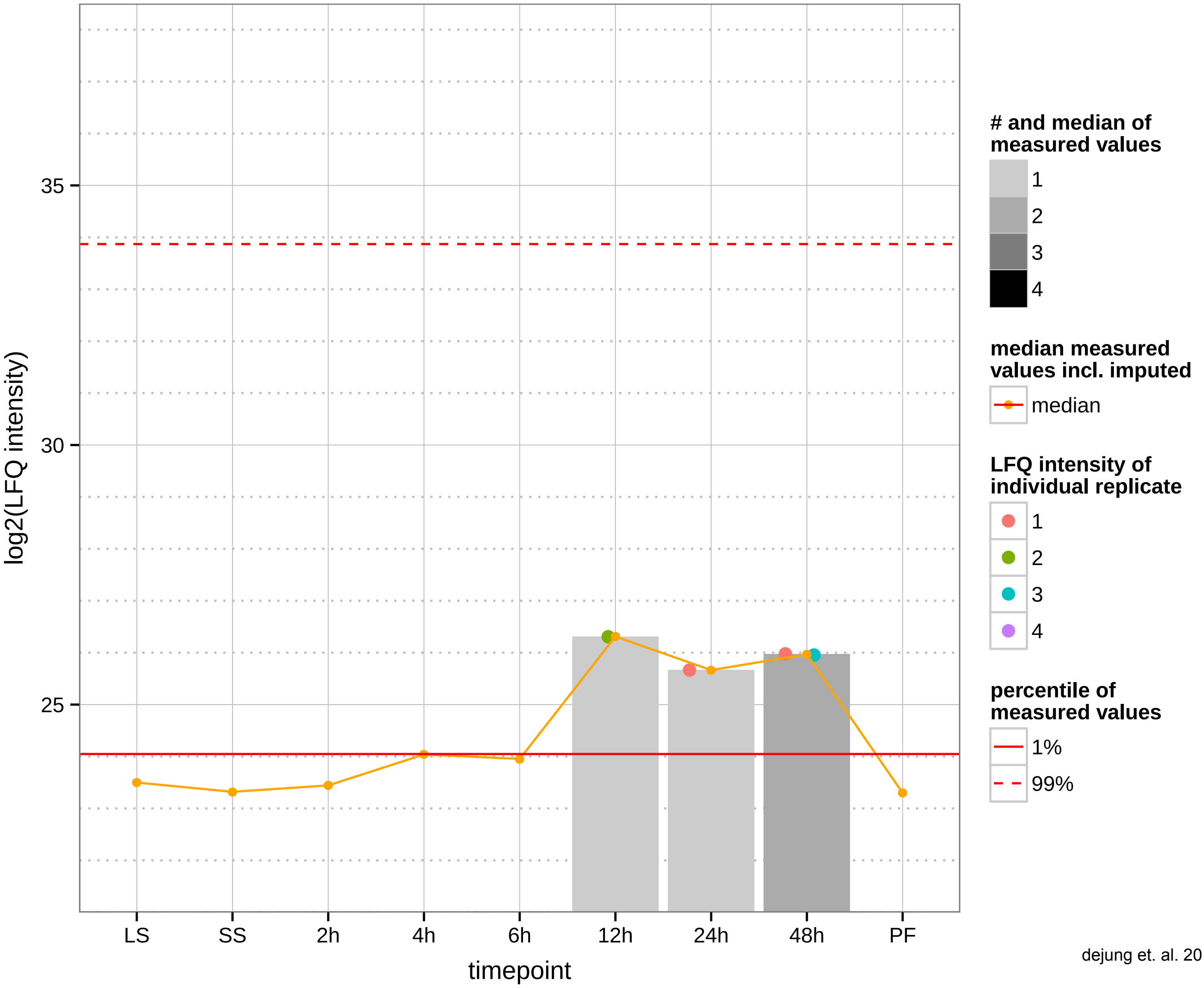
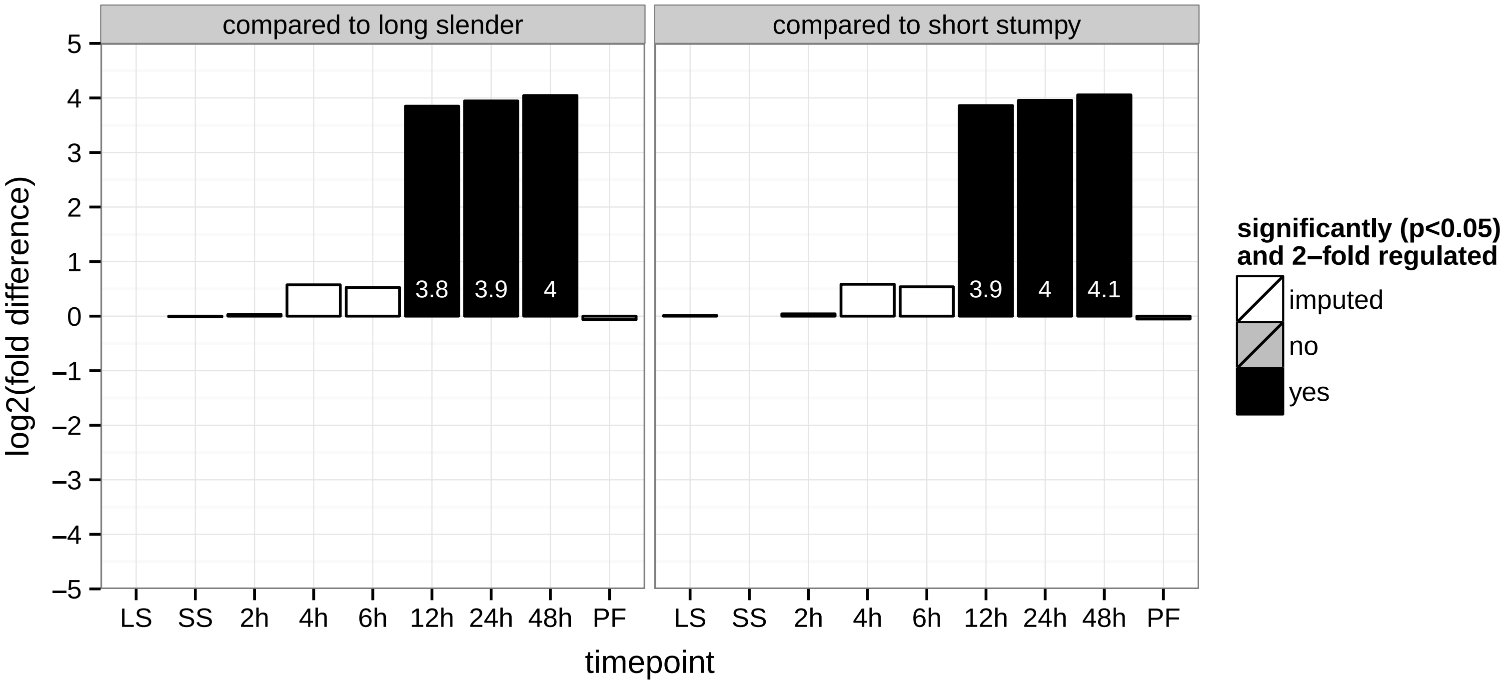
tubulin binding cofactor A, putative
Tb927.11.16150
AGOF: unfolded protein binding
AGOC: microtubule
AGOP: protein folding, tubulin complex assembly
PGOF: unfolded protein binding
PGOC: microtubule
PGOP: tubulin complex assembly

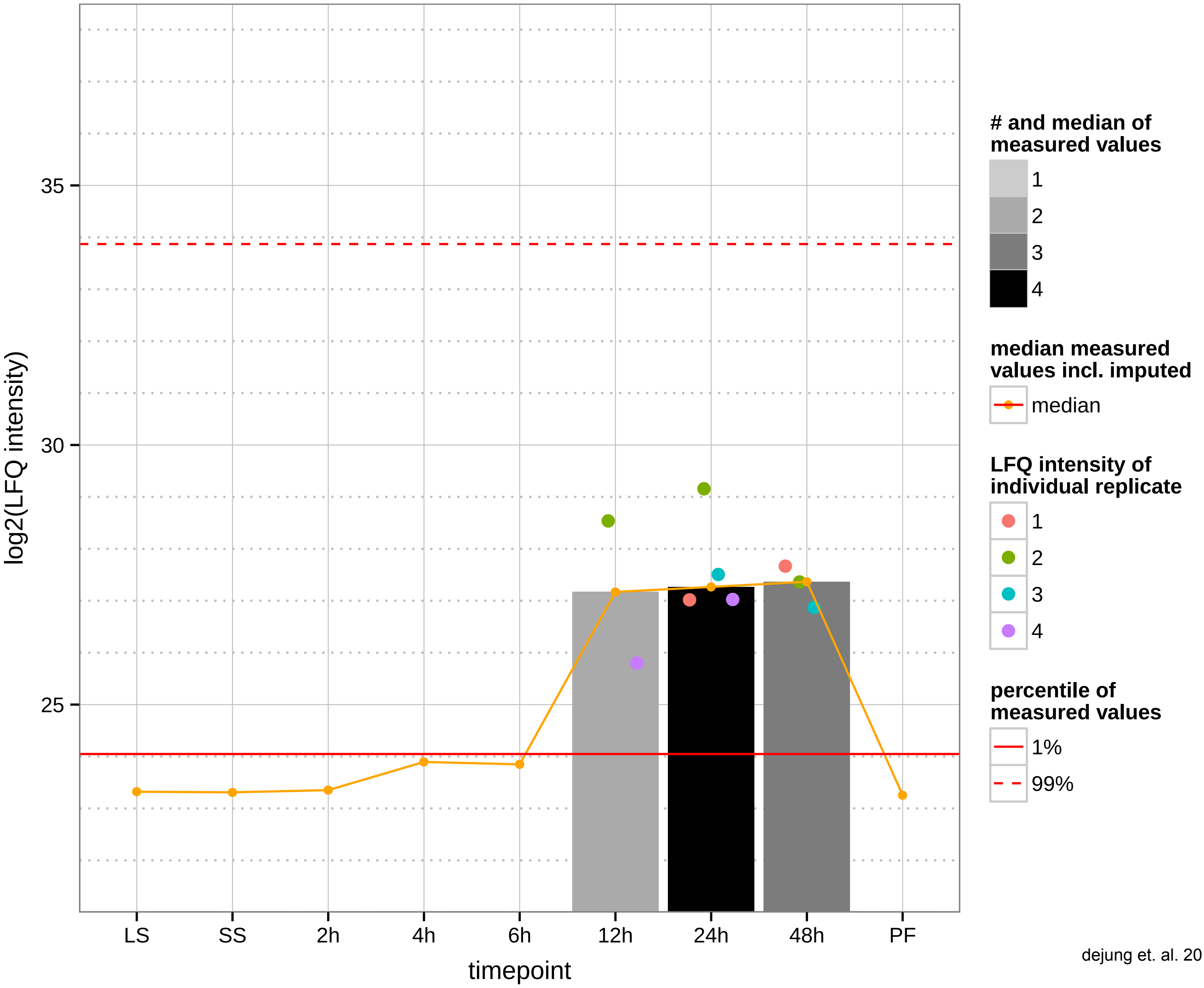




dejung et. al. 2015

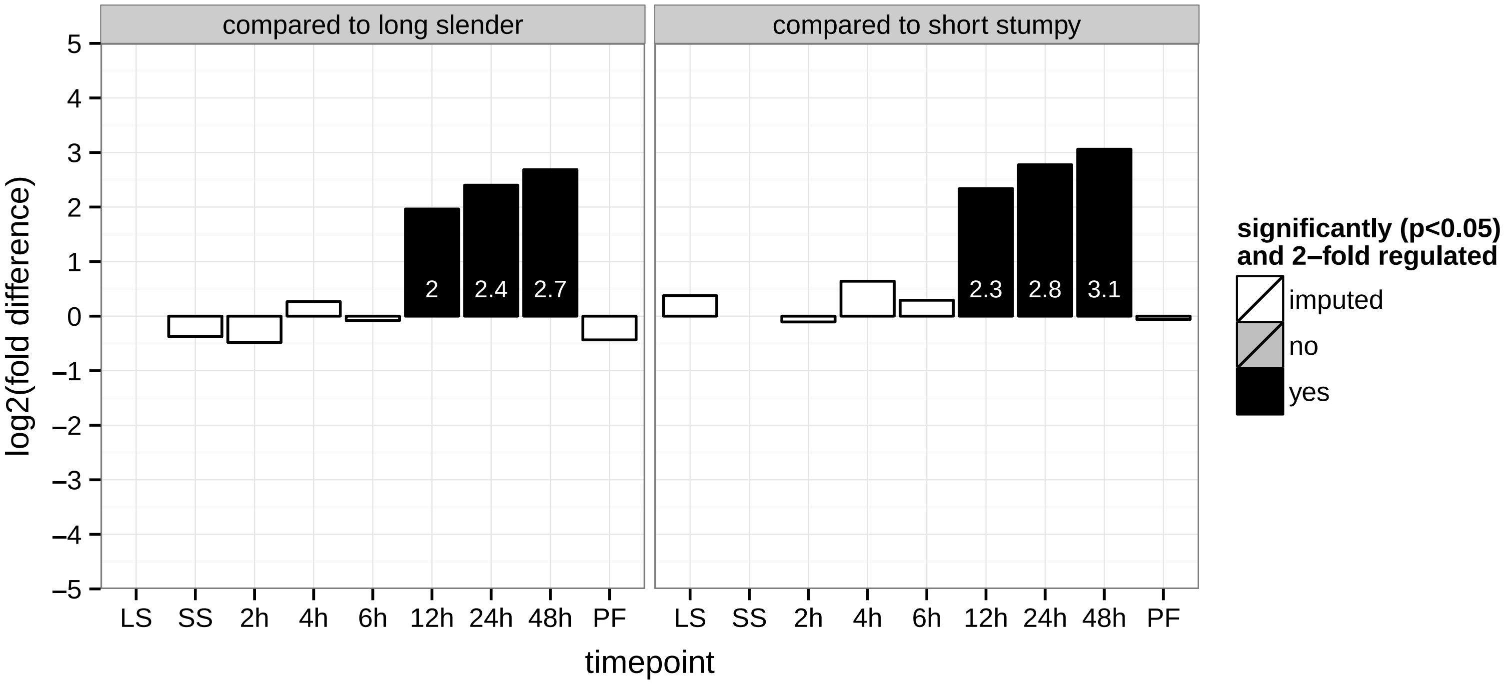
hypothetical protein, conserved
Tb927.11.4400
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

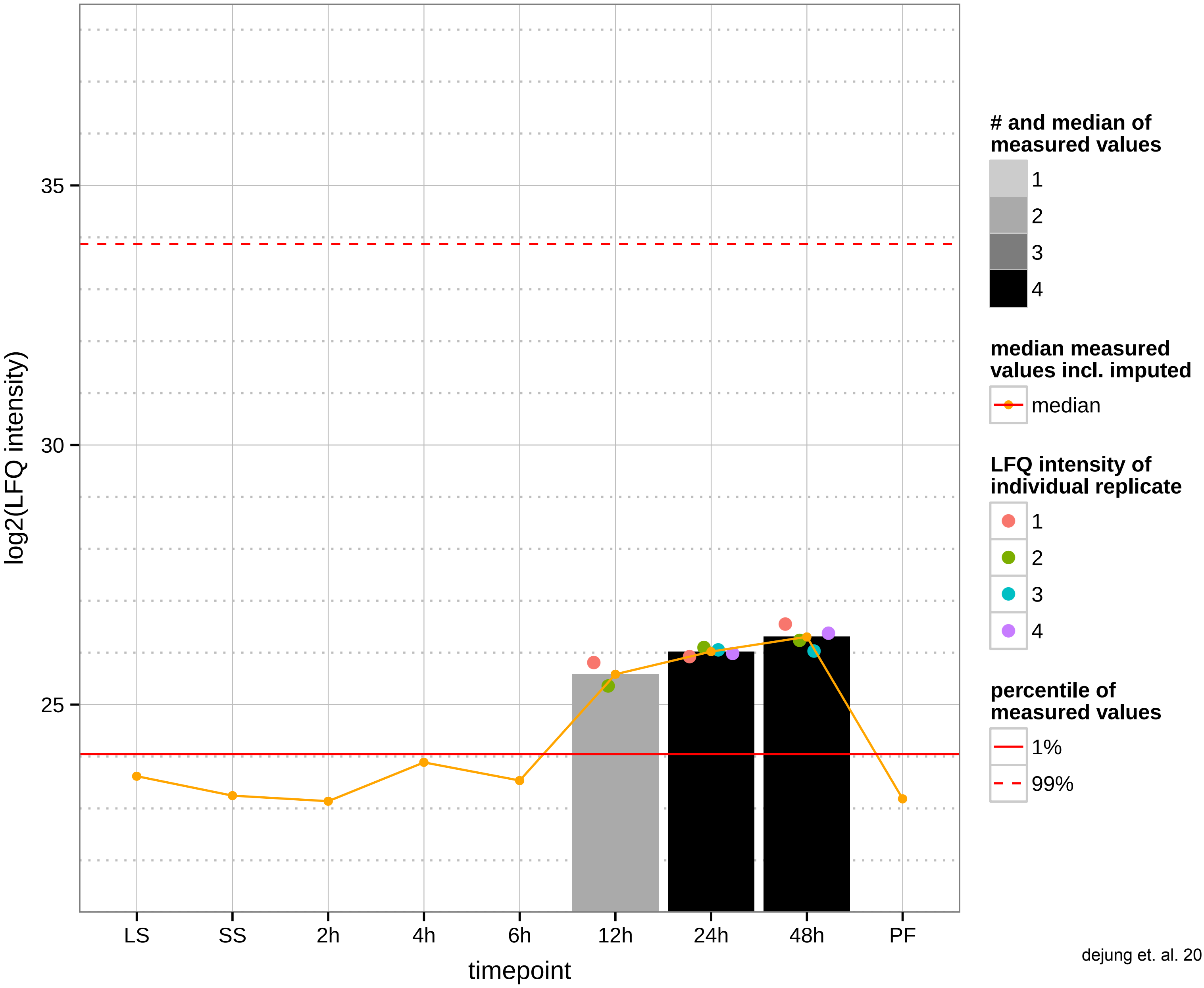




dejung et. al. 2015

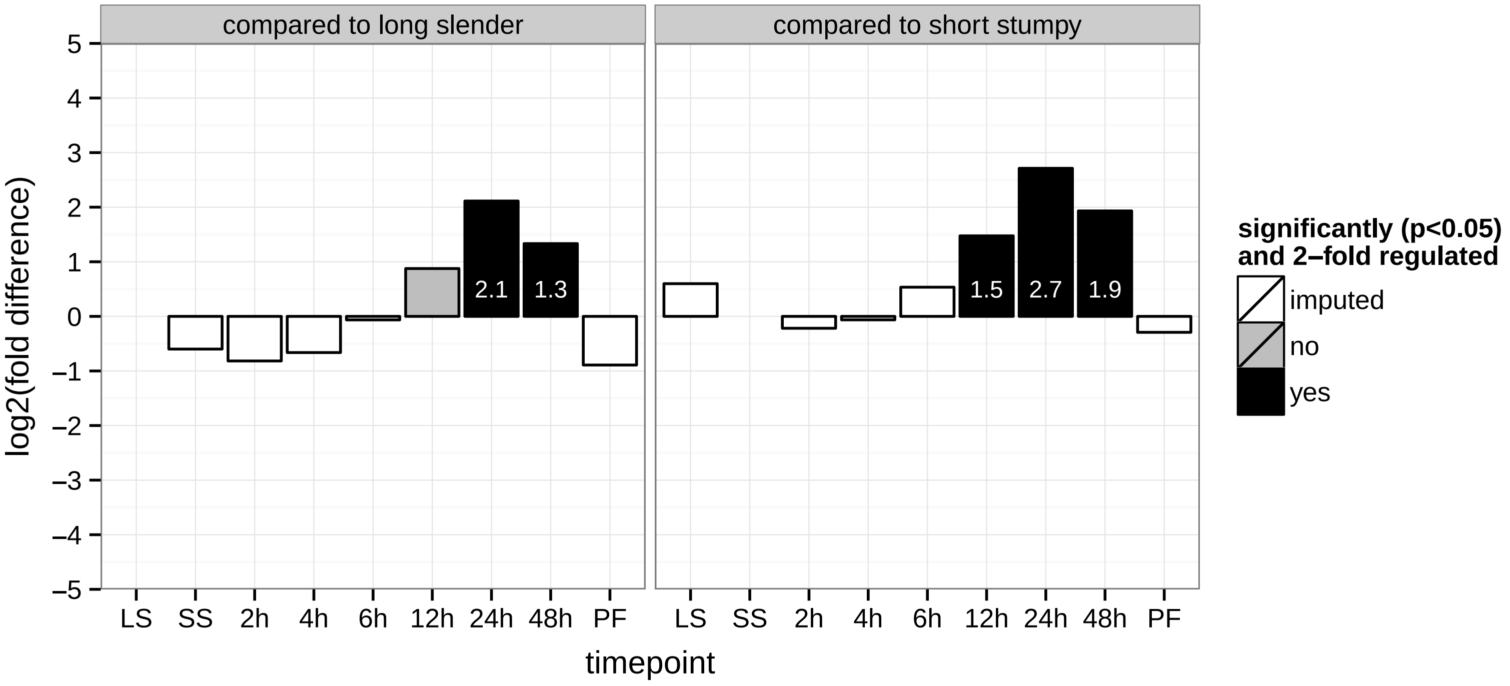
hypothetical protein, conserved
Tb927.11.4850
AGOF: heat shock protein binding
AGOC: integral to membrane, mitochondrion
AGOP: null
PGOF: heat shock protein binding
PGOC: null
PGOP: null

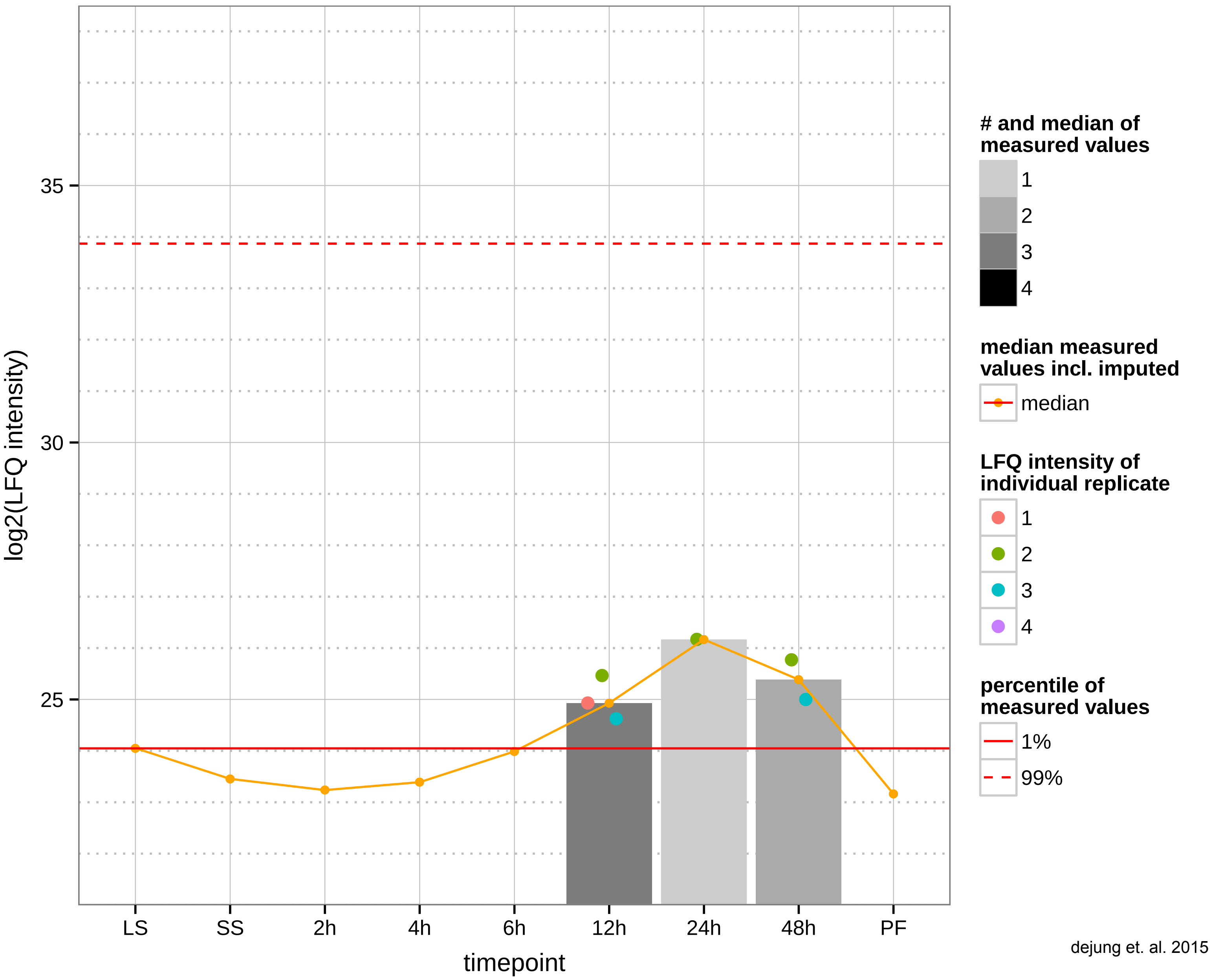




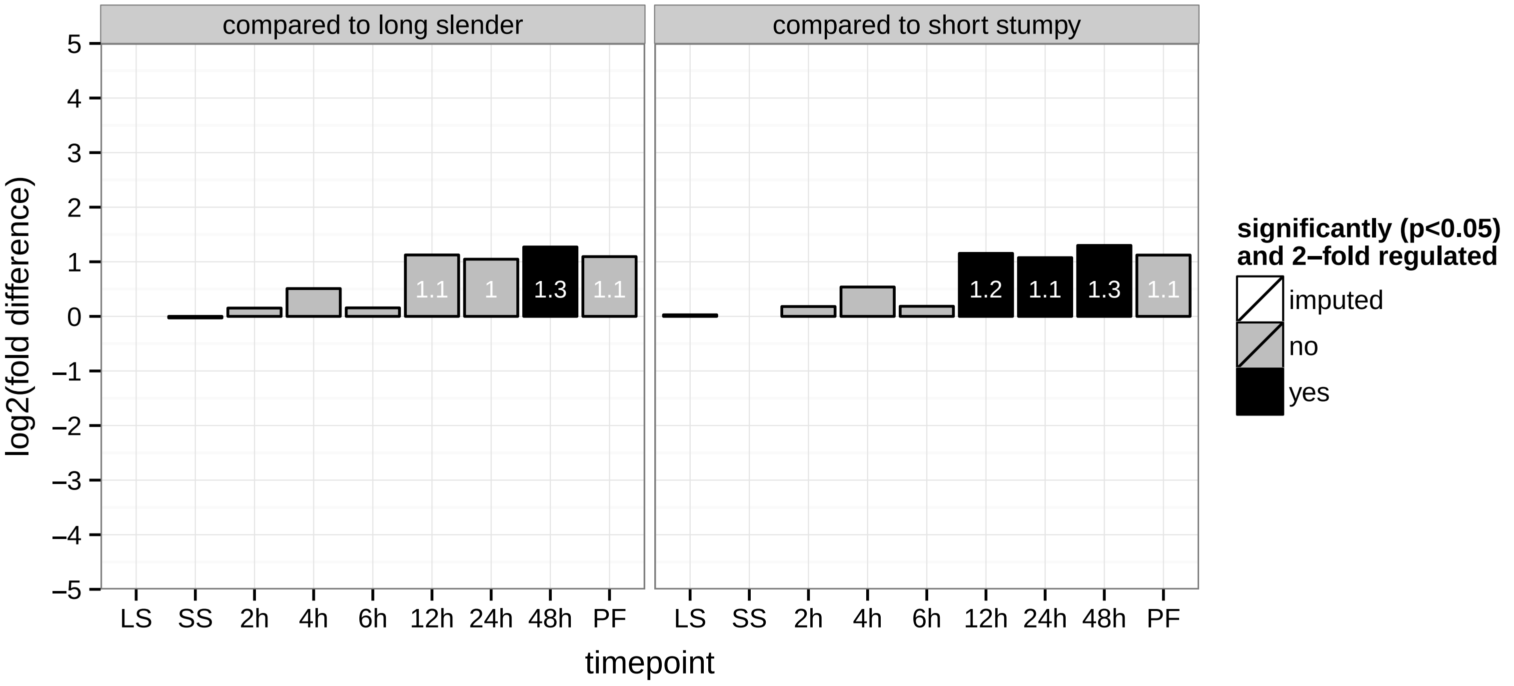
dejung et. al. 2015

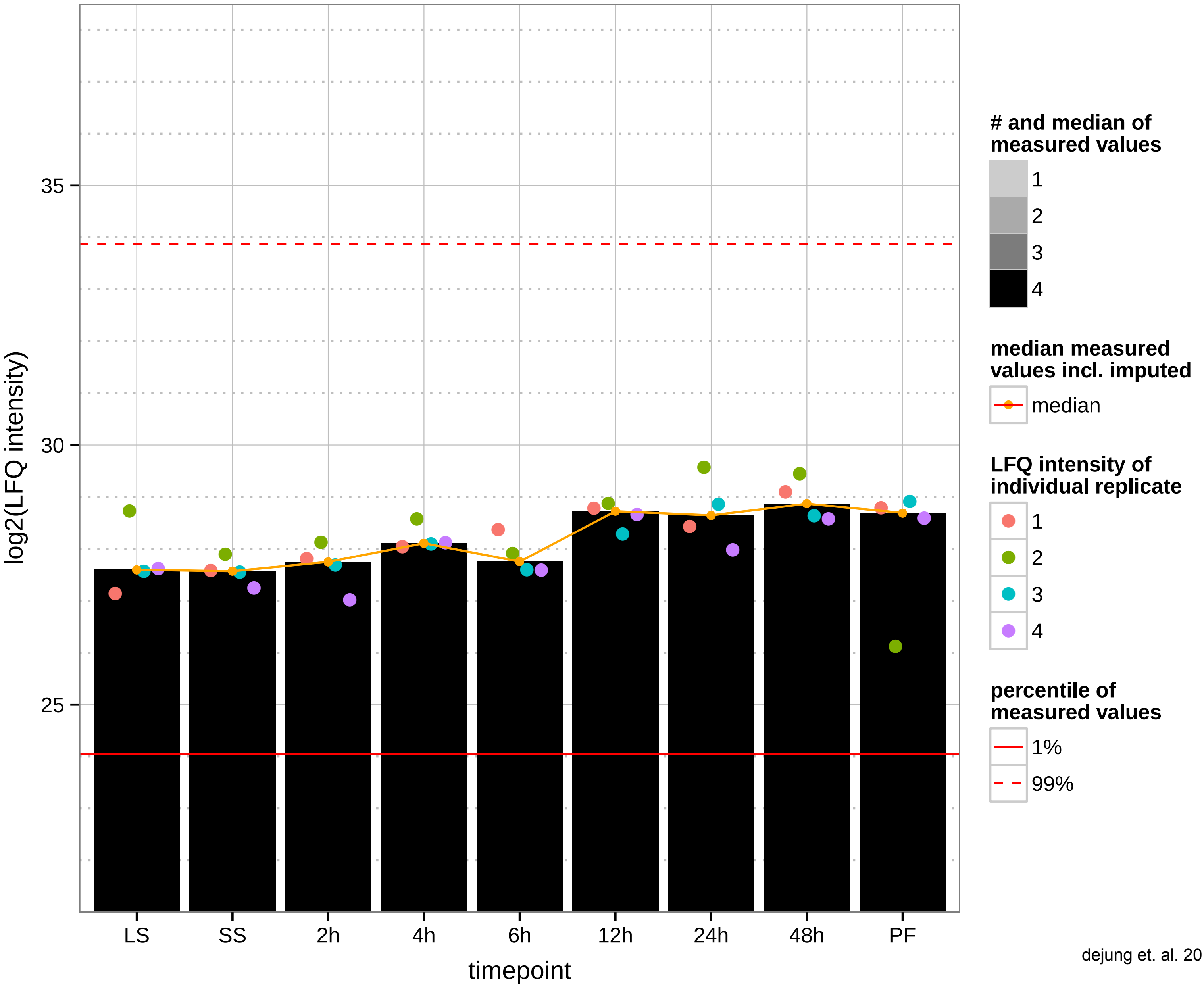
hypothetical protein, conserved
Tb927.11.5960;Tb927.11.5950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





hypothetical protein, conserved
Tb927.11.800
AGOF: unfolded protein binding
AGOC: prefoldin complex
AGOP: protein folding
PGOF: chaperone binding, unfolded protein binding
PGOC: prefoldin complex
PGOP: protein folding





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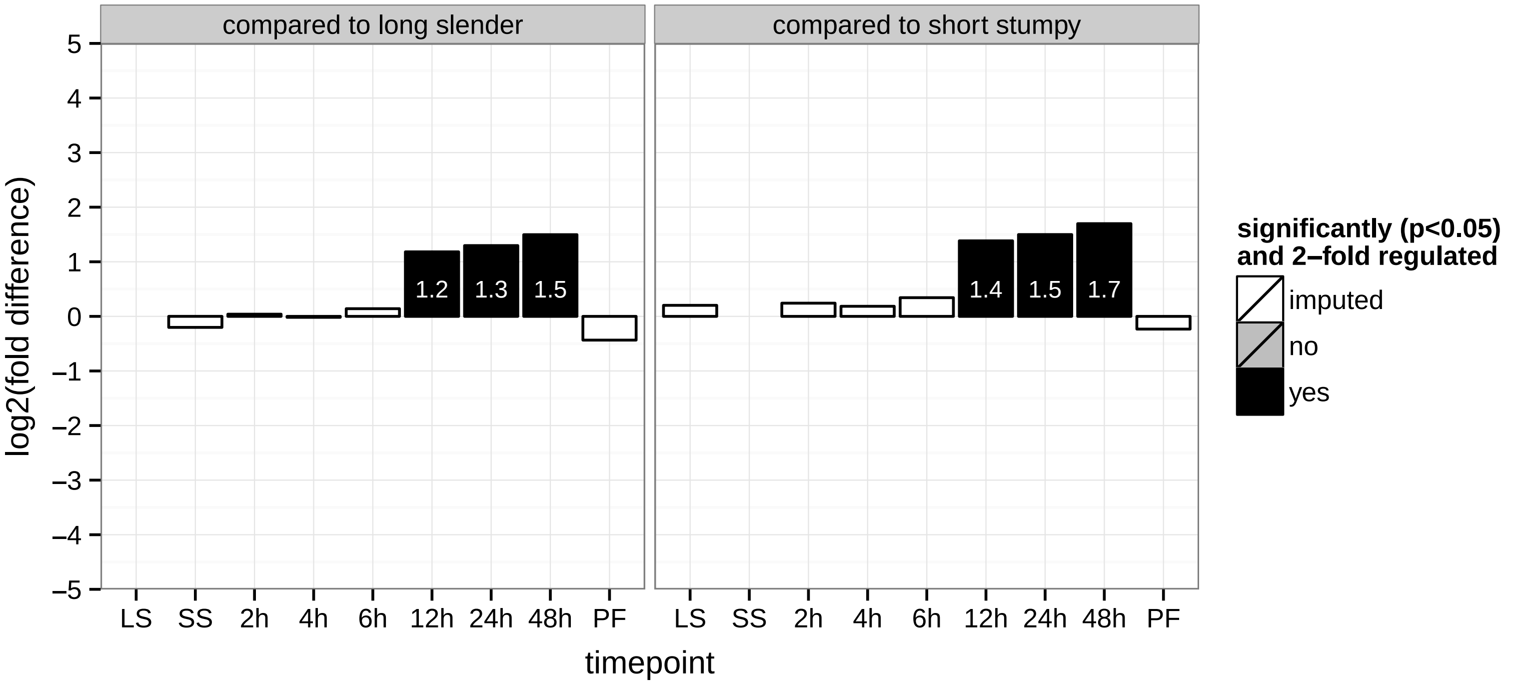
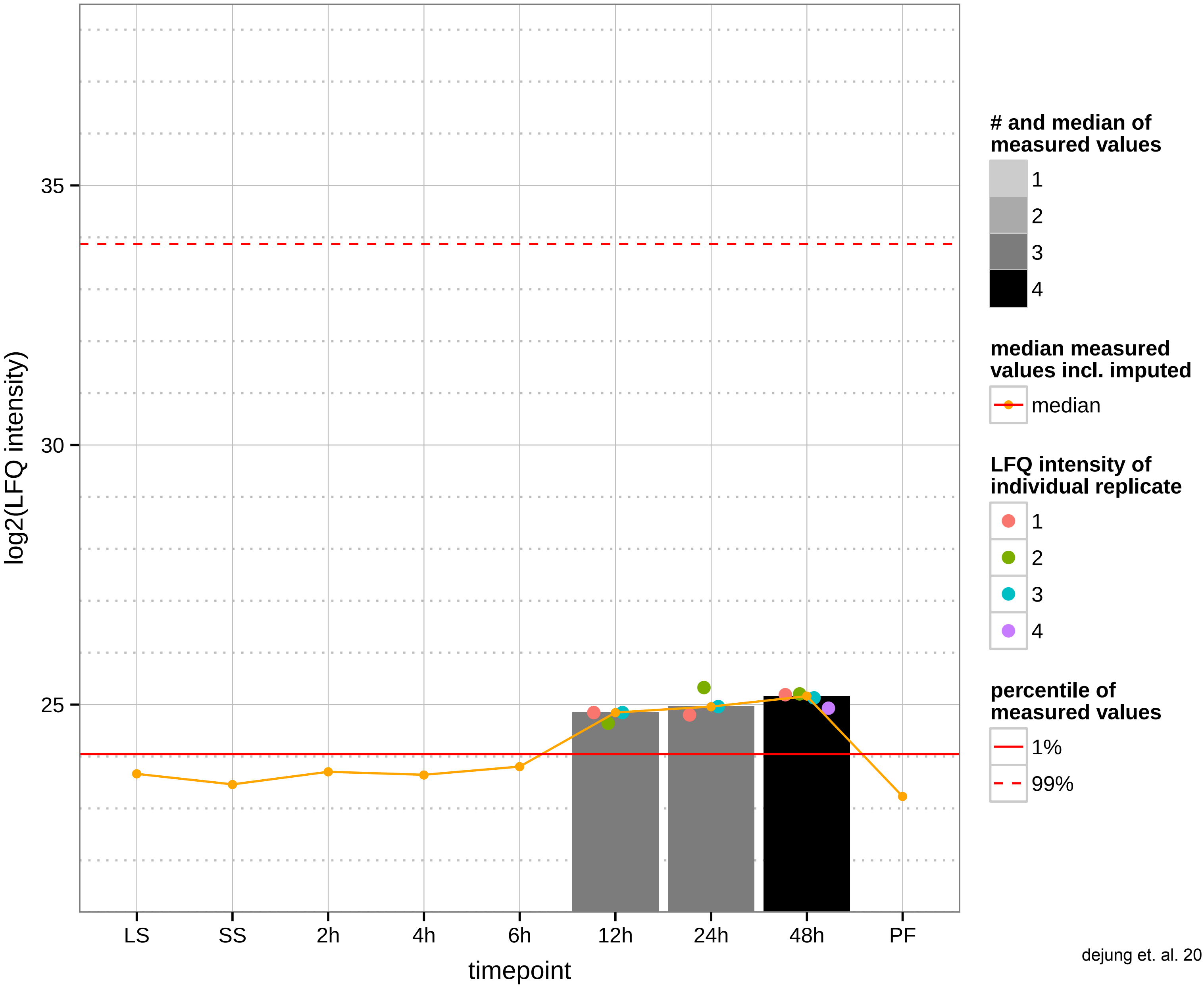
hypothetical protein, conserved
Tb927.11.8100
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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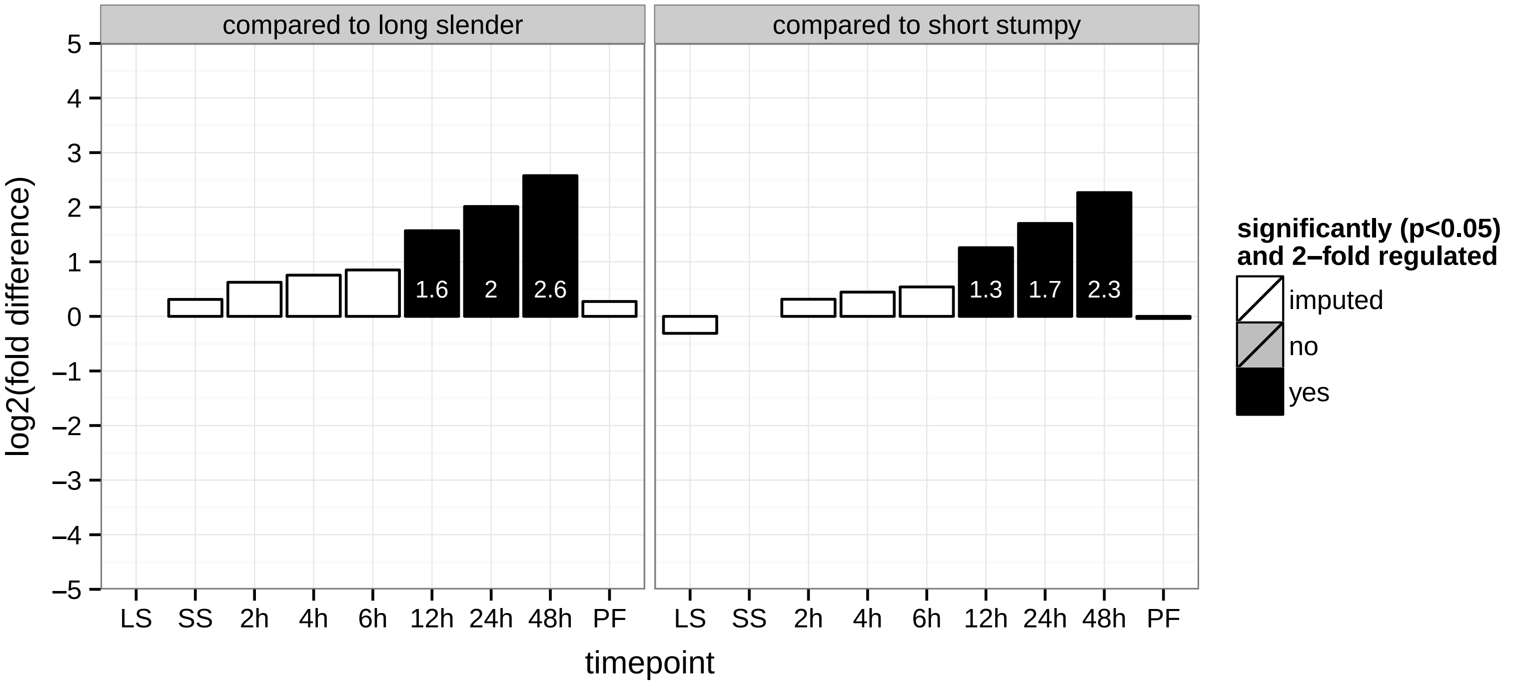
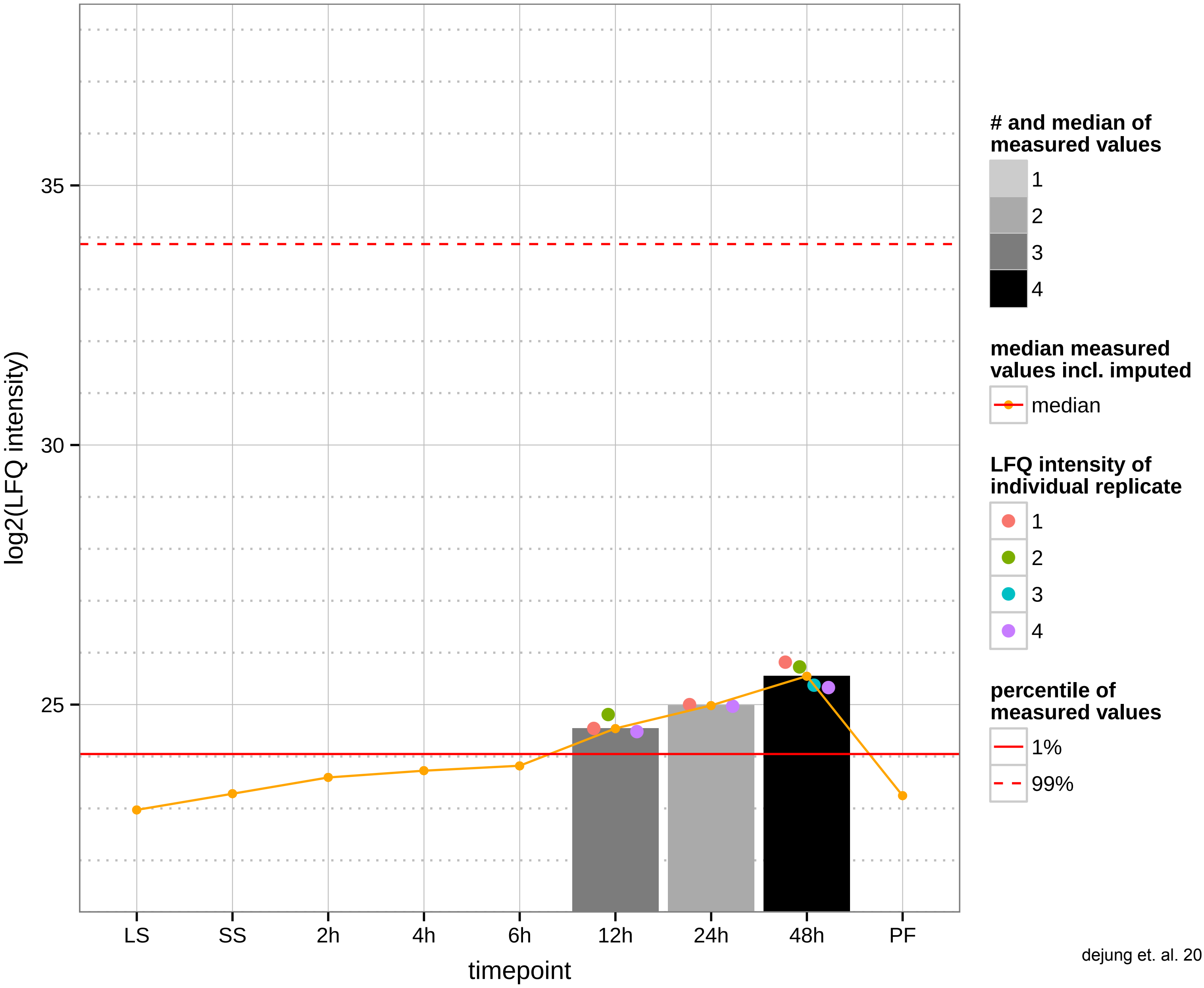
NADH dehydrogenase subunit NB6M, putative, NB6M, Complex 1, NADH−ubiquinone oxidoreductase chain NB6M
Tb927.11.8910
AGOF: NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity
AGOC: NADH dehydrogenase complex, mitochondrial membrane, mitochondrion
AGOP: NADH regeneration
PGOF: null
PGOC: null
PGOP: null





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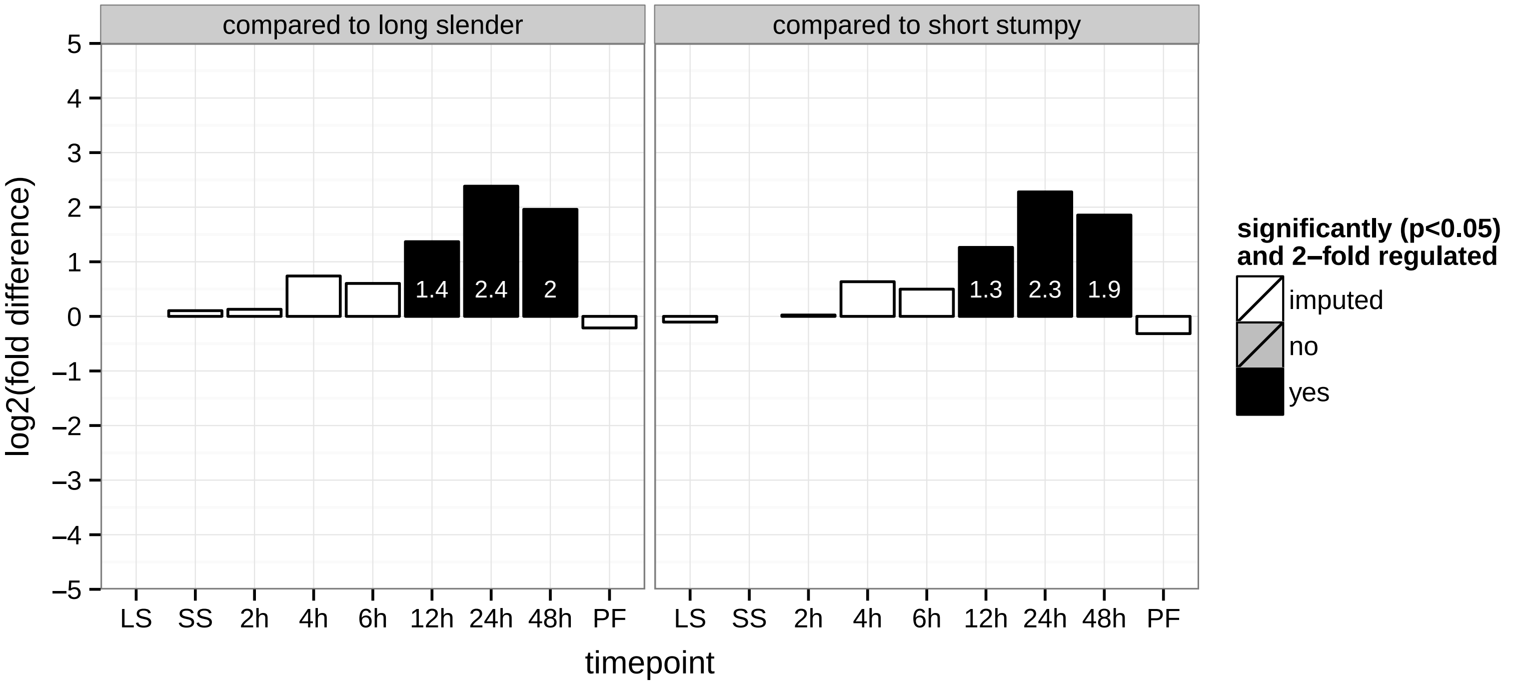
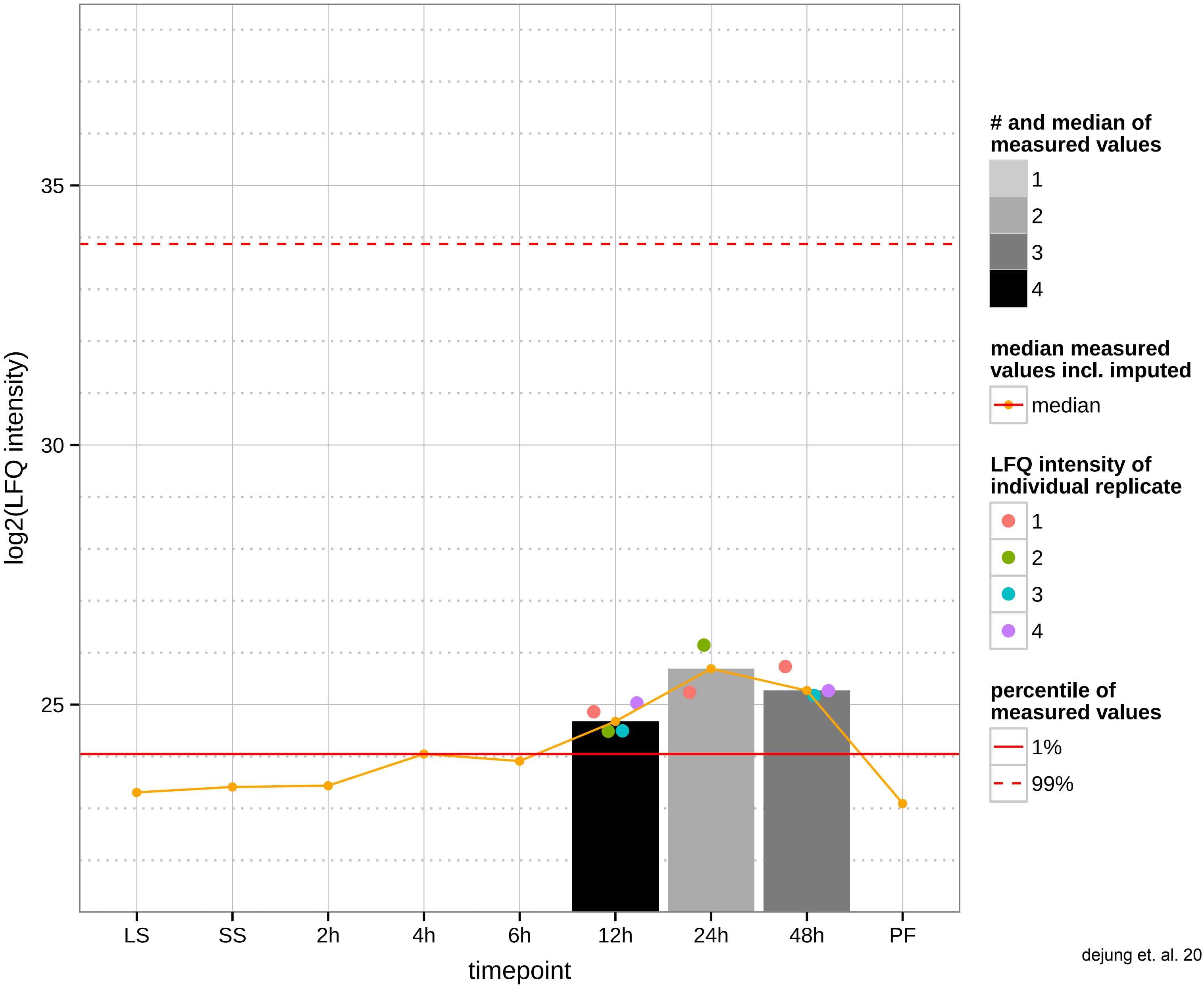
hypothetical protein, conserved
Tb927.11.9830
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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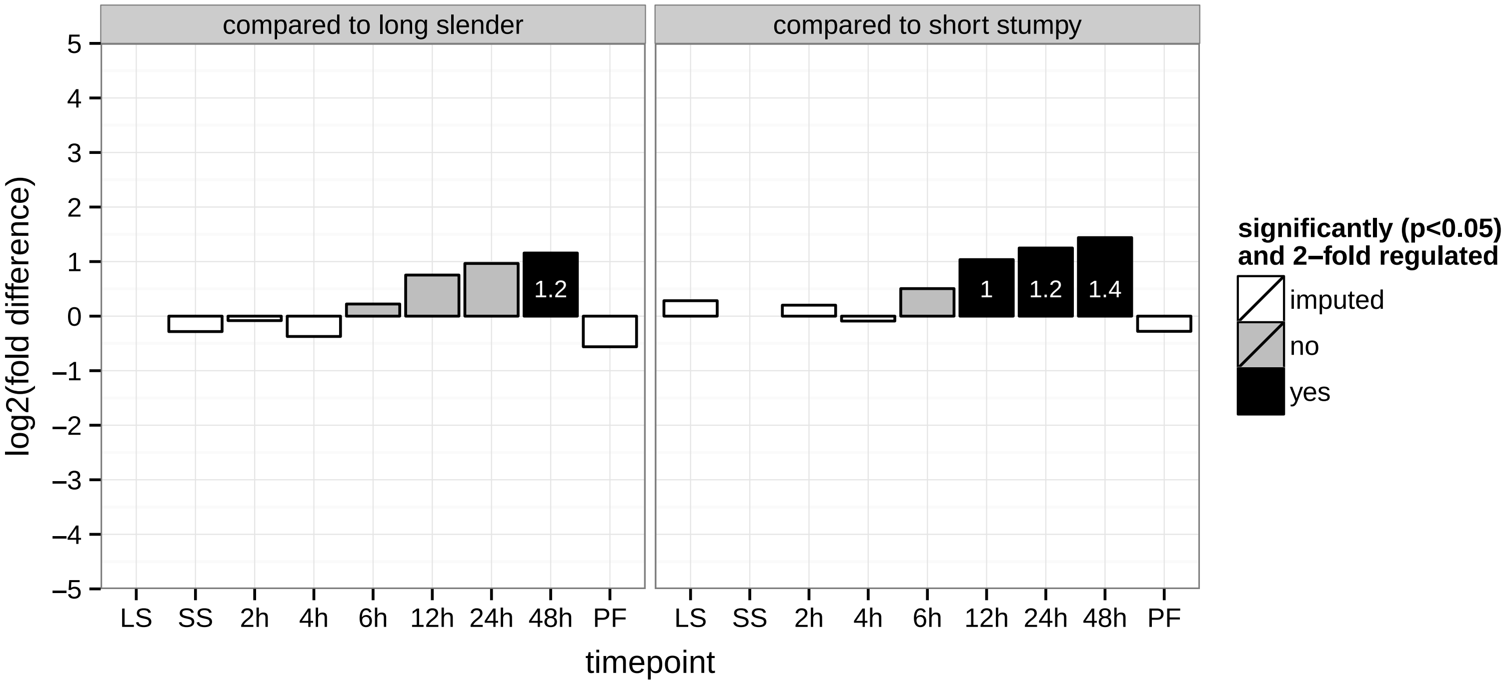
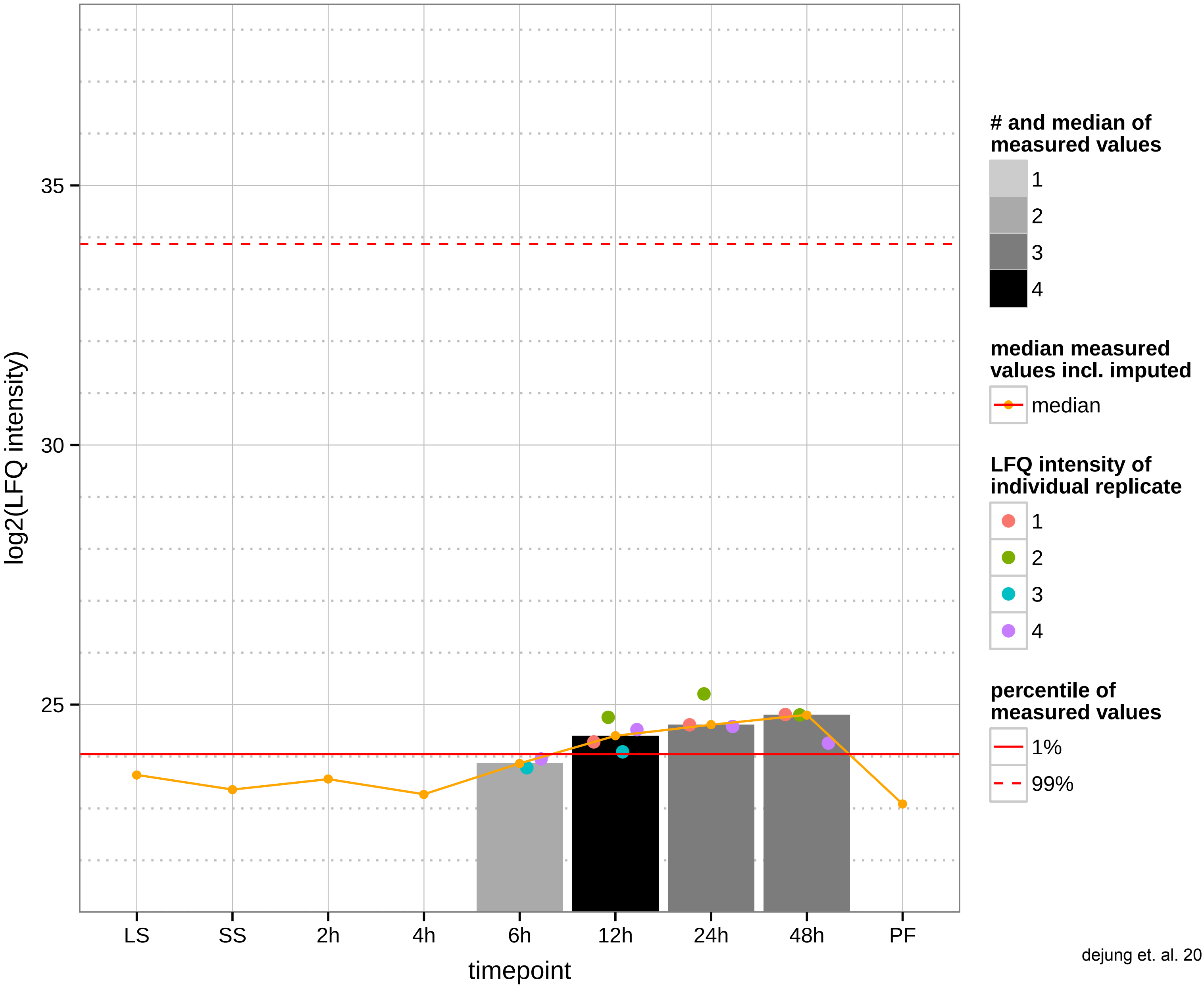
hypothetical protein, conserved
Tb927.11.9940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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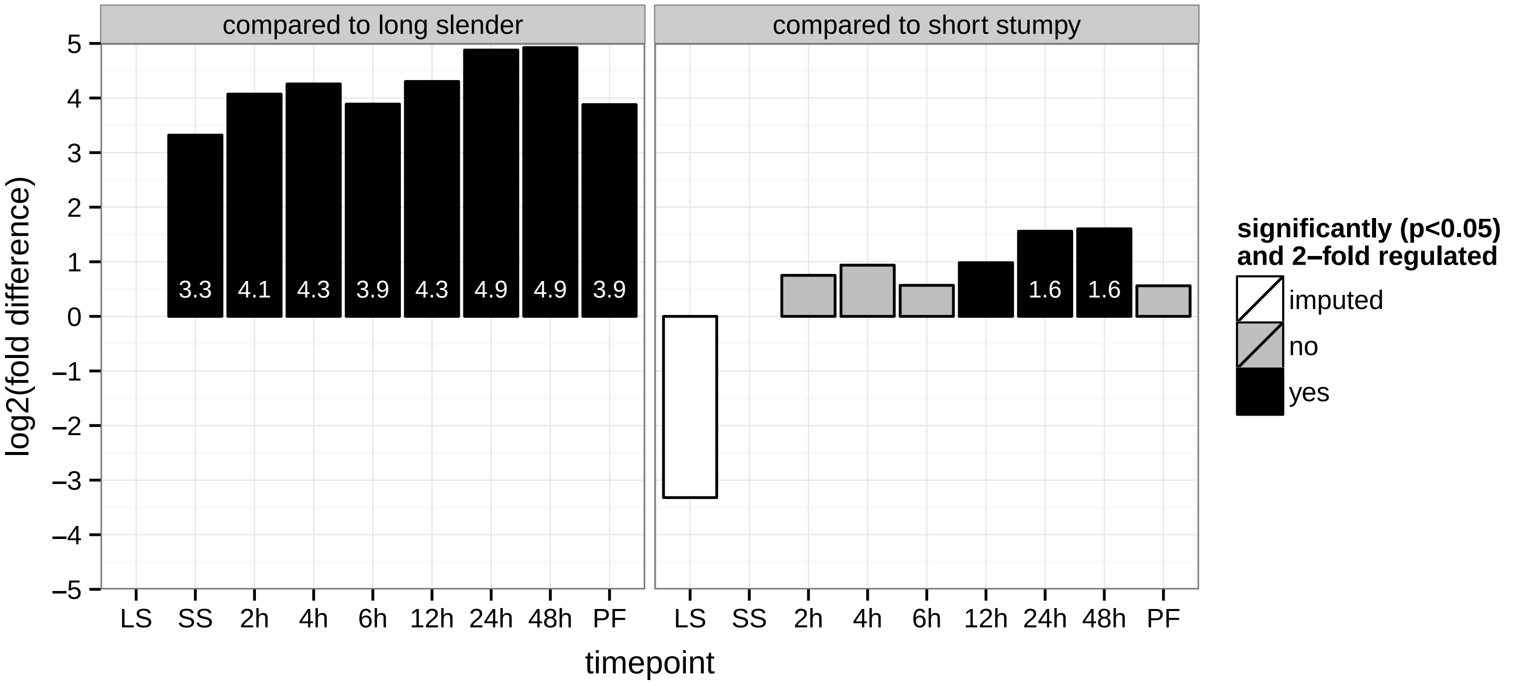
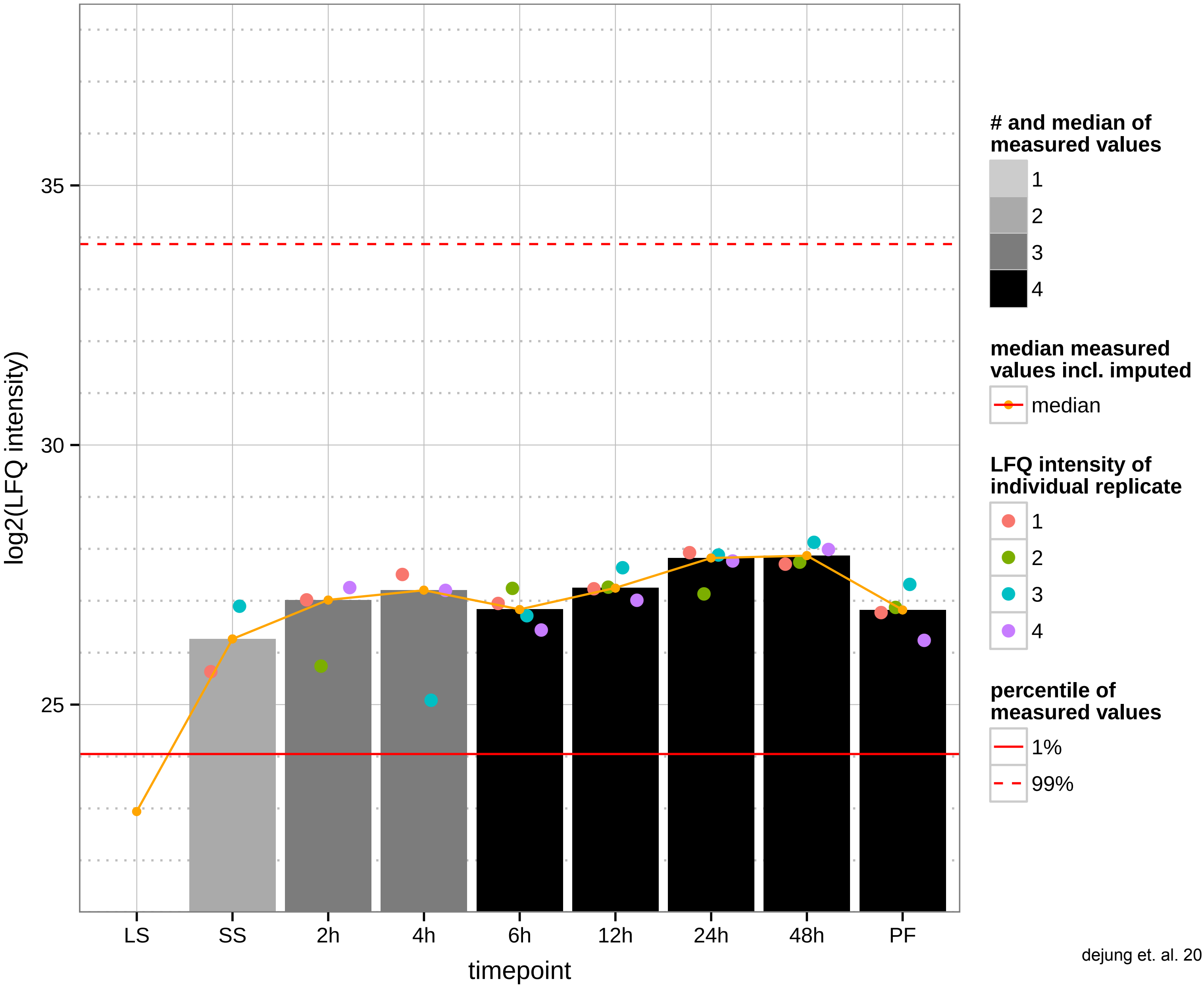
mitochondrial RNA binding complex 1 subunit (MRB1860)
Tb927.2.1860
AGOF: RNA binding
AGOC: mitochondrion
AGOP: cytidine to uridine editing, mRNA stabilization
PGOF: null
PGOC: null
PGOP: null





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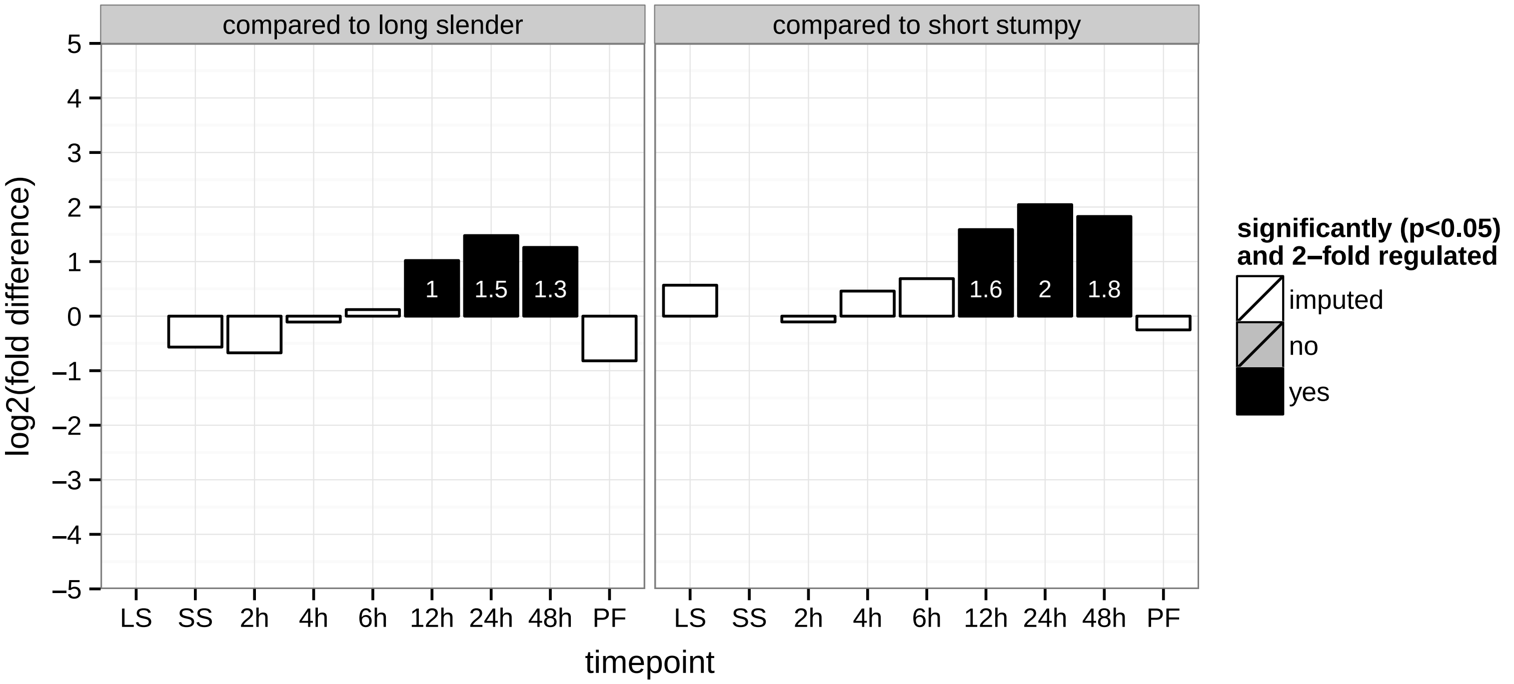
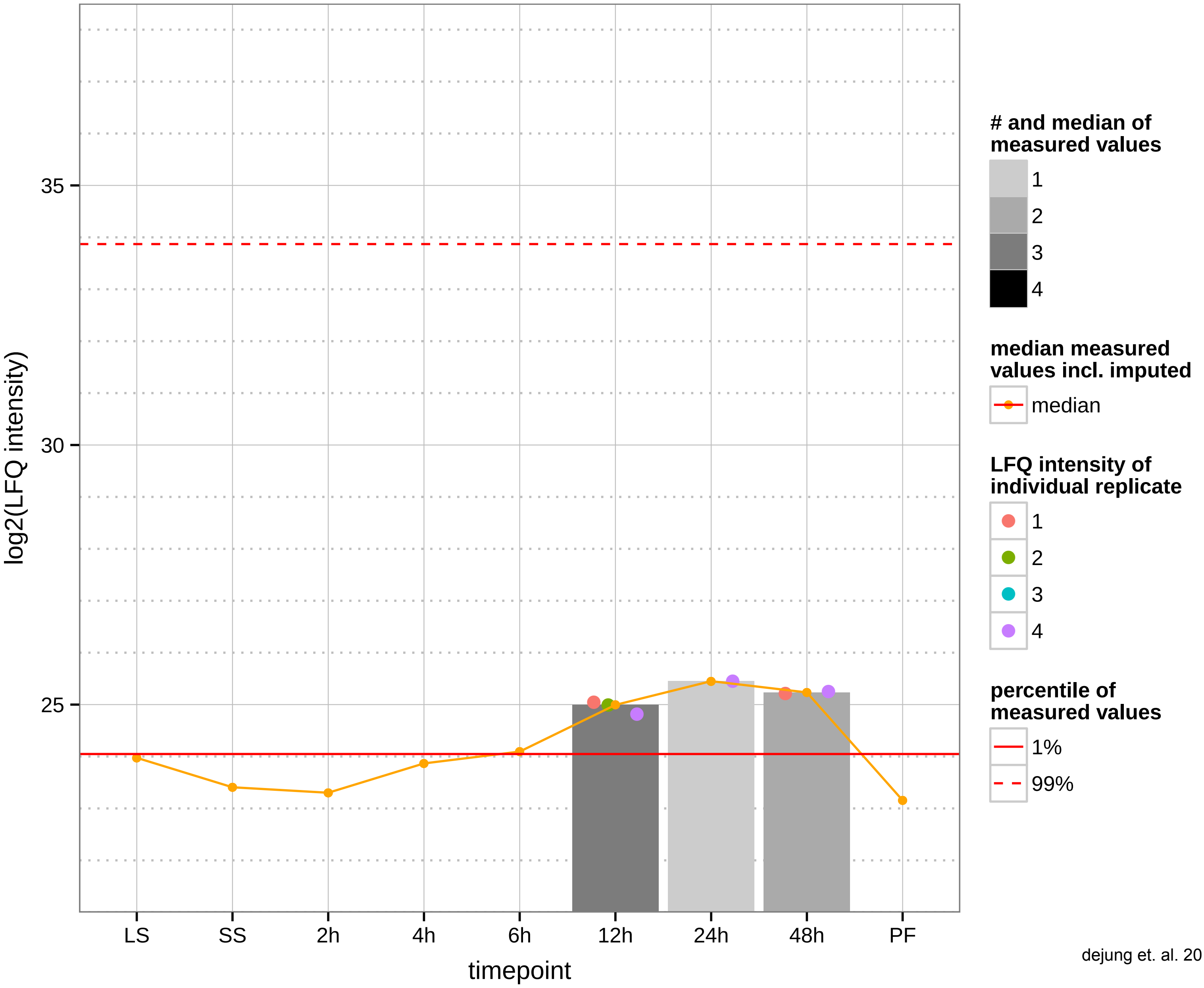
hypothetical protein, conserved
Tb927.2.3160
AGOF: null
AGOC: null
AGOP: null
PGOF: snoRNA binding
PGOC: null
PGOP: ribosome biogenesis, snRNA pseudouridine synthesis





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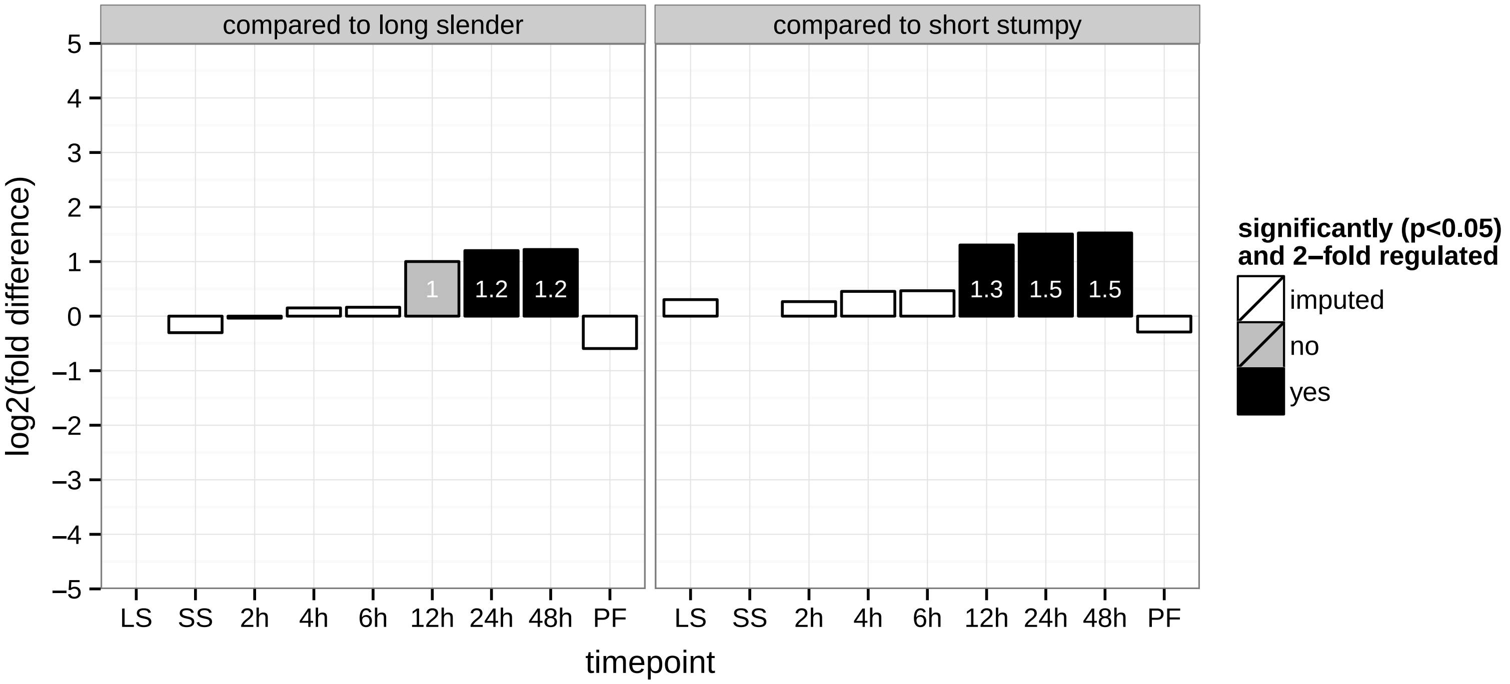
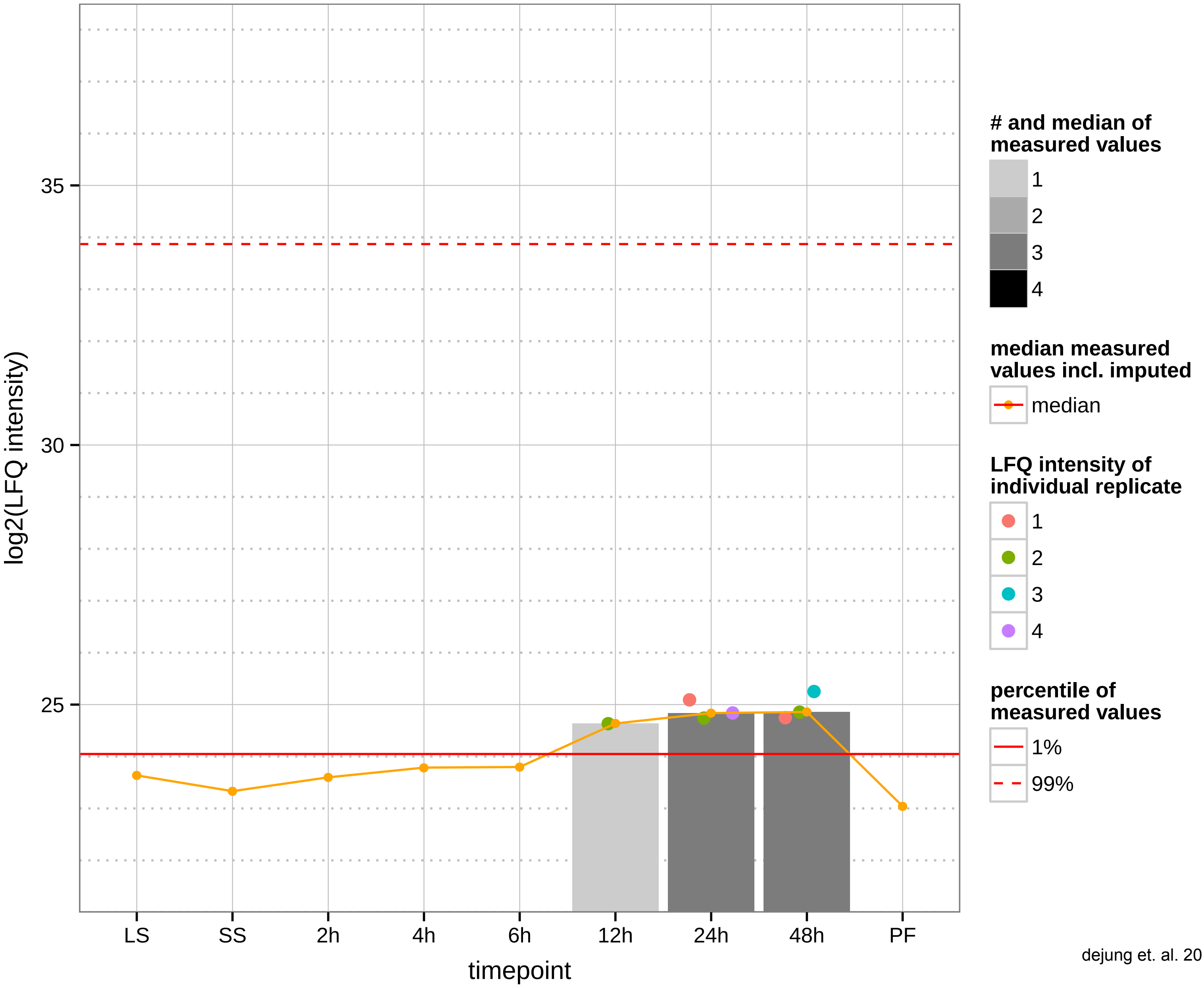
aldo–keto reductase, putative
Tb927.2.5180
AGOF: alditol:NADP+ 1–oxidoreductase activity
AGOC: mitochondrion
AGOP: oxidation–reduction process
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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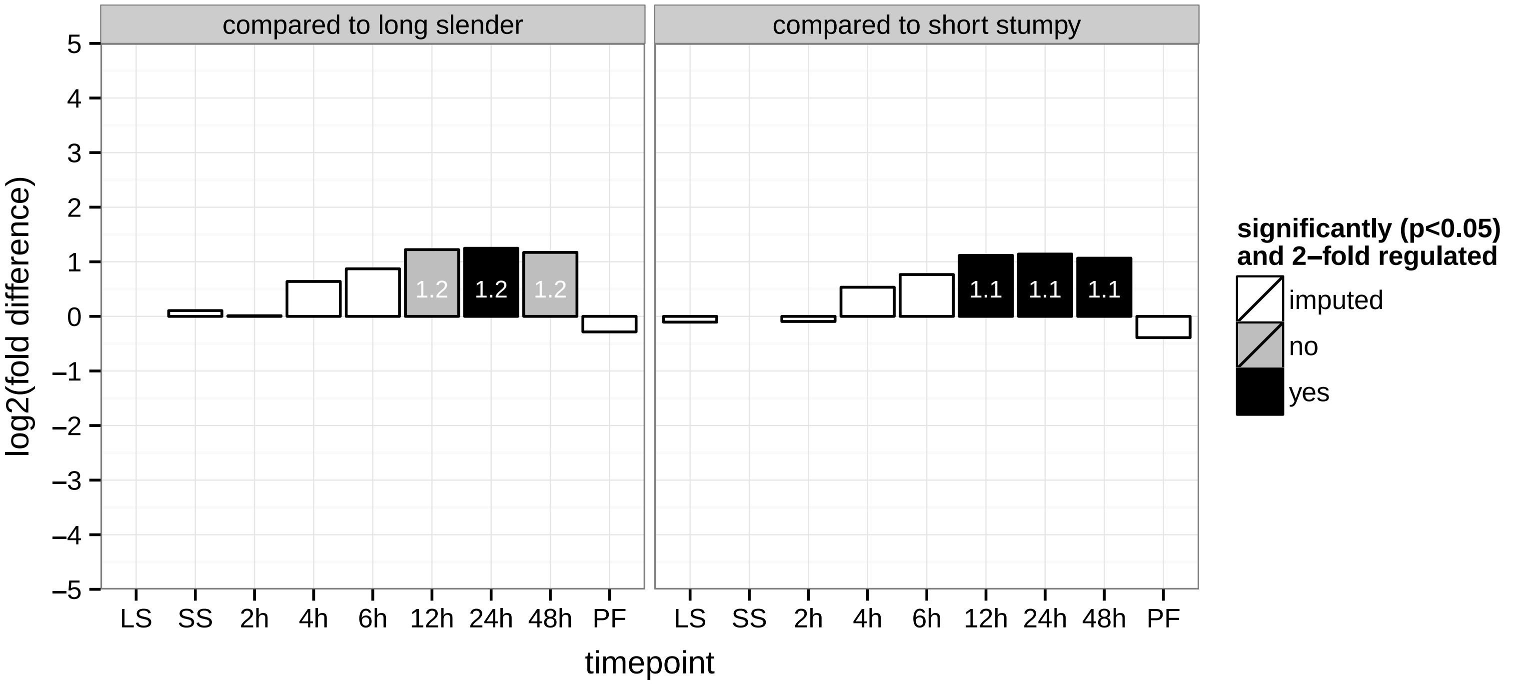
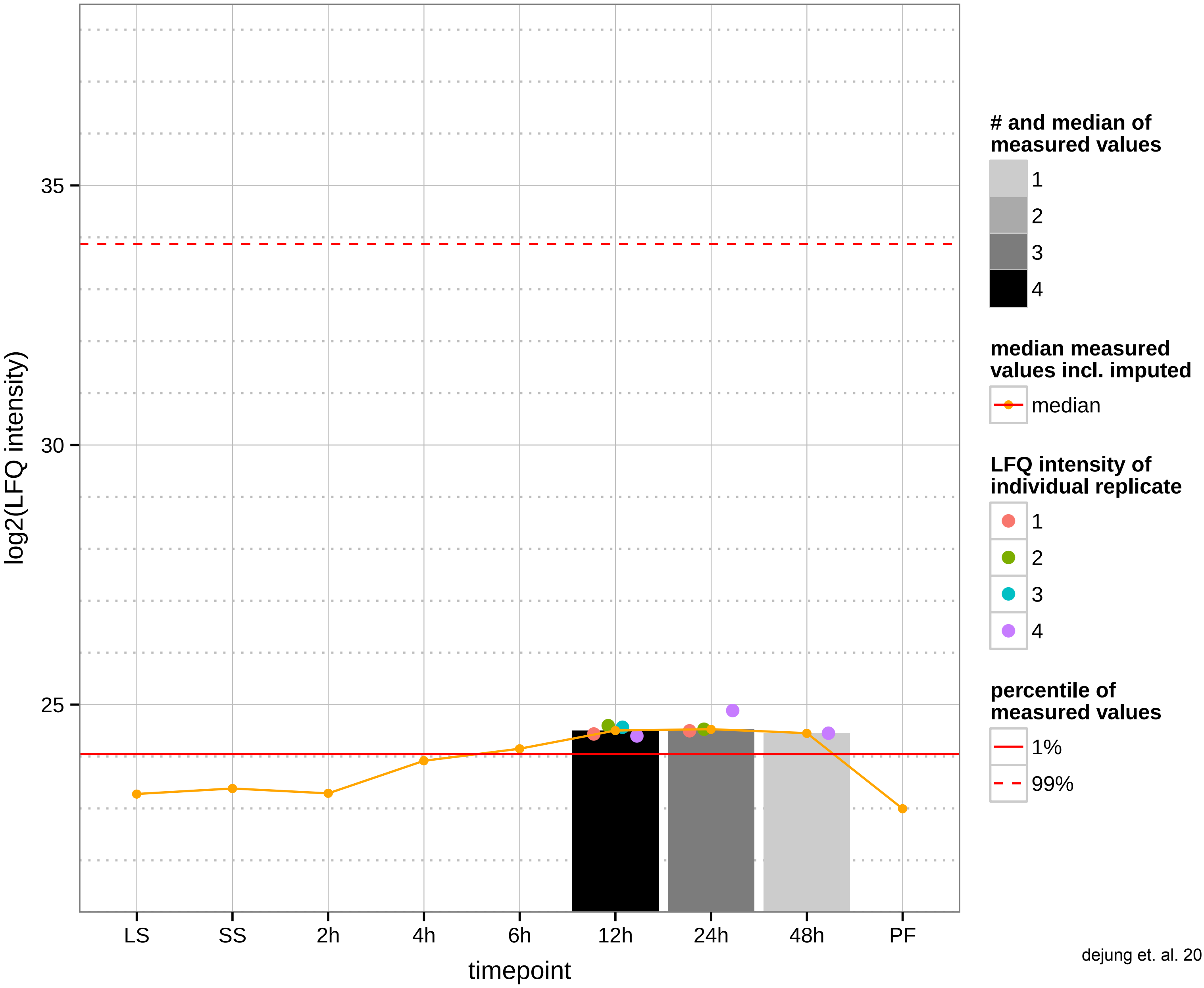
hypothetical protein, conserved
Tb927.3.2010
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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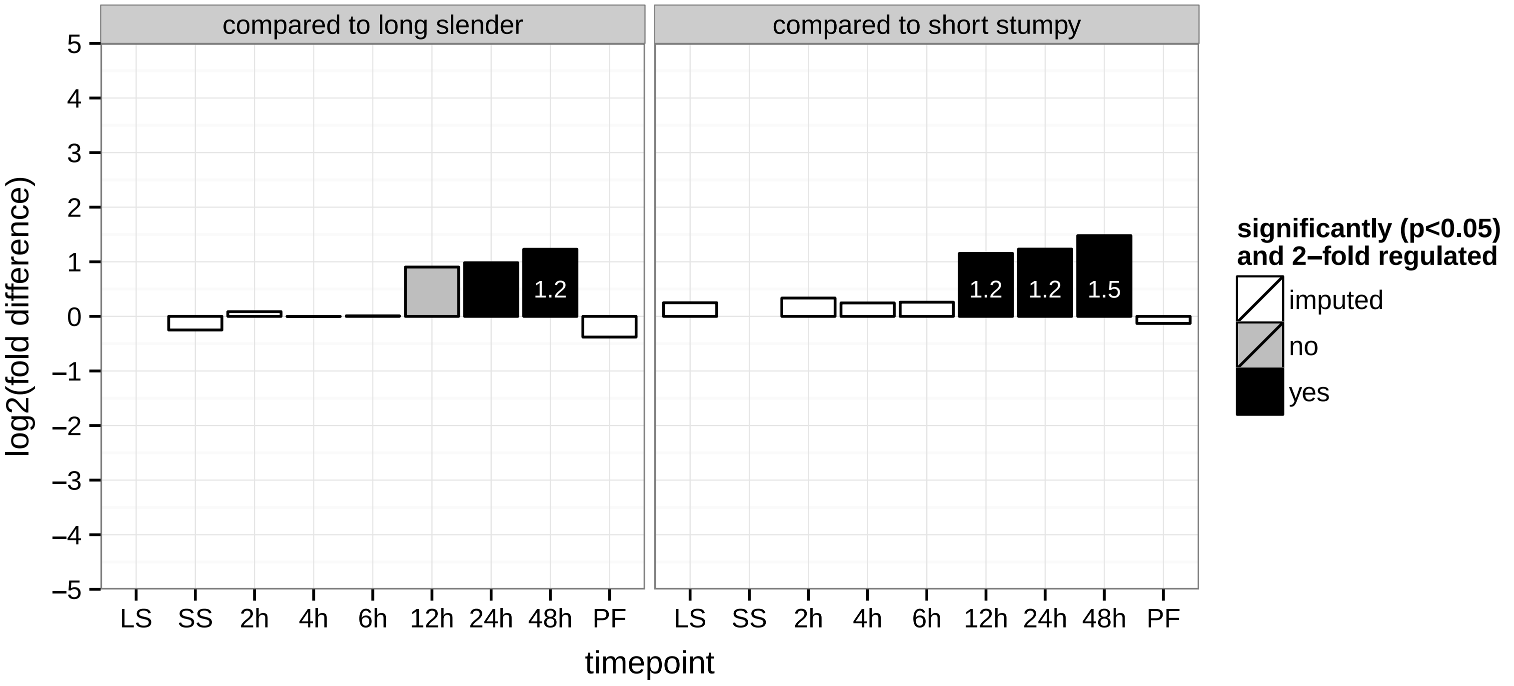
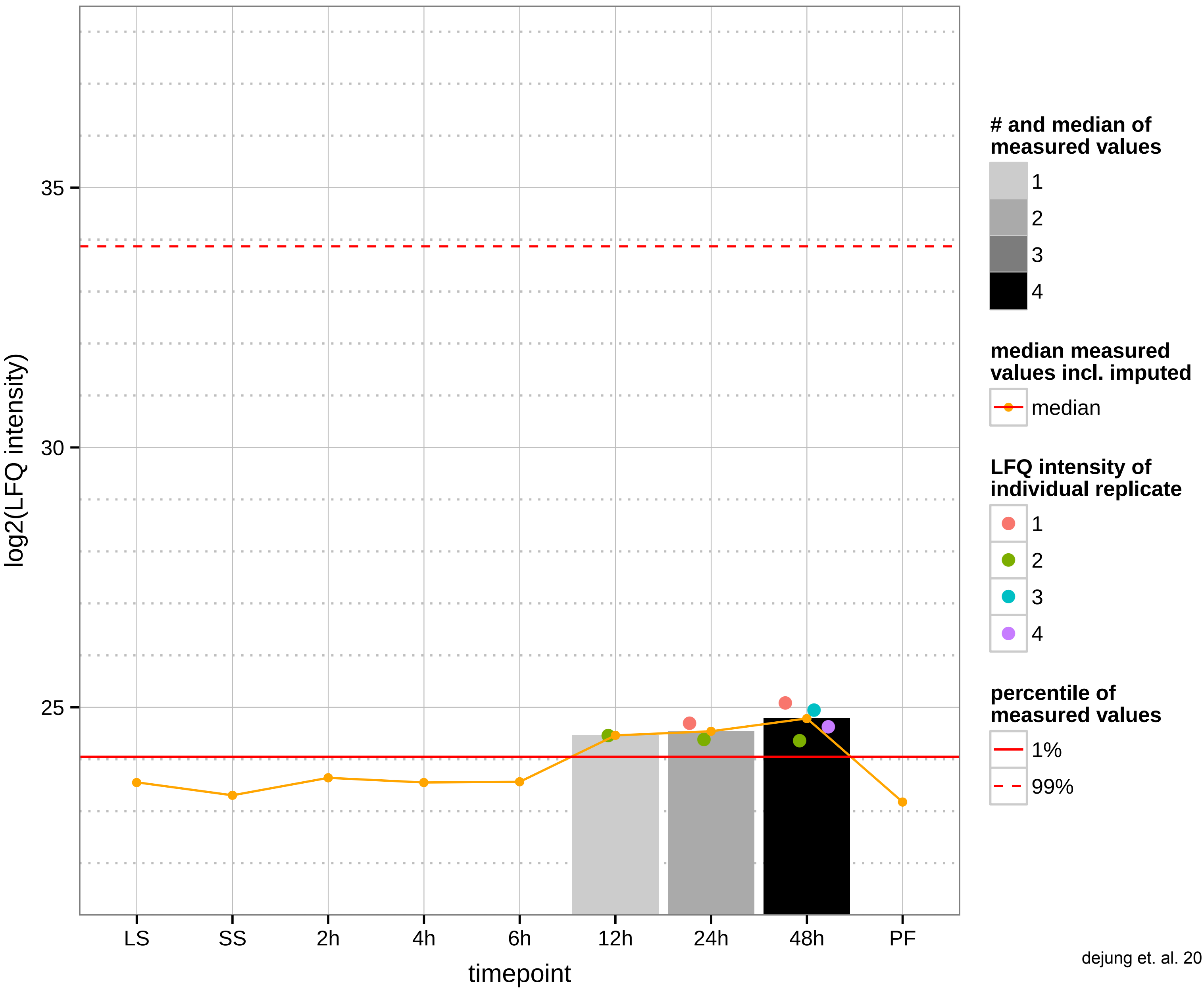
chaperone protein DNAj, putative
Tb927.3.2290
AGOF: heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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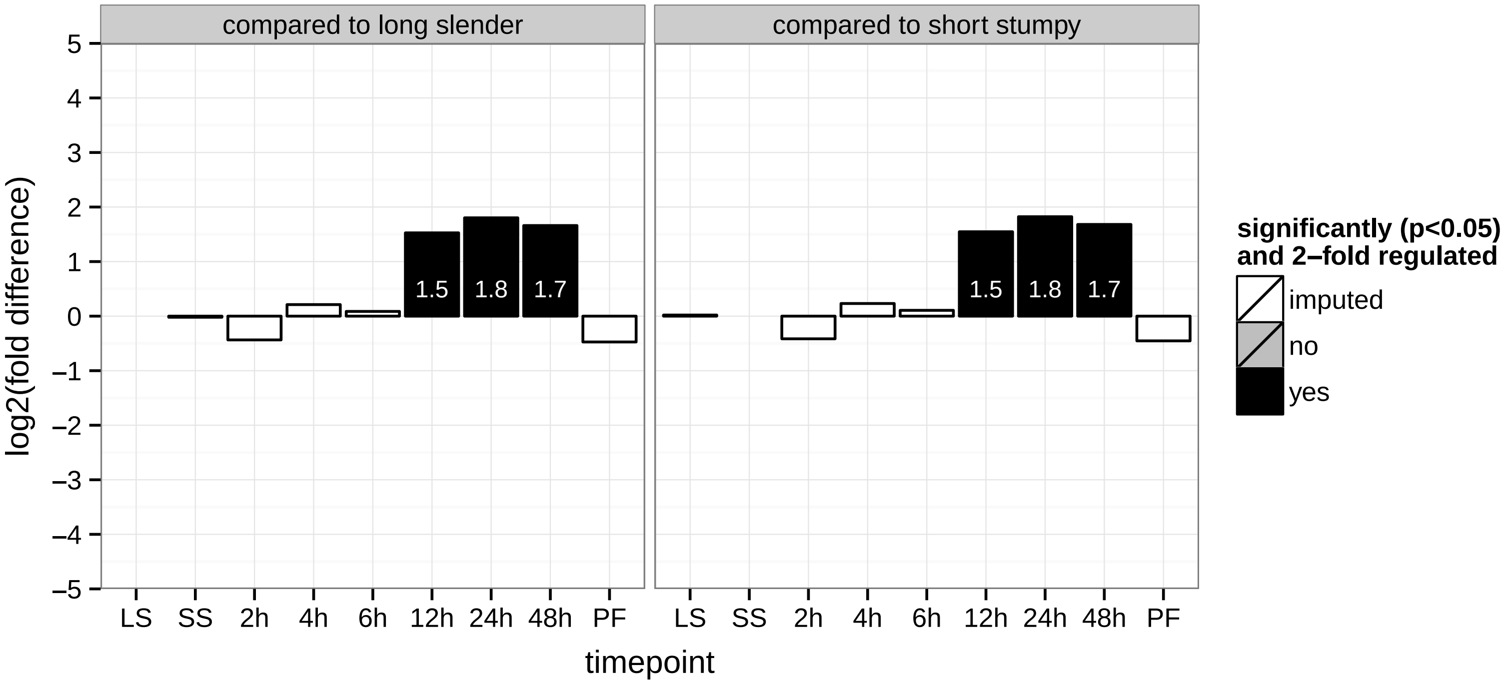
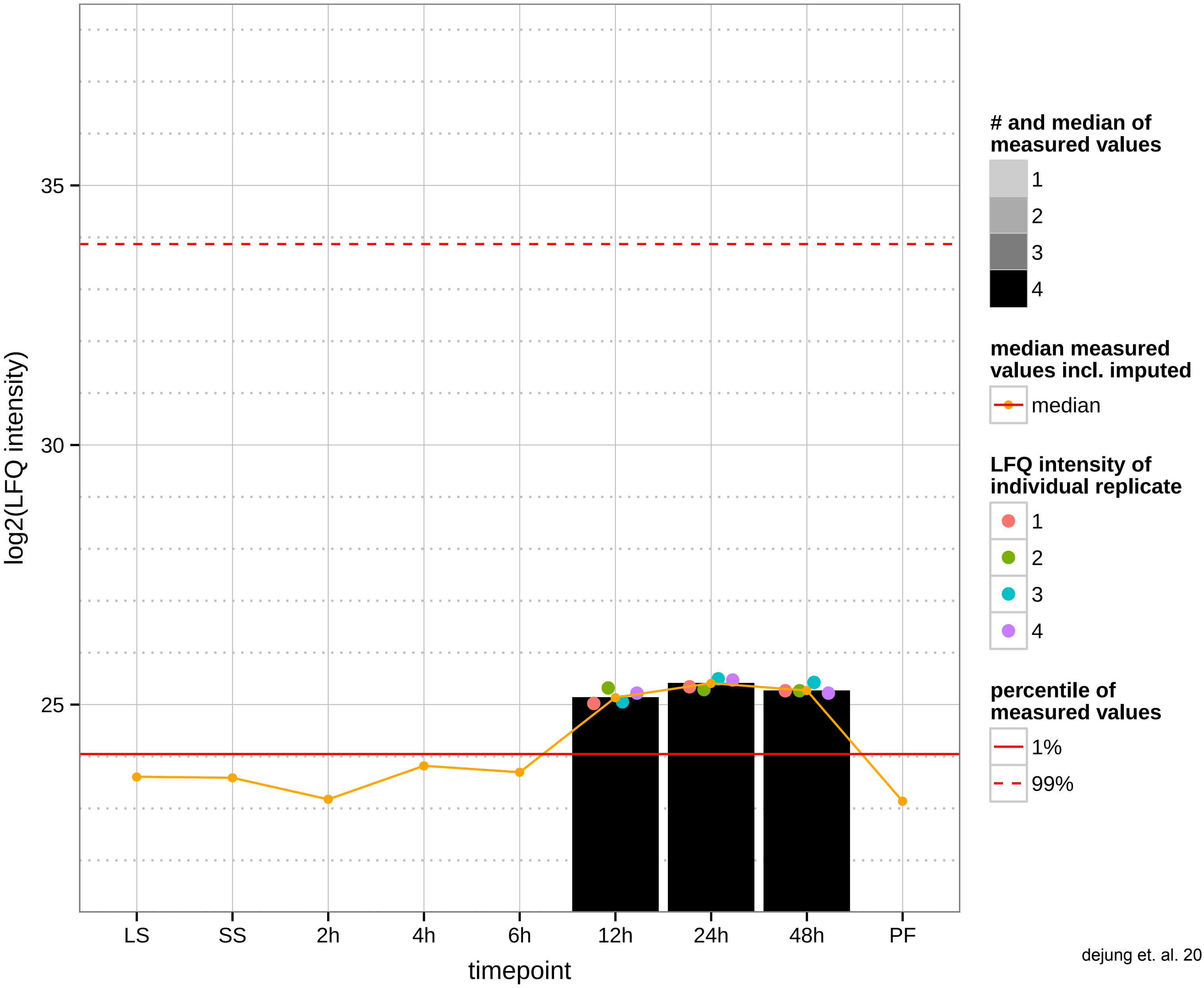
hypothetical protein, conserved
Tb927.3.3950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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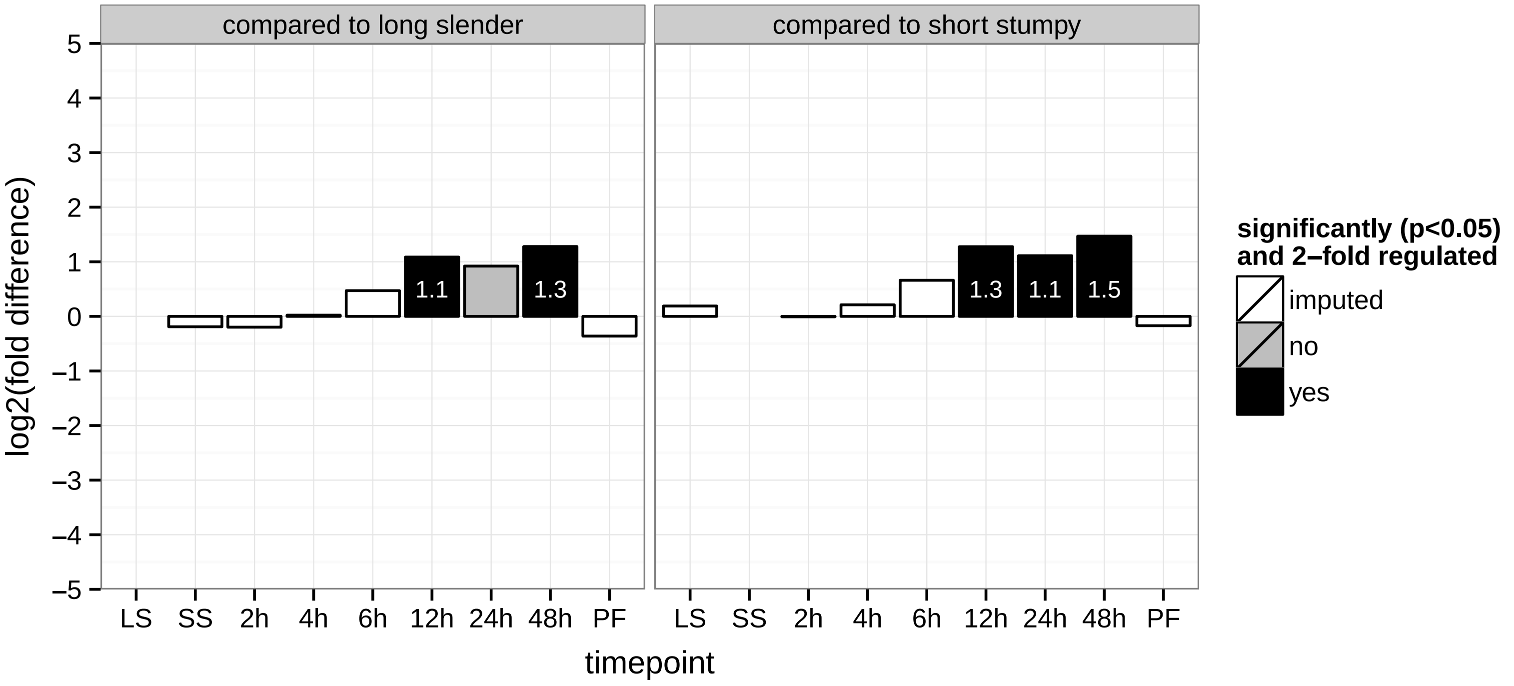
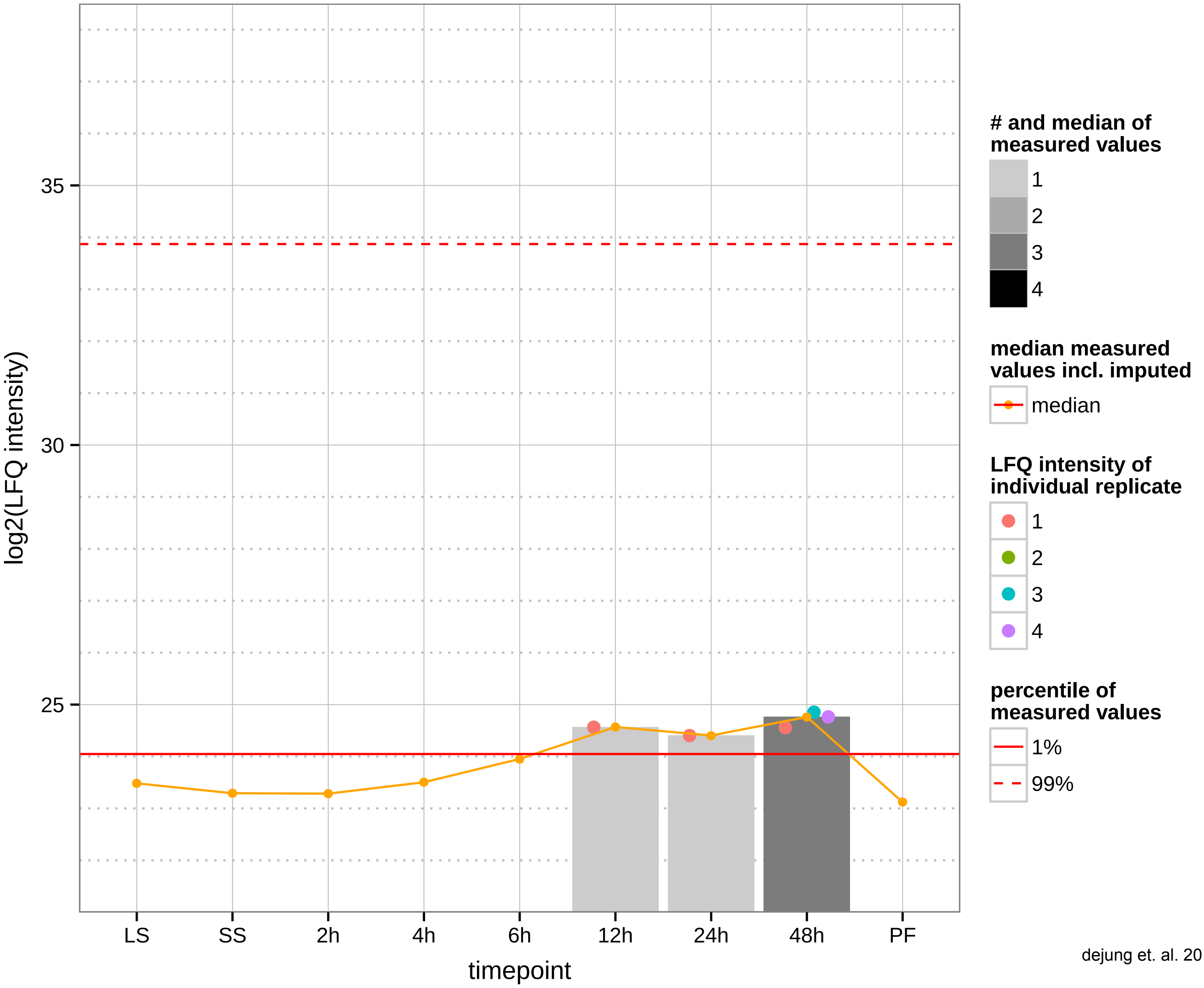
hypothetical protein, conserved, leucine−rich repeat protein (LRRP), putative
Tb927.3.4770;Tb927.3.4730
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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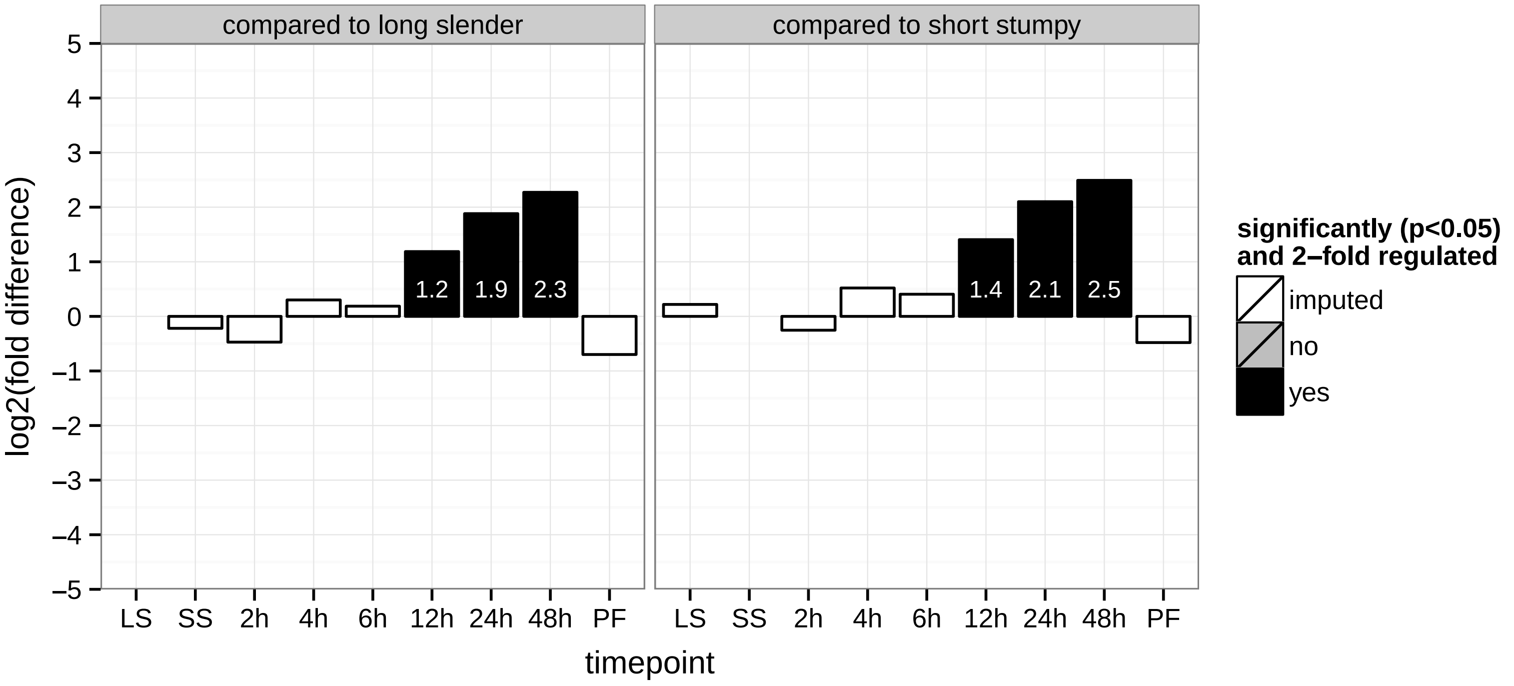
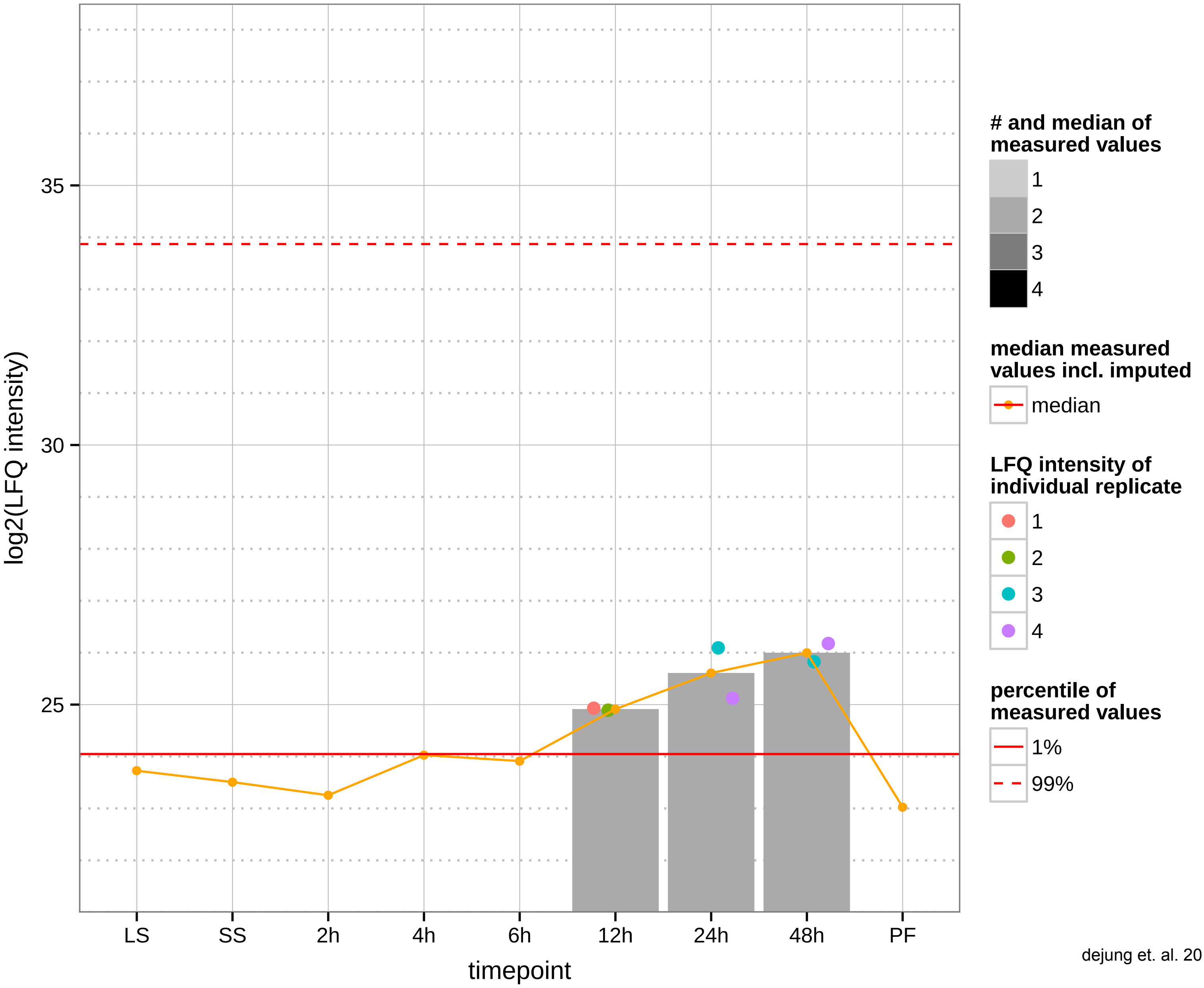
hypothetical protein, conserved
Tb927.3.4870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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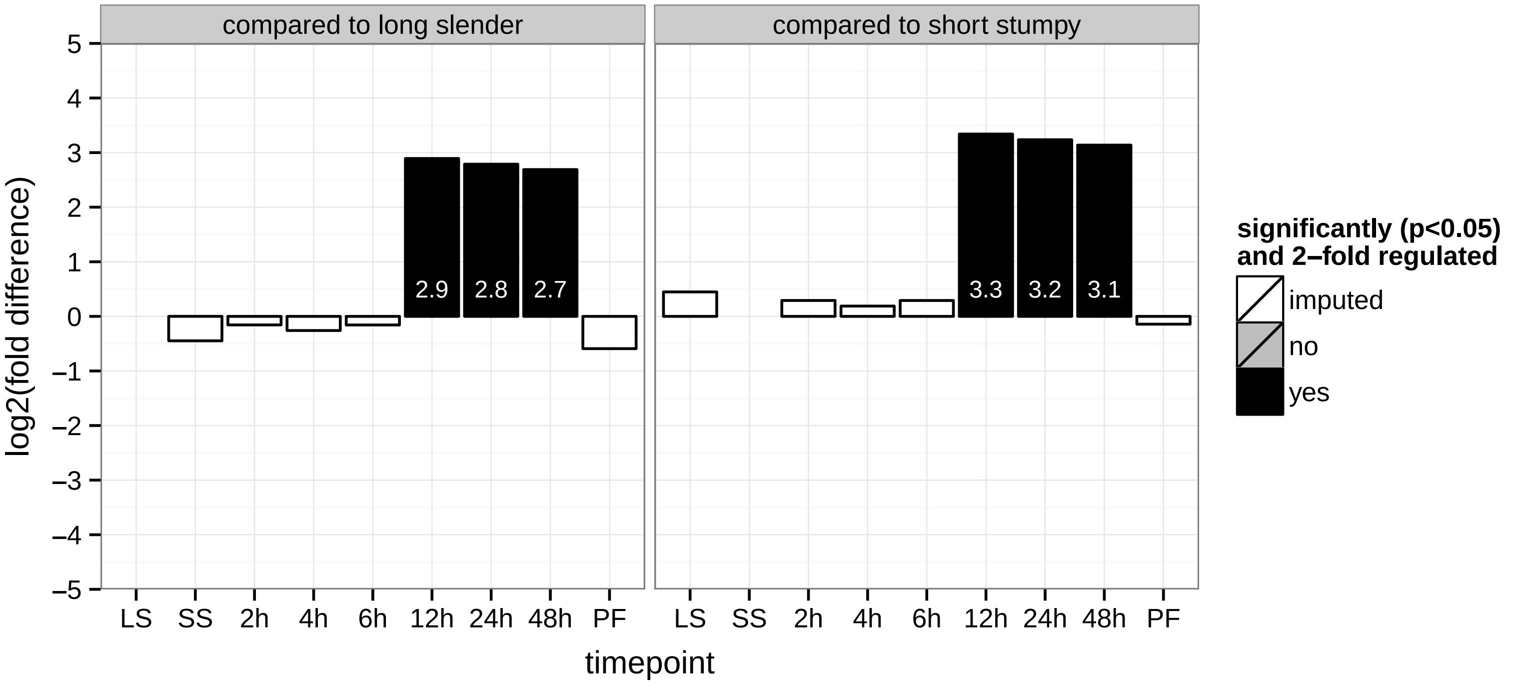
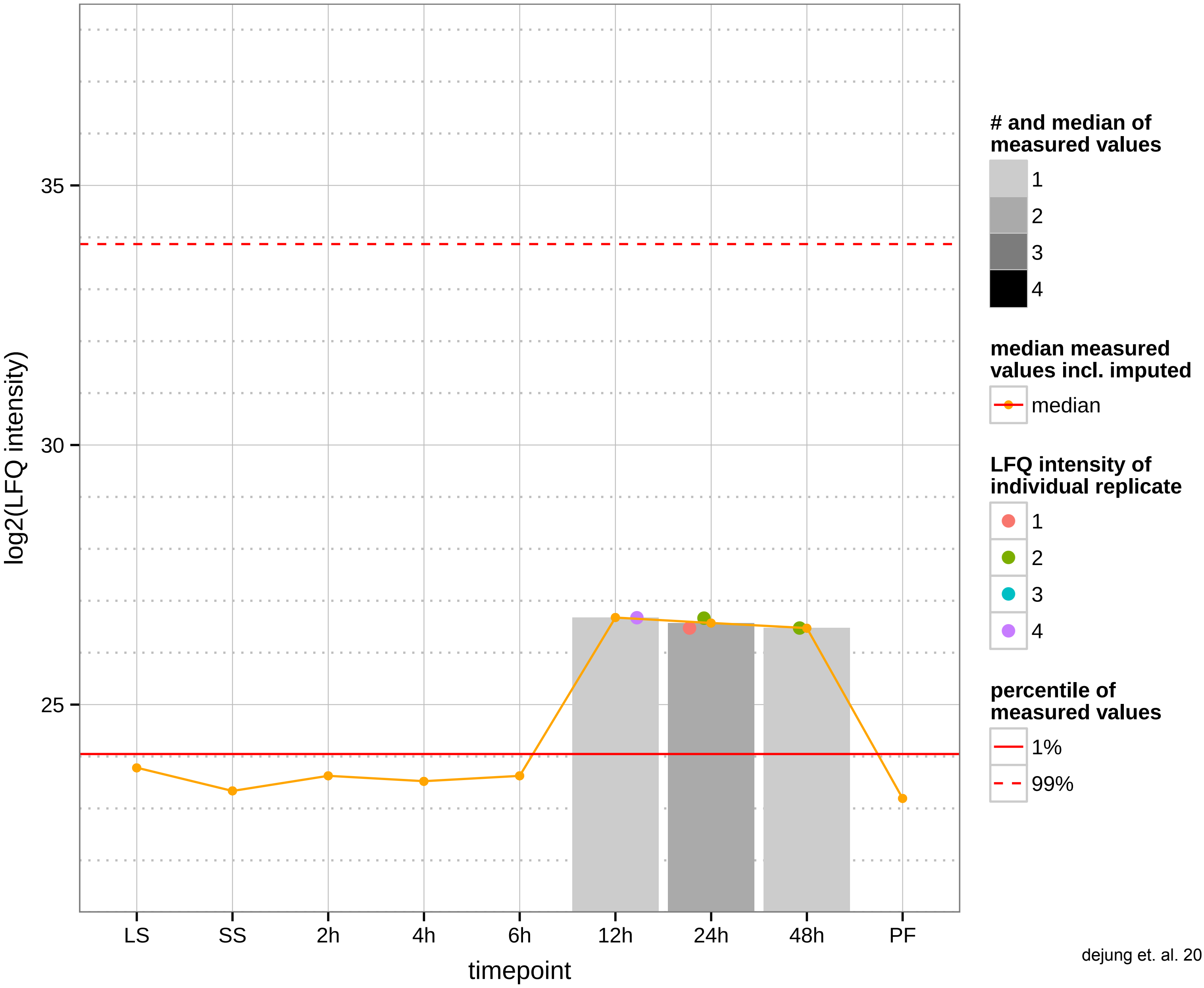
hypothetical protein, conserved
Tb927.3.5210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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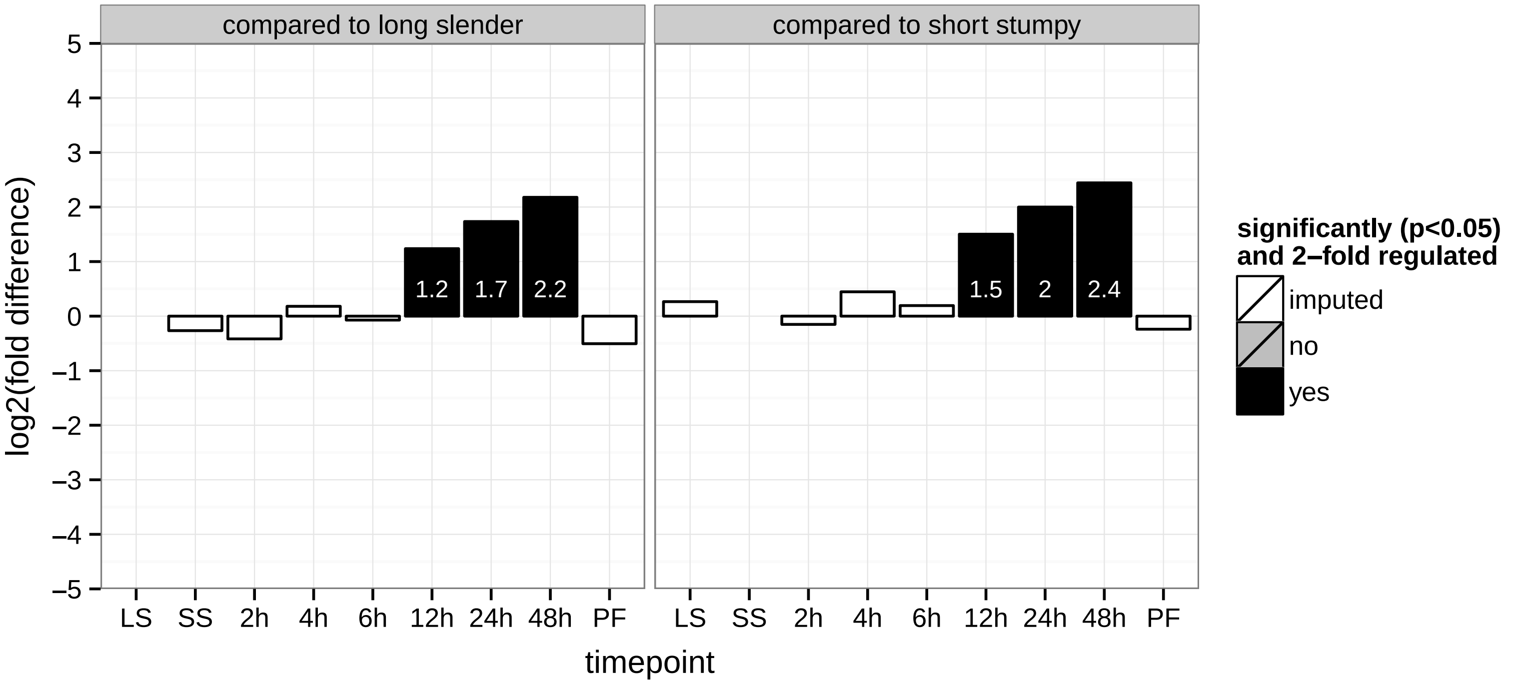
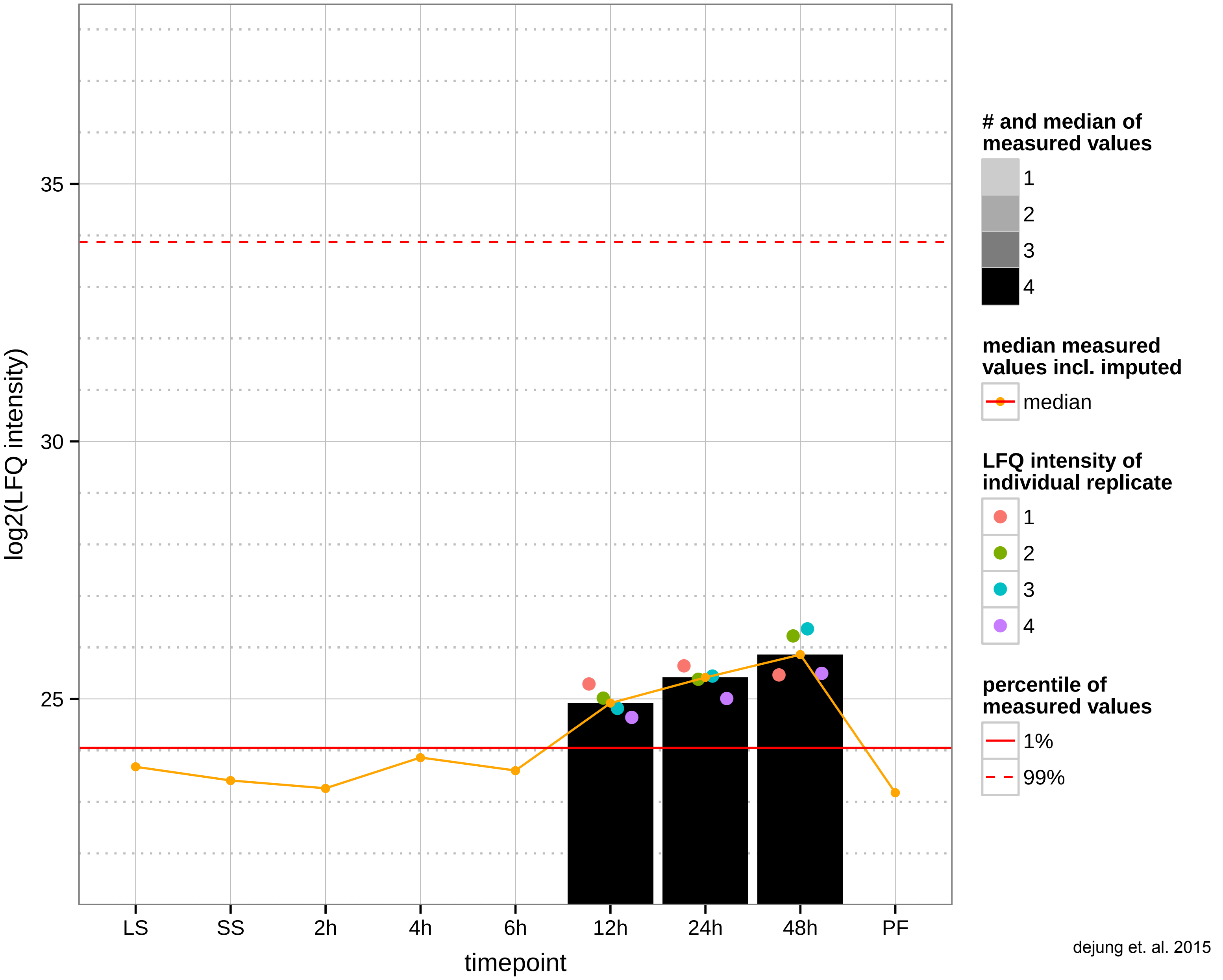
adenosine transporter, putative
Tb927.3.590
AGOF: nucleoside transmembrane transporter activity
AGOC: integral to membrane, membrane
AGOP: nucleoside transport
PGOF: nucleoside transmembrane transporter activity
PGOC: integral to membrane
PGOP: transport





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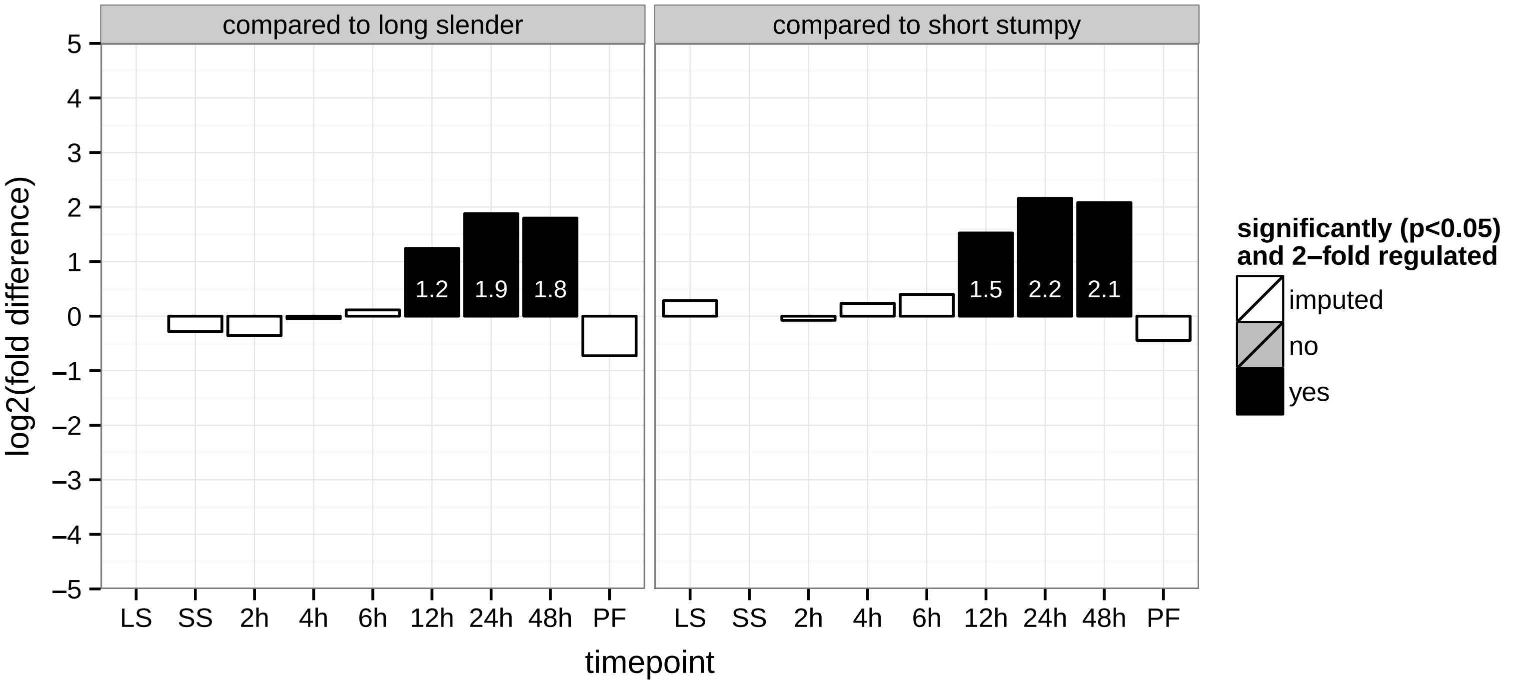
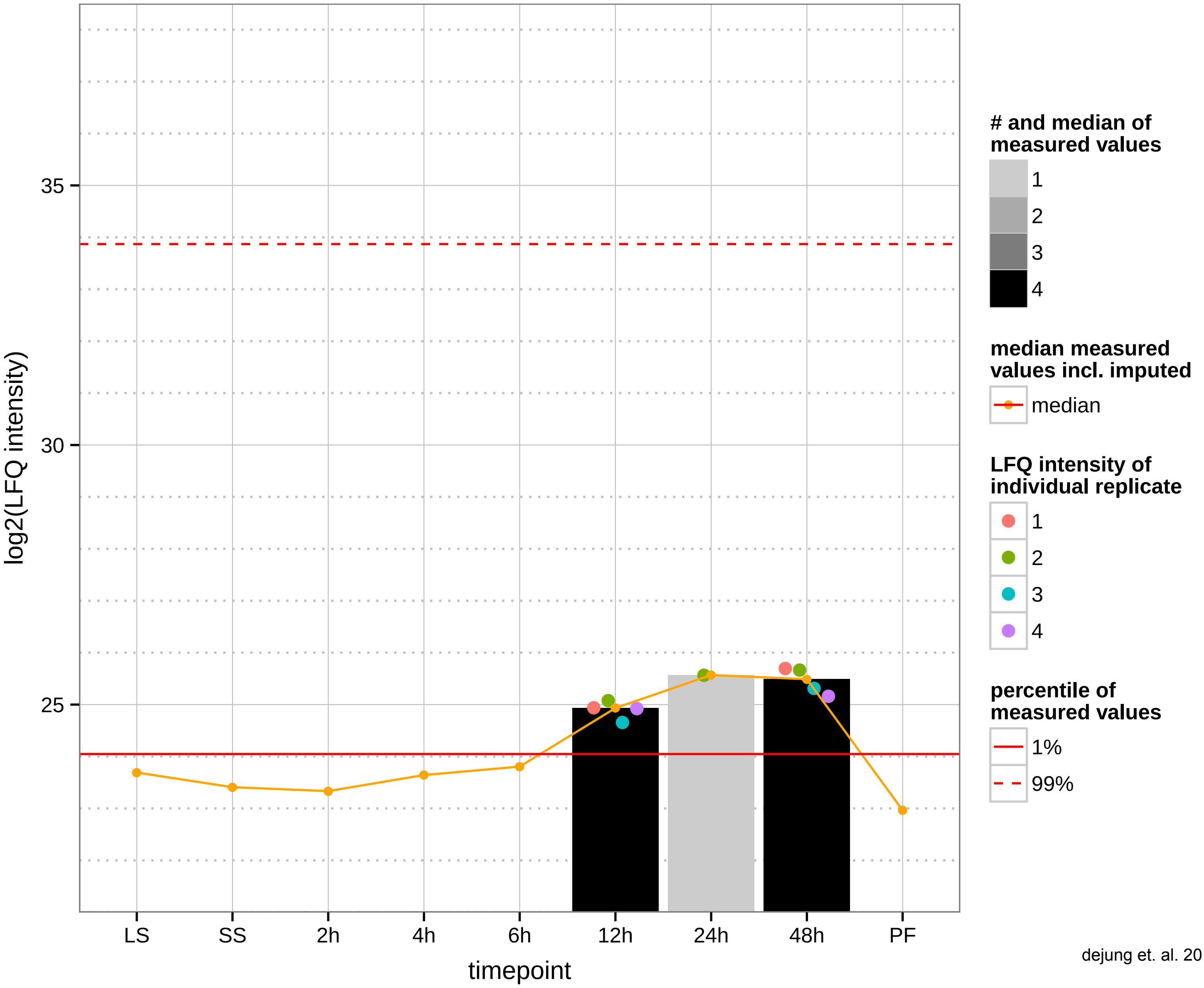
hypothetical protein, conserved
Tb927.4.1760
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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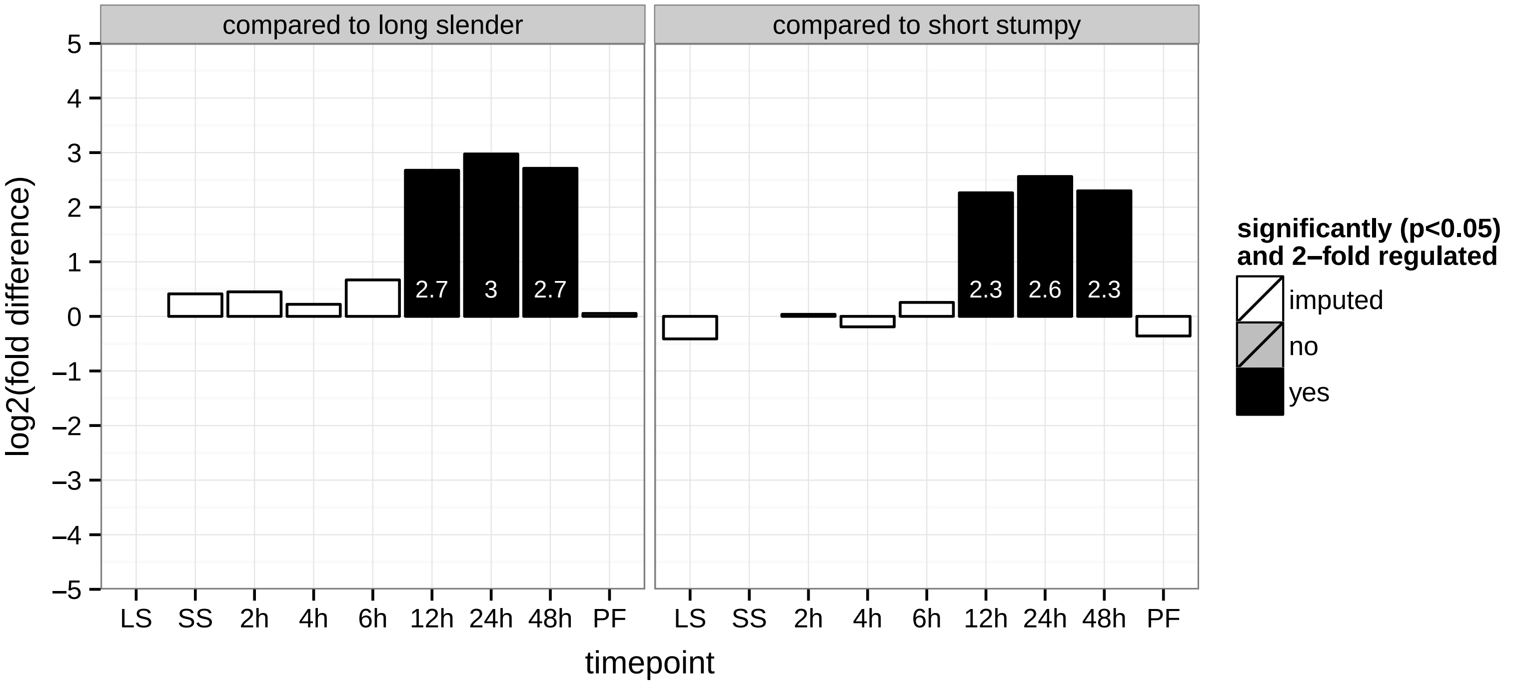
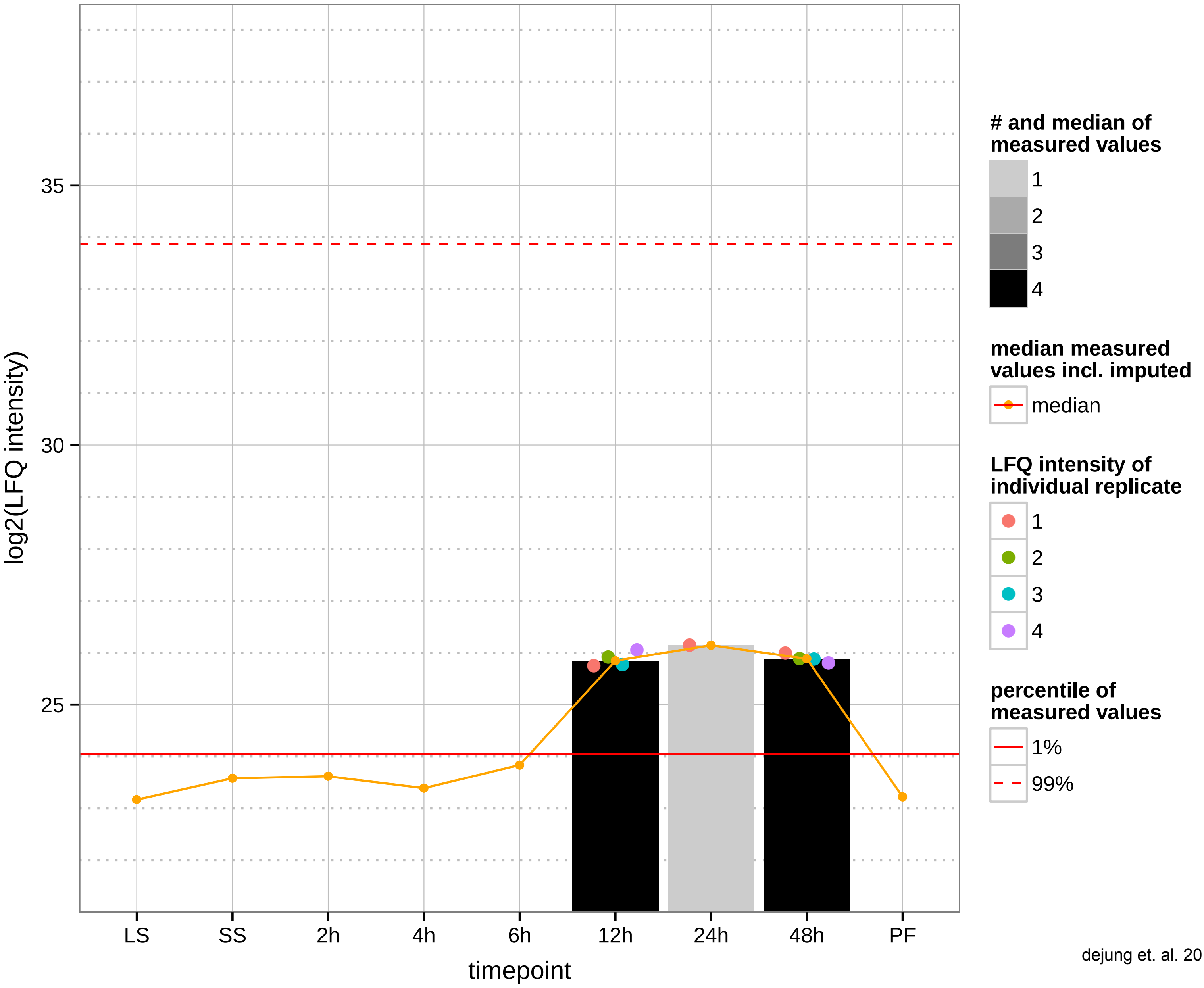
hypothetical protein, conserved
Tb927.4.4110
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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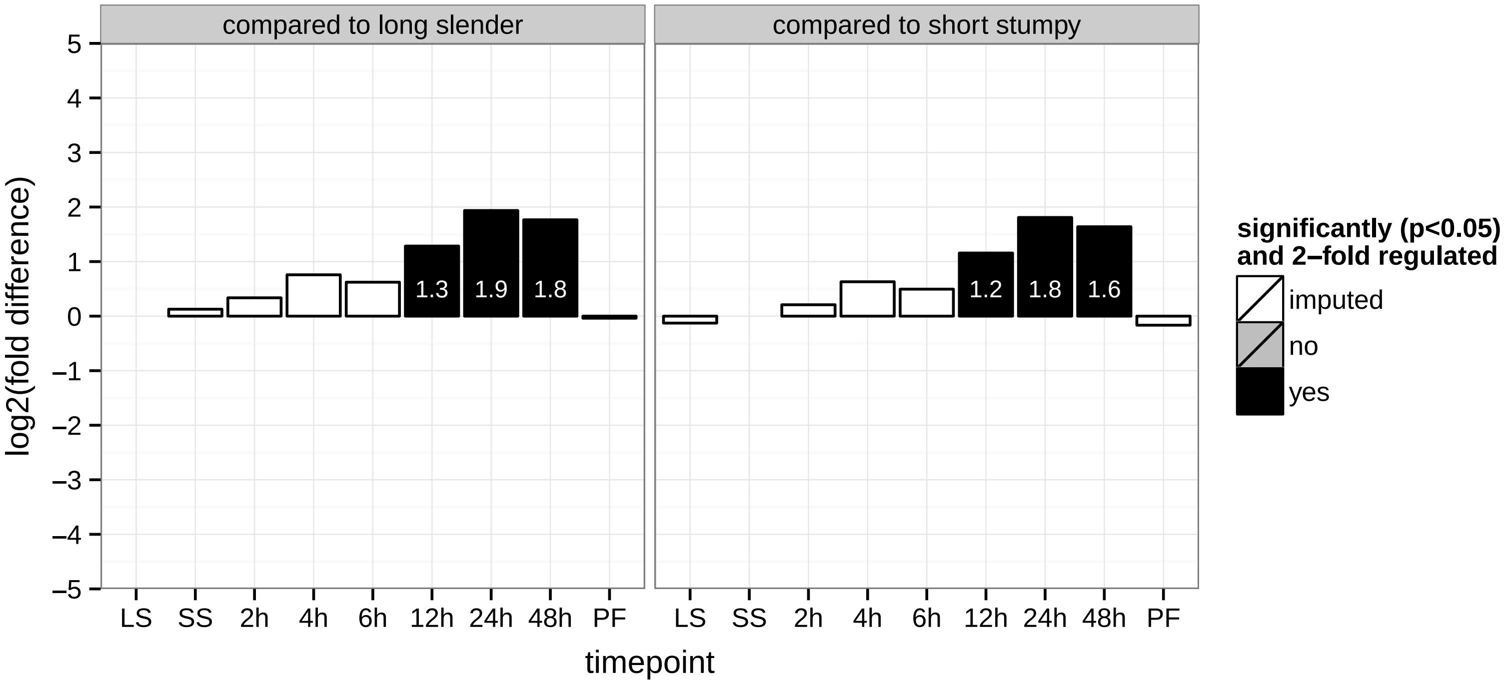
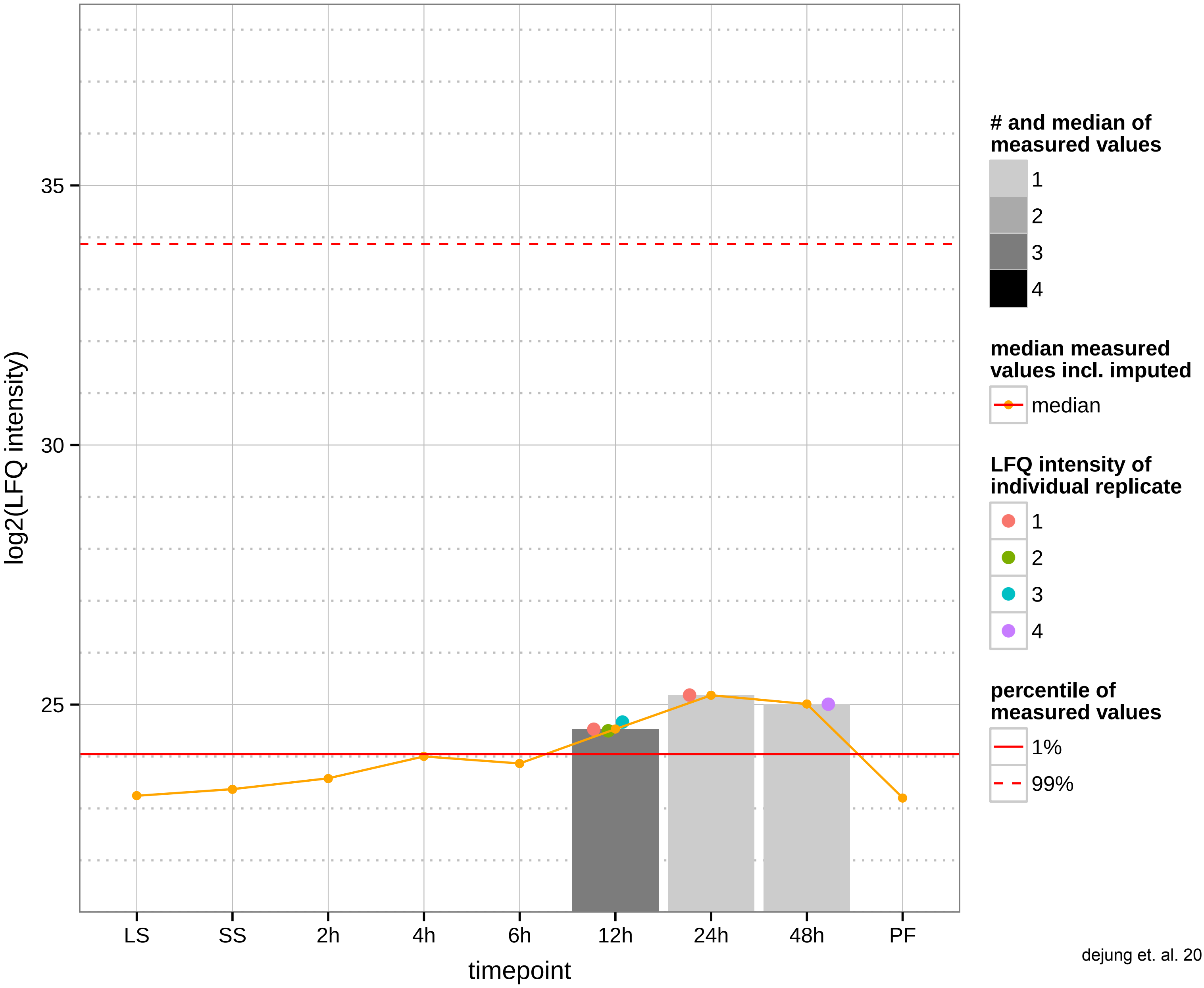
hypothetical protein, conserved
Tb927.4.940
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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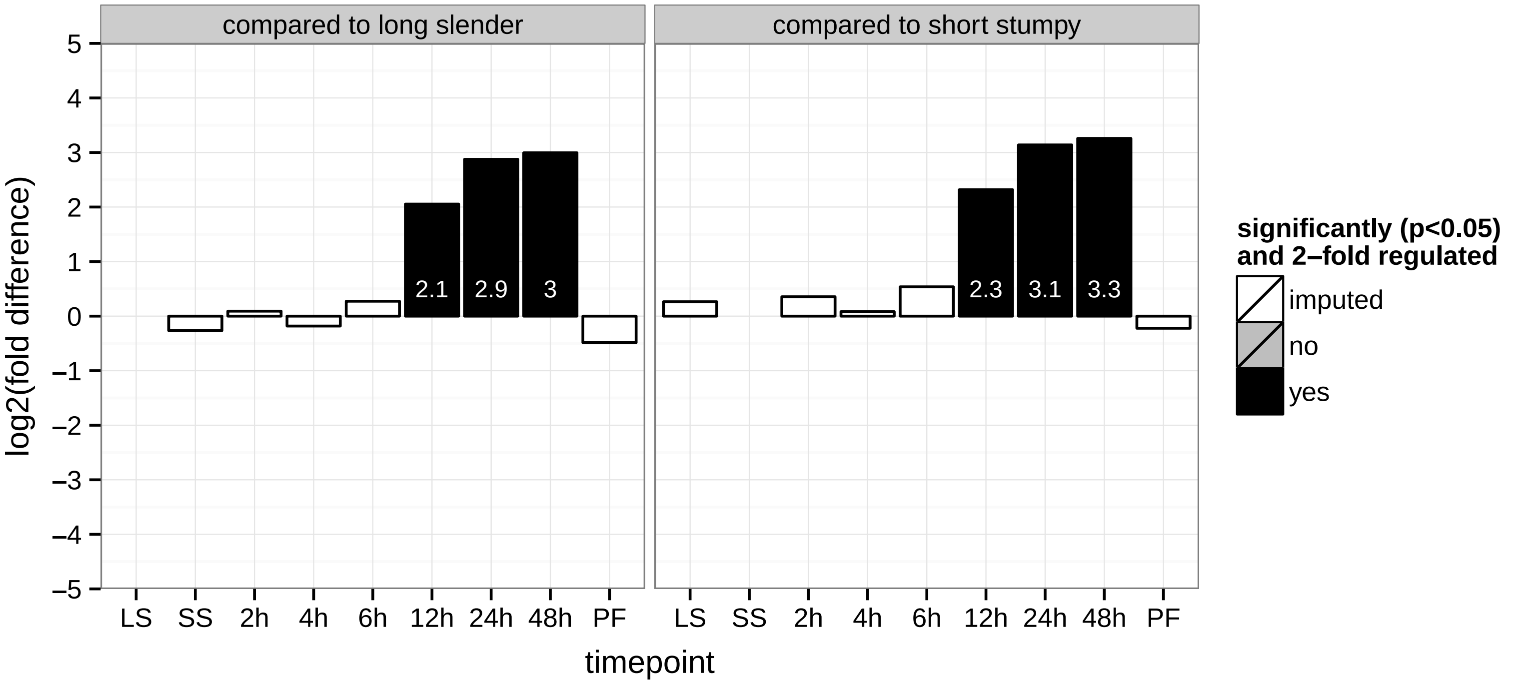
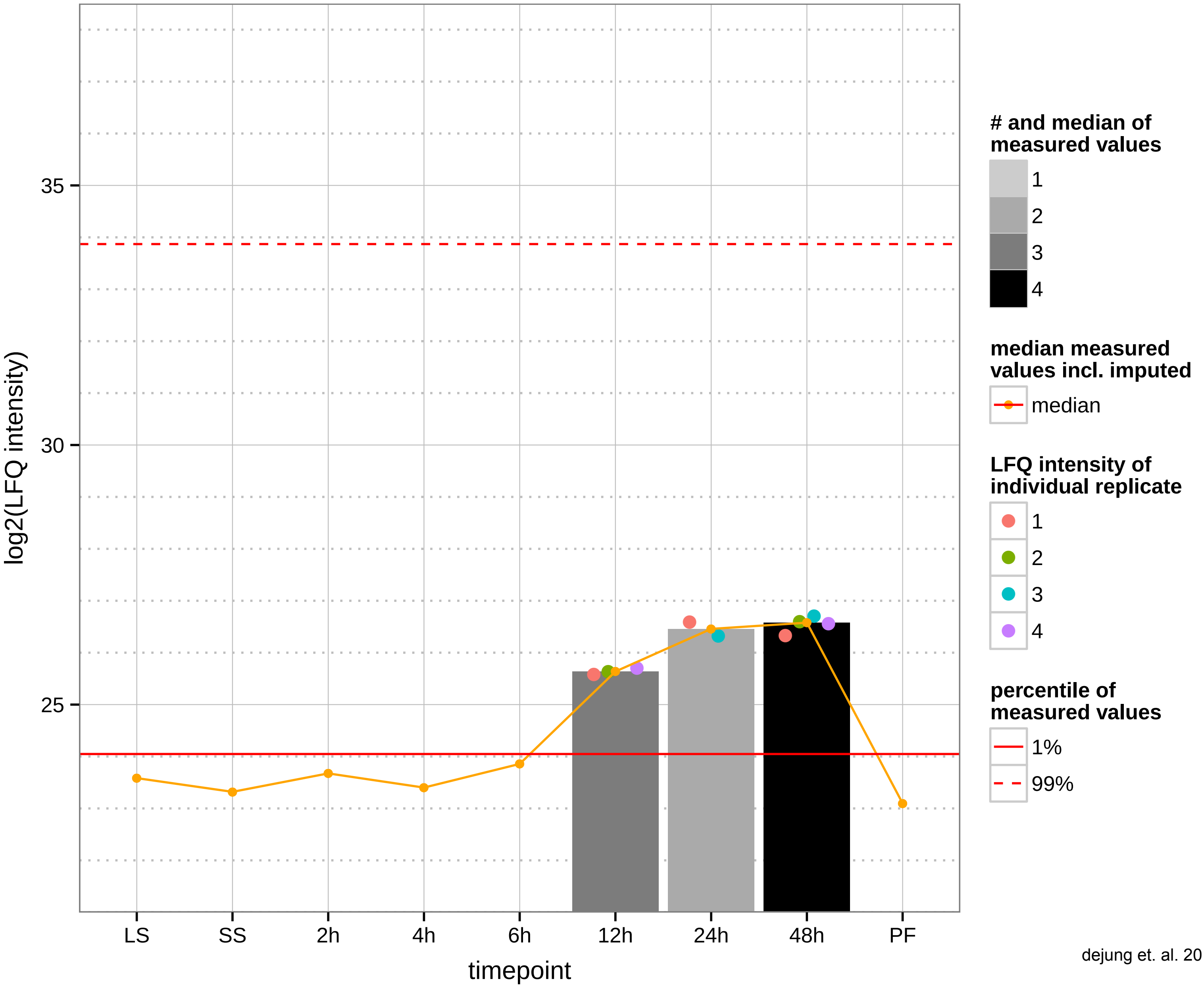
hypothetical protein, conserved
Tb927.5.2240;Tb927.5.2210;Tb927.5.2180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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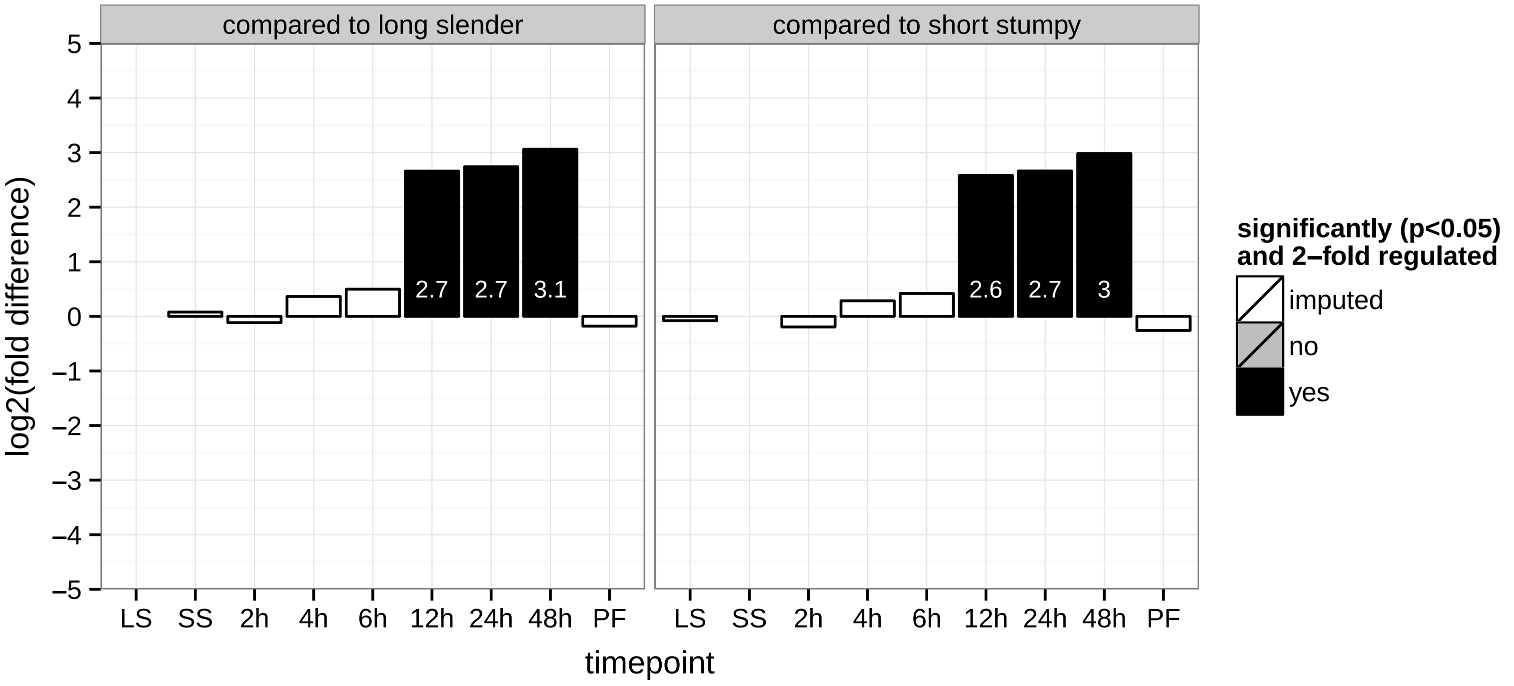
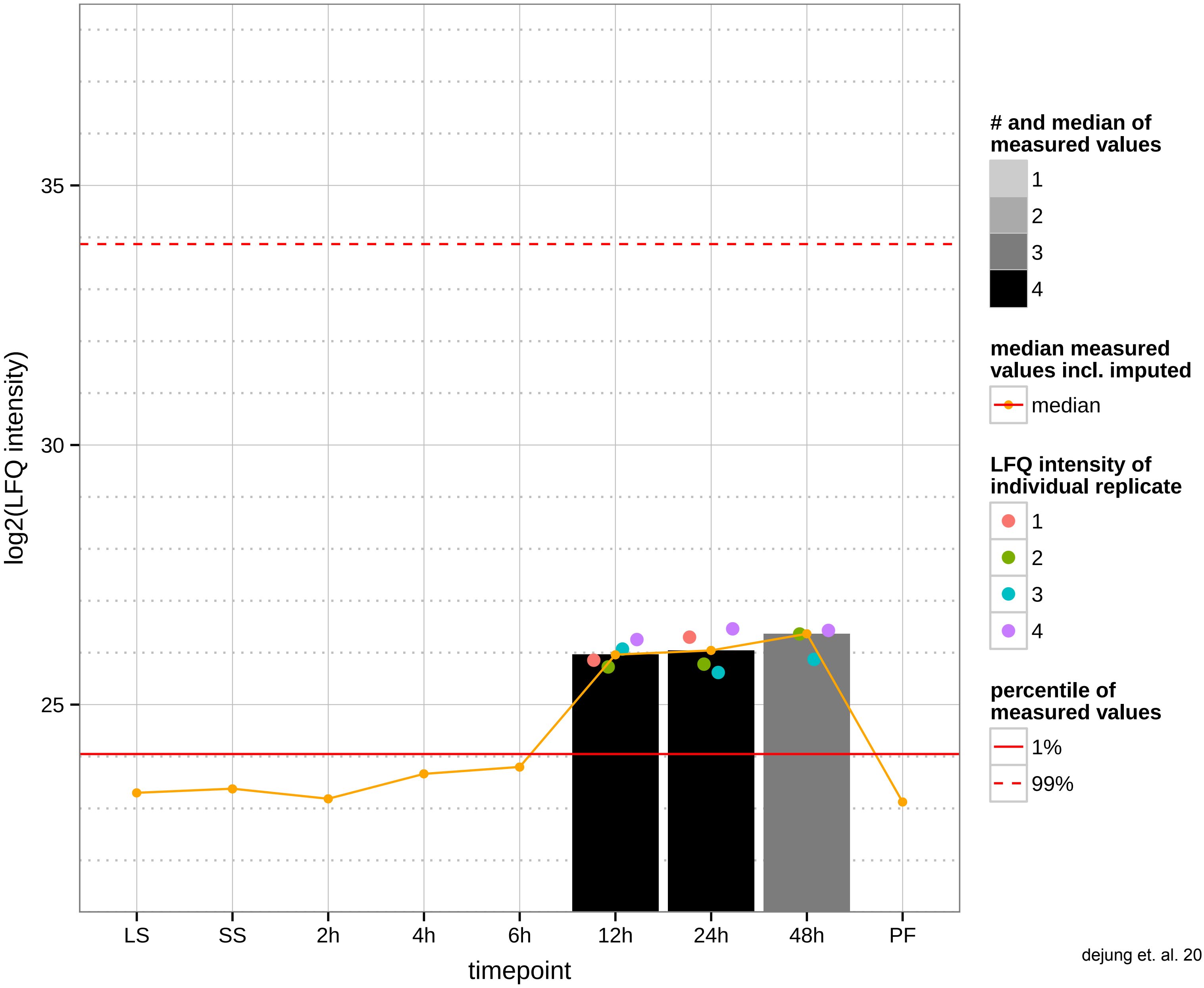
hypothetical protein, conserved
Tb927.5.680
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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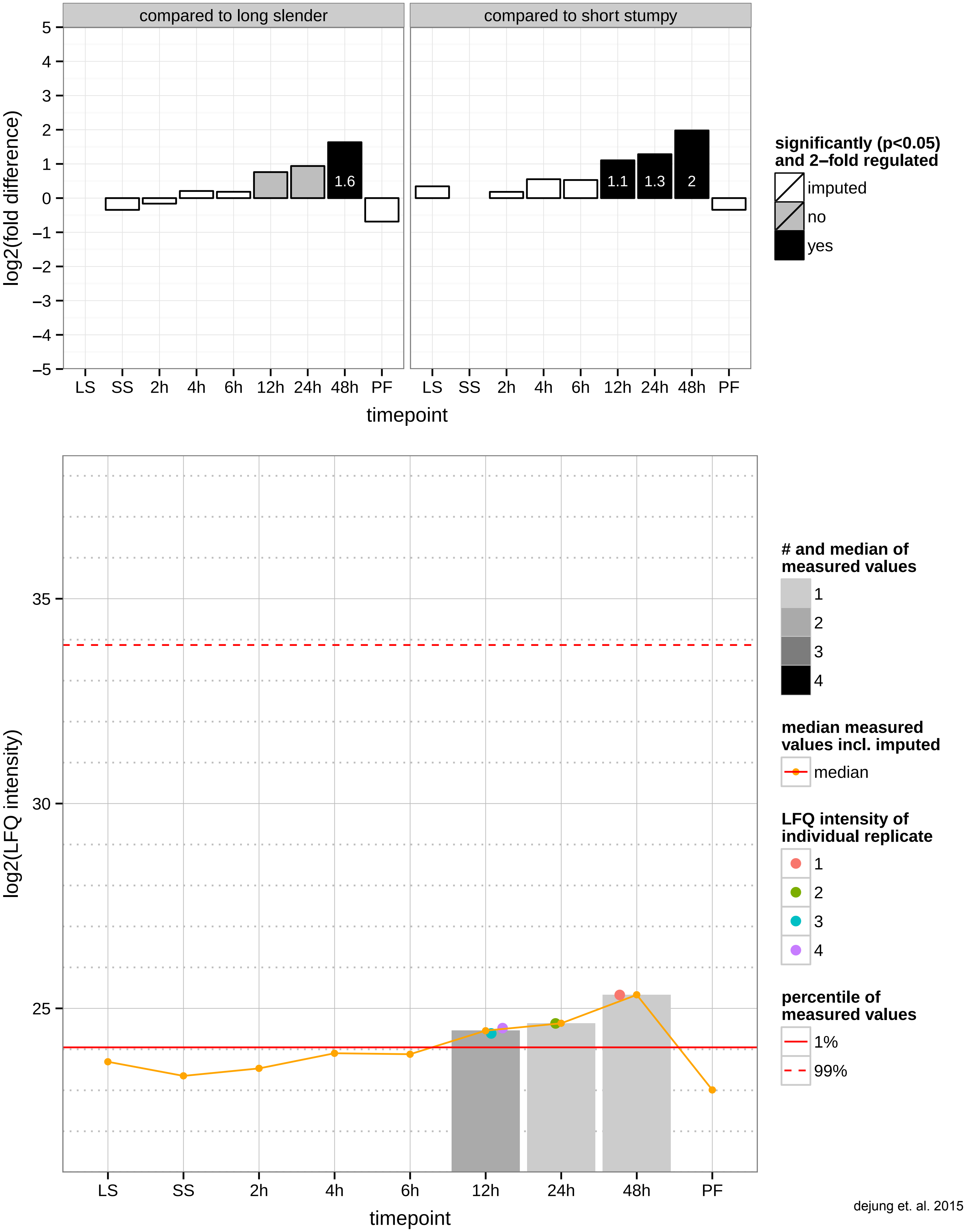
hypothetical protein, conserved
Tb927.6.1560
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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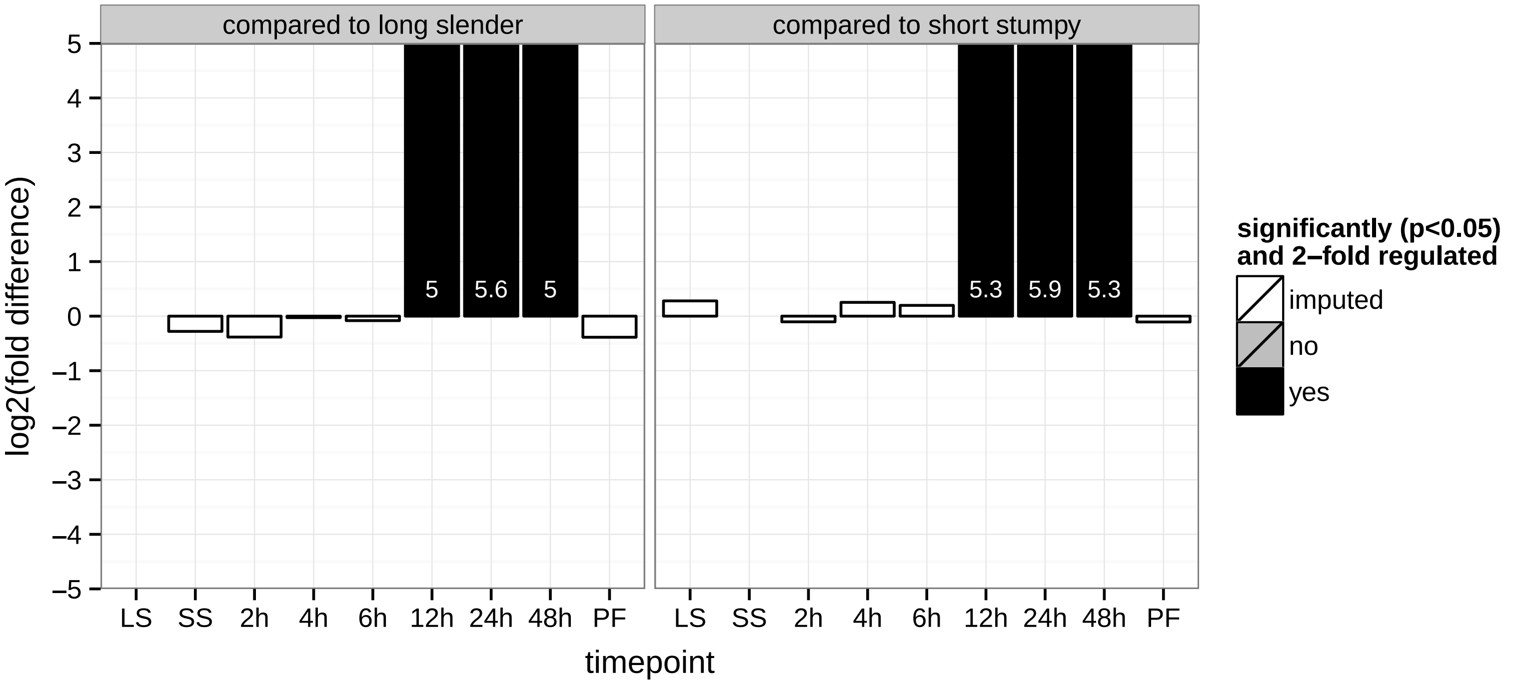
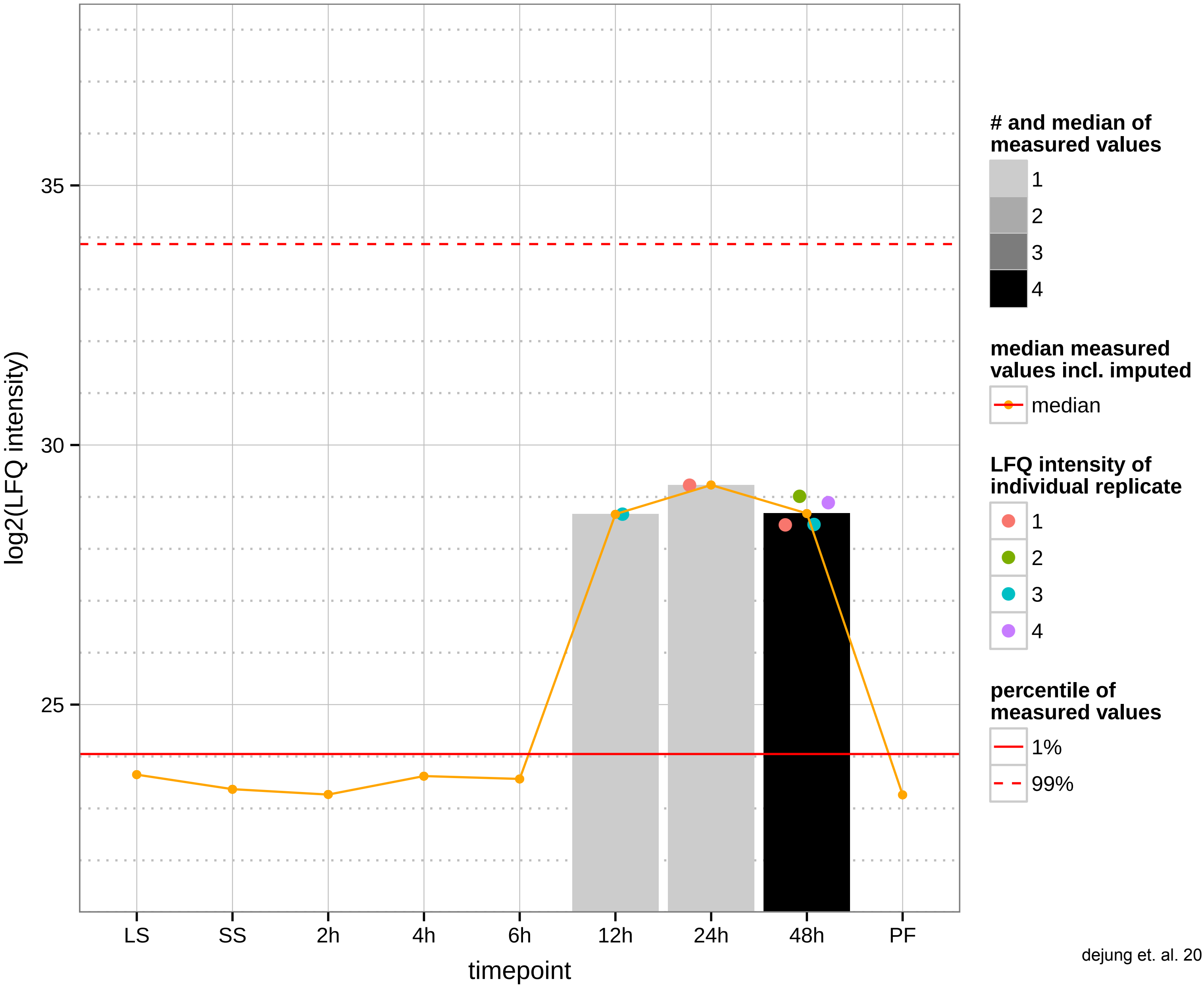
heat shock 70 kDa protein, putative (HSP70)
Tb927.7.1030
AGOF: ATP binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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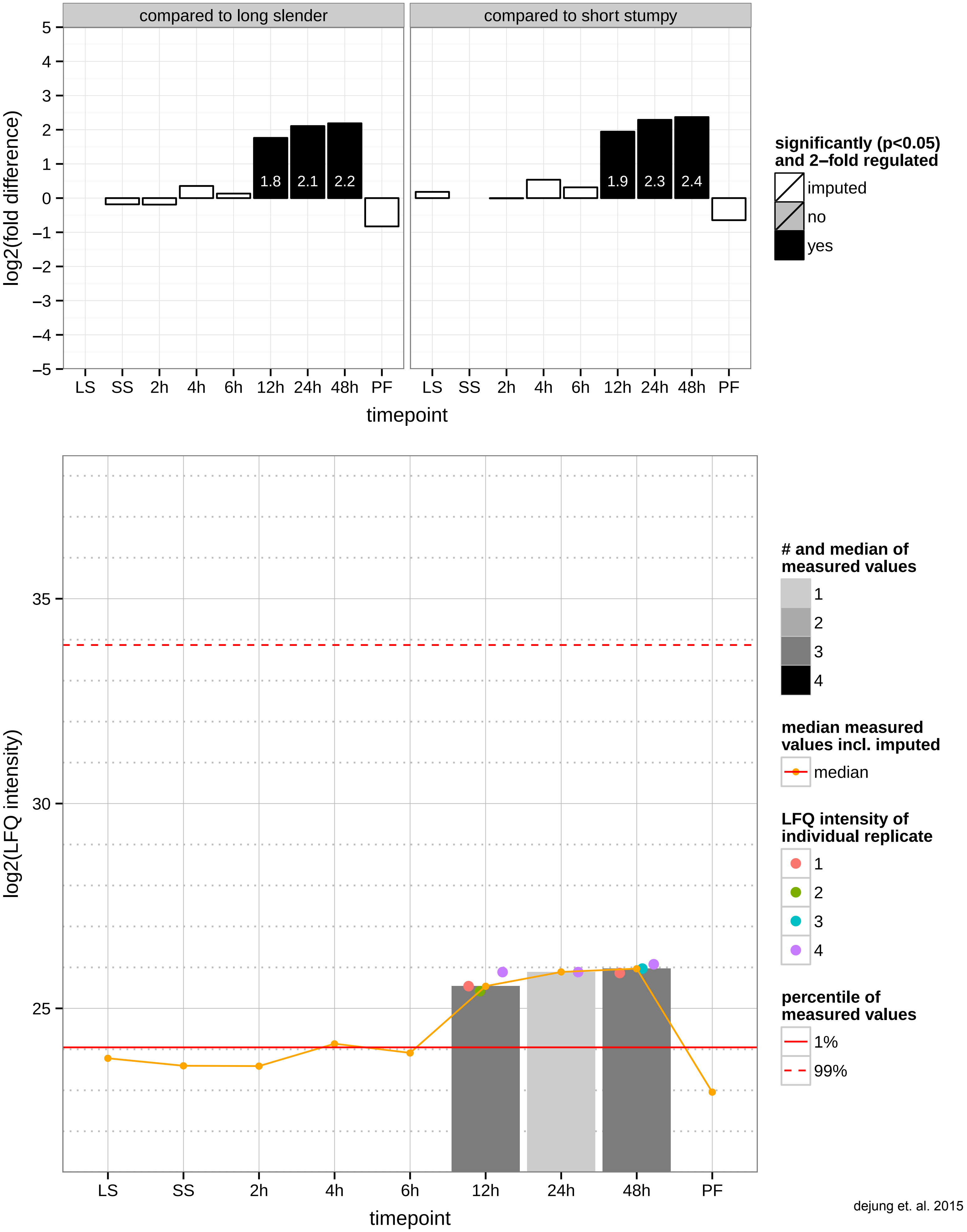
eukaryotic peptide chain release factor subunit 1, putative
Tb927.7.1710
AGOF: null
AGOC: nucleus
AGOP: translation
PGOF: null
PGOC: null
PGOP: null



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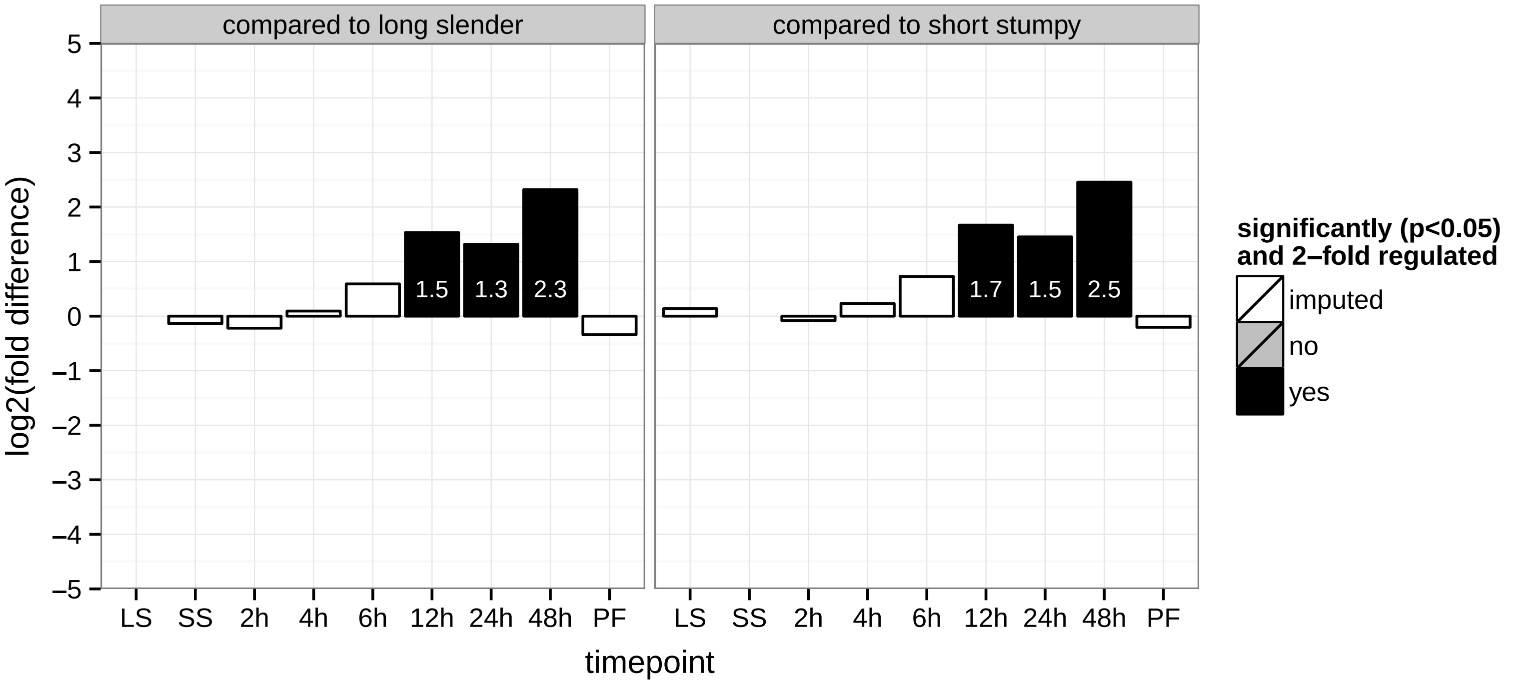
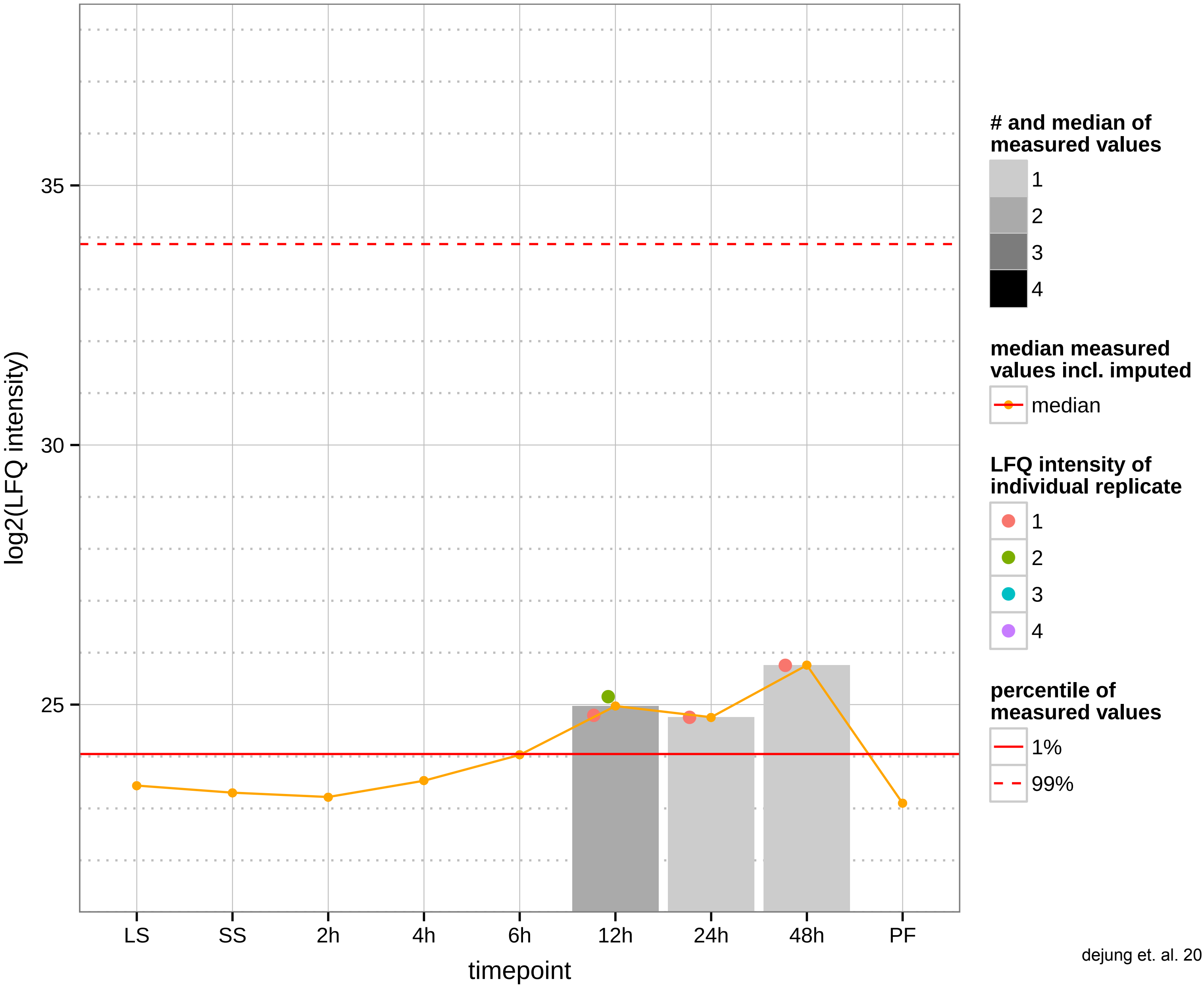
hypothetical protein, conserved
Tb927.7.3140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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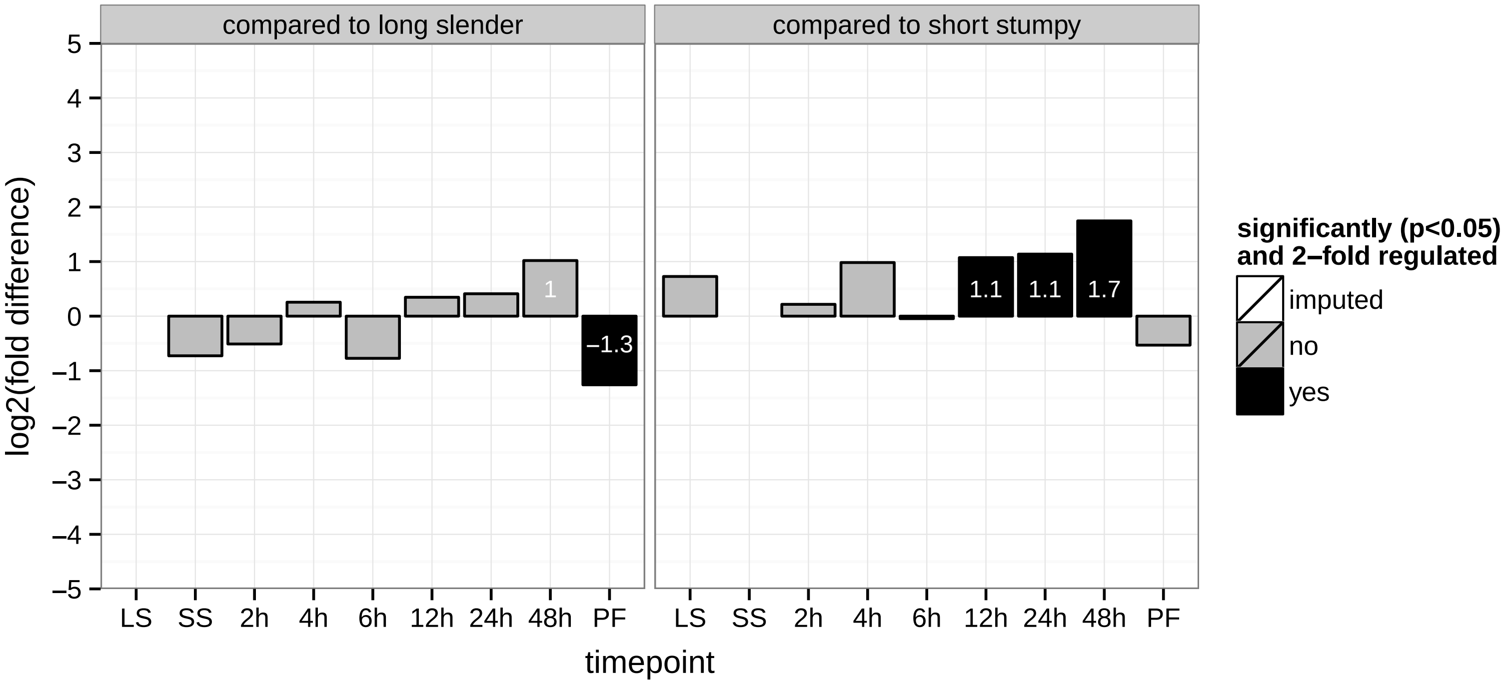
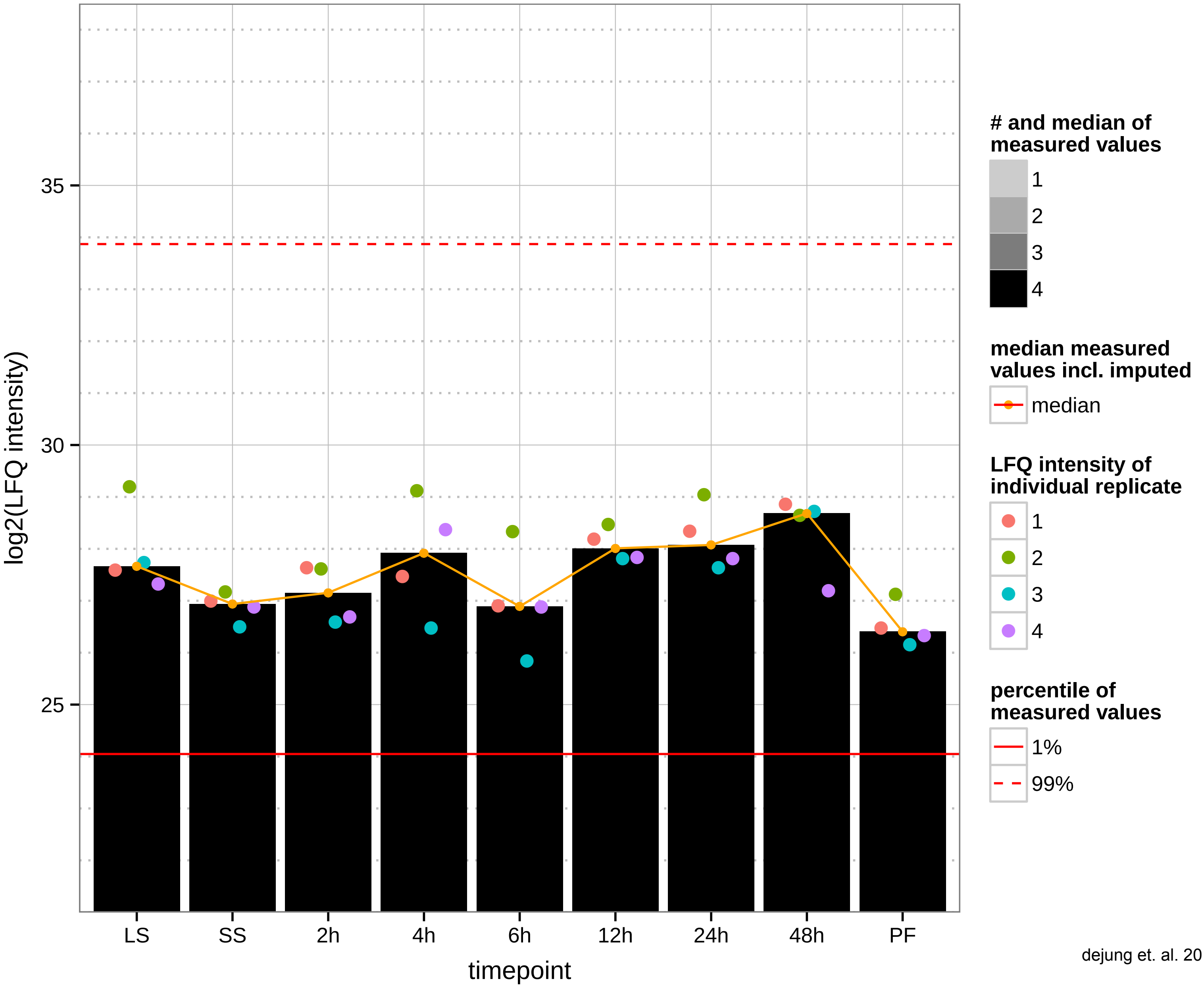
centrin, putative
Tb927.7.3410
AGOF: calcium ion binding
AGOC: cilium basal body
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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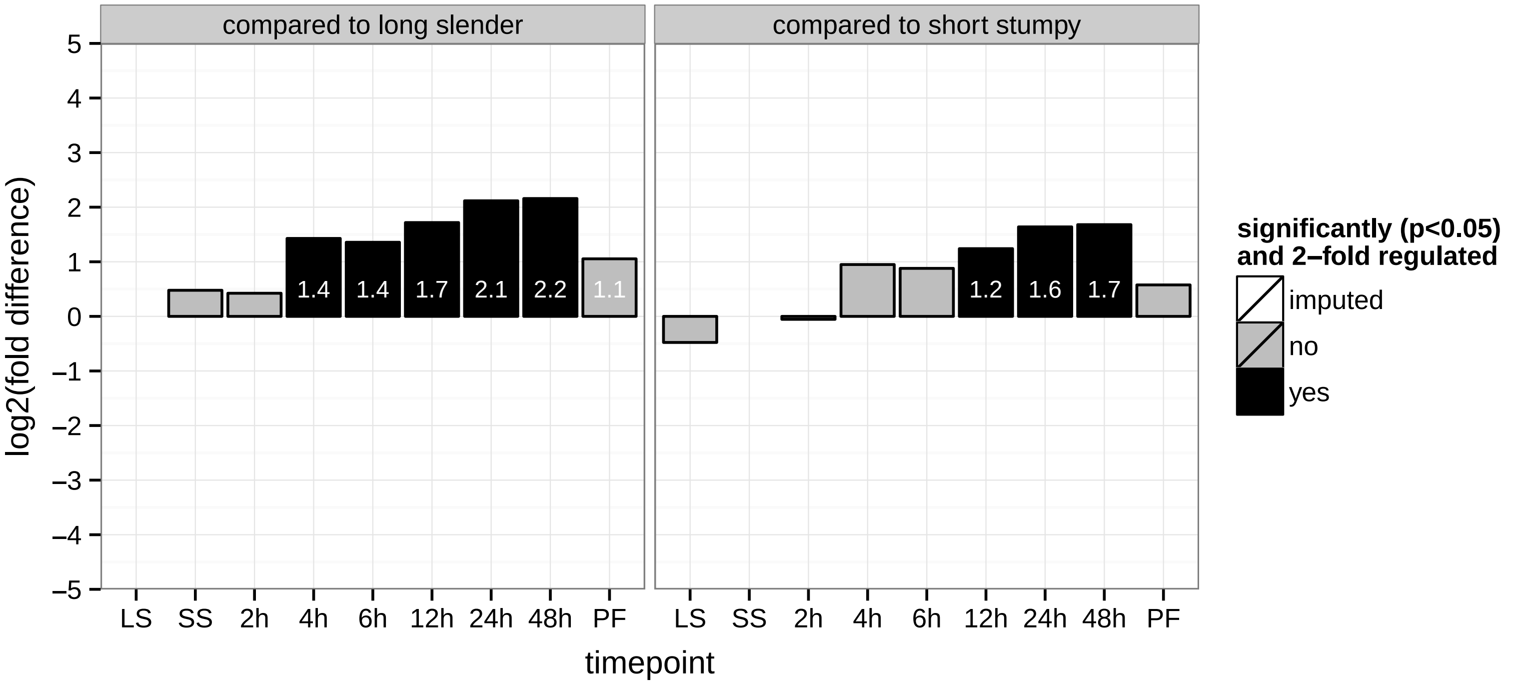
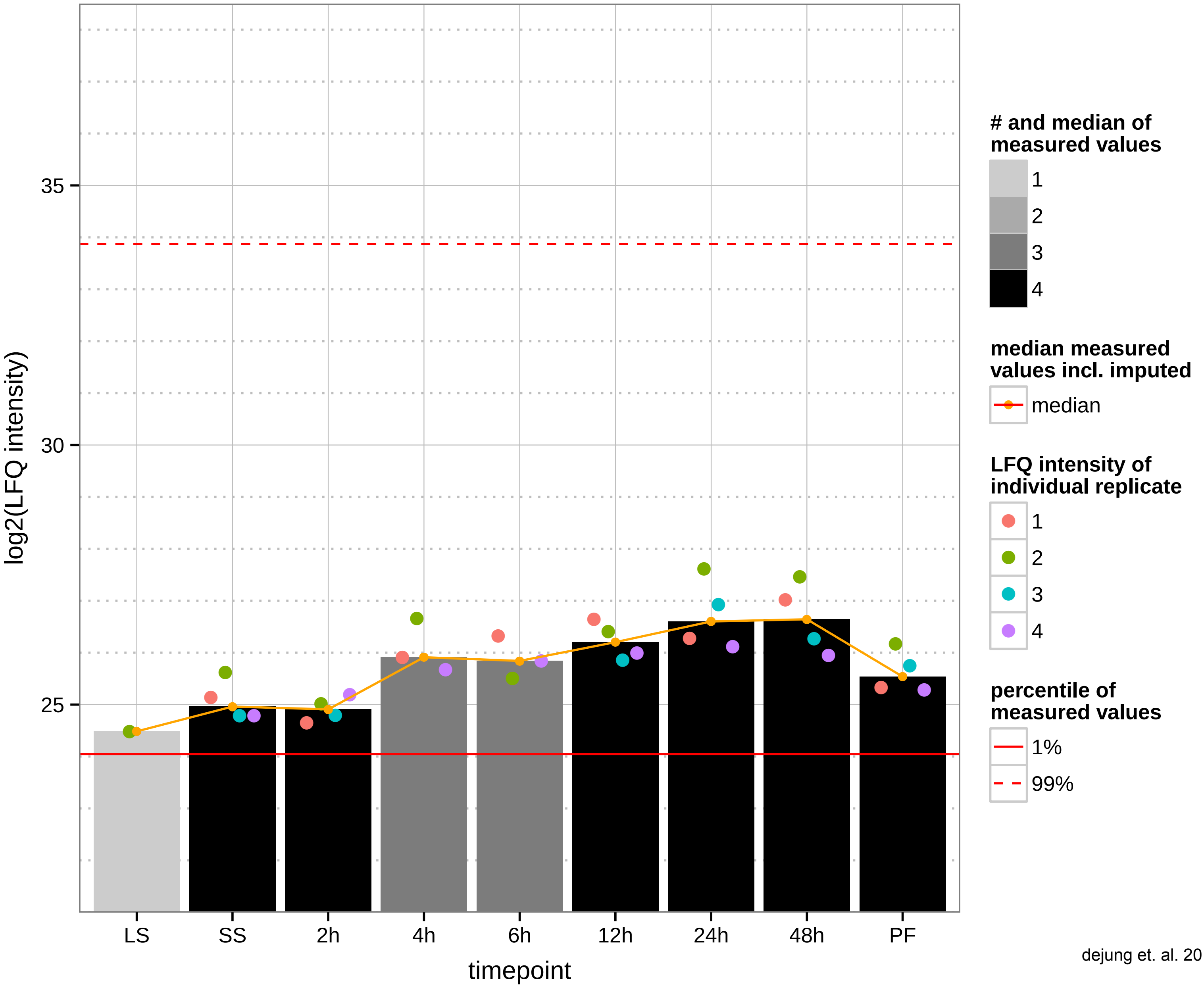
50S ribosomal protein L16, putative
Tb927.7.3960
AGOF: structural constituent of ribosome
AGOC: intracellular, mitochondrion, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: ribosome
PGOP: translation





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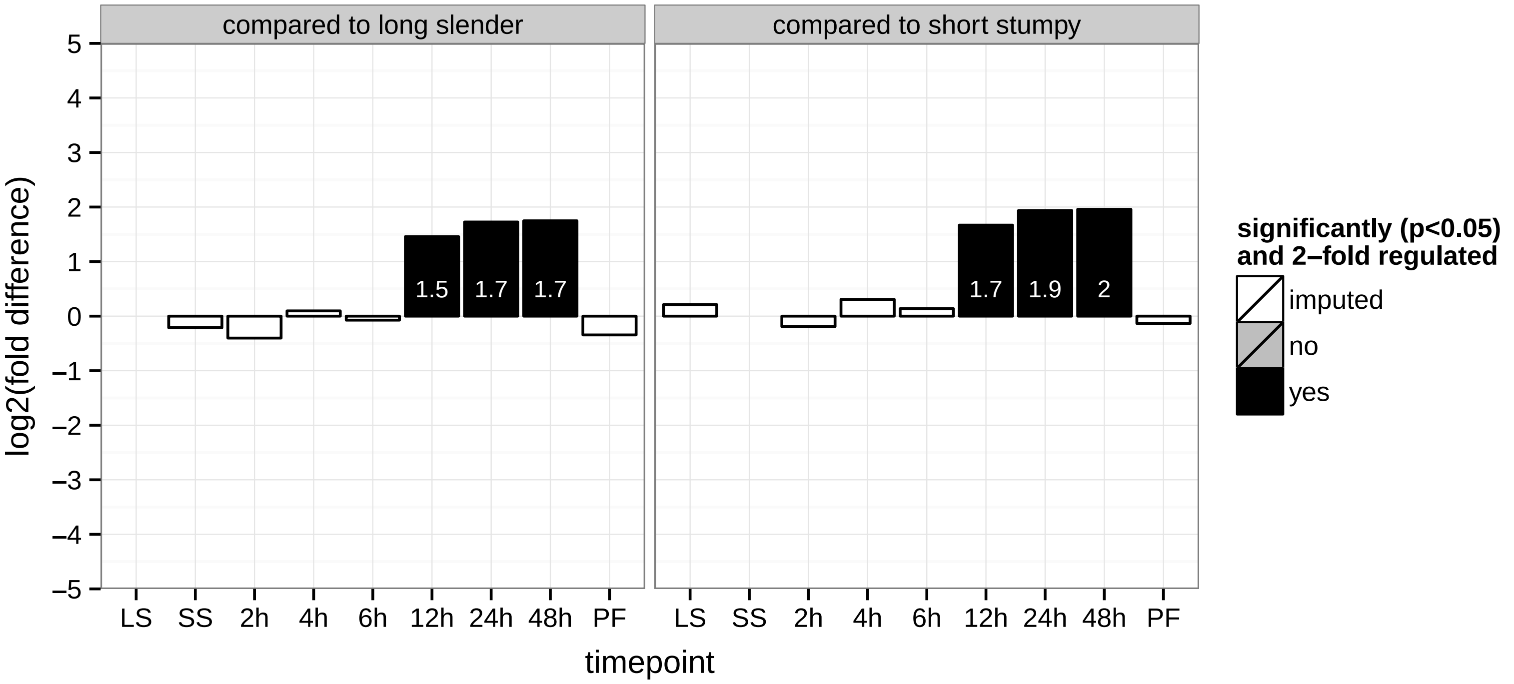
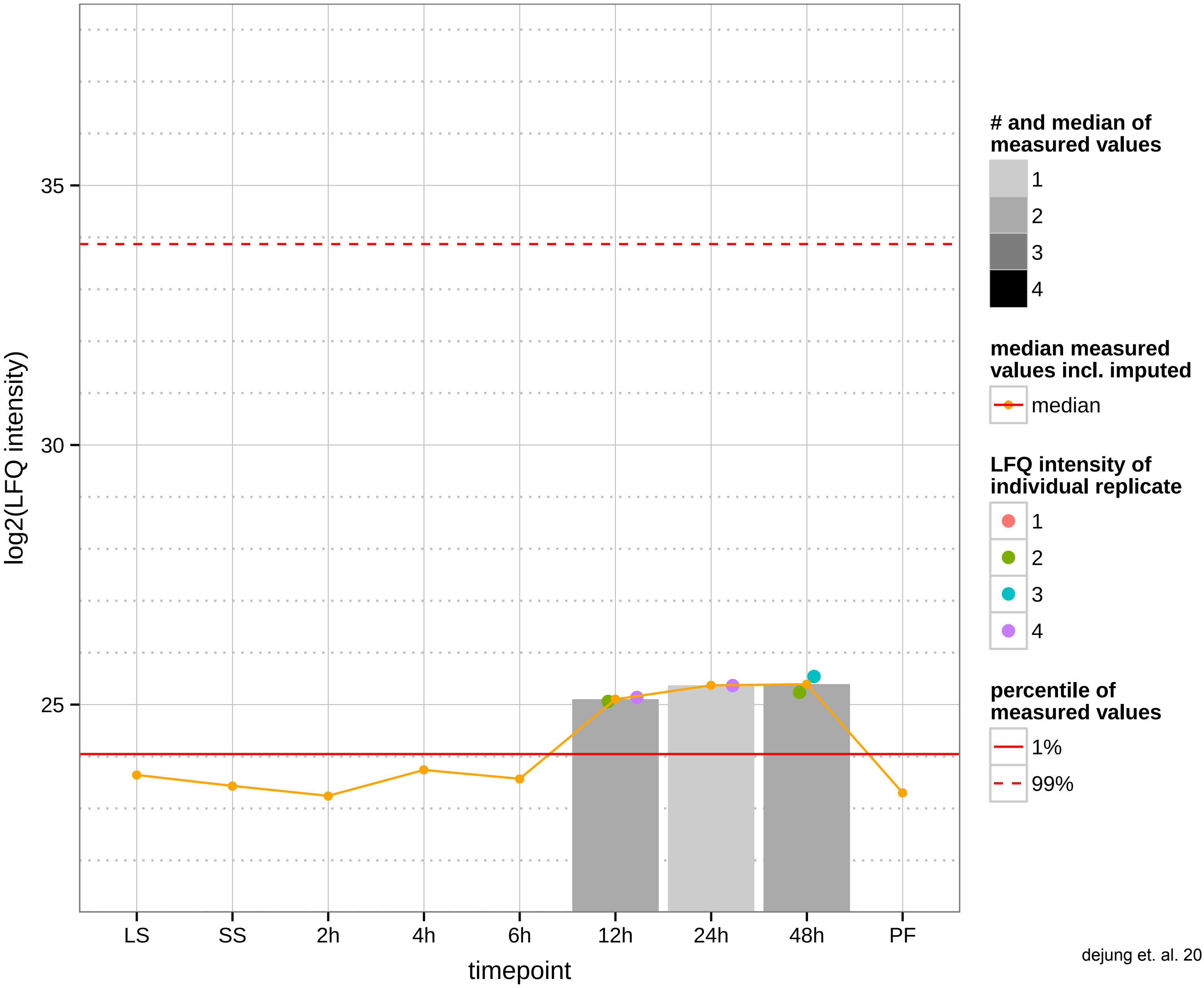
hypothetical protein, conserved
Tb927.7.5280
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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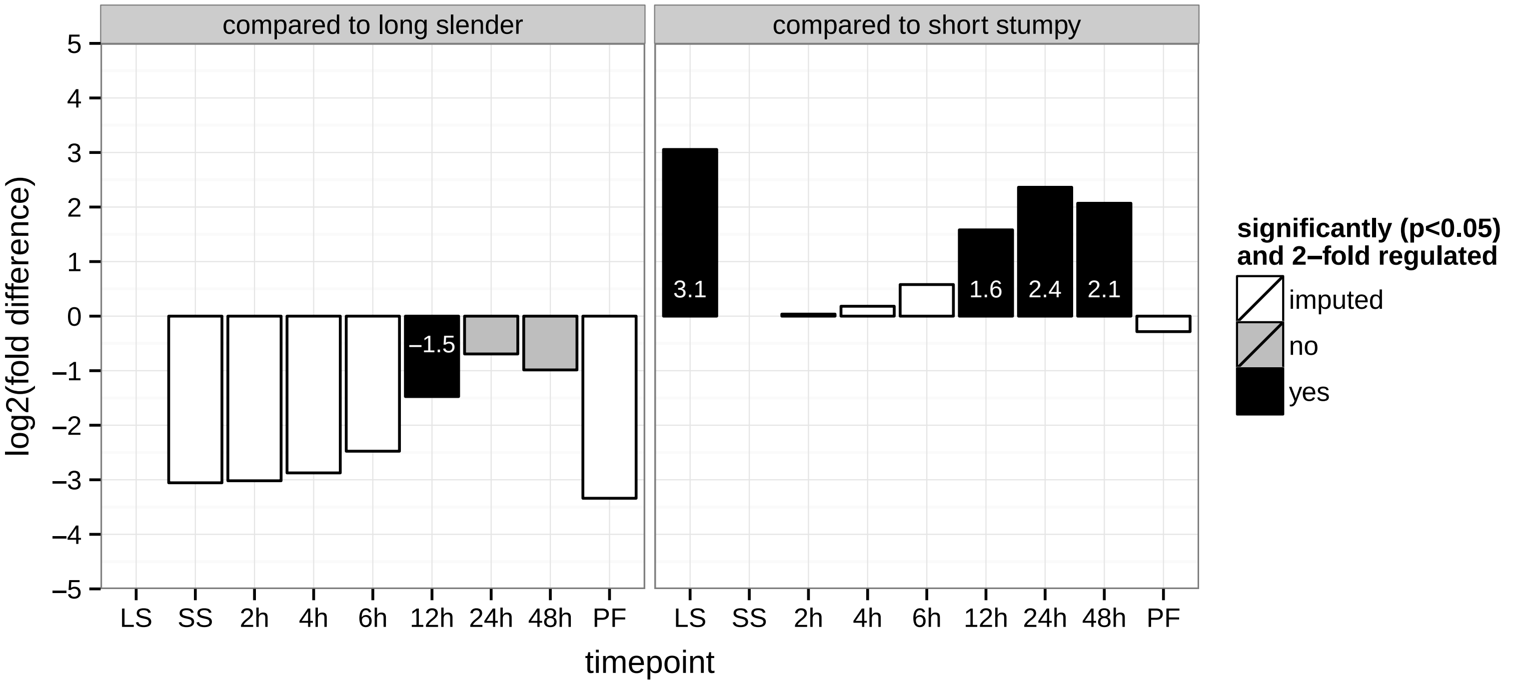
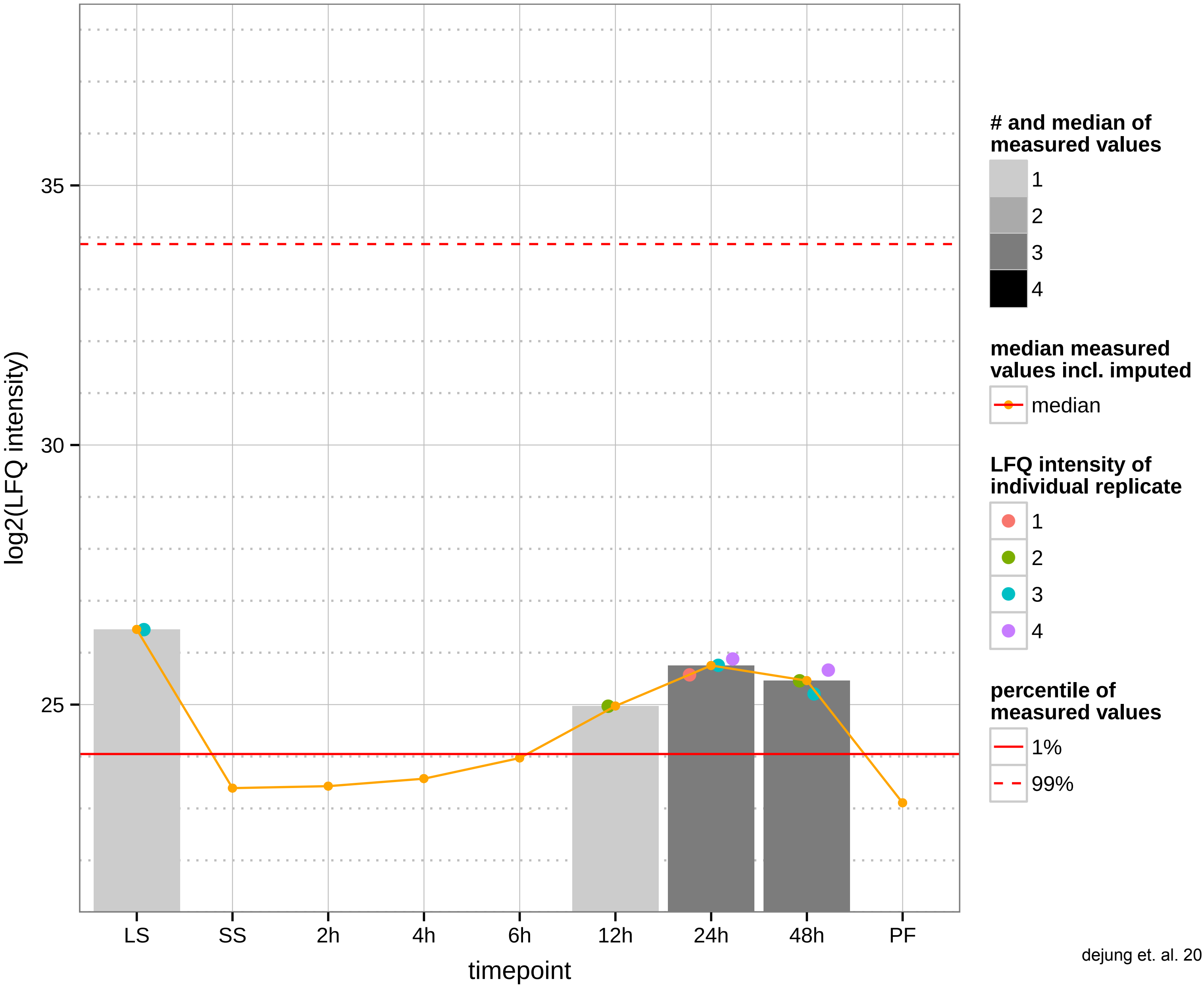
hypothetical protein, conserved
Tb927.7.5320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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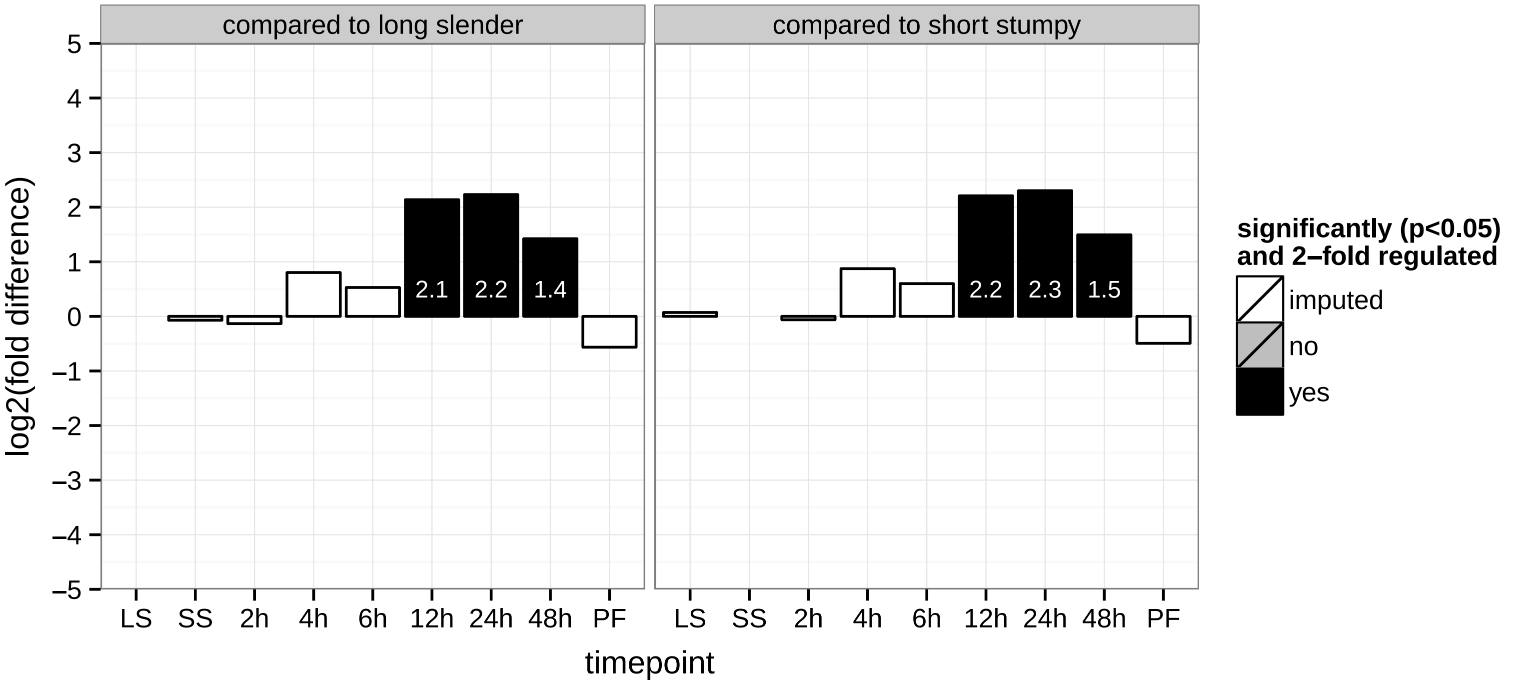
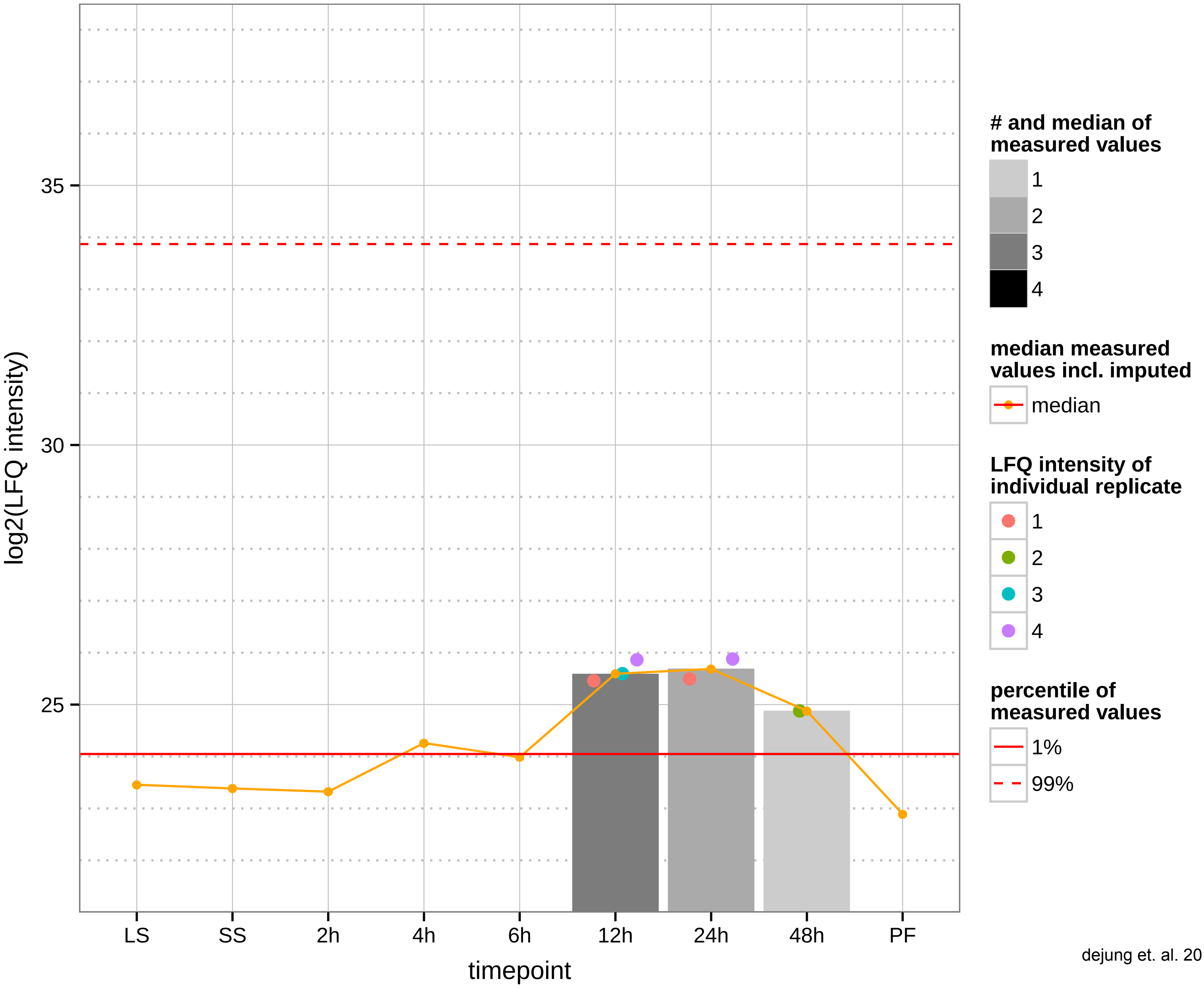
hypothetical protein, conserved
Tb927.7.5610
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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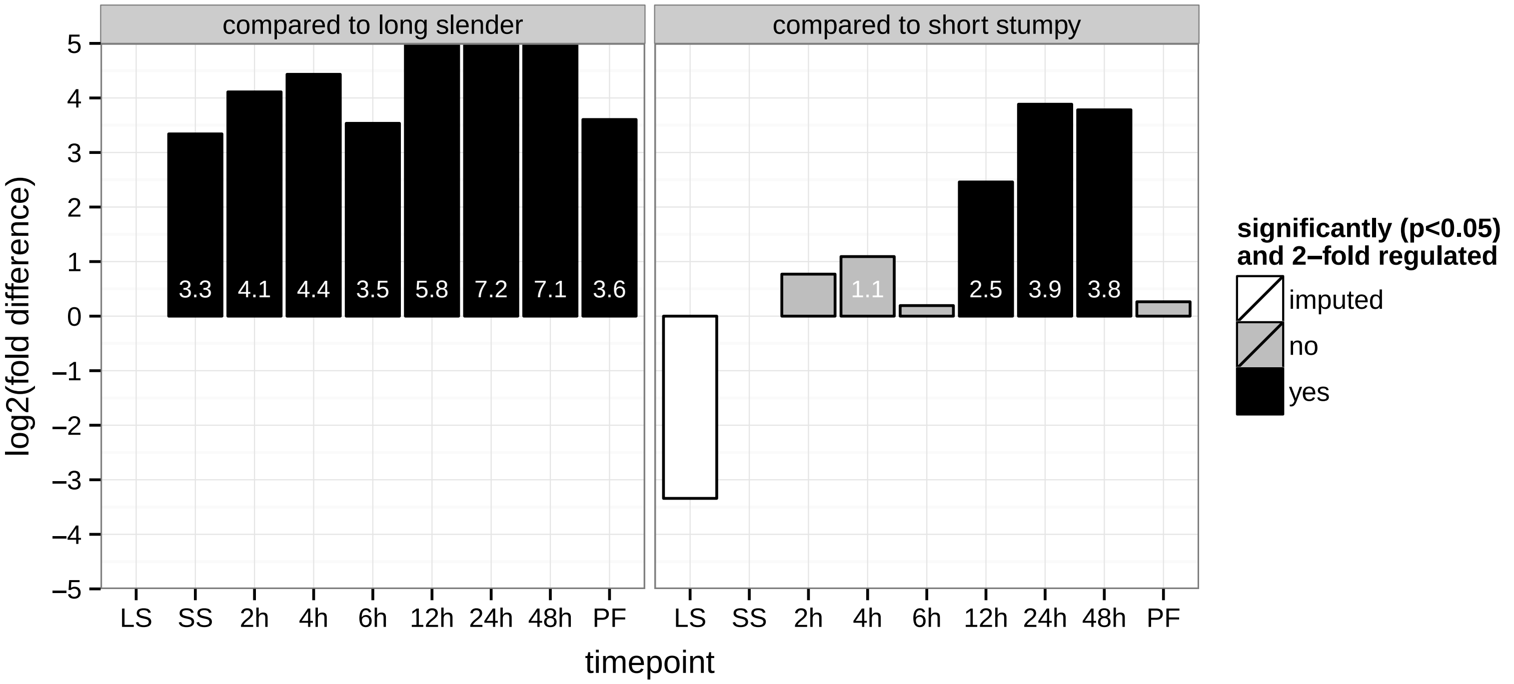
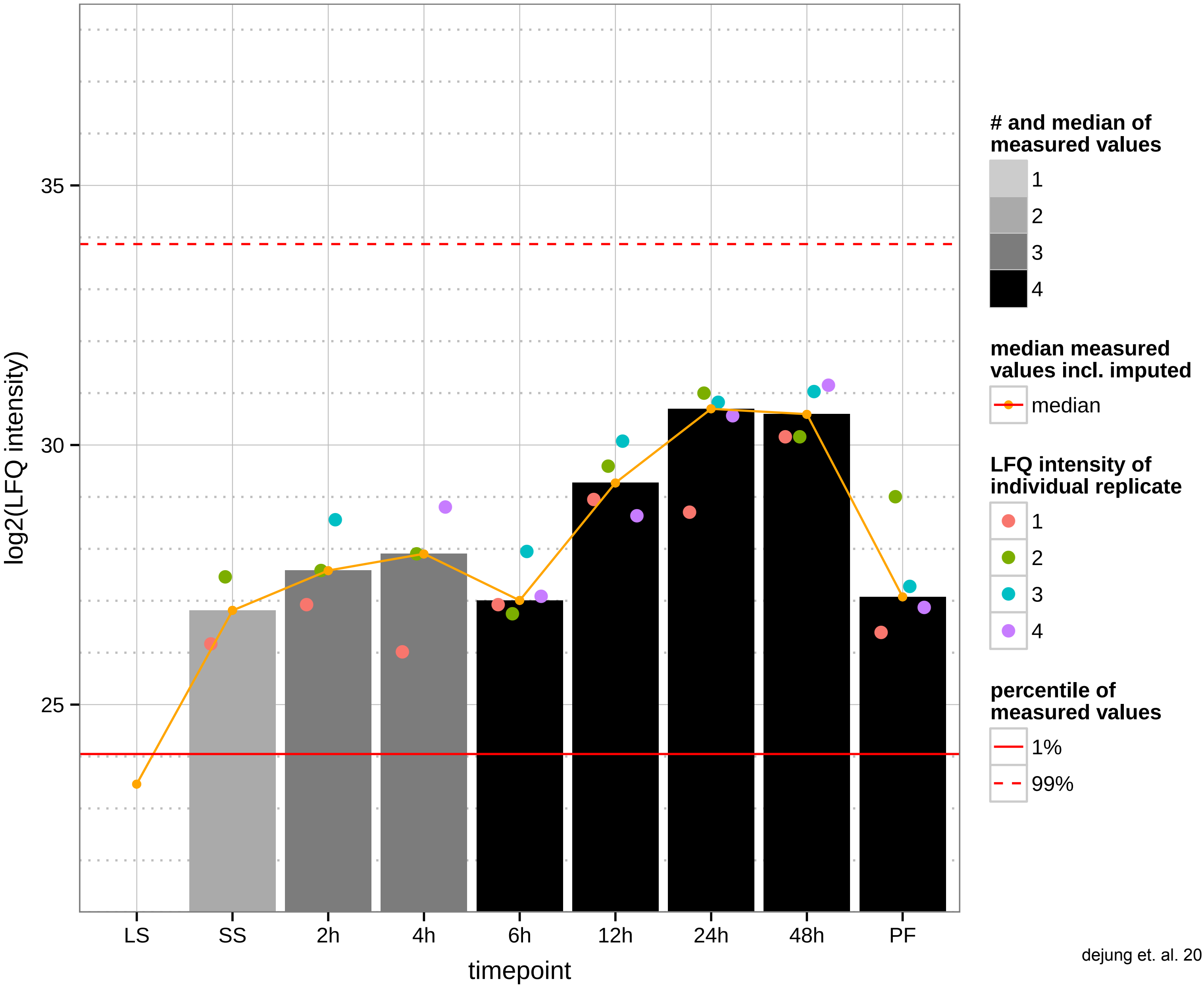
protein associated with differentiation 3, putative (PAD3)
Tb927.7.5950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: integral to membrane
PGOP: transmembrane transport





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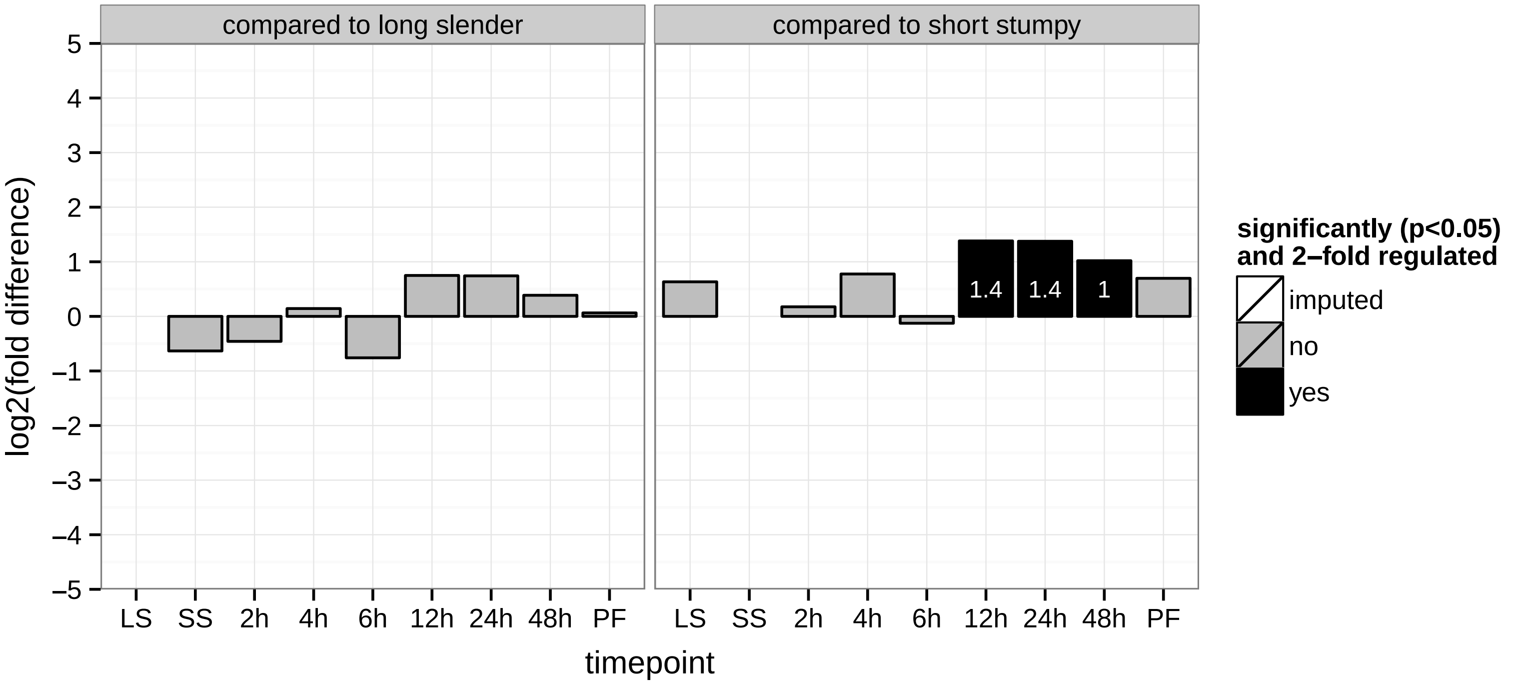
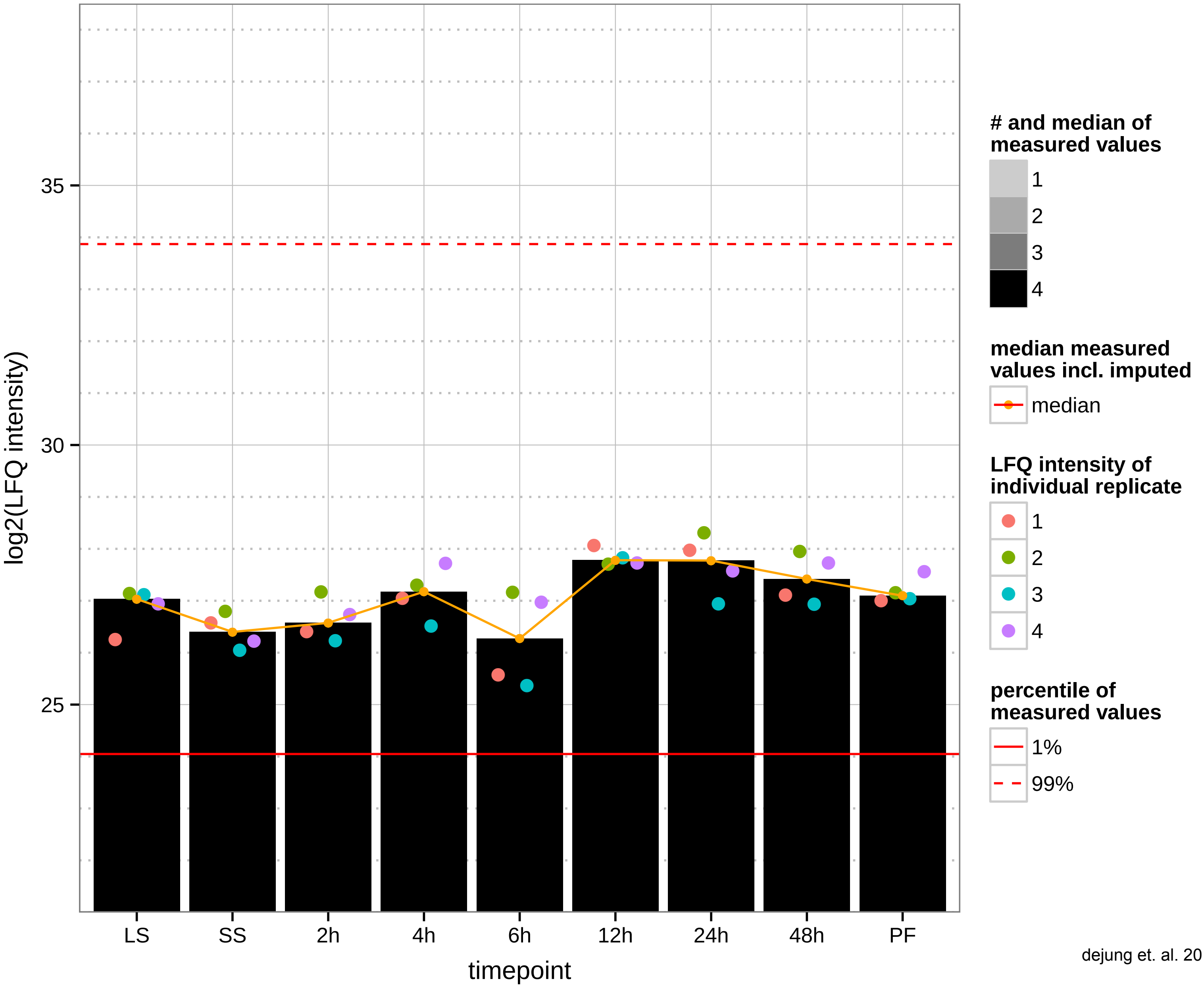
hypothetical protein, conserved
Tb927.8.4220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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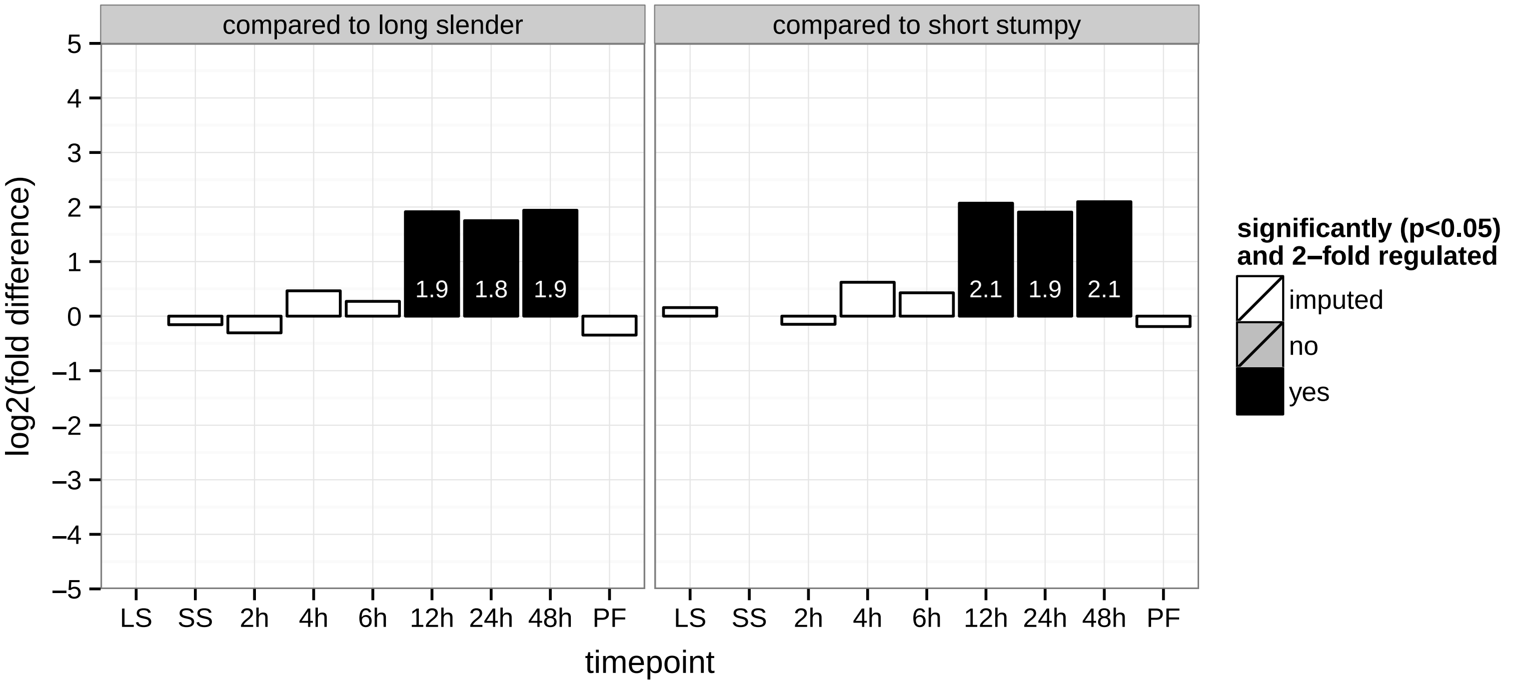
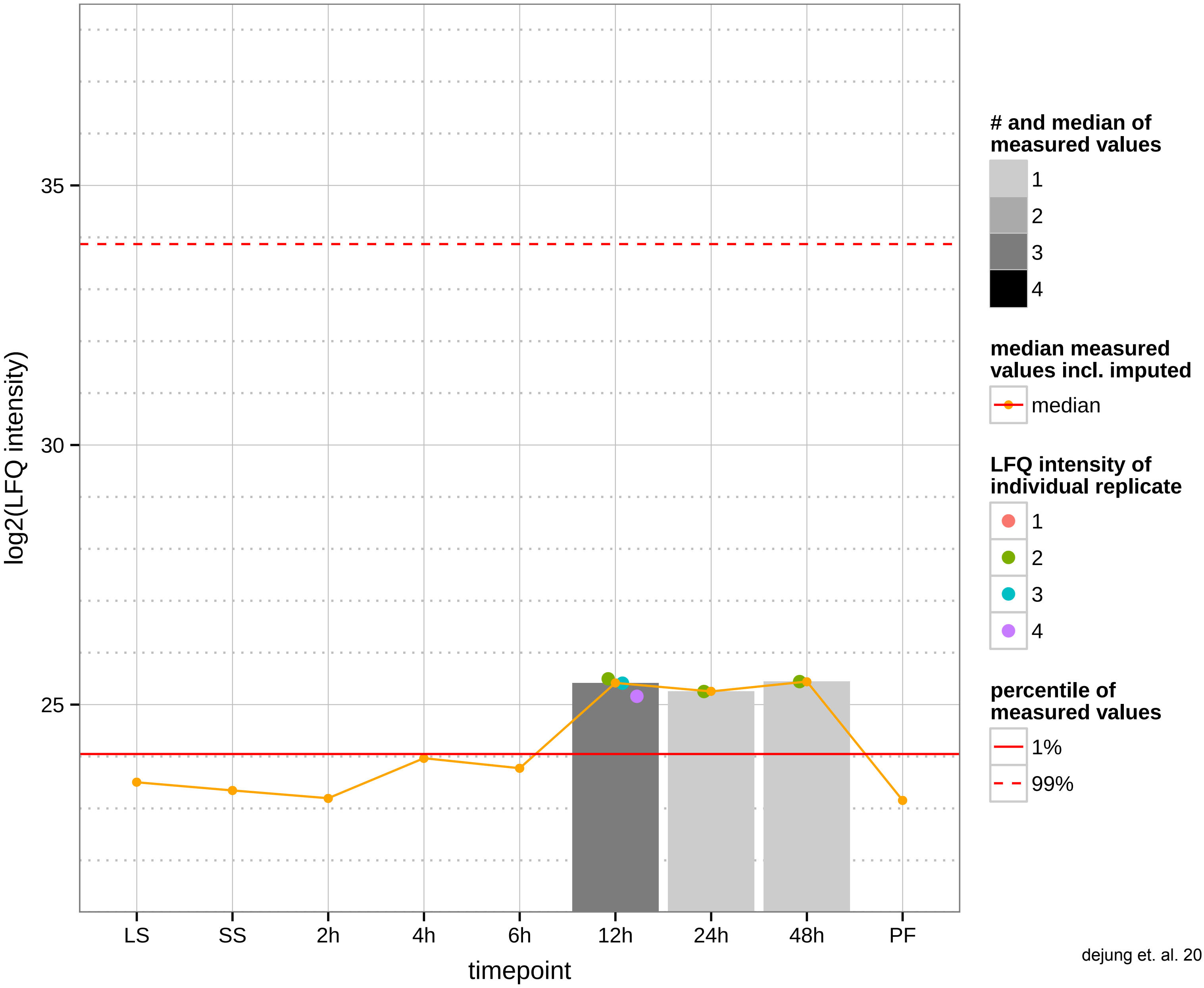
hypothetical protein, conserved
Tb927.8.5370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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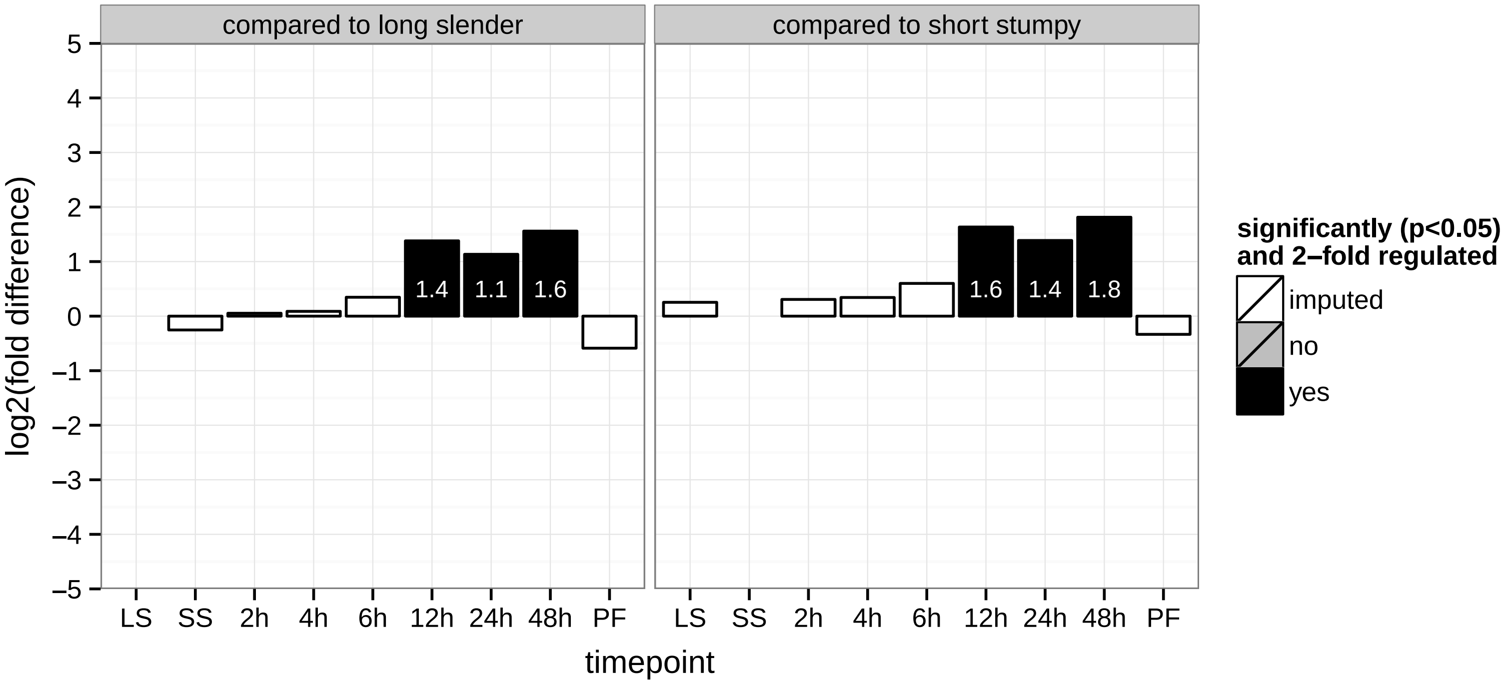
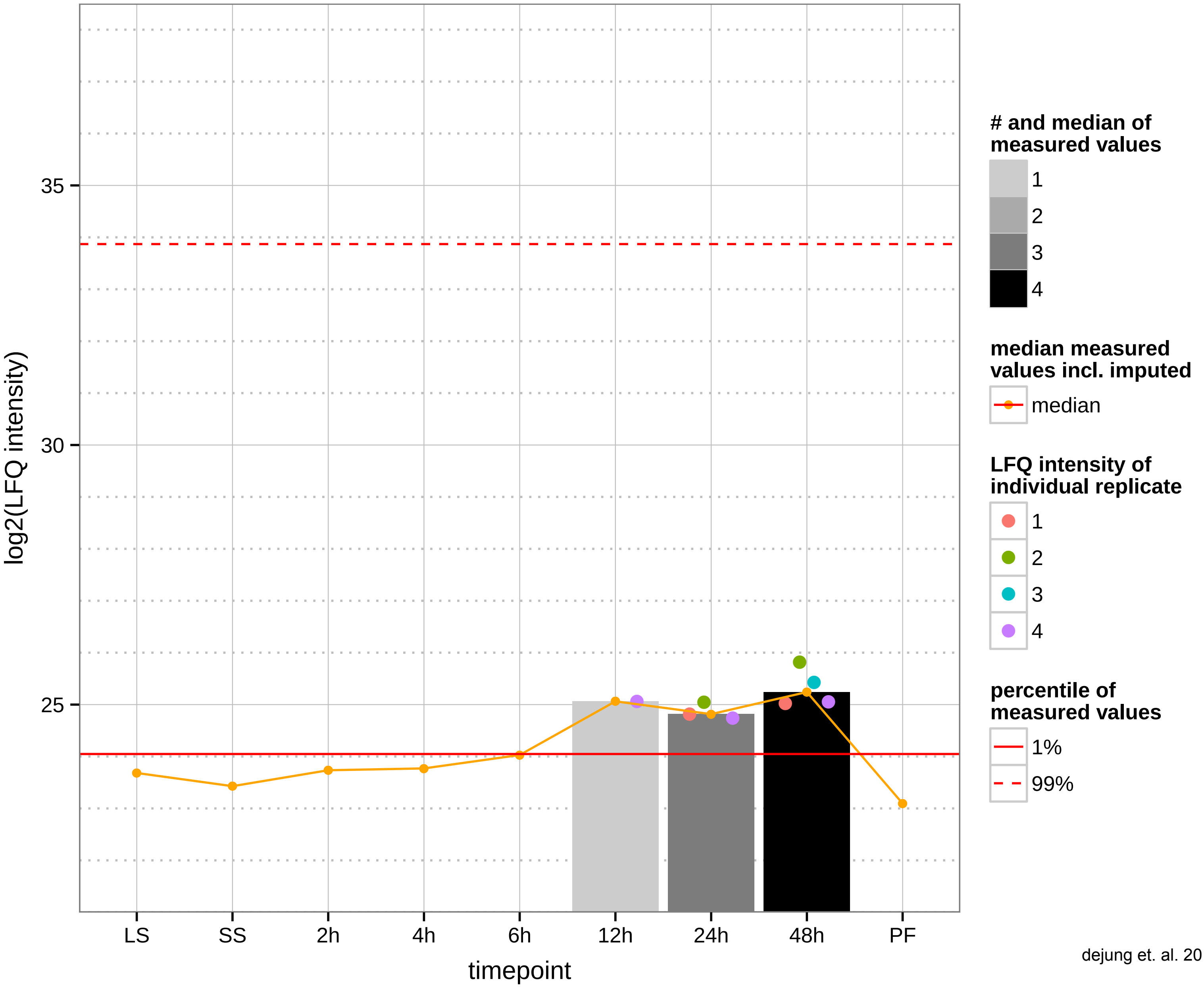
hypothetical protein, conserved
Tb927.8.5660
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrial membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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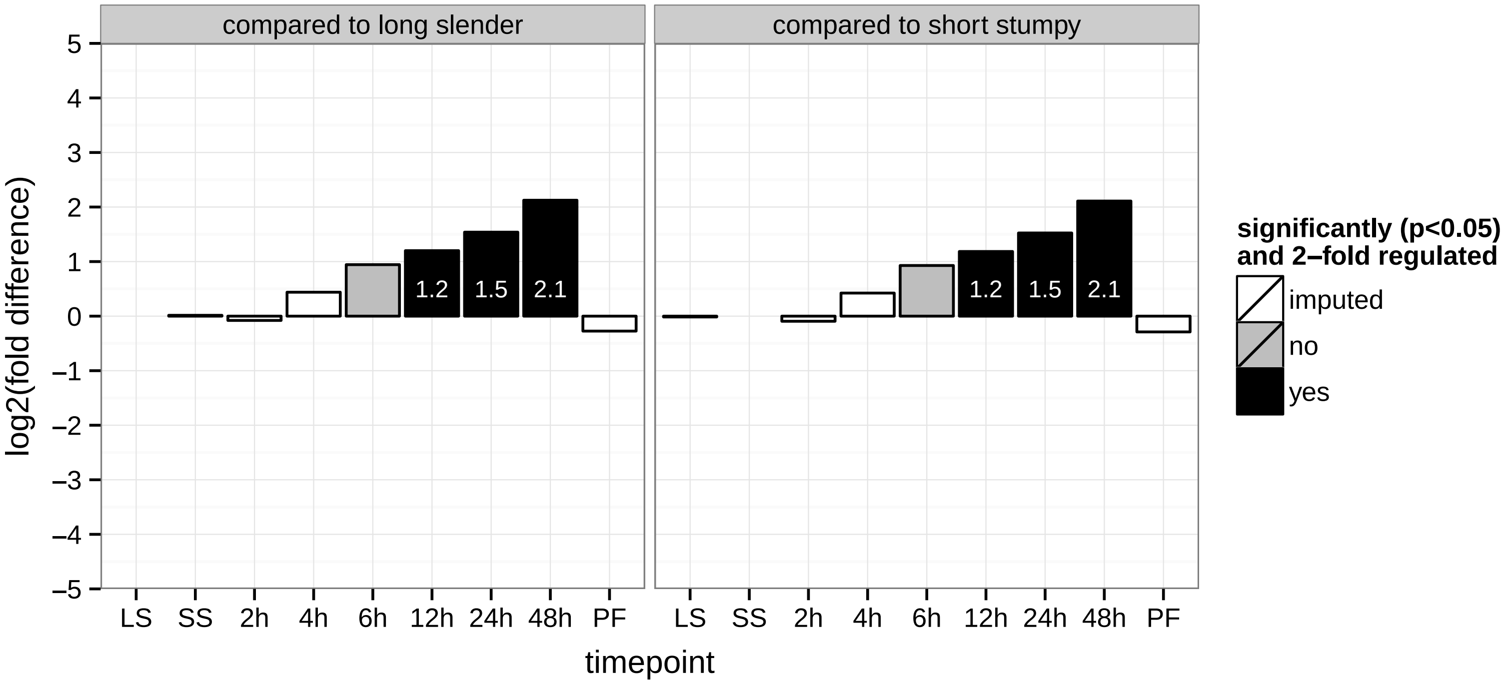
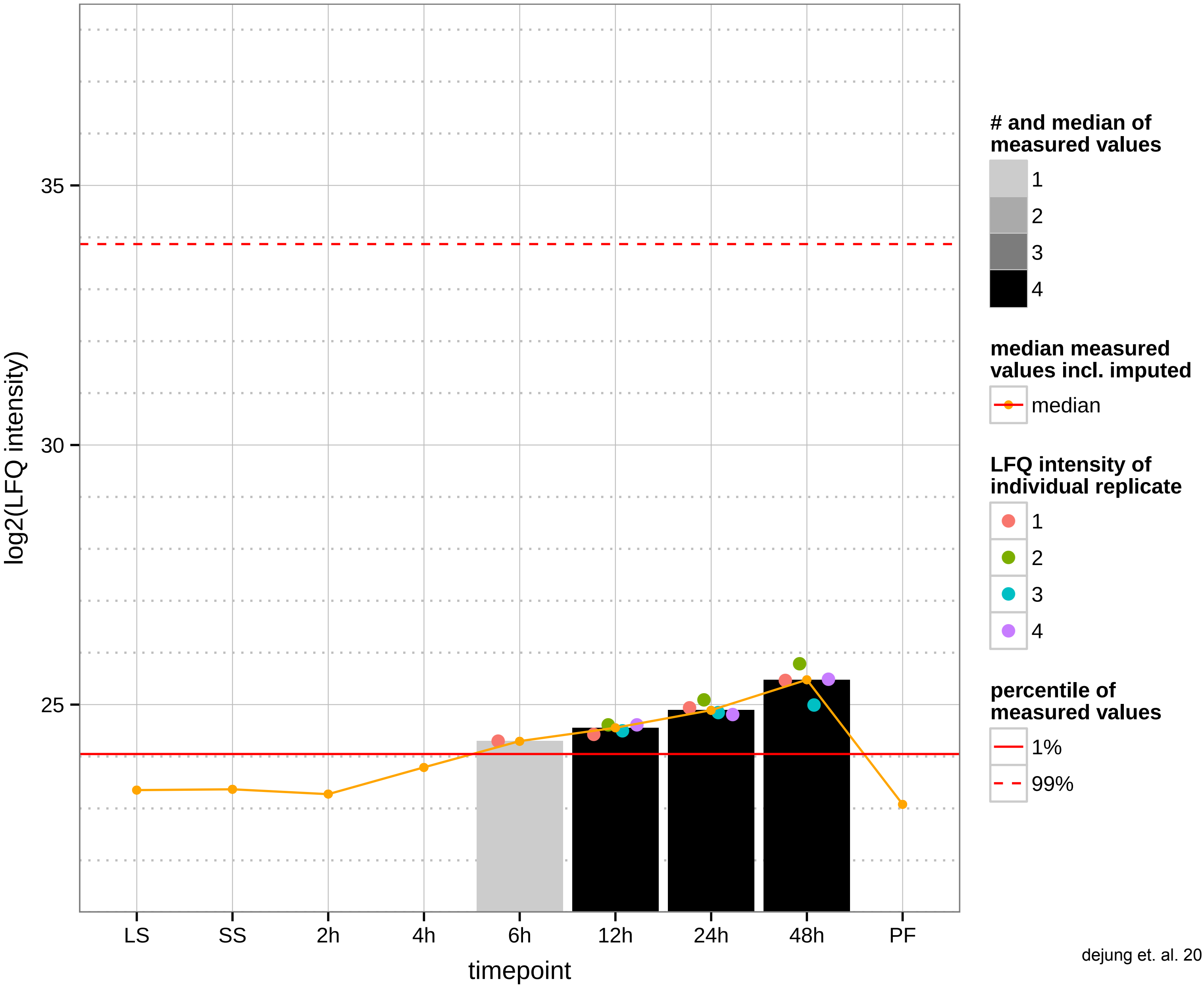
Elongator–like Protein 3a
Tb927.8.5770
AGOF: N–acetyltransferase activity, iron–sulfur cluster binding
AGOC: nucleolus
AGOP: null
PGOF: N–acetyltransferase activity, catalytic activity, iron–sulfur cluster binding
PGOC: null
PGOP: null





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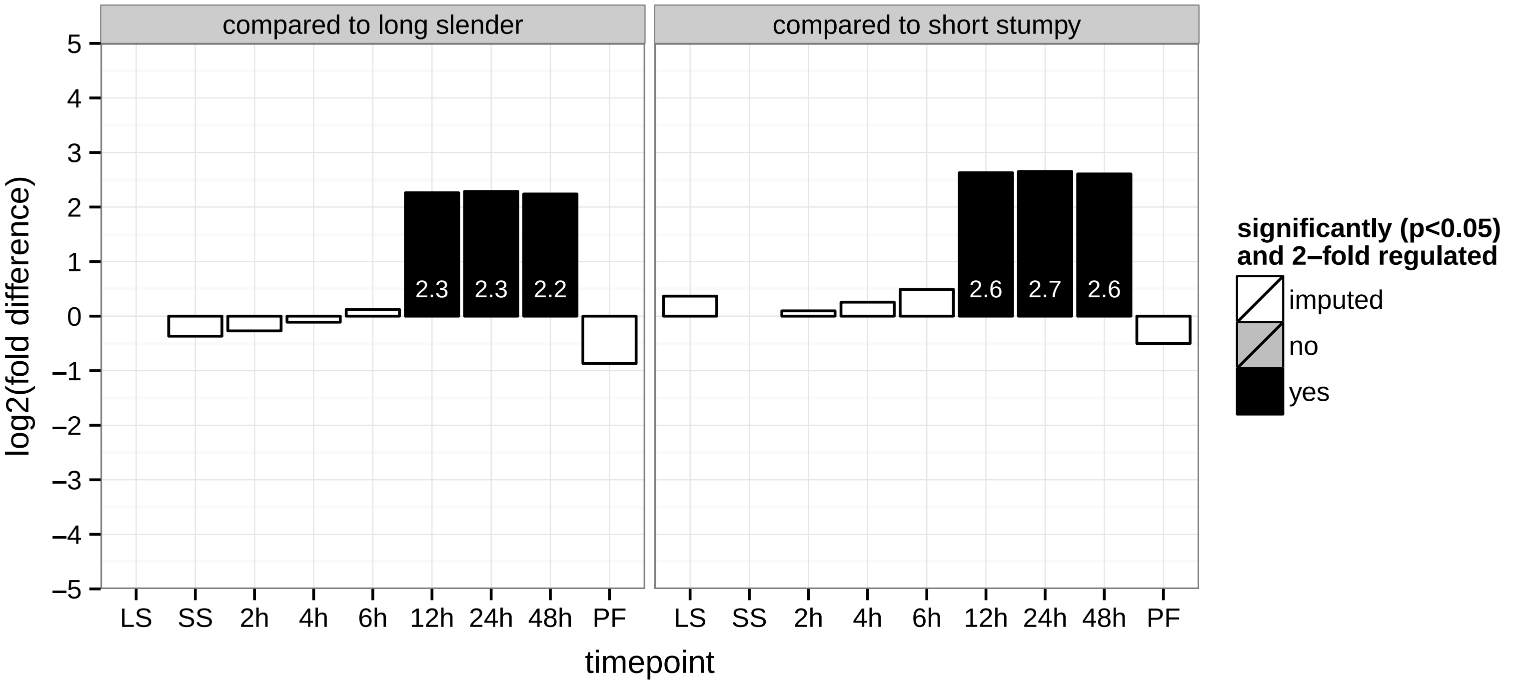
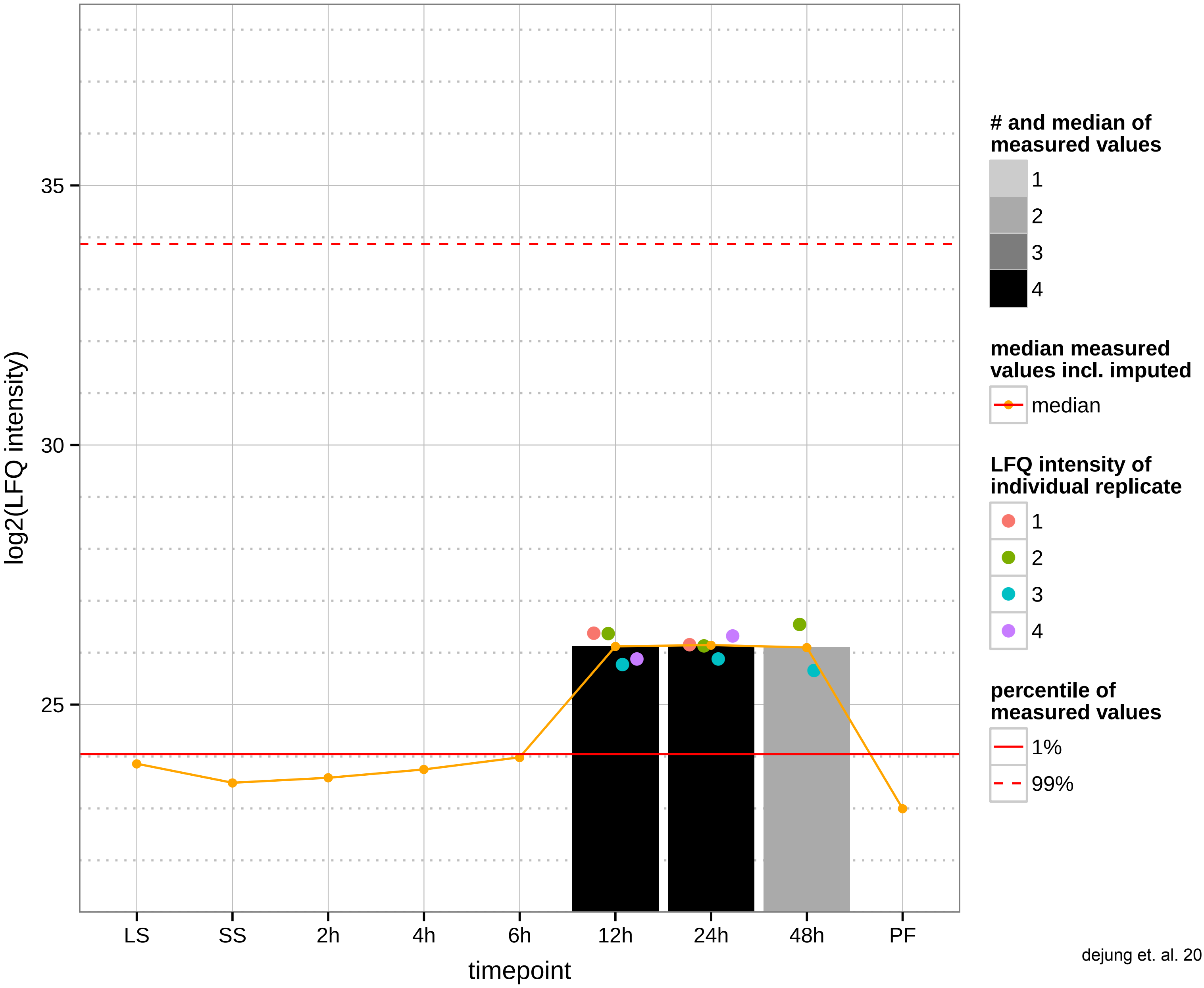
hypothetical protein, conserved
Tb927.8.6670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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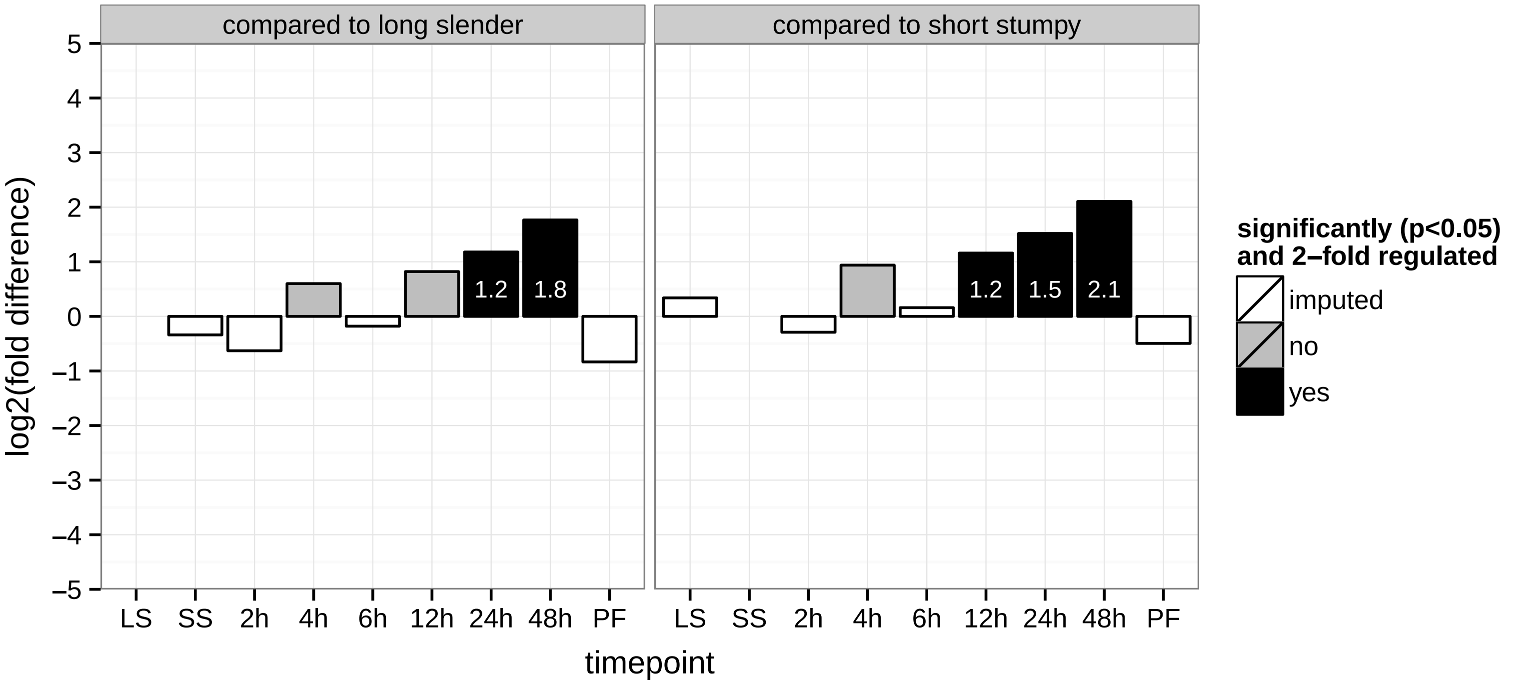
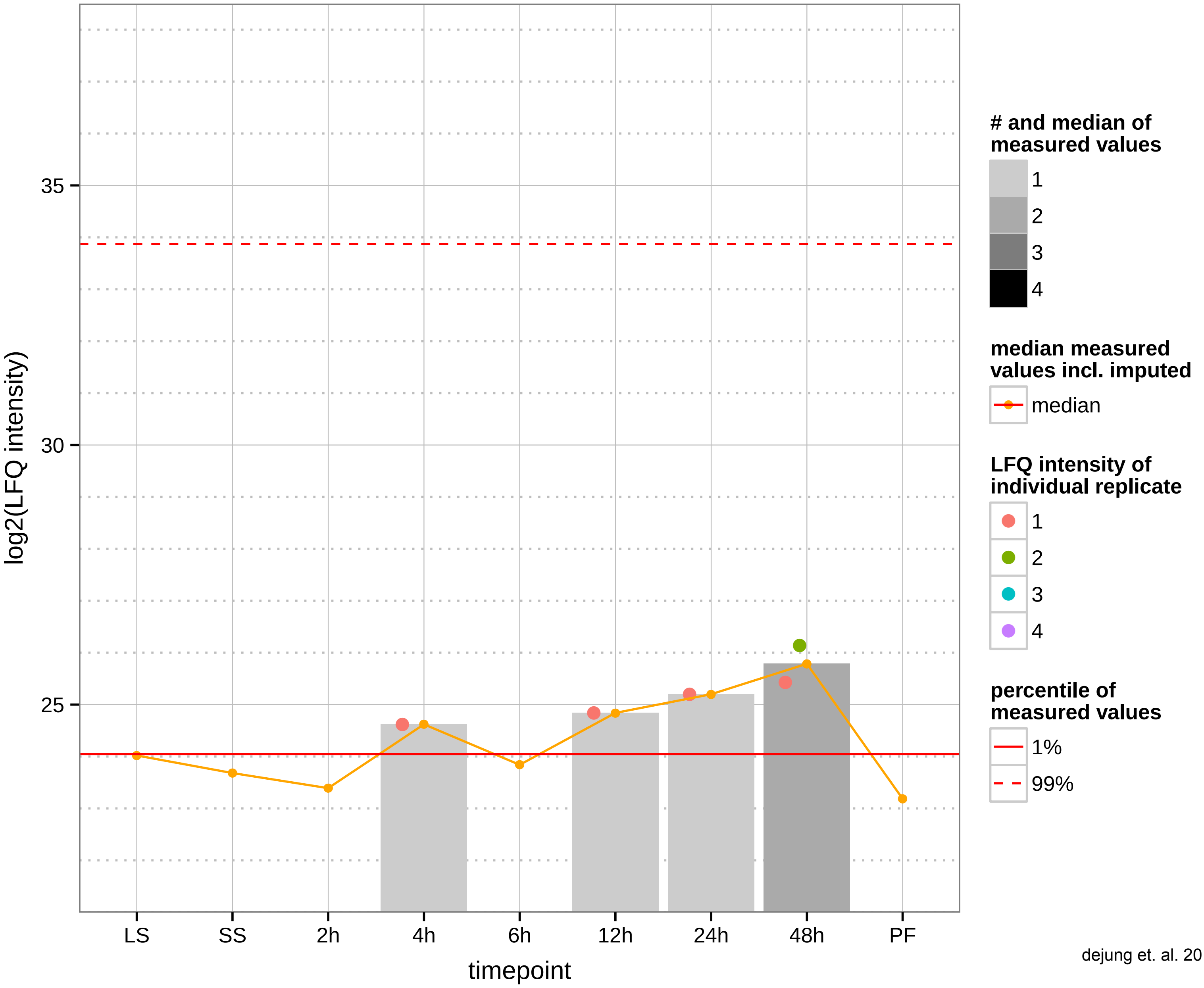
hypothetical protein, conserved
Tb927.8.6850
AGOF: calcium ion binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding, protein binding, zinc ion binding
PGOC: null
PGOP: null





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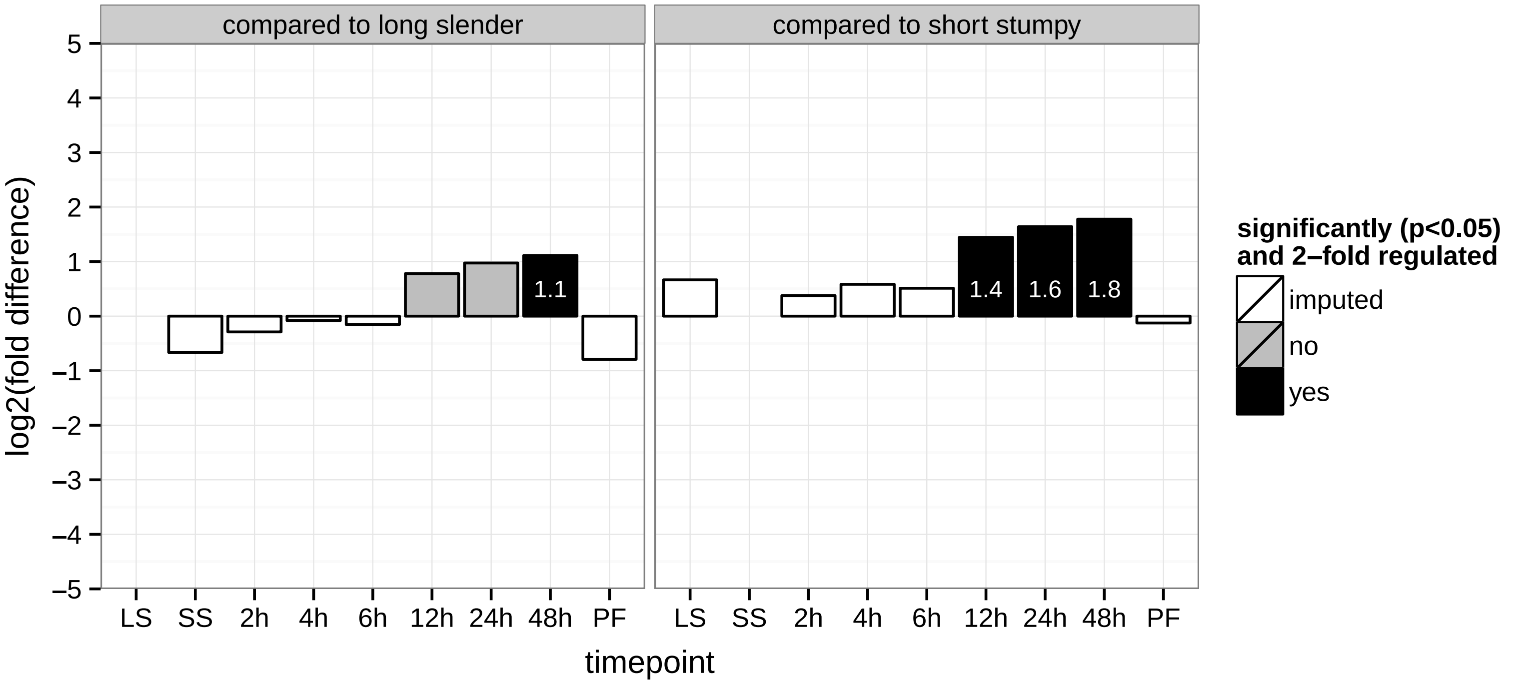
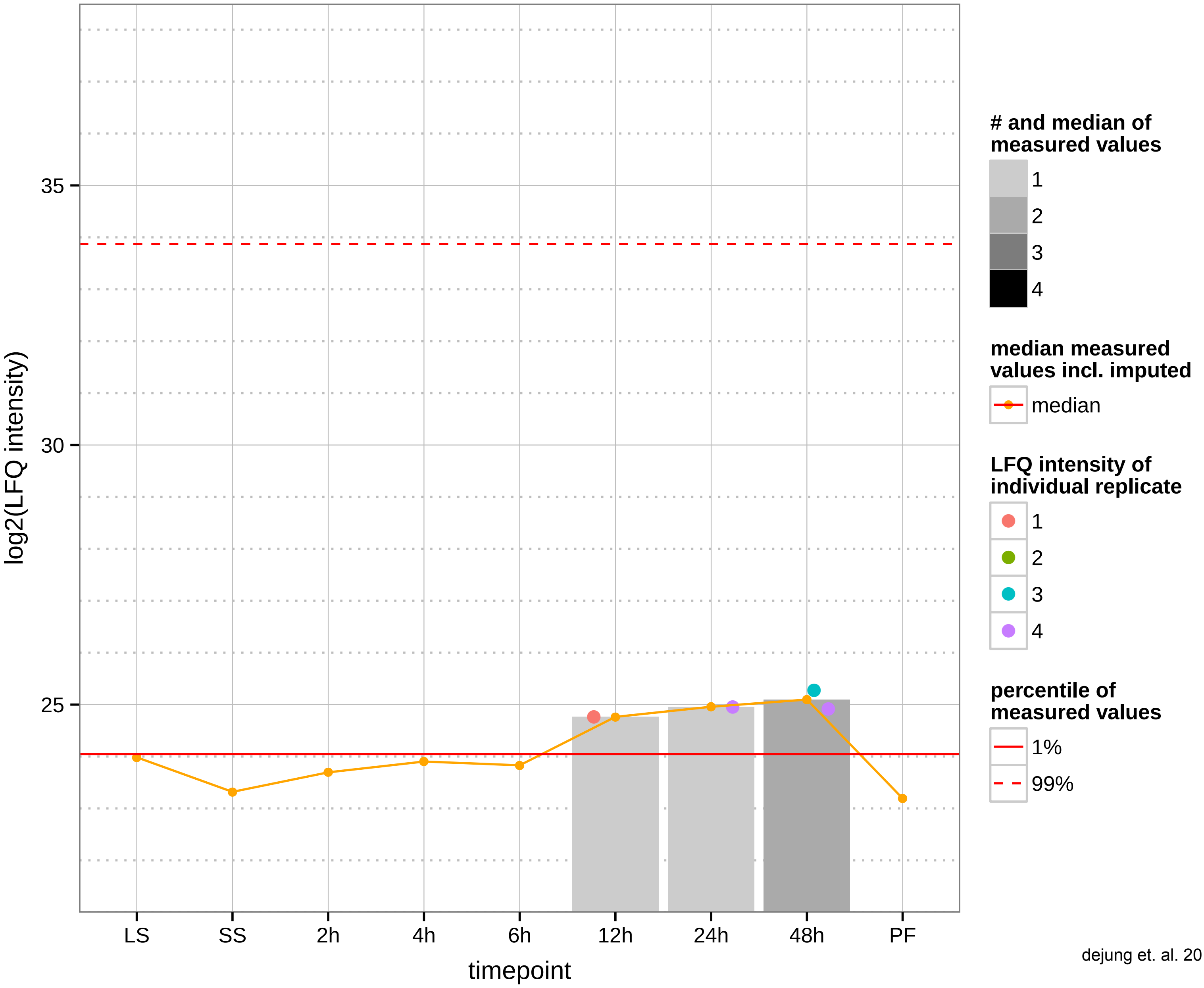
hypothetical protein, conserved
Tb927.9.12800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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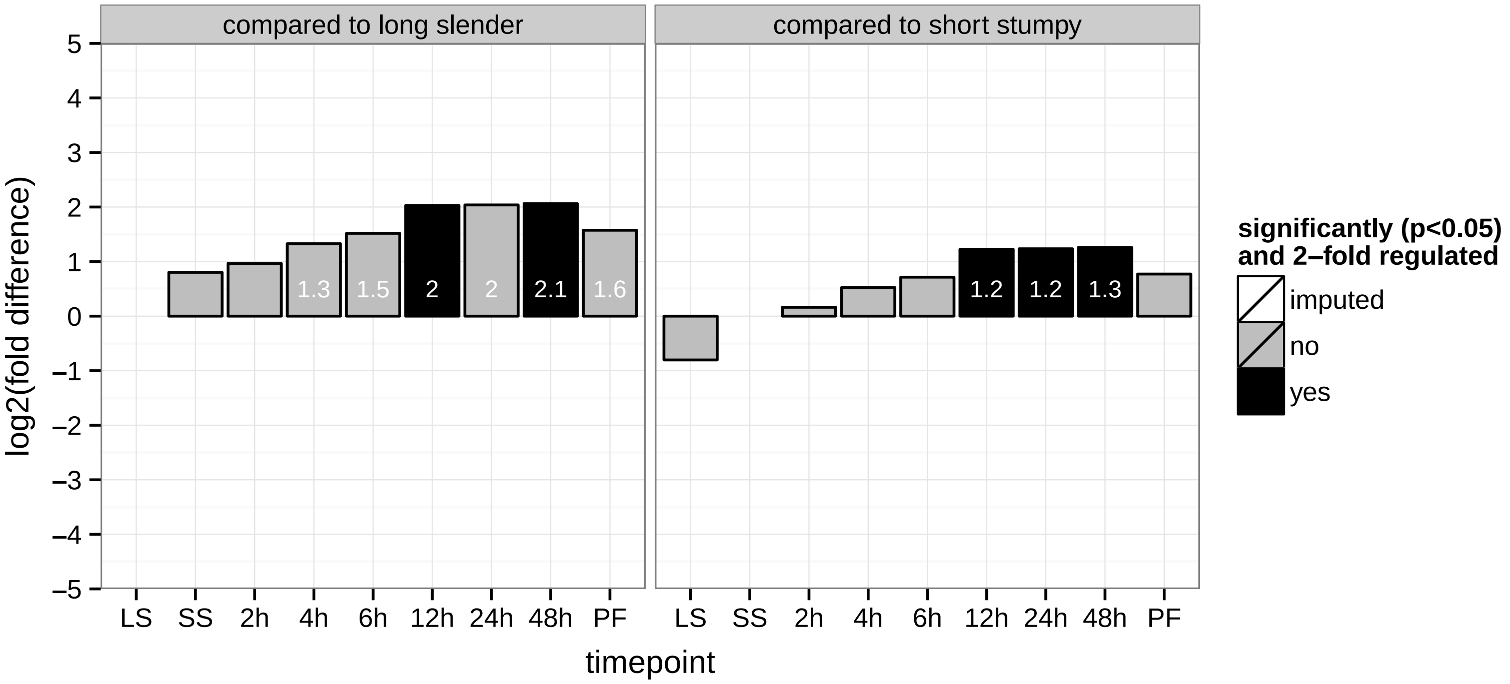
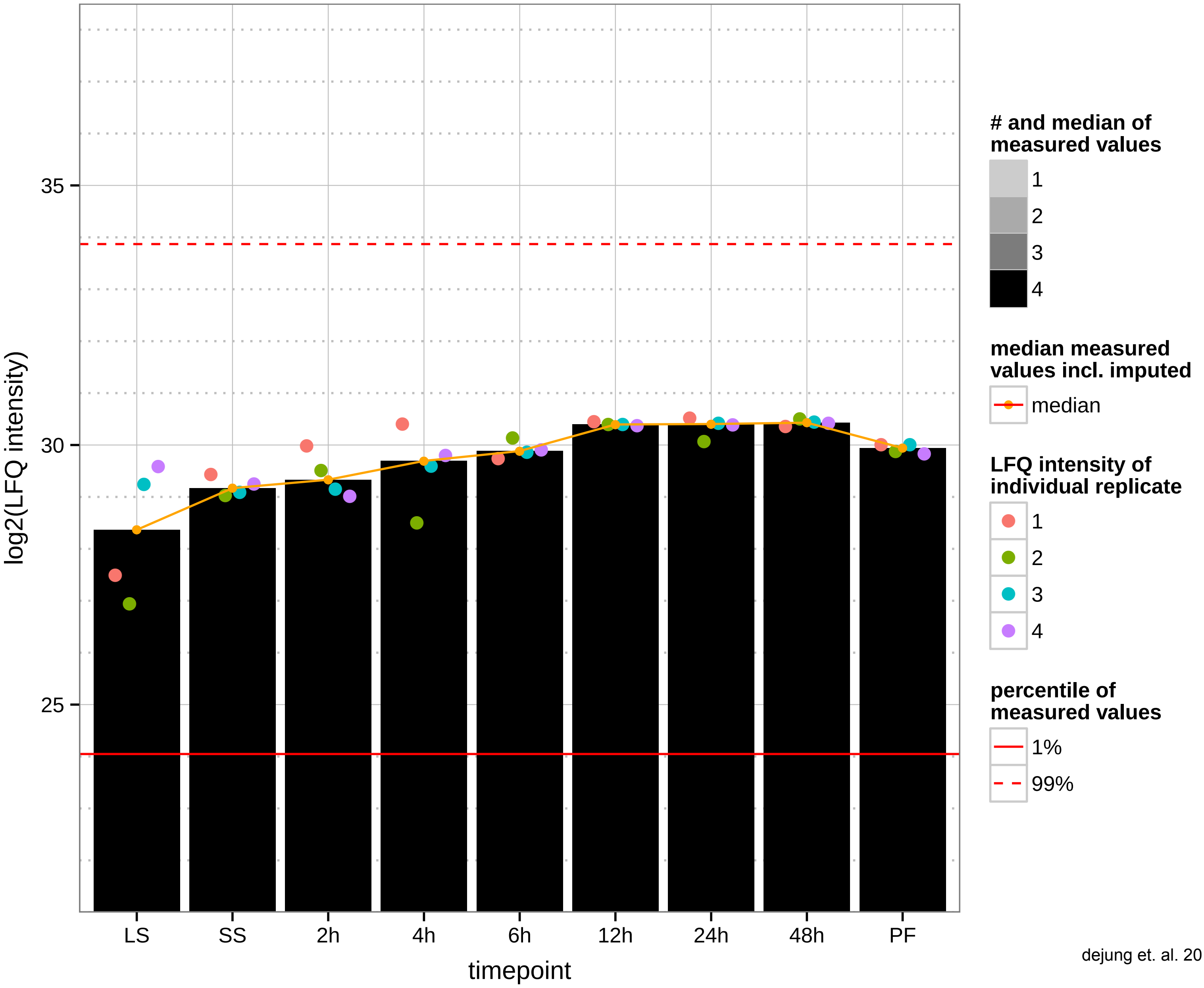
calcium motive p−type ATPase, putative
Tb927.9.15460
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, calcium−tra
AGOC: integral to membrane, plasma membrane
AGOP: ATP biosynthetic process, cation transport, metabolic process
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, catalytic acti
PGOC: membrane
PGOP: cation transport, metabolic process





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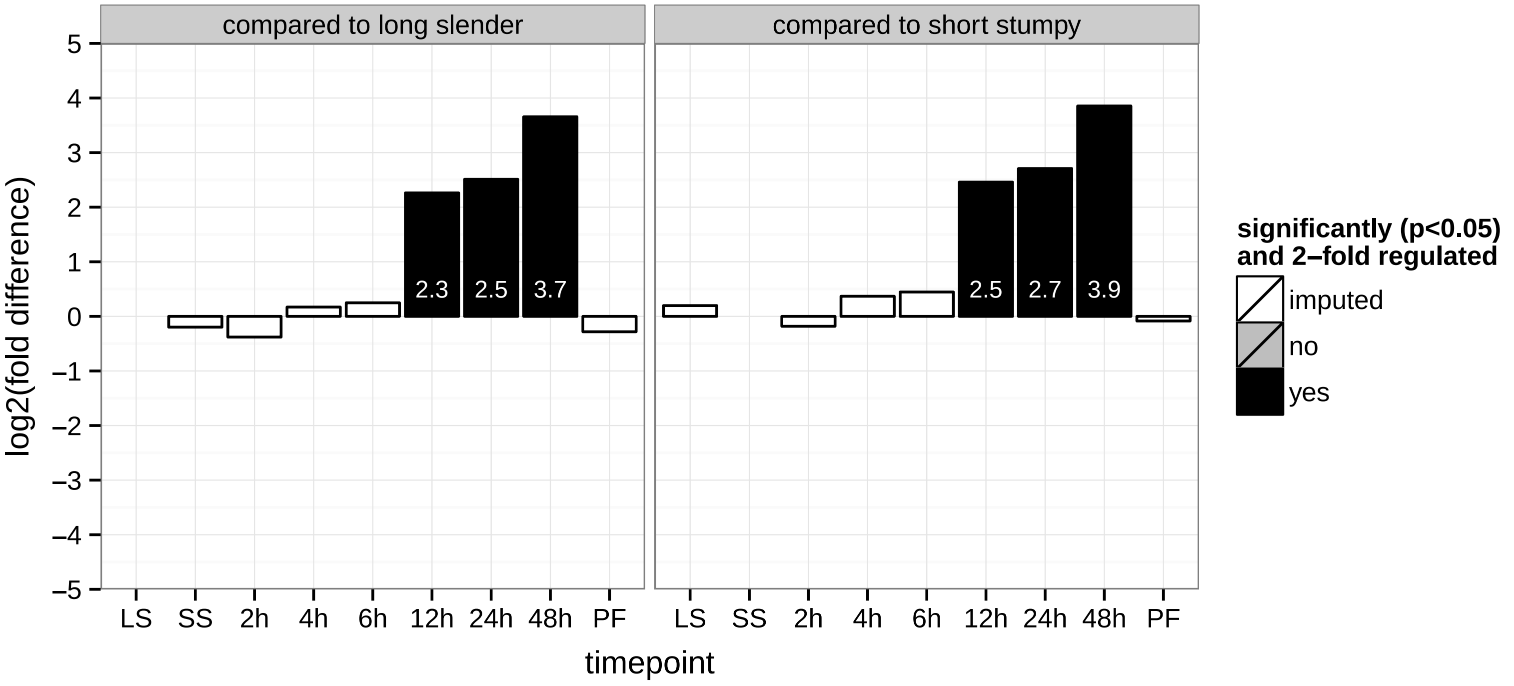
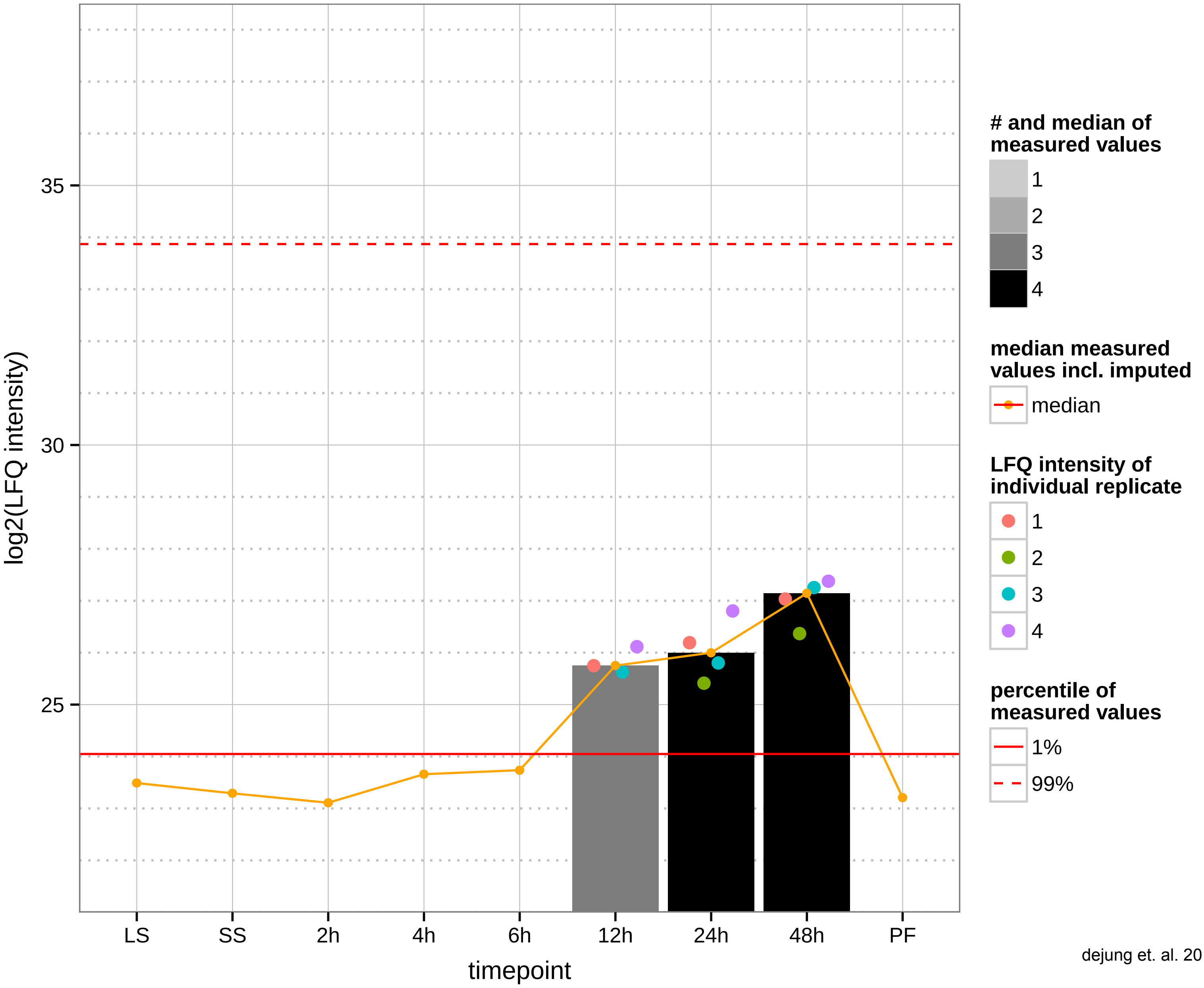
hypothetical protein, conserved
Tb927.9.6650
AGOF: ATP binding, alanine–tRNA ligase activity, nucleic acid binding
AGOC: cytoplasm
AGOP: alanyl–tRNA aminoacylation, translation
PGOF: ATP binding, alanine–tRNA ligase activity, ligase activity, forming aminoacyl–tRNA and related compounds, nucleic ac
PGOC: cytoplasm
PGOP: alanyl–tRNA aminoacylation, tRNA aminoacylation





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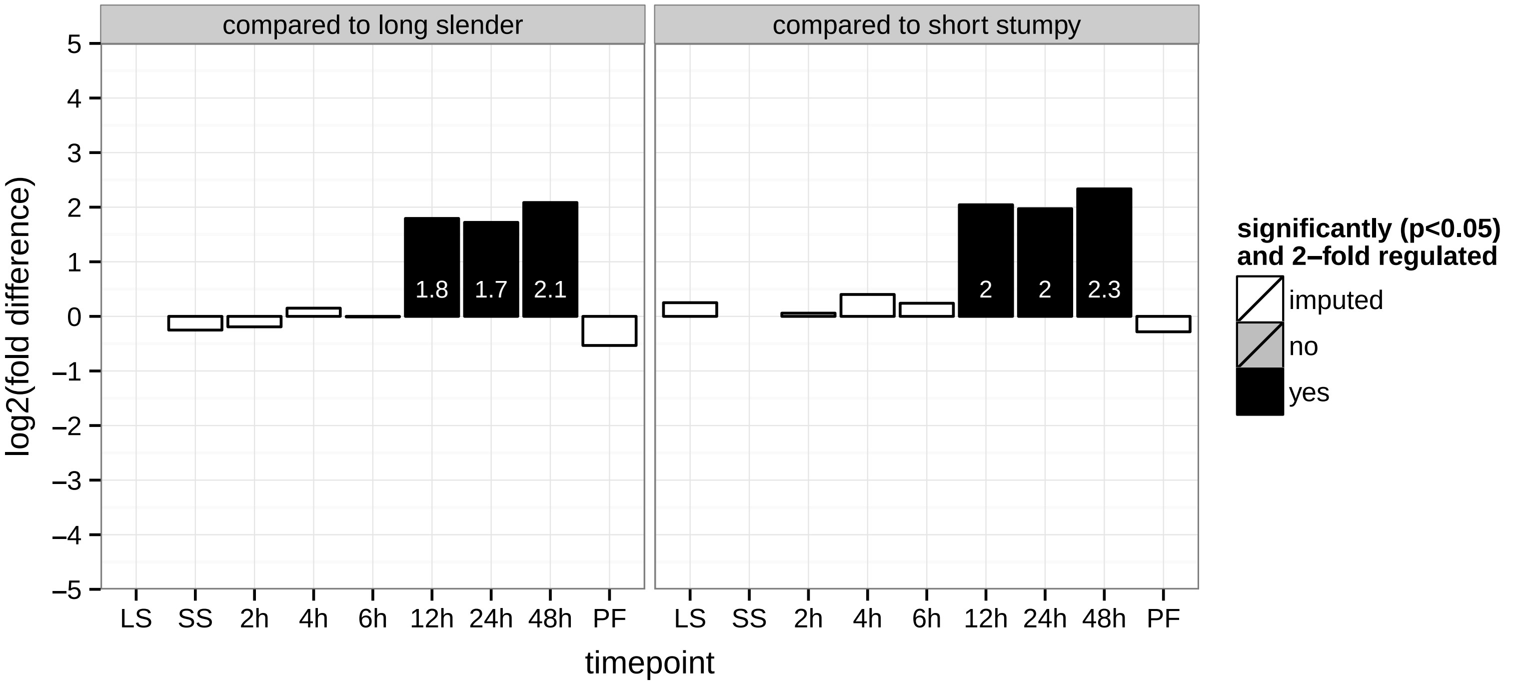
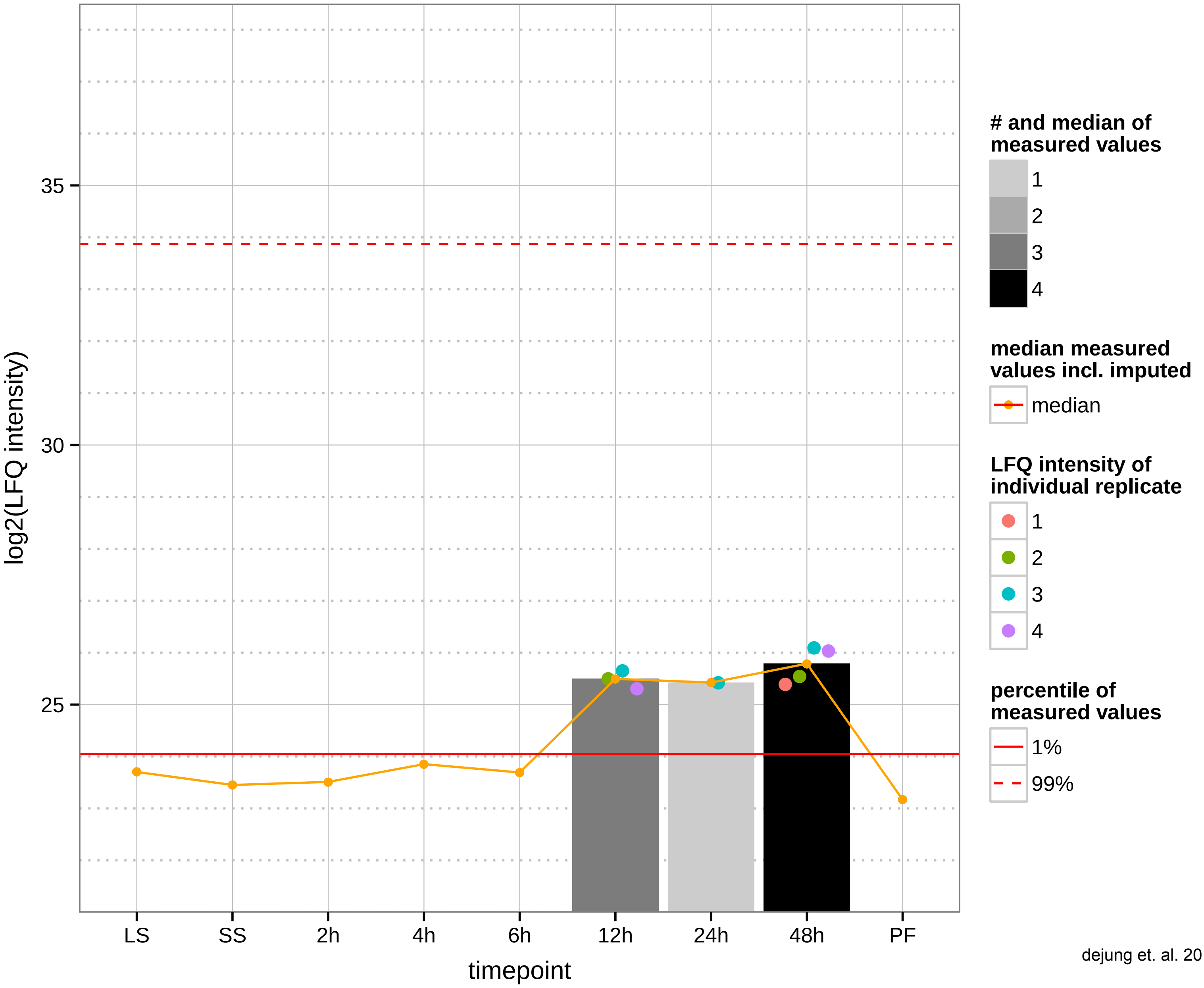
hypothetical protein, conserved
Tb927.9.6720
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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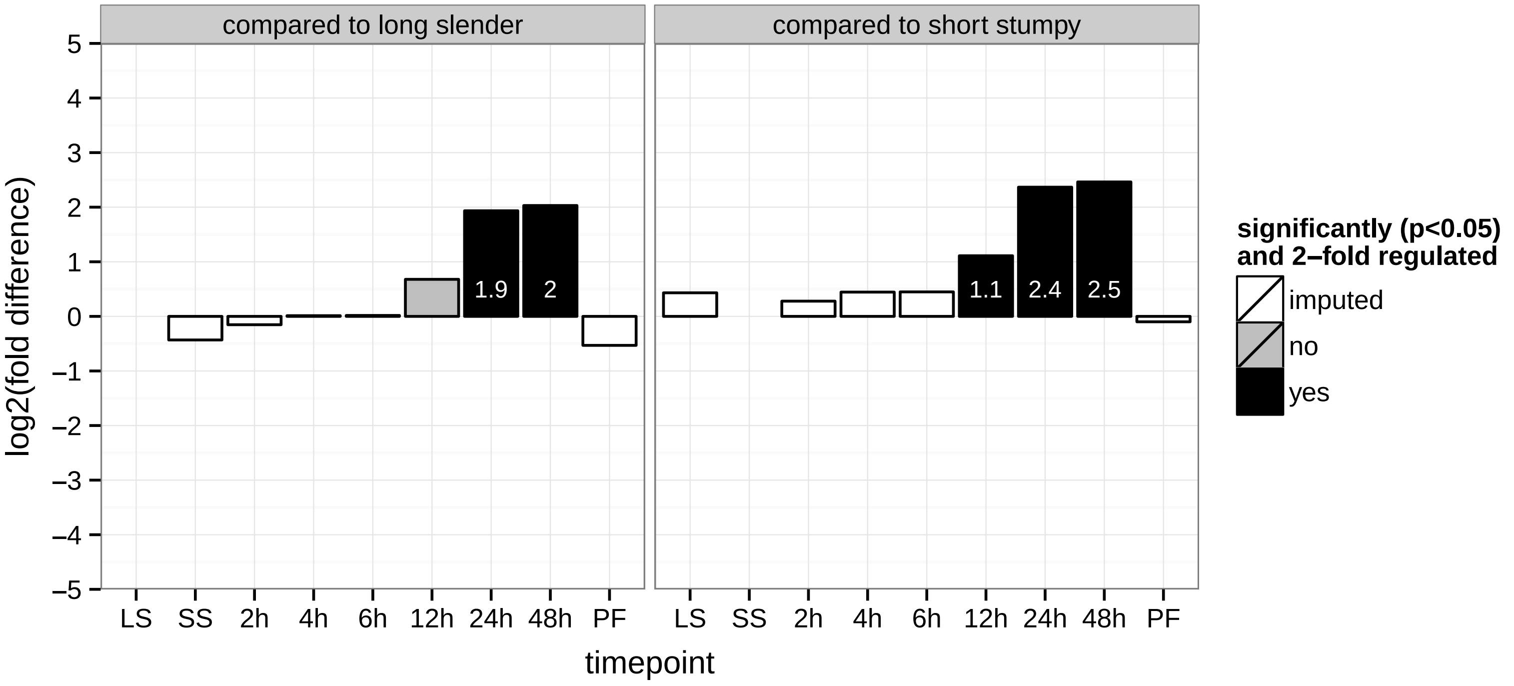
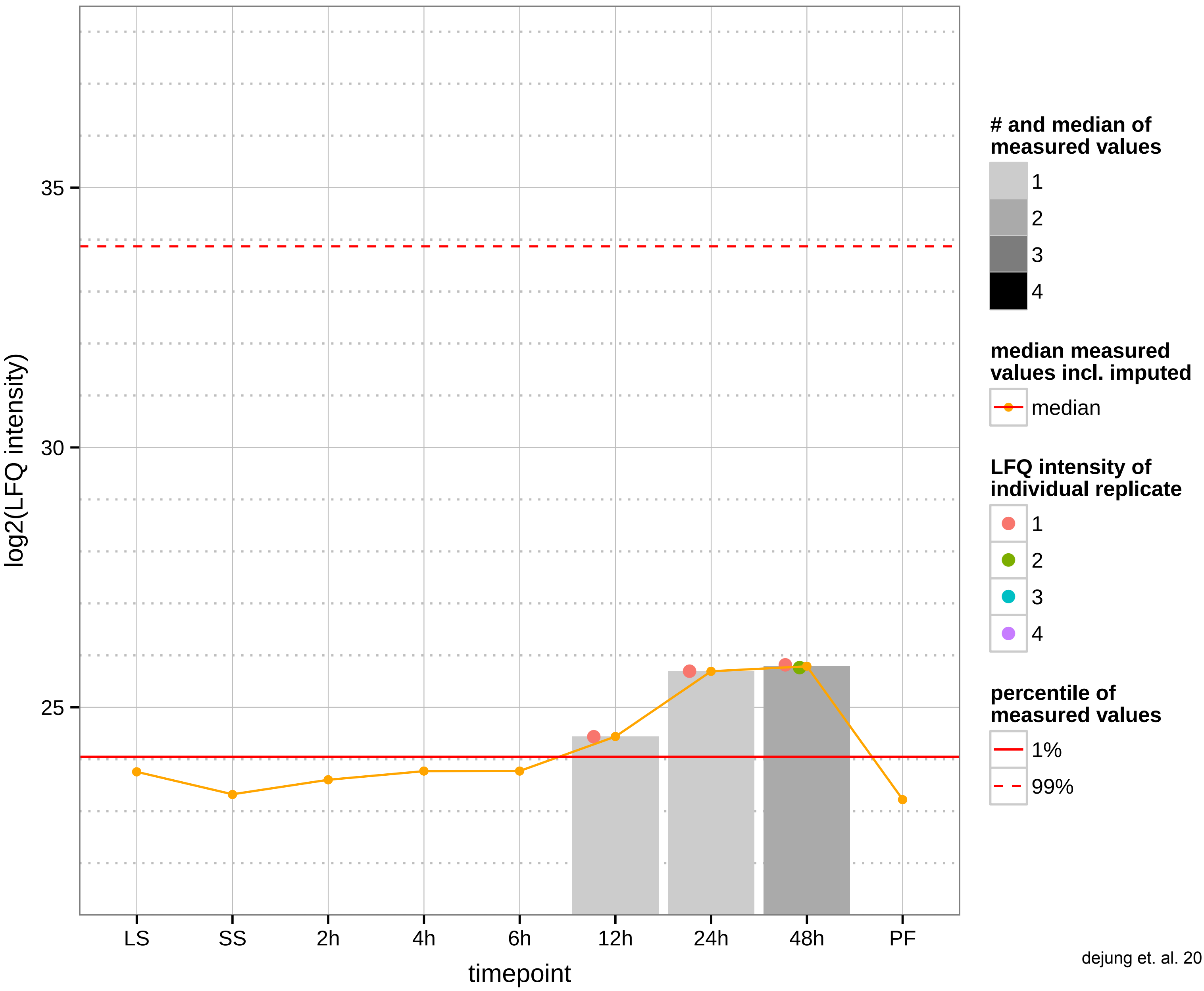
cytochrome c oxidase assembly factor, putative
Tb927.9.8680
AGOF: copper ion binding
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: cellular copper ion homeostasis, copper ion transport, oxidation–reduction process, respiratory chain complex IV asse
PGOF: copper ion binding
PGOC: mitochondrial inner membrane
PGOP: cellular copper ion homeostasis, copper ion transport, respiratory chain complex IV assembly





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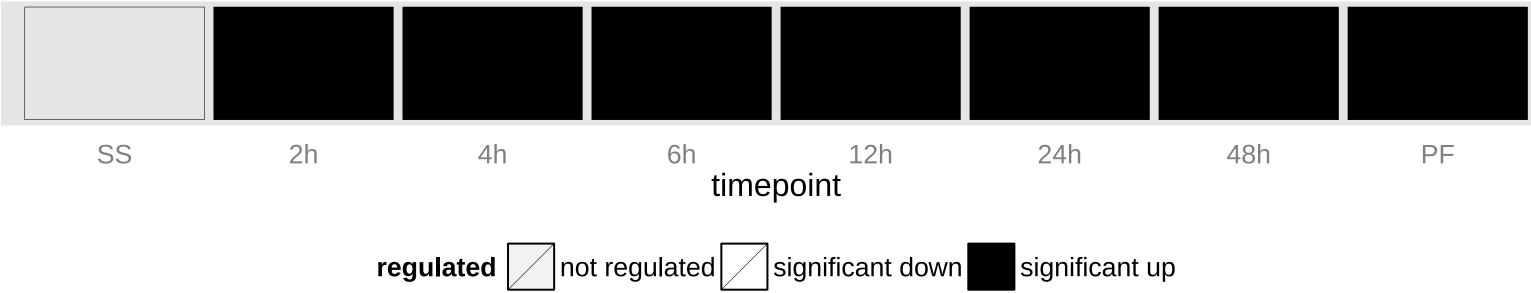

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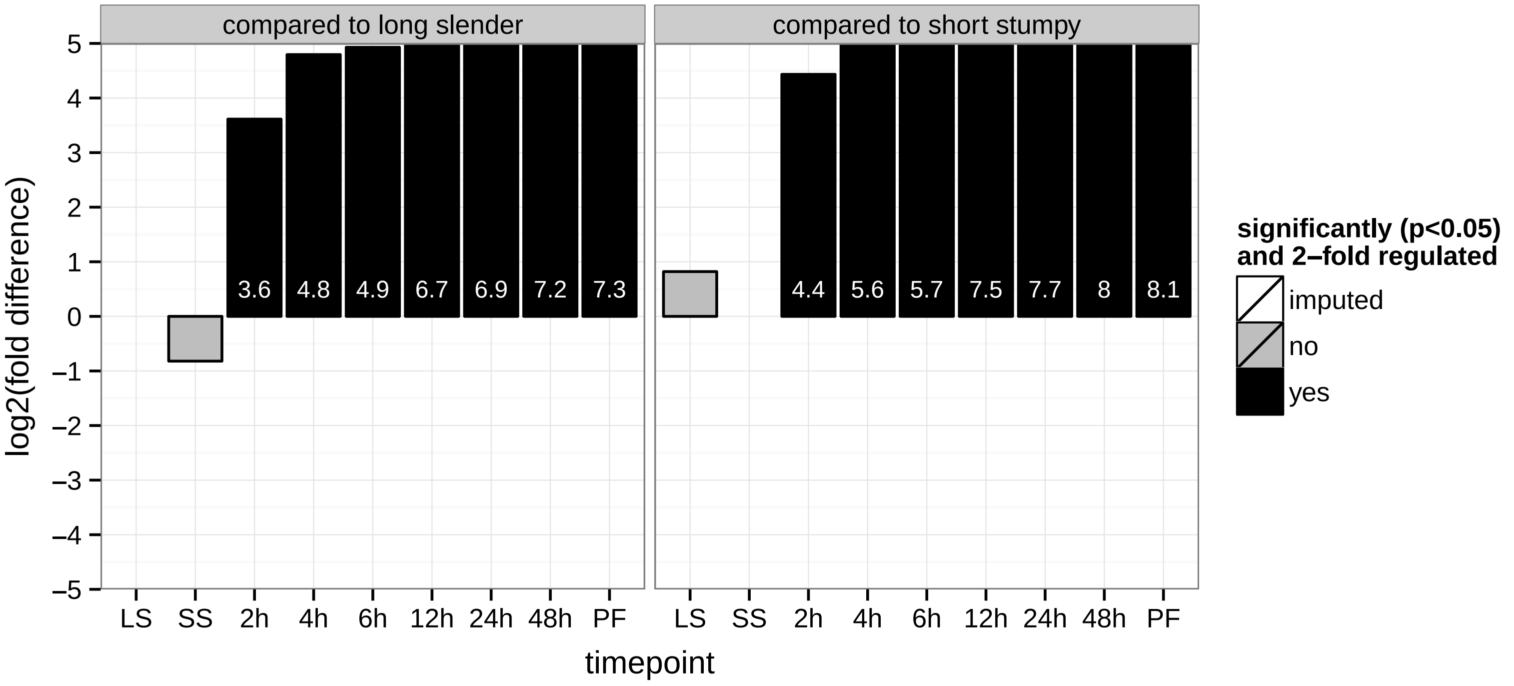
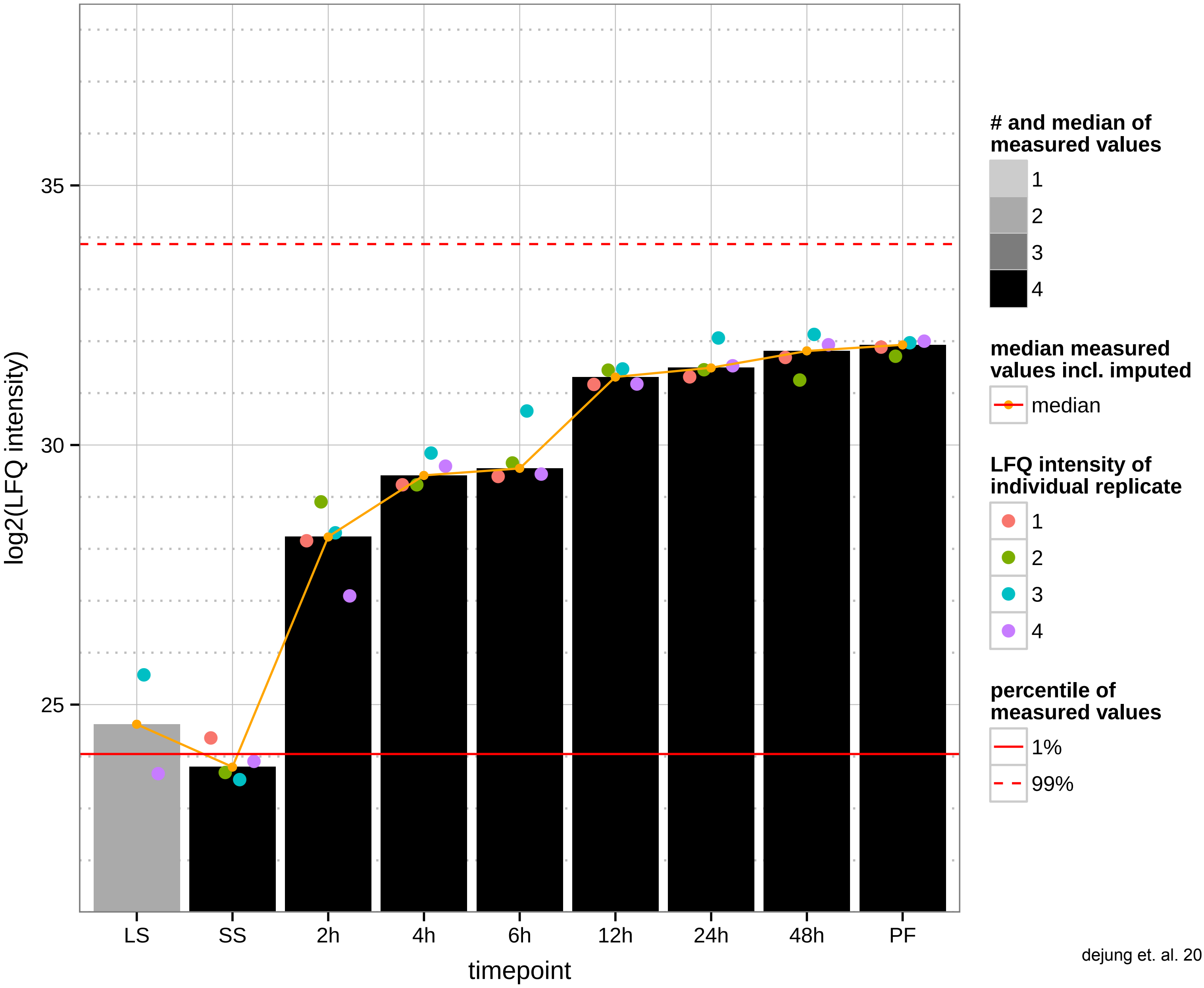
NA, cystathionine beta–synthase, putative
Tb11.02.5400b;Tb11.02.5400
AGOF: NA, cystathionine beta–synthase activity, pyridoxal phosphate binding
AGOC: NA, null
AGOP: NA, cysteine biosynthetic process
PGOF: NA, catalytic activity, pyridoxal phosphate binding
PGOC: NA, null
PGOP: NA, metabolic process





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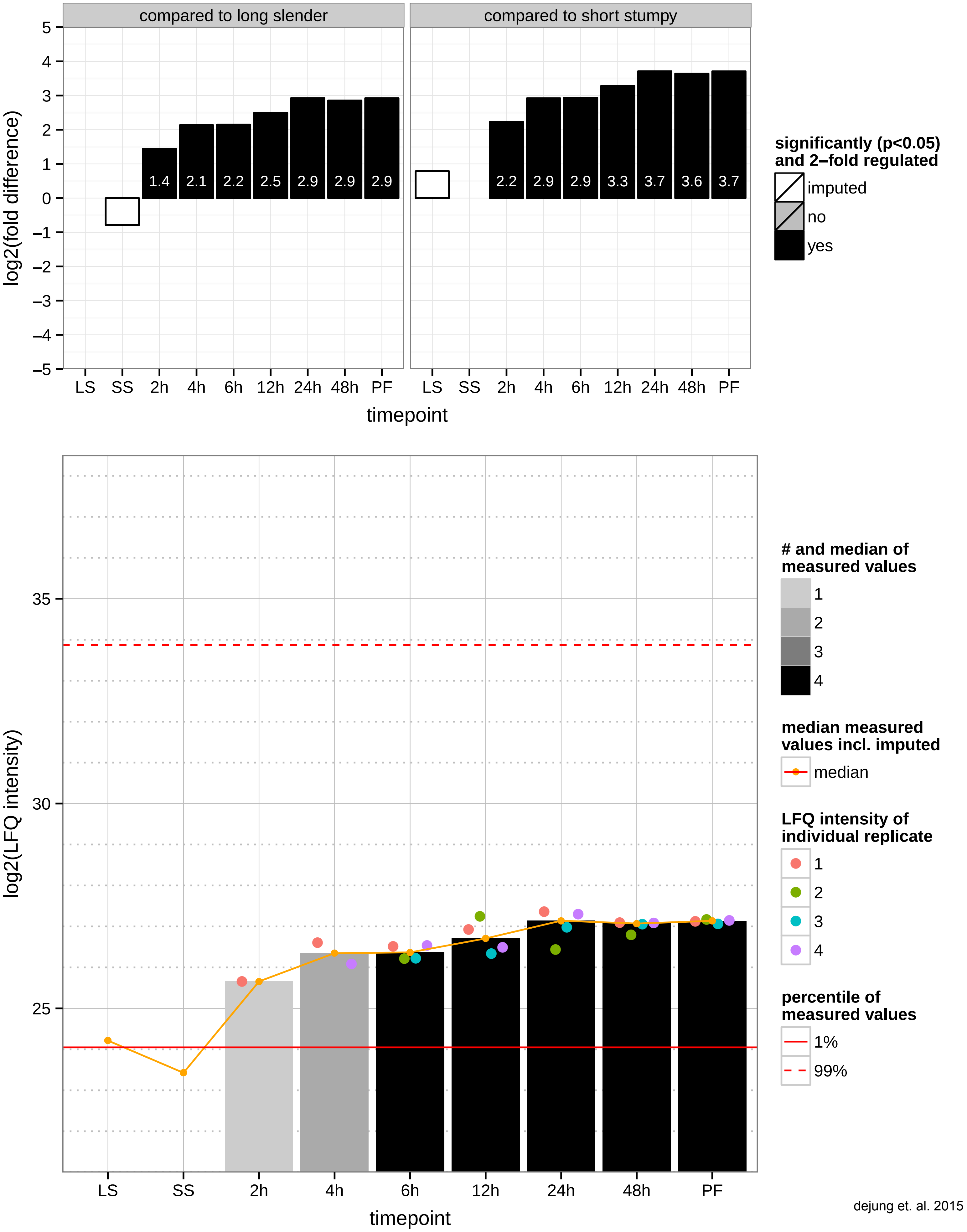
NAD(p)–dependent steroid dehydrogenase–like protein, NAD(P)–dependent steroid dehydrogenase protein, putative
Tb927.7.4950;Tb11.v5.0176
AGOF: null, 3–beta–hydroxy–delta5–steroid dehydrogenase activity, catalytic activity
AGOC: null
AGOP: null, steroid biosynthetic process
PGOF: 3–beta–hydroxy–delta5–steroid dehydrogenase activity, oxidoreductase activity, acting on the CH–OH group of donors
PGOC: null
PGOP: oxidation–reduction process, steroid biosynthetic process



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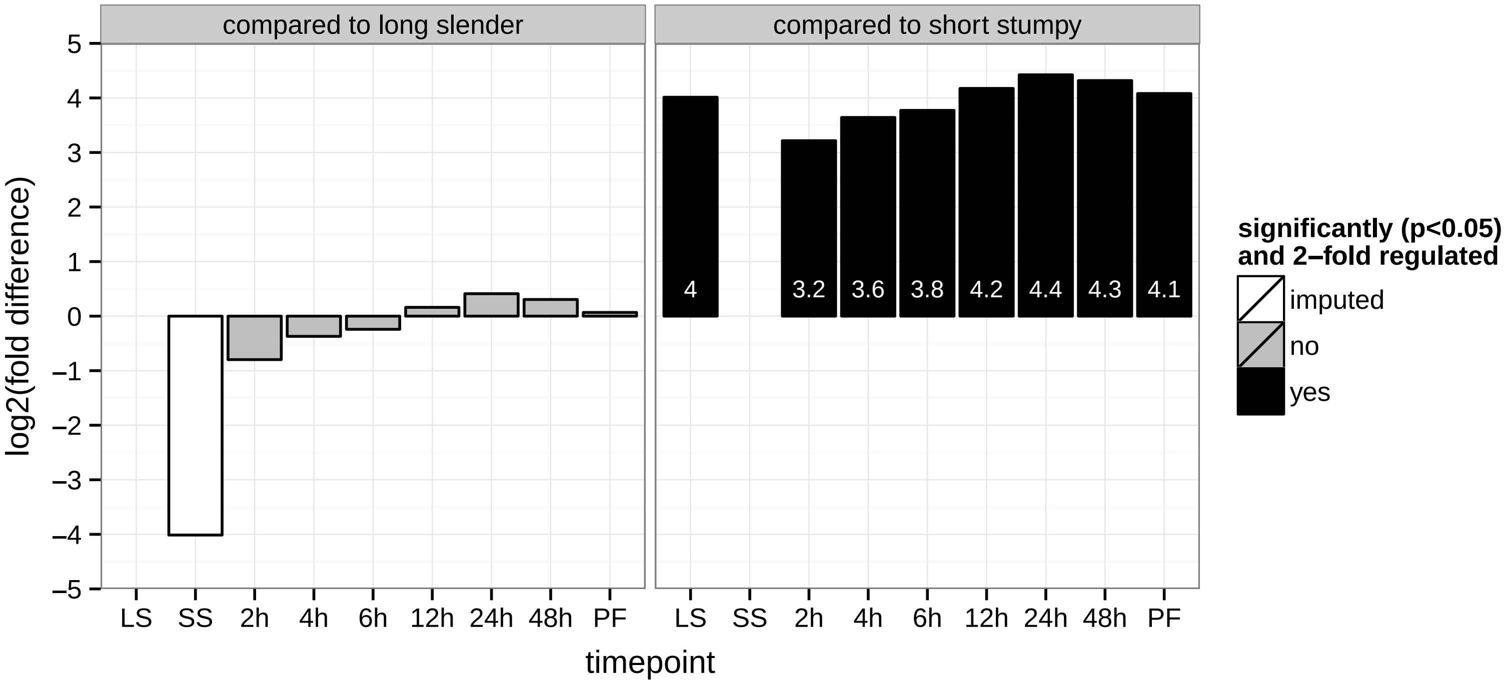
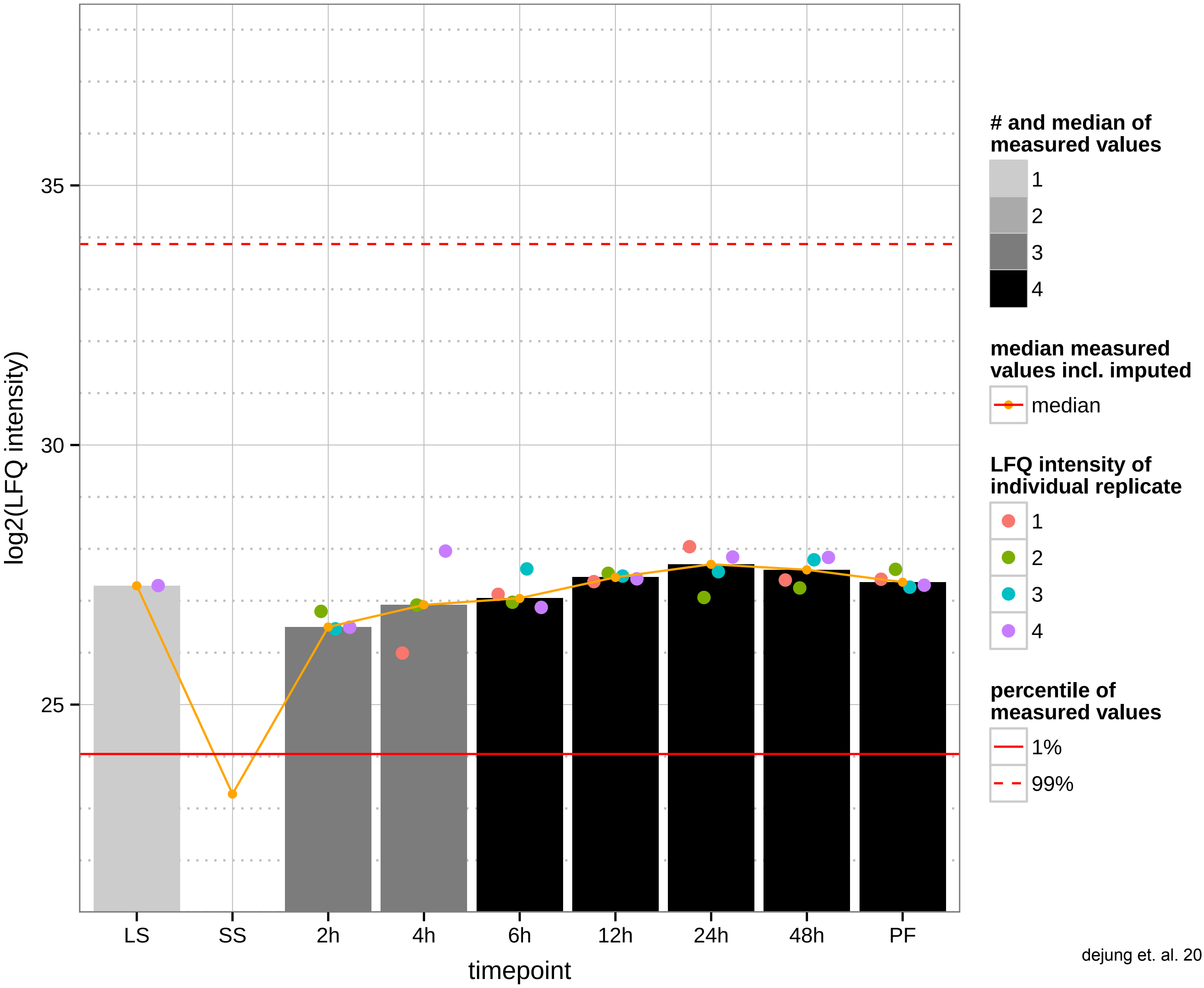
hypothetical protein, conserved, conserved protein, unknown function
Tb927.1.1470;Tb11.v5.0315
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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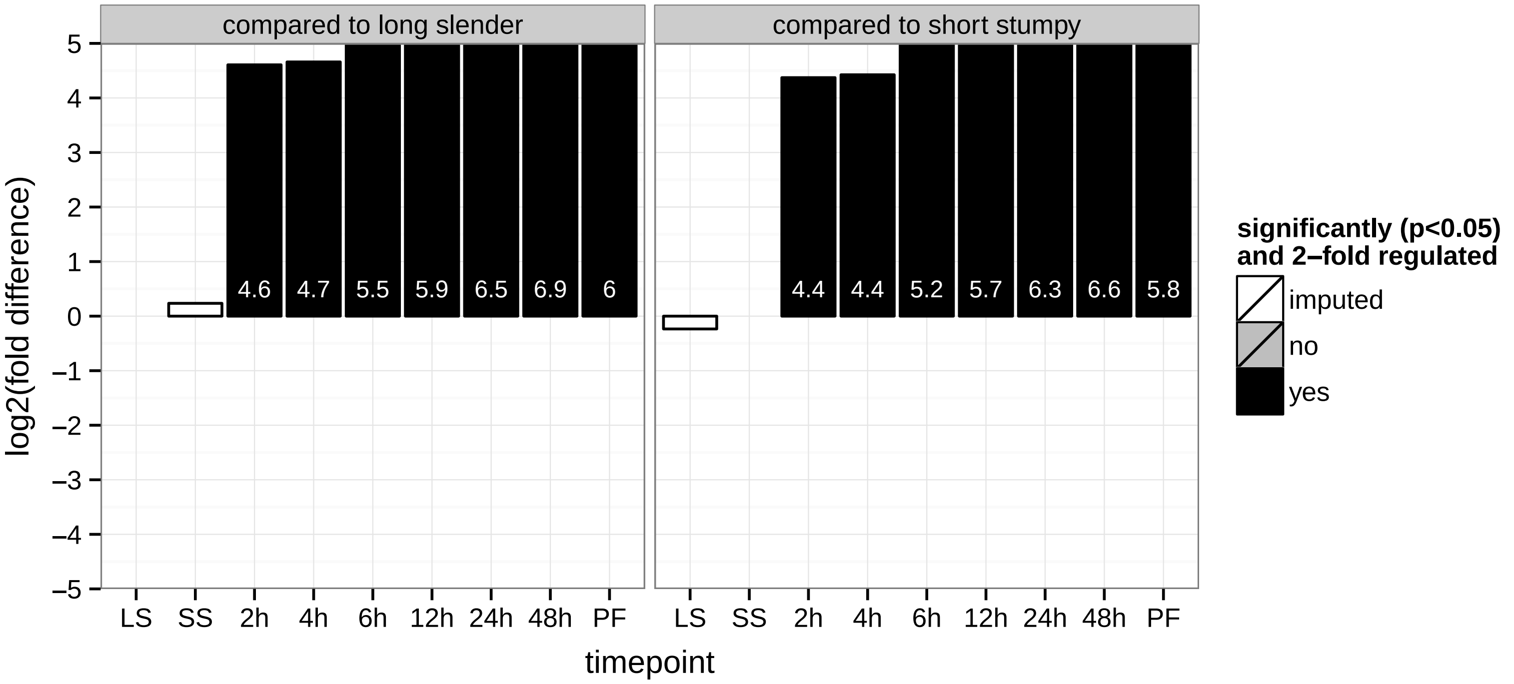
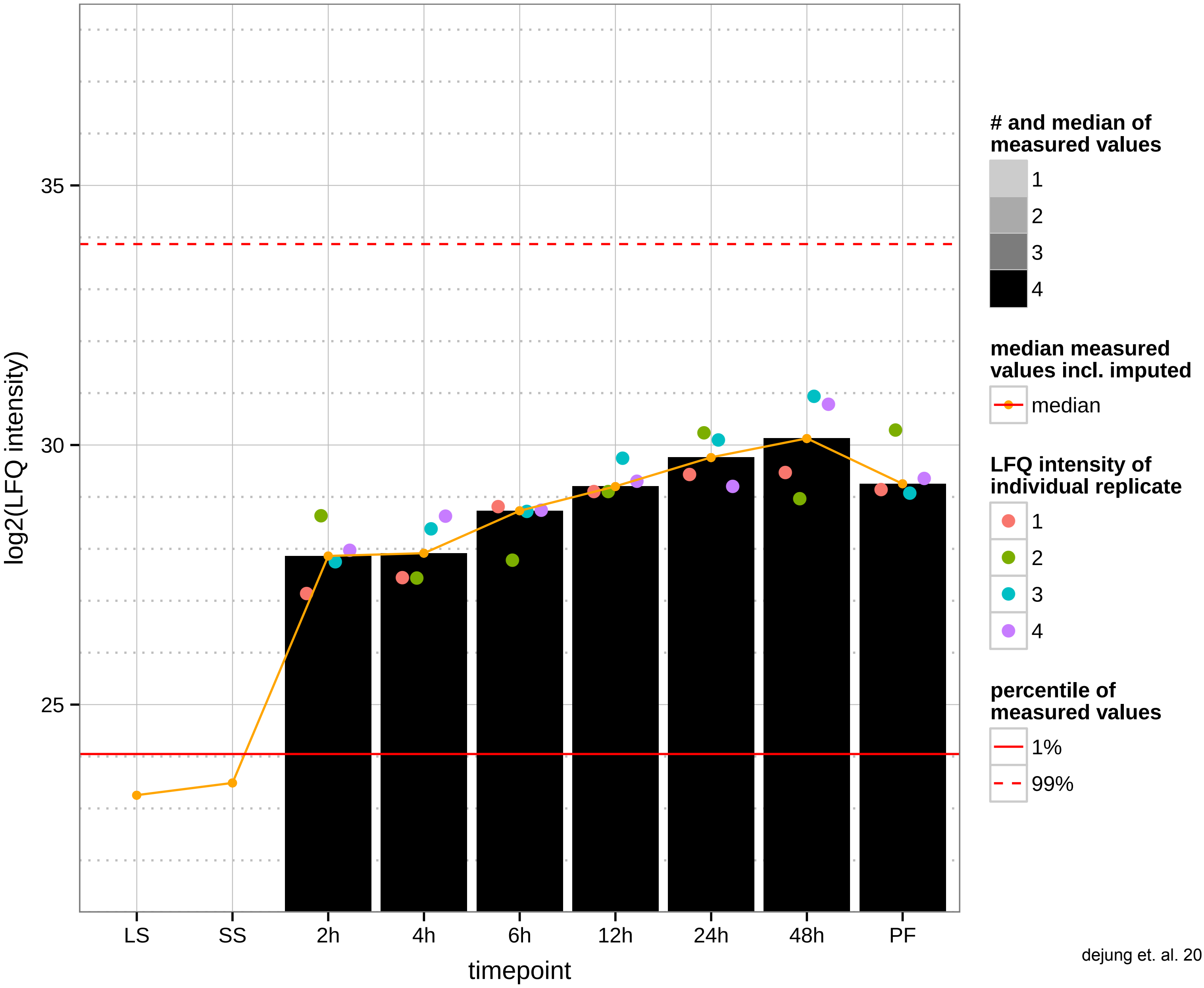
THT1 – hexose transporter, putative, THT2A – glucose transporter, fragment, glucose transporter, glucose transporter 2A (TH
Tb927.10.8520;Tb927.10.8510;Tb927.10.8500;Tb11.v5.0331;Tb927.10.8530;Tb927.10.8490;Tb11.v5.0332;Tb11.v5.0333
AGOF: null, substrate–specific transmembrane transporter activity, hexose transmembrane transporter activity
AGOC: null, integral to membrane, membrane
AGOP: null, transmembrane transport, transport, hexose transport, transmembrane transport
PGOF: substrate–specific transmembrane transporter activity, transmembrane transporter activity
PGOC: integral to membrane, membrane
PGOP: transmembrane transport





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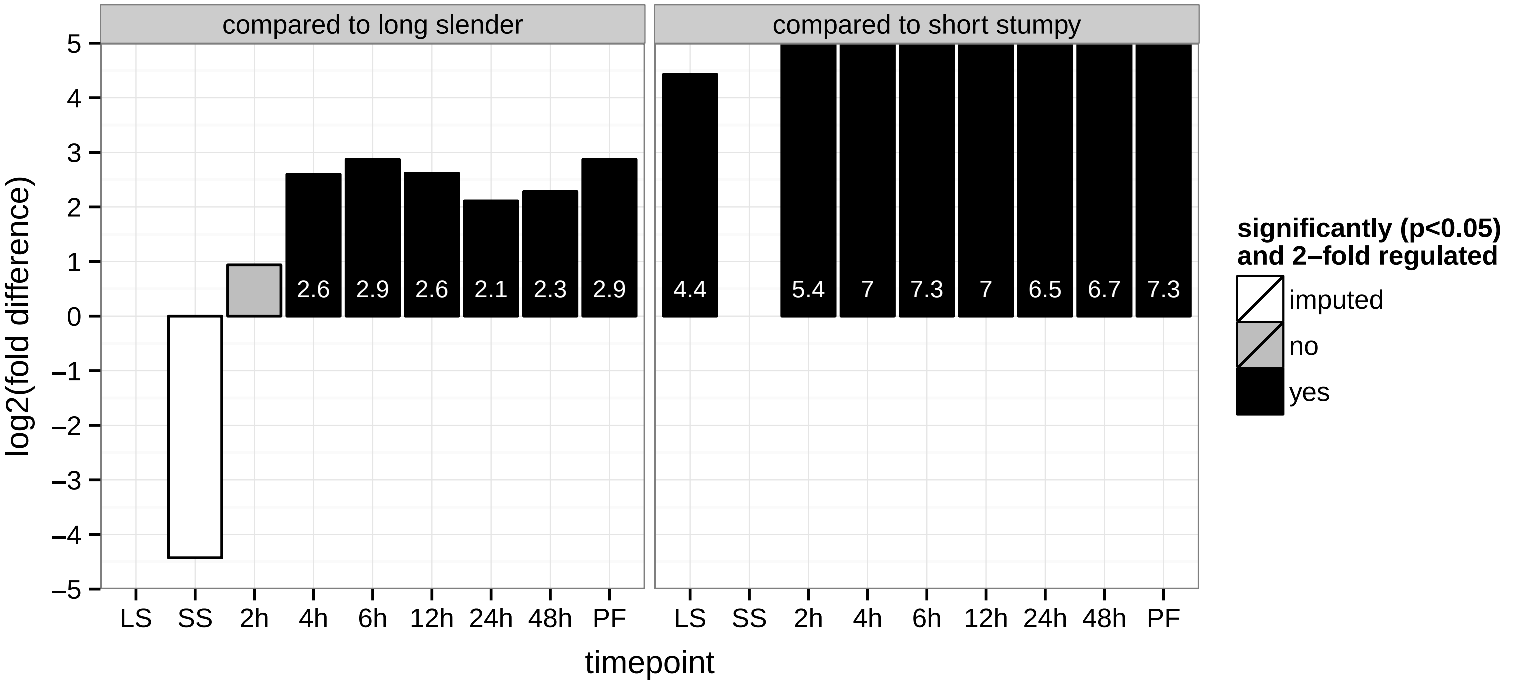
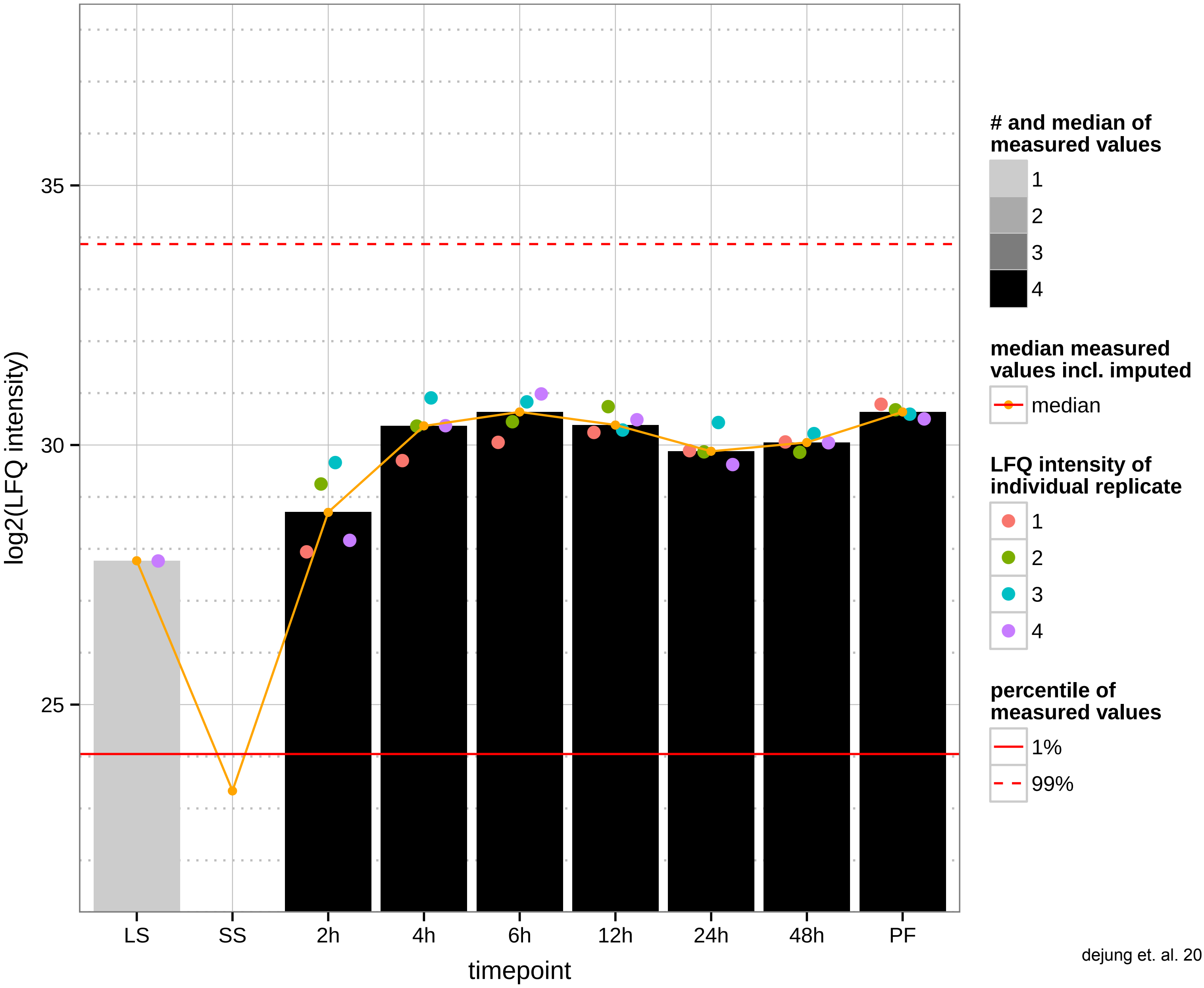
major surface protease gp63, putative, MSP−B
Tb927.8.1630;Tb927.8.1620;Tb927.8.1610;Tb11.v5.0601
AGOF: null, metalloendopeptidase activity, zinc ion binding
AGOC: null, membrane
AGOP: null, cell adhesion, proteolysis
PGOF: metalloendopeptidase activity, zinc ion binding, null
PGOC: membrane, null
PGOP: cell adhesion, proteolysis, null





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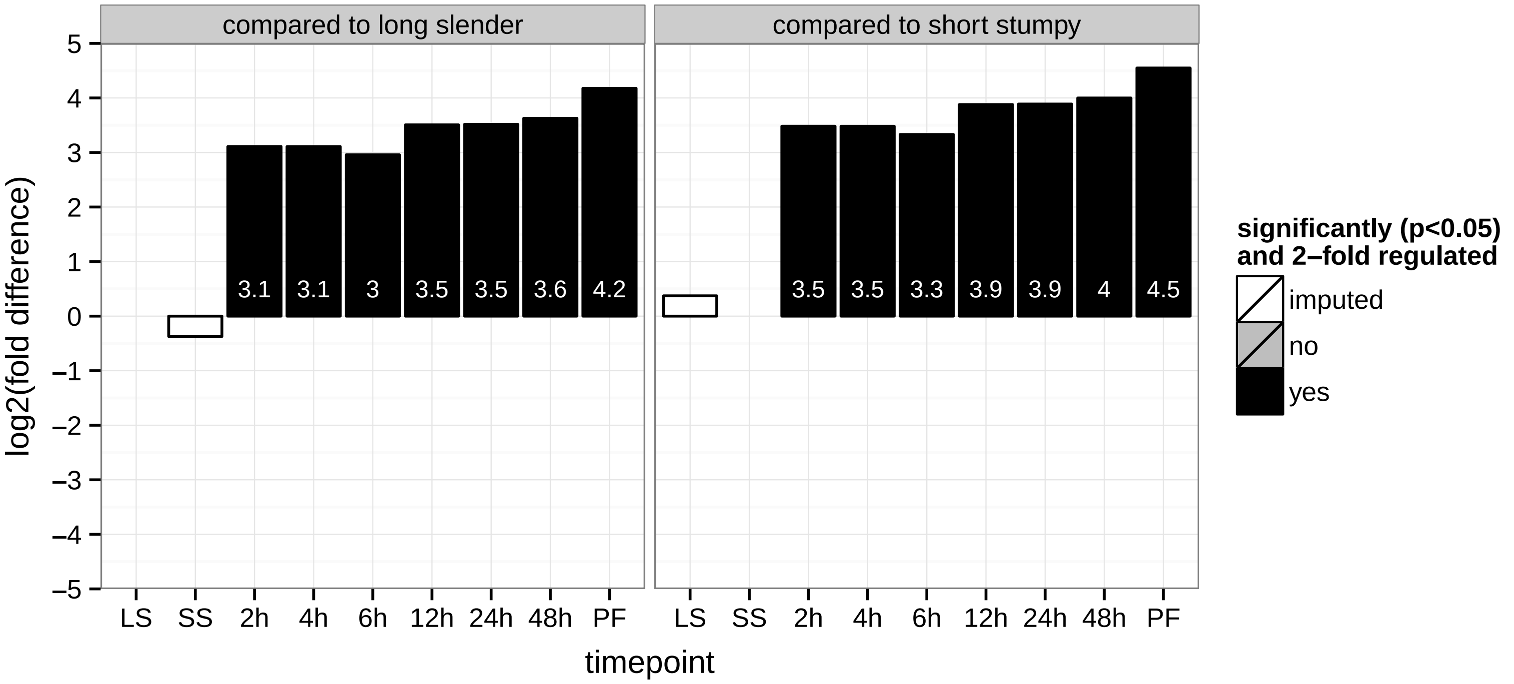
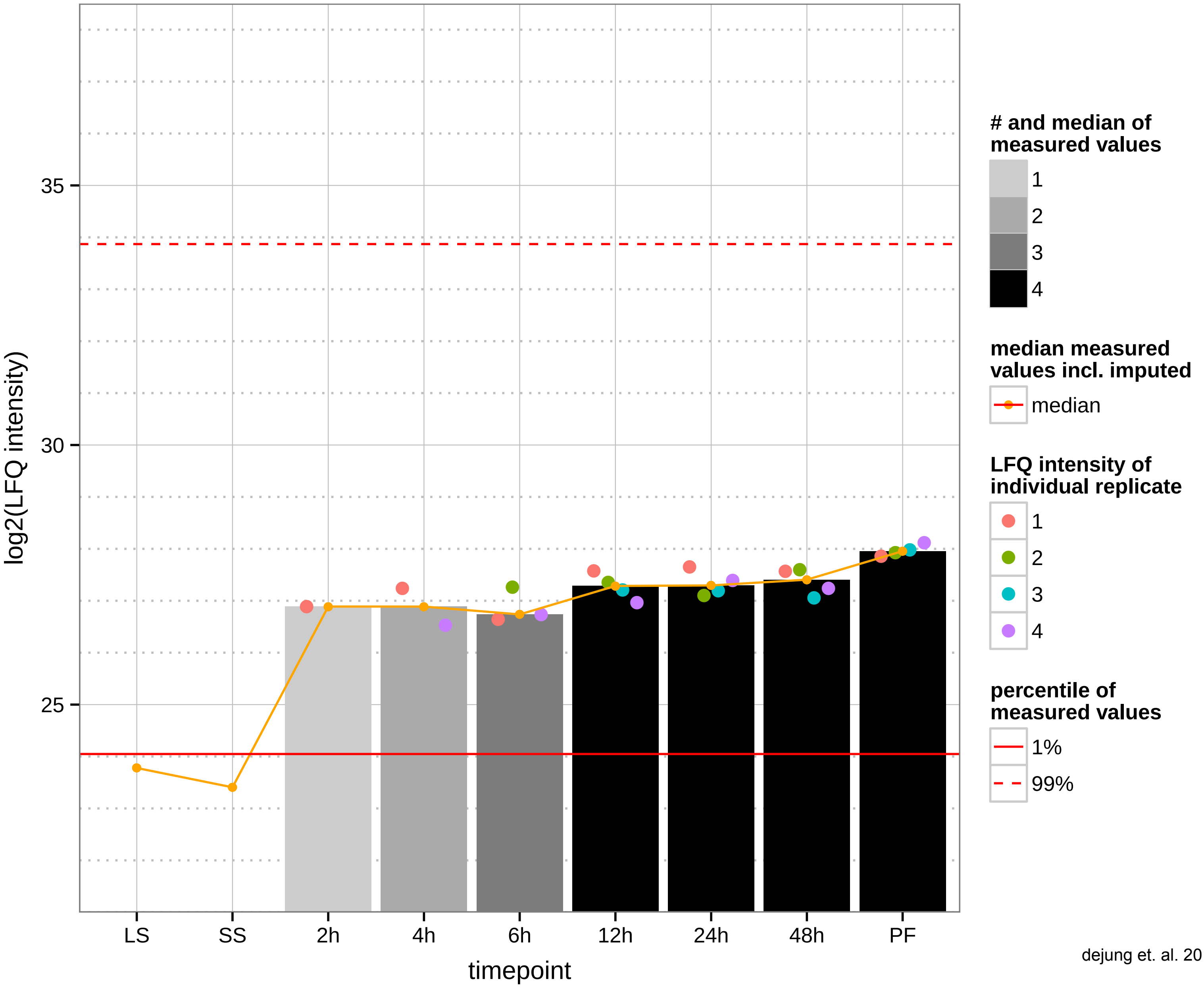
phosphatidylinositol 3−kinase, putative
Tb927.1.1930
AGOF: 1−phosphatidylinositol−3−kinase activity, phosphotransferase activity, alcohol group as acceptor
AGOC: null
AGOP: cell proliferation, phosphatidylinositol phosphorylation
PGOF: binding, phosphotransferase activity, alcohol group as acceptor, protein binding, transferase activity, transferring phosp
PGOC: null
PGOP: null





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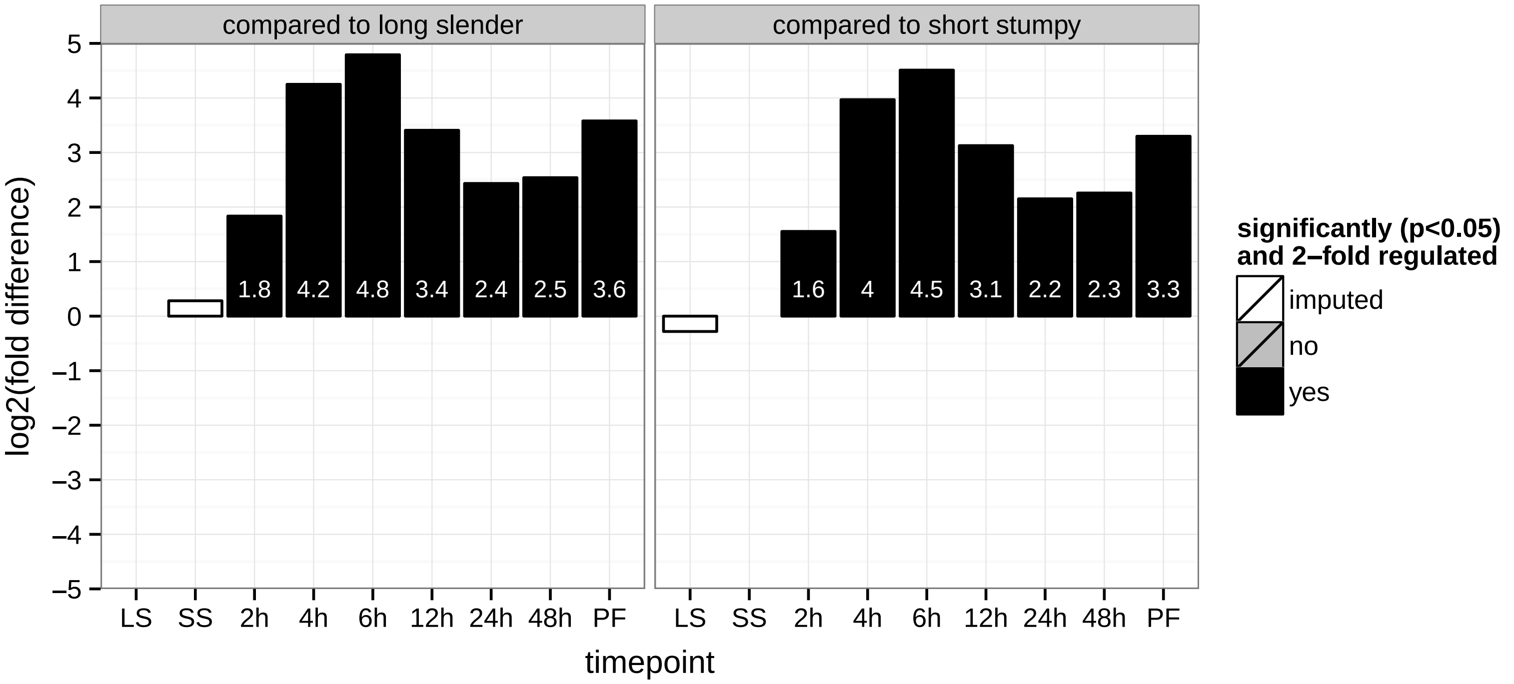
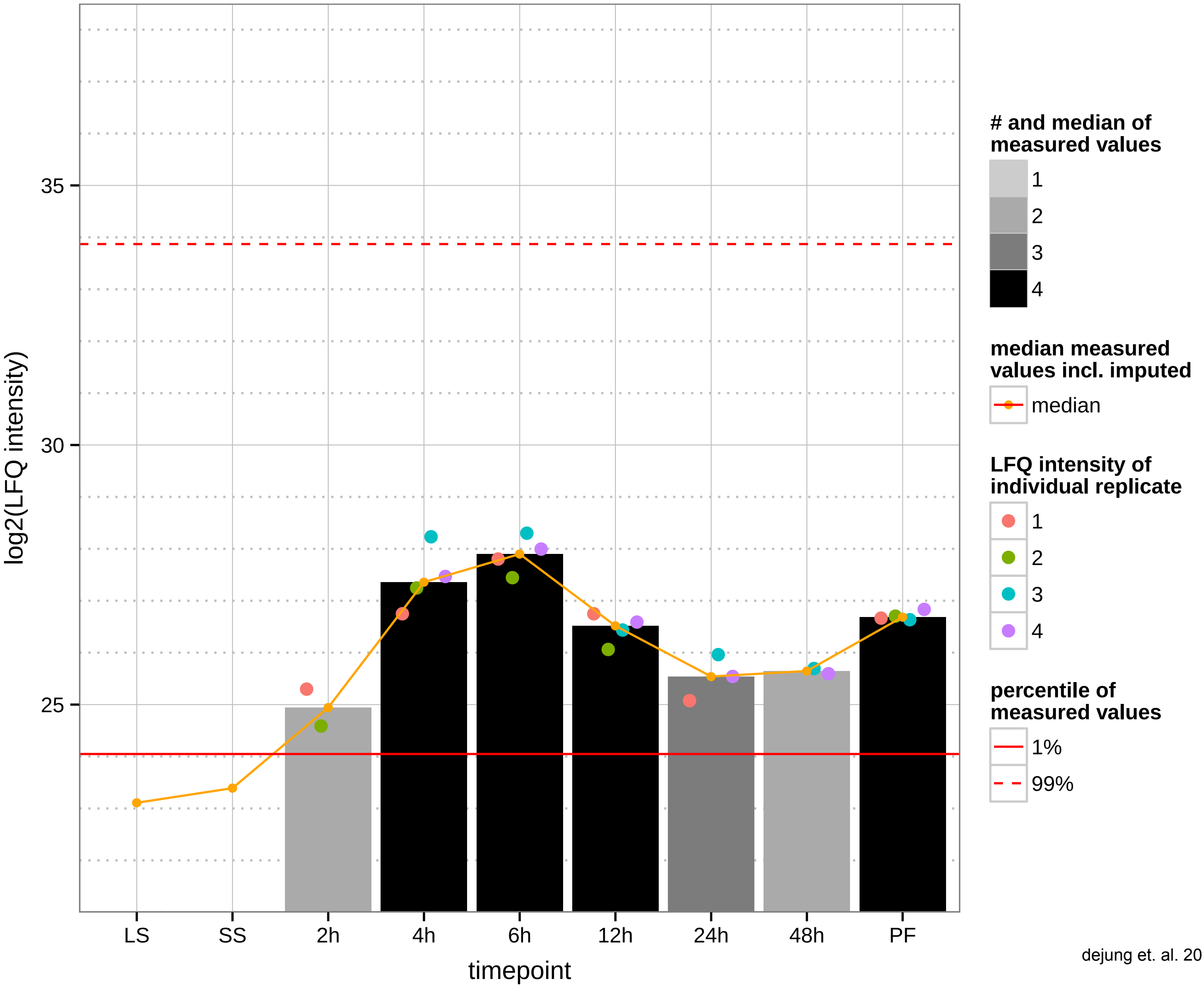
hypothetical protein, conserved
Tb927.10.10000
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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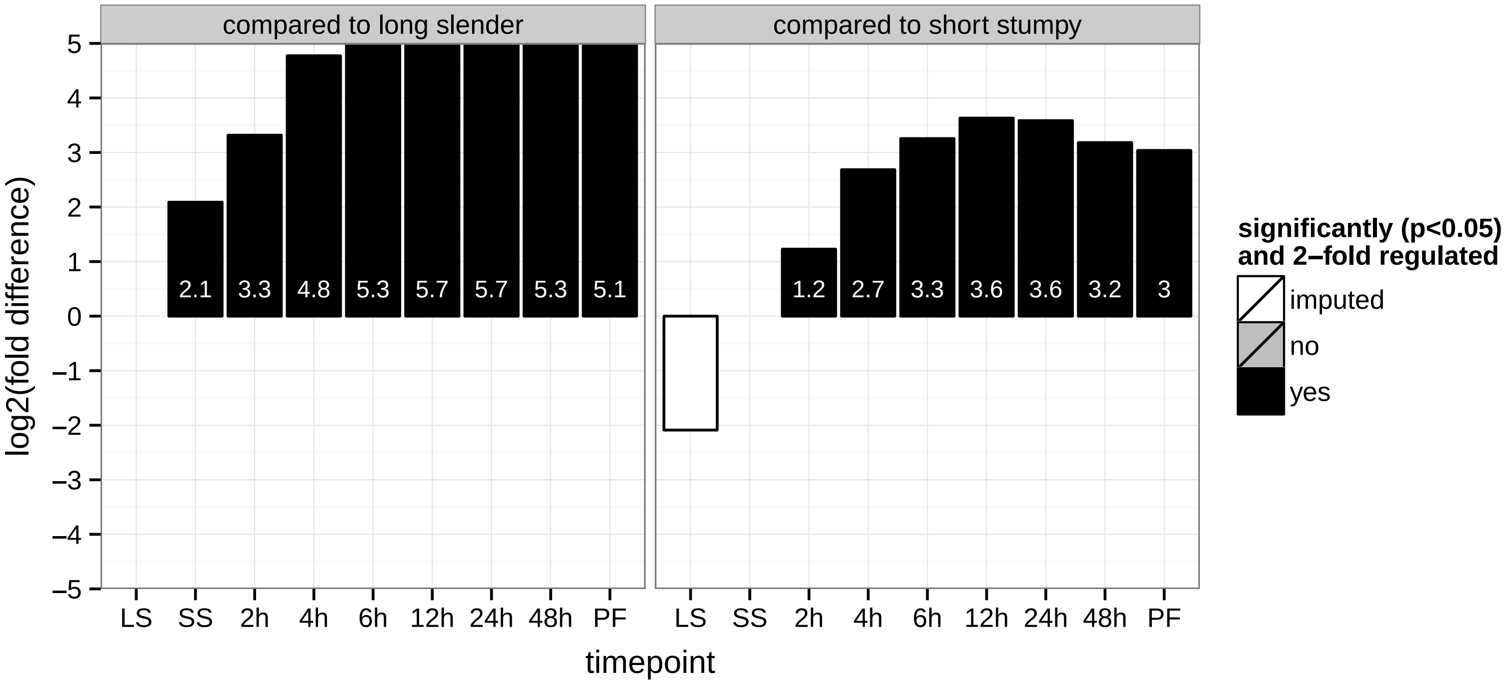
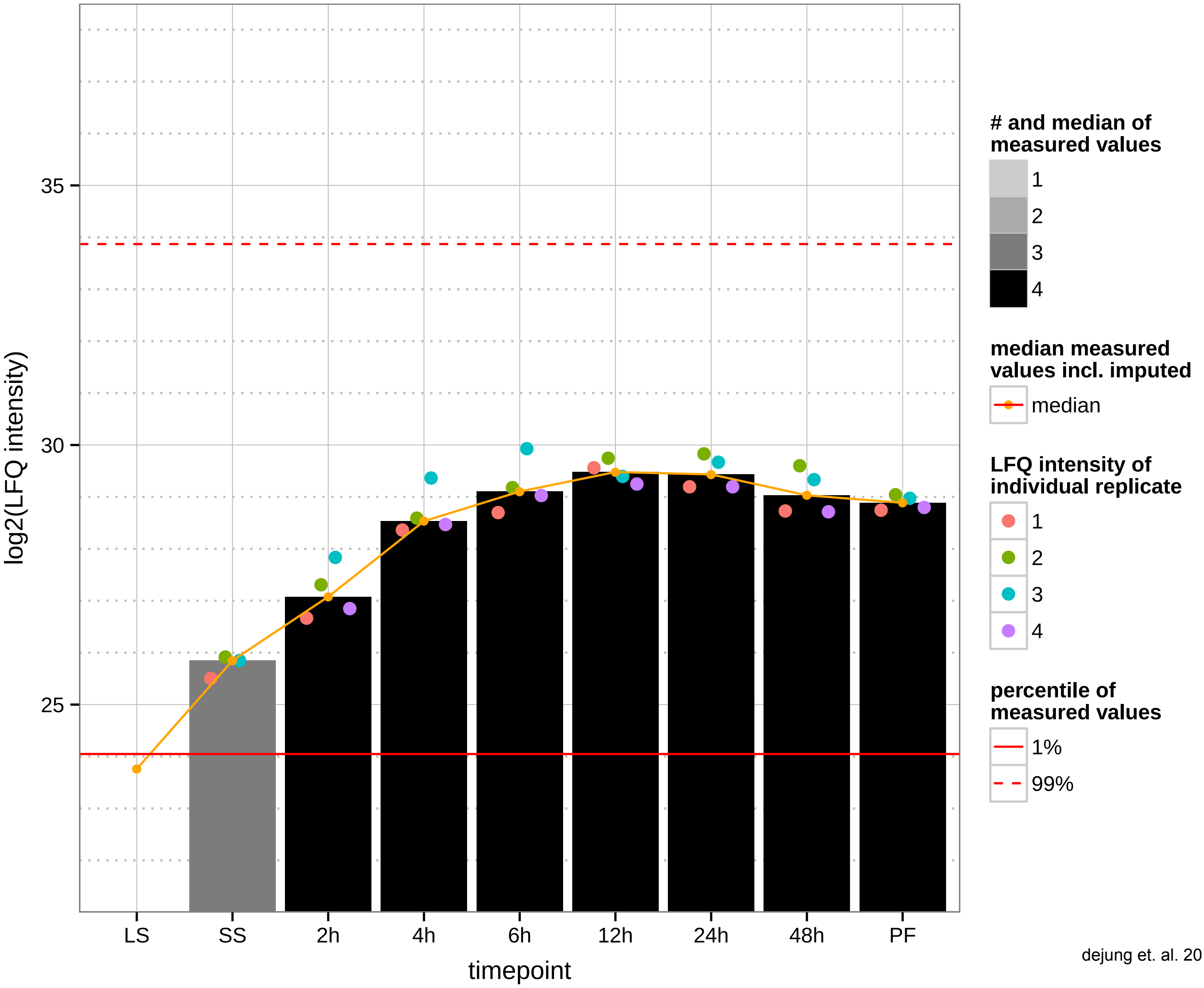
procyclic form surface phosphoprotein (PSSA–2)
Tb927.10.11220
AGOF: structural constituent of cell wall
AGOC: cell surface
AGOP: plant–type cell wall organization
PGOF: structural constituent of cell wall
PGOC: null
PGOP: plant–type cell wall organization





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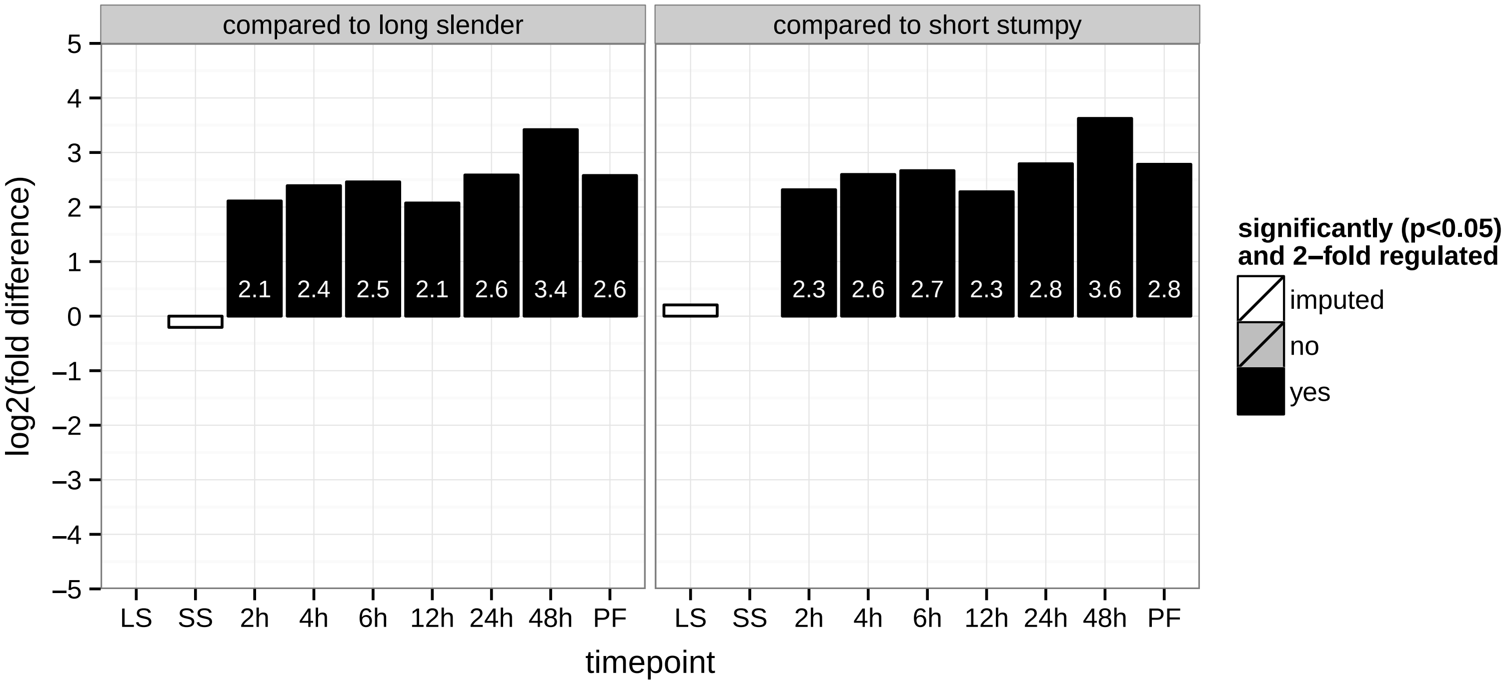
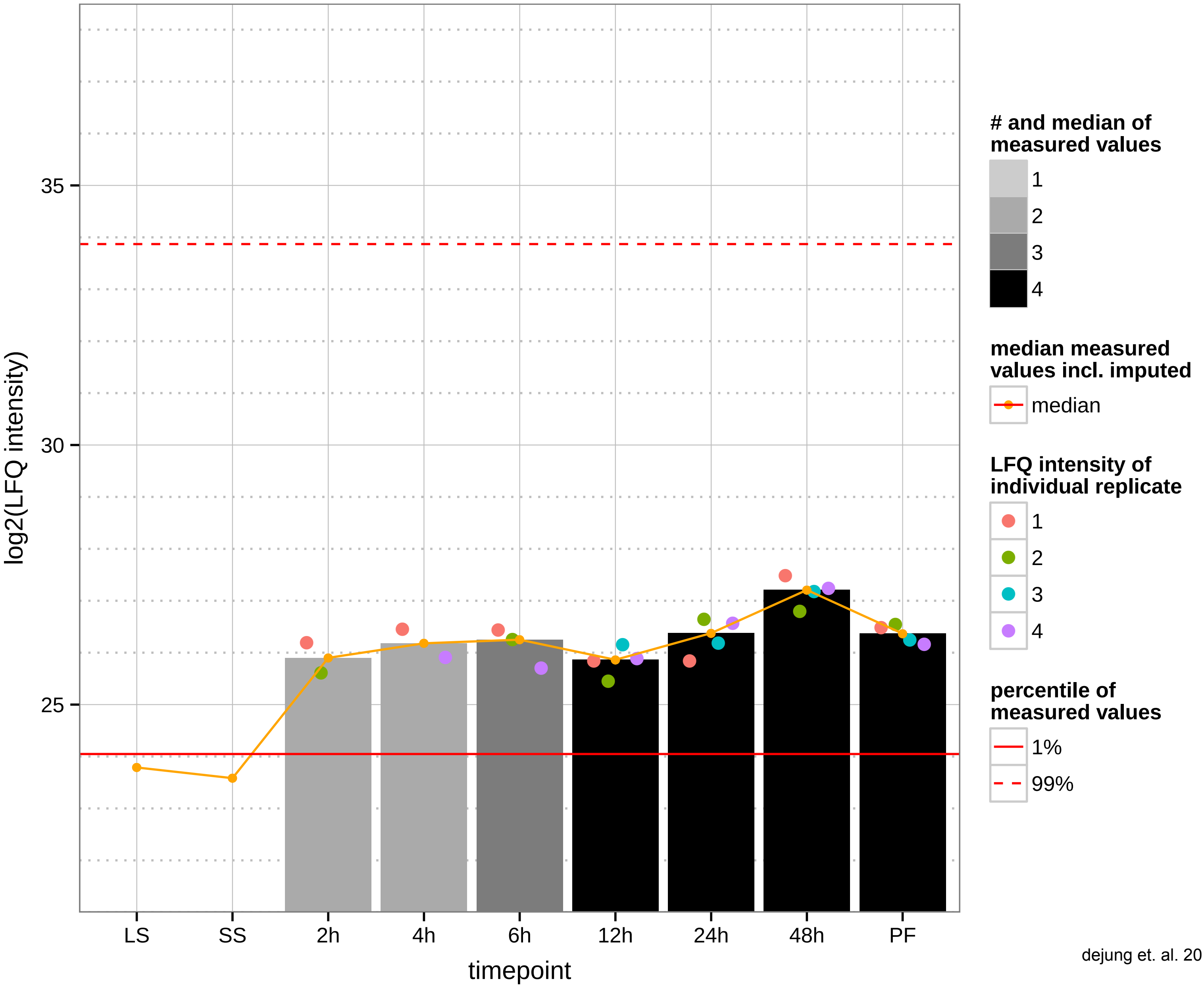
NADH–ubiquinone oxidoreductase complex I subunit, FT putative, NDUFA9 subunit, putative
Tb927.10.13620
AGOF: NAD binding, oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
AGOC: cytoplasm, mitochondrion
AGOP: cellular amino acid metabolic process
PGOF: 3–beta–hydroxy–delta5–steroid dehydrogenase activity, oxidoreductase activity, acting on the CH–OH group of donors
PGOC: null
PGOP: oxidation–reduction process, steroid biosynthetic process





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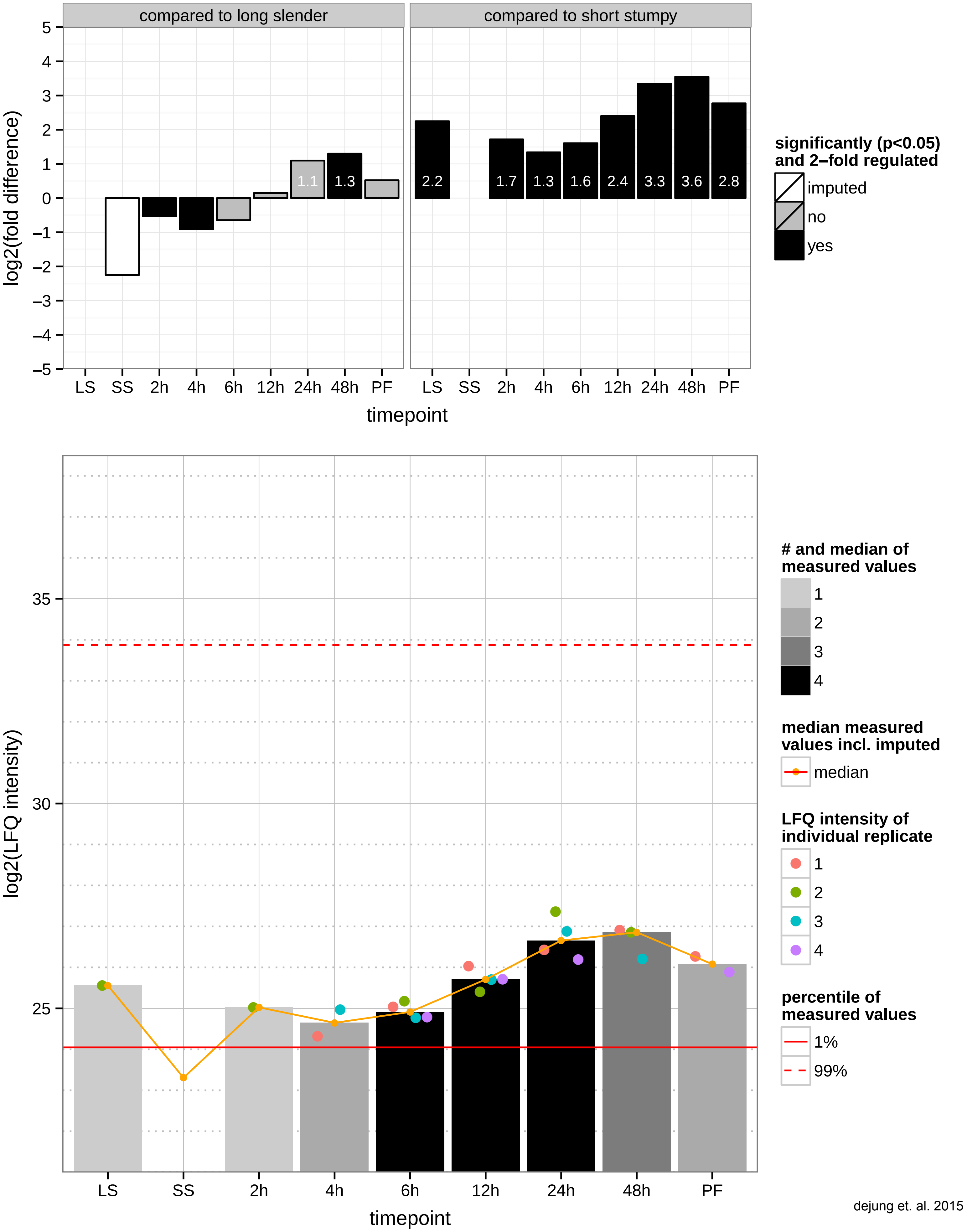
chaperone protein DNAj, putative
Tb927.10.13830
AGOF: heat shock protein binding, unfolded protein binding
AGOC: integral to membrane, mitochondrial inner membrane, mitochondrion
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null



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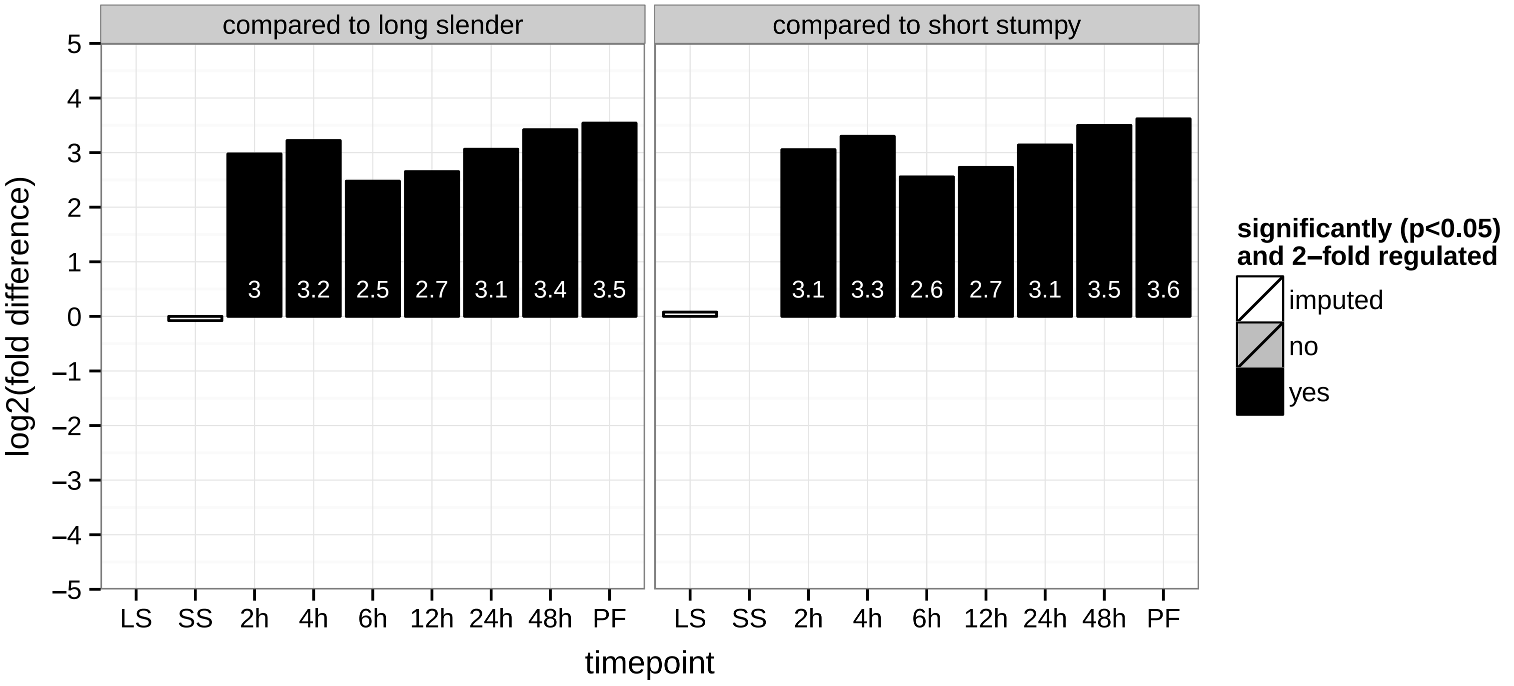
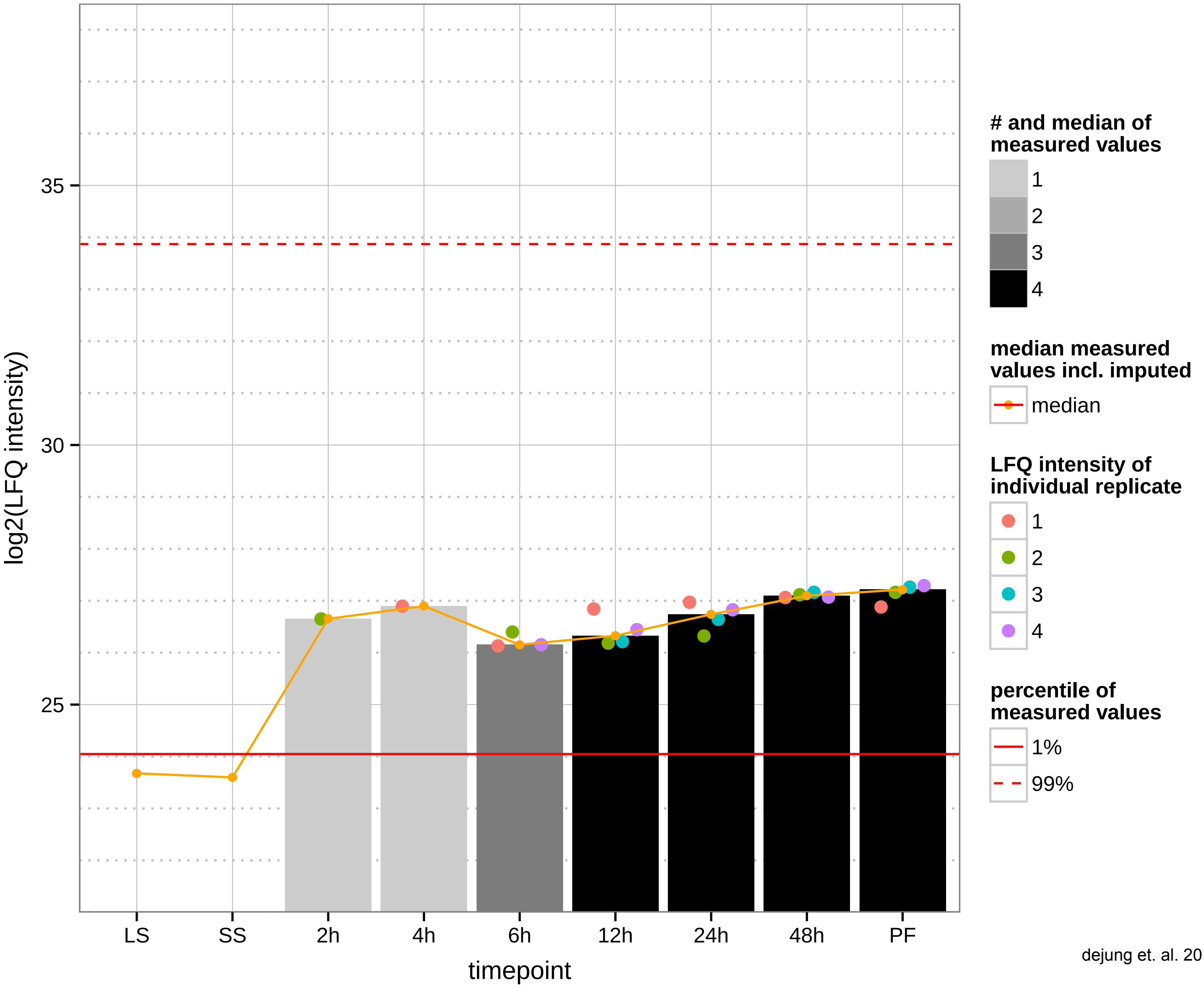
hypothetical protein, conserved
Tb927.10.13850
AGOF: null
AGOC: mitochondrion
AGOP: proton–transporting ATP synthase complex assembly
PGOF: null
PGOC: null
PGOP: proton–transporting ATP synthase complex assembly





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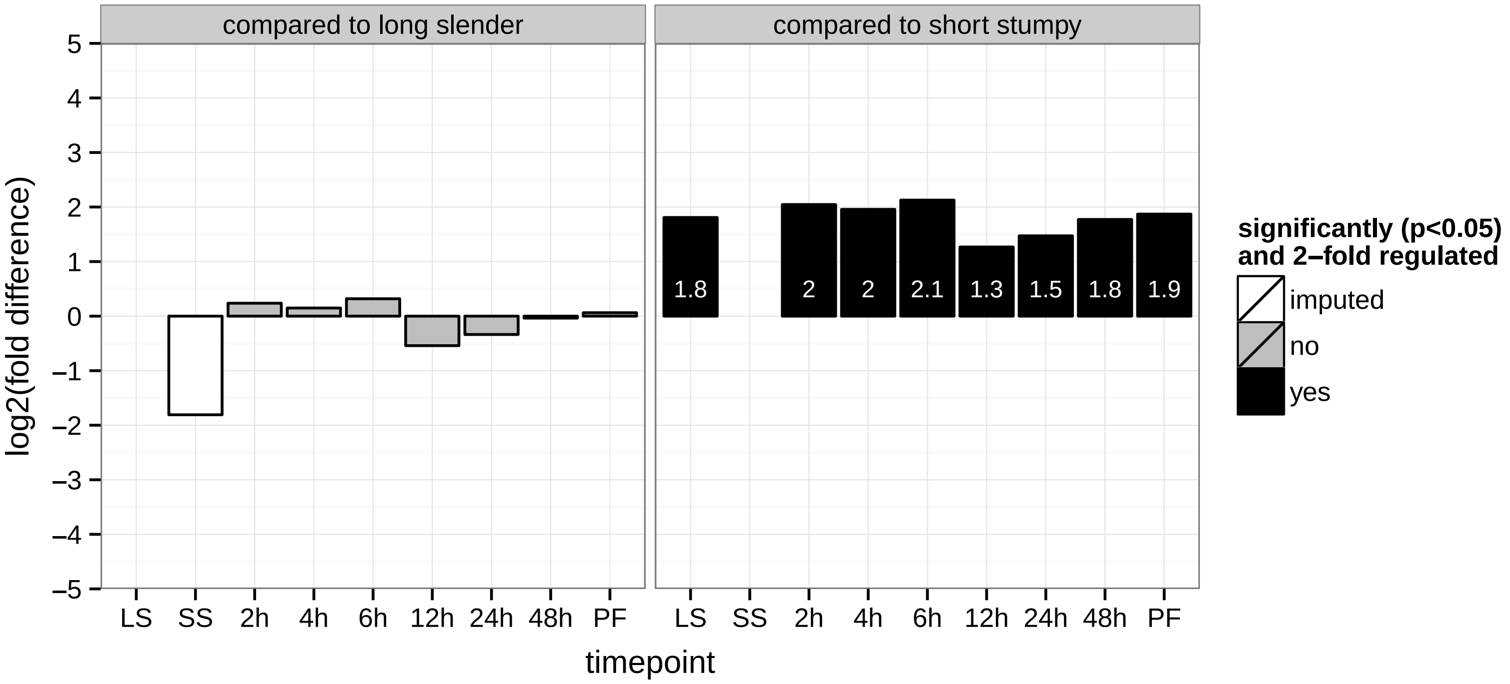
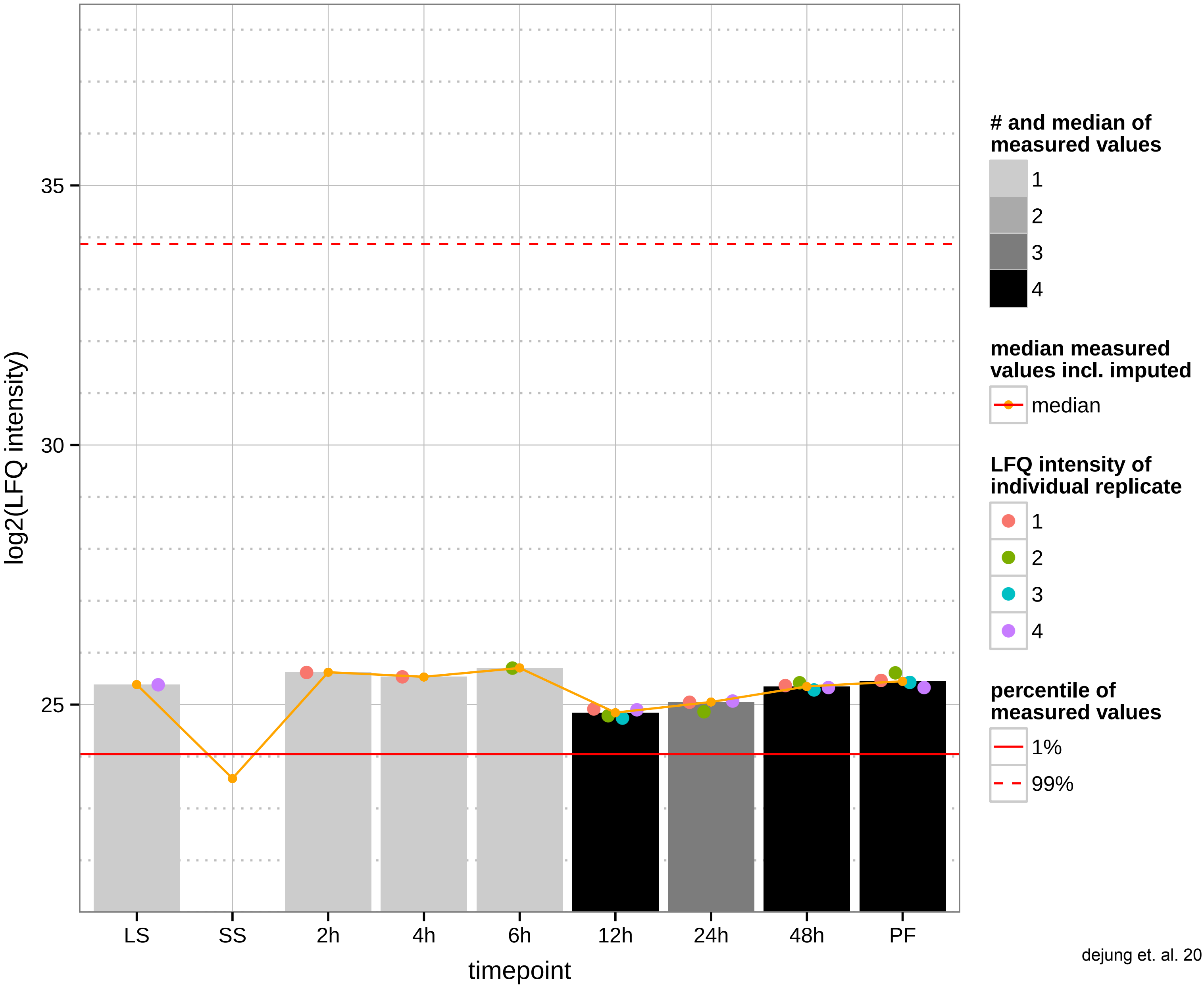
hypothetical protein, conserved
Tb927.10.15280;Tb11.v5.0999
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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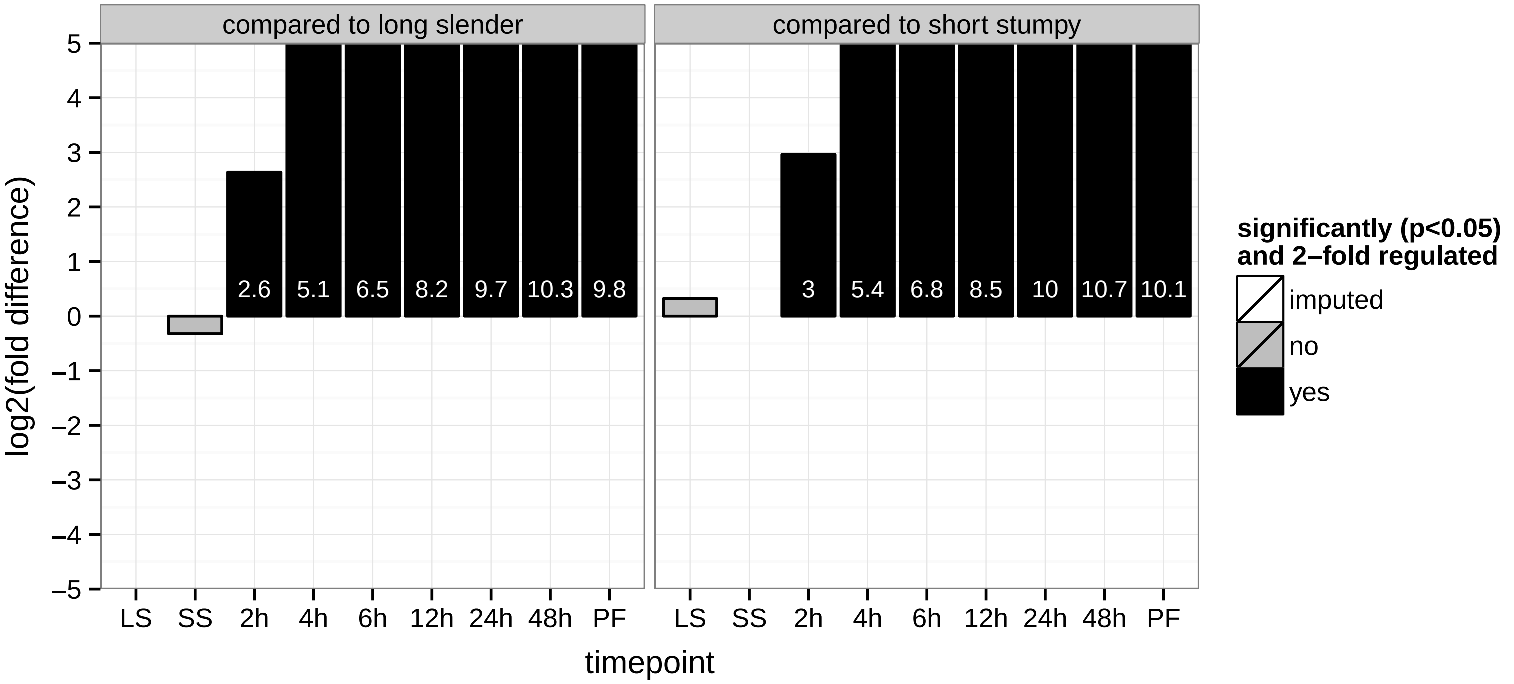
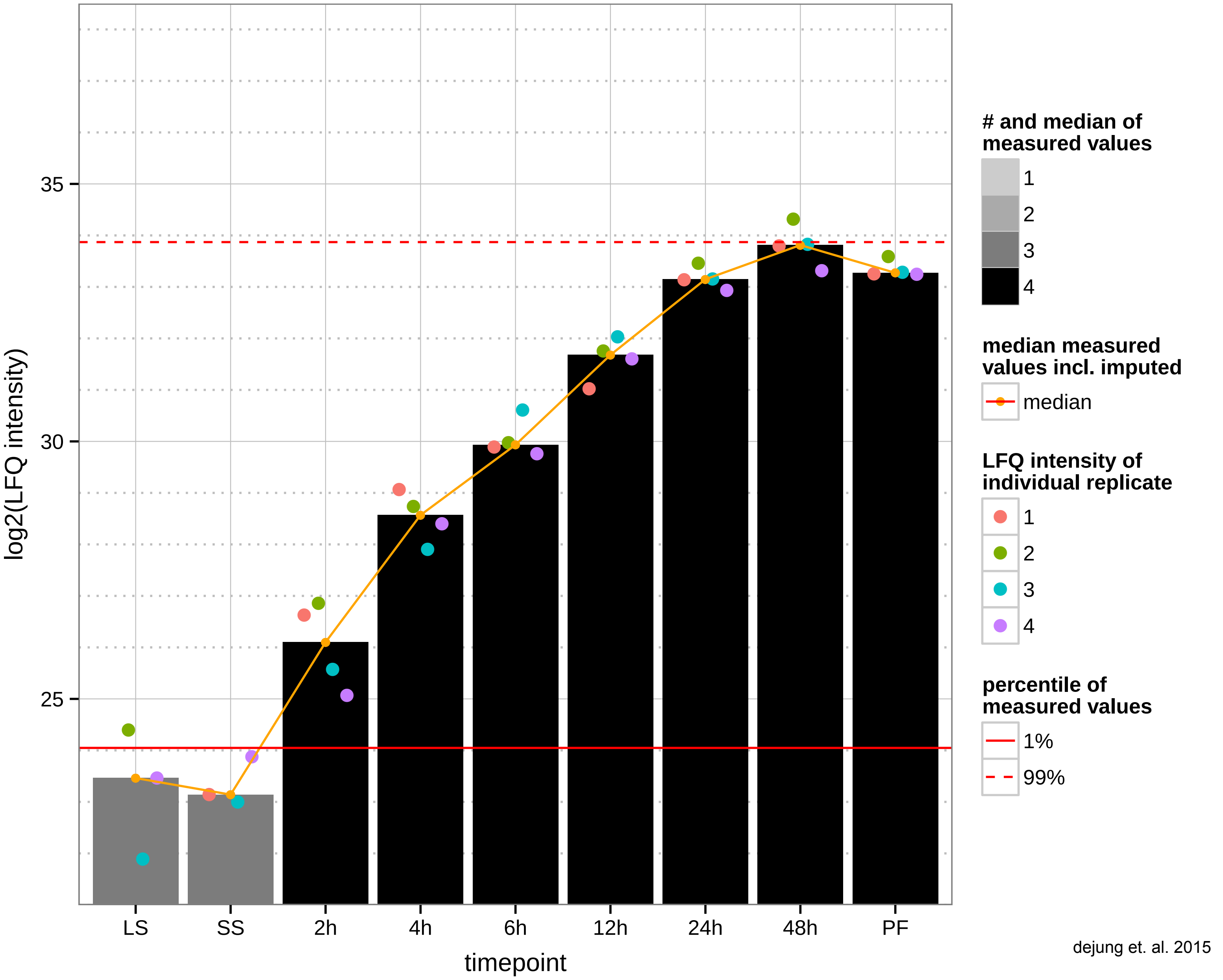
glycosomal malate dehydrogenase (gMDH)
Tb927.10.15410
AGOF: L–malate dehydrogenase activity, malate dehydrogenase activity, oxidoreductase activity
AGOC: glycosome
AGOP: glycolysis, malate metabolic process, oxidation–reduction process, tricarboxylic acid cycle
PGOF: L–malate dehydrogenase activity, catalytic activity, oxidoreductase activity, acting on the CH–OH group of donors, NA
PGOC: null
PGOP: carbohydrate metabolic process, cellular carbohydrate metabolic process, malate metabolic process, oxidation–reduct





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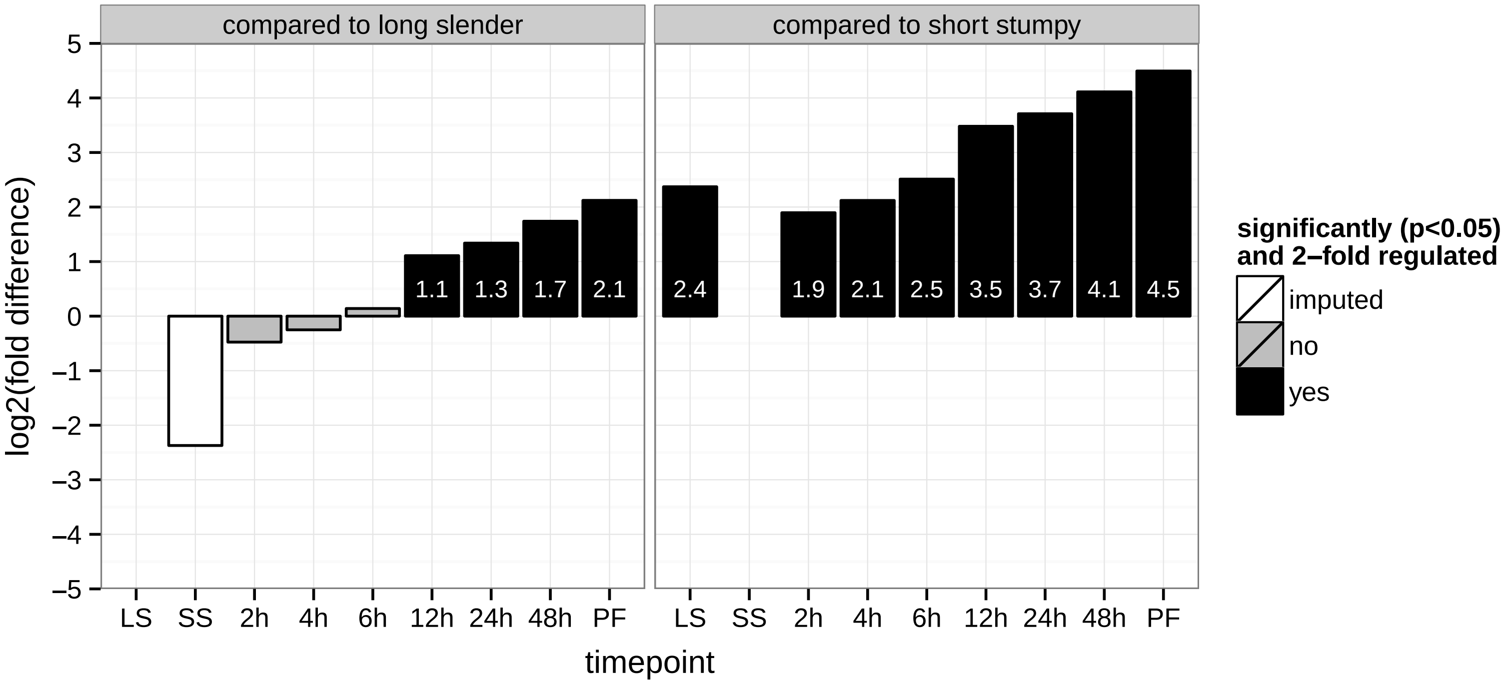
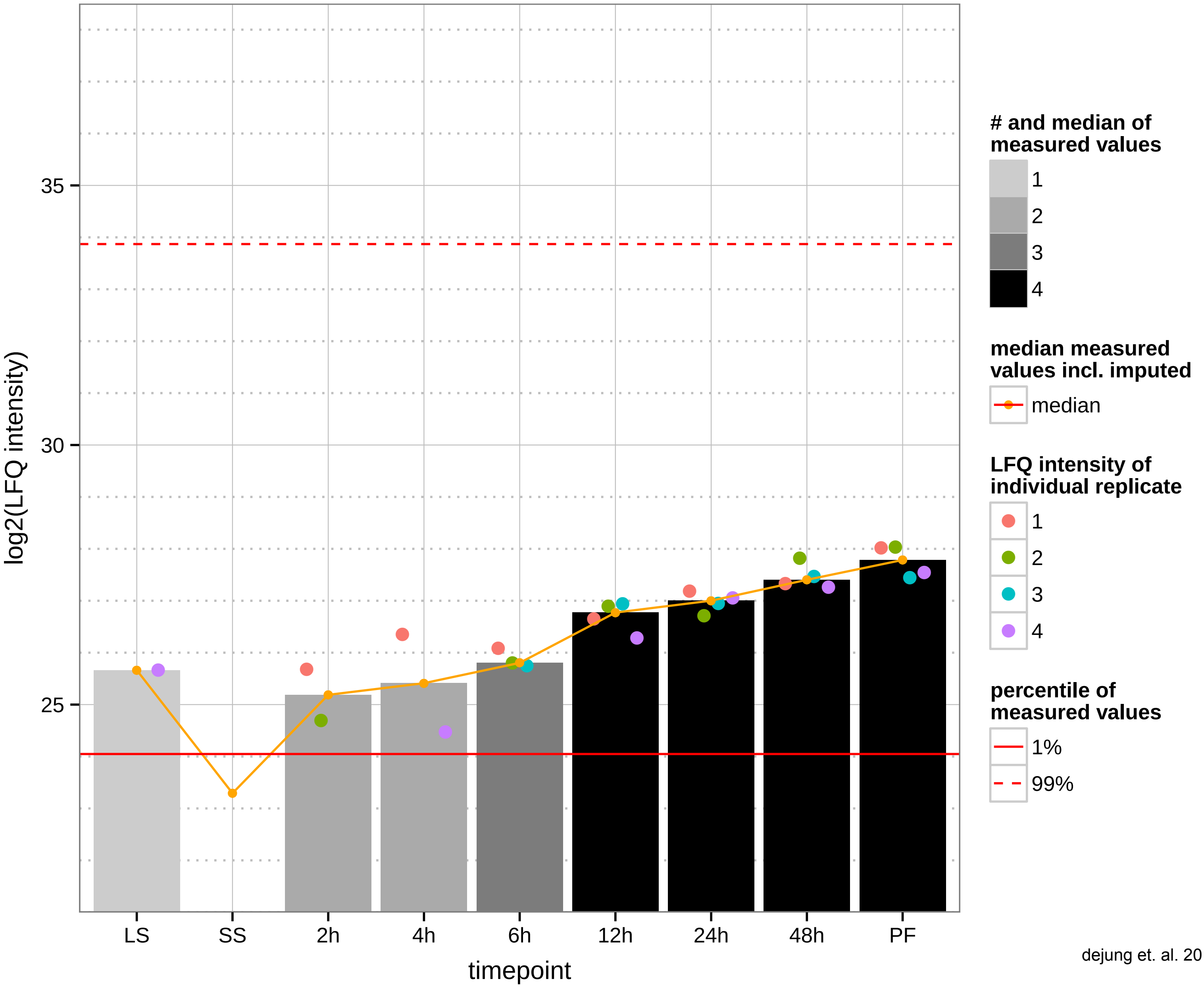
hypothetical protein, conserved
Tb927.10.1960
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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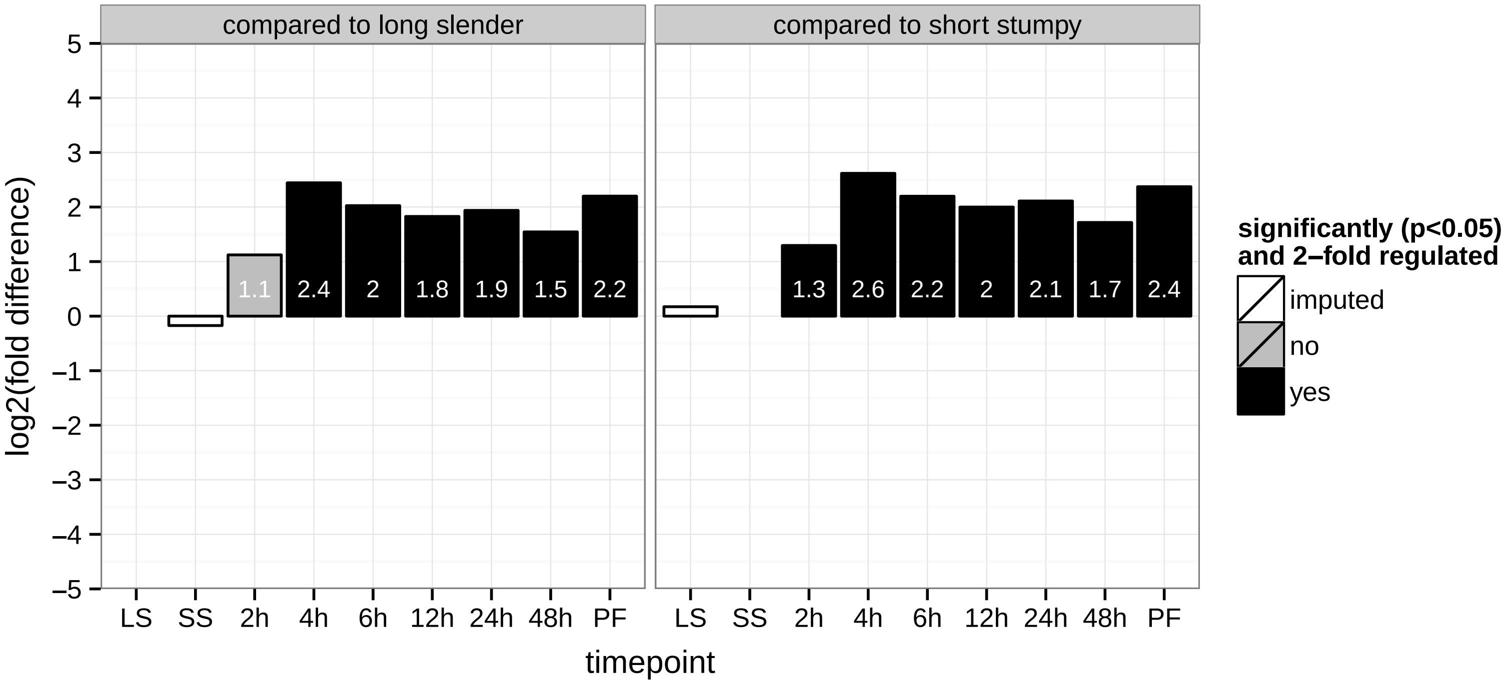
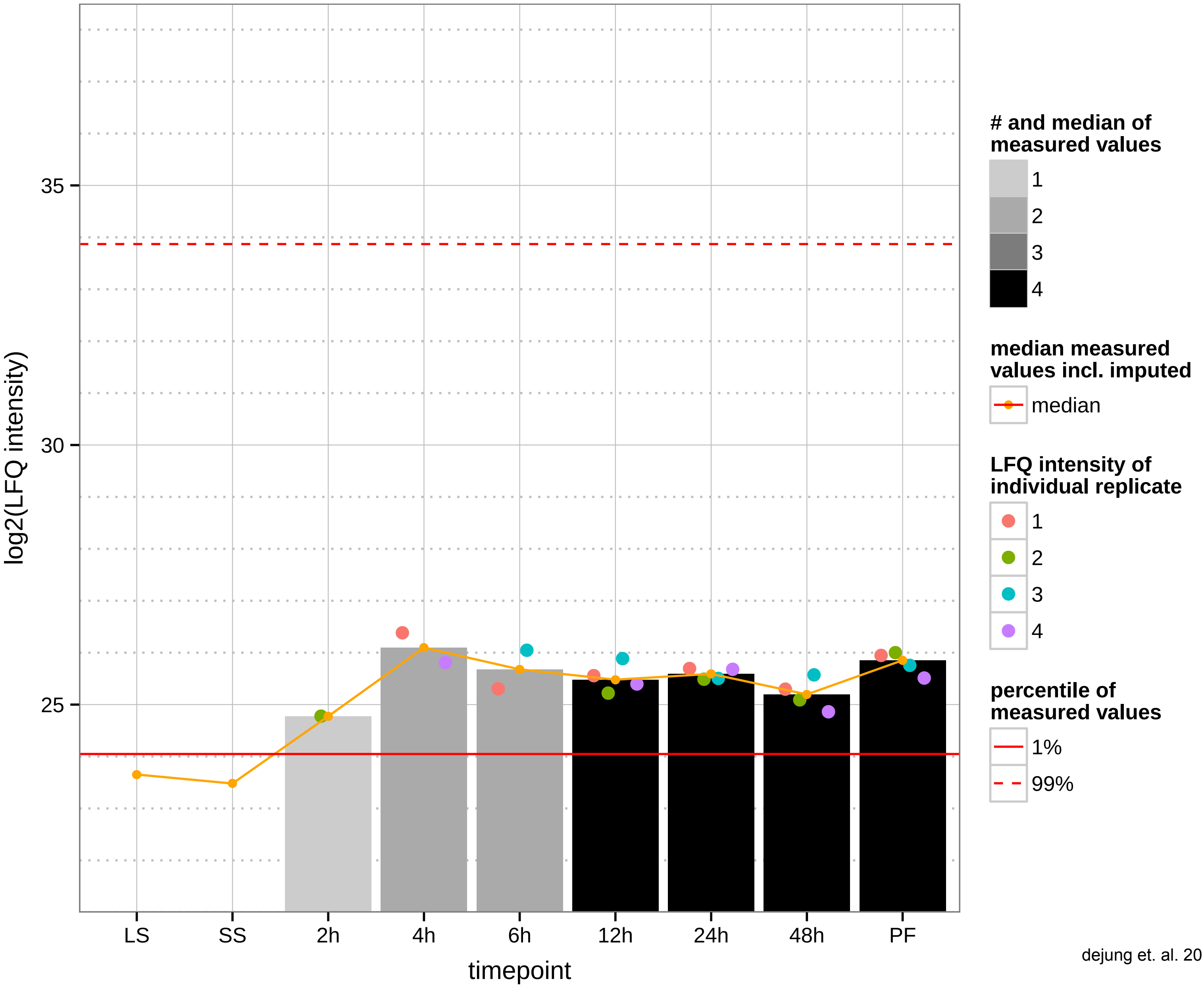
ubiquitin carboxyl–terminal hydrolase, putative, Peptidase C19, ubiquitin carboxyl–terminal hydrolase
Tb927.10.2210
AGOF: null, cysteine–type endopeptidase activity, ubiquitin thiolesterase activity
AGOC: null
AGOP: null, ubiquitin–dependent protein catabolic process
PGOF: ubiquitin thiolesterase activity
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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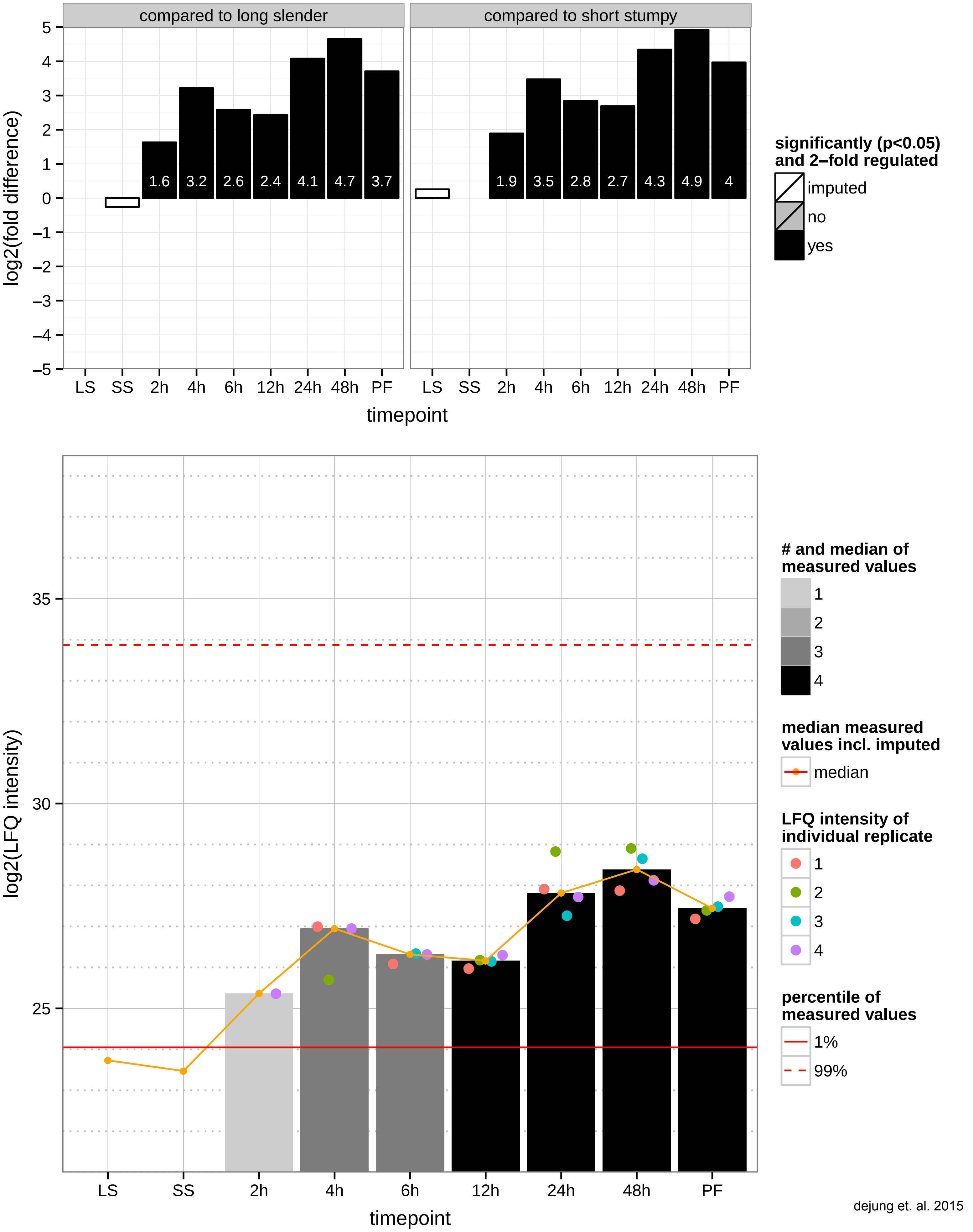
hypothetical protein, conserved
Tb927.10.3040
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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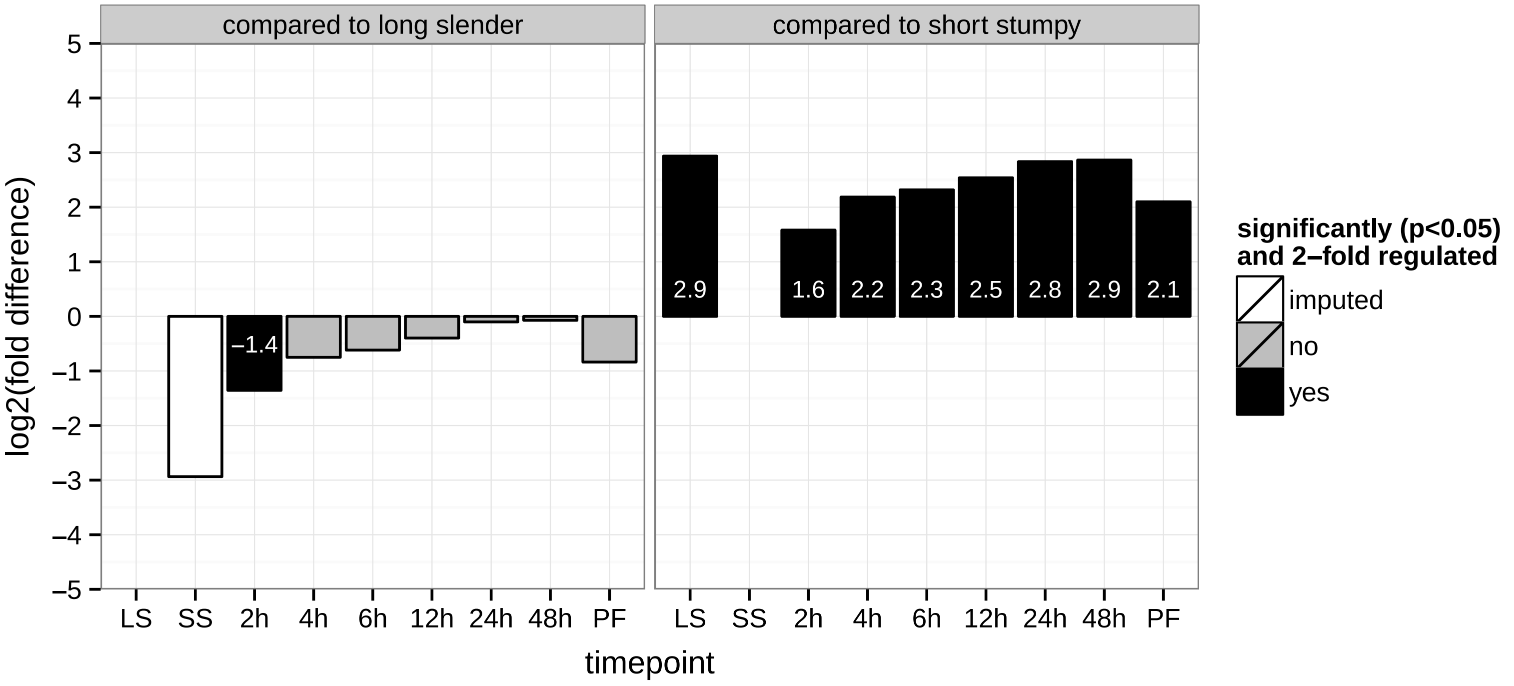
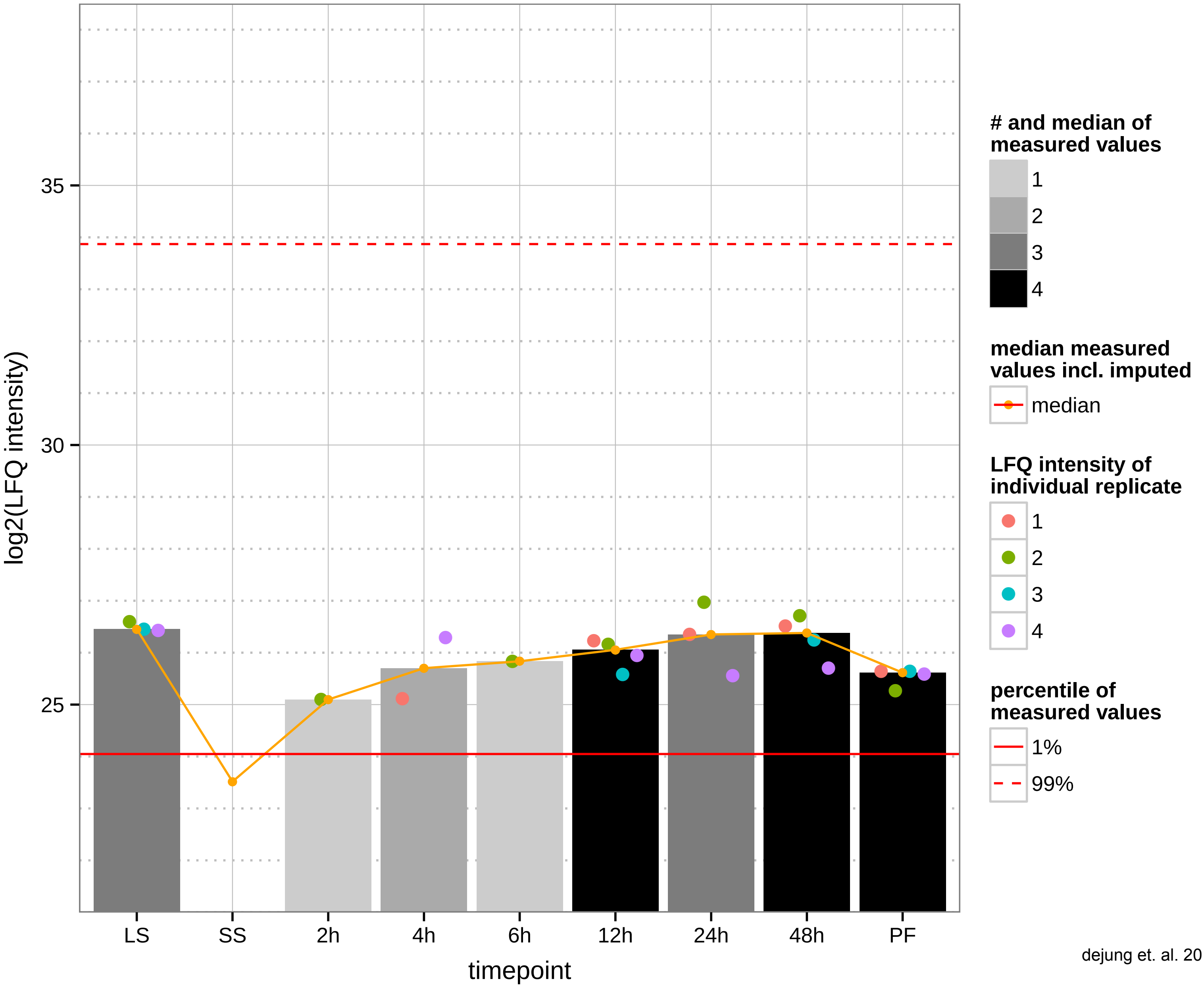
hypothetical protein, conserved
Tb927.10.3160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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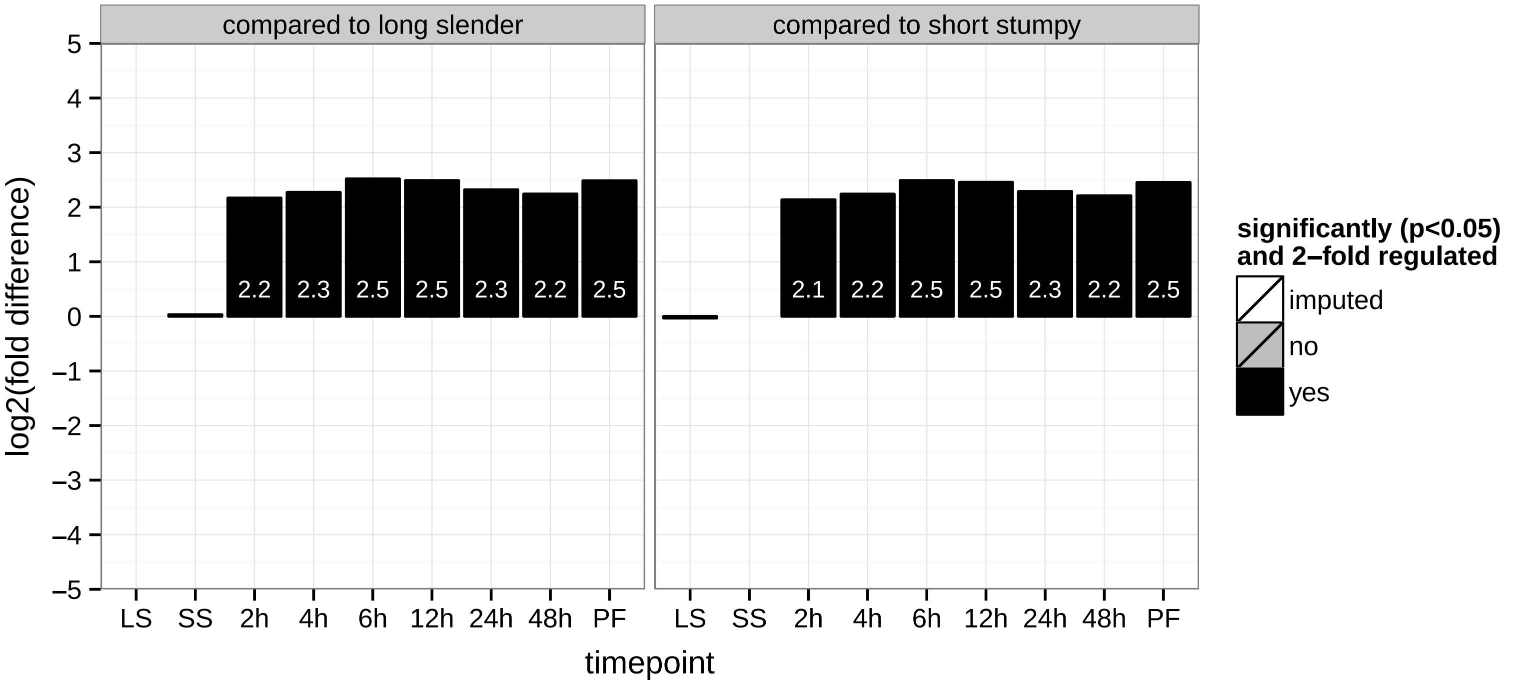
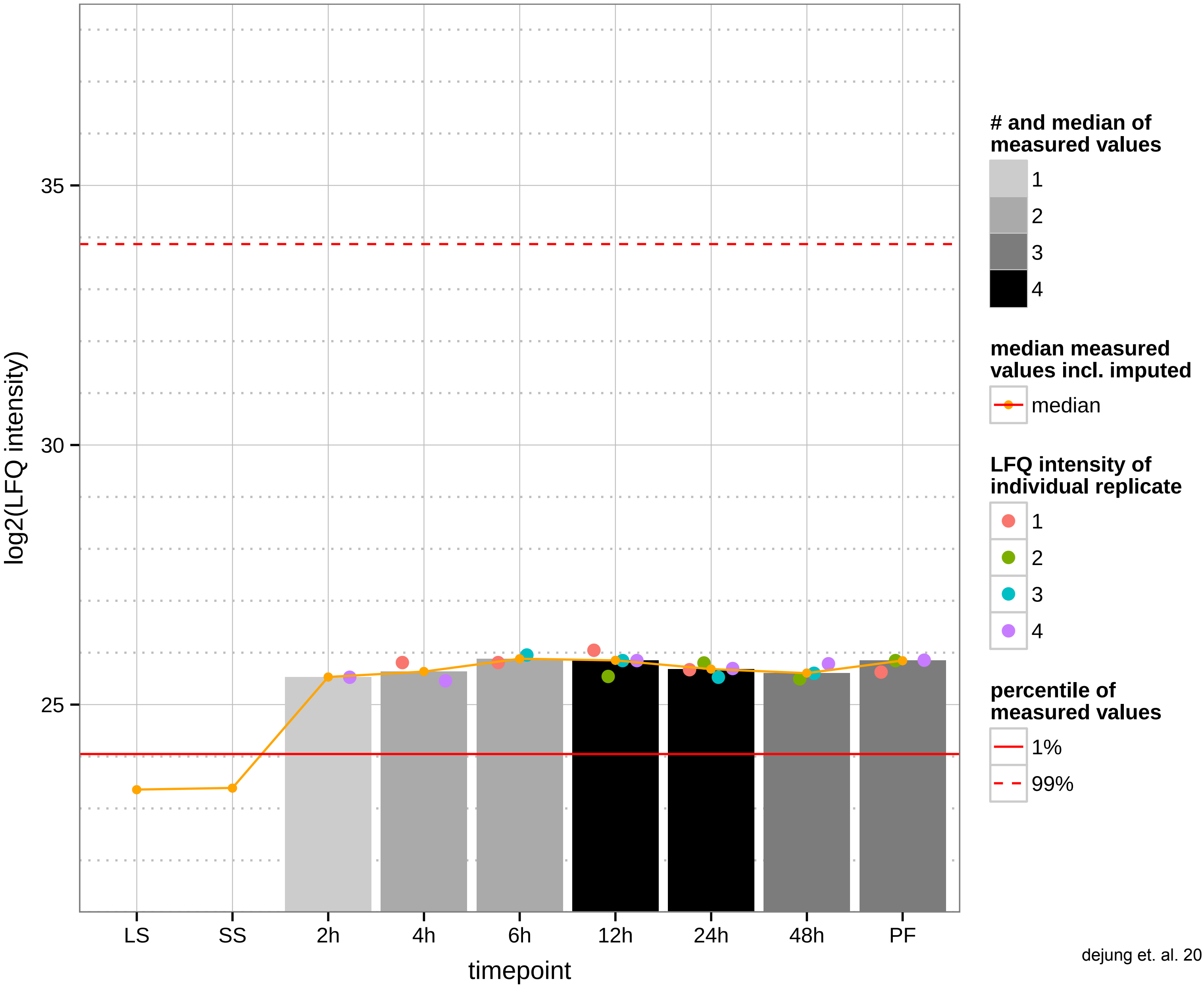
hypothetical protein, conserved
Tb927.10.6550
AGOF: DNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: DNA binding, zinc ion binding
PGOC: null
PGOP: null





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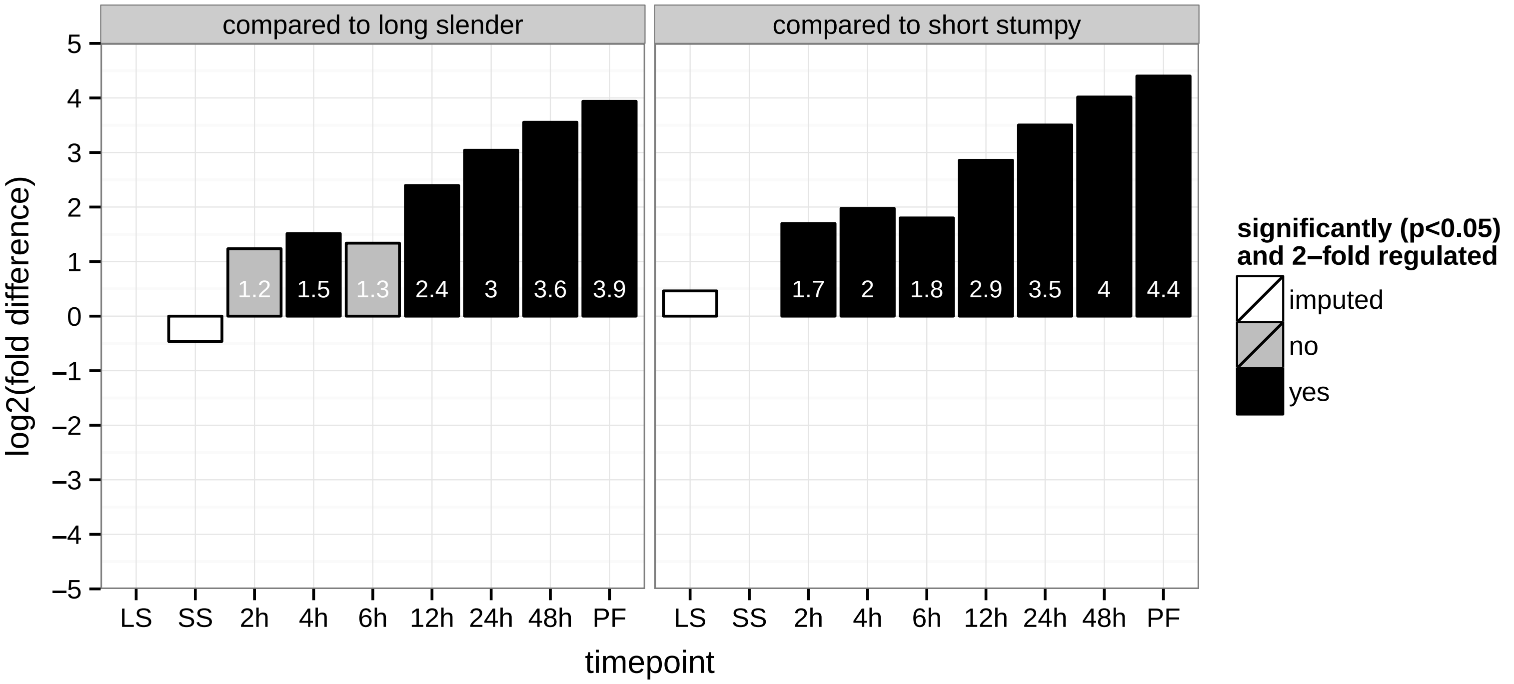
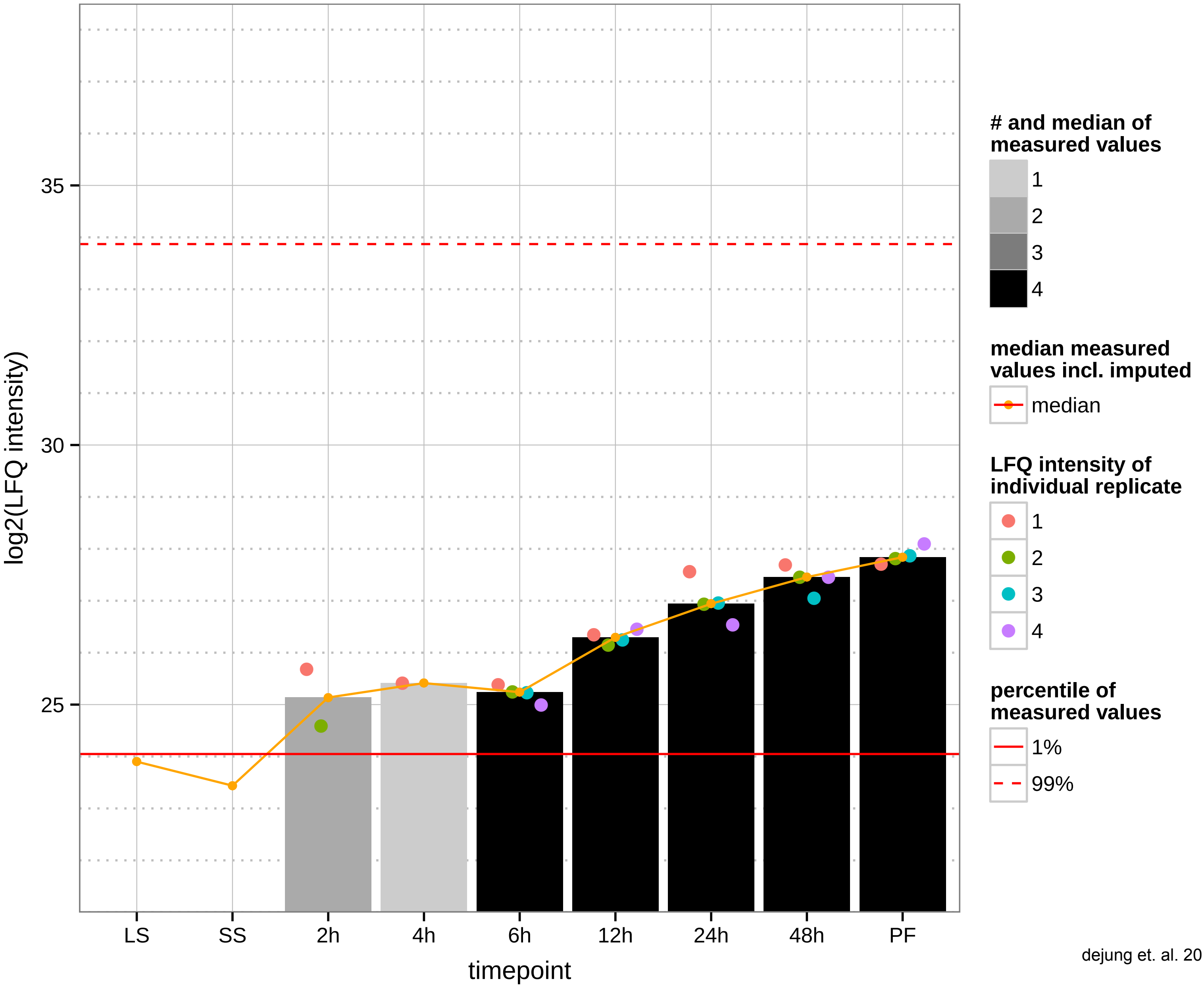
tRNA pseudouridine synthase TruD, putative, pseudouridine synthase TruD, putative (pus7)
Tb927.10.9050
AGOF: RNA binding, pseudouridine synthase activity
AGOC: null
AGOP: pseudouridine synthesis
PGOF: RNA binding, pseudouridine synthase activity
PGOC: null
PGOP: RNA modification, pseudouridine synthesis





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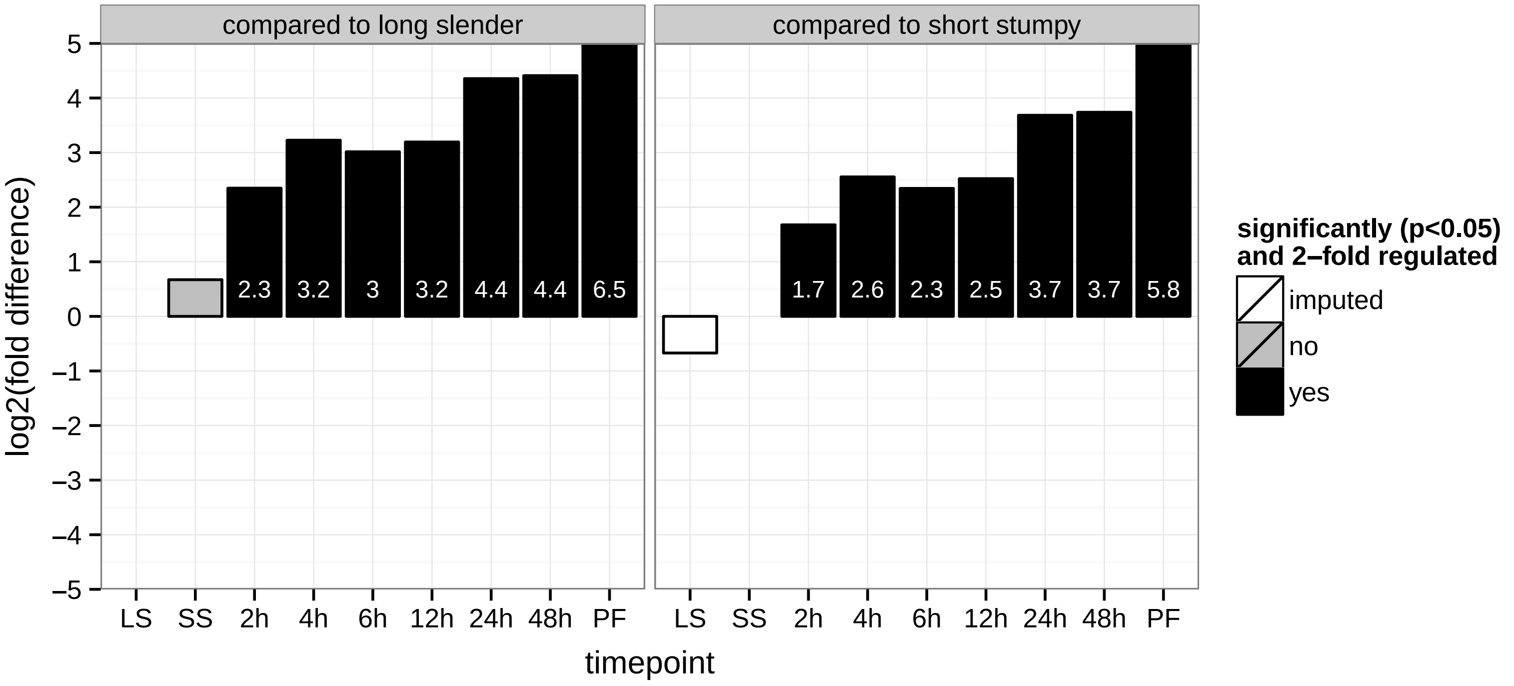
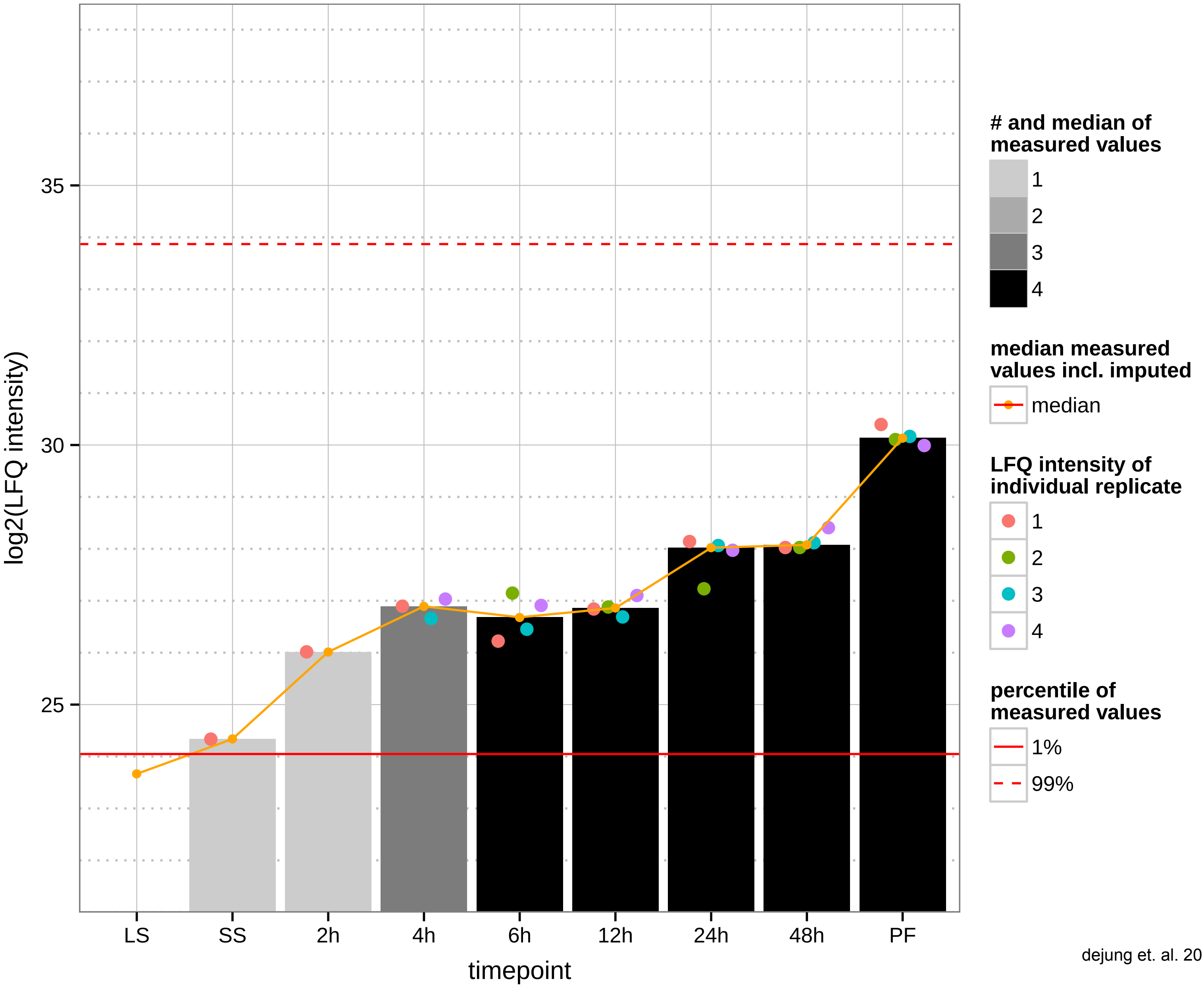
pteridine transporter, putative
Tb927.10.9080
AGOF: biopterin transporter activity
AGOC: null
AGOP: biopterin transport
PGOF: null
PGOC: null
PGOP: null





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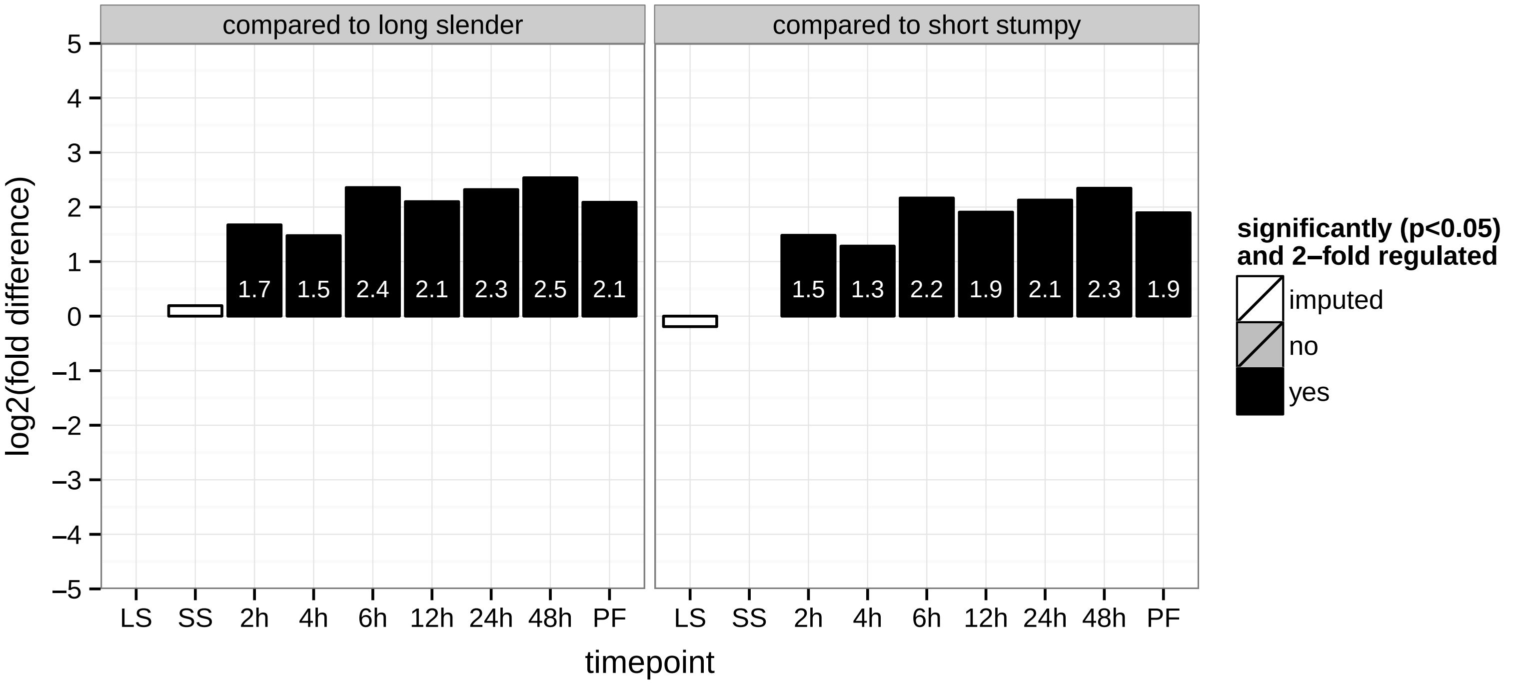
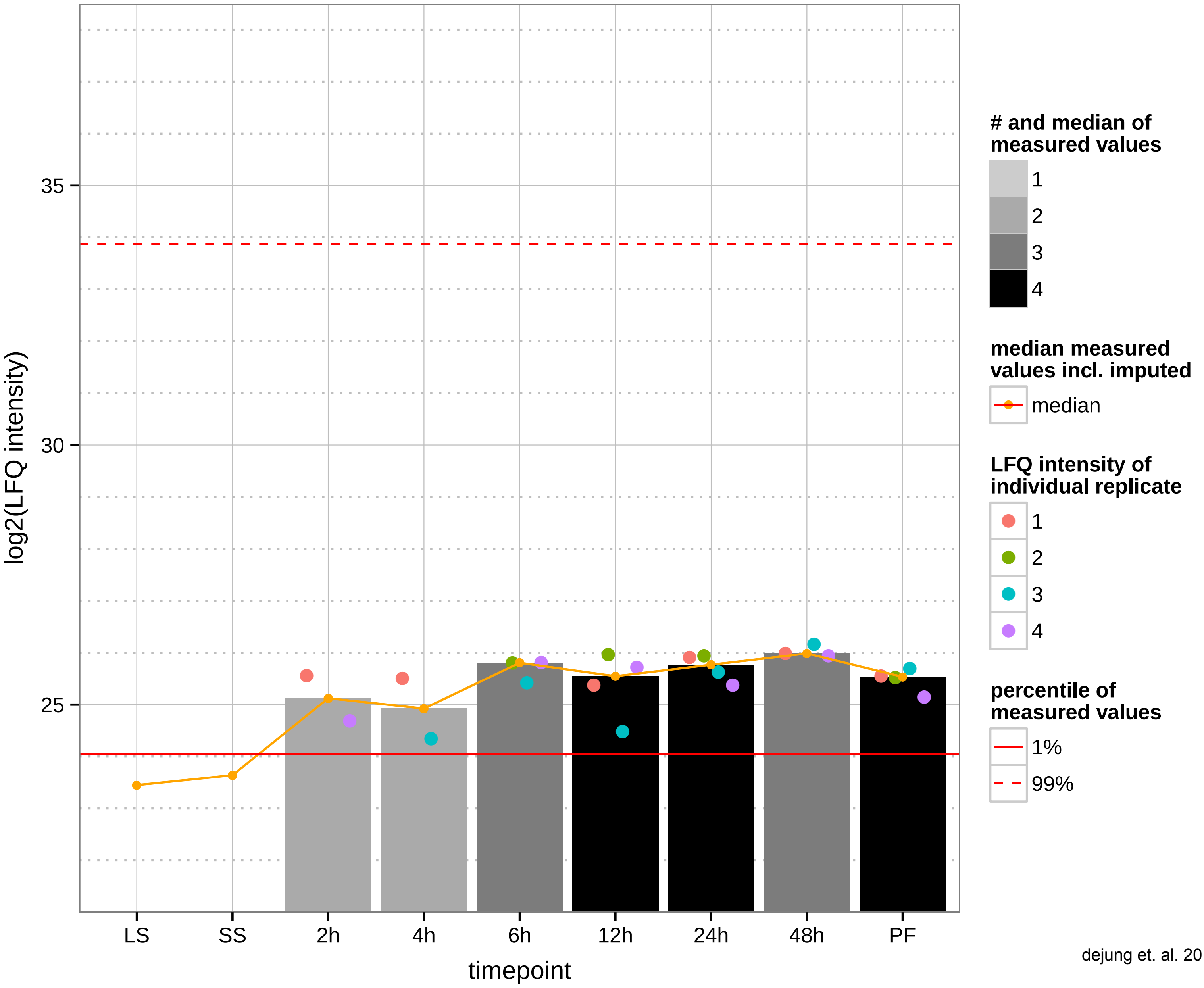
hypothetical protein, conserved
Tb927.11.10880
AGOF: transferase activity
AGOC: null
AGOP: null
PGOF: protein binding, transferase activity
PGOC: null
PGOP: null





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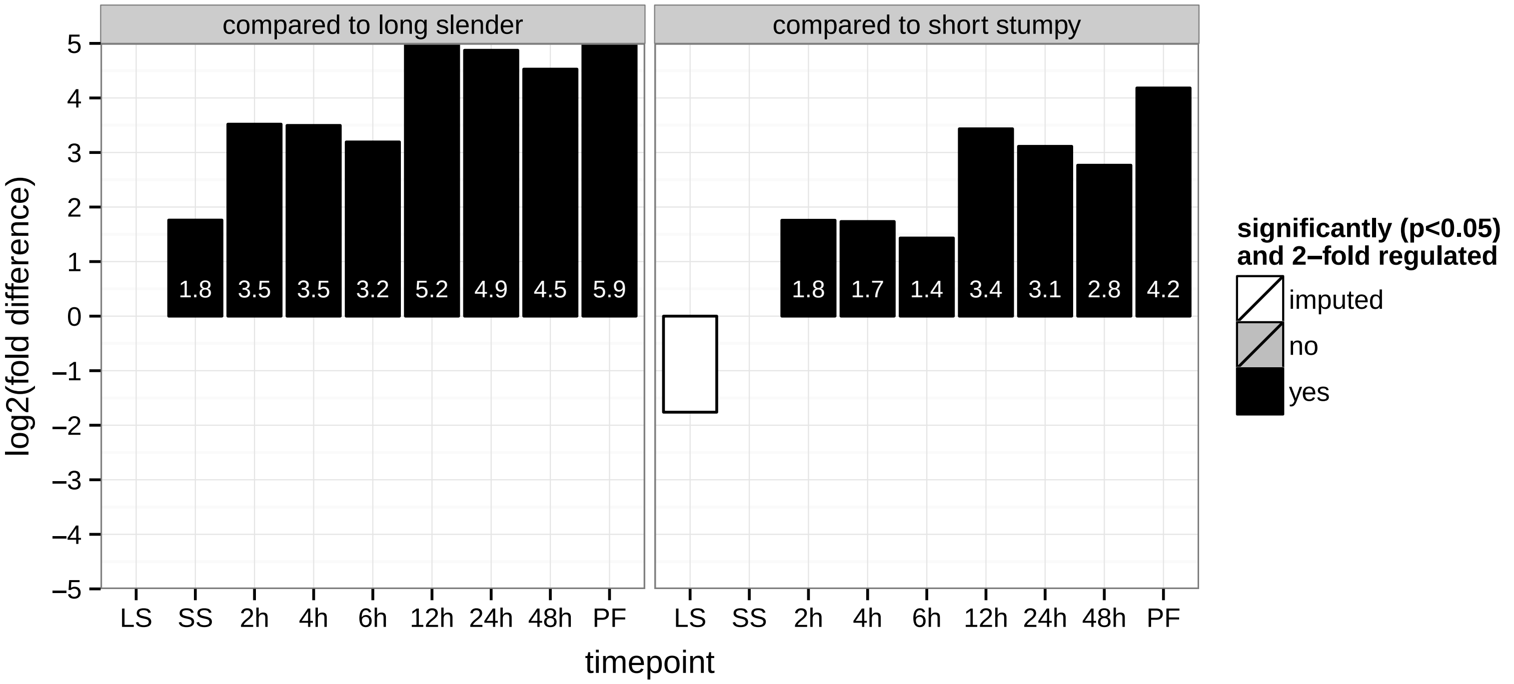
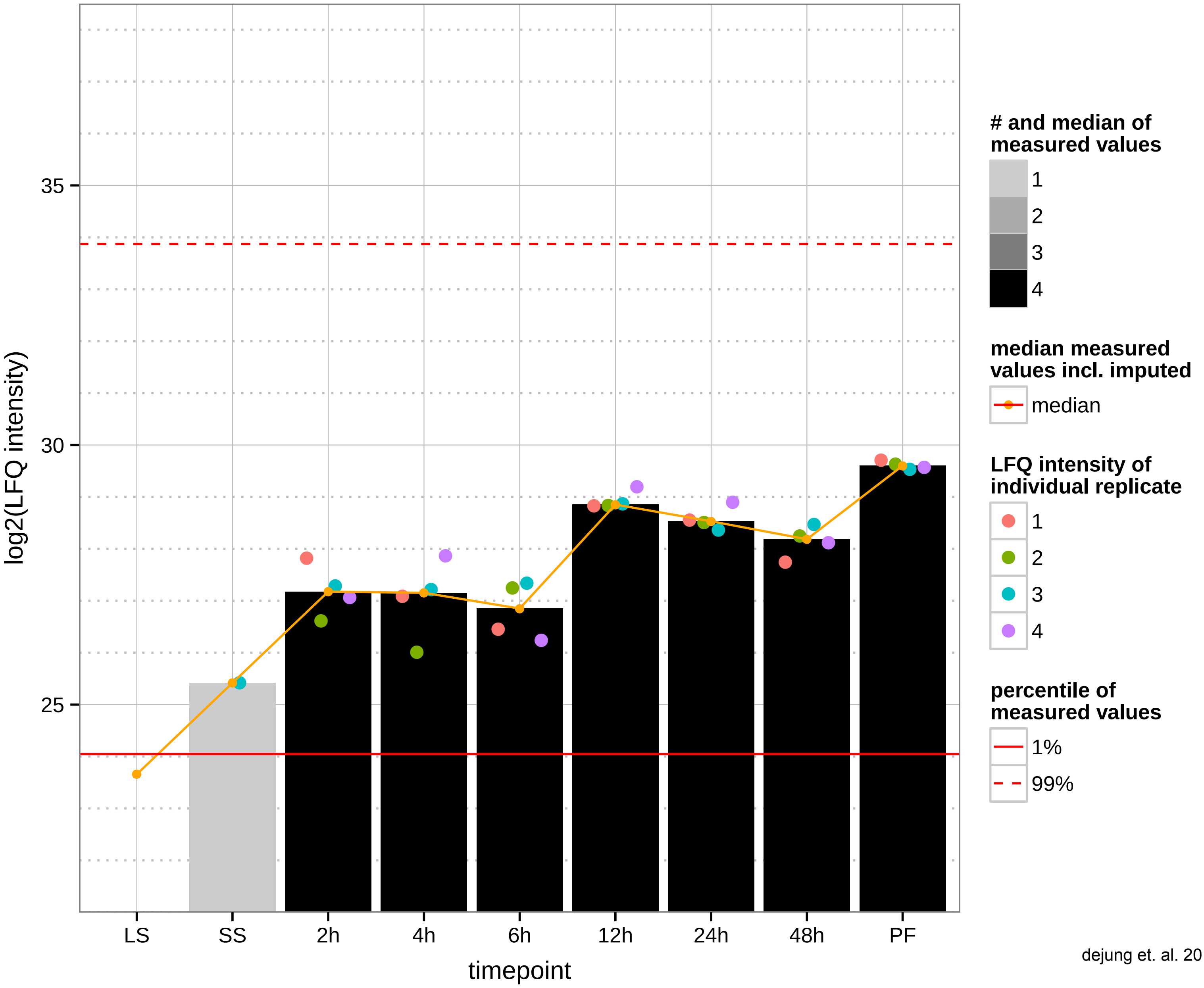
membrane–bound acid phosphatase, putative
Tb927.11.11740;Tb927.11.11750
AGOF: acid phosphatase activity
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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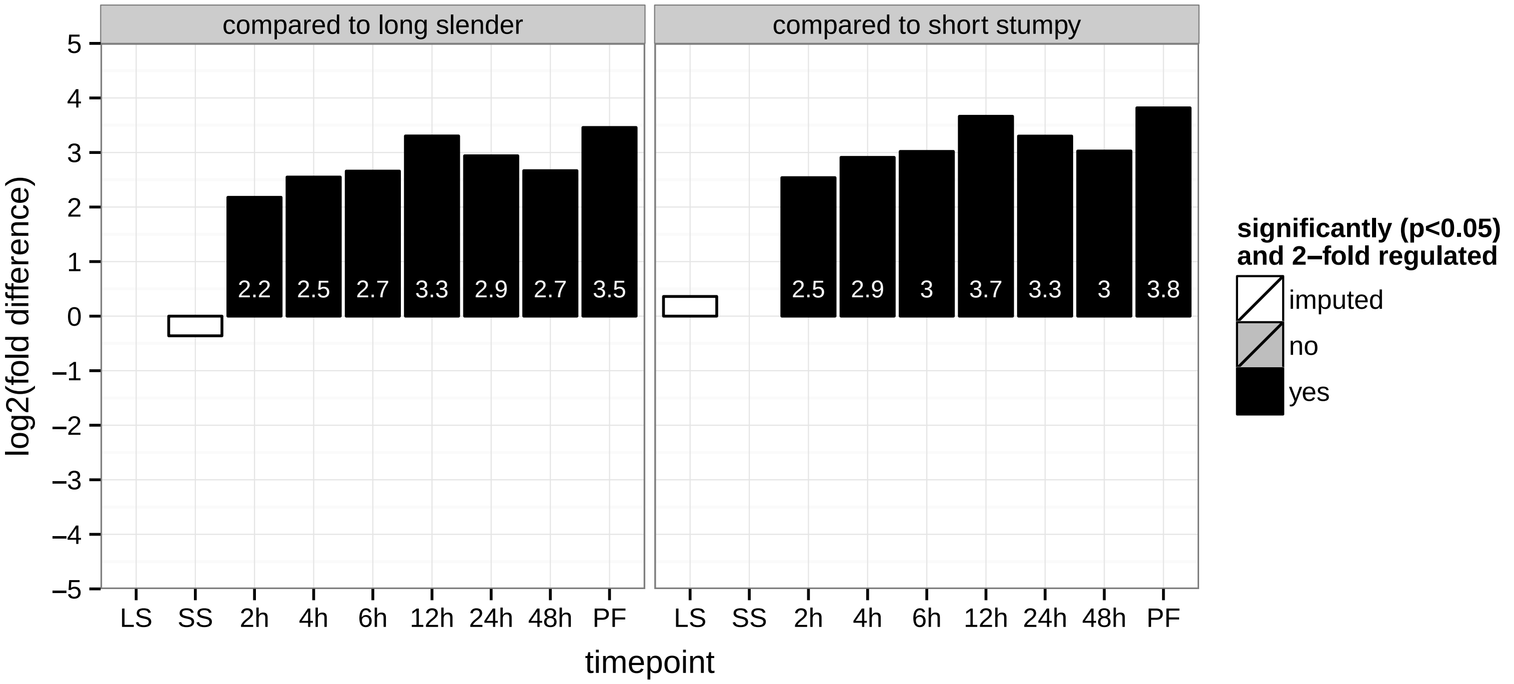
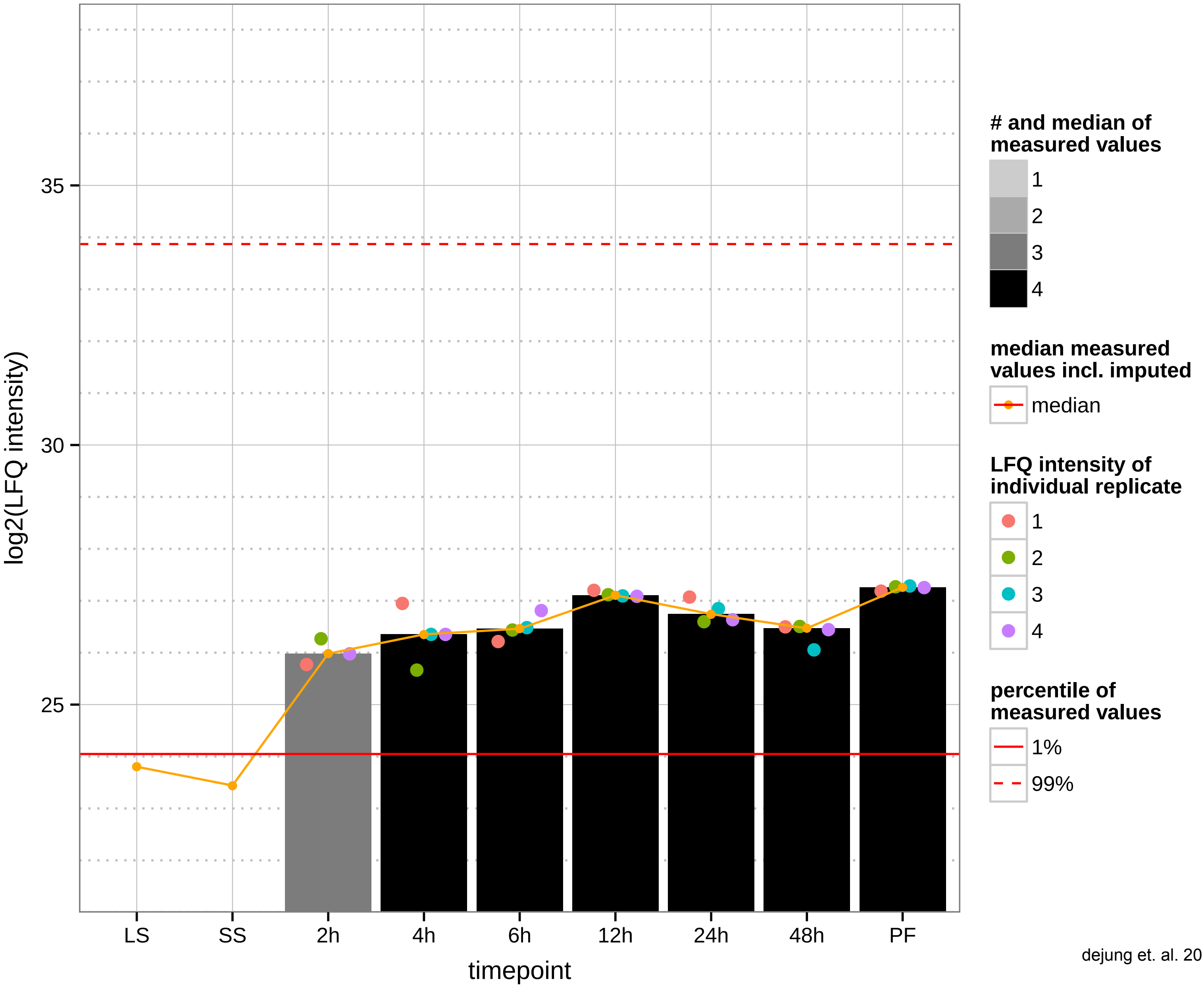
serine/threonine–protein kinase, putative
Tb927.11.15010
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, phospholipid binding, protein binding, protein kinase activity, transferase activity, transferring phosphorus
PGOC: null
PGOP: protein phosphorylation





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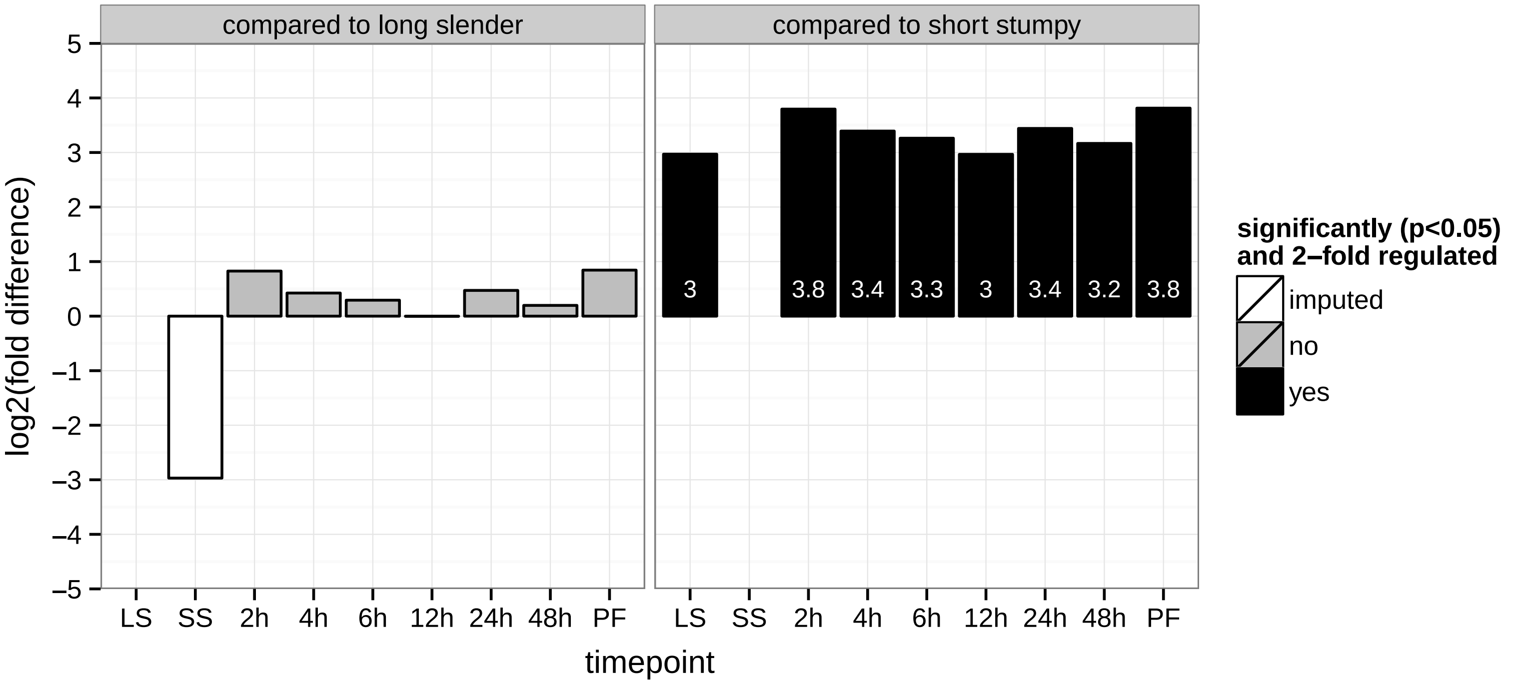
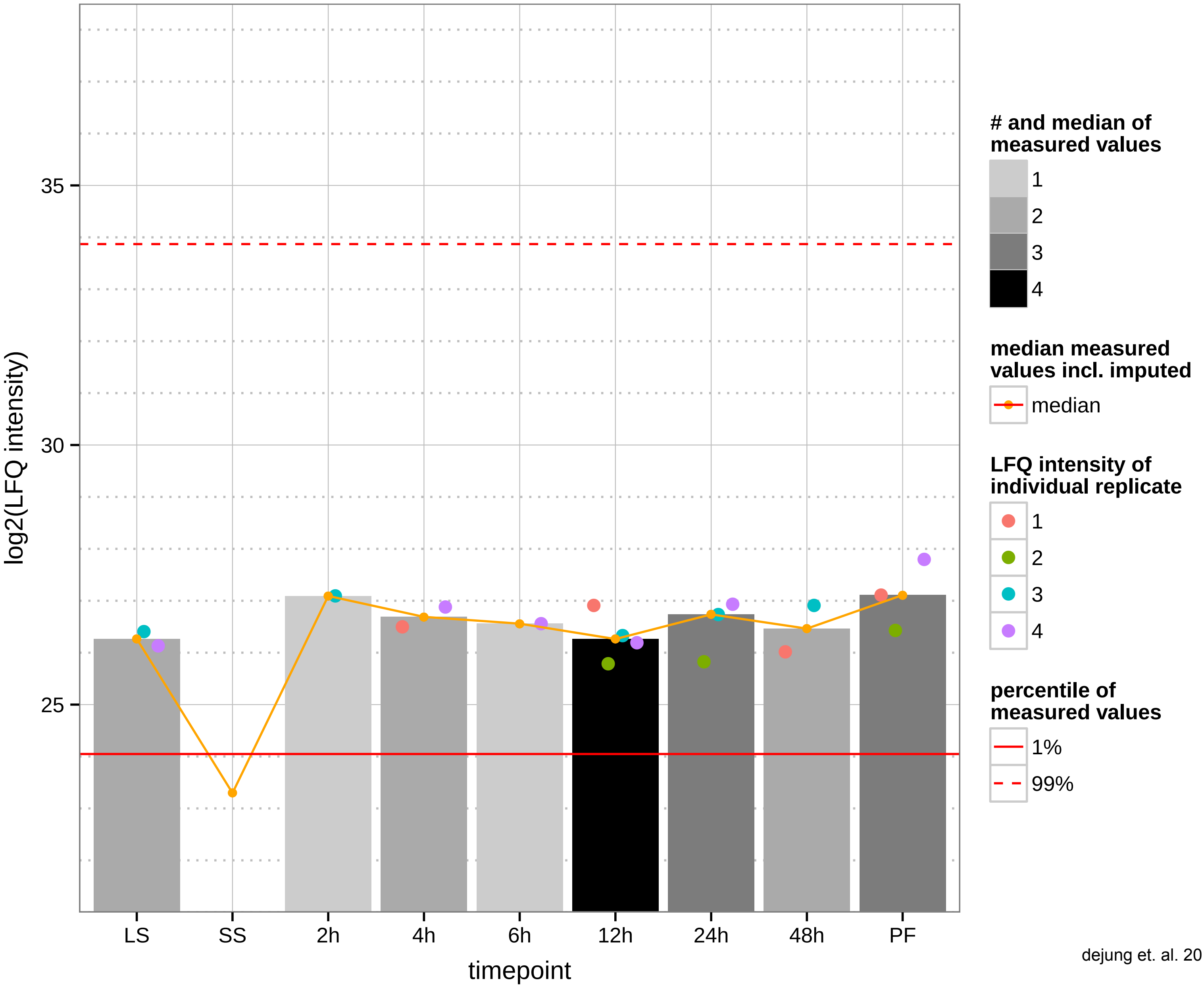
amino acid transporter, putative
Tb927.11.15950
AGOF: amine transmembrane transporter activity
AGOC: integral to membrane
AGOP: amino acid transport
PGOF: null
PGOC: null
PGOP: null





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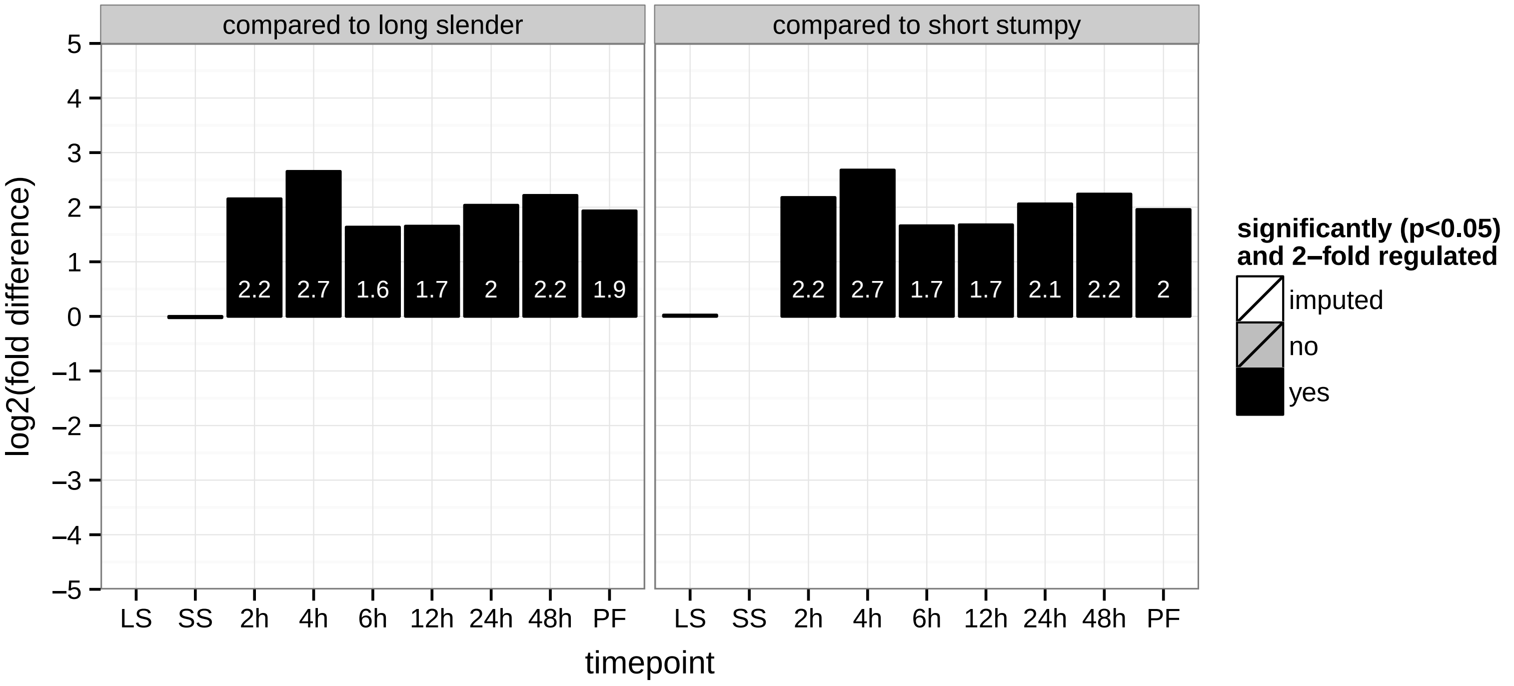
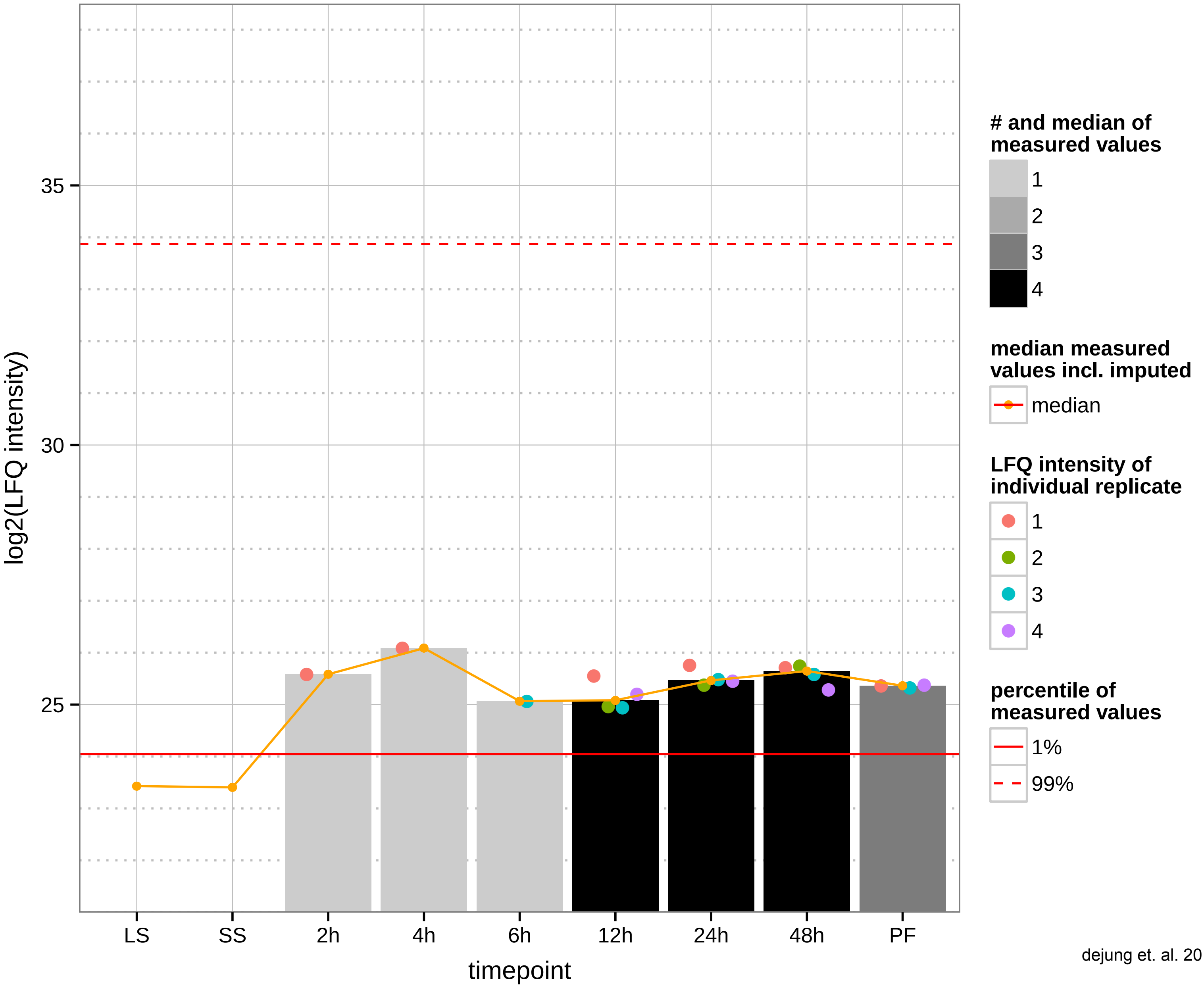
hypothetical protein, conserved
Tb927.11.2100
AGOF: null
AGOC: null
AGOP: null
PGOF: ATP binding
PGOC: null
PGOP: null





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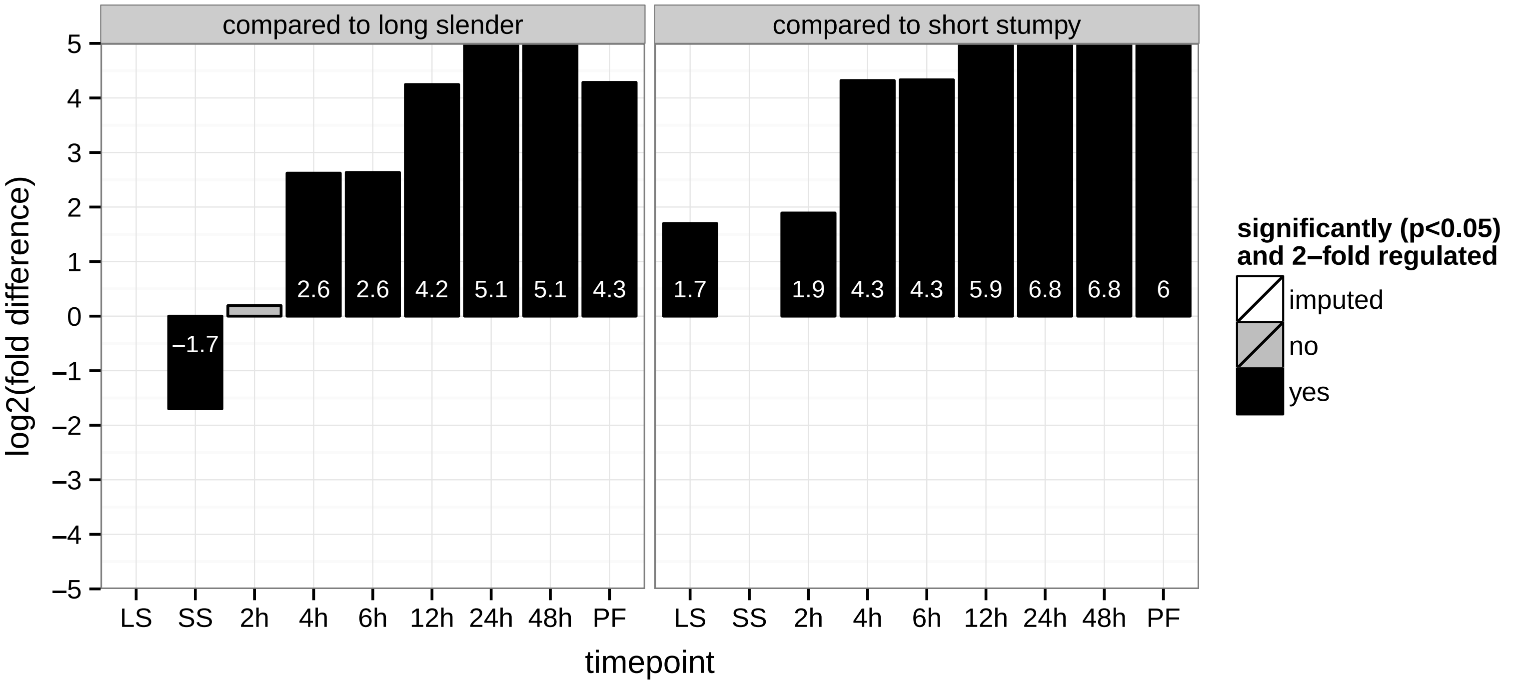
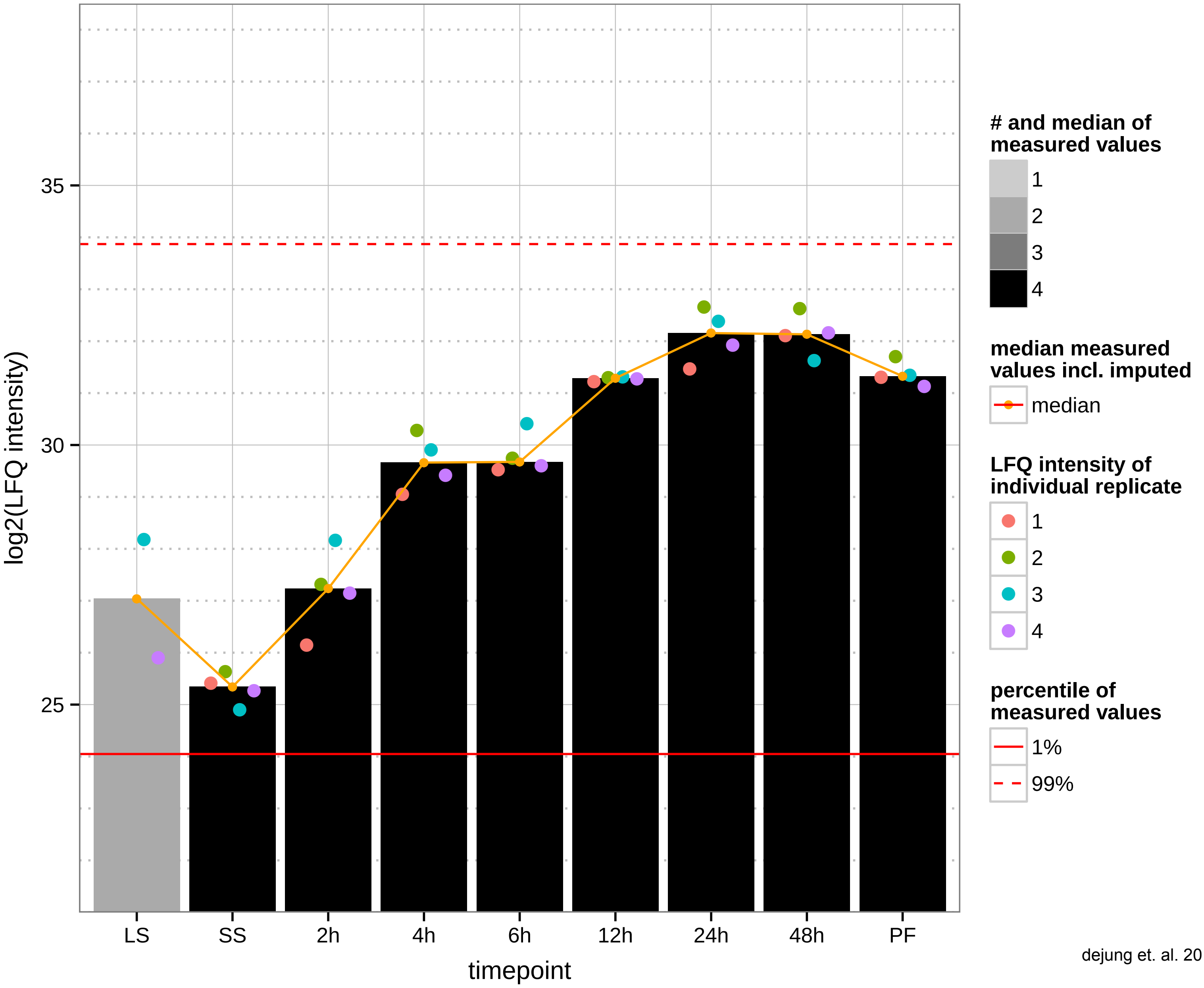
hypothetical protein, conserved
Tb927.11.2410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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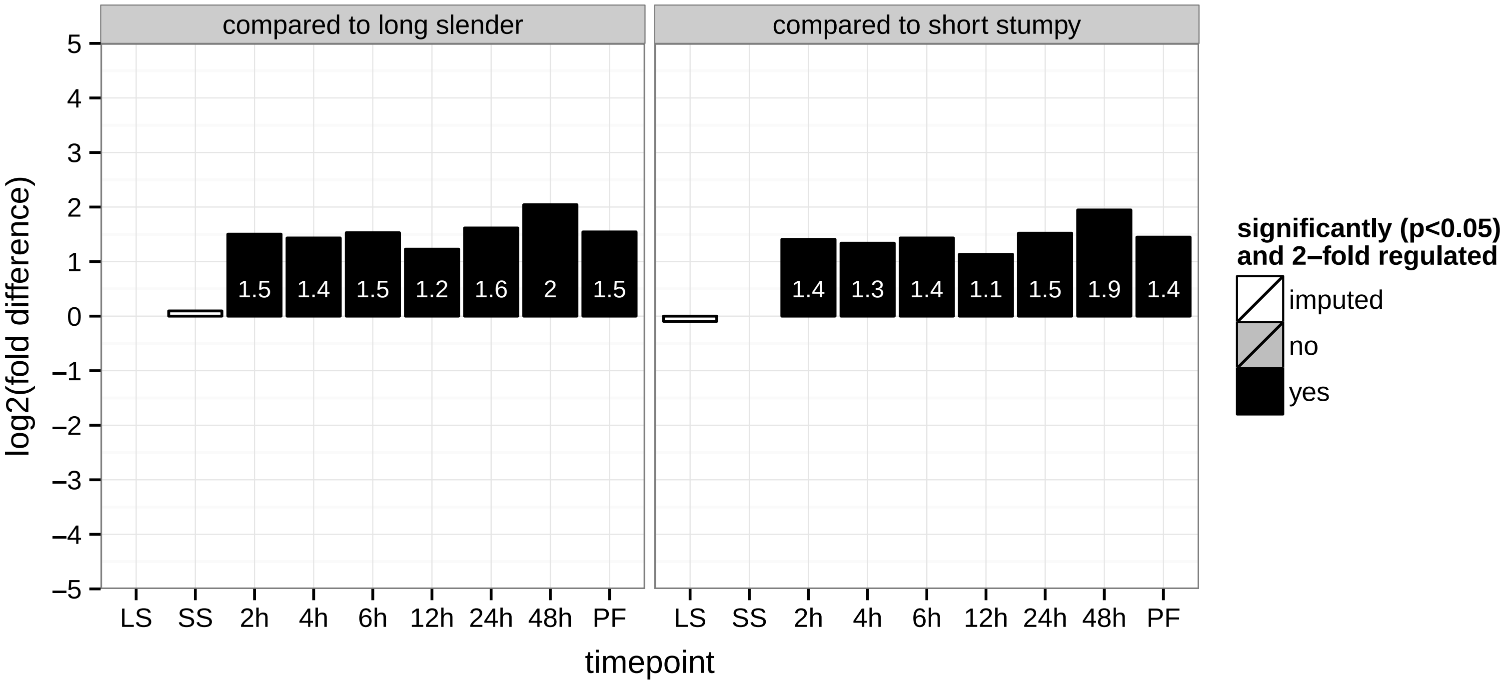
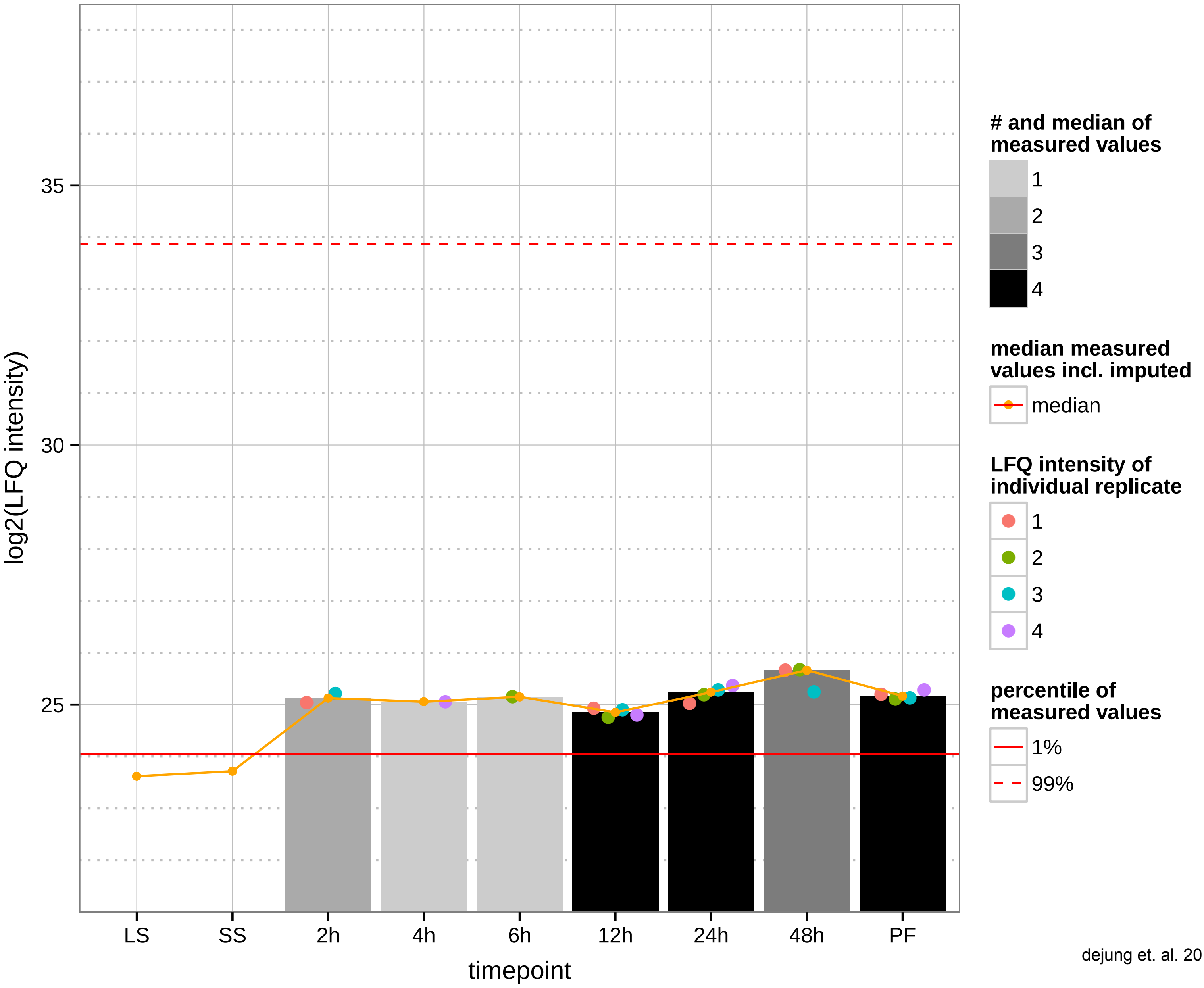
hypothetical protein, conserved (p166)
Tb927.11.3290
AGOF: null
AGOC: kinetoplast
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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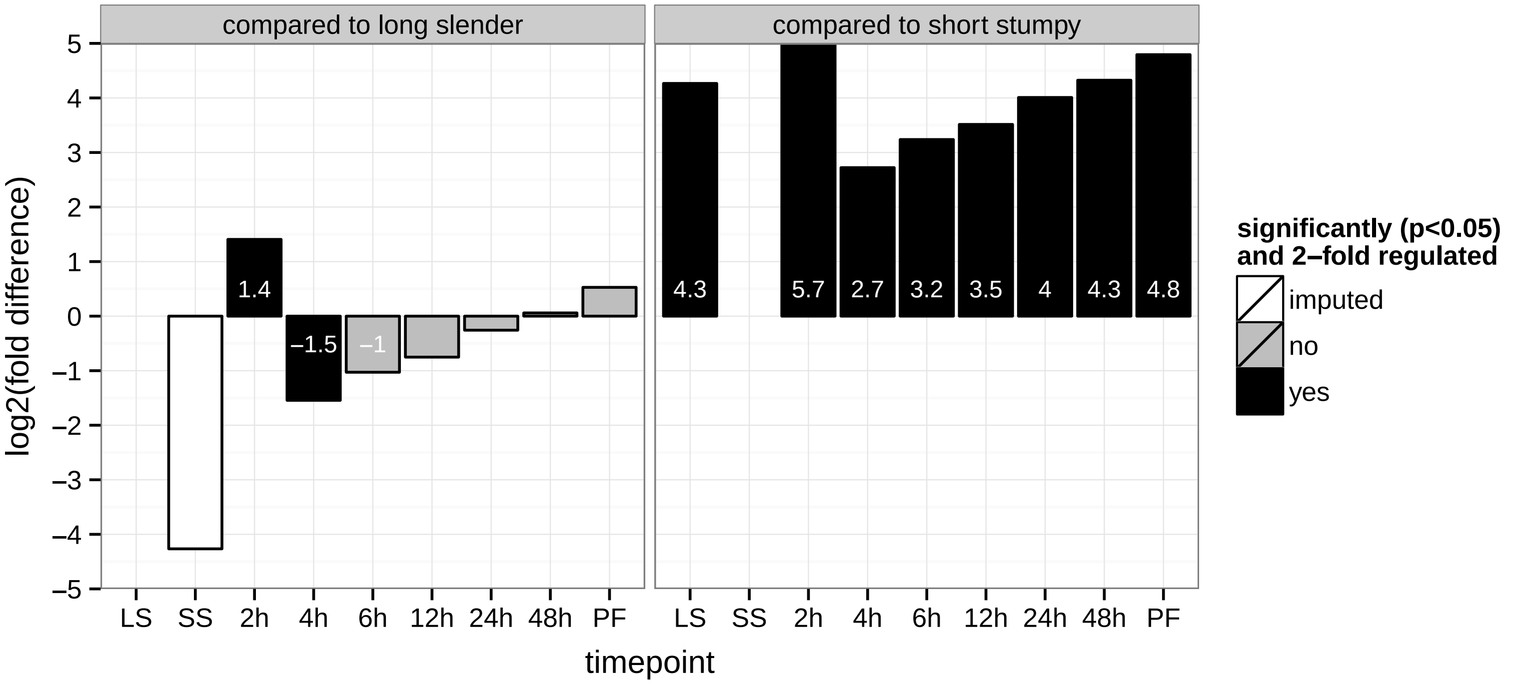
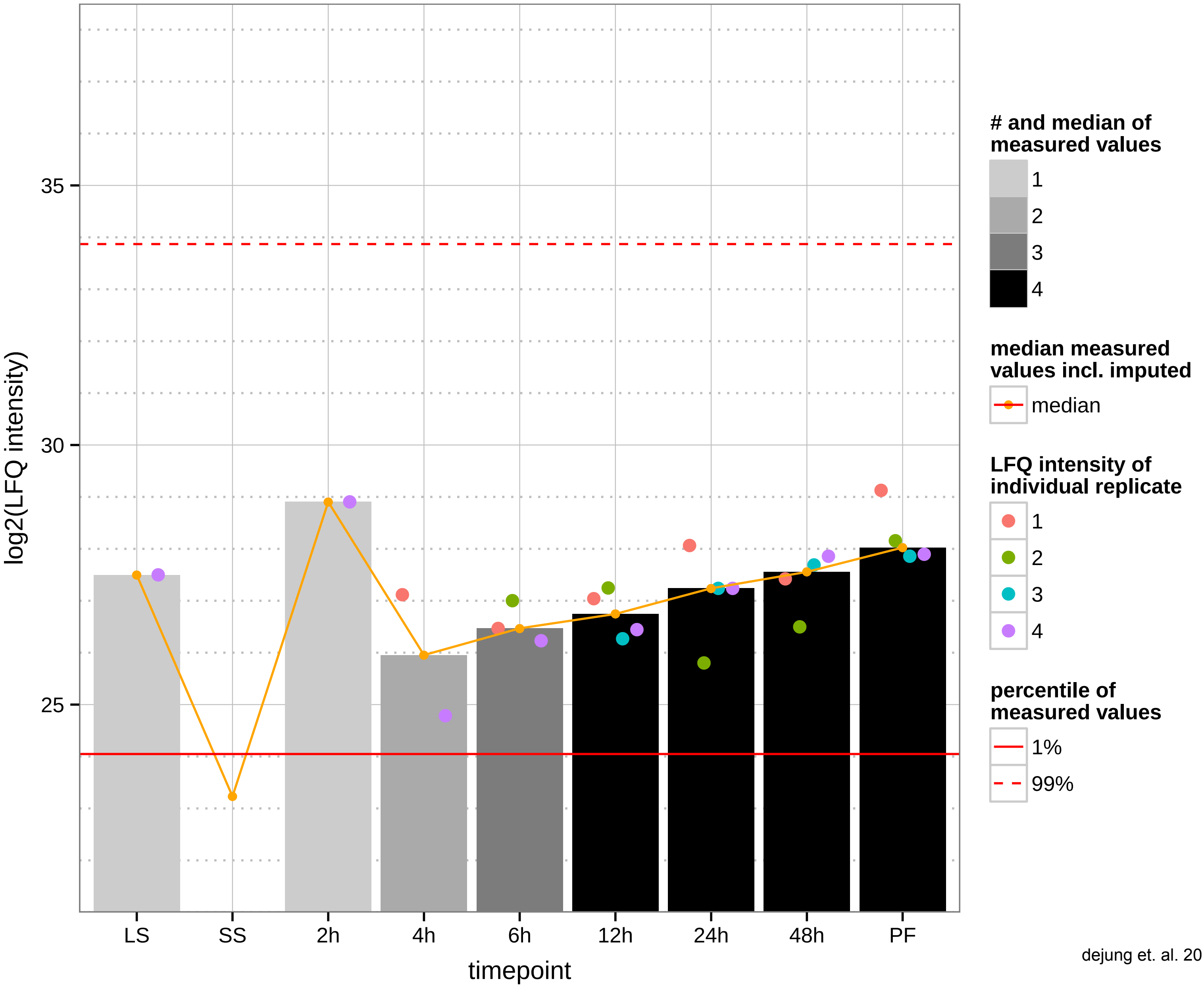
hypothetical protein, conserved
Tb927.11.4680
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: membrane
PGOP: null





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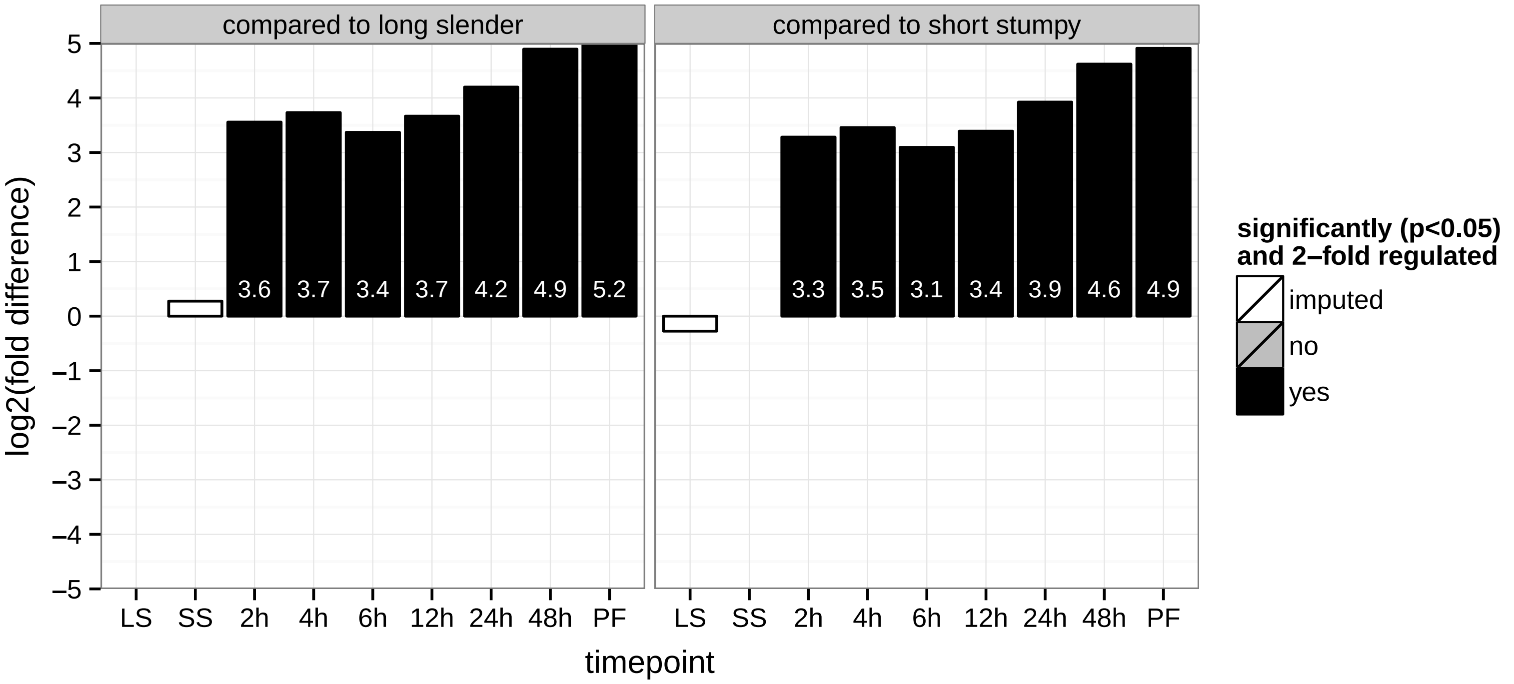
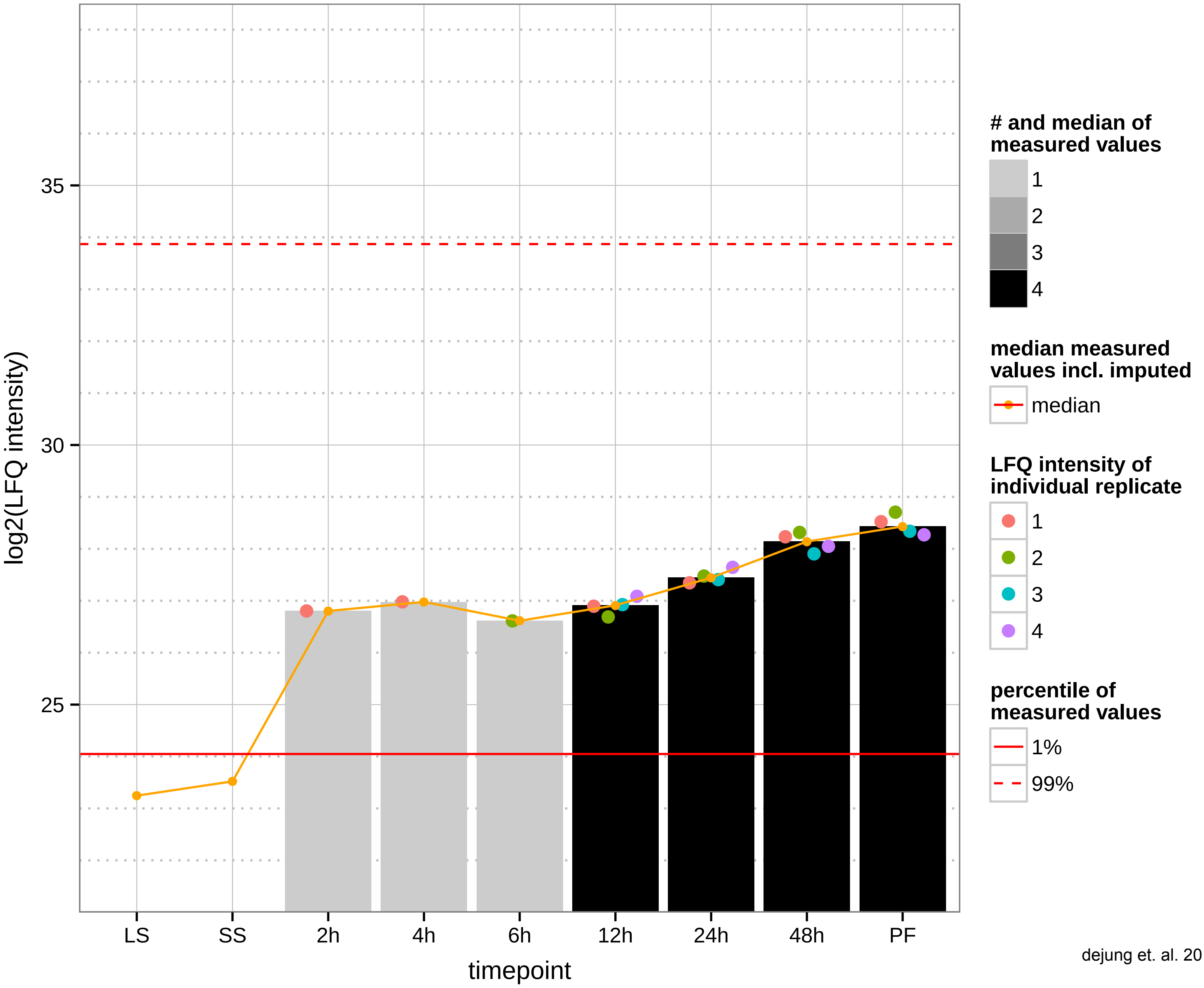
Mitochondrial SSU ribosomal protein, putative, kinetoplast ribosomal PPR−repeat containing protein 1 (KRIPP1)
Tb927.11.5500
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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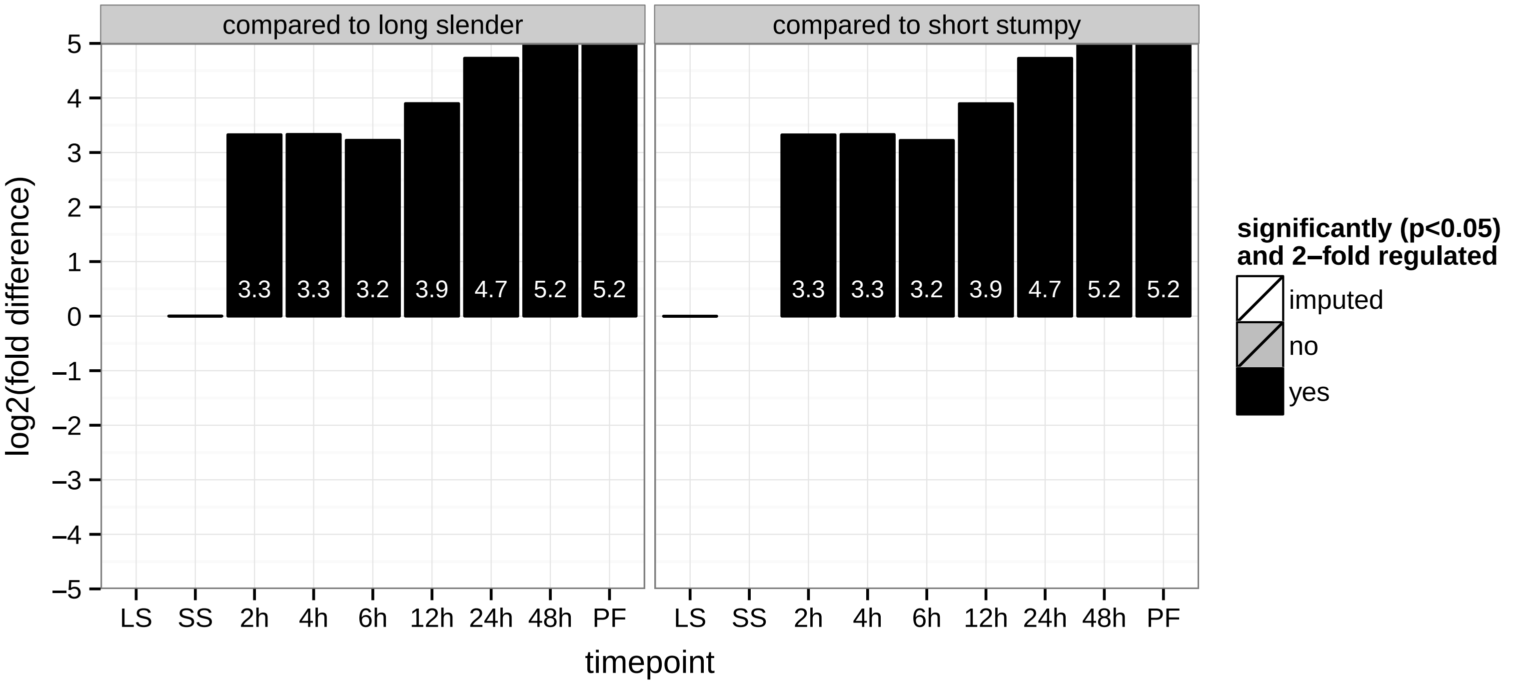
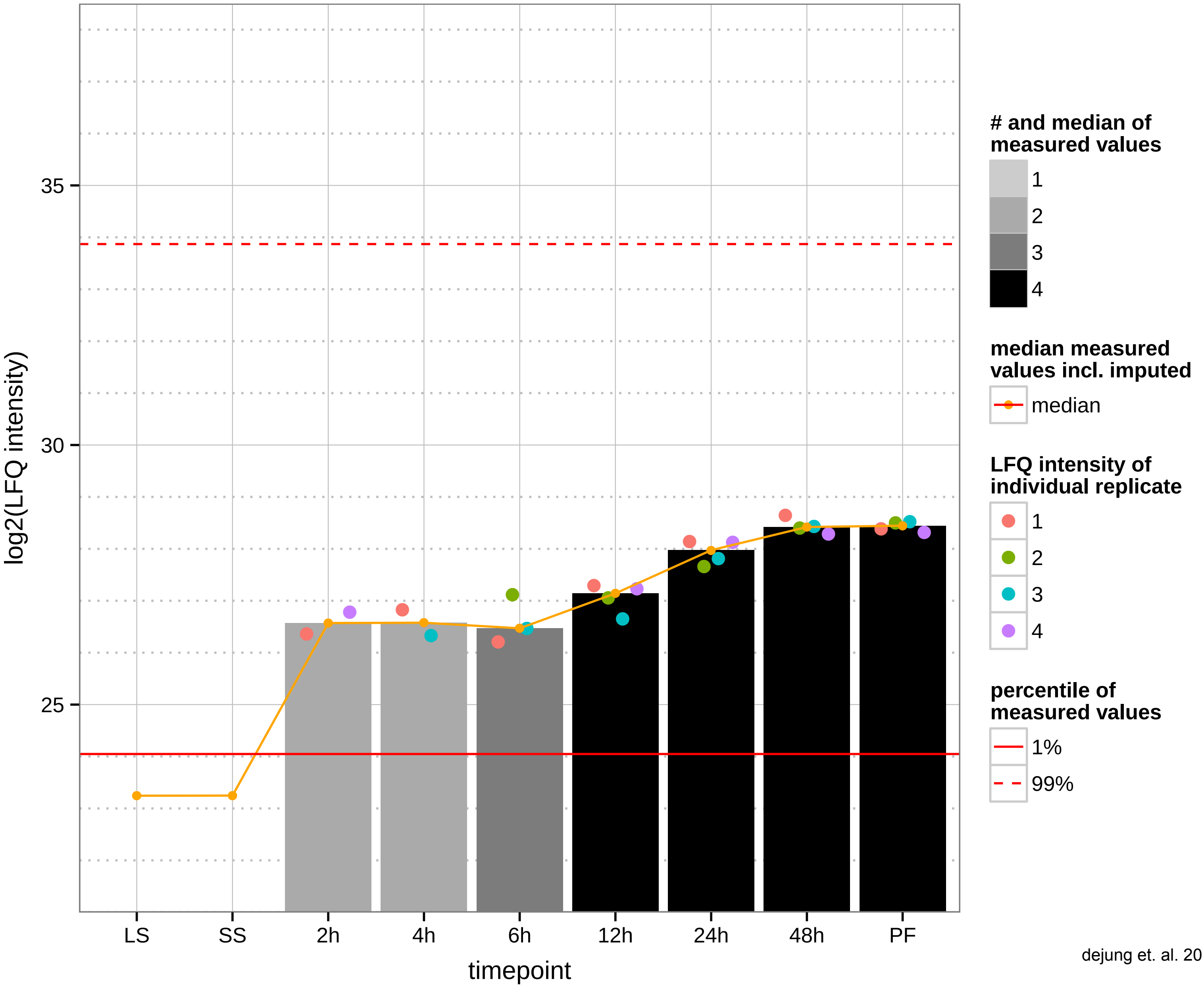
RNA–binding protein, putative (RBP38)
Tb927.11.5850
AGOF: RNA binding
AGOC: cytosol
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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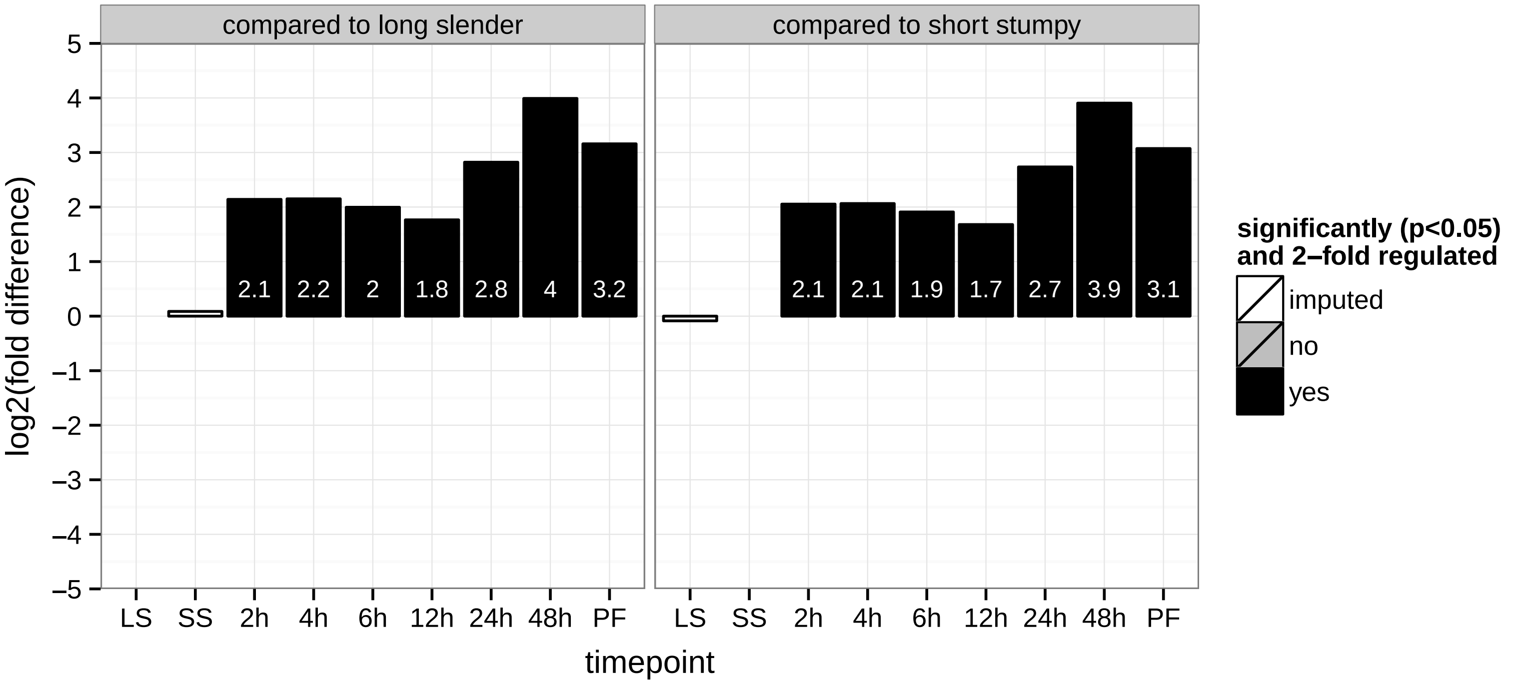
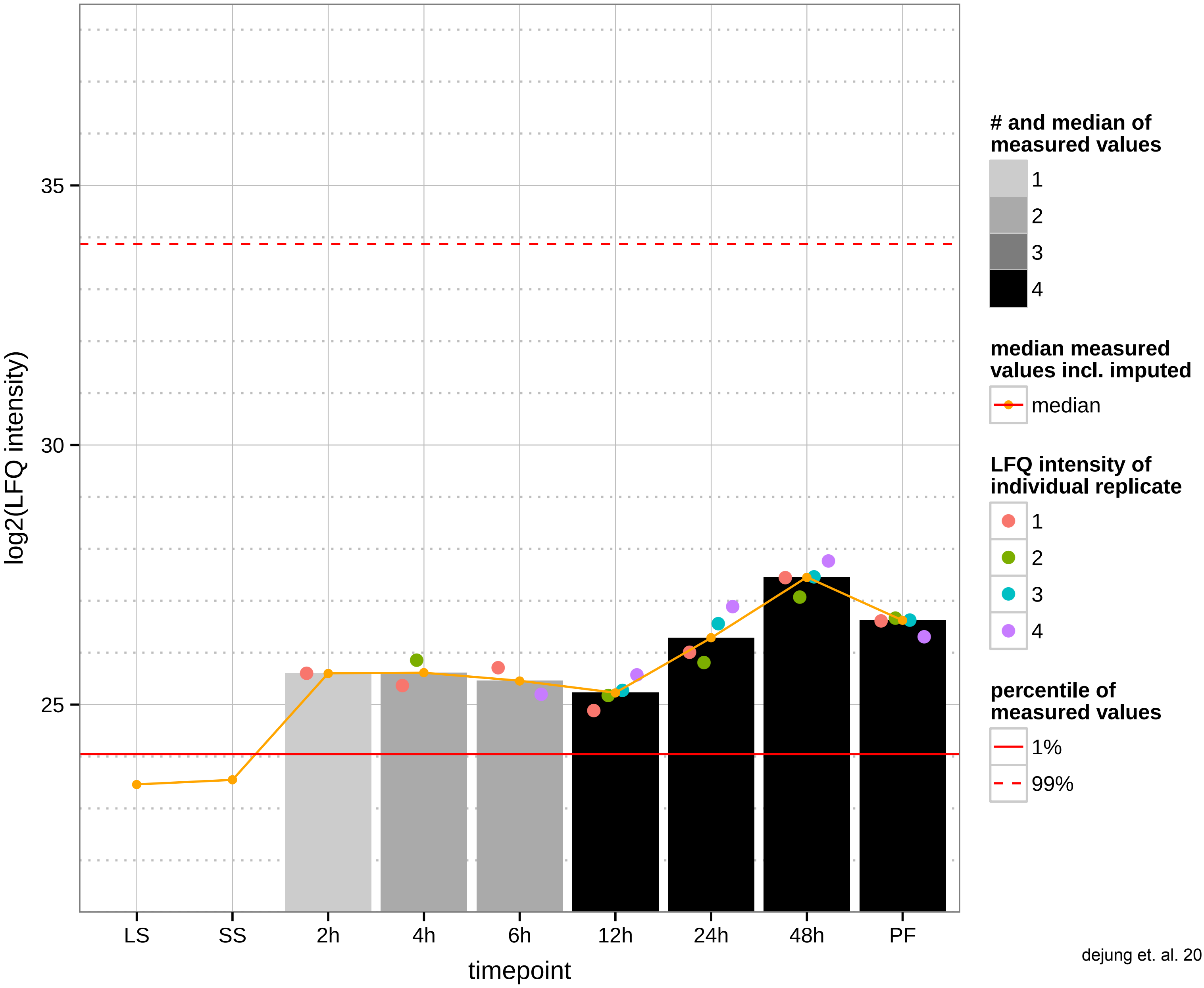
phosphoinositide–specific phospholipase C, putative
Tb927.11.5970
AGOF: phosphatidylinositol phospholipase C activity, phospholipase C activity
AGOC: membrane
AGOP: intracellular signal transduction, lipid metabolic process, signal transduction
PGOF: phosphatidylinositol phospholipase C activity, phospholipase C activity, phosphoric diester hydrolase activity, protein b
PGOC: null
PGOP: intracellular signal transduction, lipid metabolic process, signal transduction





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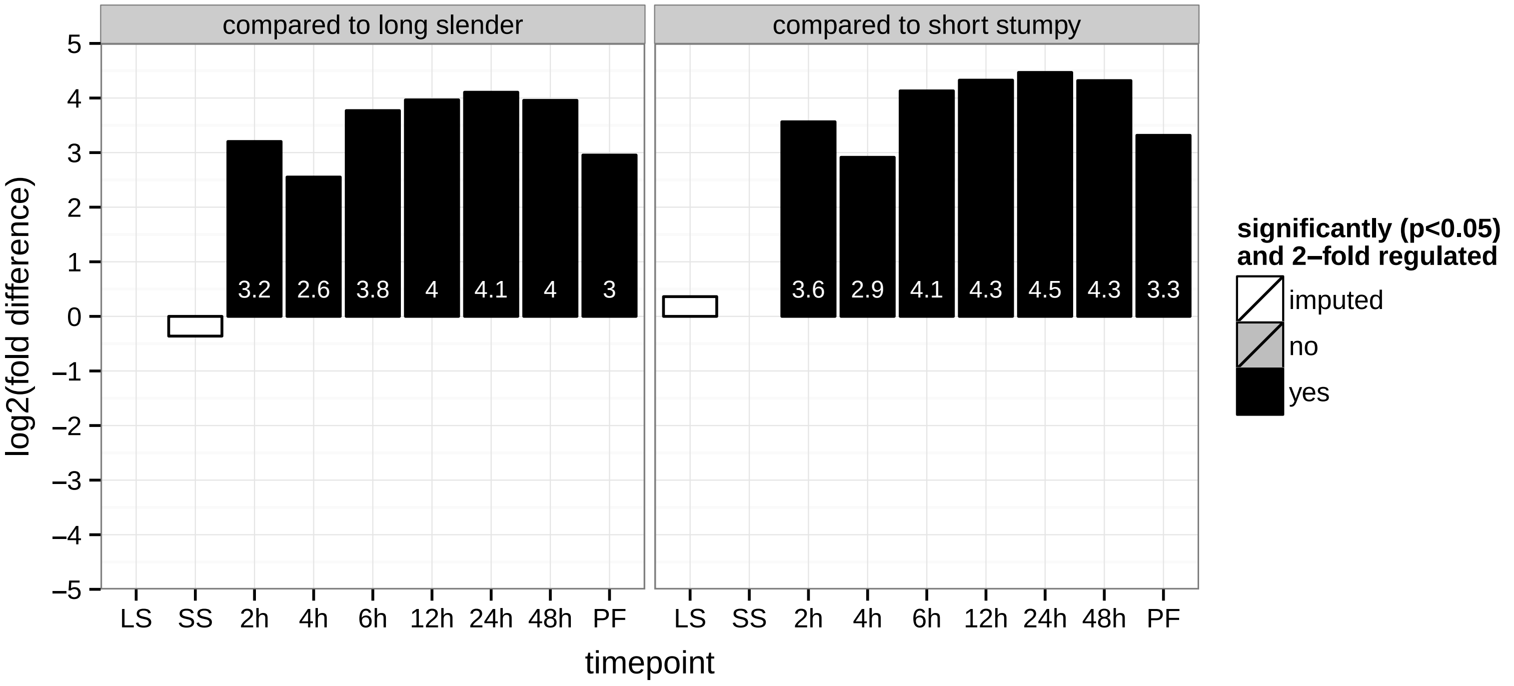
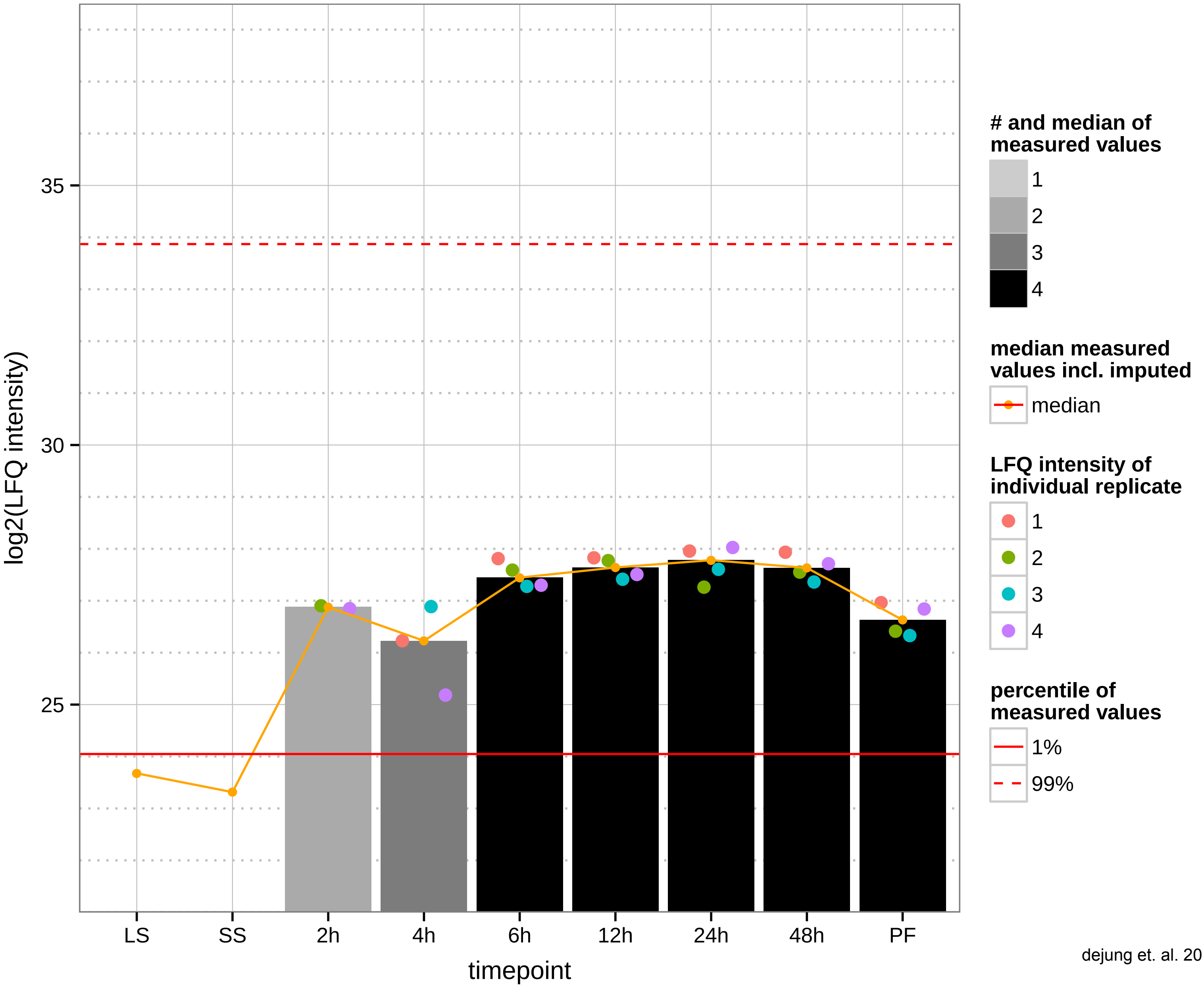
hypothetical protein, conserved
Tb927.11.6660
AGOF: hydrolase activity, acting on ester bonds
AGOC: mitochondrion
AGOP: nucleobase–containing compound metabolic process
PGOF: hydrolase activity, acting on ester bonds, nucleic acid binding
PGOC: null
PGOP: nucleobase–containing compound metabolic process





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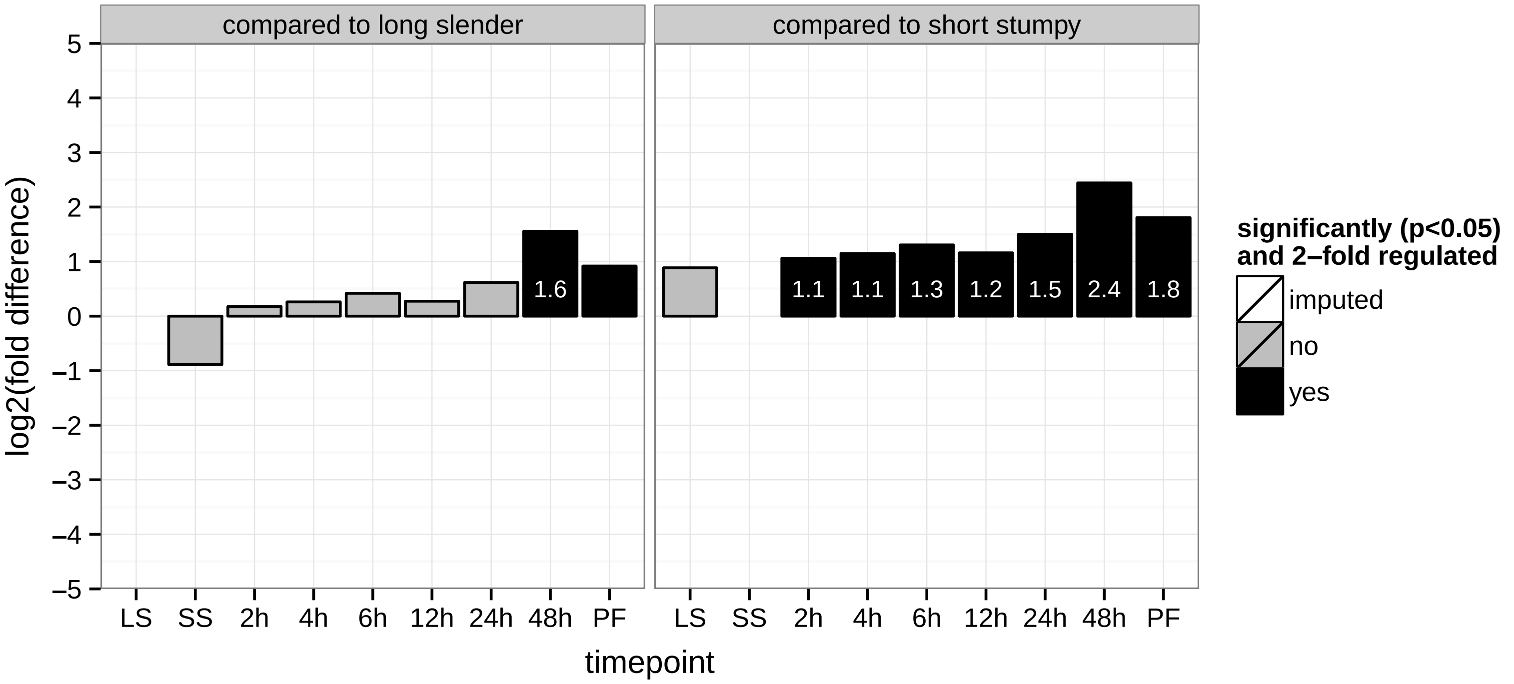
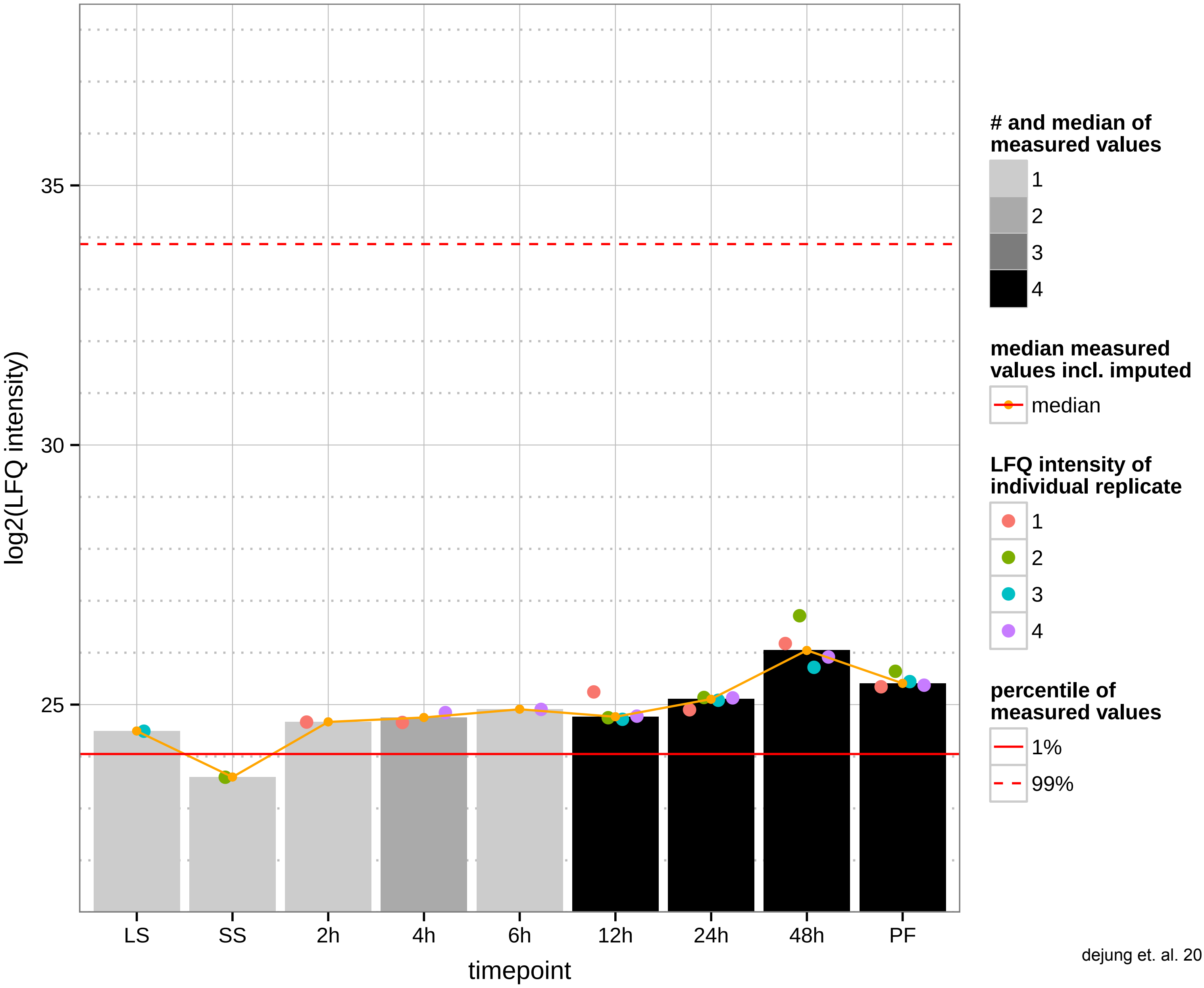
hypothetical protein, conserved
Tb927.11.840.1;Tb927.11.840.2
AGOF: solute:hydrogen antiporter activity
AGOC: integral to membrane
AGOP: cation transport
PGOF: solute:hydrogen antiporter activity
PGOC: integral to membrane
PGOP: cation transport, transmembrane transport





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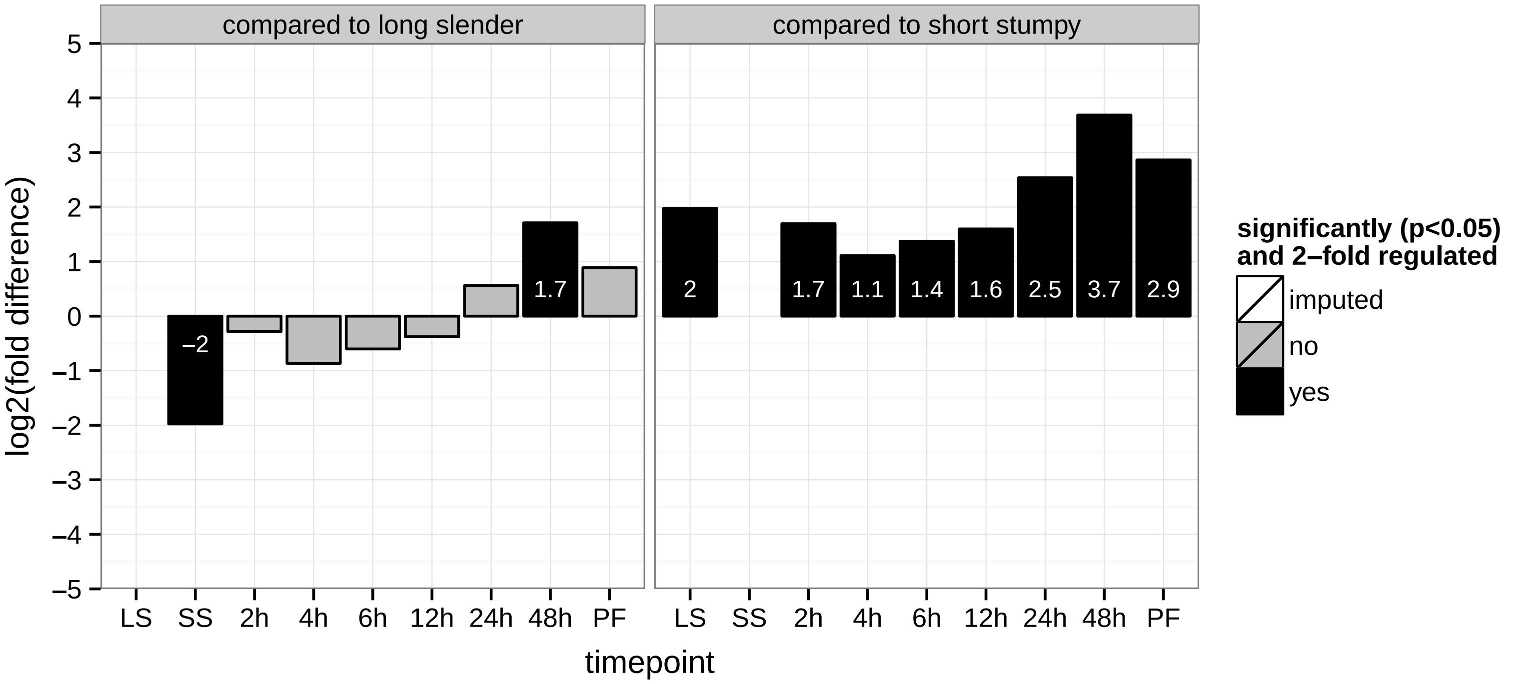
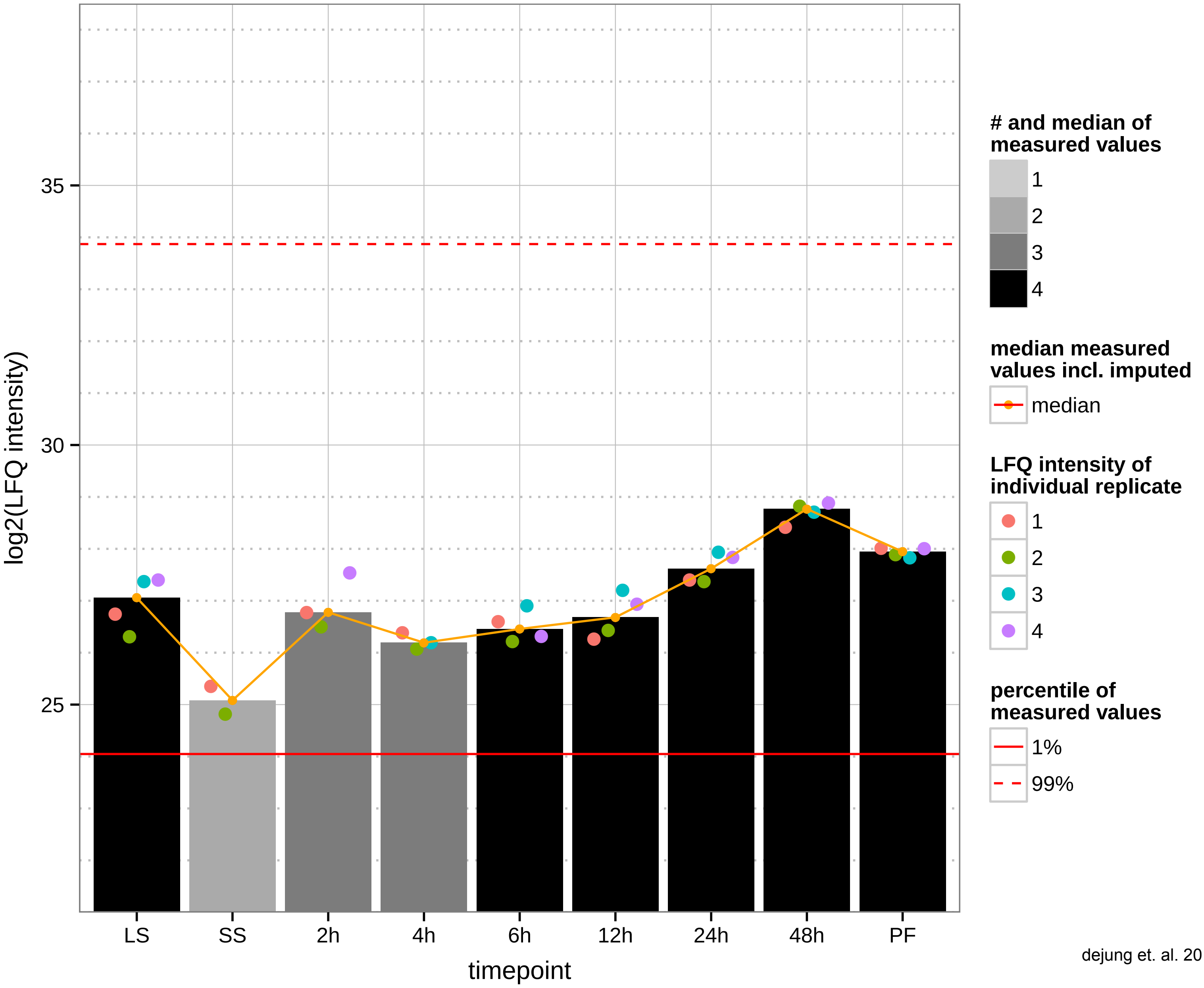
retrotransposon hot spot protein (RHS, pseudogene), putative, retrotransposon hot spot protein 6 (RHS6), degenerate
Tb927.2.1330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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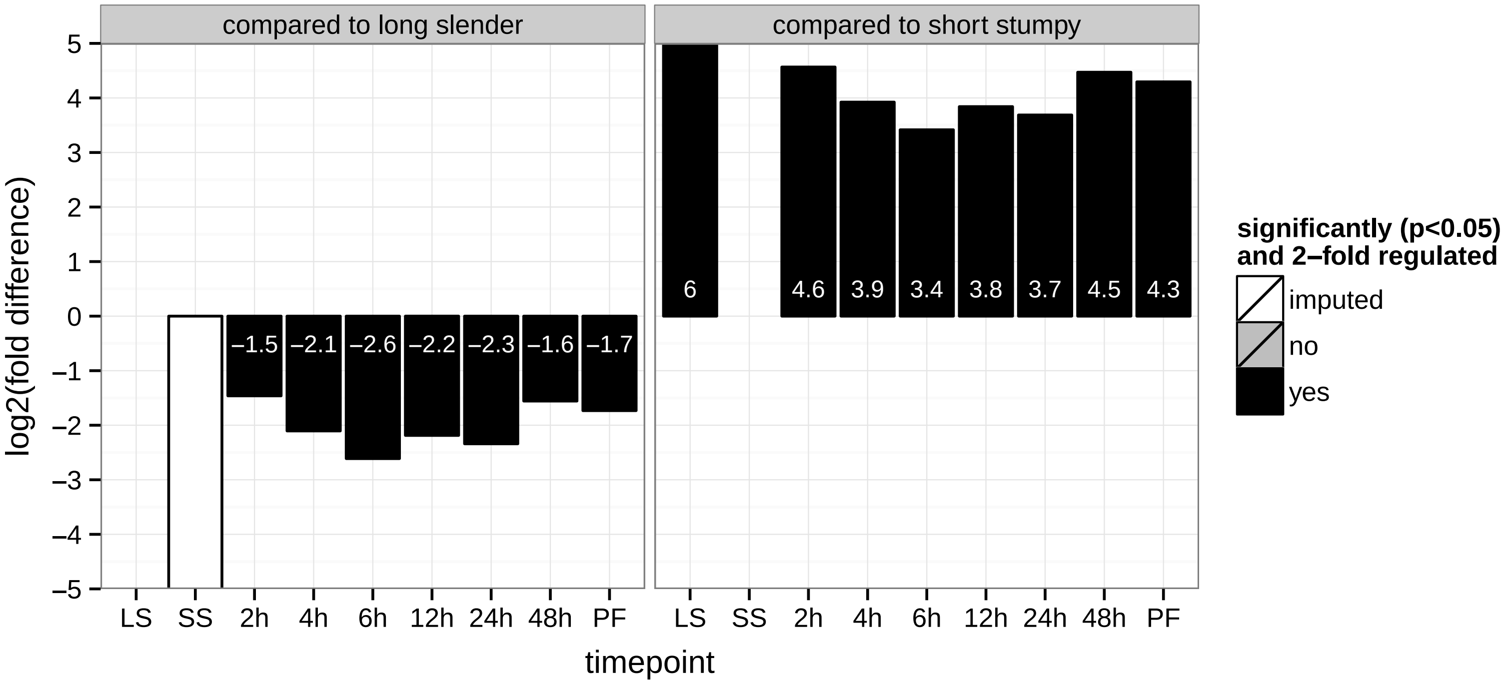
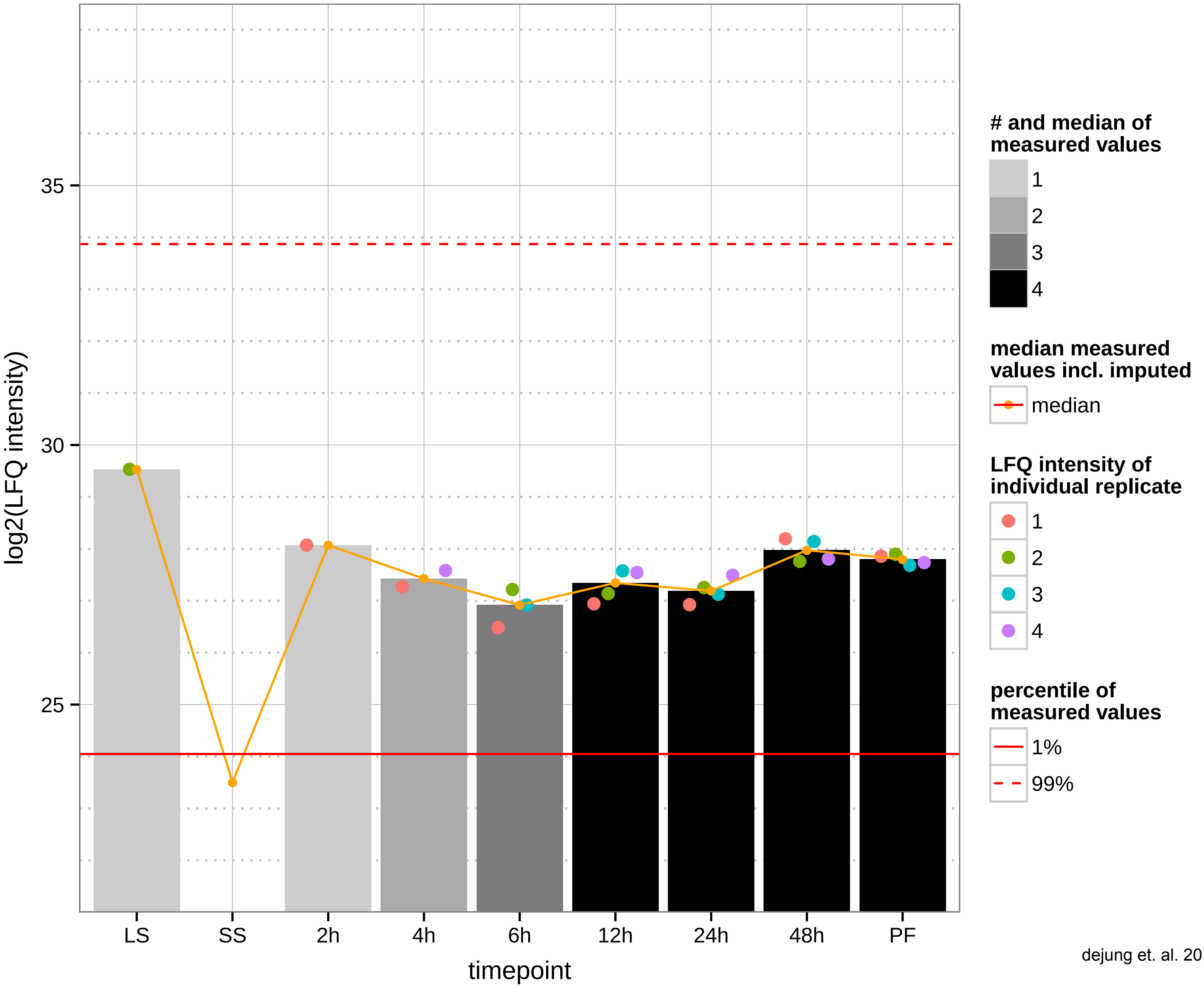
hypothetical protein, conserved
Tb927.3.1970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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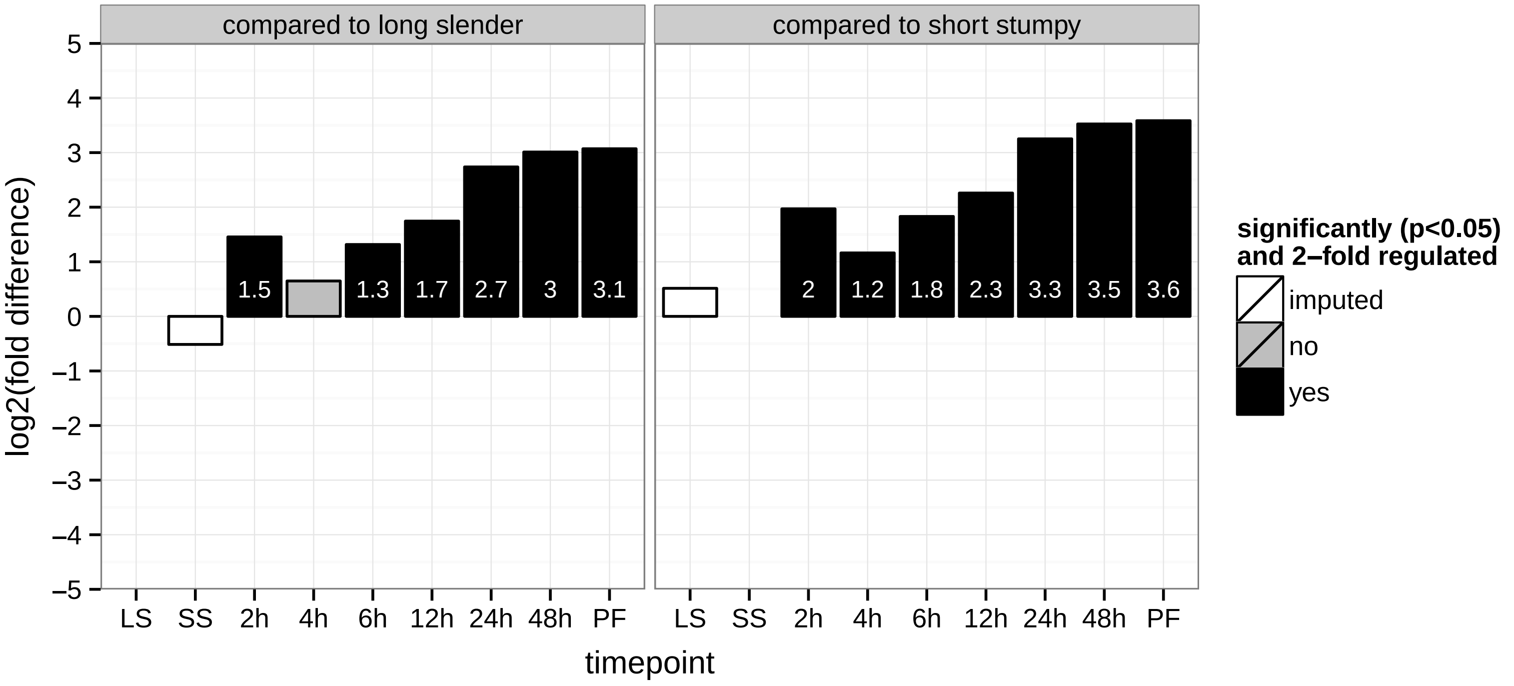
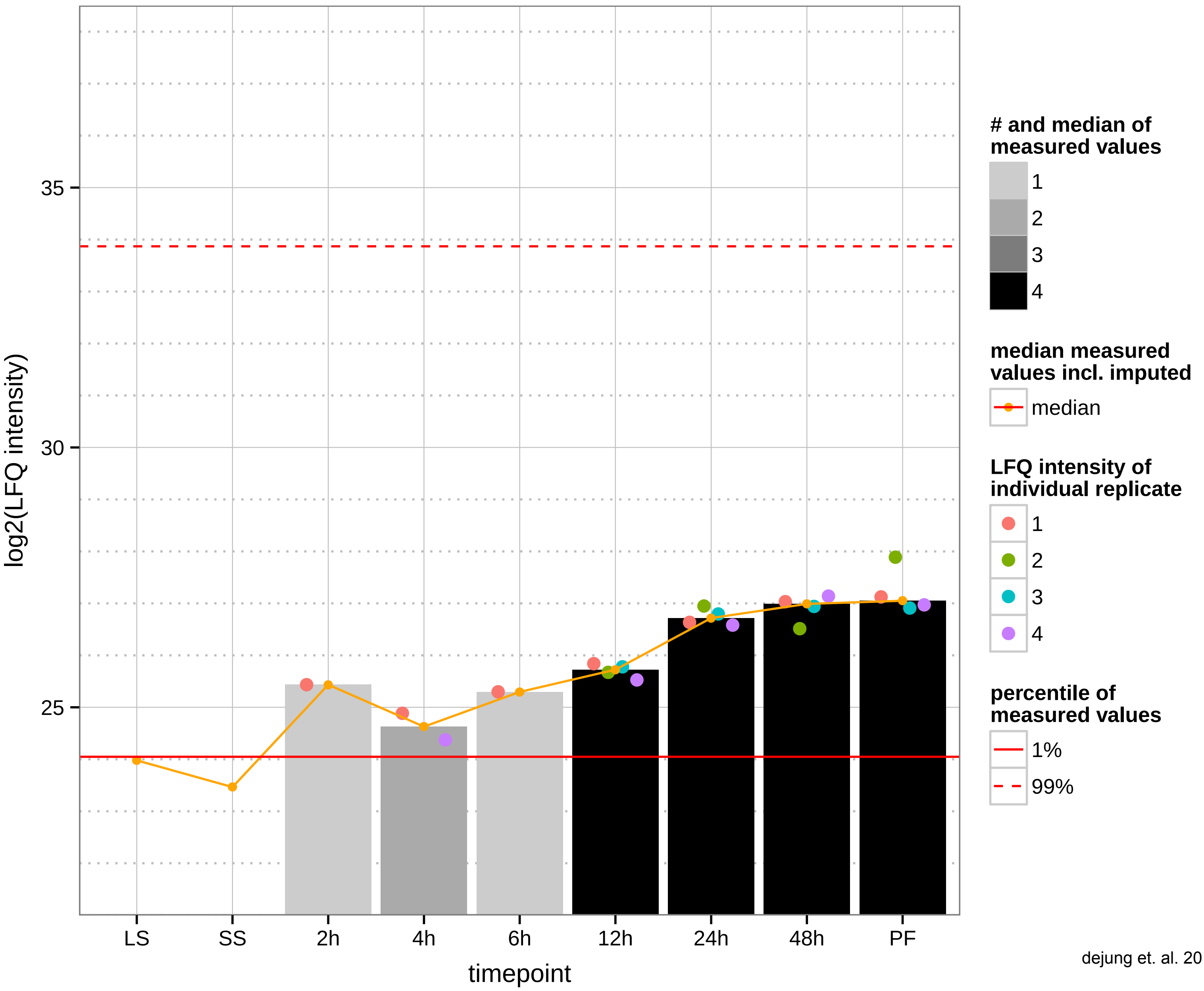
hypothetical protein, conserved
Tb927.3.750
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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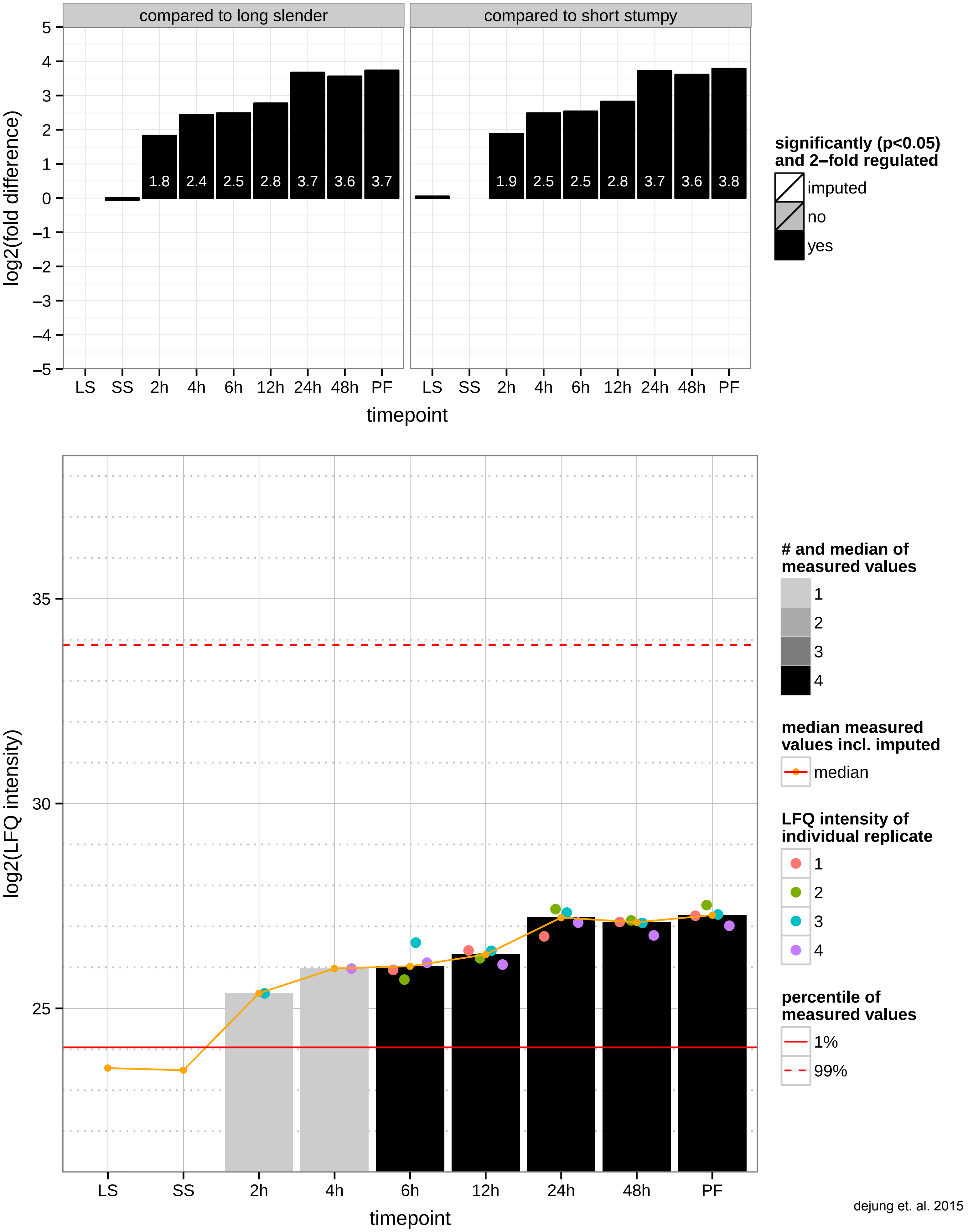
hypothetical protein, conserved
Tb927.4.1670
AGOF: heme binding
AGOC: null
AGOP: null
PGOF: heme binding
PGOC: null
PGOP: null



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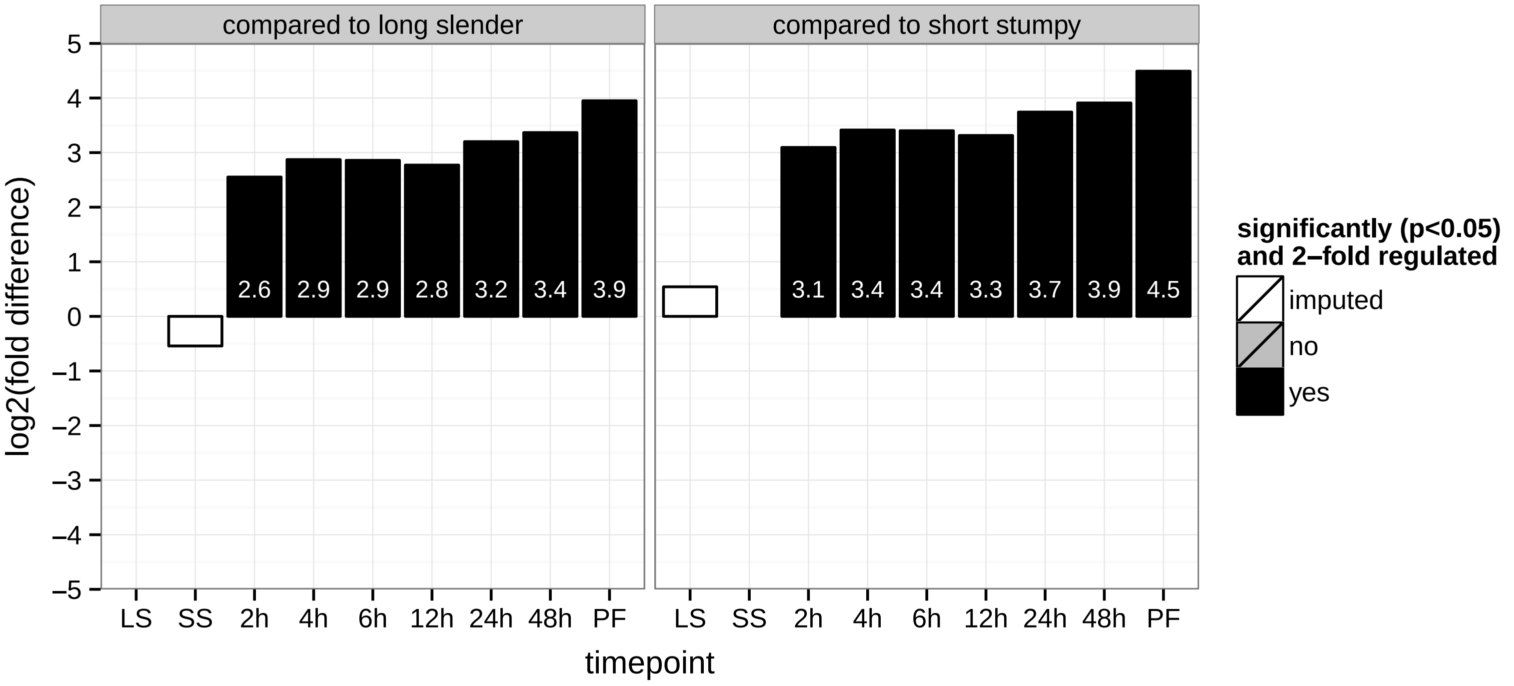
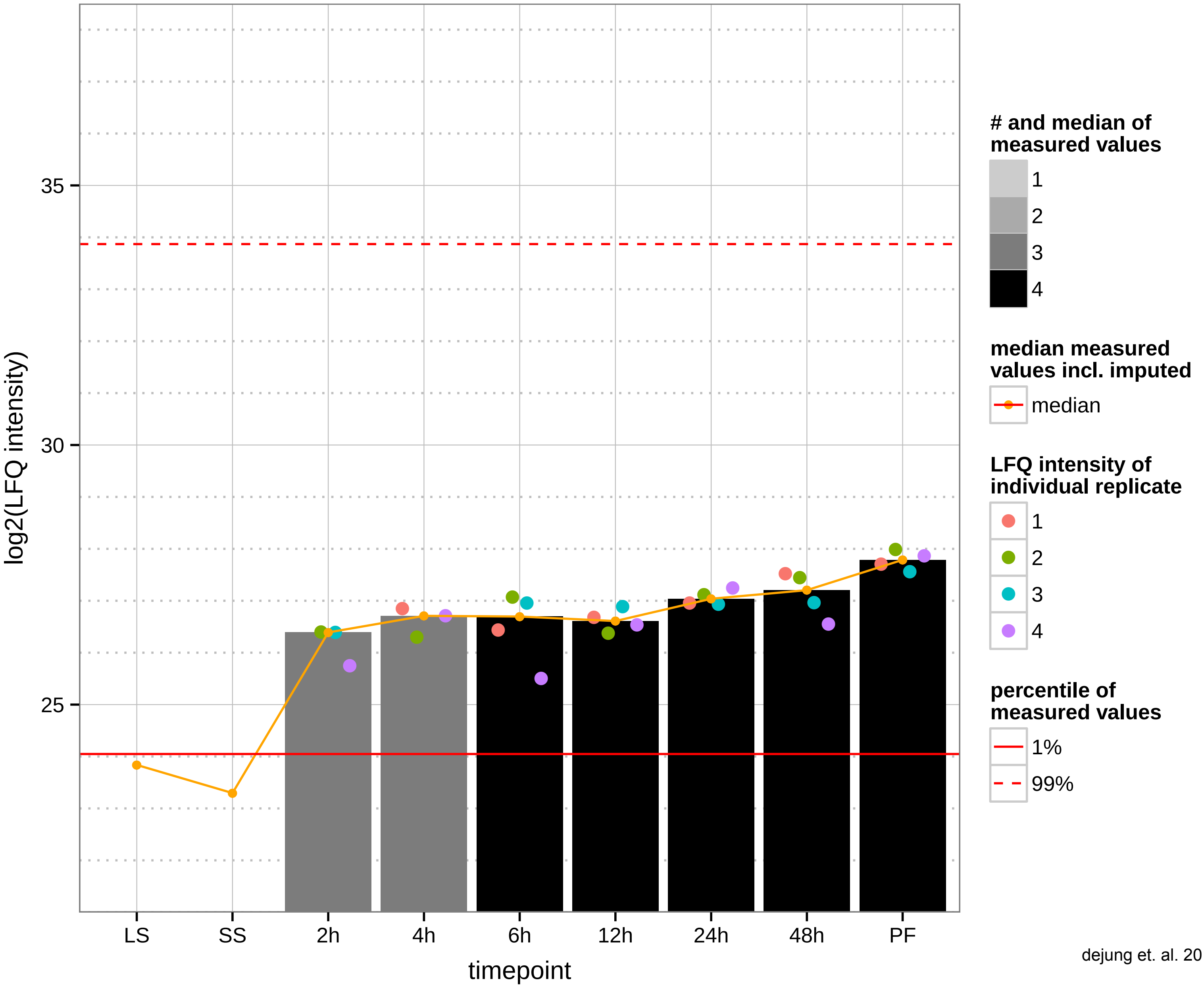
L−galactonolactone oxidase, D−arabinonolactone oxidase (GAL/ALO)
Tb927.5.2650
AGOF: D−arabinono−1, 4−lactone oxidase activity, FMN binding, L−galactonolactone oxidase activity, flavin adenine dinucleot
AGOC: glycosome, membrane
AGOP: L−ascorbic acid biosynthetic process
PGOF: D−arabinono−1, 4−lactone oxidase activity, UDP−N−acetylmuramate dehydrogenase activity, catalytic activity, flavin a
PGOC: membrane
PGOP: oxidation−reduction process





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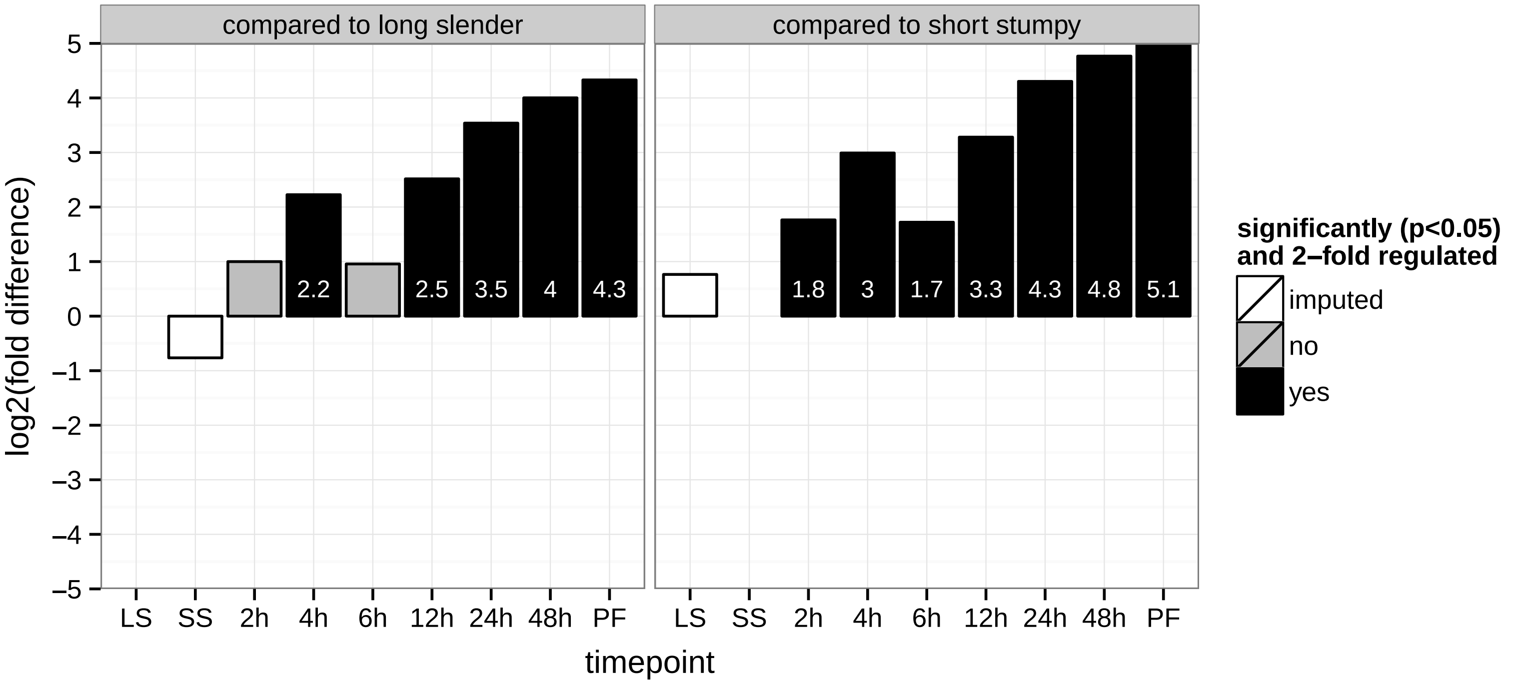
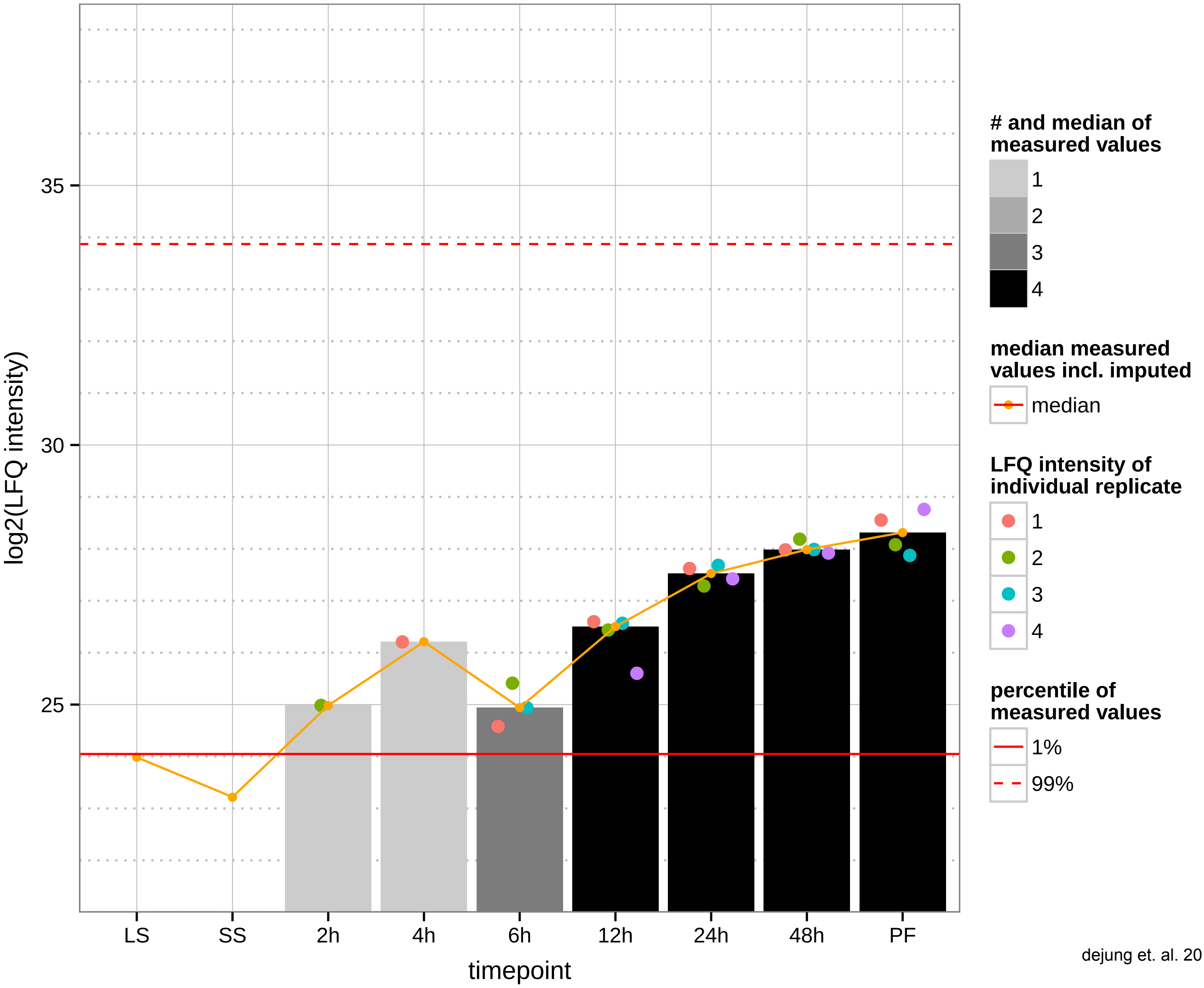
cell cycle sequence binding phosphoprotein (RBP33), putative
Tb927.5.760
AGOF: phosphoprotein binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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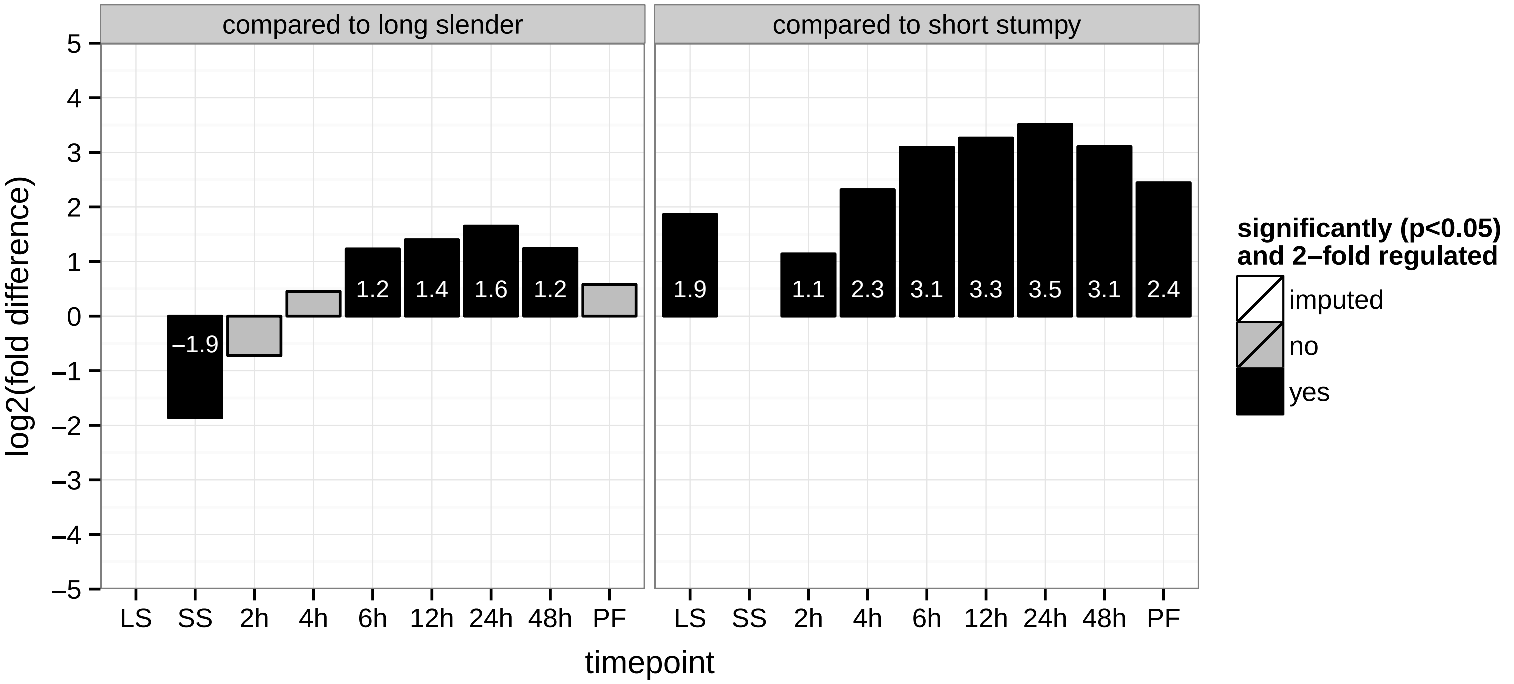
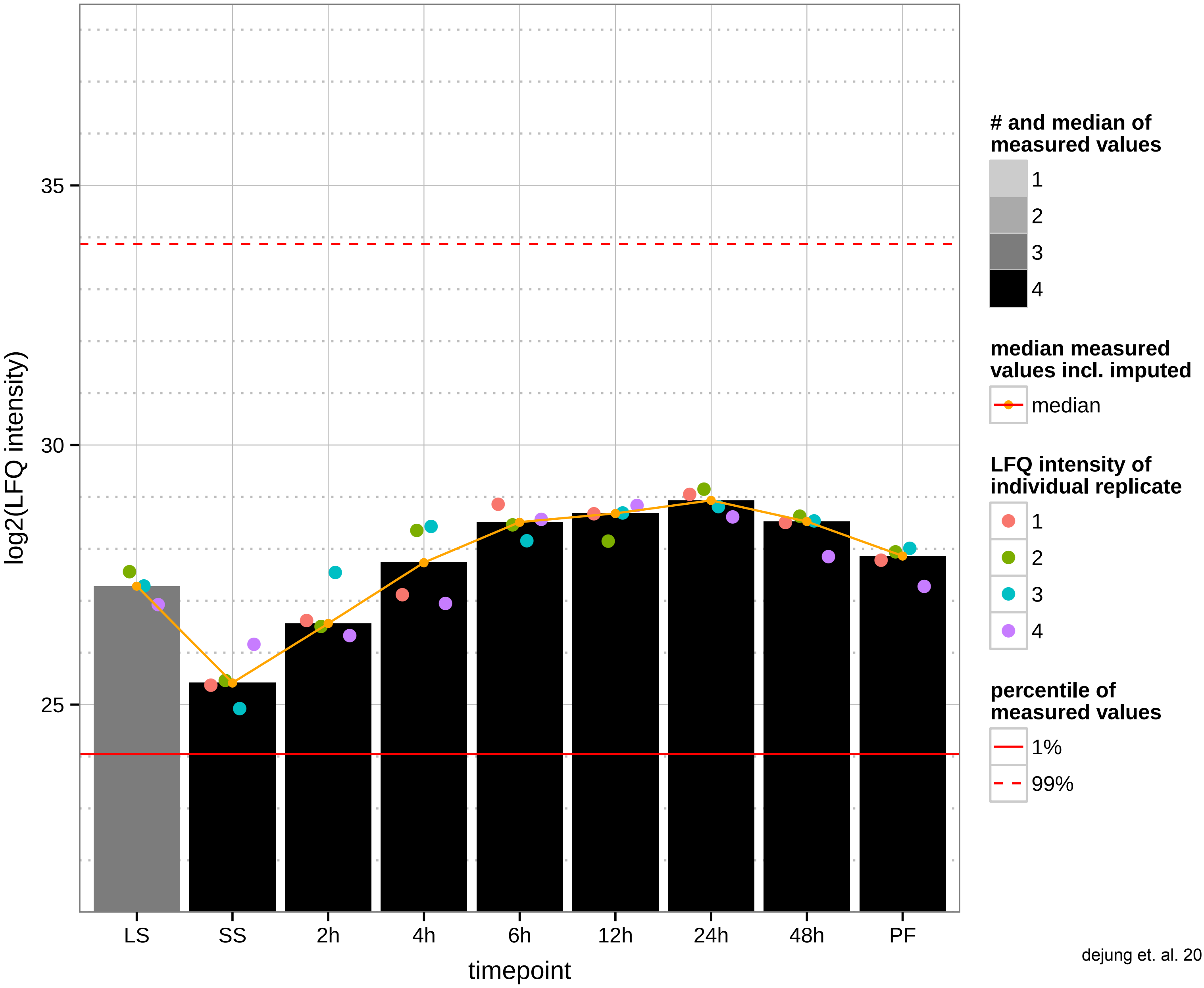
single strand–specific nuclease, putative
Tb927.6.1650
AGOF: endonuclease activity, nucleic acid binding
AGOC: null
AGOP: DNA catabolic process
PGOF: endonuclease activity, hydrolase activity, acting on ester bonds, nucleic acid binding
PGOC: null
PGOP: DNA catabolic process





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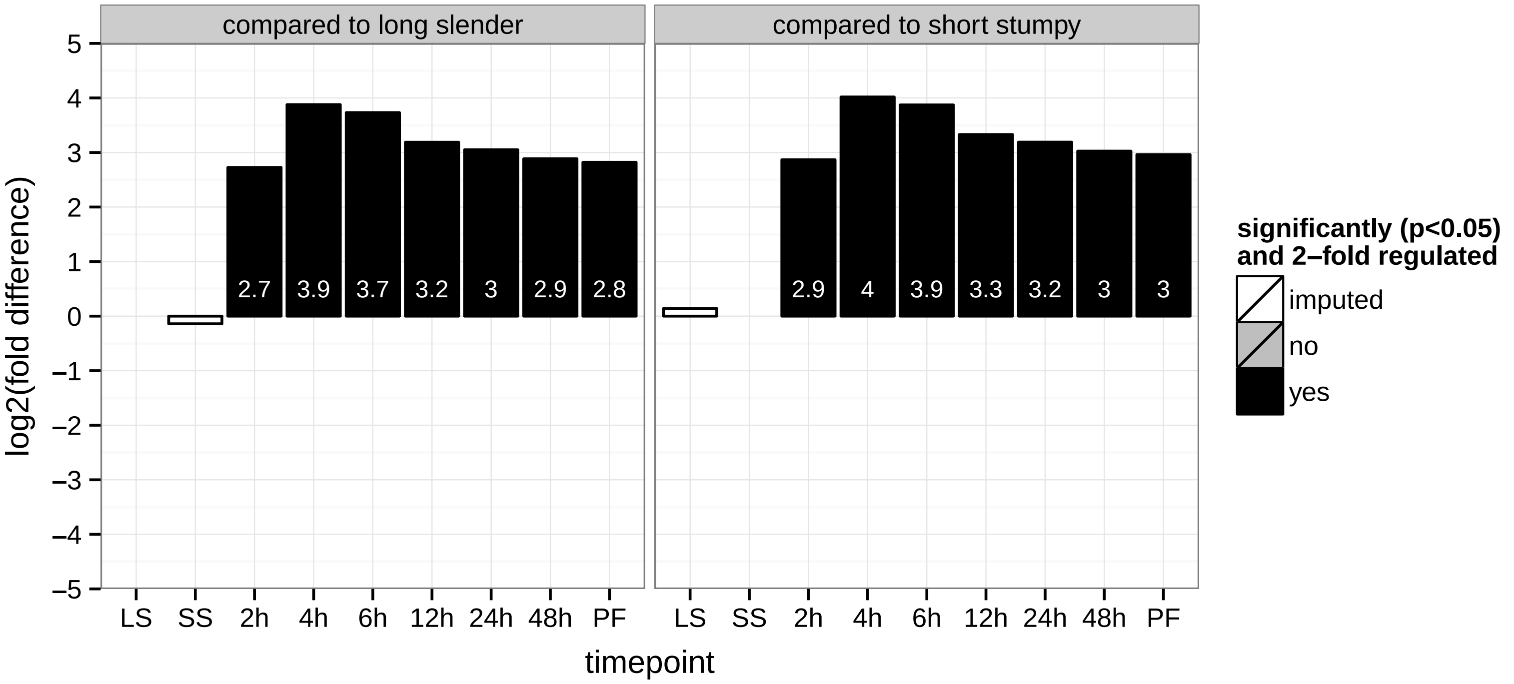
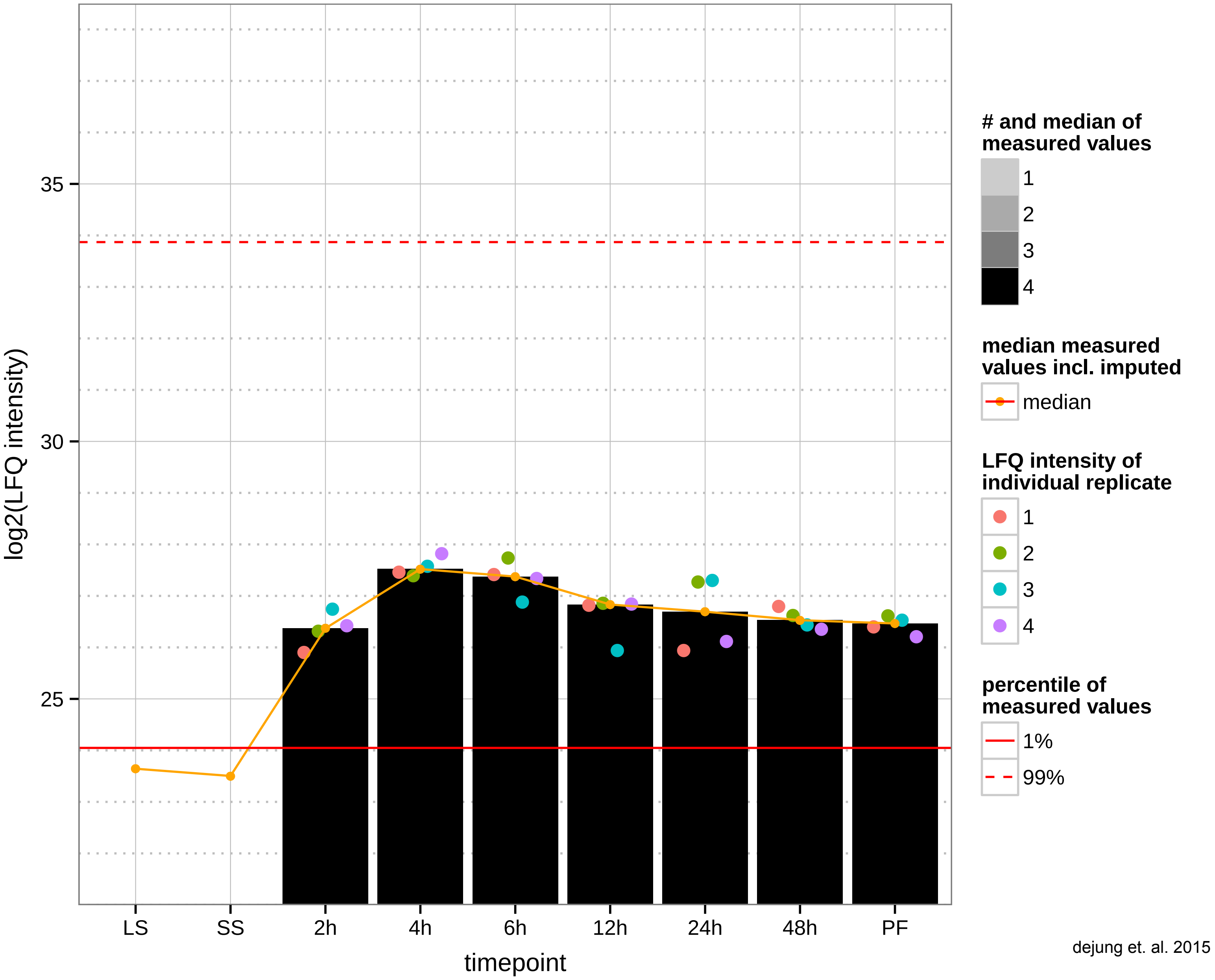
single strand–specific nuclease, putative
Tb927.6.2890
AGOF: endonuclease activity, nucleic acid binding
AGOC: null
AGOP: DNA catabolic process
PGOF: endonuclease activity, hydrolase activity, acting on ester bonds, nucleic acid binding
PGOC: null
PGOP: DNA catabolic process





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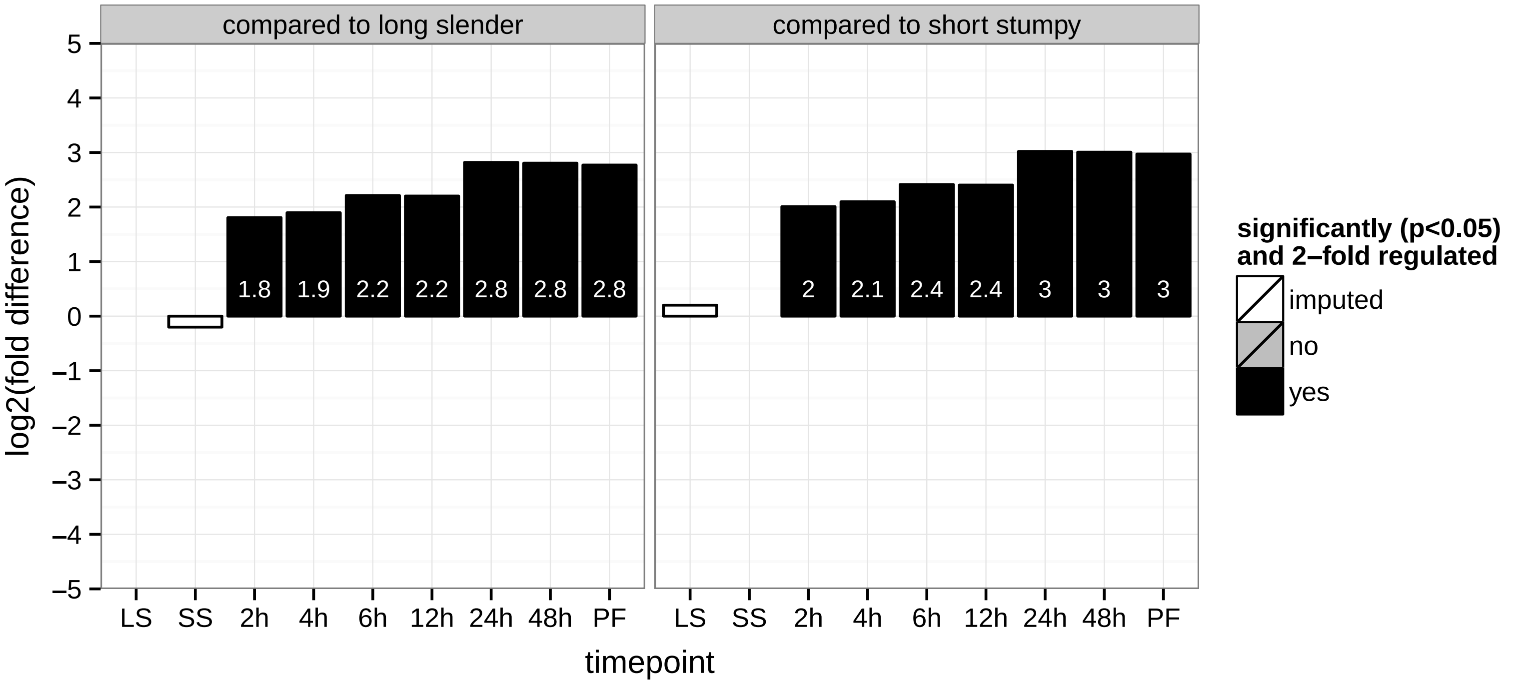
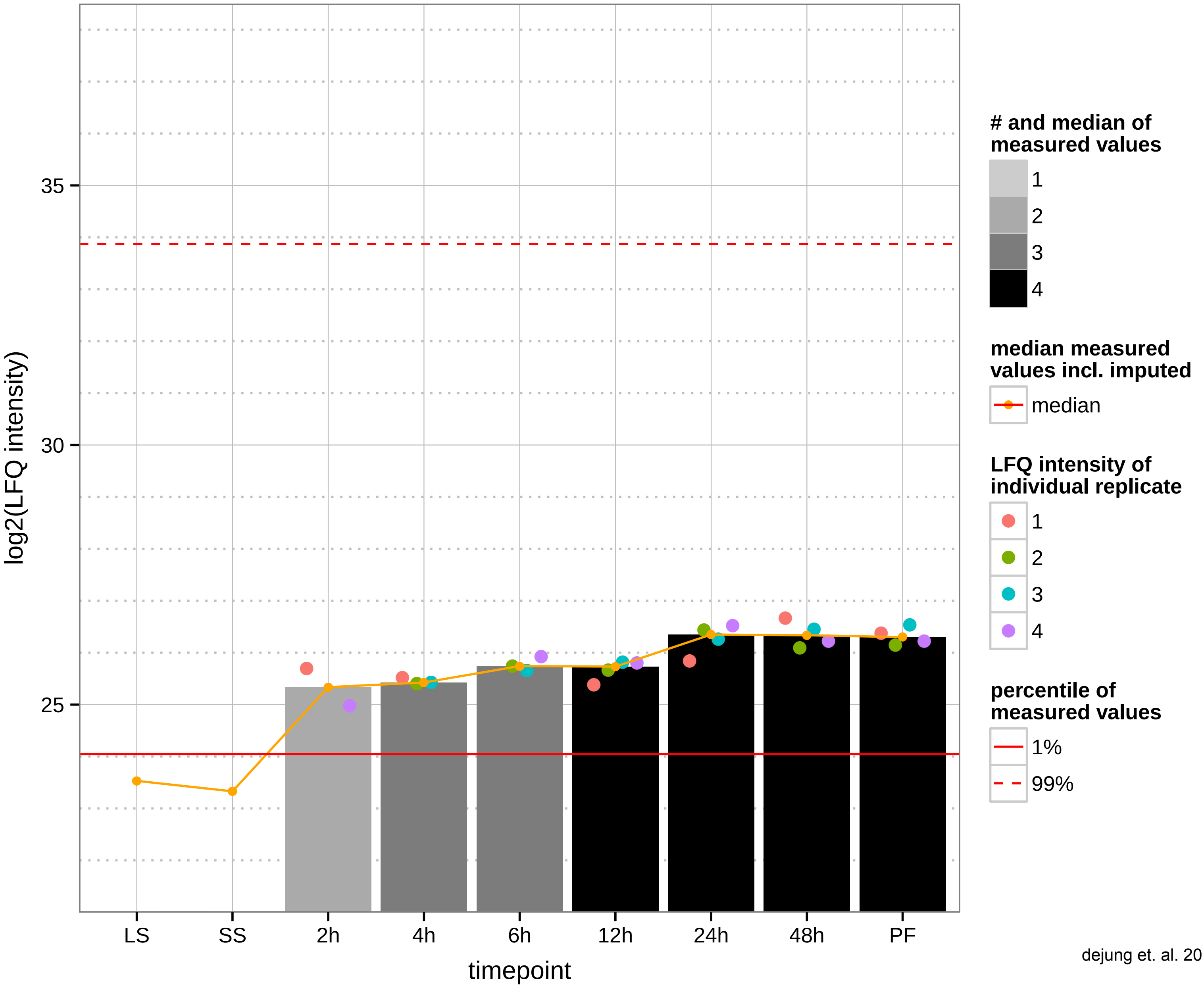
hypothetical protein, conserved
Tb927.6.4080
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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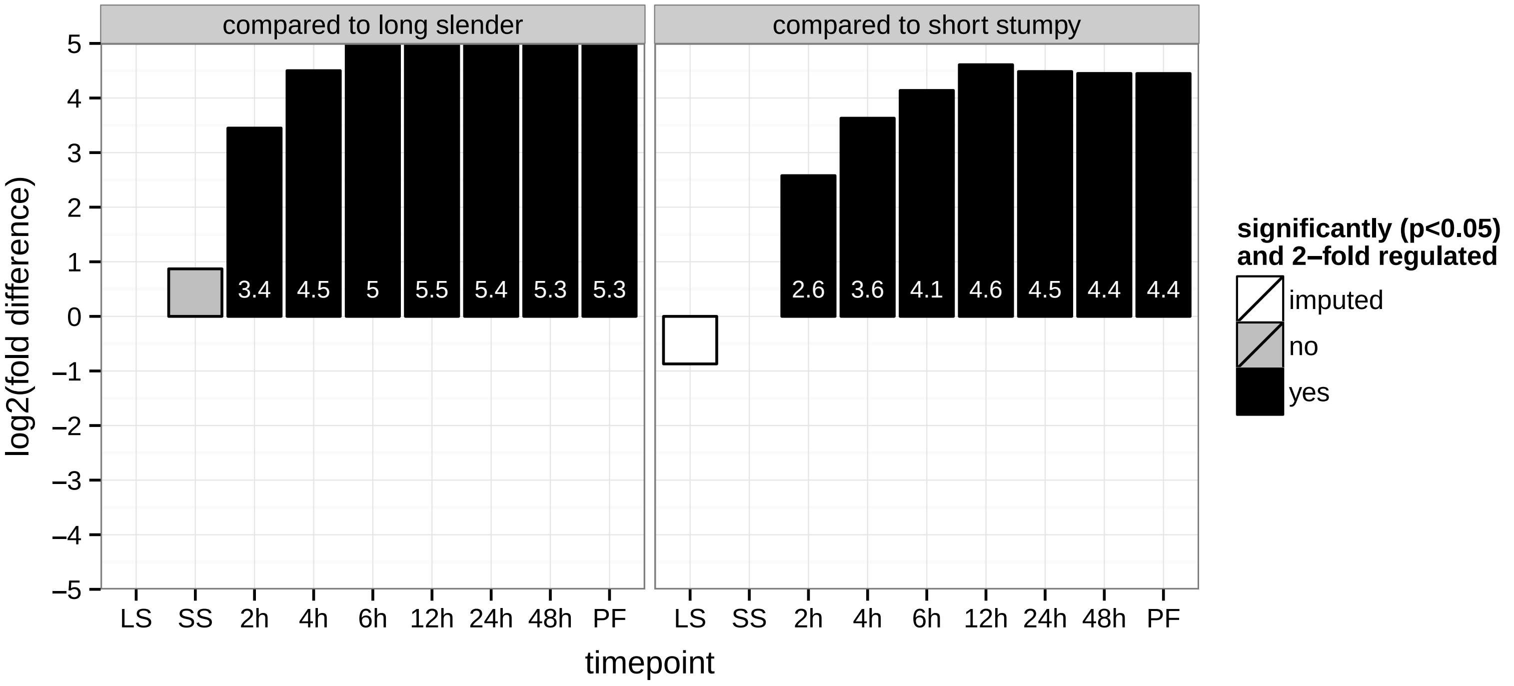
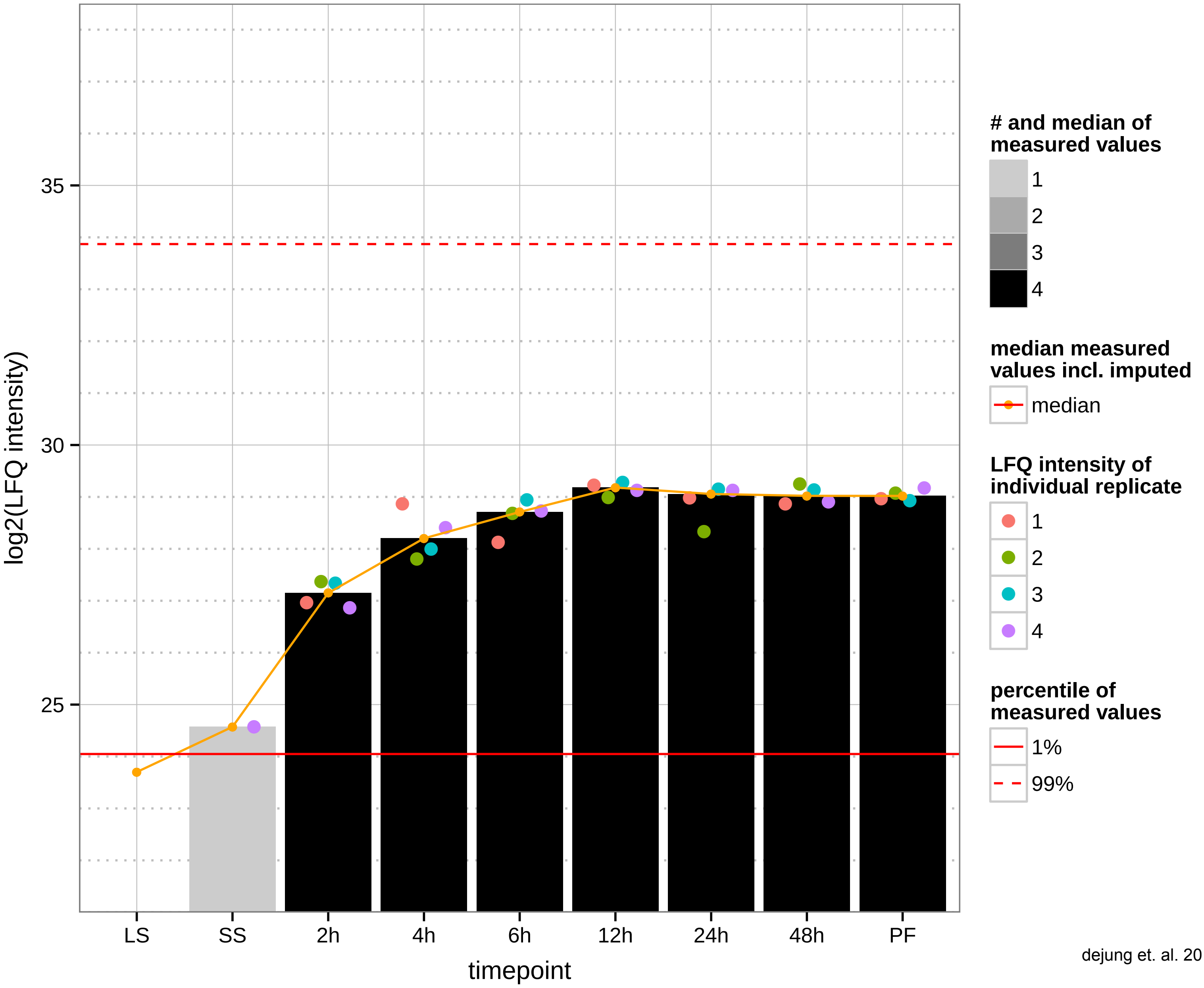
zinc finger protein family member, putative (ZC3H22)
Tb927.7.2680
AGOF: RNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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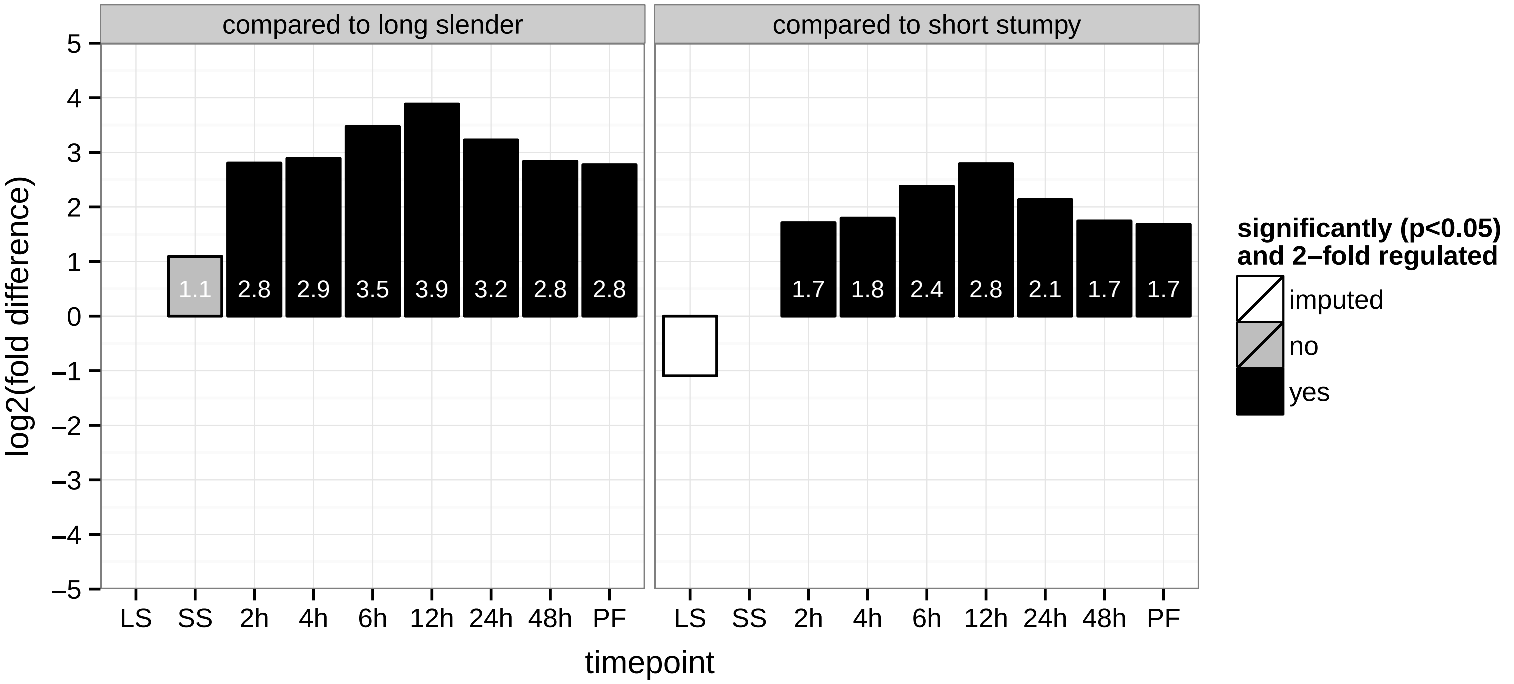
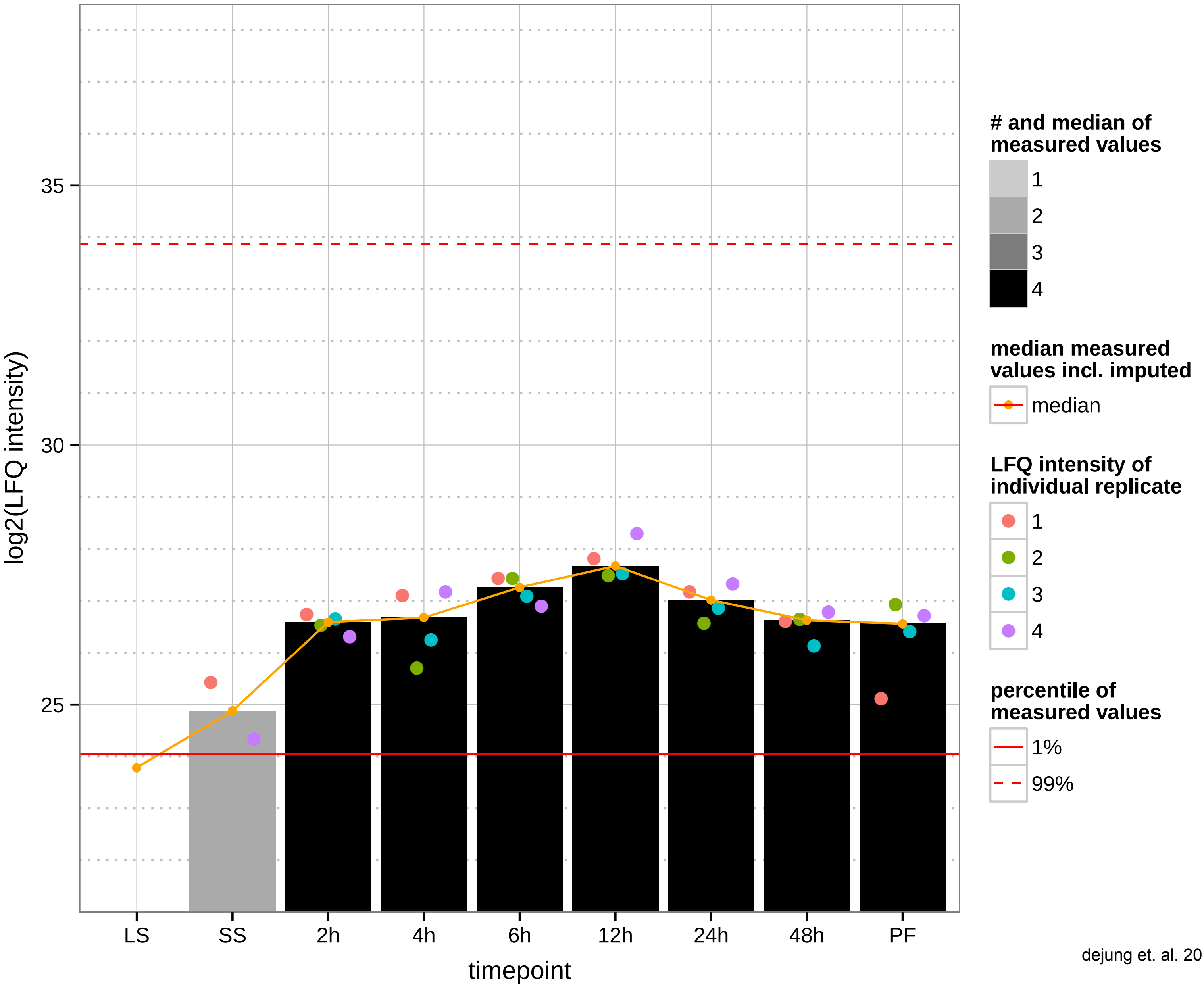
hypothetical protein, conserved
Tb927.7.3090
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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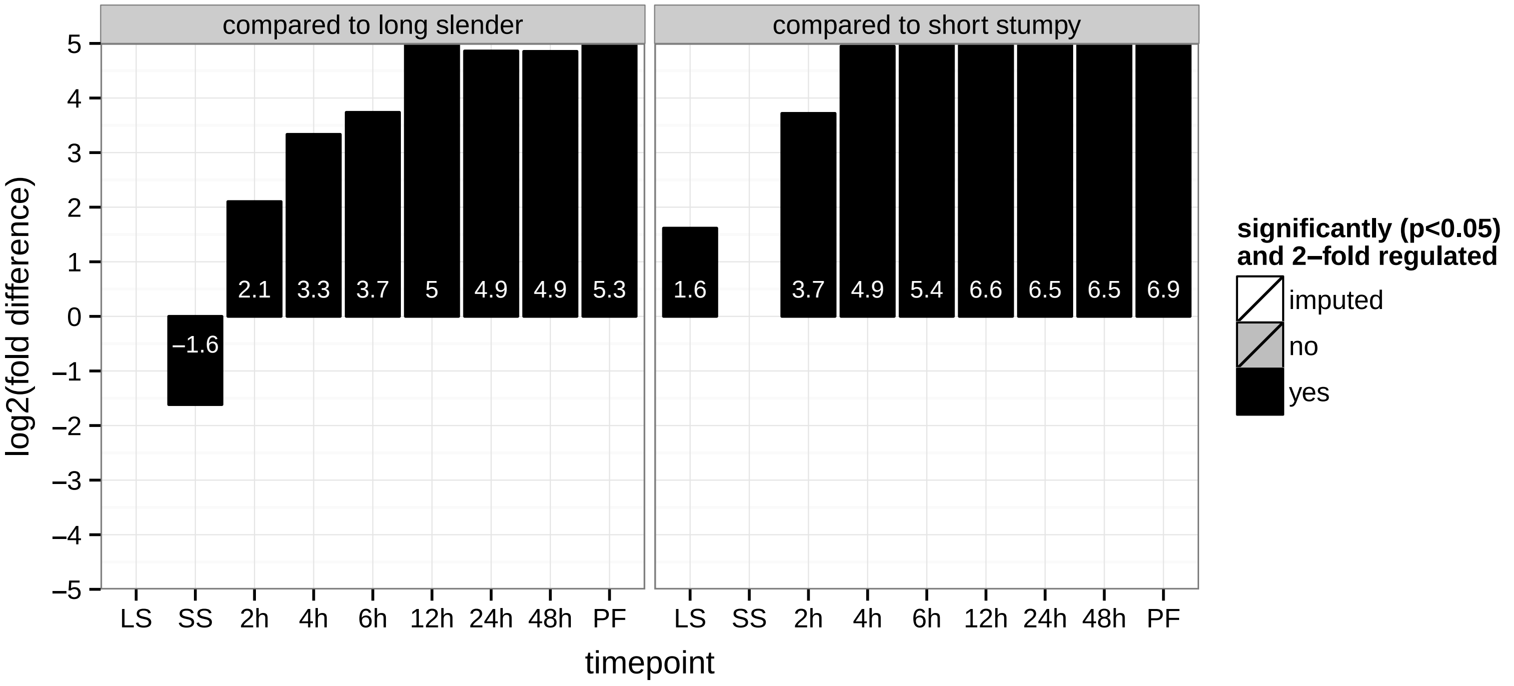
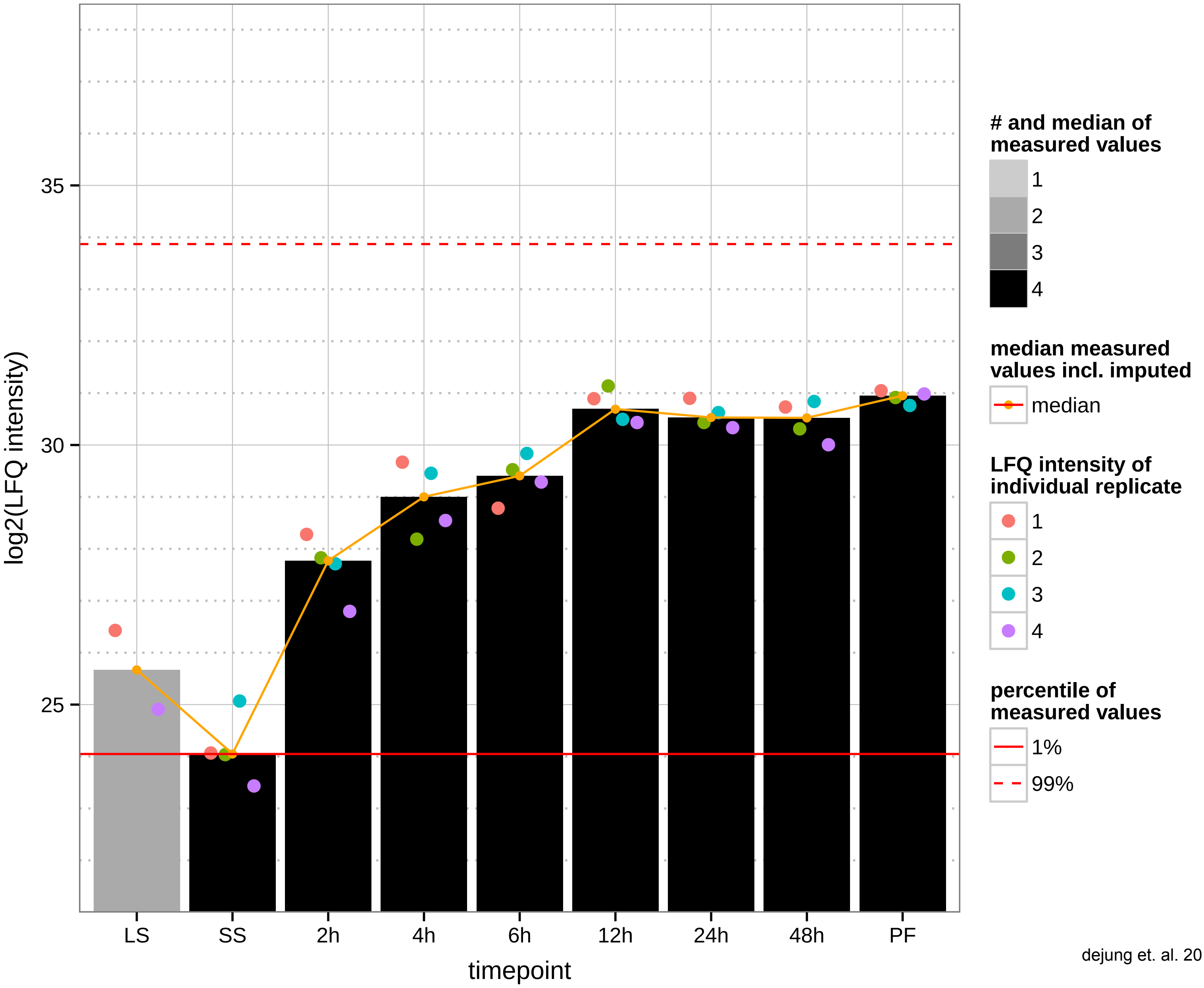
glutamine synthetase, putative, putative (GS)
Tb927.7.4970;Tb11.v5.0178
AGOF: null, glutamate–ammonia ligase activity
AGOC: null, cytoplasm, mitochondrion
AGOP: null, glutamine biosynthetic process, nitrogen compound metabolic process
PGOF: glutamate–ammonia ligase activity
PGOC: null
PGOP: glutamine biosynthetic process, nitrogen compound metabolic process





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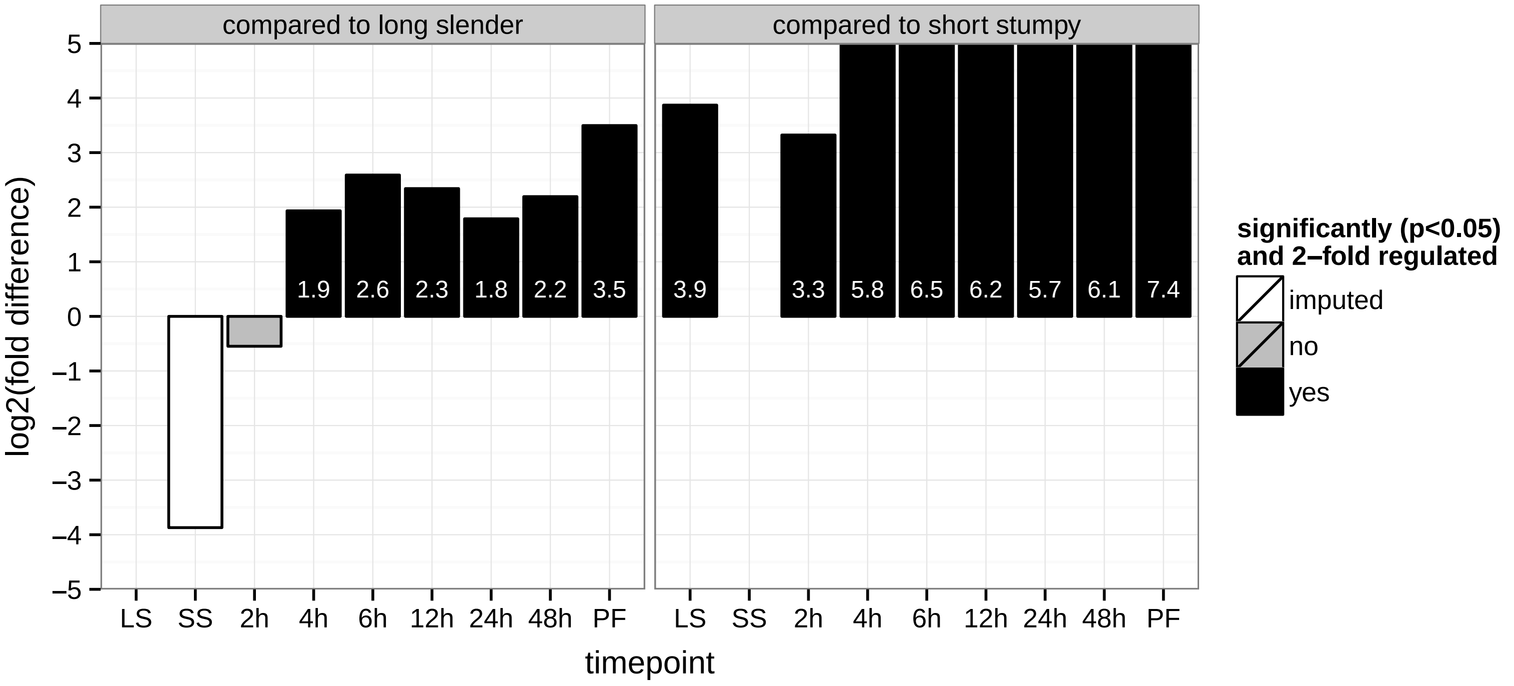
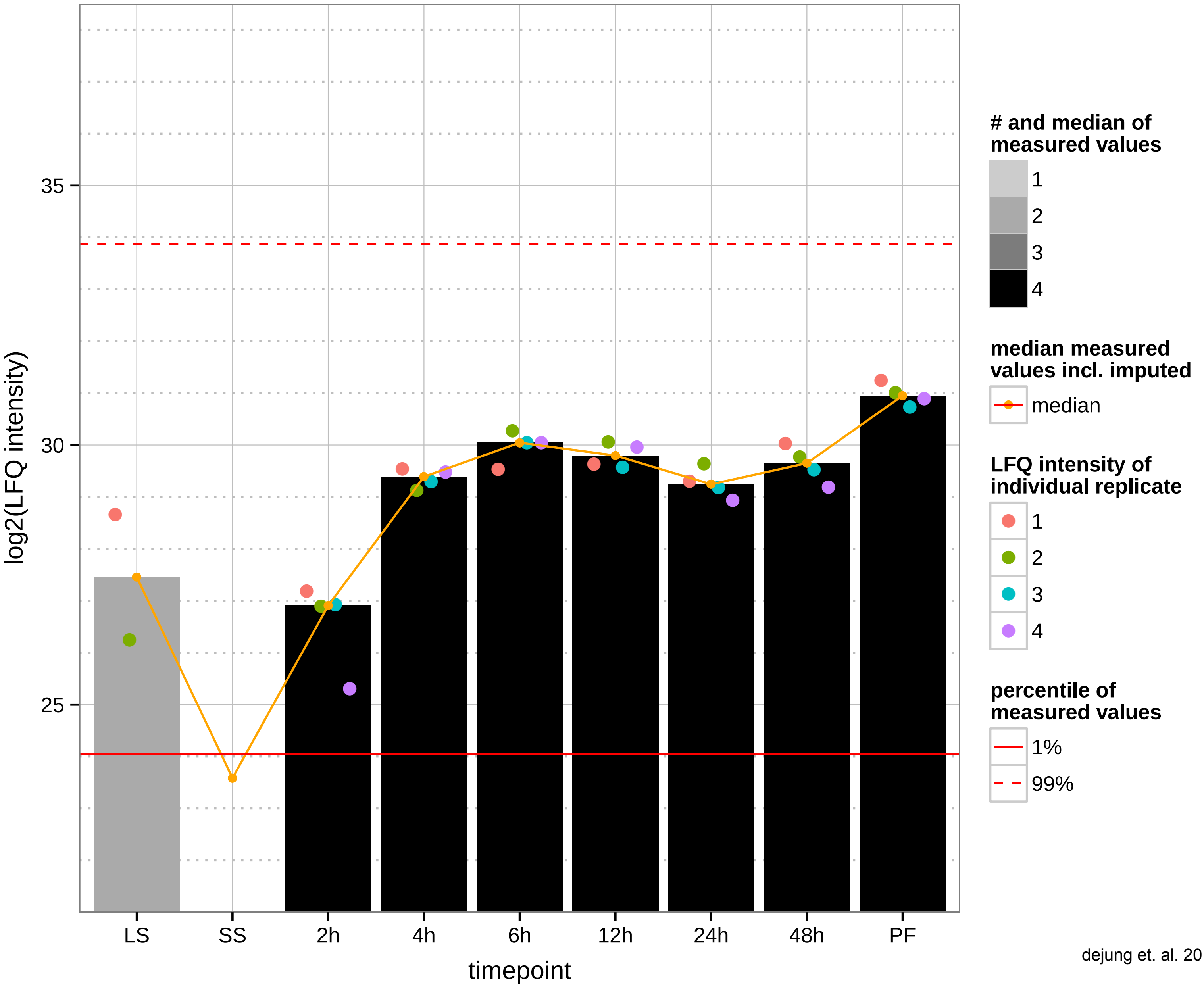
trans–sialidase (TS)
Tb927.7.6850
AGOF: exo–alpha–sialidase activity, sialyltransferase activity
AGOC: cell surface
AGOP: pathogenesis, sialic acid transport
PGOF: null
PGOC: null
PGOP: null





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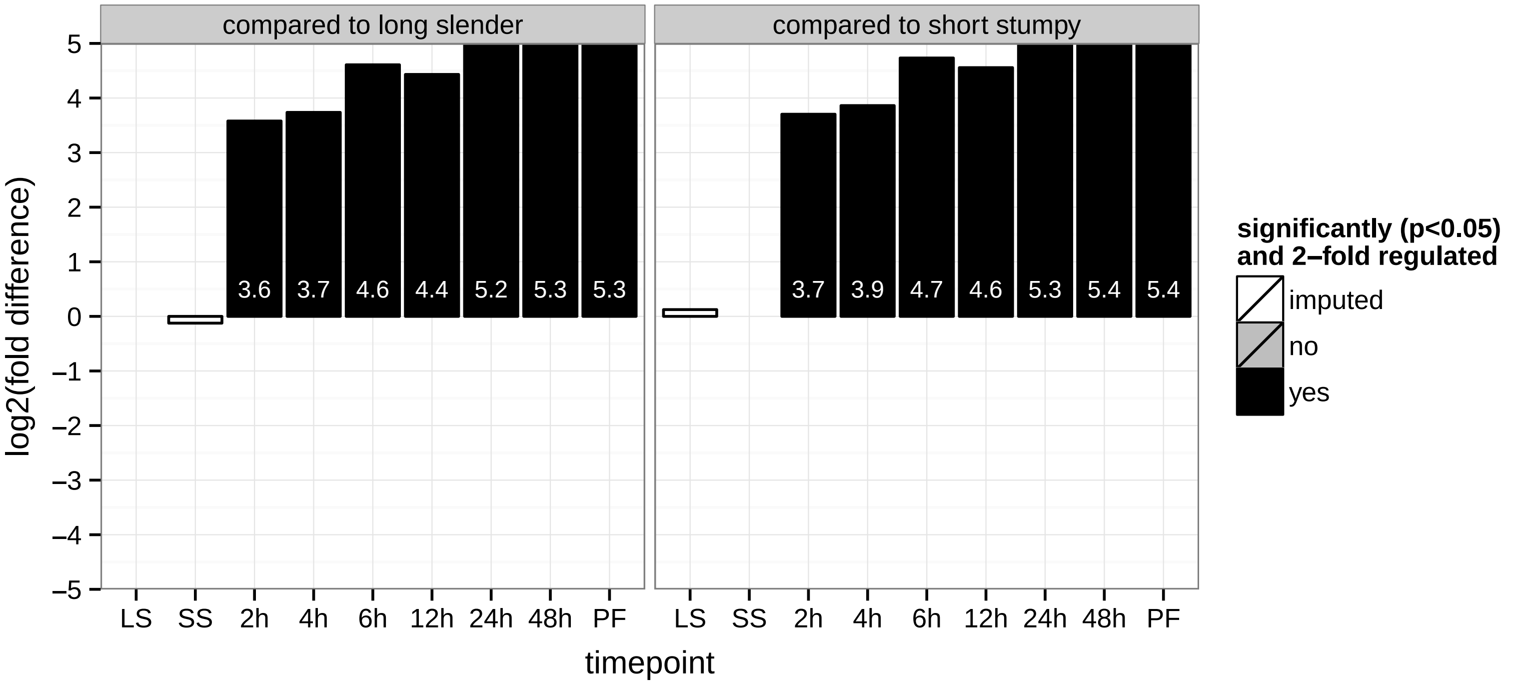
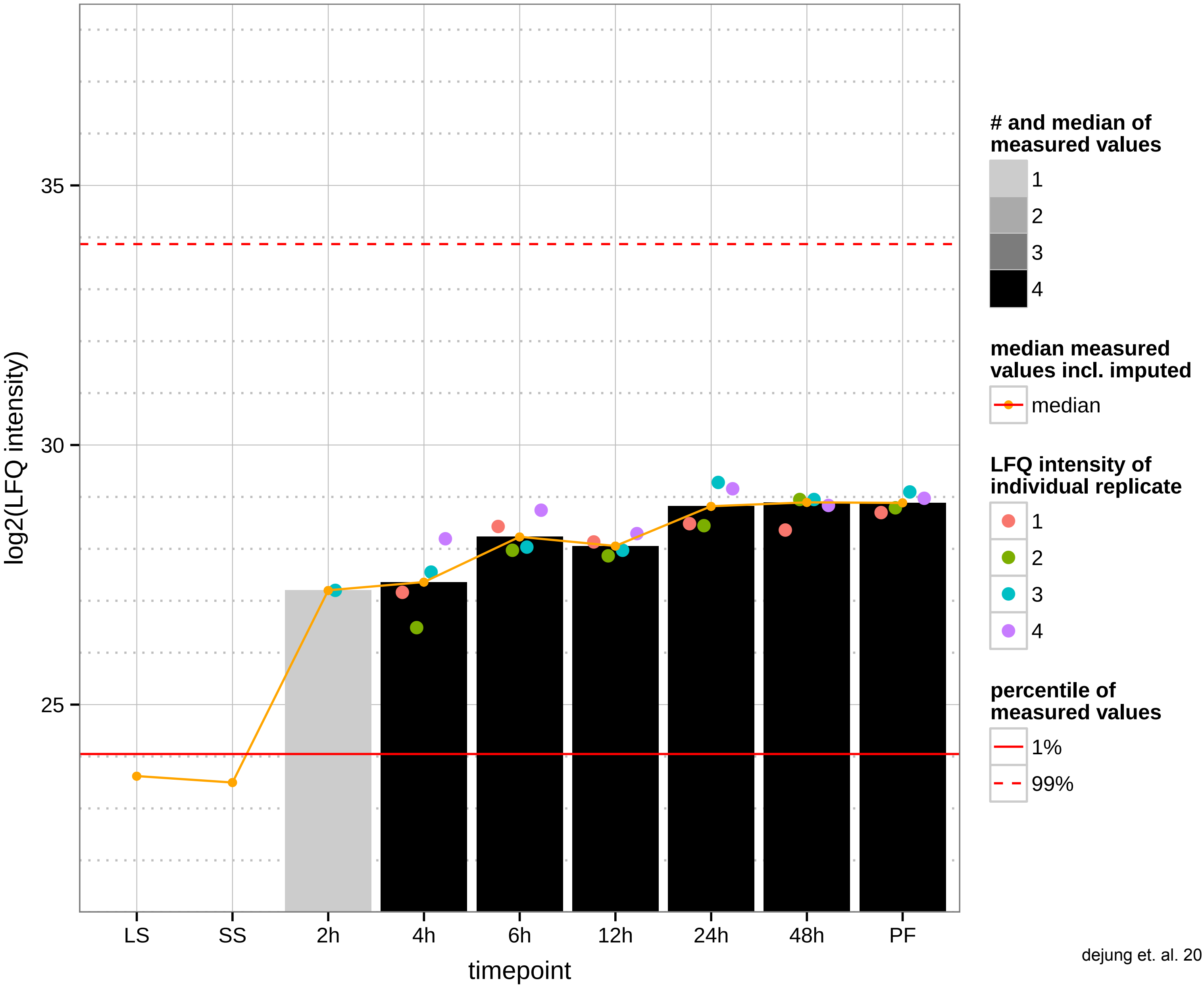
kinesin, putative
Tb927.8.4950
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: kinesin complex, microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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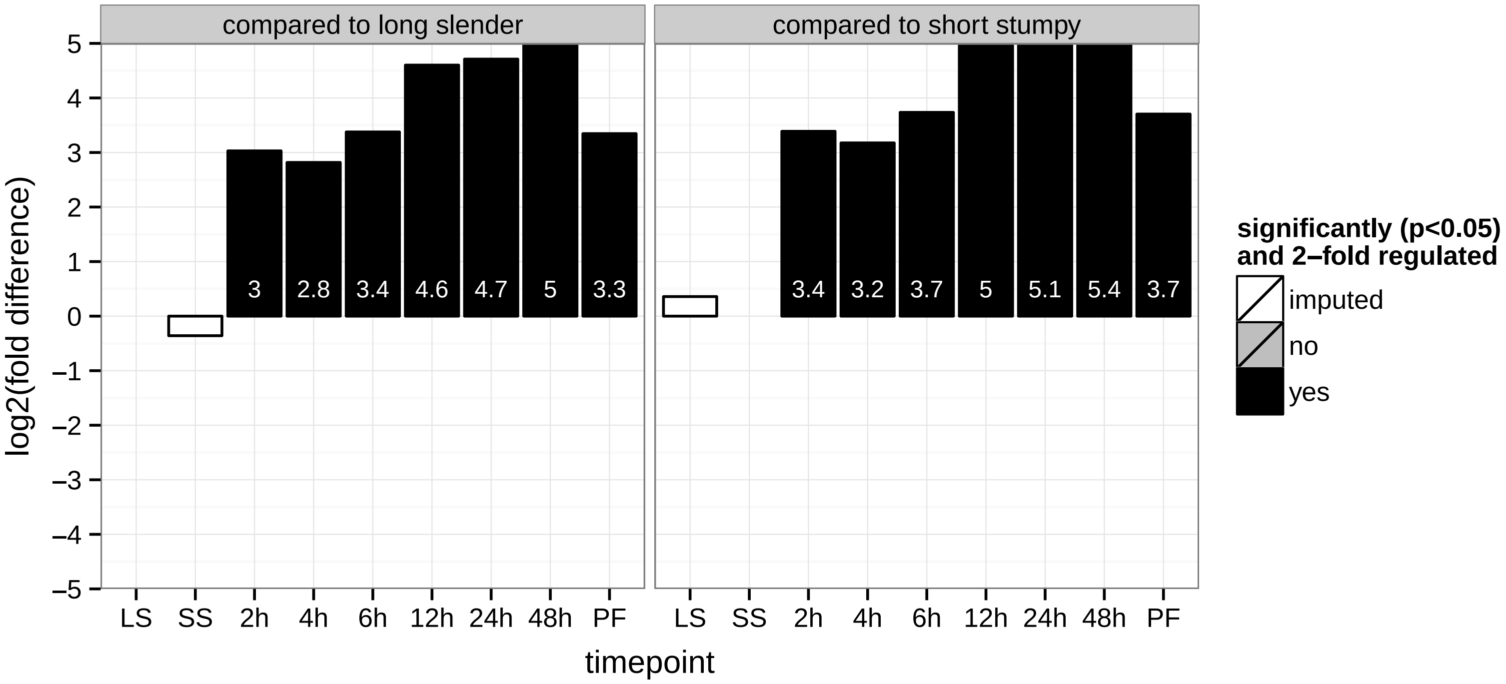
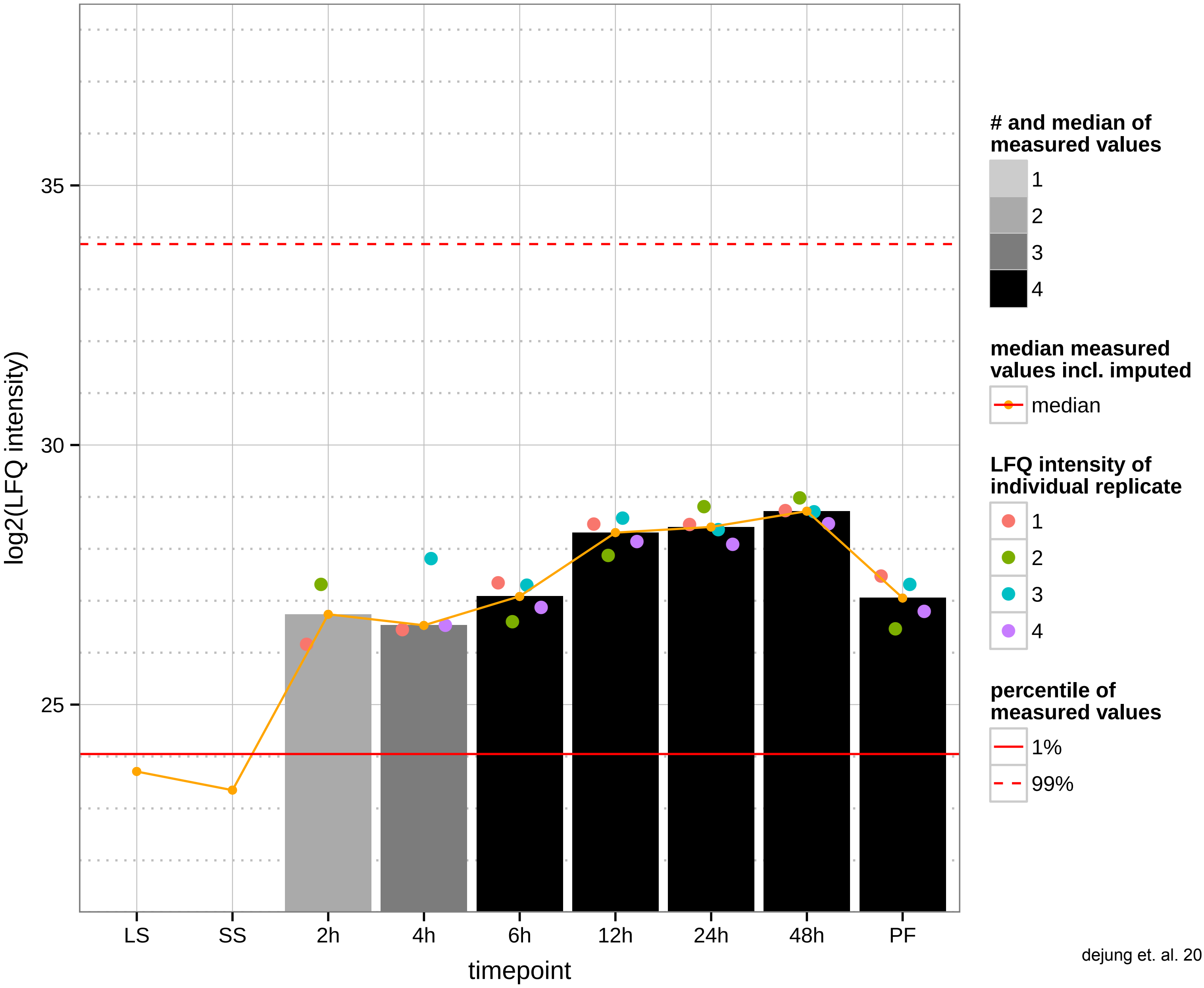
amino acid transporter, putative
Tb927.8.8300
AGOF: amine transmembrane transporter activity
AGOC: integral to membrane
AGOP: amino acid transport
PGOF: null
PGOC: null
PGOP: null





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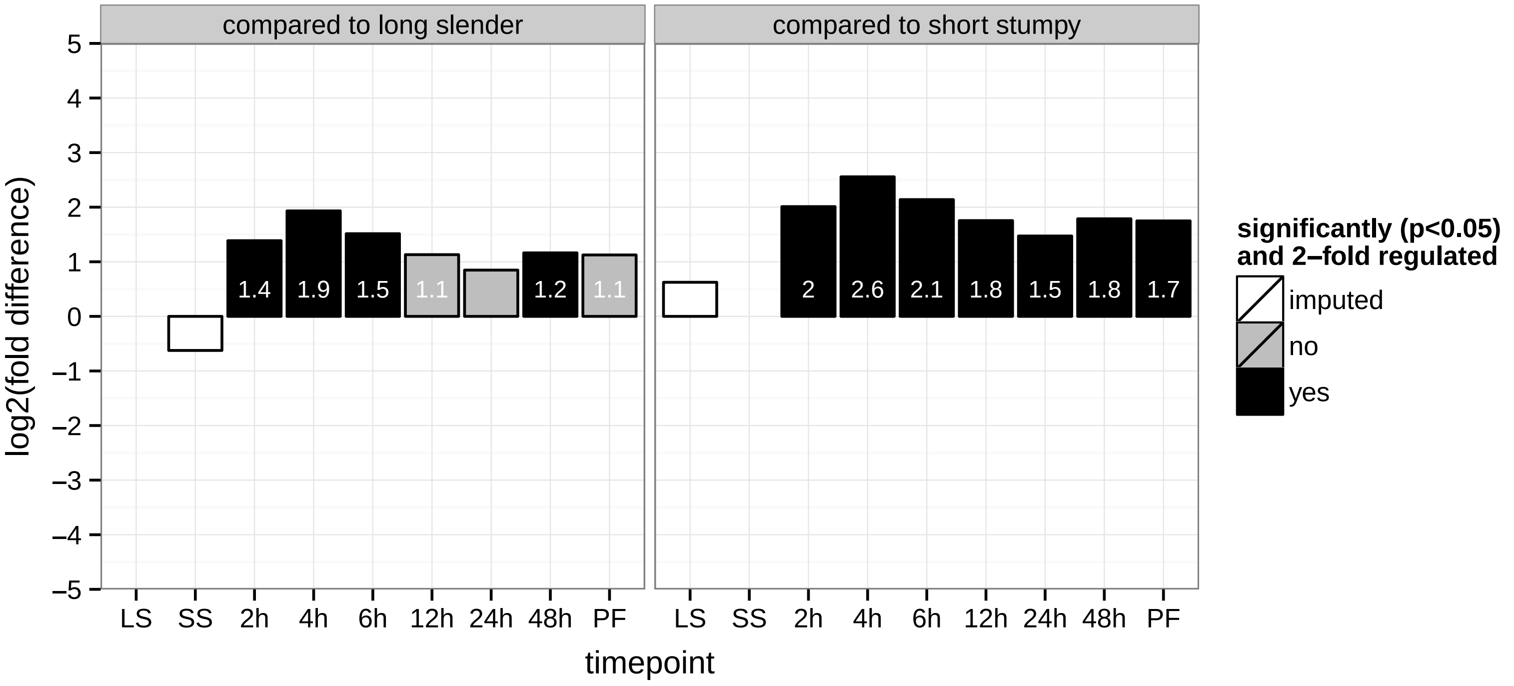
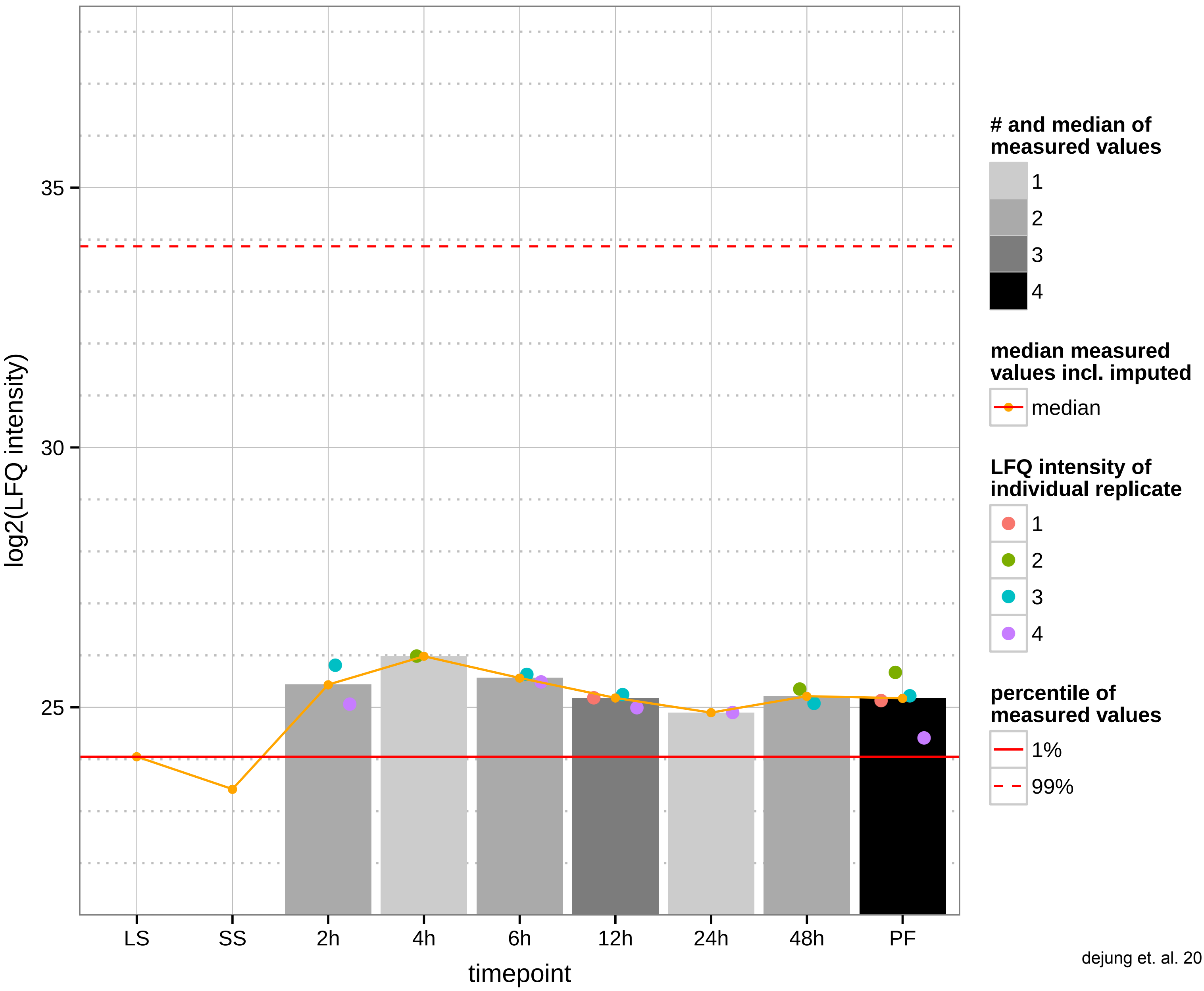
hypothetical protein, conserved
Tb927.9.13240
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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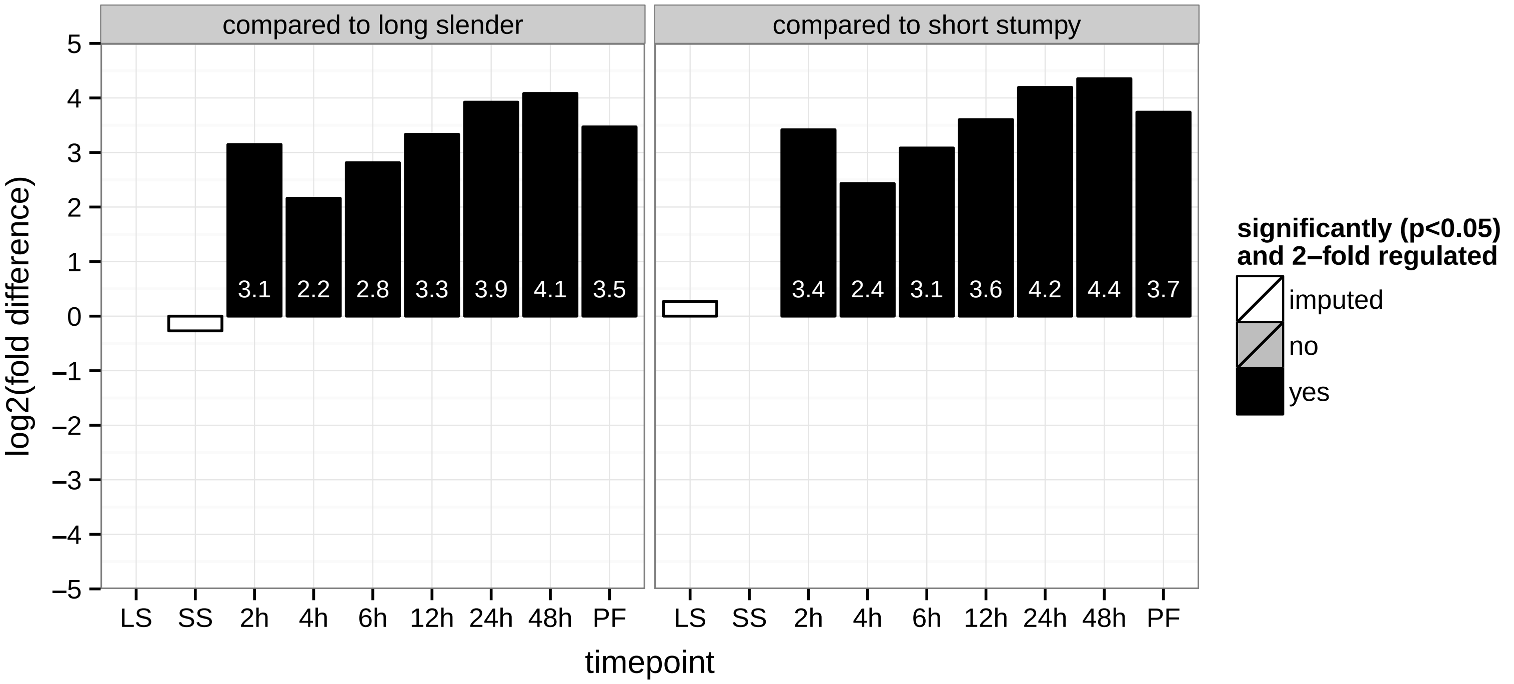
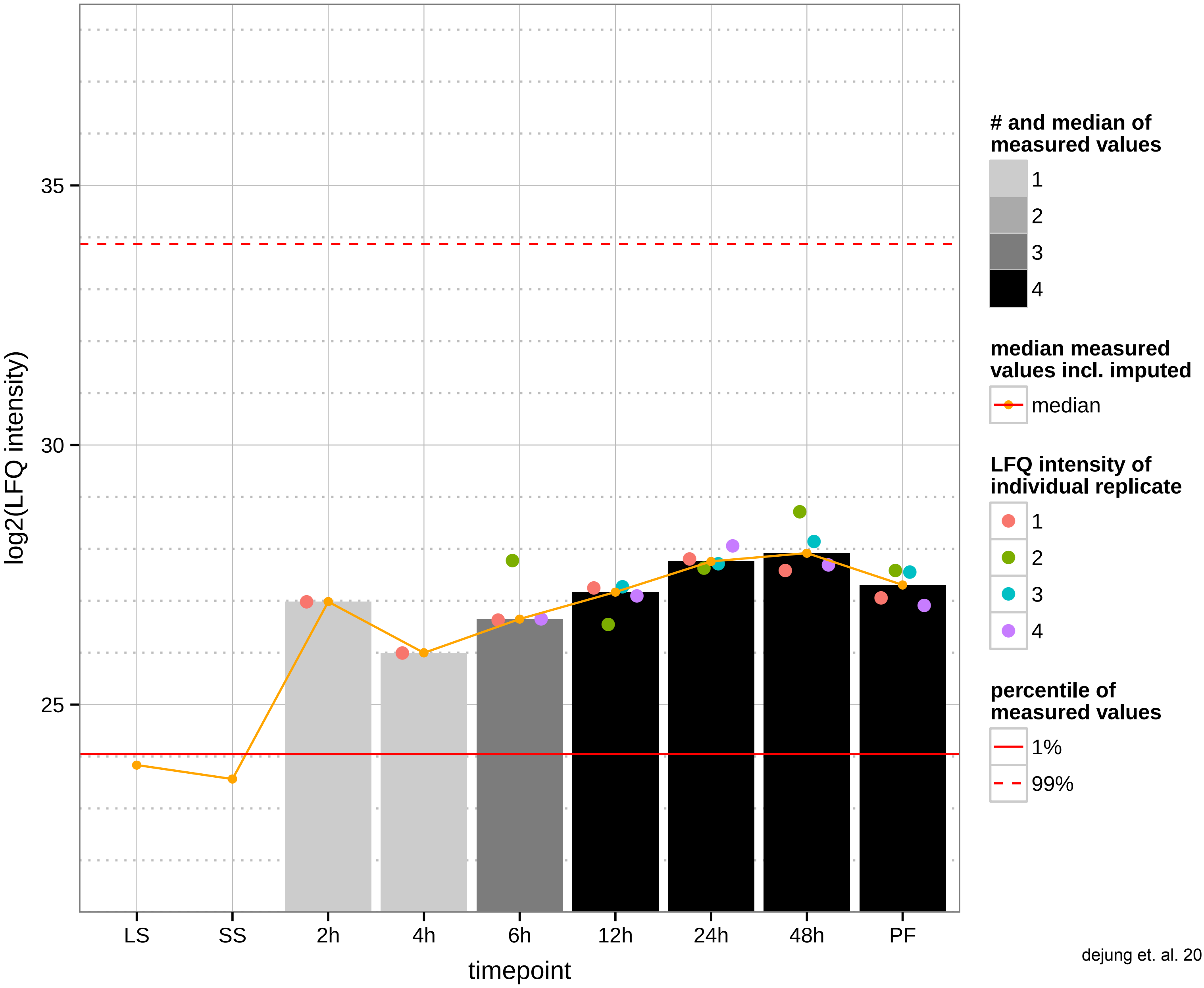
hypothetical protein, conserved
Tb927.9.14120
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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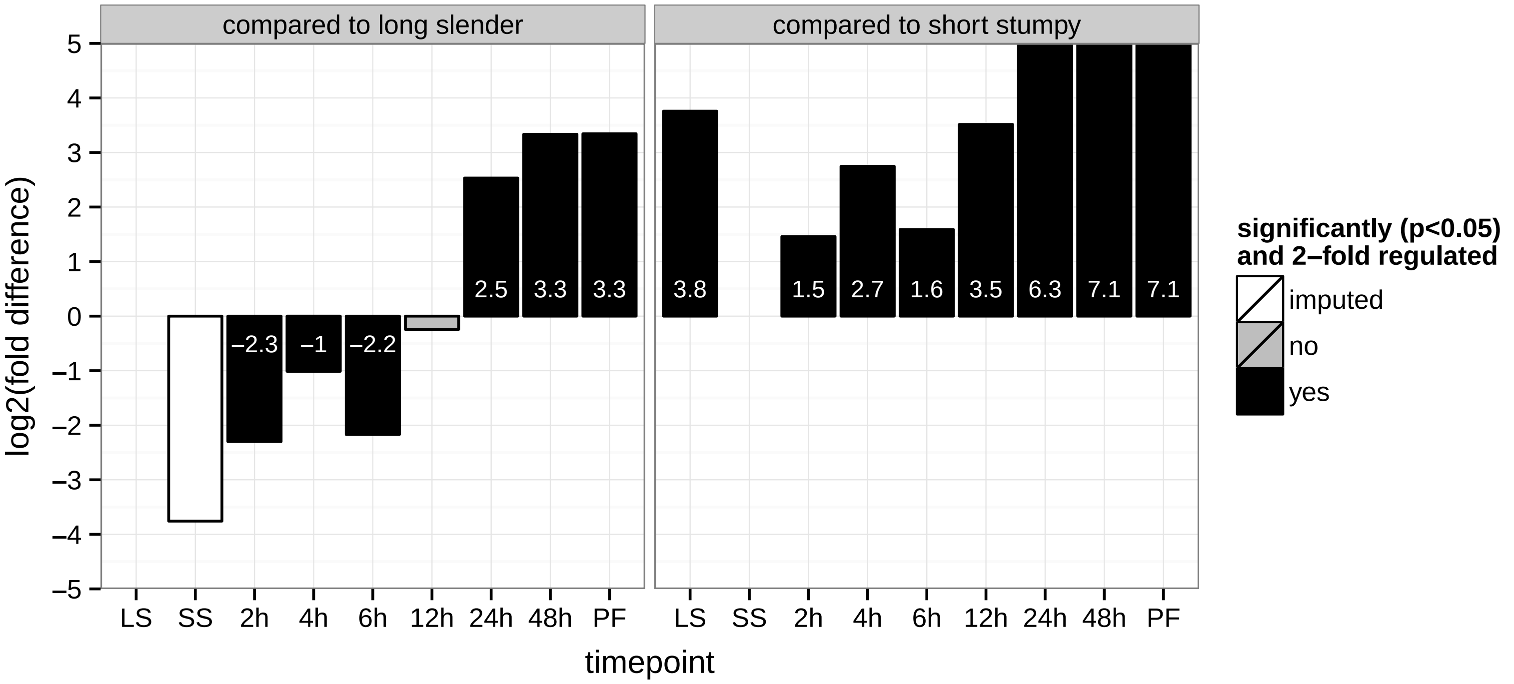
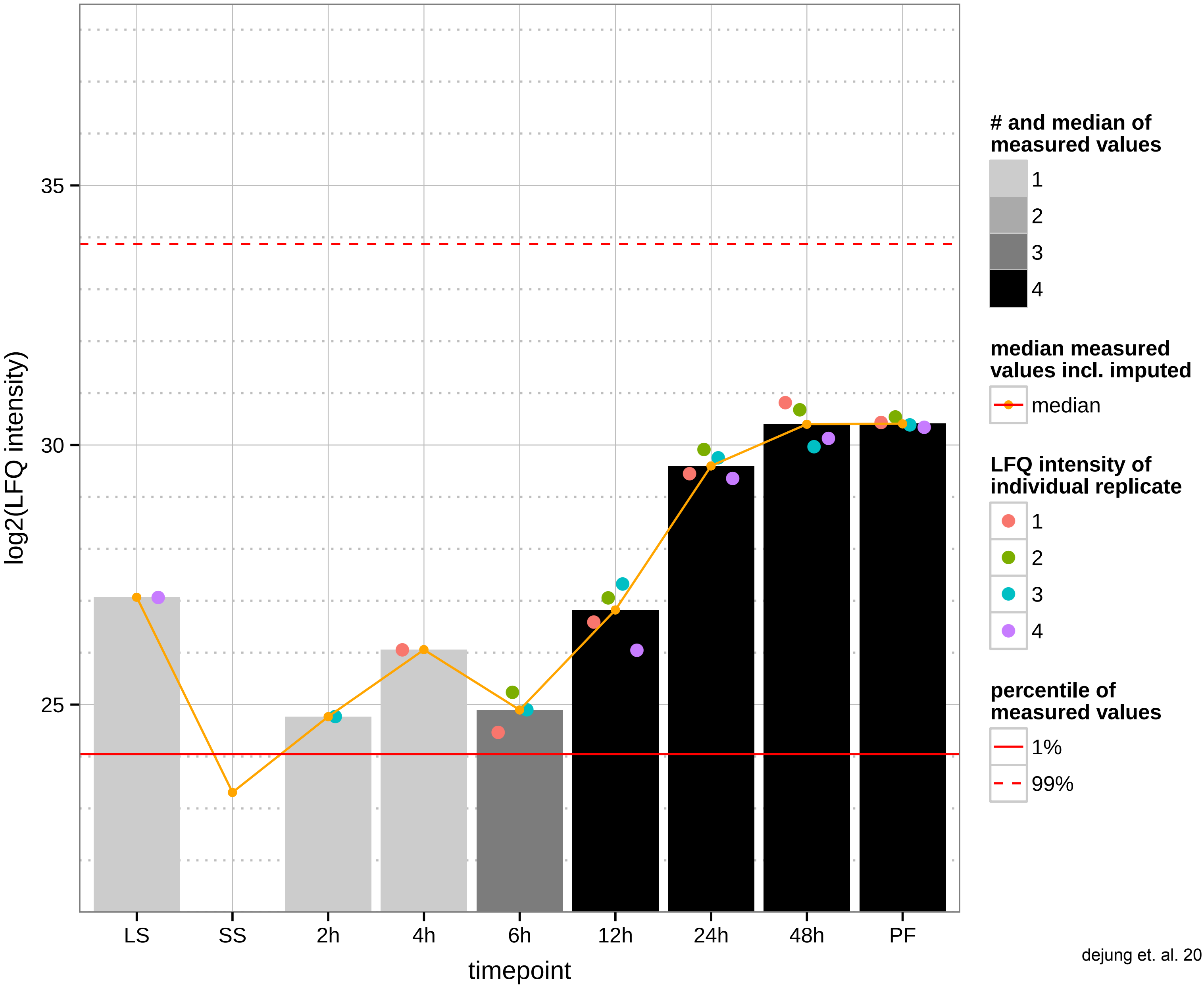
rieske iron–sulfur protein, mitochondrial precursor (RISP)
Tb927.9.14160
AGOF: 2 iron, 2 sulfur cluster binding, electron carrier activity, glutathione–disulfide reductase activity, ubiquinol–cytochrome–
AGOC: mitochondrial inner membrane, mitochondrion, respiratory chain complex III
AGOP: aerobic respiration, oxidation–reduction process
PGOF: 2 iron, 2 sulfur cluster binding, oxidoreductase activity, ubiquinol–cytochrome–c reductase activity
PGOC: null
PGOP: oxidation–reduction process





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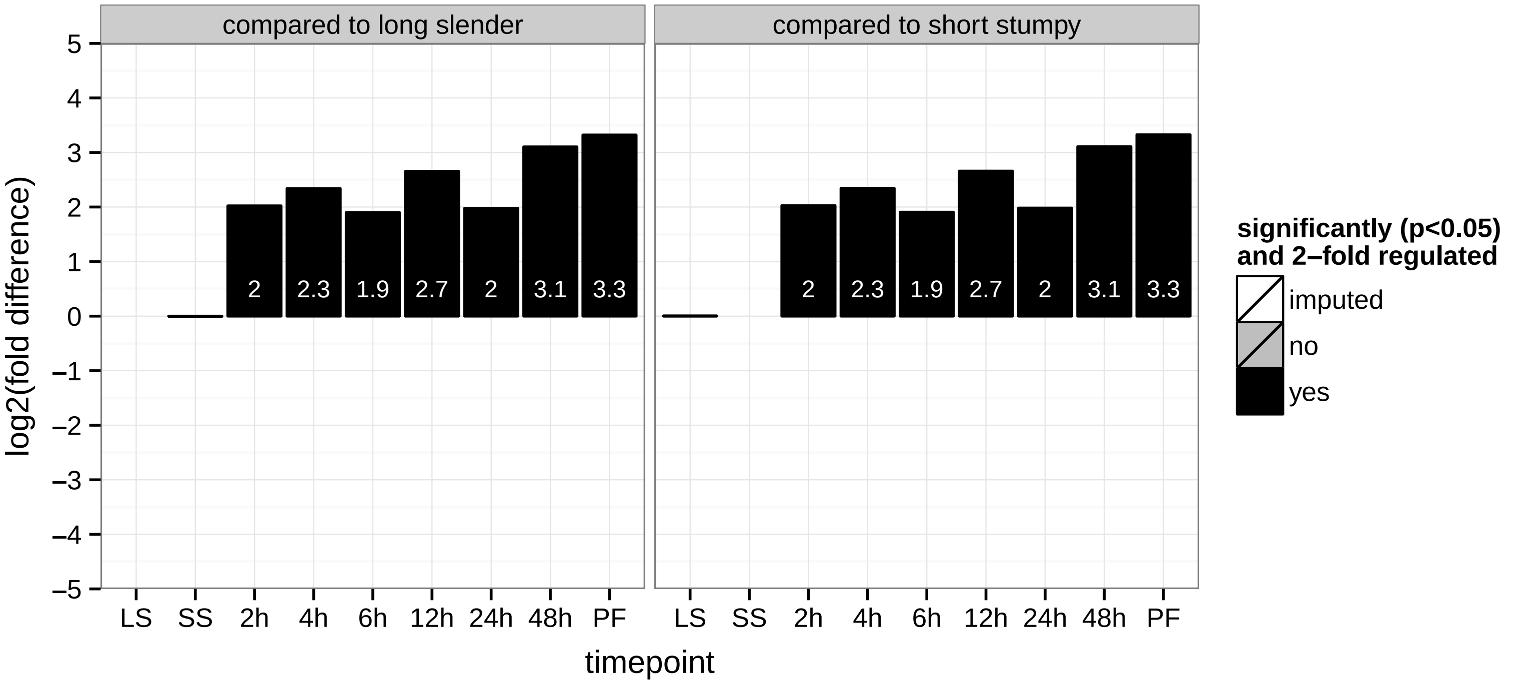
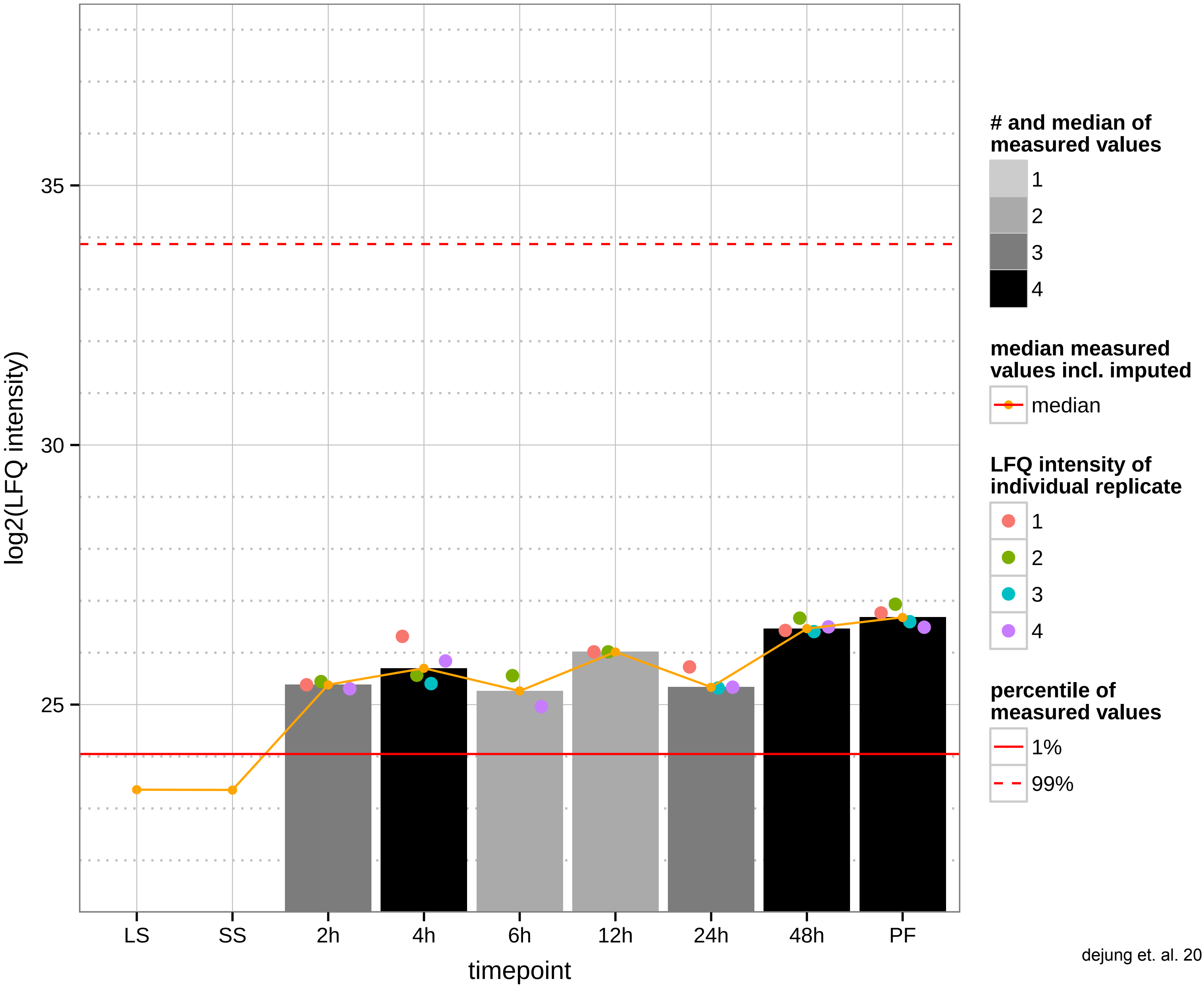
hypothetical protein, conserved
Tb927.9.15240
AGOF: null
AGOC: mitochondrion
AGOP: protein complex assembly
PGOF: null
PGOC: mitochondrion
PGOP: protein complex assembly





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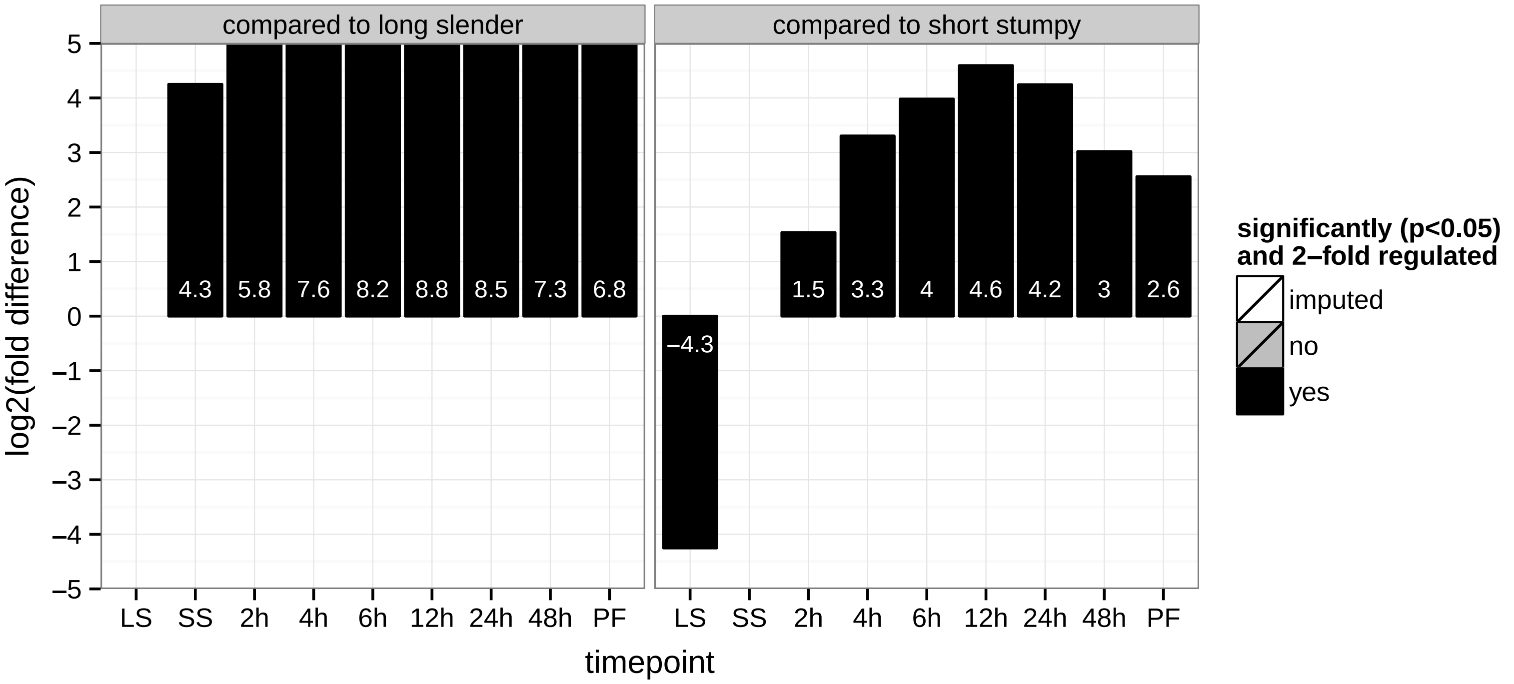
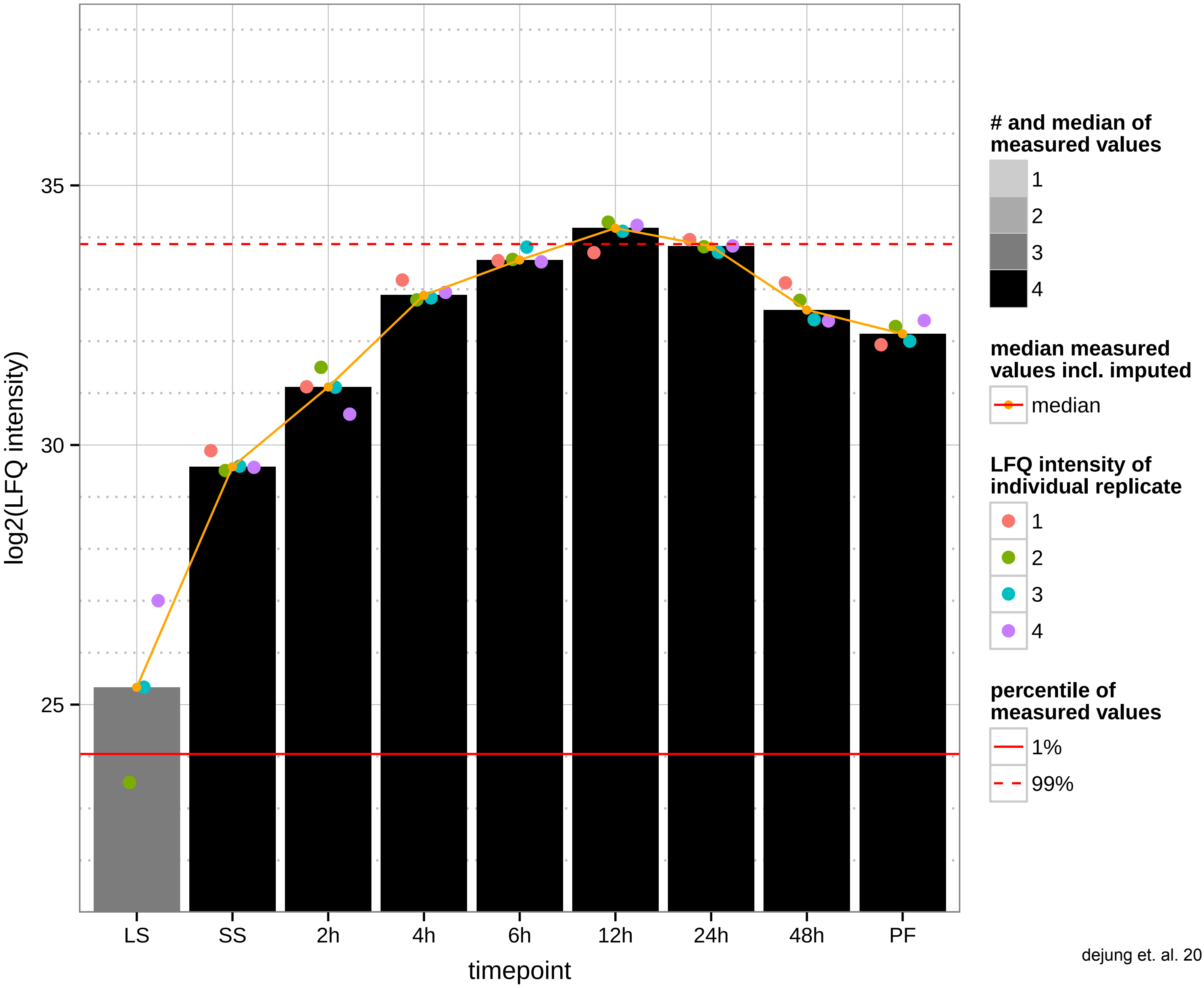
hypothetical protein, conserved, PTP1–interacting protein, 39 kDa
Tb927.9.6090
AGOF: null, magnesium–dependent protein serine/threonine phosphatase activity
AGOC: null, cytosol, glycosome, mitochondrion
AGOP: null, protein dephosphorylation
PGOF: protein binding
PGOC: null
PGOP: null





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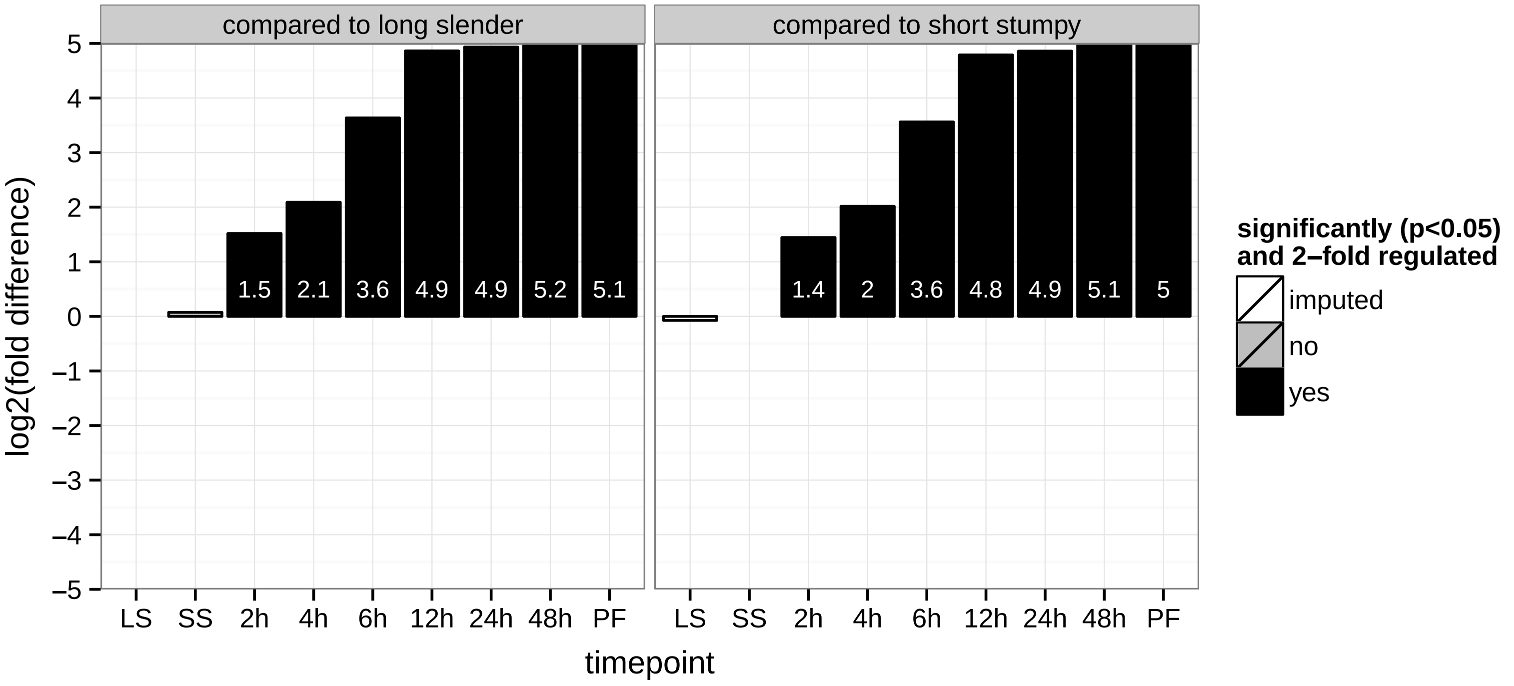
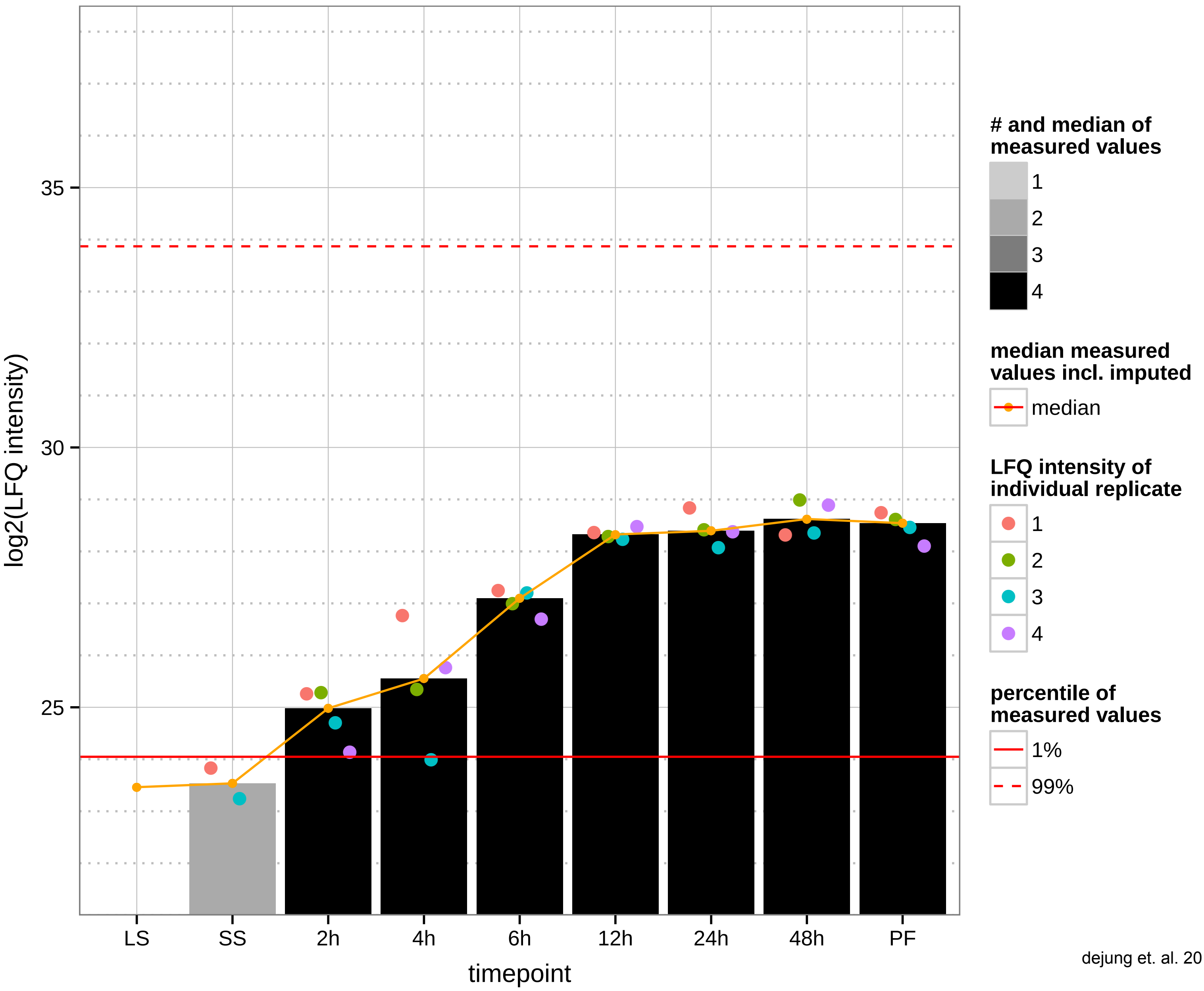
hypothetical protein, conserved
Tb927.9.9730
AGOF: null
AGOC: intracellular
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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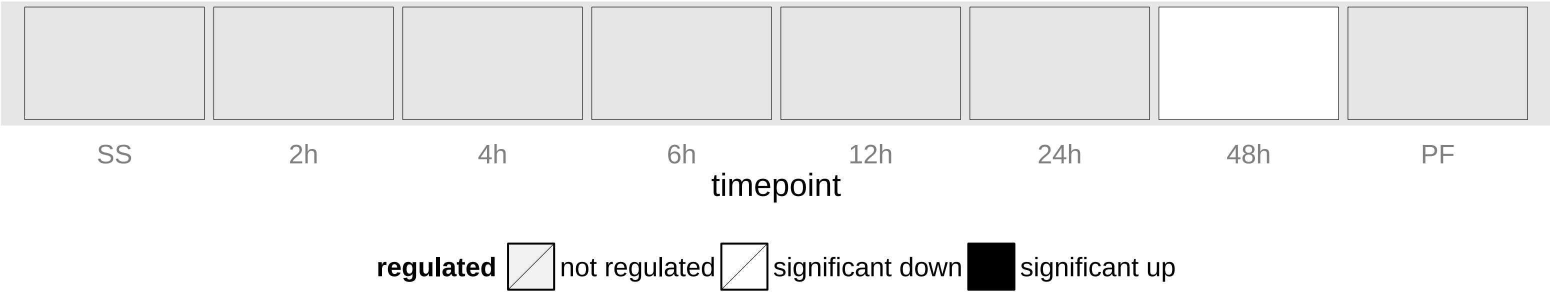

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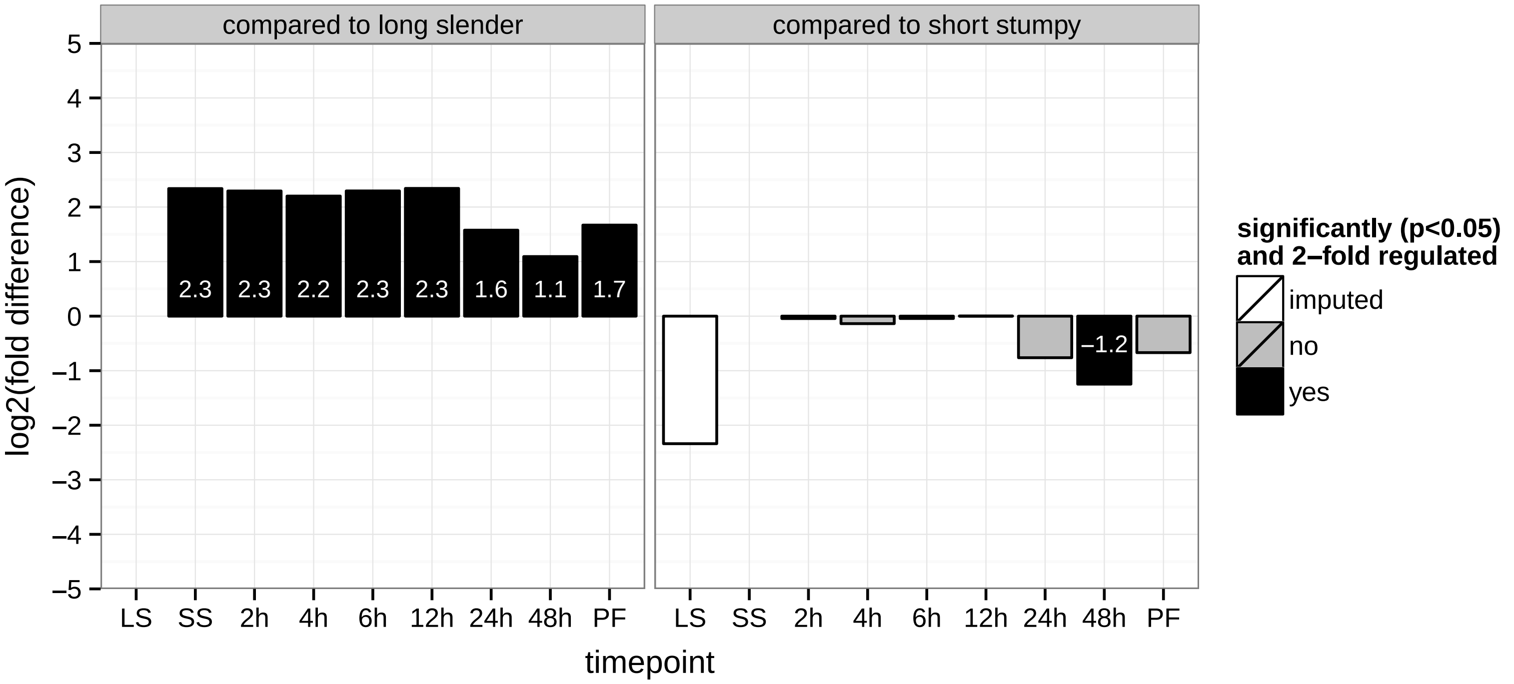
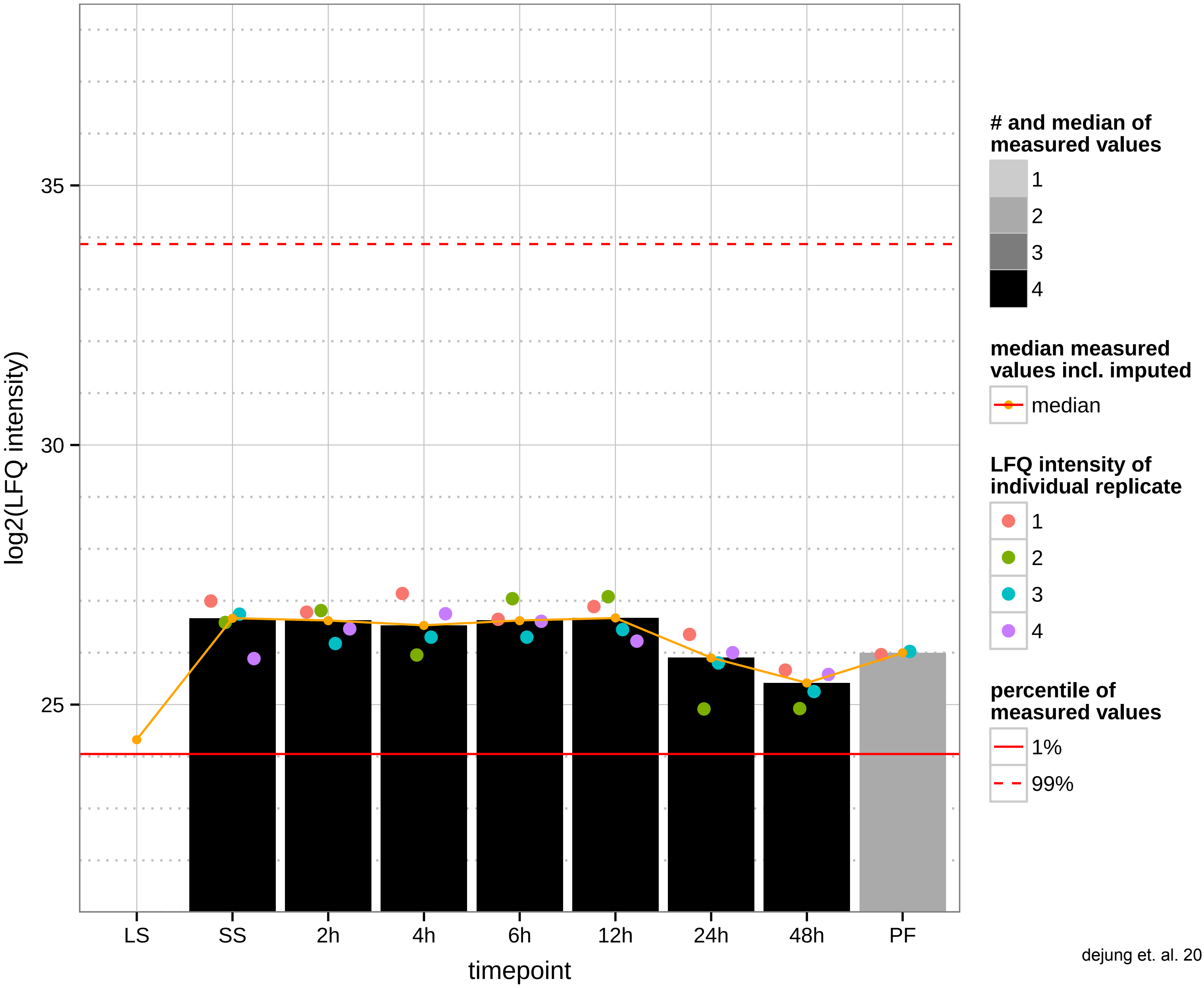
hypothetical protein, conserved
Tb927.7.4750;Tb11.v5.0158
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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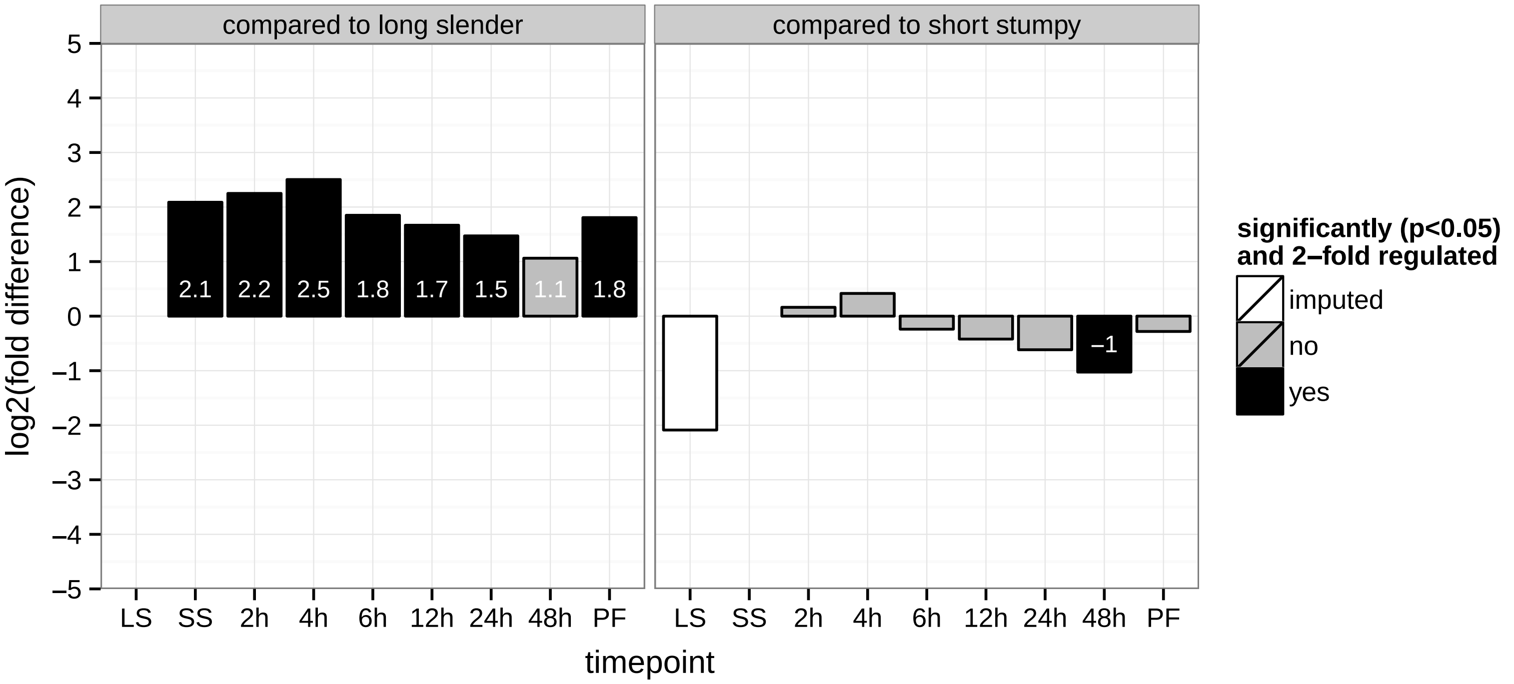
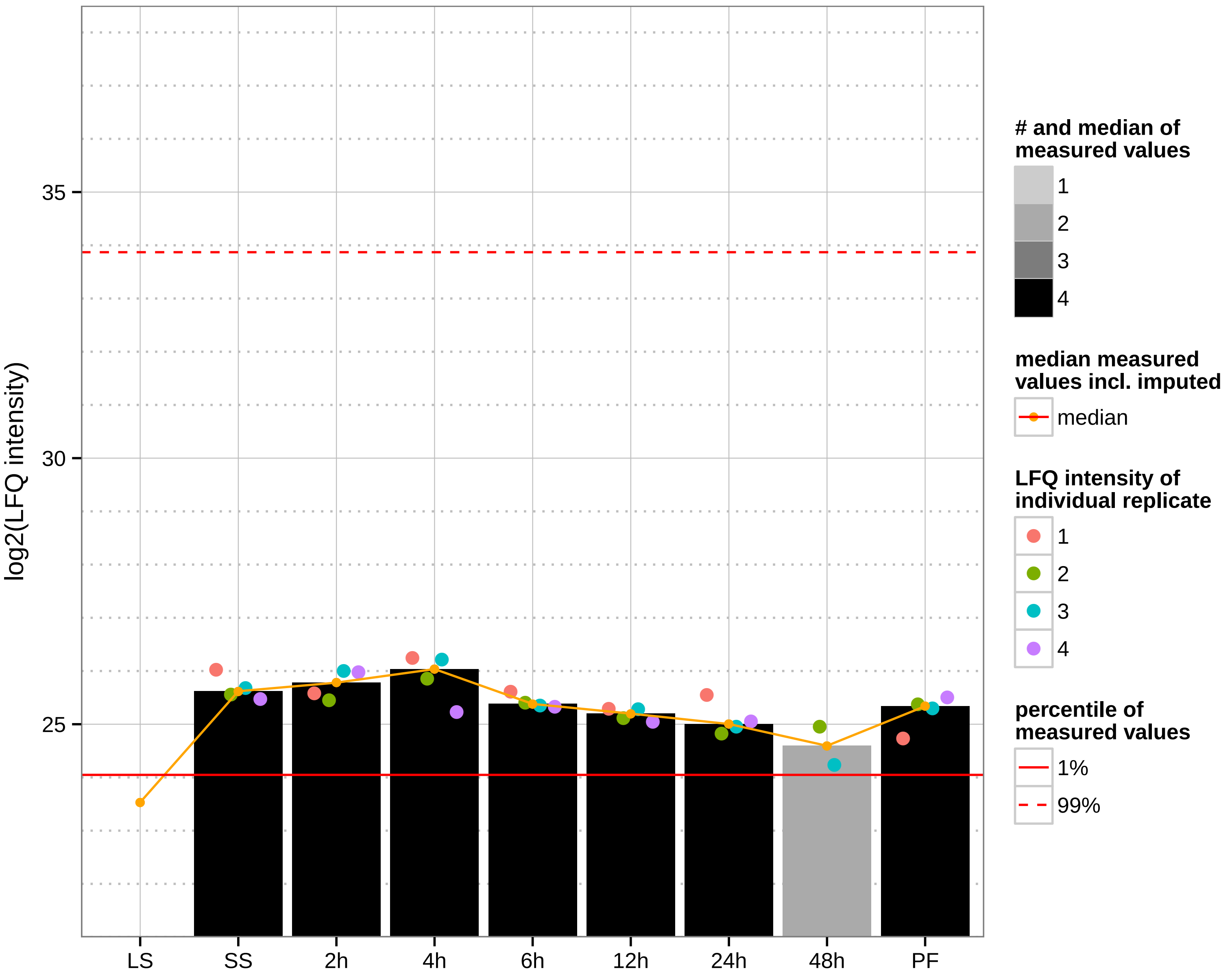
hypothetical protein, conserved
Tb927.7.4490;Tb11.v5.0262
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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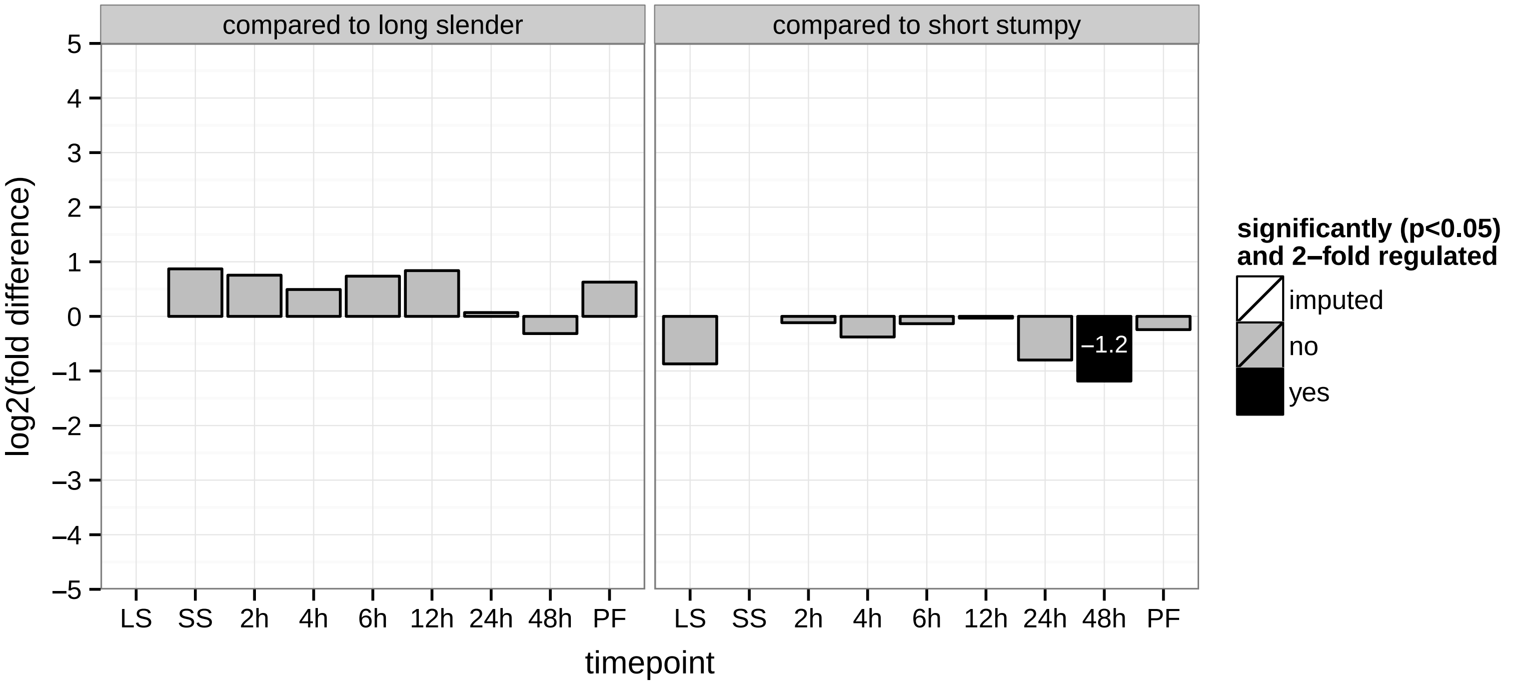
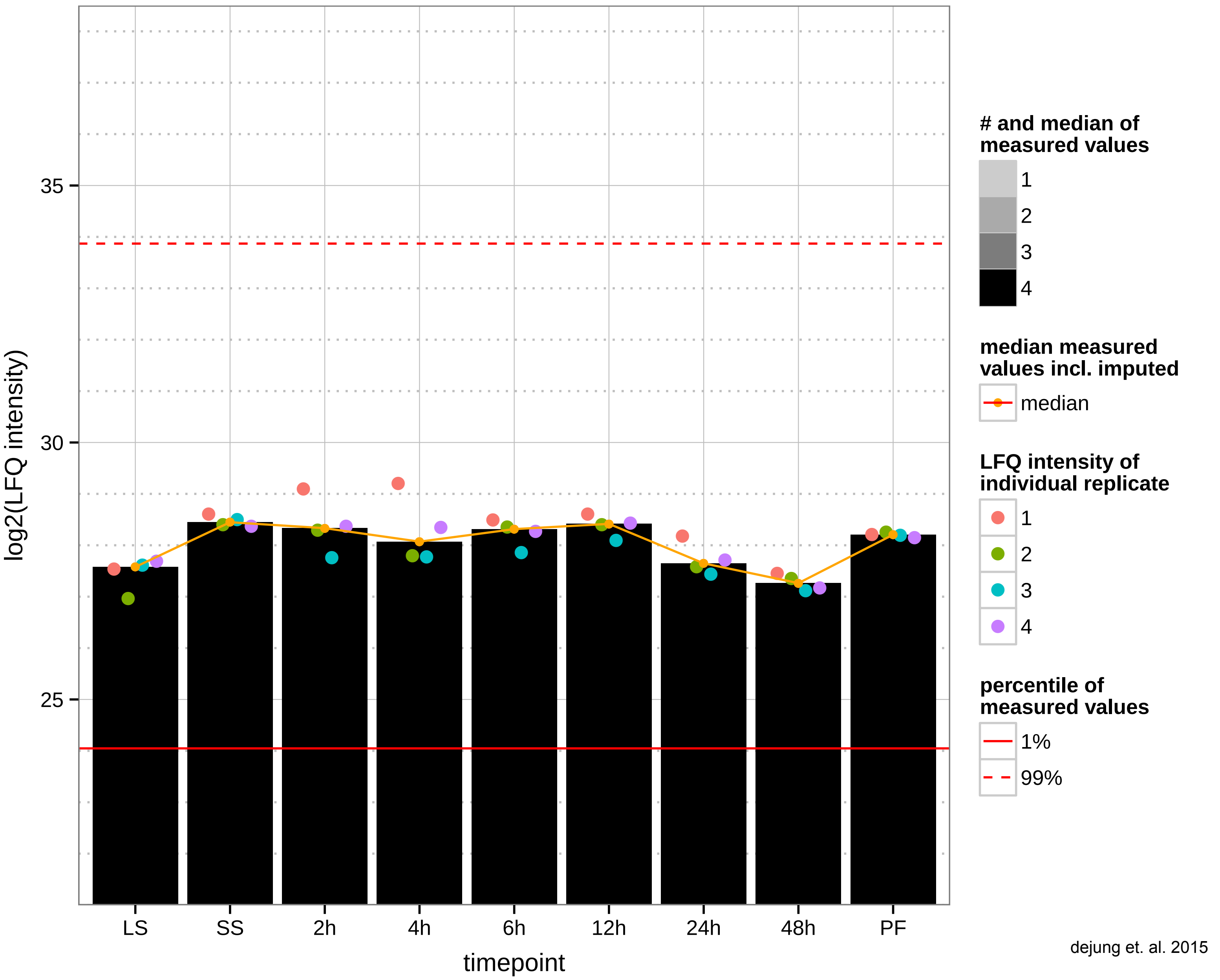
nicotinate phosphoribosyltransferase, putative
Tb927.10.11590
AGOF: nicotinate phosphoribosyltransferase activity
AGOC: null
AGOP: nicotinate nucleotide biosynthetic process, nicotinate nucleotide salvage, pyridine nucleotide biosynthetic process
PGOF: nicotinate phosphoribosyltransferase activity, nicotinate–nucleotide diphosphorylase (carboxylating) activity
PGOC: cytoplasm
PGOP: NAD biosynthetic process, nicotinate nucleotide biosynthetic process





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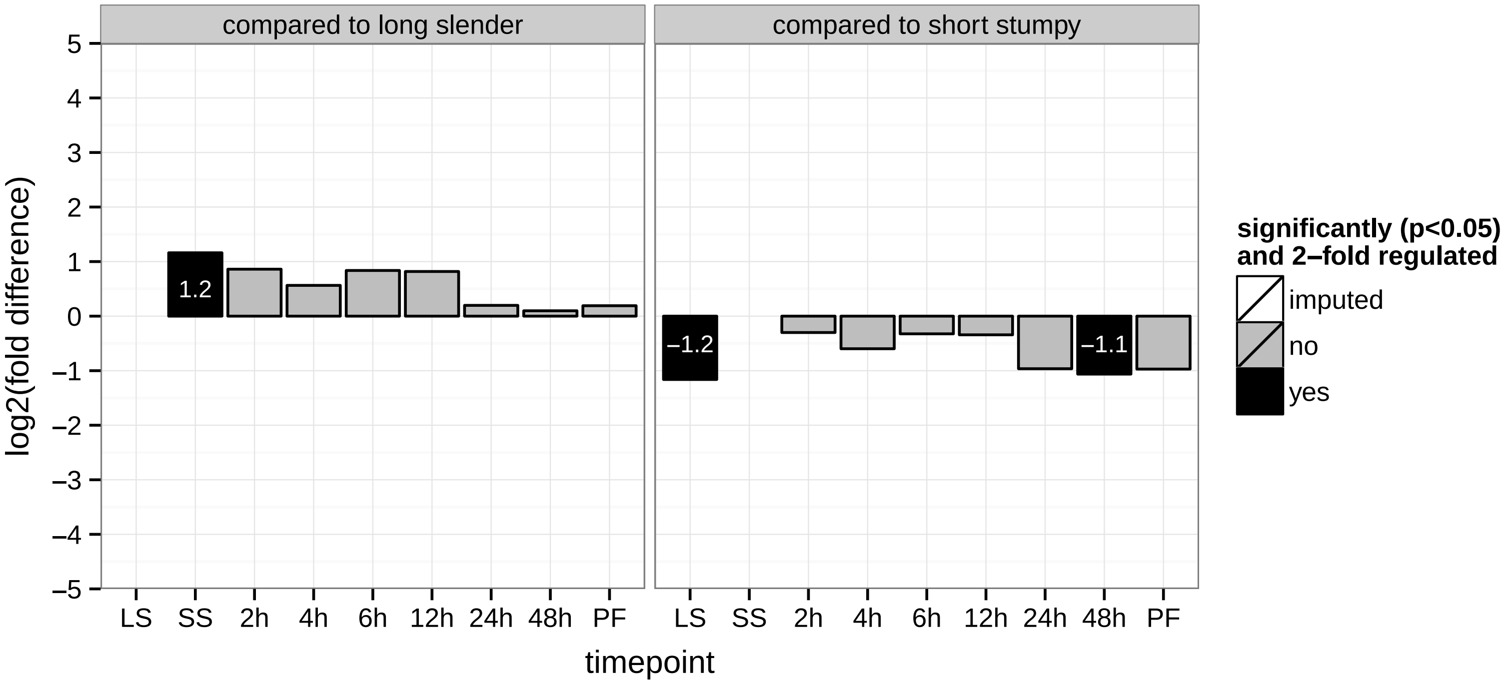
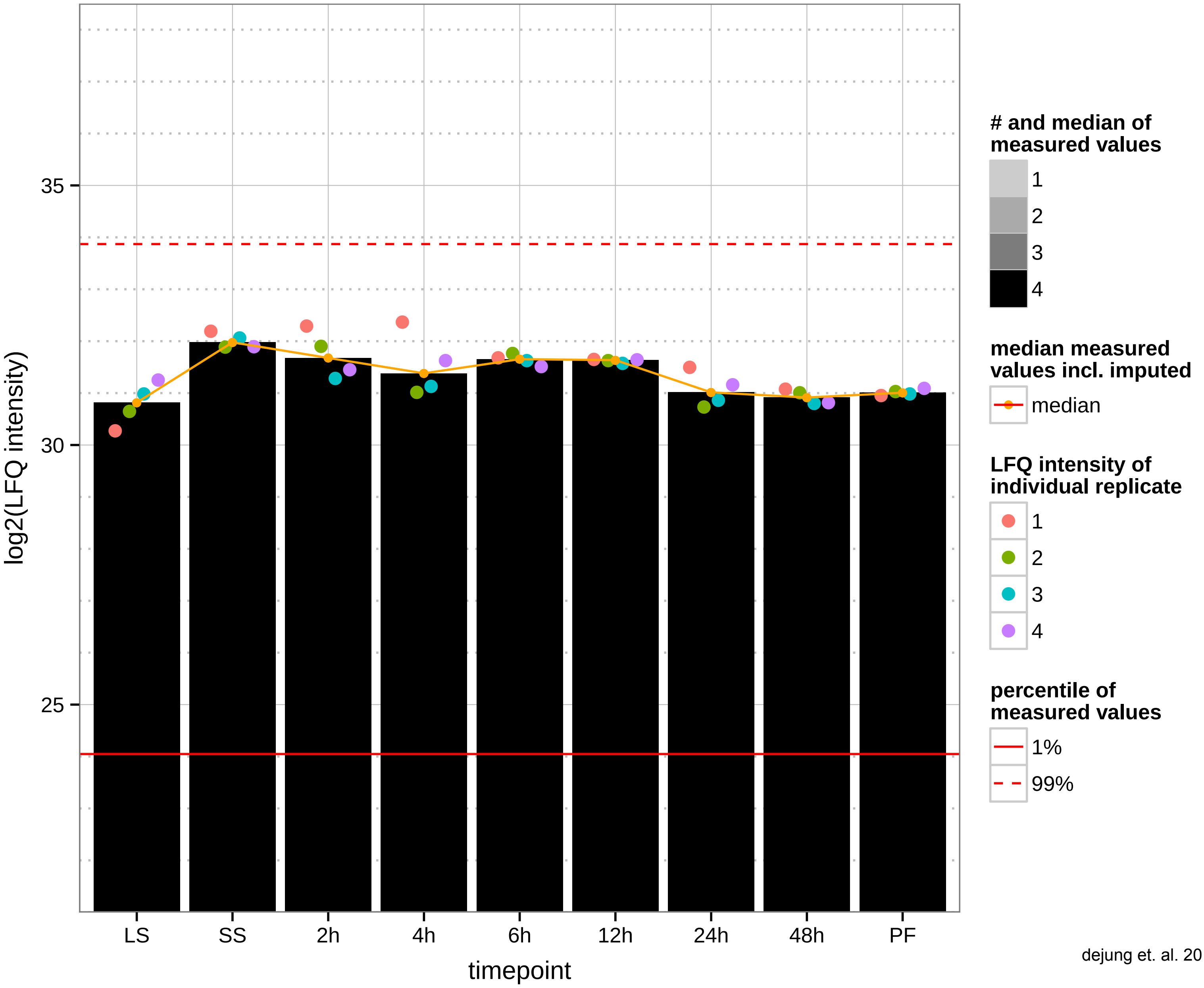
chrX additional, unordered contigs, hypothetical protein, conserved, intraflagellar transport protein IFT172, putative (IFT172)
Tb927.10.1170;Tb11.0560
AGOF: null
AGOC: null
AGOP: null
PGOF: null, protein binding
PGOC: null
PGOP: null





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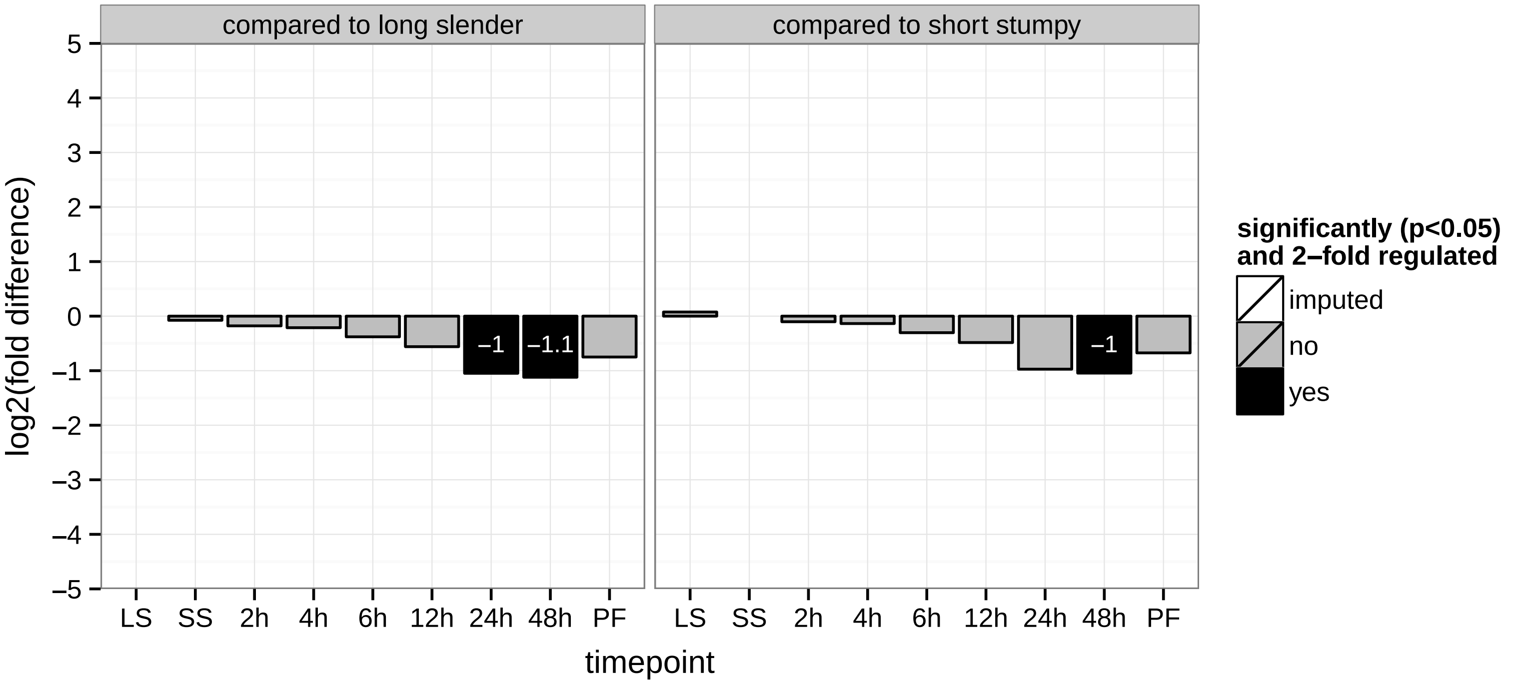
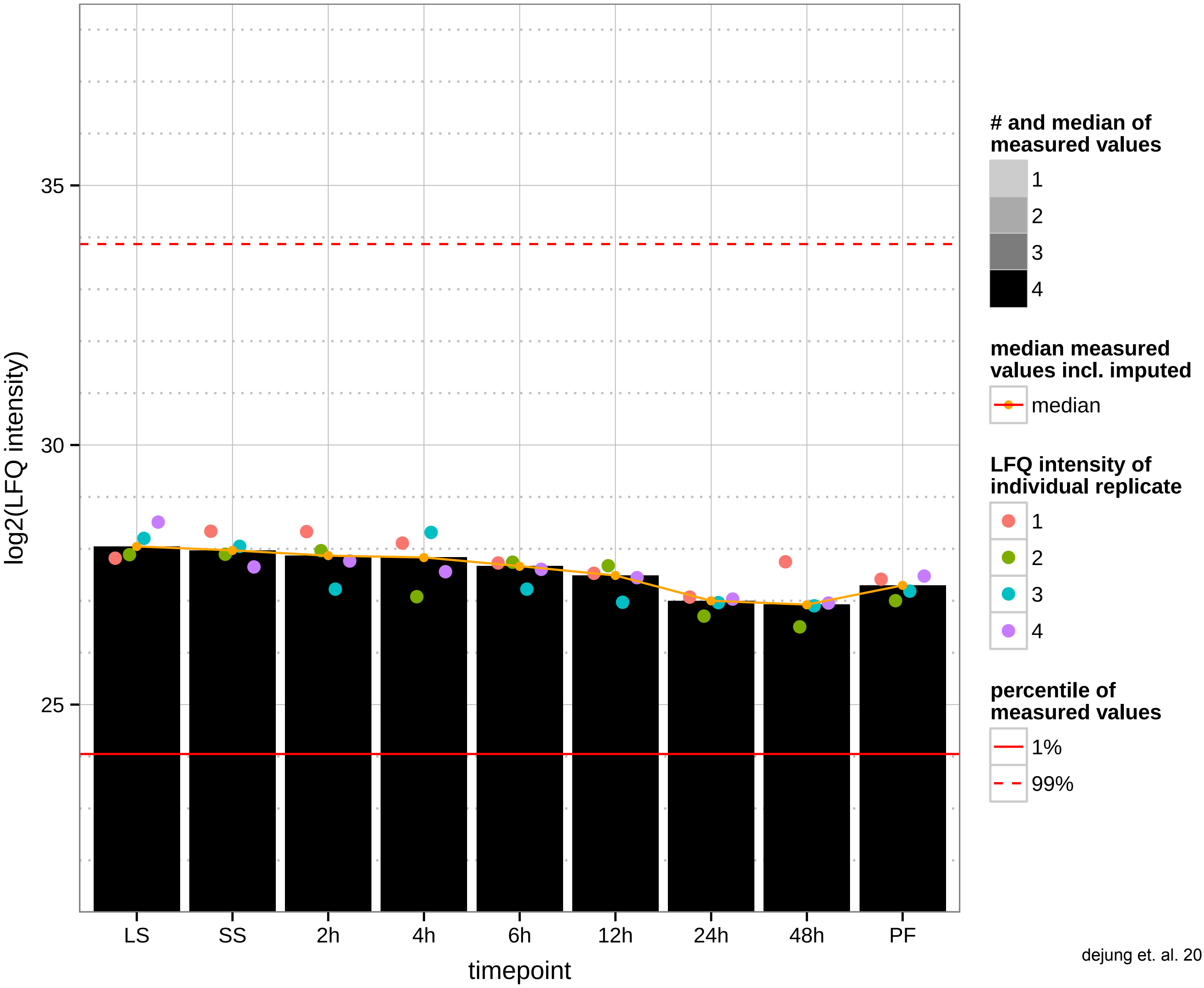
P–type H+–ATPase, putative
Tb927.10.12510
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism
AGOC: integral to membrane, plasma membrane
AGOP: ATP biosynthetic process, metabolic process, proton transport
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, catalytic acti
PGOC: integral to membrane, membrane
PGOP: ATP biosynthetic process, ATP catabolic process, cation transport, metabolic process





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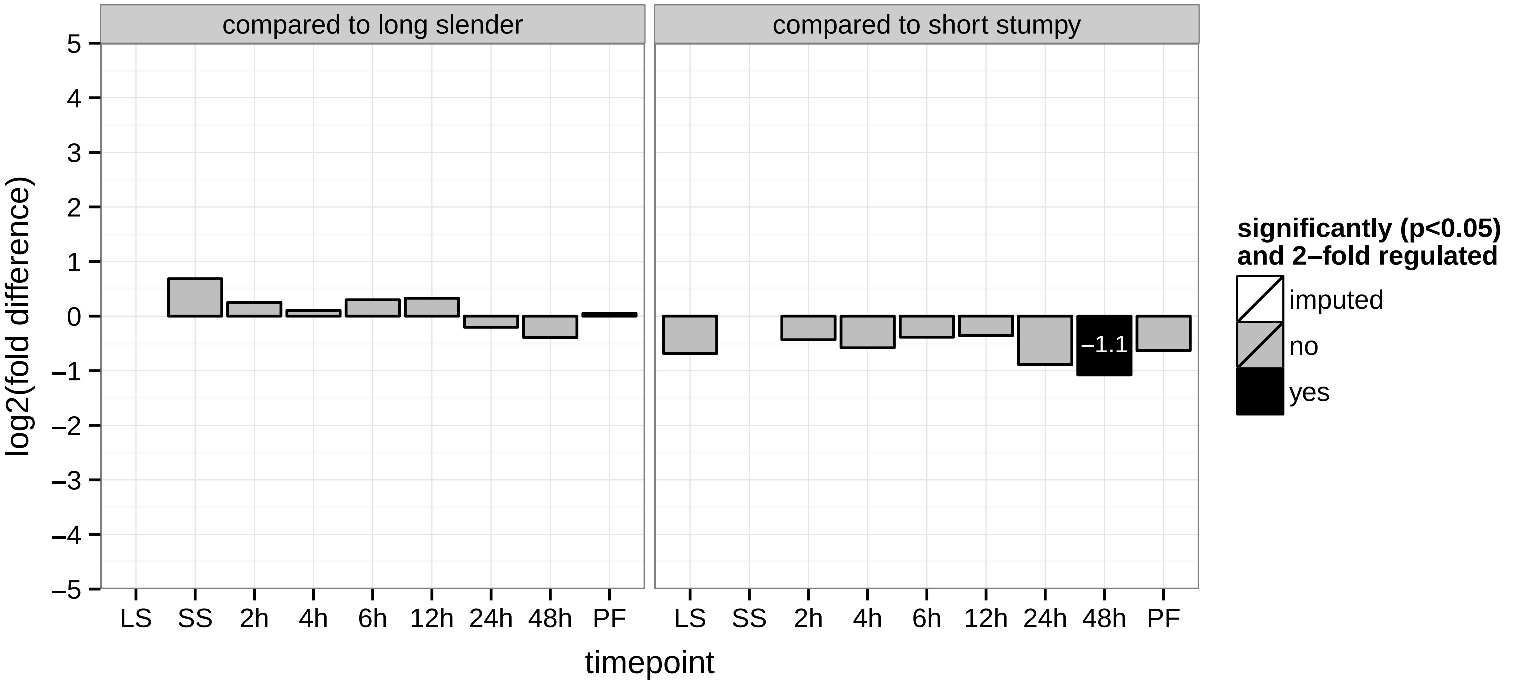
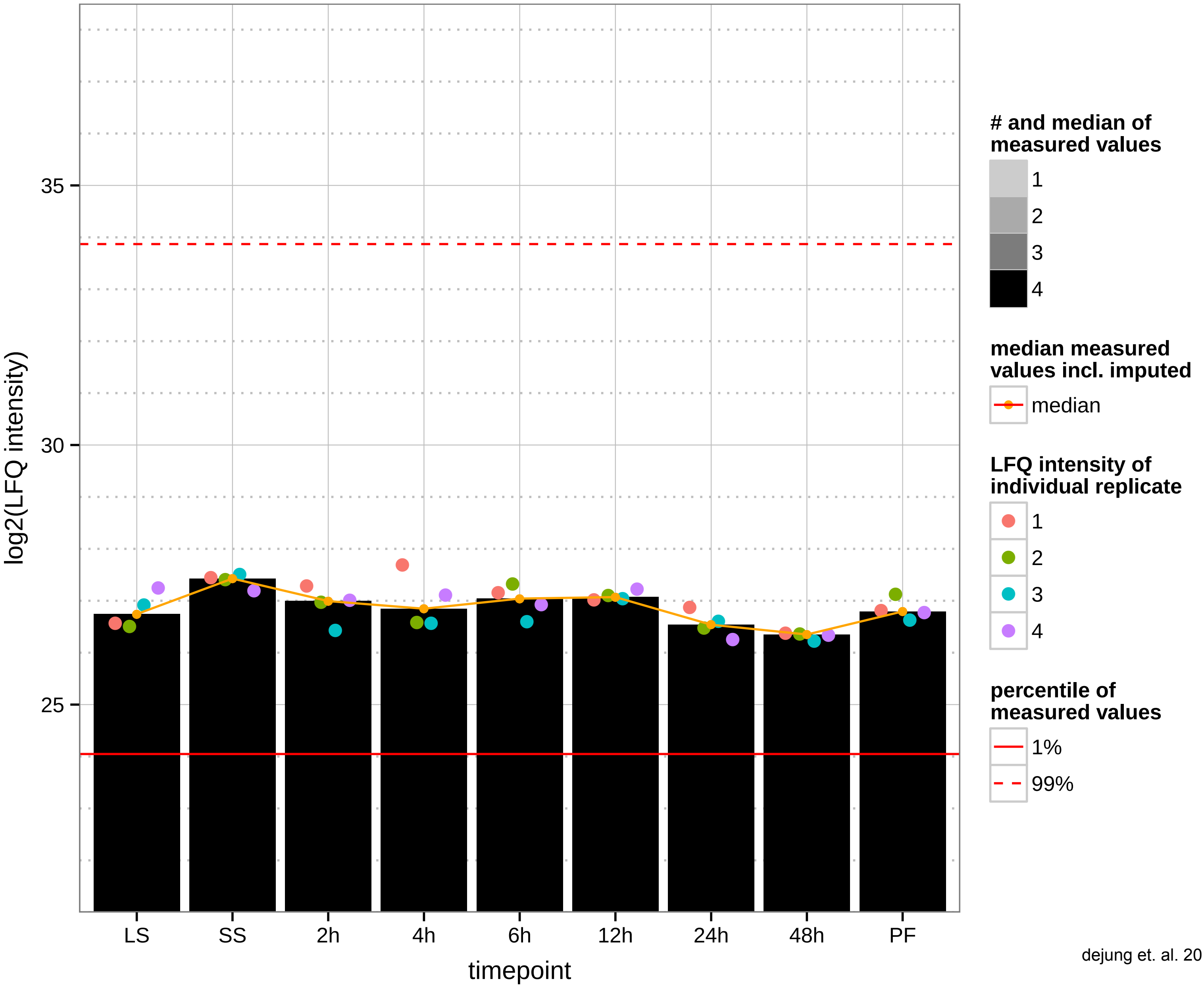
ethanolamine phosphotransferase (EPT)
Tb927.10.13290
AGOF: ethanolaminephosphotransferase activity
AGOC: membrane
AGOP: phosphatidylethanolamine biosynthetic process, phospholipid biosynthetic process
PGOF: phosphotransferase activity, for other substituted phosphate groups
PGOC: membrane
PGOP: phospholipid biosynthetic process





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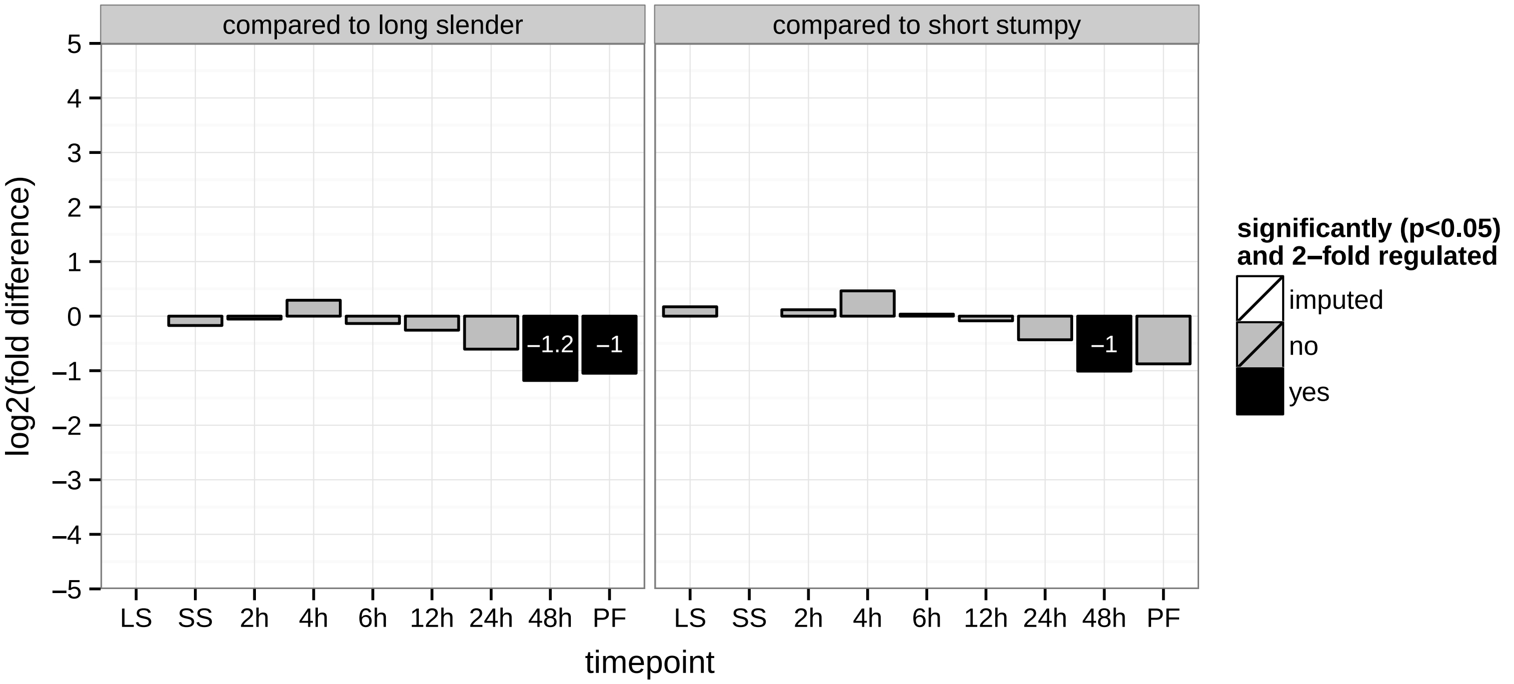
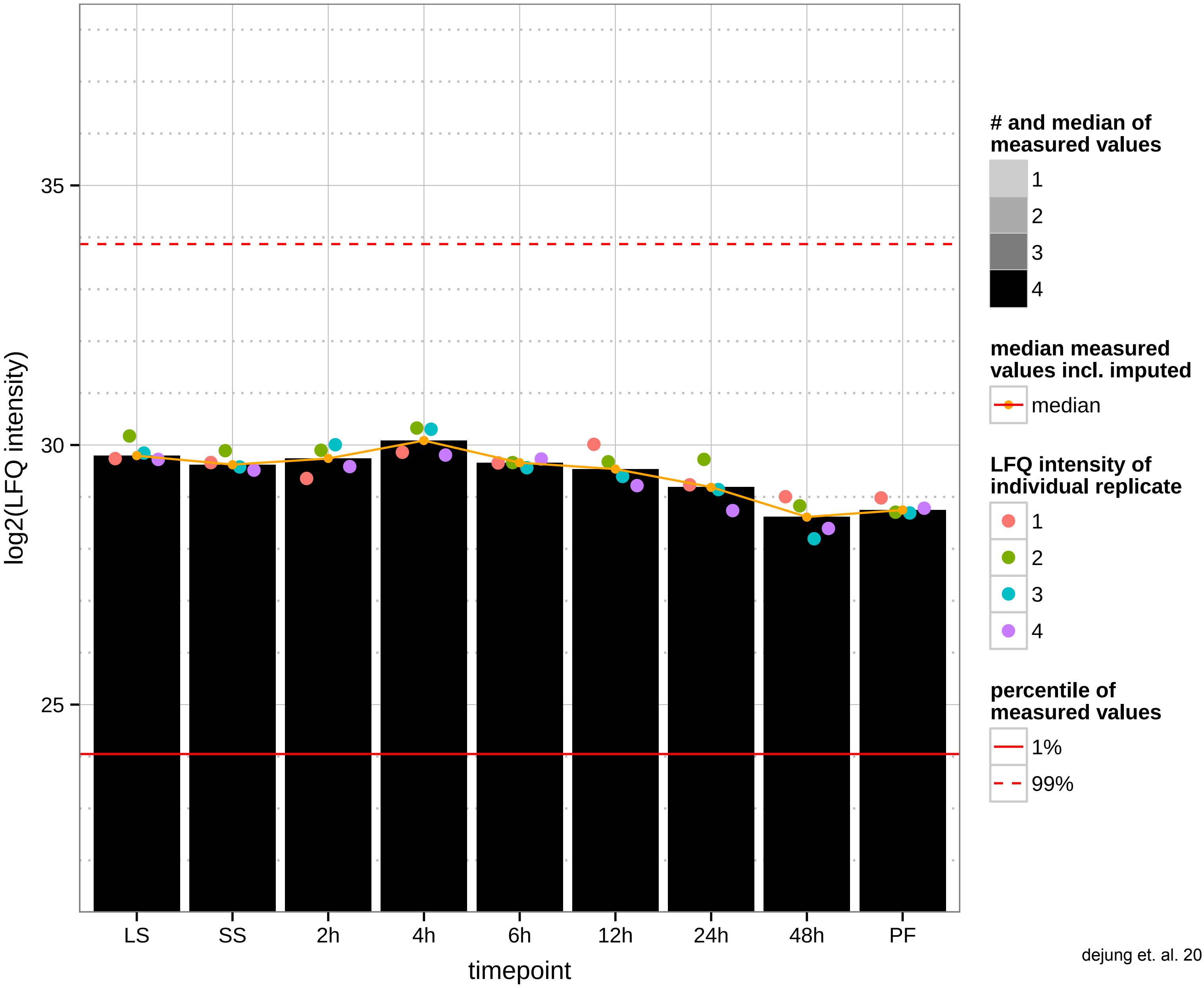
hypothetical protein, conserved, variant surface glycoprotein (VSG), pseudogene
Tb927.10.14740;Tb927.10.14620;Tb11.v5.1063
AGOF: null, heat shock protein binding
AGOC: null
AGOP: null
PGOF: heat shock protein binding, null
PGOC: null
PGOP: null





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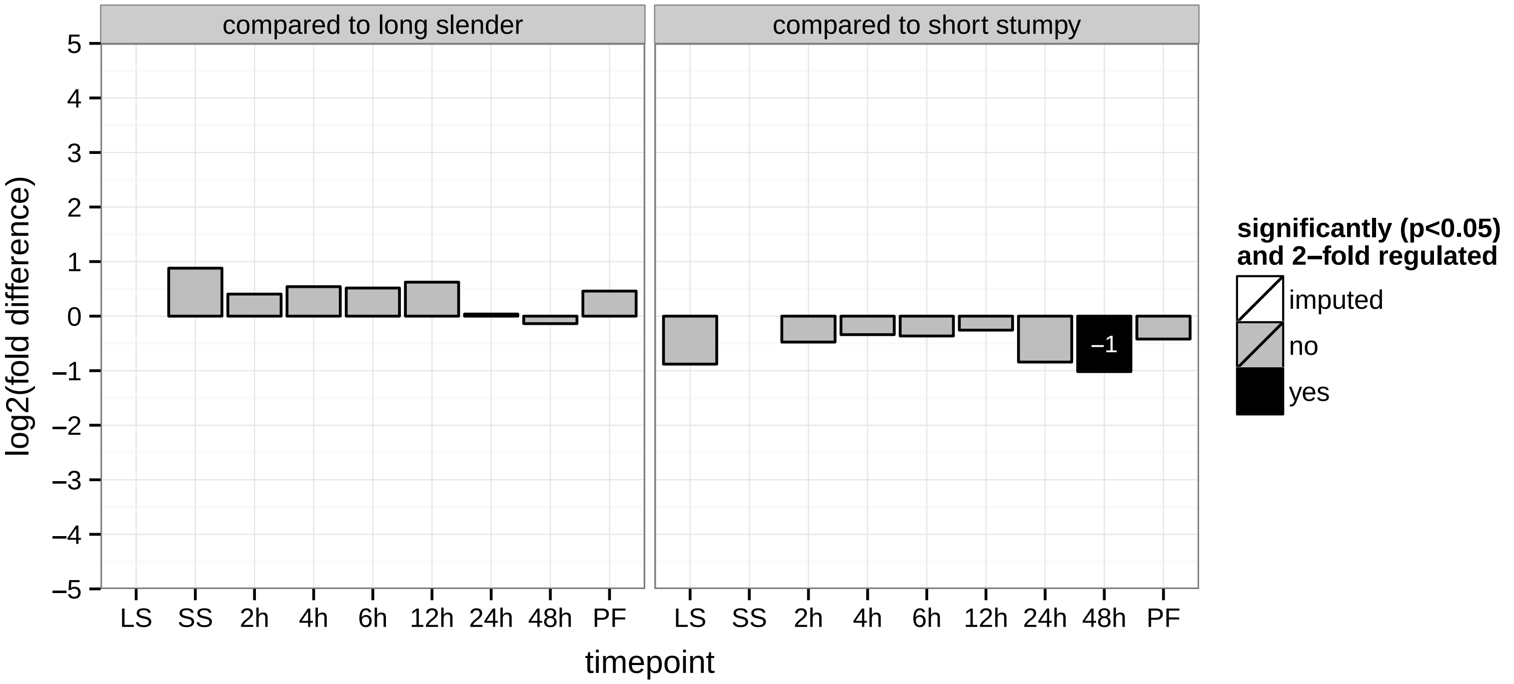
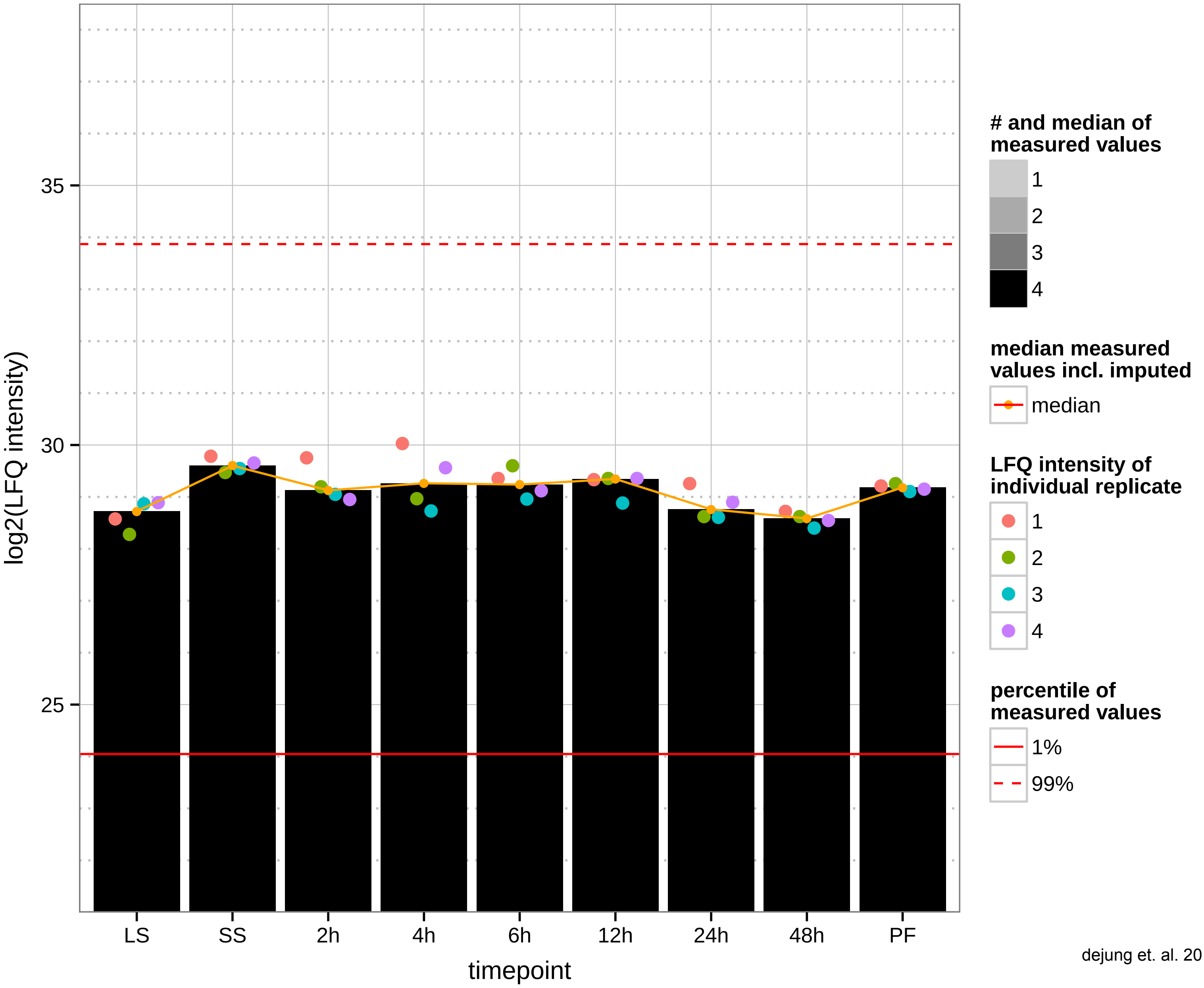
ATP synthase, putative
Tb927.10.730;Tb11.v5.0822
AGOF: null, proton−transporting ATPase activity, rotational mechanism
AGOC: null, proton−transporting two−sector ATPase complex, vacuolar proton−transporting V−type ATPase, V1 domain
AGOP: null, ATP synthesis coupled proton transport
PGOF: binding, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, proton−tra
PGOC: vacuolar proton−transporting V−type ATPase, V1 domain
PGOP: ATP hydrolysis coupled proton transport





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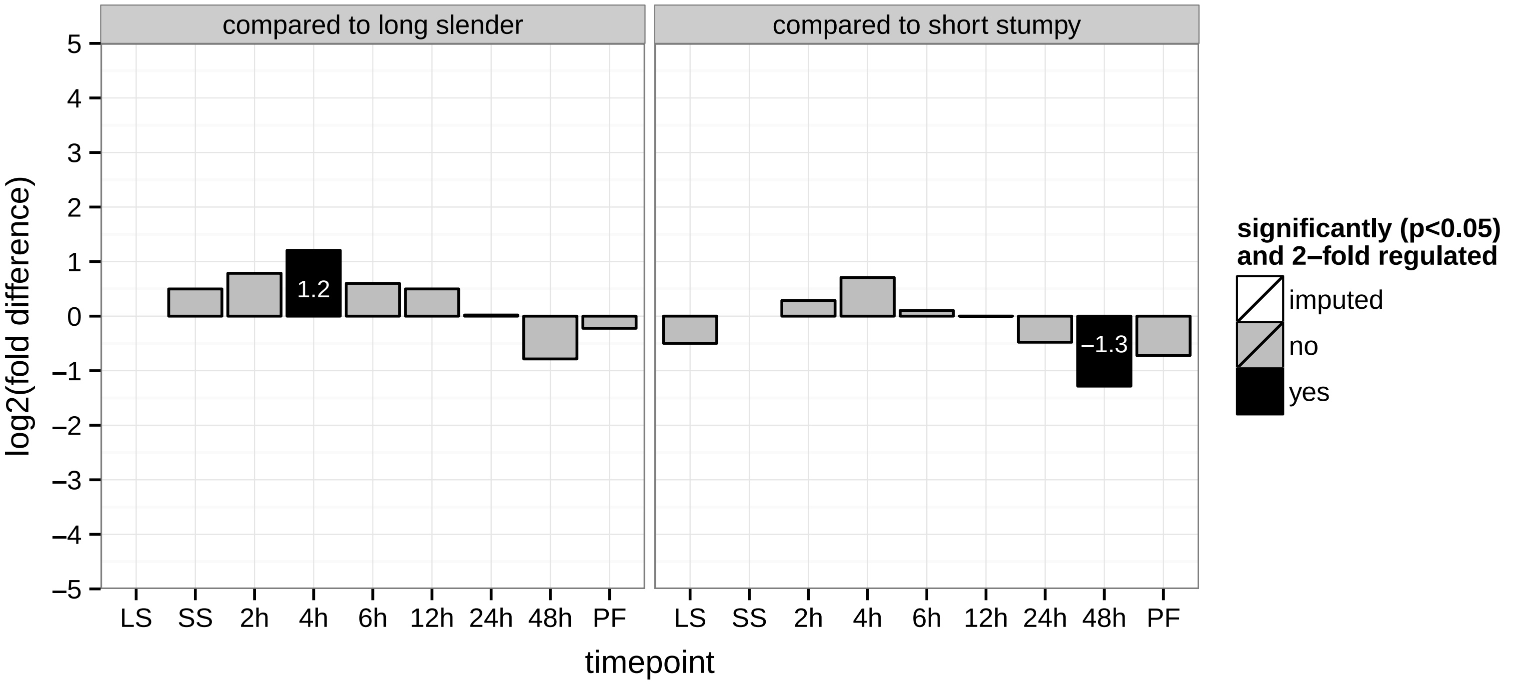
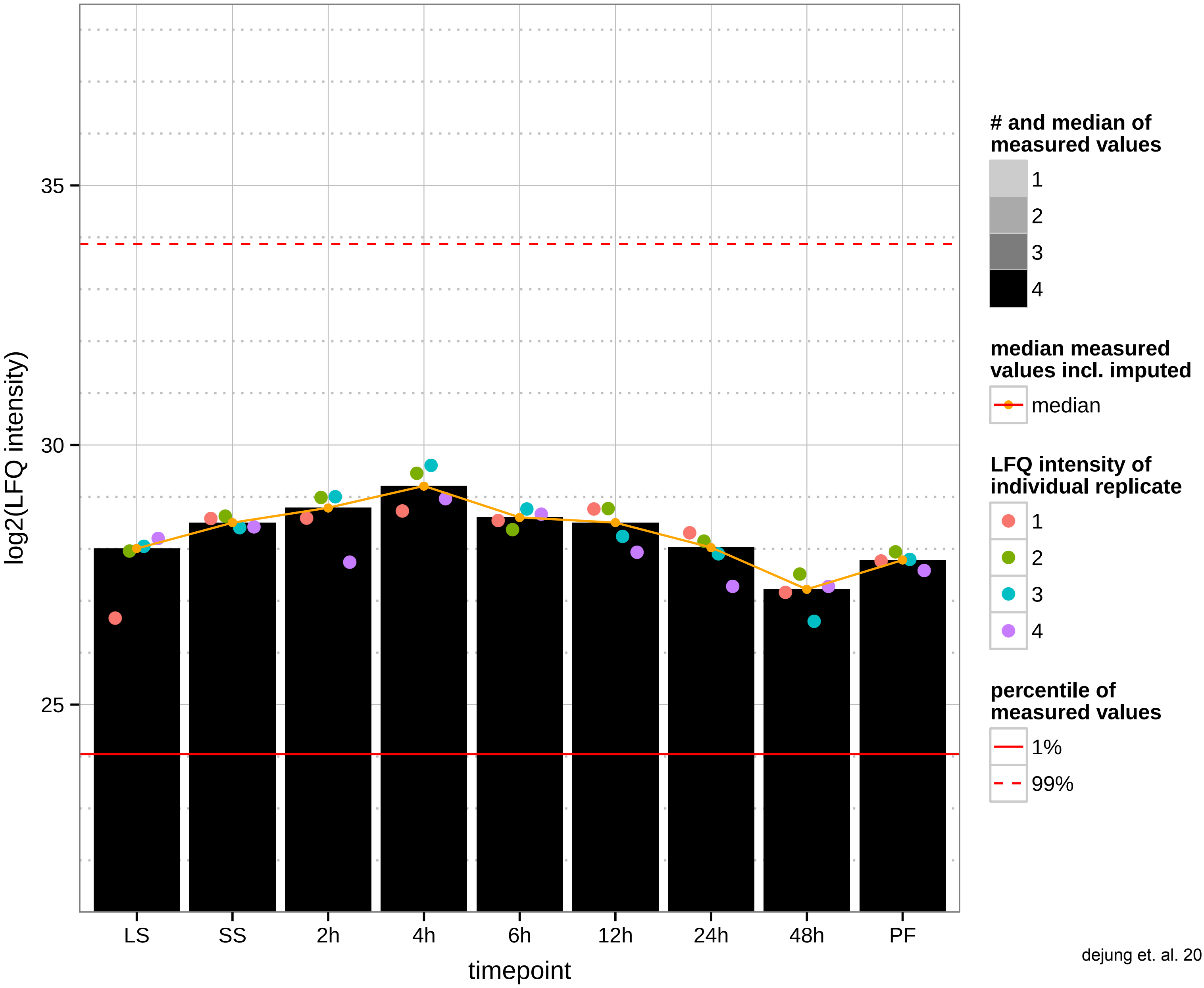
vesicle–associated membrane protein, putative, synaptobrevin, putative (VAMP)
Tb927.10.790
AGOF: SNAP receptor activity
AGOC: integral to membrane
AGOP: synaptic vesicle exocytosis
PGOF: protein binding
PGOC: integral to membrane
PGOP: vesicle–mediated transport





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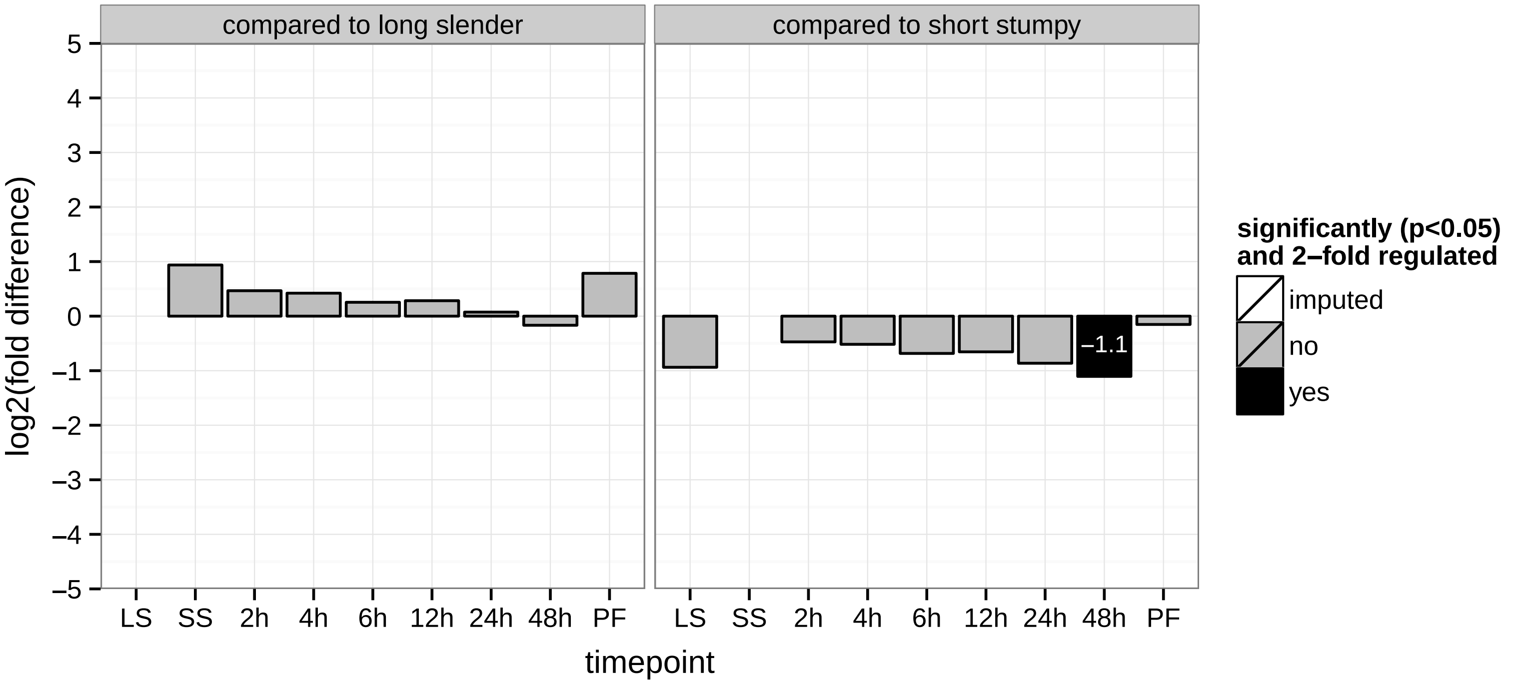
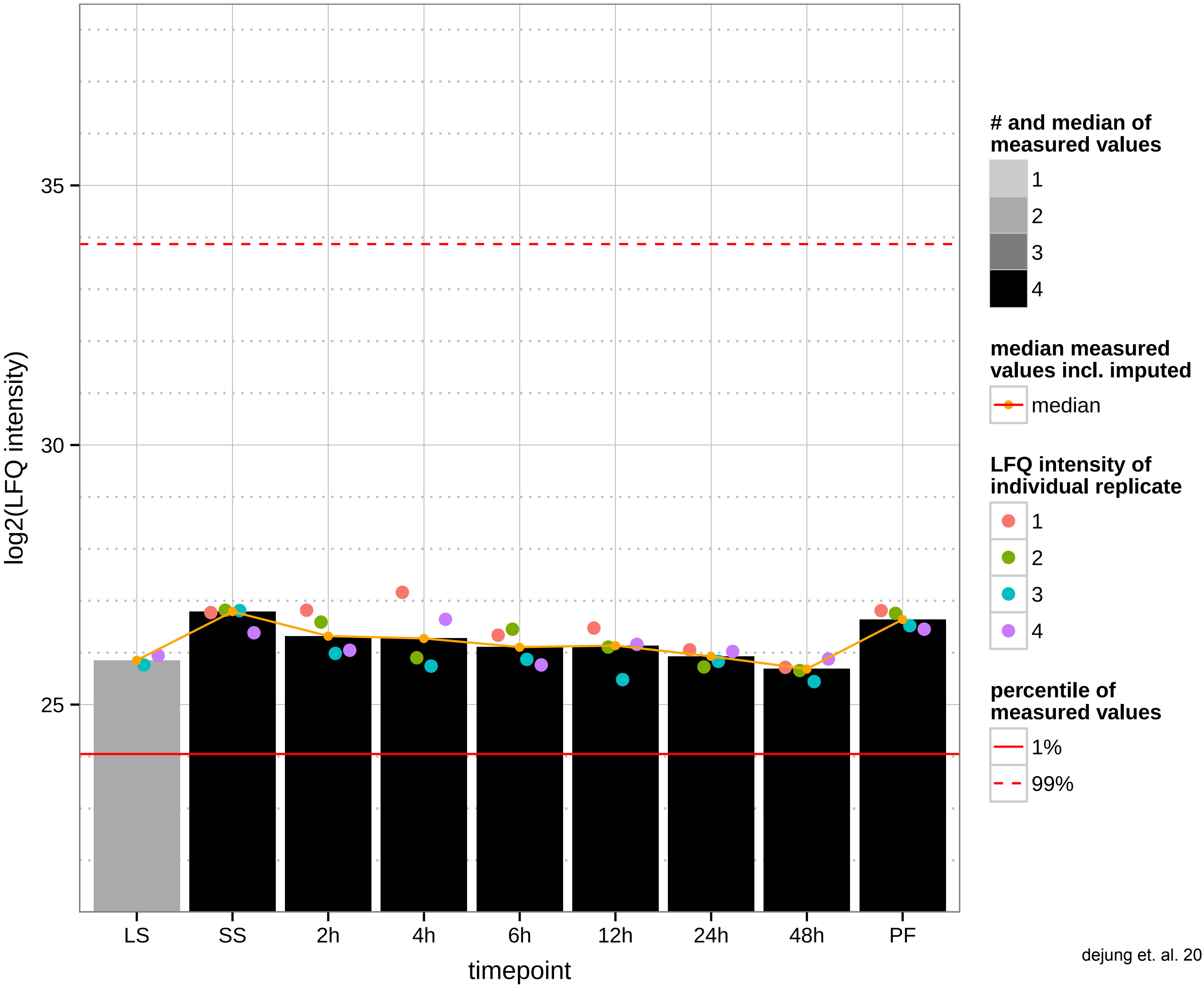
vacuolar sorting–associated protein–like, putative
Tb927.11.10010
AGOF: null
AGOC: retromer complex
AGOP: retrograde transport, endosome to Golgi, vacuolar transport
PGOF: null
PGOC: retromer complex
PGOP: vacuolar transport





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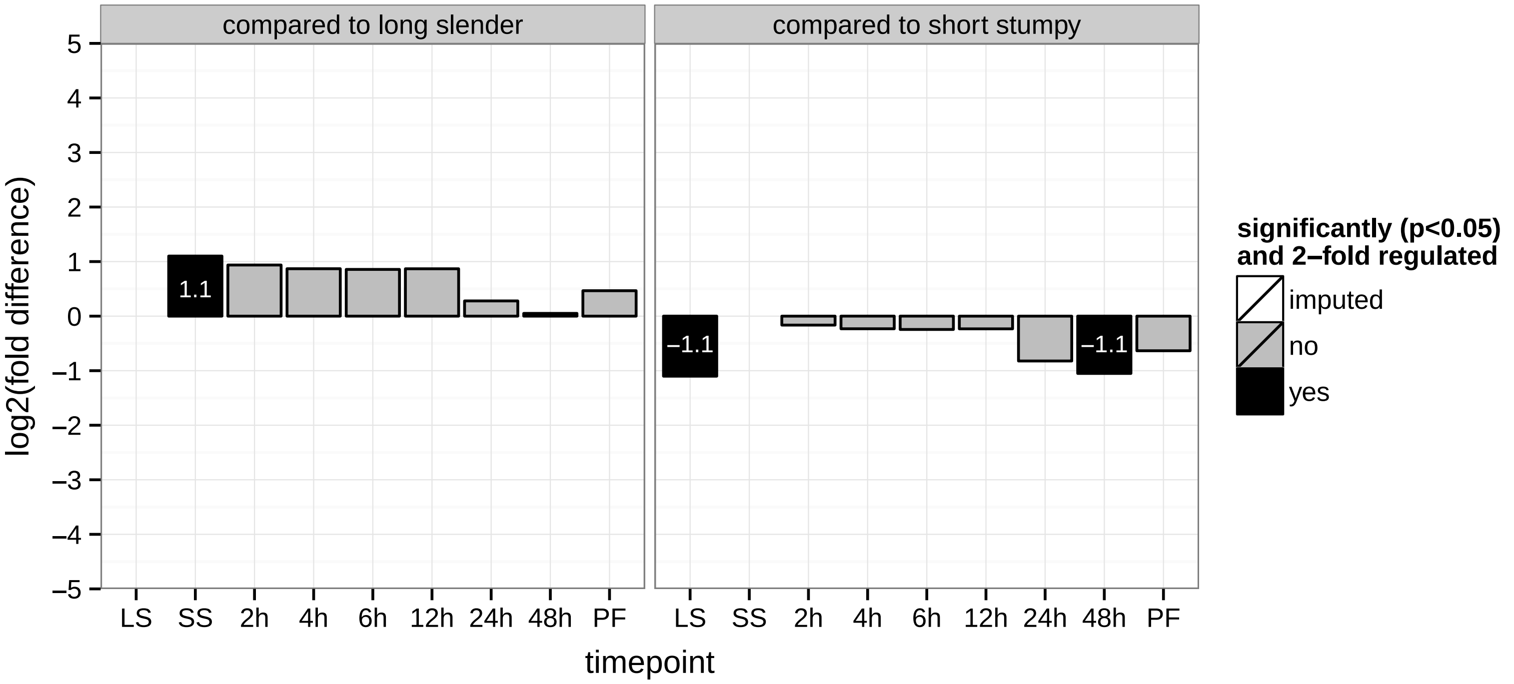
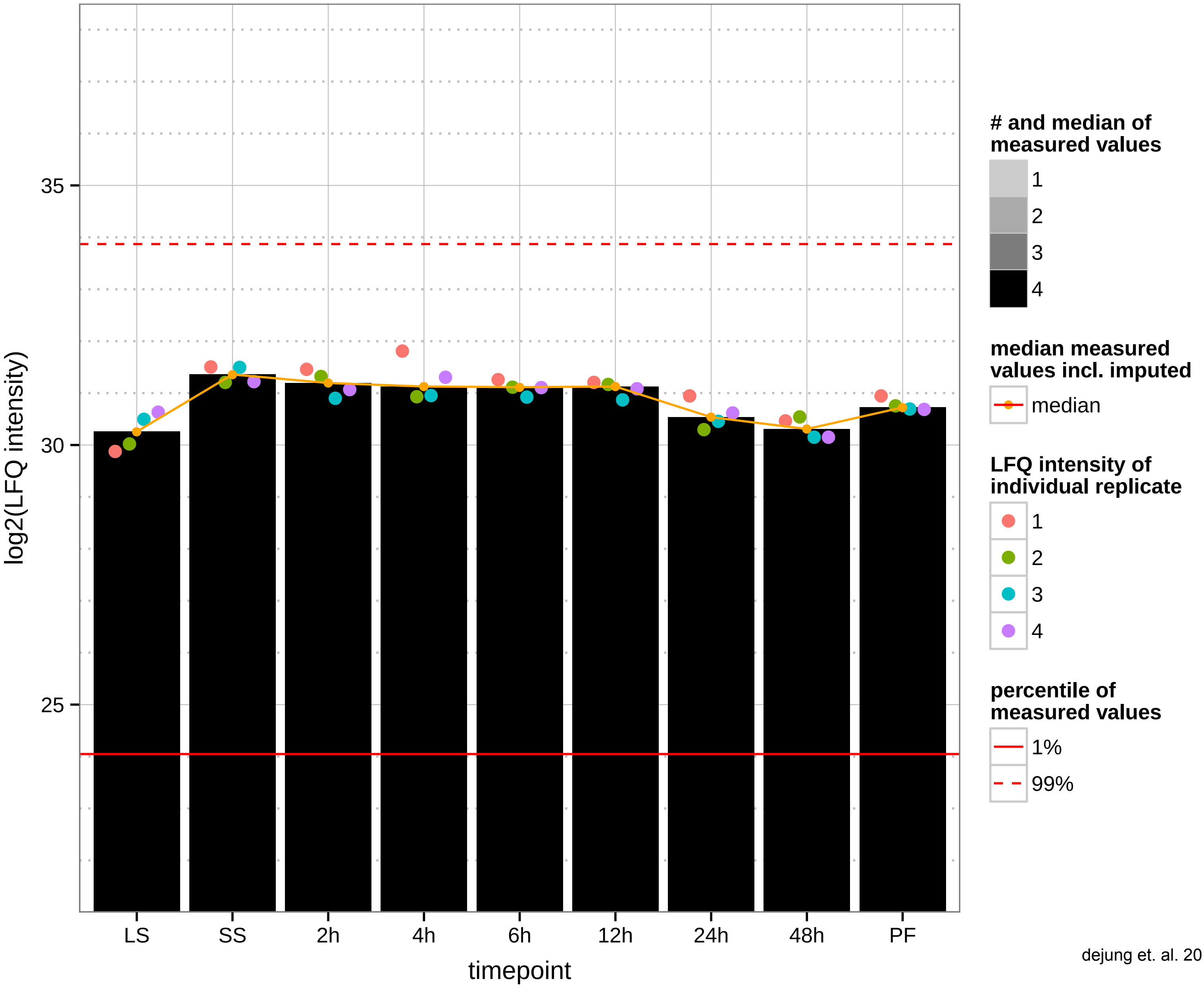
vacuolar ATP synthase subunit b, putative, v– ATPase B subunit, vacuolar proton pump B subunit
Tb927.11.11690
AGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen–exporting ATPase activity, phosphor
AGOC: contractile vacuole, lysosomal proton–transporting V–type ATPase complex, proton–transporting V–type ATPase, V1 d
AGOP: ATP hydrolysis coupled proton transport, ATP synthesis coupled proton transport
PGOF: ATP binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrolase activity, acting on acid
PGOC: proton–transporting V–type ATPase, V1 domain, proton–transporting two–sector ATPase complex, catalytic domain
PGOP: ATP hydrolysis coupled proton transport, ATP metabolic process, proton transport





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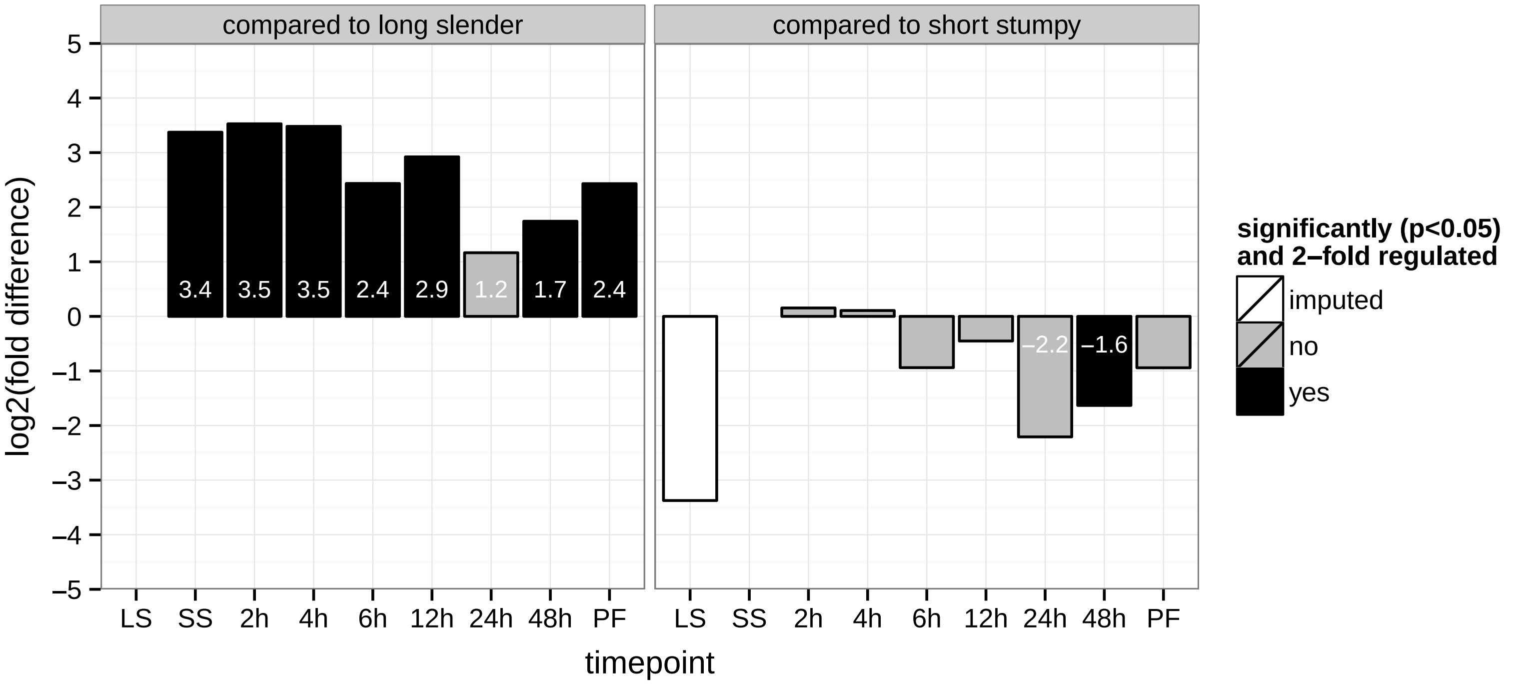
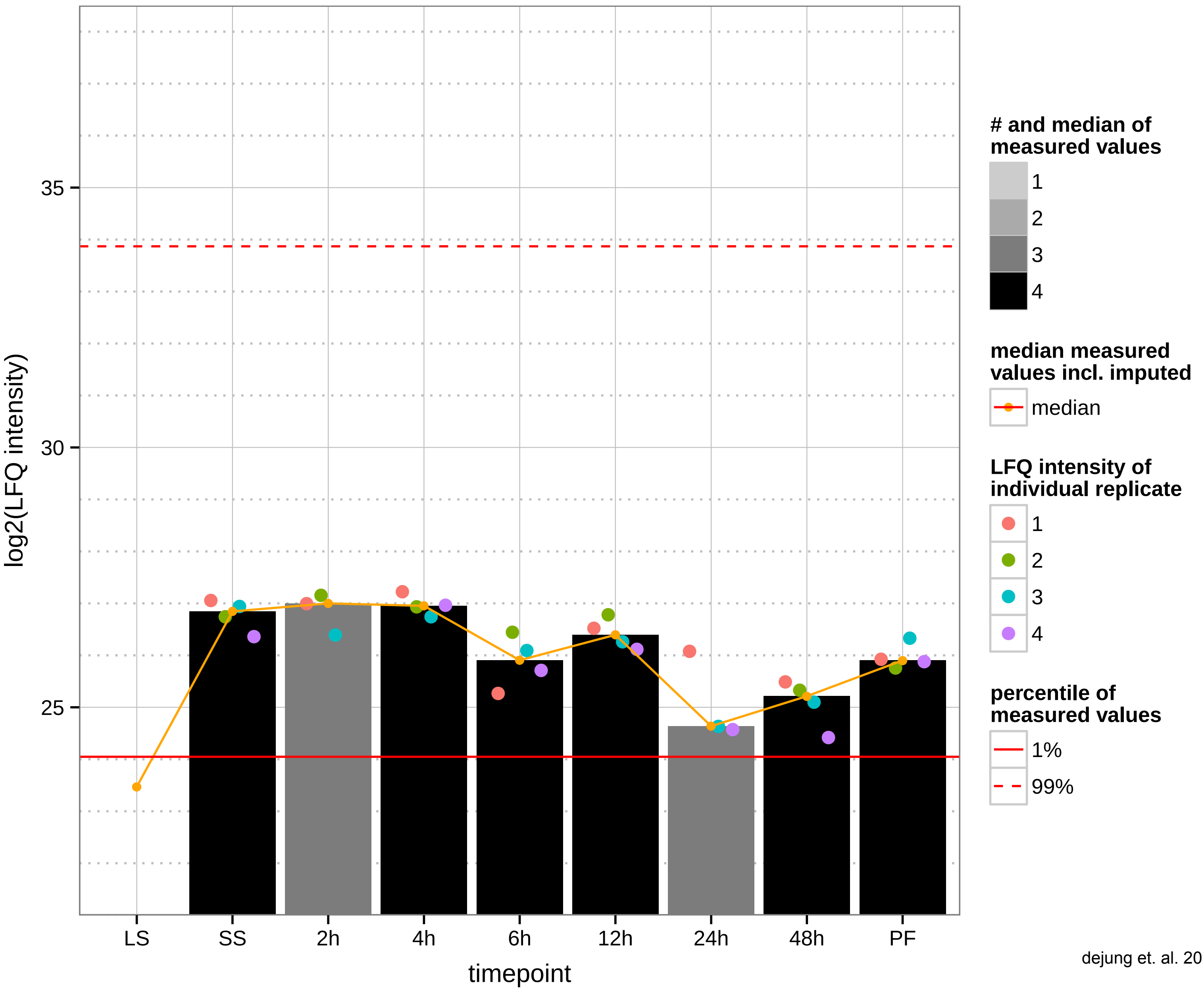
vacuolar sorting protein, putative
Tb927.11.14290
AGOF: hydrolase activity, acting on ester bonds
AGOC: cytoplasm, membrane
AGOP: protein transport, vesicle–mediated transport
PGOF: hydrolase activity, acting on ester bonds
PGOC: null
PGOP: null





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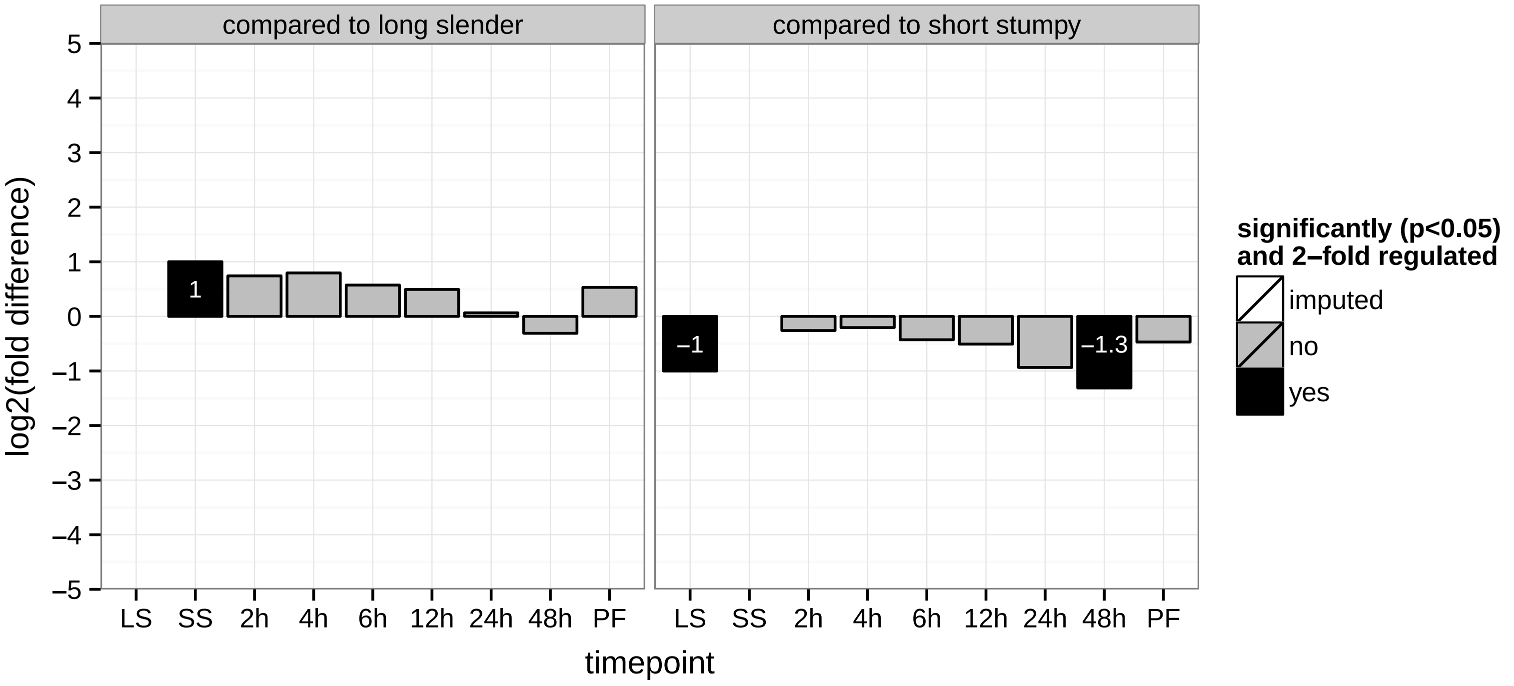
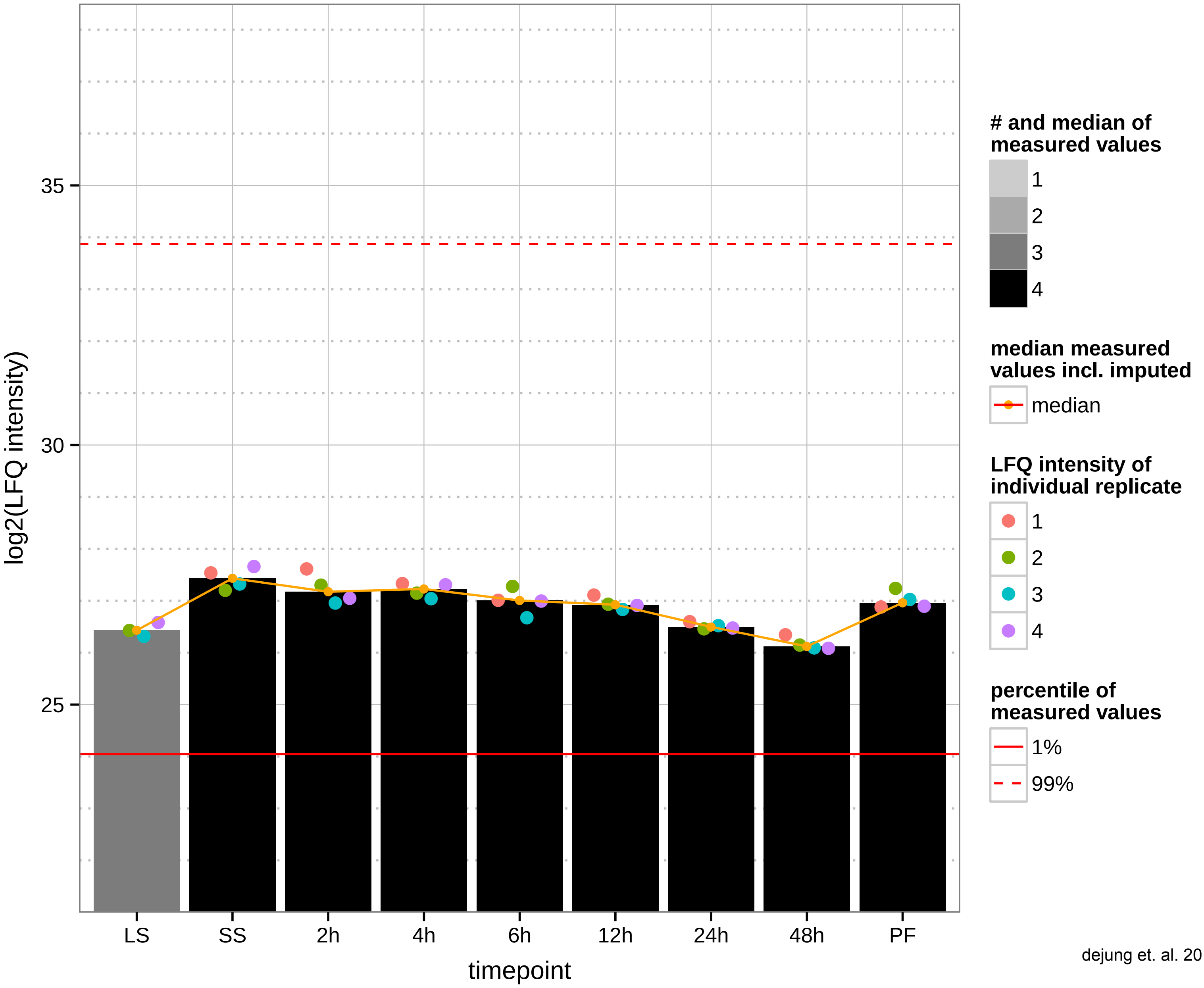
mitochondrial carrier protein (MCP2)
Tb927.11.14360
AGOF: null
AGOC: integral to membrane, mitochondrial part
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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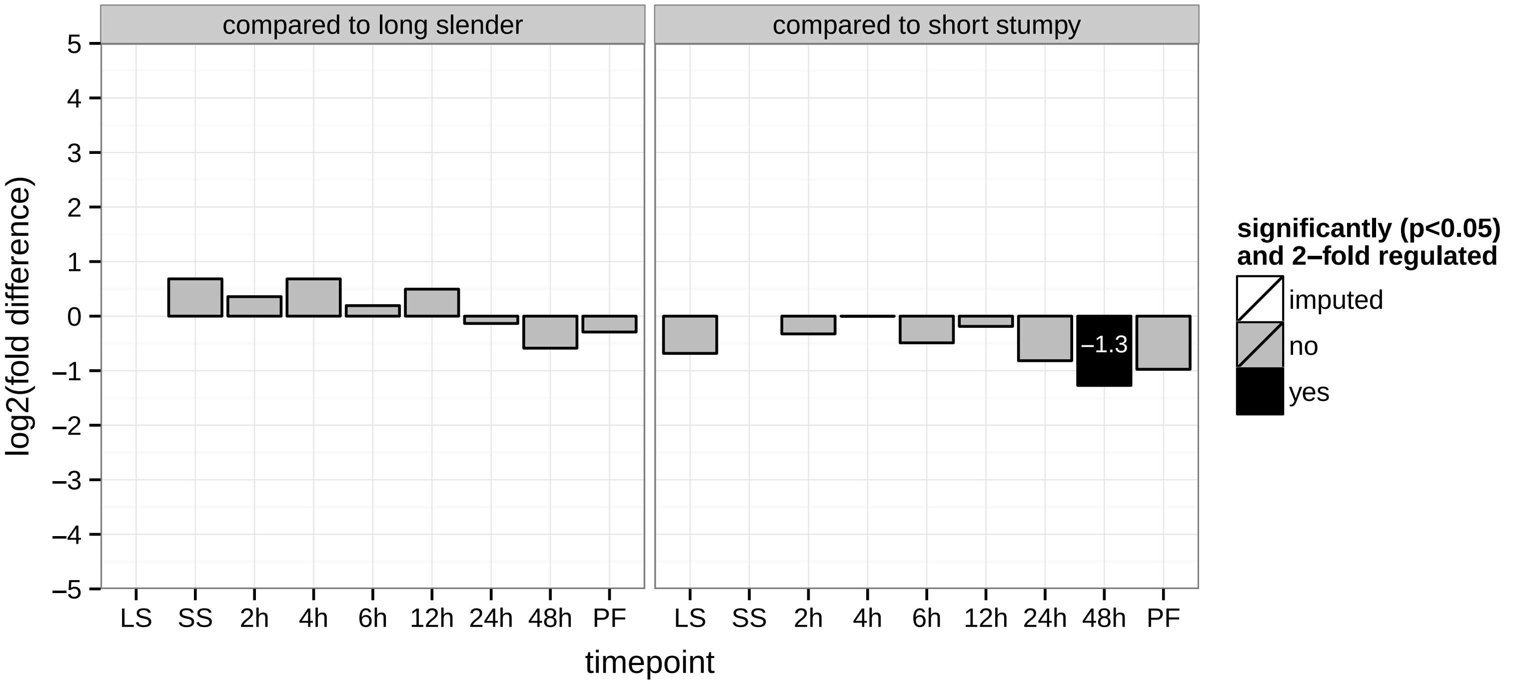
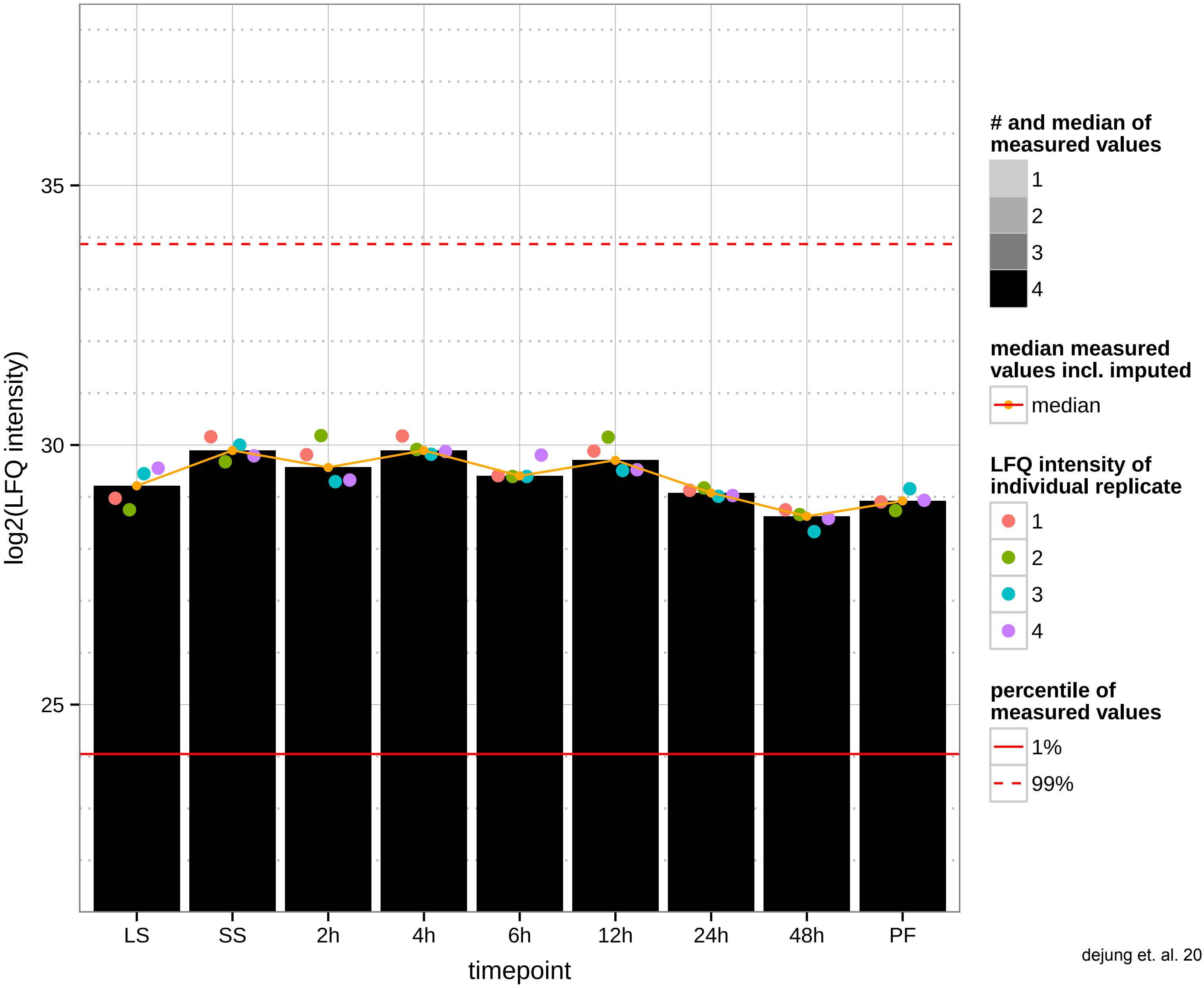
Ras–related protein Rab2 (RAB2)
Tb927.11.15240
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti





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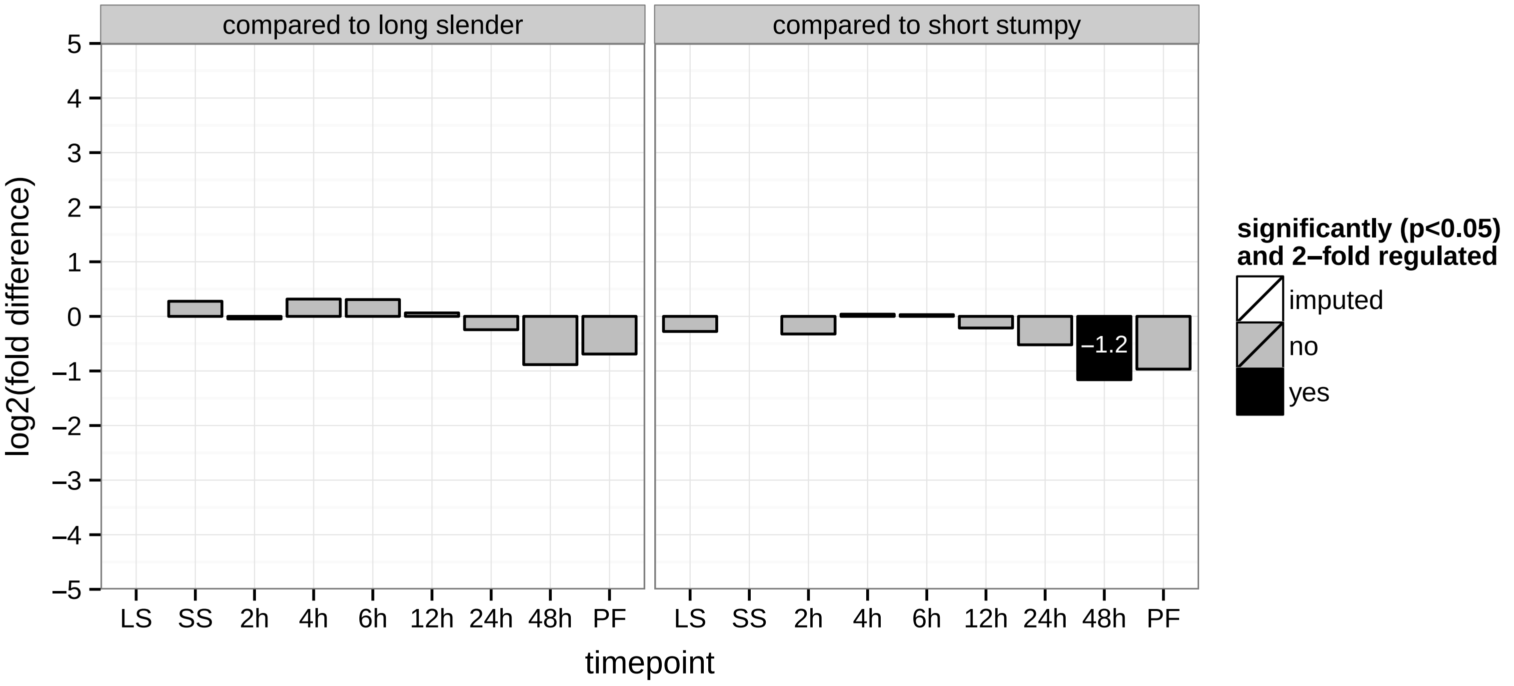
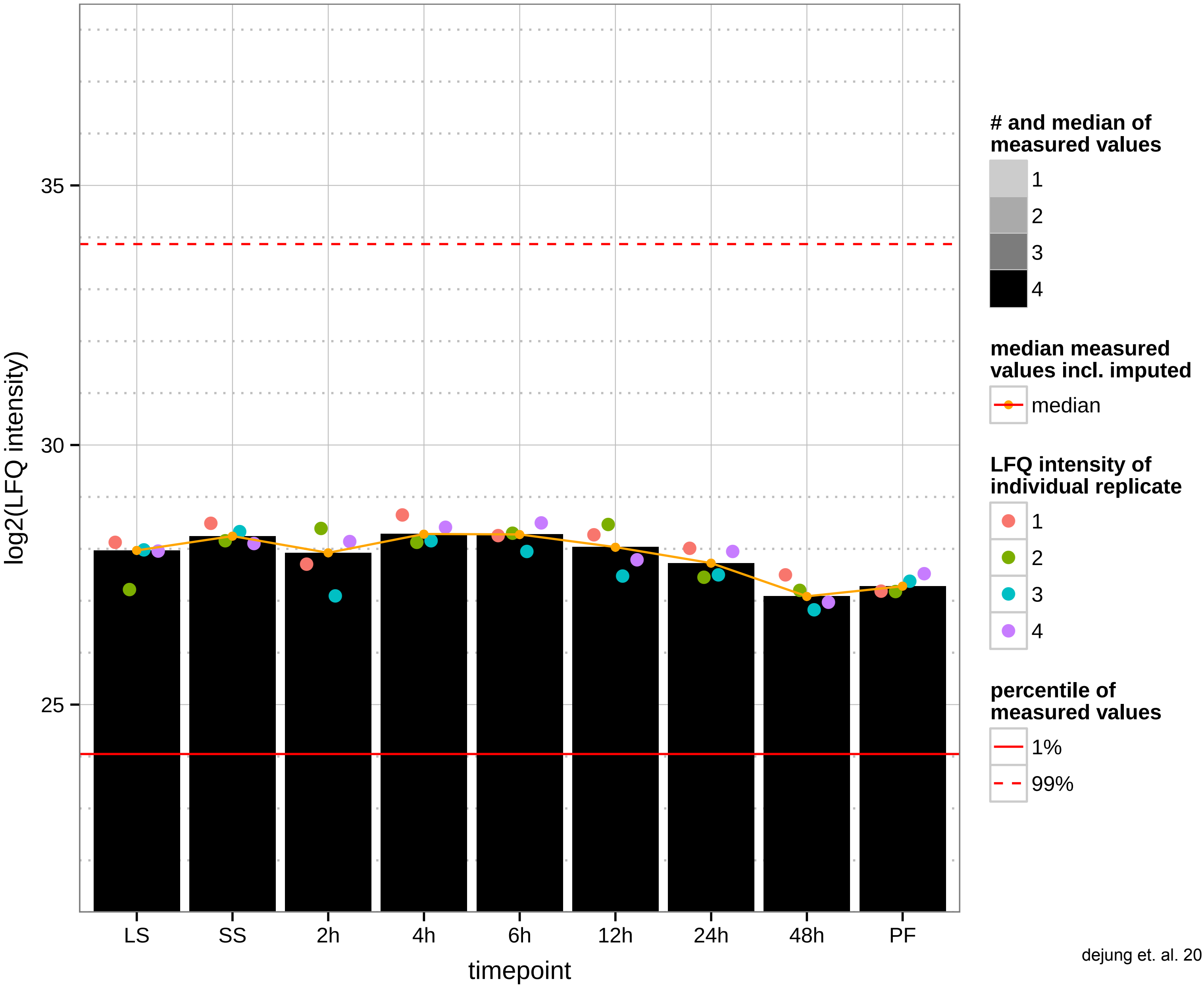
GPI transamidase subunit Tta1 (TTA1)
Tb927.11.15760
AGOF: GPI–anchor transamidase activity
AGOC: GPI–anchor transamidase complex, integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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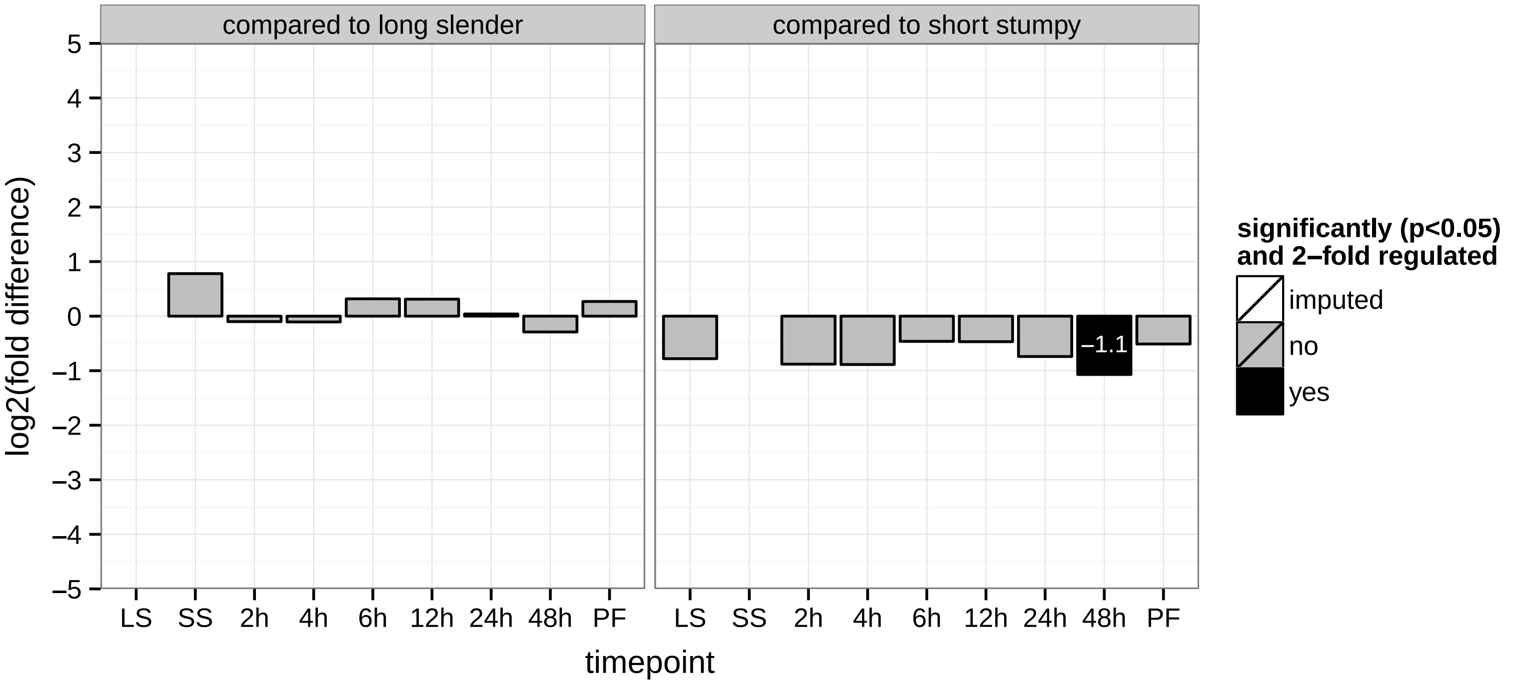
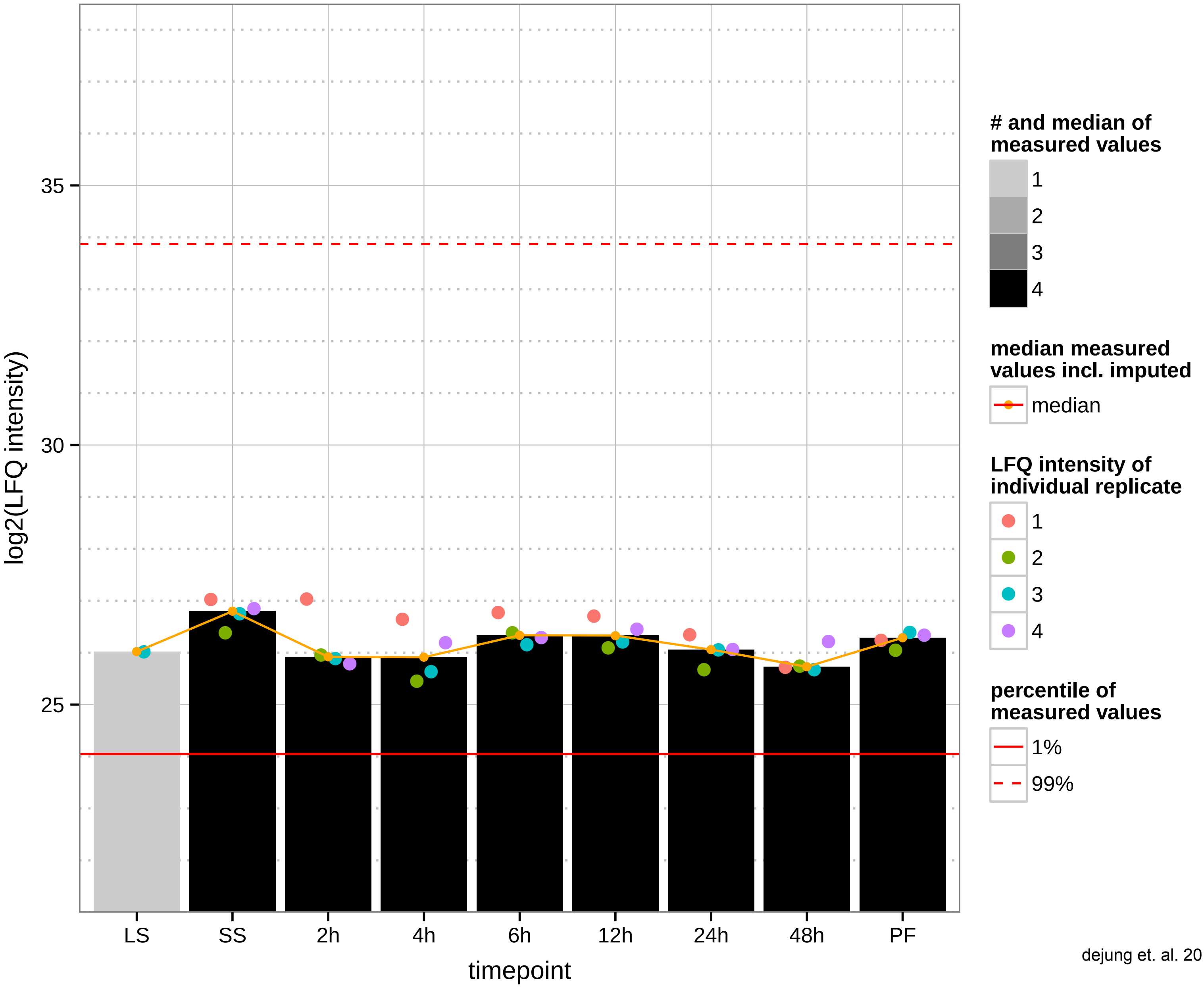
hypothetical protein, conserved
Tb927.11.15970
AGOF: ARF guanyl–nucleotide exchange factor activity
AGOC: intracellular
AGOP: regulation of ARF protein signal transduction
PGOF: ARF guanyl–nucleotide exchange factor activity
PGOC: intracellular
PGOP: regulation of ARF protein signal transduction





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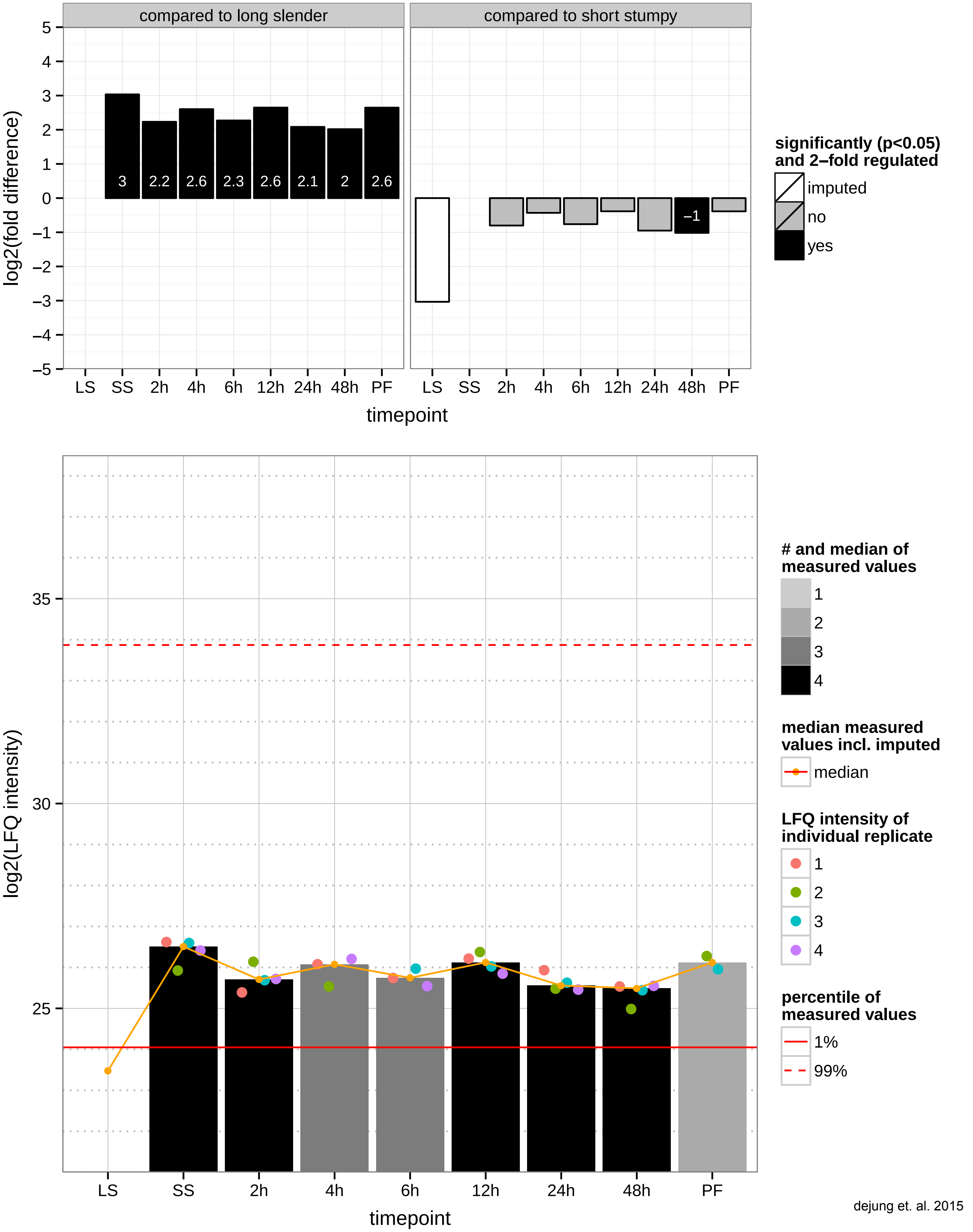
hypothetical protein, conserved
Tb927.11.16490
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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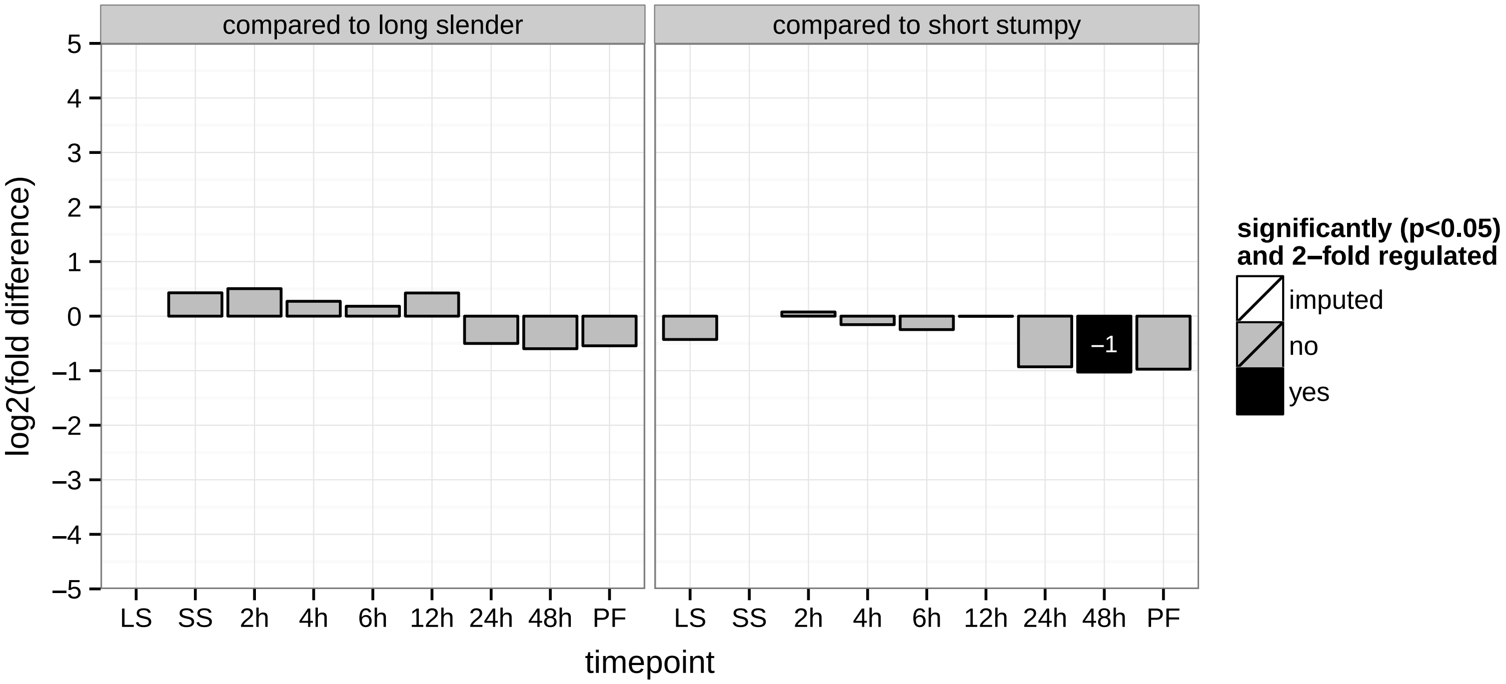
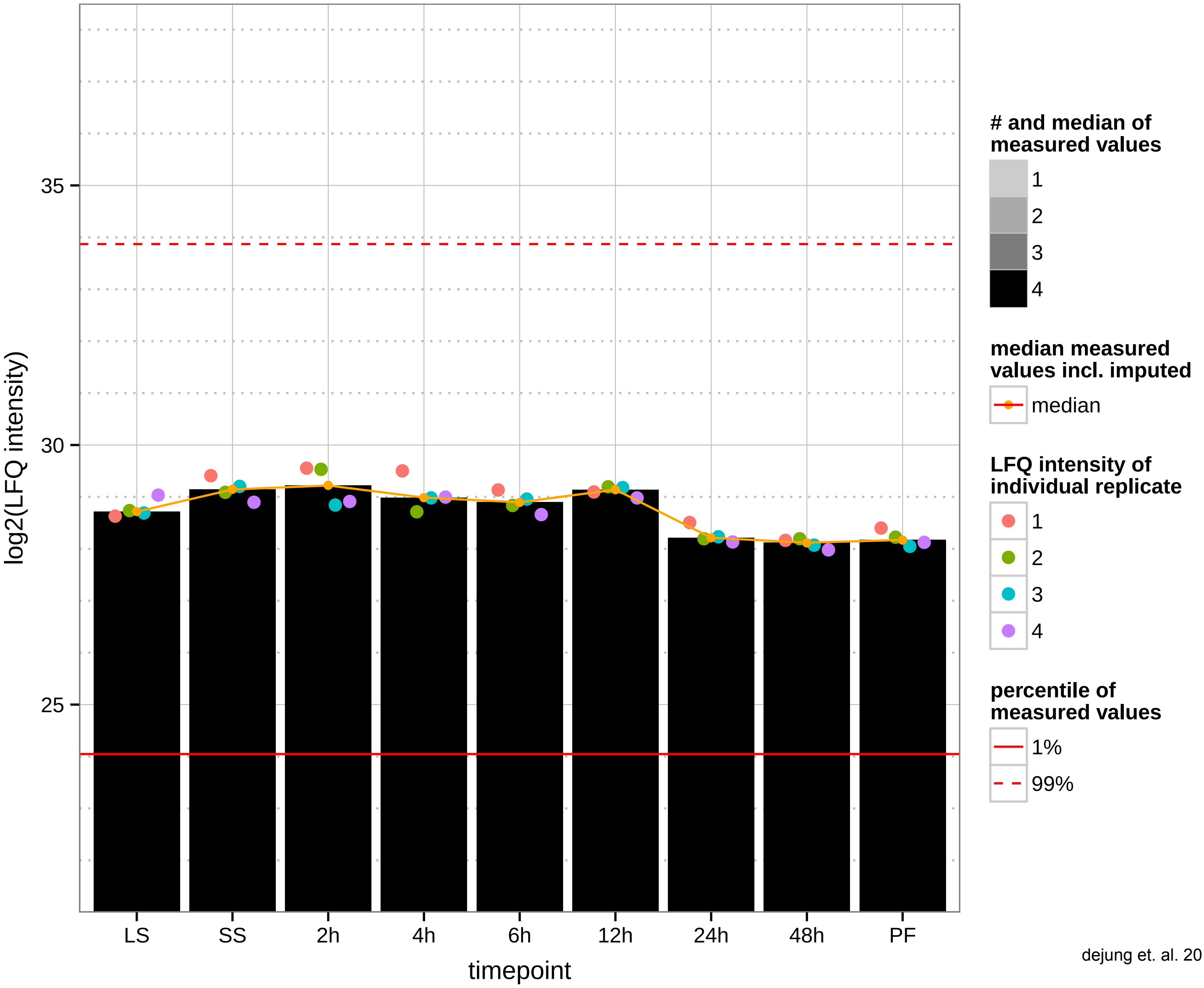
hypothetical protein, conserved
Tb927.11.8060
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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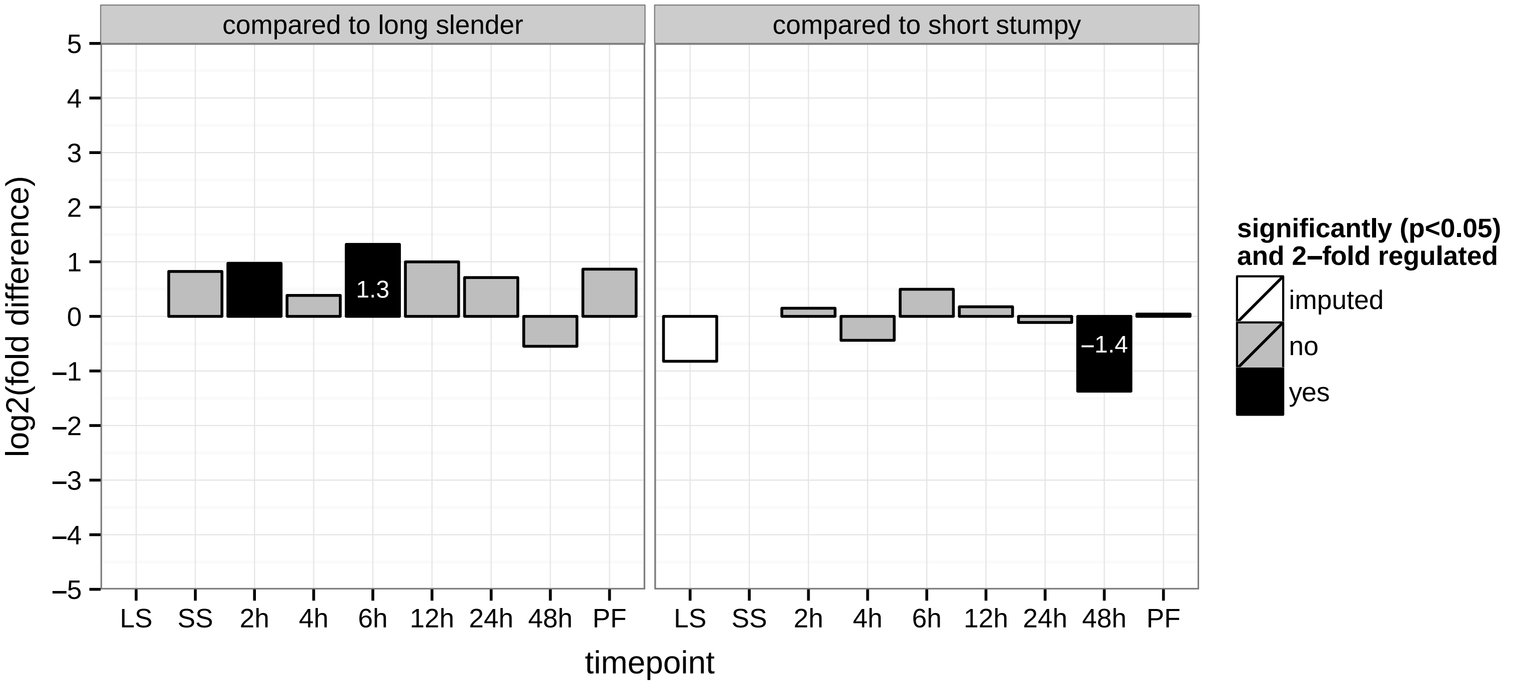
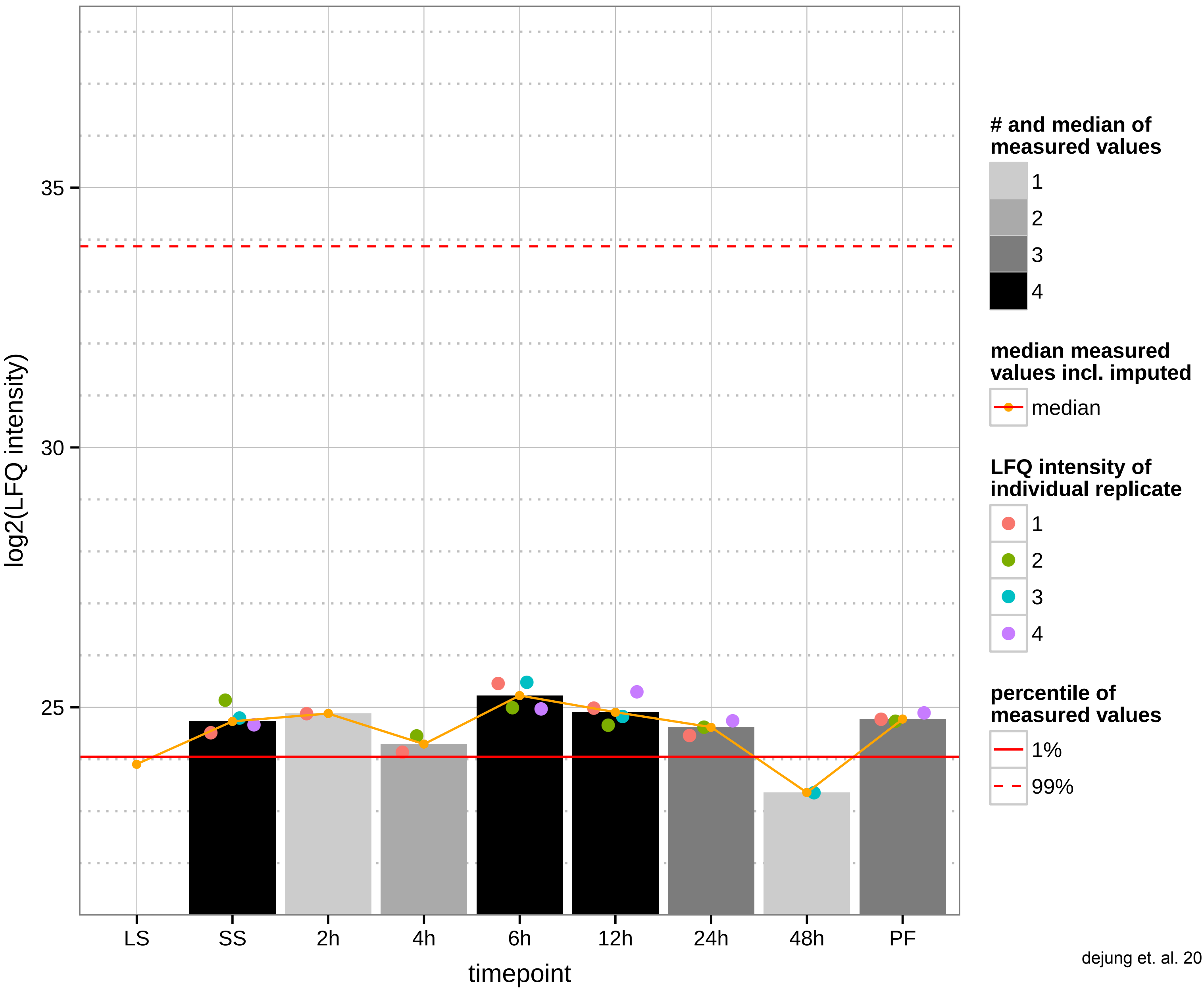
hypothetical protein, conserved
Tb927.11.9650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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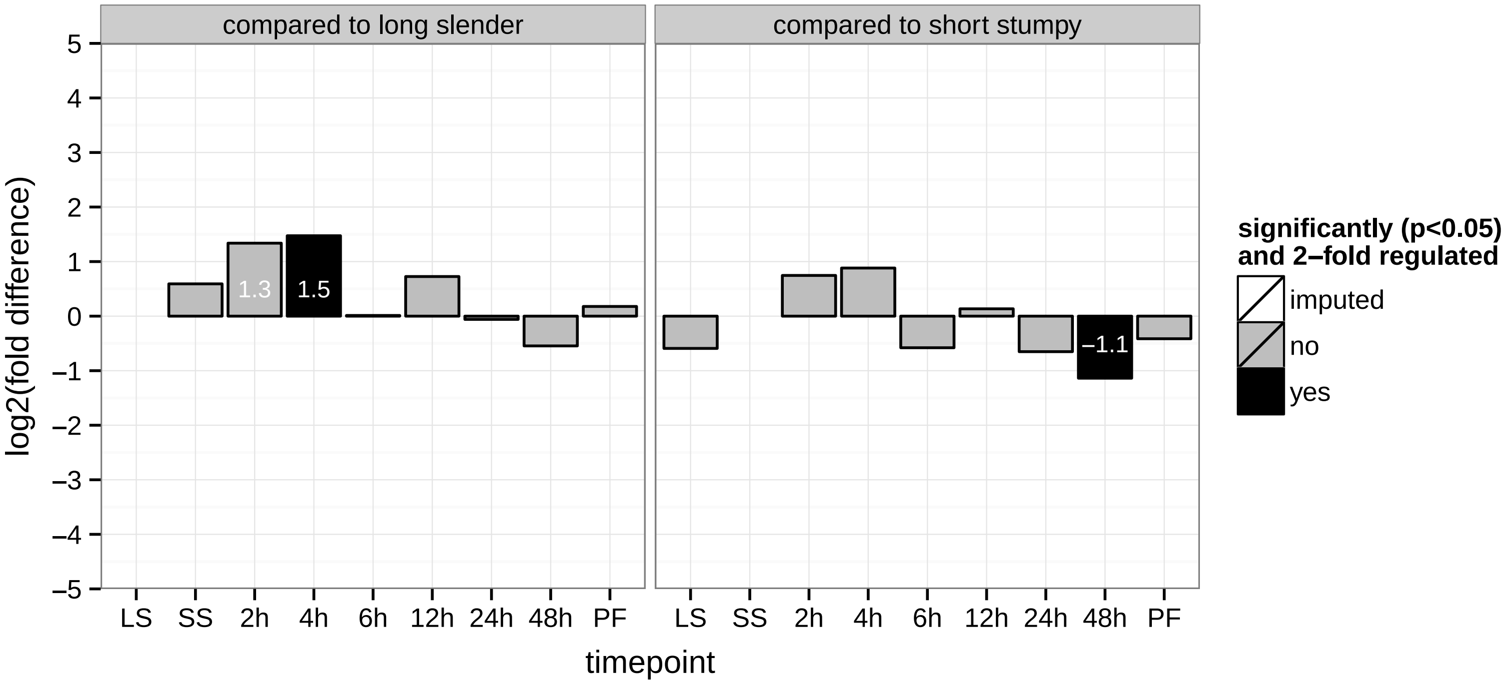
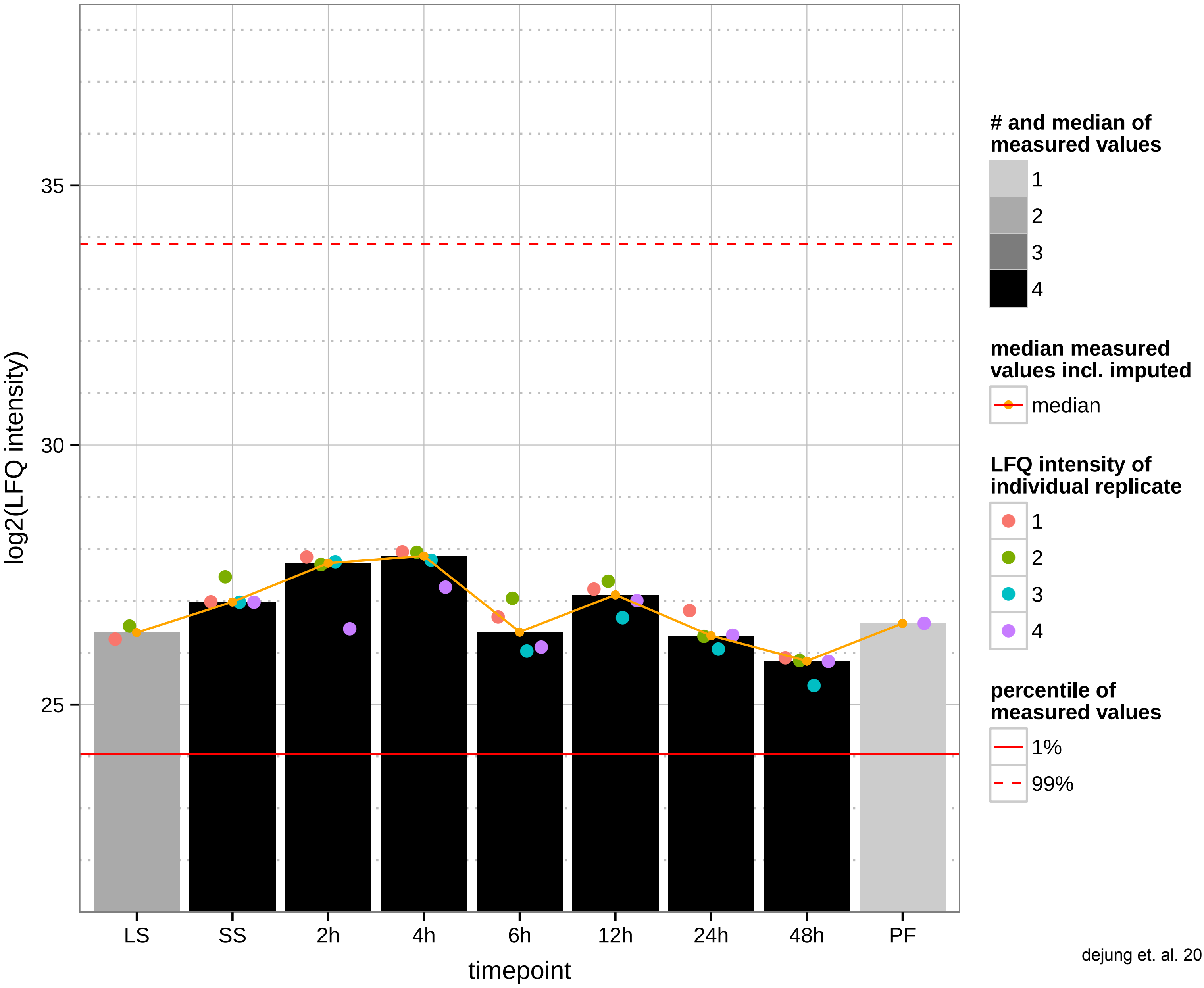
G–actin binding protein, putative, twinfilin
Tb927.4.2350
AGOF: actin binding
AGOC: intracellular
AGOP: null
PGOF: actin binding
PGOC: intracellular
PGOP: null





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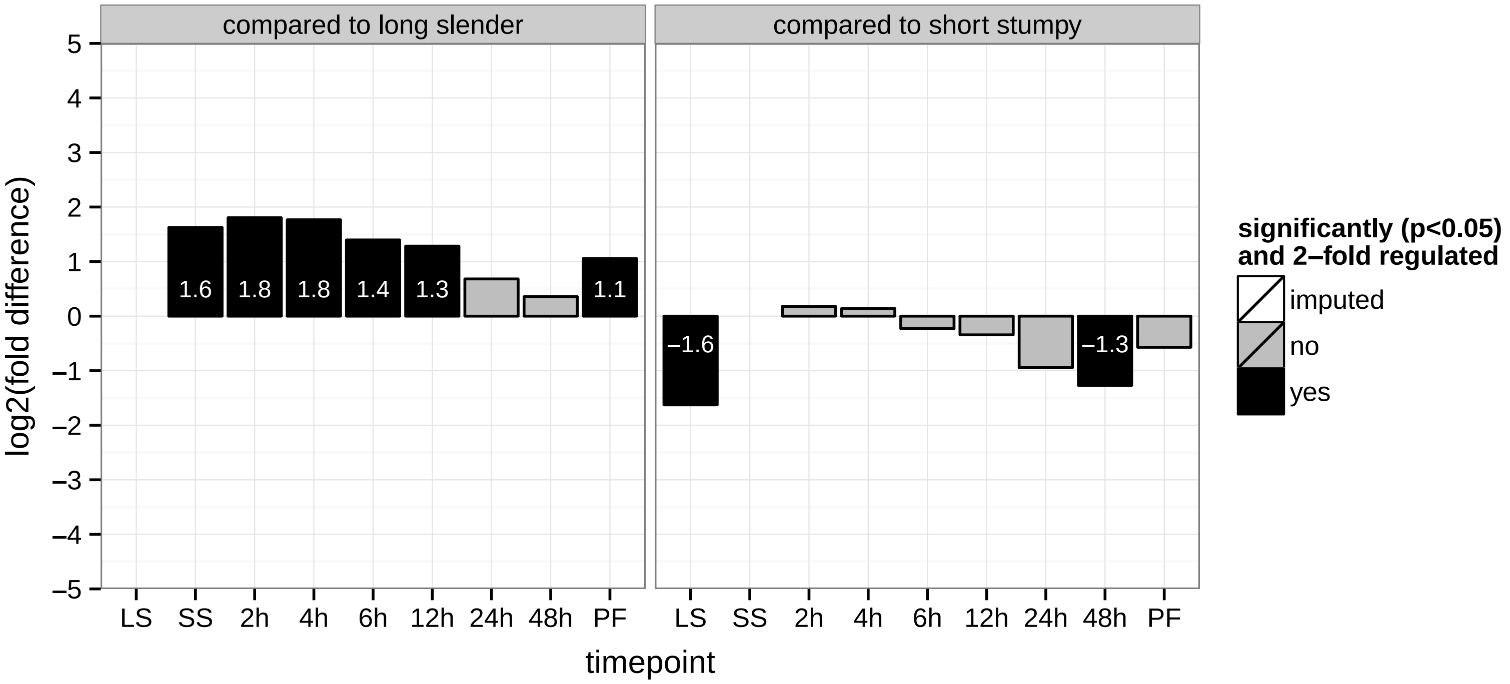
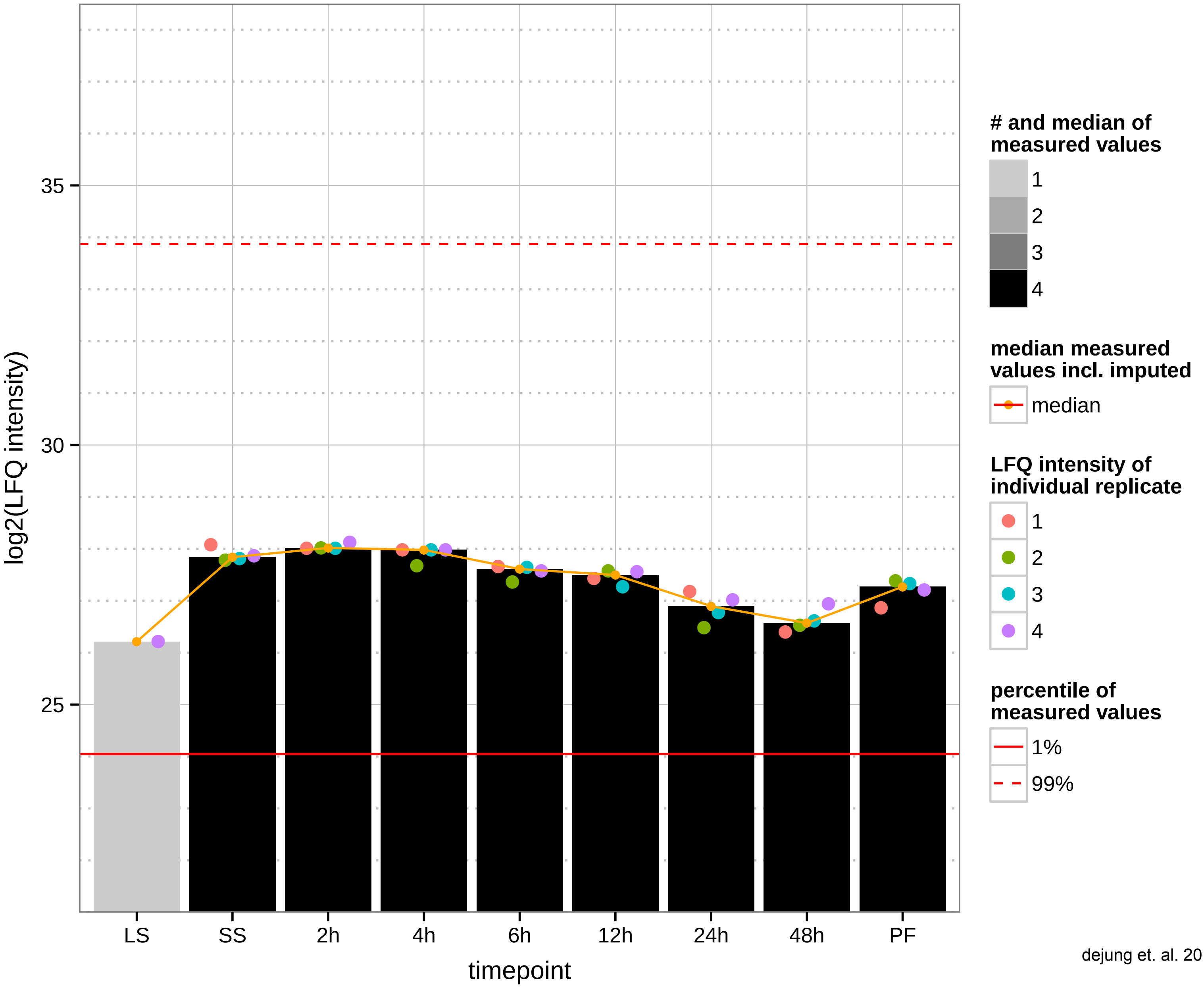
hypothetical protein, conserved
Tb927.4.3350
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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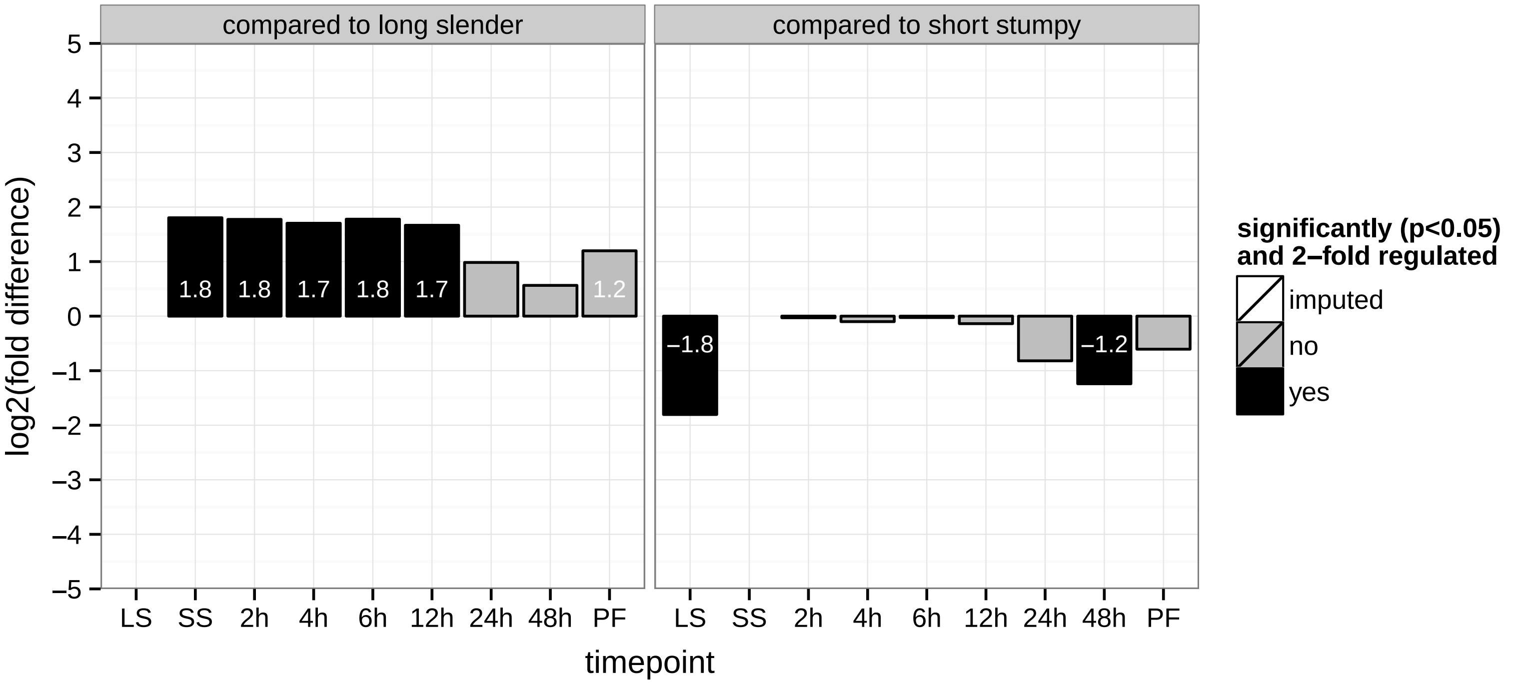
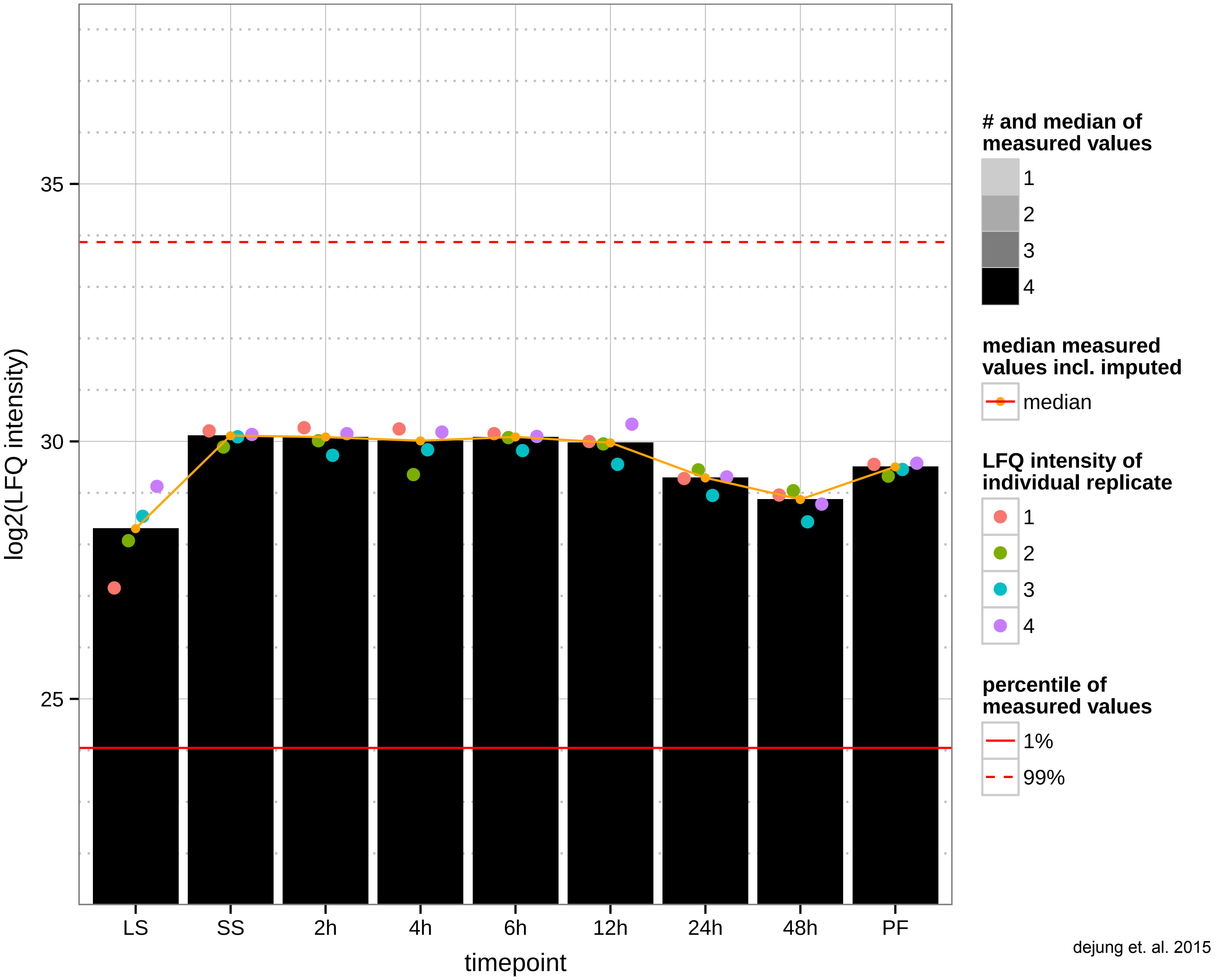
vacuolar proton translocating ATPase subunit A, putative
Tb927.5.1300
AGOF: hydrogen ion transmembrane transporter activity
AGOC: proton−transporting two−sector ATPase complex, proton−transporting domain
AGOP: ATP synthesis coupled proton transport
PGOF: hydrogen ion transmembrane transporter activity
PGOC: proton−transporting two−sector ATPase complex, proton−transporting domain, vacuolar proton−transporting V−type A
PGOP: ATP hydrolysis coupled proton transport





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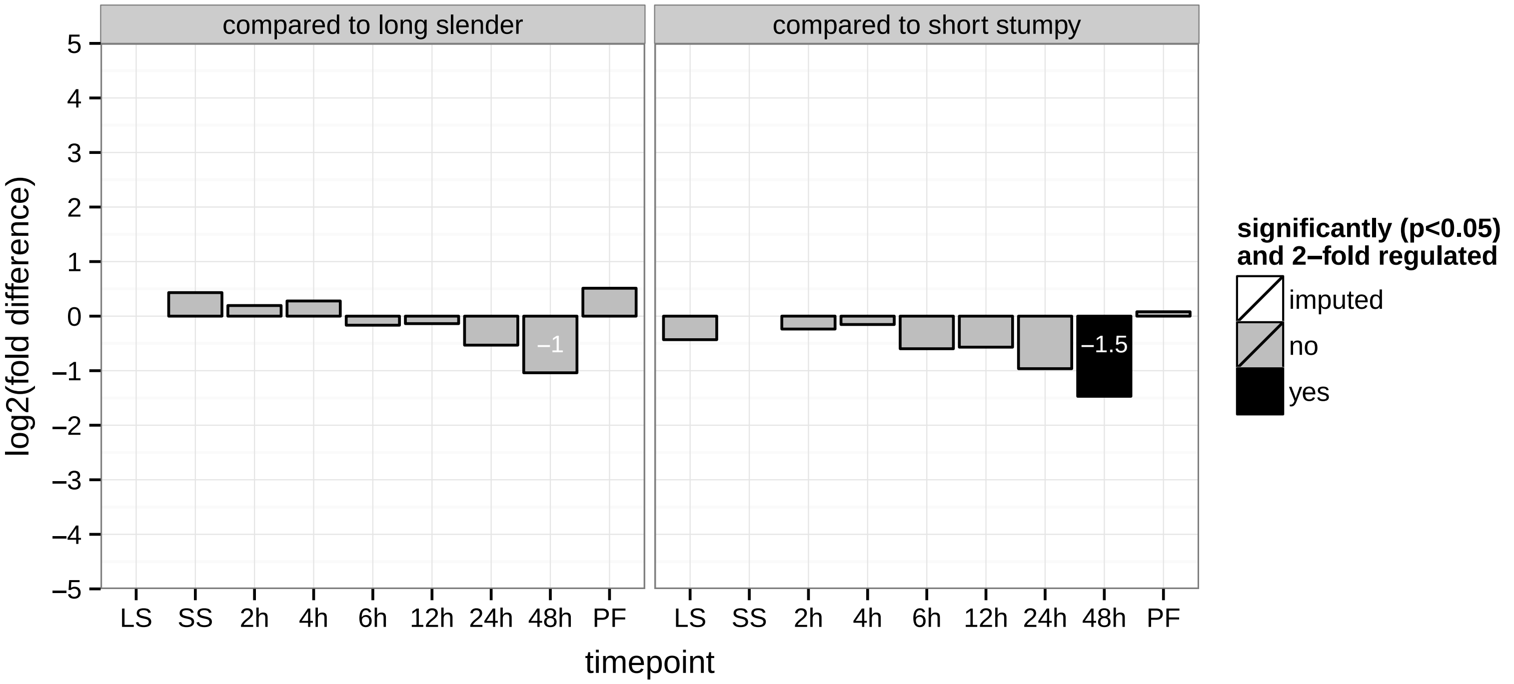
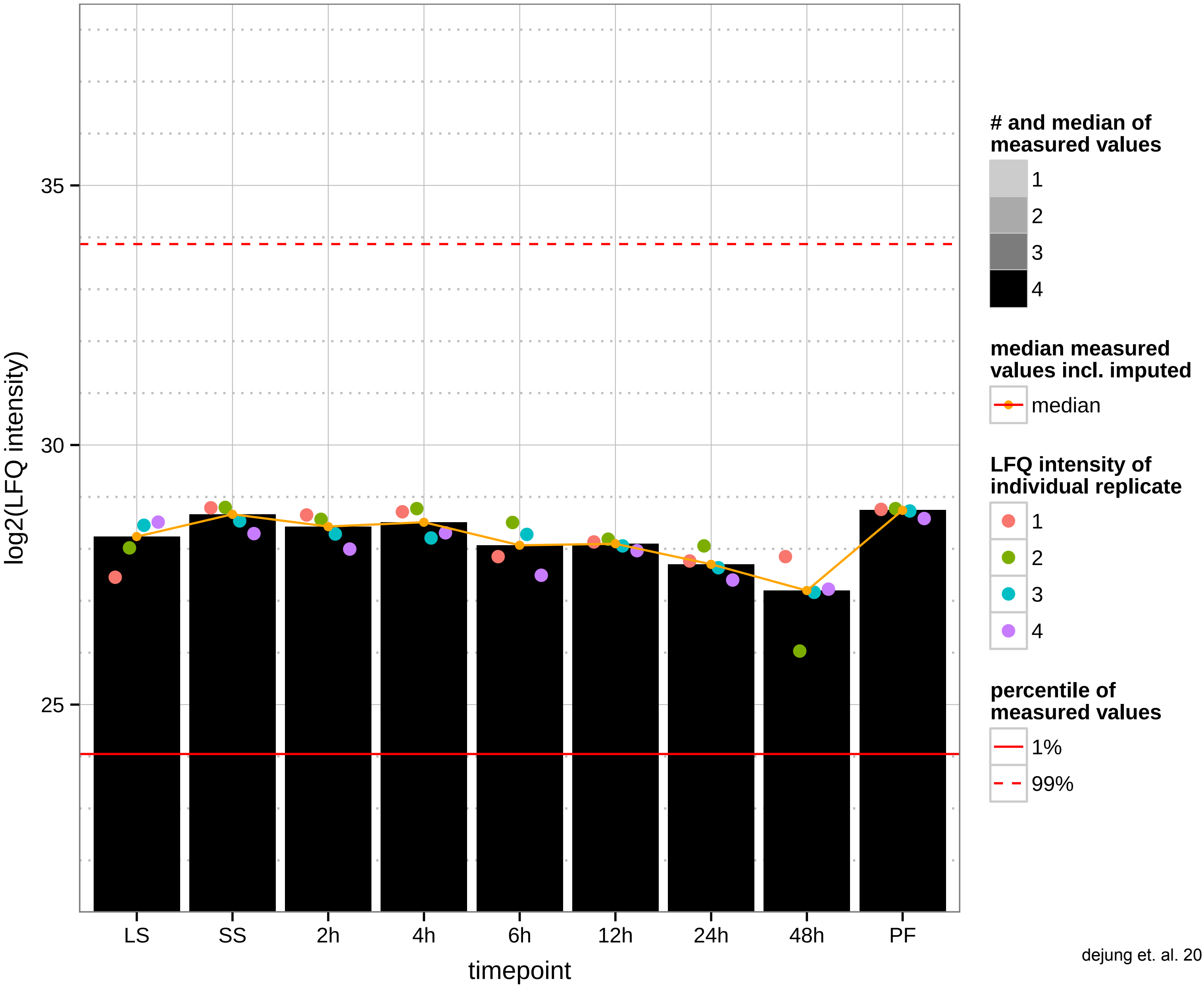
signal peptidase type I, putative, serine peptidase, Clan SF, Family S26A
Tb927.5.3220
AGOF: peptidase activity
AGOC: membrane
AGOP: proteolysis, signal peptide processing
PGOF: peptidase activity
PGOC: membrane
PGOP: signal peptide processing





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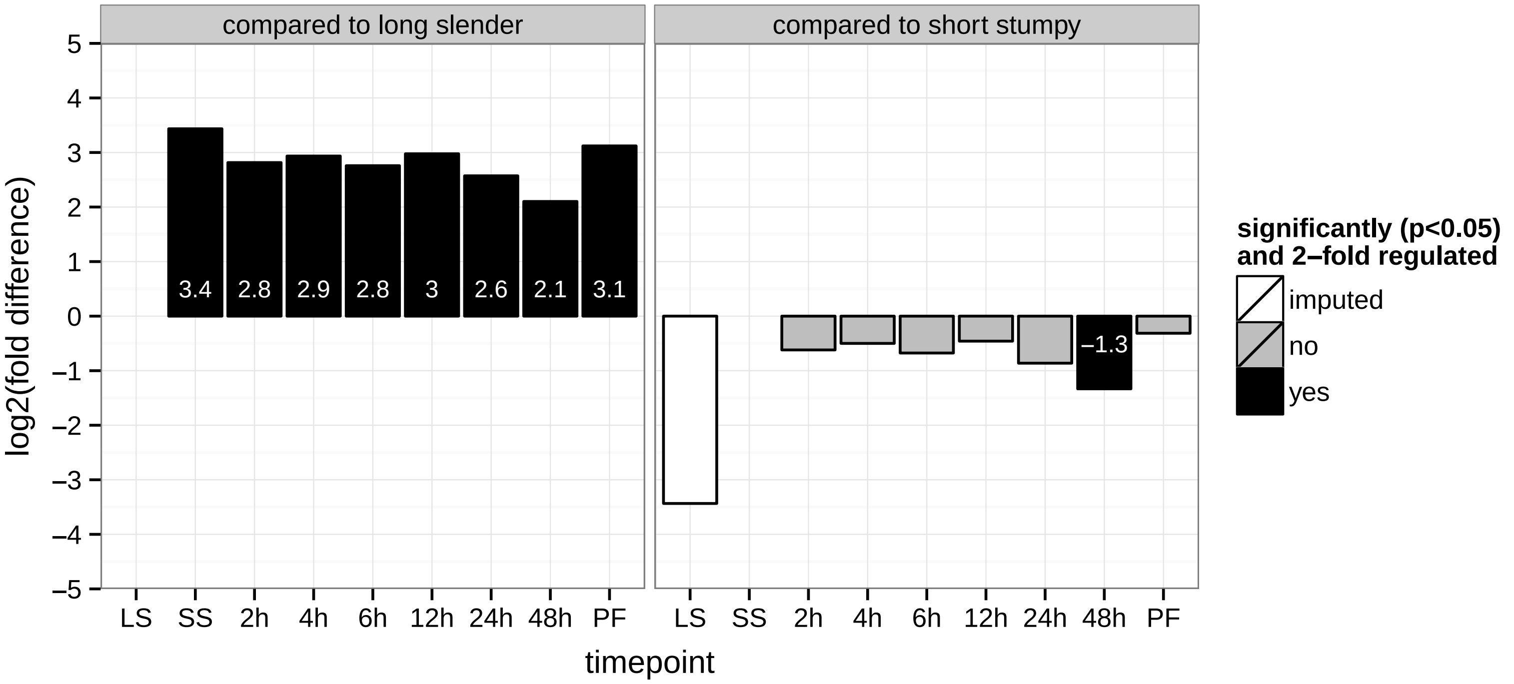
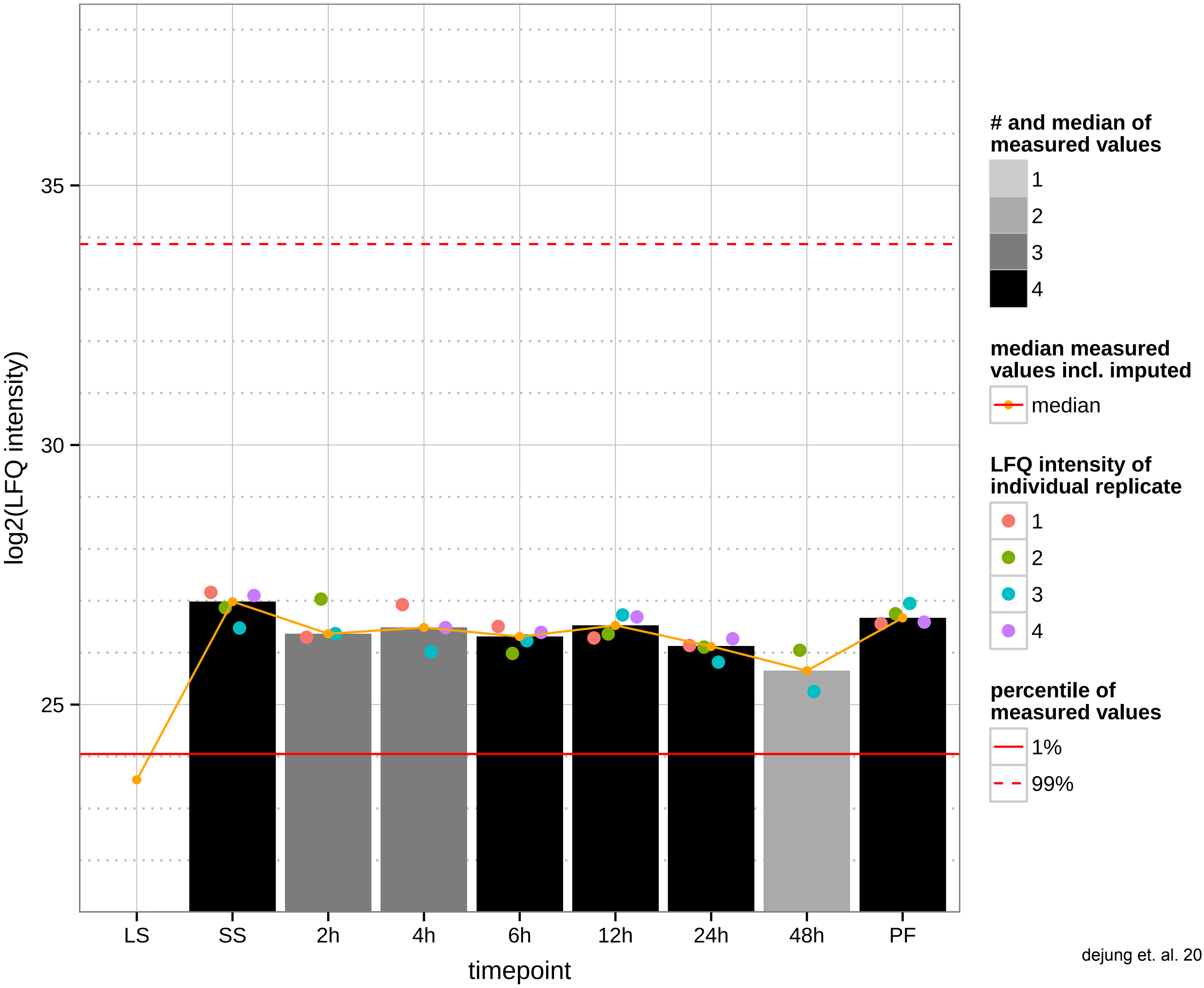
hypothetical protein, conserved
Tb927.6.3610
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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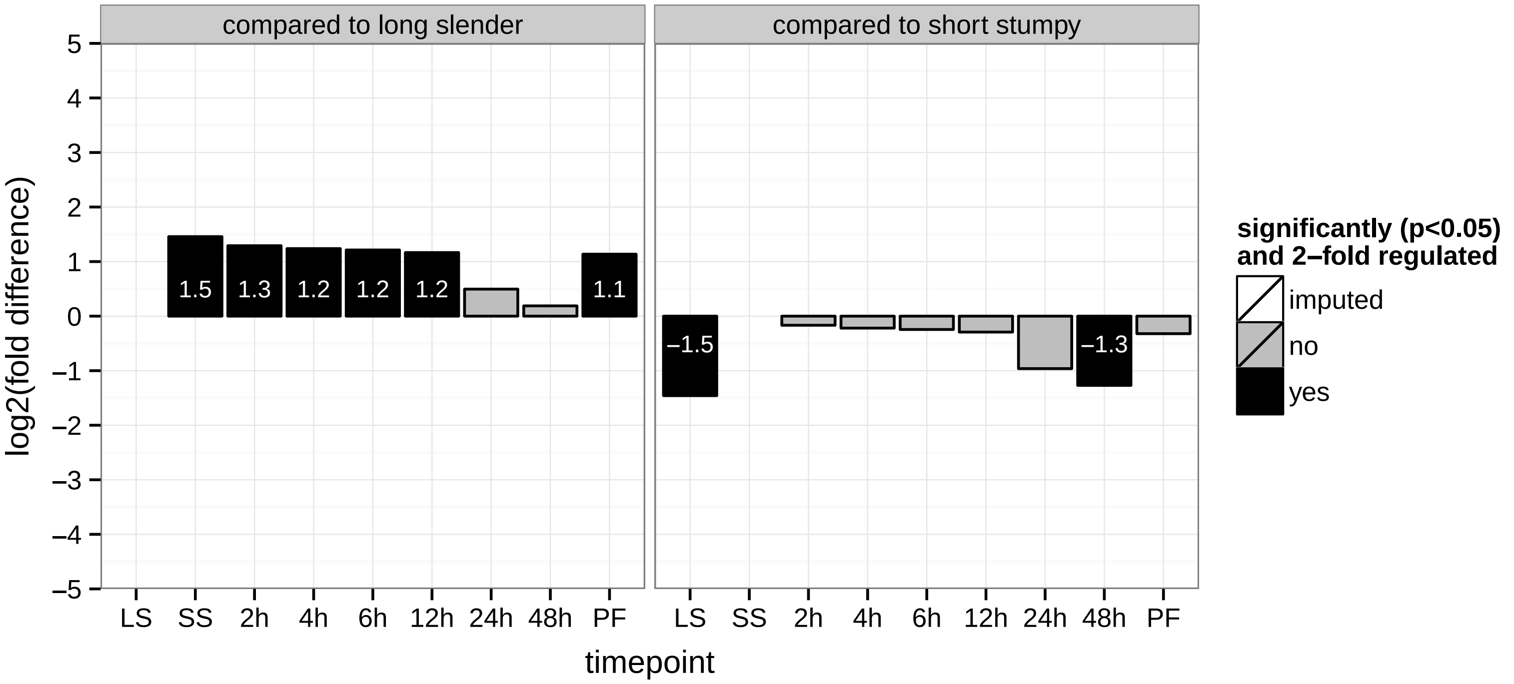
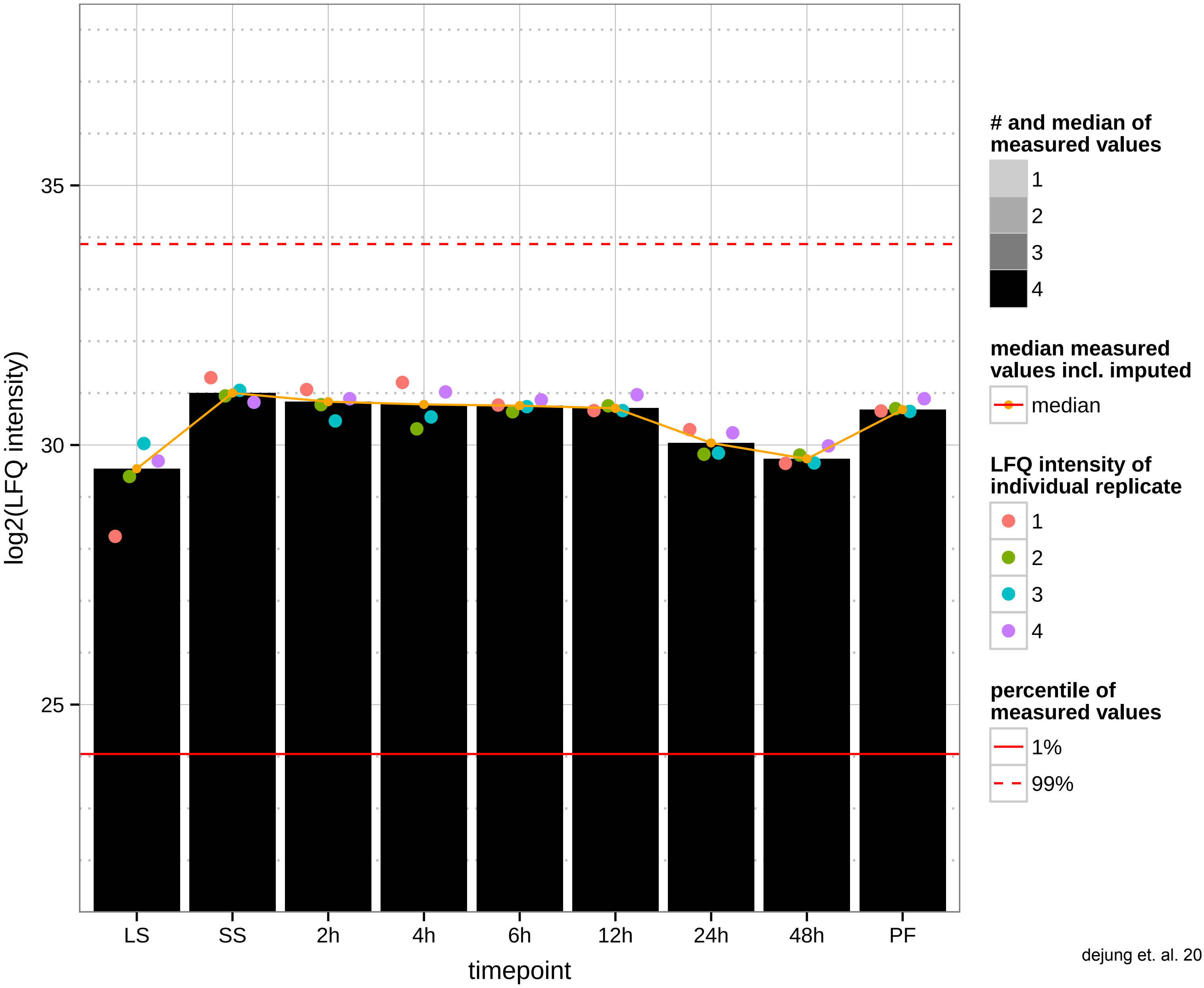
peptidase M20/M25/M40, putative
Tb927.6.400
AGOF: metallopeptidase activity
AGOC: null
AGOP: proteolysis
PGOF: hydrolase activity
PGOC: null
PGOP: metabolic process





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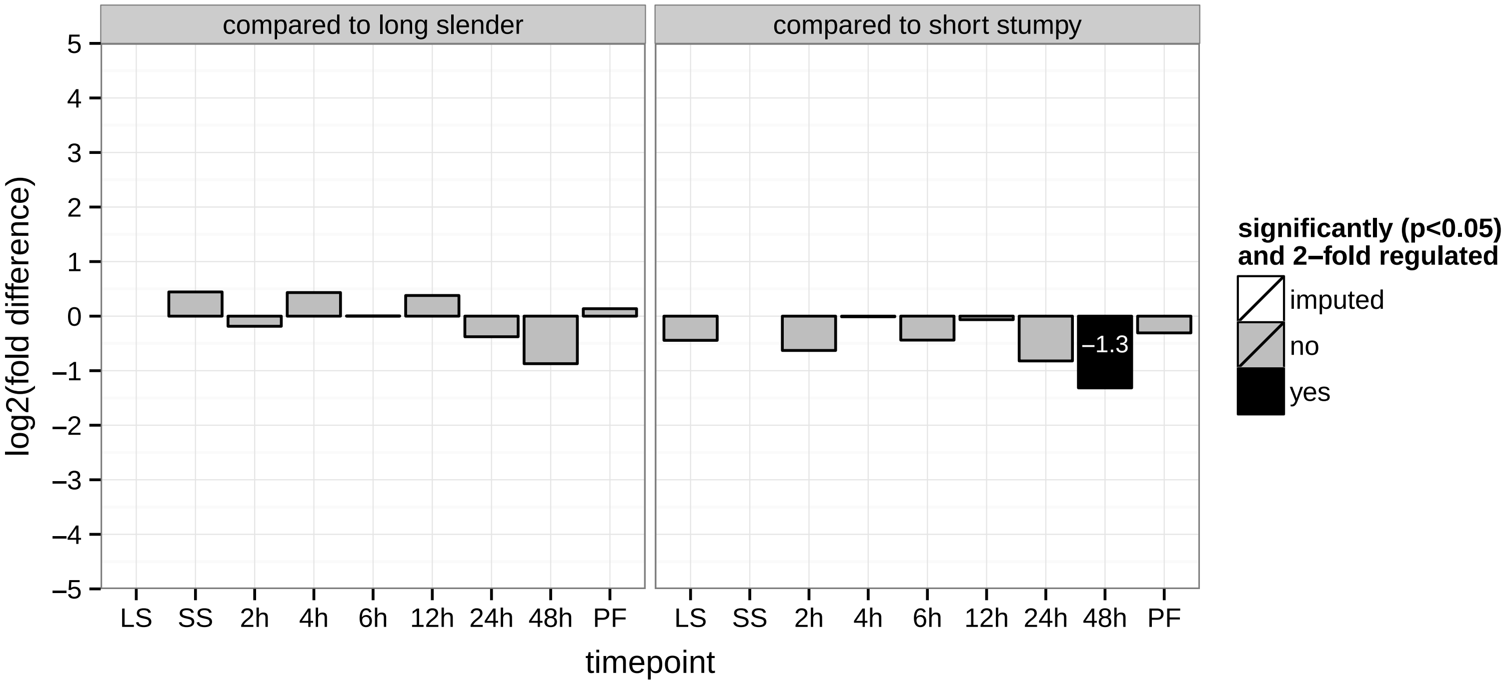
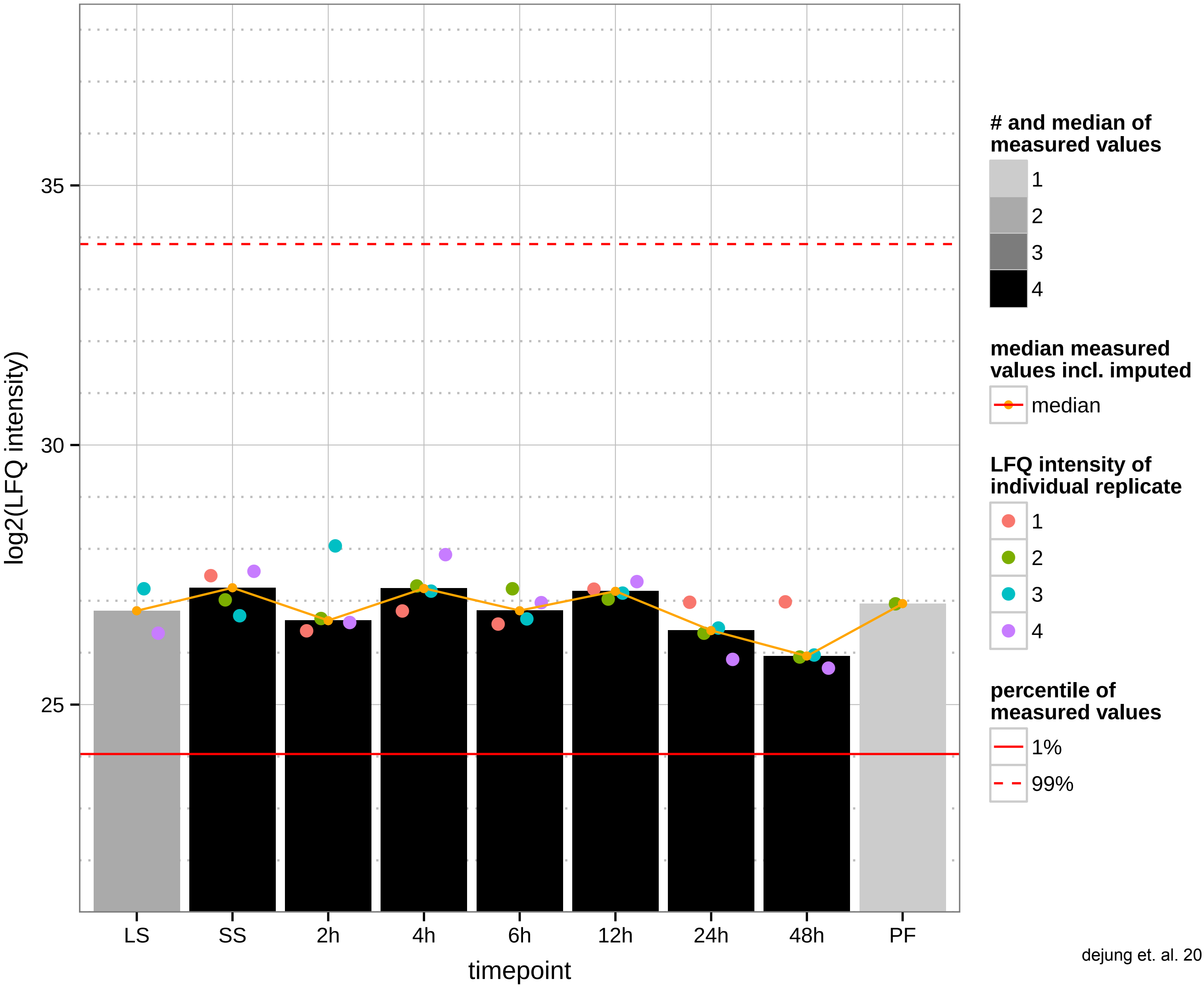
hypothetical protein, conserved
Tb927.6.5010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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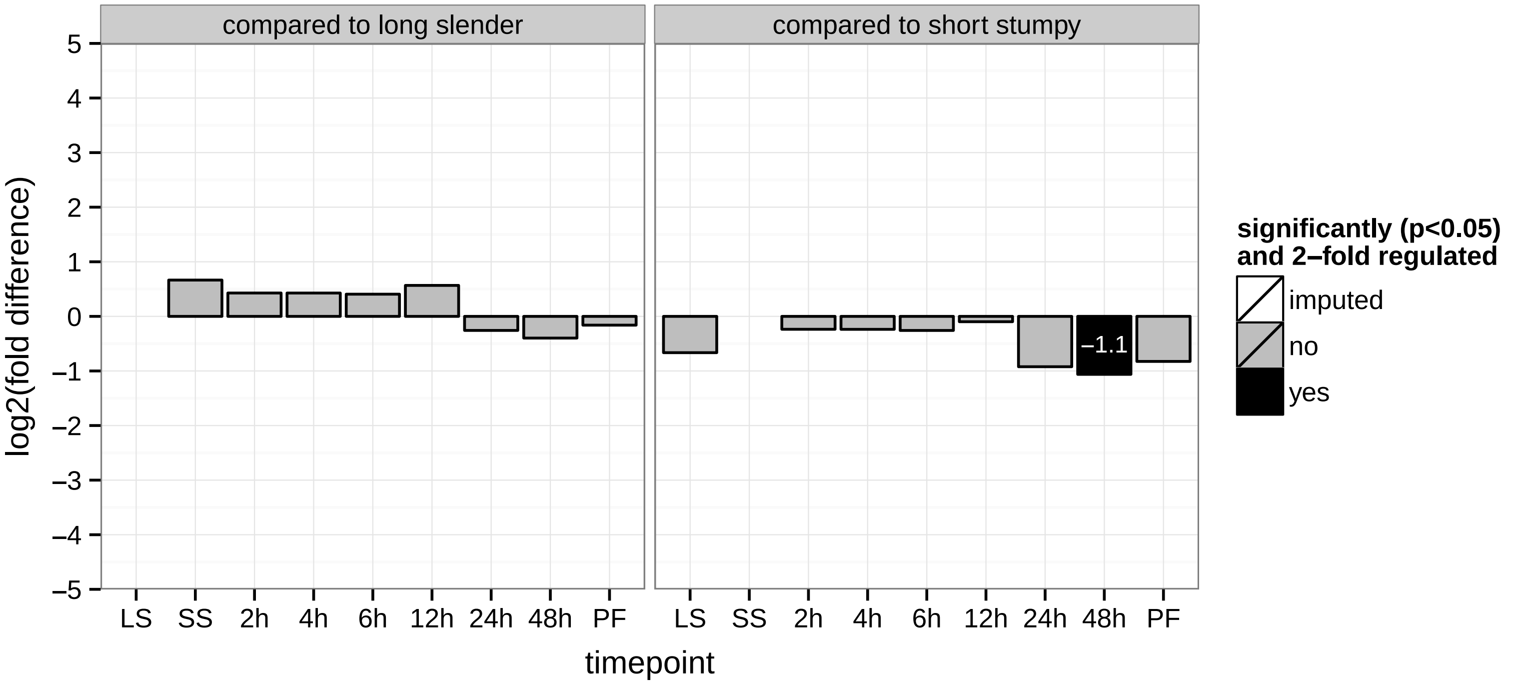
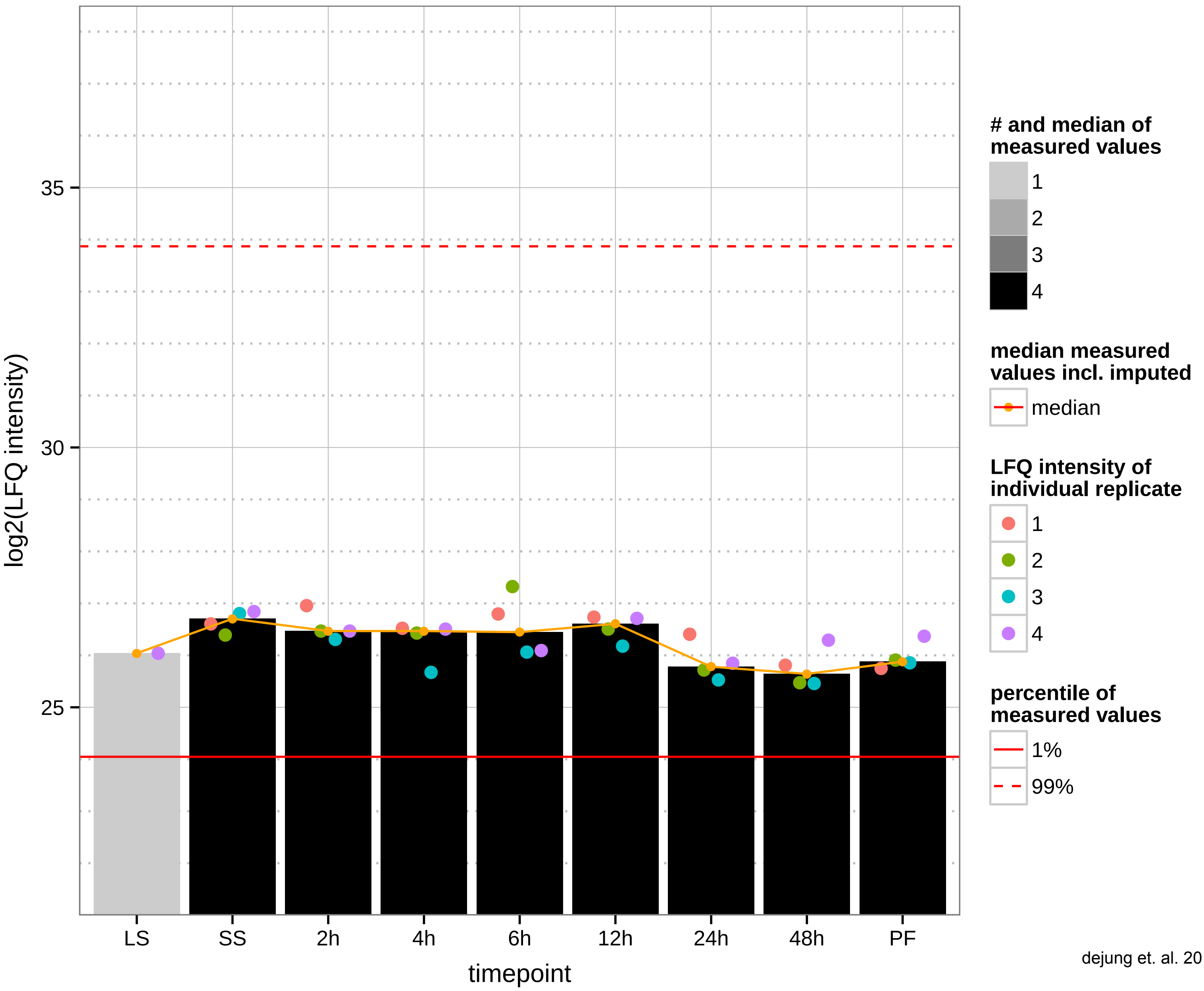
hypothetical protein, conserved
Tb927.7.2950
AGOF: ATP binding, nucleoside−triphosphatase activity
AGOC: null
AGOP: null
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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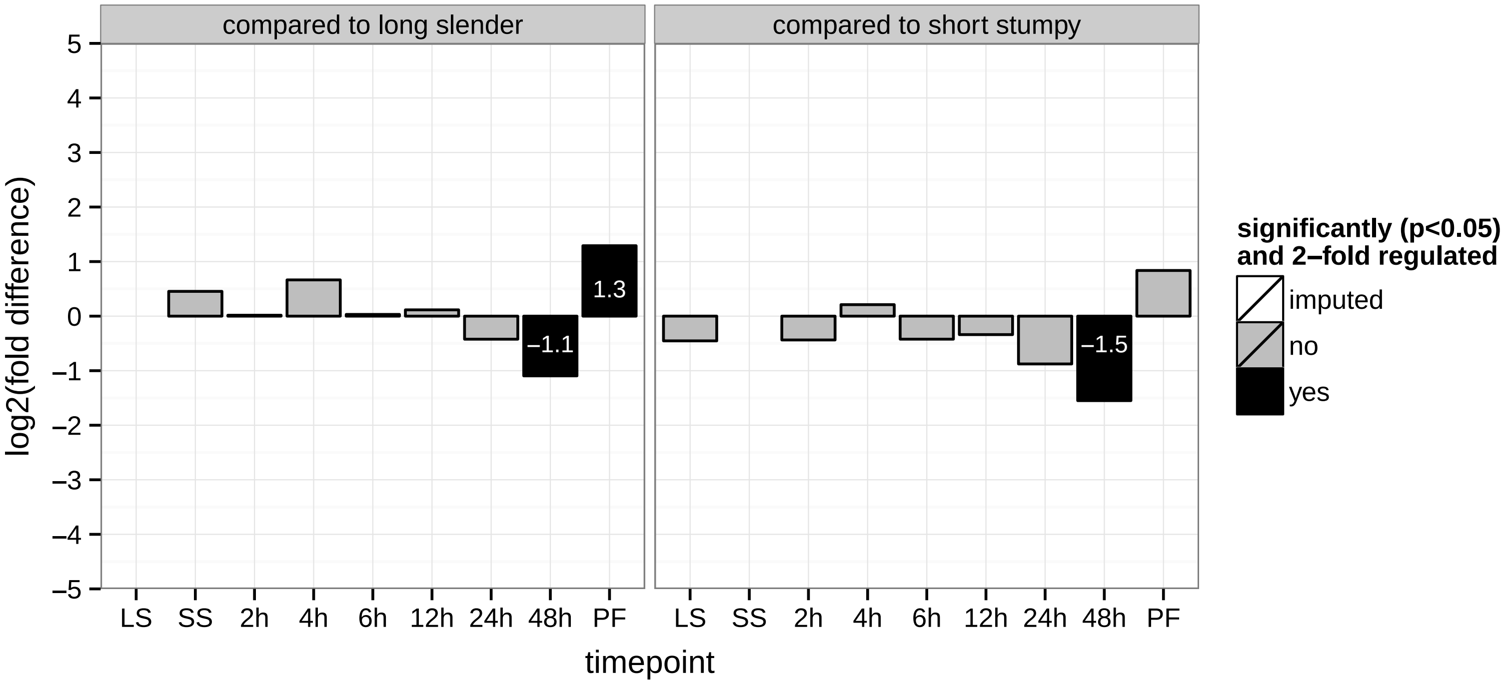
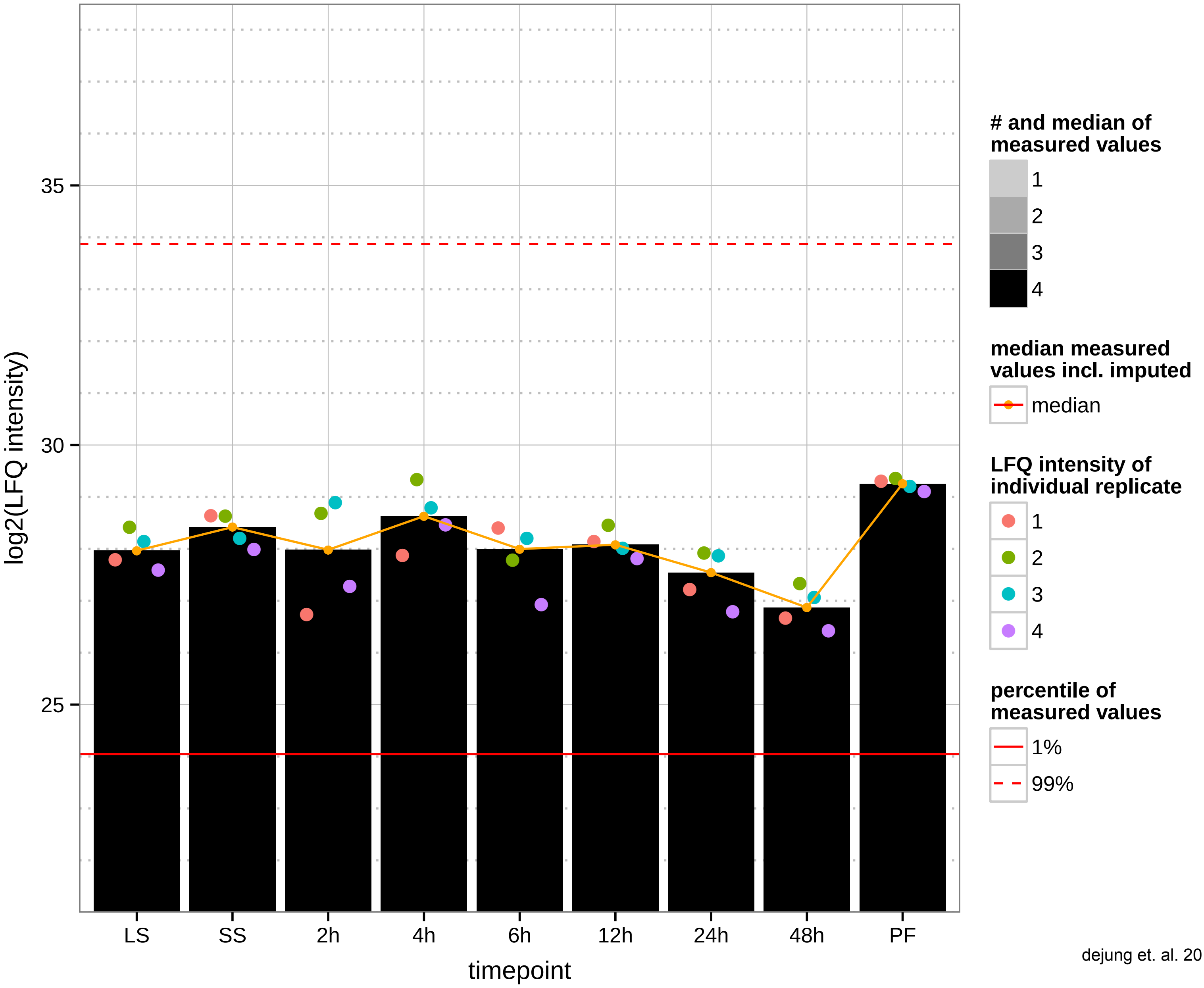
I/6 autoantigen
Tb927.7.3450
AGOF: calcium ion binding, structural constituent of cytoskeleton
AGOC: microtubule cytoskeleton
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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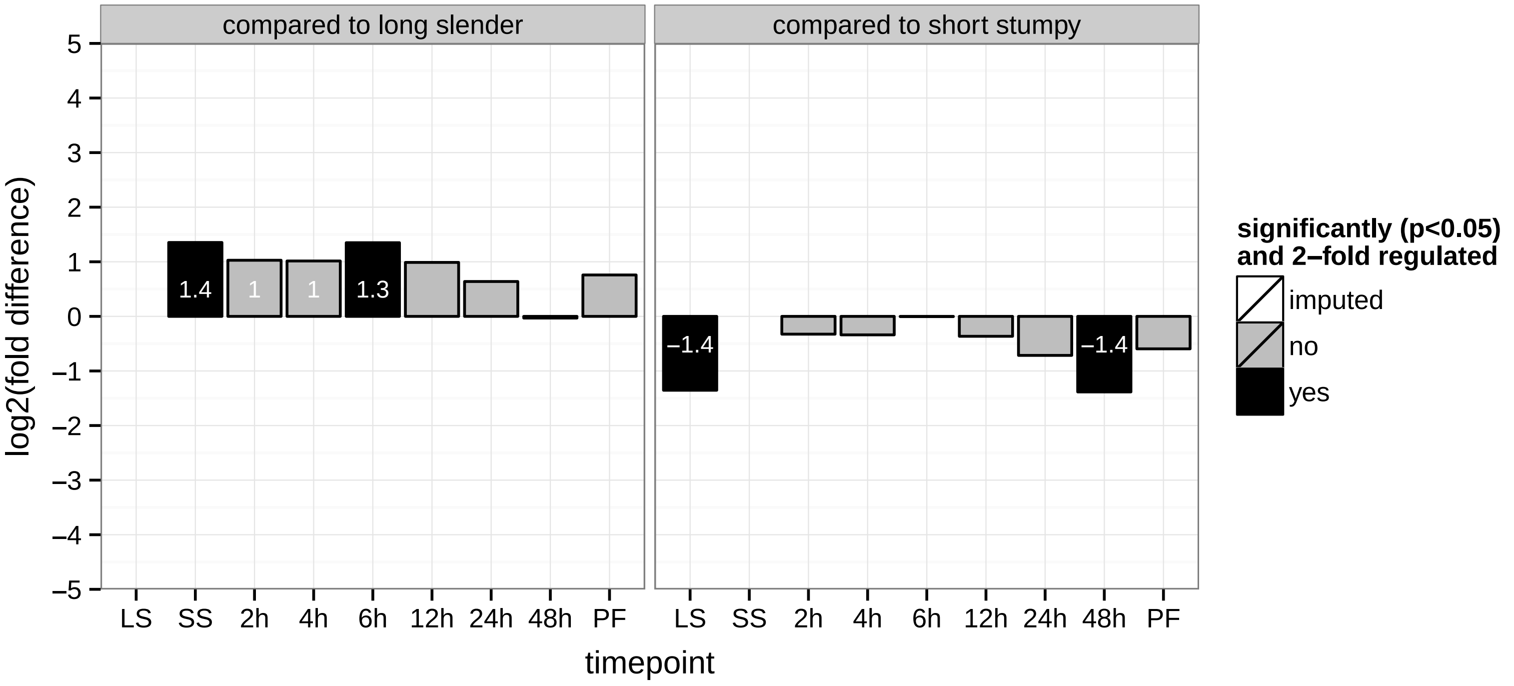
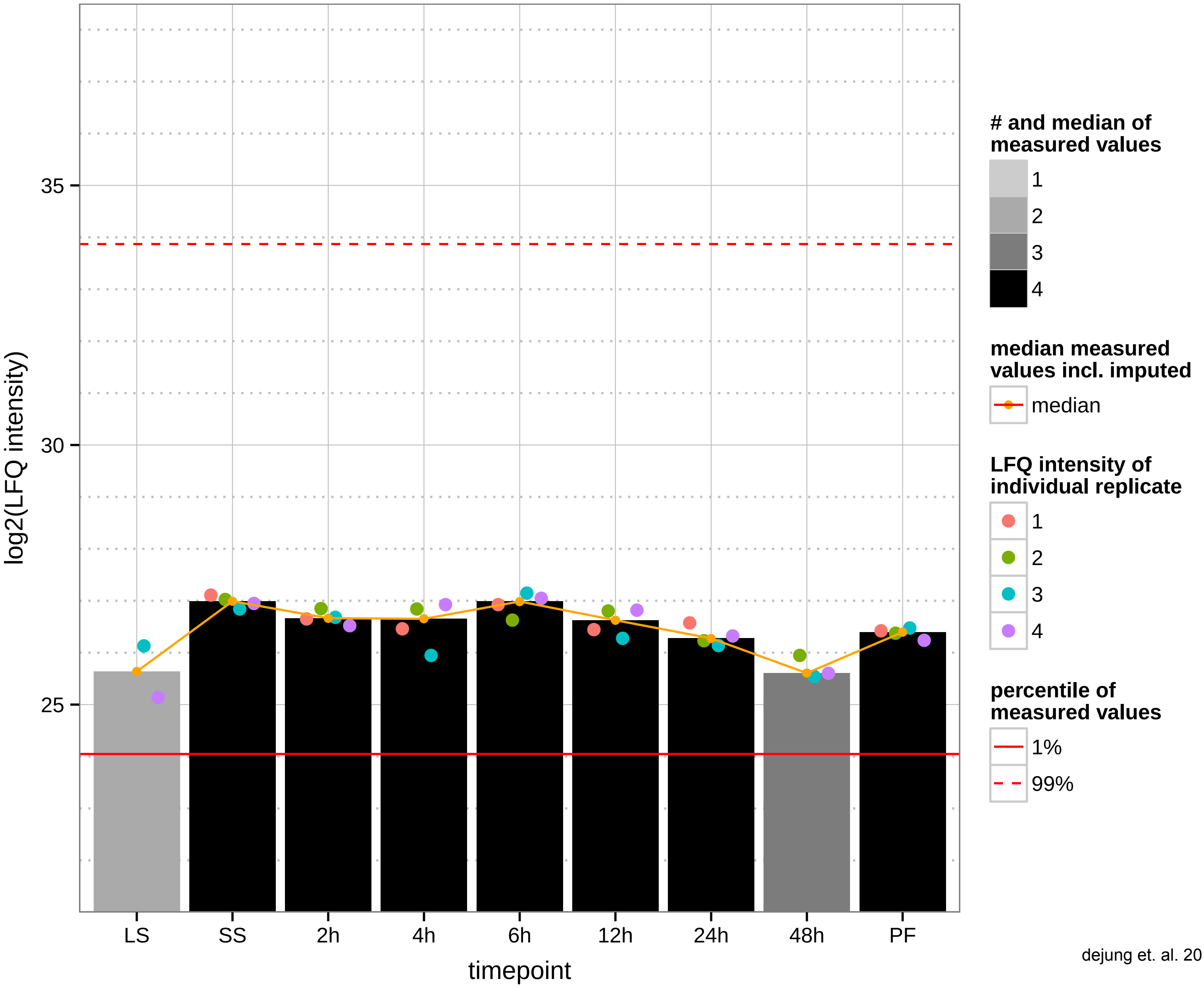
hypothetical protein, conserved
Tb927.7.590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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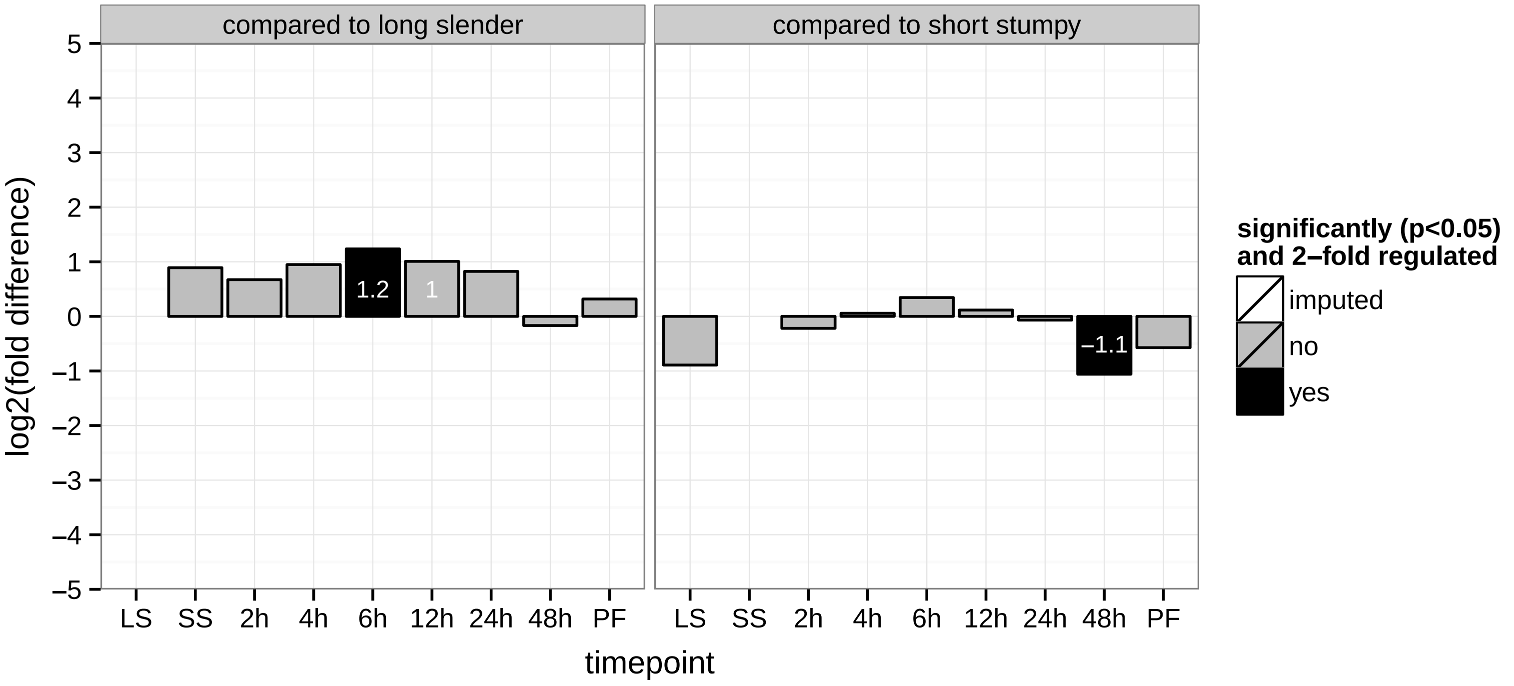
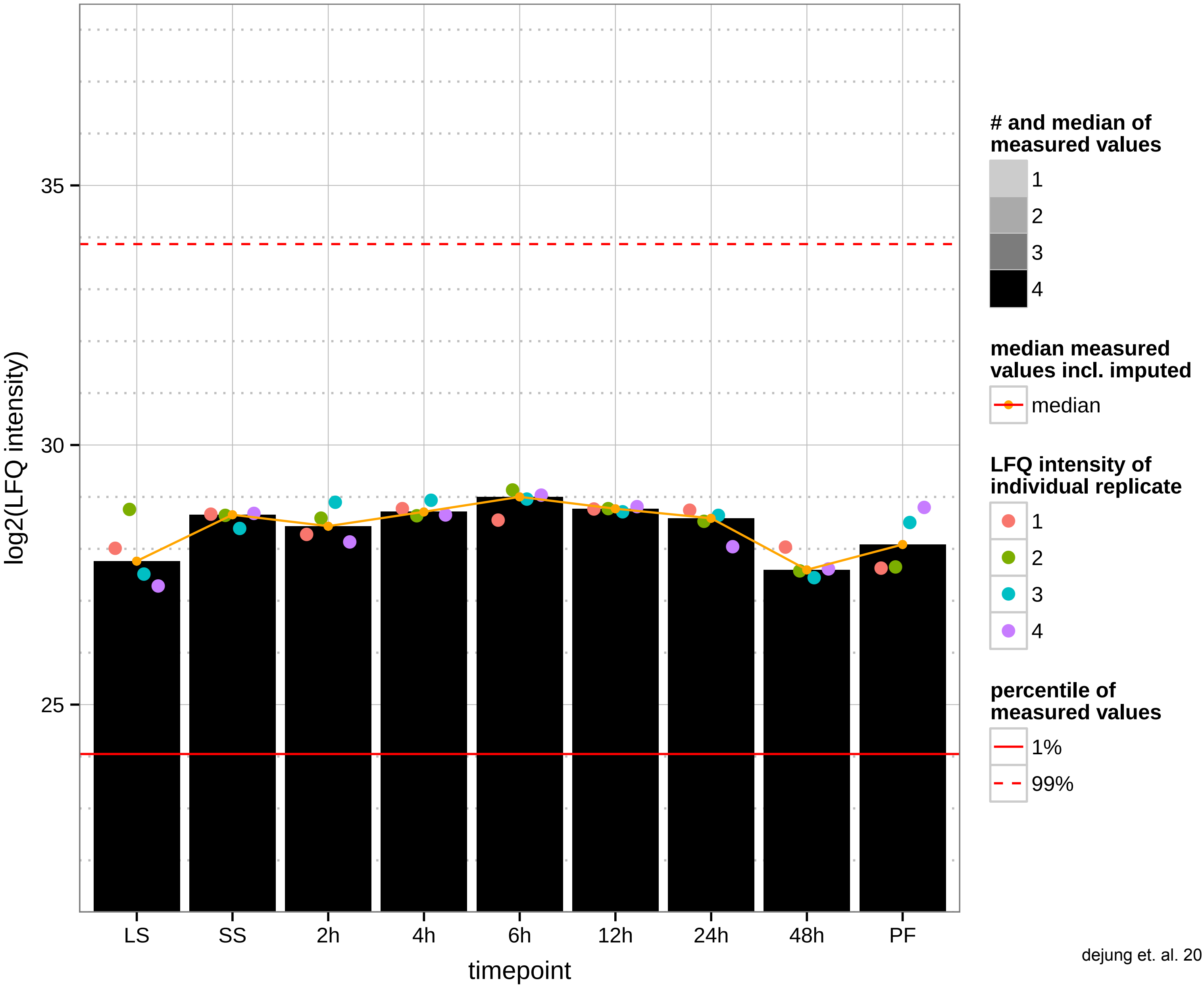
hypothetical protein, conserved
Tb927.8.1210
AGOF: DNA topoisomerase type I activity
AGOC: chromosome
AGOP: DNA topological change
PGOF: null
PGOC: null
PGOP: null





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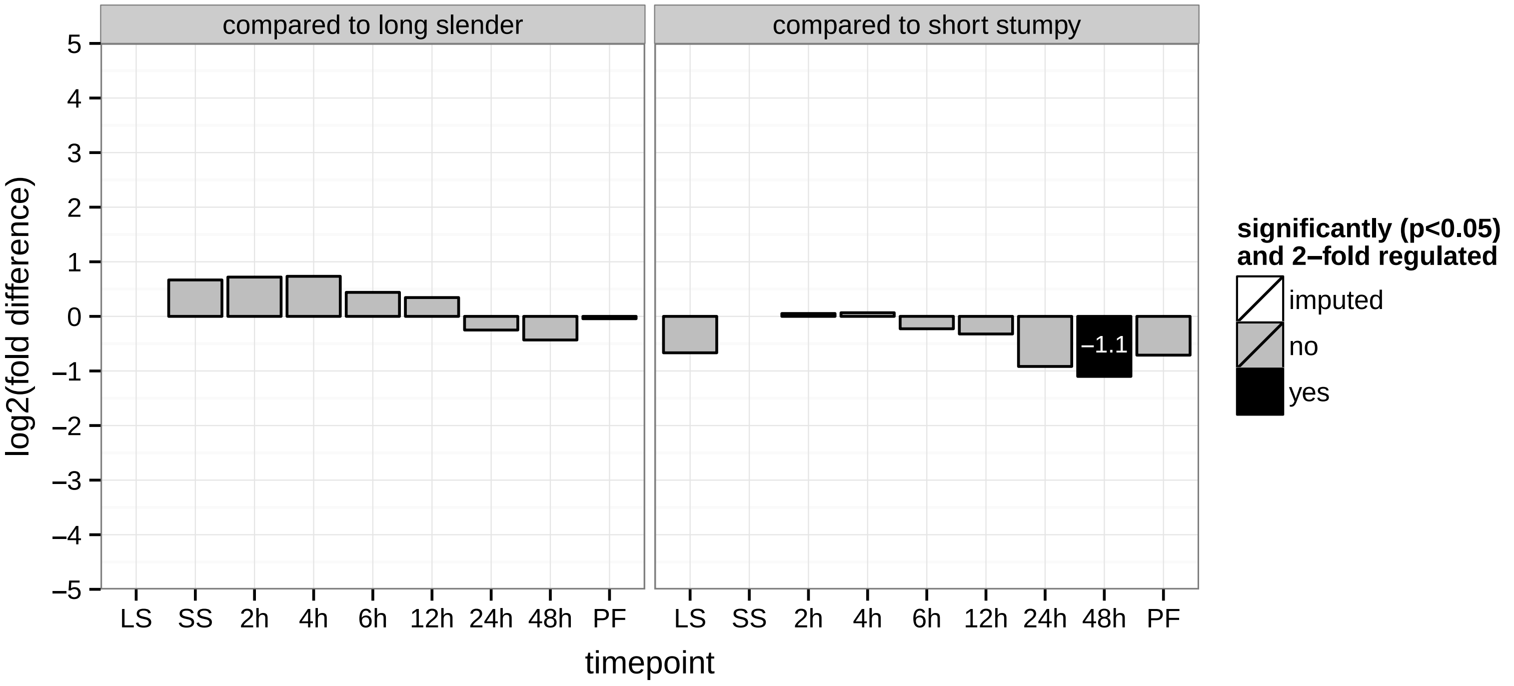
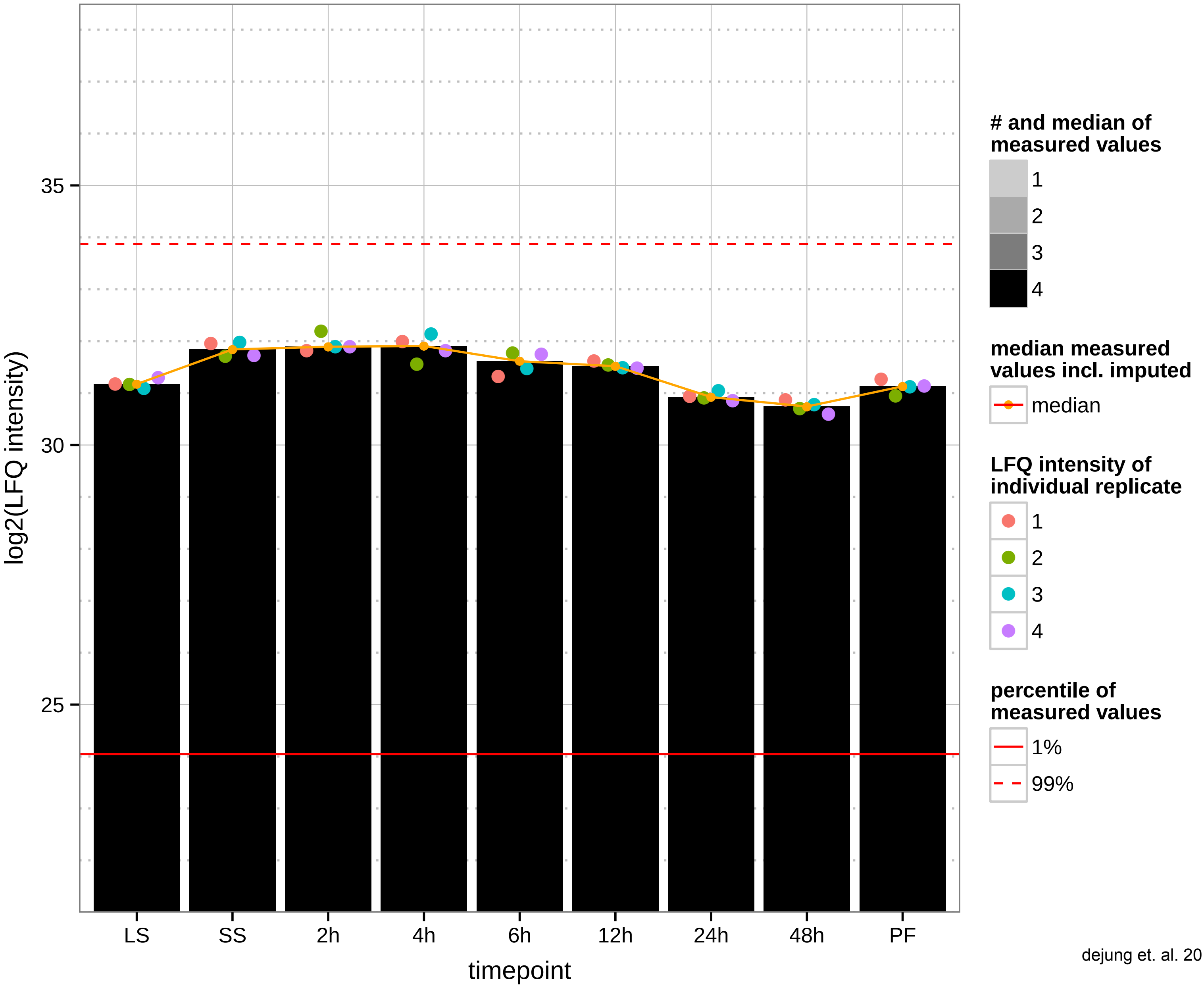
Golgi/lysosome glycoprotein 1 (tGLP1)
Tb927.8.1870
AGOF: null
AGOC: Golgi apparatus, lysosomal membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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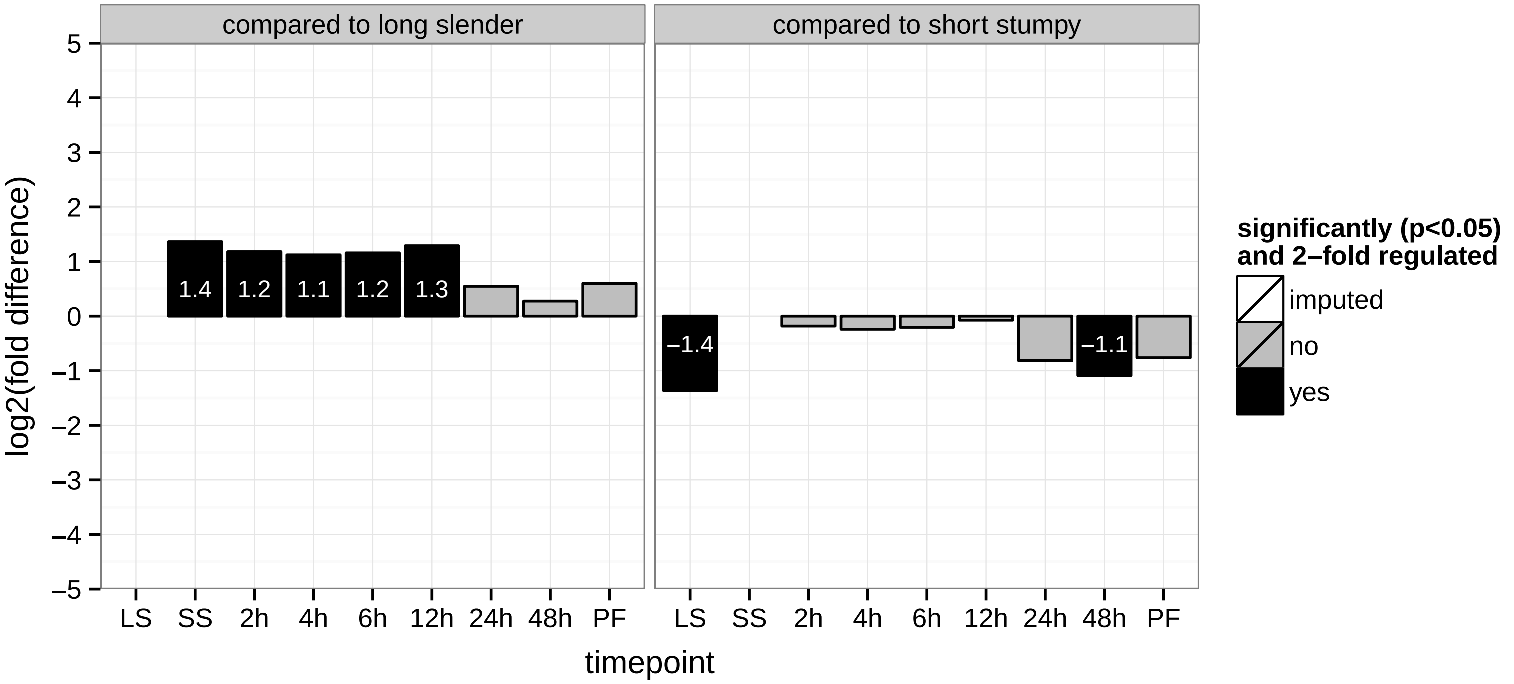
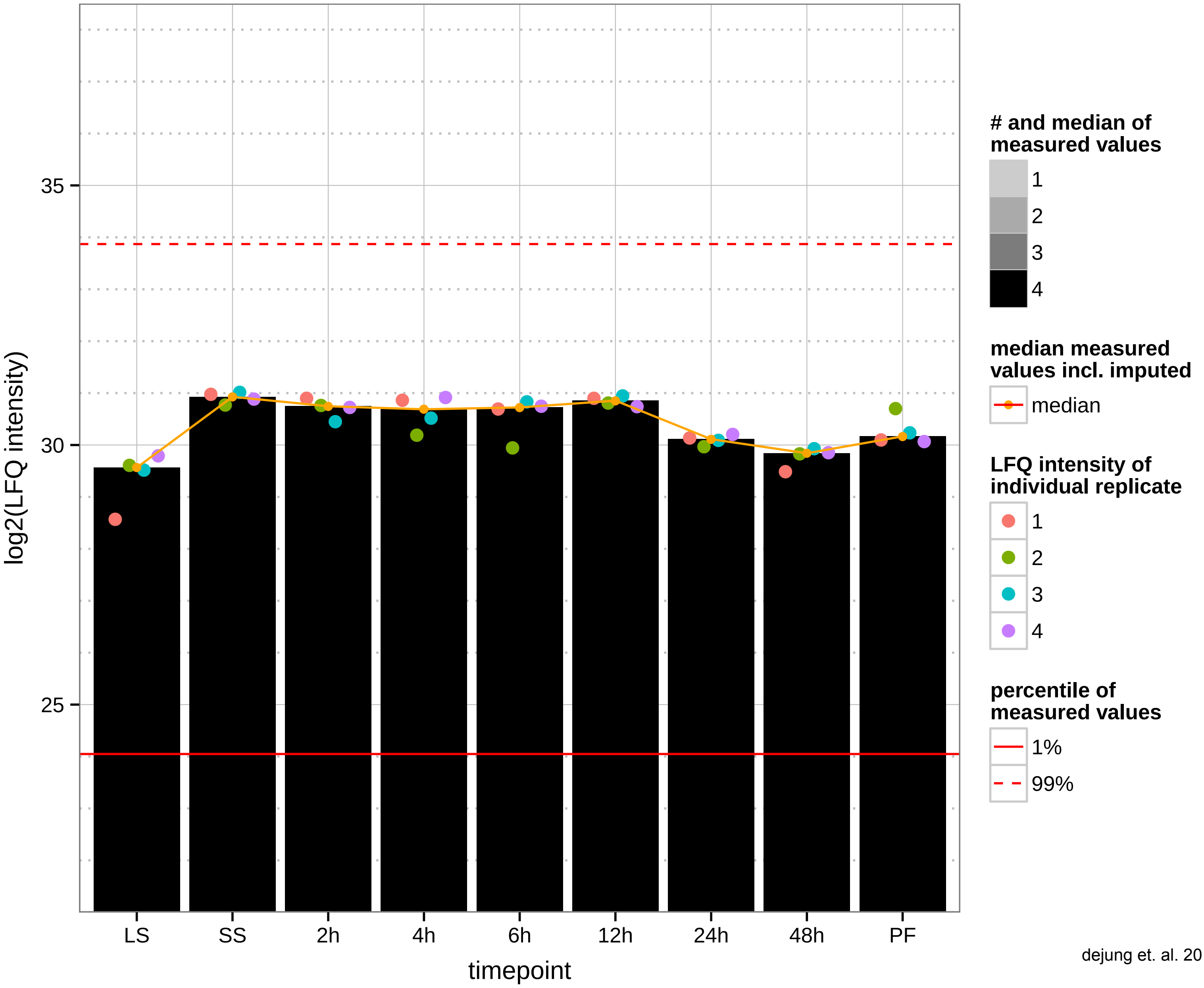
coronin, putative (CRN12)
Tb927.8.3100
AGOF: actin binding, kinesin binding, microtubule binding
AGOC: cell surface, cilium basal body, flagellar pocket
AGOP: microtubule cytoskeleton organization, microtubule−based process
PGOF: protein binding
PGOC: null
PGOP: null





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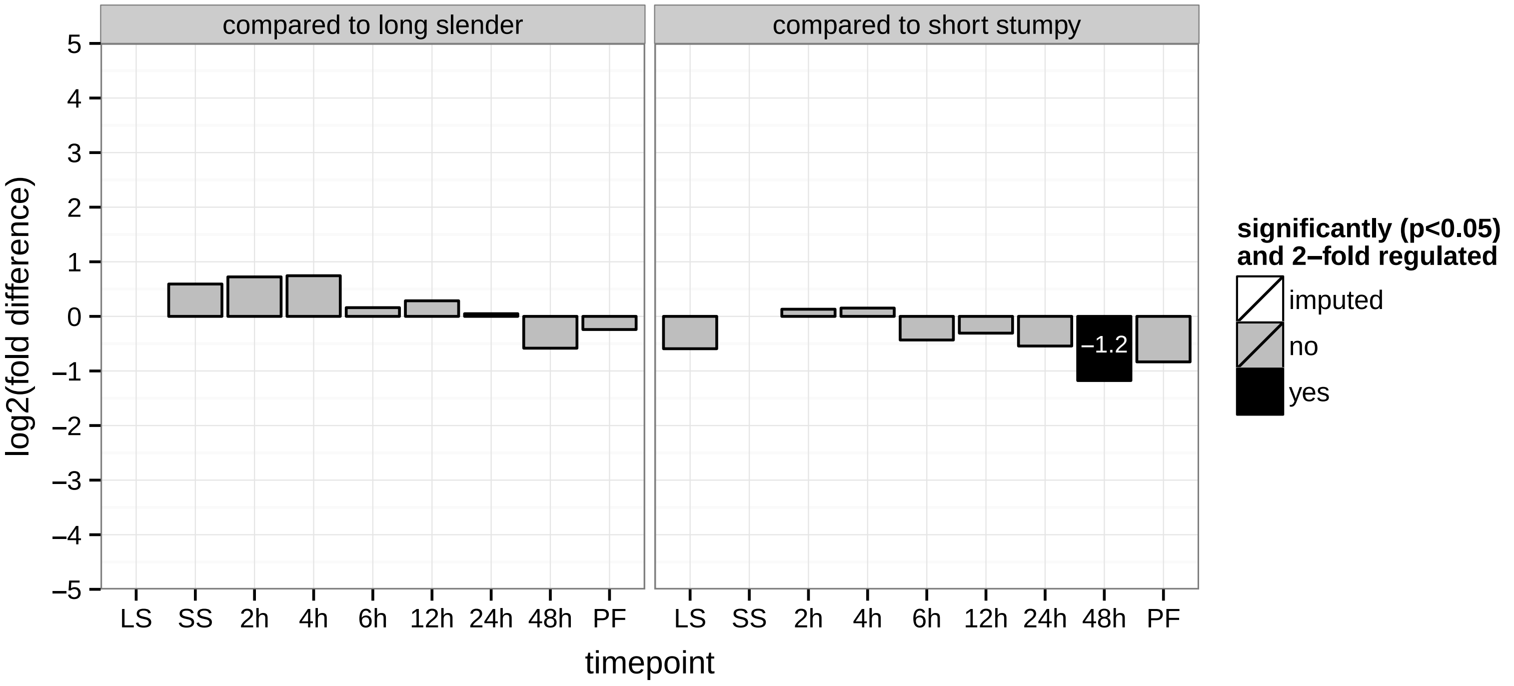
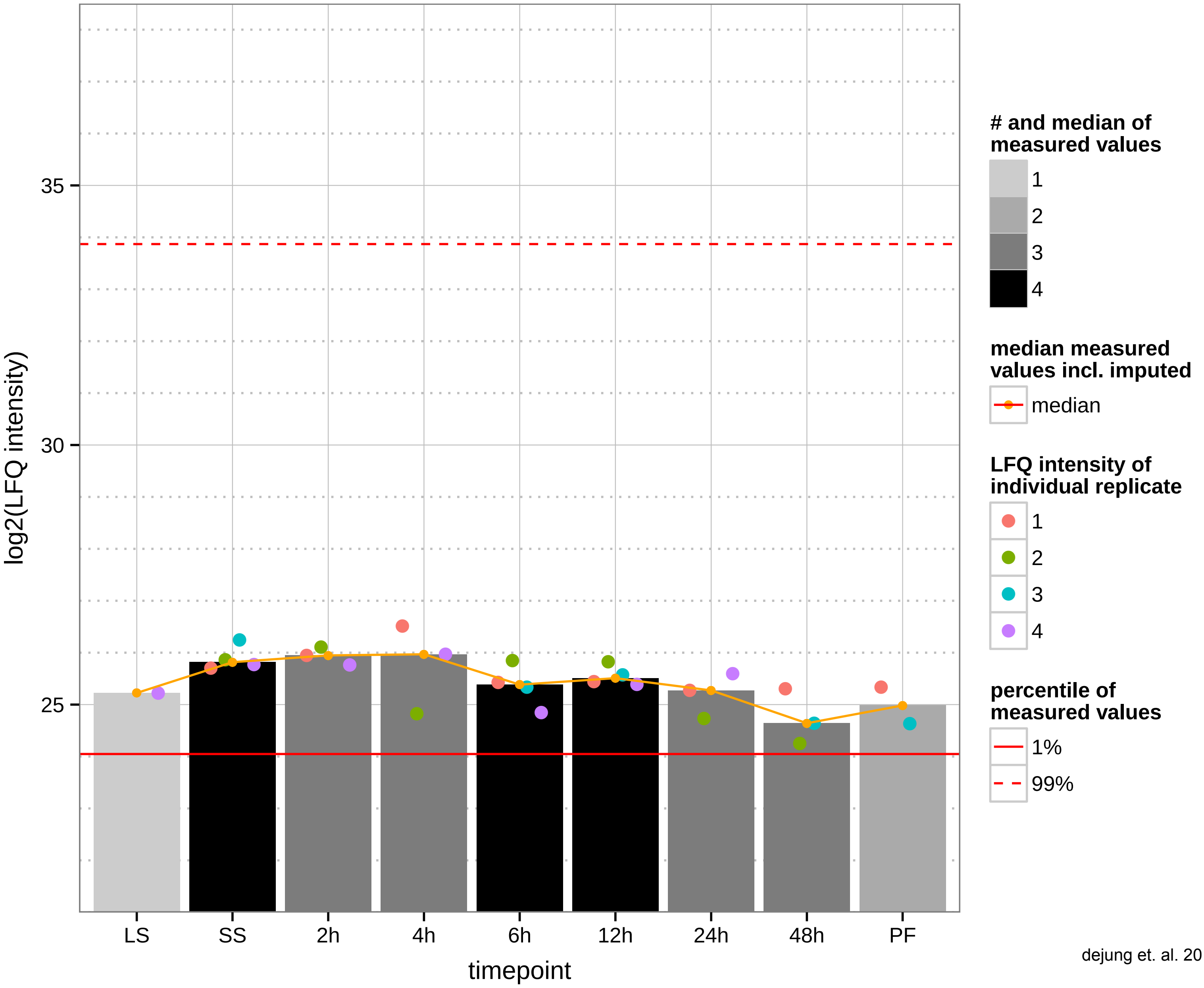
nucleoside phosphatase, putative, guanosine diphosphatase
Tb927.8.3800
AGOF: guanosine−diphosphatase activity, nucleoside−diphosphatase activity
AGOC: Golgi membrane, extracellular region
AGOP: cellular protein modification process, nucleoside metabolic process
PGOF: hydrolase activity
PGOC: null
PGOP: null





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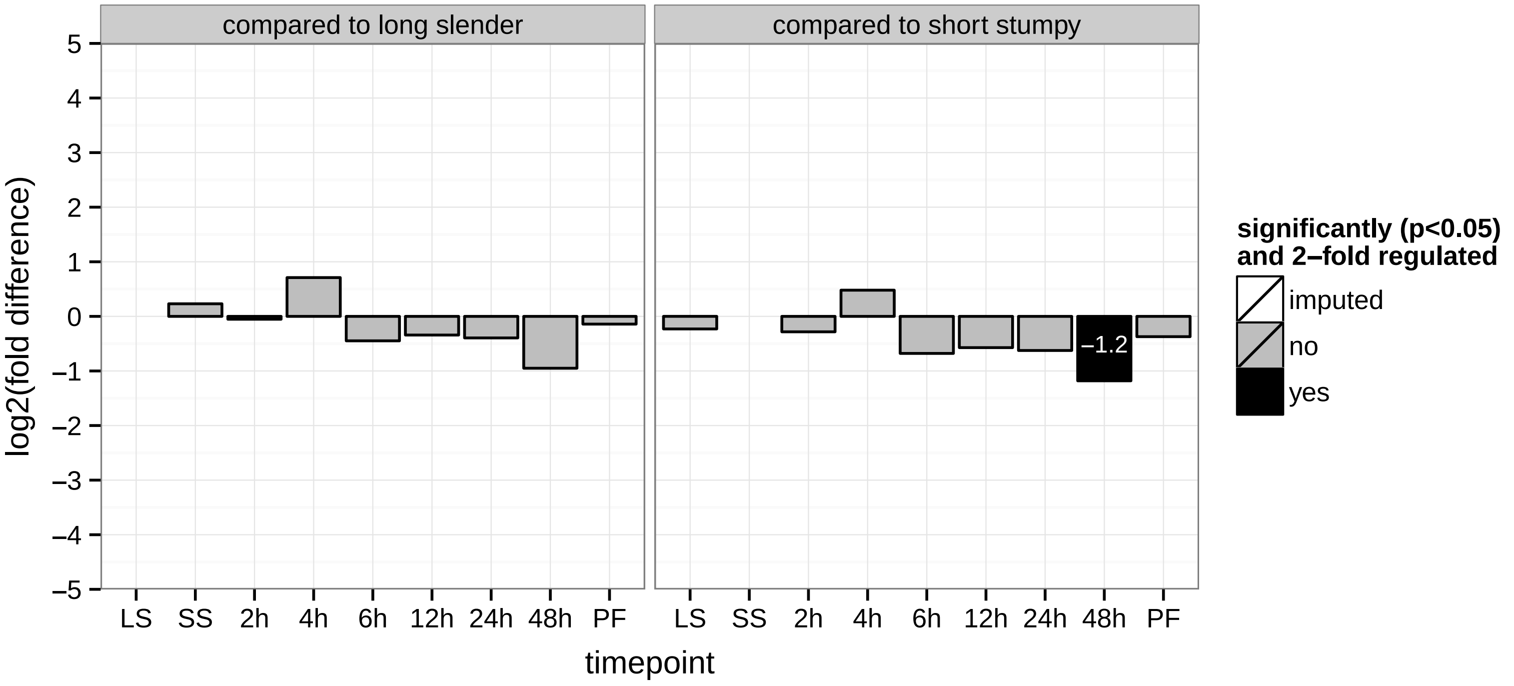
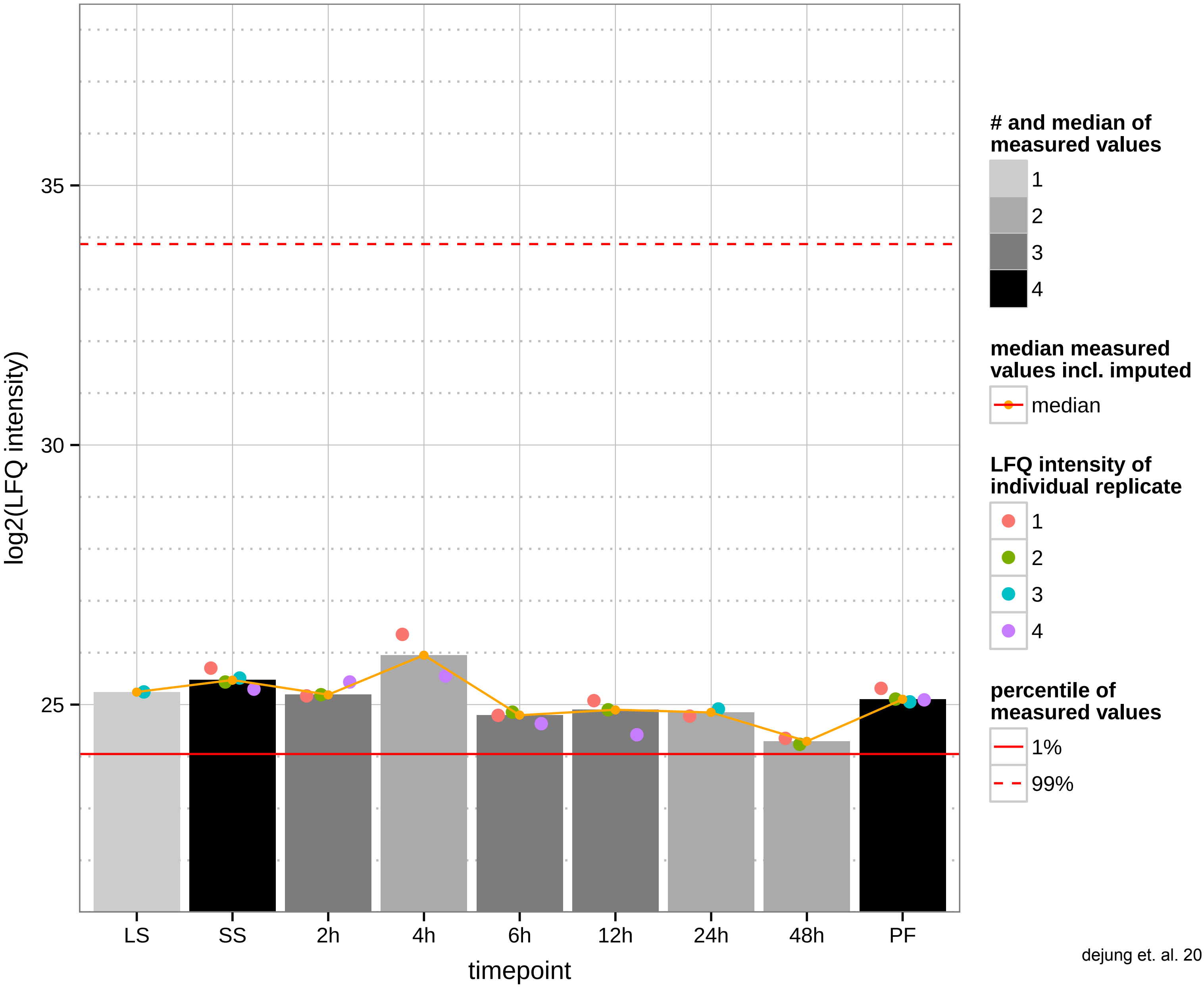
hypothetical protein, conserved
Tb927.8.4570
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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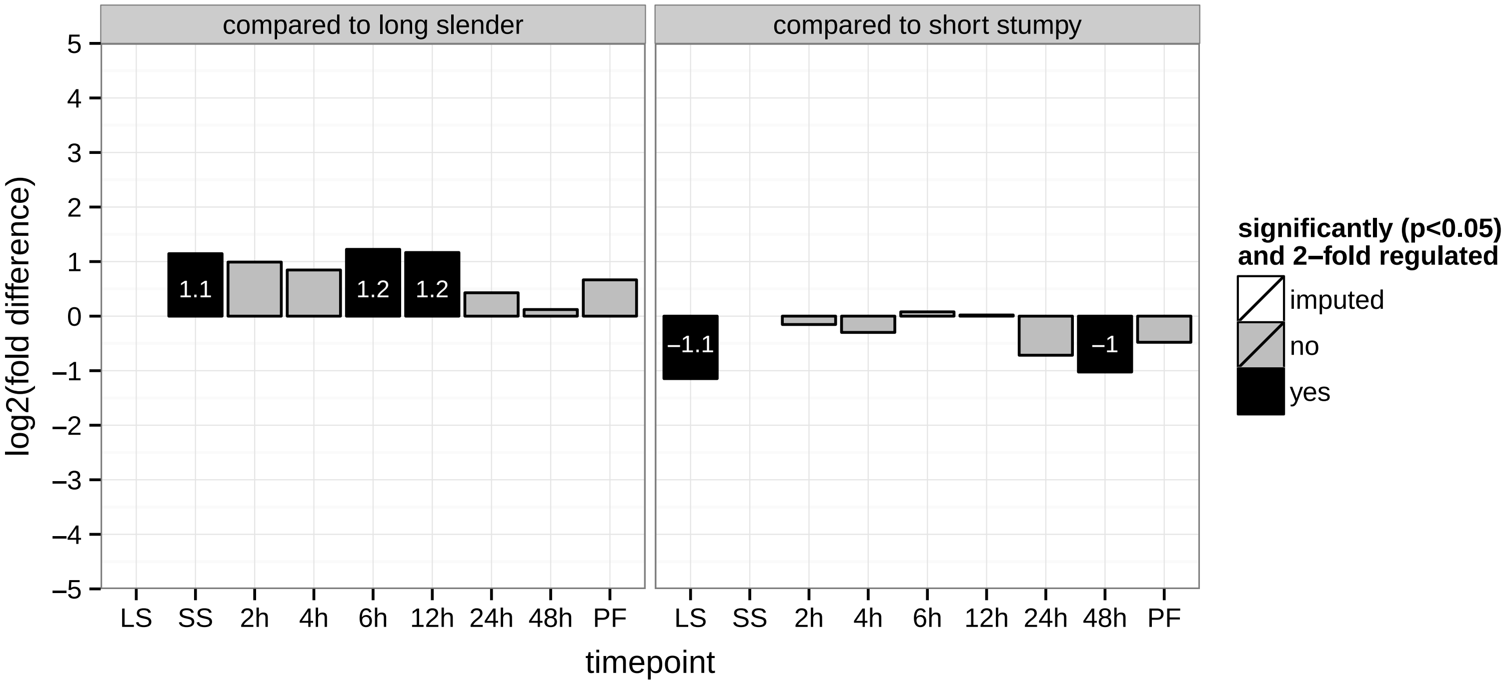
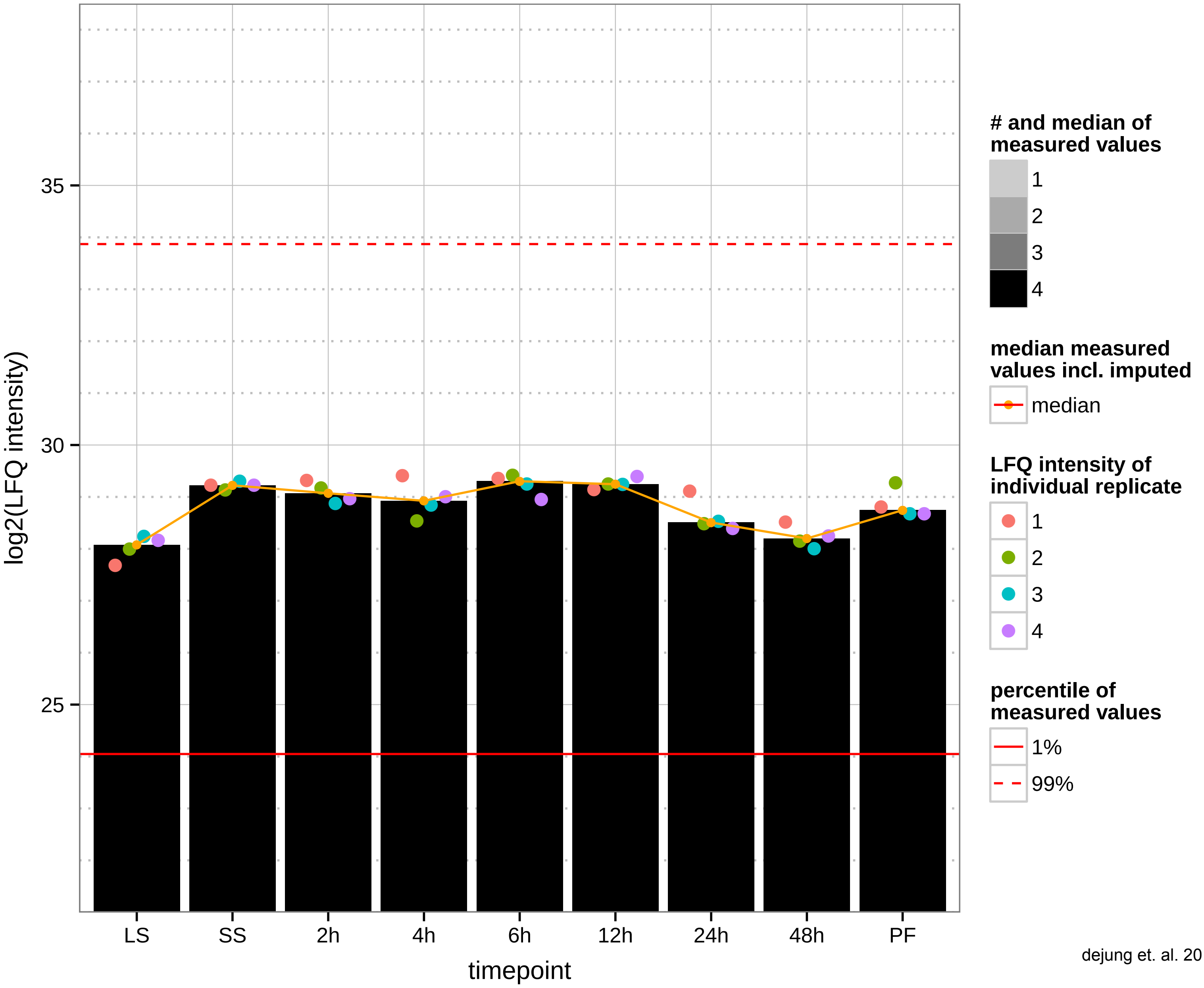
hypothetical protein, conserved
Tb927.8.5760
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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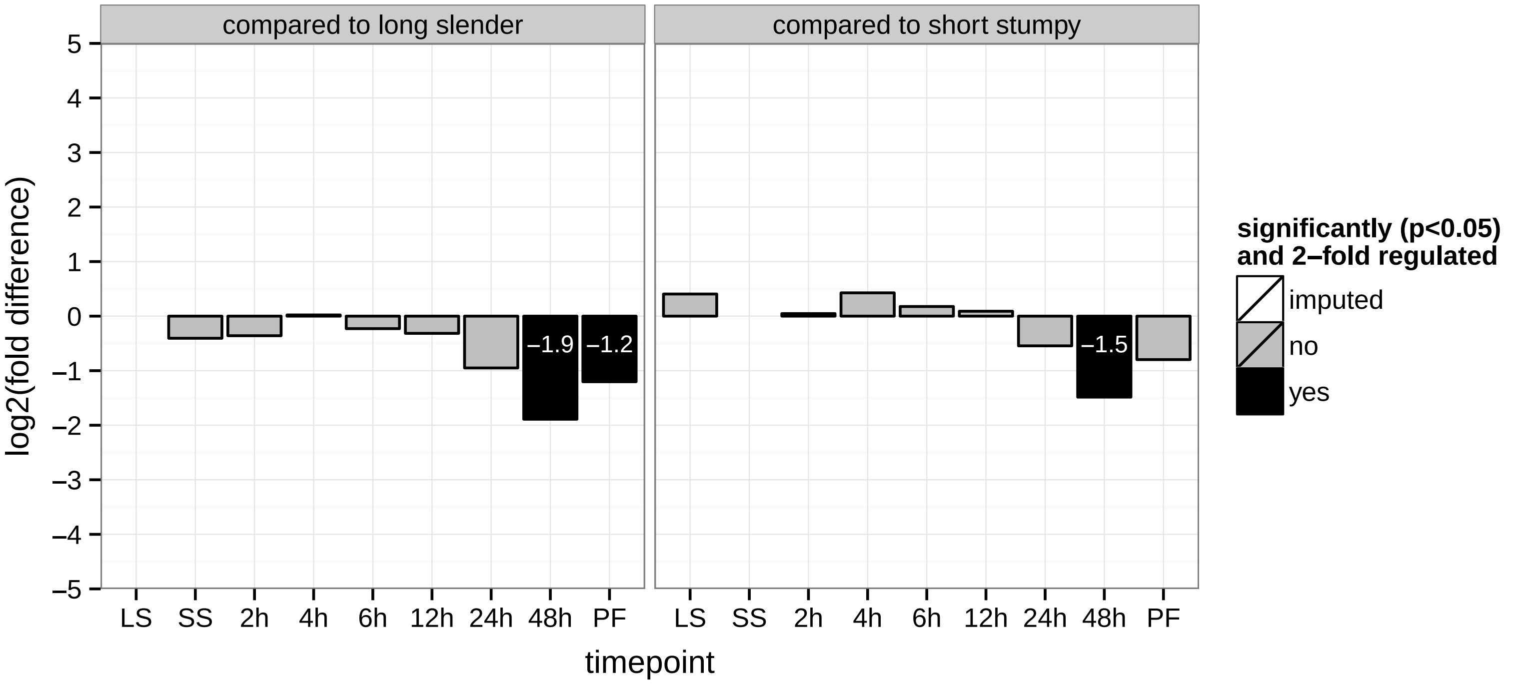
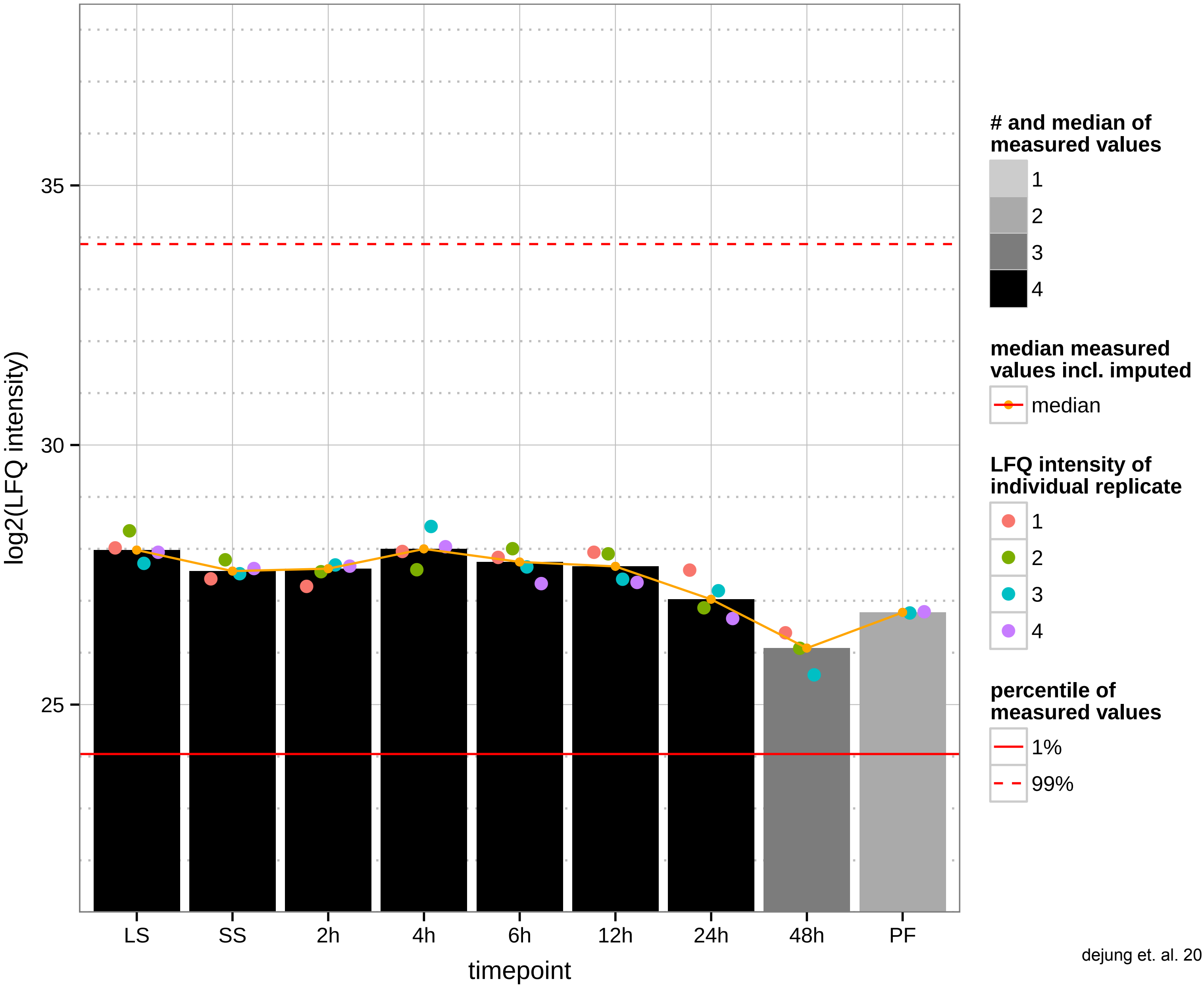
hypothetical protein, conserved
Tb927.8.7270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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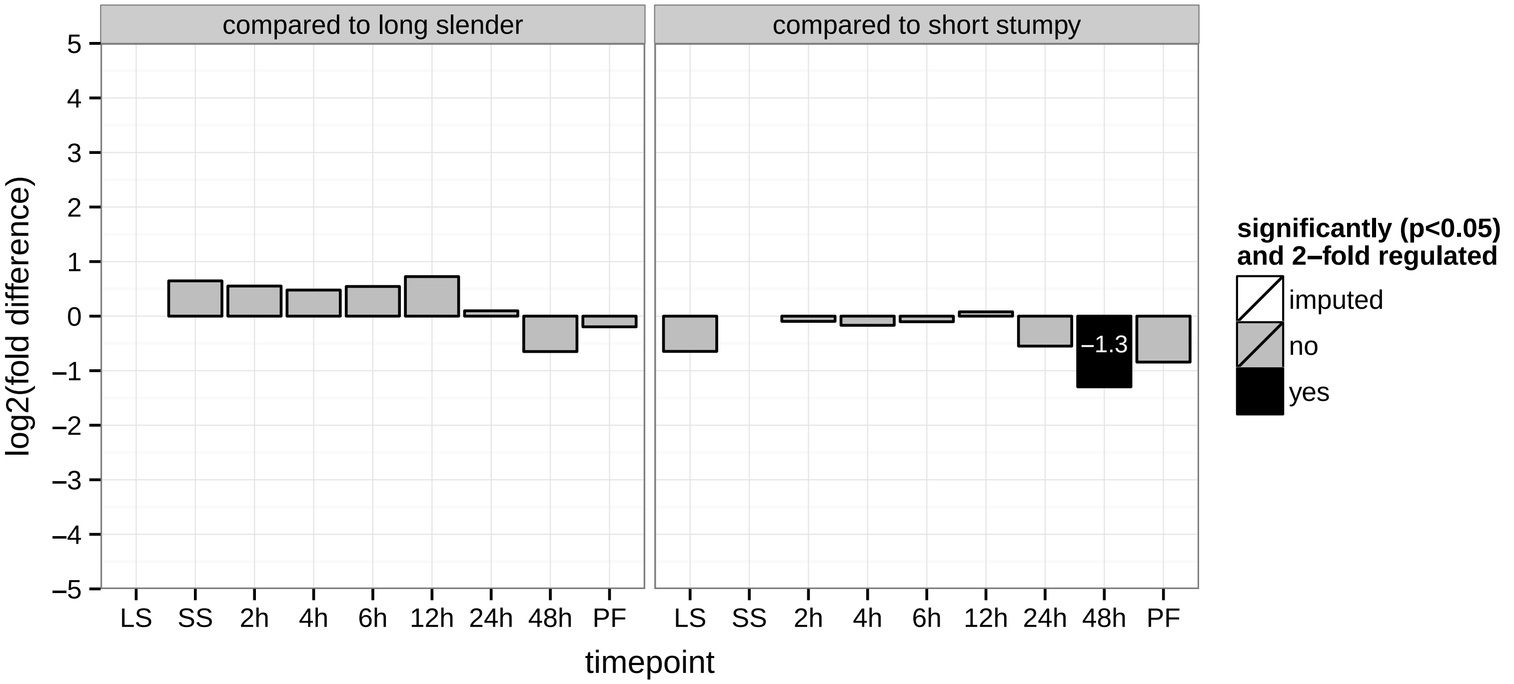
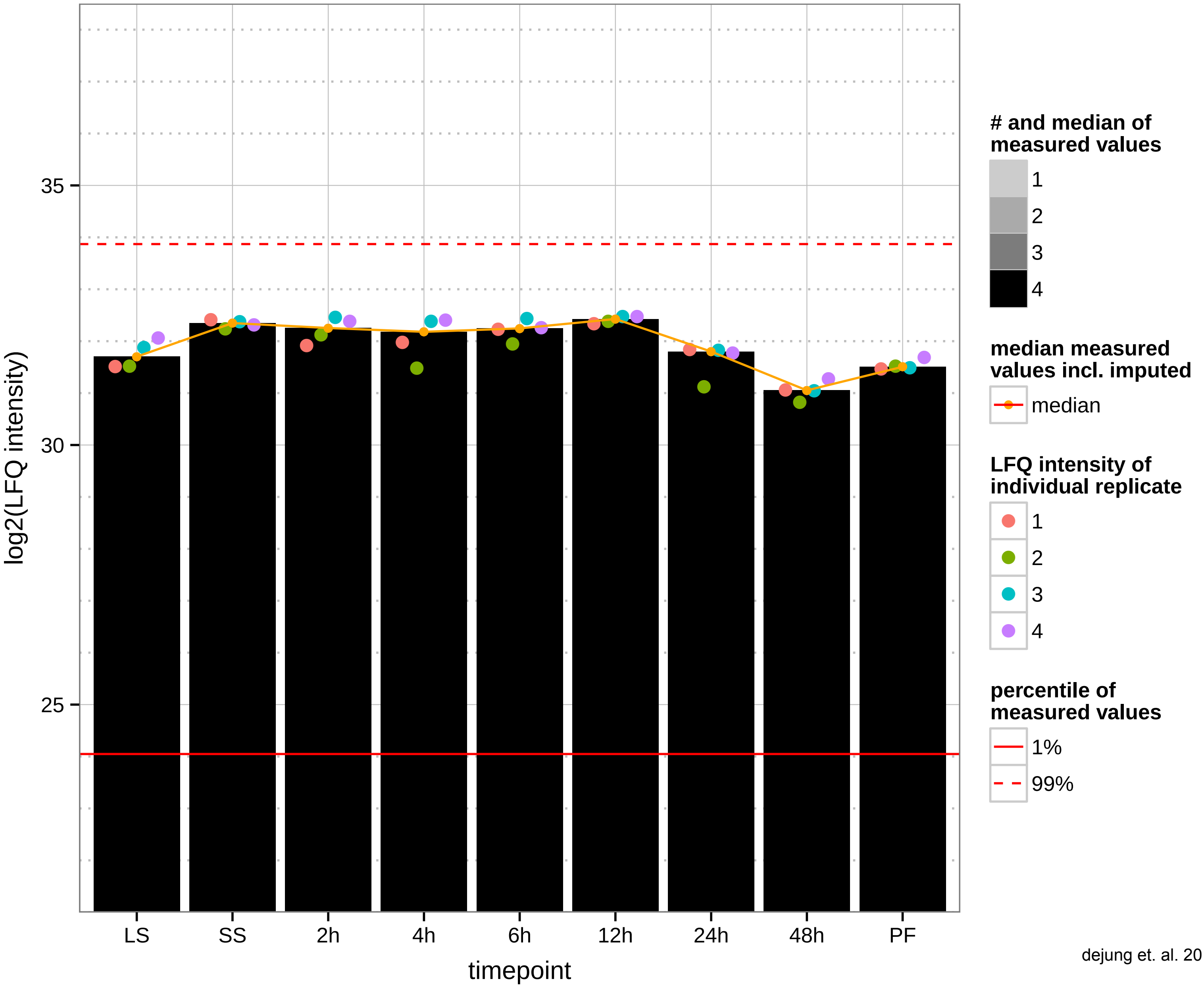
calpain, putative, cysteine peptidase
Tb927.8.8330
AGOF: calcium−dependent cysteine−type endopeptidase activity
AGOC: intracellular
AGOP: proteolysis
PGOF: calcium−dependent cysteine−type endopeptidase activity
PGOC: intracellular
PGOP: proteolysis





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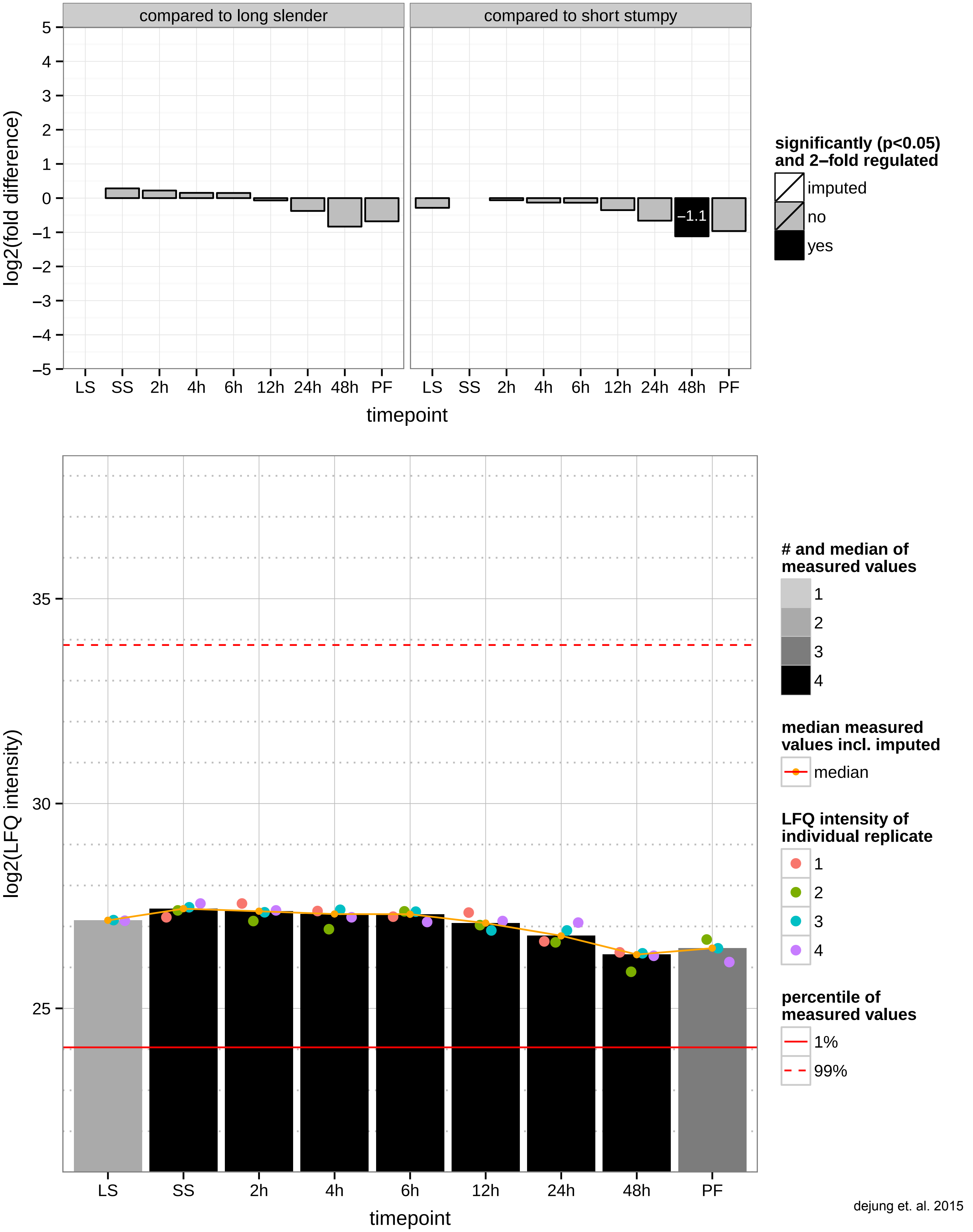
hypothetical protein, conserved
Tb927.9.11640
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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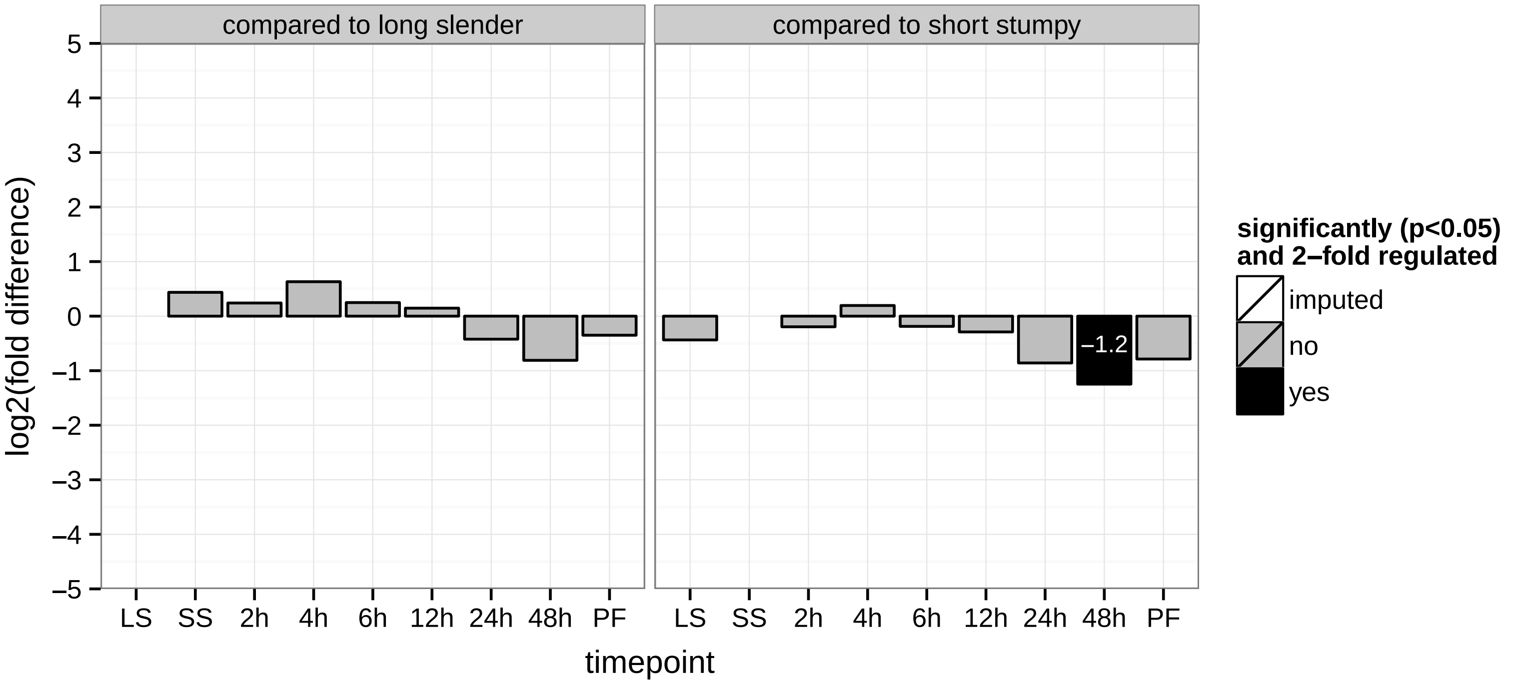
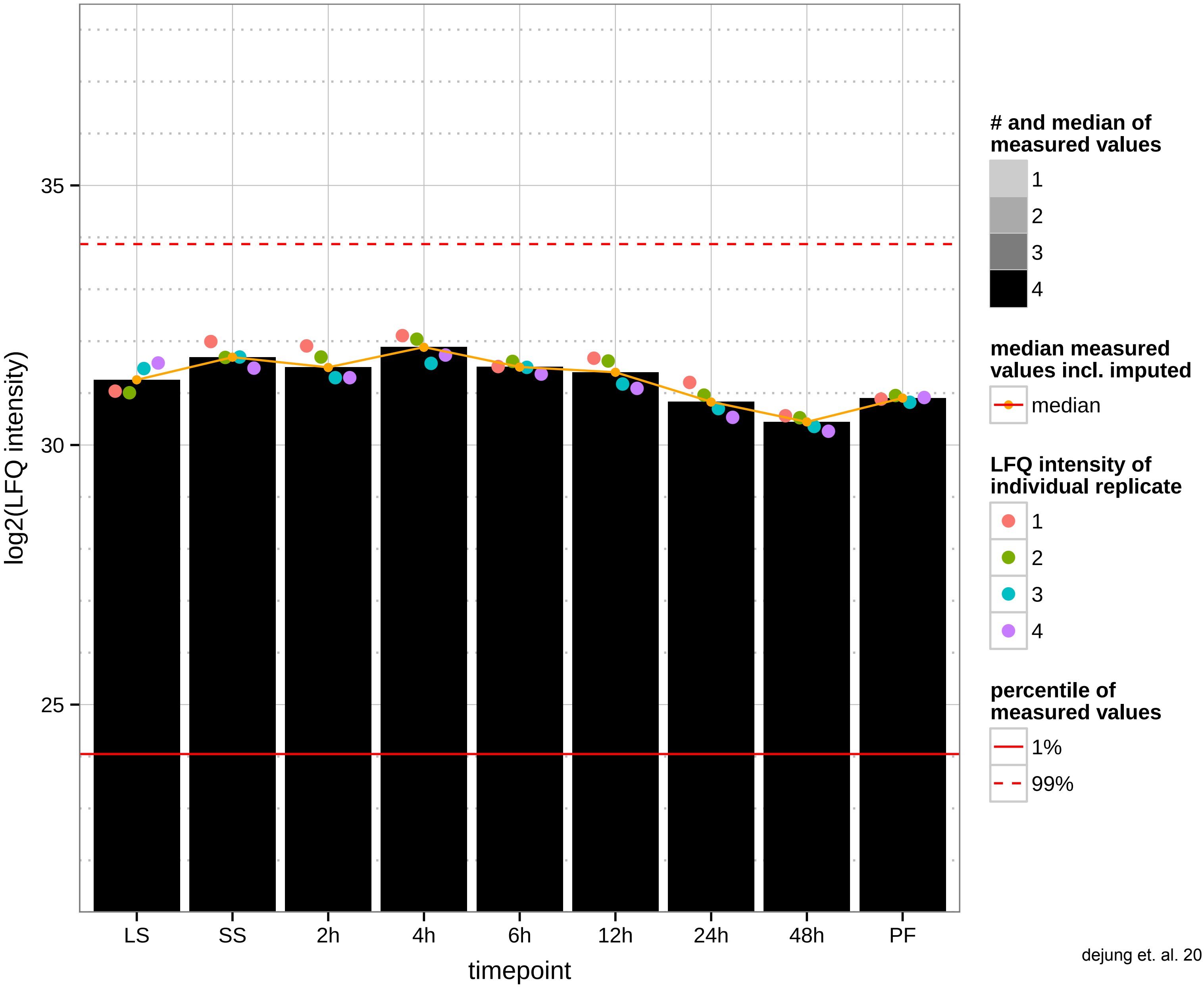
6–phosphogluconate dehydrogenase, decarboxylating (gnD)
Tb927.9.12110
AGOF: NADP binding, phosphogluconate dehydrogenase (decarboxylating) activity
AGOC: cytoplasm
AGOP: oxidation–reduction process, pentose–phosphate shunt
PGOF: NADP binding, phosphogluconate dehydrogenase (decarboxylating) activity
PGOC: null
PGOP: oxidation–reduction process, pentose–phosphate shunt





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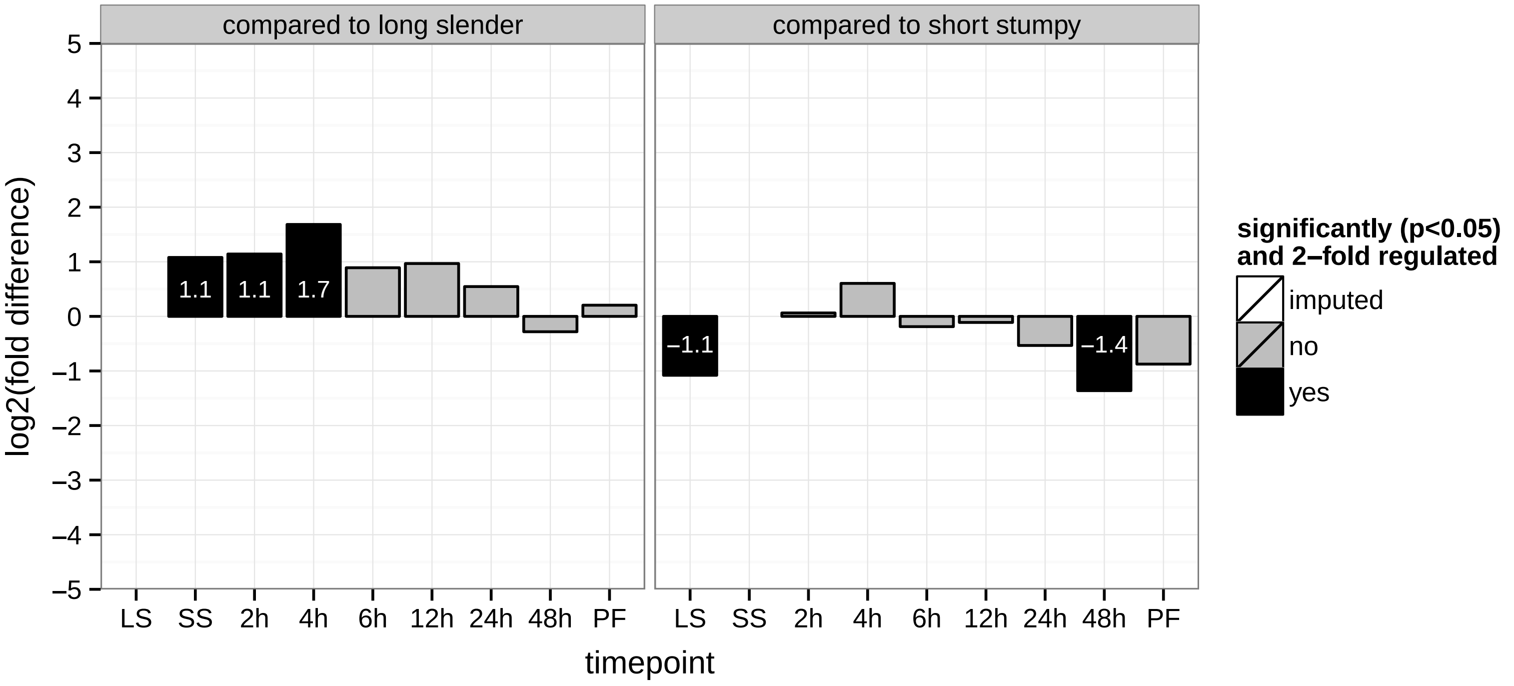
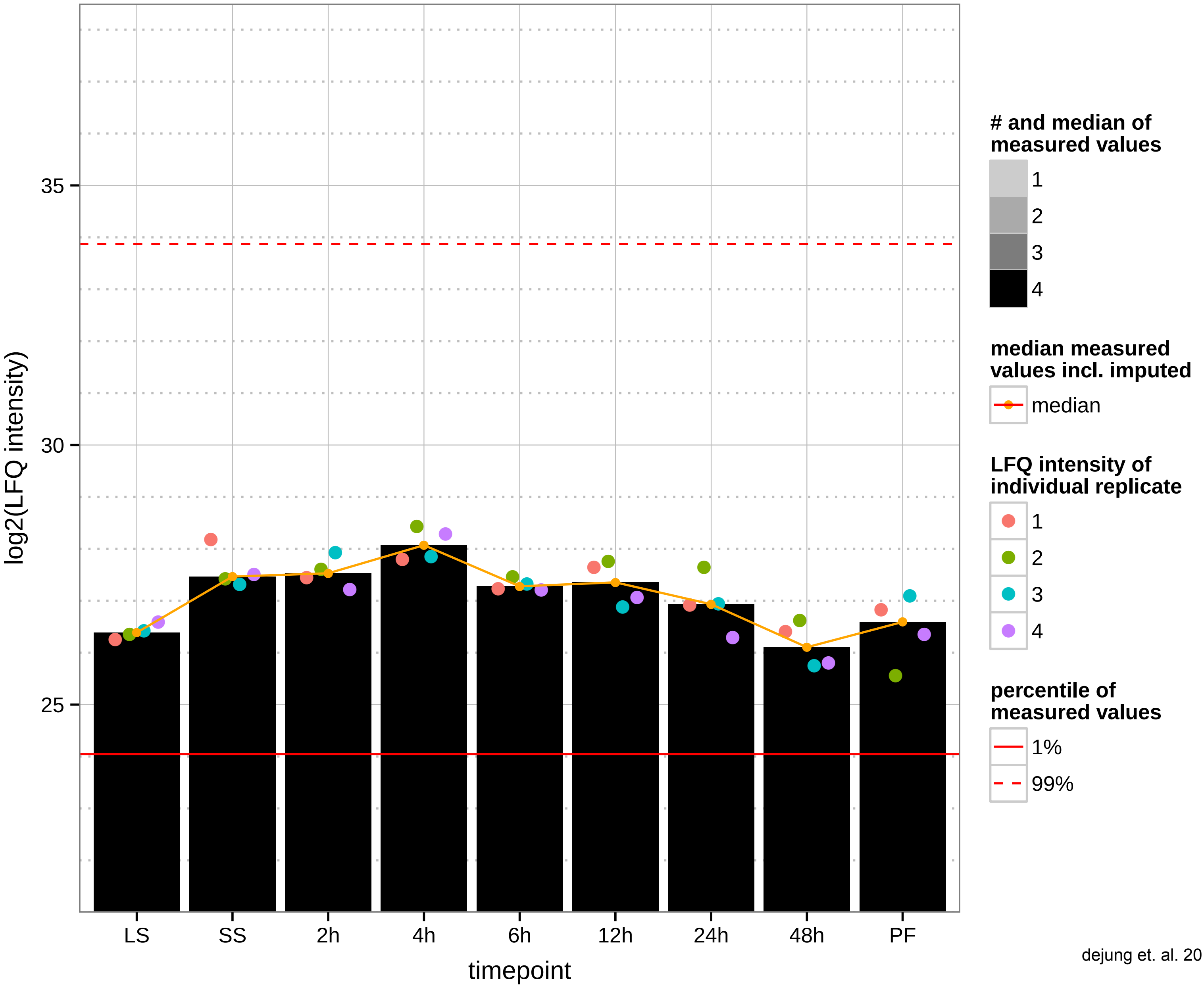
QA–SNARE protein putative
Tb927.9.13030
AGOF: SNAP receptor activity
AGOC: integral to membrane, membrane
AGOP: membrane fusion, vesicle–mediated transport
PGOF: protein binding
PGOC: membrane
PGOP: vesicle–mediated transport





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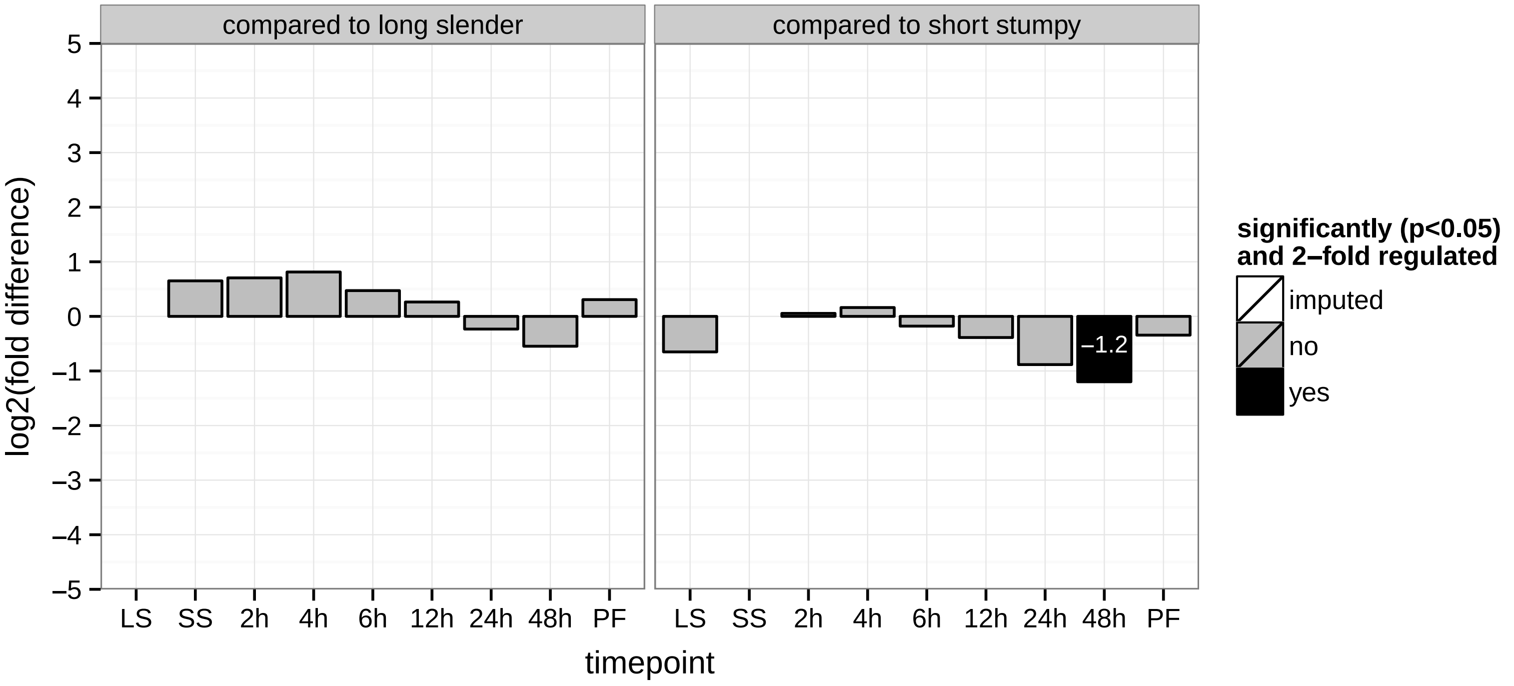
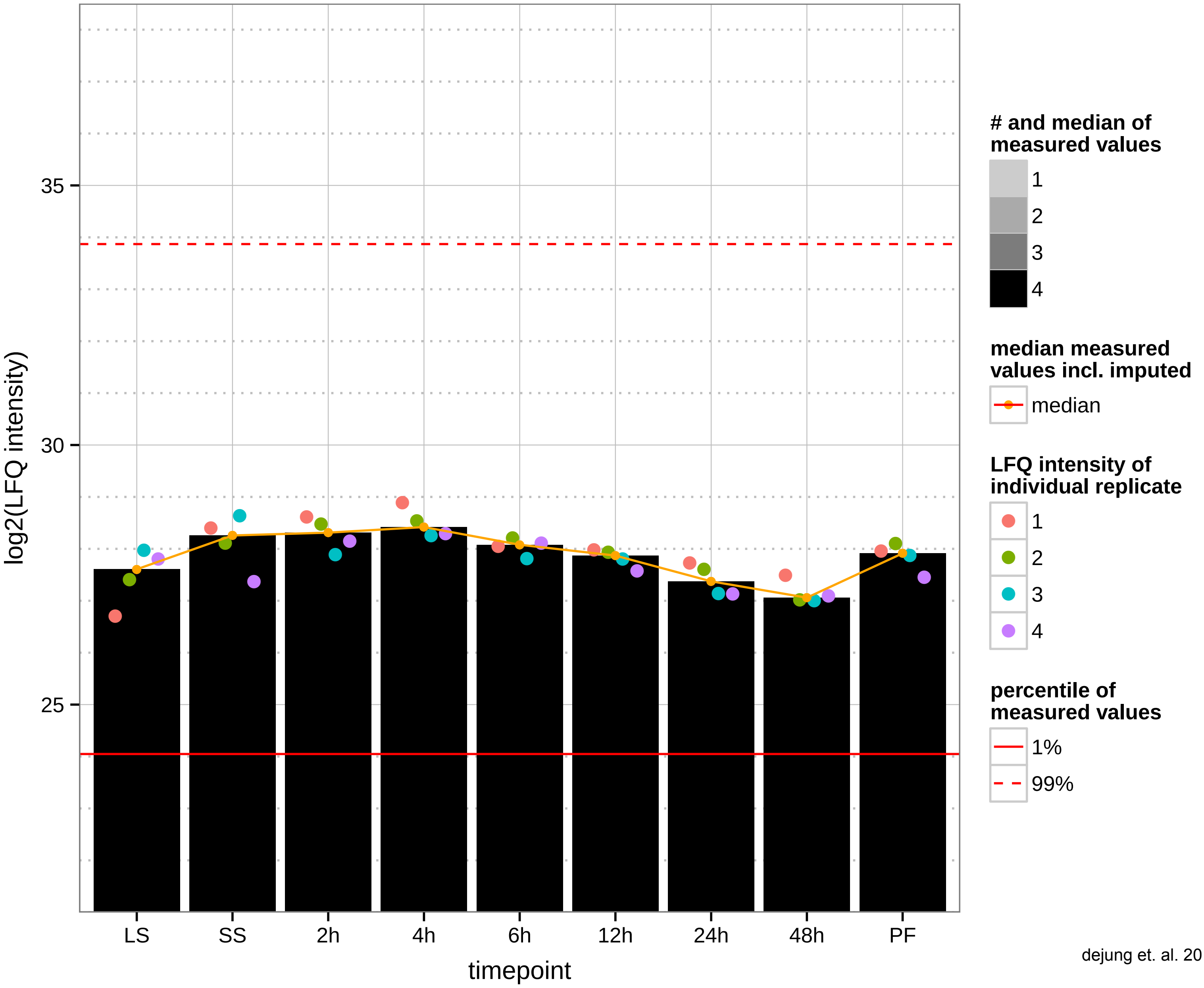
hypothetical protein, conserved
Tb927.9.3770
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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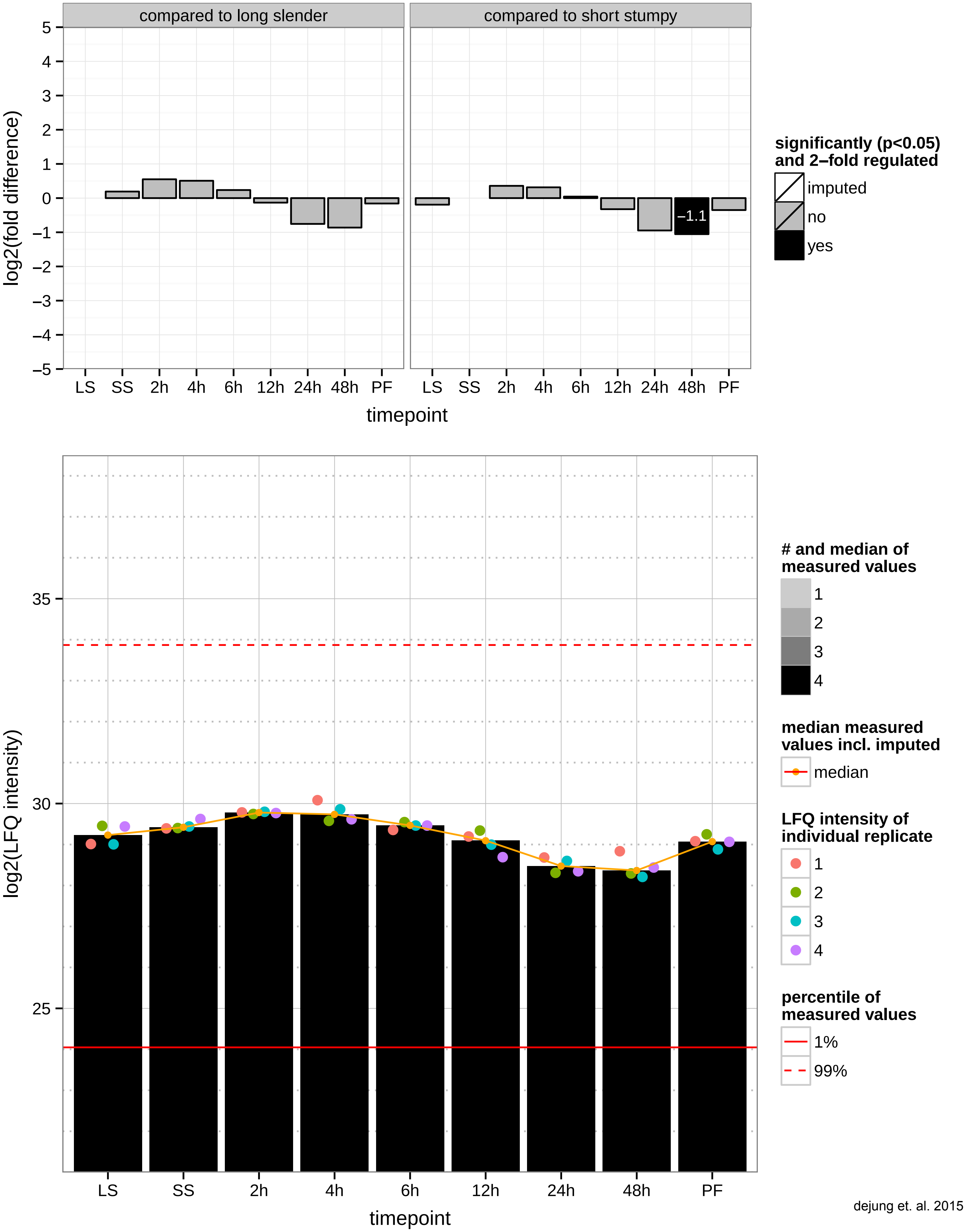
heat shock protein, putative, HSP70–like protein
Tb927.9.4500
AGOF: ATP binding
AGOC: mitochondrial inner membrane
AGOP: protein folding
PGOF: null
PGOC: null
PGOP: null



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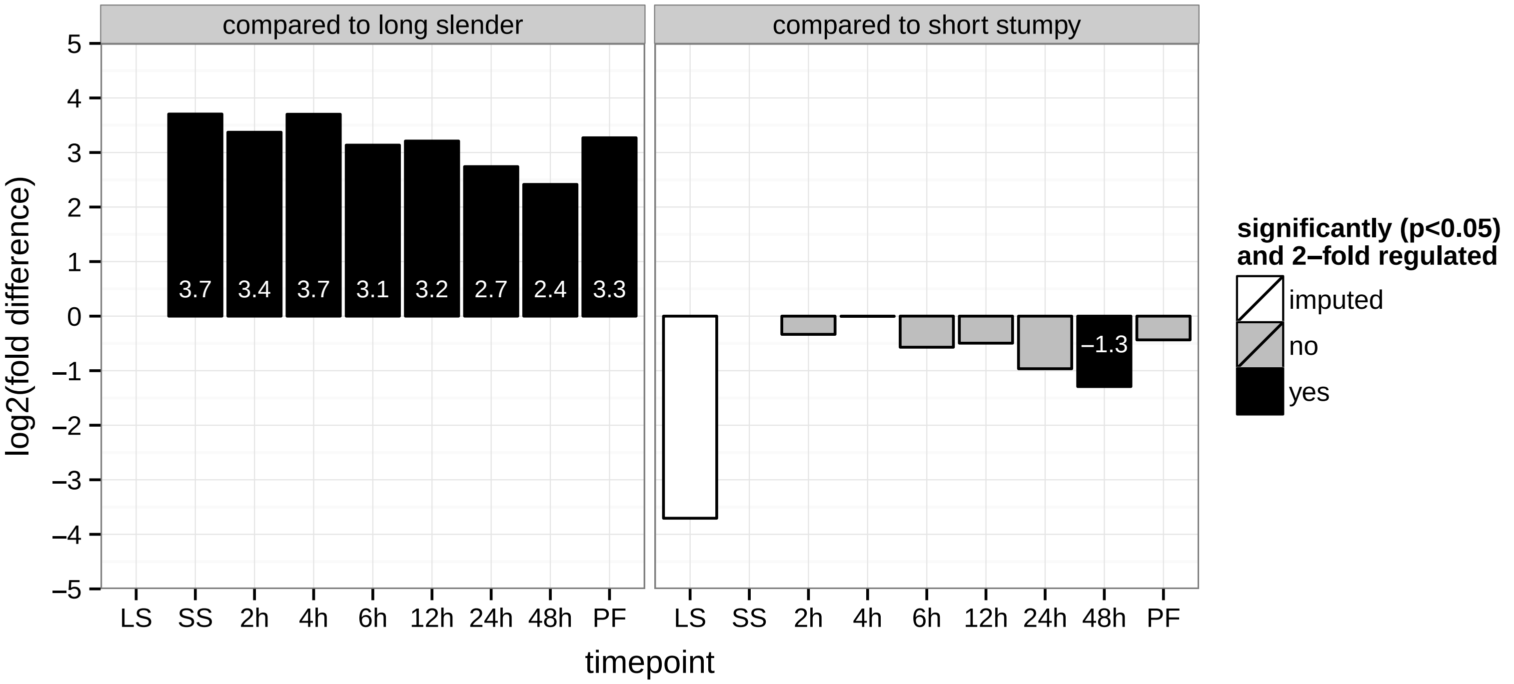
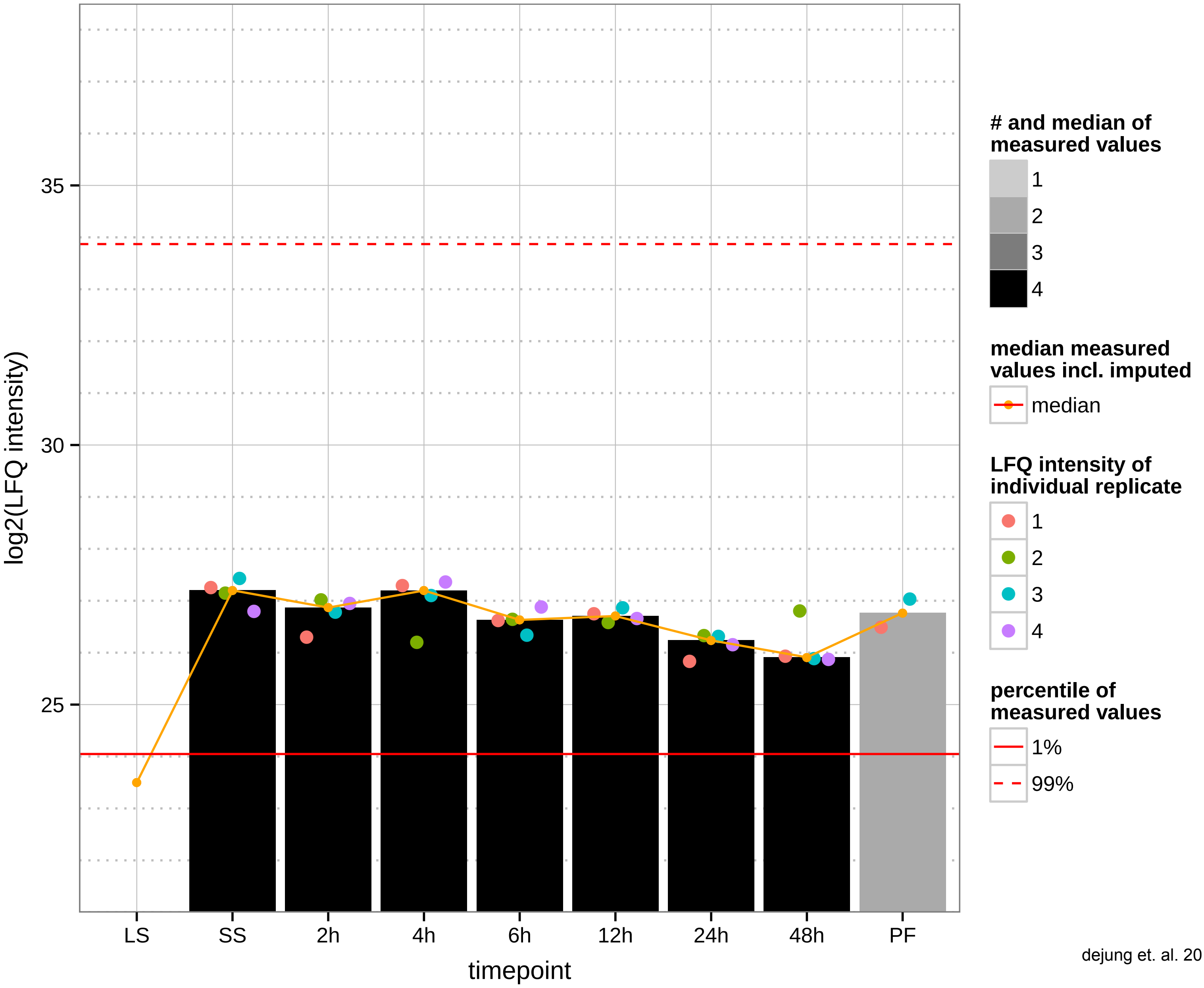
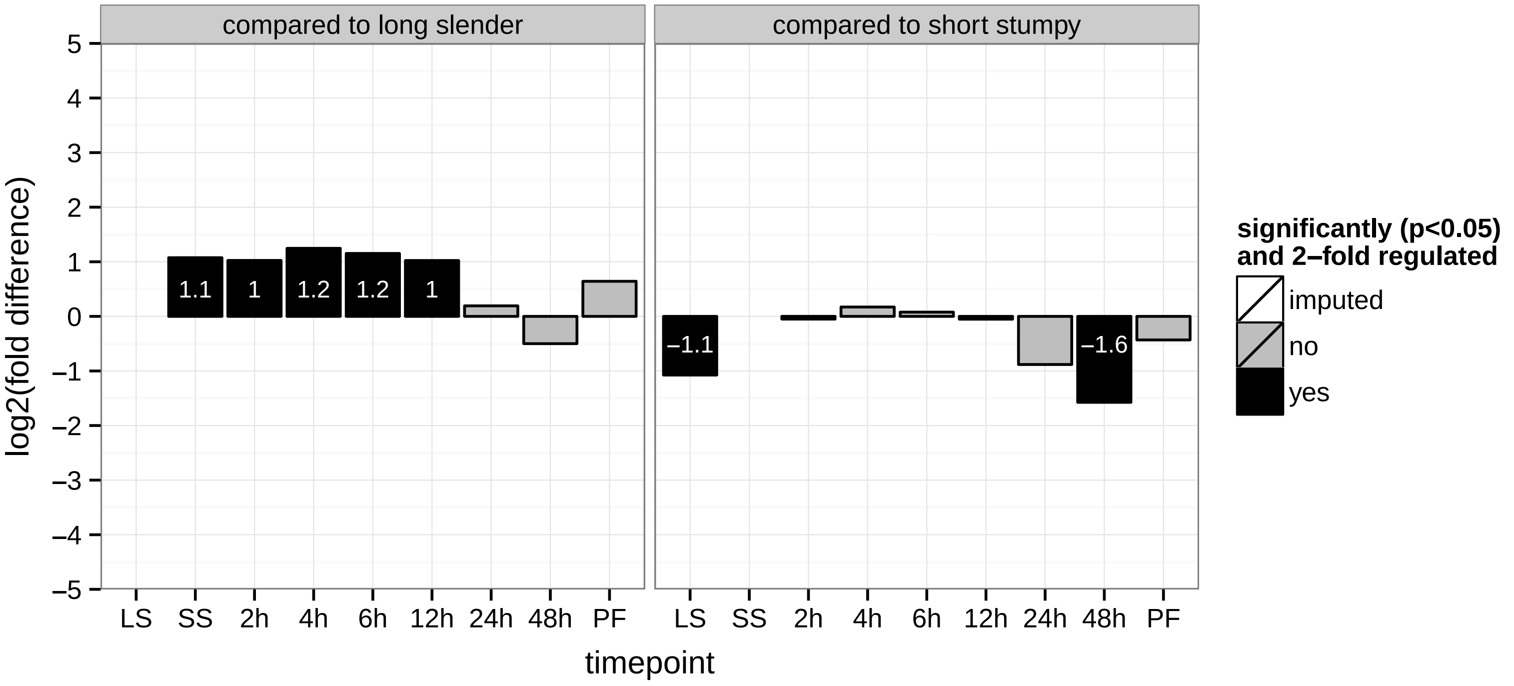
inositol–1(or 4)–monophosphatase, putative (IMPase)
Tb927.9.6350
AGOF: inositol monophosphate 1–phosphatase activity
AGOC: null
AGOP: phosphate–containing compound metabolic process, signal transduction
PGOF: null
PGOC: null
PGOP: phosphatidylinositol phosphorylation

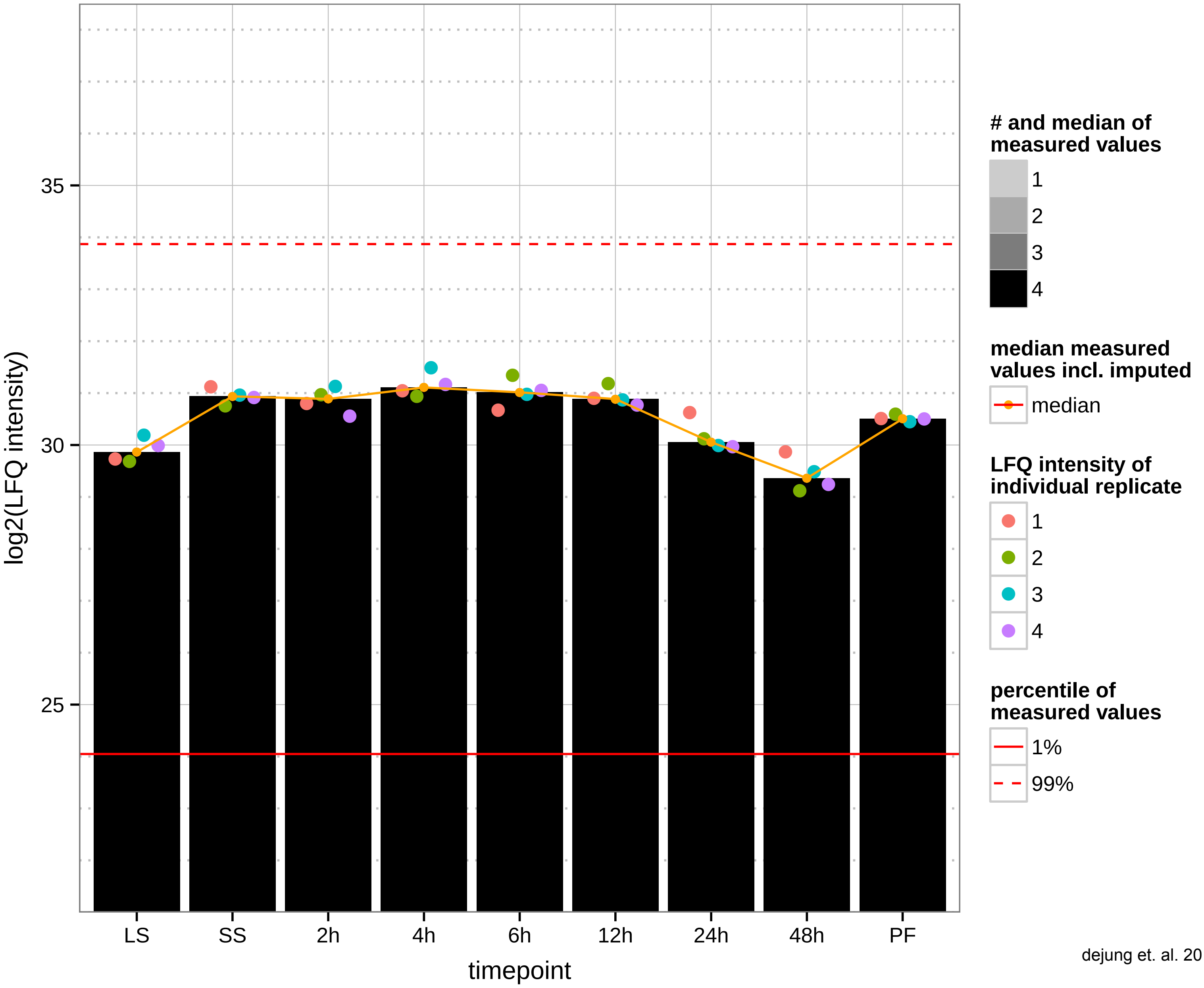




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.7110
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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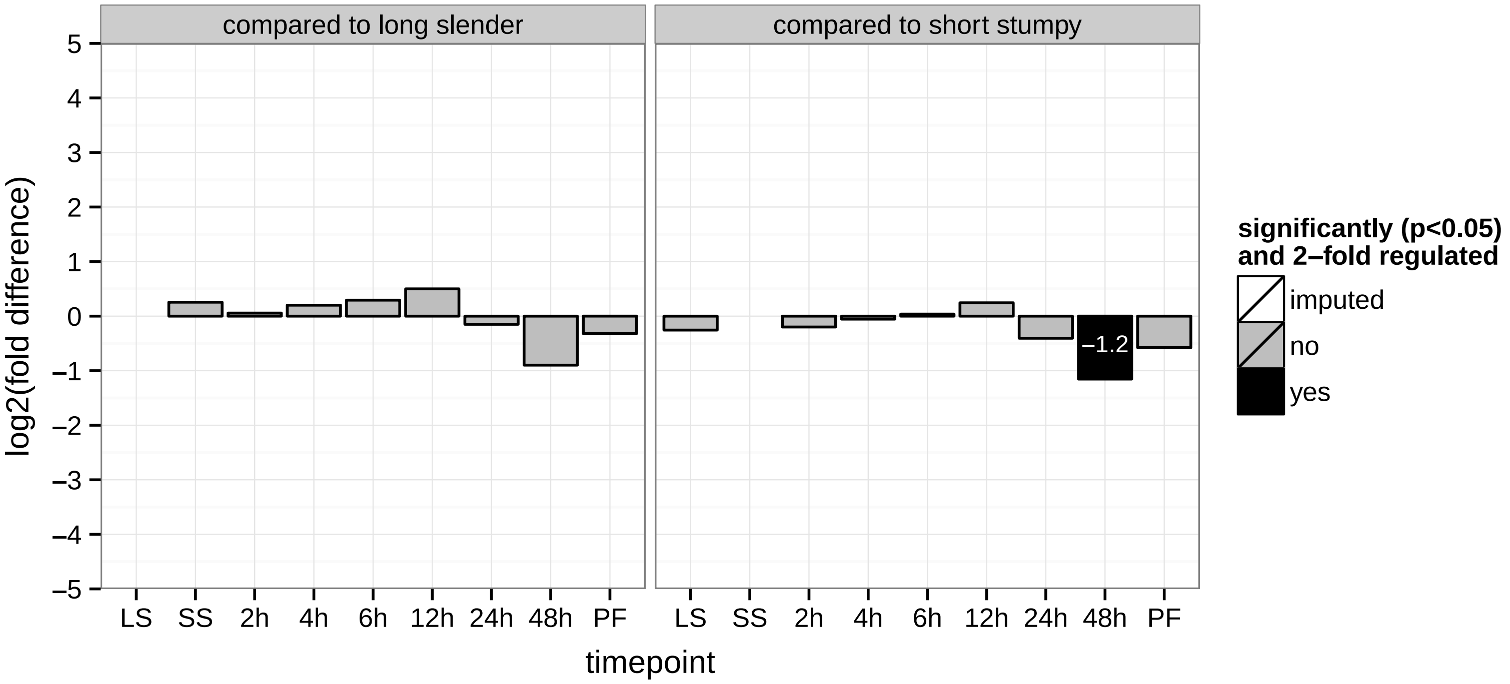
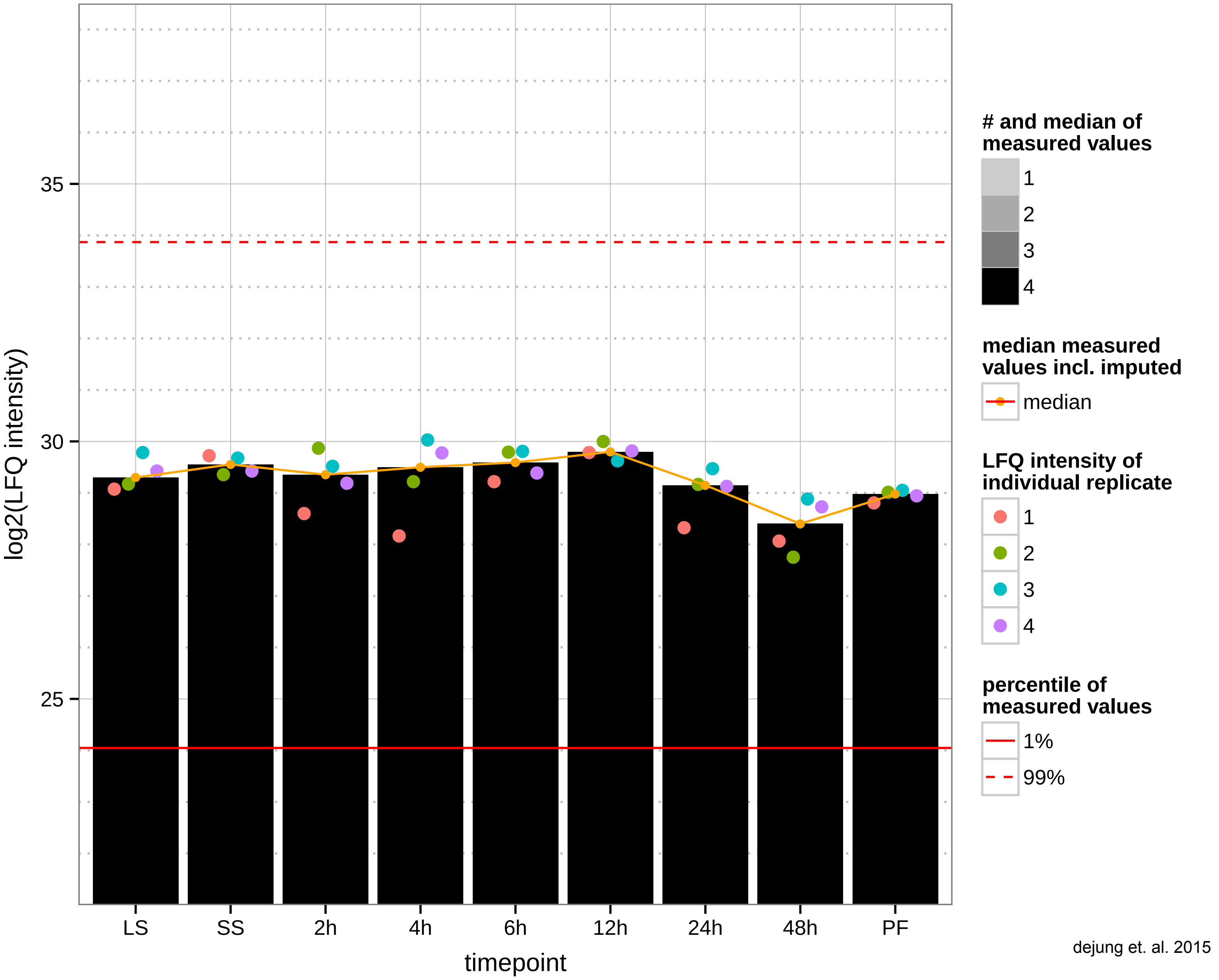
peptidyl–prolyl cis–trans isomerase (cyclophilin– 40), putative, cyclophilin–40
Tb927.9.9780
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: null
PGOF: peptidyl–prolyl cis–trans isomerase activity, protein binding
PGOC: null
PGOP: protein folding





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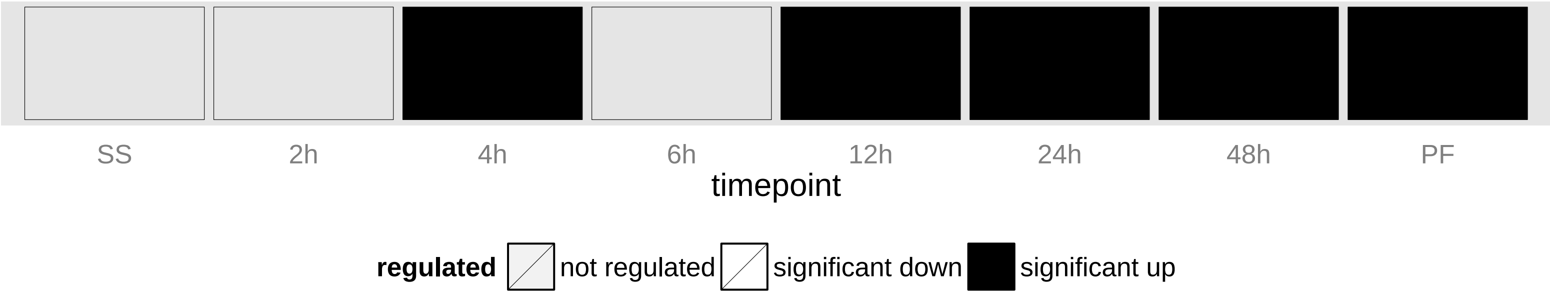

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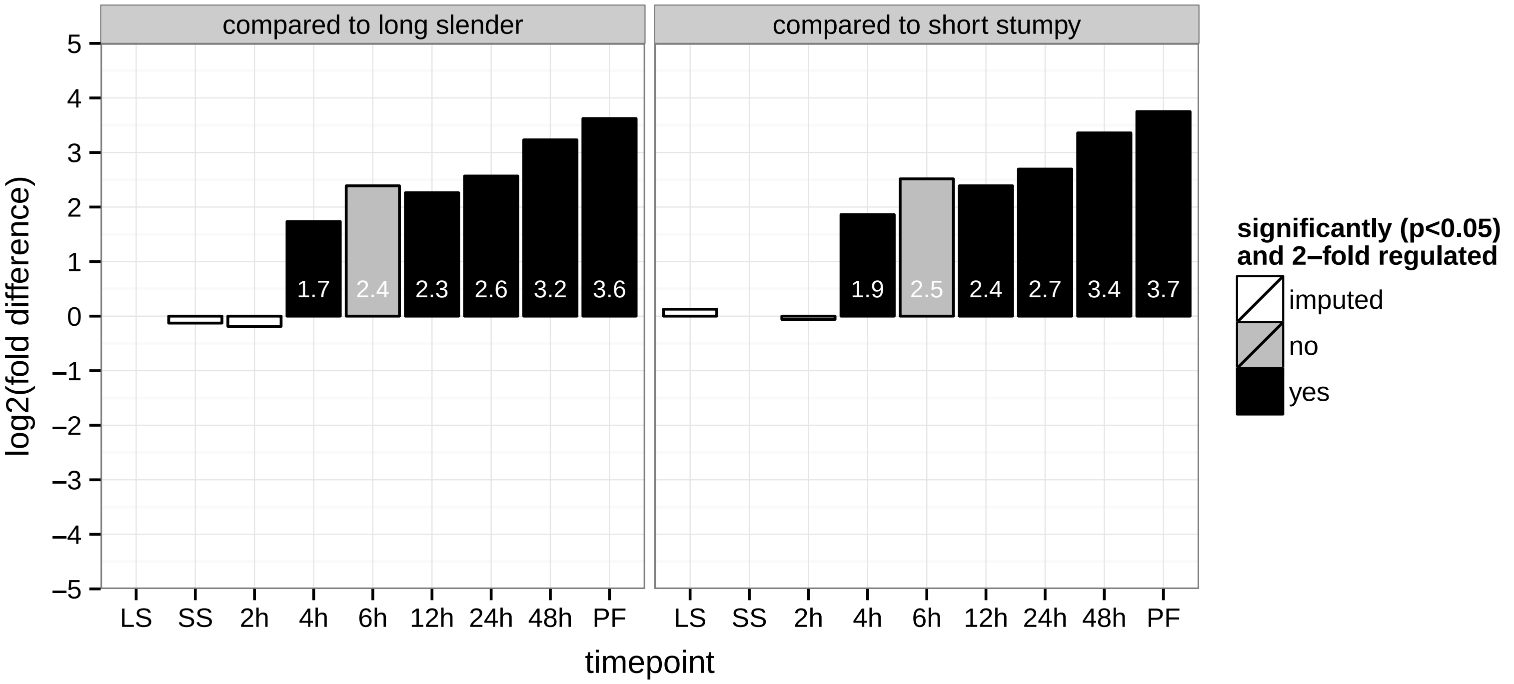
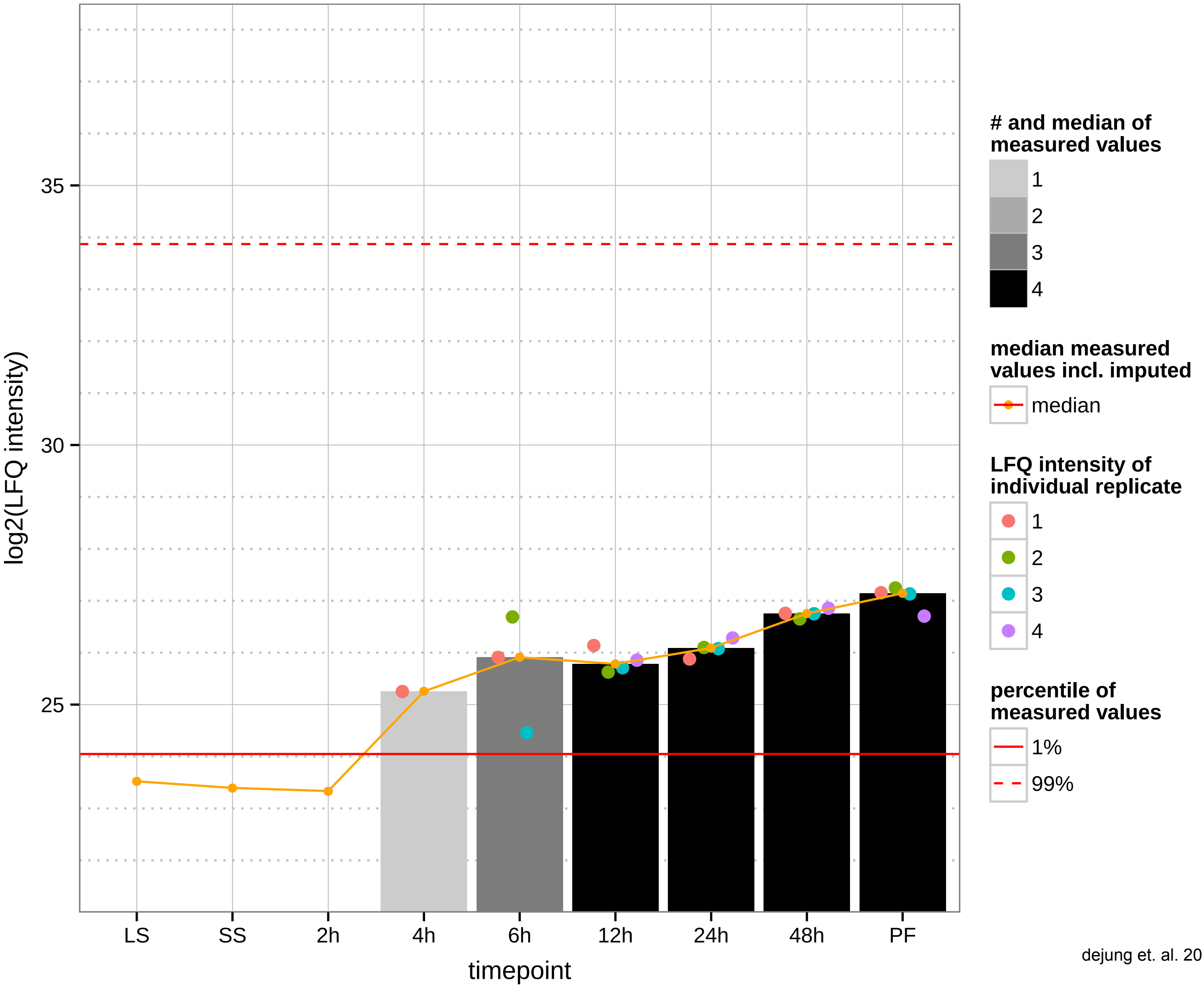
branched–chain alpha–keto acid dehydrogenase e1–beta subunit precursor, putative, chrX additional, unordered contigs, 2–o
Tb927.10.4330;Tb11.v5.1012;Tb10.v4.0043
AGOF: catalytic activity, null, 3–methyl–2–oxobutanoate dehydrogenase (2–methylpropanoyl–transferring) activity
AGOC: null, mitochondrial alpha–ketoglutarate dehydrogenase complex, mitochondrion
AGOP: metabolic process, null
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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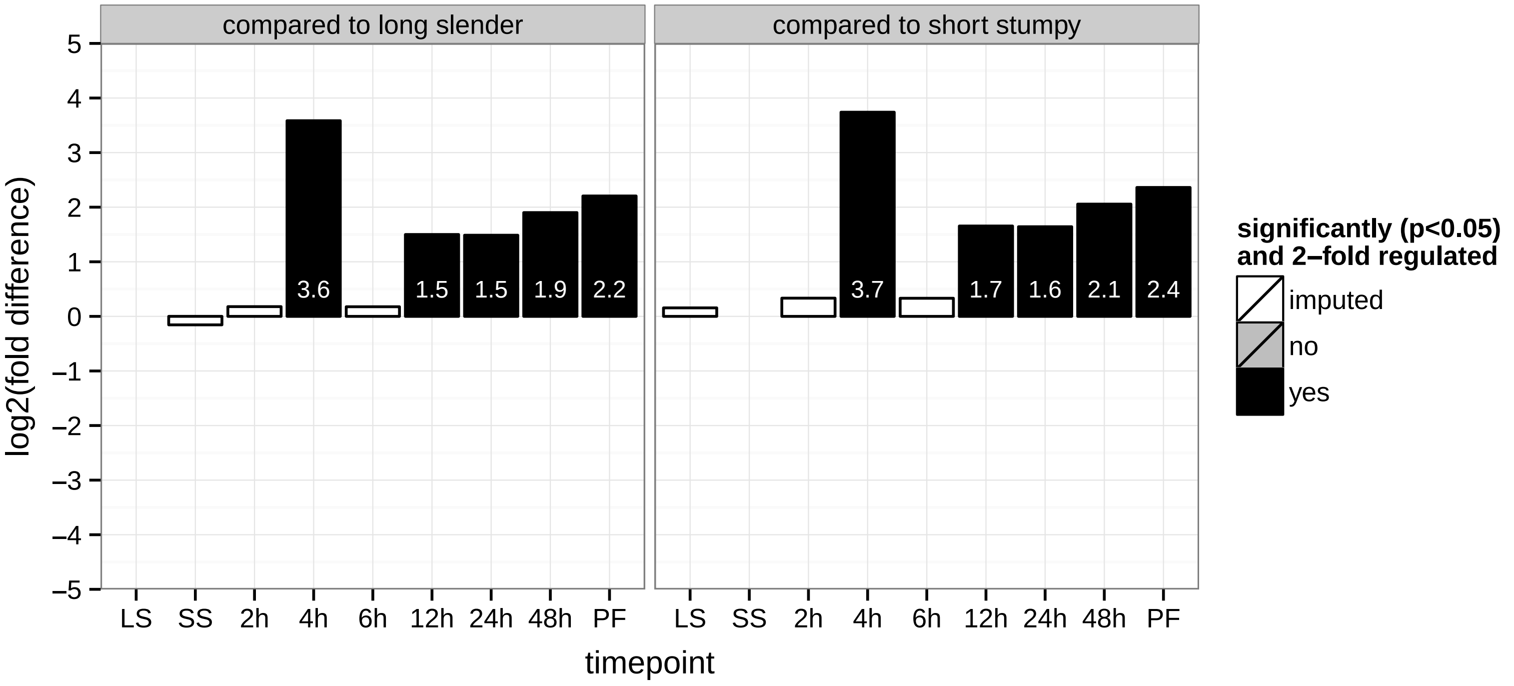
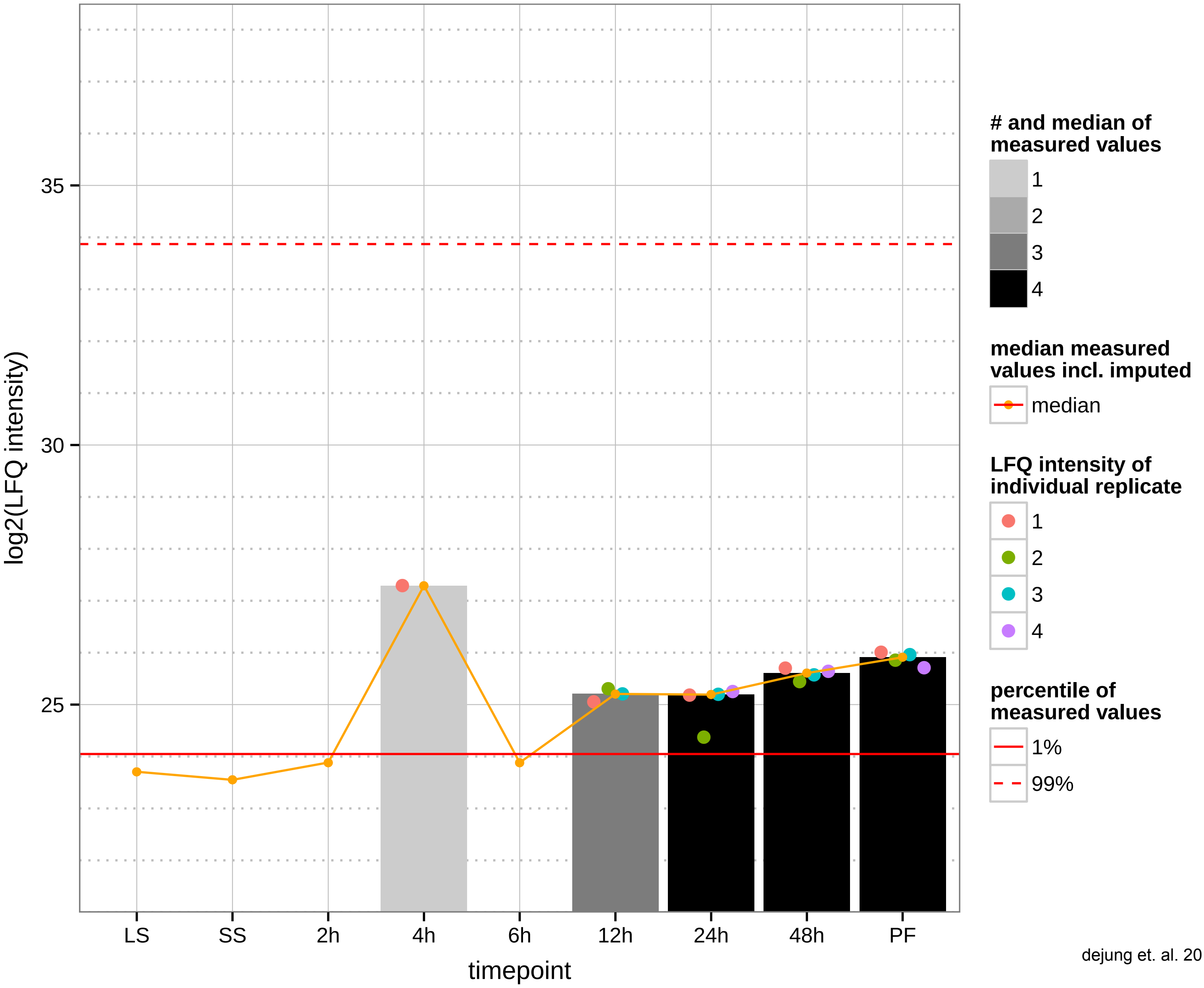
chrX additional, unordered contigs, epsilon tubulin, epsilon tubulin (TUBE1)
Tb927.10.1140;Tb11.0530
AGOF: GTP binding, GTPase activity, structural molecule activity
AGOC: microtubule, protein complex
AGOP: microtubule–based movement, protein polymerization, microtubule polymerization, microtubule–based movement
PGOF: GTP binding, GTPase activity
PGOC: protein complex
PGOP: GTP catabolic process, protein polymerization





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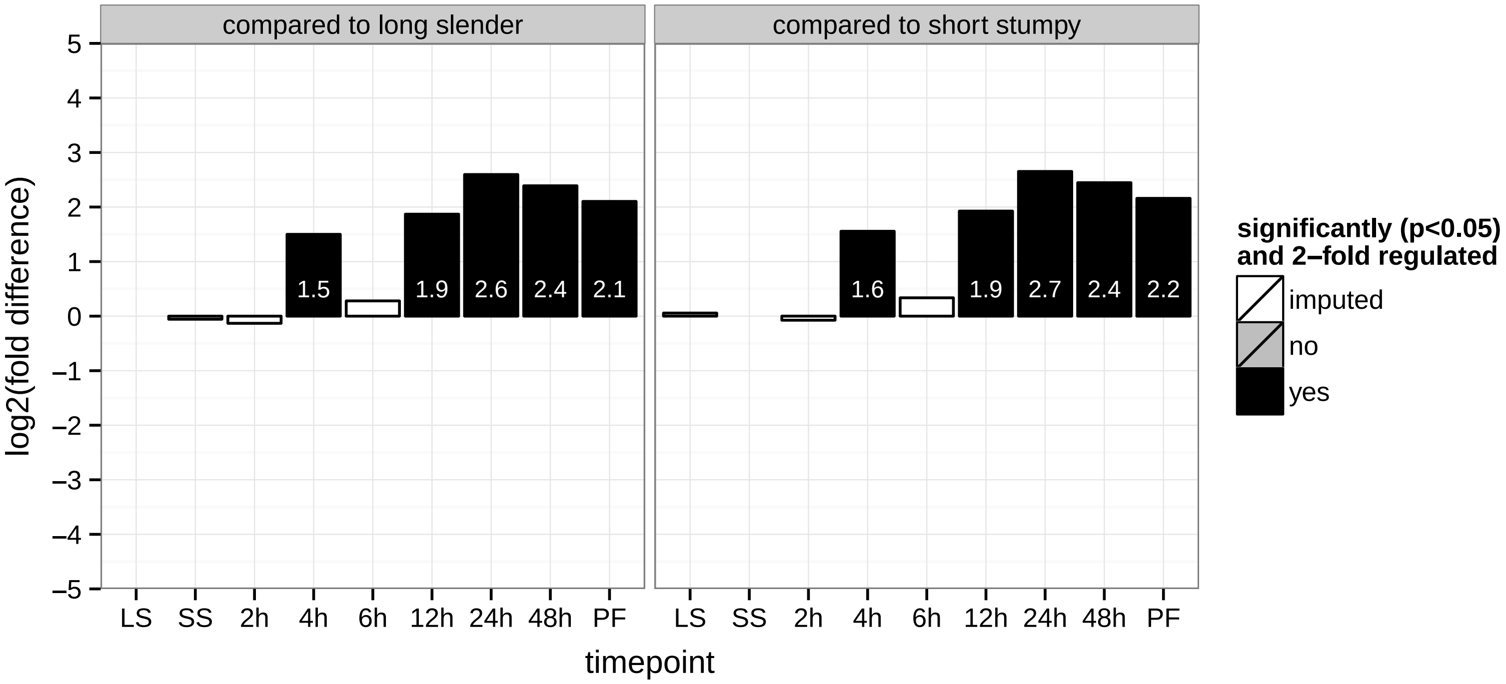
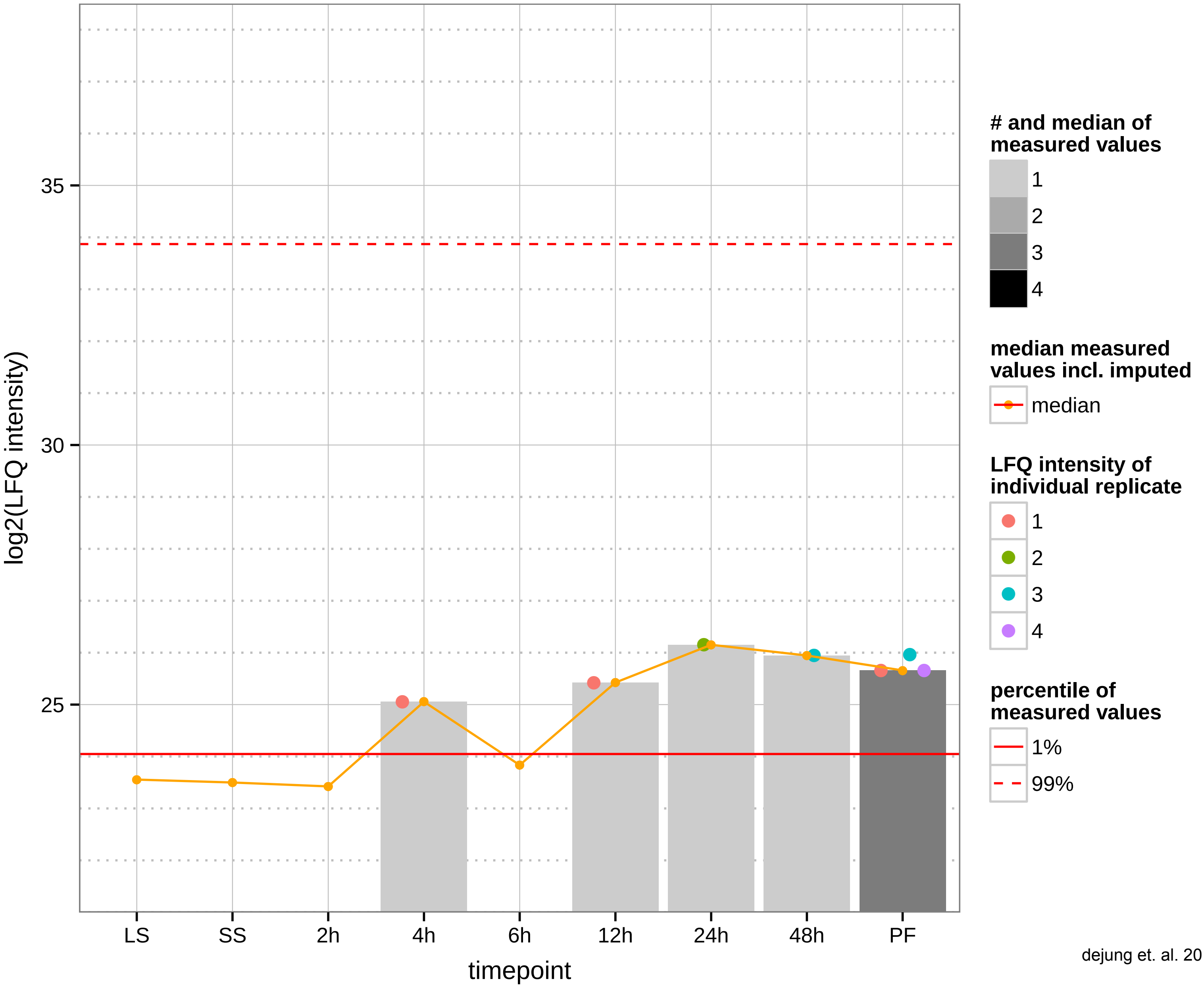
amino acid transporter, putative, putative (AATP6)
Tb927.8.4740;Tb927.8.4730;Tb927.8.4720;Tb927.8.4710;Tb927.8.4700;Tb11.v5.0569
AGOF: null, amine transmembrane transporter activity
AGOC: null, integral to membrane, membrane
AGOP: null, amino acid transport
PGOF: null
PGOC: null
PGOP: null





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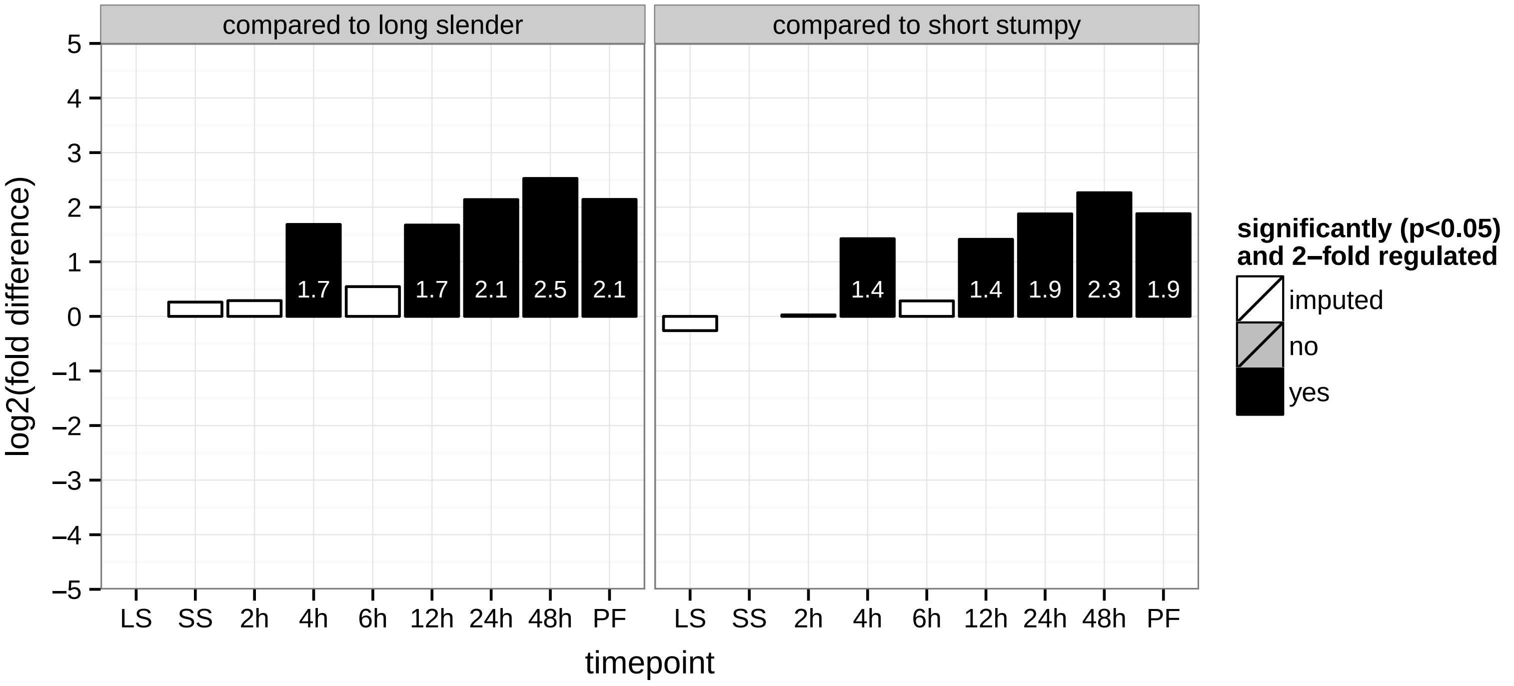
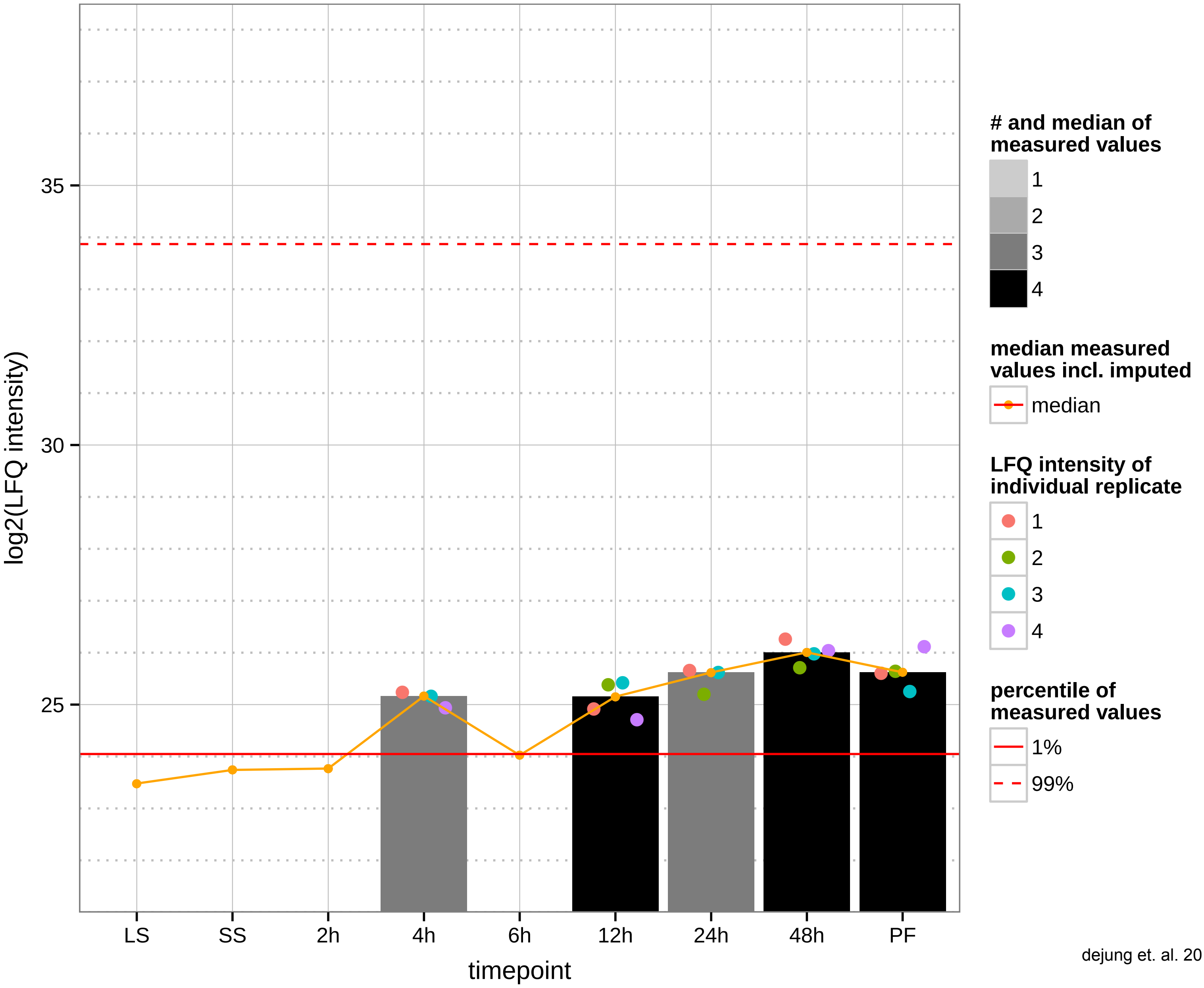
cytochrome c oxidase assembly factor, putative, electron transport protein SCO1/2
Tb927.1.1580
AGOF: copper ion binding
AGOC: mitochondrion
AGOP: respiratory chain complex IV assembly
PGOF: null
PGOC: null
PGOP: null





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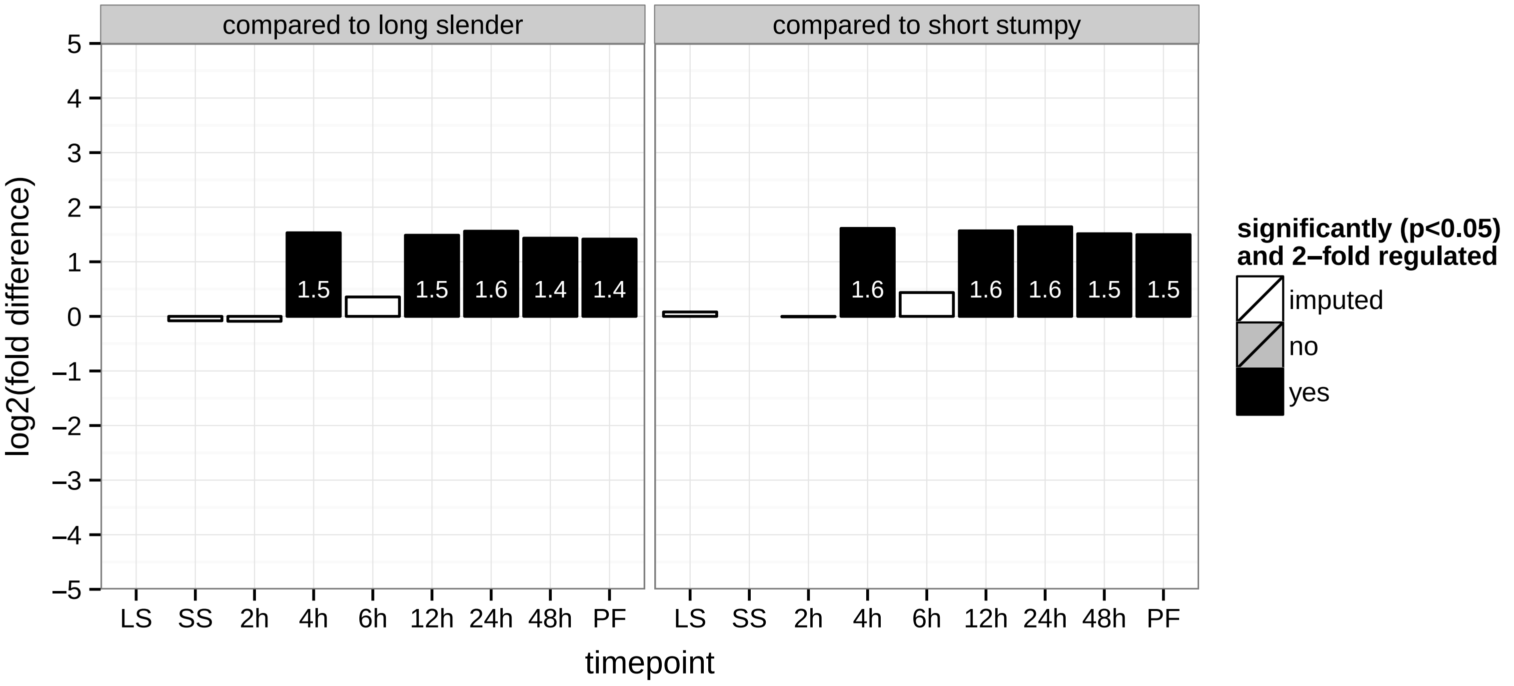
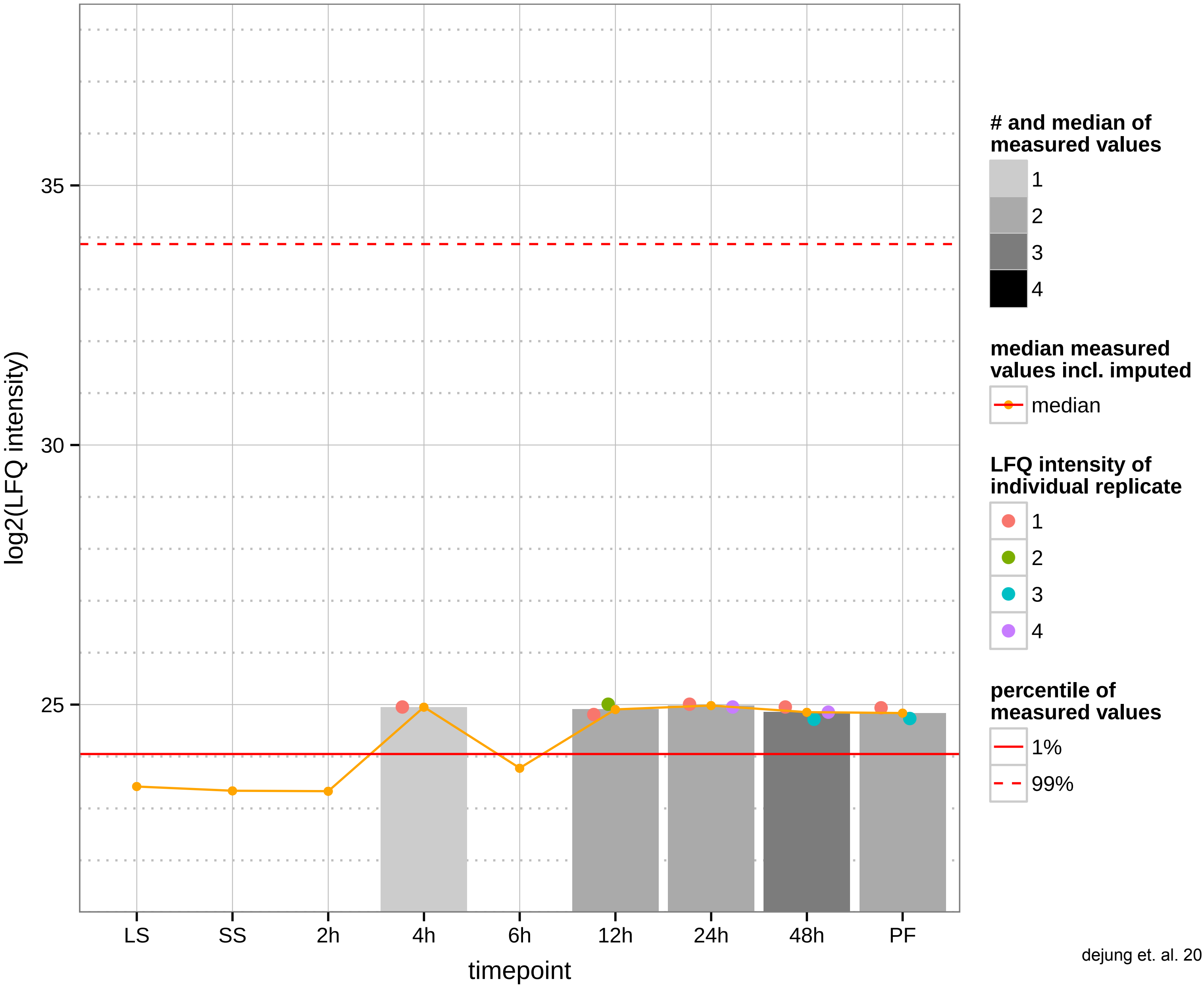
palmitoyl acyltransferase 2, putative
Tb927.10.10800
AGOF: zinc ion binding
AGOC: integral to membrane
AGOP: endocytosis, protein palmitoylation, transport
PGOF: zinc ion binding
PGOC: null
PGOP: null





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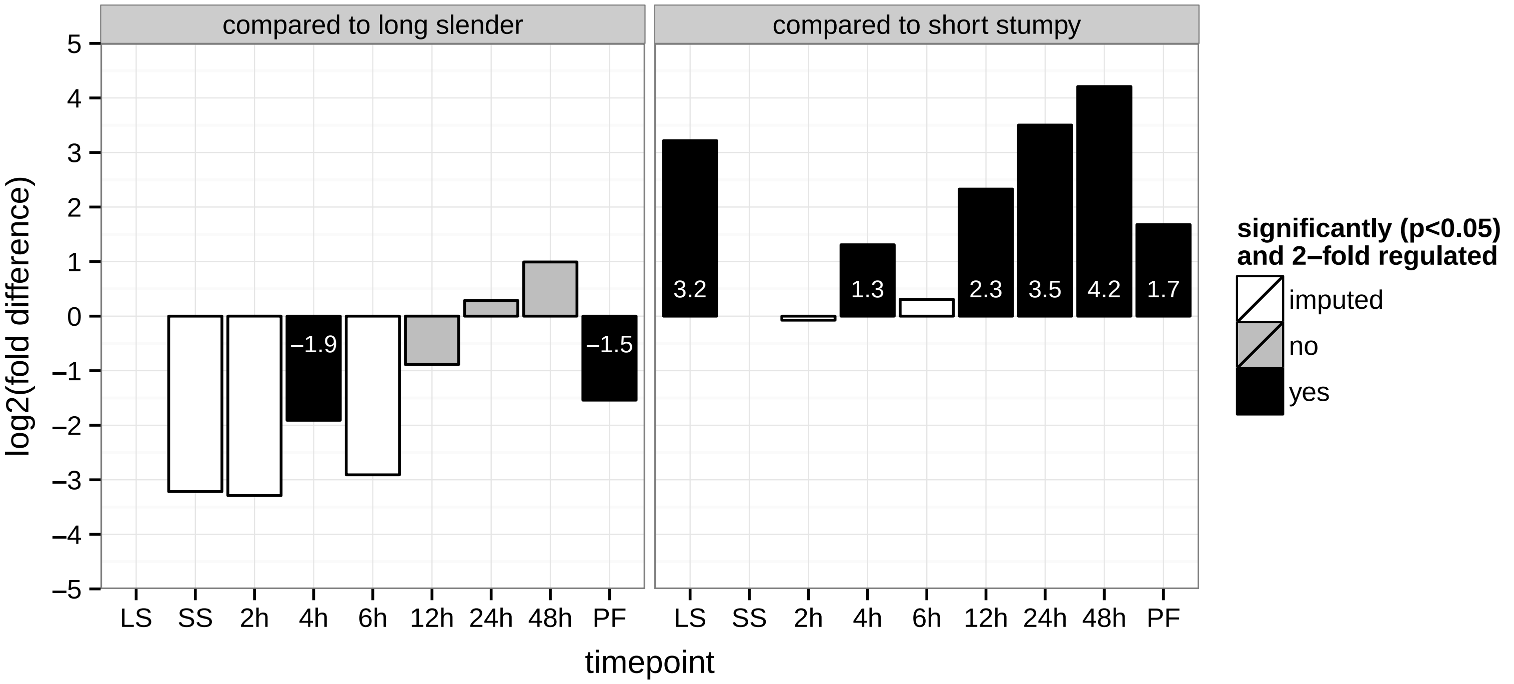
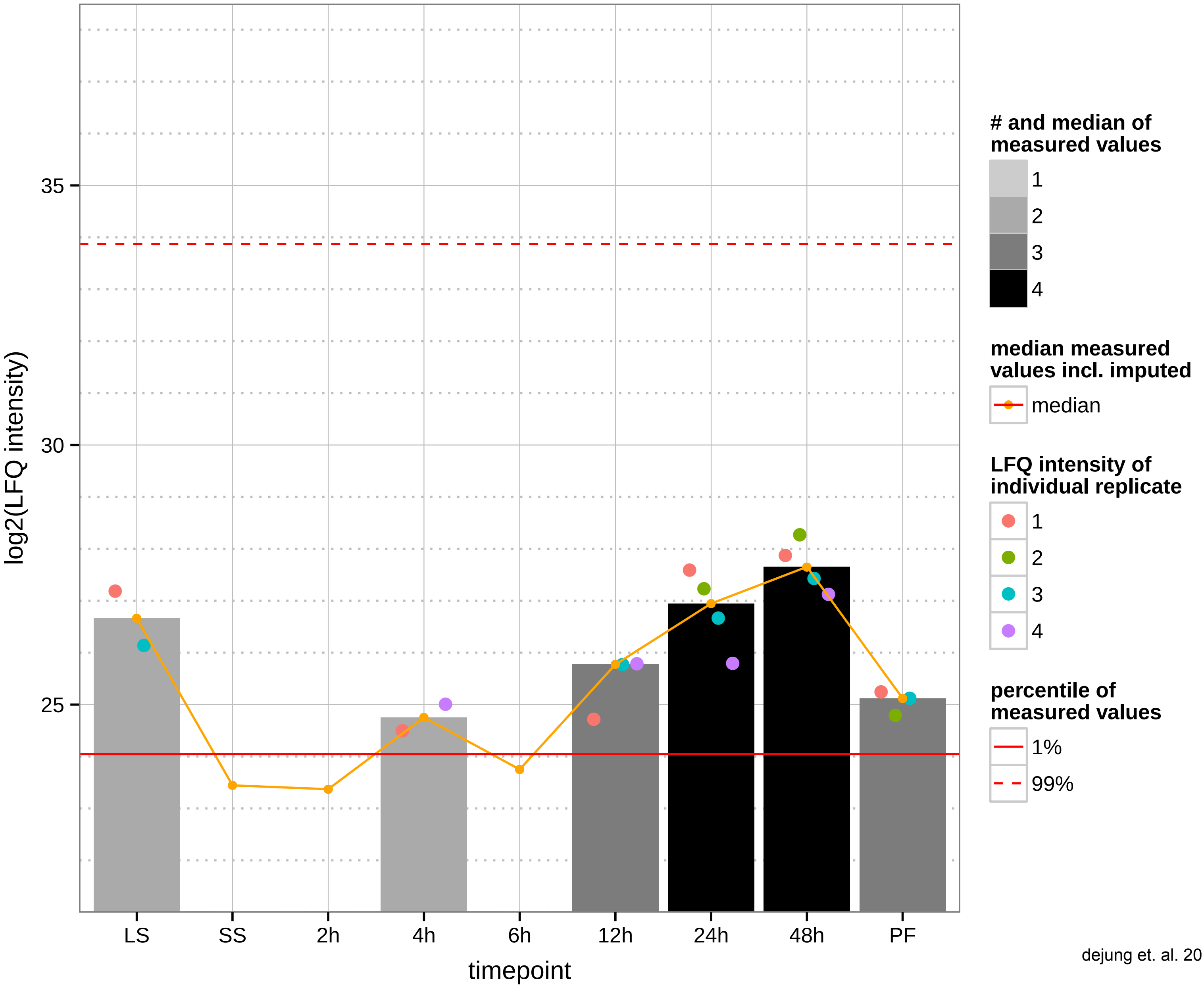
hypothetical protein, conserved
Tb927.10.13600
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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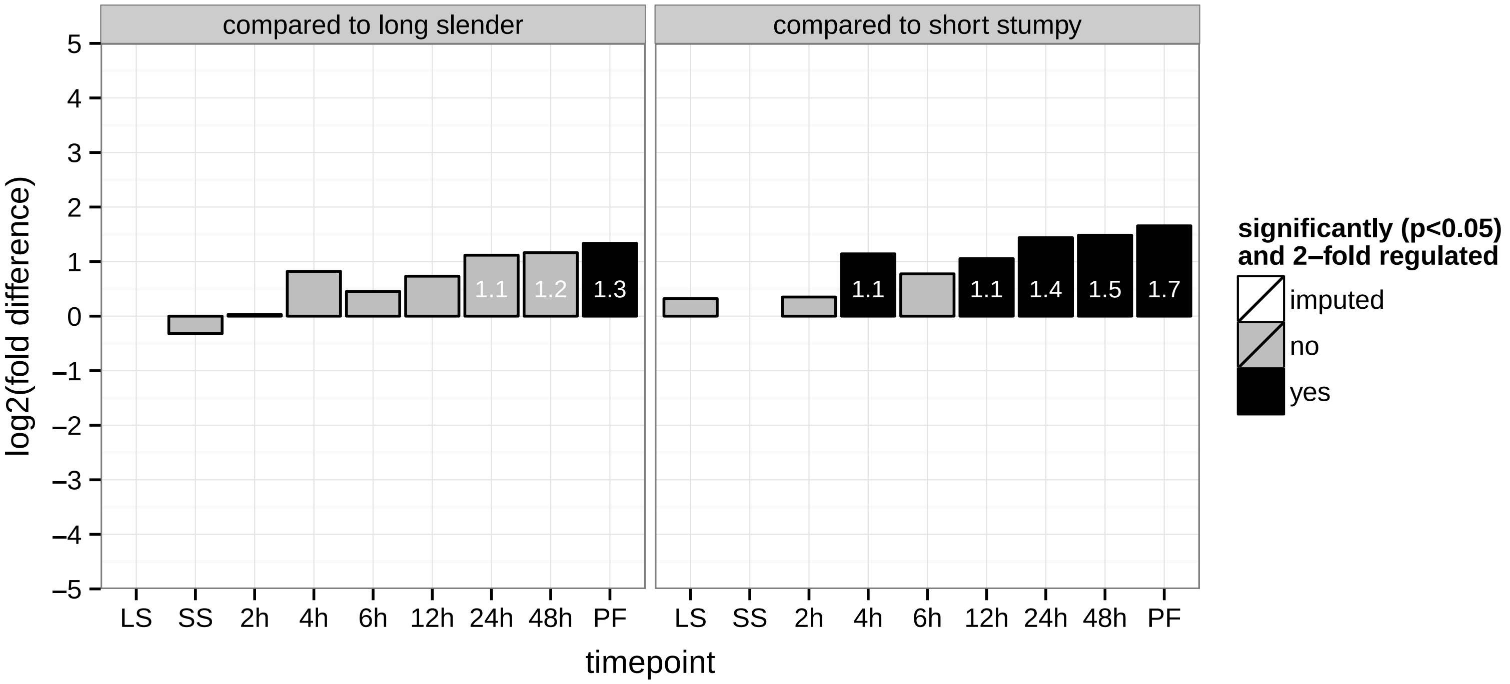
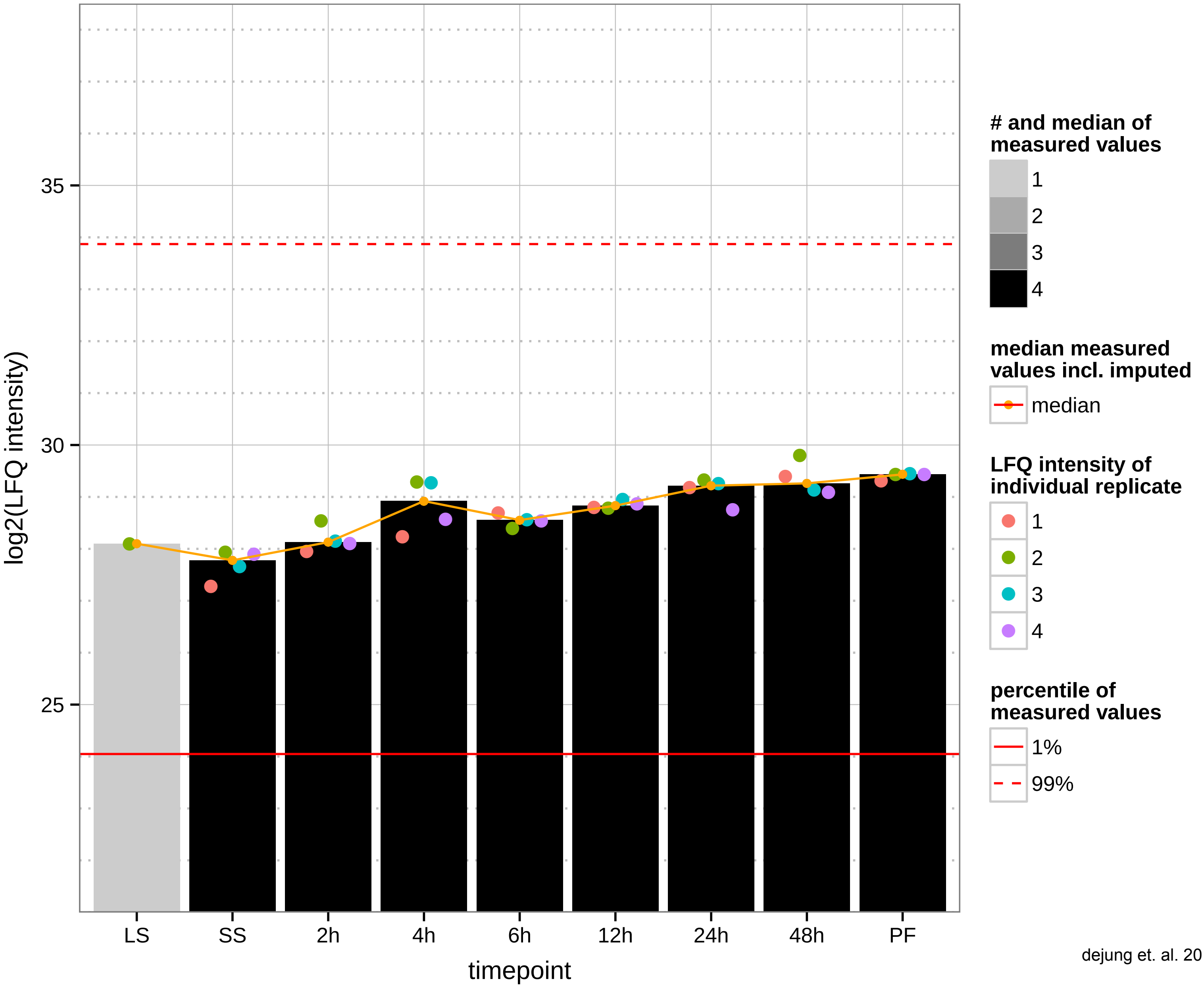
Zinc finger CCCH domain−containing protein 40, RNA binding protein, putative (ZC3H40)
Tb927.10.14950
AGOF: RNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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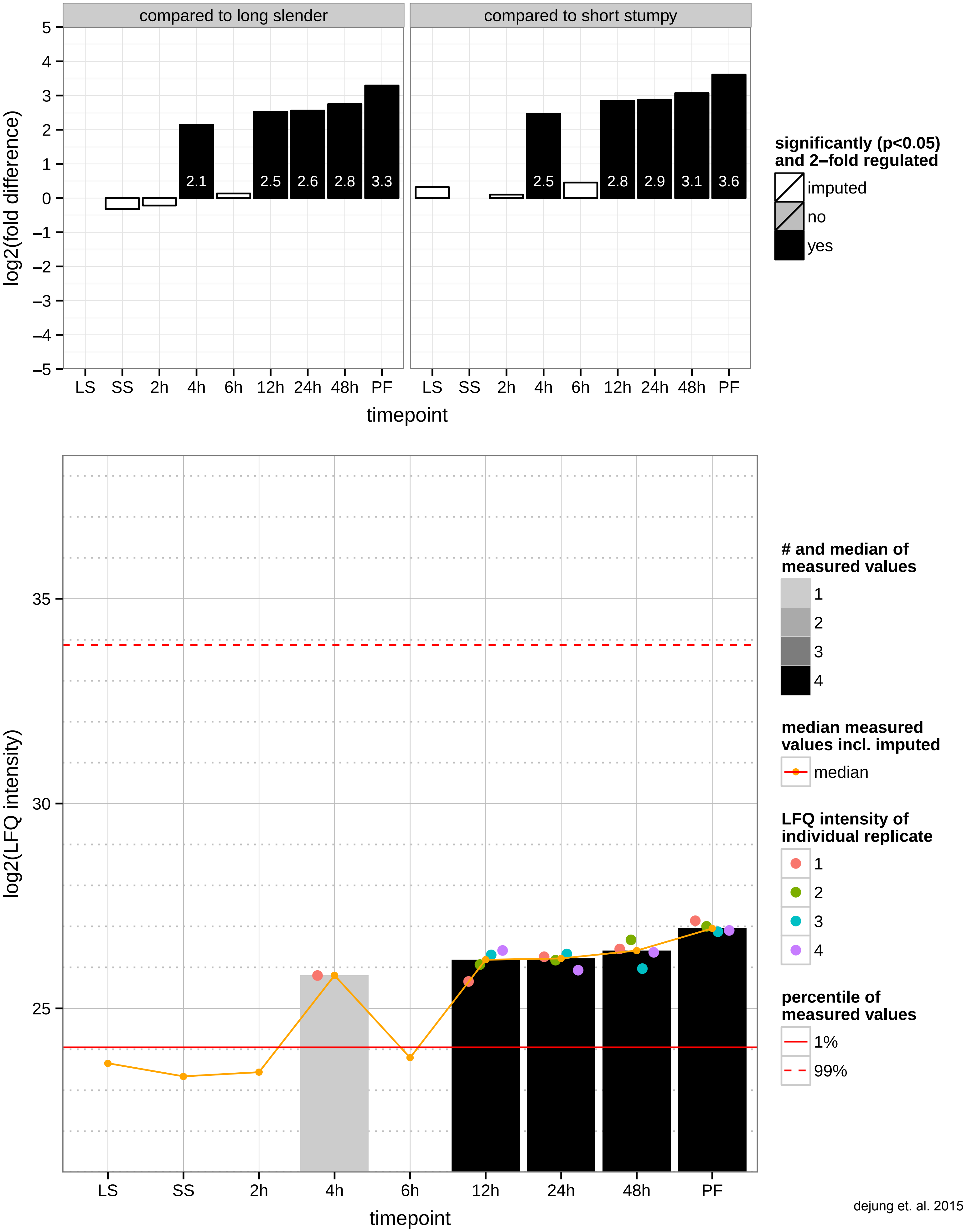
hypothetical protein, conserved
Tb927.10.2310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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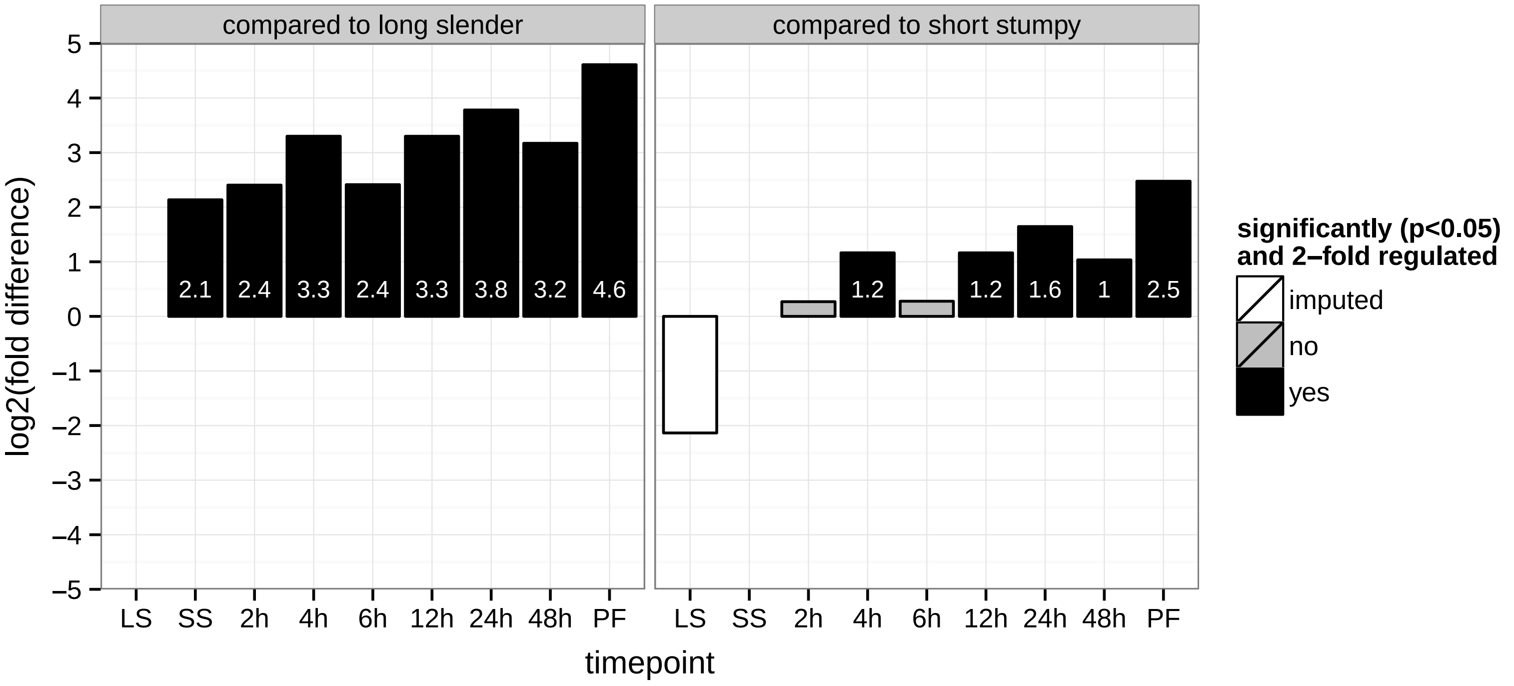
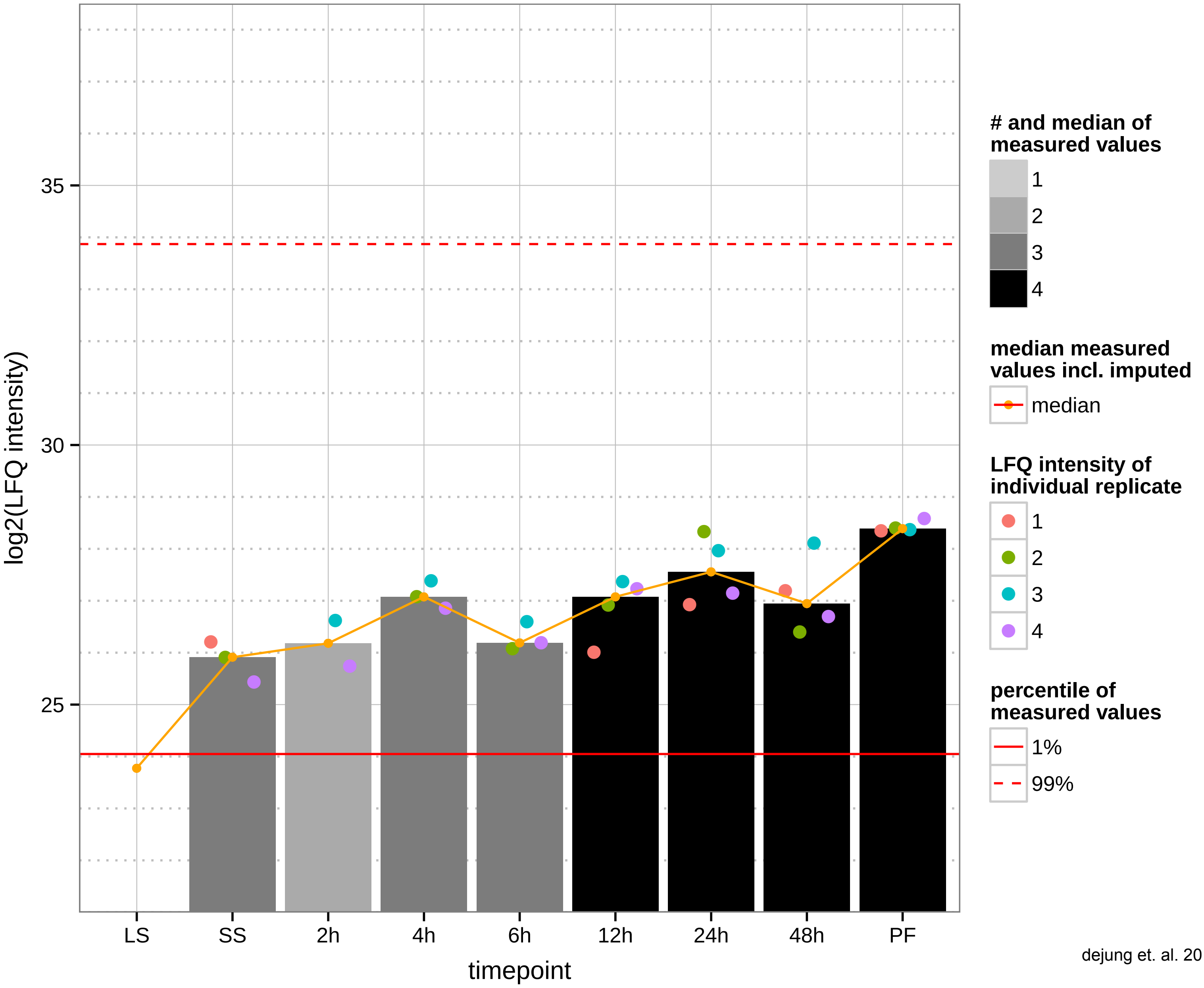
hypothetical protein, conserved
Tb927.10.5050
AGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, proton−transporting ATPase activity
AGOC: mitochondrial proton−transporting ATP synthase complex, catalytic core F(1), mitochondrion
AGOP: ATP synthesis coupled proton transport
PGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, proton−transporting ATPase activity
PGOC: mitochondrial proton−transporting ATP synthase complex, catalytic core F(1)
PGOP: ATP synthesis coupled proton transport





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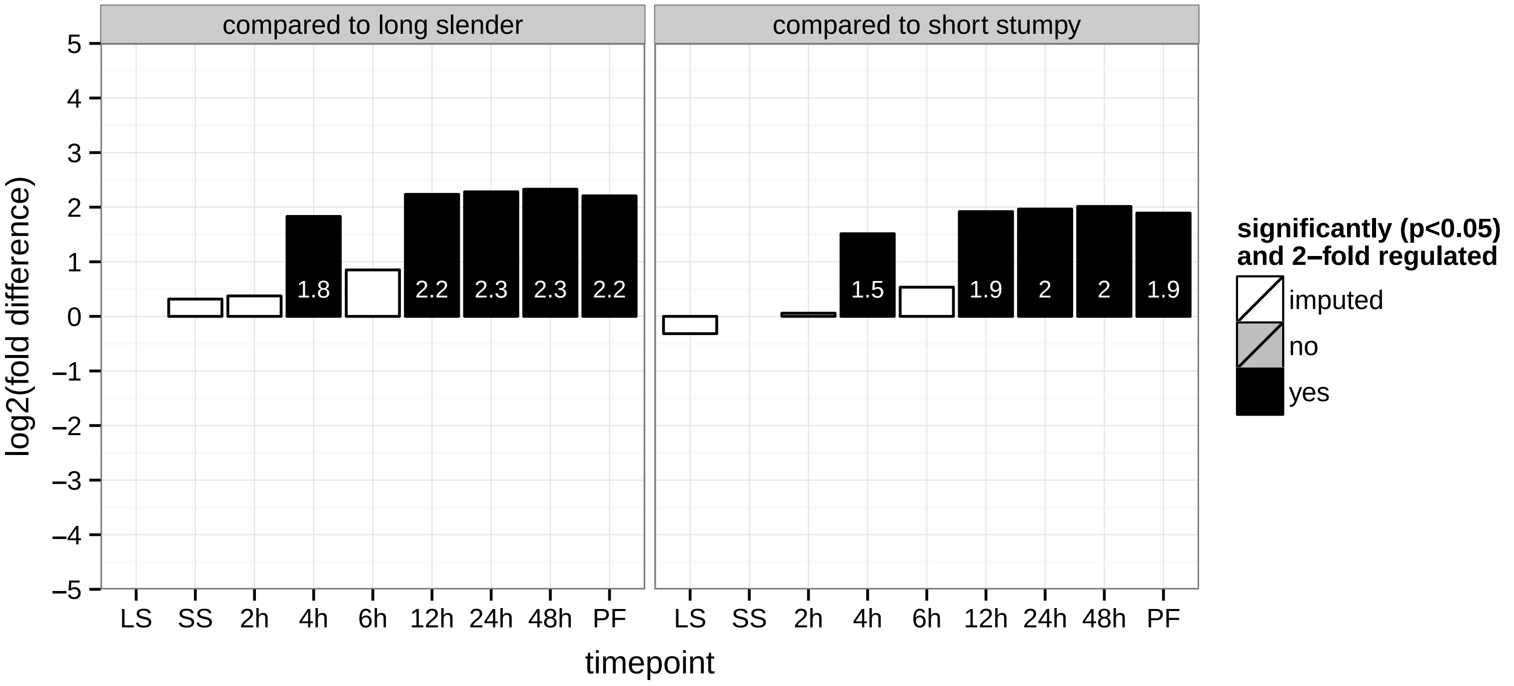
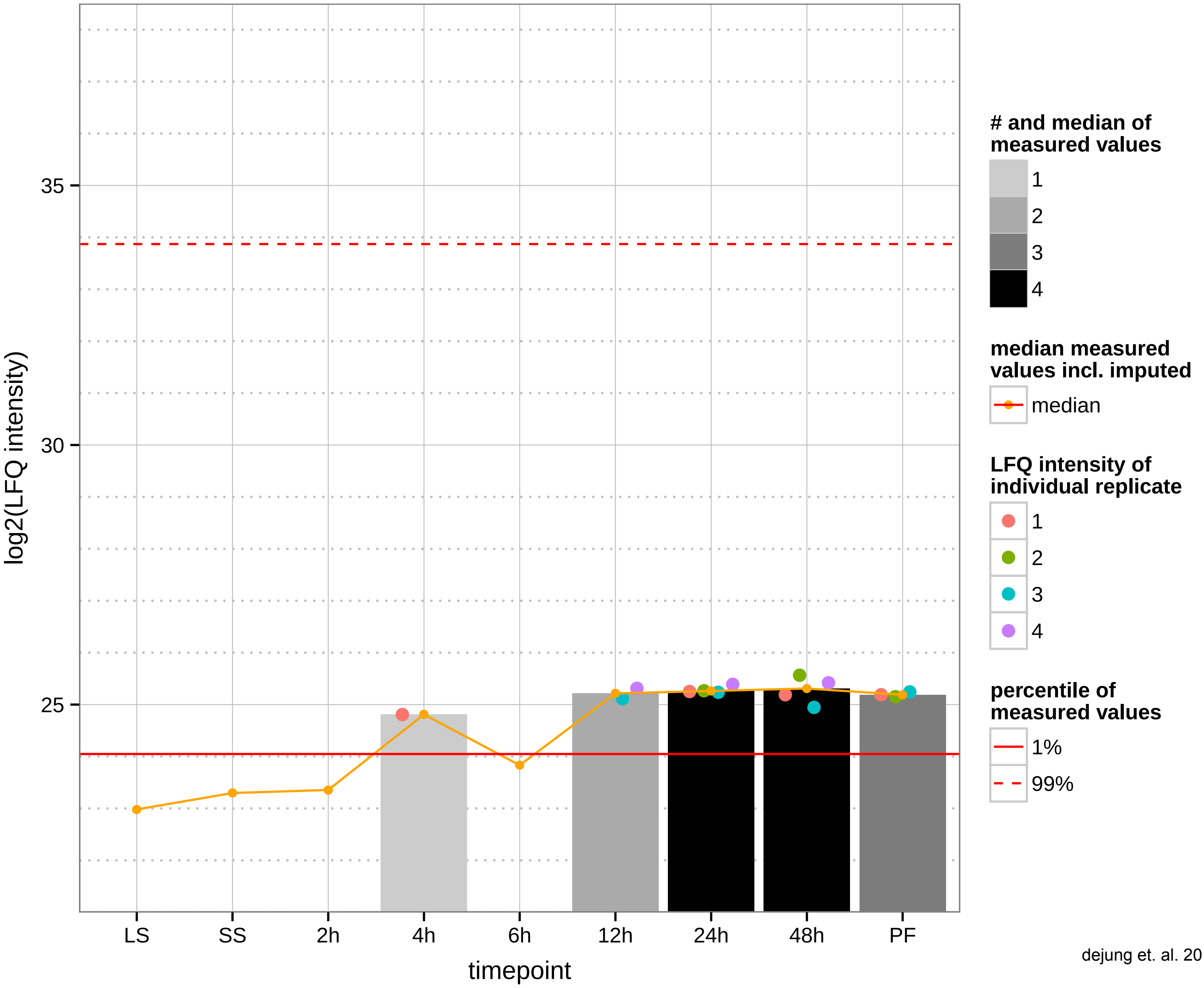
hypothetical protein, conserved
Tb927.10.5870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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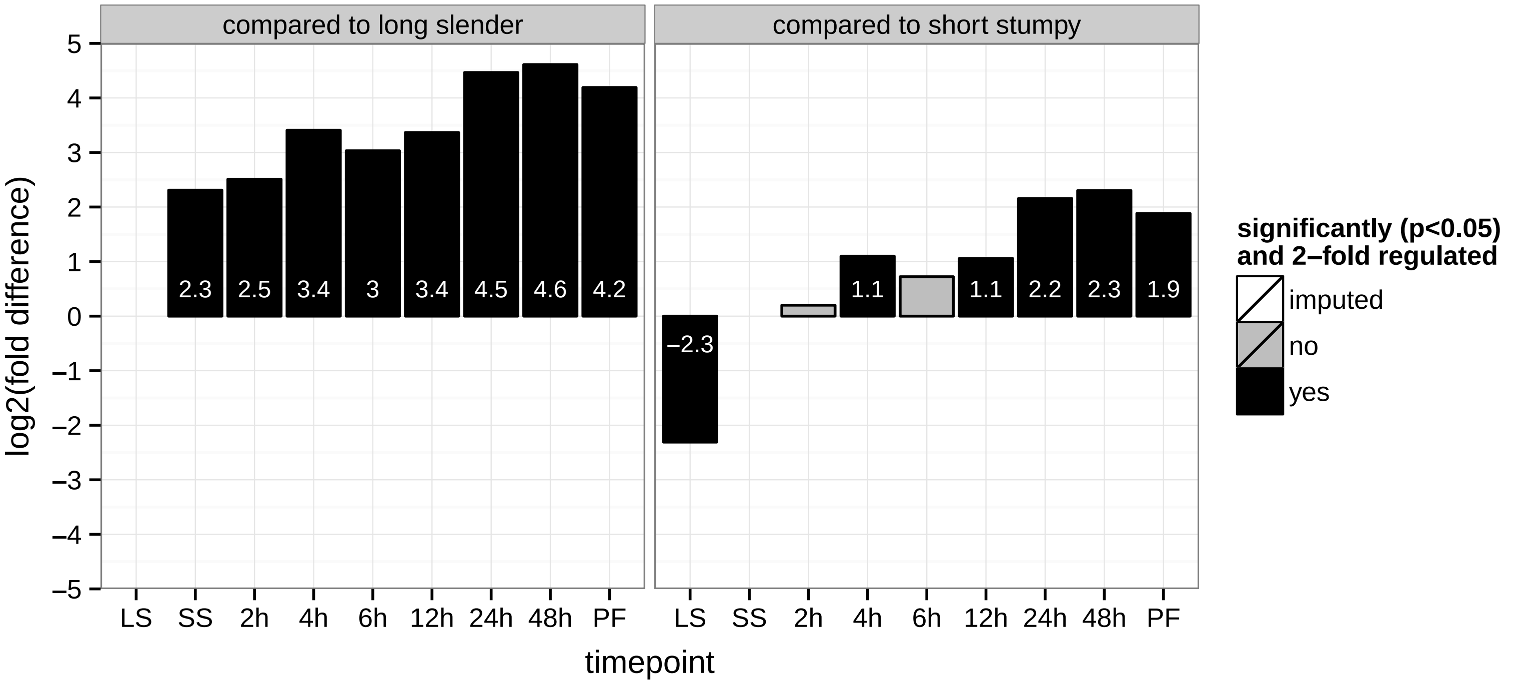
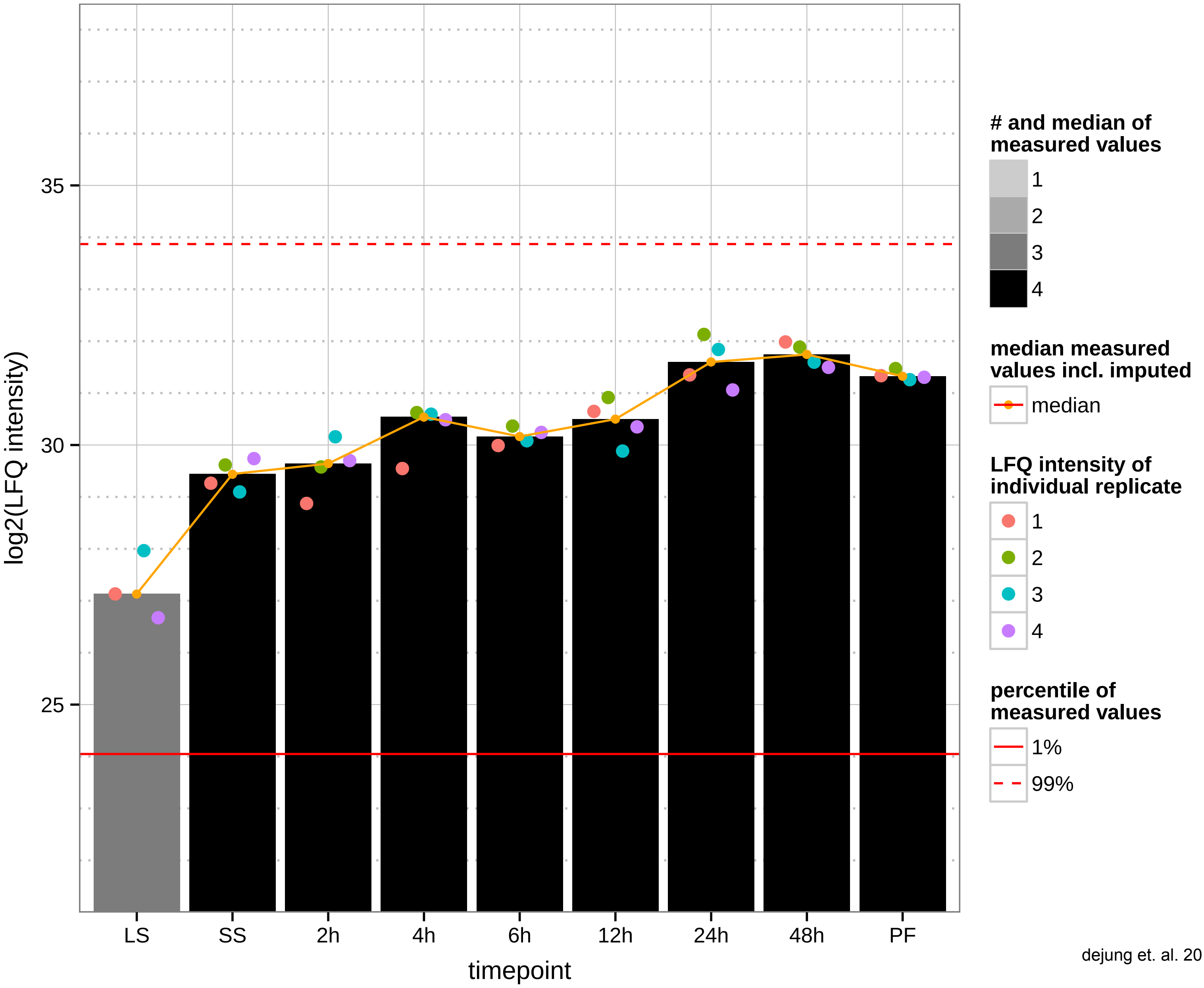
hypothetical protein, conserved
Tb927.10.8030
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism
PGOC: null
PGOP: ATP synthesis coupled proton transport





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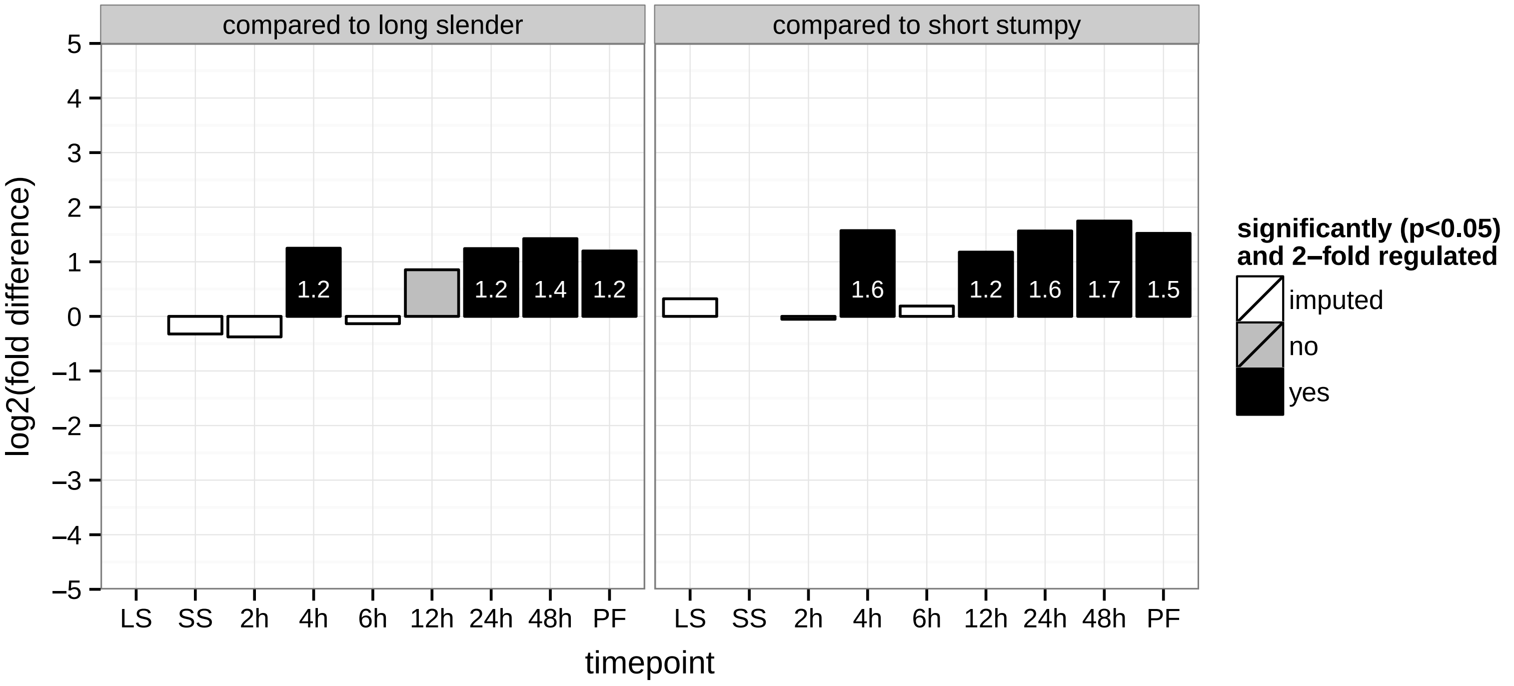
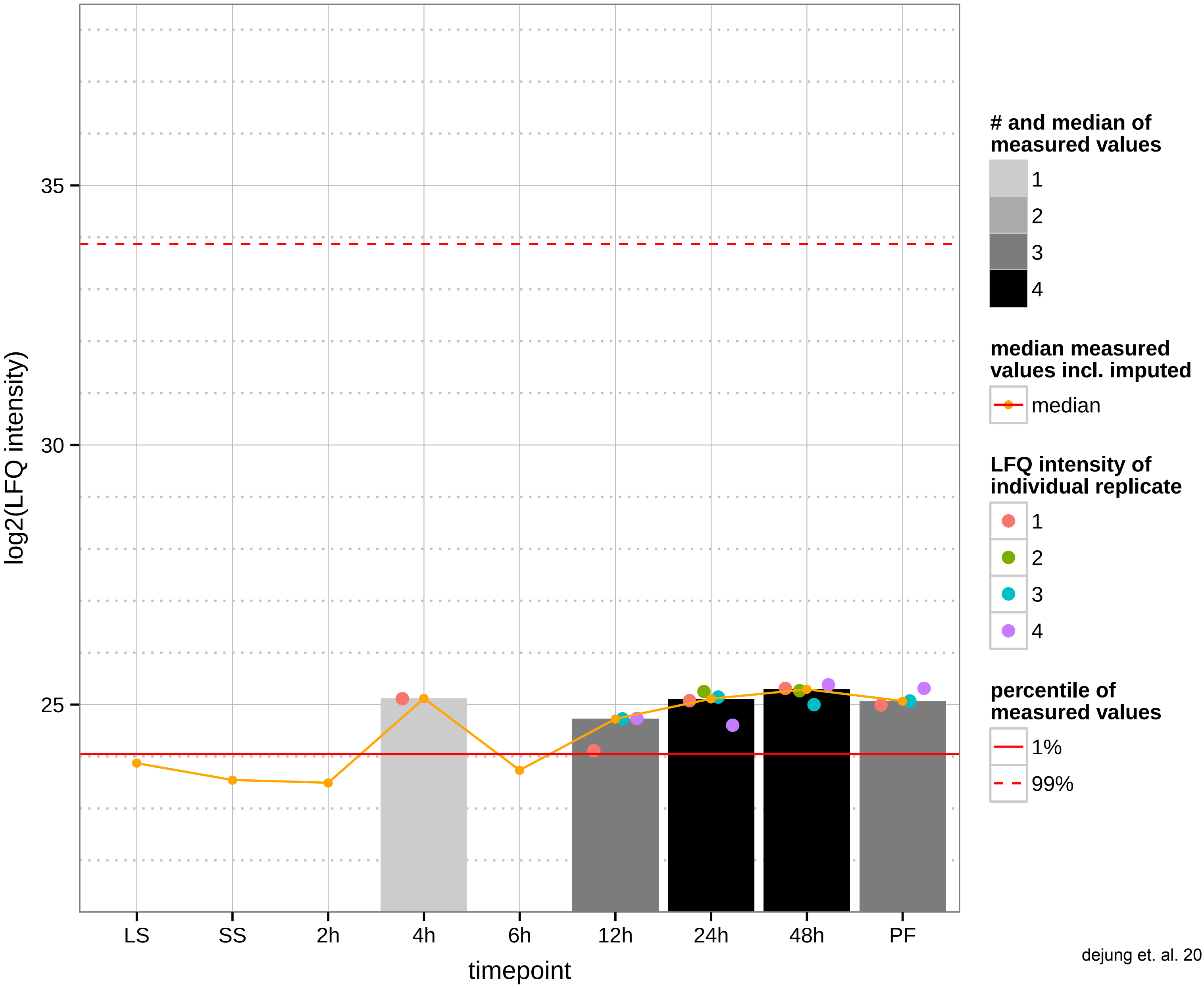
hypothetical protein, conserved
Tb927.10.8240
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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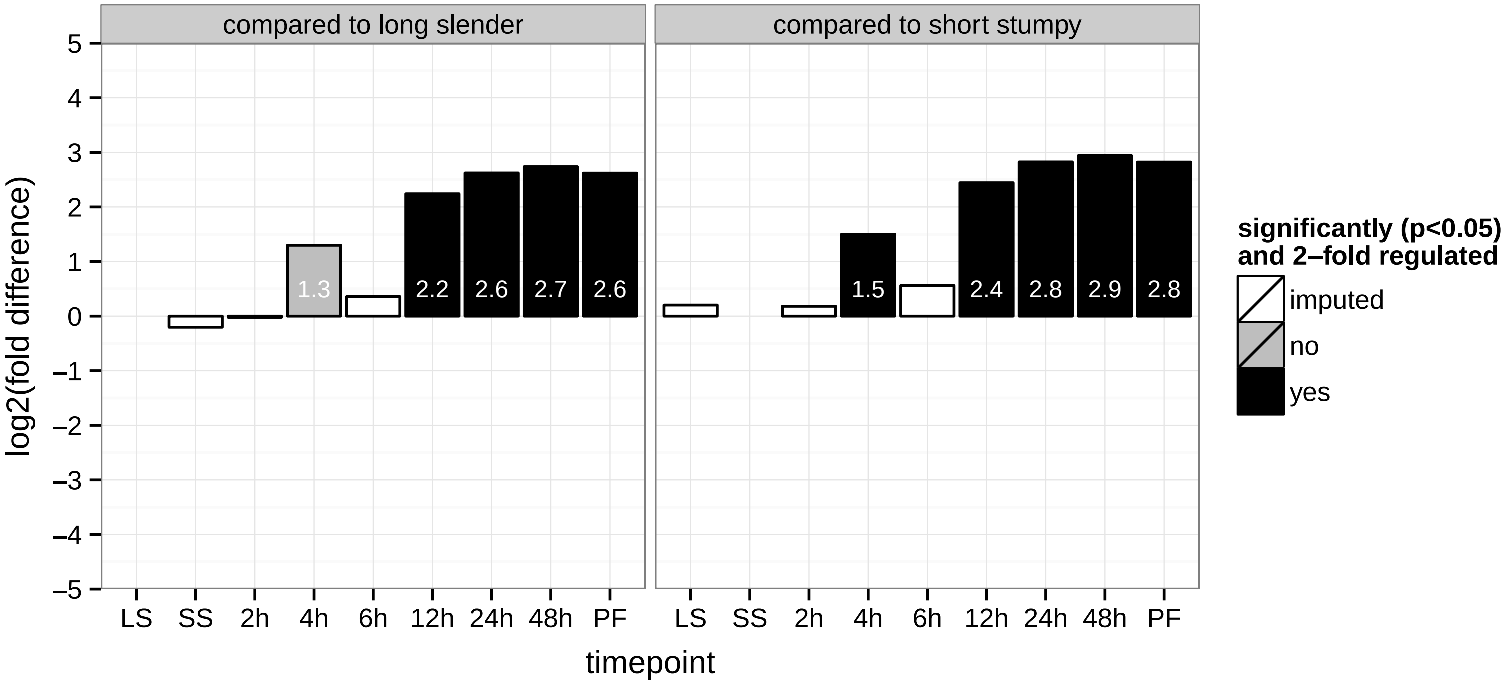
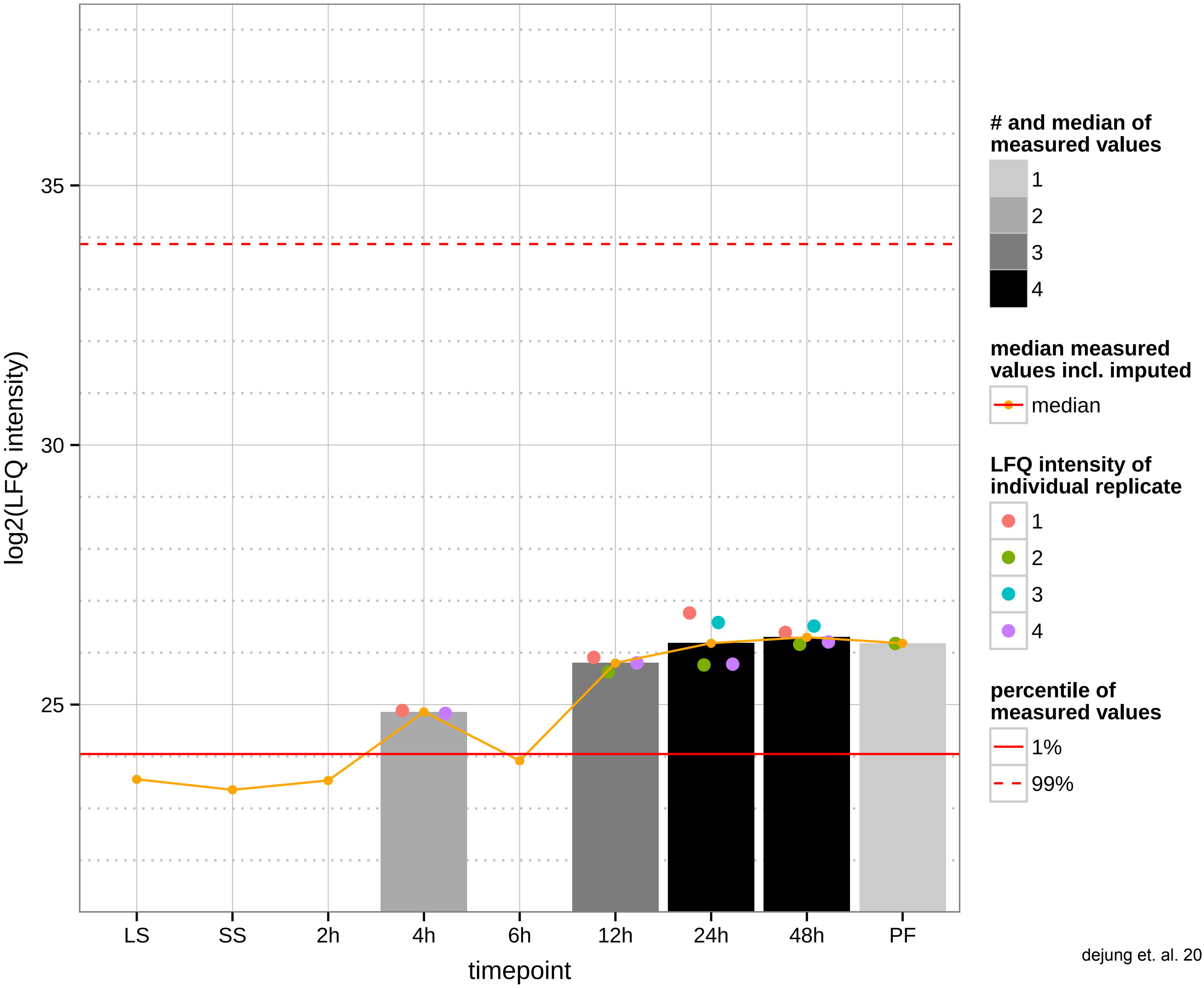
hypothetical protein, conserved
Tb927.11.10040
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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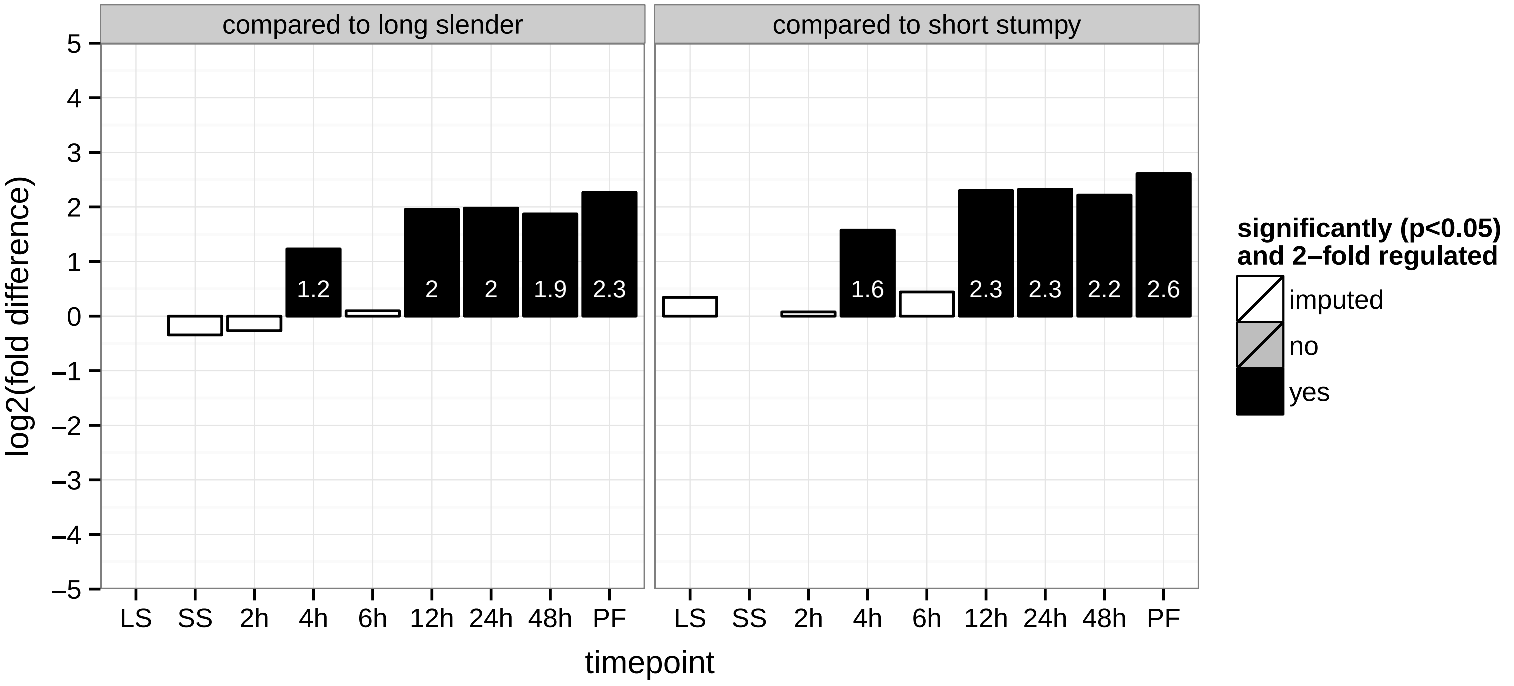
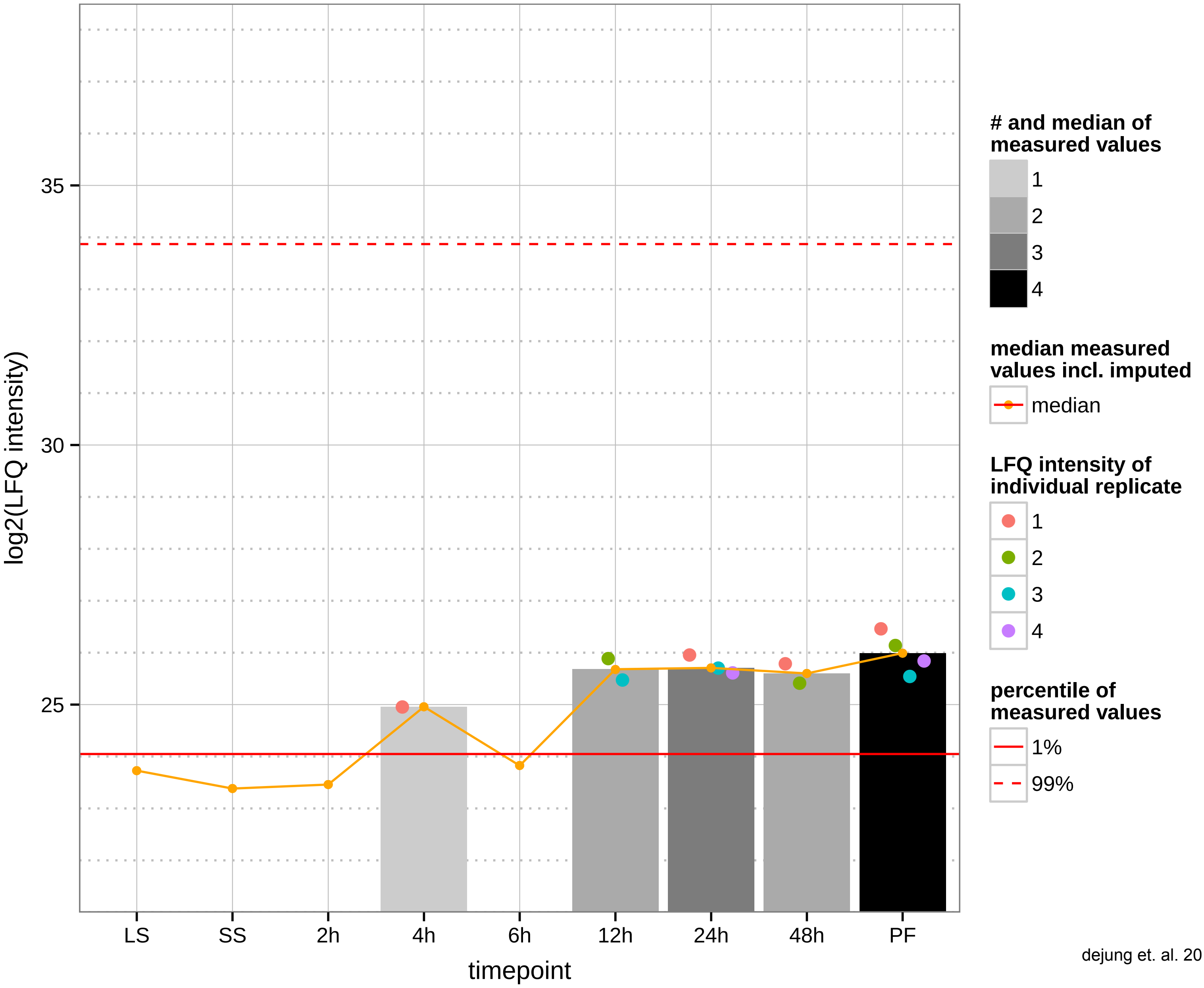
RNA processing factor 1, putative, ribosome biogenesis protein
Tb927.11.1050
AGOF: rRNA primary transcript binding
AGOC: nucleolus
AGOP: RNA processing
PGOF: null
PGOC: null
PGOP: null





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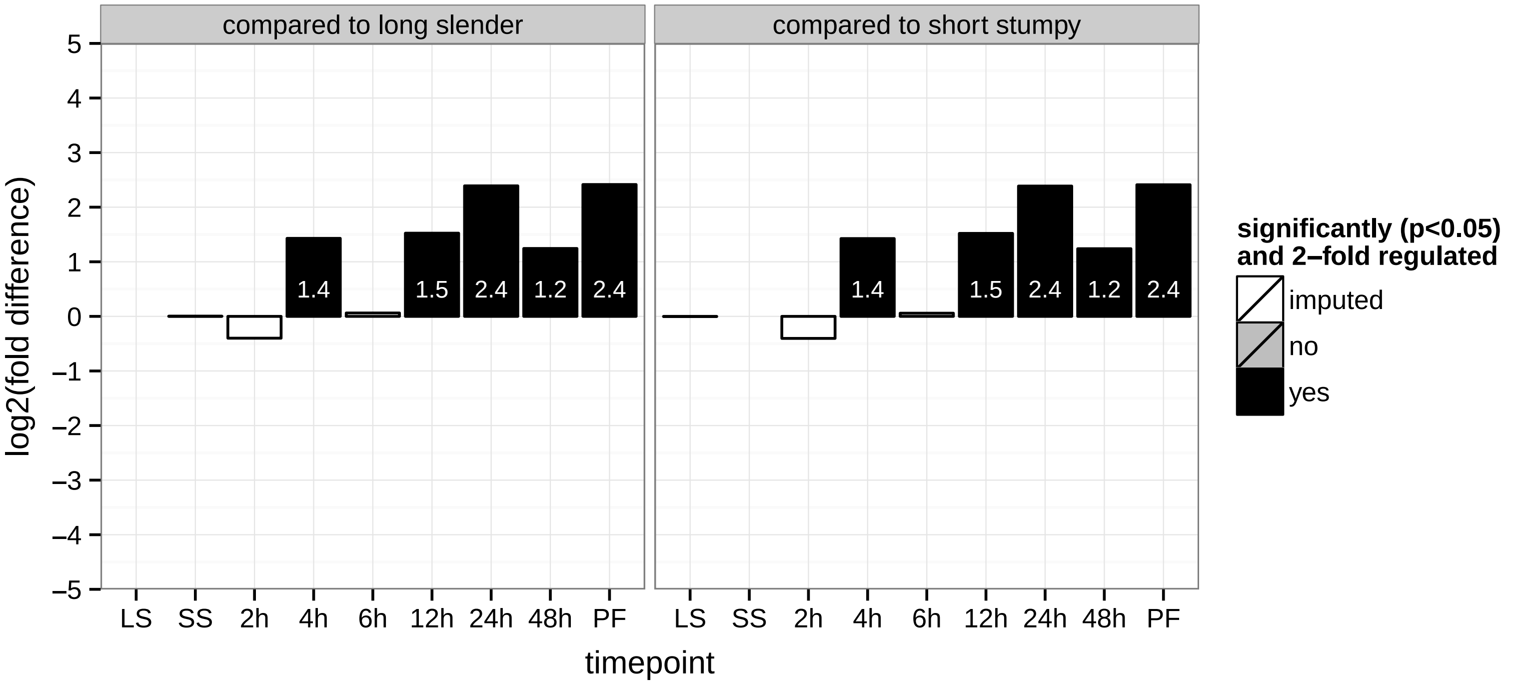
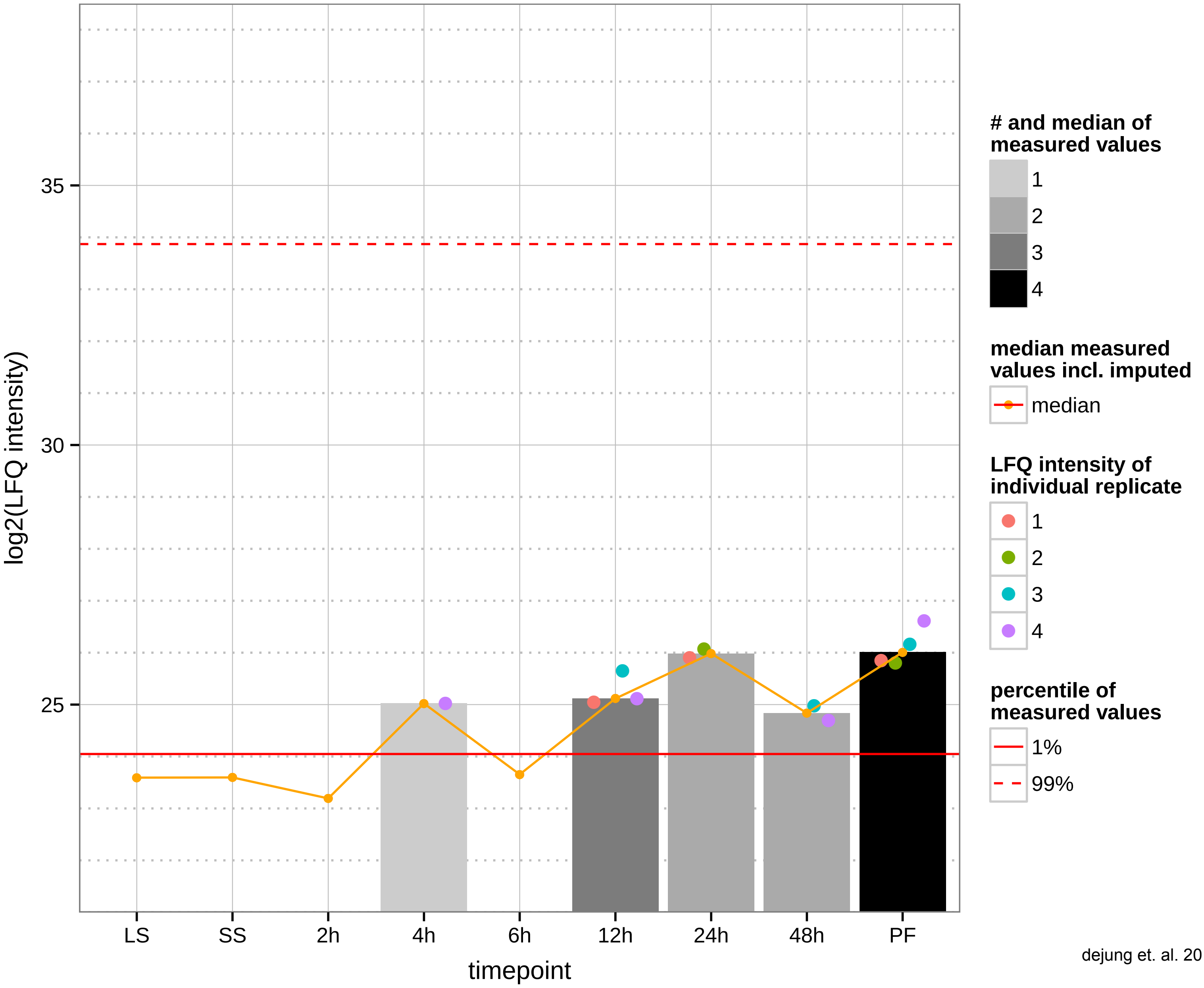
DNA–directed RNA polymerase II, putative, RNA polymerase subunit, putative (RPB11)
Tb927.11.2200
AGOF: DNA binding, DNA–directed RNA polymerase activity, protein dimerization activity
AGOC: nucleus
AGOP: transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA–dependent





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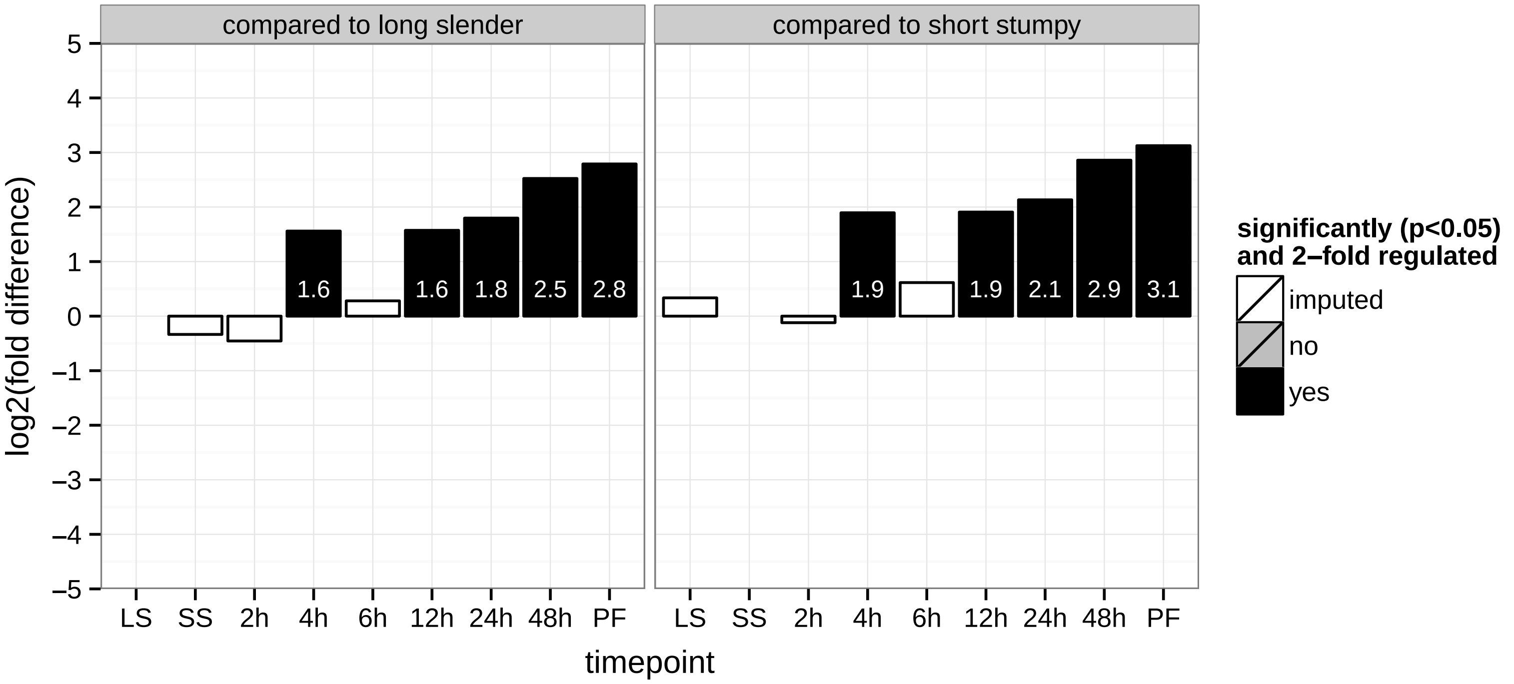
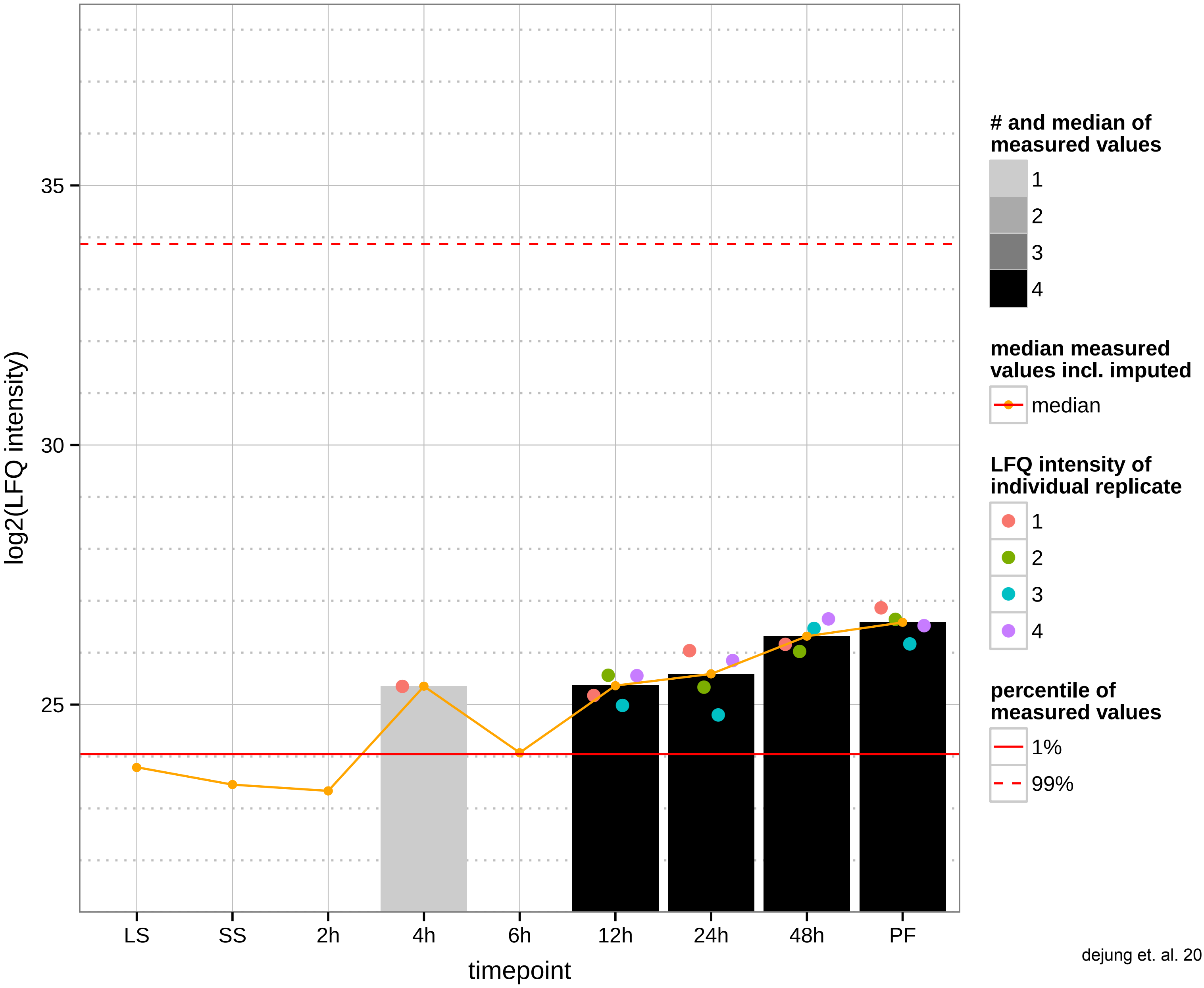
glycosomal transporter (GAT2) (GAT2)
Tb927.11.3130
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances
AGOC: glycosome membrane, integral to membrane
AGOP: fatty acid transport
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of substances, nucleoside–triphosphatase activity
PGOC: integral to membrane, membrane
PGOP: transmembrane transport, transport





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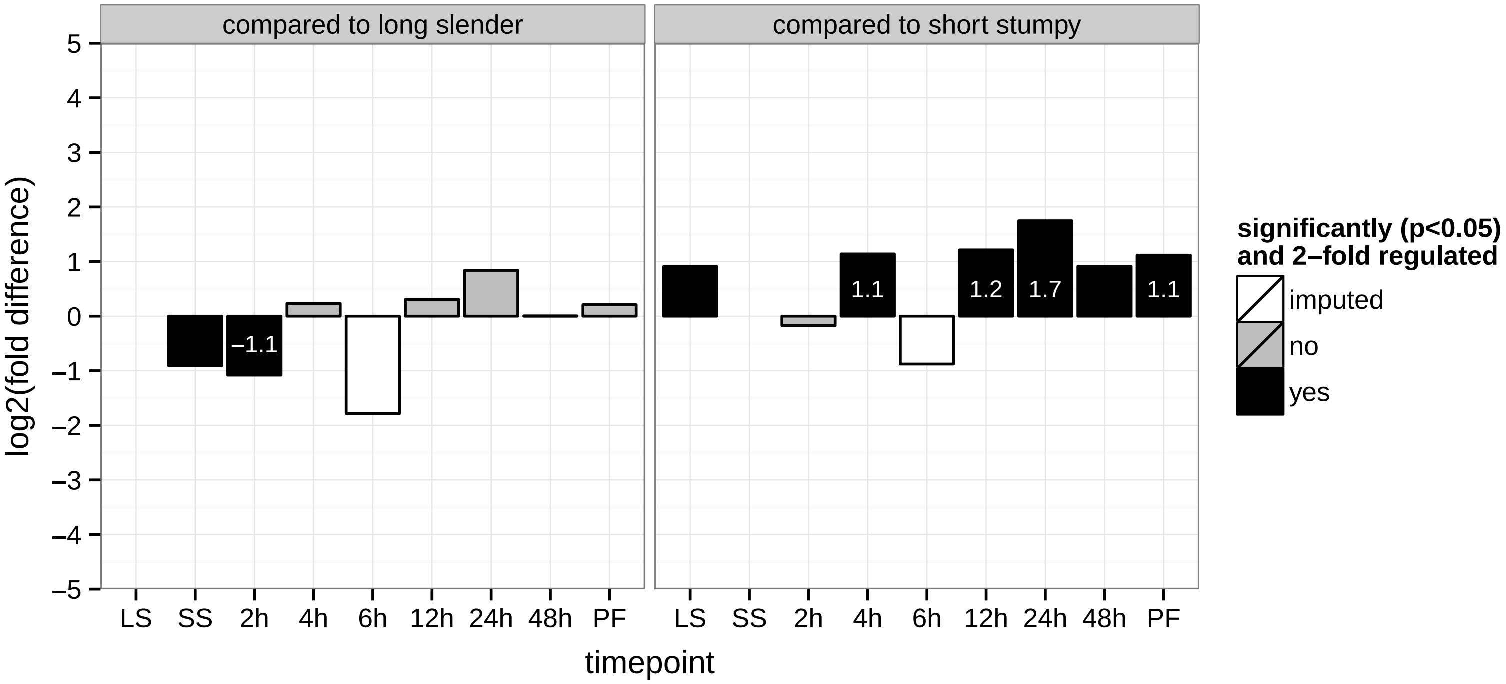
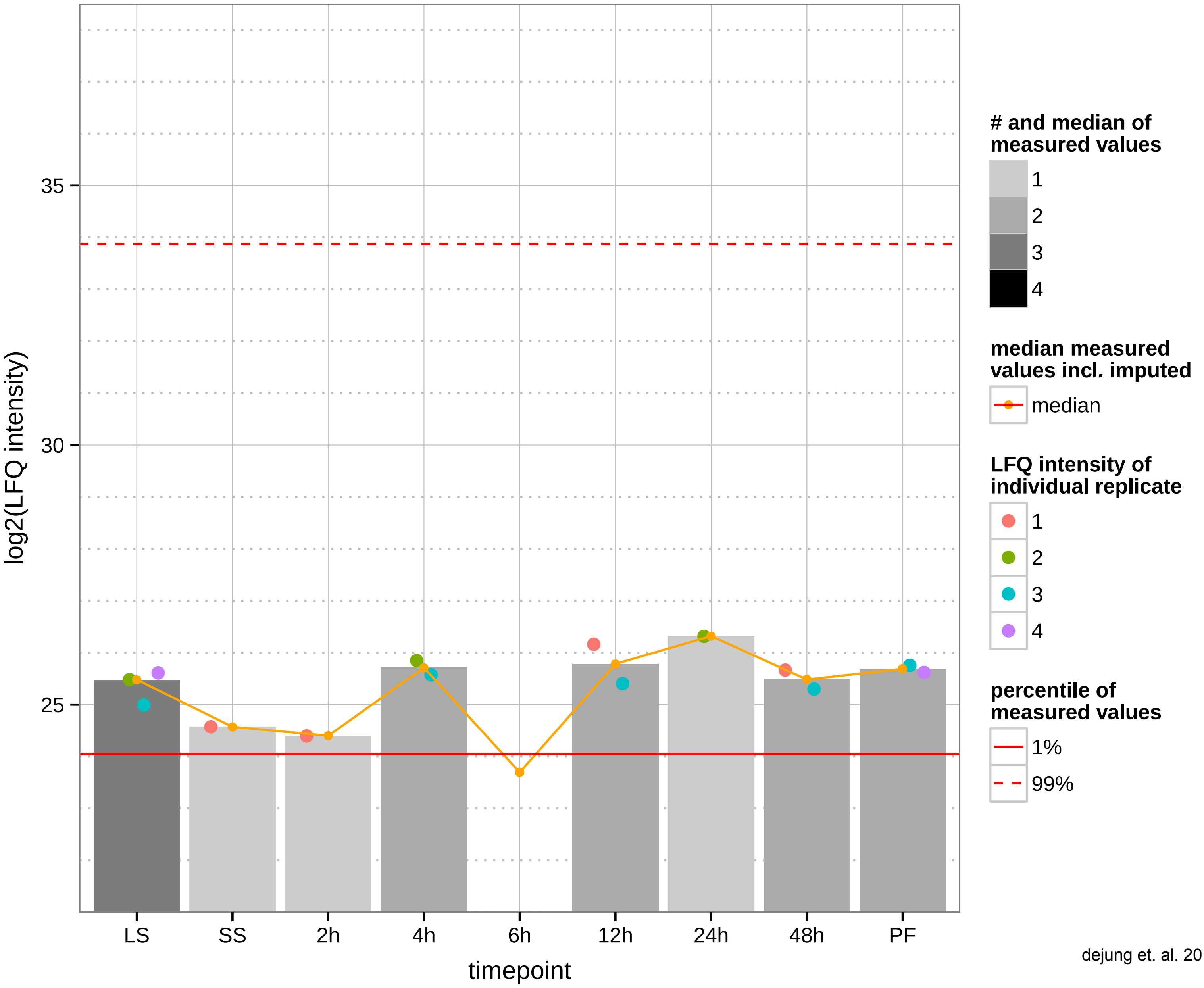
hypothetical protein
Tb927.11.3370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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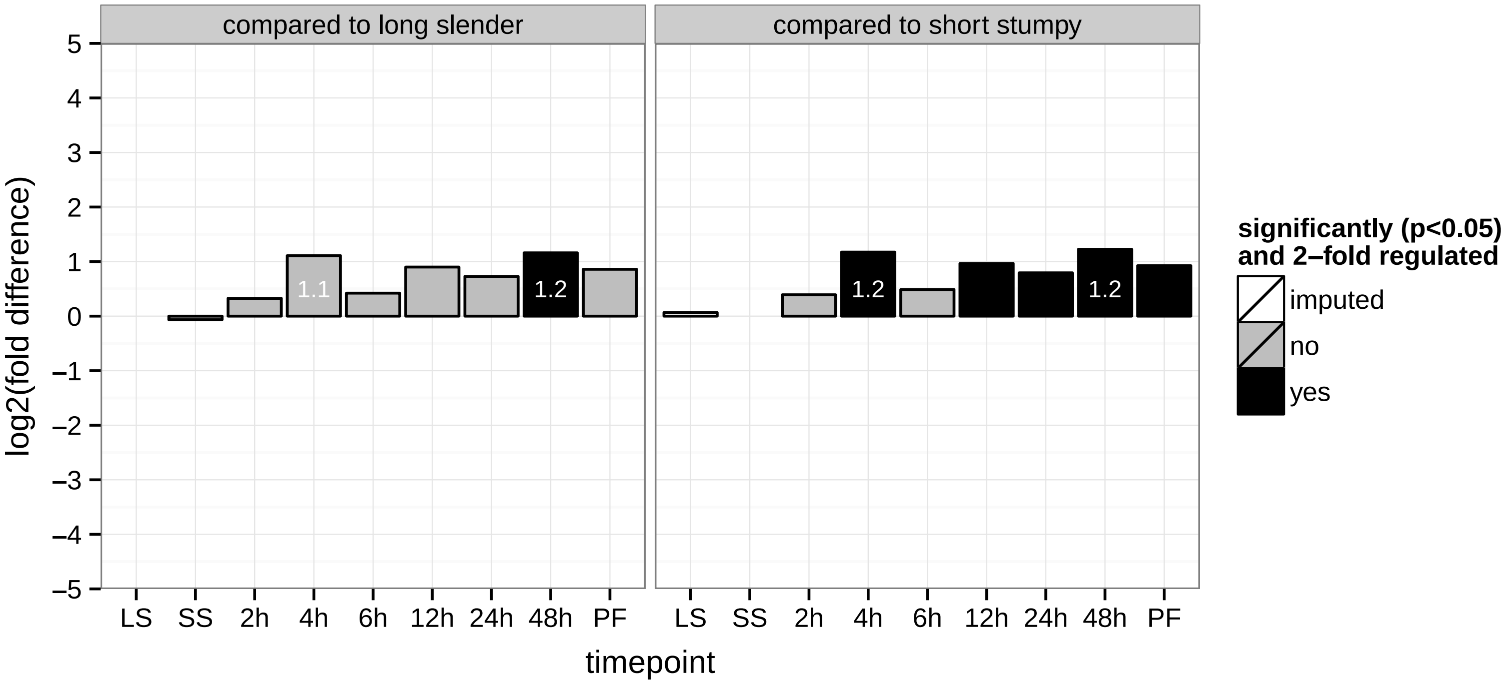
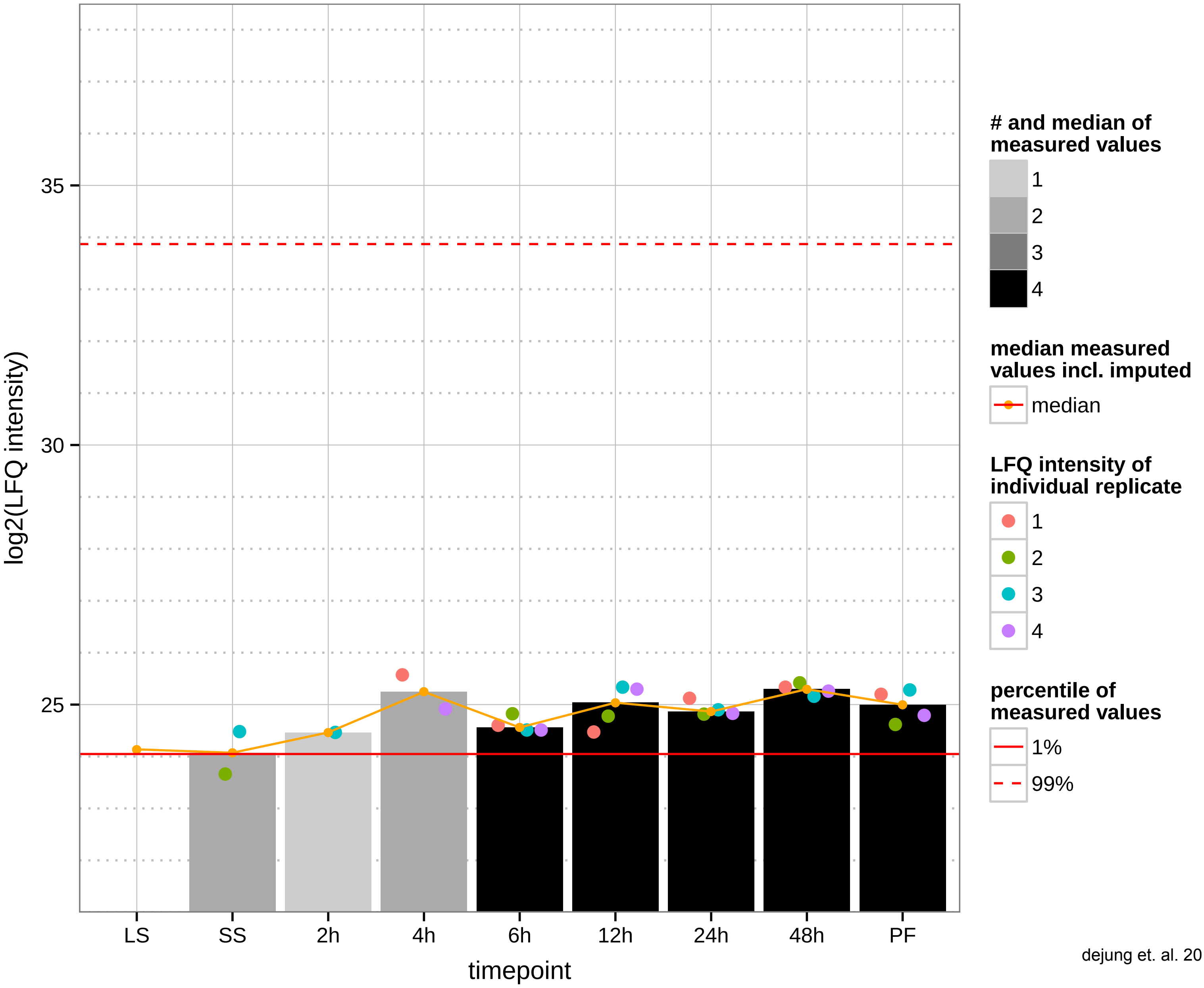
nucleic acid binding protein, putative
Tb927.11.6620
AGOF: nucleic acid binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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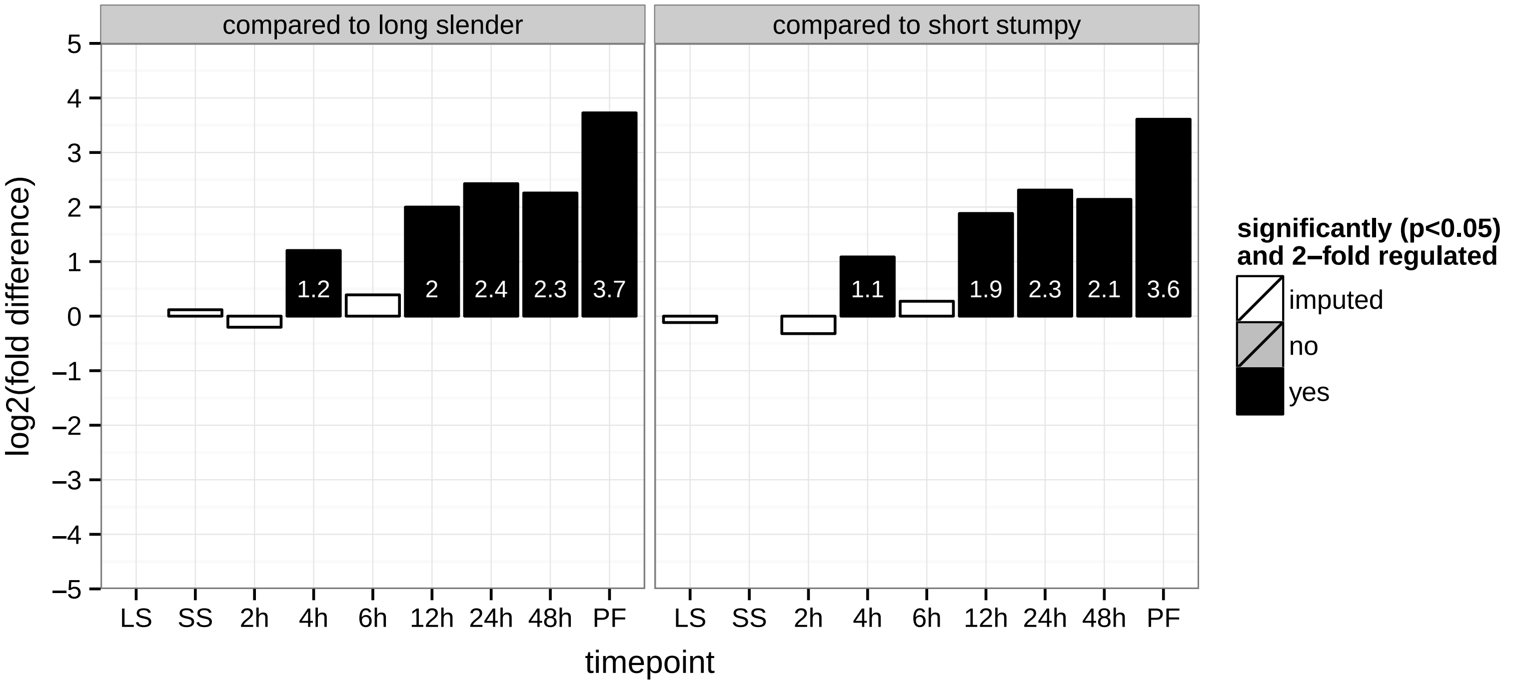
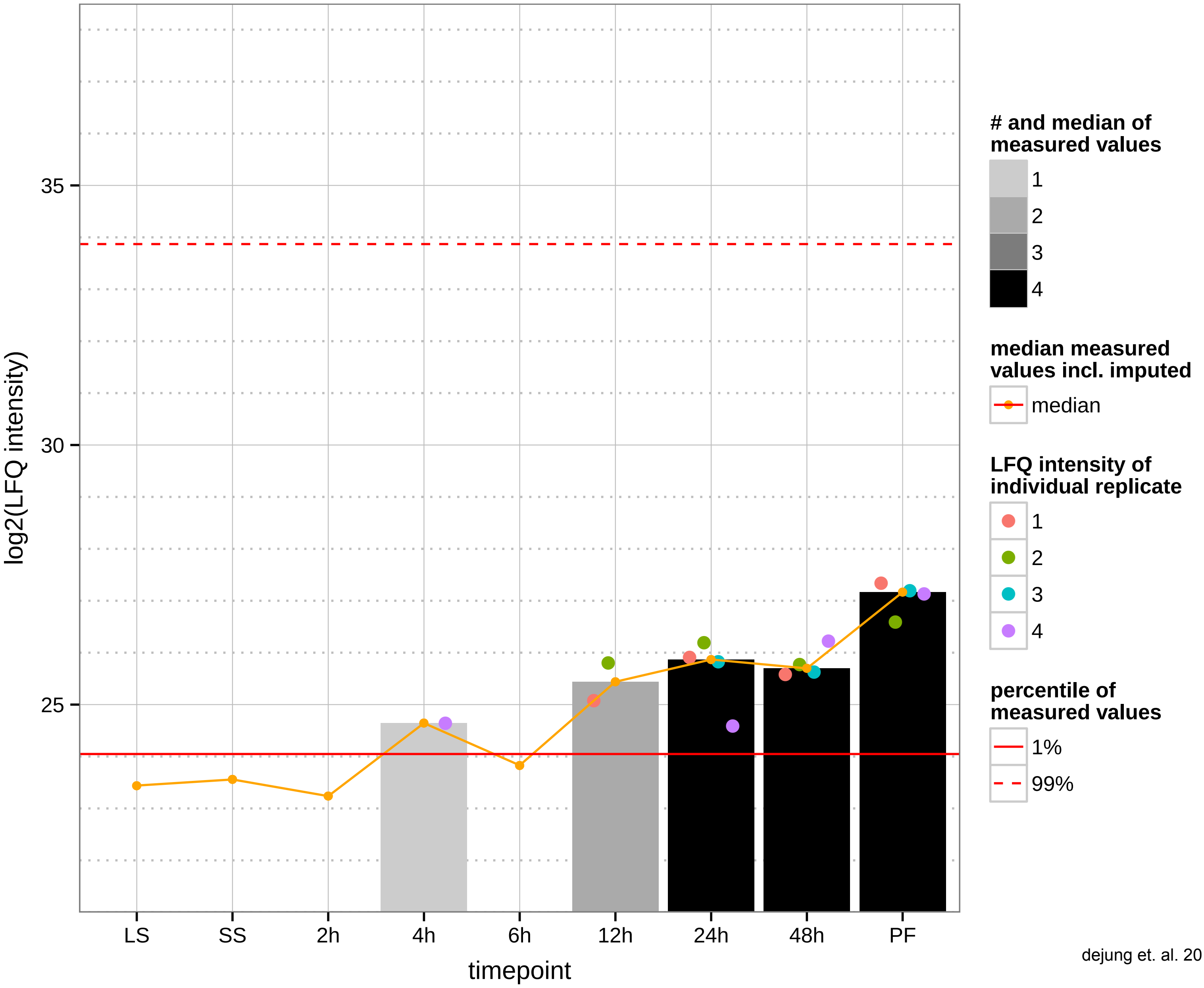
cytochrome b5, putative (CYB5)
Tb927.11.6640
AGOF: glutathione−disulfide reductase activity, heme binding
AGOC: integral to membrane, mitochondrial inner membrane
AGOP: oxidation−reduction process
PGOF: heme binding
PGOC: null
PGOP: null





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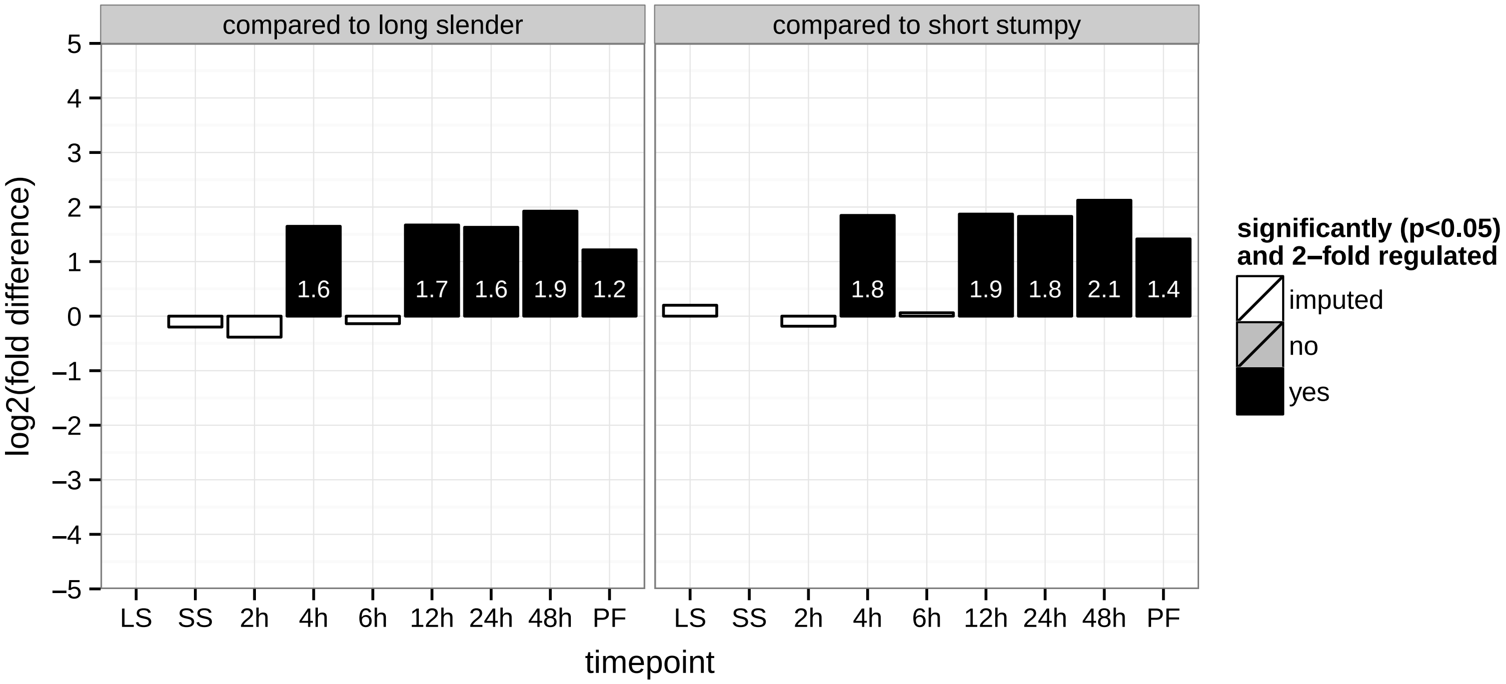
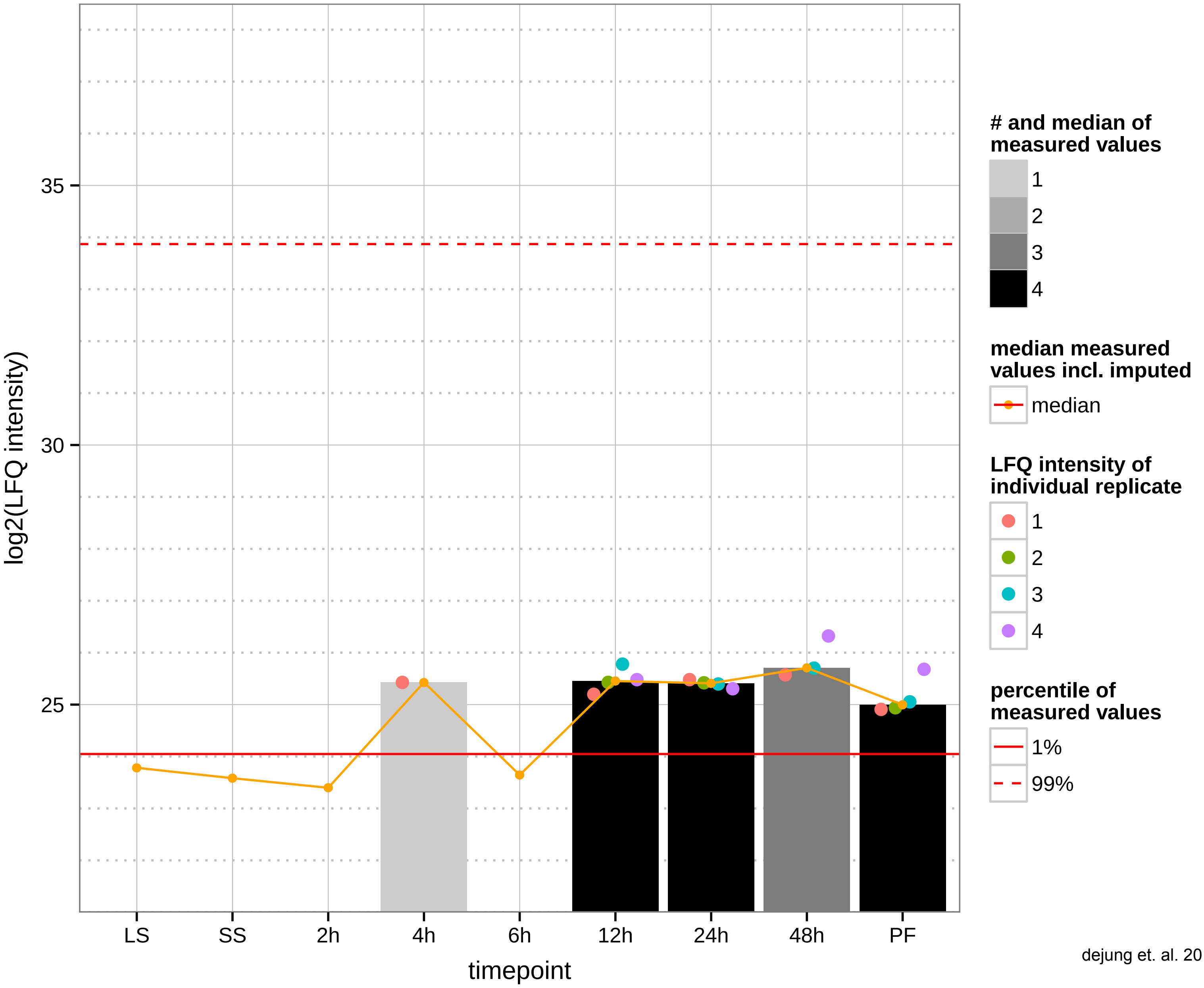
hypothetical protein, conserved
Tb927.11.6830
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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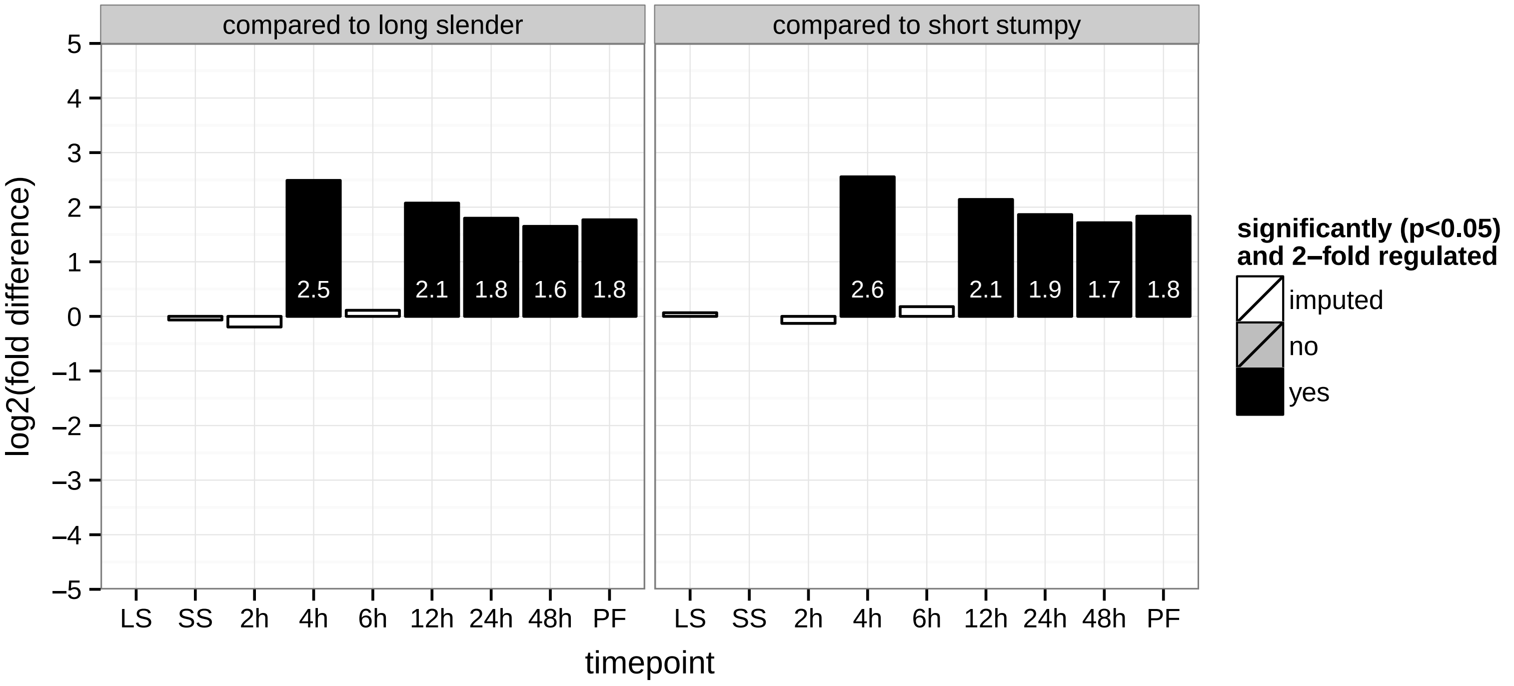
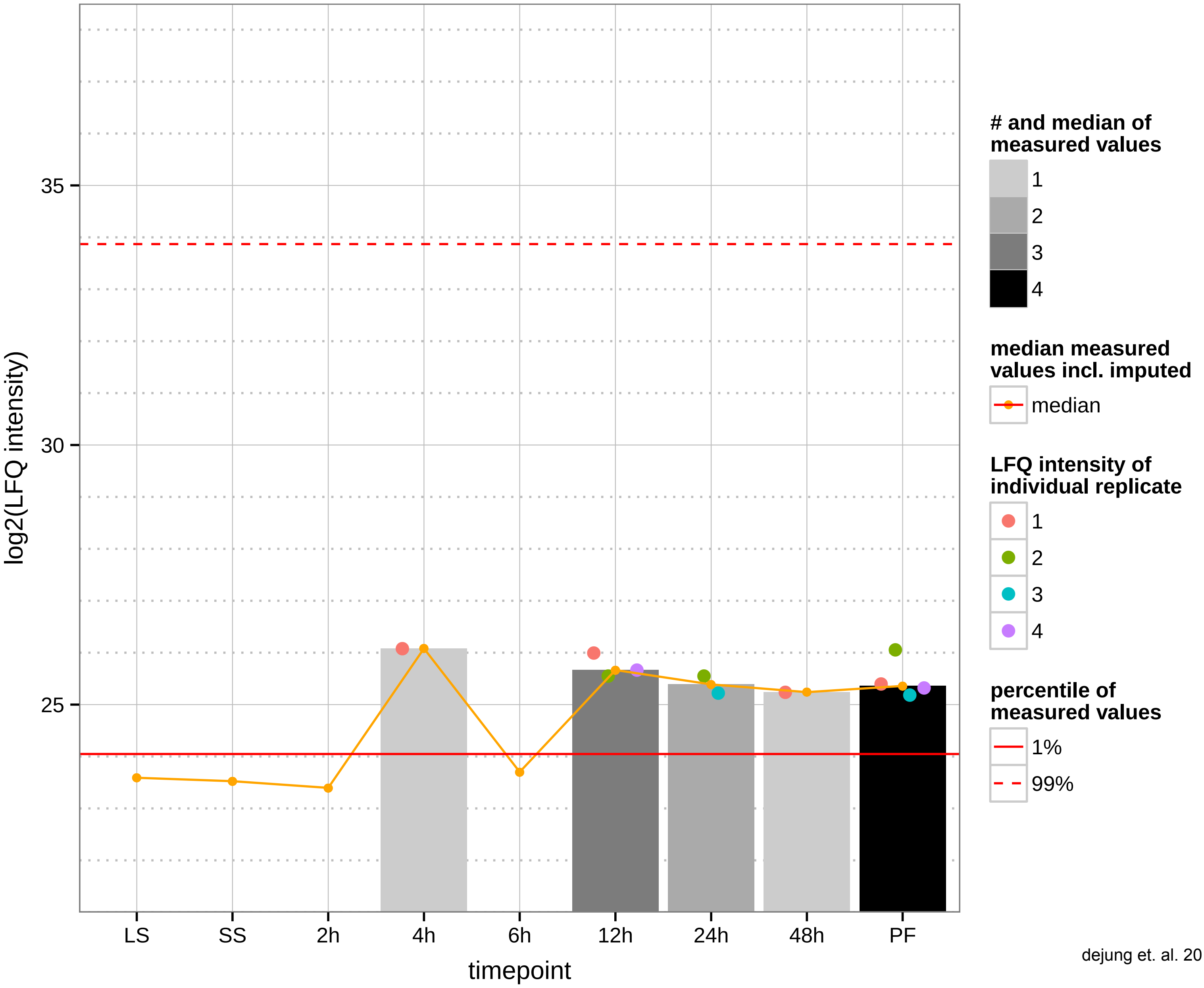
hypothetical protein, conserved
Tb927.11.9600
AGOF: null
AGOC: mitochondrial matrix, mitochondrion
AGOP: null
PGOF: null
PGOC: mitochondrial matrix
PGOP: null





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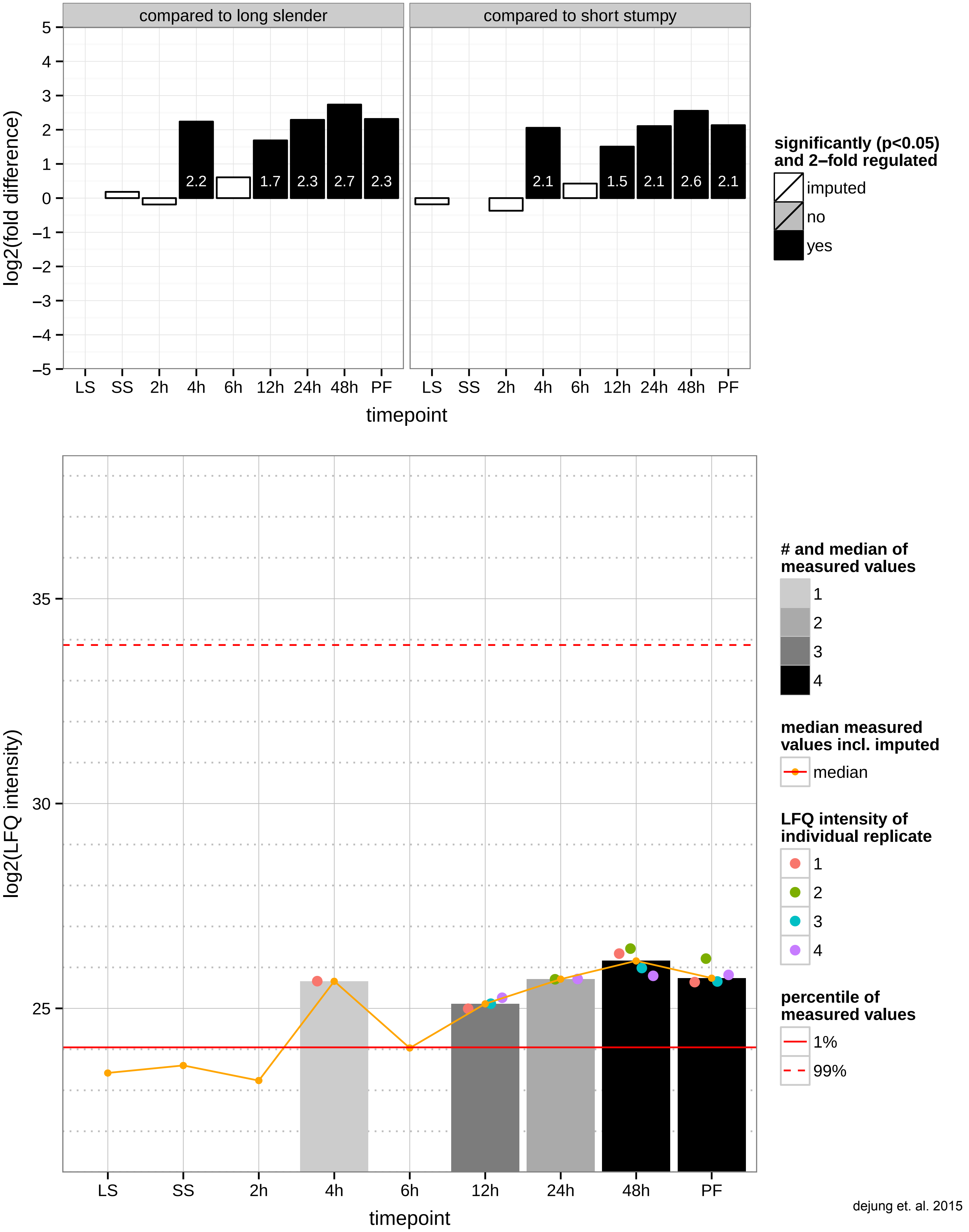
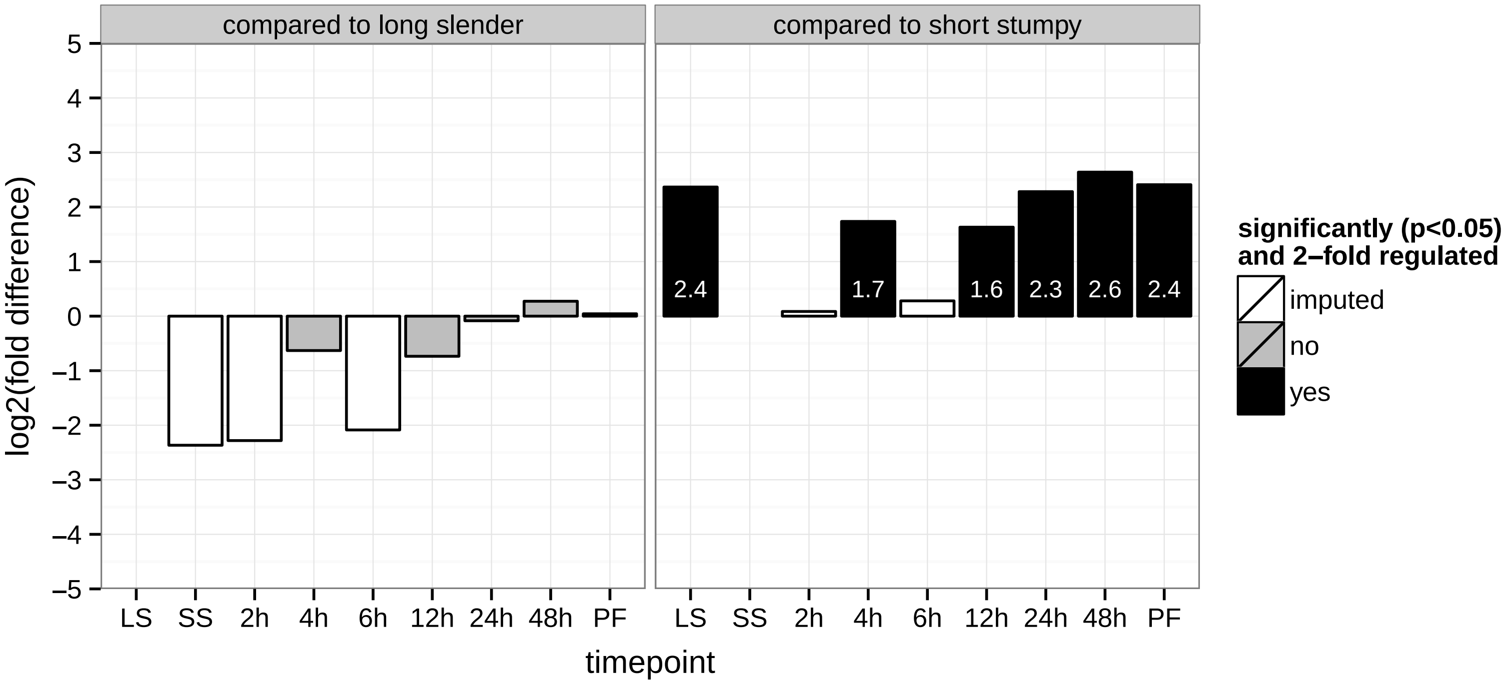
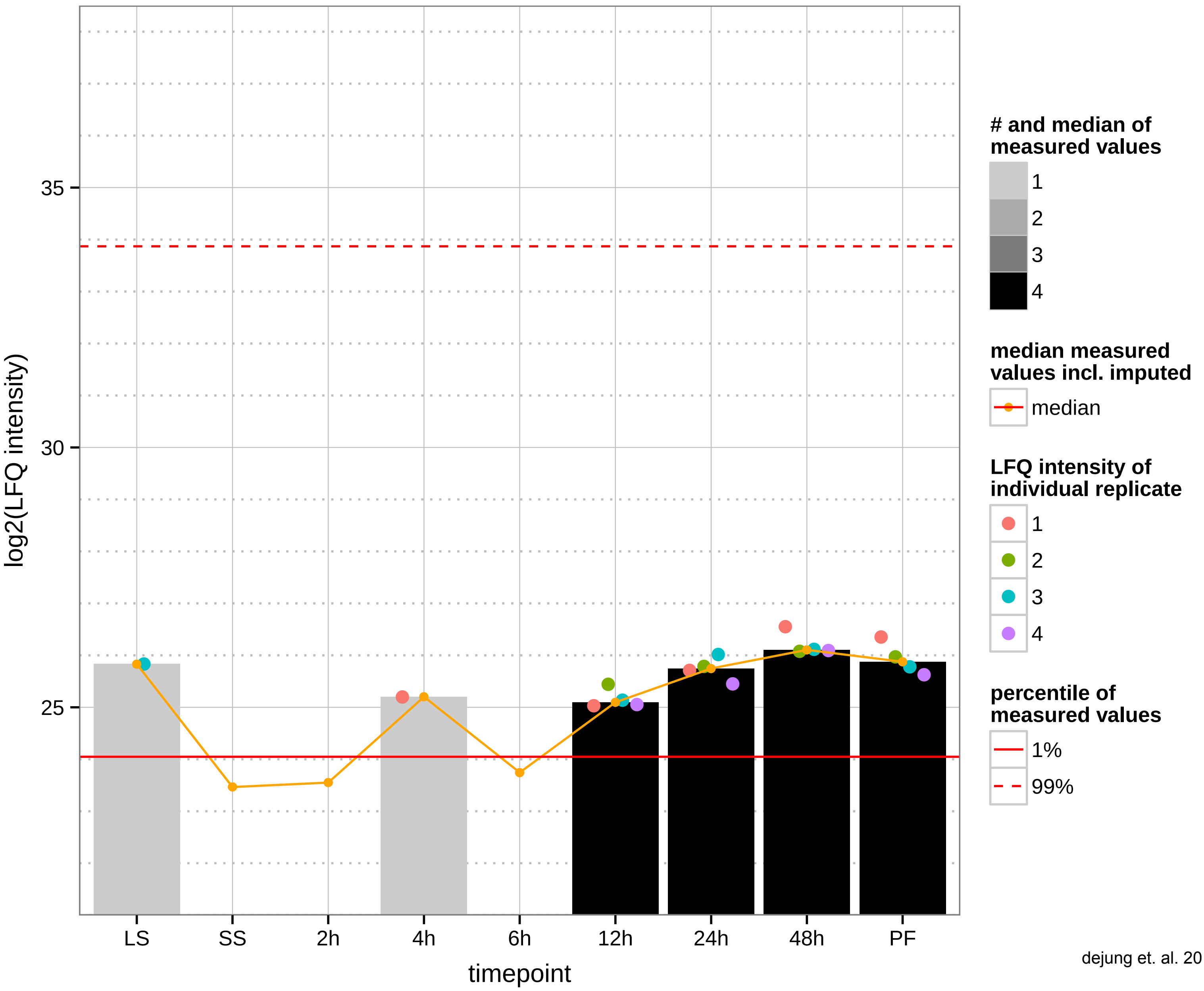
hypothetical protein, conserved
Tb927.11.9750
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



endo/exonuclease Mre11 (MRE11)
Tb927.2.4390
AGOF: damaged DNA binding, endonuclease activity, exonuclease activity, hydrolase activity, manganese ion binding
AGOC: nucleus
AGOP: double−strand break repair
PGOF: endonuclease activity, exonuclease activity, hydrolase activity, manganese ion binding
PGOC: nucleus
PGOP: DNA metabolic process, double−strand break repair





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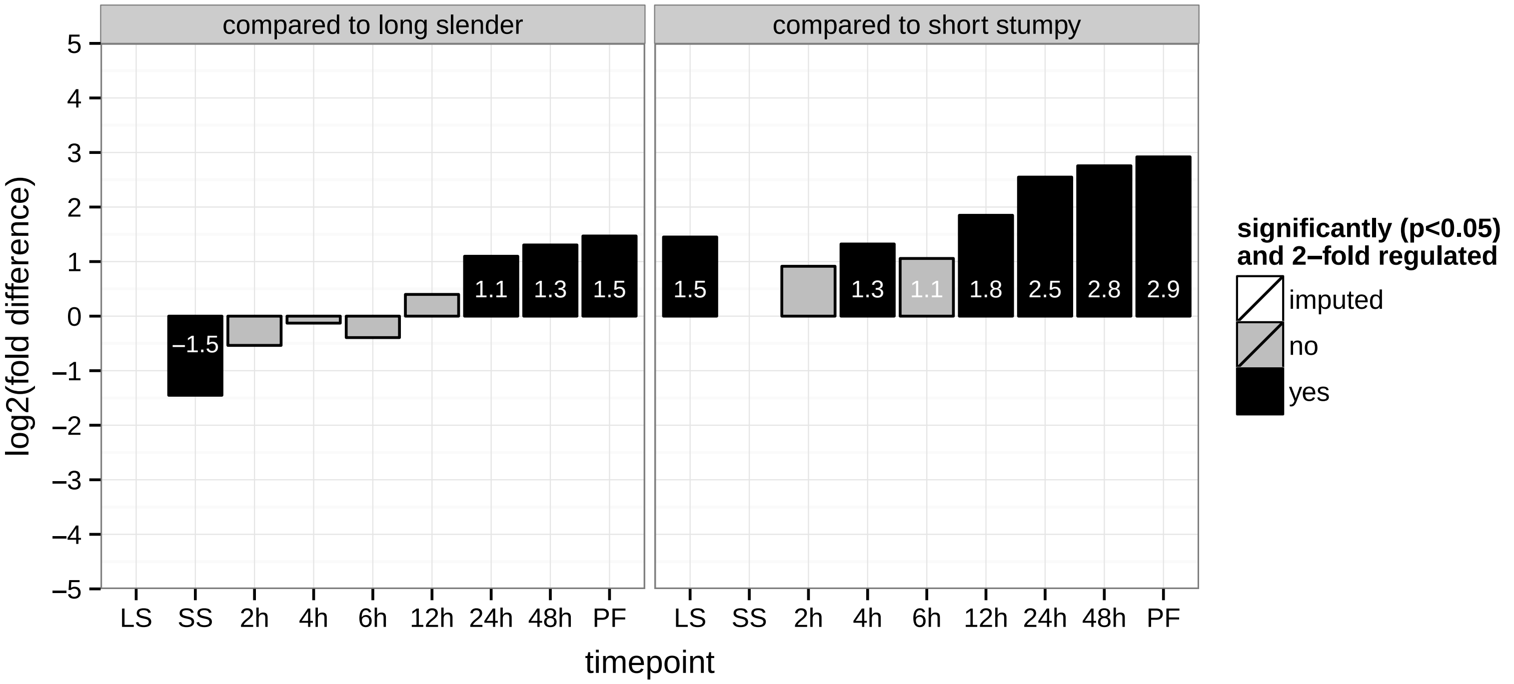
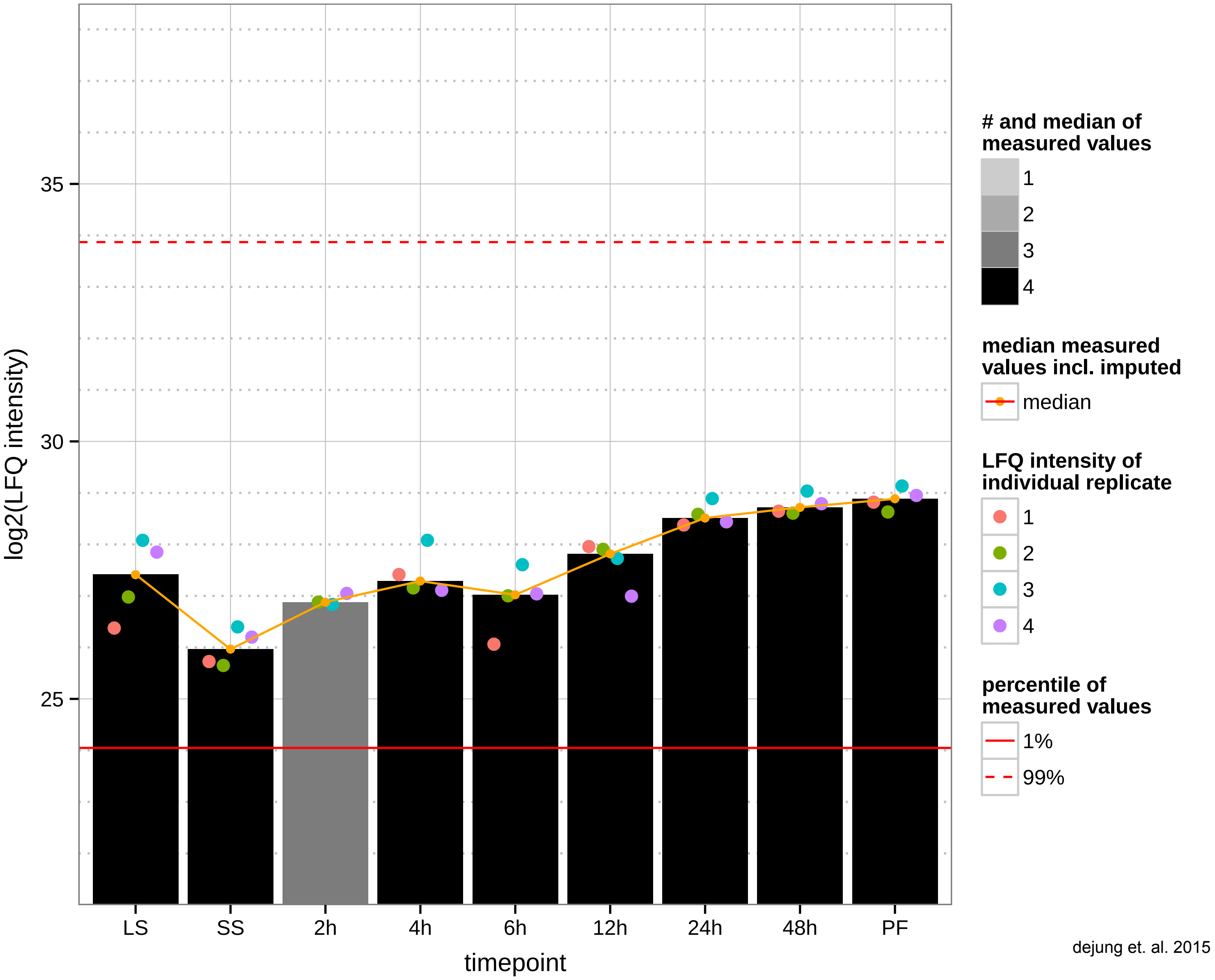
hypothetical protein, conserved
Tb927.2.4850
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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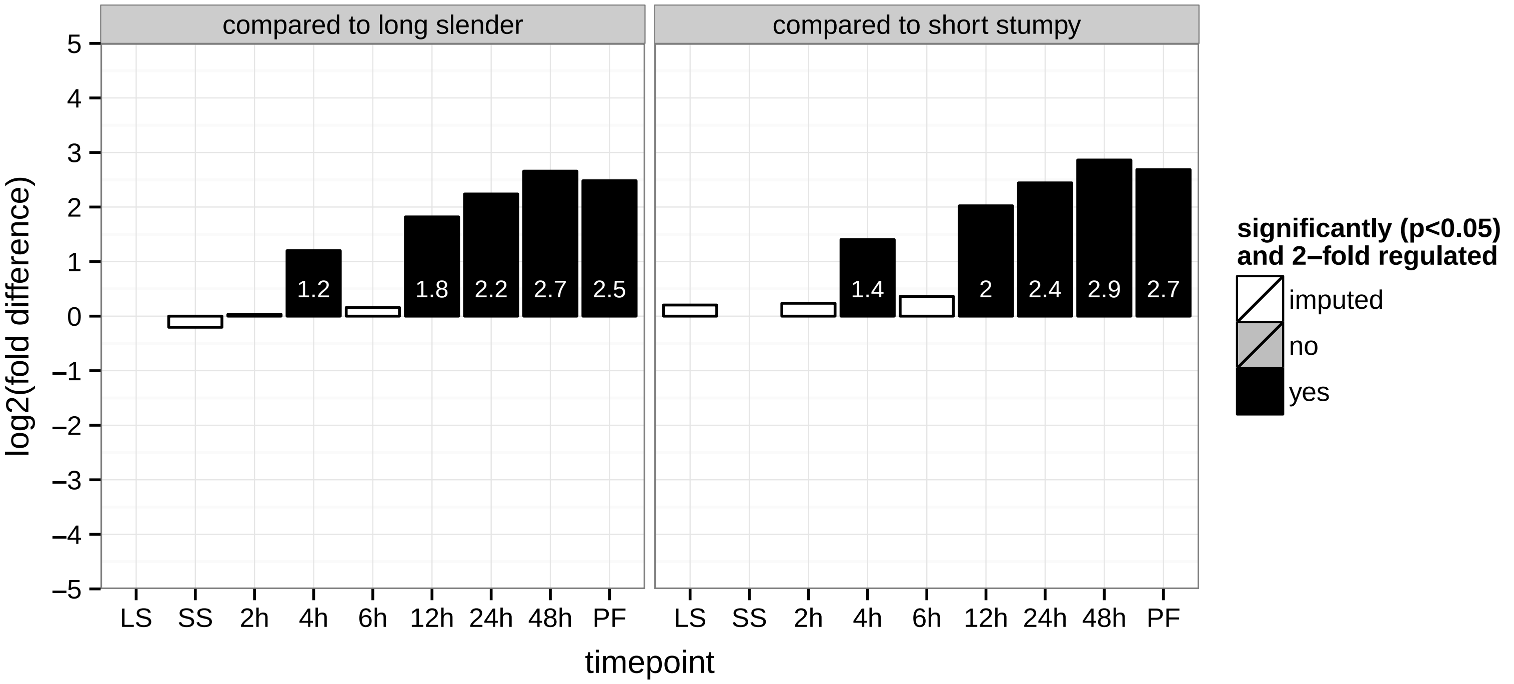
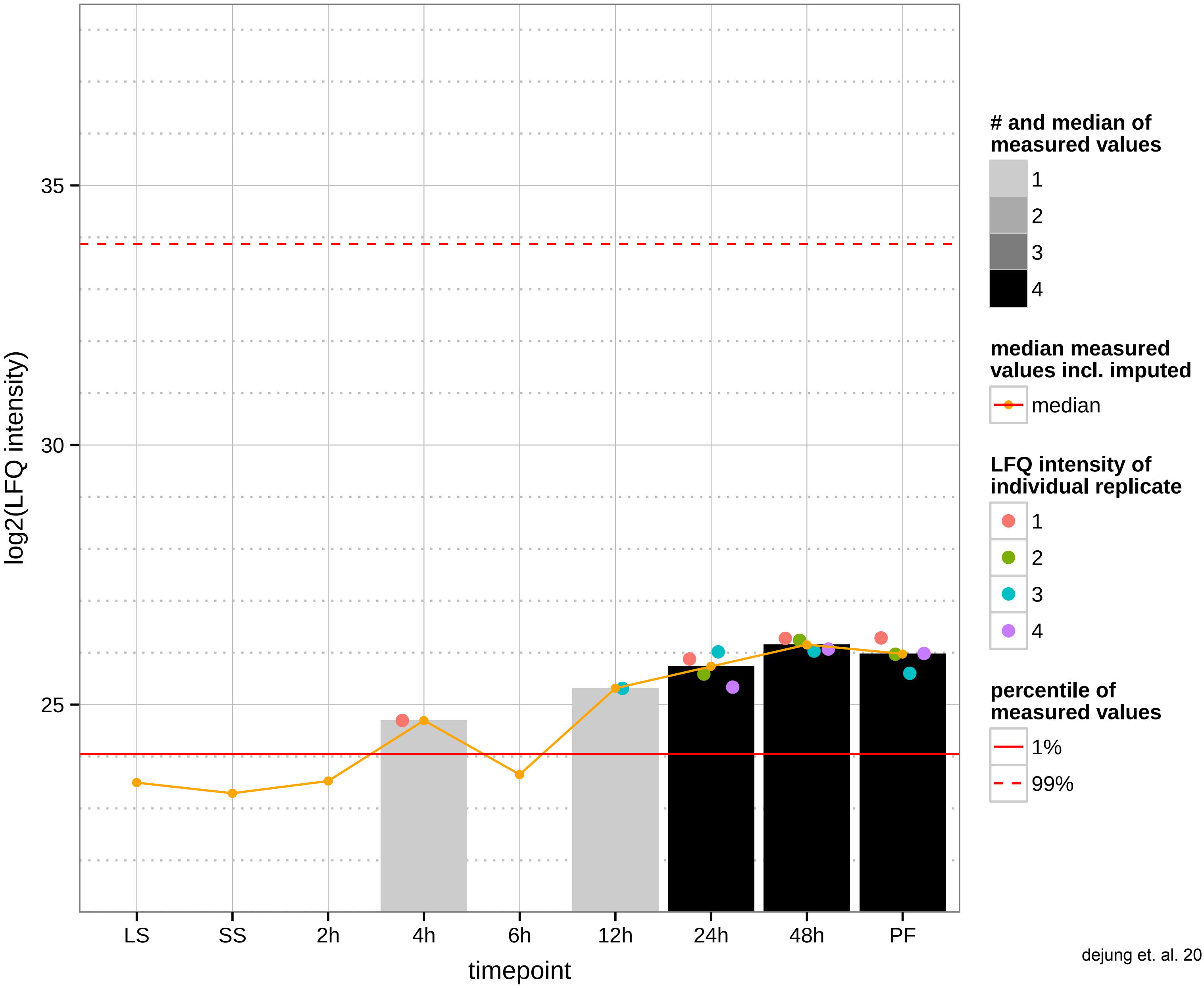
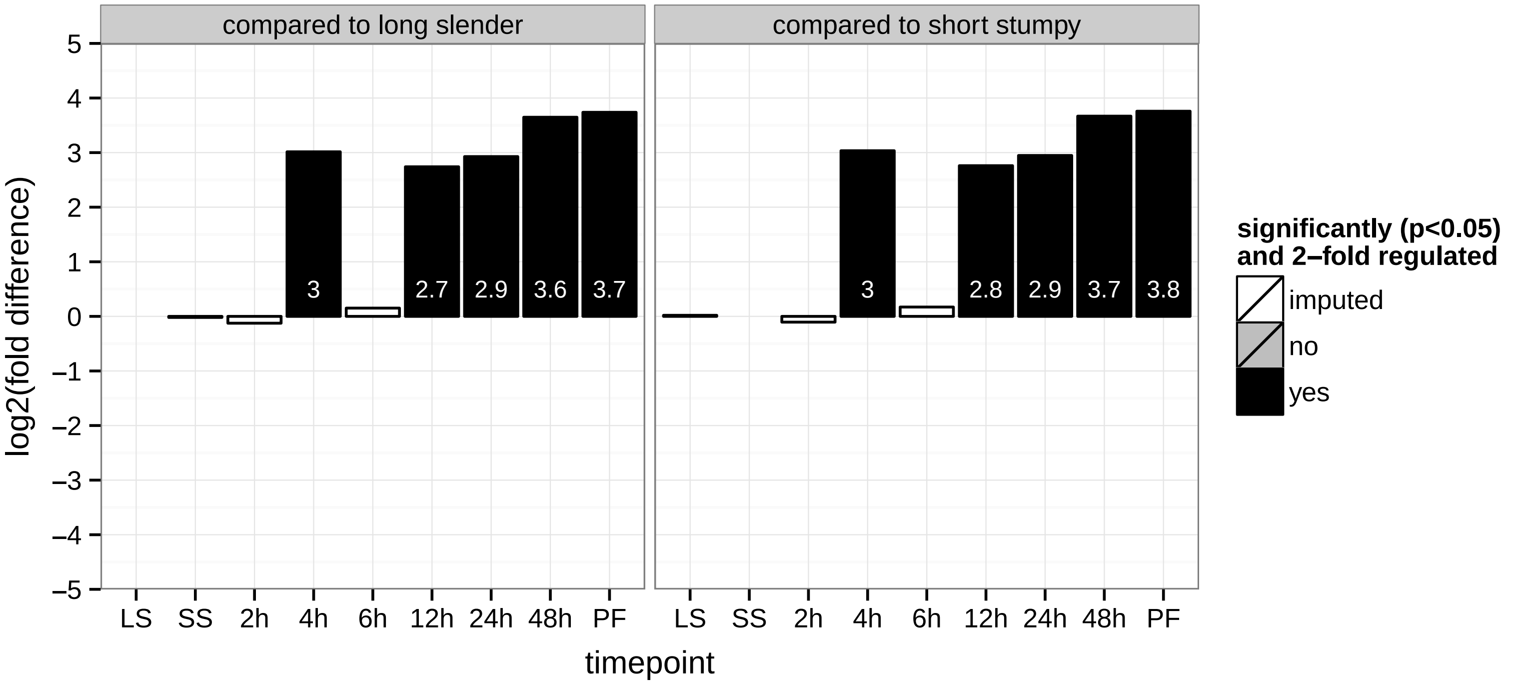
hypothetical protein, conserved
Tb927.2.5970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

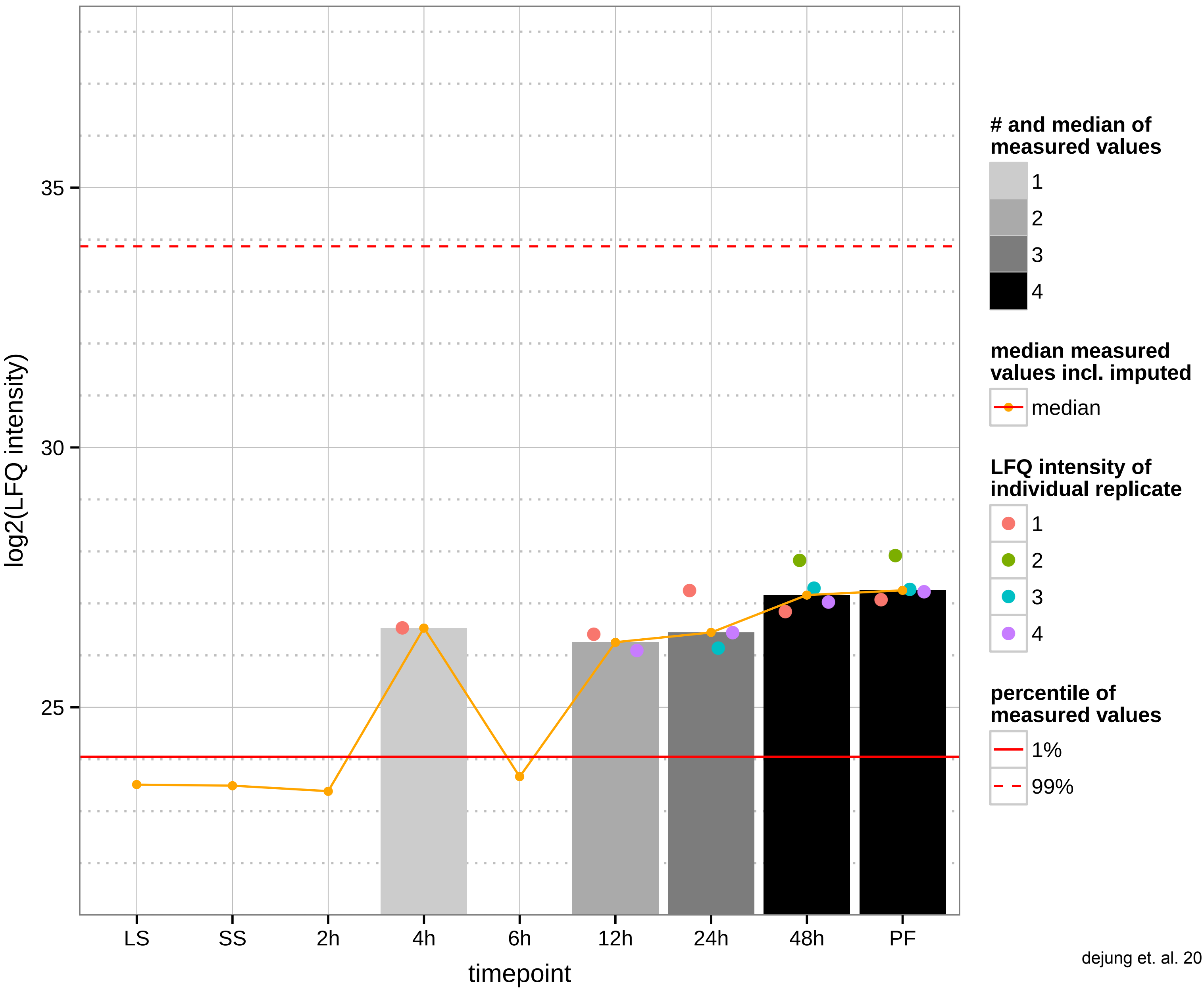




dejung et. al. 2015

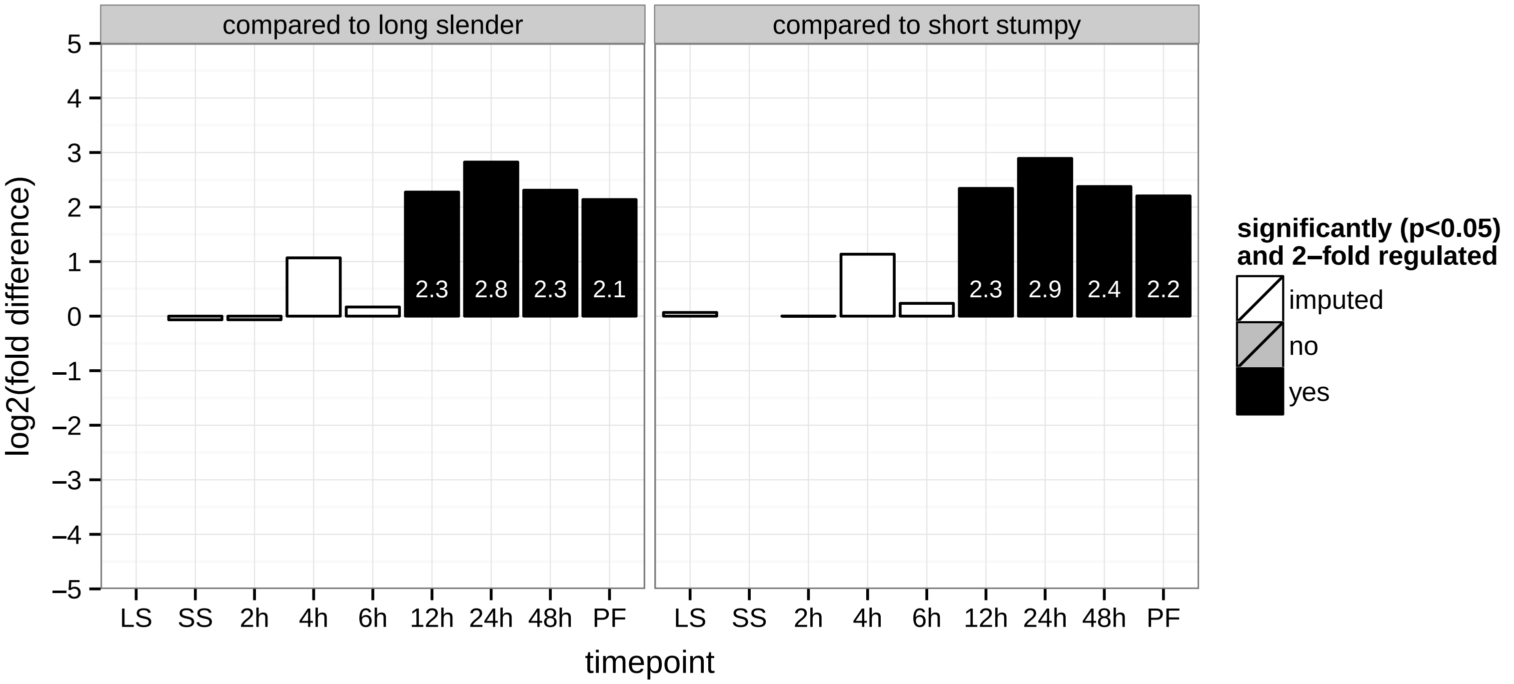
hypothetical protein, conserved
Tb927.3.2080
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

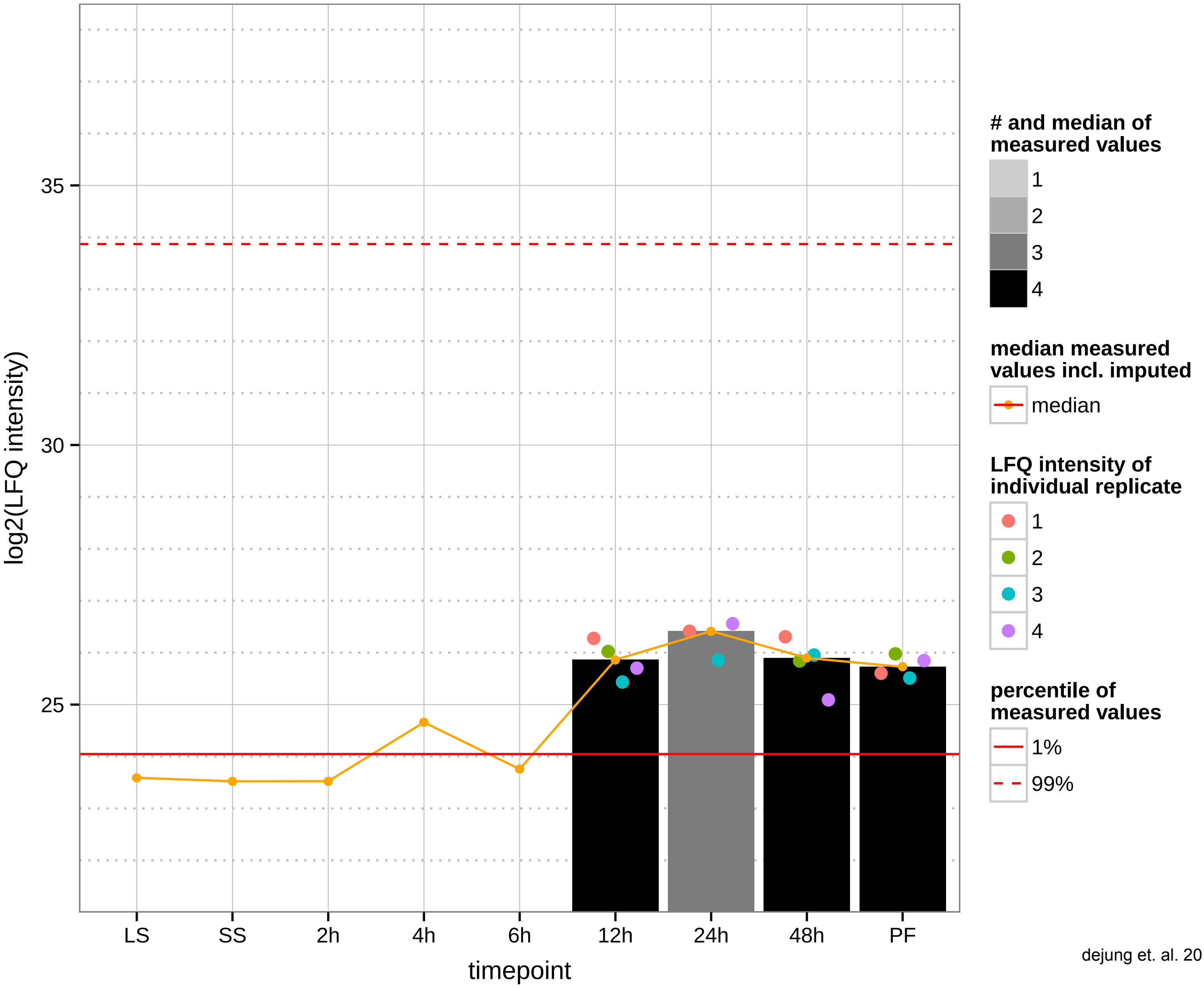




dejung et. al. 2015

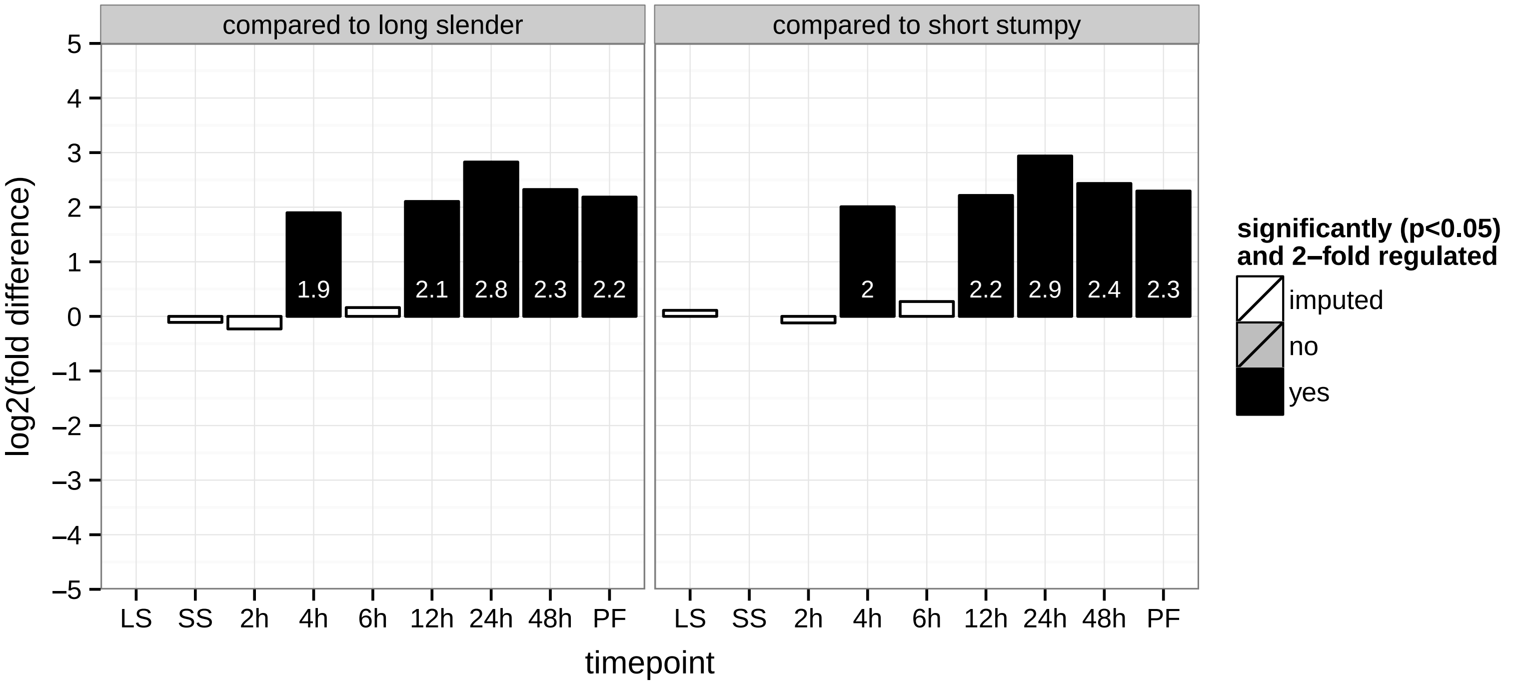
hypothetical protein, conserved
Tb927.3.2130
AGOF: RNA binding, pseudouridine synthase activity
AGOC: mitochondrion
AGOP: pseudouridine synthesis
PGOF: RNA binding, pseudouridine synthase activity
PGOC: null
PGOP: RNA modification, pseudouridine synthesis

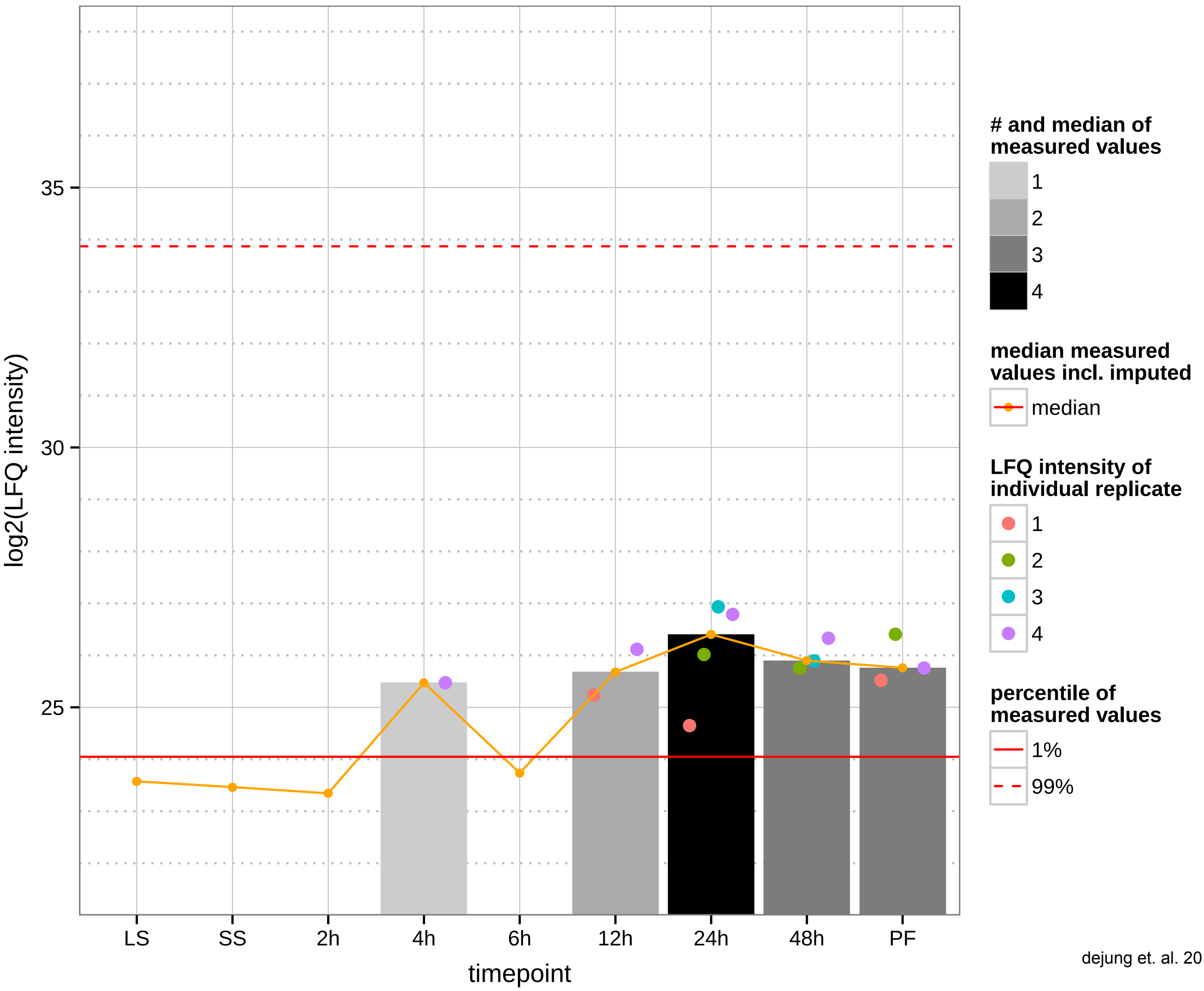




dejung et. al. 2015

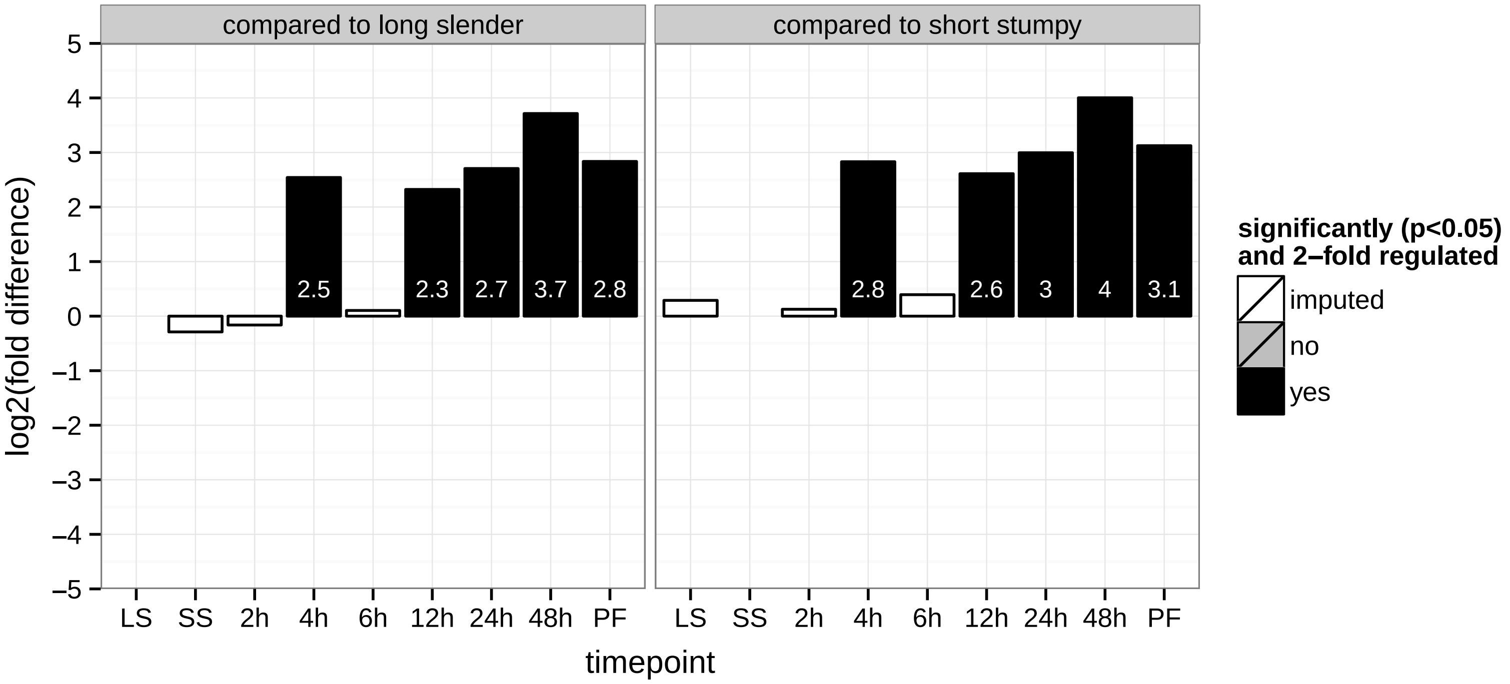
C–8 sterol isomerase, putative
Tb927.3.4650
AGOF: C–8 sterol isomerase activity
AGOC: endoplasmic reticulum
AGOP: ergosterol biosynthetic process
PGOF: C–8 sterol isomerase activity
PGOC: endoplasmic reticulum
PGOP: ergosterol biosynthetic process

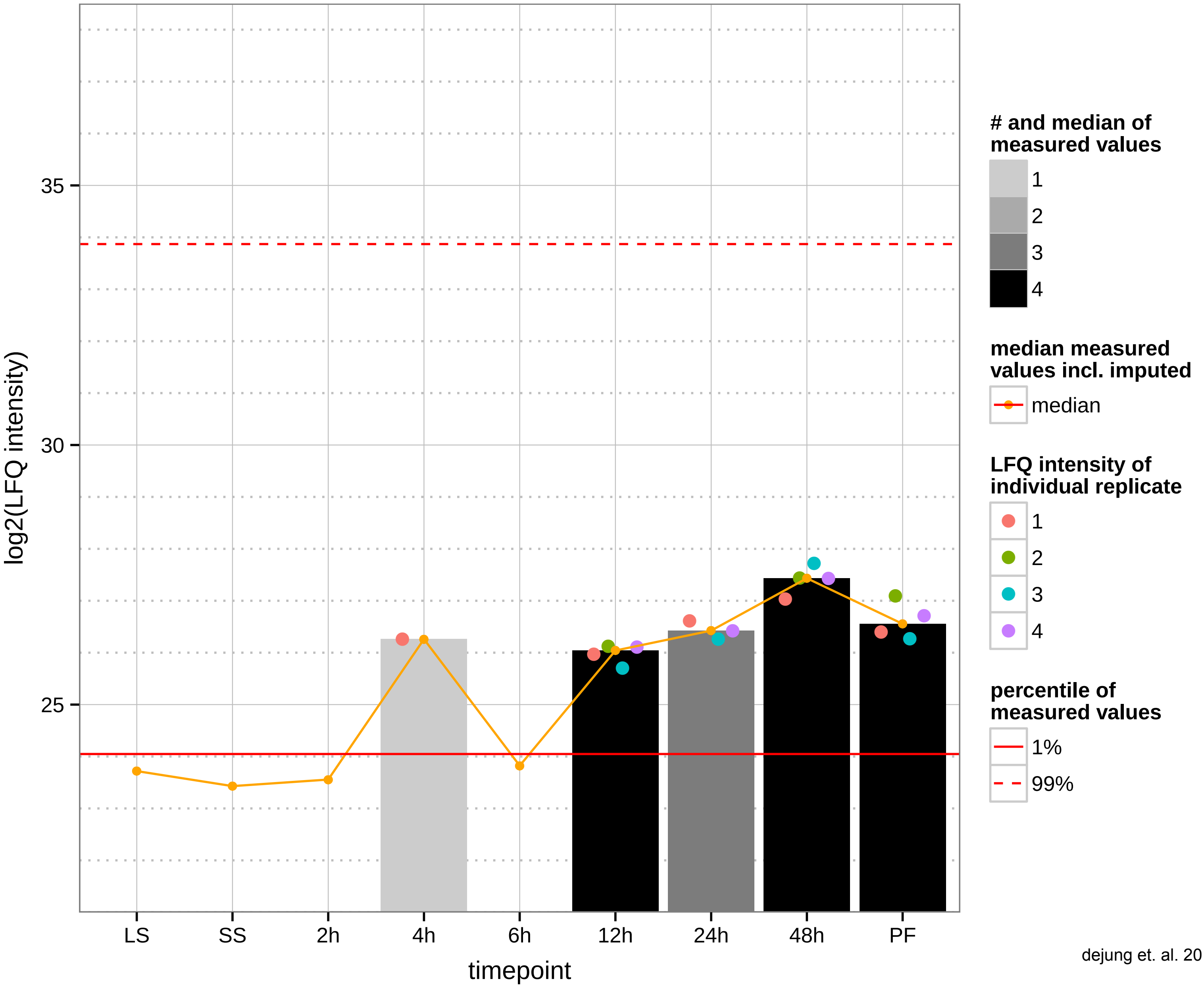




dejung et. al. 2015

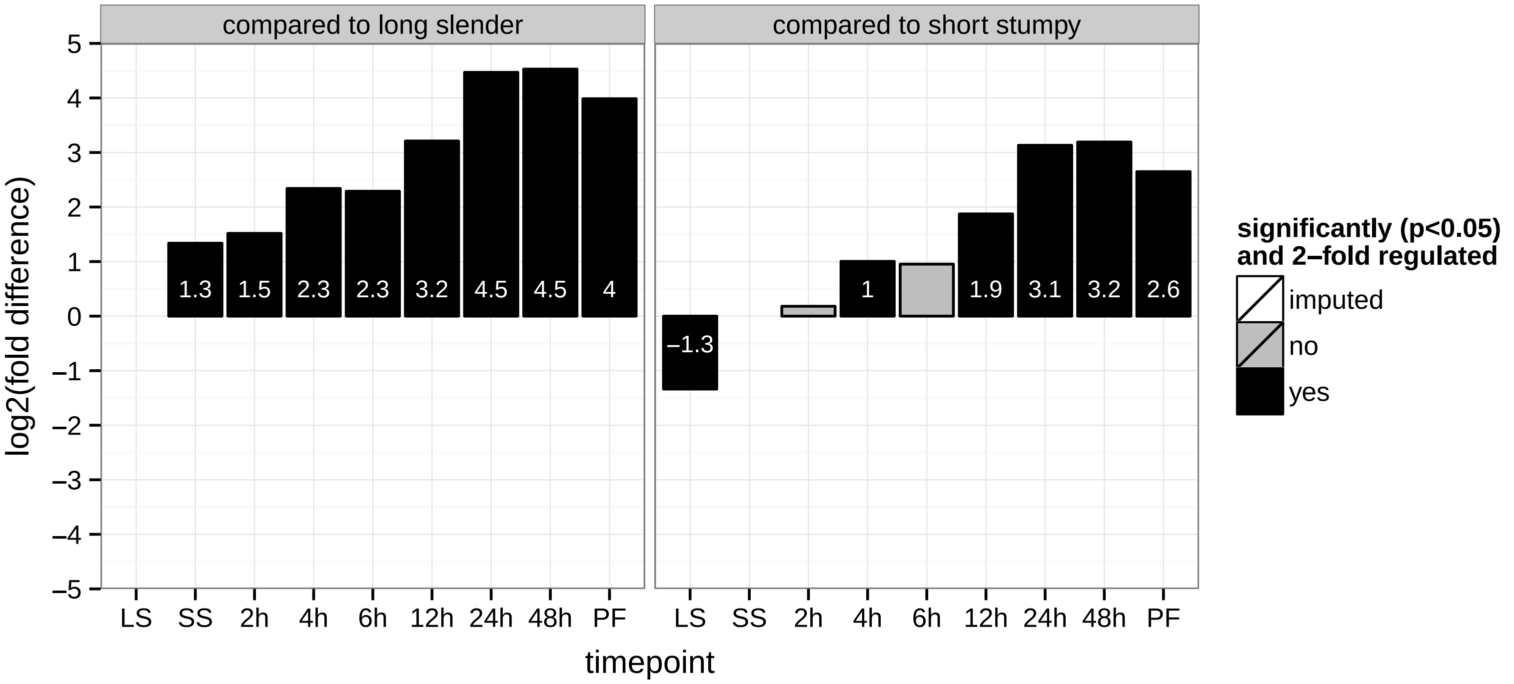
hypothetical protein, conserved
Tb927.5.1120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

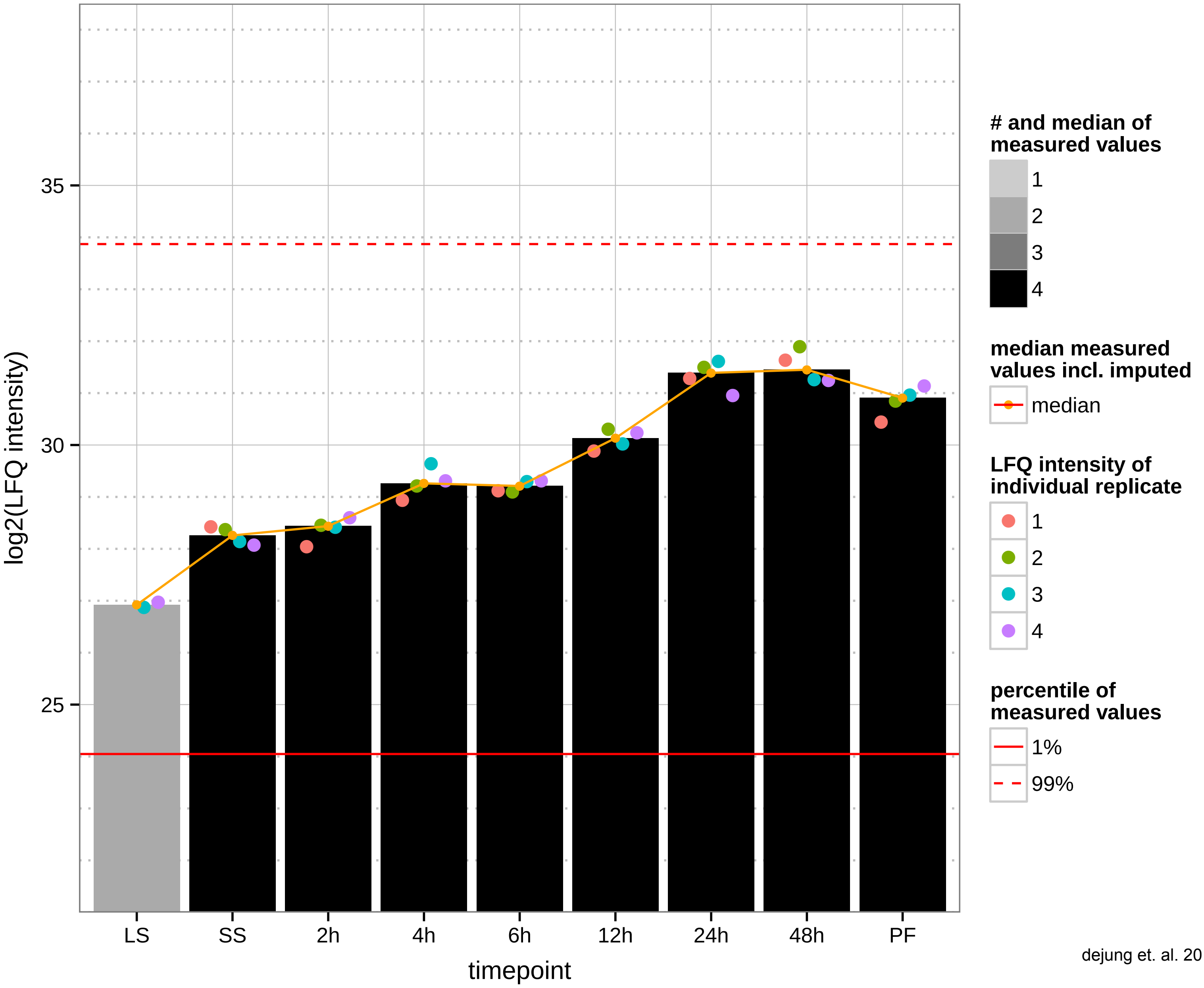




dejung et. al. 2015

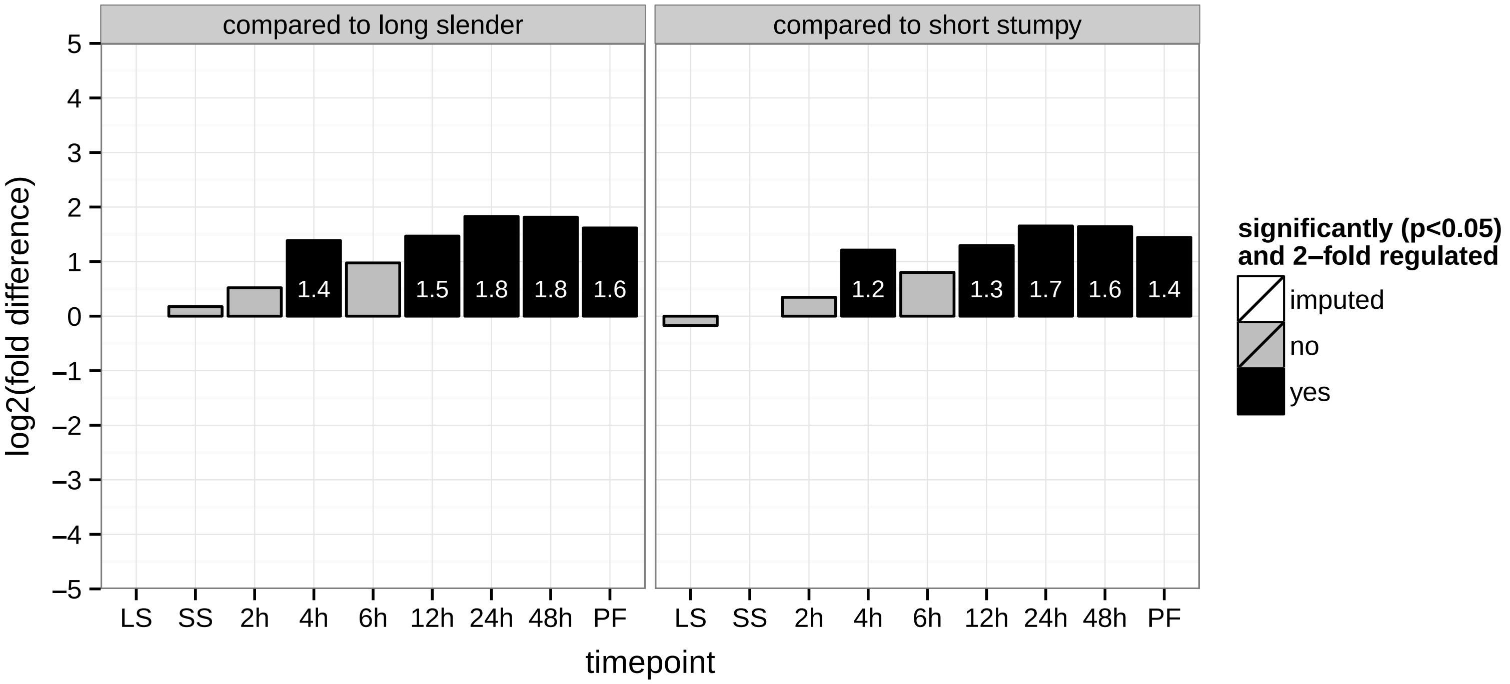
conserved protein
Tb927.5.2260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

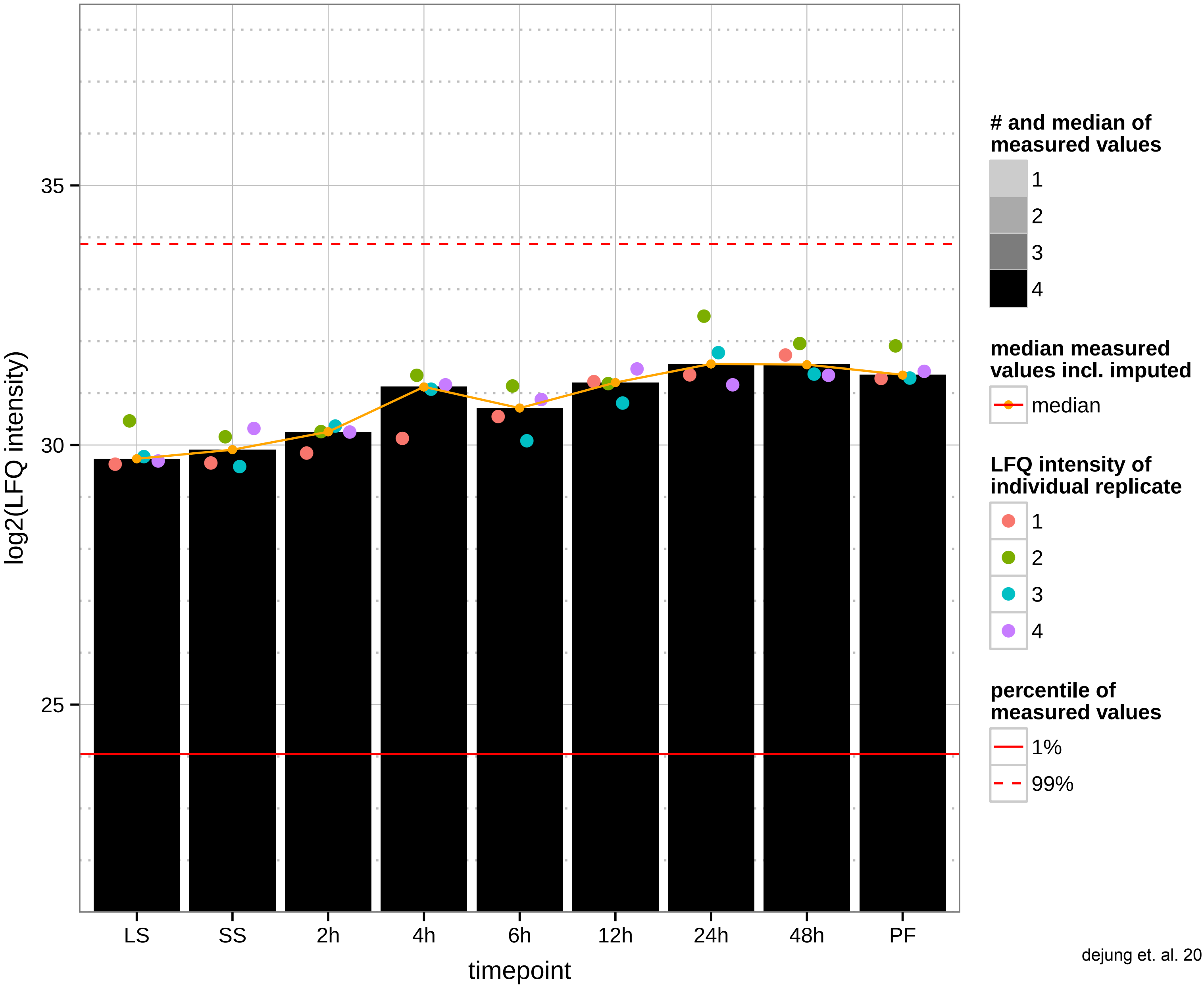




dejung et. al. 2015

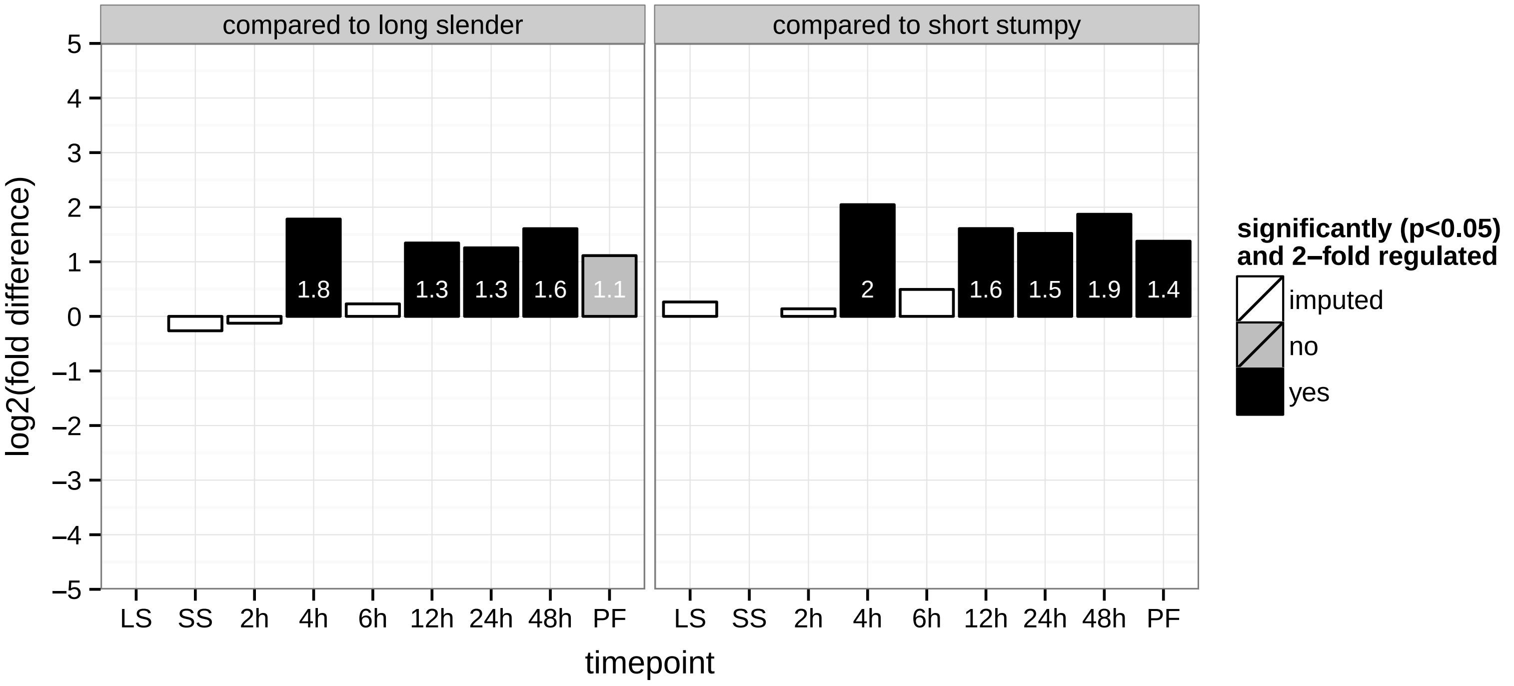
co–chaperone GrpE, putative
Tb927.6.2170
AGOF: adenyl–nucleotide exchange factor activity, chaperone binding, protein homodimerization activity
AGOC: mitochondrion
AGOP: protein folding, protein import into mitochondrial matrix
PGOF: adenyl–nucleotide exchange factor activity, chaperone binding, protein homodimerization activity
PGOC: null
PGOP: protein folding

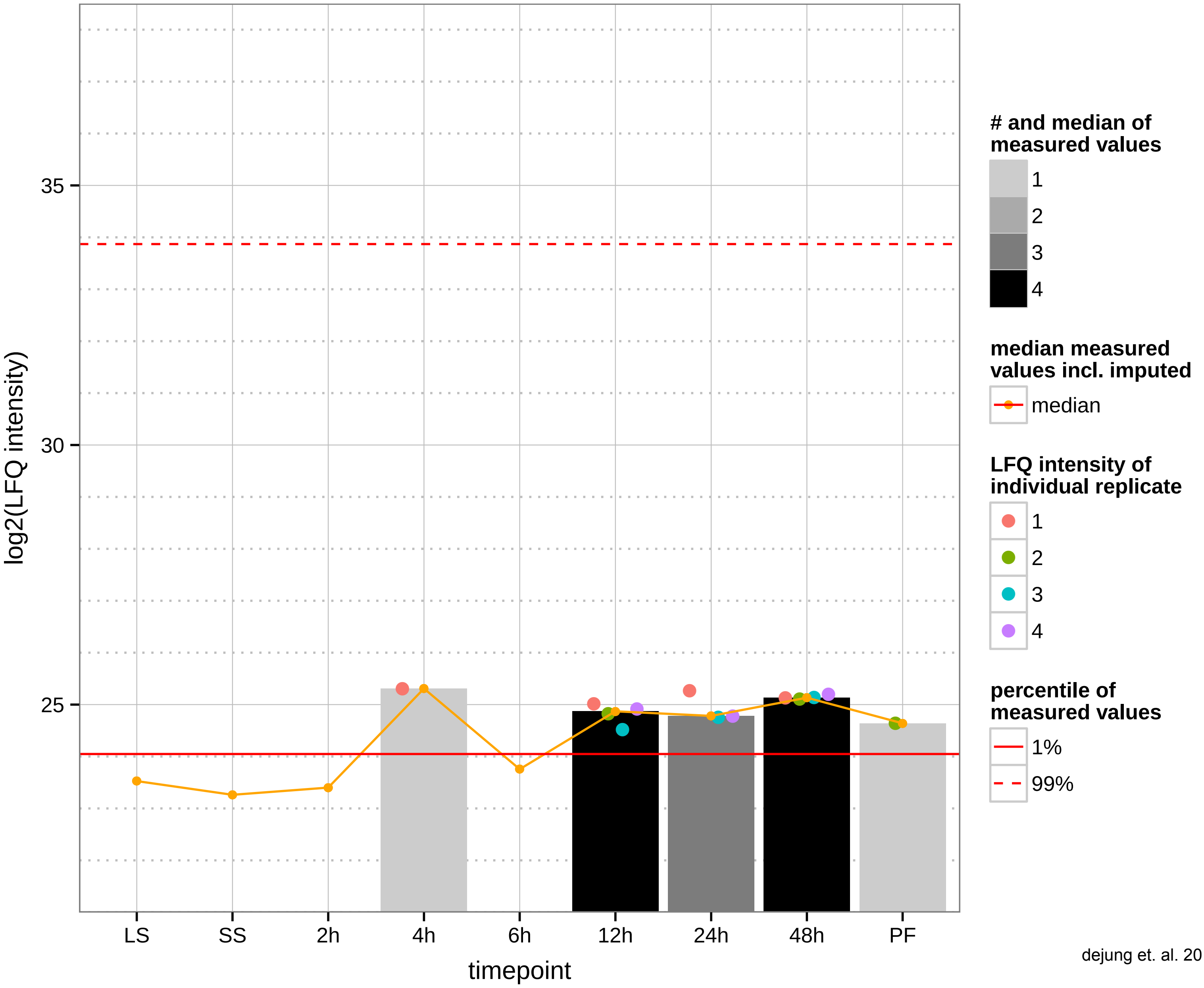




dejung et. al. 2015

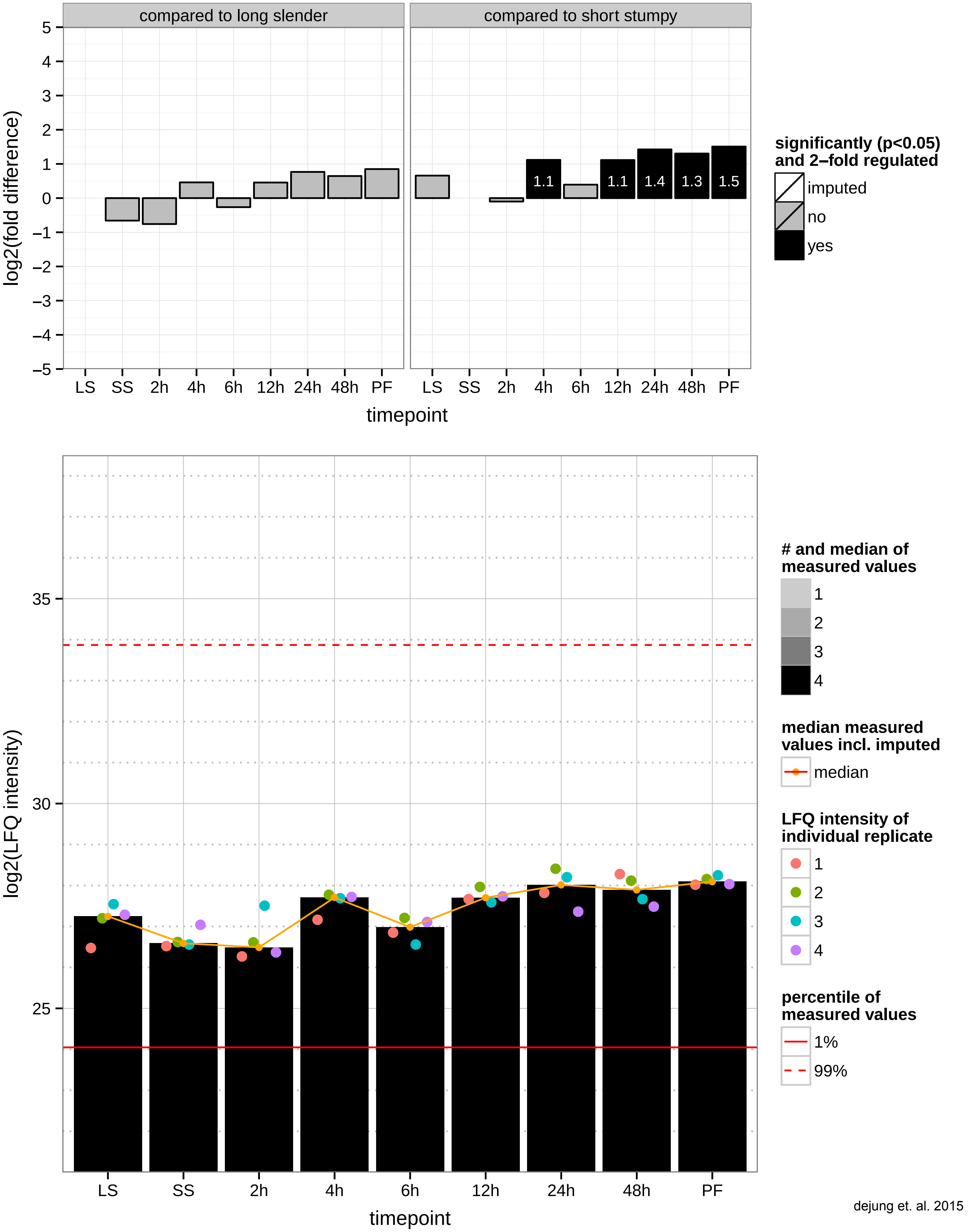
tRNA modification enzyme, putative
Tb927.6.3510
AGOF: null, catalytic activity, iron−sulfur cluster binding
AGOC: null
AGOP: null
PGOF: 4 iron, 4 sulfur cluster binding, catalytic activity, iron−sulfur cluster binding, transferase activity
PGOC: null
PGOP: RNA modification, macromolecule modification





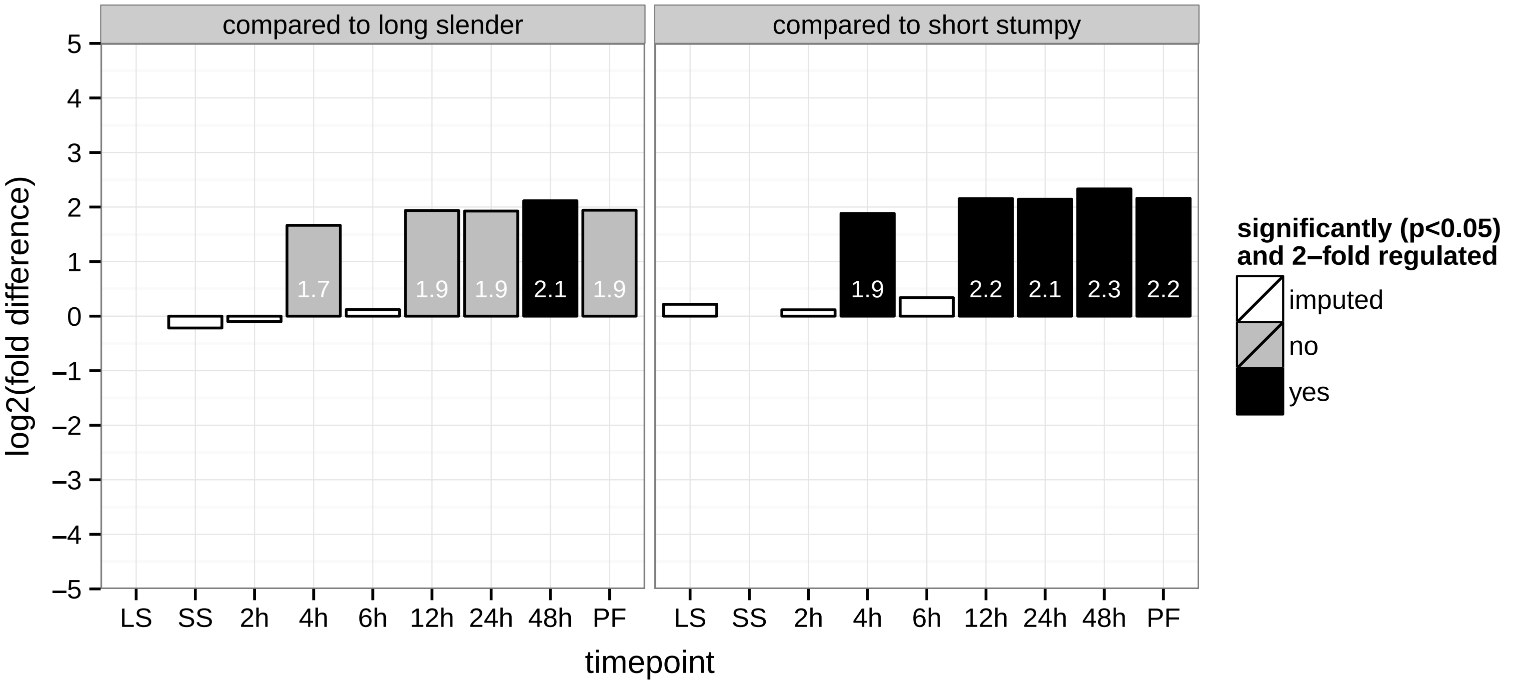
dejung et. al. 2015

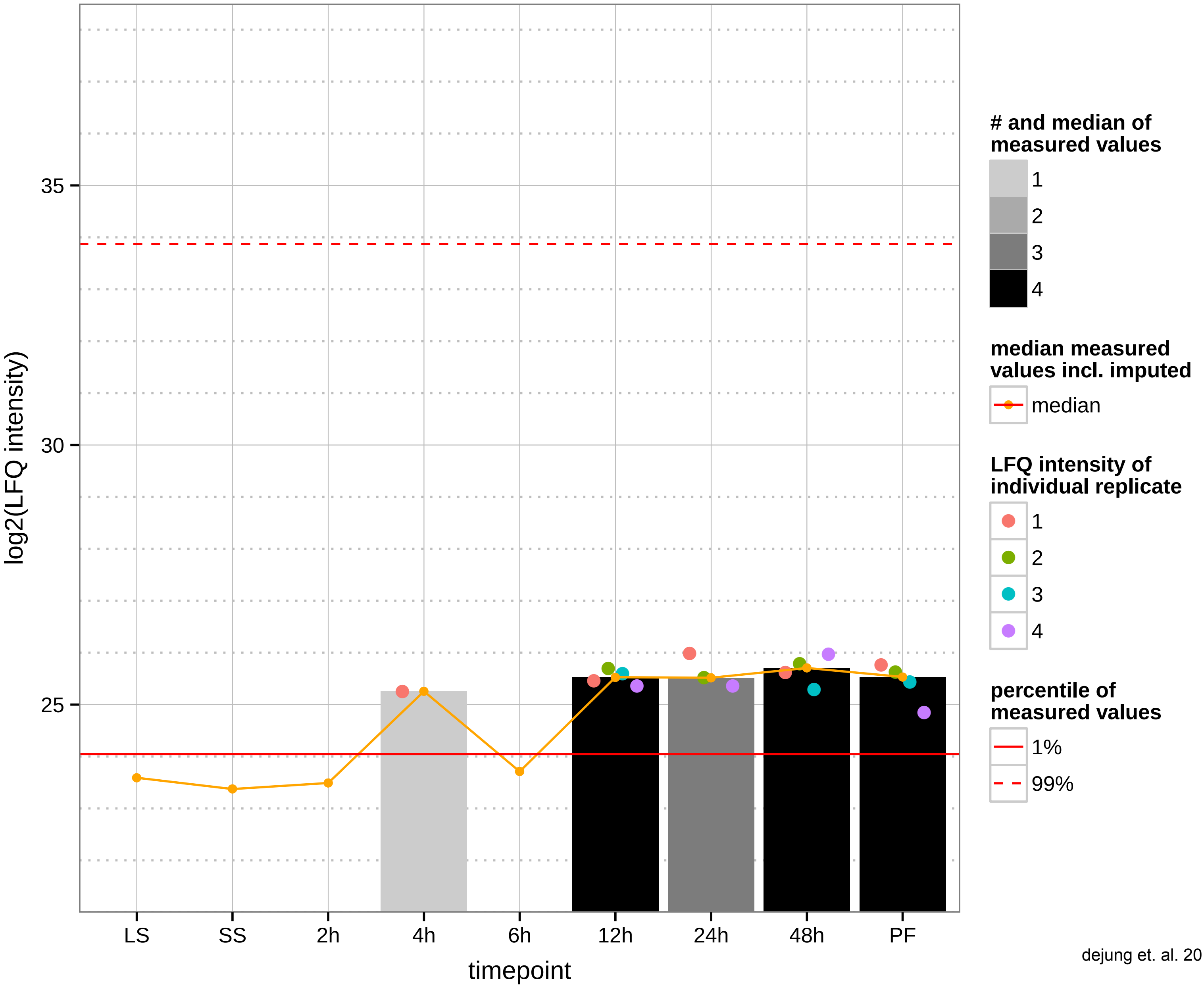
UV excision repair RAD23 protein, putative
Tb927.6.4650
AGOF: damaged DNA binding
AGOC: null
AGOP: nucleotide–excision repair, proteasomal ubiquitin–dependent protein catabolic process
PGOF: damaged DNA binding, protein binding
PGOC: null
PGOP: nucleotide–excision repair, proteasomal ubiquitin–dependent protein catabolic process



dejung et. al. 2015

ras–like small GTPase, putative (TbEAR)
Tb927.7.1640
AGOF: GTP binding
AGOC: intracellular, mitochondrion
AGOP: null
PGOF: GTP binding
PGOC: null
PGOP: null





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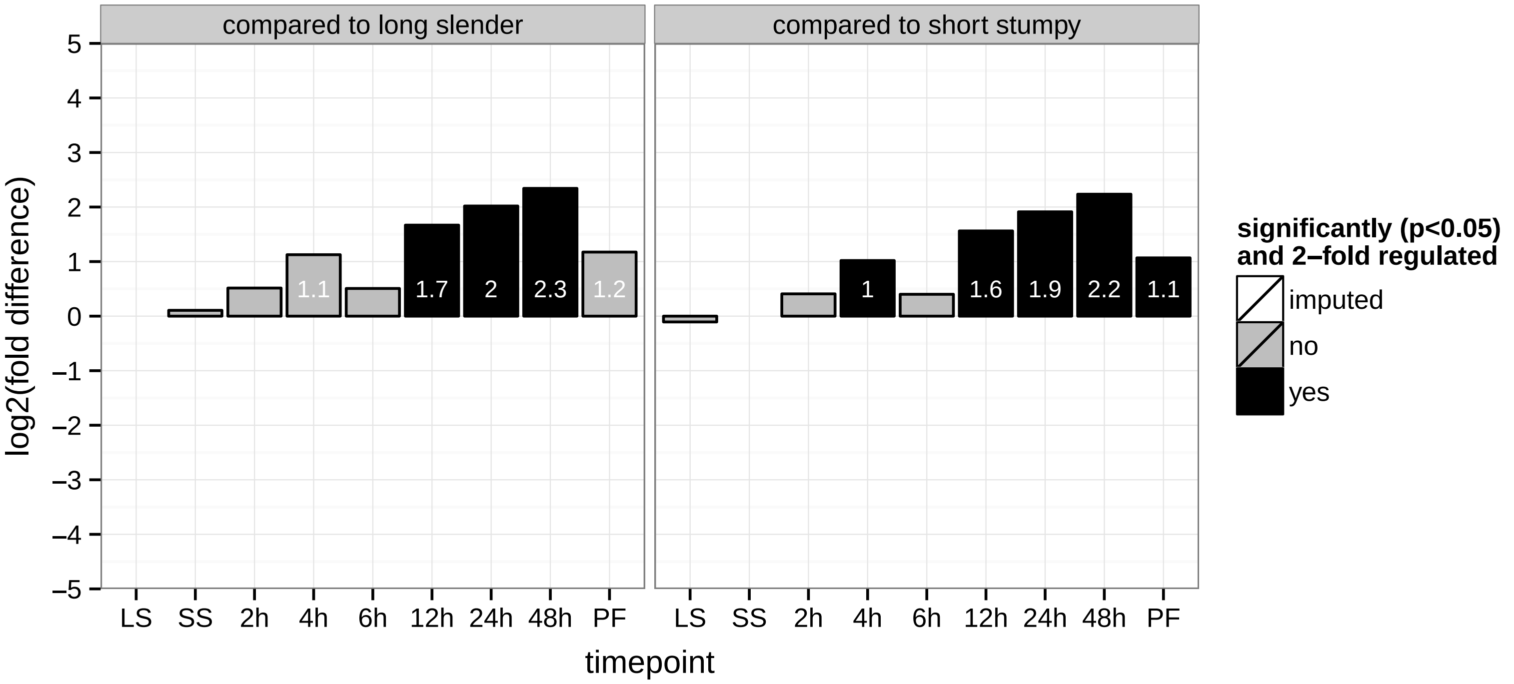
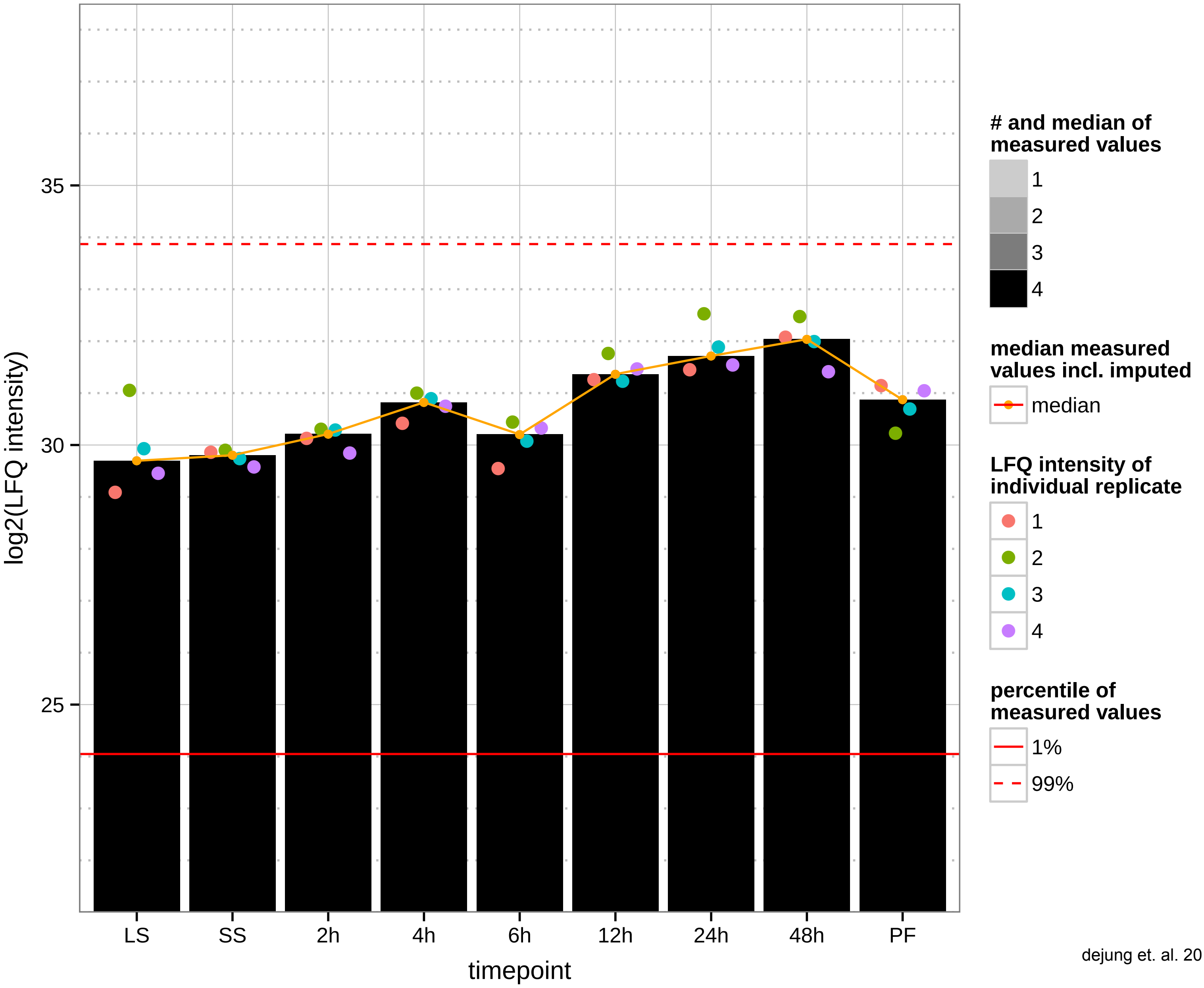
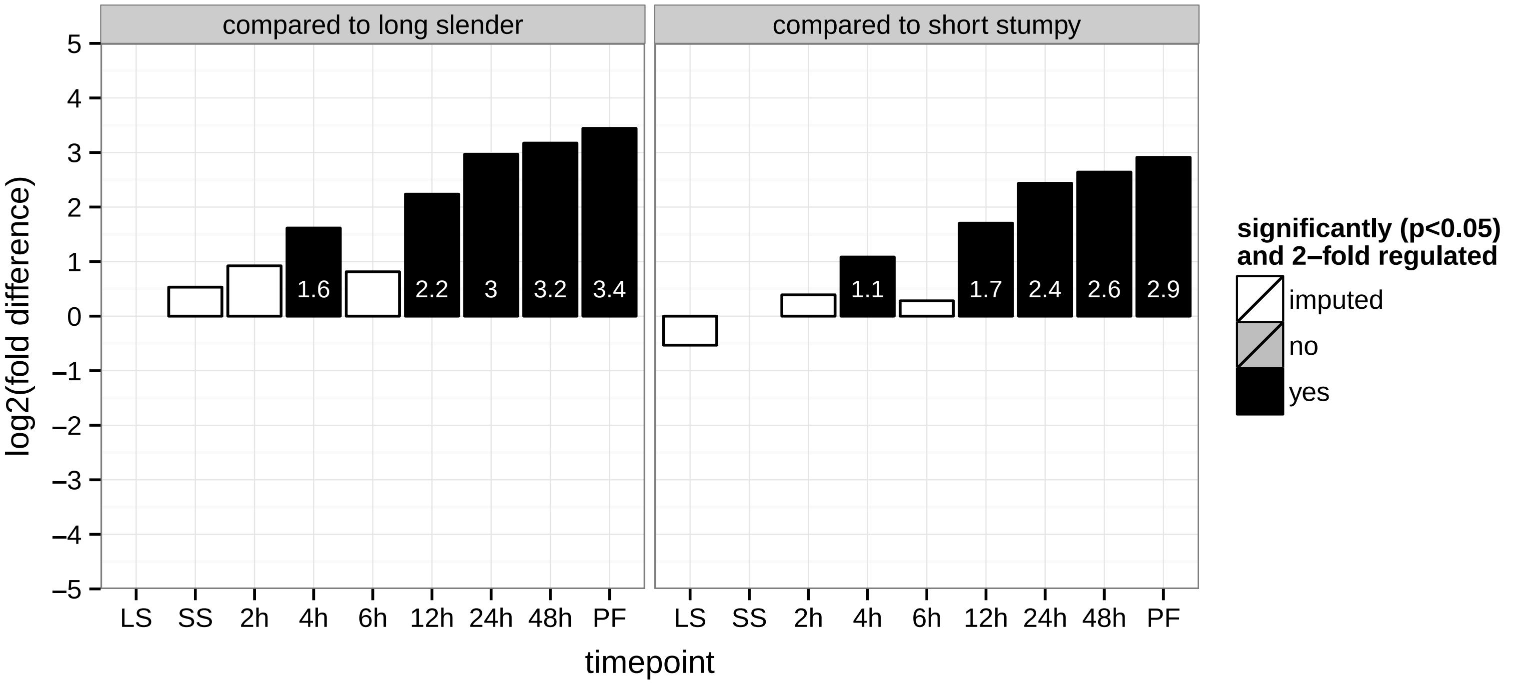
calpain–like cysteine peptidase, putative, cysteine peptidase, Clan CA, family C2
Tb927.7.4070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

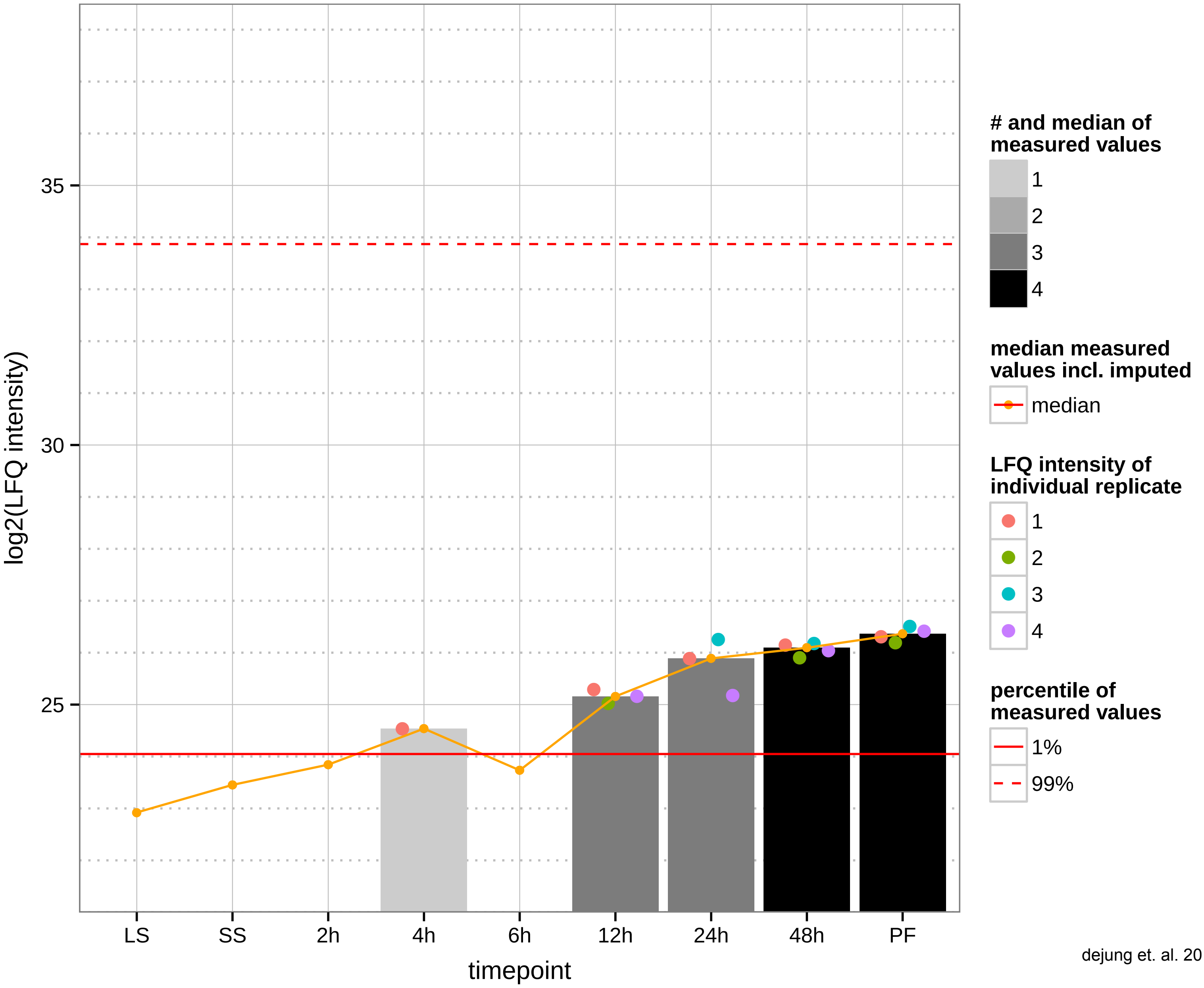




dejung et. al. 2015

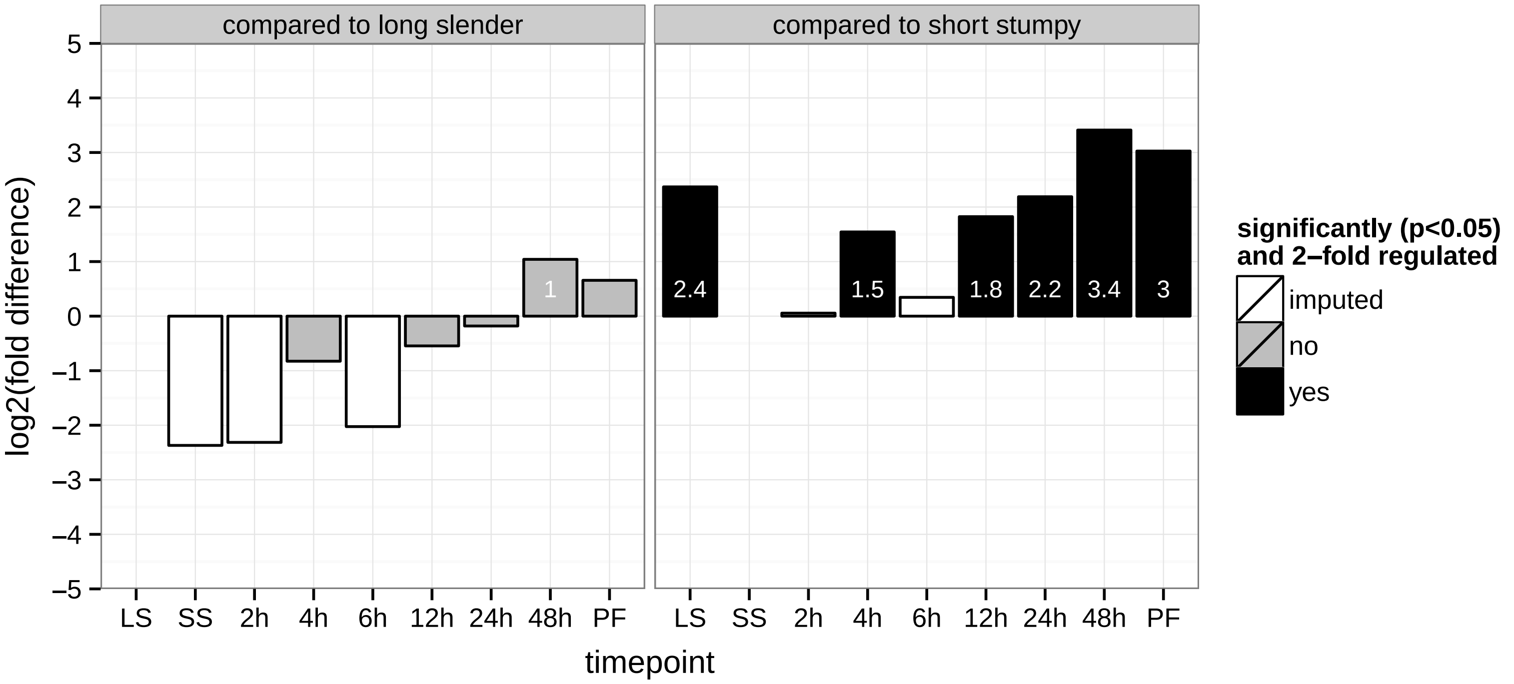
zinc finger CCCH domain containing protein 17 (ZC3H17)
Tb927.7.930
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

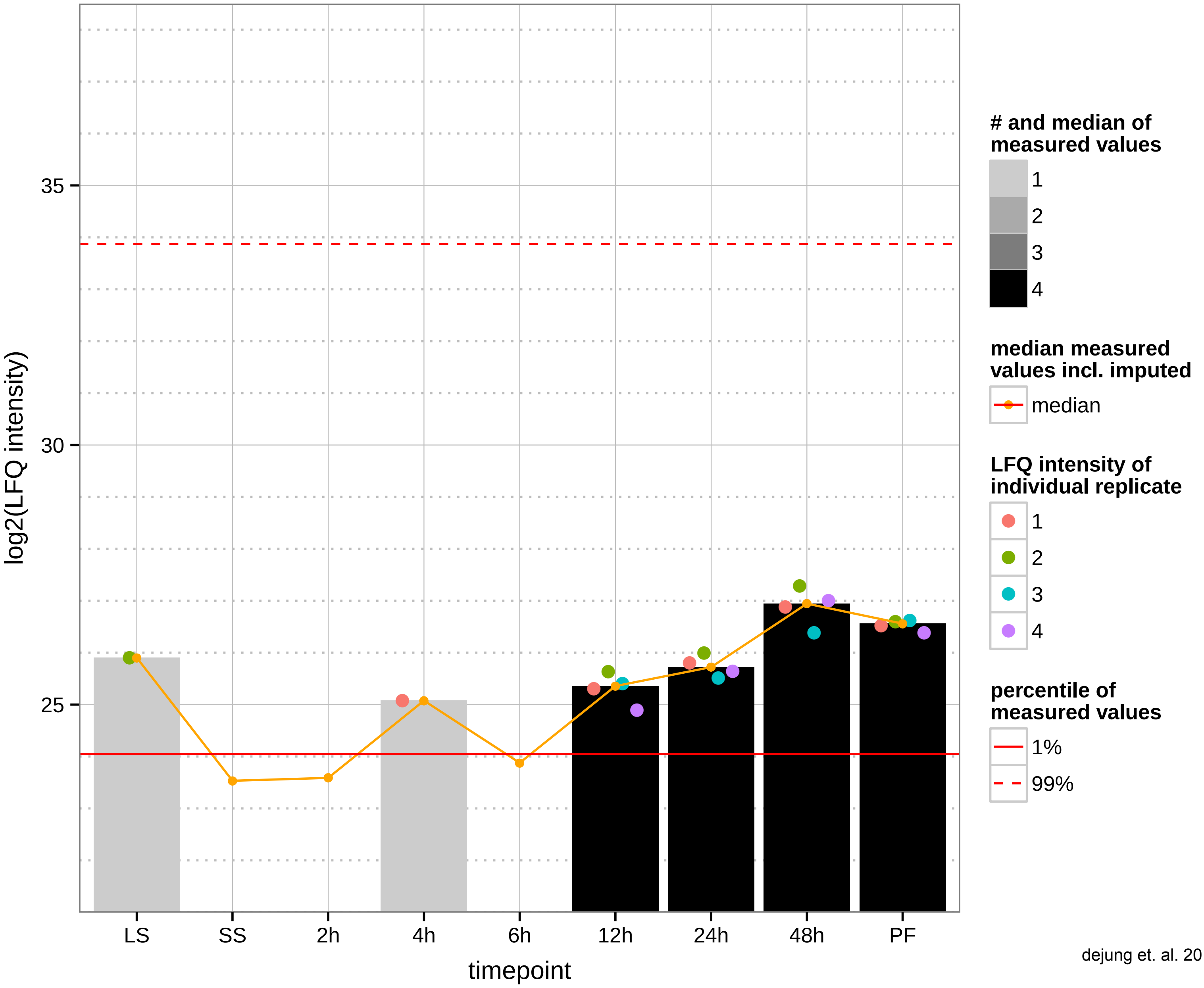




dejung et. al. 2015

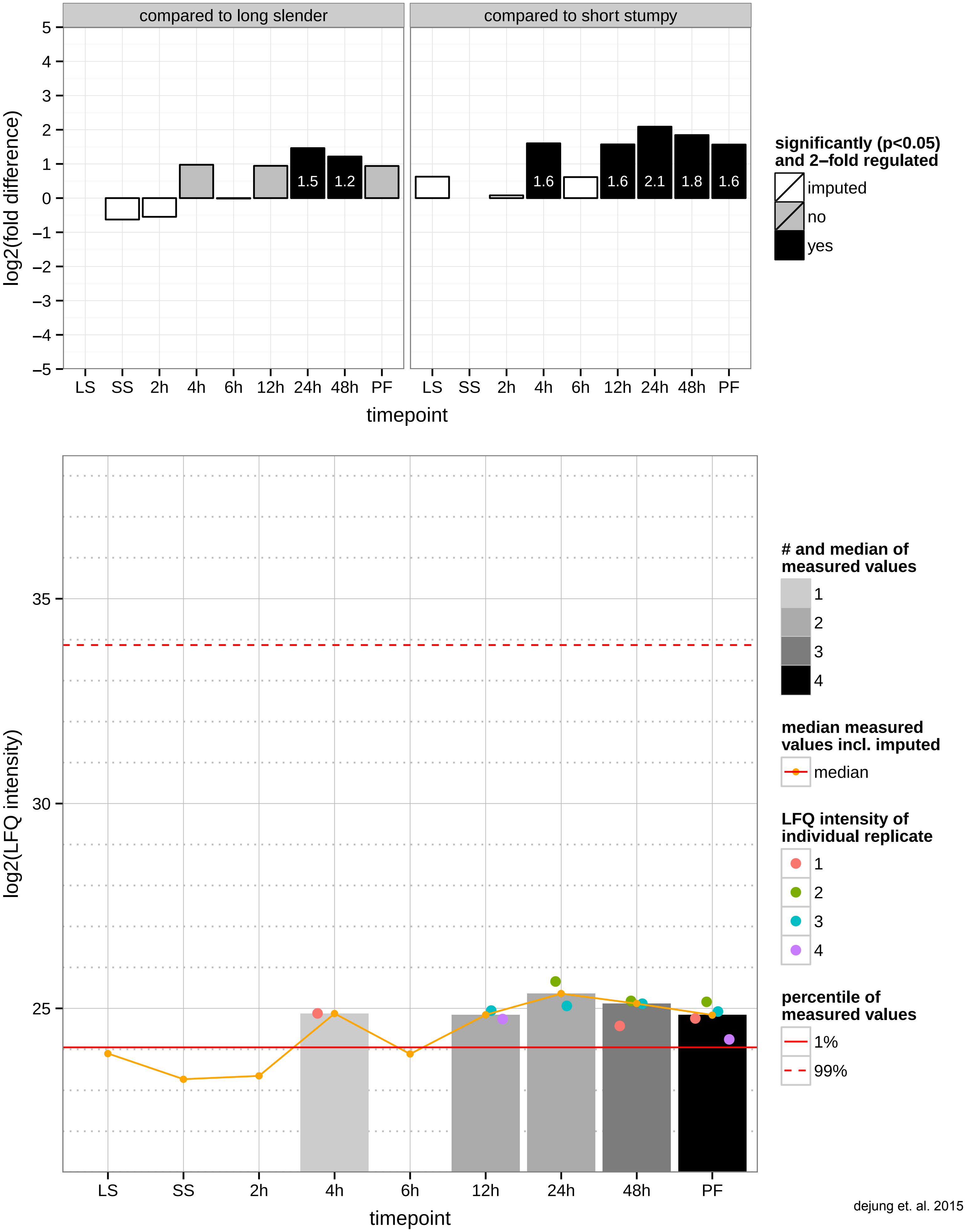
hypothetical protein, conserved
Tb927.8.5300
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.6380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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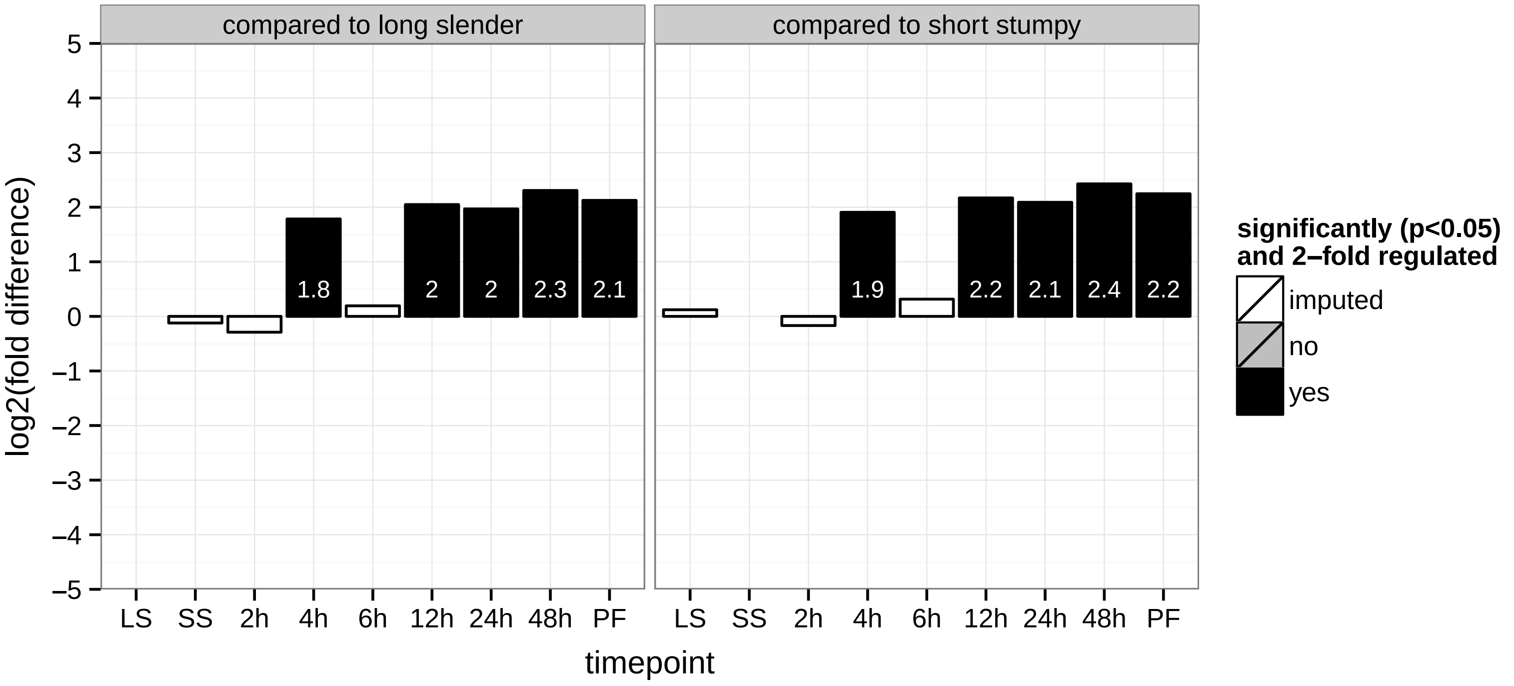
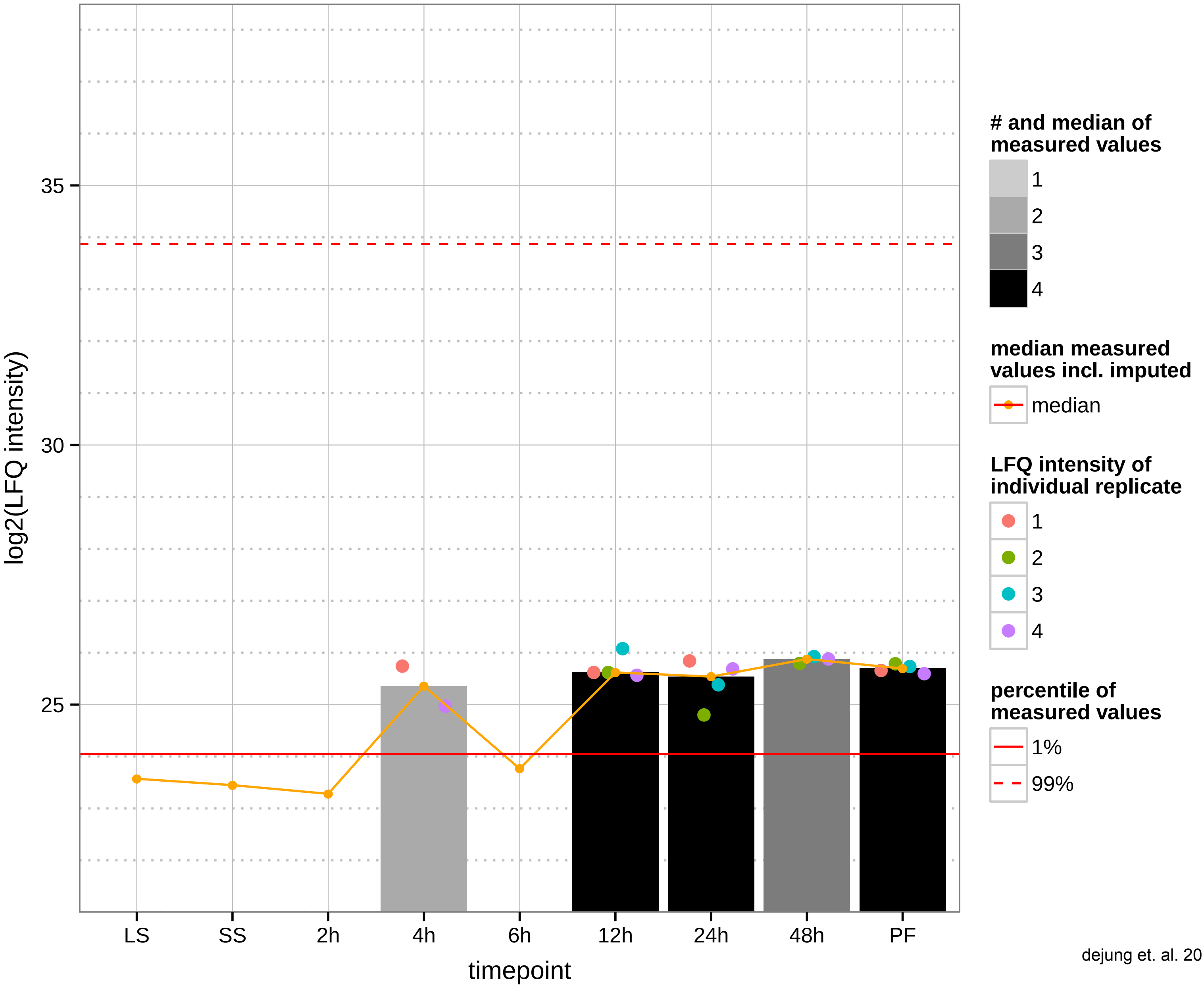
dihydrolipoamide dehydrogenase, pseudogene, putative, acetoin dehydrogenase e3 component, point mutation
Tb927.8.7380;Tb927.4.5050
AGOF: dihydrolipoyl dehydrogenase activity, flavin adenine dinucleotide binding, disulfide oxidoreductase activity
AGOC: cytoplasm, mitochondrion
AGOP: cell redox homeostasis, oxidation–reduction process
PGOF: flavin adenine dinucleotide binding, oxidoreductase activity
PGOC: cytoplasm
PGOP: cell redox homeostasis, oxidation–reduction process





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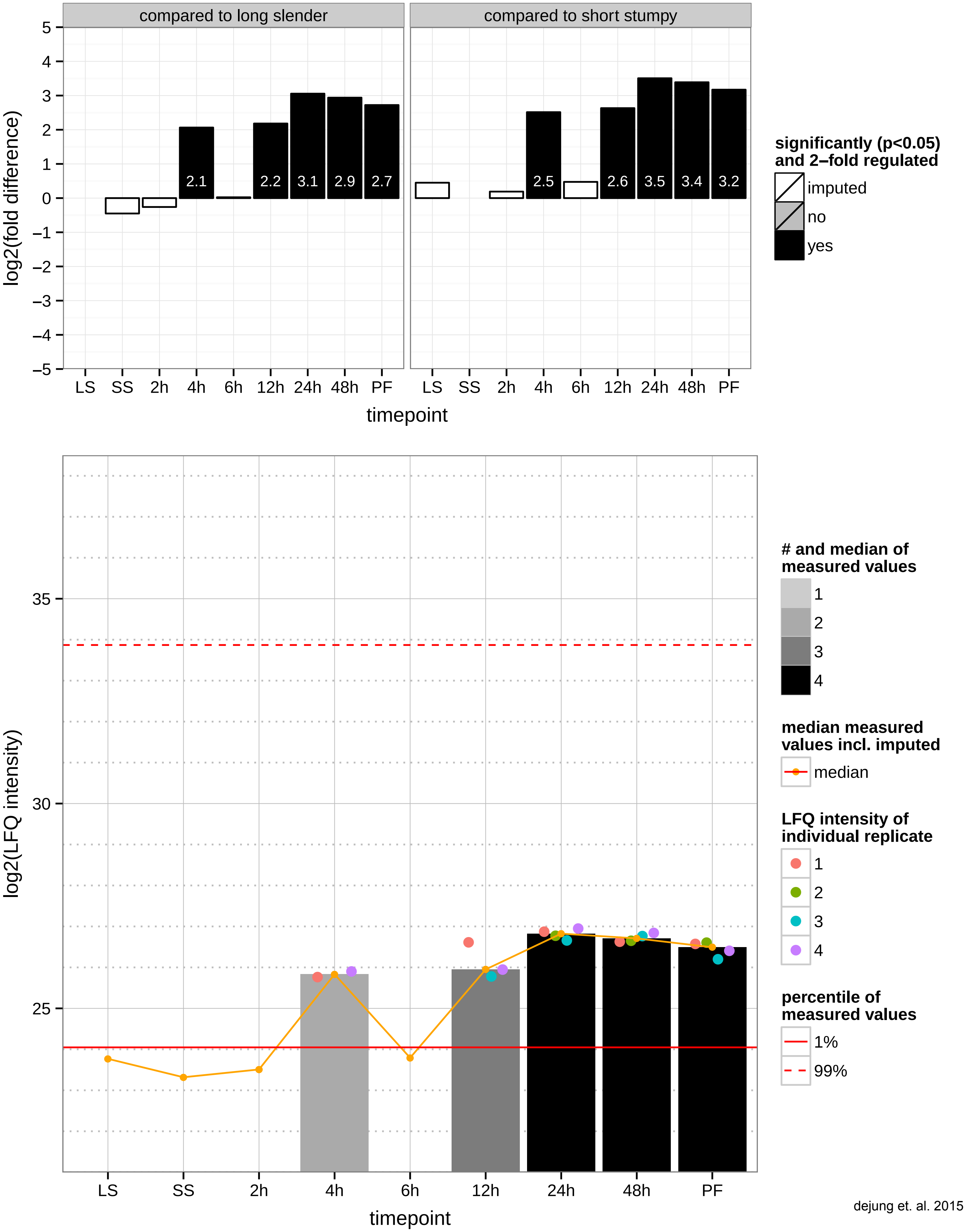
hypothetical protein, conserved
Tb927.9.10470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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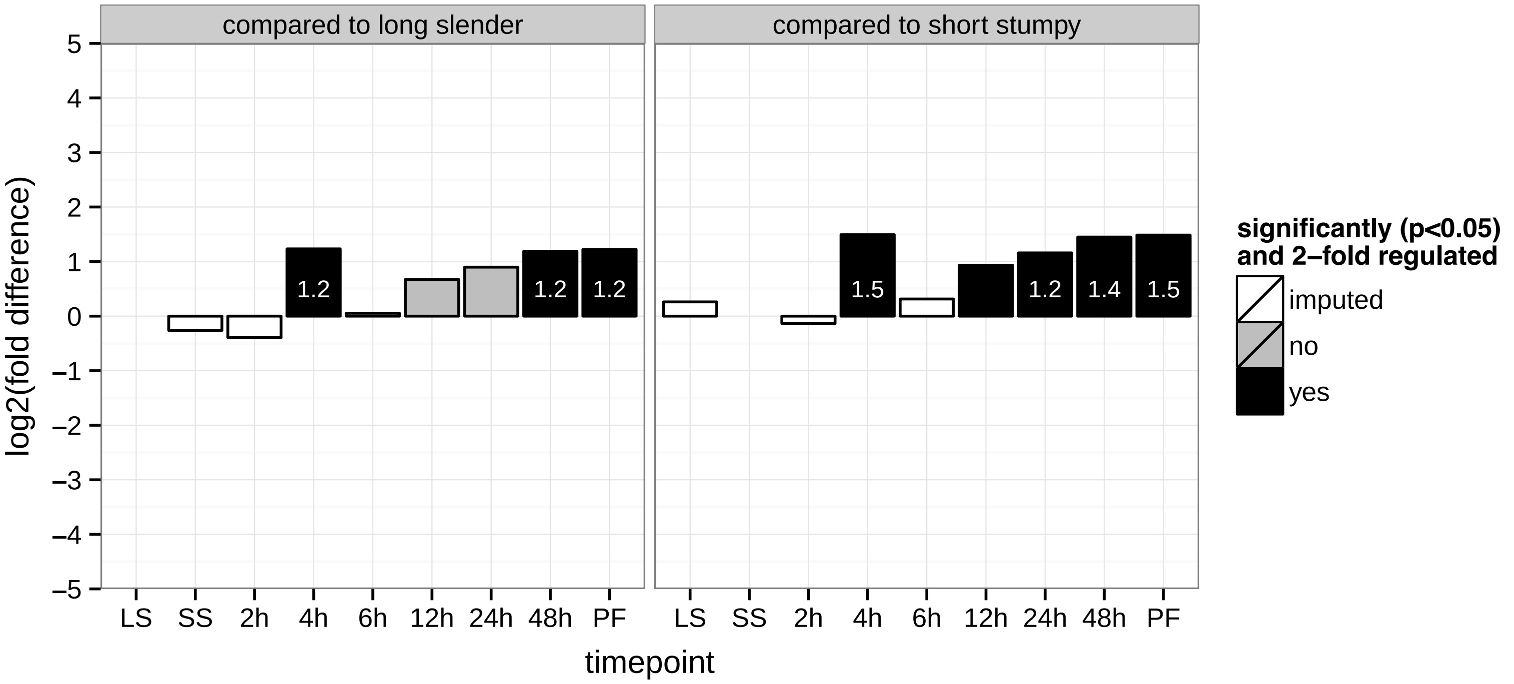
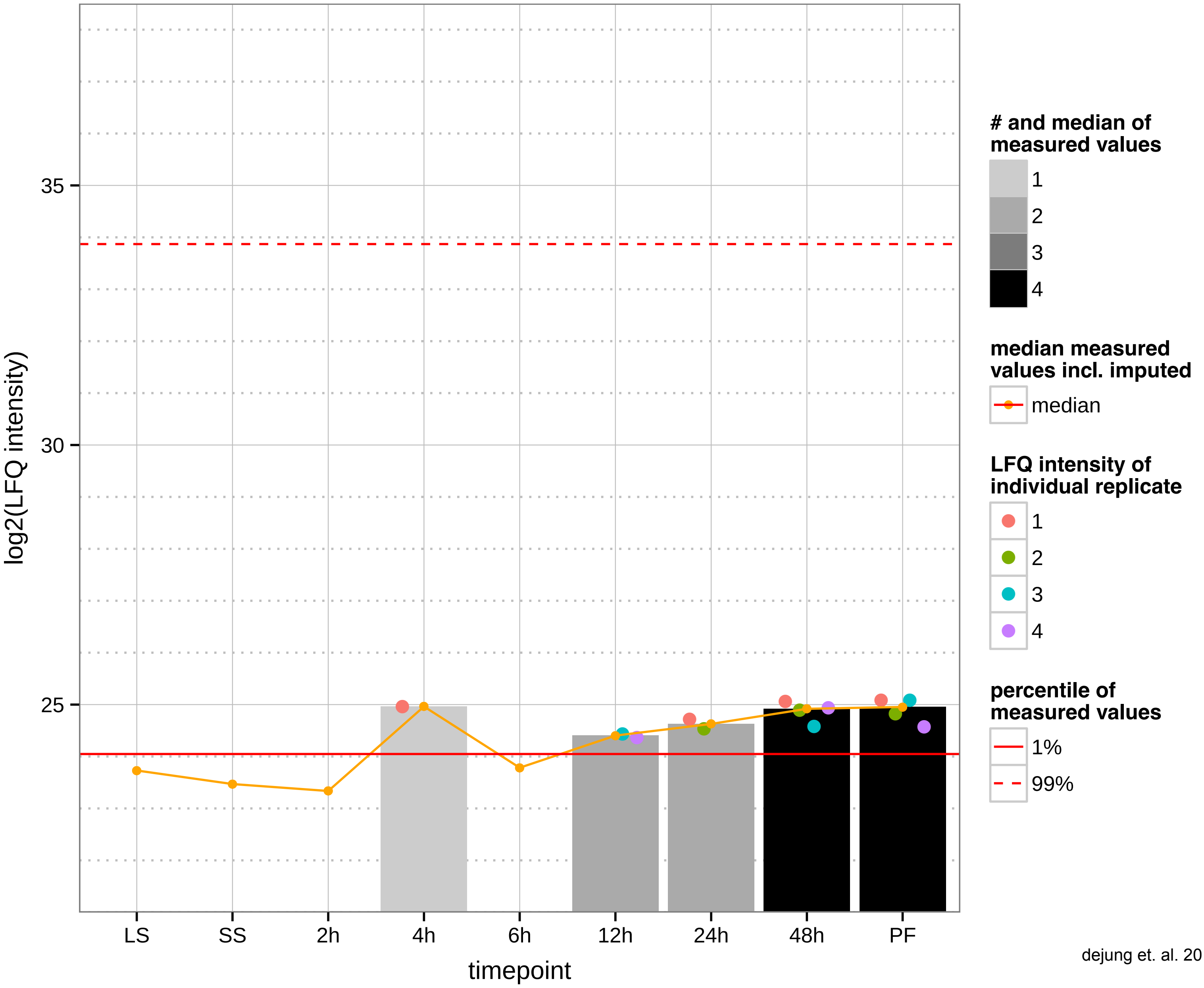
hypothetical protein, conserved
Tb927.9.12750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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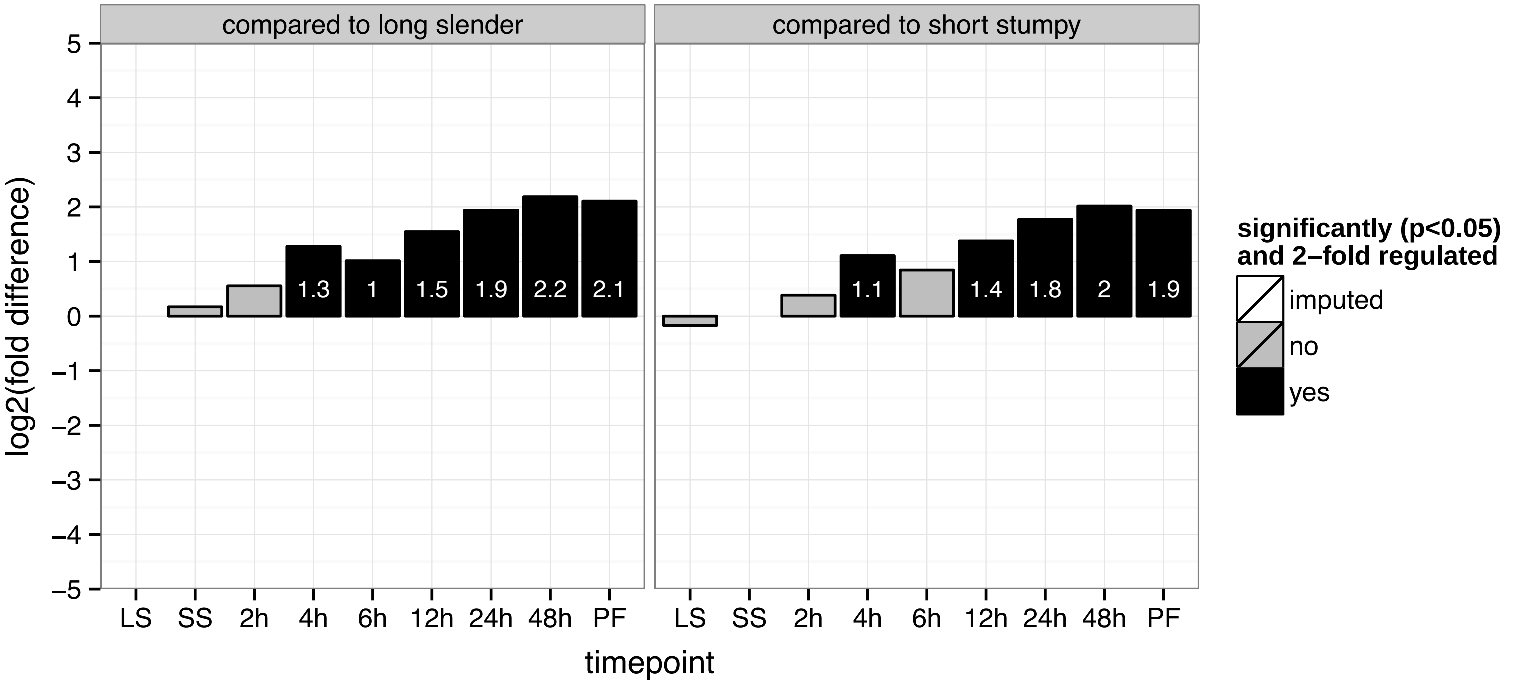
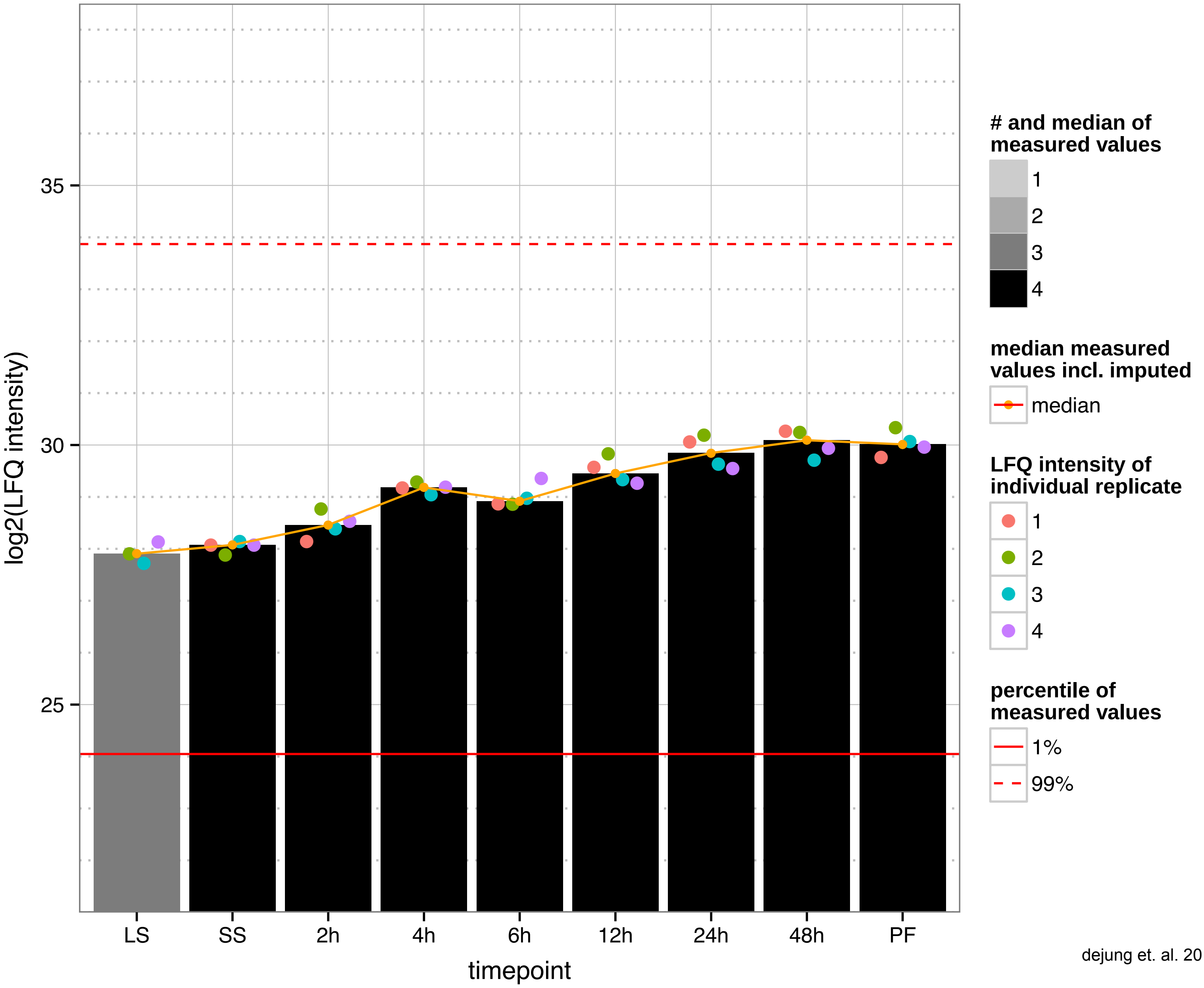
hypothetical protein, conserved
Tb927.9.7000
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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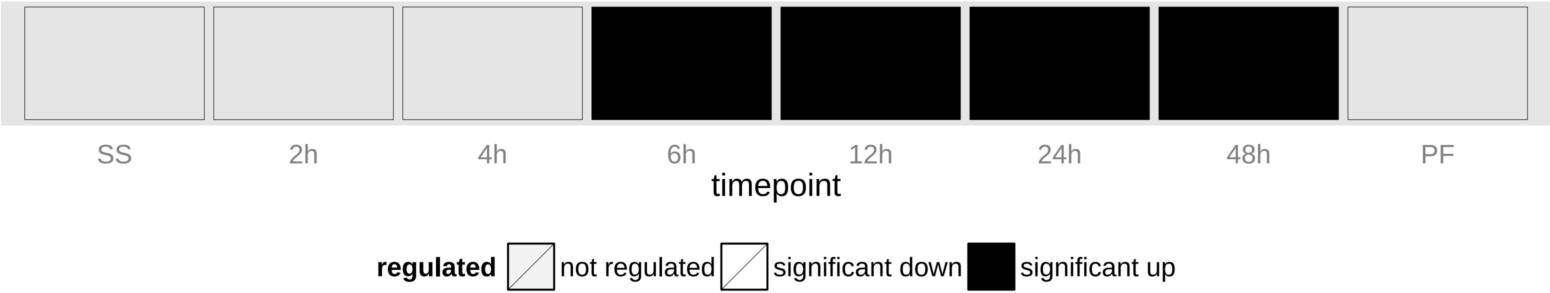
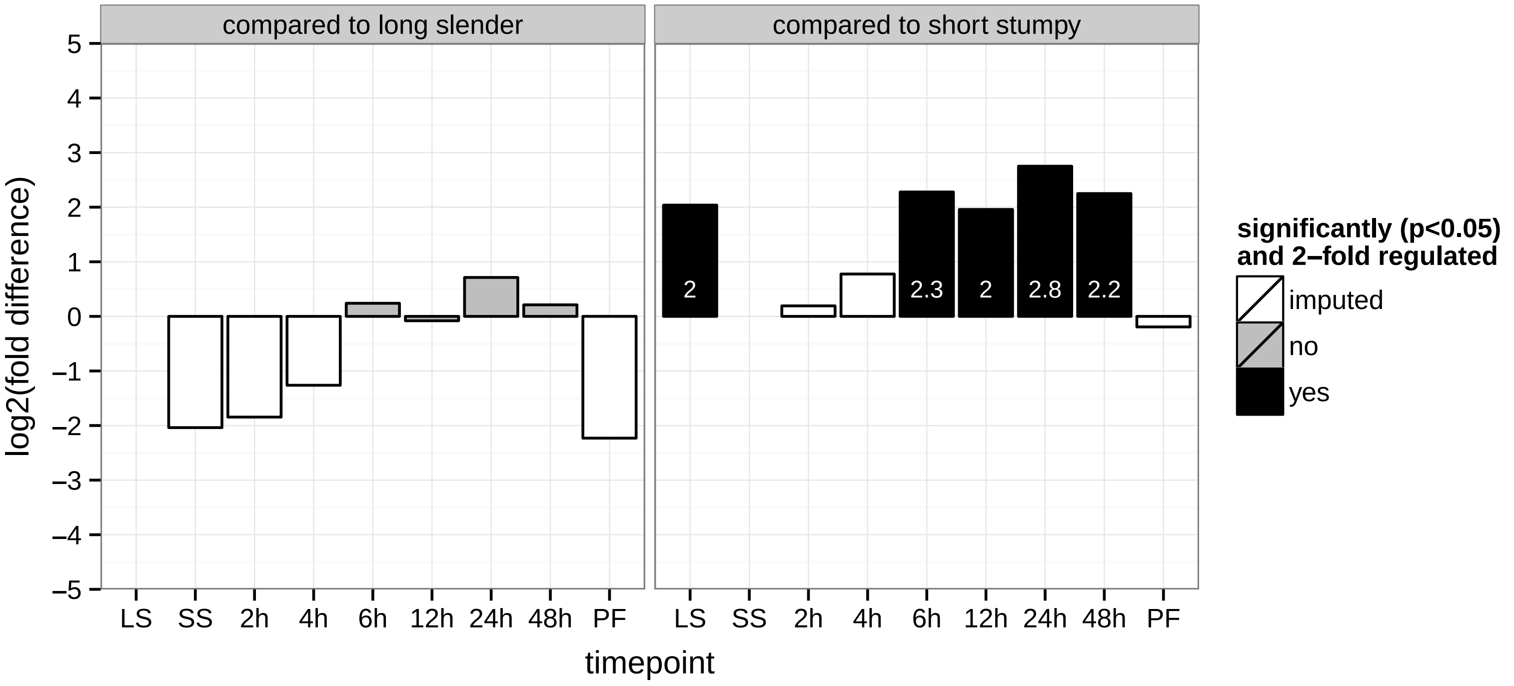
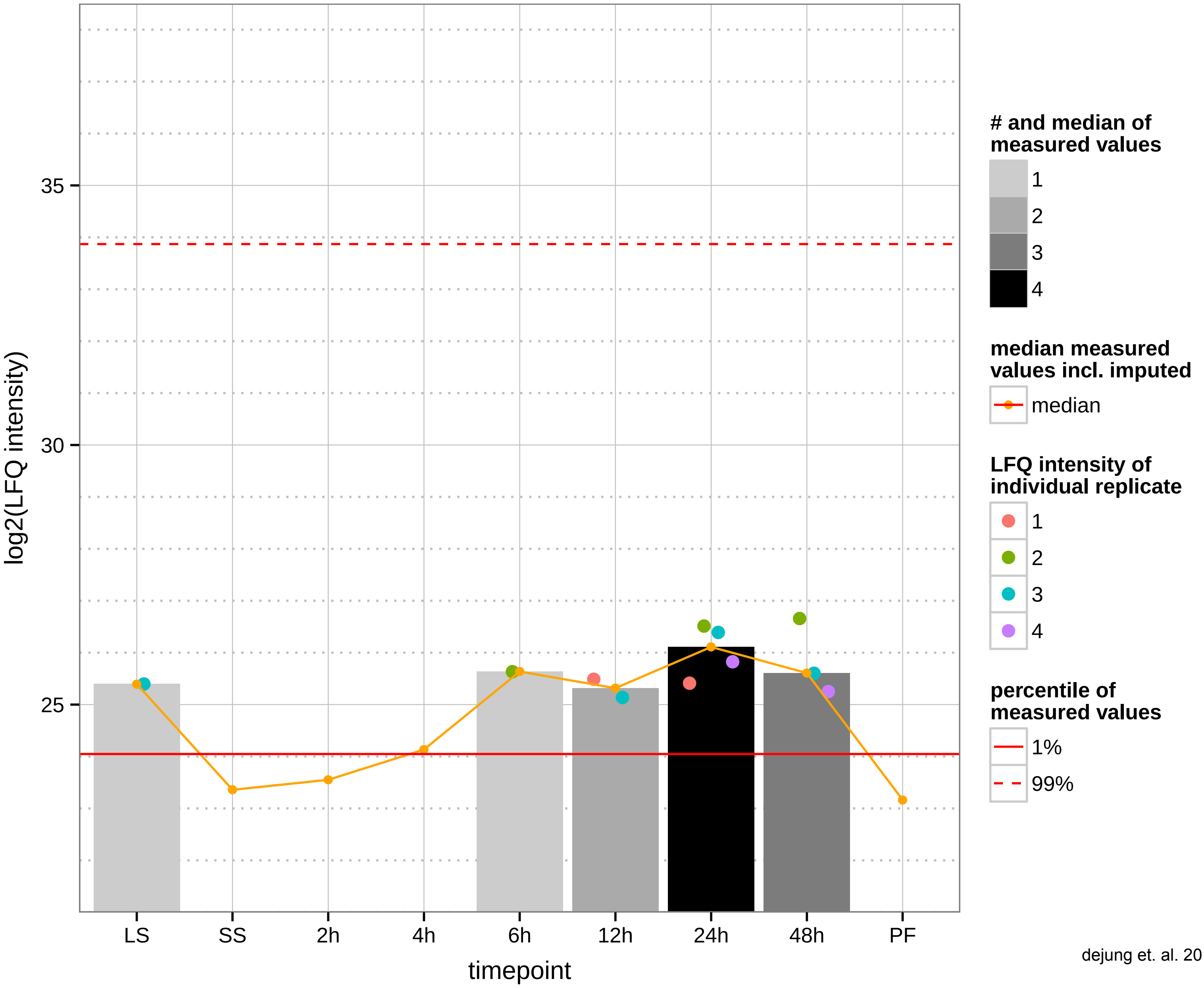


dejung et. al. 2015

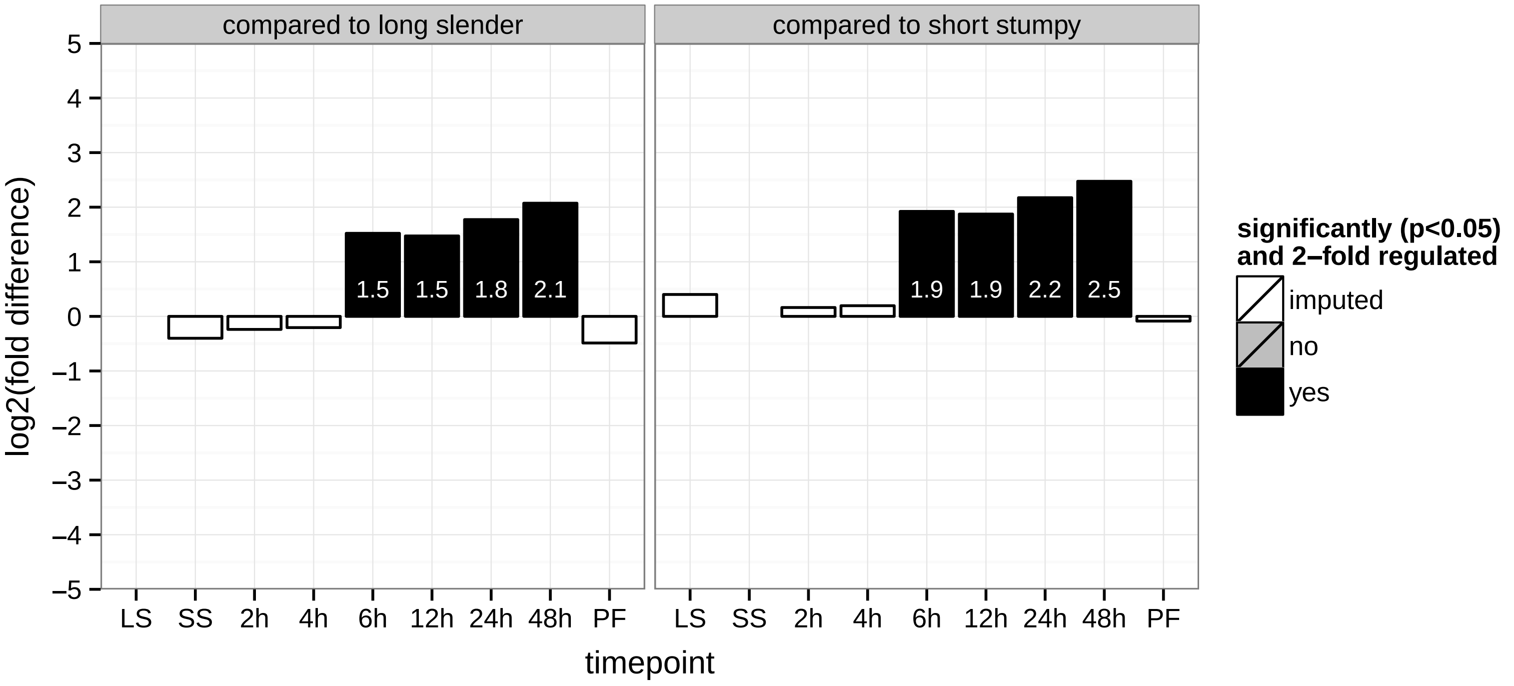
hypothetical protein, conserved
Tb927.1.3800
AGOF: null
AGOC: mitochondrion
AGOP: response to stress
PGOF: null
PGOC: null
PGOP: response to stress

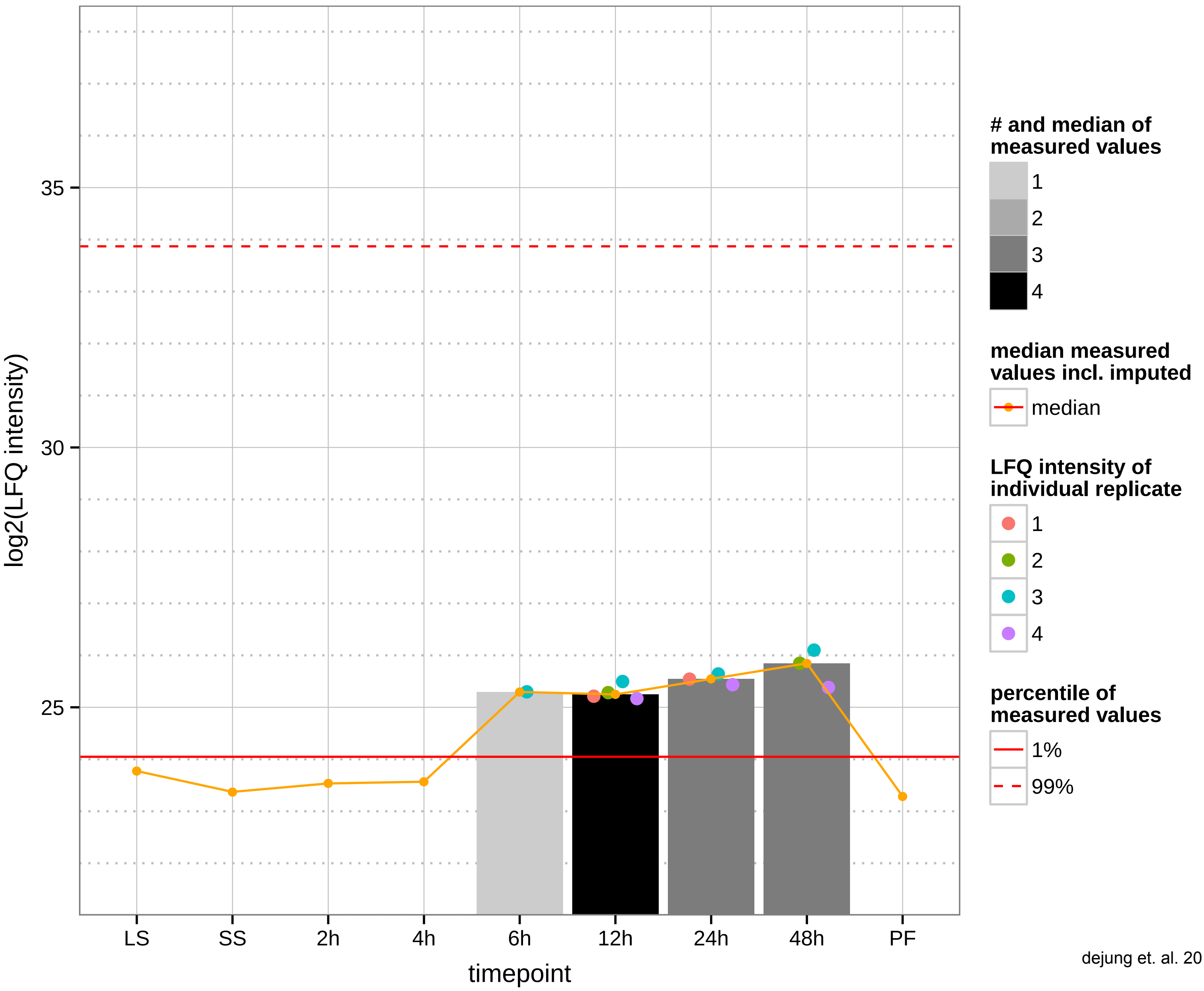




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.12050
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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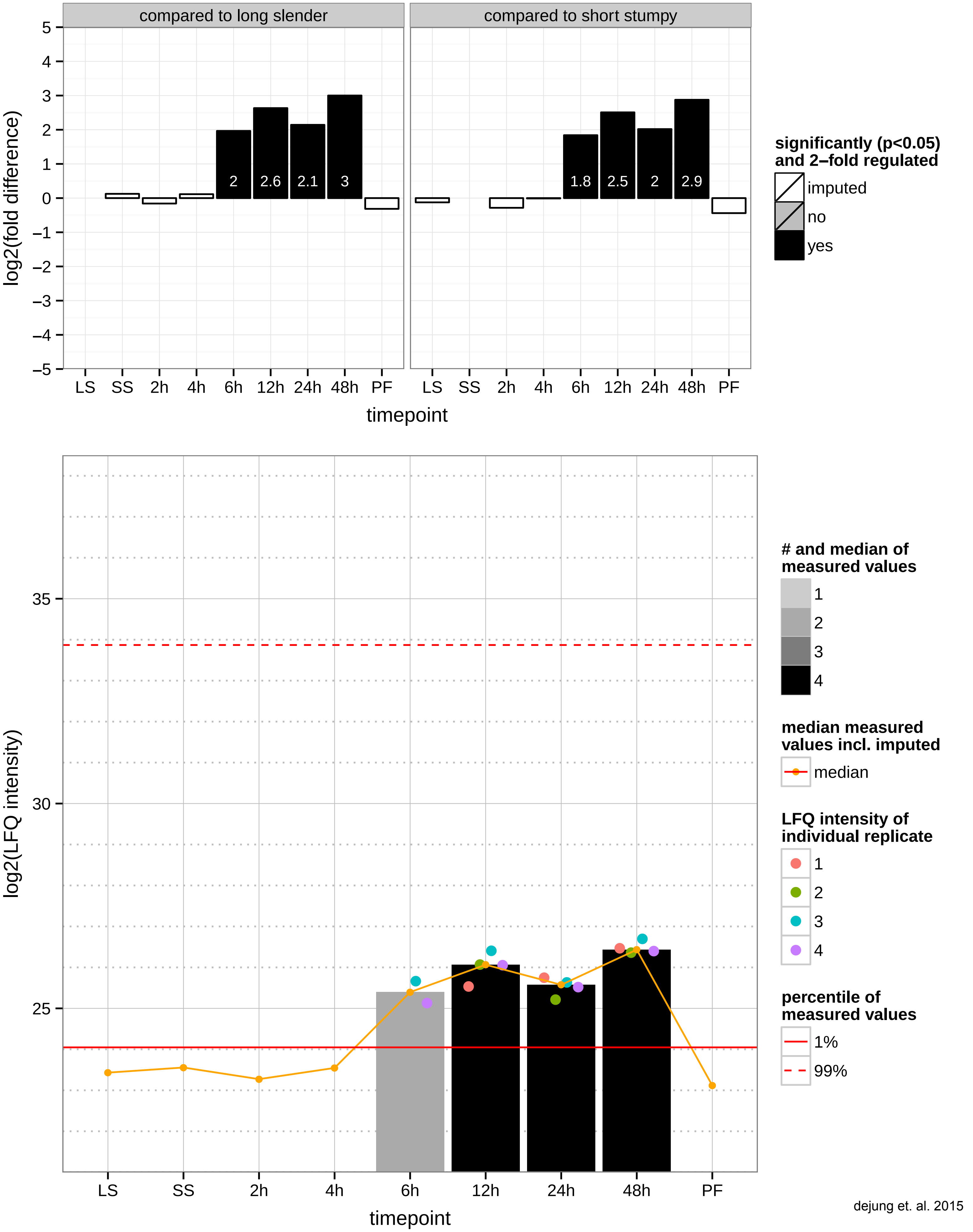
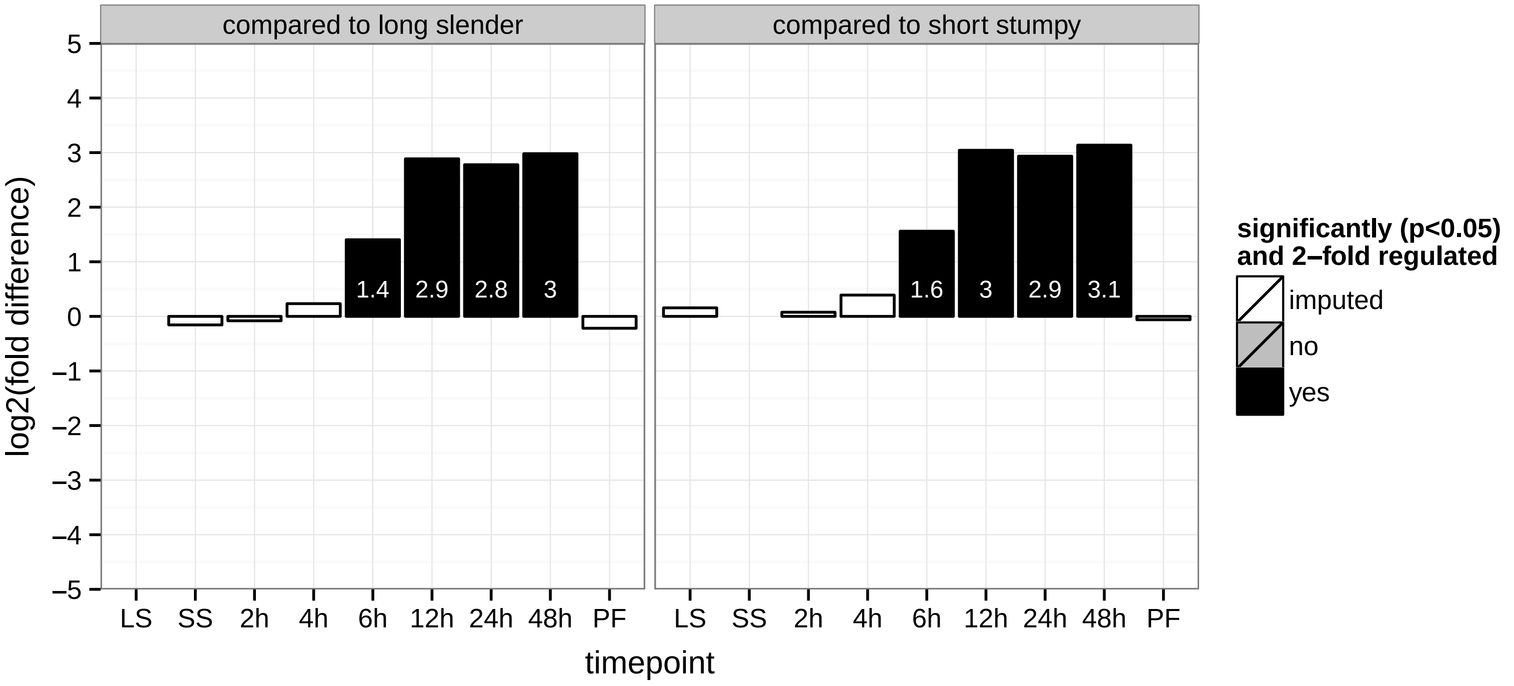
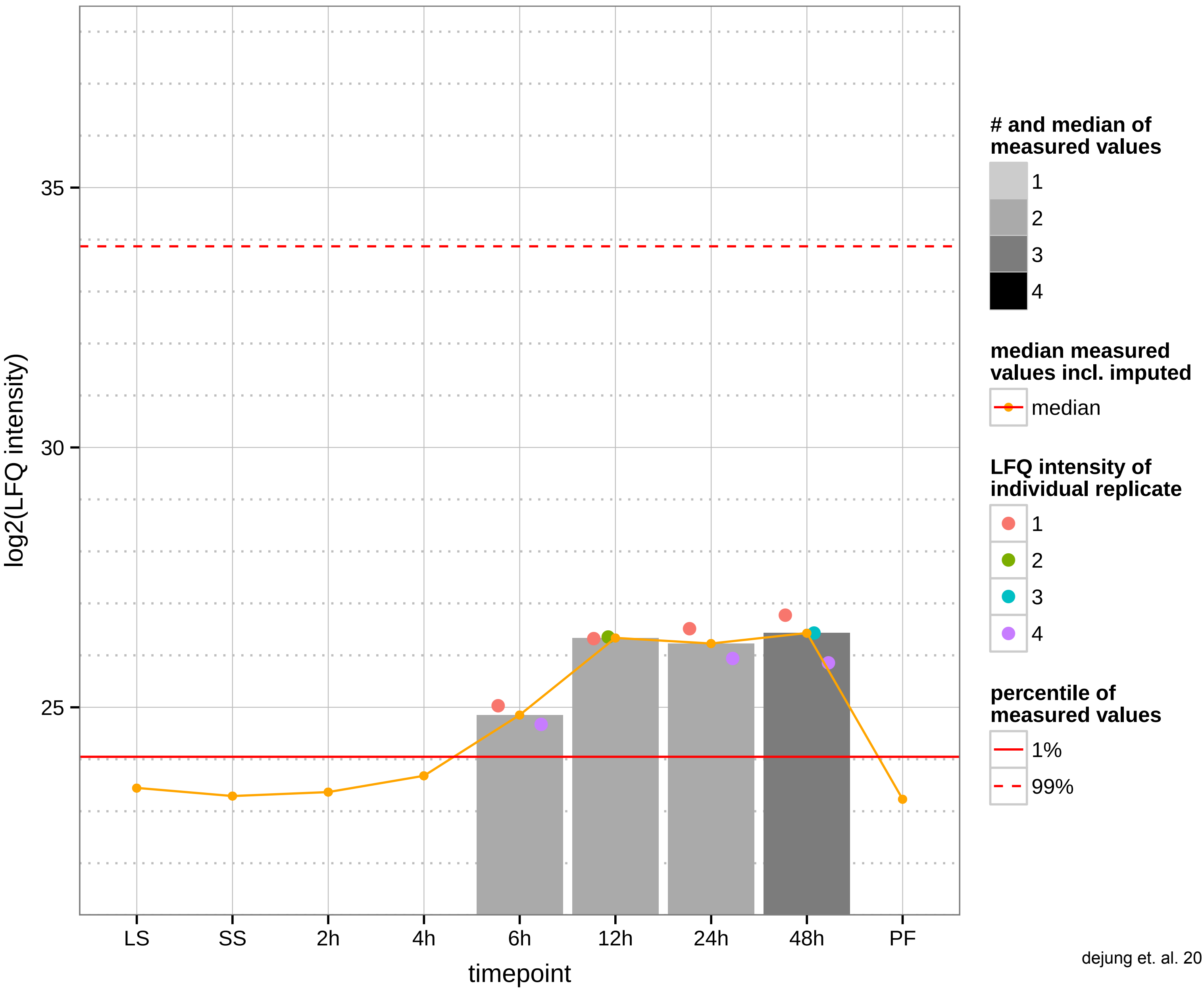
Zinc finger CCCH domain–containing protein 37 (ZC3H37), Zinc finger CCCH domain–containing protein 38 (ZC3H38)
Tb927.10.12780
AGOF: RNA binding, nucleic acid binding, zinc ion binding, nucleic acid binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null



dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.5860
AGOF: null
AGOC: null
AGOP: null
PGOF: cAMP−dependent protein kinase regulator activity
PGOC: null
PGOP: signal transduction





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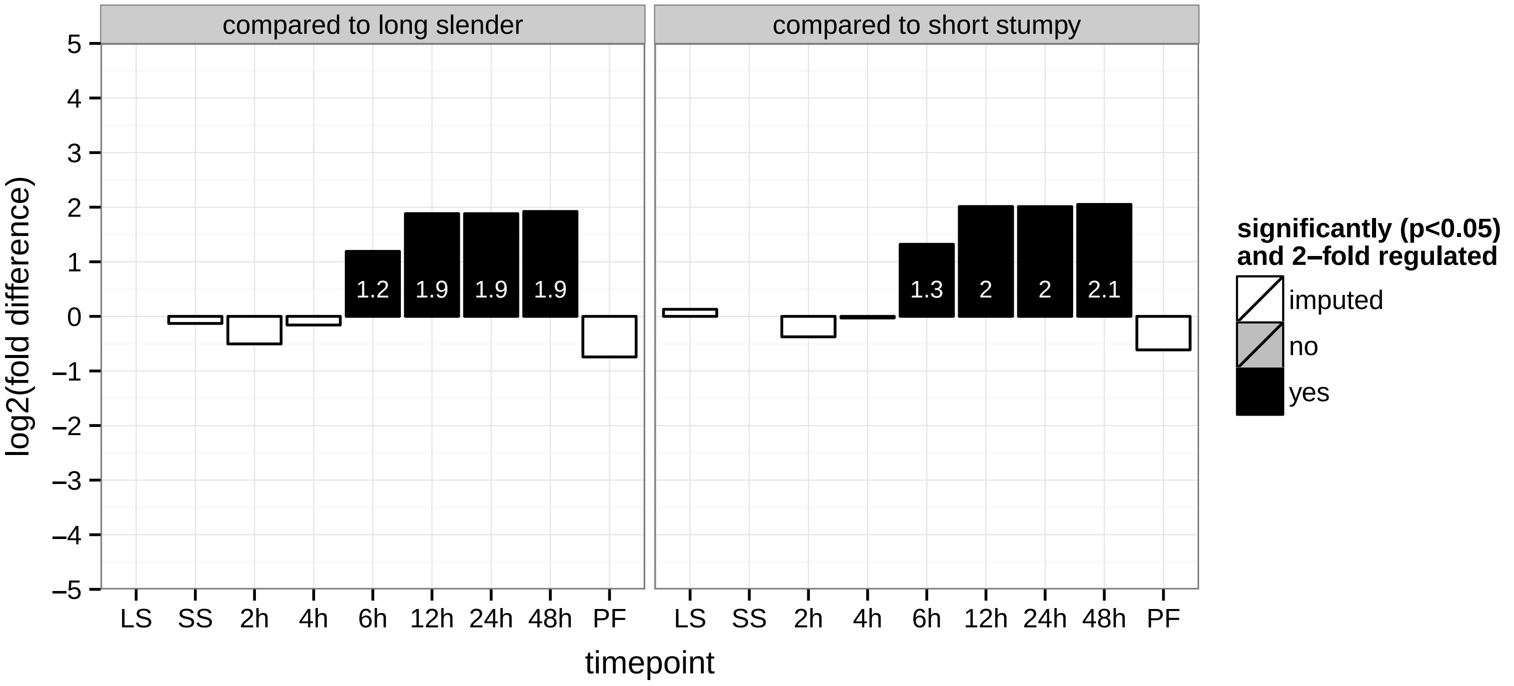
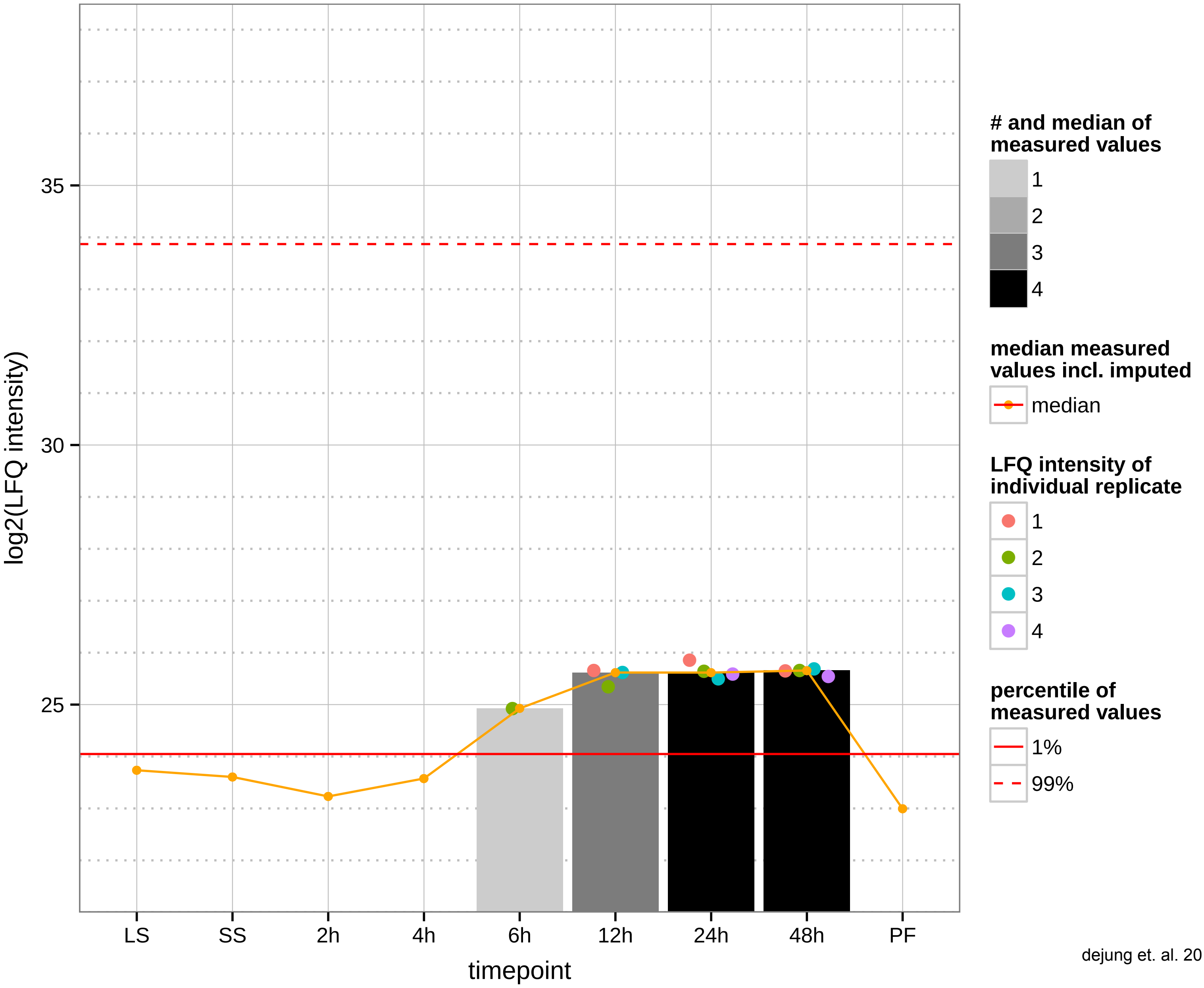
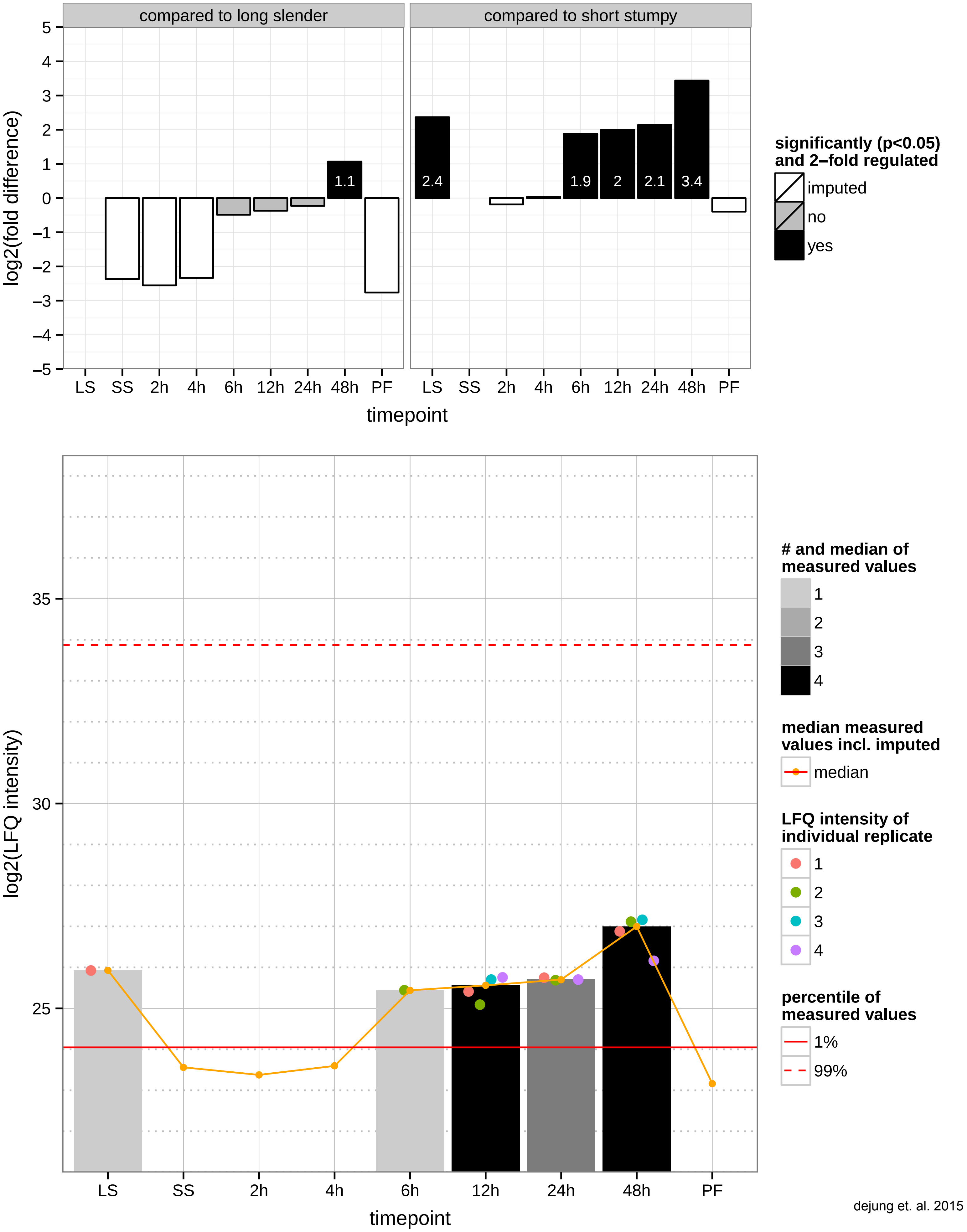
ras–like small GTPase, putative (TbRHP)
Tb927.10.6240
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: protein transport
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, protein transport, signal transduction, small GTPase mediated signal transduction





dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.6360
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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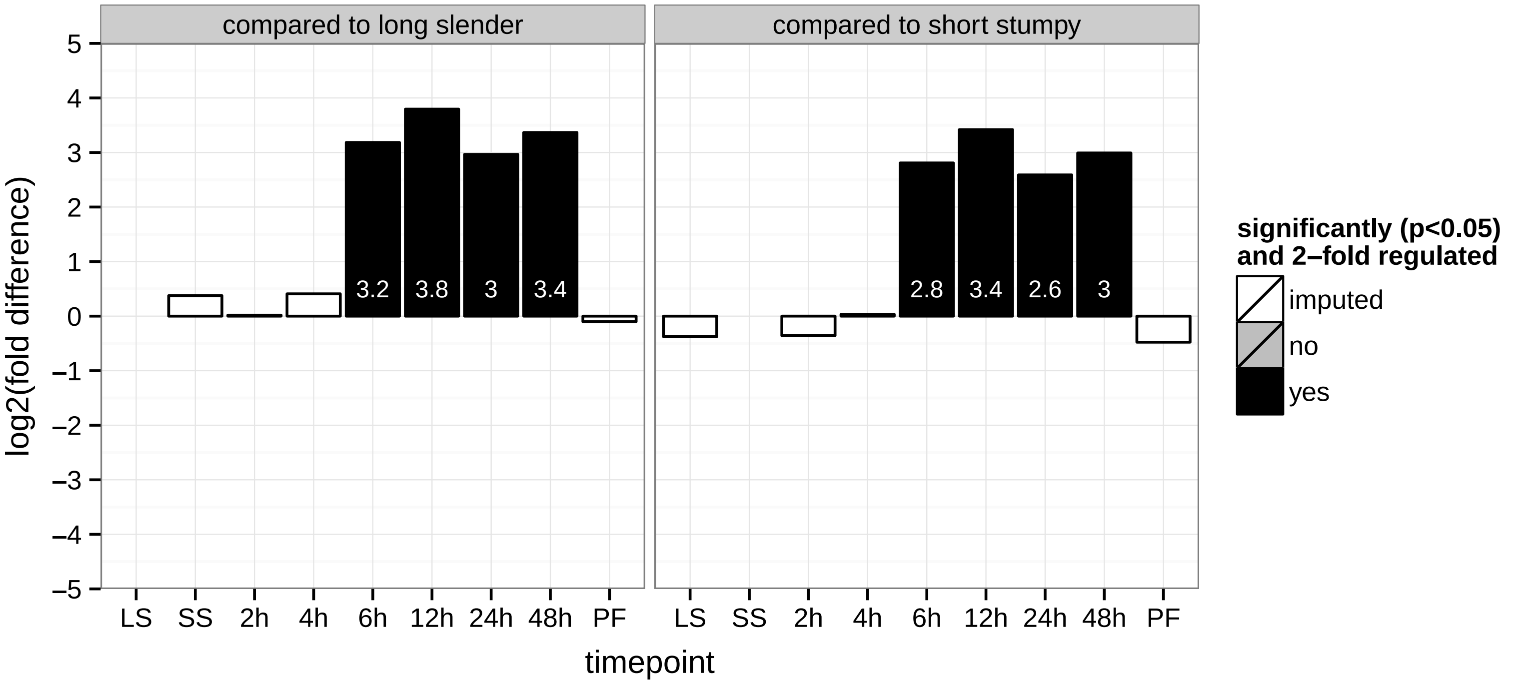
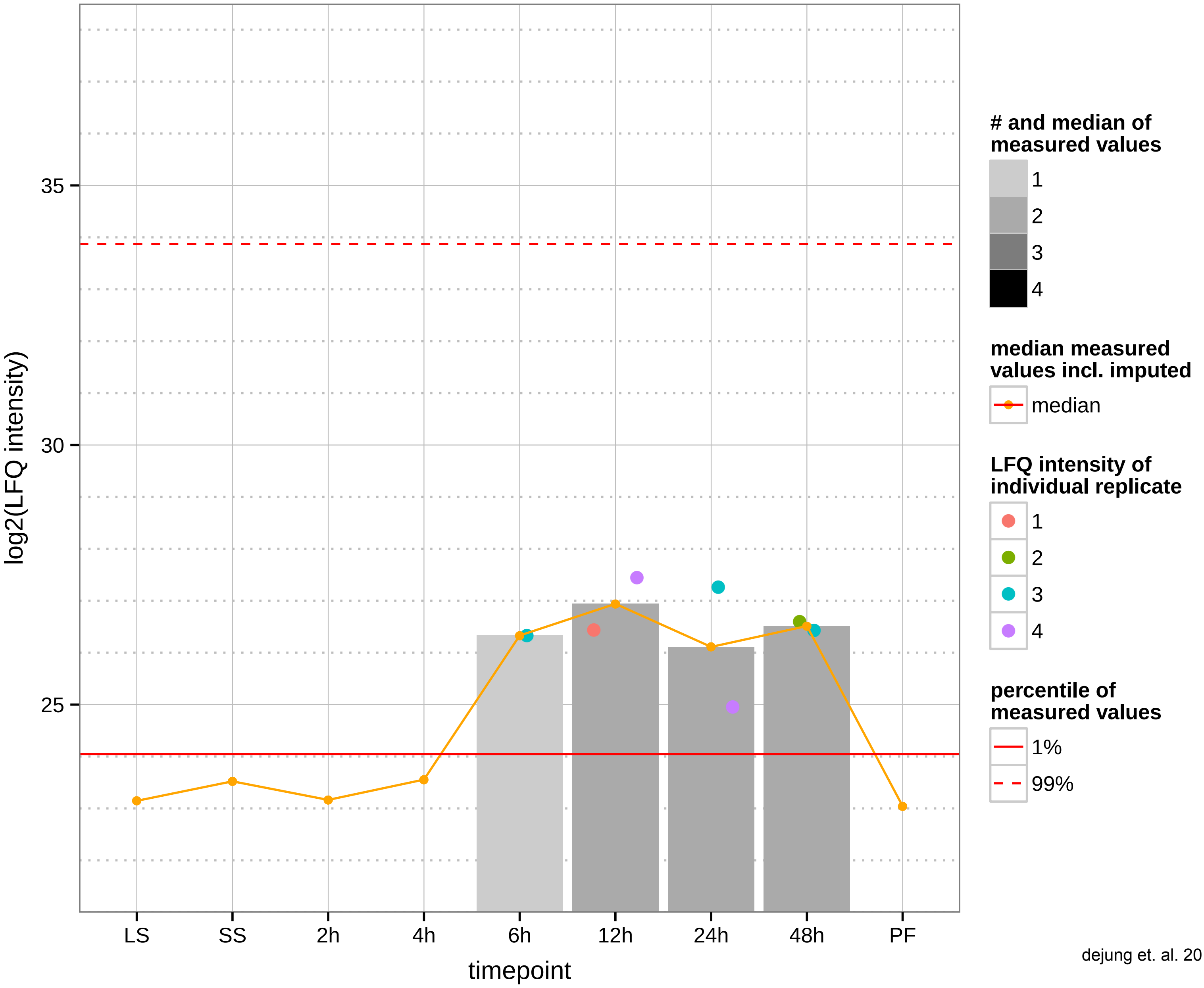
hypothetical protein, conserved
Tb927.10.9280;Tb11.v5.0485
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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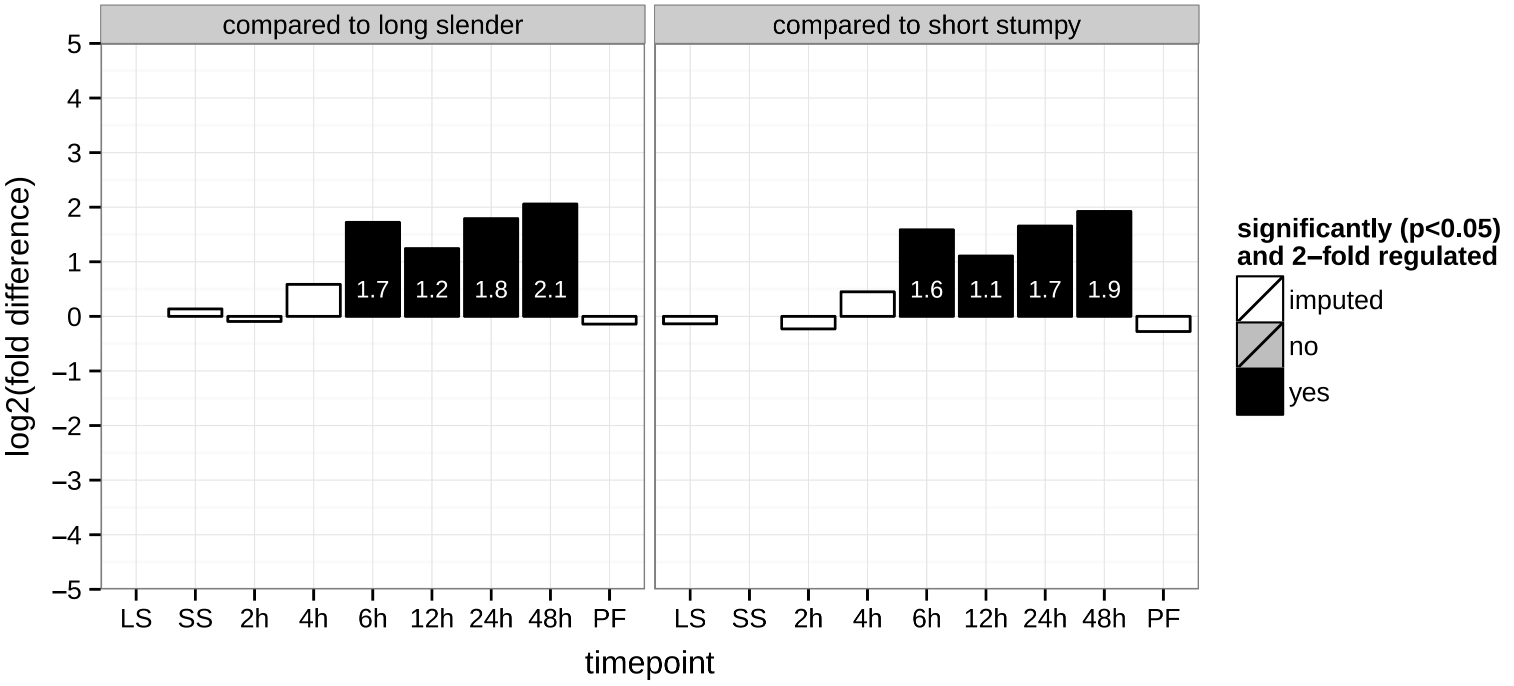
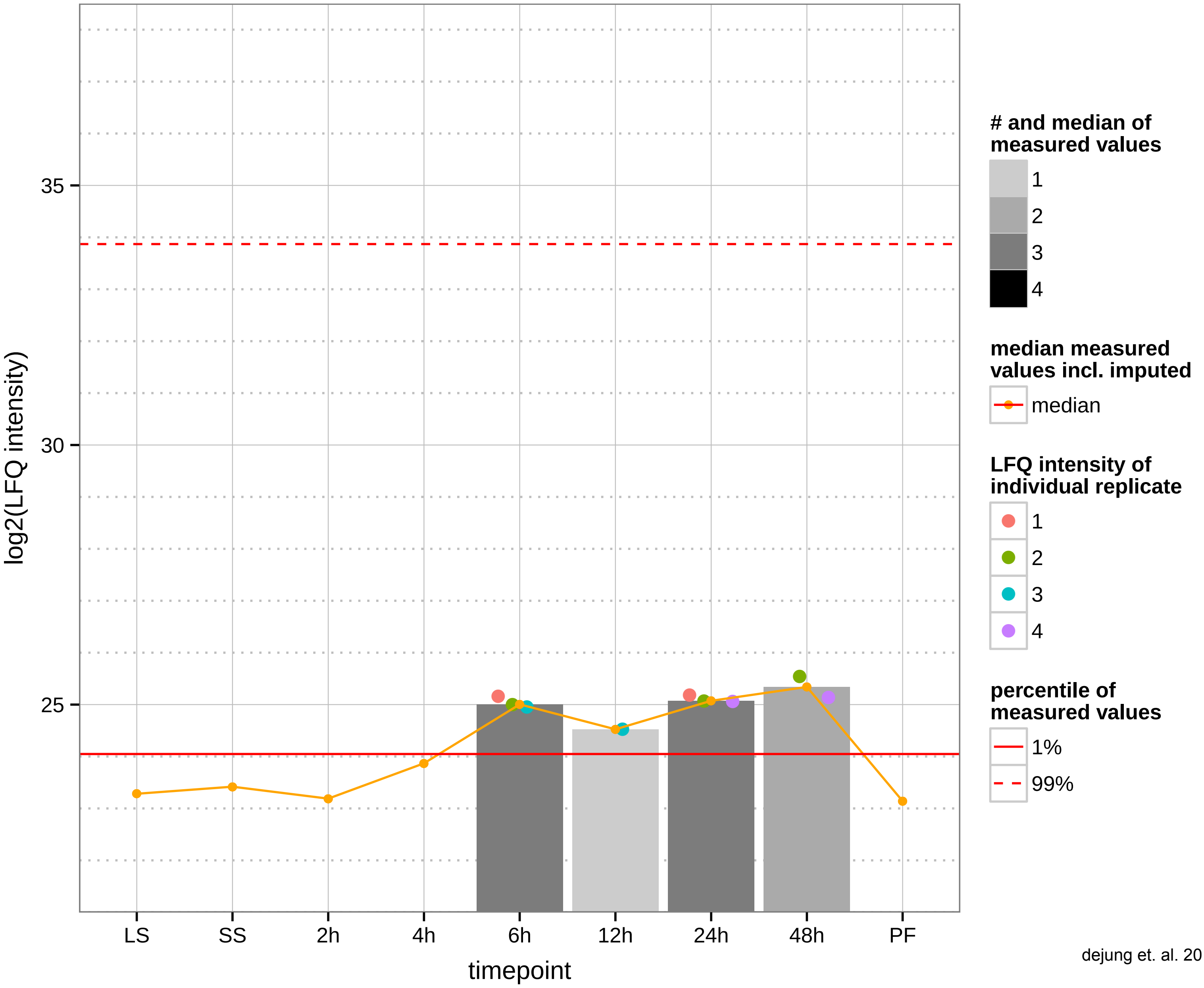
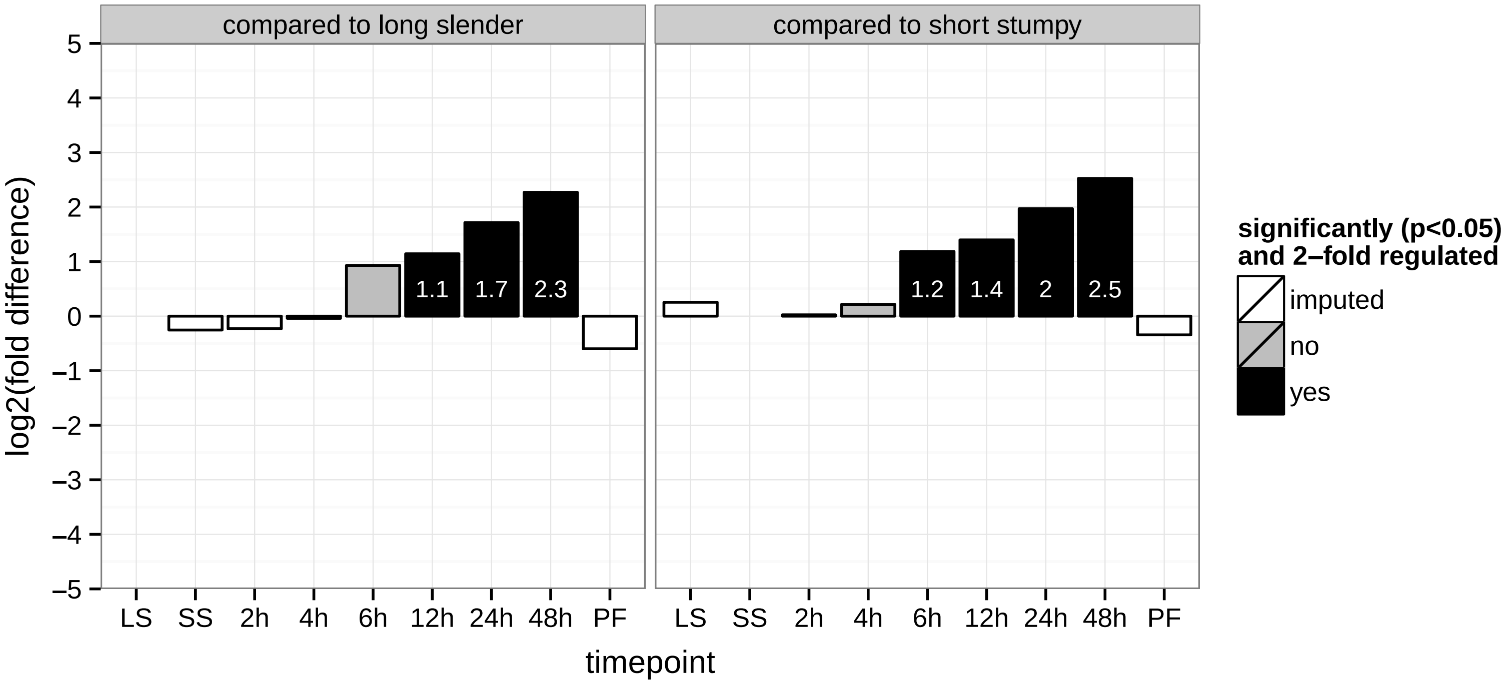
actin–like protein, putative
Tb927.11.10110
AGOF: structural constituent of cytoskeleton
AGOC: actin cytoskeleton
AGOP: cytoskeleton organization
PGOF: null
PGOC: null
PGOP: null

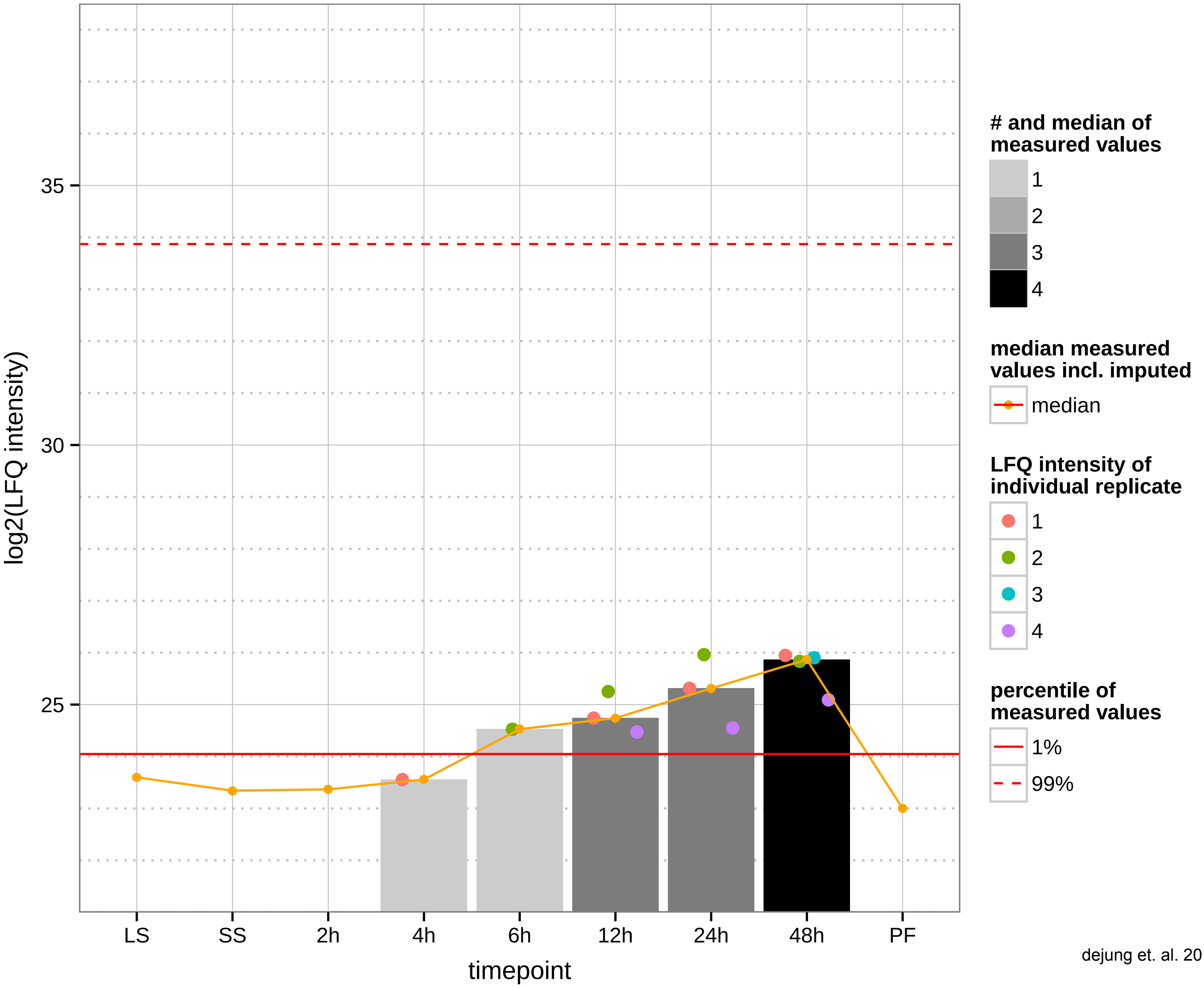




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.1300
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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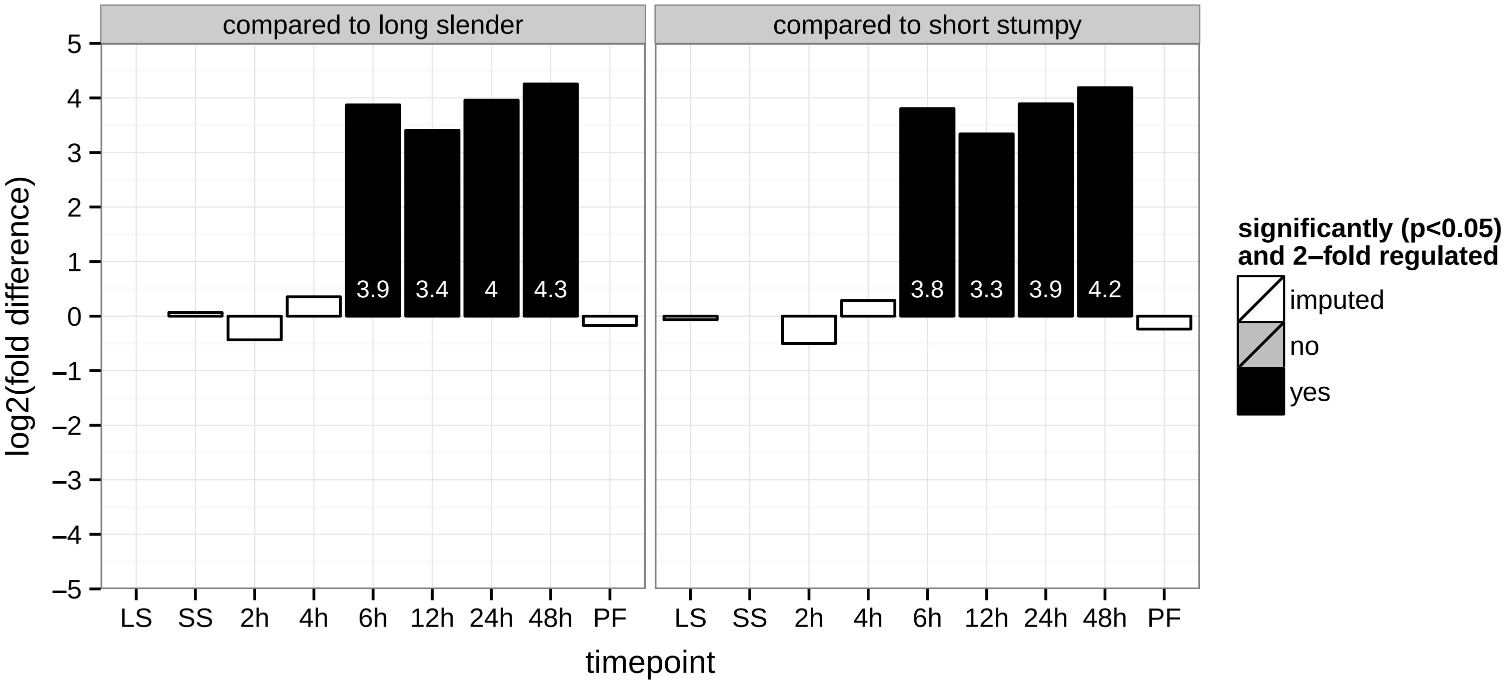
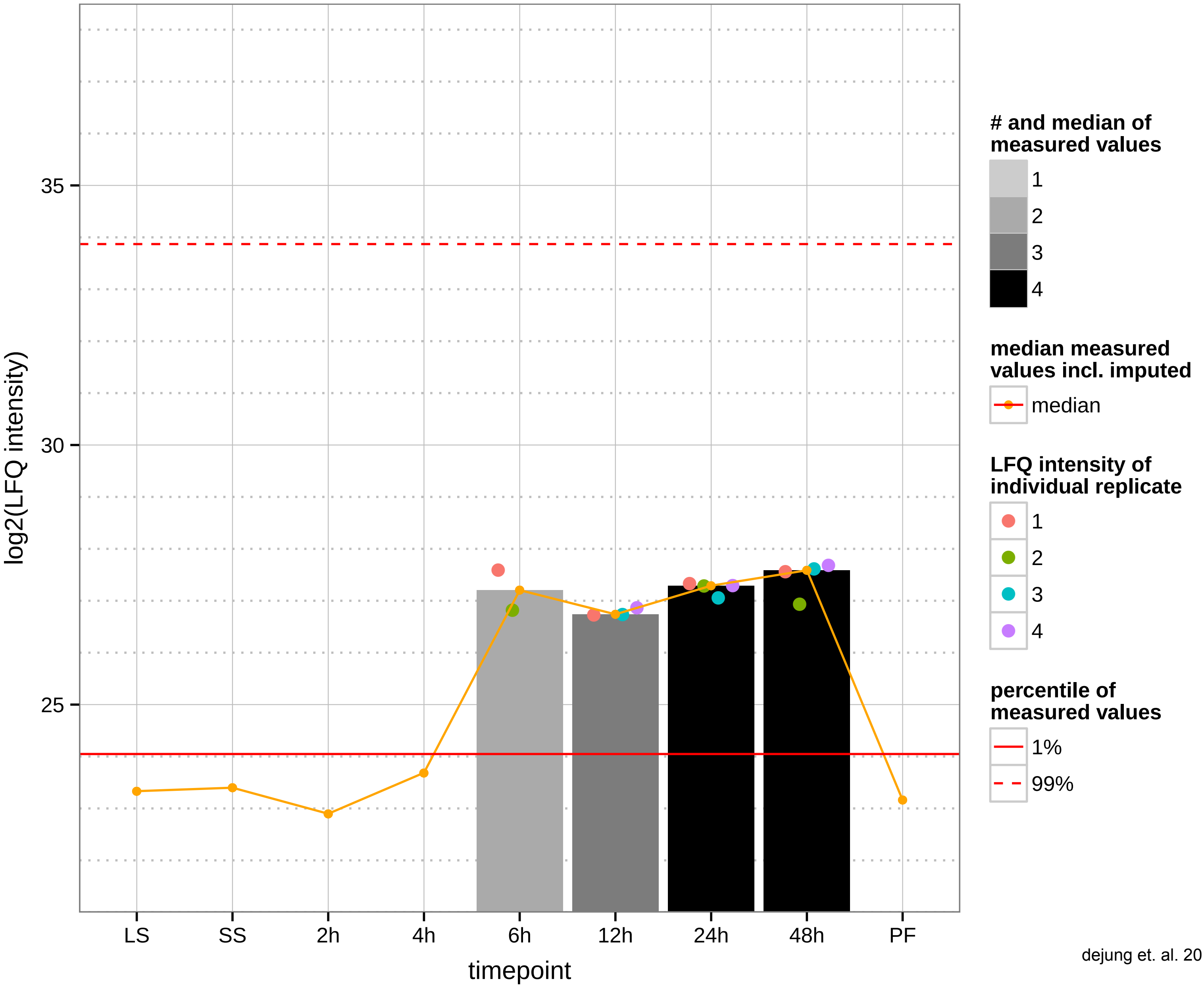
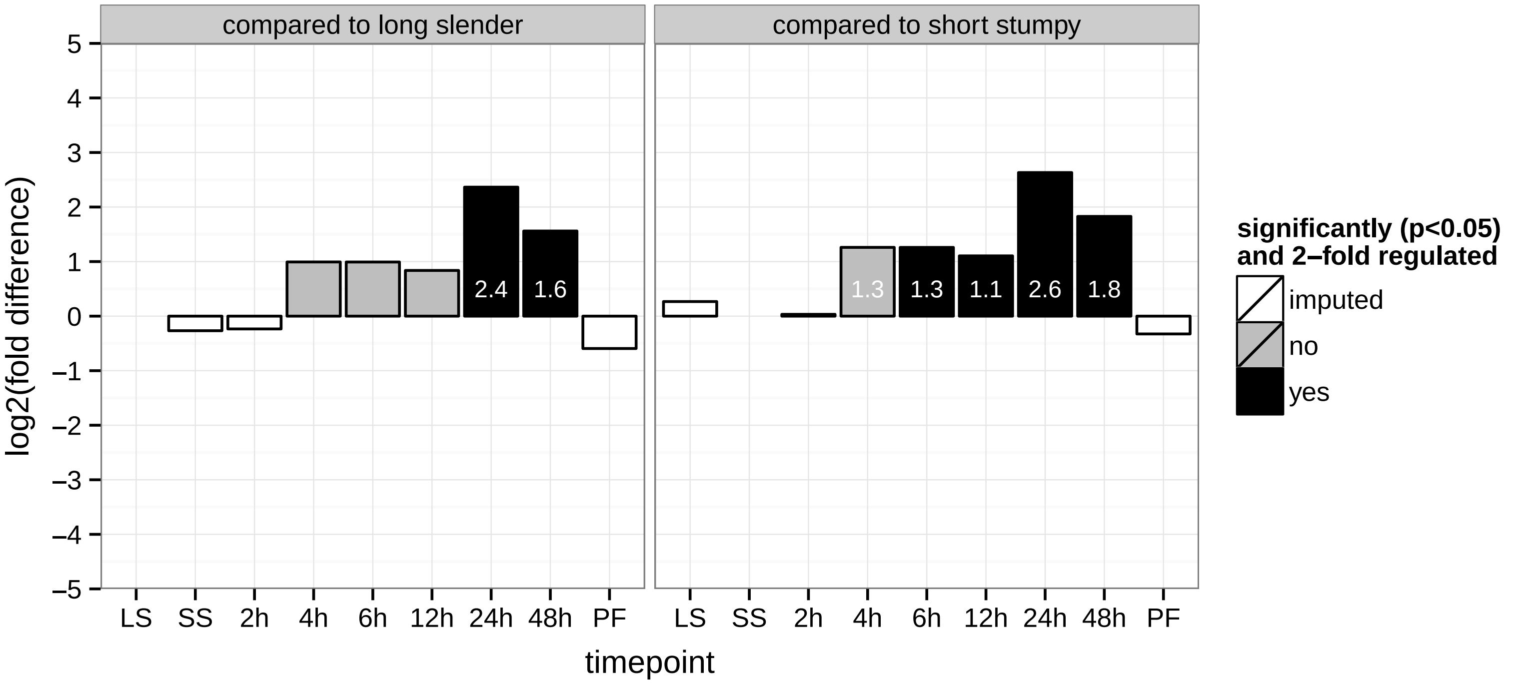
hypothetical protein, conserved
Tb927.11.13840
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

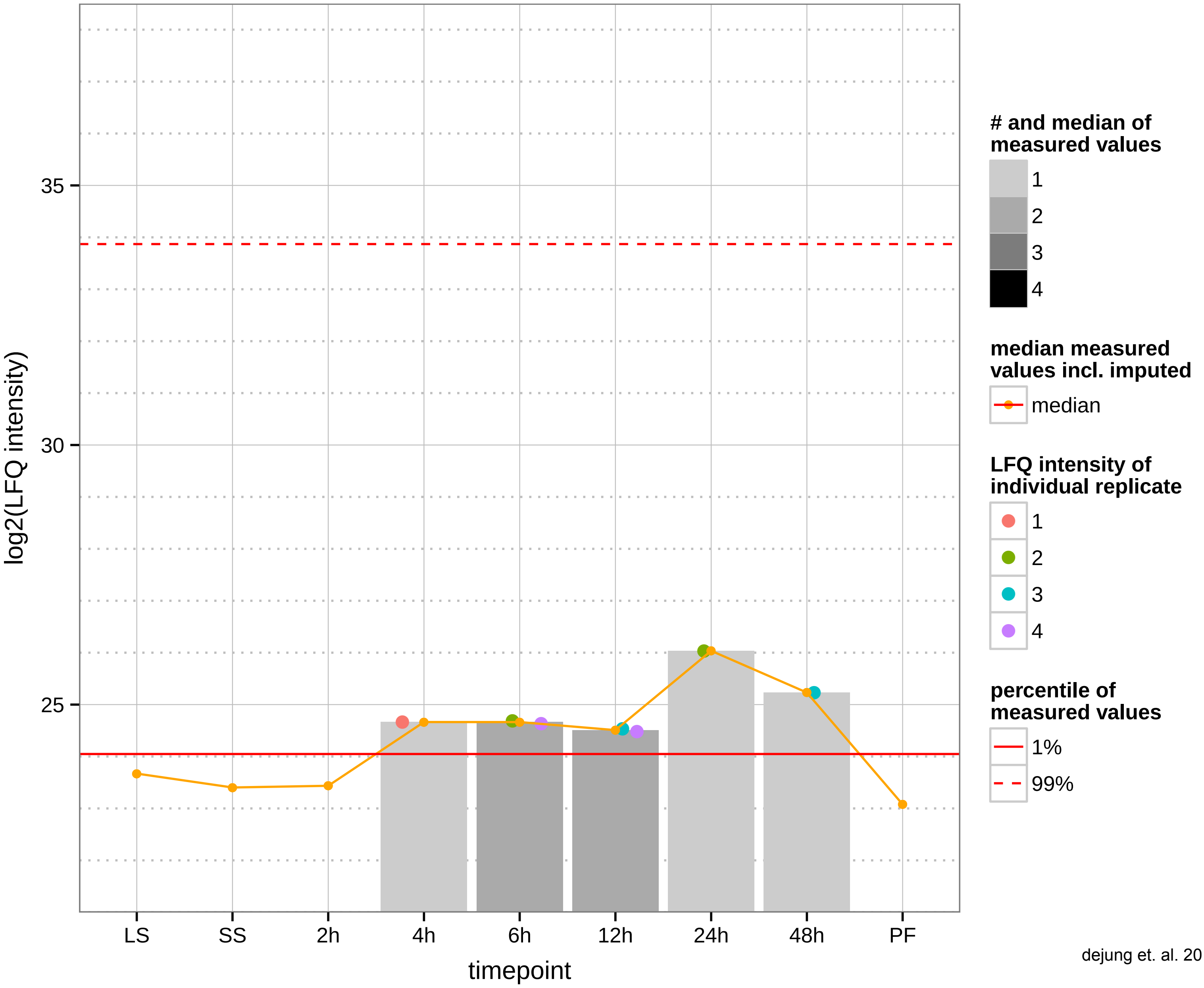




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.15440
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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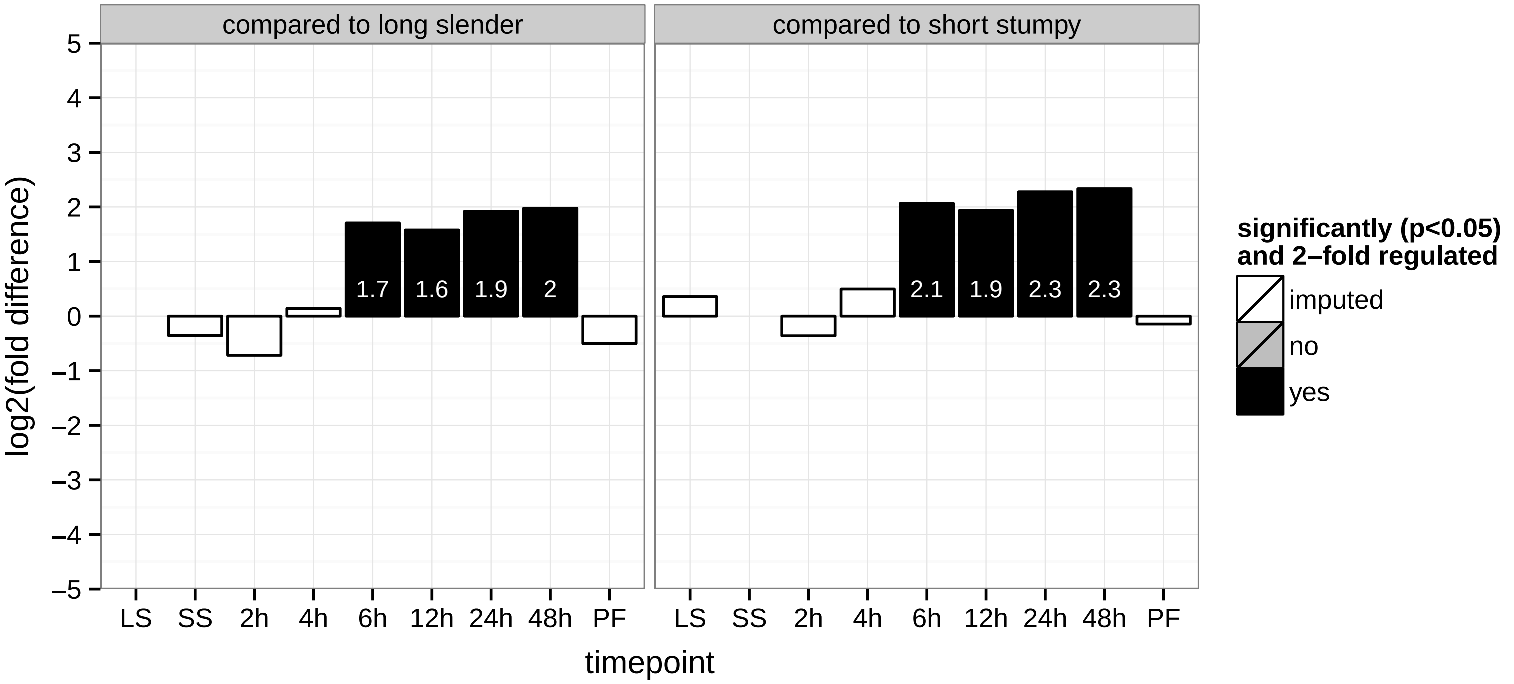
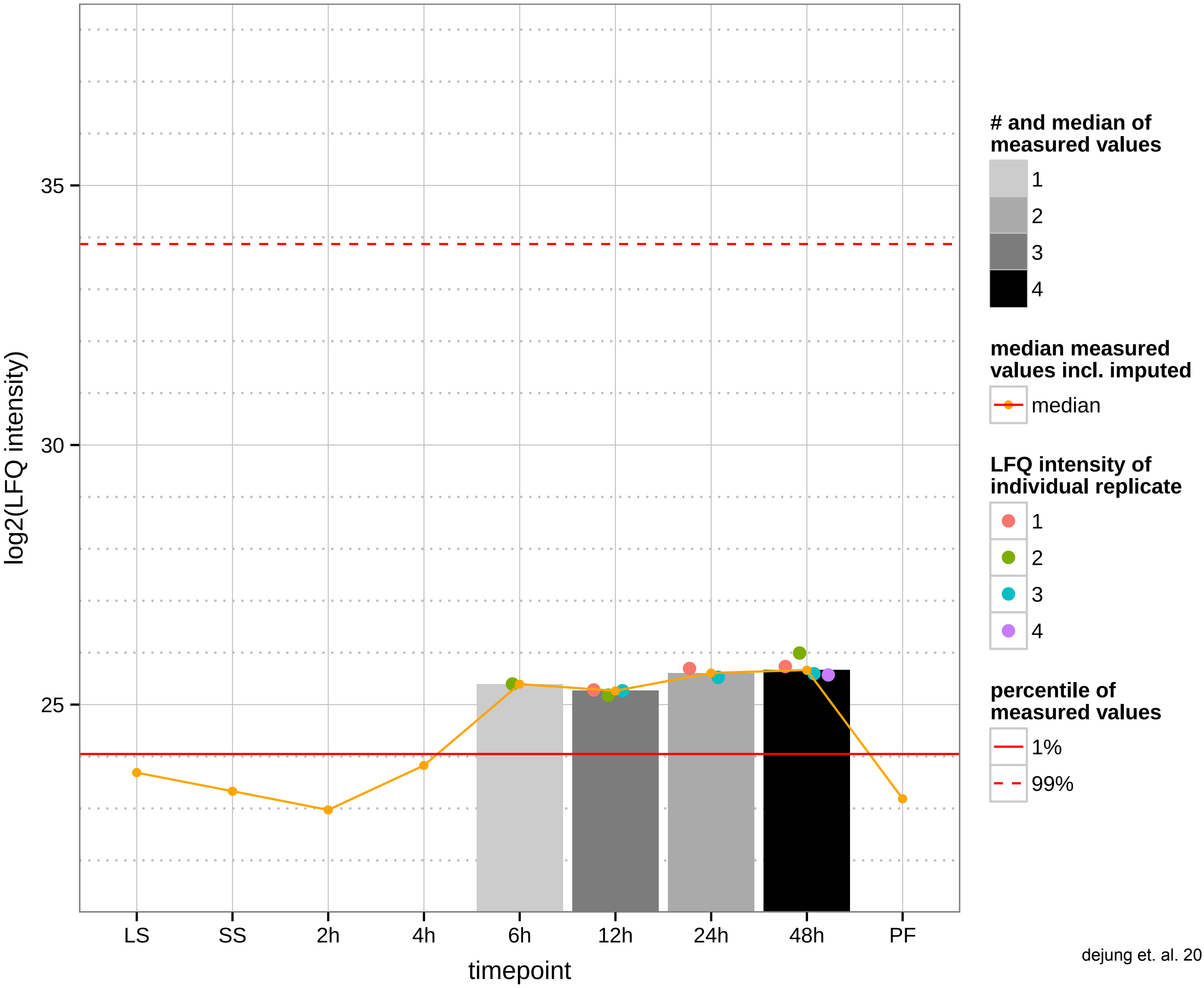
hypothetical protein, conserved
Tb927.11.15580
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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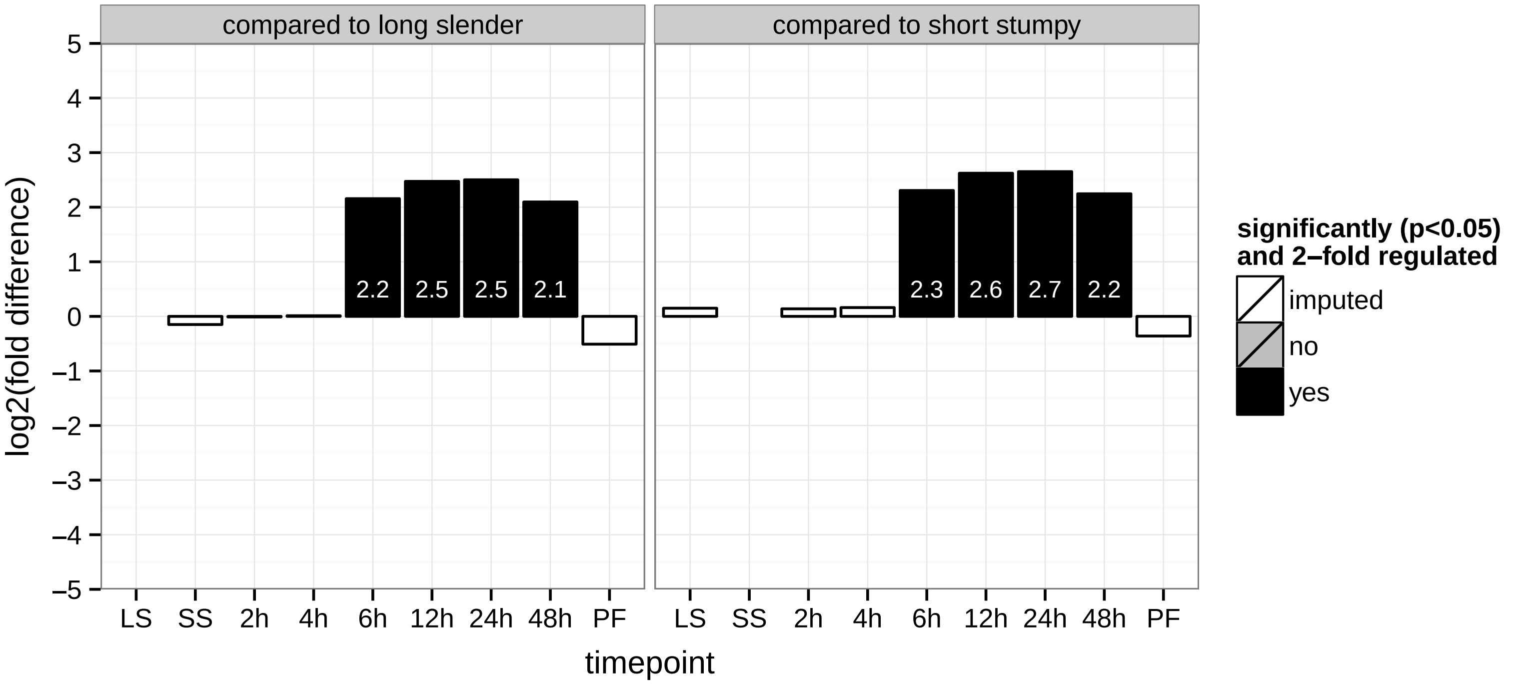
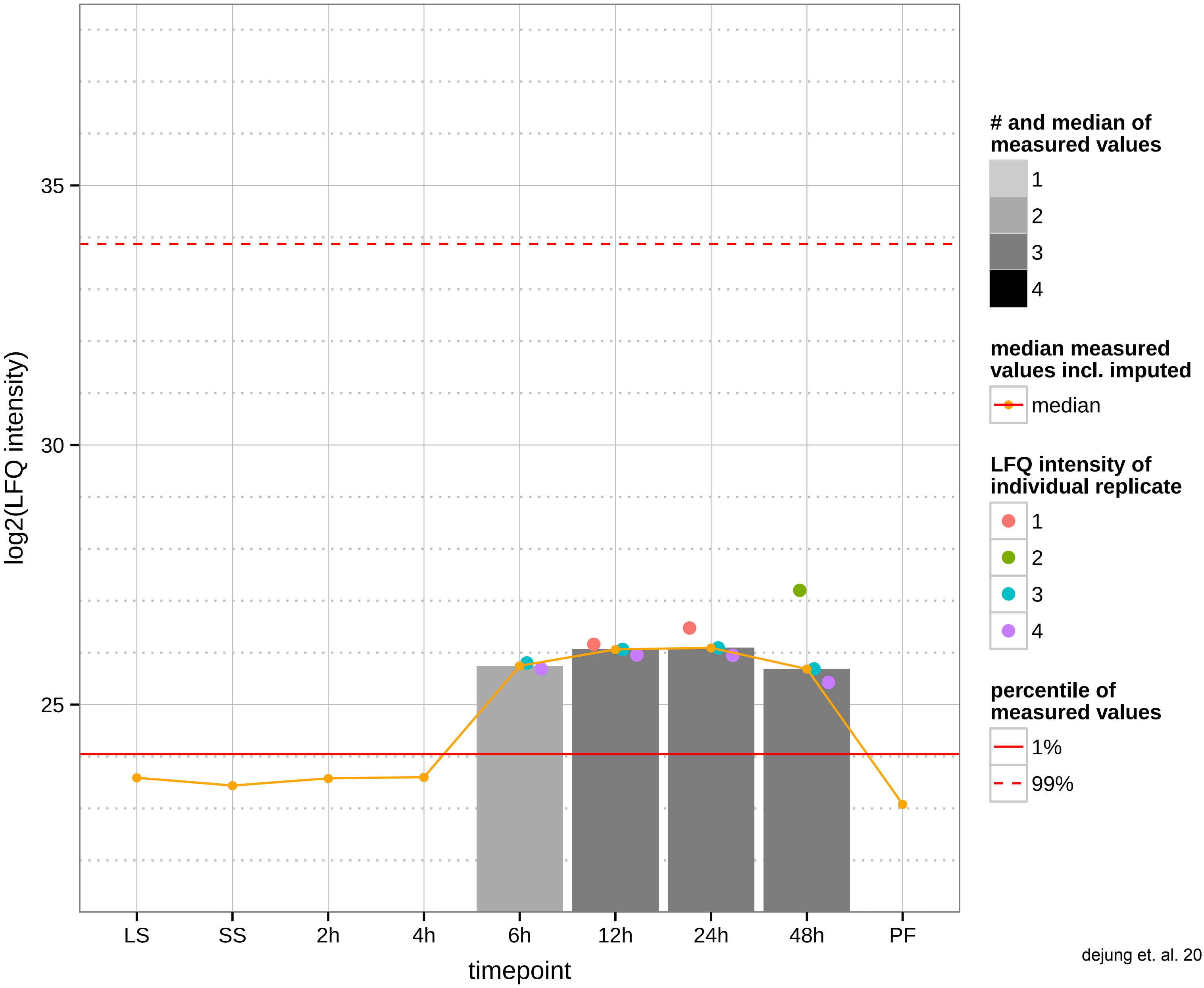
hypothetical protein, conserved
Tb927.11.17020
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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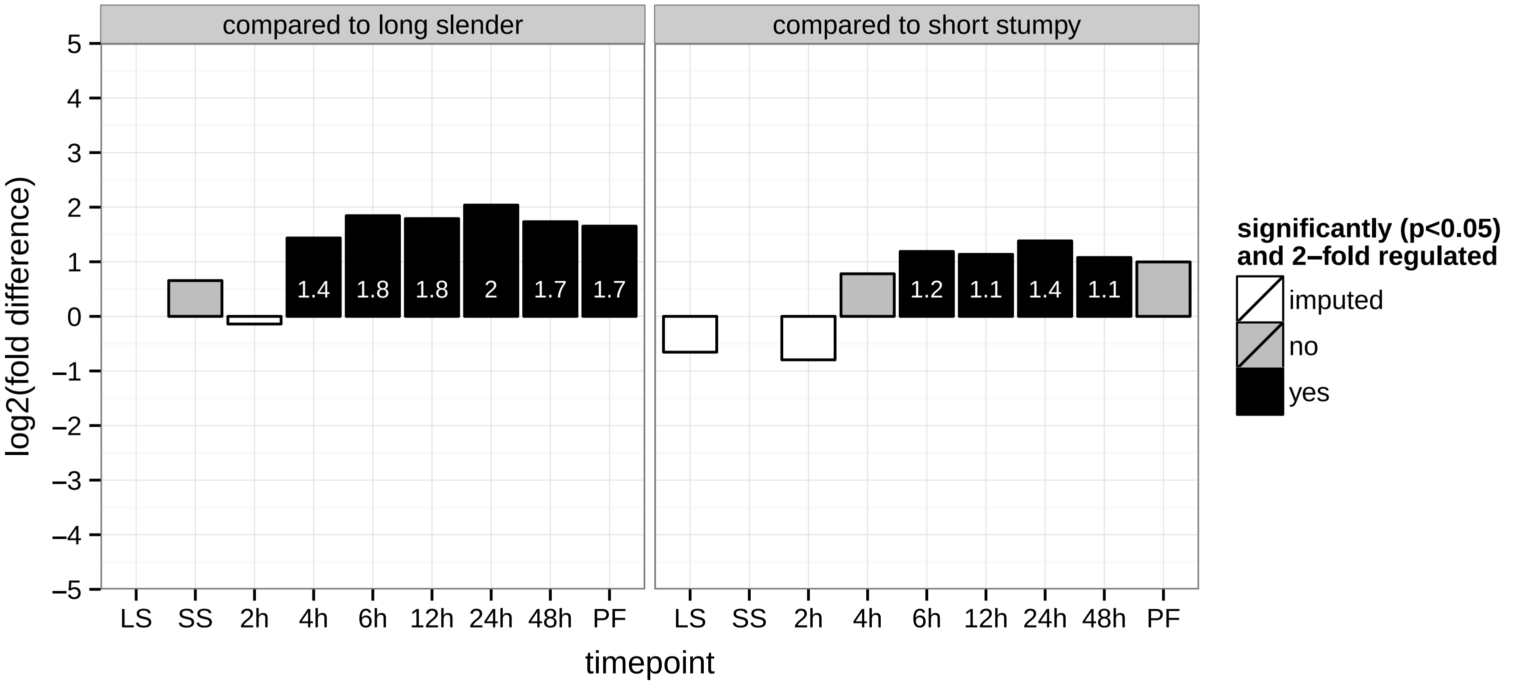
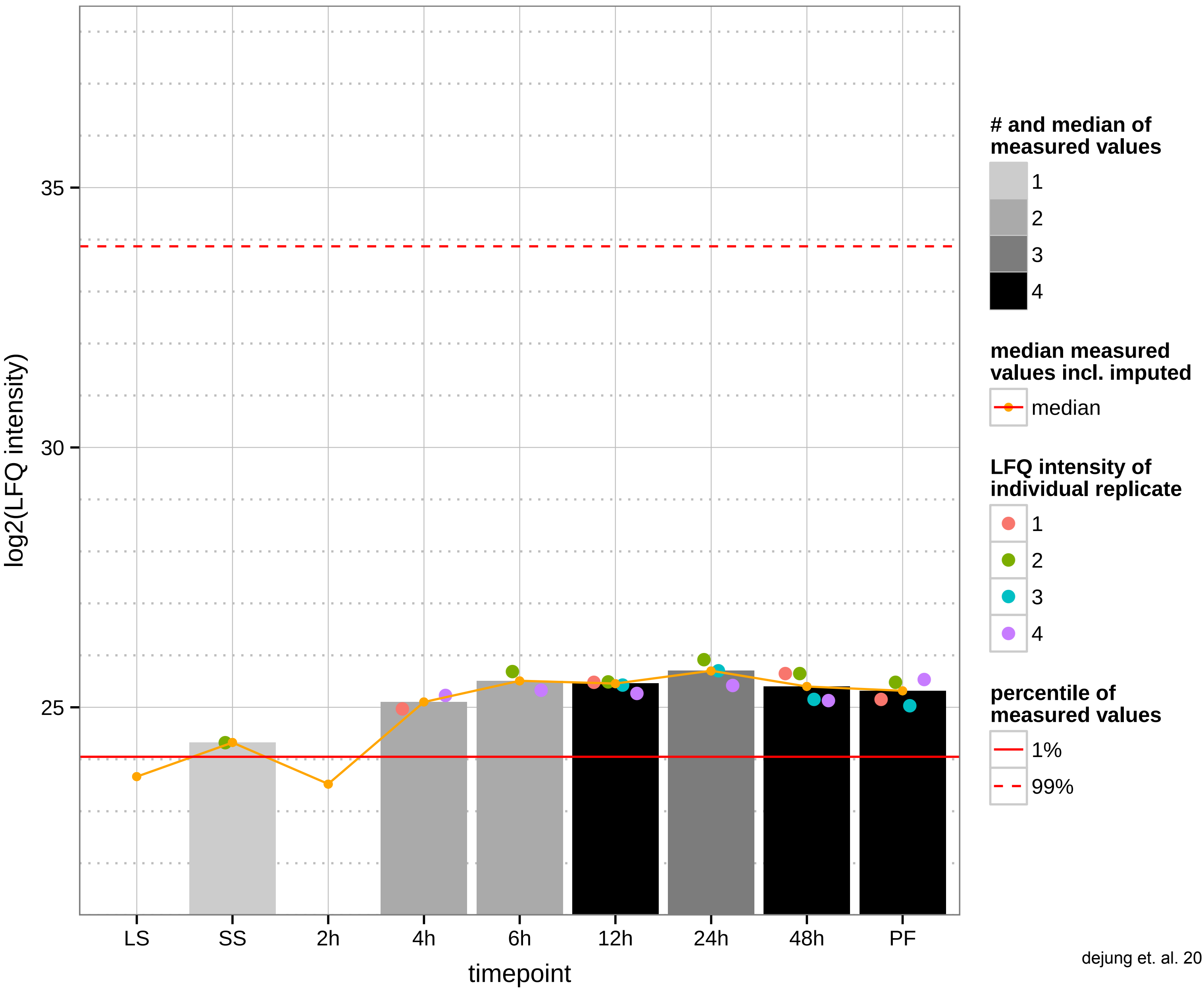
hypothetical protein, conserved
Tb927.11.1770
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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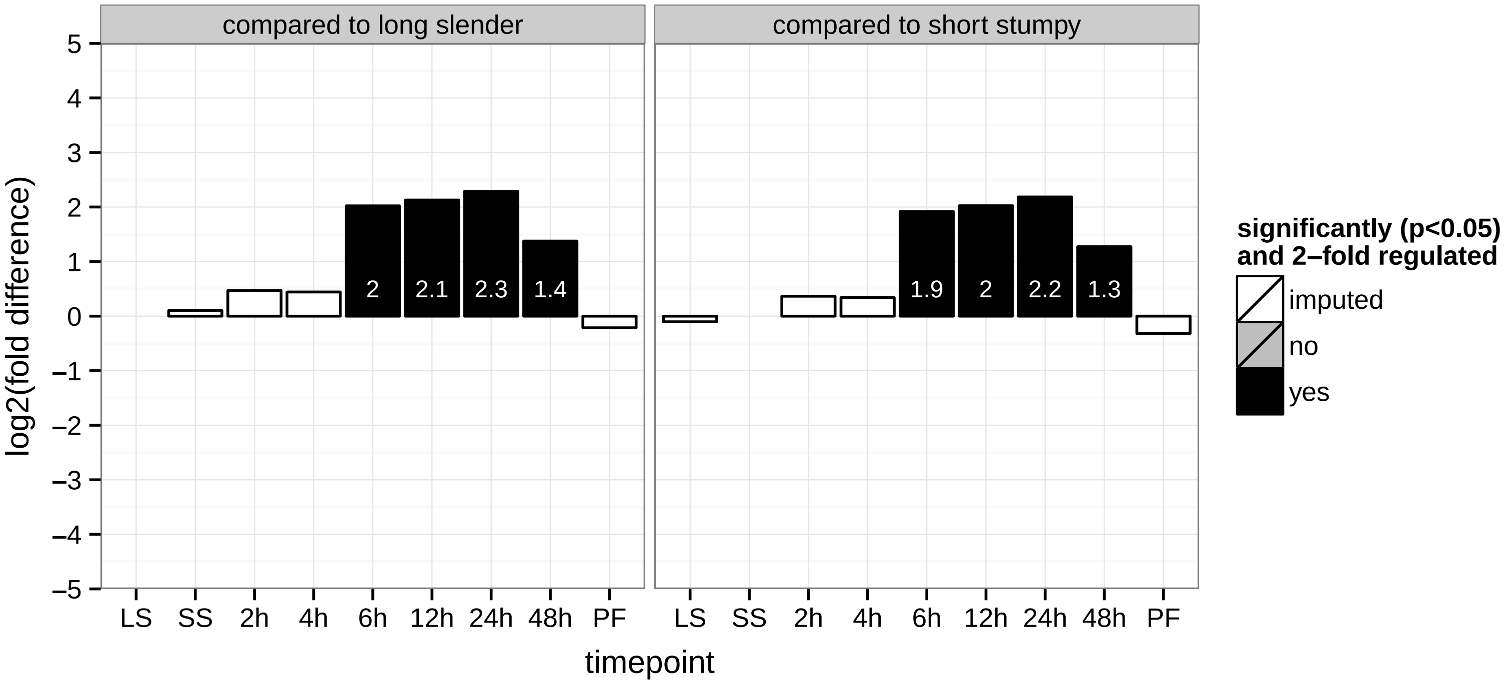
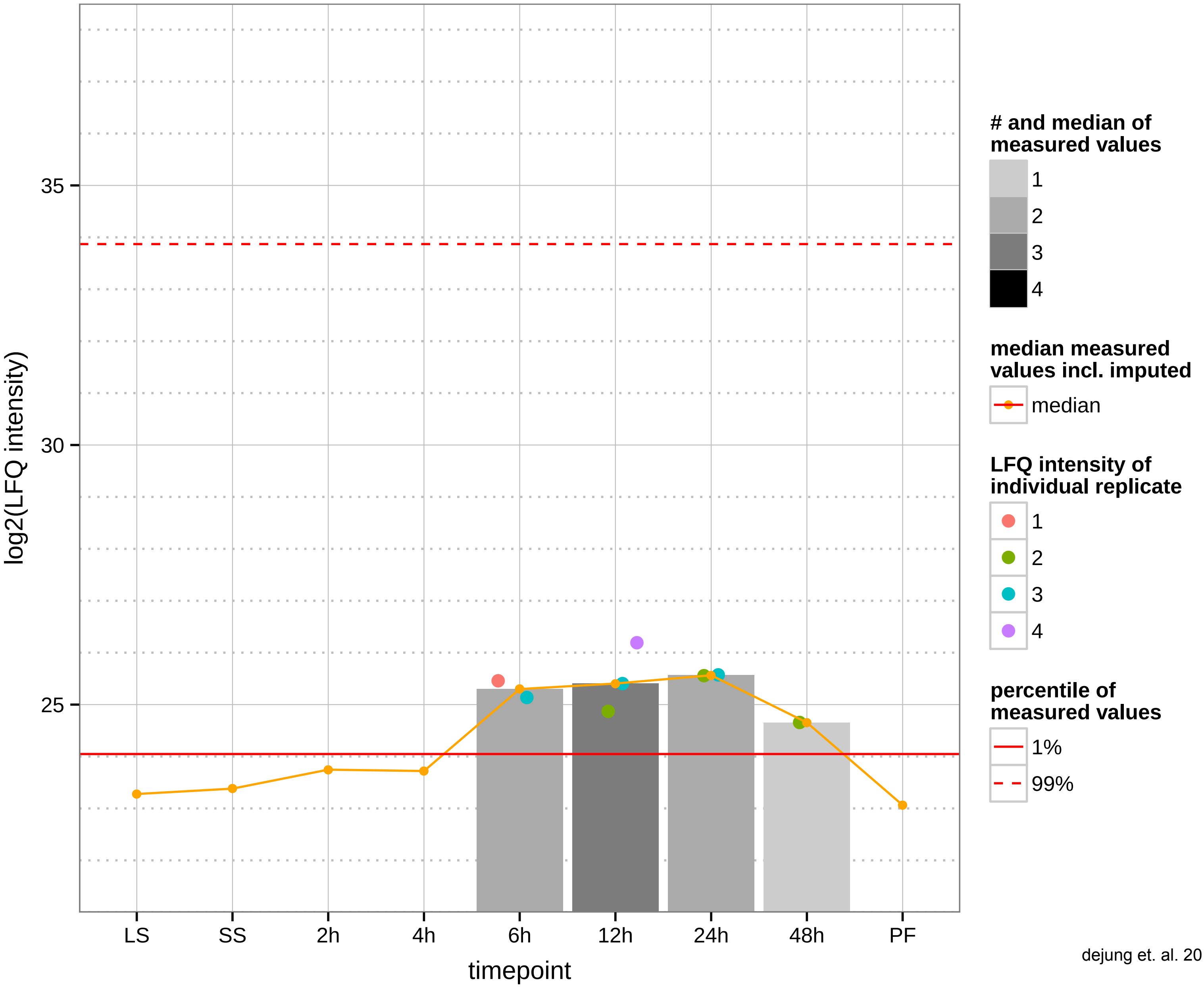
hypothetical protein, conserved
Tb927.11.2070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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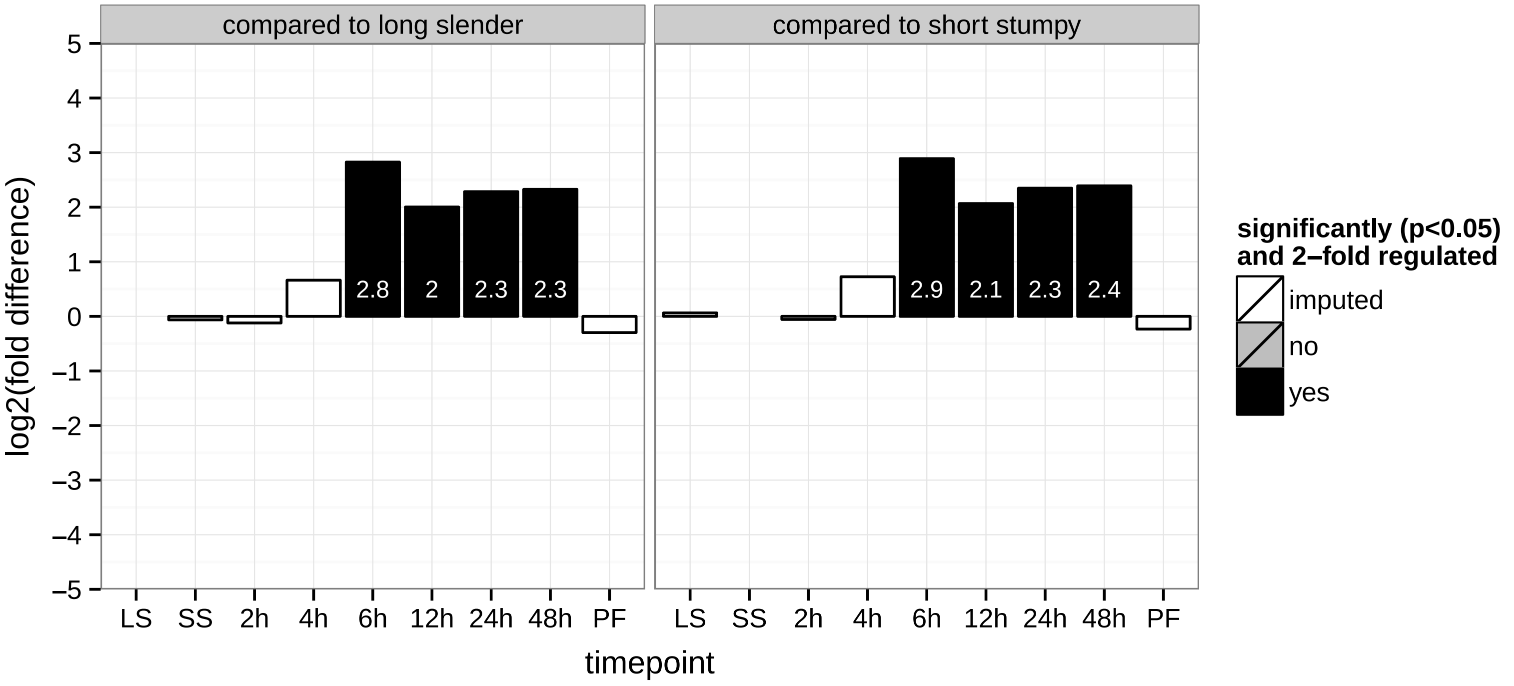
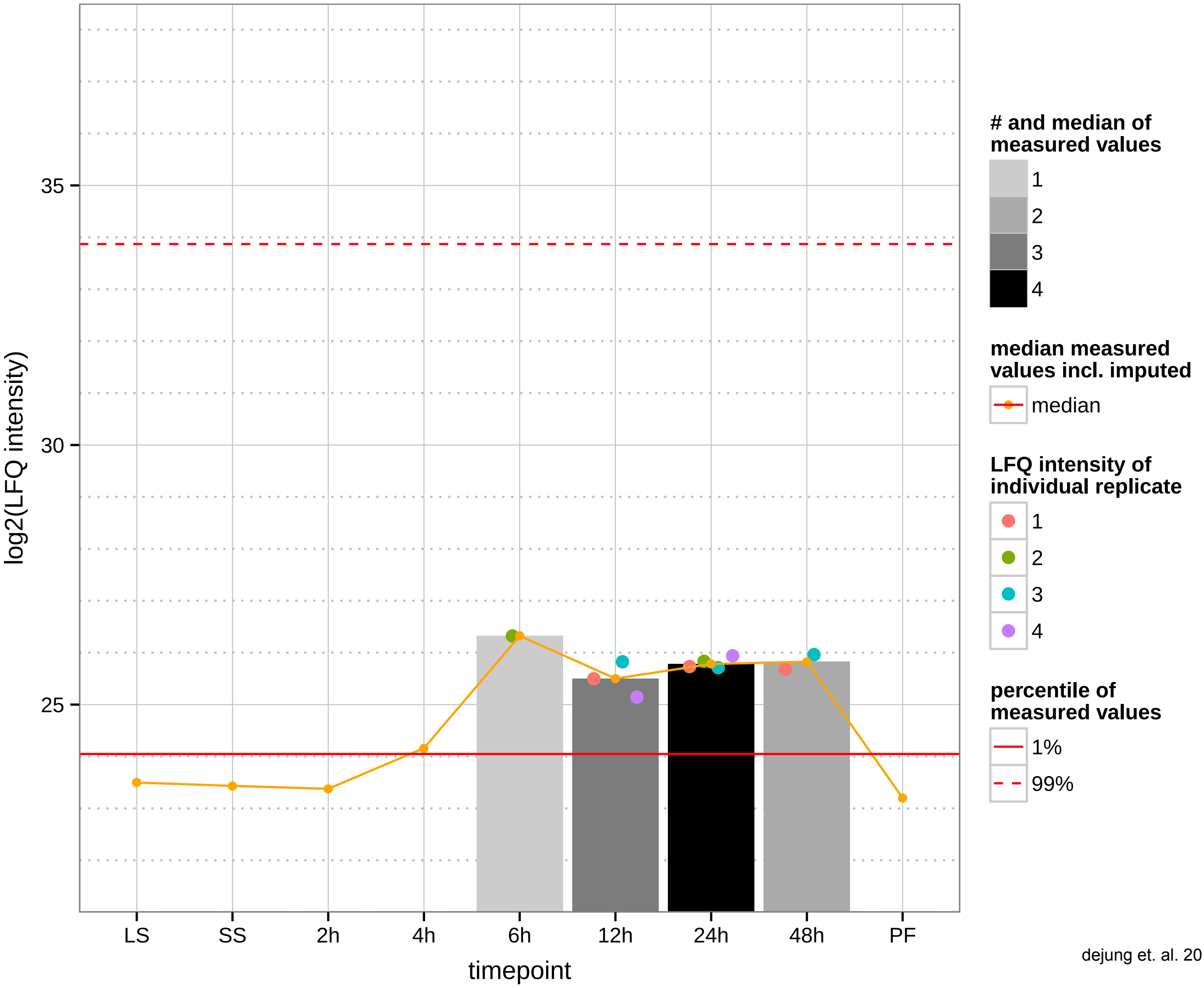
hypothetical protein, conserved
Tb927.11.2150
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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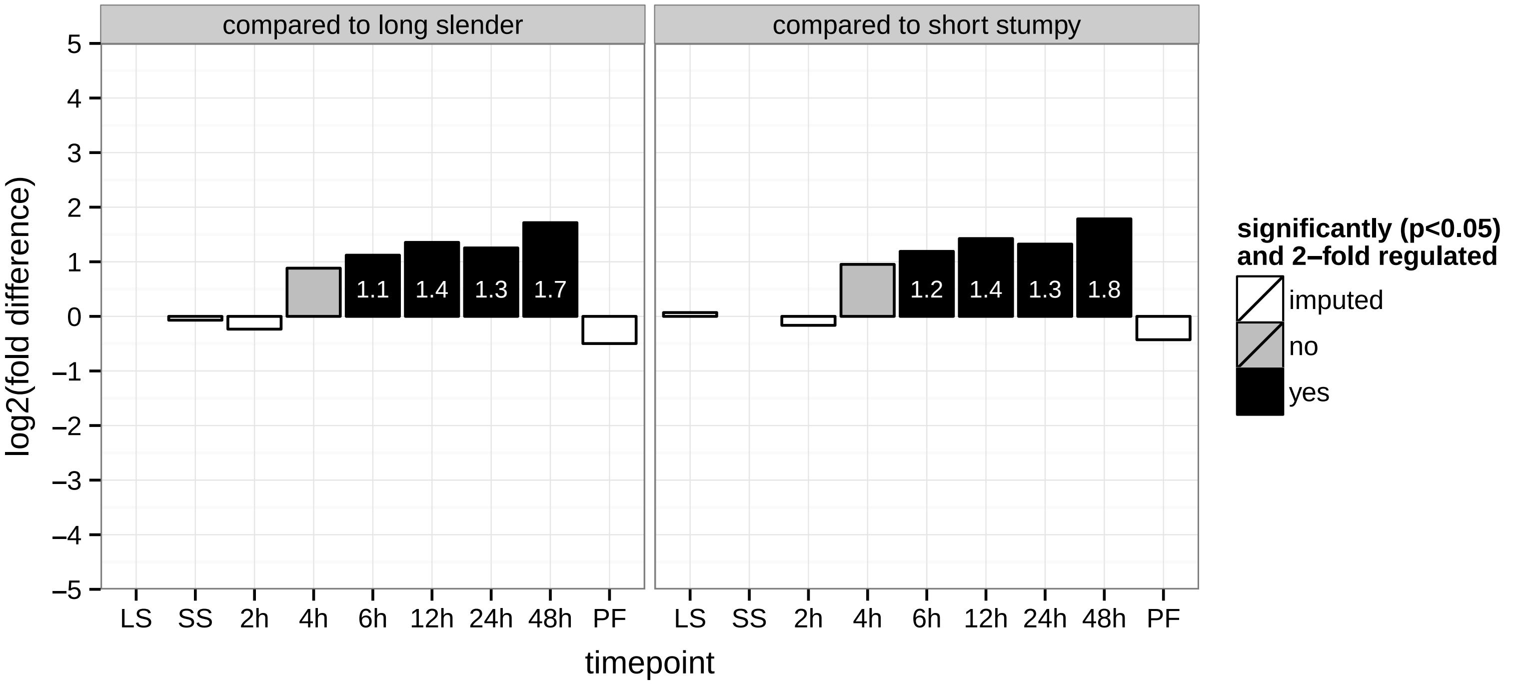
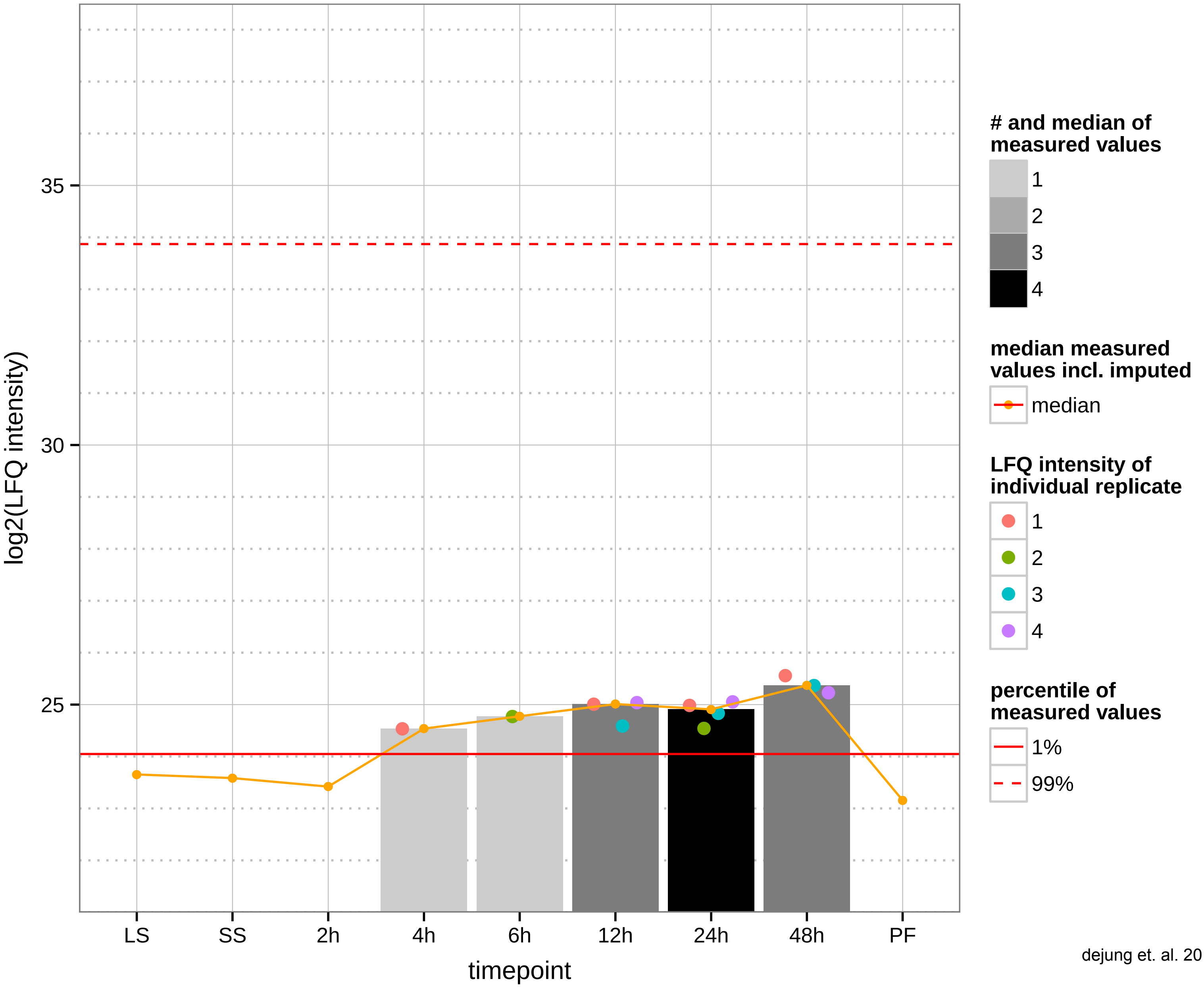
molybdopterin synthase sulphurylase protein, putative
Tb927.11.2330
AGOF: catalytic activity
AGOC: integral to membrane
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null





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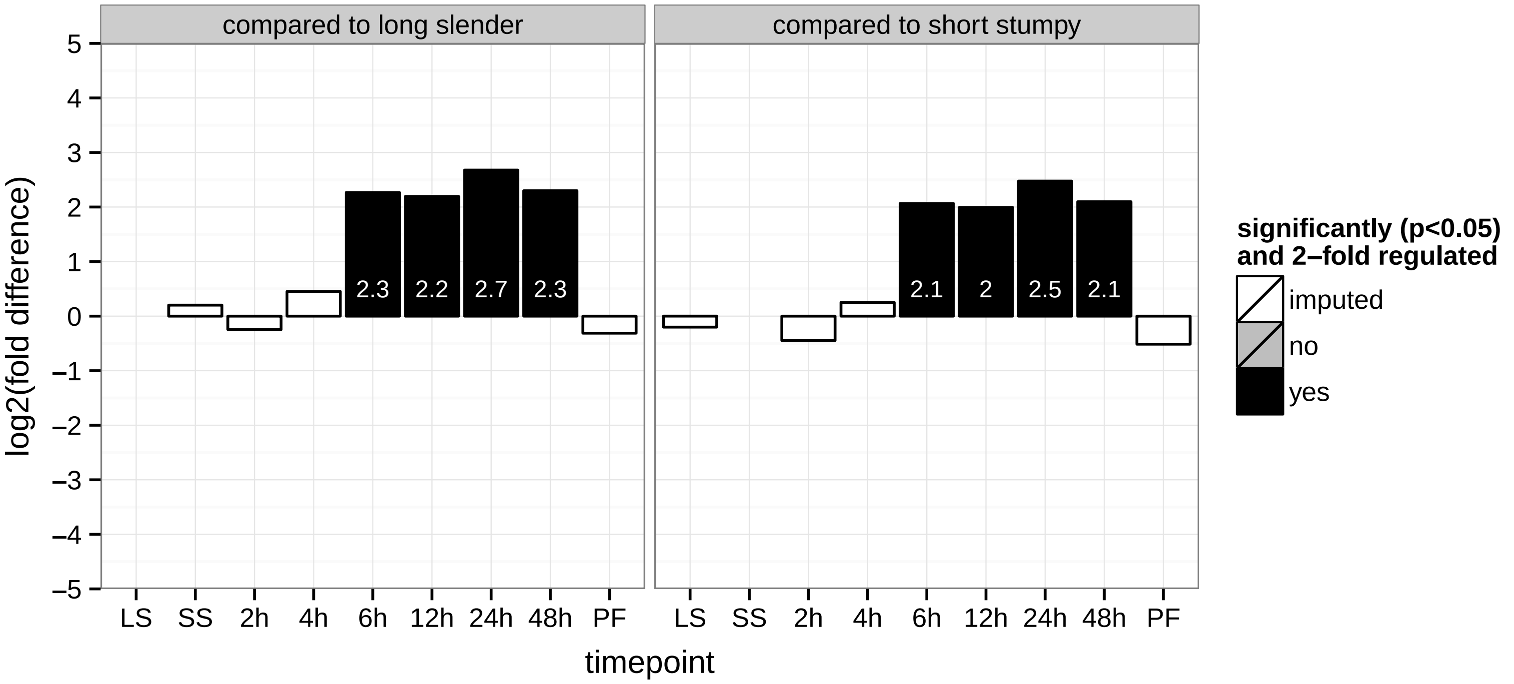
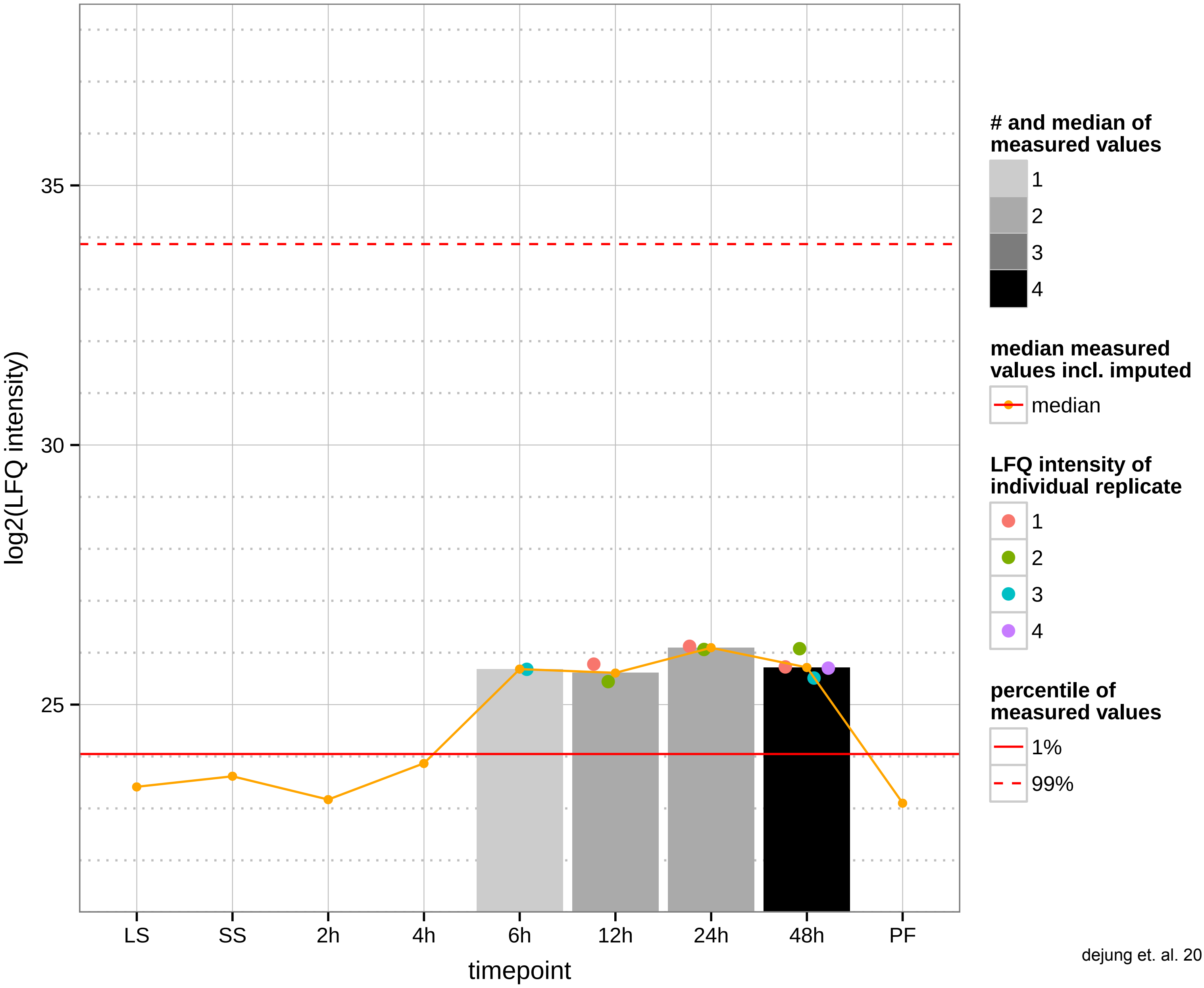
NUDIX hydrolase, conserved
Tb927.11.9810
AGOF: hydrolase activity
AGOC: null
AGOP: metabolic process
PGOF: hydrolase activity
PGOC: null
PGOP: null





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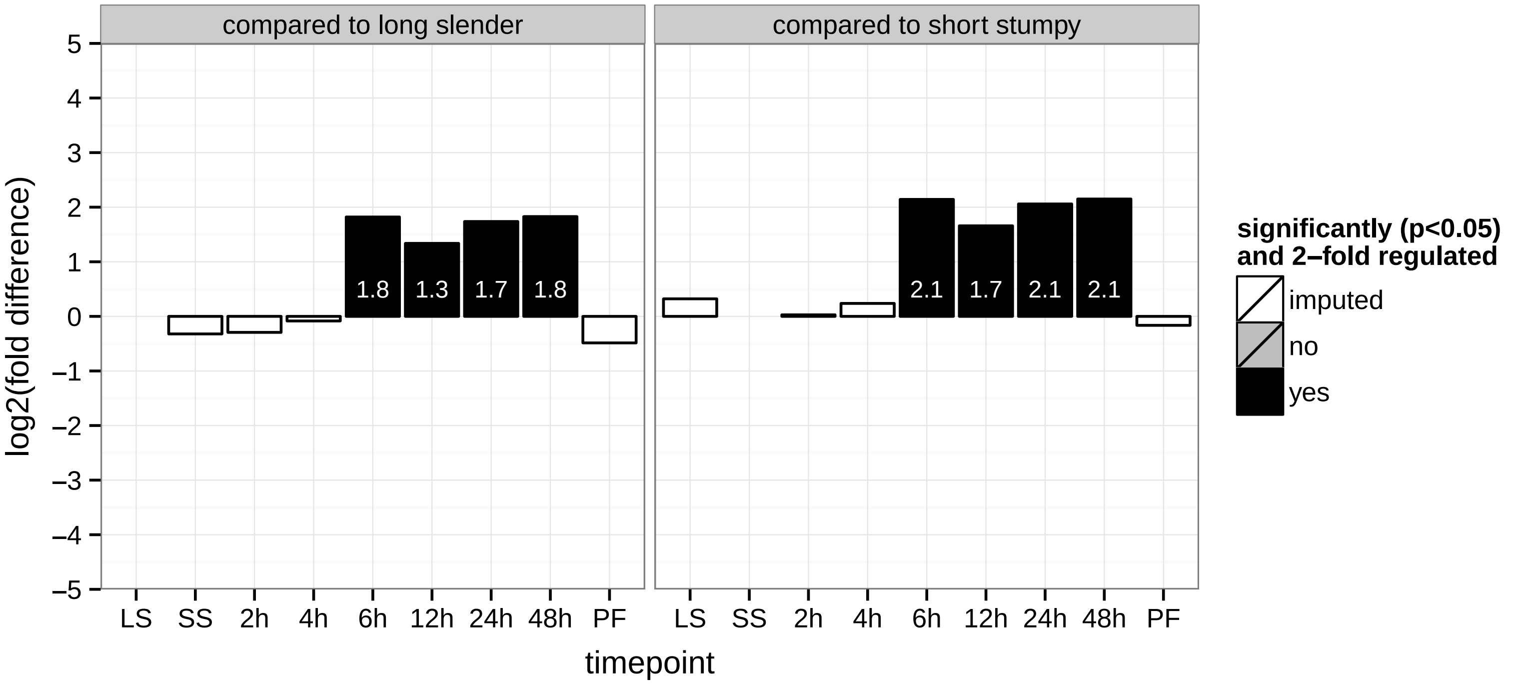
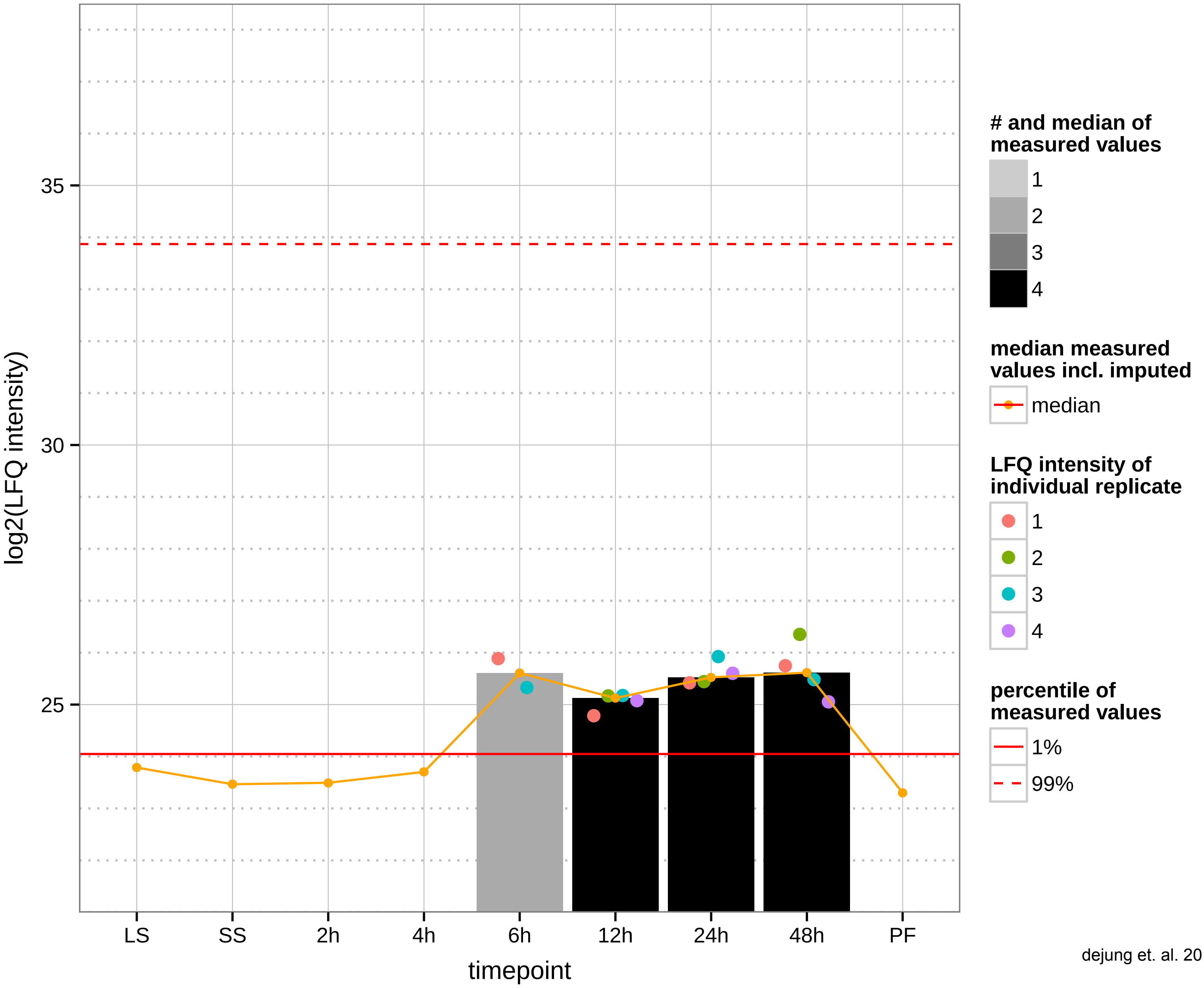
minichromosome maintenance (MCM) complex subunit, putative, DNA replication licensing factor MCM3
Tb927.2.3930;Tb11.v5.0640
AGOF: null, ATP binding, DNA binding
AGOC: null, nucleus
AGOP: null, DNA replication, DNA–dependent DNA replication initiation
PGOF: ATP binding, DNA binding
PGOC: null
PGOP: DNA replication





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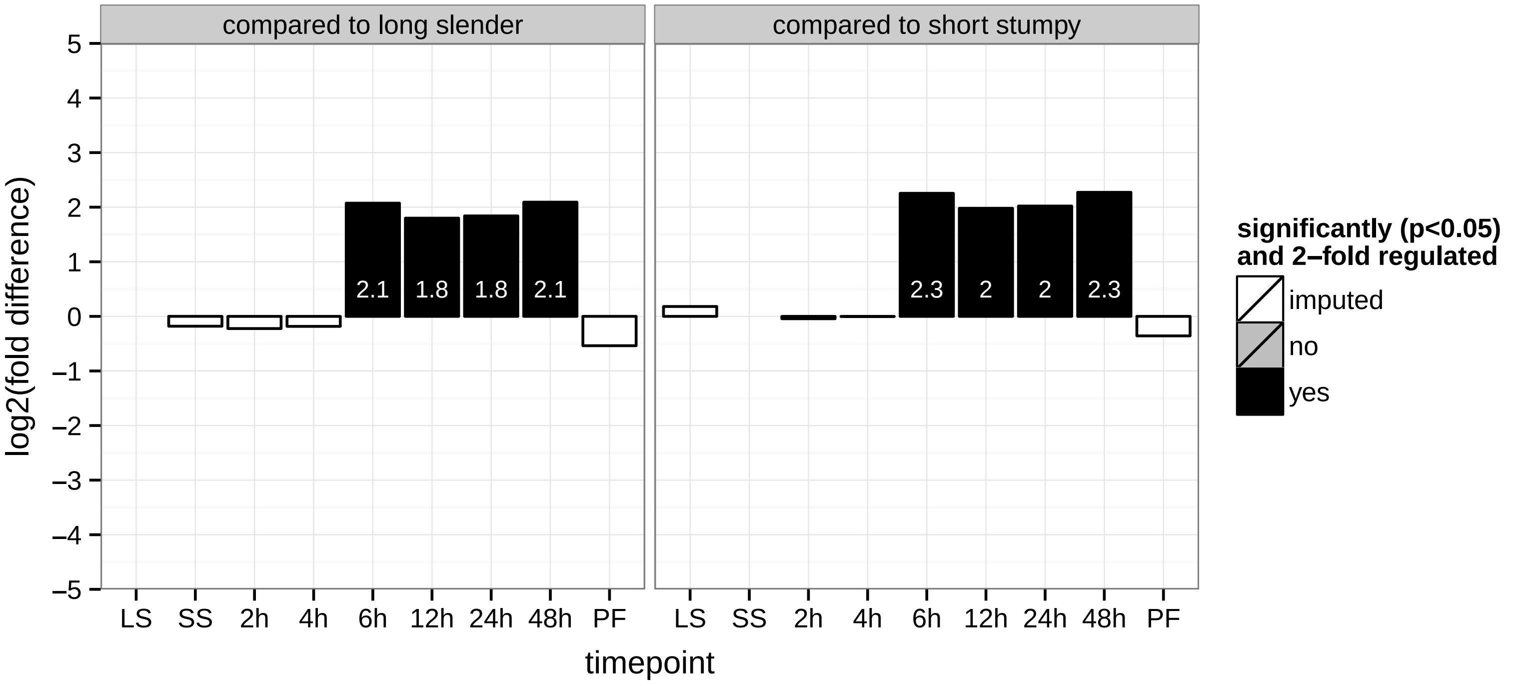
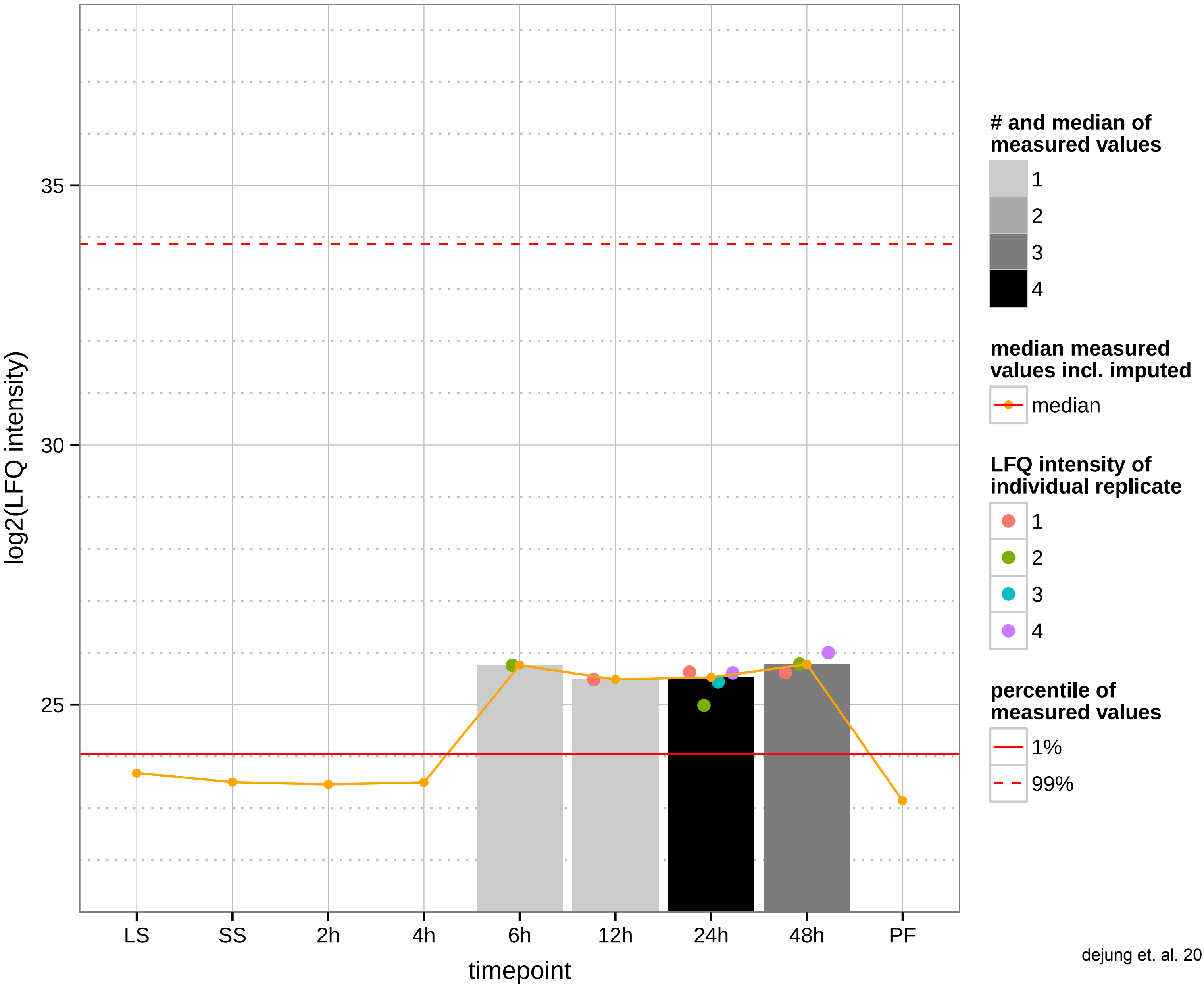
hypothetical protein, conserved
Tb927.2.5870
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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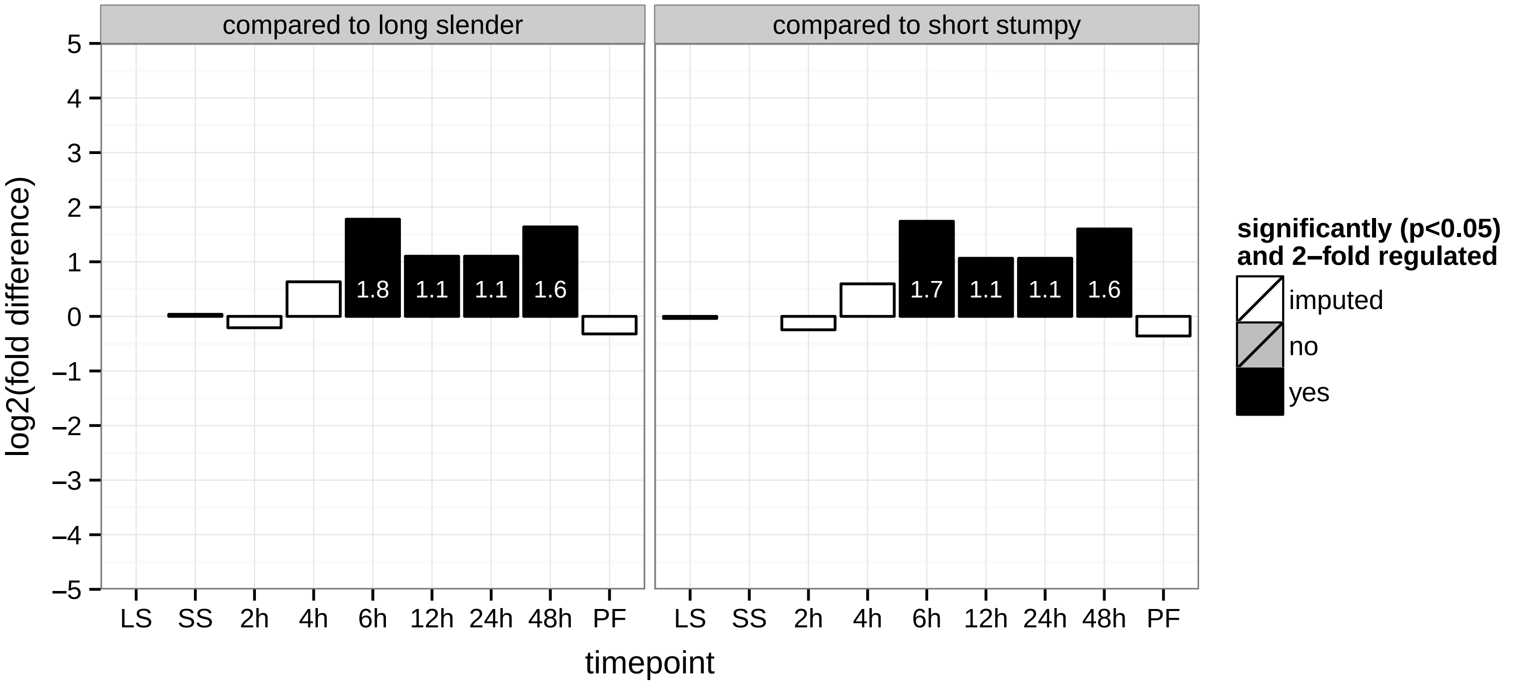
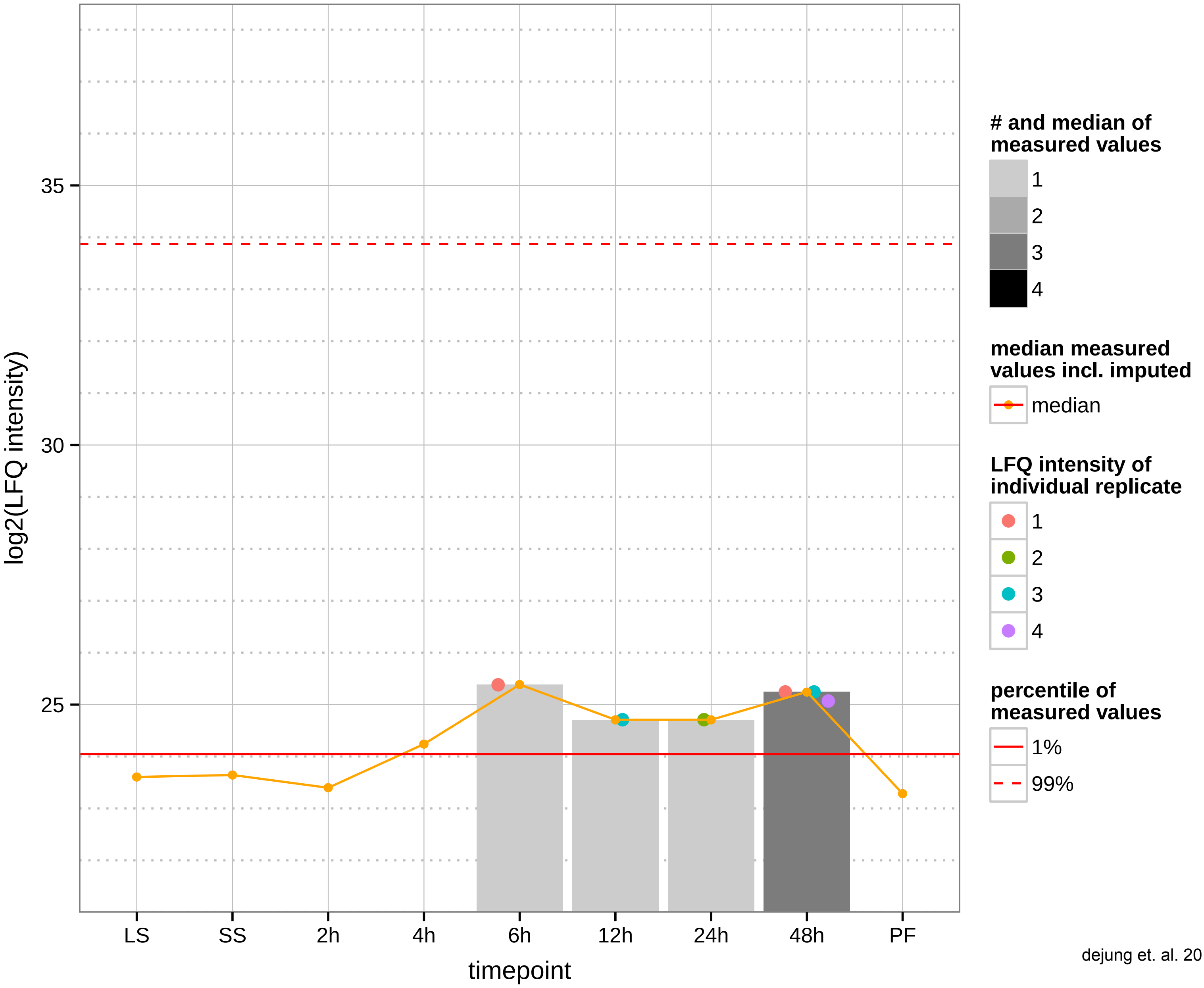
peroxisome biogenesis factor 1, putative
Tb927.4.1250
AGOF: ATP binding, nucleoside–triphosphatase activity
AGOC: peroxisome
AGOP: peroxisome organization, protein import into peroxisome membrane
PGOF: ATP binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: peroxisome
PGOP: peroxisome organization





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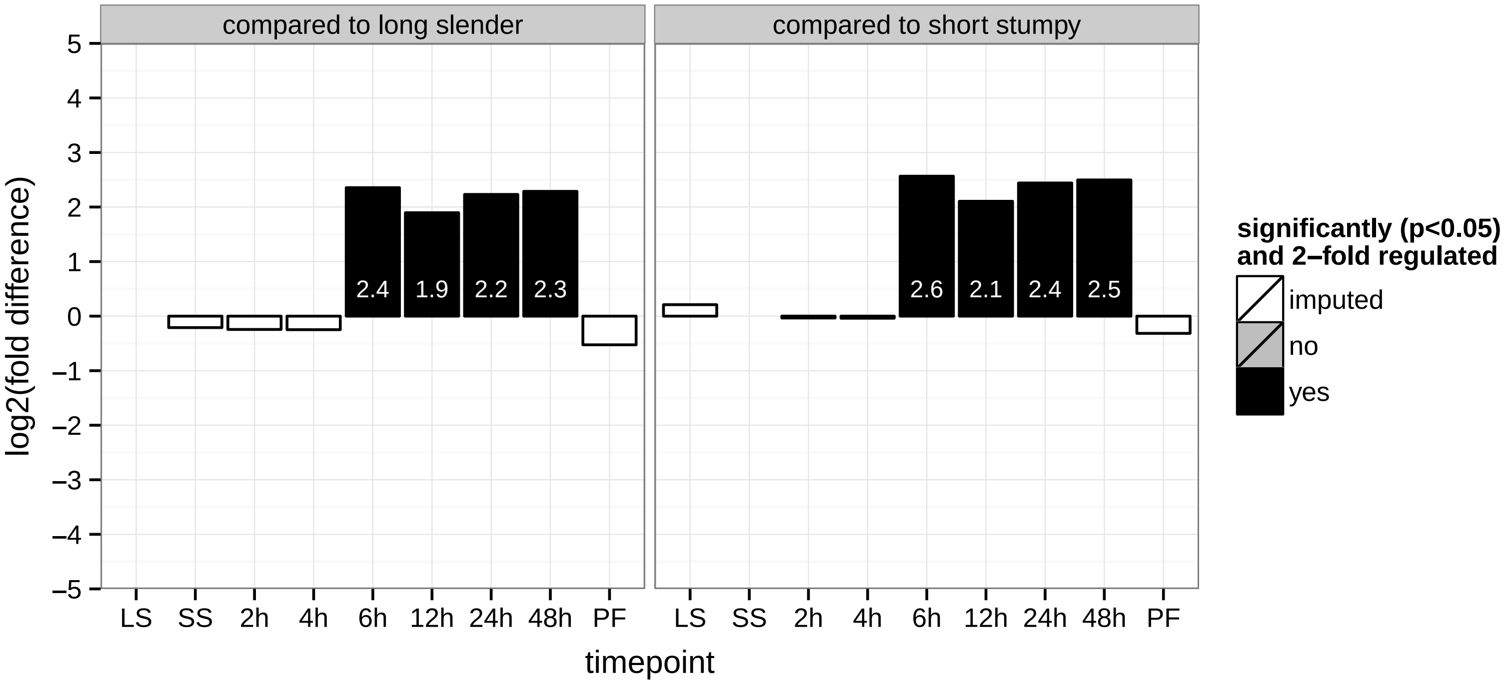
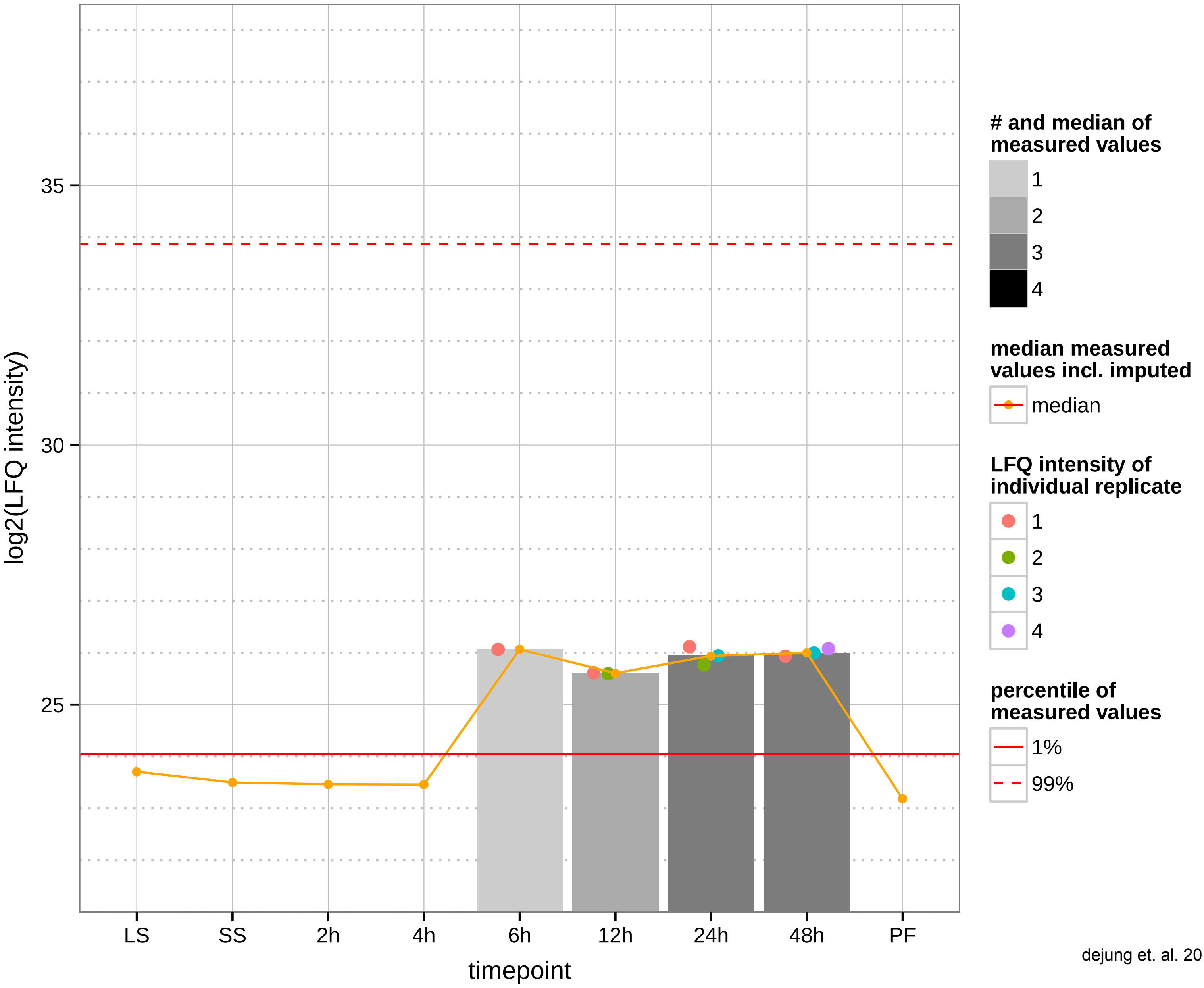
leucine–rich repeat protein (LRRP, pseudogene), putative, leucine–rich repeat protein 1 (LRRP1), frameshift
Tb927.4.160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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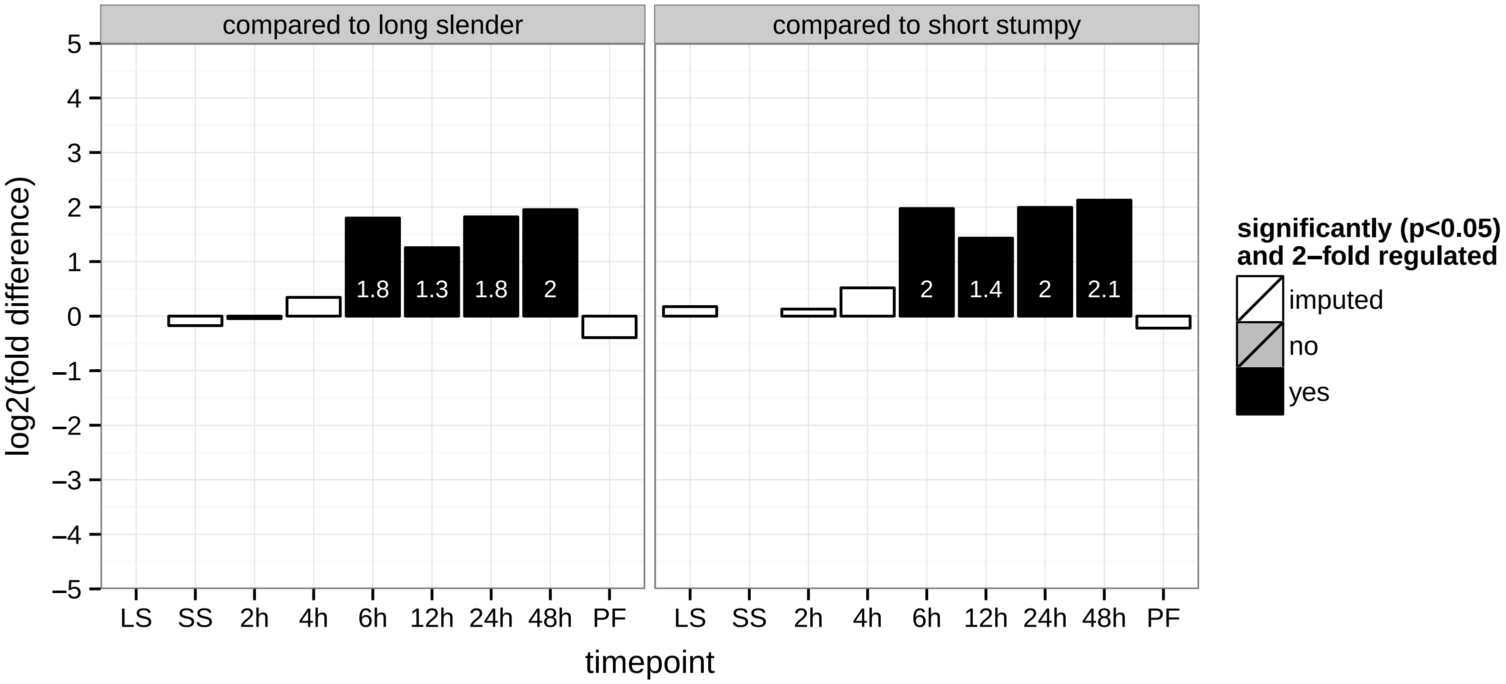
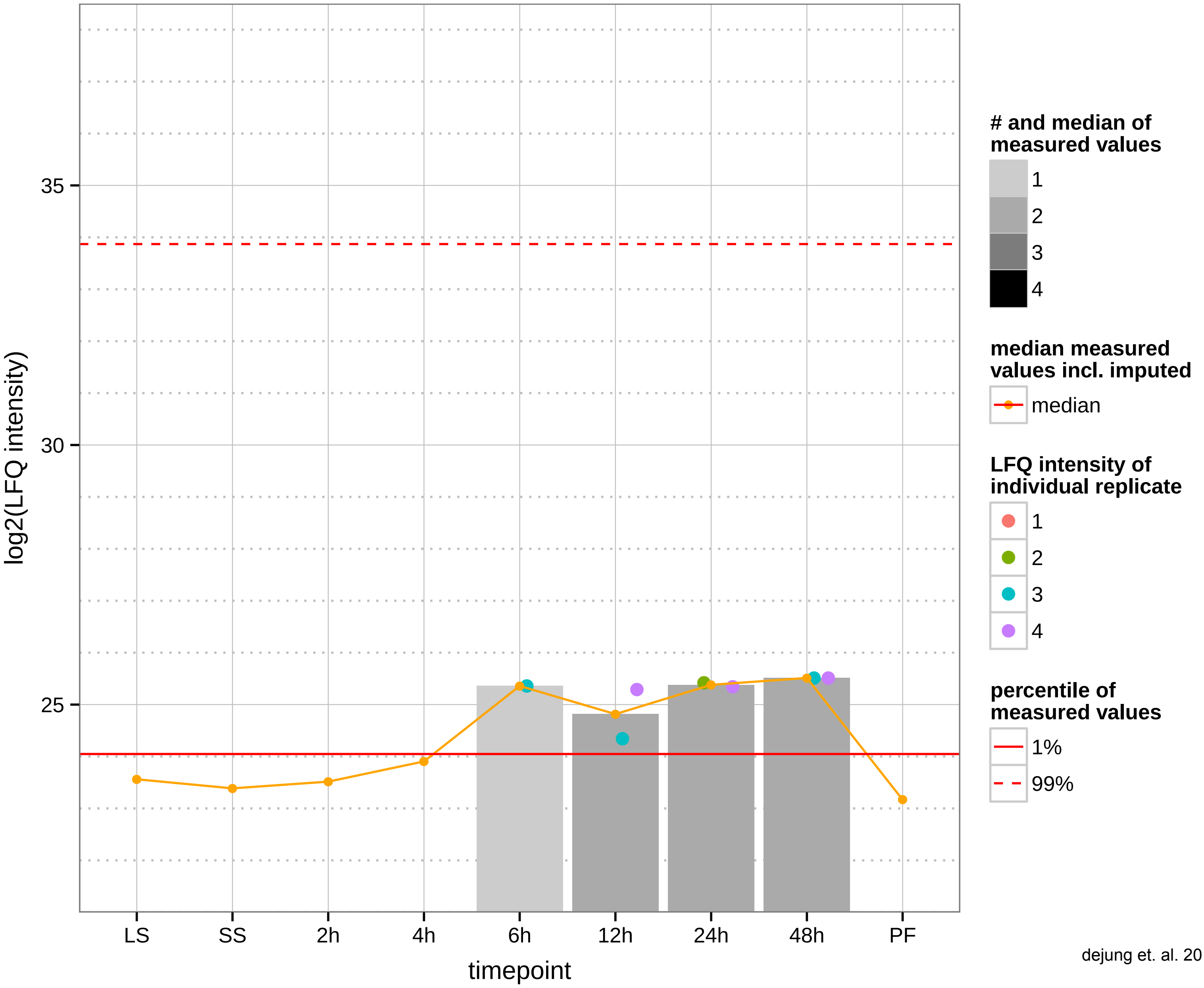
hypothetical protein, conserved
Tb927.4.5190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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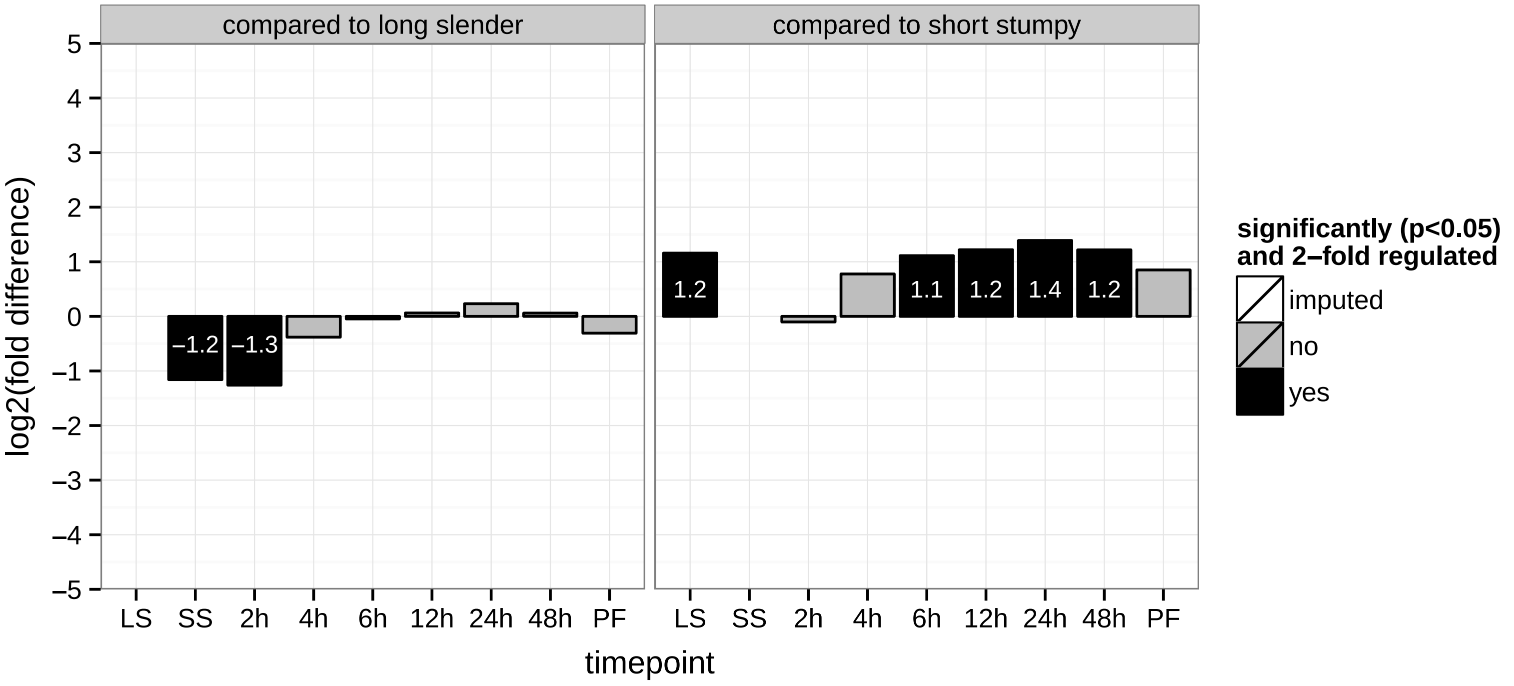
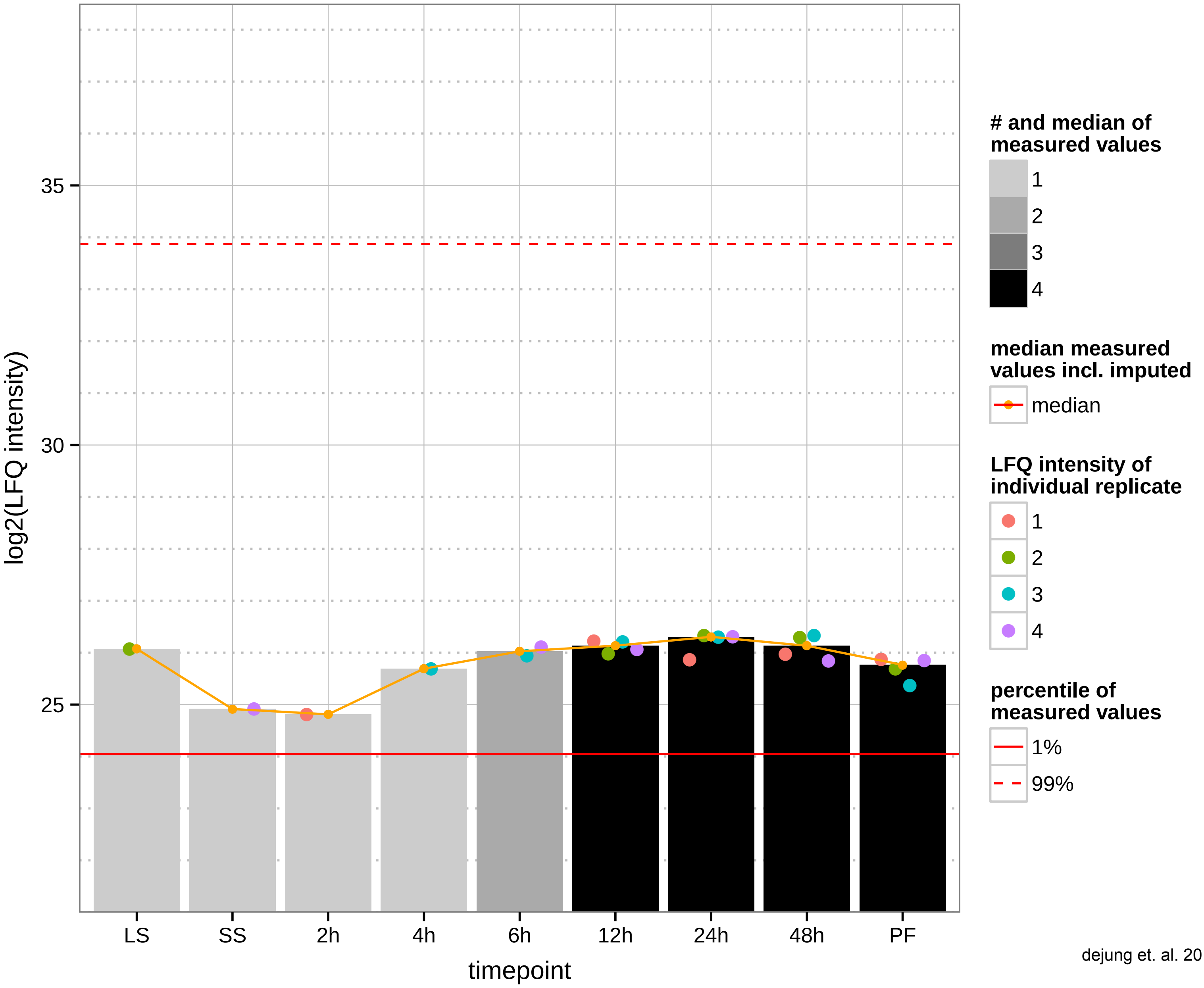
hypothetical protein, conserved
Tb927.7.3380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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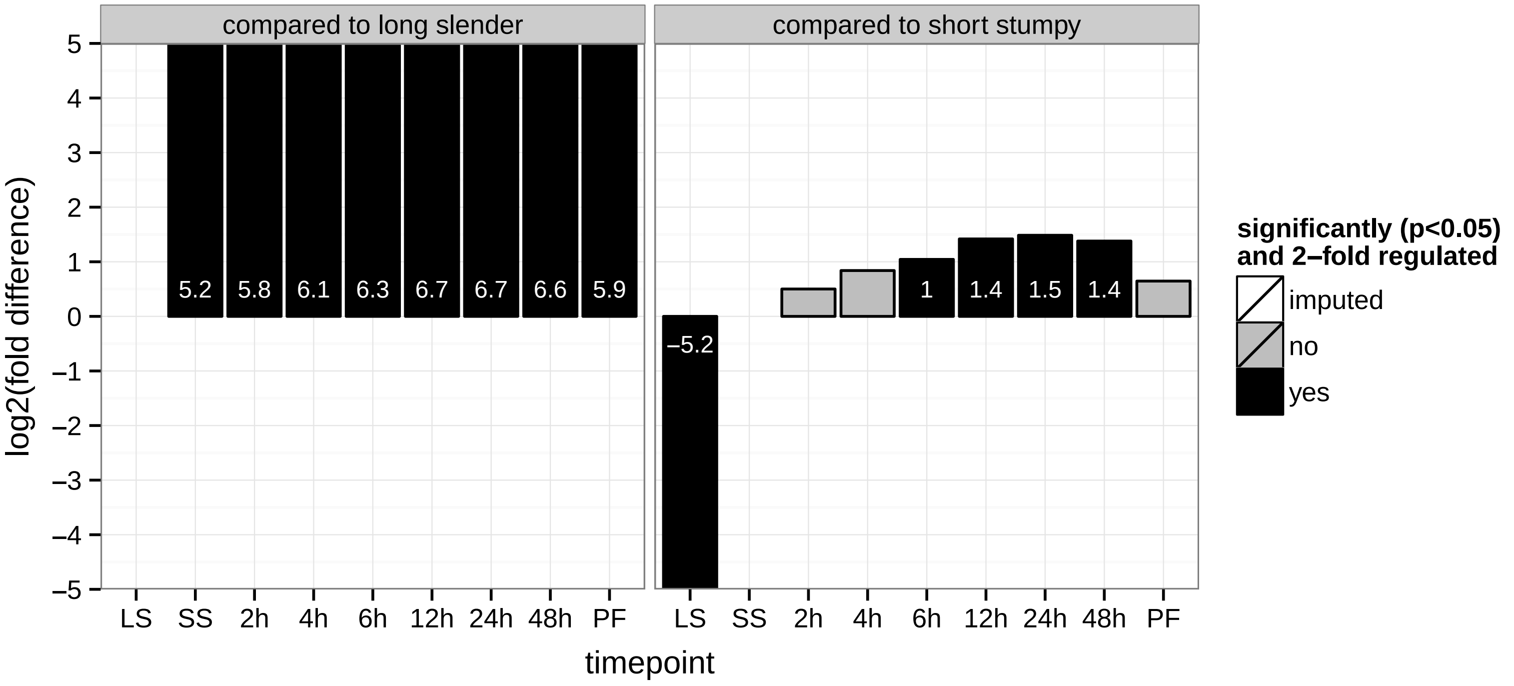
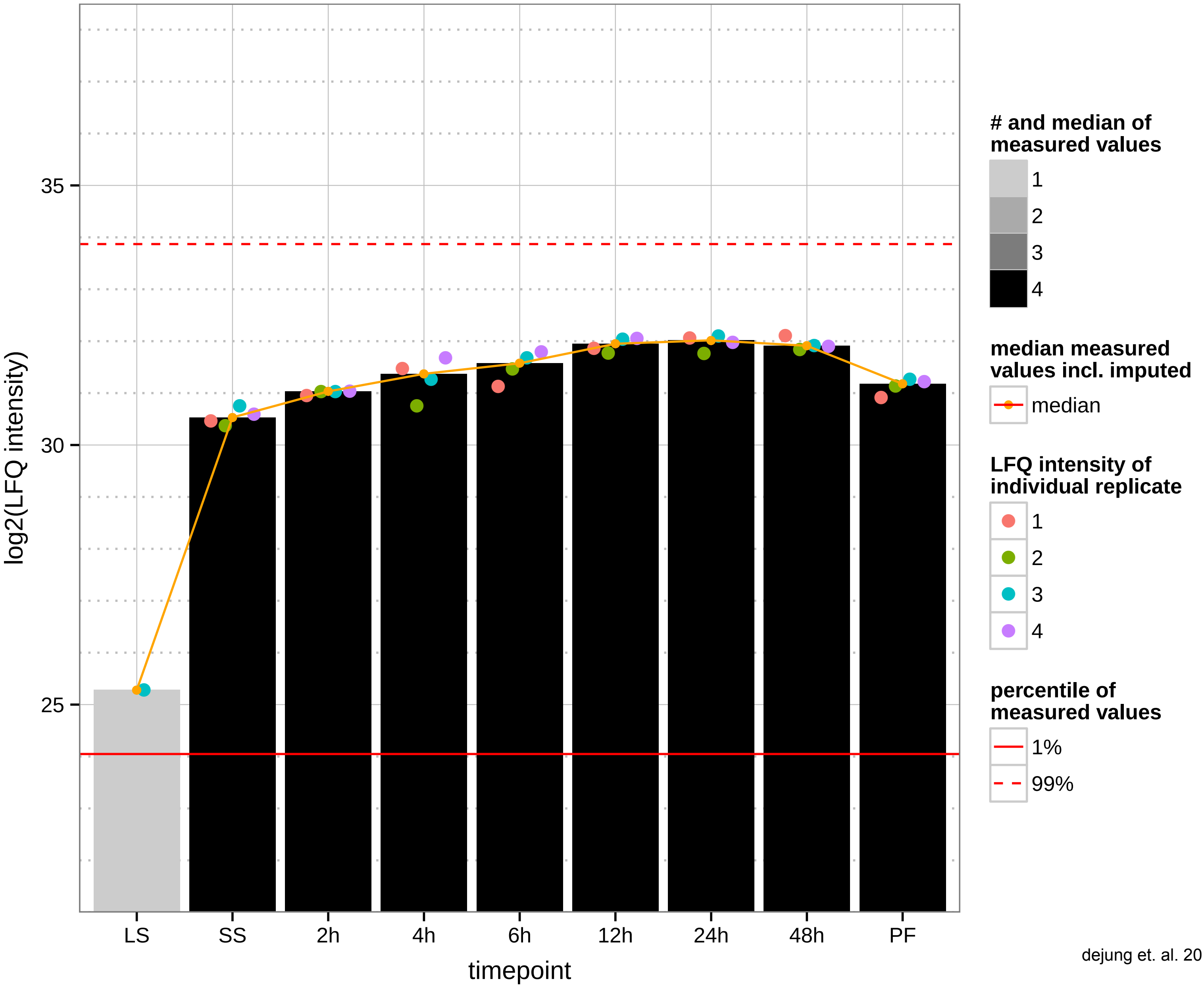
Protein Associated with Differentiation (PAD2)
Tb927.7.5940
AGOF: null
AGOC: flagellar pocket, plasma membrane
AGOP: citrate transport, regulation of developmental process, response to temperature stimulus
PGOF: null
PGOC: integral to membrane
PGOP: transmembrane transport





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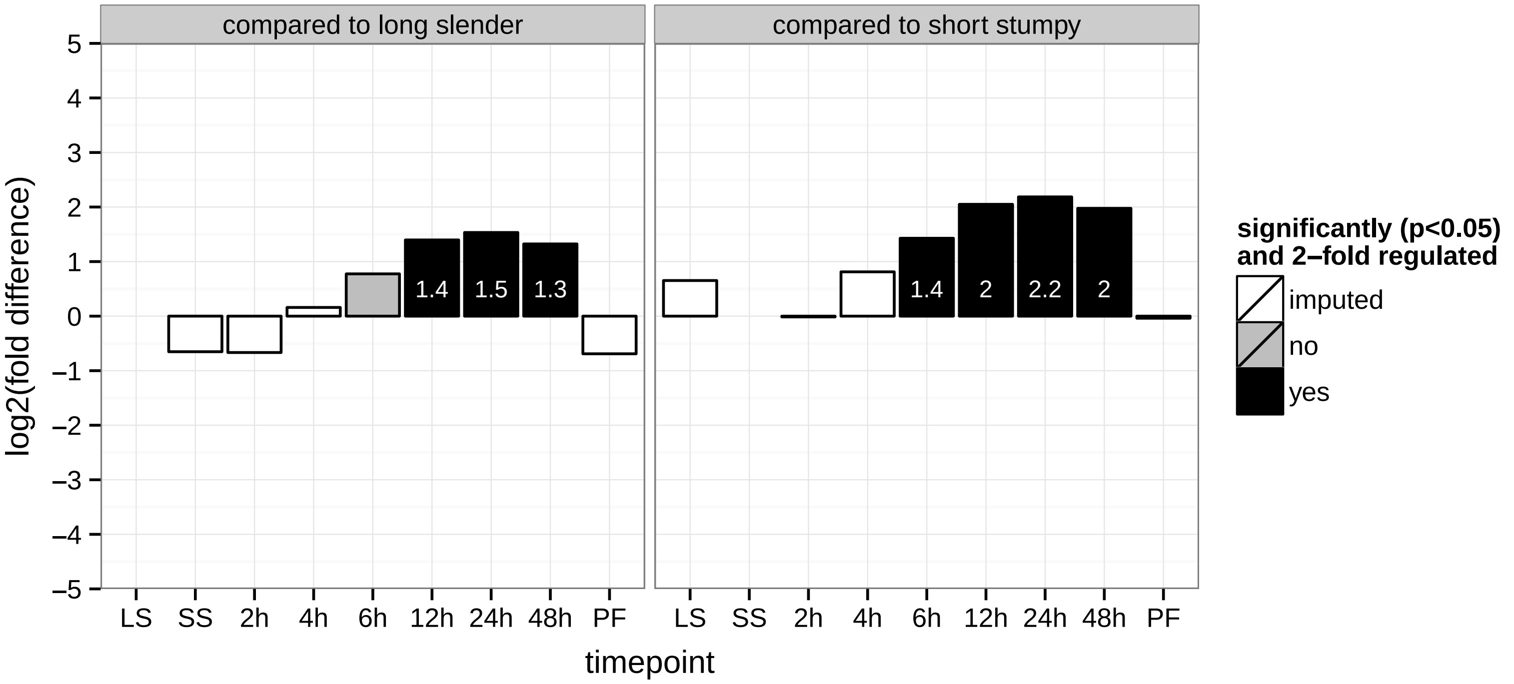
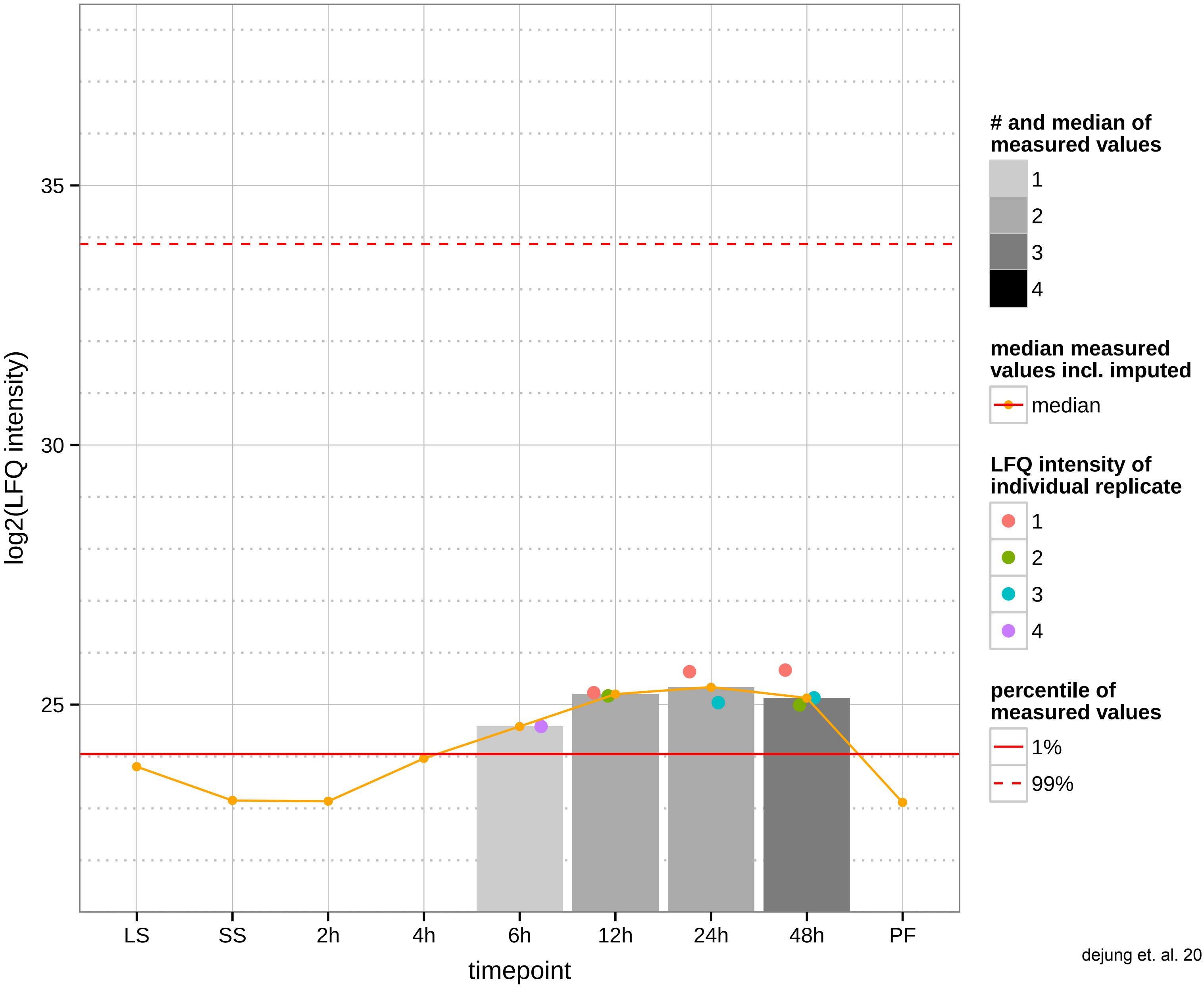
nitroreductase, NADH dehydrogenase, putative (NTR)
Tb927.7.7230
AGOF: oxidoreductase activity
AGOC: mitochondrion
AGOP: drug metabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: null





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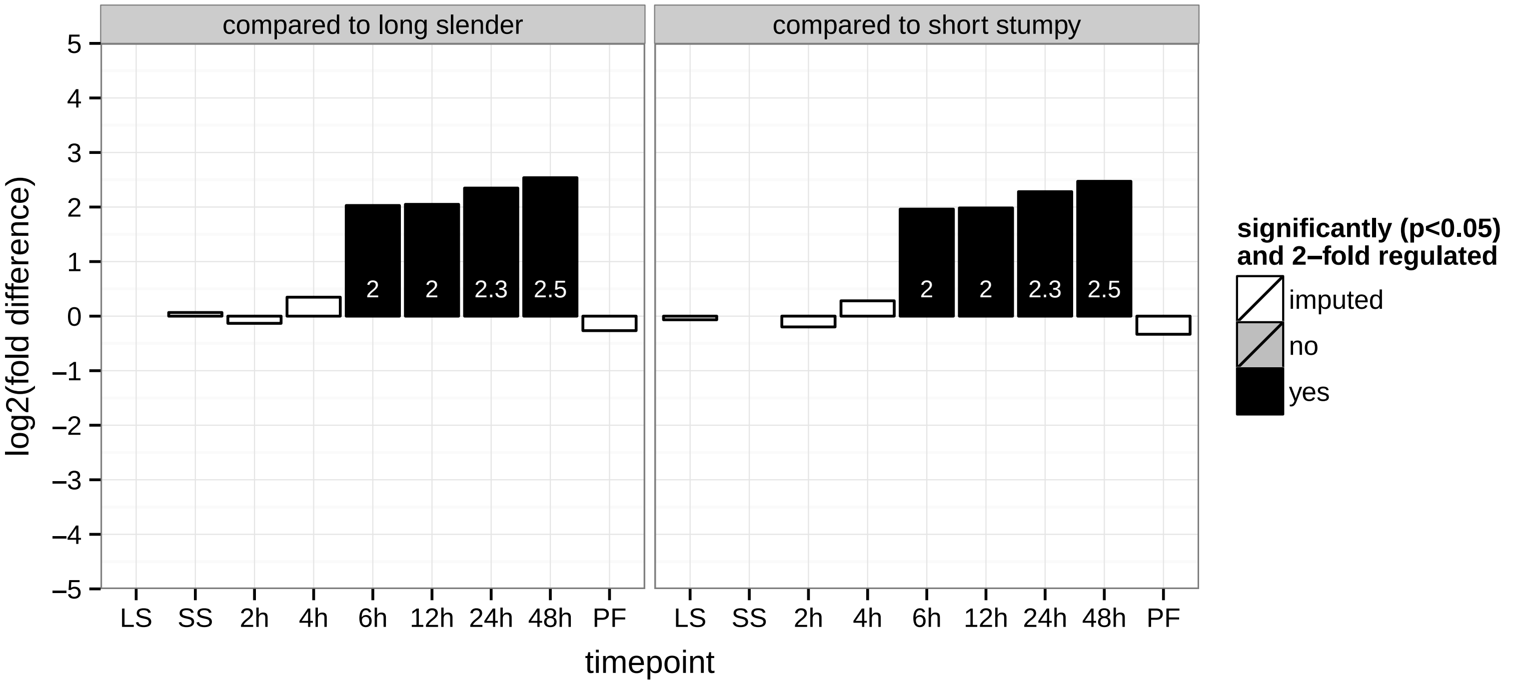
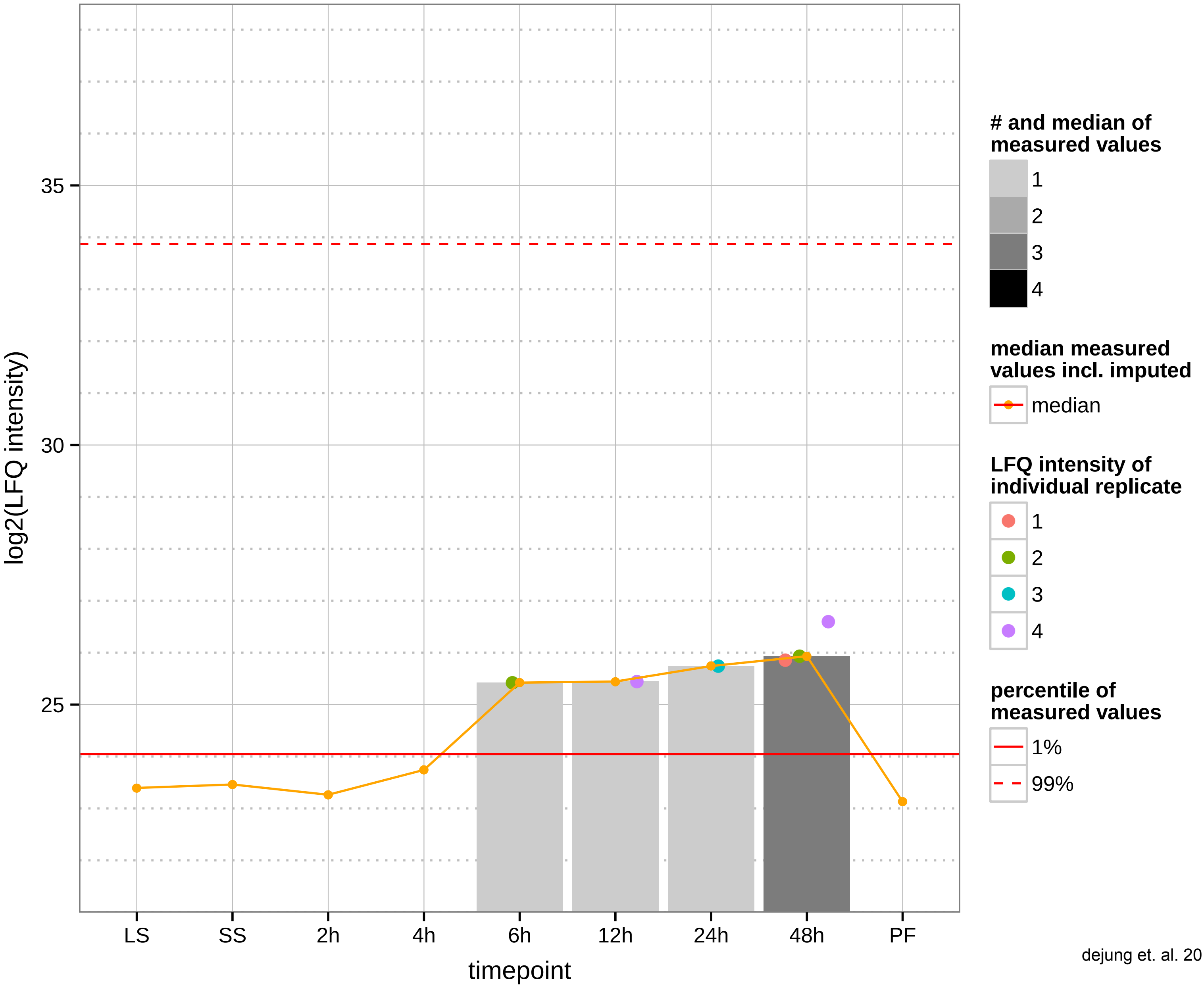
hypothetical protein, conserved
Tb927.8.4860
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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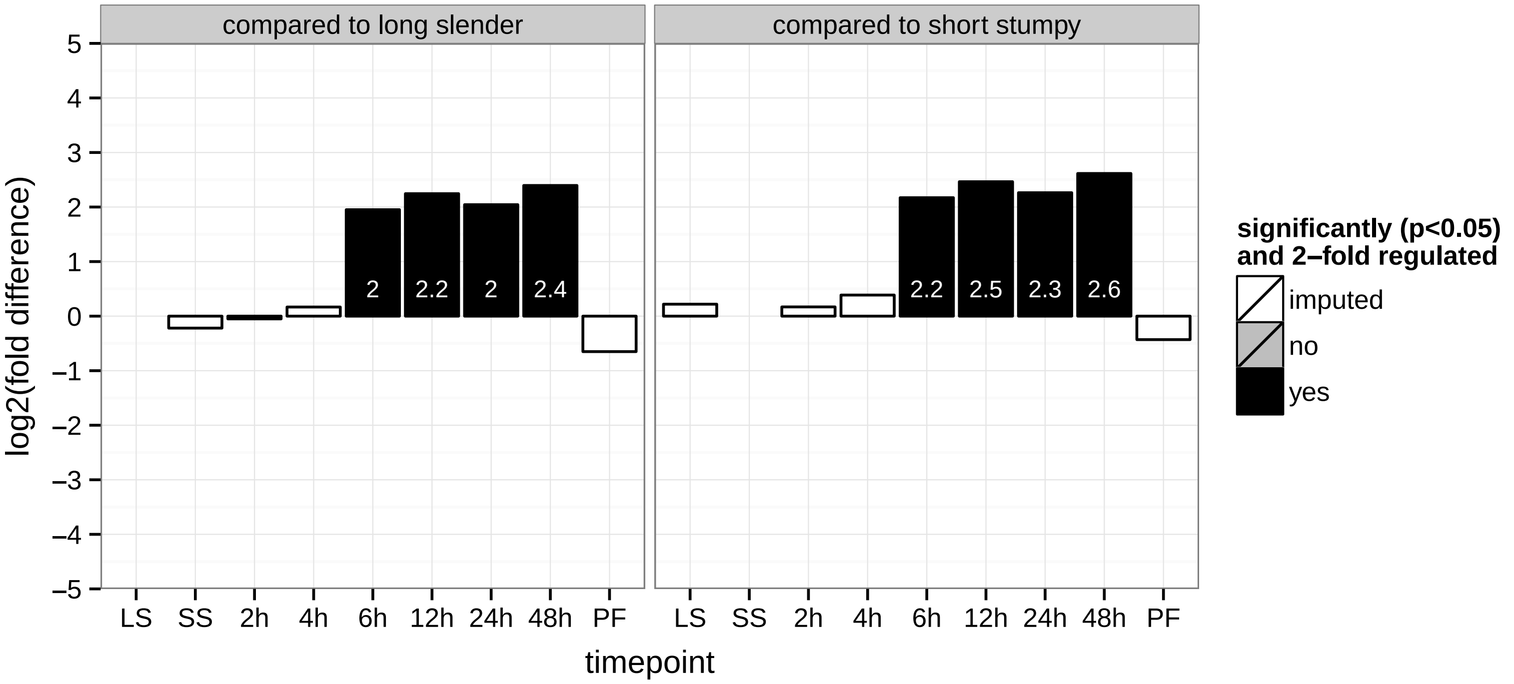
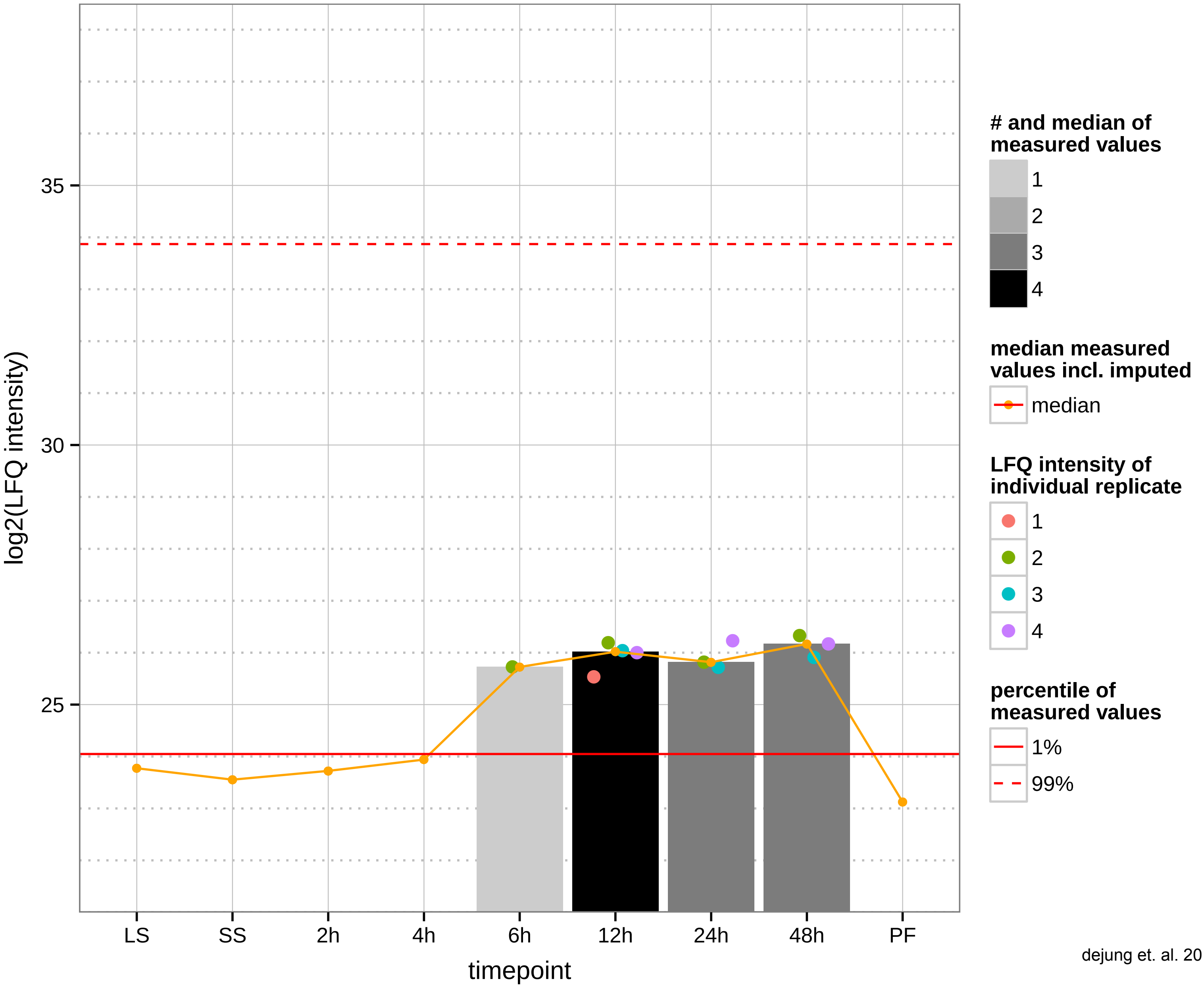
hypothetical protein, conserved
Tb927.9.11820
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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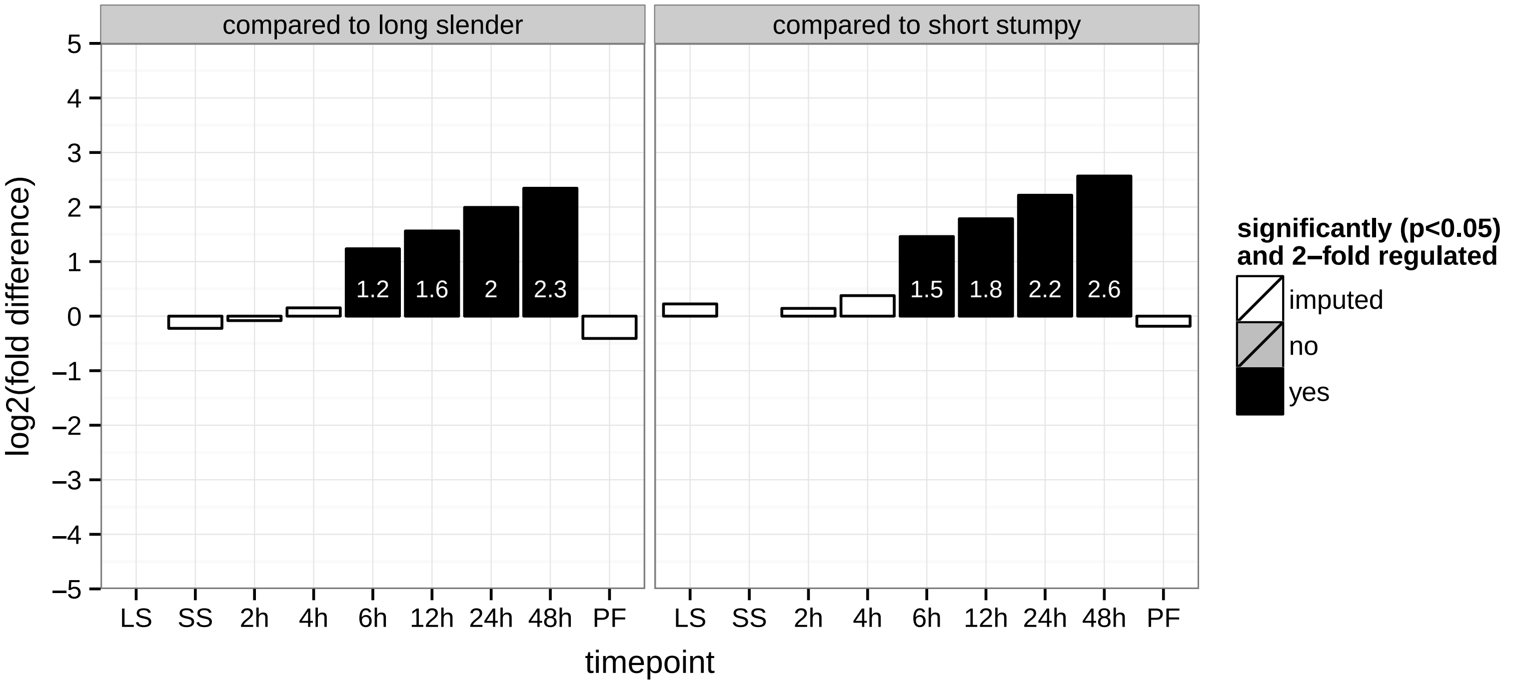
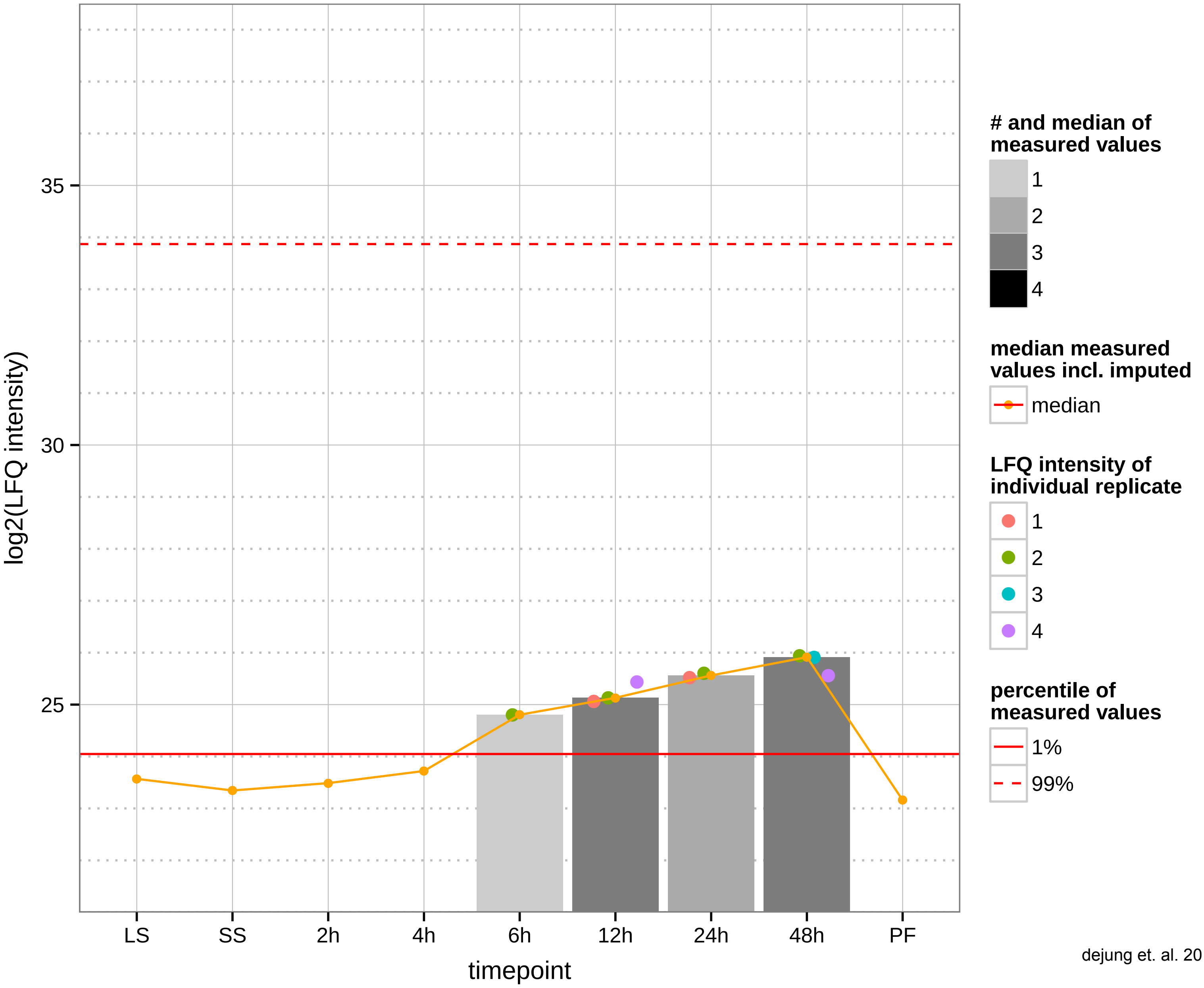
ankyrin repeat protein, putative
Tb927.9.13100
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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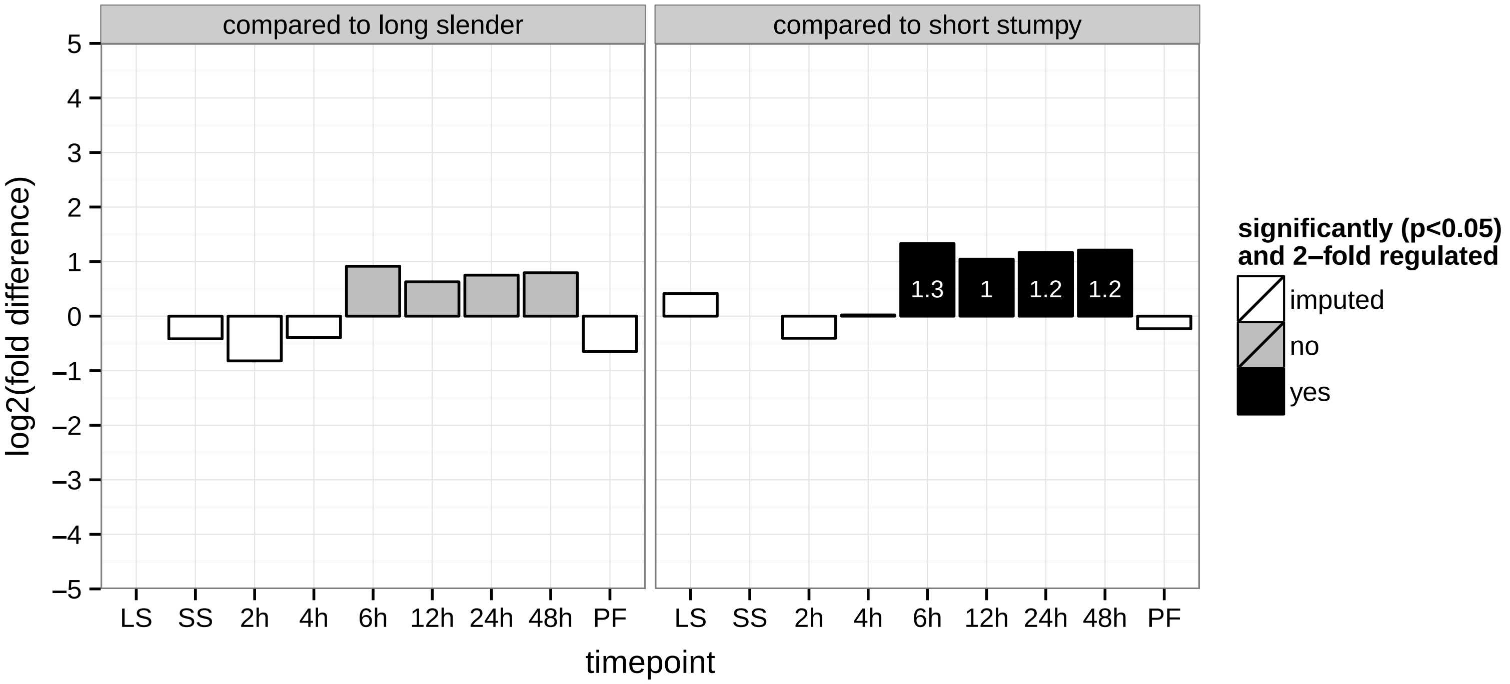
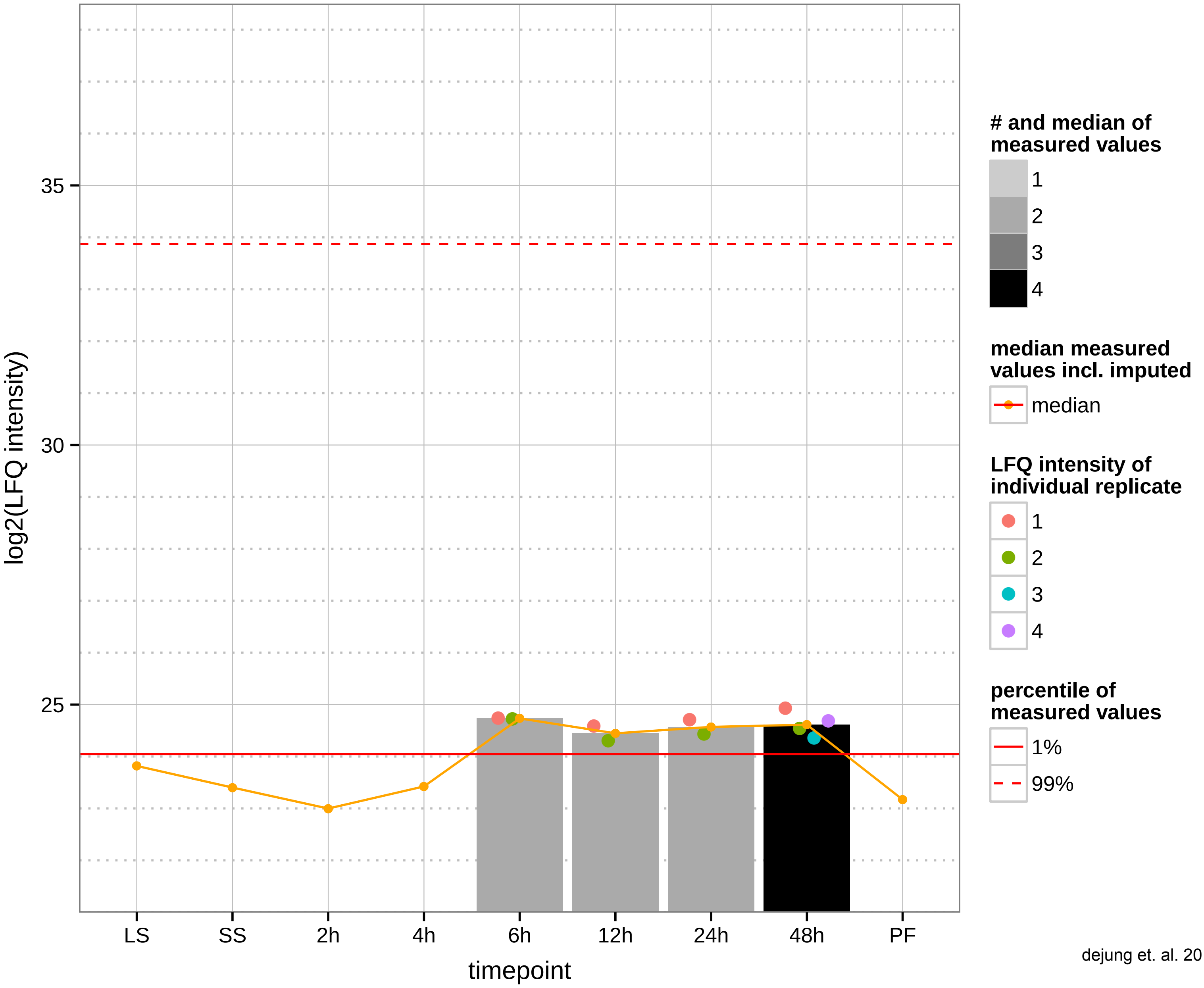
hypothetical protein, conserved
Tb927.9.13120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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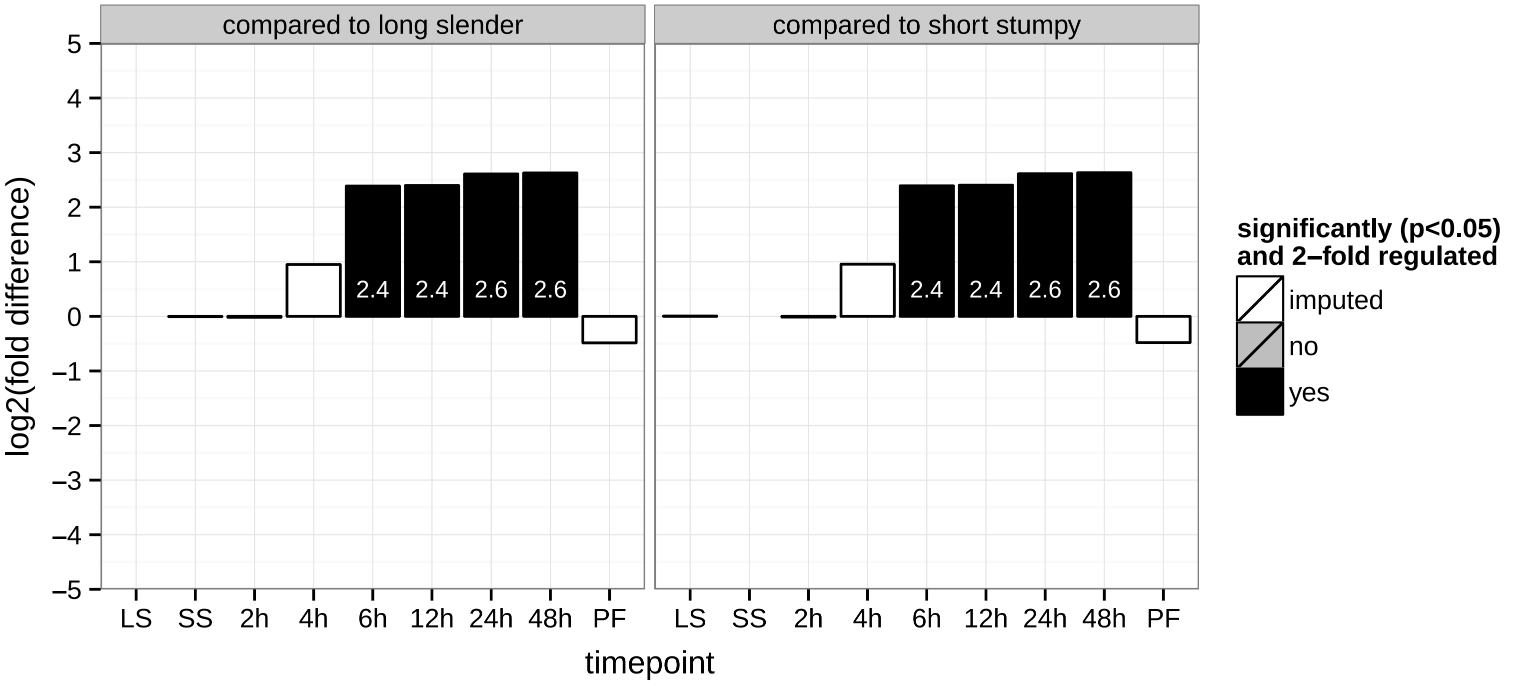
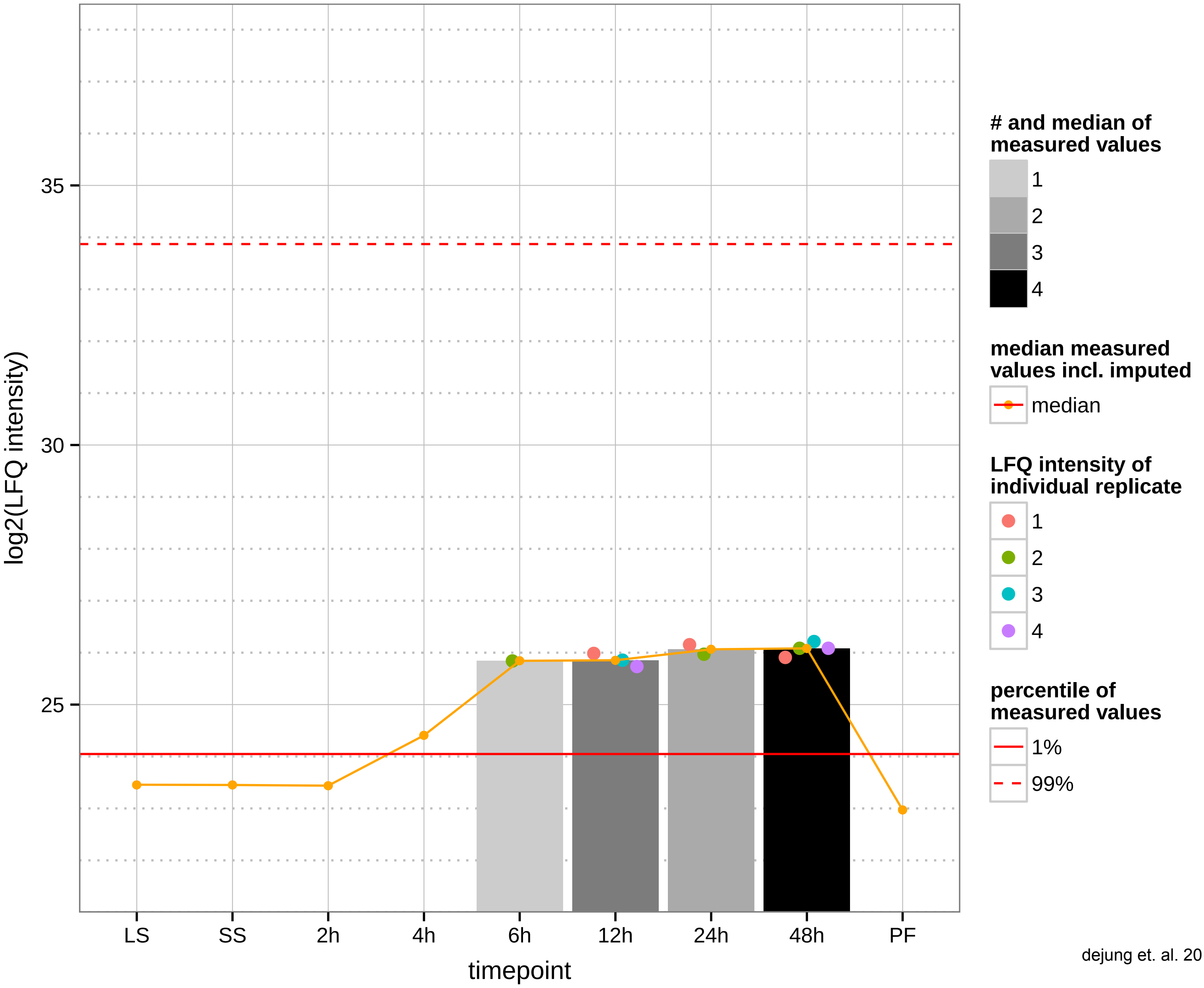
hypothetical protein, conserved
Tb927.9.1440
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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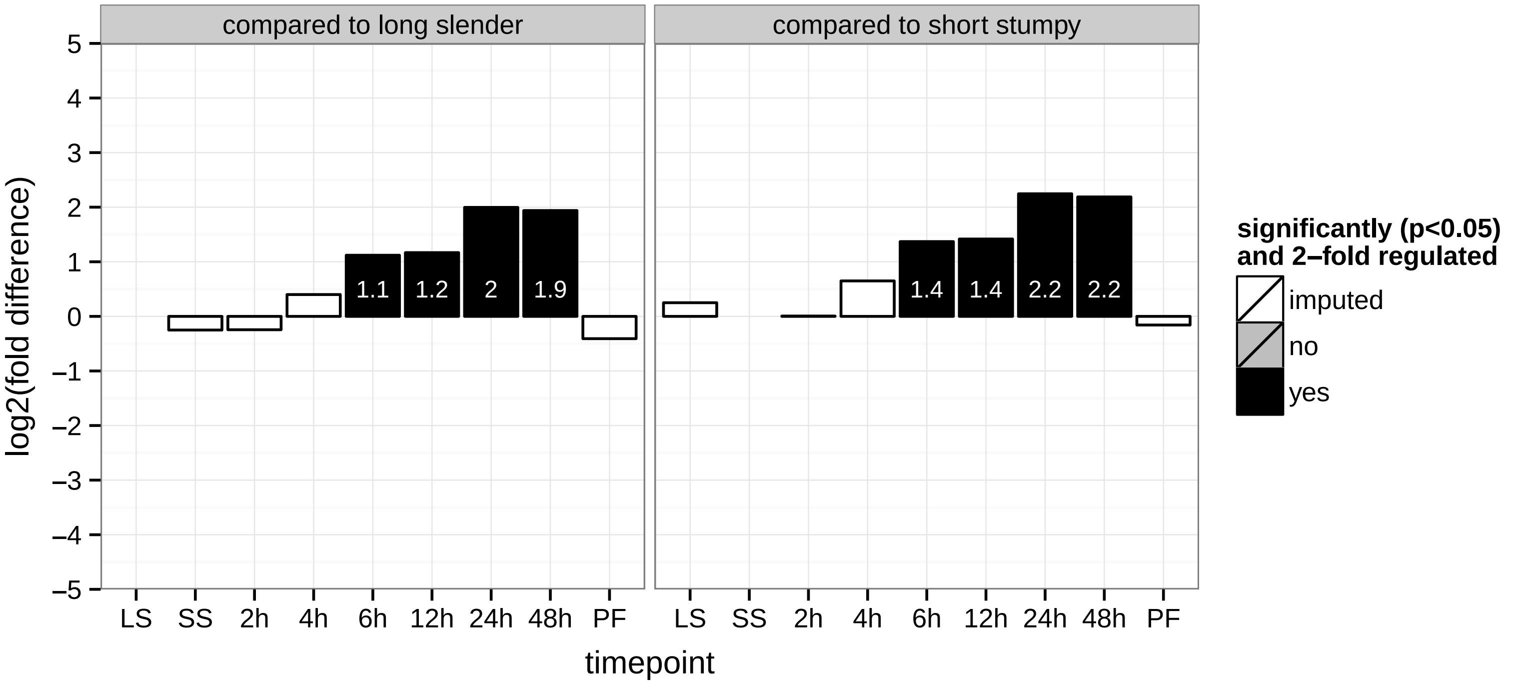
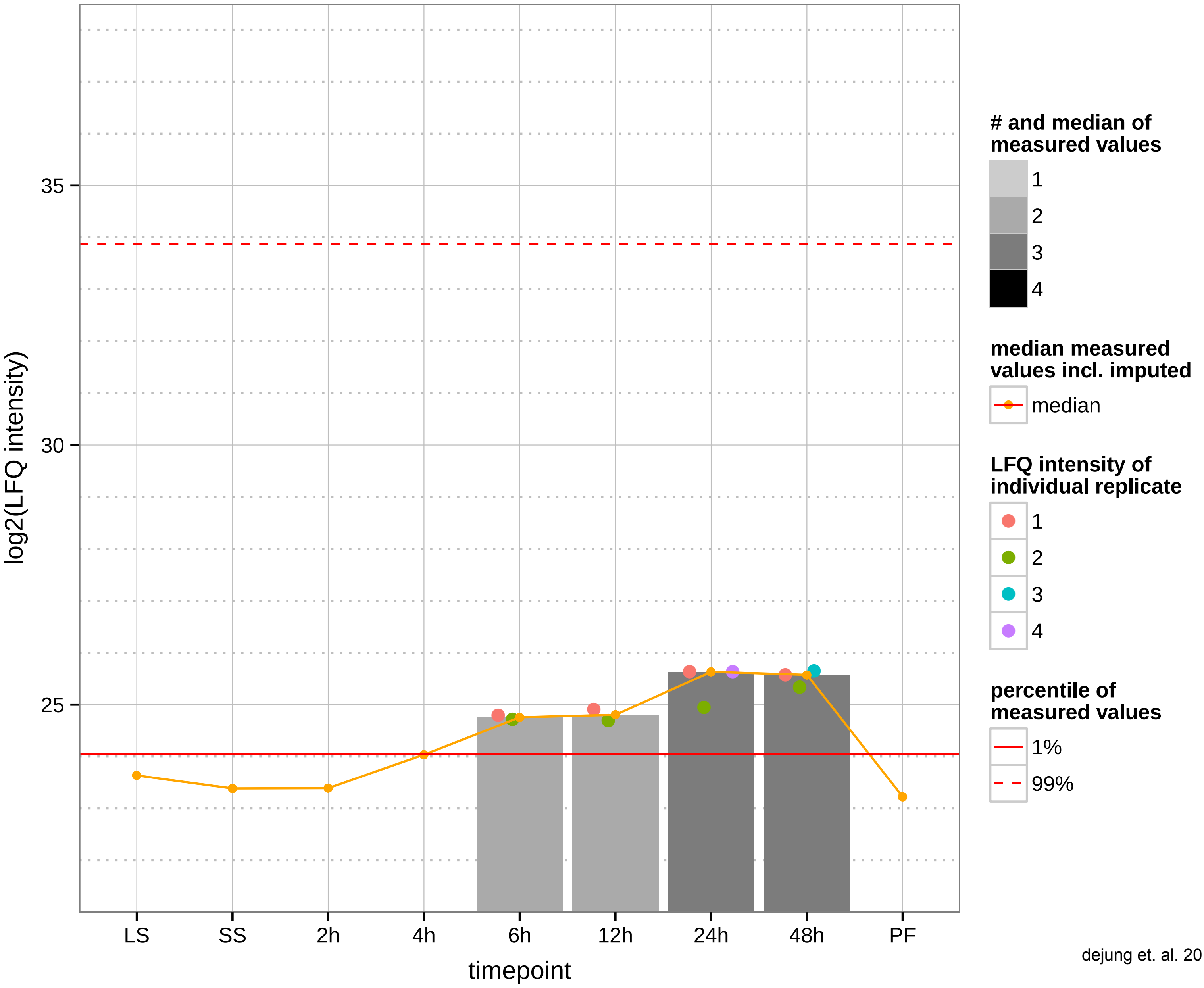
hypothetical protein, conserved
Tb927.9.15040
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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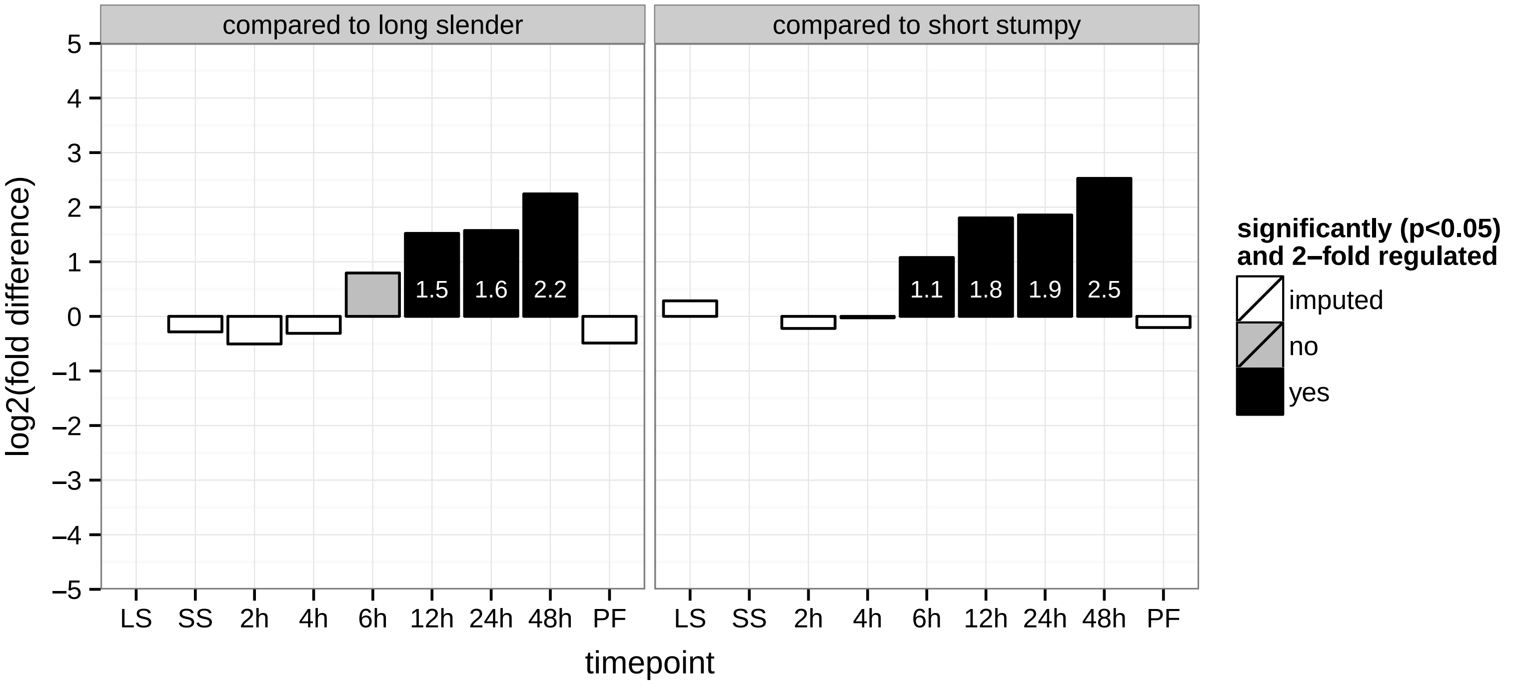
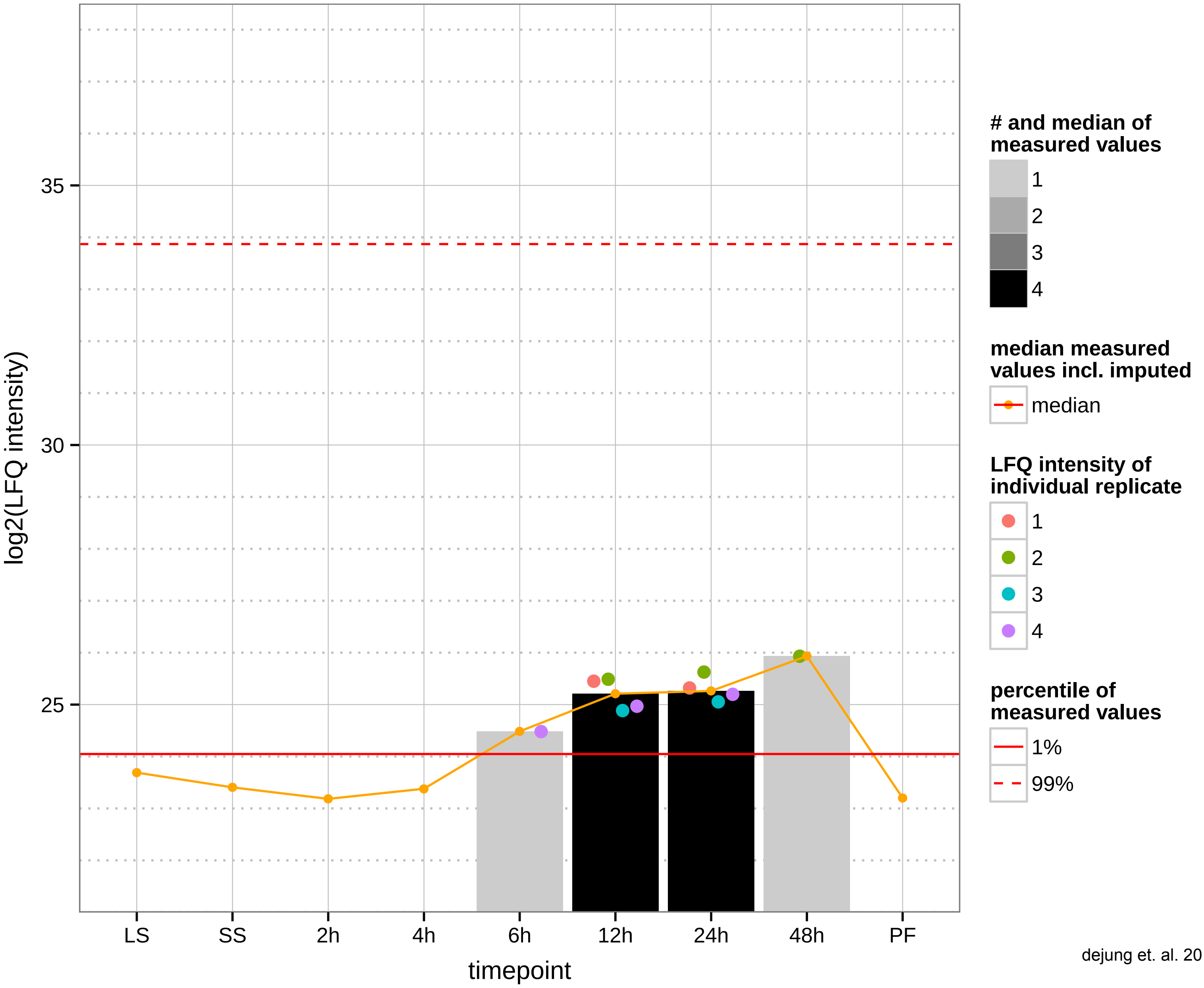
hypothetical protein, conserved
Tb927.9.2060
AGOF: GTP binding
AGOC: null
AGOP: null
PGOF: GTP binding
PGOC: intracellular
PGOP: small GTPase mediated signal transduction





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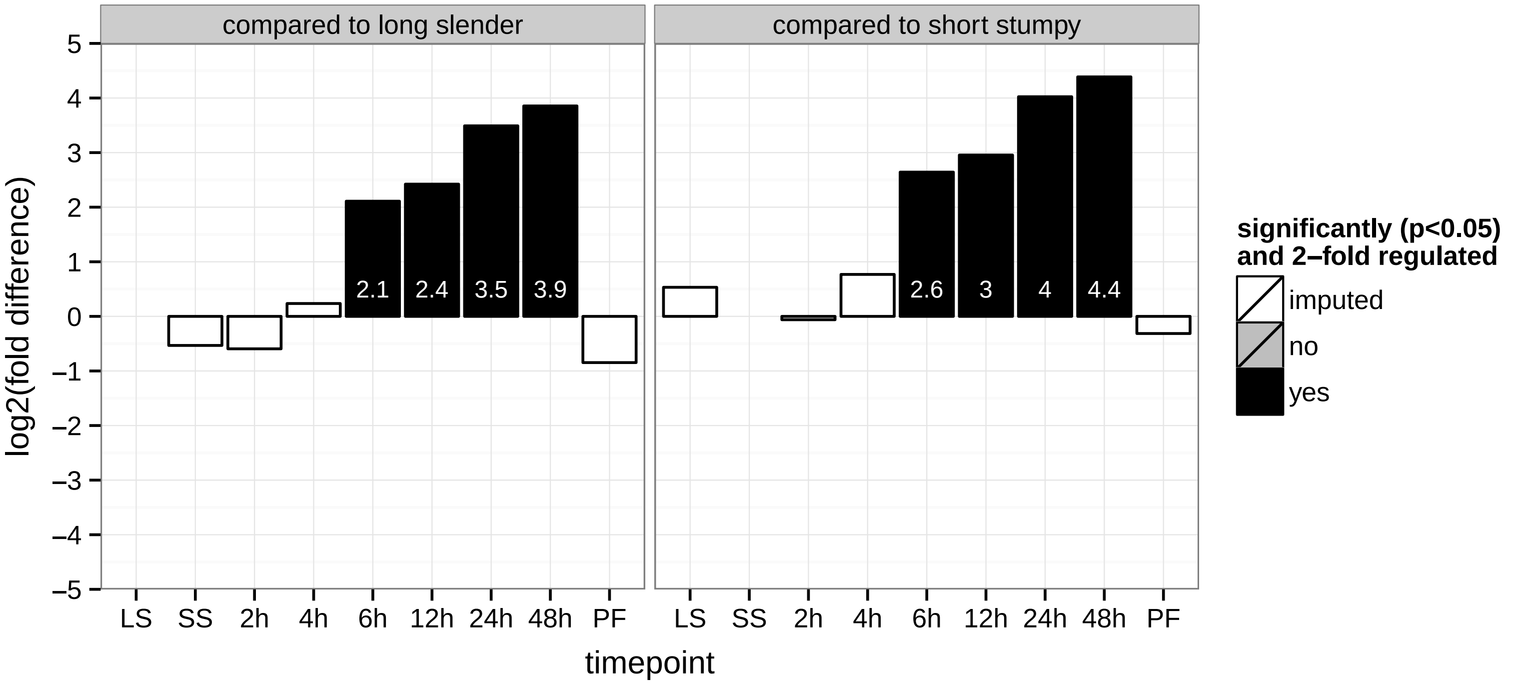
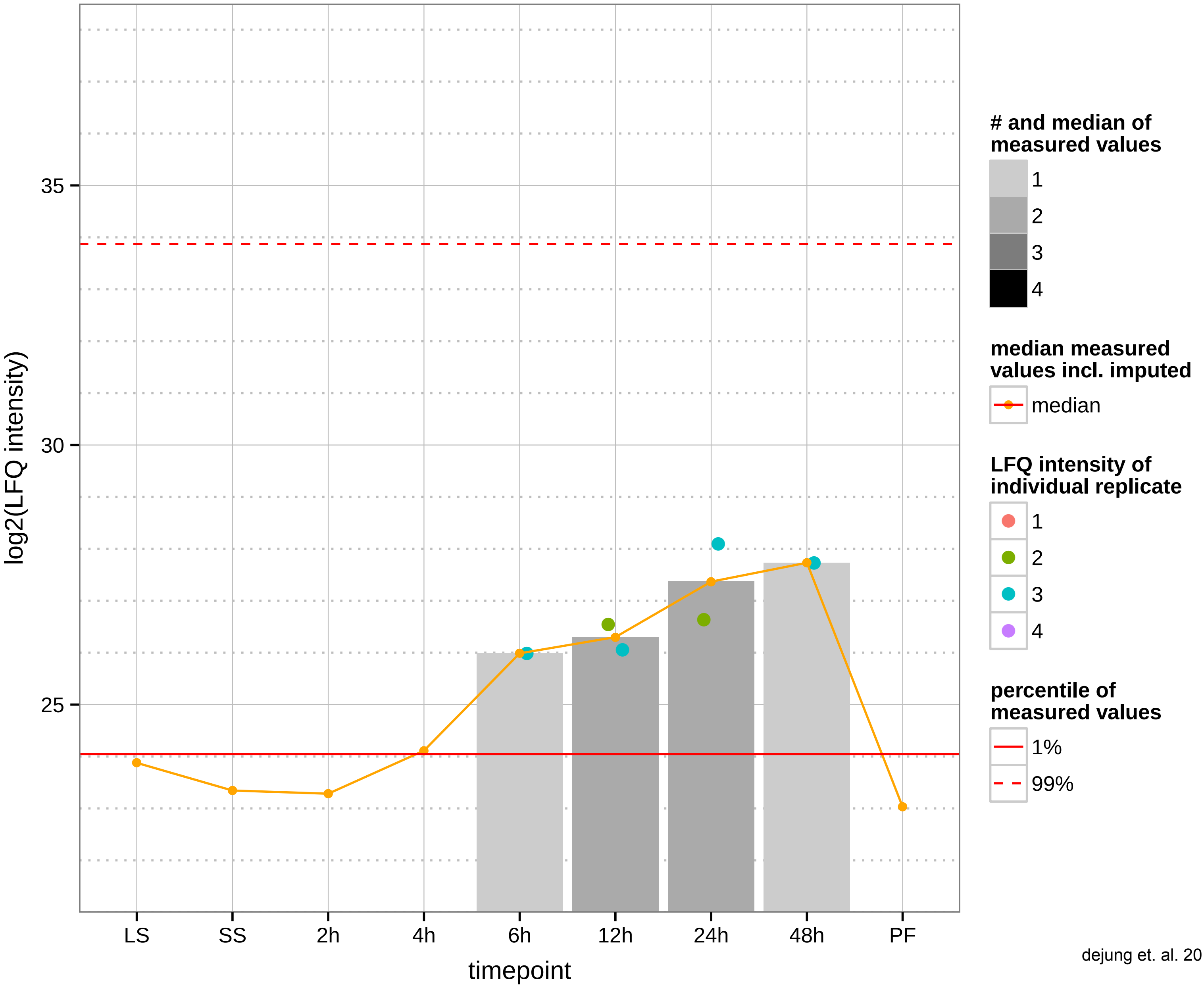
hypothetical protein, conserved
Tb927.9.7980
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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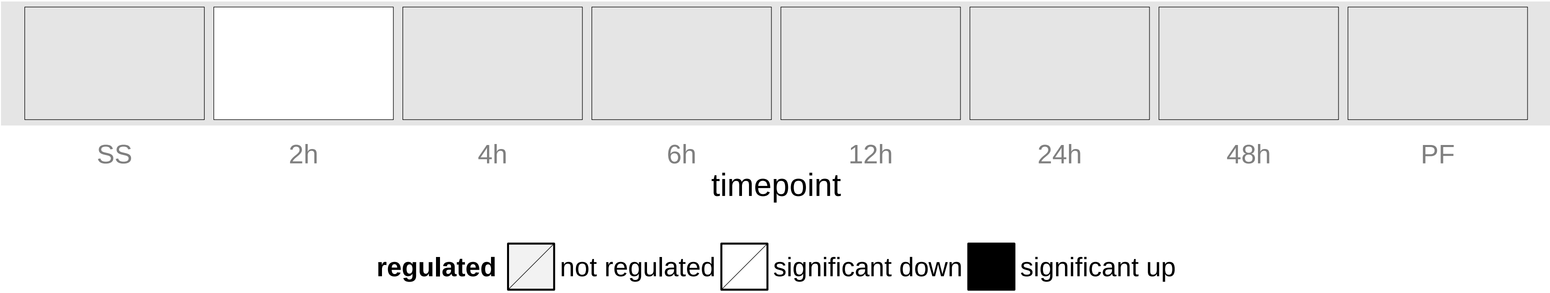

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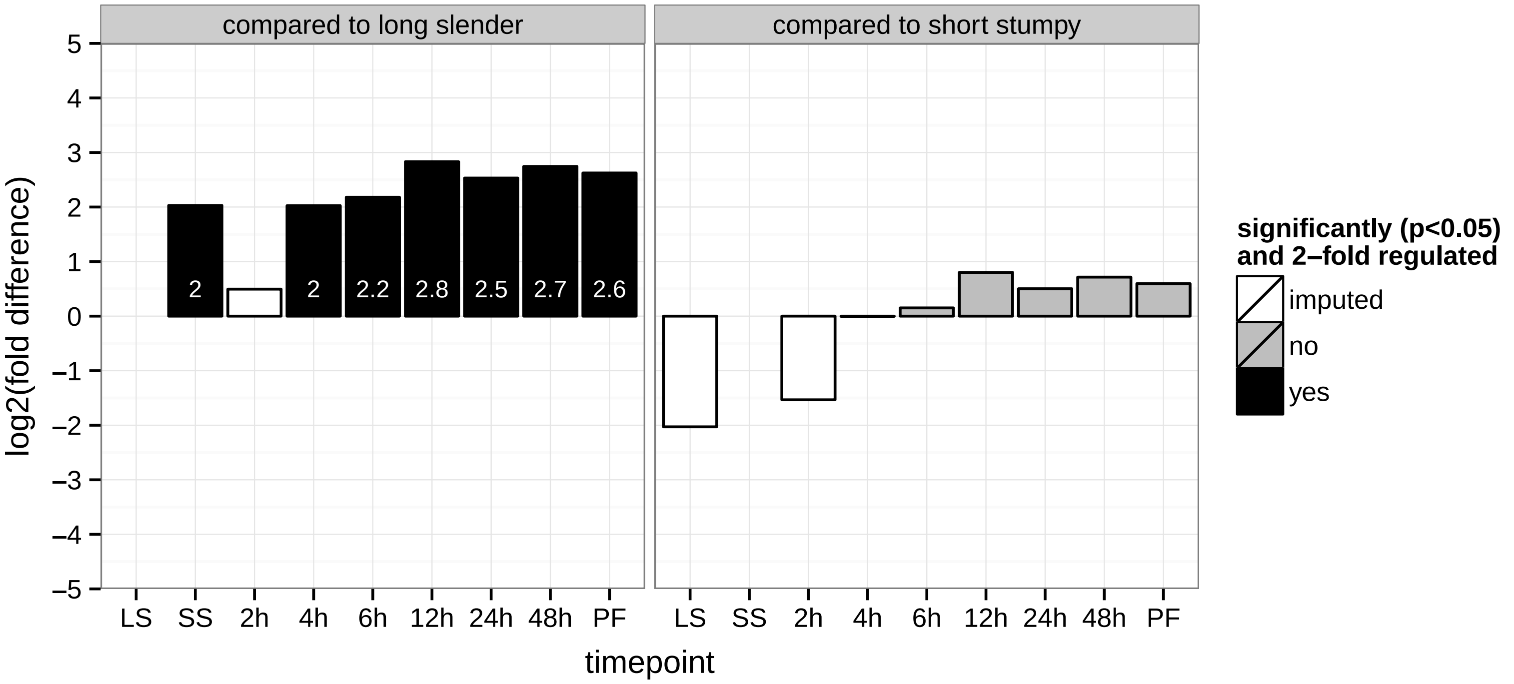
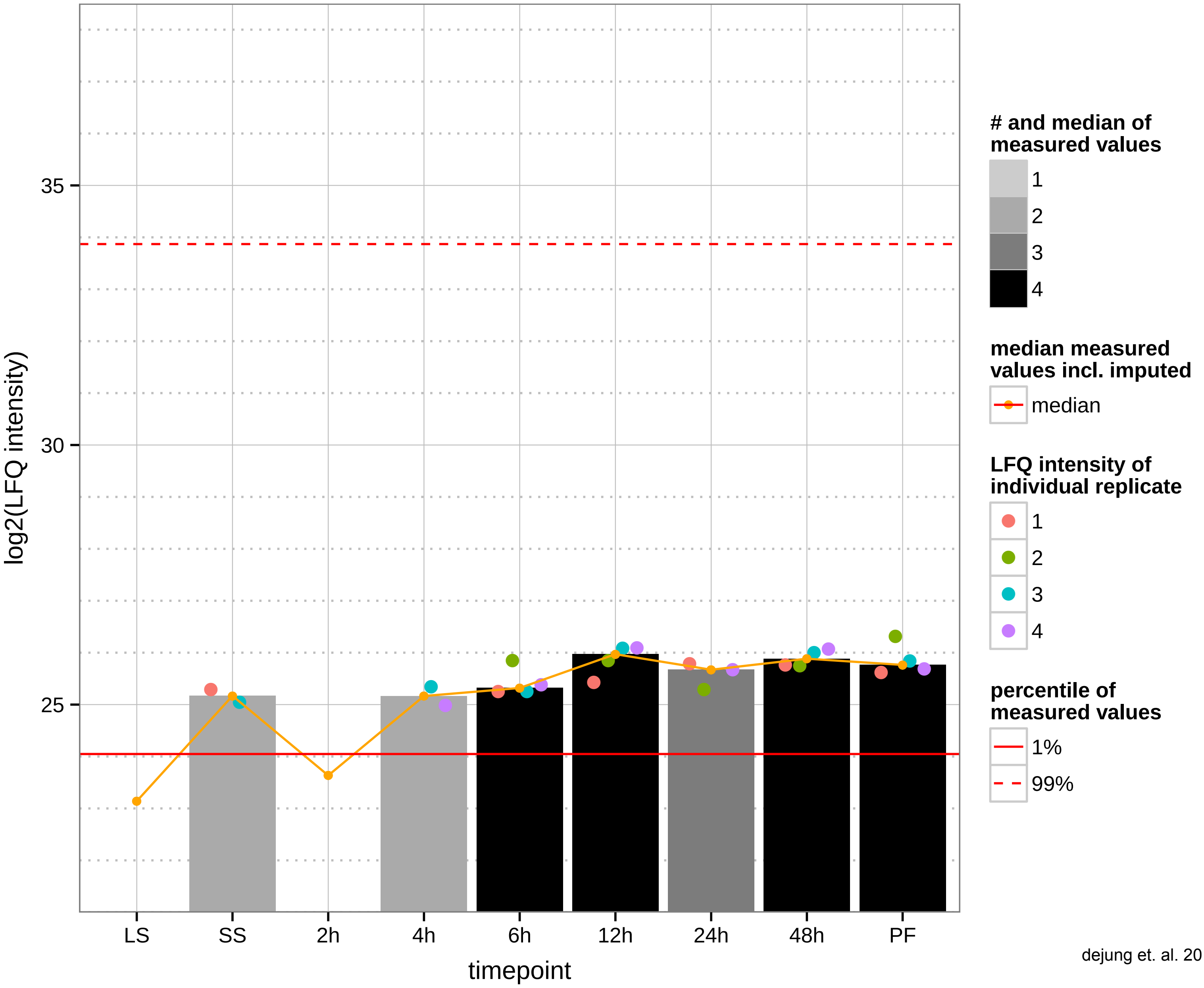
hypothetical protein, conserved, chrX additional, unordered contigs
Tb927.10.4470;Tb10.v4.0037
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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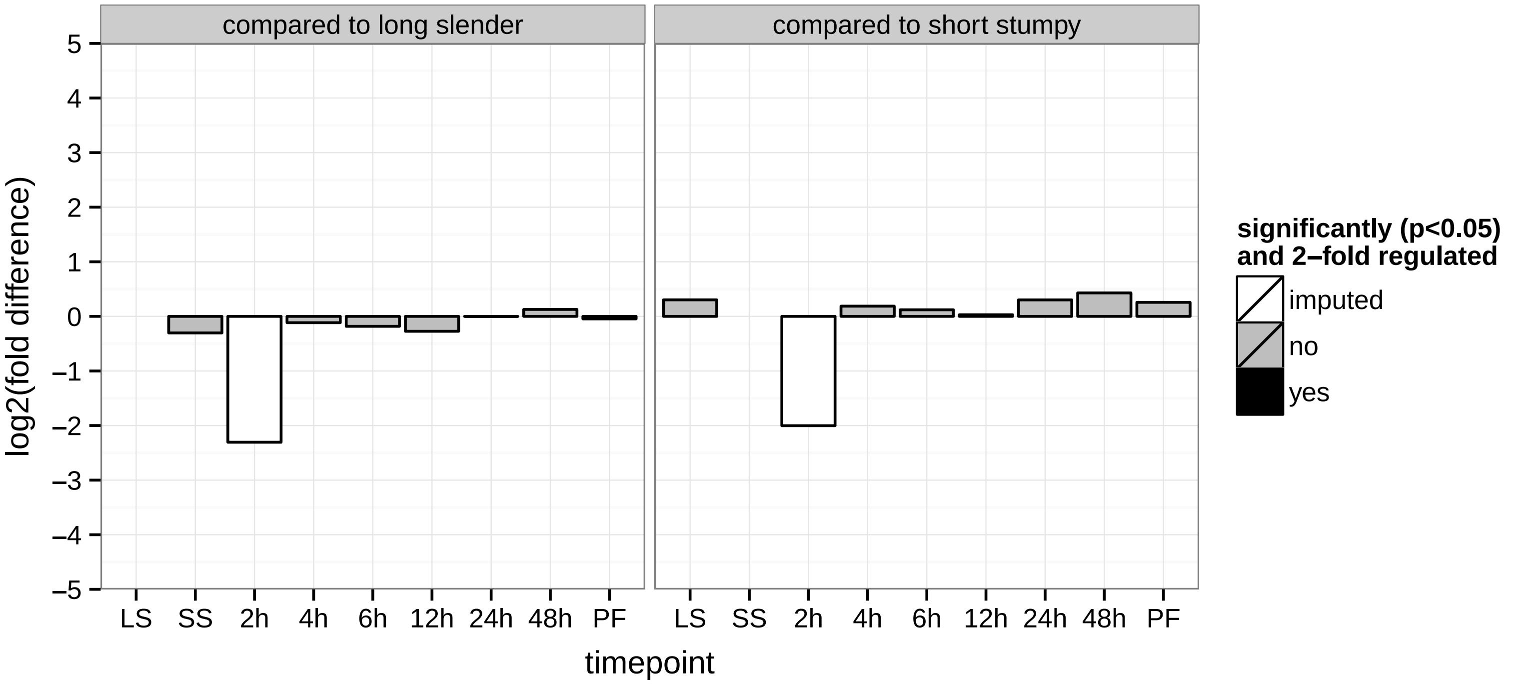
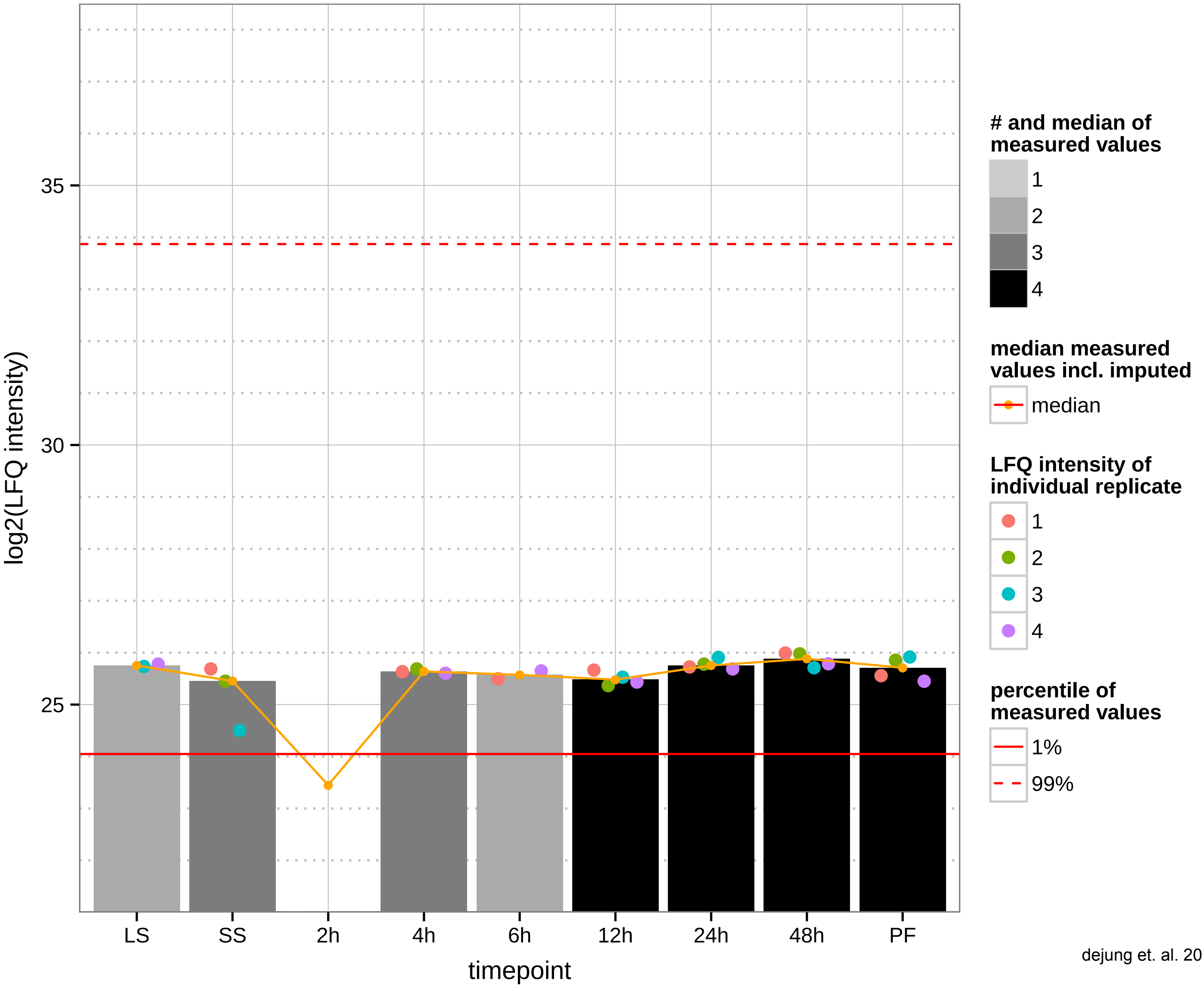
hypothetical protein, conserved
Tb927.7.4840;Tb11.v5.0166
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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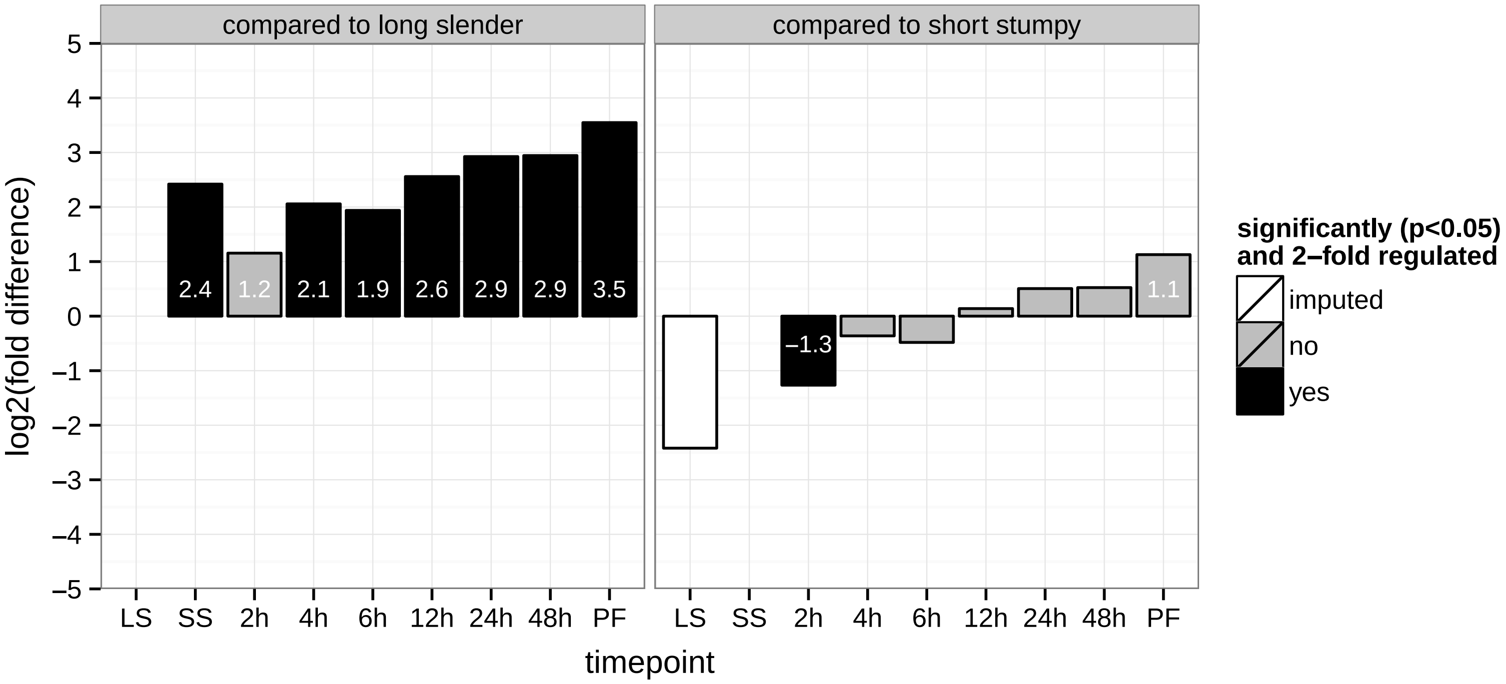
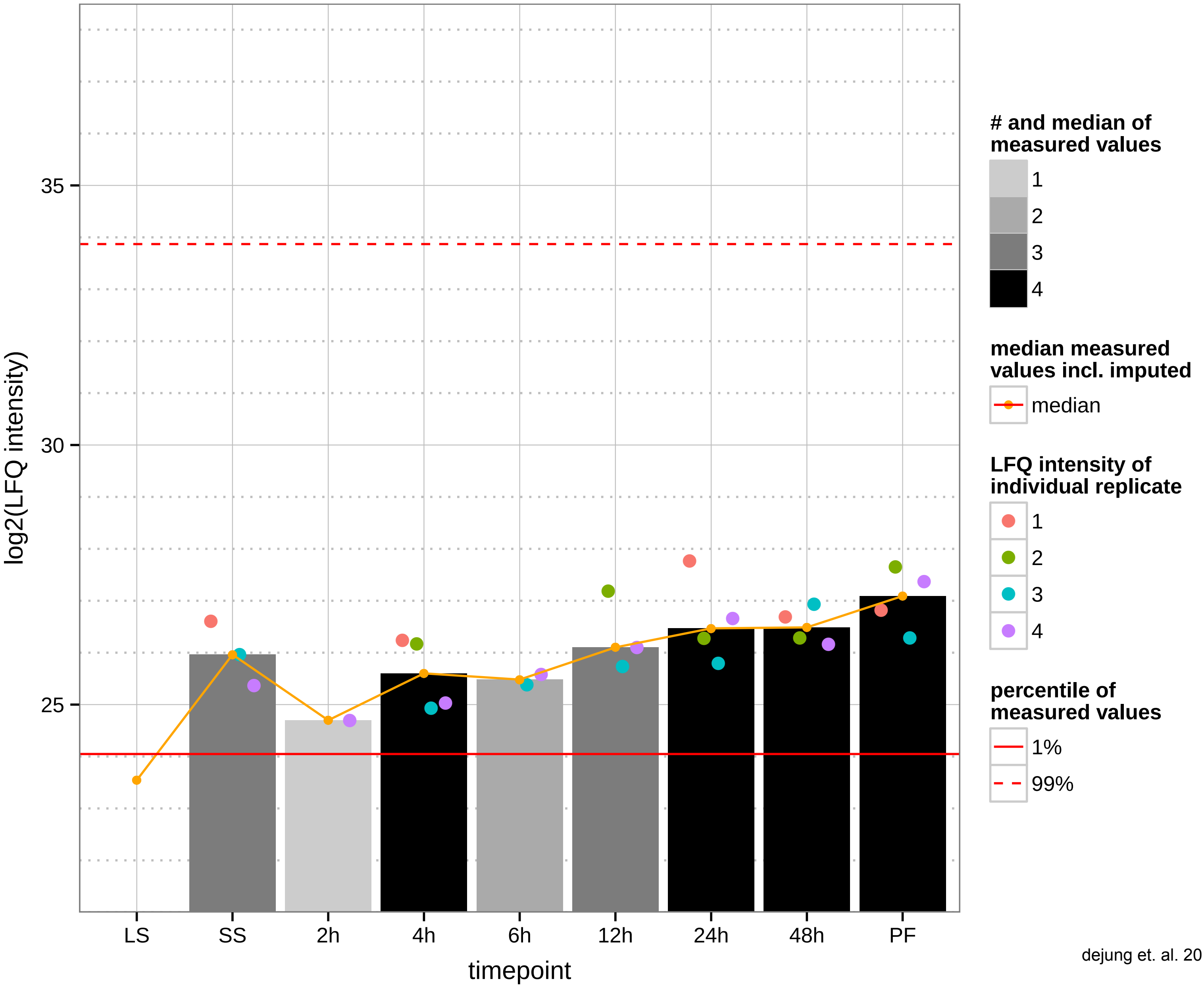
hypothetical protein, conserved
Tb927.11.7250;Tb11.v5.0257
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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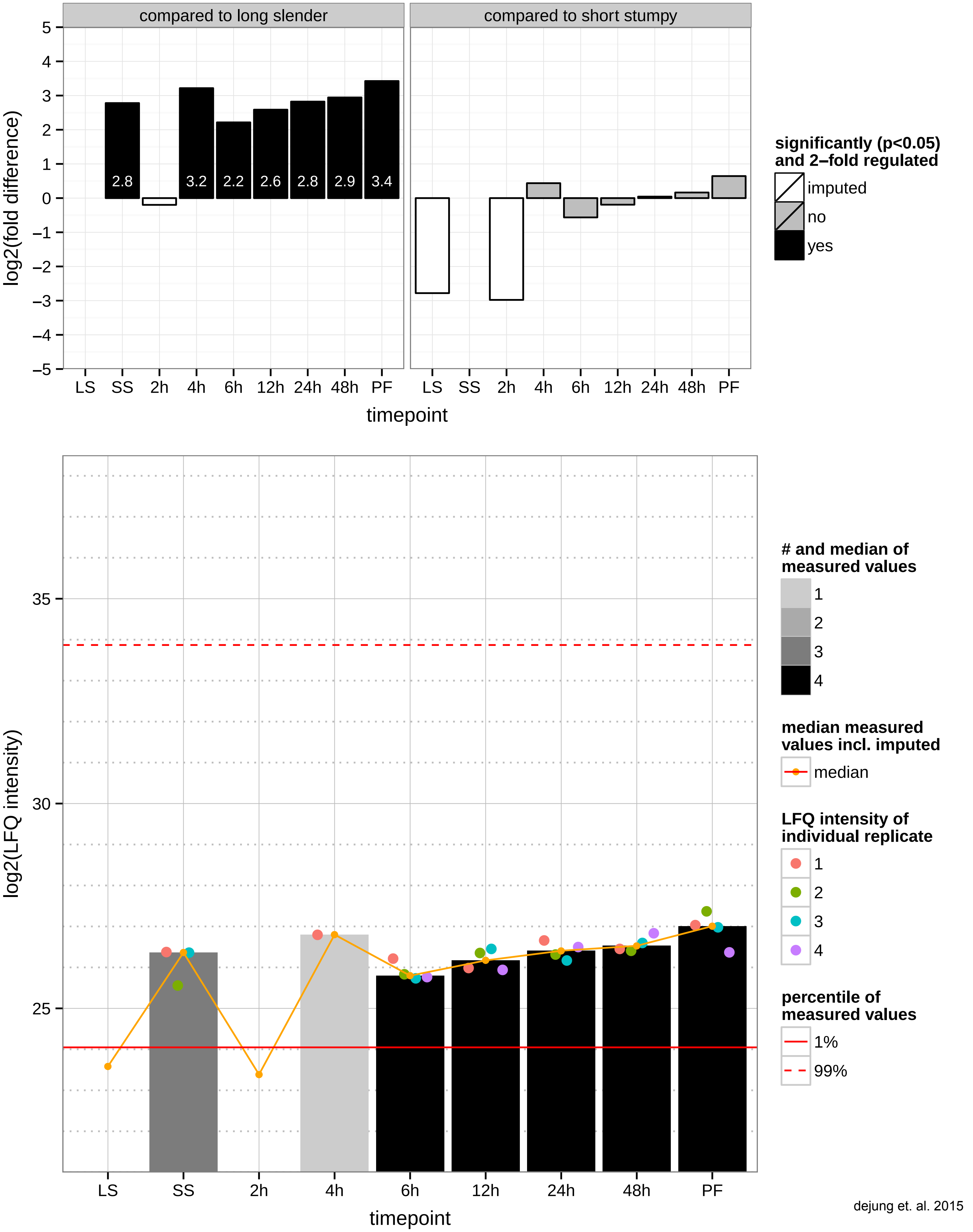
hypothetical protein, conserved
Tb11.v5.0562;Tb927.8.1260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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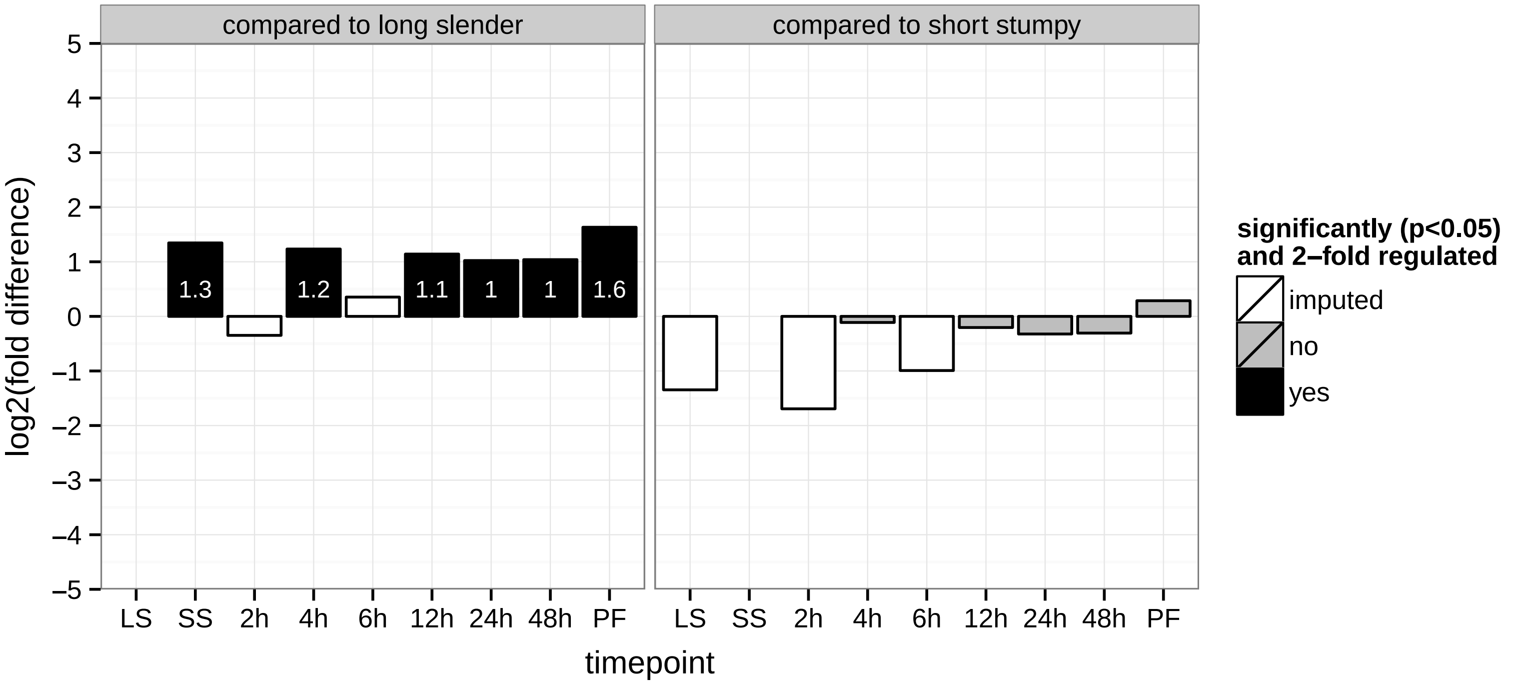
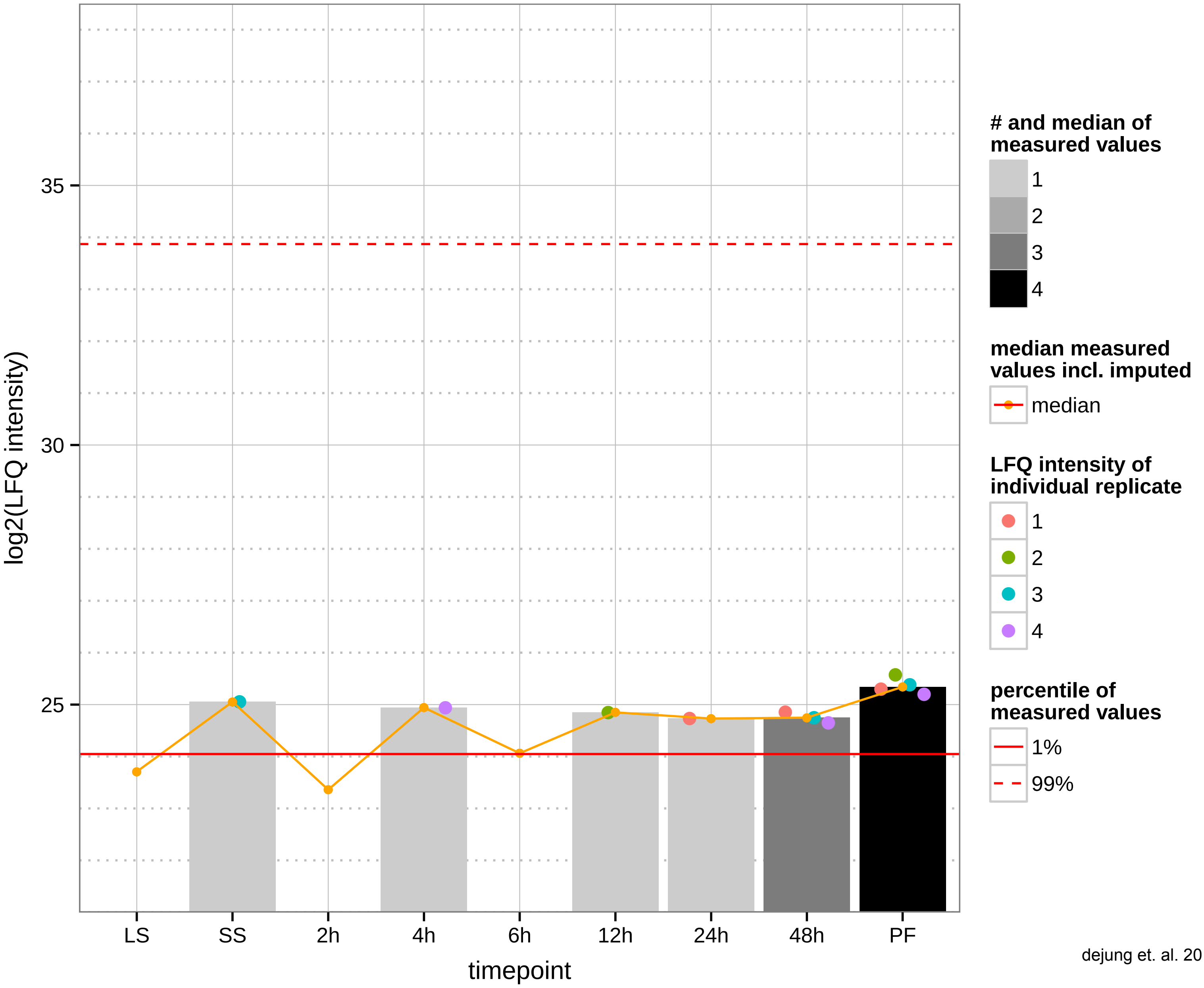
hypothetical protein, conserved
Tb927.10.3470
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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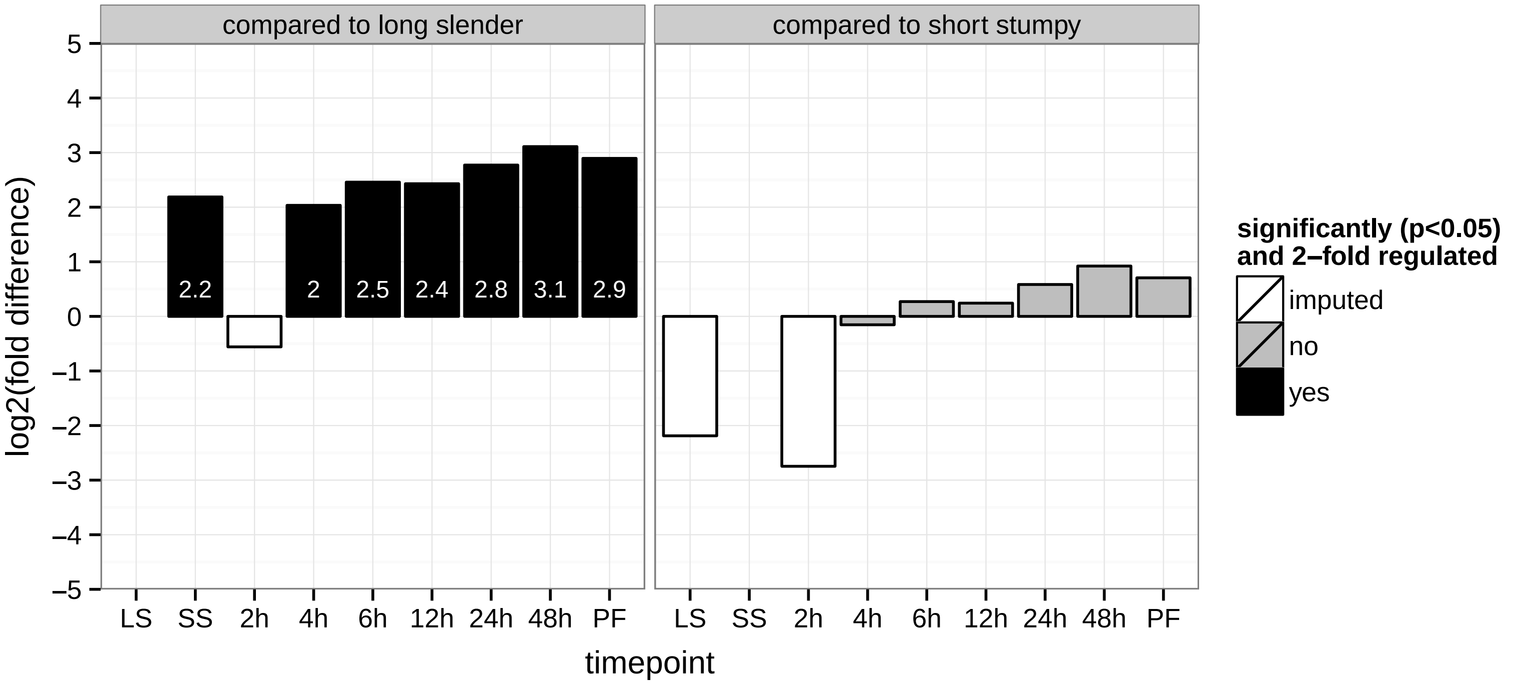
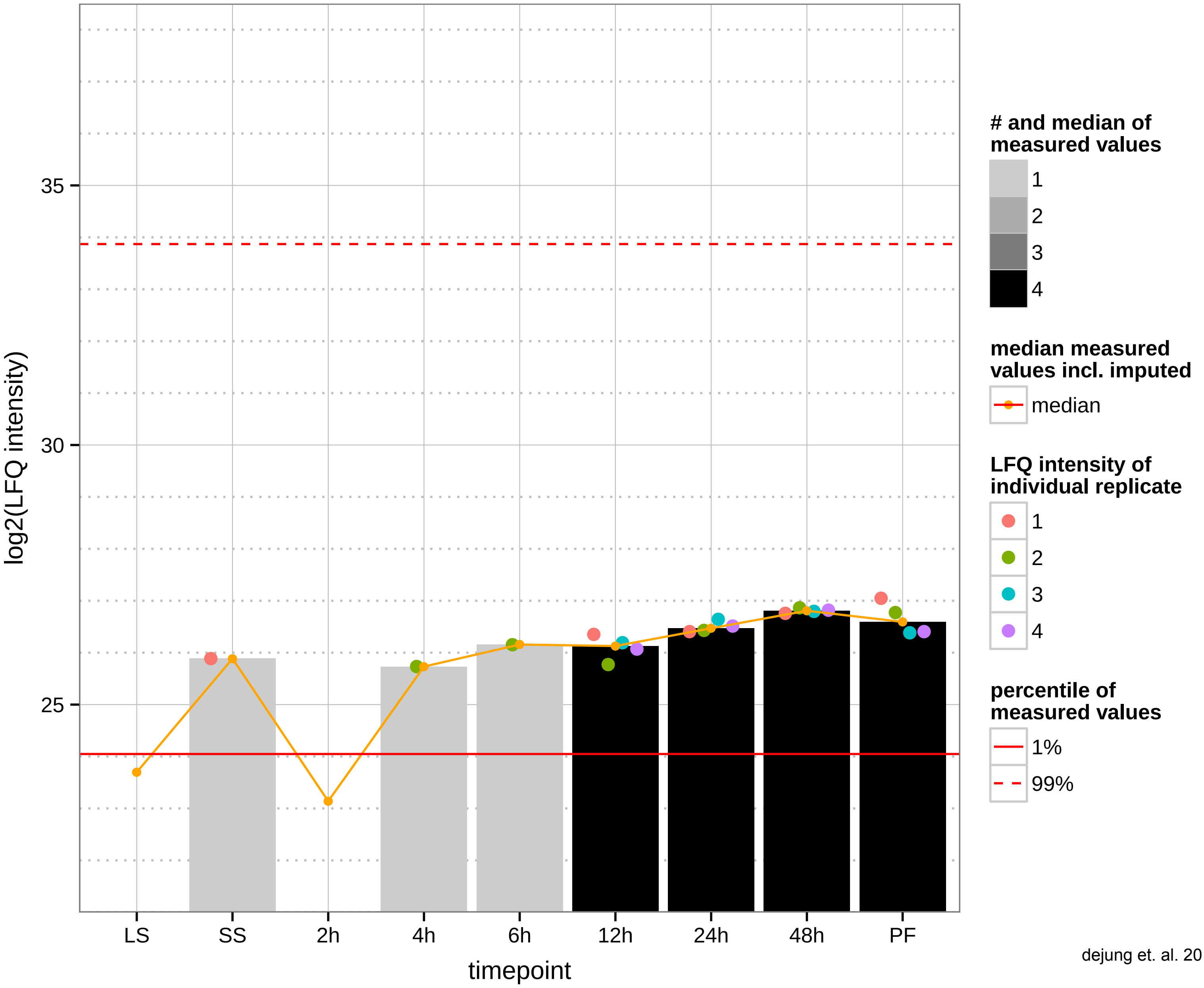
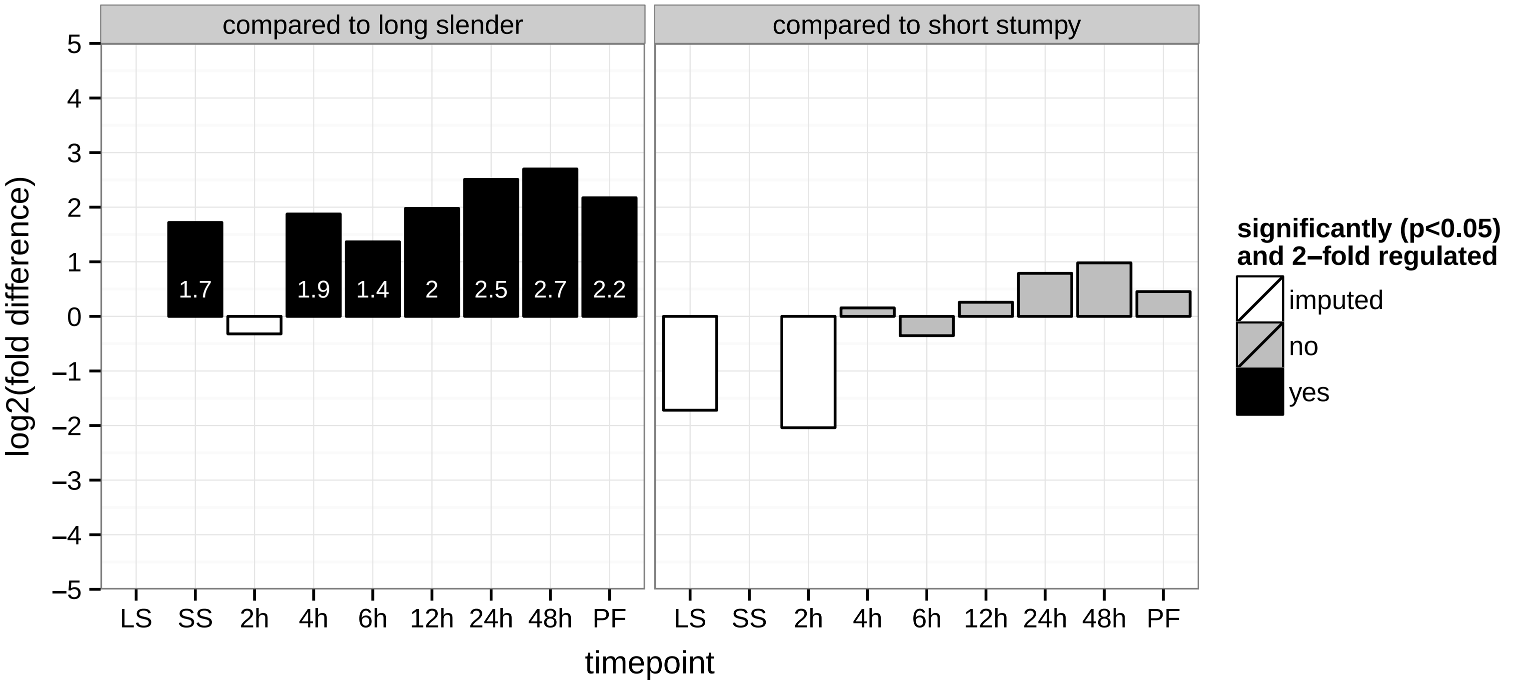
hypothetical protein, conserved
Tb927.10.3580
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

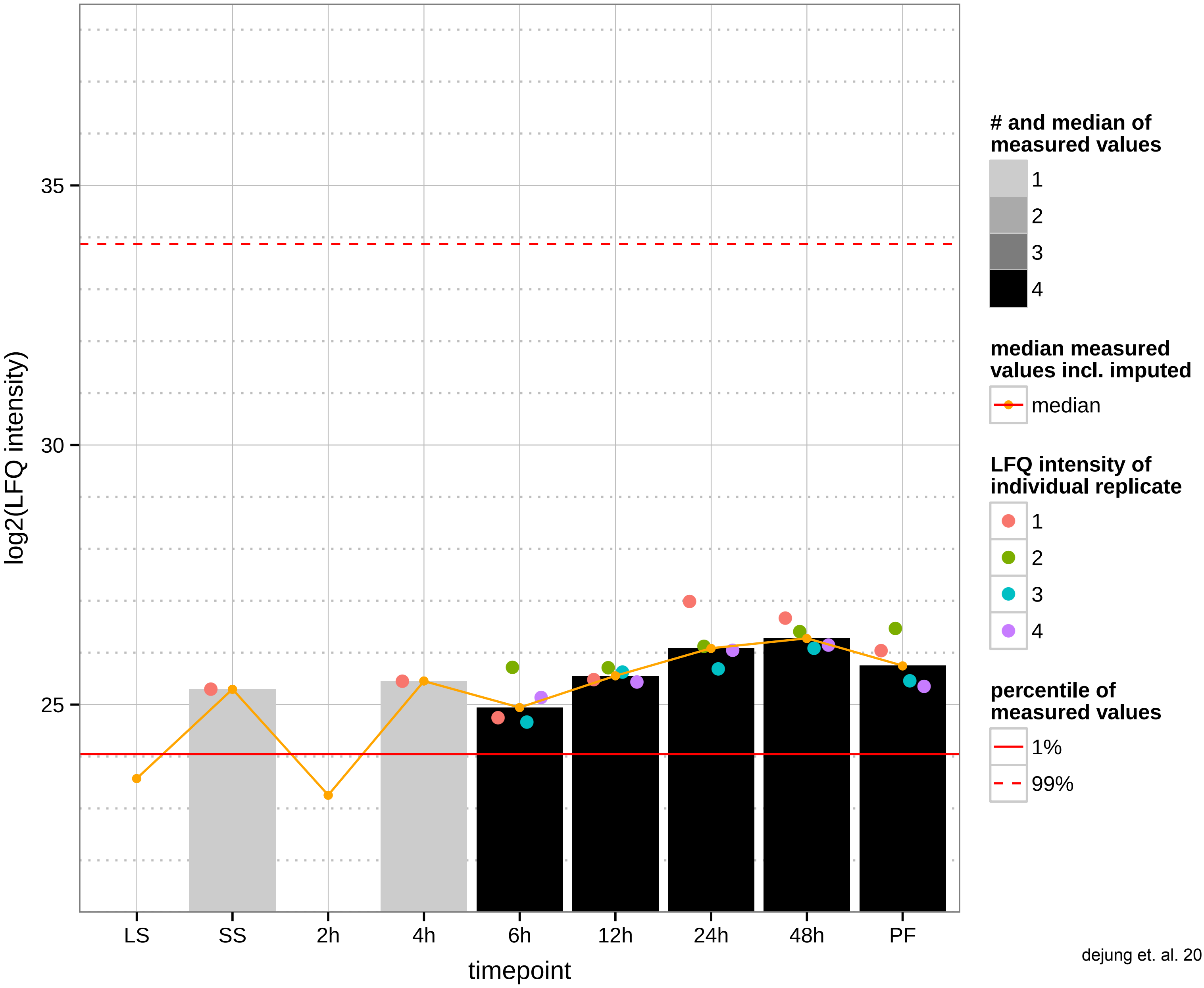




dejung et. al. 2015

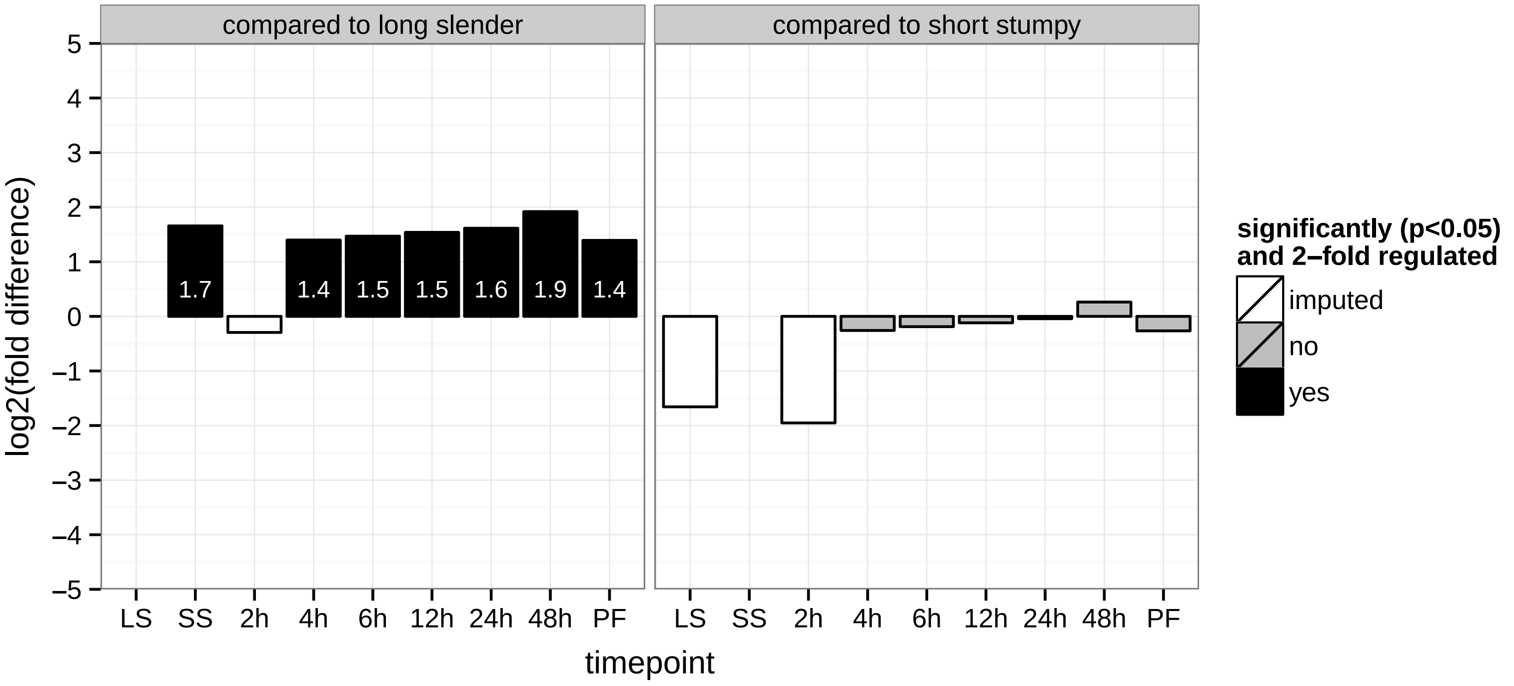
hypothetical protein, conserved
Tb927.10.4220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

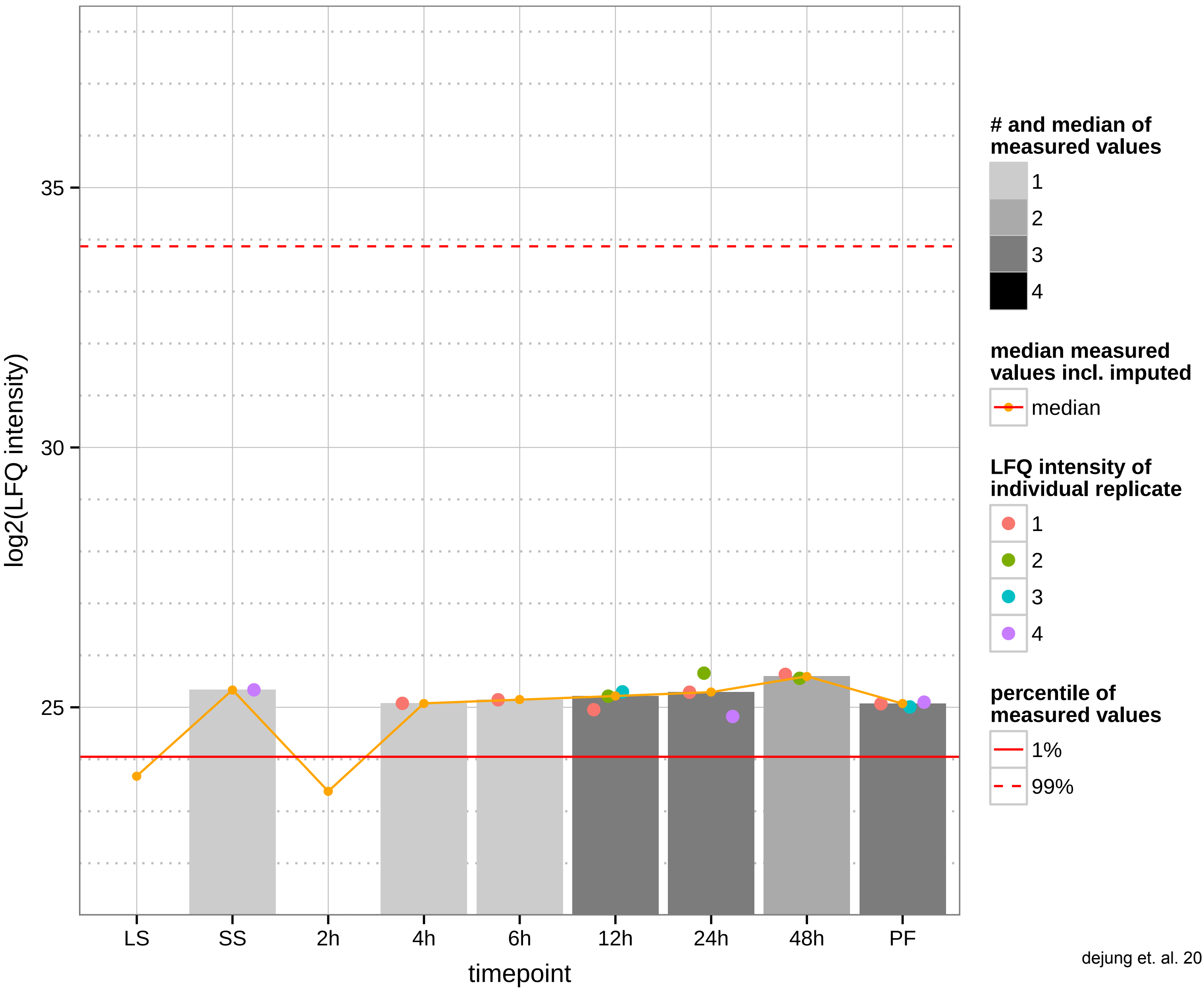




dejung et. al. 2015

caltractin, putative
Tb927.10.6980
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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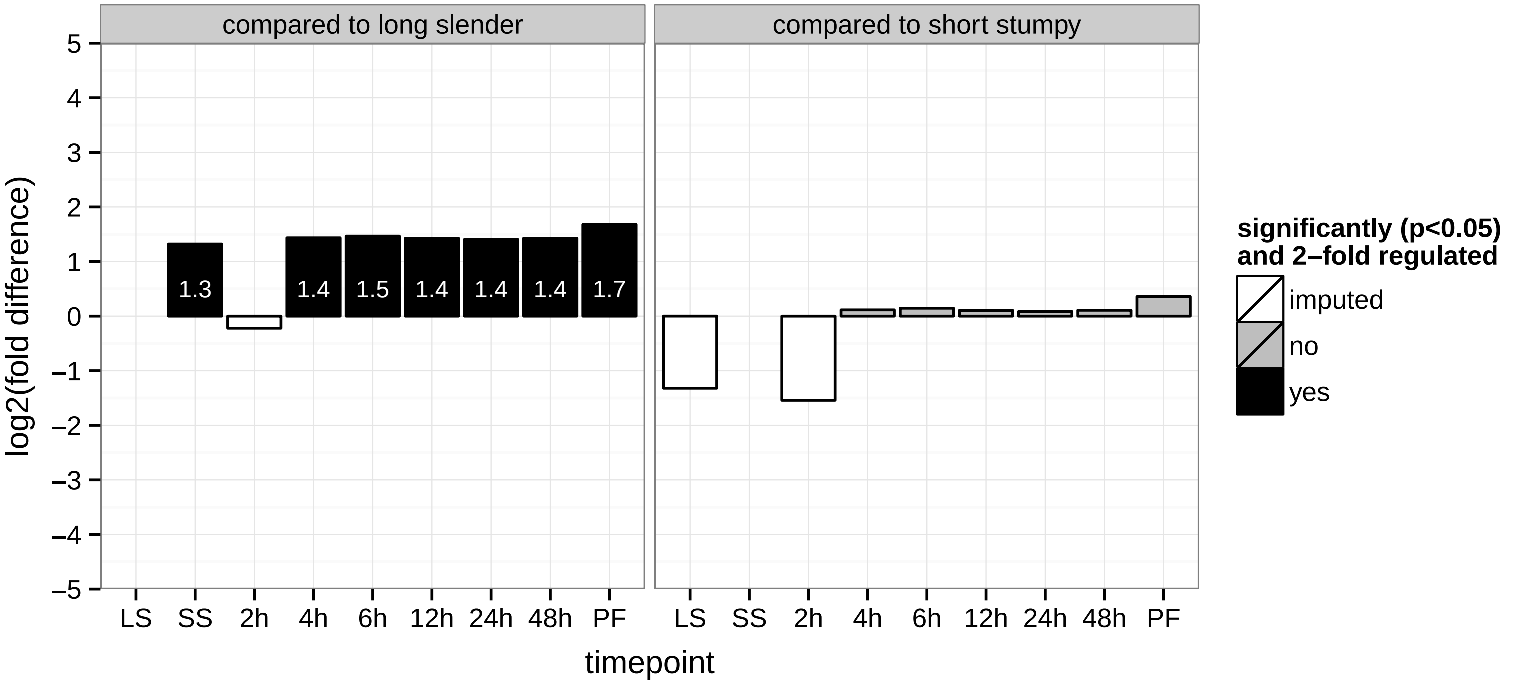
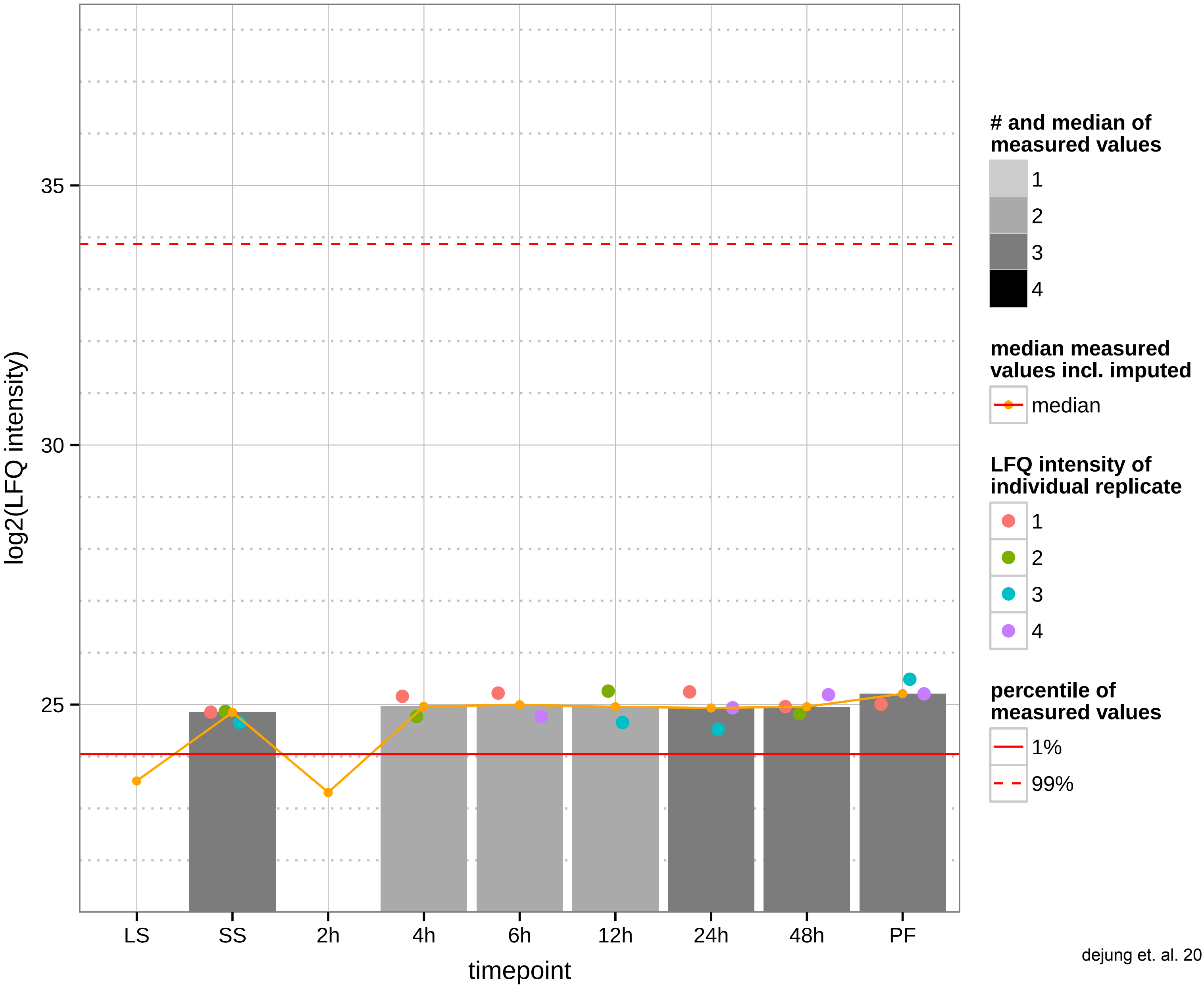
beta–adaptin 3, putative, adaptin complex 3 subunit
Tb927.11.10650
AGOF: null
AGOC: Golgi apparatus, coated pit, membrane coat
AGOP: intracellular protein transport, vesicle–mediated transport
PGOF: binding
PGOC: membrane coat
PGOP: intracellular protein transport, vesicle–mediated transport





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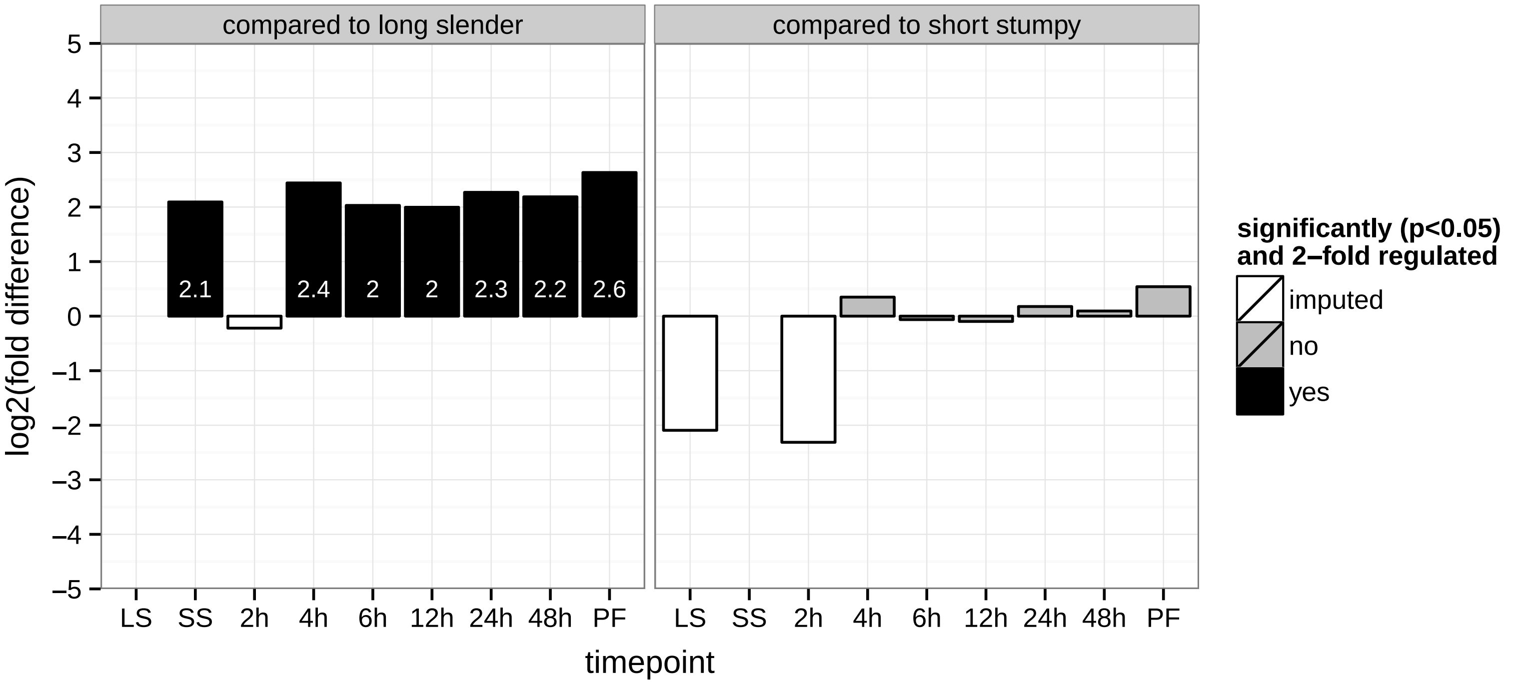
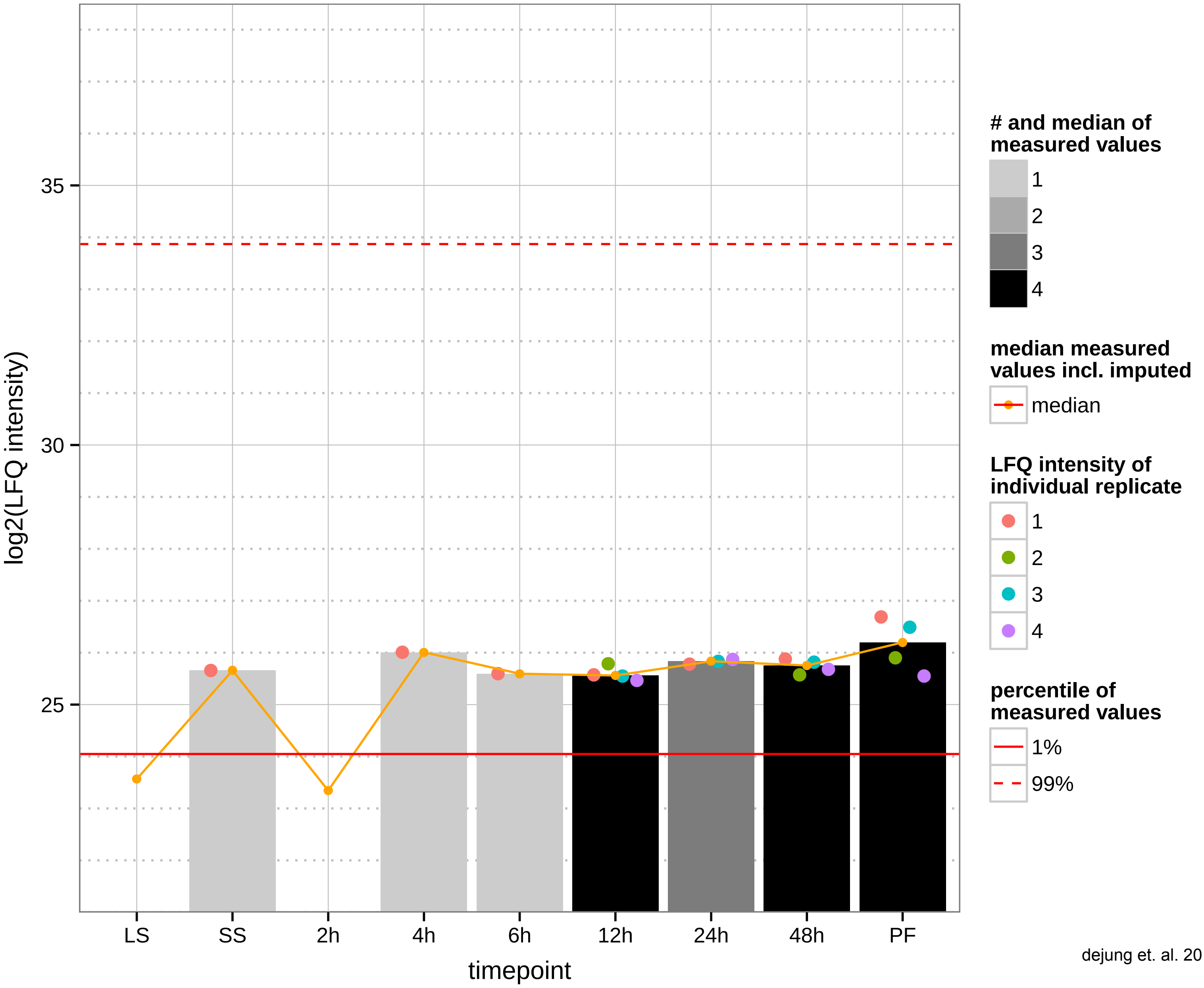
RNA helicase, putative
Tb927.11.12110
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding, zinc ion binding
AGOC: intracellular
AGOP: nucleobase−containing compound metabolic process, transport
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding, protein binding, zinc ion binding
PGOC: null
PGOP: null





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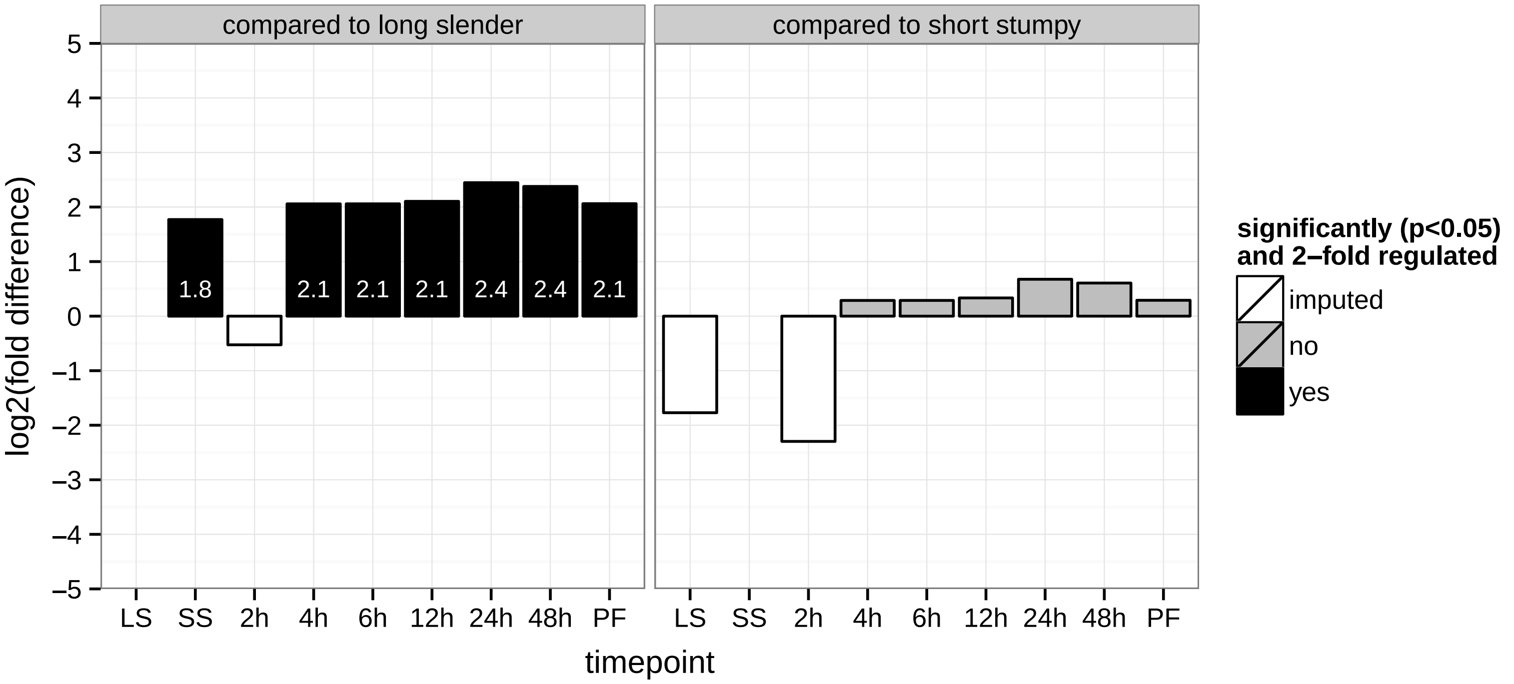
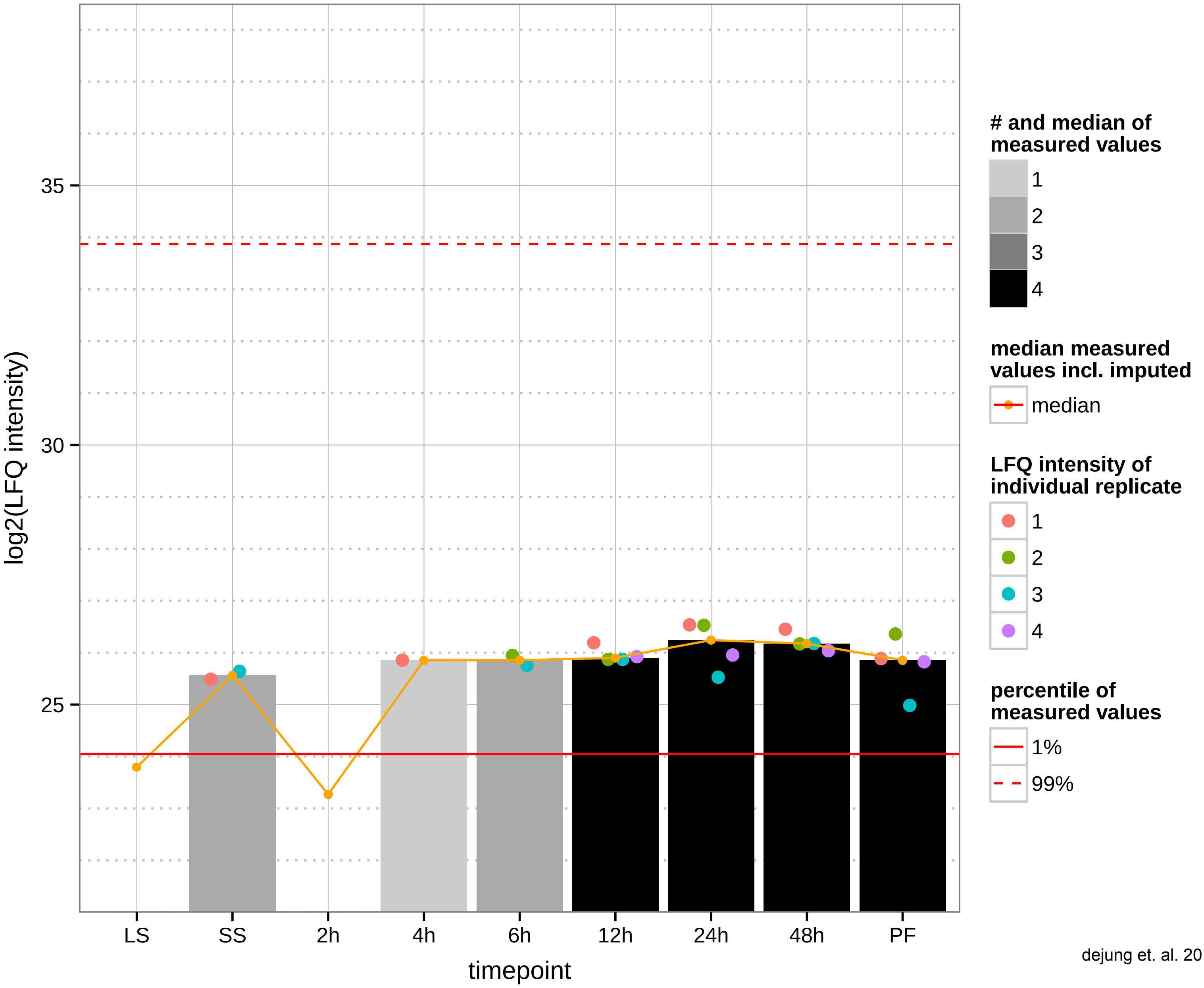
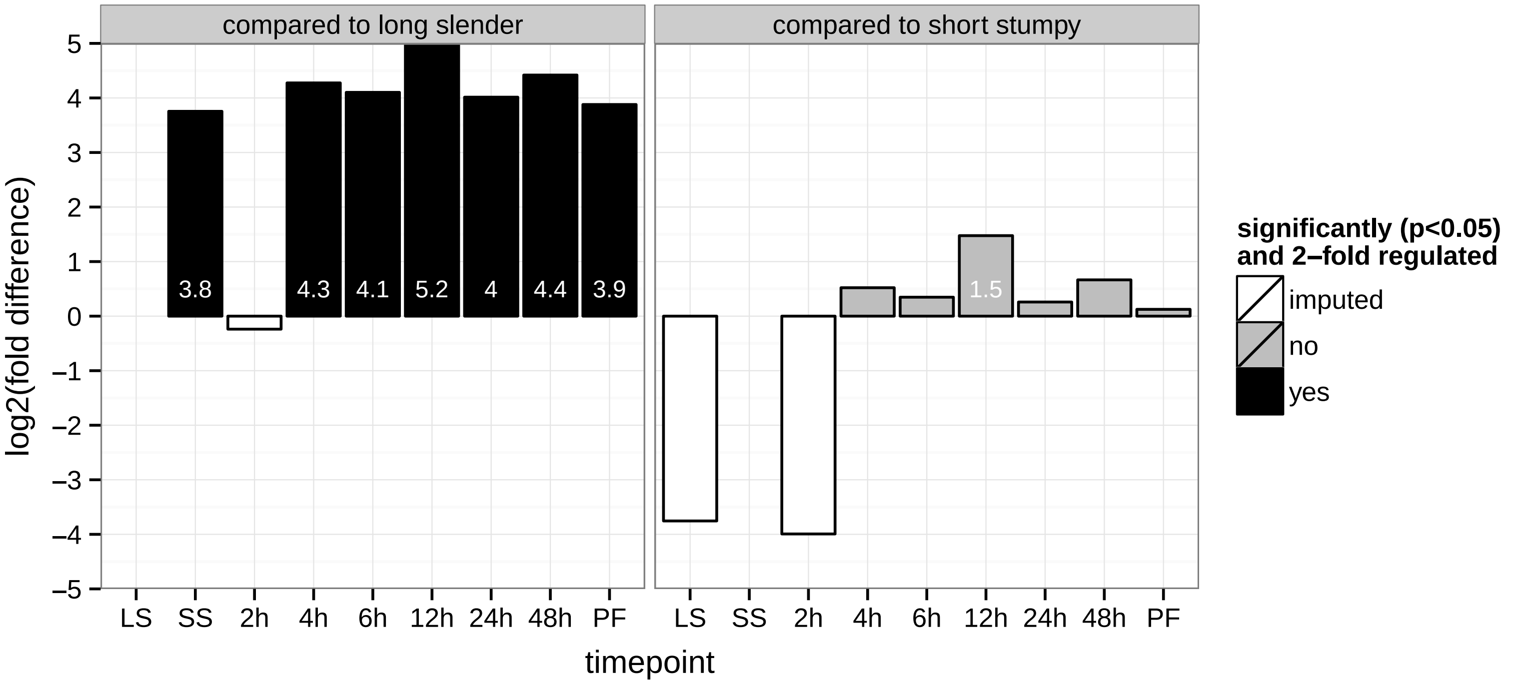
phospholipid:diacylglycerol acyltransferase–like protein
Tb927.11.13220
AGOF: phosphatidylcholine–sterol O–acyltransferase activity
AGOC: null
AGOP: lipid metabolic process
PGOF: O–acyltransferase activity
PGOC: null
PGOP: lipid metabolic process

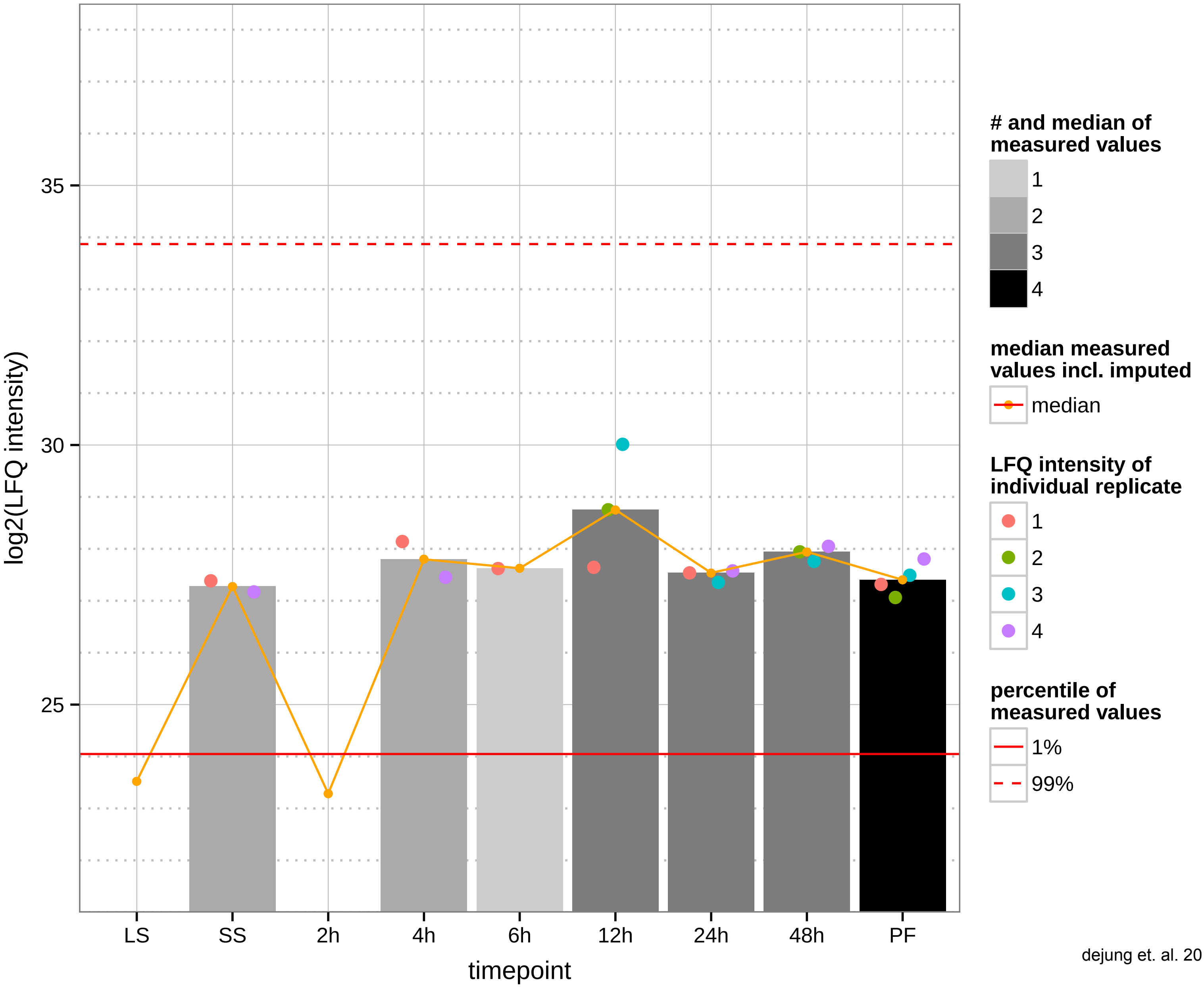




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.16230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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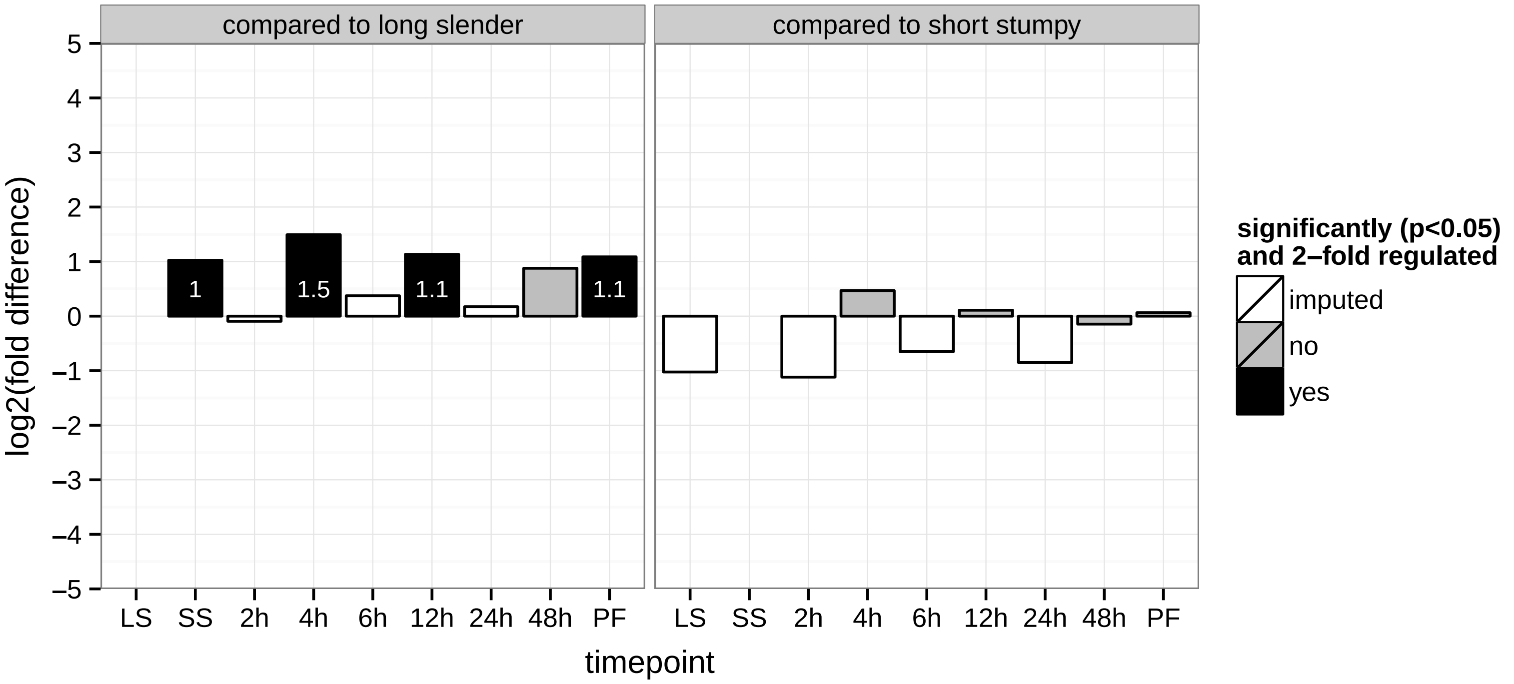
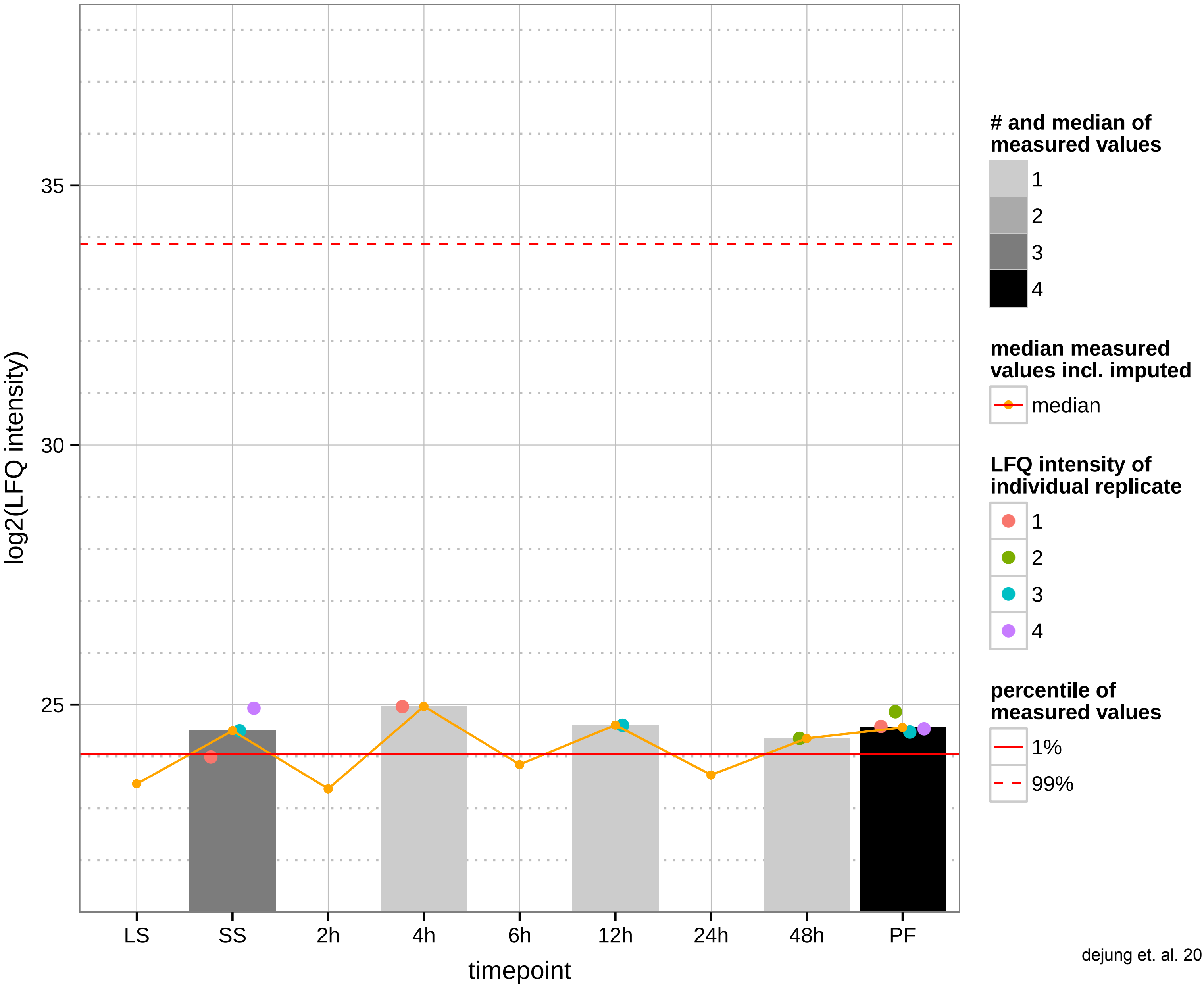
KREPB4, RNA–editing complex protein (KREPB4)
Tb927.11.2990
AGOF: RNA binding
AGOC: mRNA editing complex, mitochondrial mRNA editing complex, mitochondrion
AGOP: RNA modification
PGOF: null
PGOC: null
PGOP: null





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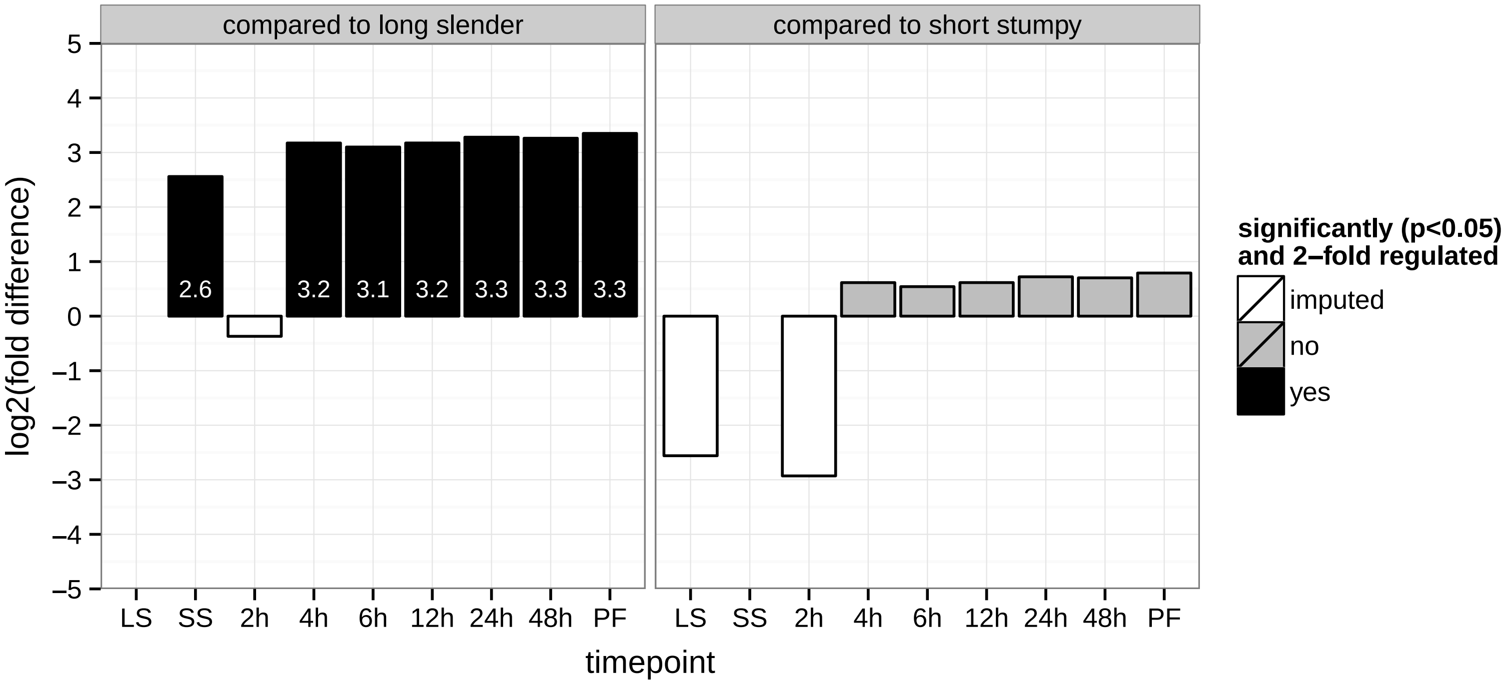
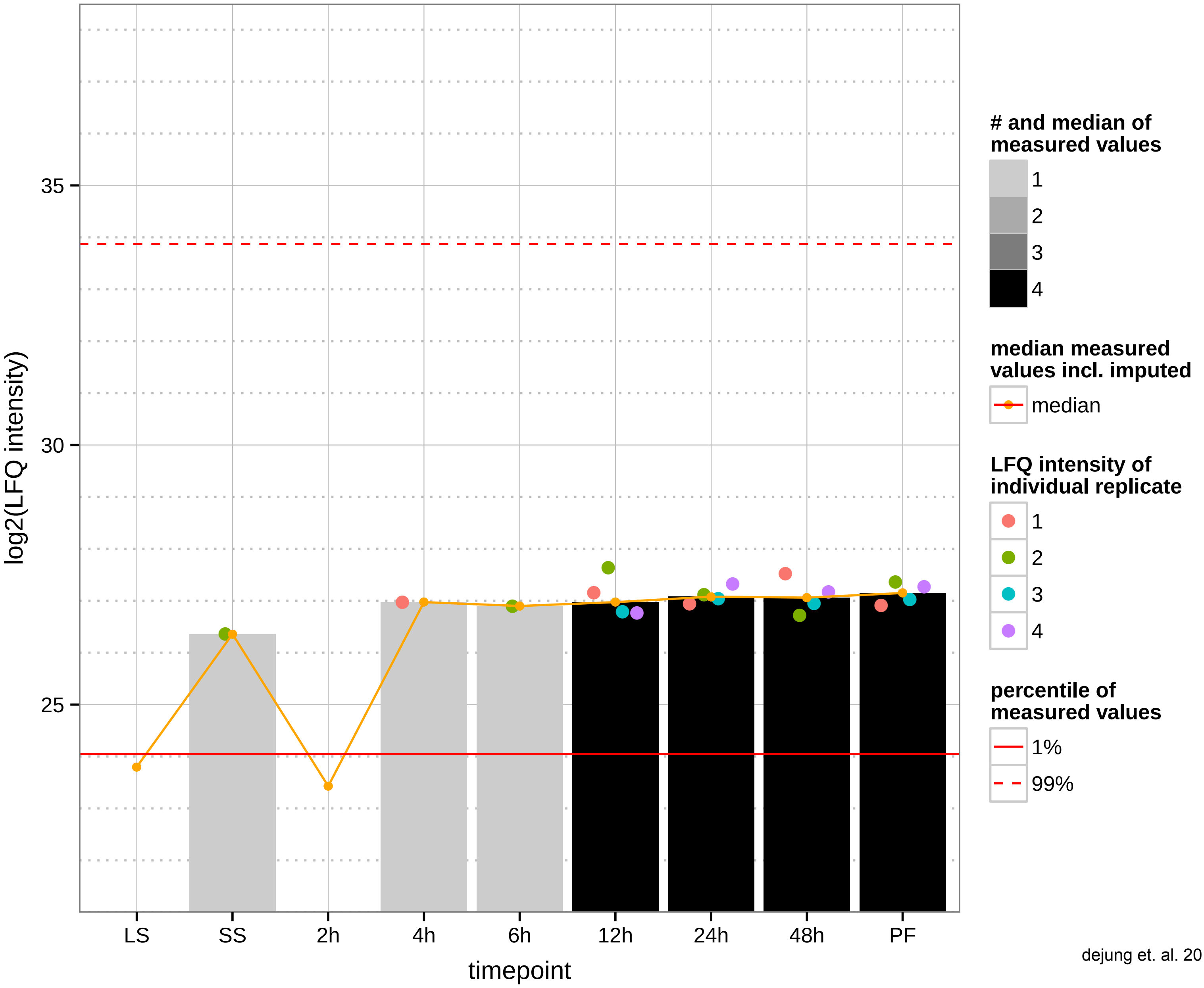
glycosyltransferase family–like protein, putative
Tb927.11.3900
AGOF: null
AGOC: null
AGOP: lipopolysaccharide biosynthetic process
PGOF: null
PGOC: null
PGOP: lipopolysaccharide biosynthetic process





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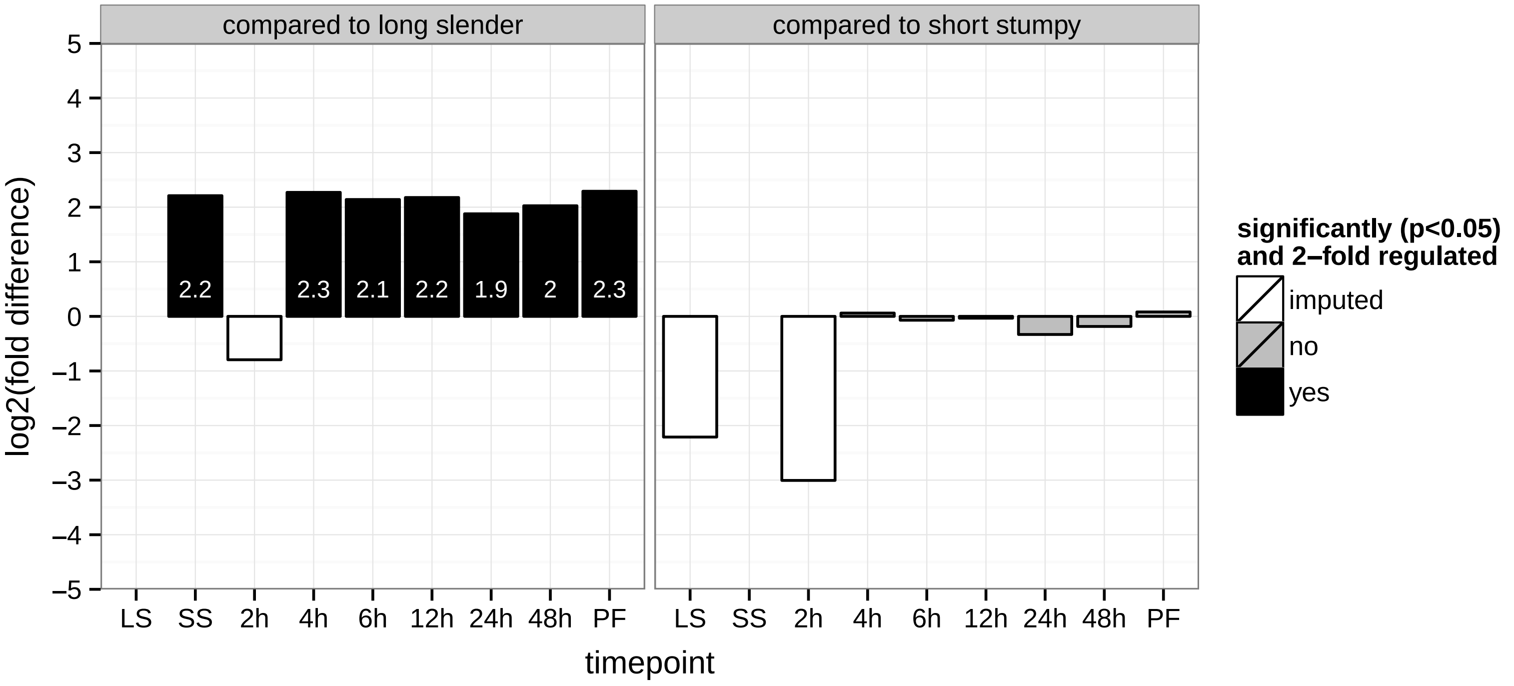
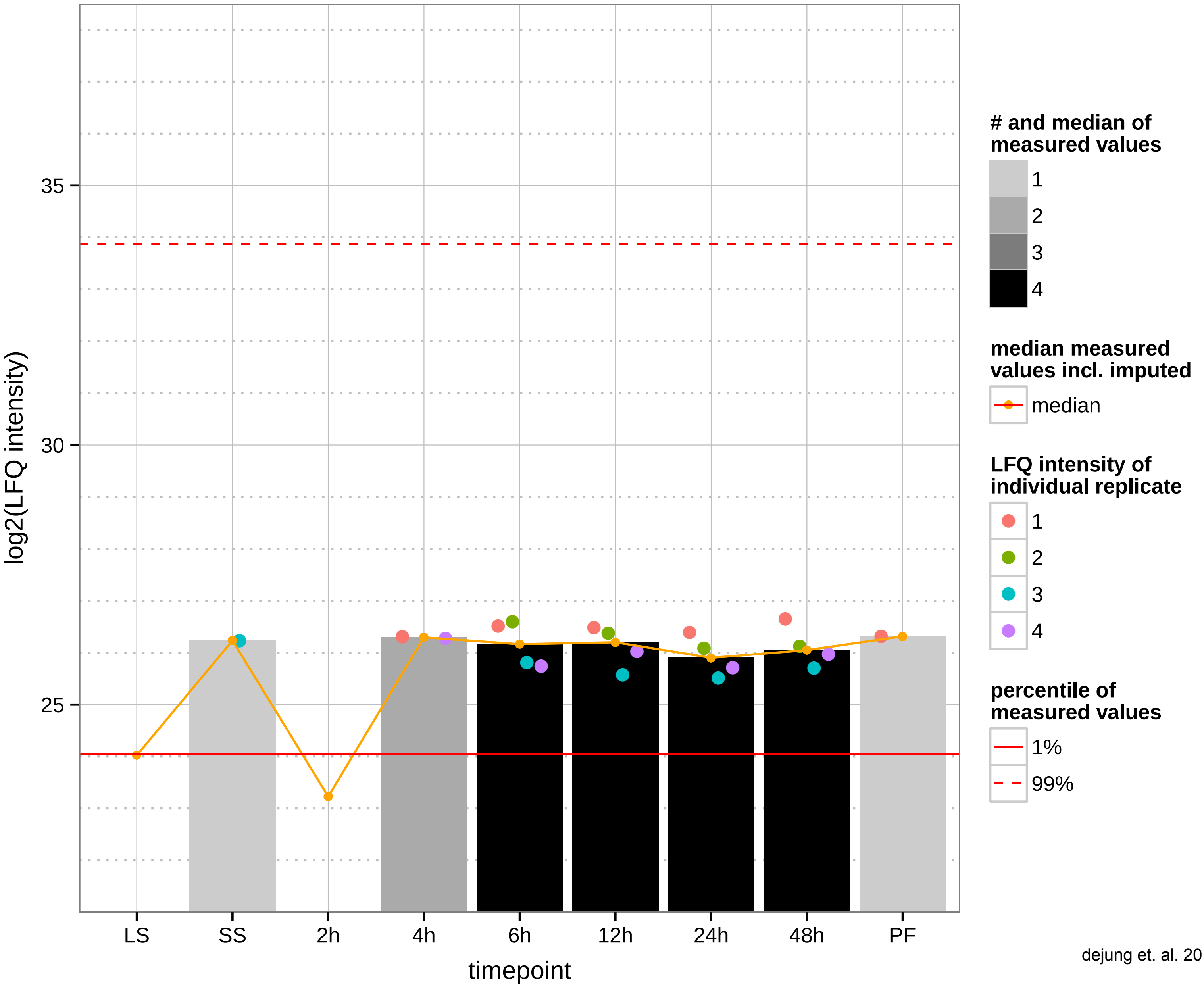
NADH–cytochrome b5 reductase–like protein
Tb927.11.6970
AGOF: cytochrome–b5 reductase activity, electron carrier activity
AGOC: mitochondrion
AGOP: oxidation–reduction process
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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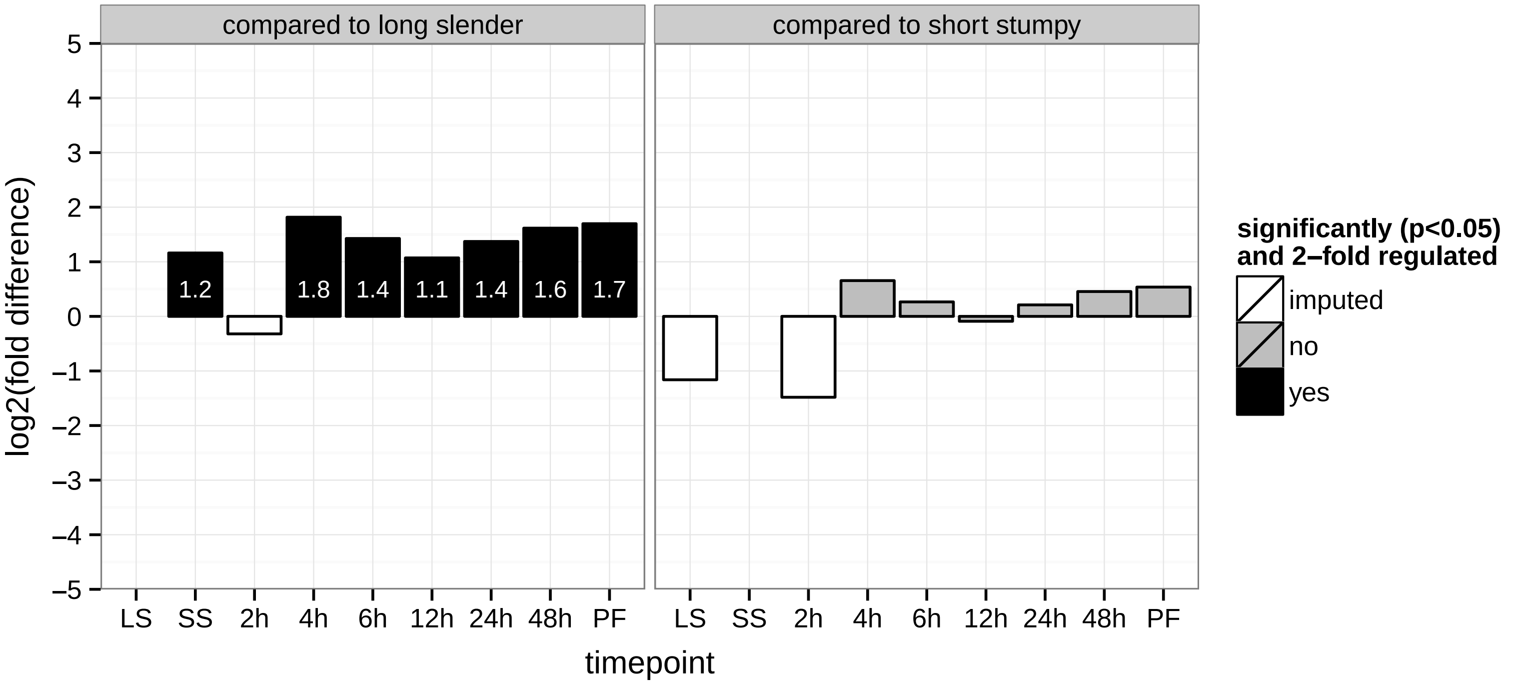
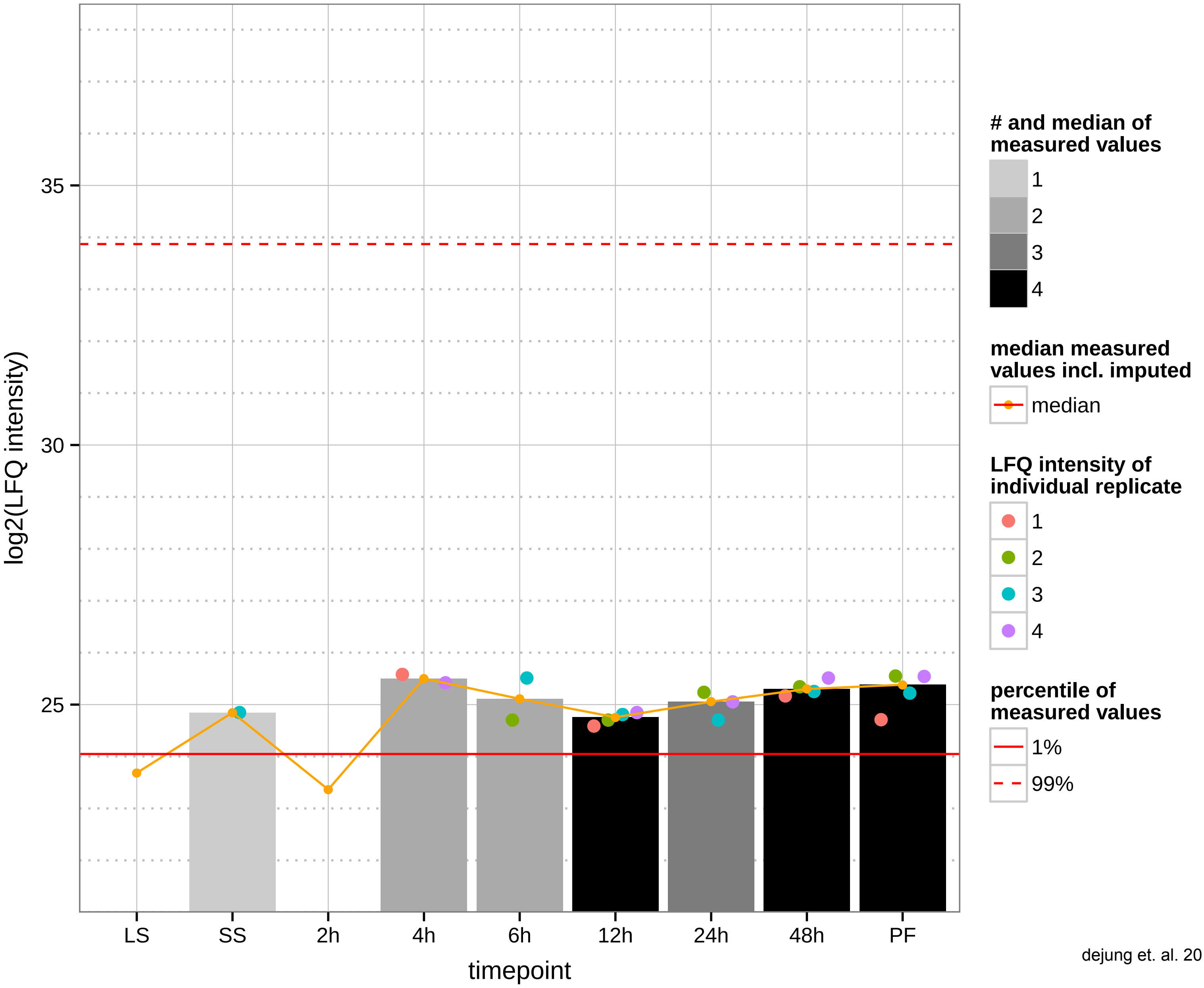
prenyltransferase, putative
Tb927.11.9360
AGOF: 4−hydroxybenzoate octaprenyltransferase activity
AGOC: integral to membrane, mitochondrion
AGOP: ubiquinone biosynthetic process
PGOF: prenyltransferase activity
PGOC: integral to membrane
PGOP: null





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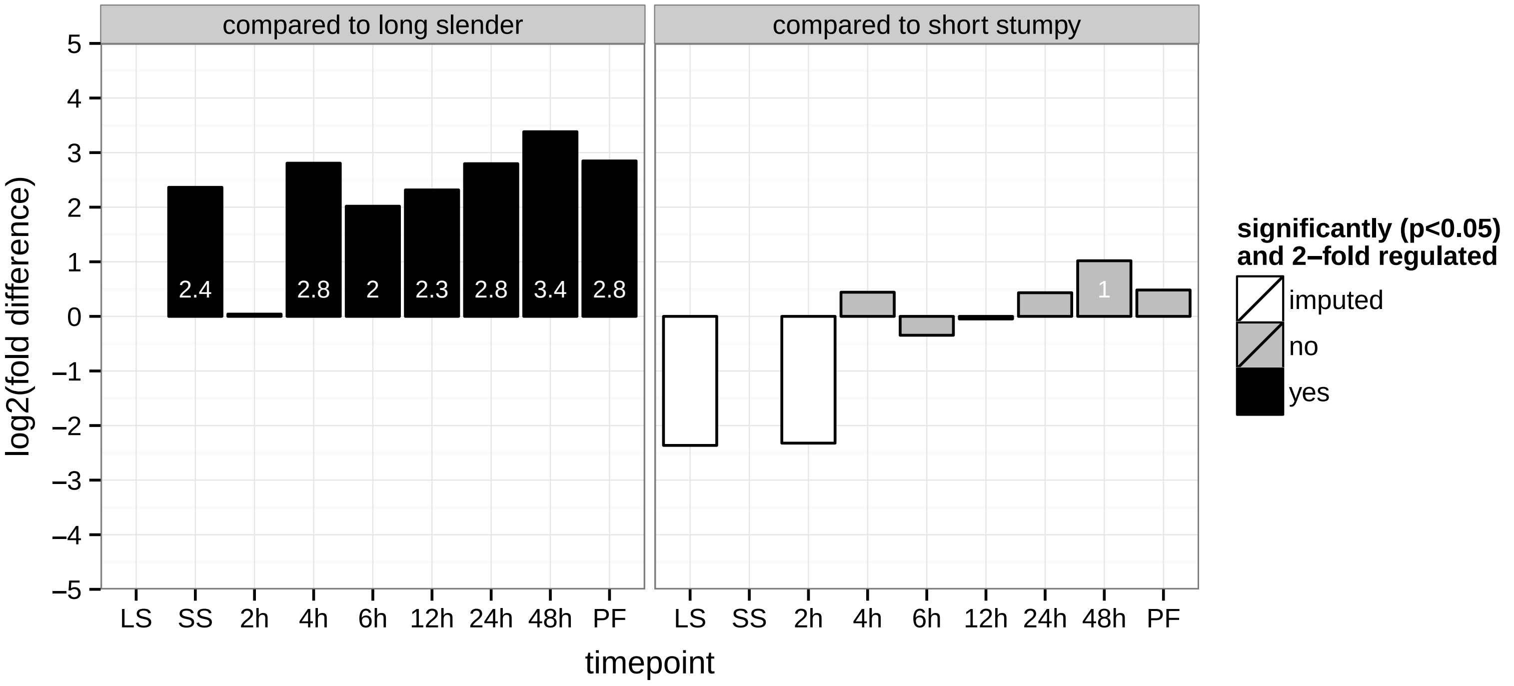
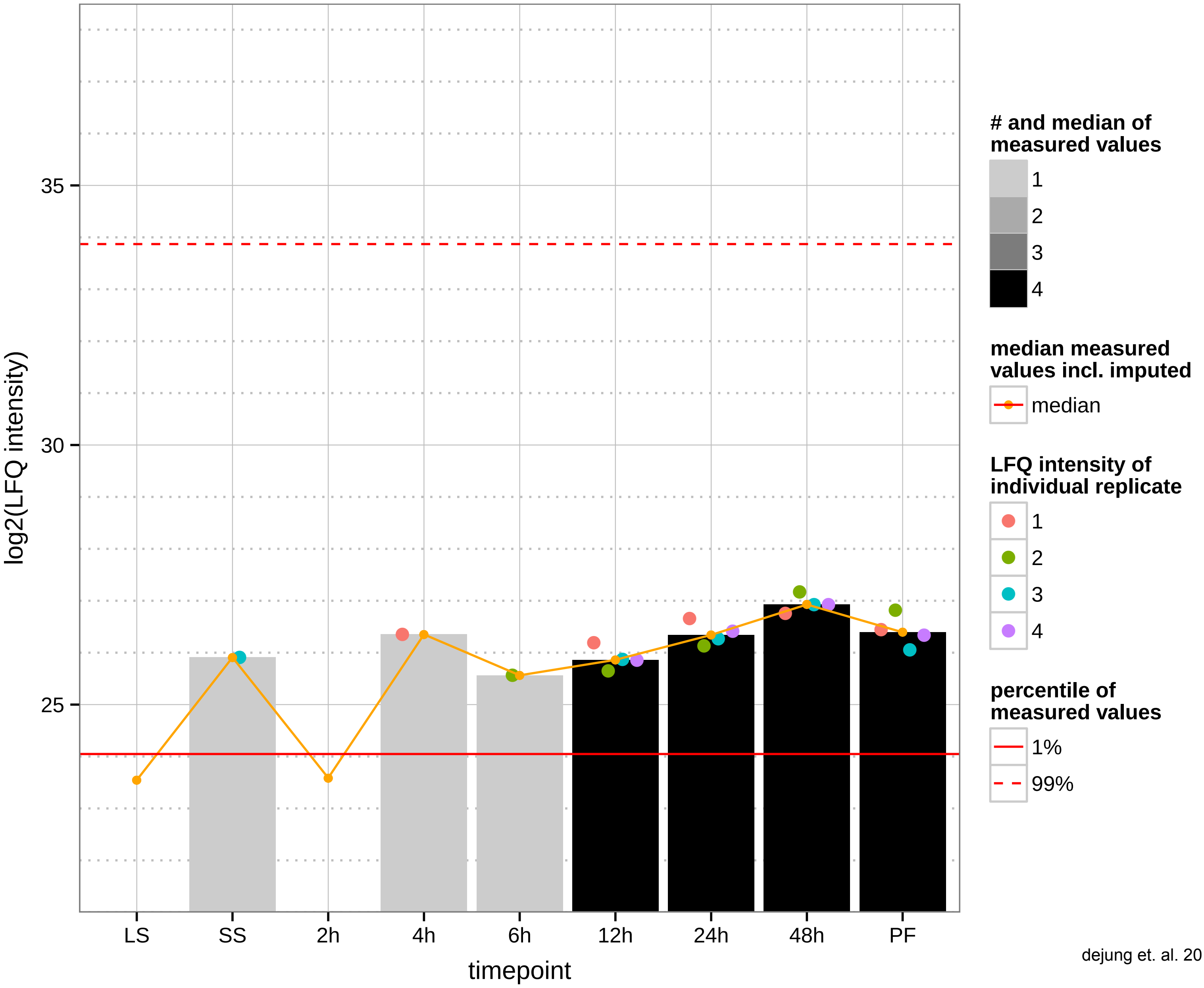
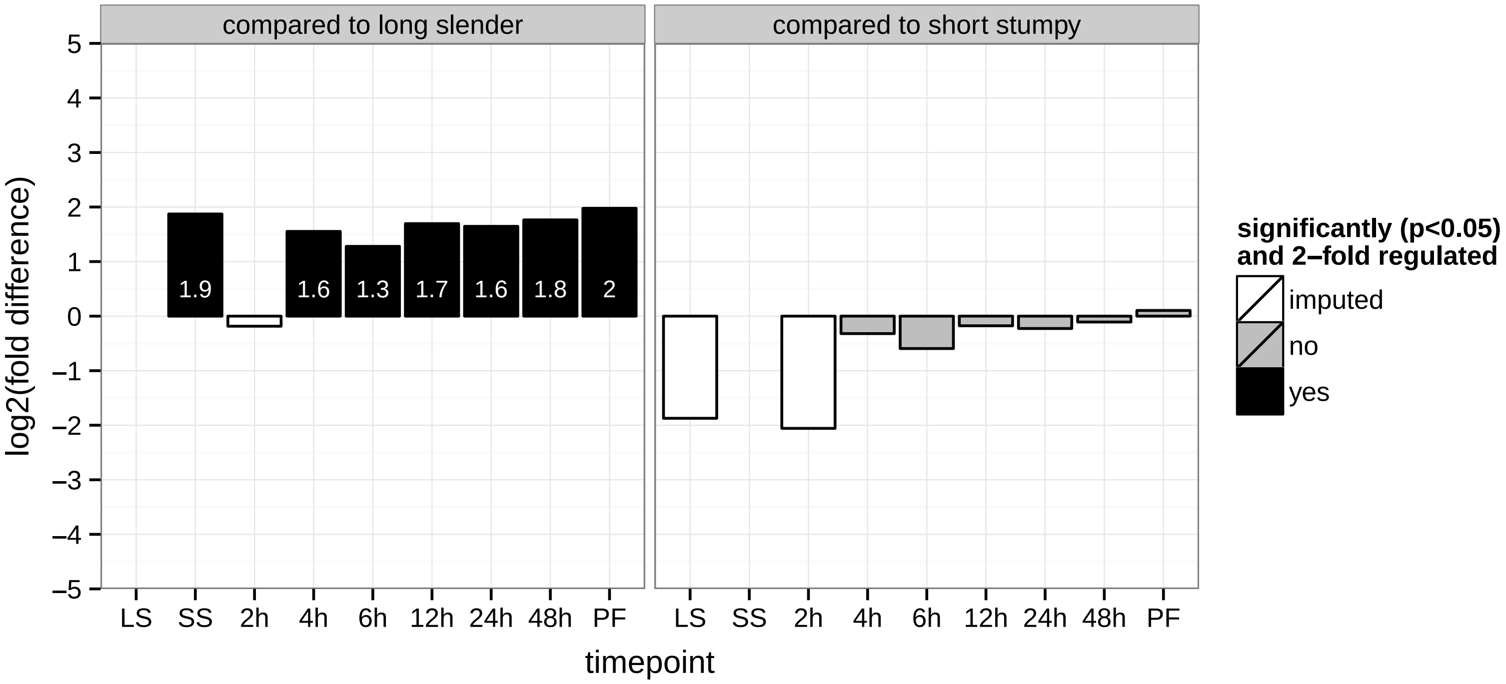
DNA polymerase delta catalytic subunit, putative
Tb927.2.1800
AGOF: DNA binding, DNA−directed DNA polymerase activity, nucleotide binding
AGOC: null
AGOP: DNA replication
PGOF: DNA binding, DNA−directed DNA polymerase activity, nucleic acid binding, nucleotide binding
PGOC: null
PGOP: DNA replication, nucleobase−containing compound metabolic process

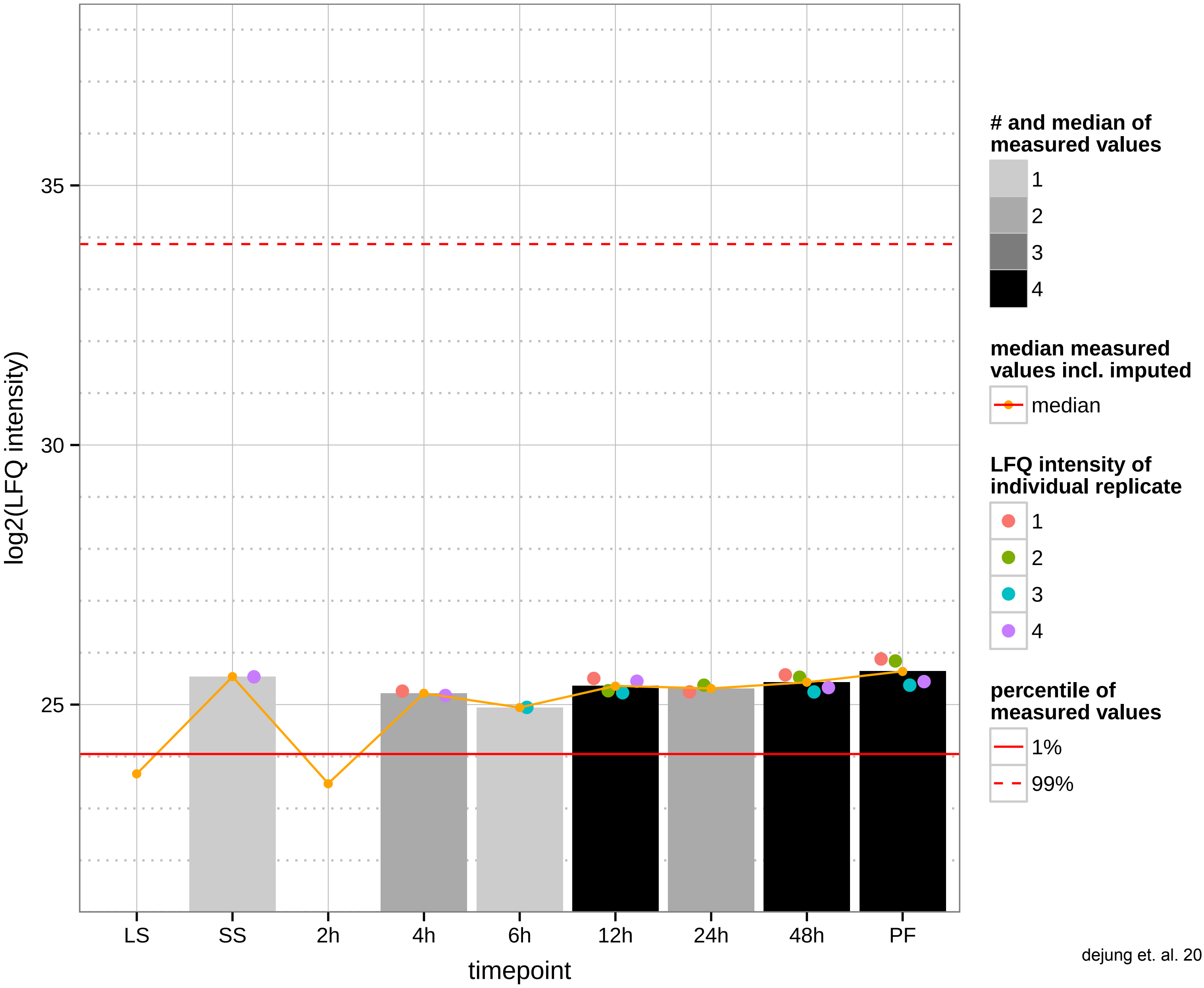




dejung et. al. 2015

hypothetical protein, conserved
Tb927.2.2370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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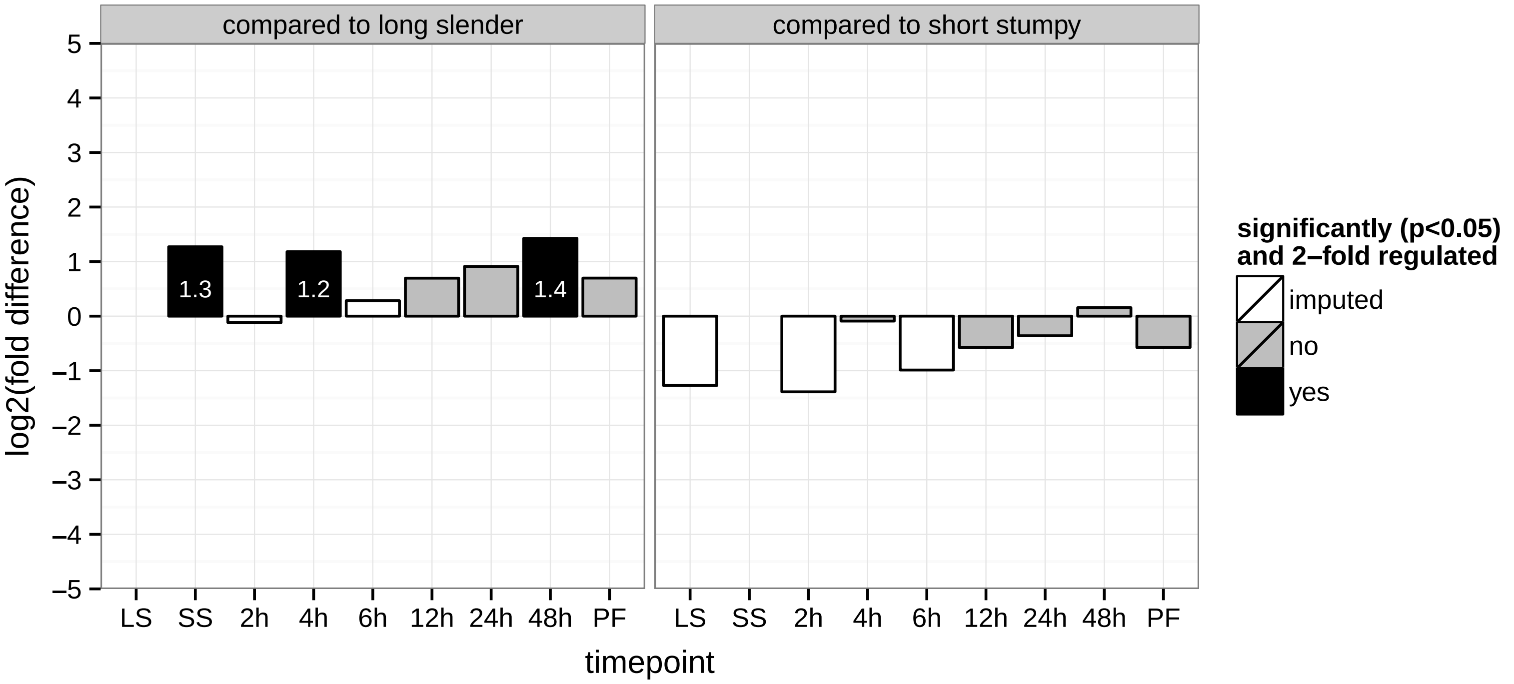
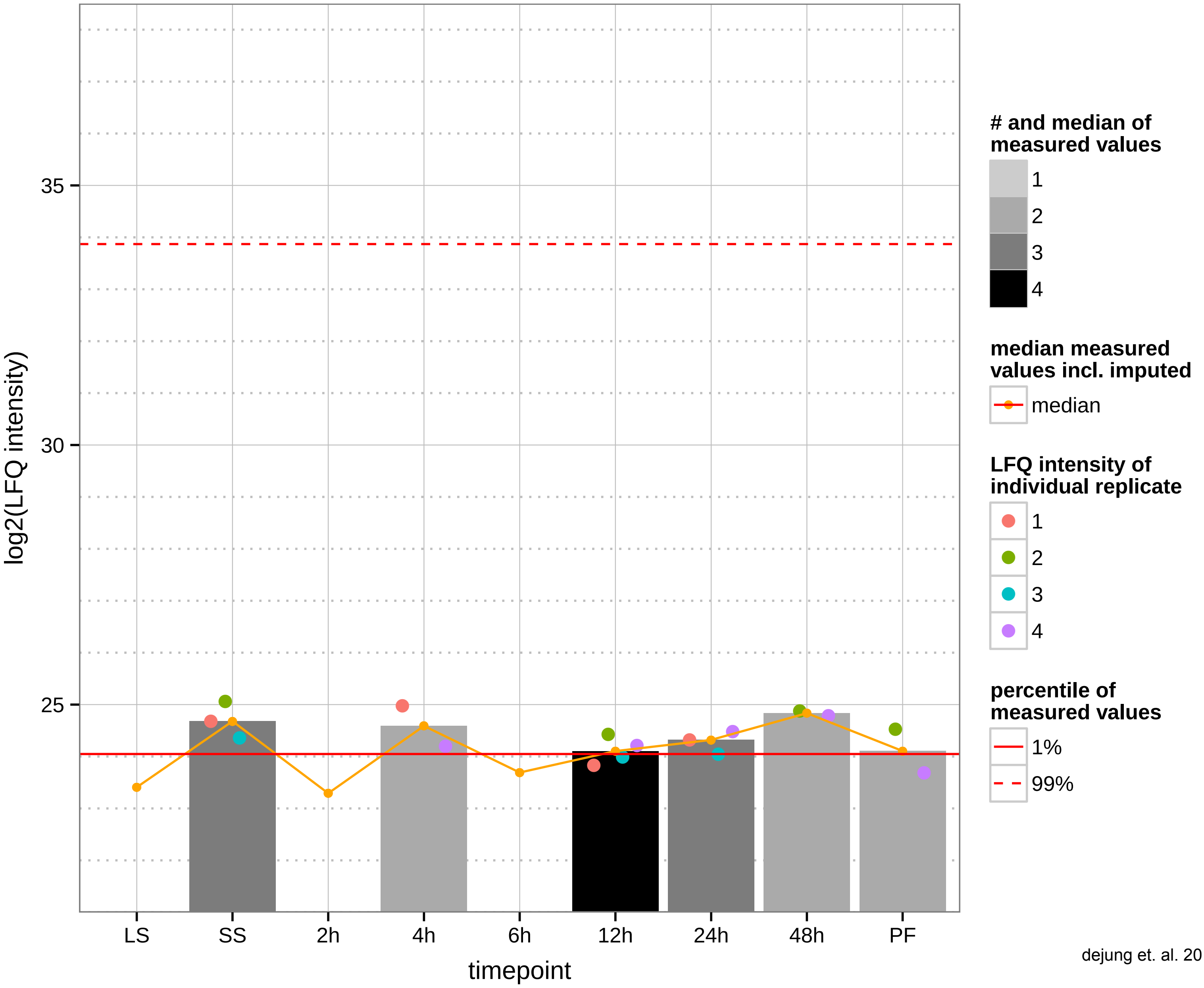
hypothetical protein, conserved
Tb927.2.6080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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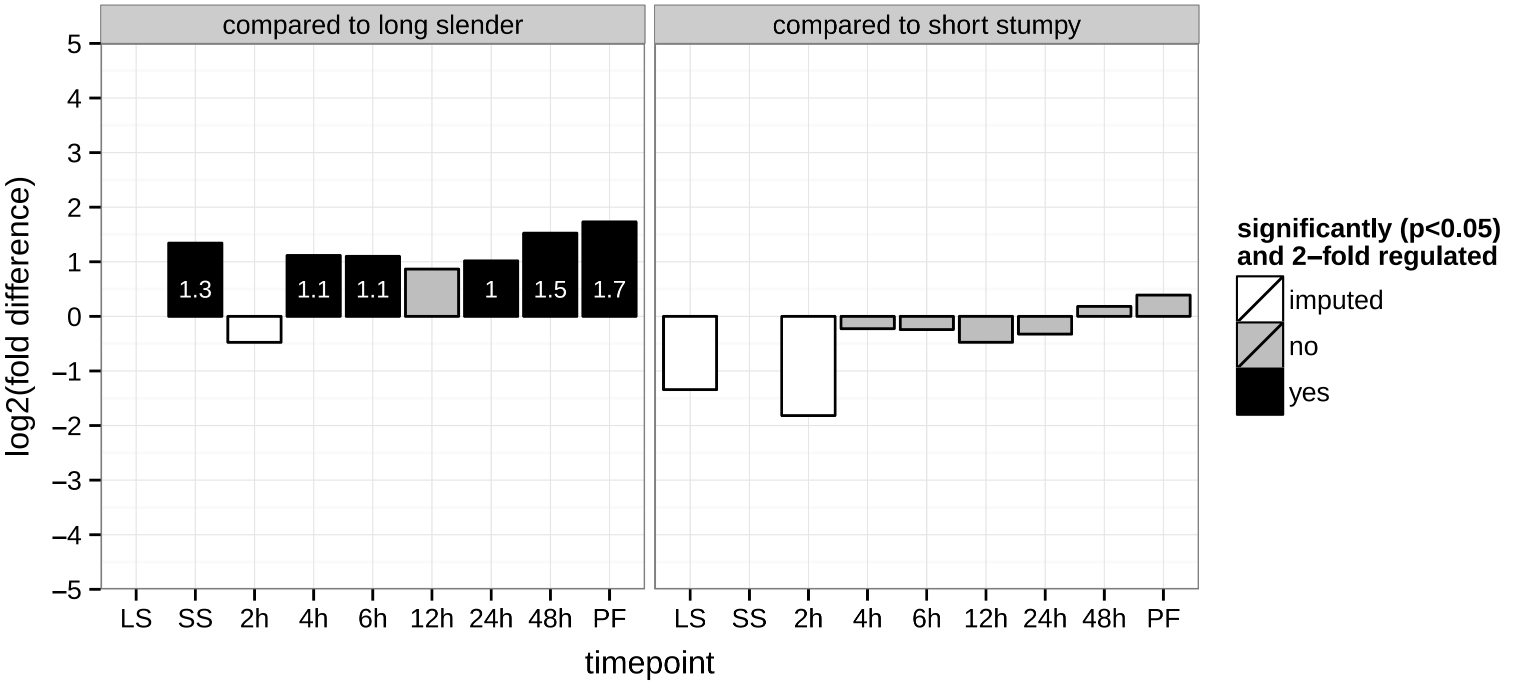
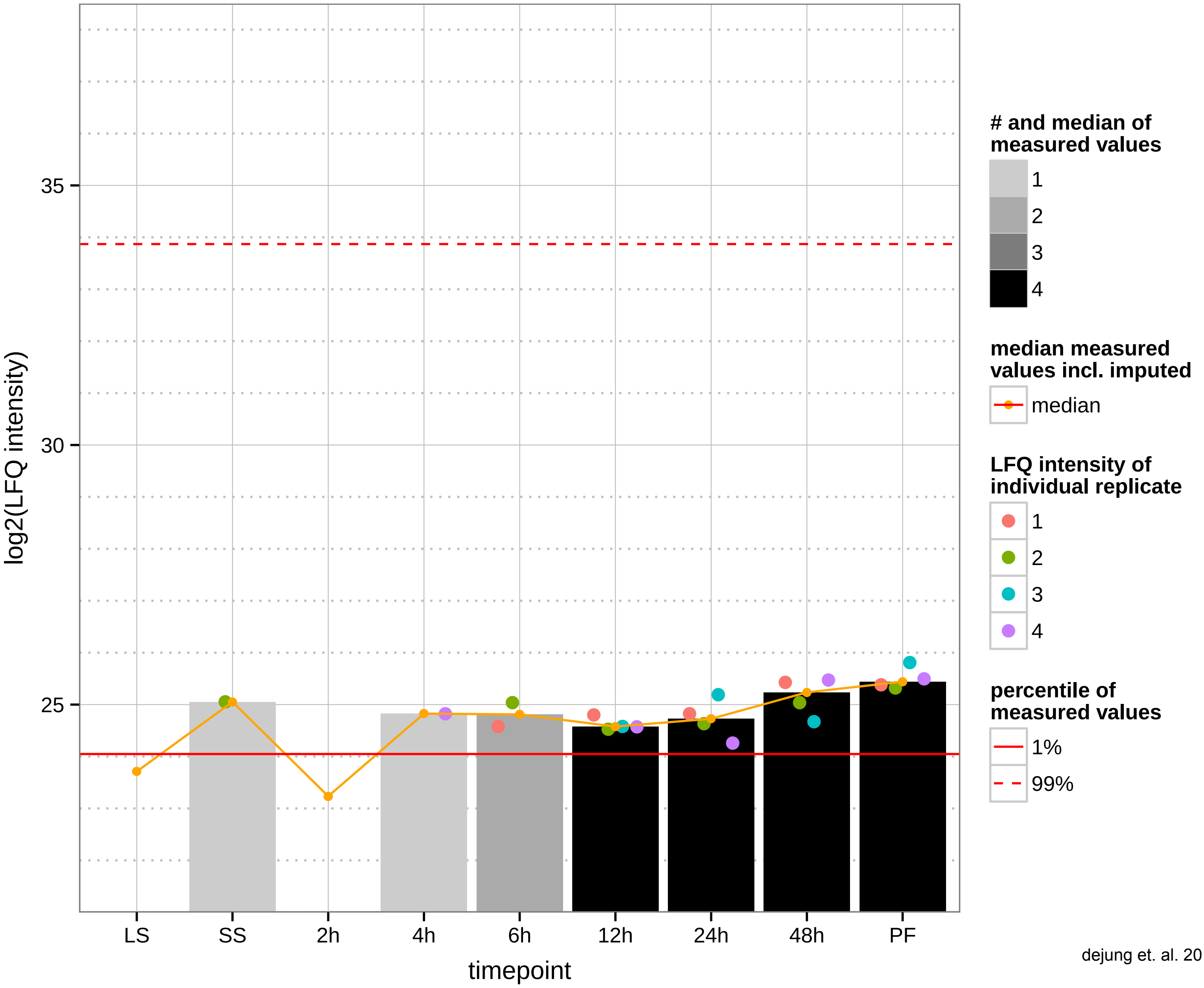
hypothetical protein, conserved
Tb927.3.1100
AGOF: exonuclease activity, nucleic acid binding
AGOC: intracellular, mitochondrion
AGOP: null
PGOF: exonuclease activity, nucleic acid binding
PGOC: intracellular
PGOP: null





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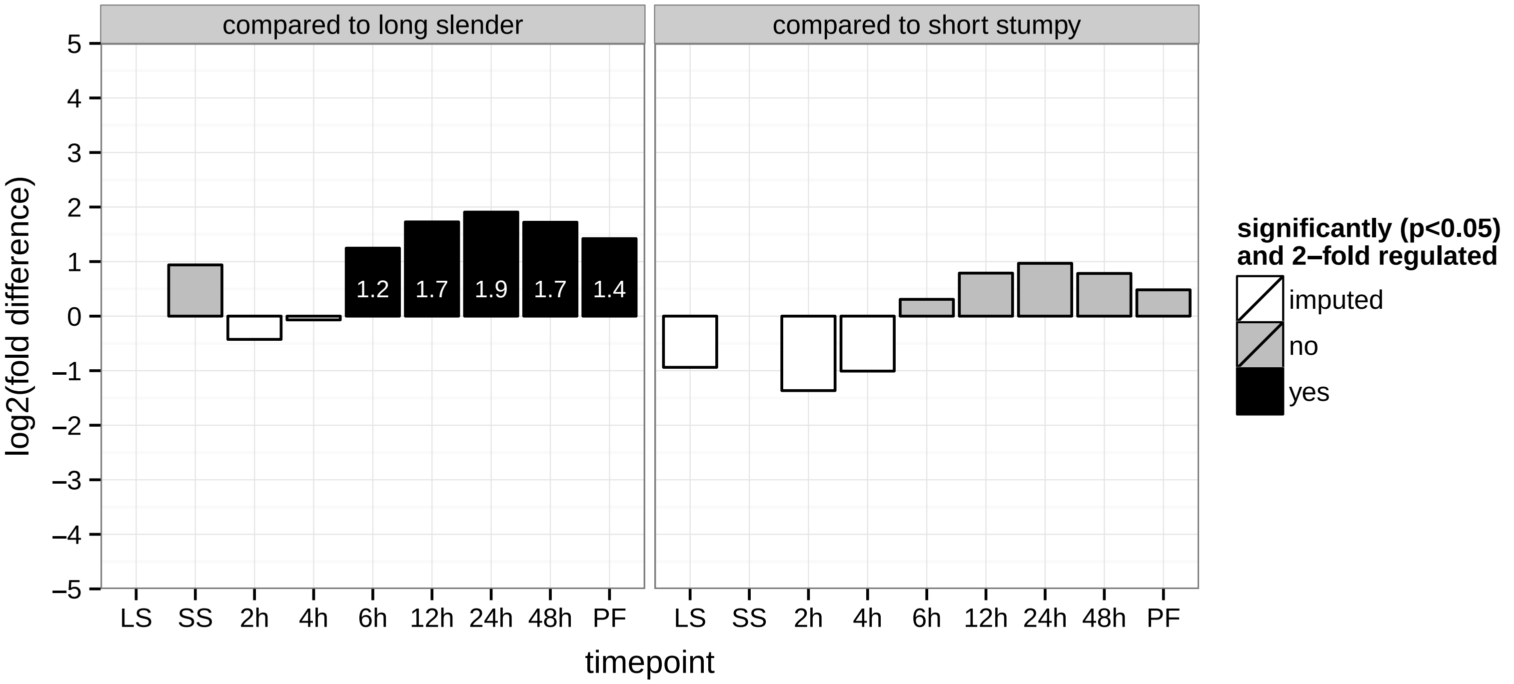
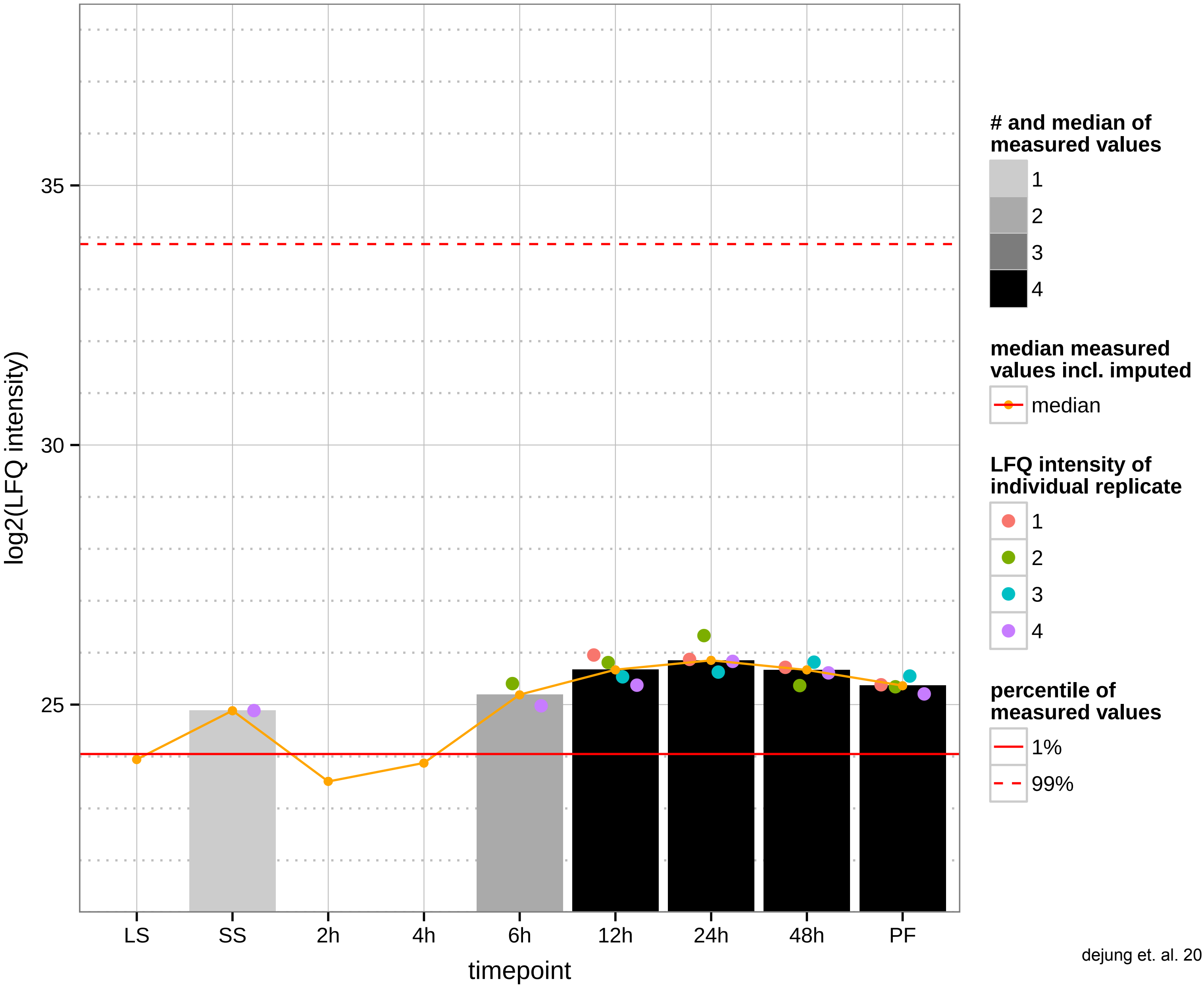
hypothetical protein, conserved
Tb927.3.2300
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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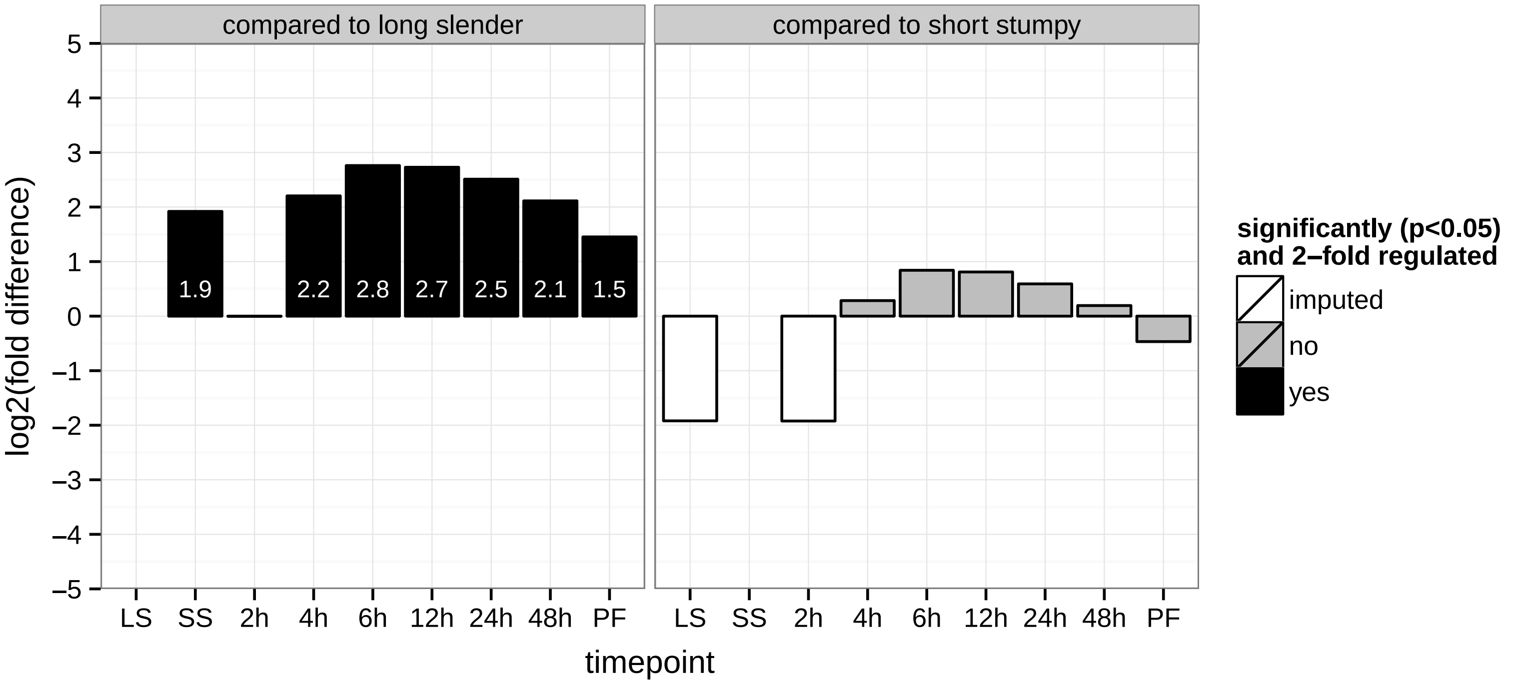
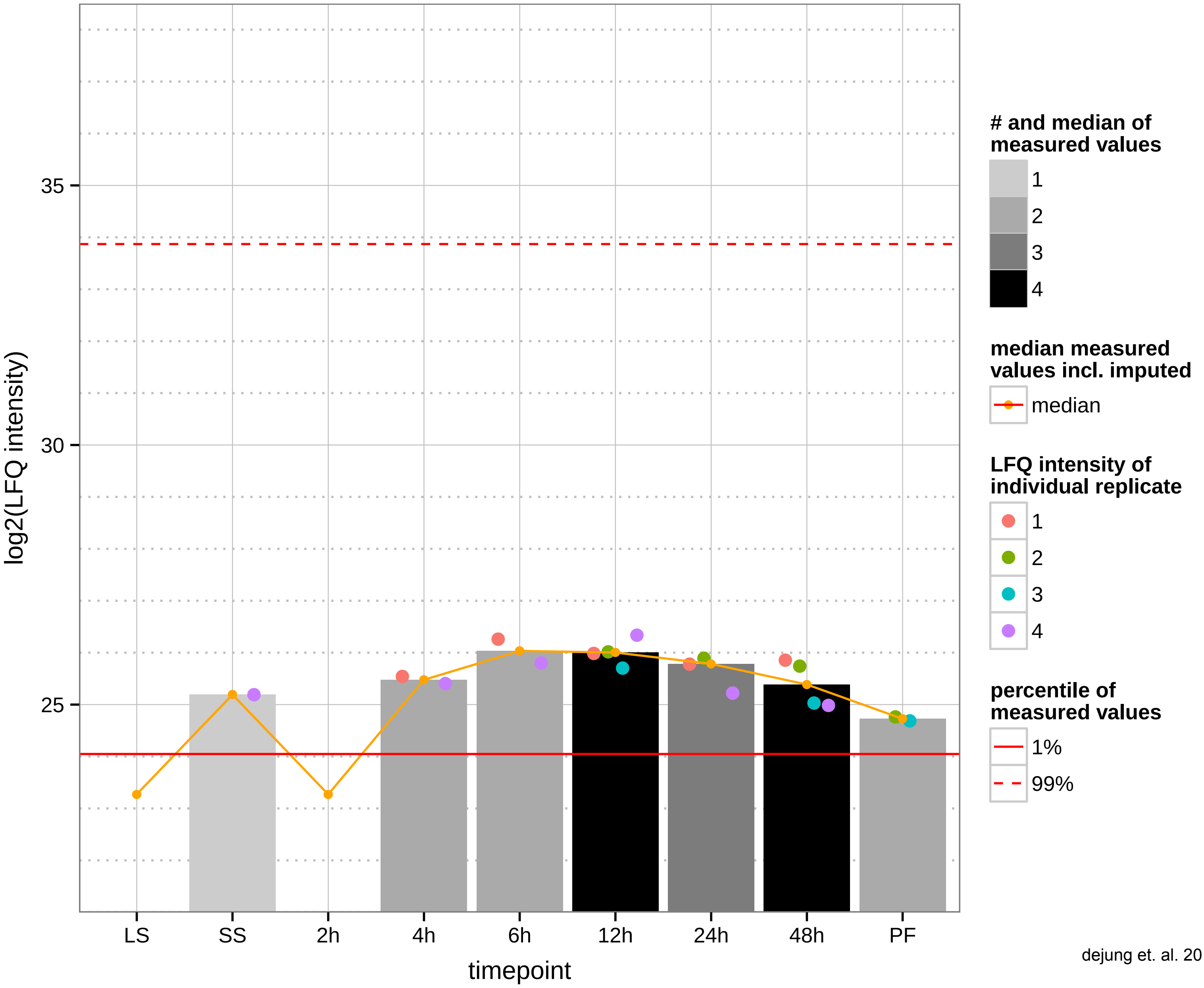
ubiquinone biosynthesis protein COQ7 homolog, putative
Tb927.3.4890
AGOF: null
AGOC: mitochondrion
AGOP: protein metabolic process, ubiquinone biosynthetic process
PGOF: null
PGOC: null
PGOP: oxidation–reduction process, ubiquinone biosynthetic process





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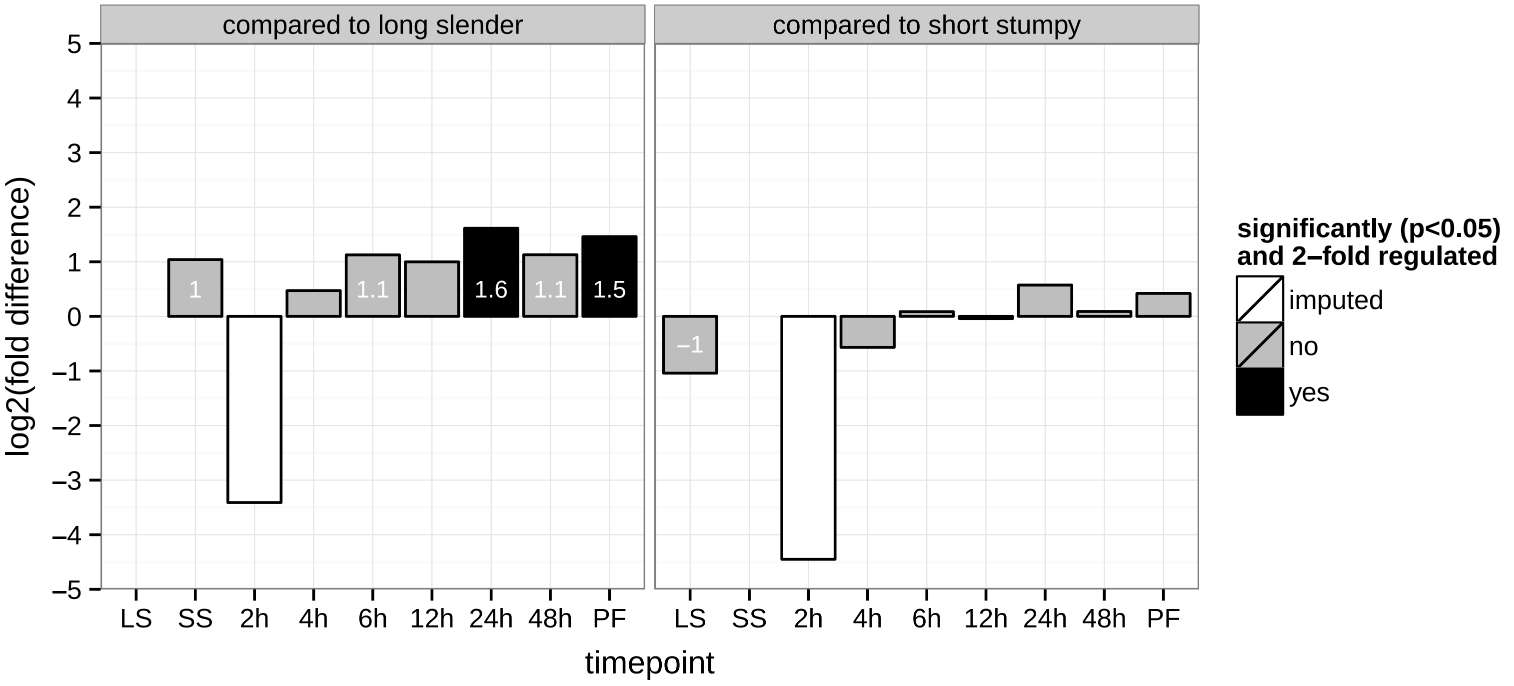
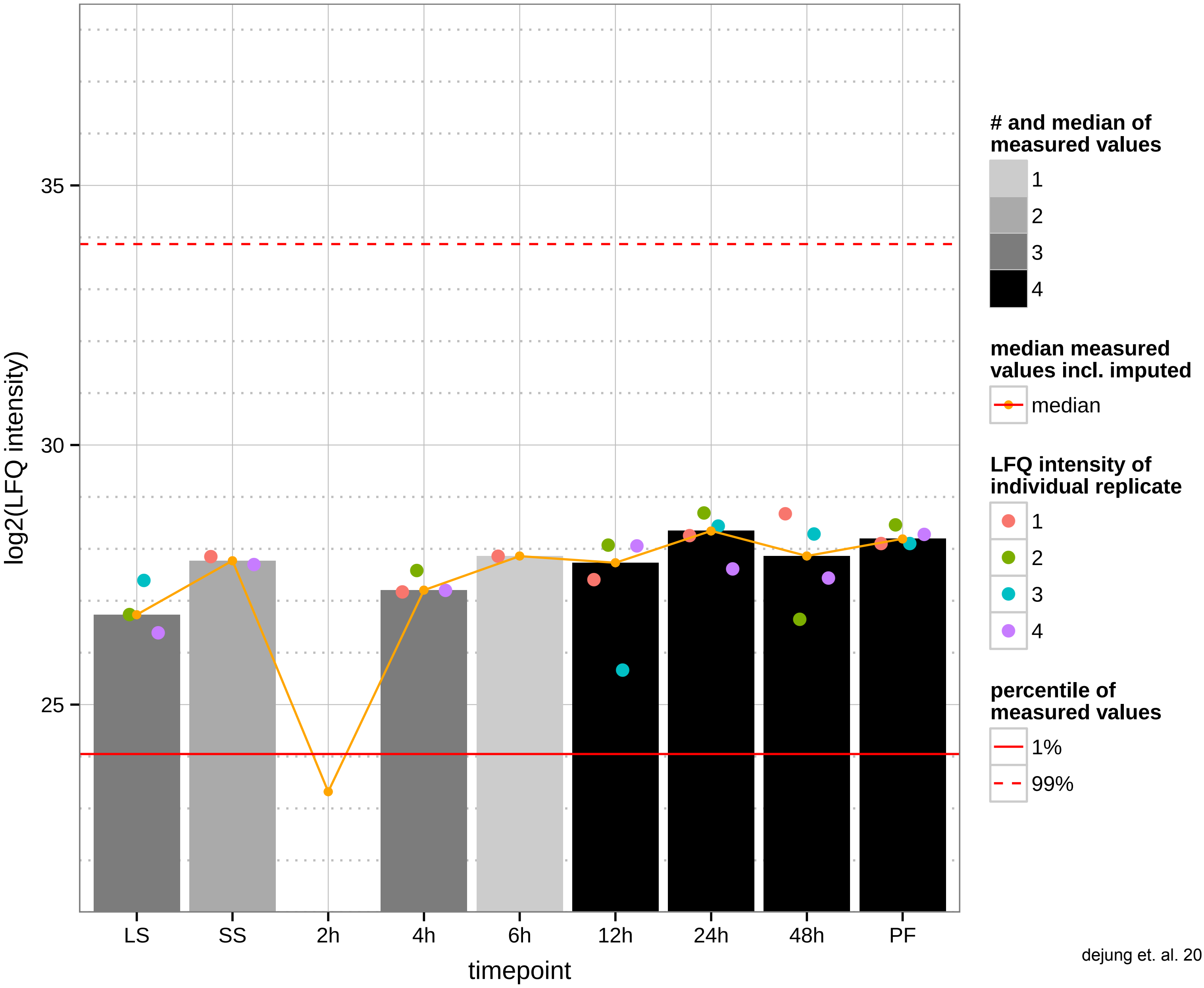
centrin, putative (centrin1)
Tb927.4.2260
AGOF: calcium ion binding
AGOC: centrosome, mitochondrion
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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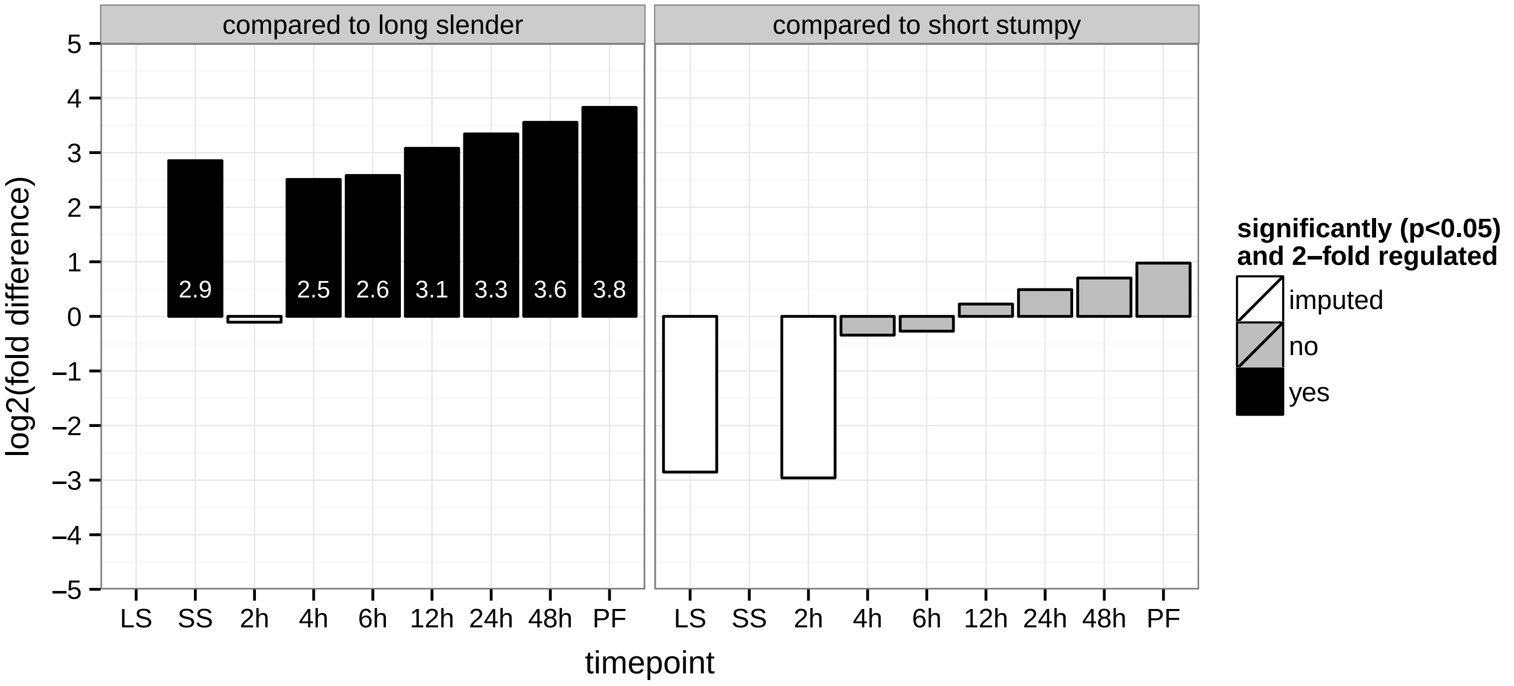
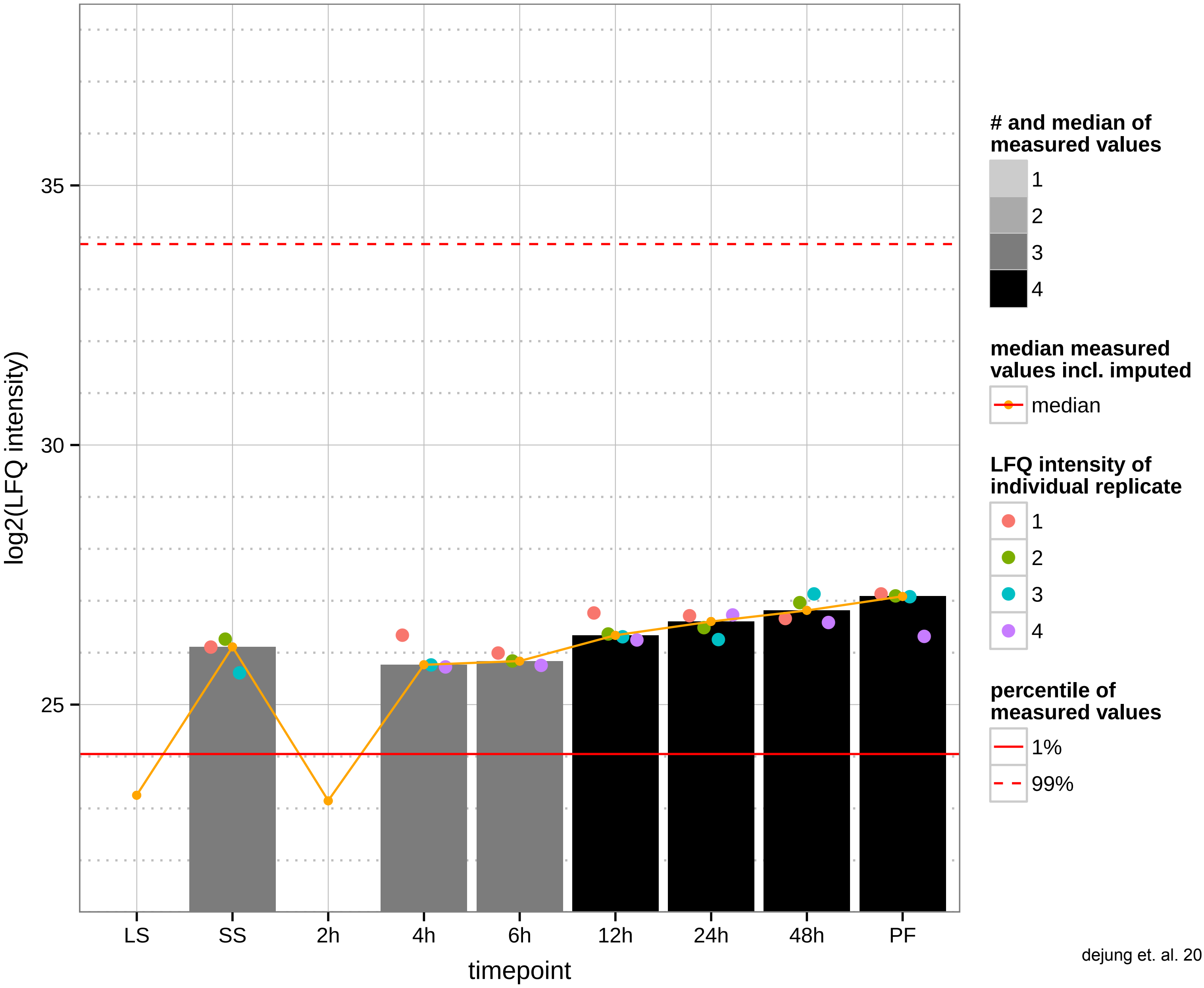
protein phosphatase 1 (PP1)
Tb927.4.5030
AGOF: protein serine/threonine phosphatase activity
AGOC: nucleus
AGOP: null
PGOF: hydrolase activity
PGOC: null
PGOP: null





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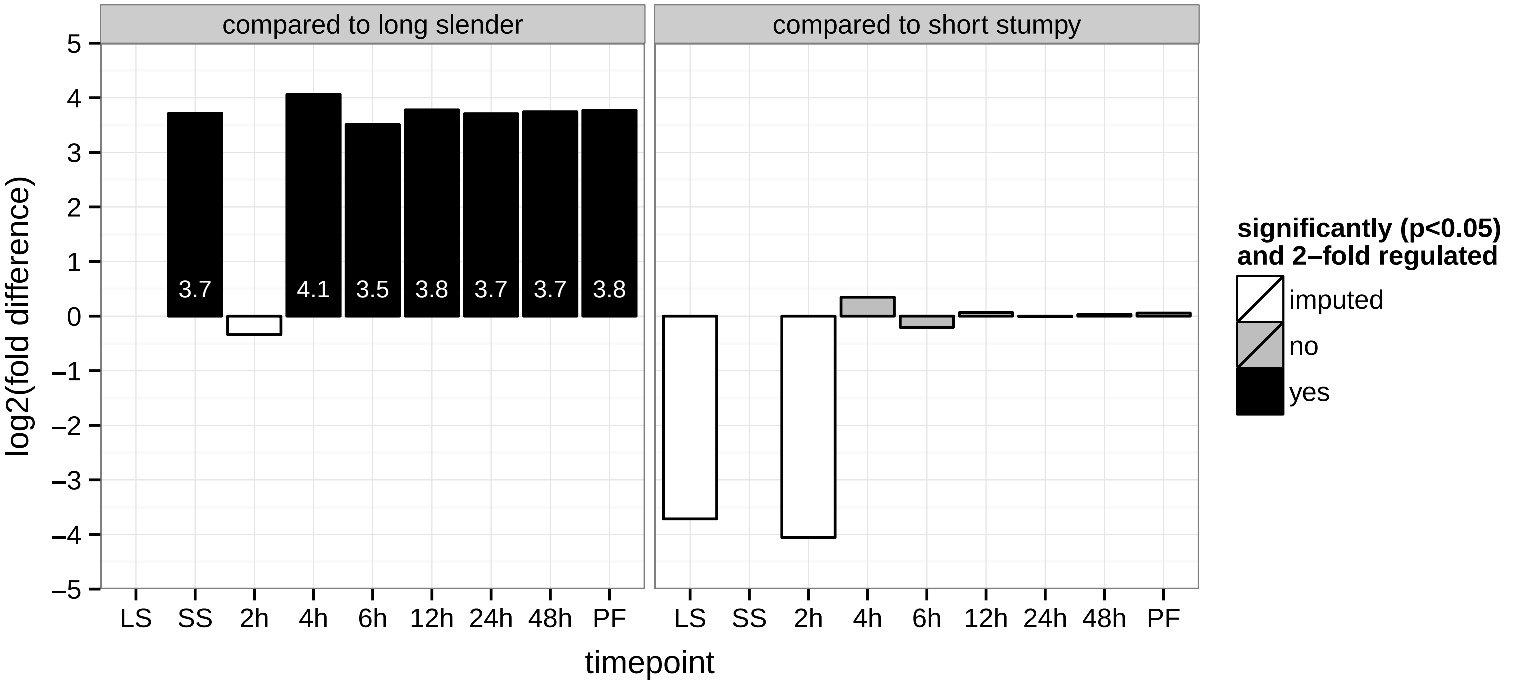
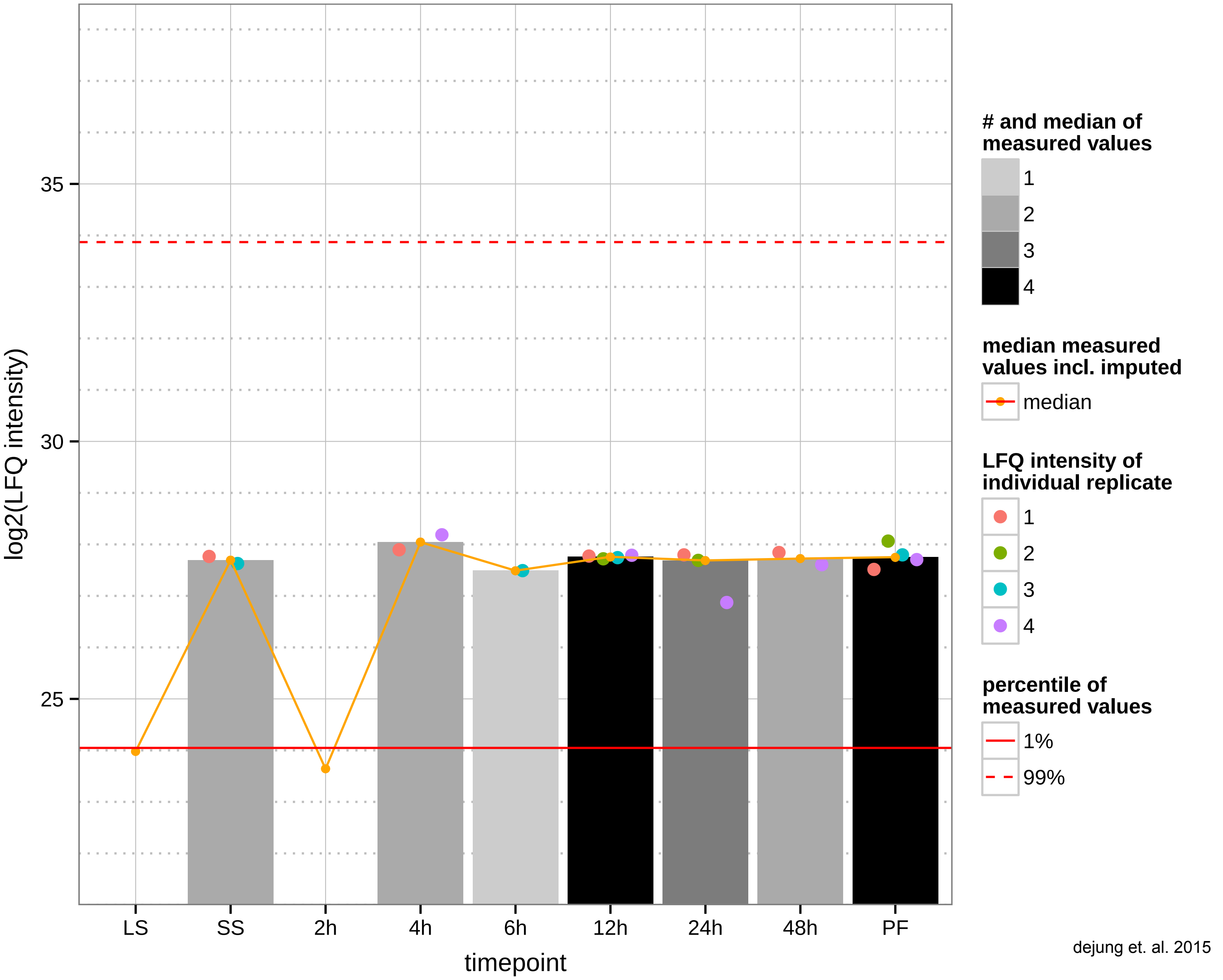
geranylgeranyl transferase type II beta subunit, putative
Tb927.4.690
AGOF: catalytic activity
AGOC: null
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null





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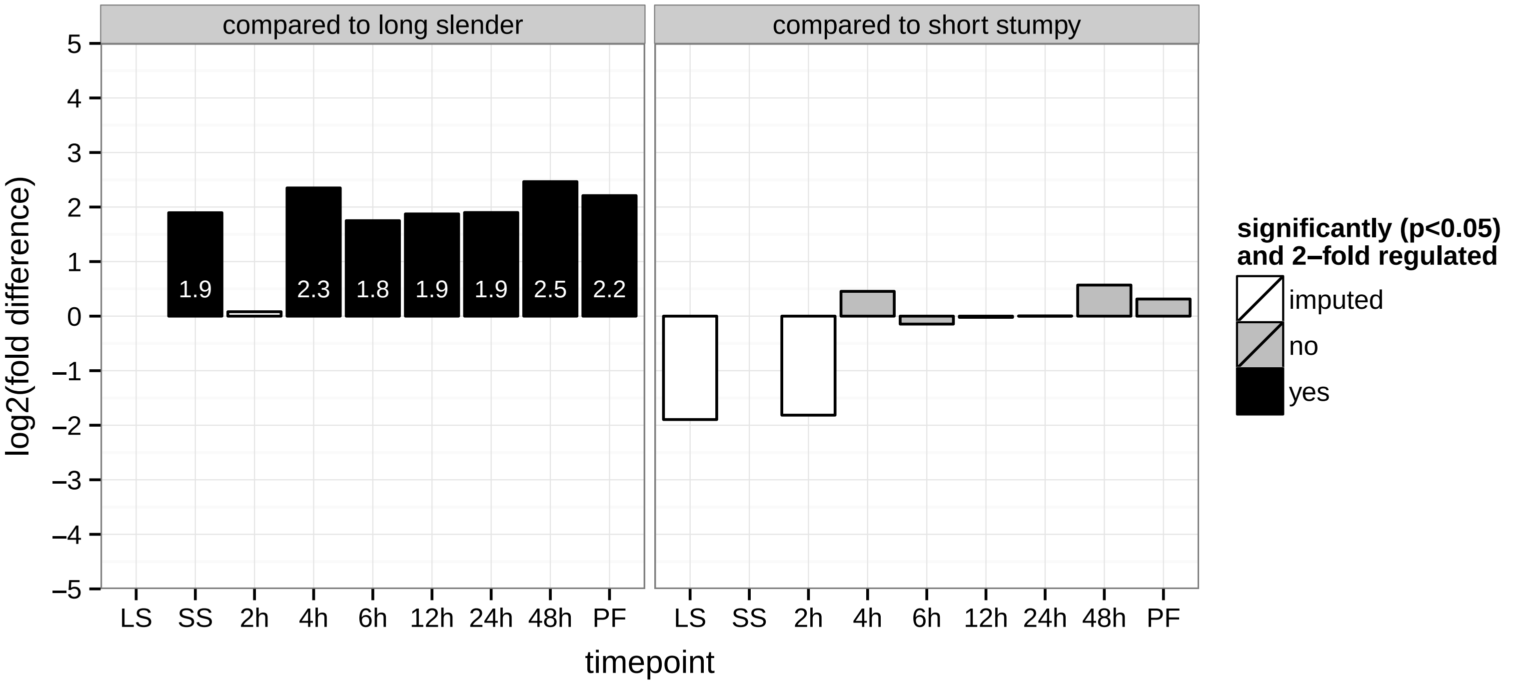
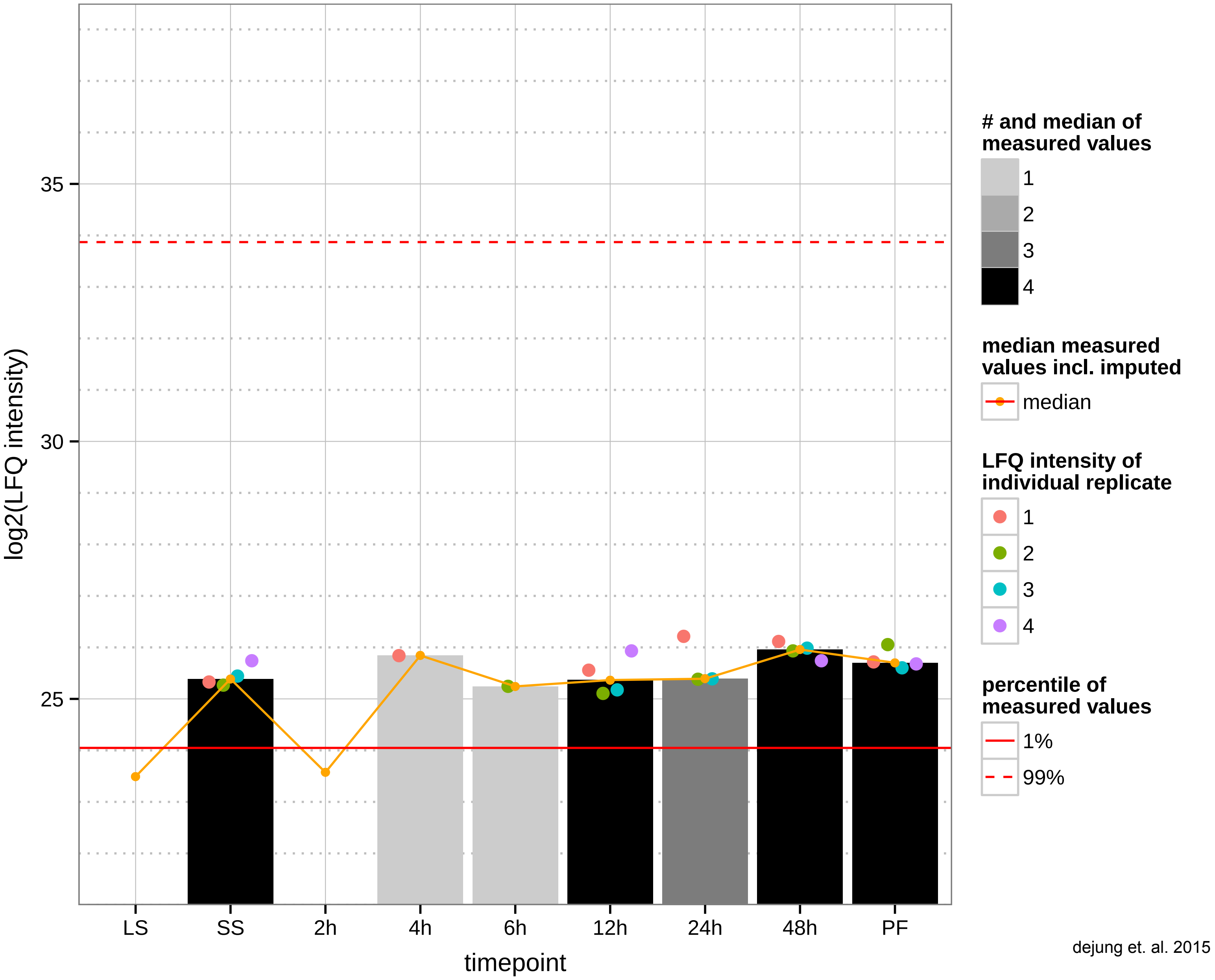
hypothetical protein, conserved
Tb927.5.2070
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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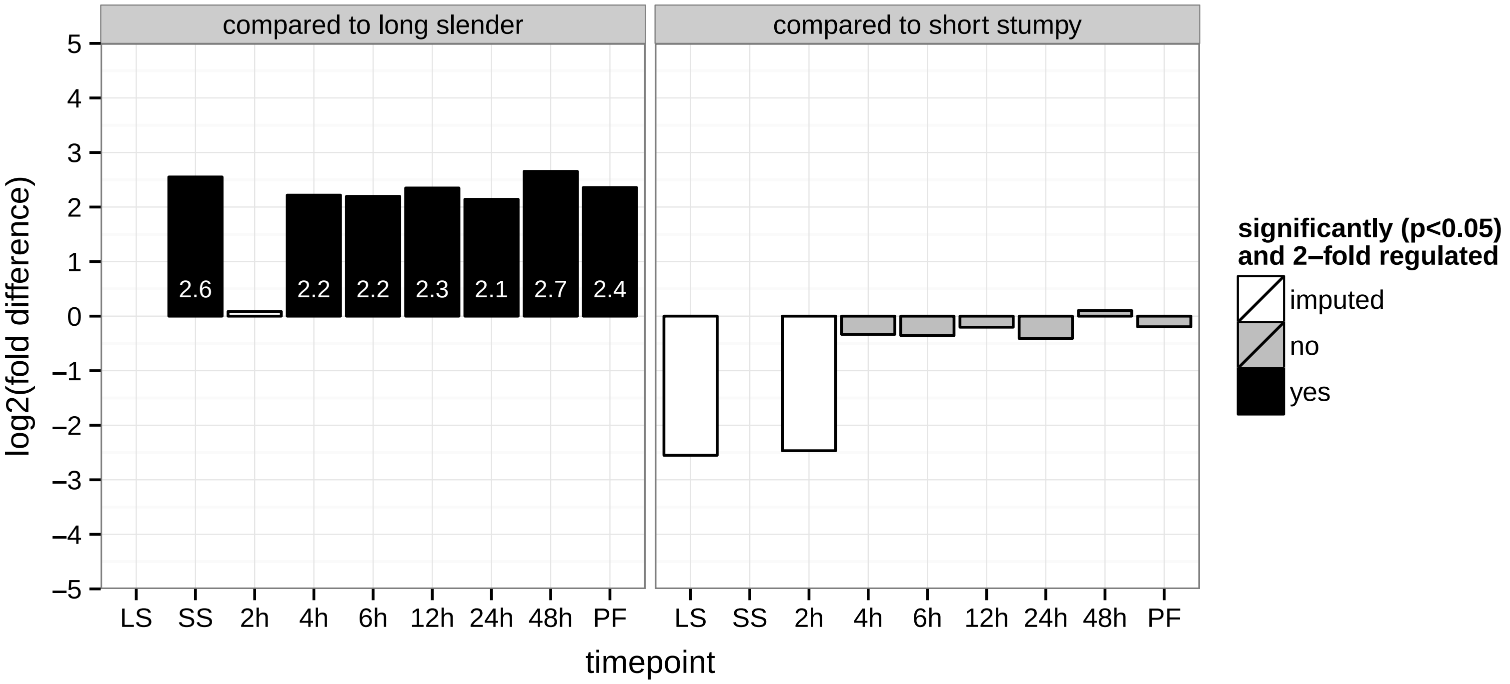
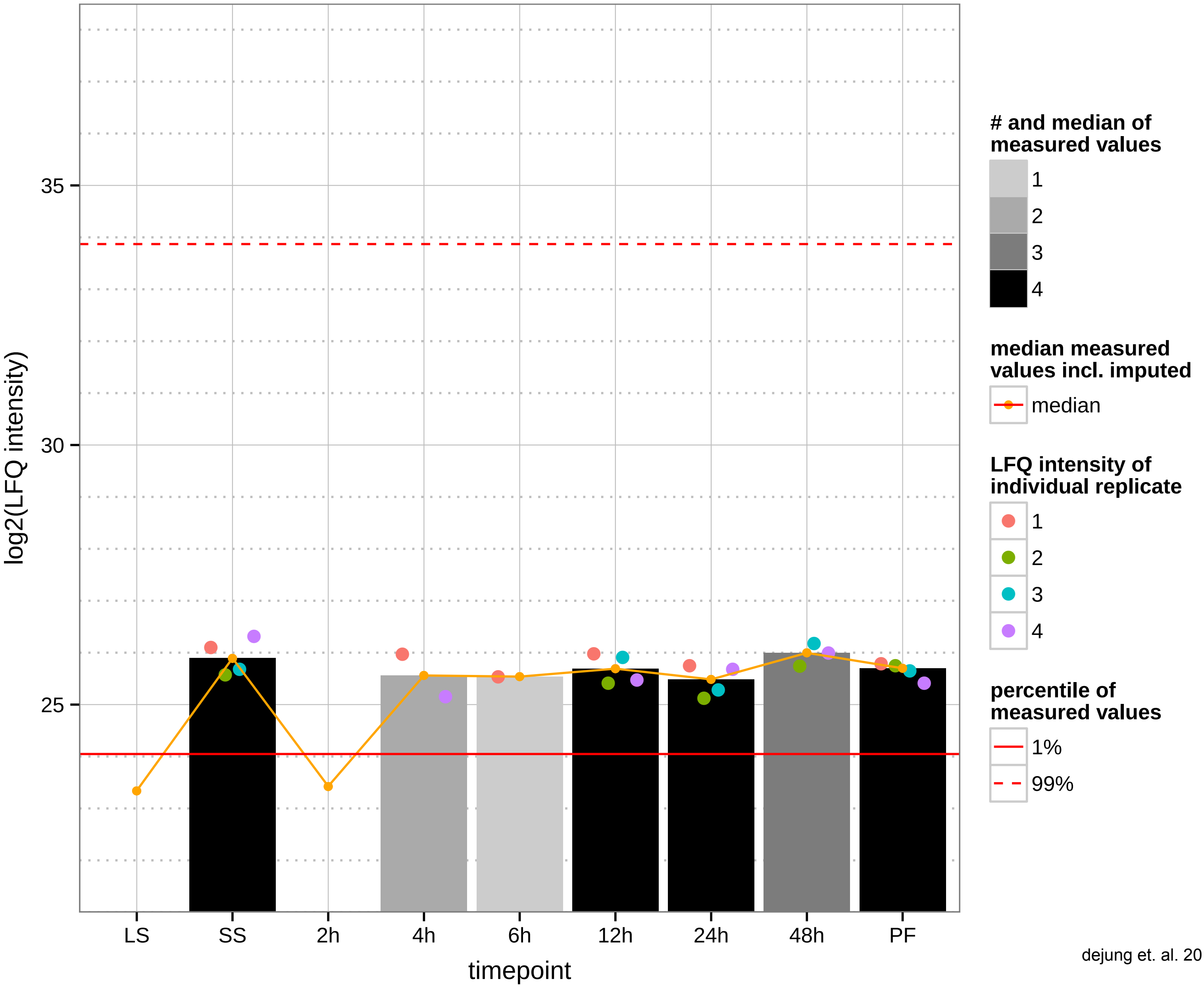
hypothetical protein, conserved
Tb927.5.3240
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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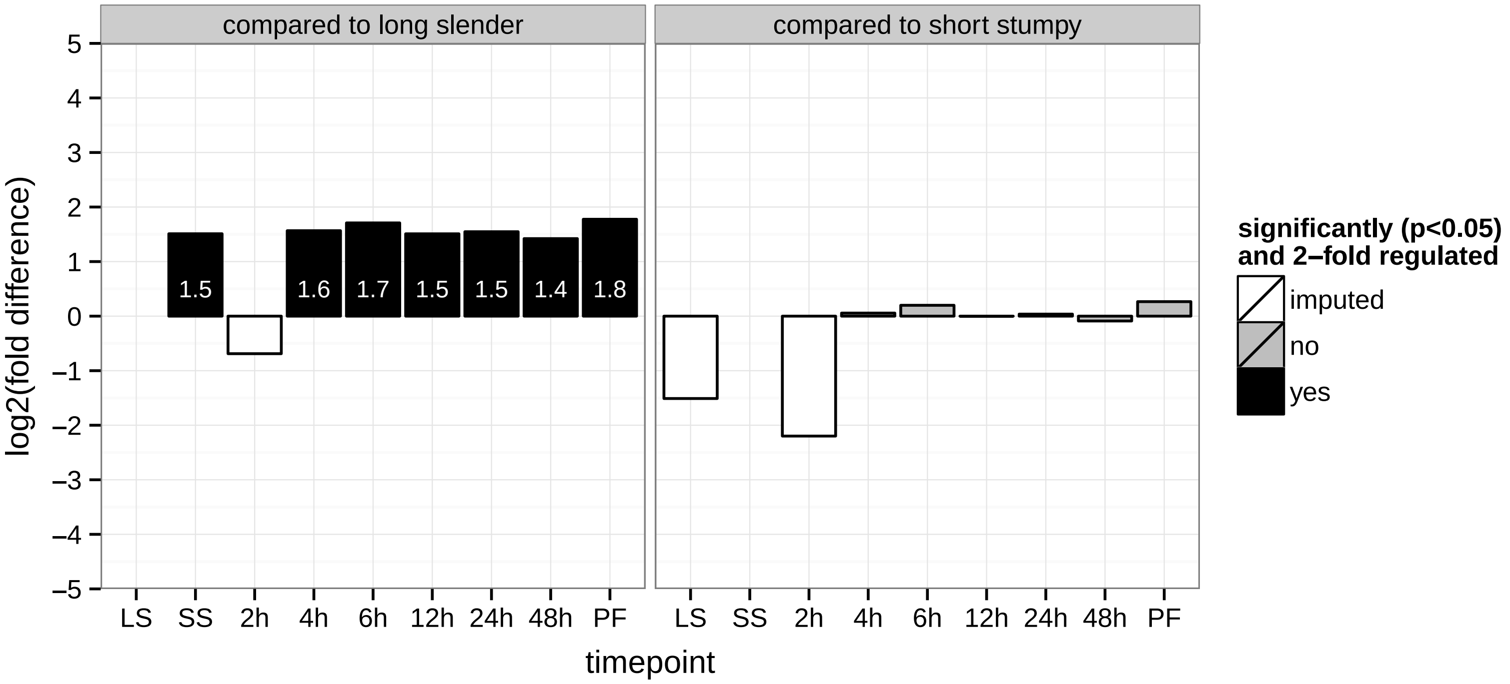
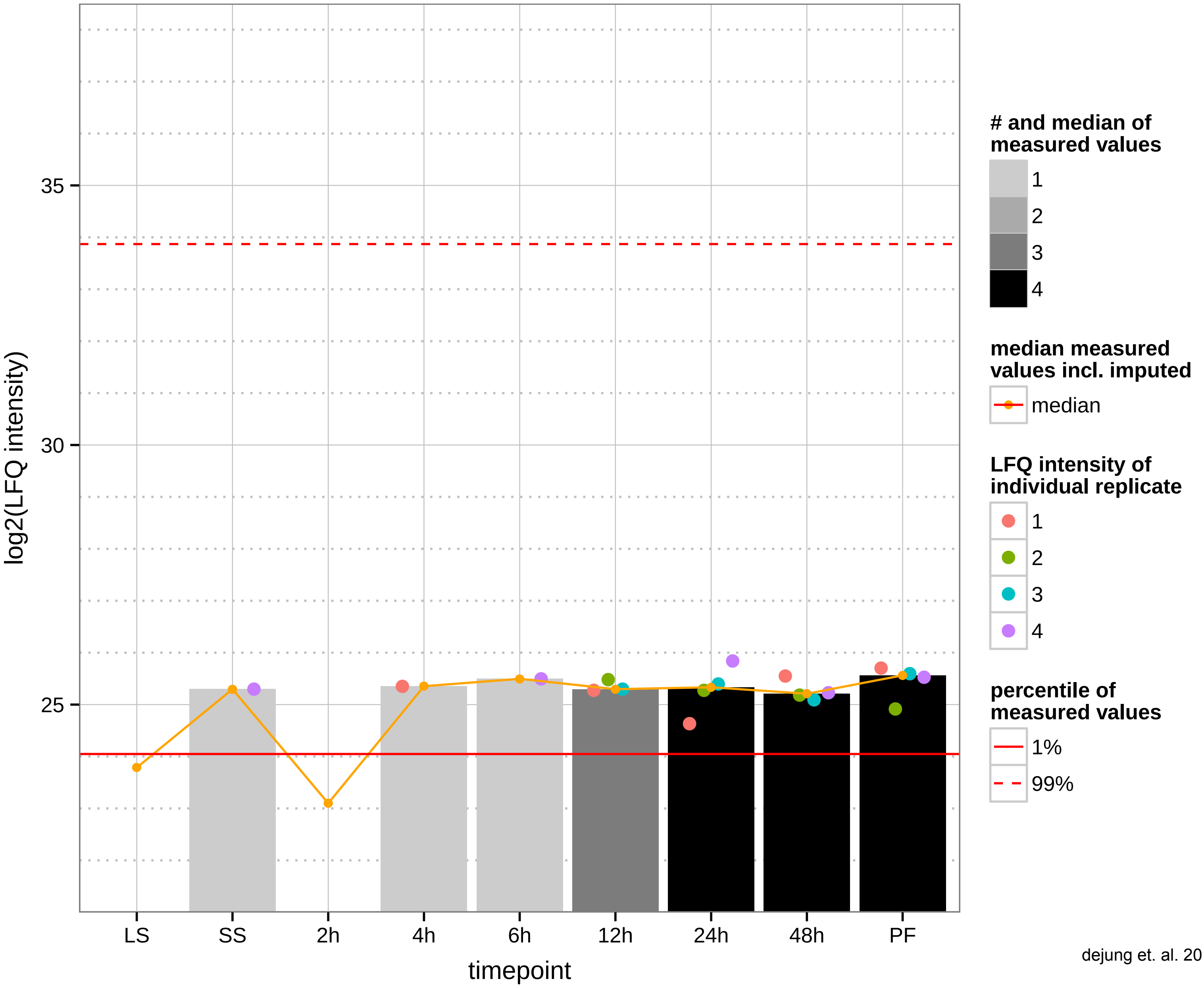
hypothetical protein, conserved
Tb927.6.1830
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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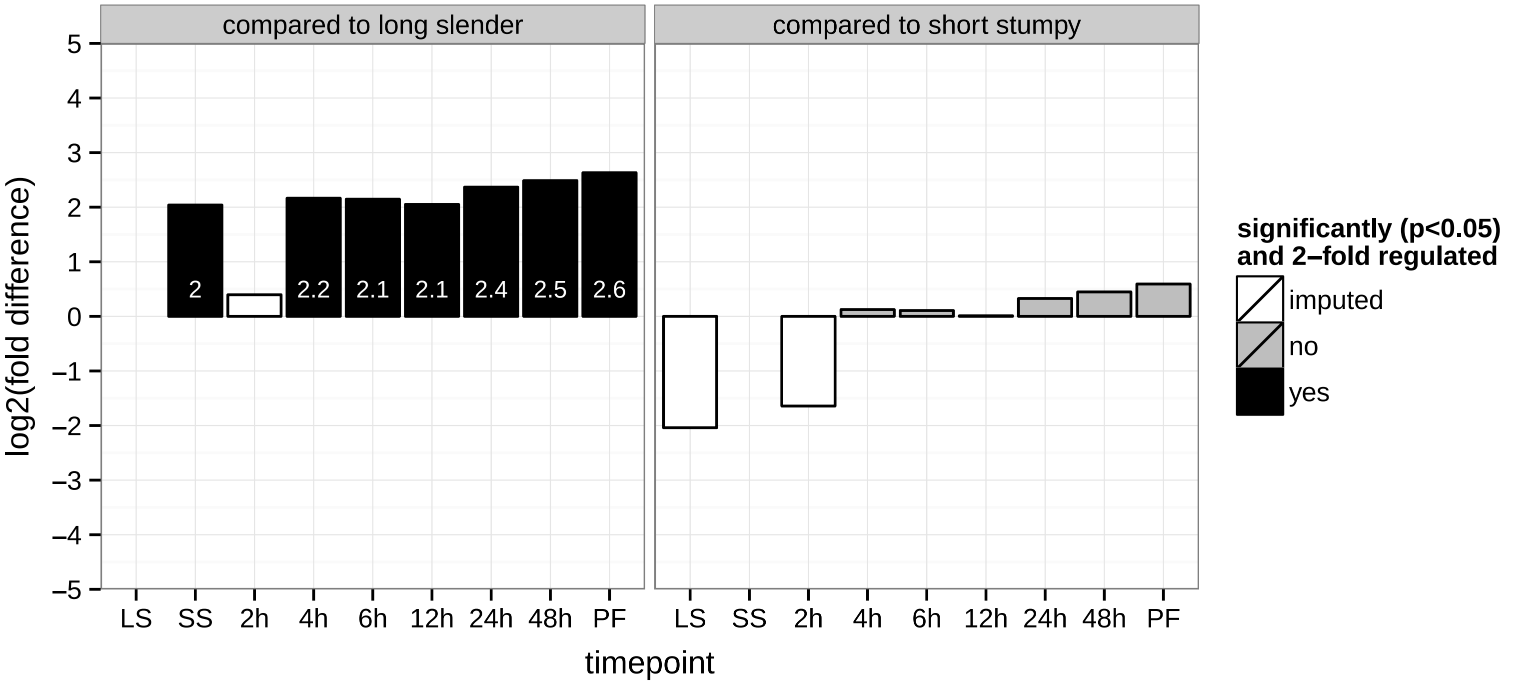
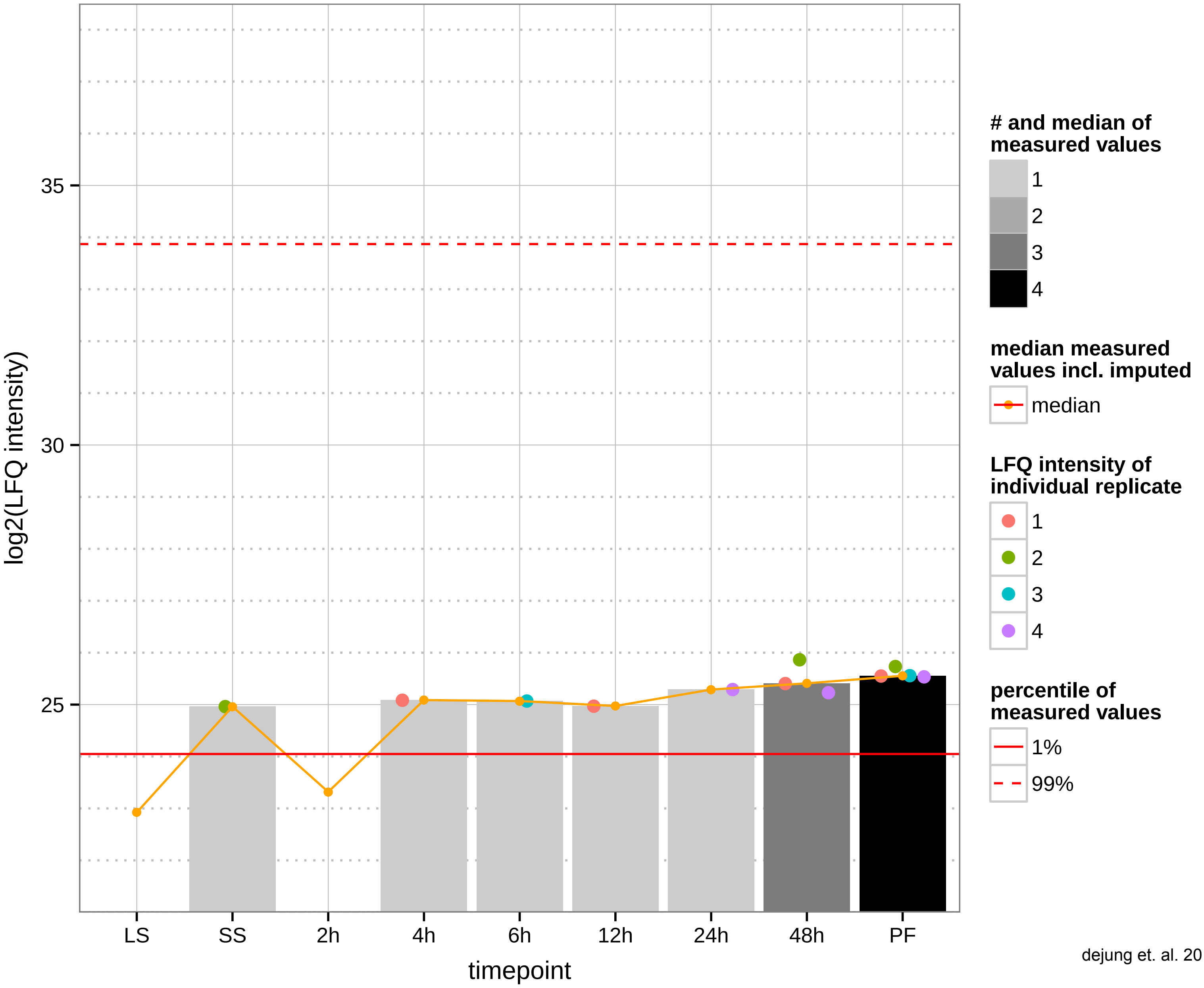
hypothetical protein, conserved
Tb927.7.1530
AGOF: oxidoreductase activity
AGOC: null
AGOP: null
PGOF: oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular o
PGOC: null
PGOP: oxidation–reduction process





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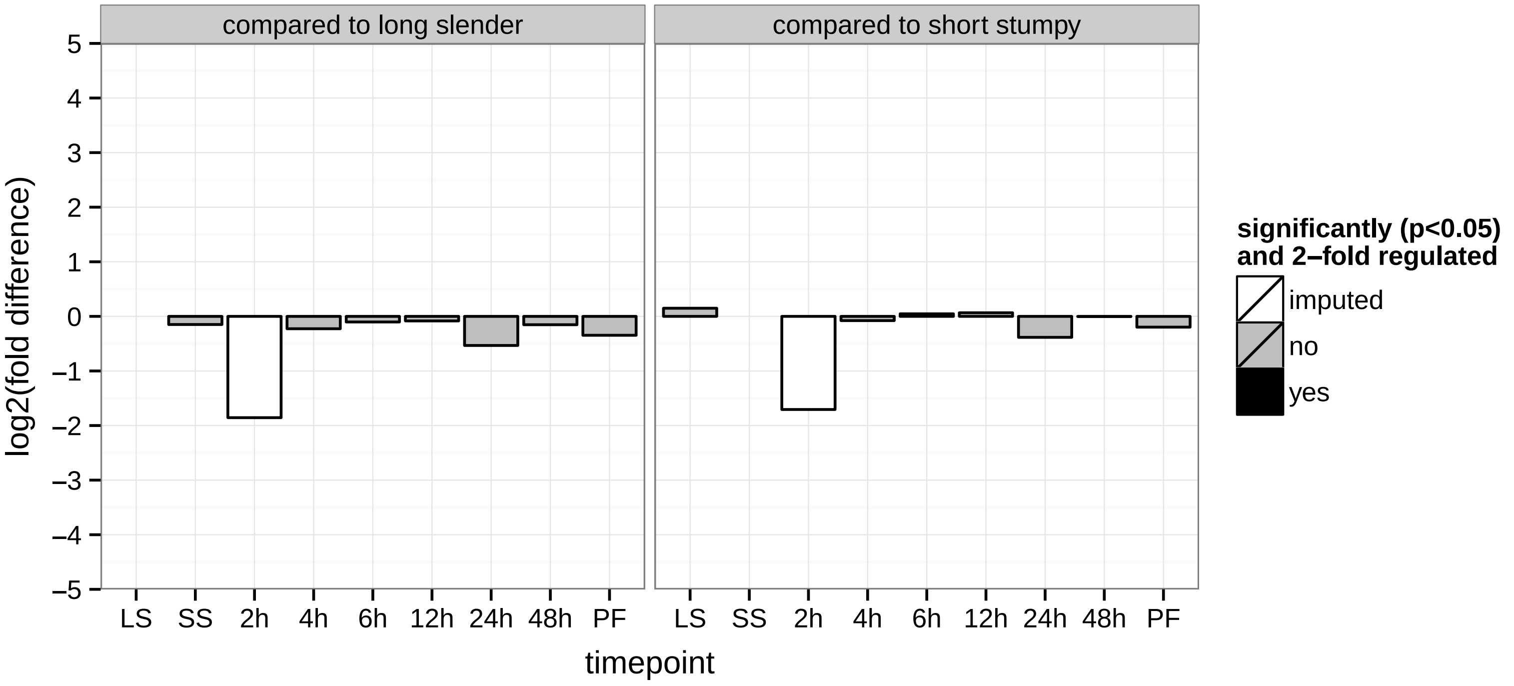
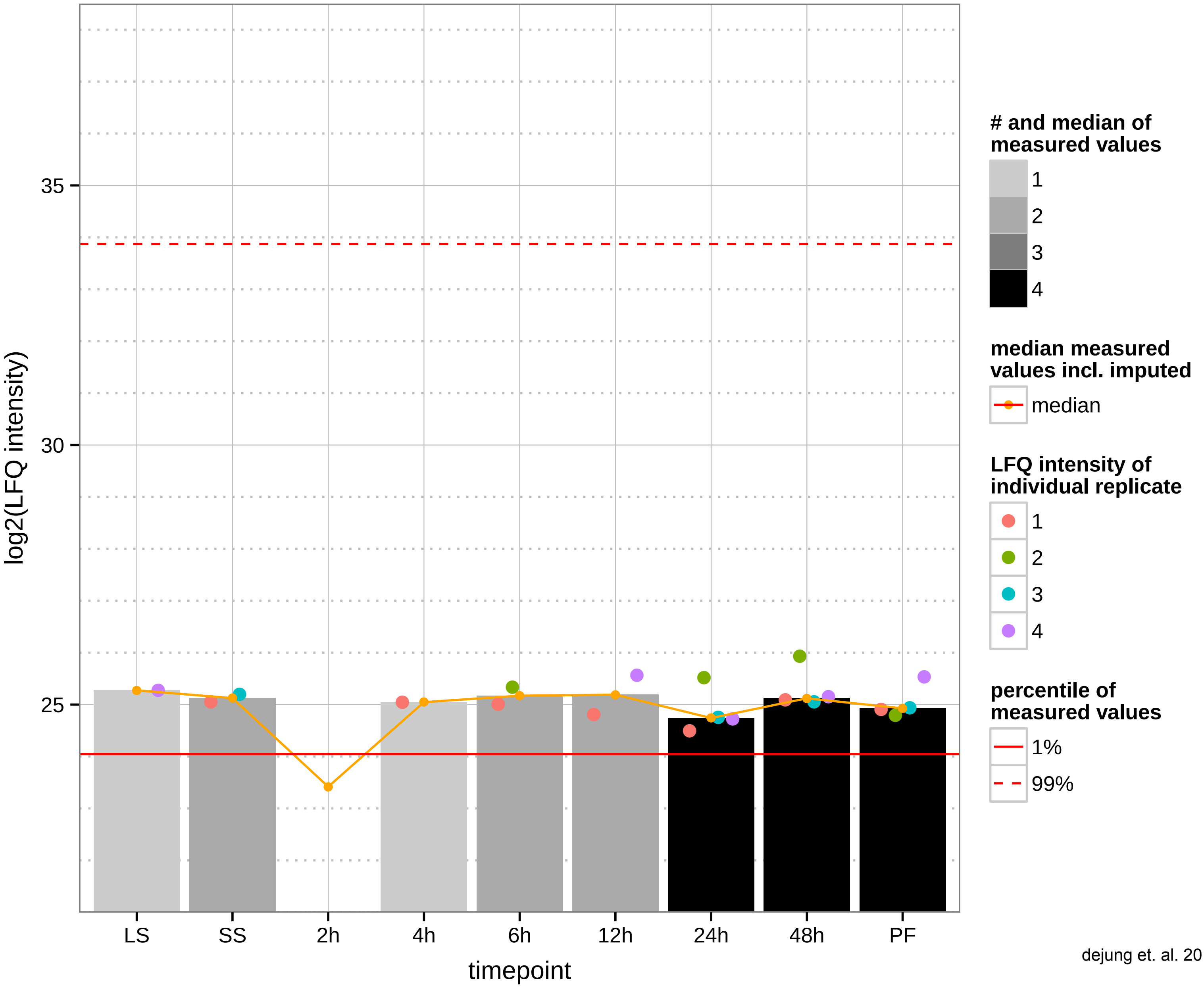
hypothetical protein, conserved
Tb927.7.5750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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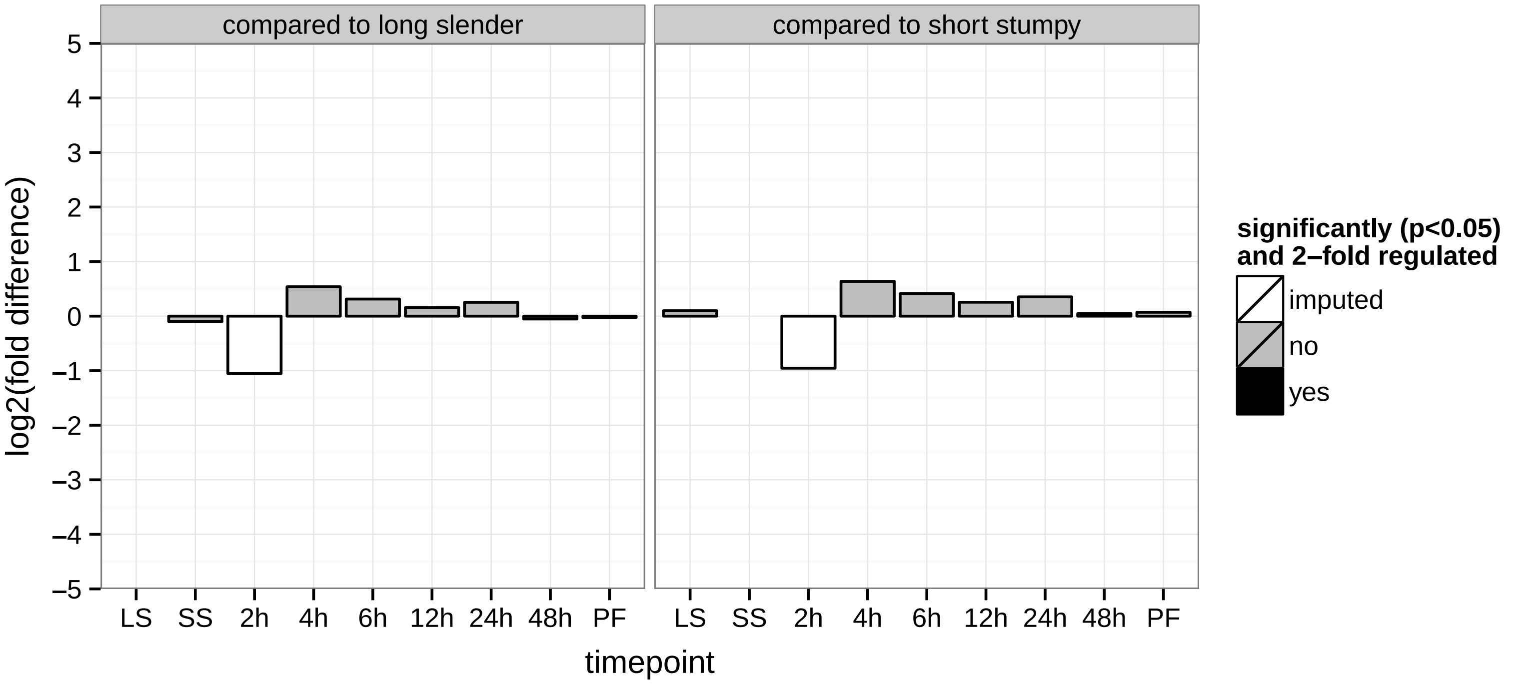
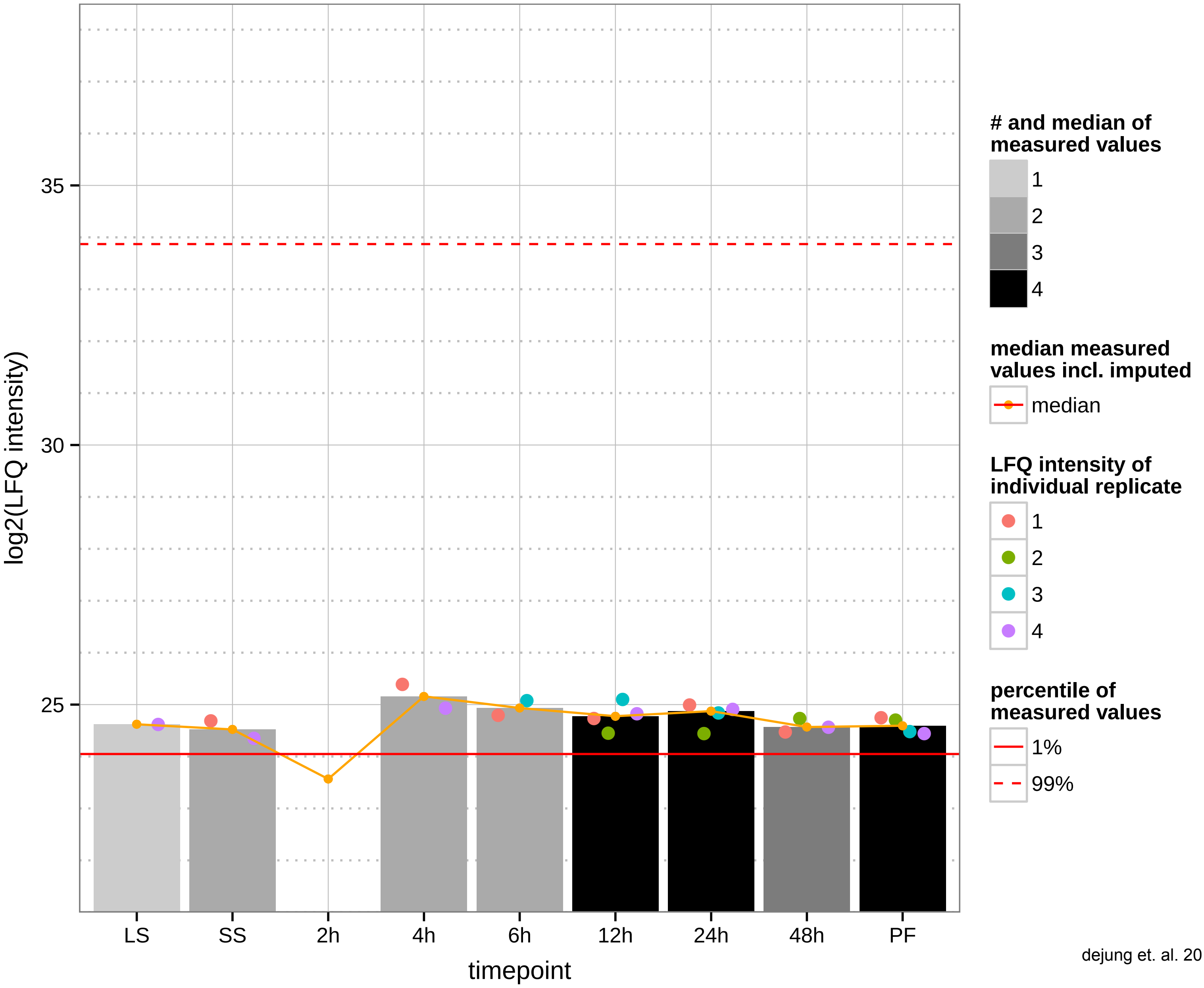
telomerase–associated protein, putative
Tb927.7.830
AGOF: RNA binding
AGOC: ribonucleoprotein complex
AGOP: null
PGOF: RNA binding, protein binding
PGOC: ribonucleoprotein complex
PGOP: null





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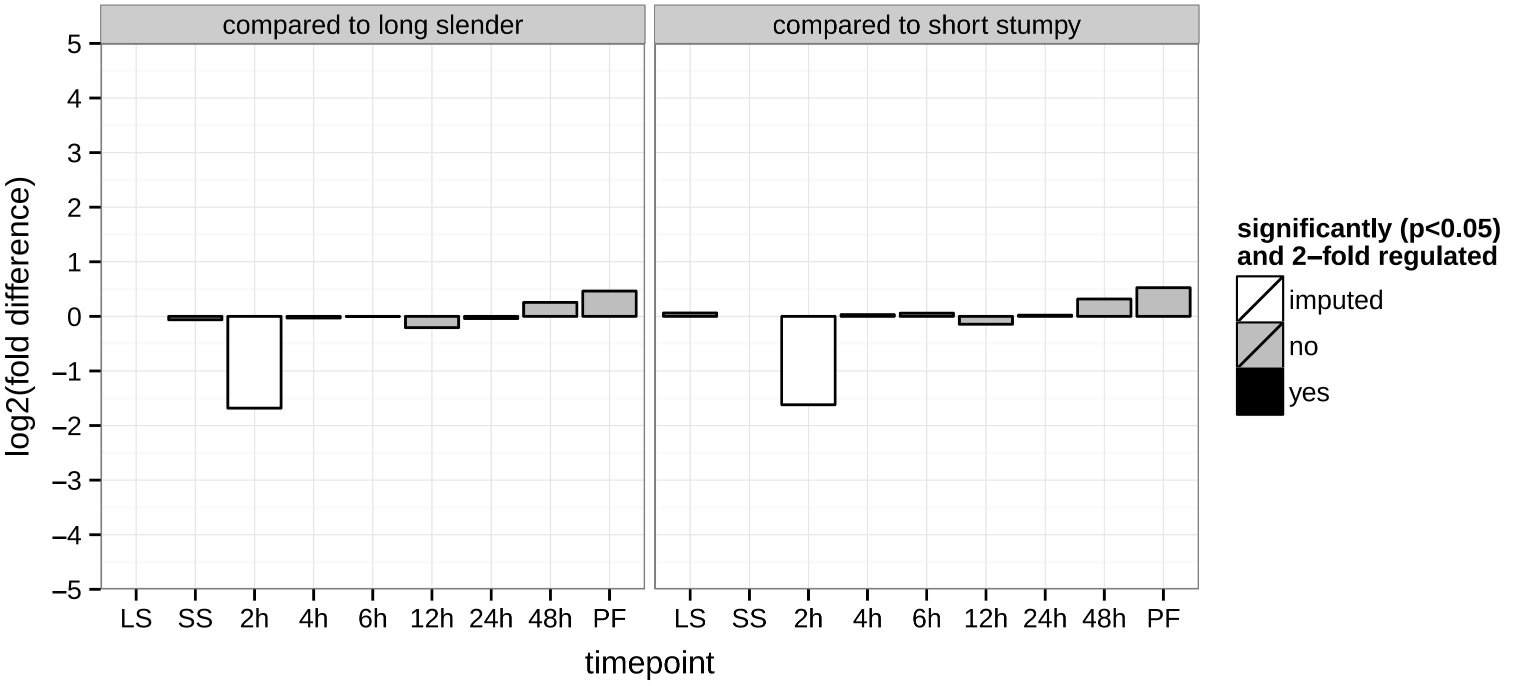
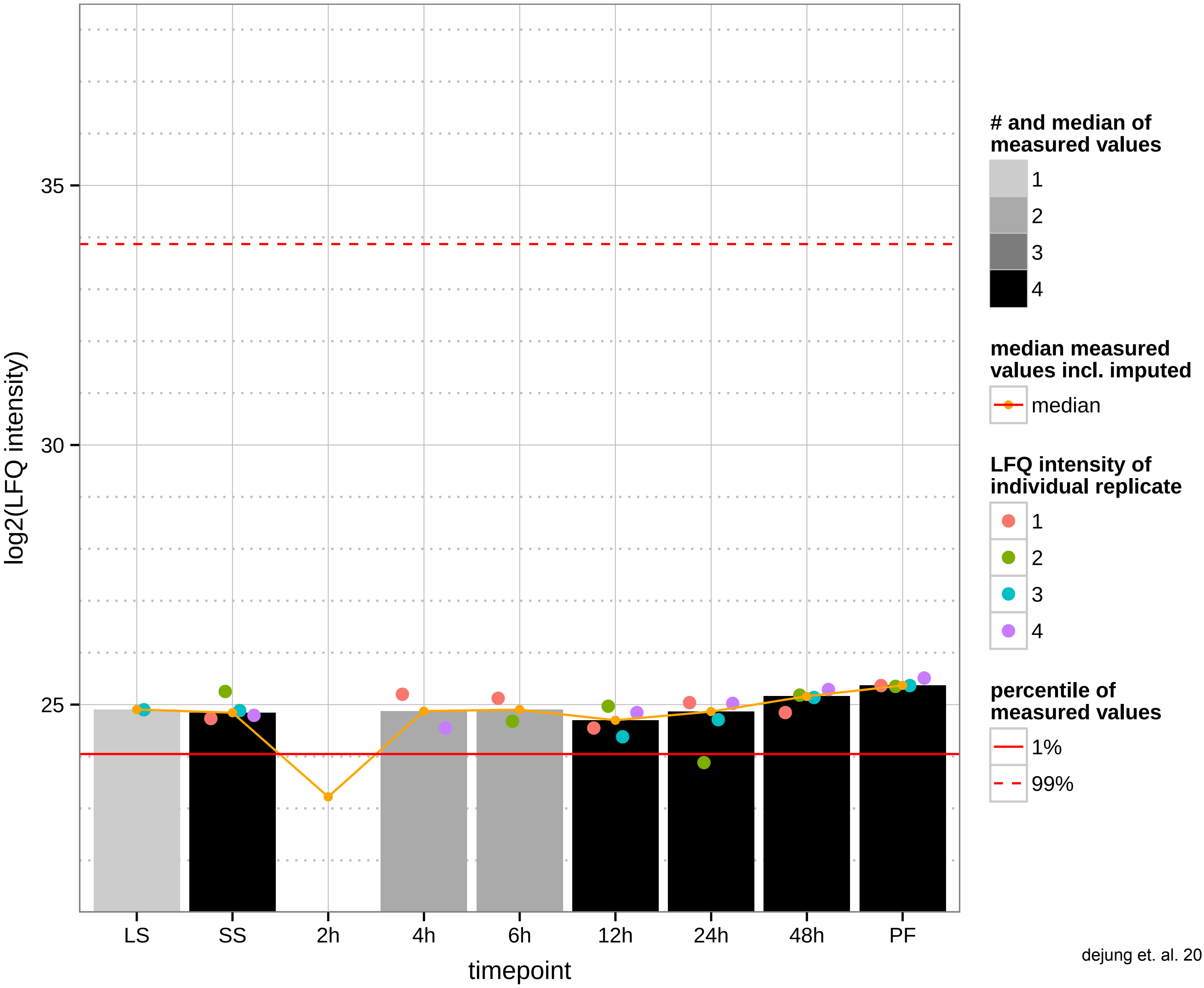
hypothetical protein, conserved
Tb927.8.5650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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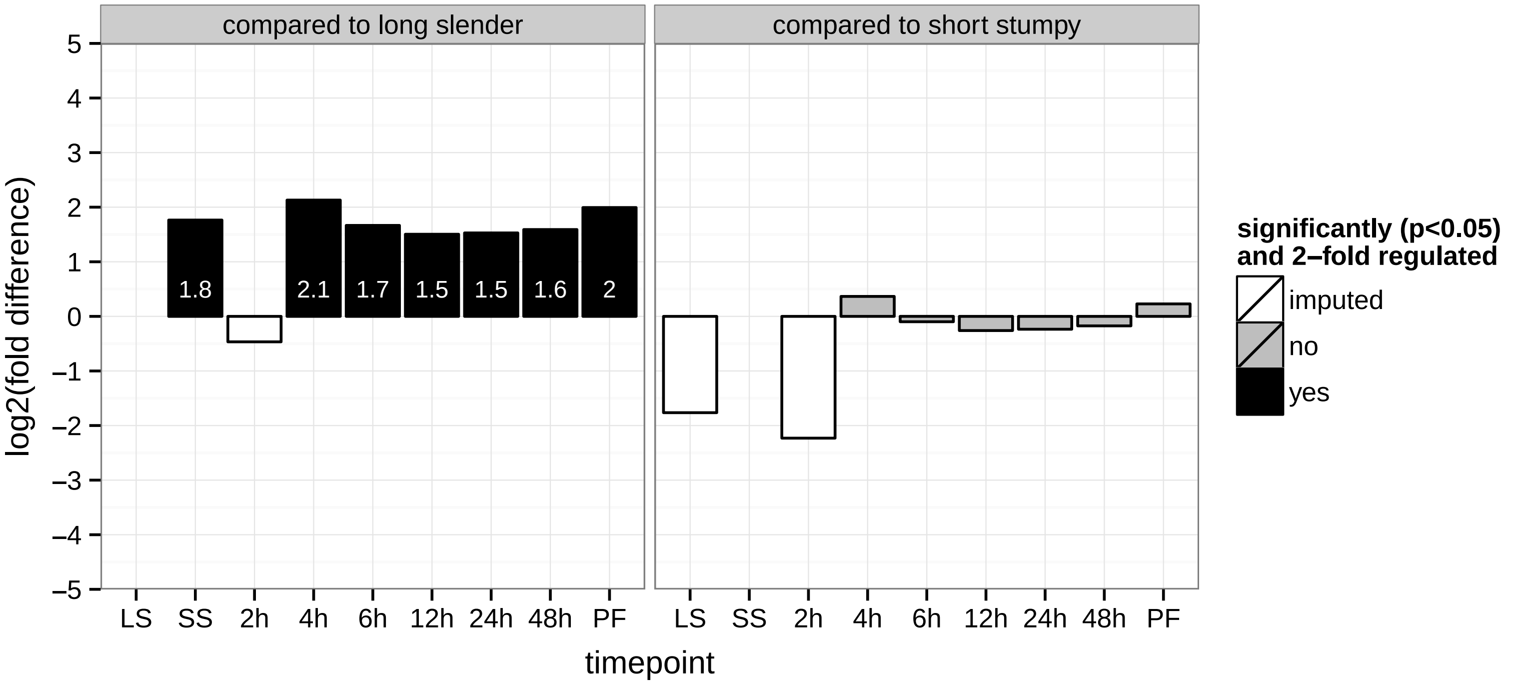
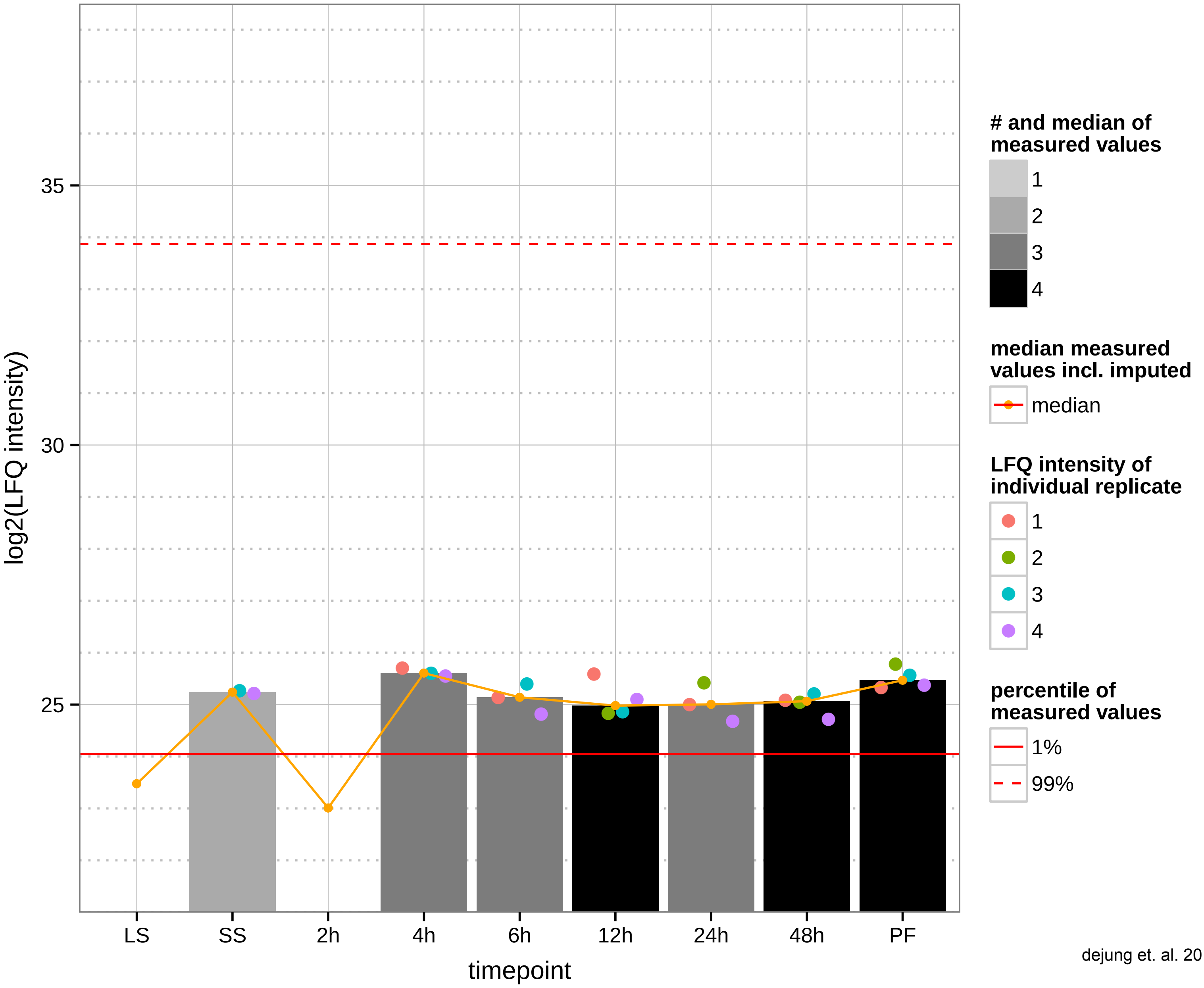
hypothetical protein, conserved
Tb927.8.6460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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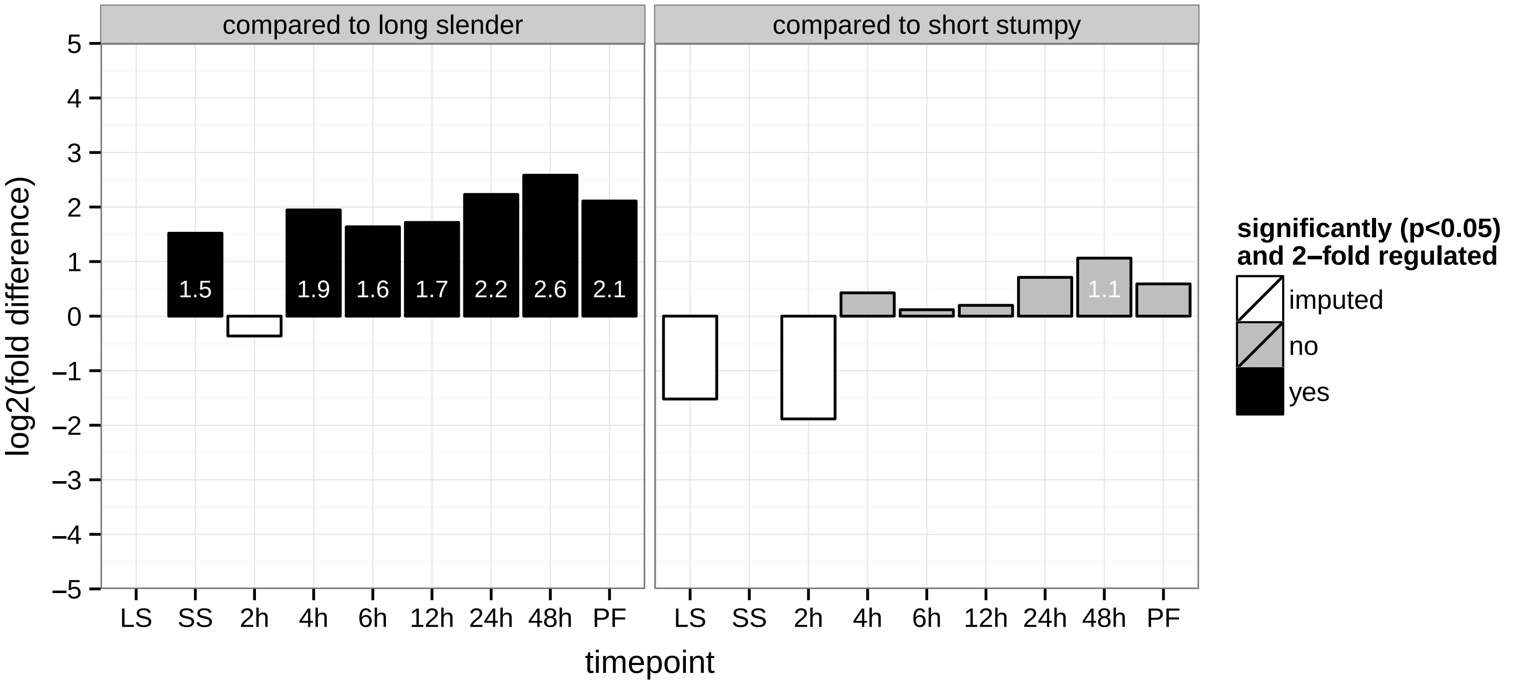
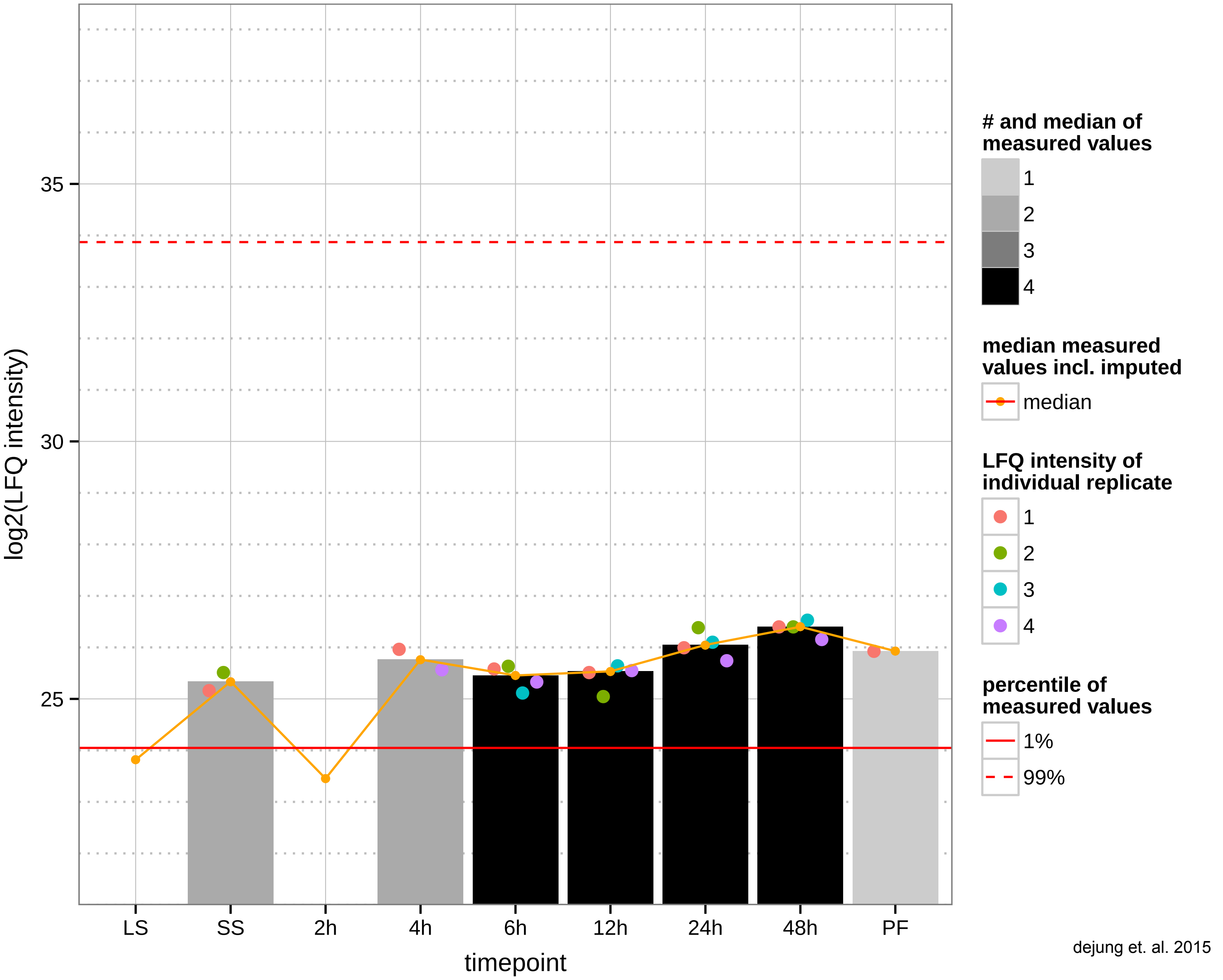
kinetoplast–associated protein, putative
Tb927.8.7260
AGOF: structural molecule activity
AGOC: kinetoplast, mitochondrion
AGOP: cell morphogenesis
PGOF: null
PGOC: null
PGOP: null





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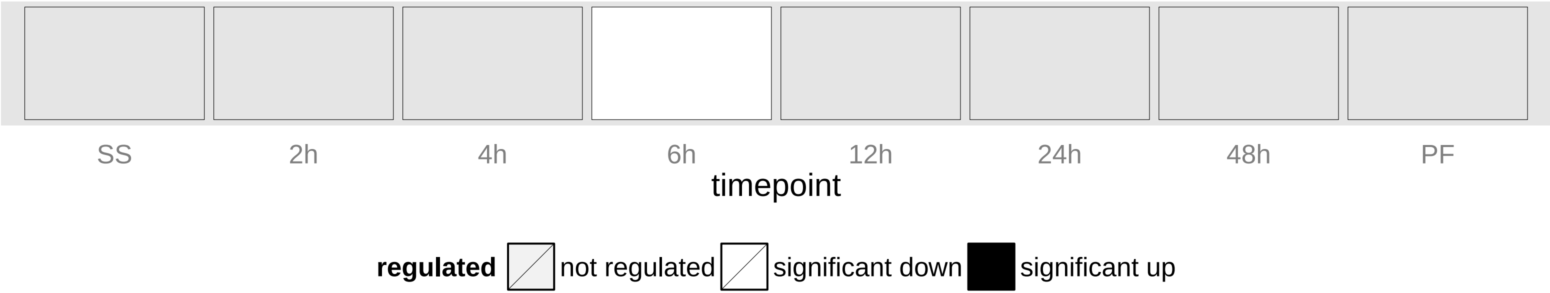

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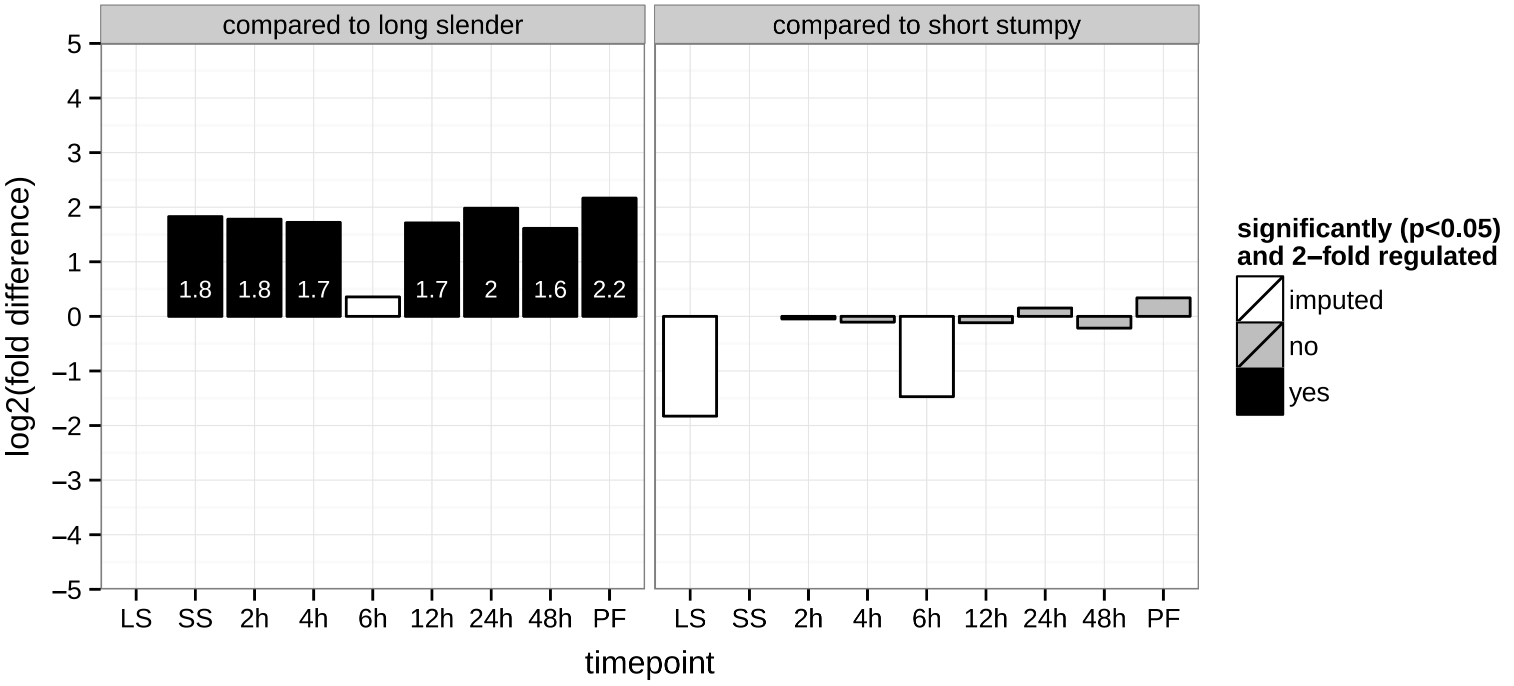
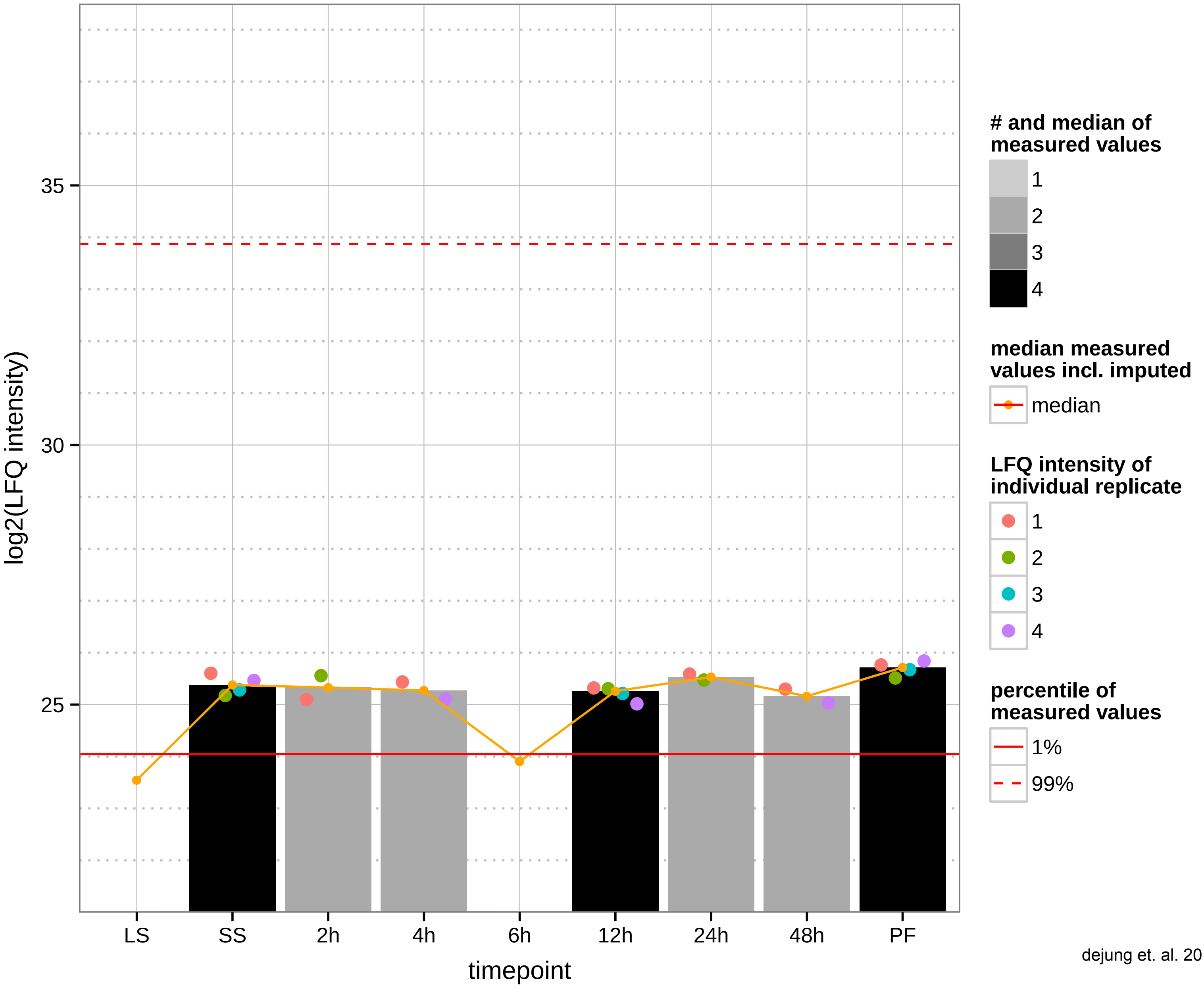
tRNA pseudouridine synthase A–like protein, putative
Tb927.10.15650;Tb11.v5.0465
AGOF: null, RNA binding, pseudouridine synthase activity
AGOC: null, mitochondrion
AGOP: null, pseudouridine synthesis, tRNA modification
PGOF: RNA binding, pseudouridine synthase activity
PGOC: null
PGOP: RNA modification, pseudouridine synthesis





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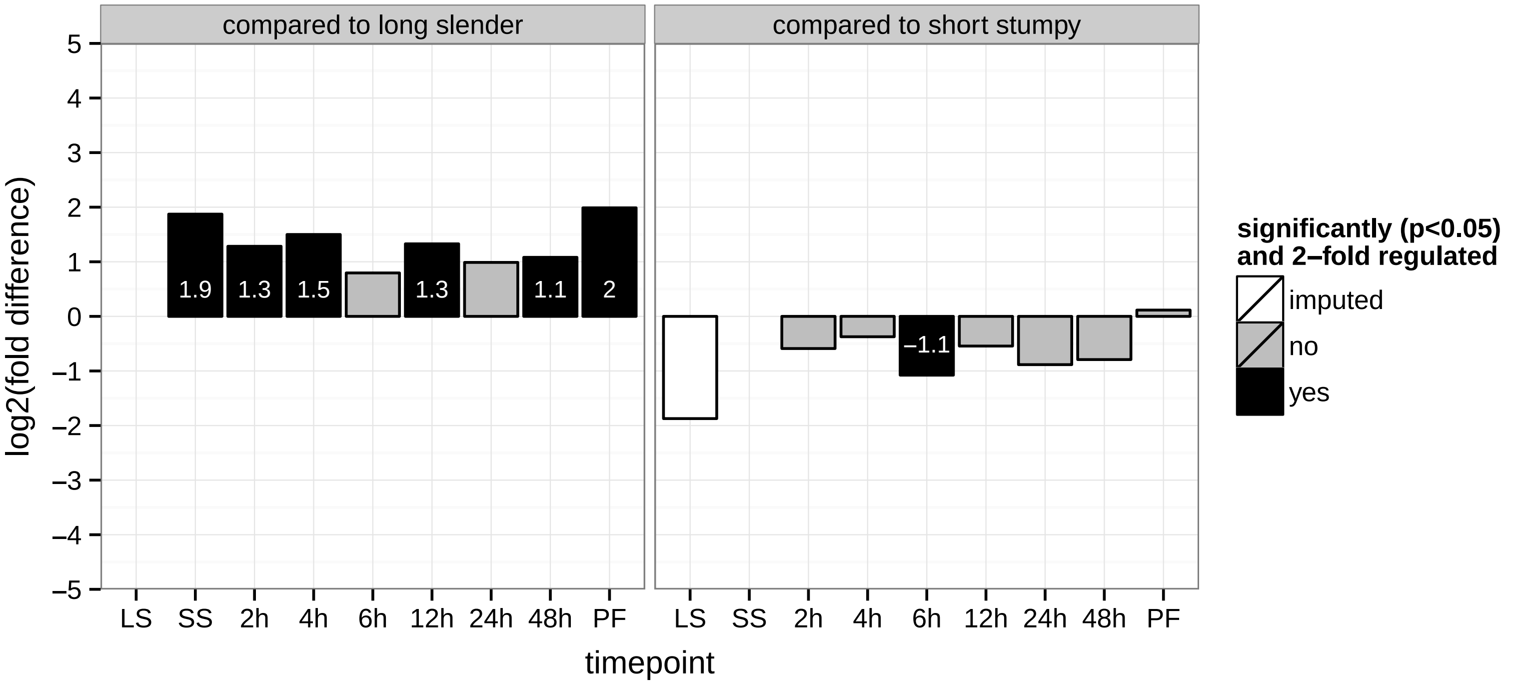
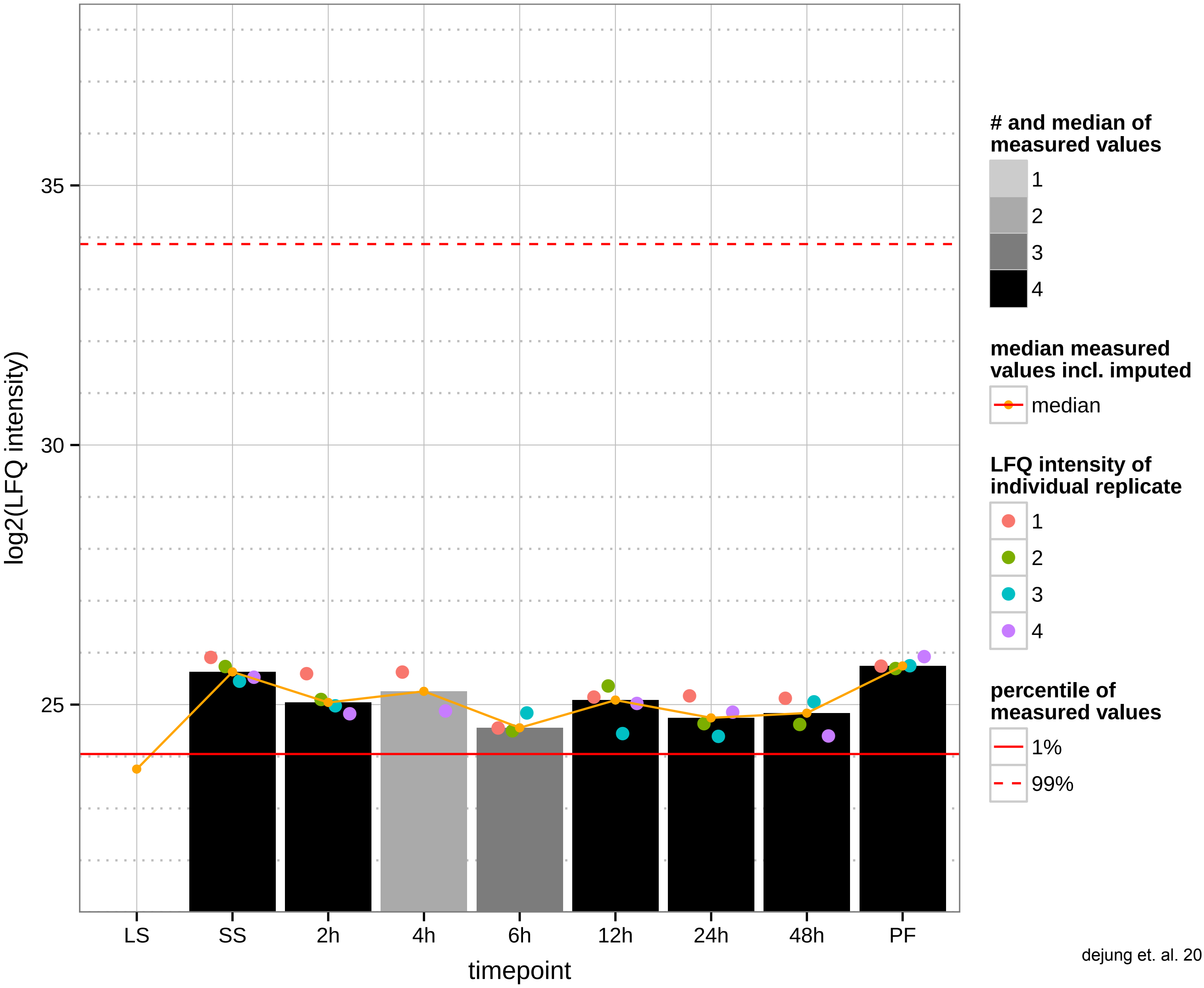
hypothetical protein, conserved
Tb927.10.1800;Tb11.v5.0832
AGOF: null, methyltransferase activity
AGOC: null
AGOP: null
PGOF: methyltransferase activity
PGOC: null
PGOP: null





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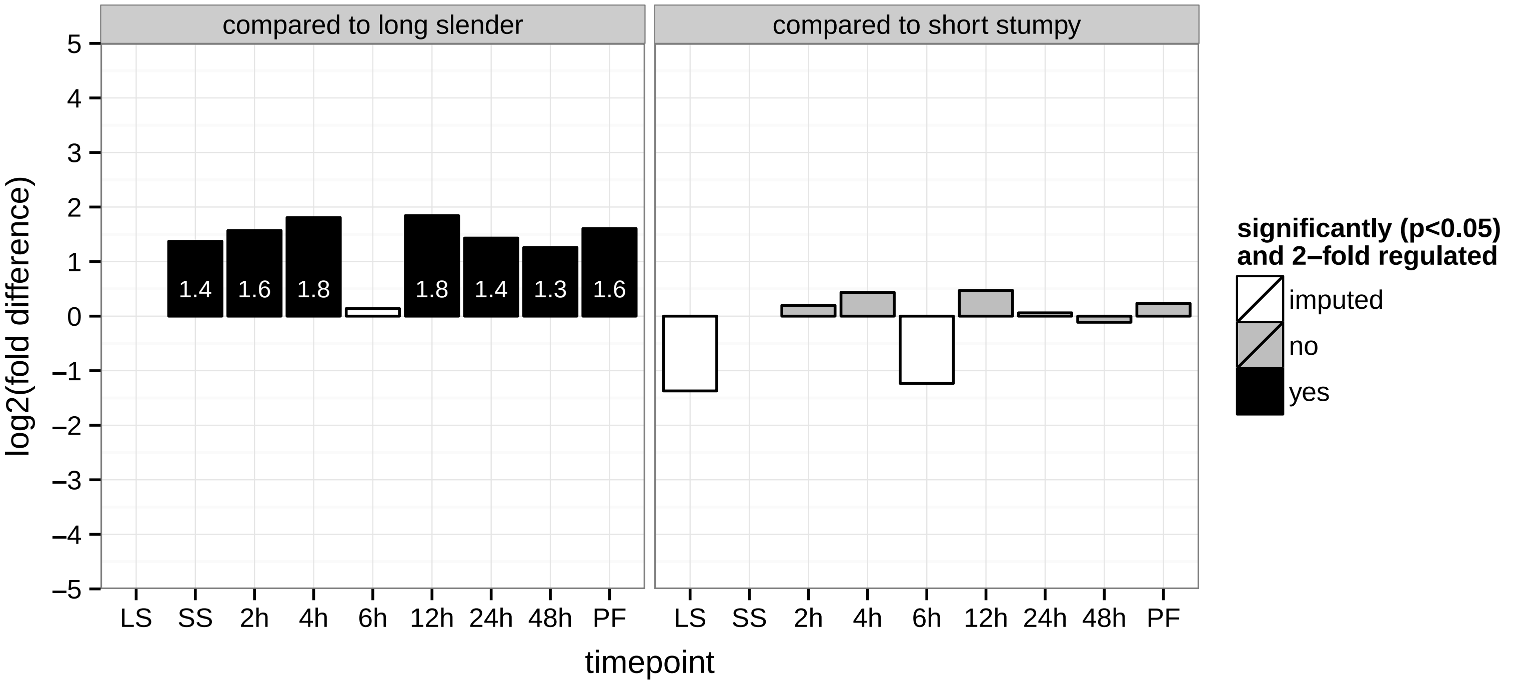
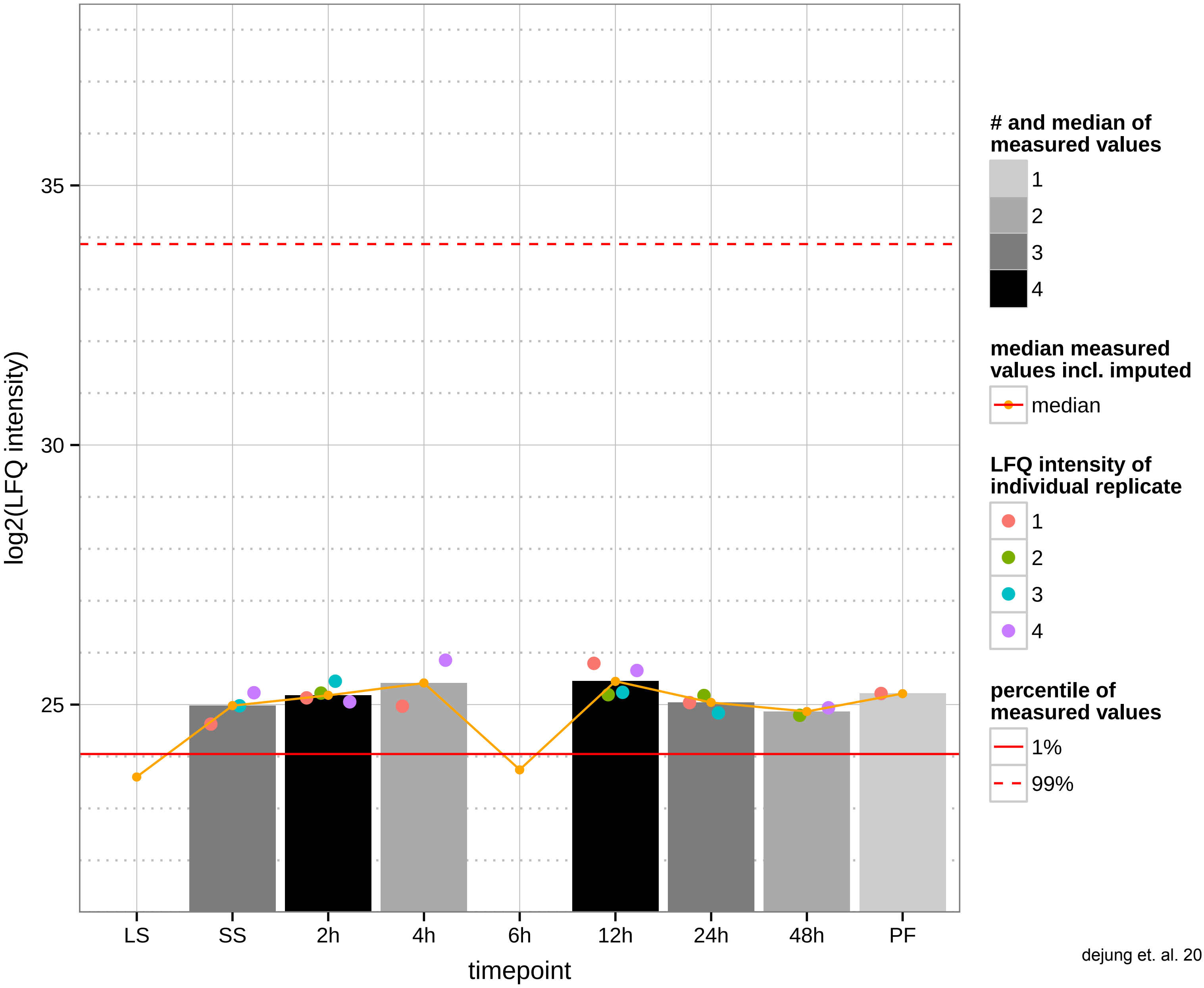
hypothetical protein, conserved
Tb927.10.2930
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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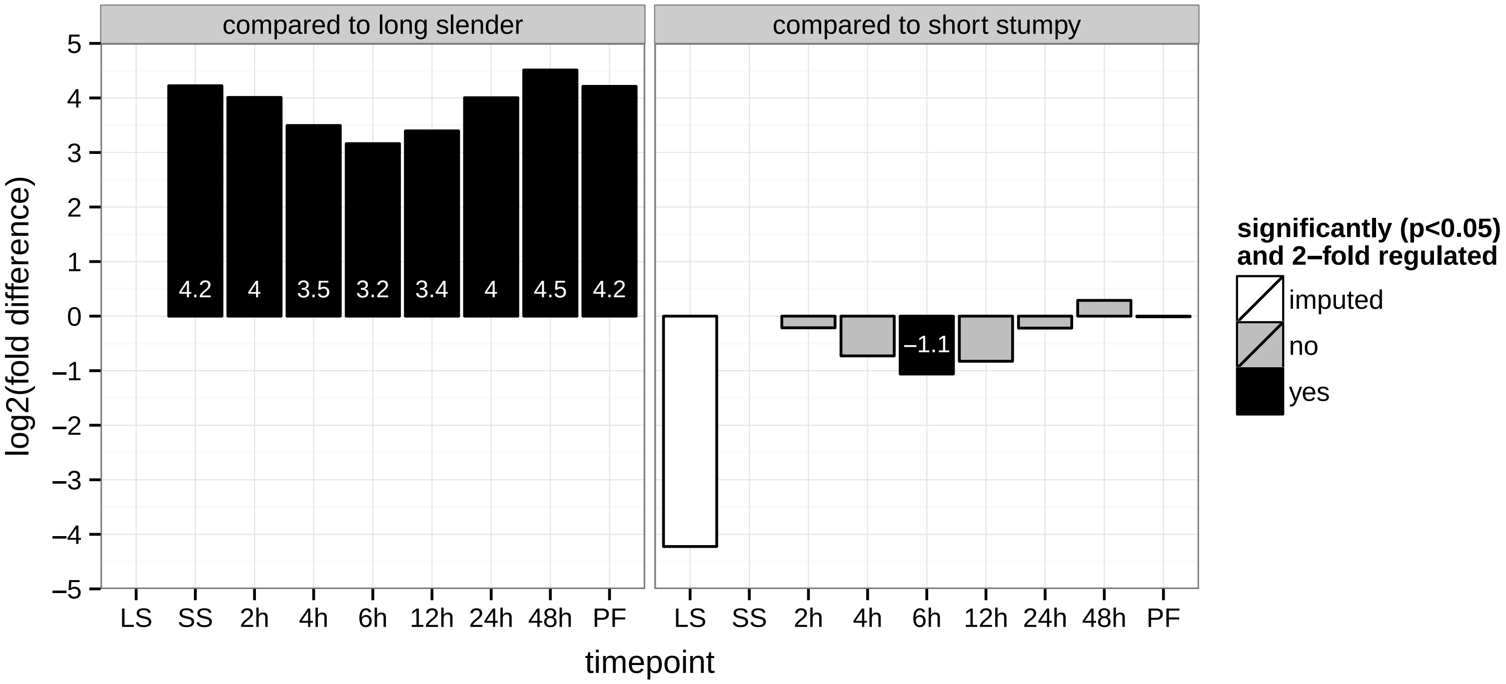
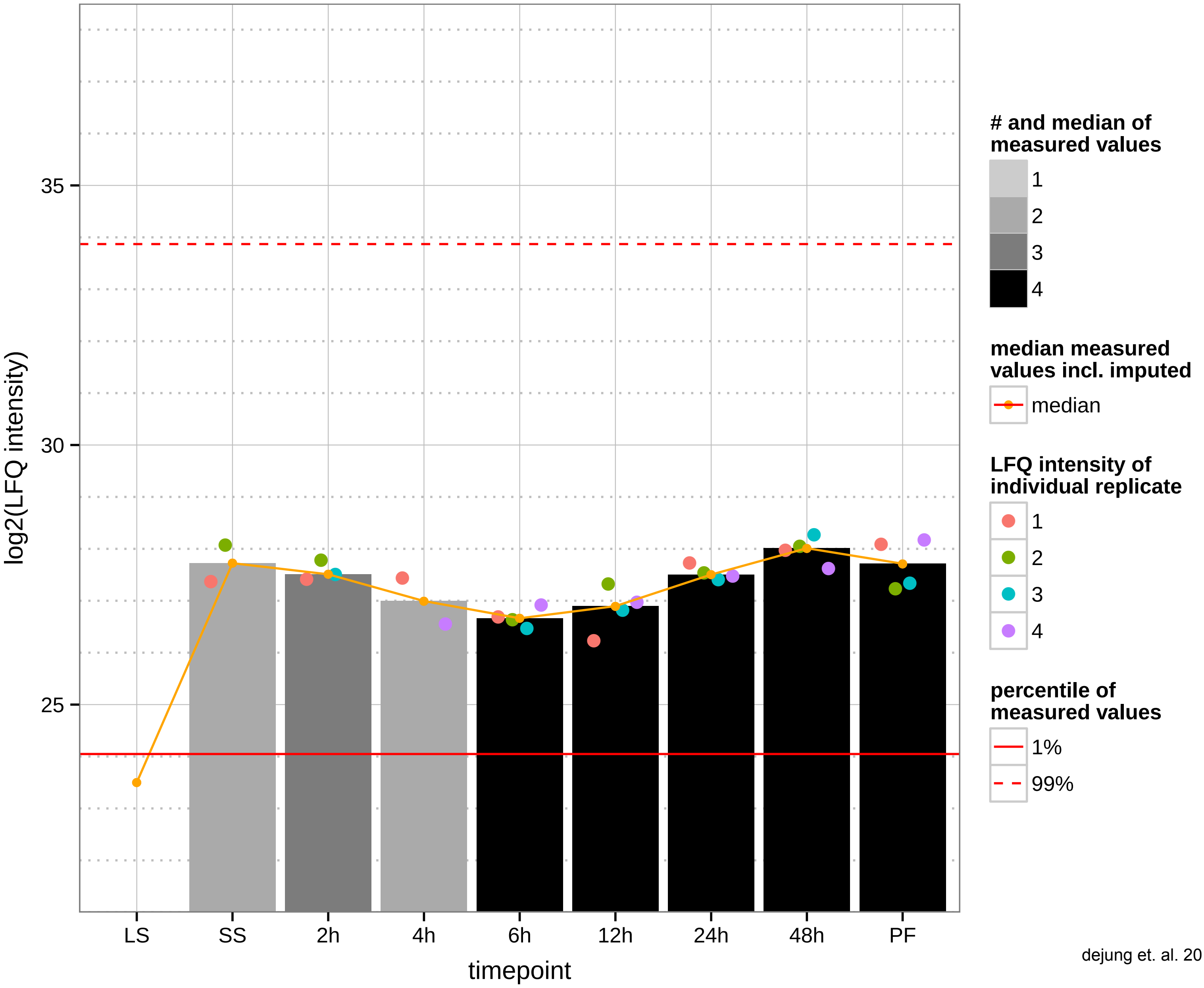
TPR–repeat–containing chaperone protein DNAJ, putative, TPR repeat protein
Tb927.10.4900
AGOF: heat shock protein binding
AGOC: null
AGOP: protein folding
PGOF: heat shock protein binding, protein binding
PGOC: null
PGOP: null





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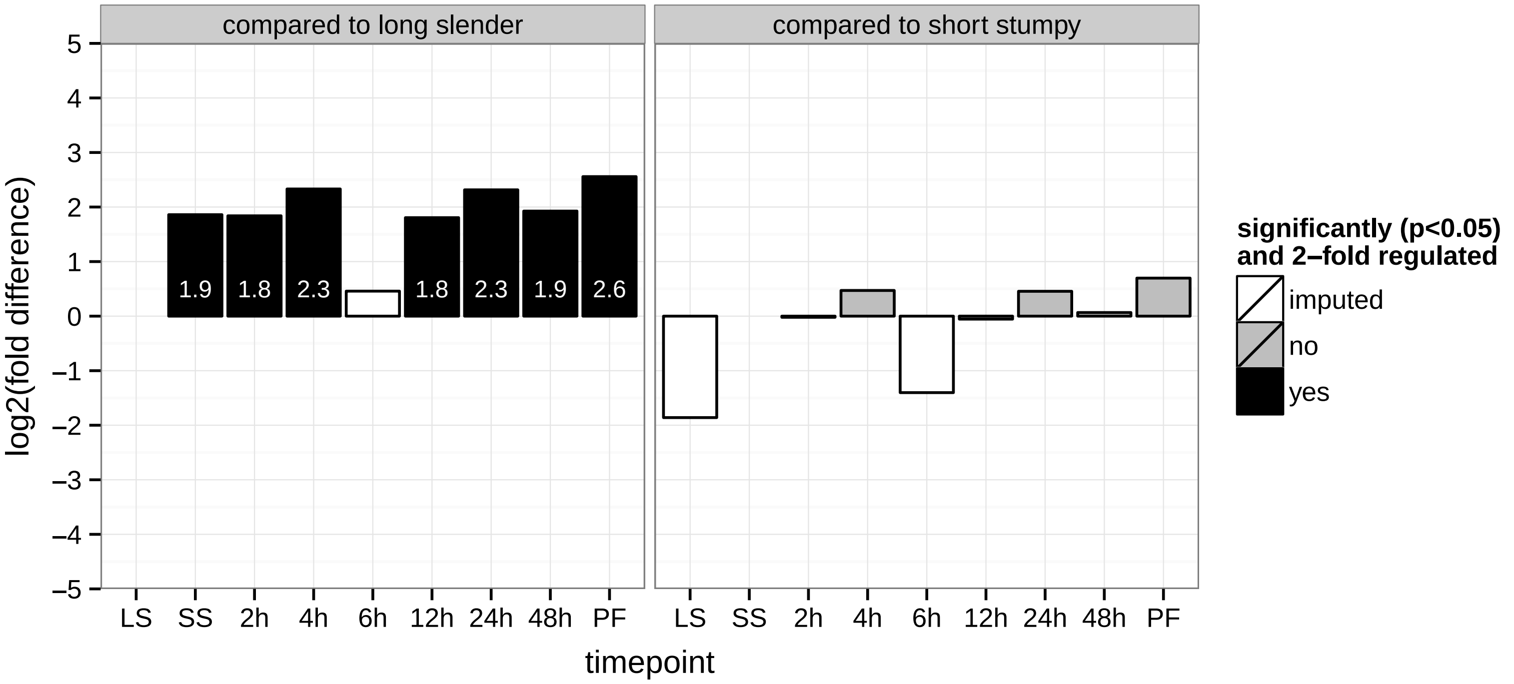
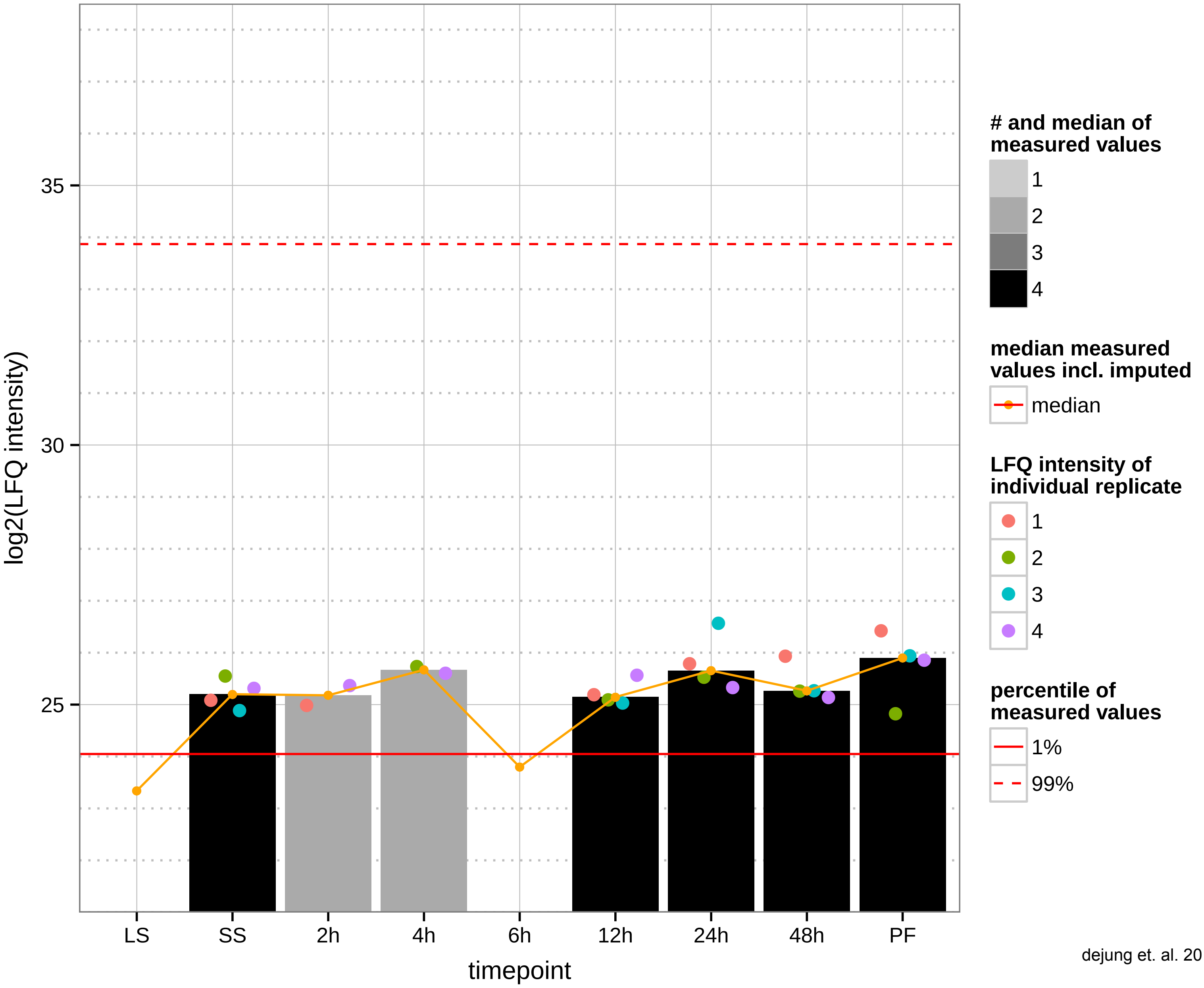
hypothetical protein, conserved
Tb927.10.7380
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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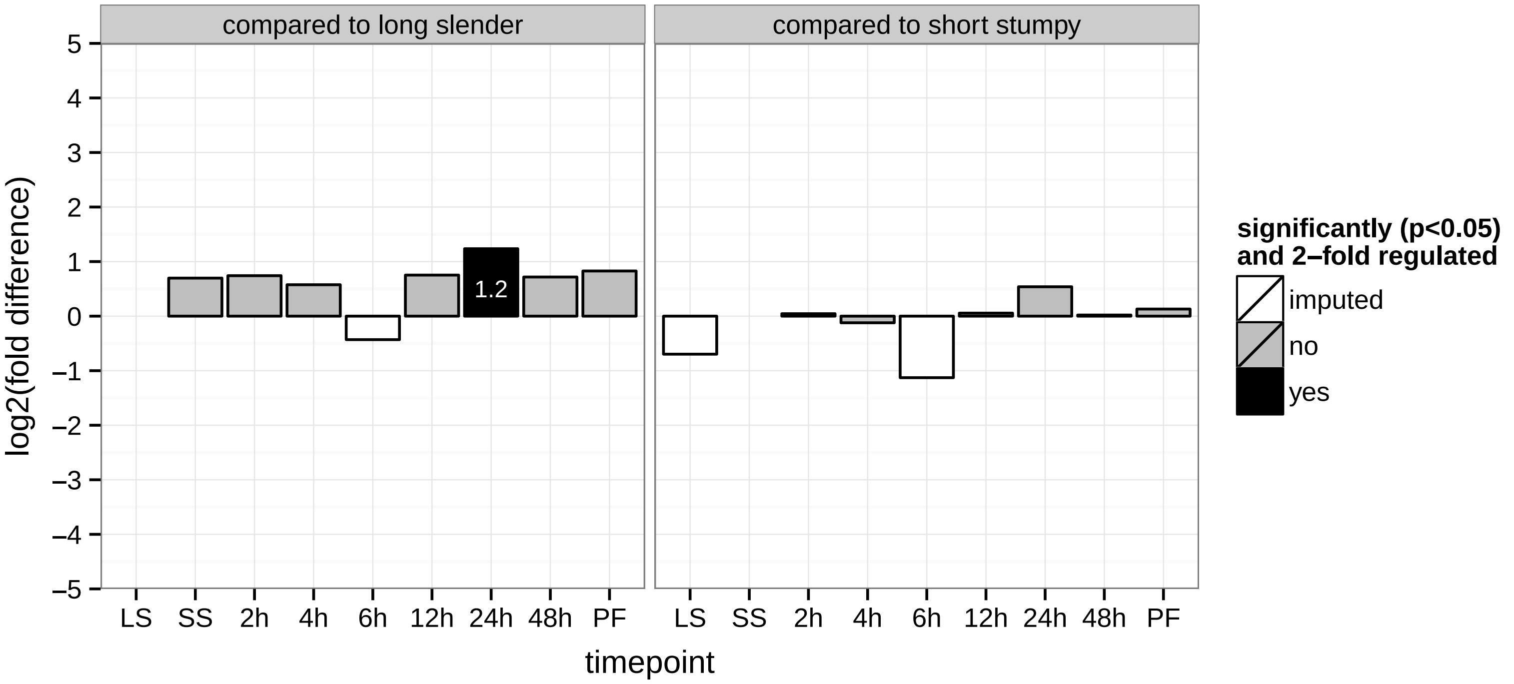
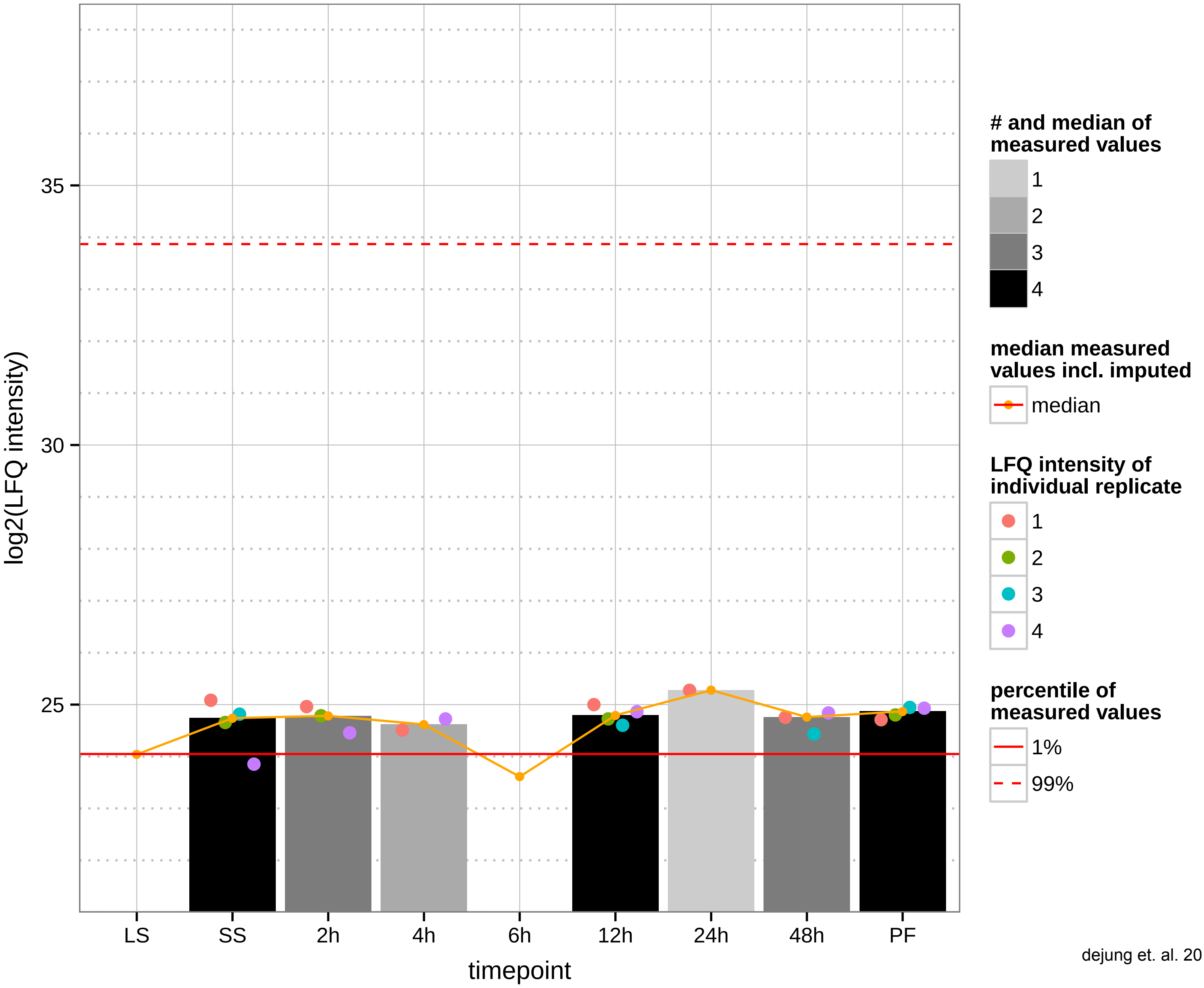
gamma–tubulin complex subunit, putative, spindle pole body protein, putative (GCP2)
Tb927.10.9770;Tb11.v5.0848
AGOF: null
AGOC: null, microtubule organizing center, spindle pole
AGOP: null, microtubule cytoskeleton organization
PGOF: null
PGOC: microtubule organizing center, spindle pole
PGOP: microtubule cytoskeleton organization





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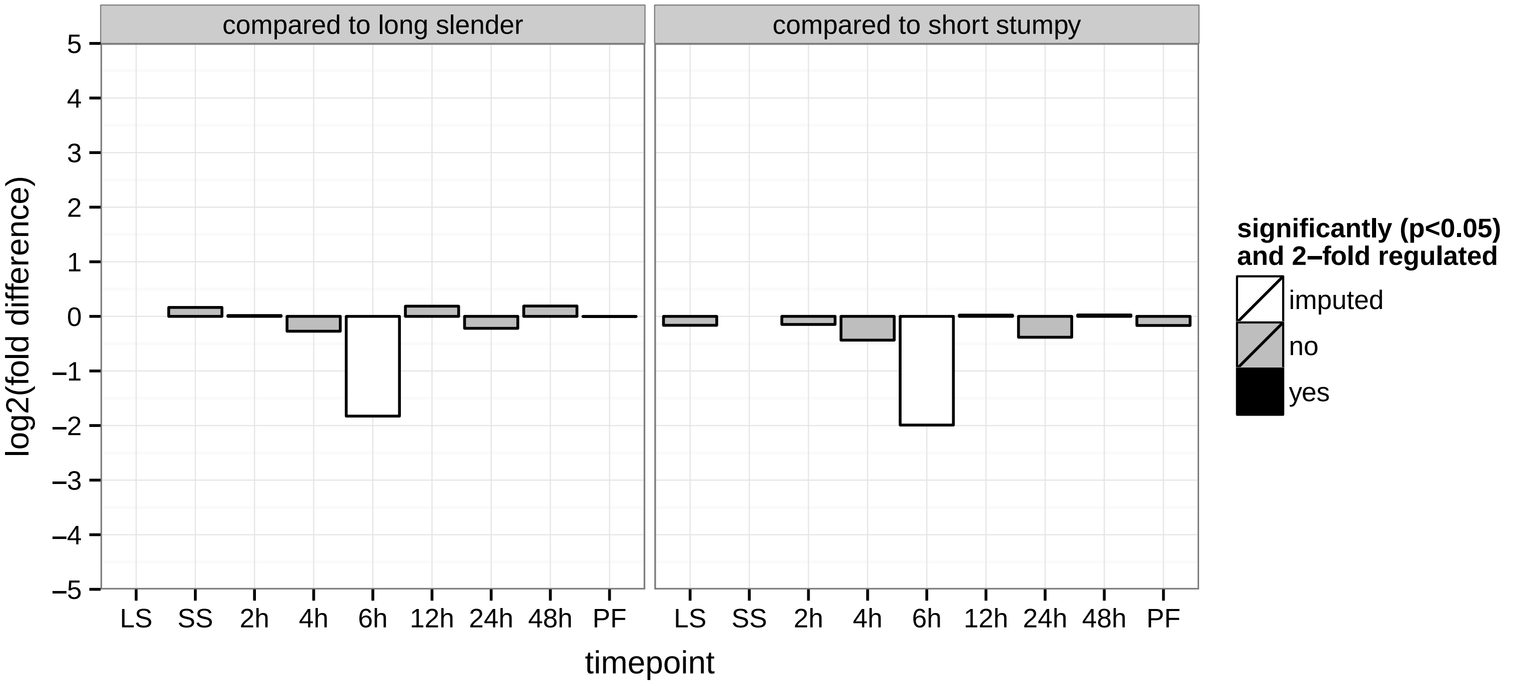
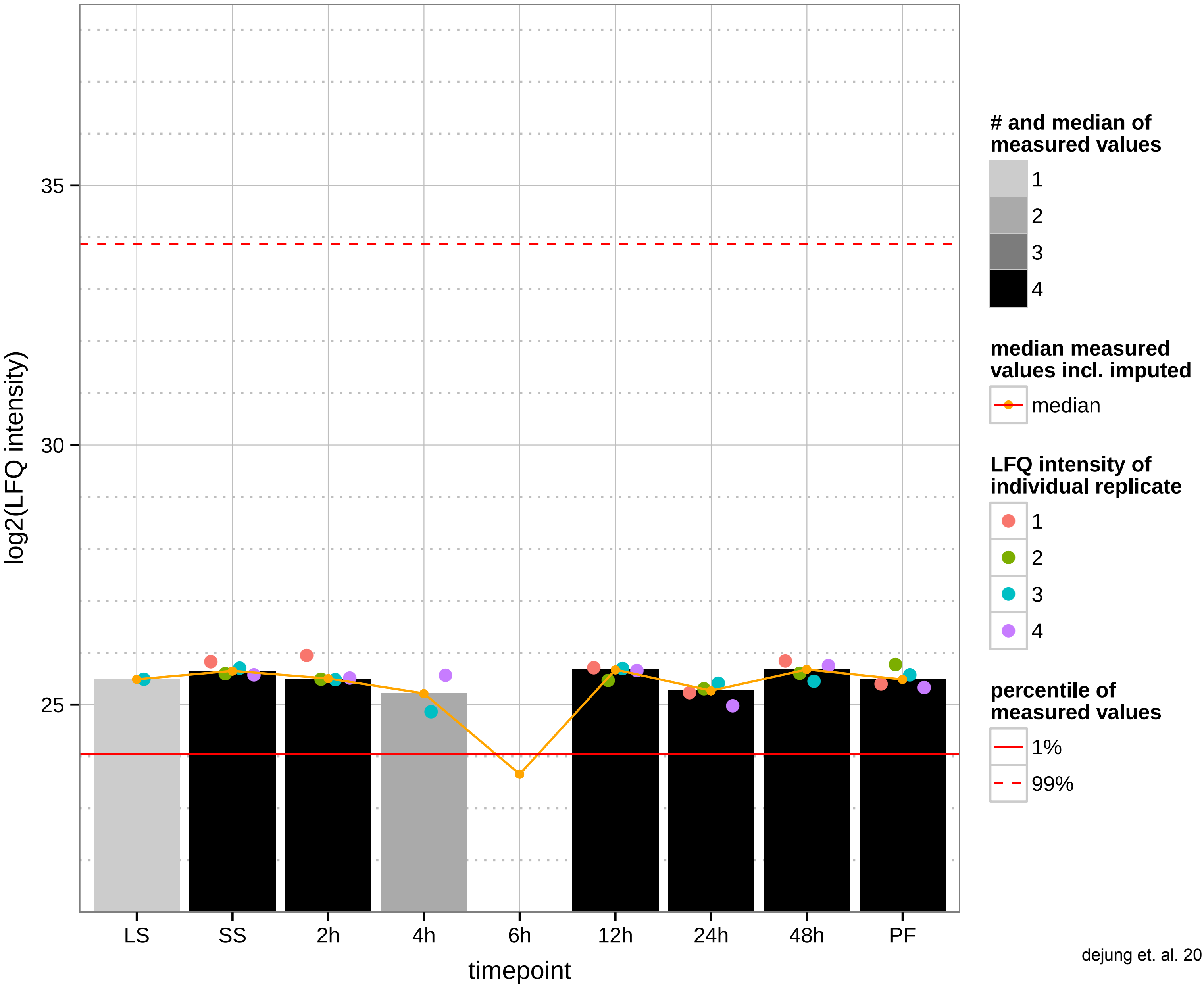
calpain–like cysteine peptidase, putative, antigen
Tb927.11.1130
AGOF: null, calcium–dependent cysteine–type endopeptidase activity
AGOC: null, intracellular
AGOP: null, proteolysis
PGOF: null, calcium–dependent cysteine–type endopeptidase activity
PGOC: null, intracellular
PGOP: null, proteolysis





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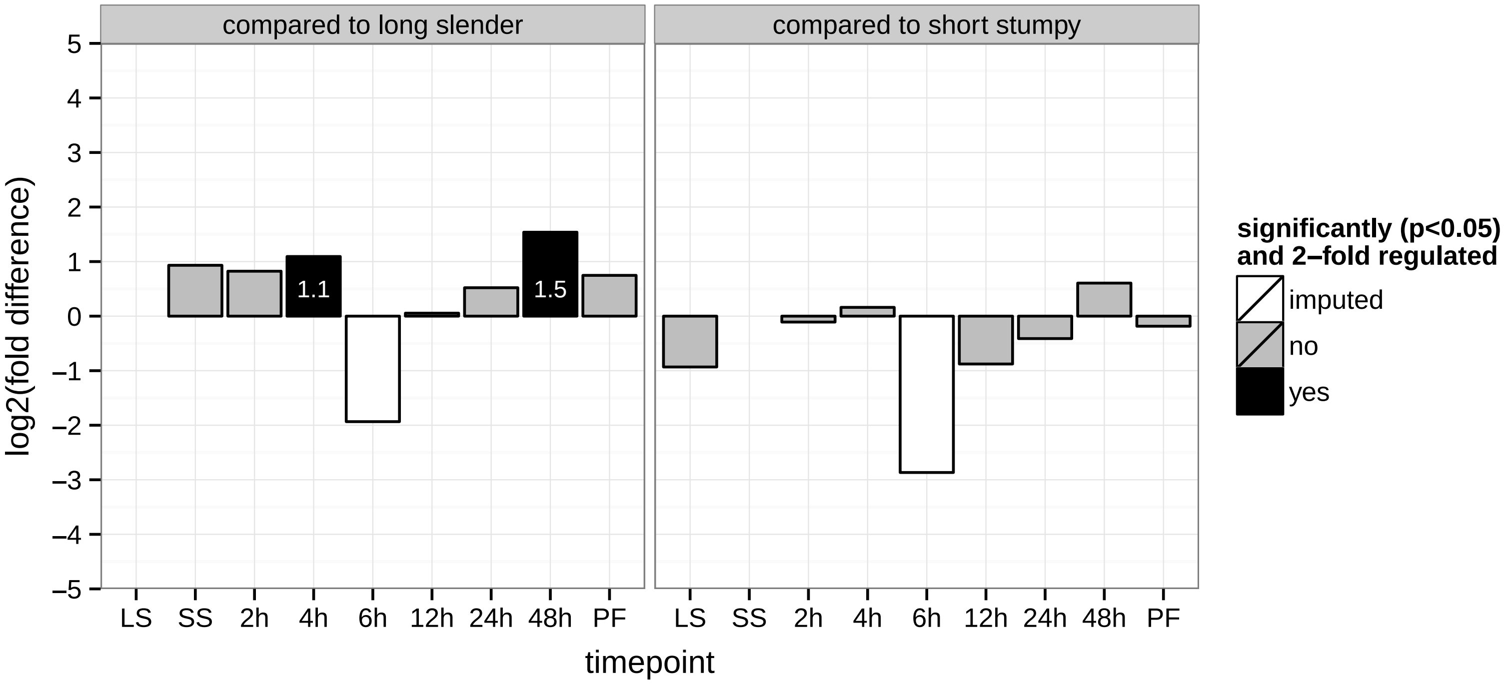
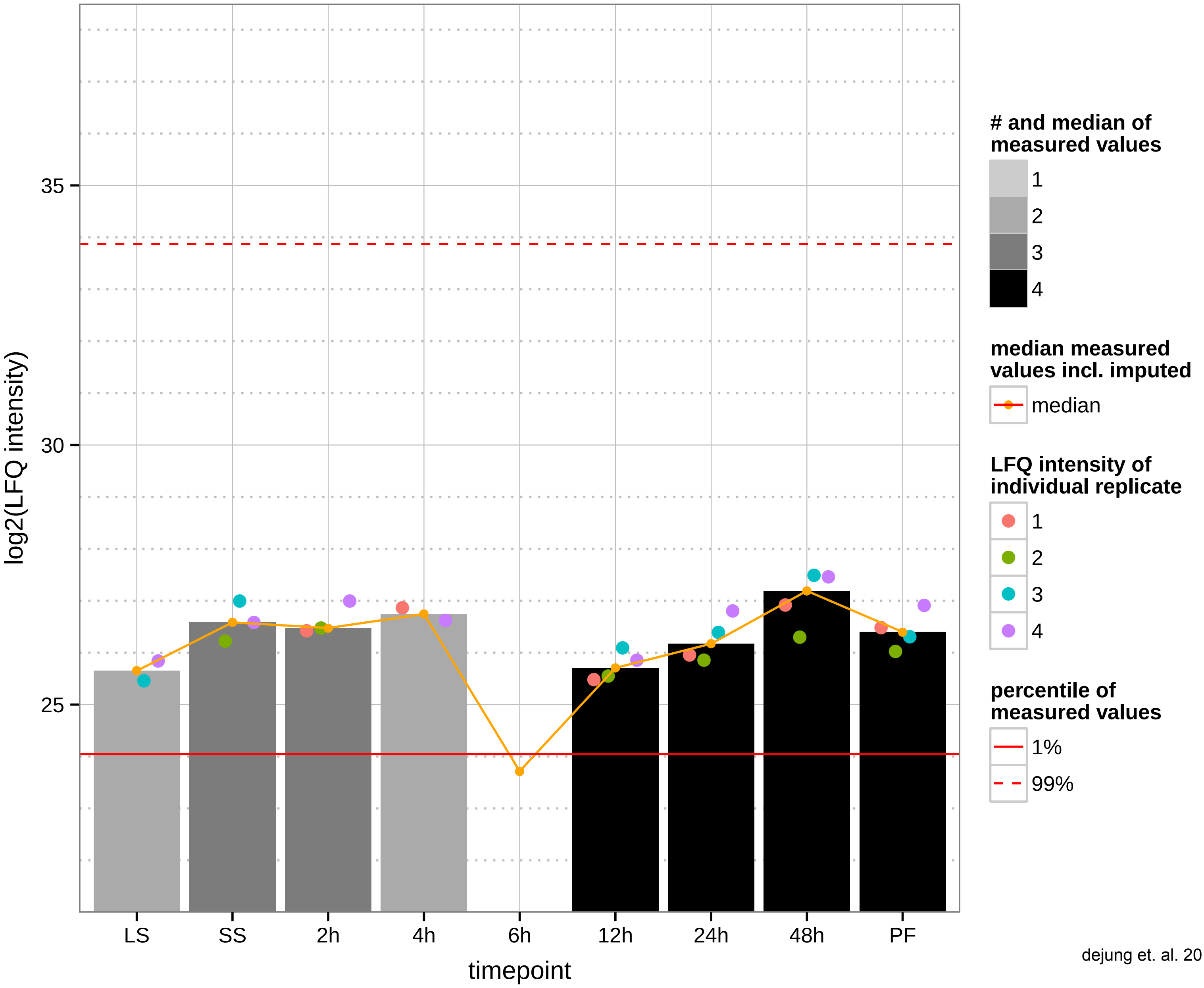
ornithine decarboxylase (ODC)
Tb927.11.13730
AGOF: ornithine decarboxylase activity
AGOC: null
AGOP: polyamine biosynthetic process
PGOF: catalytic activity
PGOC: null
PGOP: null





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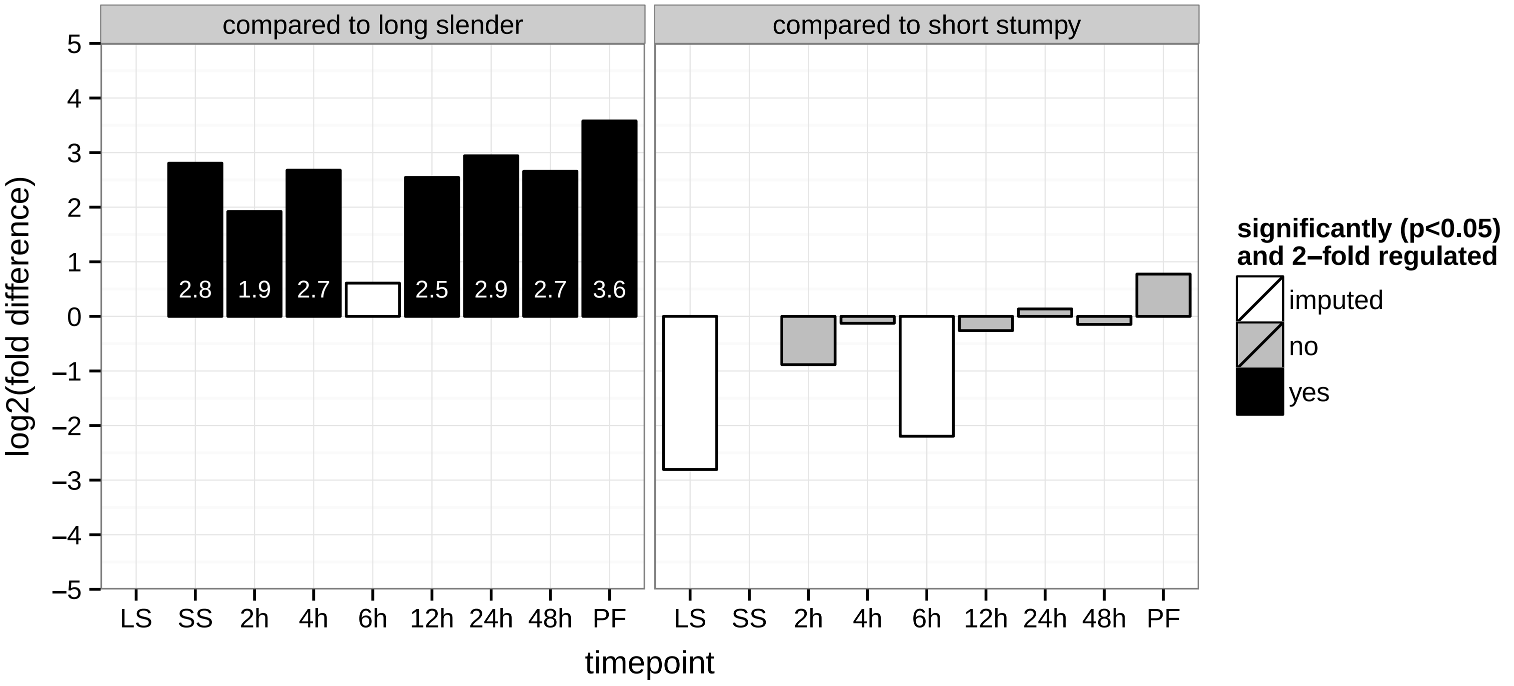
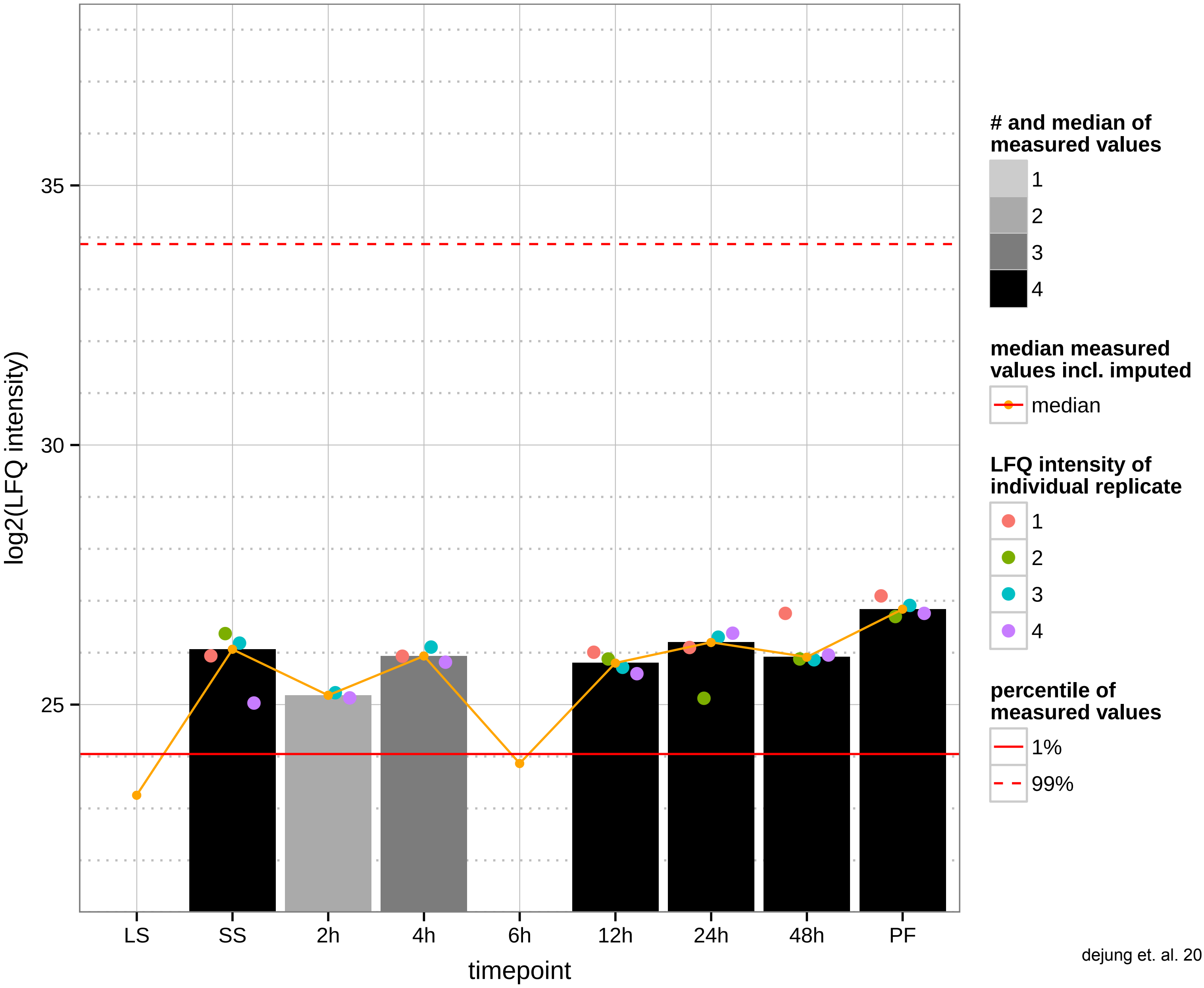
hypothetical protein, conserved
Tb927.11.15940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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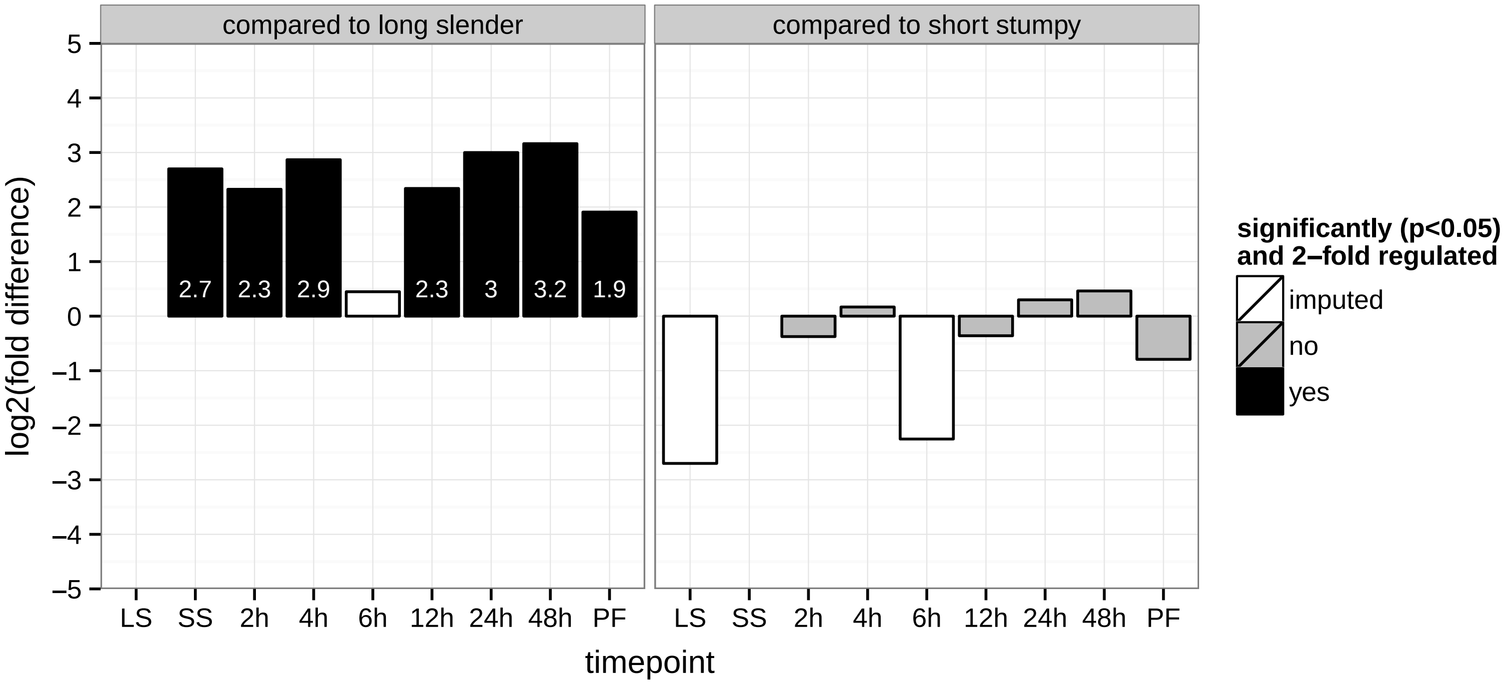
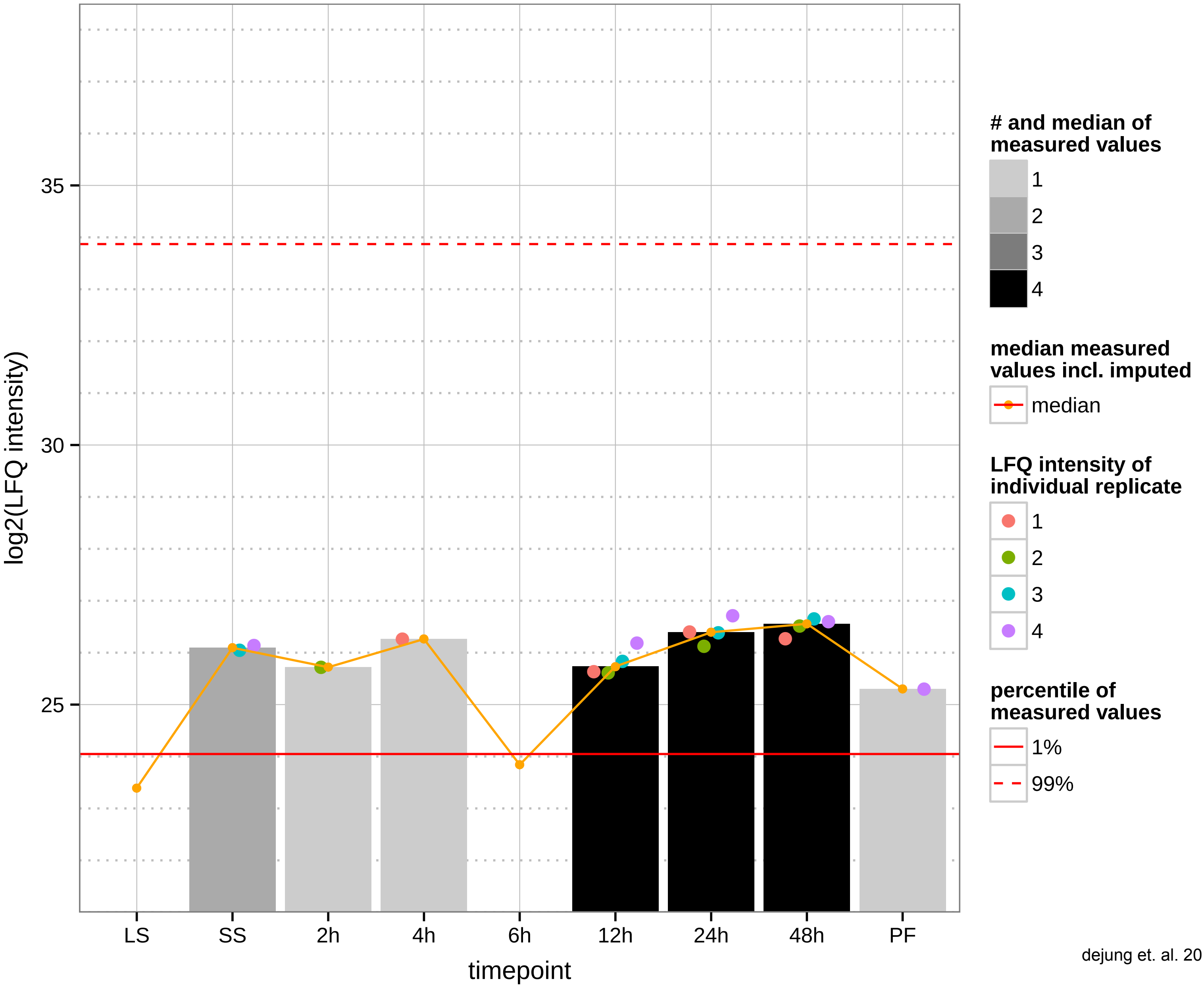
hypothetical protein, conserved
Tb927.11.2580
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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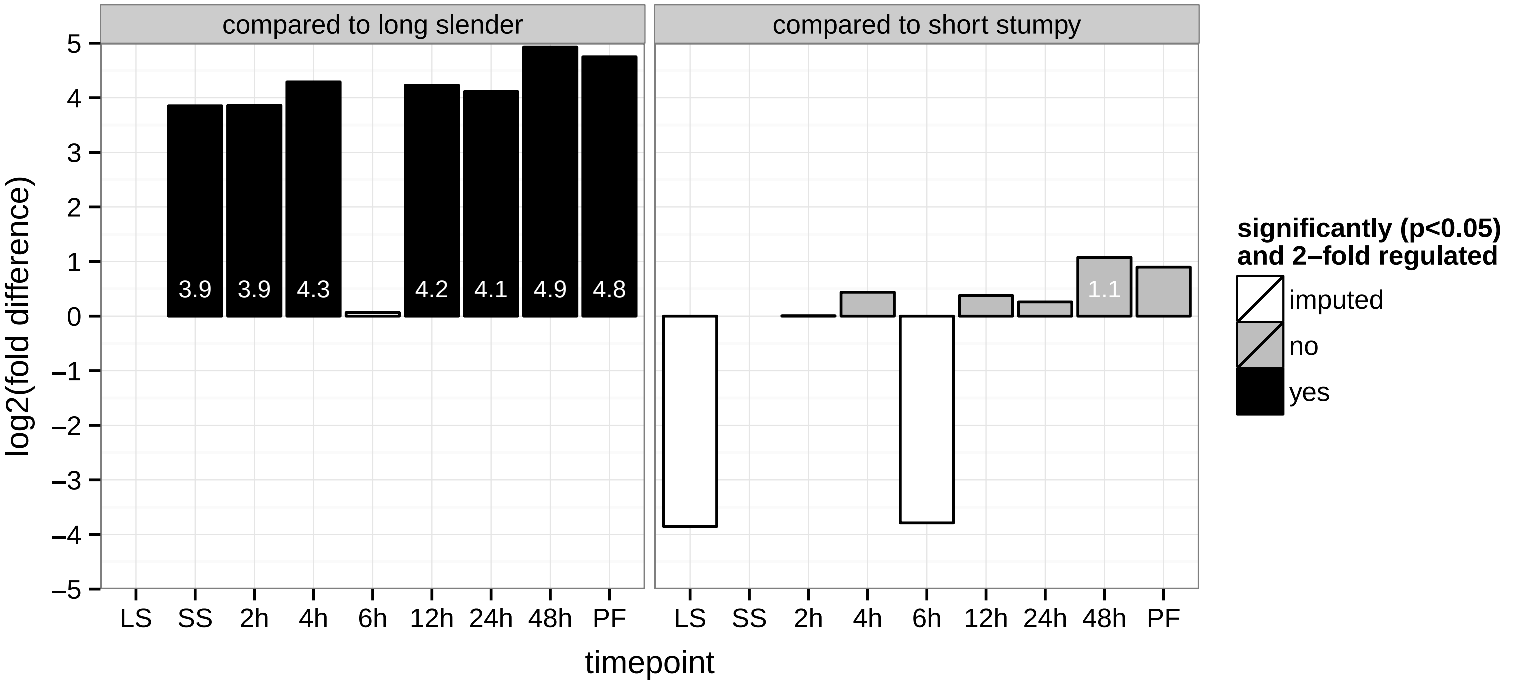
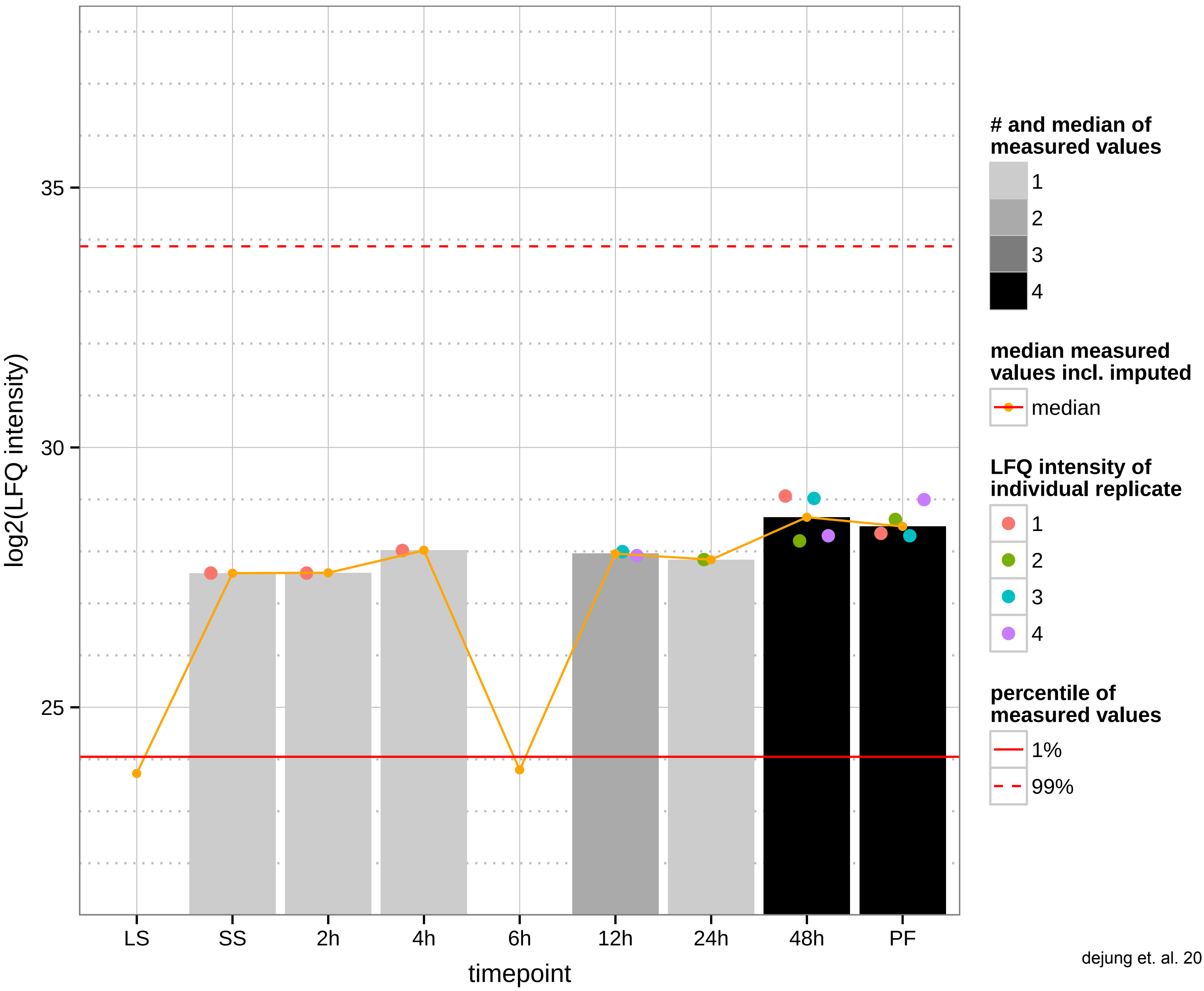
long–chain–fatty–acid–CoA ligase, putative, acyl–CoA synthetase, fatty acid thiokinase (long chain)
Tb927.11.4490
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: metabolic process





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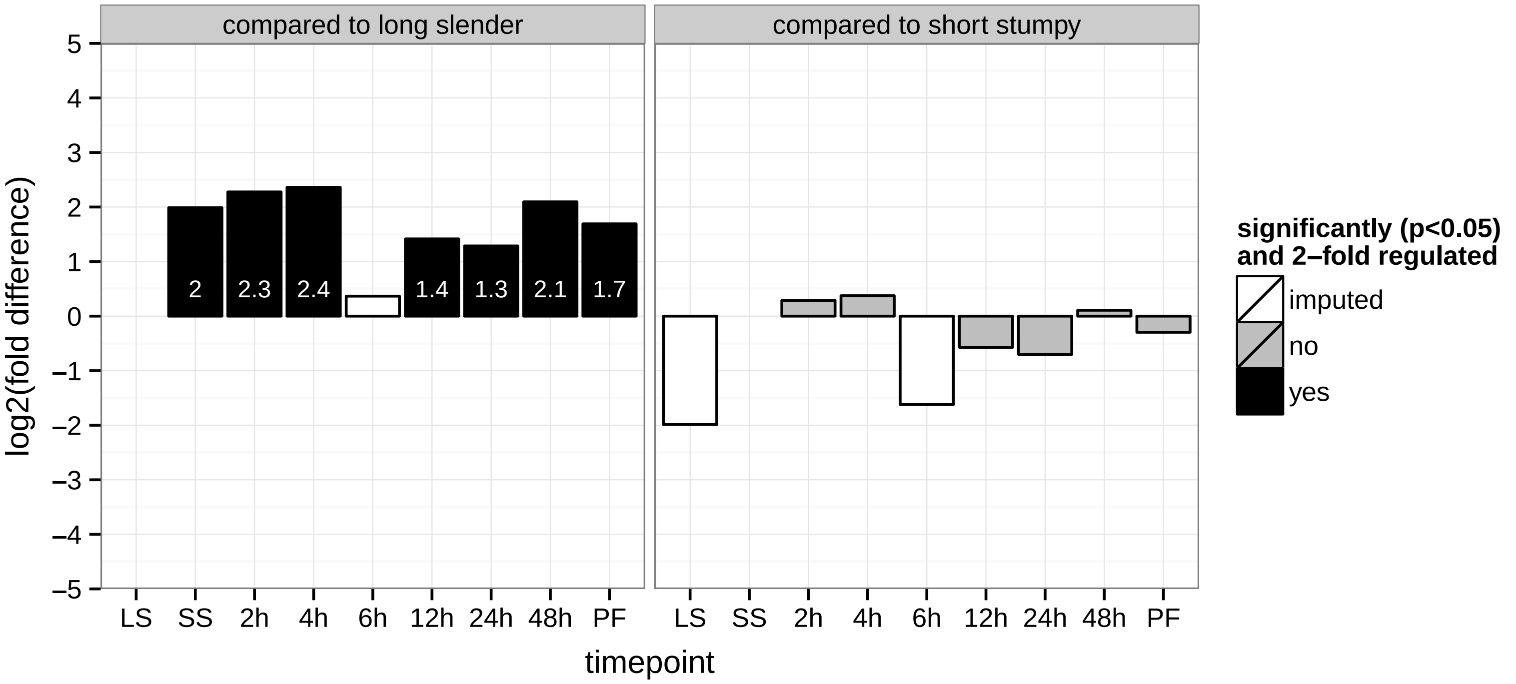
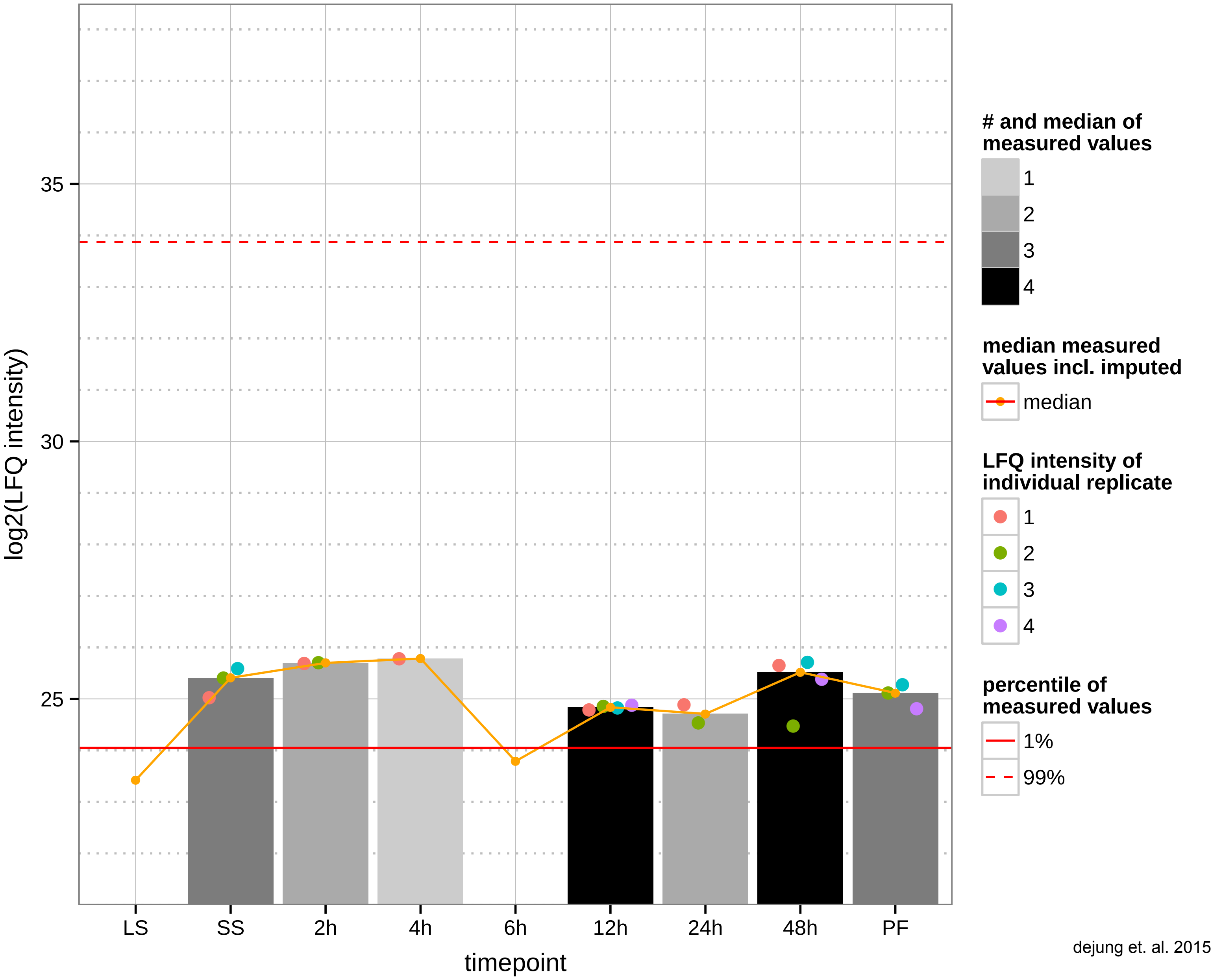
protein kinase, putative
Tb927.11.7210
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity, histone serine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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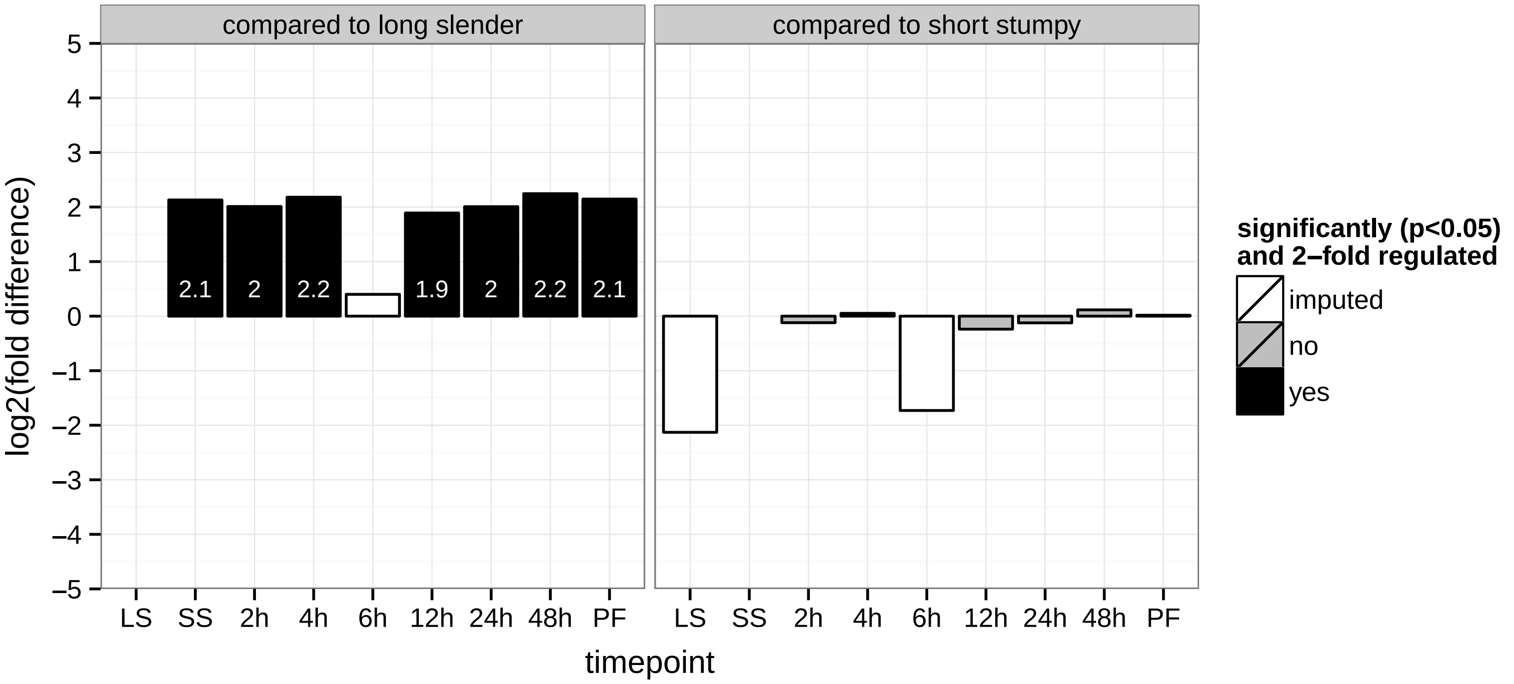
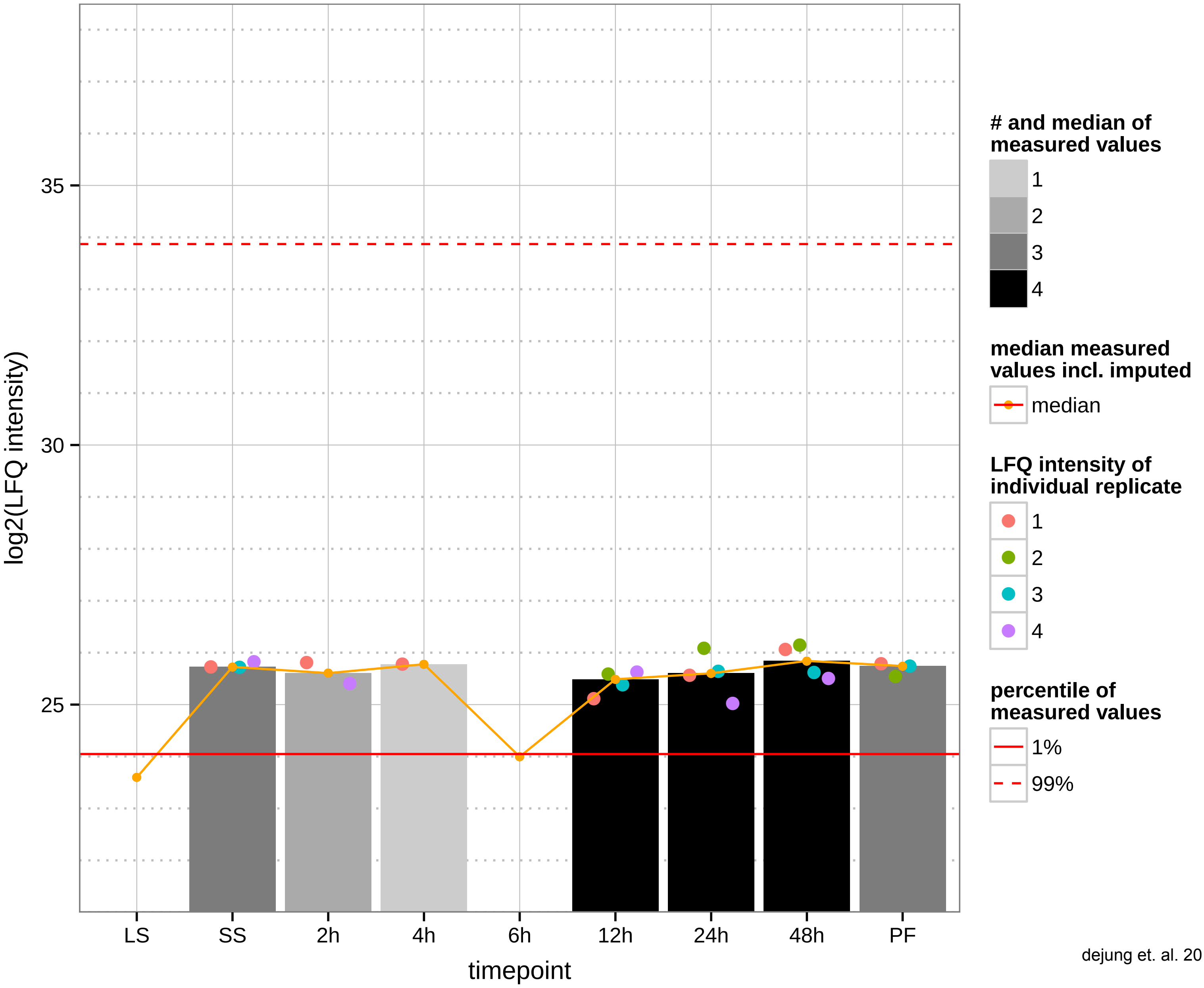
hypothetical protein, conserved
Tb927.11.7330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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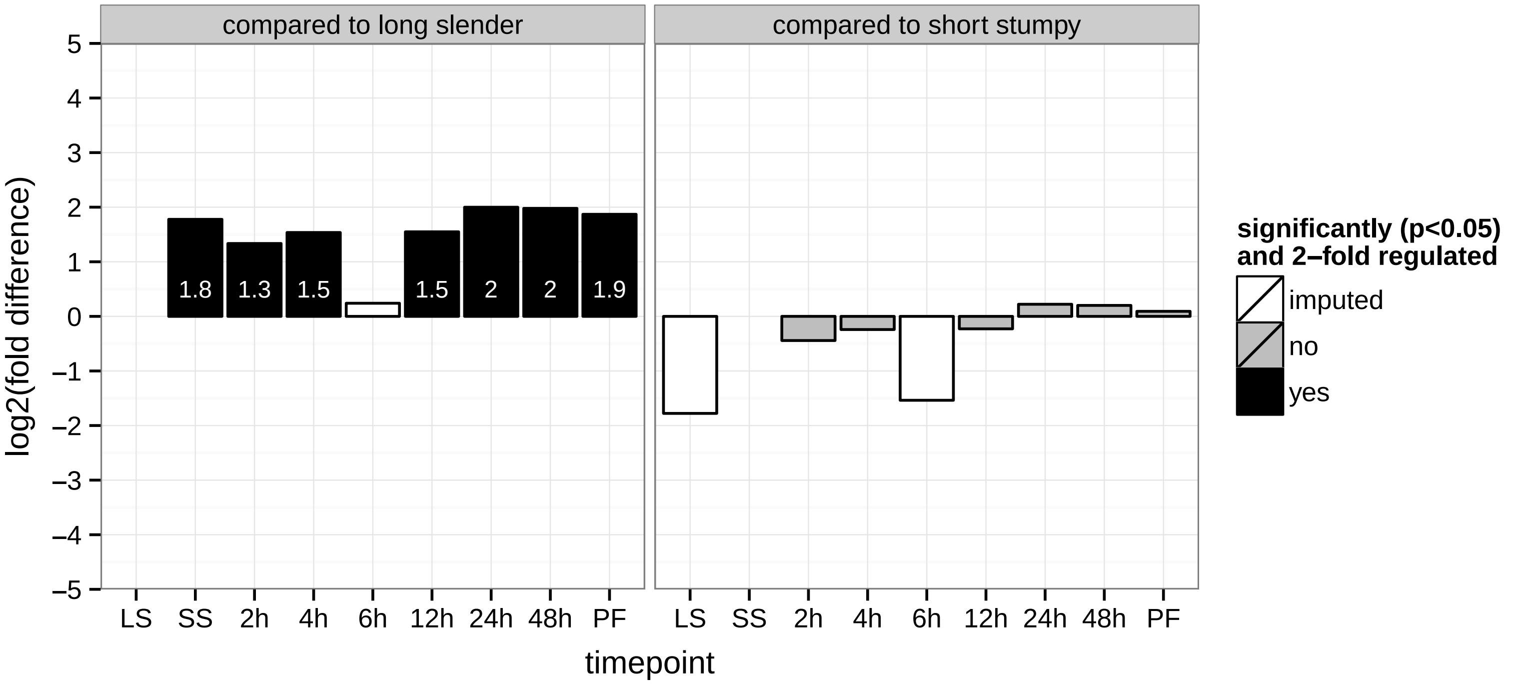
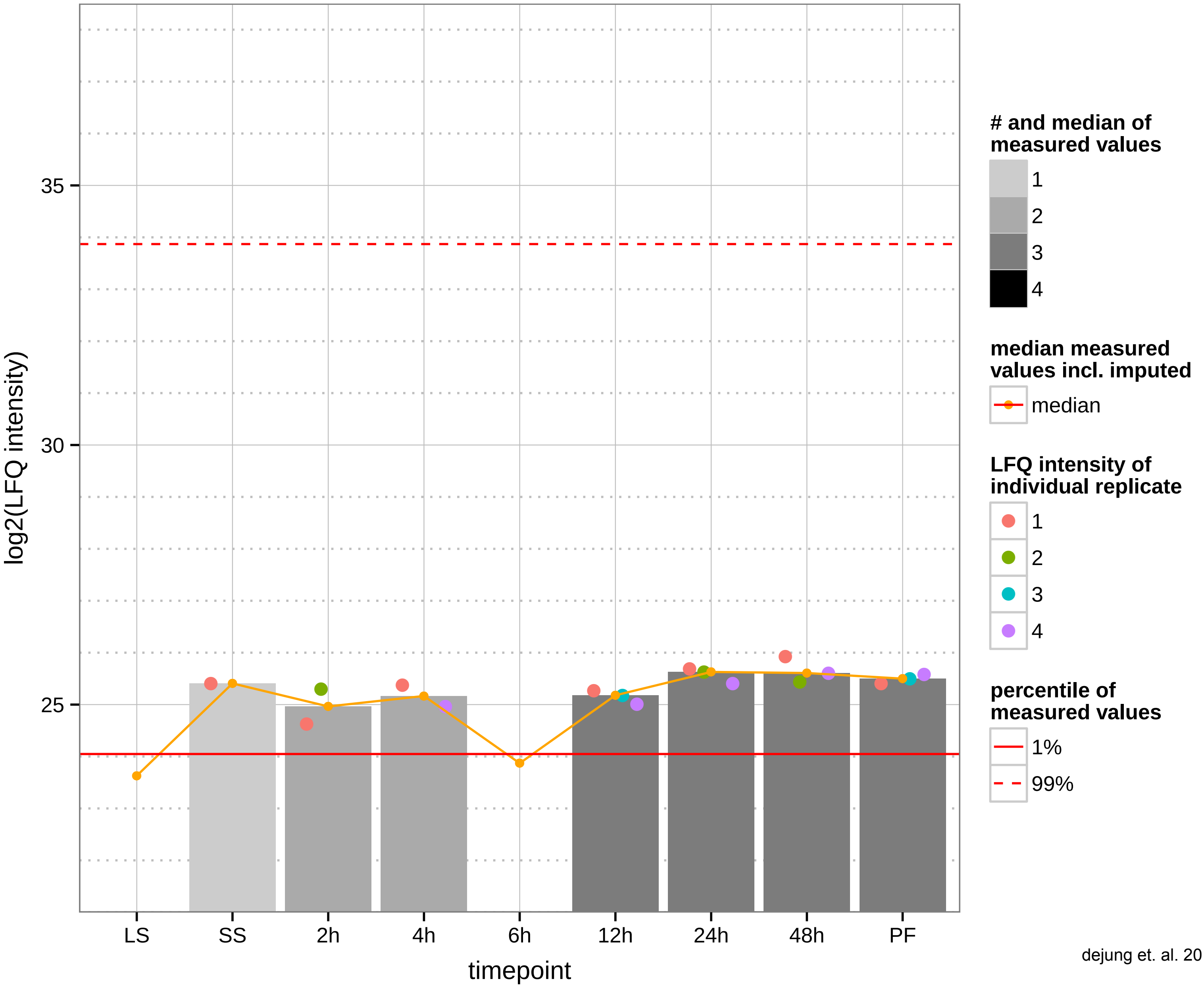
hypothetical protein, conserved
Tb927.2.2200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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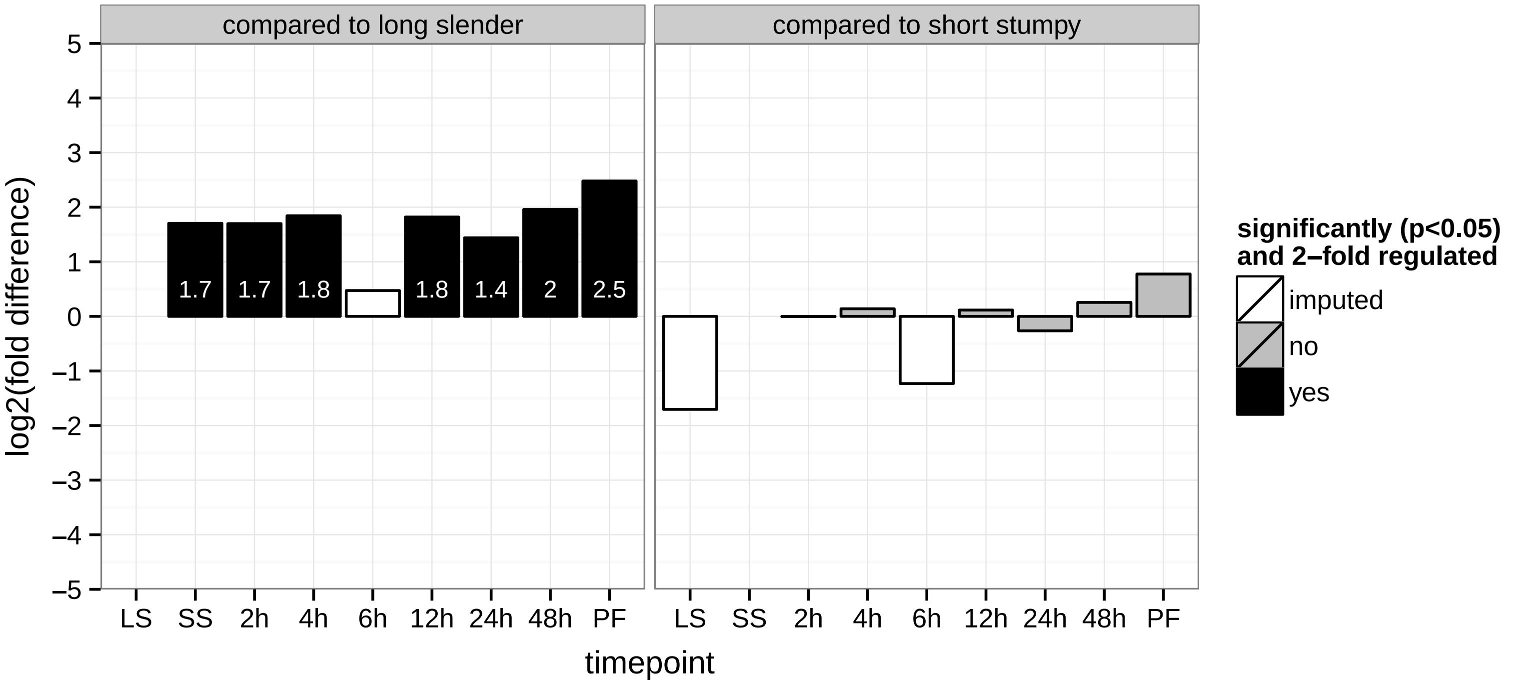
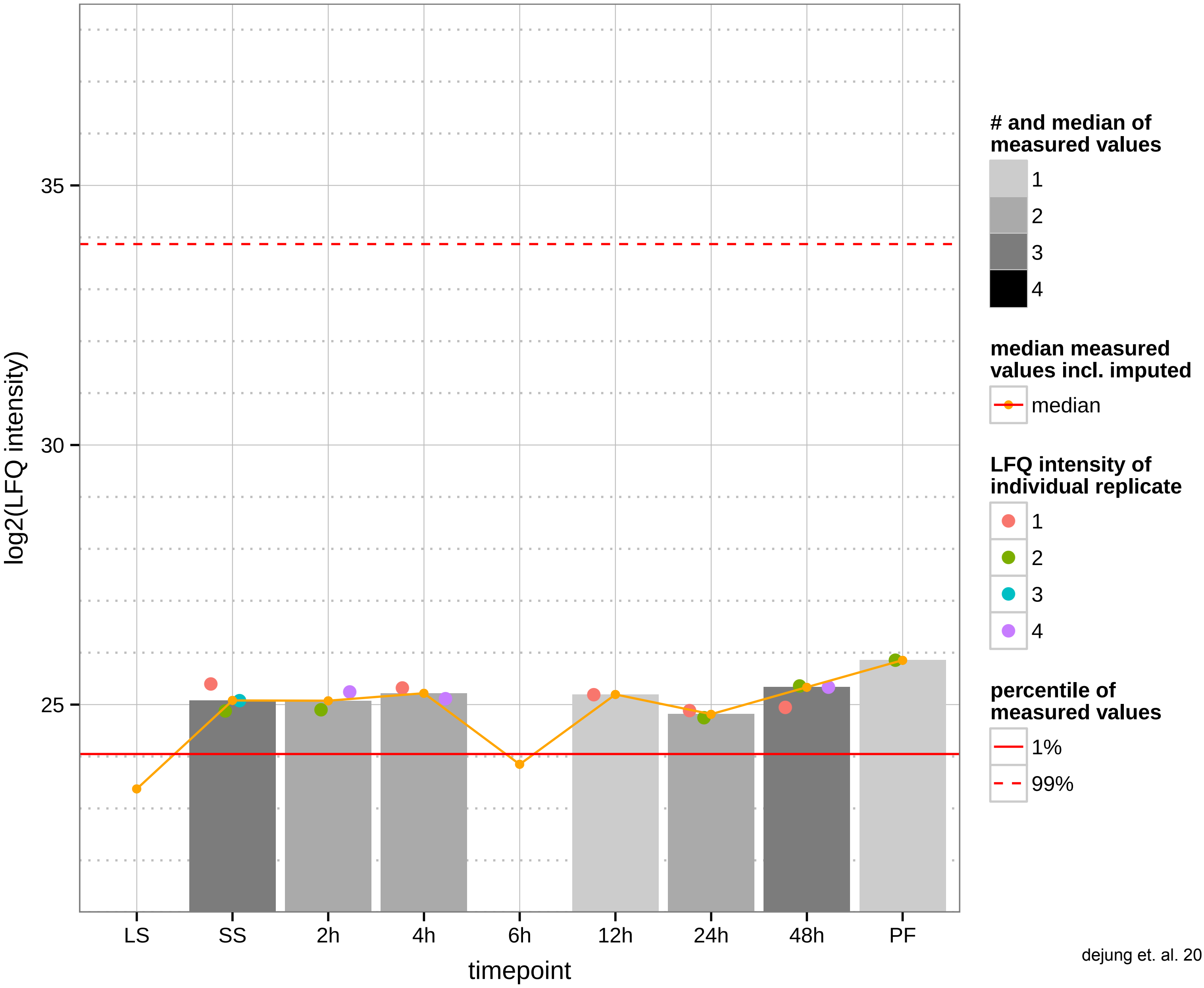
protein kinase, putative
Tb927.2.5230
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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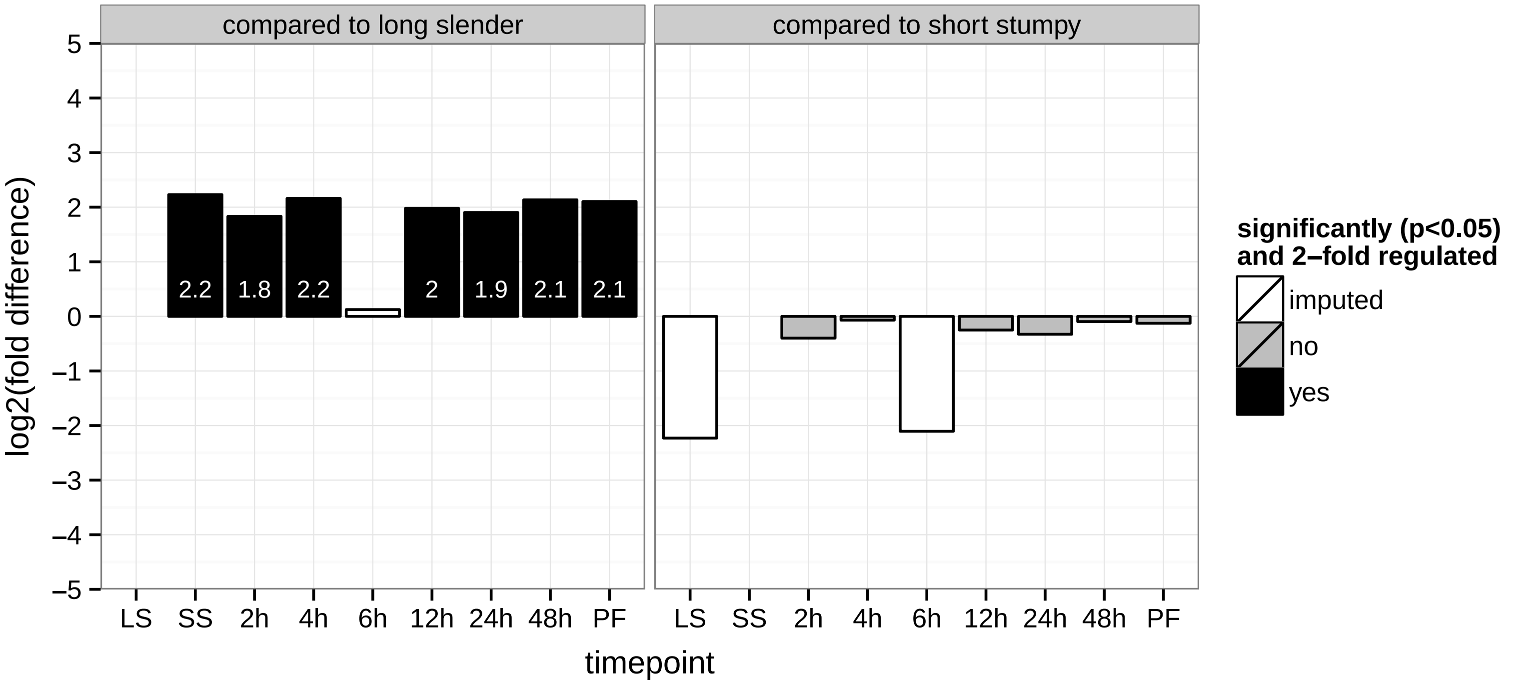
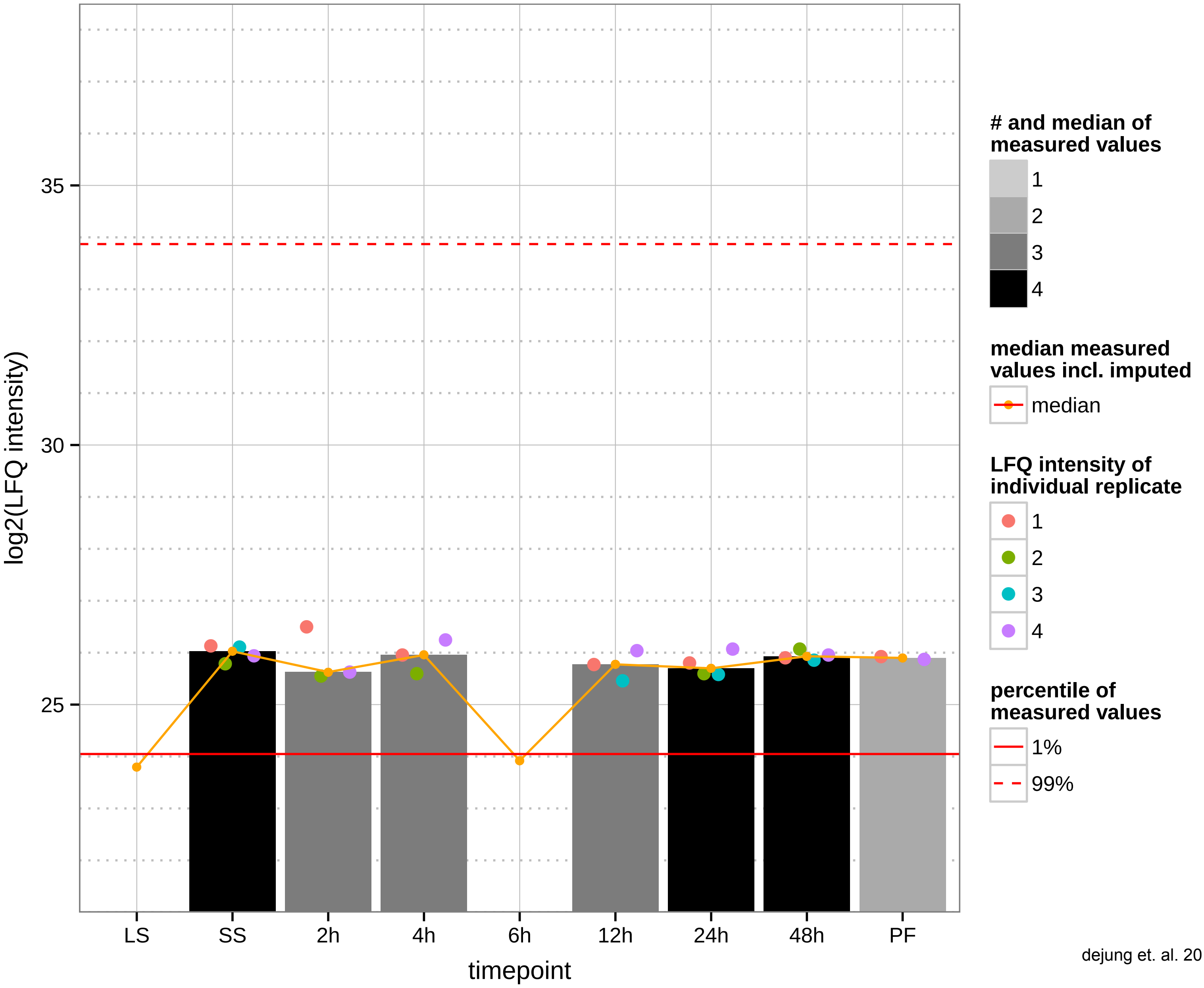
hypothetical protein, conserved
Tb927.3.2210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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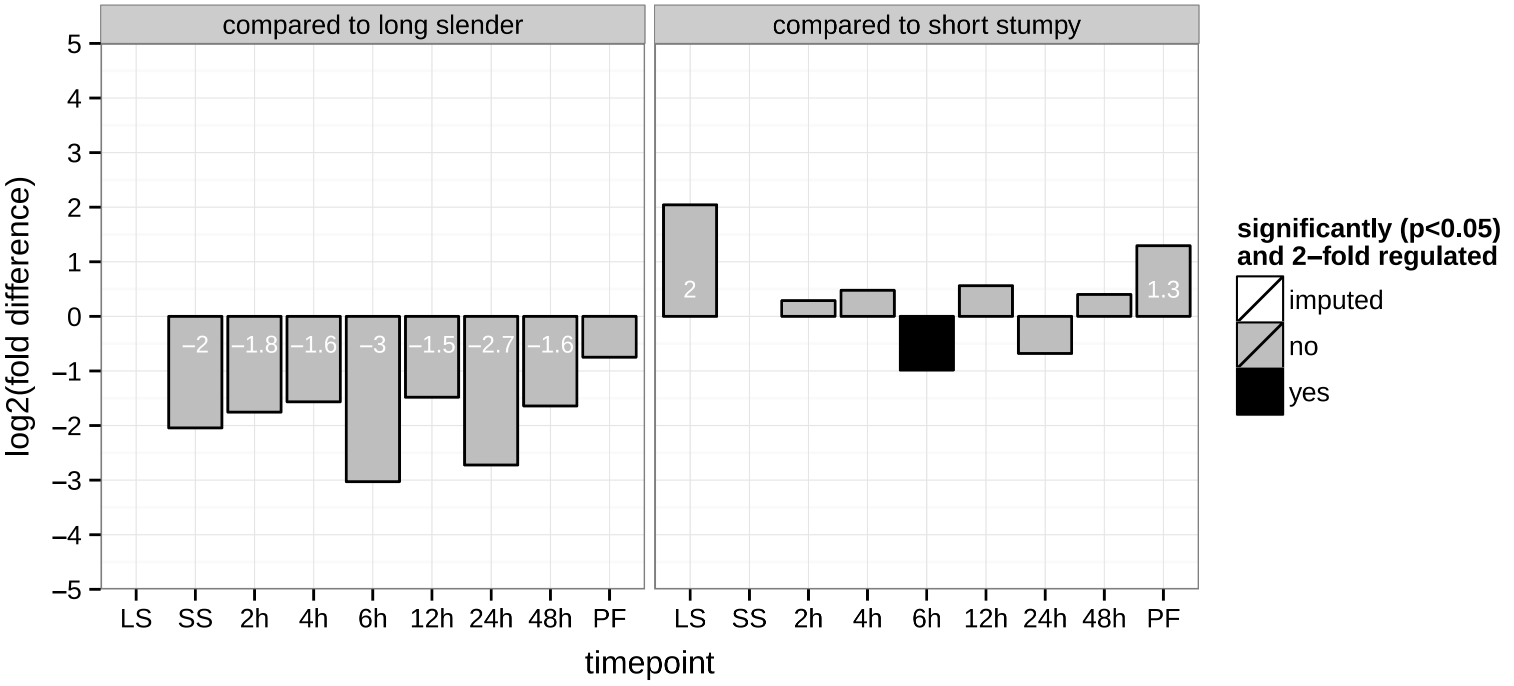
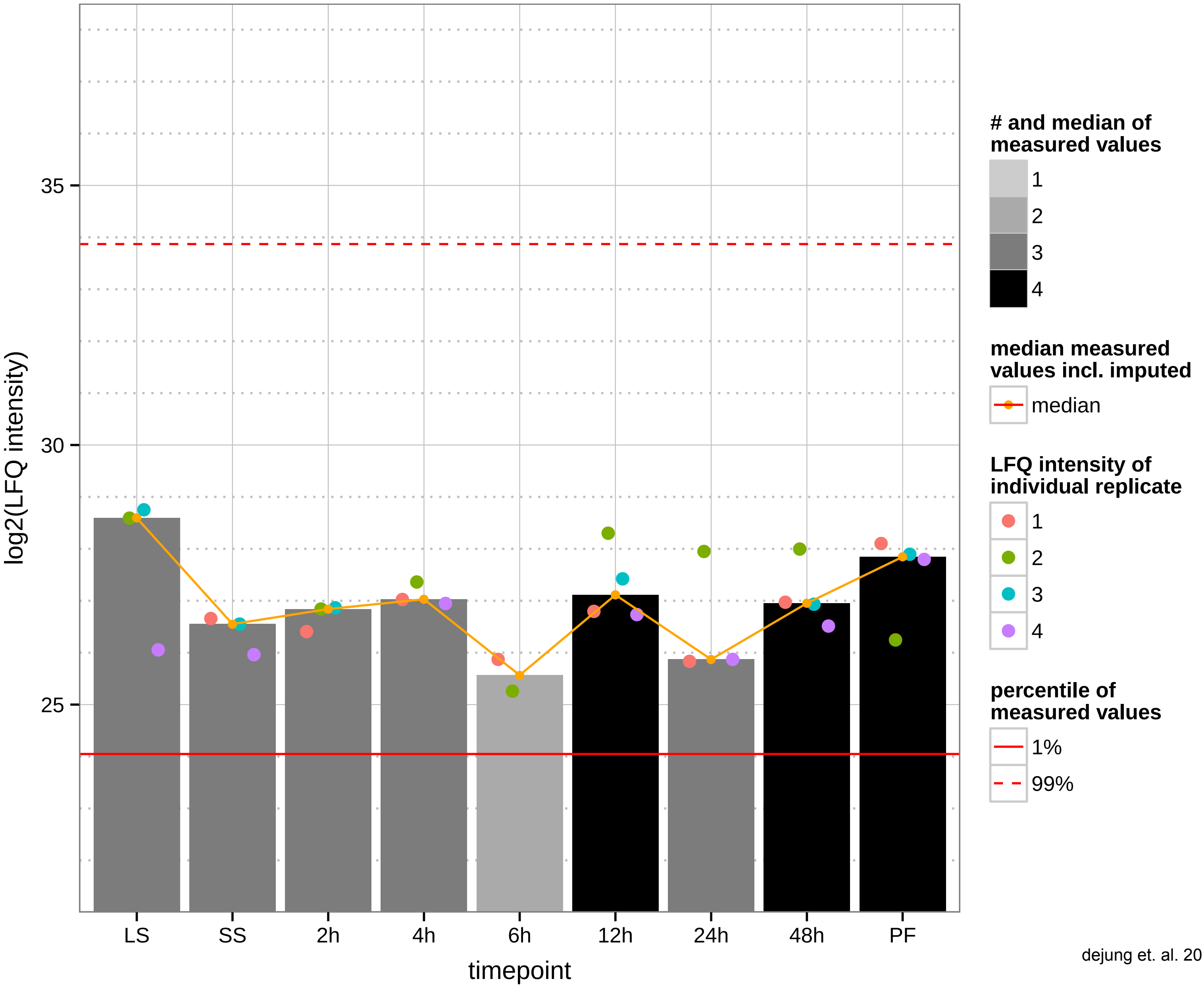
hypothetical protein, conserved
Tb927.3.5350
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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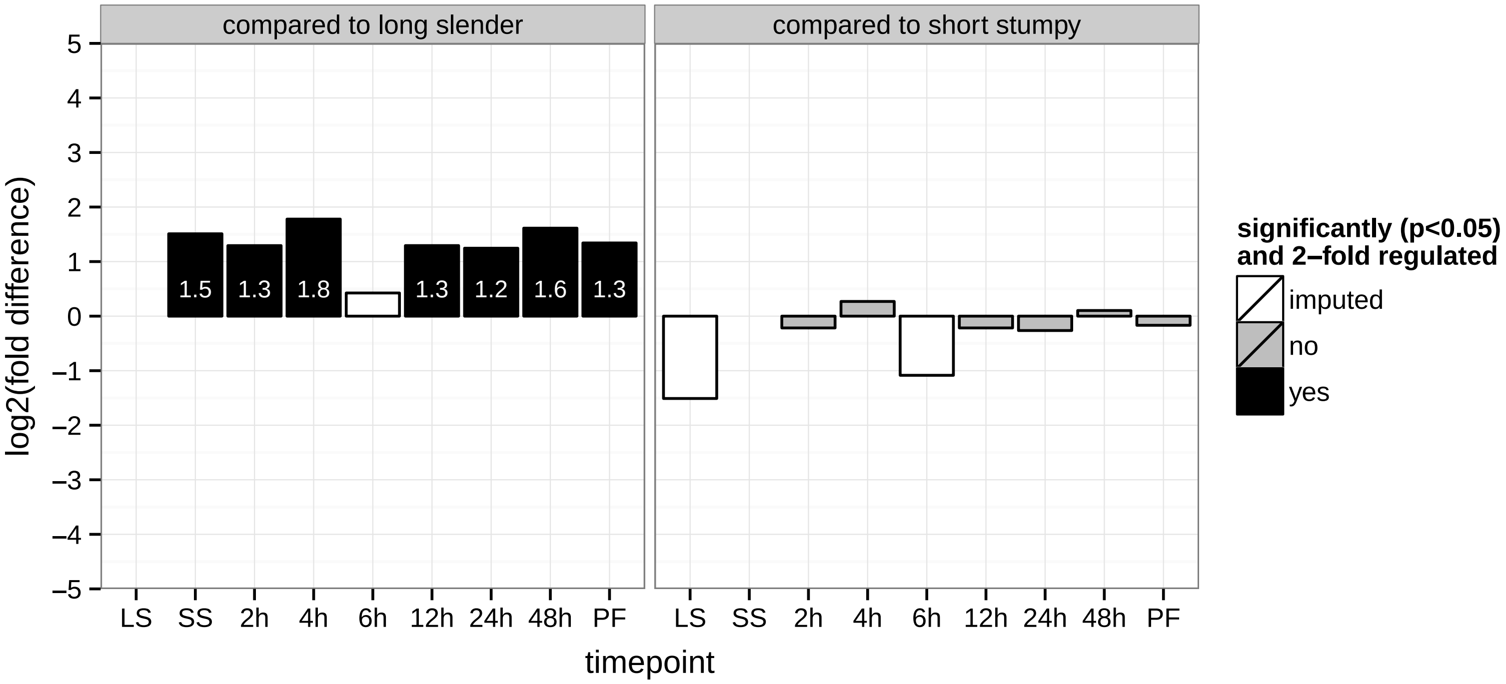
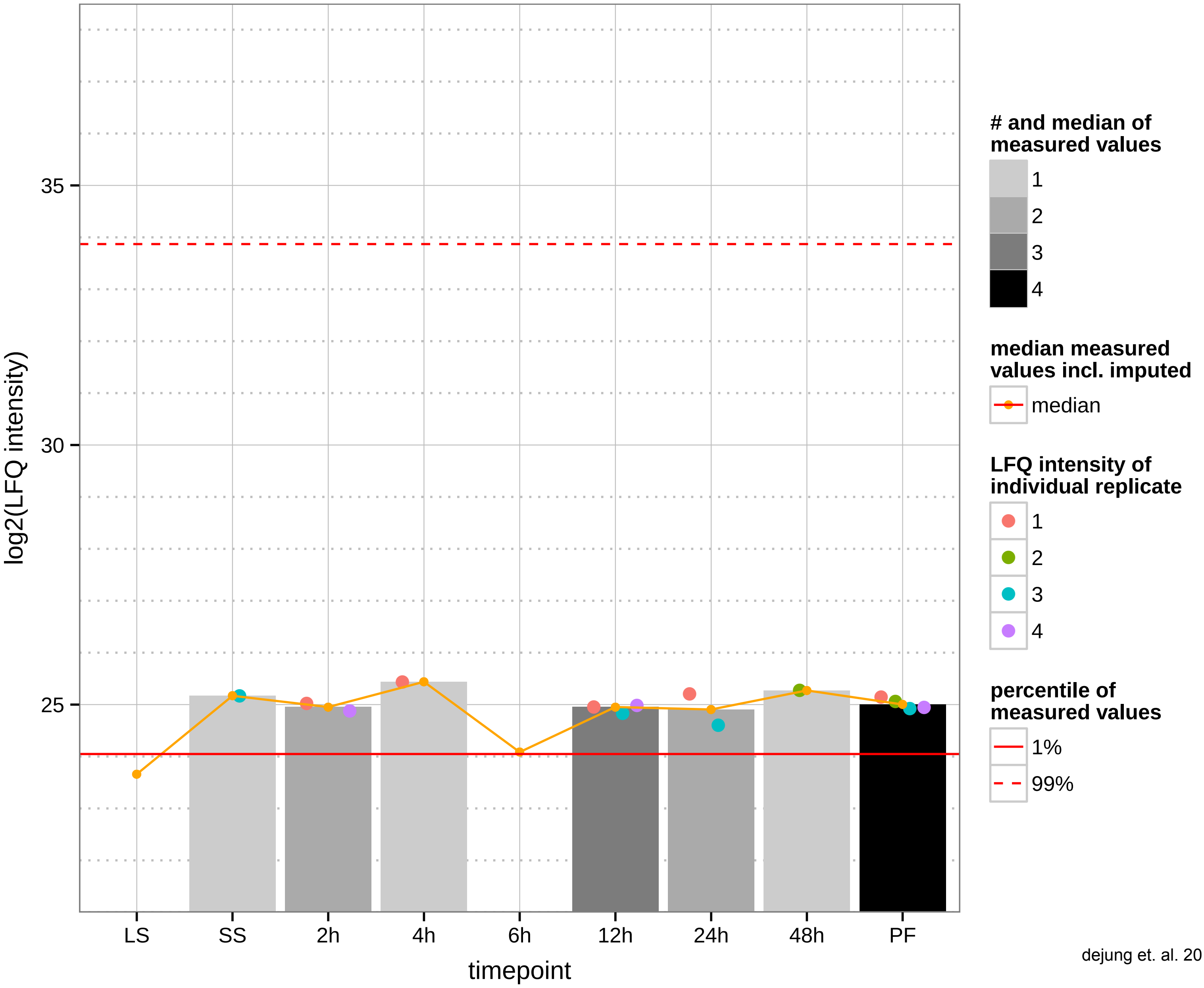
hypothetical protein, conserved
Tb927.4.4560
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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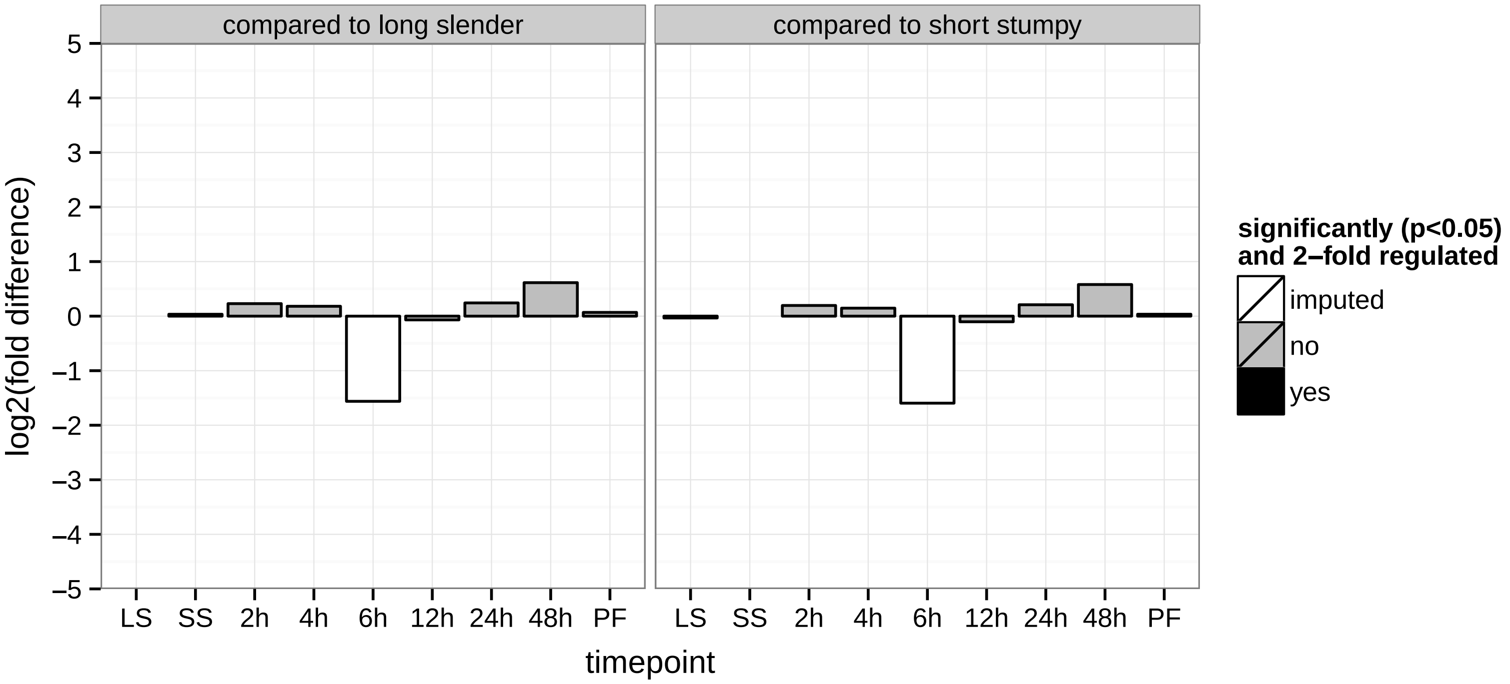
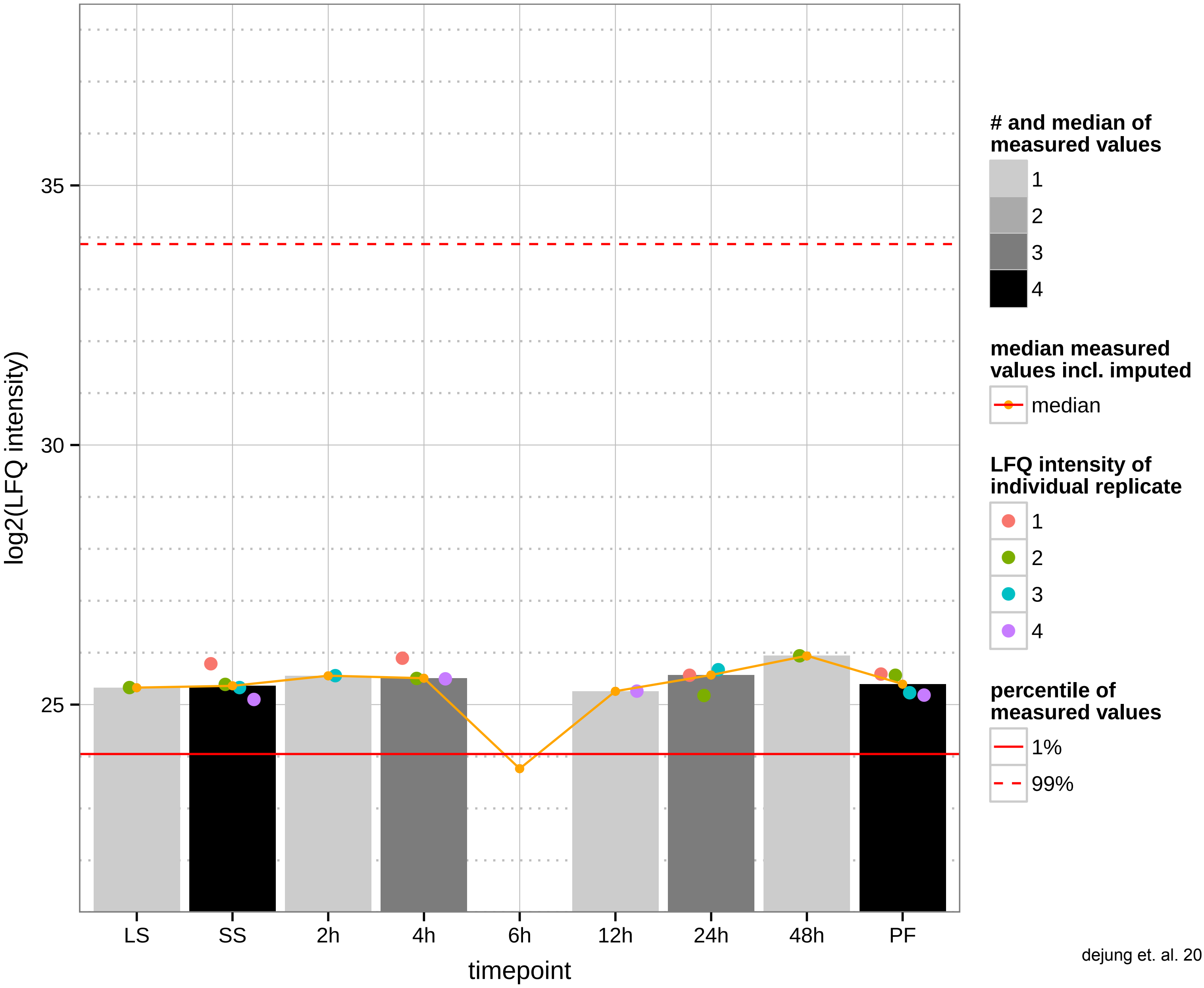
hypothetical protein, conserved
Tb927.5.1940
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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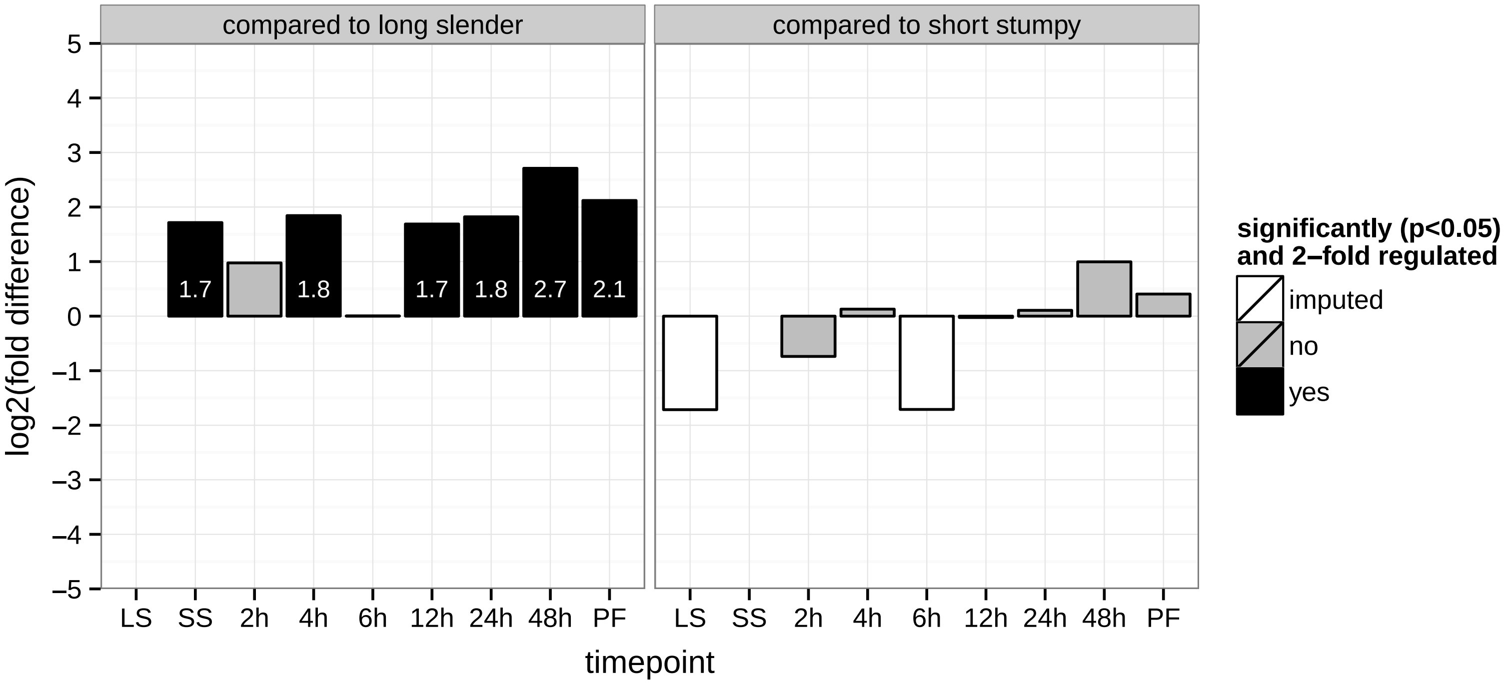
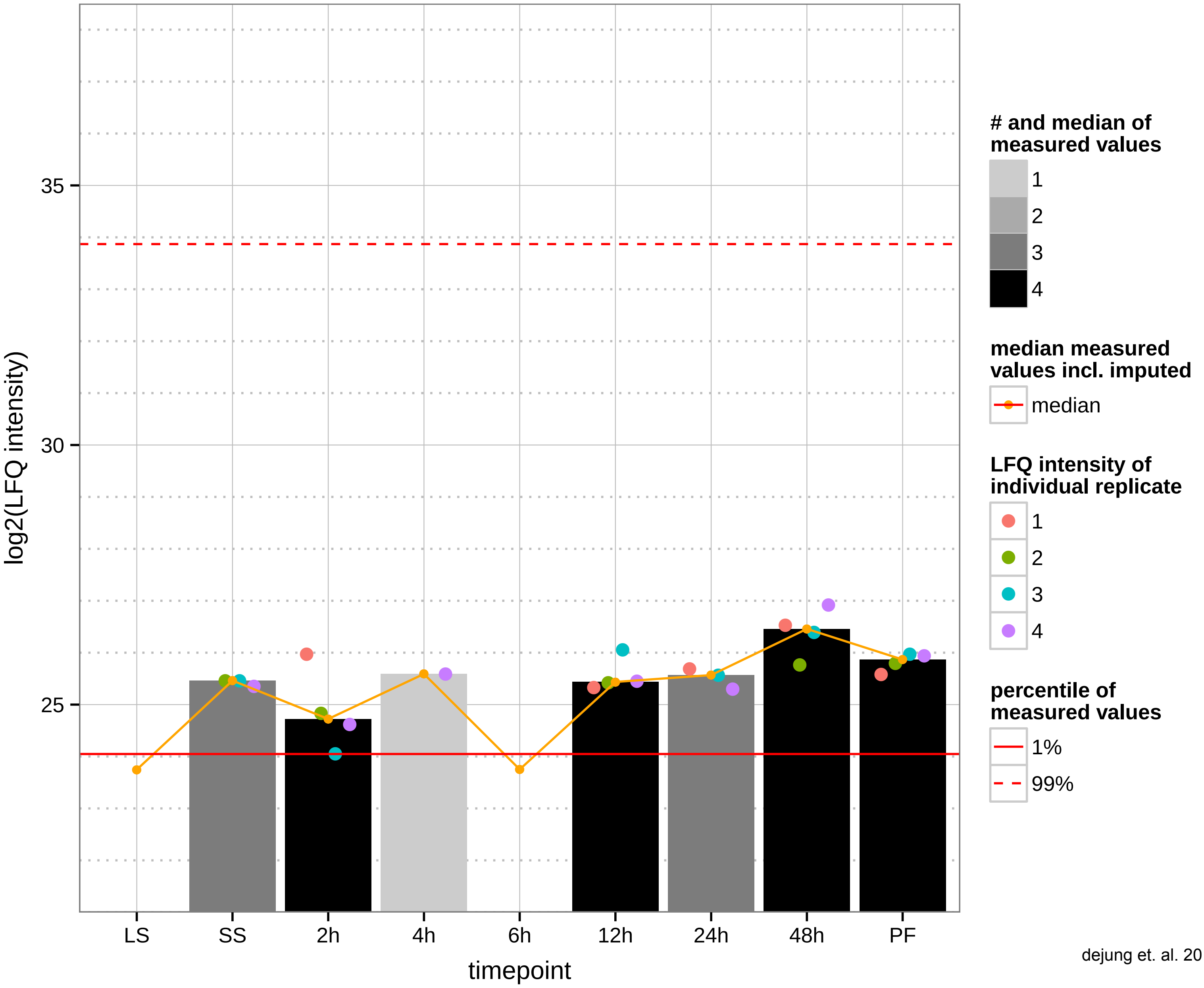
hypothetical protein, conserved
Tb927.6.1590
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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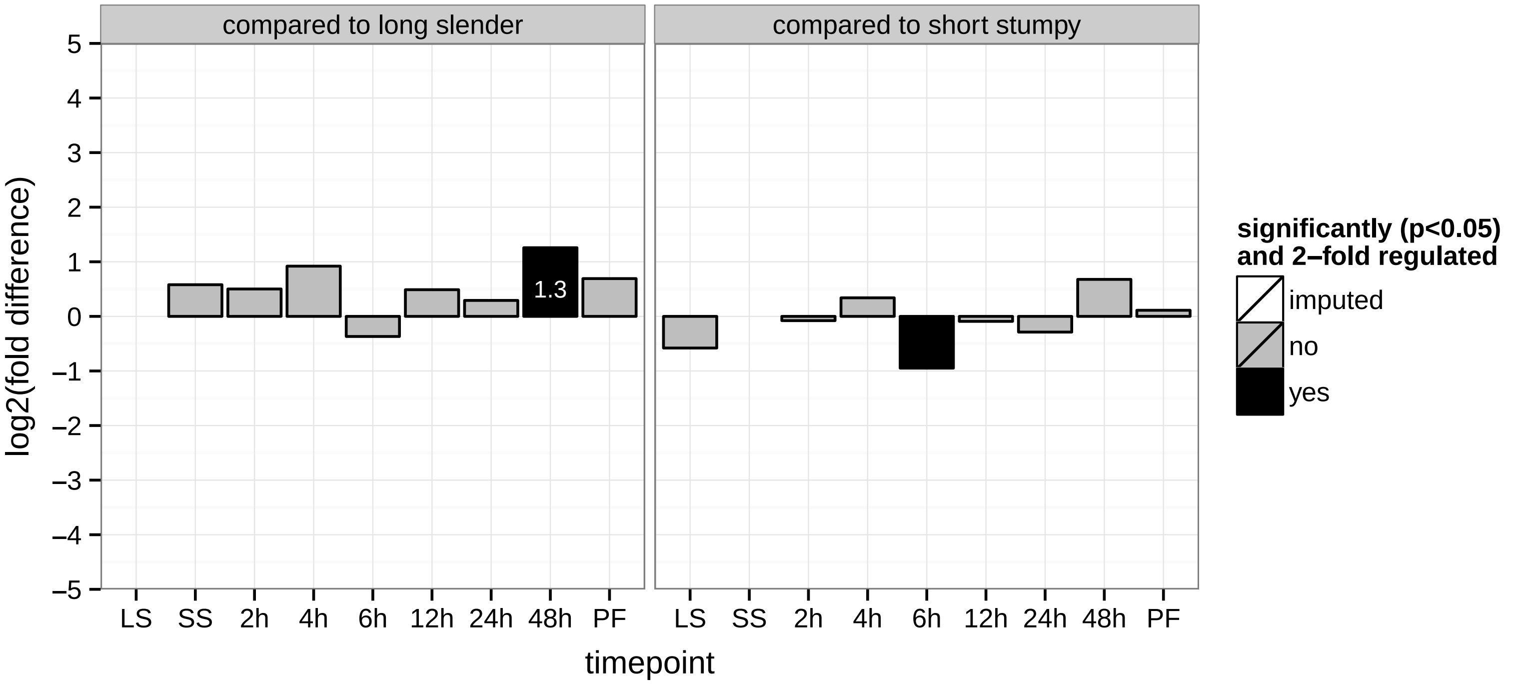
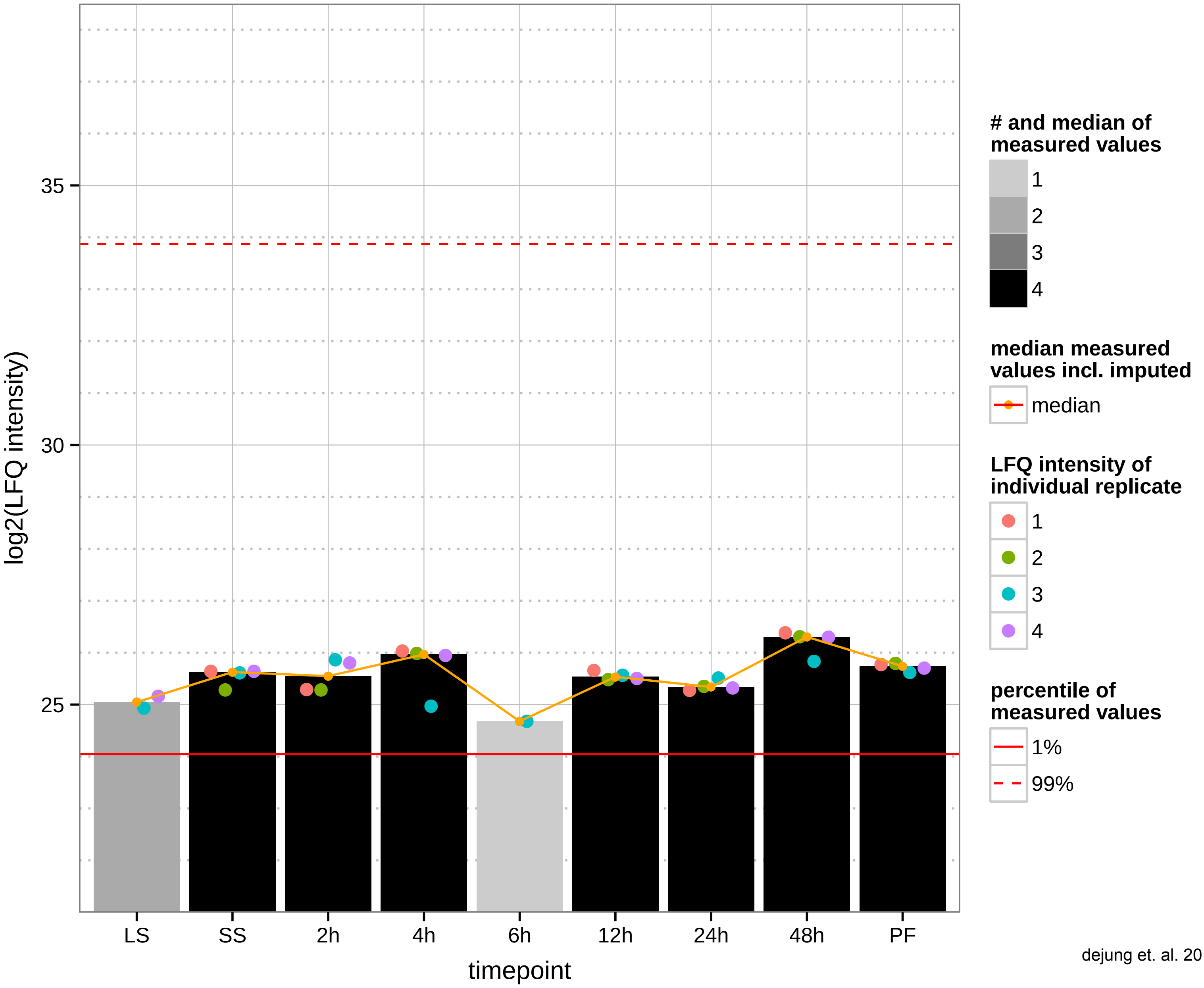
mitochondrial RNA binding protein 1 (MRB1680)
Tb927.6.1680
AGOF: zinc ion binding
AGOC: intracellular, mitochondrion
AGOP: RNA processing
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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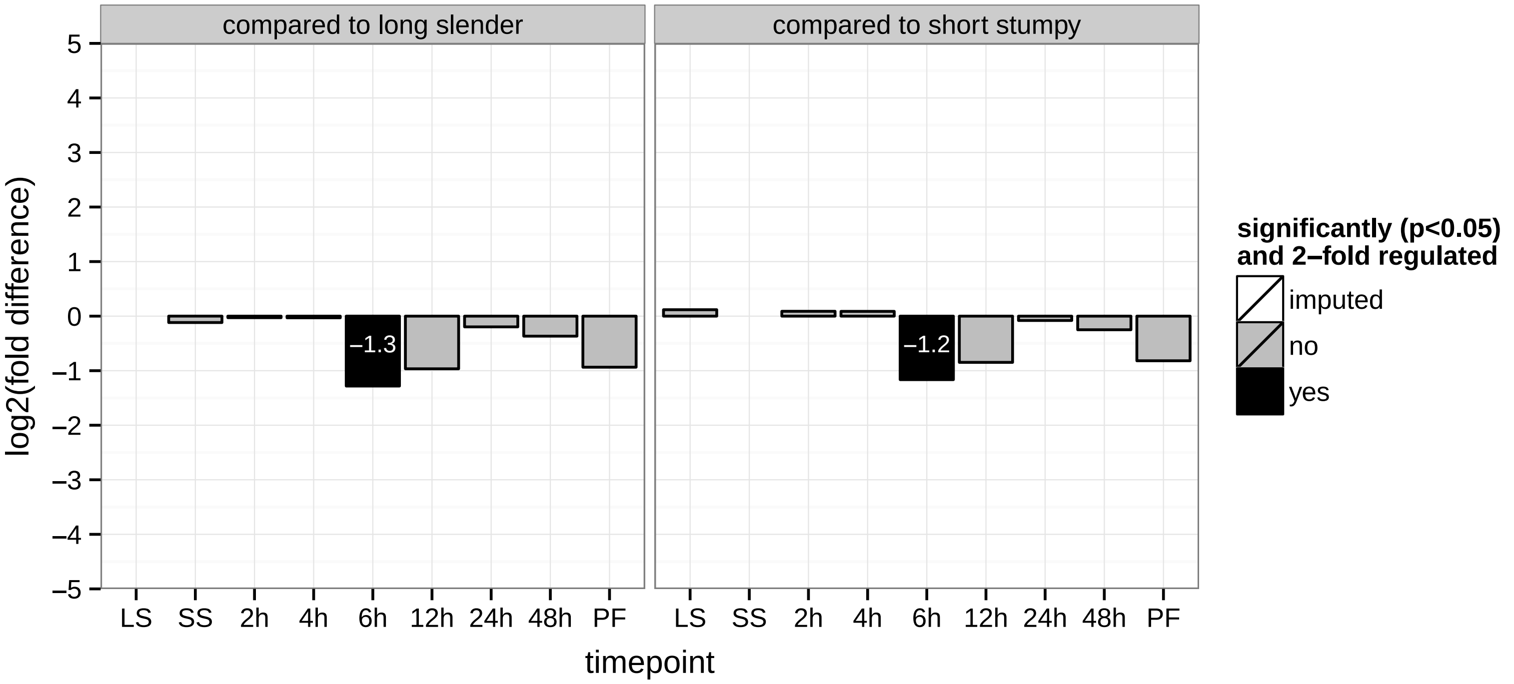
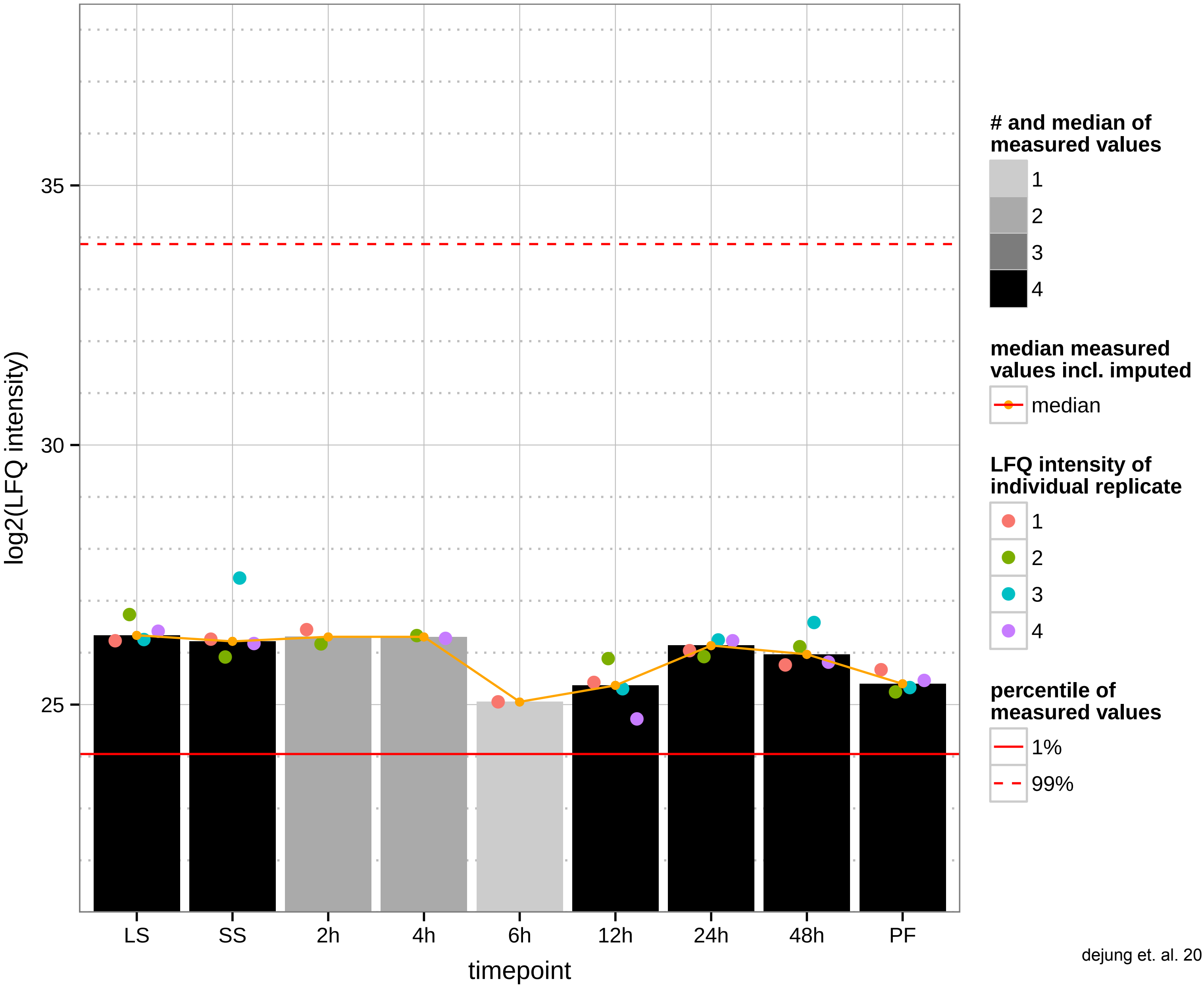
prozyme, S–adenosylmethionine decarboxylaseregulator
Tb927.6.4470
AGOF: adenosylmethionine decarboxylase activity
AGOC: null
AGOP: spermidine biosynthetic process, spermine biosynthetic process
PGOF: adenosylmethionine decarboxylase activity
PGOC: null
PGOP: spermidine biosynthetic process, spermine biosynthetic process





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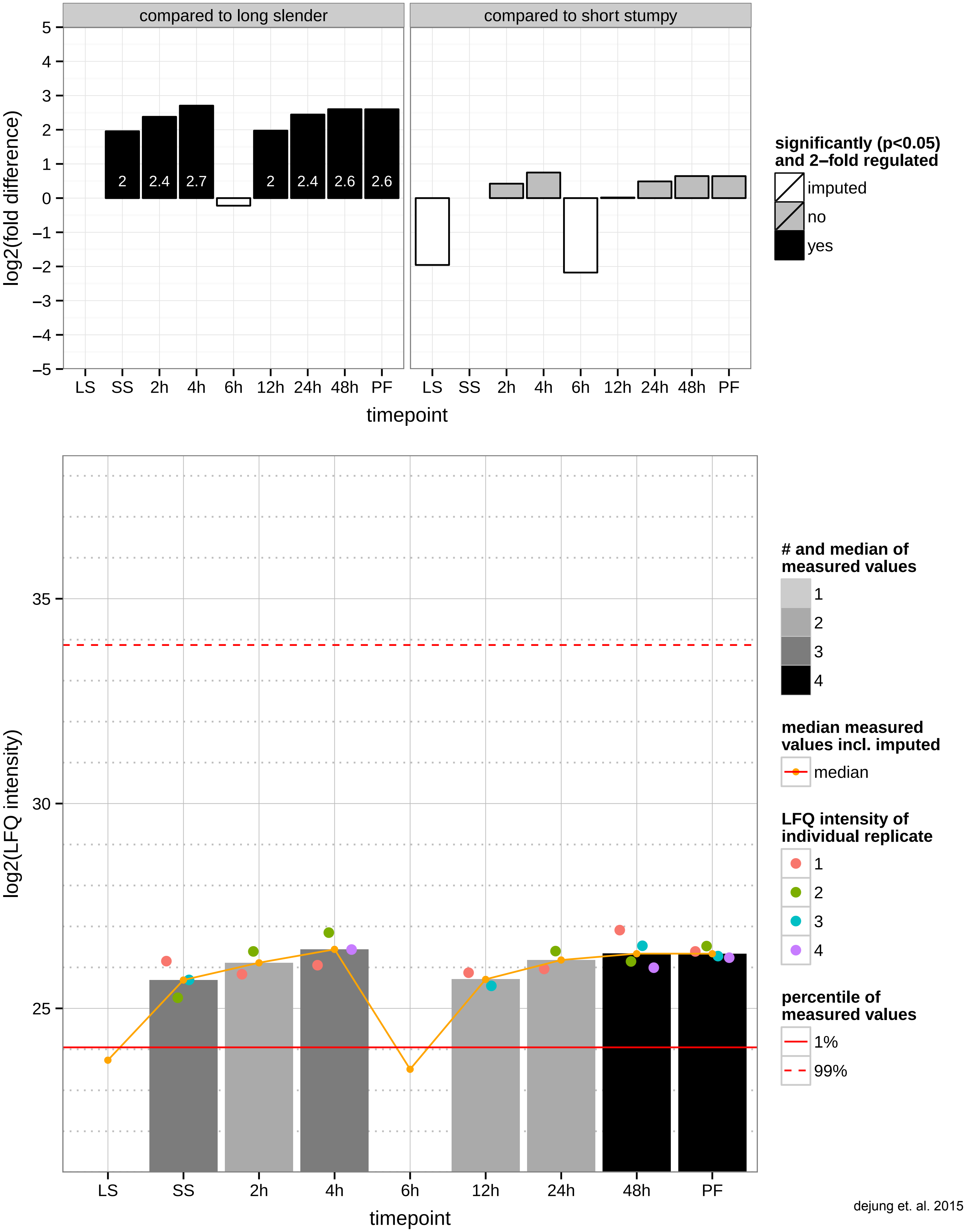
RNA–binding protein, putative (Y14)
Tb927.7.1170
AGOF: RNA binding, protein binding
AGOC: exon–exon junction complex, nucleus
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null



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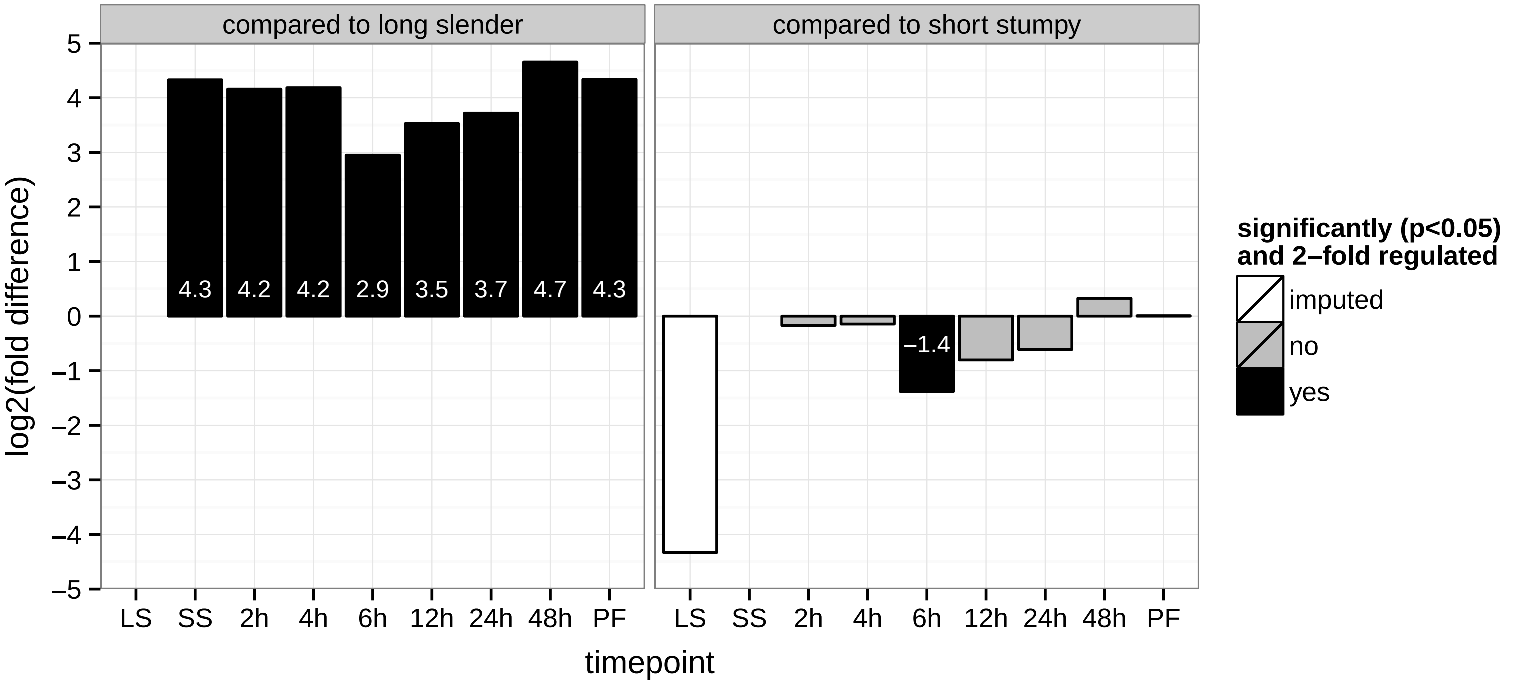
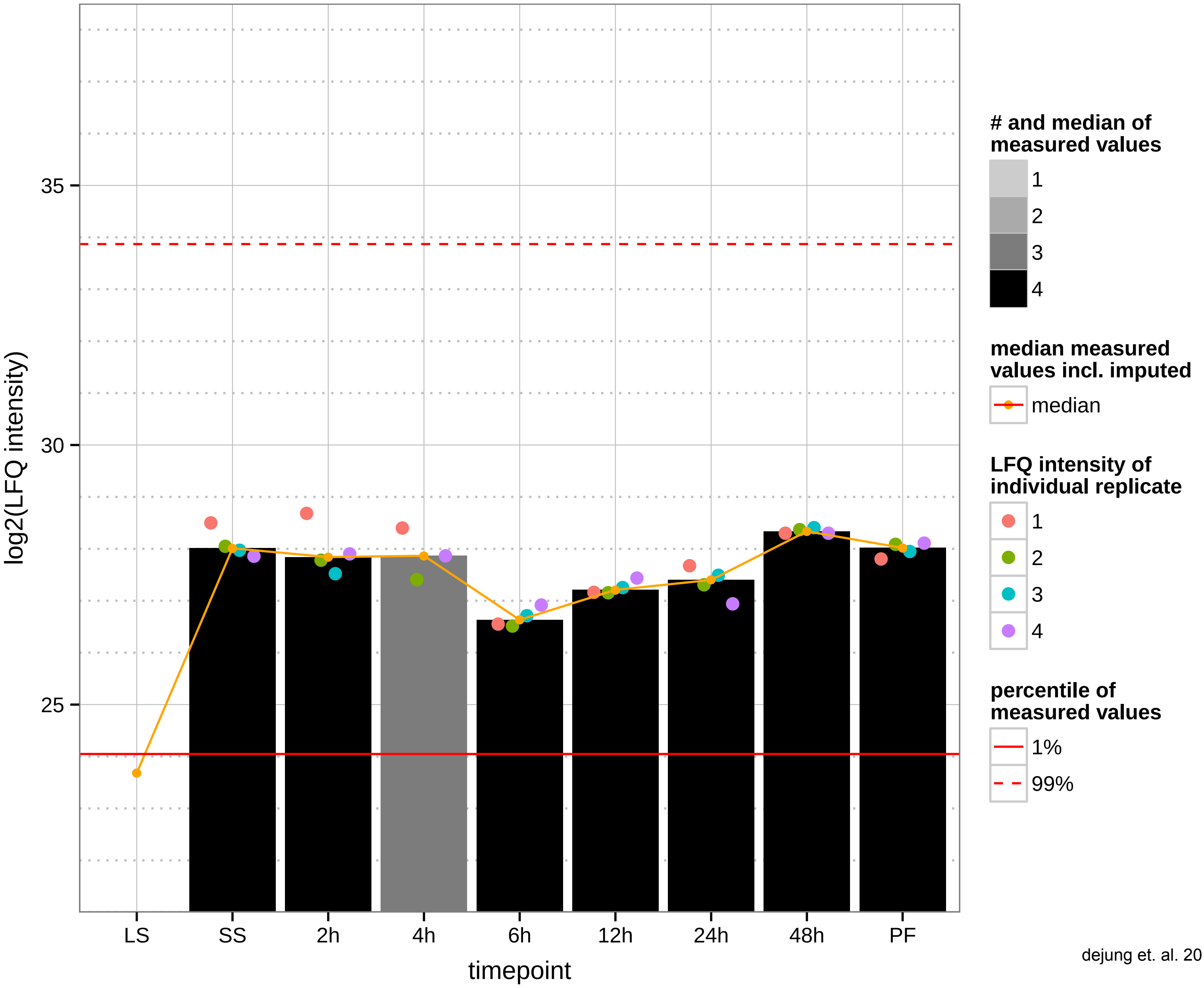
zinc finger protein family member, putative (ZC3H21)
Tb927.7.2670
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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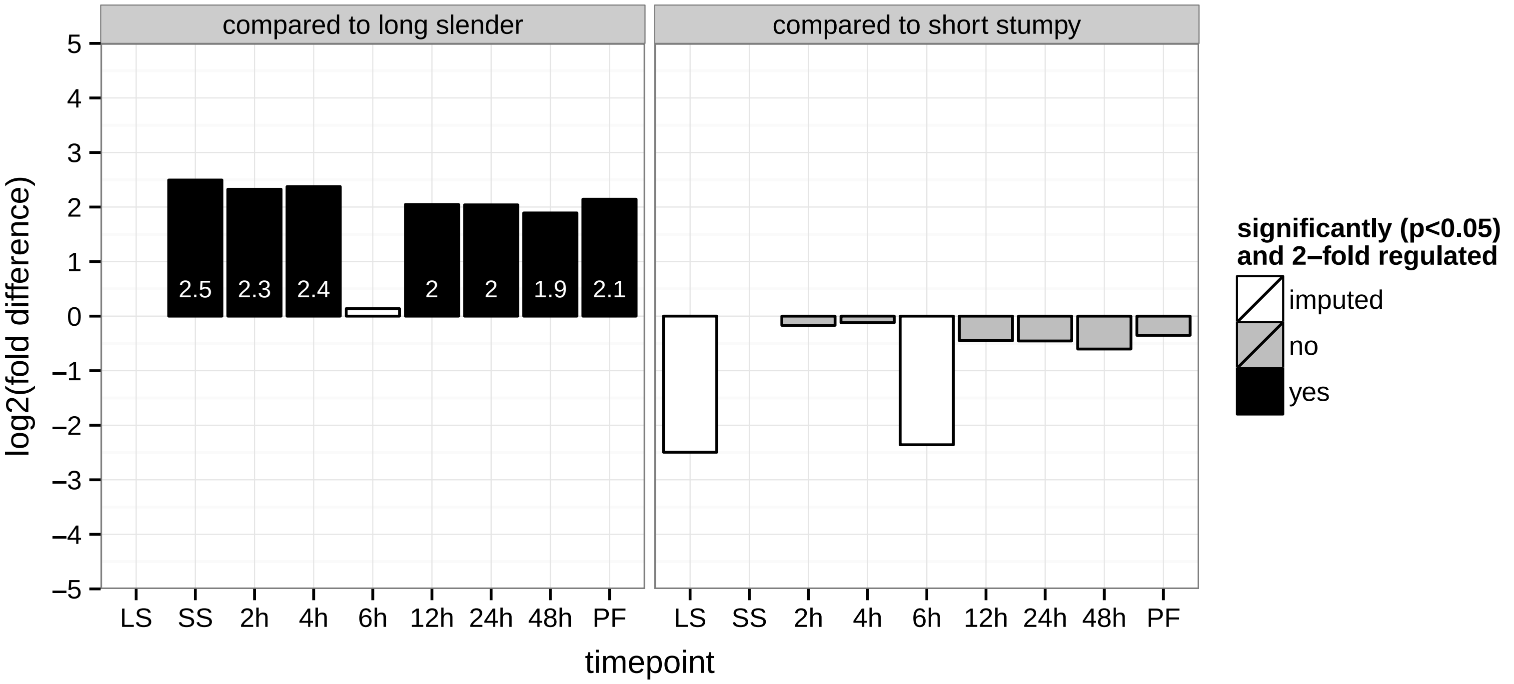
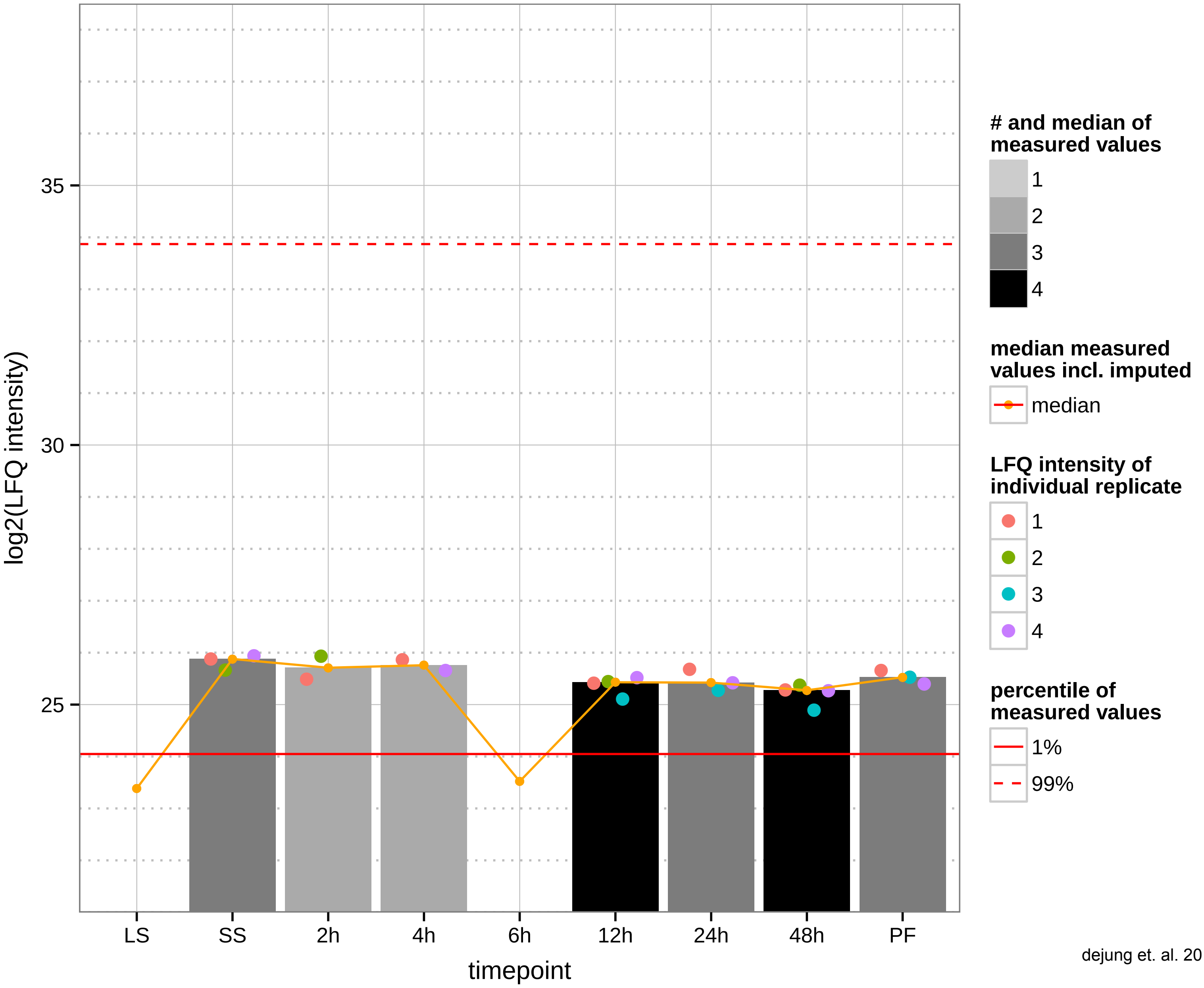
hypothetical protein, conserved
Tb927.8.1770
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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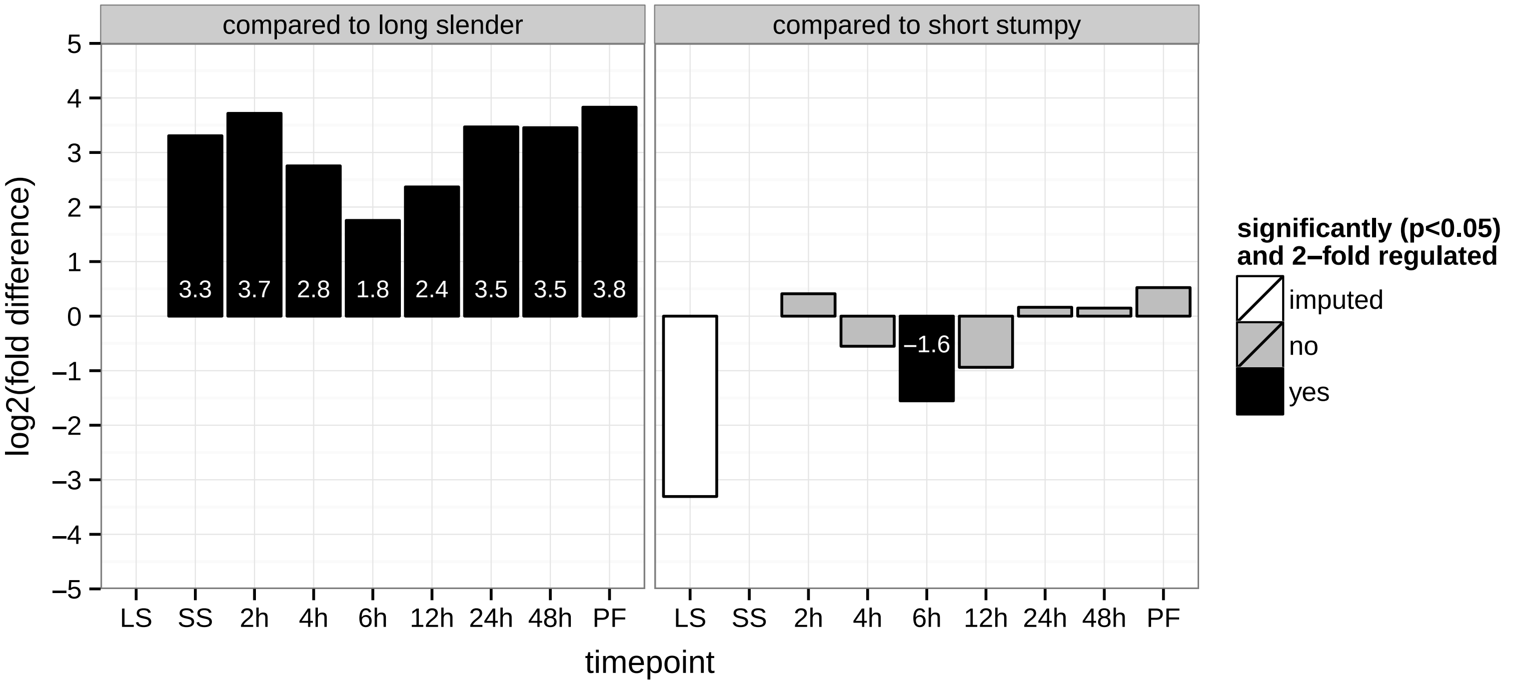
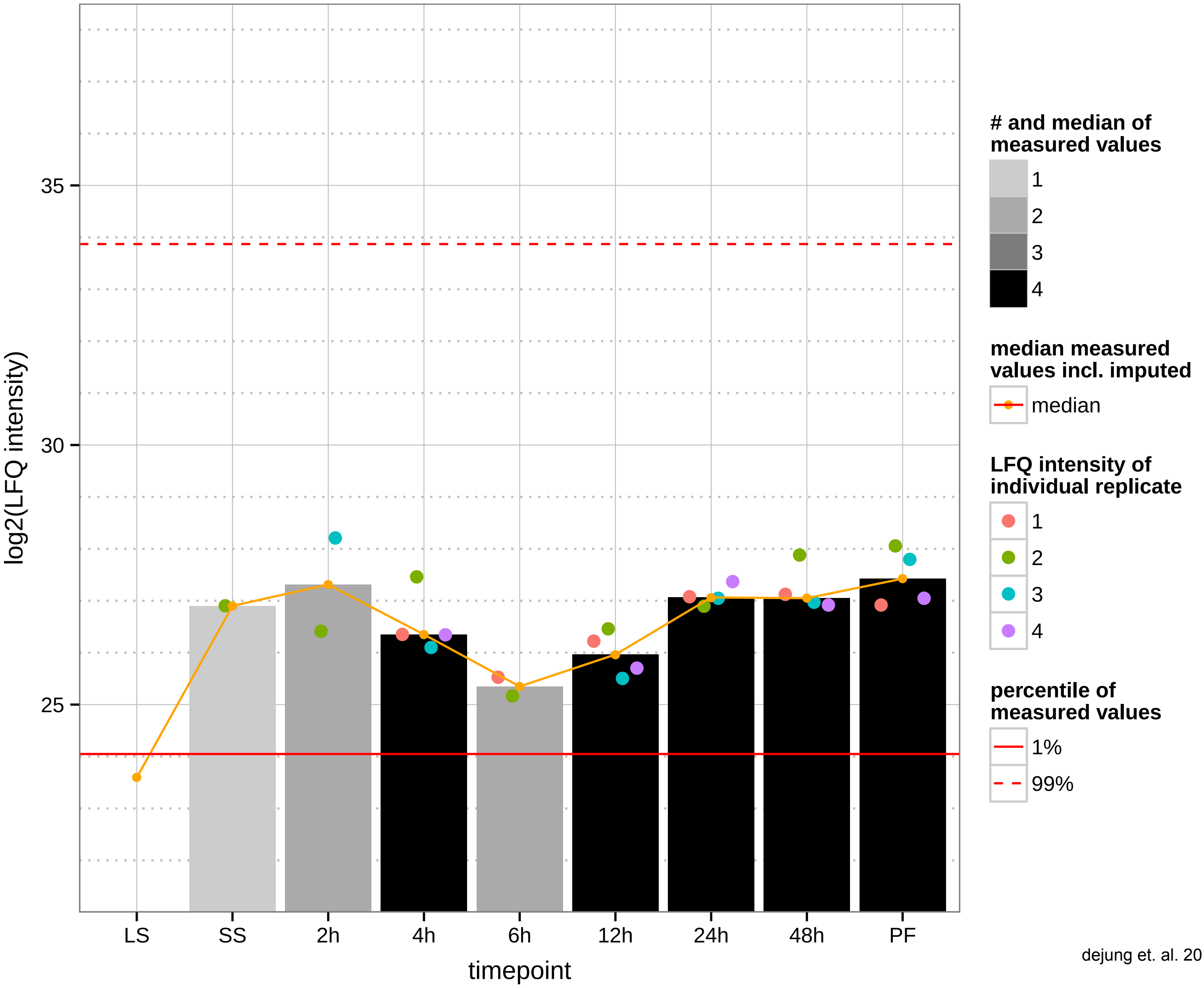
cullin, putative
Tb927.8.5970
AGOF: ubiquitin protein ligase binding
AGOC: cullin–RING ubiquitin ligase complex
AGOP: cell cycle, ubiquitin–dependent protein catabolic process
PGOF: ubiquitin protein ligase binding
PGOC: cullin–RING ubiquitin ligase complex
PGOP: ubiquitin–dependent protein catabolic process





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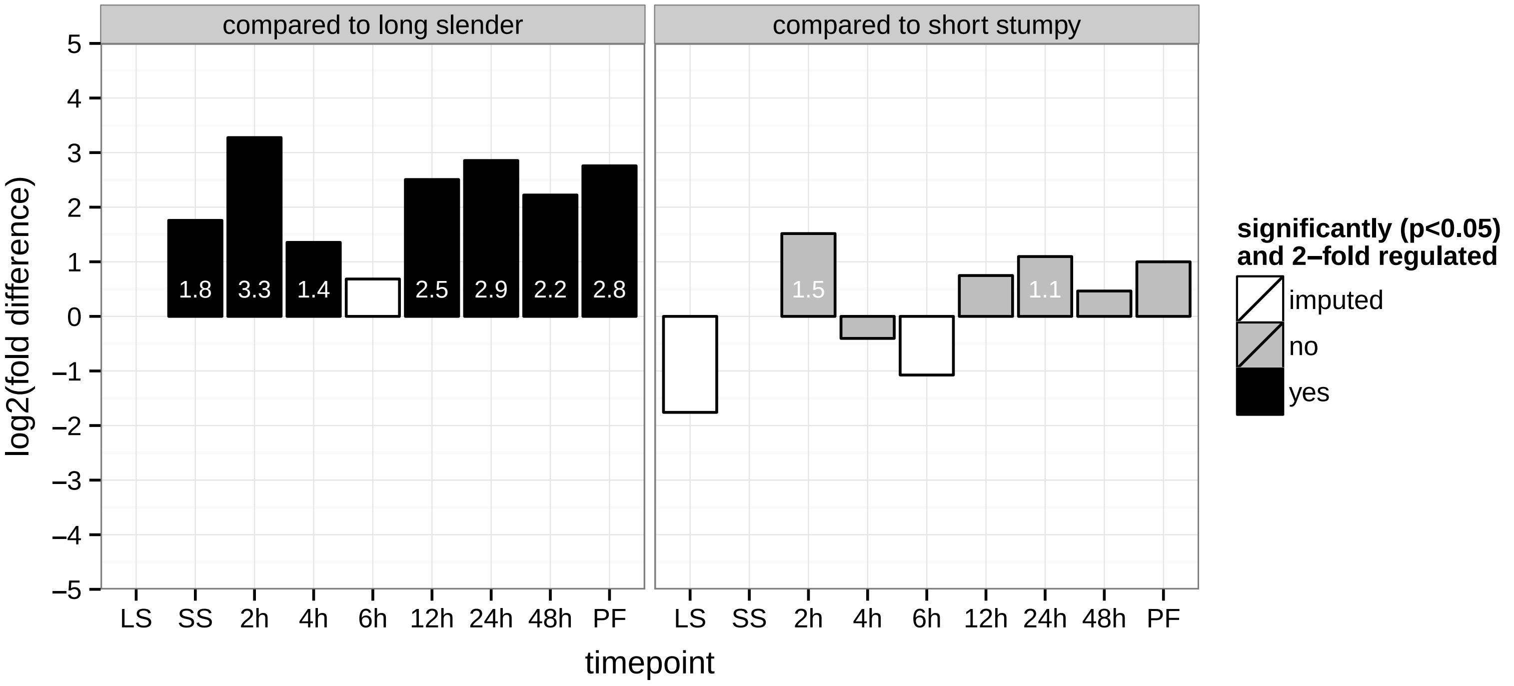
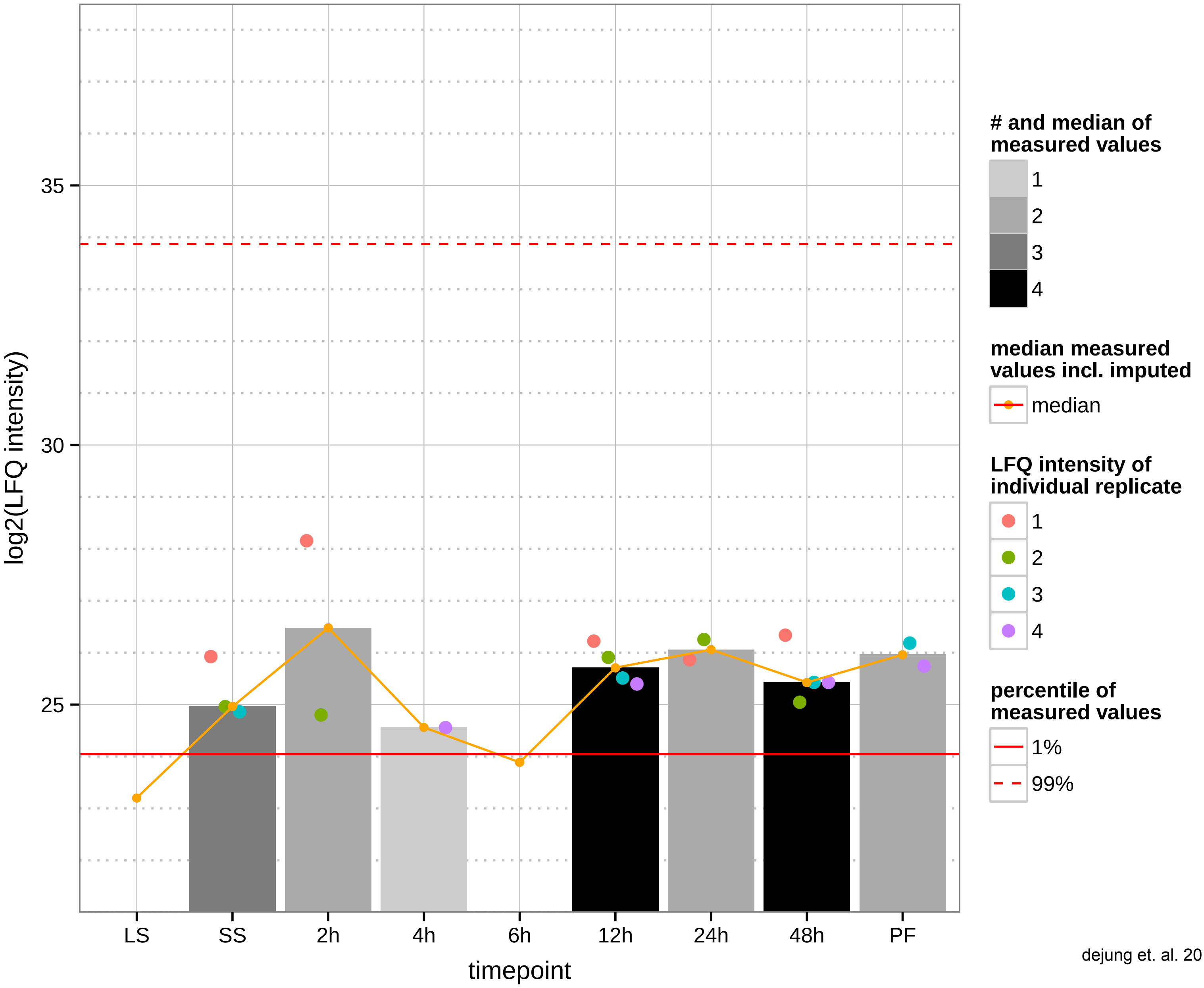
hypothetical protein, conserved
Tb927.8.6050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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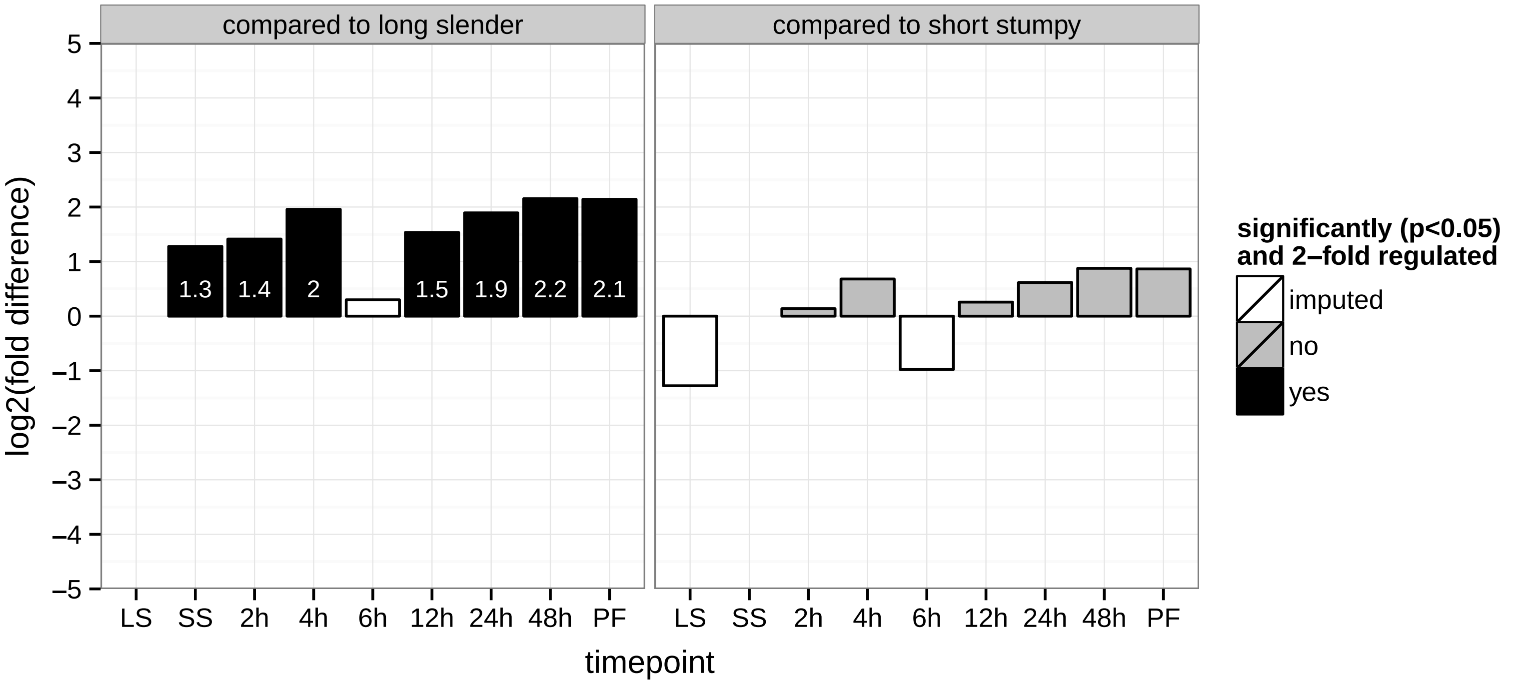
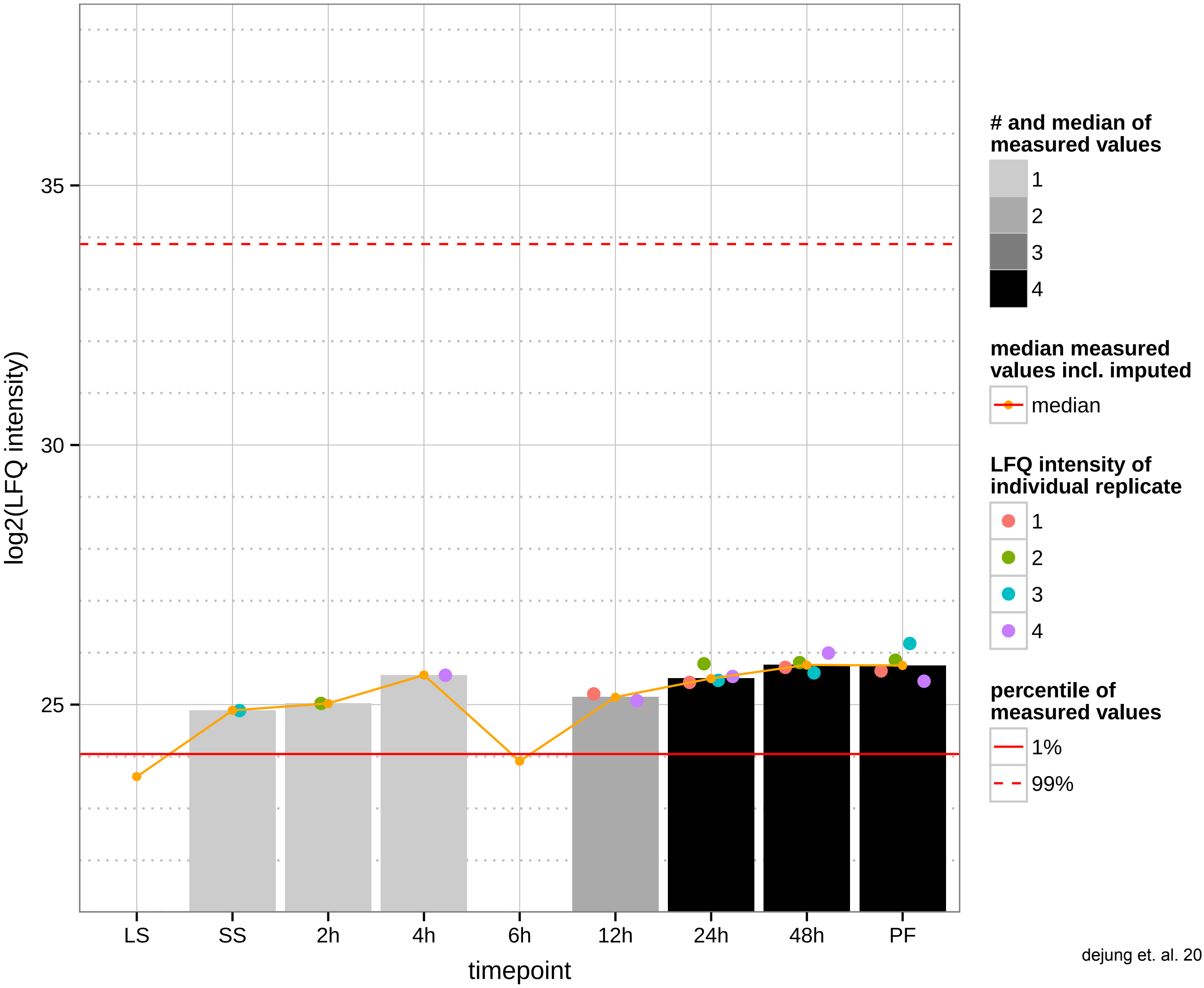
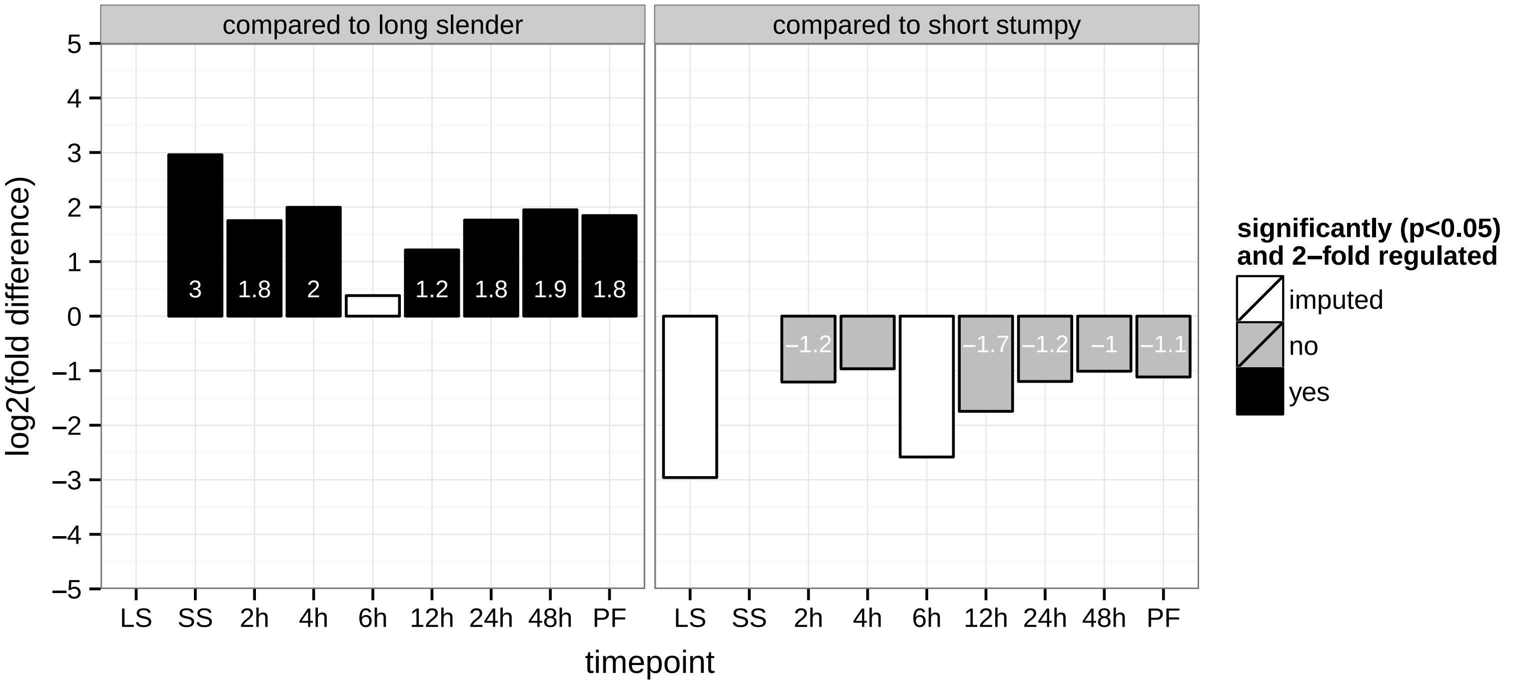
hypothetical protein, conserved
Tb927.8.610
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

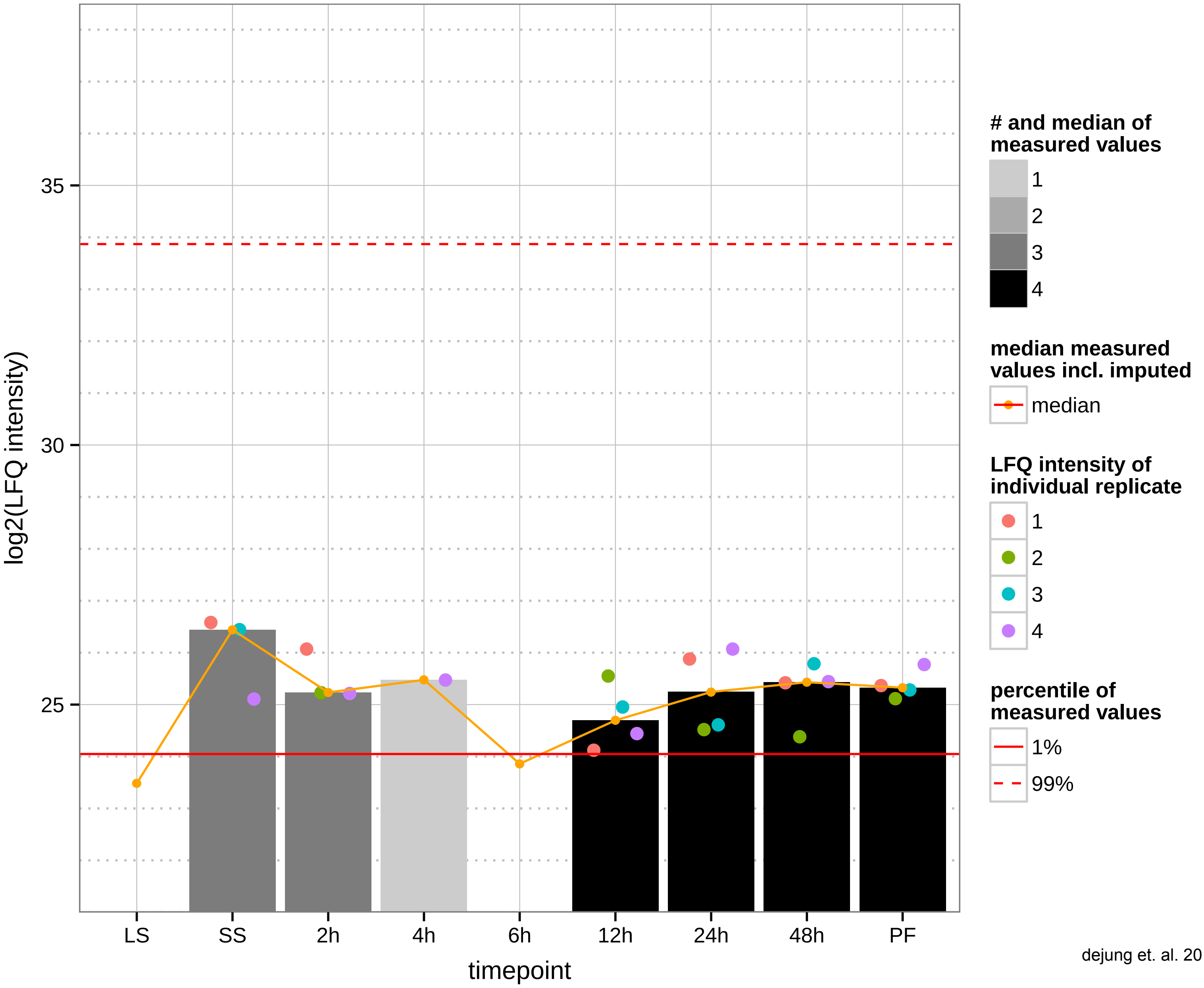




dejung et. al. 2015

kinetoplastid kinetochore protein 3, protein kinase, putative (kkt3)
Tb927.9.10920
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity, zinc ion binding
AGOC: intracellular, kinetochore
AGOP: cell proliferation, chromosome segregation, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups, zinc ion binding
PGOC: intracellular
PGOP: protein phosphorylation





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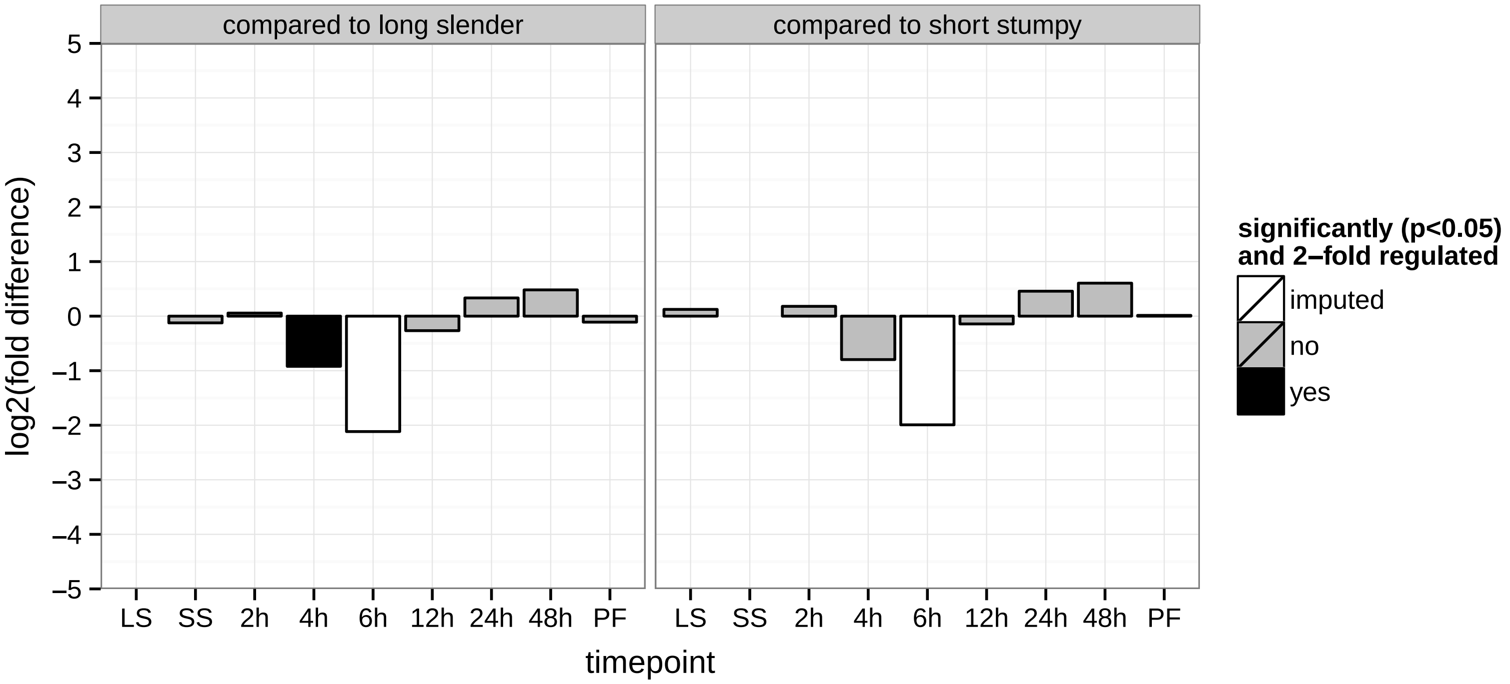
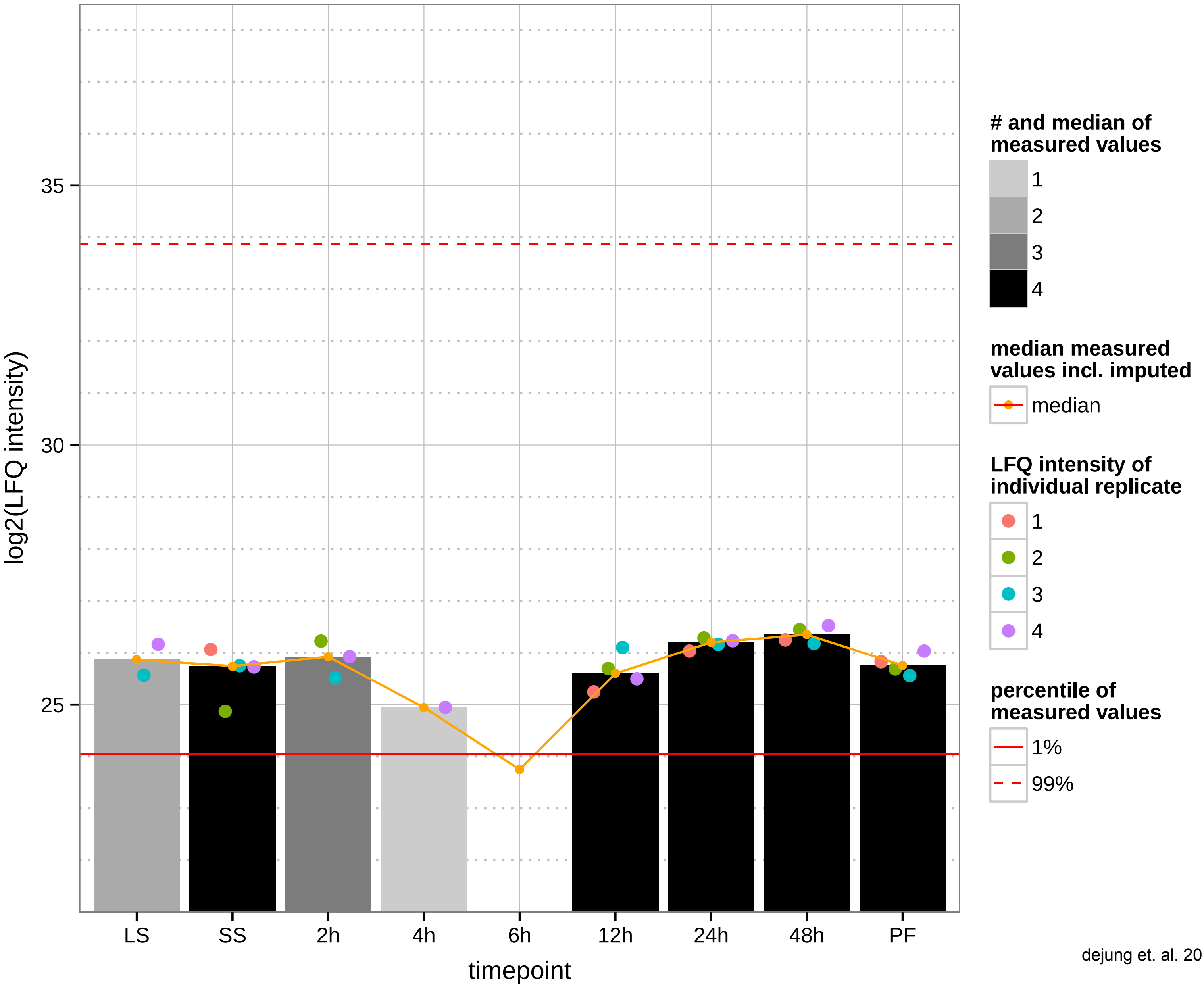
hypothetical protein, conserved
Tb927.9.8180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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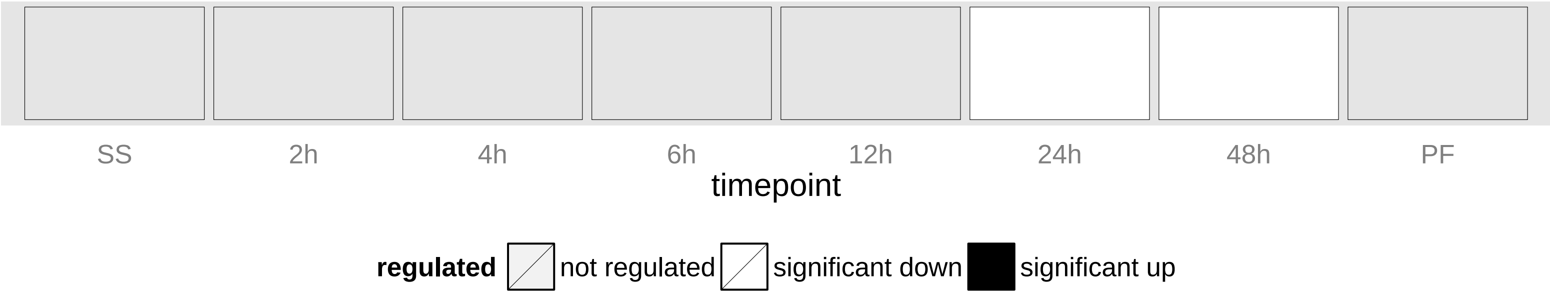

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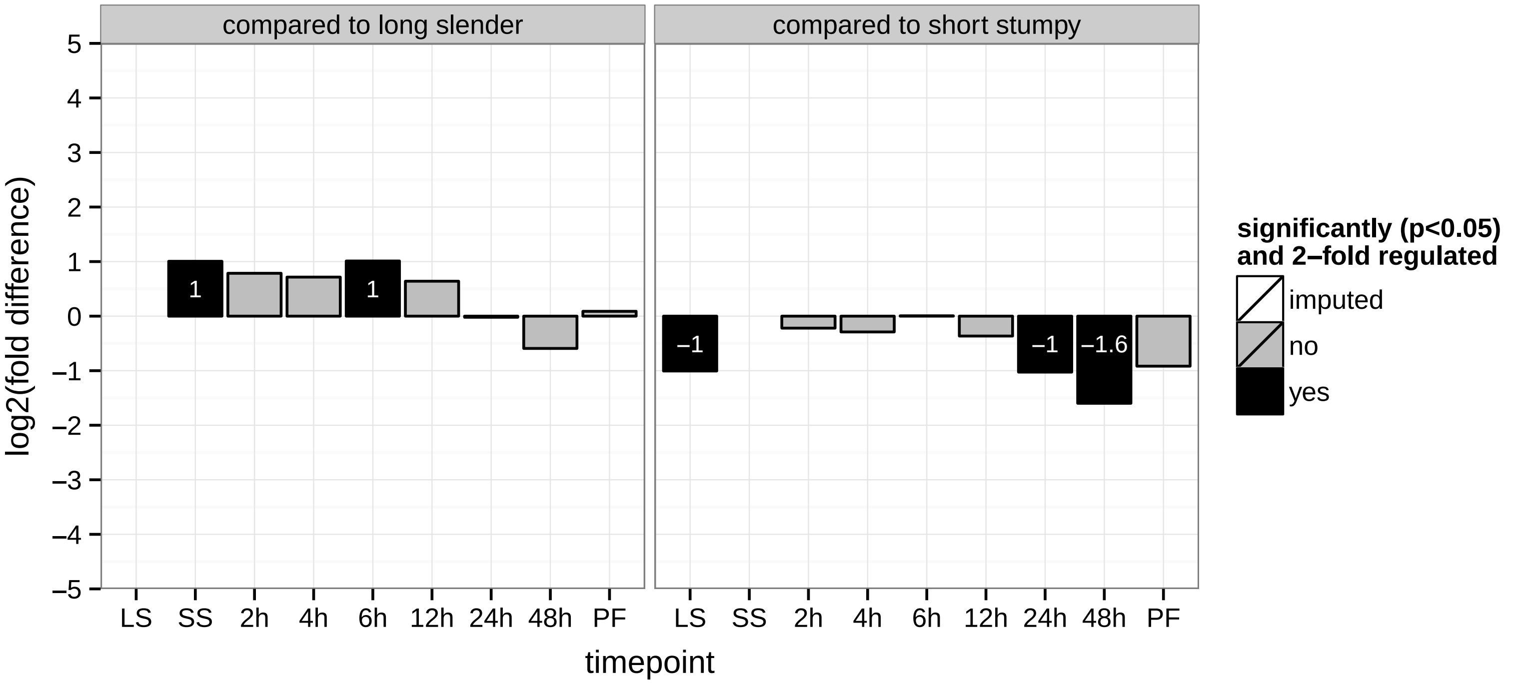
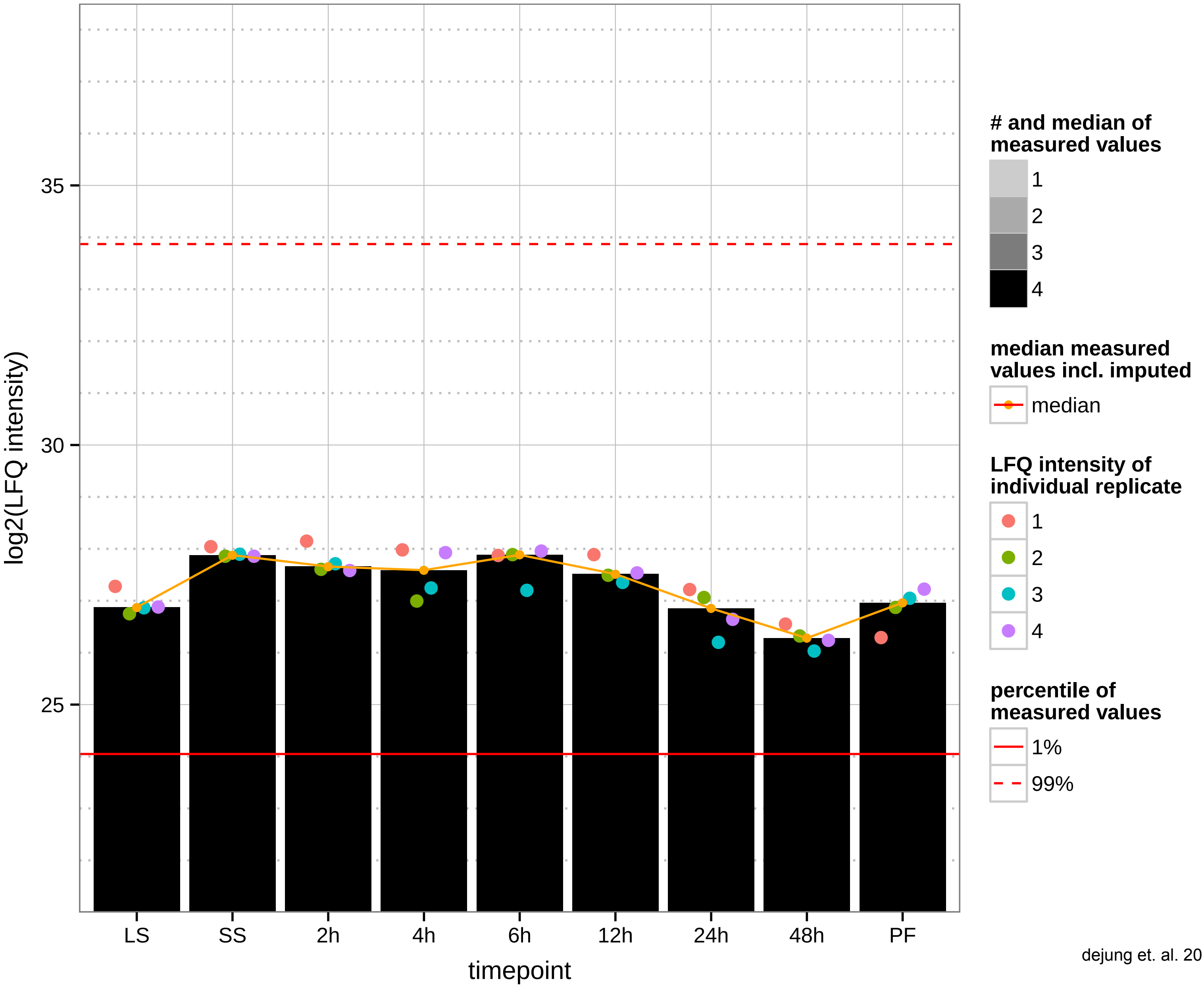
protein kinase, putative, mitogen–activated protein kinase 9, putative (MPK9)
Tb927.10.14800;Tb11.v5.0626
AGOF: null, ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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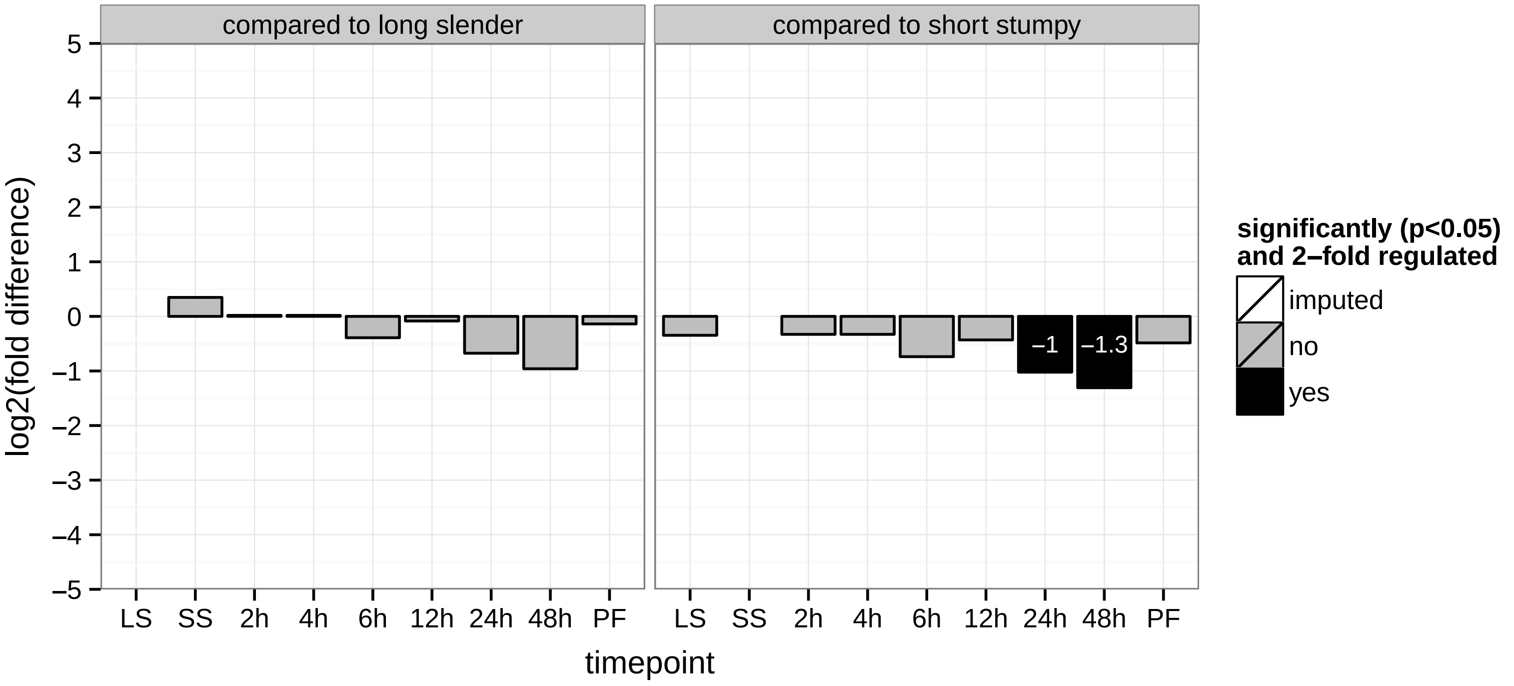
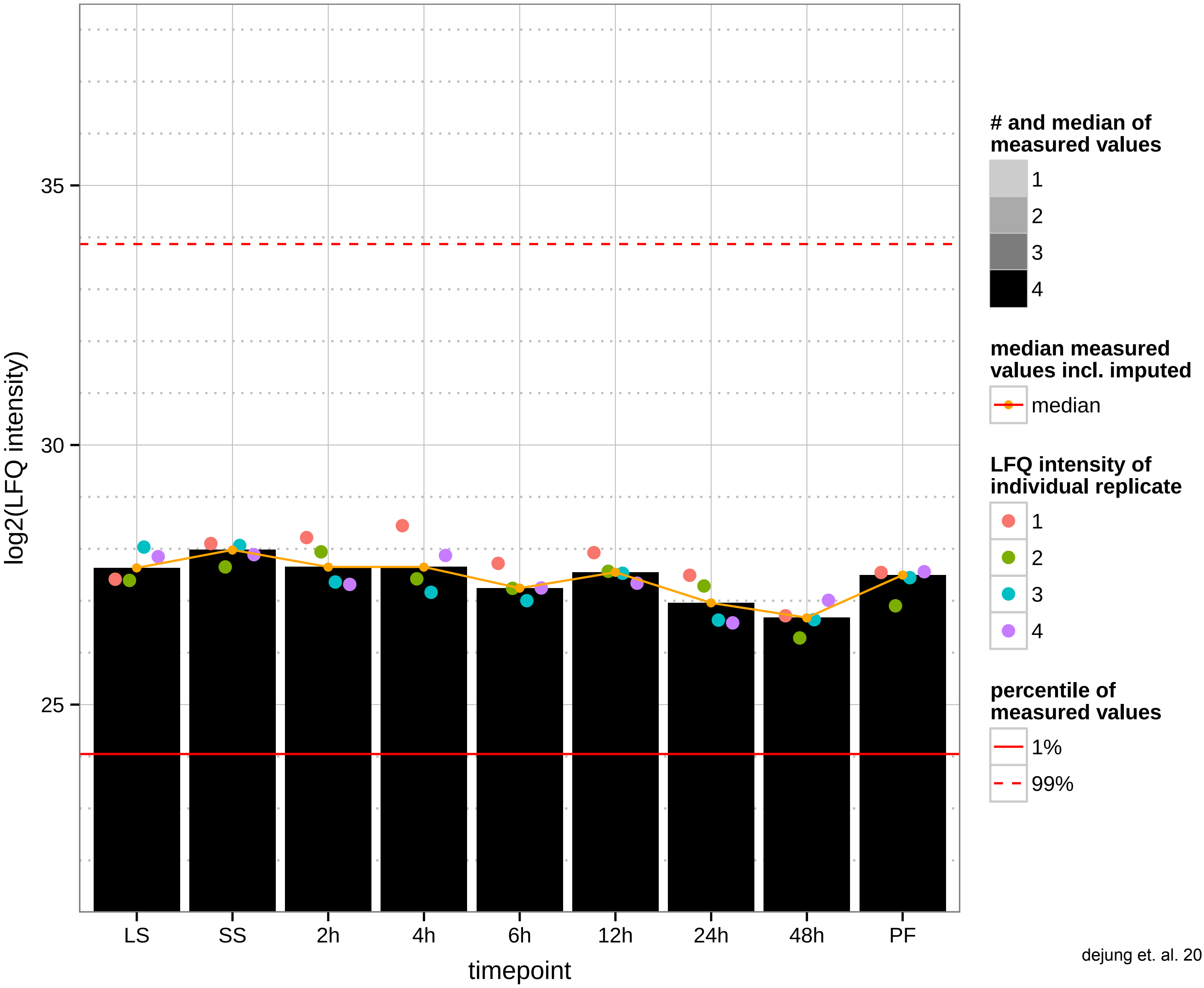
hypothetical protein, conserved
Tb927.1.4500
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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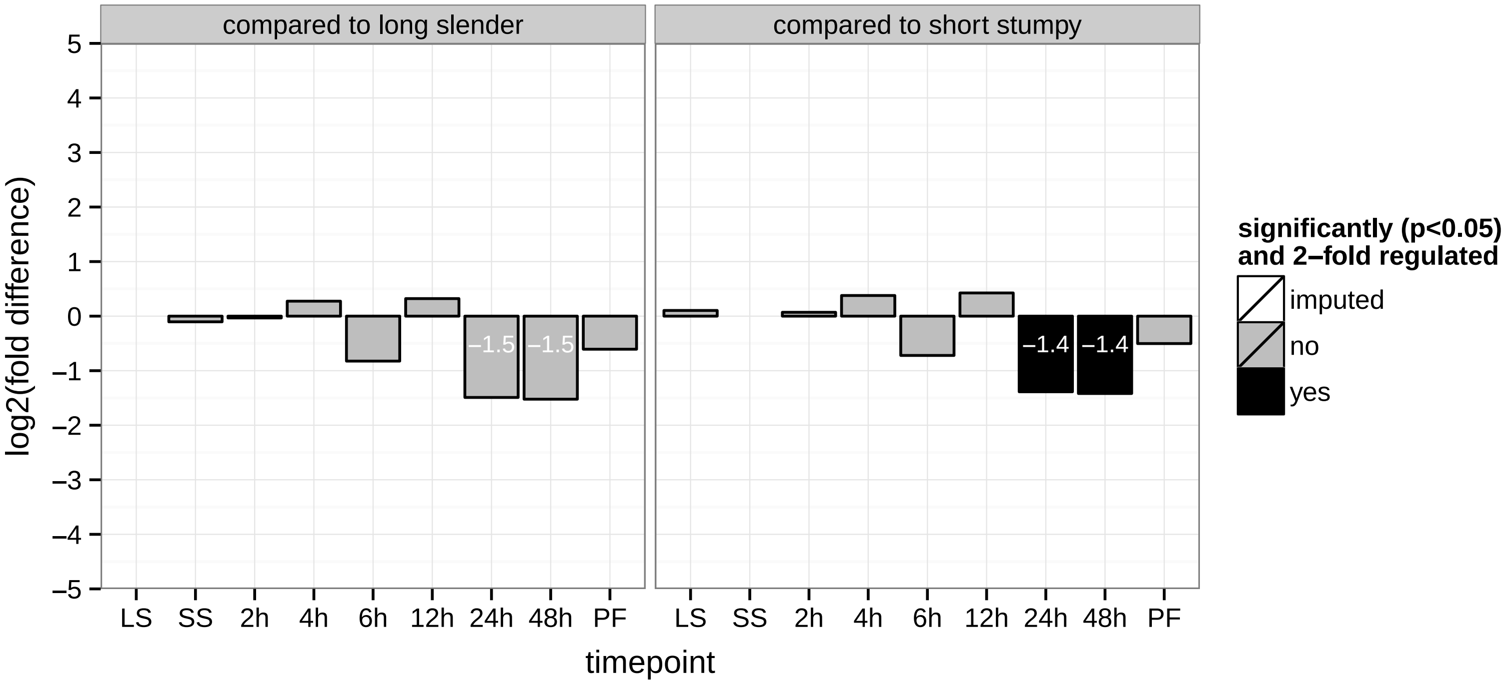
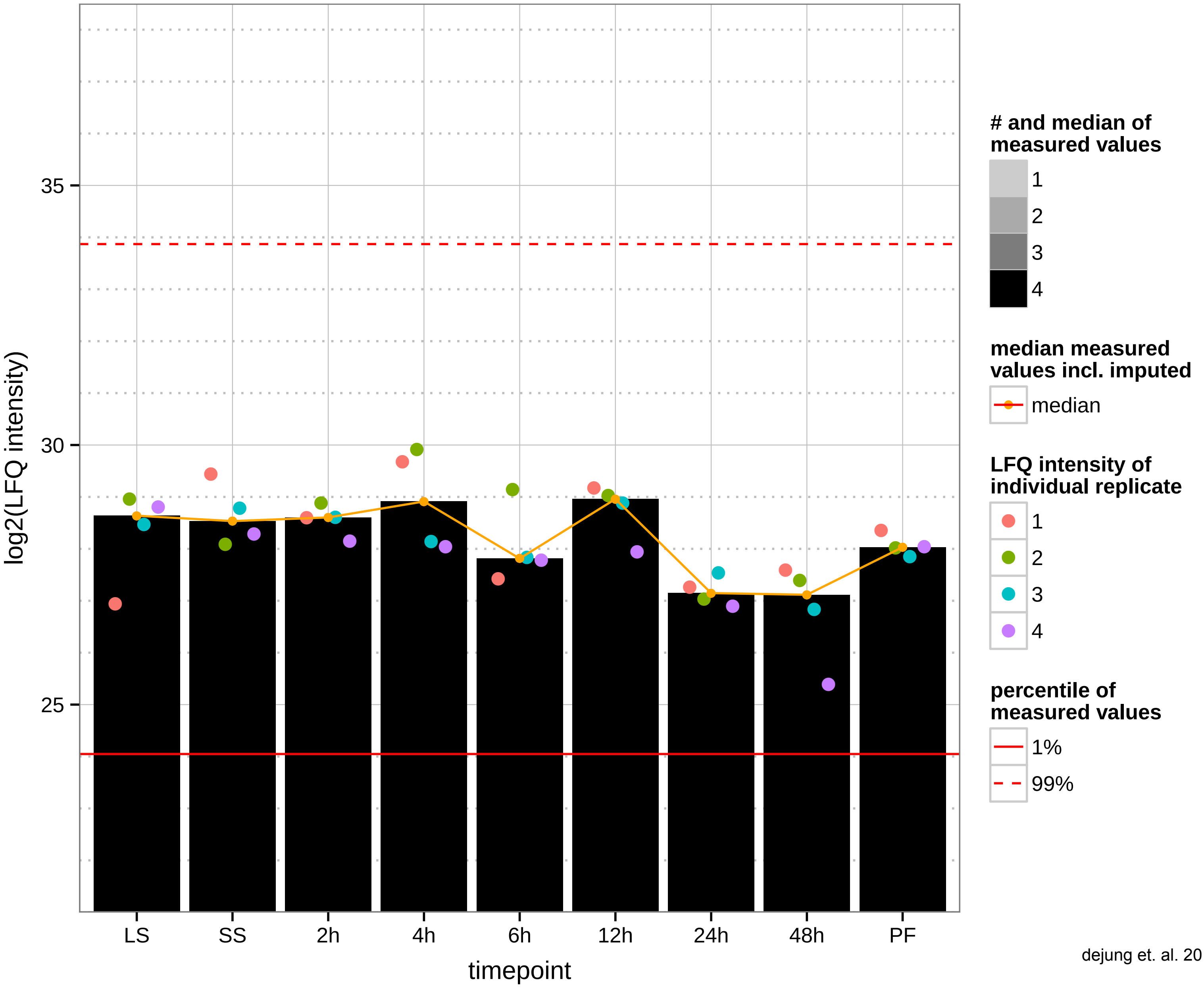
vacuolar ATP synthase, putative
Tb927.10.200
AGOF: hydrogen–exporting ATPase activity, phosphorylative mechanism
AGOC: proton–transporting V–type ATPase, V0 domain, vacuolar proton–transporting V–type ATPase complex
AGOP: ATP hydrolysis coupled proton transport, ATP synthesis coupled proton transport
PGOF: hydrogen ion transmembrane transporter activity
PGOC: proton–transporting V–type ATPase, V0 domain, proton–transporting two–sector ATPase complex, proton–transportin
PGOP: ATP hydrolysis coupled proton transport





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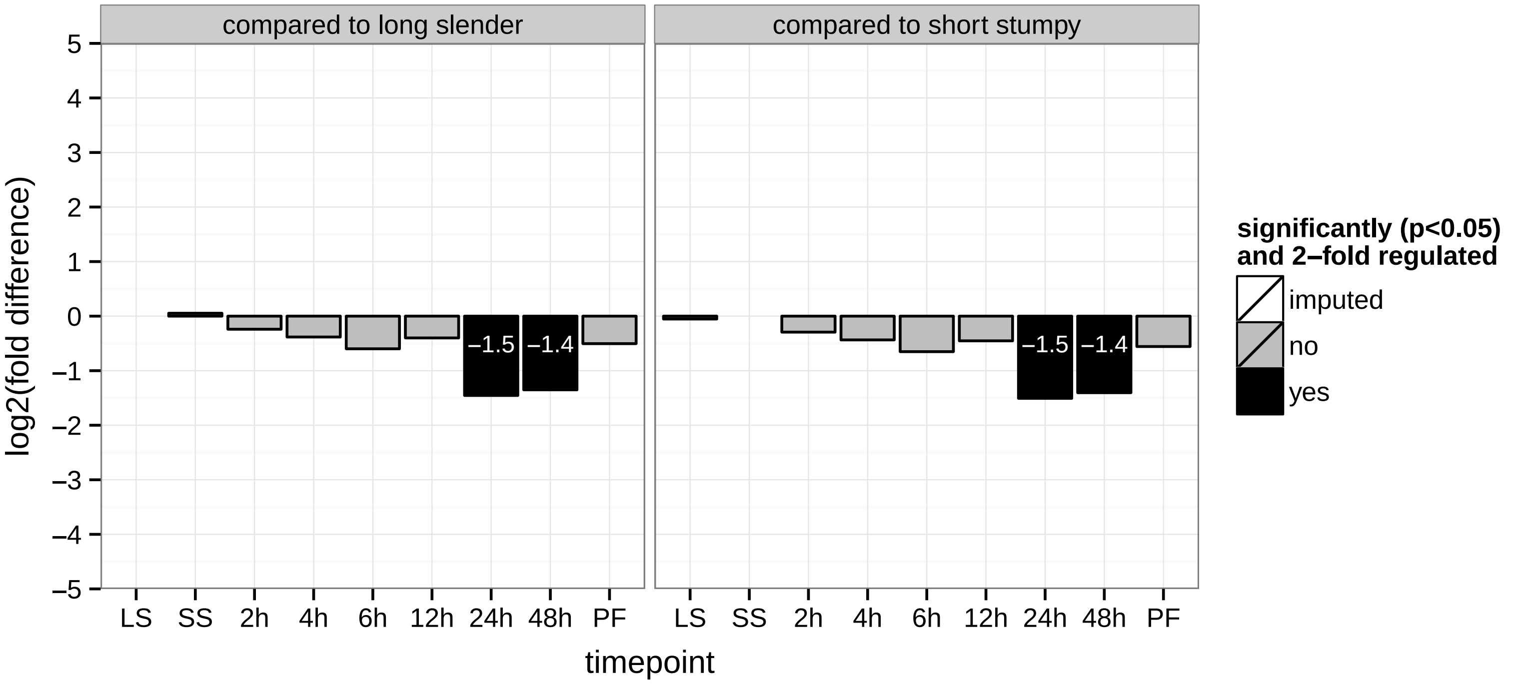
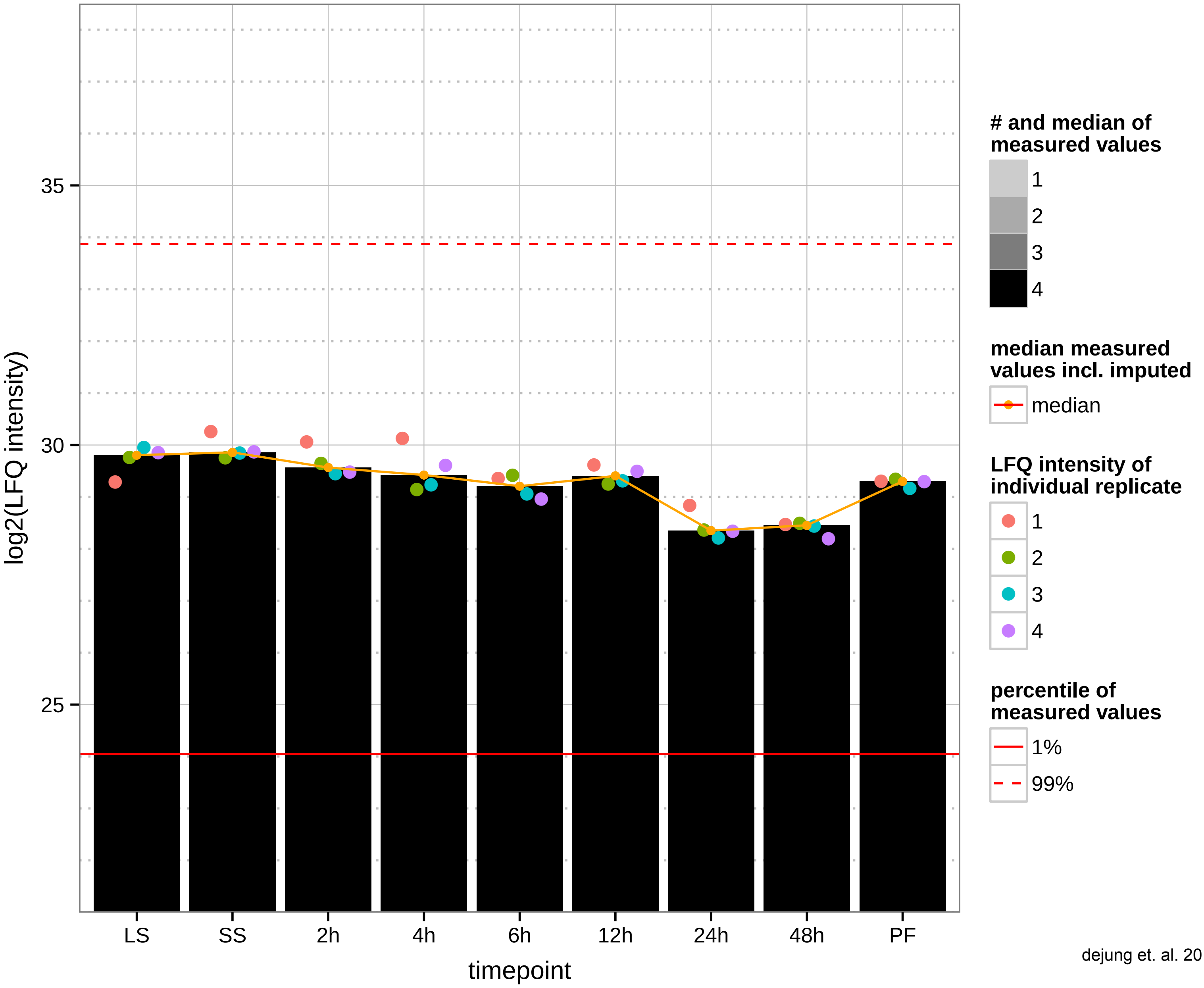
hypothetical protein, conserved
Tb927.11.15140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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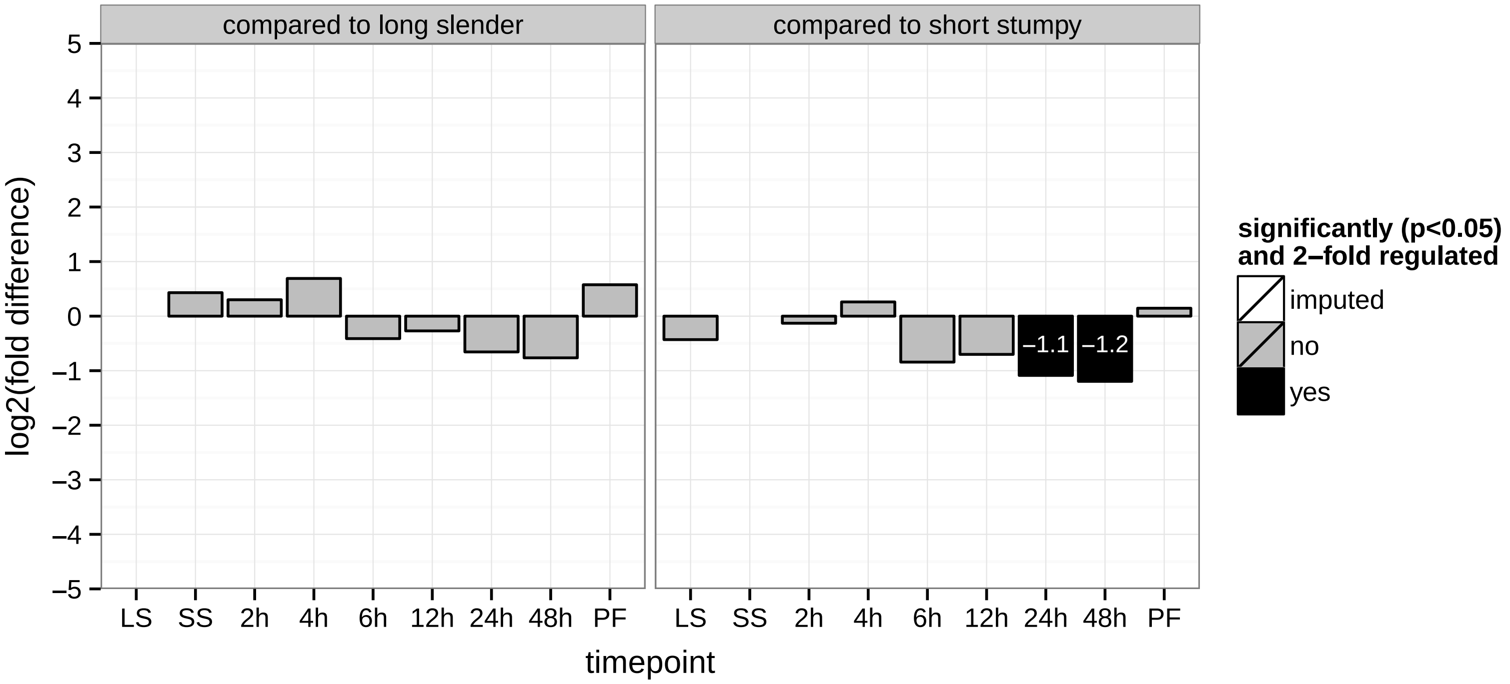
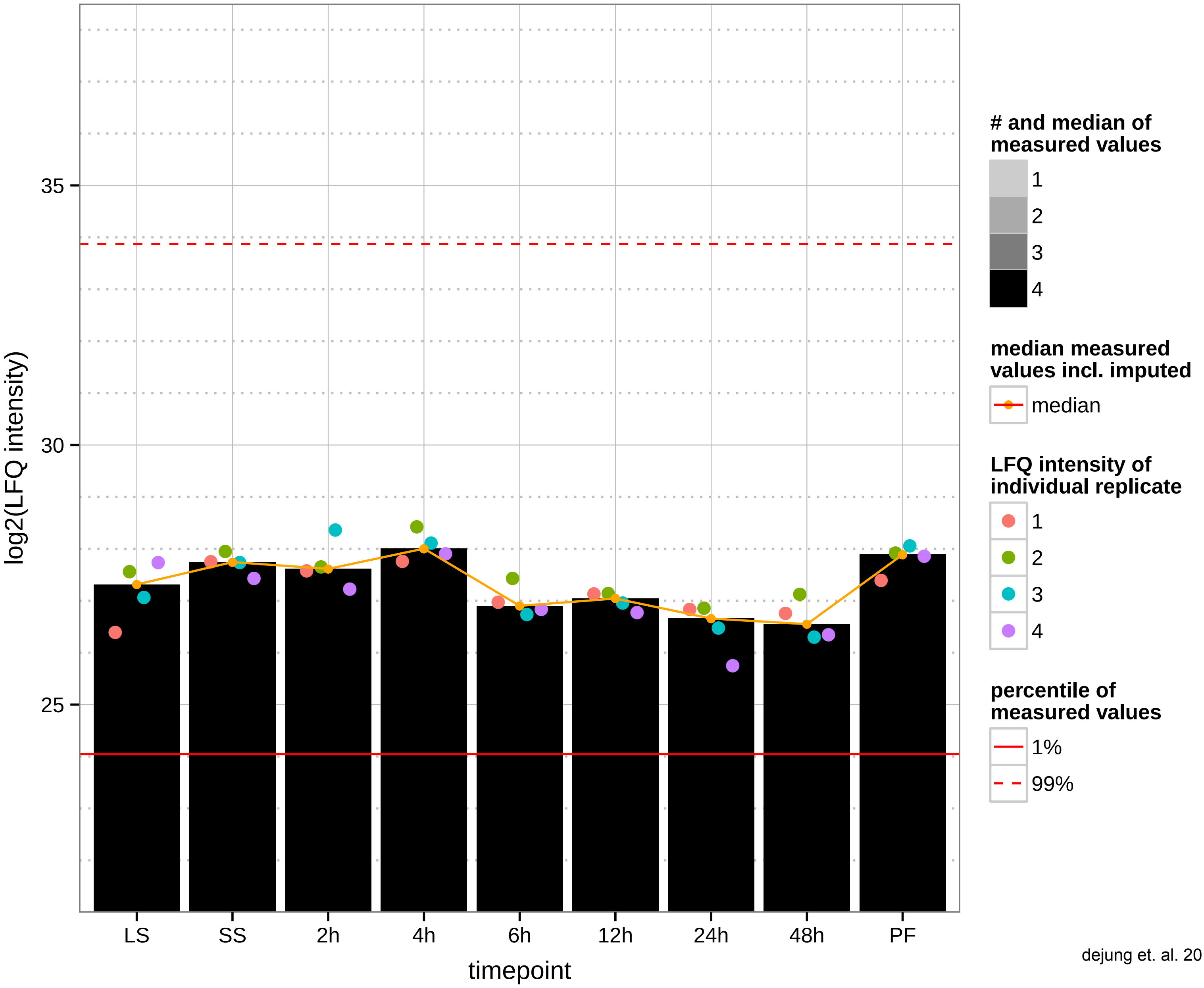
6–phosphogluconolactonase (6PGL)
Tb927.11.6330
AGOF: 6–phosphogluconolactonase activity
AGOC: cytoplasm, glycosome
AGOP: pentose–phosphate shunt
PGOF: 6–phosphogluconolactonase activity
PGOC: null
PGOP: carbohydrate metabolic process, pentose–phosphate shunt





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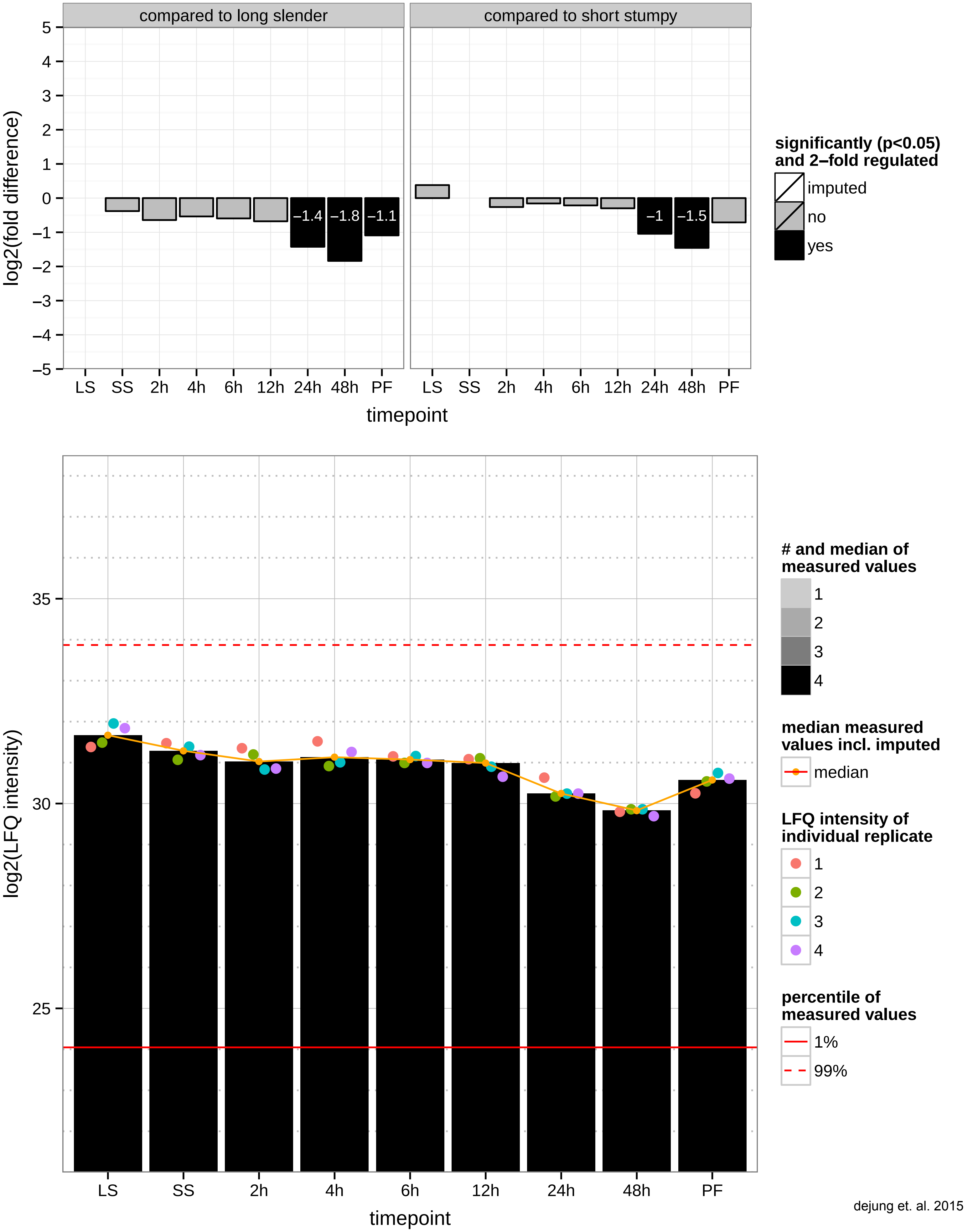
branched−chain amino acid aminotransferase, putative
Tb927.2.4590;Tb11.v5.0820;Tb927.2.4610
AGOF: null, branched−chain−amino−acid transaminase activity
AGOC: null, mitochondrion
AGOP: null, branched chain family amino acid metabolic process, cellular amino acid metabolic process, branched chain fami
PGOF: branched−chain−amino−acid transaminase activity, catalytic activity
PGOC: null
PGOP: branched chain family amino acid metabolic process, metabolic process



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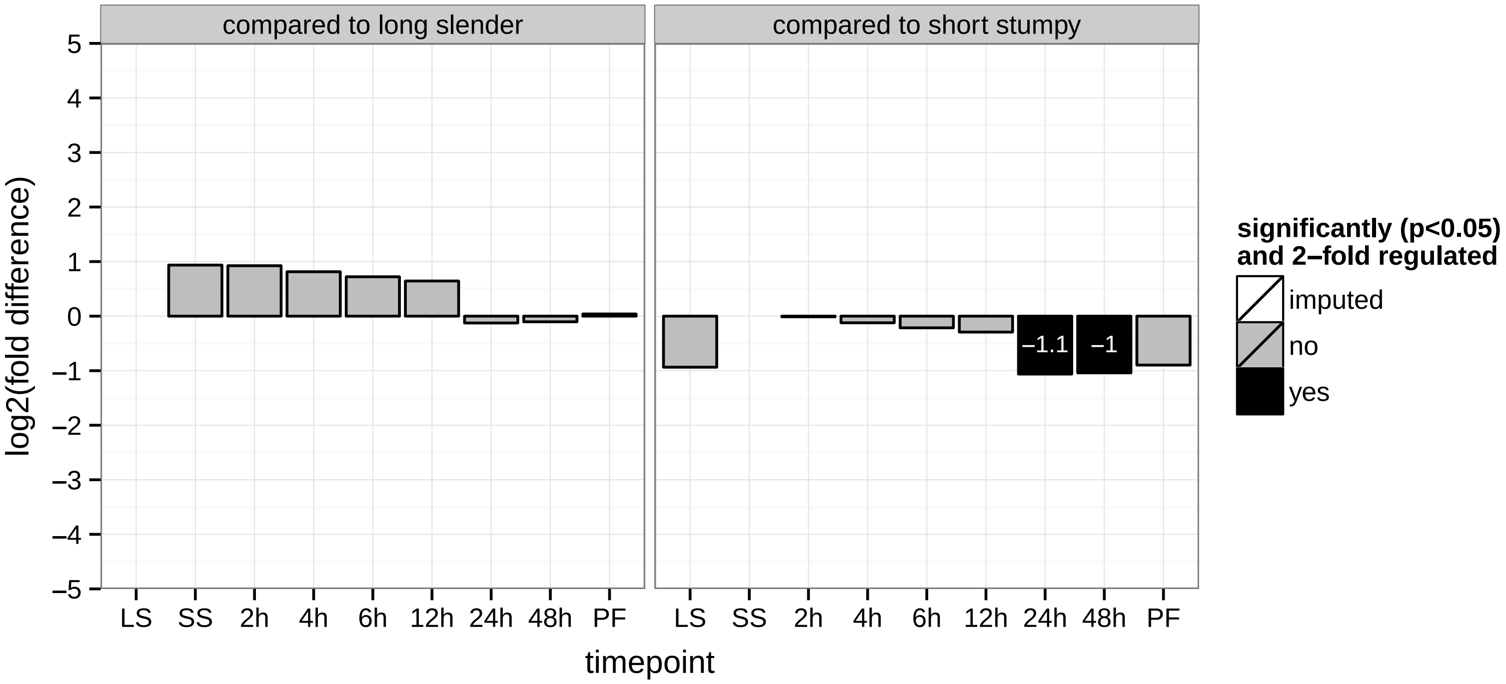
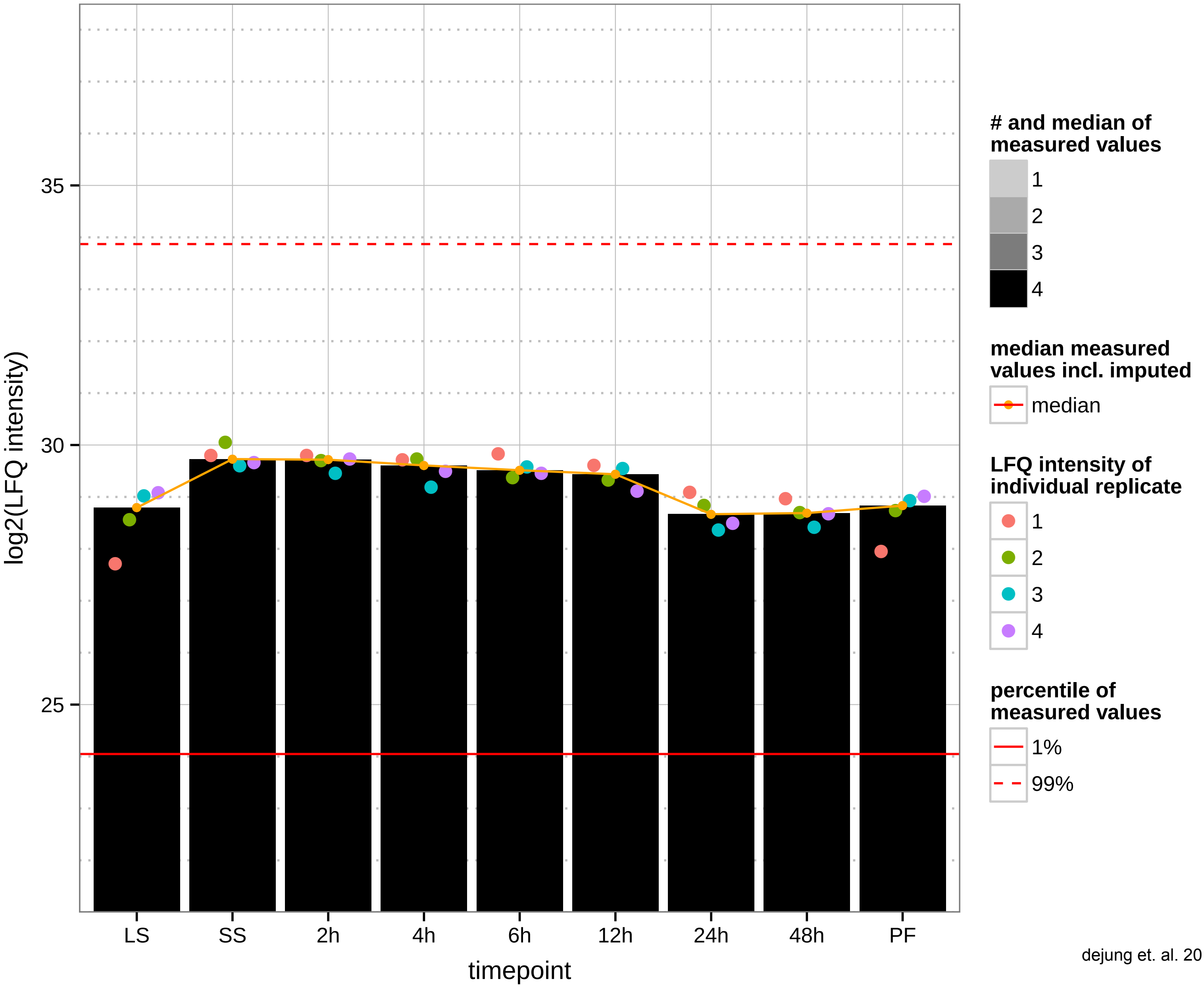
hypothetical protein, conserved, flagellar transport protein, putative (PIFTA1)
Tb927.3.1110;Tb11.v5.0589
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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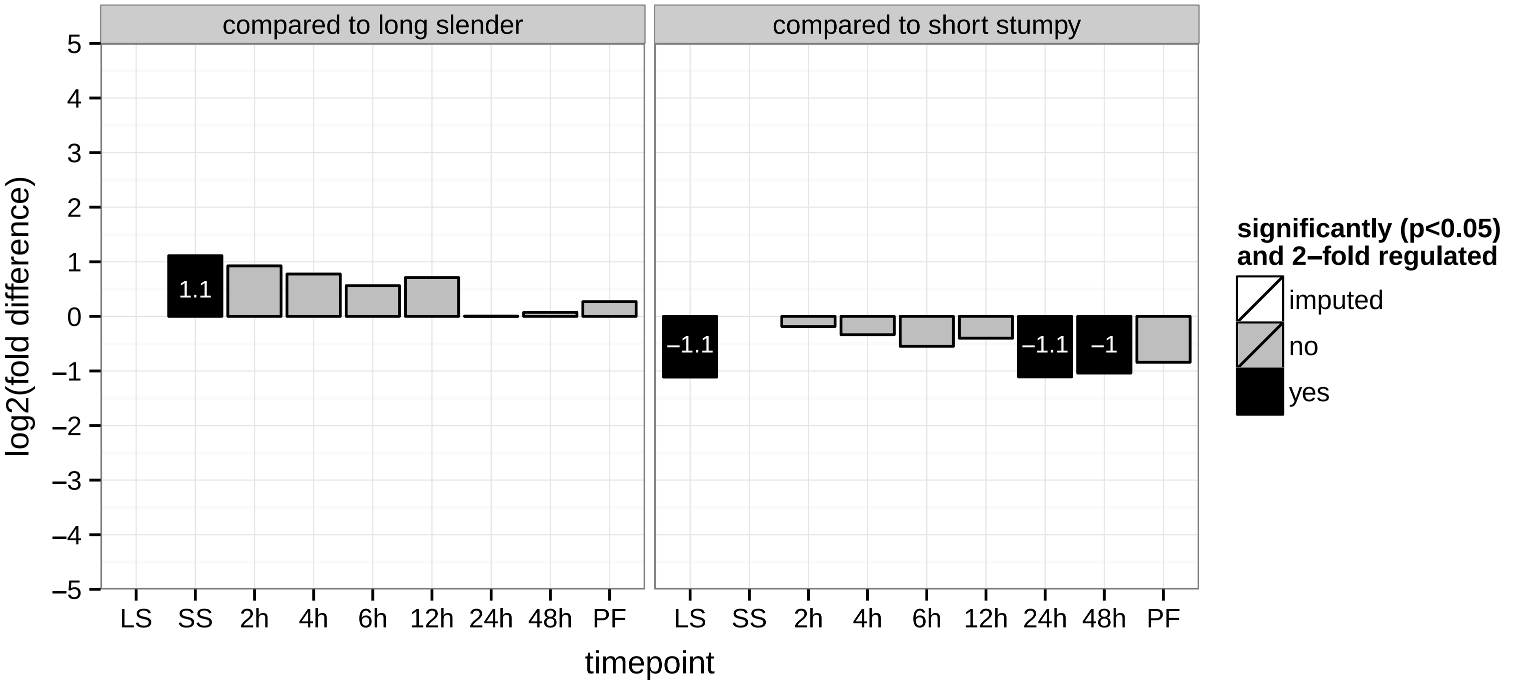
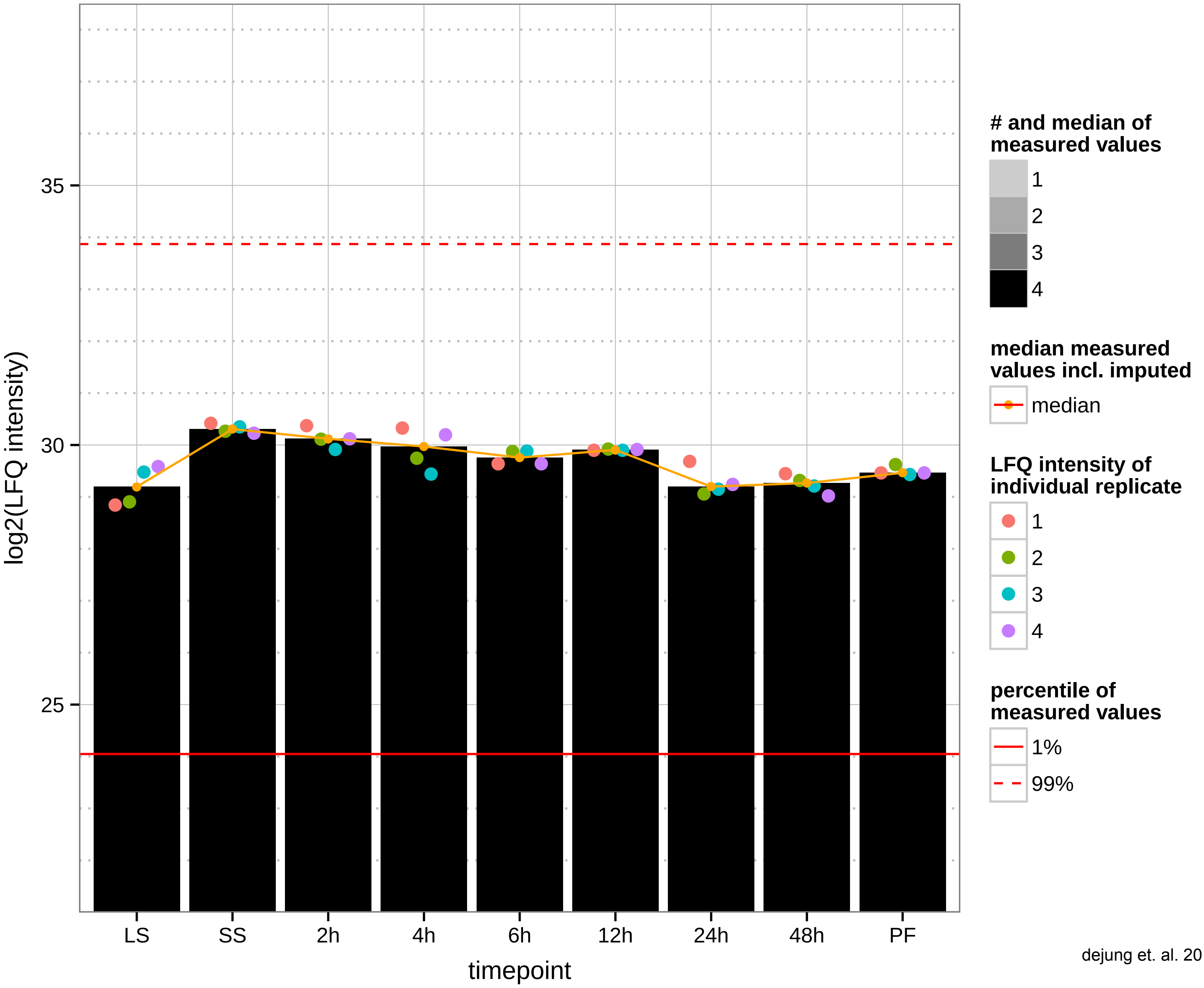
flagellar transport protein, putative (PIFTC3)
Tb927.3.3000
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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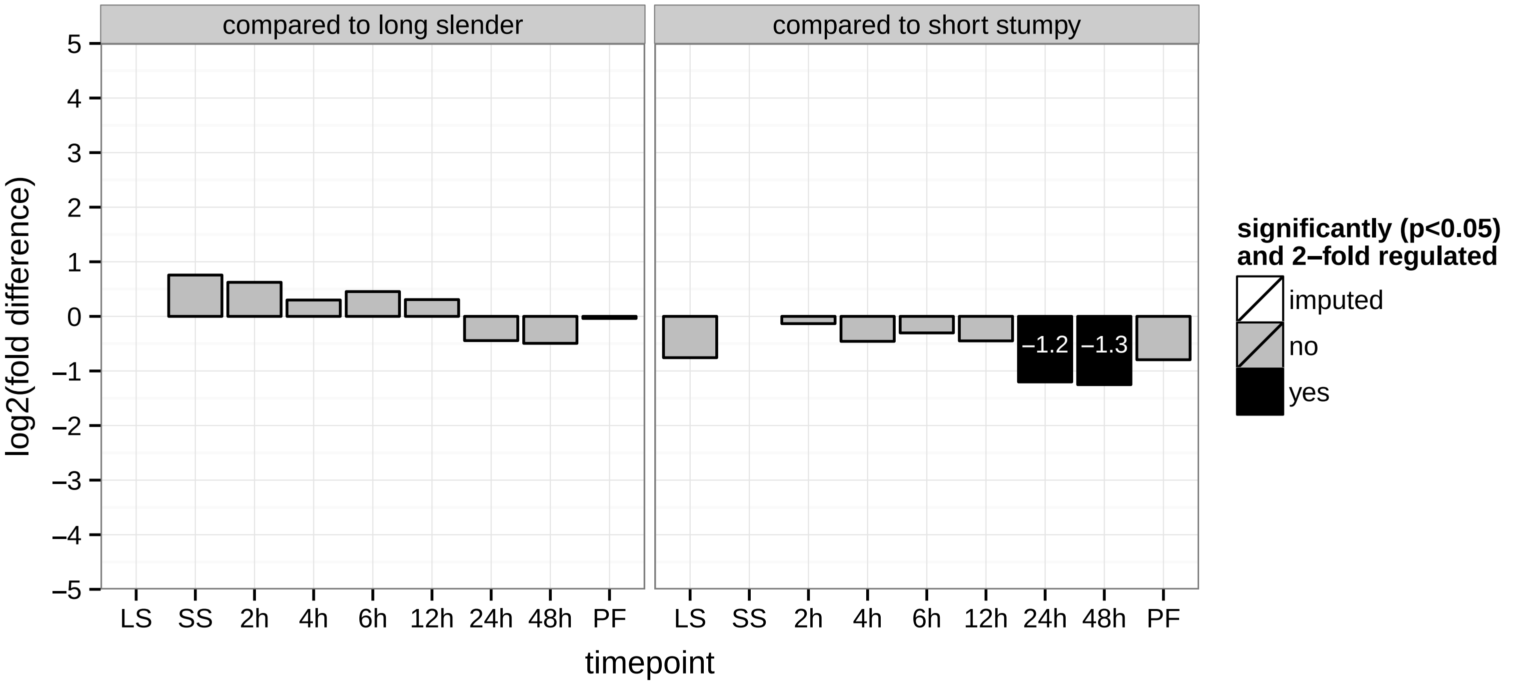
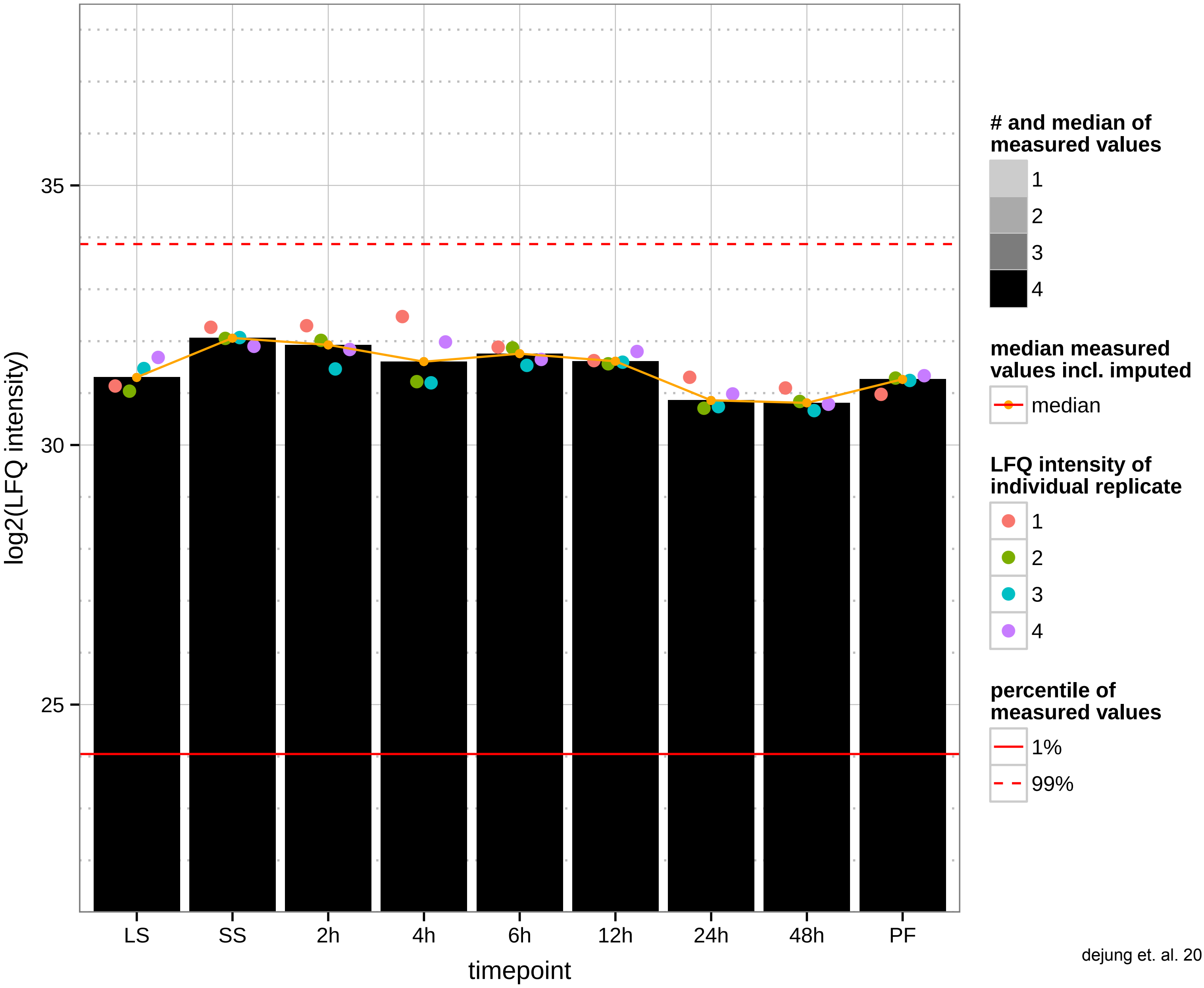
hypothetical protein, conserved
Tb927.3.3560
AGOF: ubiquitin–protein ligase activity
AGOC: ubiquitin ligase complex
AGOP: protein ubiquitination
PGOF: ubiquitin–protein ligase activity
PGOC: ubiquitin ligase complex
PGOP: protein ubiquitination





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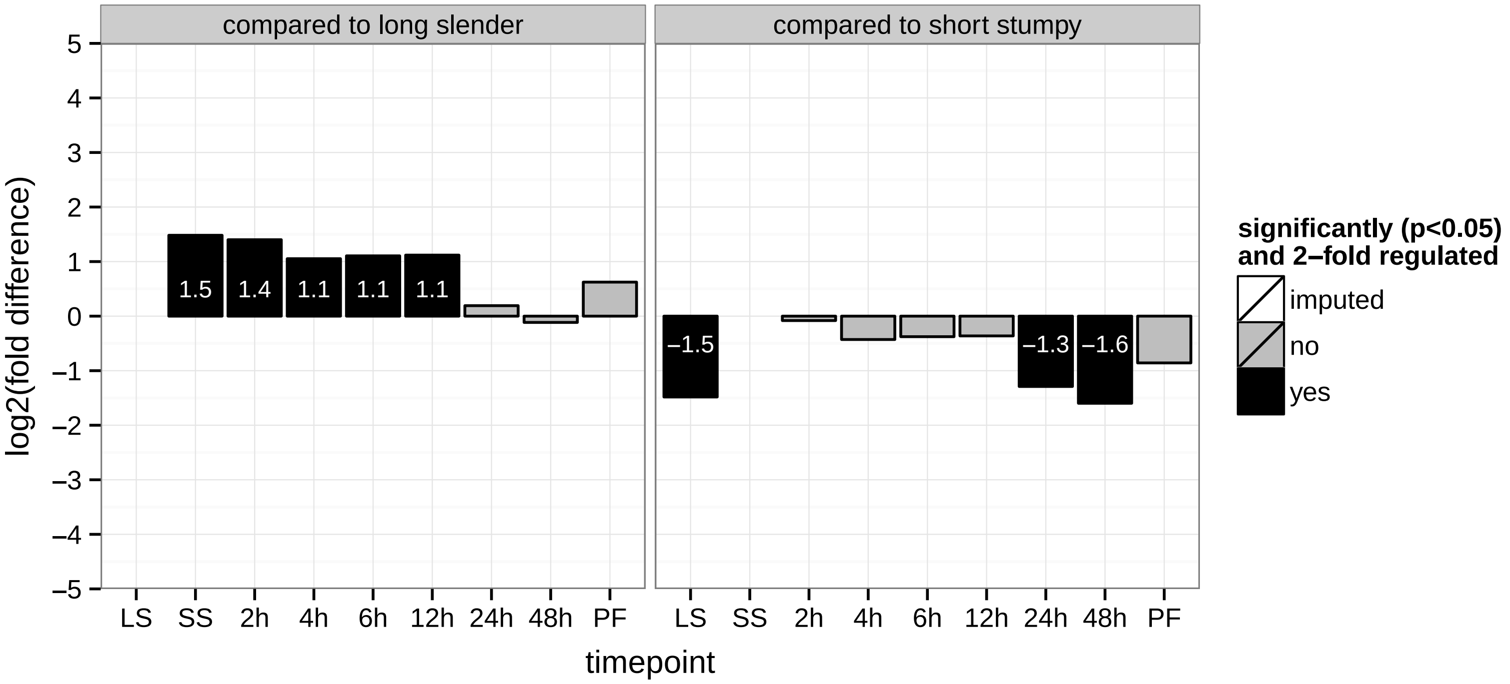
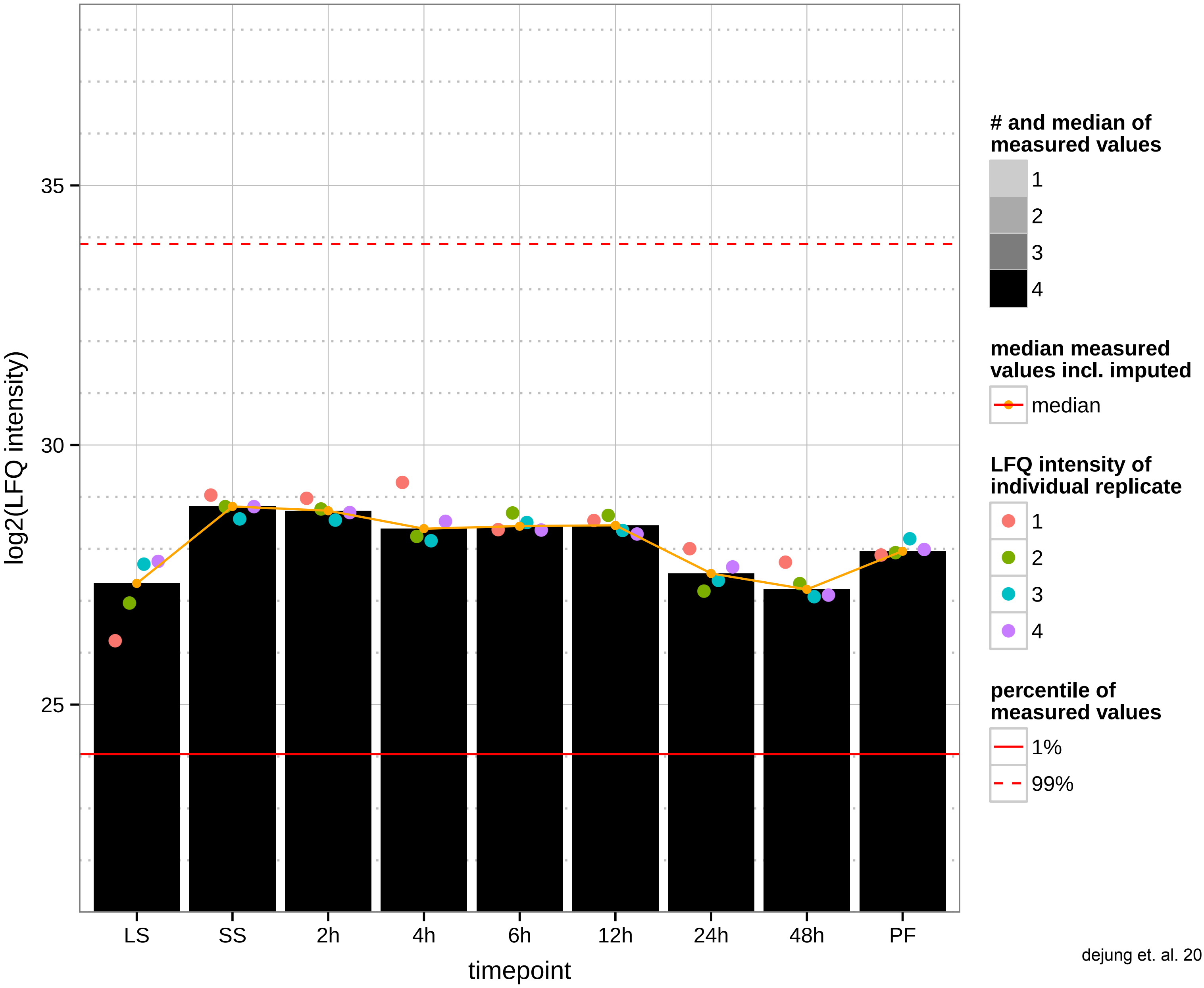
dynein intermediate chain WDRD34, putative
Tb927.3.5540
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null





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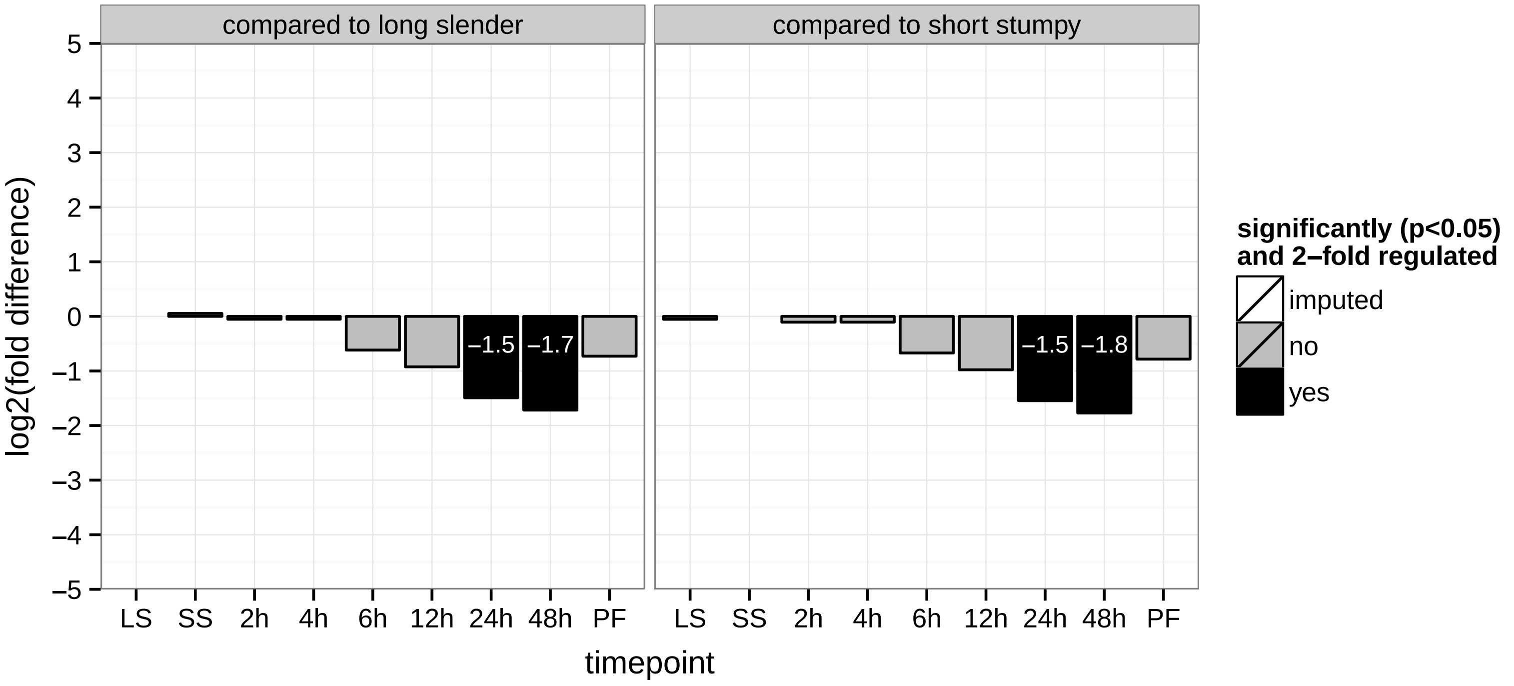
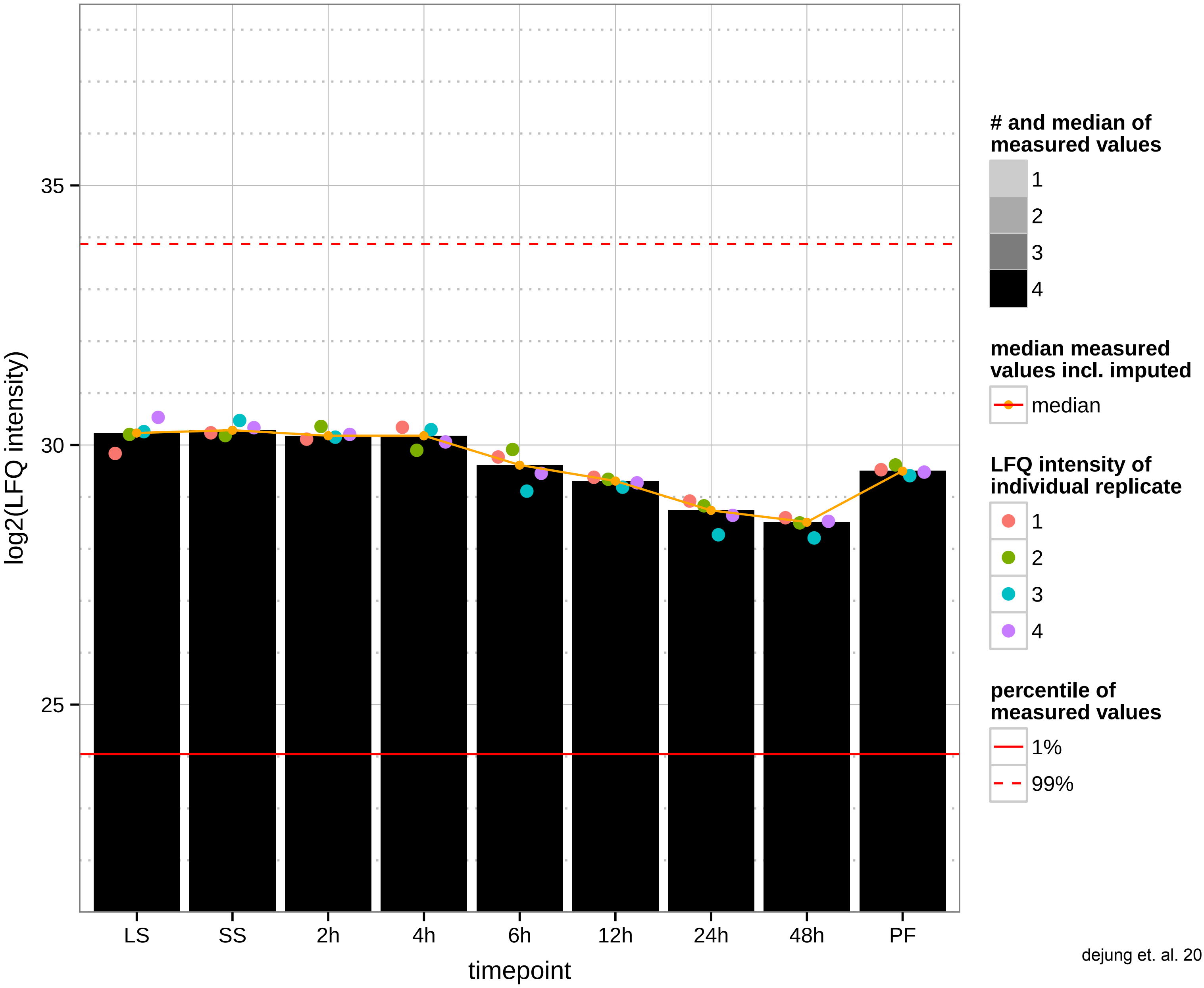
thioredoxin, putative
Tb927.4.2450
AGOF: glutathione−disulfide reductase activity
AGOC: null
AGOP: cell redox homeostasis, oxidation−reduction process
PGOF: null
PGOC: null
PGOP: cell redox homeostasis





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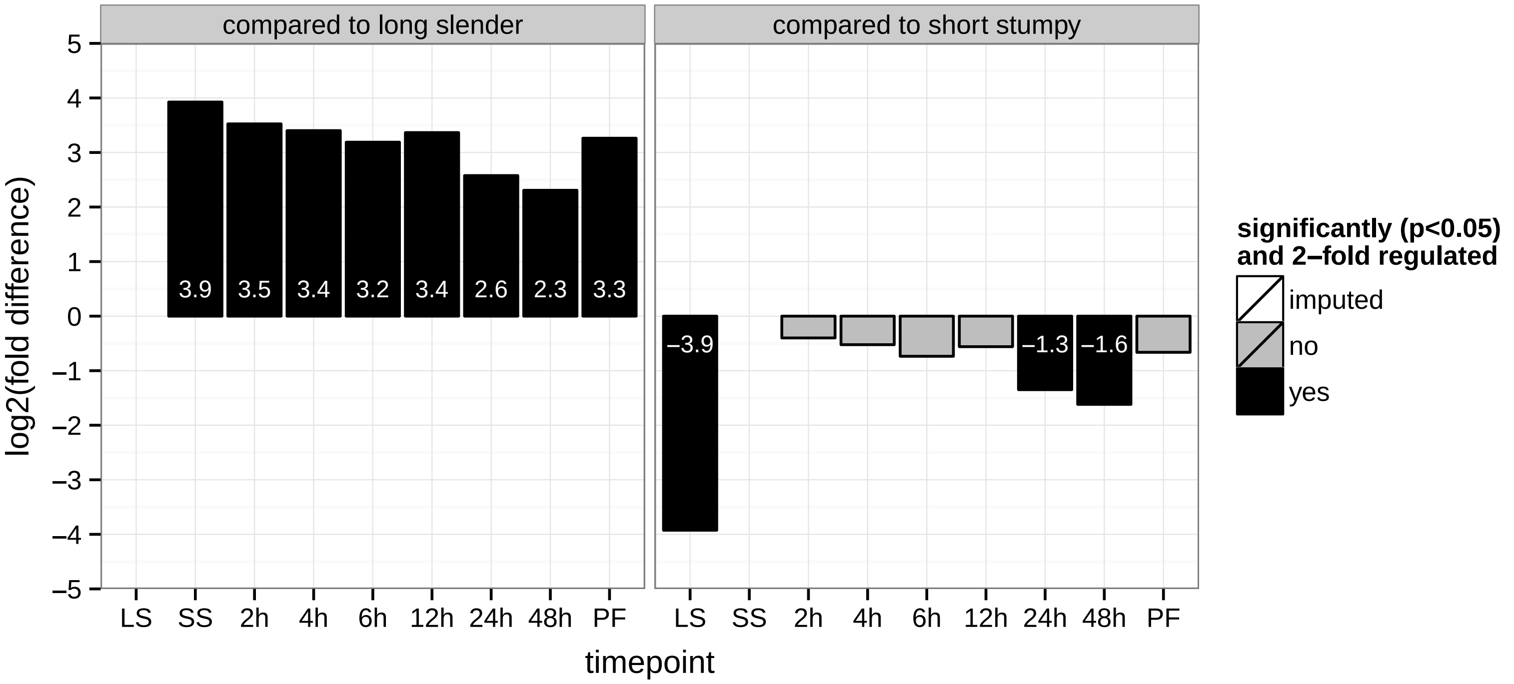
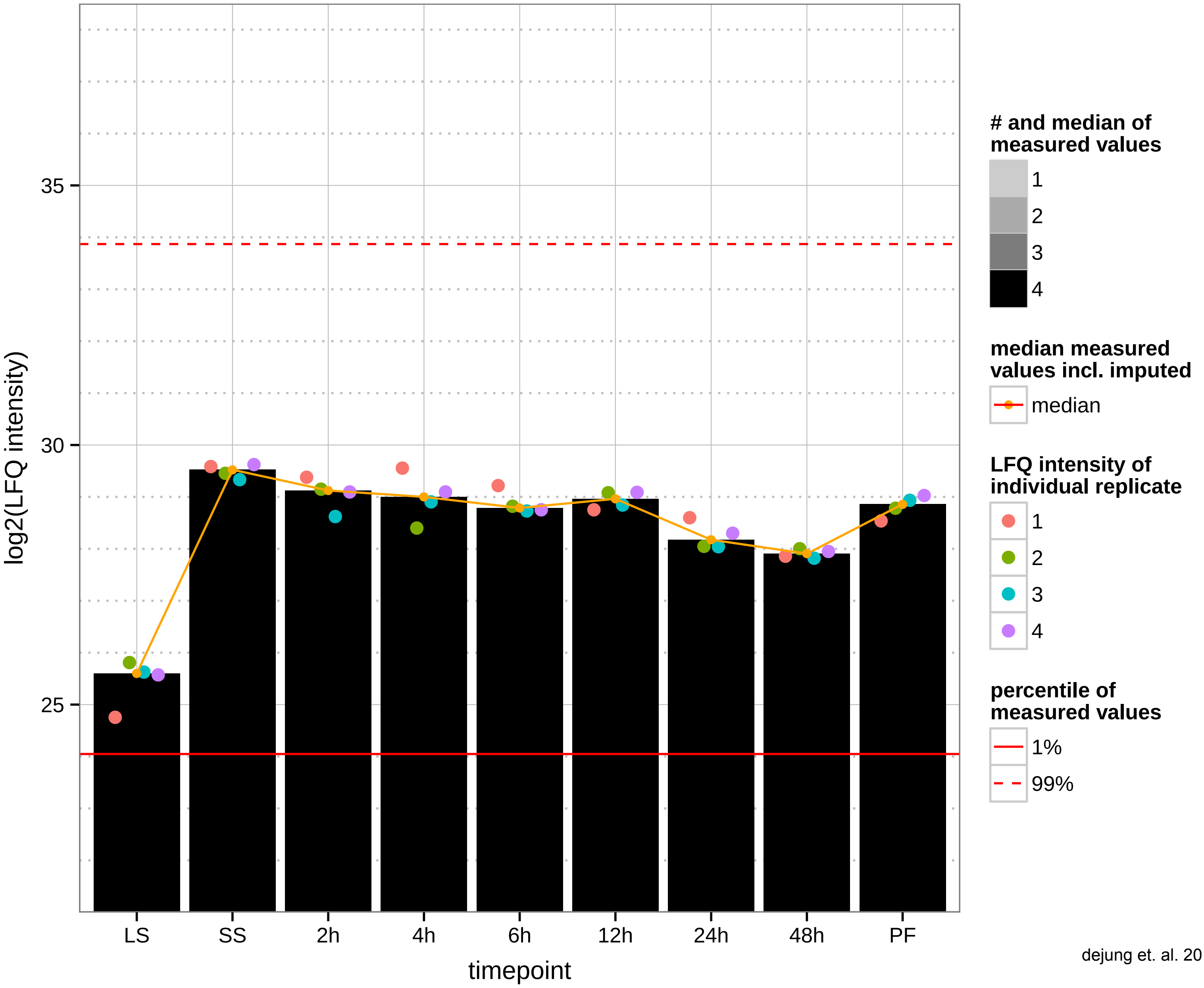
choline/ethanolamine kinase (C/EK1)
Tb927.5.1140
AGOF: choline kinase activity, ethanolamine kinase activity
AGOC: cytoplasm
AGOP: phosphatidylcholine biosynthetic process, phosphatidylethanolamine biosynthetic process
PGOF: phosphotransferase activity, alcohol group as acceptor, transferase activity, transferring phosphorus–containing group
PGOC: null
PGOP: null





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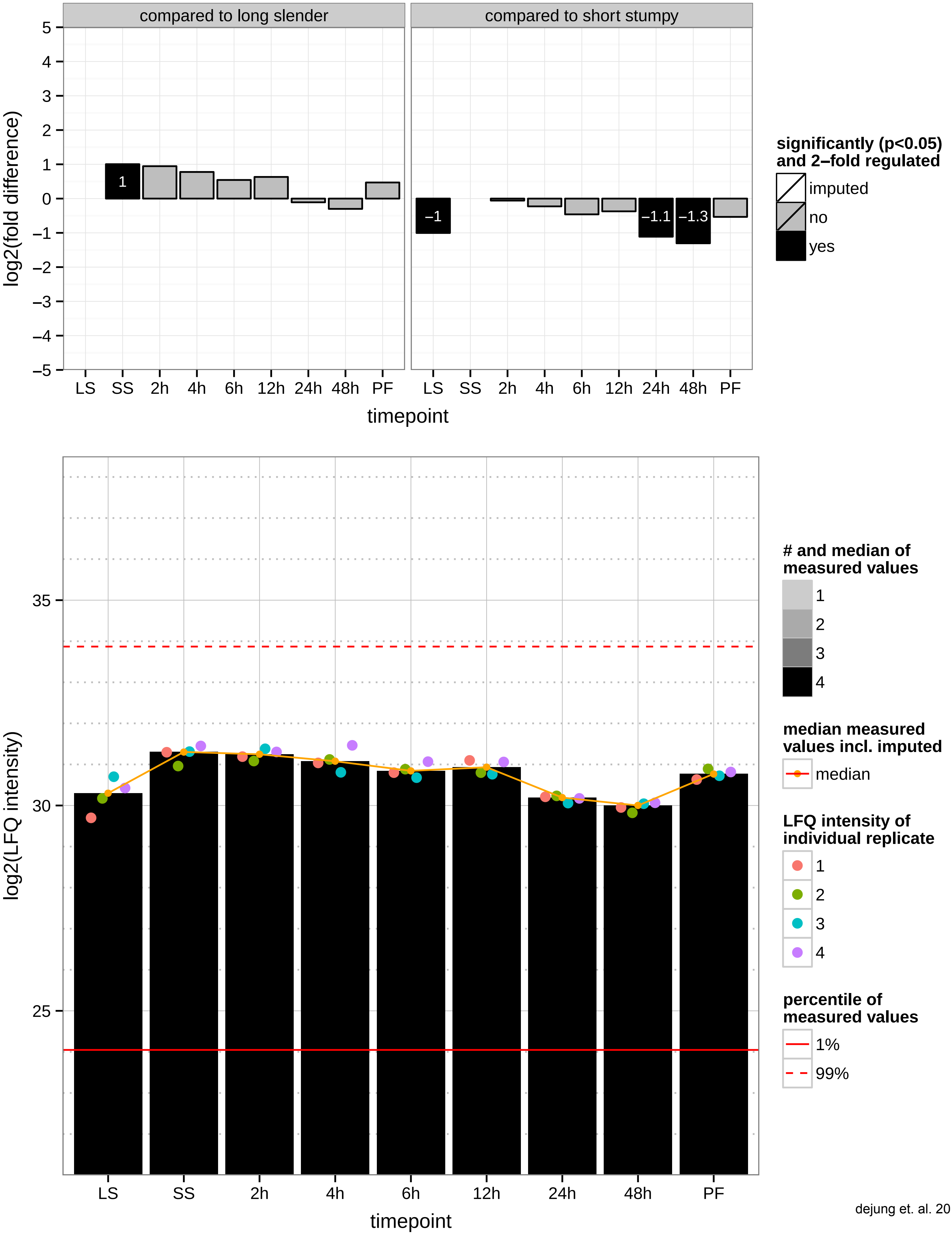
hypothetical protein, conserved
Tb927.5.1460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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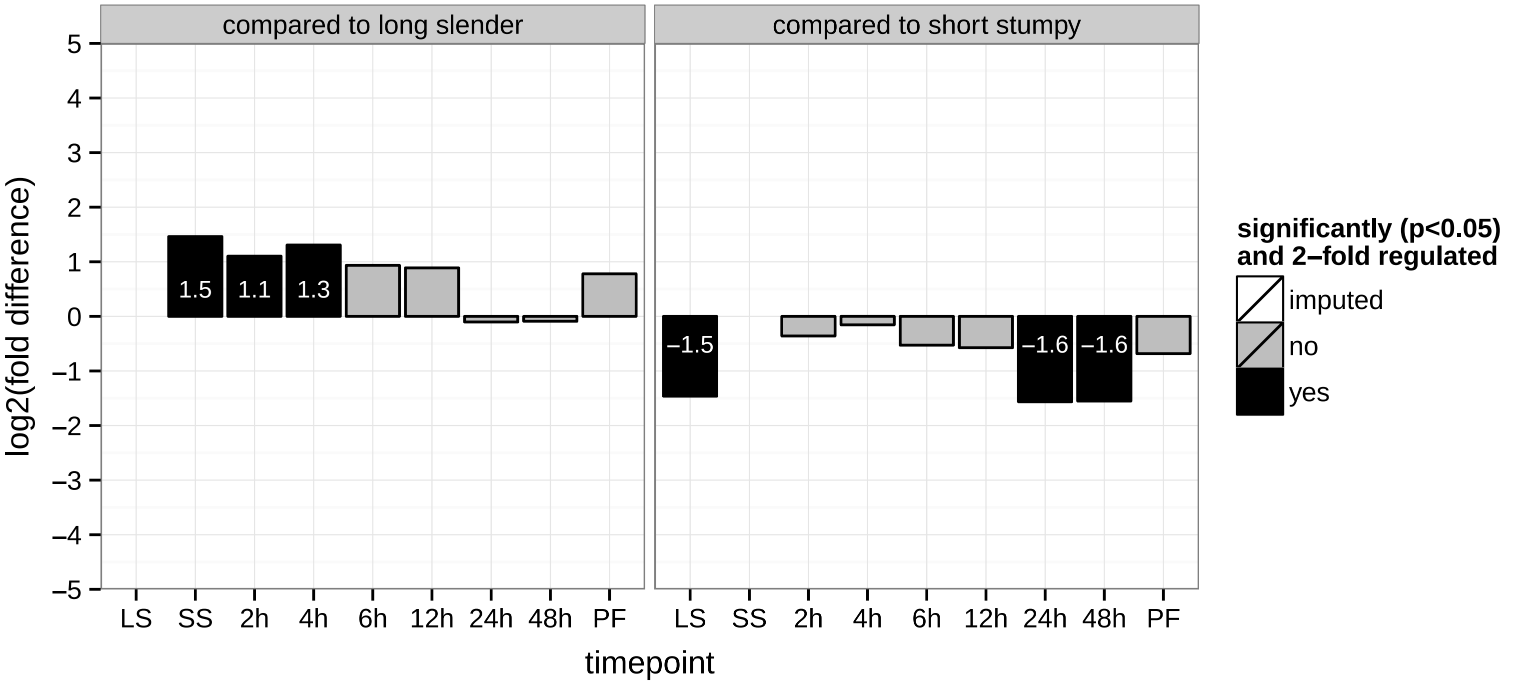
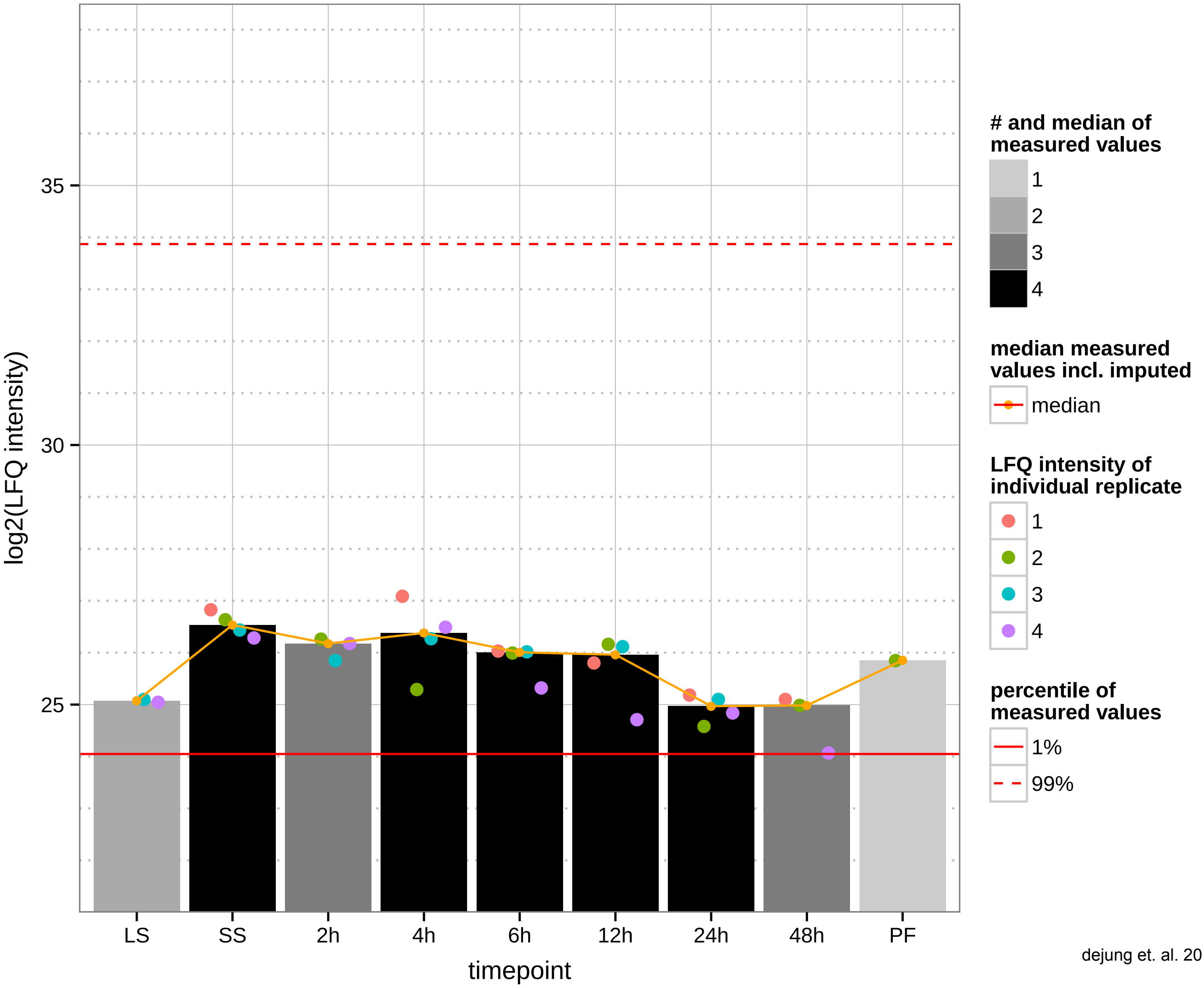
protein kinase, putative
Tb927.5.2820
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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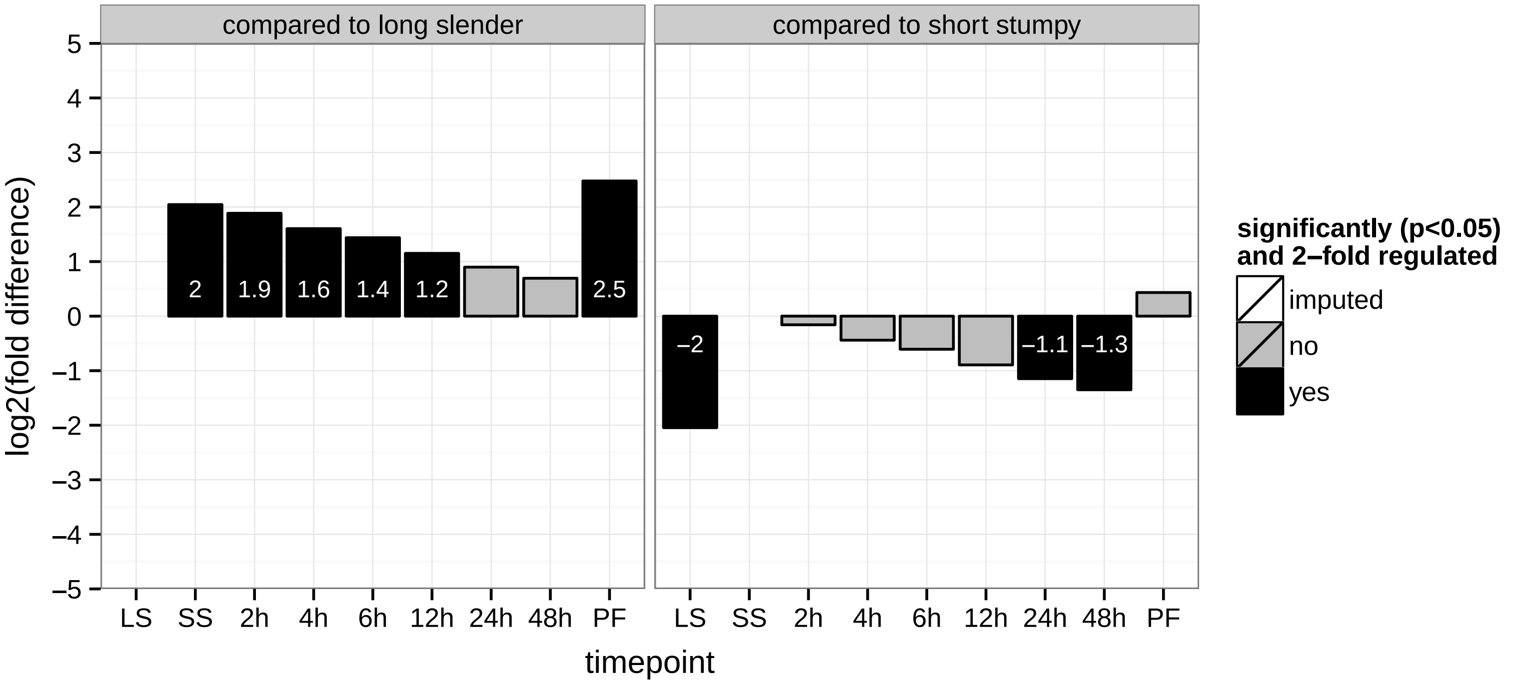
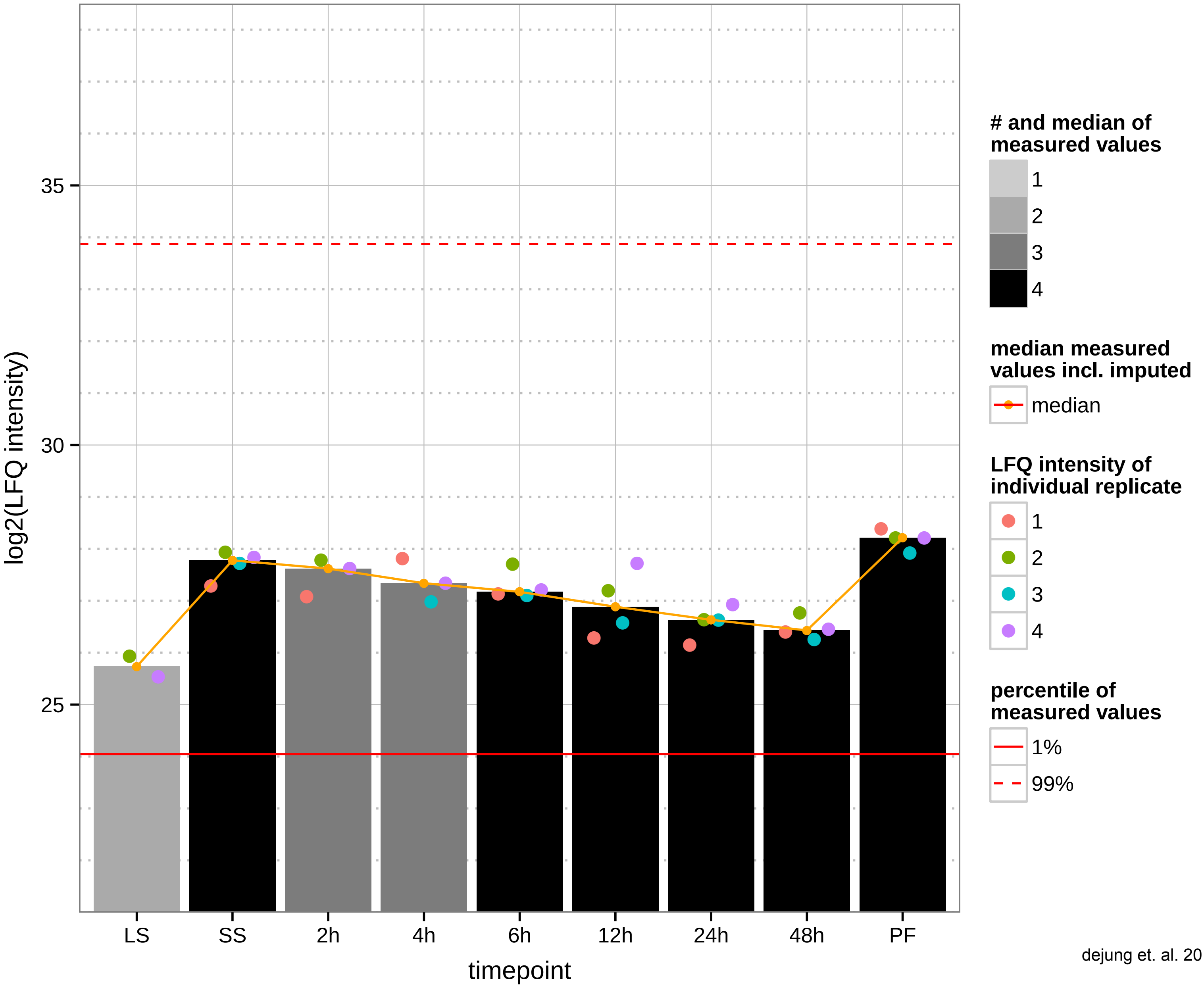
NADH–dependent fumarate reductase, putative
Tb927.5.940
AGOF: electron carrier activity, succinate dehydrogenase activity
AGOC: null
AGOP: null
PGOF: oxidoreductase activity, succinate dehydrogenase activity
PGOC: null
PGOP: oxidation–reduction process





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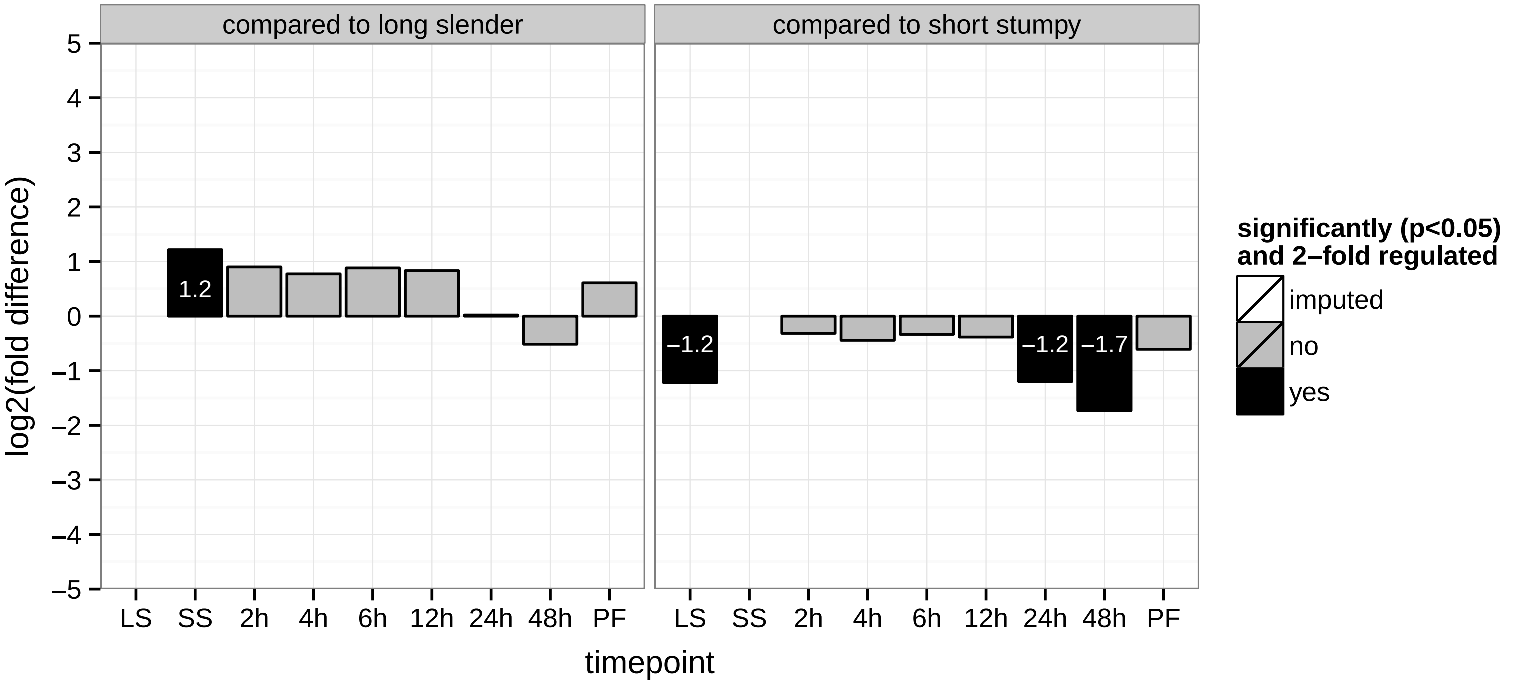
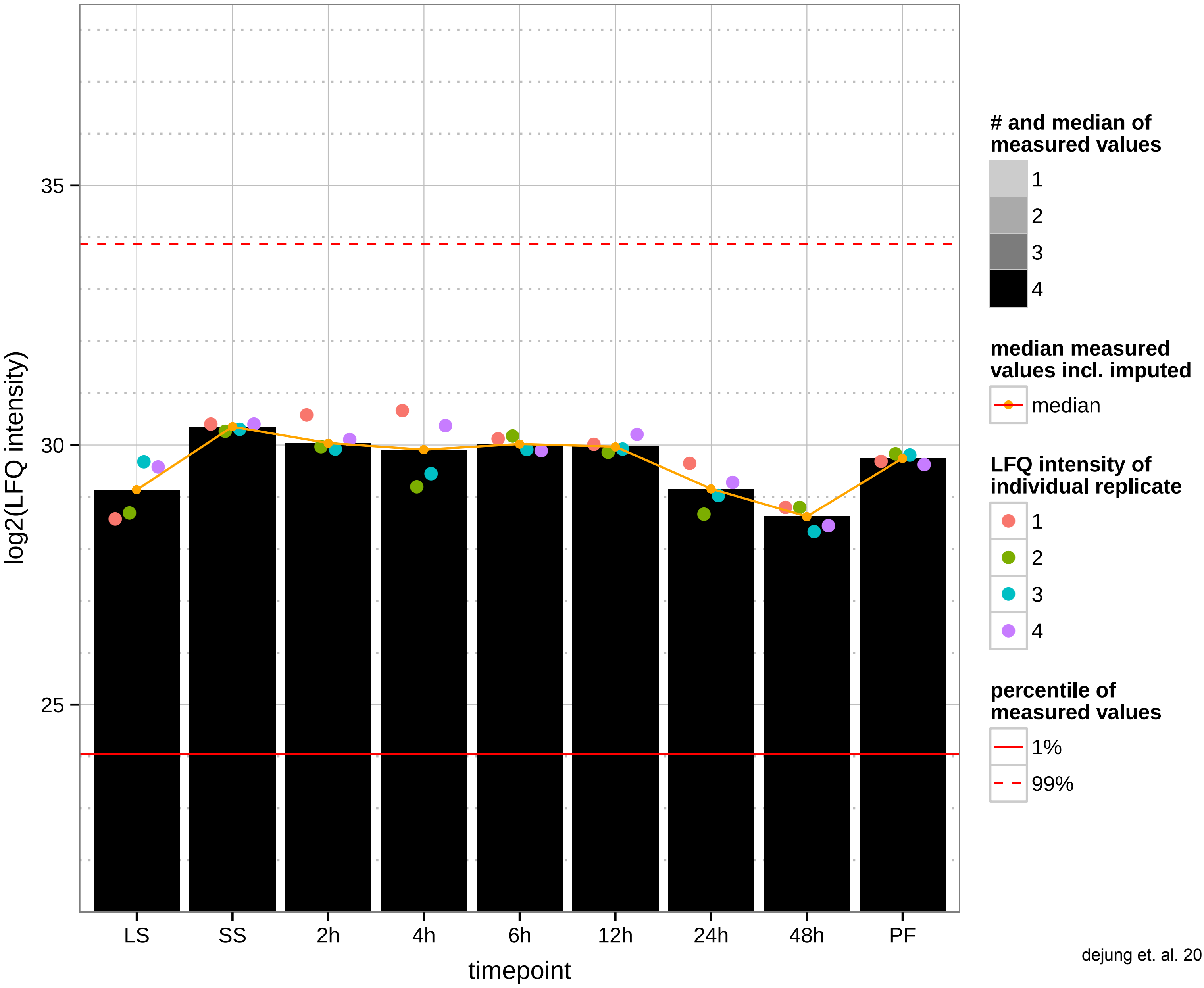
endosomal trafficking protein RME−8, putative
Tb927.6.3500
AGOF: heat shock protein binding
AGOC: null
AGOP: endocytosis
PGOF: binding, heat shock protein binding
PGOC: null
PGOP: null





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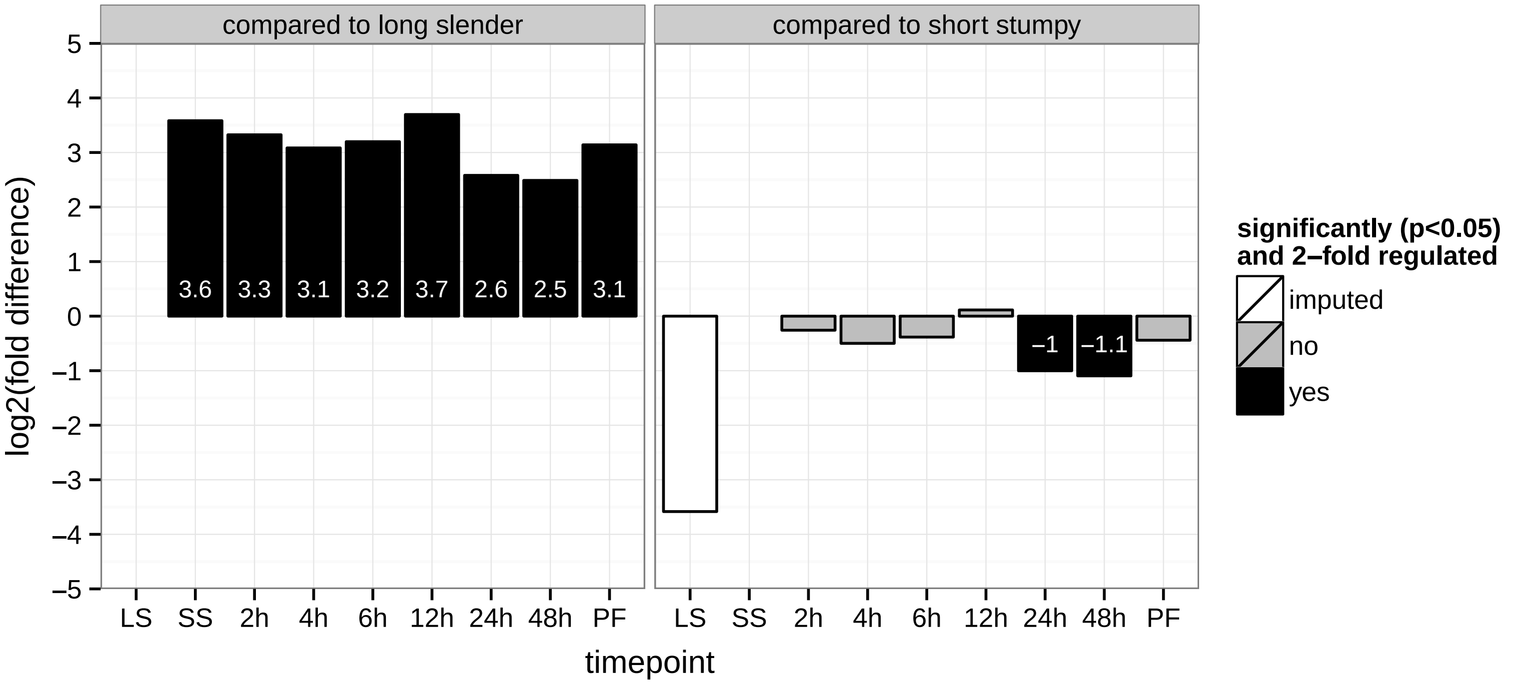
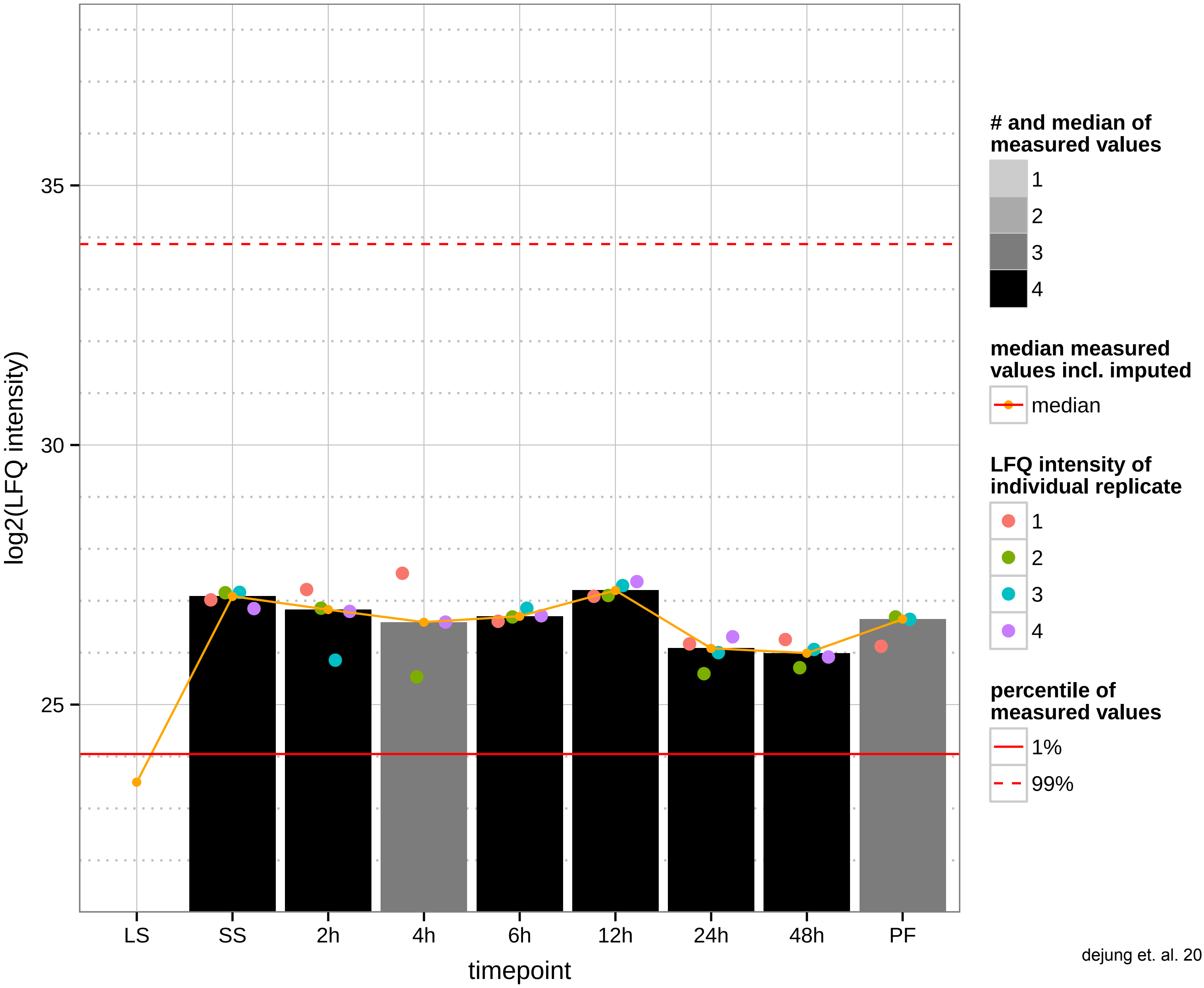
pre−mRNA splicing factor ATP−dependent RNA helicase, putative, ATP−dependent RNA helicase
Tb927.6.4600
AGOF: ATP binding, helicase activity, nucleic acid binding
AGOC: null
AGOP: null
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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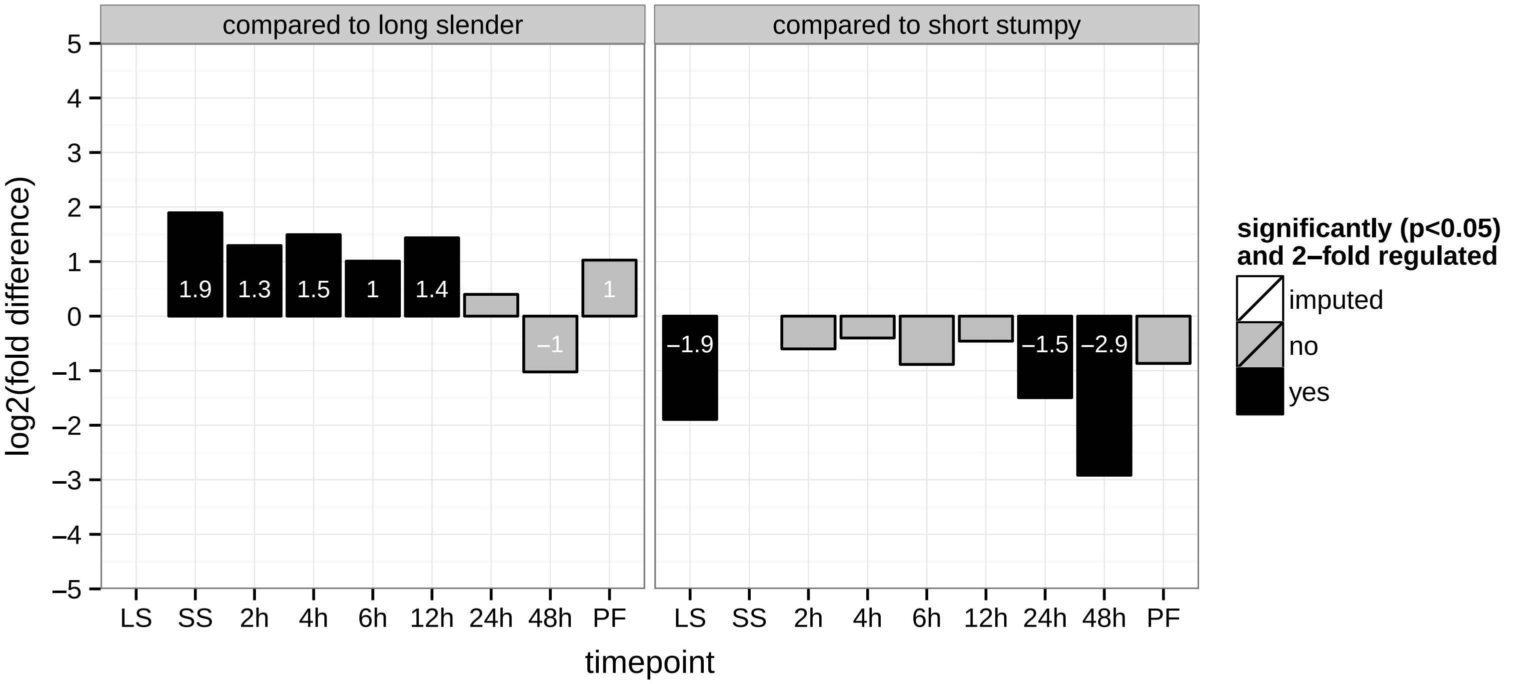
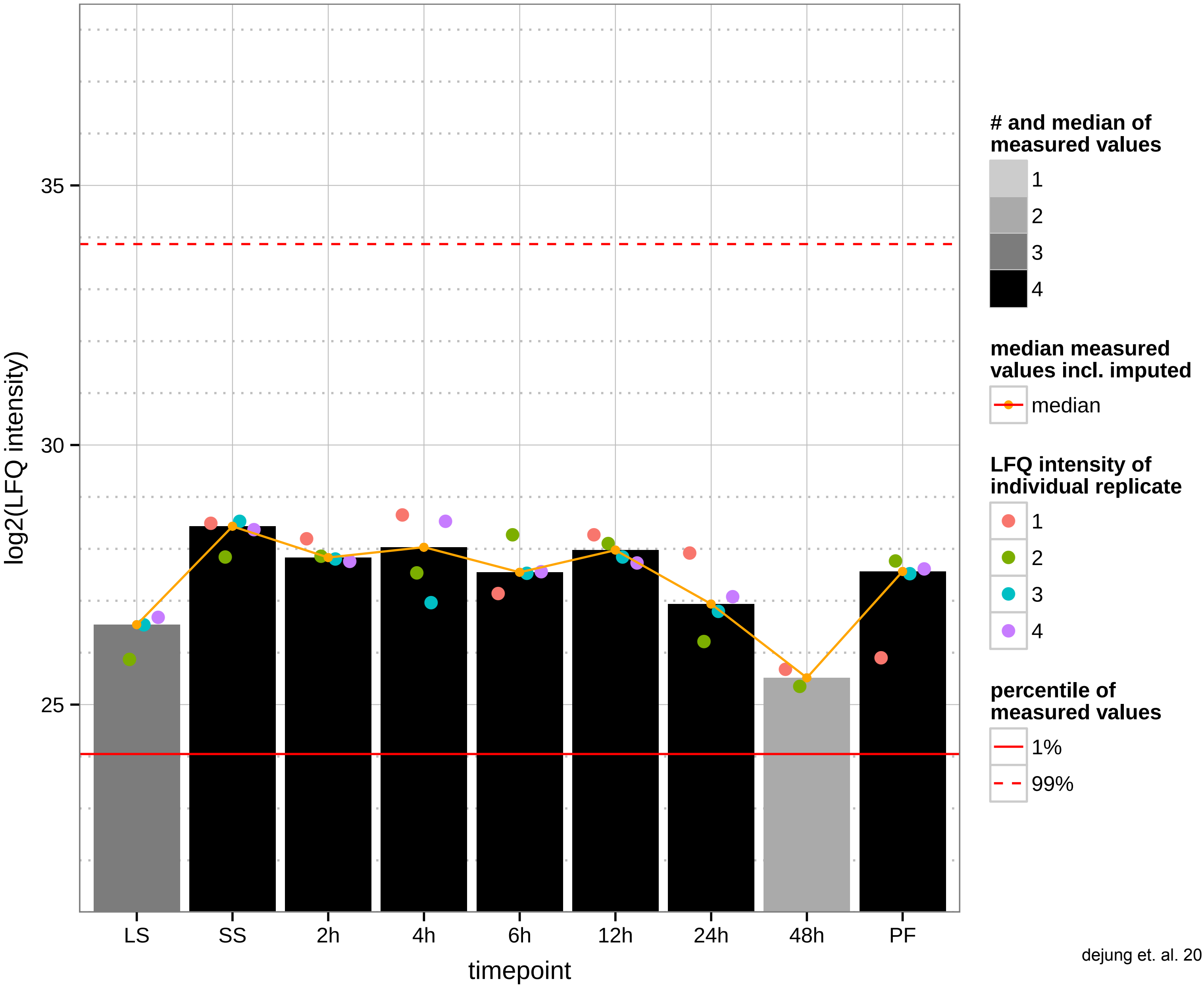
cysteine peptidase C (CPC), CPC cysteine peptidase, Clan CA, family C1, Cathepsin B–like (TbcatB)
Tb927.6.560
AGOF: cysteine–type peptidase activity
AGOC: null
AGOP: proteolysis
PGOF: cysteine–type peptidase activity
PGOC: null
PGOP: proteolysis





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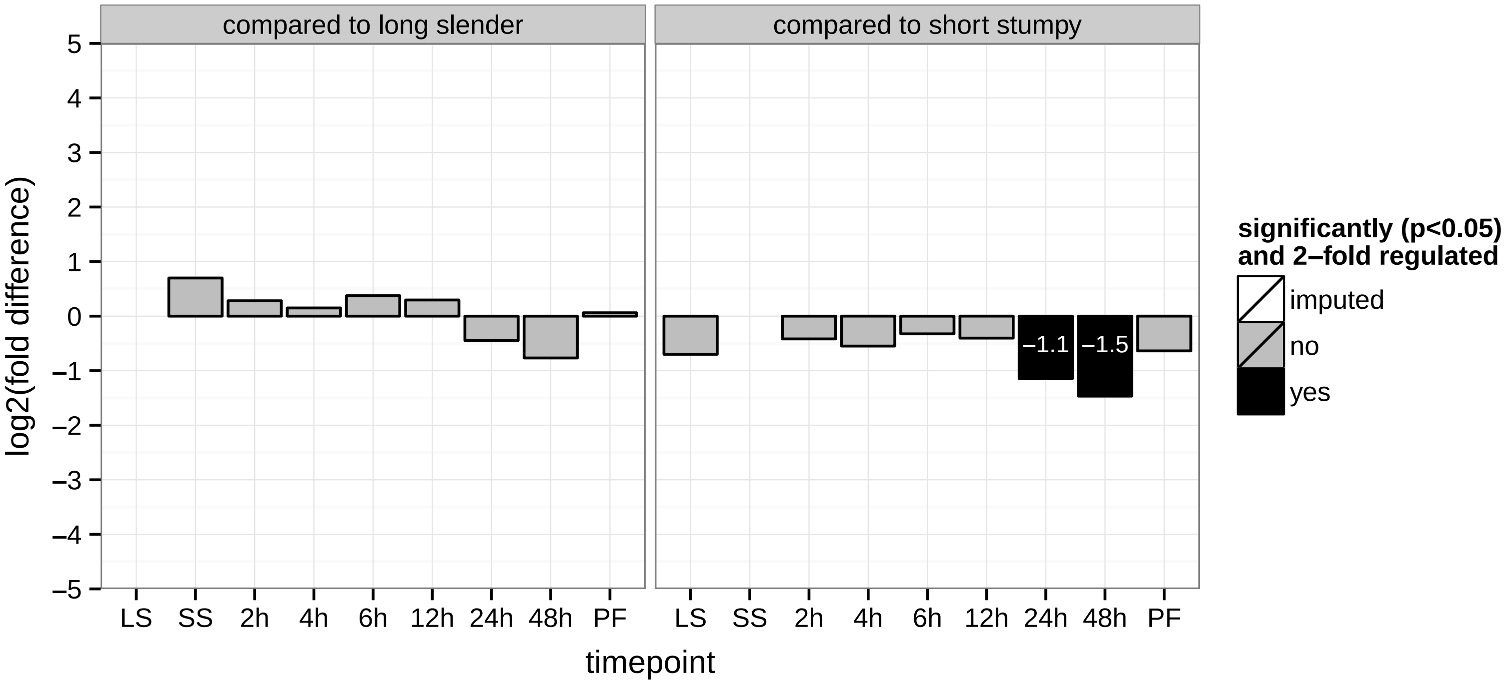
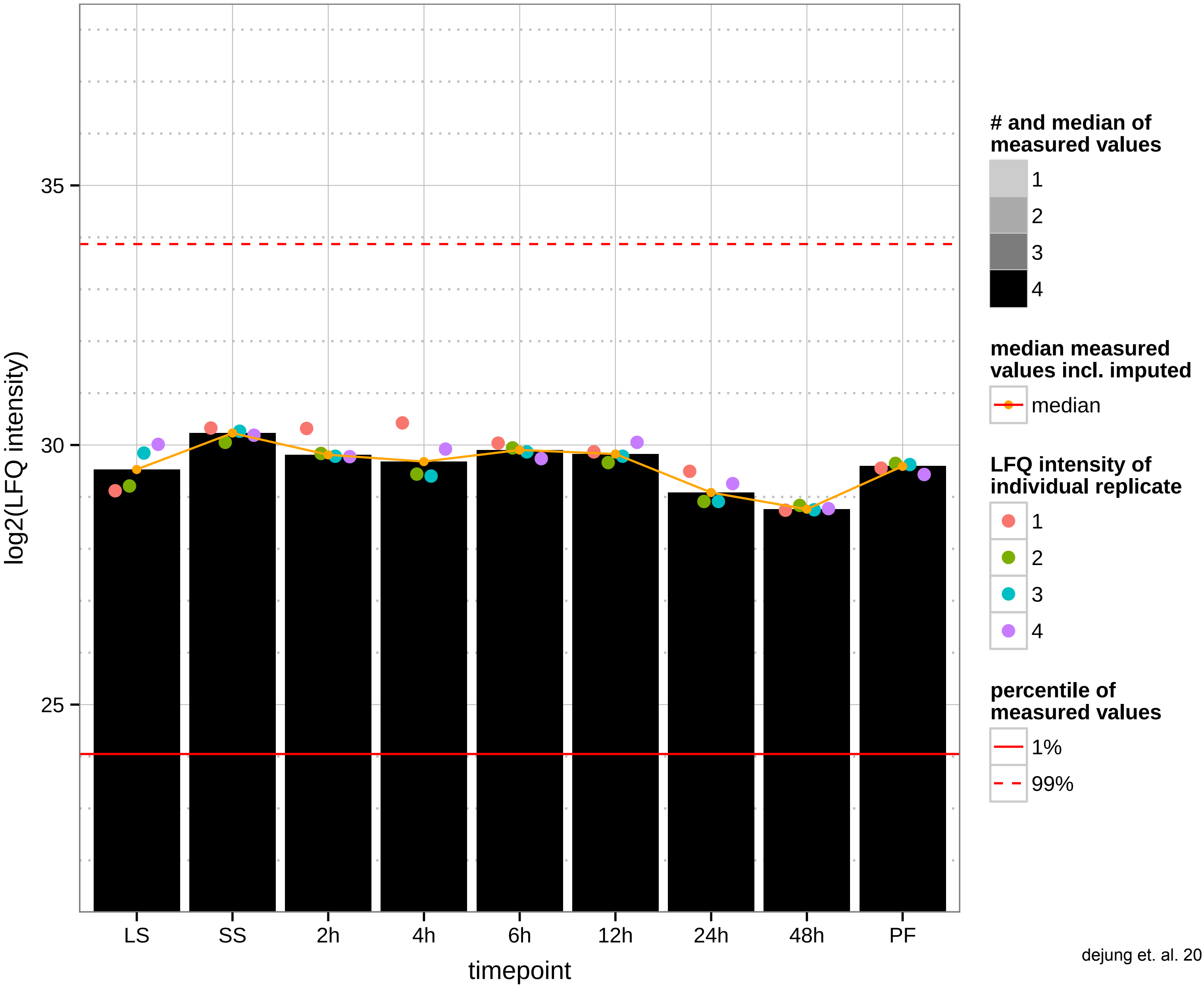
Mu−adaptin 1, putative, adaptor complex AP−1 medium subunit
Tb927.7.3180
AGOF: null
AGOC: clathrin adaptor complex
AGOP: intracellular protein transport, vesicle−mediated transport
PGOF: protein binding
PGOC: clathrin adaptor complex
PGOP: intracellular protein transport, transport, vesicle−mediated transport





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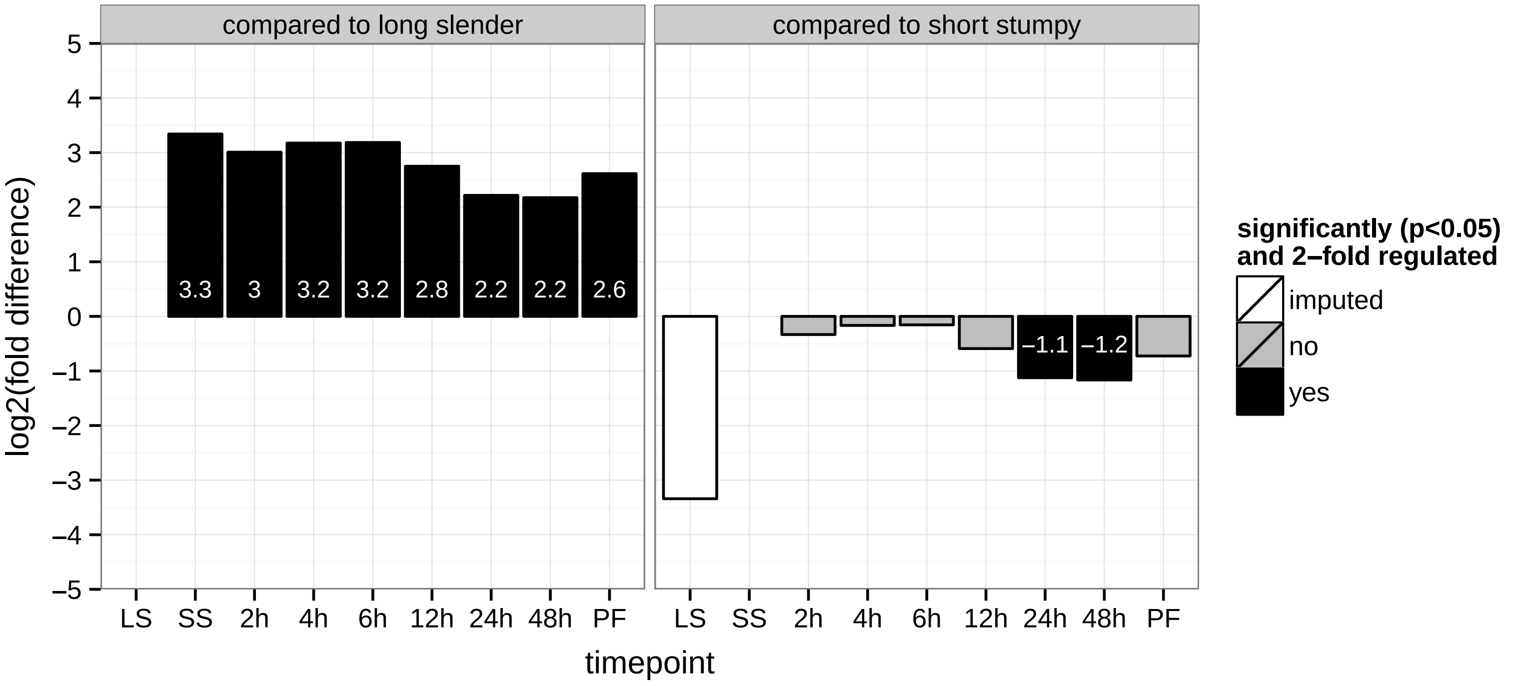
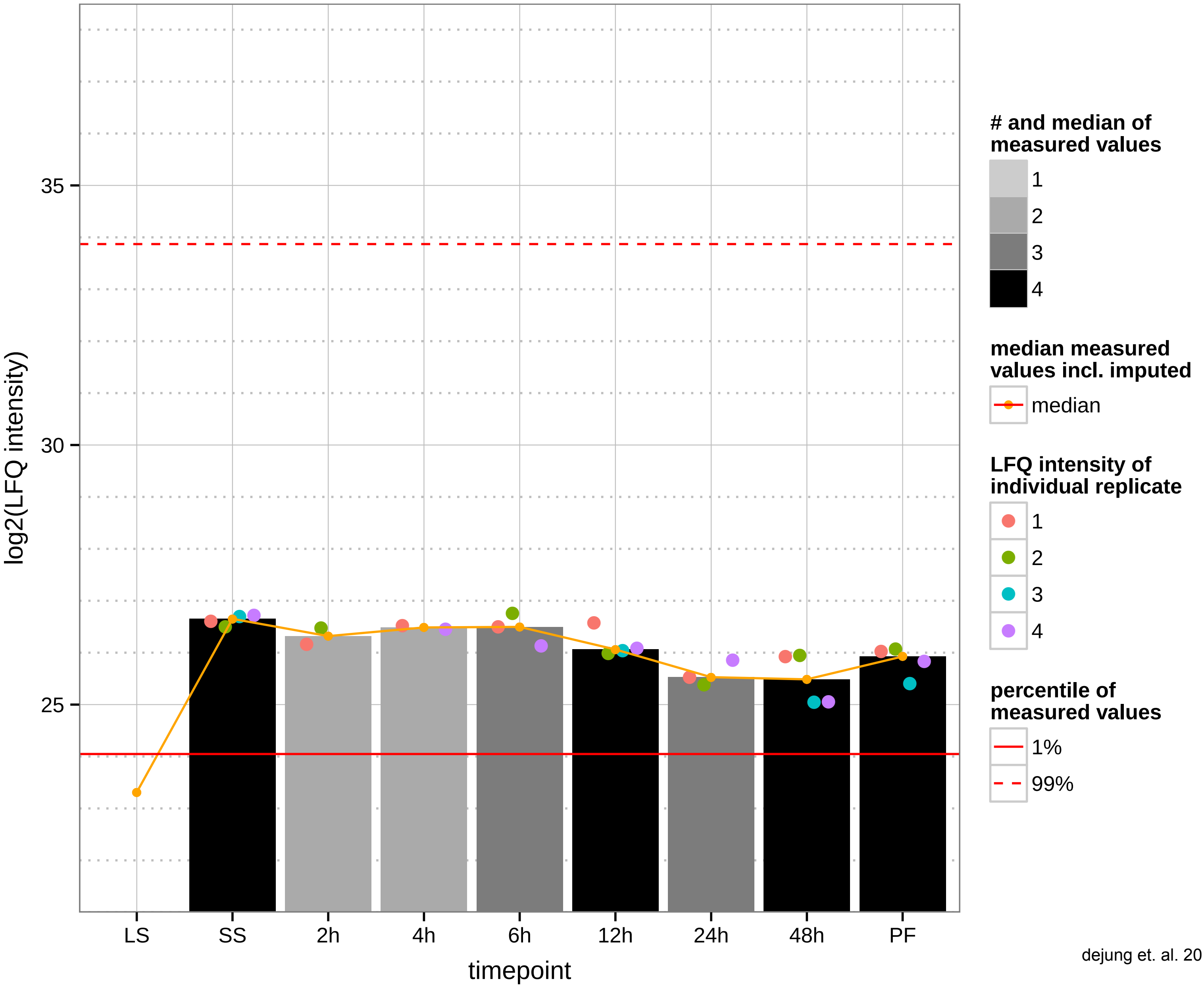
hypothetical protein, conserved
Tb927.7.550
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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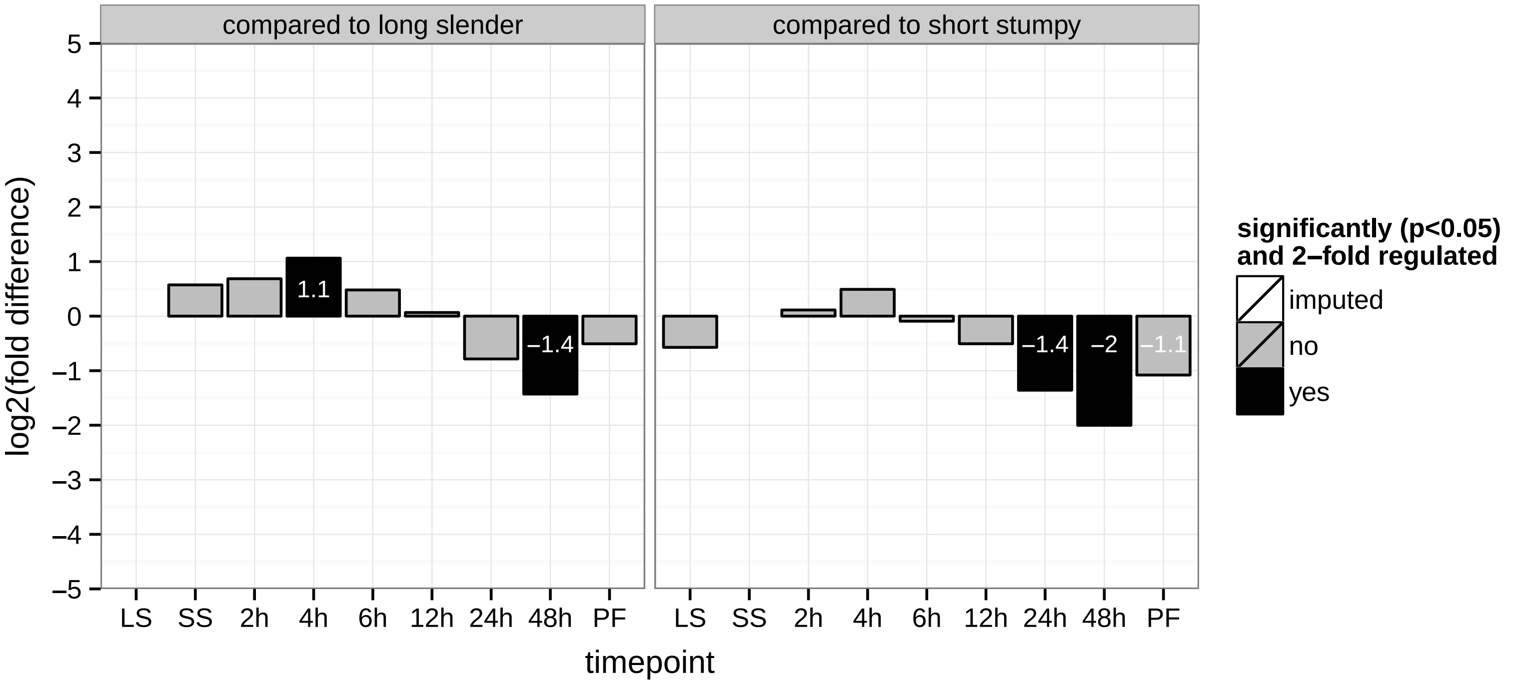
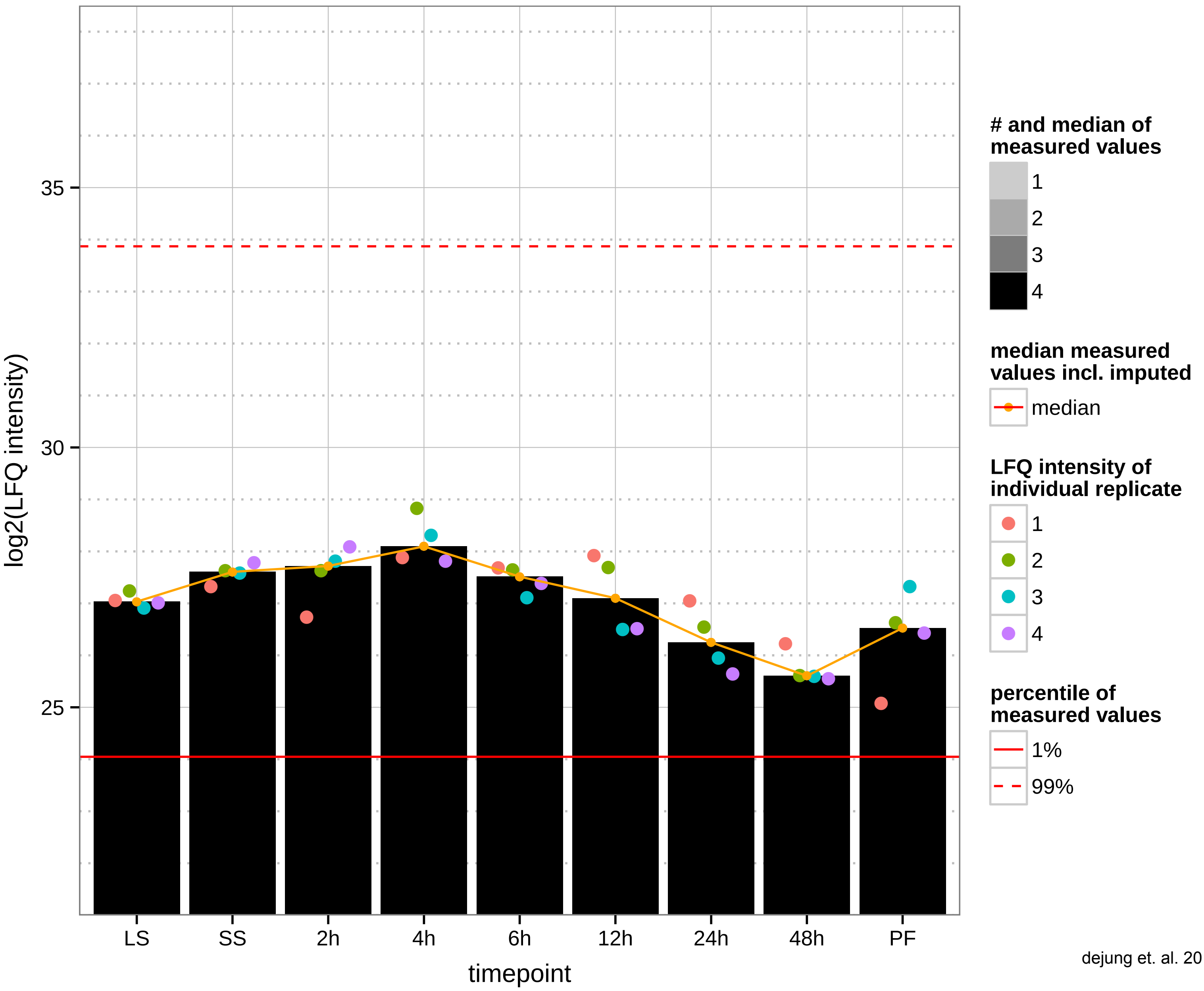
hypothetical protein, conserved
Tb927.8.3470
AGOF: null
AGOC: membrane
AGOP: intracellular protein transport
PGOF: null
PGOC: membrane
PGOP: intracellular protein transport, vesicle–mediated transport





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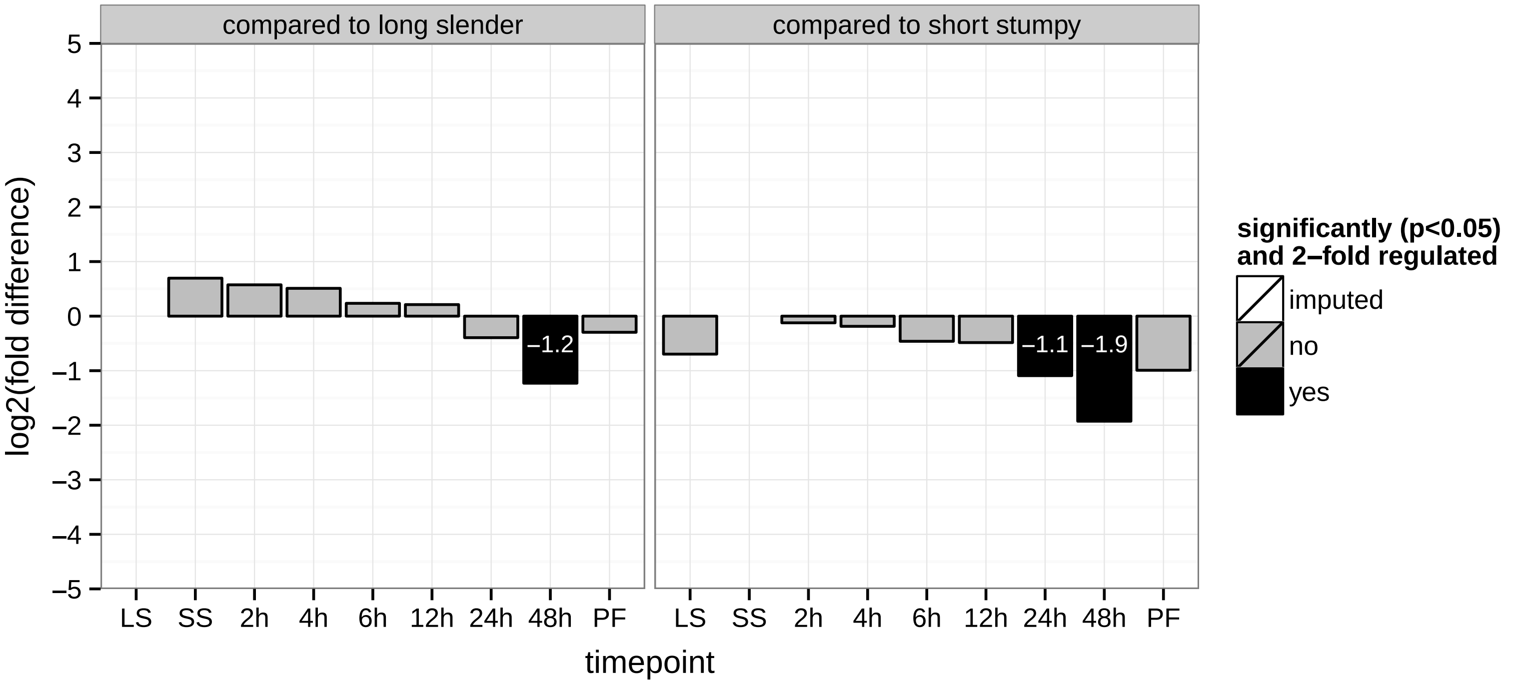
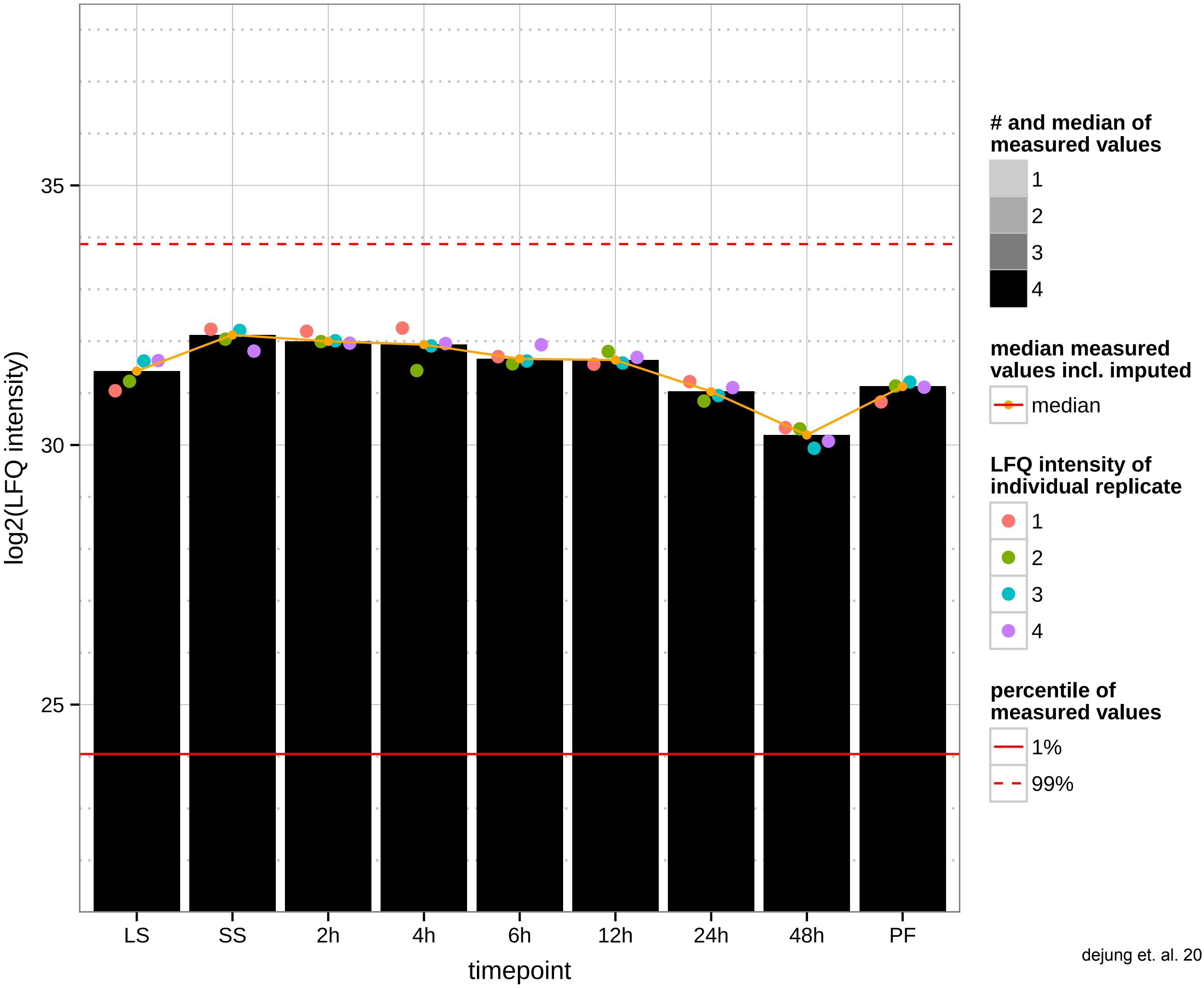
uridine phosphorylase
Tb927.8.4430
AGOF: purine–nucleoside phosphorylase activity, uridine phosphorylase activity
AGOC: null
AGOP: nucleoside metabolic process
PGOF: catalytic activity
PGOC: null
PGOP: nucleoside metabolic process





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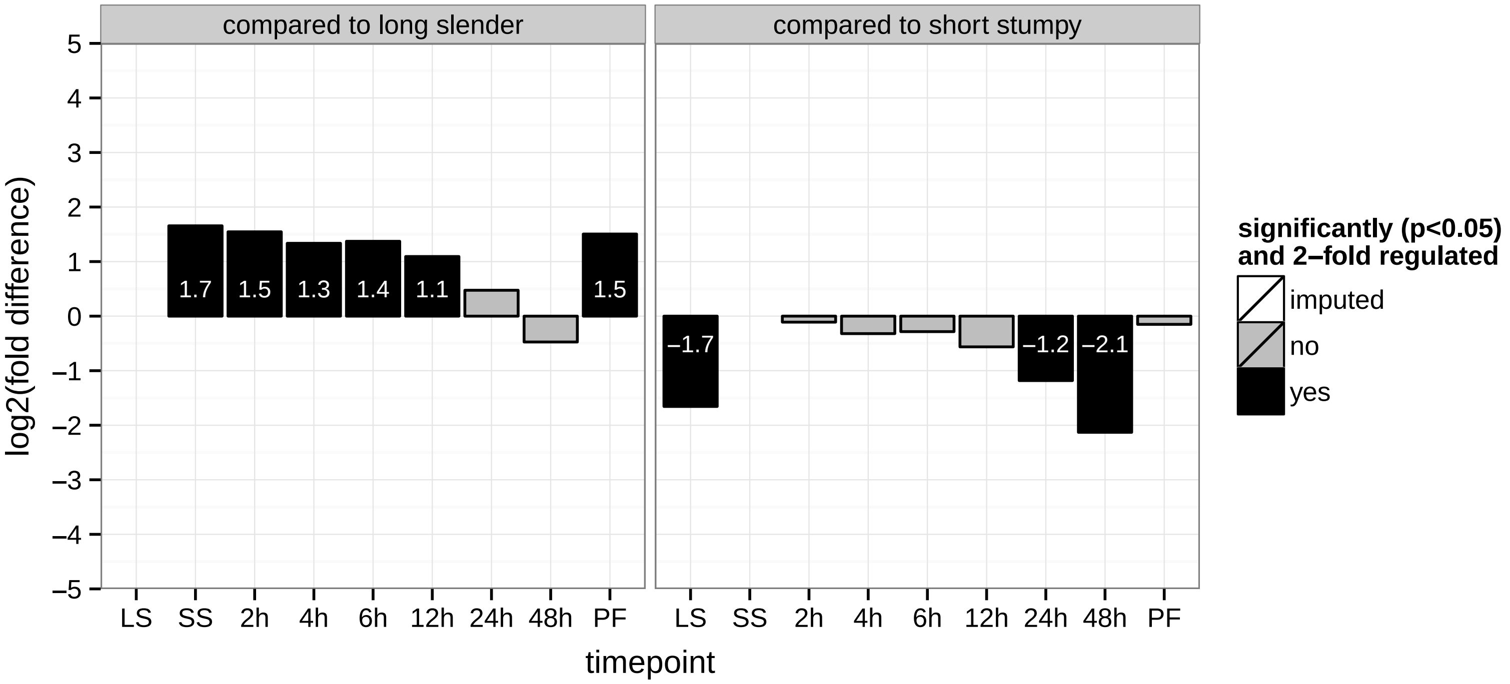
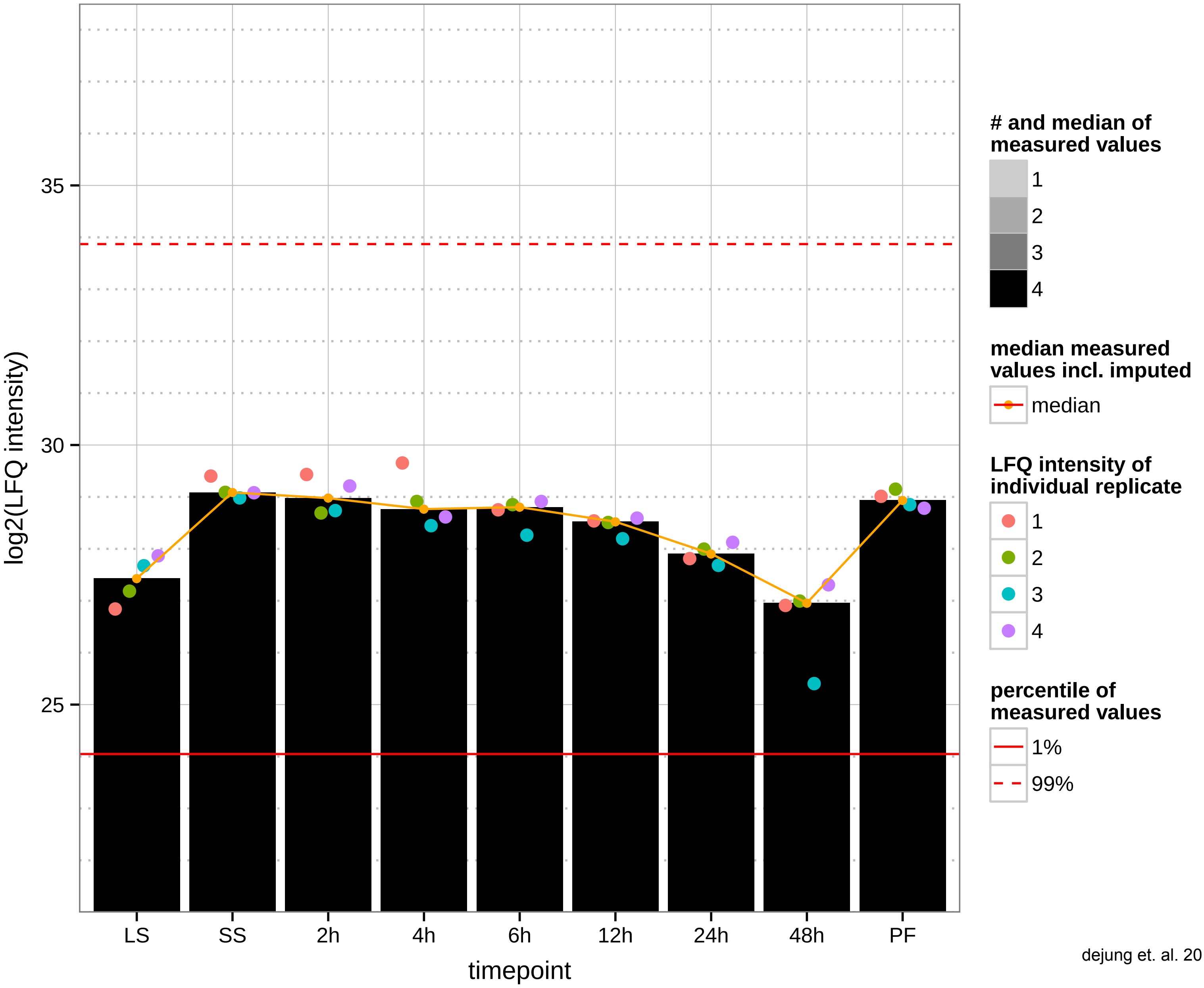
hypothetical protein, conserved
Tb927.9.6380;Tb927.9.6360;Tb927.9.6370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null, integral to membrane
PGOP: null, transmembrane transport





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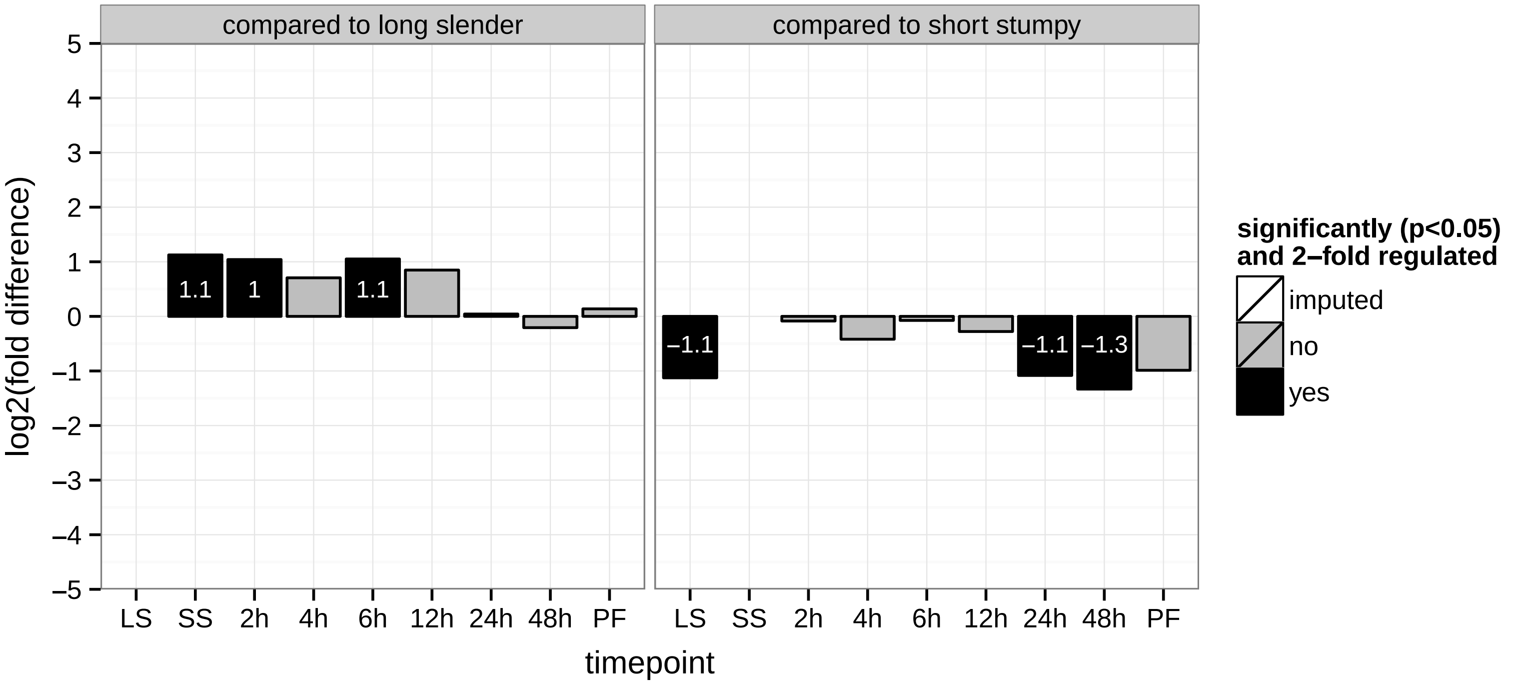
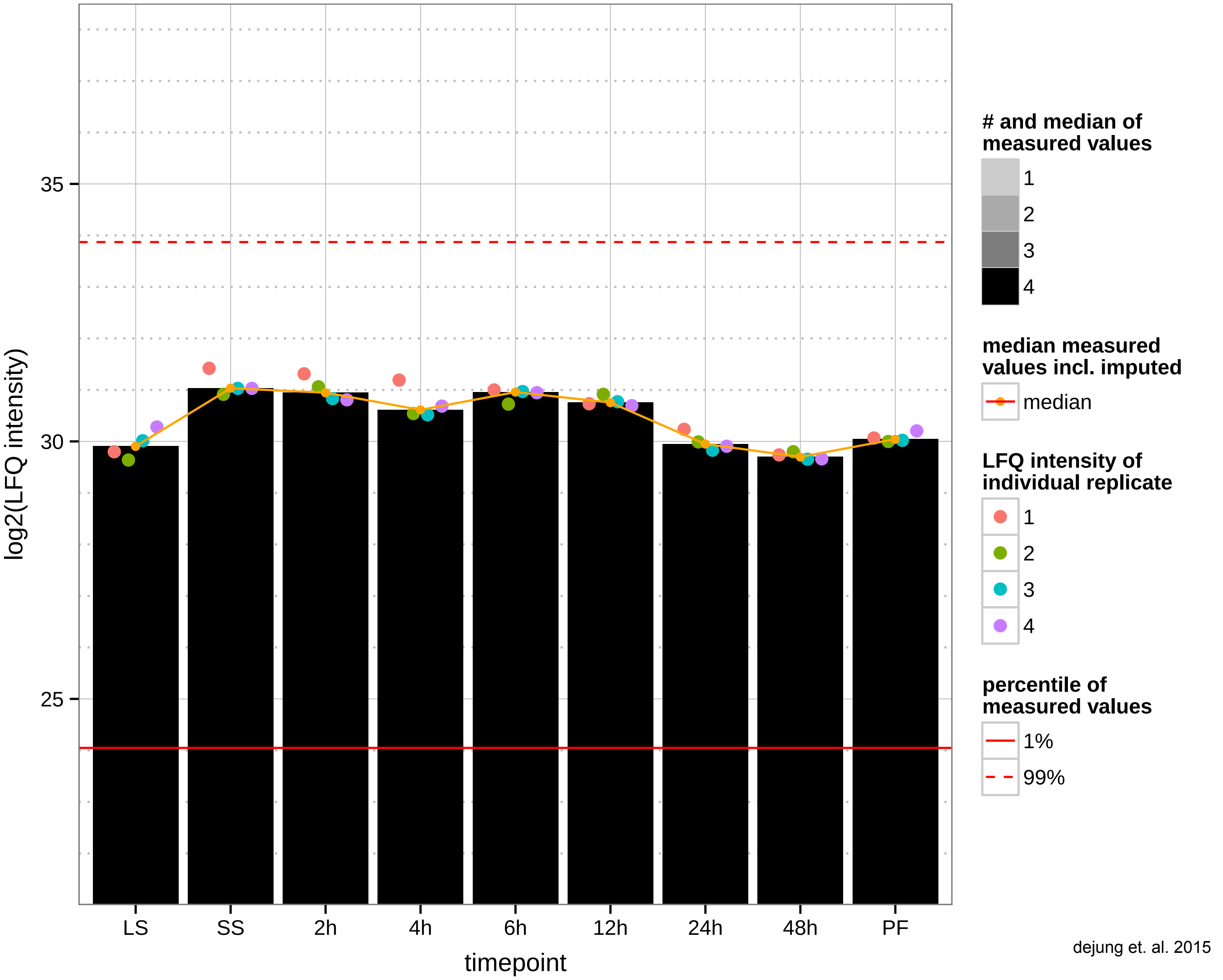
protein kinase, putative
Tb927.9.6560
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity
AGOC: null
AGOP: growth, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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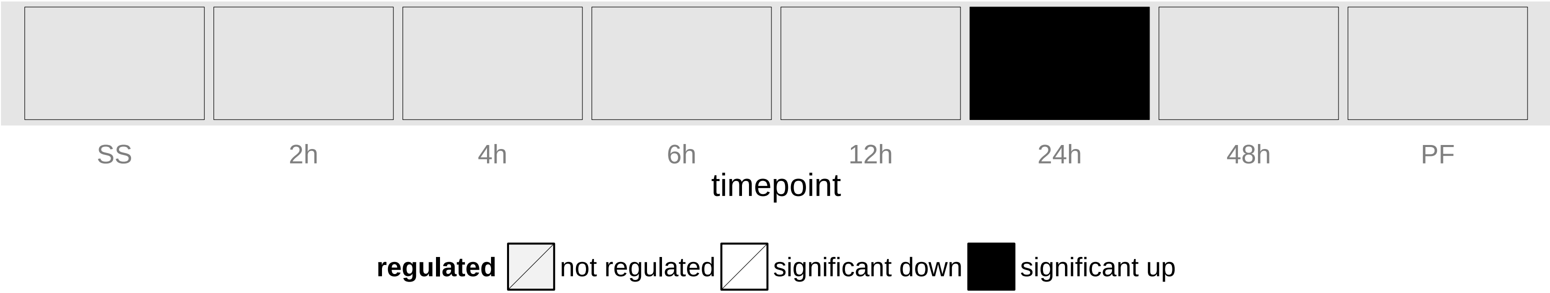
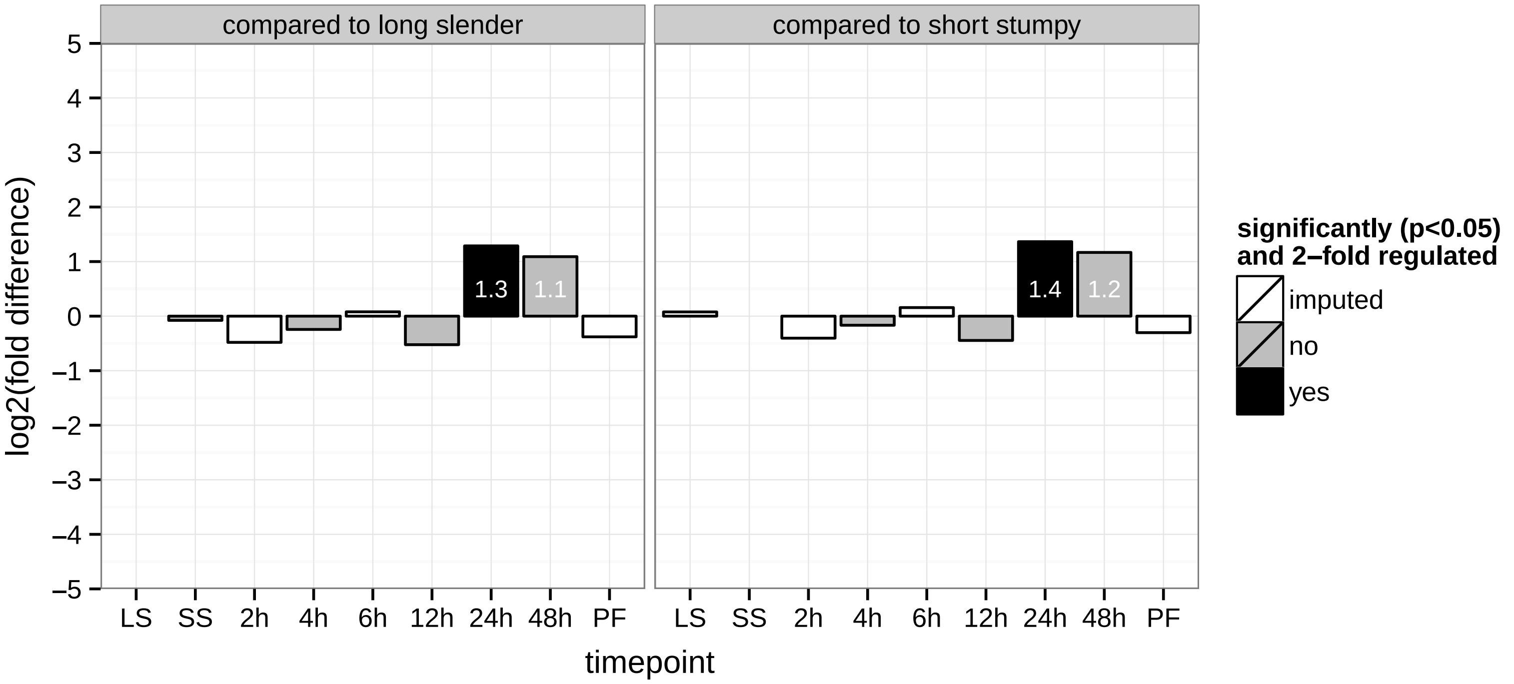
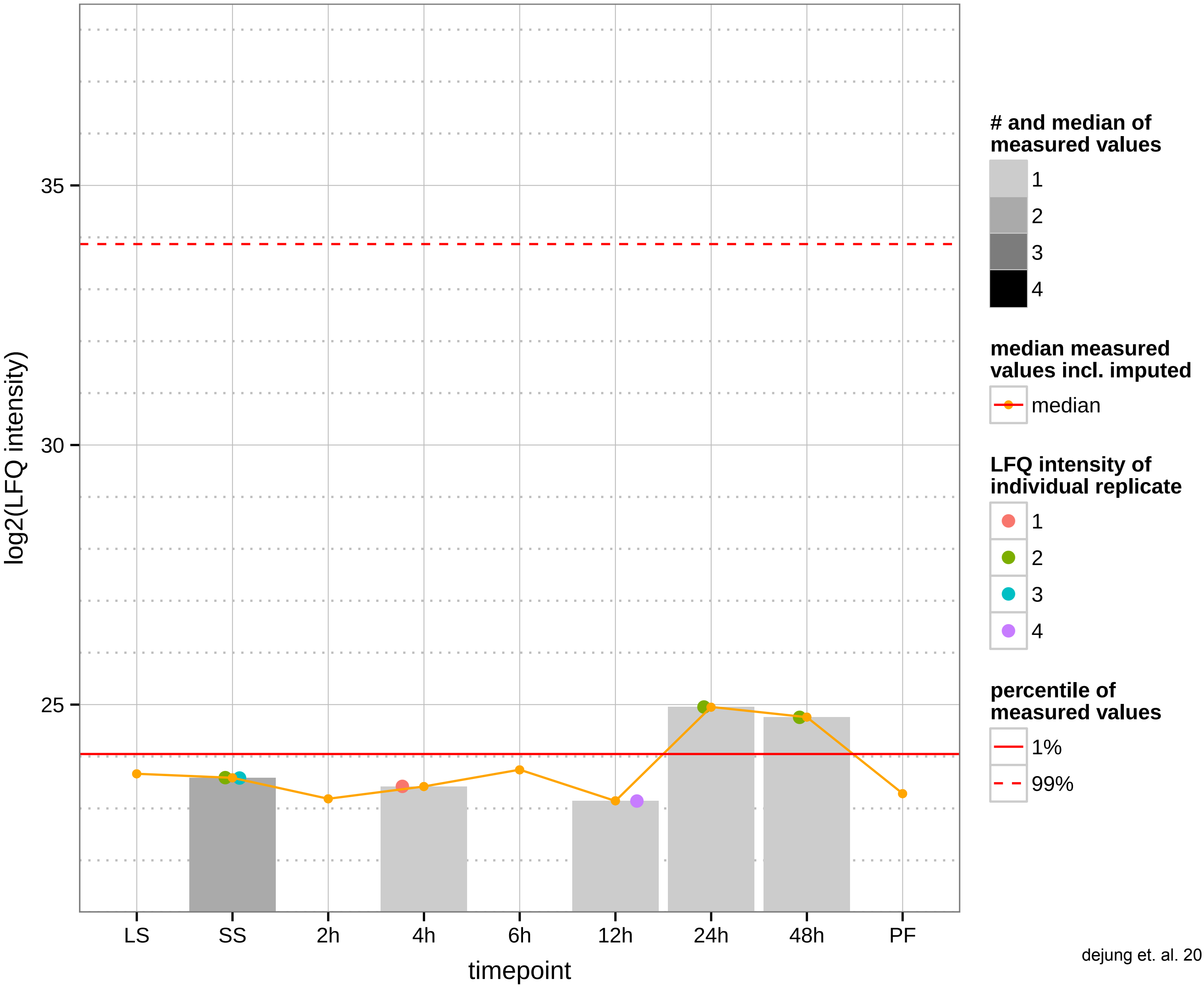


dejung et. al. 2015

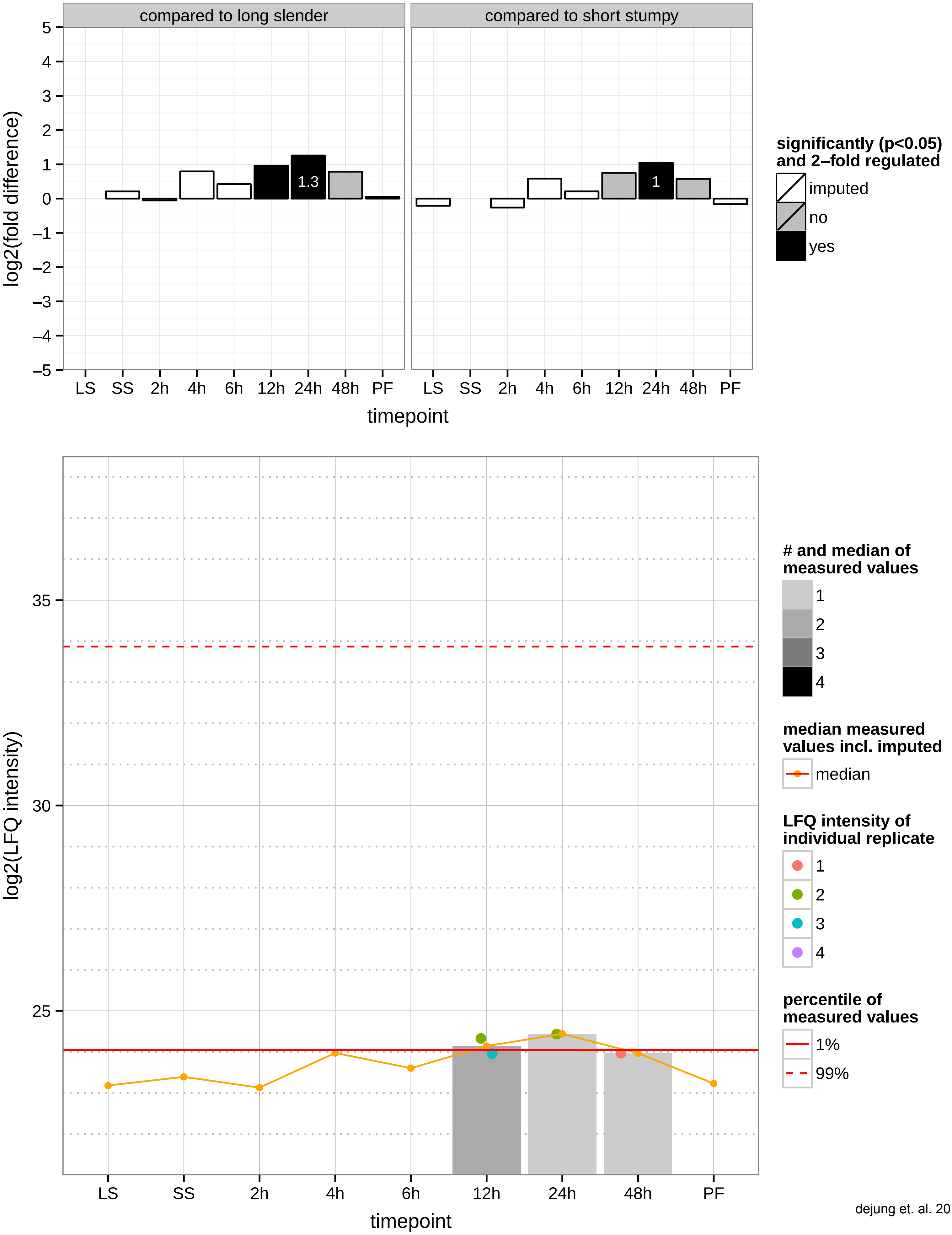
hypothetical protein, conserved
Tb11.v5.0685;Tb927.8.3110
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null, structural constituent of ribosome
PGOC: null, intracellular, ribosome
PGOP: null, translation





dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.11750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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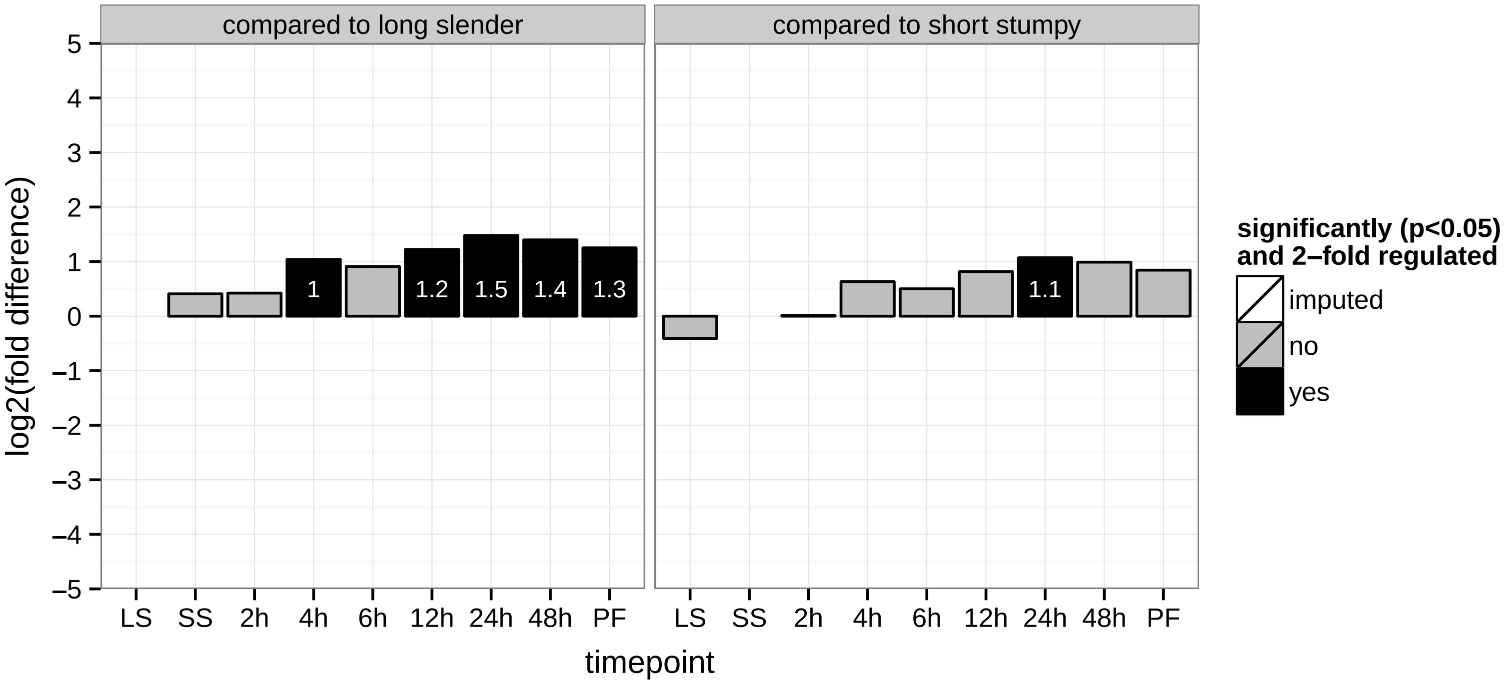
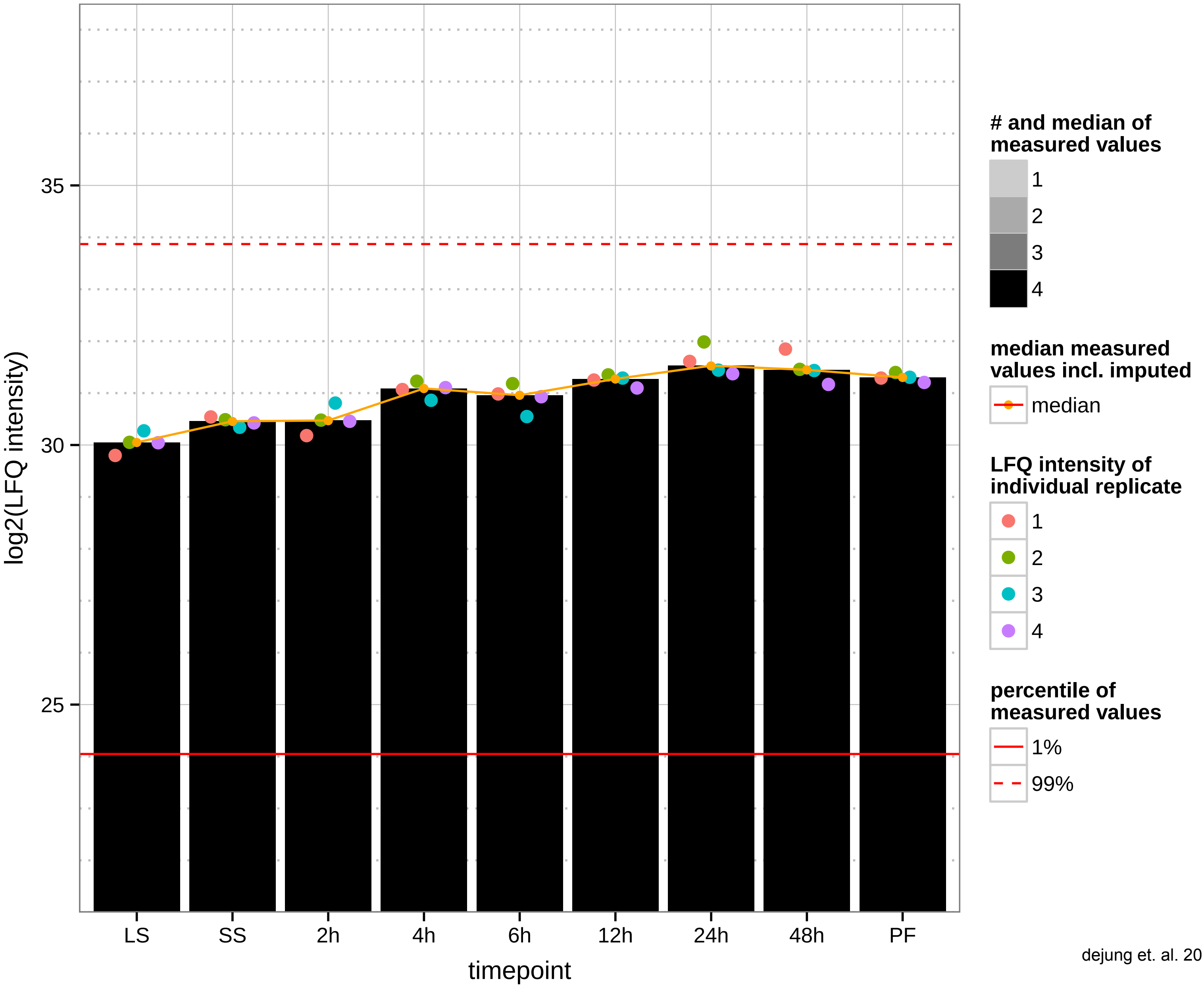
nucleosome assembly protein, putative
Tb927.10.15180
AGOF: histone binding
AGOC: nucleus
AGOP: nucleosome assembly
PGOF: null
PGOC: nucleus
PGOP: nucleosome assembly





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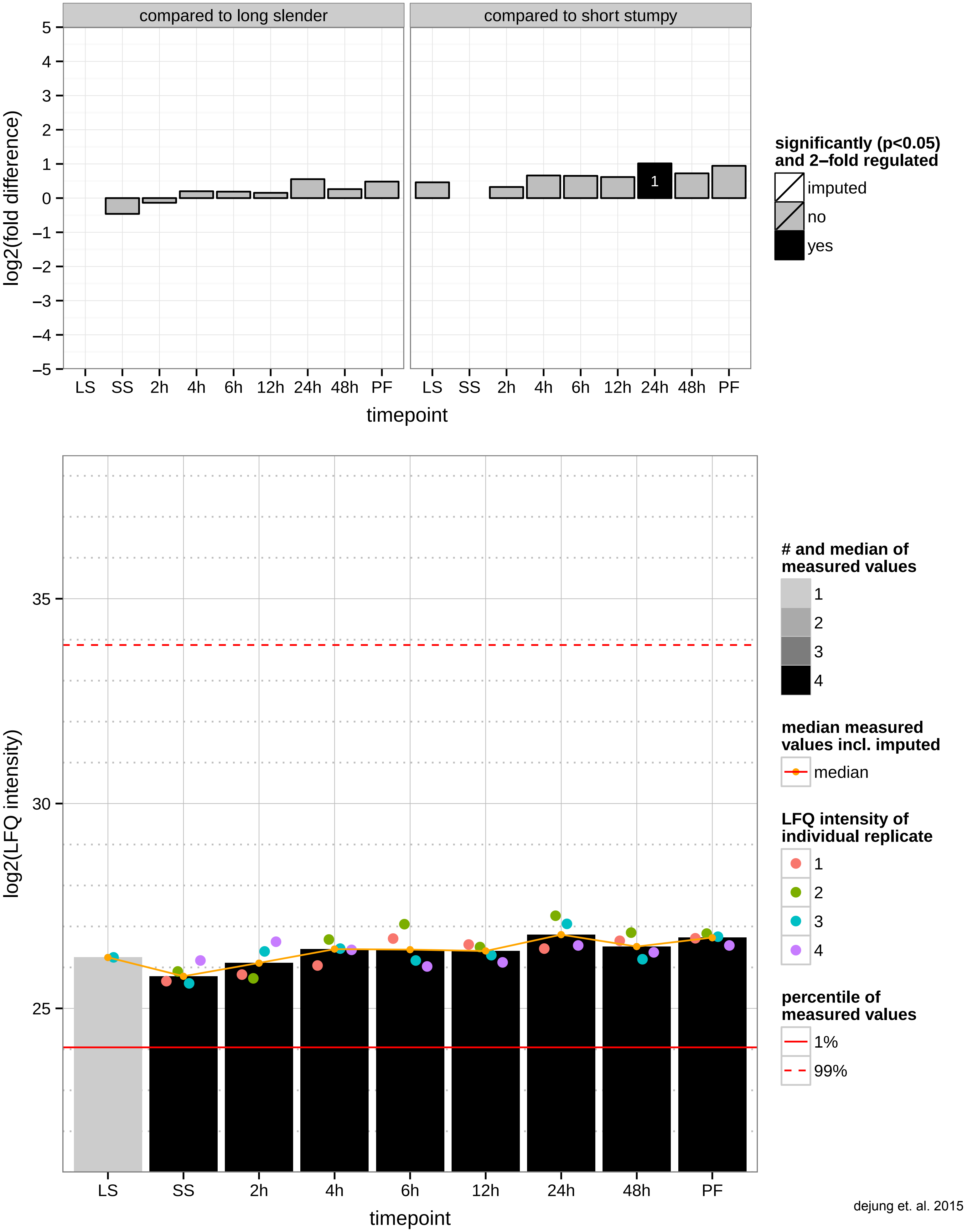
hypothetical protein, conserved
Tb927.10.7750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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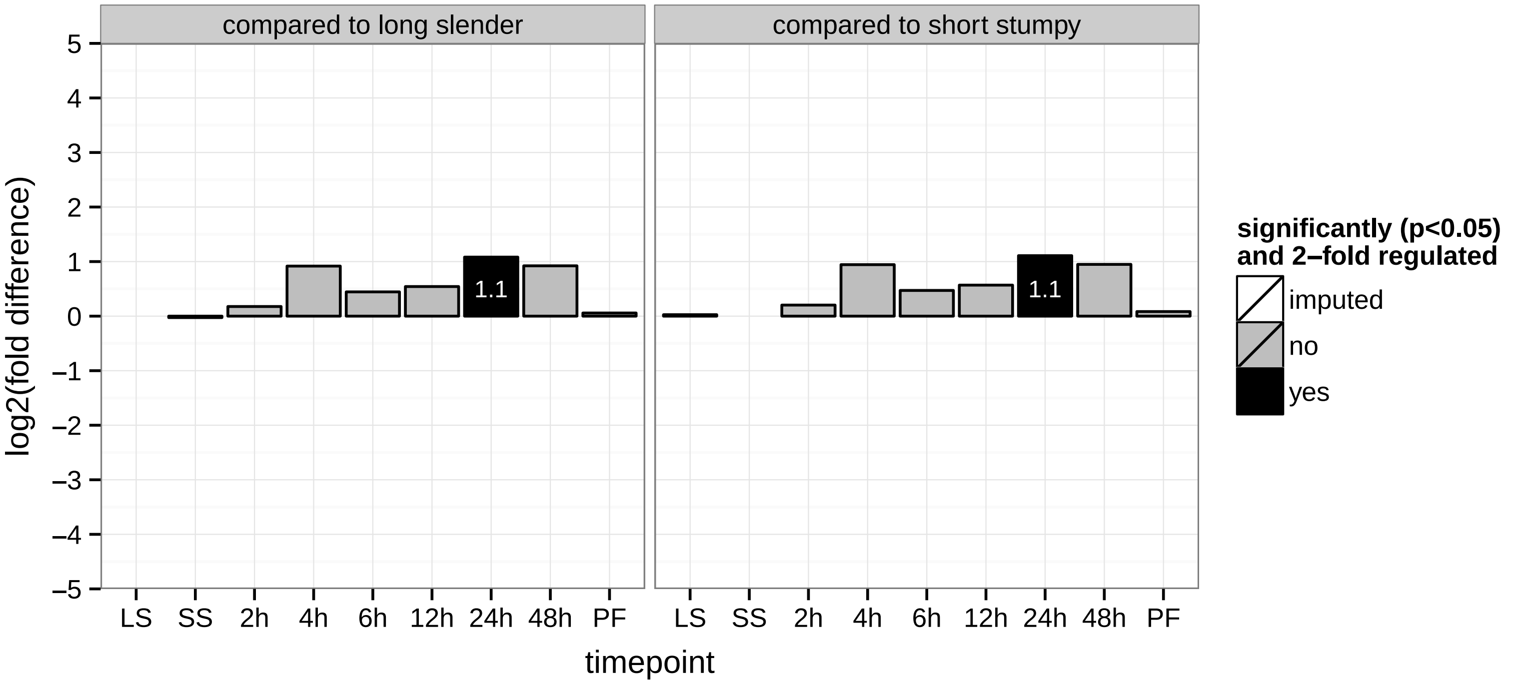
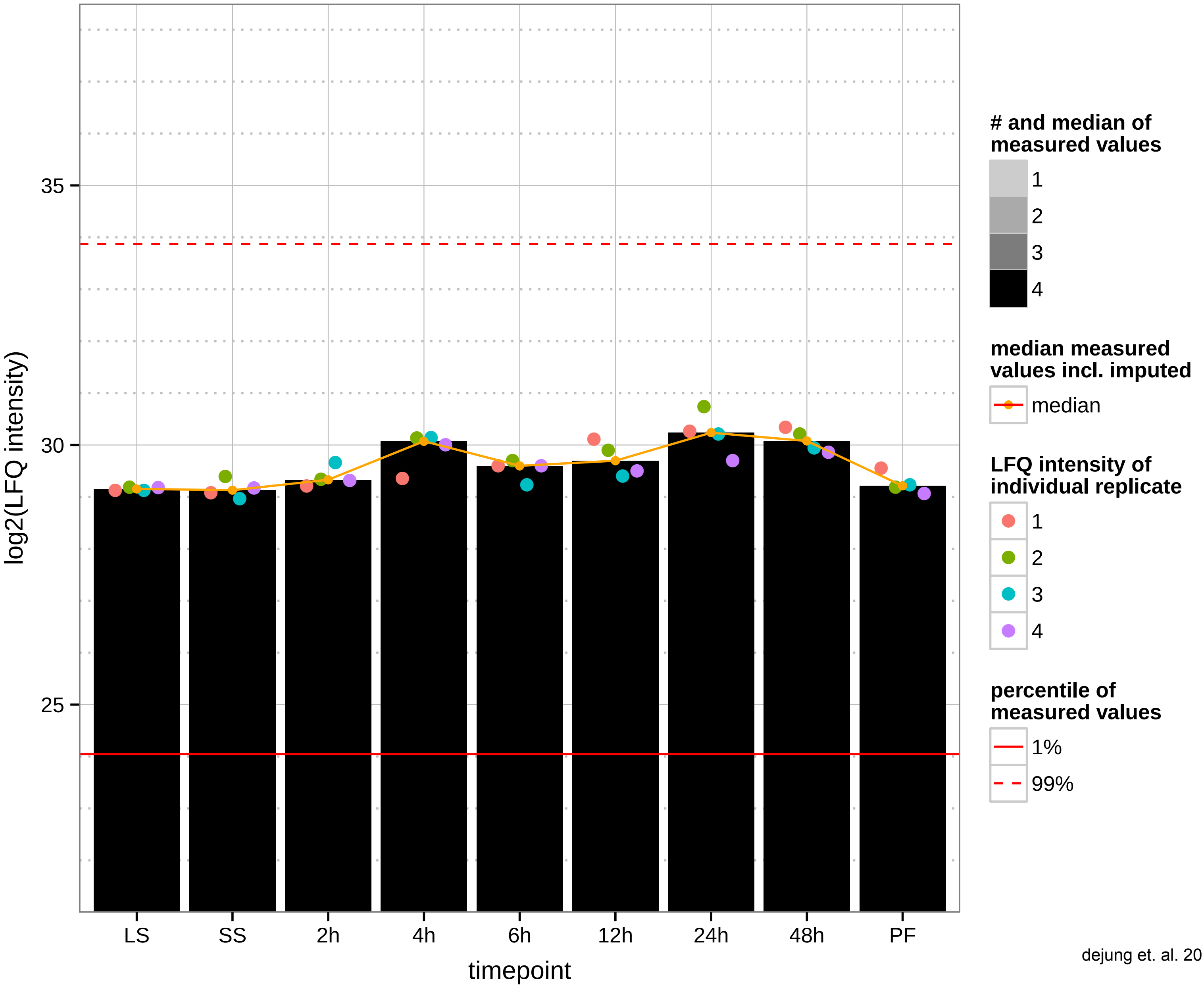
hslVU complex proteolytic subunit, putative, threonine peptidase, Clan T(1), family T1B
Tb927.11.10240
AGOF: endopeptidase activity, threonine–type endopeptidase activity
AGOC: HslUV protease complex, mitochondrion, proteasome core complex
AGOP: protein catabolic process, proteolysis involved in cellular protein catabolic process, rolling circle DNA replication
PGOF: threonine–type endopeptidase activity
PGOC: HslUV protease complex, proteasome core complex
PGOP: proteolysis, proteolysis involved in cellular protein catabolic process





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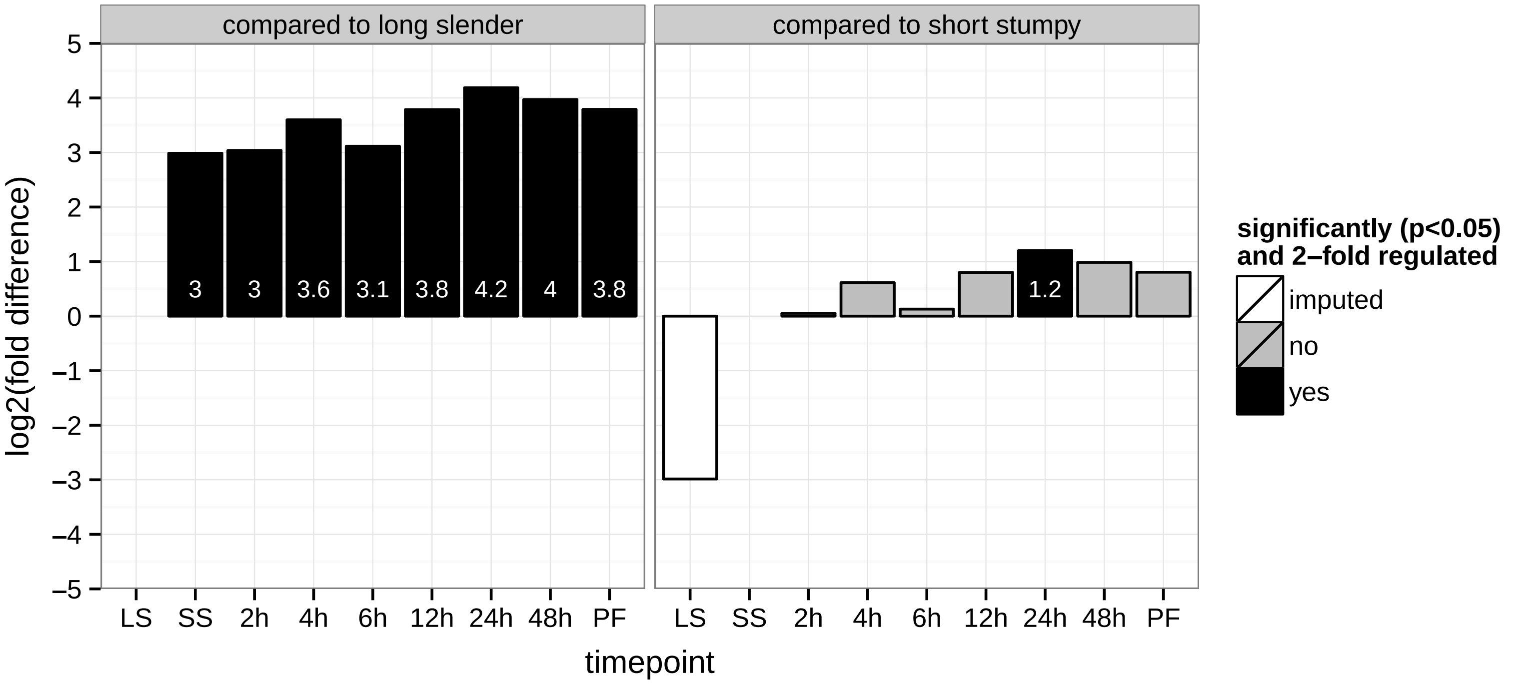
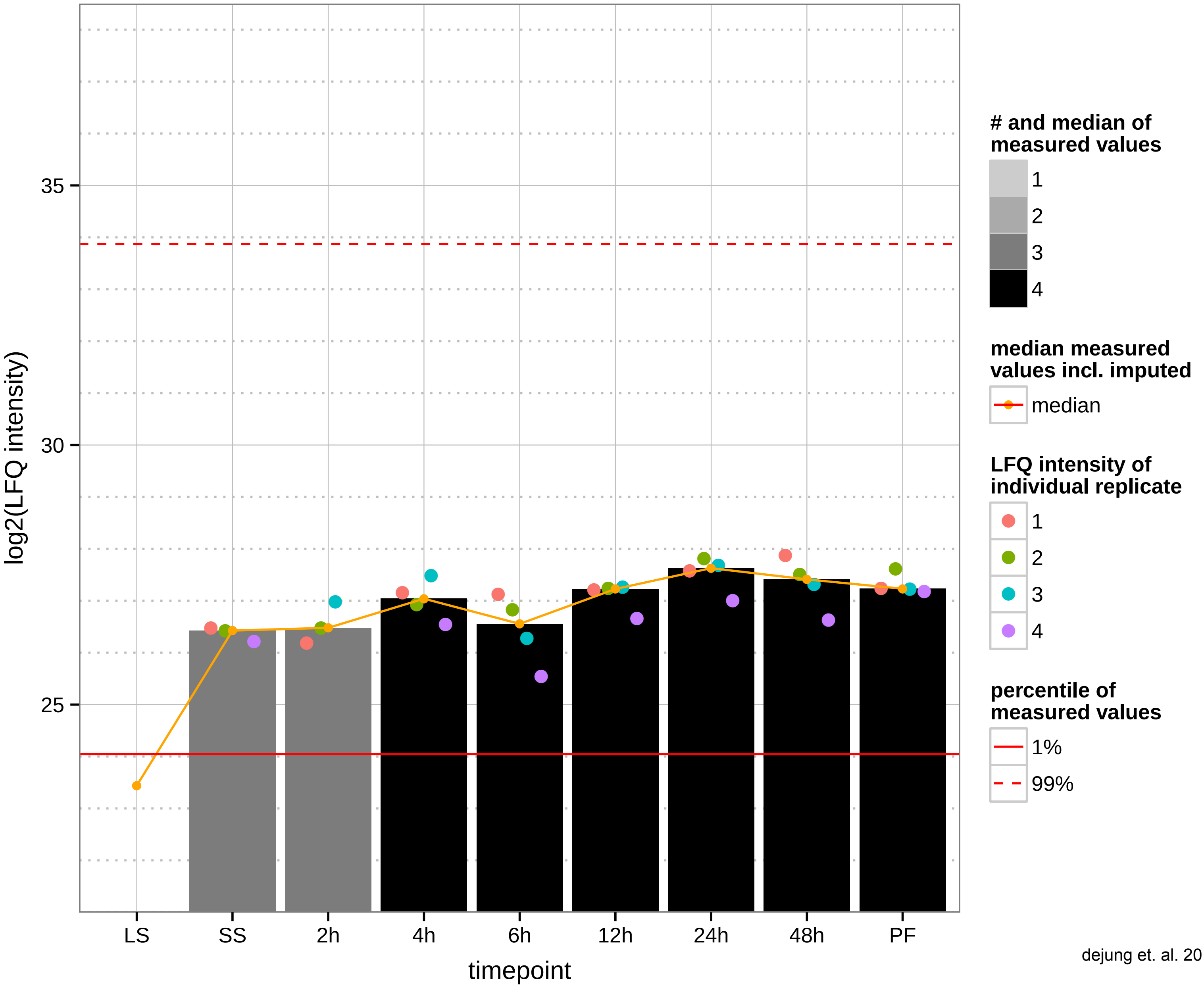
hypothetical protein, conserved
Tb927.11.10570
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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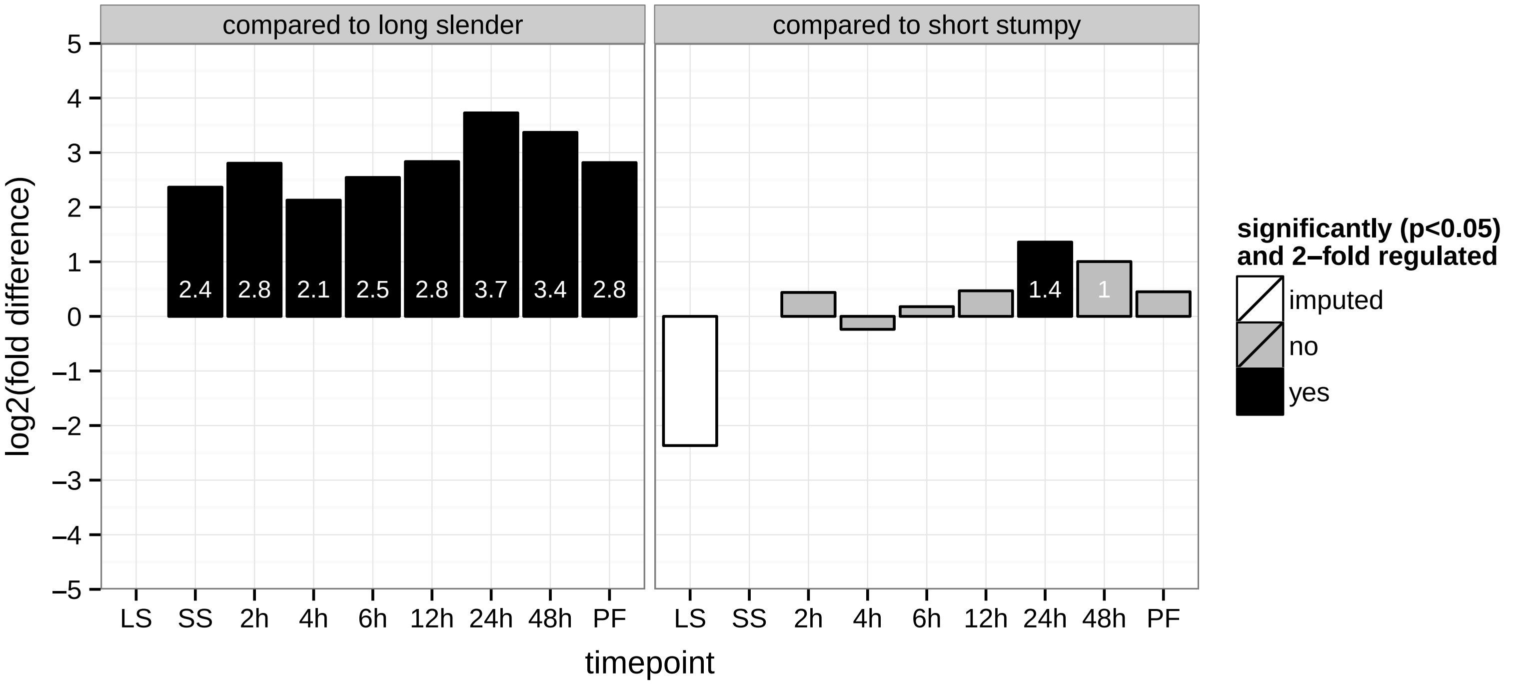
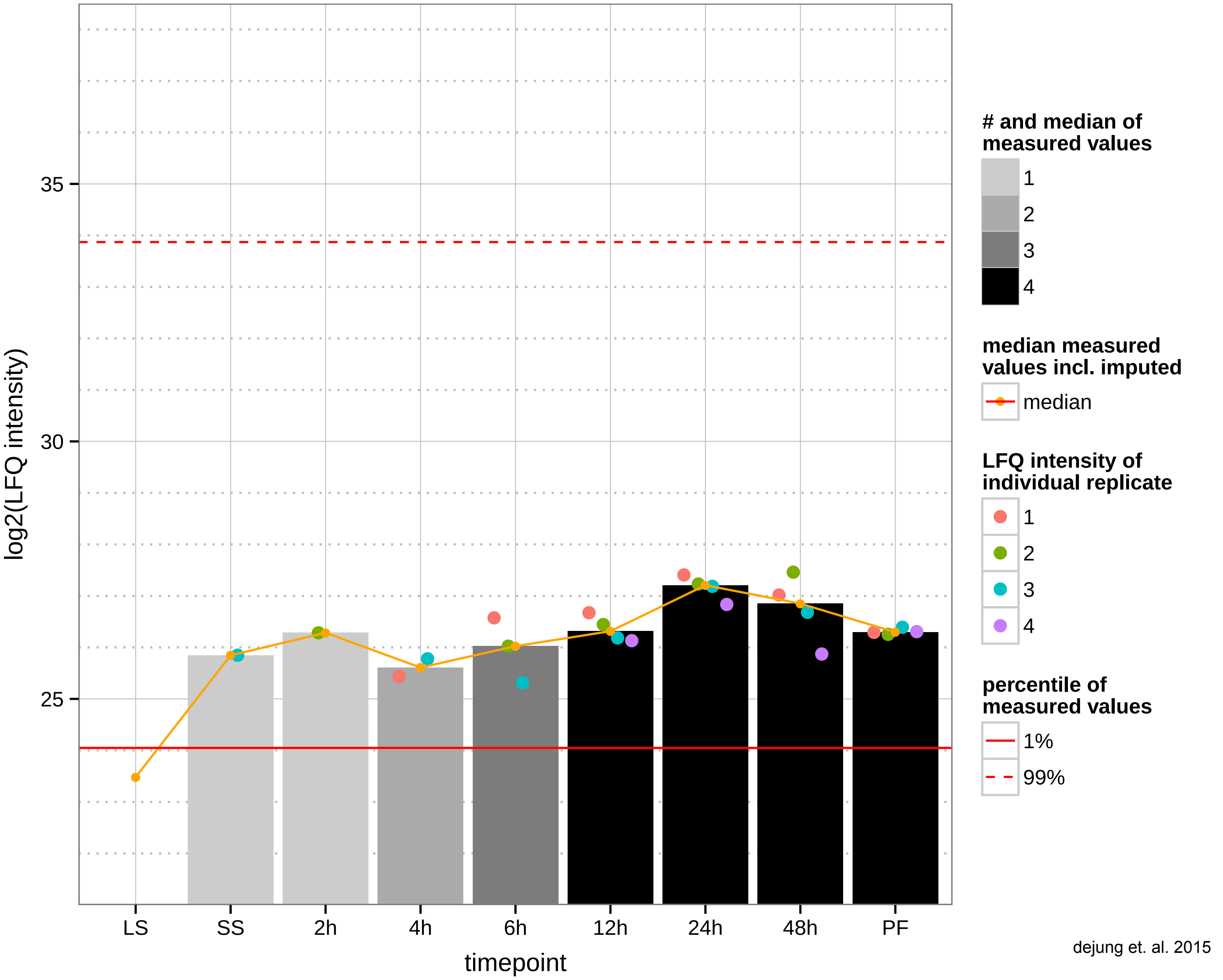
mitochondrial import inner membrane translocase subunit tim17 (Tim17)
Tb927.11.13290
AGOF: protein transporter activity
AGOC: integral to mitochondrial inner membrane, mitochondrial inner membrane, mitochondrial inner membrane presequenc
AGOP: protein targeting to mitochondrion, stabilization of membrane potential
PGOF: null
PGOC: null
PGOP: null





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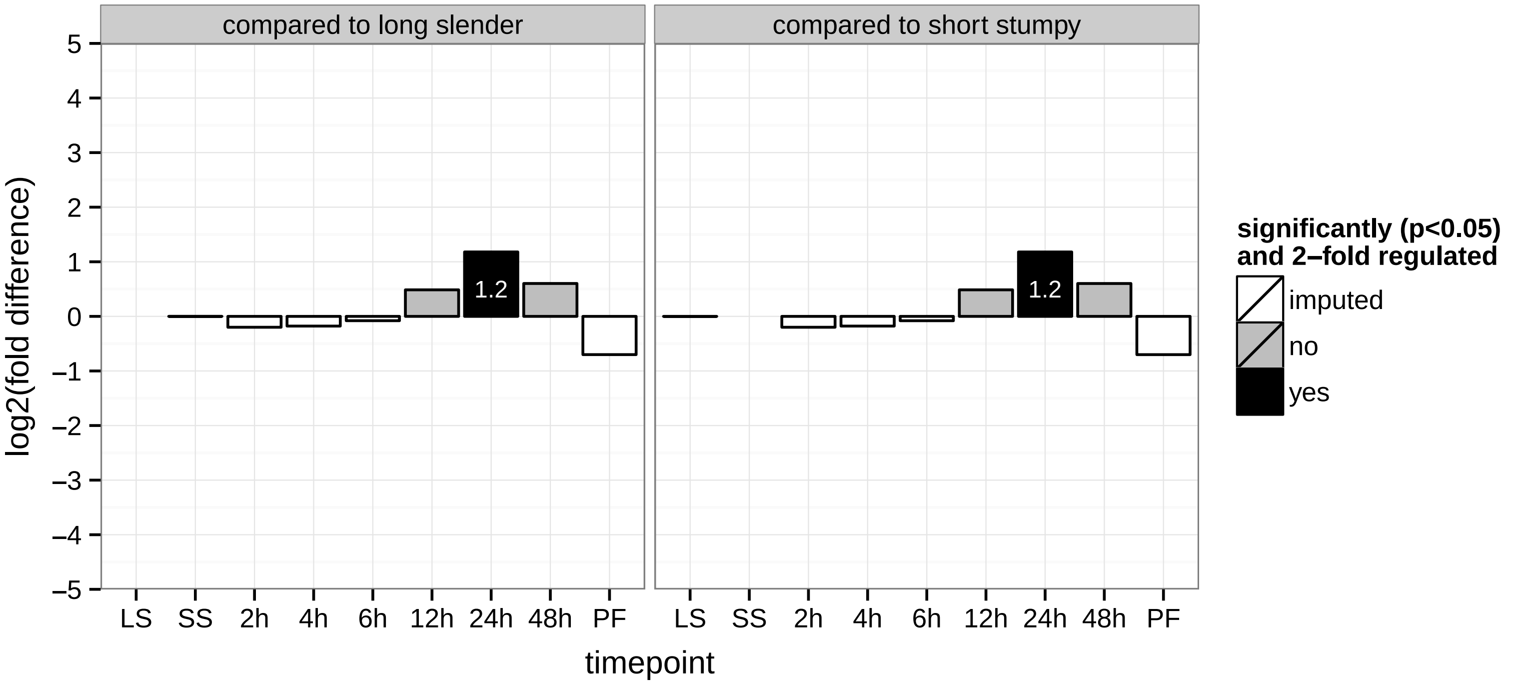
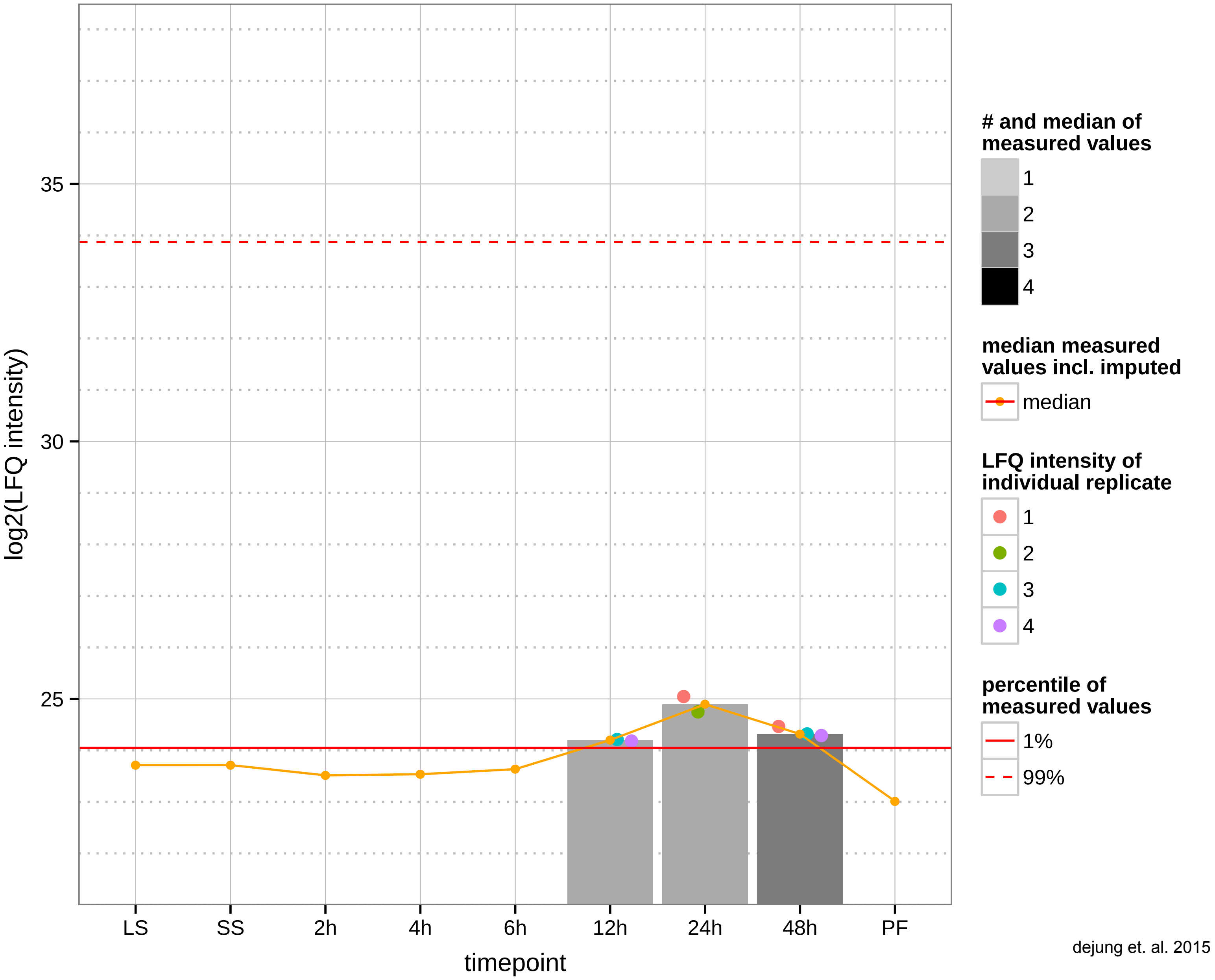
hypothetical protein, conserved
Tb927.11.13950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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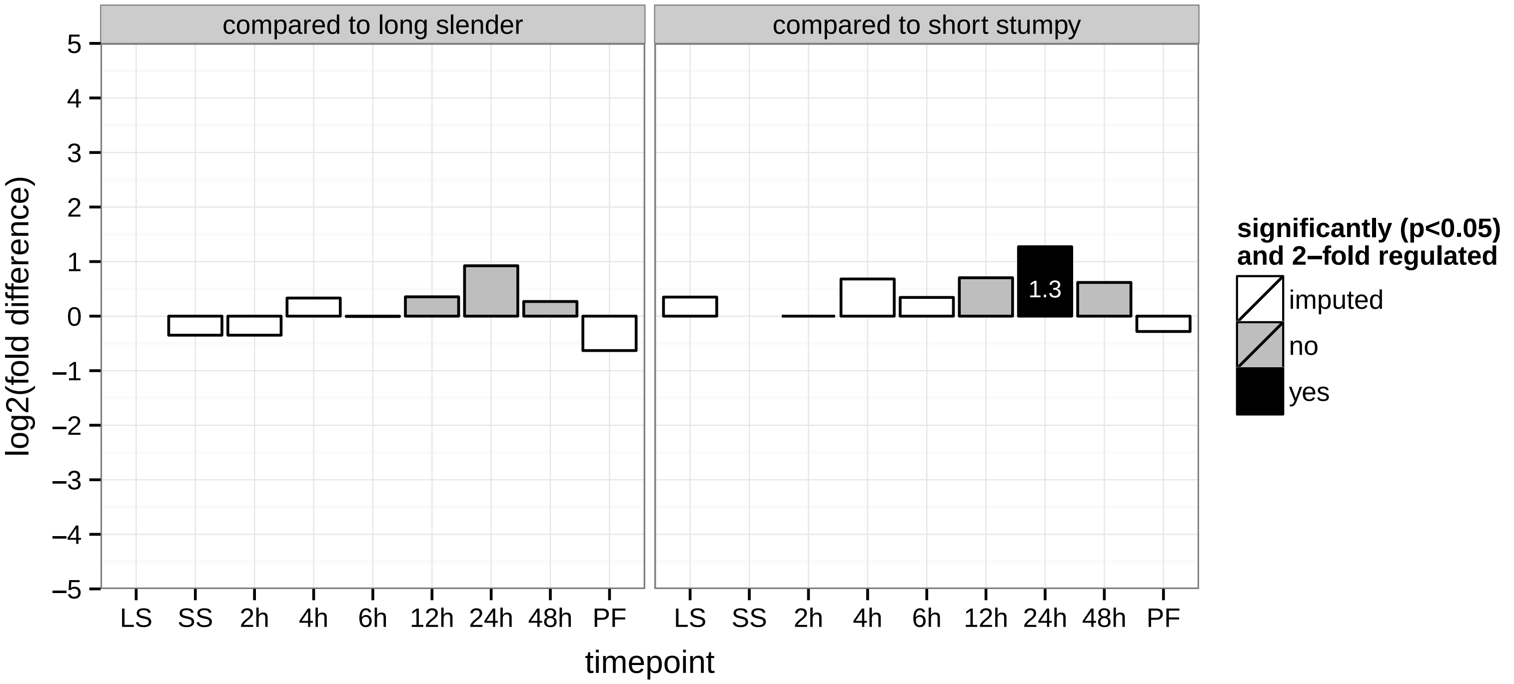
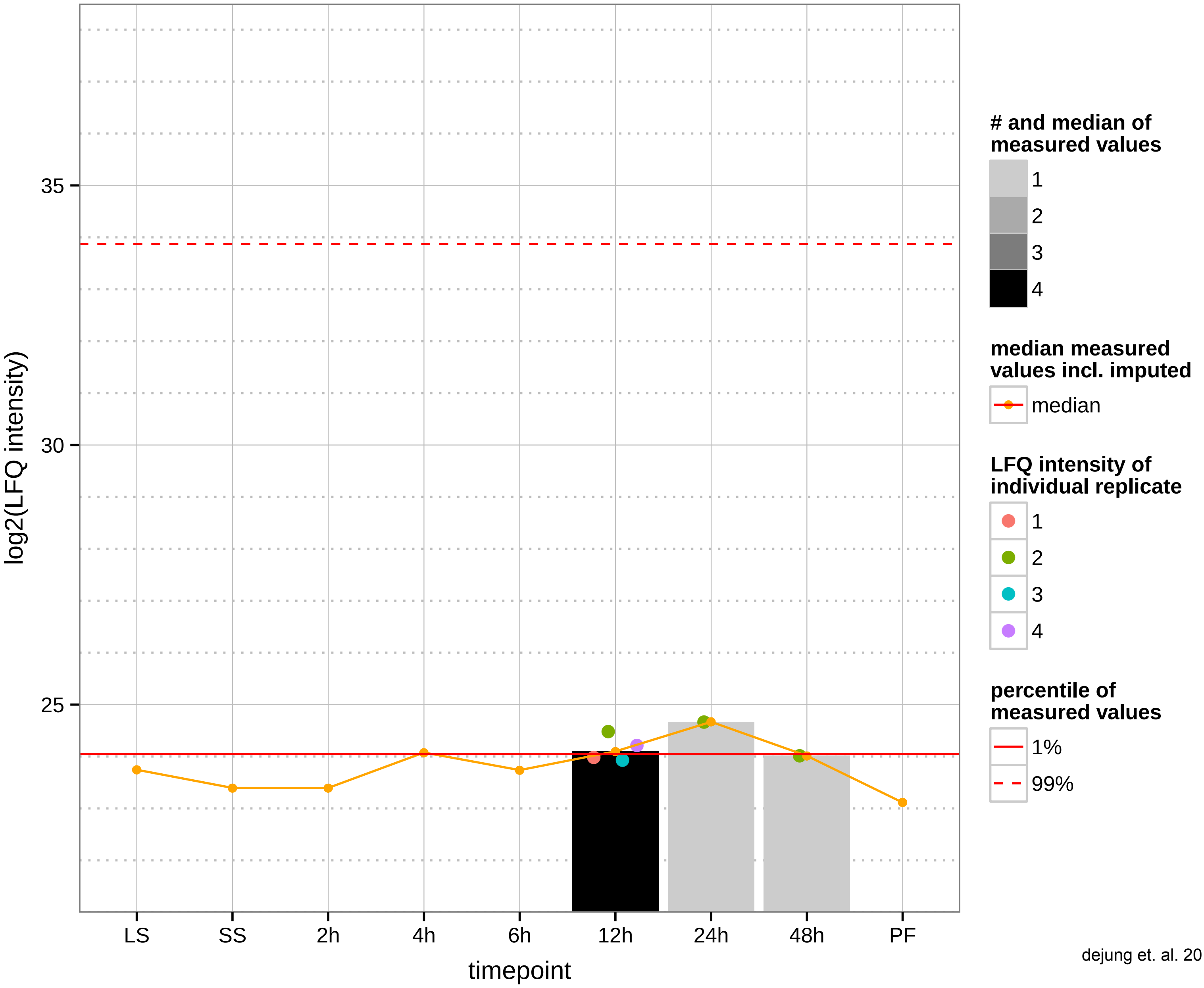
hypothetical protein, conserved
Tb927.11.16040
AGOF: null
AGOC: null
AGOP: null
PGOF: unfolded protein binding
PGOC: prefoldin complex
PGOP: protein folding





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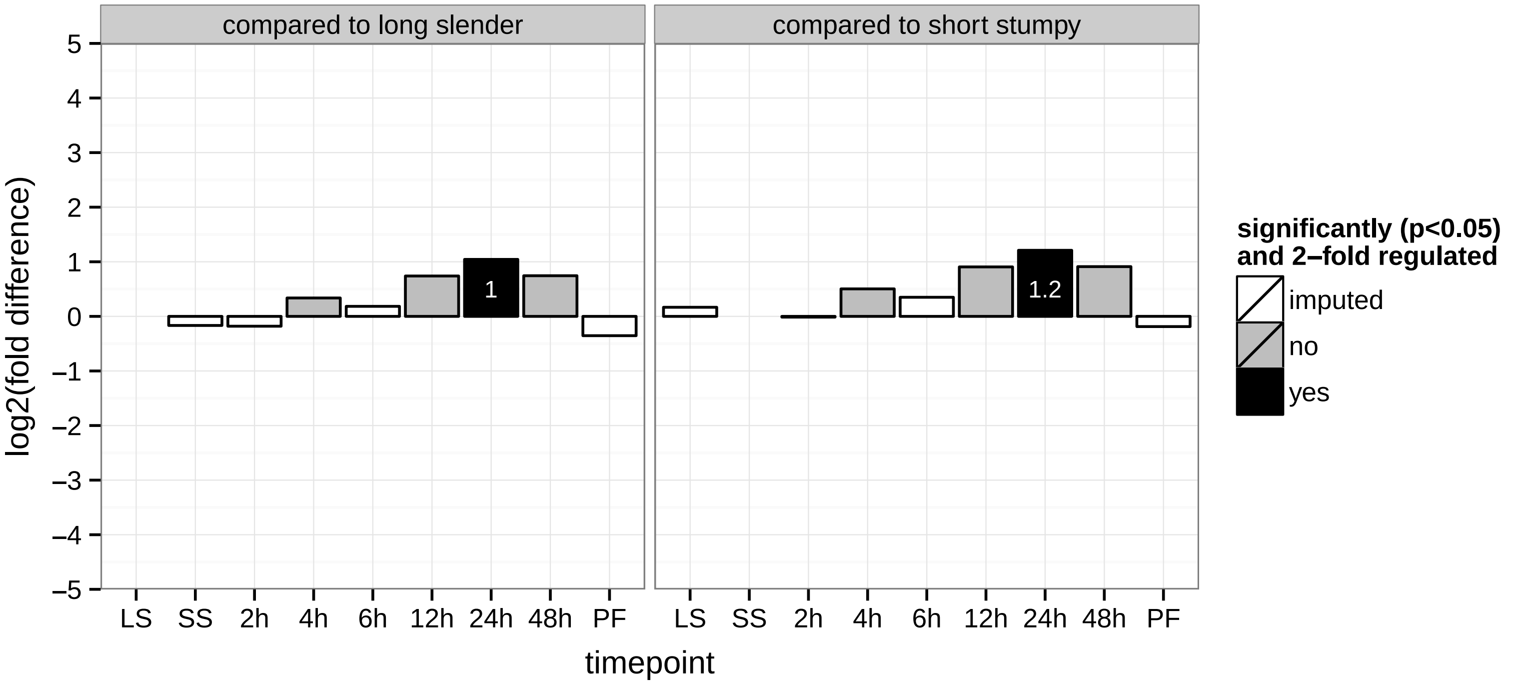
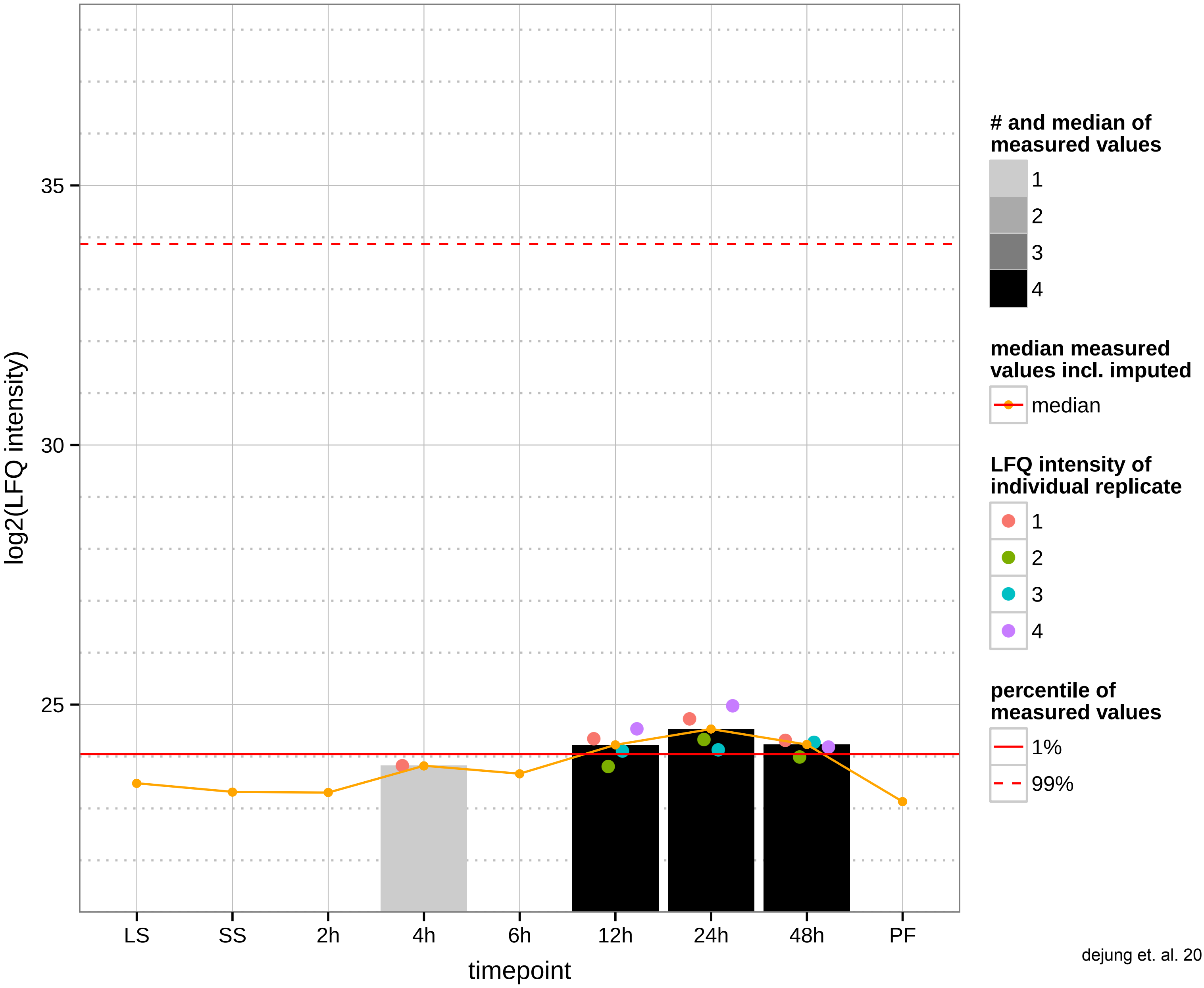
glycerolphosphate mutase, putative
Tb927.11.2920
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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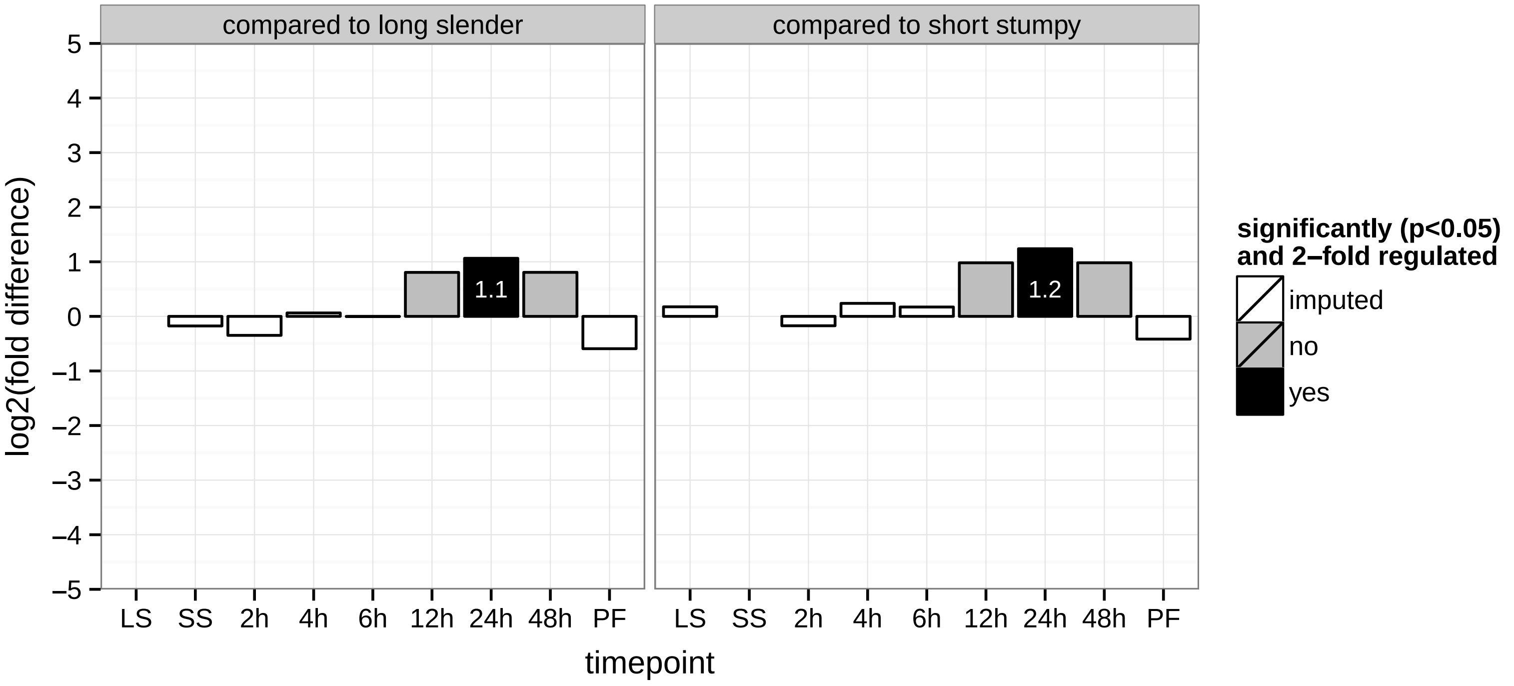
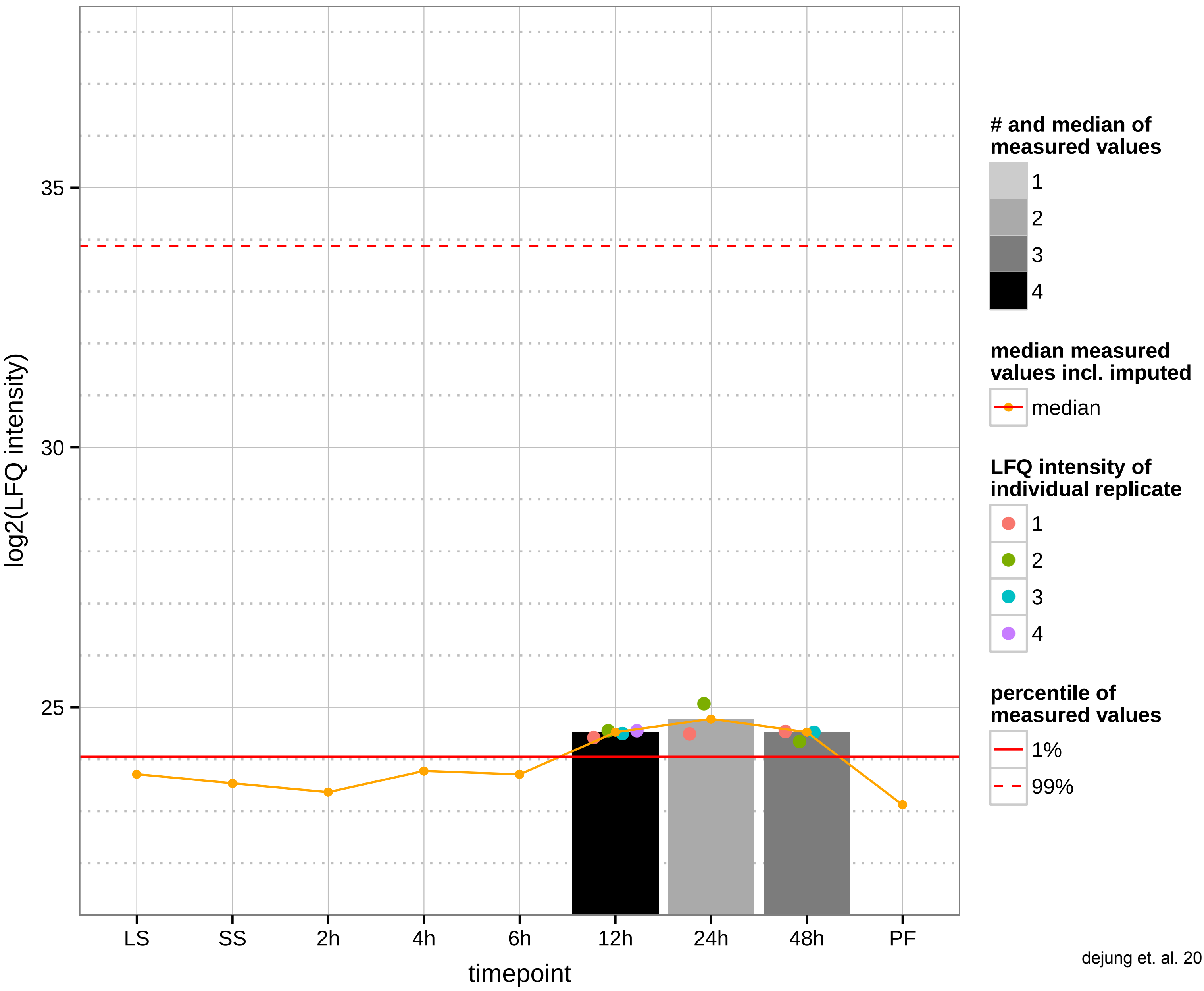
hypothetical protein, conserved
Tb927.11.5200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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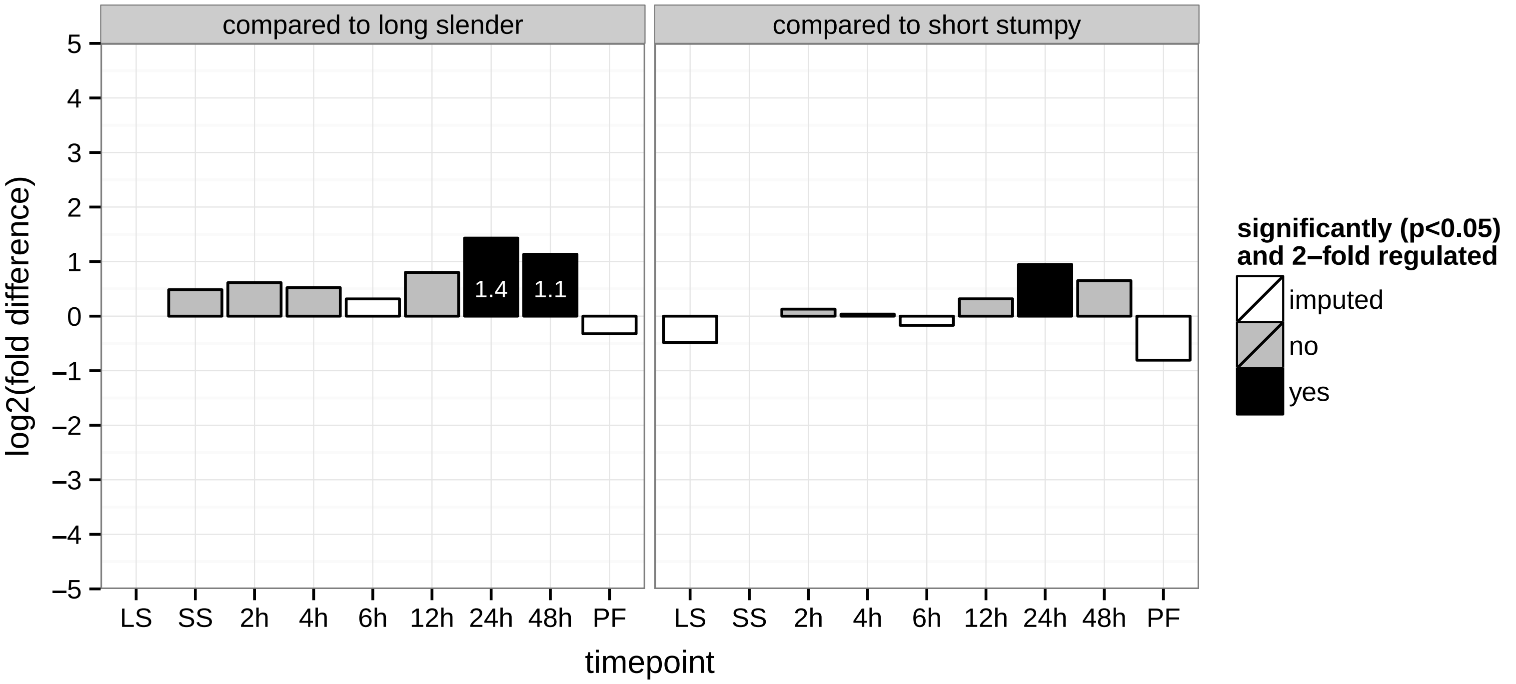
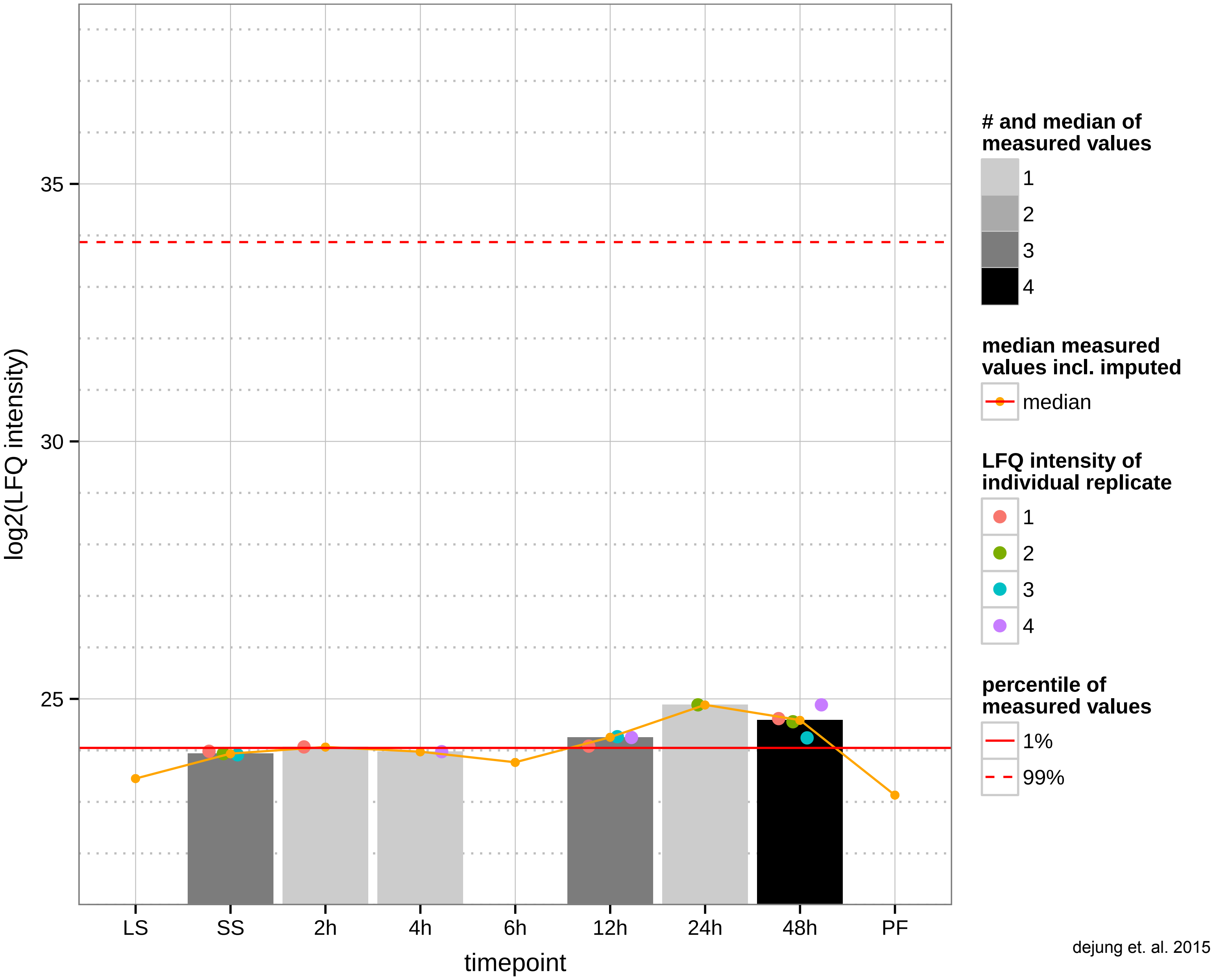
hypothetical protein, conserved
Tb927.3.4450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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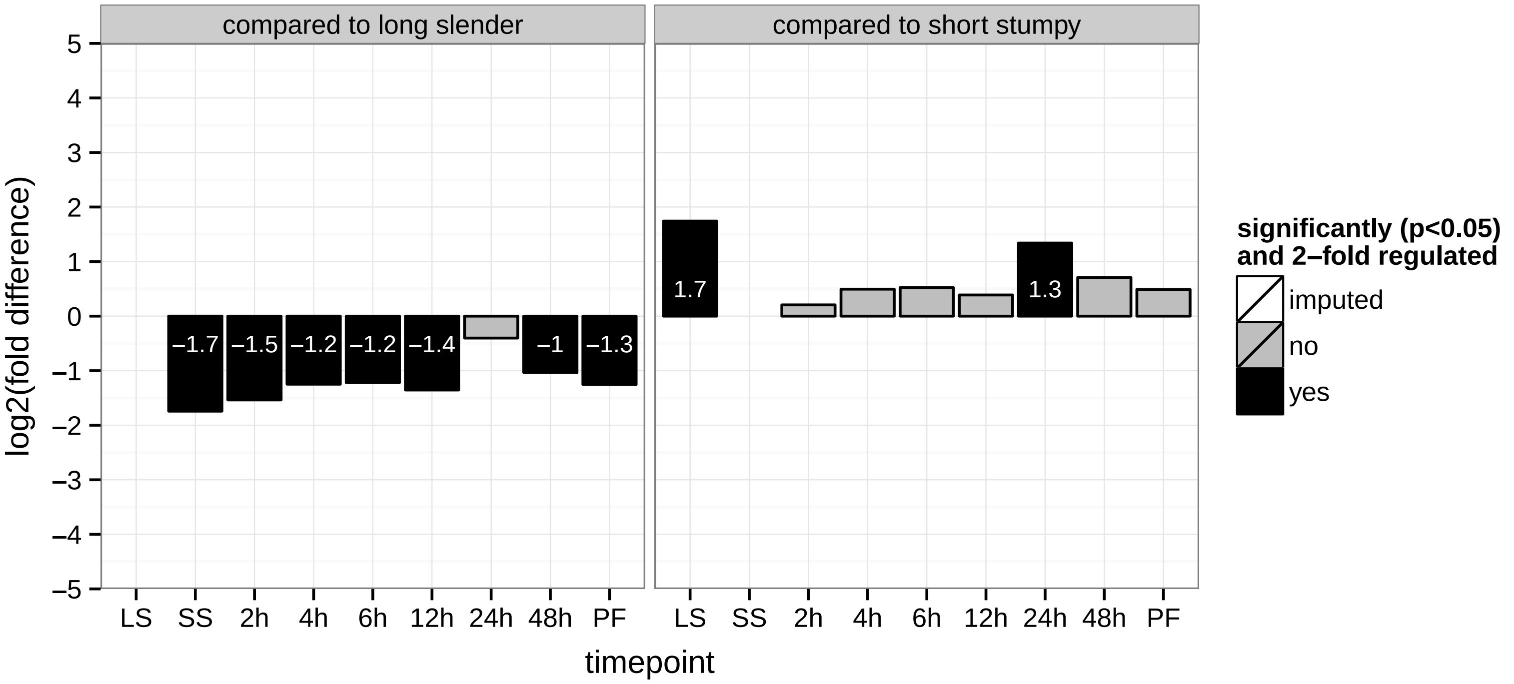
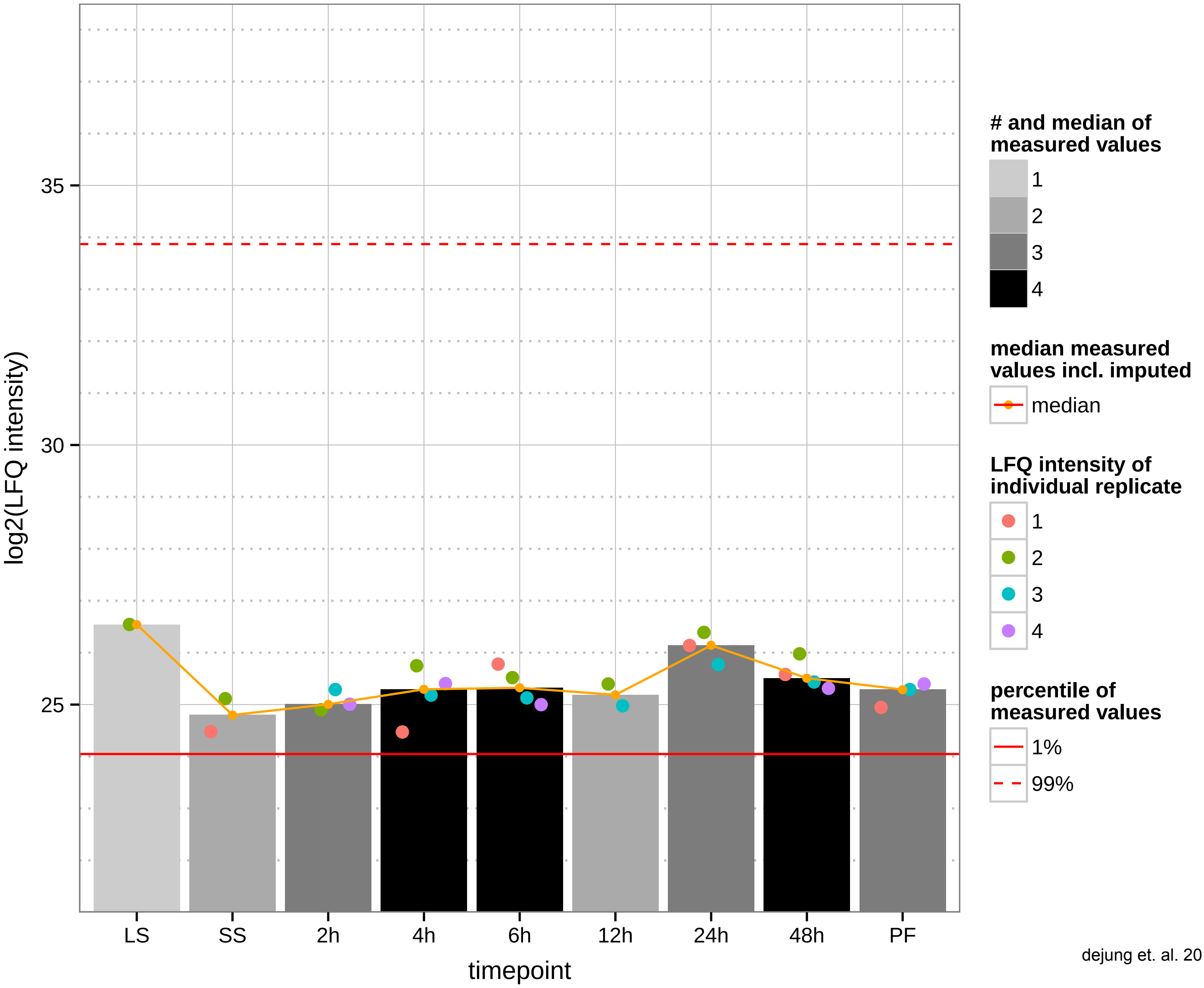
Spef1, flagellar component
Tb927.4.3130
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: protein binding
PGOC: null
PGOP: null





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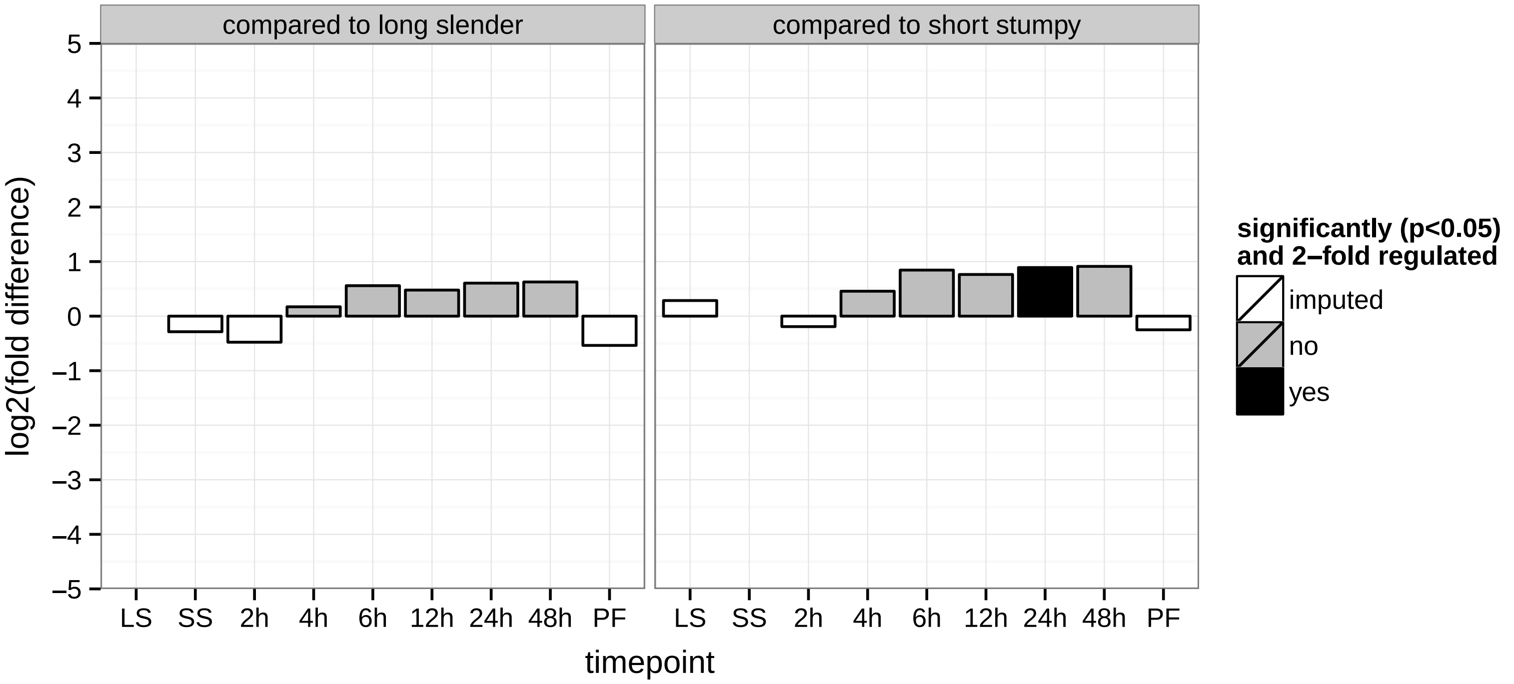
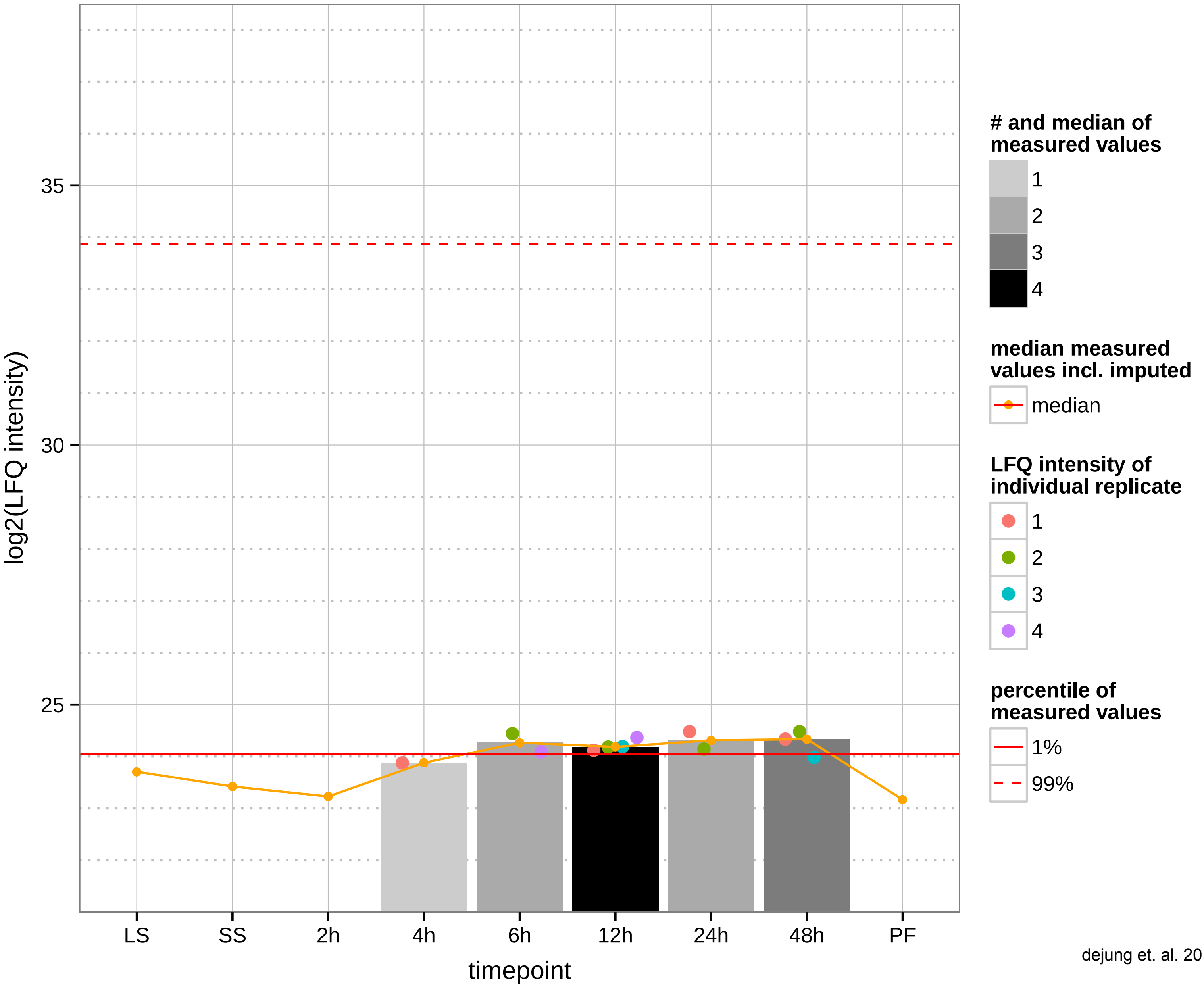
hypothetical protein, conserved
Tb927.5.1340
AGOF: null
AGOC: null, intracellular
AGOP: null, RNA processing
PGOF: null
PGOC: null, intracellular
PGOP: null, RNA processing





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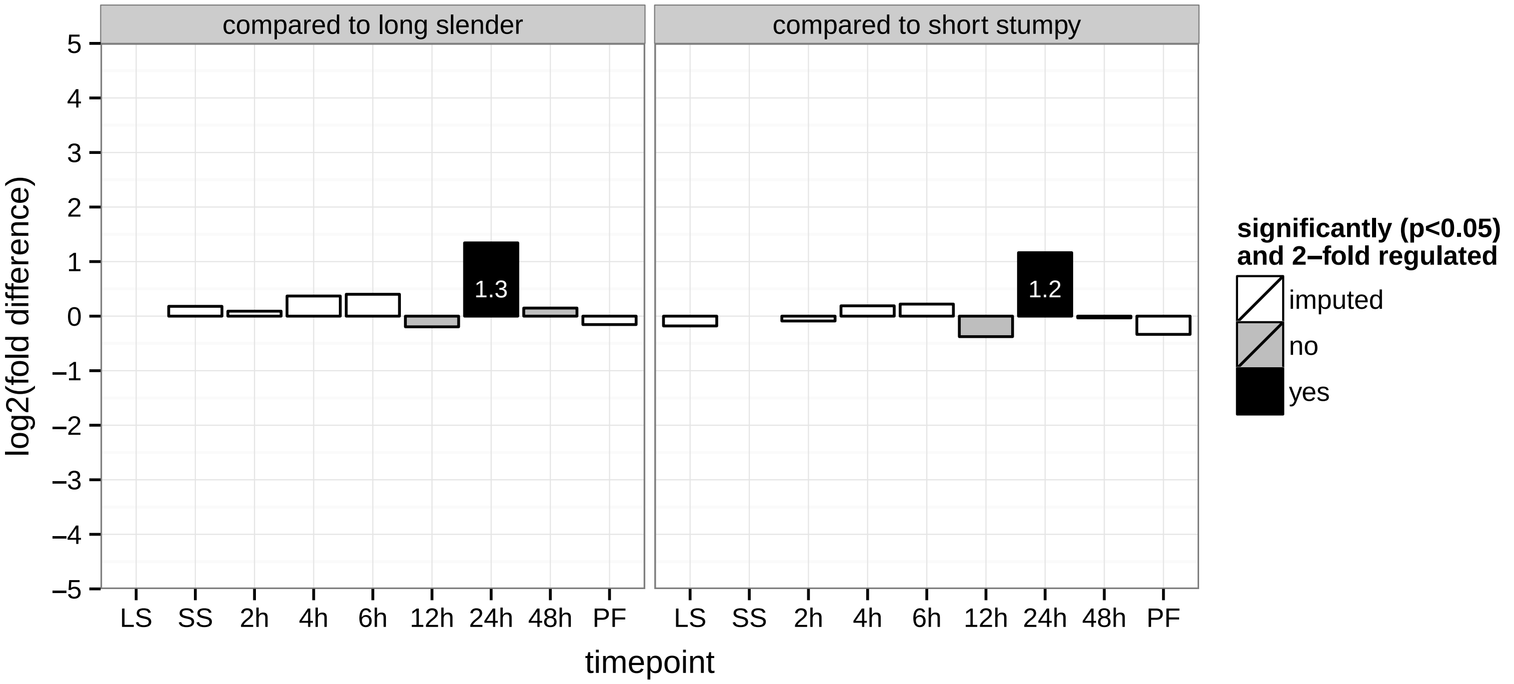
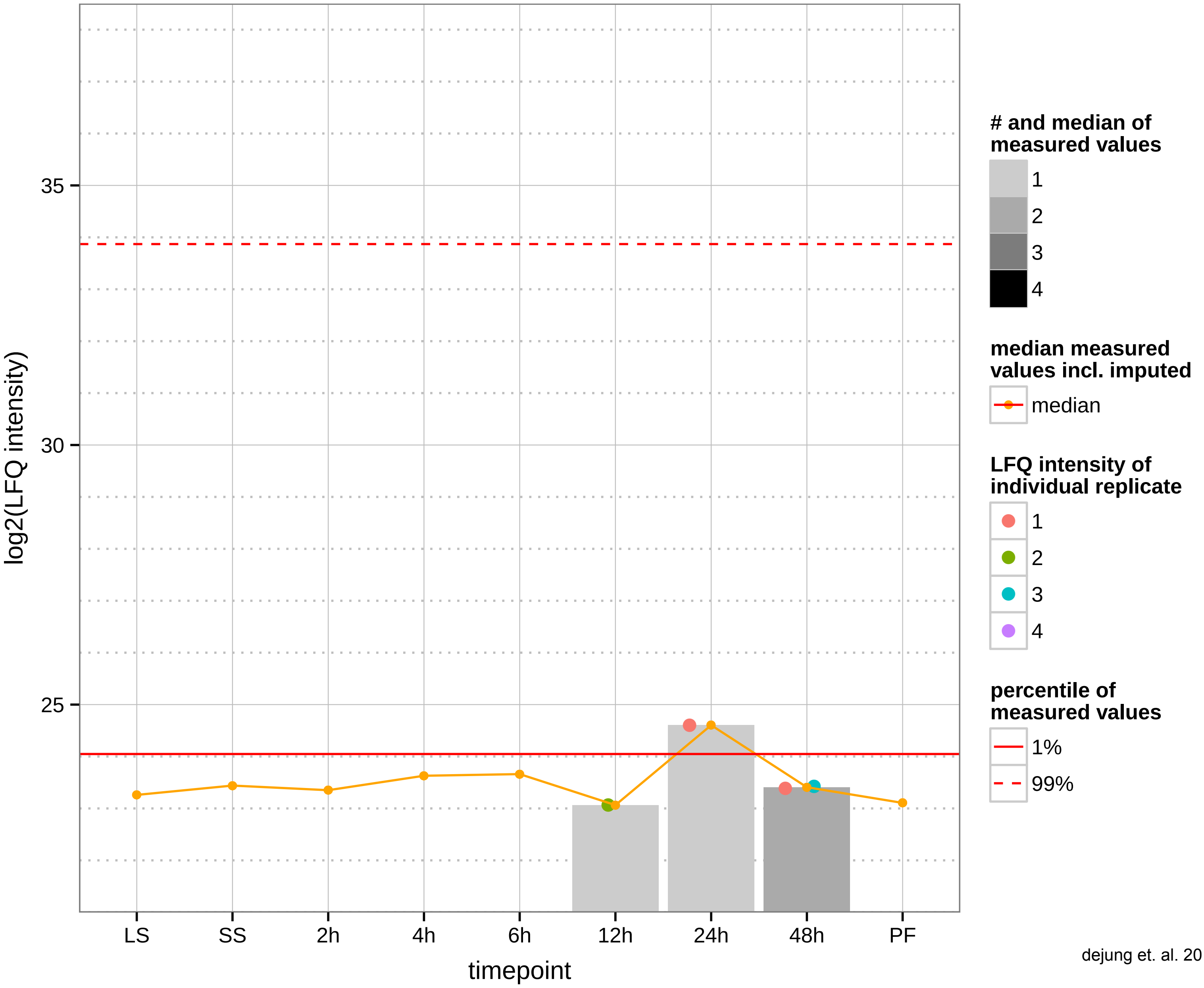
DNA repair and recombination helicase protein PIF1, putative (TbPIF8)
Tb927.7.1000
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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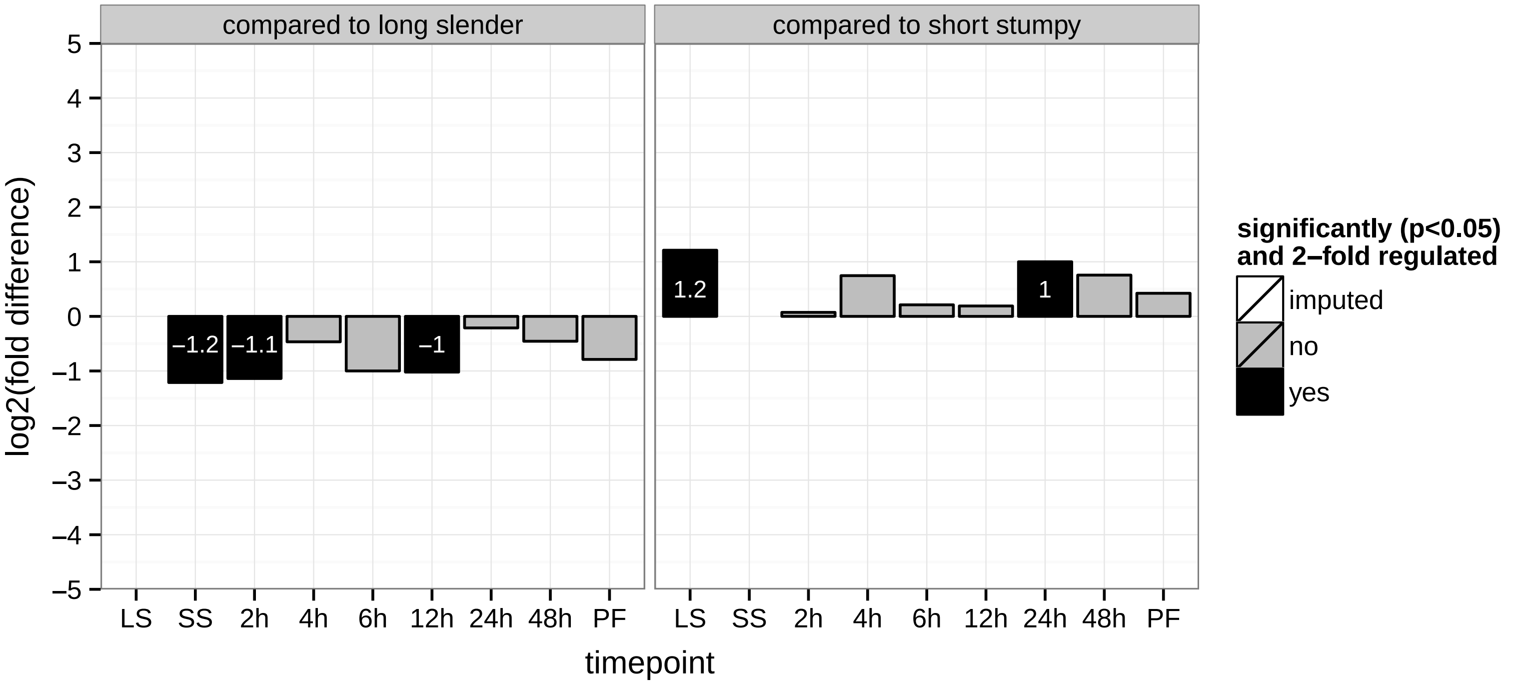
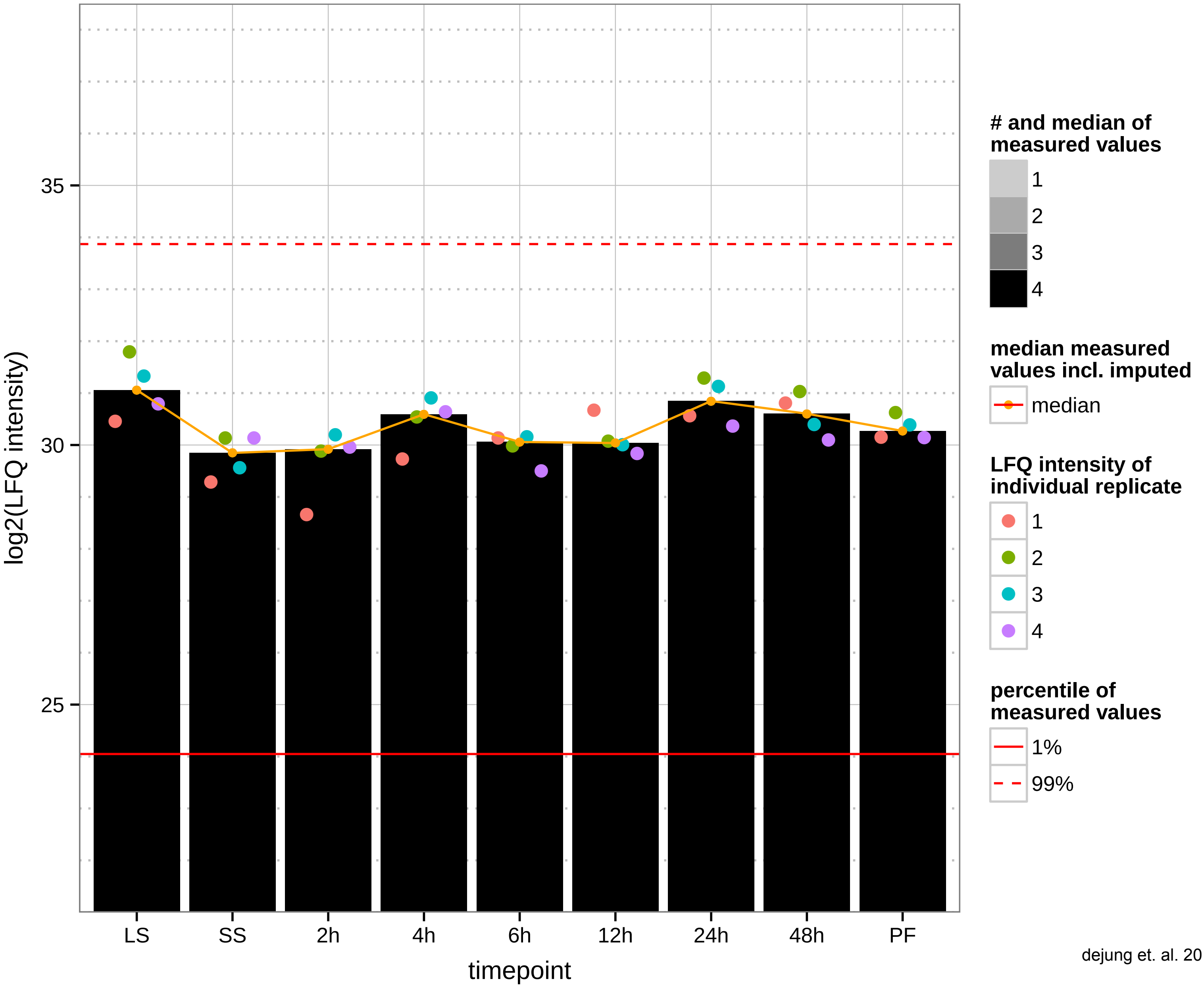
Eukaryotic translation initiation factor 4E type 6 (eif4e6)
Tb927.7.1670
AGOF: RNA 7−methylguanosine cap binding, RNA cap 4 binding, protein binding, translation initiation factor activity
AGOC: cytoplasm, eukaryotic translation initiation factor 4F complex
AGOP: cell motility, motile cilium assembly, translational initiation
PGOF: RNA binding, translation initiation factor activity
PGOC: cytoplasm
PGOP: translational initiation





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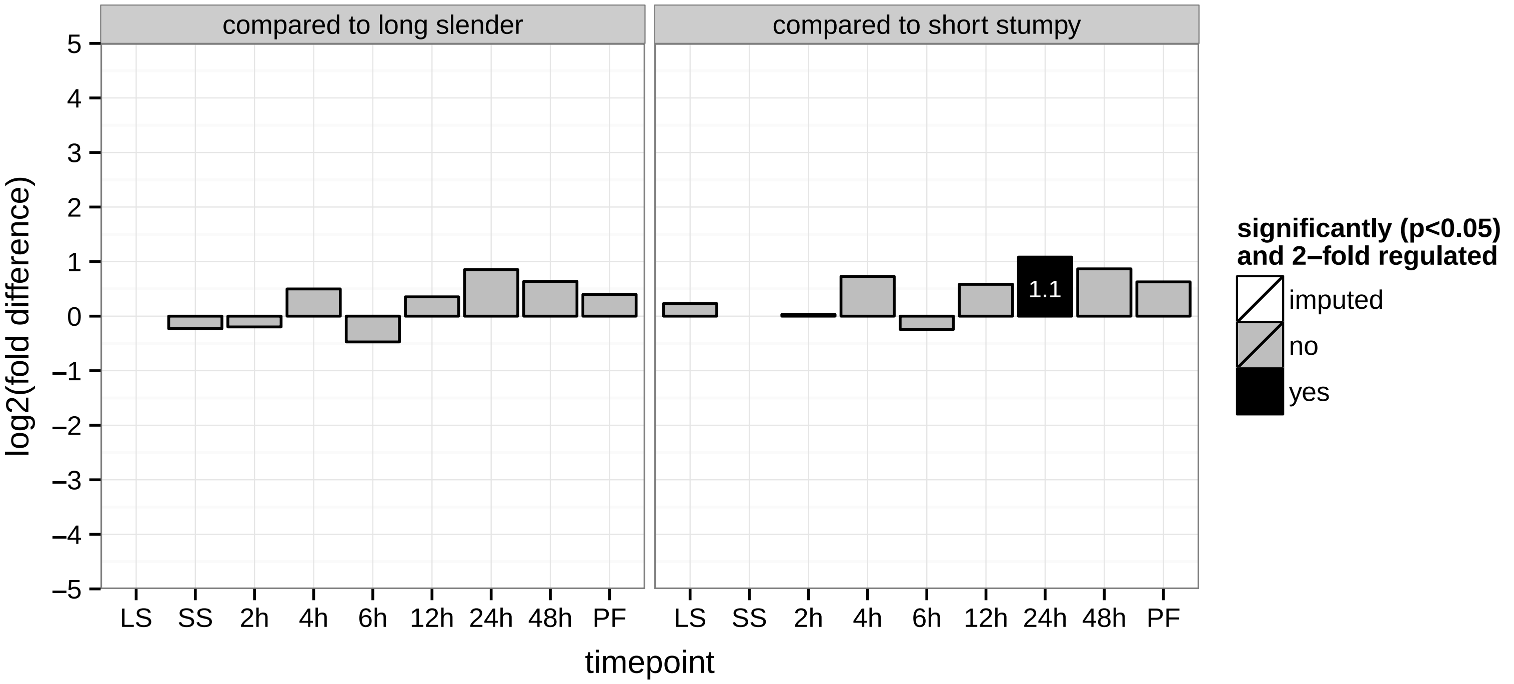
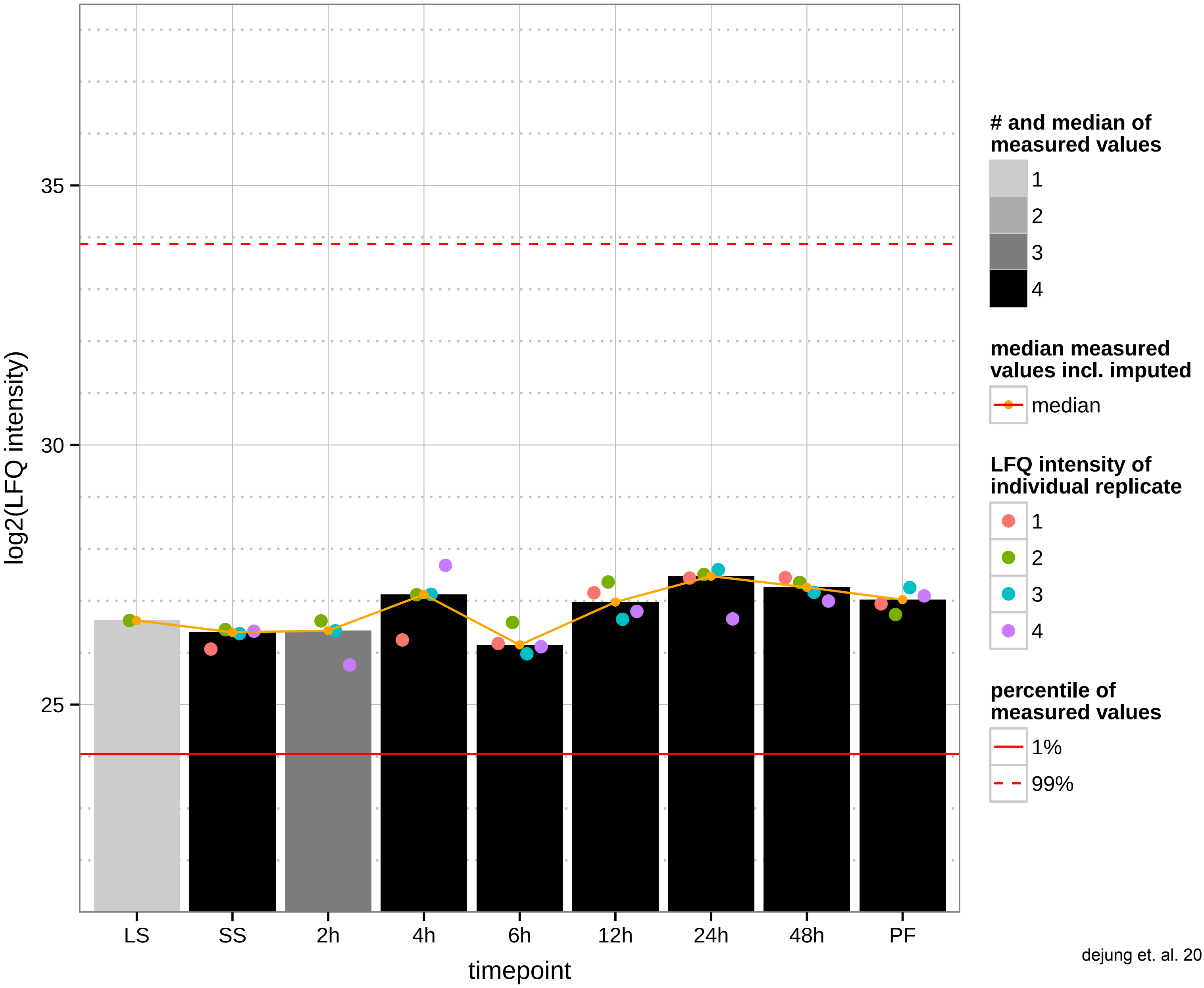
prefoldin, putative
Tb927.7.2590
AGOF: unfolded protein binding
AGOC: prefoldin complex
AGOP: protein folding
PGOF: unfolded protein binding
PGOC: prefoldin complex
PGOP: protein folding





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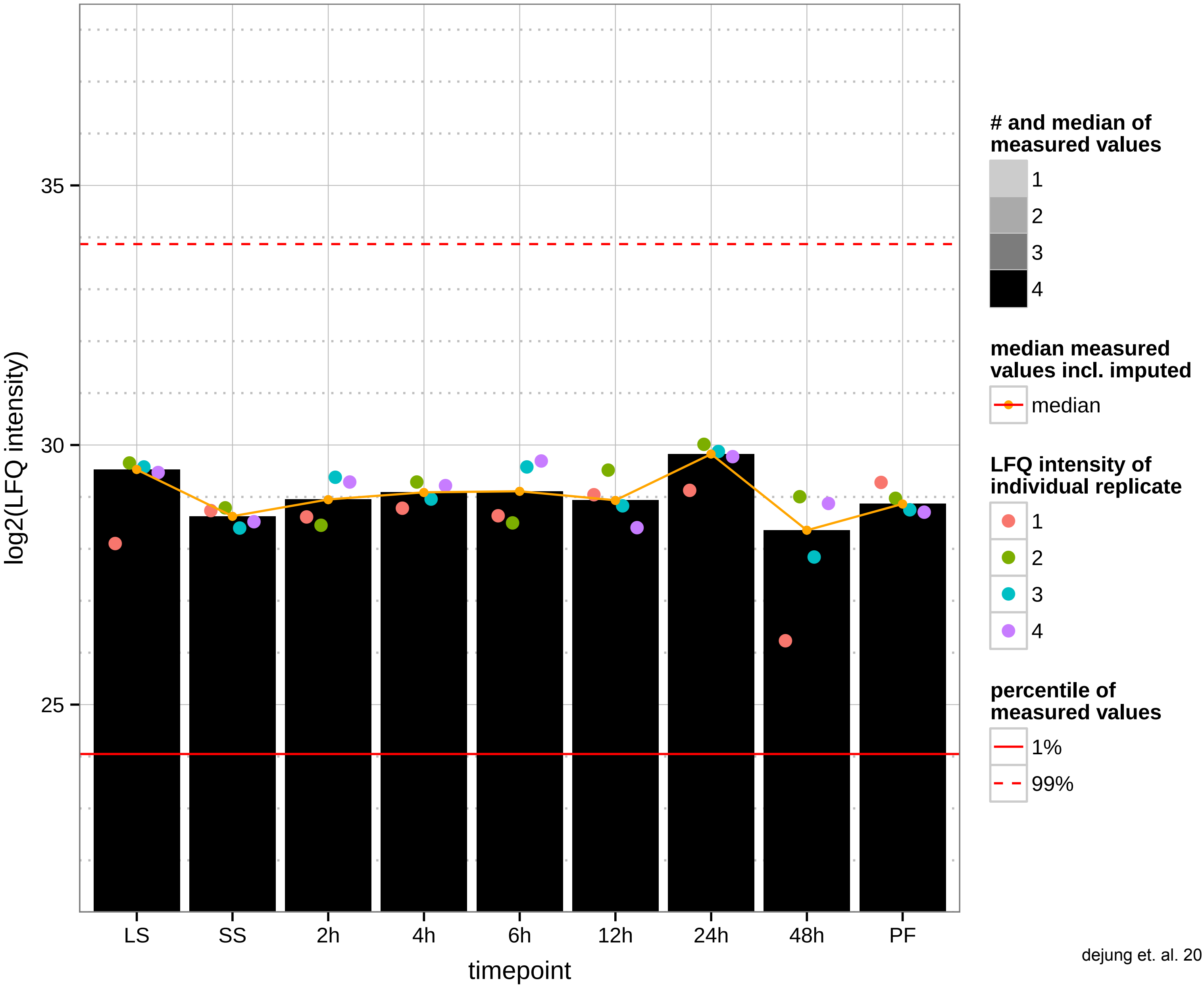
hypothetical protein, conserved
Tb927.7.4470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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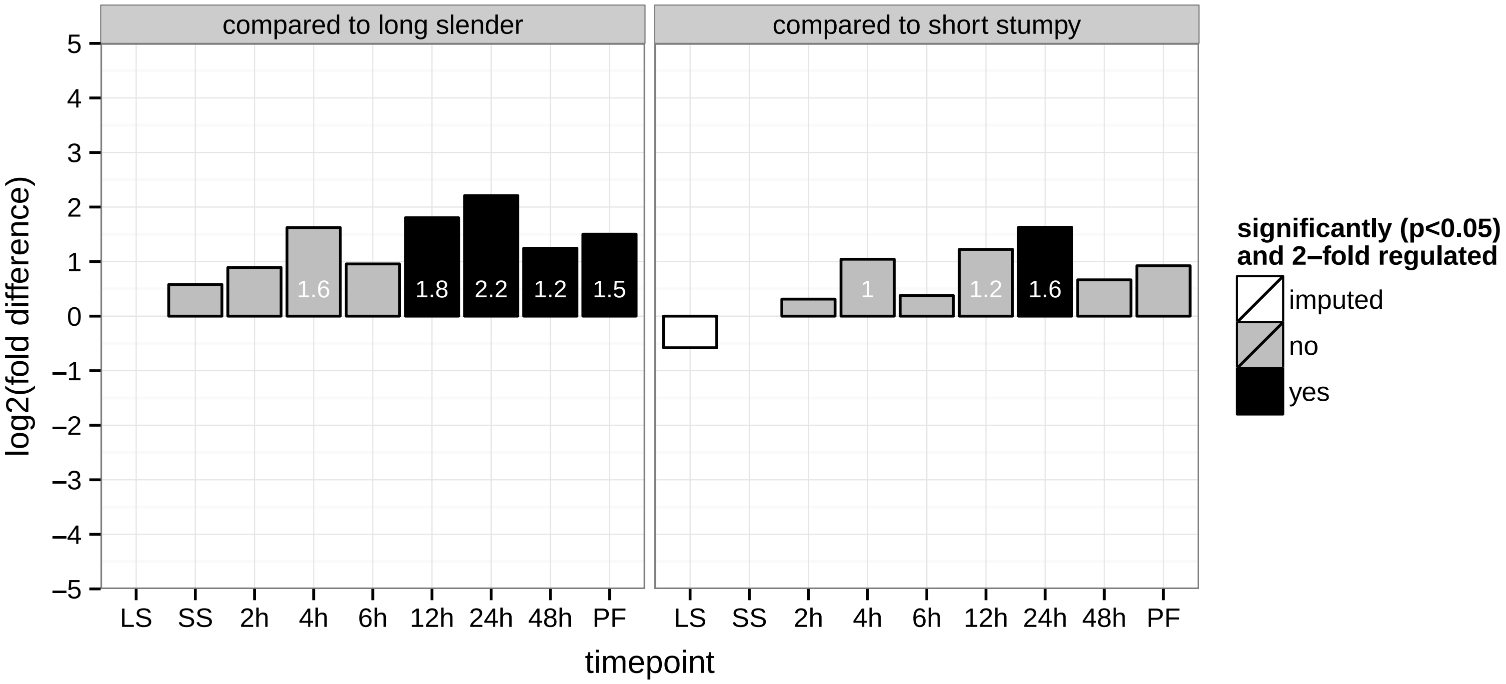
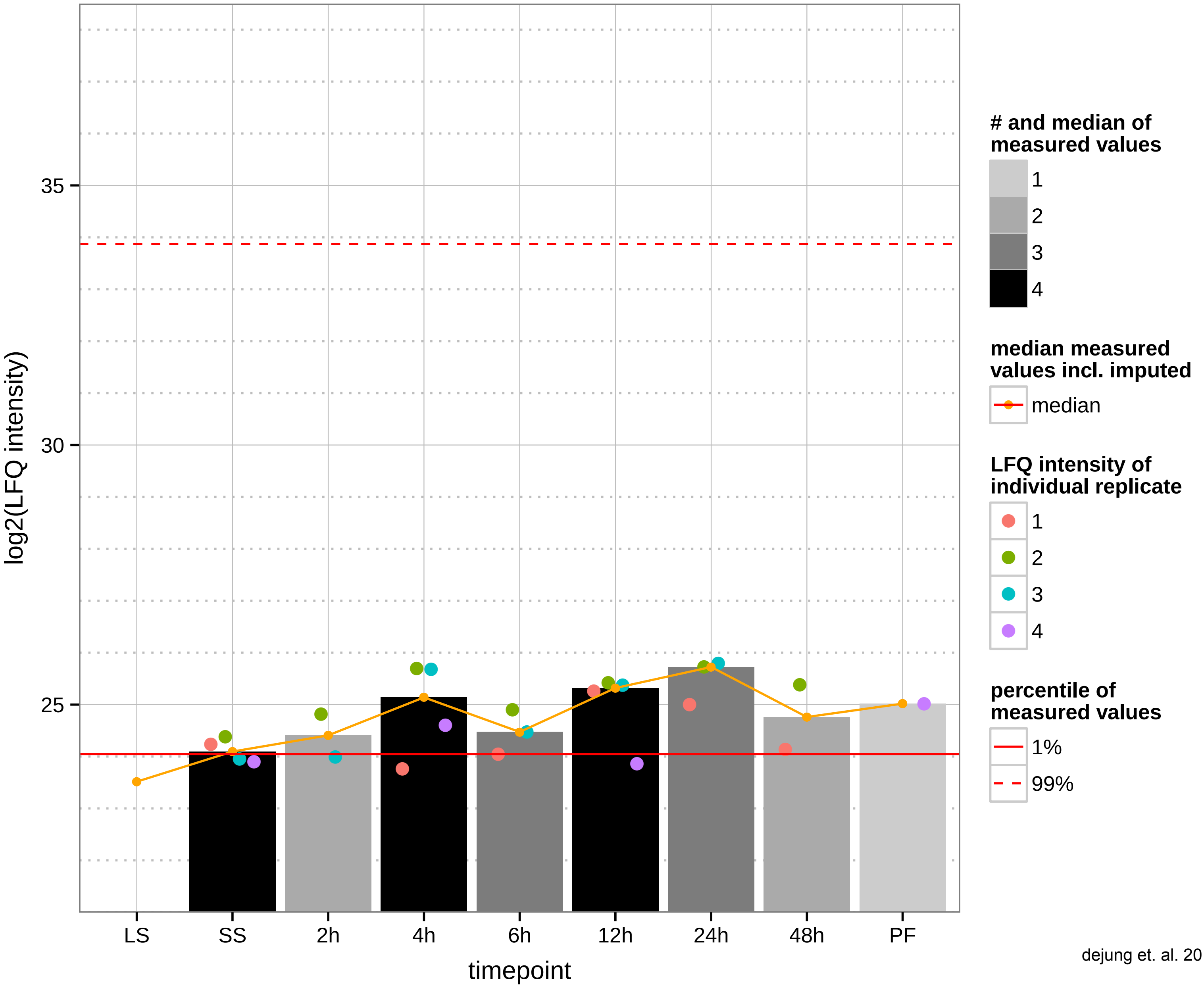
exosome–associated protein 3, 3' exoribonuclease, putative (EAP3)
Tb927.7.5460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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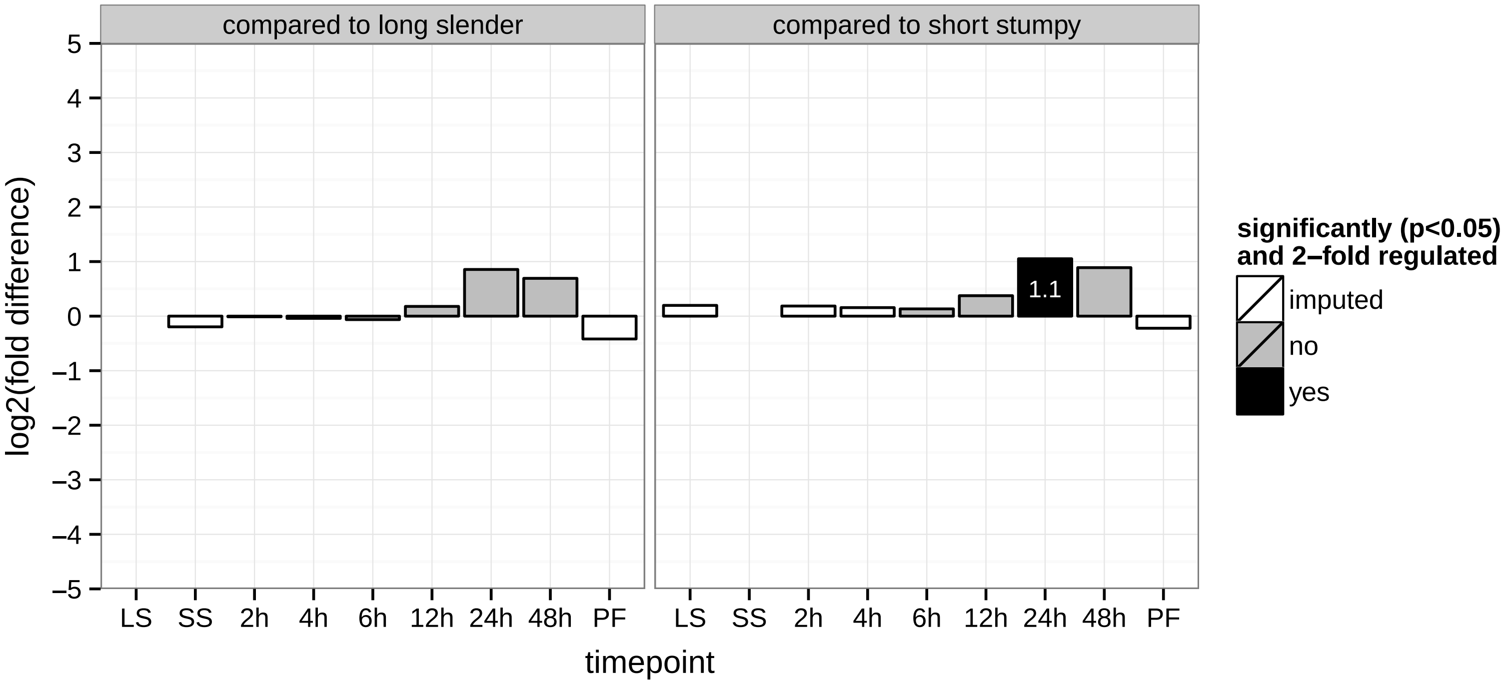
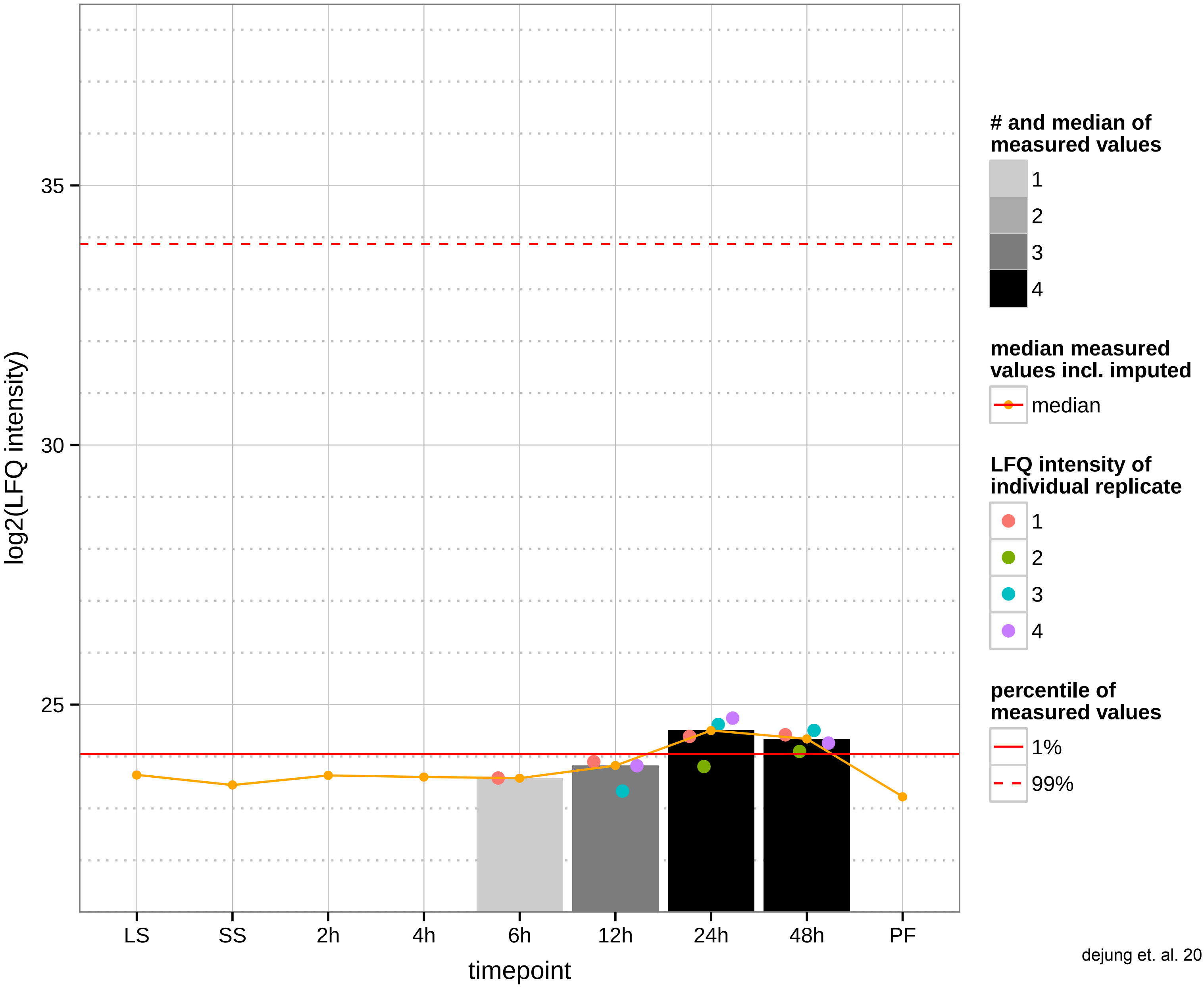
hypothetical protein, conserved
Tb927.8.6520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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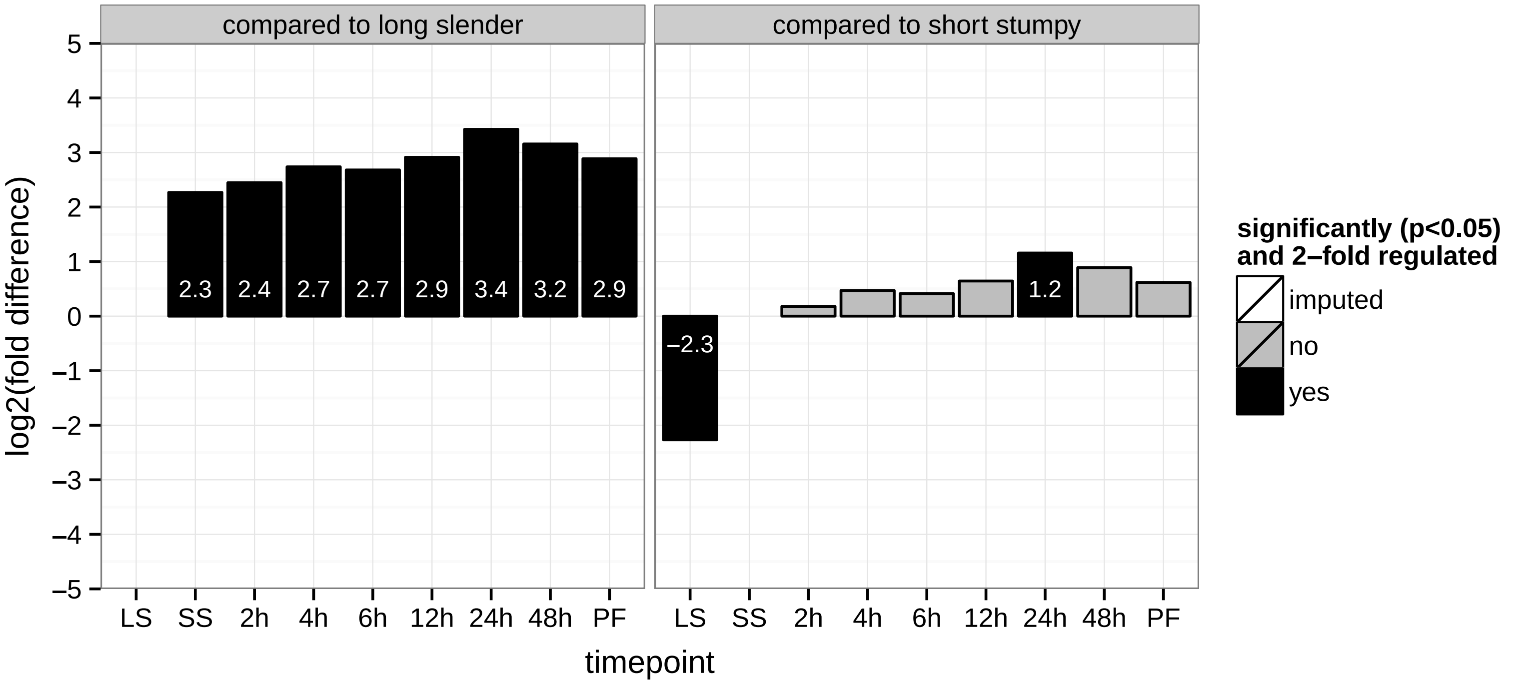
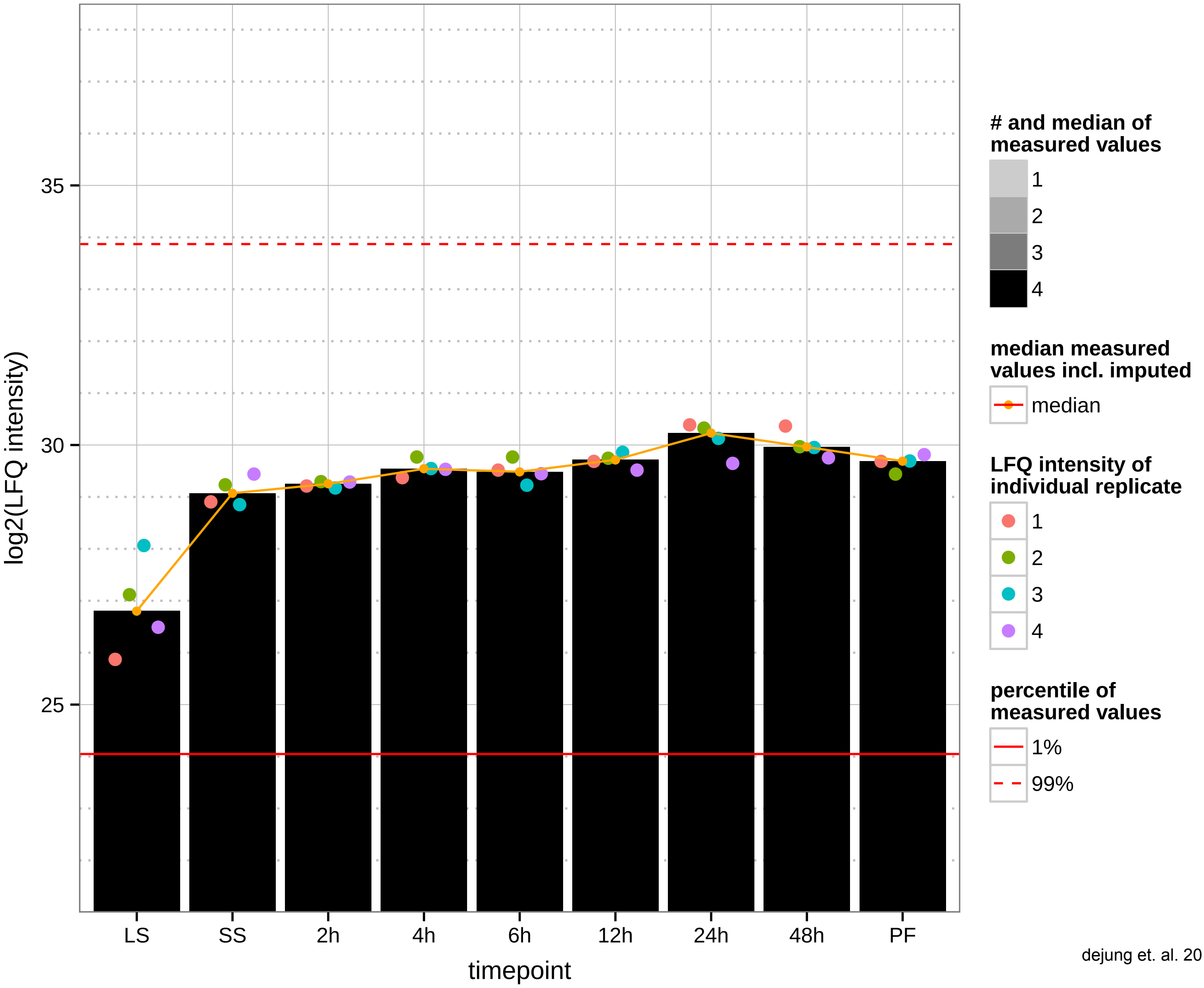
hypothetical protein, conserved
Tb927.9.11220
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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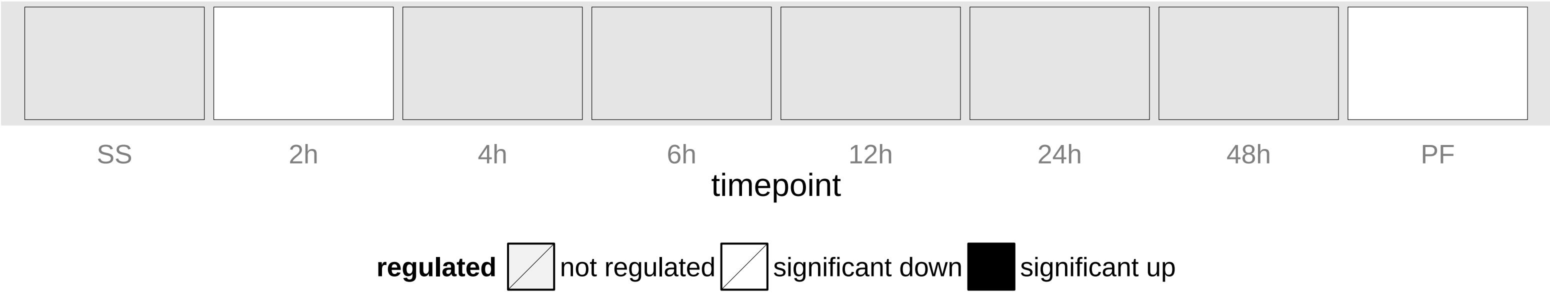

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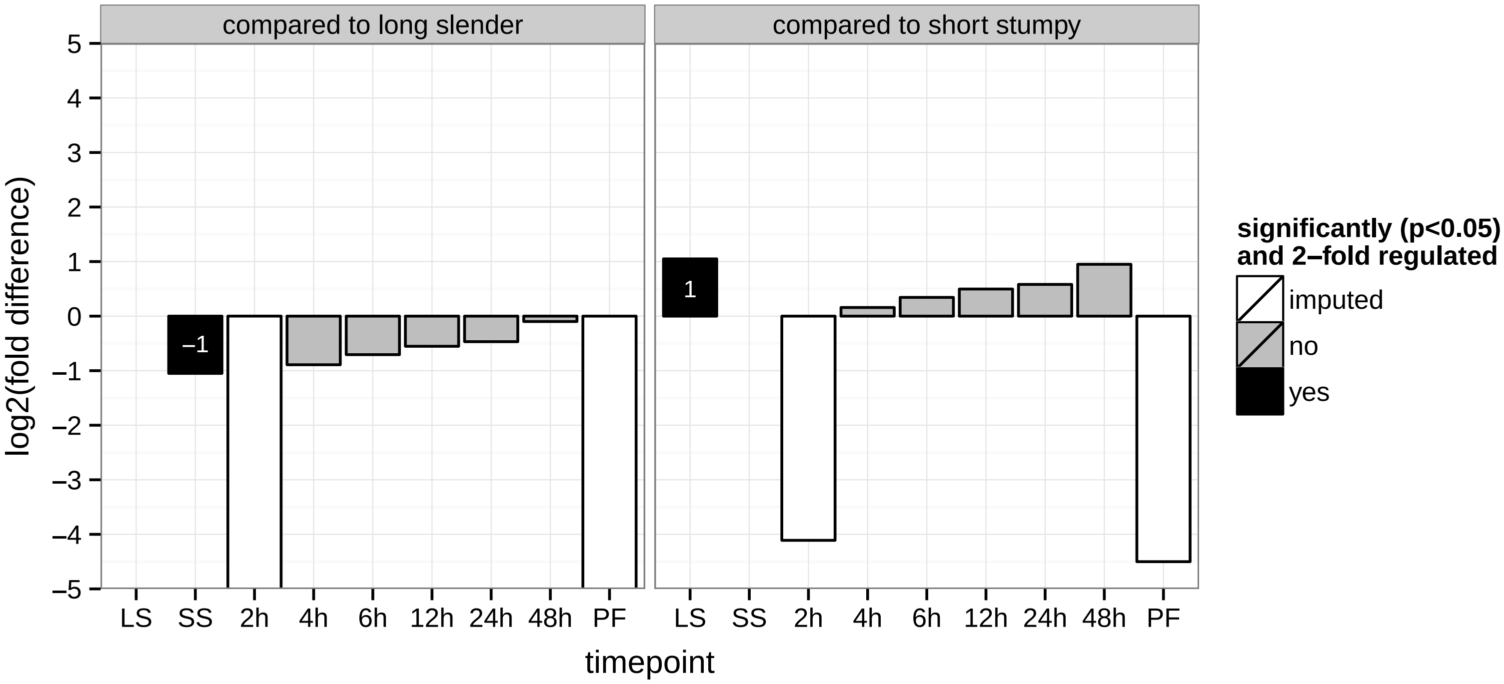
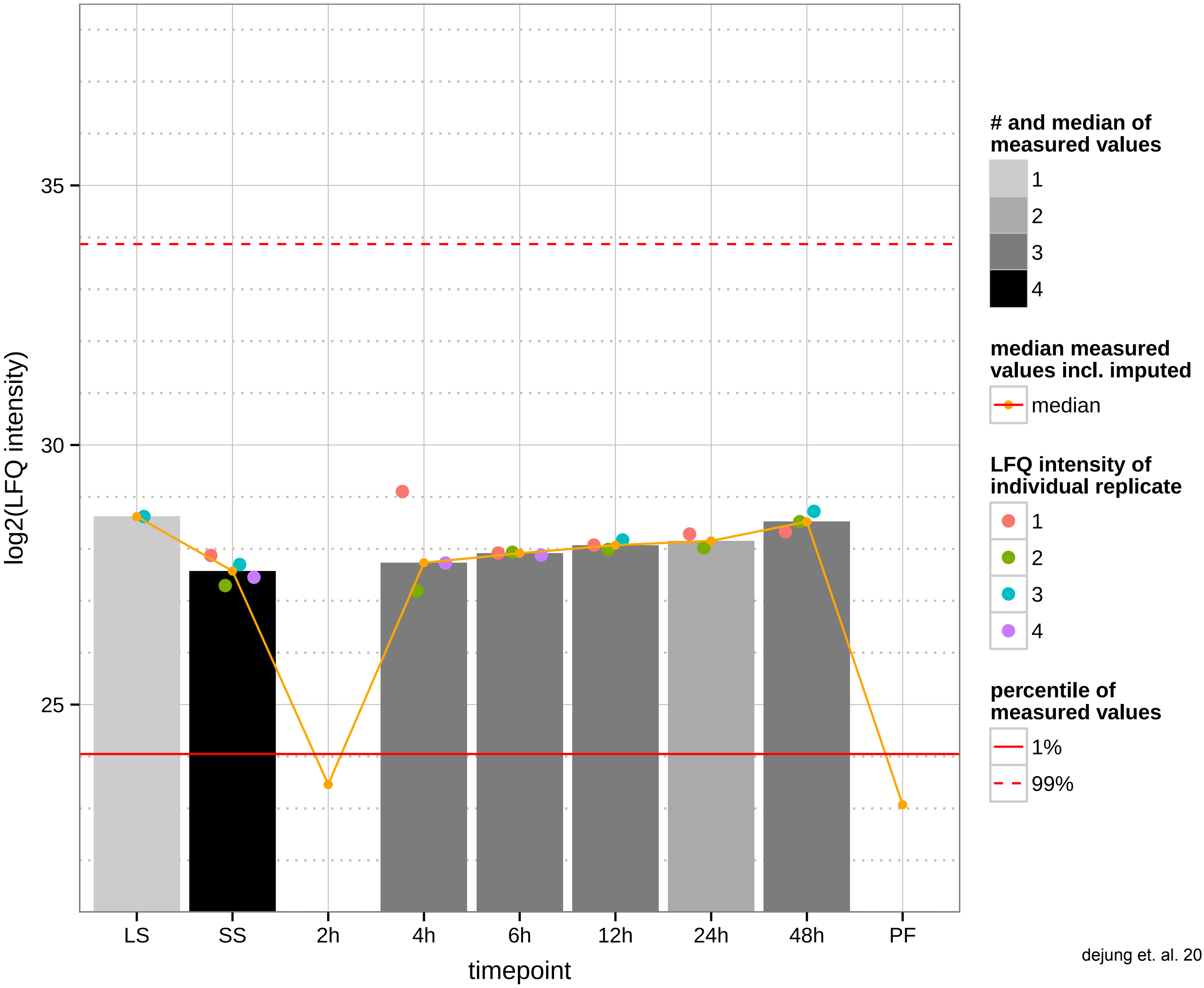
kinesin, putative
Tb927.10.15390;Tb11.v5.0434
AGOF: null, microtubule motor activity, motor activity
AGOC: null, kinesin complex, microtubule associated complex
AGOP: null, microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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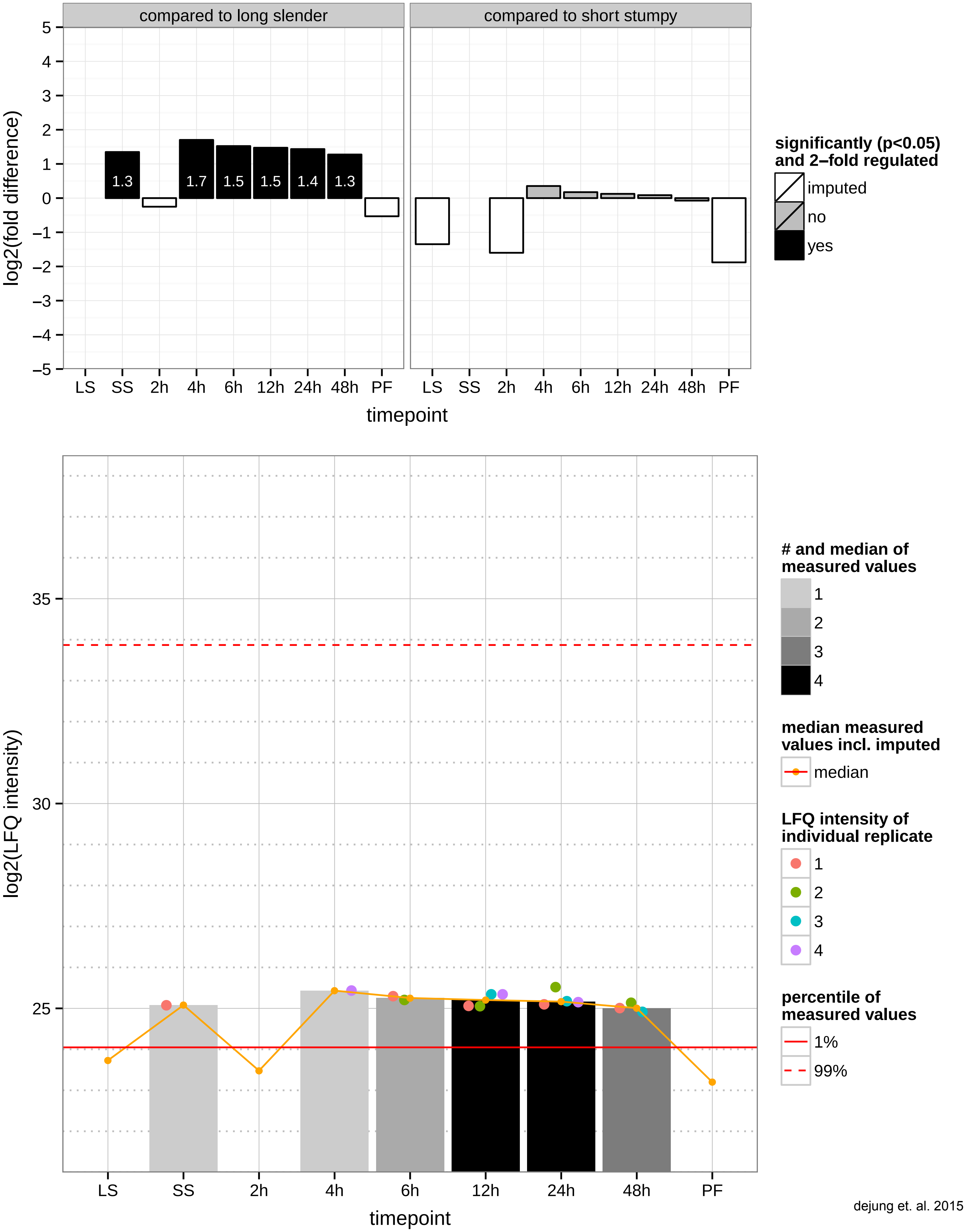
hypothetical protein, conserved
Tb11.v5.0736;Tb927.5.3420
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: null



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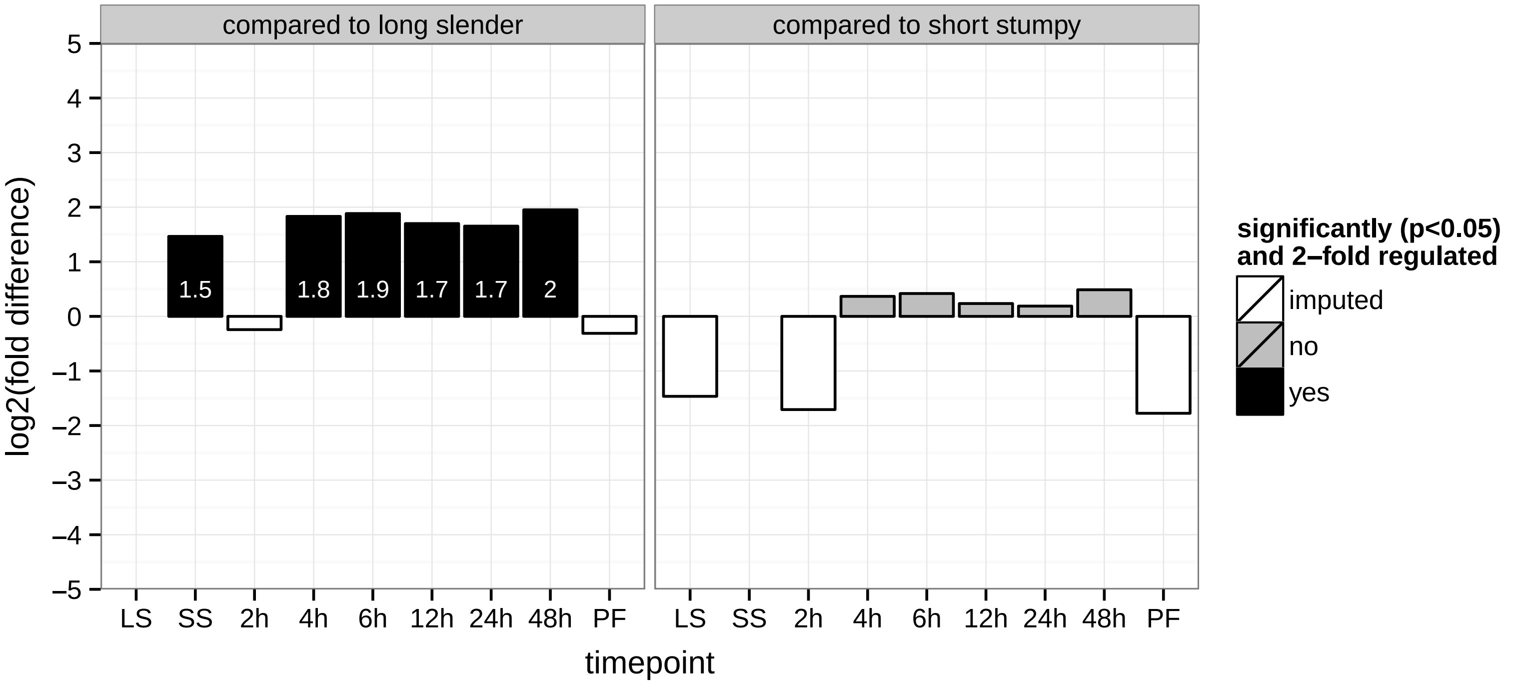
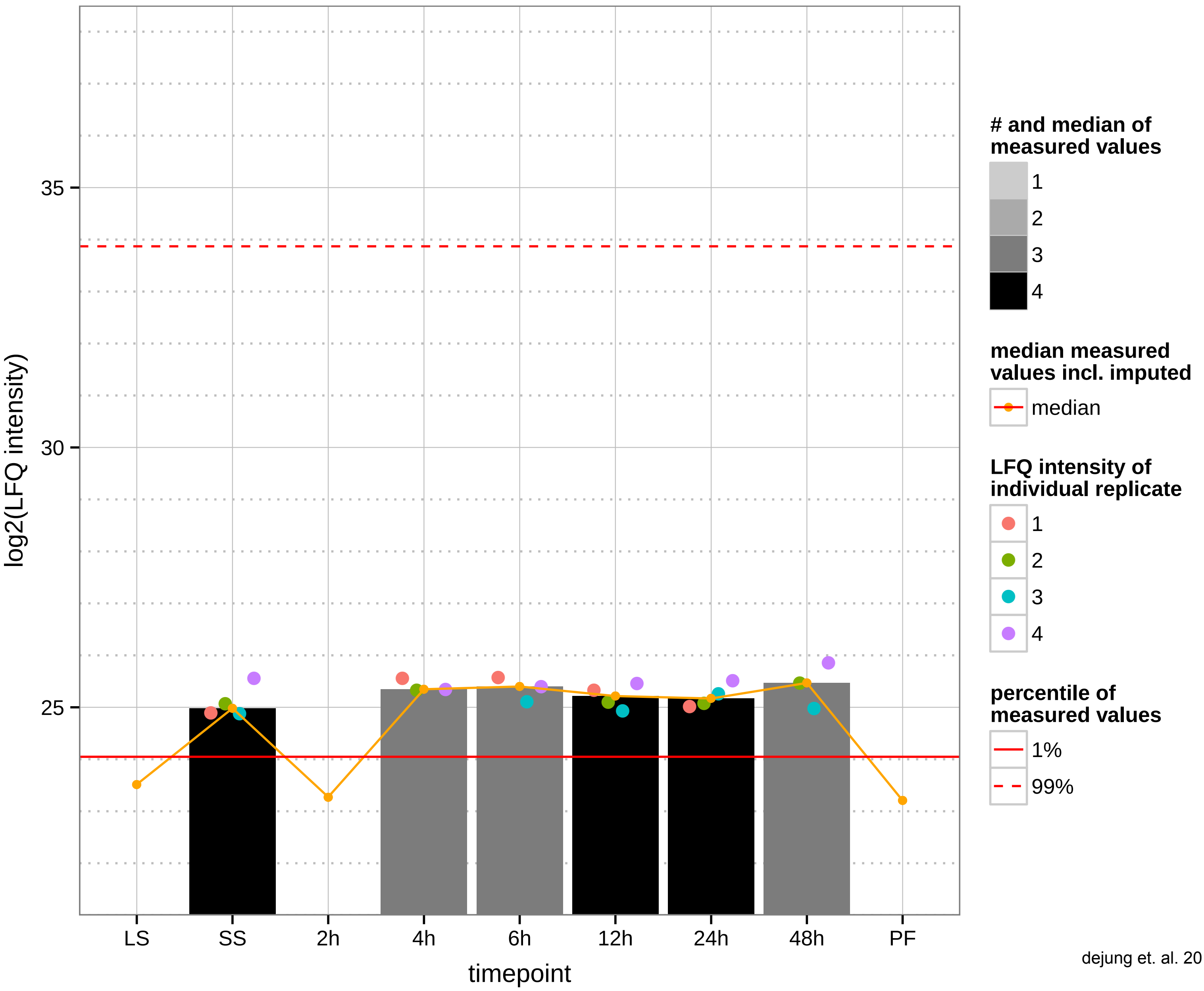
hypothetical protein, conserved
Tb927.10.15430
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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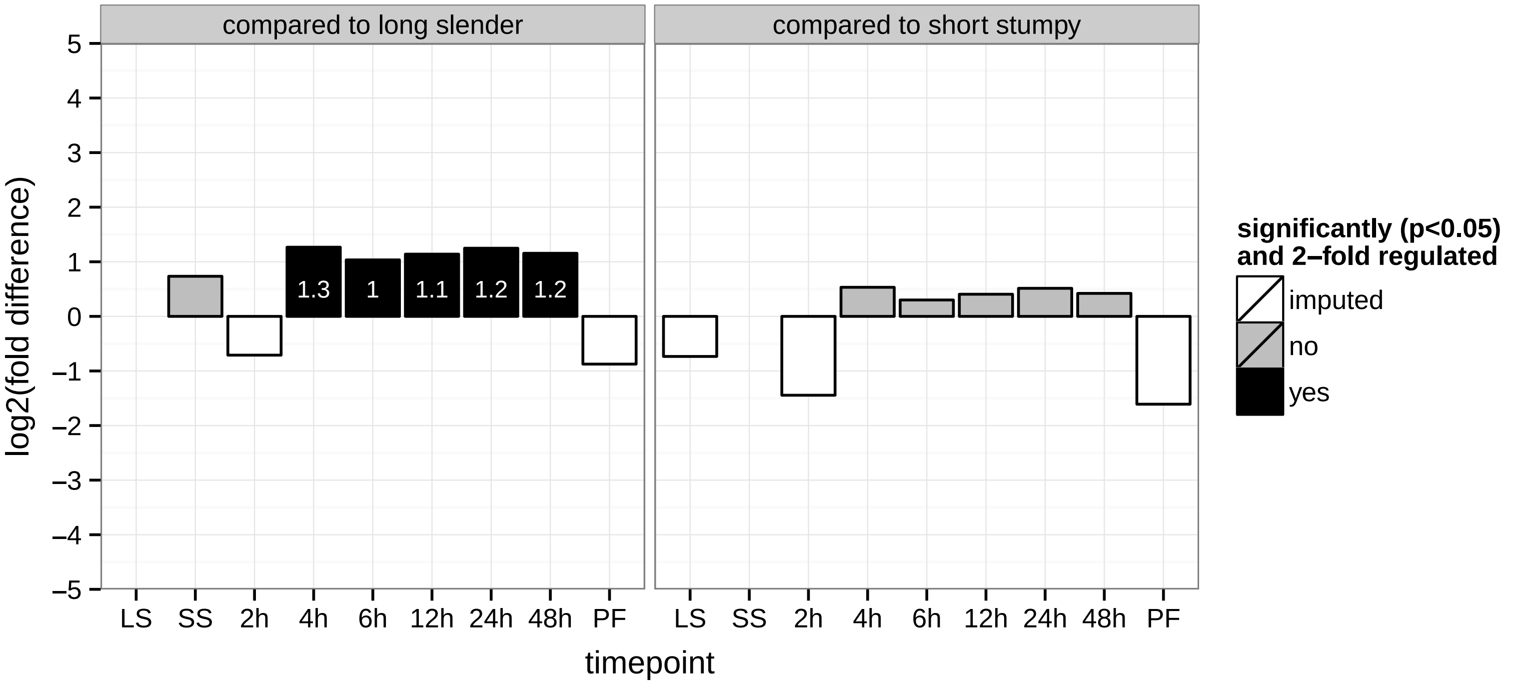
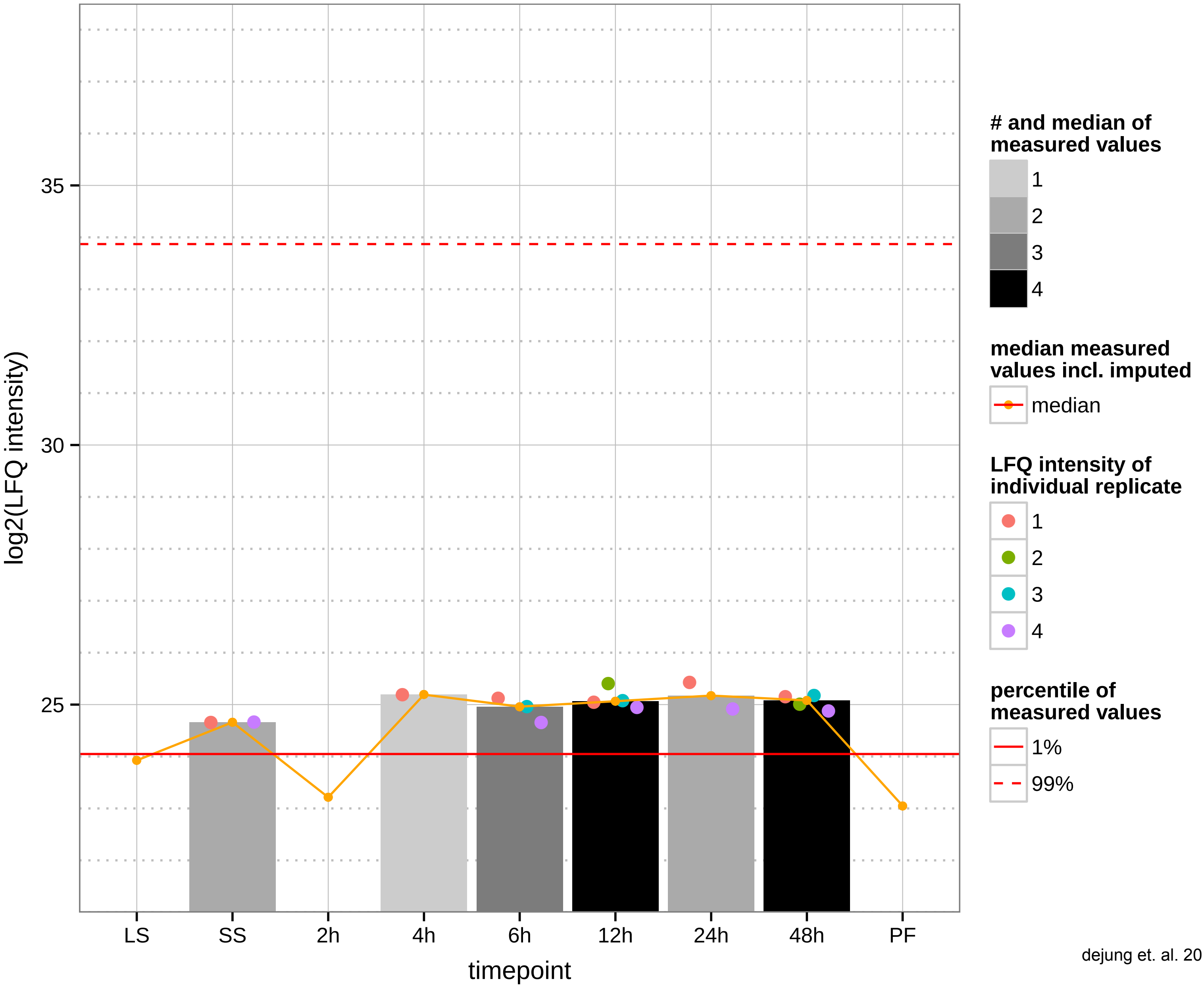
Pre–mRNA–splicing factor CWC22, putative (TbCWC22)
Tb927.11.10750
AGOF: RNA binding
AGOC: null
AGOP: RNA metabolic process, translation
PGOF: DNA binding, RNA binding, binding, protein binding
PGOC: null
PGOP: null





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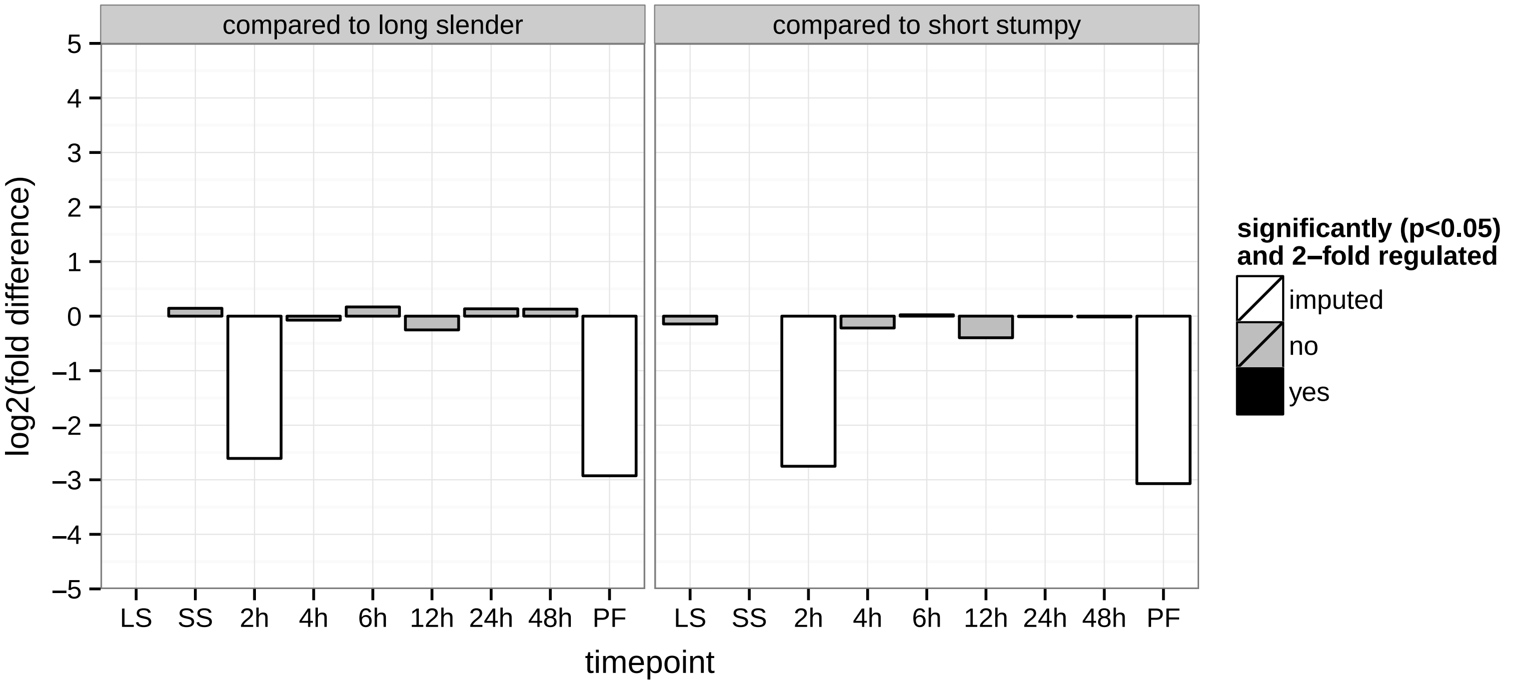
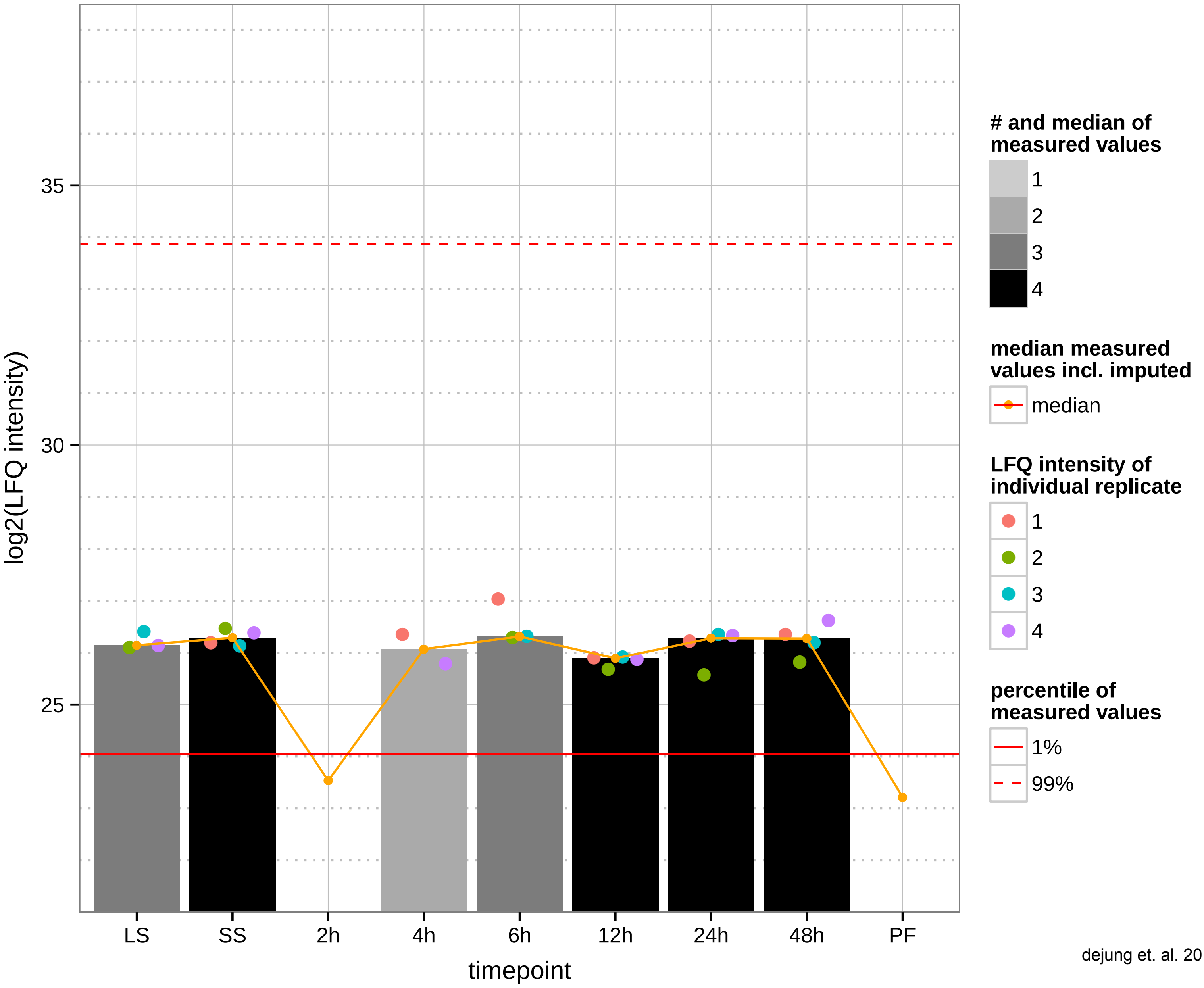
hypothetical protein, conserved
Tb927.11.14450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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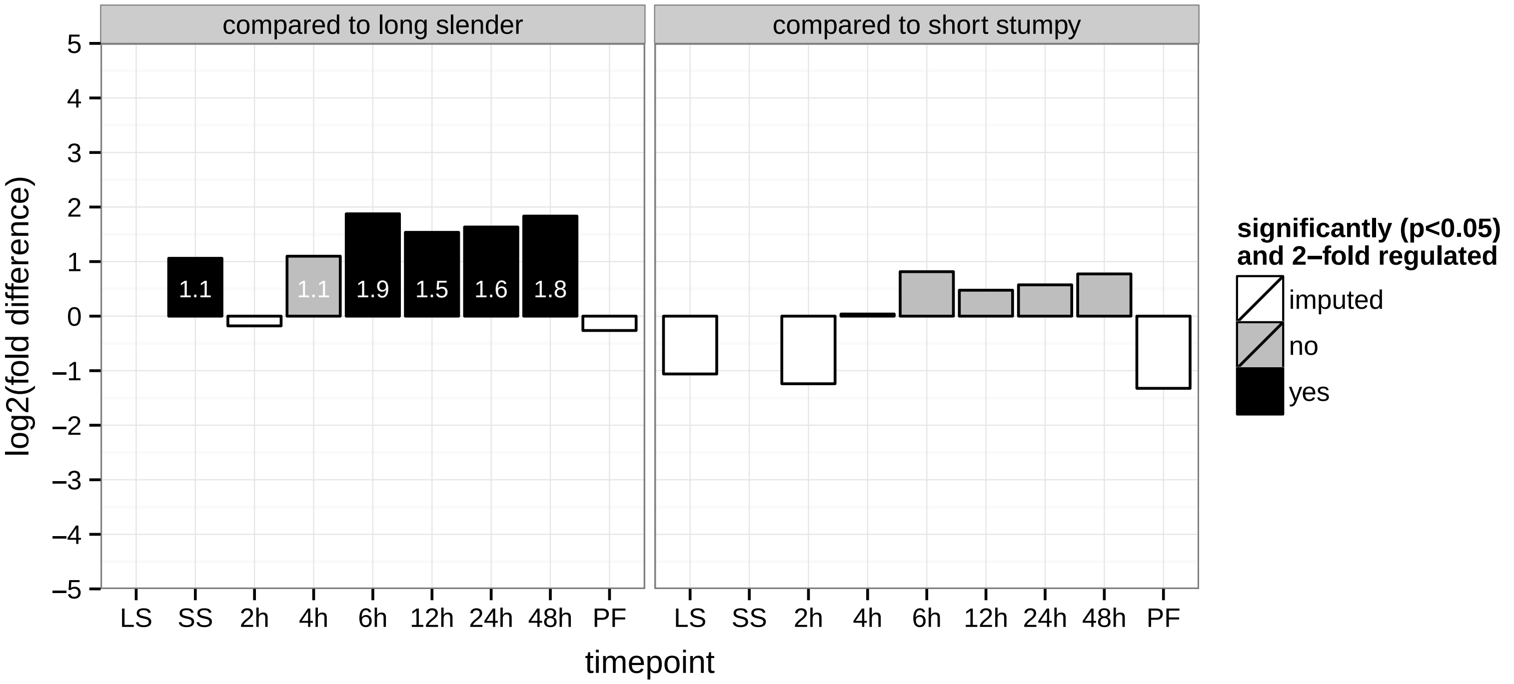
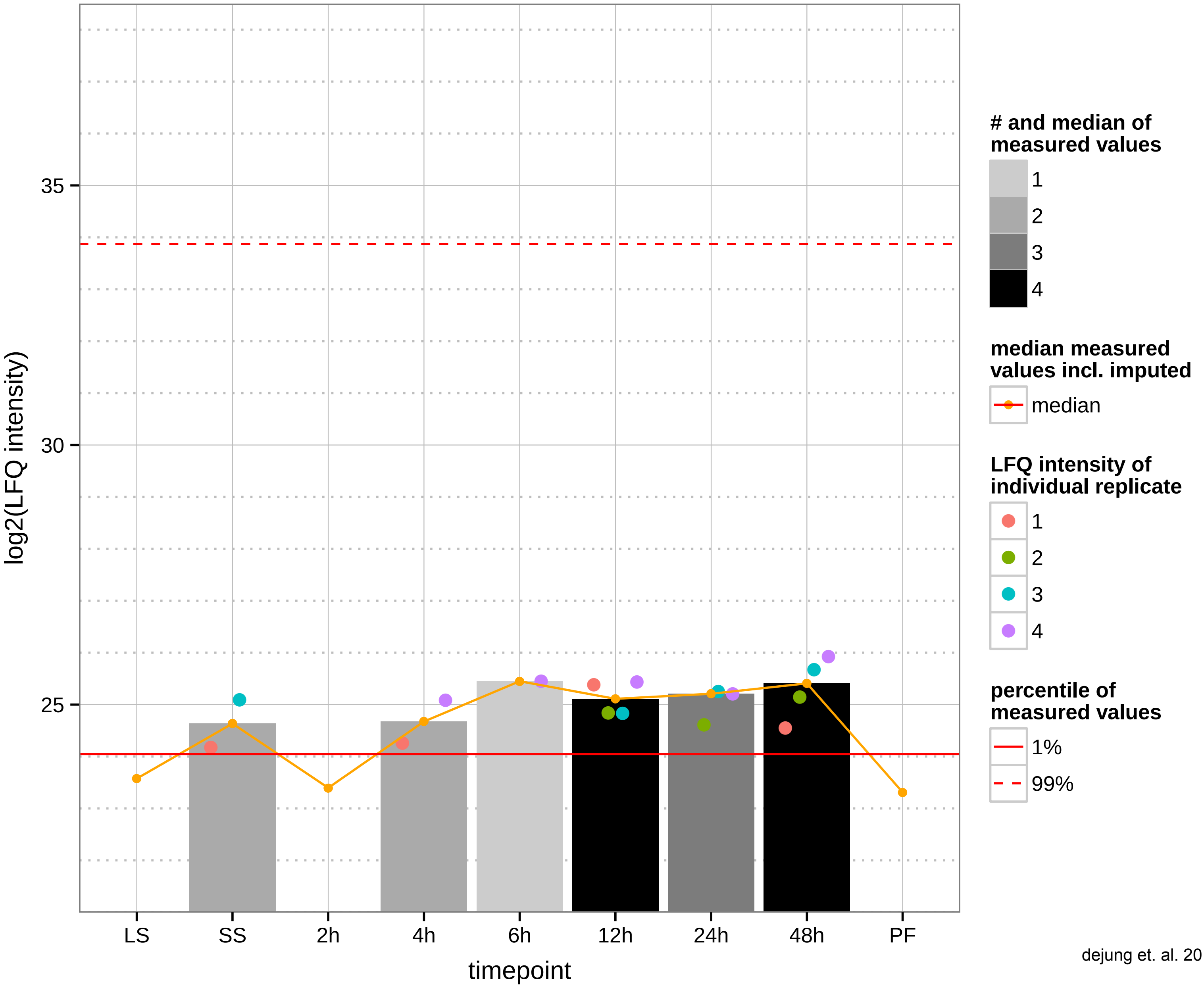
tatD related deoxyribonuclease, putative
Tb927.11.1600
AGOF: deoxyribonuclease activity, endodeoxyribonuclease activity, producing 5'–phosphomonoesters
AGOC: null
AGOP: metabolic process
PGOF: endodeoxyribonuclease activity, producing 5'–phosphomonoesters
PGOC: null
PGOP: null





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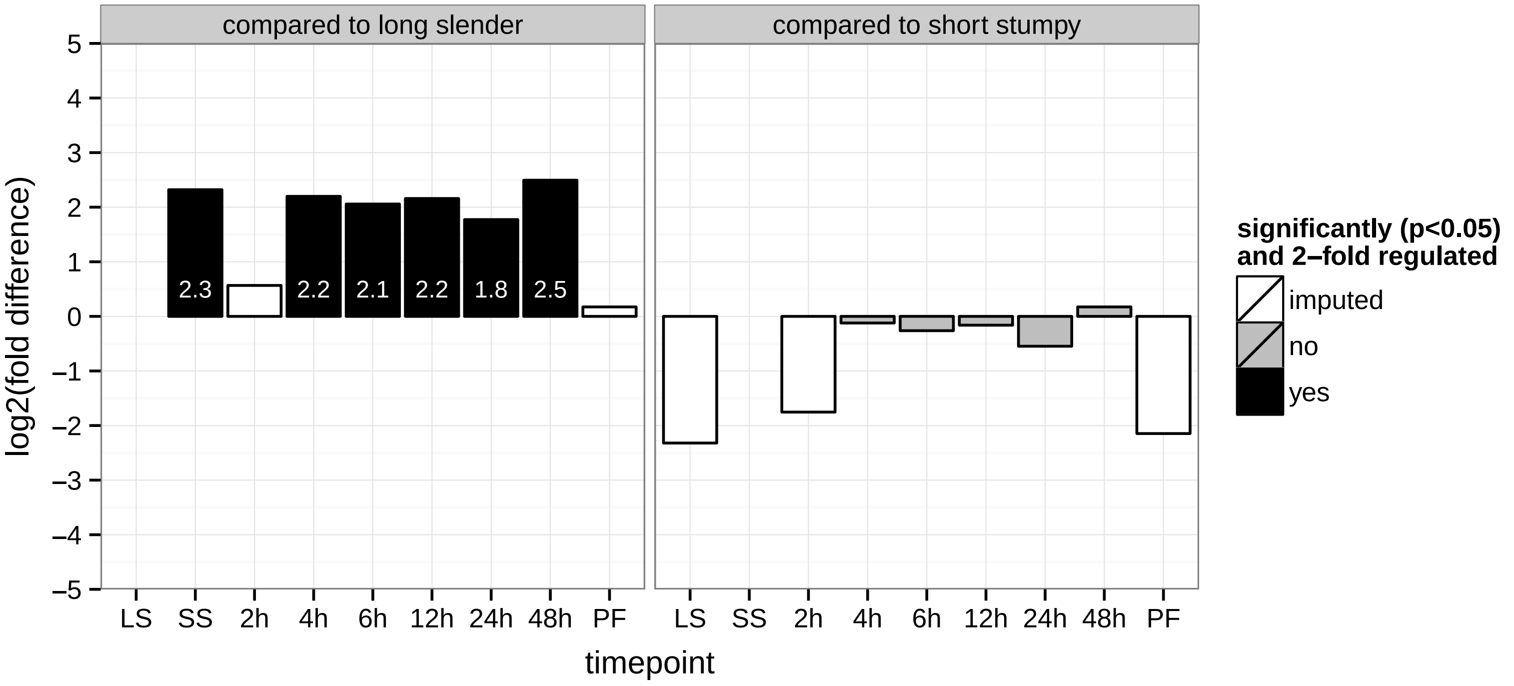
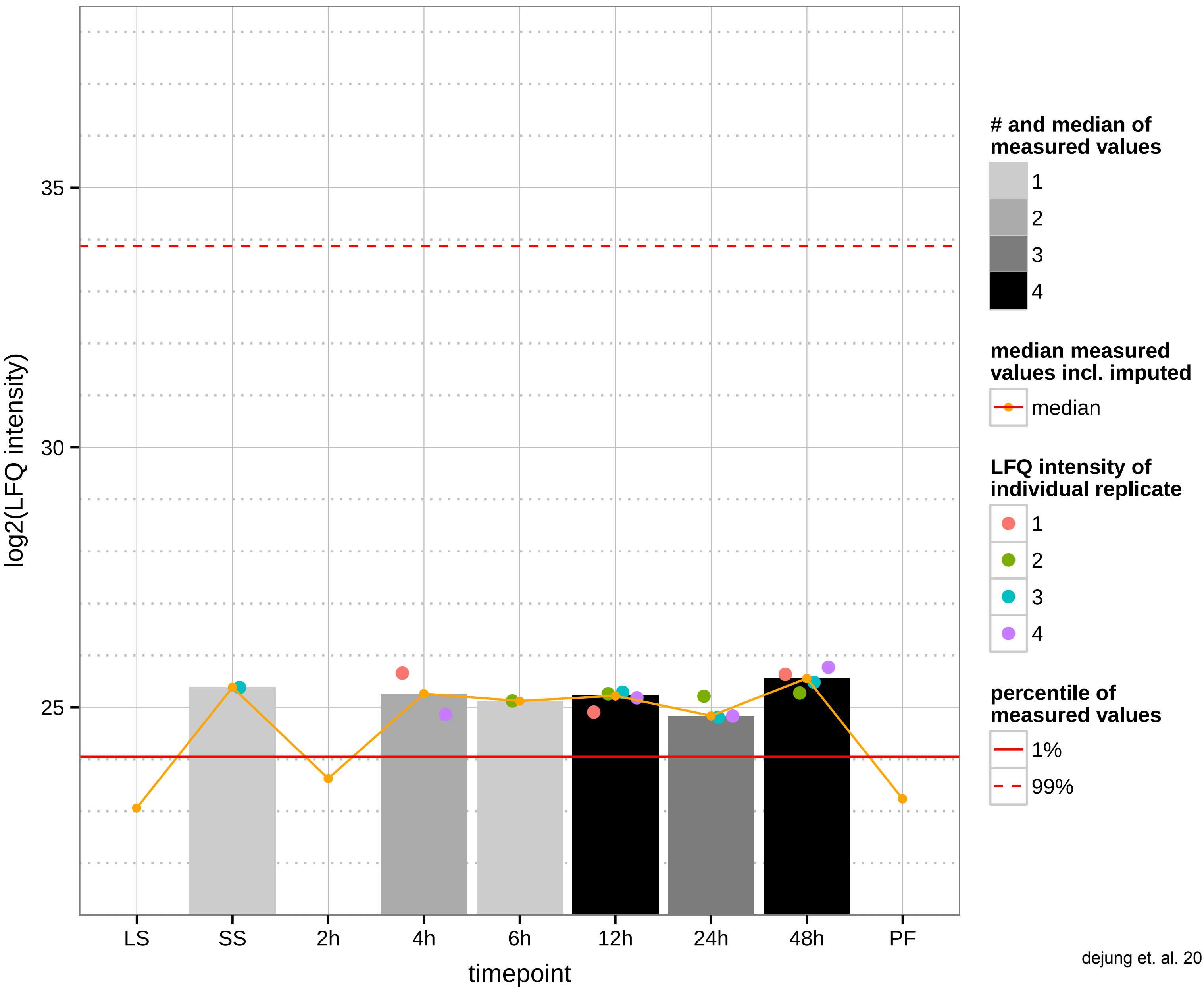
ras–like small GTPase, putative (TbGTR)
Tb927.11.3320
AGOF: GTP binding
AGOC: cytoplasm, nucleus
AGOP: null
PGOF: GTP binding
PGOC: cytoplasm, nucleus
PGOP: null





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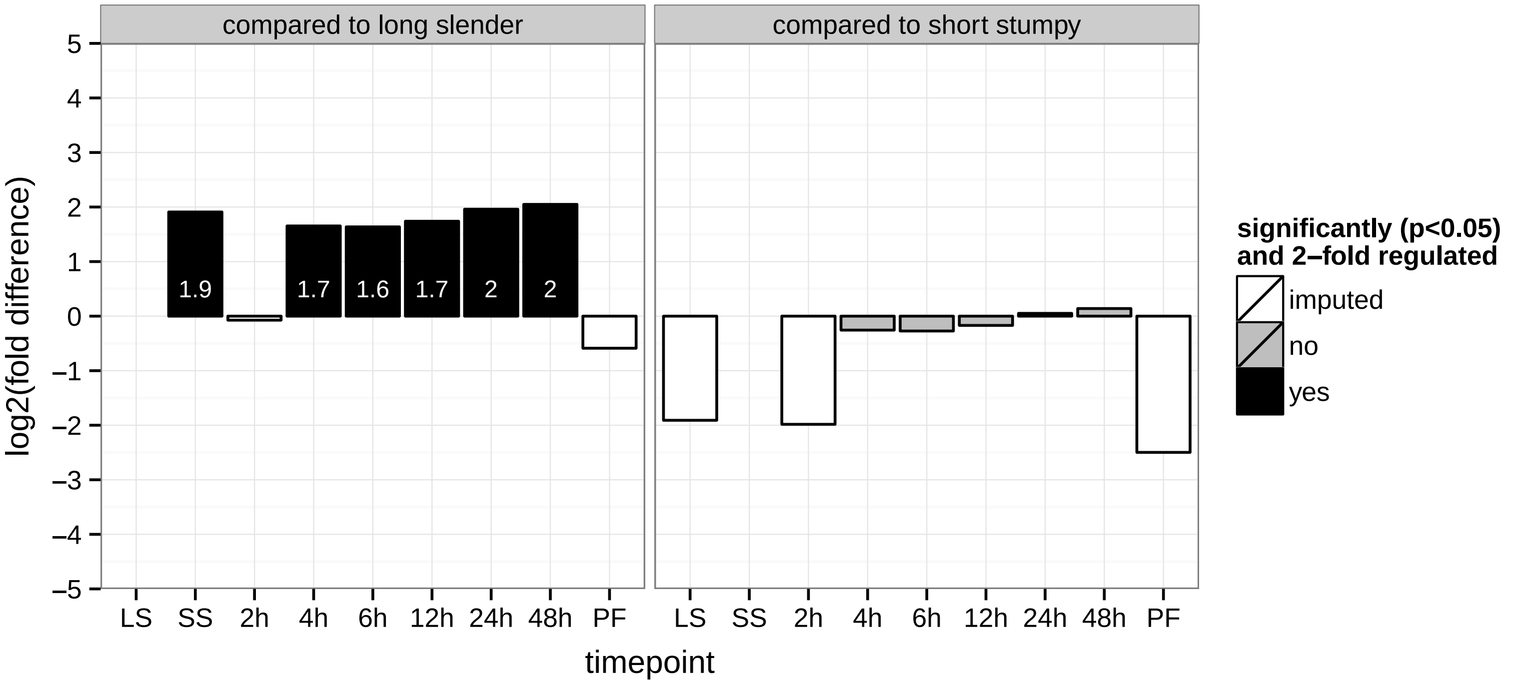
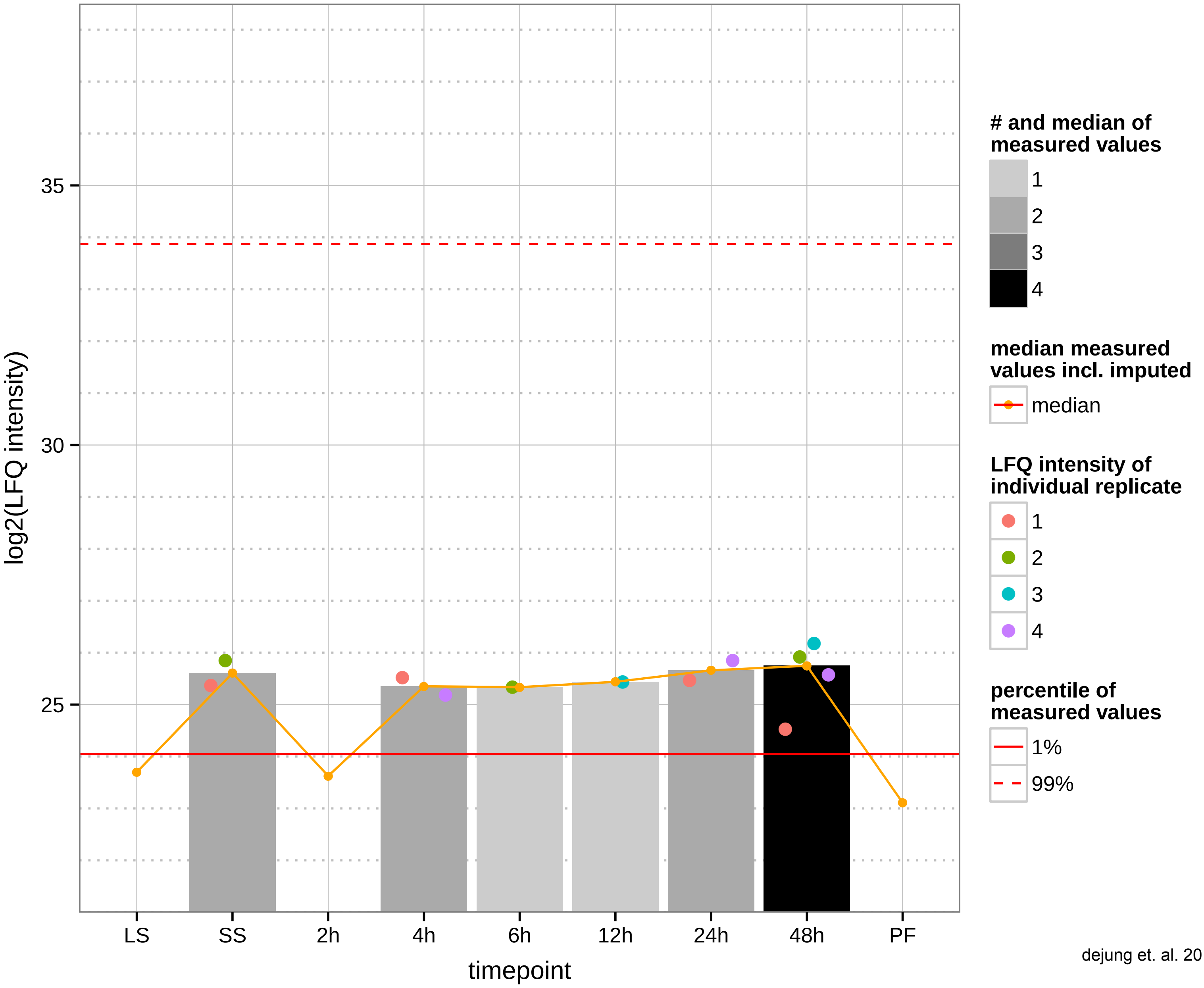
leucine–rich repeat protein (LRRP), putative
Tb927.11.5190
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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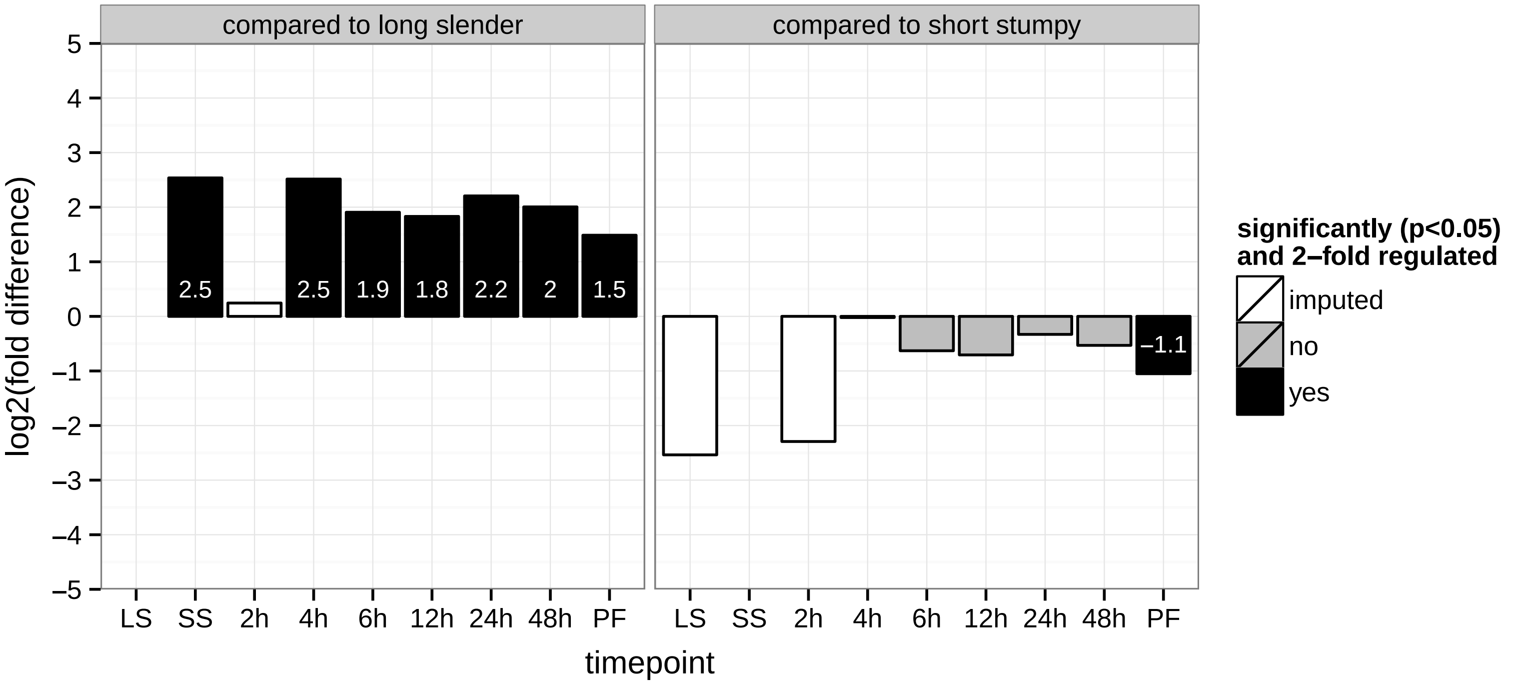
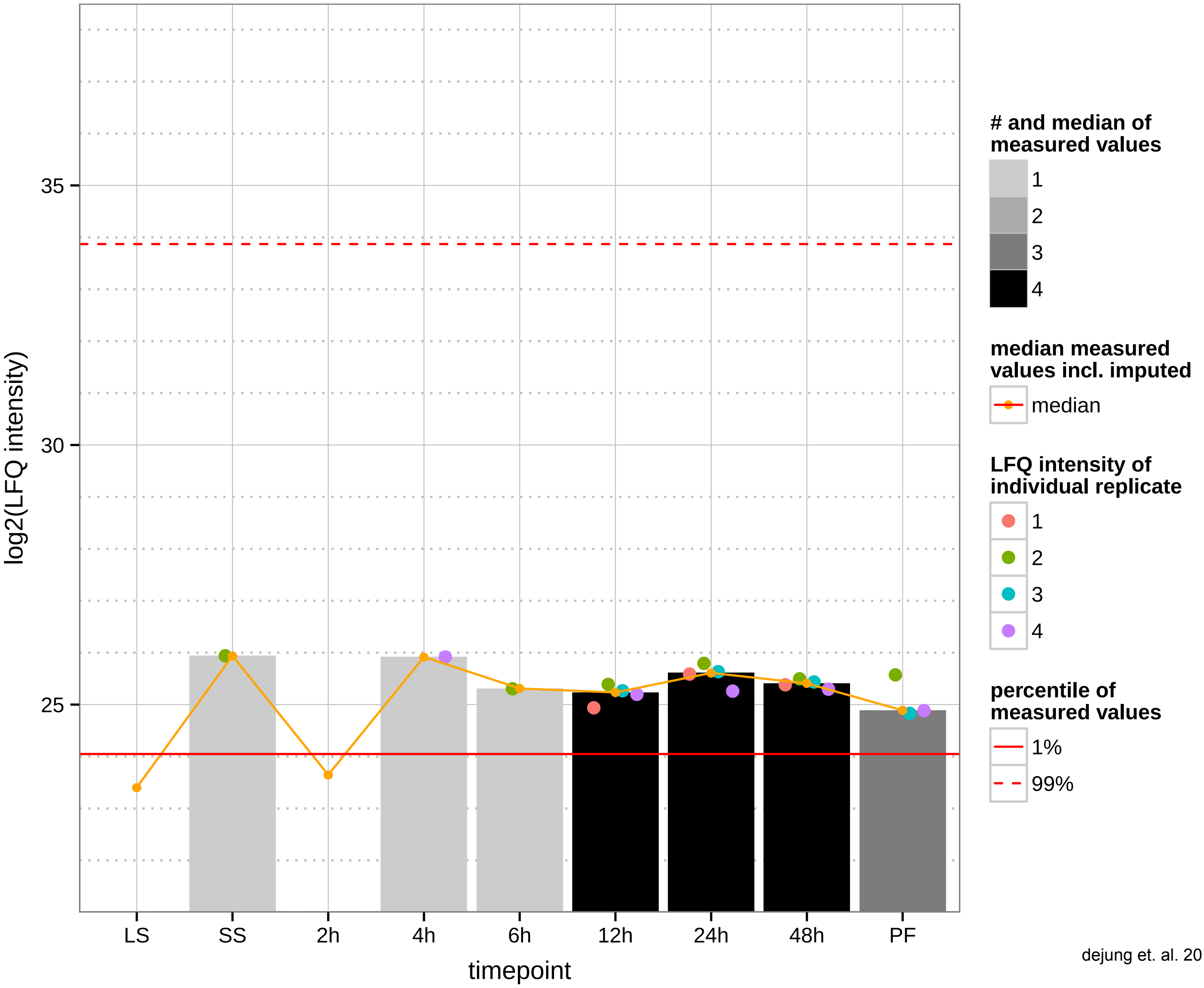
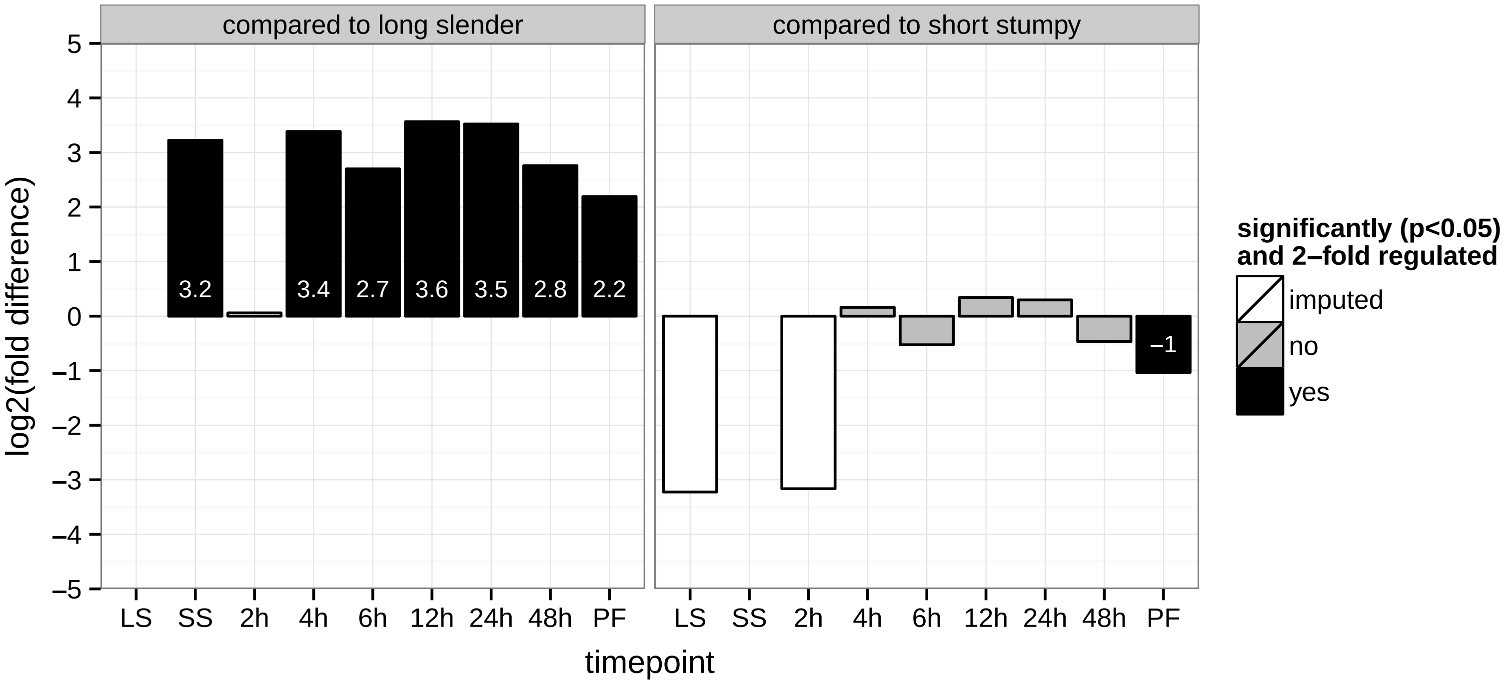
hypothetical protein, conserved
Tb927.11.6190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

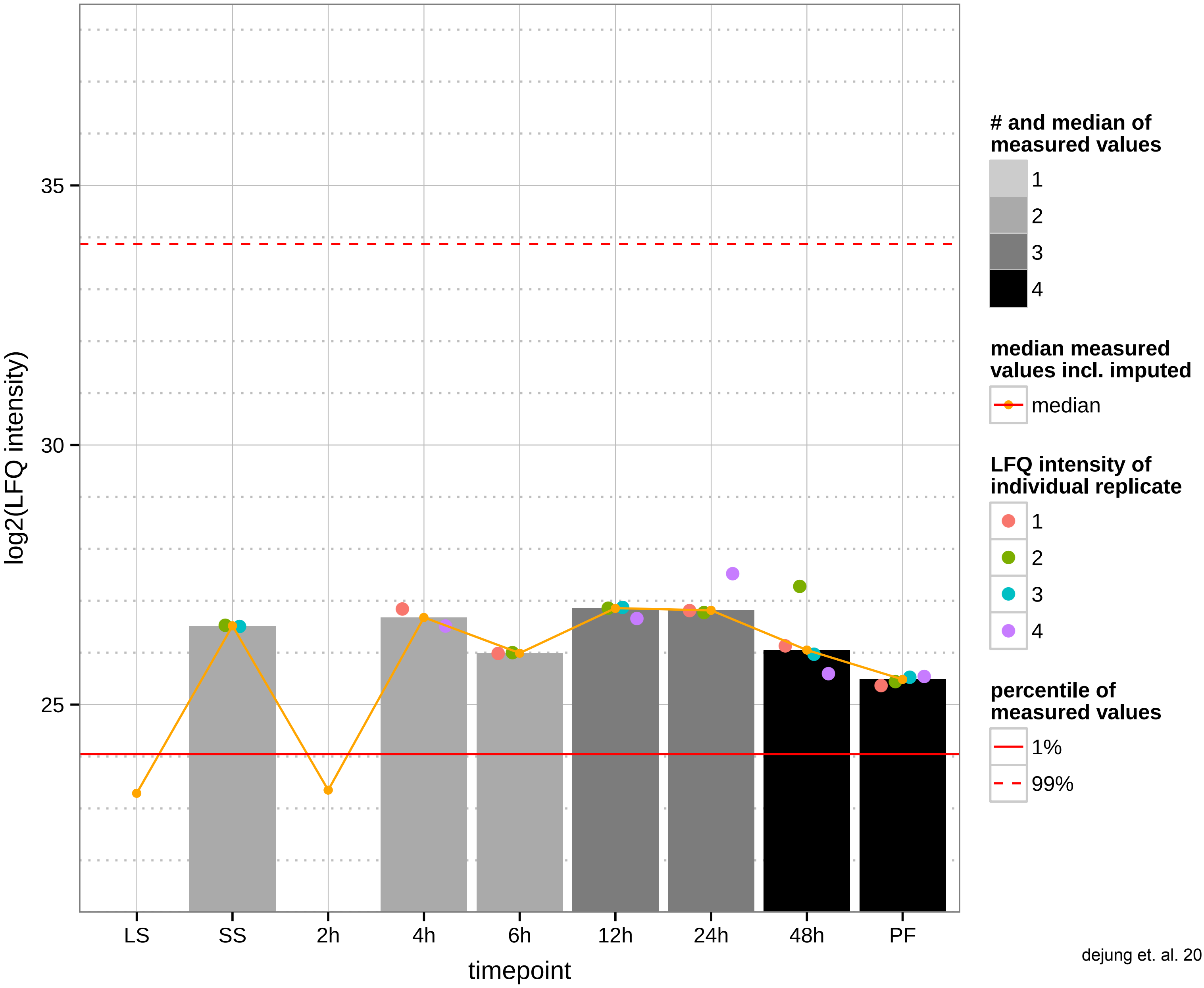




dejung et. al. 2015

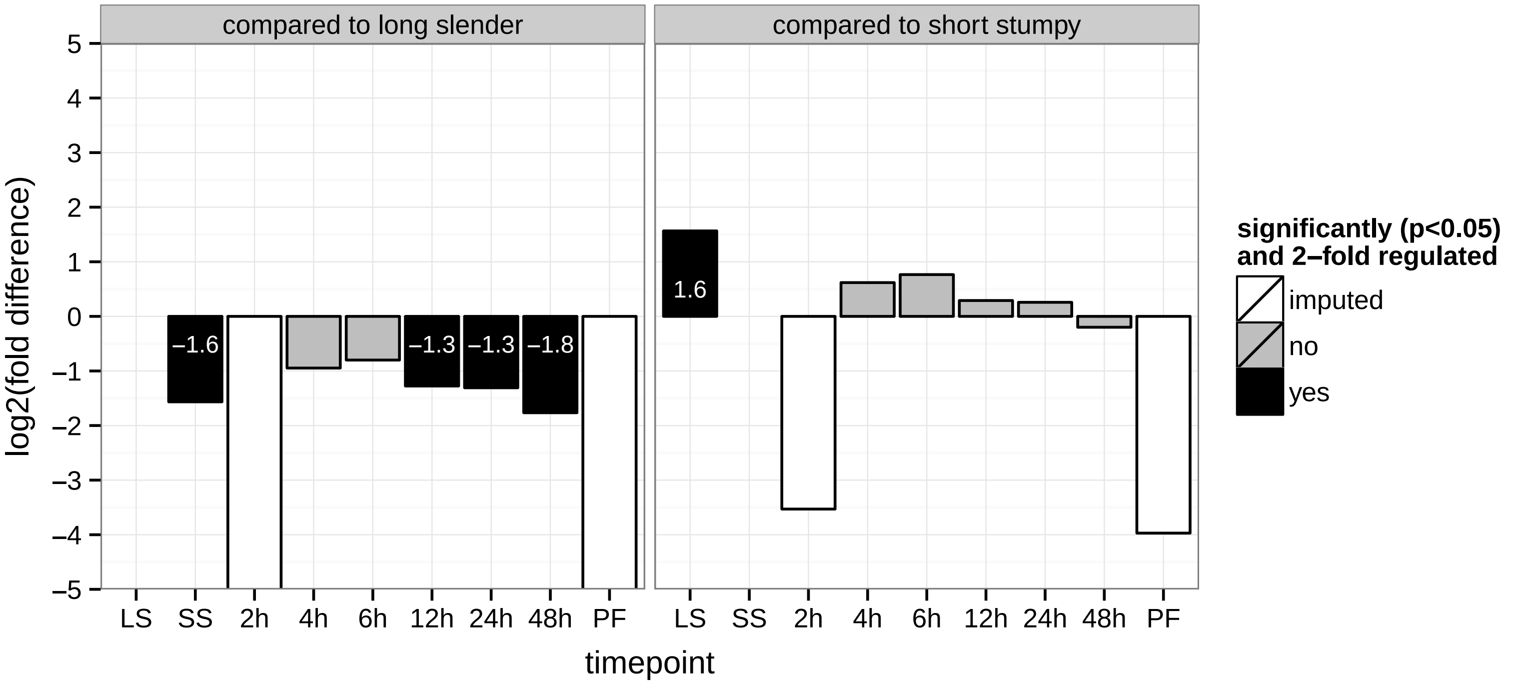
hypothetical protein, conserved
Tb927.11.8700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

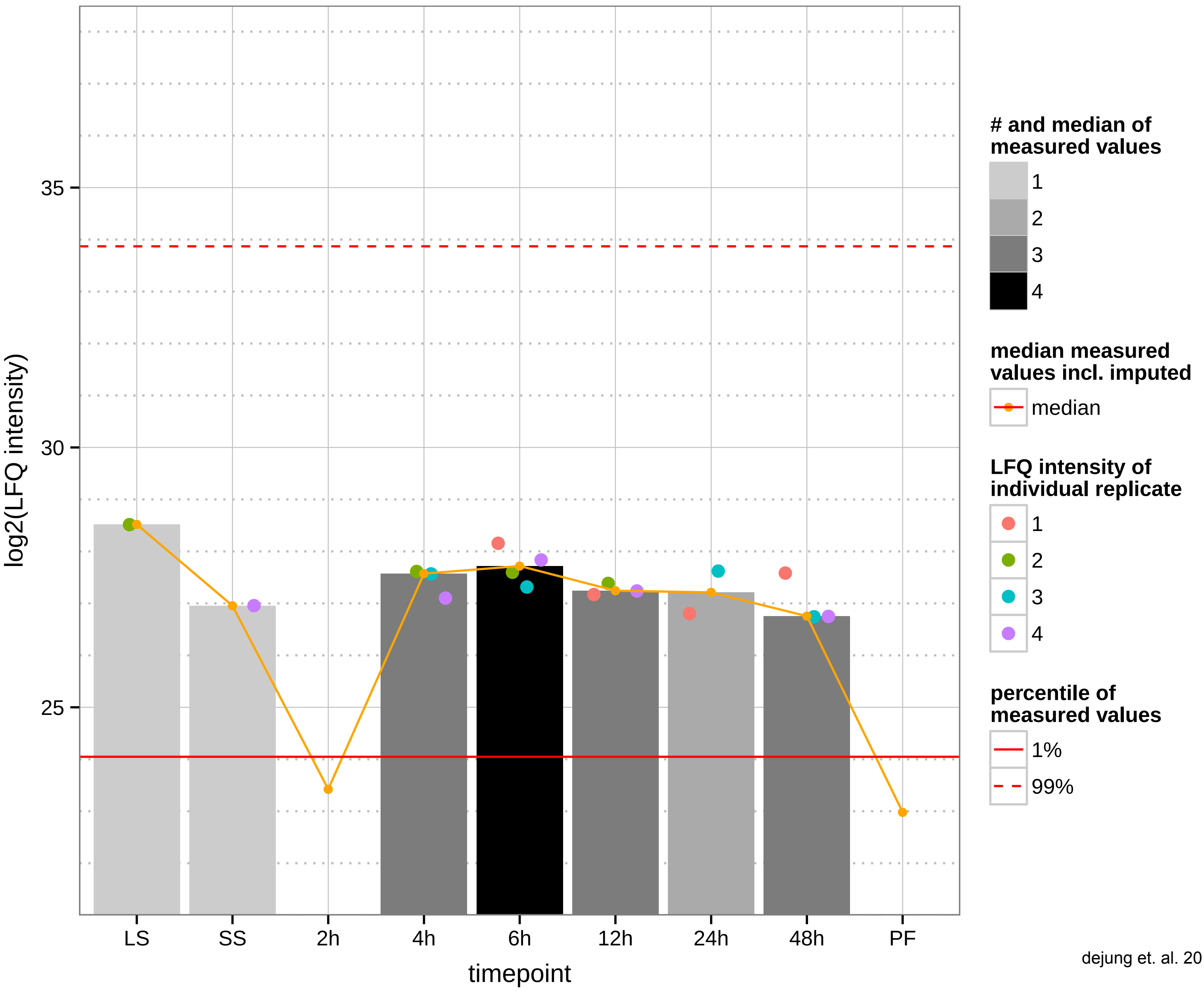




dejung et. al. 2015

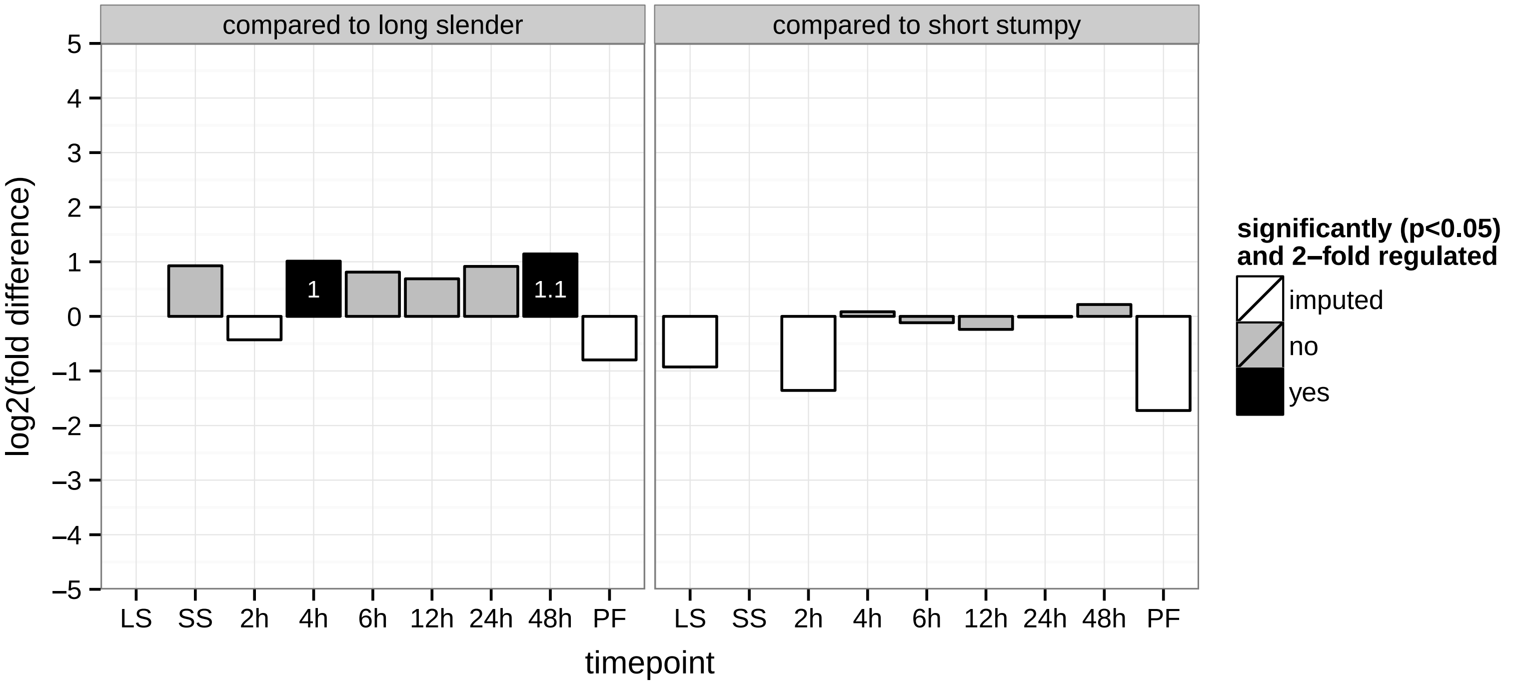
acyl–CoA binding protein, putative (ACBP)
Tb927.4.2010
AGOF: fatty–acyl–CoA binding
AGOC: null
AGOP: fatty acid metabolic process
PGOF: fatty–acyl–CoA binding
PGOC: null
PGOP: null

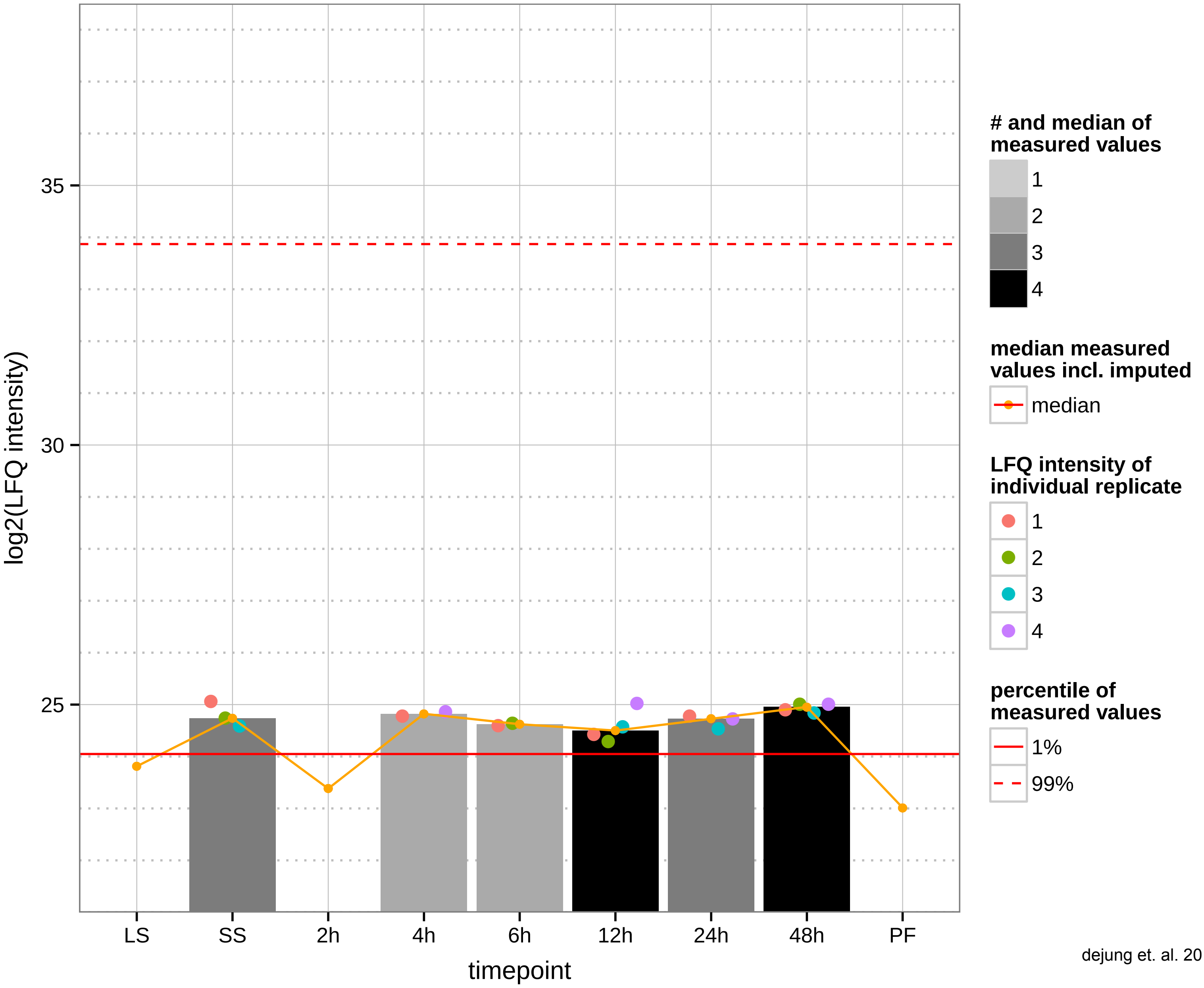




dejung et. al. 2015

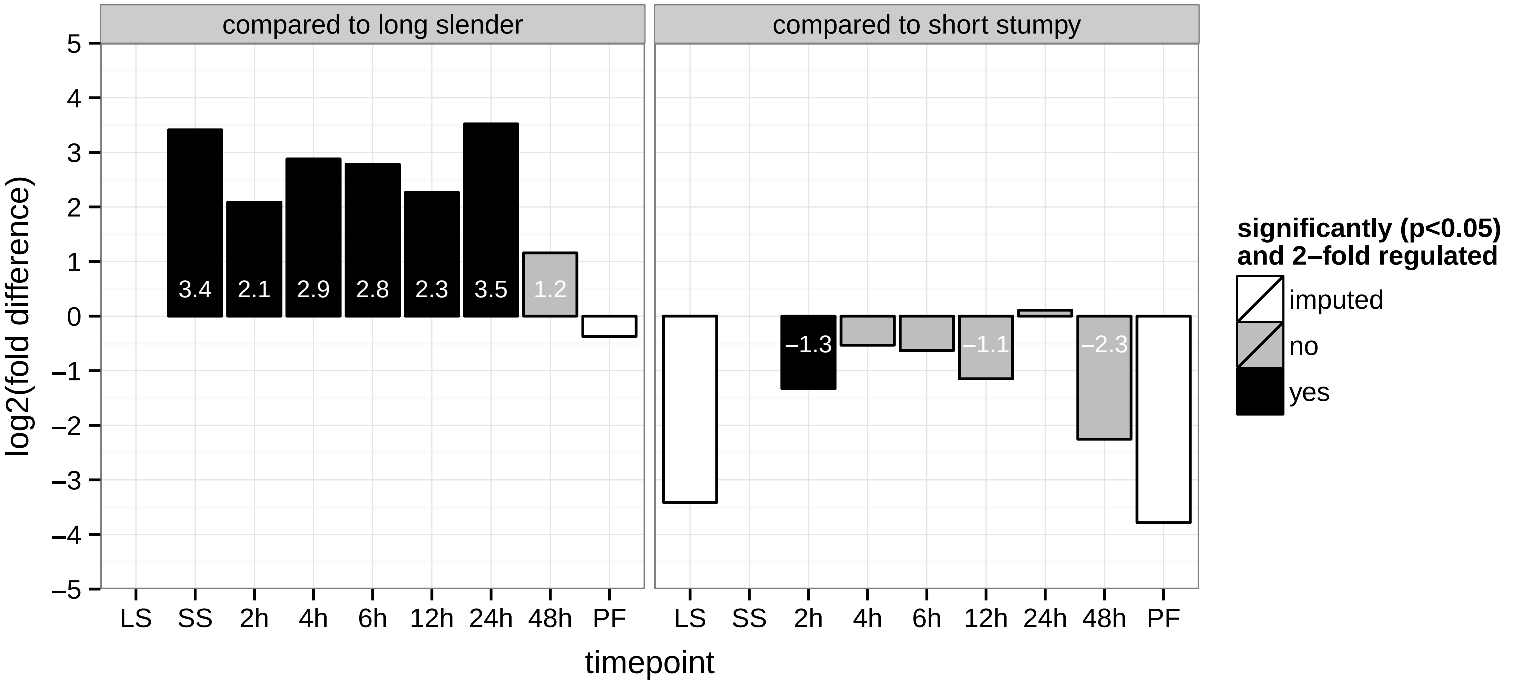
hypothetical protein, conserved
Tb927.4.2130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

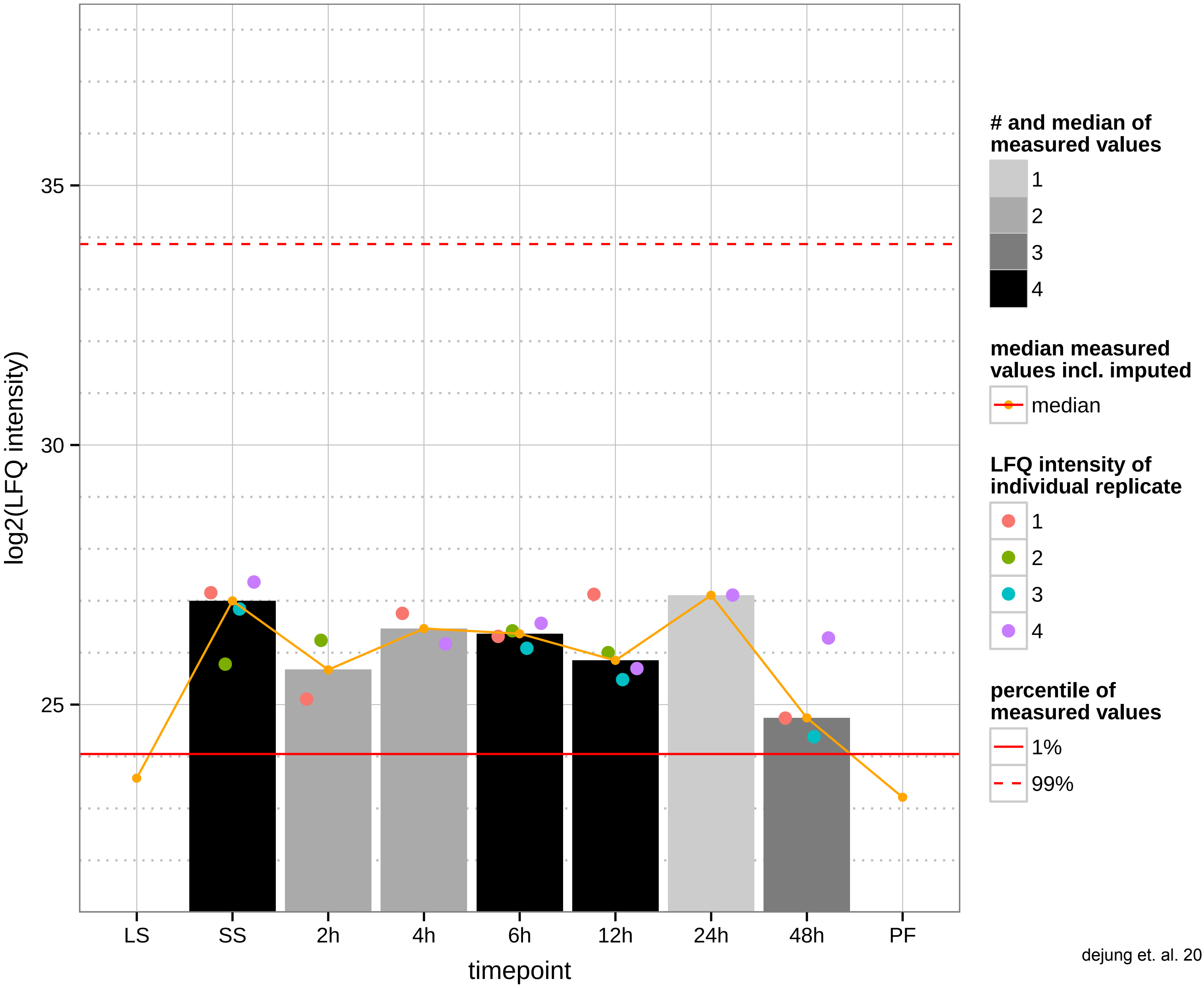




dejung et. al. 2015

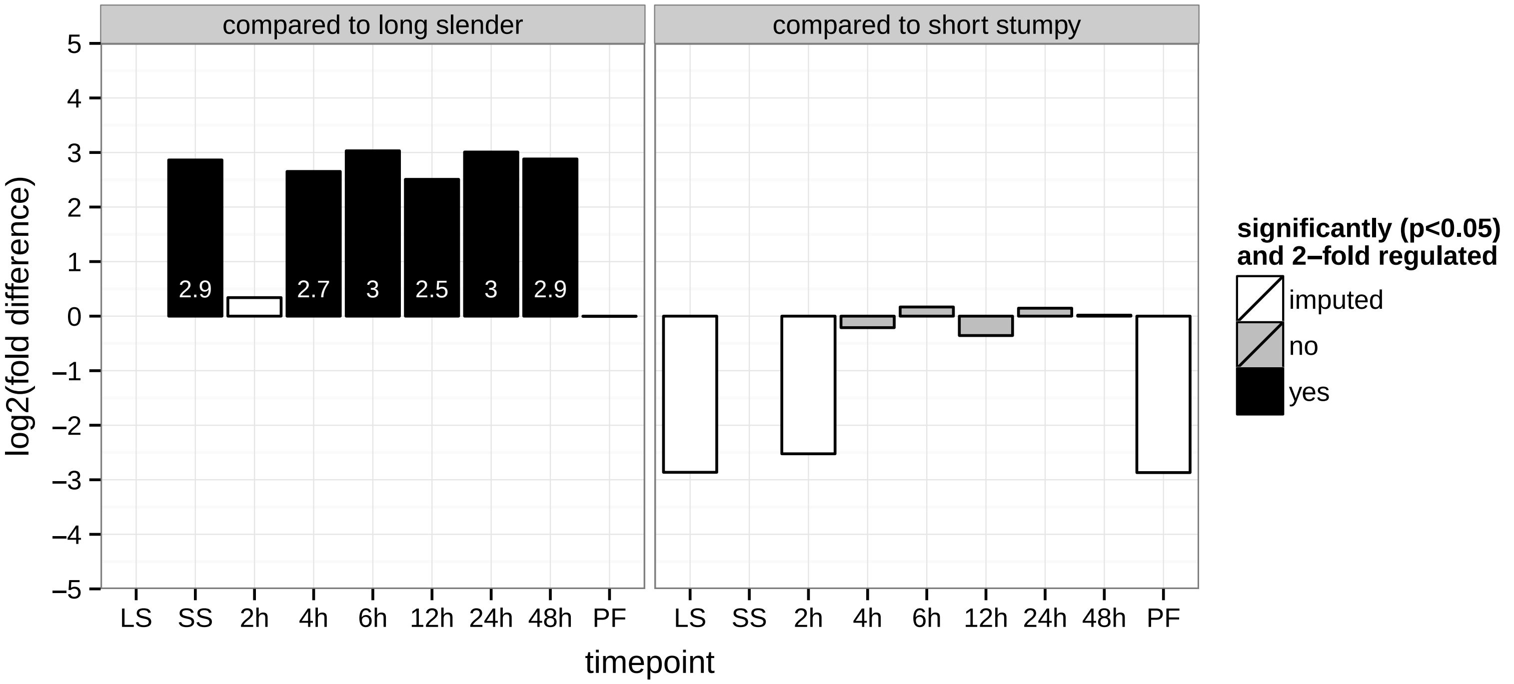
regulator of chromosome condensation, putative
Tb927.7.1190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

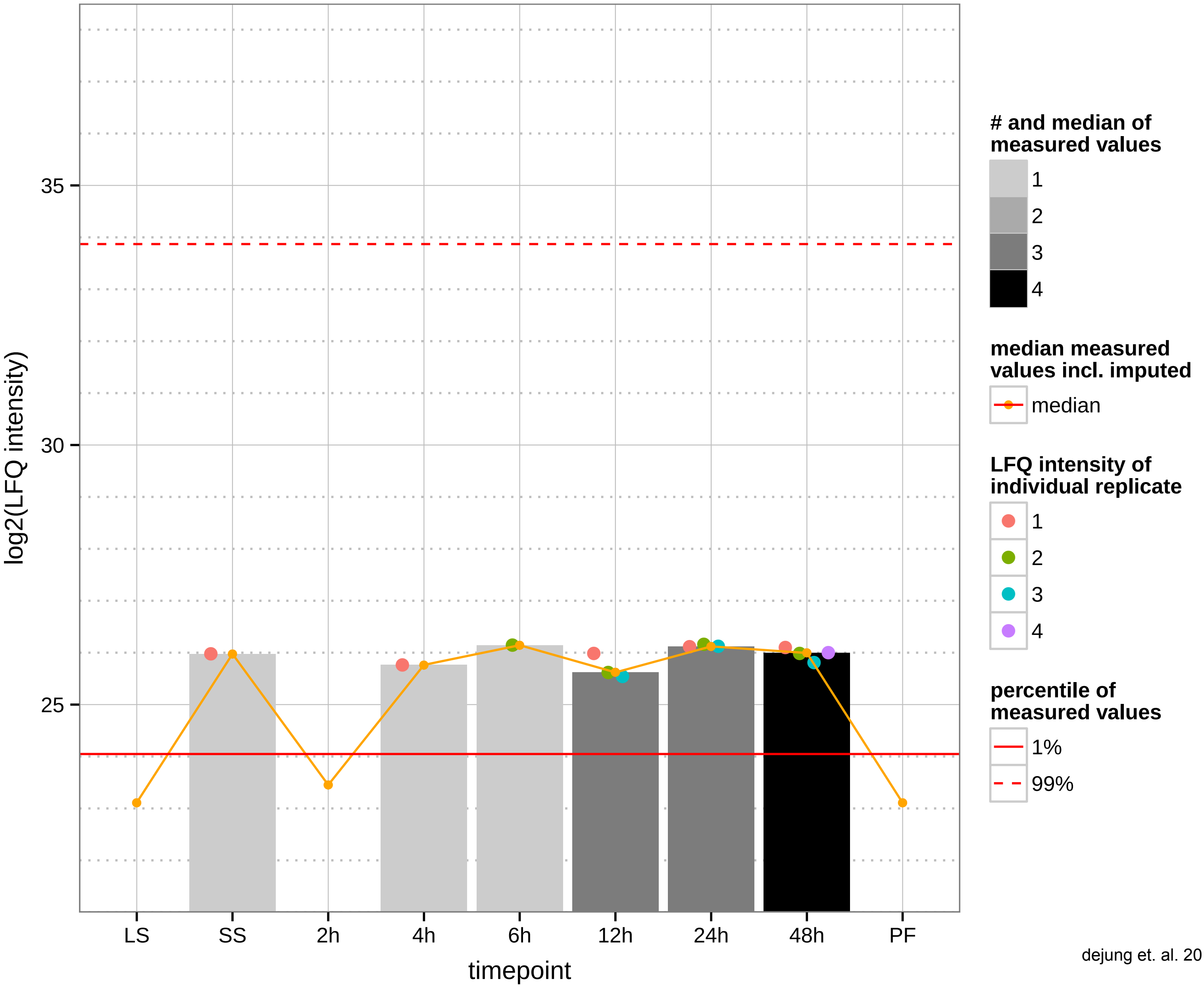




dejung et. al. 2015

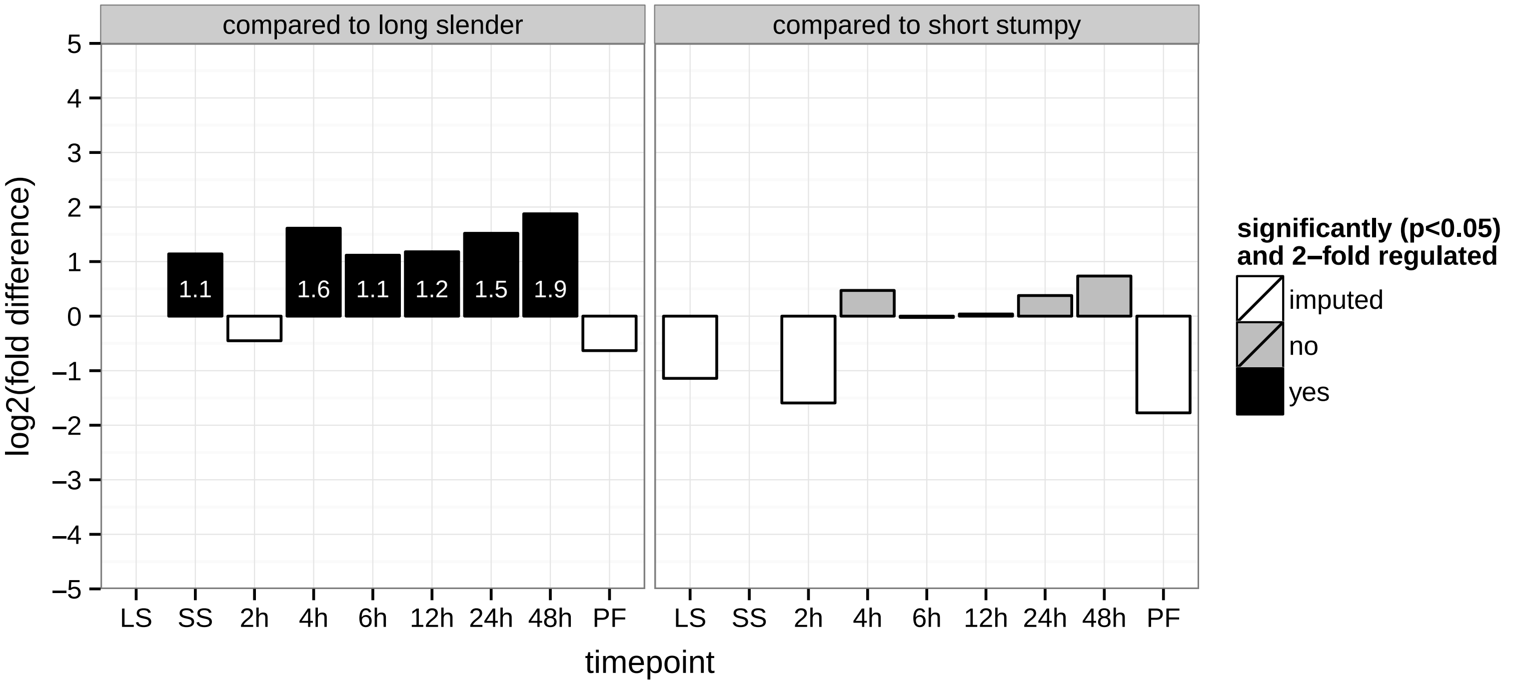
hypothetical protein, conserved
Tb927.7.4140
AGOF: RNA binding, structural constituent of ribosome
AGOC: intracellular, mitochondrion, ribosome
AGOP: translation
PGOF: RNA binding, structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation

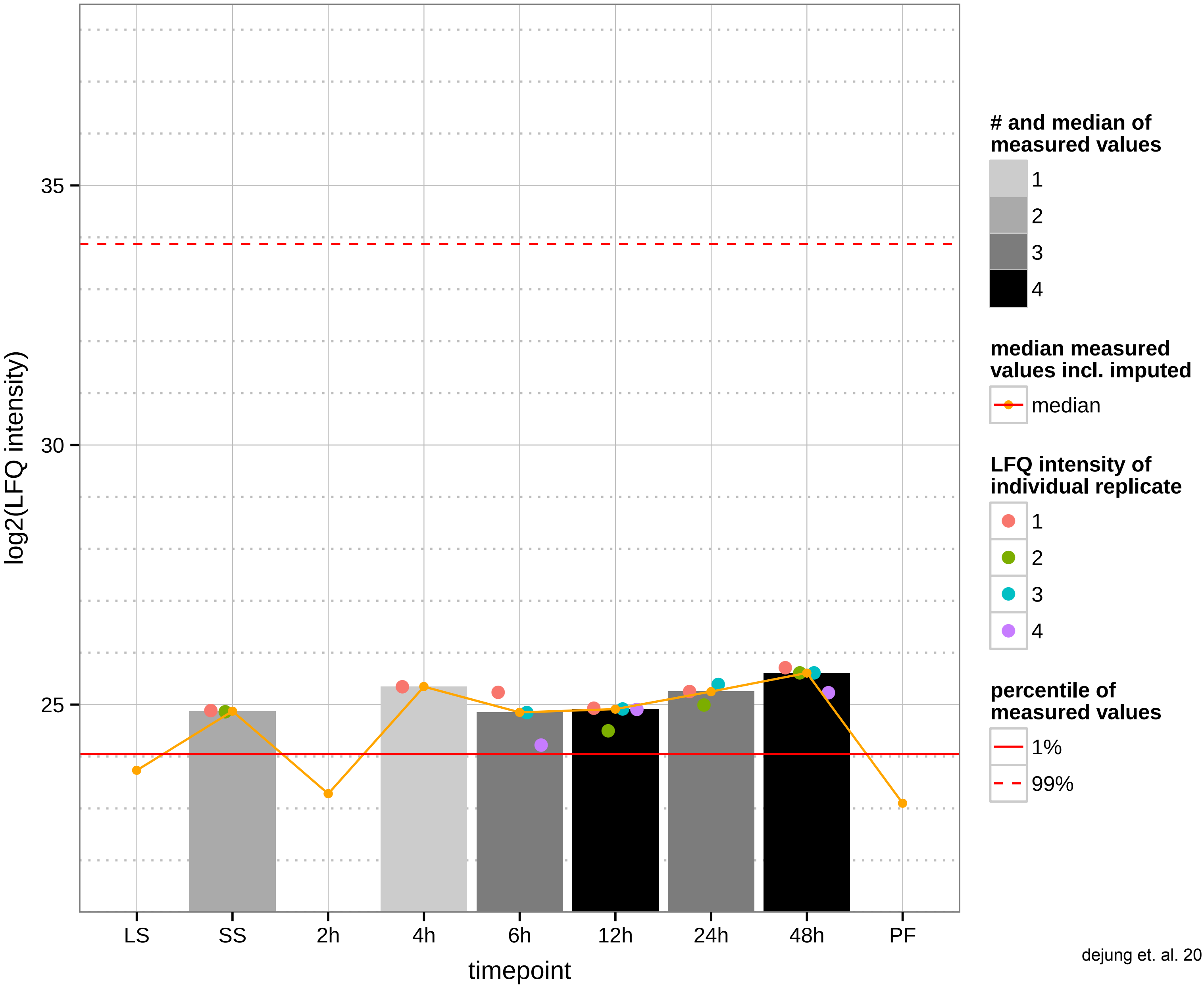




dejung et. al. 2015

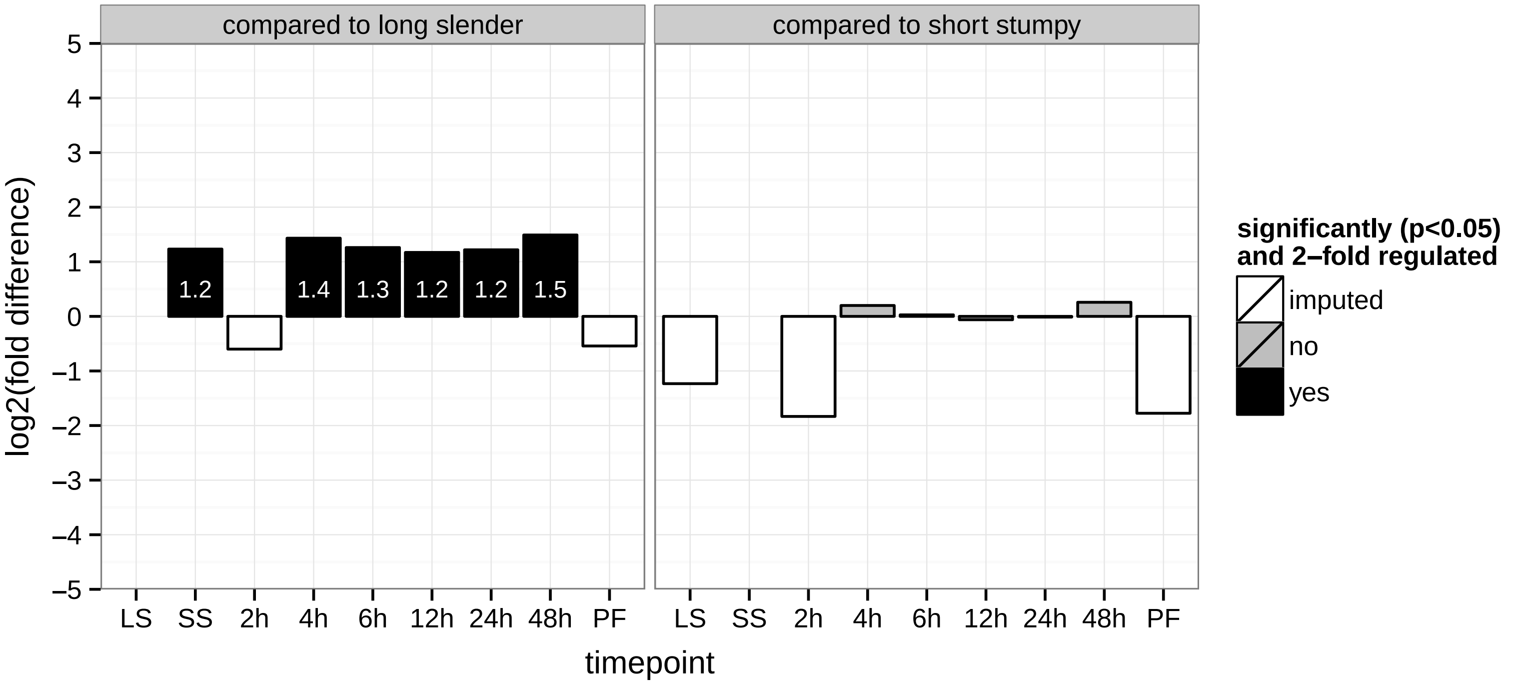
protein kinase, putative
Tb927.7.6220
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: cytokinesis after mitosis, growth, protein phosphorylation
PGOF: ATP binding, protein binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation

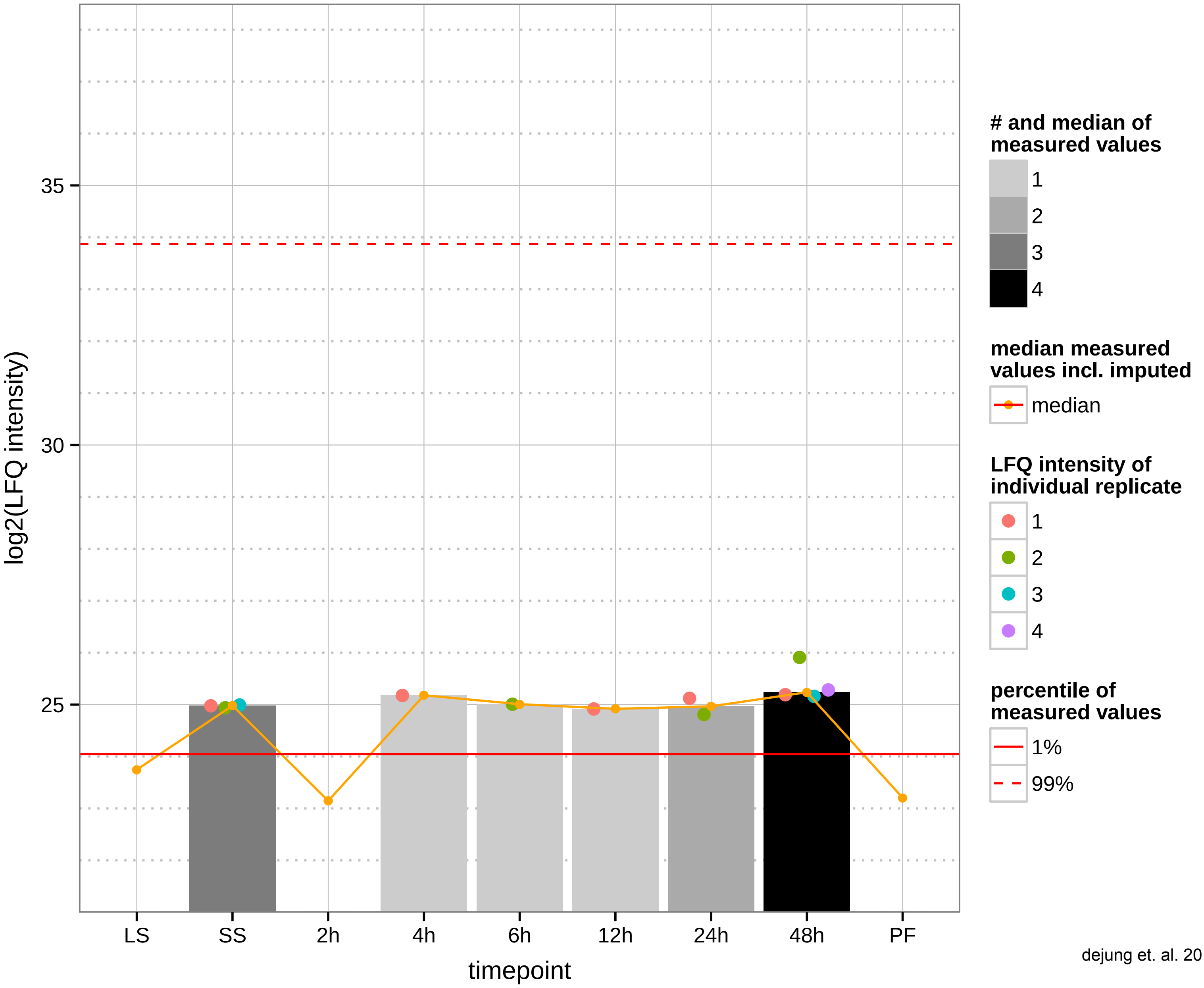




dejung et. al. 2015

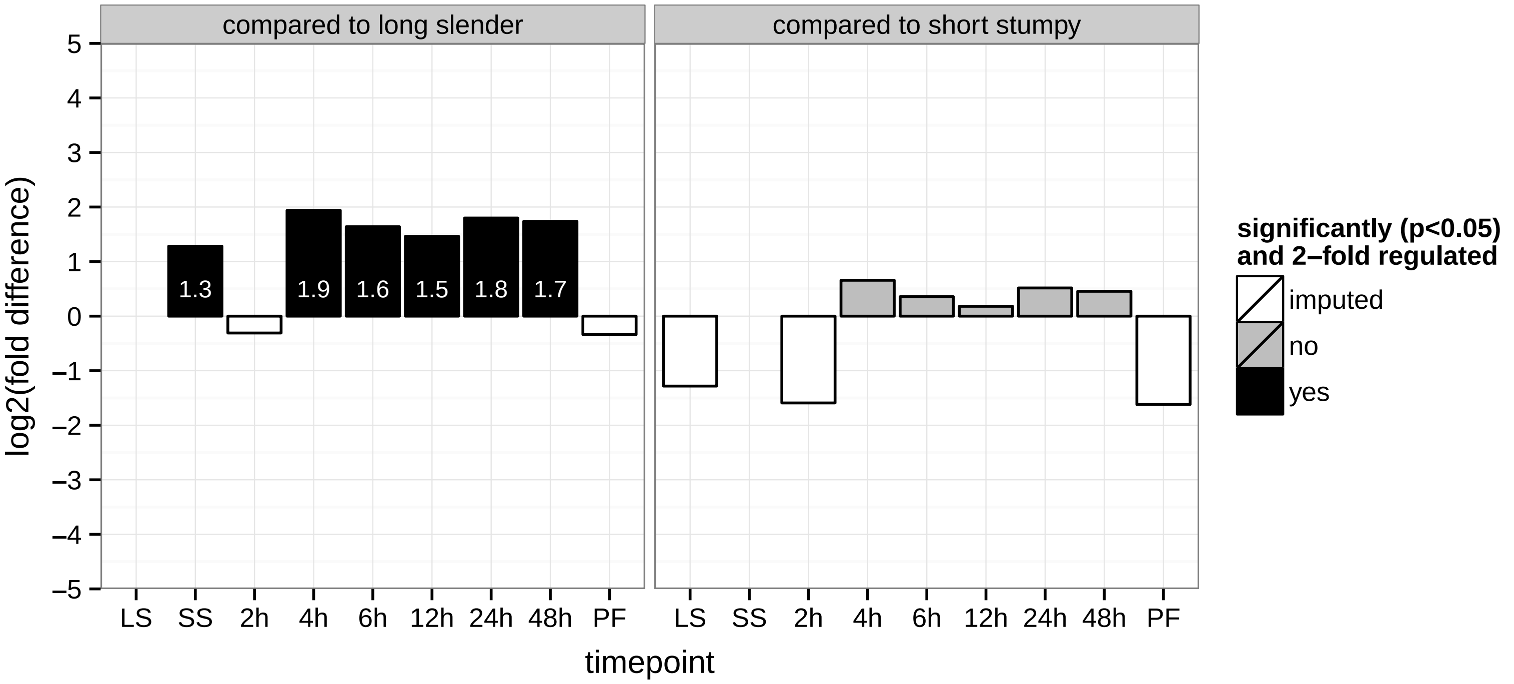
hypothetical protein, conserved
Tb927.8.1050
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

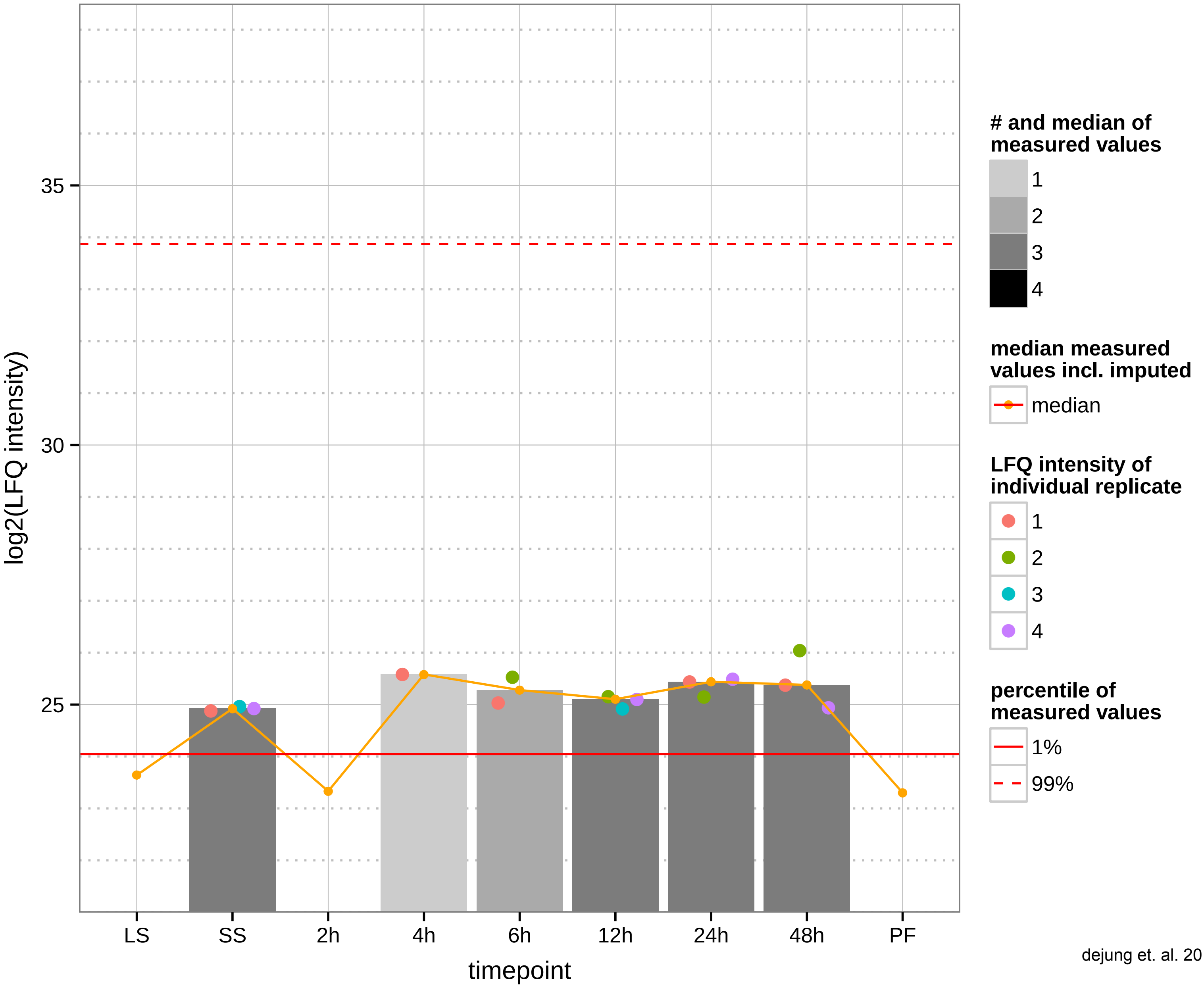




dejung et. al. 2015

vacuolar−type Ca2+−ATPase, putative
Tb927.8.1160
AGOF: ATP binding, calcium−transporting ATPase activity
AGOC: acidocalcisome, integral to membrane, membrane
AGOP: ATP biosynthetic process, calcium ion transport, cell growth, cellular calcium ion homeostasis, metabolic process
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, calcium−trar
PGOC: membrane
PGOP: ATP biosynthetic process, calcium ion transmembrane transport, cation transport, metabolic process





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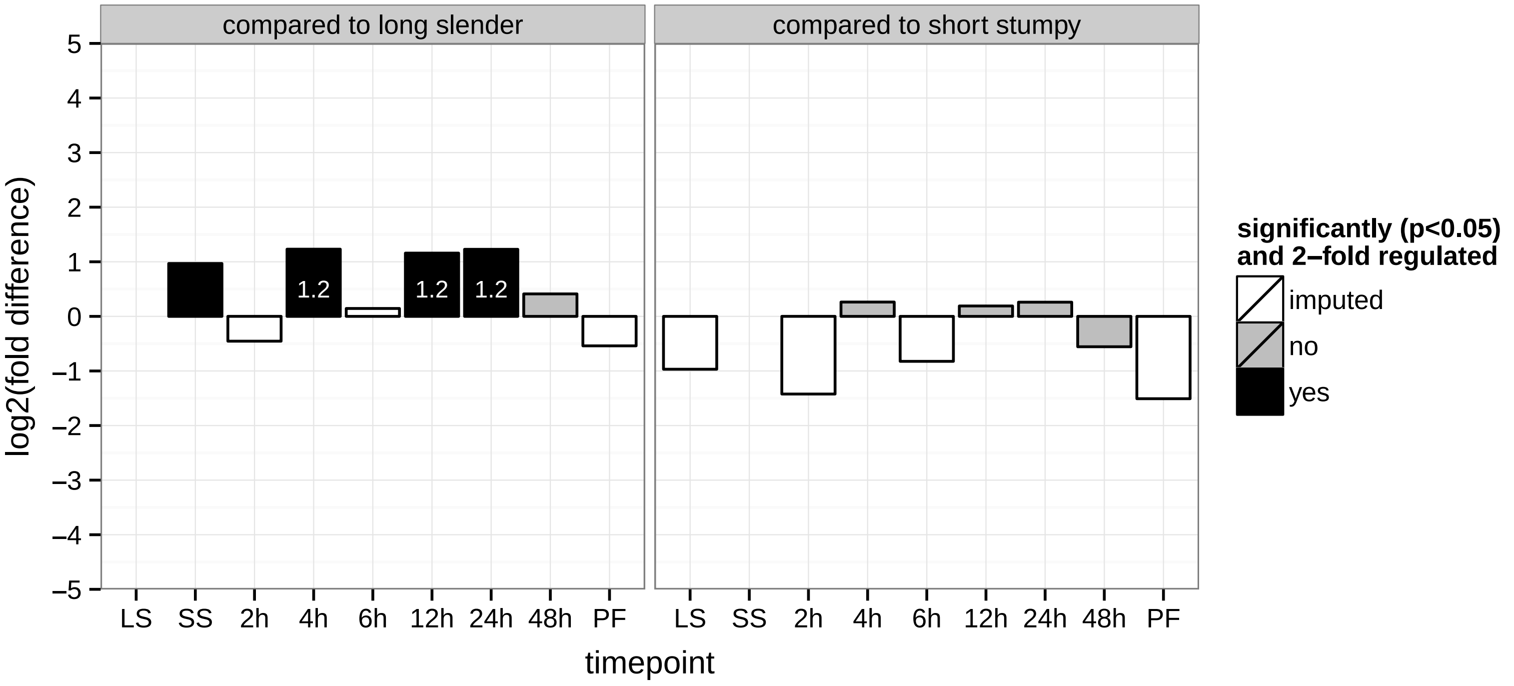
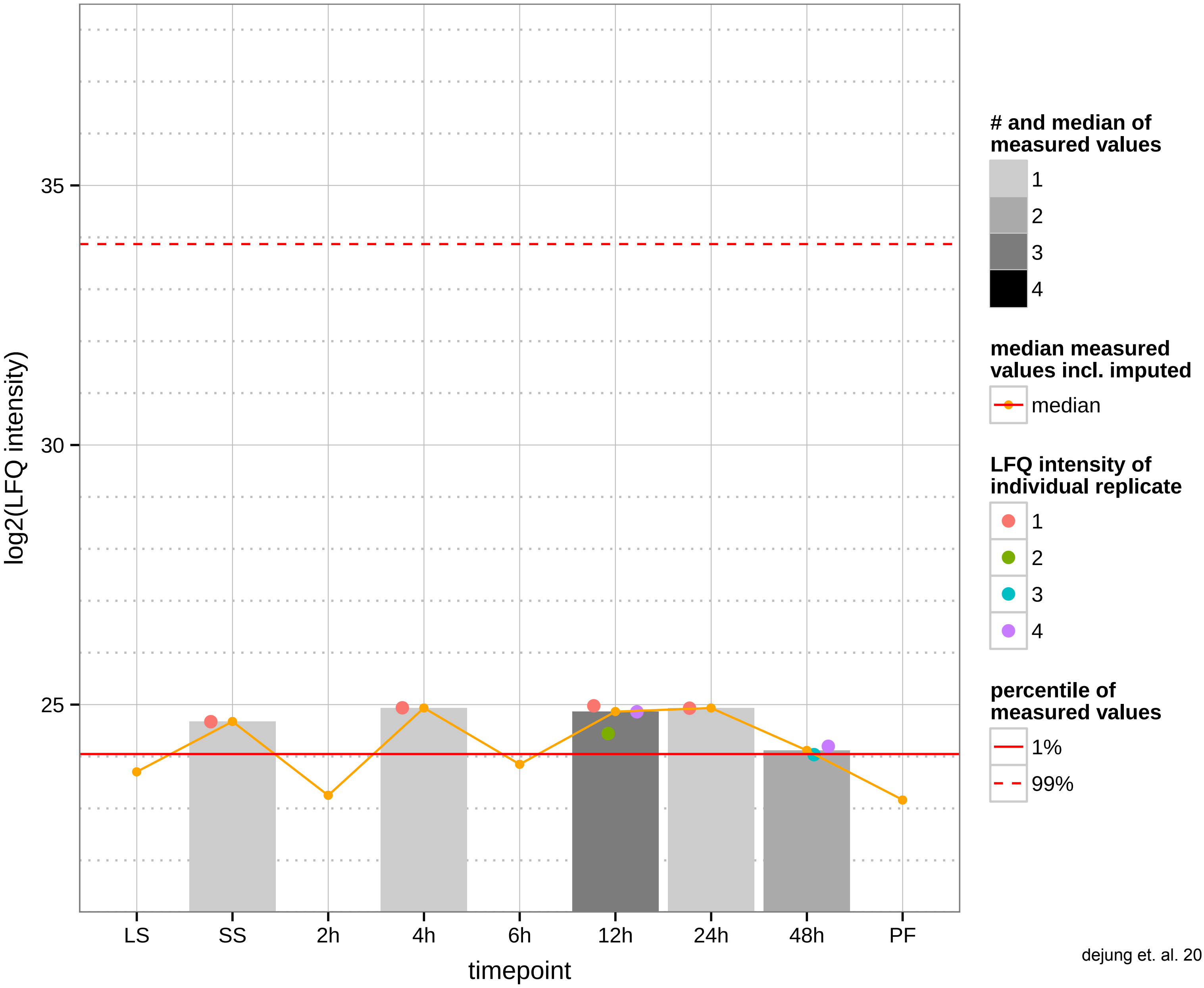
electron transfer flavoprotein–ubiquinone oxidoreductase, putative
Tb927.8.1240
AGOF: electron–transferring–flavoprotein dehydrogenase activity
AGOC: mitochondrion
AGOP: oxidation–reduction process
PGOF: electron–transferring–flavoprotein dehydrogenase activity, iron–sulfur cluster binding
PGOC: null
PGOP: oxidation–reduction process





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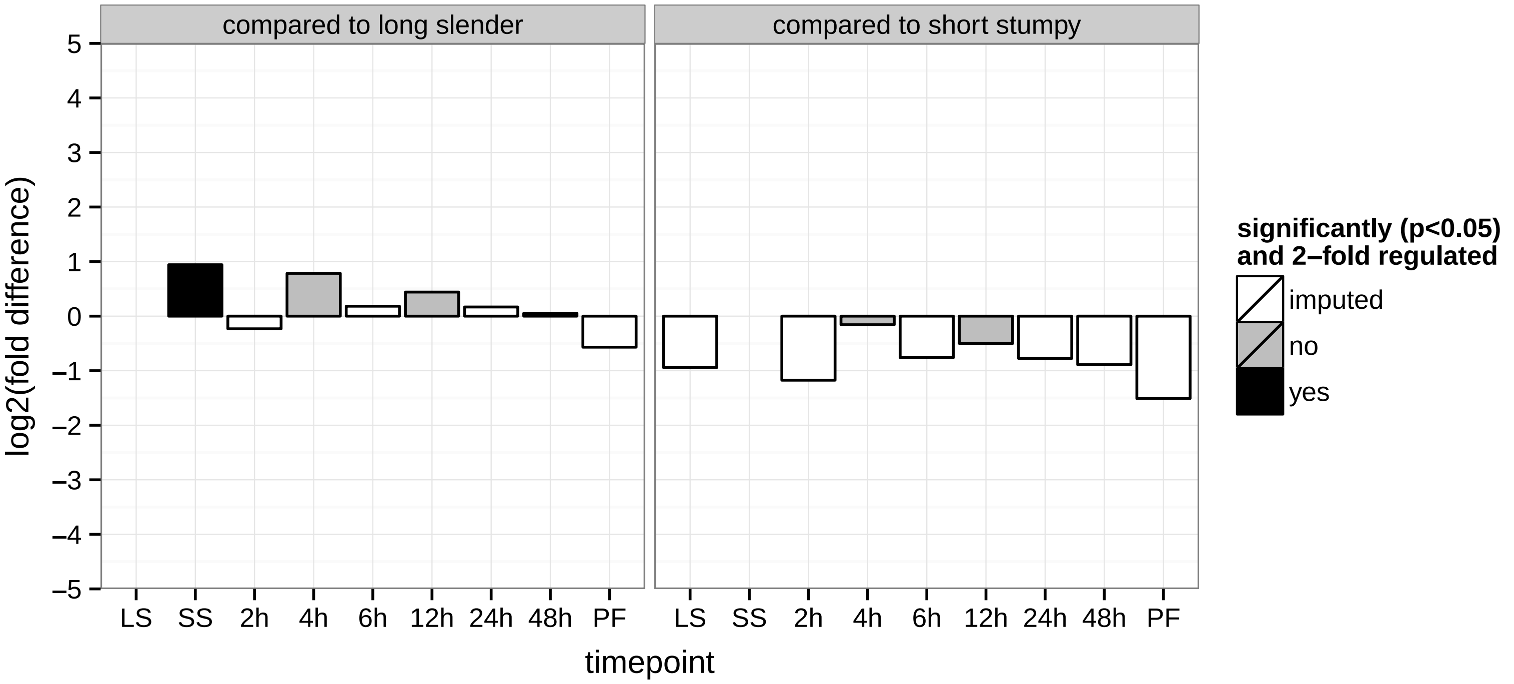
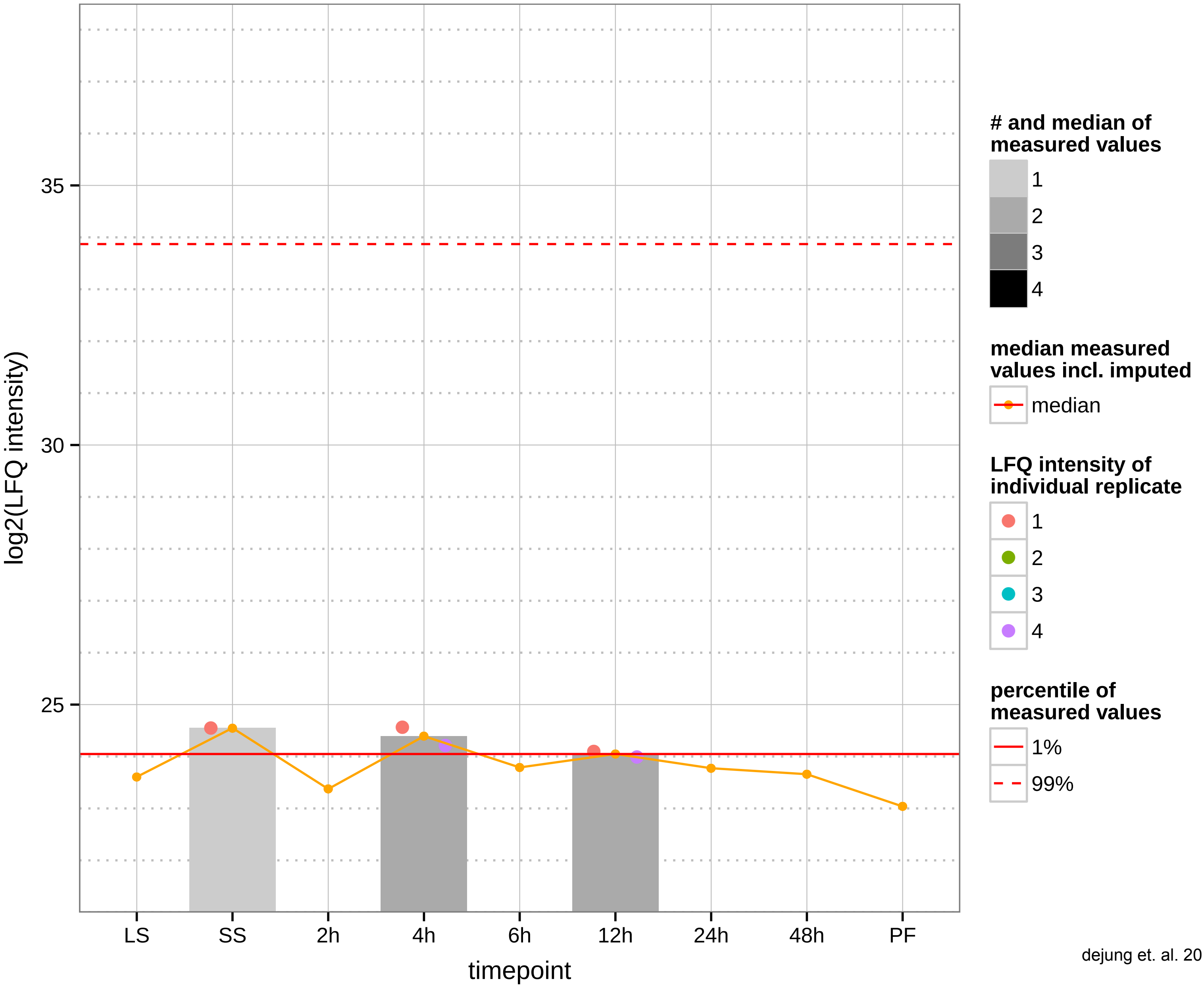
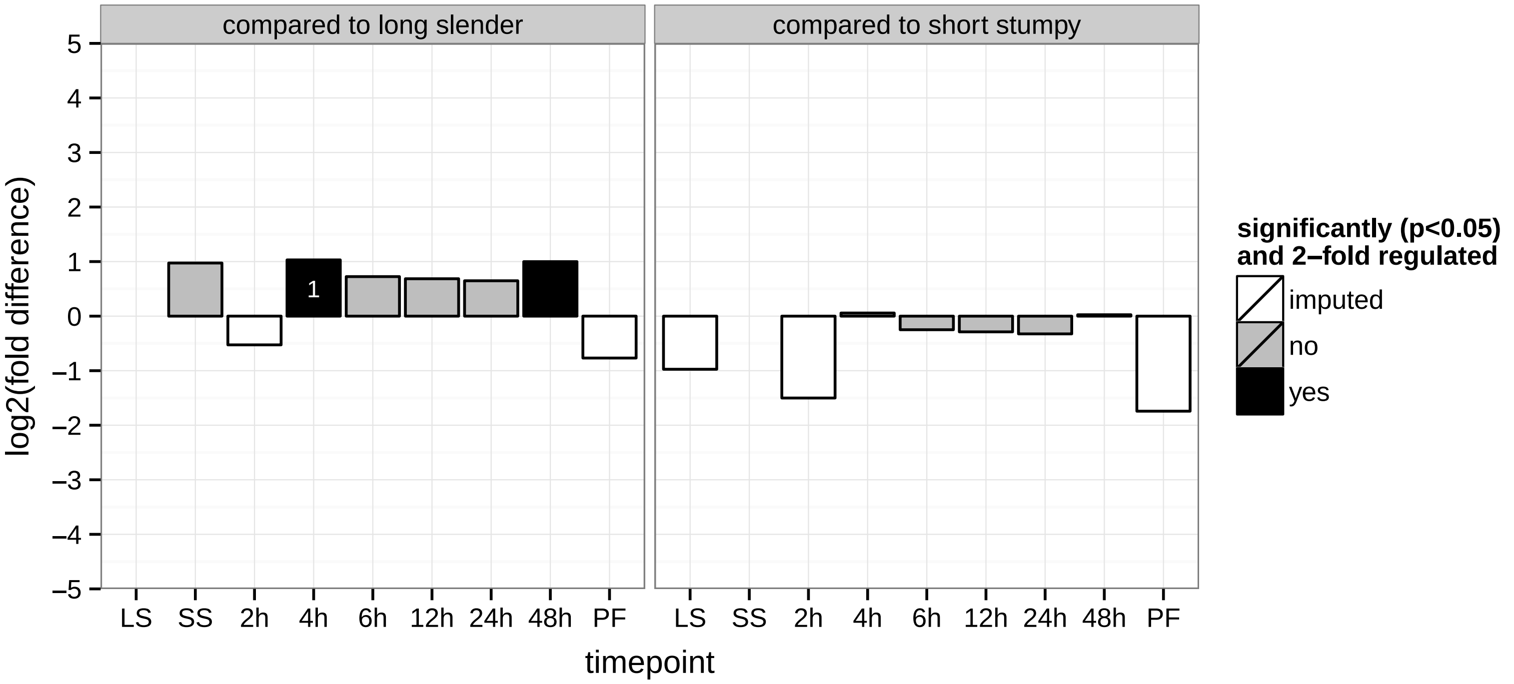
phosphatidylinositol 3–kinase, putative, PI3–kinase, putative (PI3K)
Tb927.8.6210
AGOF: 1–phosphatidylinositol–3–kinase activity, phosphotransferase activity, alcohol group as acceptor
AGOC: phosphatidylinositol 3–kinase complex
AGOP: phosphatidylinositol phosphorylation, phosphatidylinositol–mediated signaling
PGOF: binding, phosphotransferase activity, alcohol group as acceptor, protein binding, transferase activity, transferring phosp
PGOC: null
PGOP: null

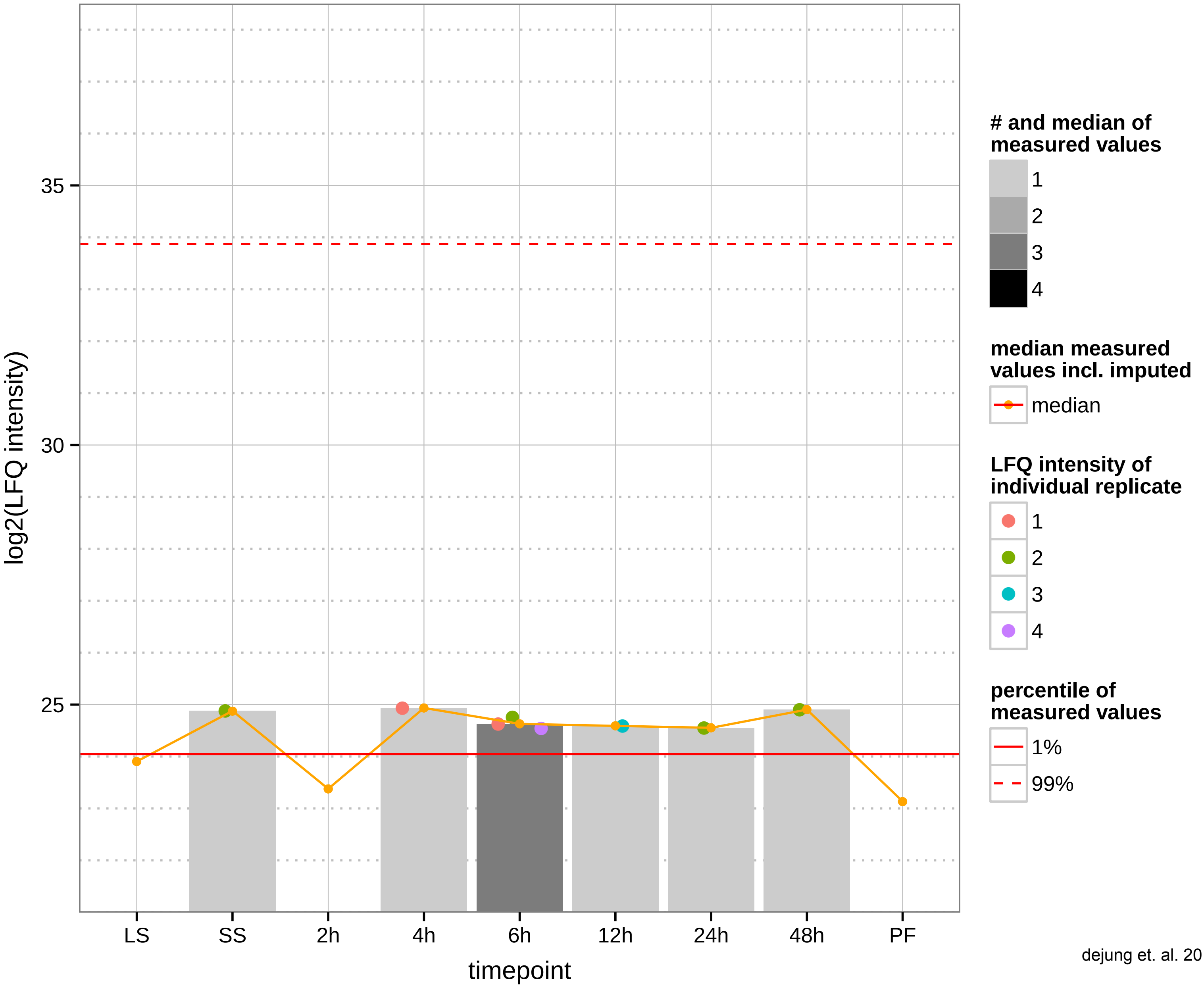




dejung et. al. 2015

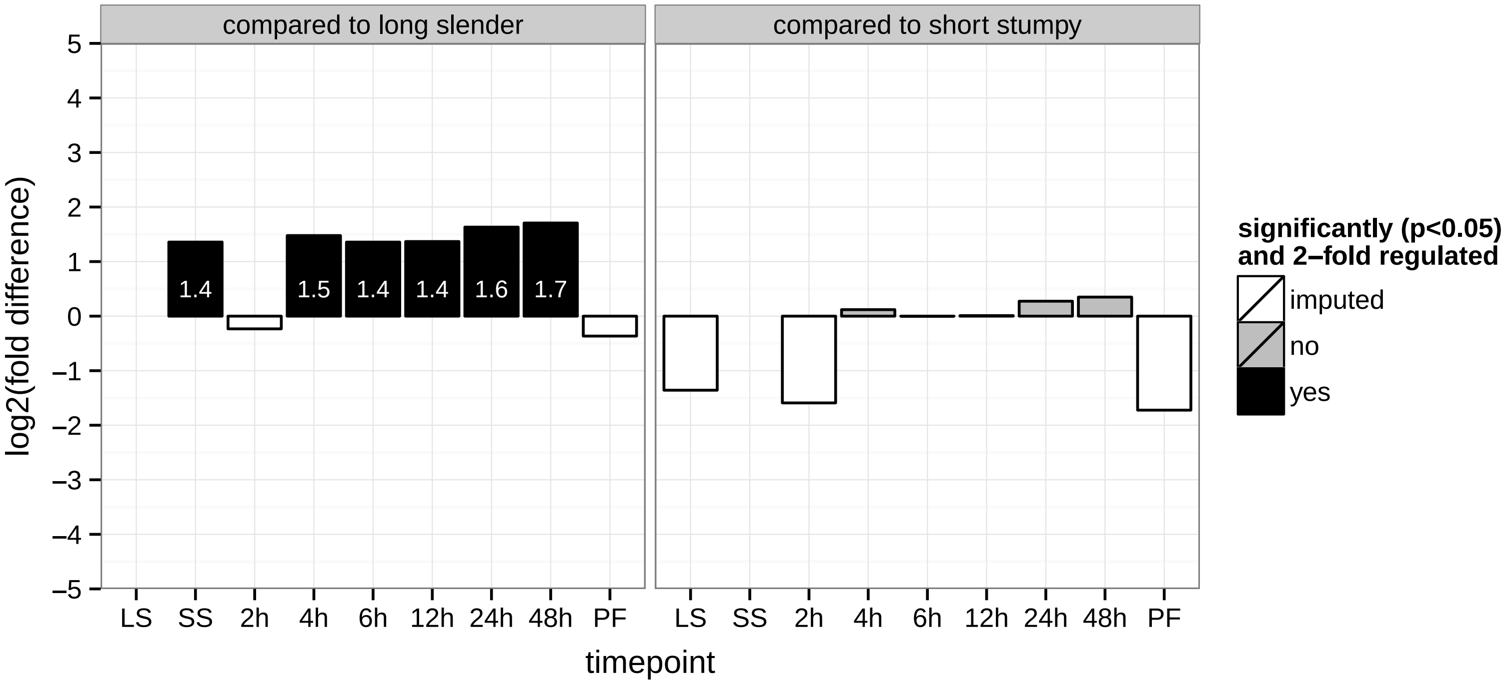
hypothetical protein, conserved
Tb927.9.13060
AGOF: voltage−gated potassium channel activity
AGOC: membrane, voltage−gated potassium channel complex
AGOP: potassium ion transport
PGOF: protein binding
PGOC: null
PGOP: protein homooligomerization

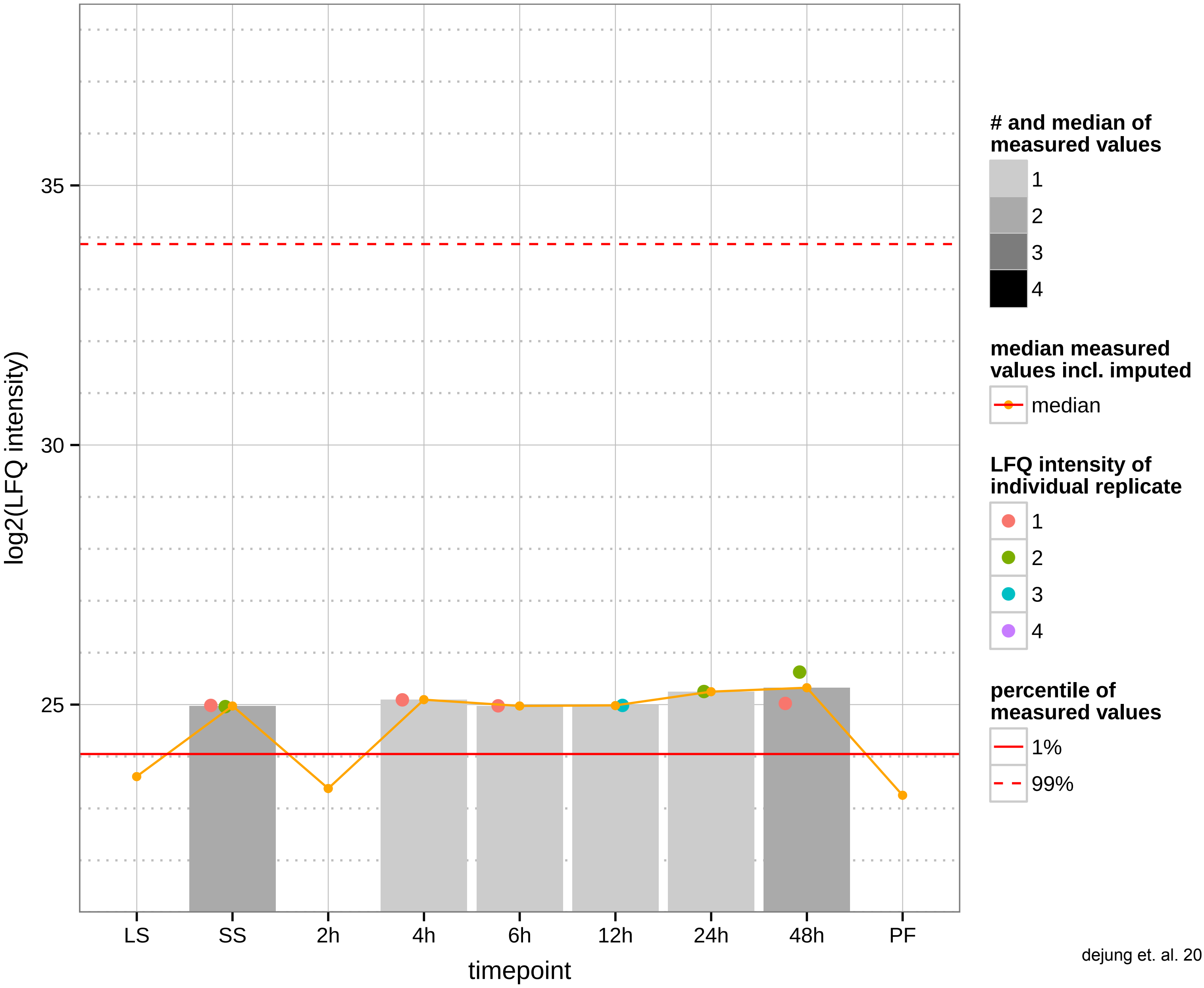




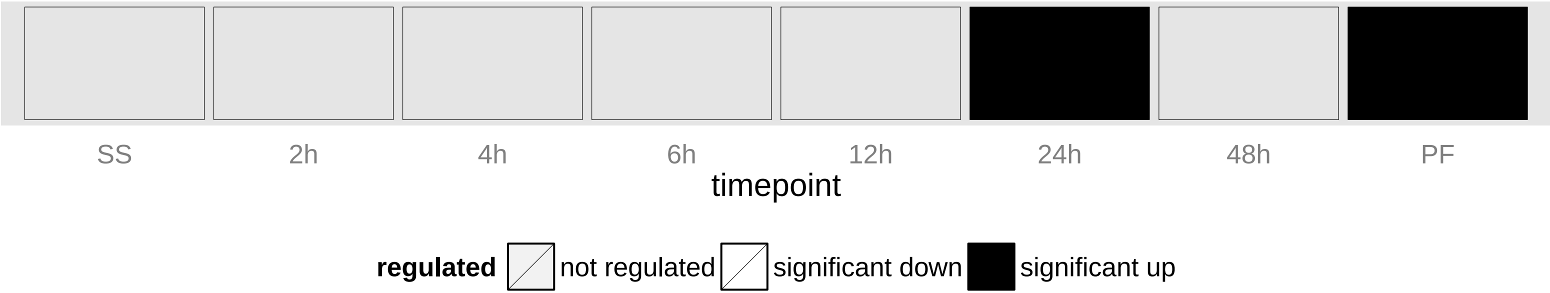
dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.9420
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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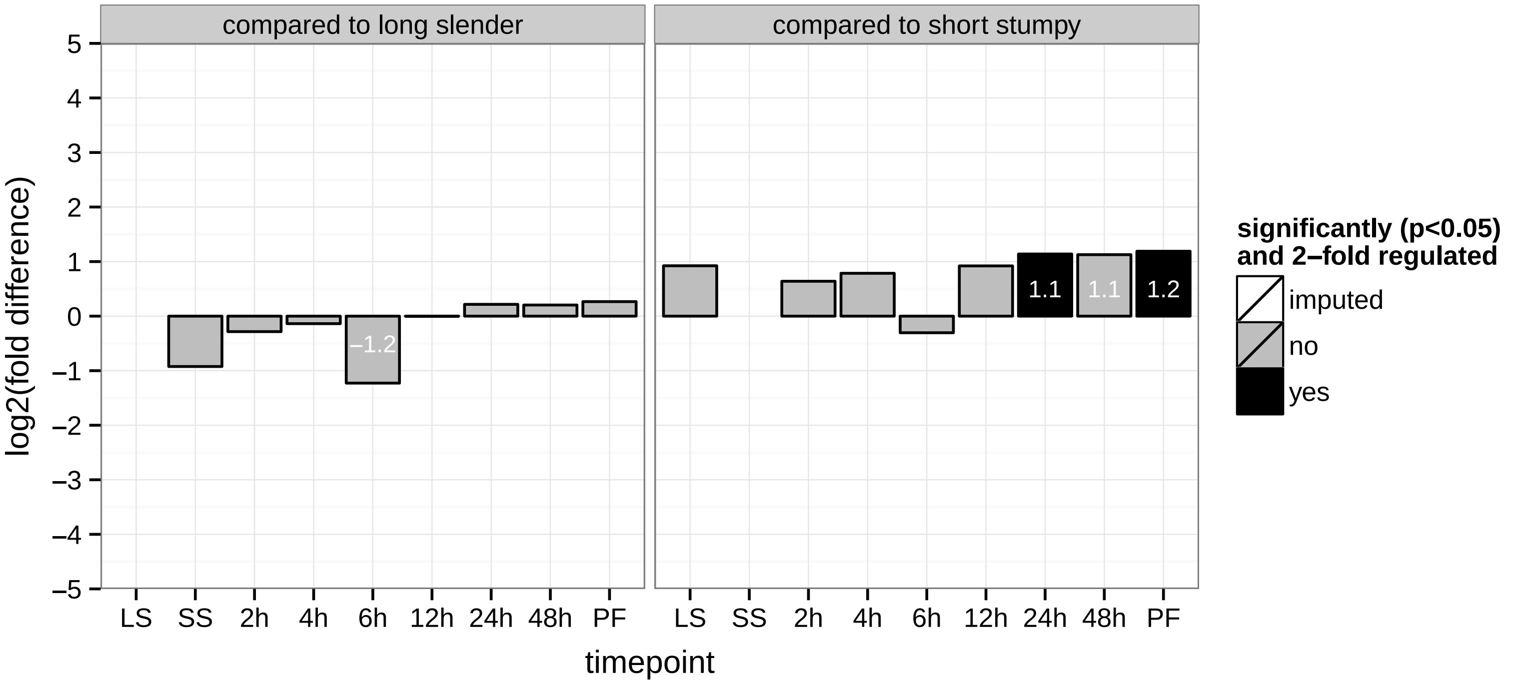
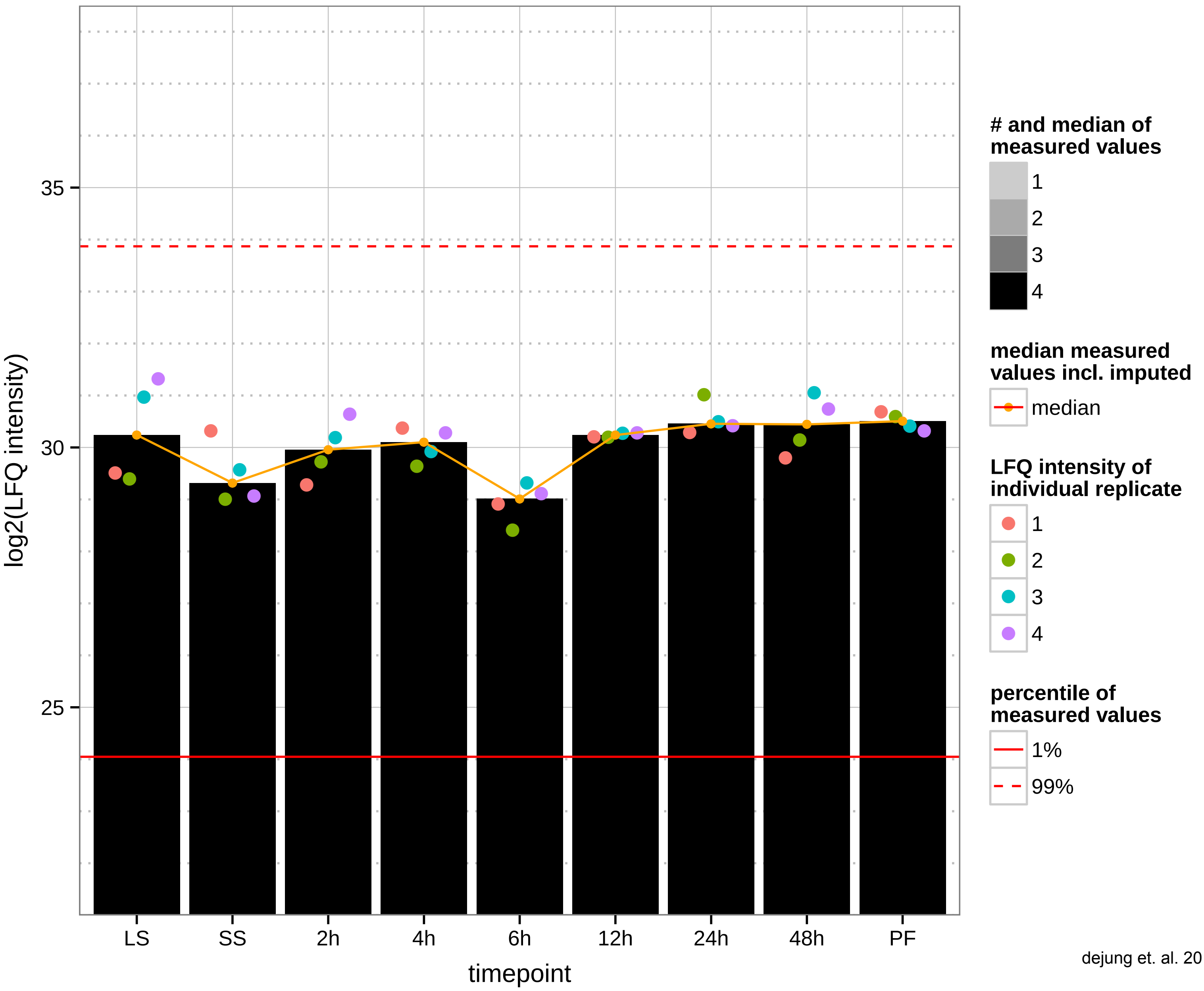
dynein light chain LC8, putative, chrXI additional, unordered contigs (DYNLL2), putative (DYNLL1)
Tb927.11.18680;Tb11.0845
AGOF: microtubule motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based process
PGOF: null
PGOC: microtubule associated complex
PGOP: microtubule–based process





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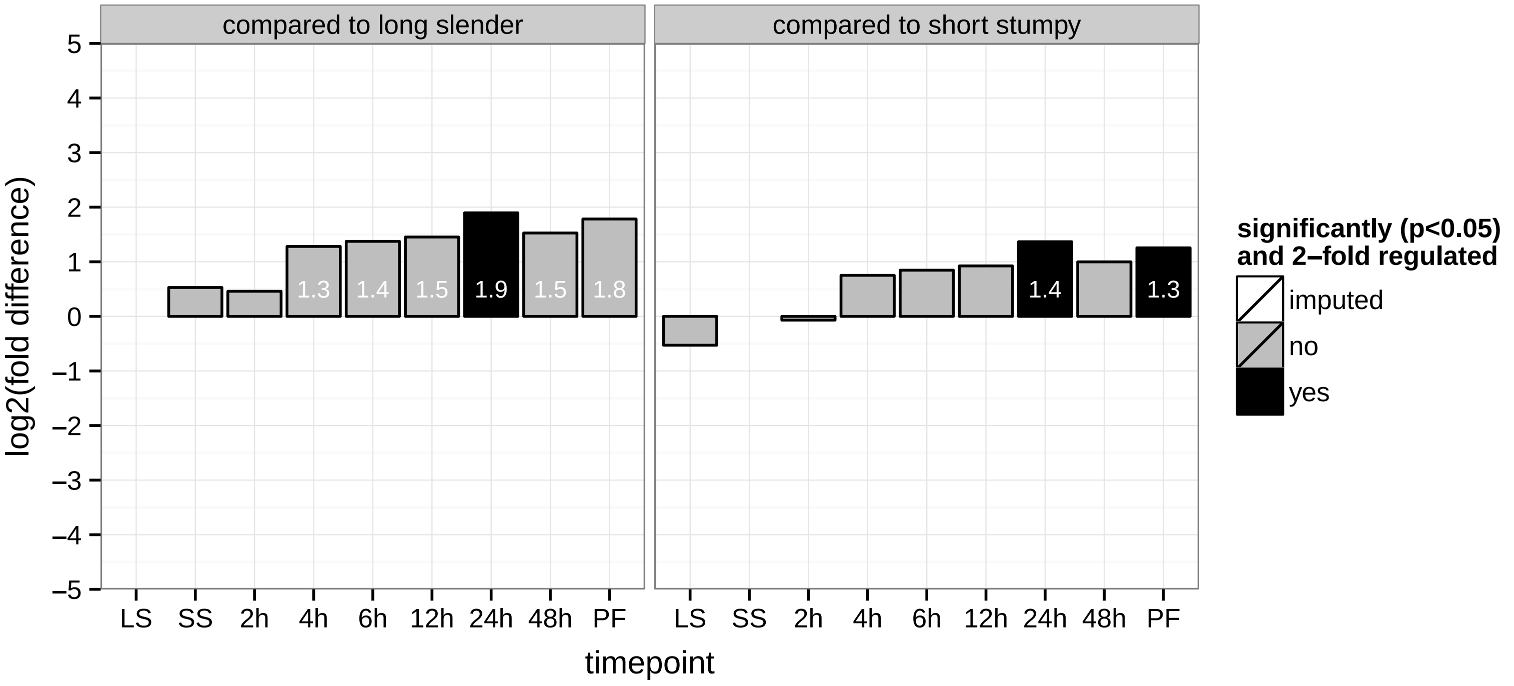
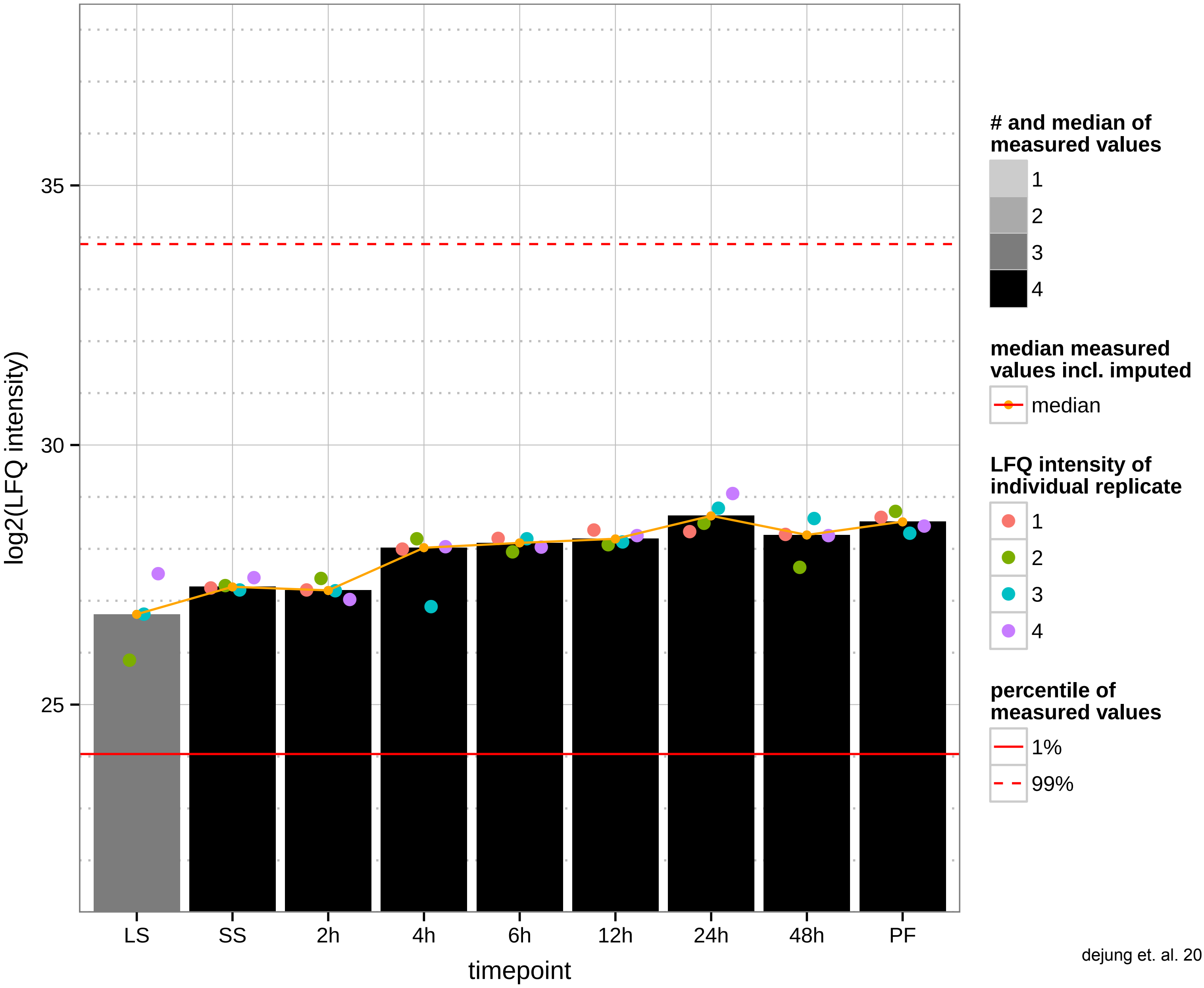
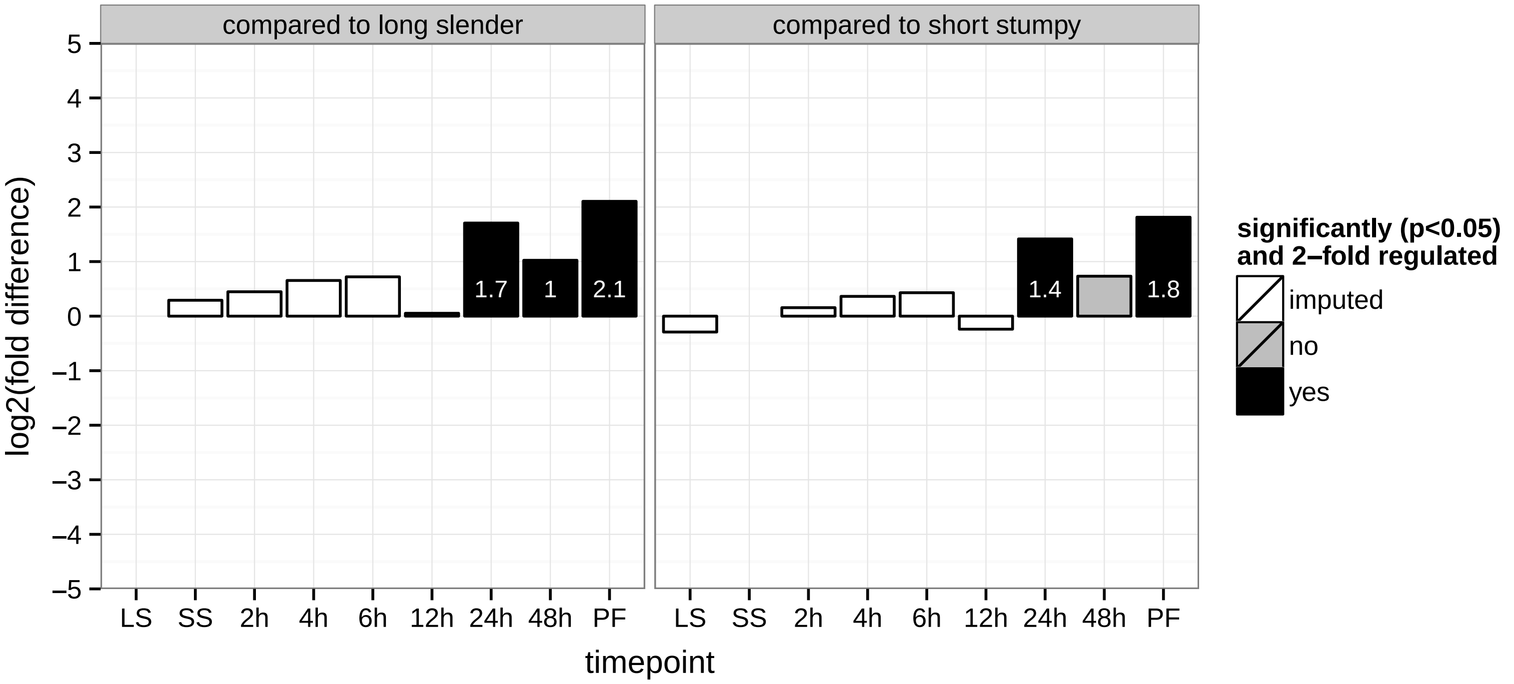
60S ribosomal protein L7, putative
Tb927.10.13730
AGOF: structural constituent of ribosome
AGOC: ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null

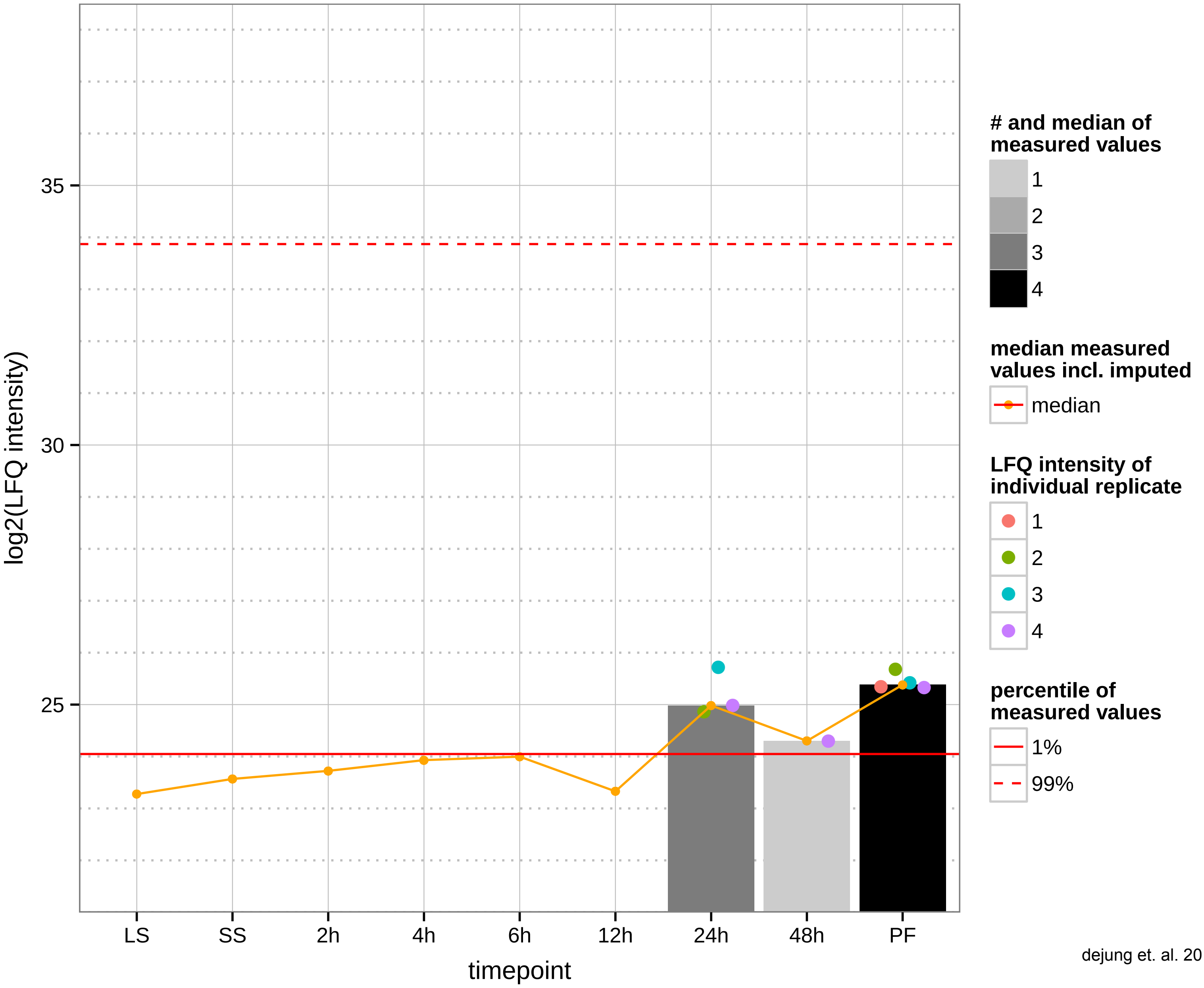




dejung et. al. 2015

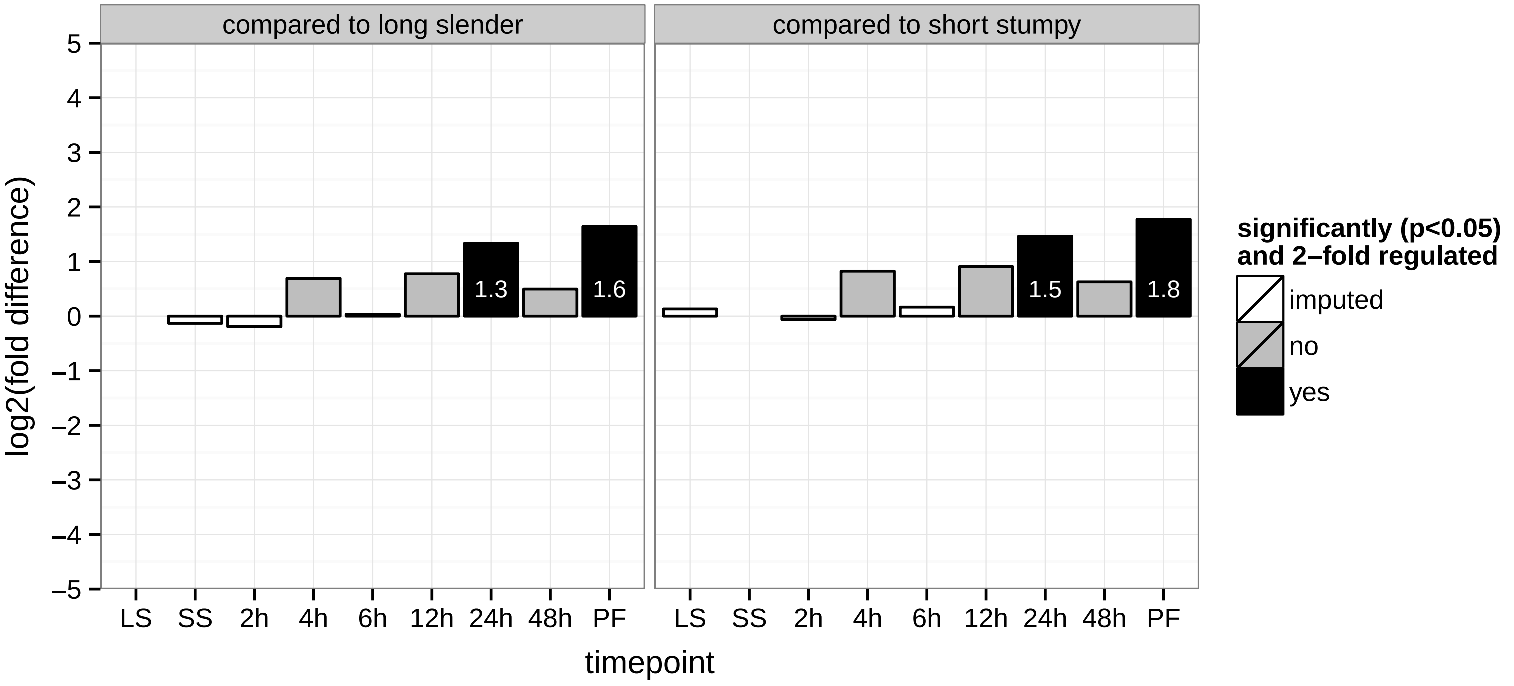
cell division related protein kinase 2, putative, CDC2−related protein kinase (CRK3)
Tb927.10.4990
AGOF: ATP binding, protein binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: mitochondrion
AGOP: cell cycle, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus−containing groups
PGOC: null
PGOP: protein phosphorylation

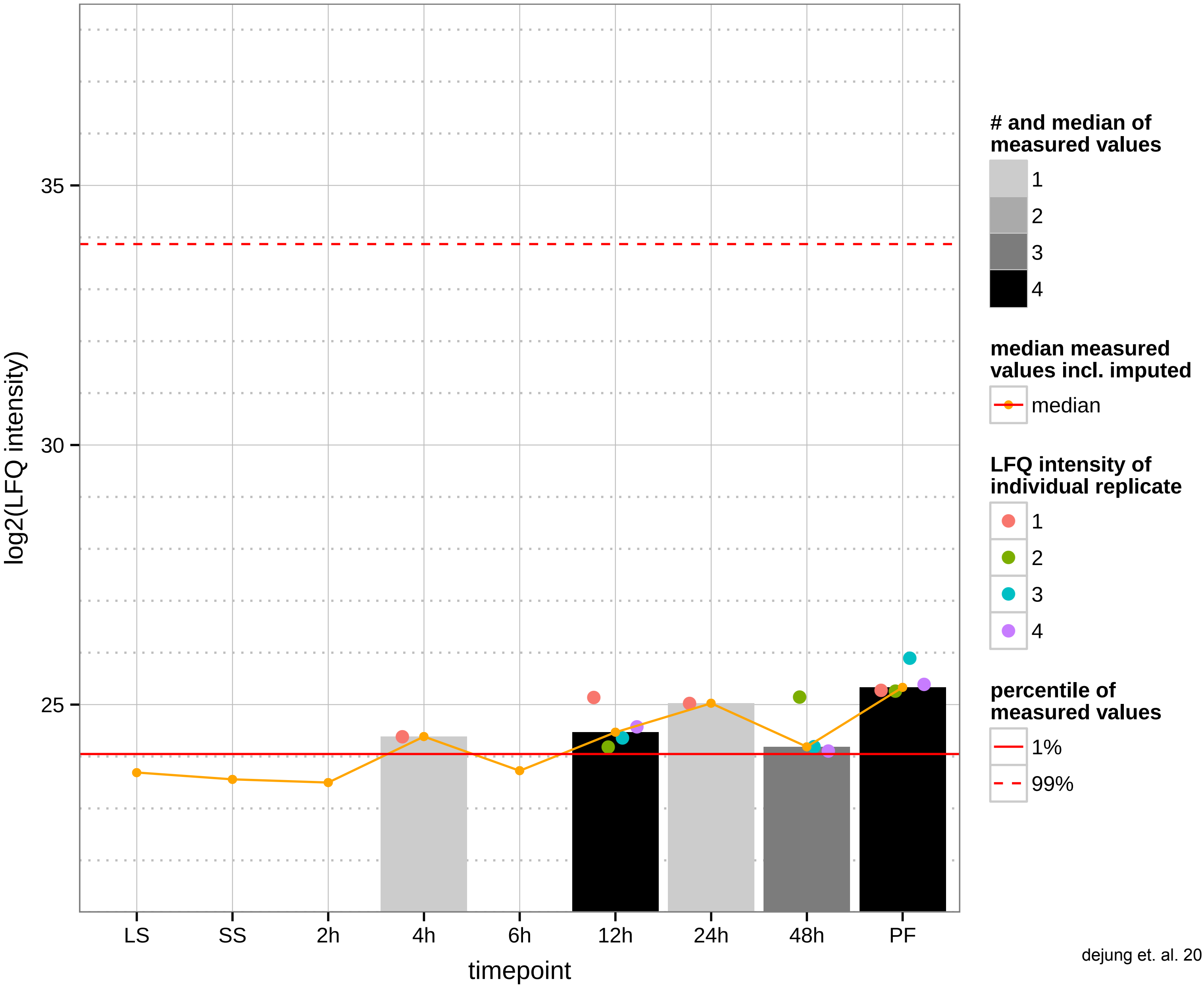




dejung et. al. 2015

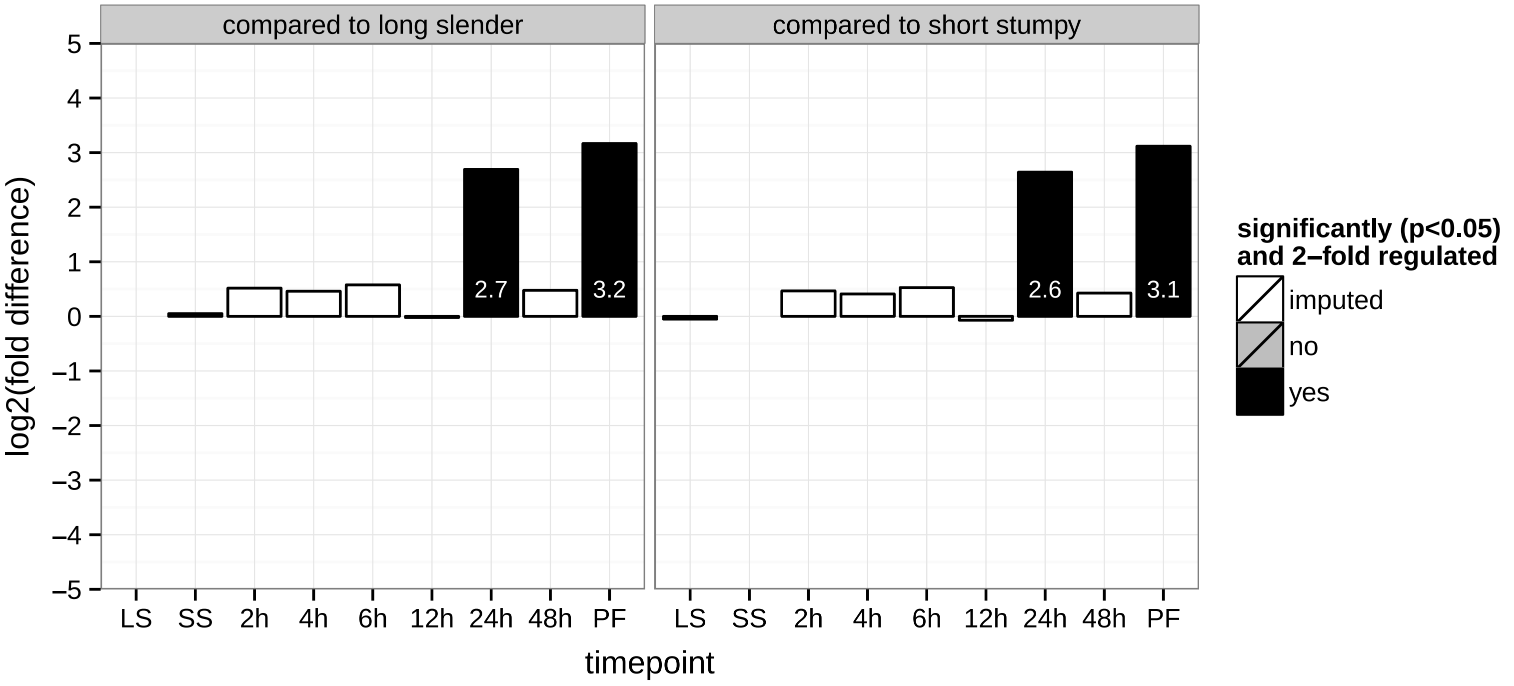
hypothetical protein, conserved
Tb927.10.7010;Tb11.v5.0806
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

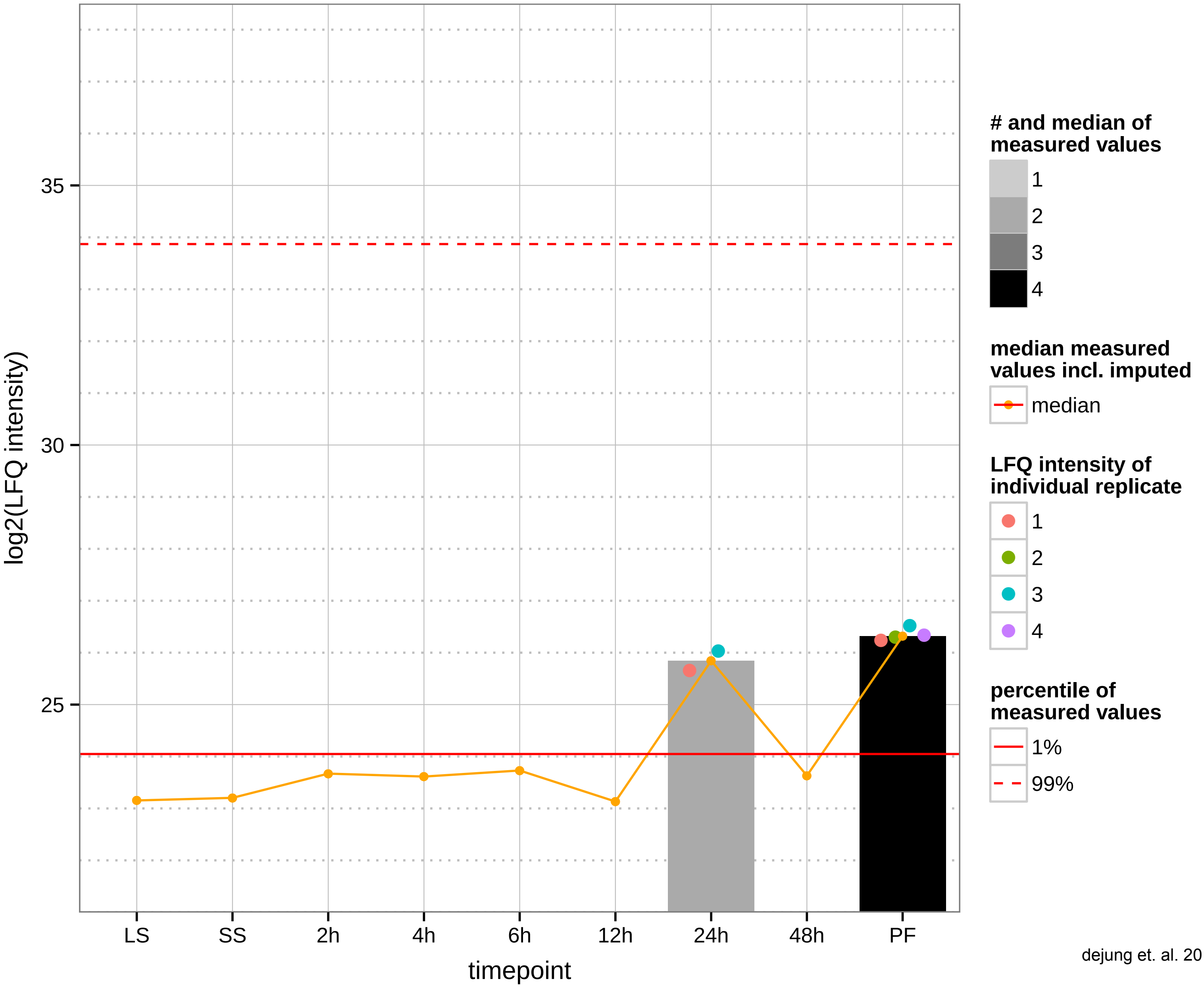




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.9870
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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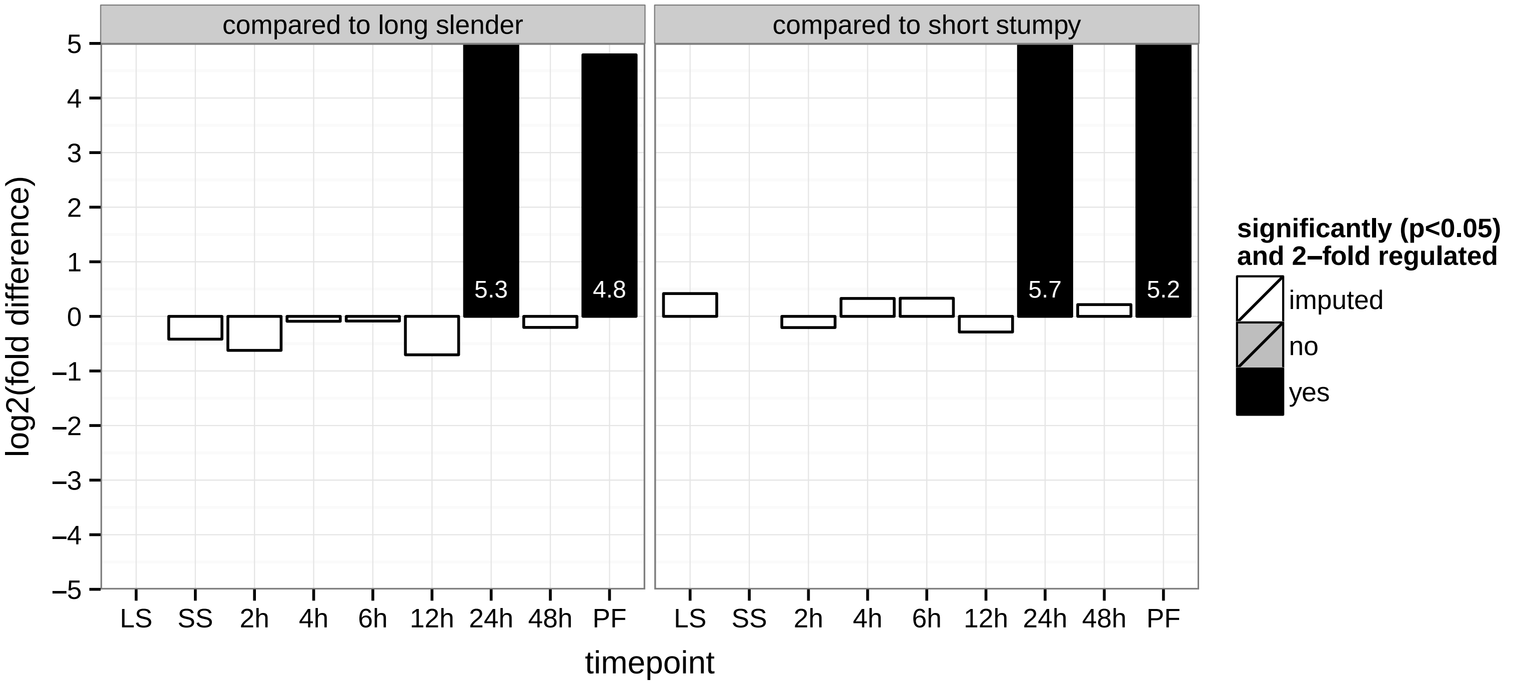
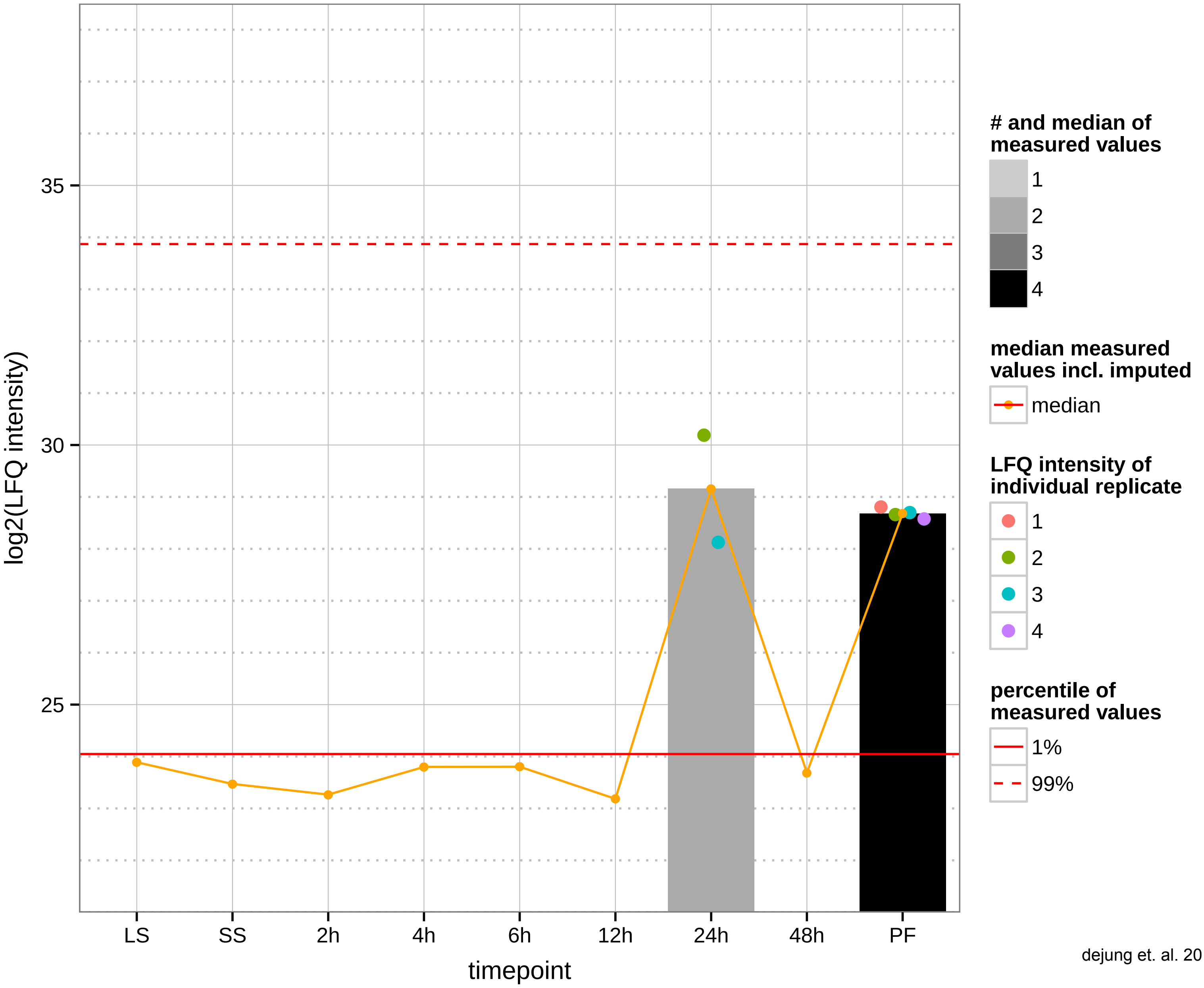
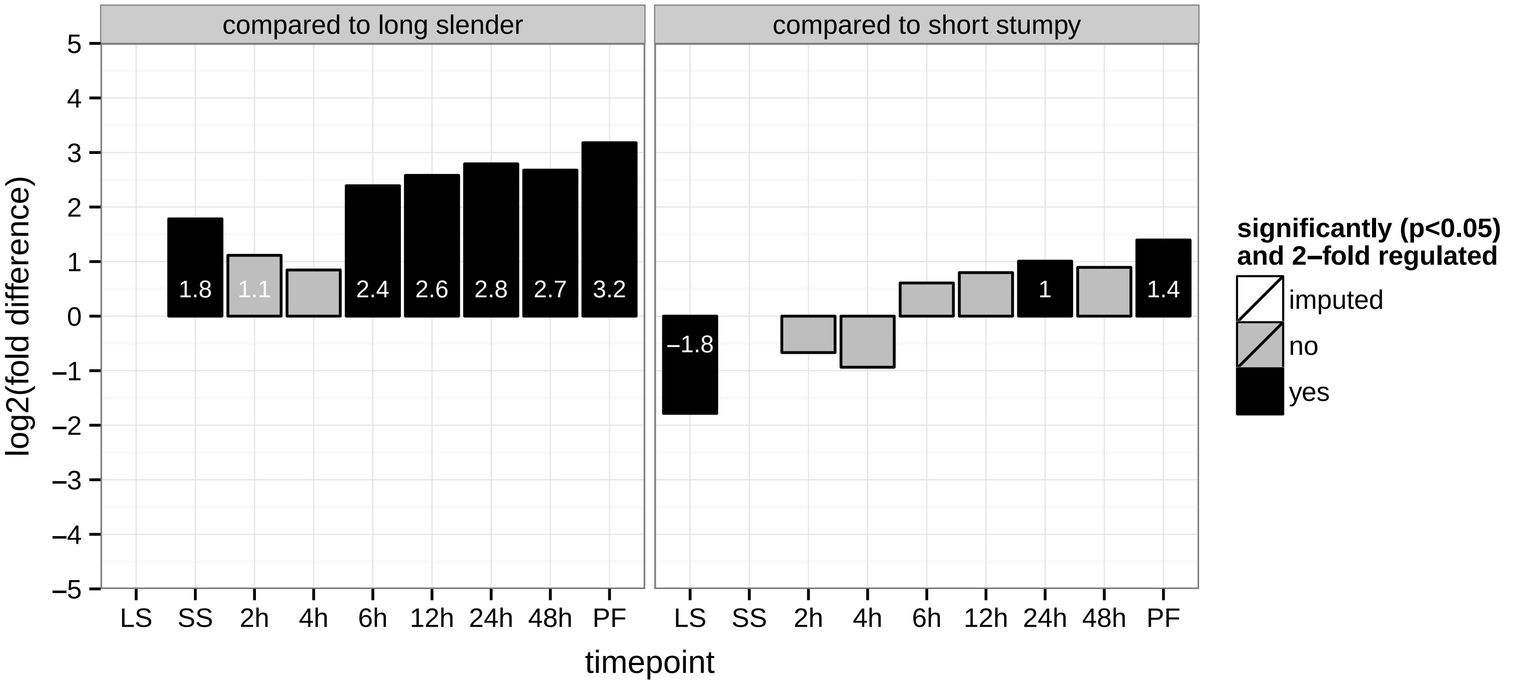
hypothetical protein, conserved
Tb927.11.1690
AGOF: cholestenol delta–isomerase activity
AGOC: endoplasmic reticulum, integral to membrane
AGOP: sterol metabolic process
PGOF: cholestenol delta–isomerase activity
PGOC: endoplasmic reticulum, integral to membrane
PGOP: sterol metabolic process

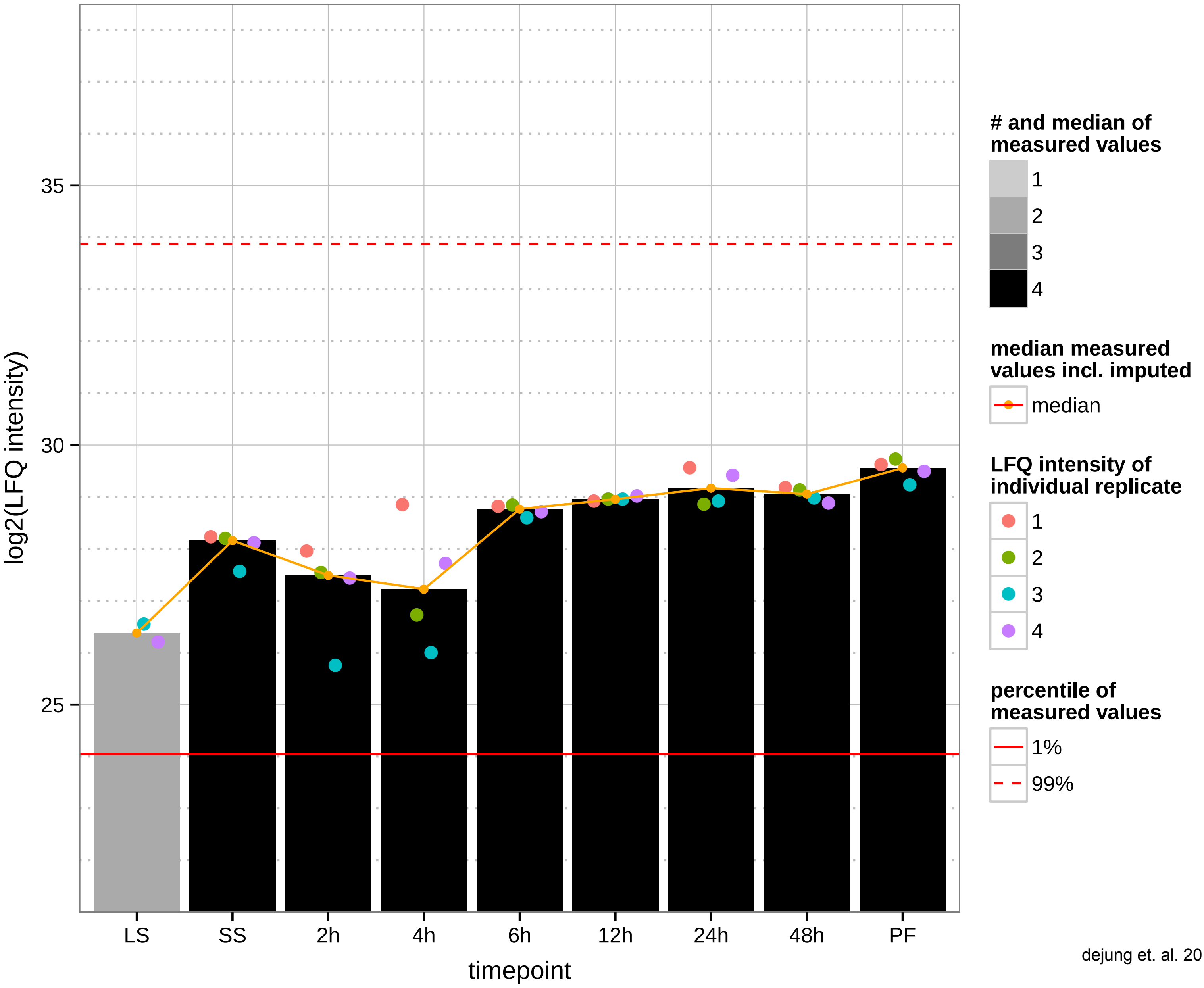




dejung et. al. 2015

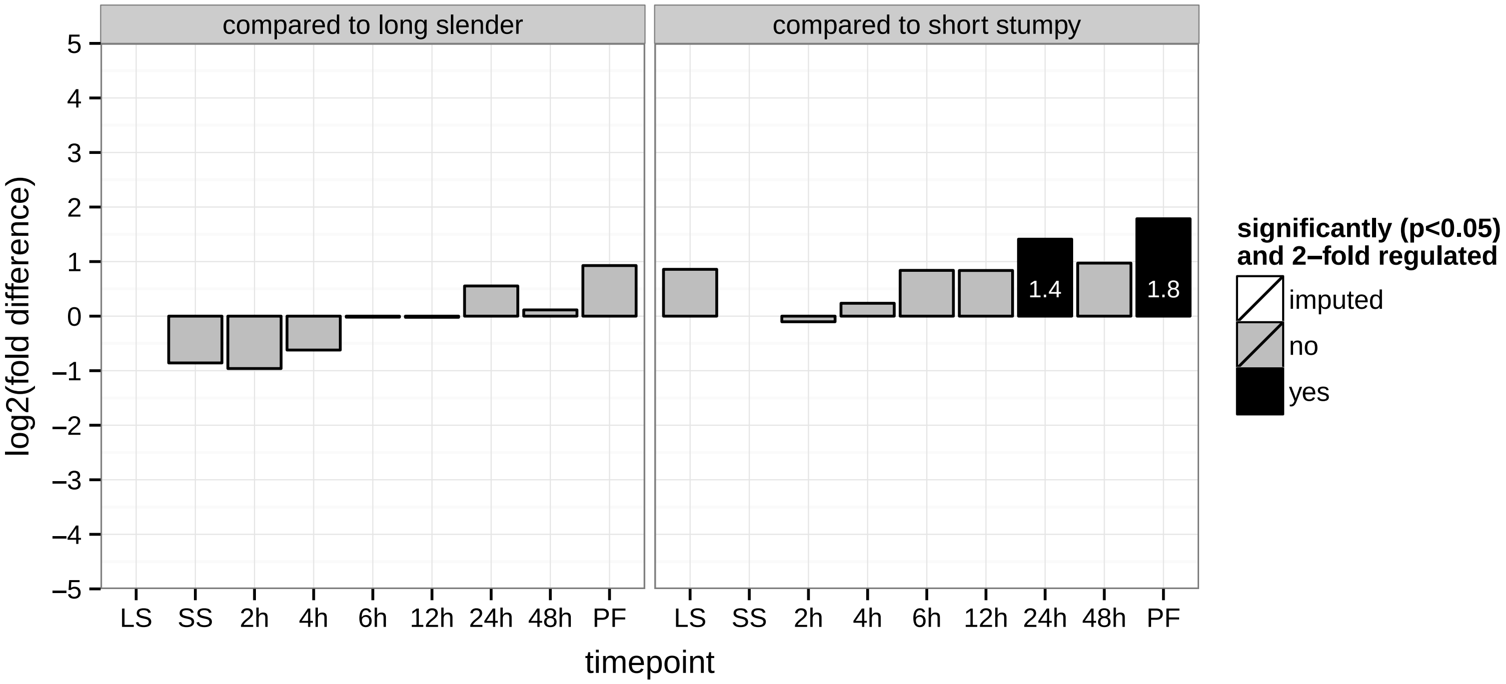
hypothetical protein, conserved
Tb927.11.2510
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

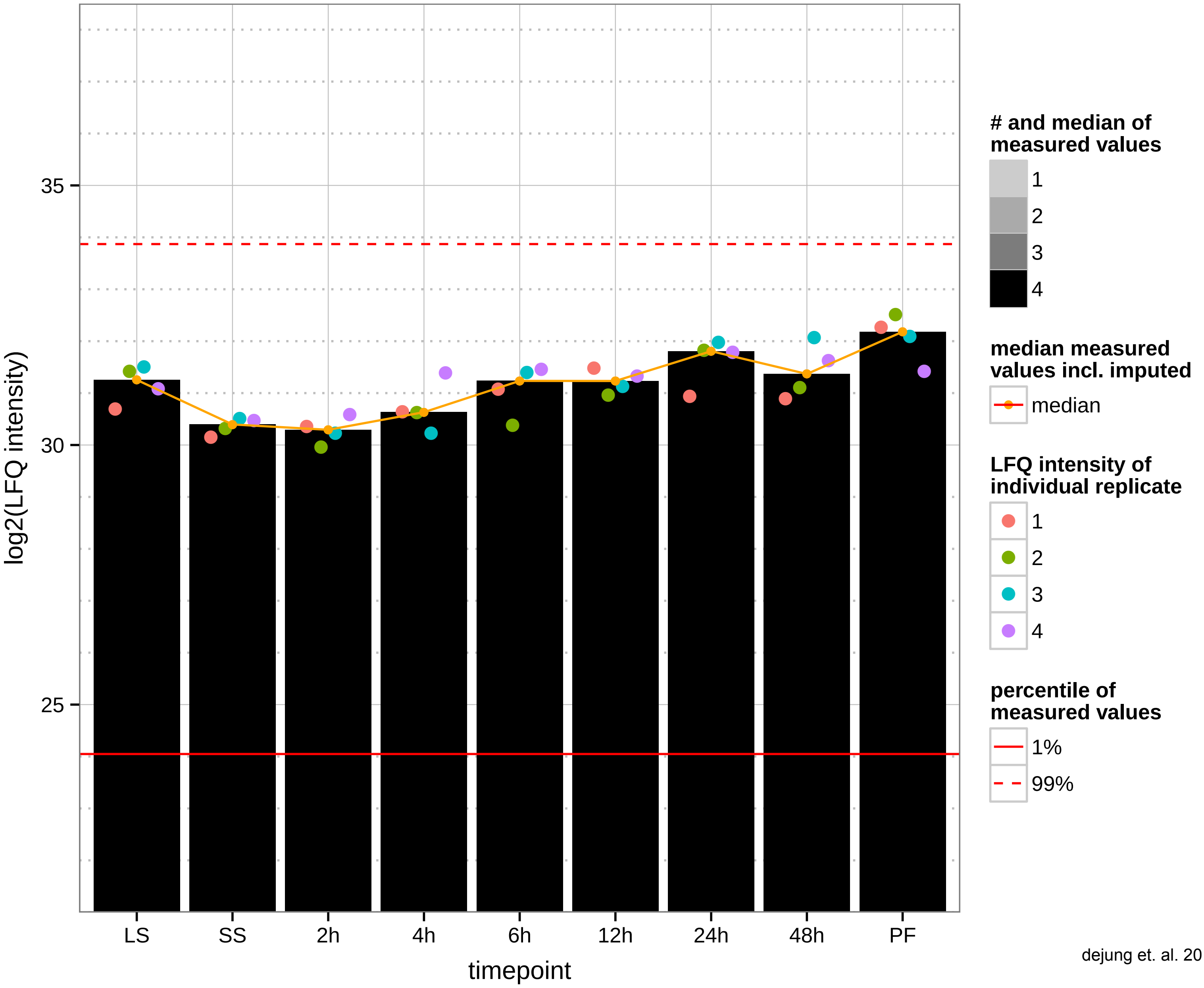




dejung et. al. 2015

60S ribosomal protein L44, ribosomal protein L36a.e (RPL44)
Tb927.2.6090;Tb927.11.3230
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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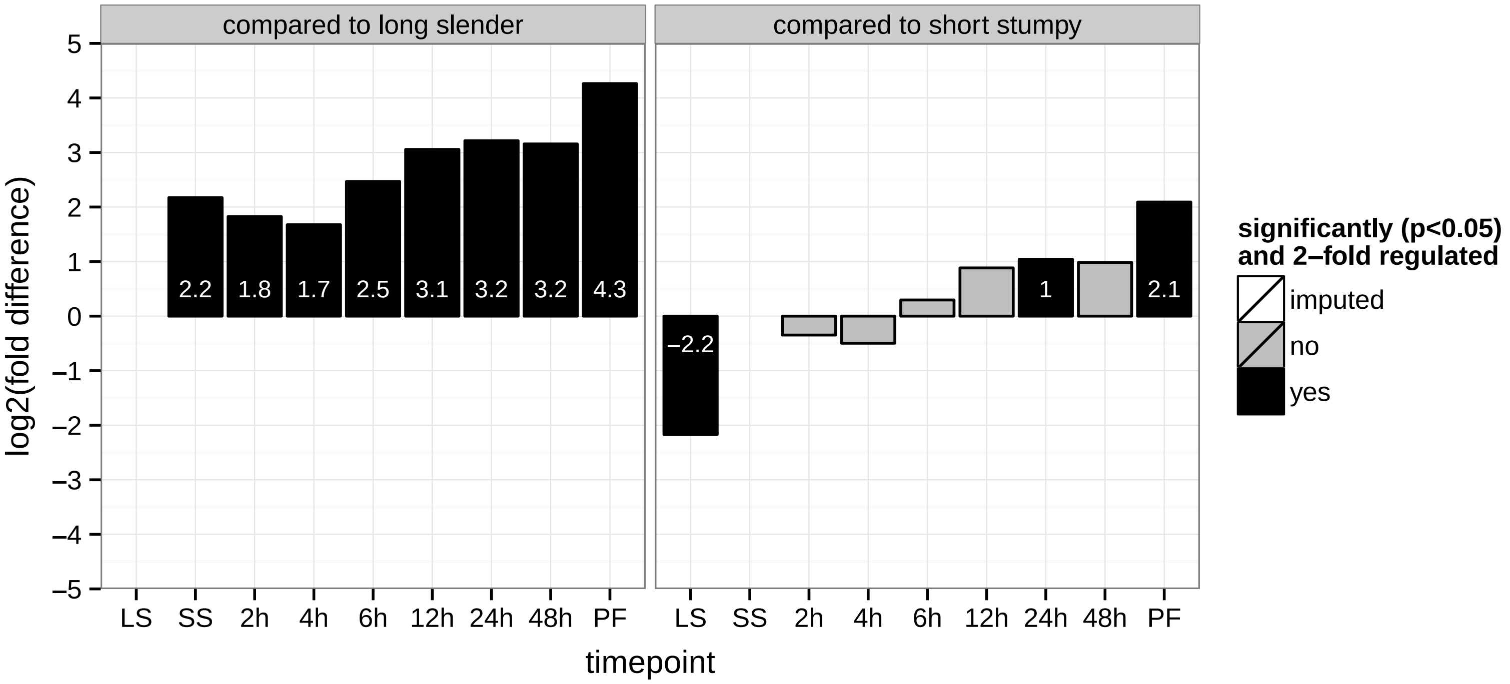
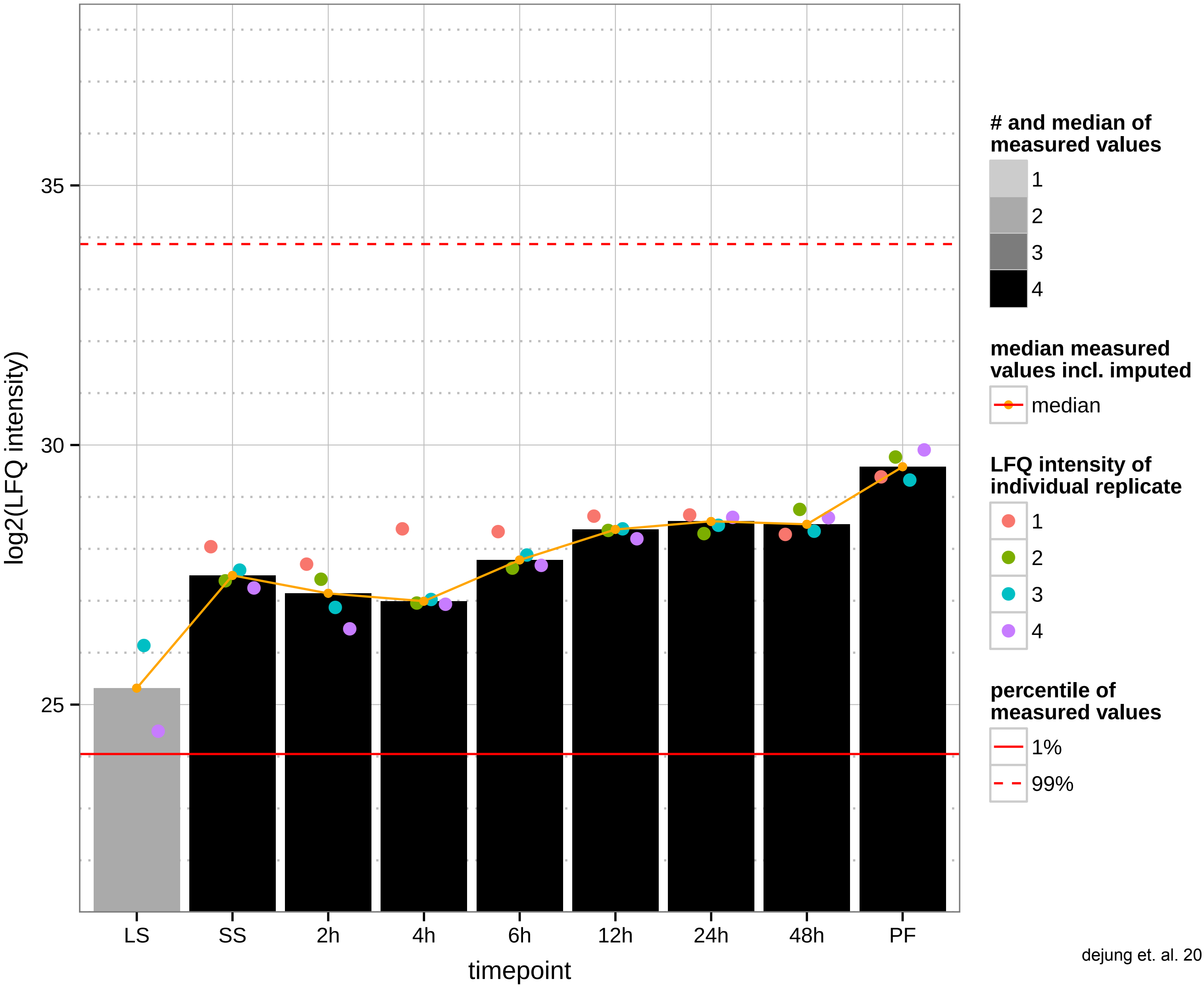
hypothetical protein, conserved
Tb927.11.4190
AGOF: null
AGOC: null
AGOP: cellular process
PGOF: null
PGOC: null
PGOP: cellular process





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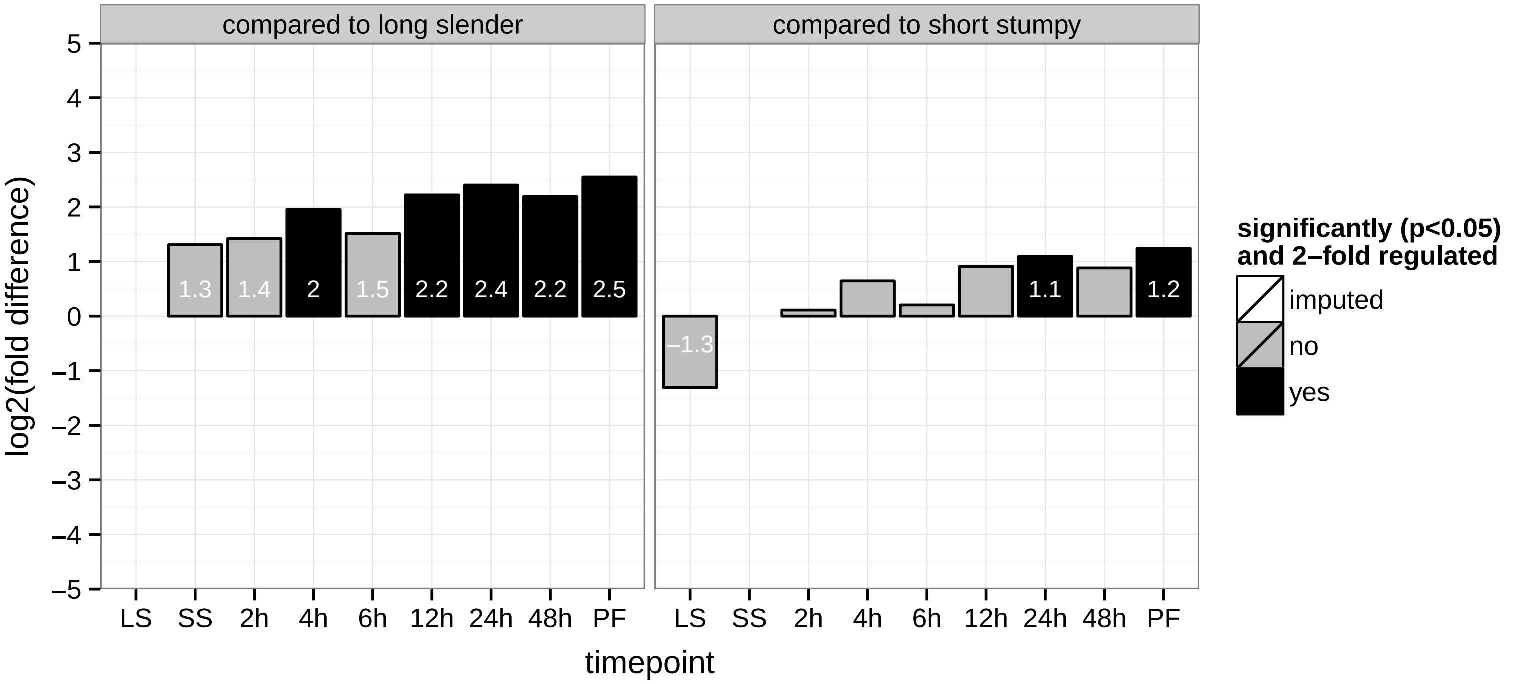
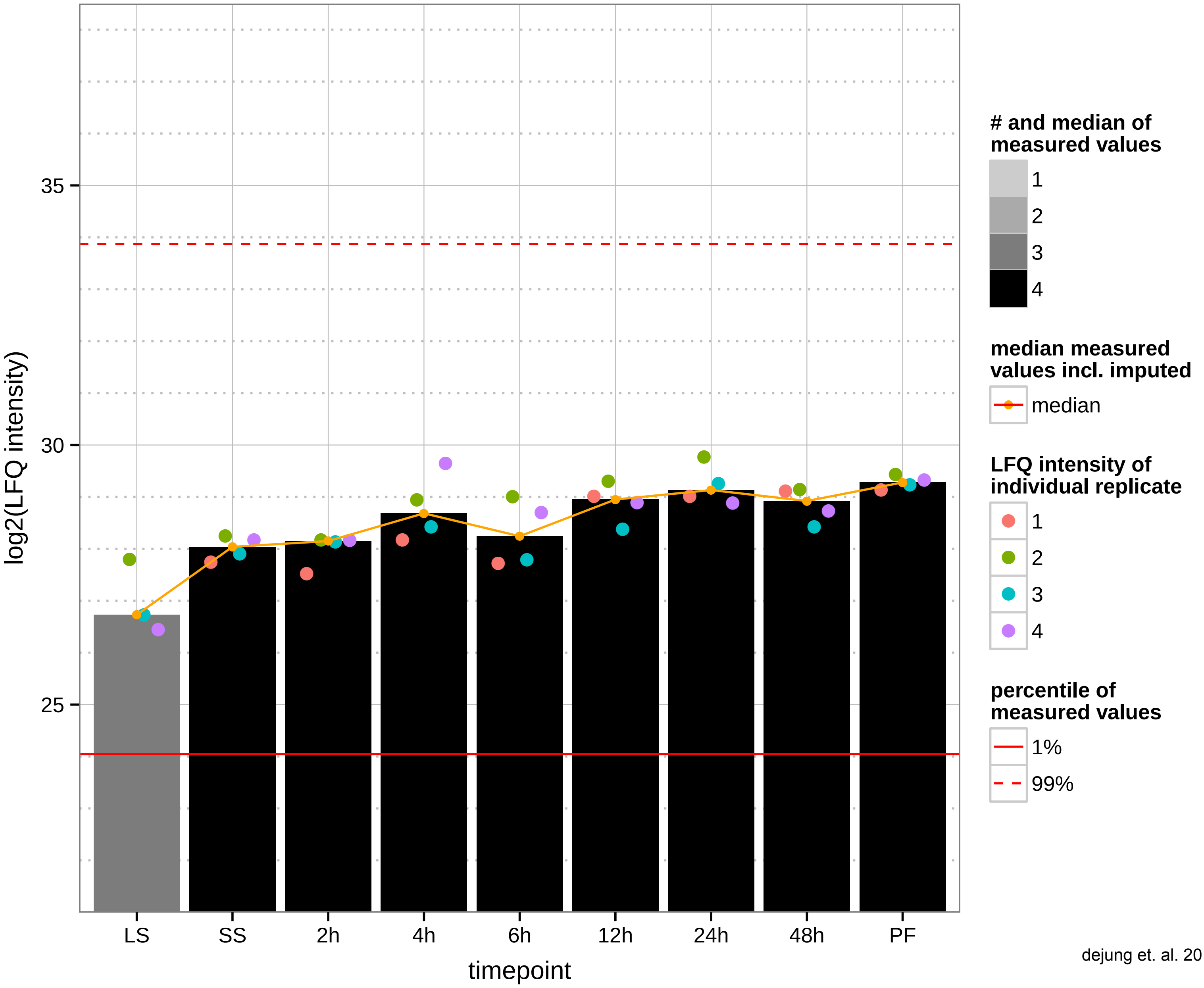
hypothetical protein, conserved
Tb927.11.5180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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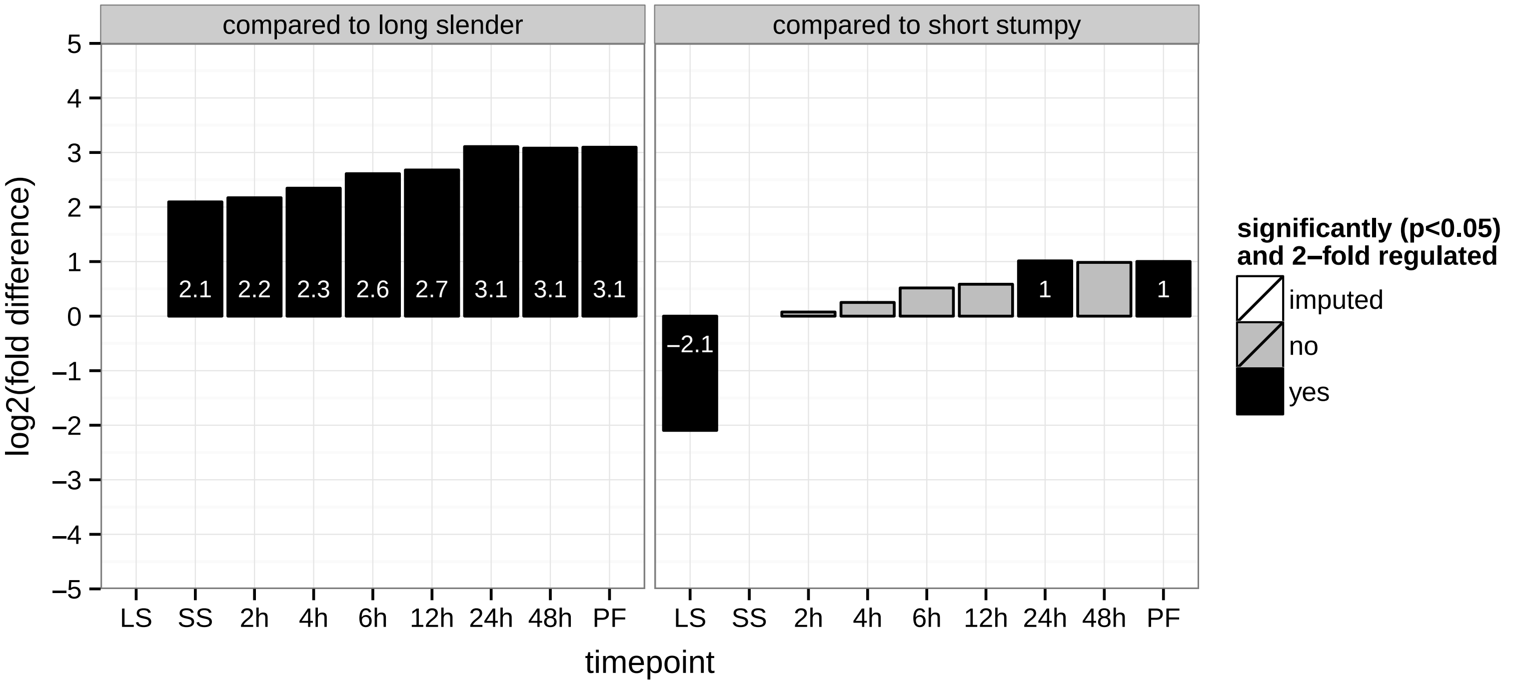
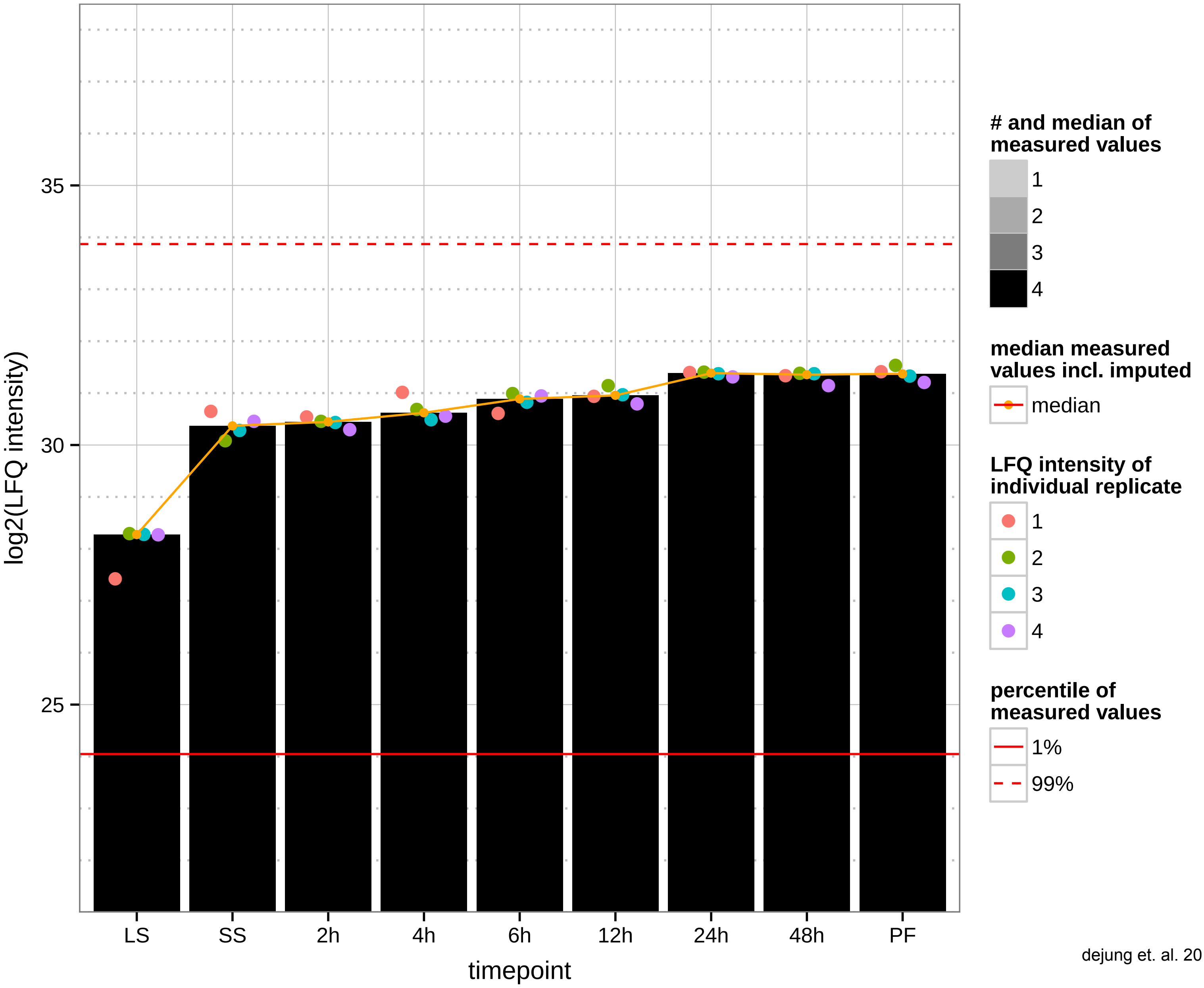
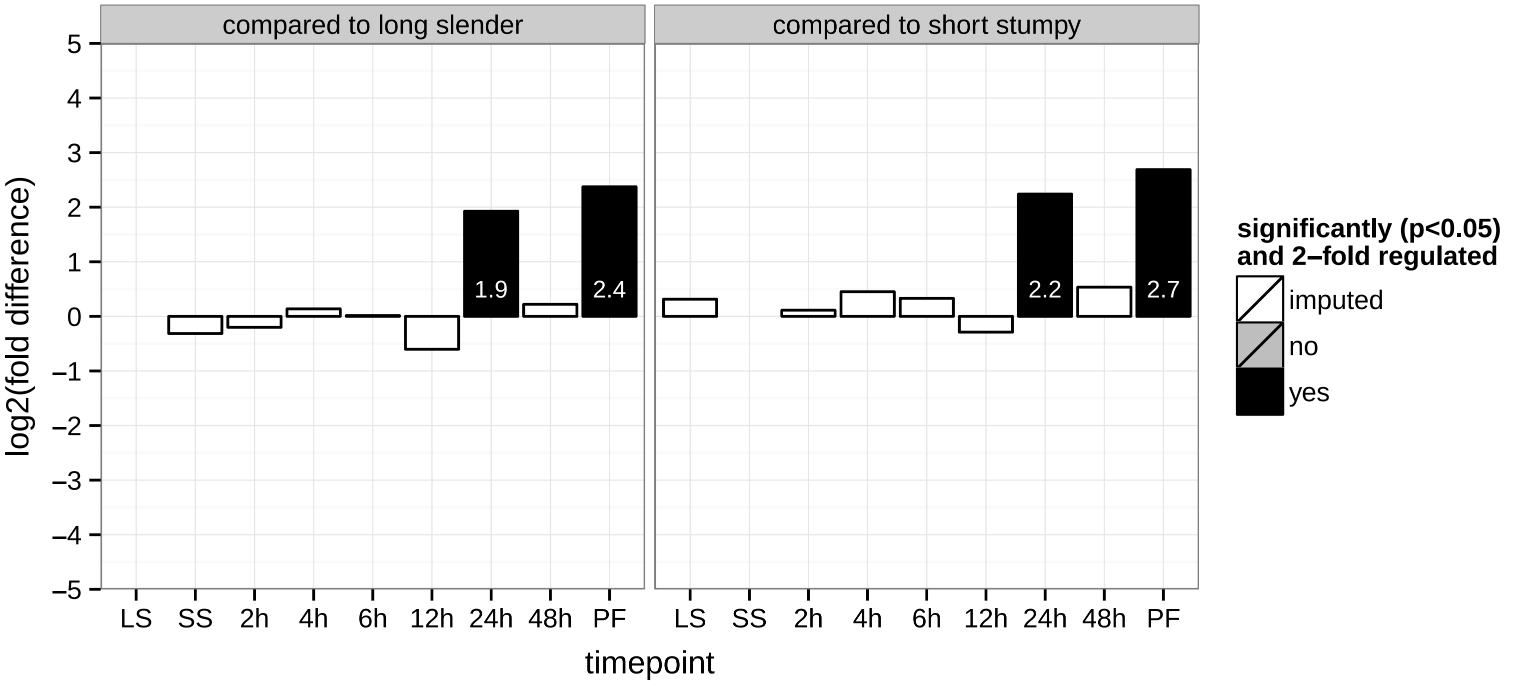
hypothetical protein, conserved
Tb927.11.7780
AGOF: null
AGOC: mitochondrial inner membrane, mitochondrion
AGOP: null
PGOF: binding
PGOC: null
PGOP: null

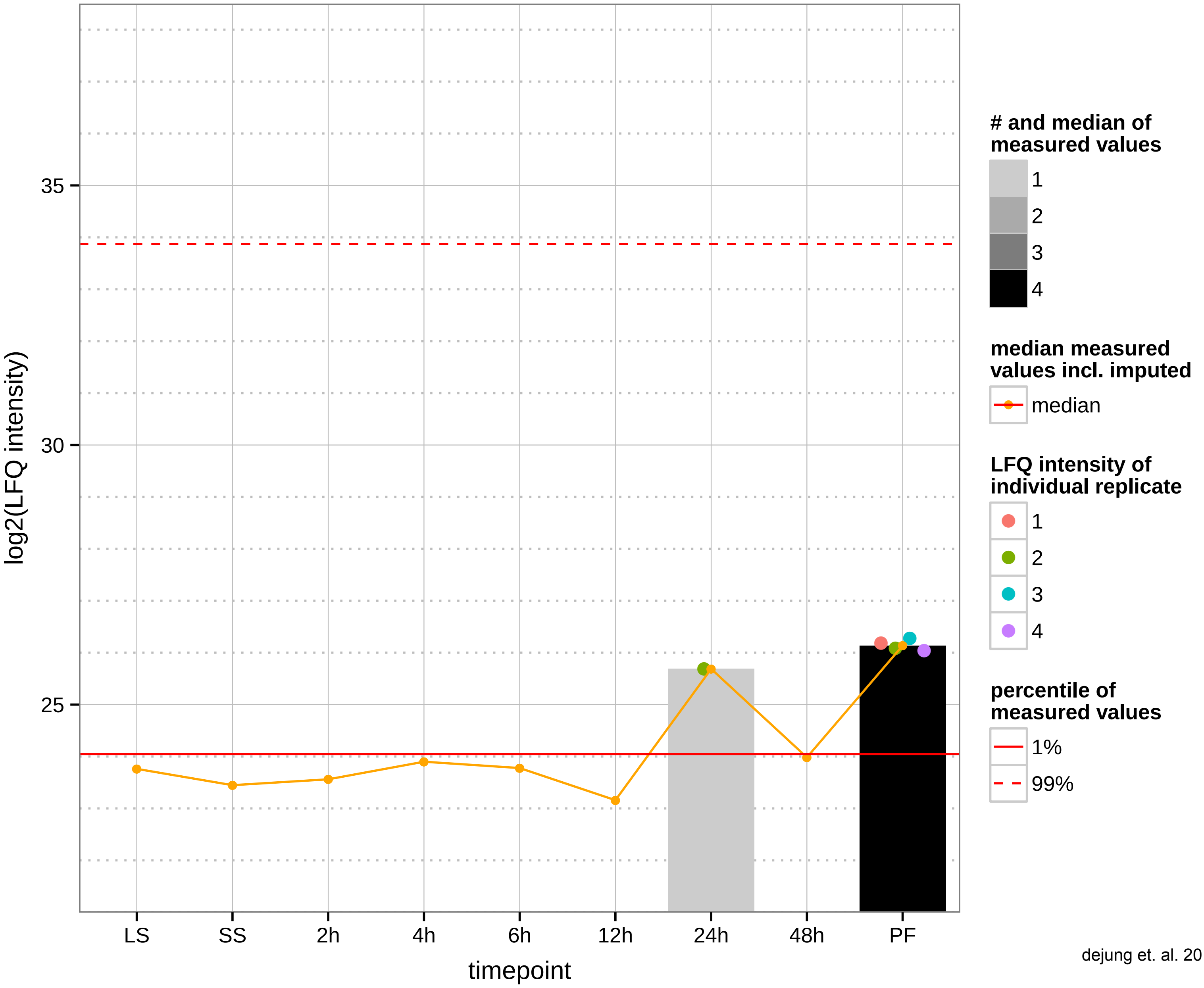




dejung et. al. 2015

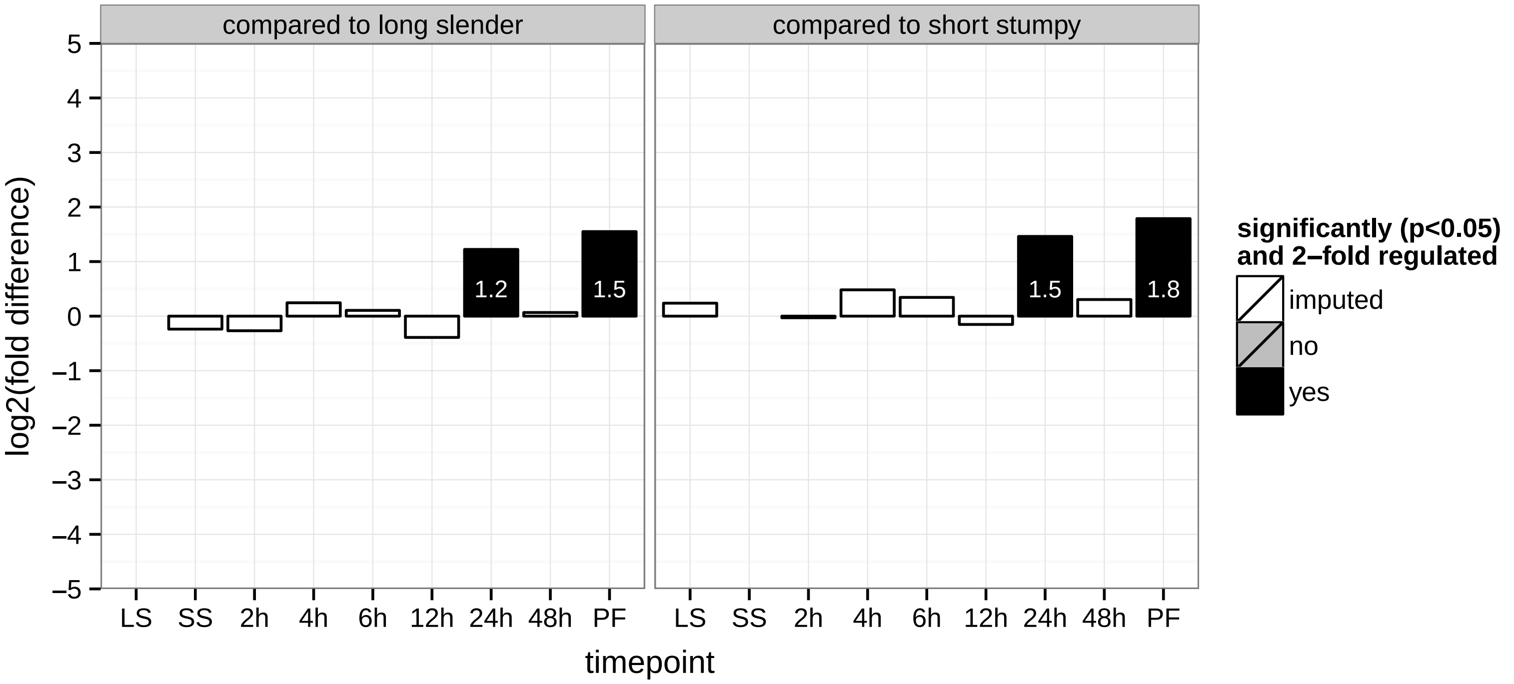
retrotransposon hot spot (RHS) protein, putative, retrotransposon hot spot protein (RHS, pseudogene), retrotransposon hot sp
Tb927.2.1100;Tb11.v5.0800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

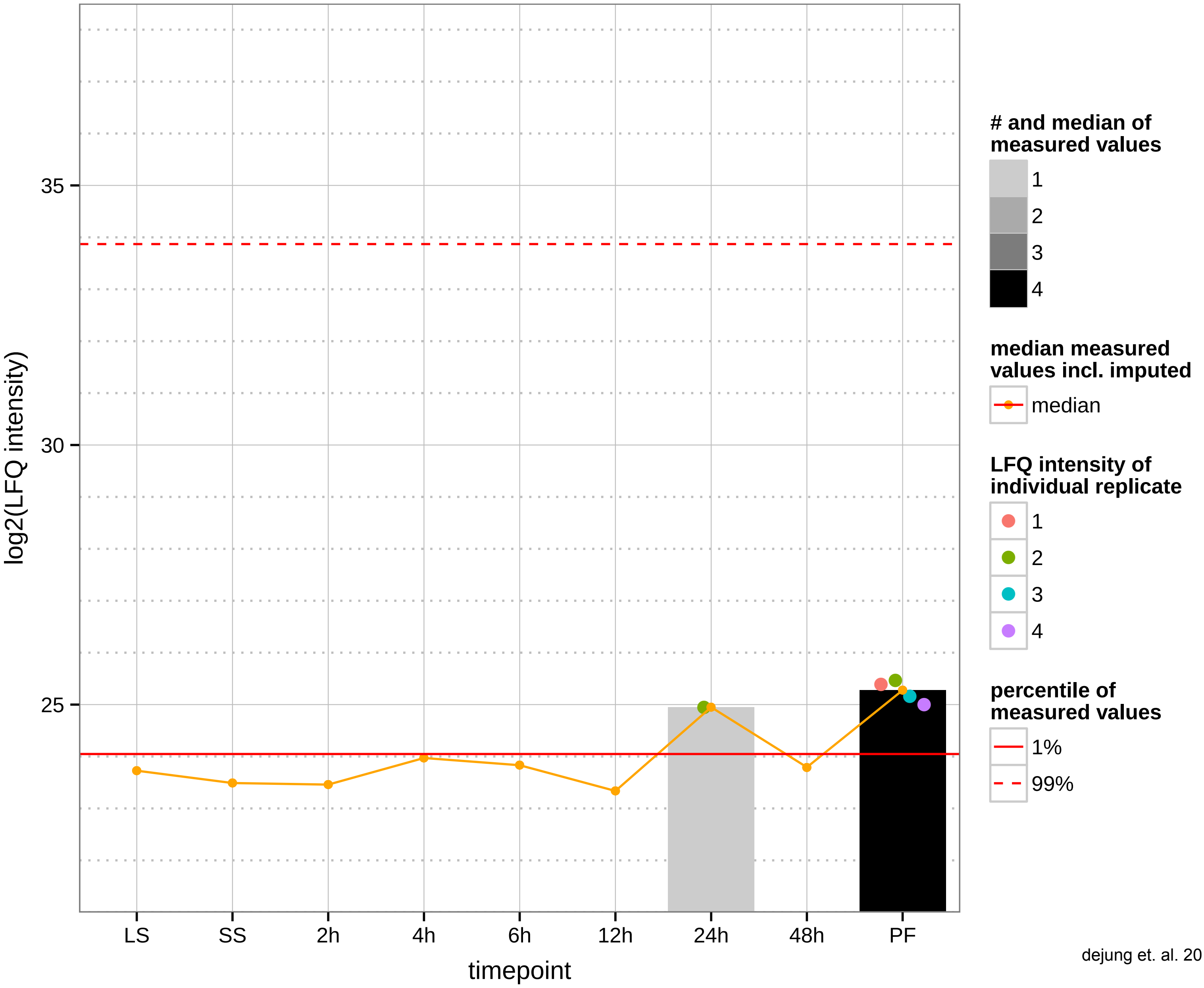




dejung et. al. 2015

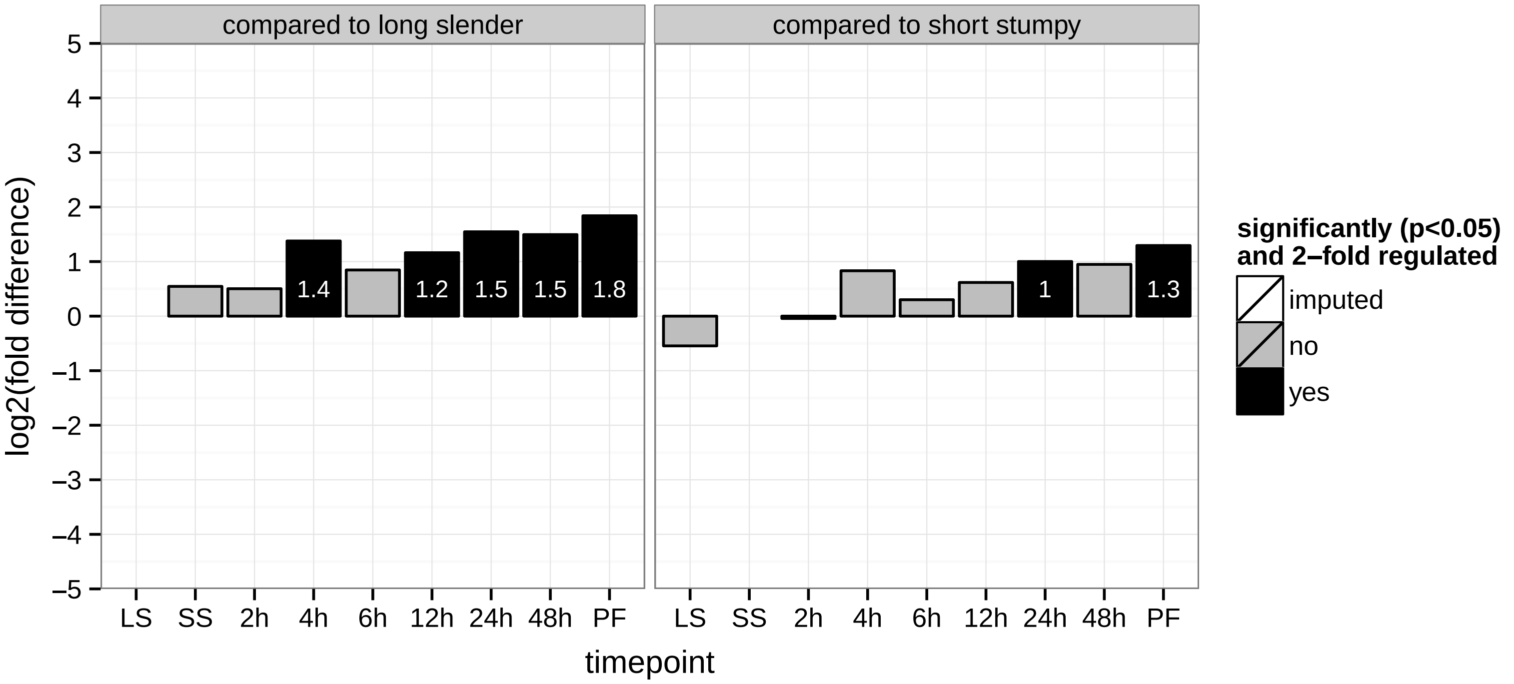
hypothetical protein, conserved
Tb927.6.1410
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

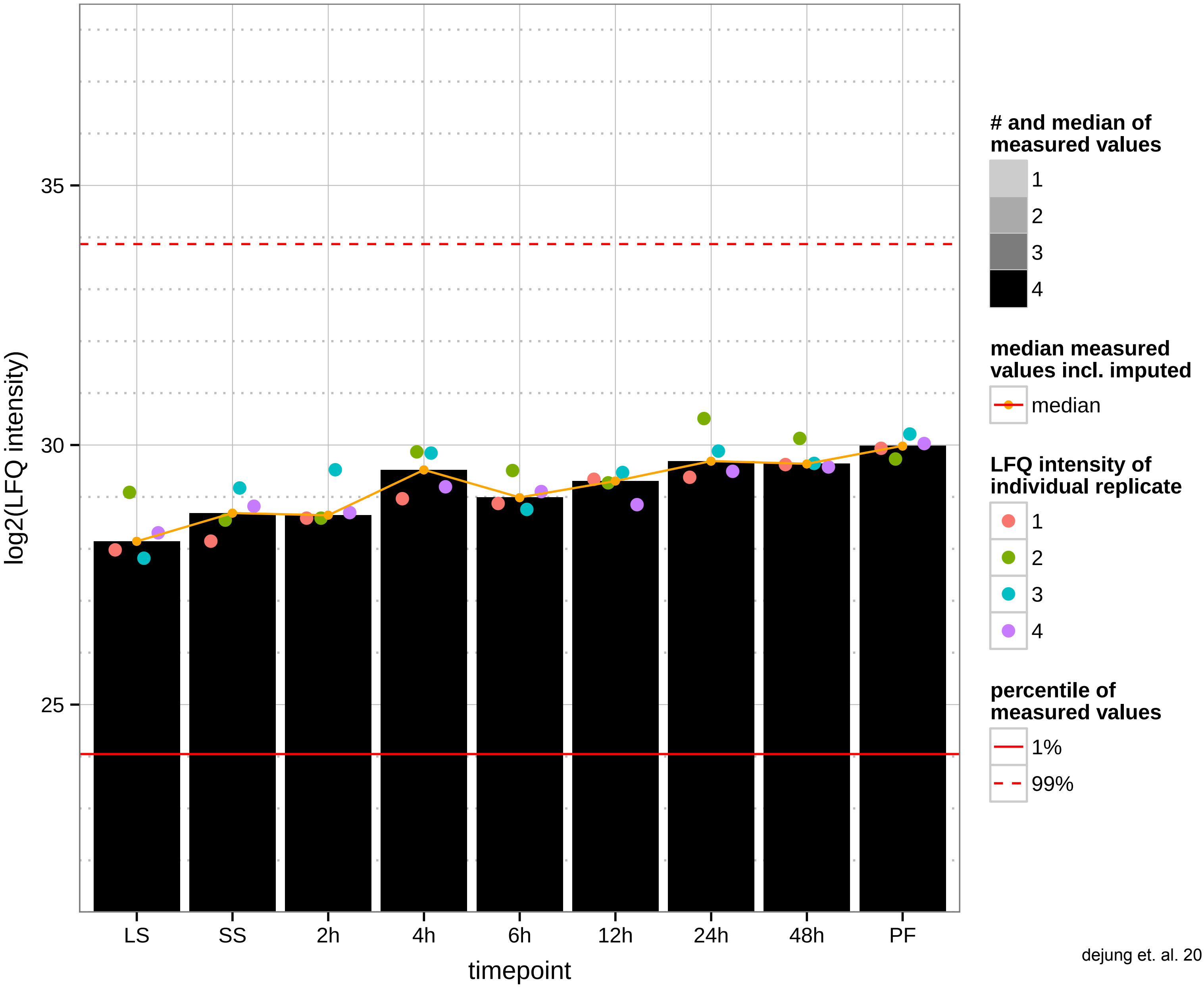




dejung et. al. 2015

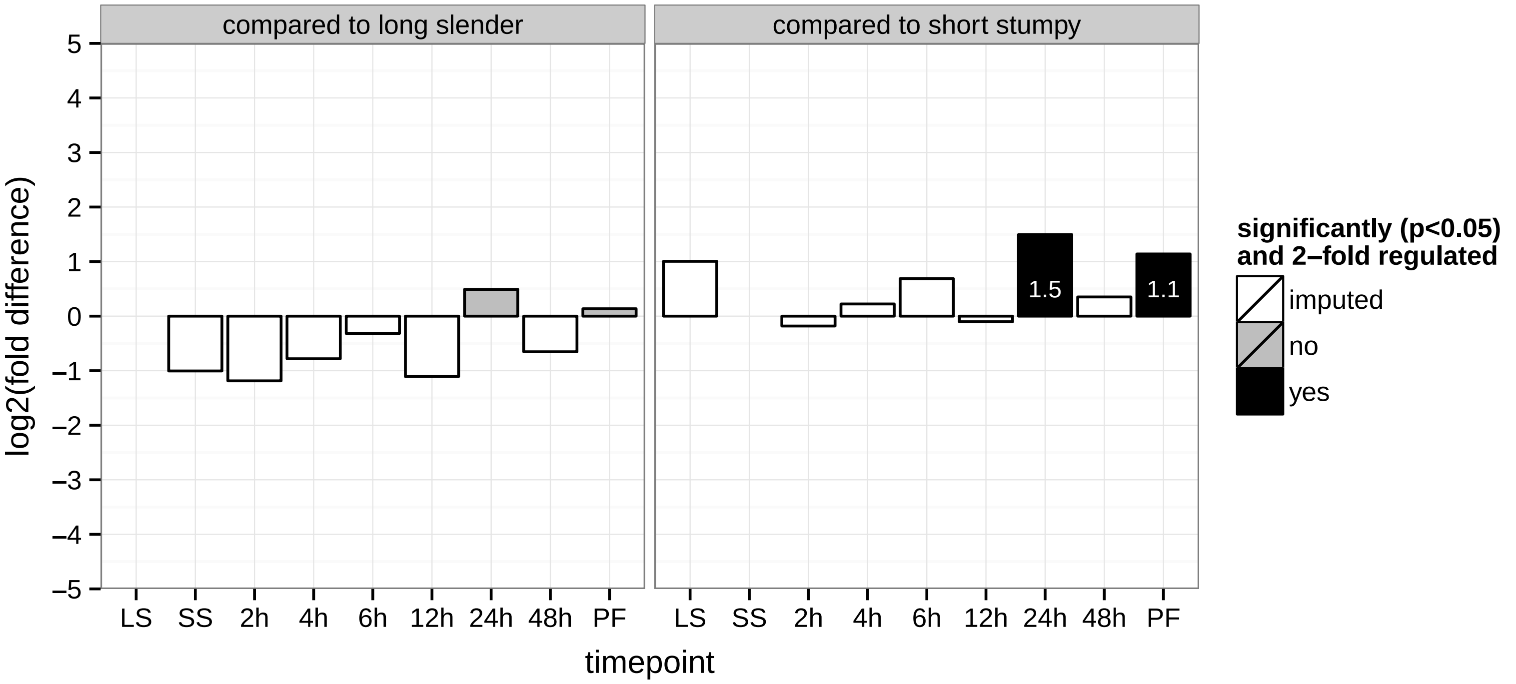
hypothetical protein, conserved
Tb927.6.2340;Tb927.6.2280
AGOF: unfolded protein binding
AGOC: prefoldin complex
AGOP: protein folding
PGOF: unfolded protein binding
PGOC: prefoldin complex
PGOP: protein folding

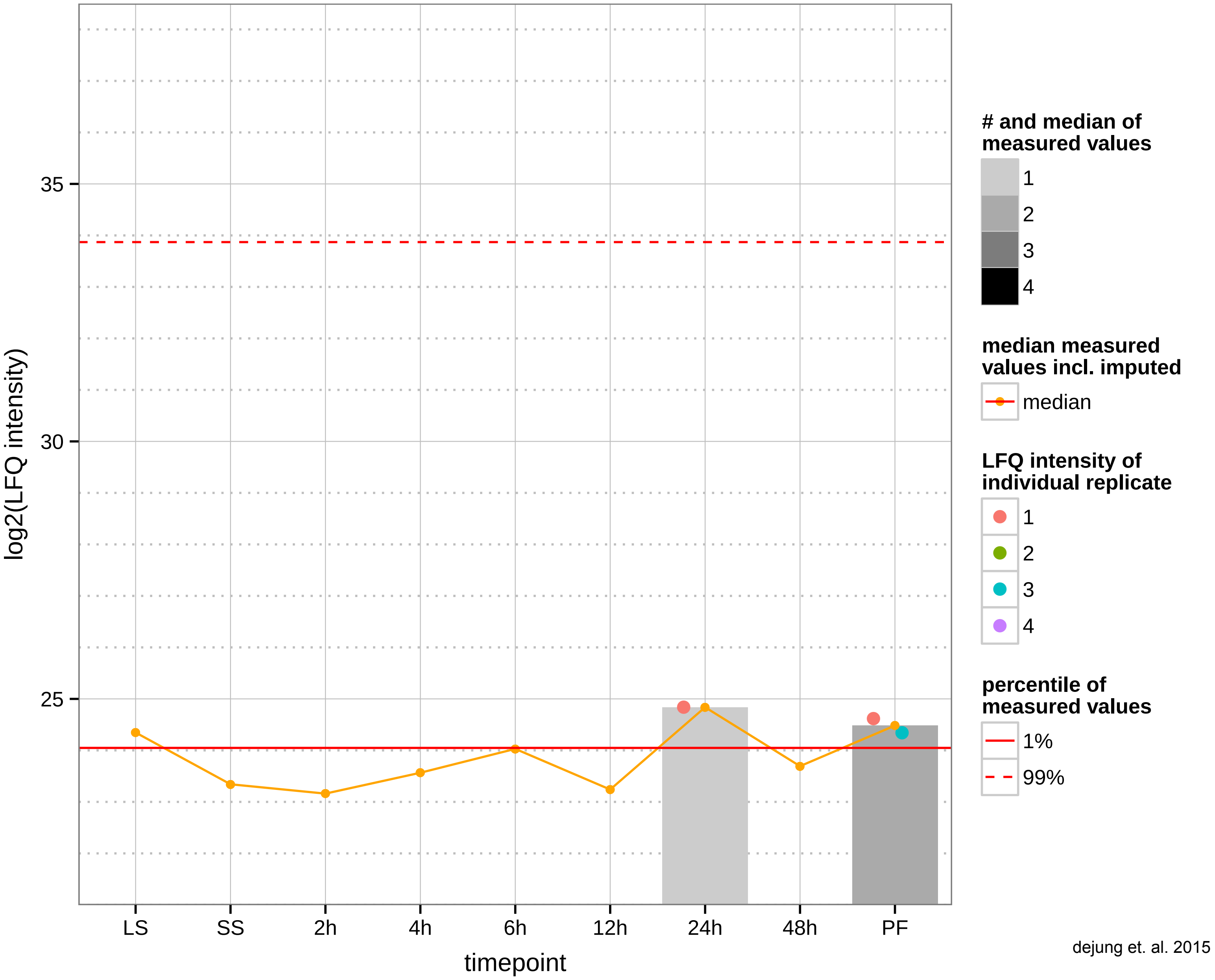




dejung et. al. 2015

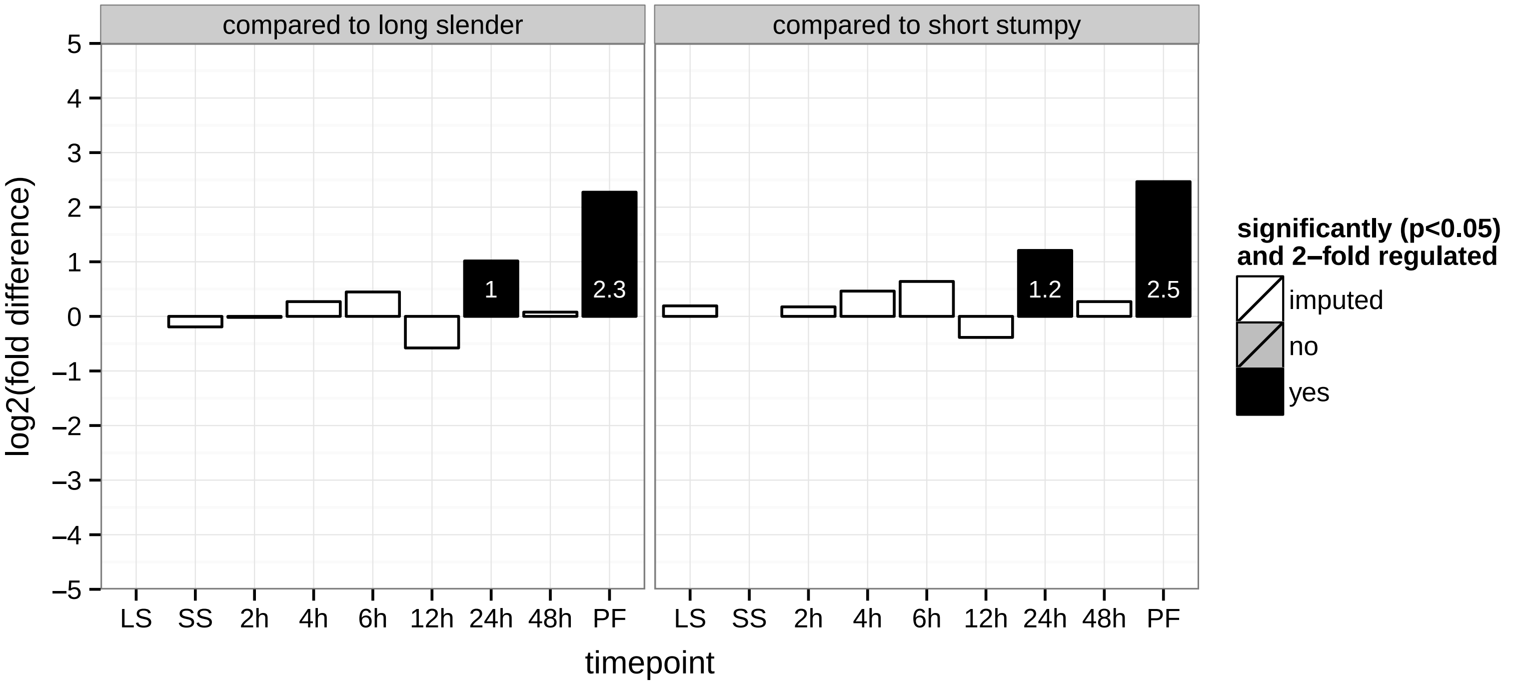
hypothetical protein, conserved
Tb927.7.2620
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

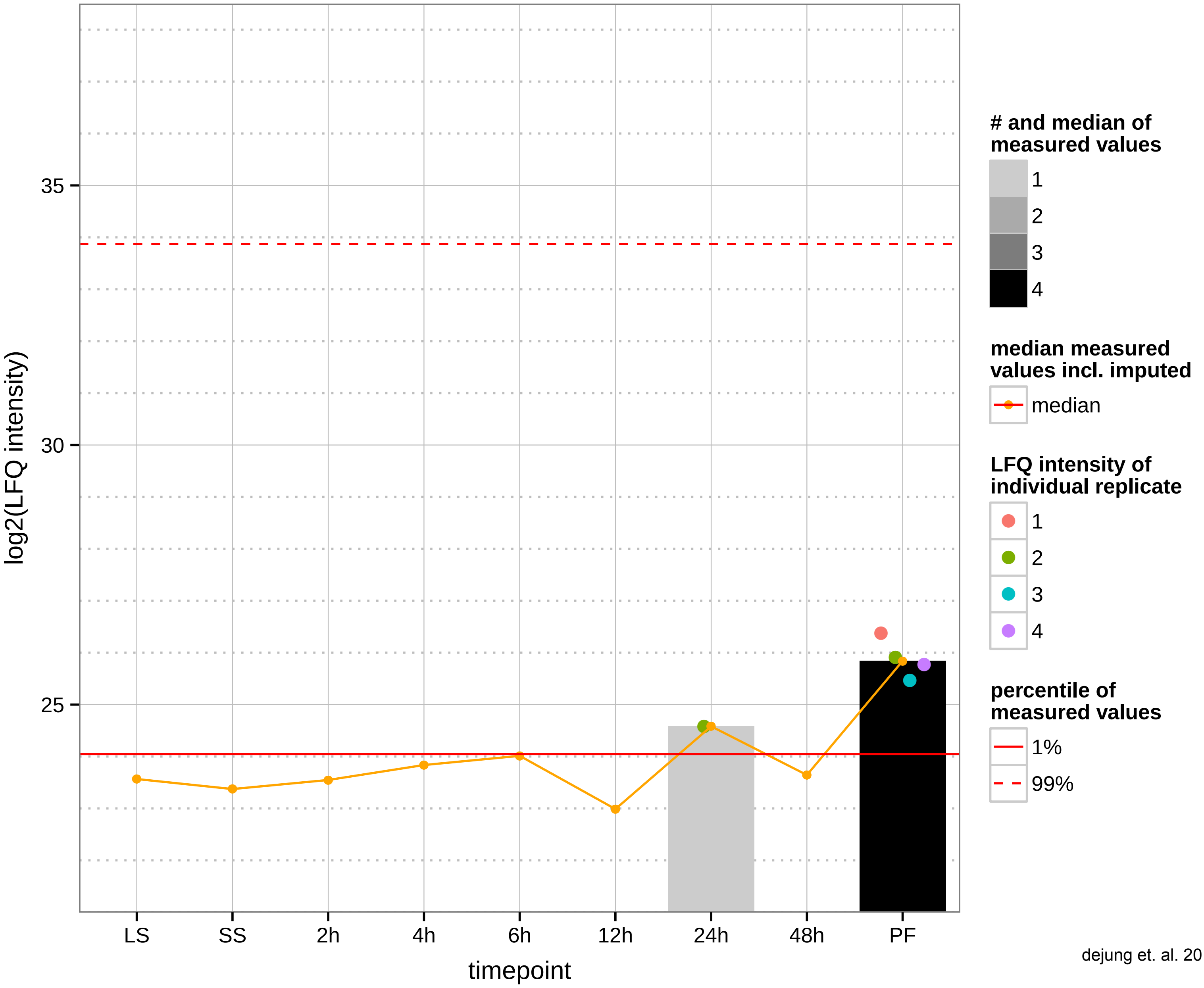




dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.3700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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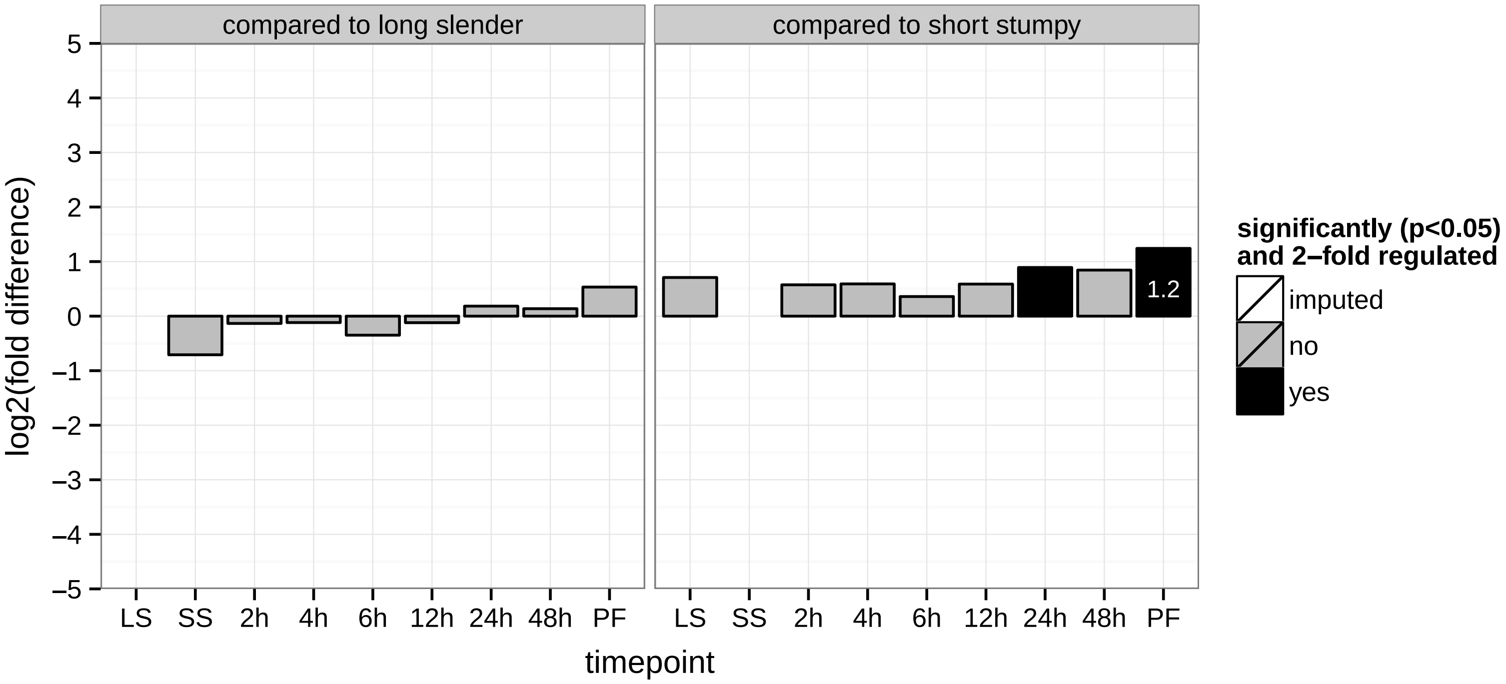
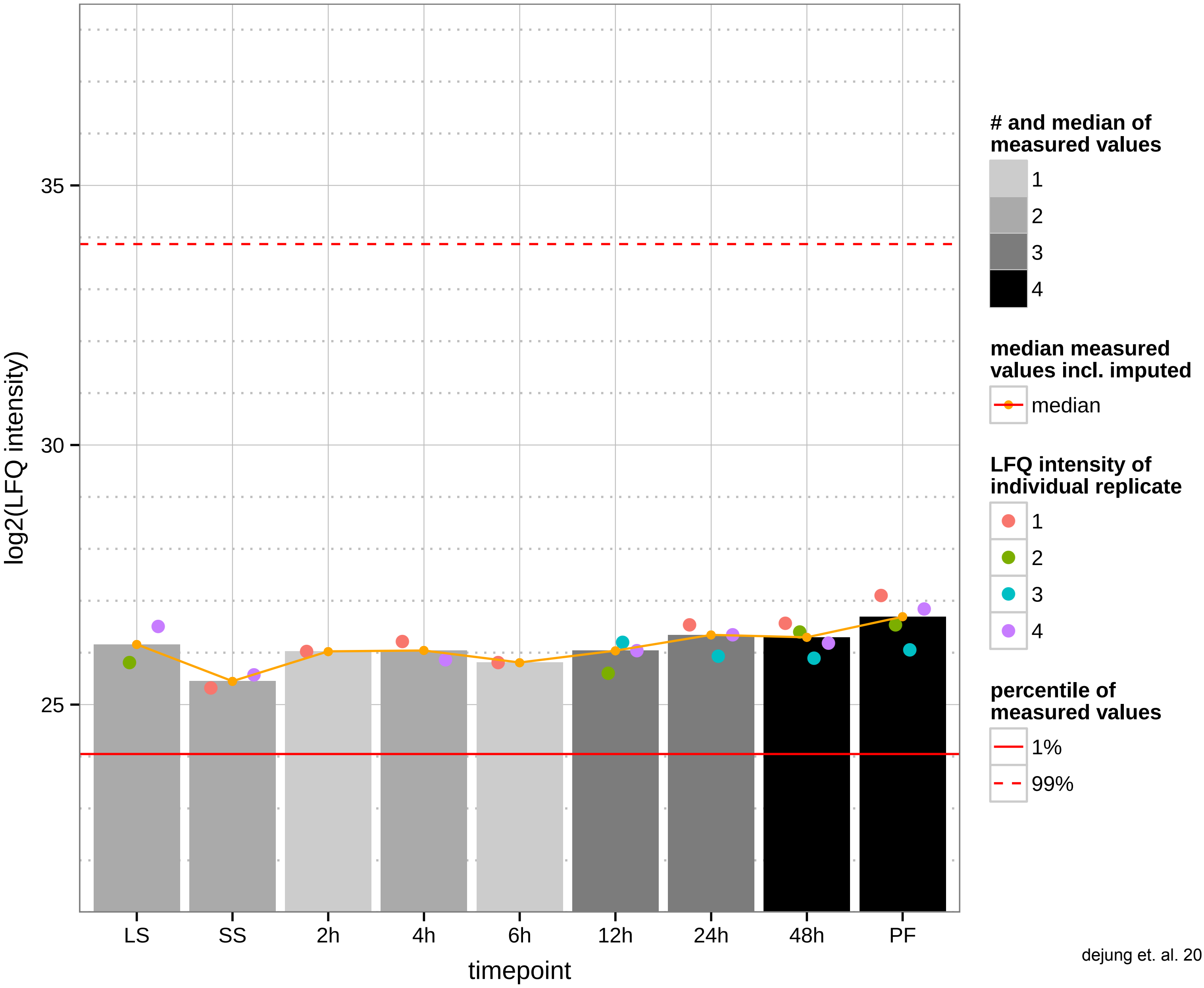
lanosterol synthase
Tb927.7.5230
AGOF: lanosterol synthase activity
AGOC: integral to membrane
AGOP: sterol biosynthetic process
PGOF: catalytic activity, intramolecular transferase activity
PGOC: null
PGOP: null





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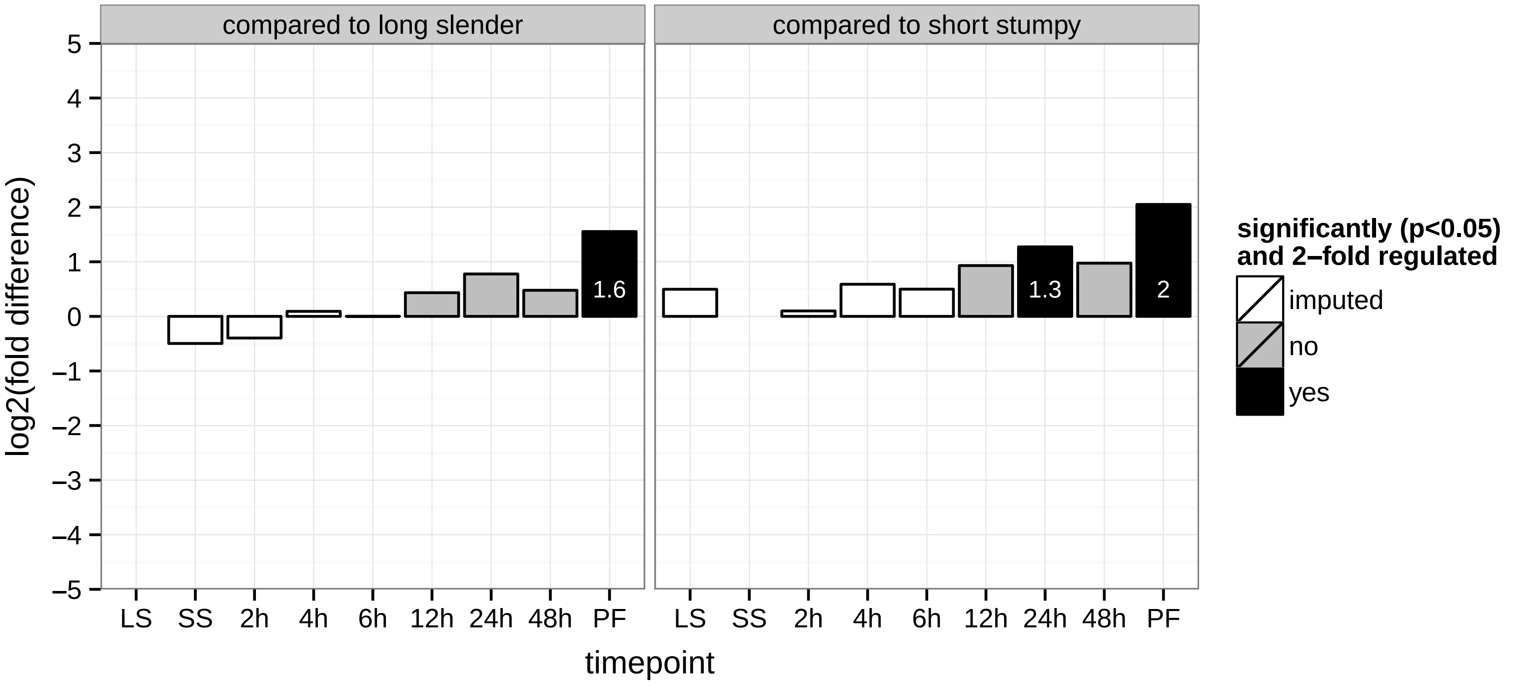
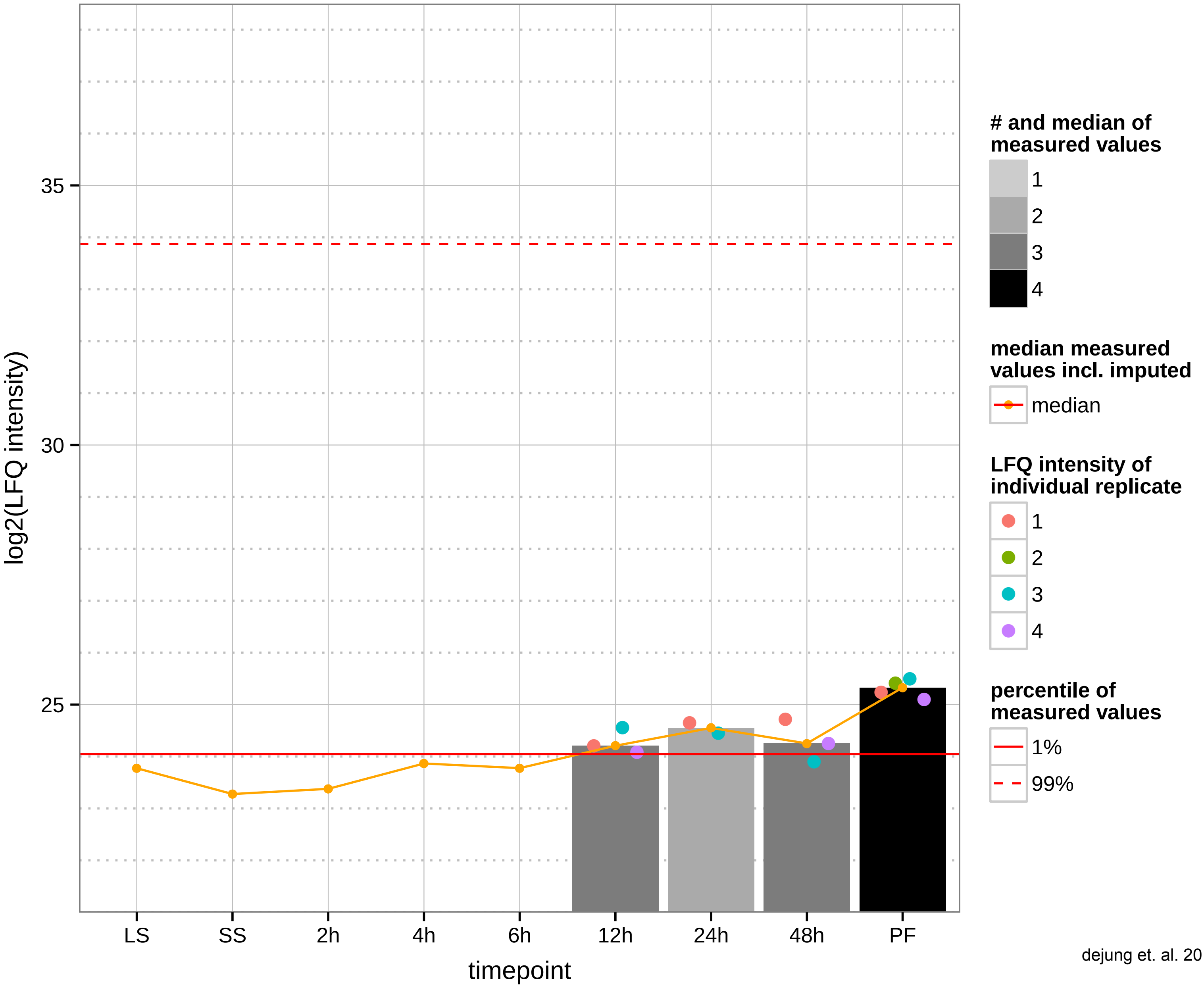
5'–3' exonuclease XRNC, putative, exoribonuclease 2, putative (XRNC)
Tb927.8.2810
AGOF: exonuclease activity, nucleic acid binding
AGOC: intracellular, nucleus
AGOP: RNA processing
PGOF: exonuclease activity, nucleic acid binding
PGOC: intracellular
PGOP: null





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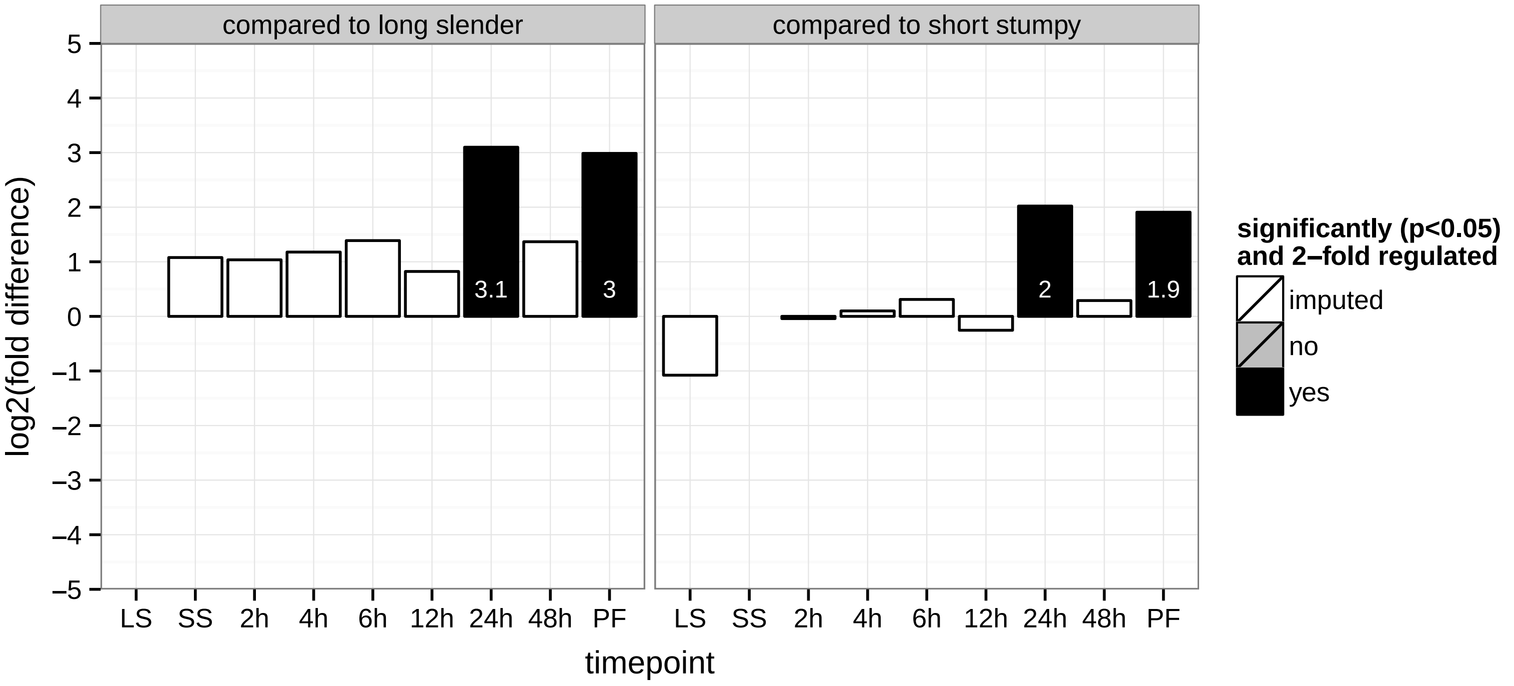
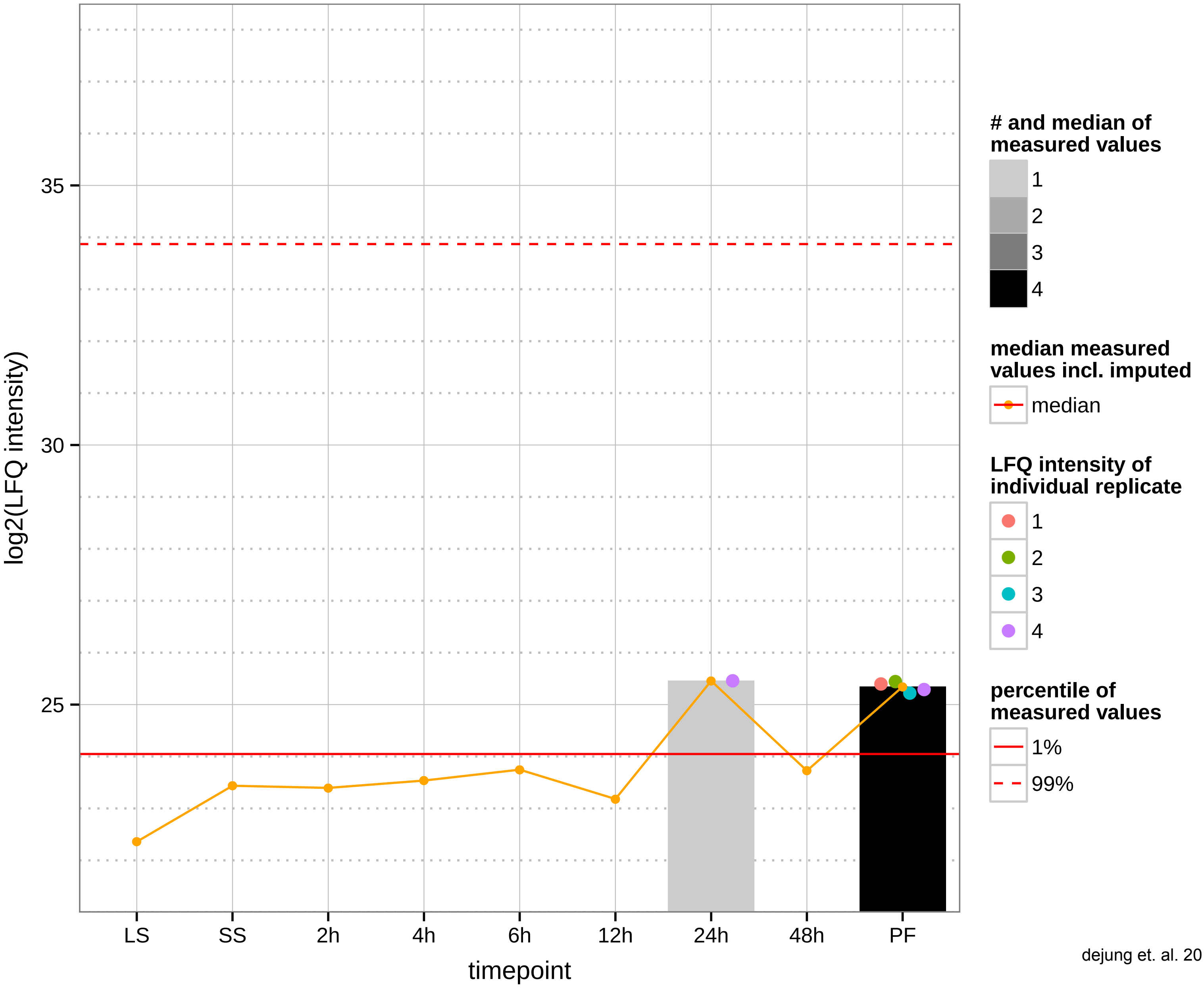
hypothetical protein, conserved
Tb927.8.5220
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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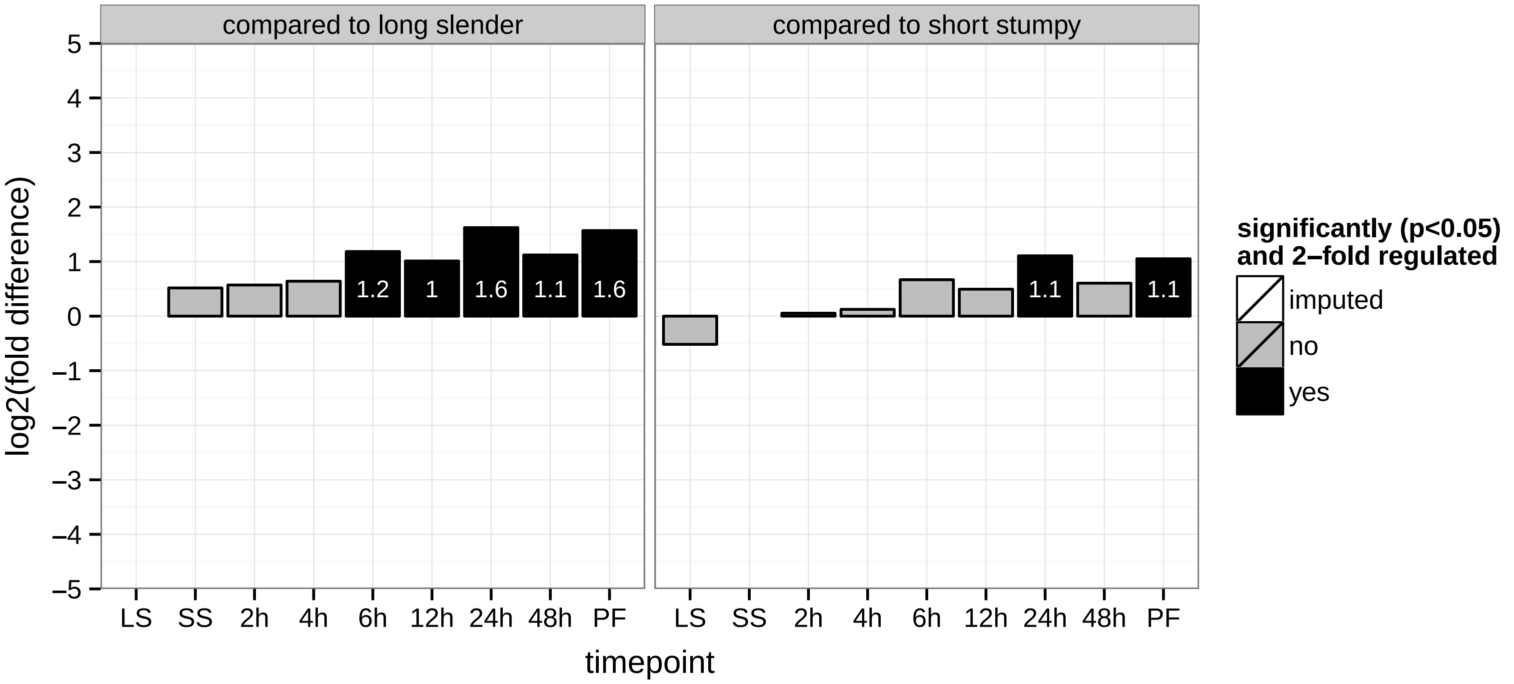
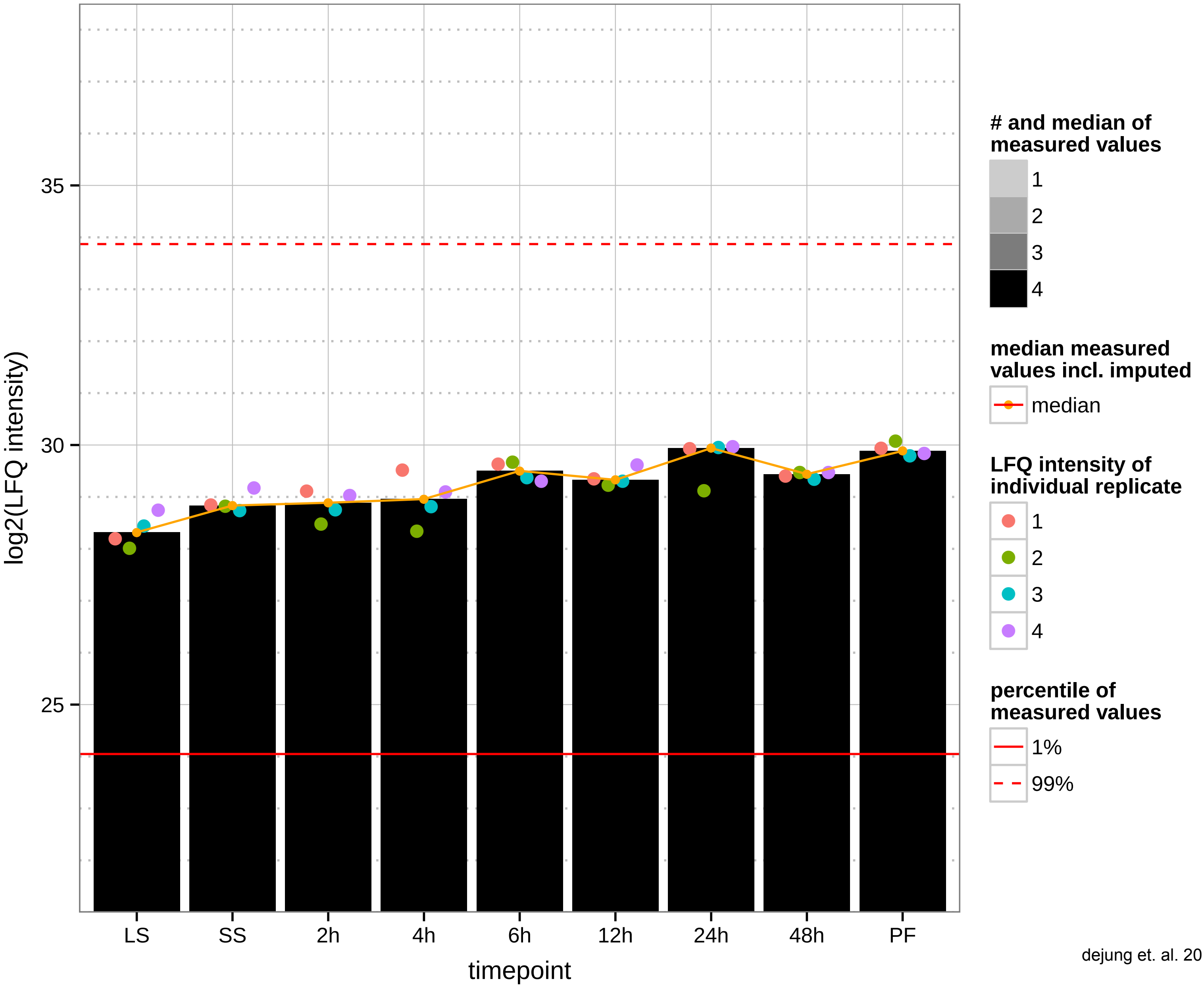
hypothetical protein, conserved
Tb927.9.9630
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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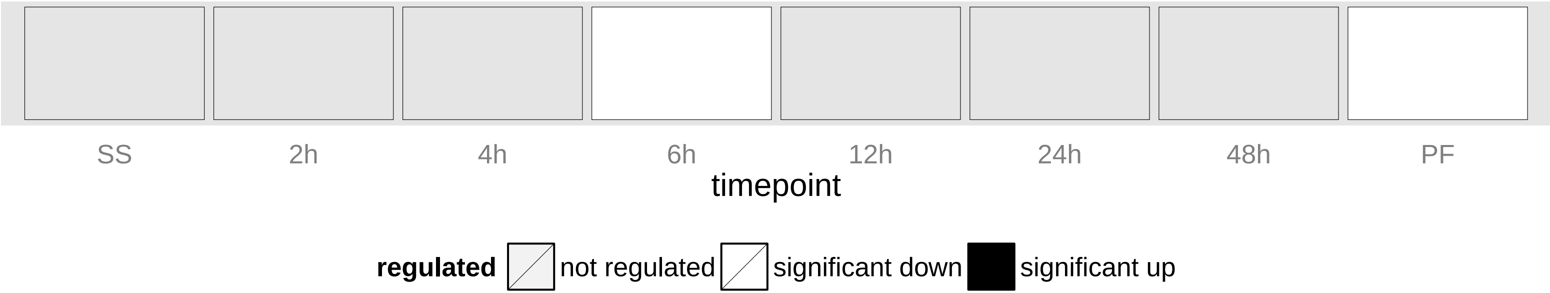

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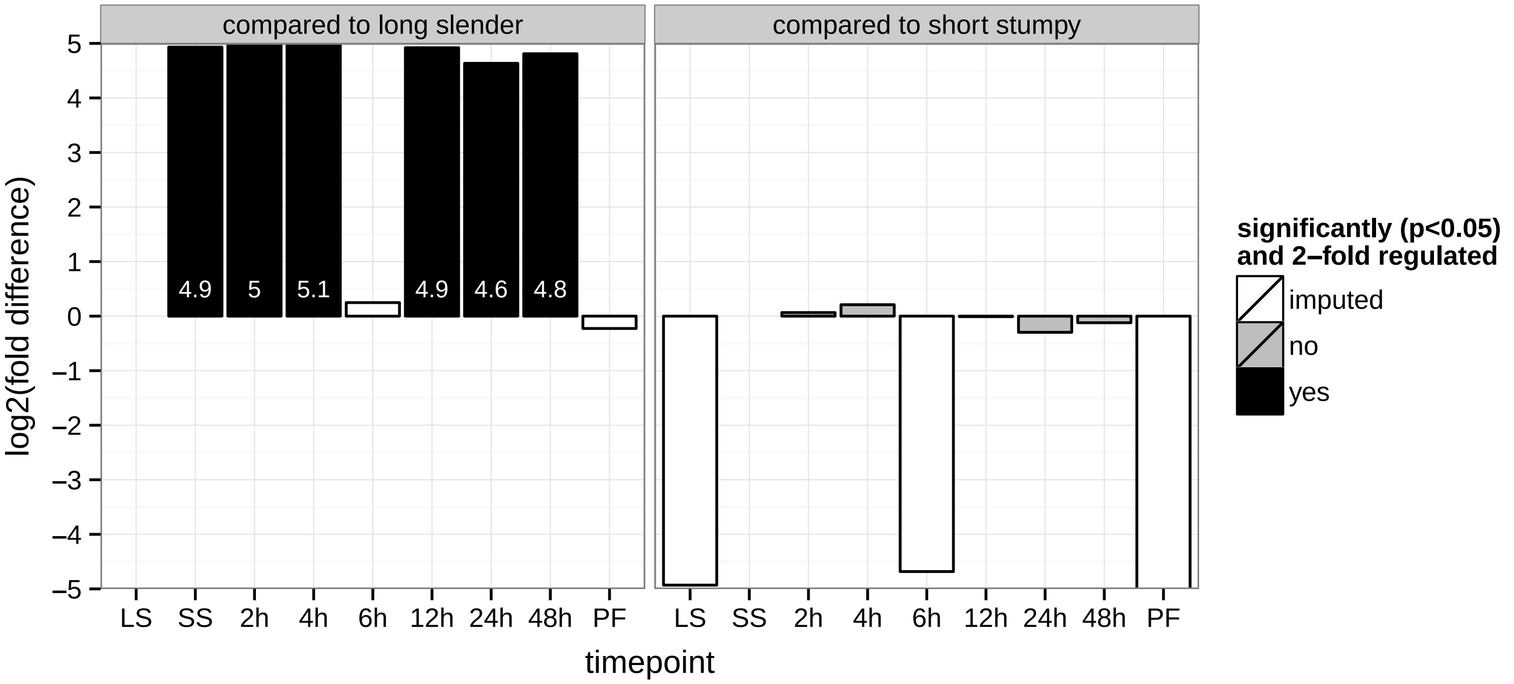
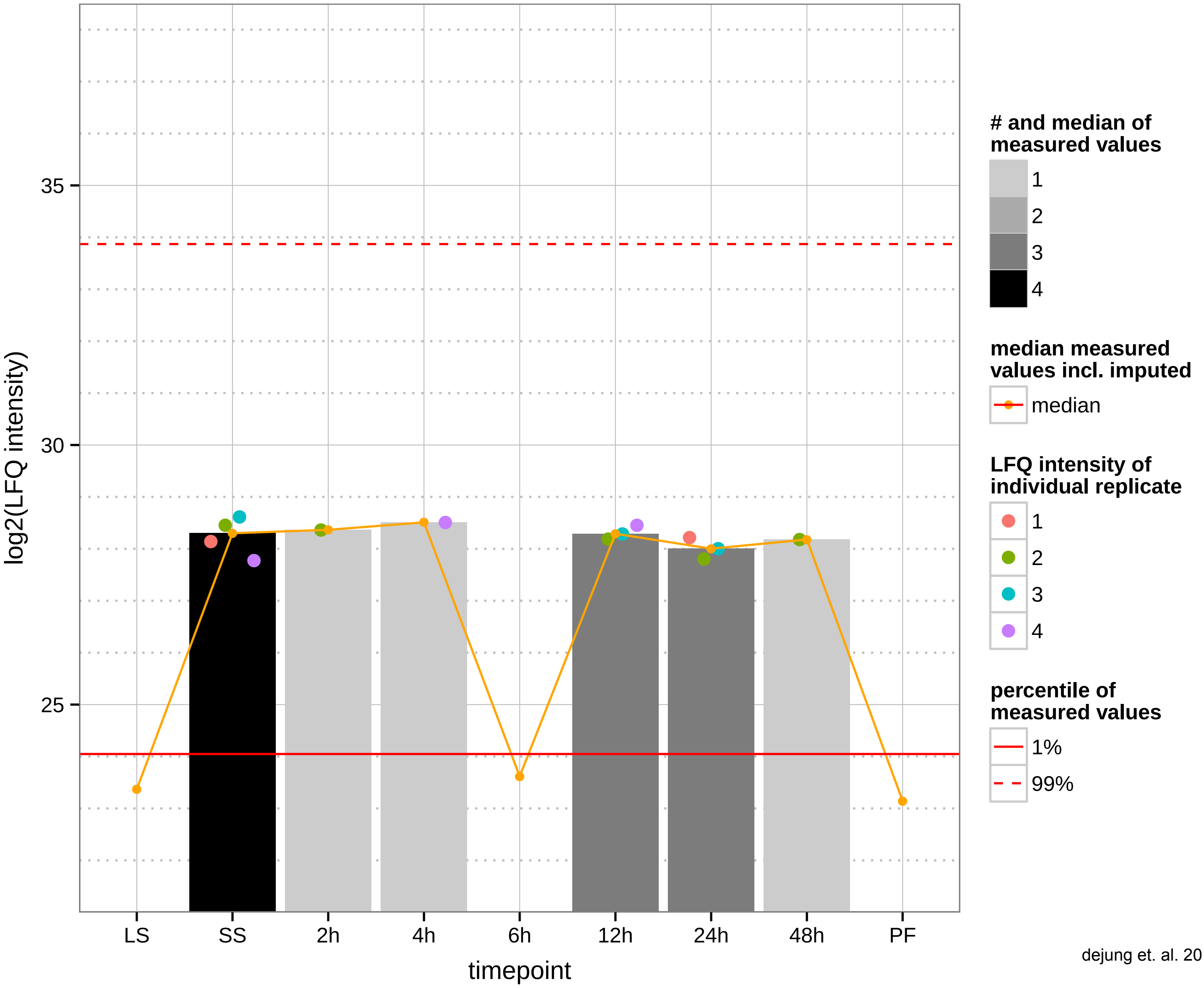
hypothetical protein, conserved, hypothetical transmembrane protein
Tb927.1.790;Tb11.v5.0524
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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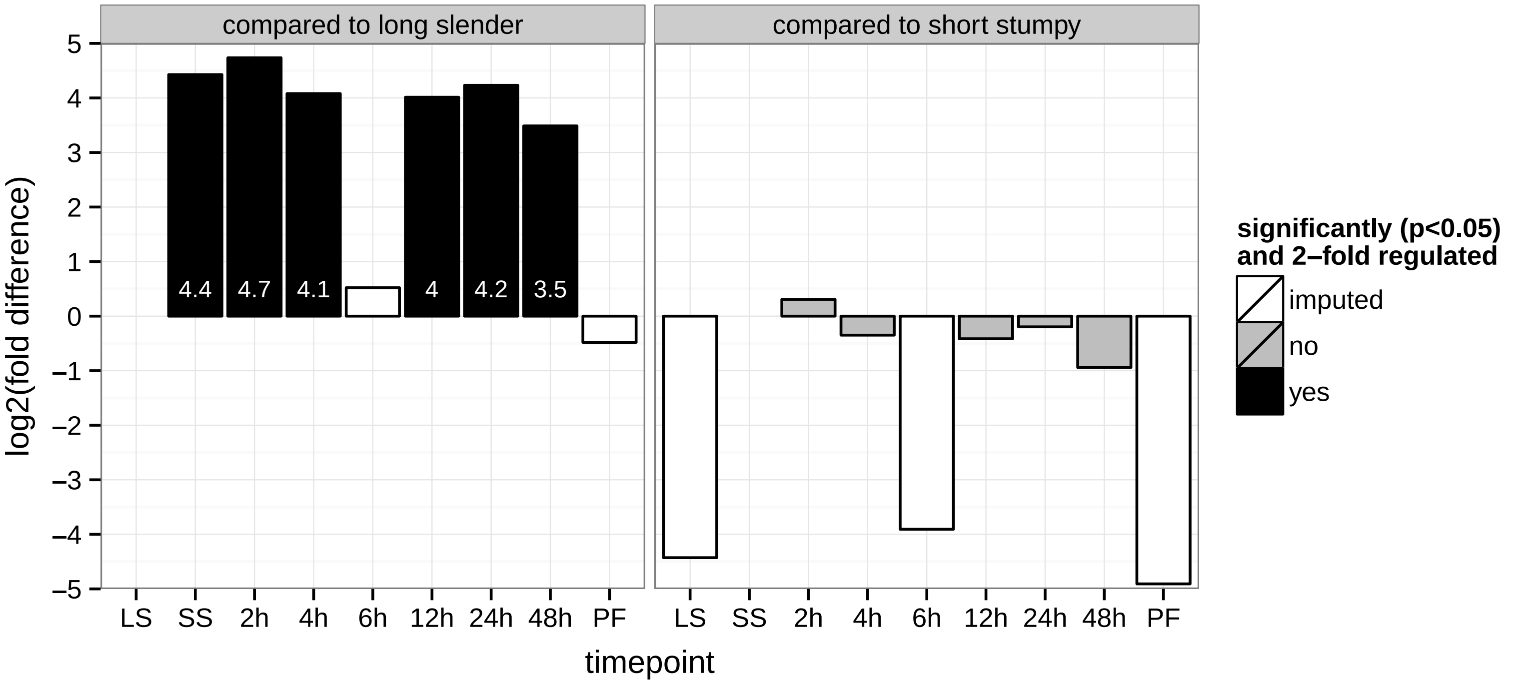
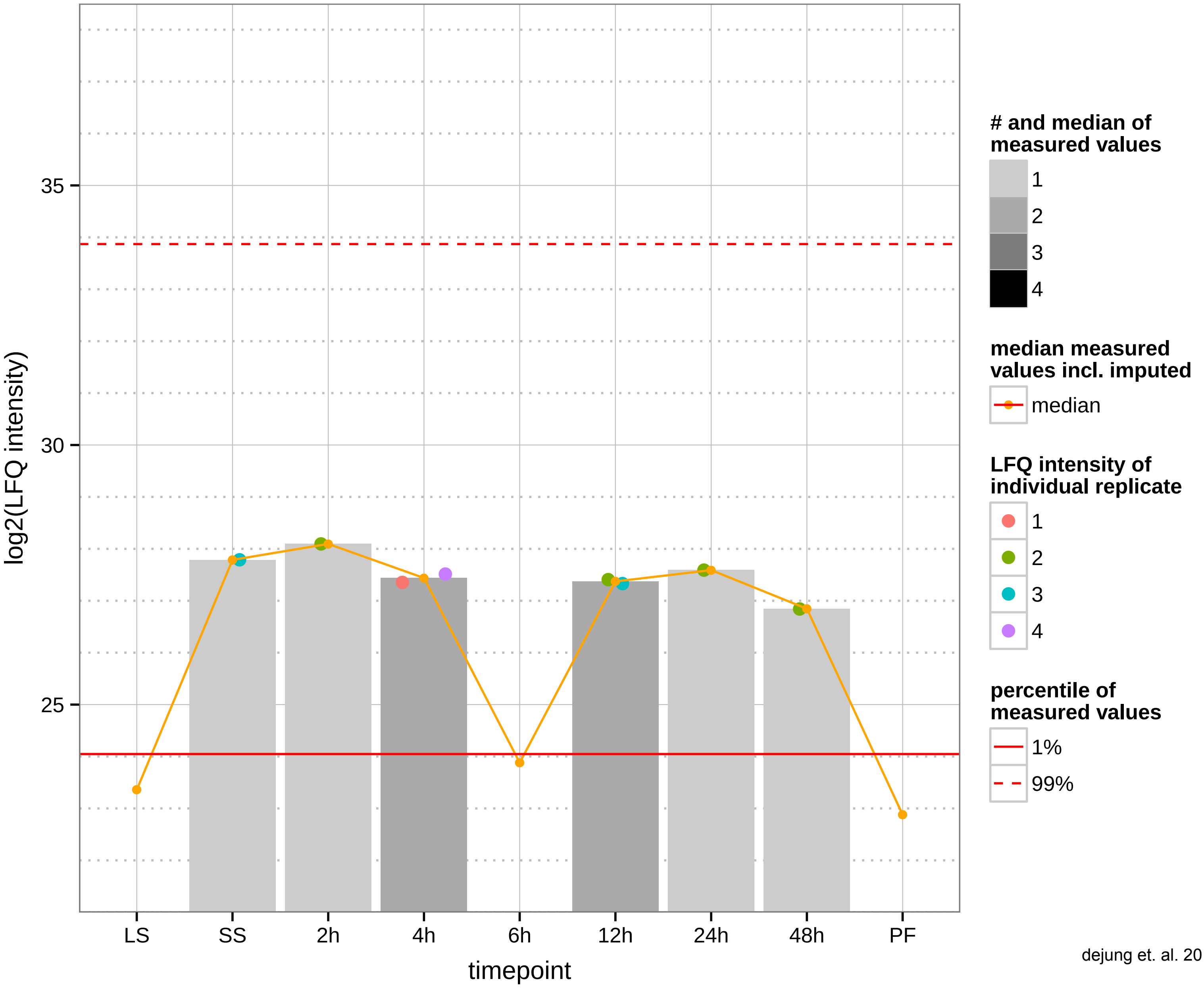
RNA–binding protein, putative (RBP27), RNA–binding protein 27
Tb927.10.14080;Tb927.10.13570
AGOF: RNA binding, nucleic acid binding
AGOC: null
AGOP: null
PGOF: null, nucleic acid binding
PGOC: null
PGOP: null





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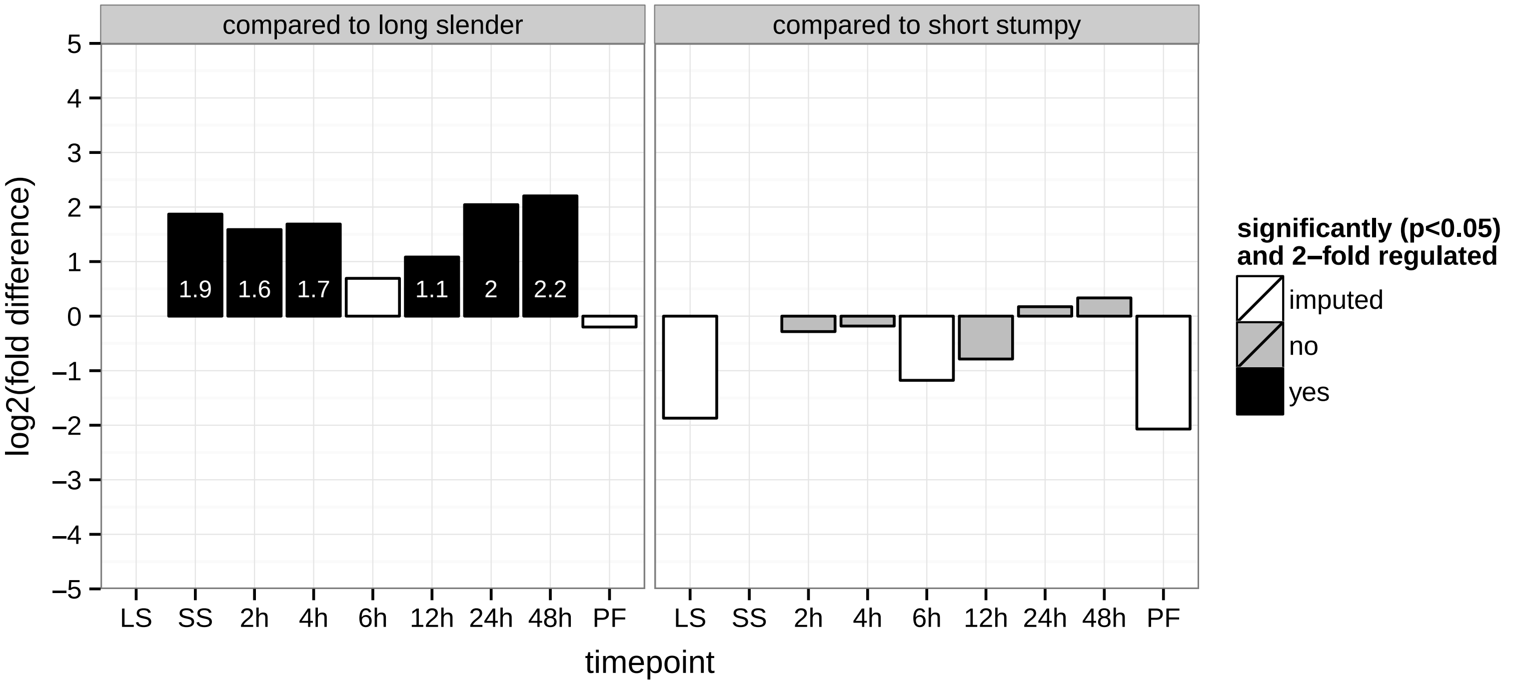
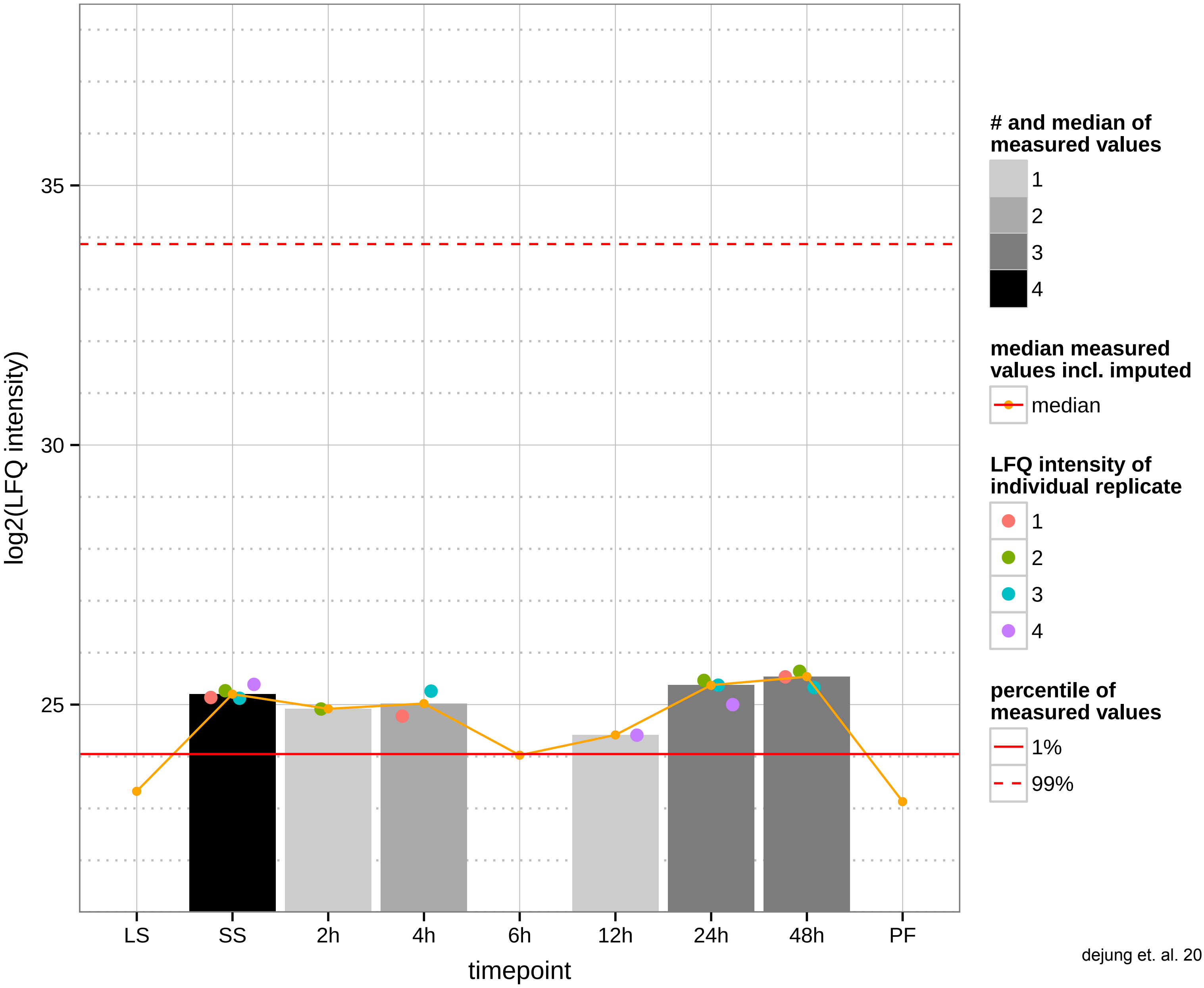
uracil–DNA glycosylase, putative
Tb927.10.13970
AGOF: uracil DNA N–glycosylase activity
AGOC: null
AGOP: base–excision repair
PGOF: uracil DNA N–glycosylase activity
PGOC: null
PGOP: base–excision repair





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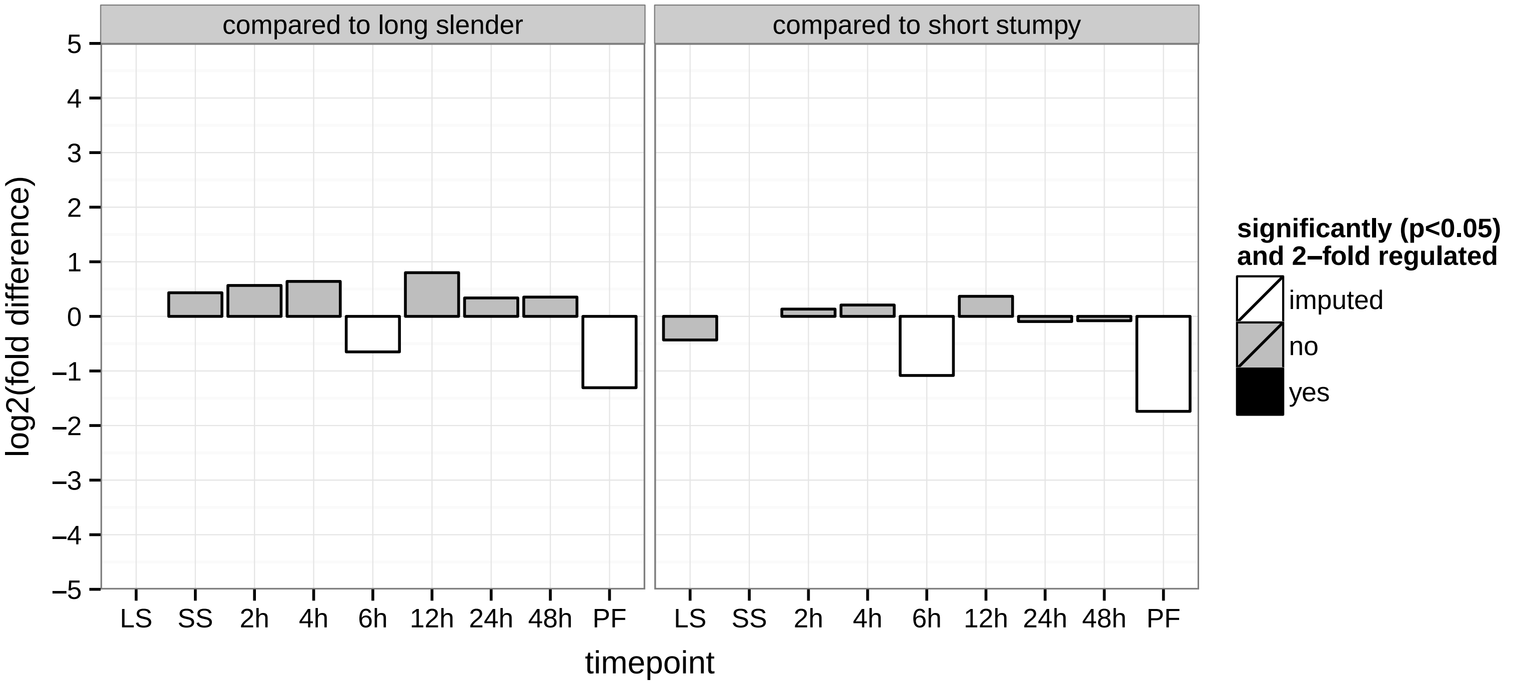
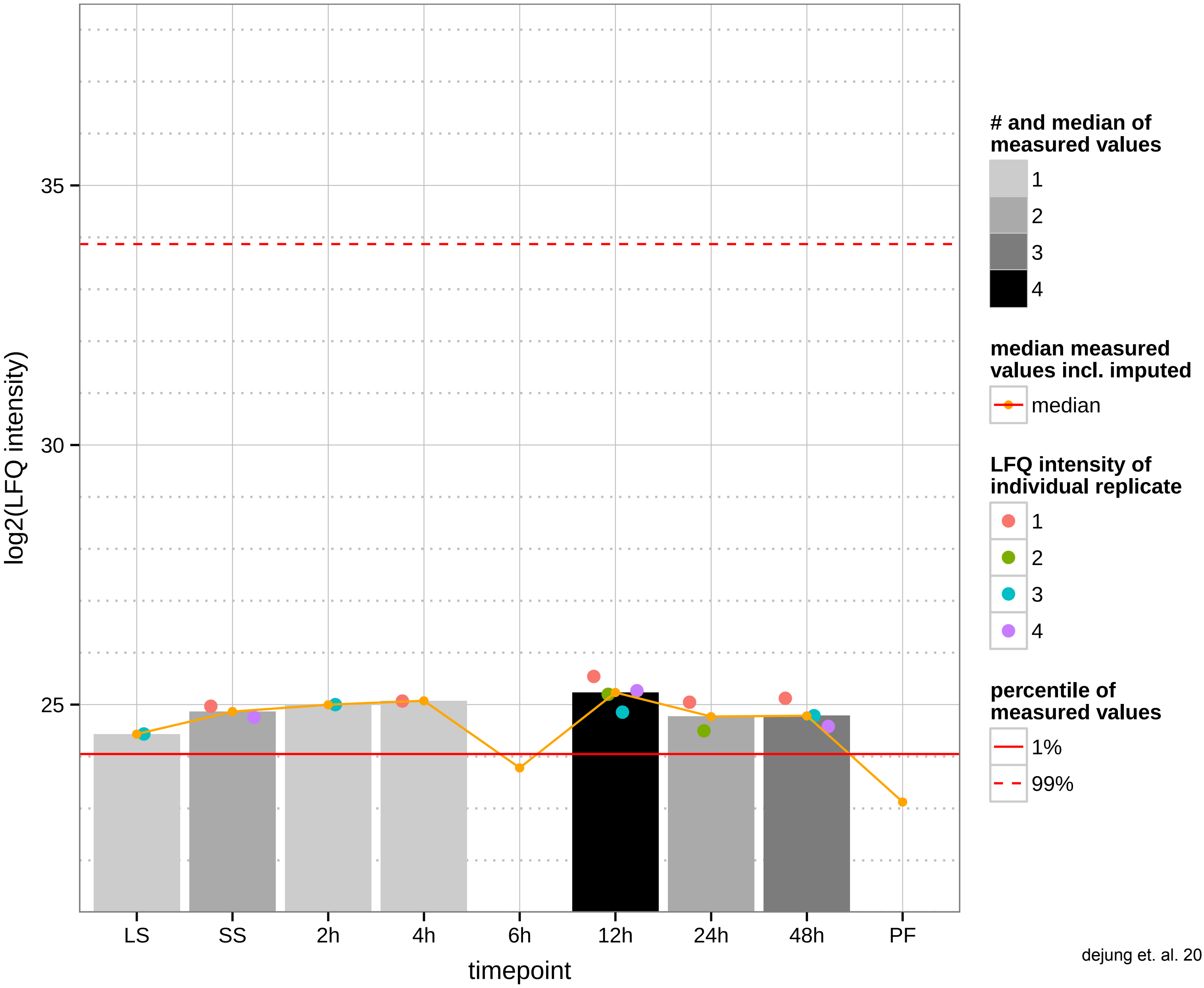
G10 protein homologue, putative
Tb927.10.6650
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: nucleus
PGOP: null





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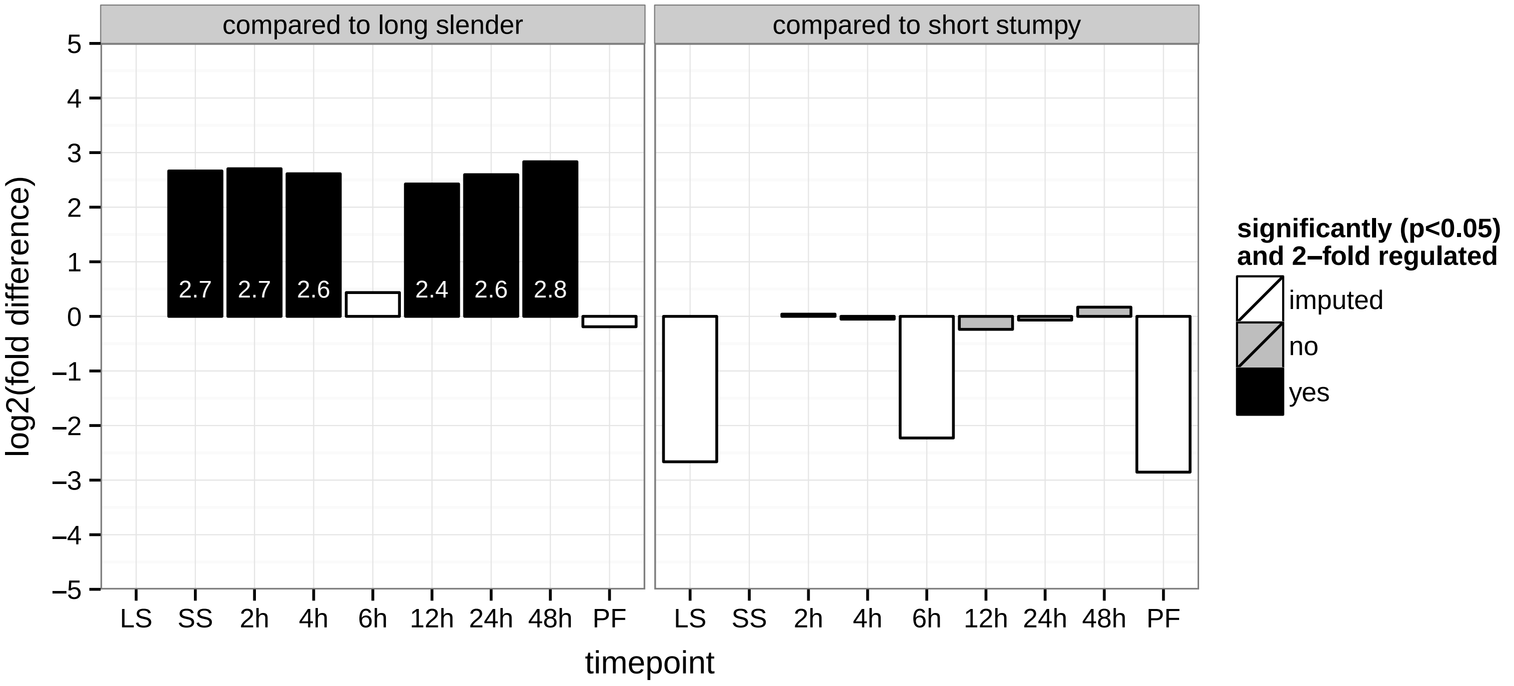
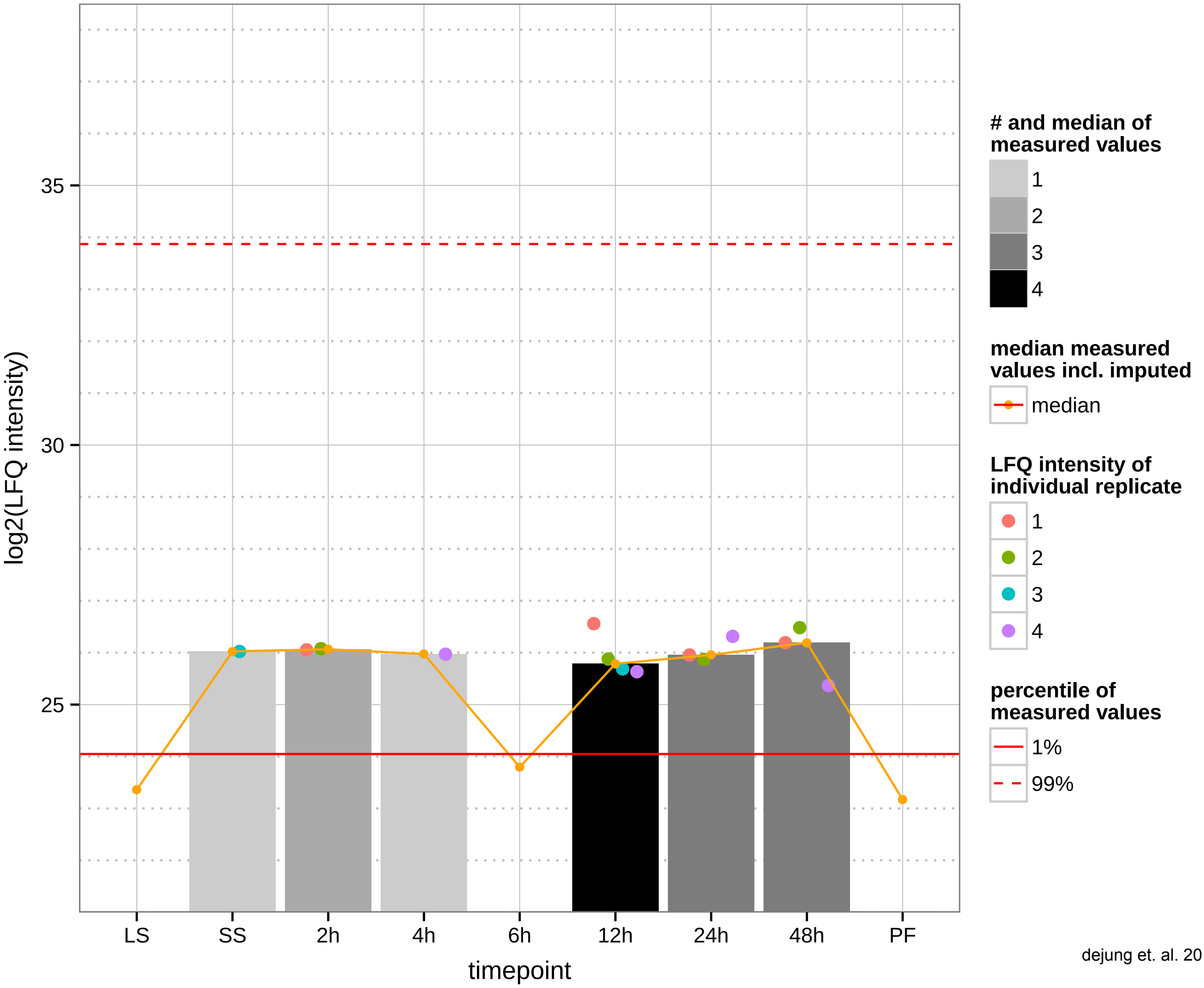
Poly(A)–specific ribonuclease PARN–2
Tb927.10.8360
AGOF: nuclease activity, nucleic acid binding
AGOC: nucleus
AGOP: null
PGOF: nucleic acid binding
PGOC: nucleus
PGOP: null





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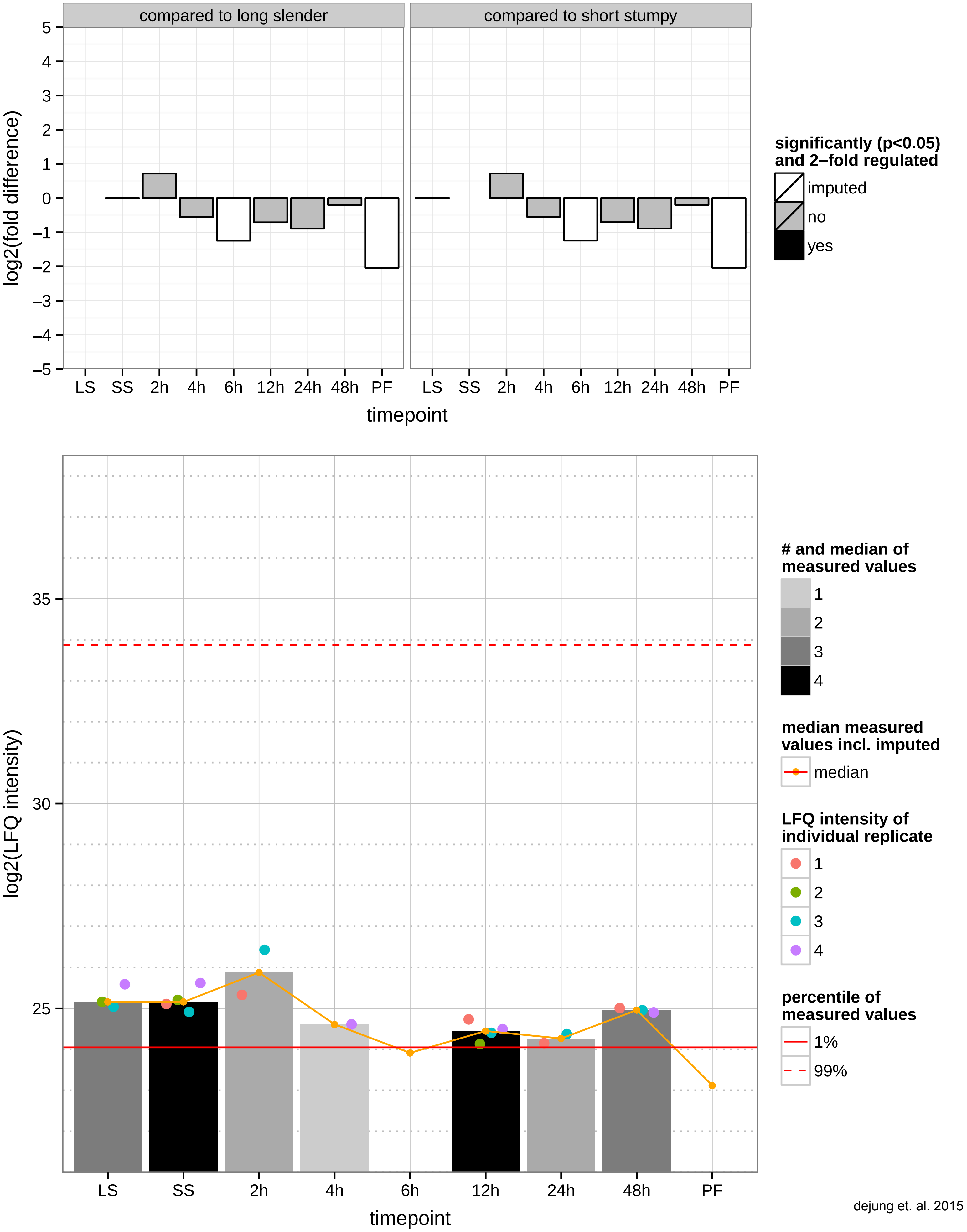
hypothetical protein, conserved
Tb927.11.13460
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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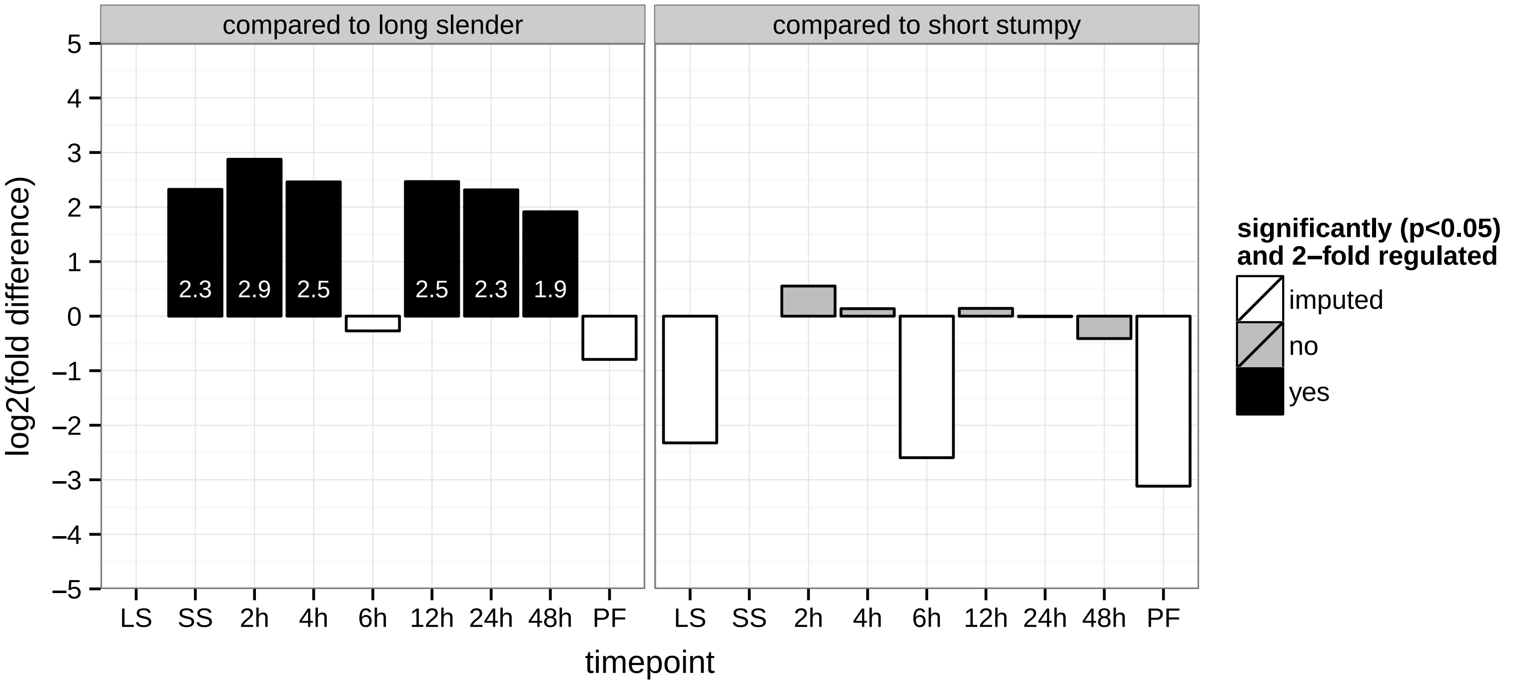
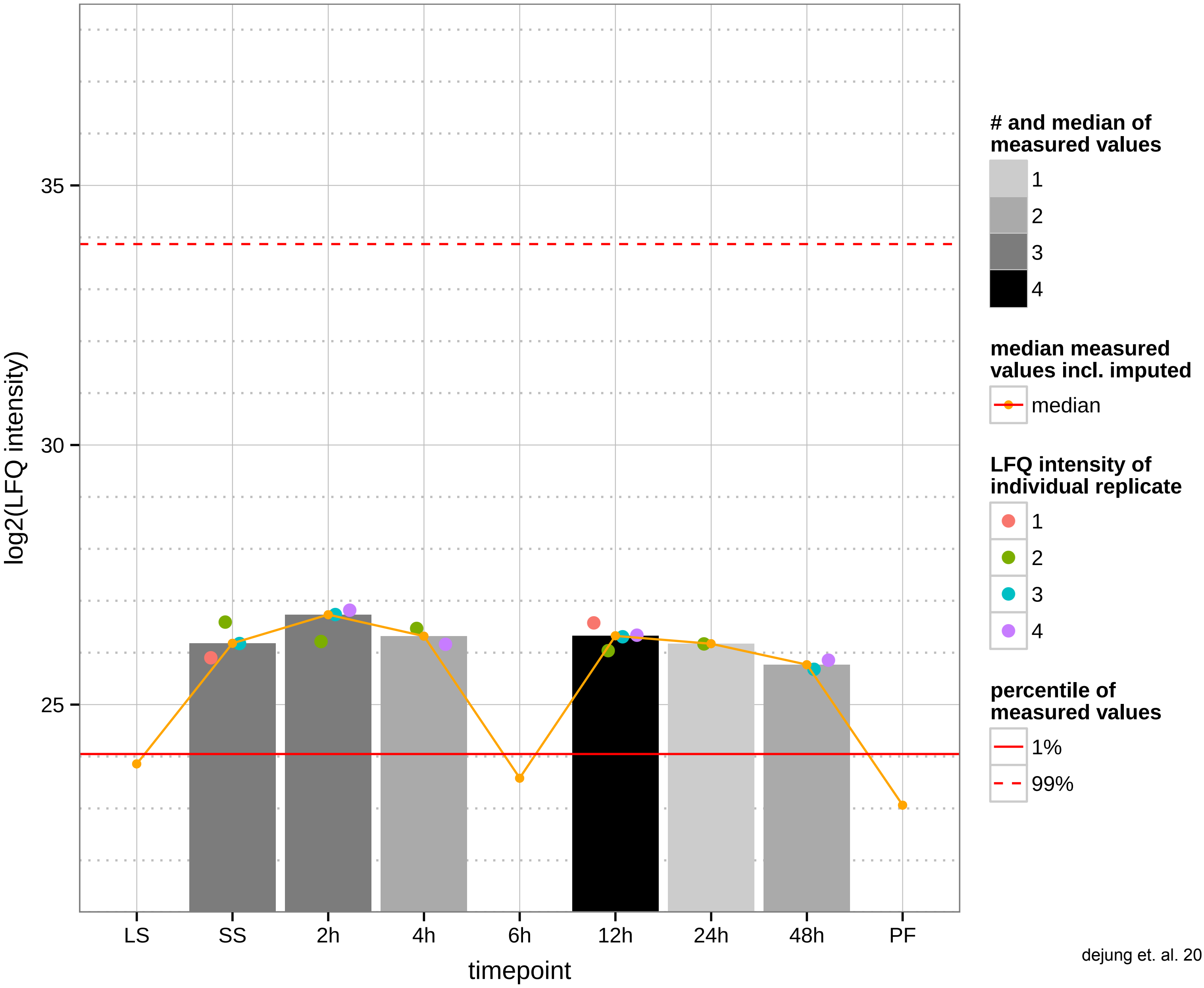
hypothetical protein, conserved
Tb927.11.620
AGOF: null
AGOC: null
AGOP: null
PGOF: binding, protein binding
PGOC: null
PGOP: null





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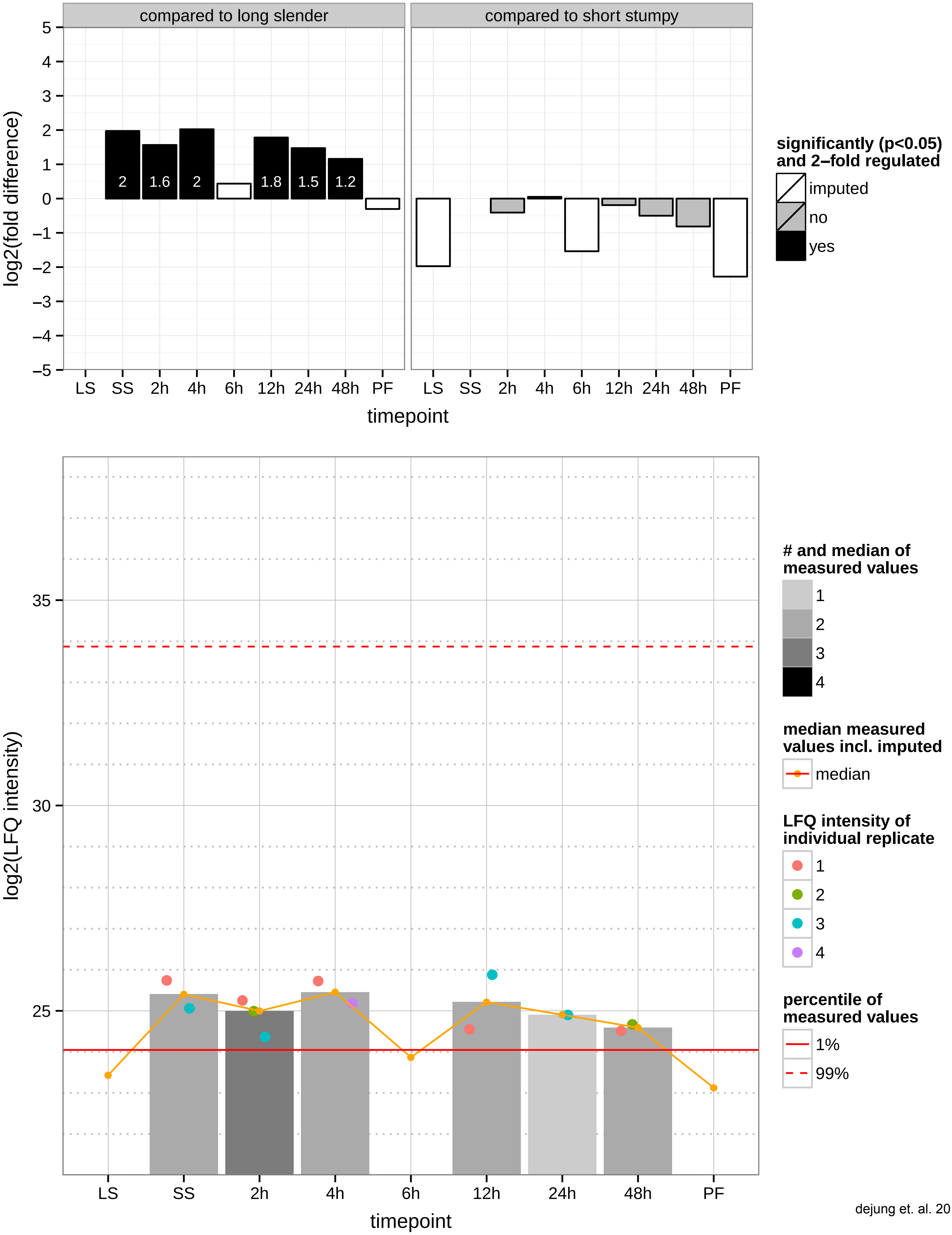
protein phosphatase 2C, putative
Tb927.2.5050
AGOF: phosphatase activity
AGOC: null
AGOP: dephosphorylation
PGOF: catalytic activity
PGOC: null
PGOP: null



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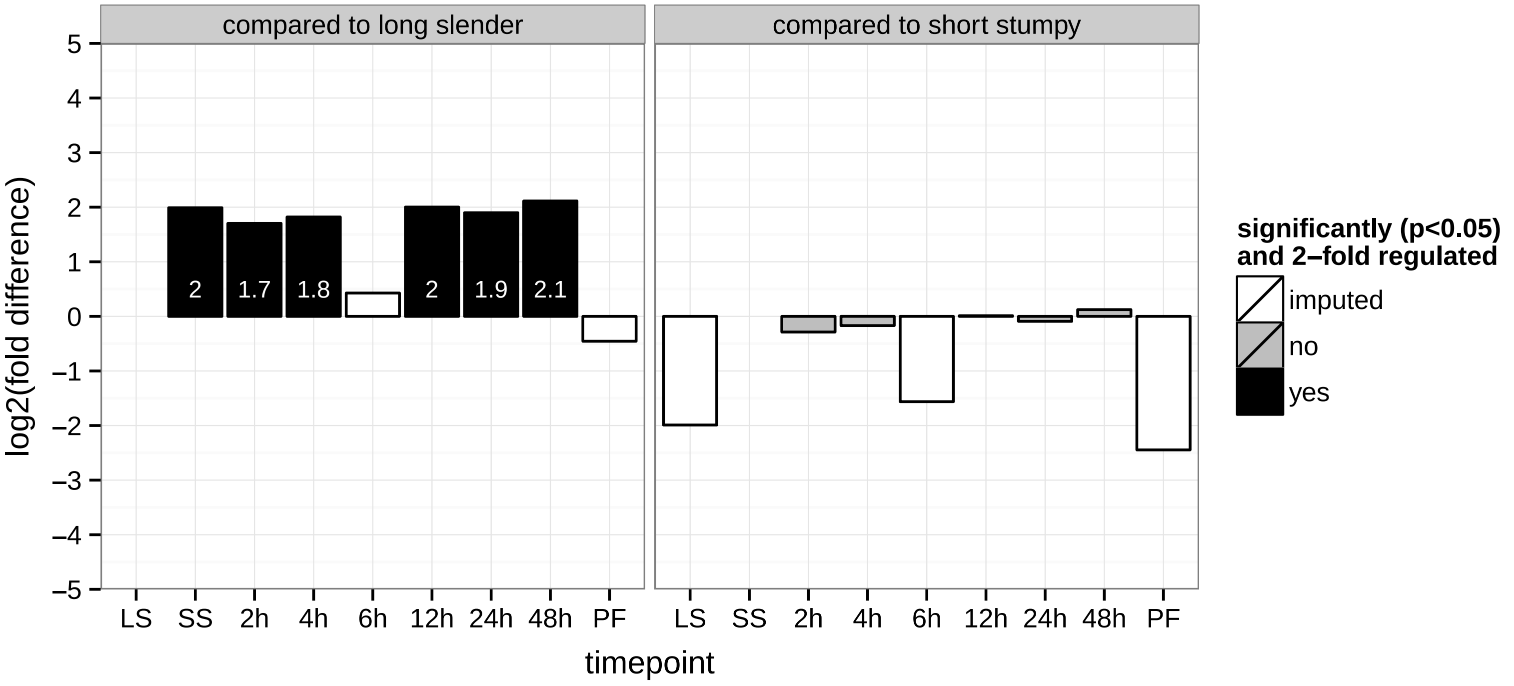
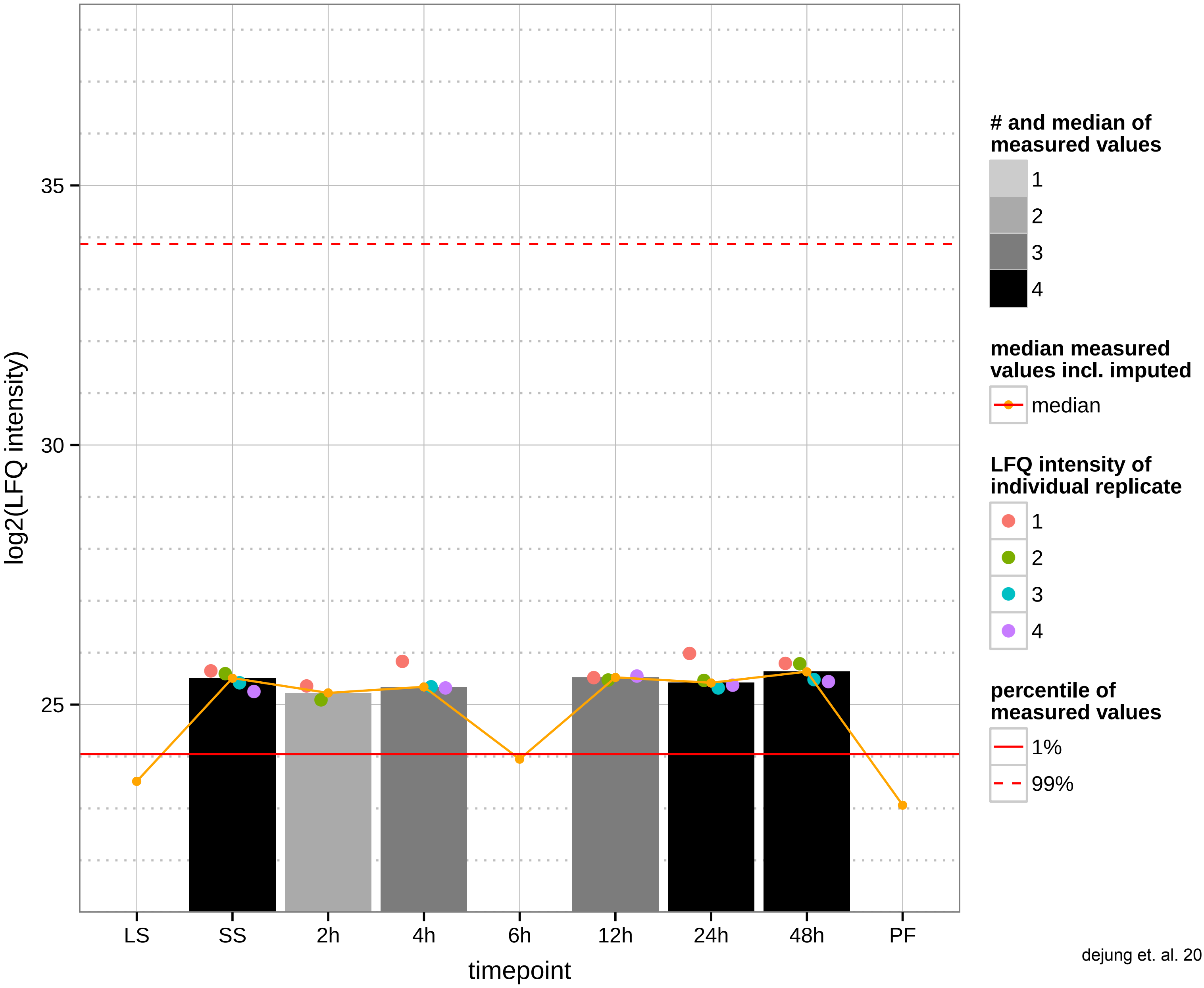
vesicle–associated membrane protein, putative, synaptobrevin
Tb927.2.5120
AGOF: null
AGOC: integral to membrane
AGOP: membrane fusion, vesicle–mediated transport
PGOF: null
PGOC: integral to membrane
PGOP: transport, vesicle–mediated transport





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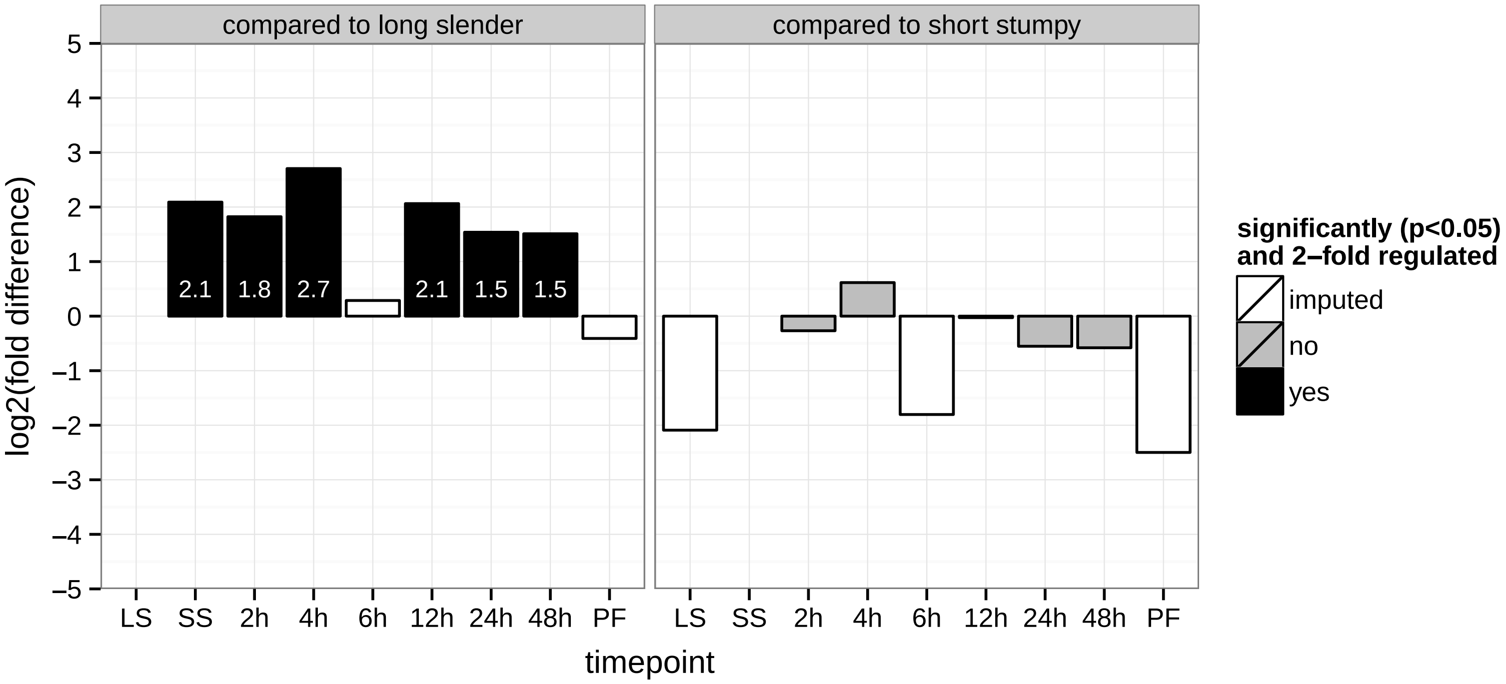
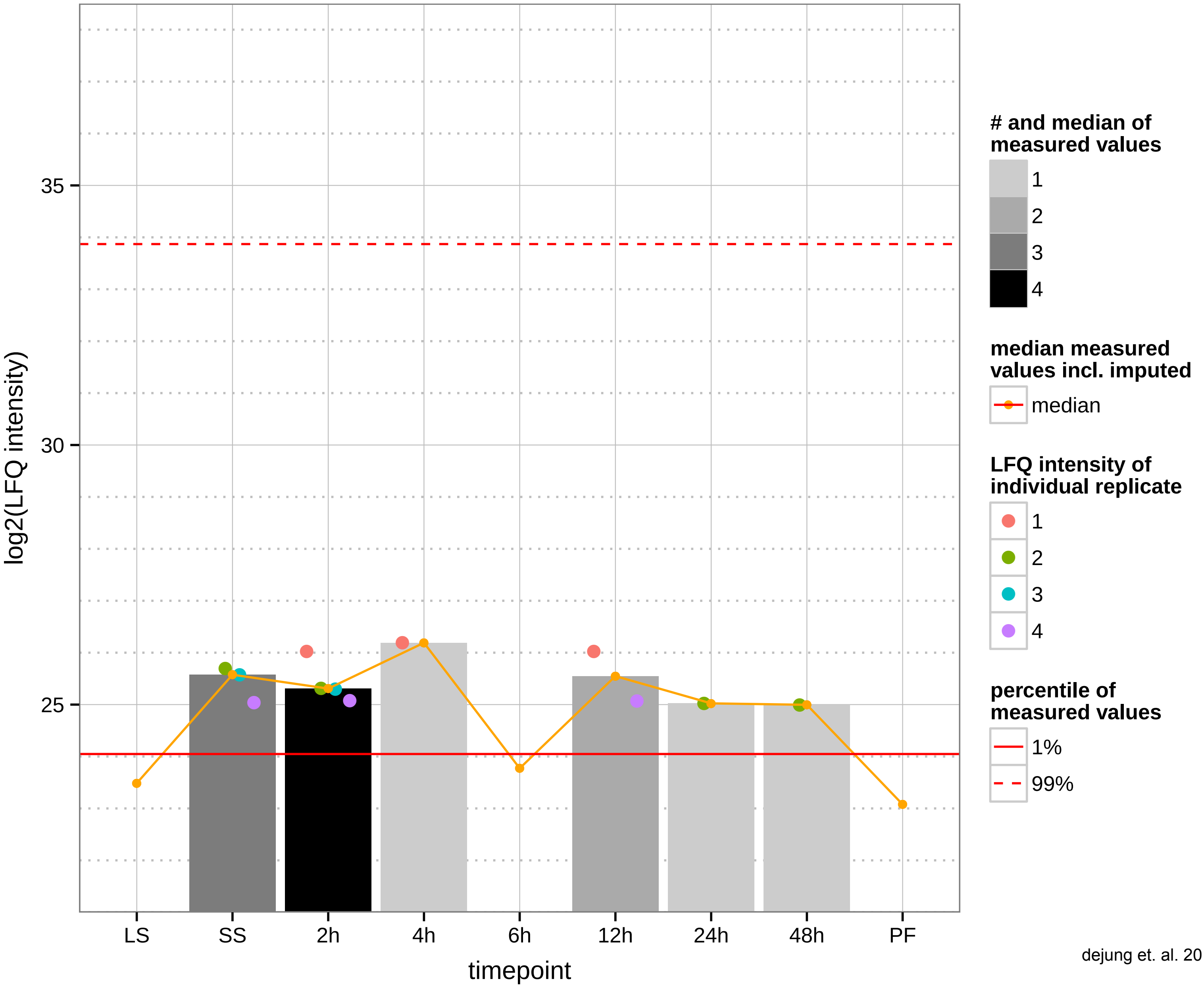
casein kinase 1, putative (CK1)
Tb927.3.1630
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: cytoplasm, cytoskeleton, integral to membrane, nucleus
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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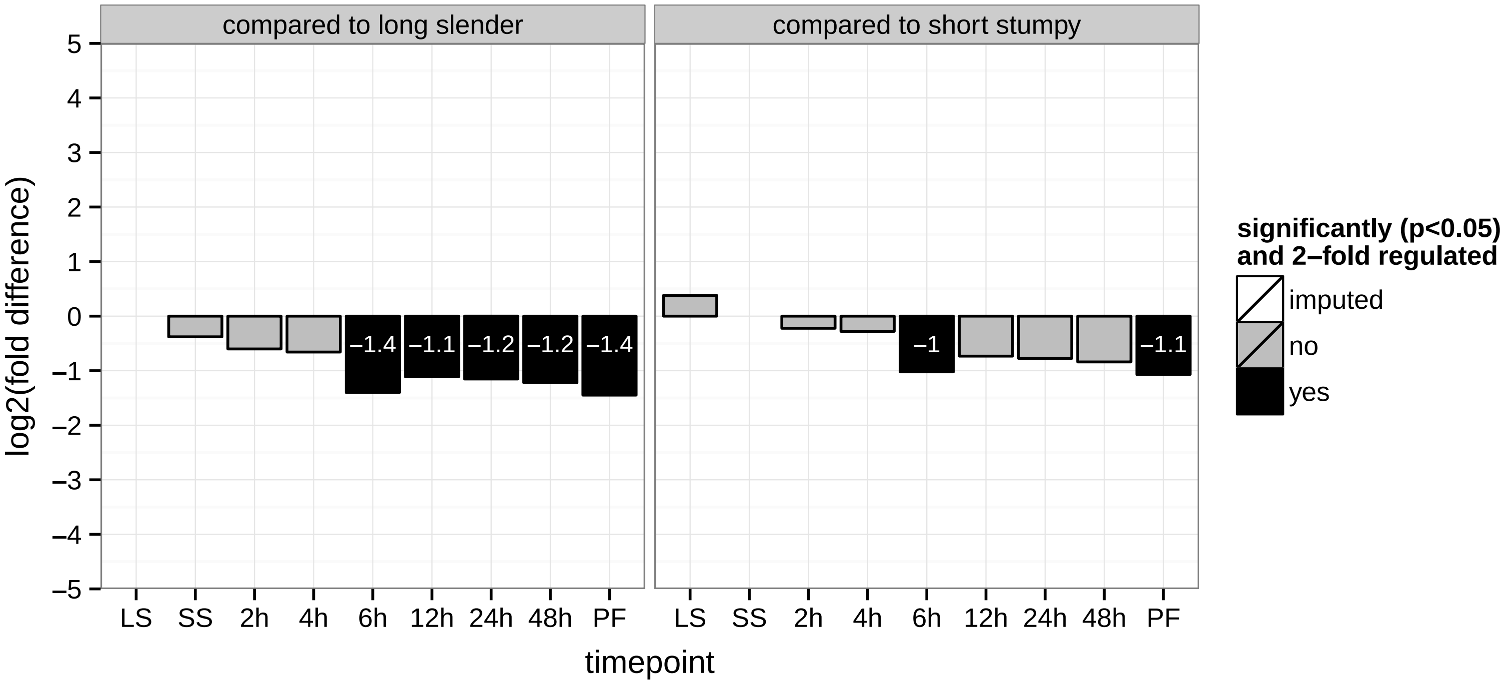
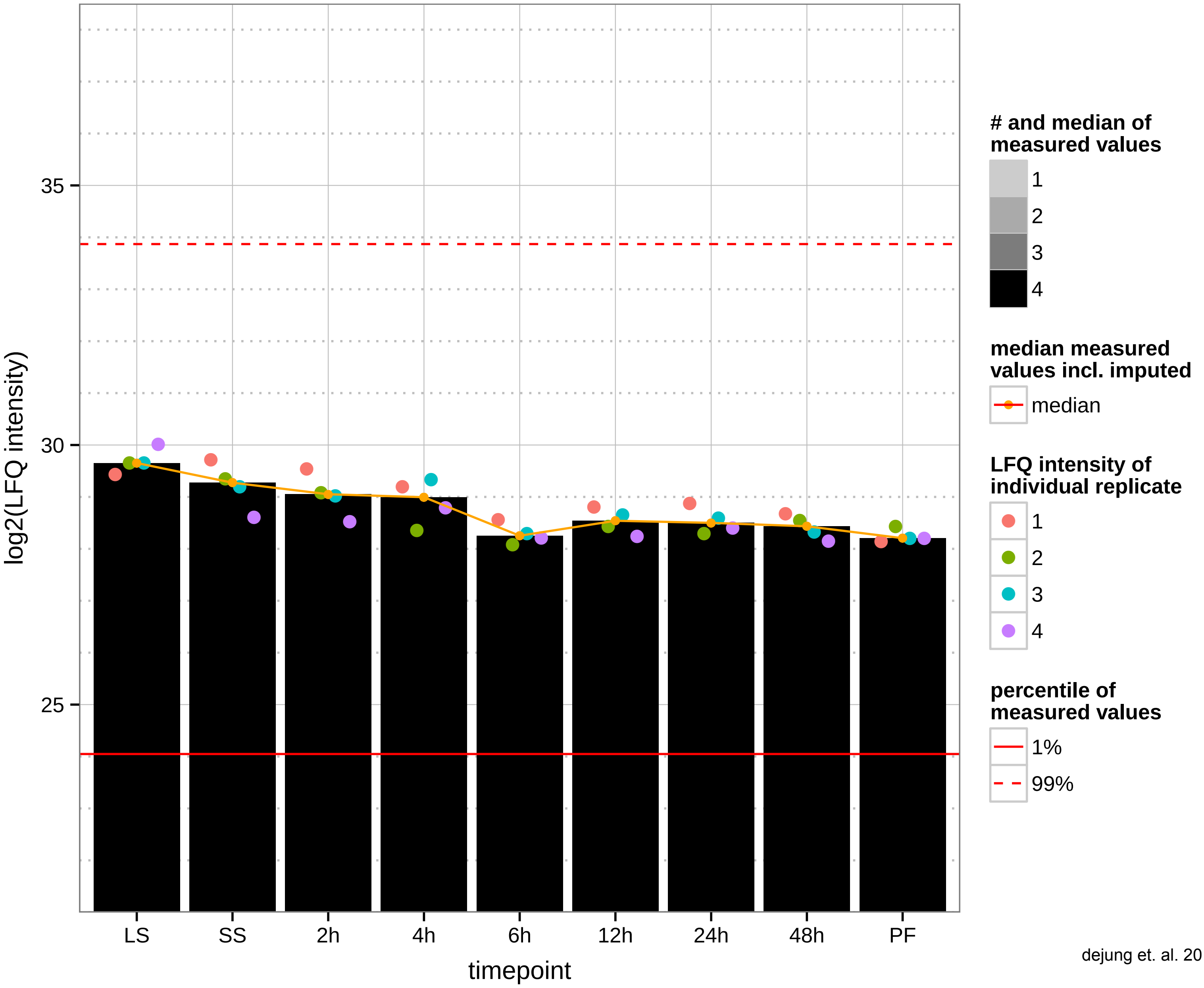
hypothetical protein, conserved
Tb927.3.4070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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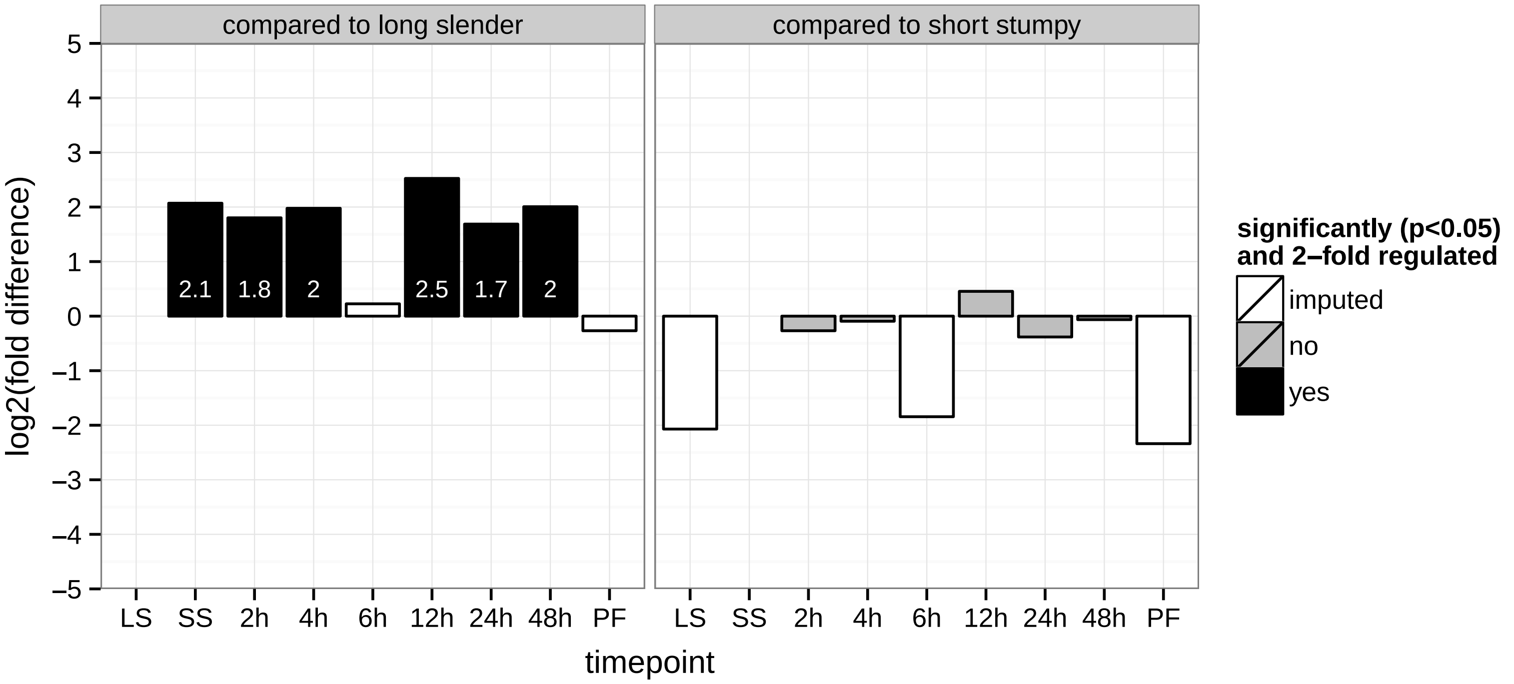
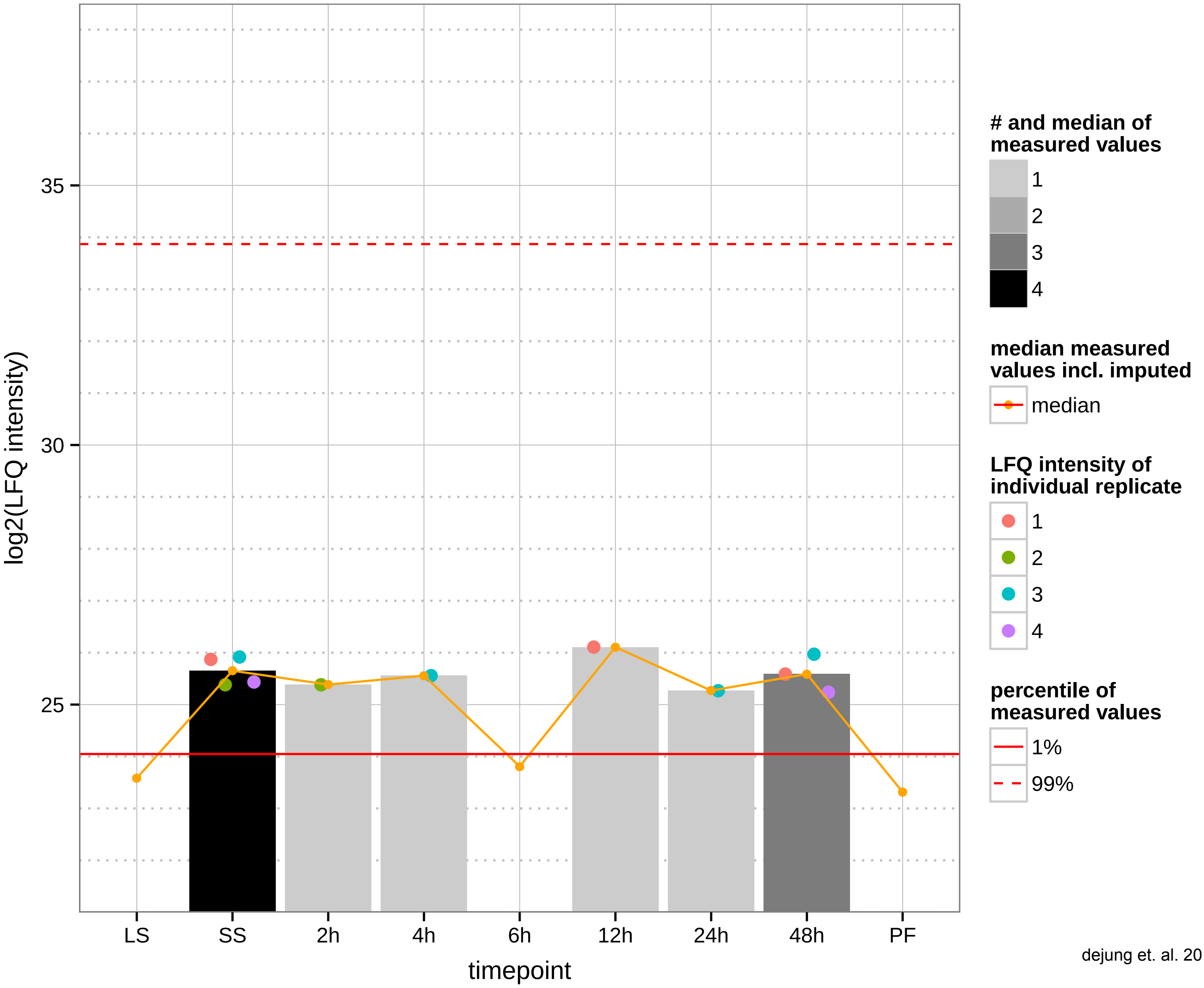
hypothetical protein, conserved
Tb927.4.3310
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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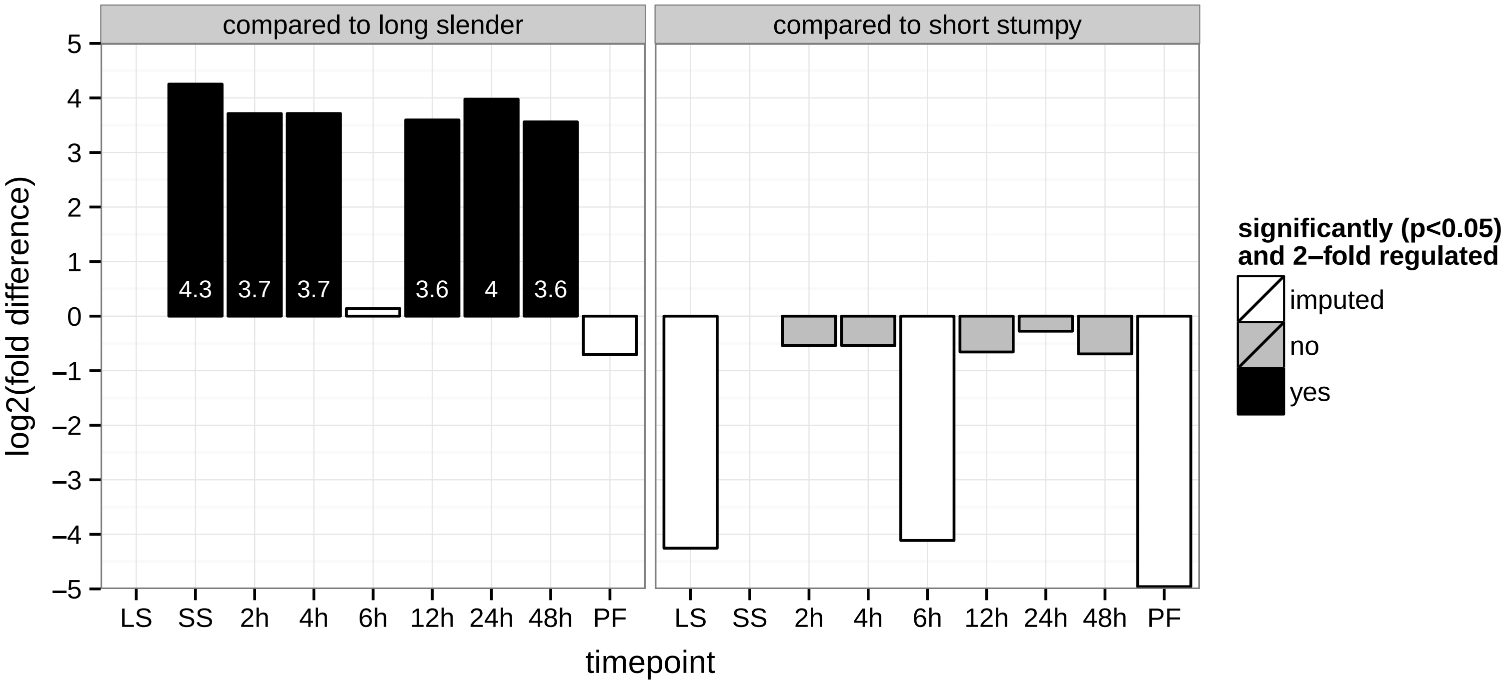
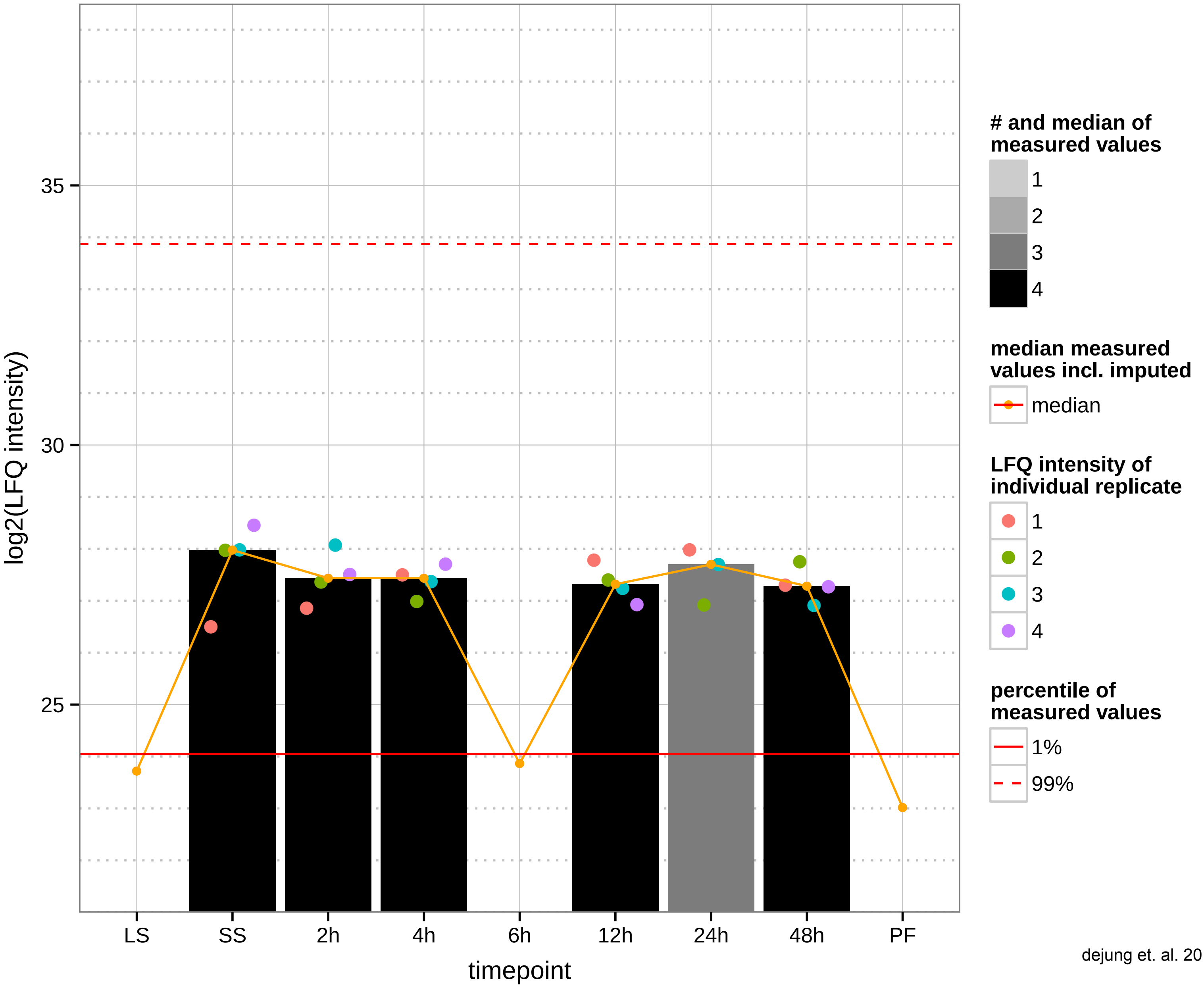
hypothetical protein, conserved
Tb927.5.3550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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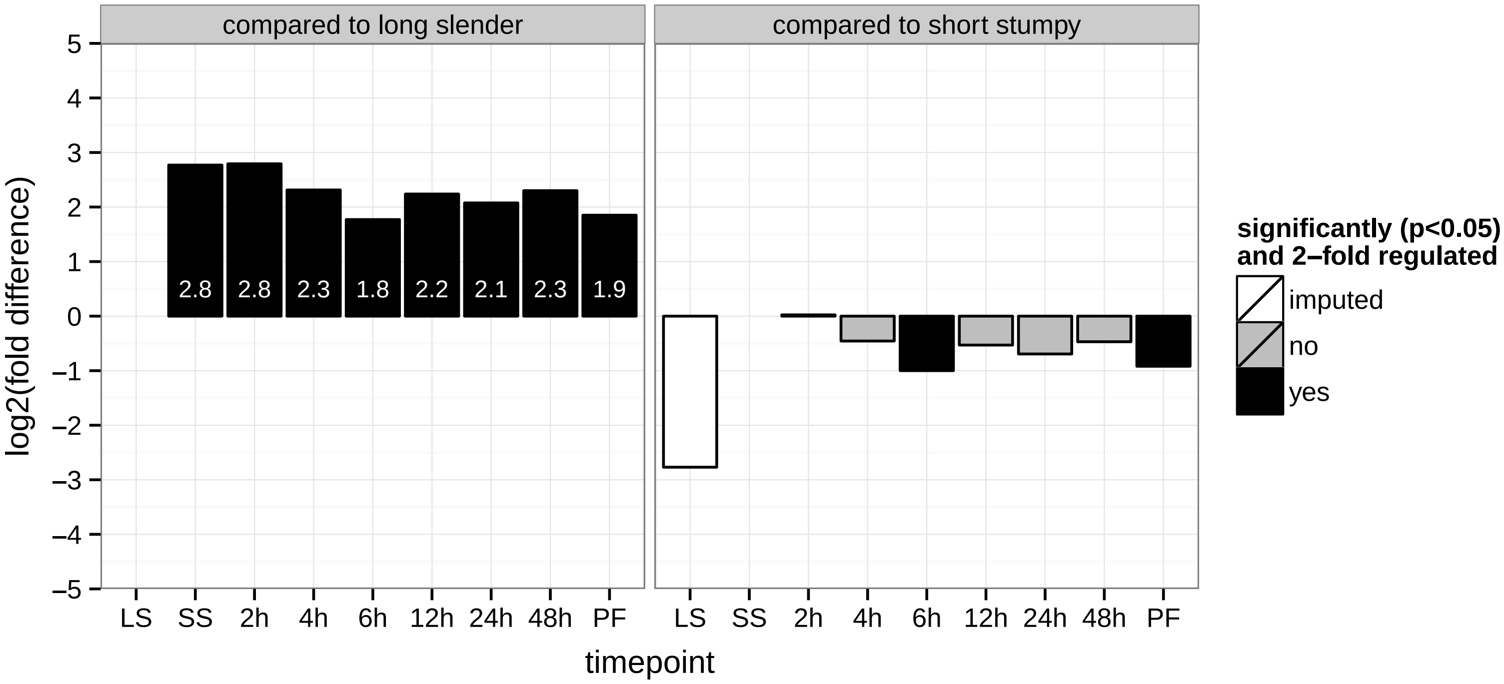
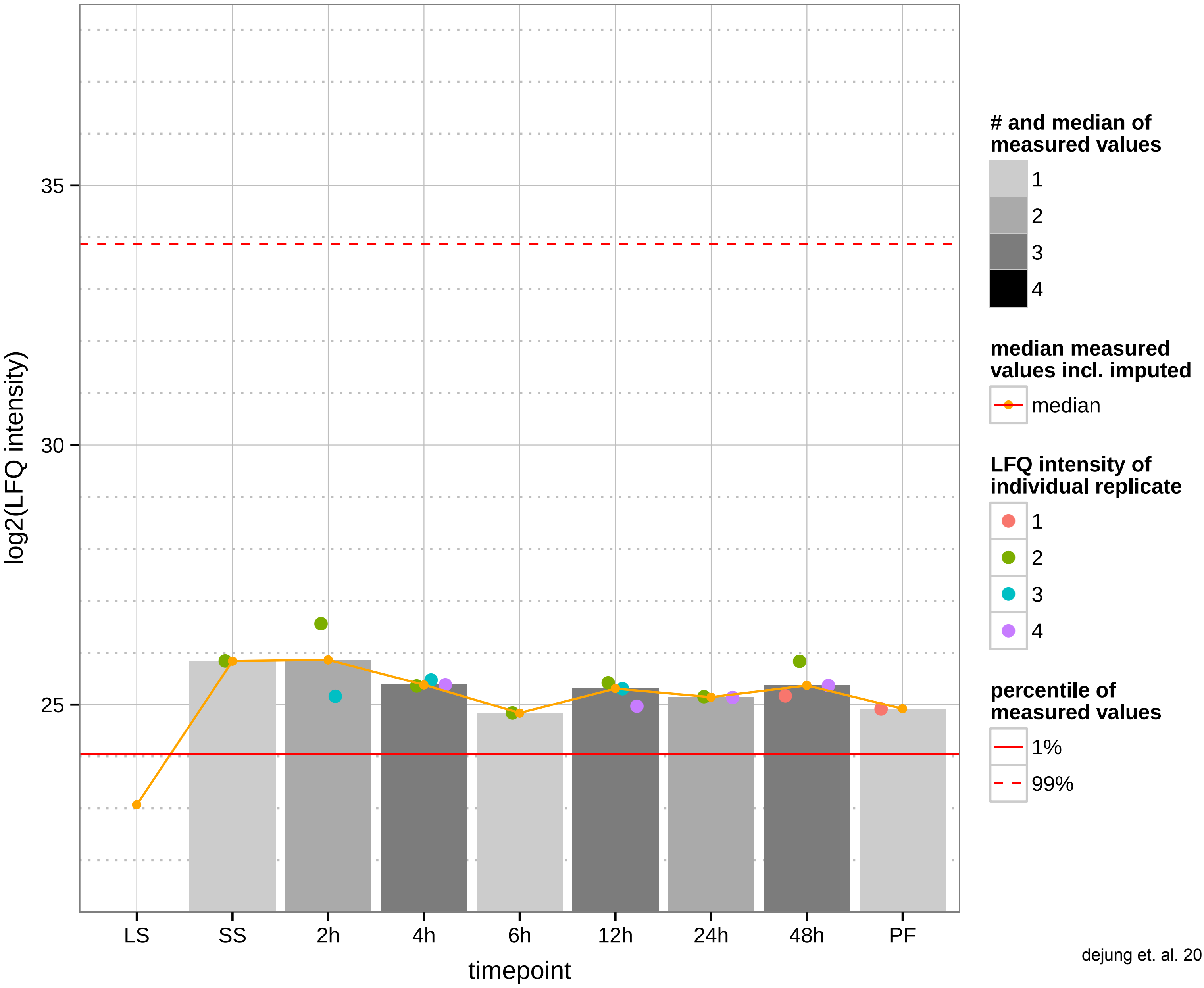
hypothetical protein, conserved
Tb927.6.1270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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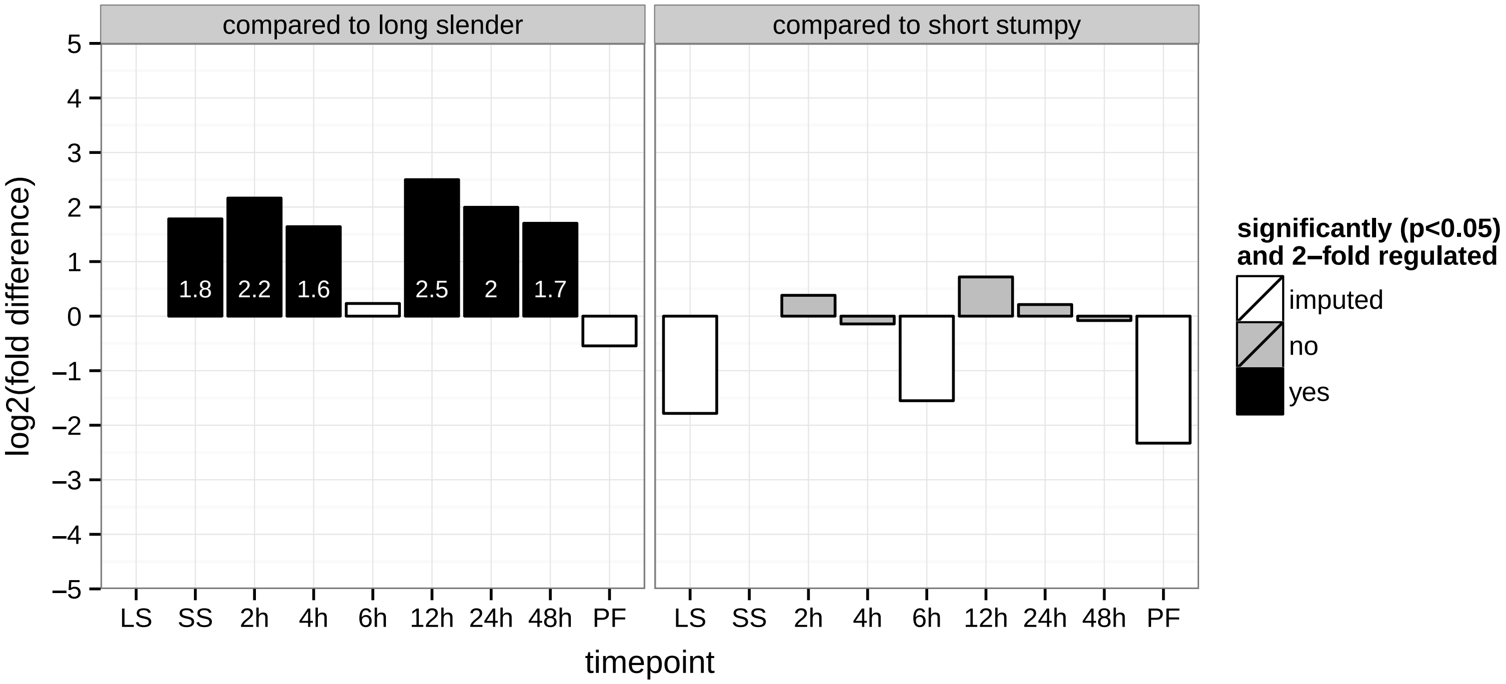
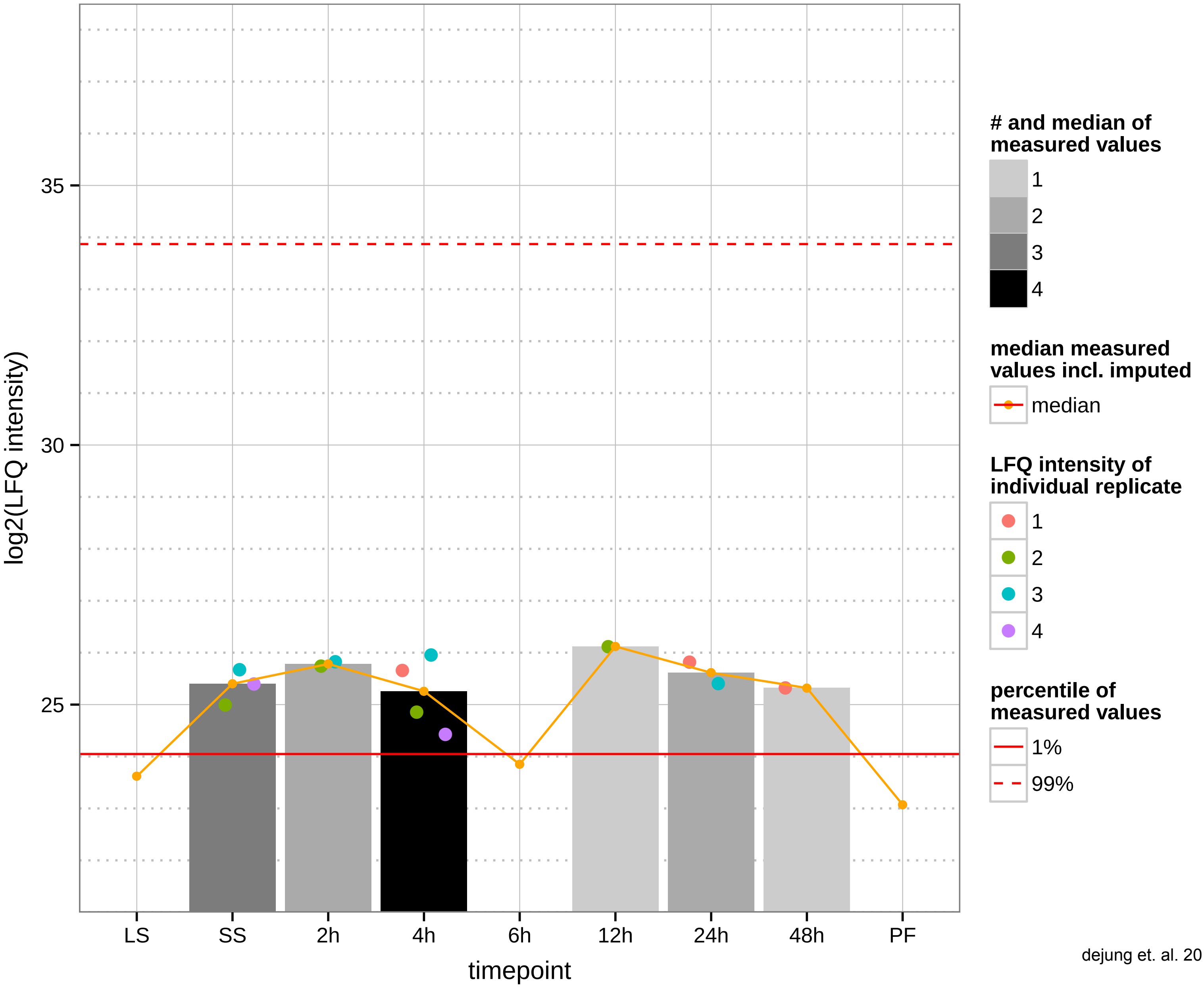
hypothetical protein, conserved
Tb927.6.1930
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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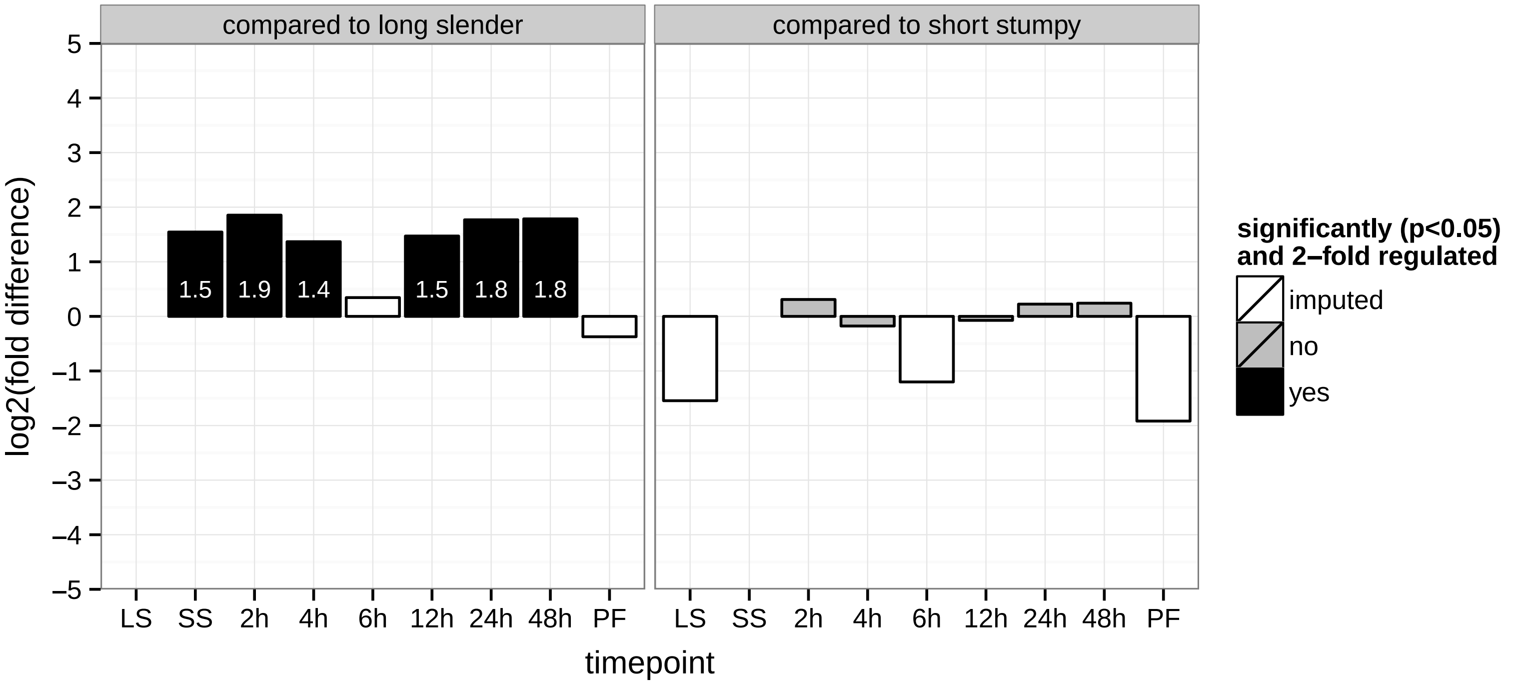
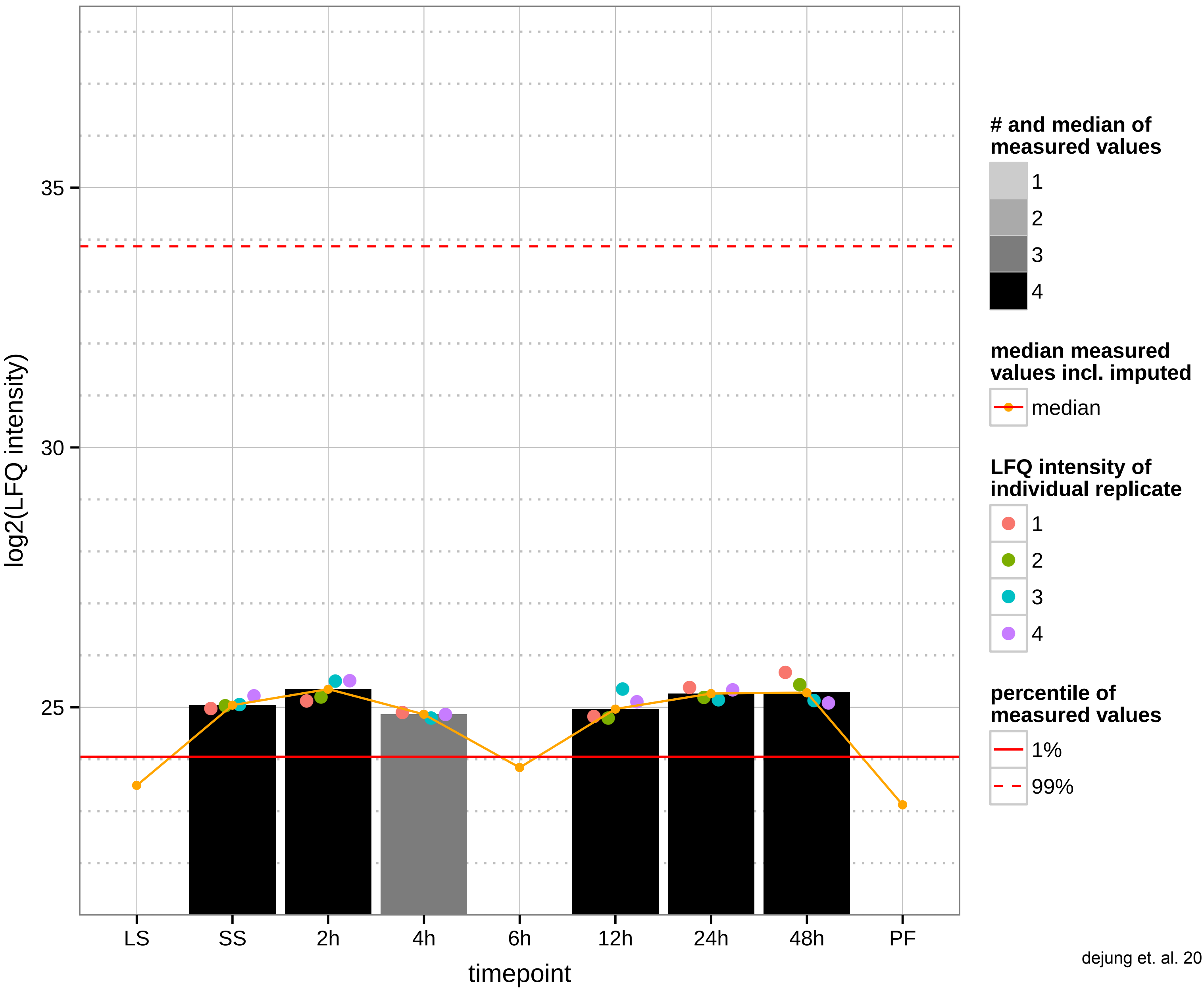
acetyltransferase, putative, Elongator–like Protein 3b (ELP3b)
Tb927.8.3310;Tb11.v5.0520
AGOF: null, N–acetyltransferase activity, iron–sulfur cluster binding
AGOC: null, nucleolus
AGOP: null, histone acetylation, maintenance of rDNA, negative regulation of DNA–dependent transcription, elongation
PGOF: N–acetyltransferase activity, catalytic activity, iron–sulfur cluster binding
PGOC: null
PGOP: null





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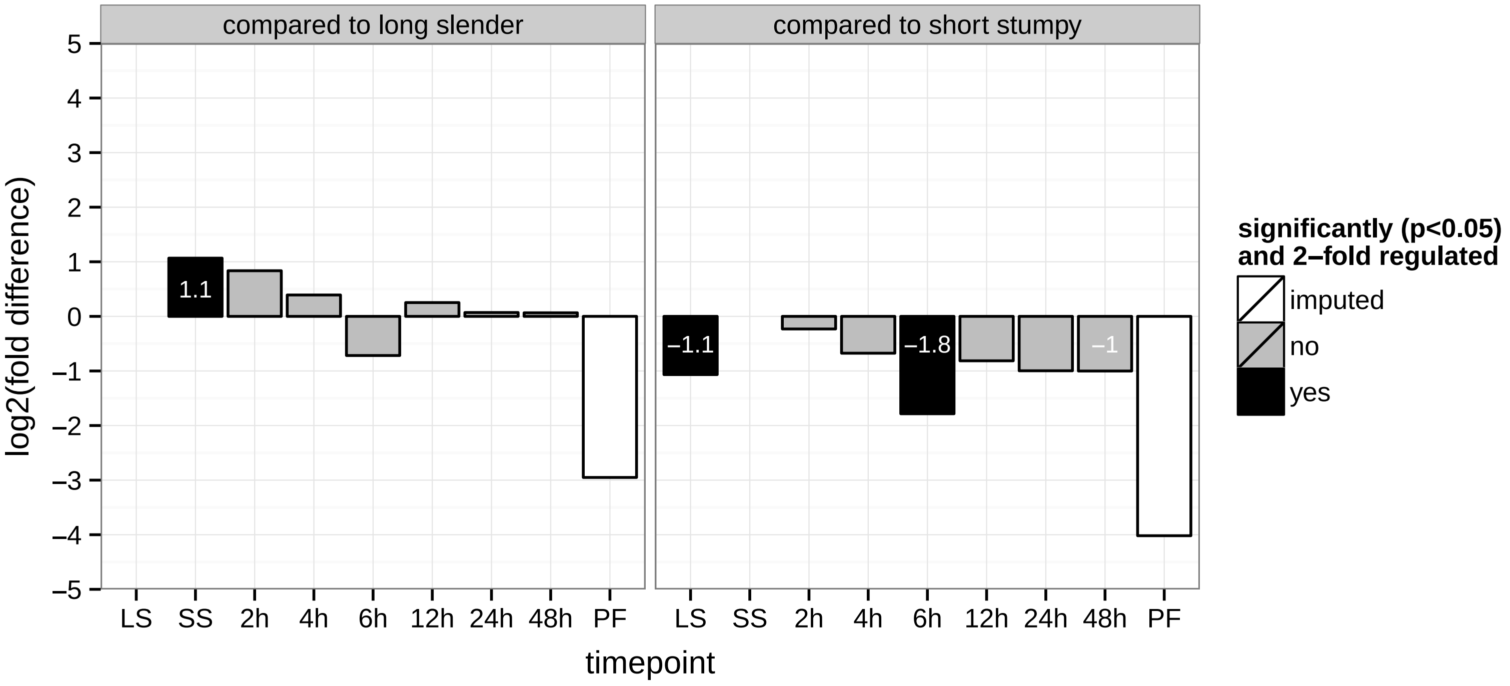
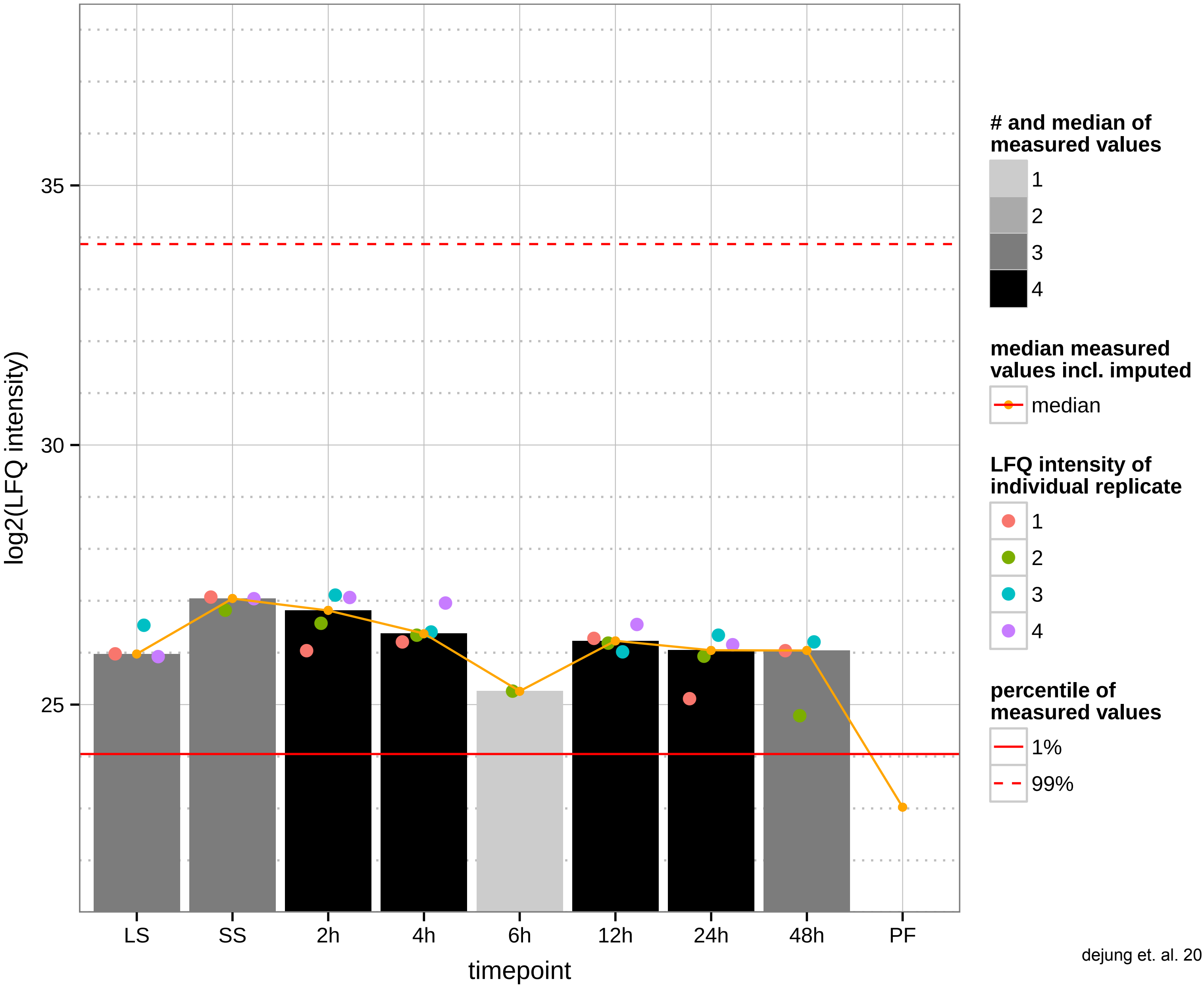
hypothetical protein, conserved
Tb927.8.4480
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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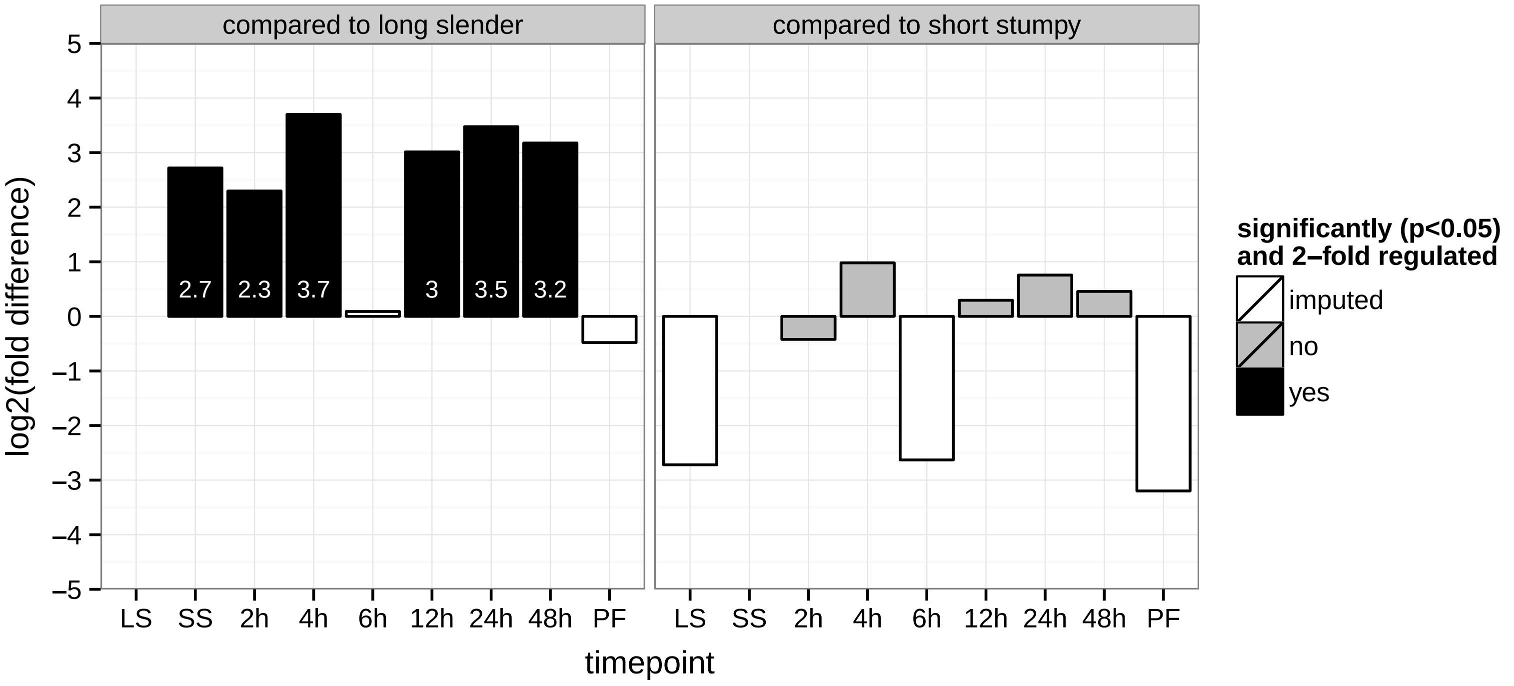
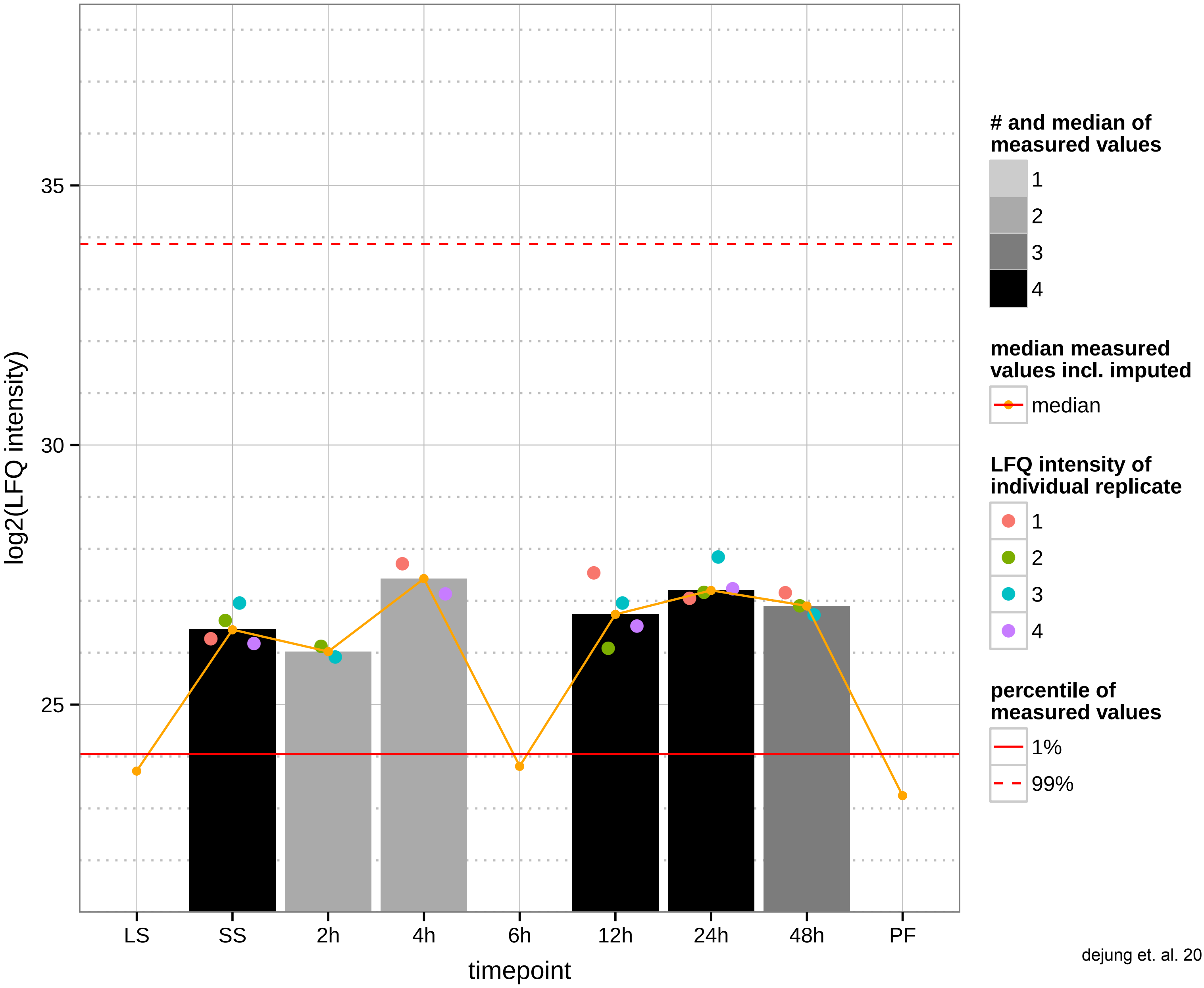
60S ribosomal protein L38, putative
Tb927.9.2020
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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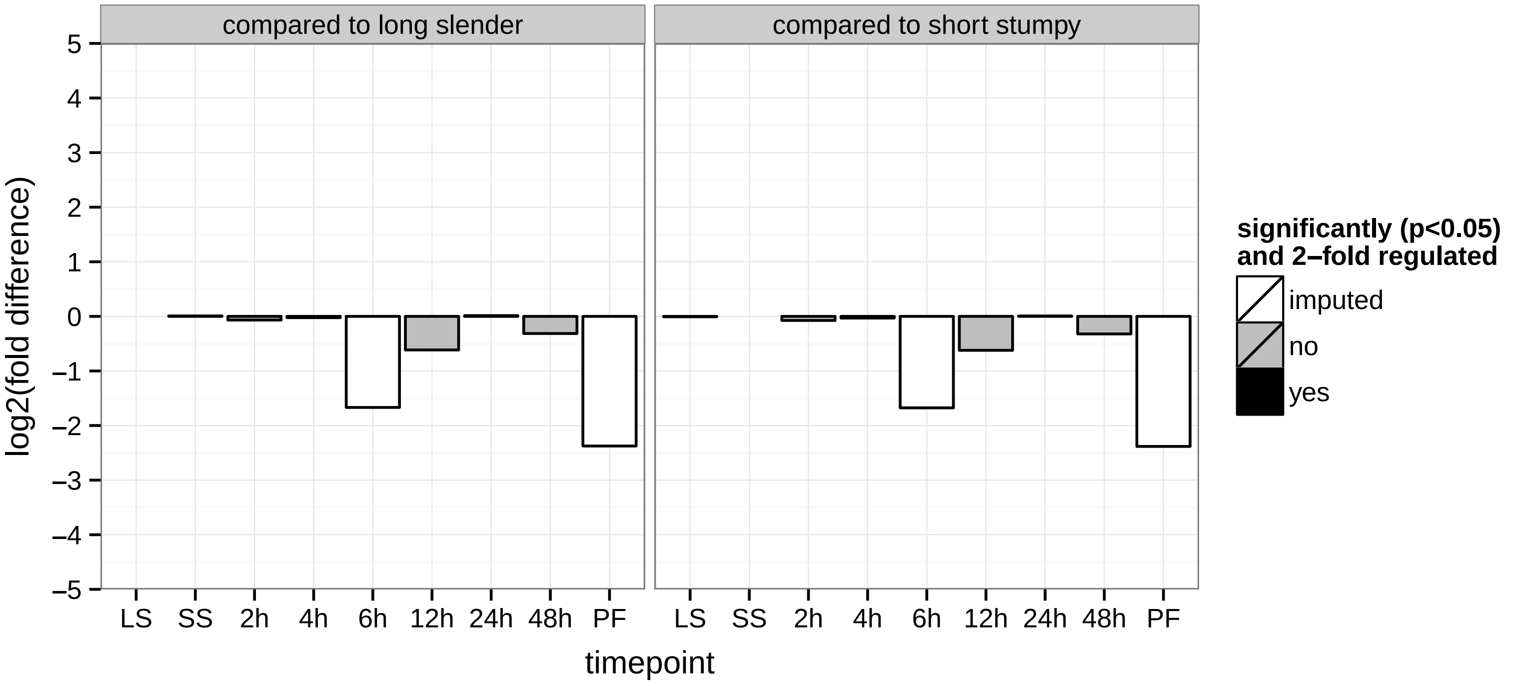
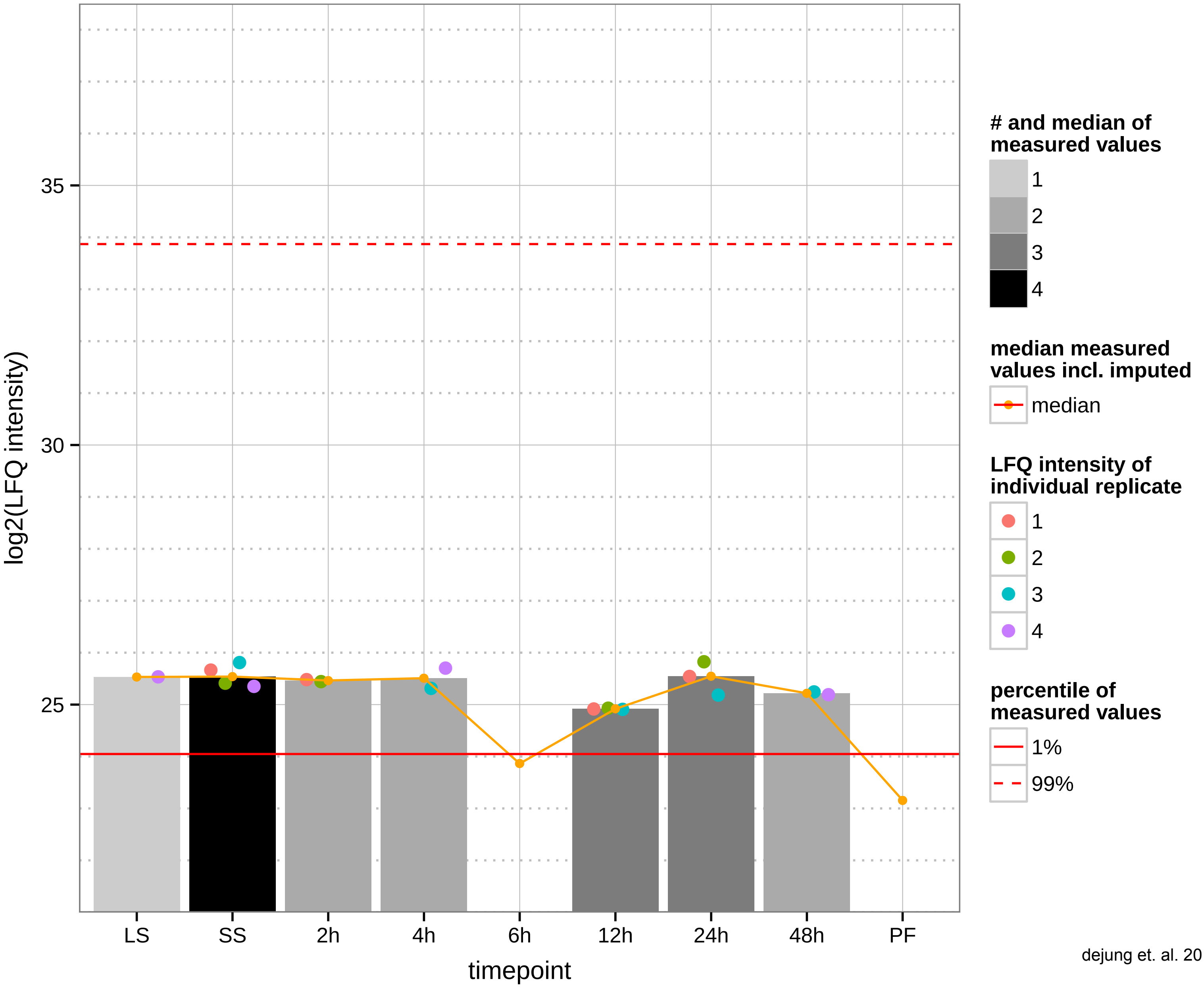
hypothetical protein, conserved
Tb927.9.9090
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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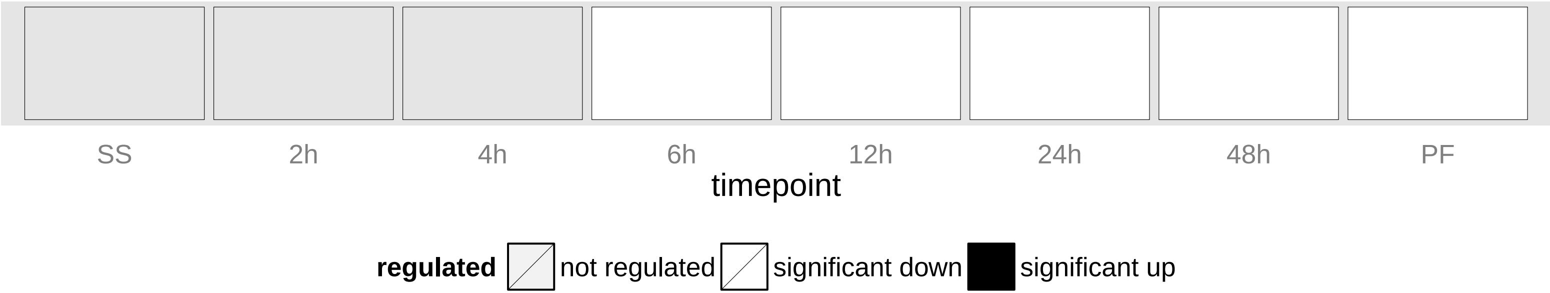

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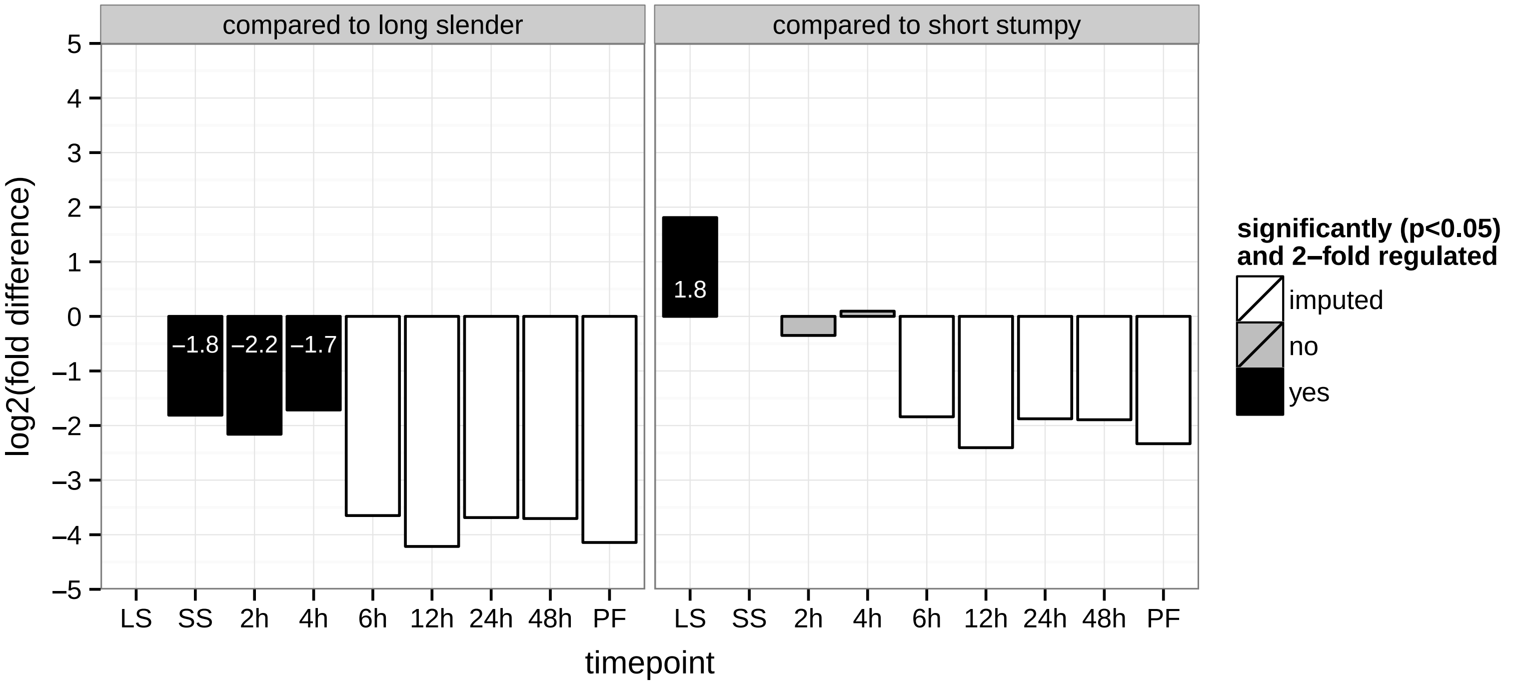
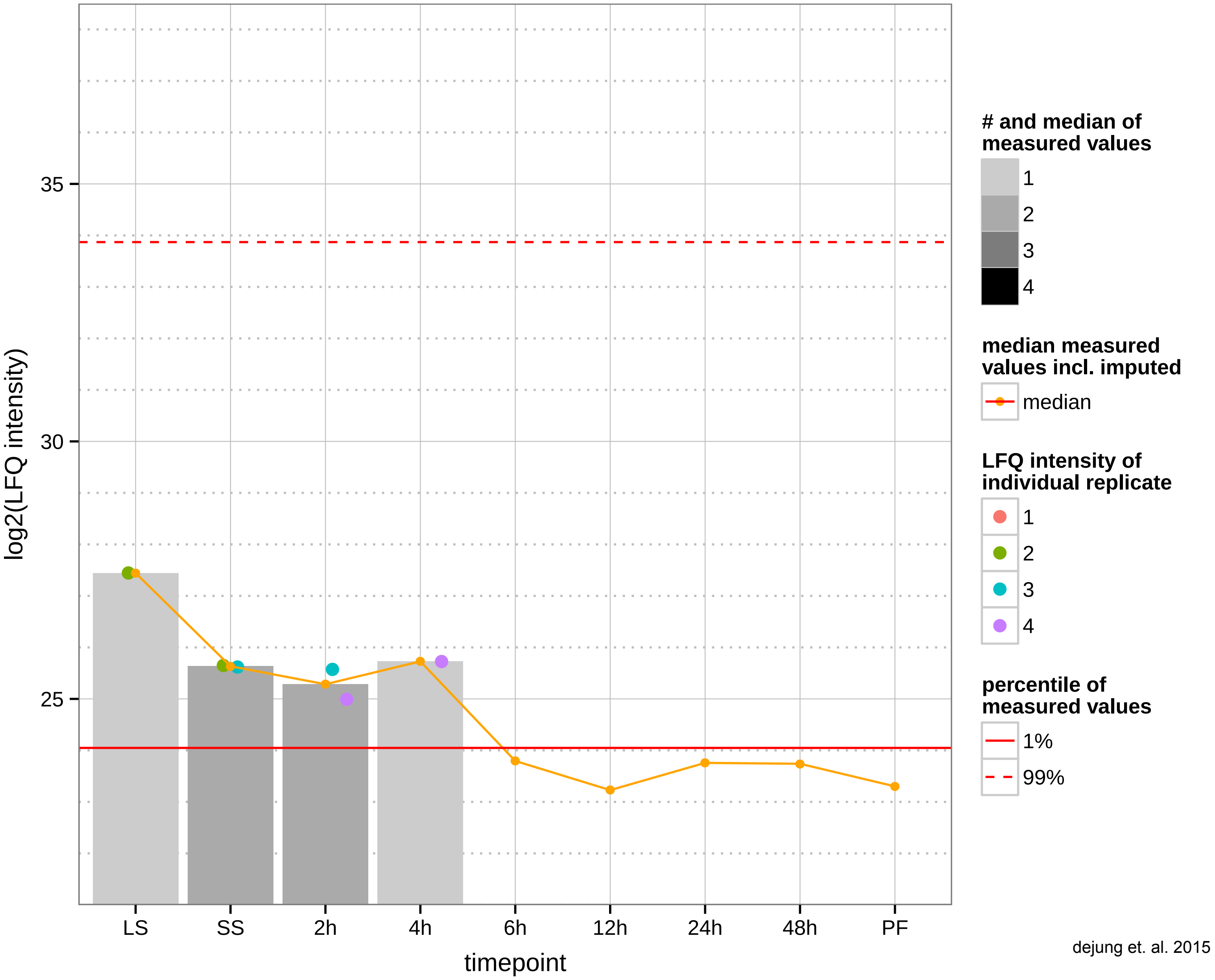
hypothetical protein, conserved, BAC from homologous region on chr5
Tb927.5.4390;Tb05.5K5.40
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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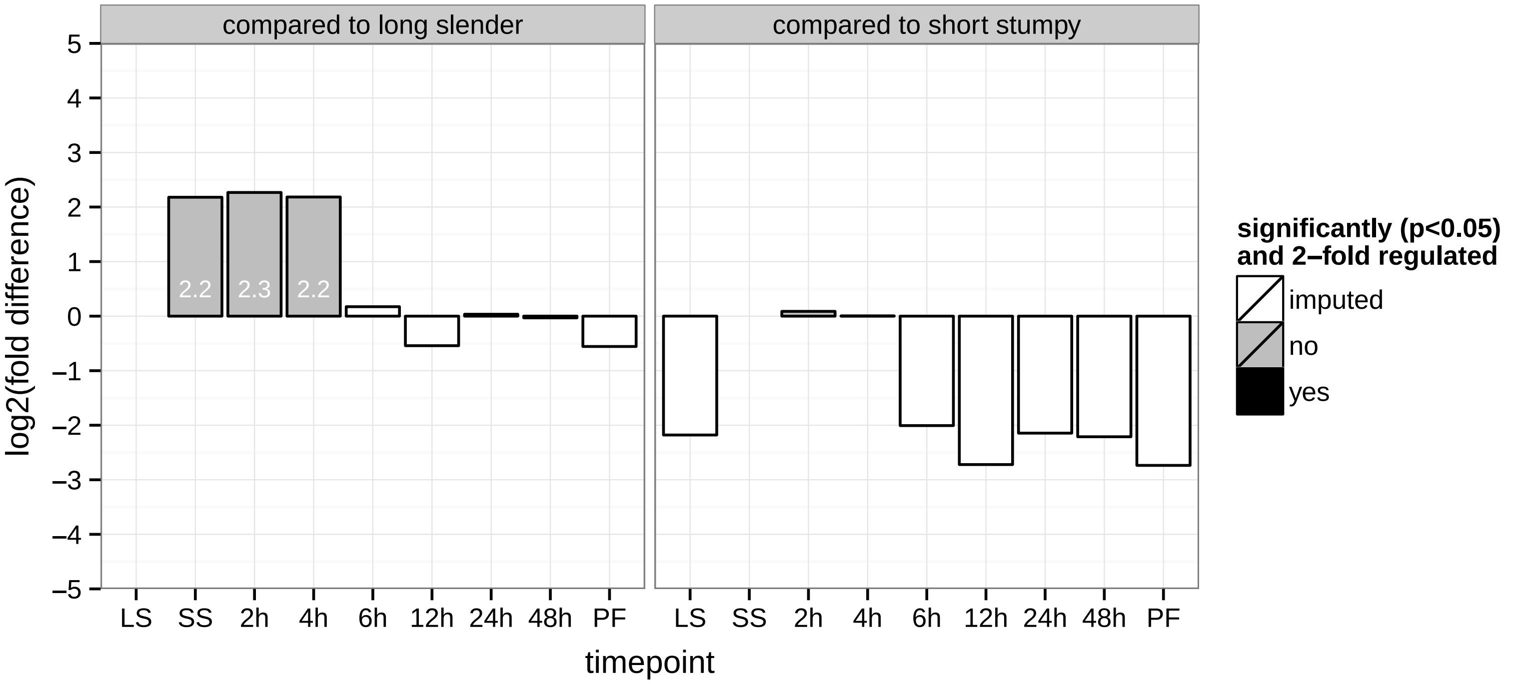
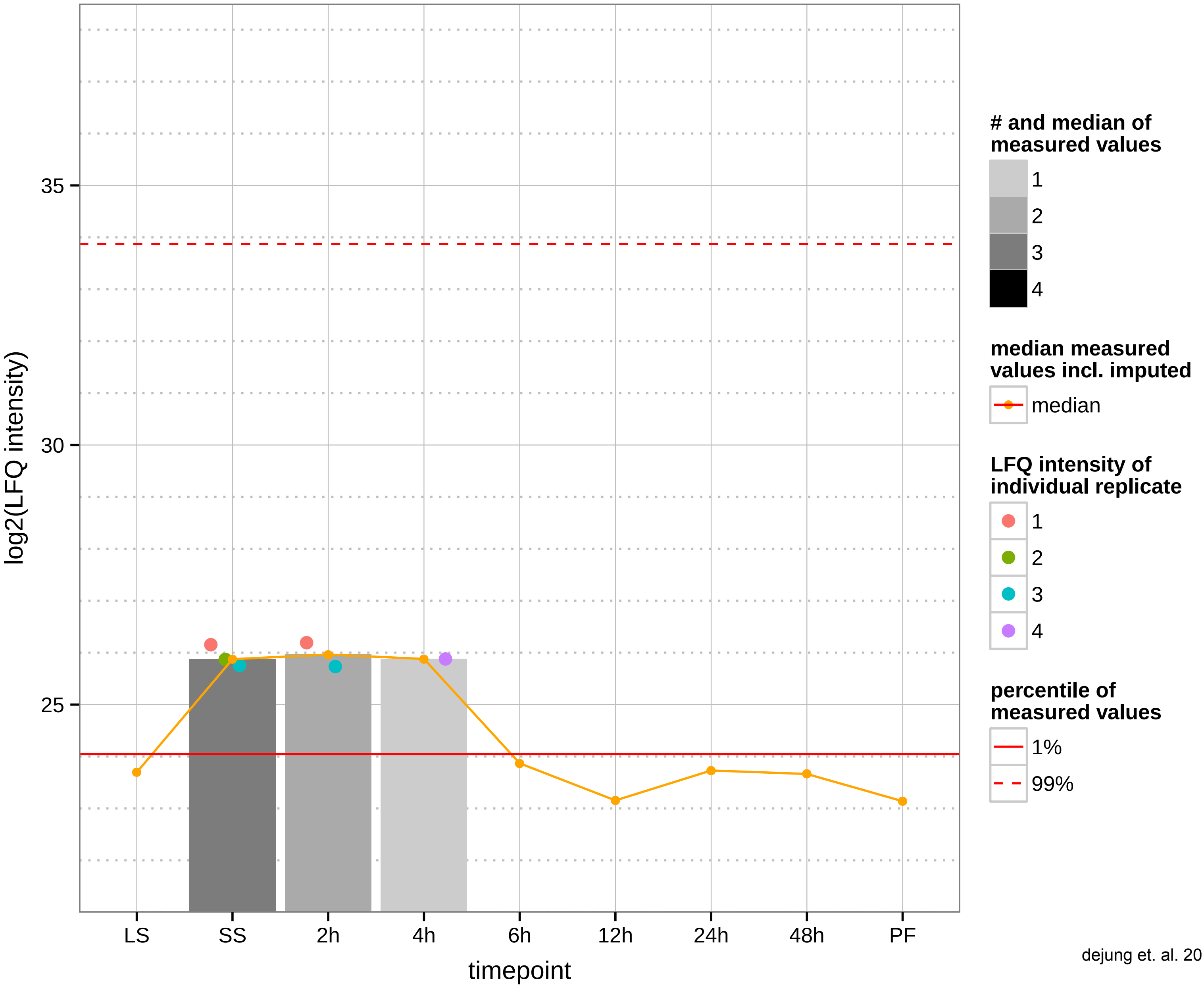
retrotransposon hot spot protein (RHS, pseudogene), putative, retrotransposon hot spot protein 4 (RHS4, chrXI additional, un
Tb11.0820;Tb11.v5.0295
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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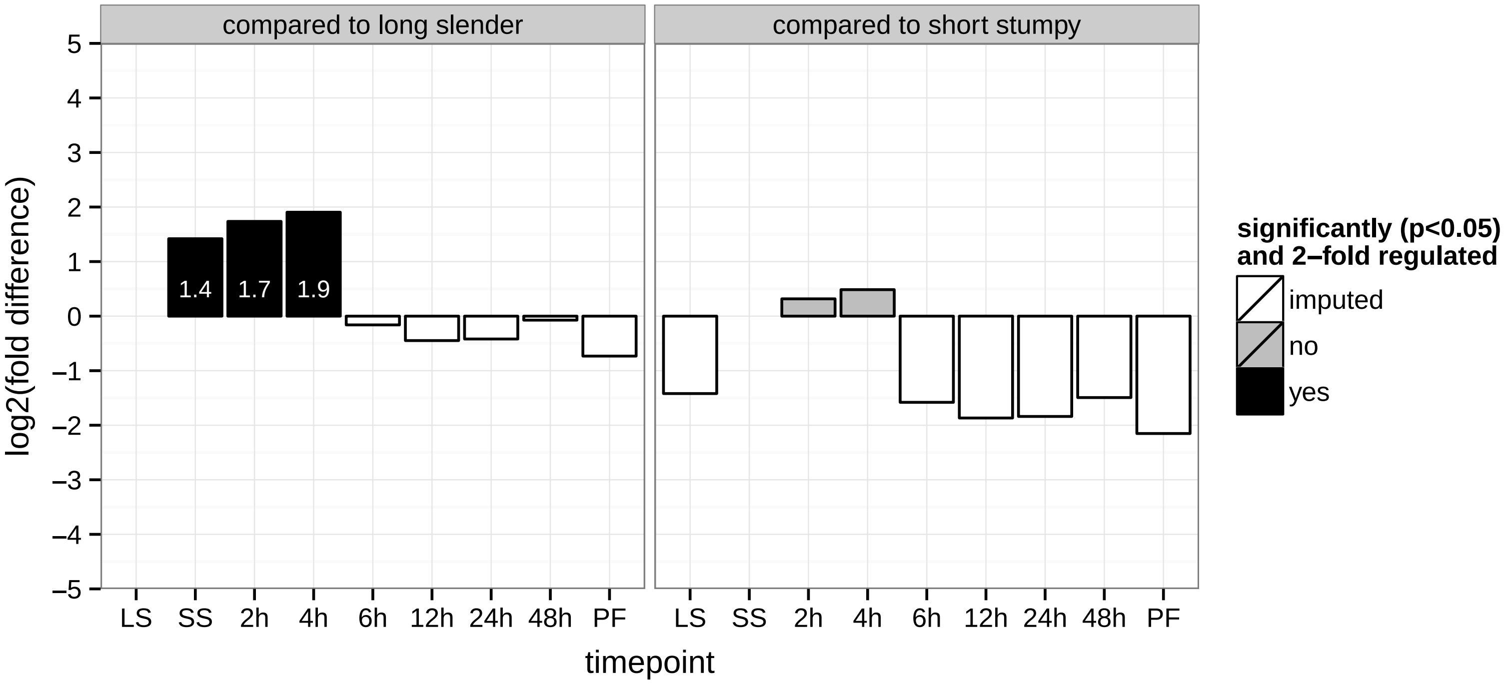
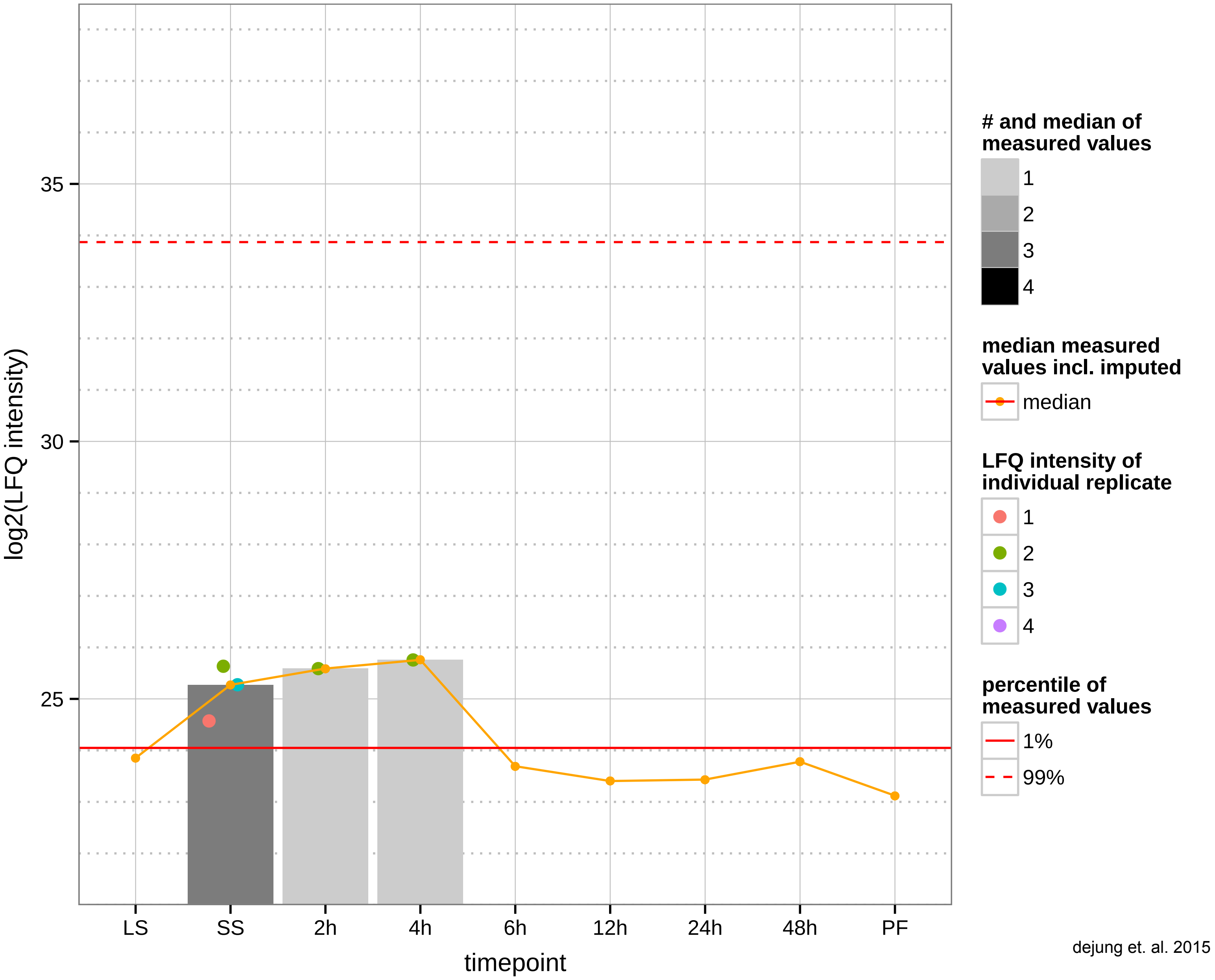
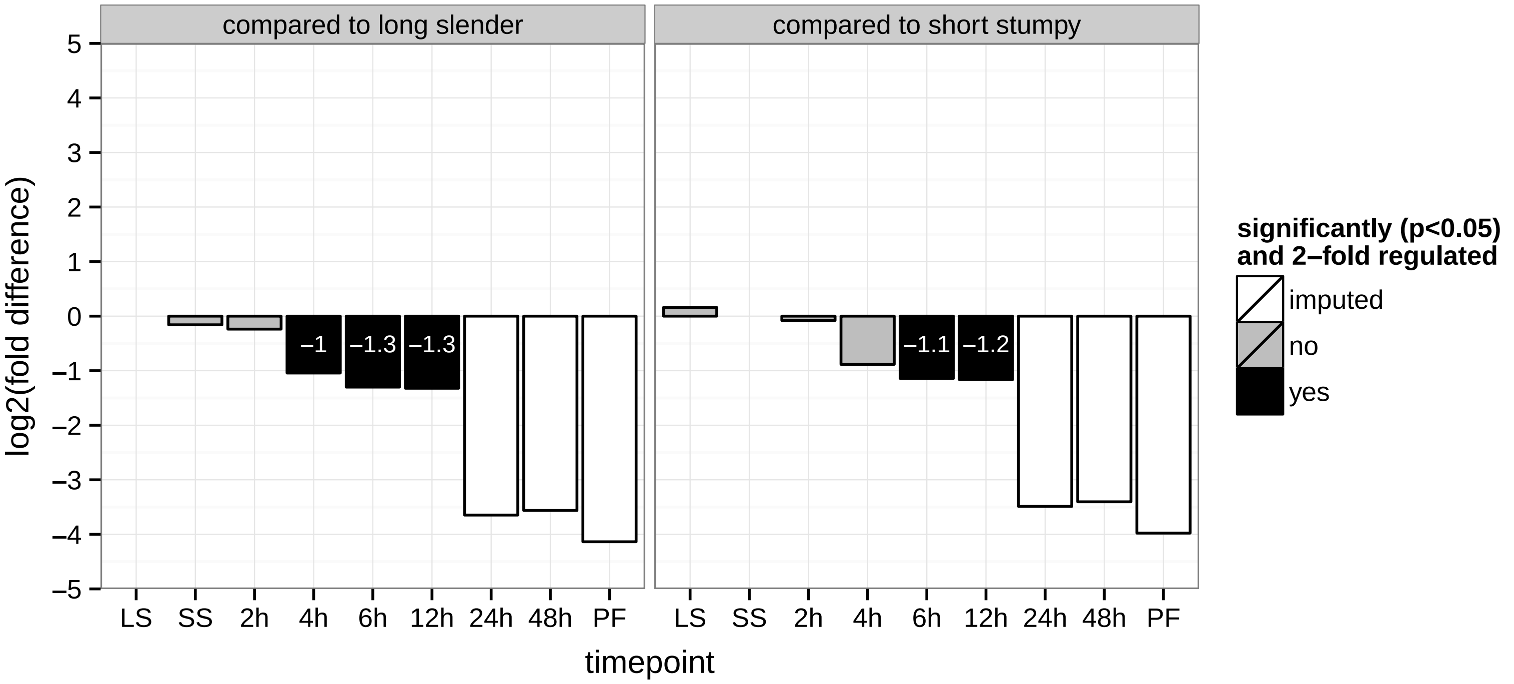
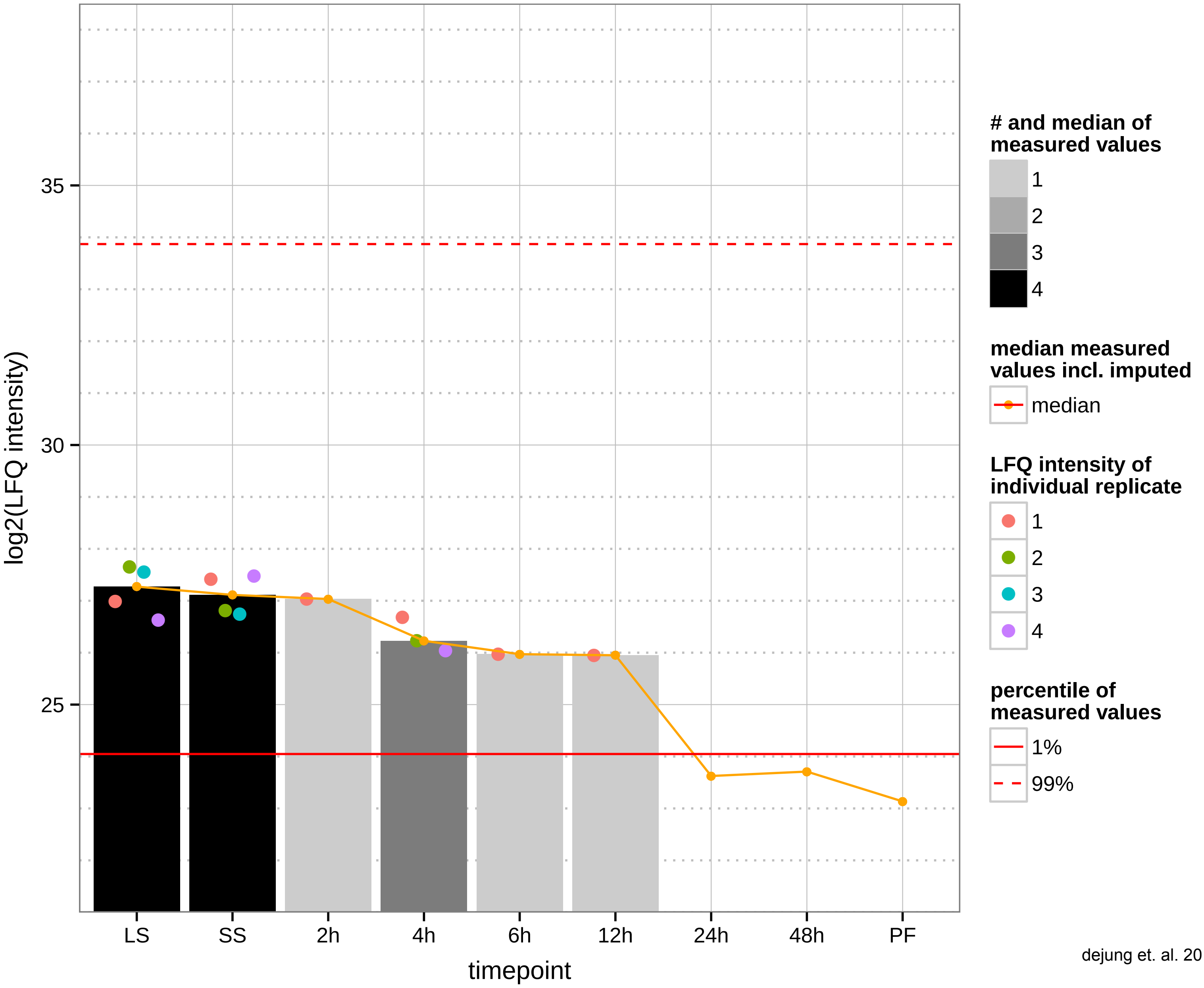
BarP protein, putative, hypothetical protein
Tb927.7.4690;Tb11.v5.0153
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





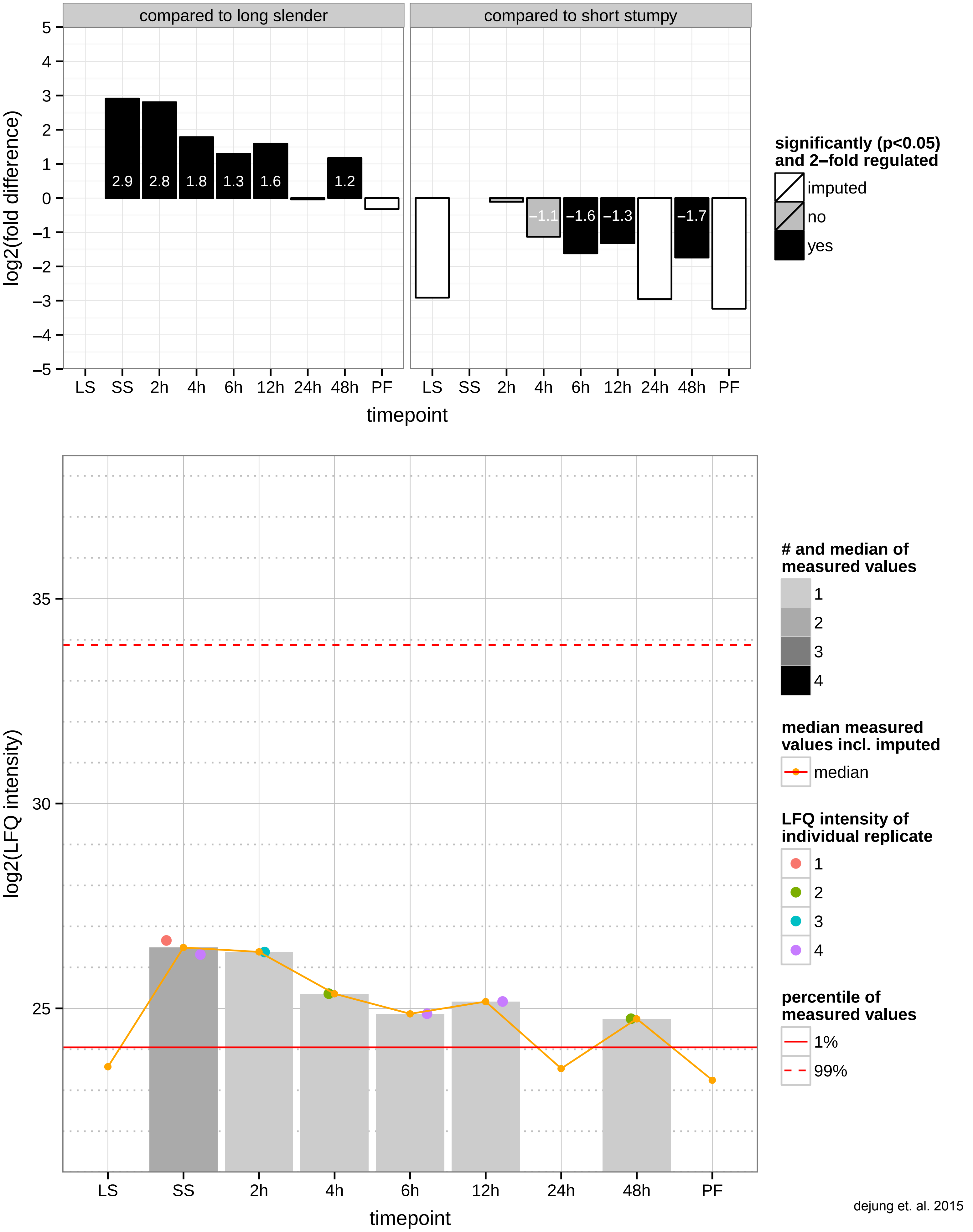
75 kDa invariant surface glycoprotein, putative, putative (ISG75)
Tb927.5.370;Tb11.v5.0230
AGOF: null
AGOC: null, plasma membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





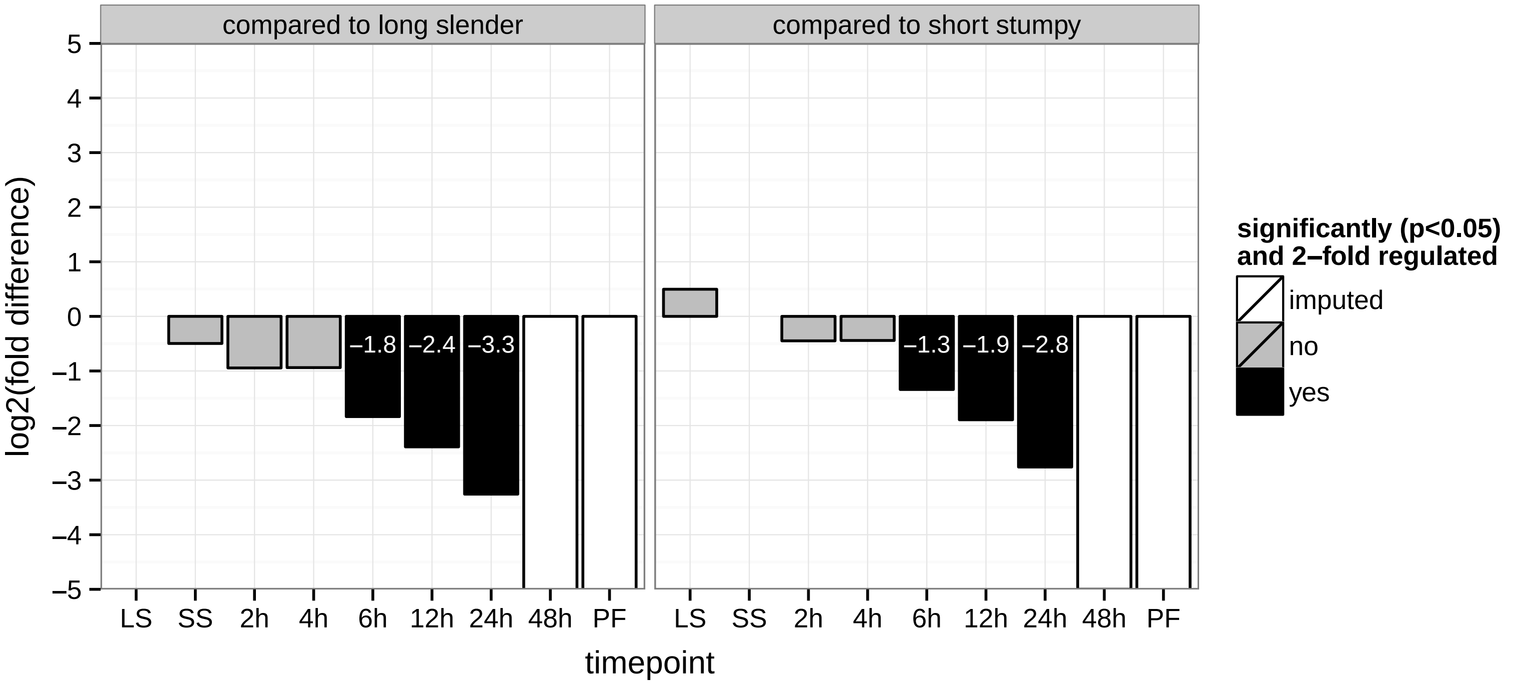
dejung et. al. 2015

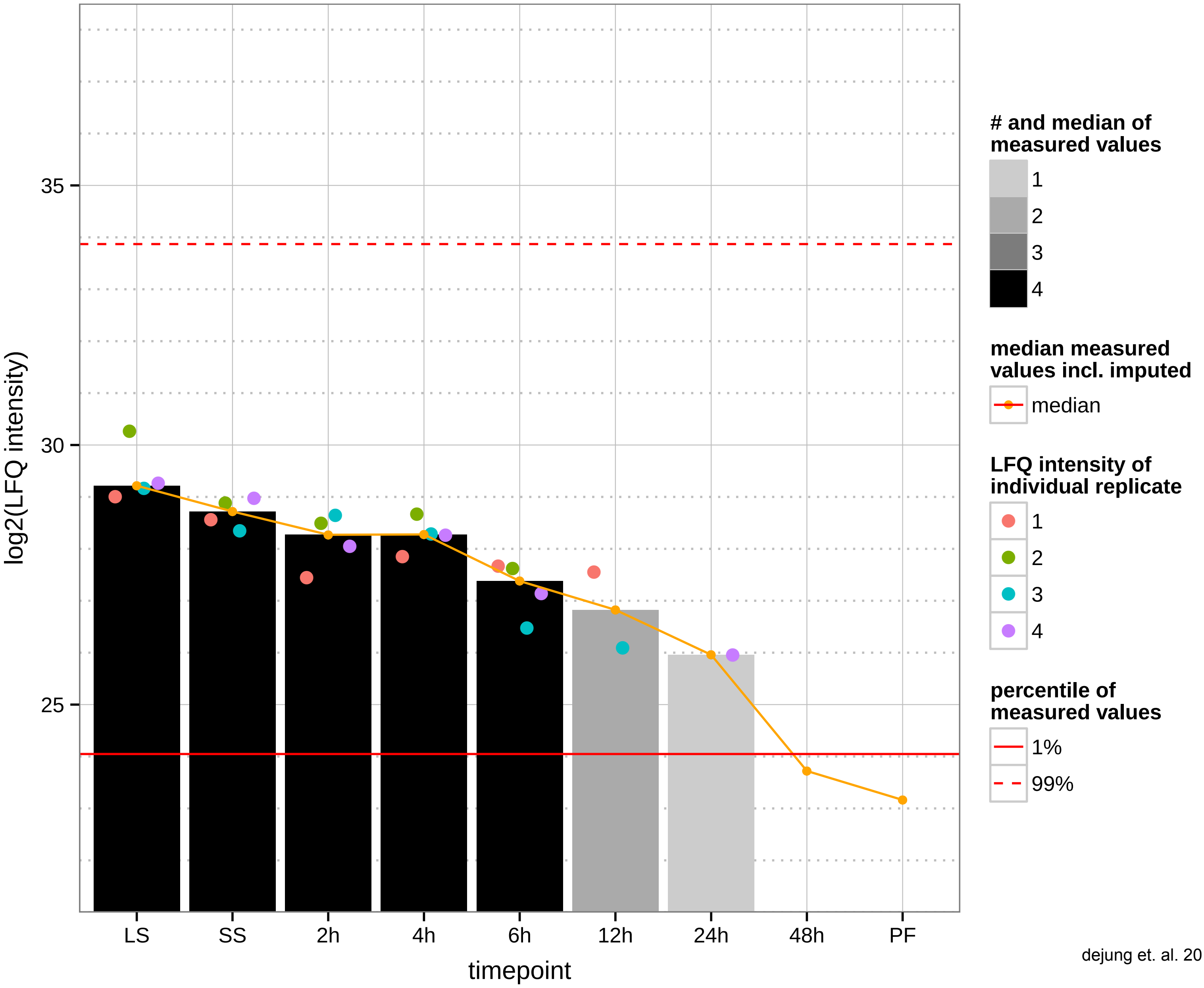
hypothetical protein, conserved
Tb11.v5.0365
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015

65 kDa invariant surface glycoprotein, putative
Tb11.v5.0731
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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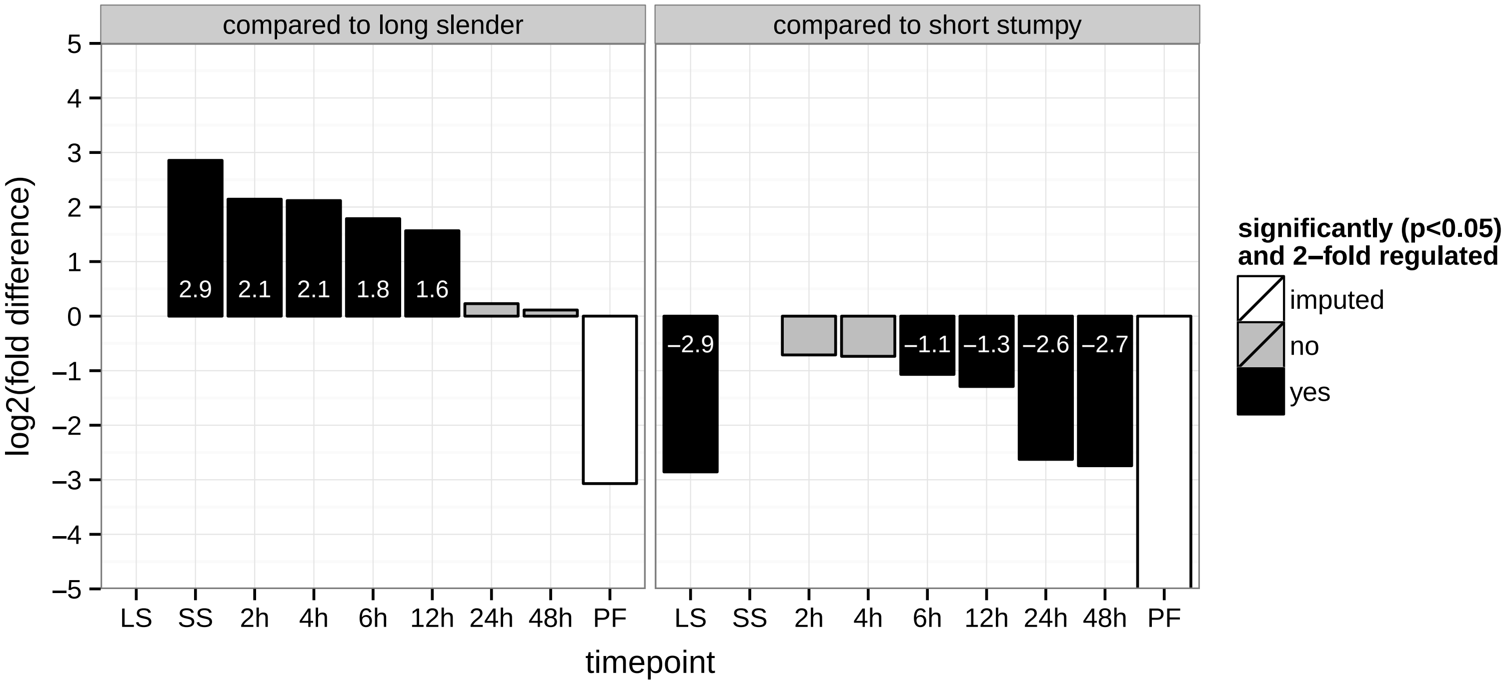
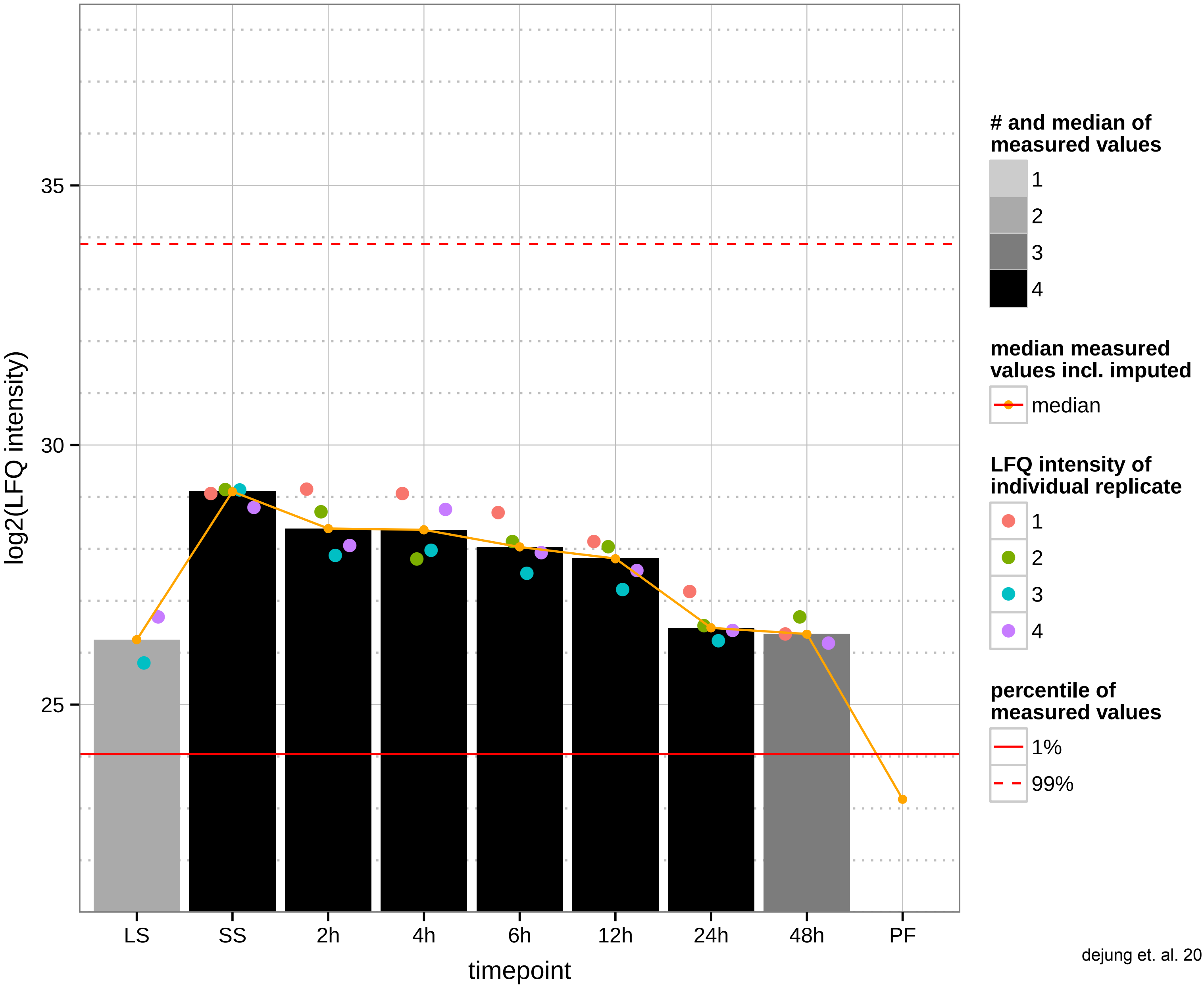
Sarcalumenin, putative, sarcoplasmic reticulum glycoprotein
Tb927.10.14910
AGOF: GTP binding, calcium ion binding
AGOC: intracellular, sarcoplasmic reticulum
AGOP: endosomal transport
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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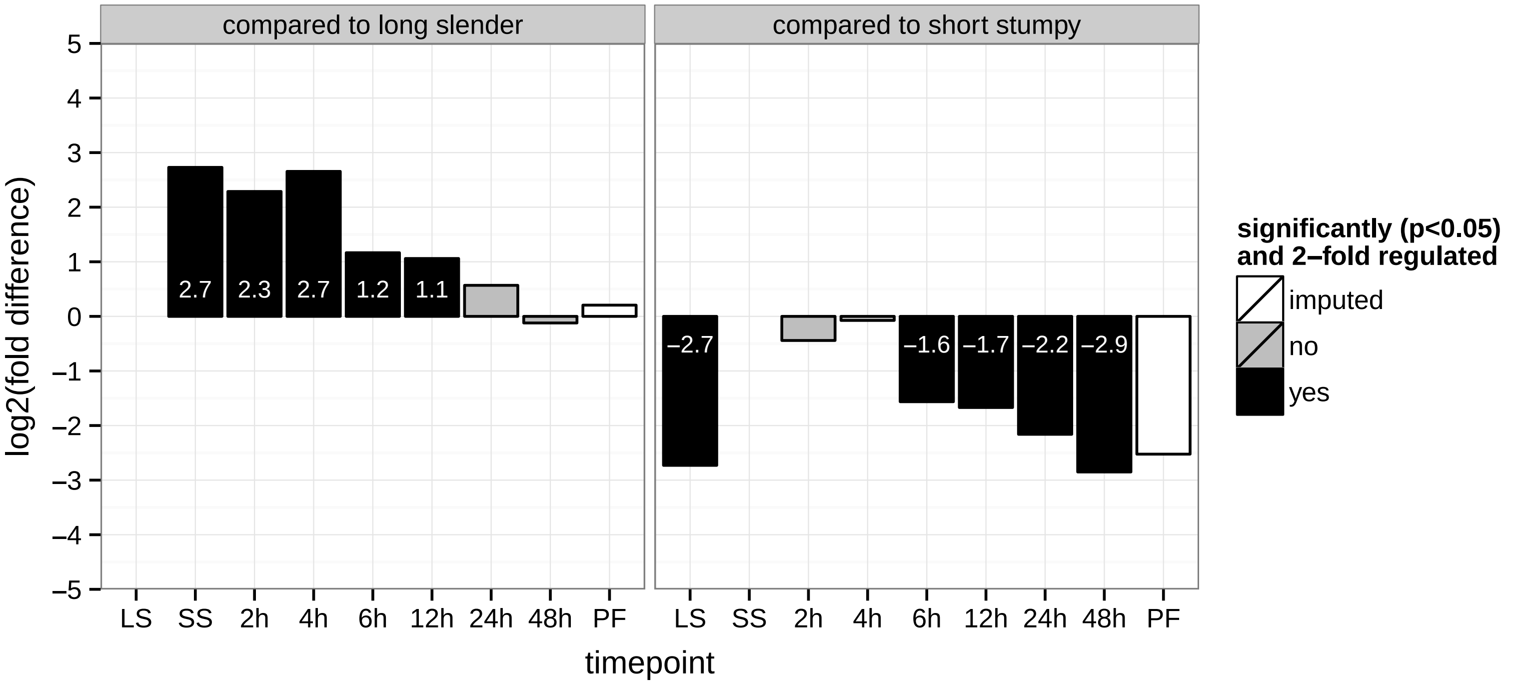
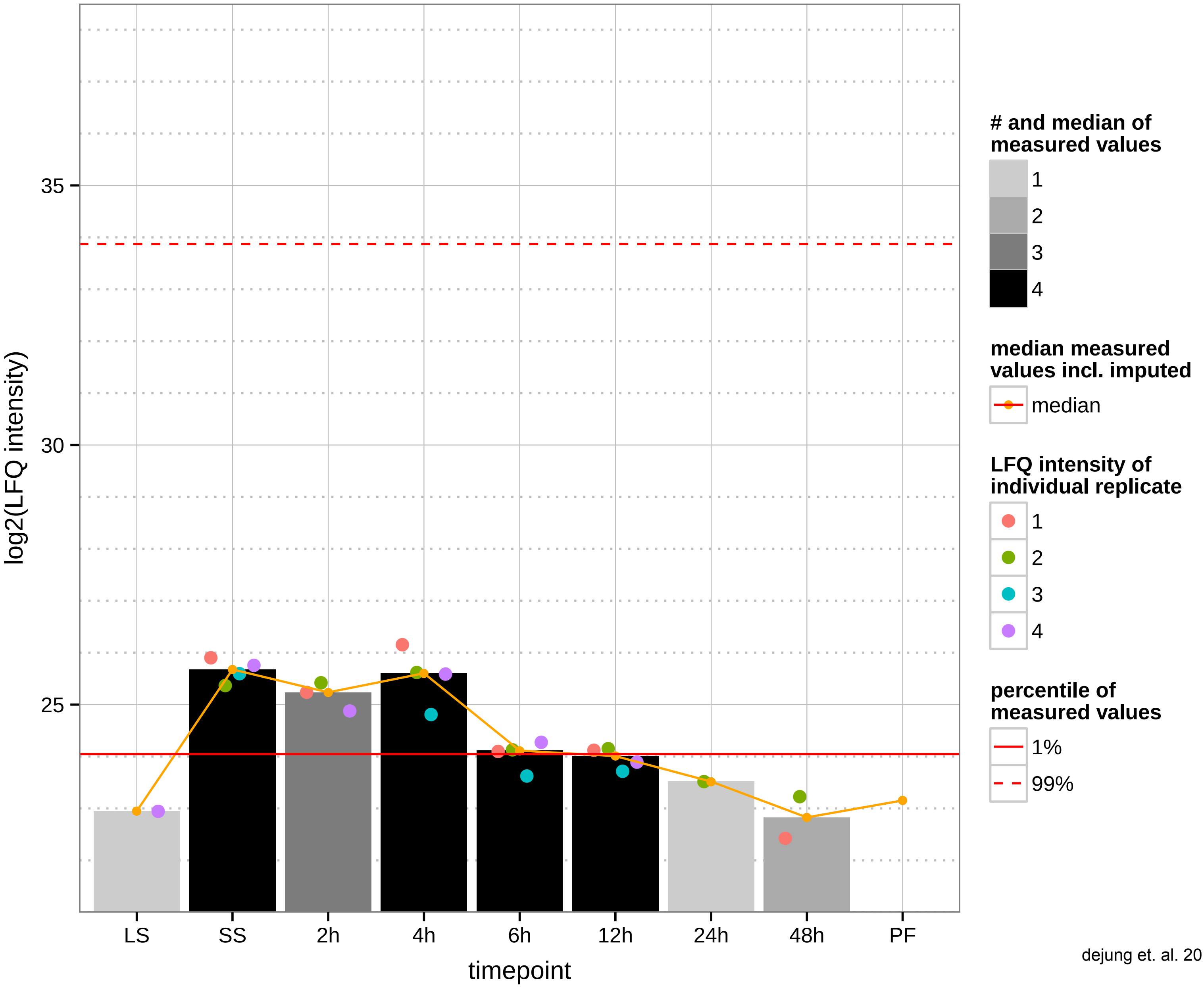
protein–L–isoaspartate, putative
Tb927.10.7850
AGOF: protein–L–isoaspartate (D–aspartate) O–methyltransferase activity
AGOC: null
AGOP: cellular protein modification process
PGOF: protein–L–isoaspartate (D–aspartate) O–methyltransferase activity
PGOC: null
PGOP: cellular protein modification process





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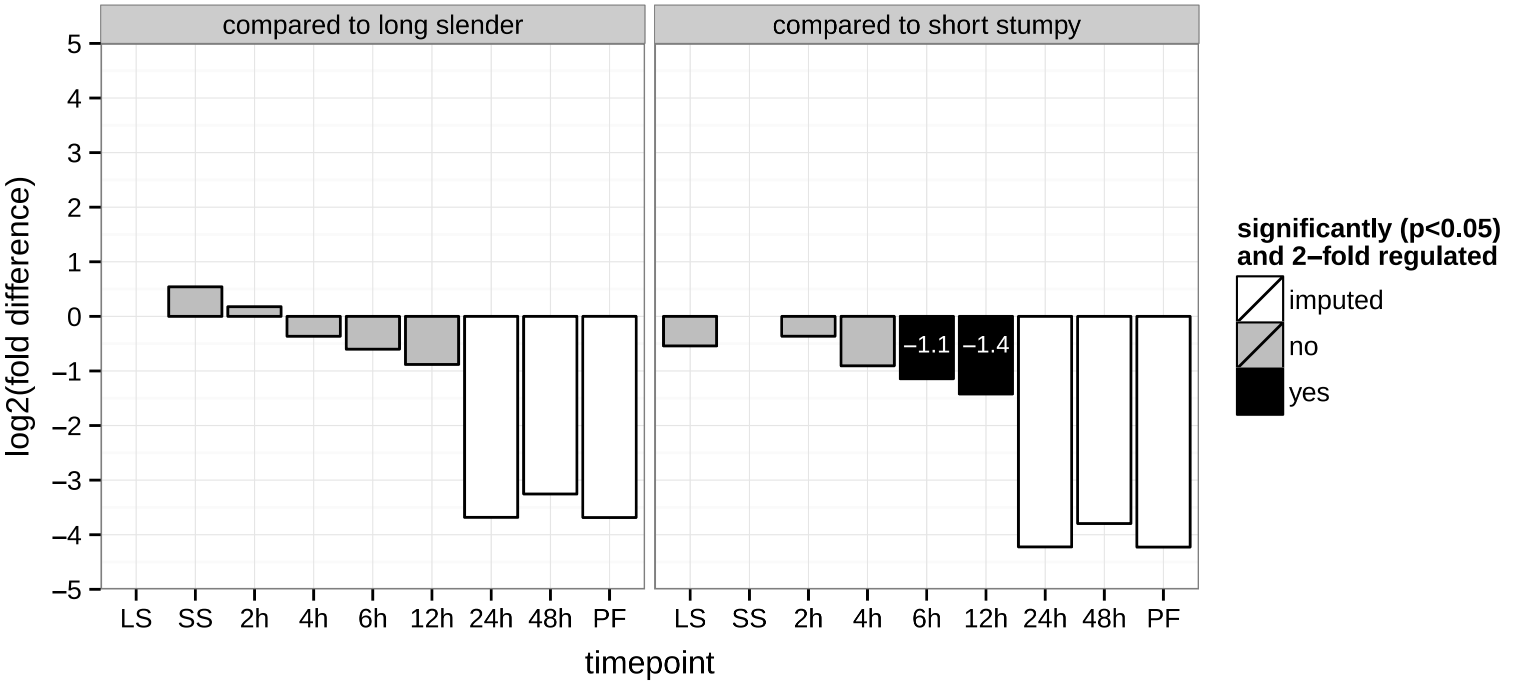
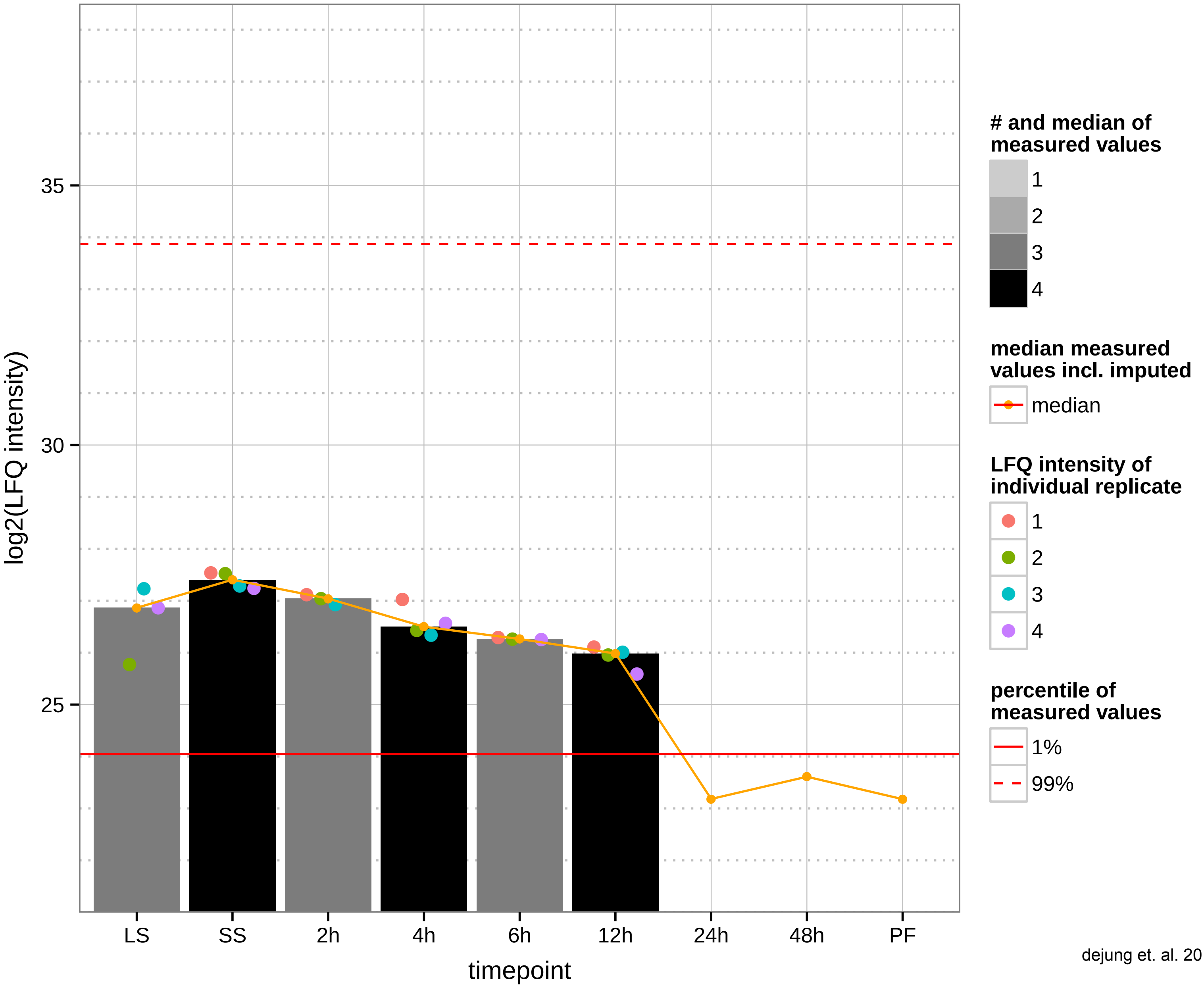
hypothetical protein, conserved
Tb927.11.7550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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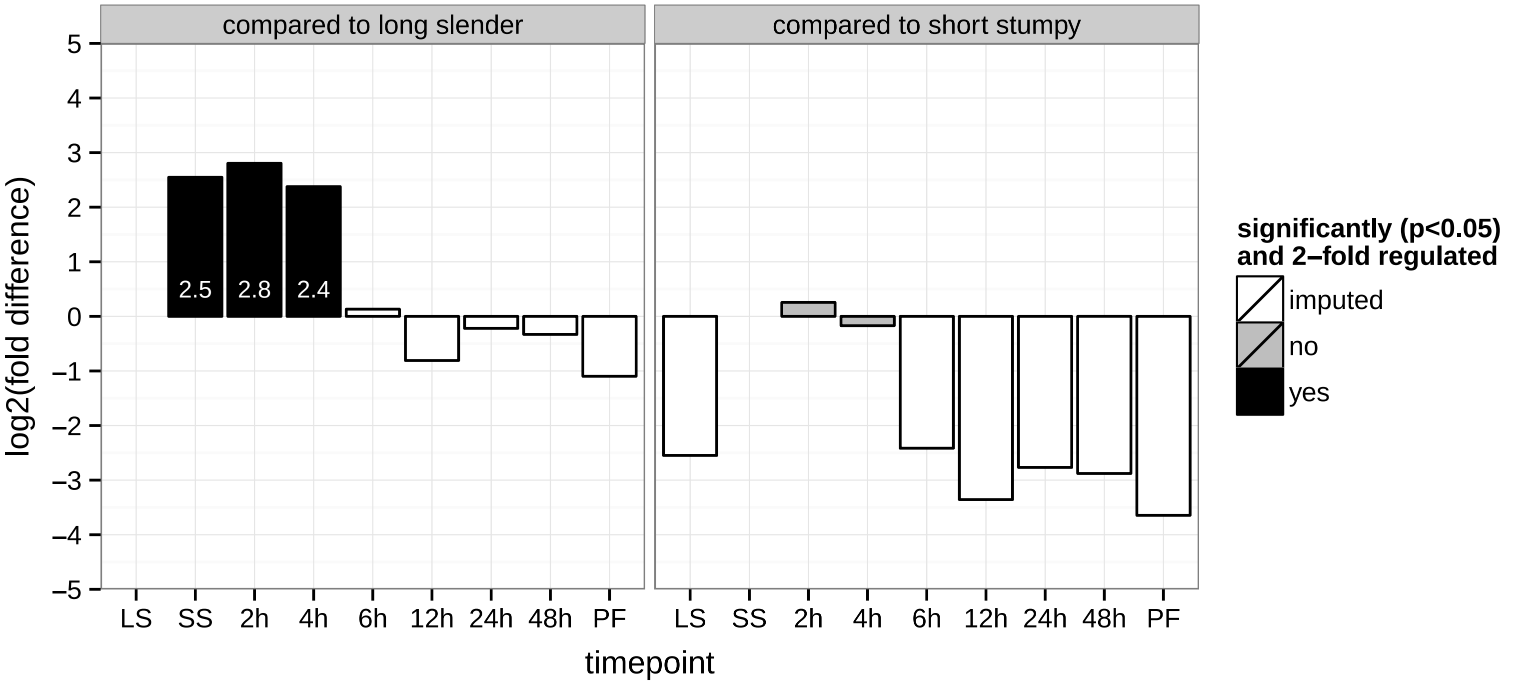
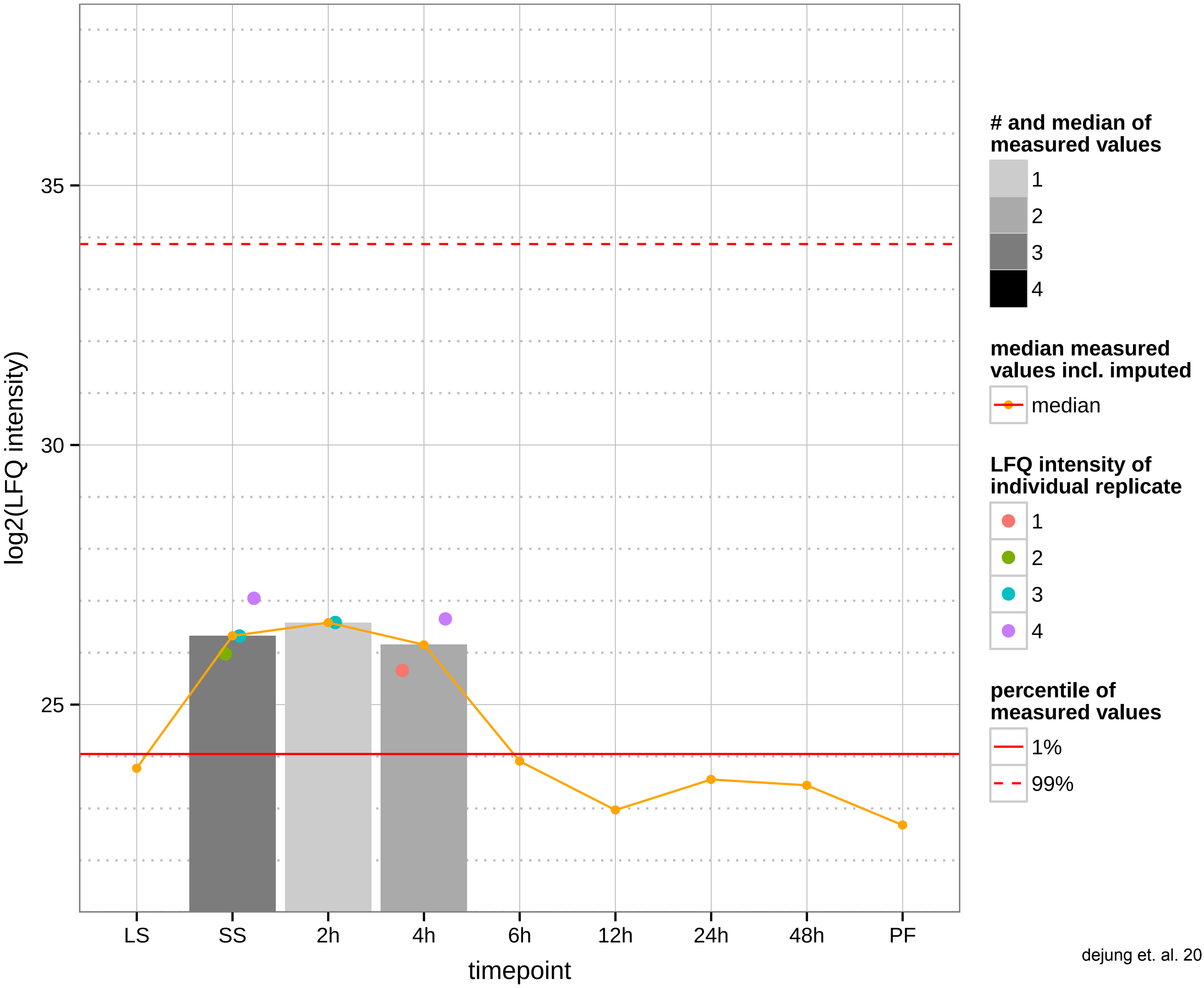
hypothetical protein, conserved
Tb927.11.9150
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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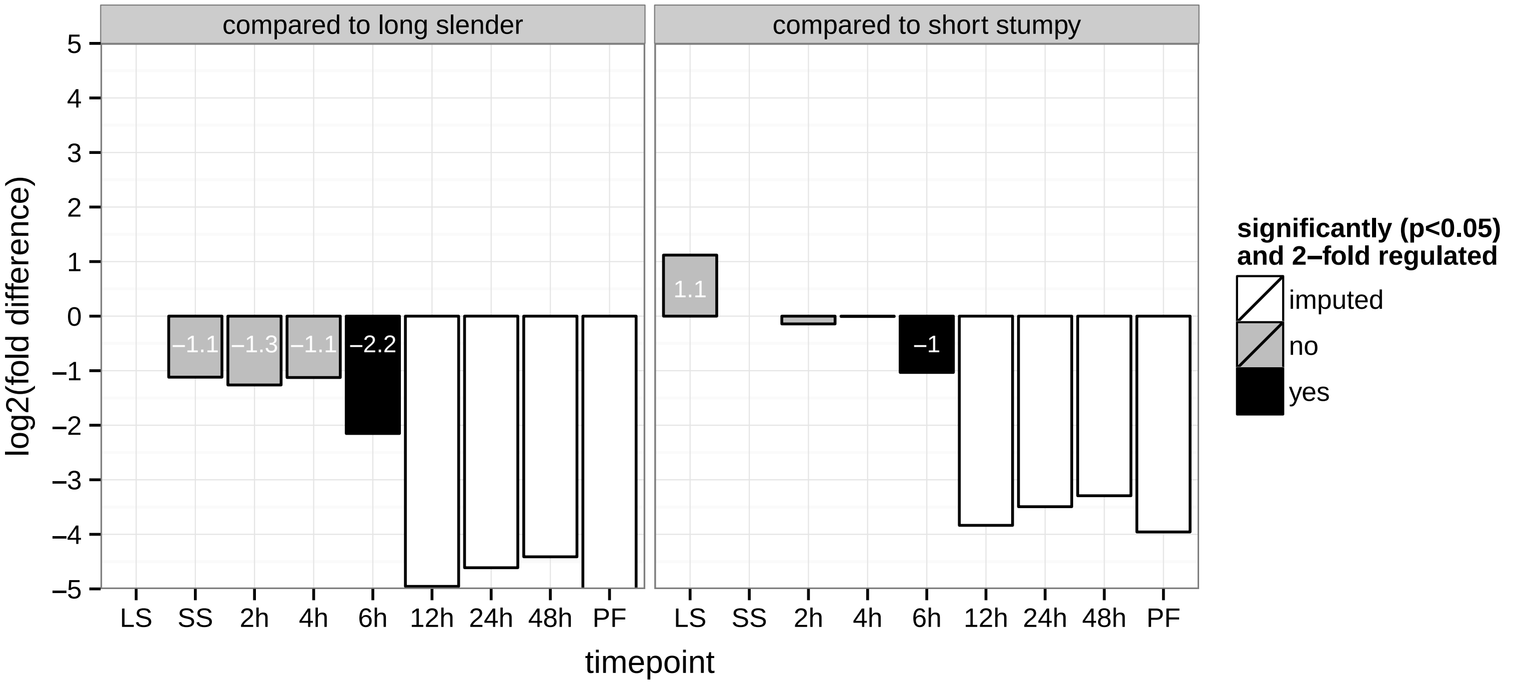
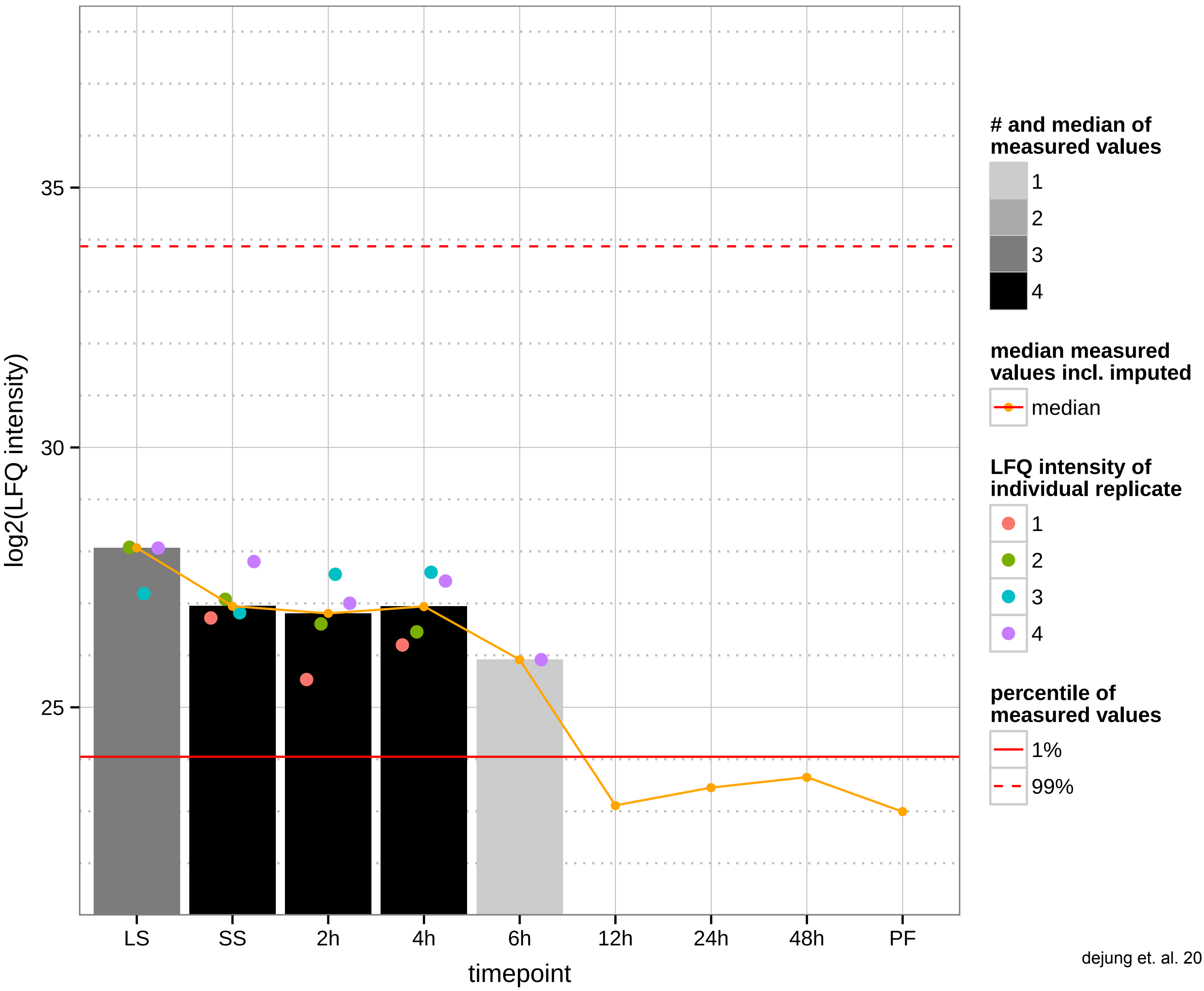
65 kDa invariant surface glycoprotein
Tb927.2.3320
AGOF: null
AGOC: plasma membrane
AGOP: plasma membrane organization
PGOF: null
PGOC: null
PGOP: null





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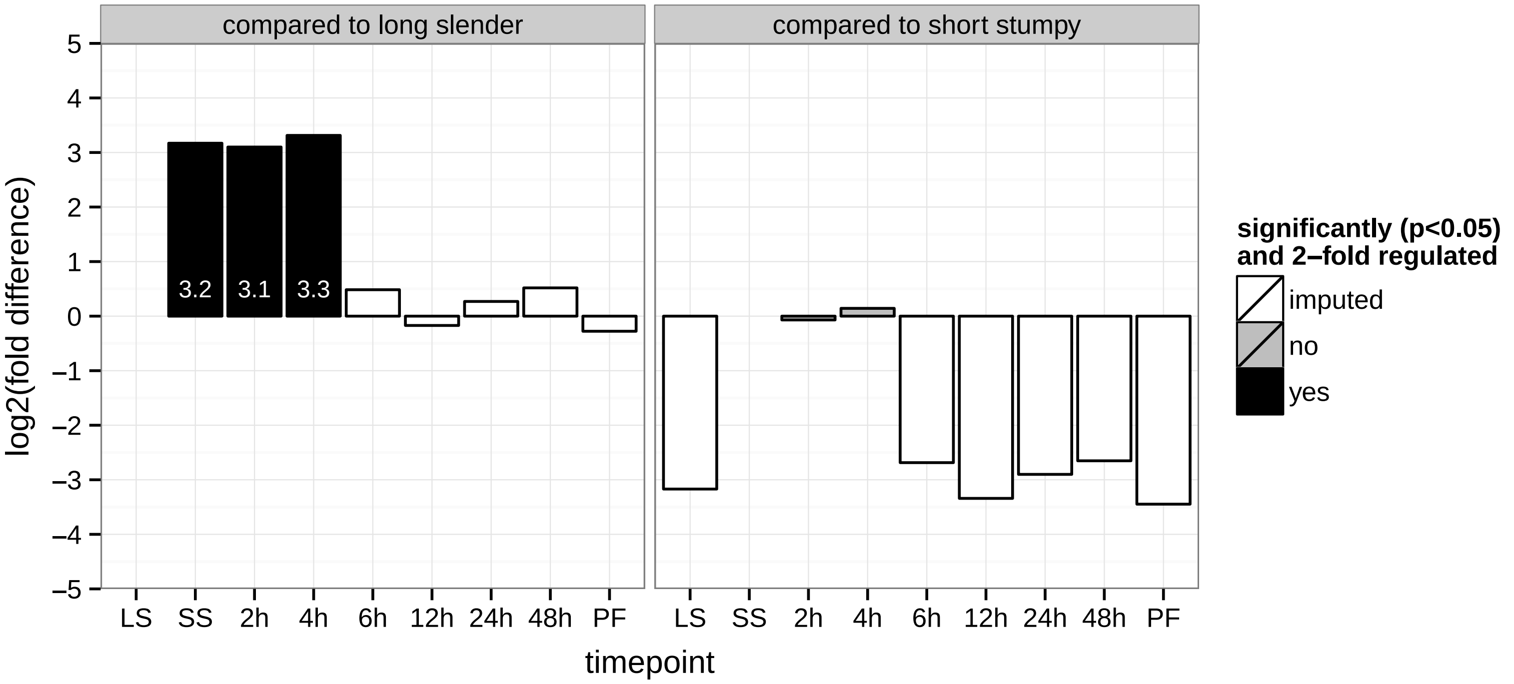
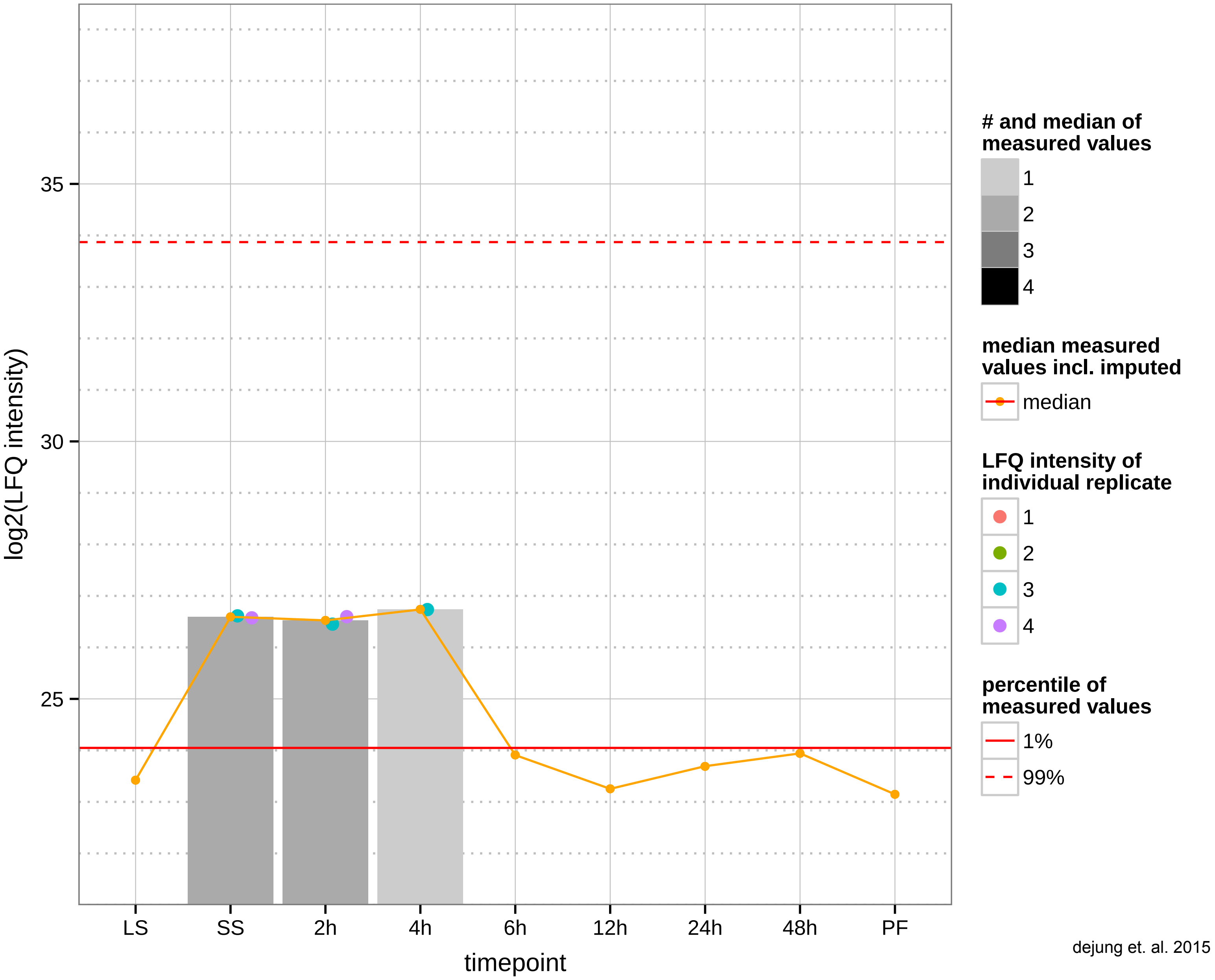
hypothetical protein, conserved
Tb927.2.5200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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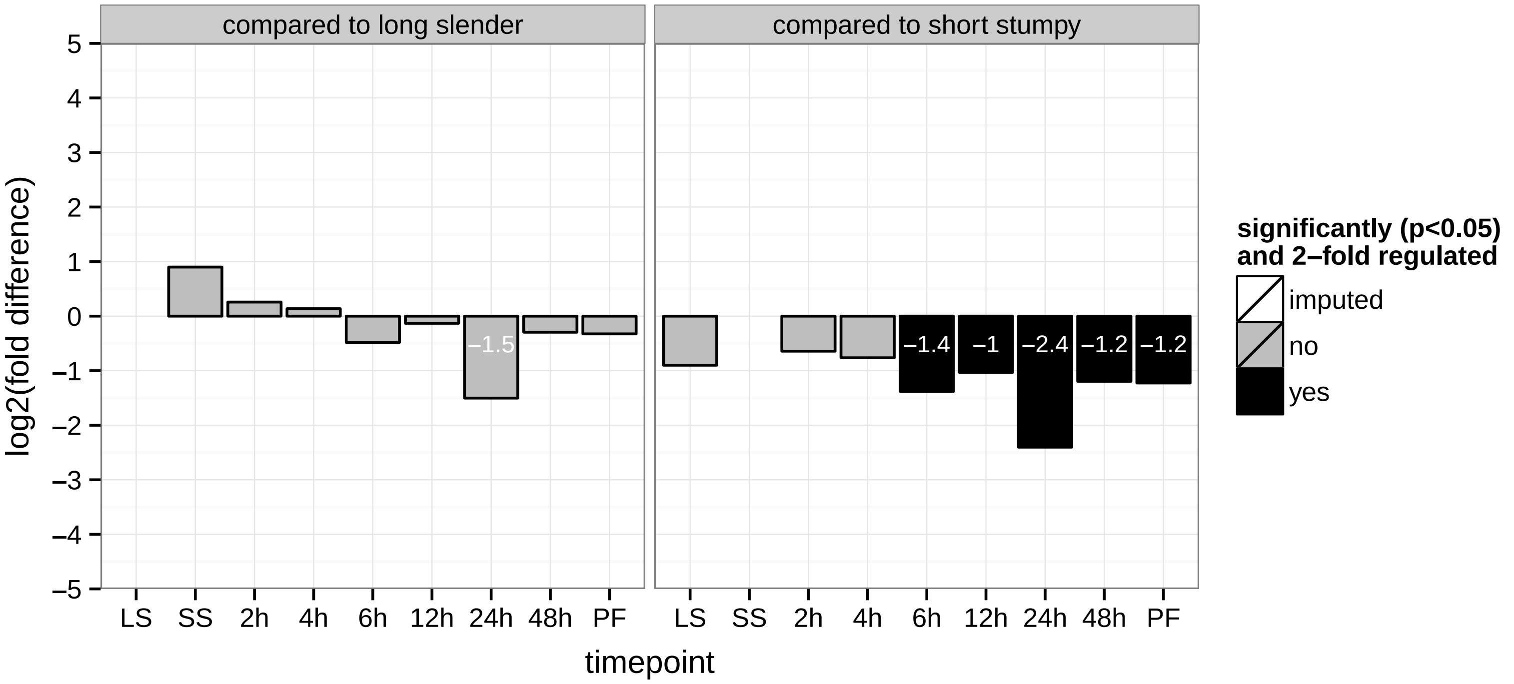
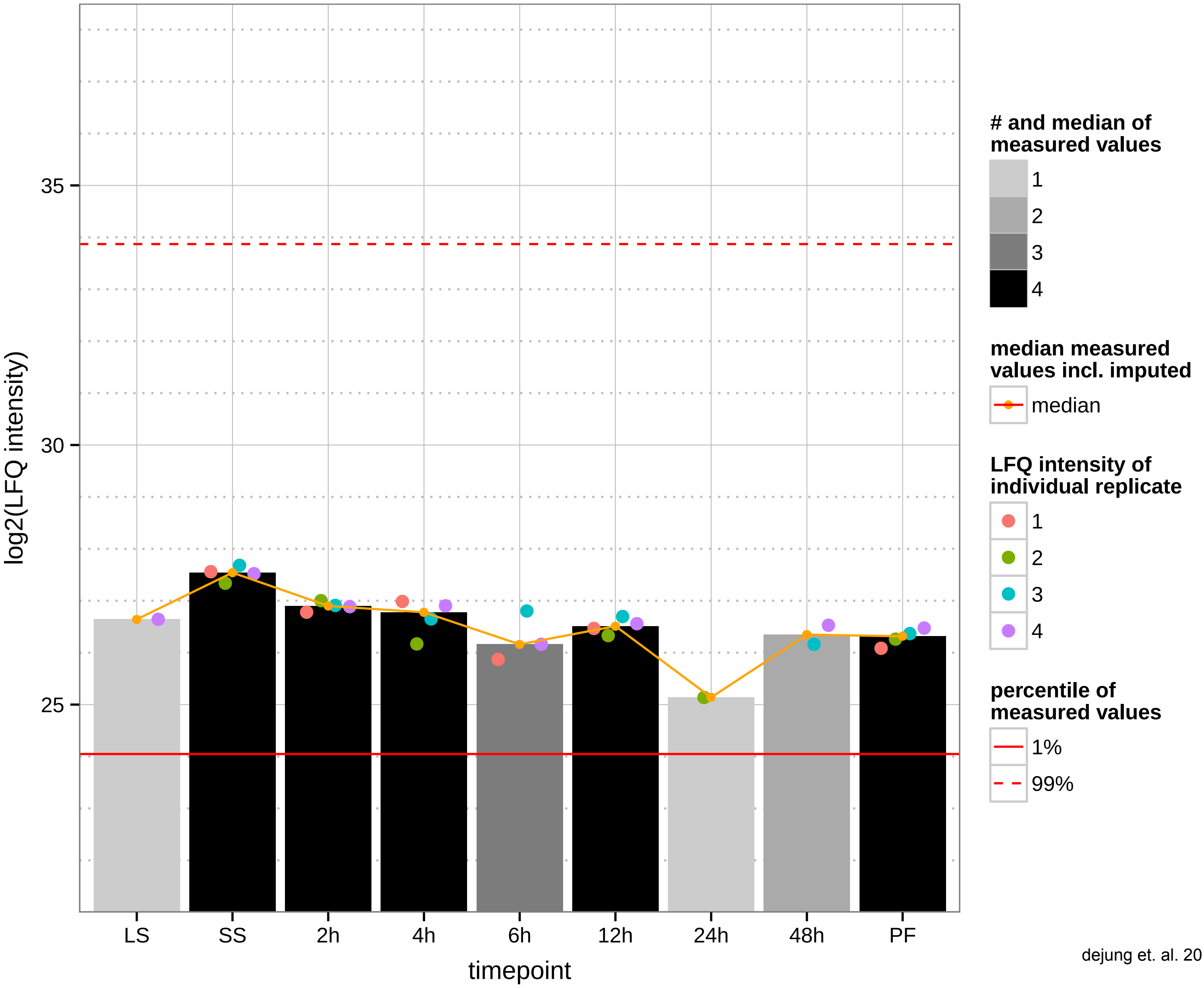
zinc finger protein family member, putative (ZC3H20)
Tb927.7.2660
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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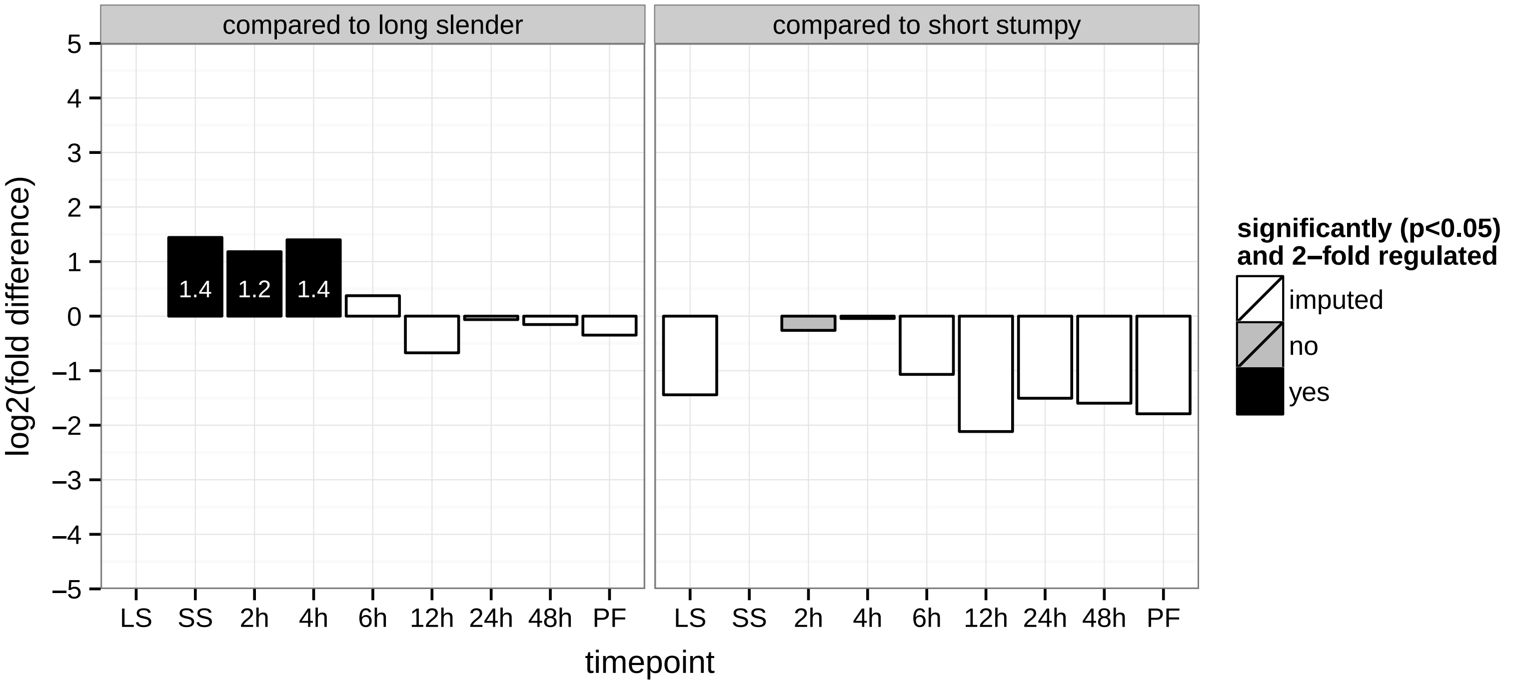
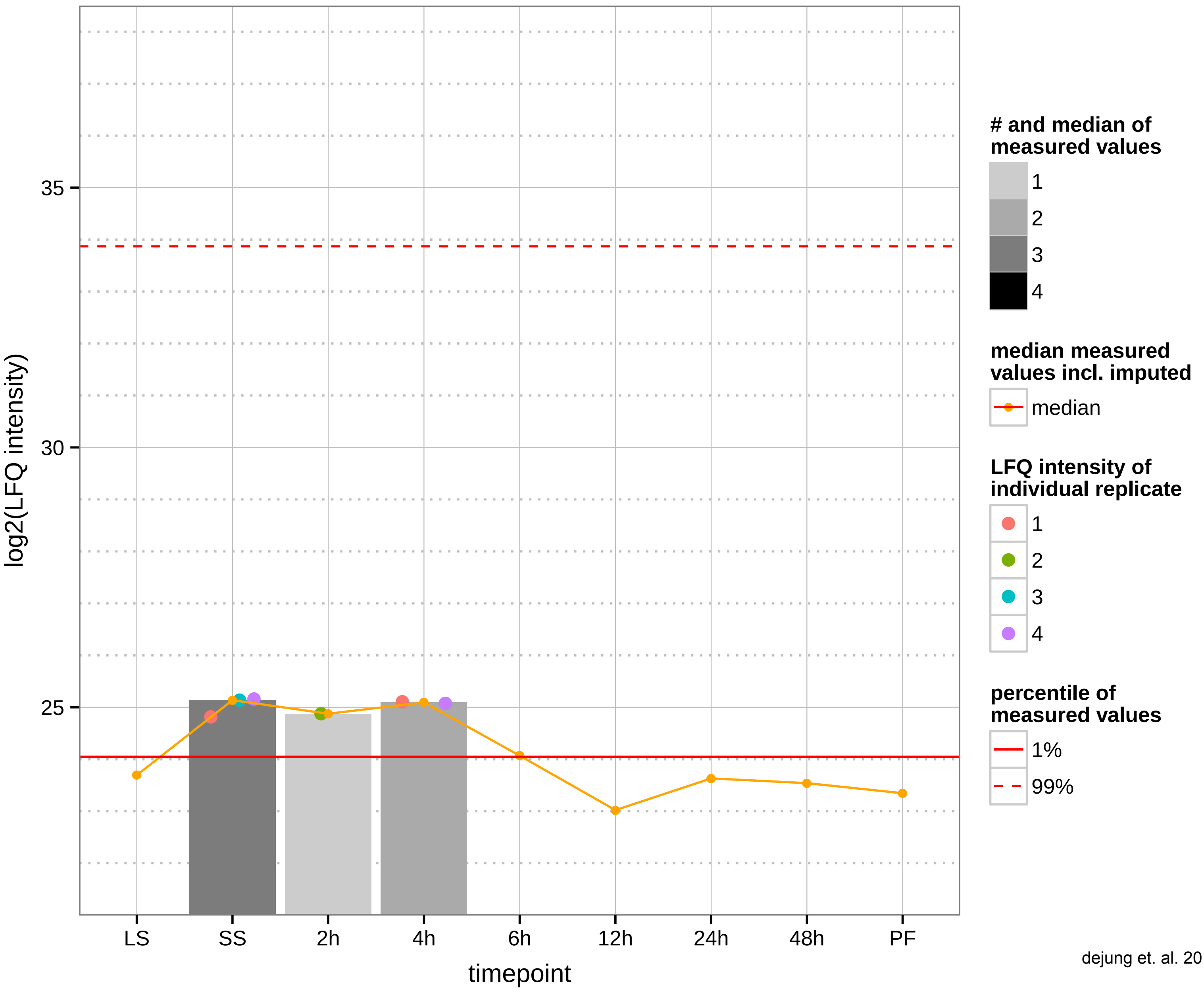
ras–like small GTPase, putative (TbFRP)
Tb927.7.3790
AGOF: GTP binding, zinc ion binding
AGOC: intracellular
AGOP: protein transport, small GTPase mediated signal transduction
PGOF: GTP binding, metal ion binding, protein binding
PGOC: null
PGOP: protein transport, small GTPase mediated signal transduction





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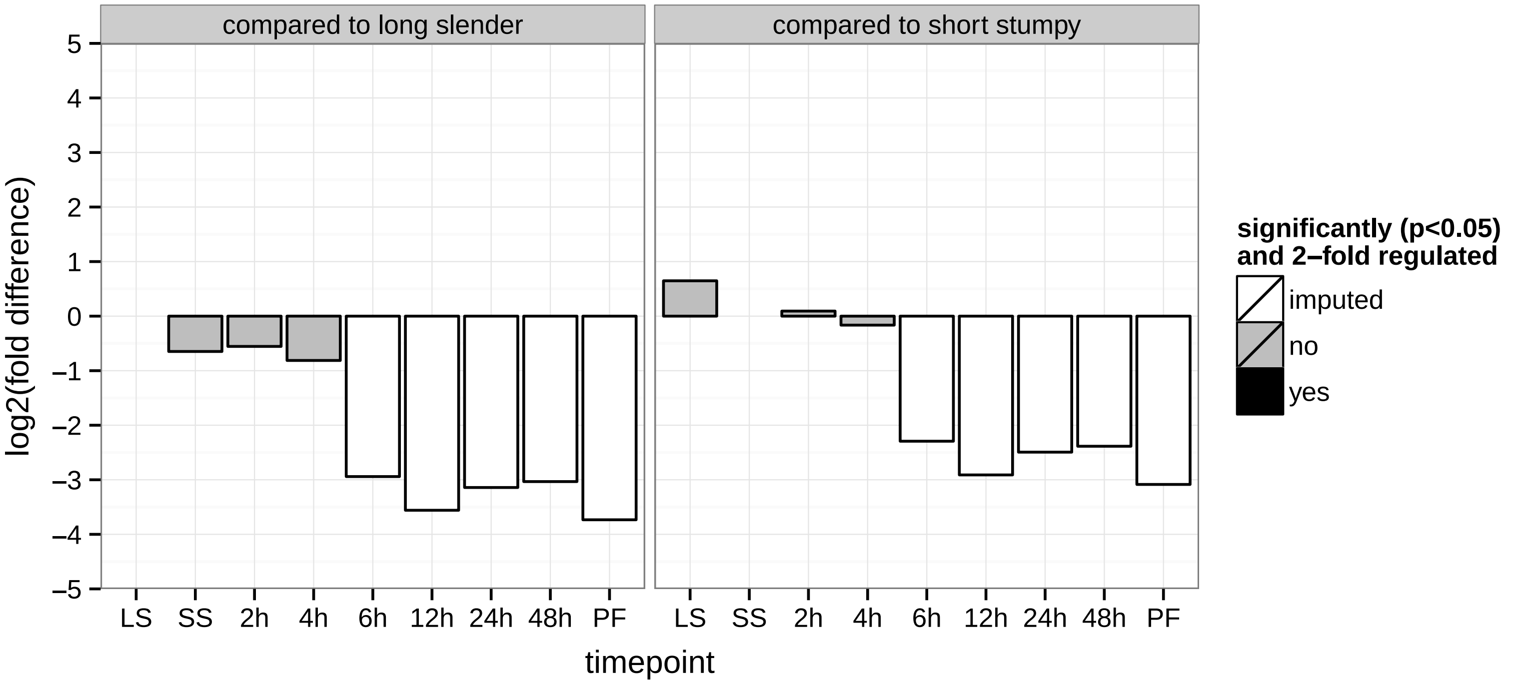
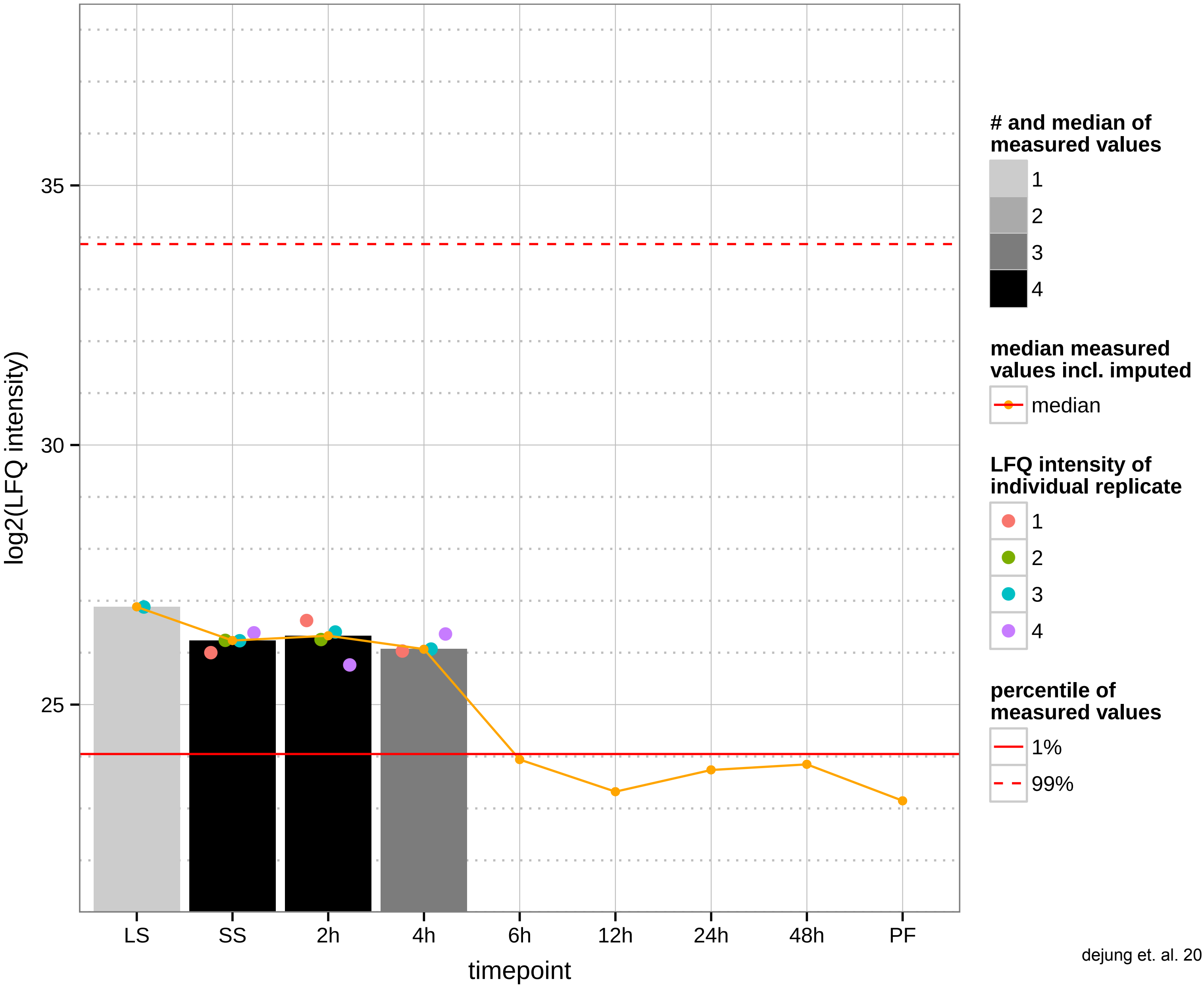
hypothetical protein, conserved
Tb927.7.4410
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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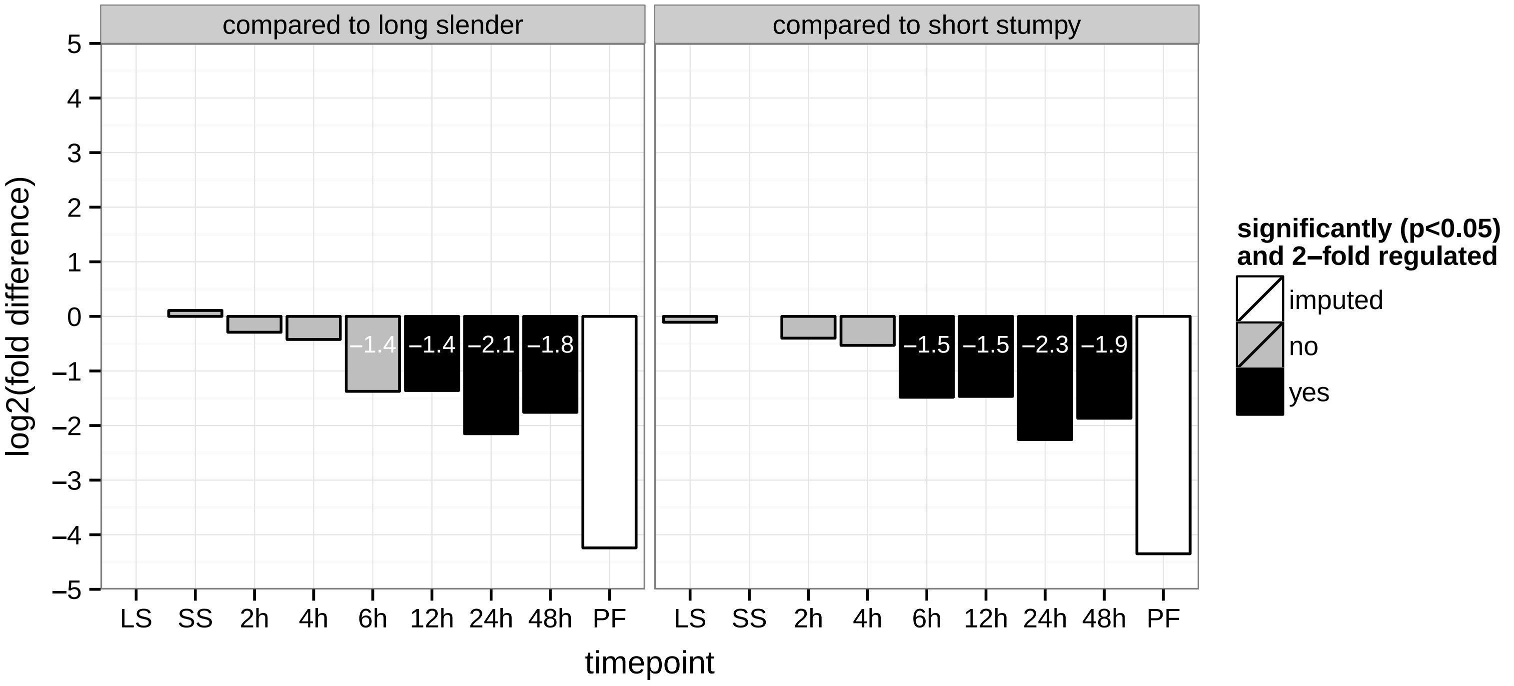
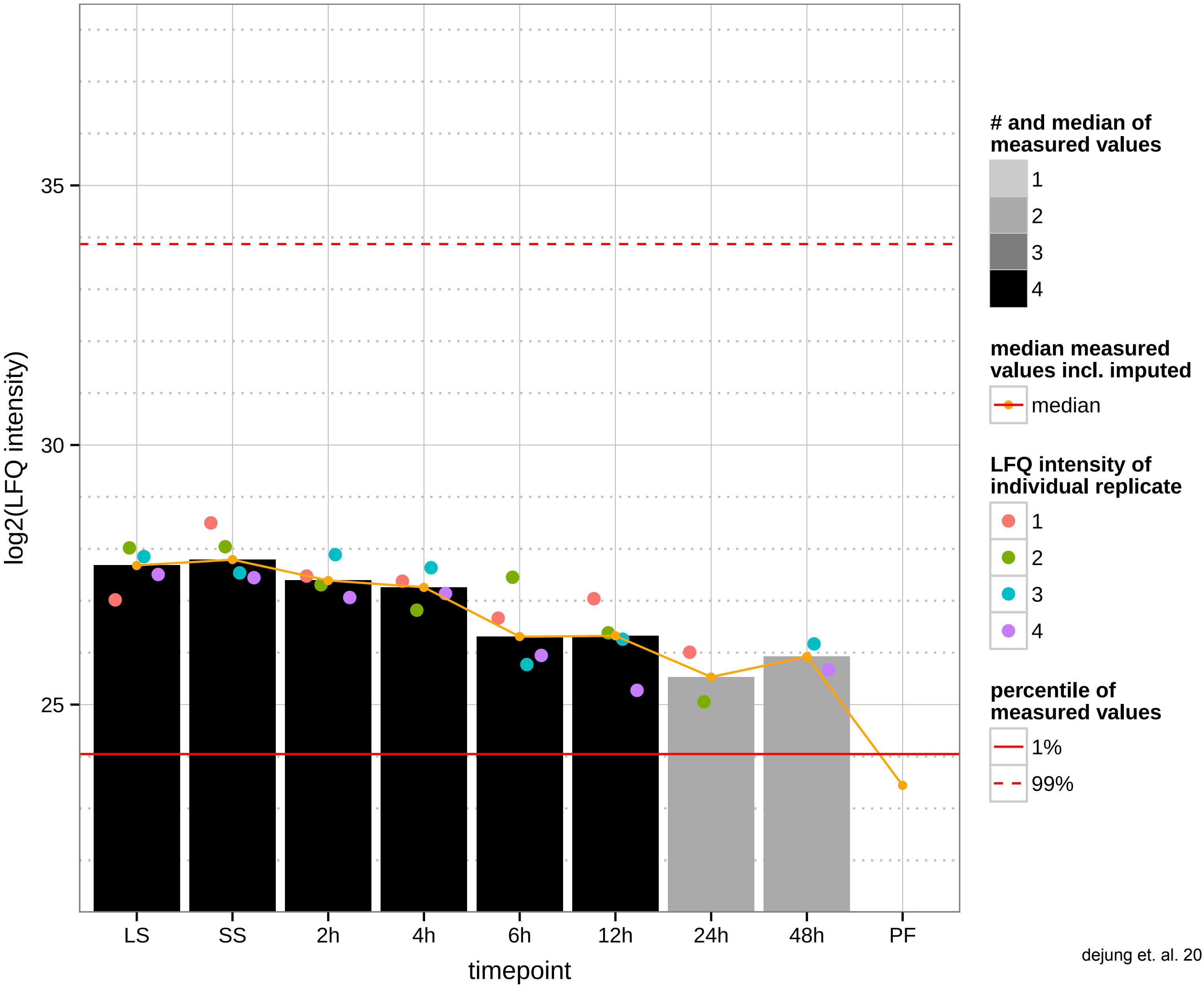
hypothetical protein
Tb927.7.470
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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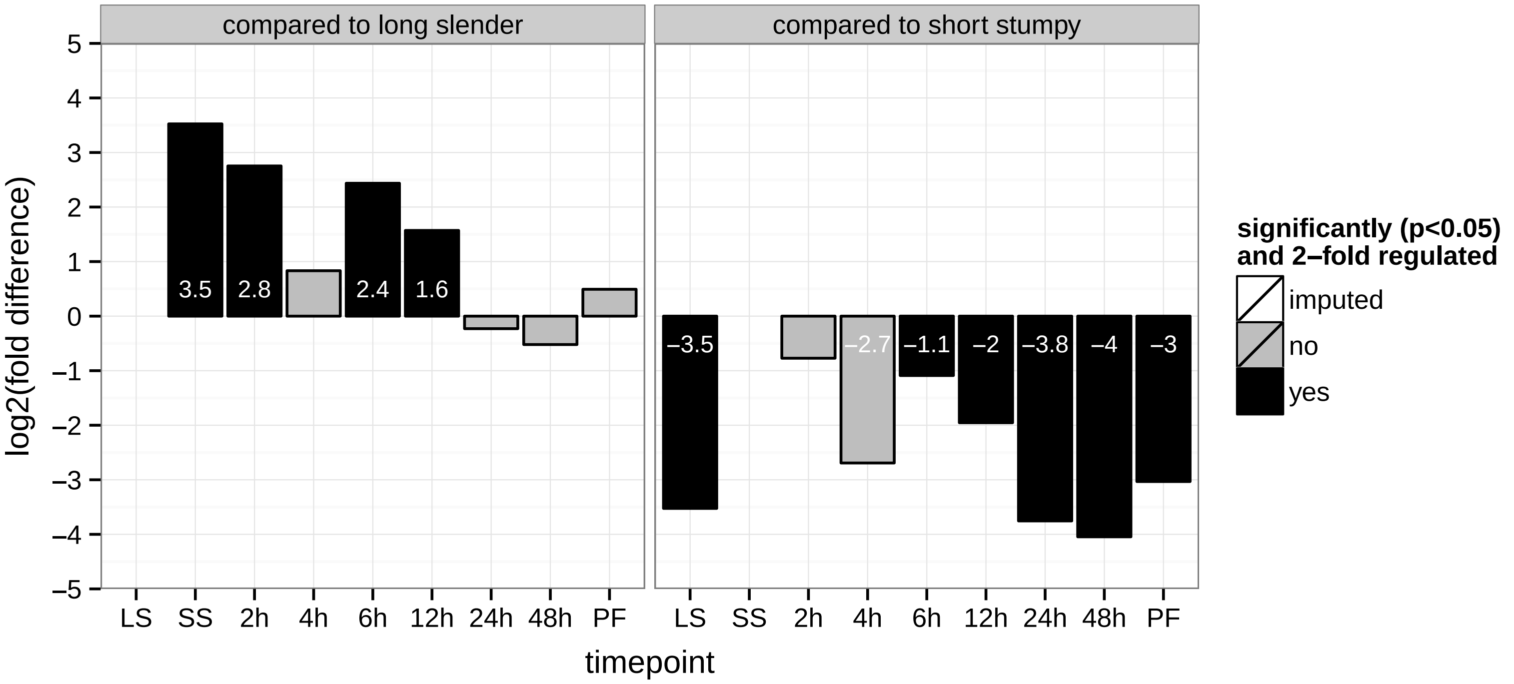
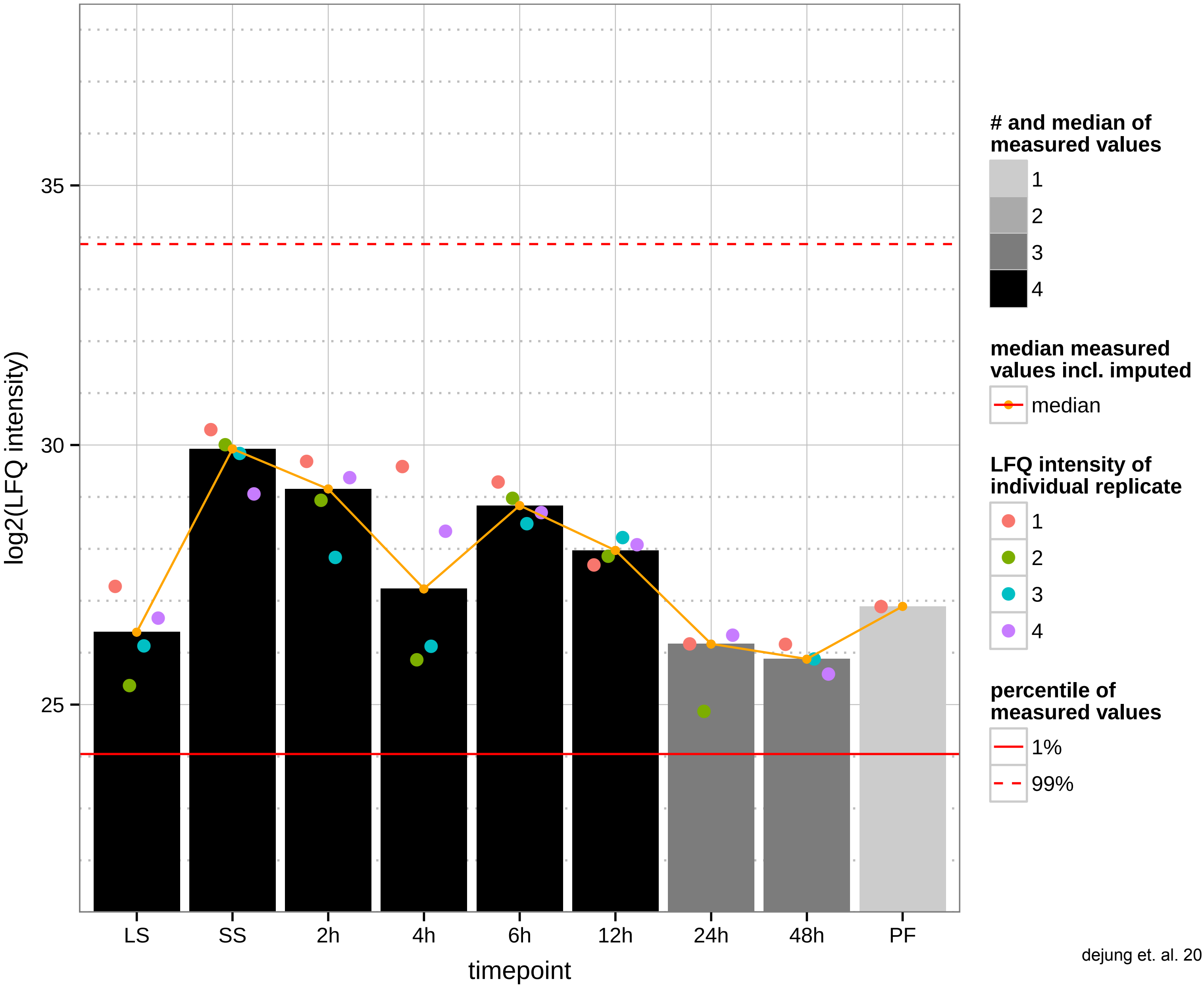
hypothetical protein, conserved
Tb927.7.7000
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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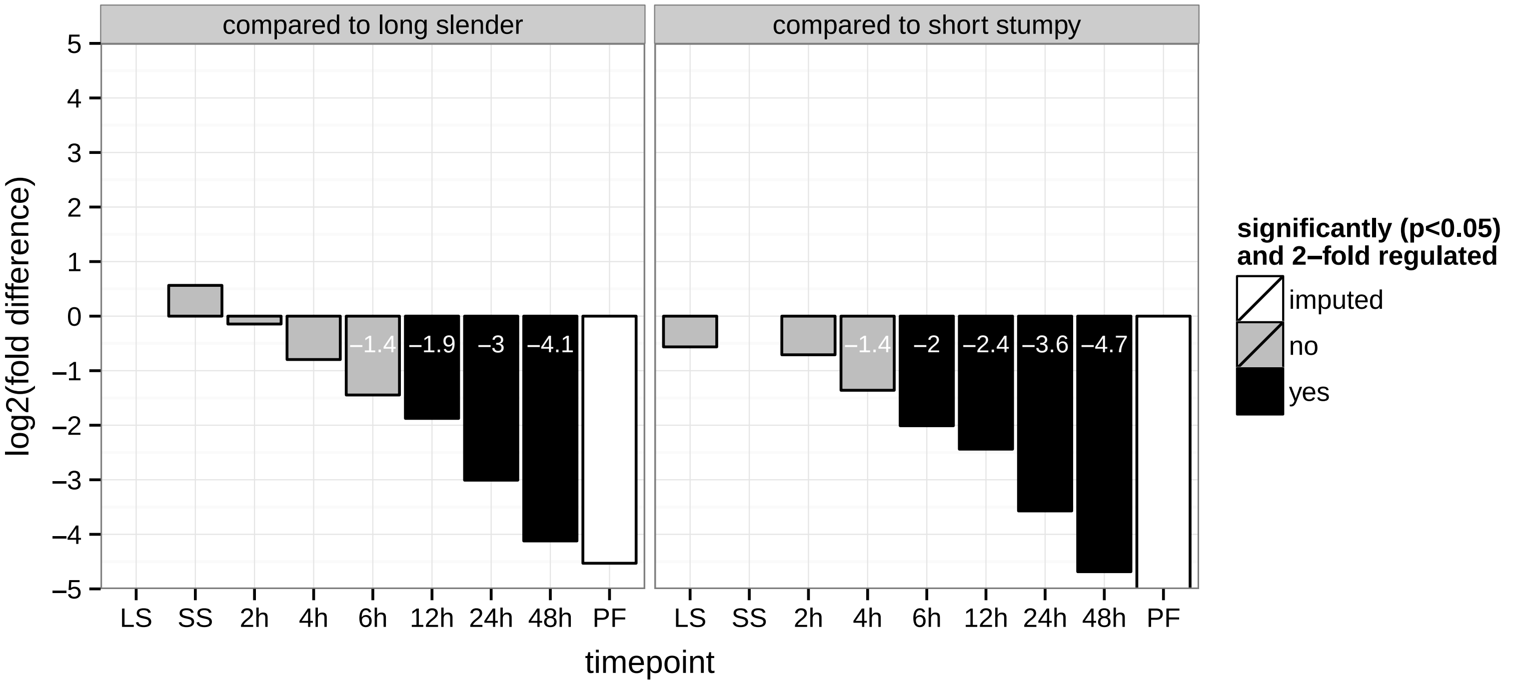
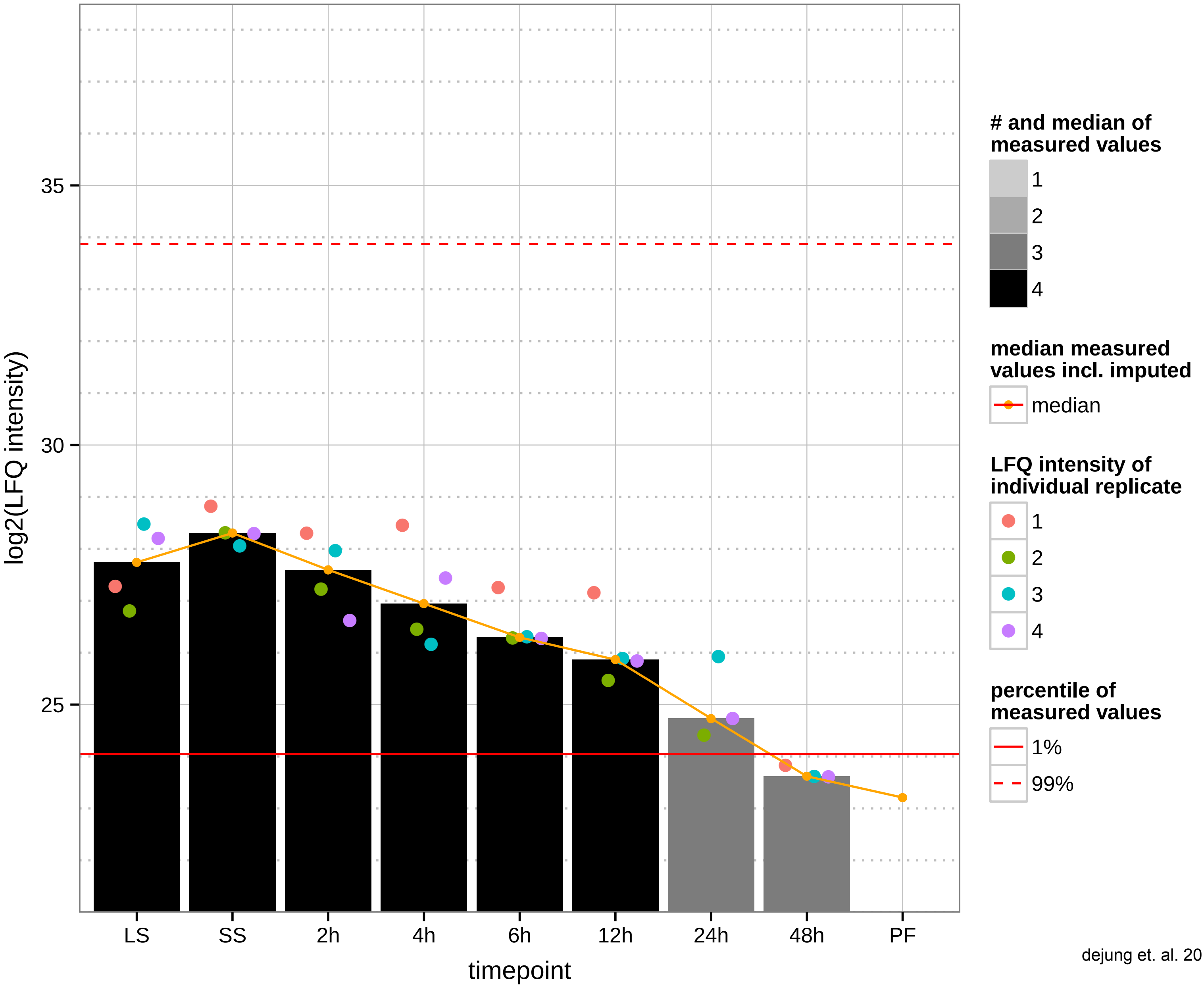
hypothetical protein, conserved
Tb927.9.11480
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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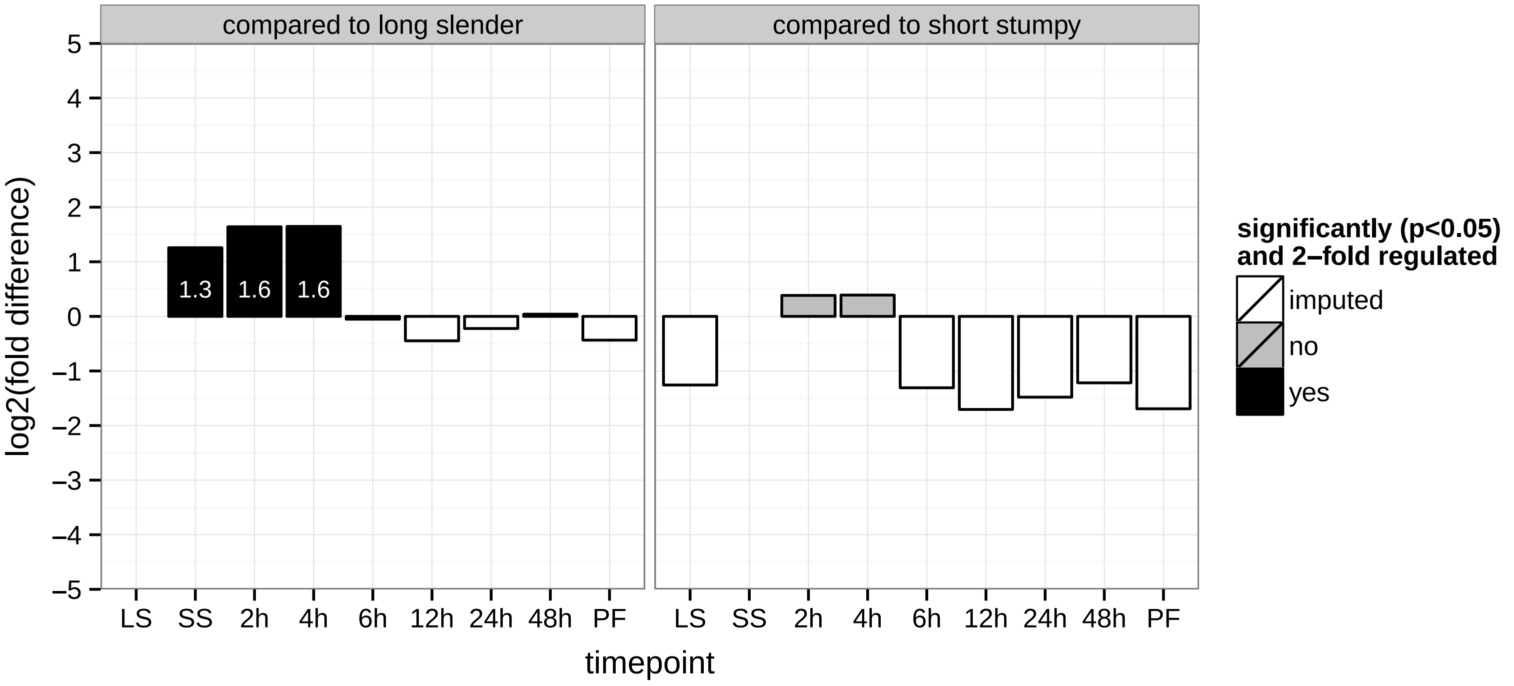
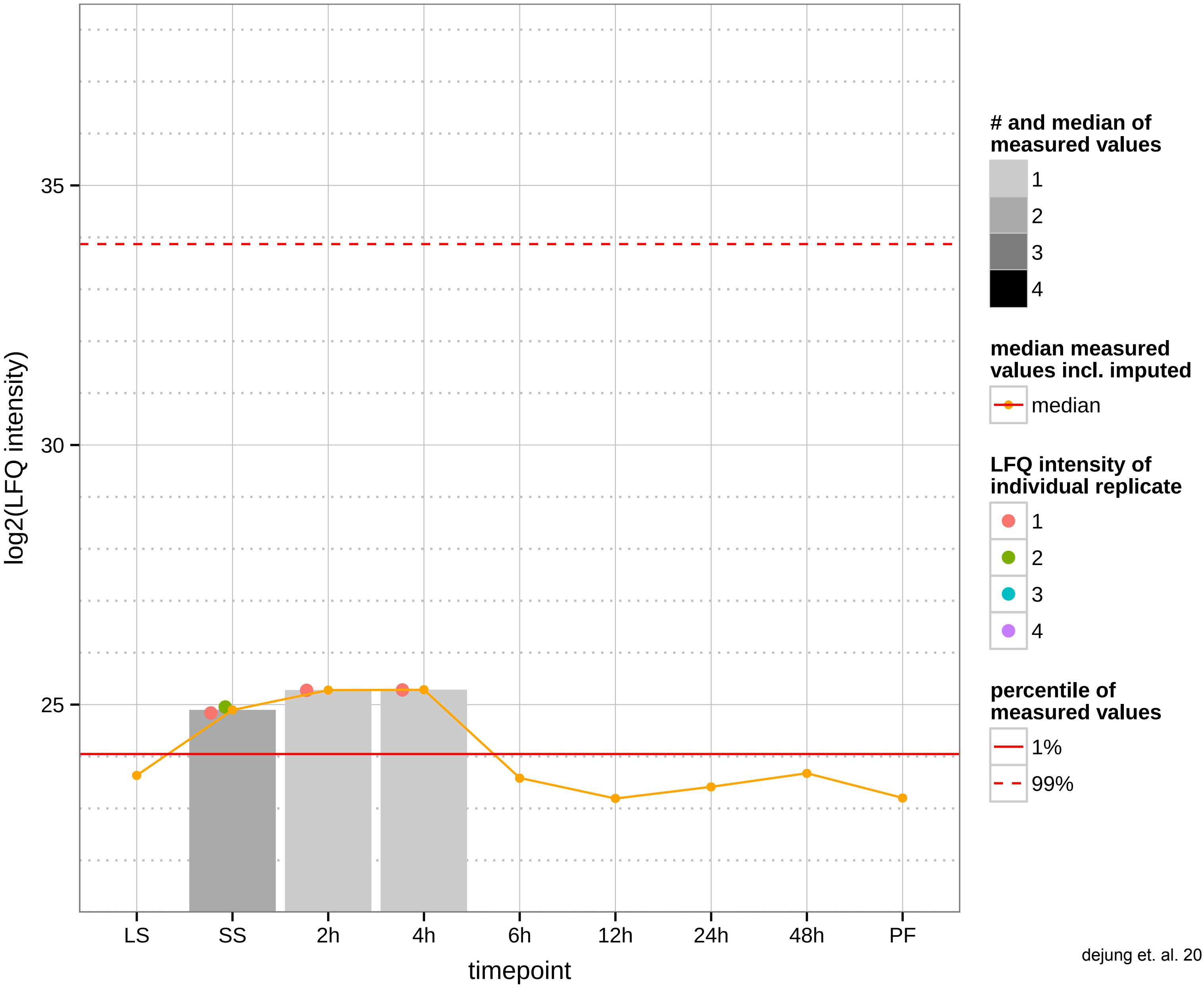
hypothetical protein, conserved
Tb927.9.3130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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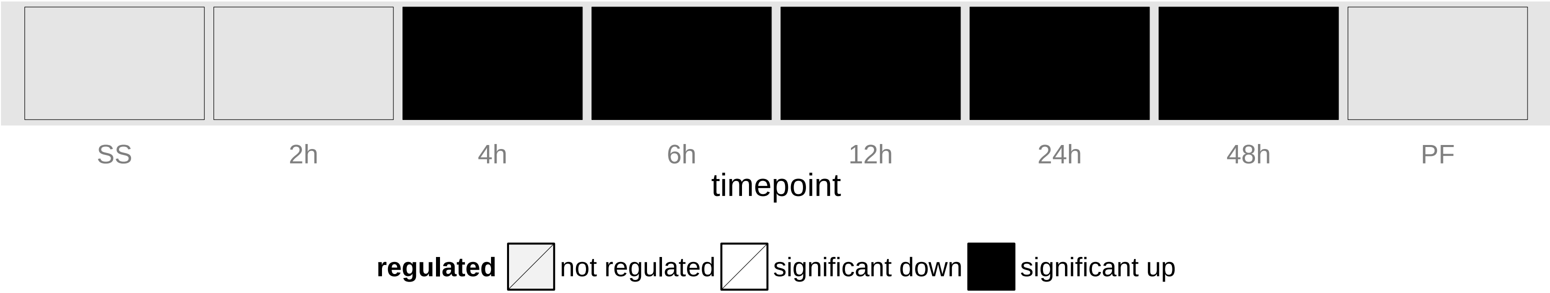

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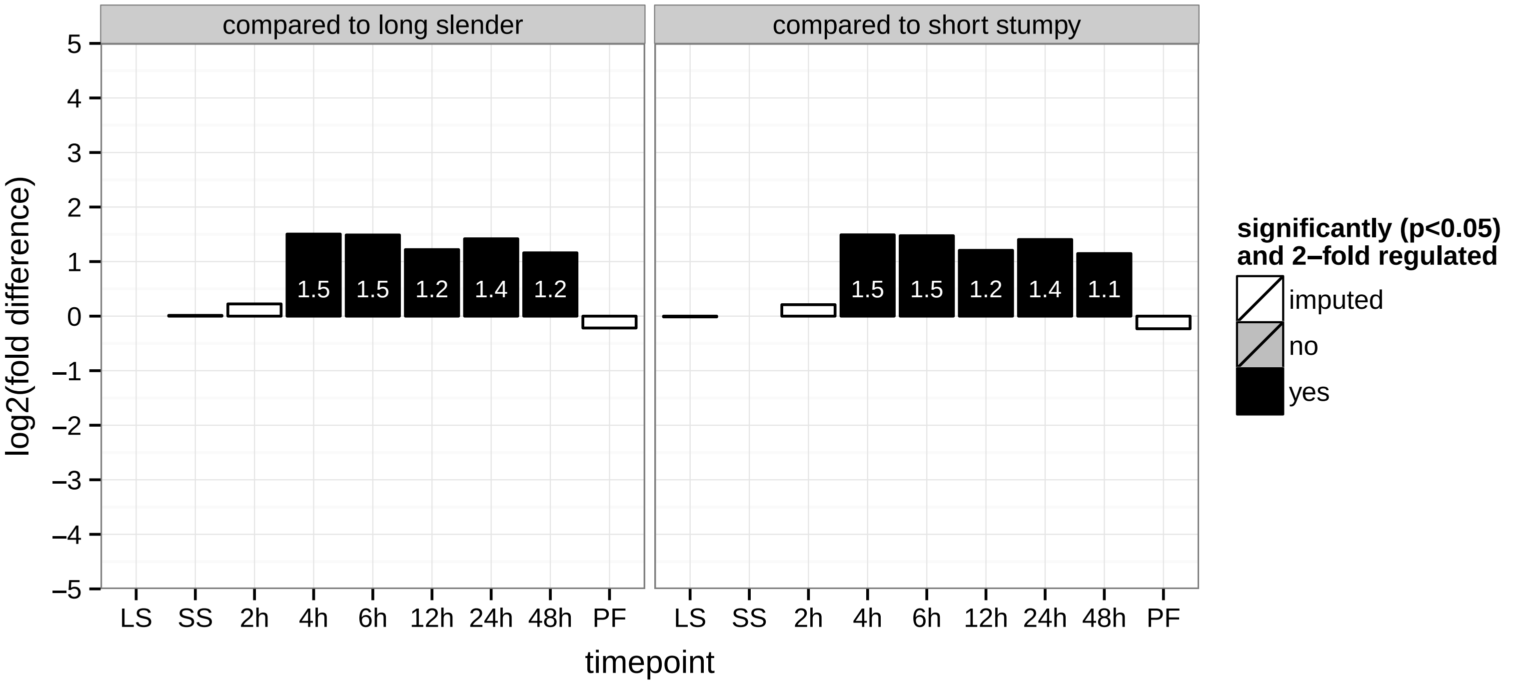
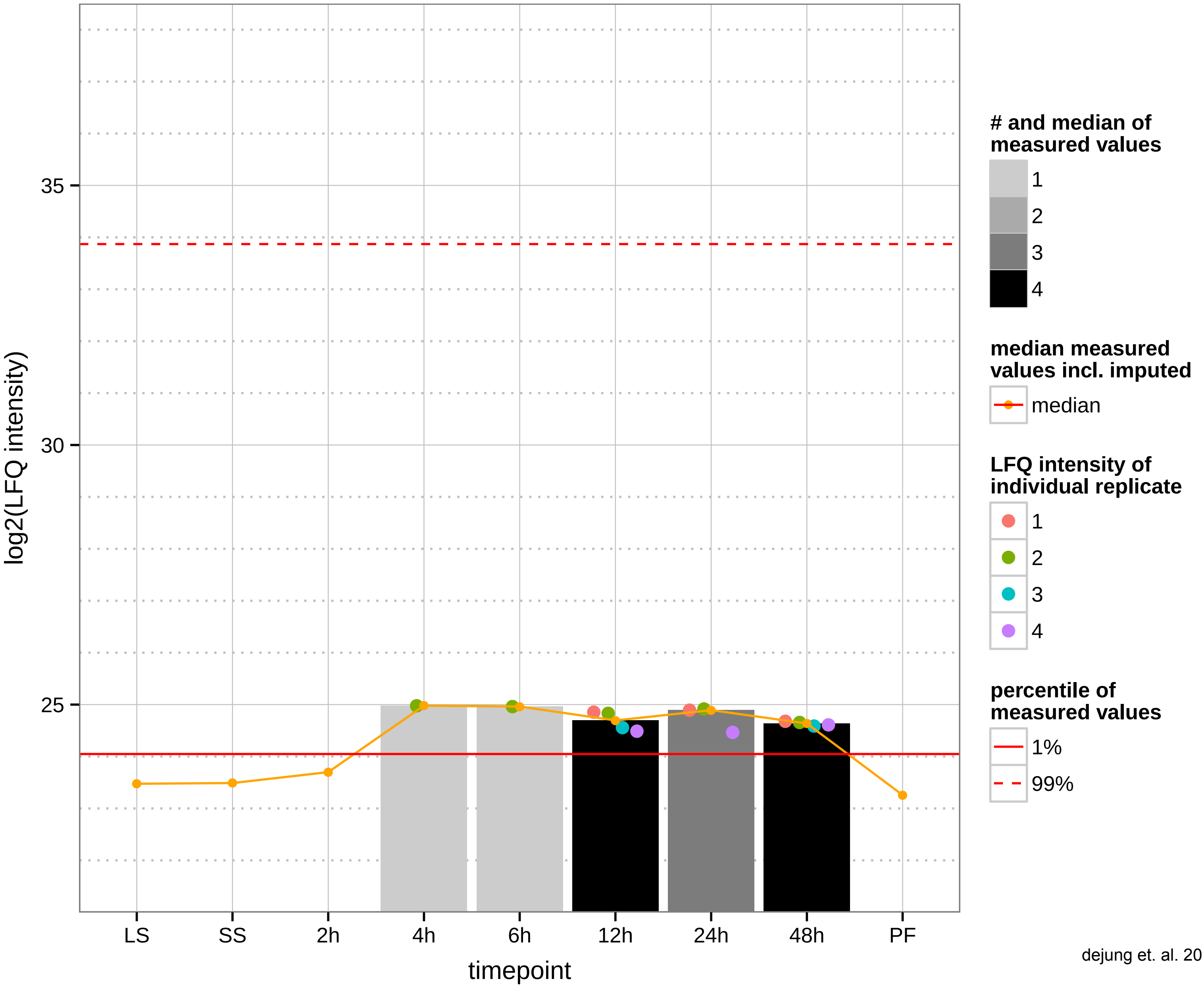
hypothetical protein, conserved
Tb927.7.4740;Tb11.v5.0157
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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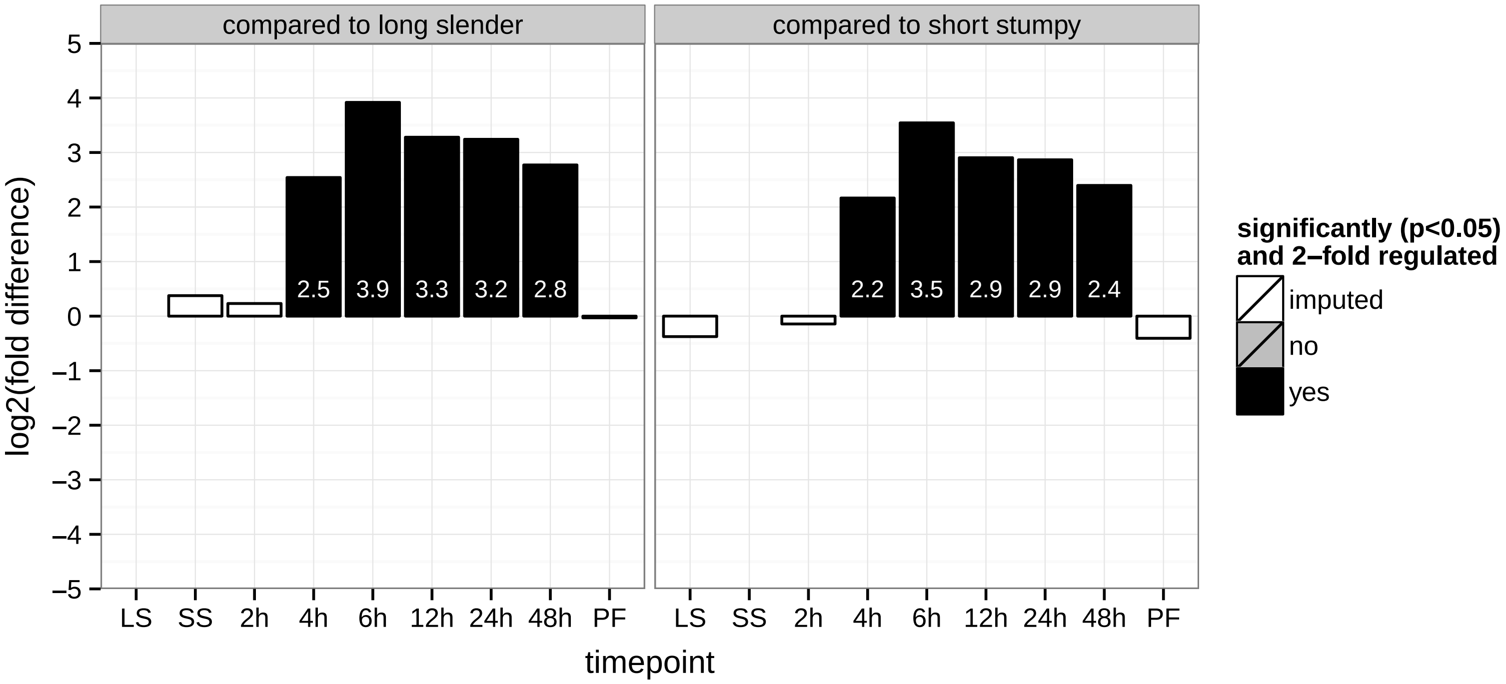
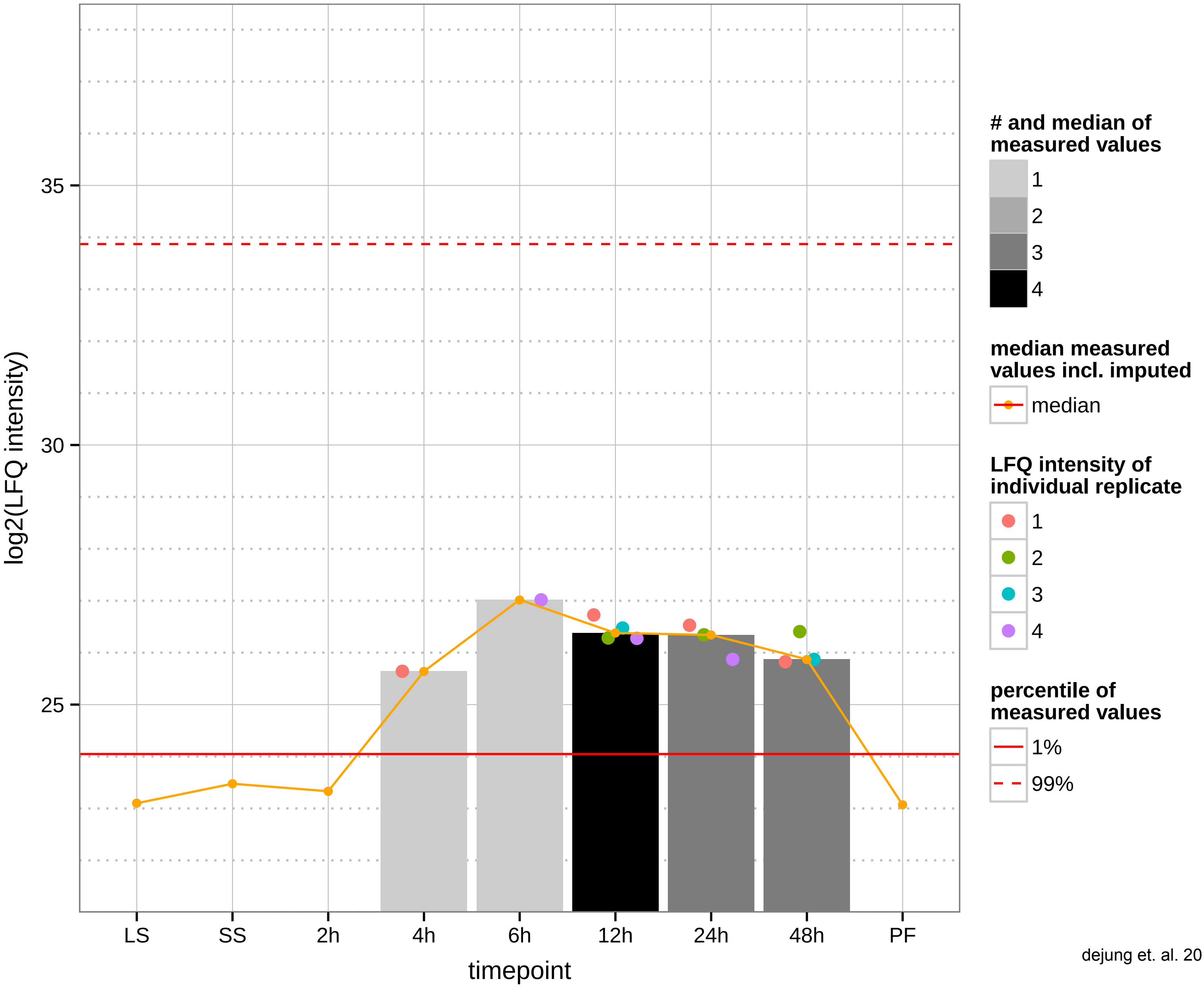
protein kinase, putative
Tb927.10.3230
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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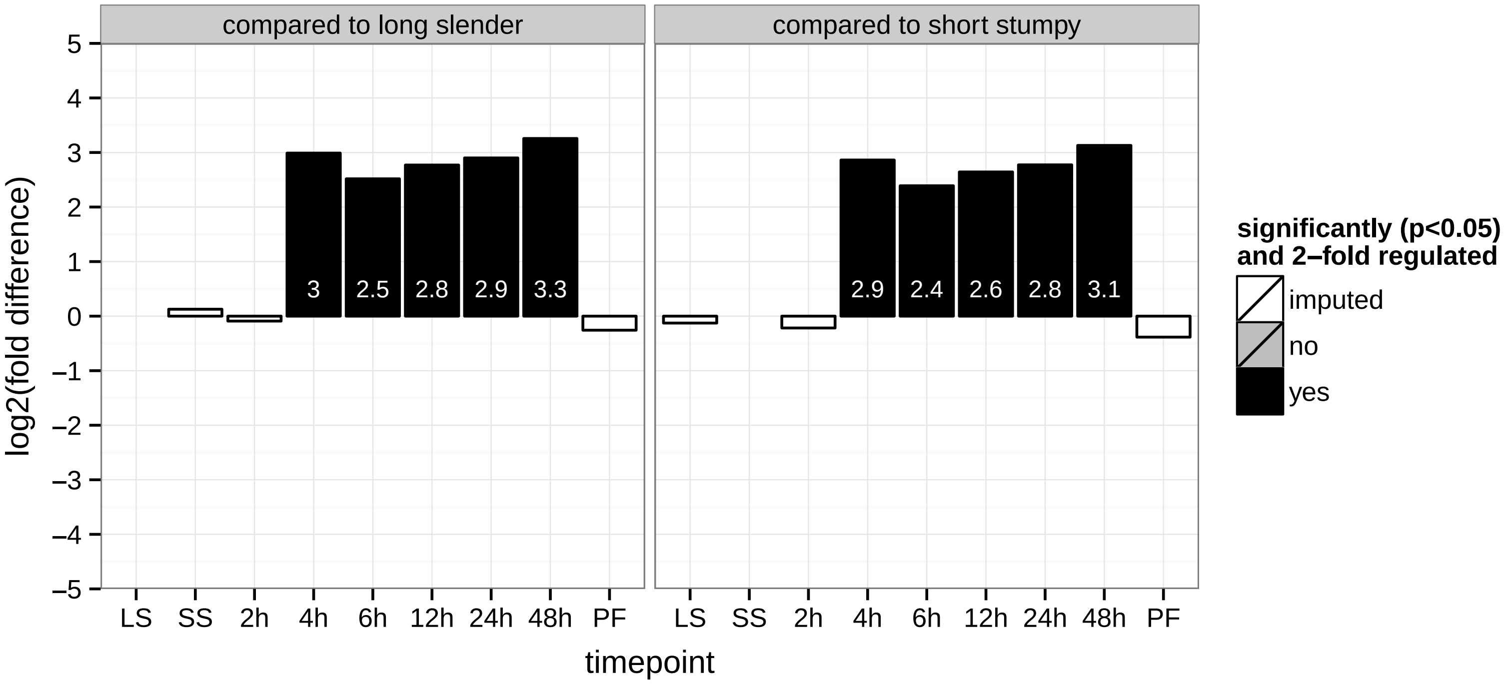
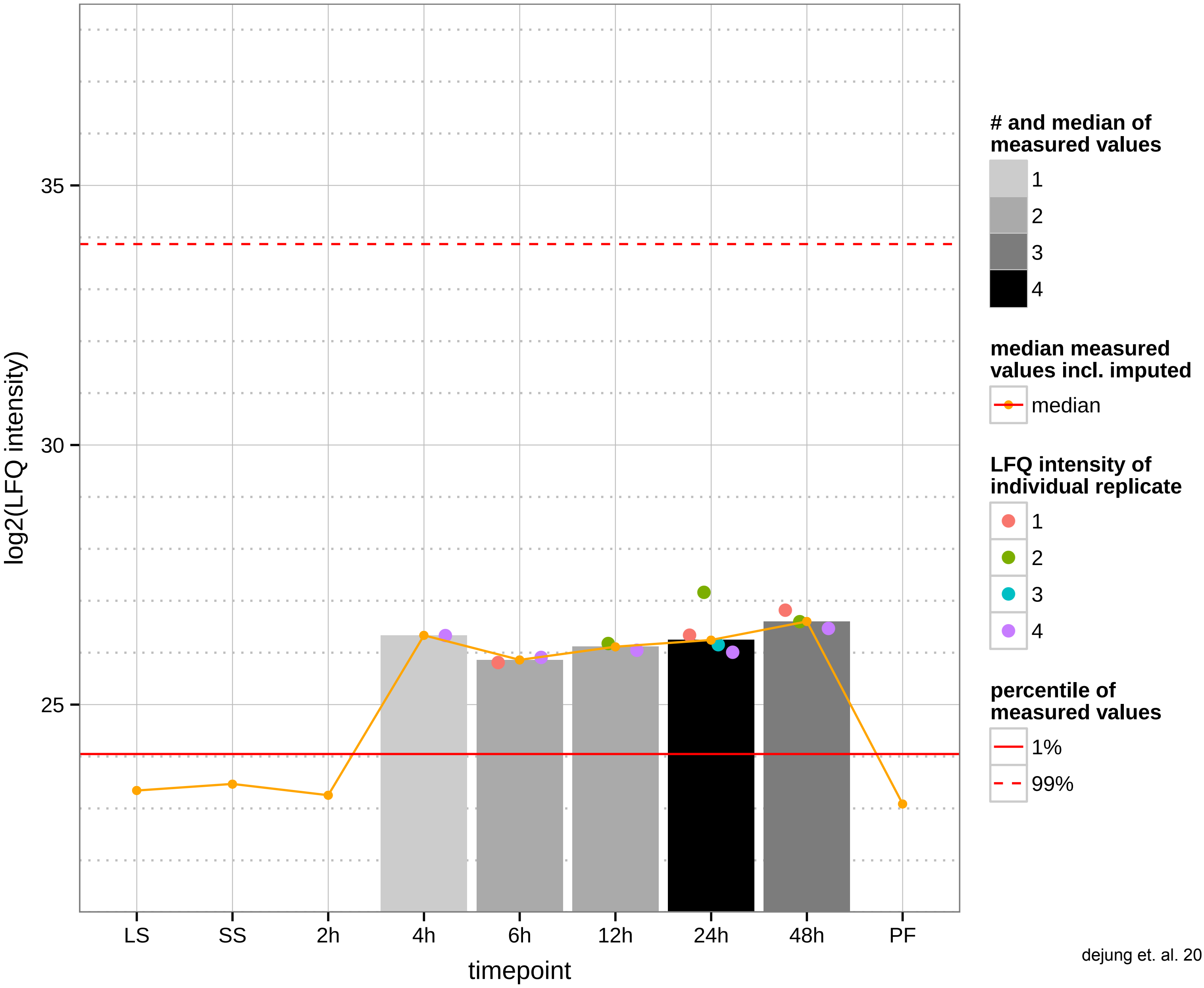
hypothetical protein, conserved
Tb927.10.7910
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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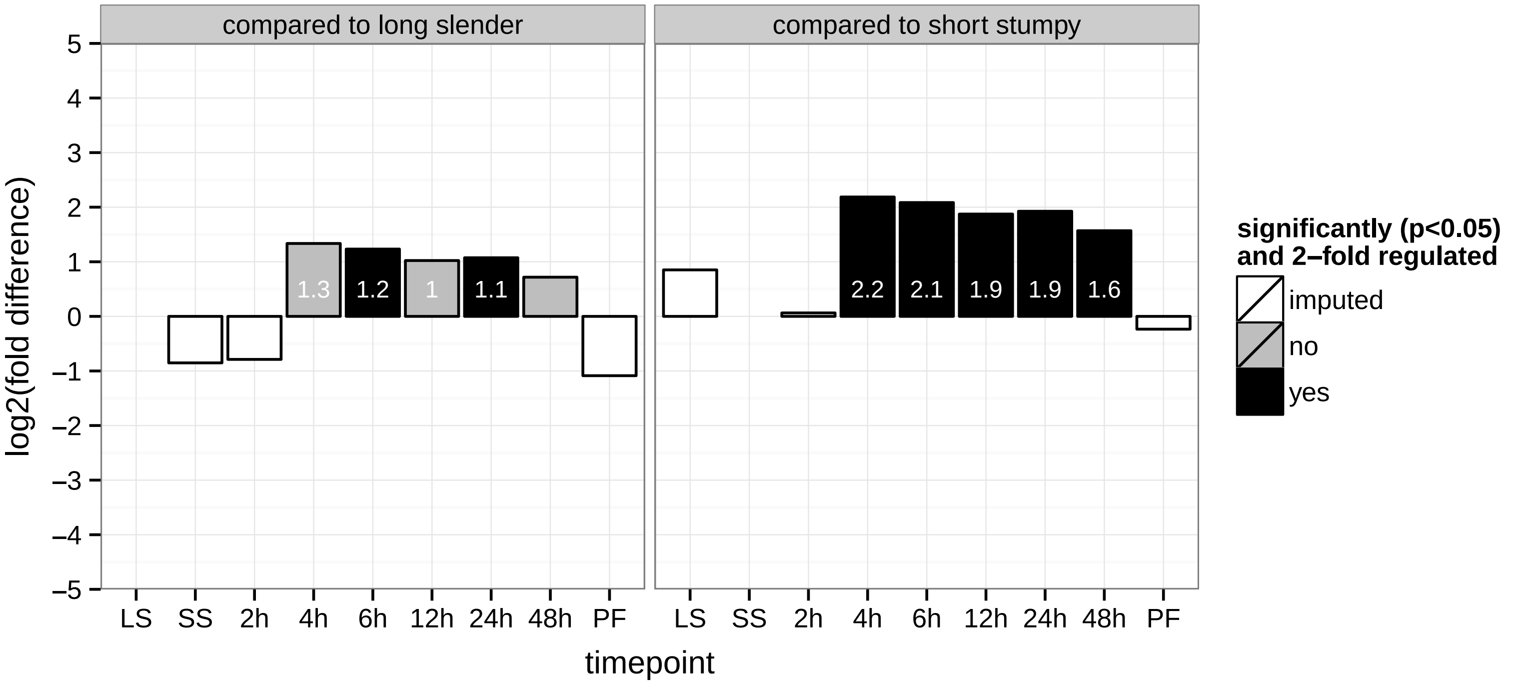
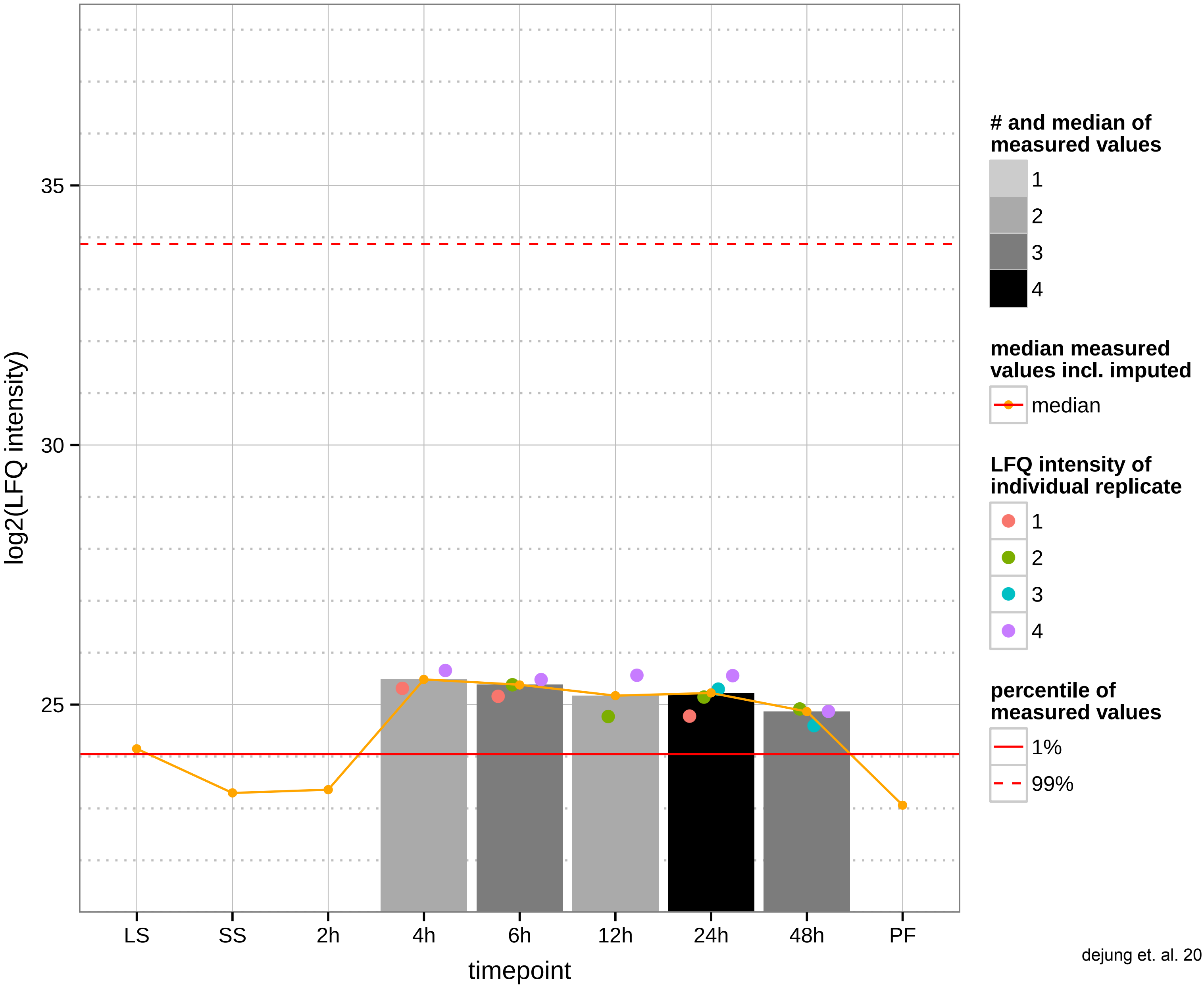
hypothetical protein, conserved
Tb927.11.12320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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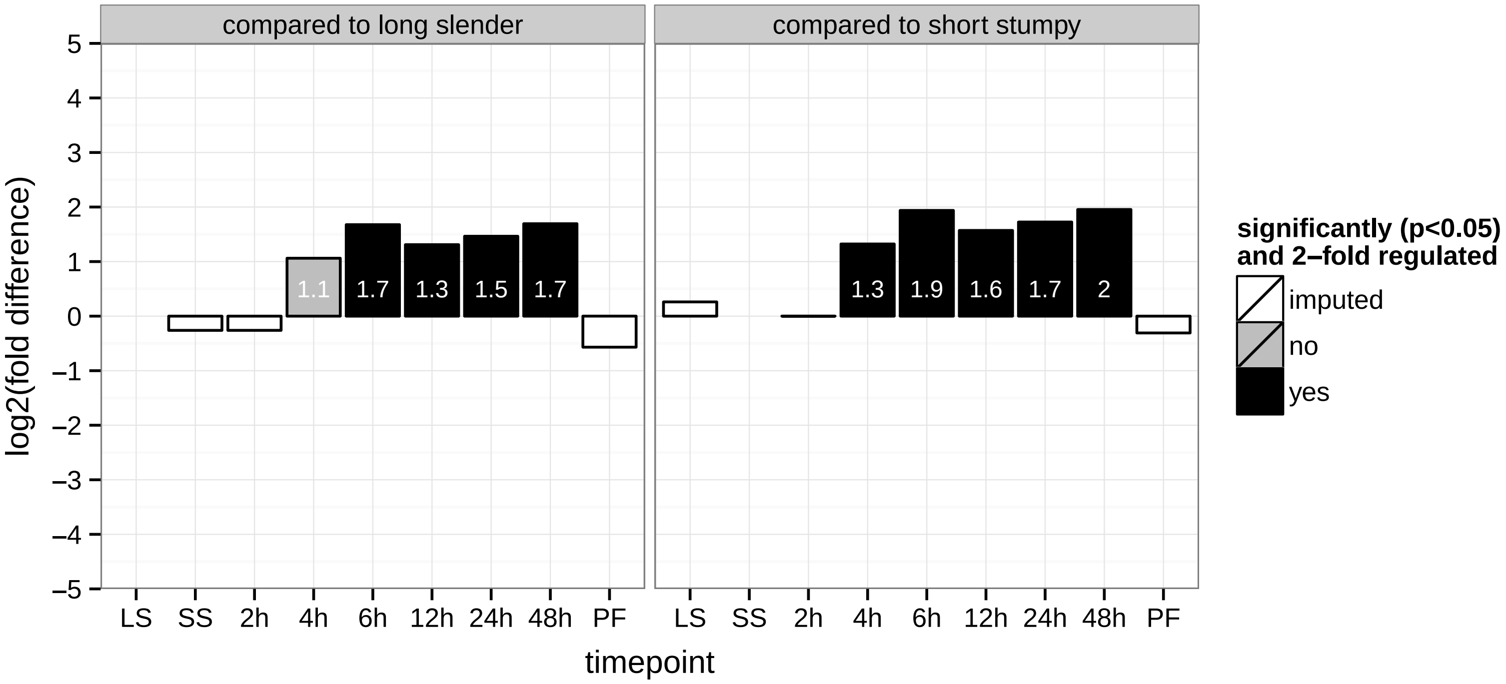
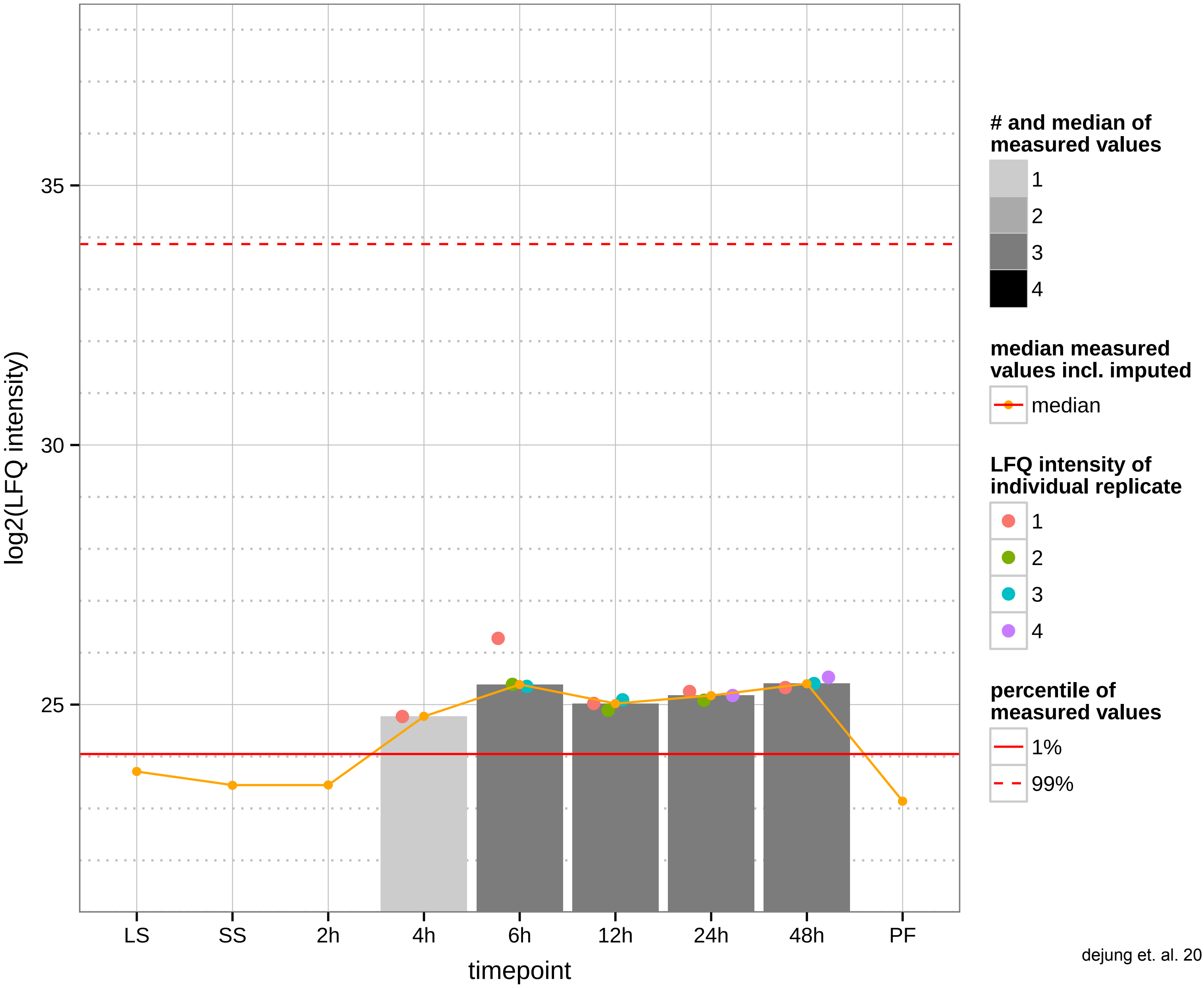
hypothetical protein, conserved
Tb927.11.2590
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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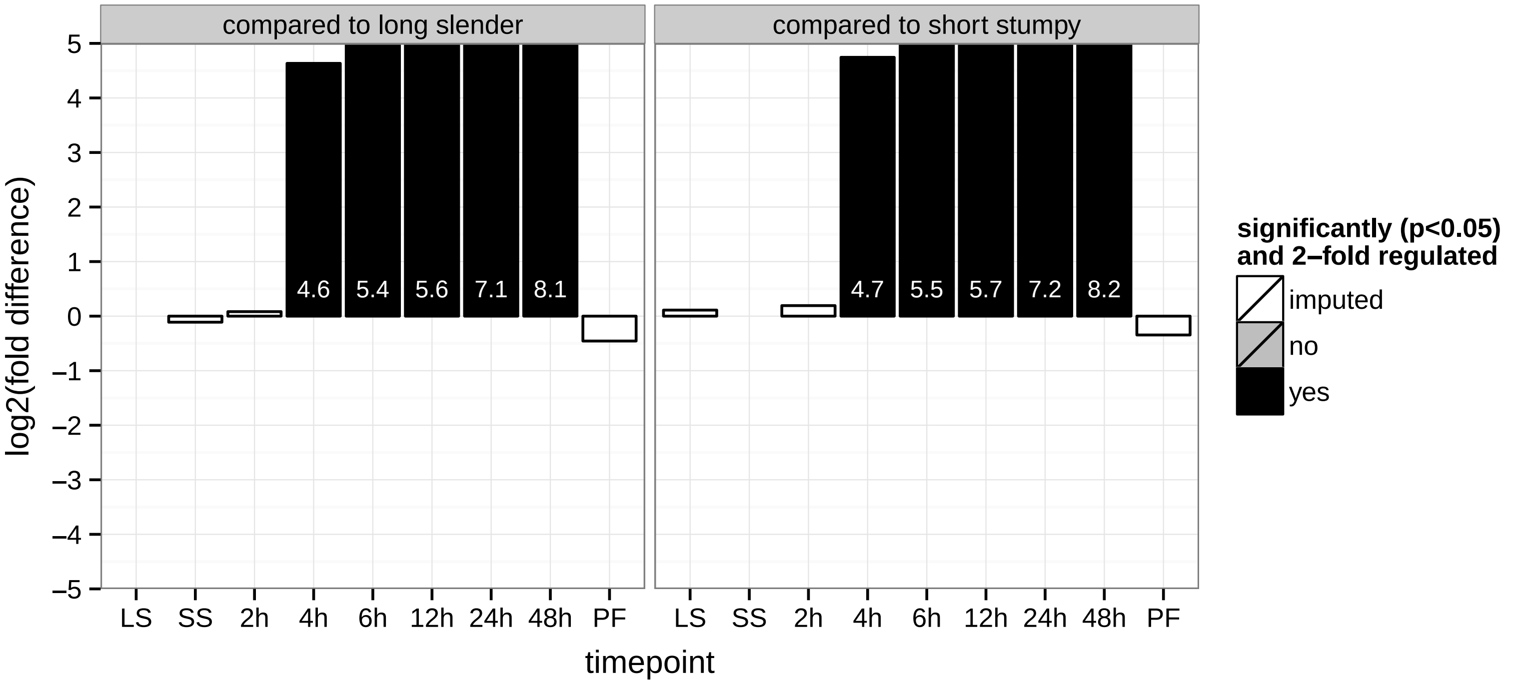
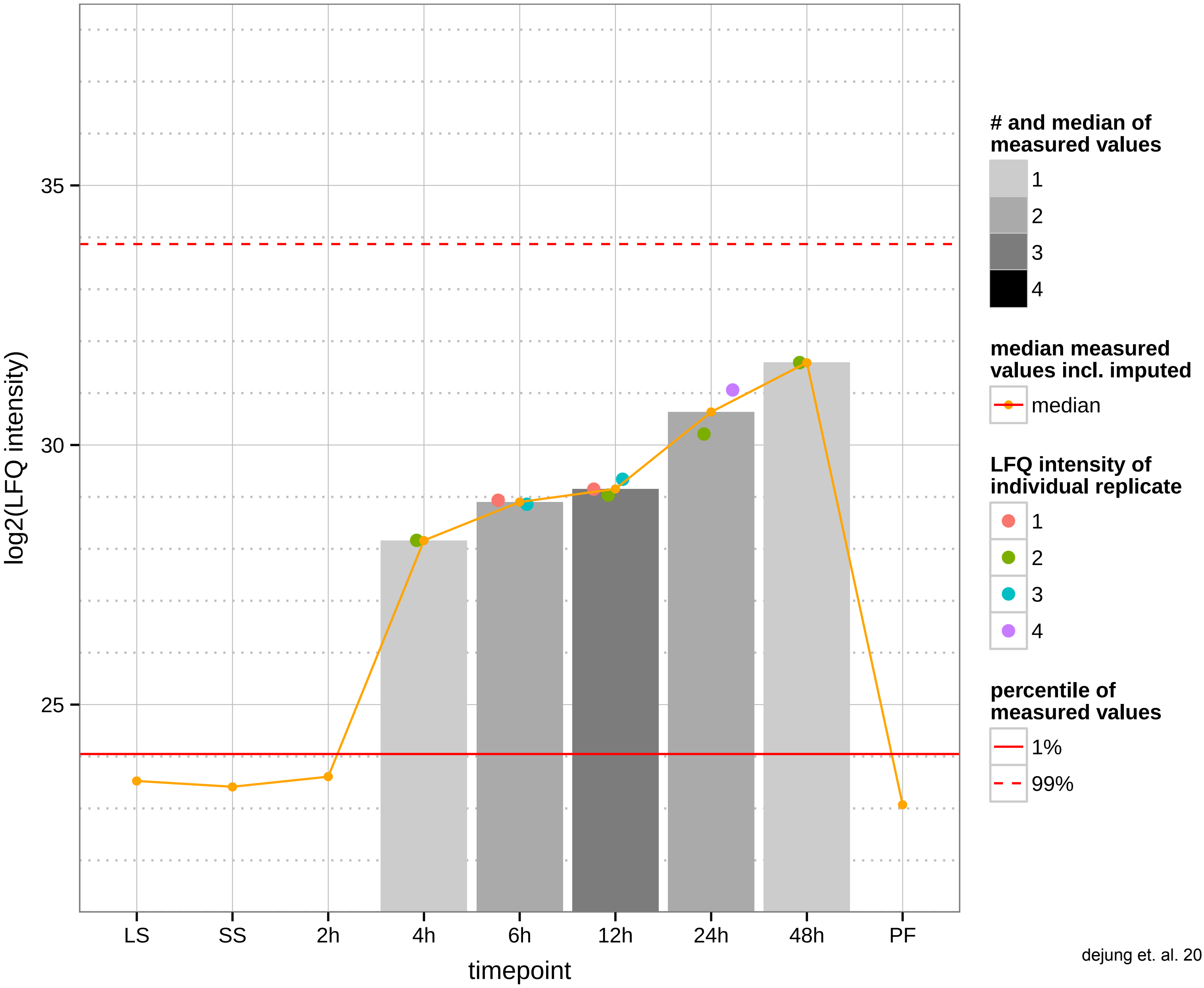
hypothetical protein, conserved
Tb927.11.7500;Tb927.11.7490
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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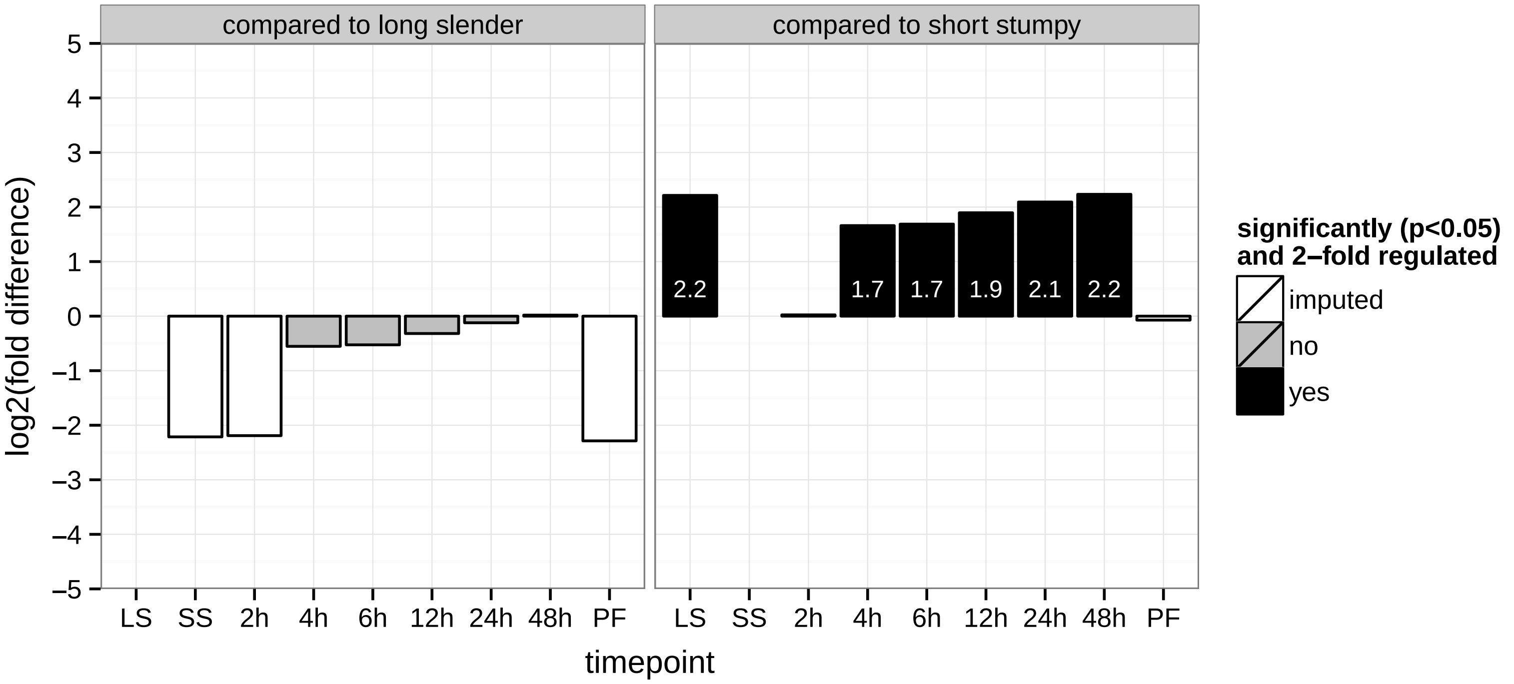
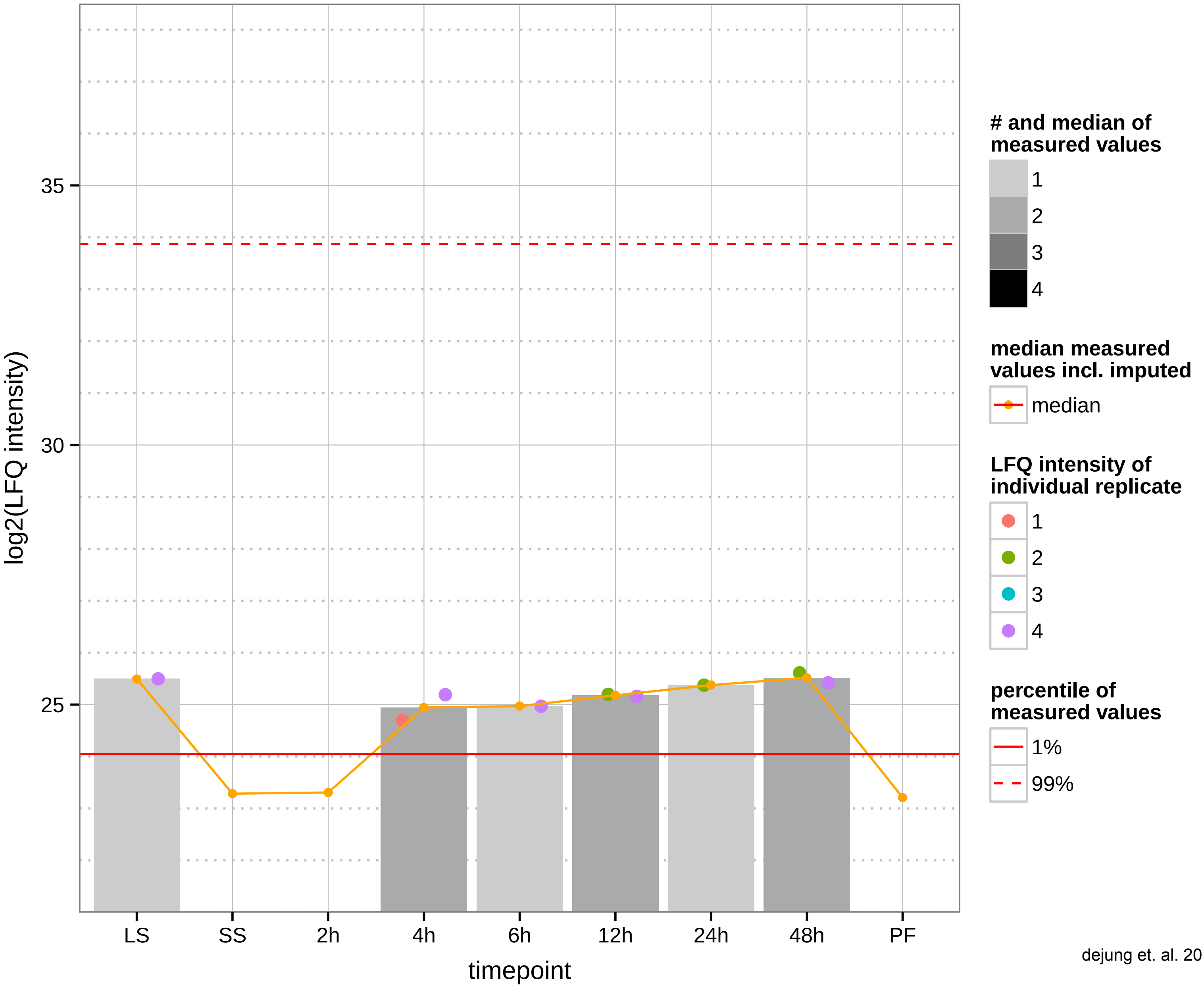
calmodulin, putative
Tb927.11.7940
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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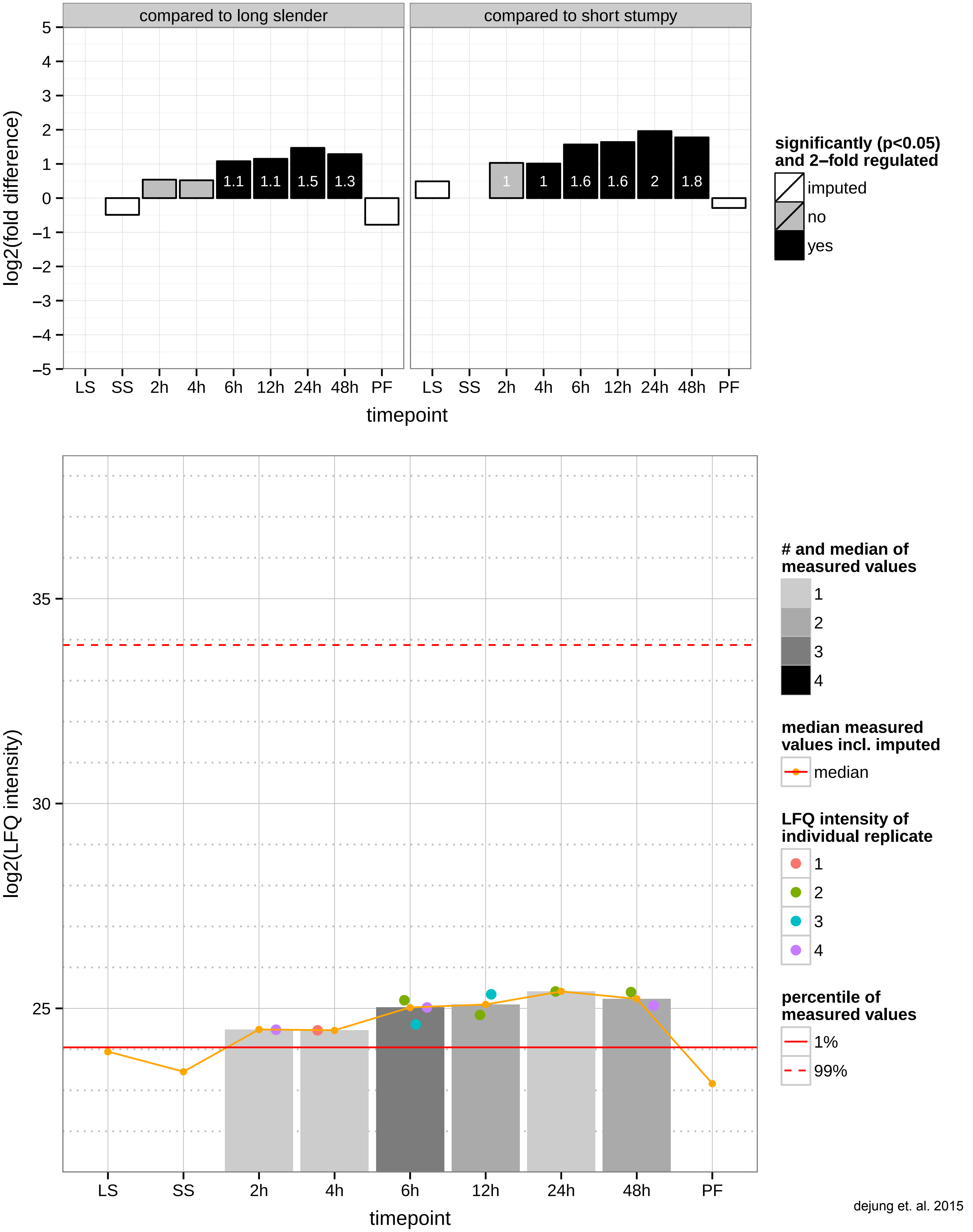
hypothetical protein, conserved
Tb927.11.9320
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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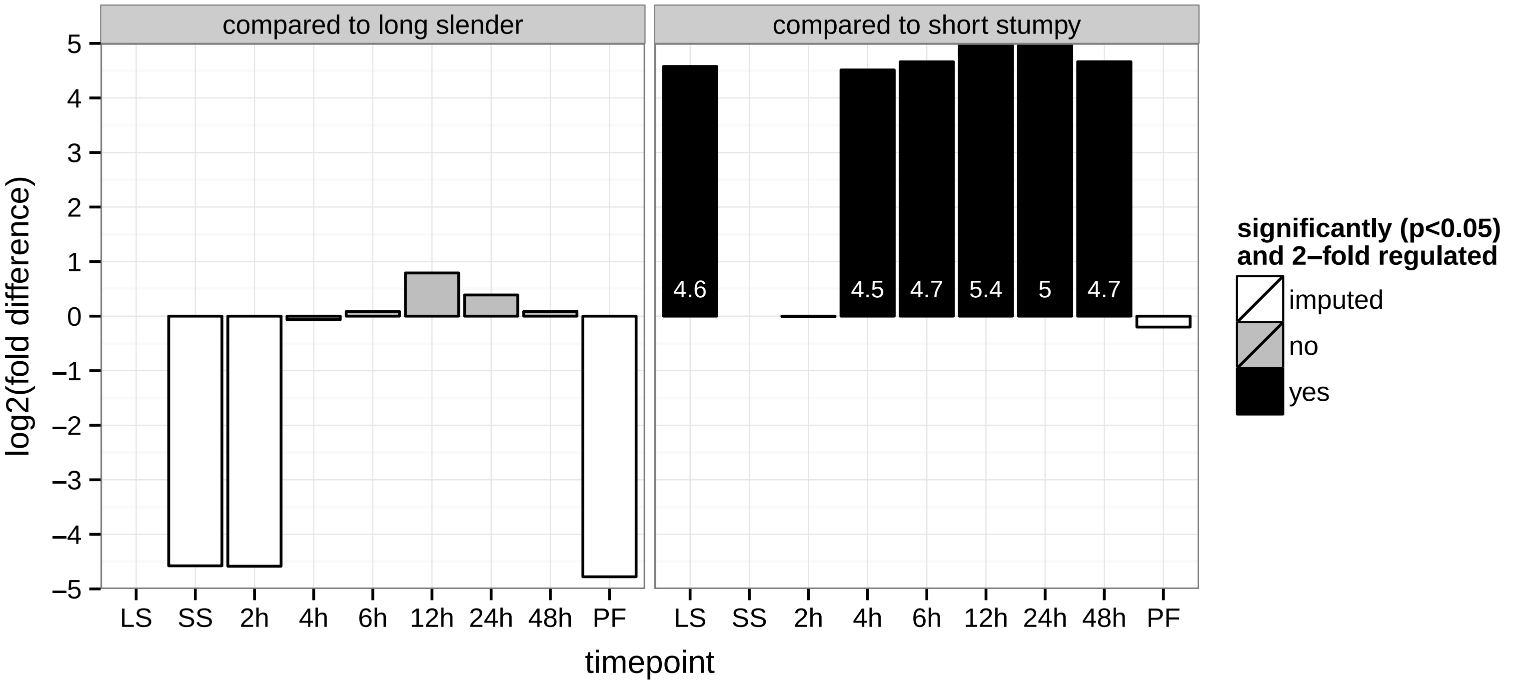
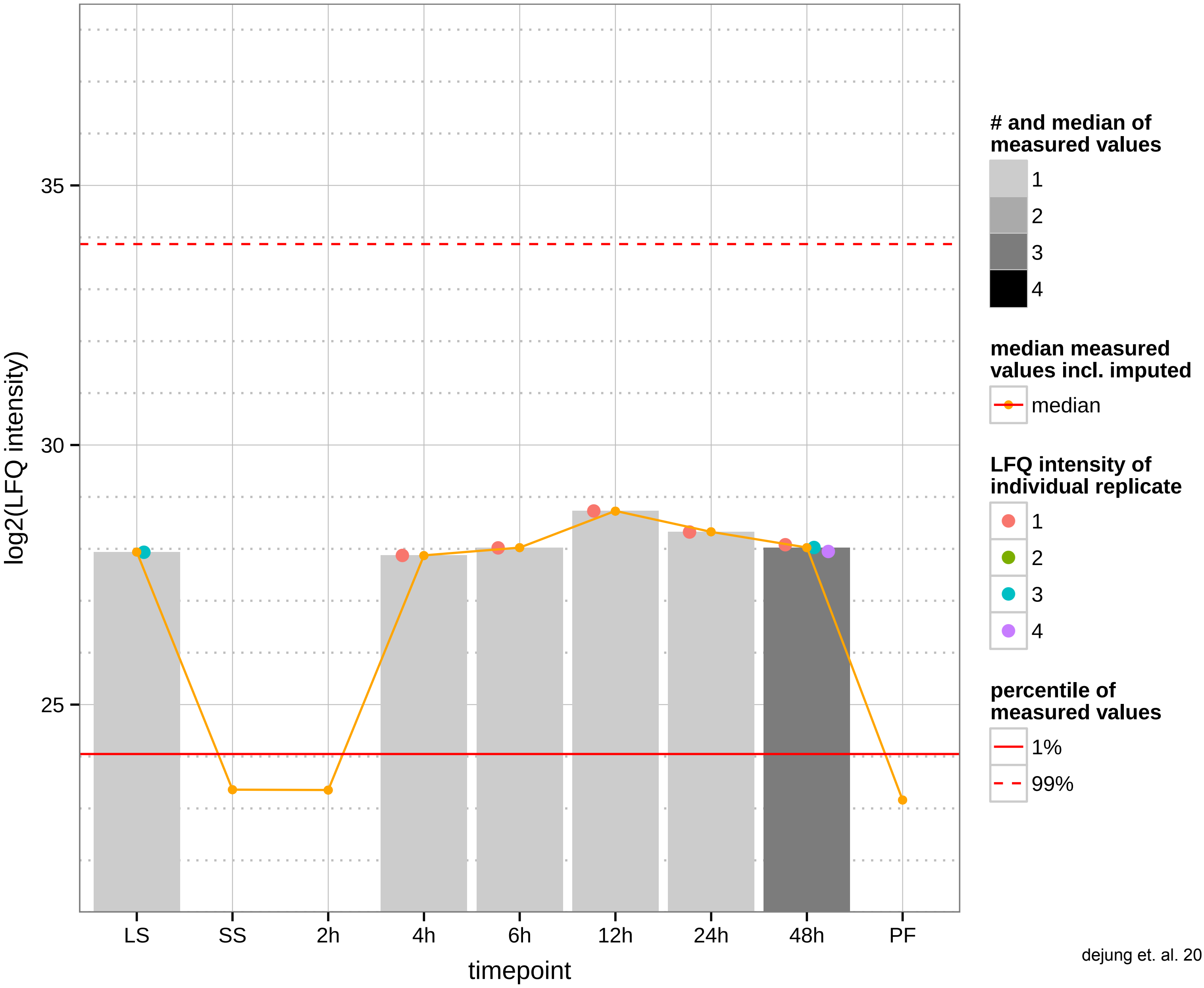
calreticulin, putative
Tb927.4.5010
AGOF: calcium ion binding, unfolded protein binding
AGOC: endoplasmic reticulum
AGOP: protein folding
PGOF: calcium ion binding, unfolded protein binding
PGOC: endoplasmic reticulum
PGOP: protein folding





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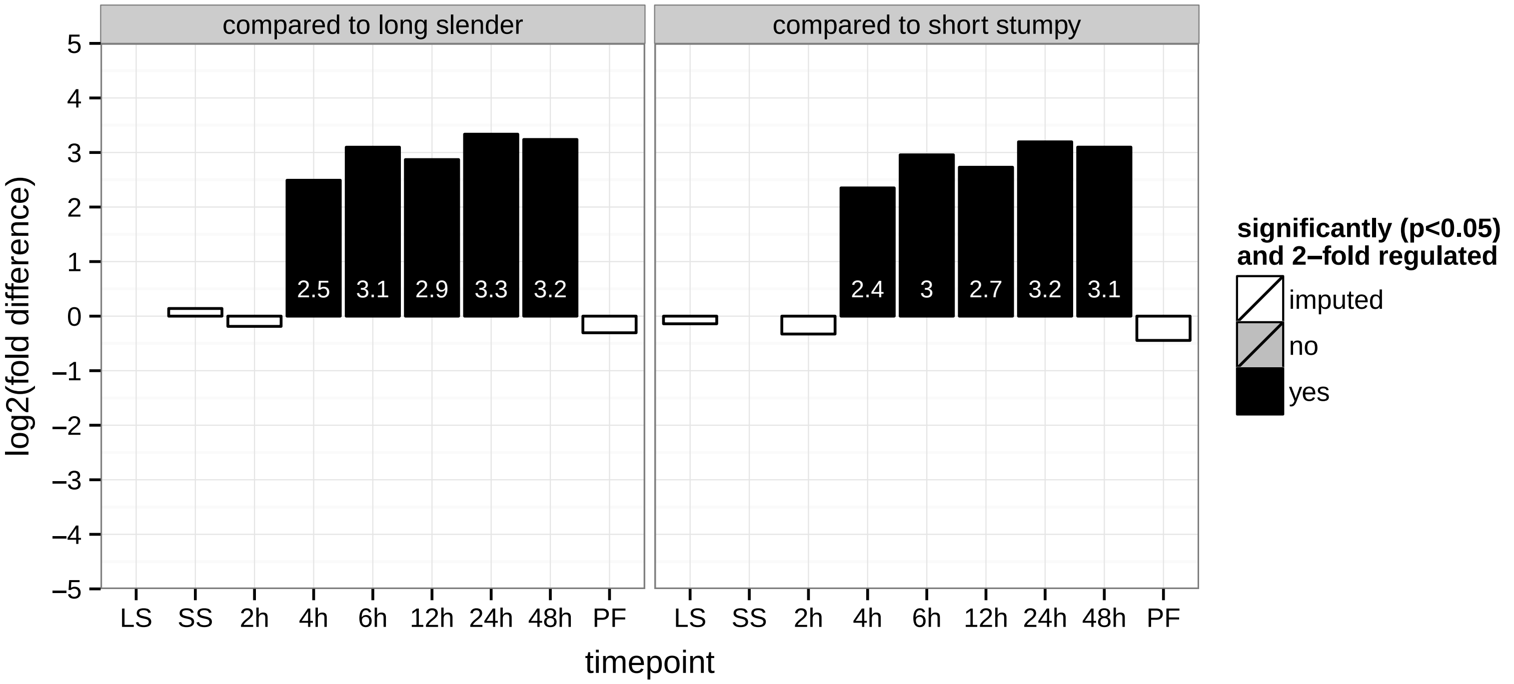
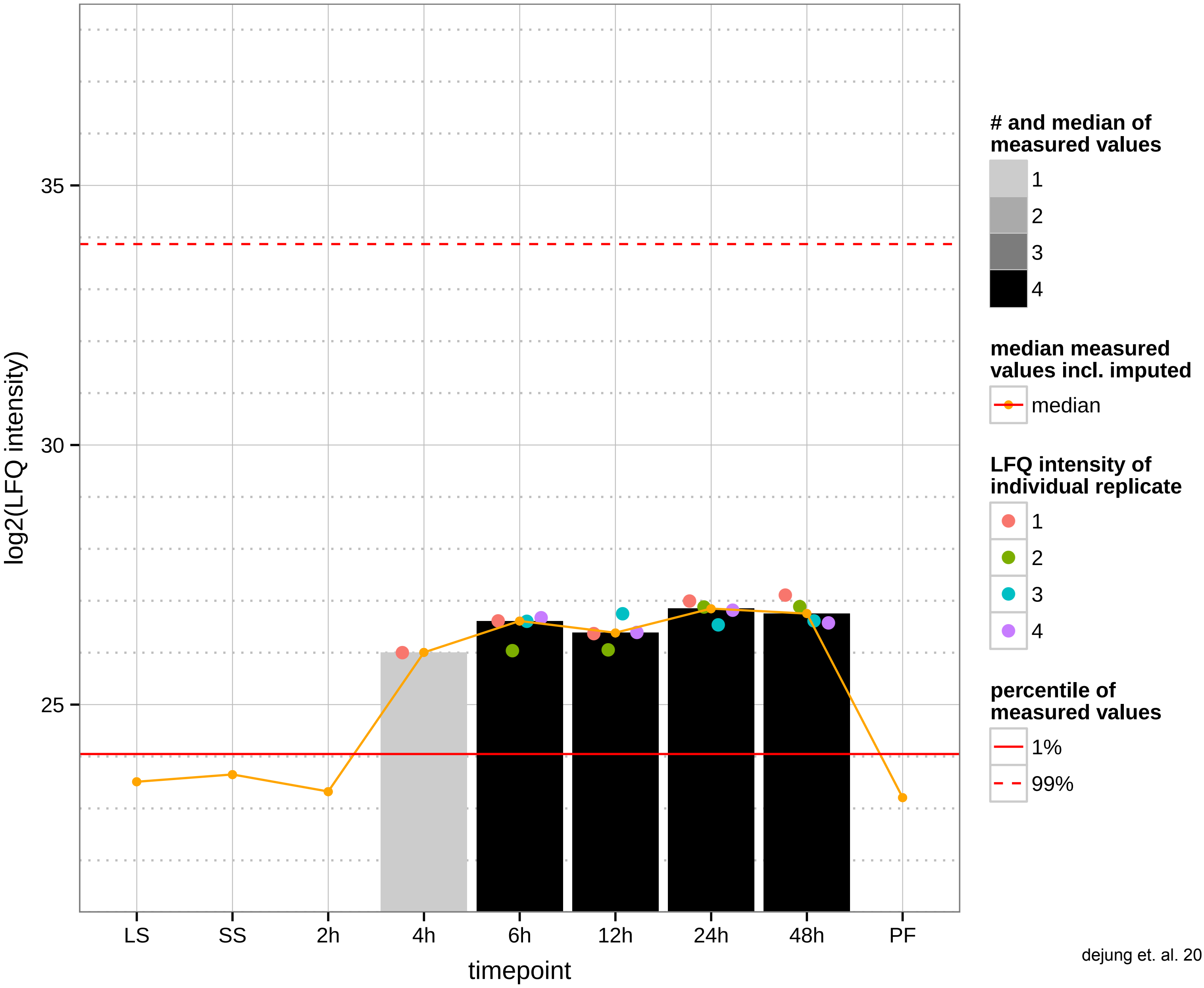
hypothetical protein, conserved
Tb927.5.840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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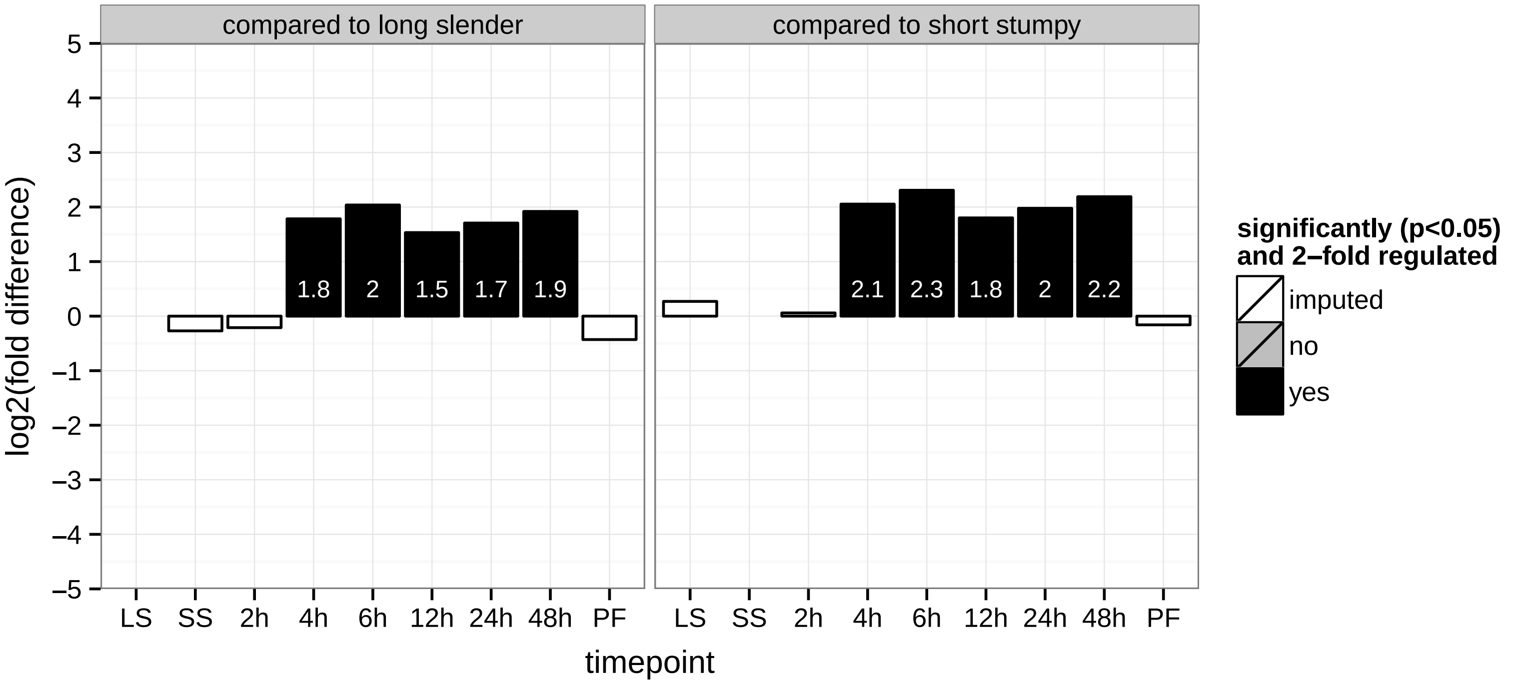
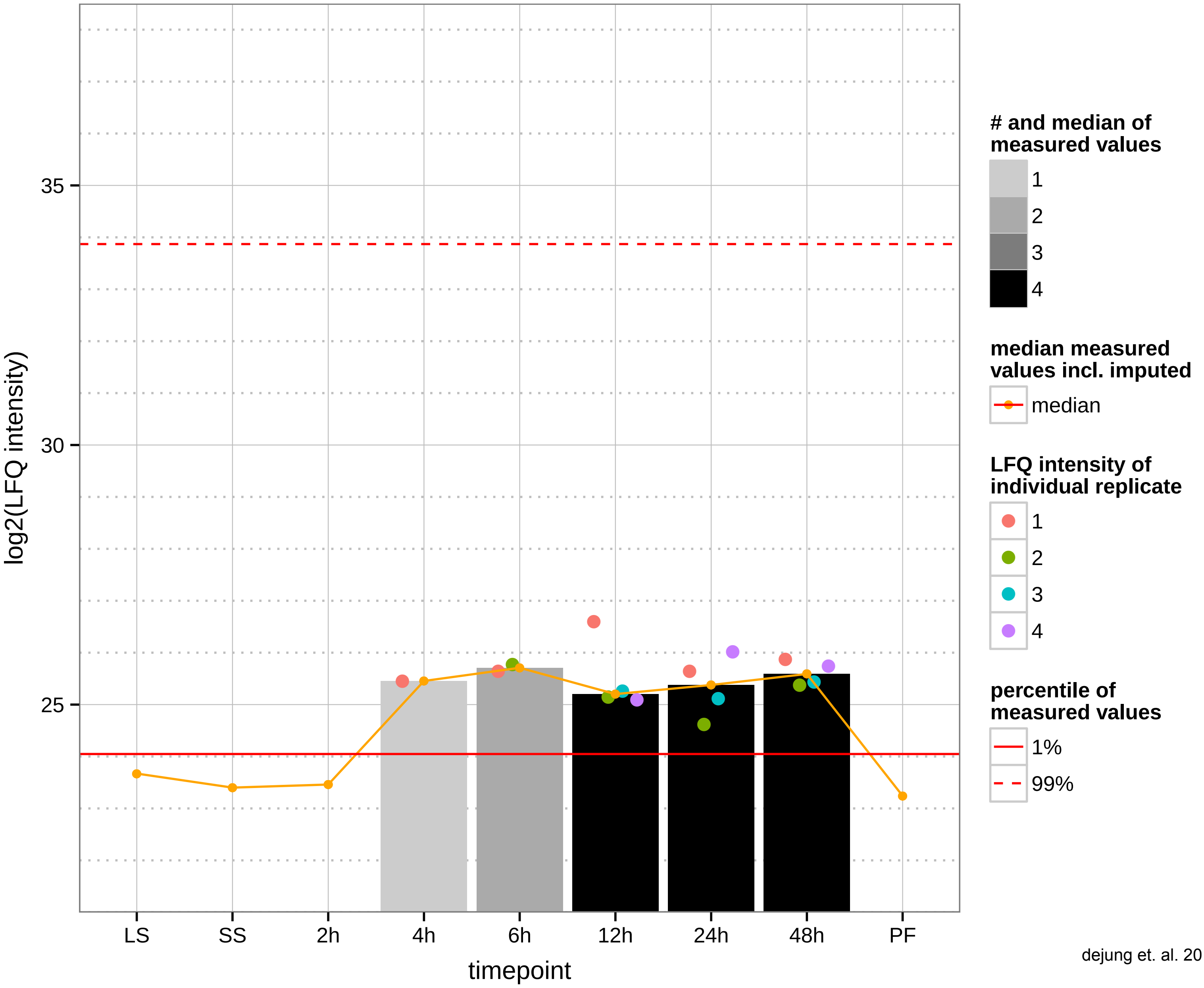
leucine−rich repeat protein (LRRP), putative
Tb927.6.1940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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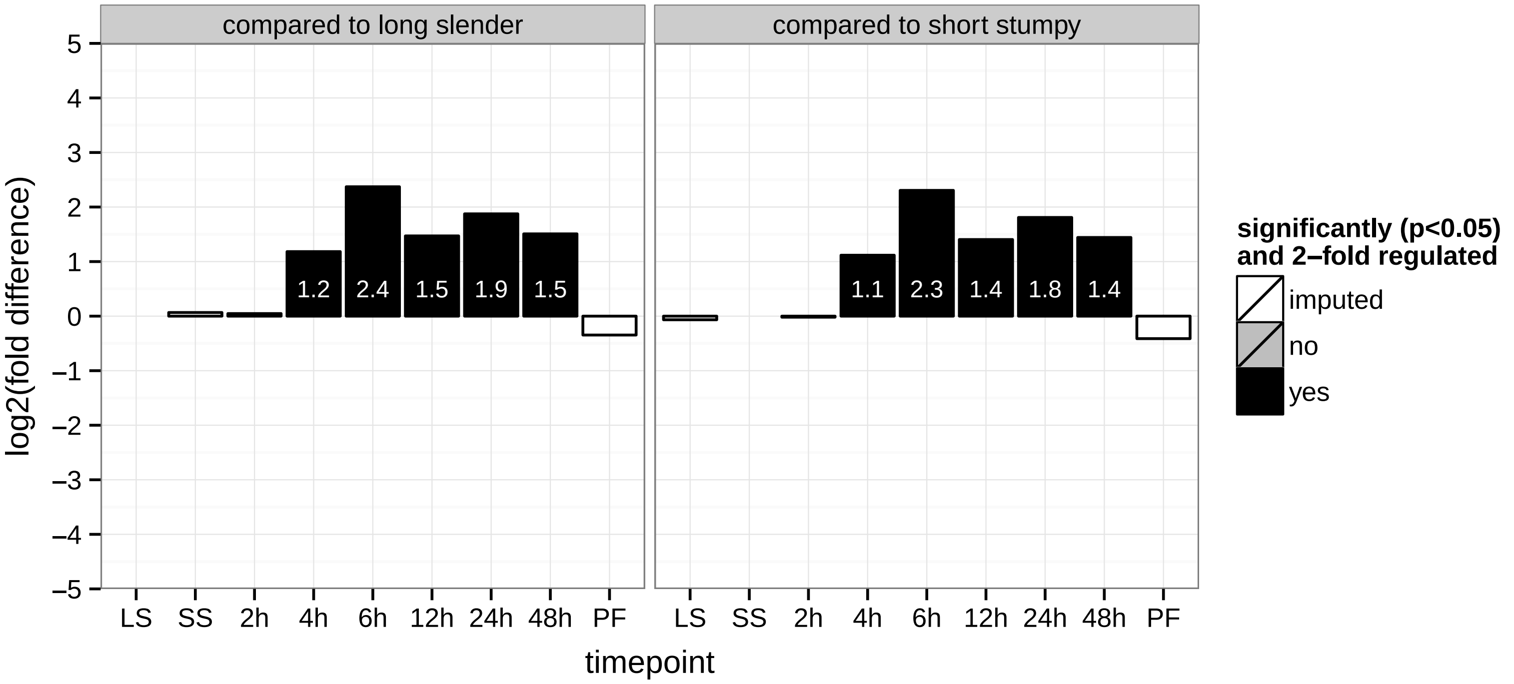
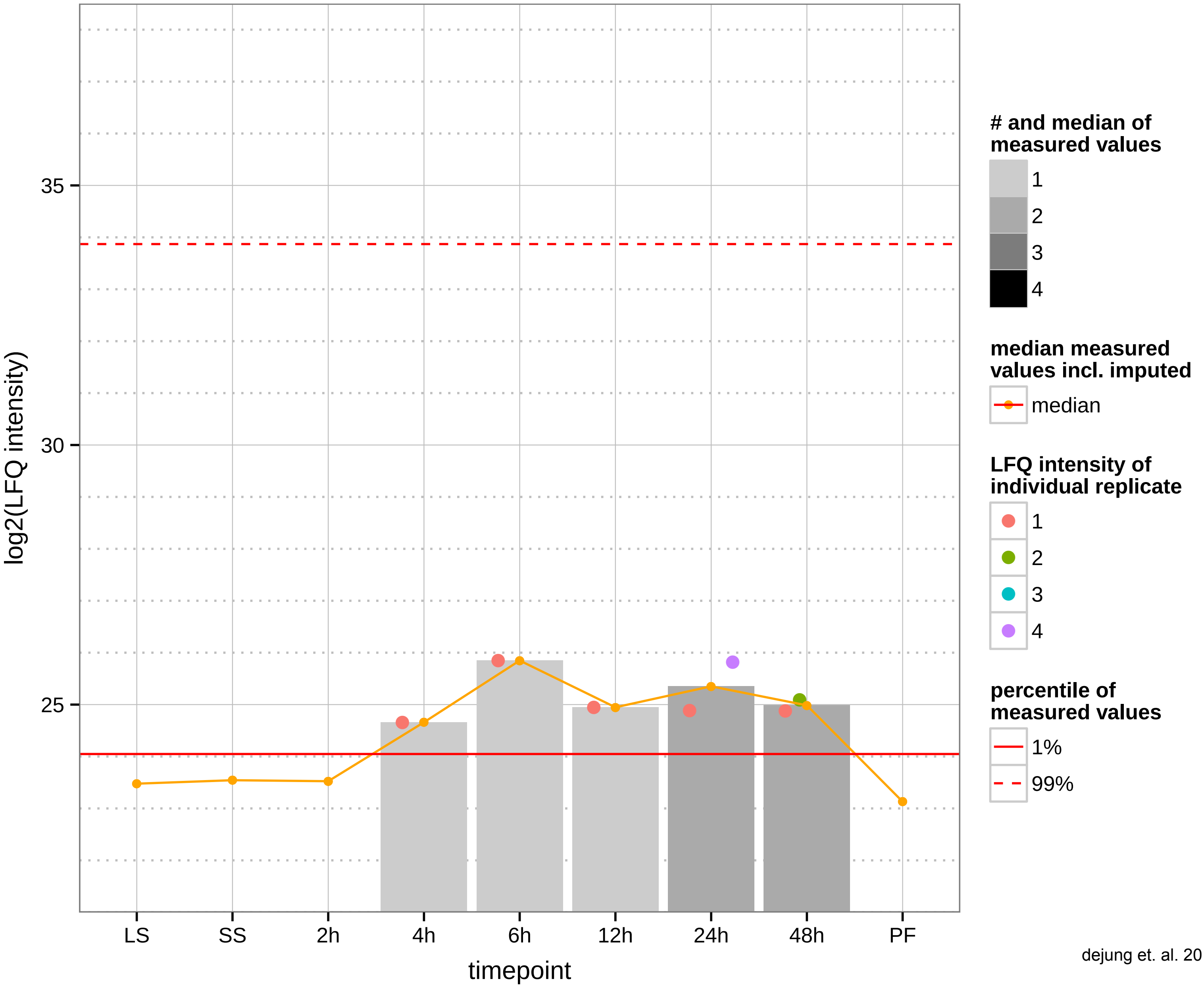
hypothetical protein, conserved (YCF45)
Tb927.6.3350
AGOF: nucleoside–triphosphatase activity, nucleotide binding
AGOC: mitochondrion
AGOP: null
PGOF: nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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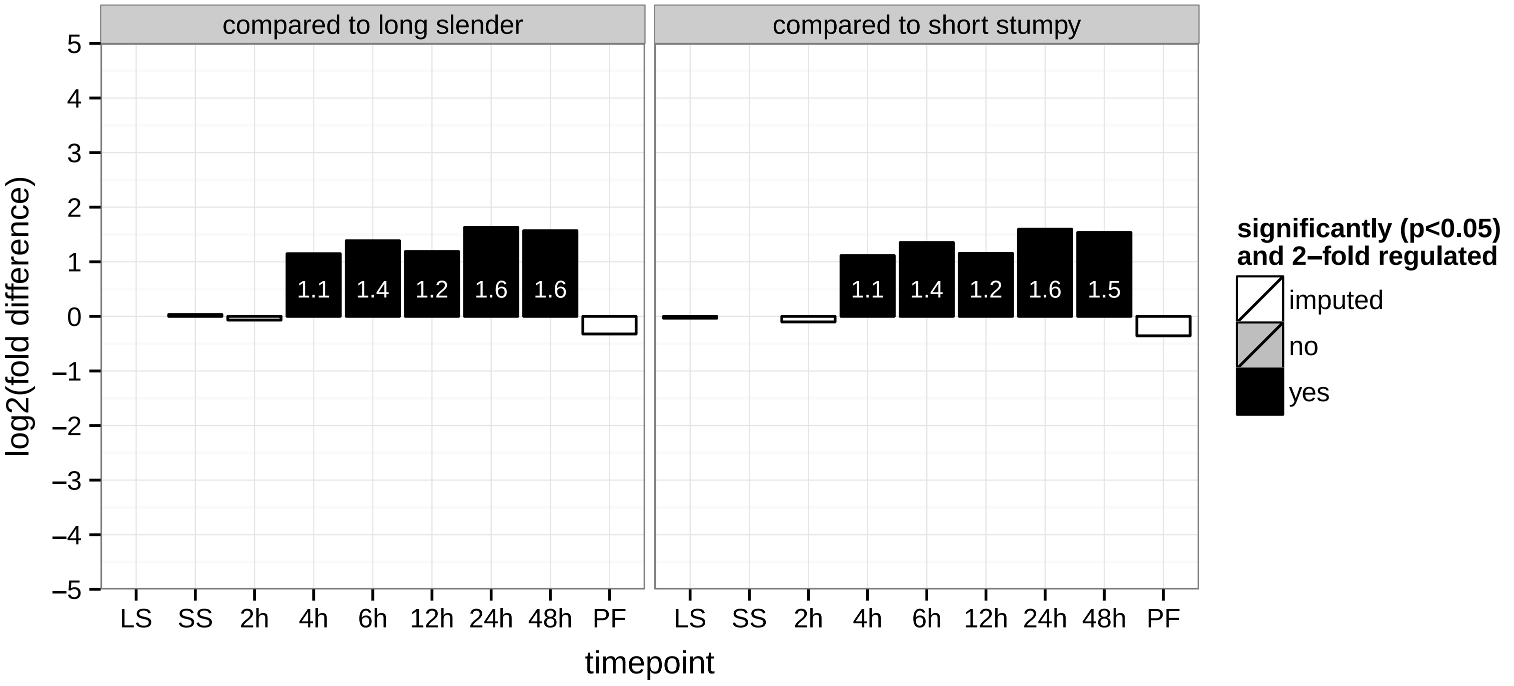
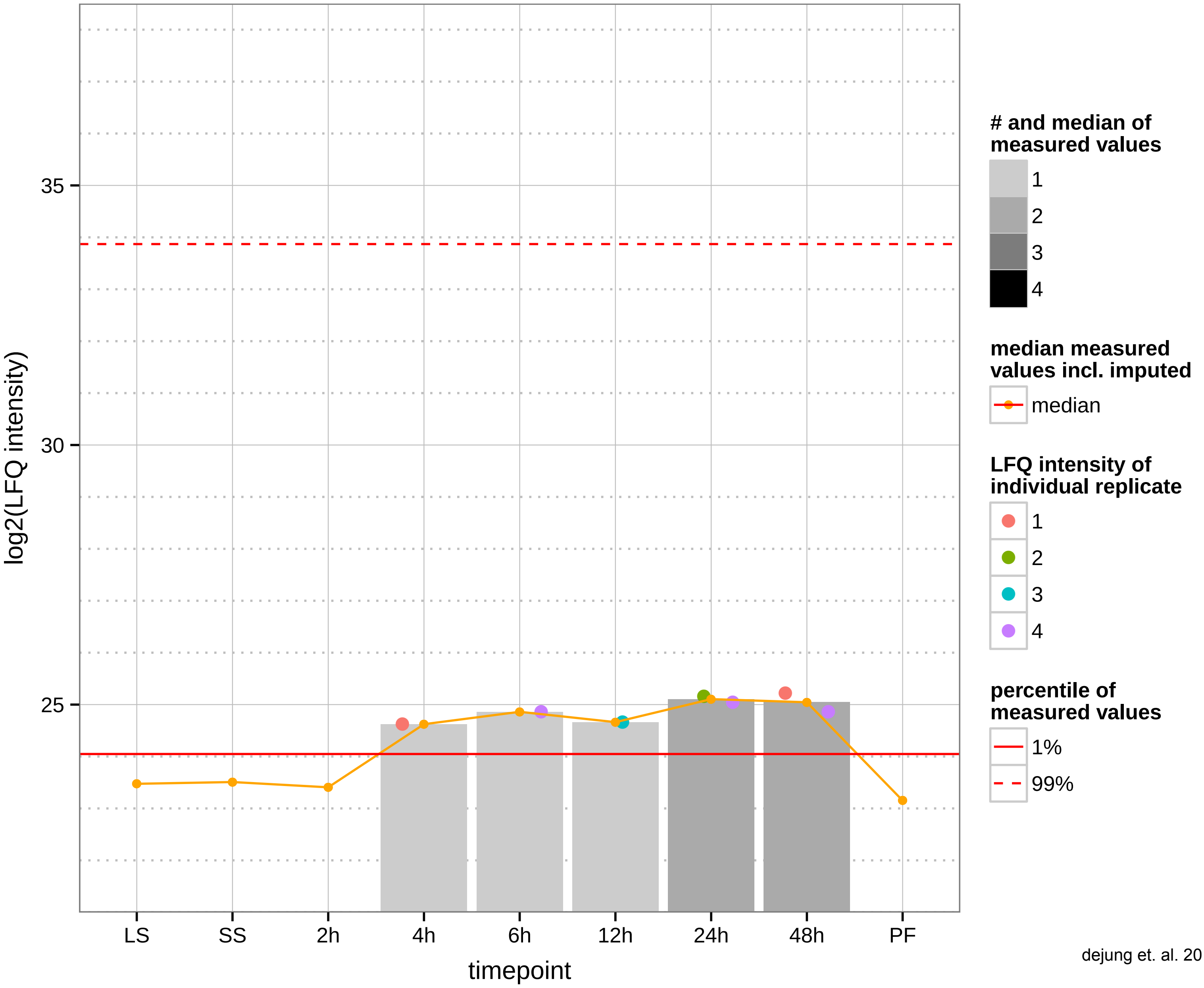
hypothetical protein, conserved
Tb927.7.5240
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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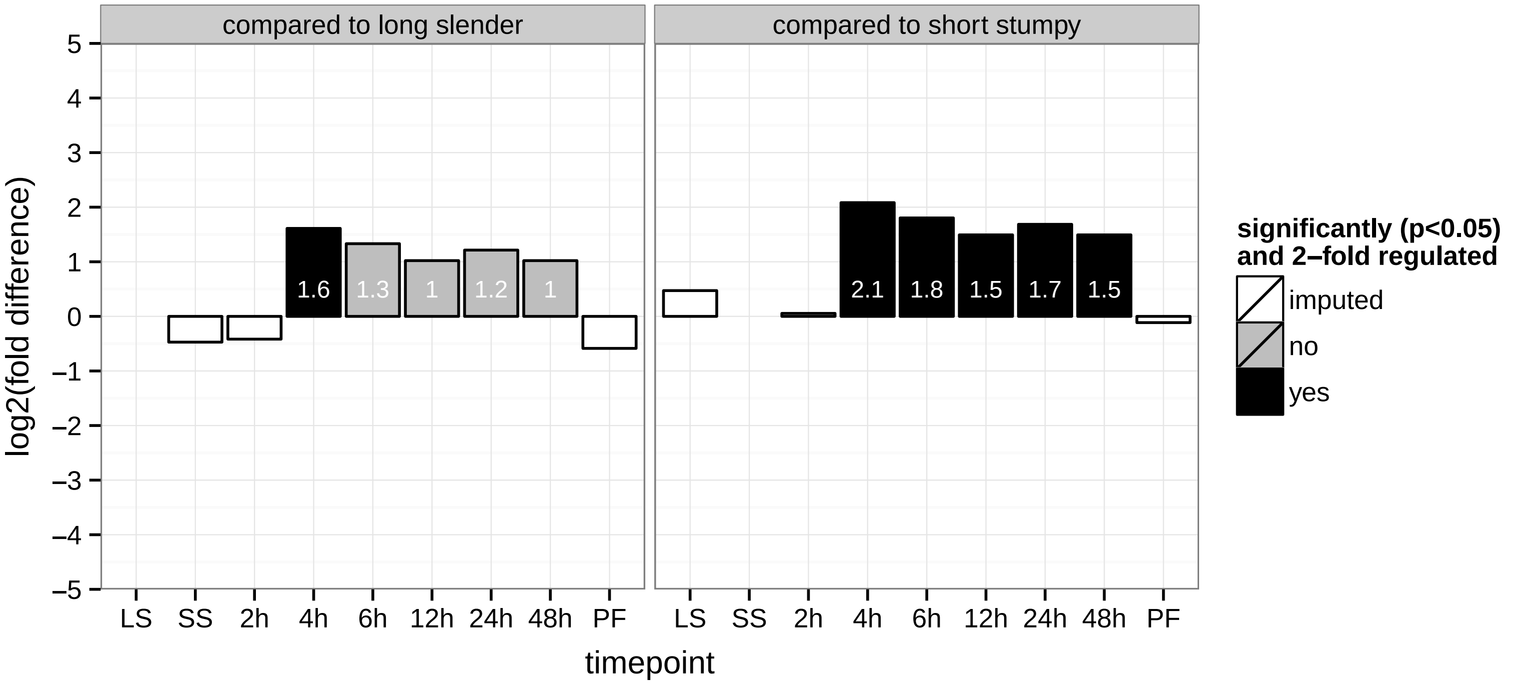
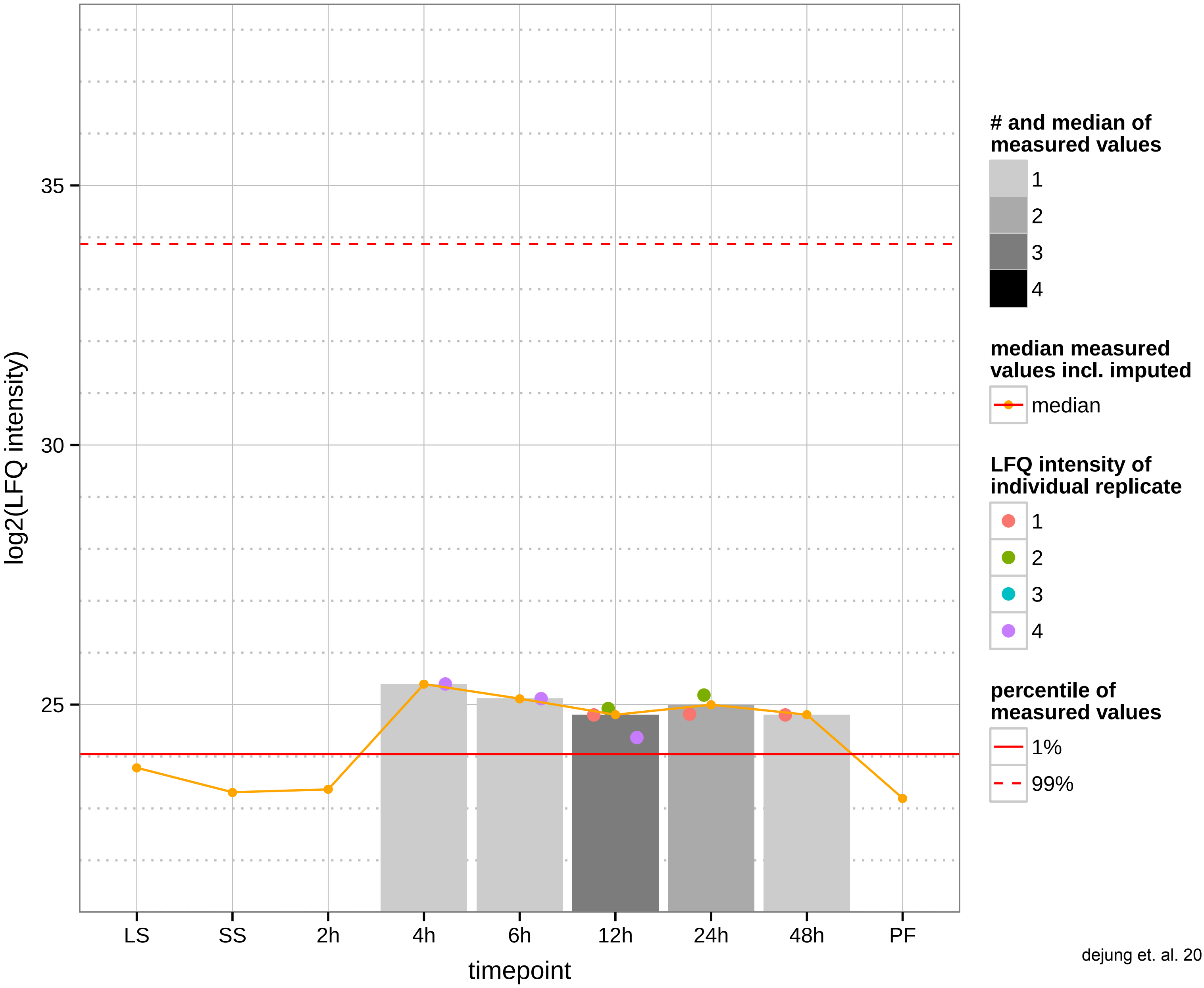
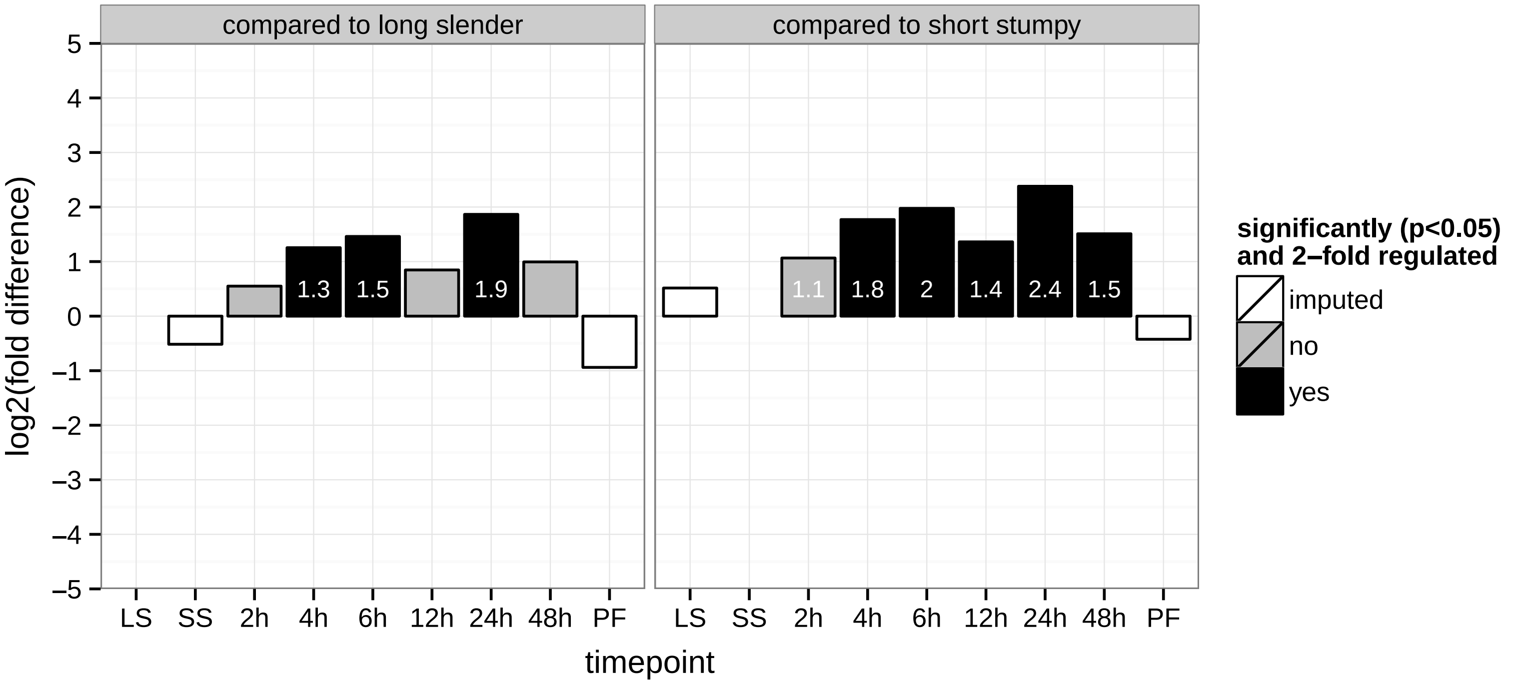
hypothetical protein, conserved
Tb927.8.1120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

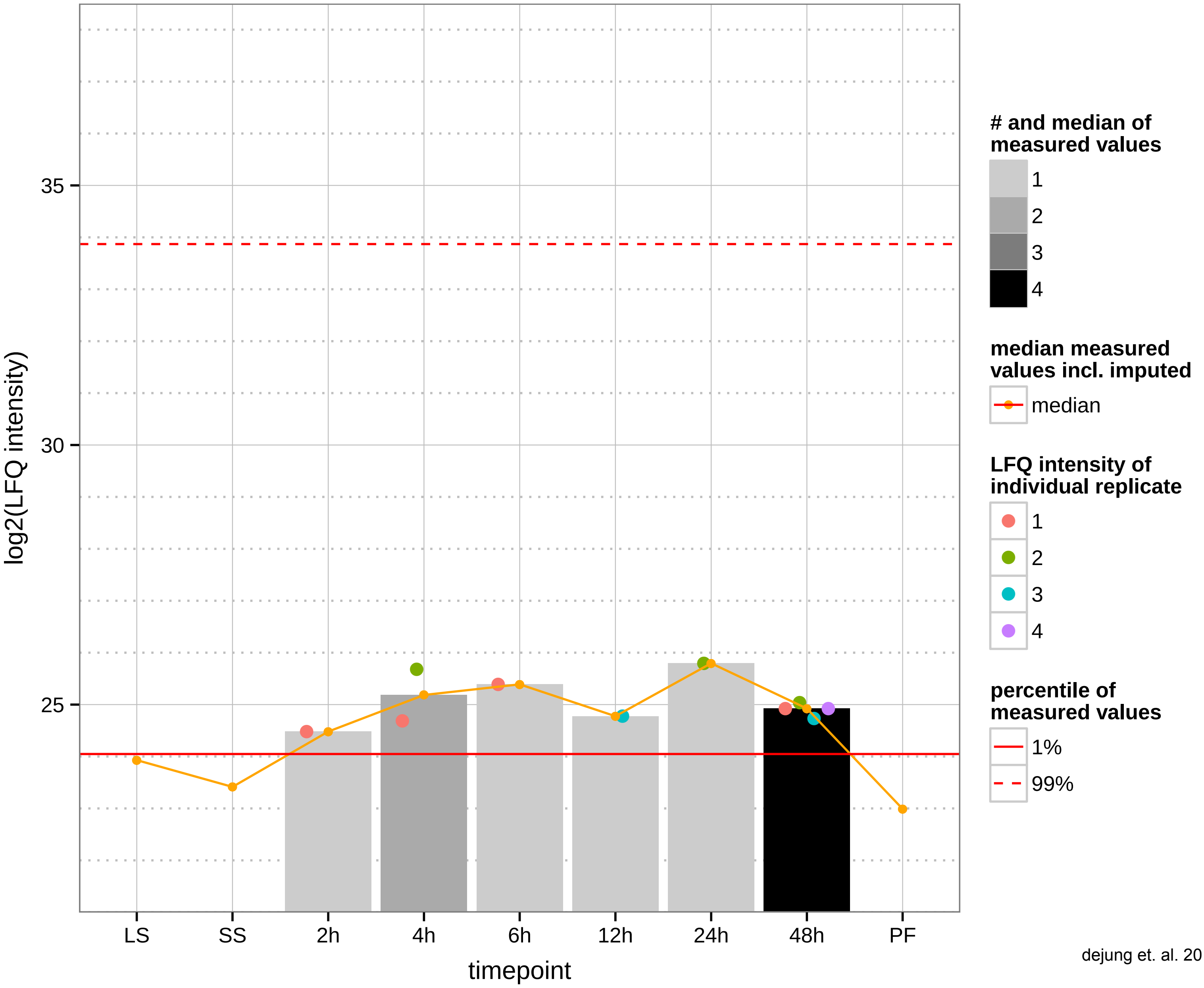




dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.12890
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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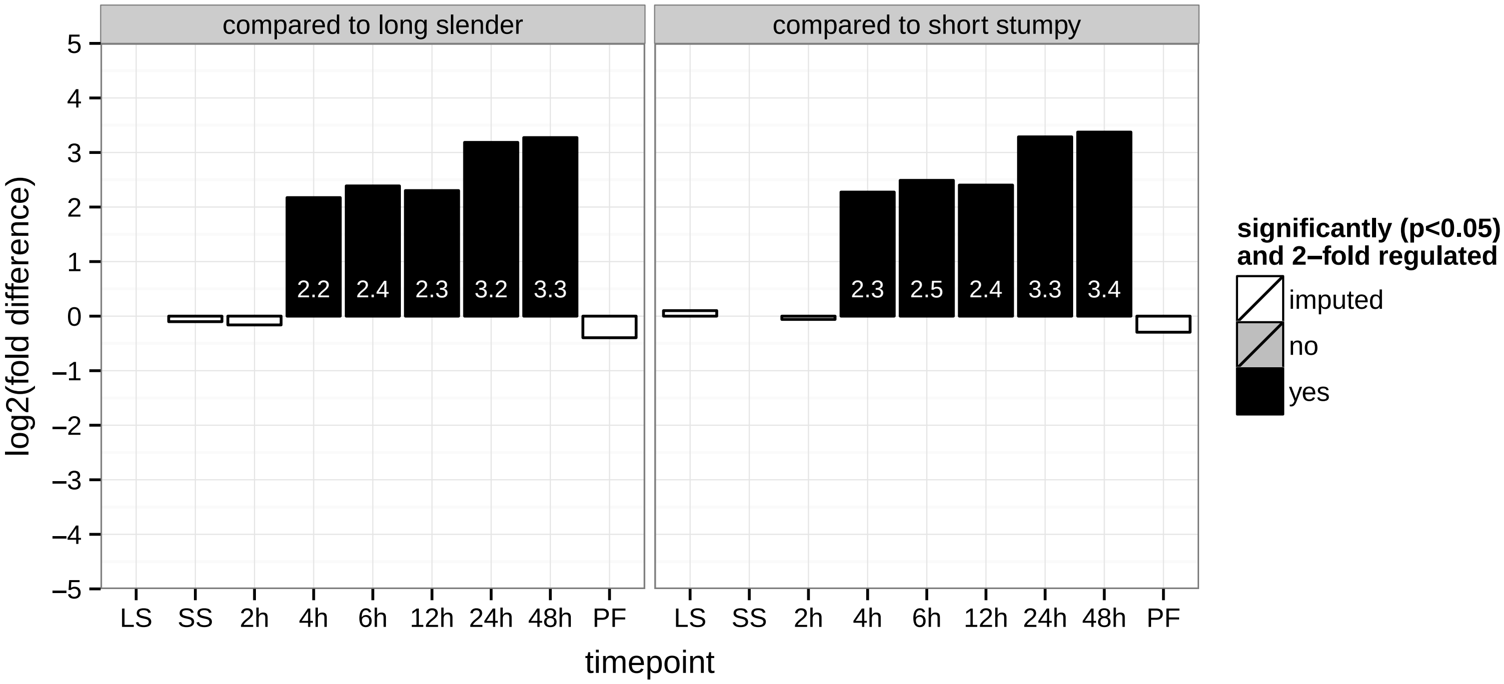
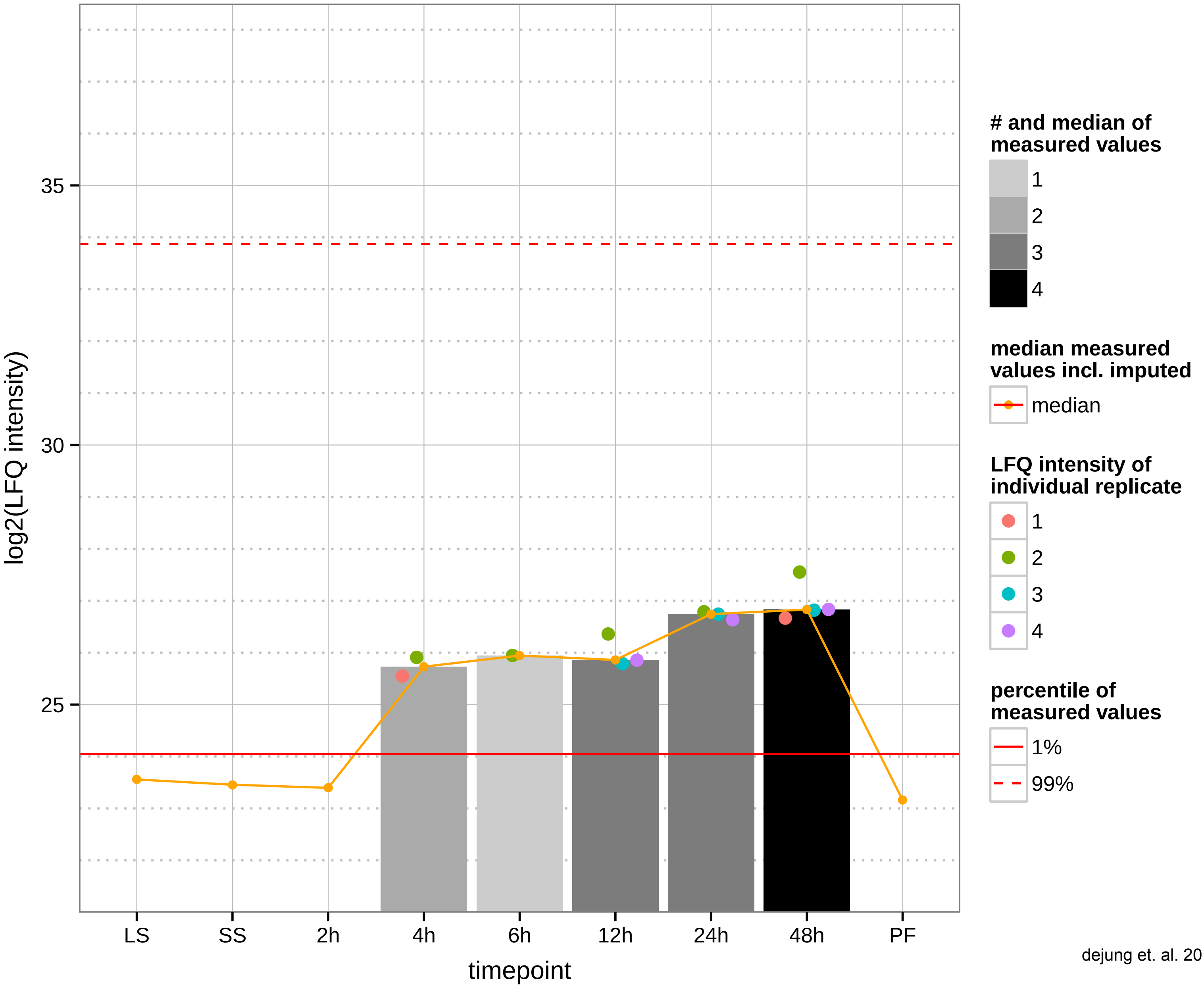
hypothetical protein, conserved
Tb927.9.2160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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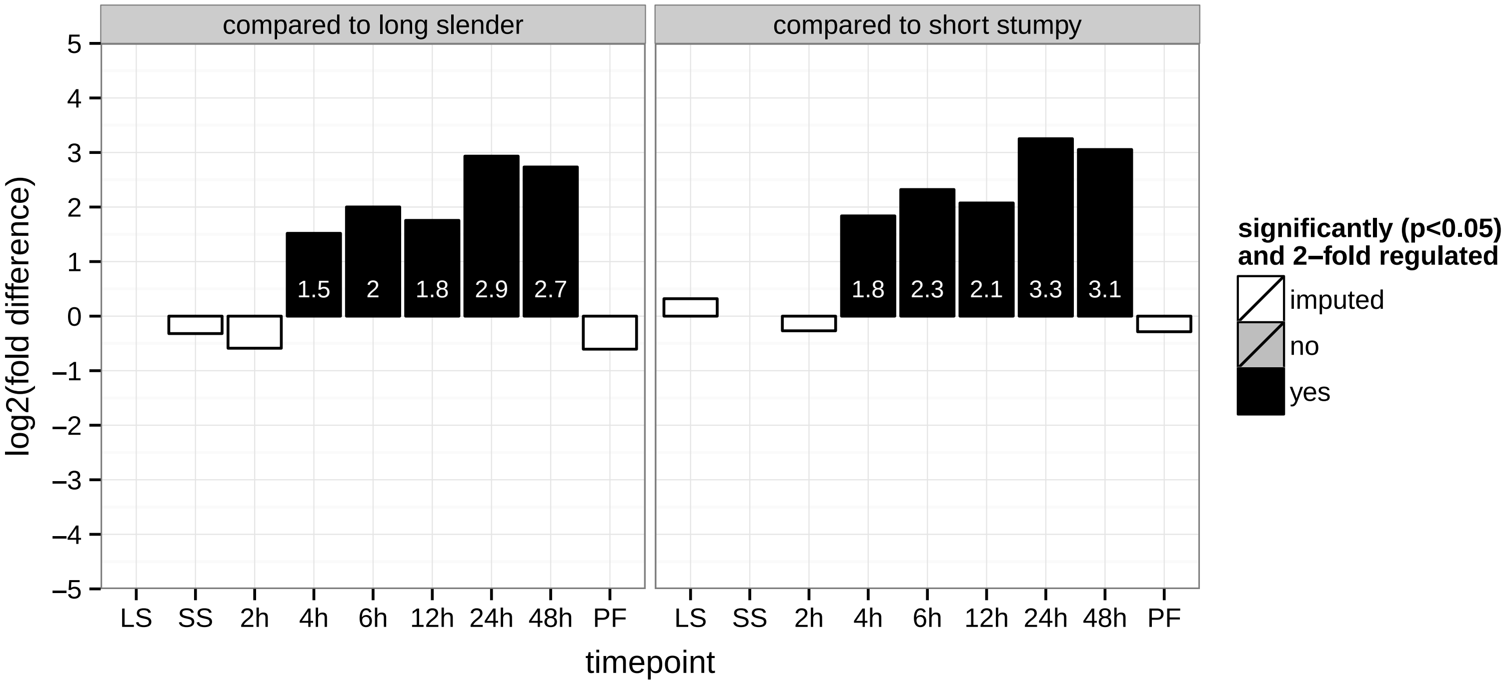
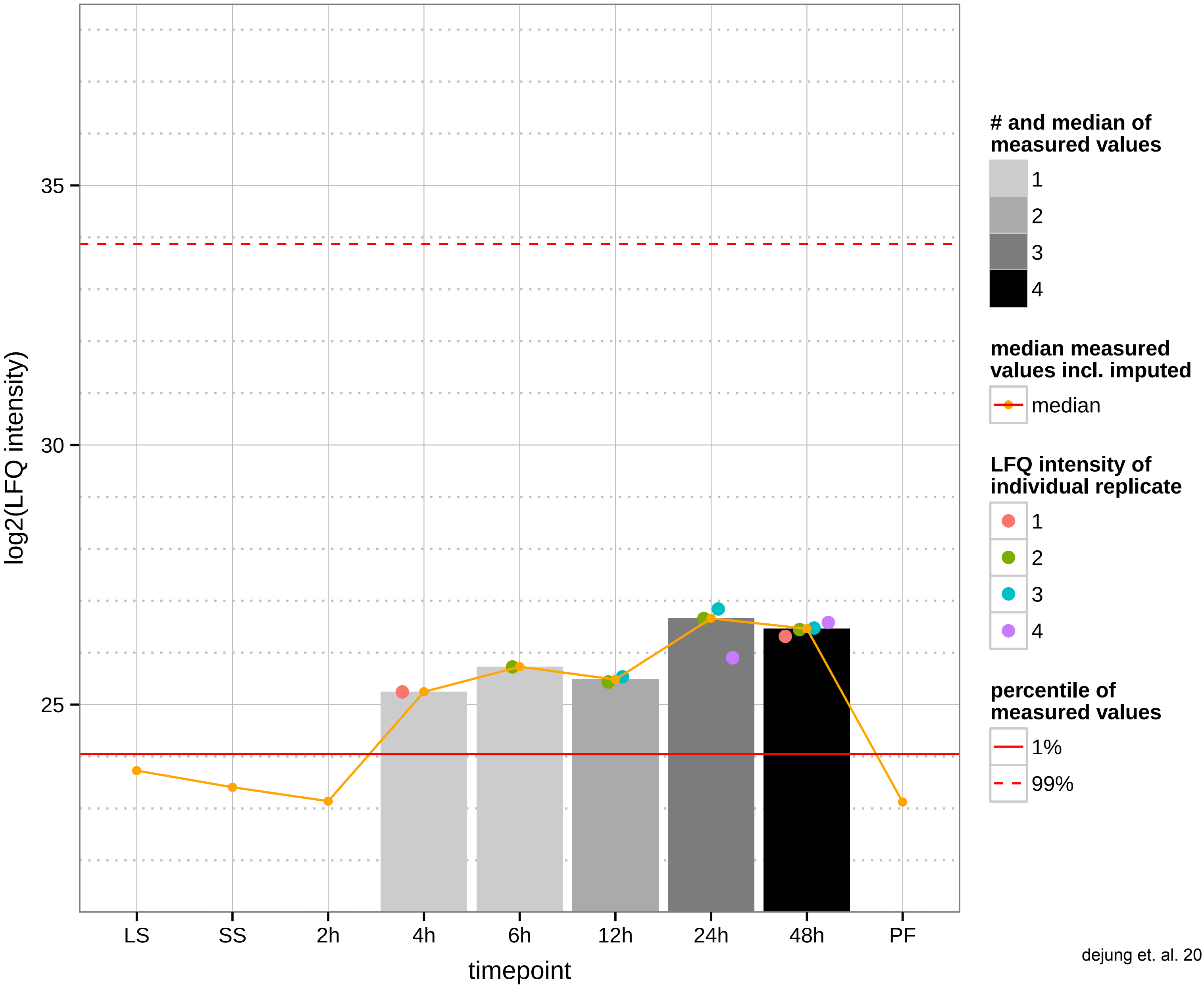
thioredoxin (trx)
Tb927.9.3370
AGOF: disulfide oxidoreductase activity, protein disulfide isomerase activity
AGOC: null
AGOP: cell redox homeostasis
PGOF: electron carrier activity, protein disulfide oxidoreductase activity
PGOC: null
PGOP: cell redox homeostasis, glycerol ether metabolic process





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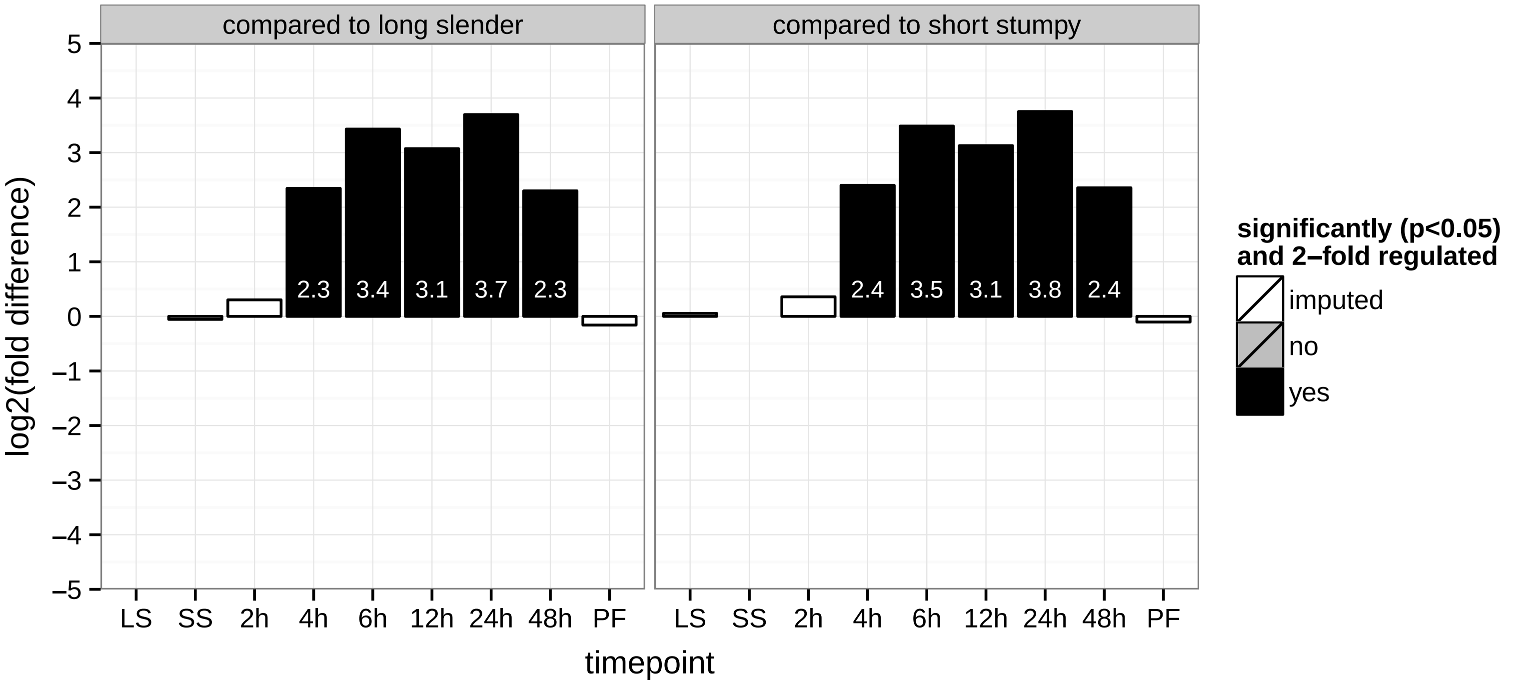
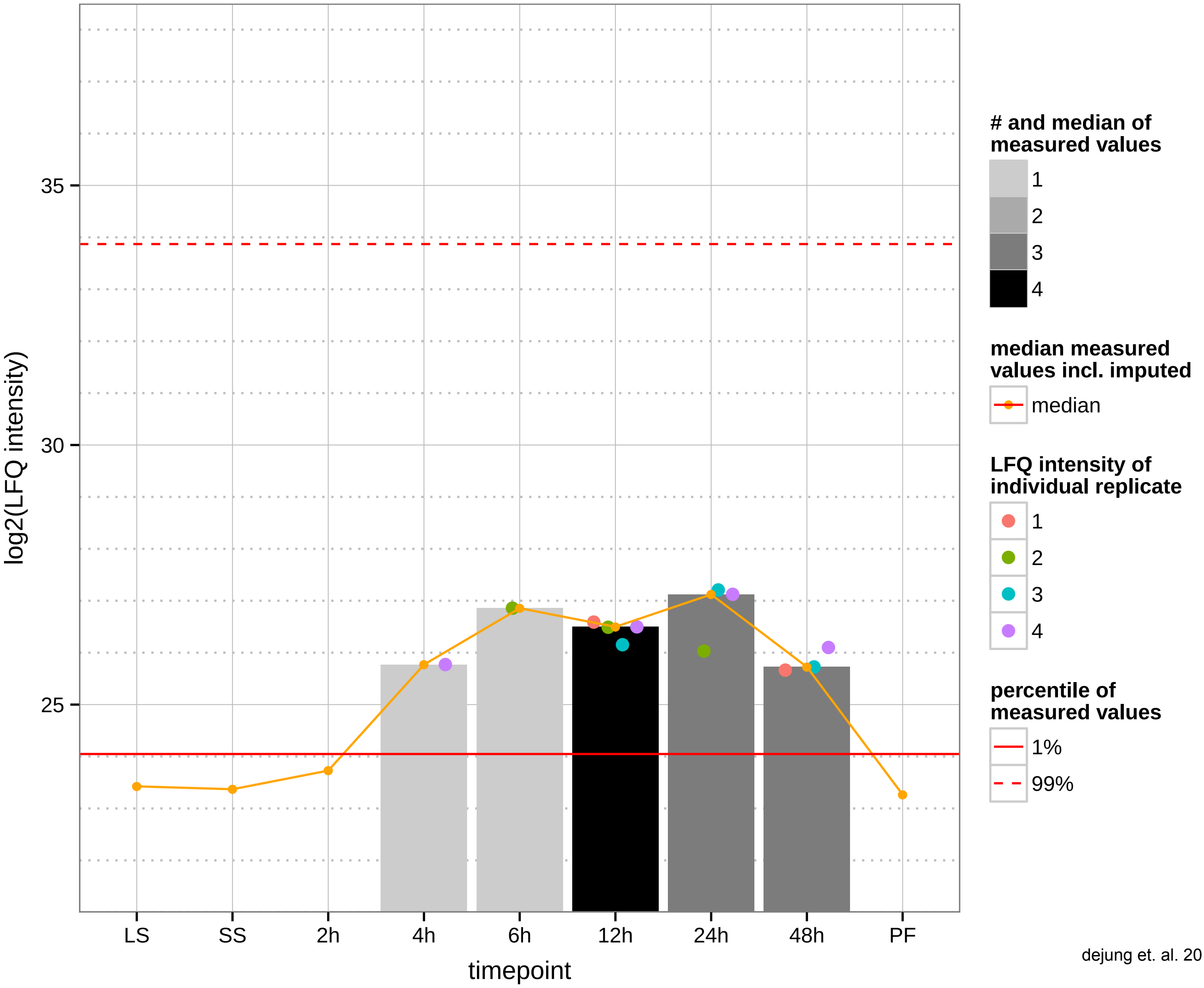
hypothetical protein, conserved
Tb927.9.4350
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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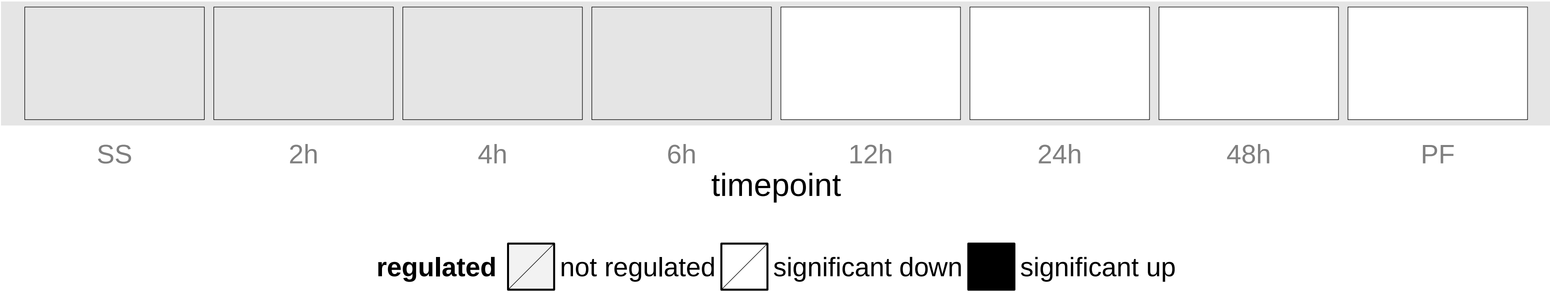

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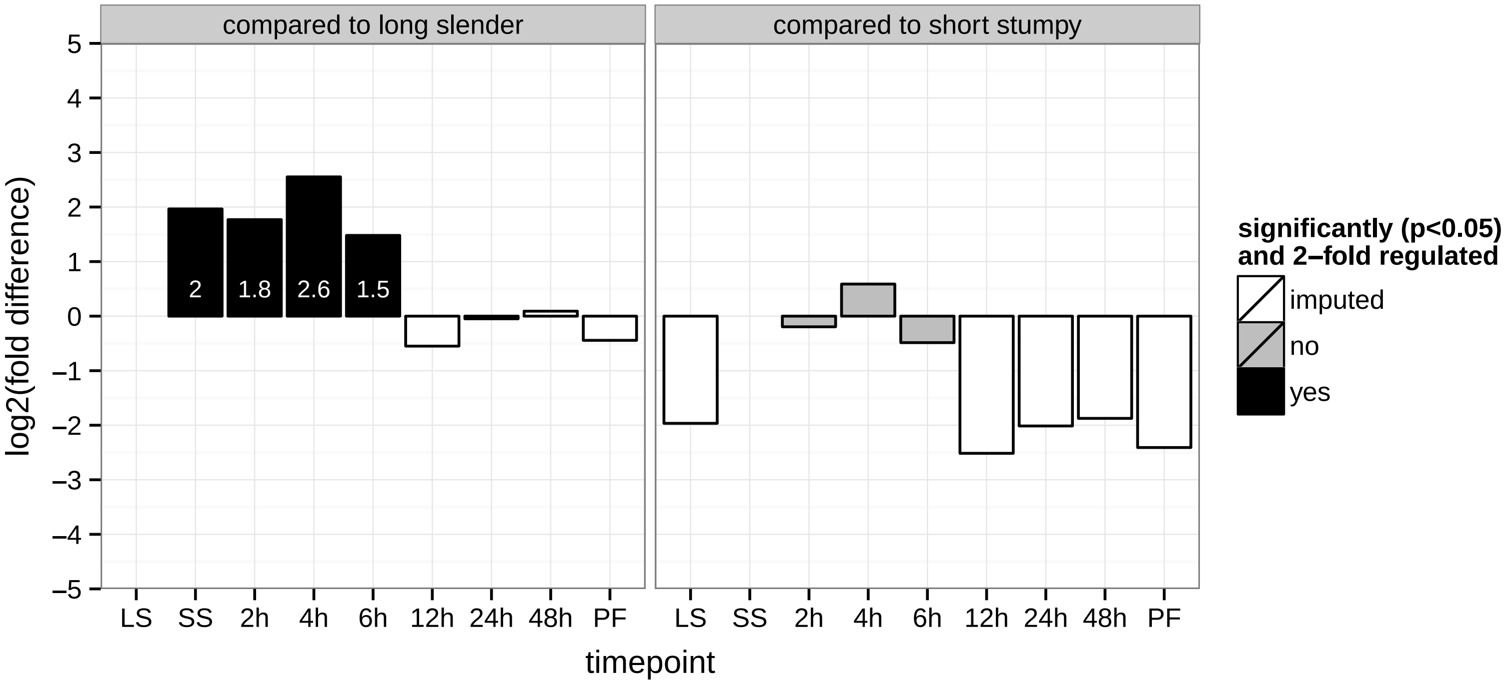
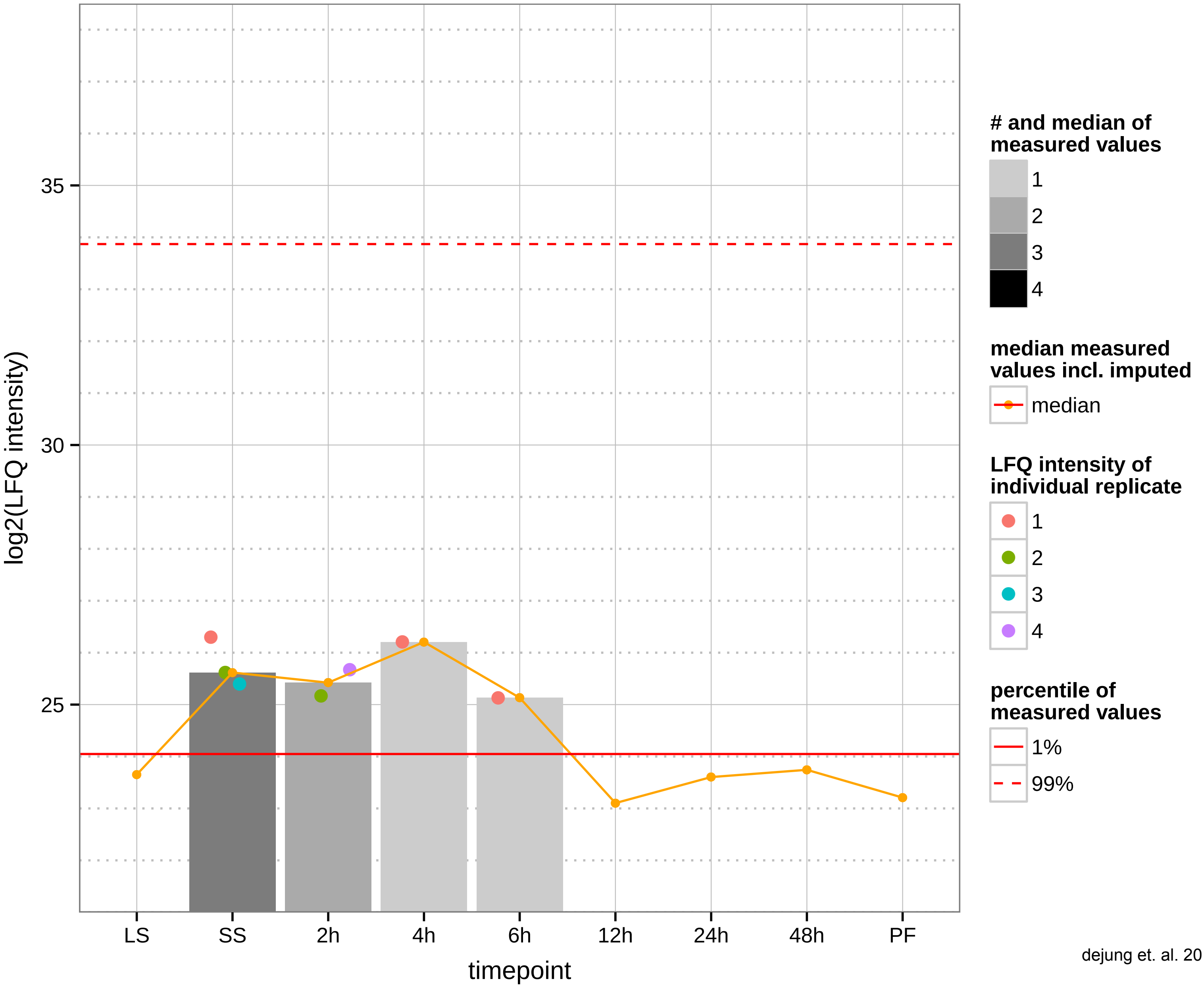
MSP−A, putative, chrXI additional, unordered contigs, Gp63−1 surface protease homolog
Tb927.11.7640;Tb11.0360;Tb927.11.7620
AGOF: metalloendopeptidase activity, zinc ion binding
AGOC: membrane
AGOP: cell adhesion, proteolysis
PGOF: metalloendopeptidase activity, zinc ion binding
PGOC: membrane
PGOP: cell adhesion, proteolysis





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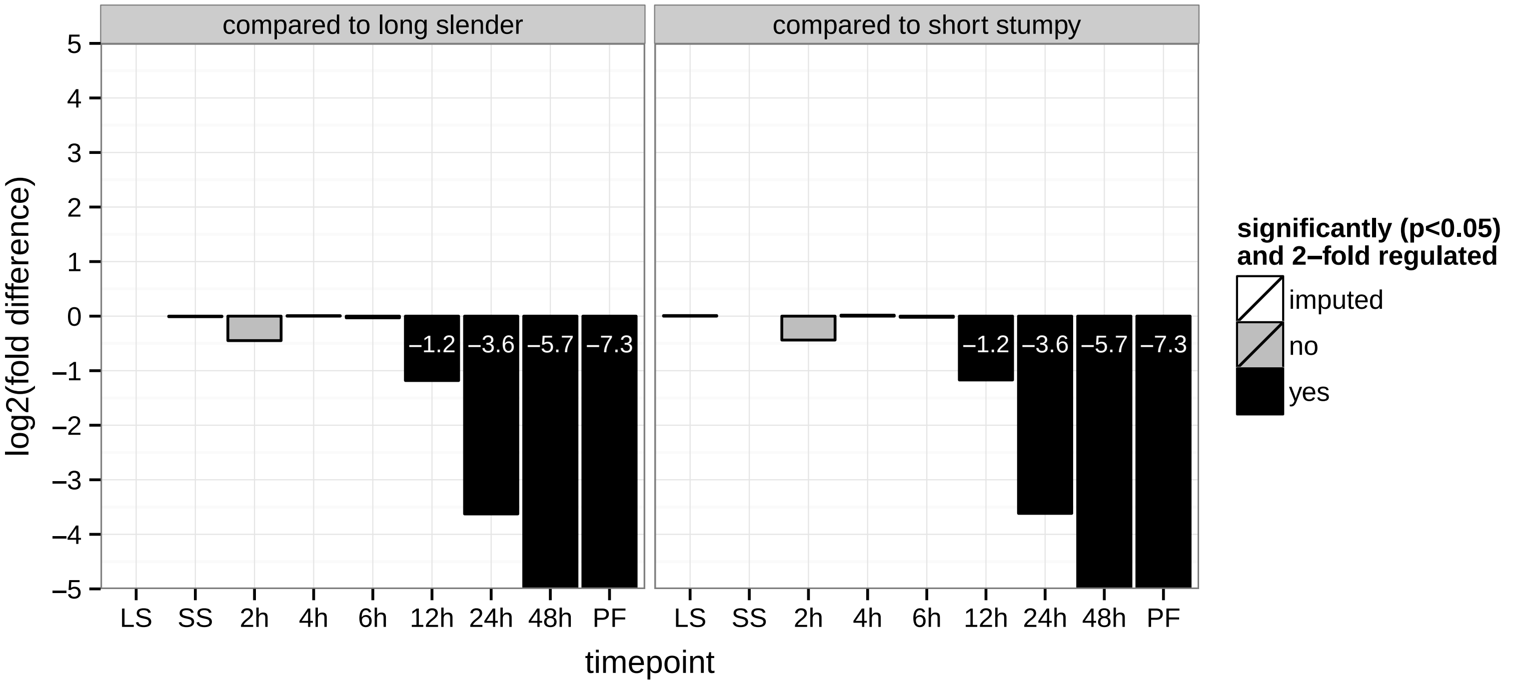
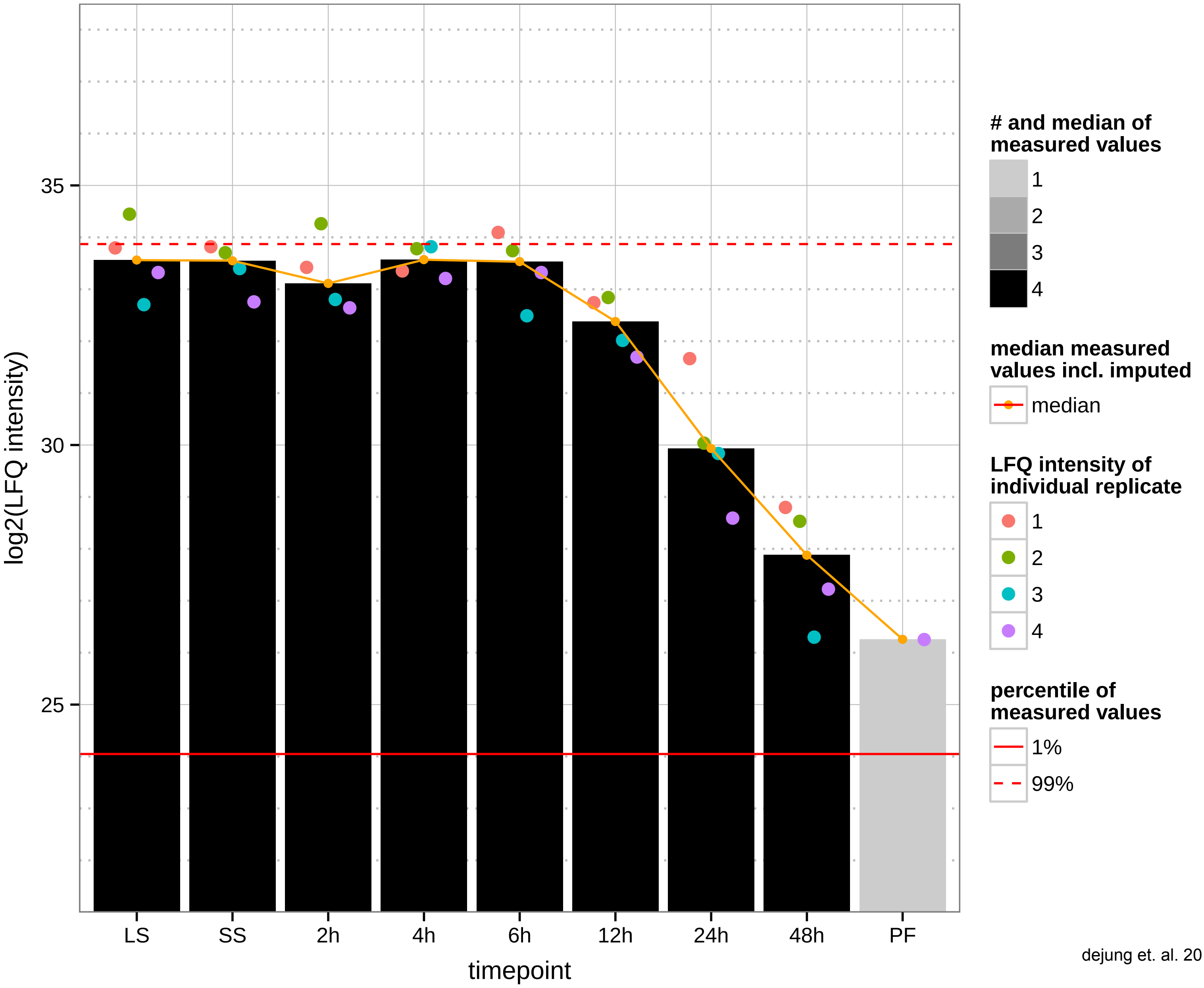
variant surface glycoprotein (VSG, pseudogene), putative, chrXI additional, unordered contigs, variant surface protein (VSG)
Tb11.1690;Tb11.v5.0142
AGOF: null
AGOC: null
AGOP: evasion or tolerance of host immune response, null
PGOF: null
PGOC: null
PGOP: null





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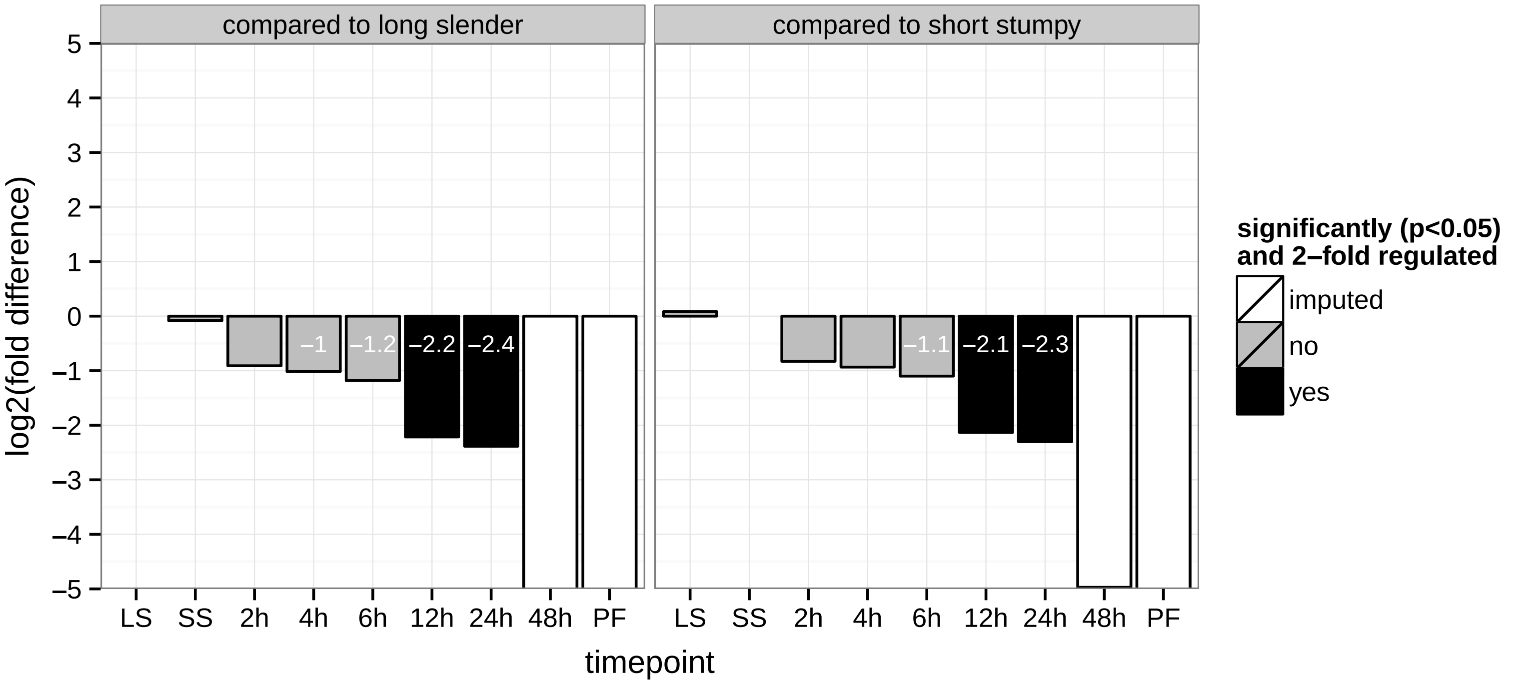
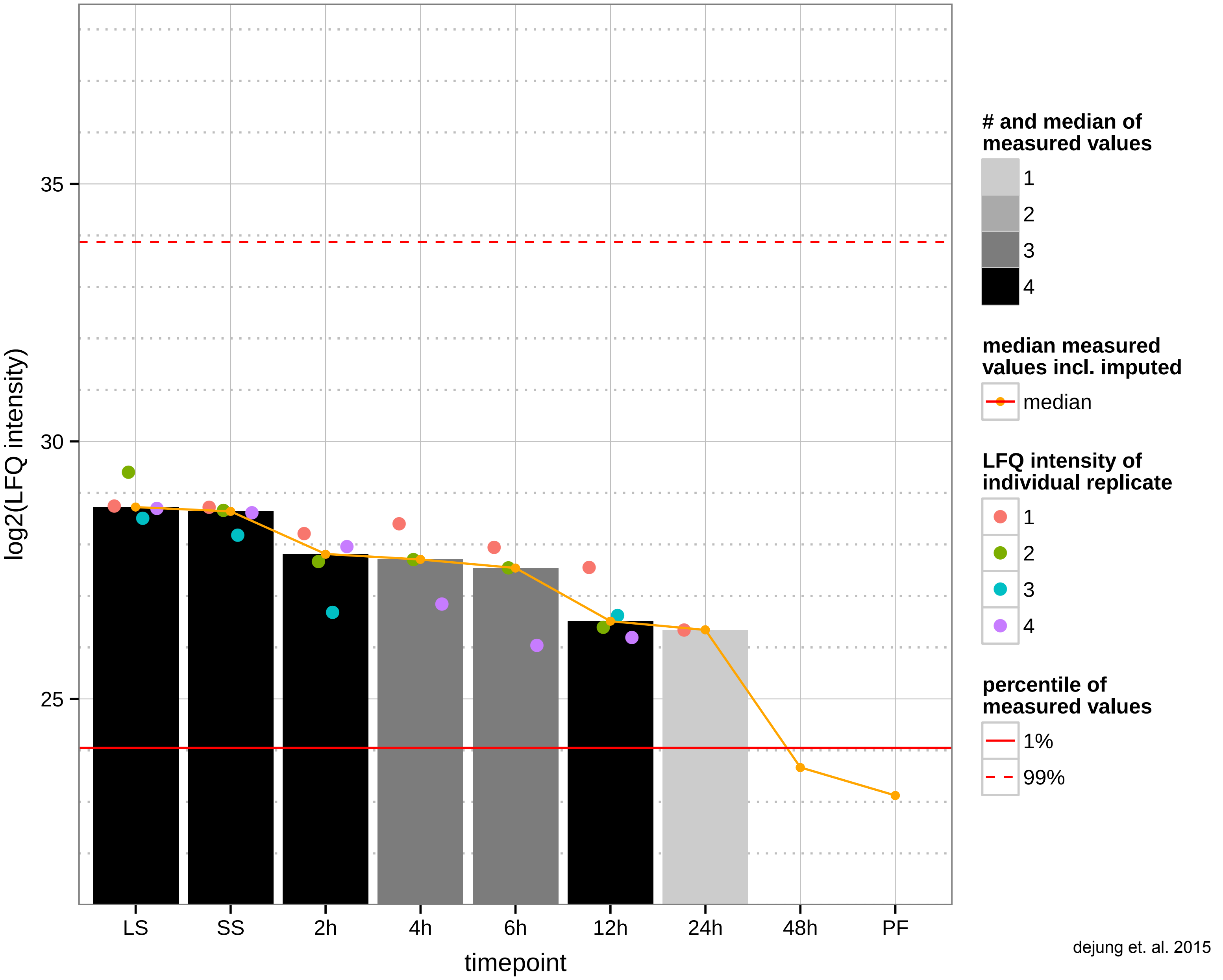
75 kDa invariant surface glycoprotein, putative, 75 kDa invariant surface glycoprotein (ISG75)
Tb927.5.360;Tb11.v5.0231
AGOF: null
AGOC: null, plasma membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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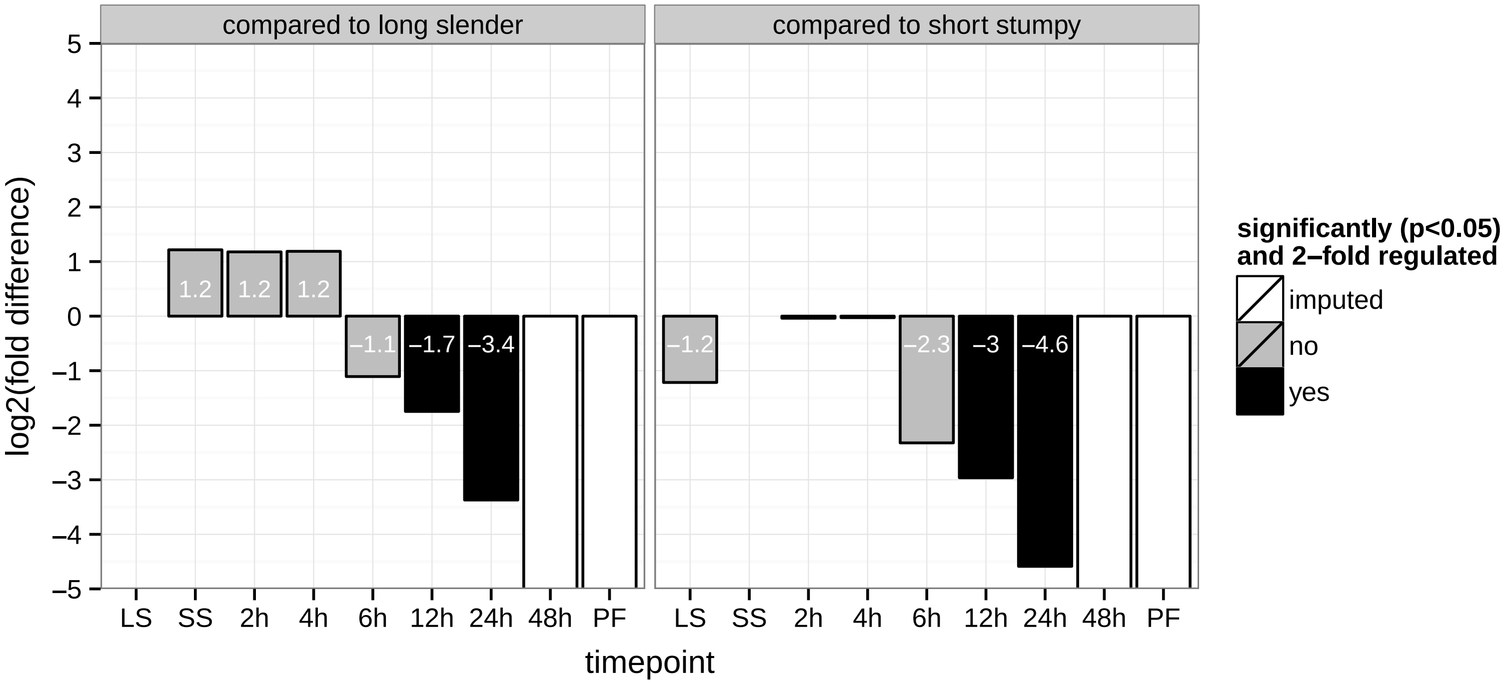
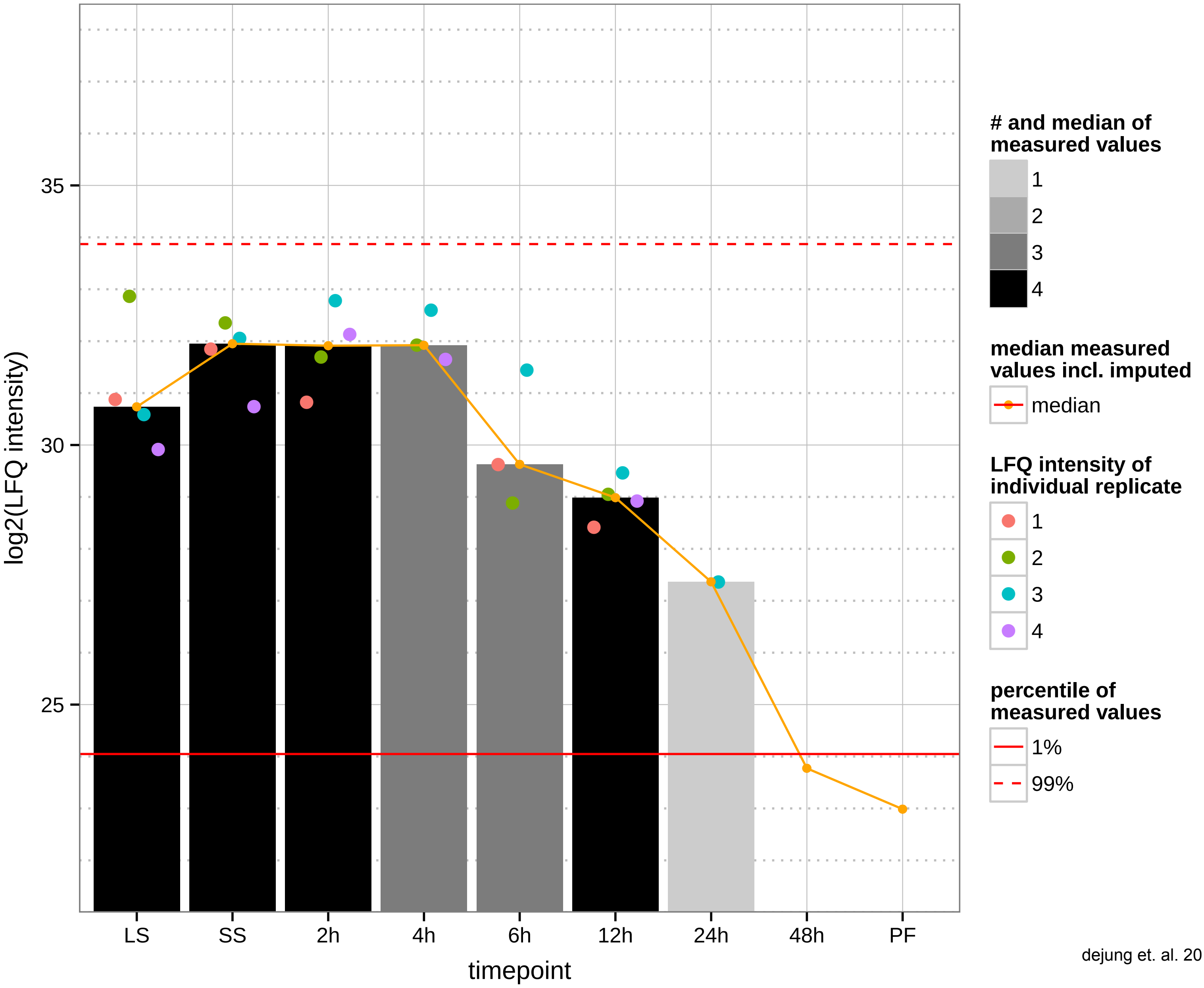
variant surface glycoprotein (VSG), putative
Tb927.1.05
AGOF: null
AGOC: integral to membrane
AGOP: antigenic variation
PGOF: null
PGOC: null
PGOP: null





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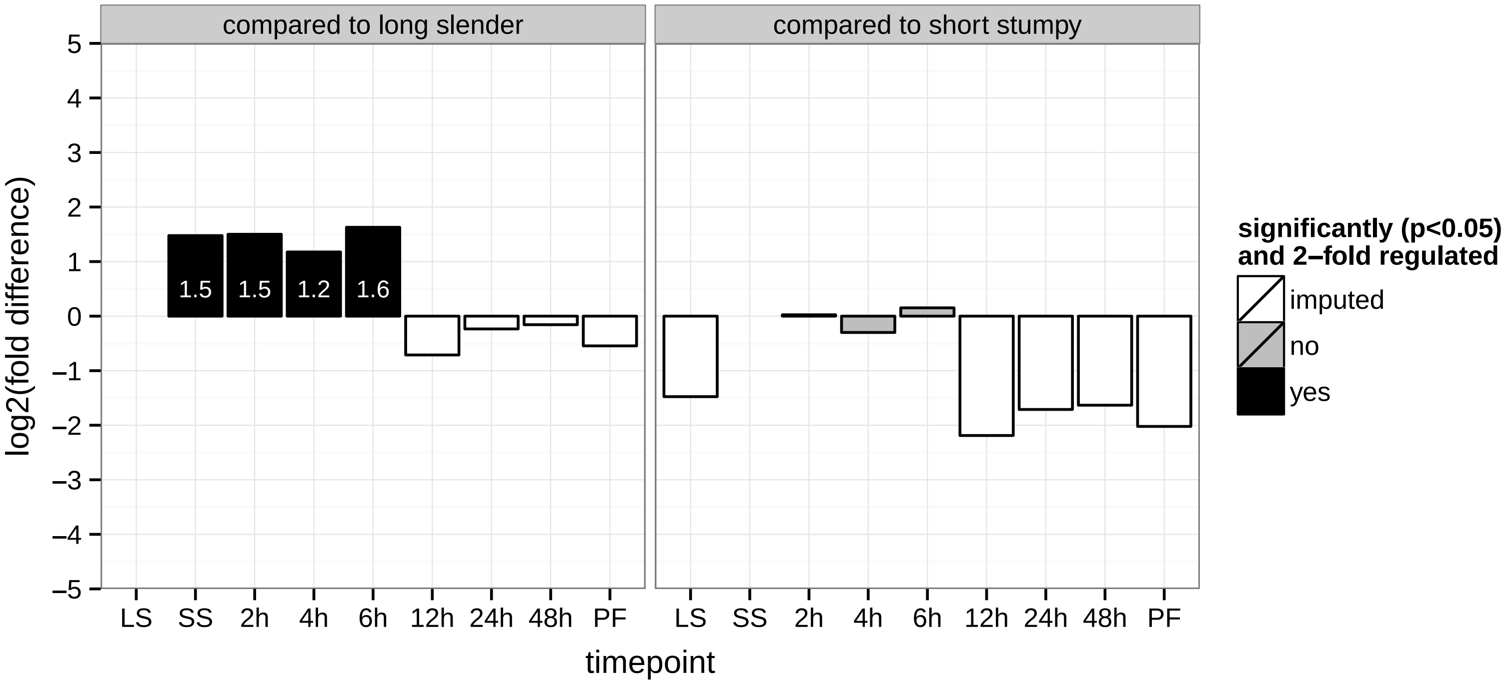
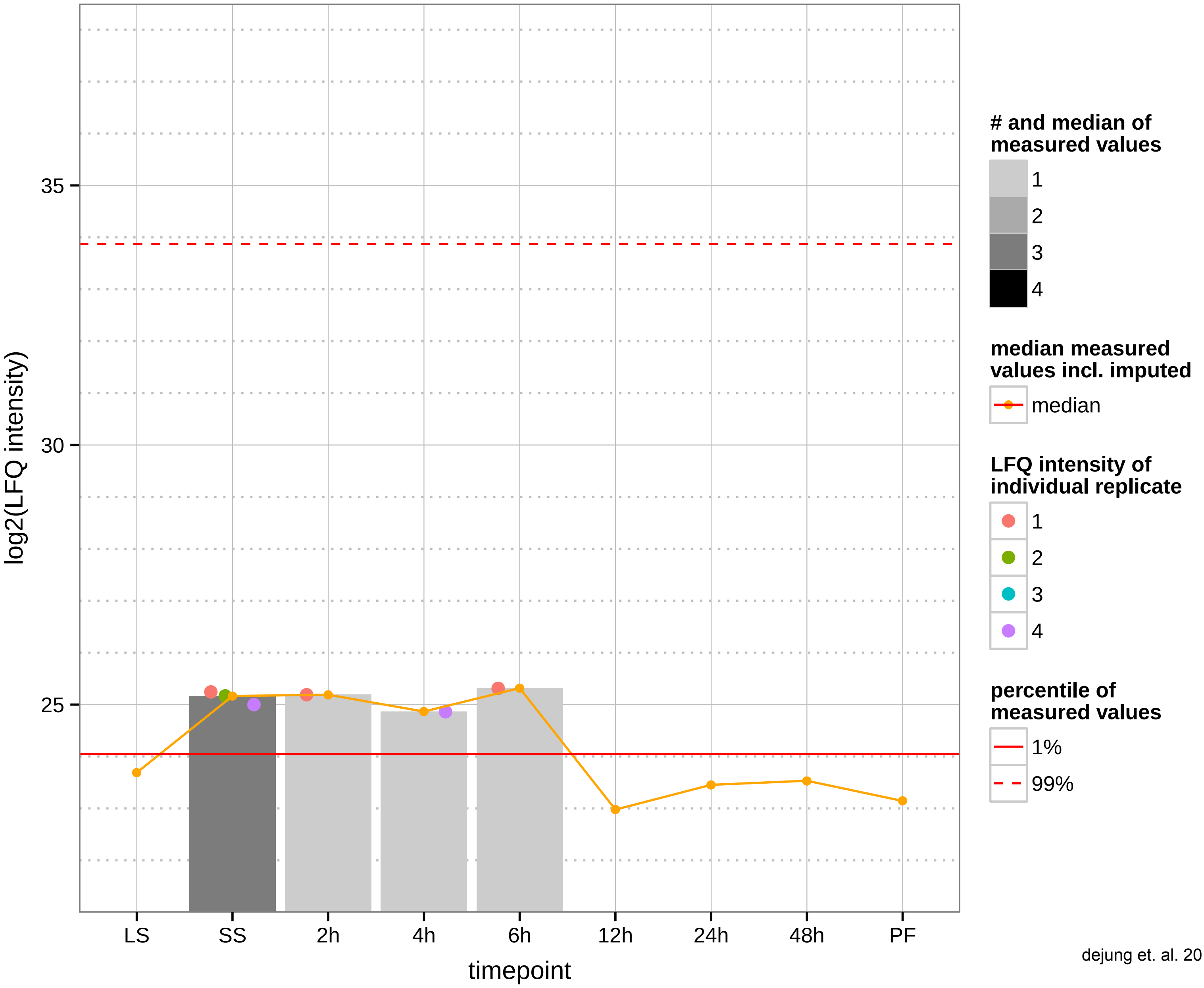
actin related protein 2, putative
Tb927.10.15800
AGOF: structural constituent of cytoskeleton
AGOC: actin cytoskeleton
AGOP: cytoskeleton organization
PGOF: null
PGOC: null
PGOP: null





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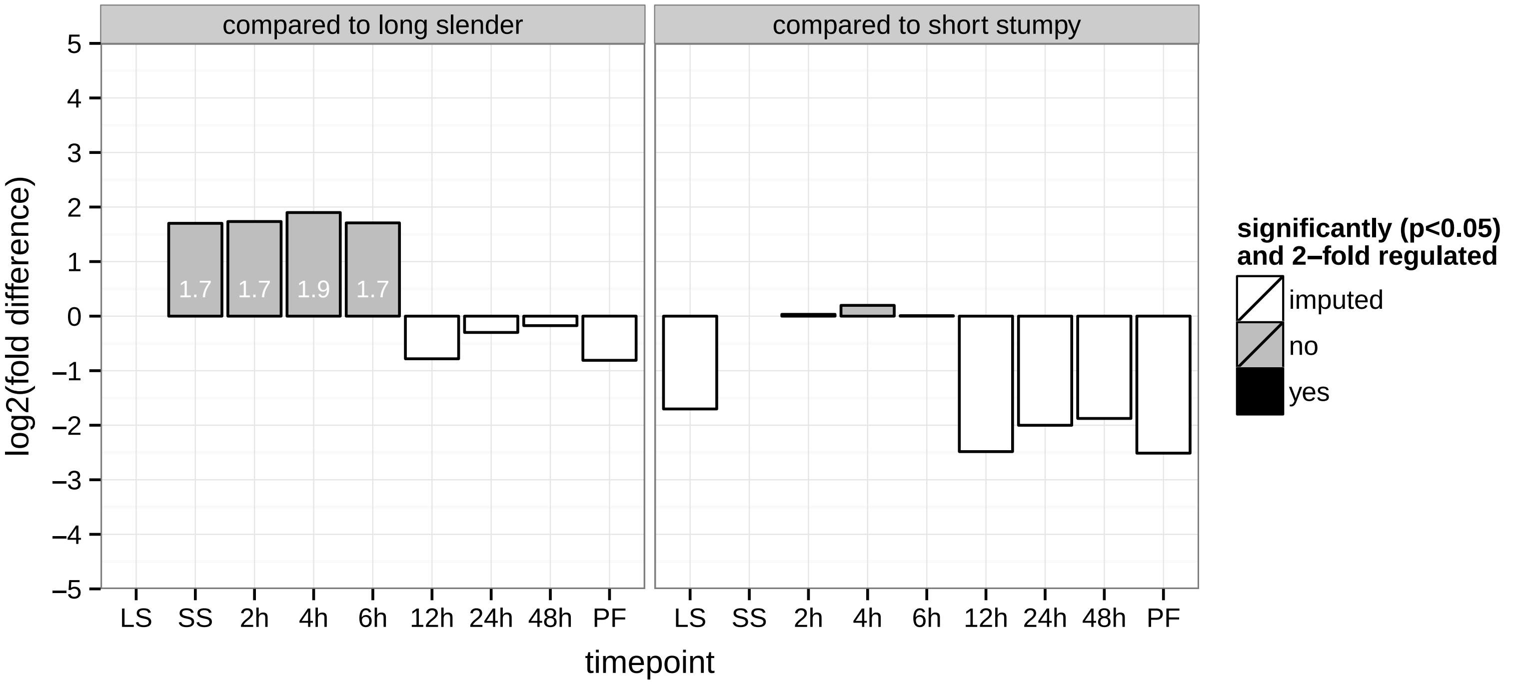
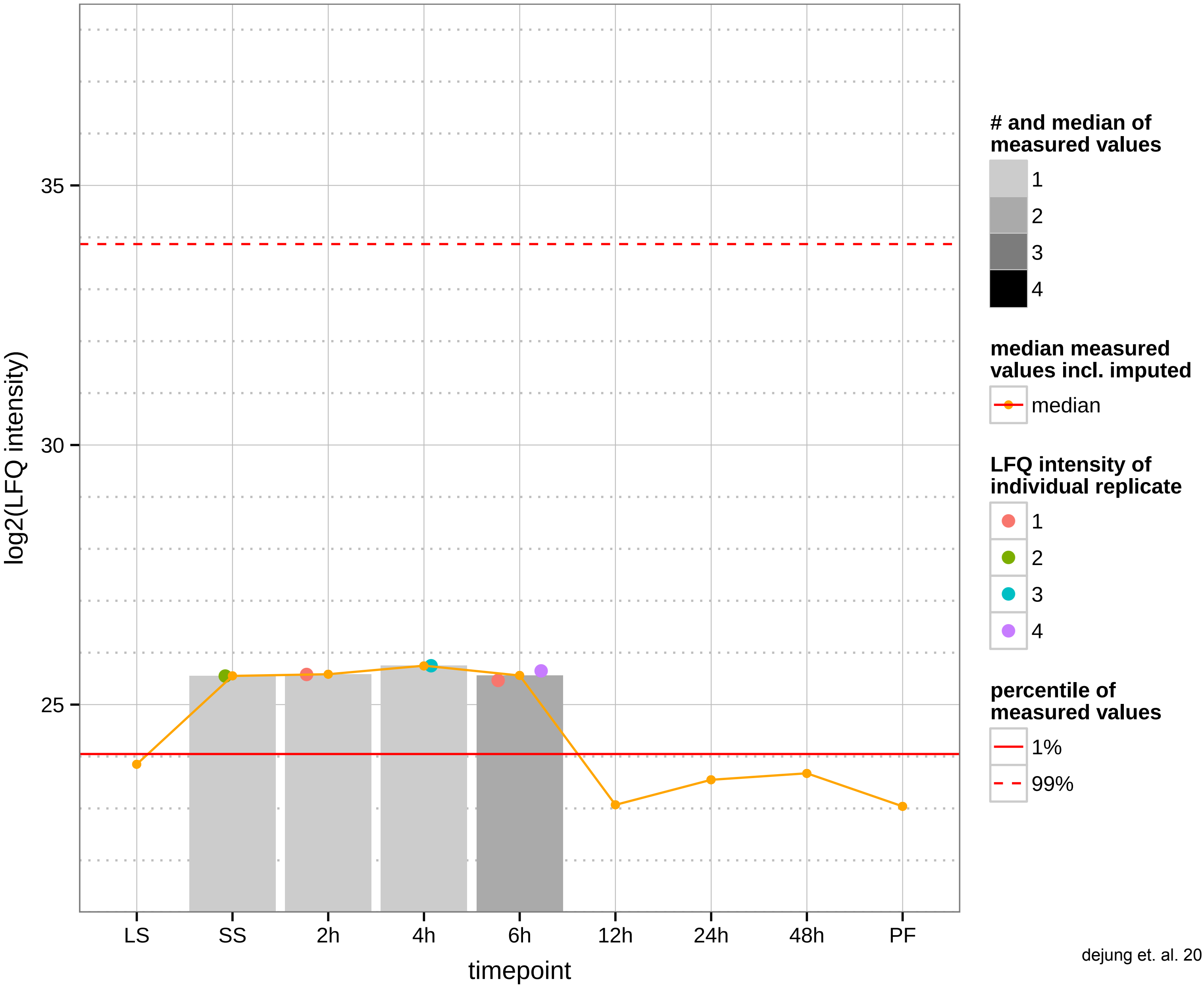
ribosomal RNA processing protein 41B, RNase PH–like protein, putative, exosome complex exonuclease 1, putative (RRP41B
Tb927.2.2180
AGOF: 3'–5' exonuclease activity, 3'–5'–exoribonuclease activity, RNA binding
AGOC: cellular_component
AGOP: RNA processing, rRNA metabolic process
PGOF: null
PGOC: null
PGOP: null





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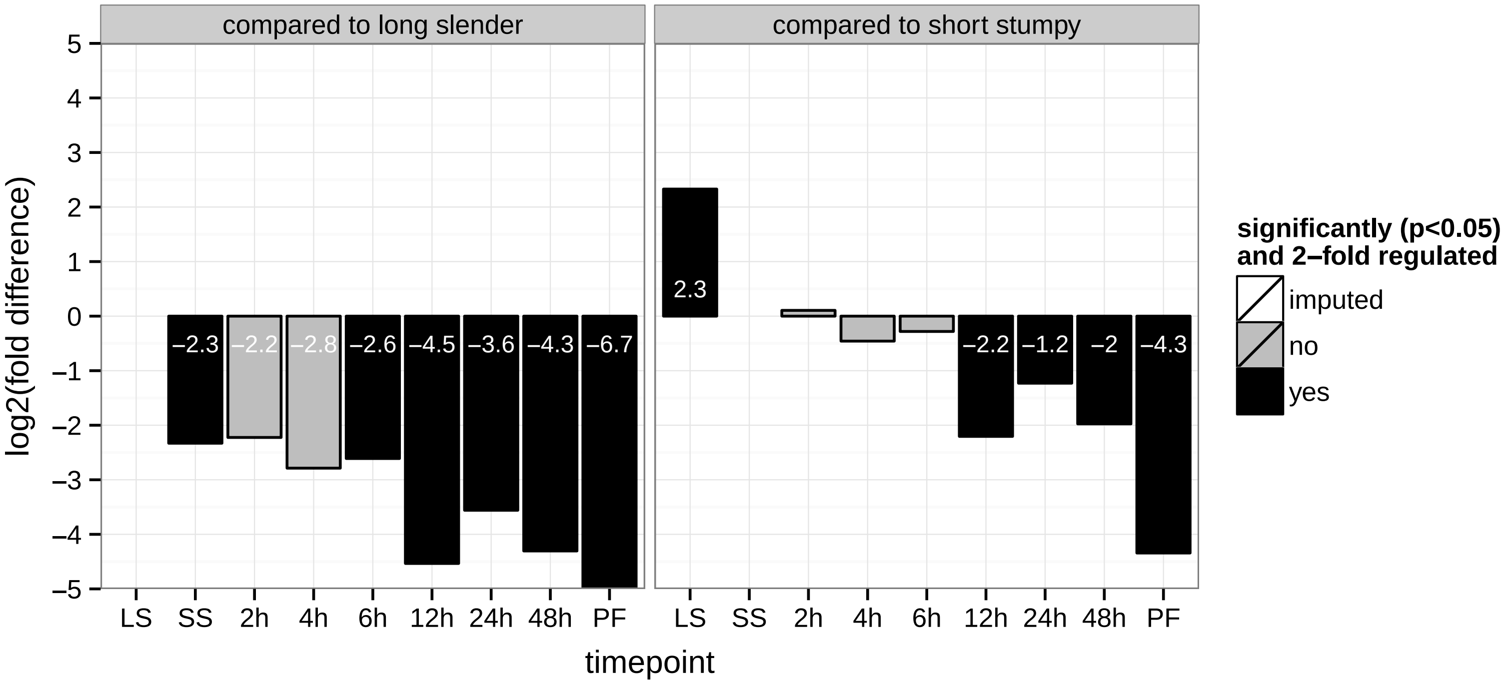
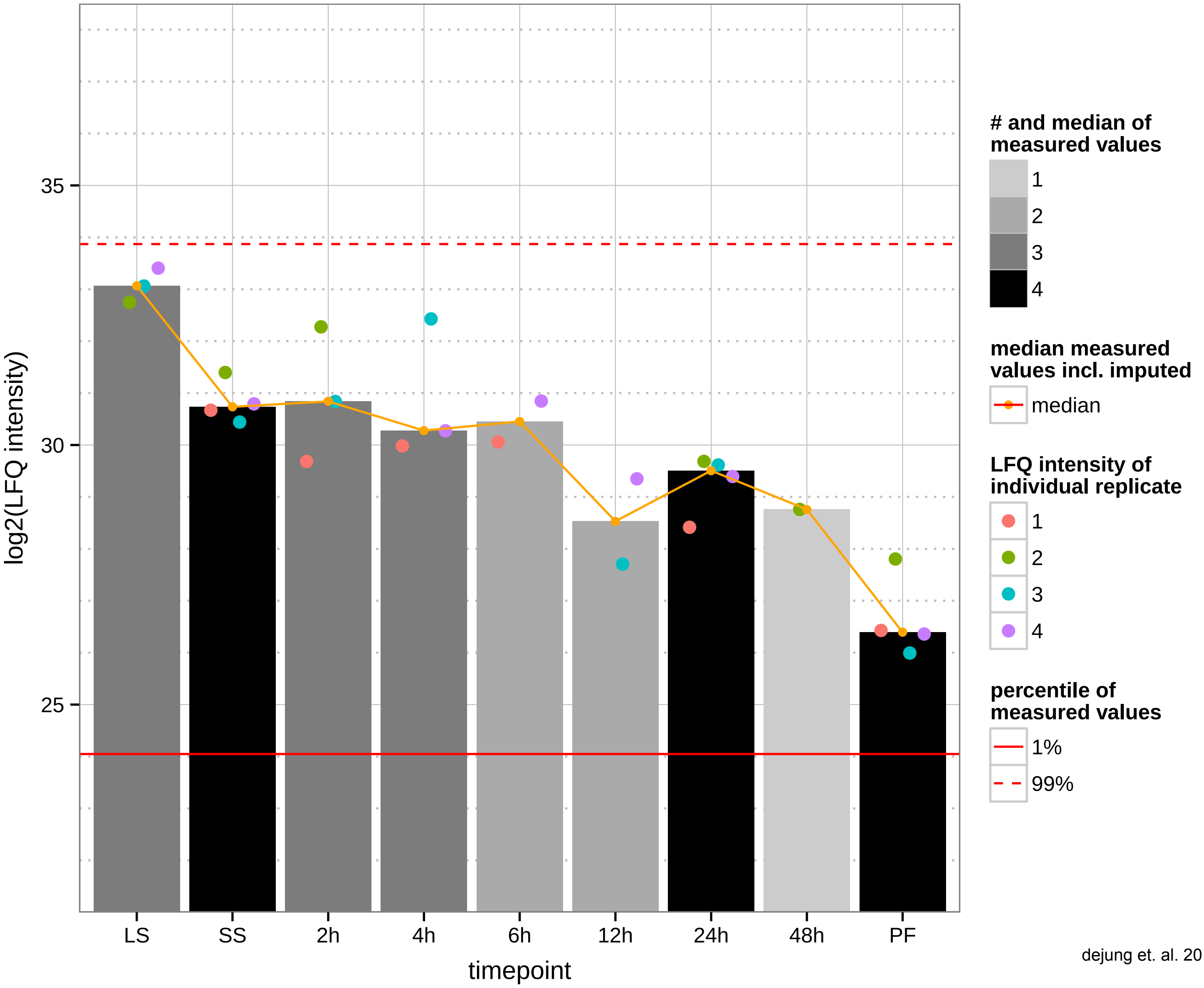
kinesin, putative
Tb927.3.3390;Tb927.3.3400
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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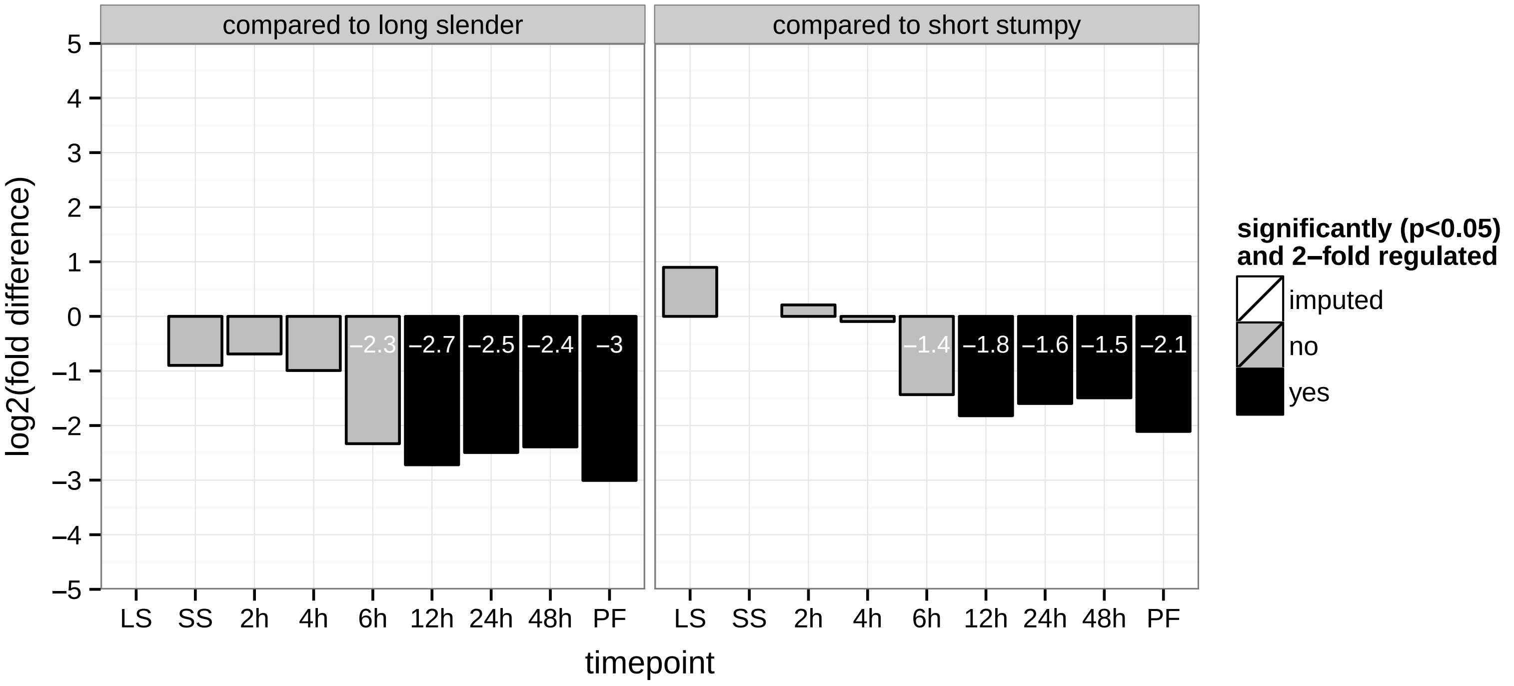
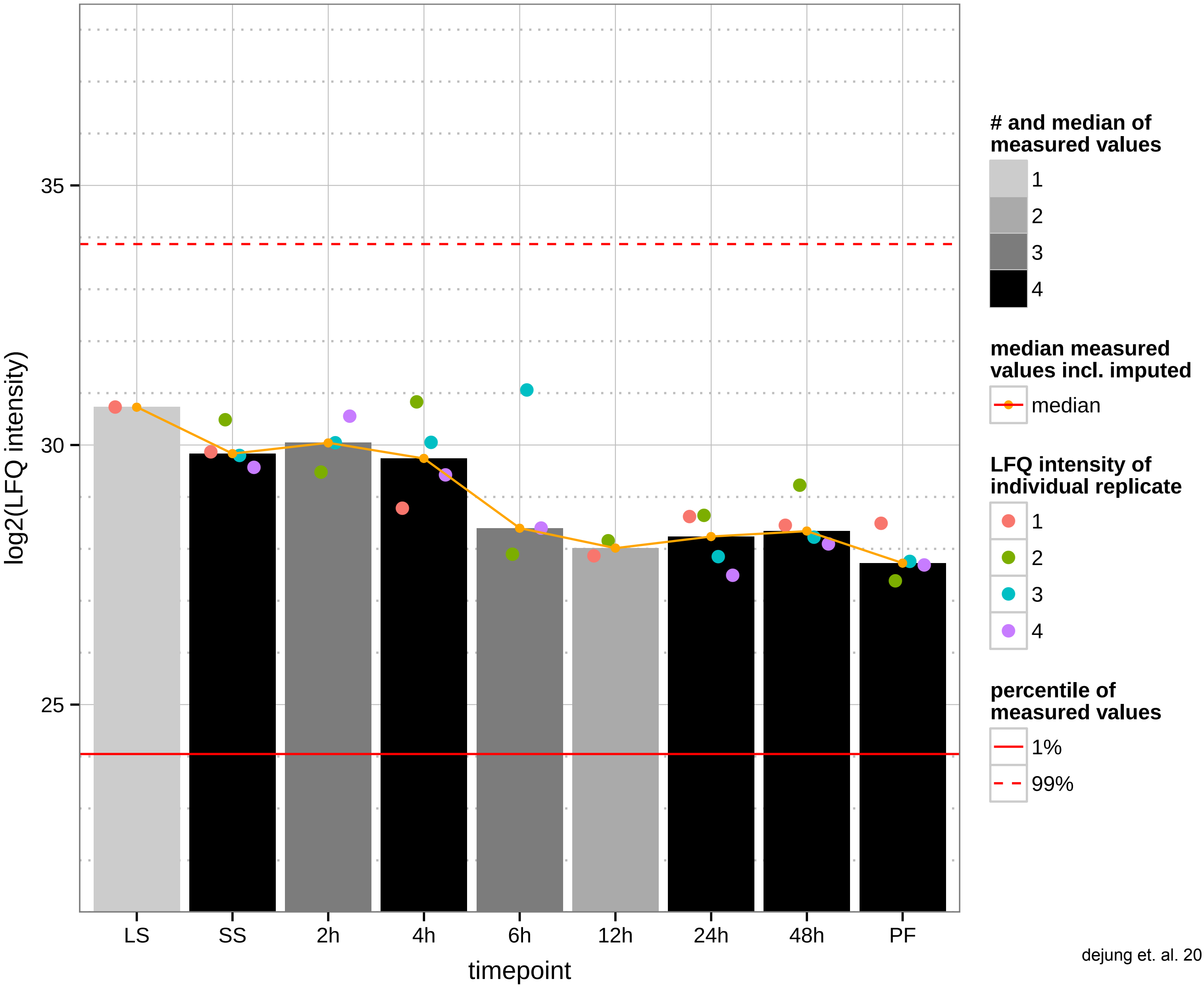
protein phosphatase 2C, putative
Tb927.4.3680
AGOF: catalytic activity
AGOC: mitochondrion
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null





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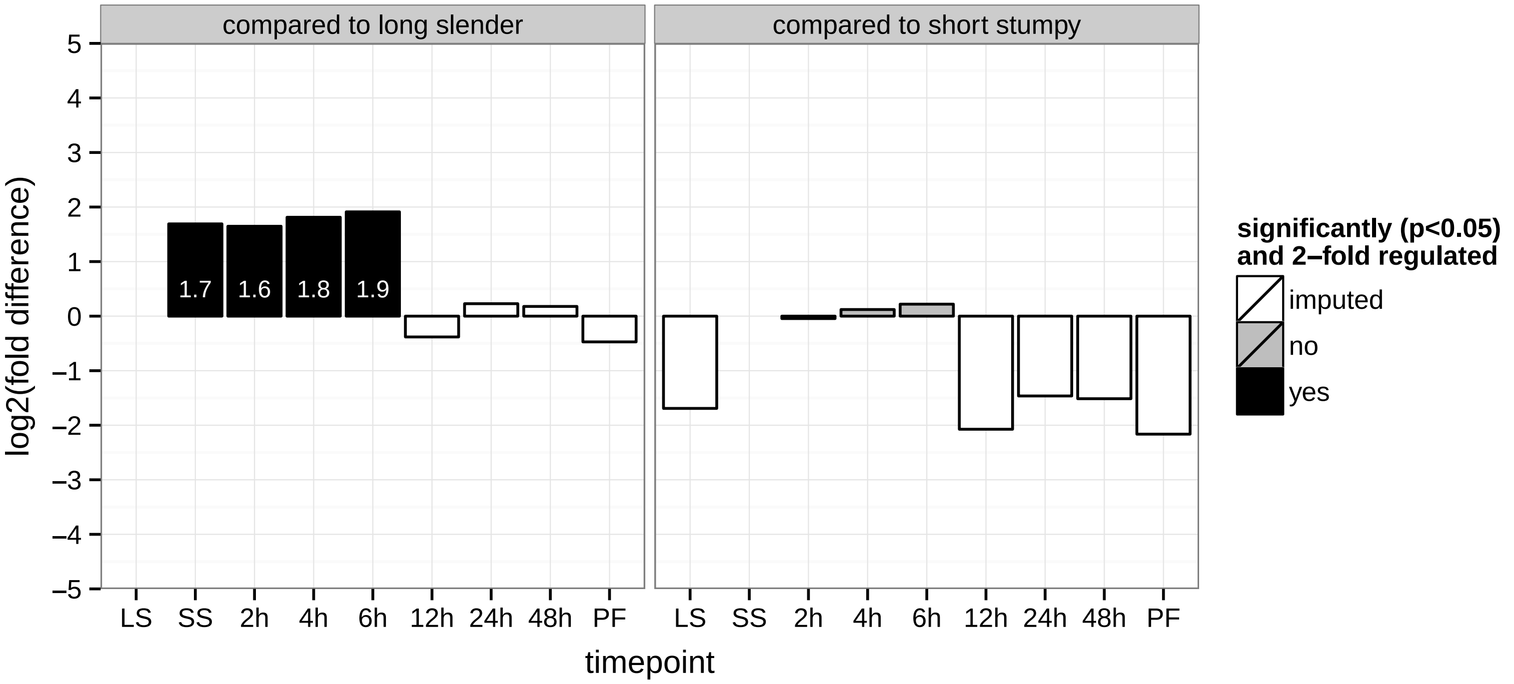
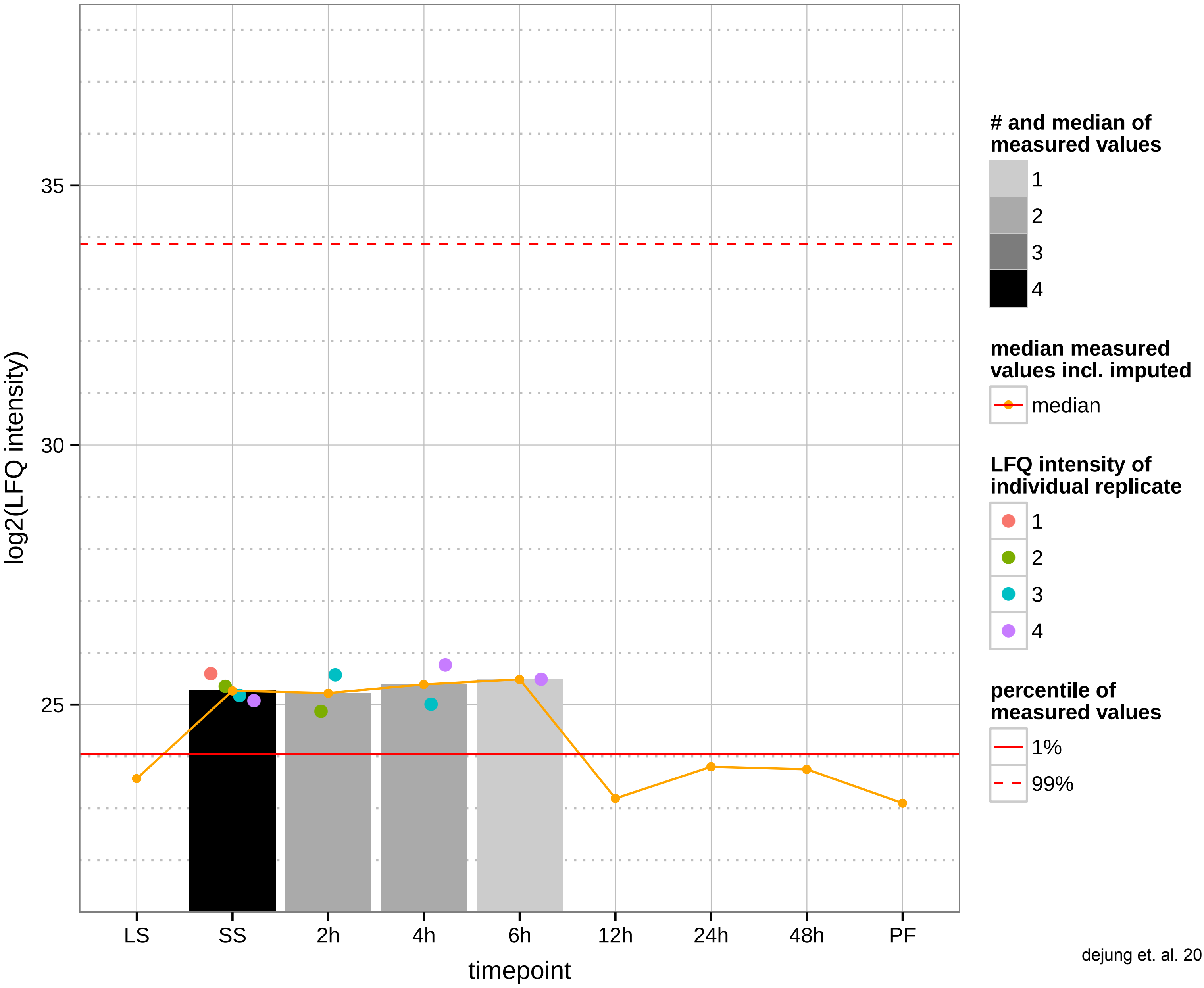
64 kDa invariant surface glycoprotein (ISG64)
Tb927.5.1430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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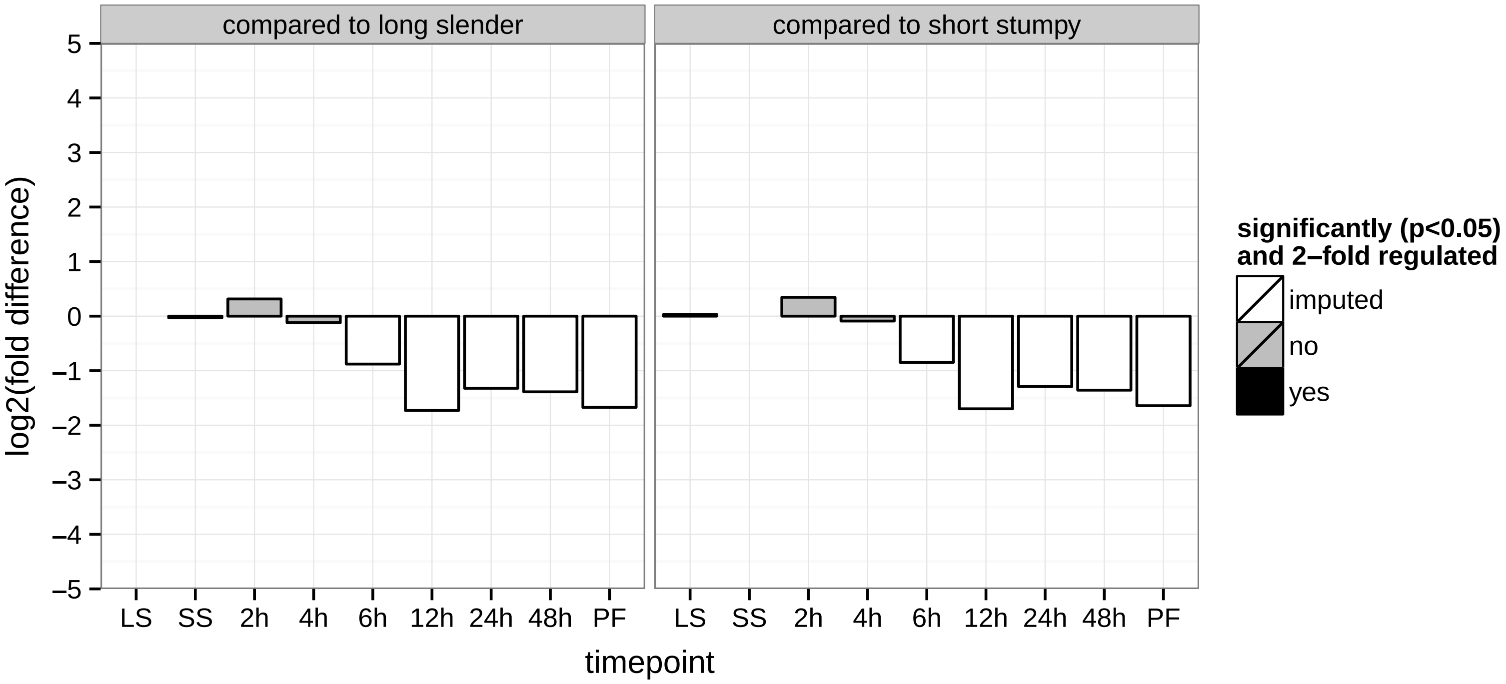
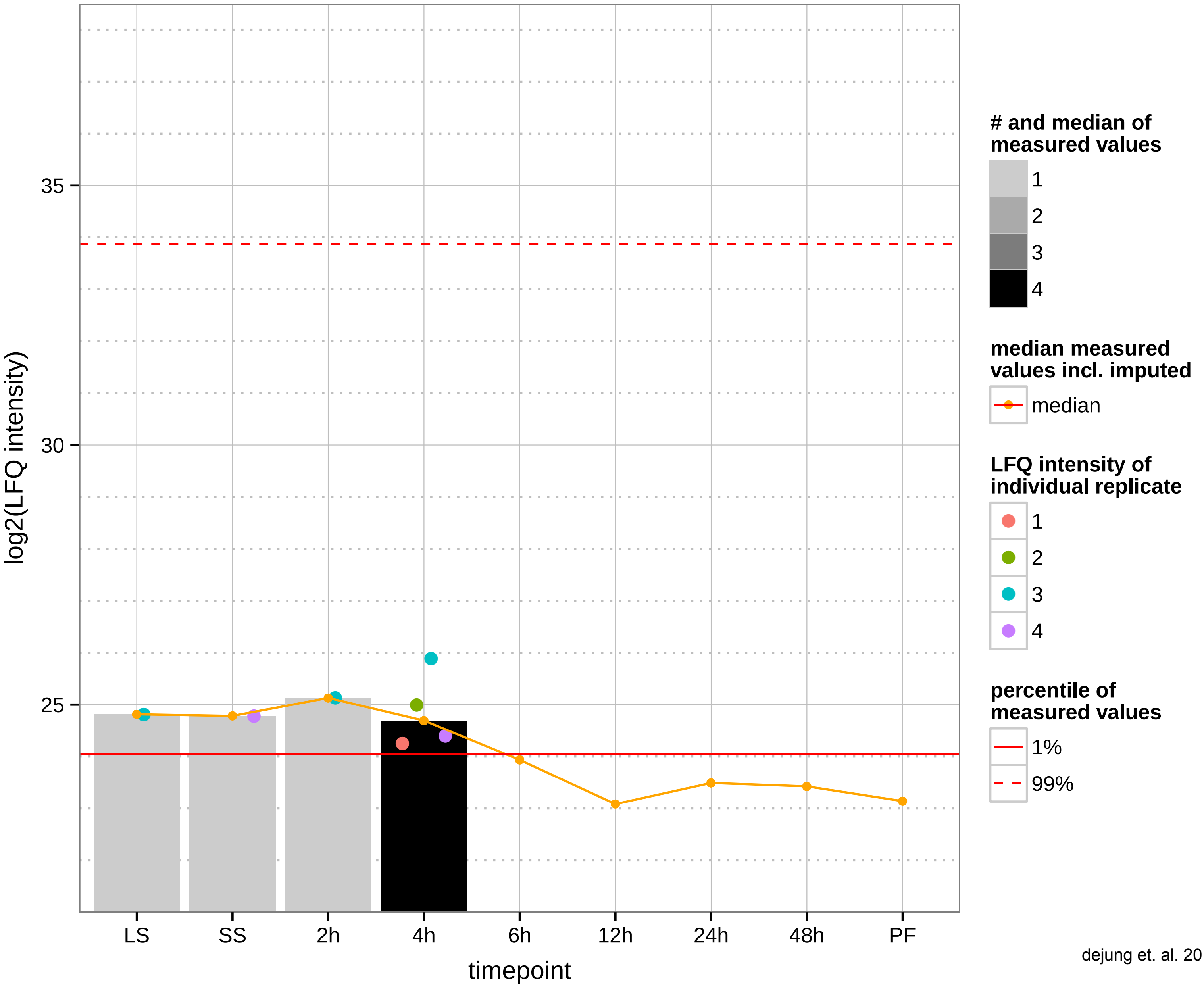
hypothetical protein
Tb927.5.3100
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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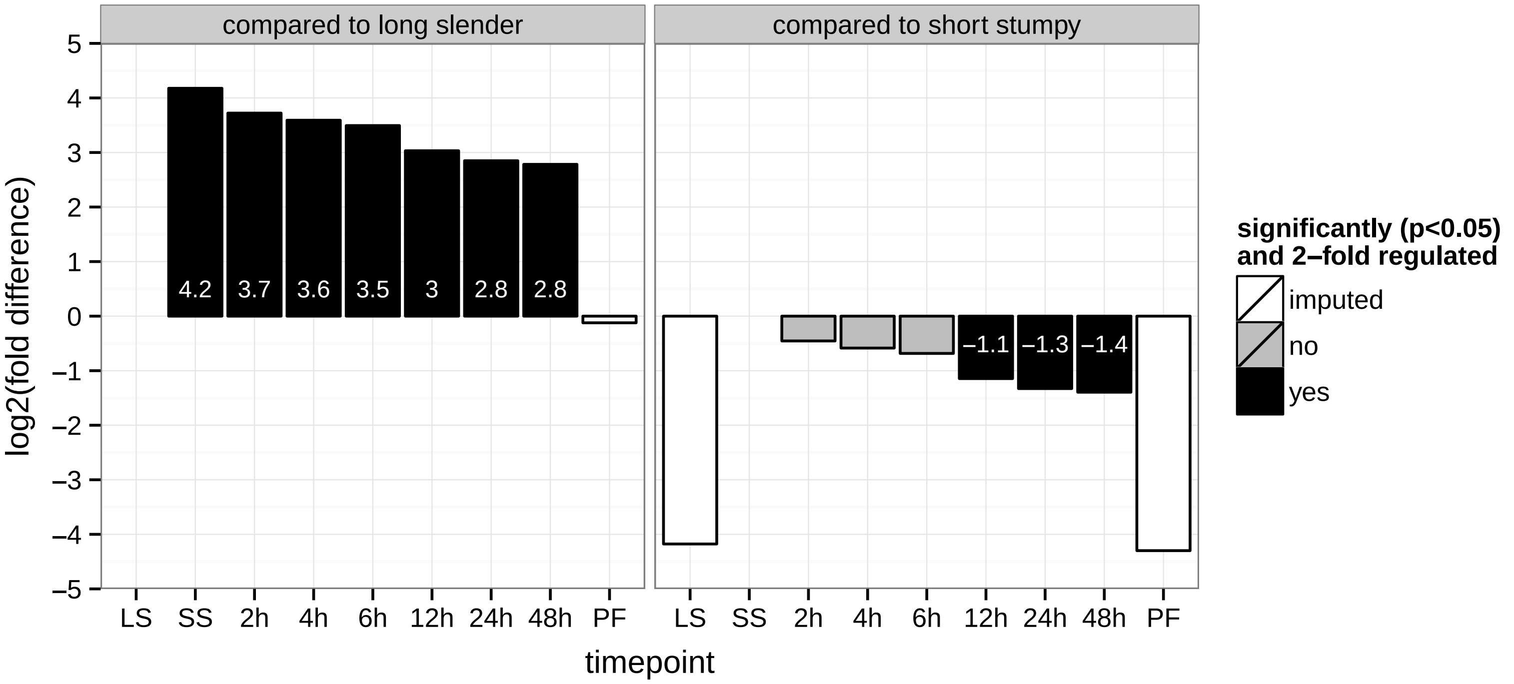
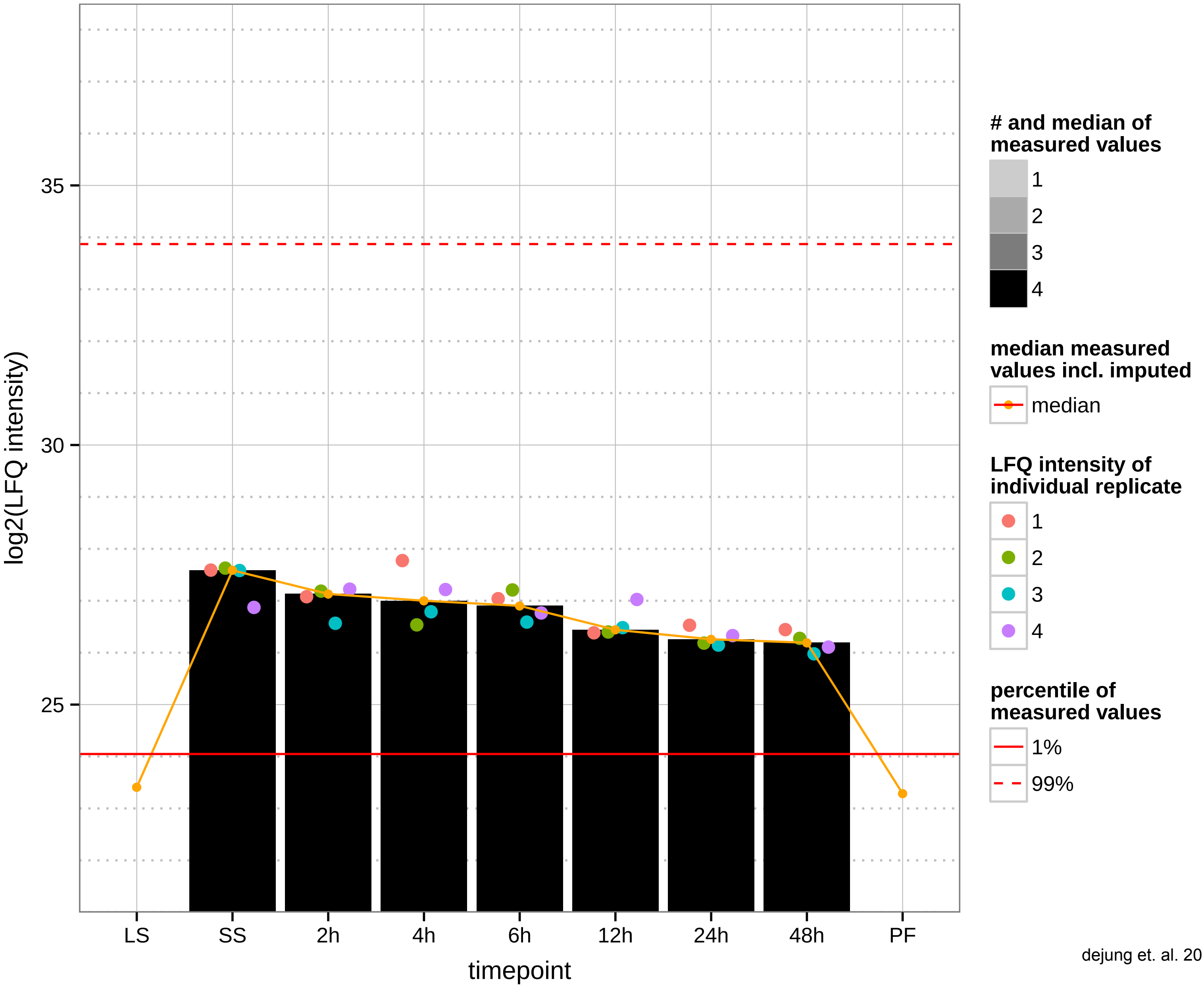
hypothetical protein, conserved
Tb927.6.1750
AGOF: Rab GTPase activator activity
AGOC: intracellular
AGOP: regulation of Rab GTPase activity
PGOF: Rab GTPase activator activity
PGOC: intracellular
PGOP: regulation of Rab GTPase activity





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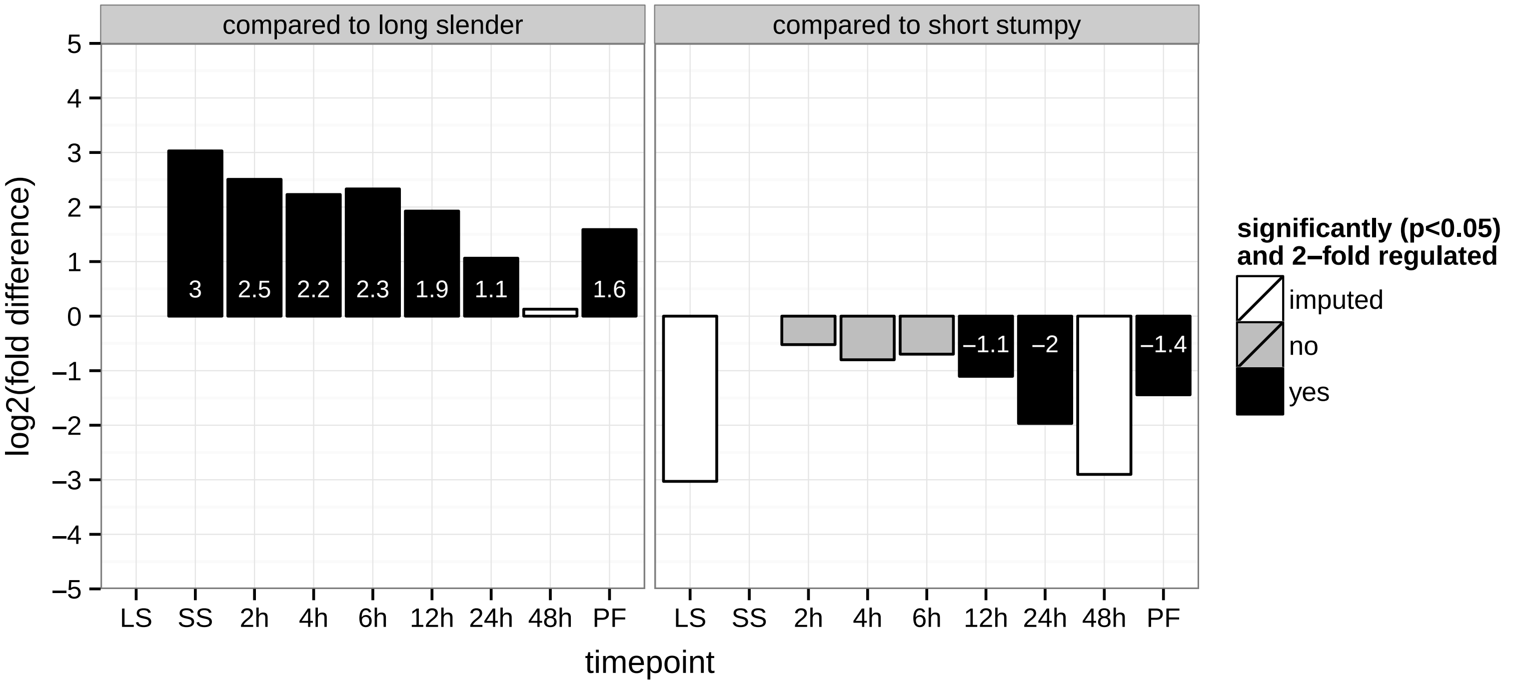
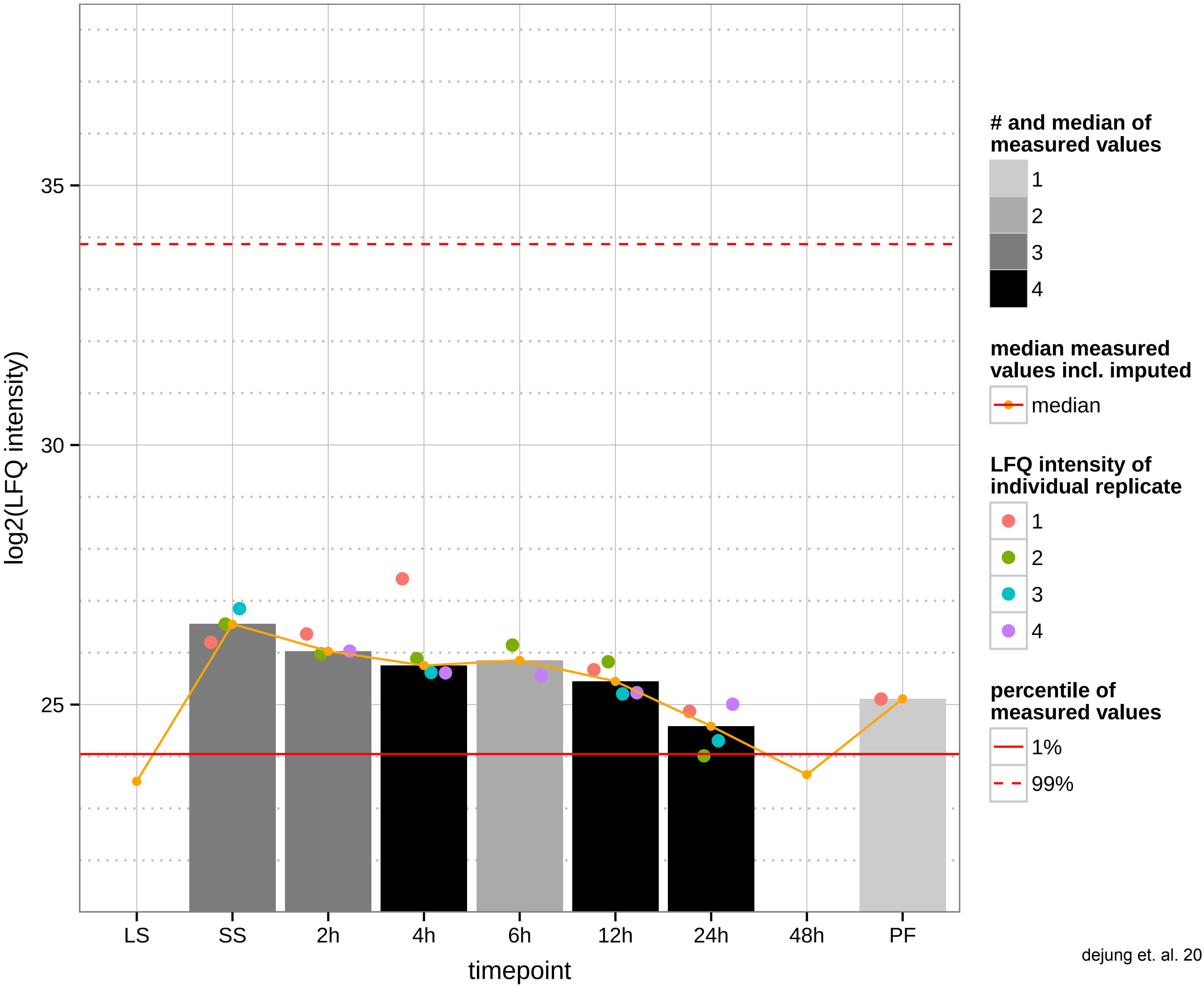
hypothetical protein, conserved
Tb927.6.1980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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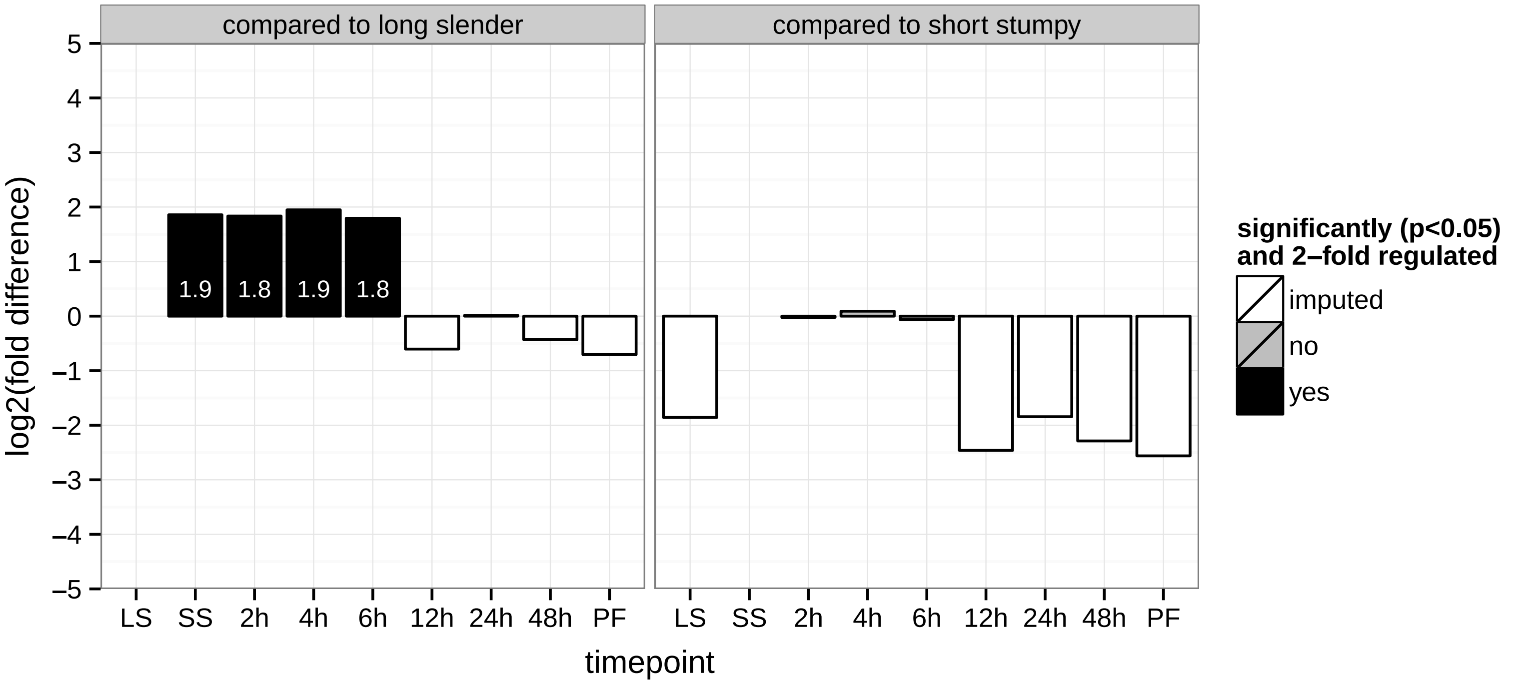
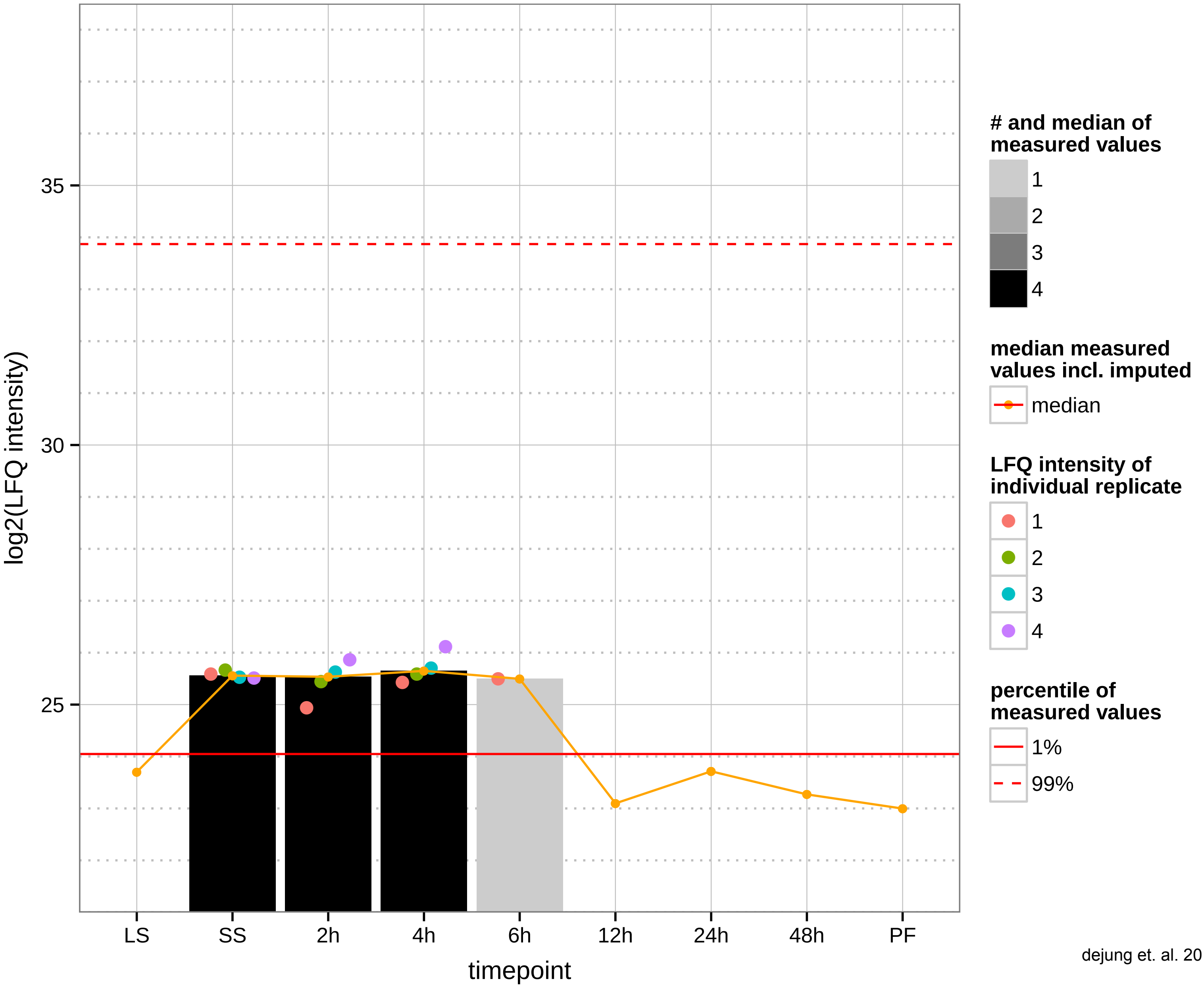
palmitoyl acyltransferase 11, putative
Tb927.7.3350
AGOF: zinc ion binding
AGOC: integral to membrane
AGOP: endocytosis, protein palmitoylation, transport
PGOF: zinc ion binding
PGOC: null
PGOP: null





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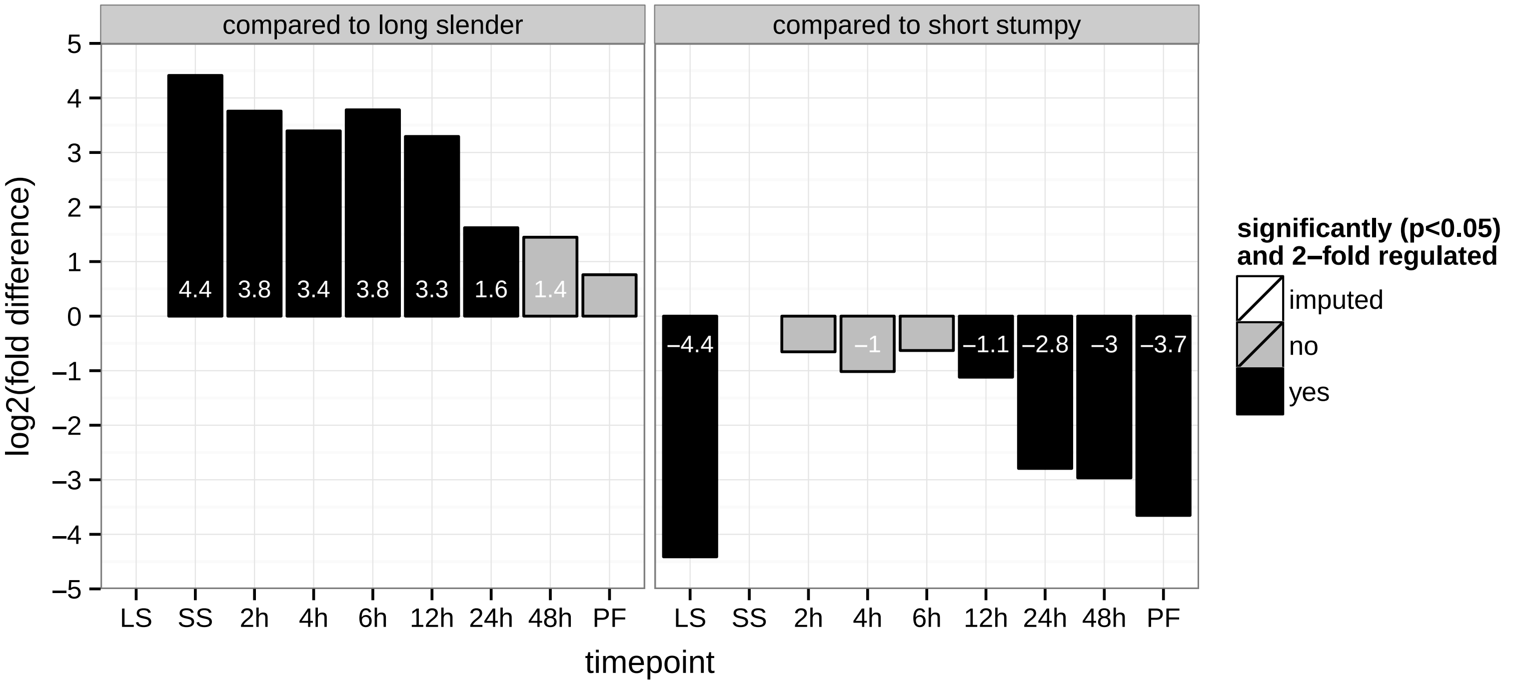
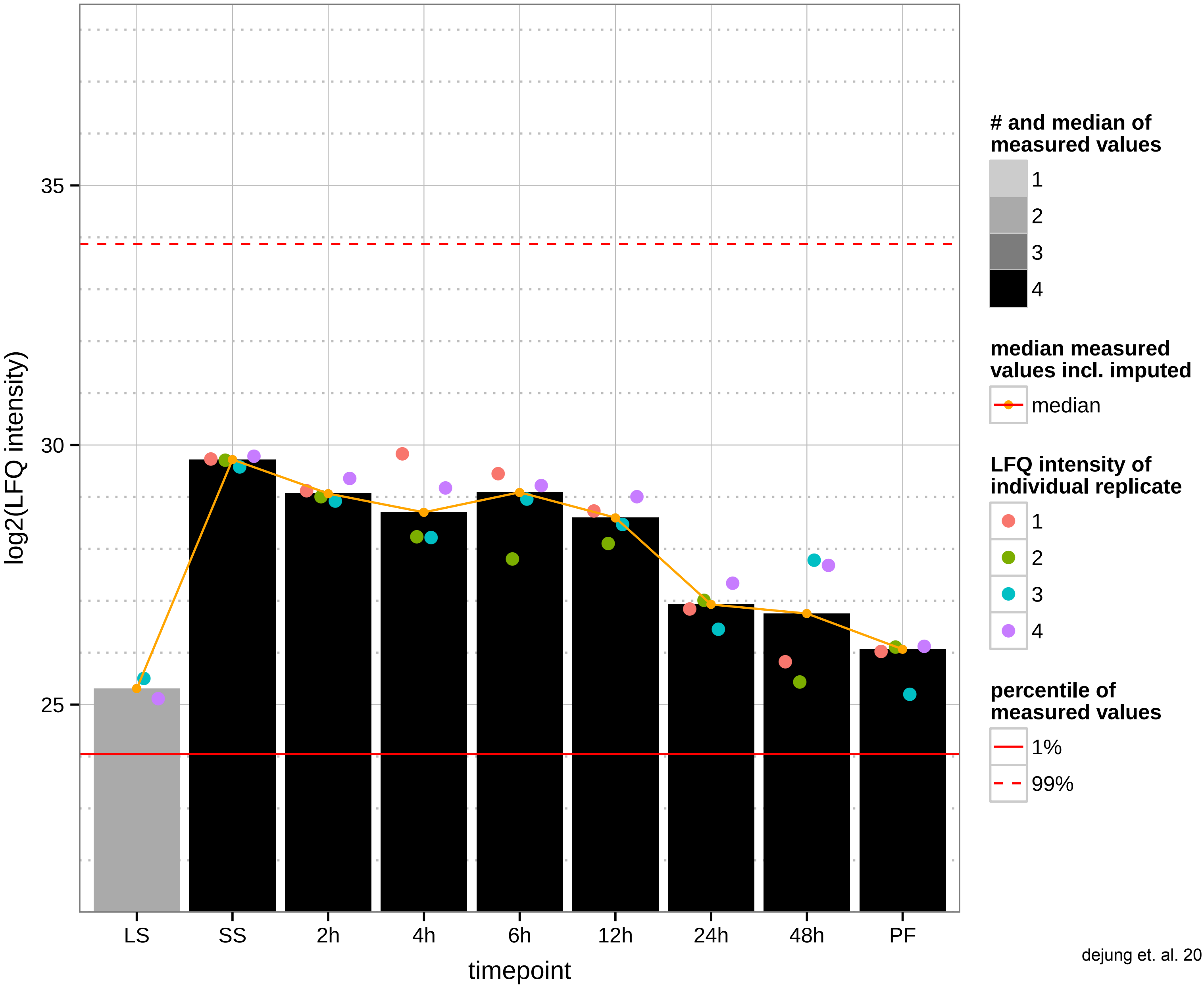
hypothetical protein, conserved
Tb927.7.3970
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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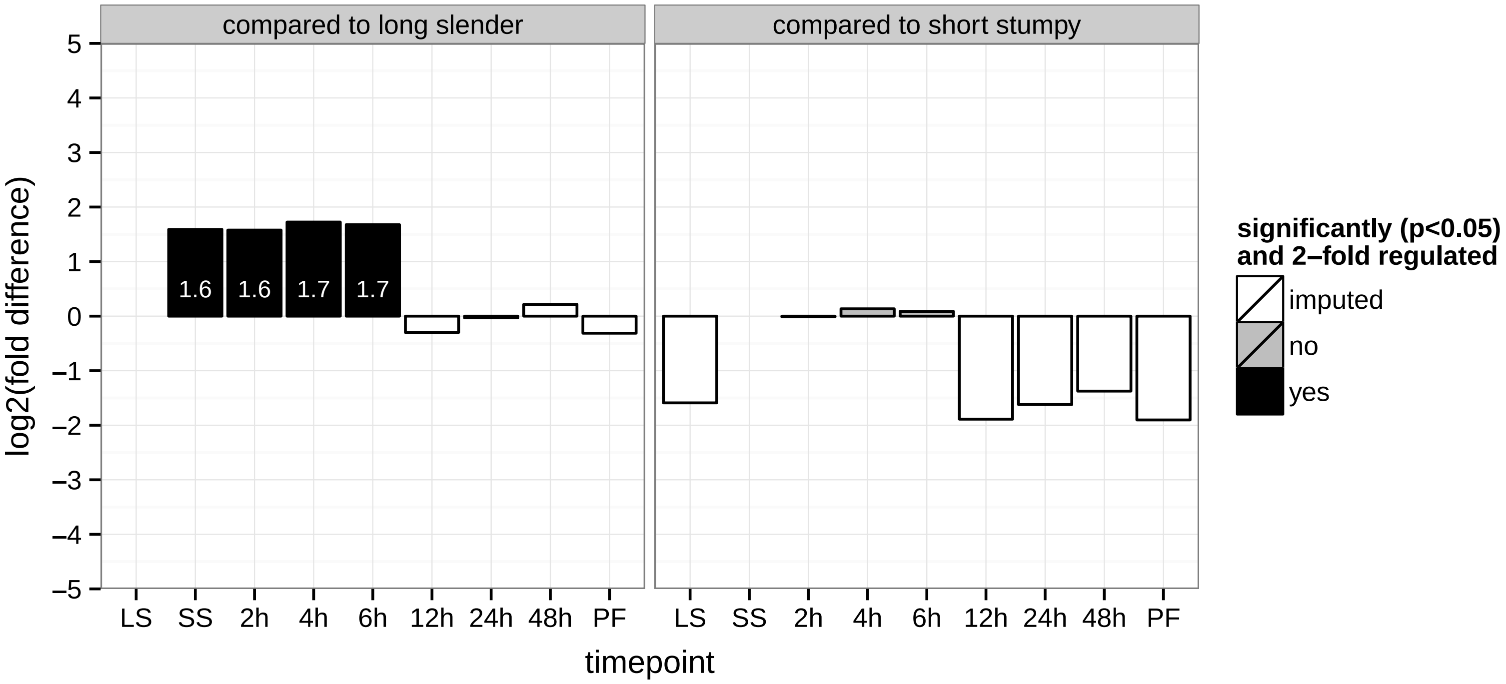
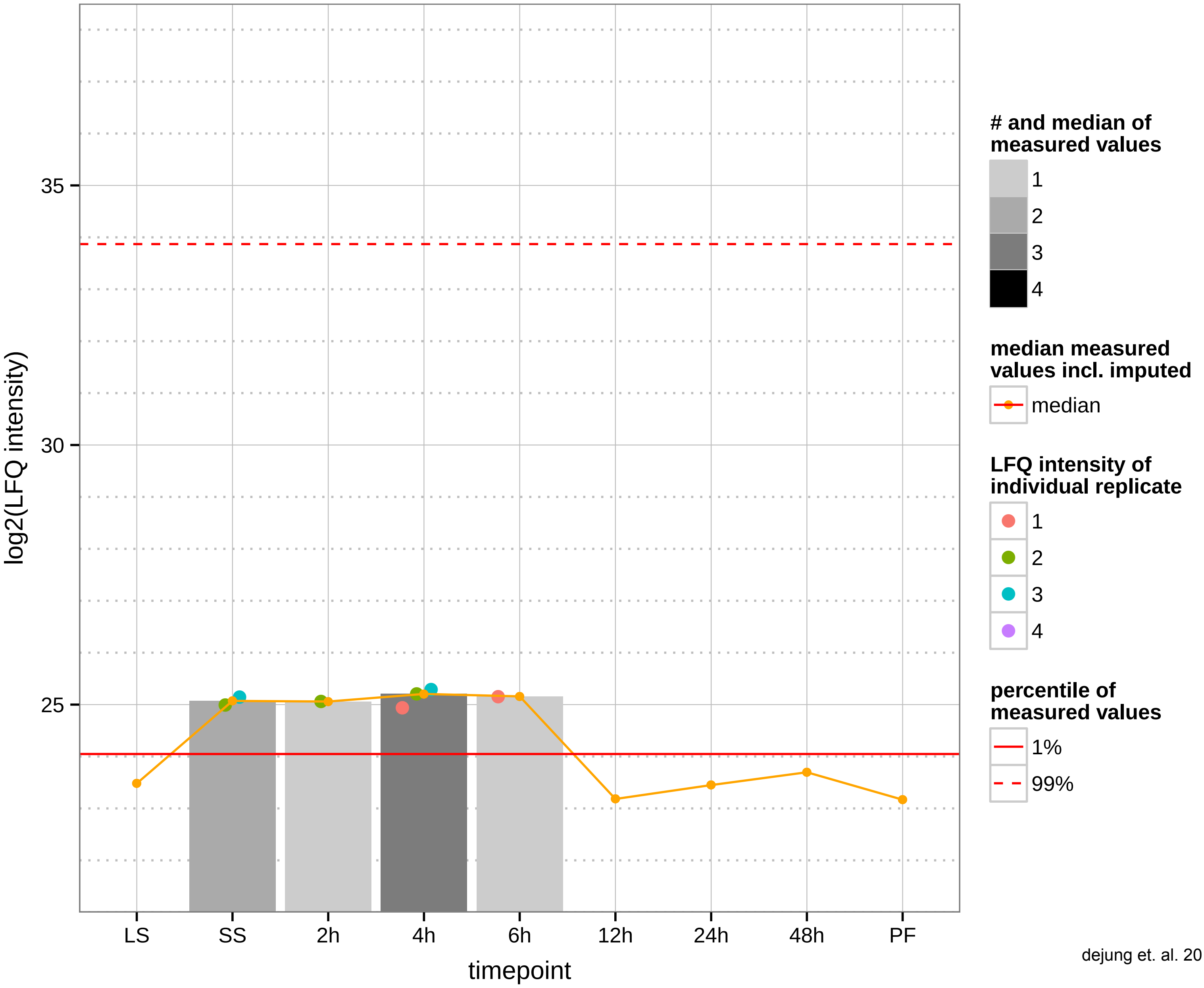
hypothetical protein, conserved
Tb927.7.520
AGOF: heme binding
AGOC: null
AGOP: null
PGOF: heme binding
PGOC: null
PGOP: null





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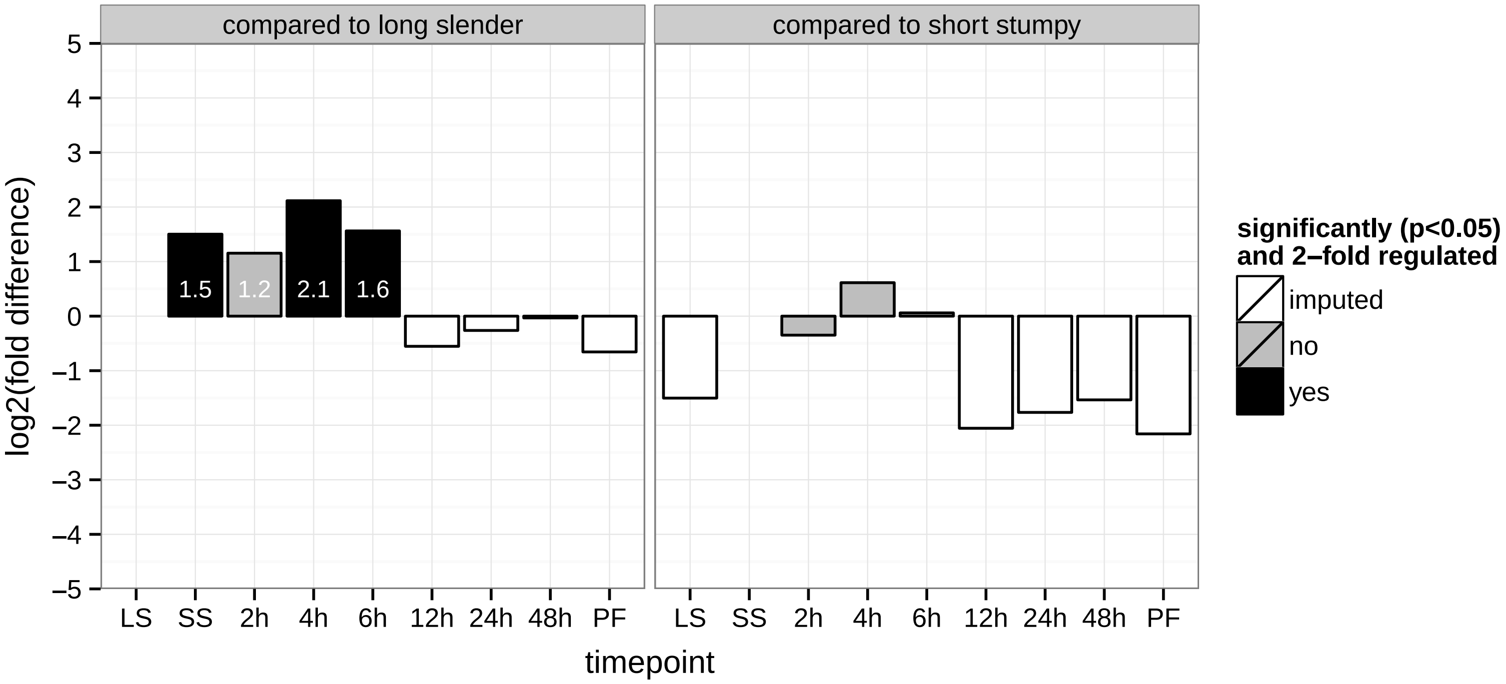
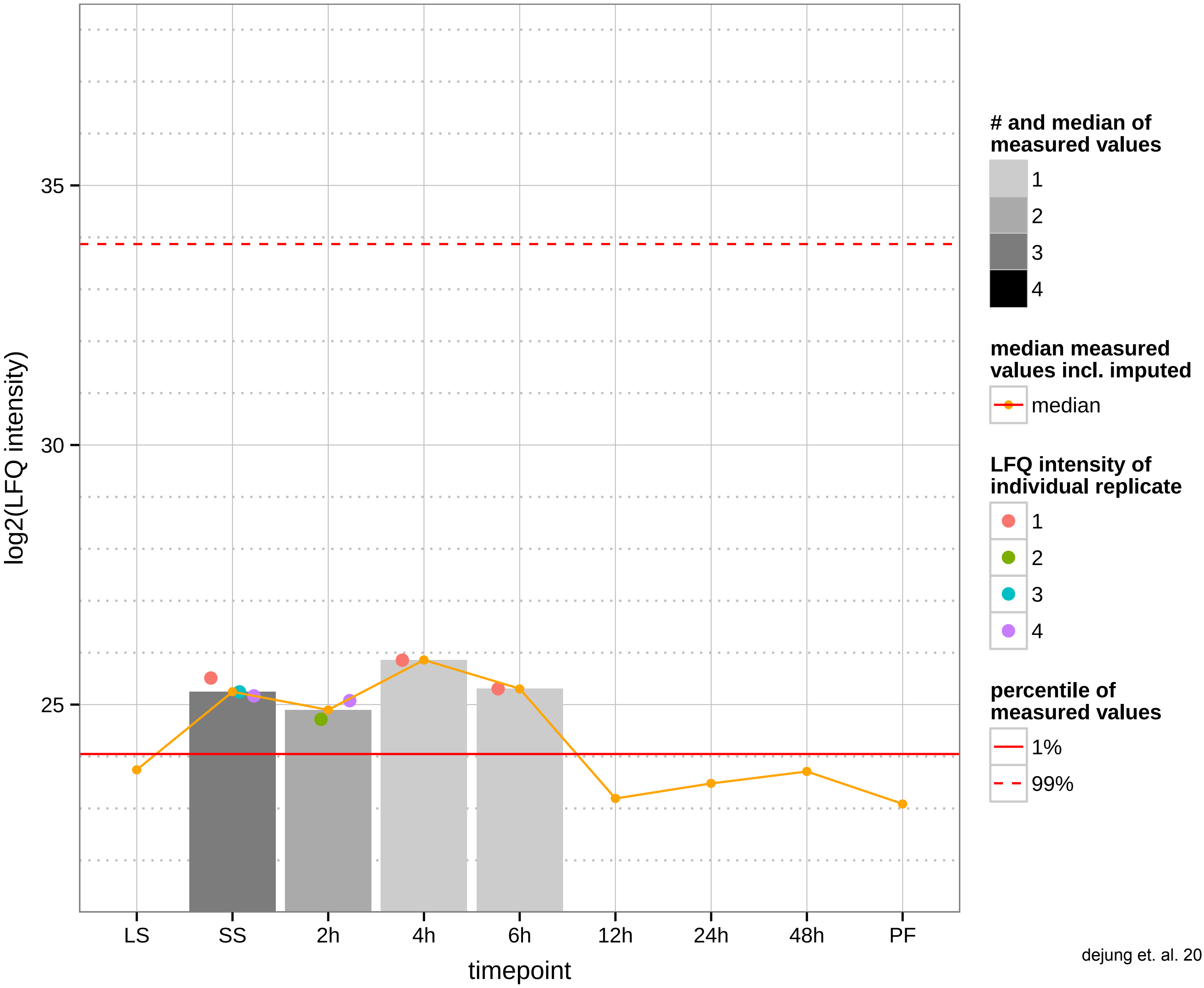
lipin, putative
Tb927.7.5450
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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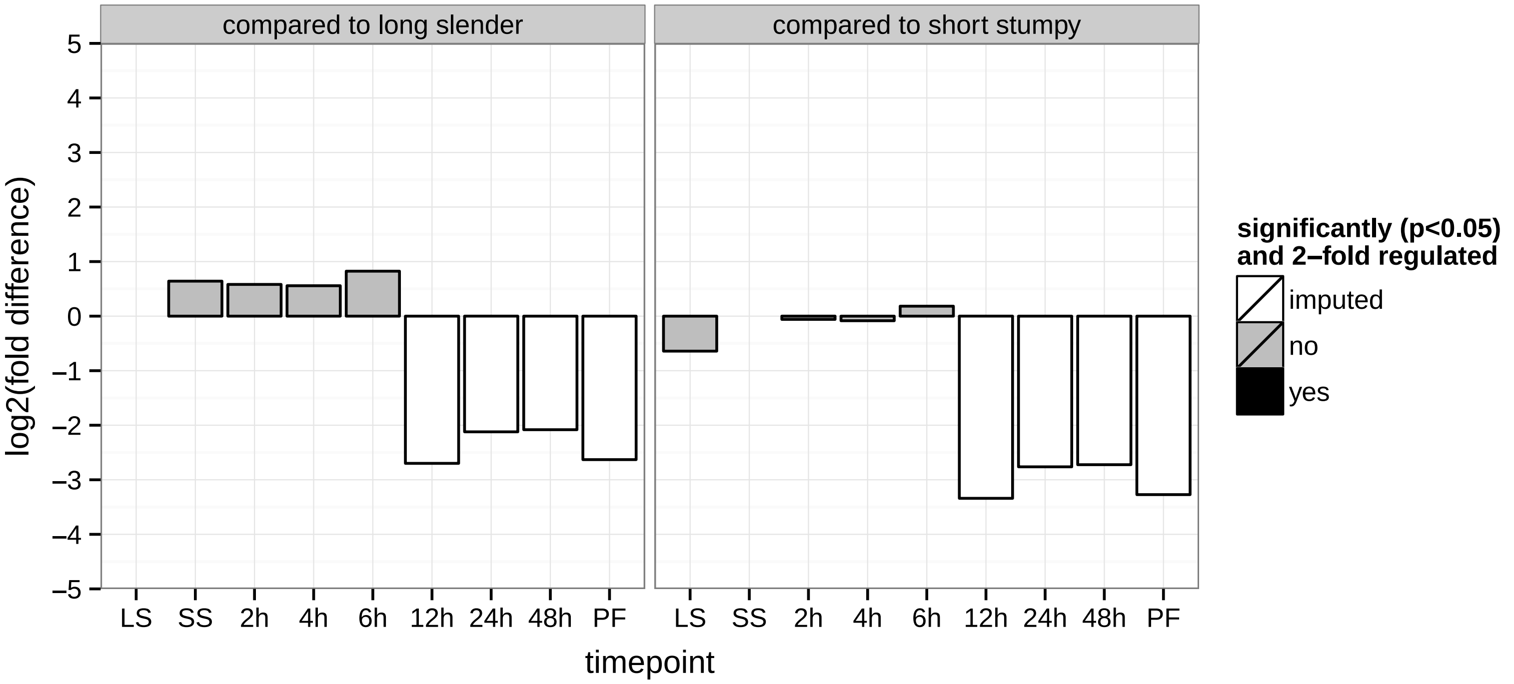
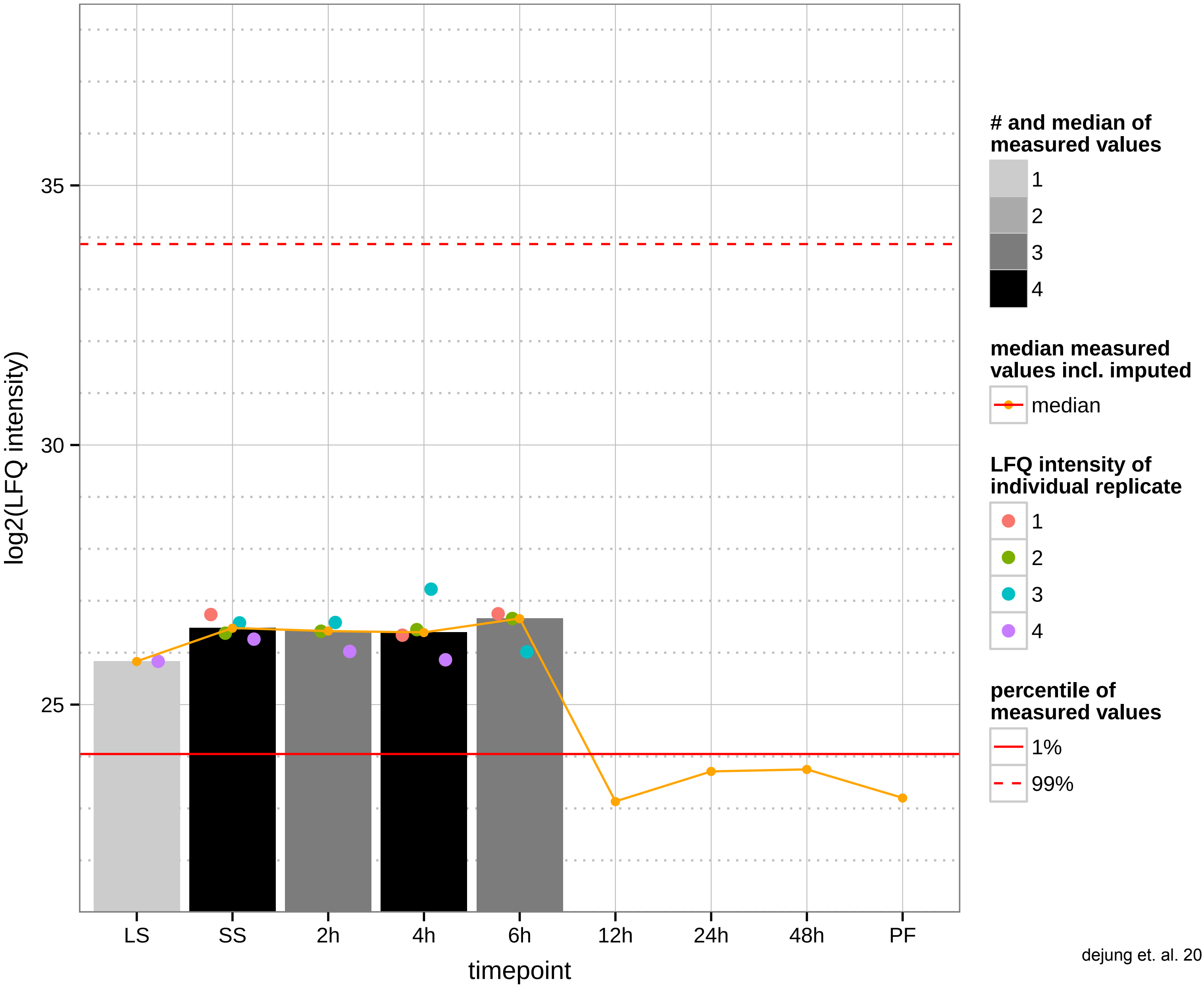
hypothetical protein, conserved
Tb927.7.6600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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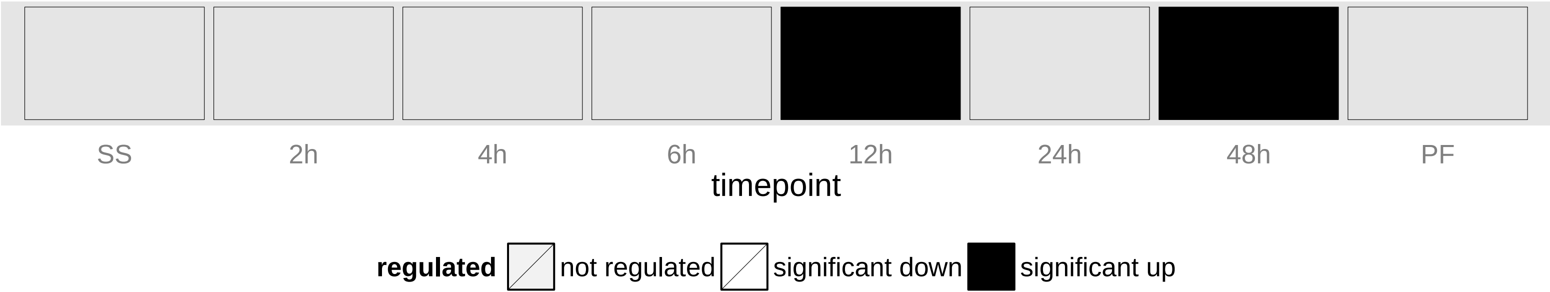

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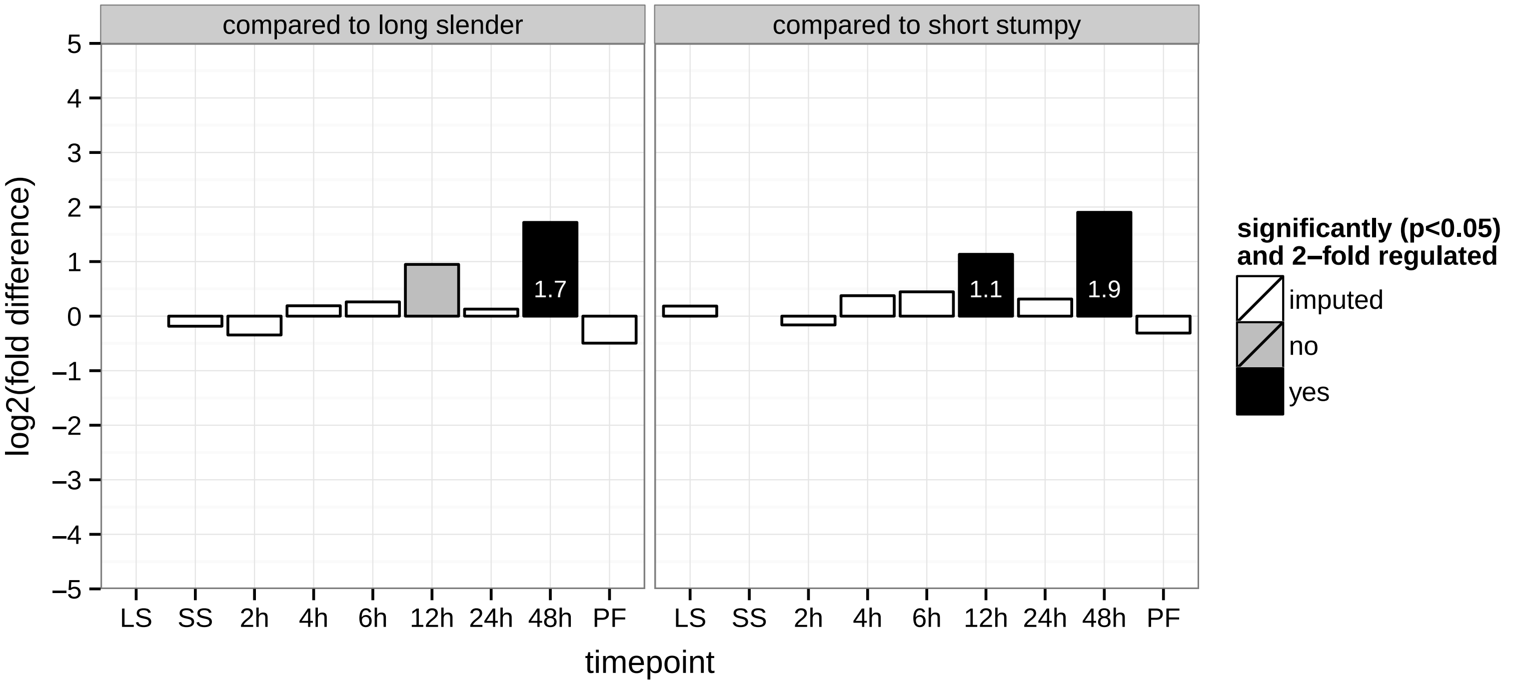
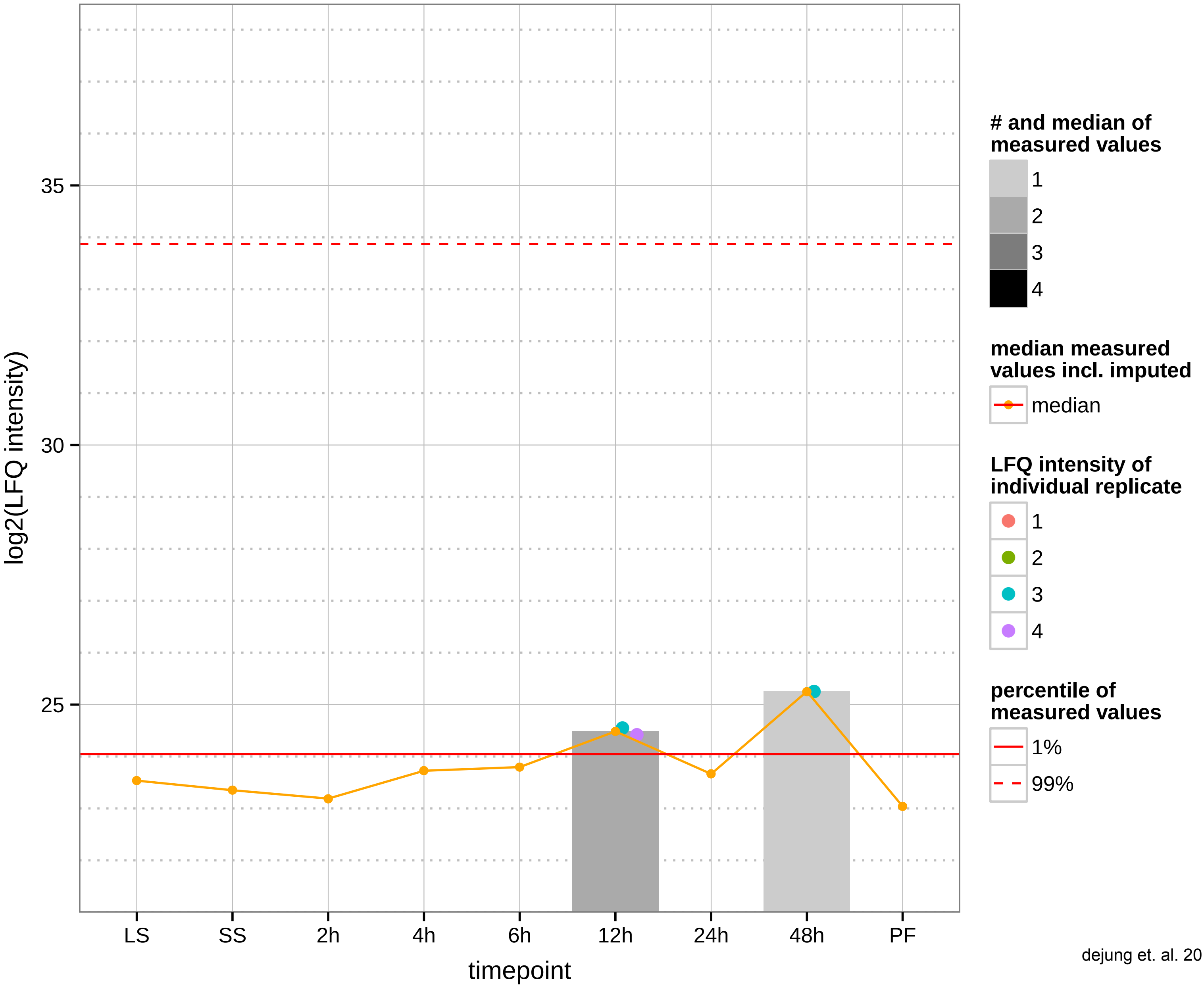
retrotransposon hot spot protein (RHS, pseudogene), putative, chrXI additional, unordered contigs, retrotransposon hot spot p
Tb11.v5.0442;Tb11.1800
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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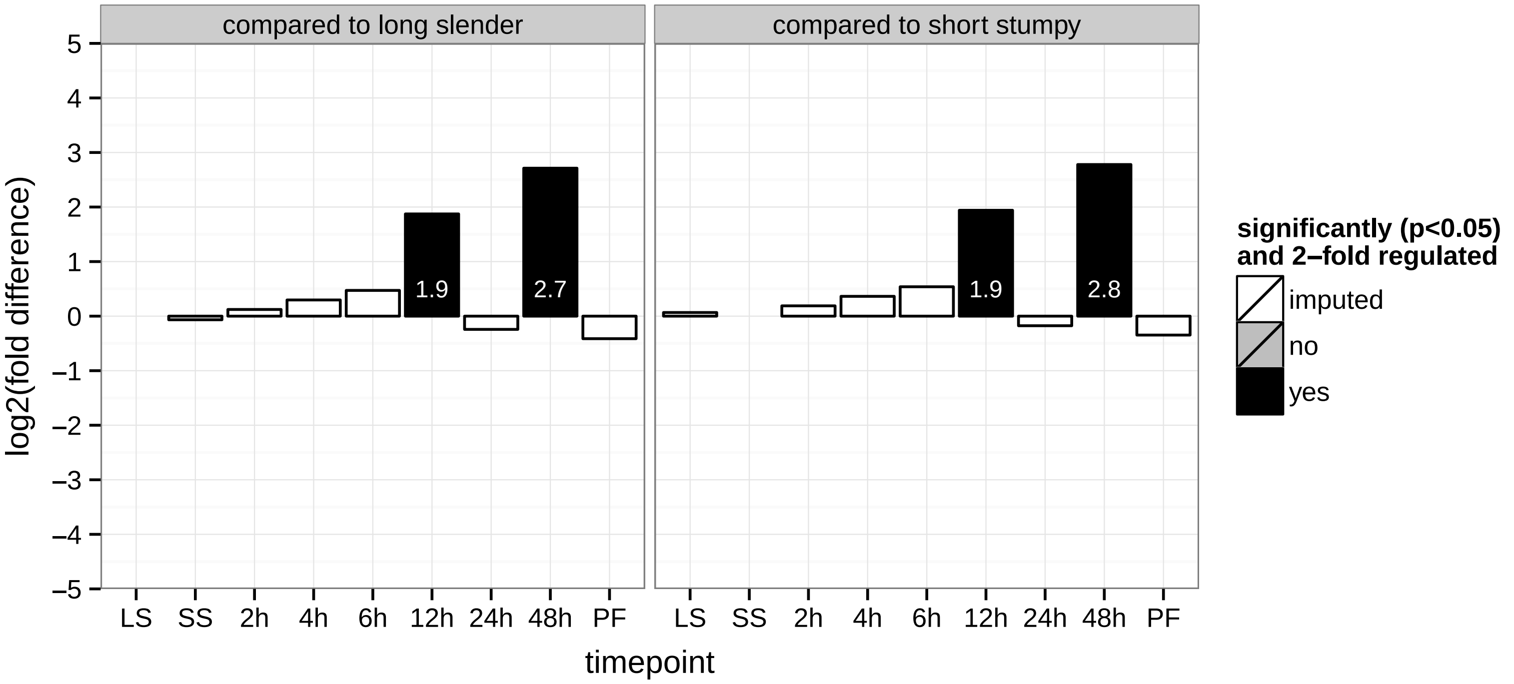
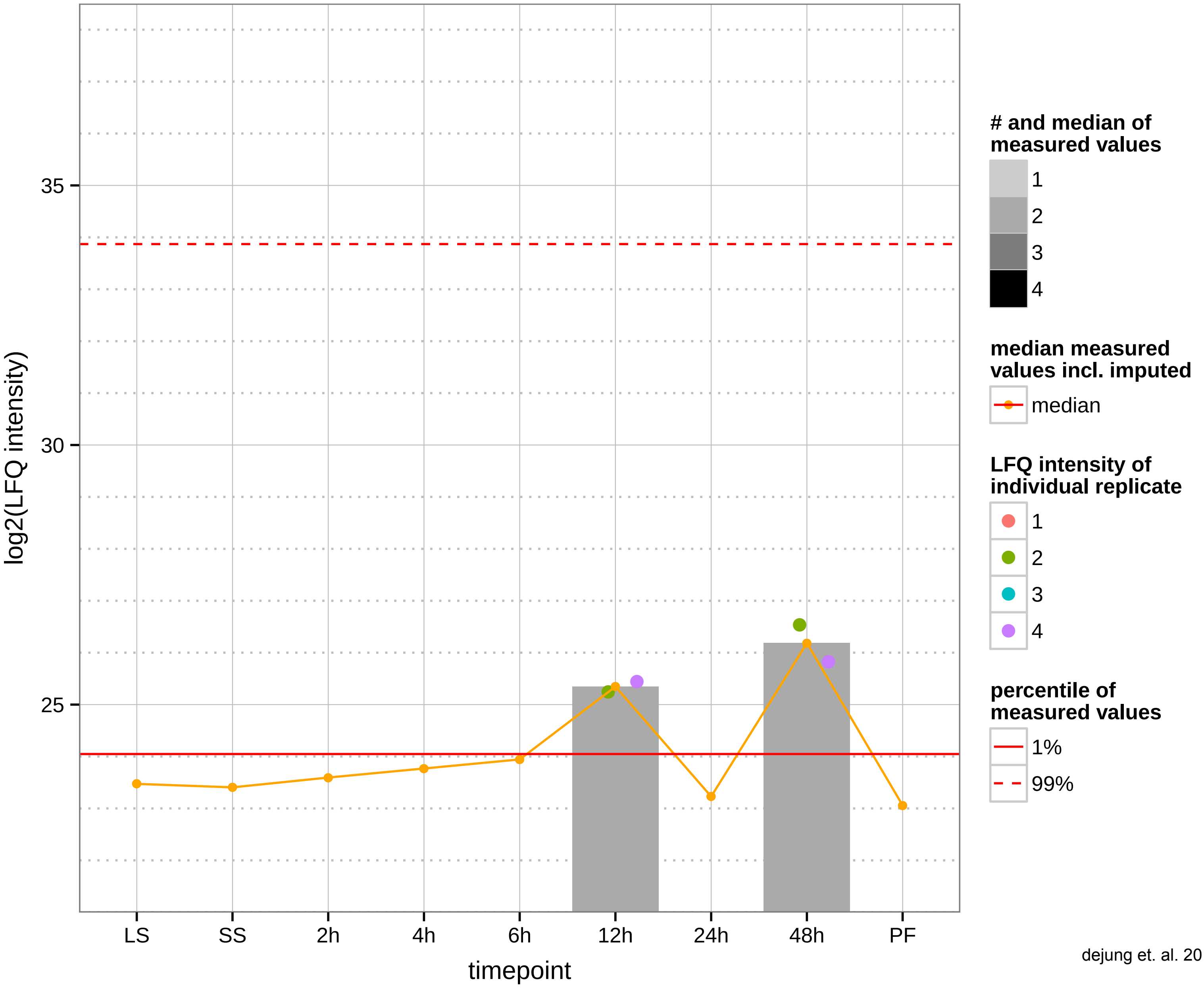
hypothetical protein, conserved
Tb927.7.4510;Tb11.v5.0264
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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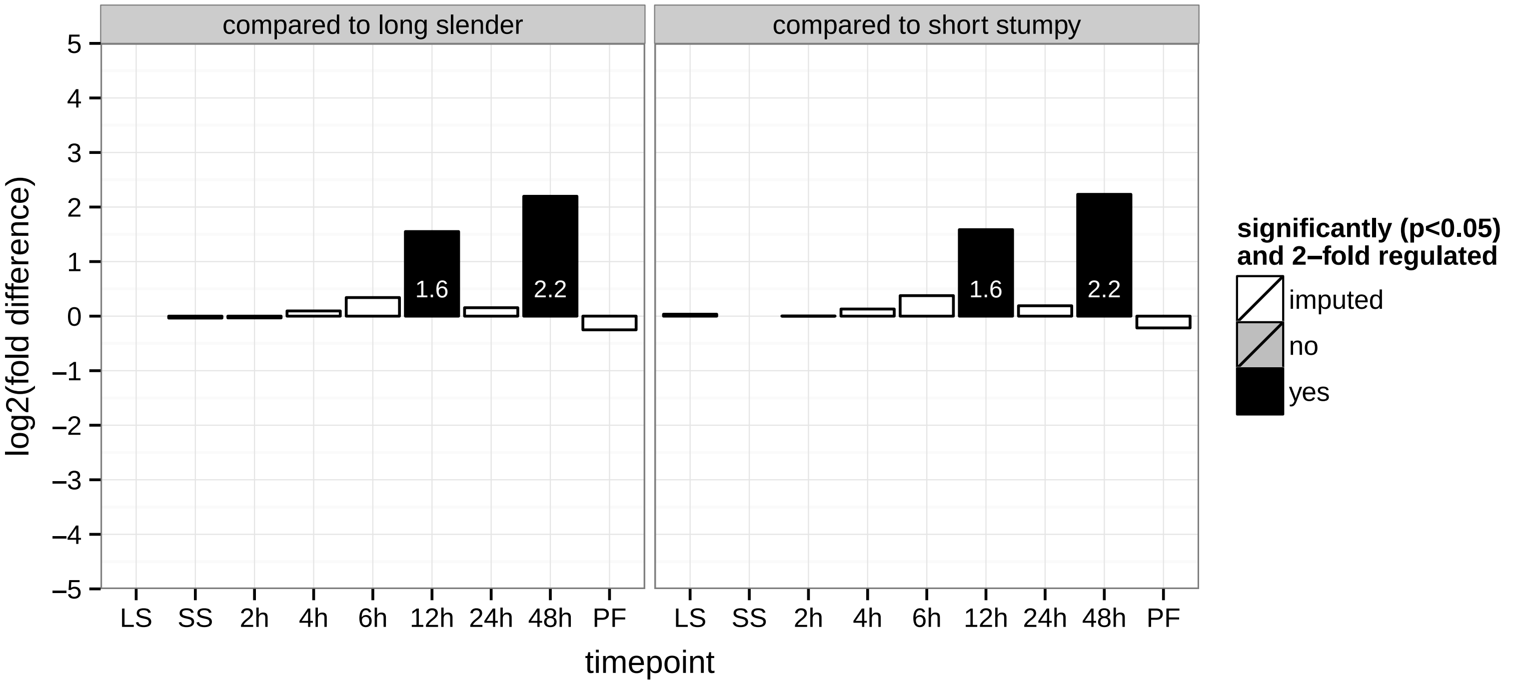
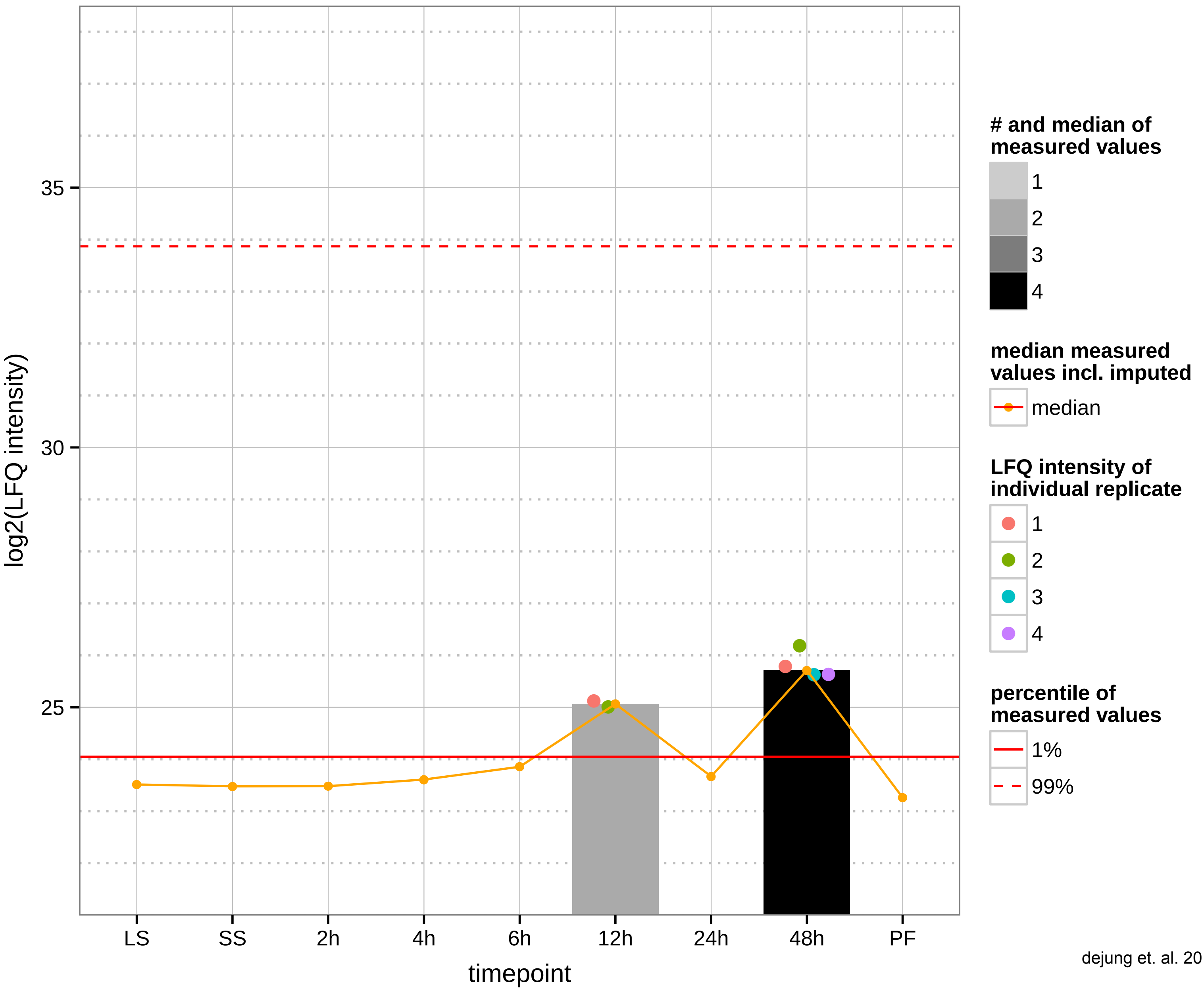
hypothetical protein, conserved
Tb927.1.4220
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: nucleus
PGOP: null





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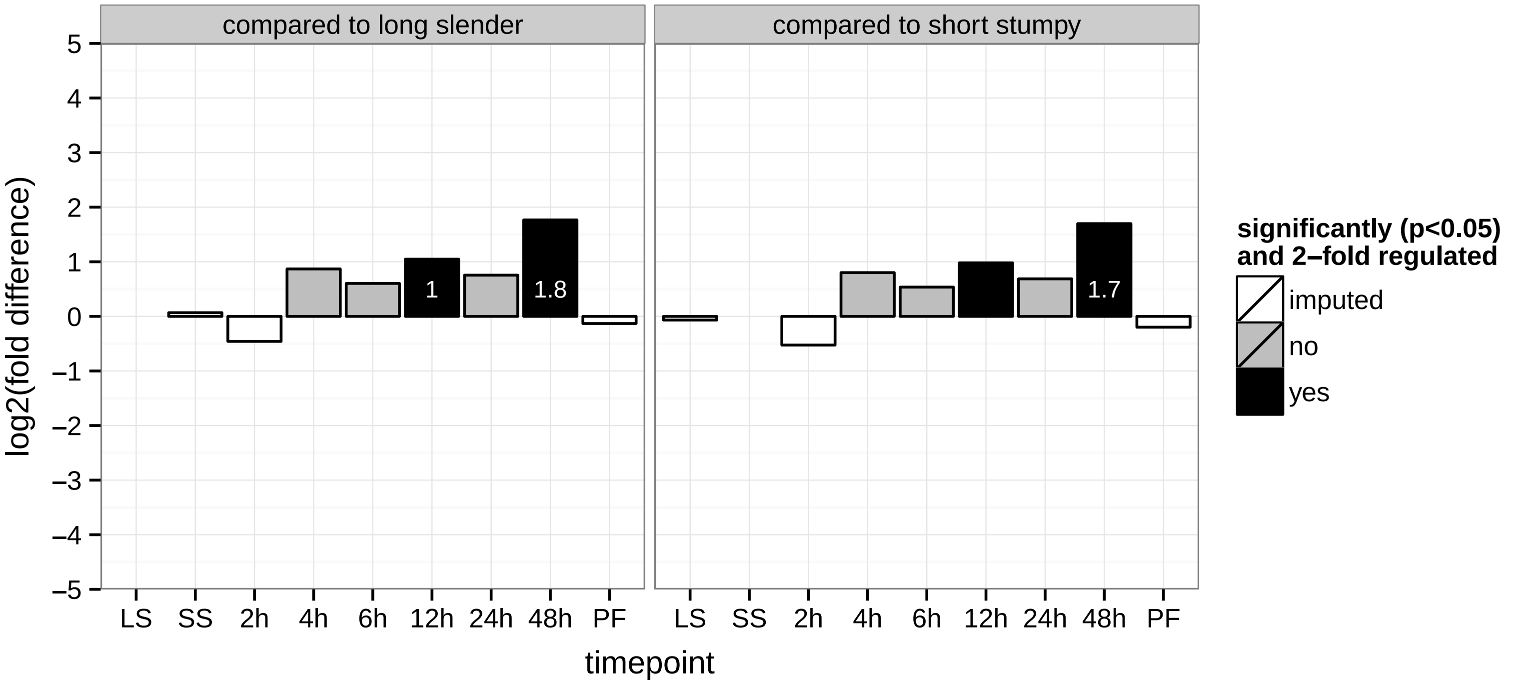
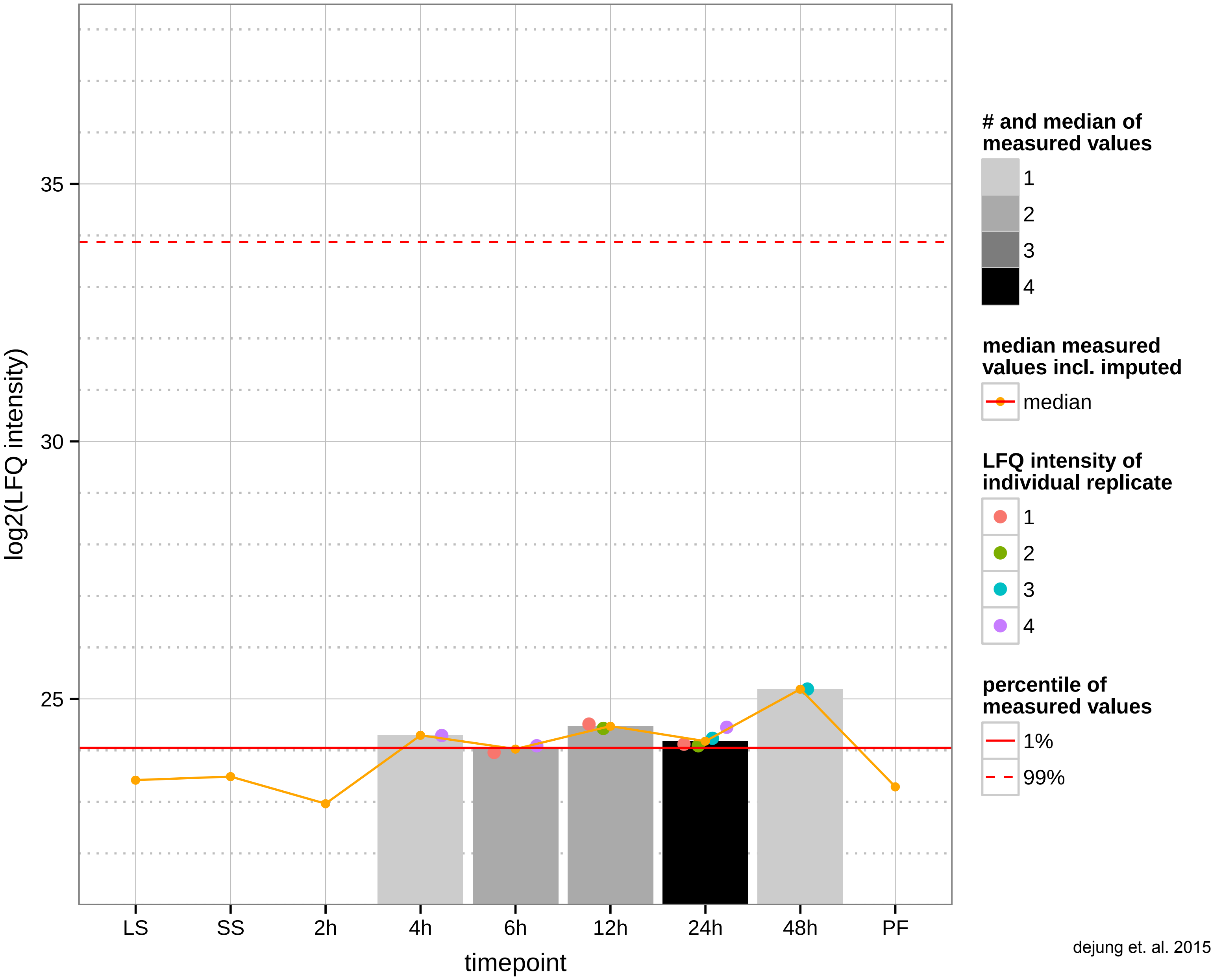
Zinc finger CCCH domain−containing protein 35 (ZC3H35)
Tb927.10.12740
AGOF: RNA binding, nucleic acid binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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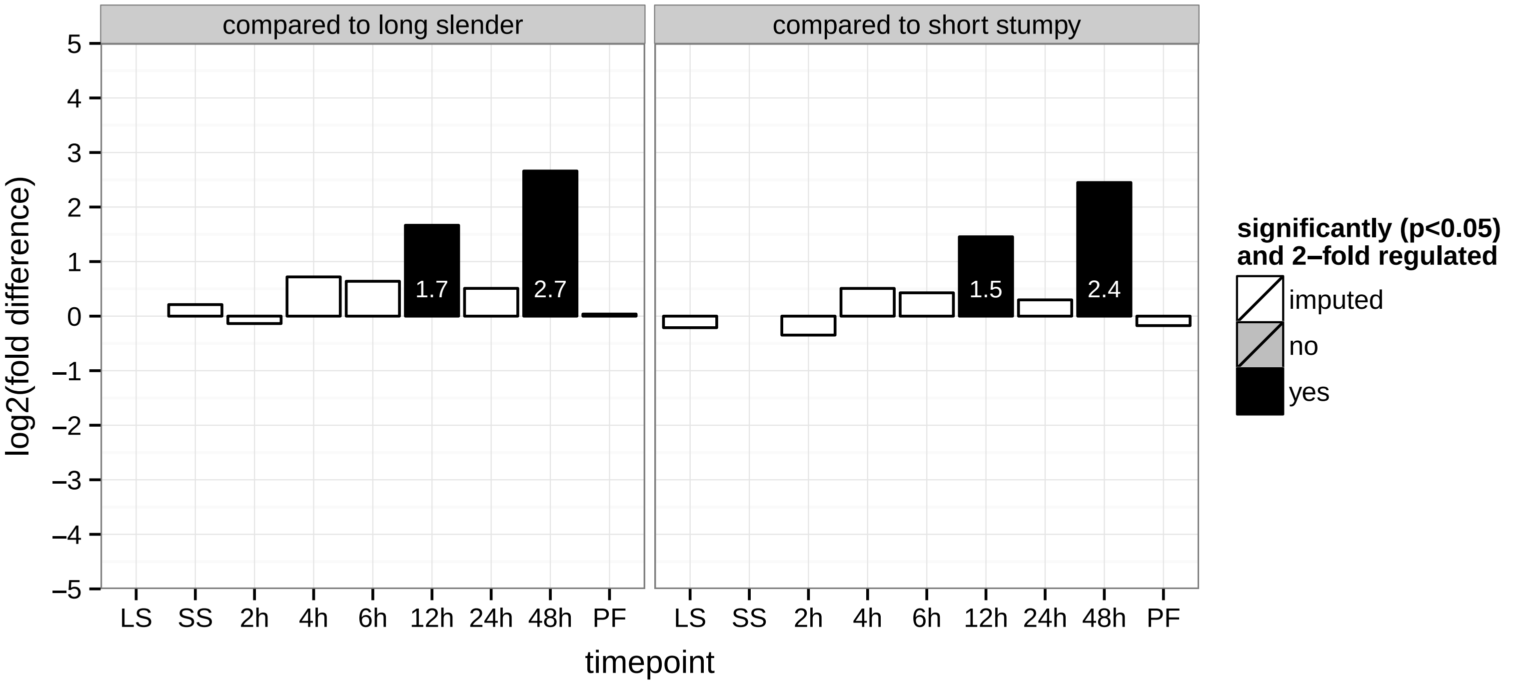
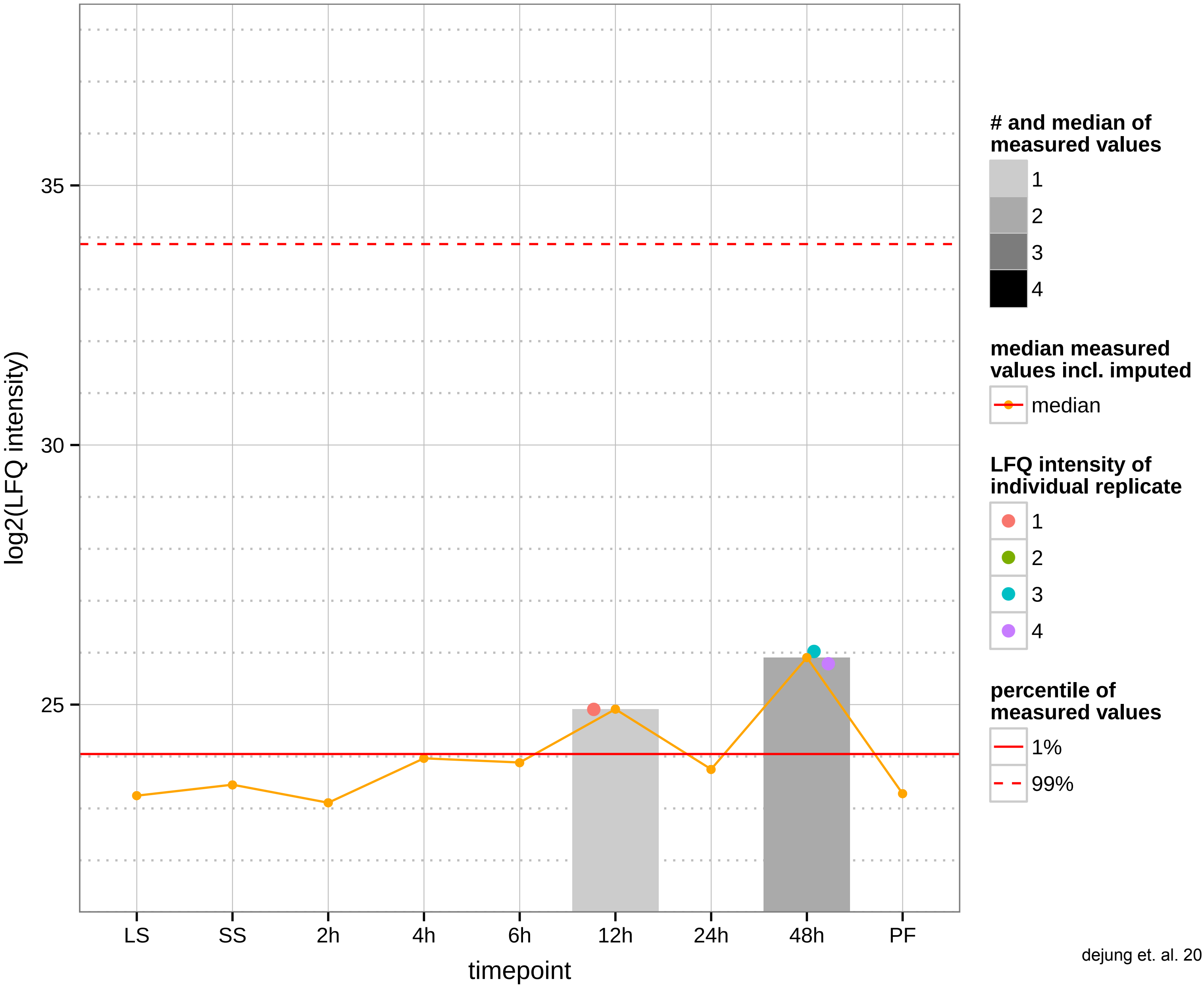
sjogren s syndrome nuclear autoantigen 1, putative
Tb927.10.14110
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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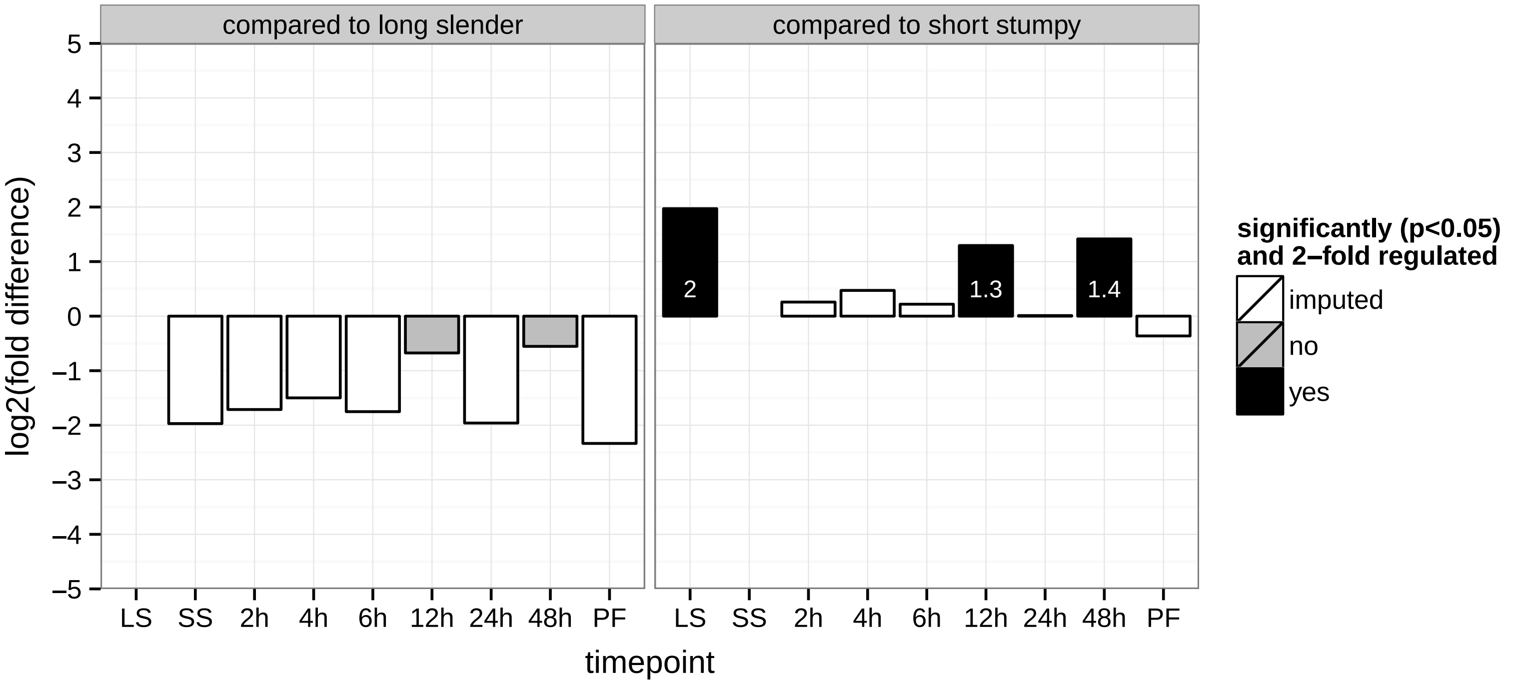
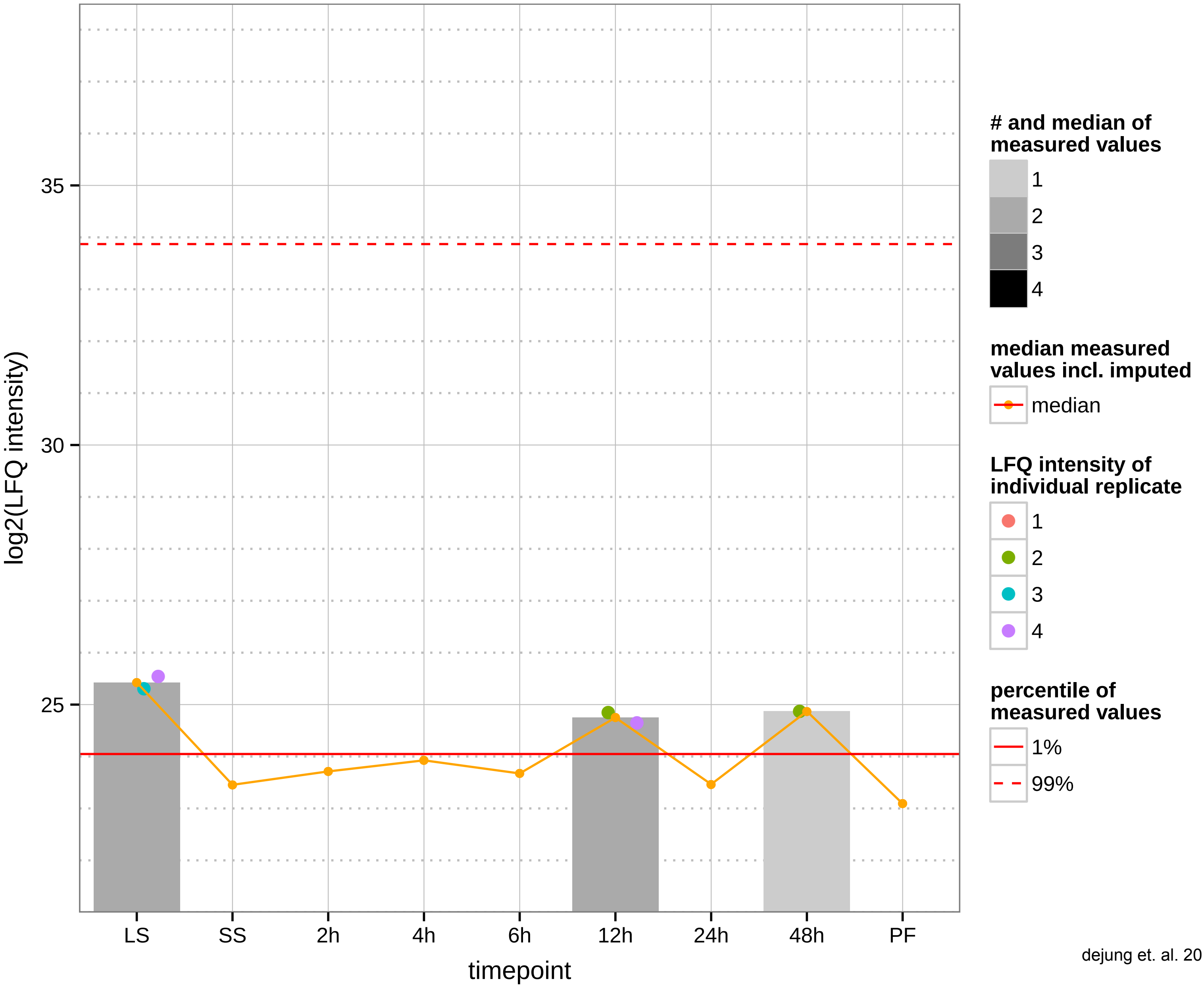
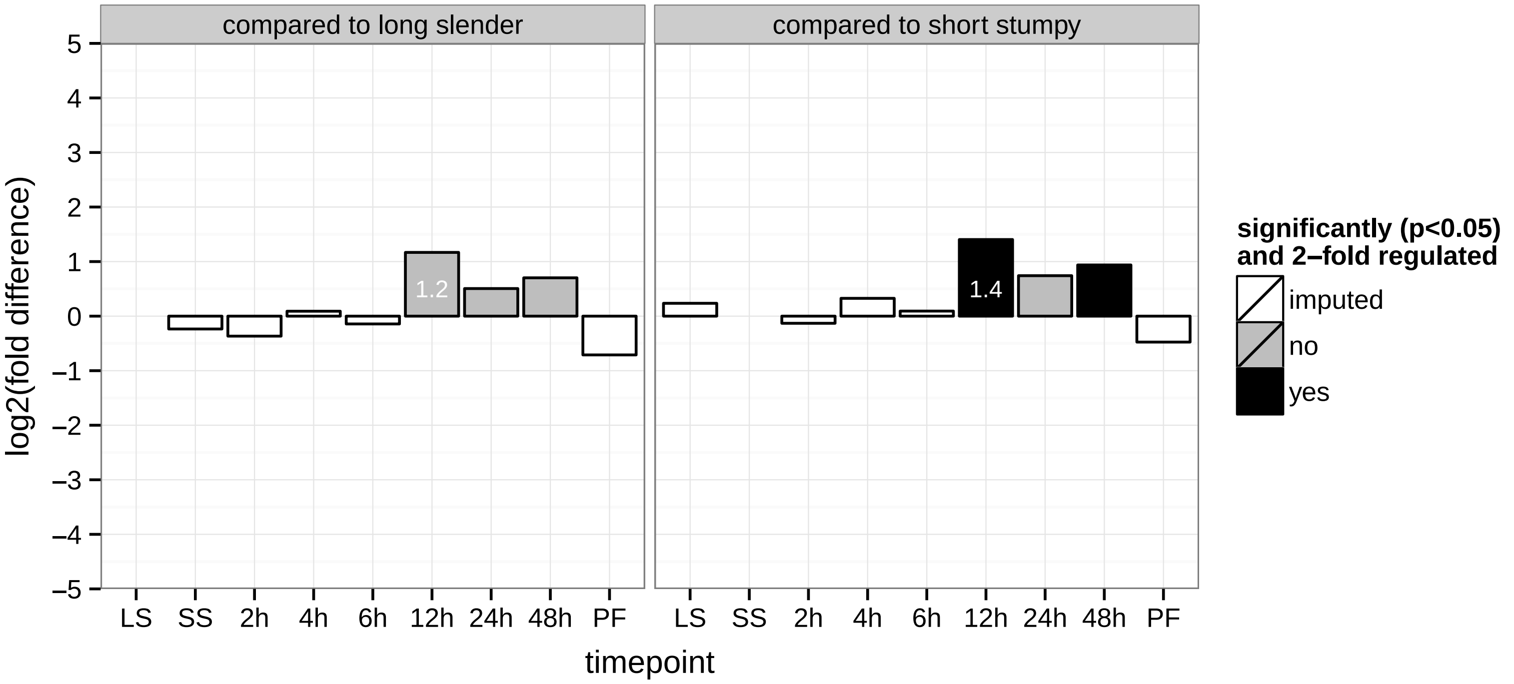
hypothetical protein, conserved
Tb927.11.11790
AGOF: nucleic acid binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null

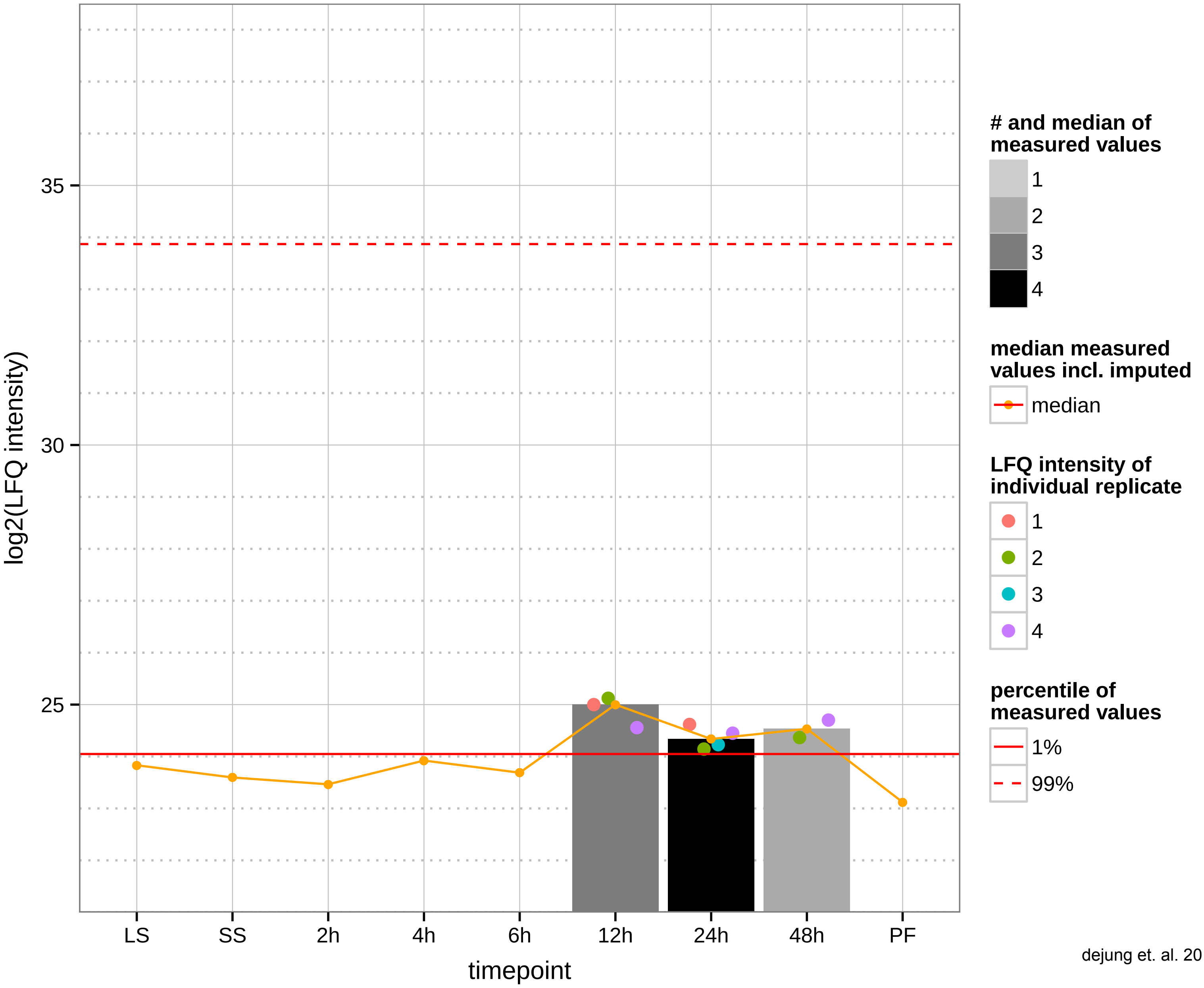




dejung et. al. 2015

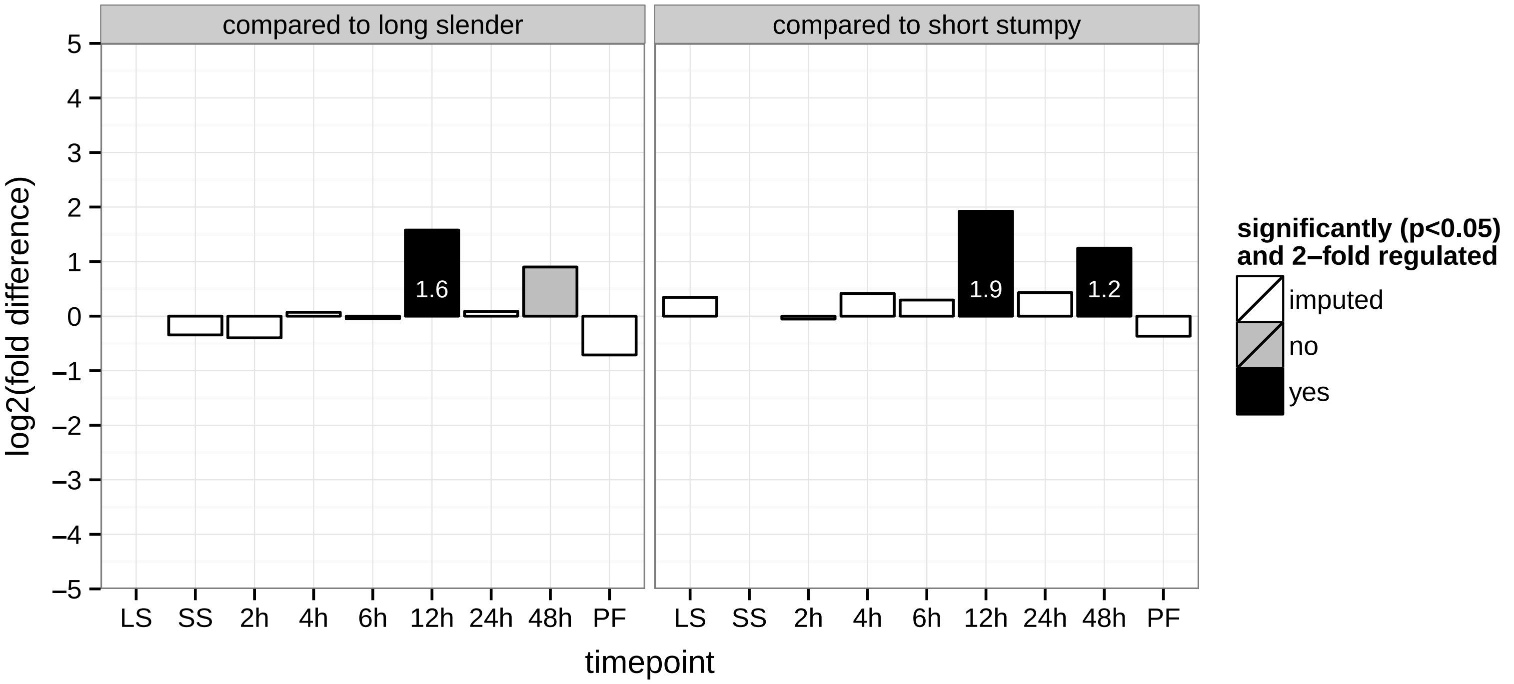
Polypeptide deformylase 1
Tb927.11.14520
AGOF: formylmethionine deformylase activity, iron ion binding, peptide deformylase activity
AGOC: null
AGOP: cellular protein modification process, translation
PGOF: null
PGOC: null
PGOP: null

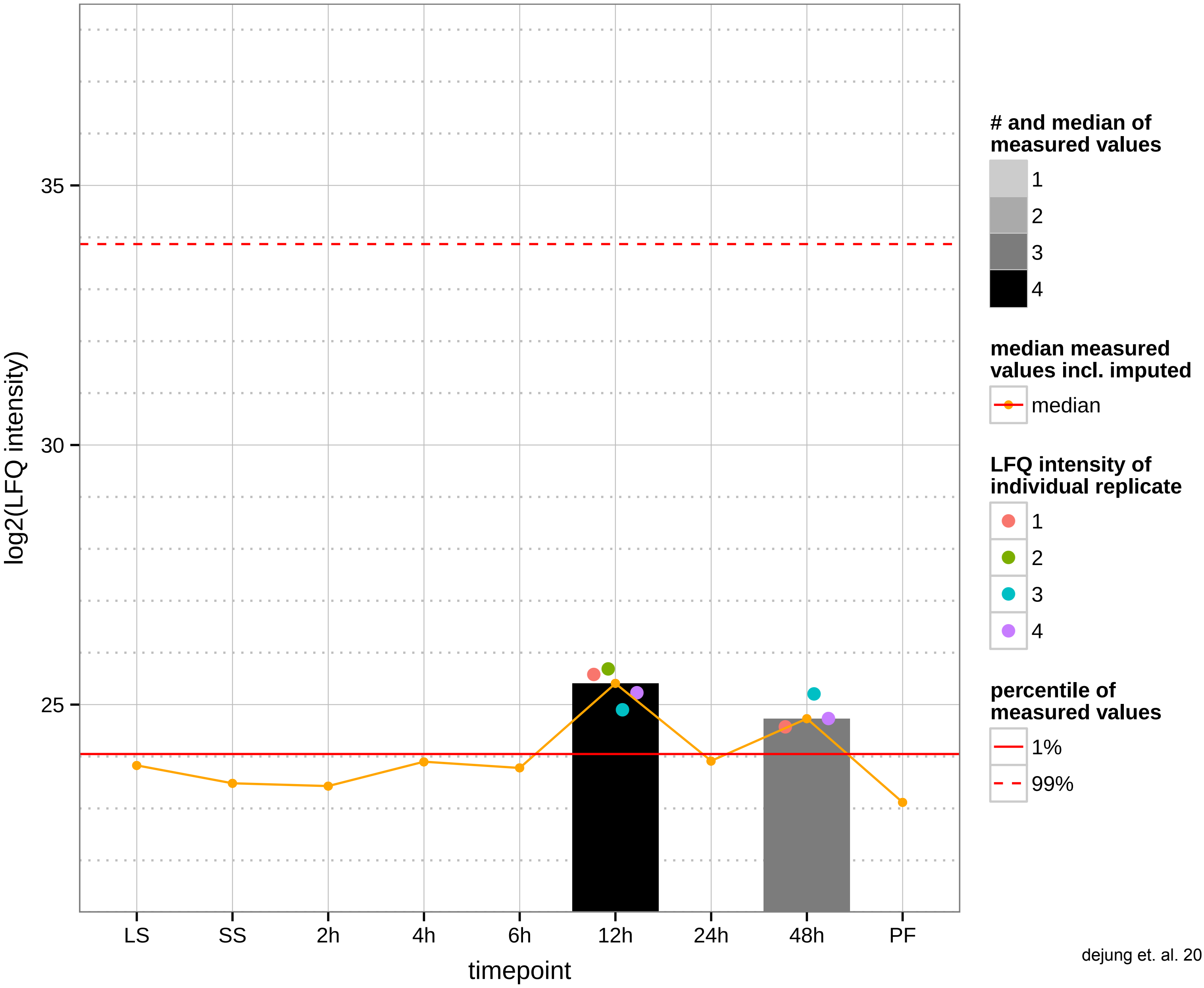




dejung et. al. 2015

aldo/keto reductase, putative
Tb927.11.5360
AGOF: aldo–keto reductase (NADP) activity
AGOC: cytoplasm, nucleus
AGOP: metabolic process, oxidation–reduction process
PGOF: null
PGOC: null
PGOP: null





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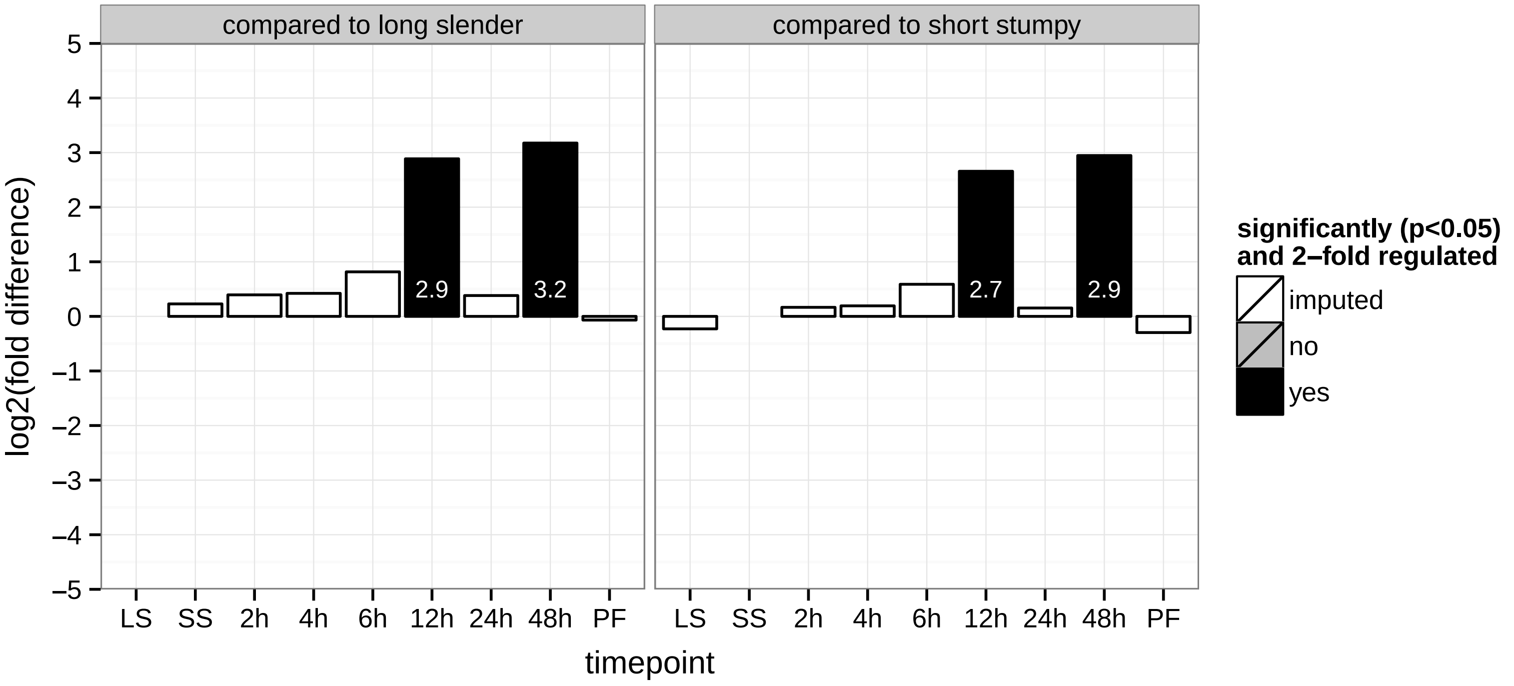
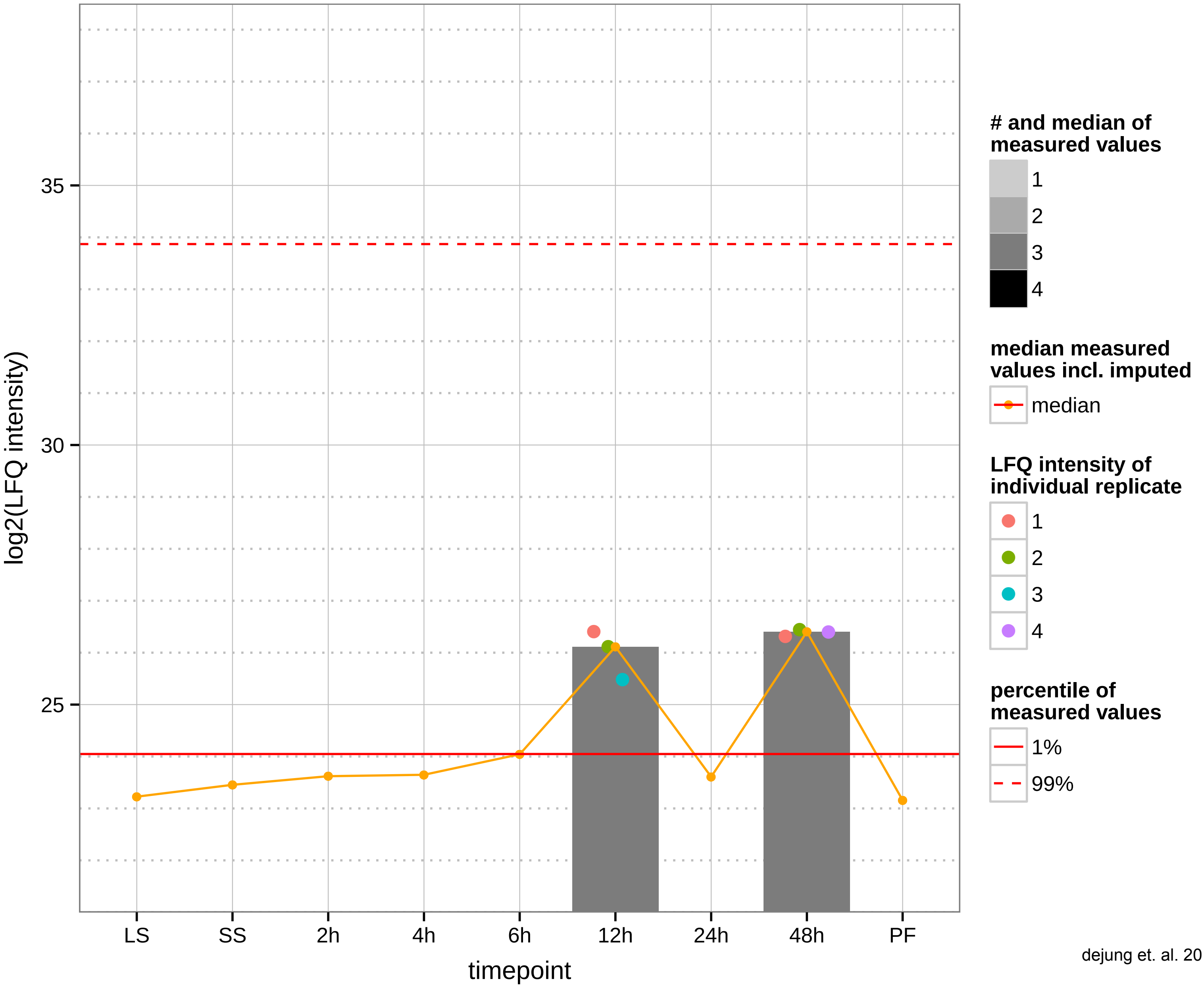
hypothetical protein, conserved
Tb927.11.8860
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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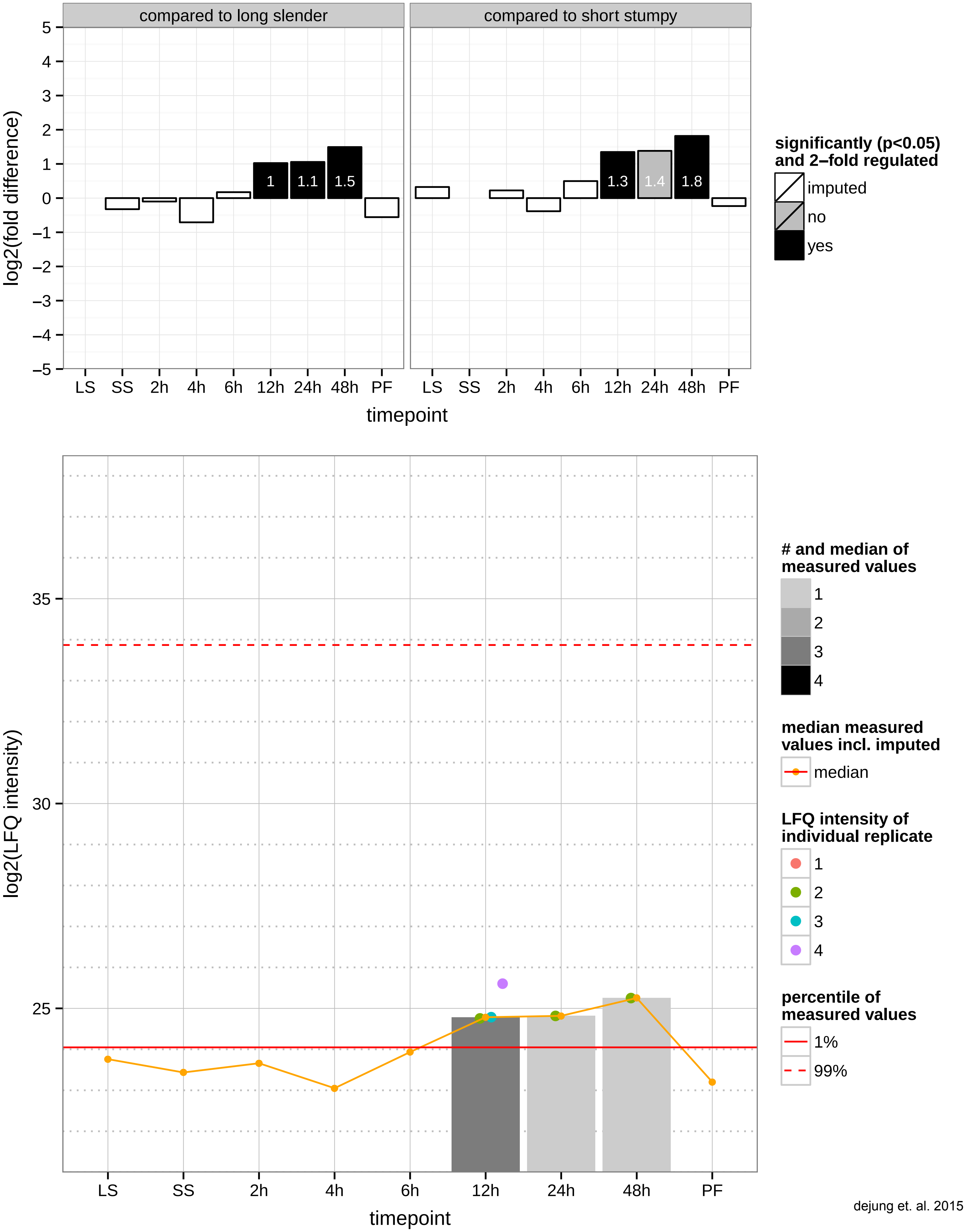
hypothetical protein, conserved
Tb927.2.2270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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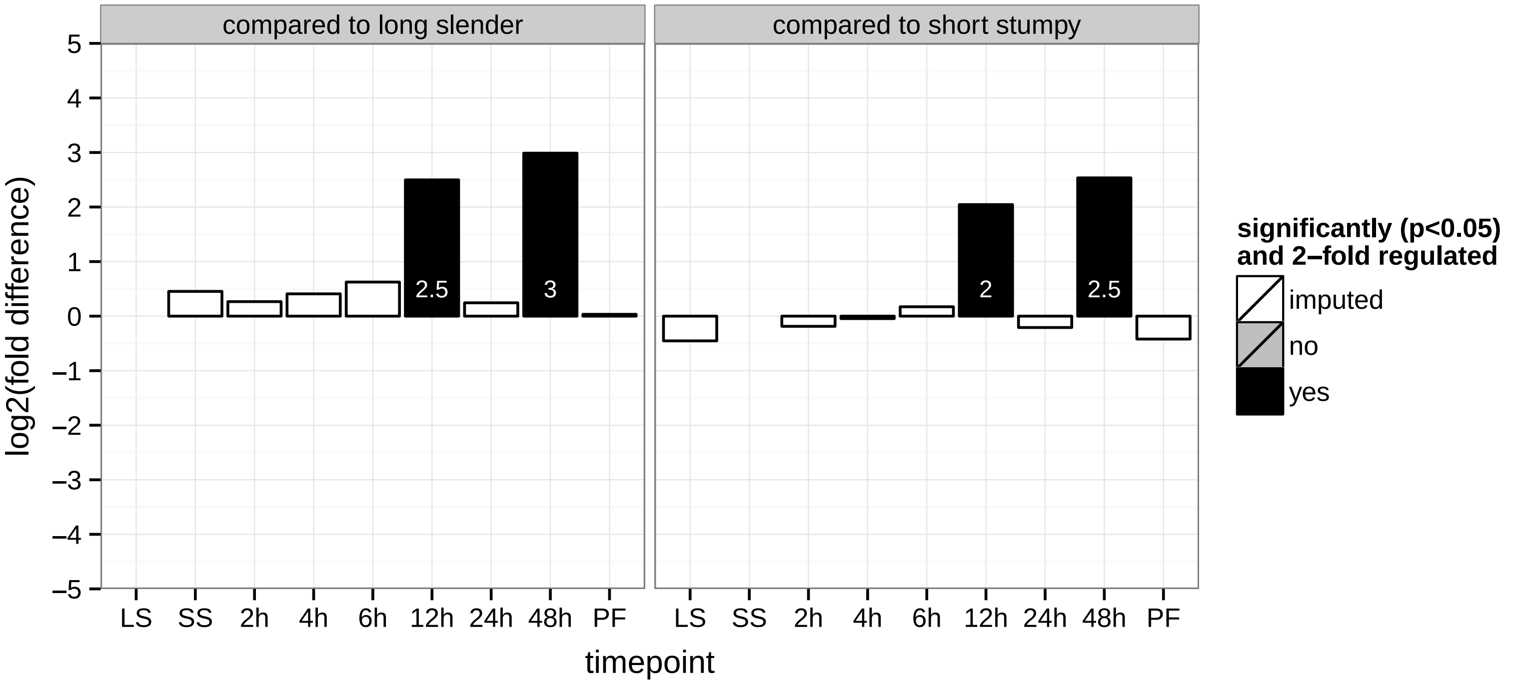
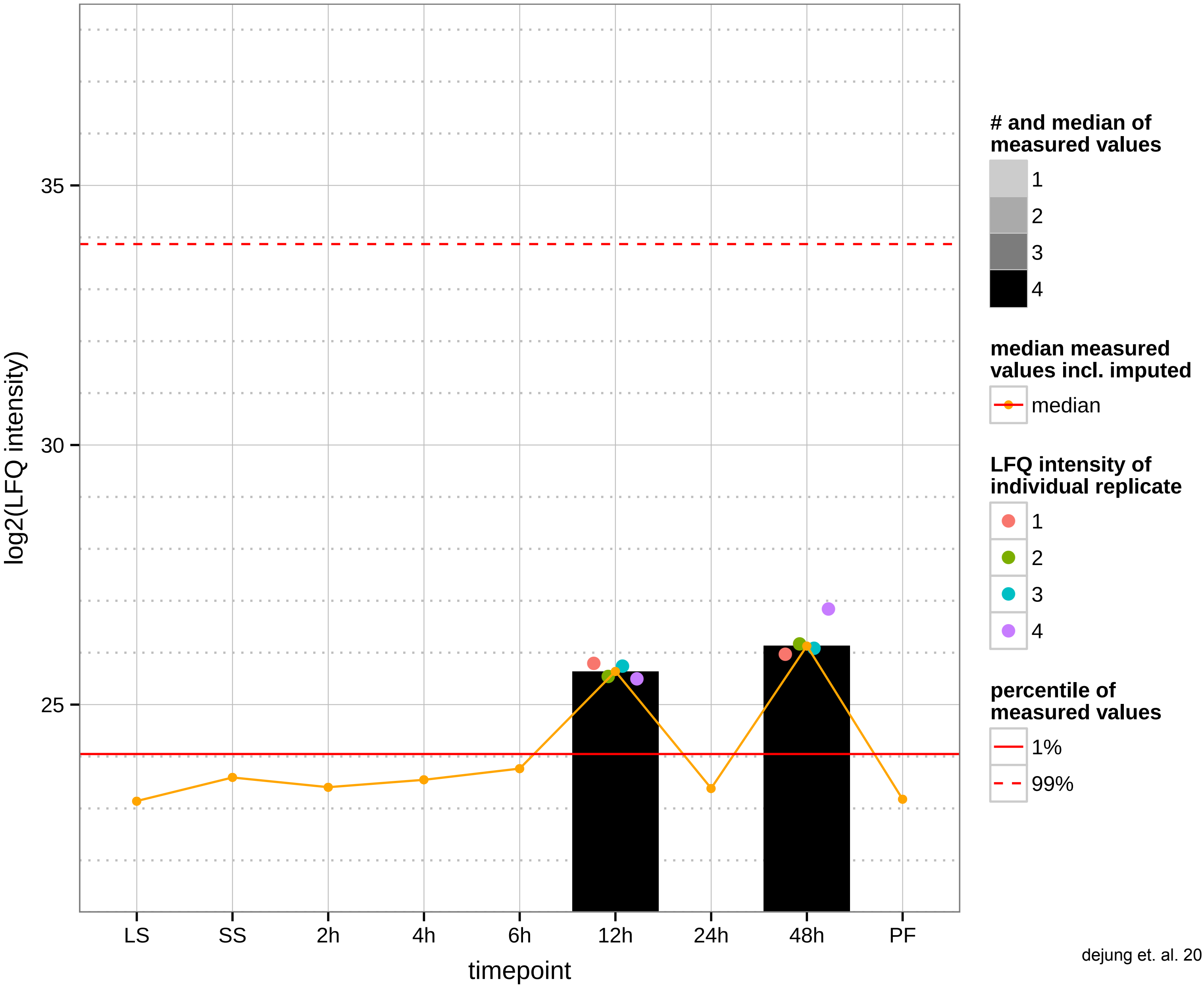
hypothetical protein, conserved
Tb927.2.4000
AGOF: nucleic acid binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null





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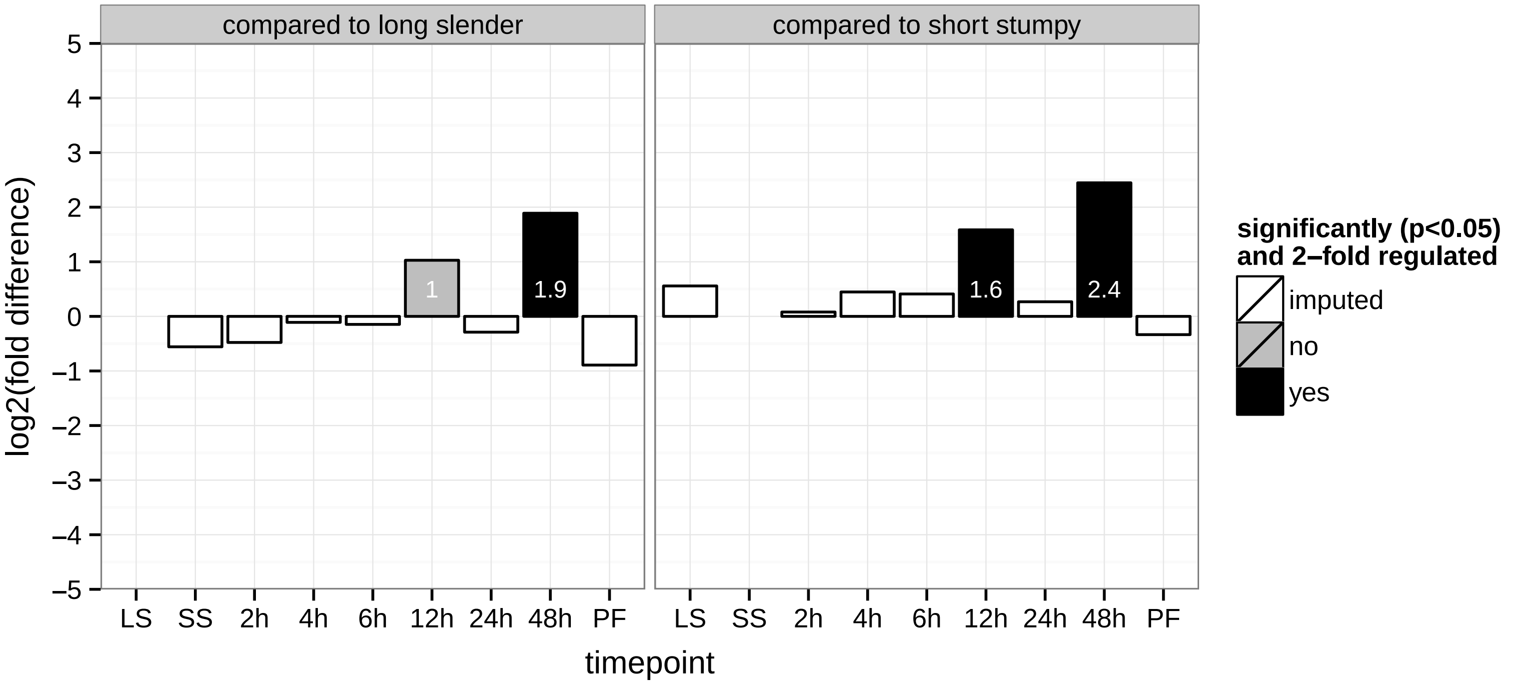
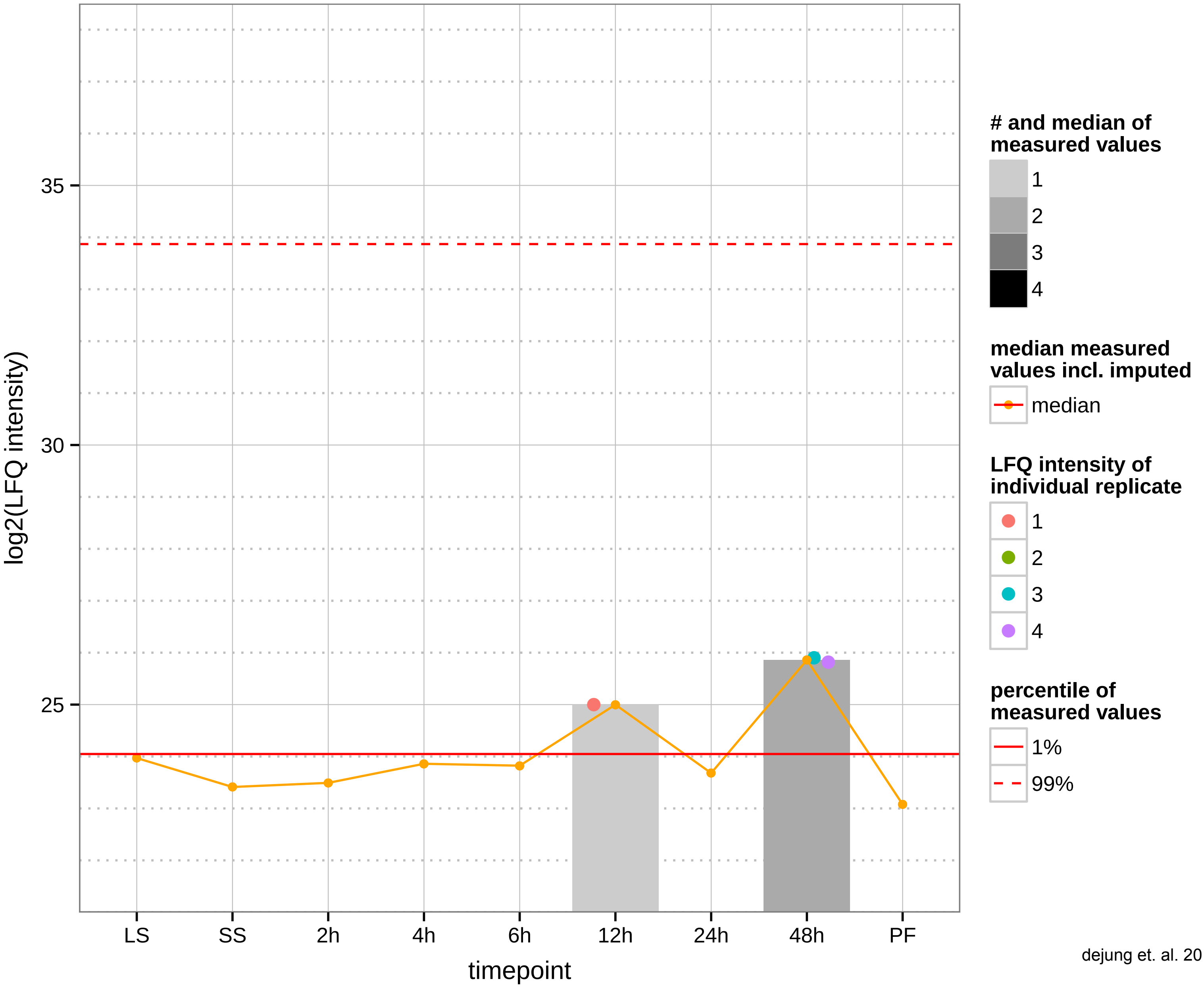
DNA polymerase delta subunit 2, putative
Tb927.3.1130
AGOF: DNA binding, DNA−directed DNA polymerase activity
AGOC: nucleus
AGOP: DNA replication
PGOF: DNA binding, DNA−directed DNA polymerase activity
PGOC: null
PGOP: DNA replication





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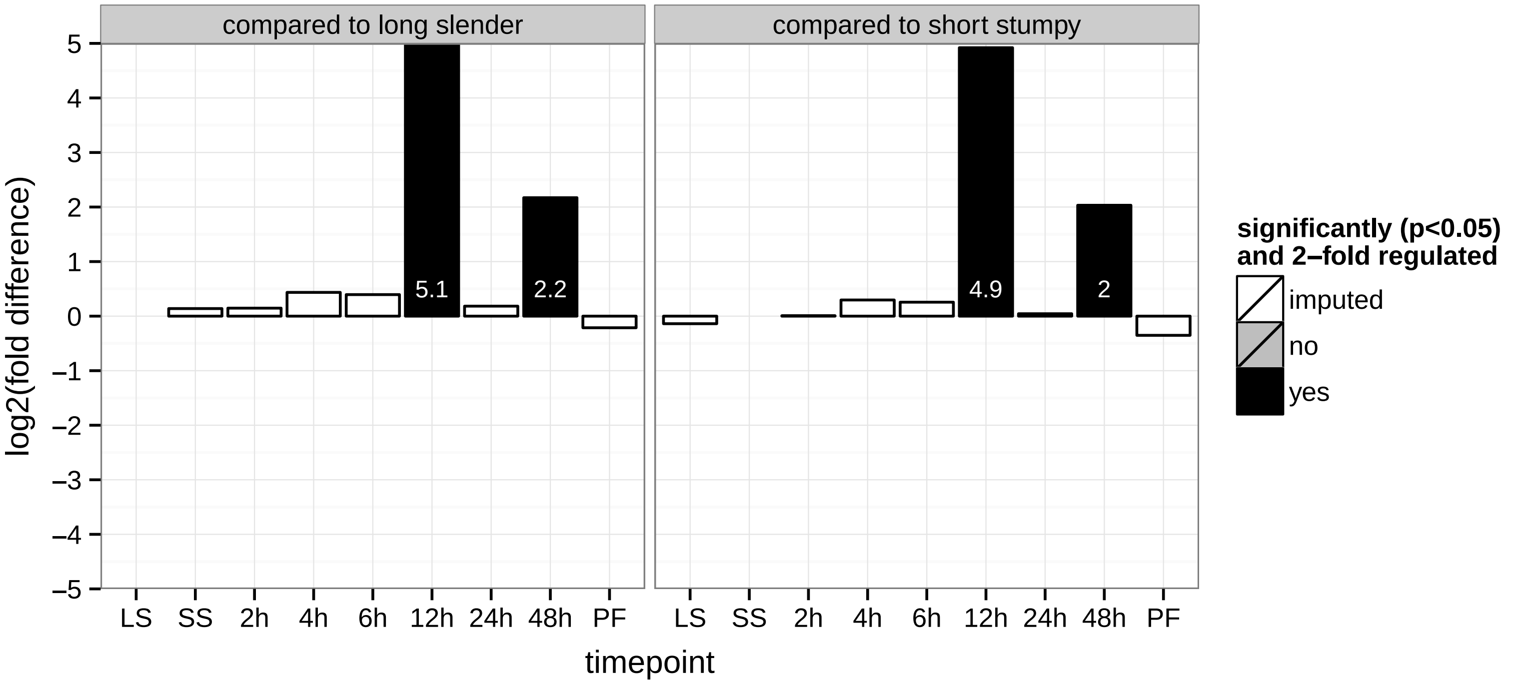
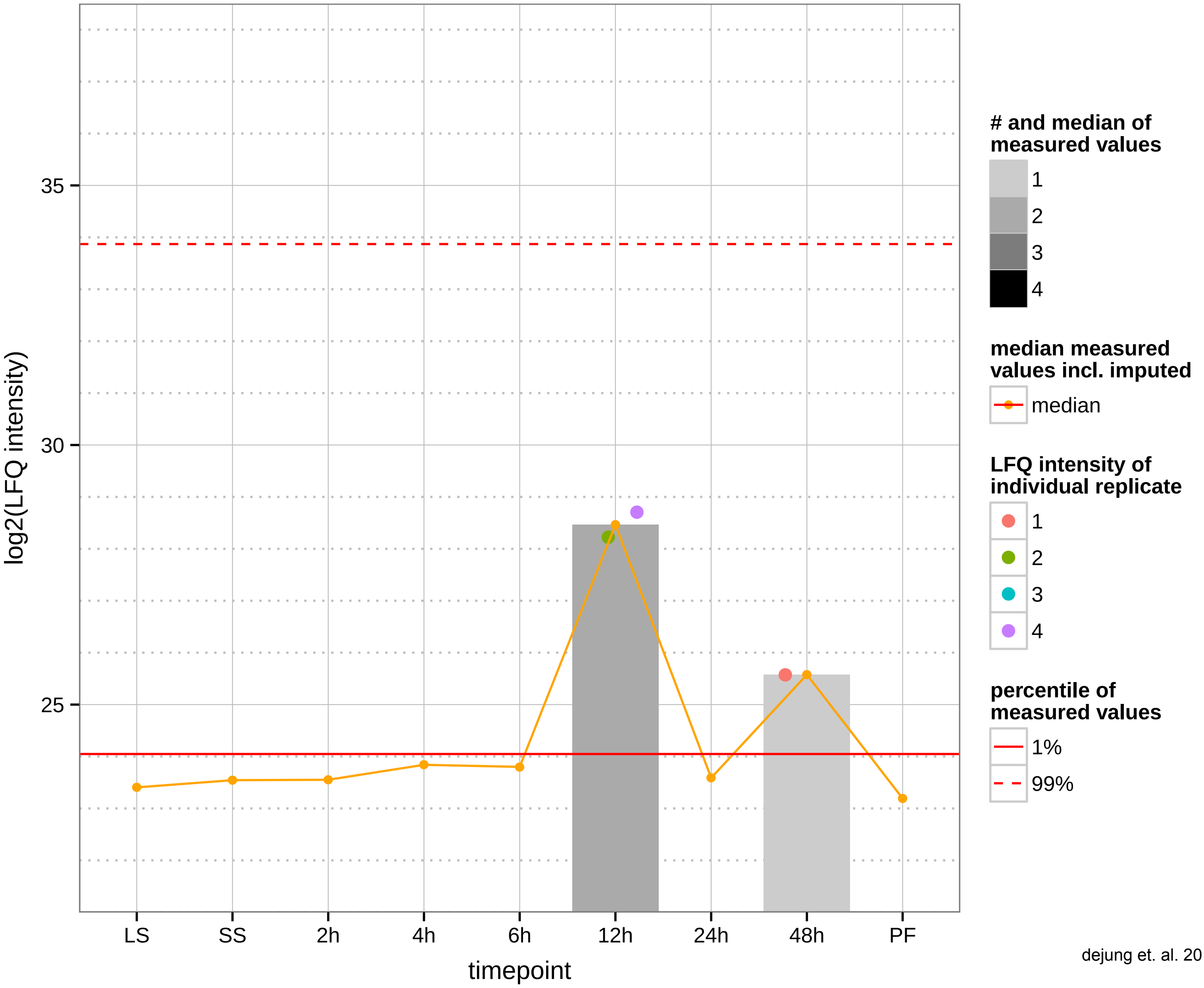
hypothetical protein, conserved
Tb927.3.4060
AGOF: asparagine synthase (glutamine−hydrolyzing) activity
AGOC: null
AGOP: asparagine biosynthetic process
PGOF: asparagine synthase (glutamine−hydrolyzing) activity
PGOC: null
PGOP: asparagine biosynthetic process





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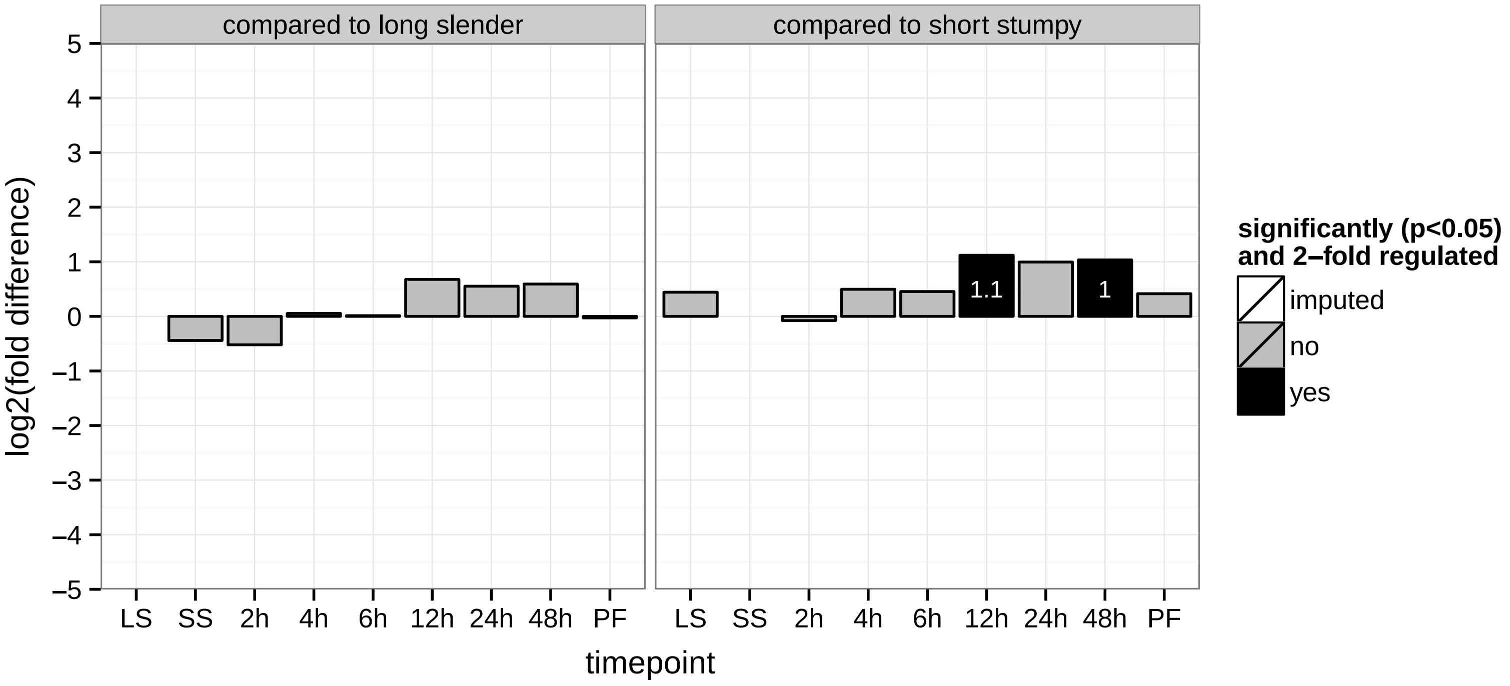
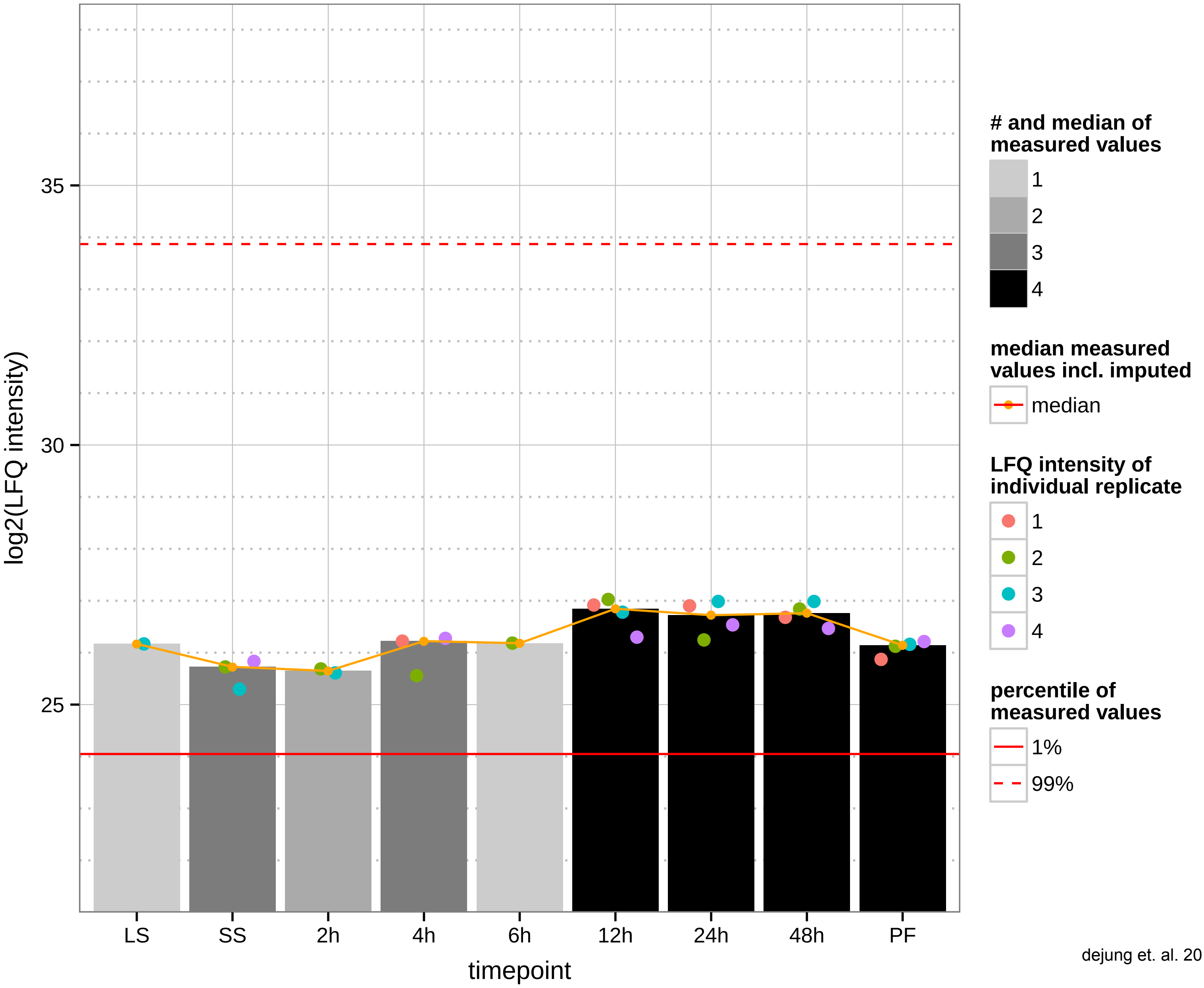
hypothetical protein, conserved
Tb927.4.2280
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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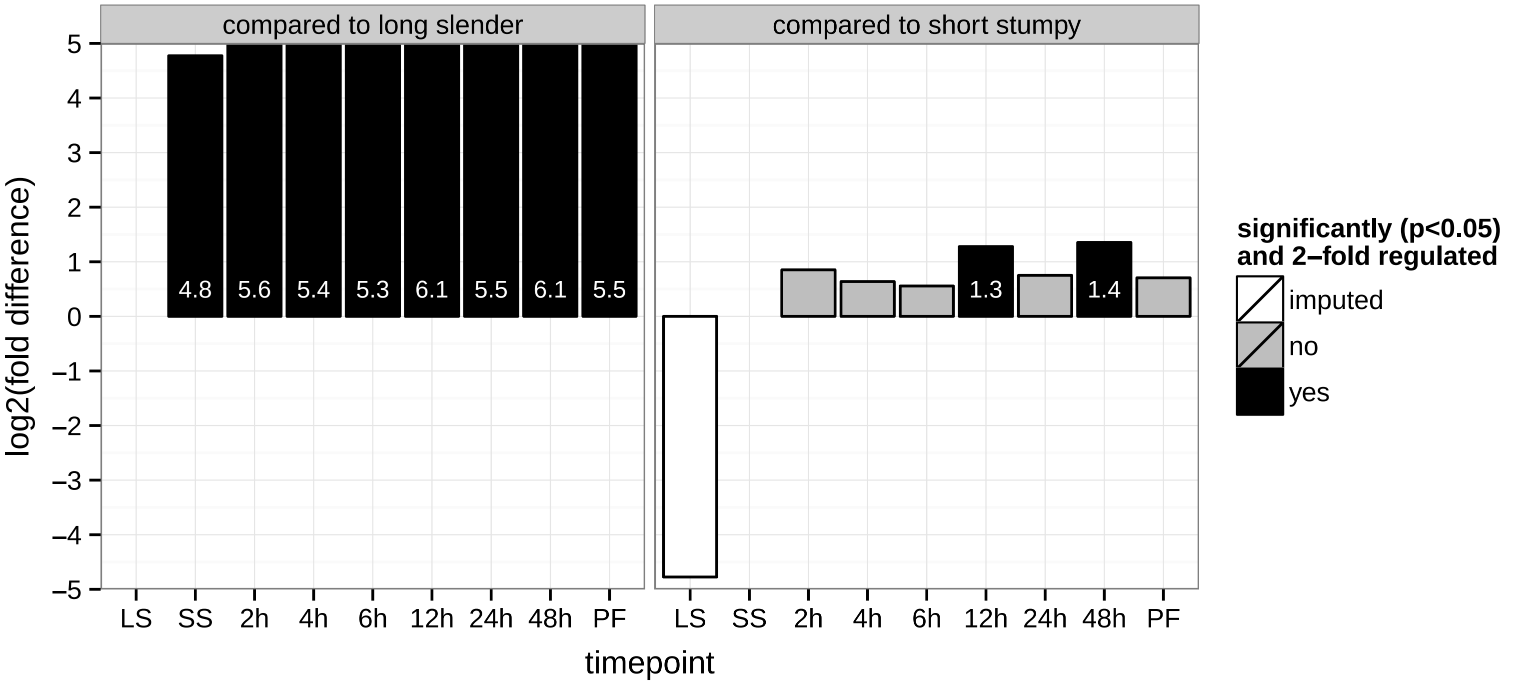
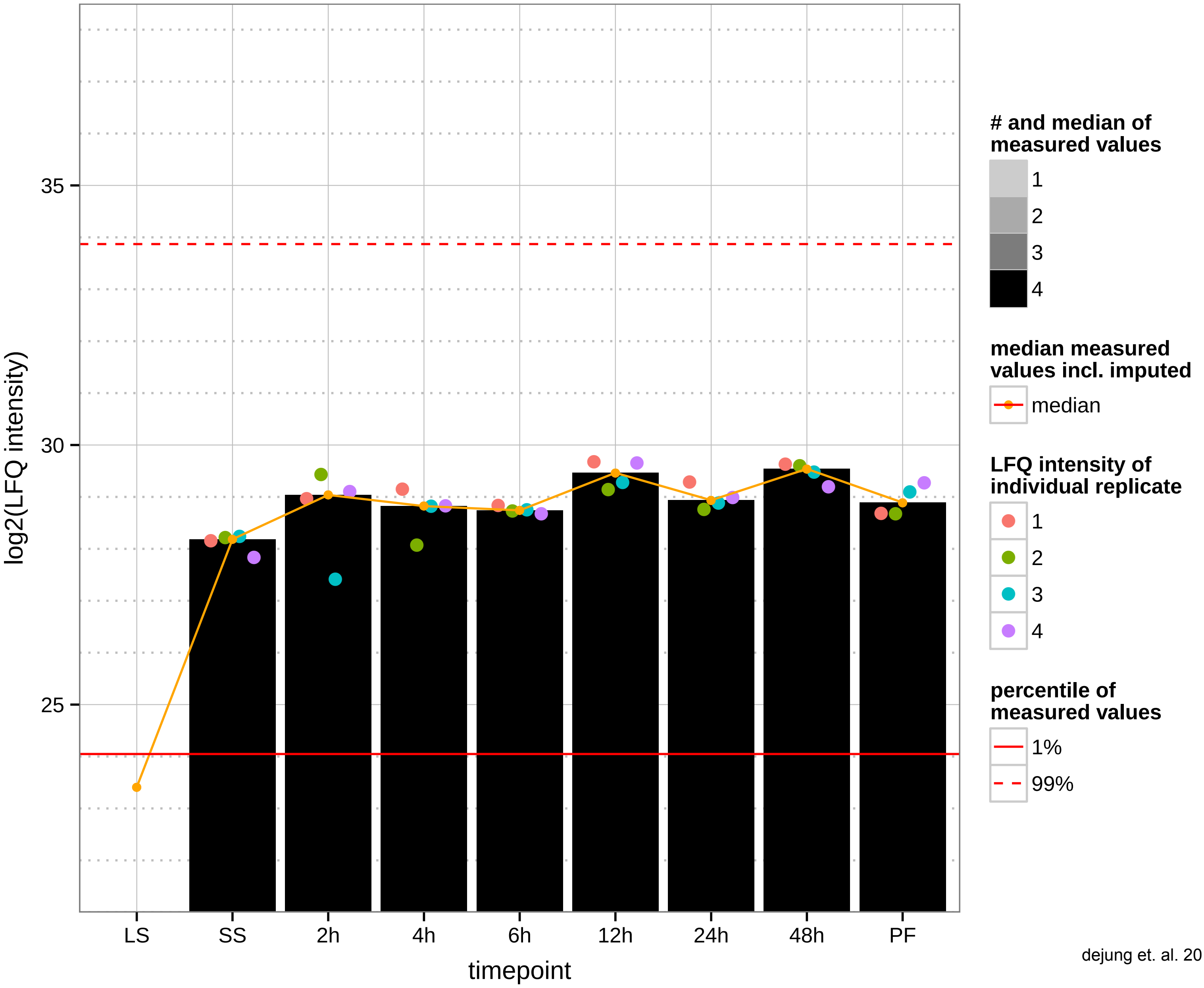
hypothetical protein, conserved
Tb927.6.2390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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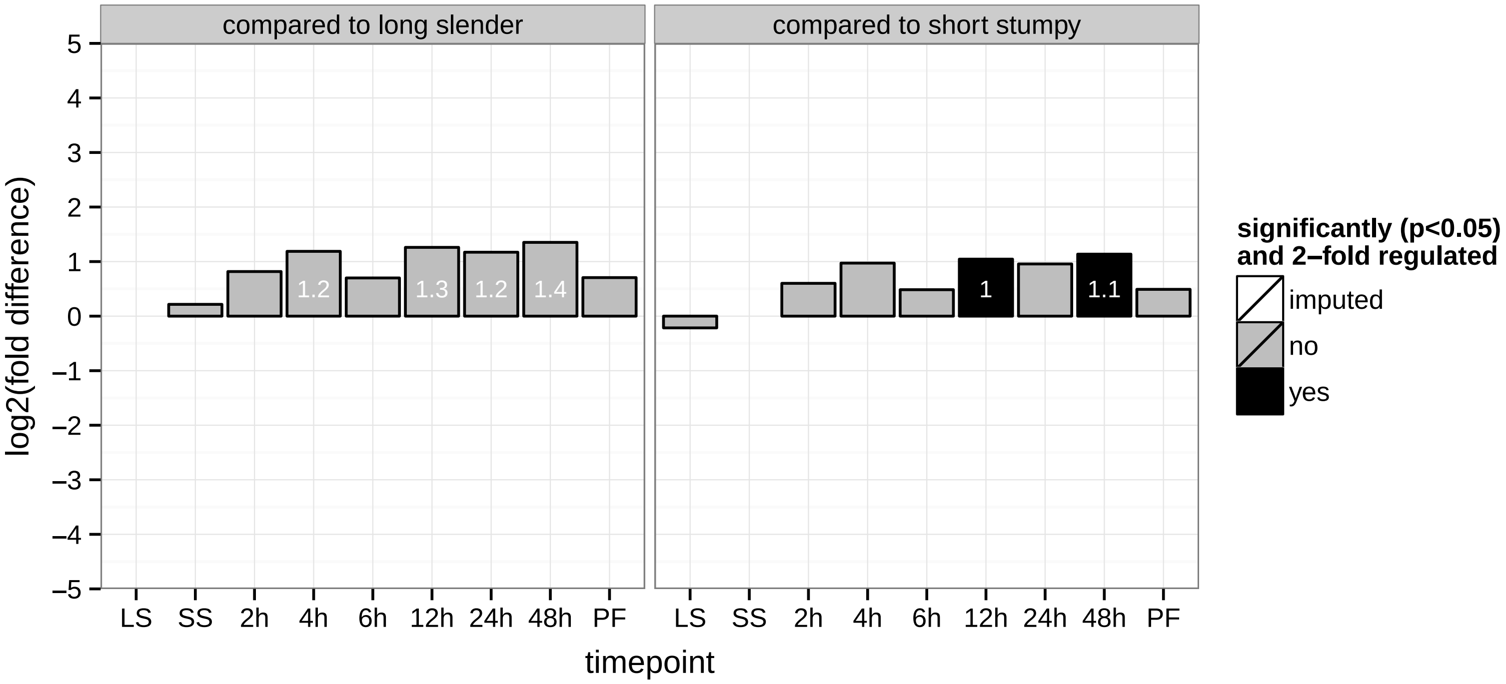
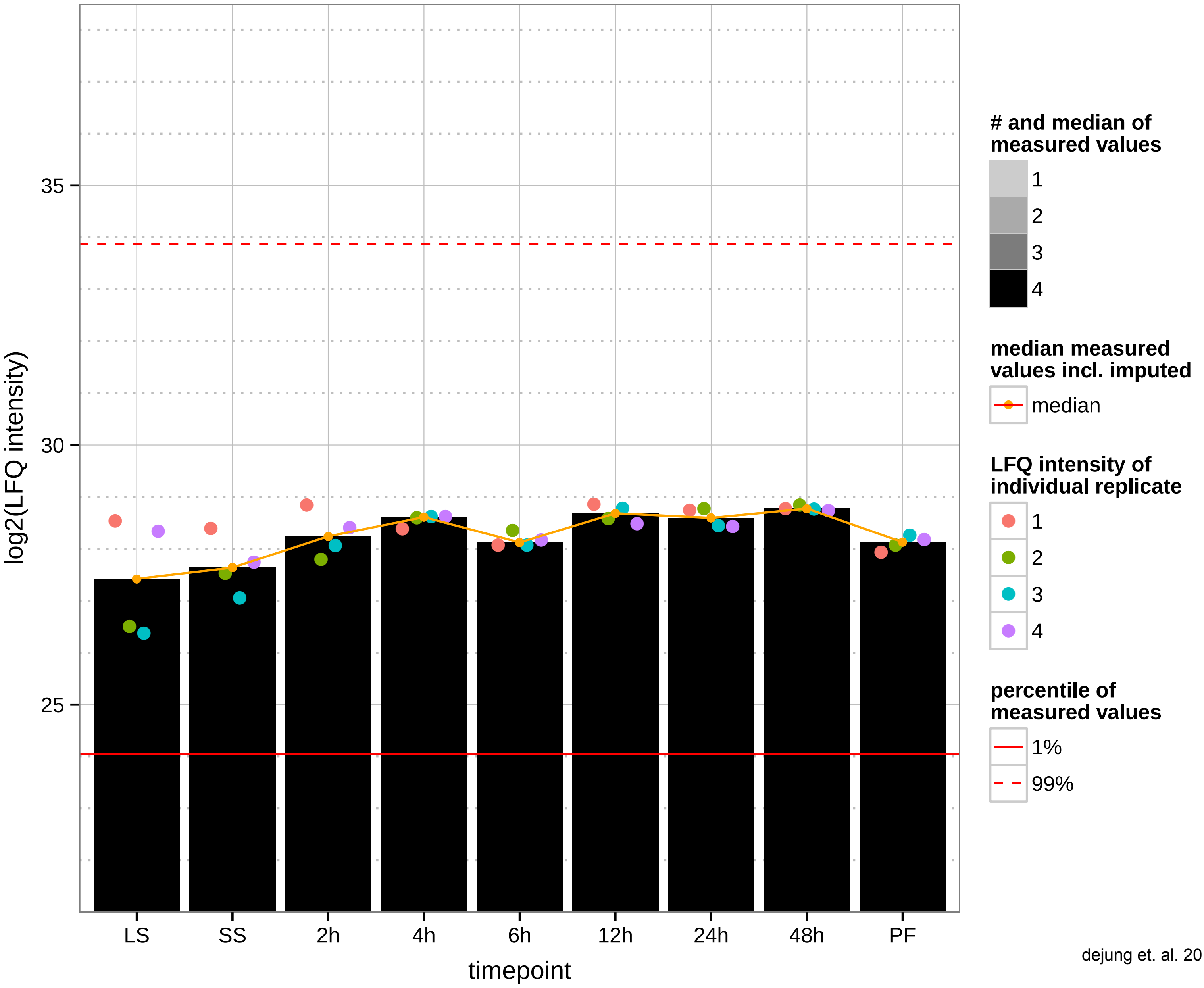
hypothetical protein, conserved
Tb927.7.6180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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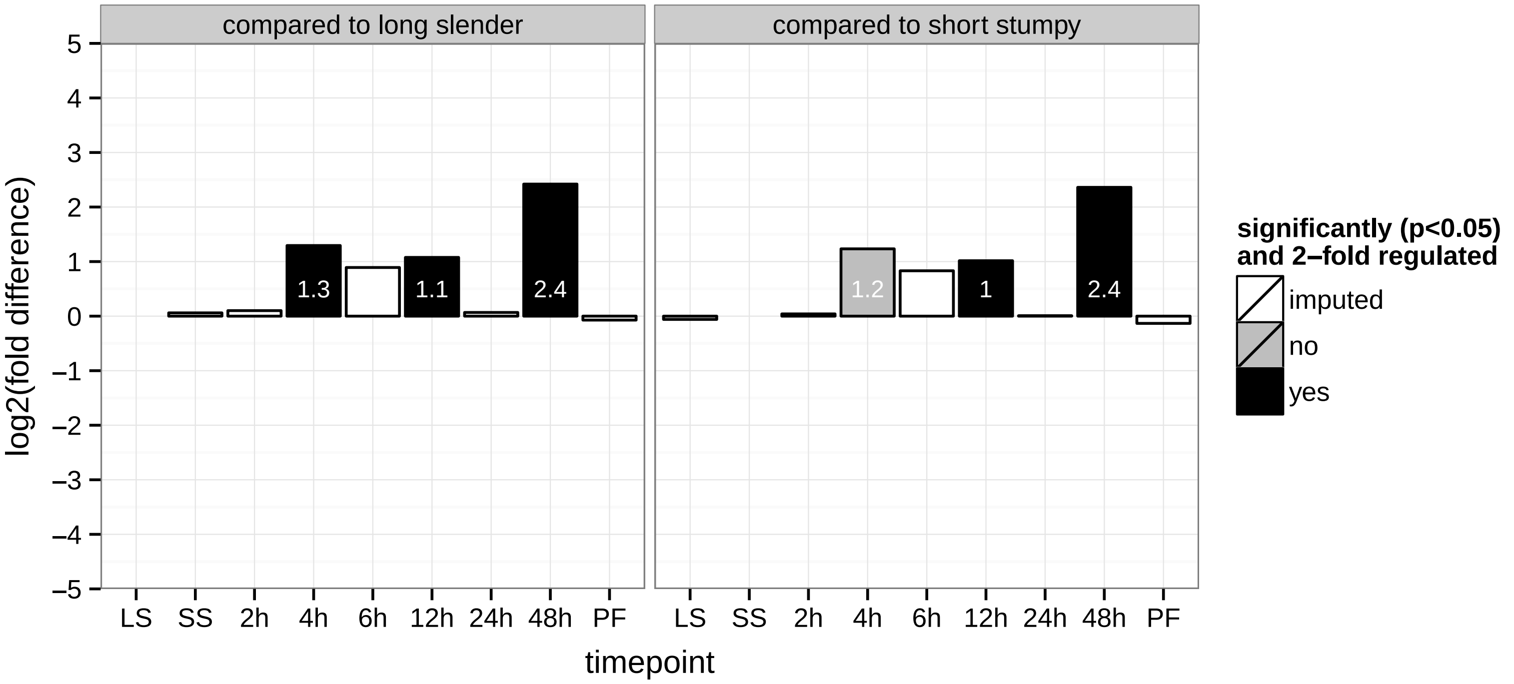
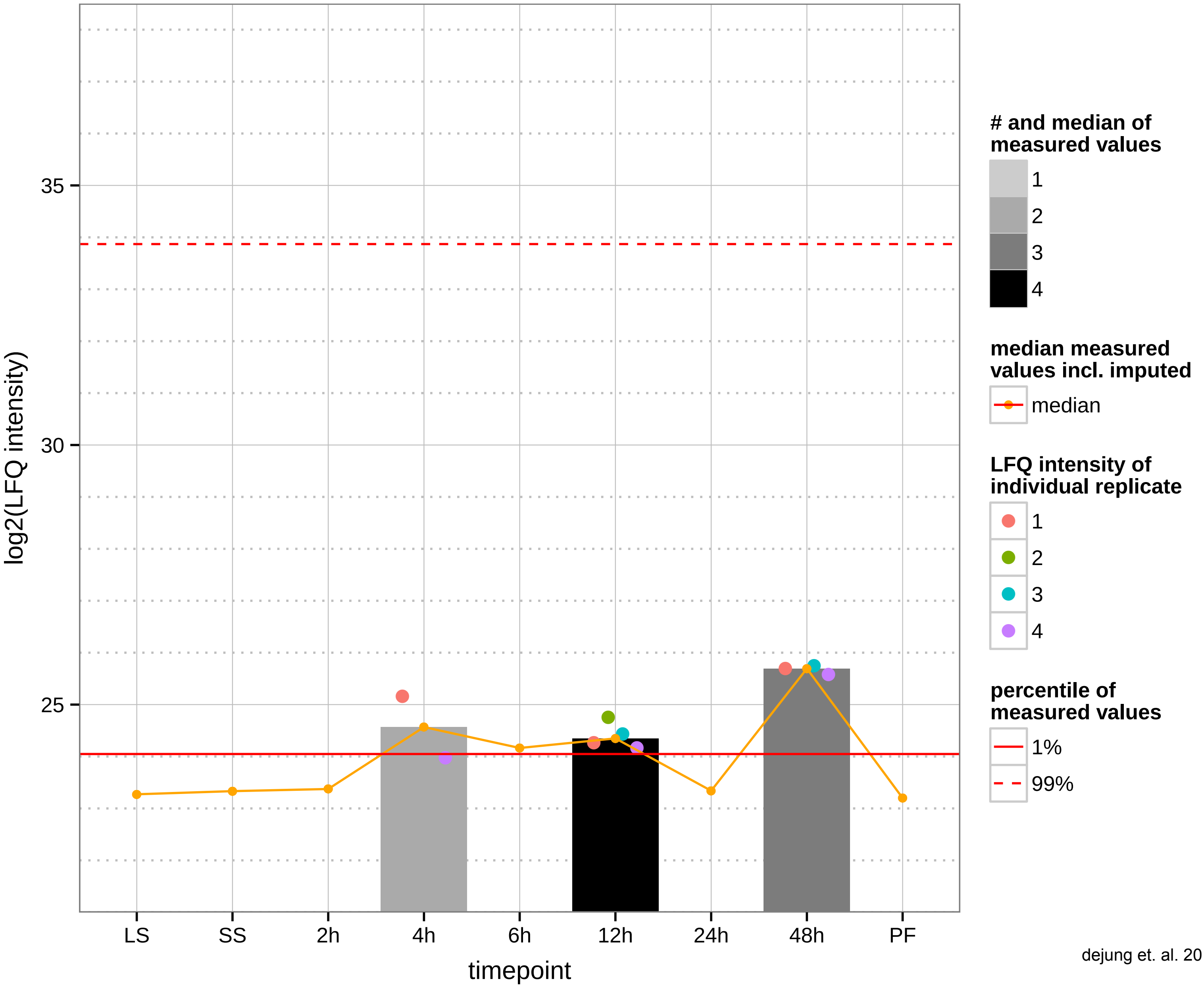
hypothetical protein, conserved
Tb927.8.8200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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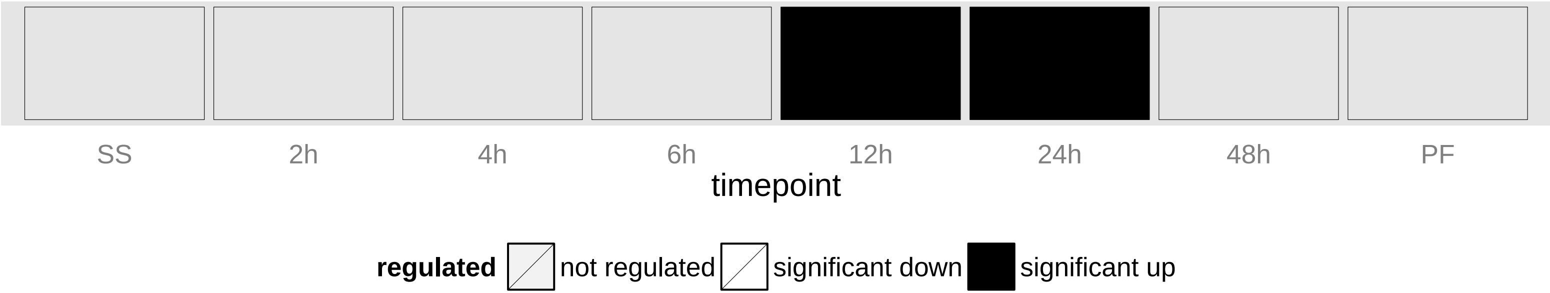

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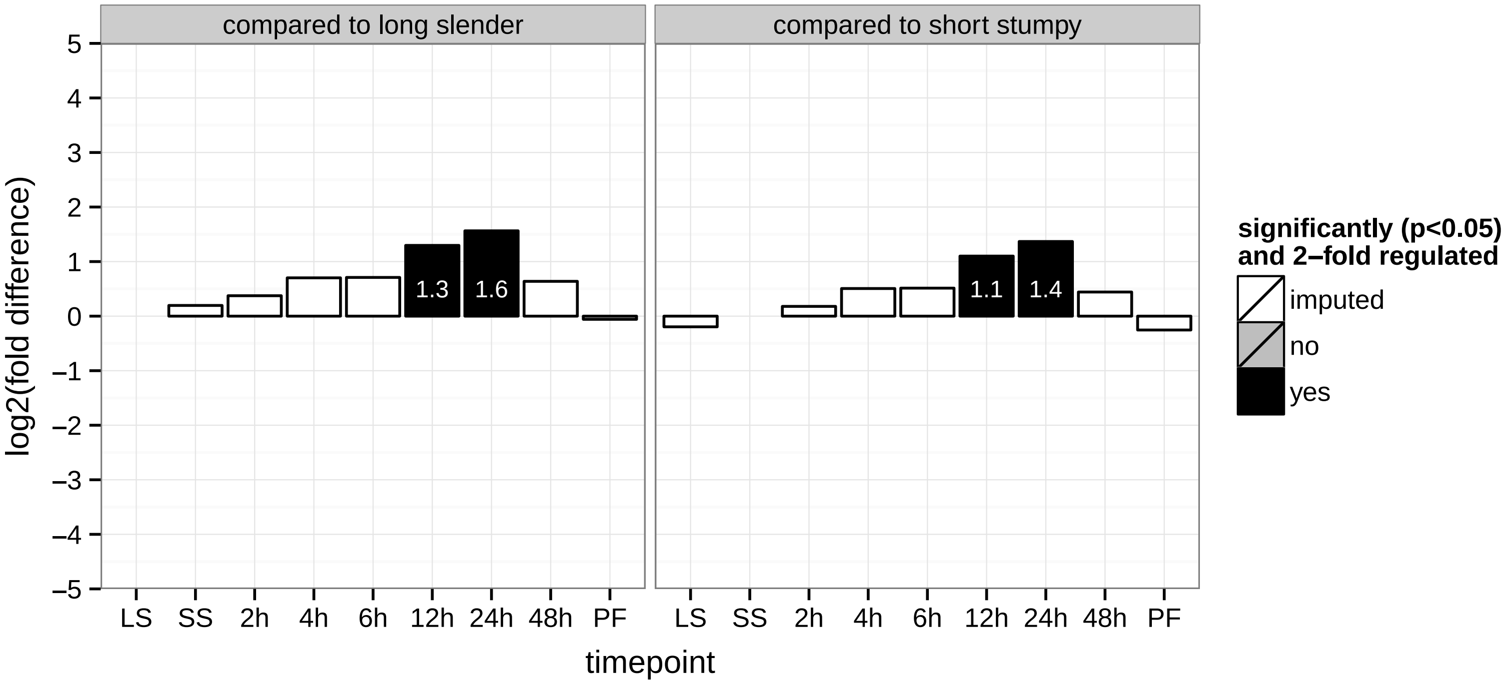
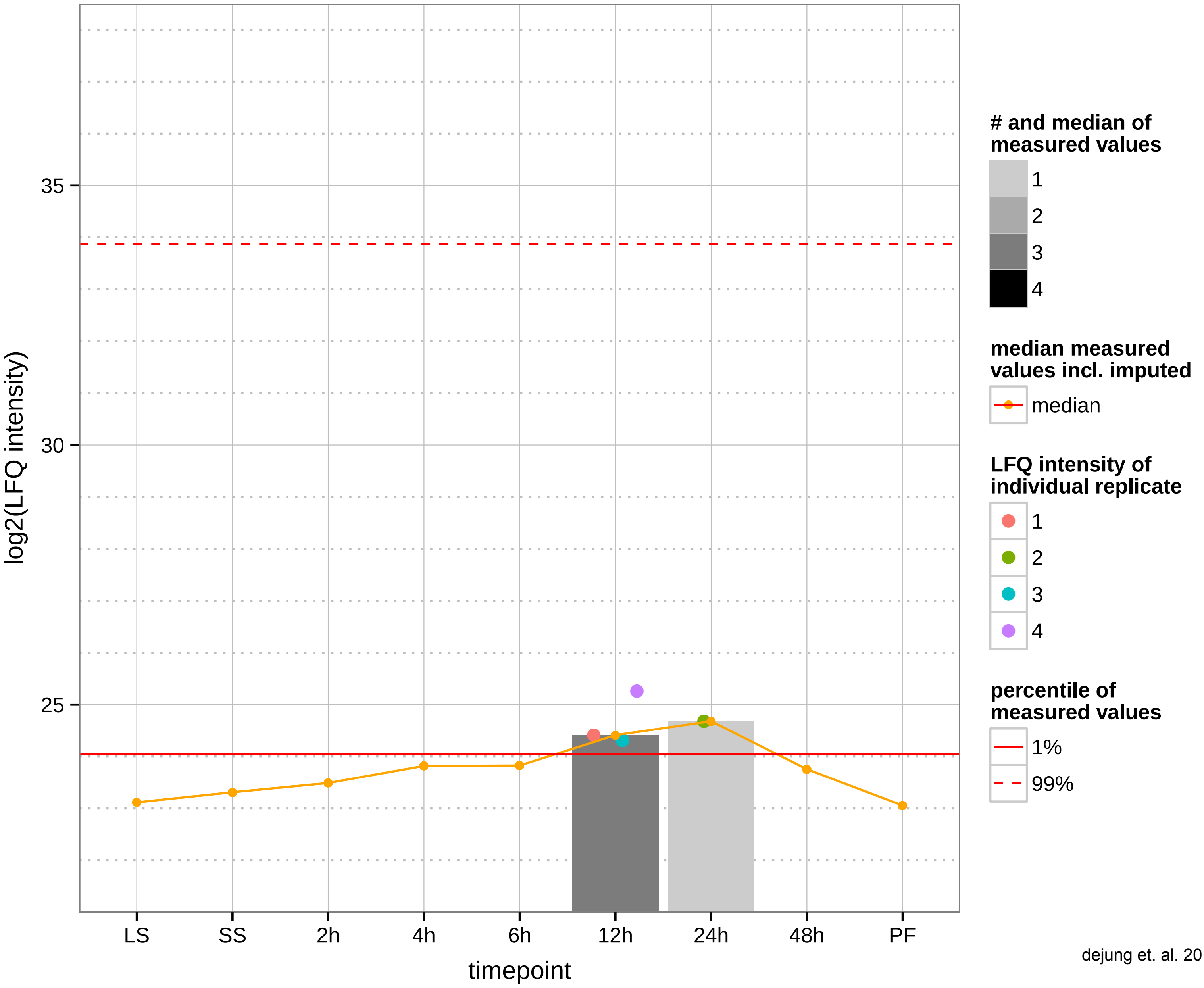
hypothetical protein, conserved
Tb11.v5.0581;Tb927.10.570
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: exocyst
PGOP: protein transport, vesicle docking involved in exocytosis





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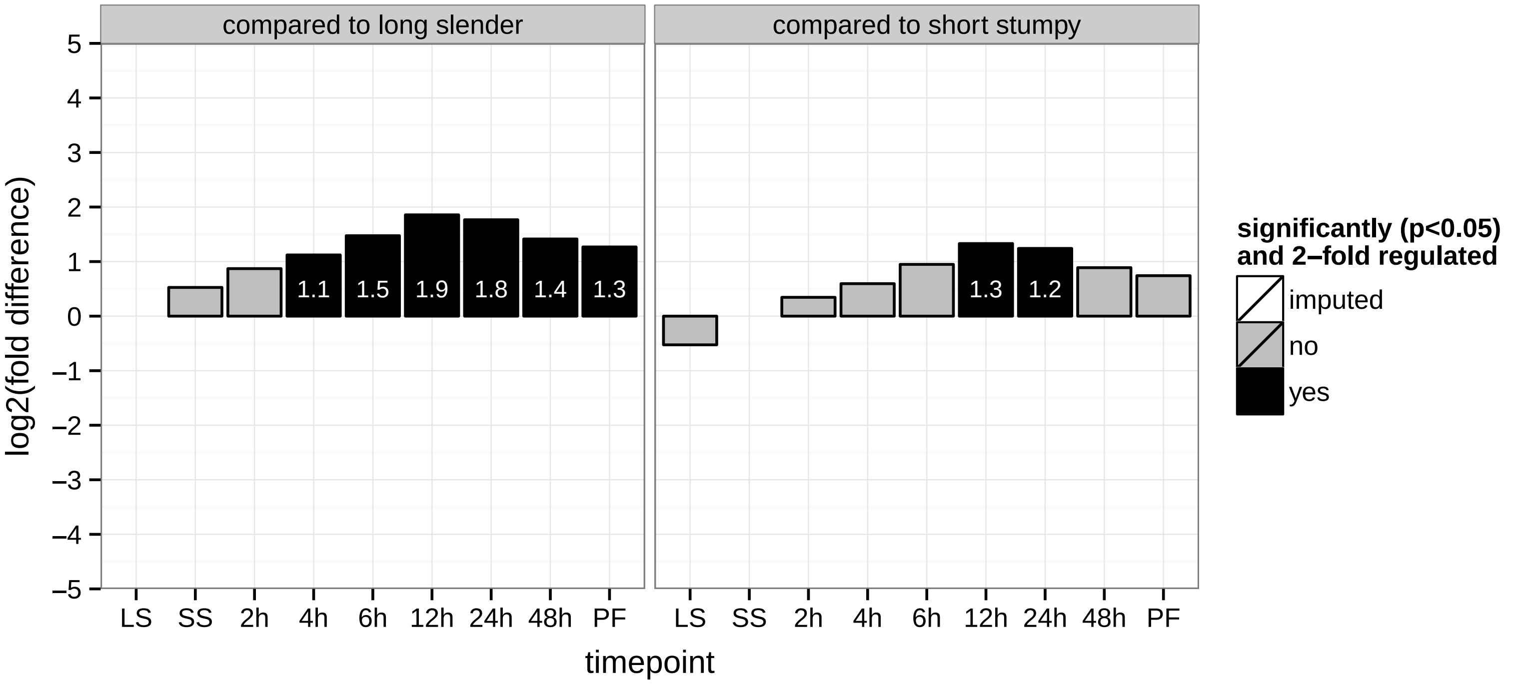
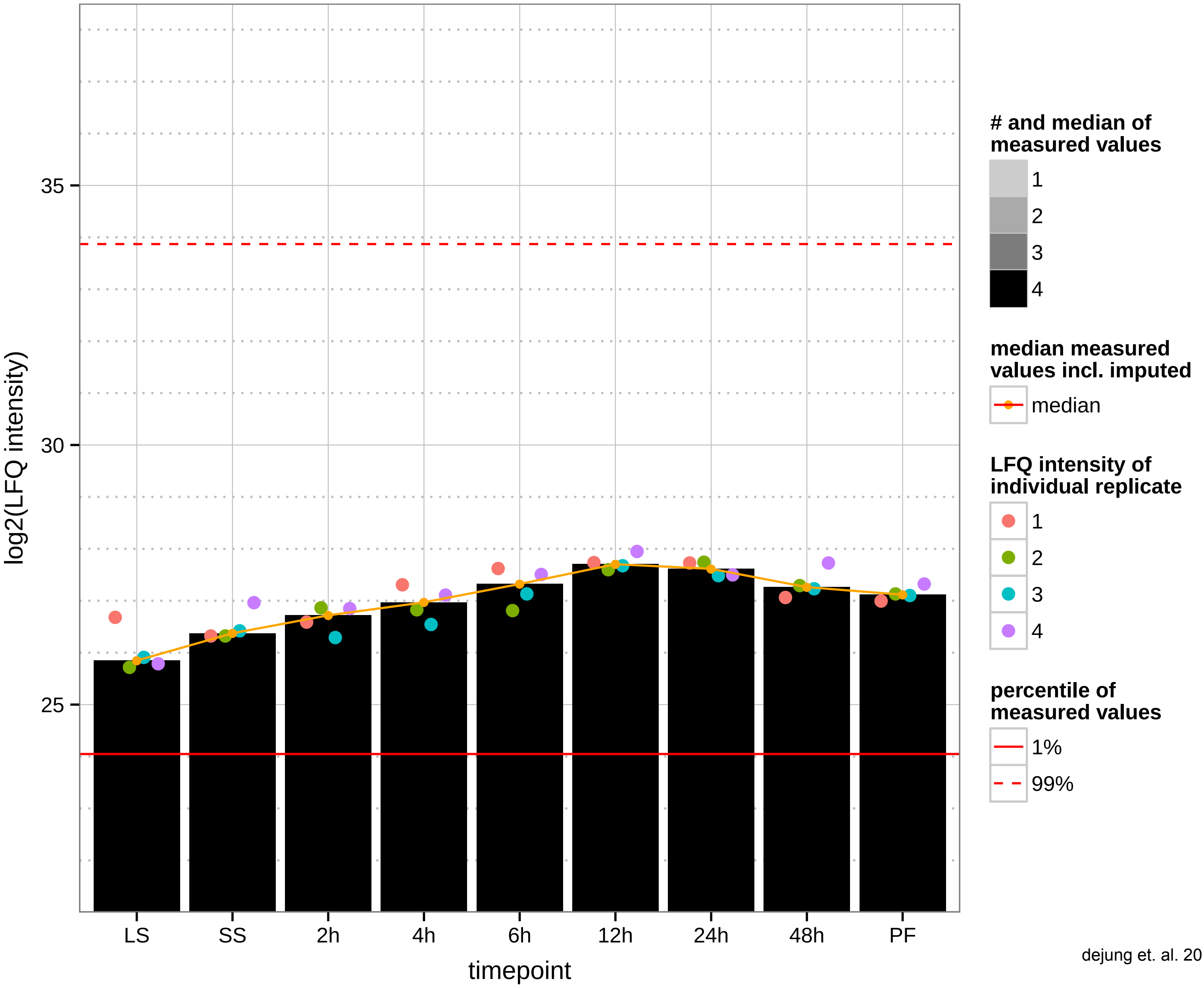
hypothetical protein, conserved
Tb927.11.10860
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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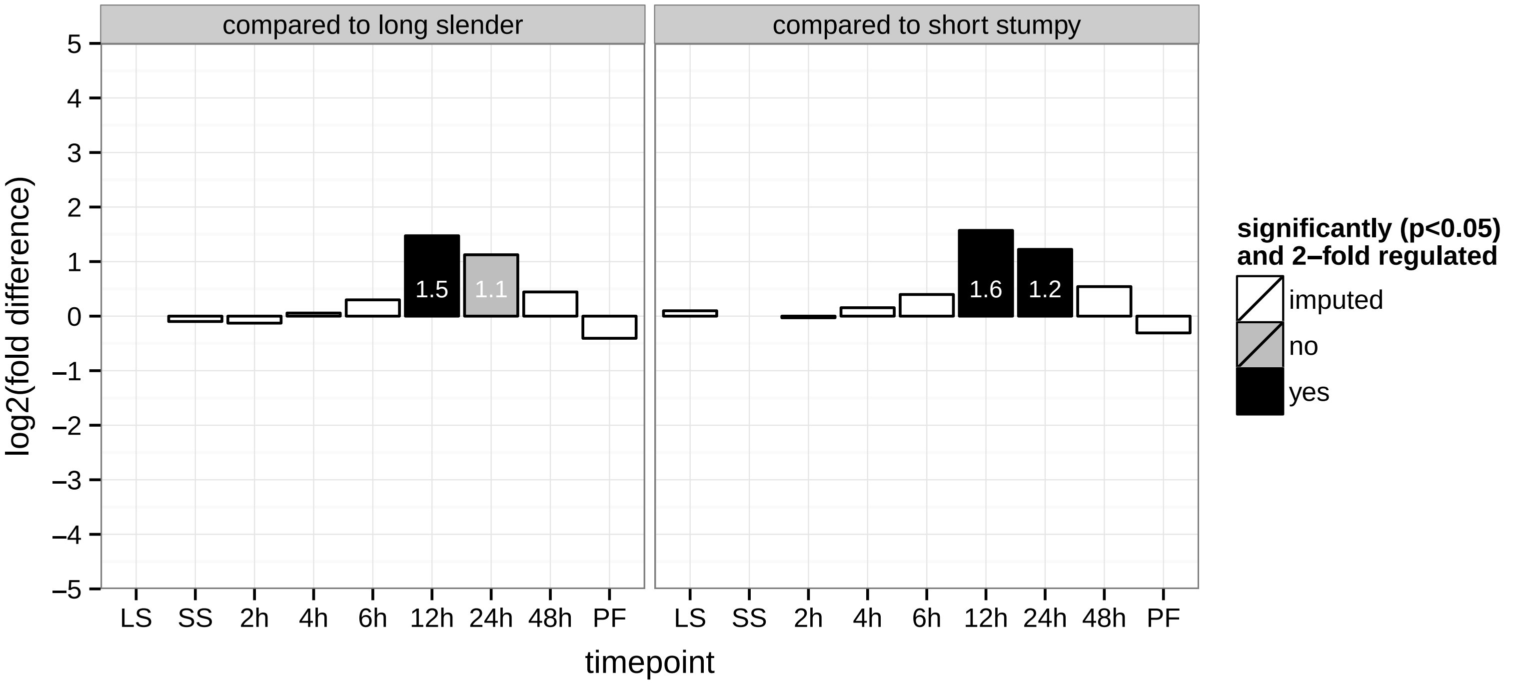
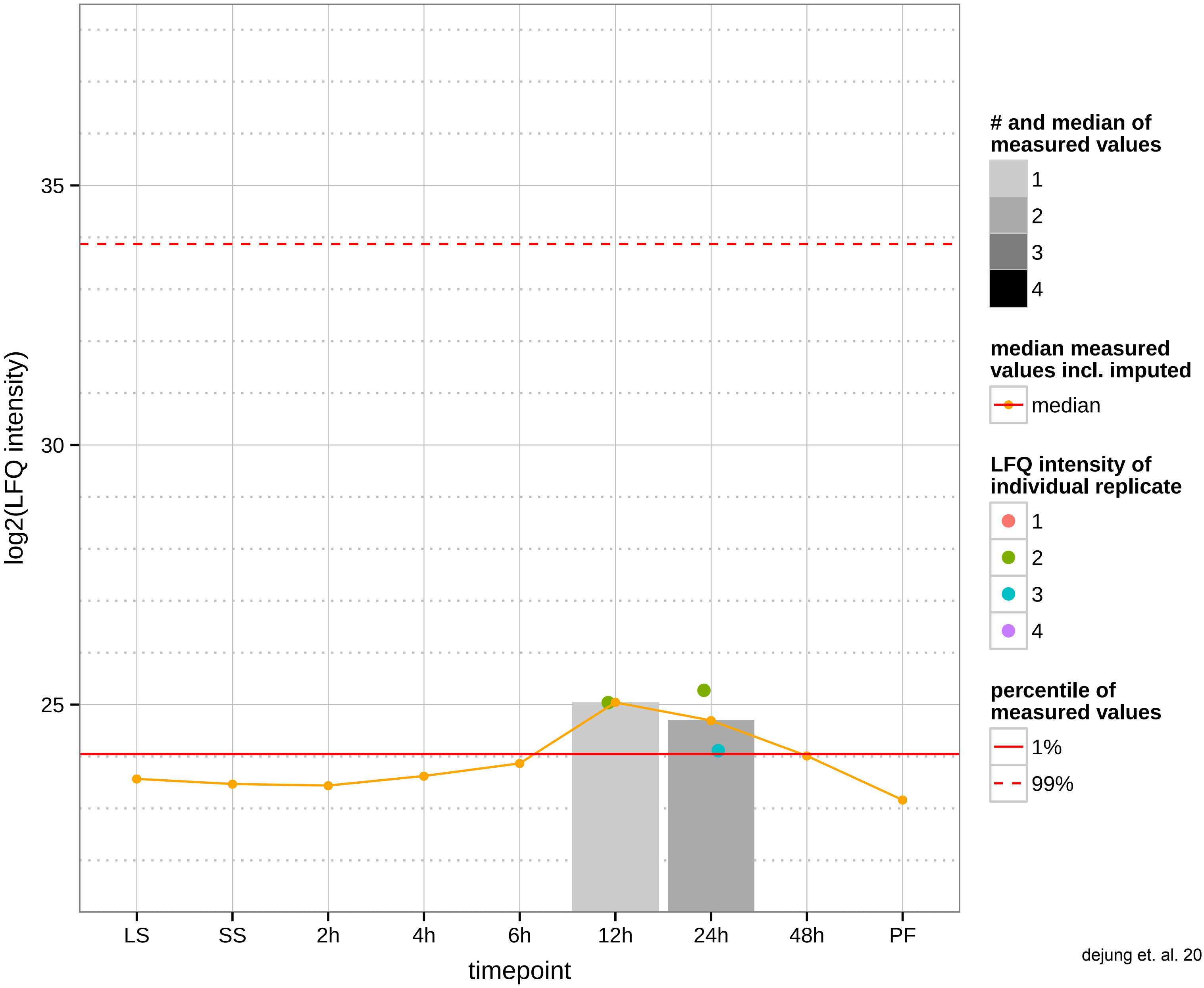
hypothetical protein, conserved
Tb927.11.13590
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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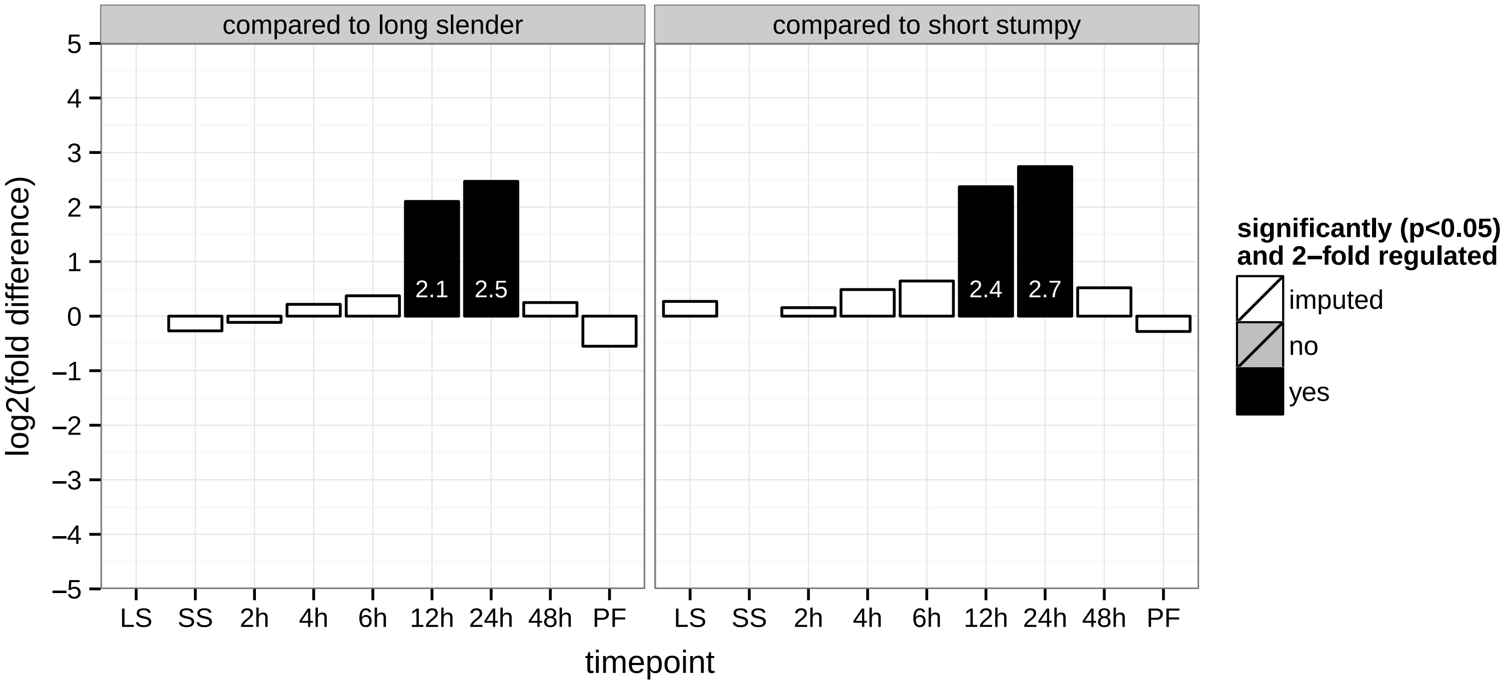
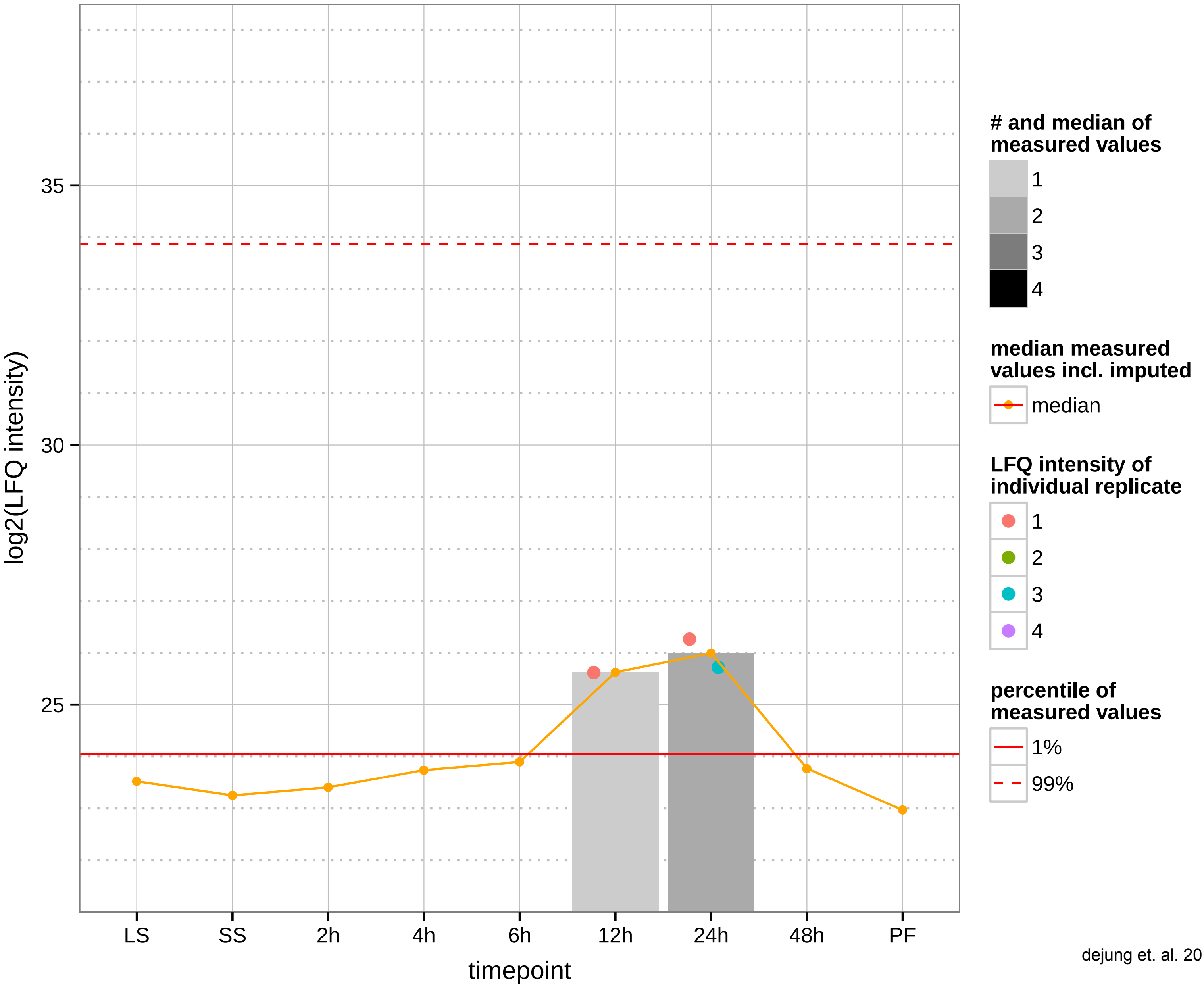
hypothetical protein, conserved
Tb927.11.5760
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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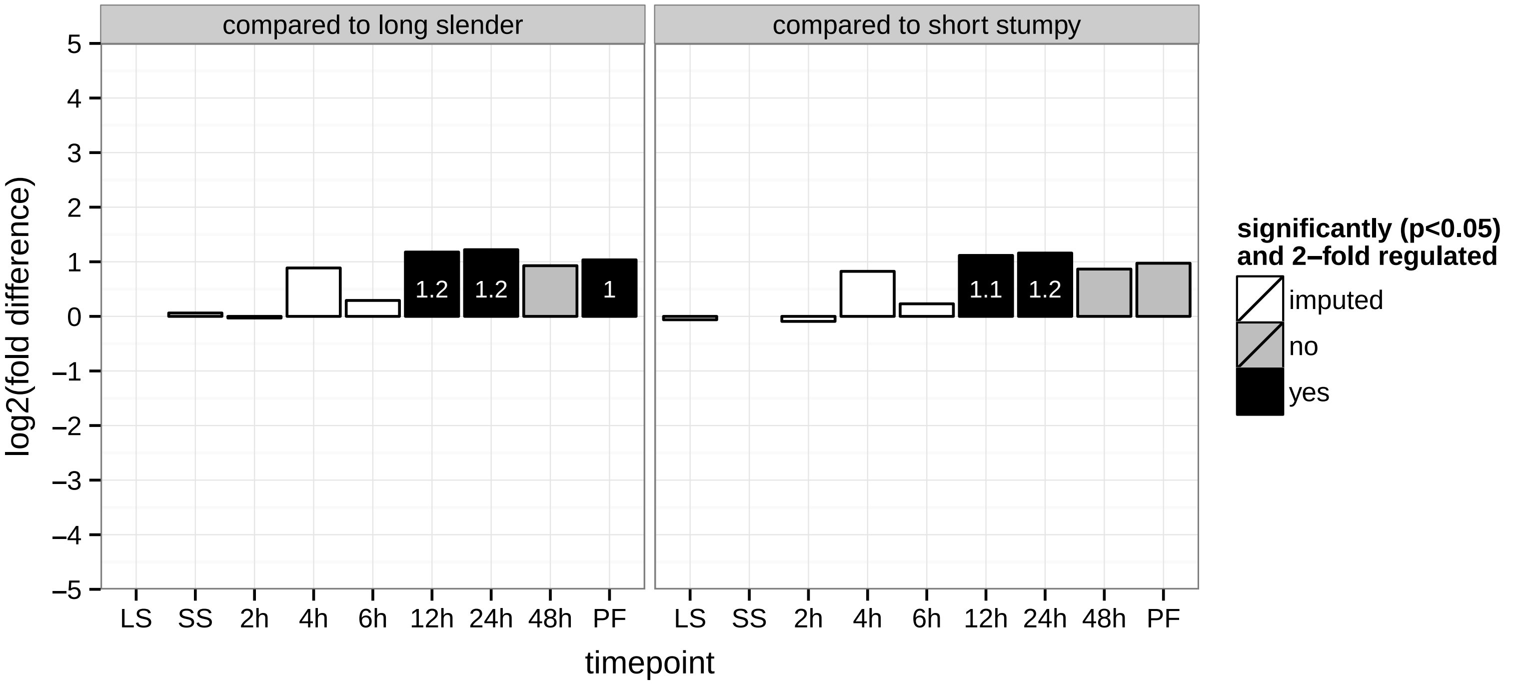
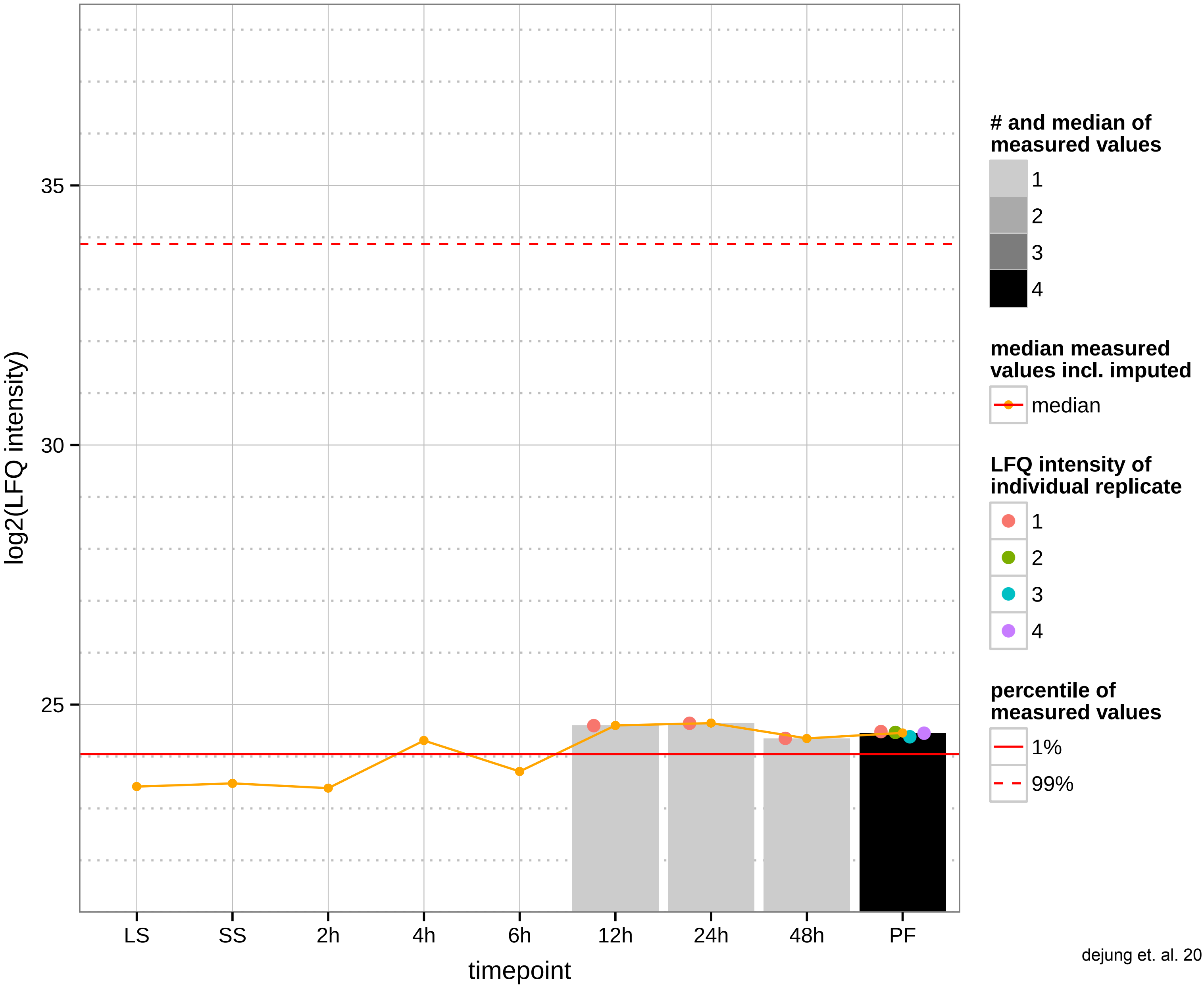
hypothetical protein, conserved
Tb927.2.4900;Tb927.2.4750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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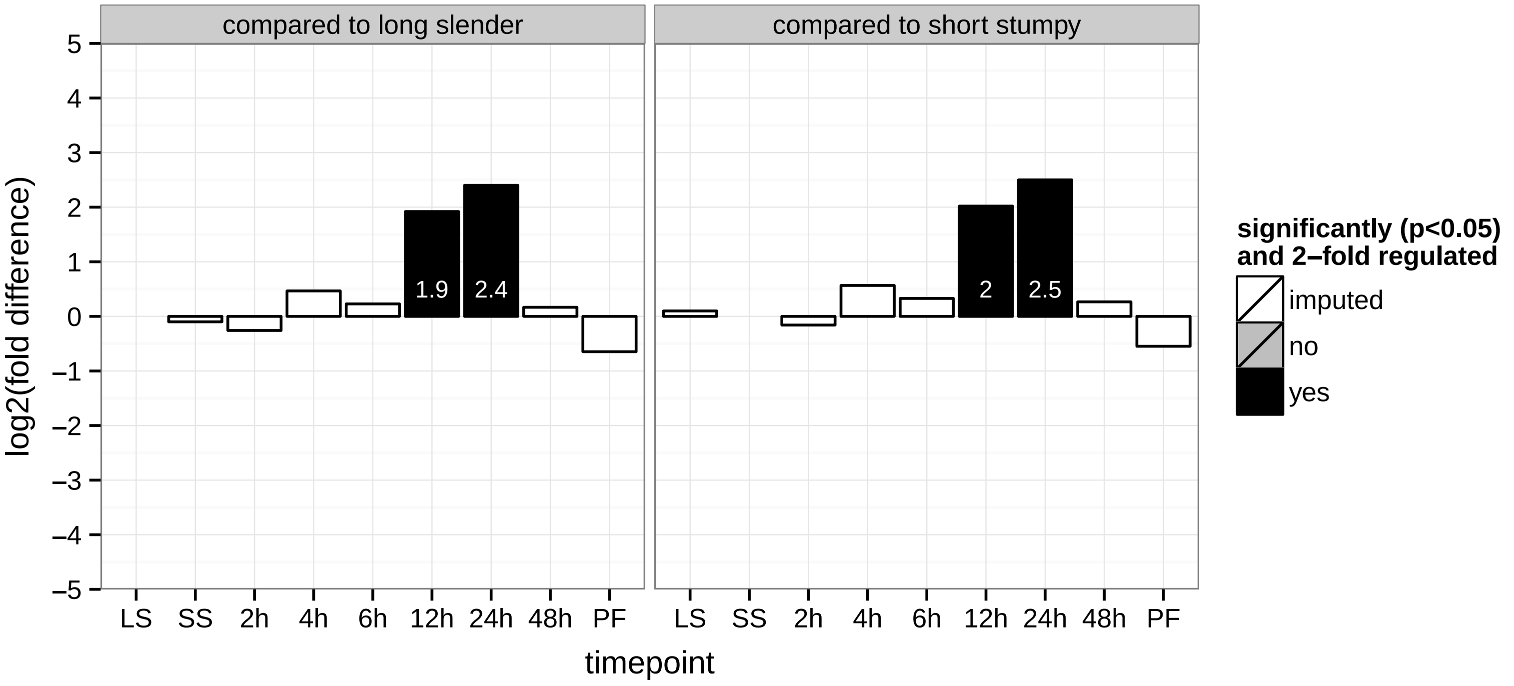
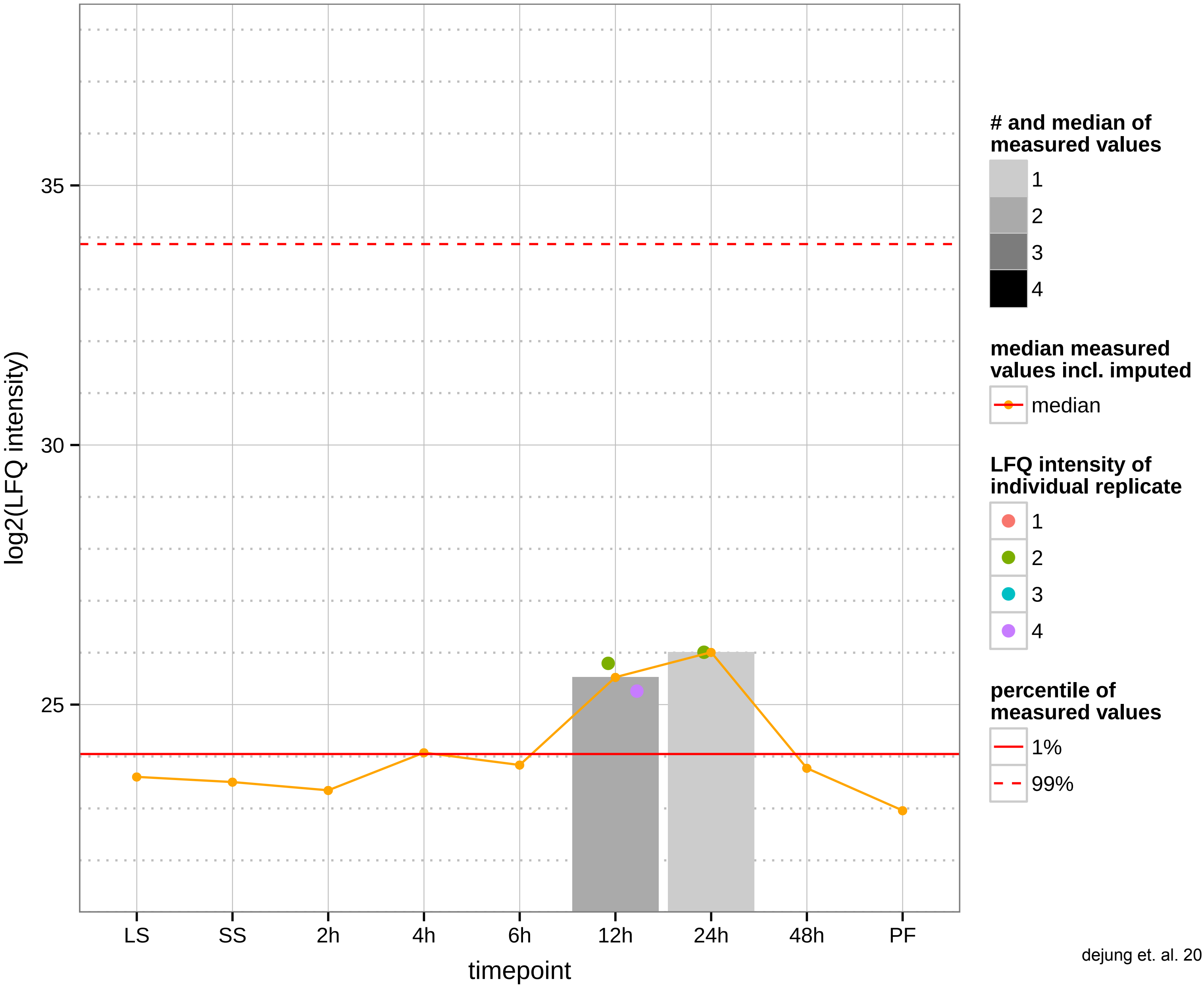
hypothetical protein, conserved
Tb927.3.1260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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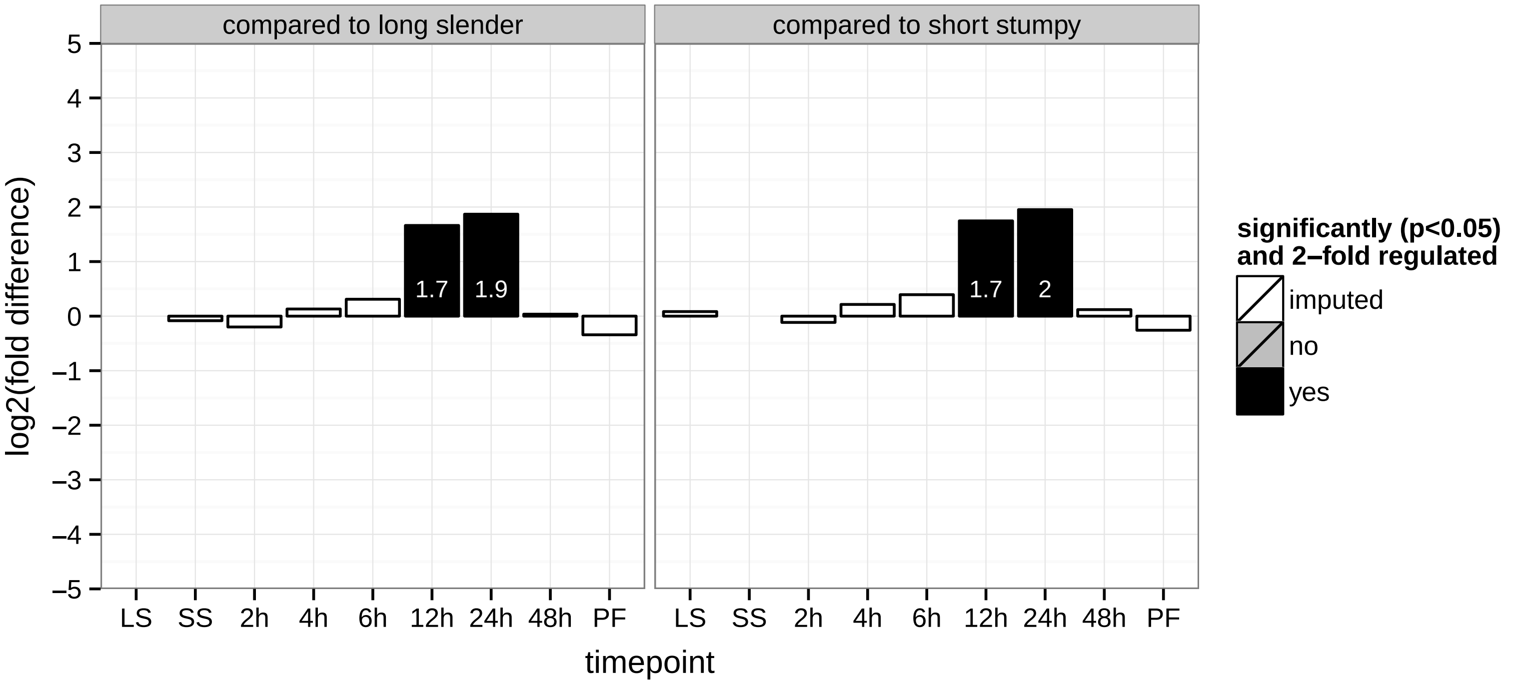
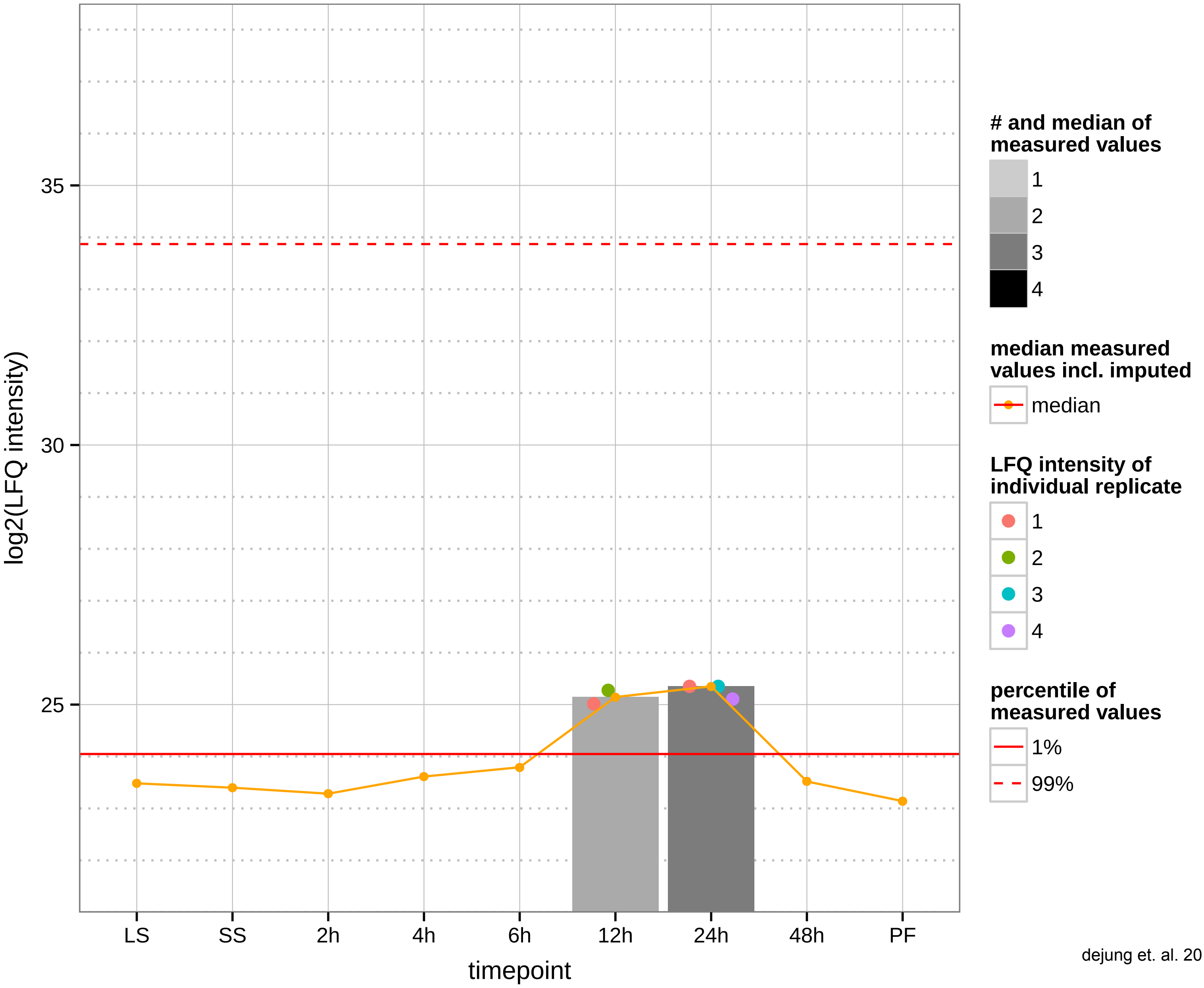
hypothetical protein, conserved
Tb927.3.1600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: mitochondrial intermembrane space protein transporter complex
PGOP: protein import into mitochondrial inner membrane, protein targeting to mitochondrion





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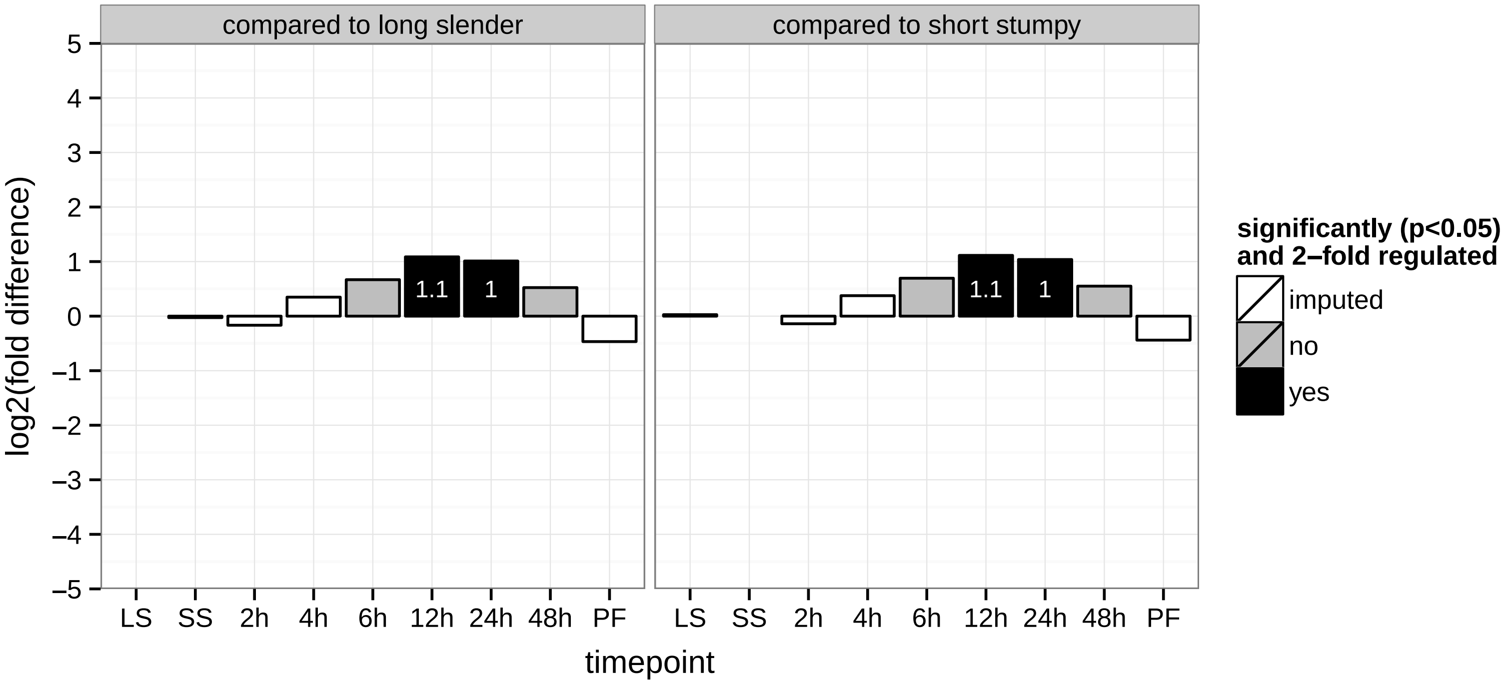
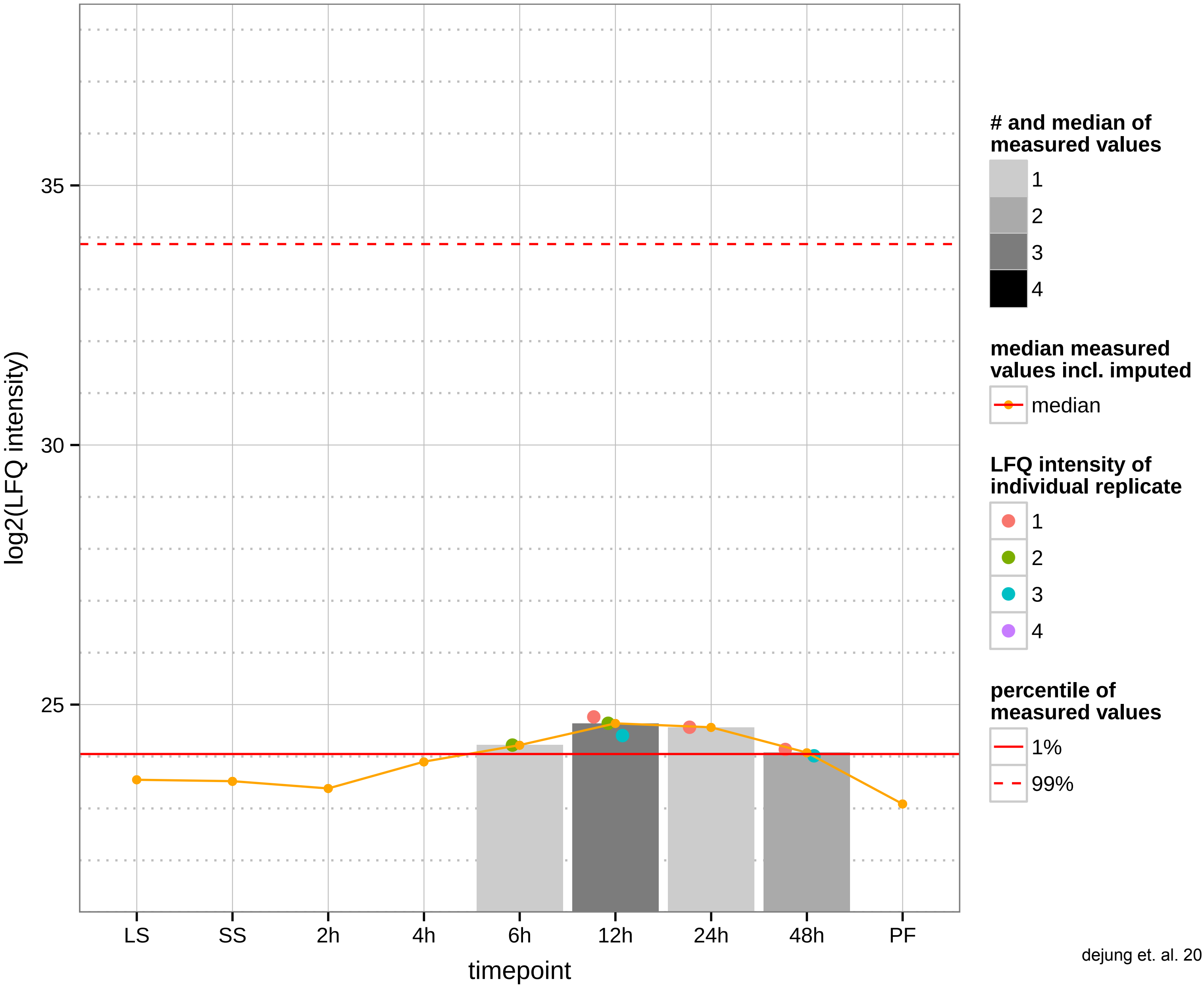
hypothetical protein, conserved
Tb927.4.1120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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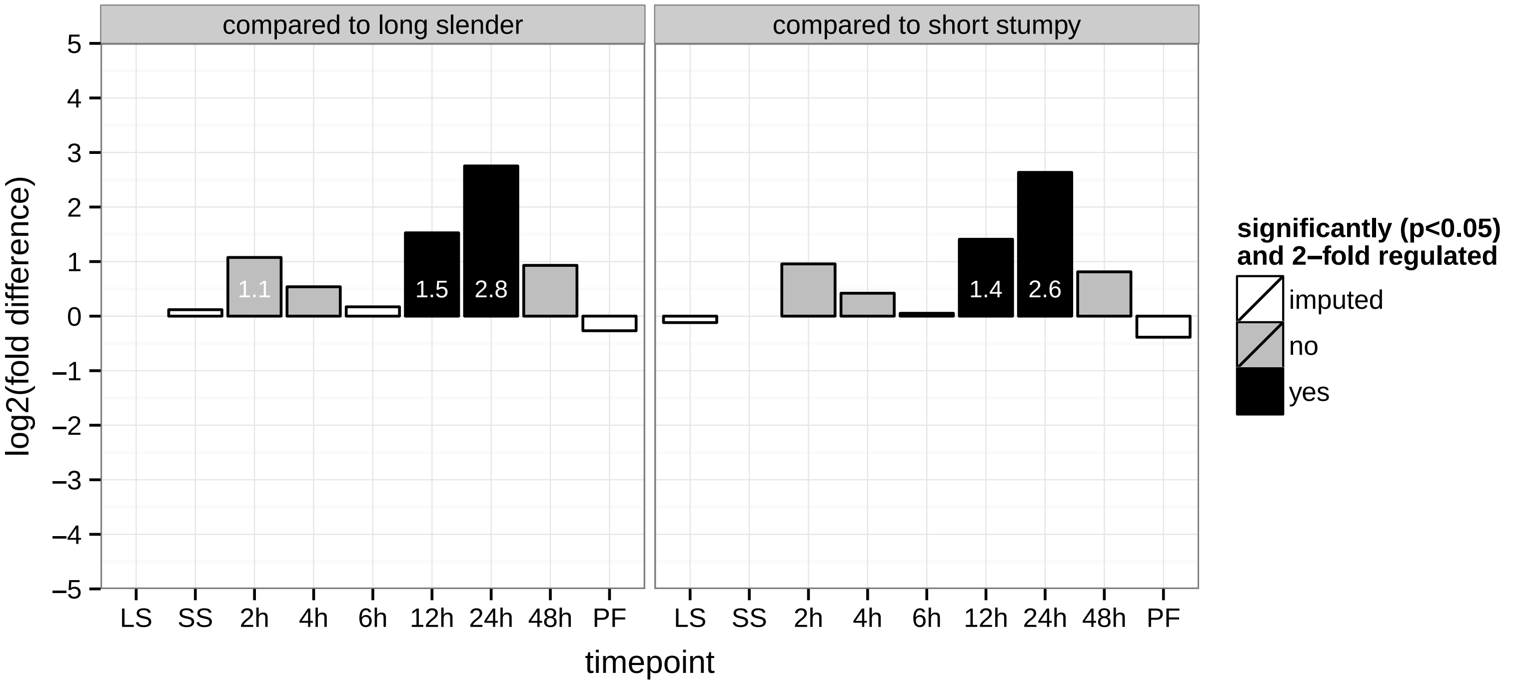
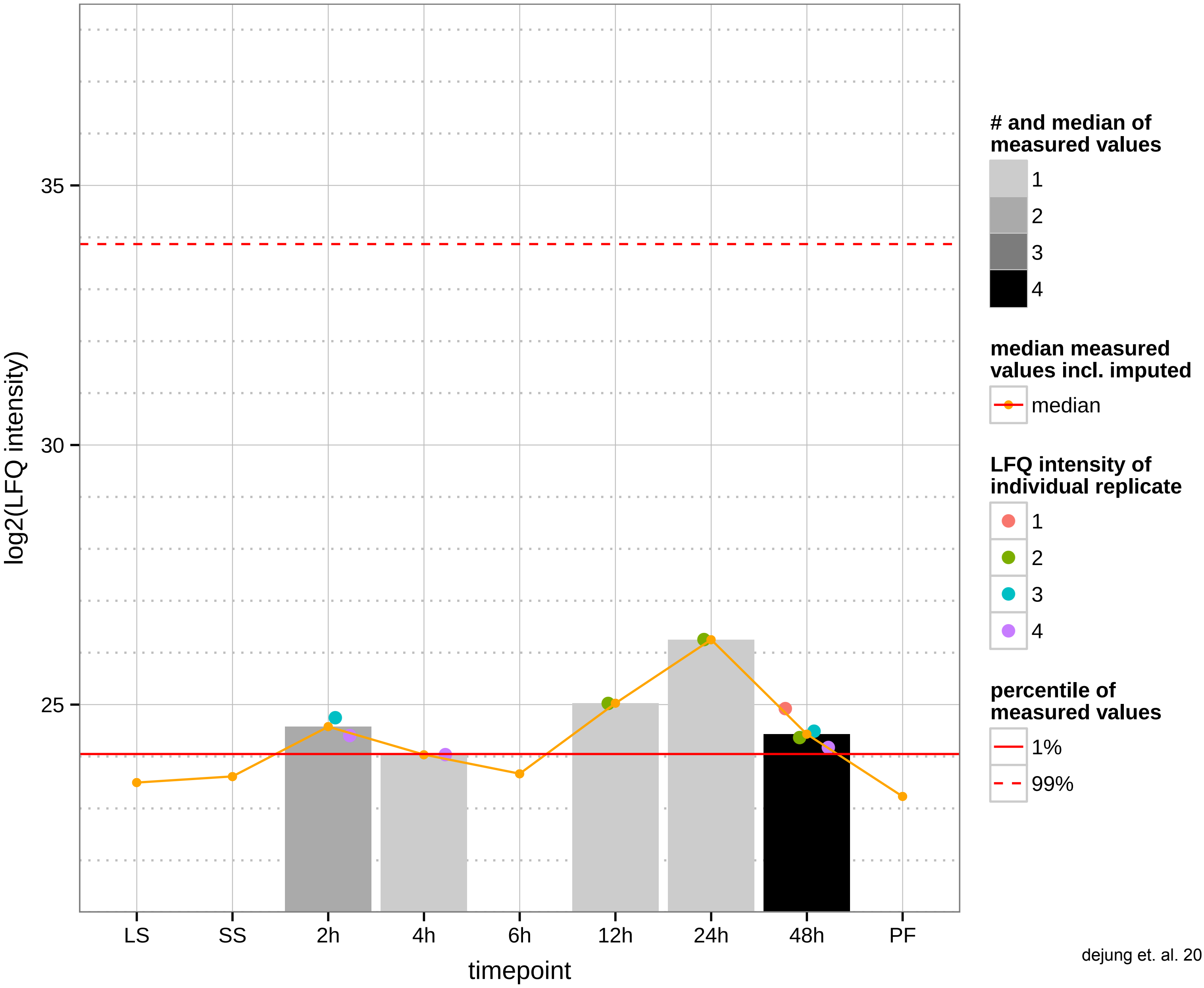
ubiquitin, putative
Tb927.4.2540
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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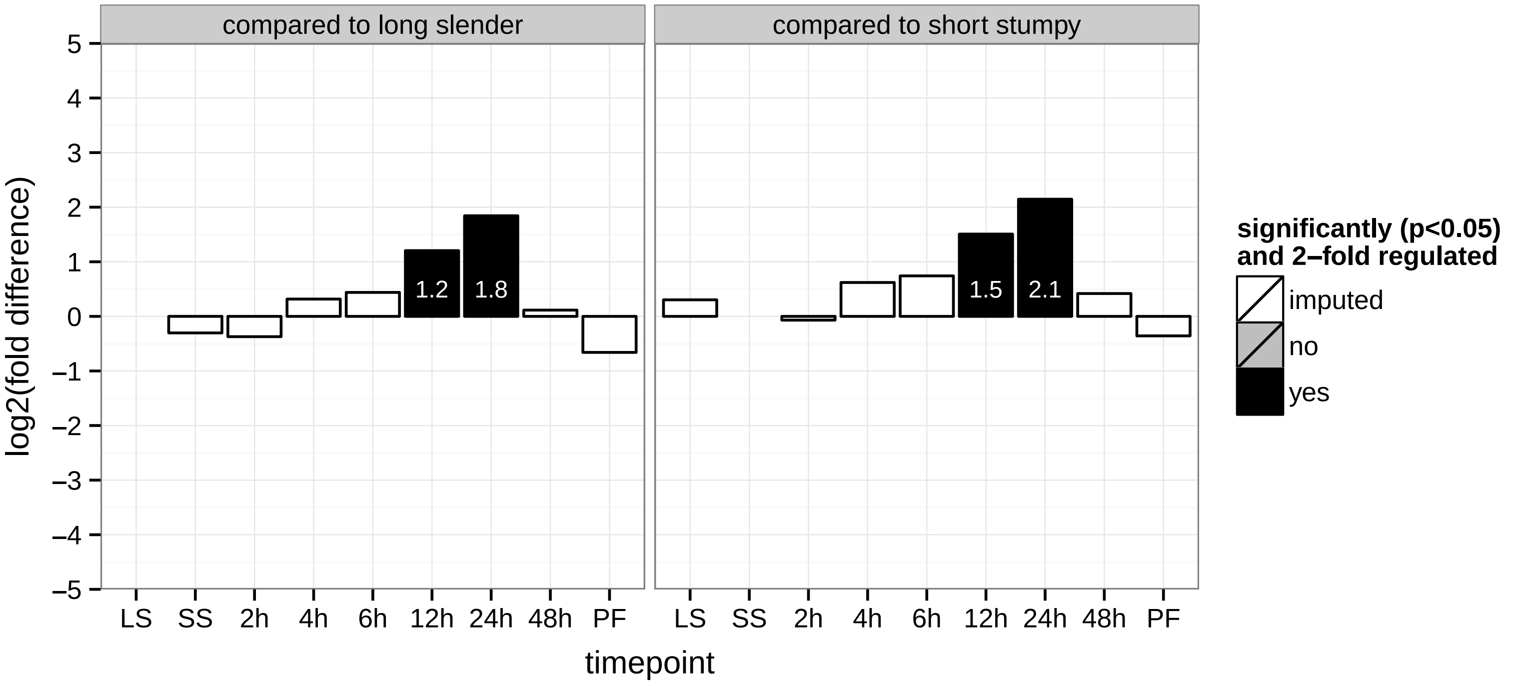
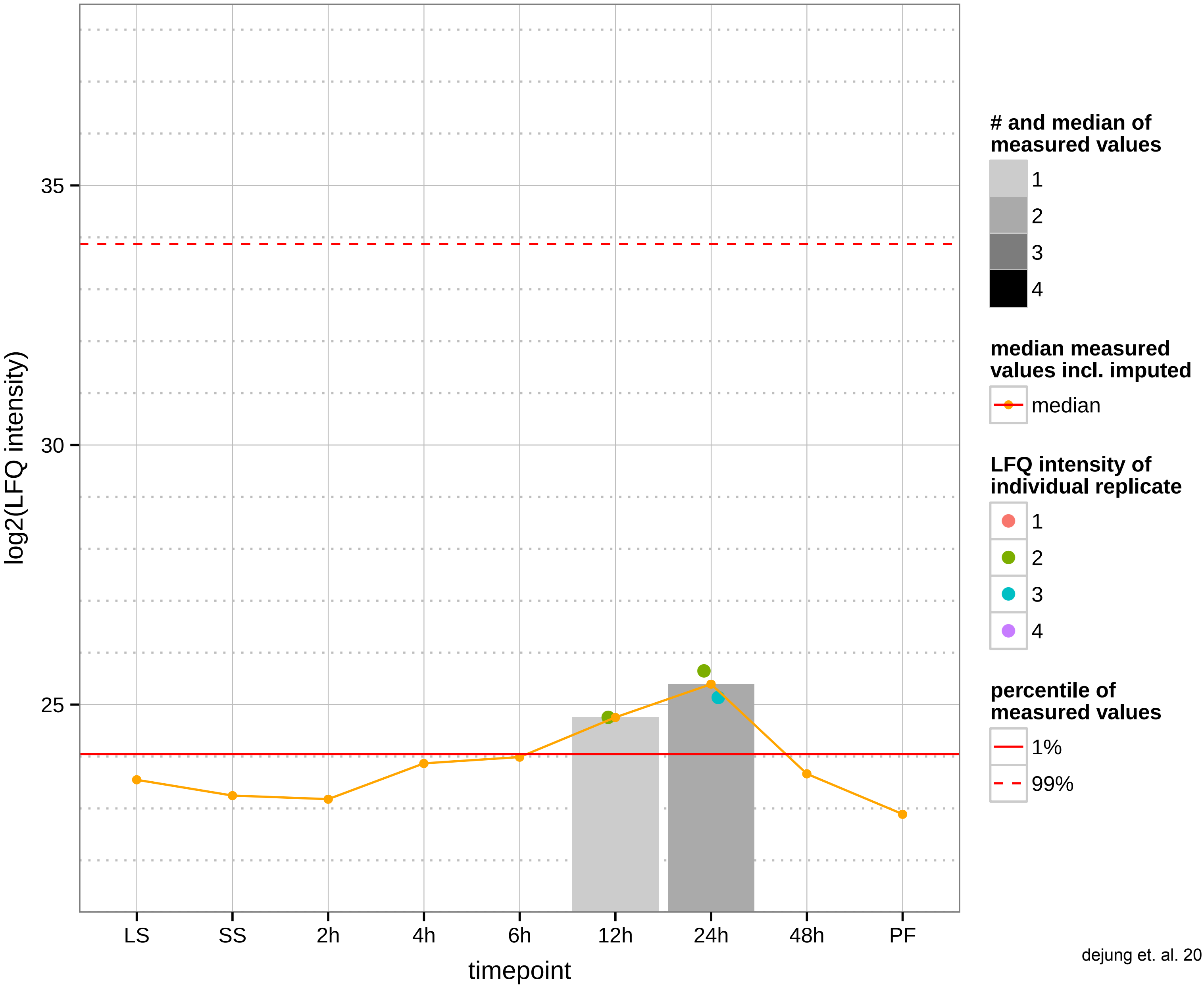
hypothetical protein, conserved
Tb927.4.3430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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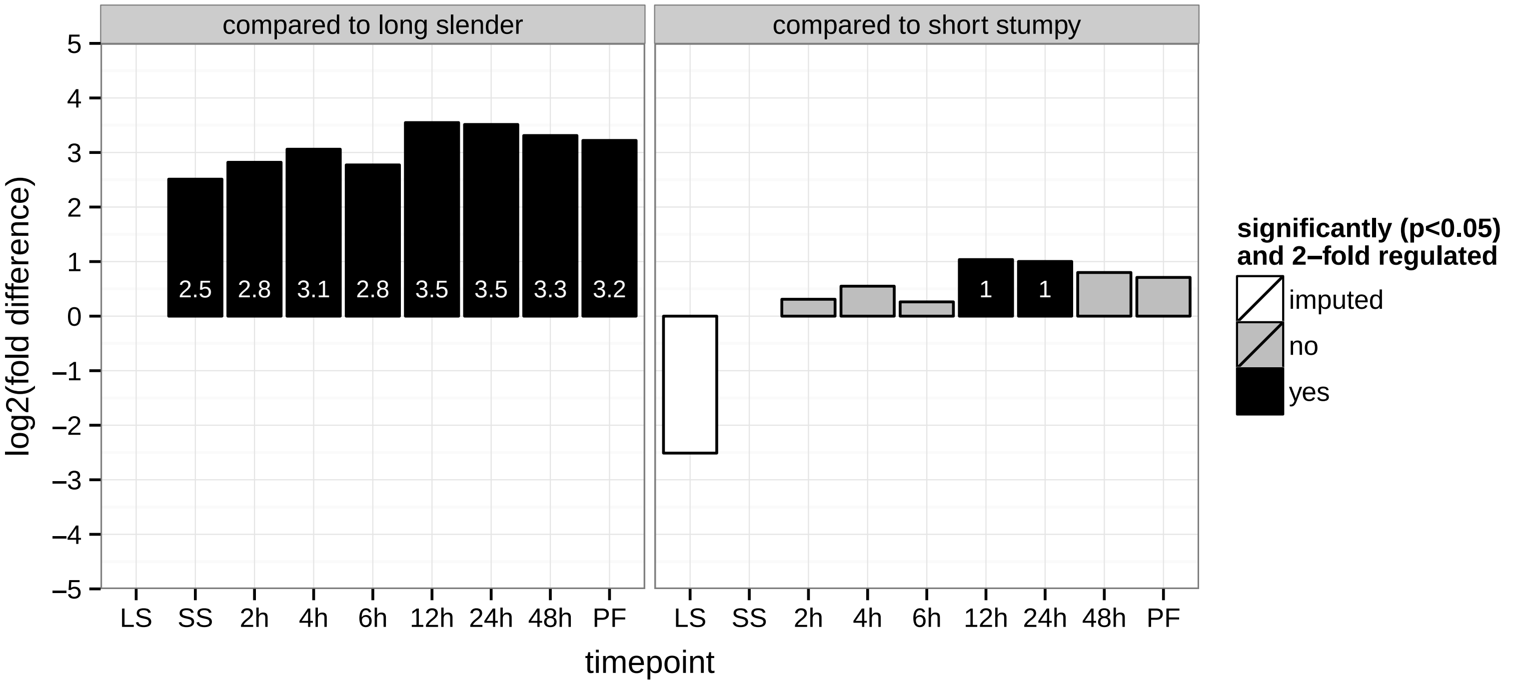
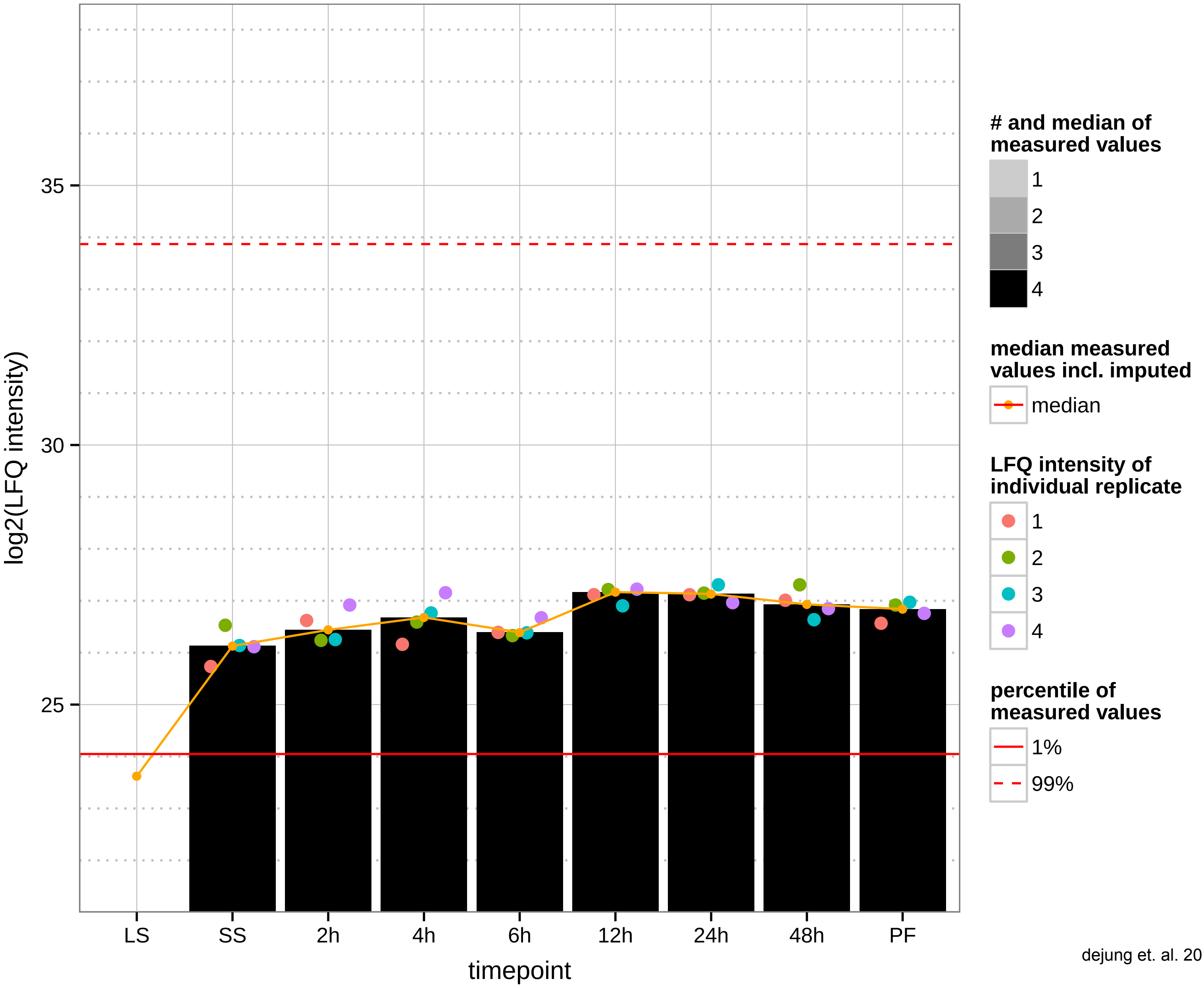
phosphoglycerate mutase protein, putative
Tb927.5.3580
AGOF: catalytic activity
AGOC: null
AGOP: metabolic process, purine ribonucleotide biosynthetic process
PGOF: null
PGOC: null
PGOP: null





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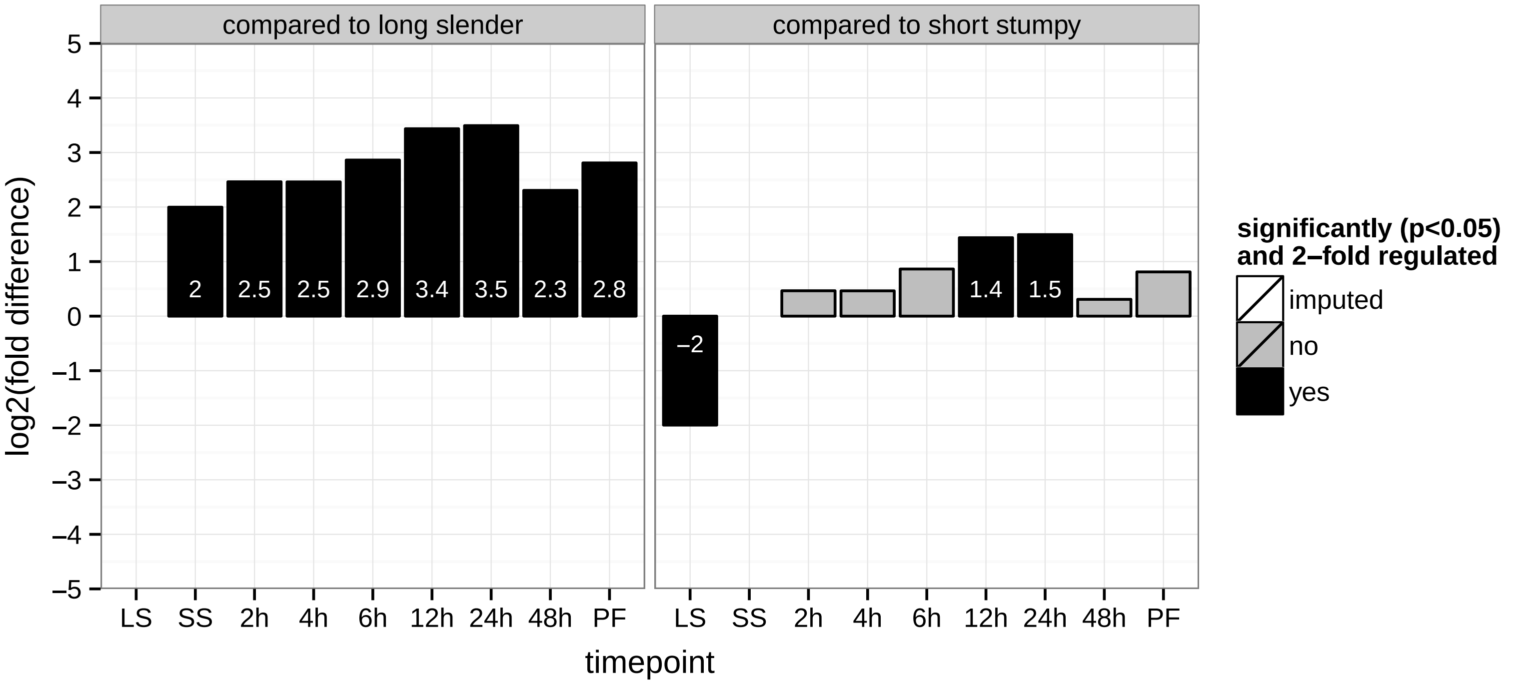
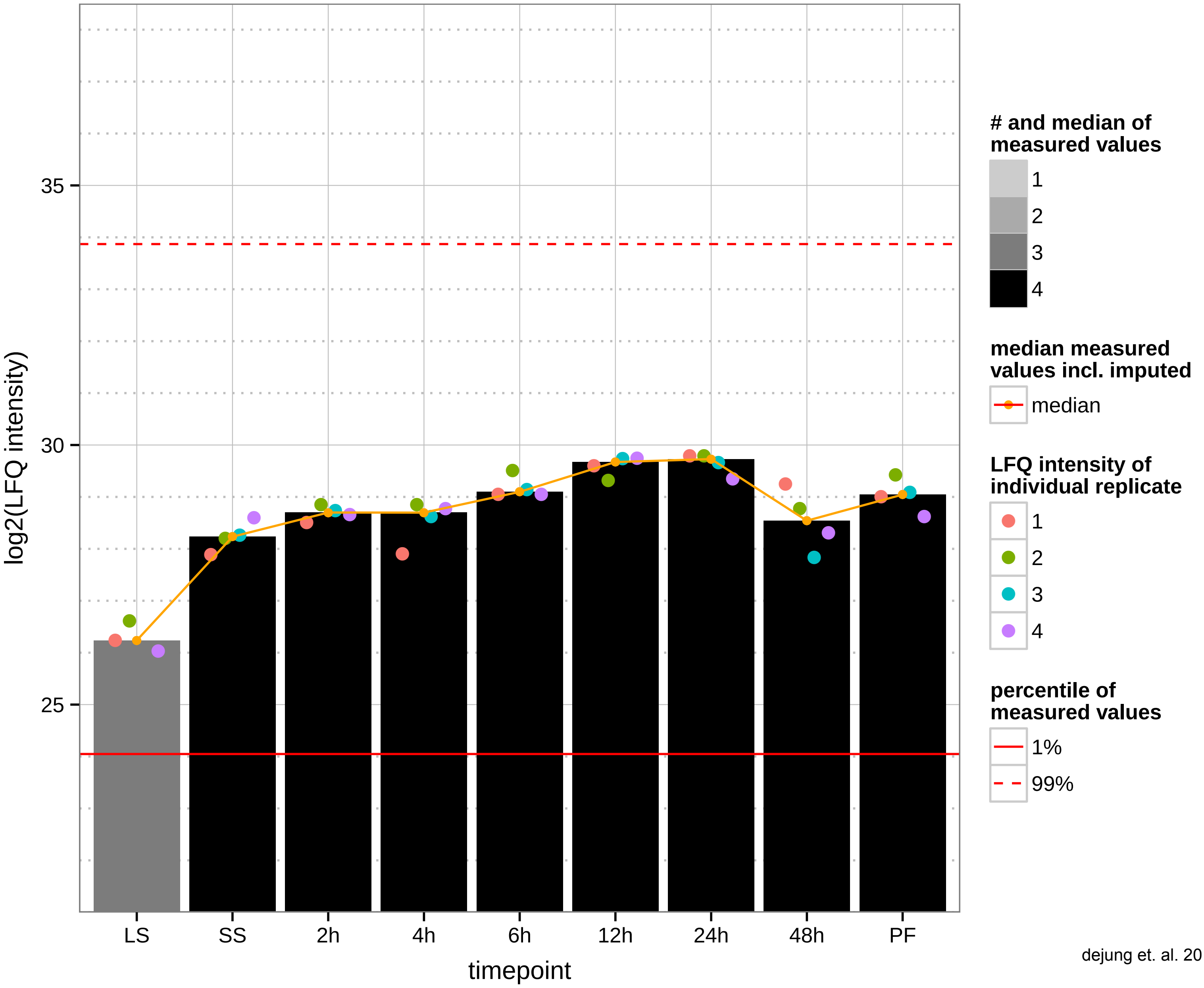
hypothetical protein, conserved
Tb927.7.2160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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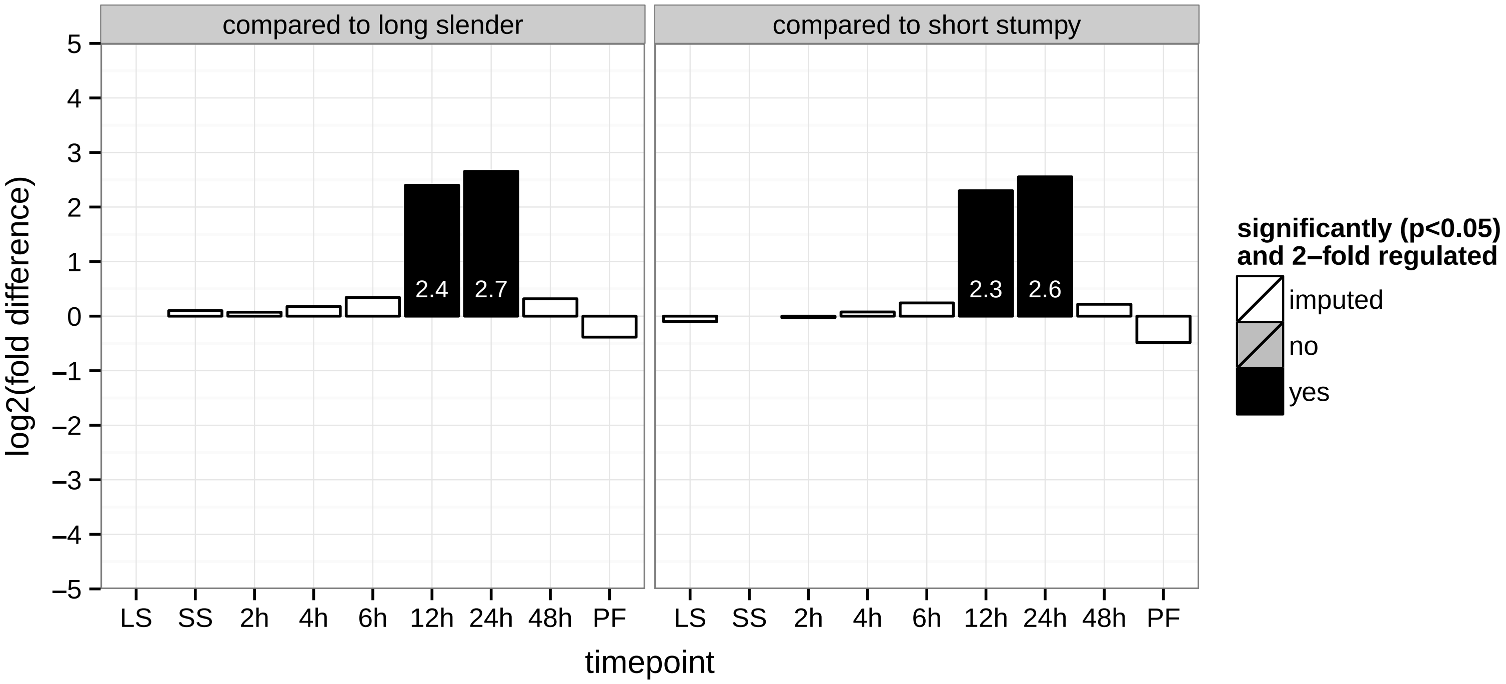
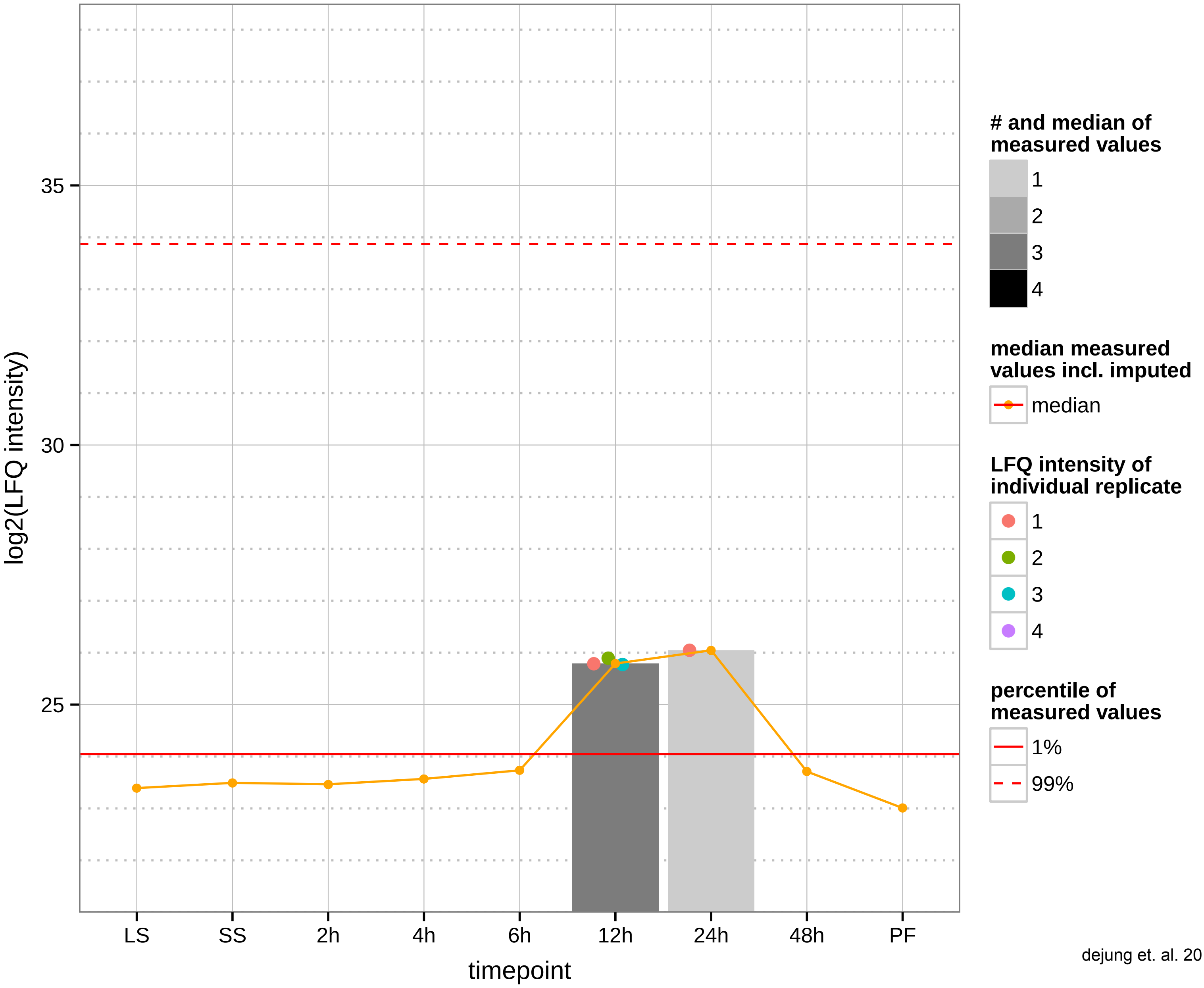
hypothetical protein, conserved
Tb927.7.6110;Tb927.7.6170;Tb927.7.6150;Tb927.7.6130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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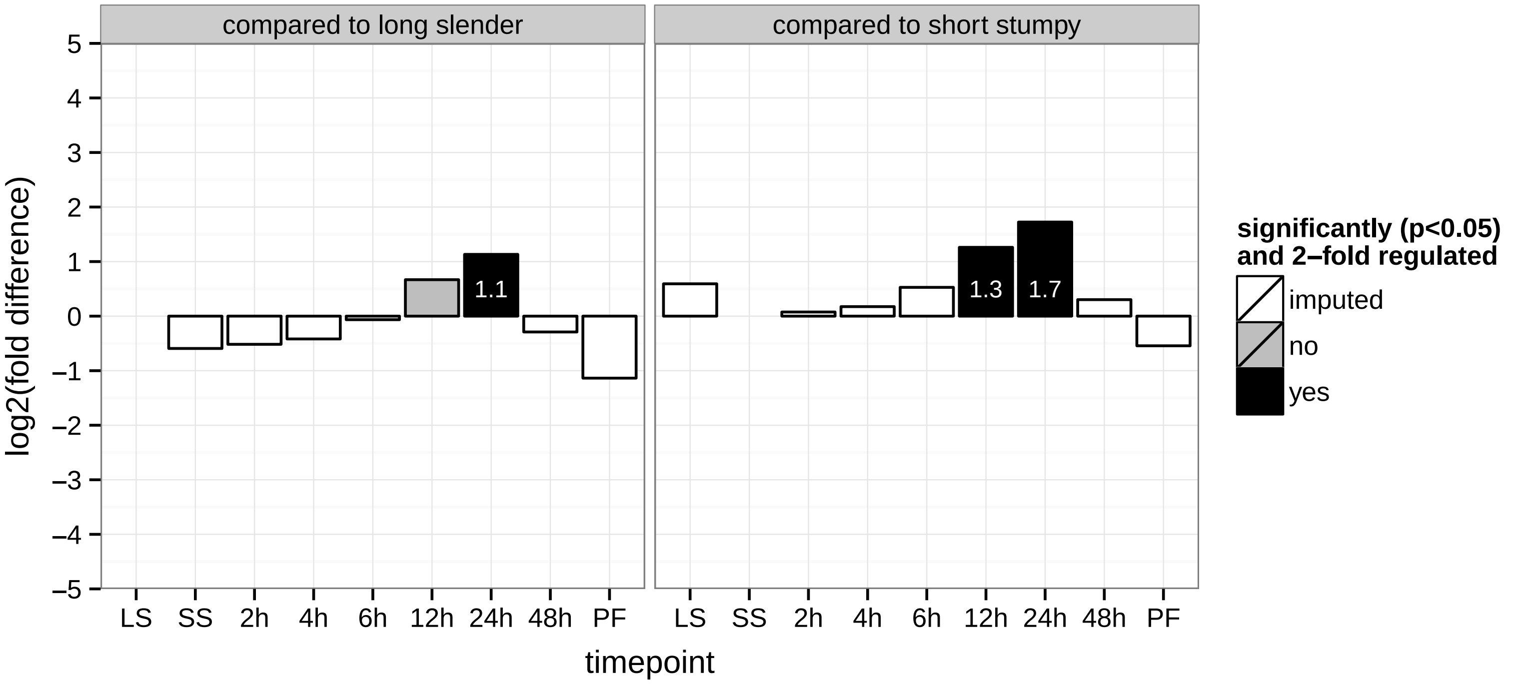
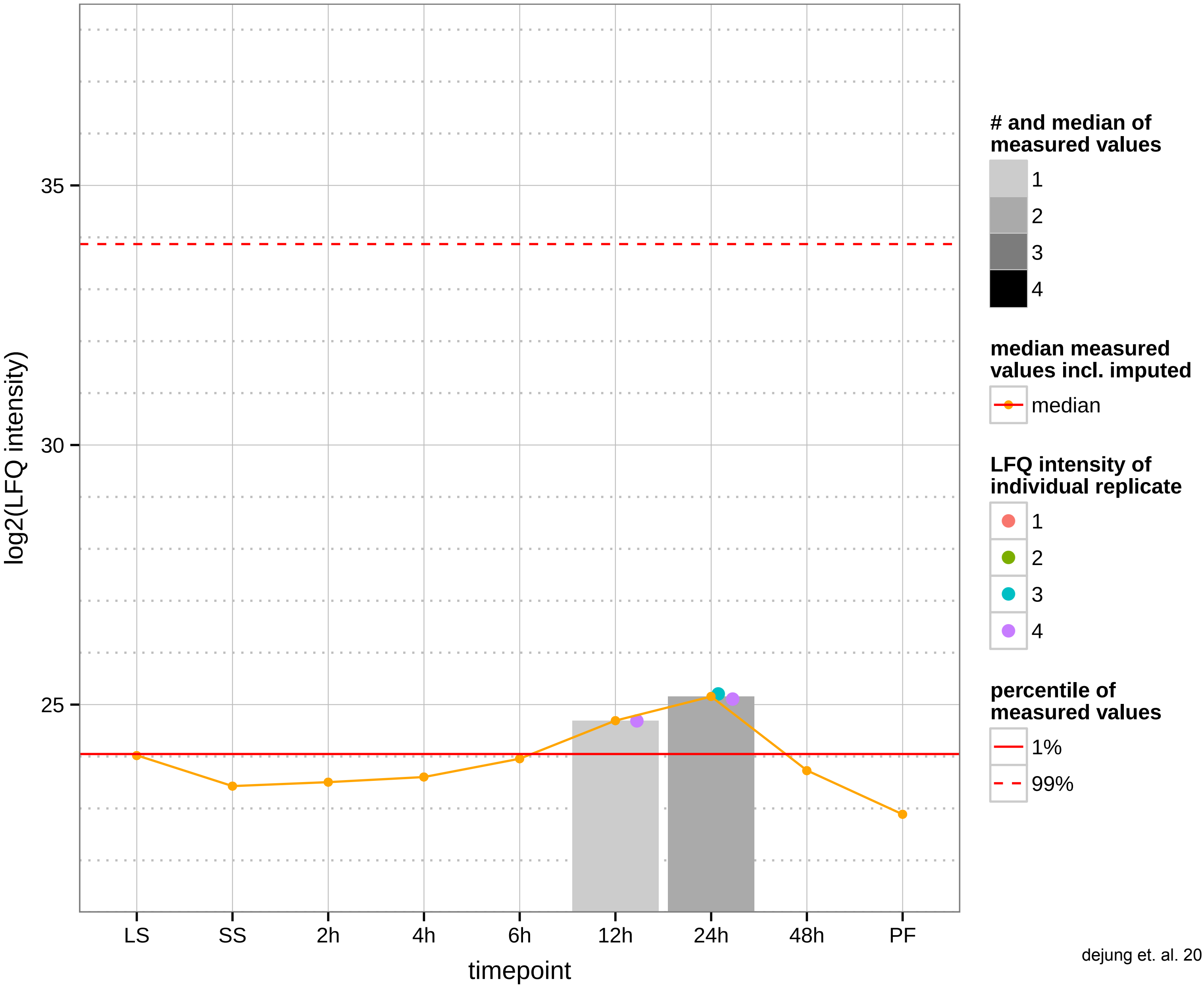
hypothetical protein, conserved
Tb927.8.1250
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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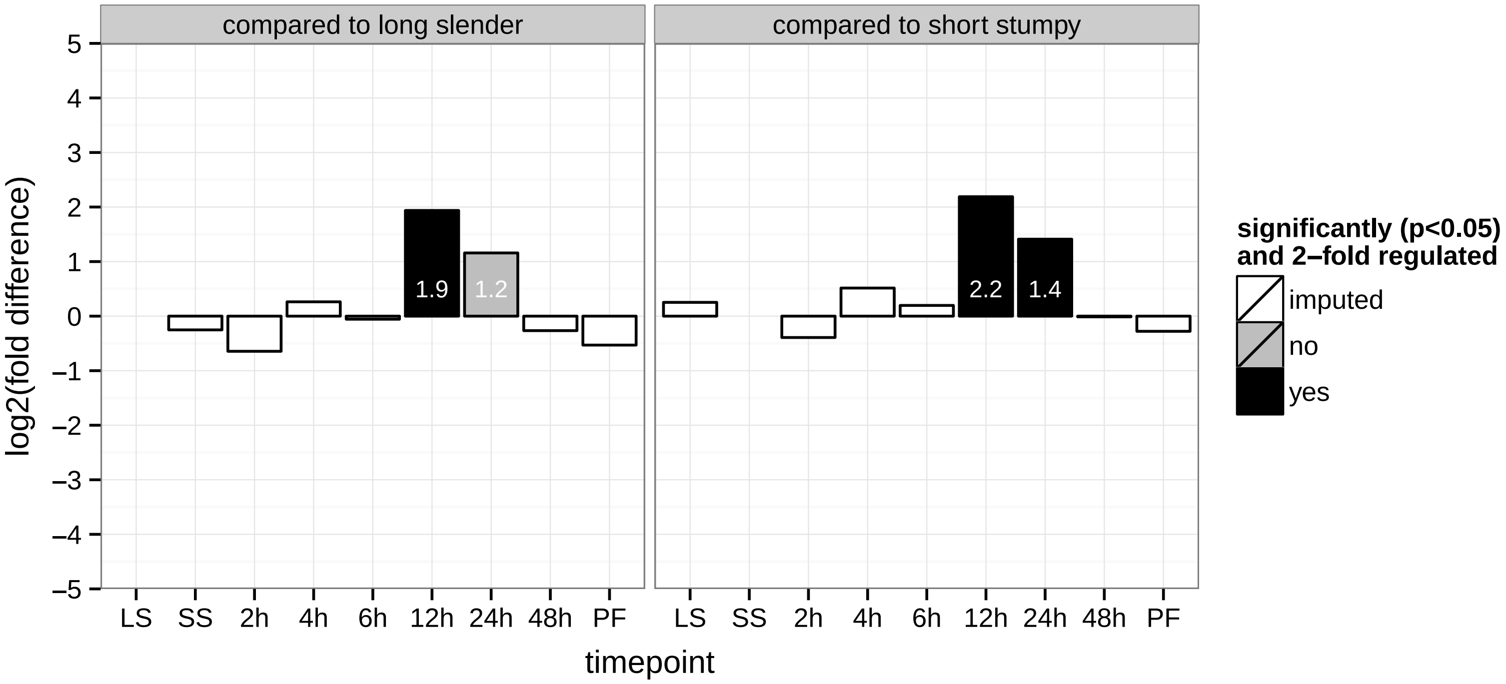
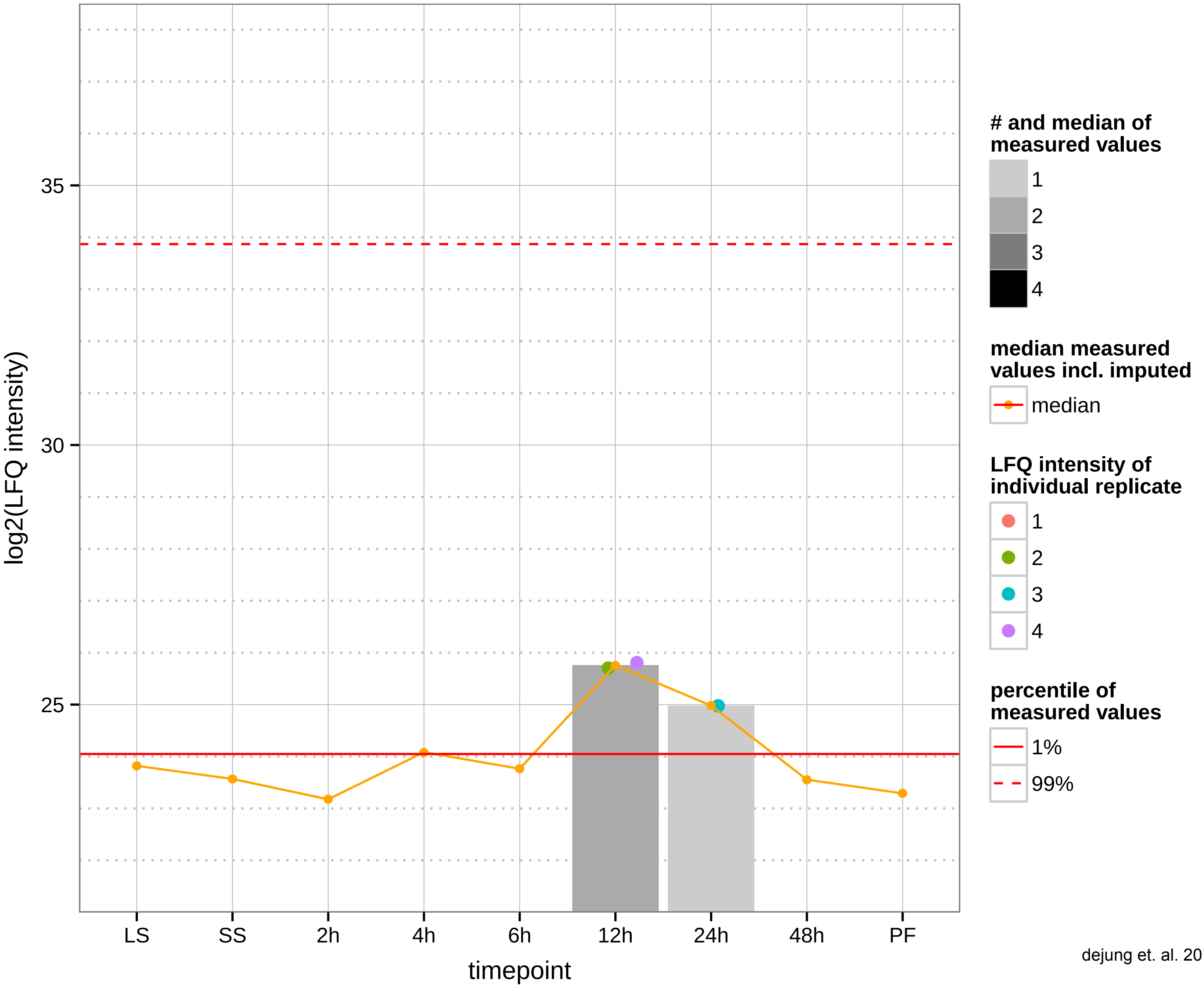
metal–ion transporter, putative
Tb927.8.7460;Tb927.4.4960;Tb11.v5.0836
AGOF: null, cation transmembrane transporter activity, metal ion transmembrane transporter activity
AGOC: null, membrane, acidocalcisome, integral to membrane, membrane
AGOP: null, cation transport, response to metal ion
PGOF: cation transmembrane transporter activity
PGOC: integral to membrane
PGOP: cation transport, transmembrane transport





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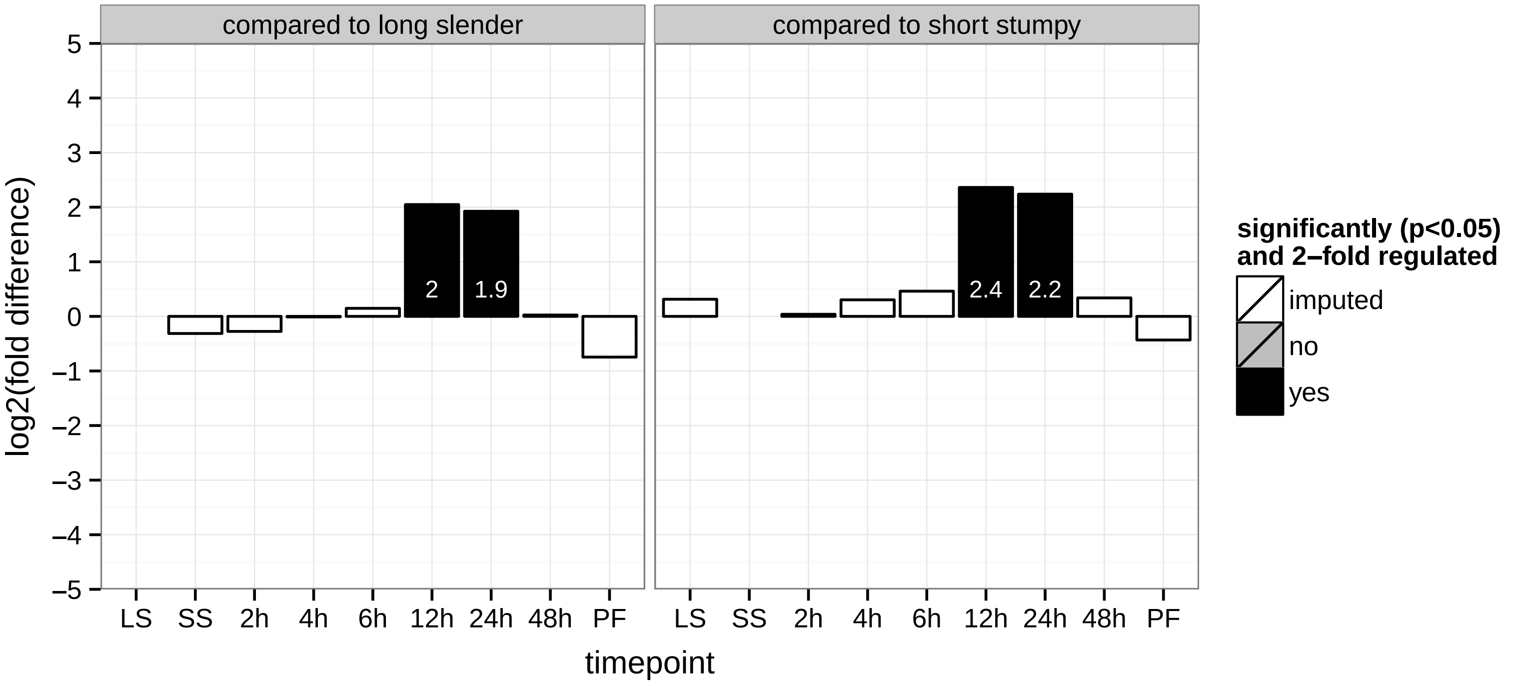
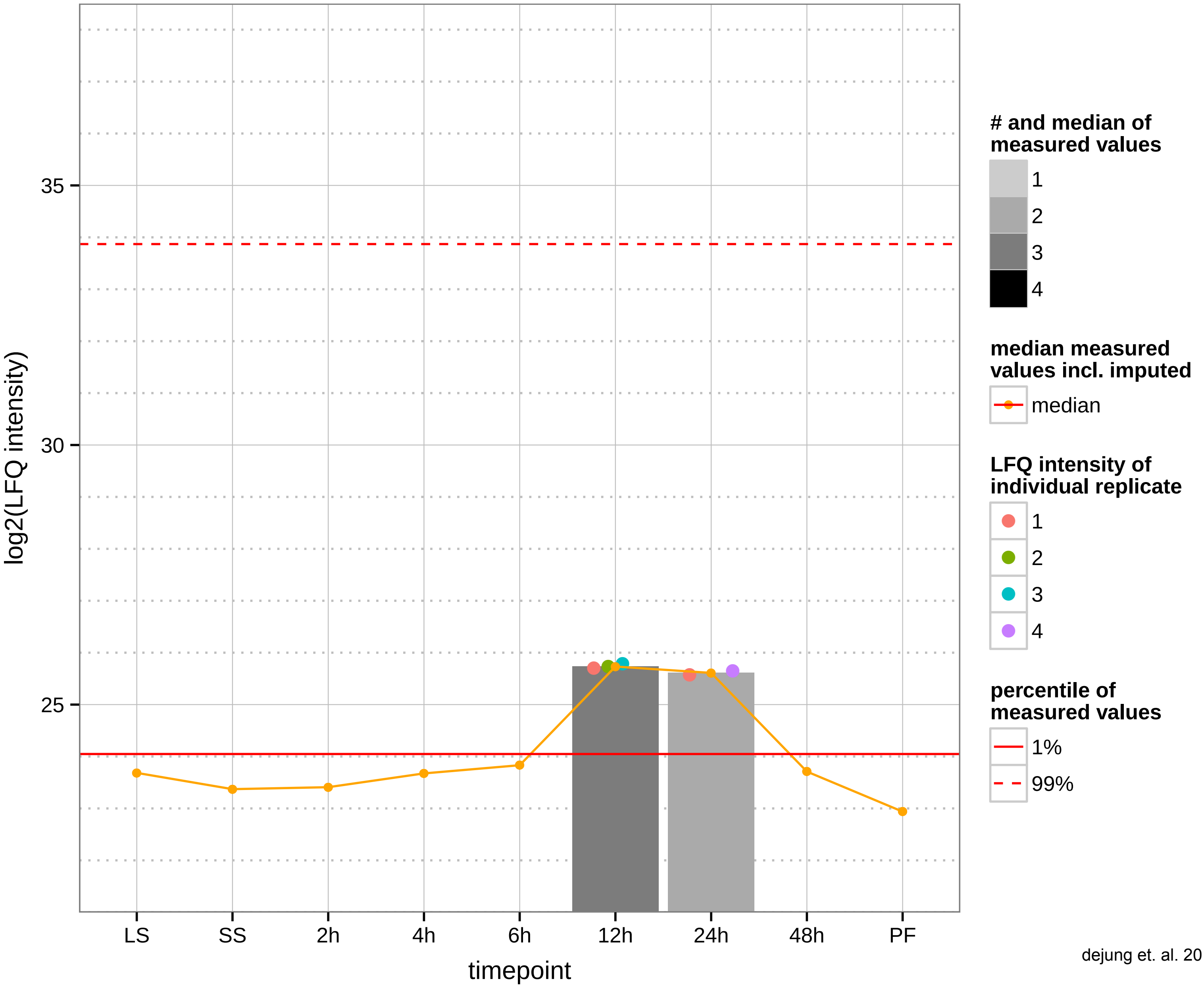
hypothetical protein, conserved
Tb927.9.12330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: cell redox homeostasis





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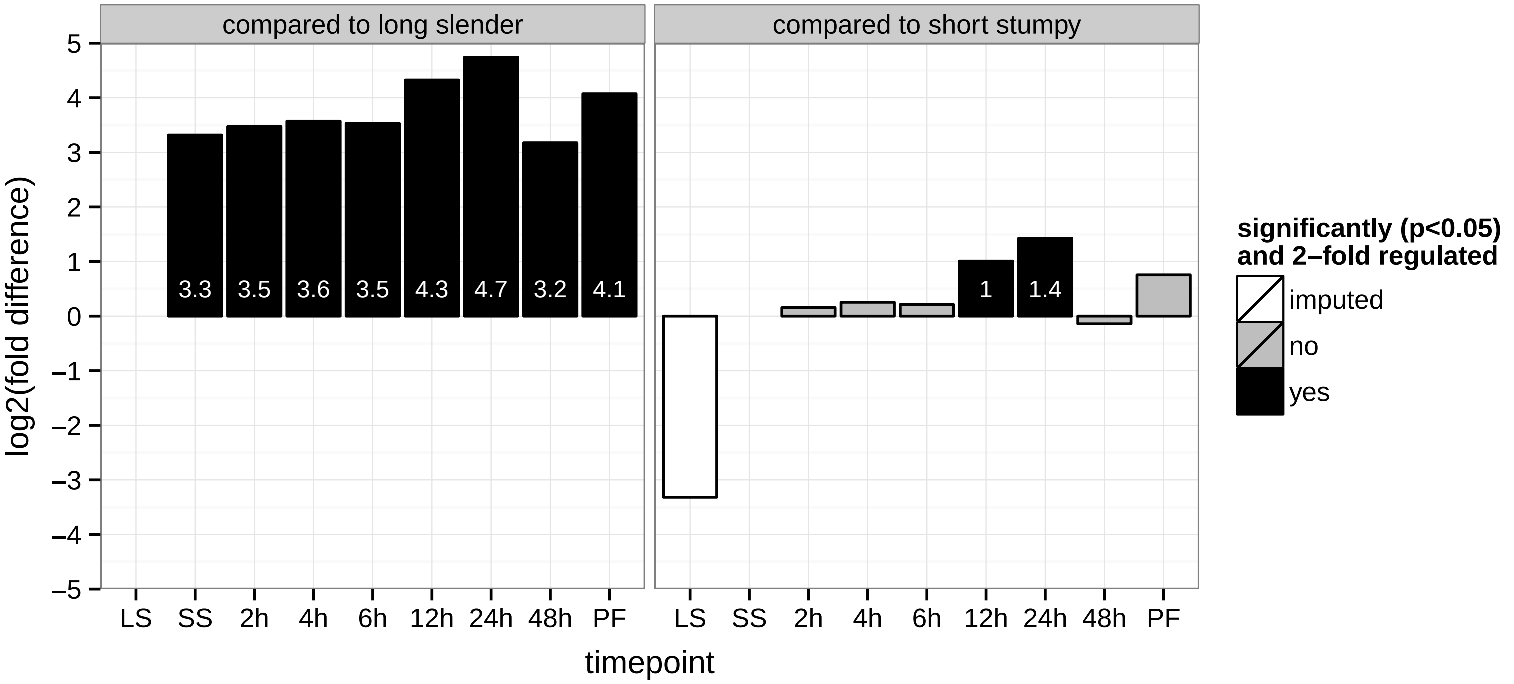
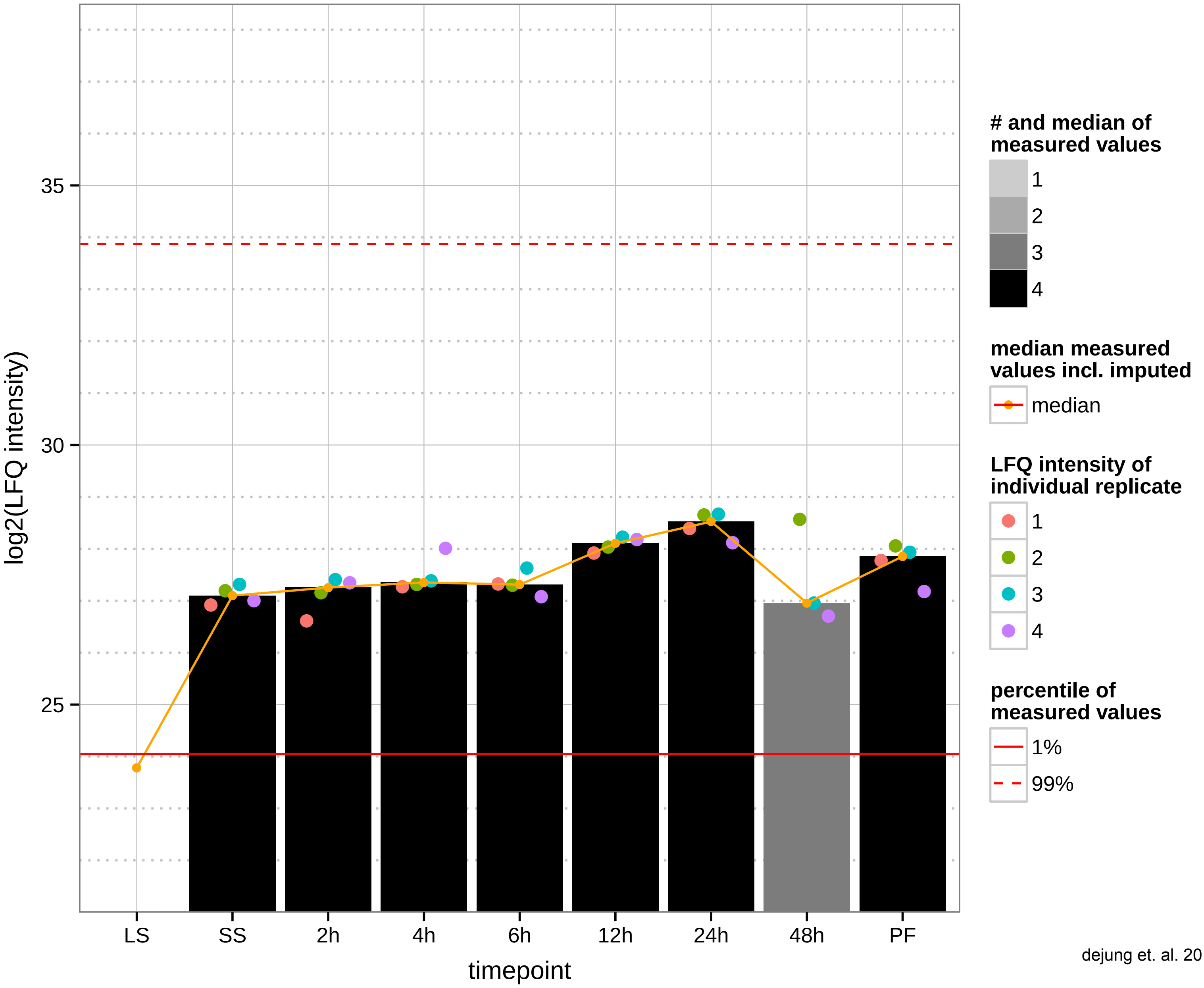
hypothetical protein, conserved
Tb927.9.3780
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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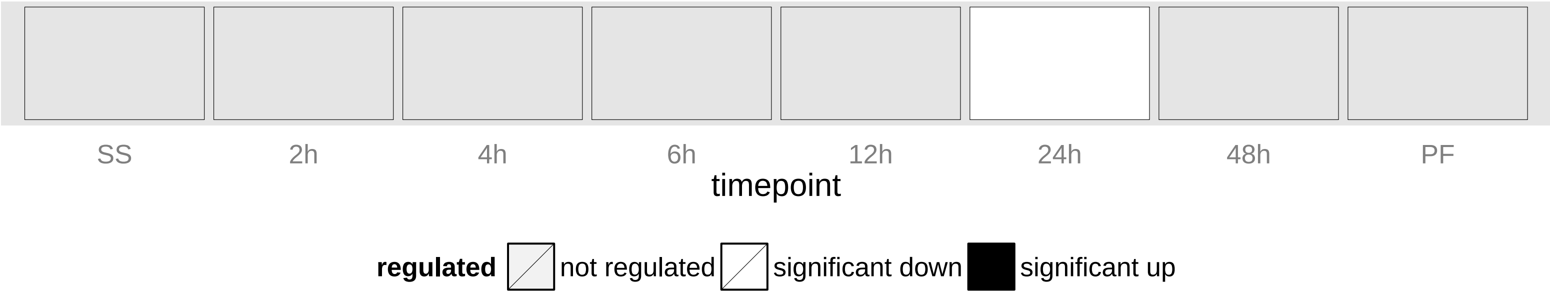

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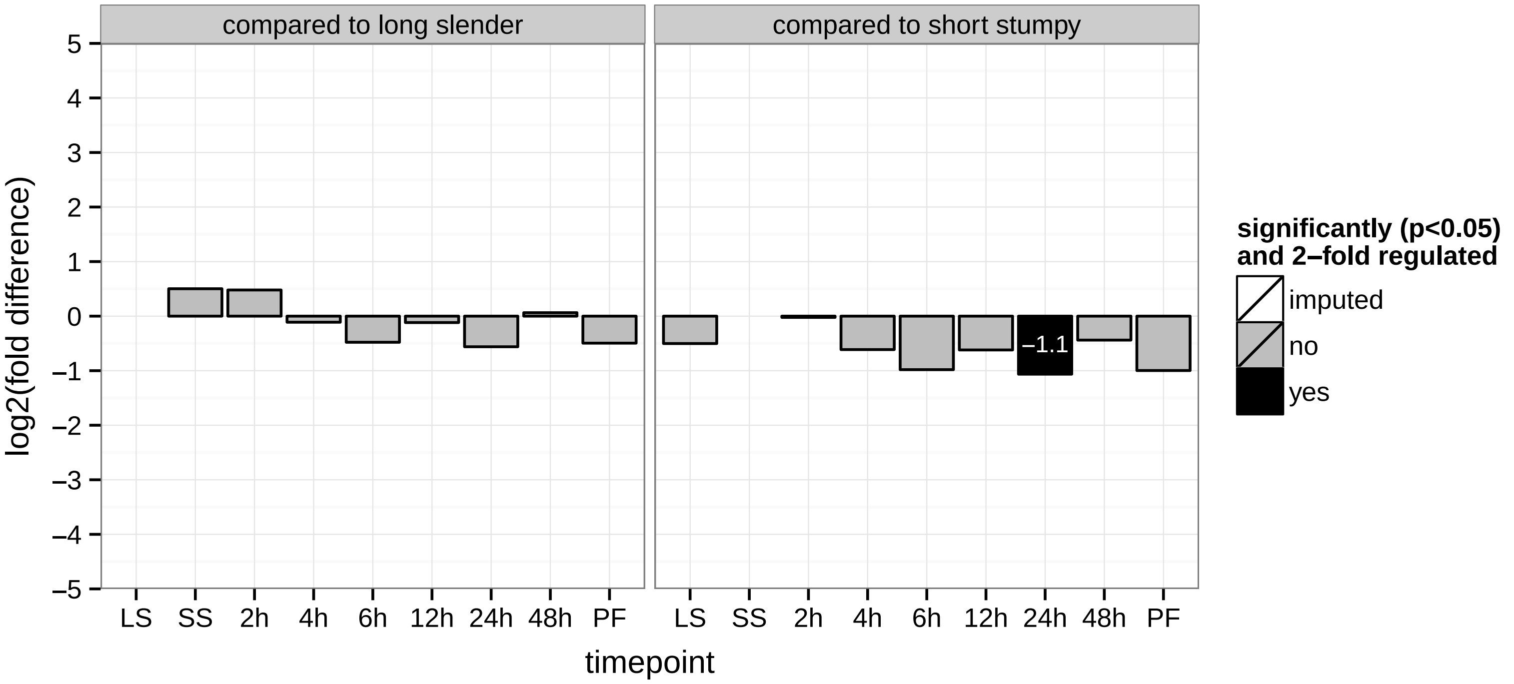
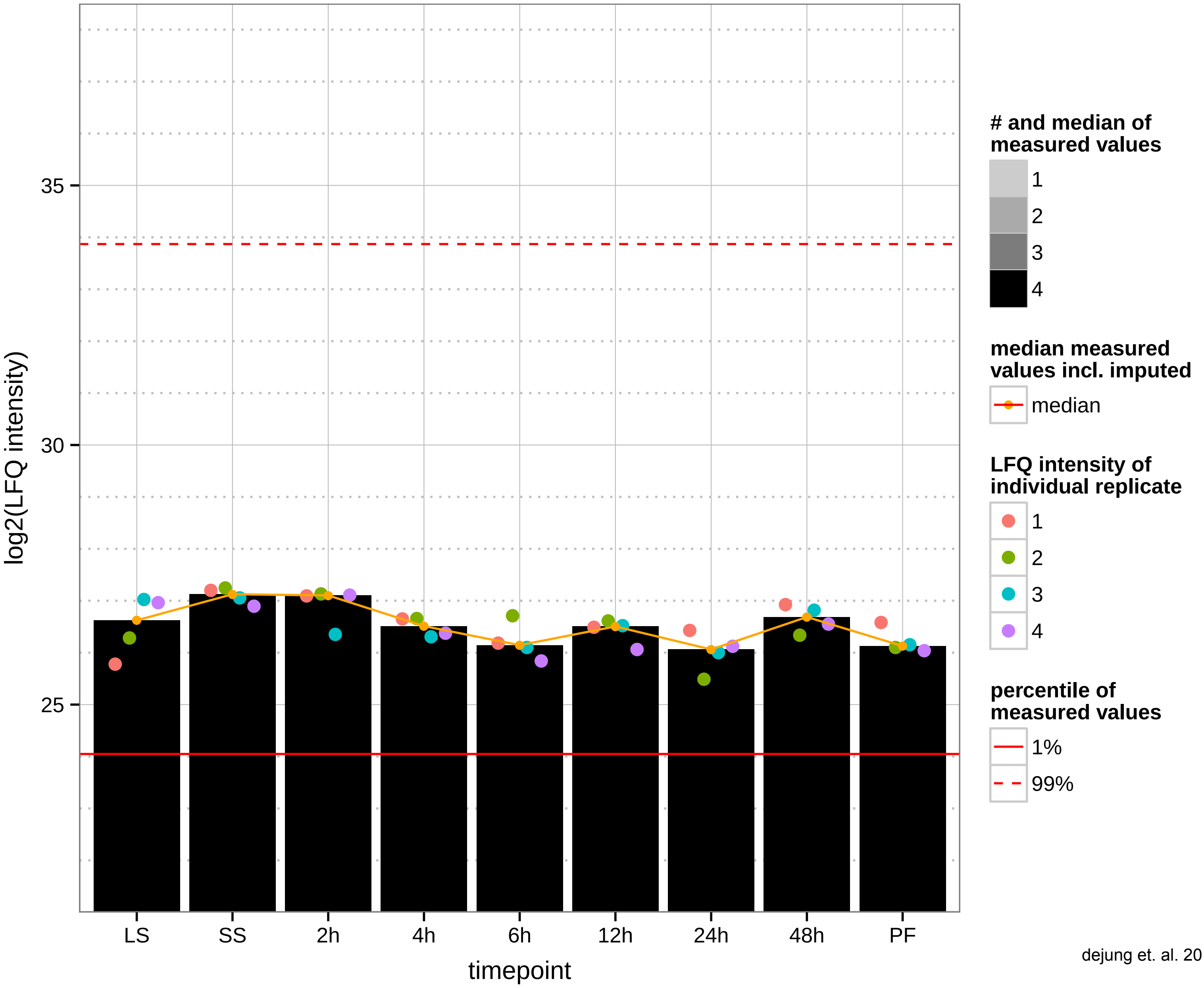
leucine–rich repeat protein (LRRP), putative
Tb927.1.4180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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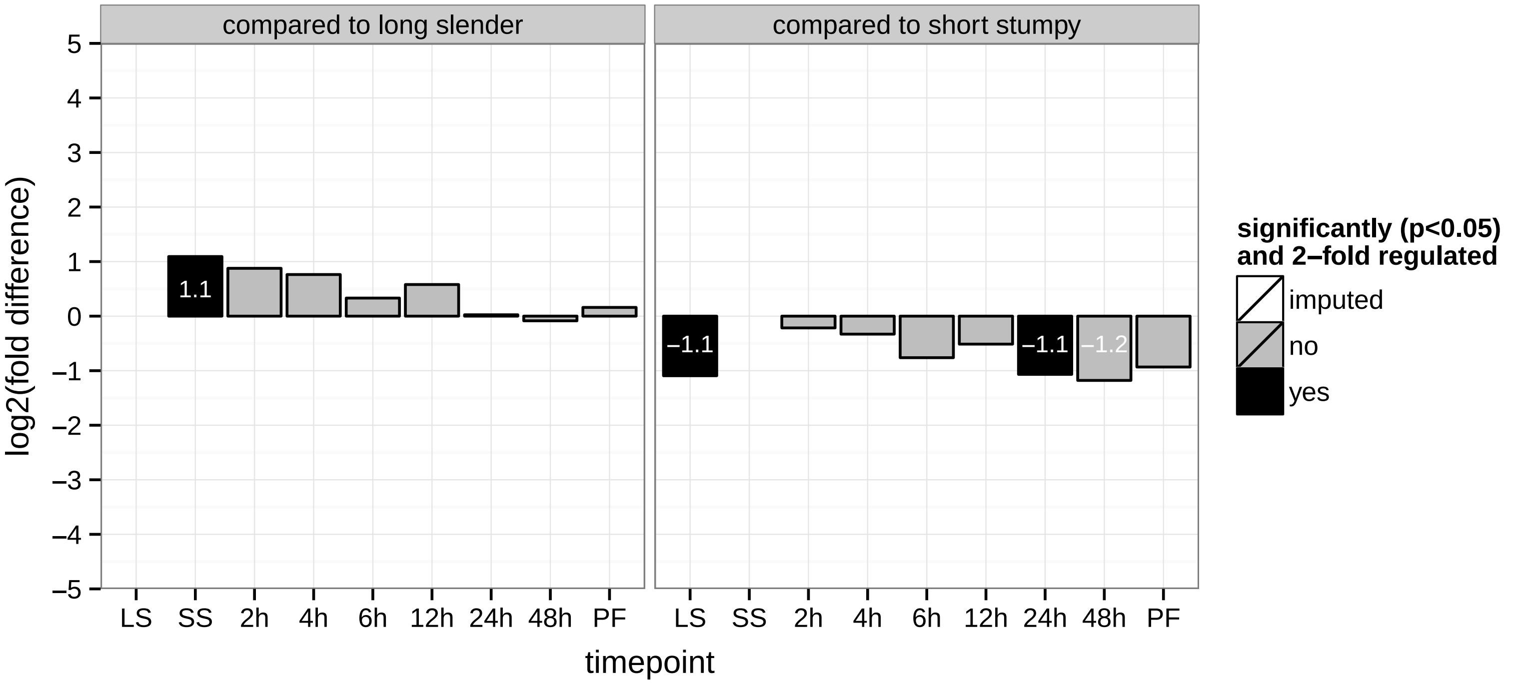
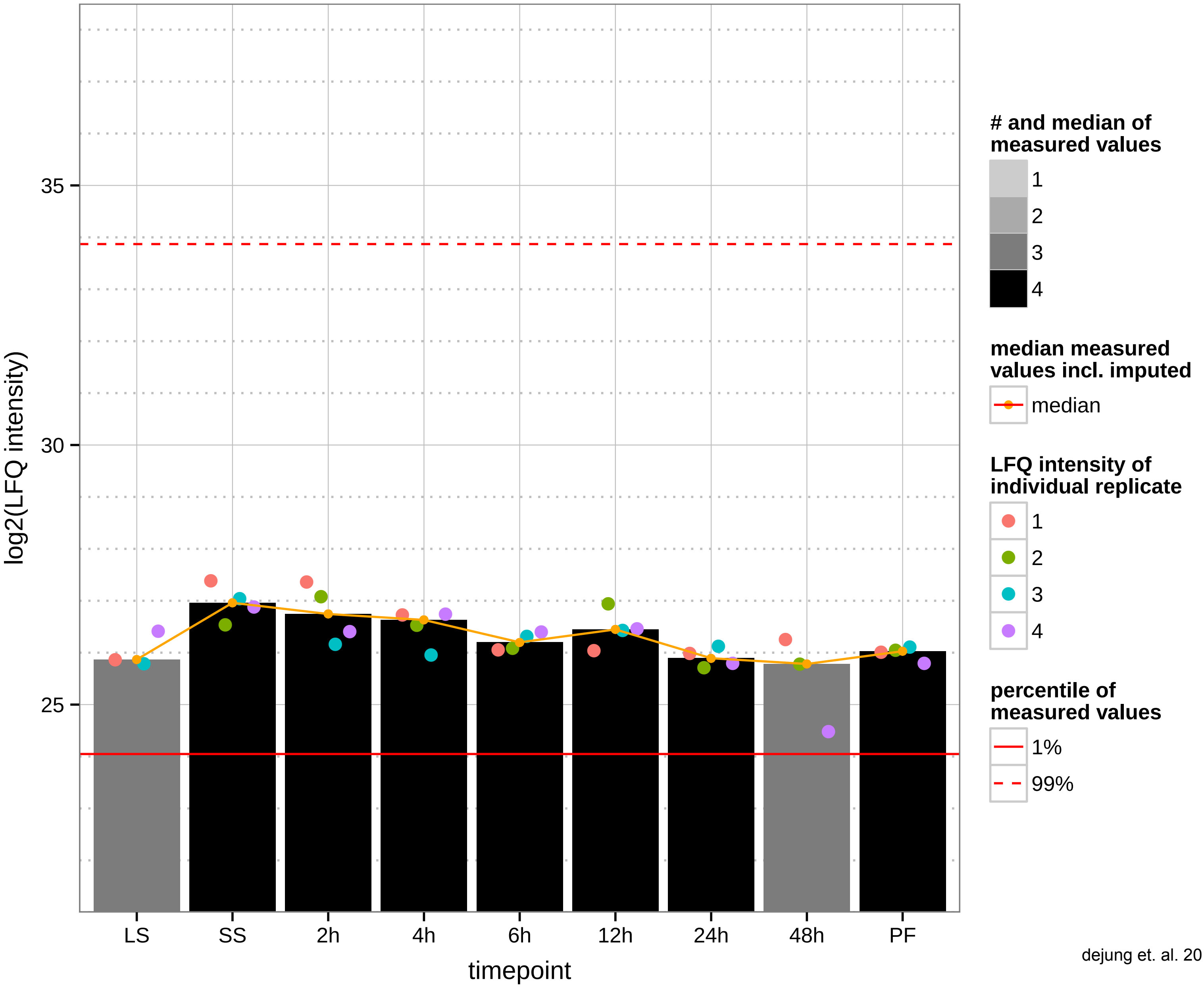
GPI transamidase component GAA1 (TbGAA1)
Tb927.10.210
AGOF: GPI–anchor transamidase activity
AGOC: GPI–anchor transamidase complex, anchored to plasma membrane
AGOP: GPI anchor biosynthetic process
PGOF: null
PGOC: GPI–anchor transamidase complex, integral to membrane
PGOP: null





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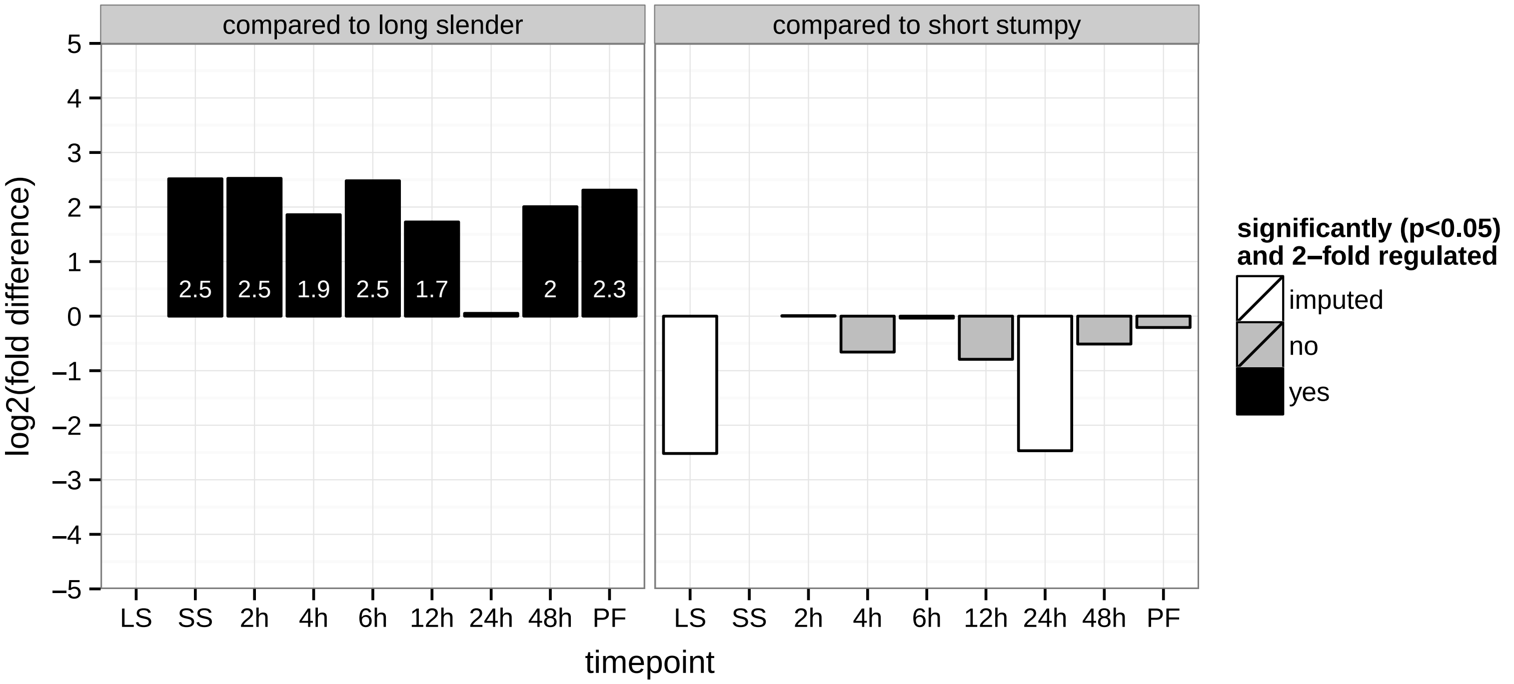
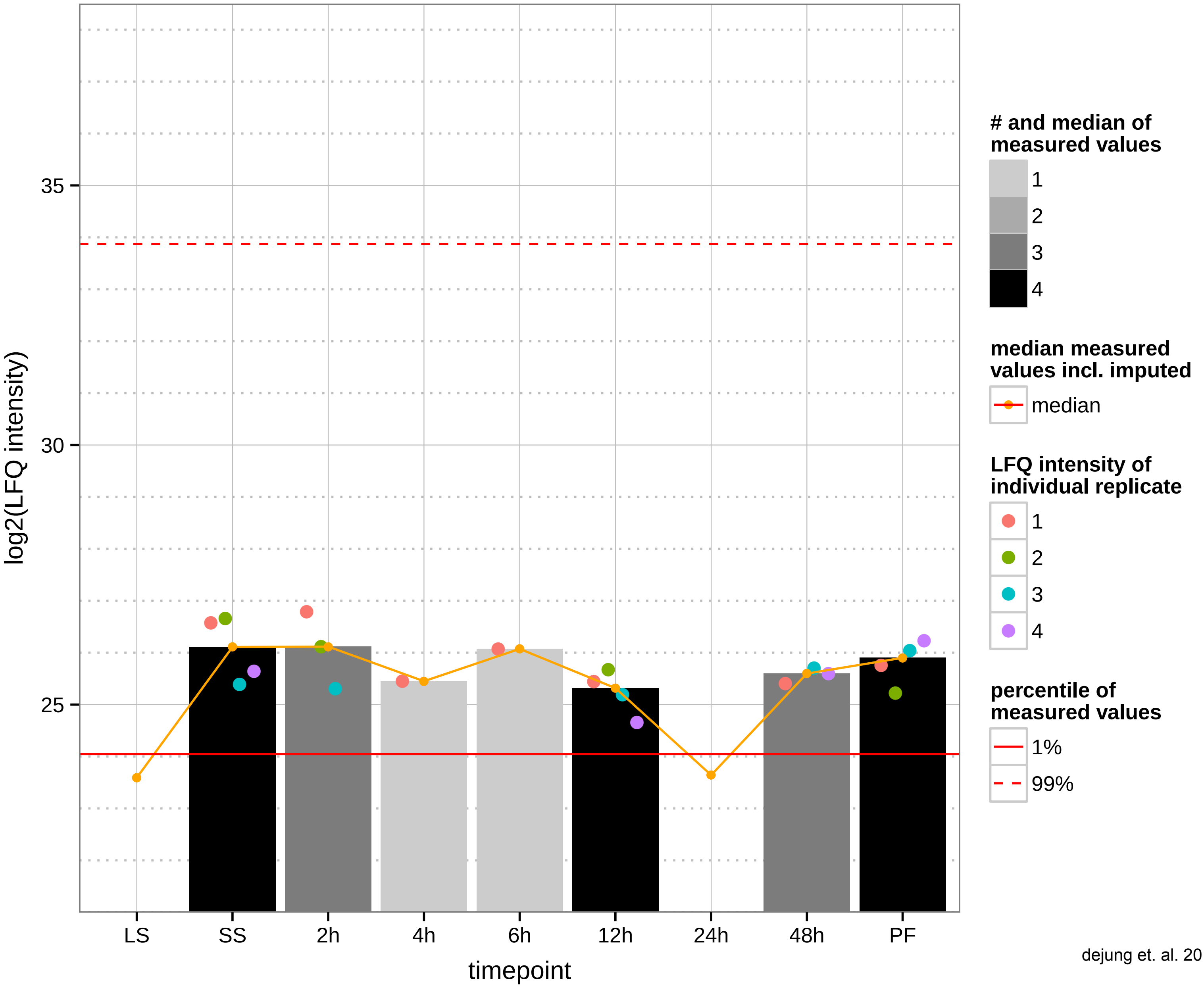
hypothetical protein, conserved
Tb927.10.3310
AGOF: null
AGOC: null
AGOP: ciliary or flagellar motility
PGOF: null
PGOC: null
PGOP: null





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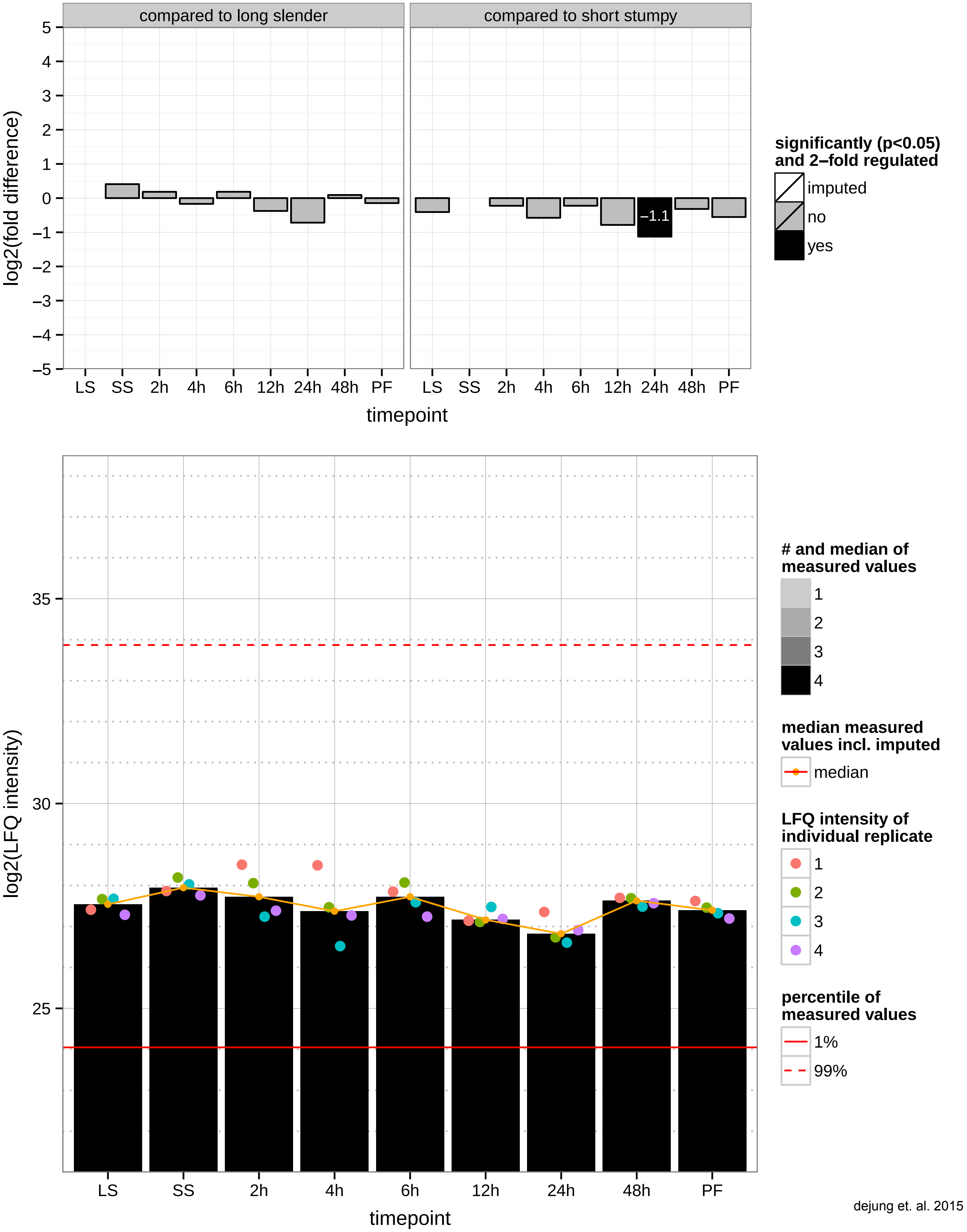
paraflagellar rod component, putative (PFC17)
Tb927.11.11210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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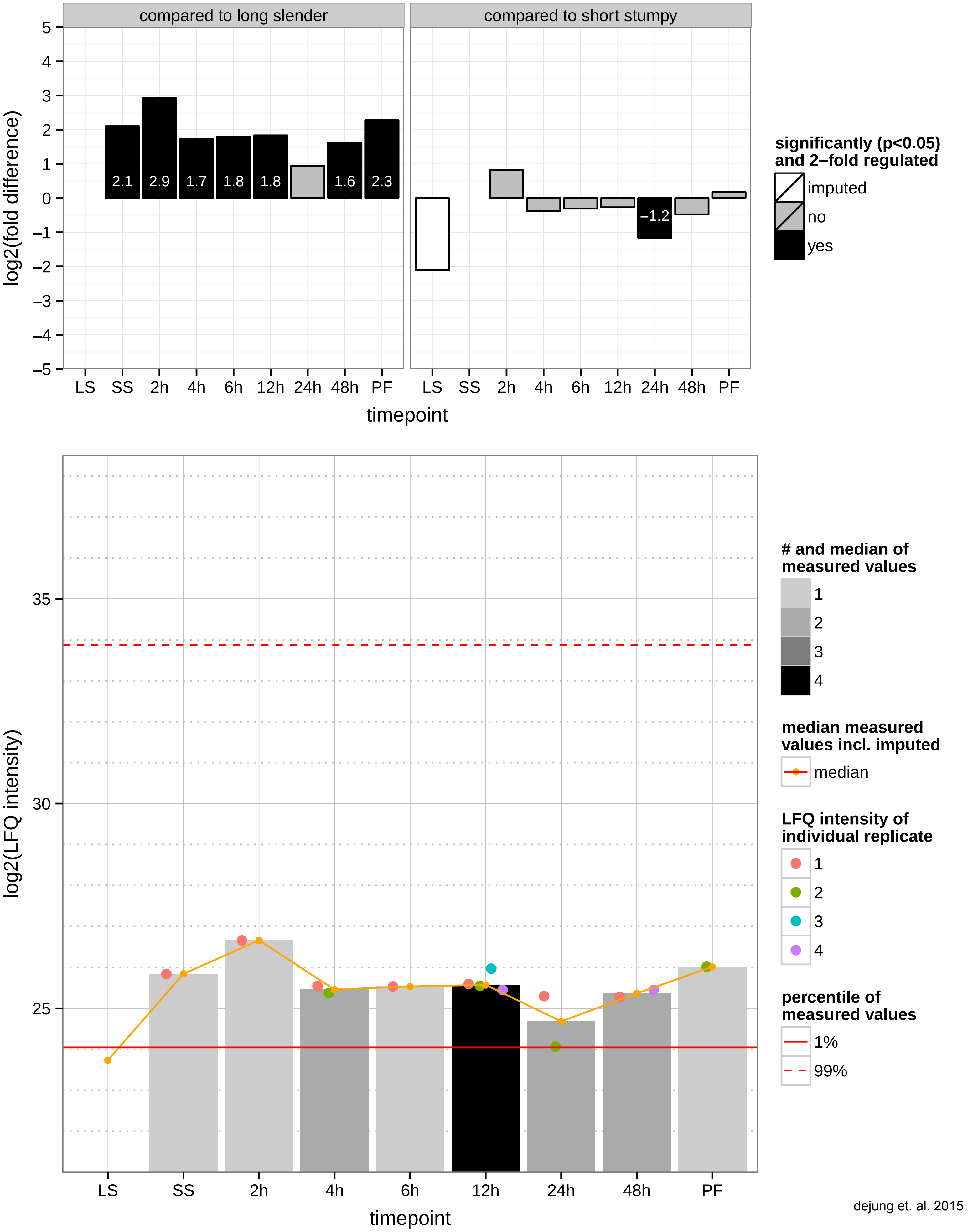
hypothetical protein, conserved
Tb927.11.11260
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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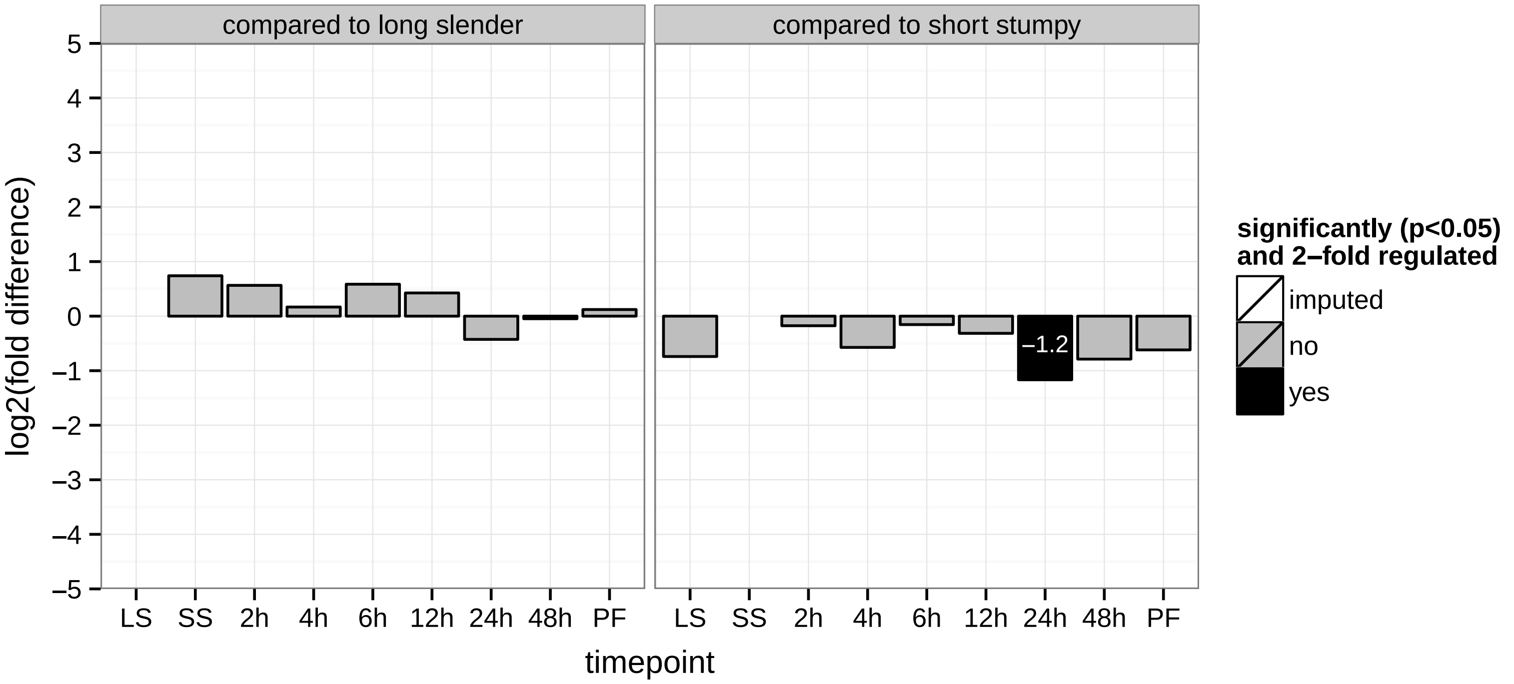
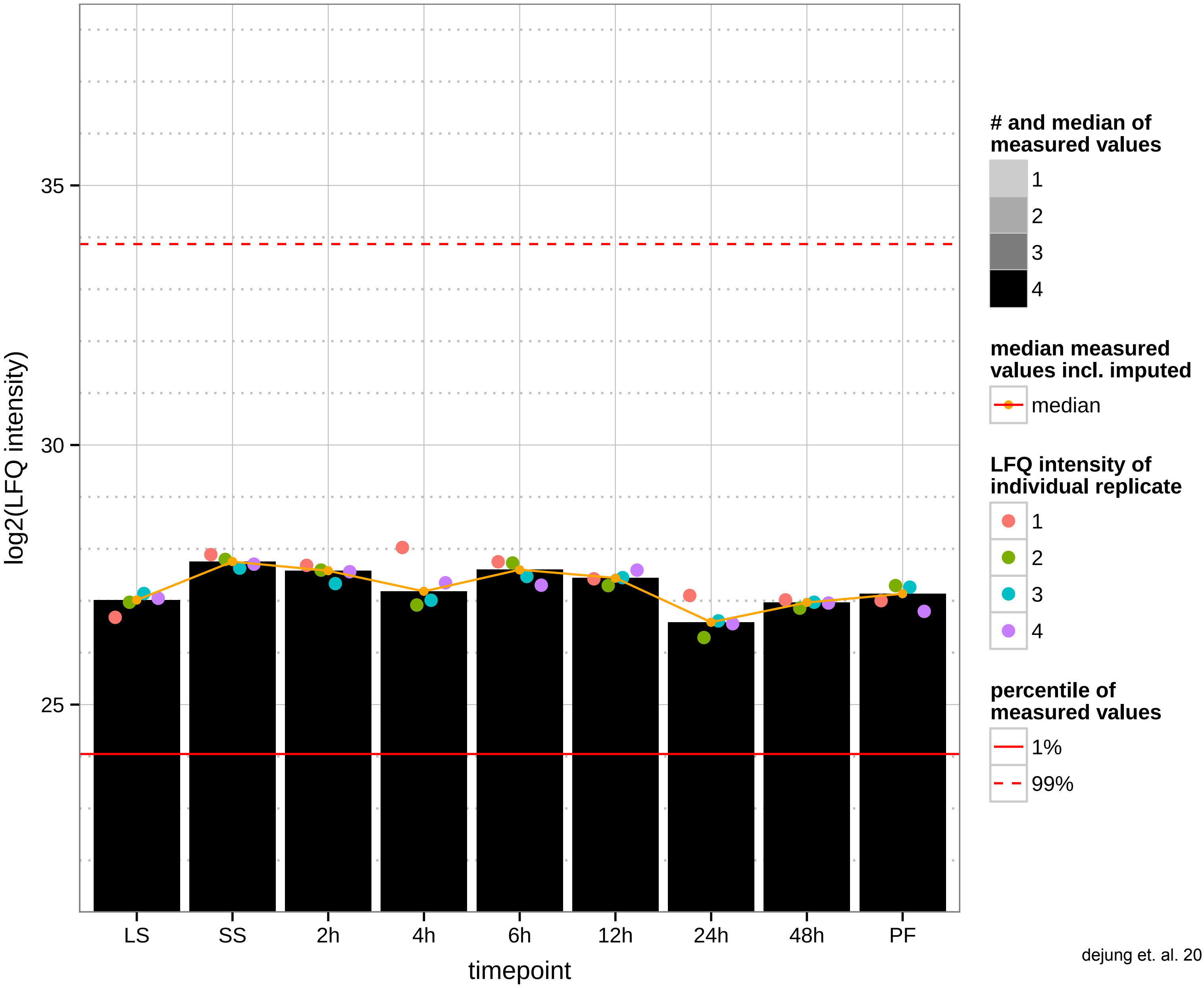
hypothetical protein, conserved
Tb927.3.1200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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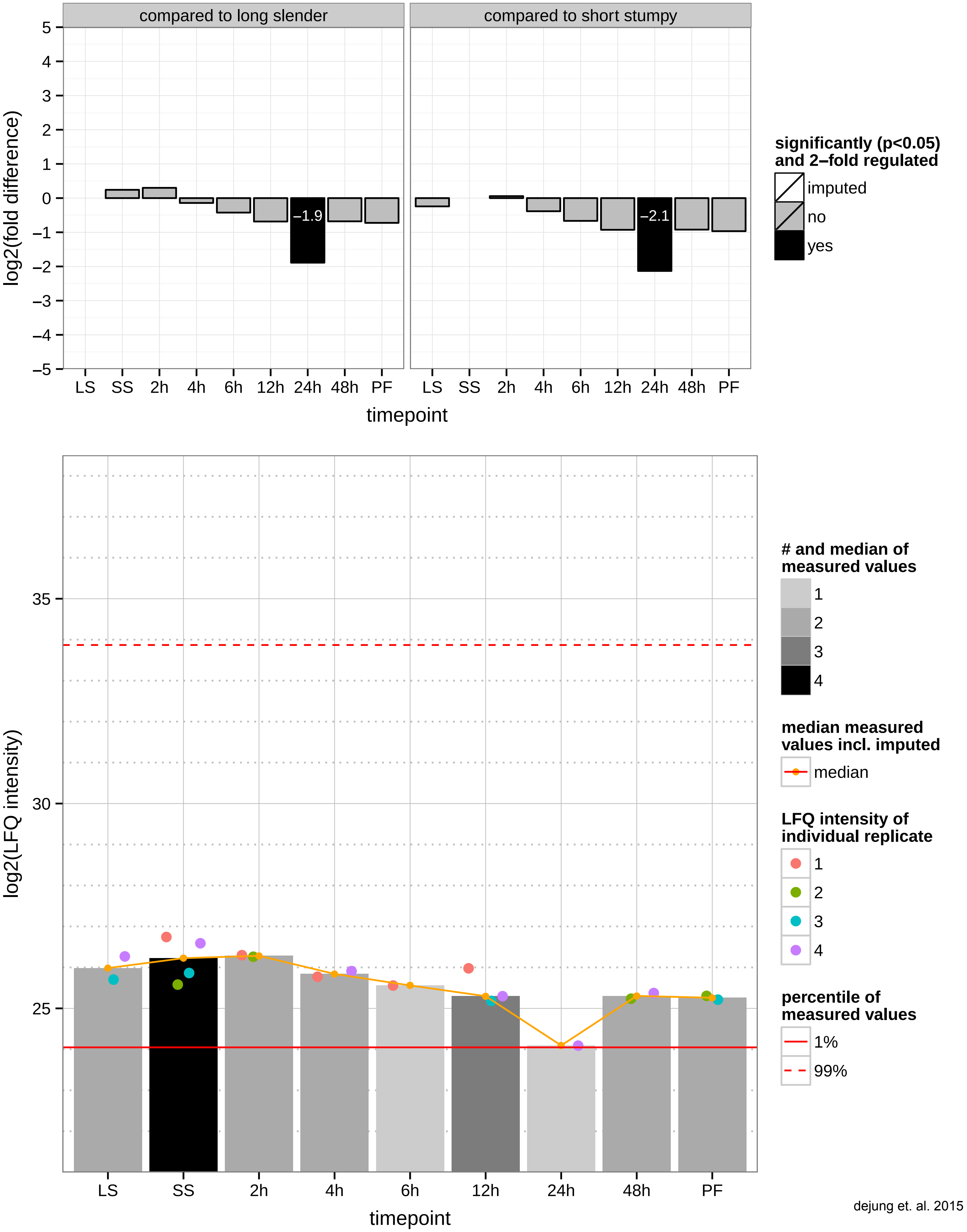
hypothetical protein, conserved
Tb927.3.4270
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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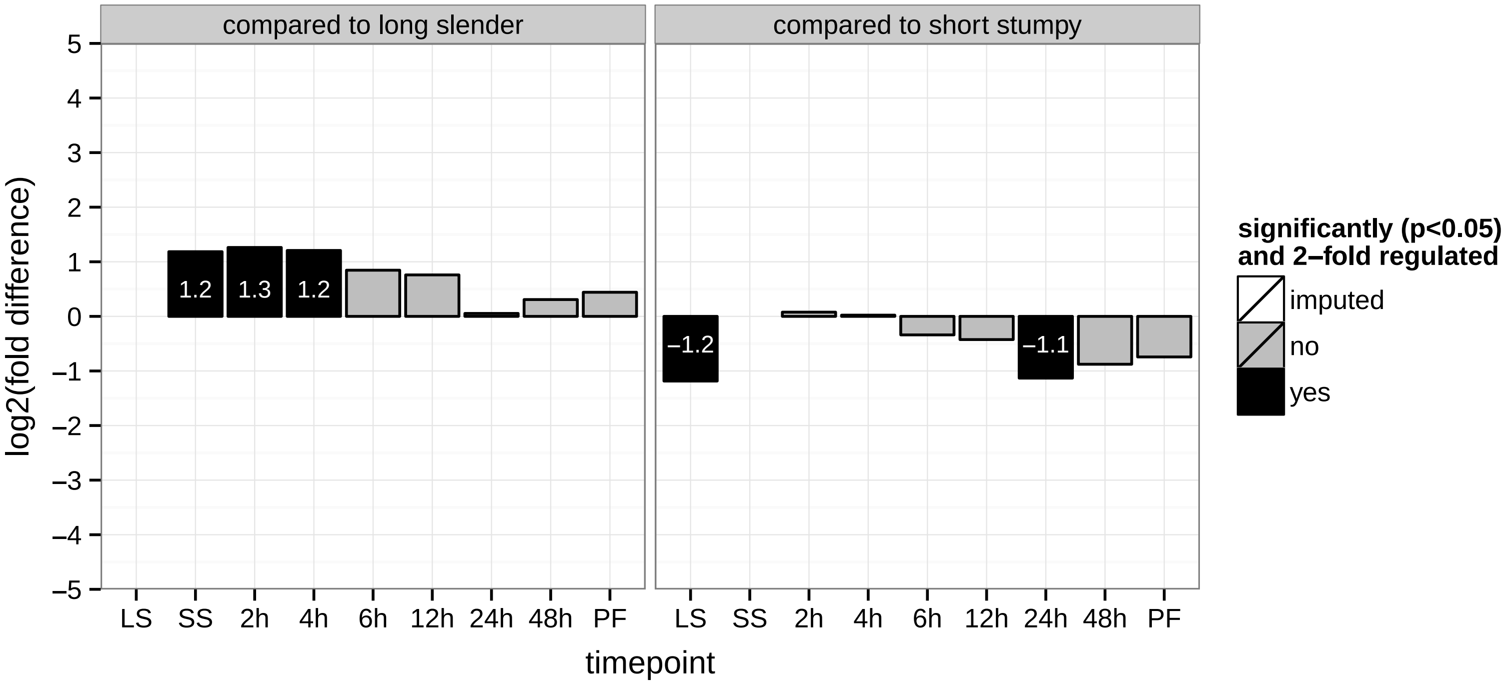
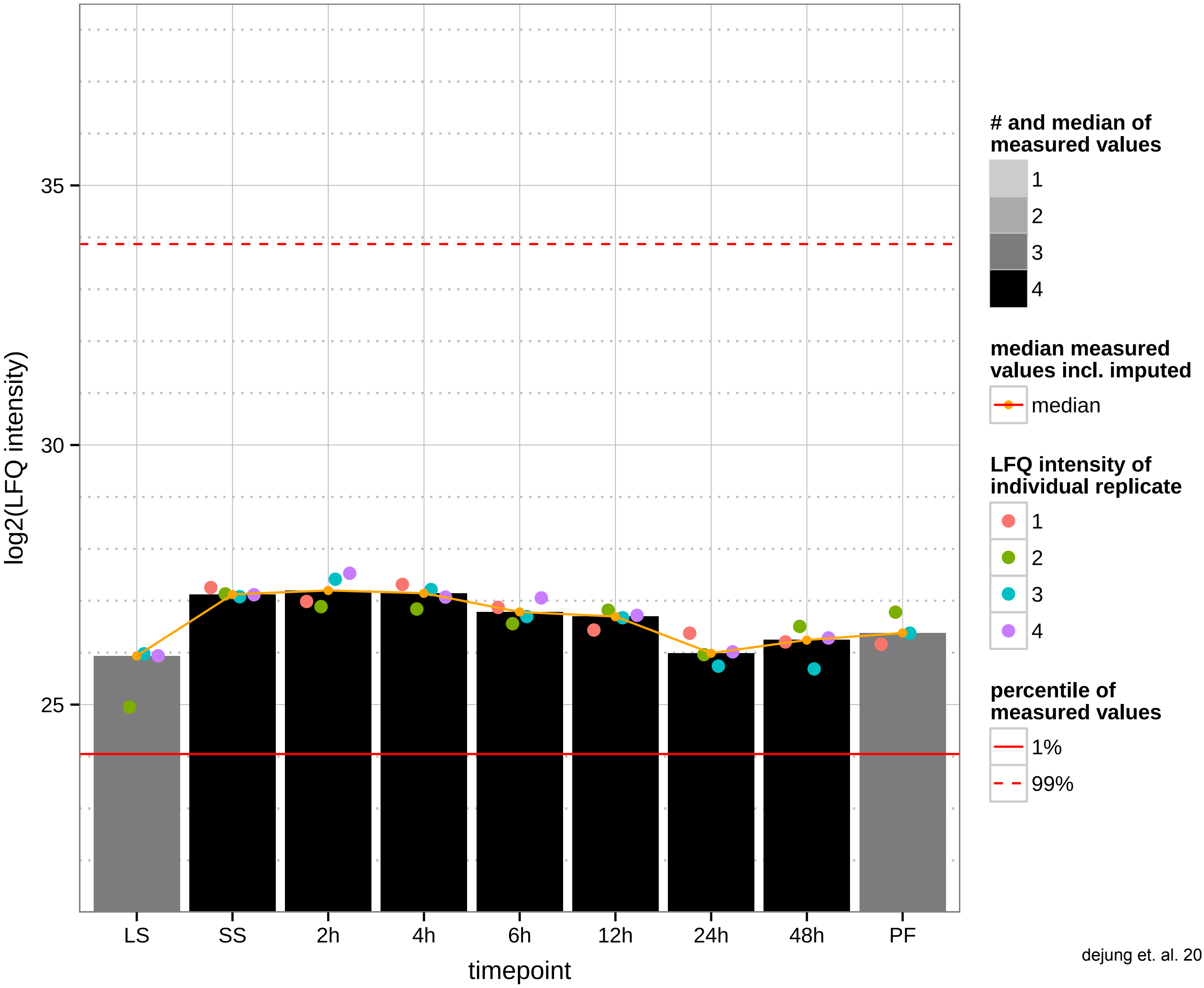
kinesin, putative
Tb927.6.2880
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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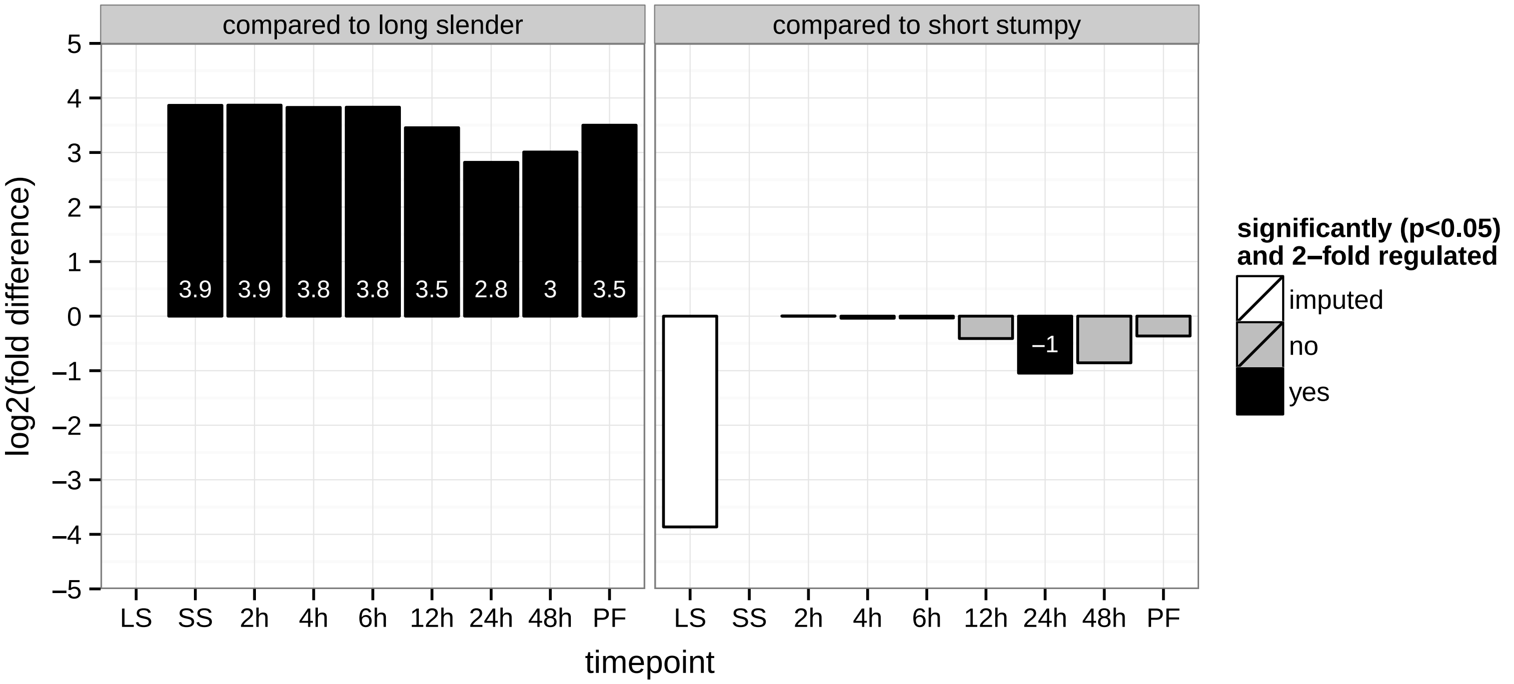
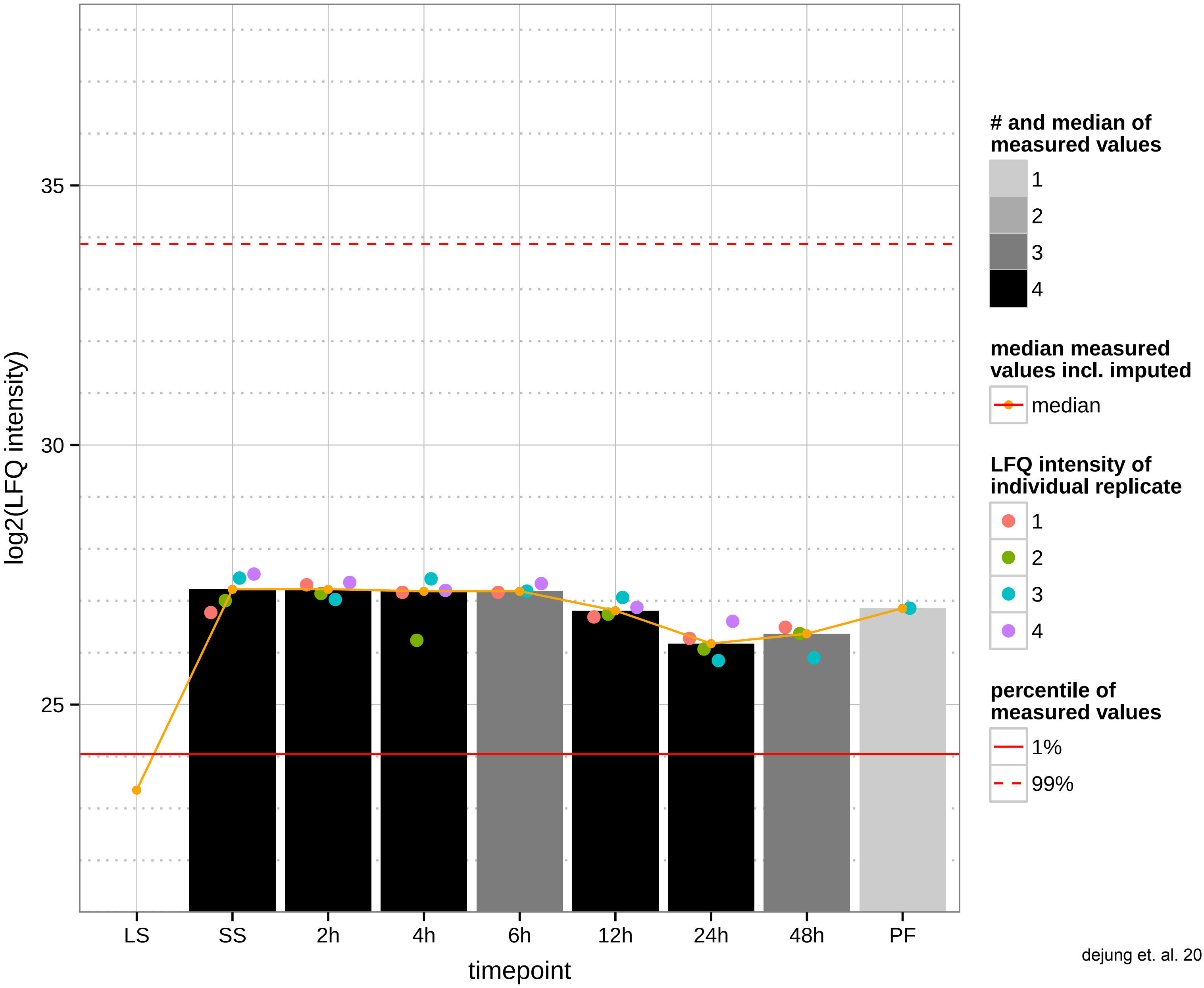
RING finger protein, putative
Tb927.6.3780
AGOF: nucleic acid binding, ubiquitin–protein ligase activity, zinc ion binding
AGOC: null
AGOP: histone ubiquitination
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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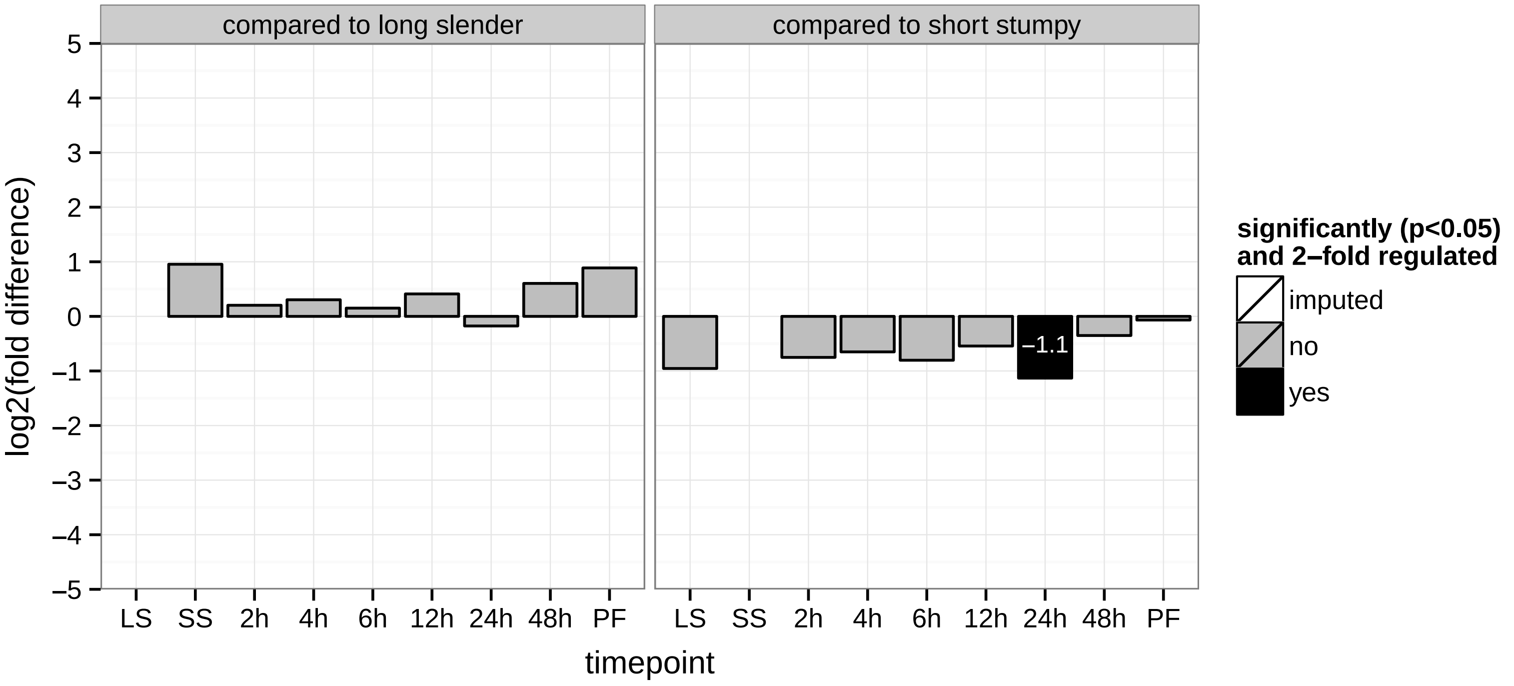
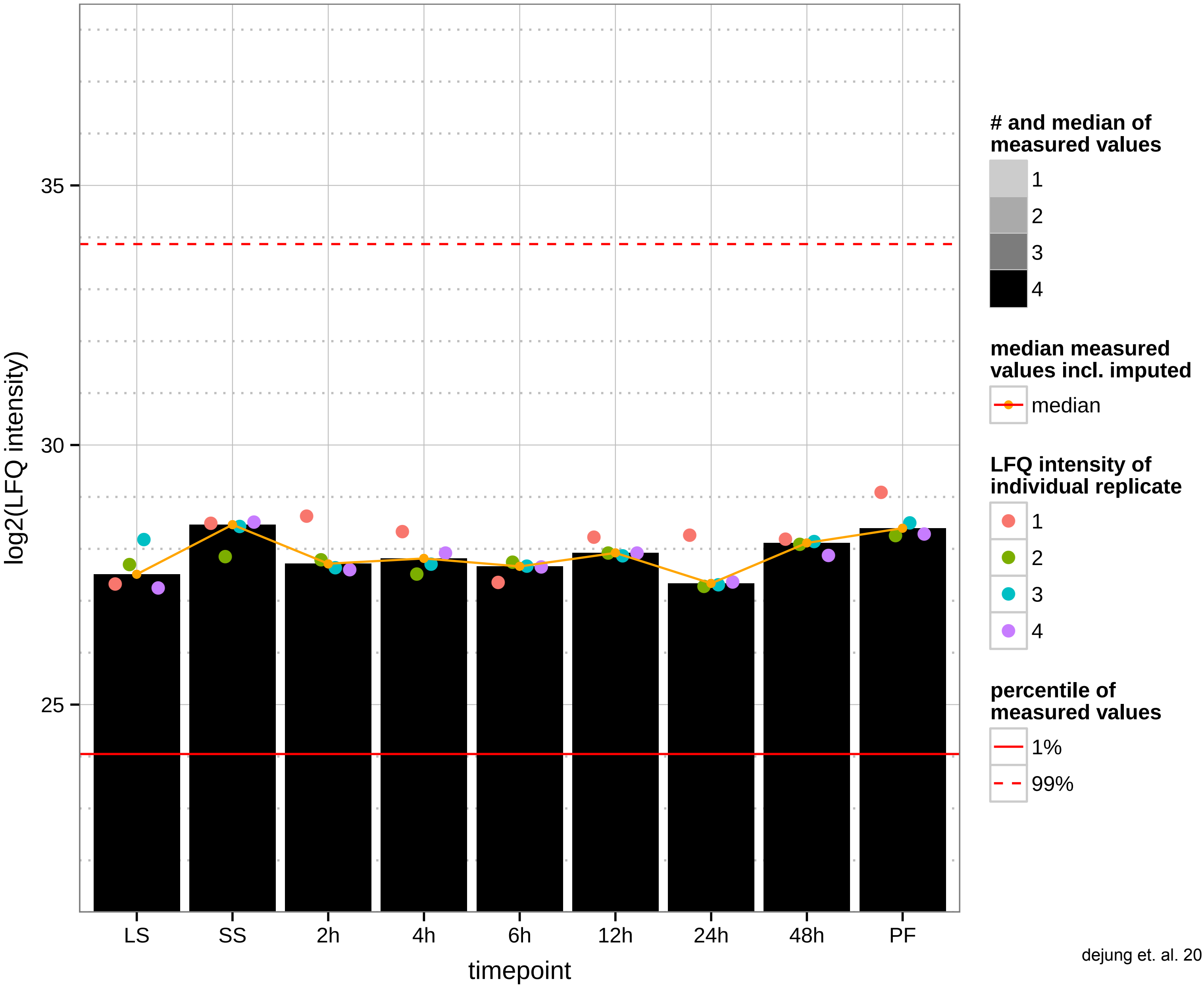
hypothetical protein, conserved
Tb927.6.840
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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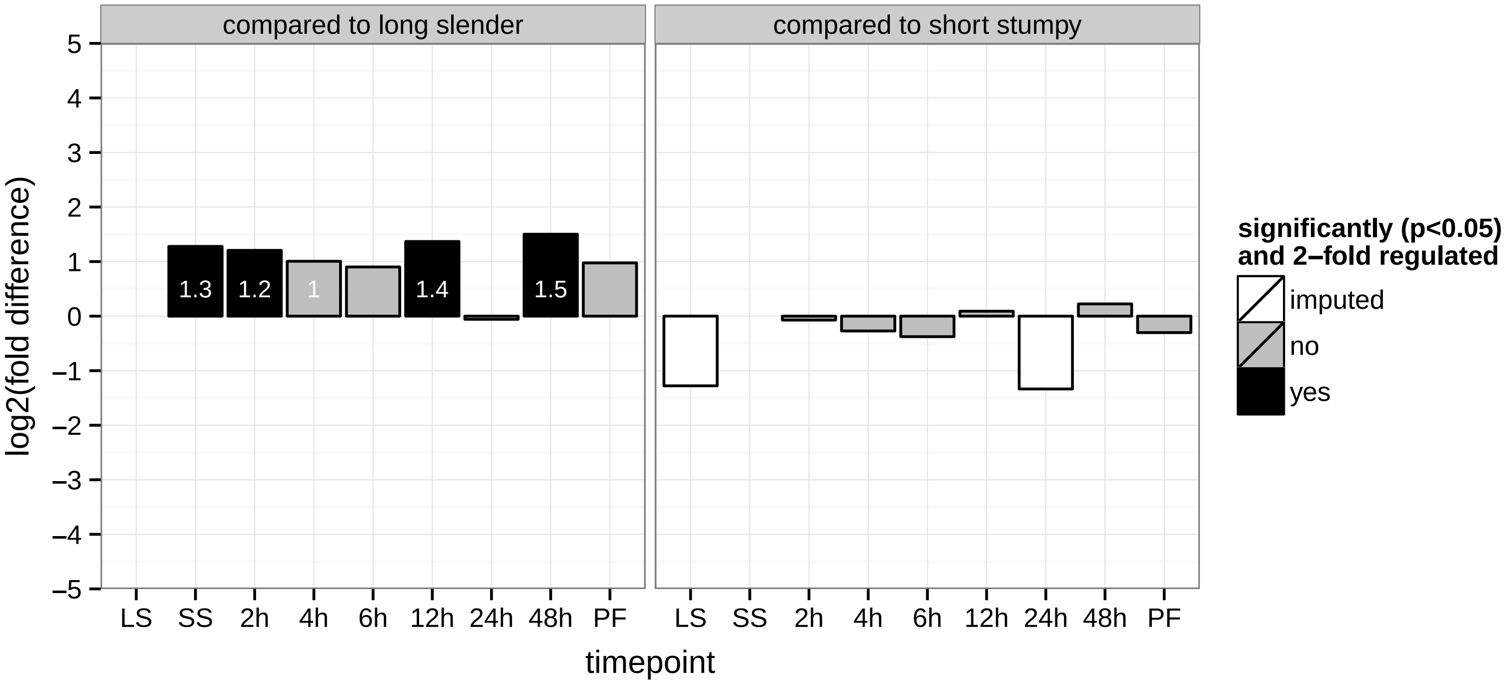
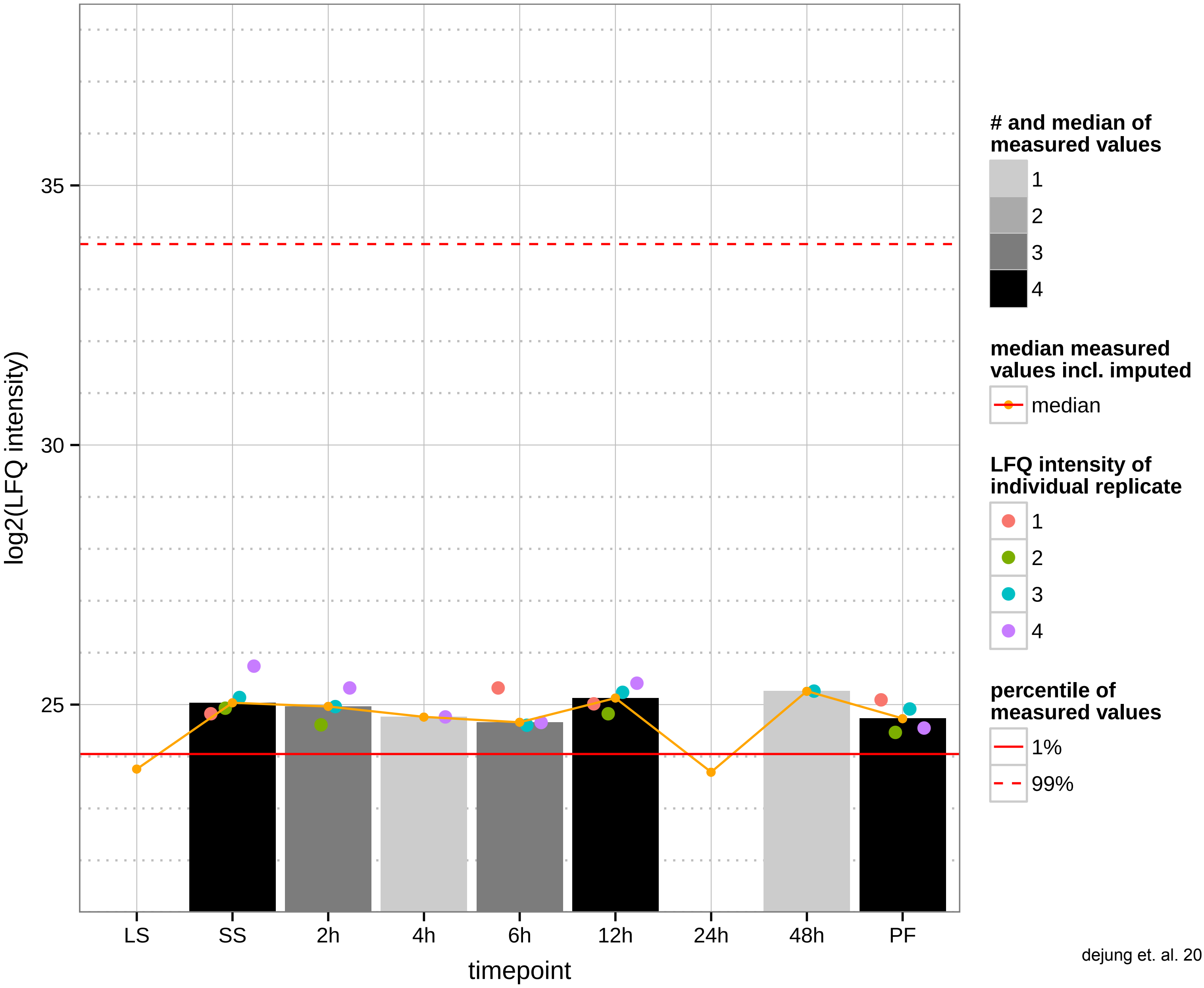
hypothetical protein, conserved
Tb927.7.1200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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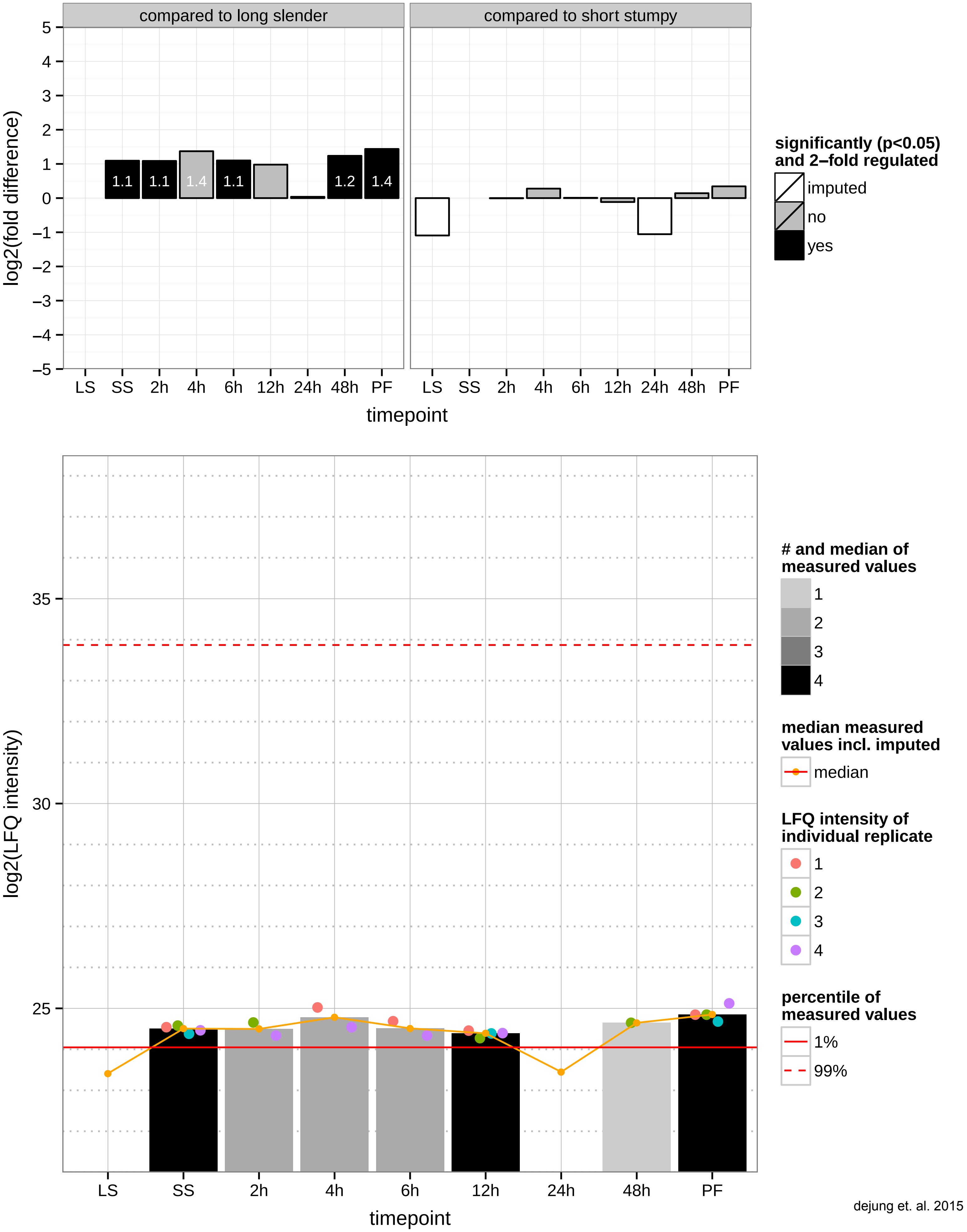
hypothetical protein, conserved
Tb927.7.3910
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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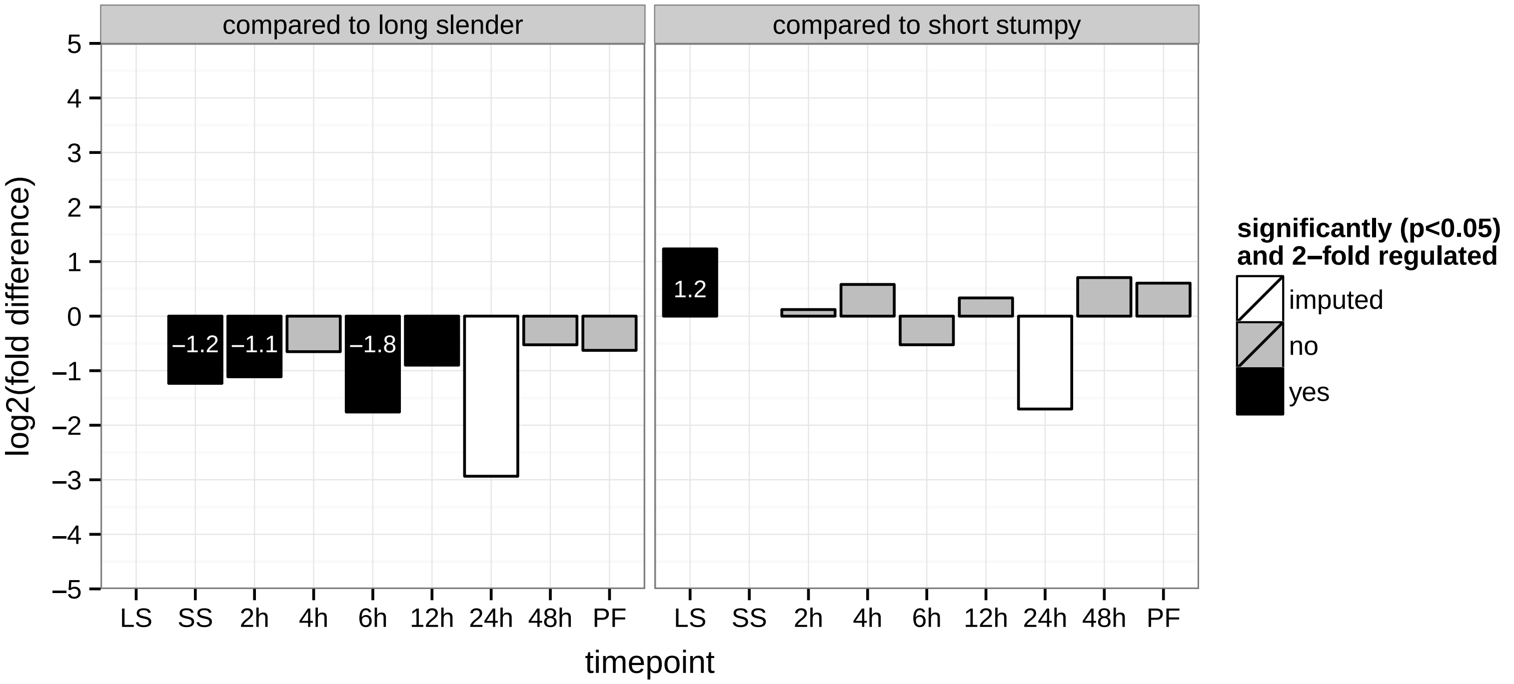
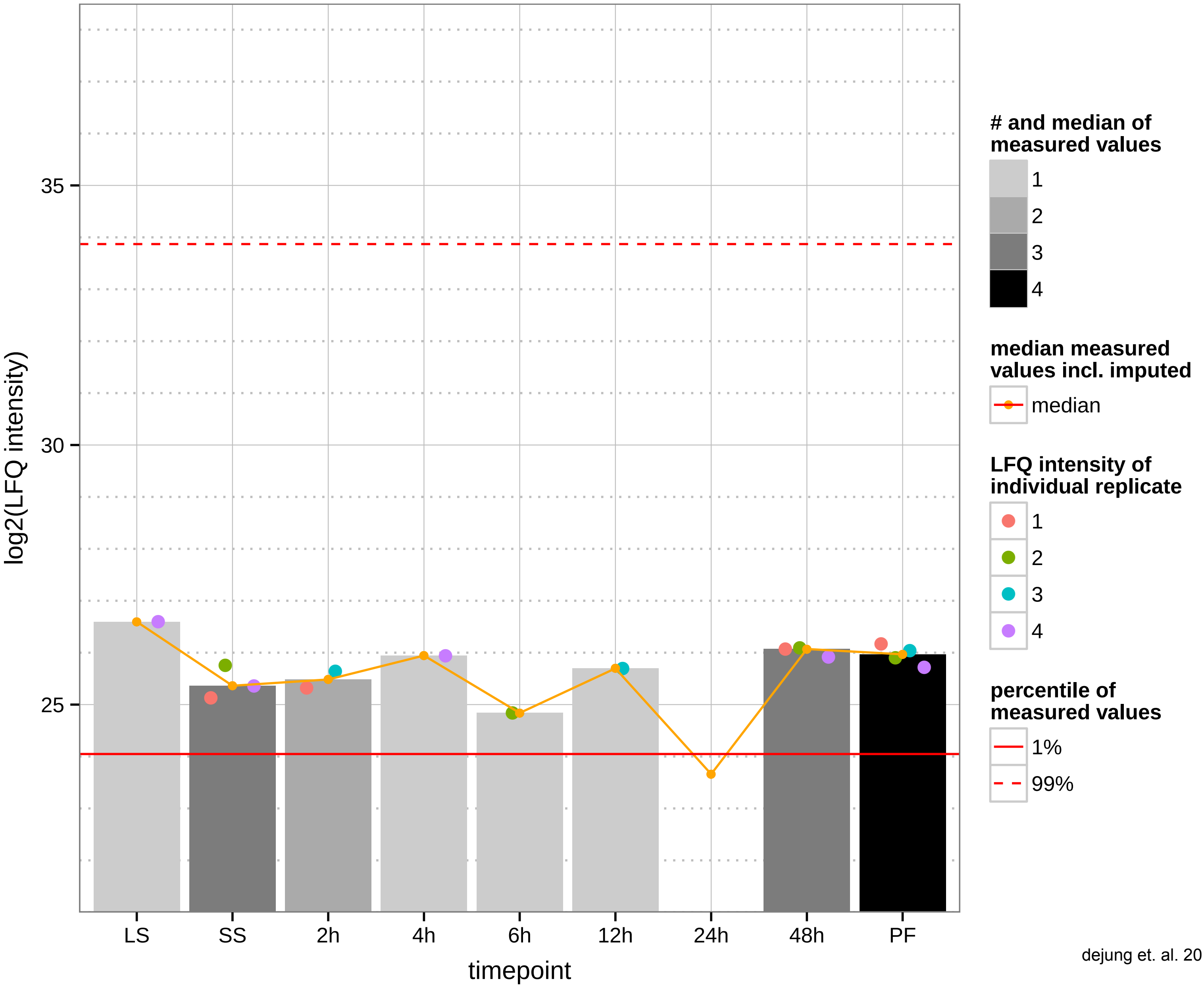
NADH–ubiquinone oxidoreductase, mitochondrial, putative
Tb927.7.6350
AGOF: NAD binding, electron carrier activity, oxidoreductase activity
AGOC: mitochondrion
AGOP: null
PGOF: NAD binding, oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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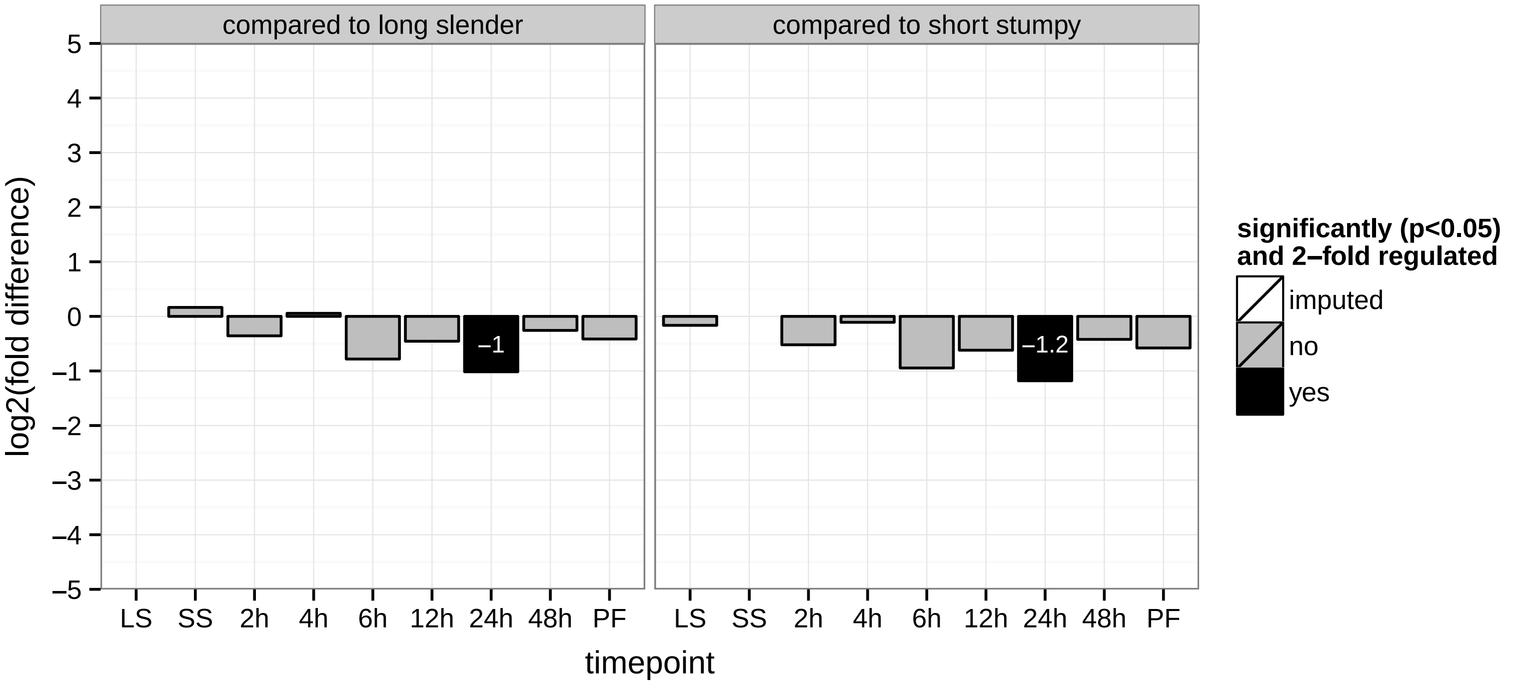
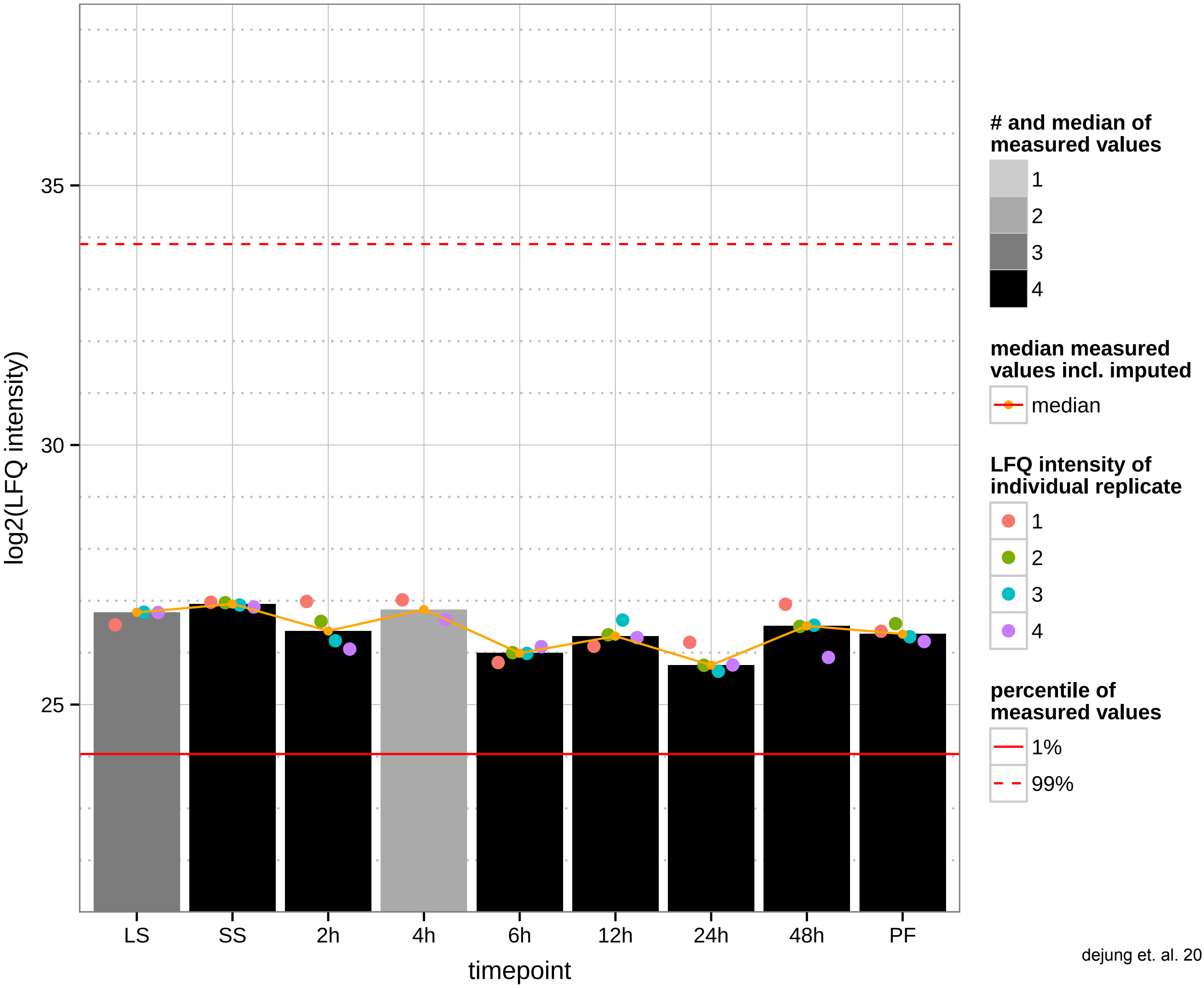
actin, putative
Tb927.9.5440
AGOF: structural constituent of cytoskeleton
AGOC: actin cytoskeleton
AGOP: cytoskeleton organization
PGOF: null
PGOC: null
PGOP: null





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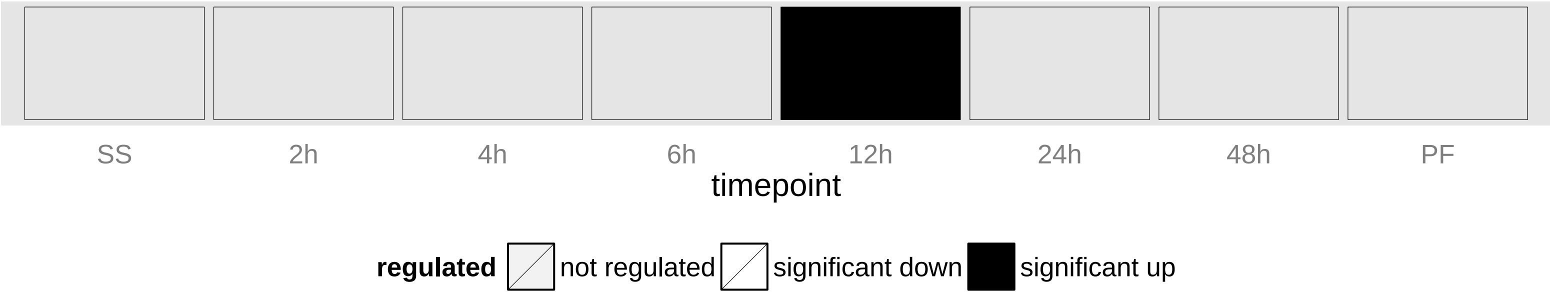

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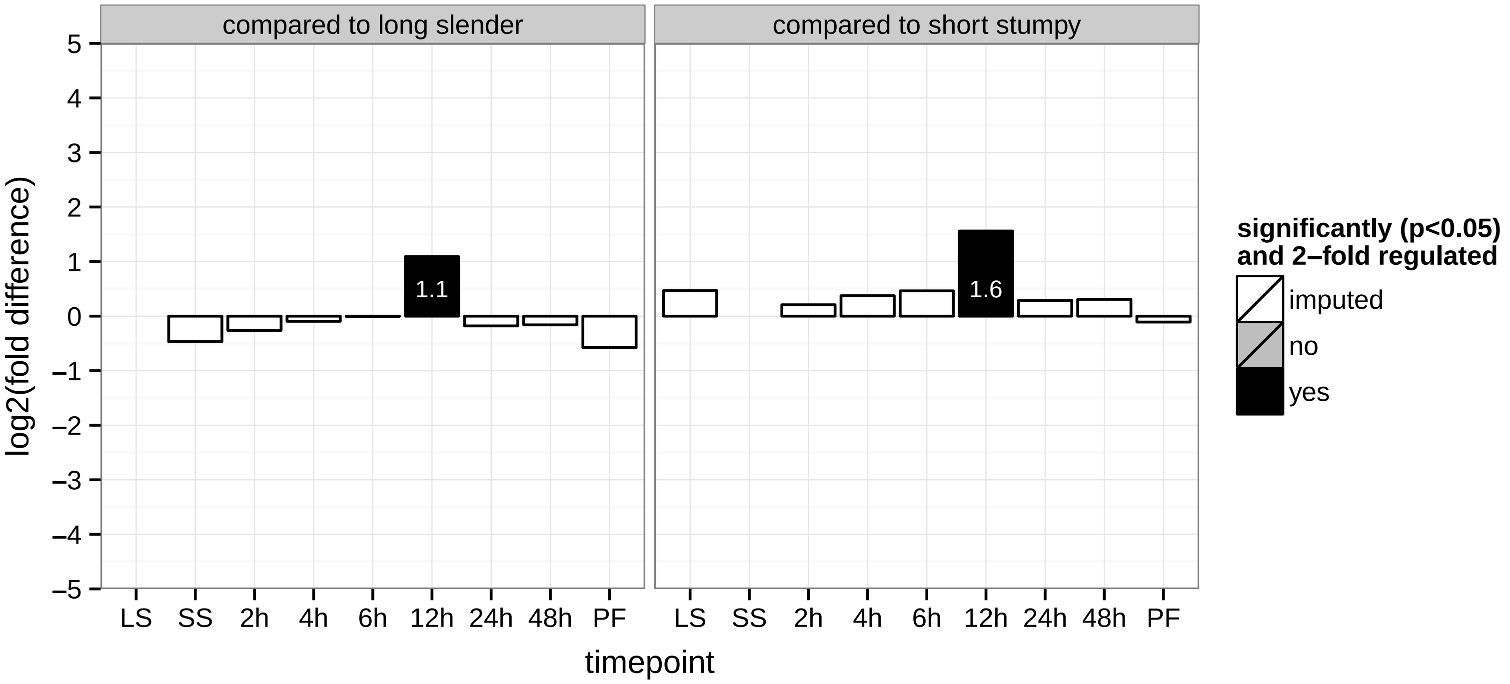
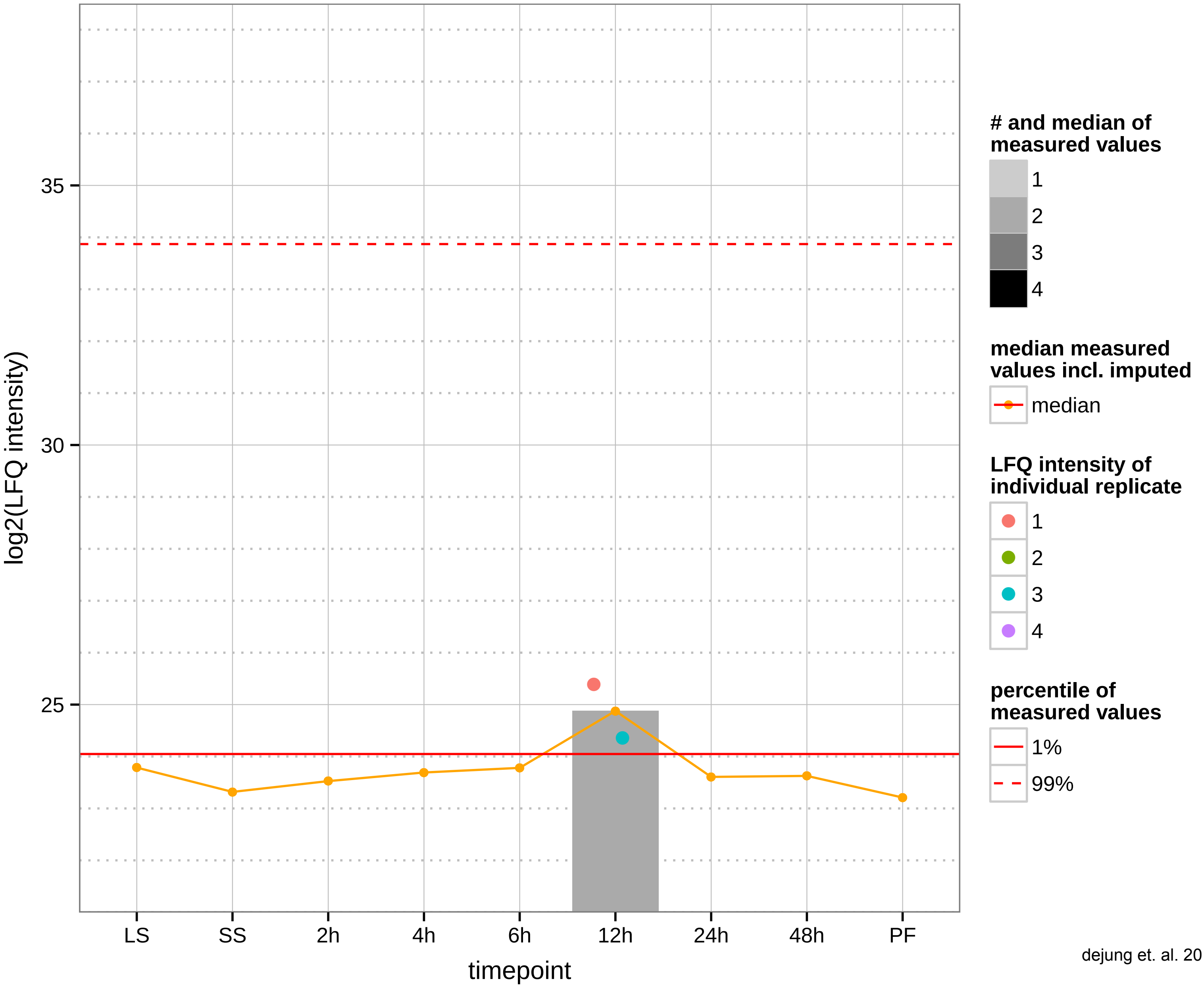
hypothetical PIN domain−containing protein, conserved
Tb927.1.1790
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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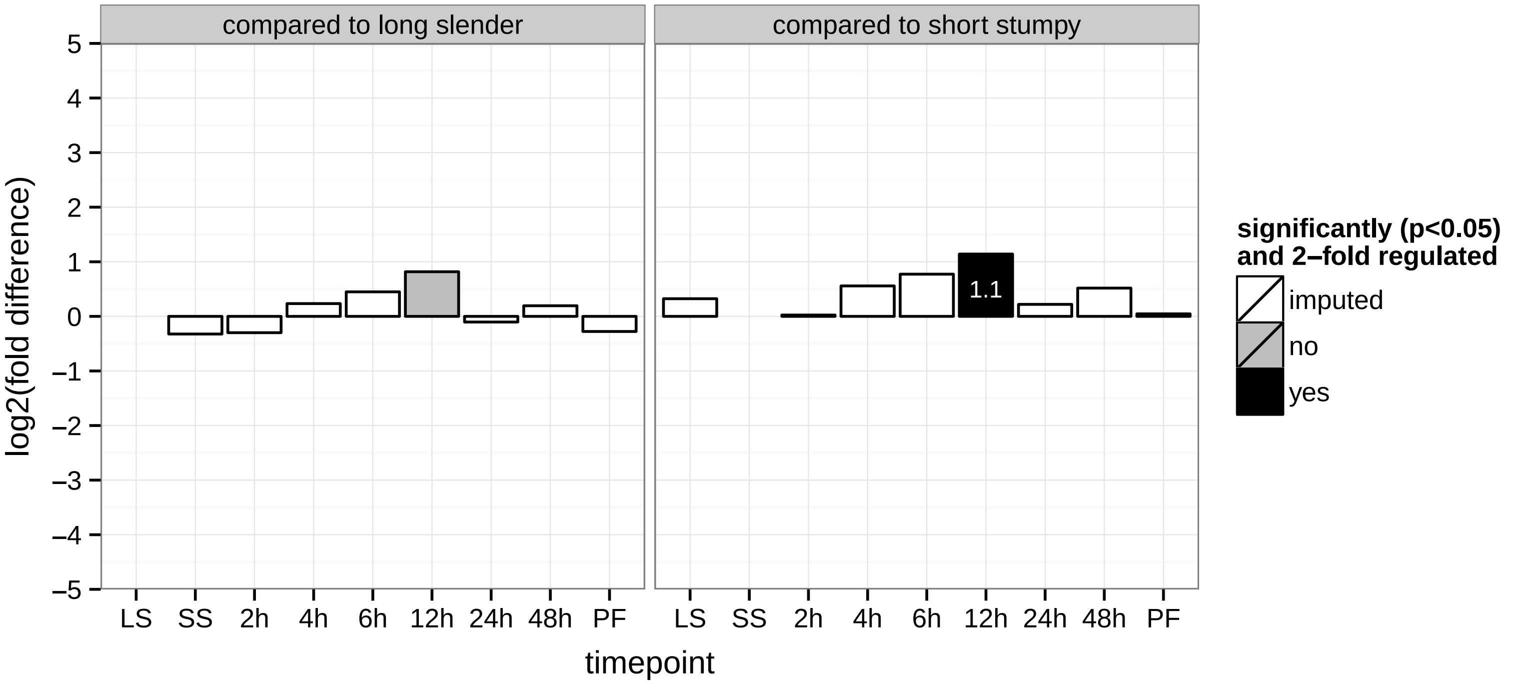
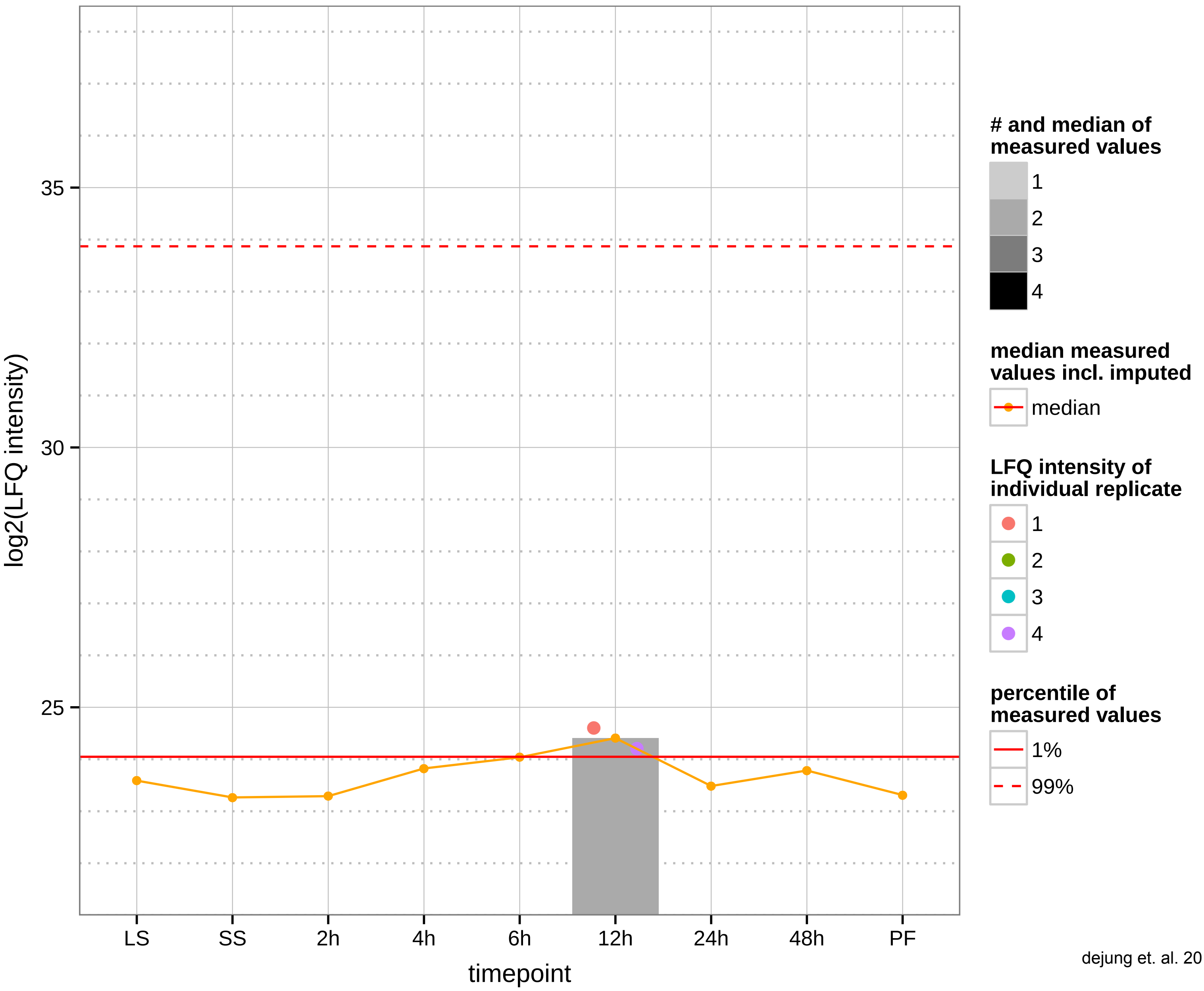
hypothetical protein, conserved
Tb927.1.2190
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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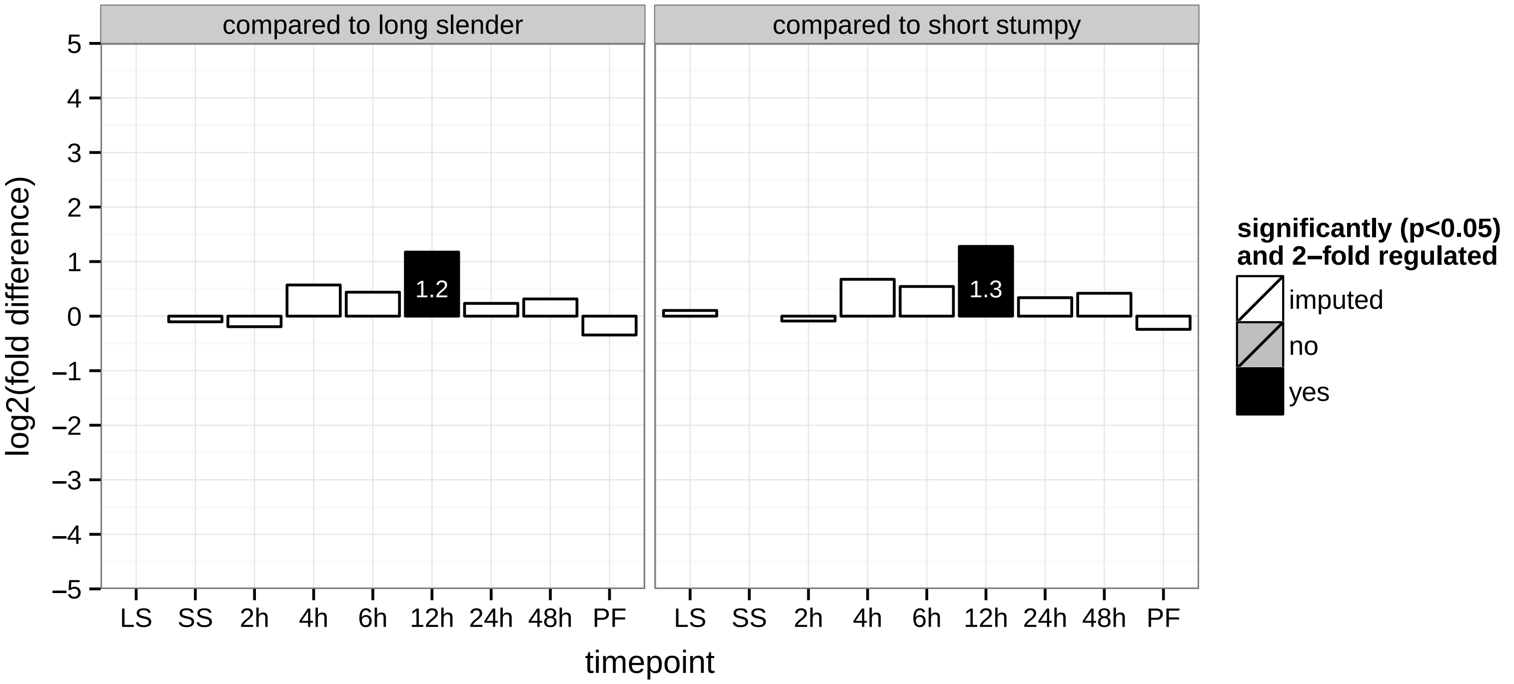
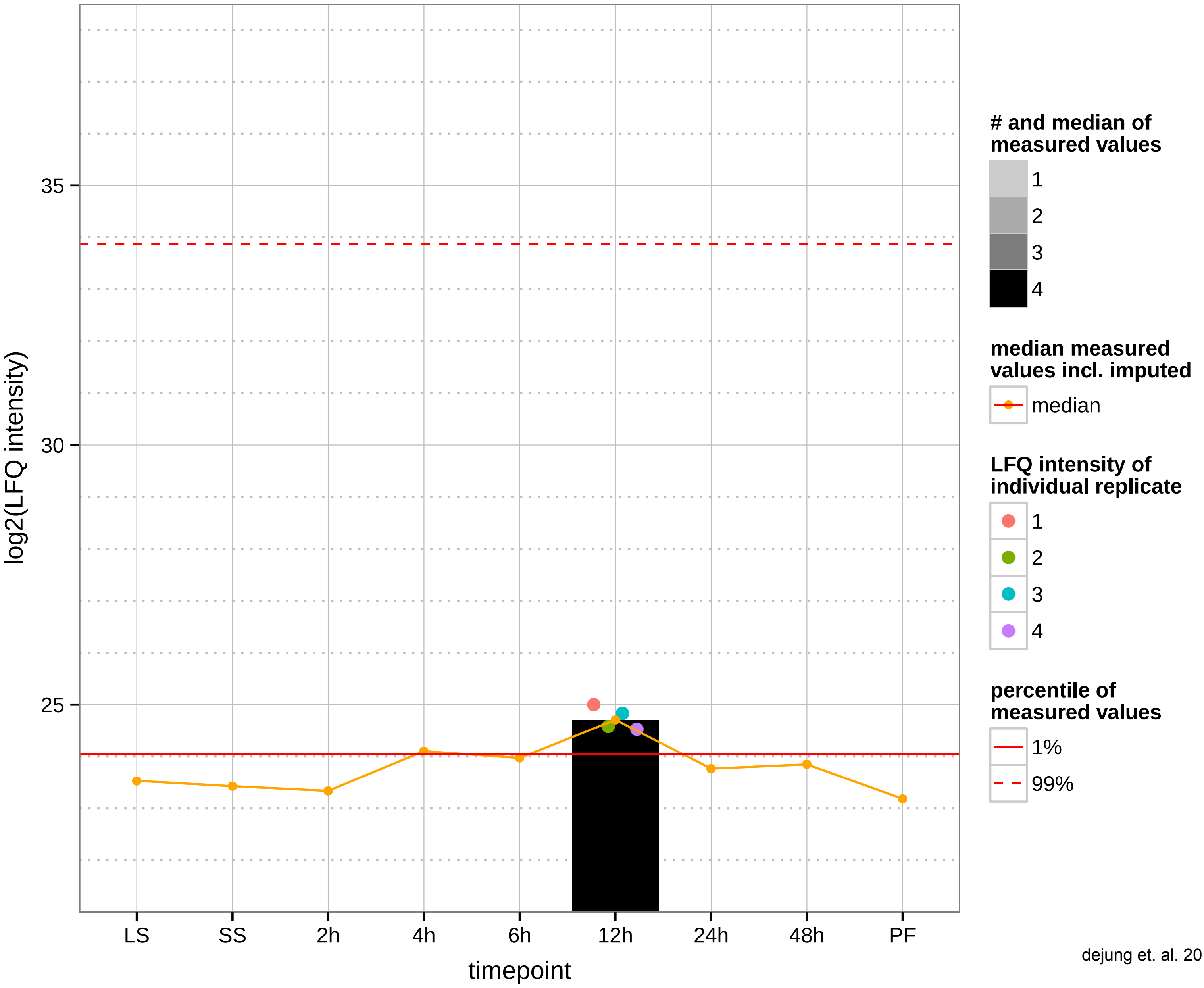
Histone–lysine N–methyltransferase, H3 lysine–76 specific, Histone H3–K76 methyltransferase (DOT1B)
Tb927.1.570
AGOF: histone–lysine N–methyltransferase activity
AGOC: null
AGOP: antigenic variation, regulation of cell cycle
PGOF: histone–lysine N–methyltransferase activity
PGOC: null
PGOP: null





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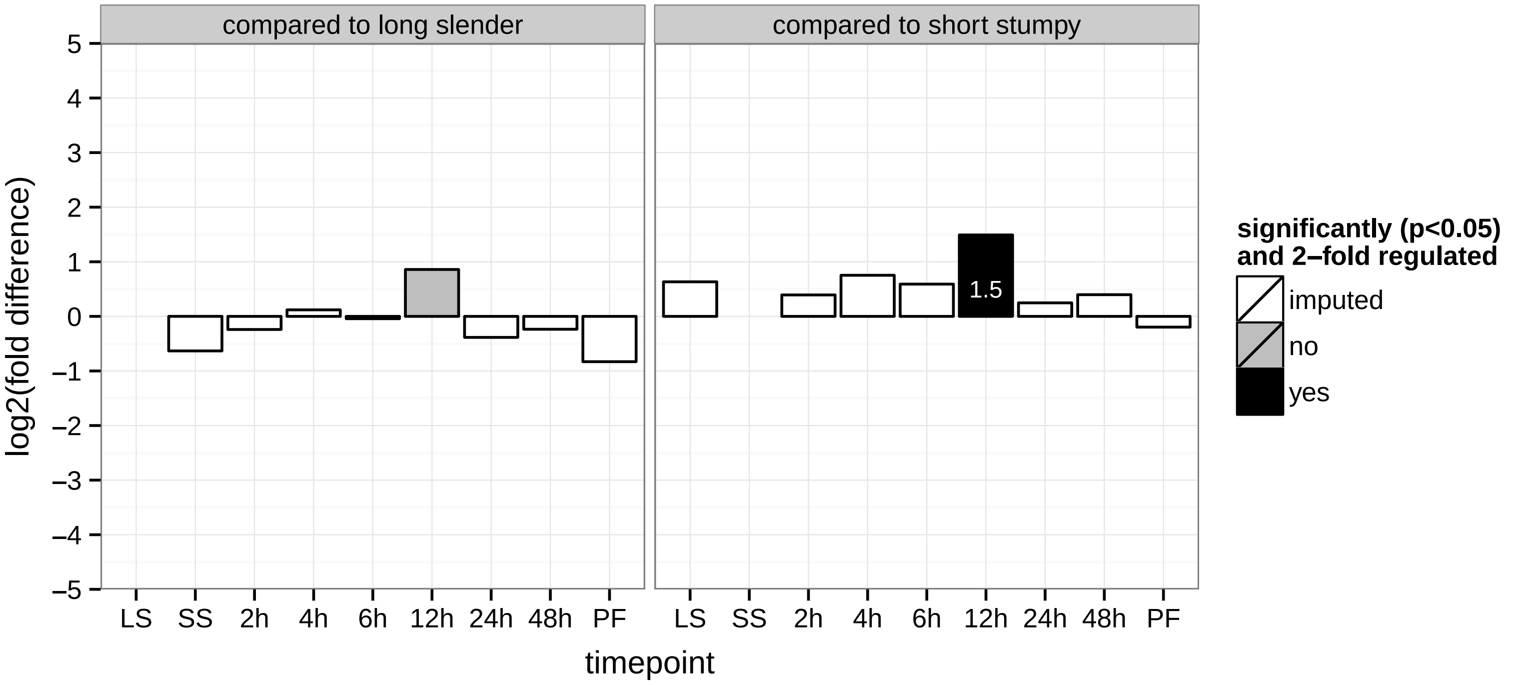
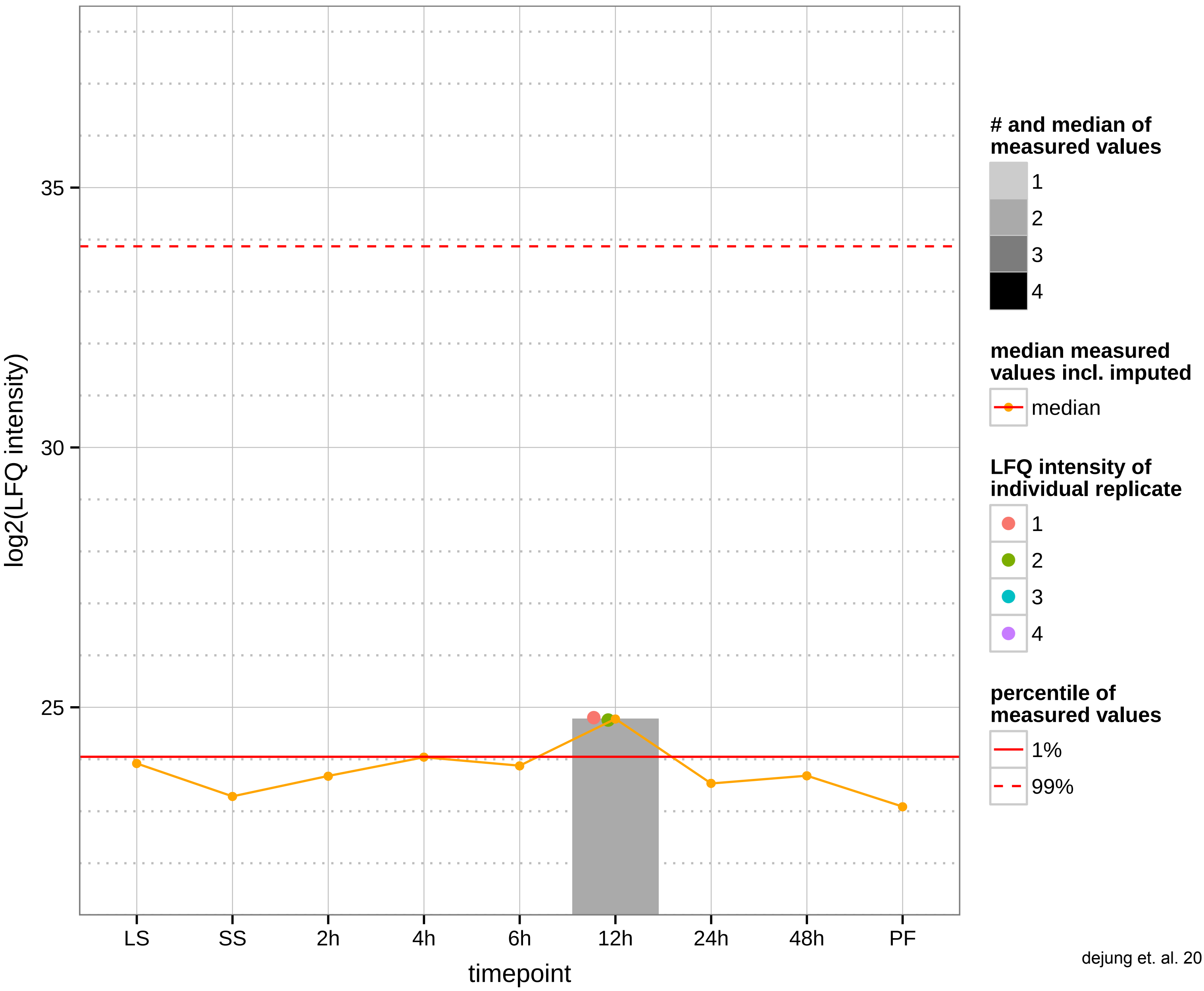
hypothetical protein, conserved
Tb927.10.14650
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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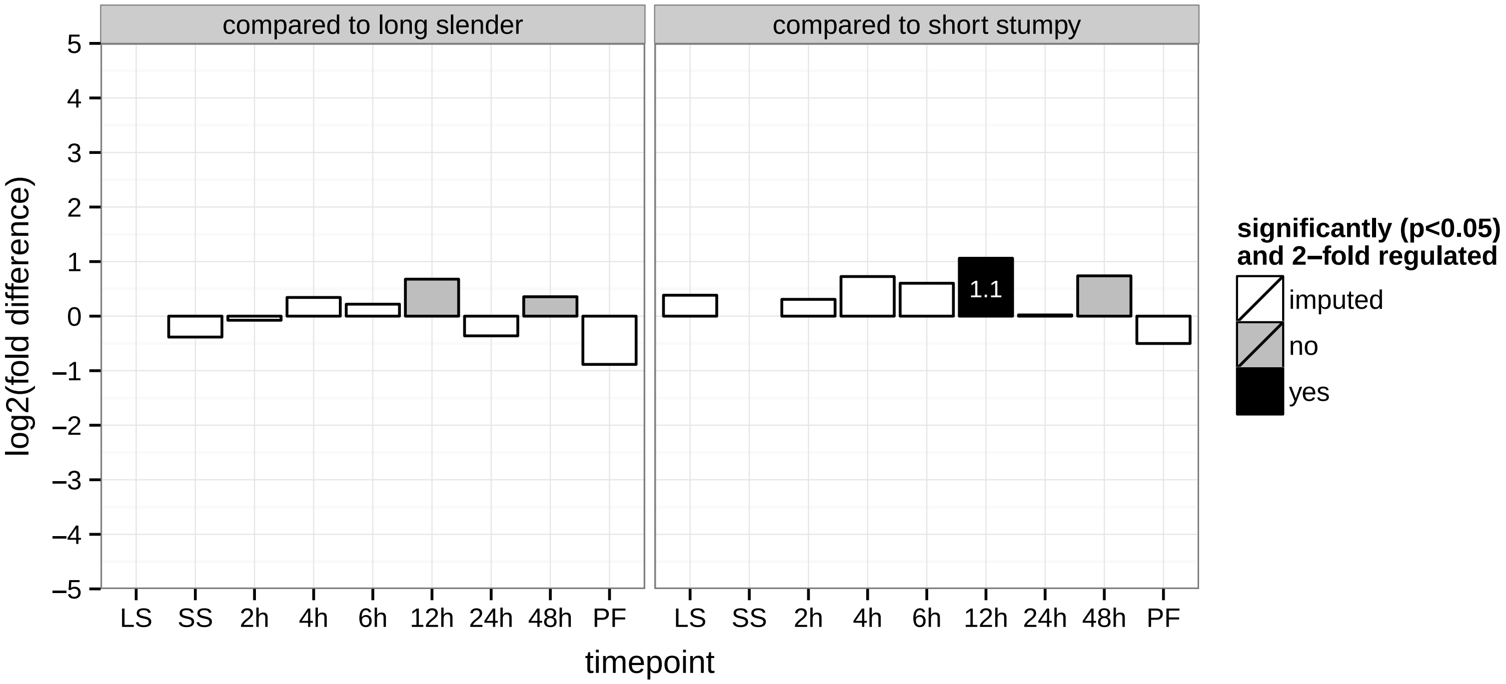
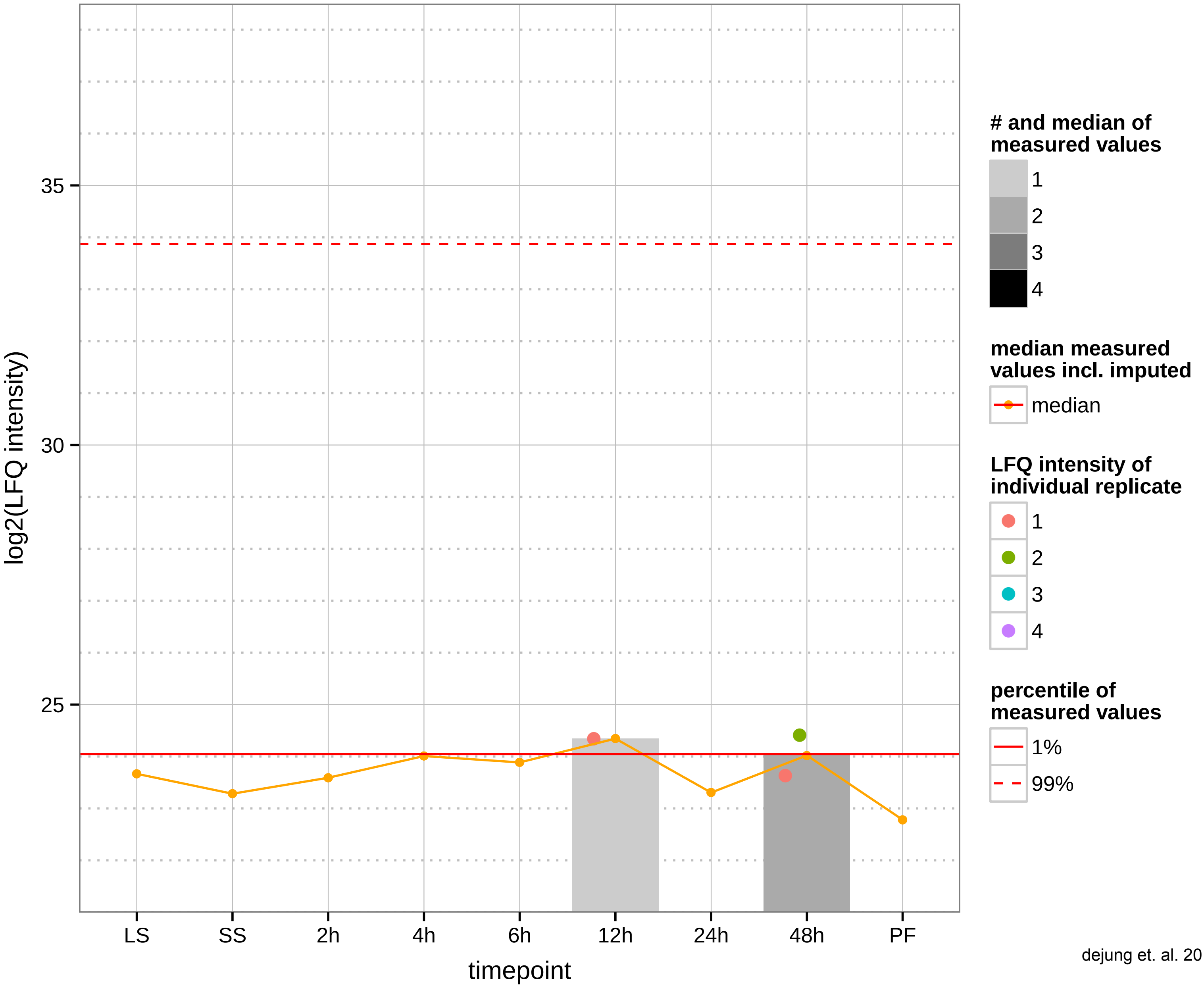
calcineurin B subunit, putative
Tb927.10.370
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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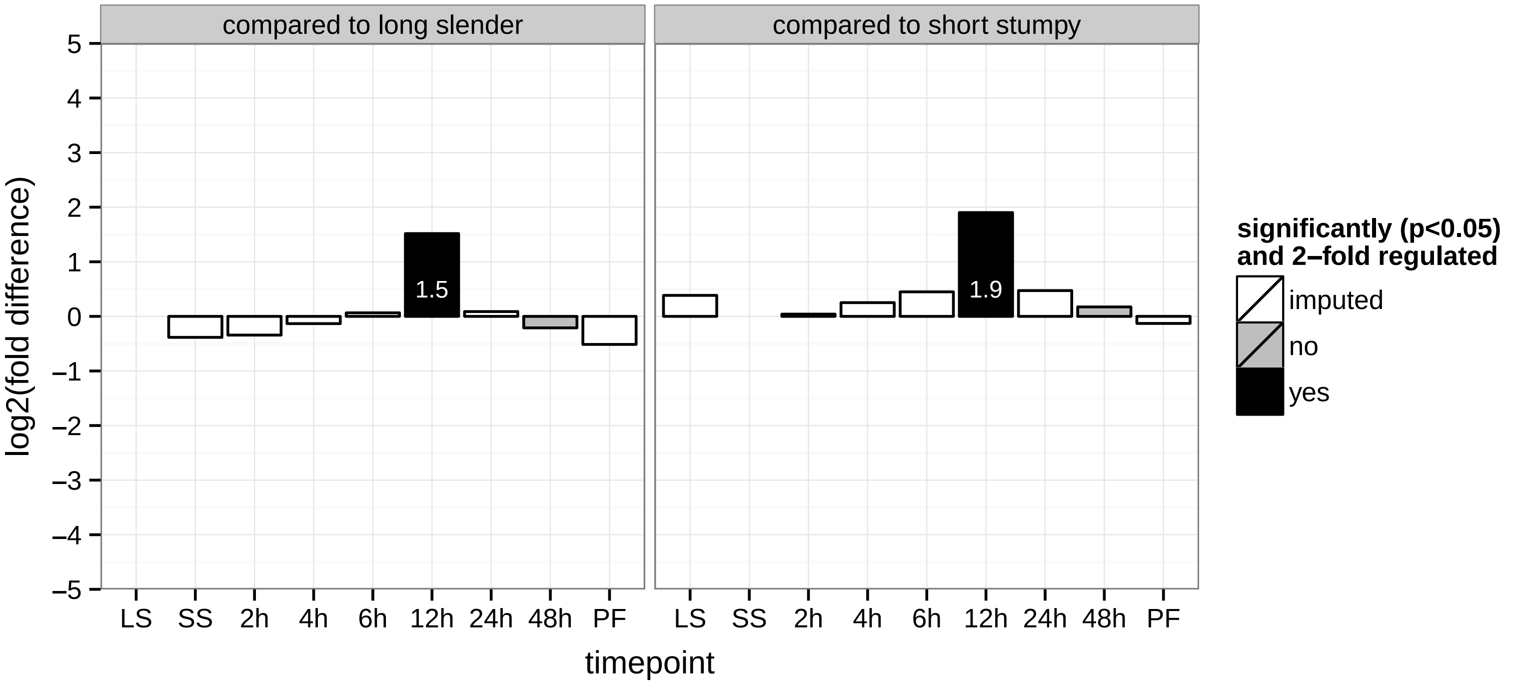
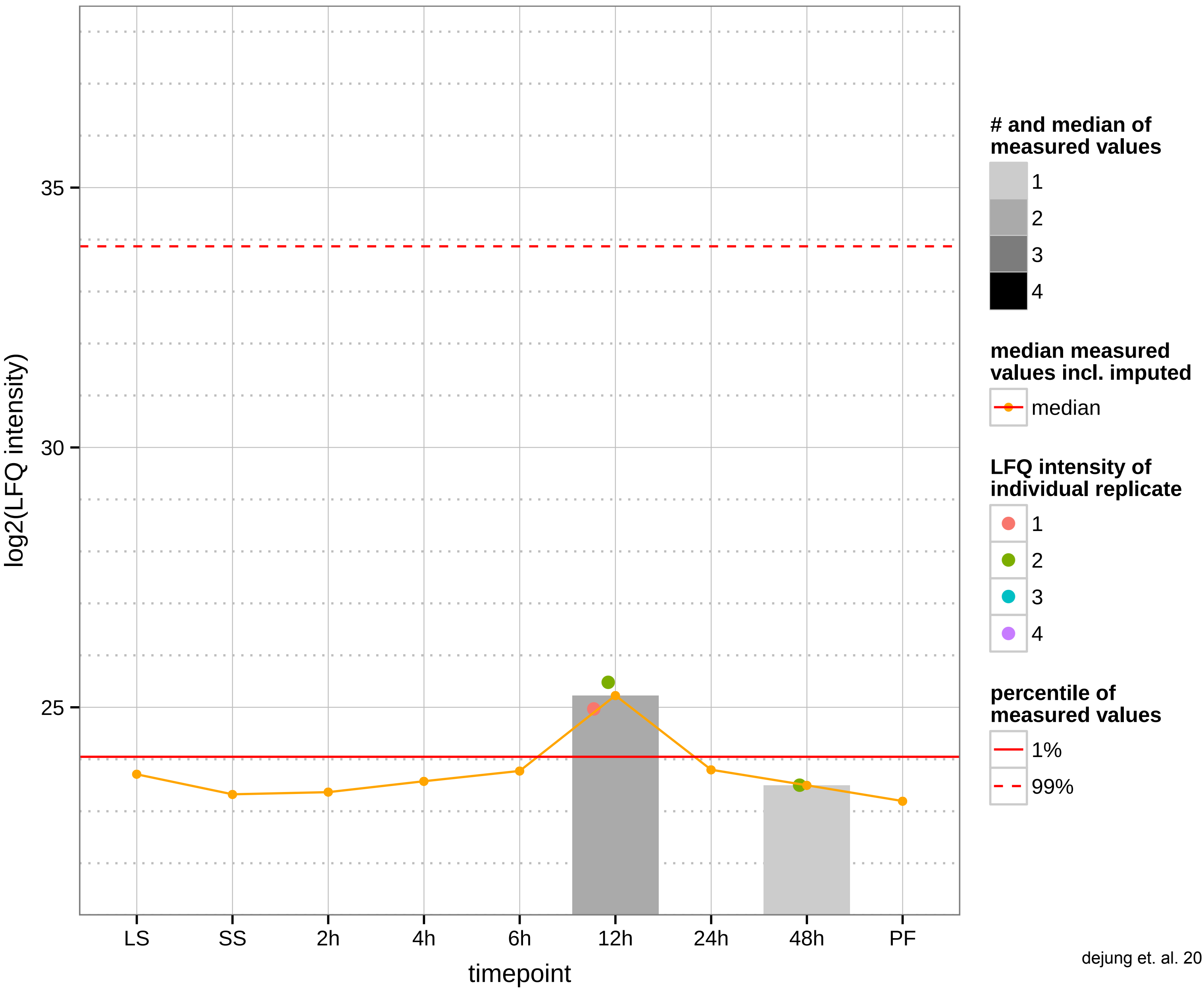
hypothetical protein, conserved
Tb927.10.4830
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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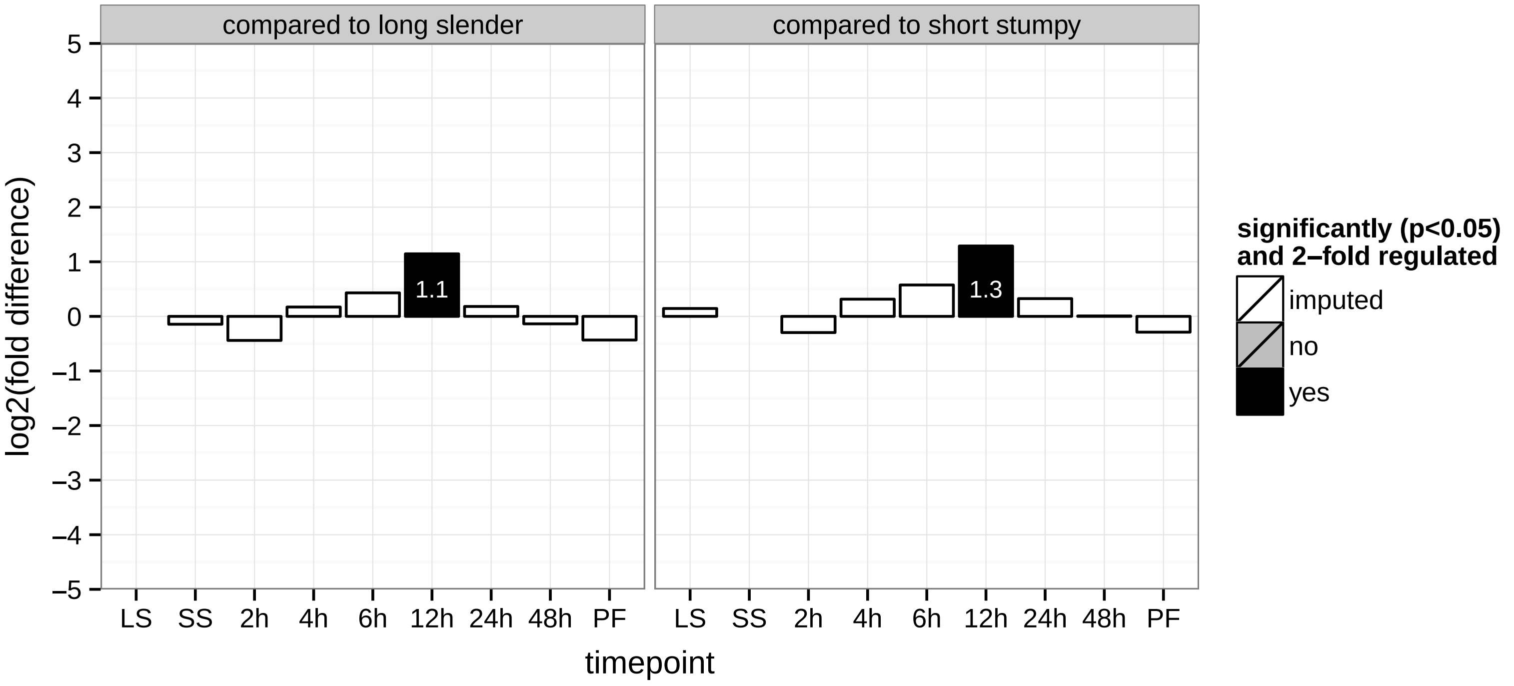
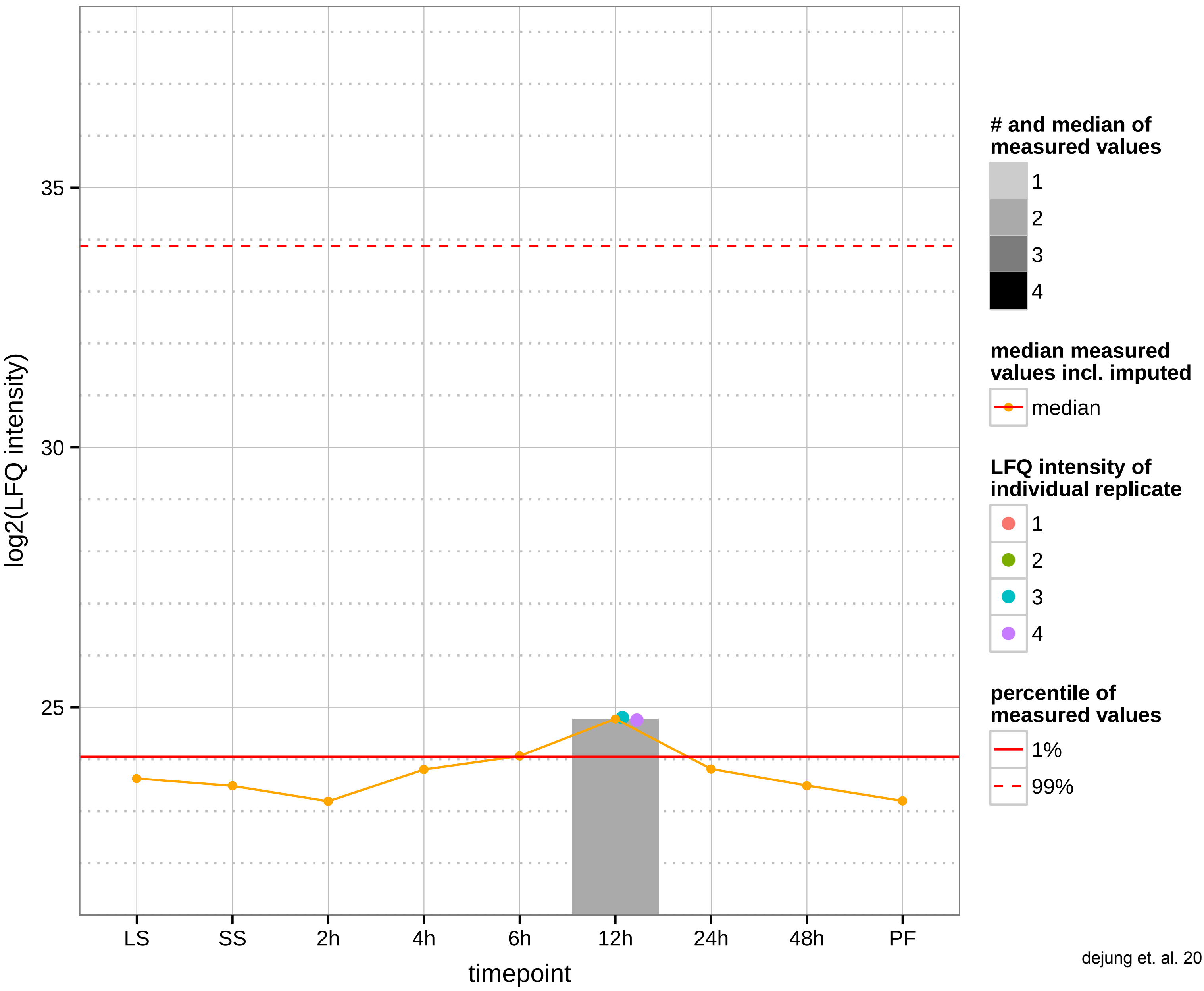
amino acid tansporter, putative
Tb927.10.5780
AGOF: null
AGOC: membrane
AGOP: amino acid transport
PGOF: null
PGOC: null
PGOP: null





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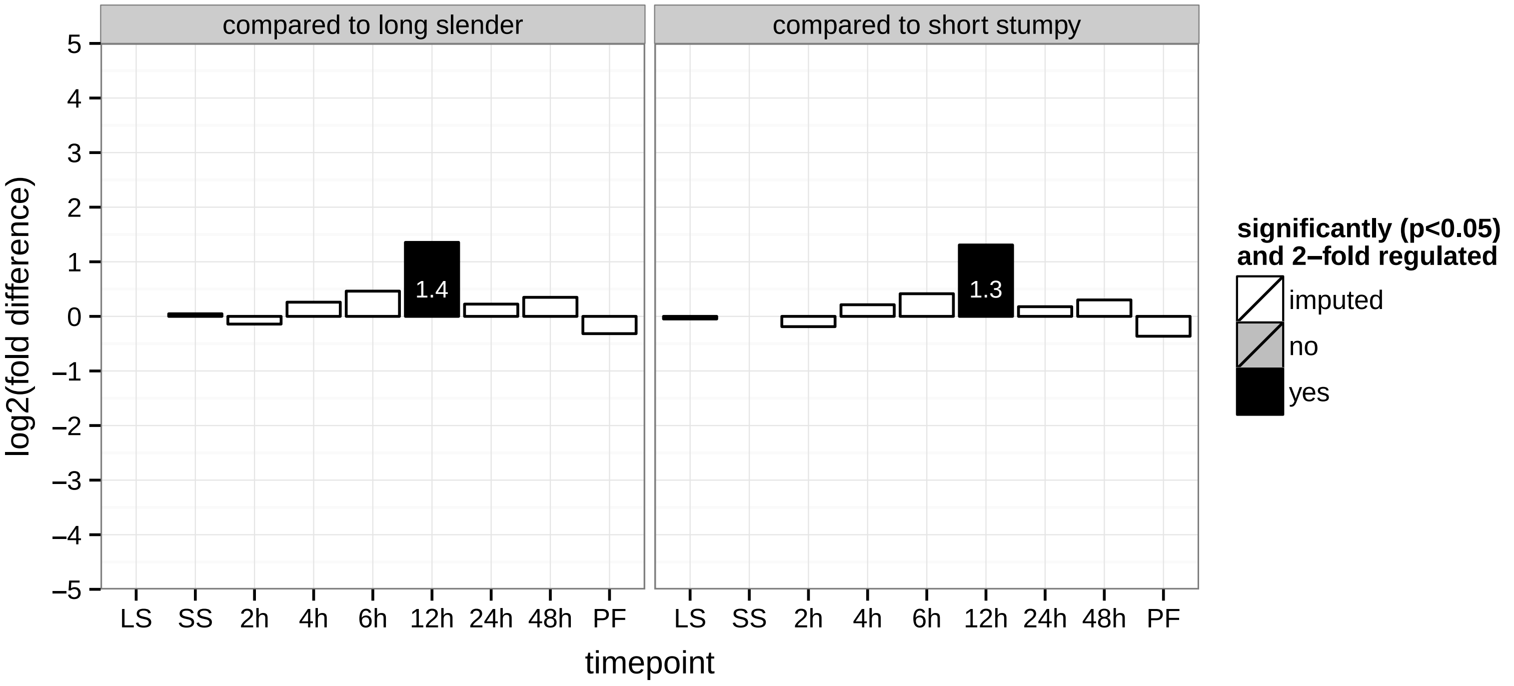
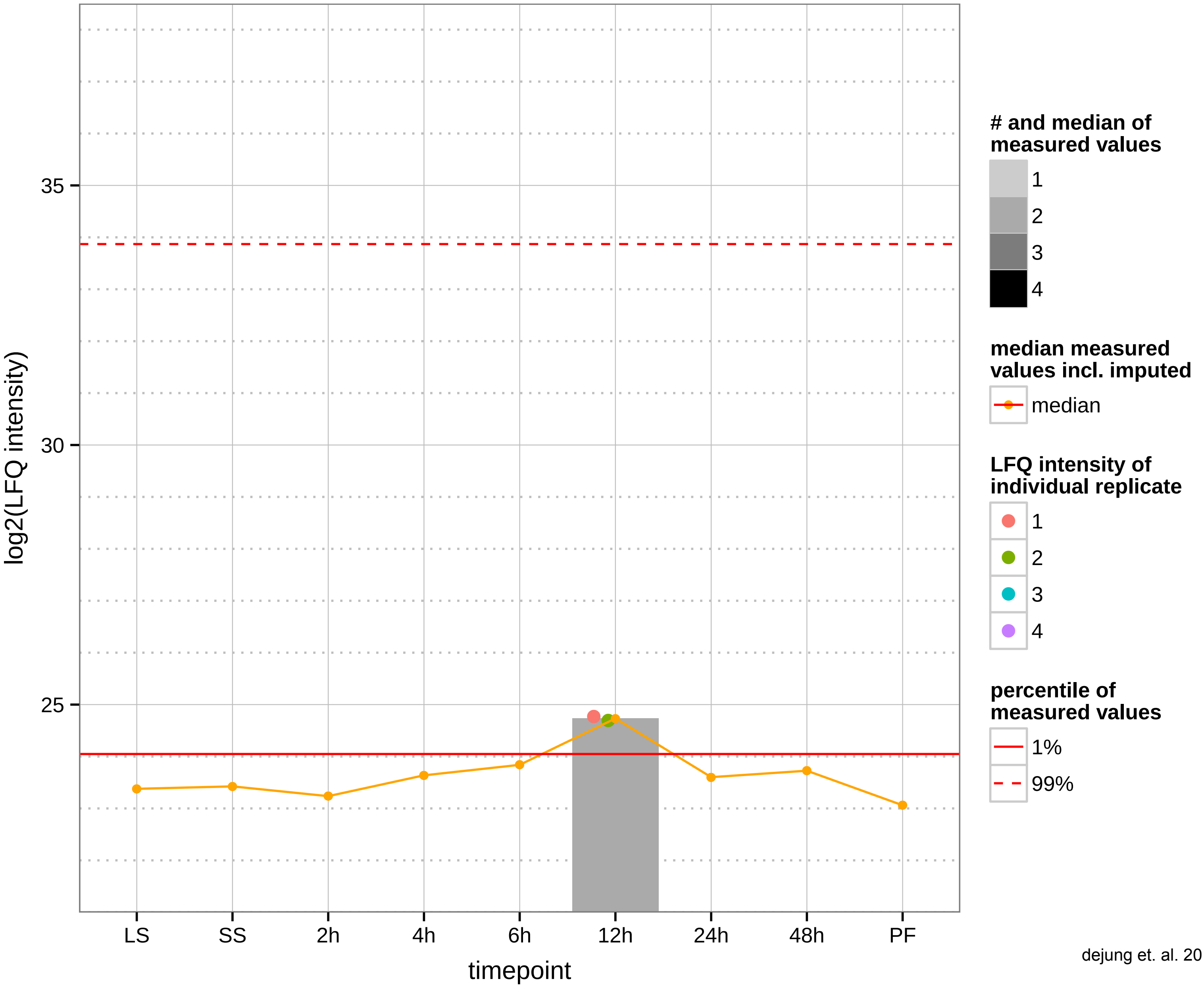
hypothetical protein, conserved
Tb927.11.1750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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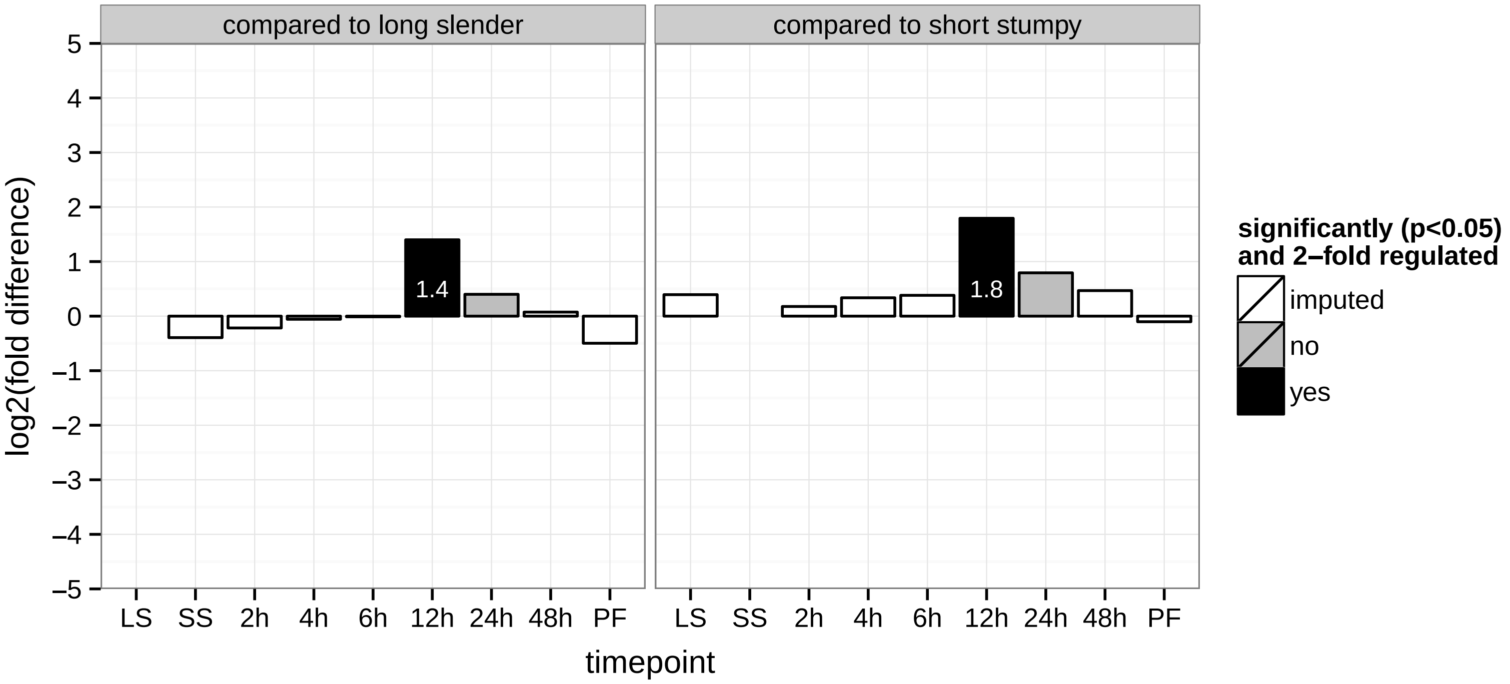
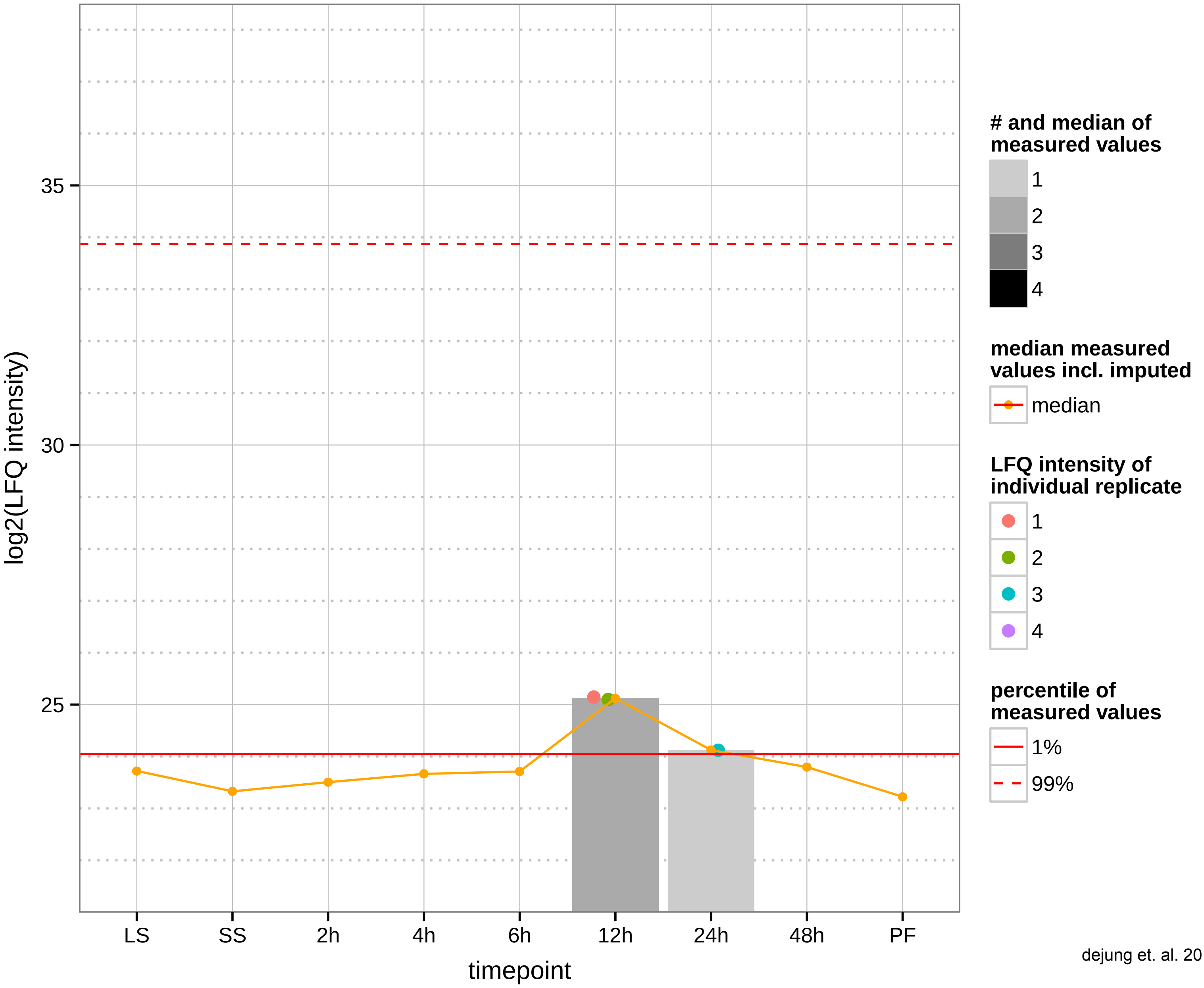
hypothetical protein, conserved
Tb927.2.5930
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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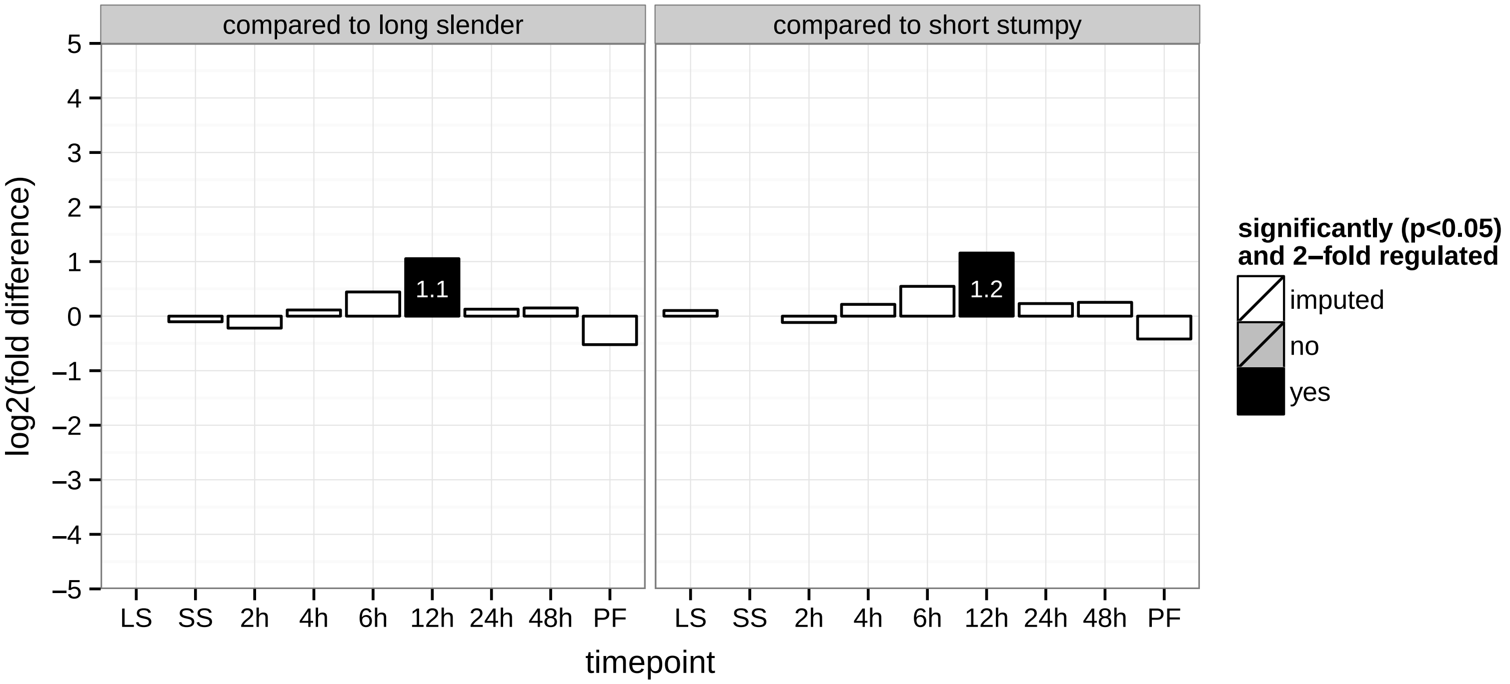
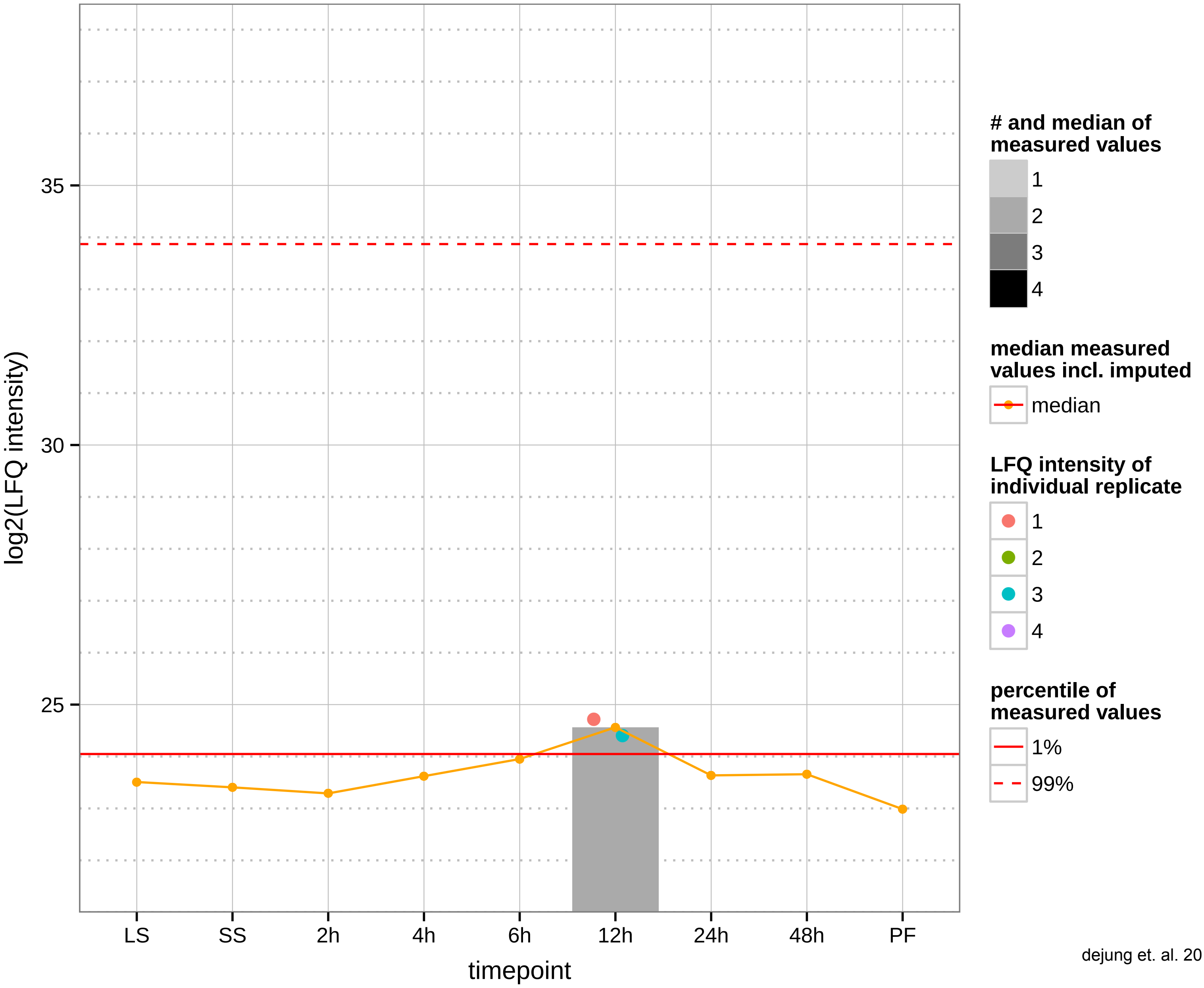
metalloprotease, putative
Tb927.5.1870
AGOF: ATP binding, nucleoside−triphosphatase activity
AGOC: null
AGOP: null
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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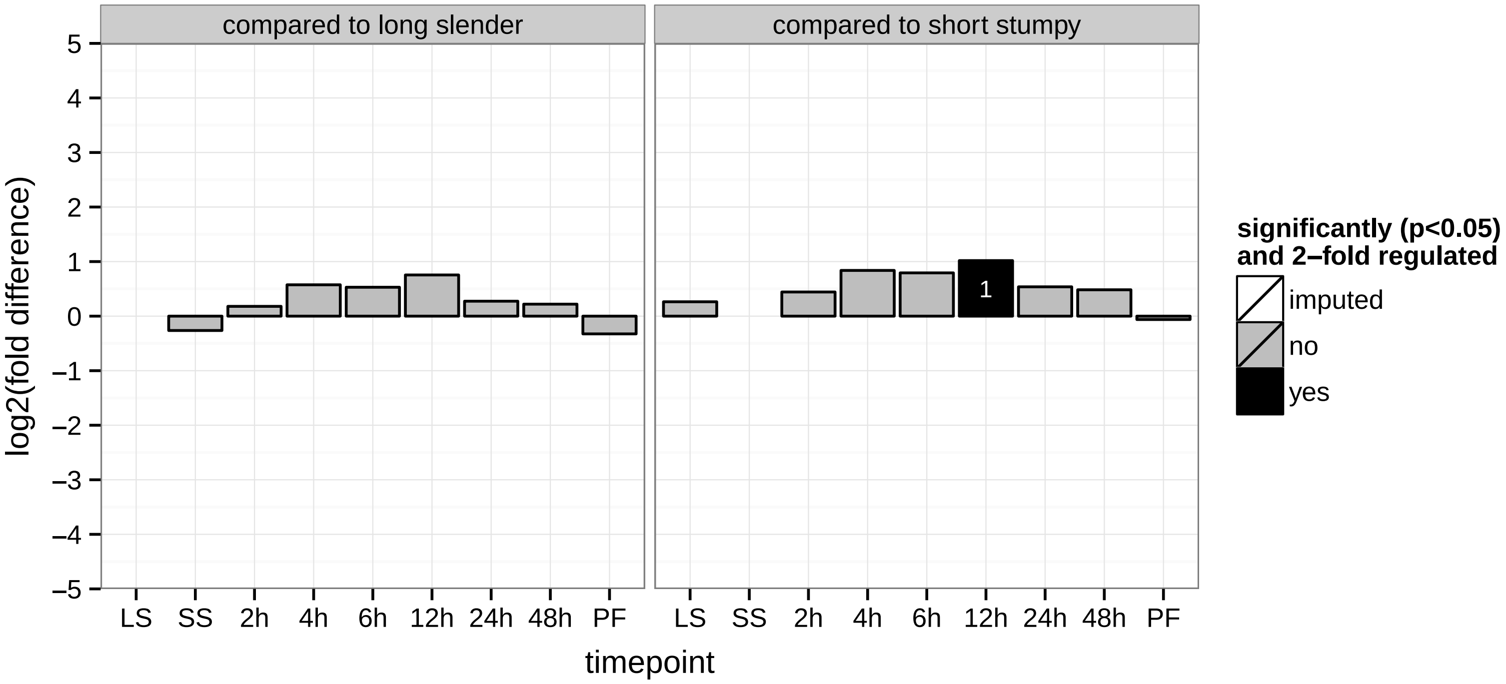
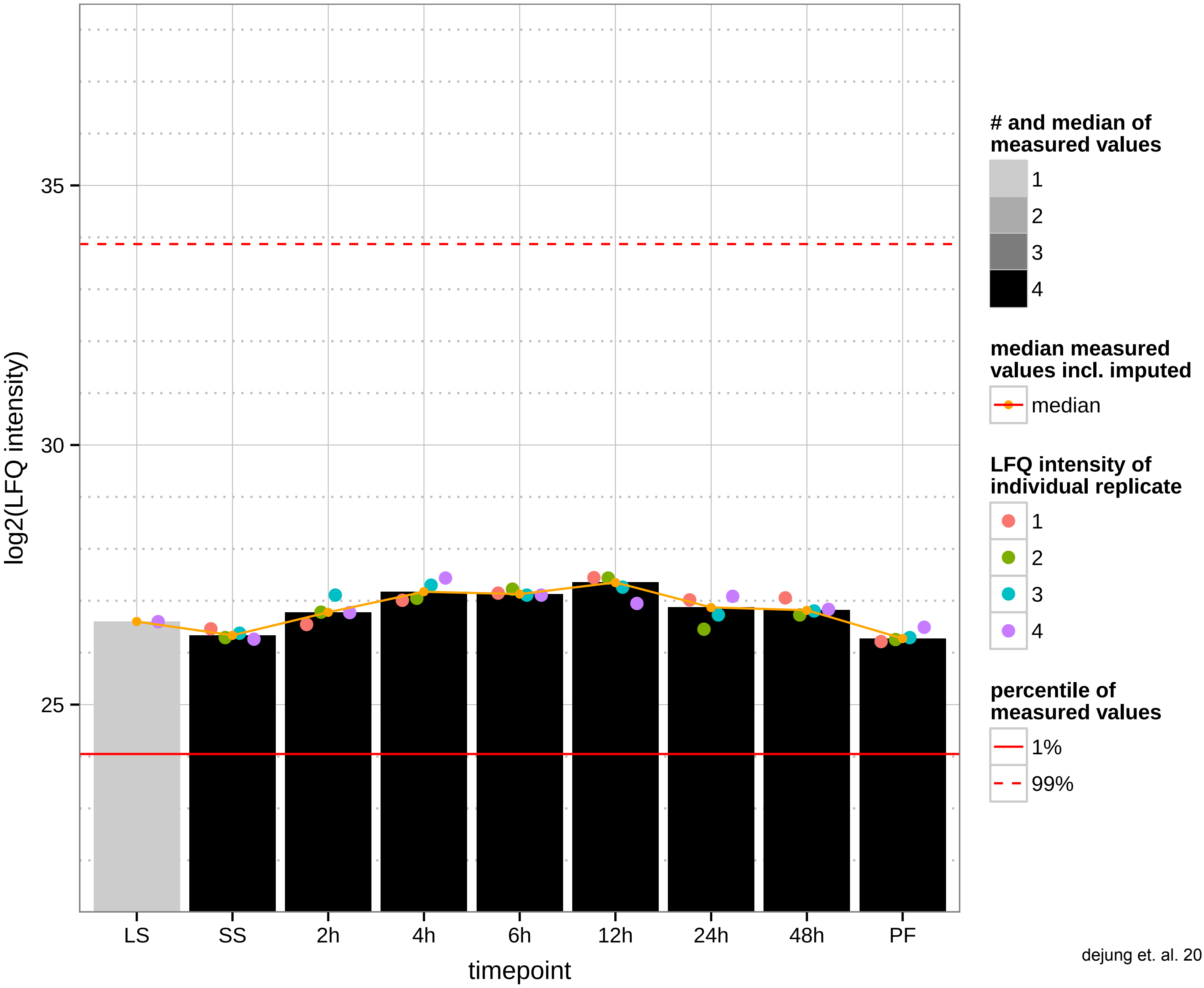
hypothetical protein, conserved
Tb927.5.2620
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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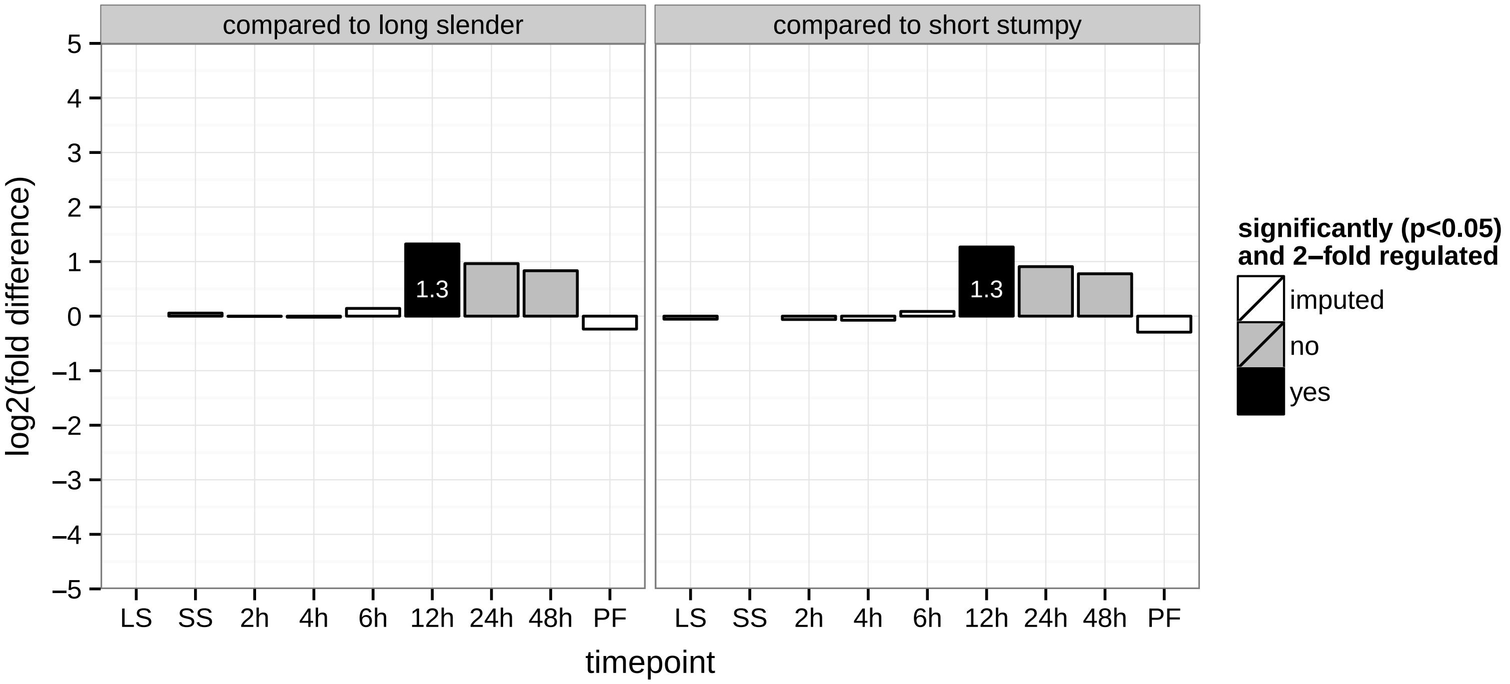
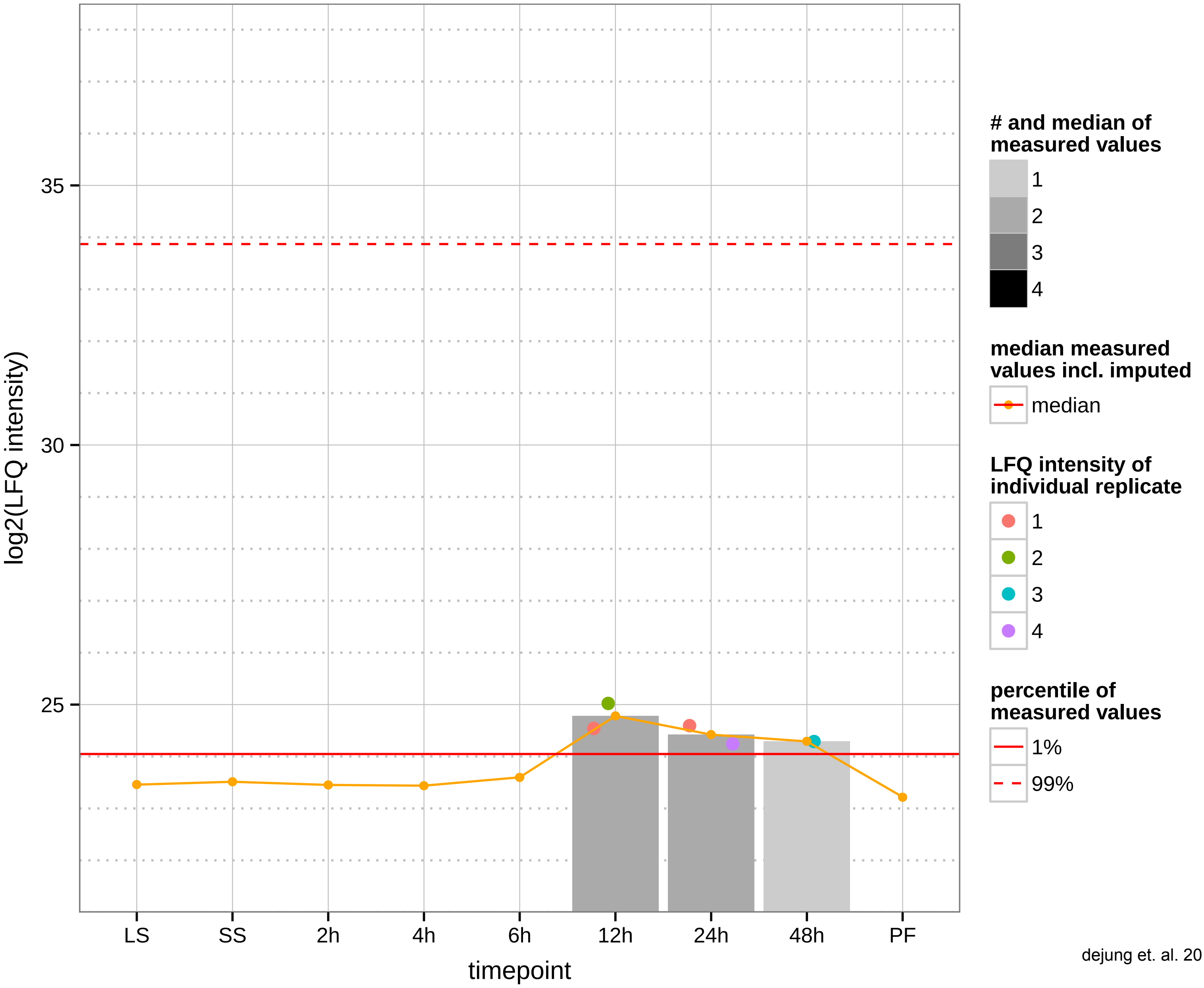
hypothetical protein, conserved
Tb927.5.3190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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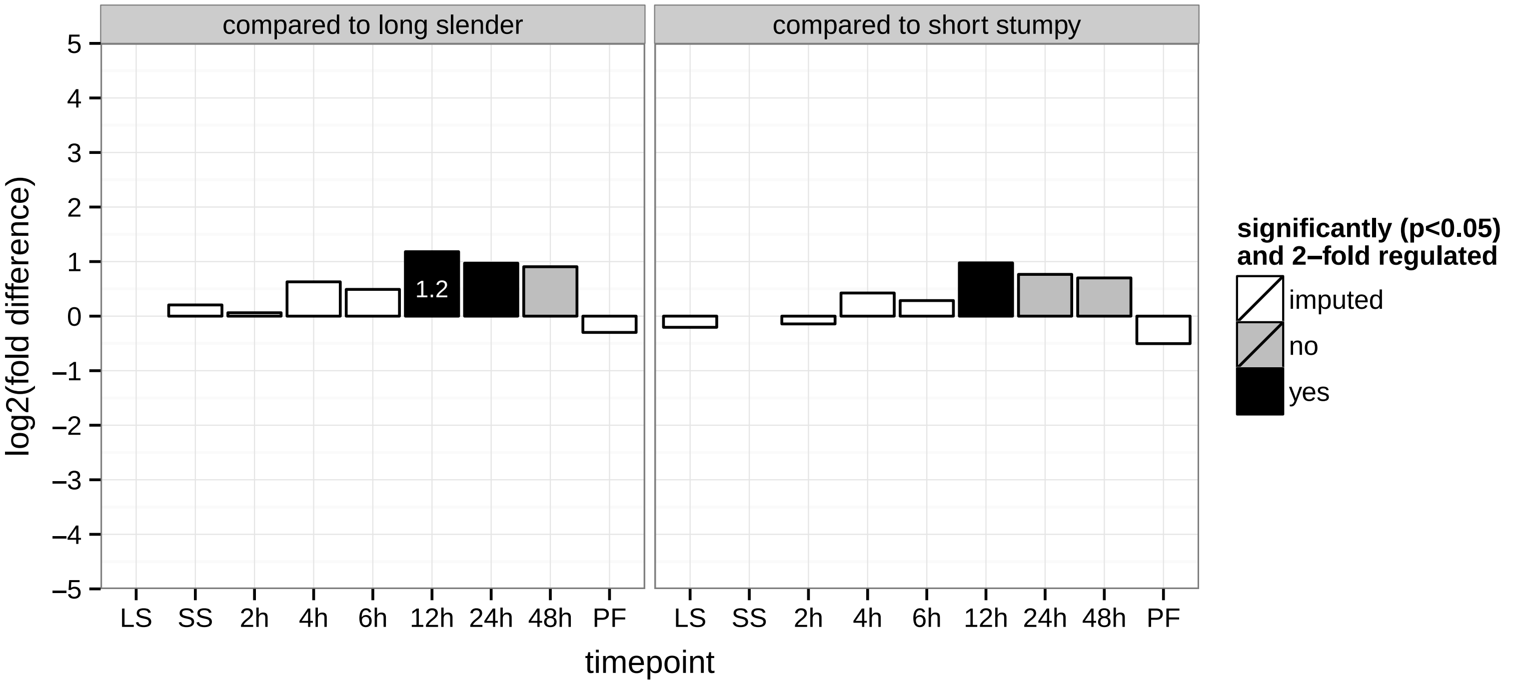
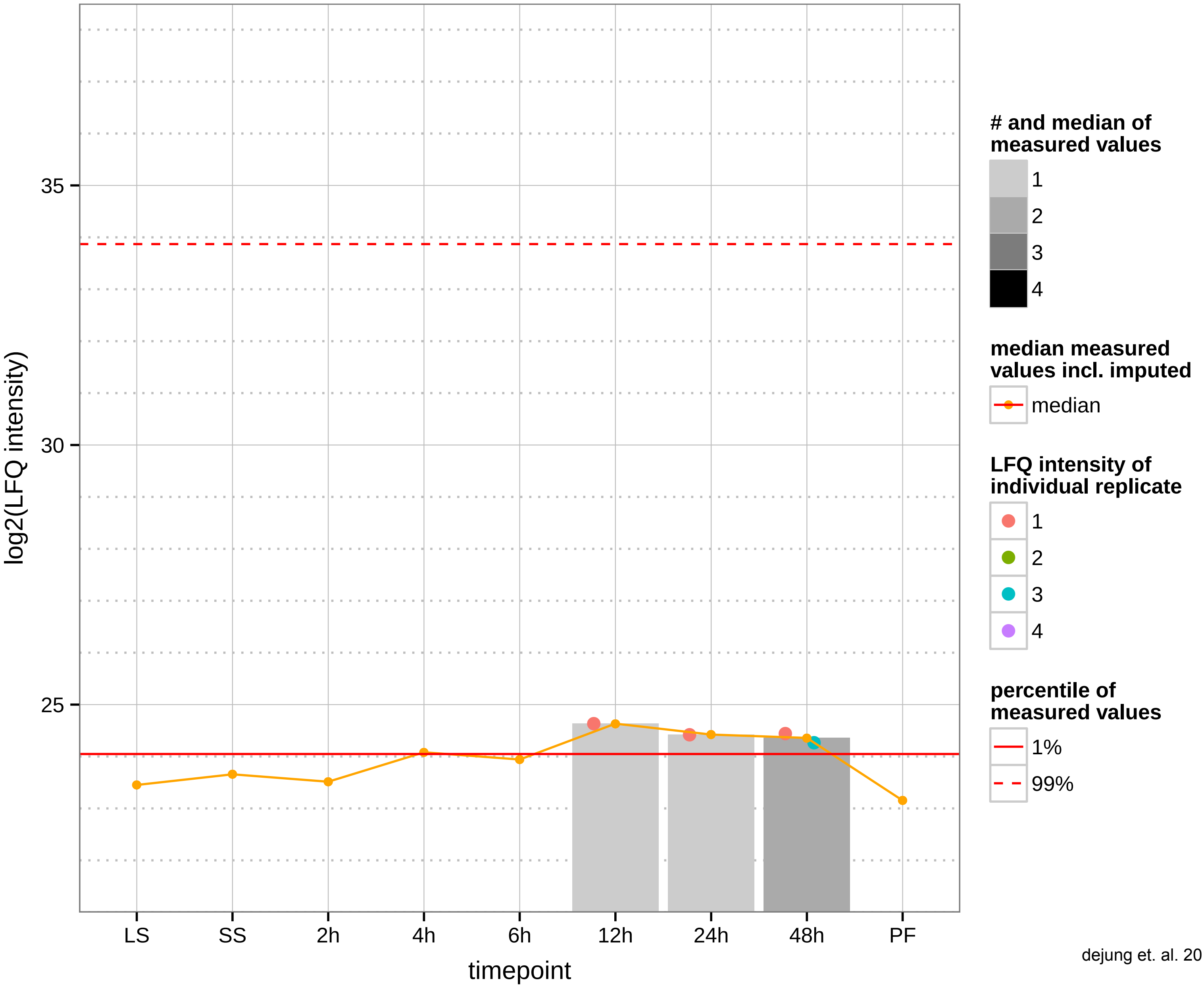
hypothetical protein, conserved
Tb927.7.1680
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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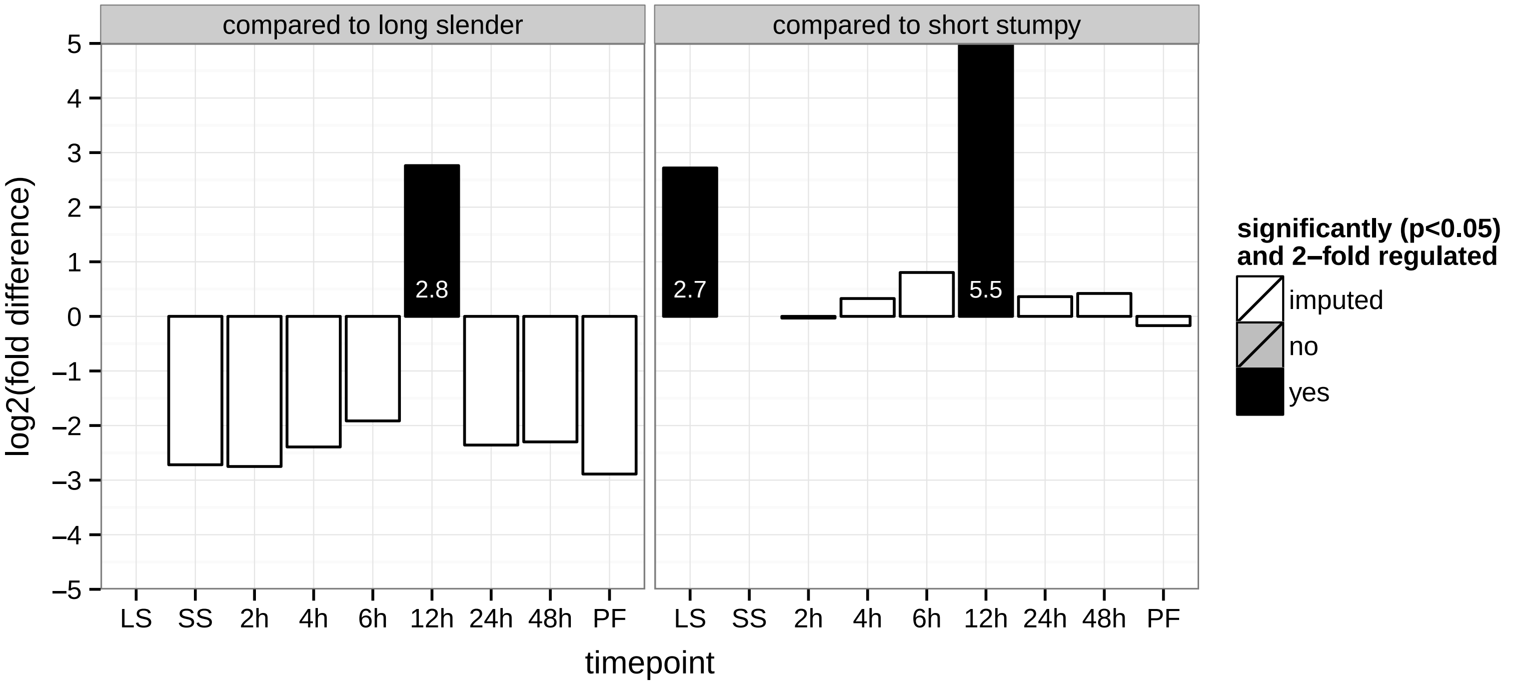
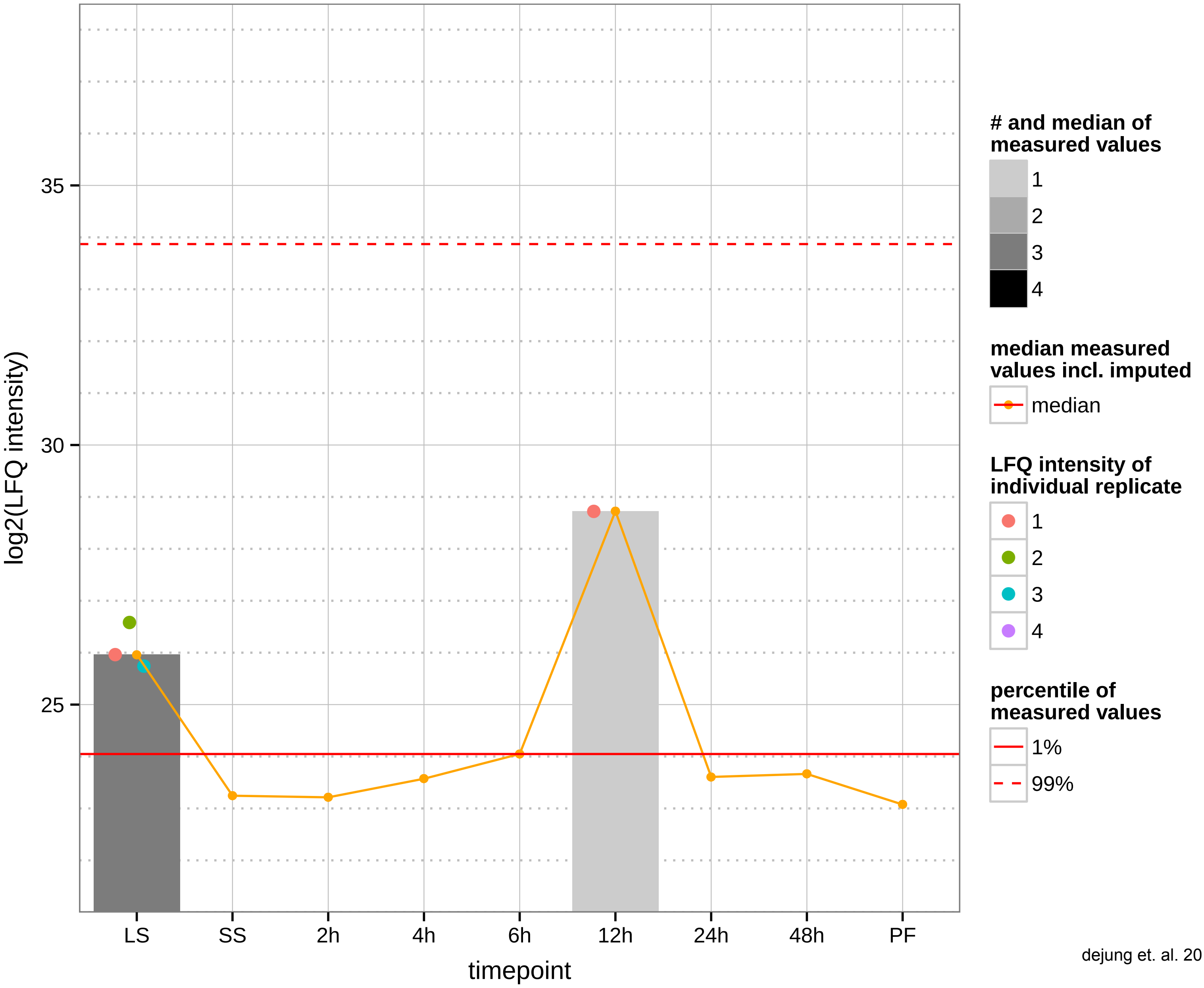
hypothetical protein, conserved, unspecified product
Tb927.9.4000;Tb927.9.3930
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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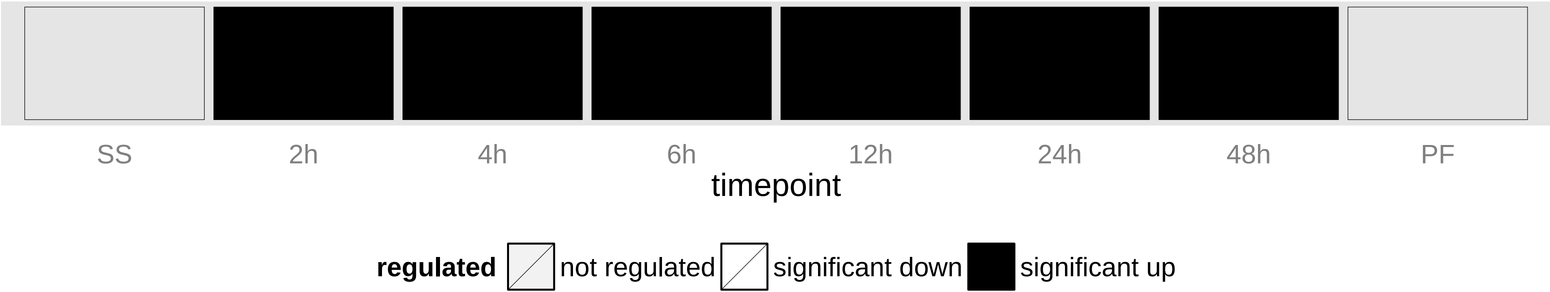

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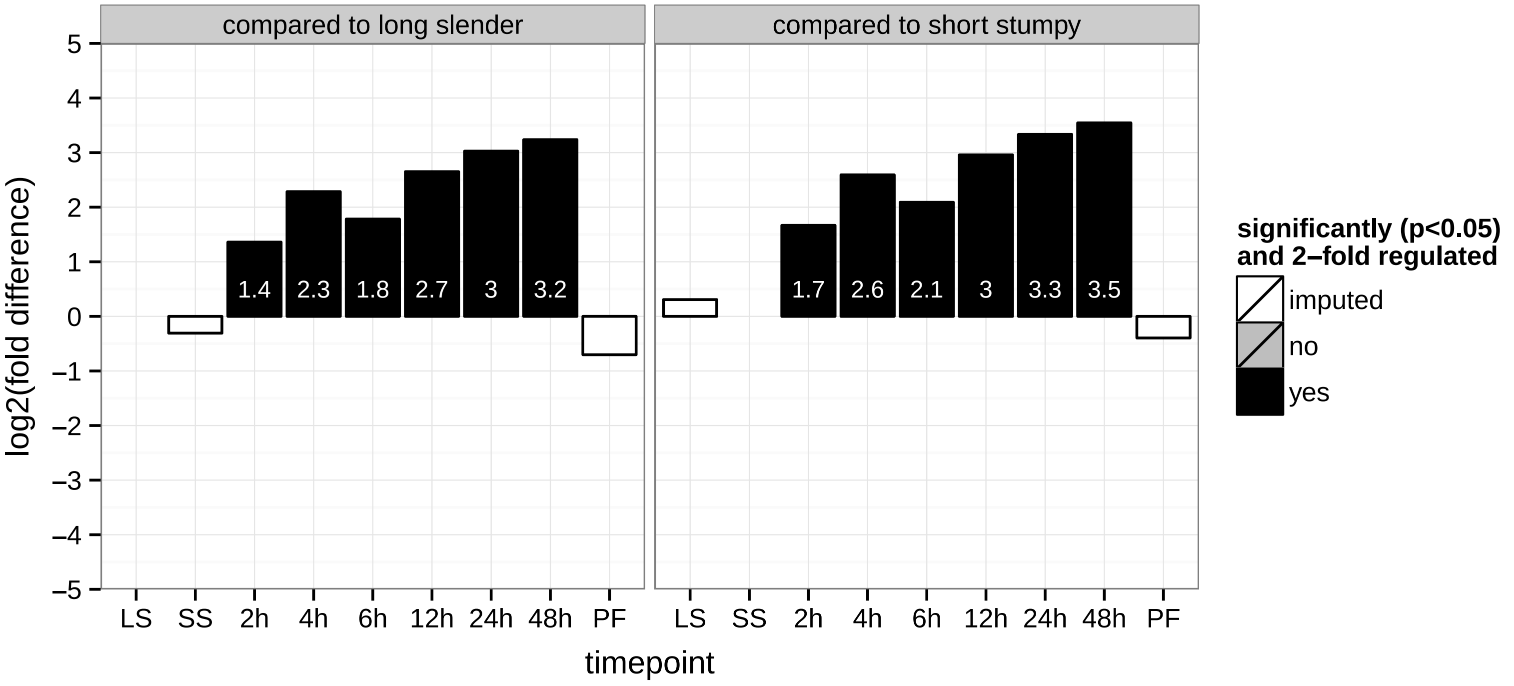
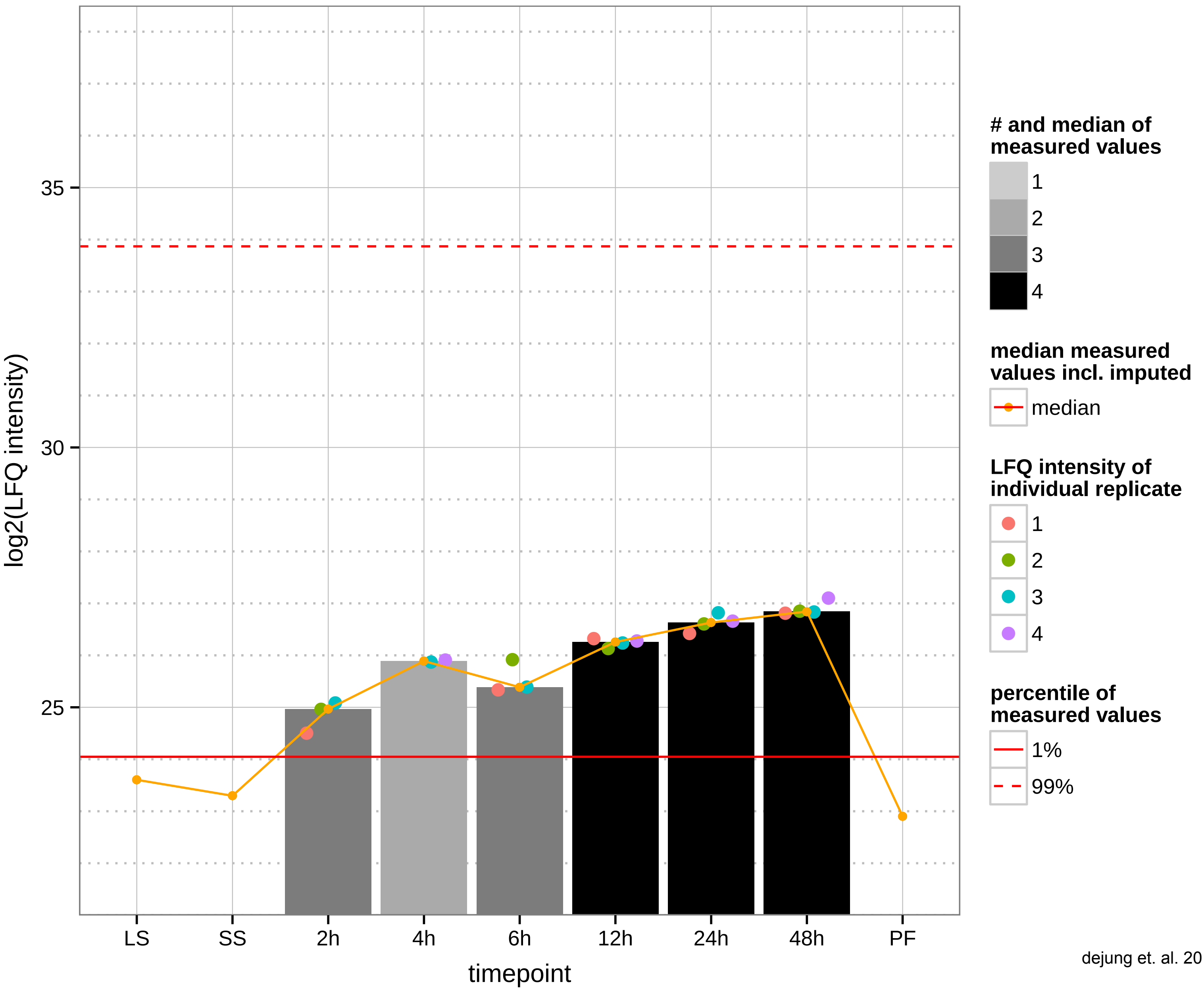
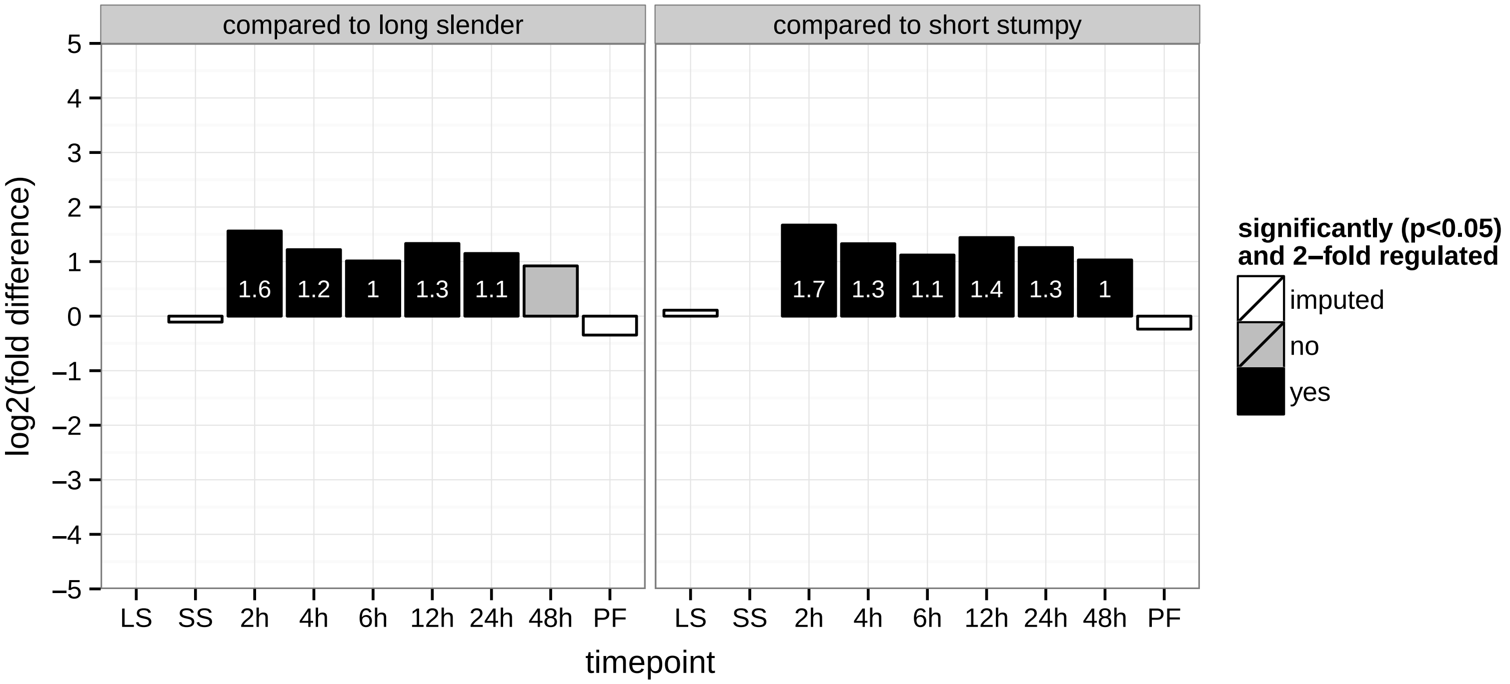
expression site–associated gene (ESAG) protein, putative, expression site–associated gene 5 (ESAG5) protein
Tb927.5.340;Tb11.v5.0282
AGOF: null, lipid binding
AGOC: null
AGOP: null
PGOF: lipid binding
PGOC: null
PGOP: null

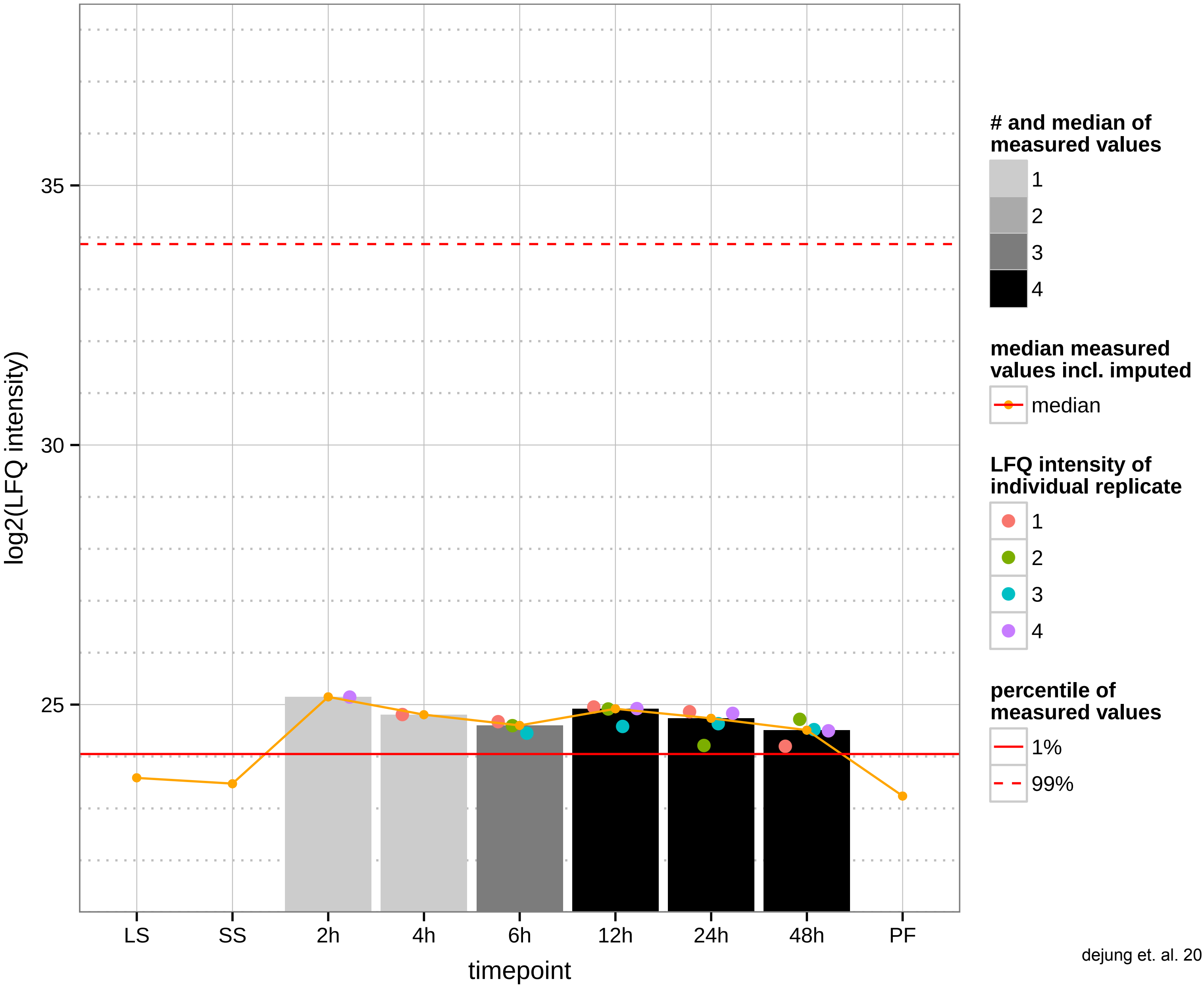




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.2790
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: Golgi transport complex
PGOP: intra–Golgi vesicle–mediated transport





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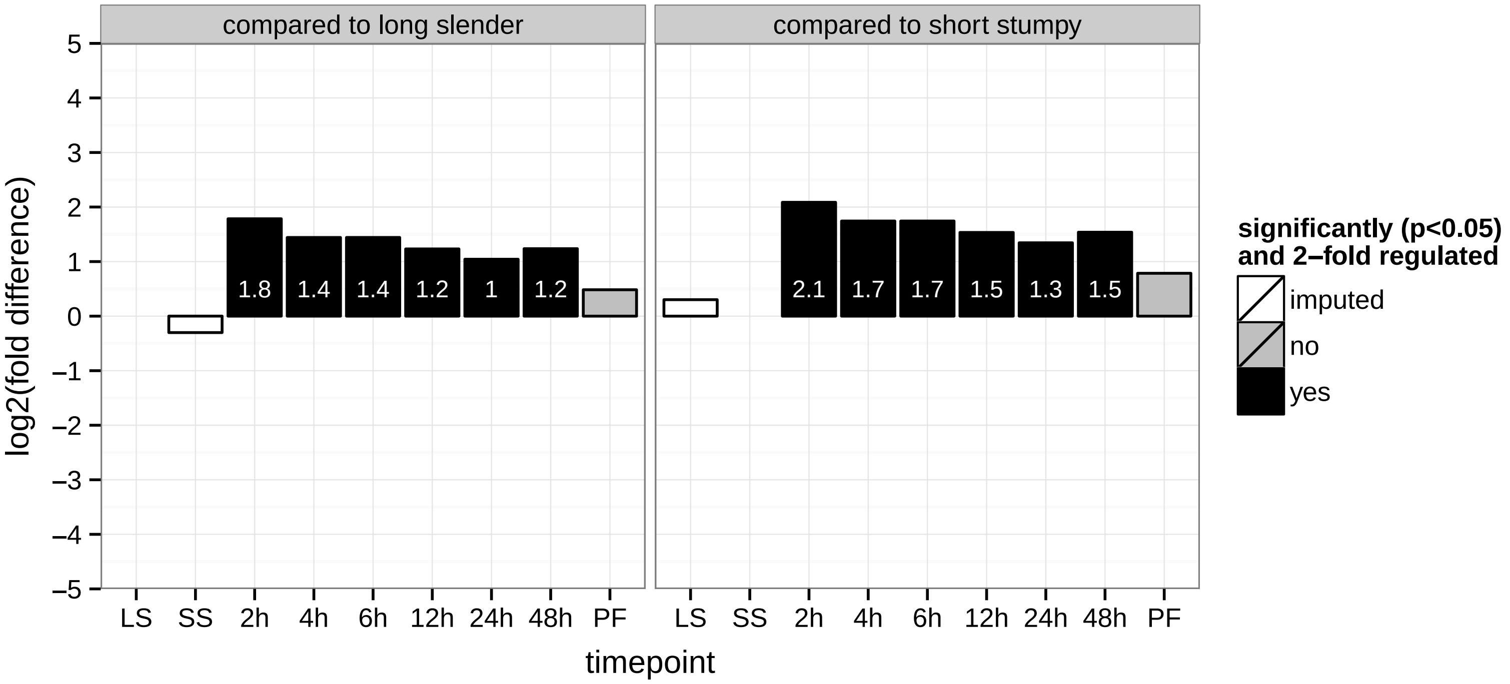
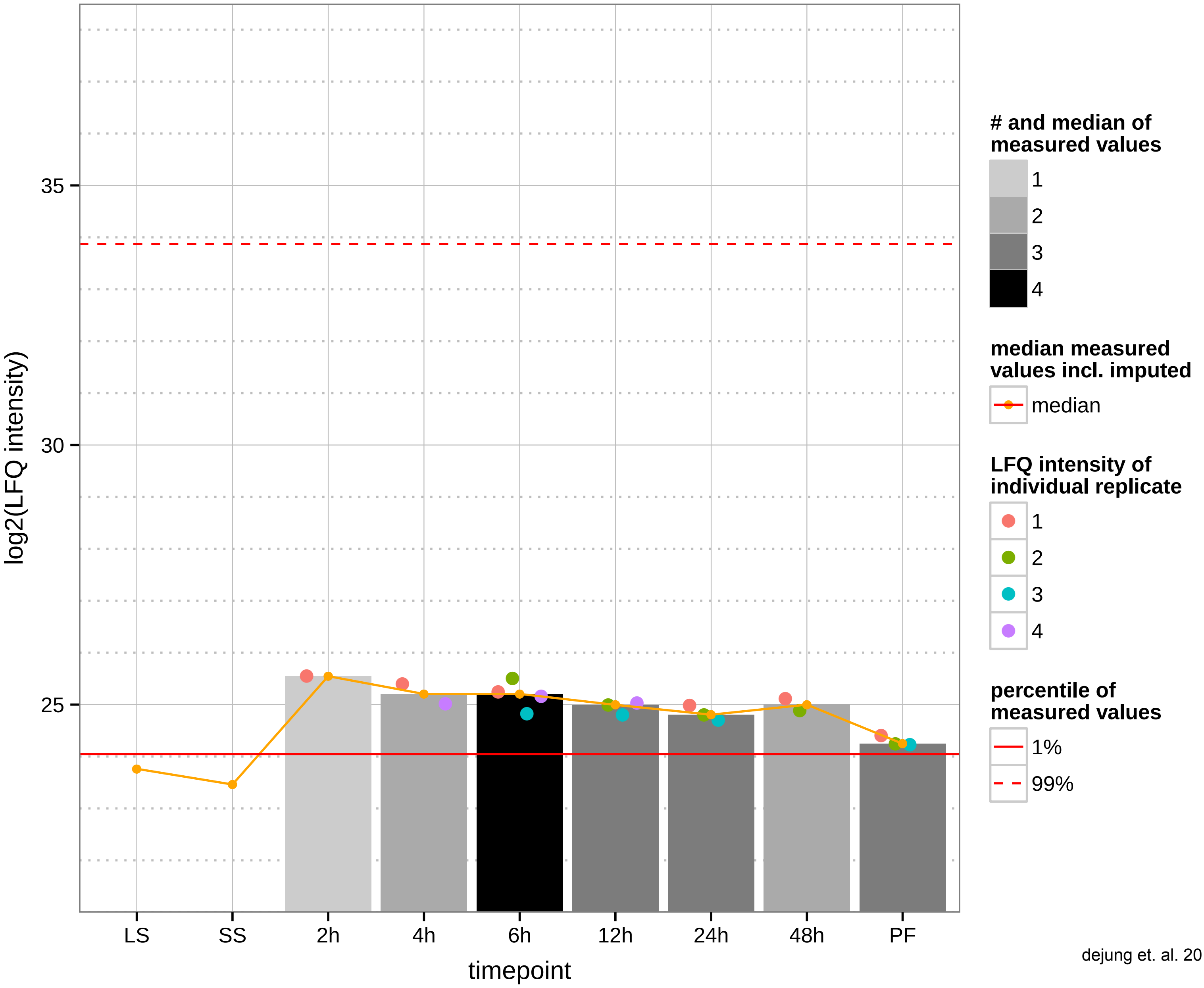
small GTPase, putative (RAB23)
Tb927.10.8560
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti





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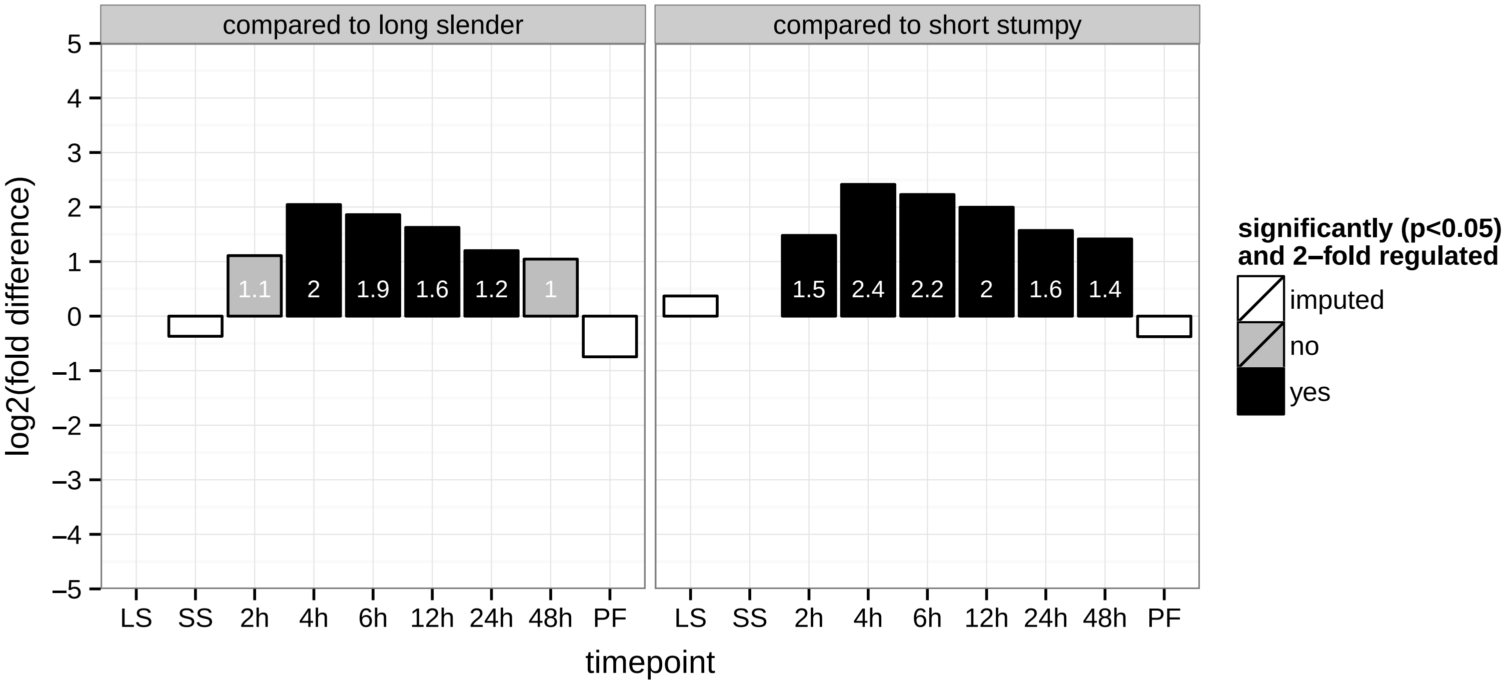
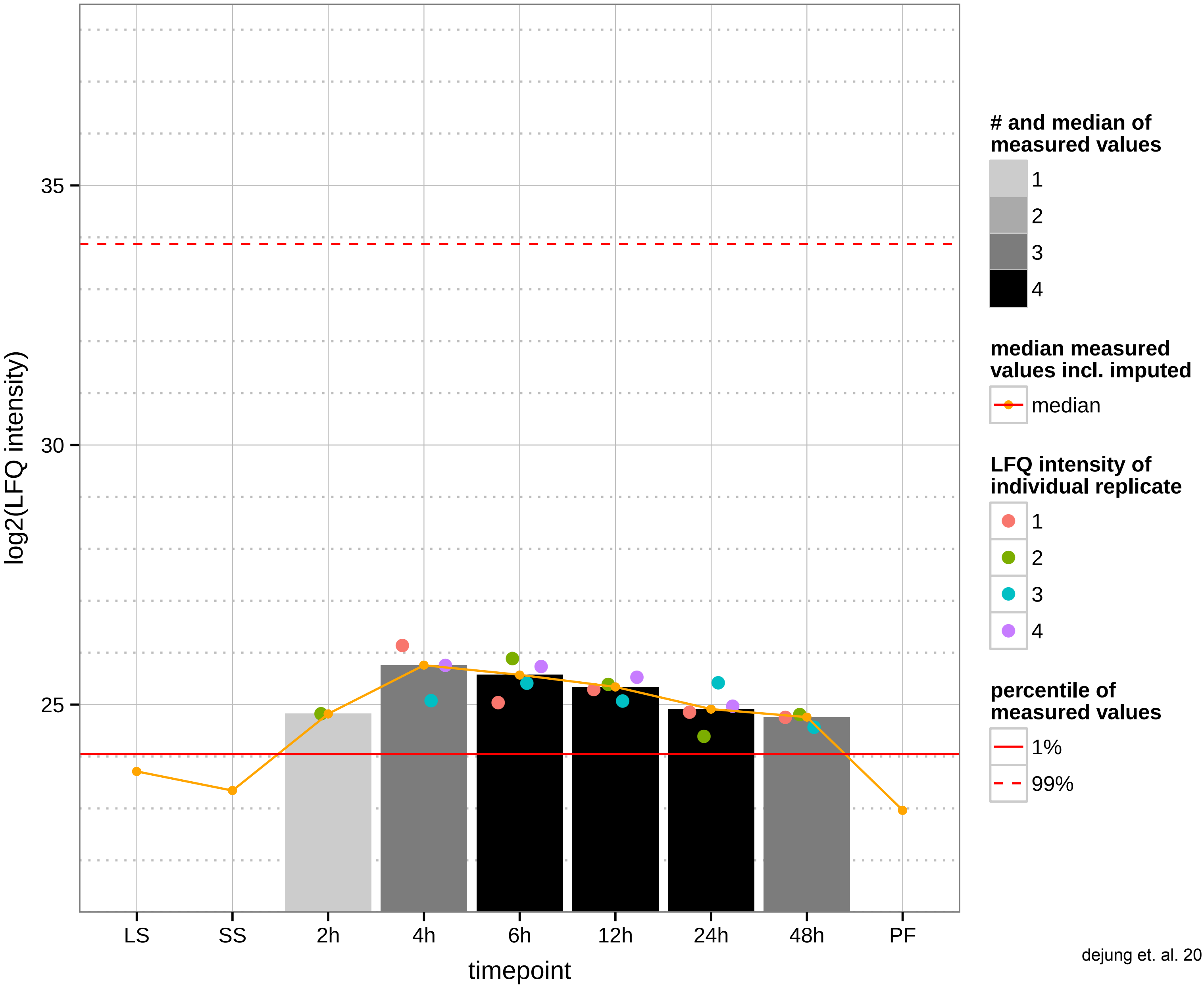
expression site–associated gene 4 (ESAG4) protein, putative, receptor–type adenylate cyclase GRESAG 4
Tb927.11.150;Tb11.v5.1015
AGOF: null, adenylate cyclase activity
AGOC: null, integral to membrane
AGOP: null, cyclic nucleotide biosynthetic process, intracellular signal transduction
PGOF: phosphorus–oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction





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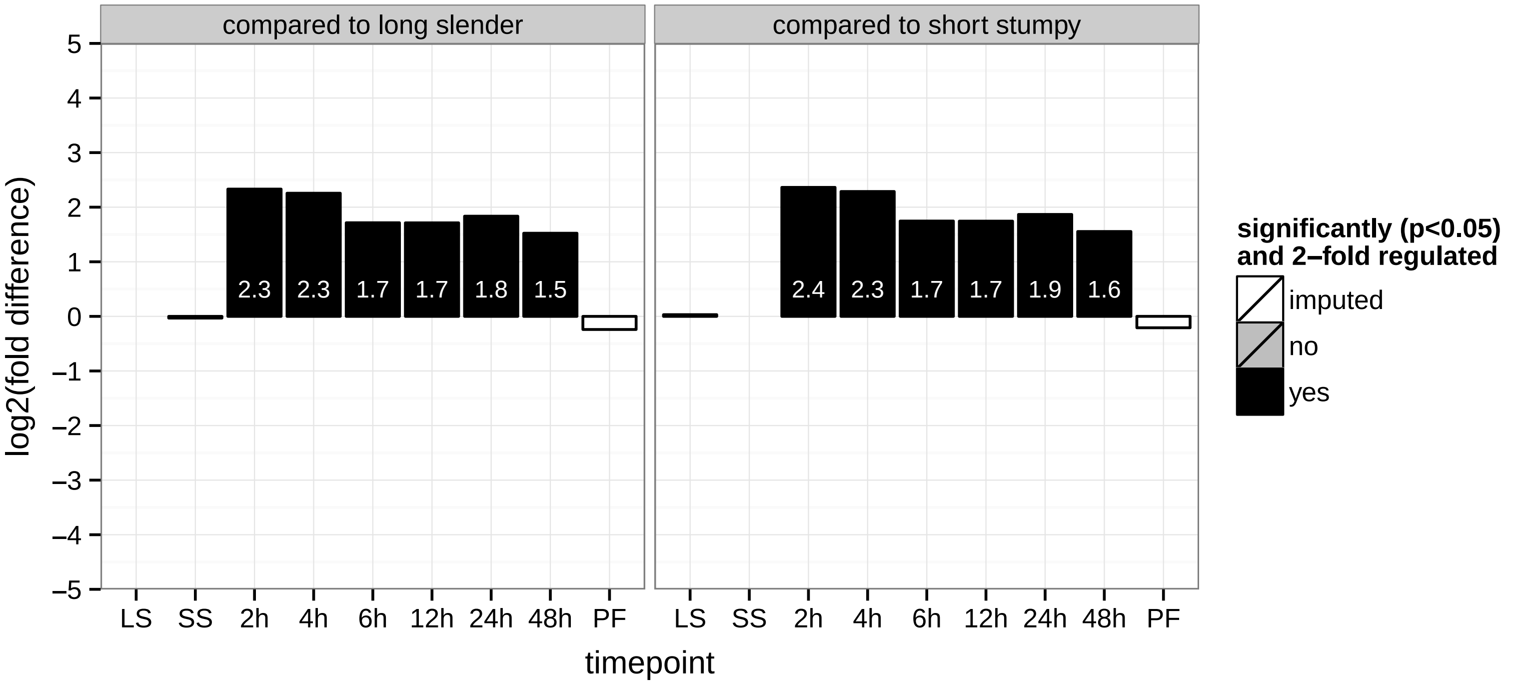
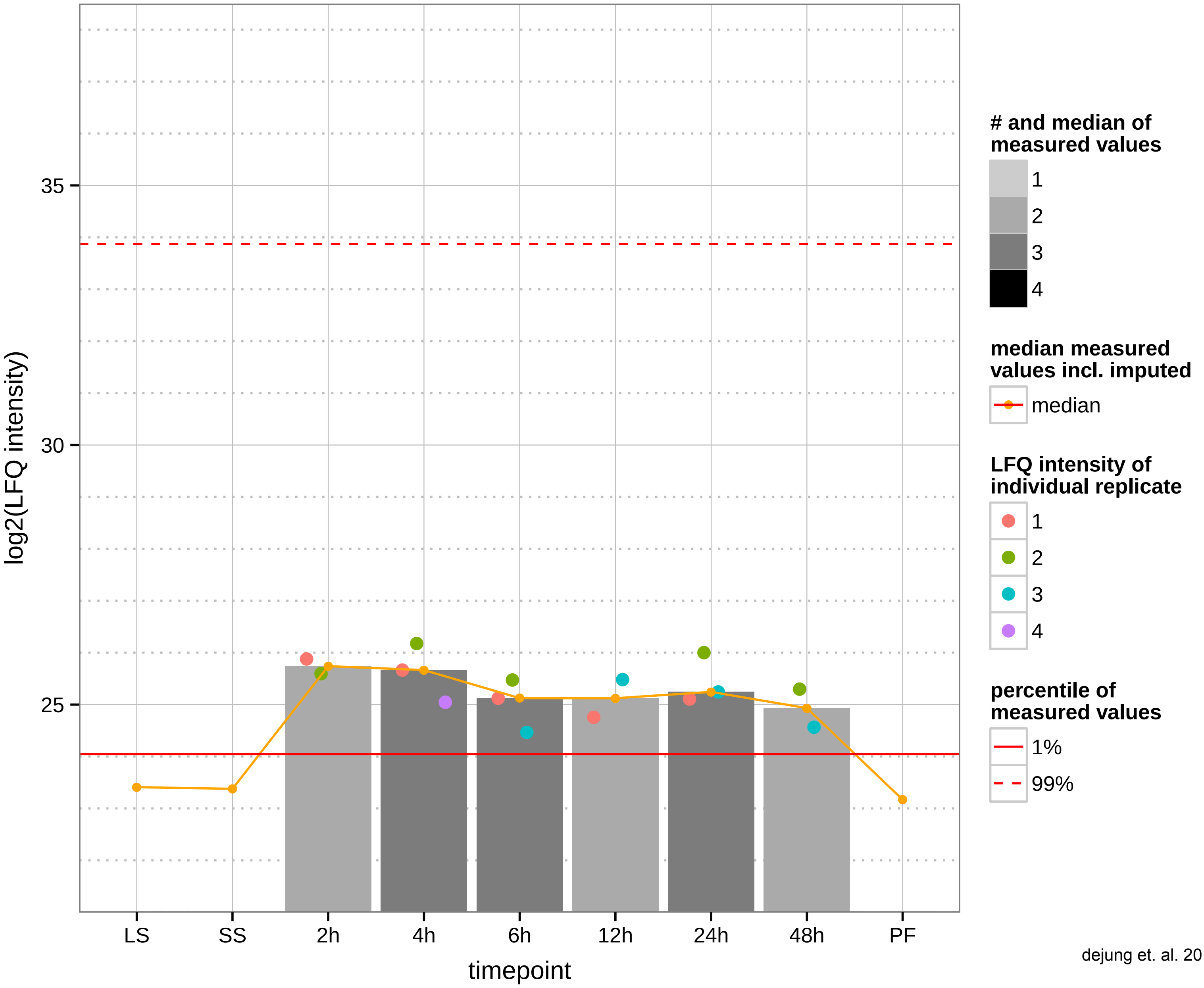
hypothetical protein, conserved
Tb927.11.6100
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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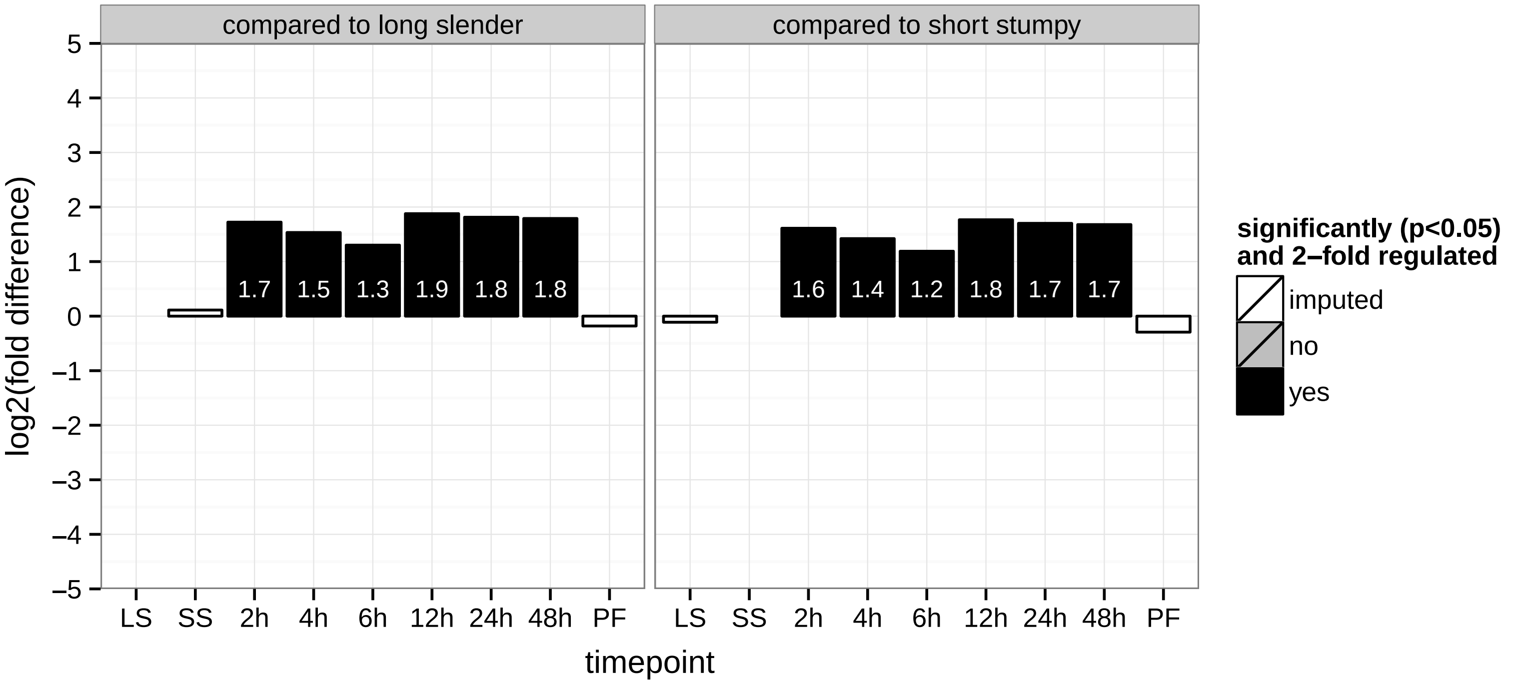
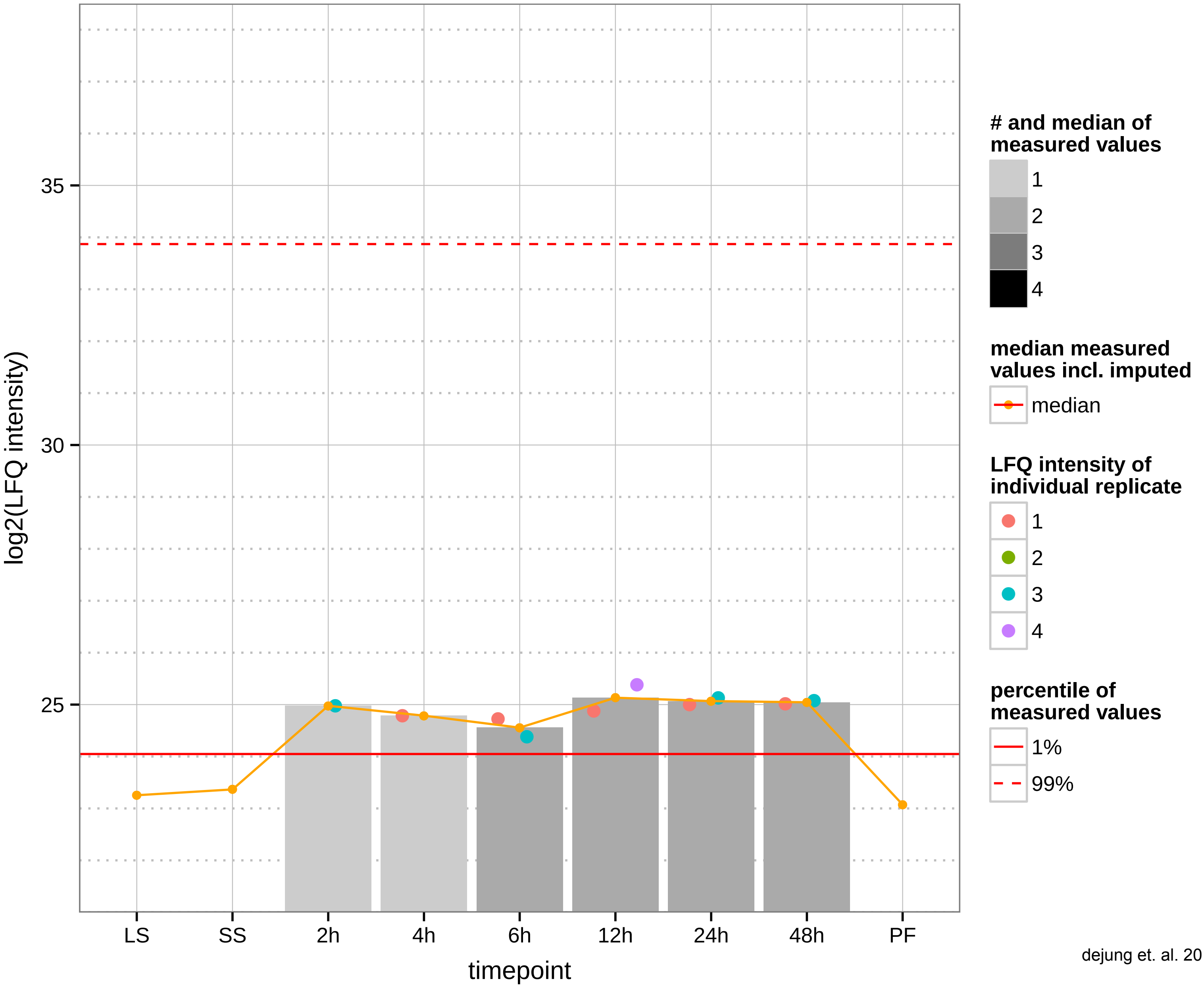
hypothetical protein, conserved
Tb927.3.2350
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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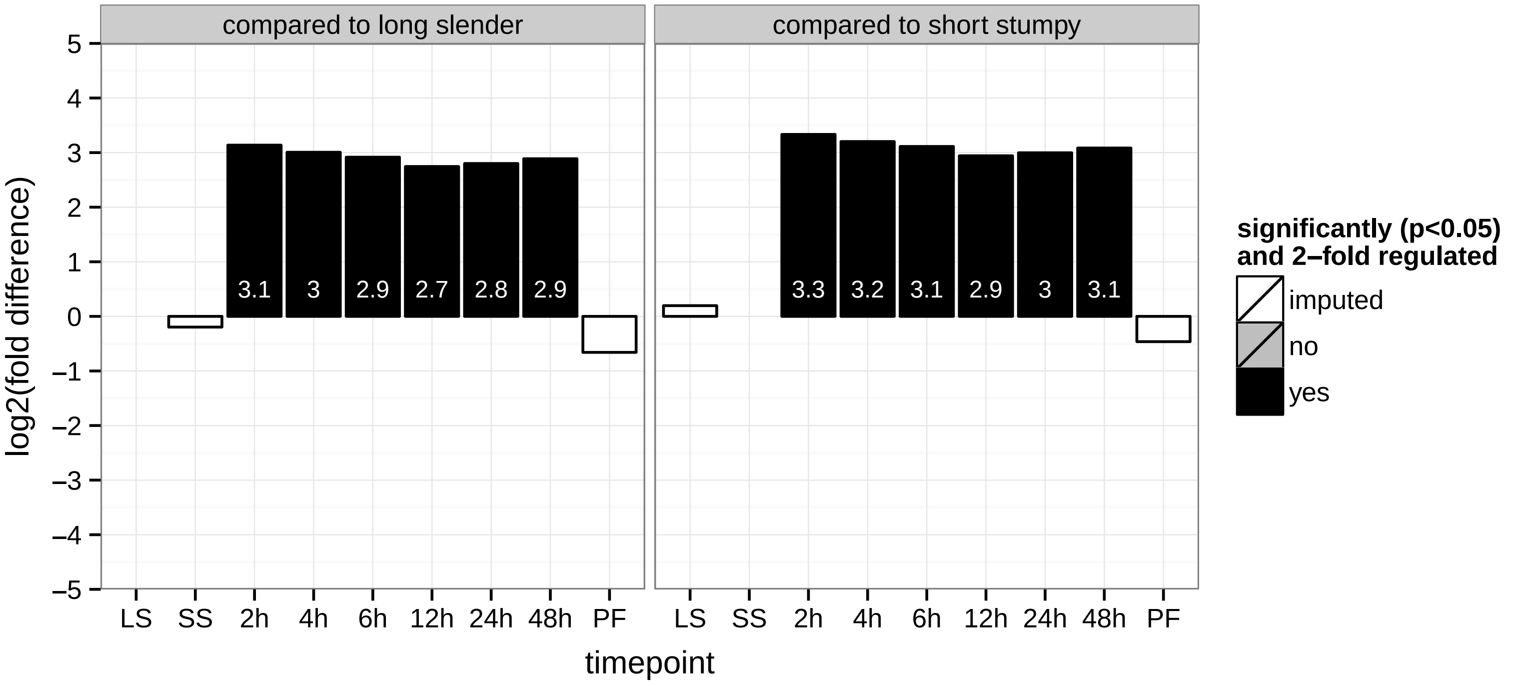
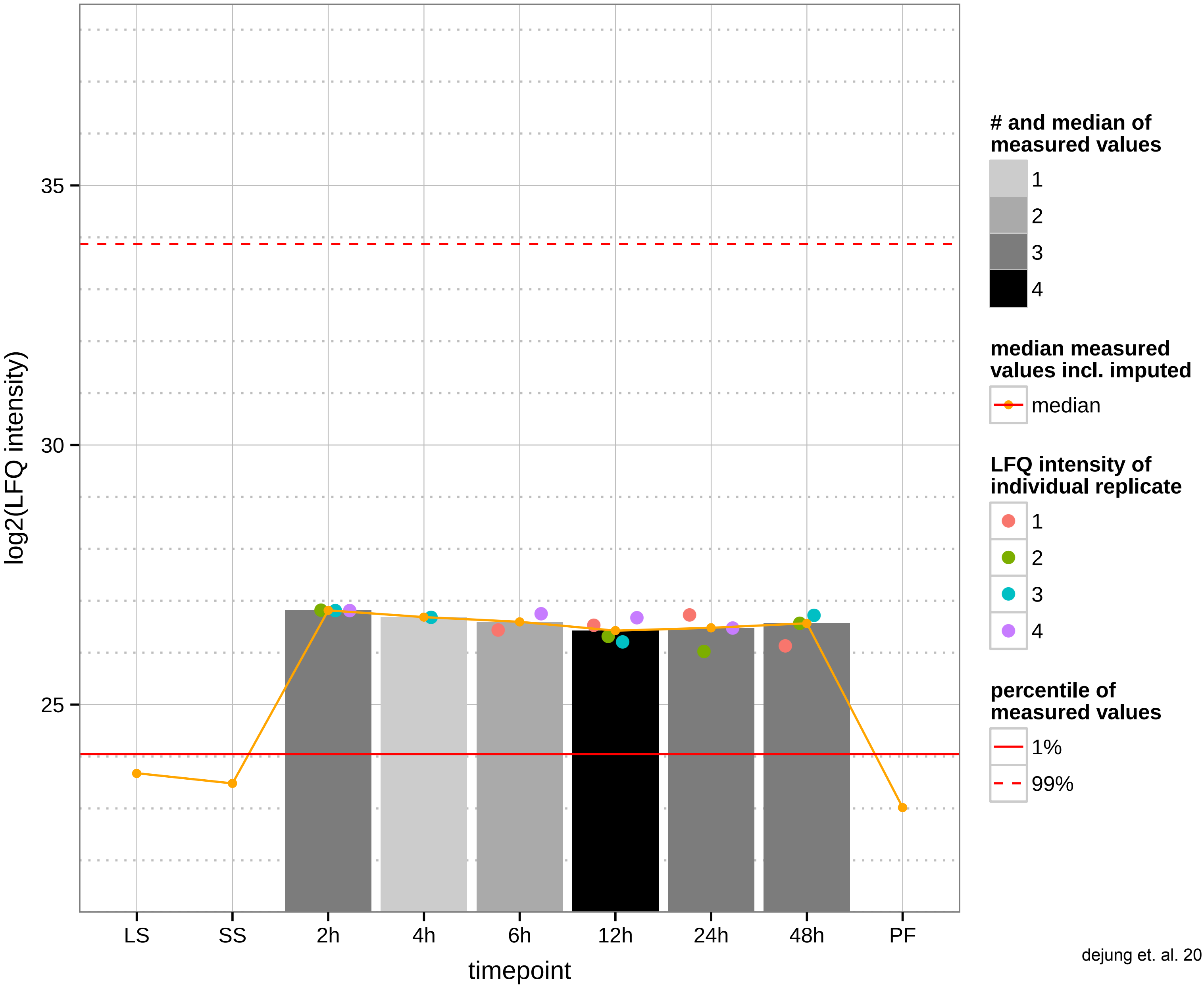
hypothetical protein, conserved
Tb927.3.4580
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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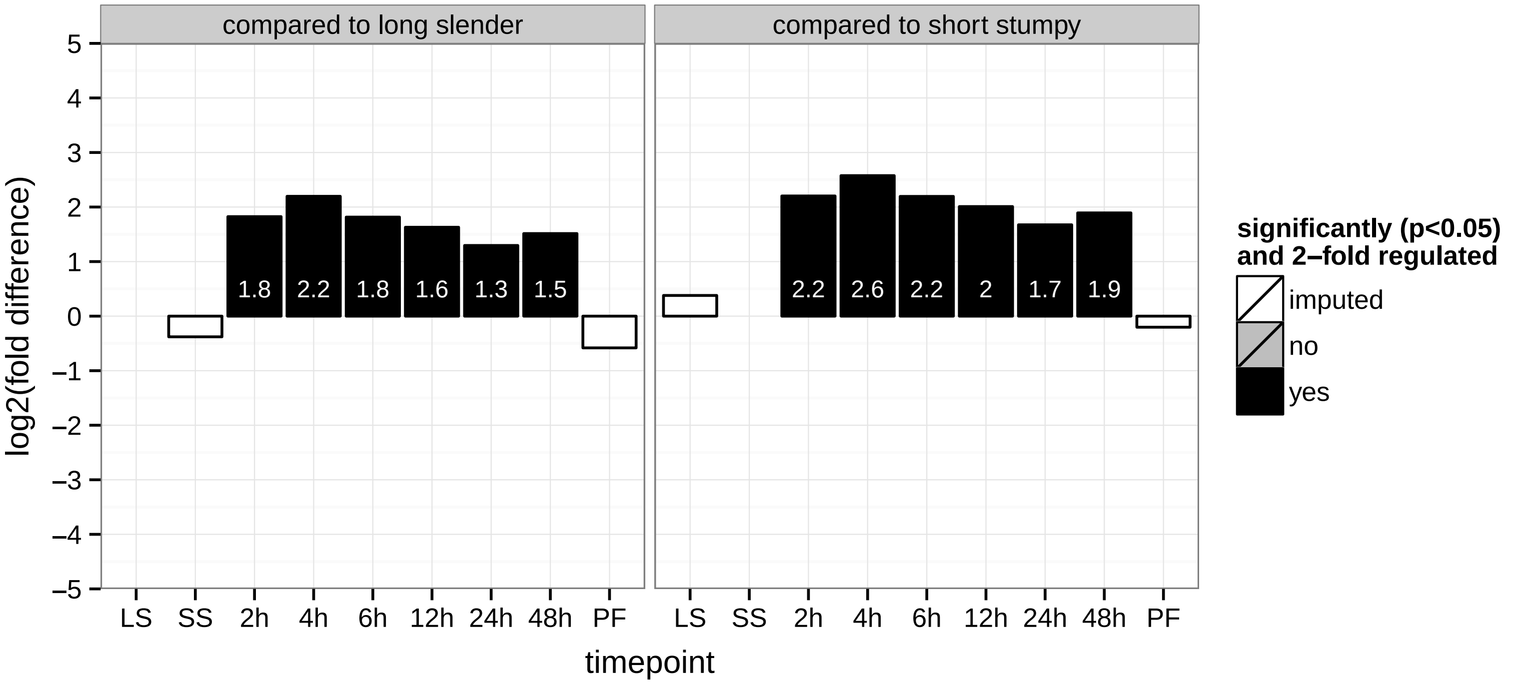
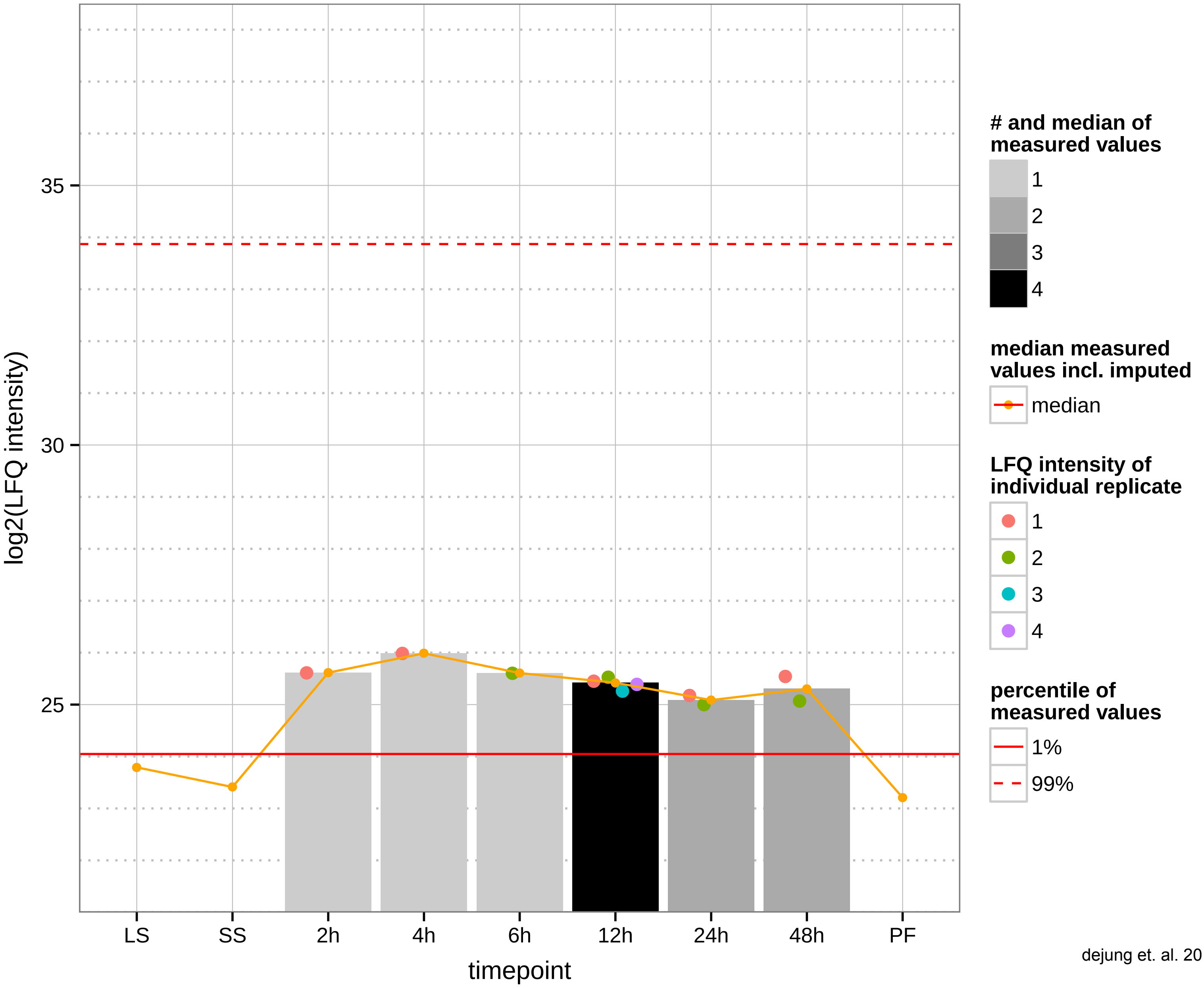
protein kinase, putative, eukaryotic translation initiation factor 2–alpha kinase precursor
Tb927.4.2500
AGOF: ATP binding, elongation factor–2 kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: integral to membrane
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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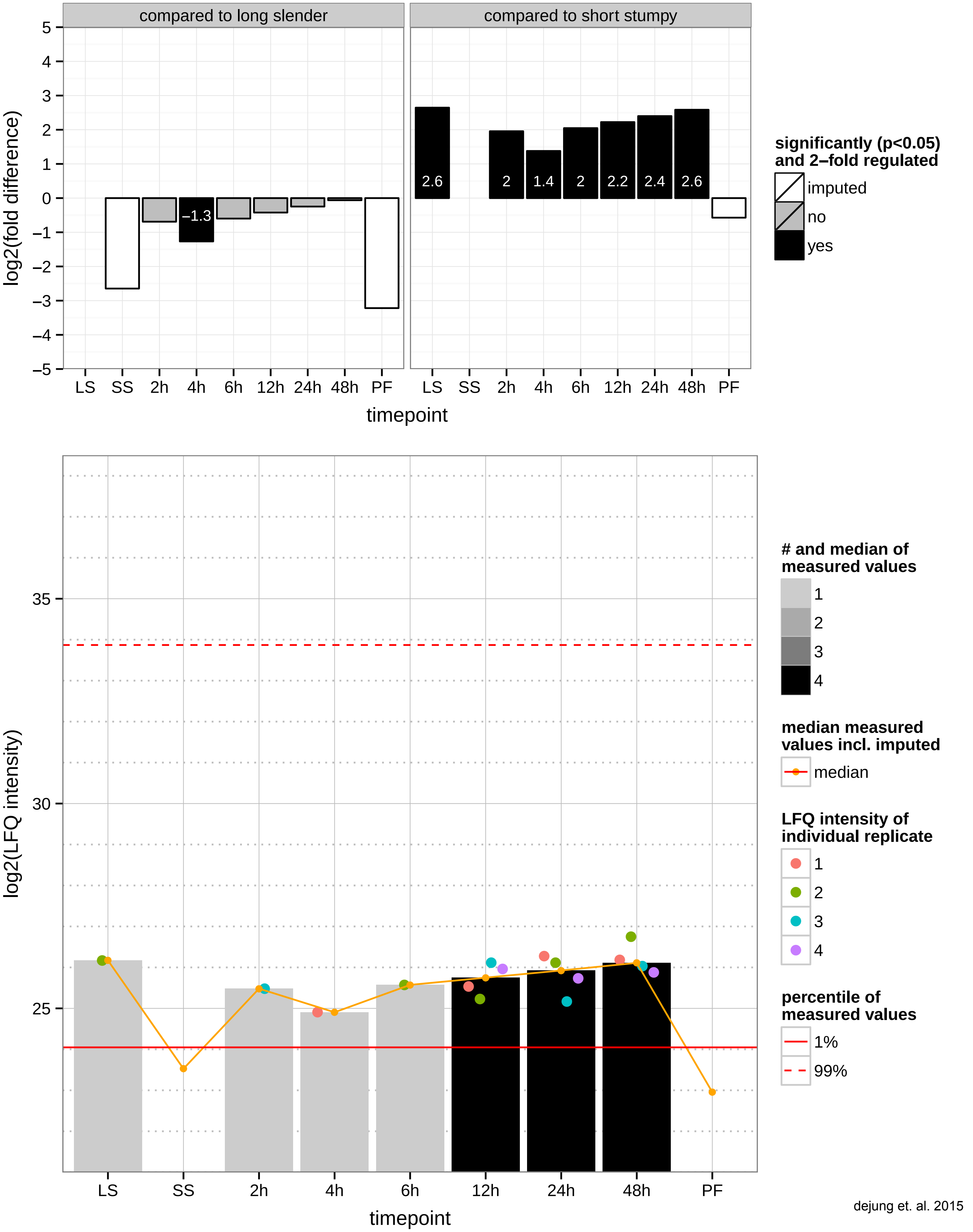
hypothetical protein, conserved
Tb927.4.2750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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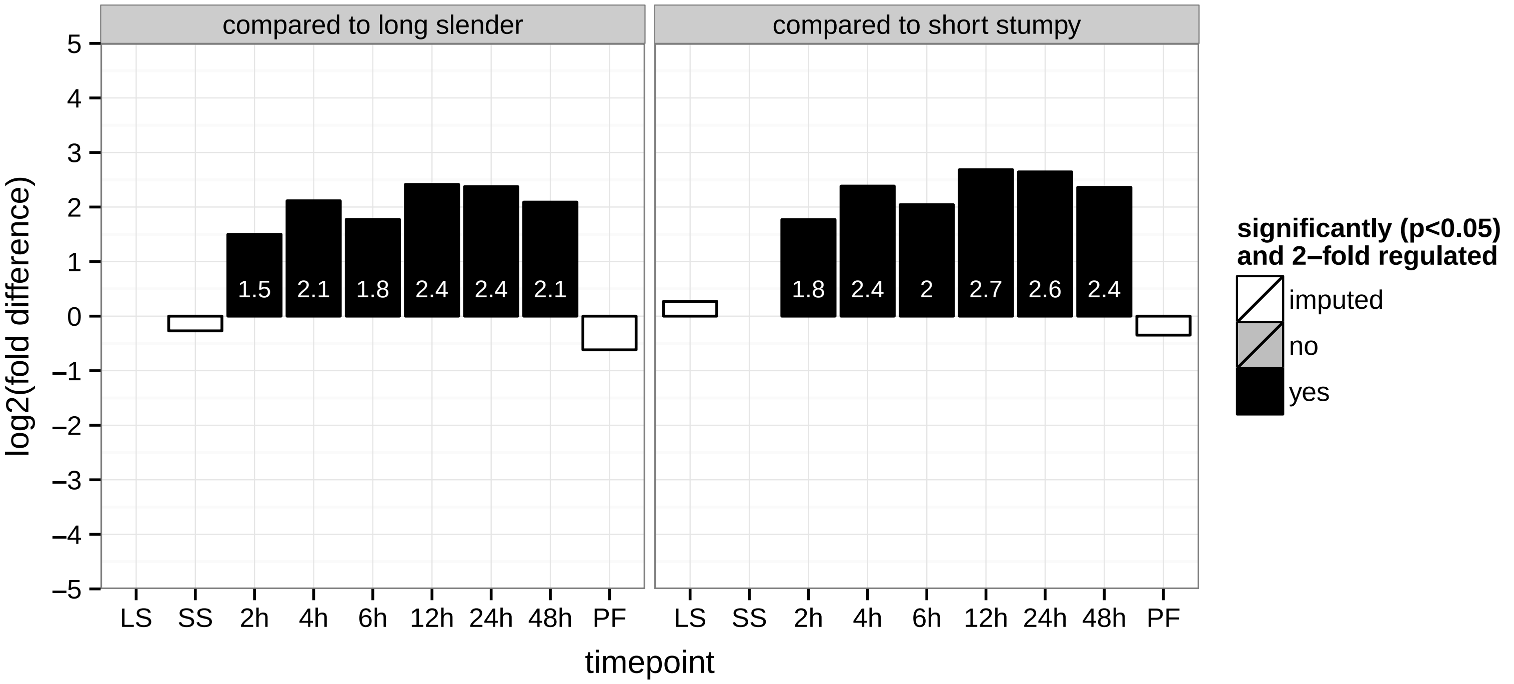
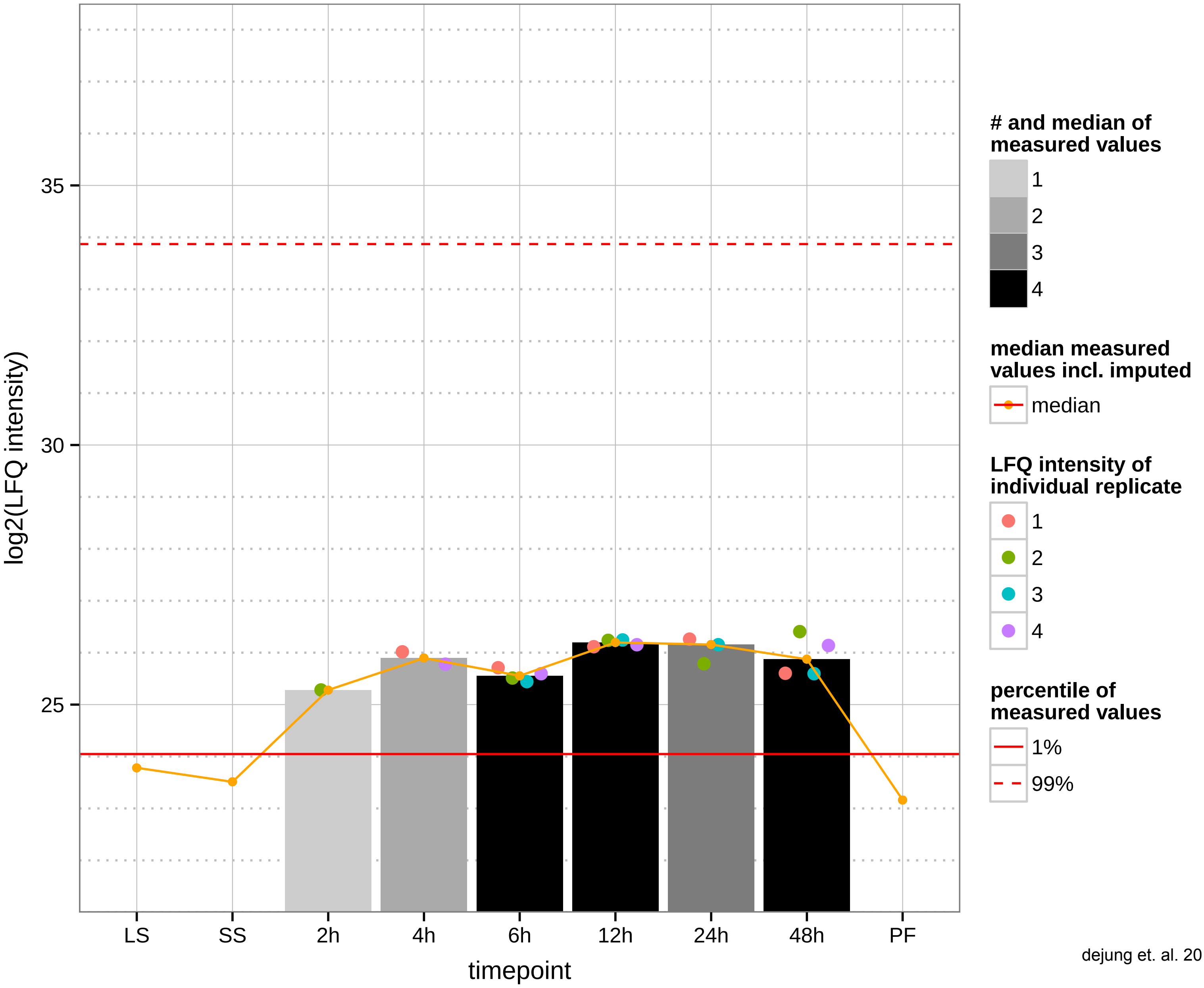
amino acid transporter, putative
Tb927.4.3930
AGOF: amine transmembrane transporter activity
AGOC: integral to membrane
AGOP: amino acid transport
PGOF: null
PGOC: null
PGOP: null





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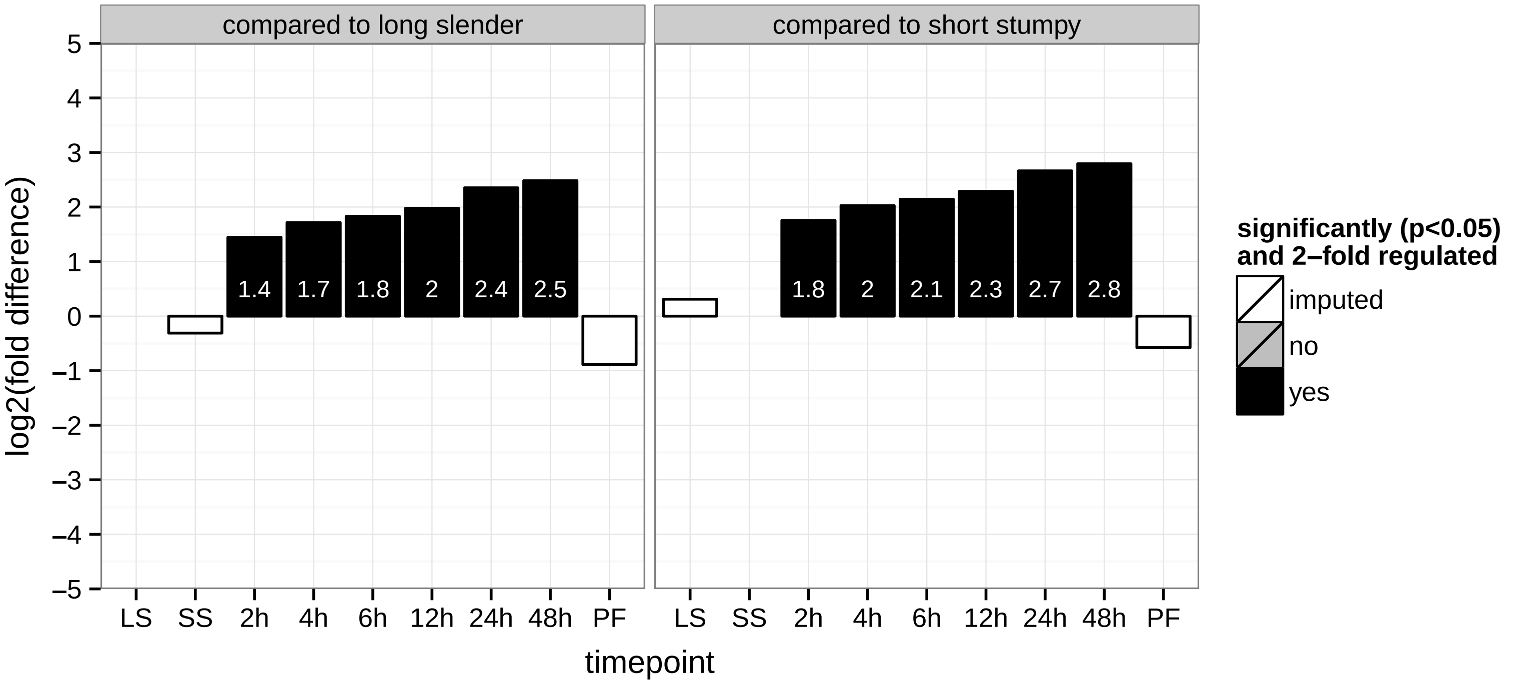
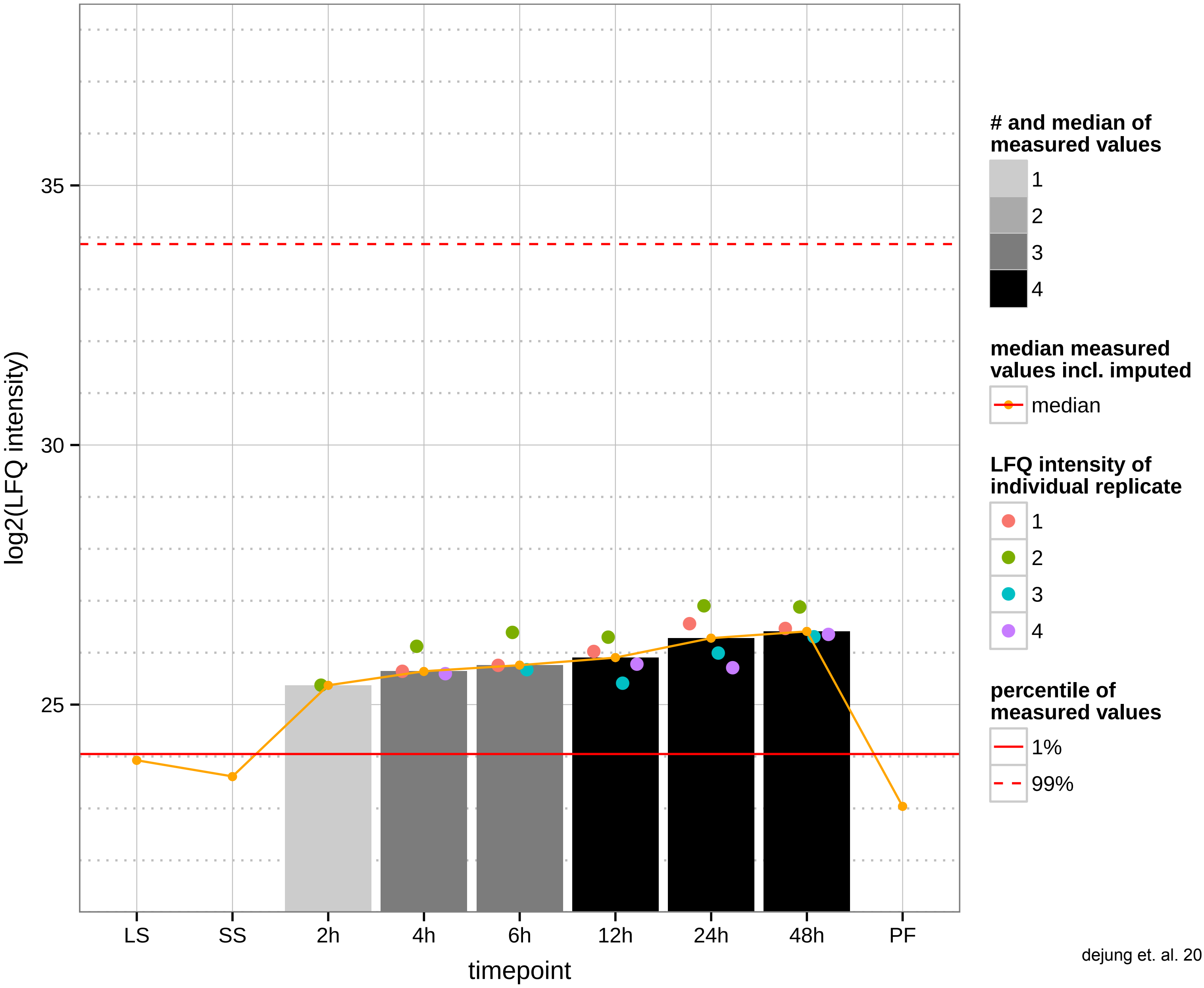
centrin, putative, caltractin
Tb927.8.1080
AGOF: calcium ion binding
AGOC: centrosome
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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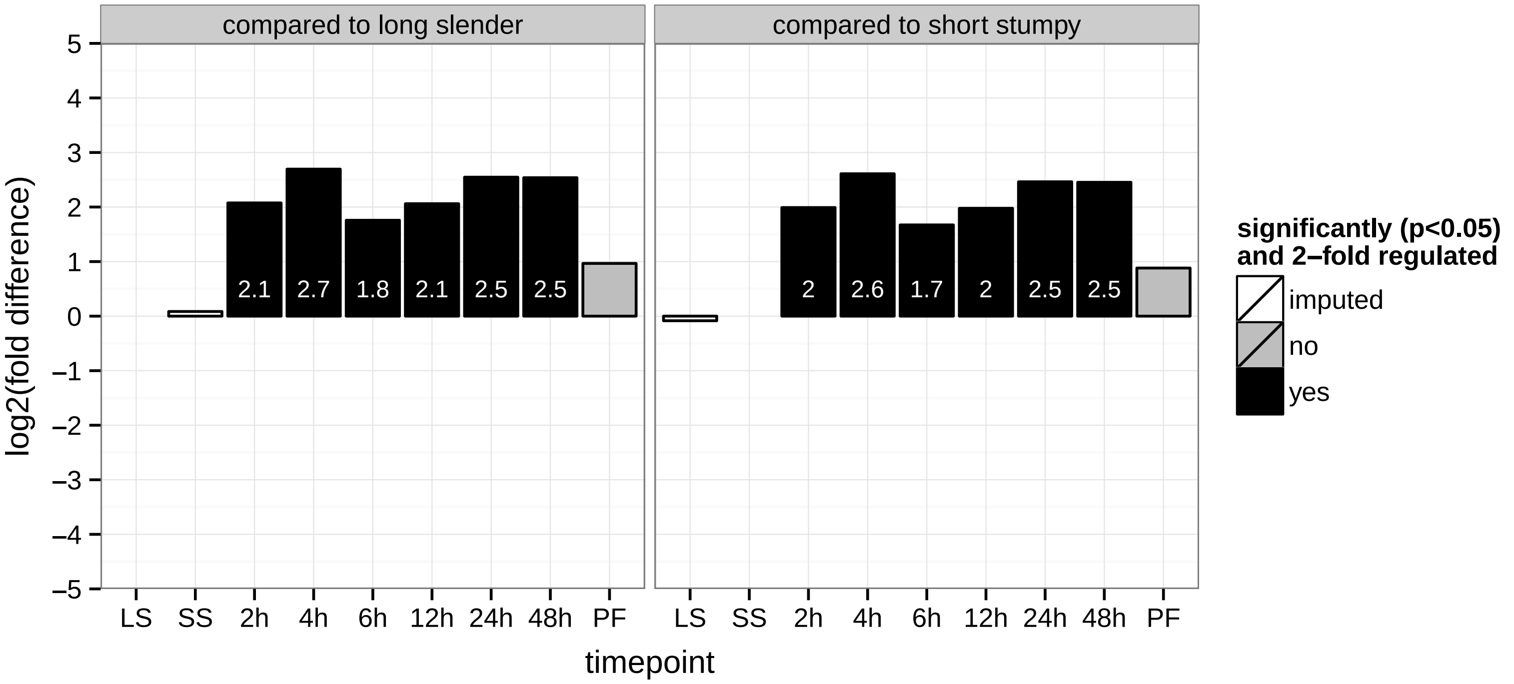
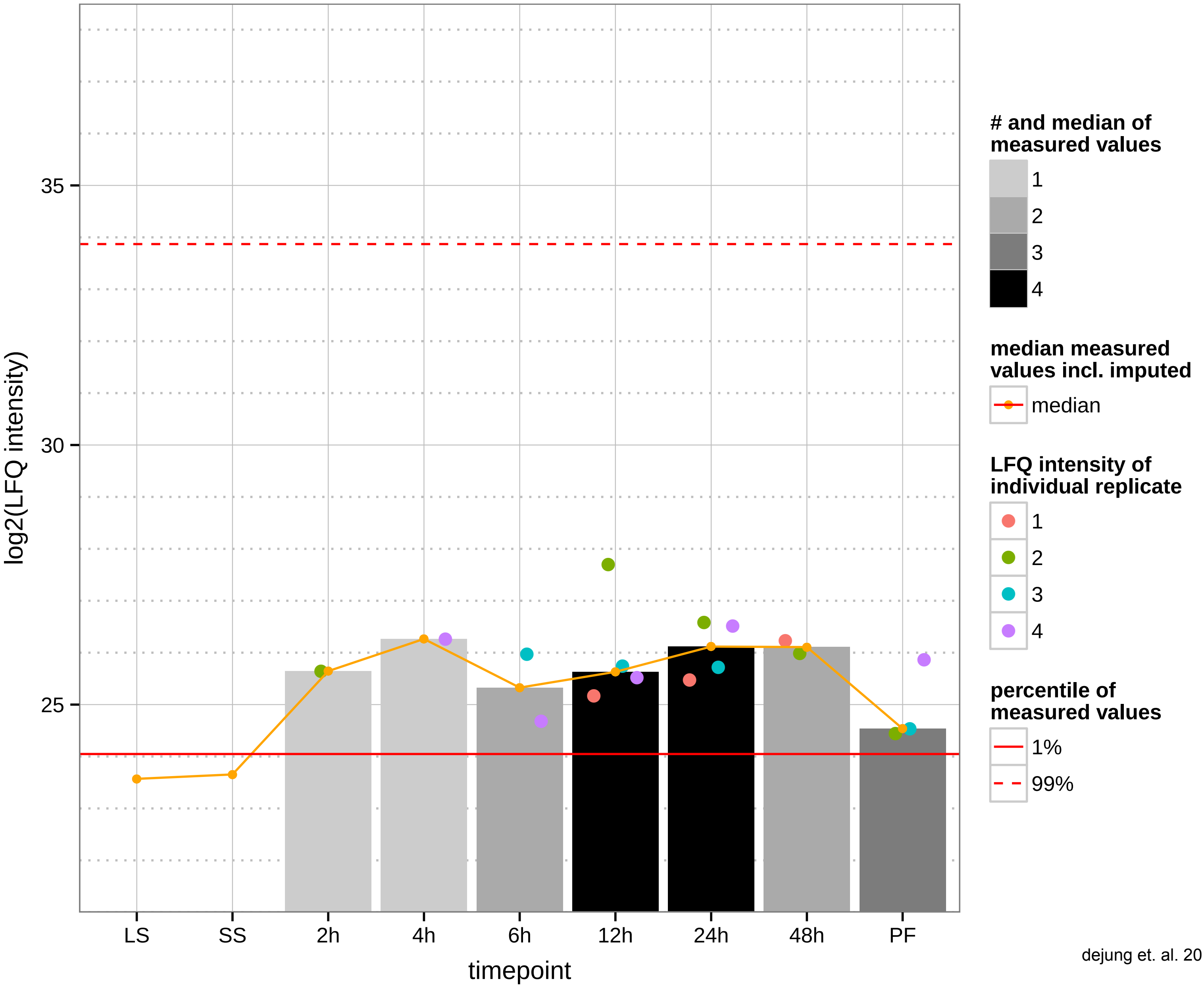
hypothetical protein, conserved
Tb927.8.3070
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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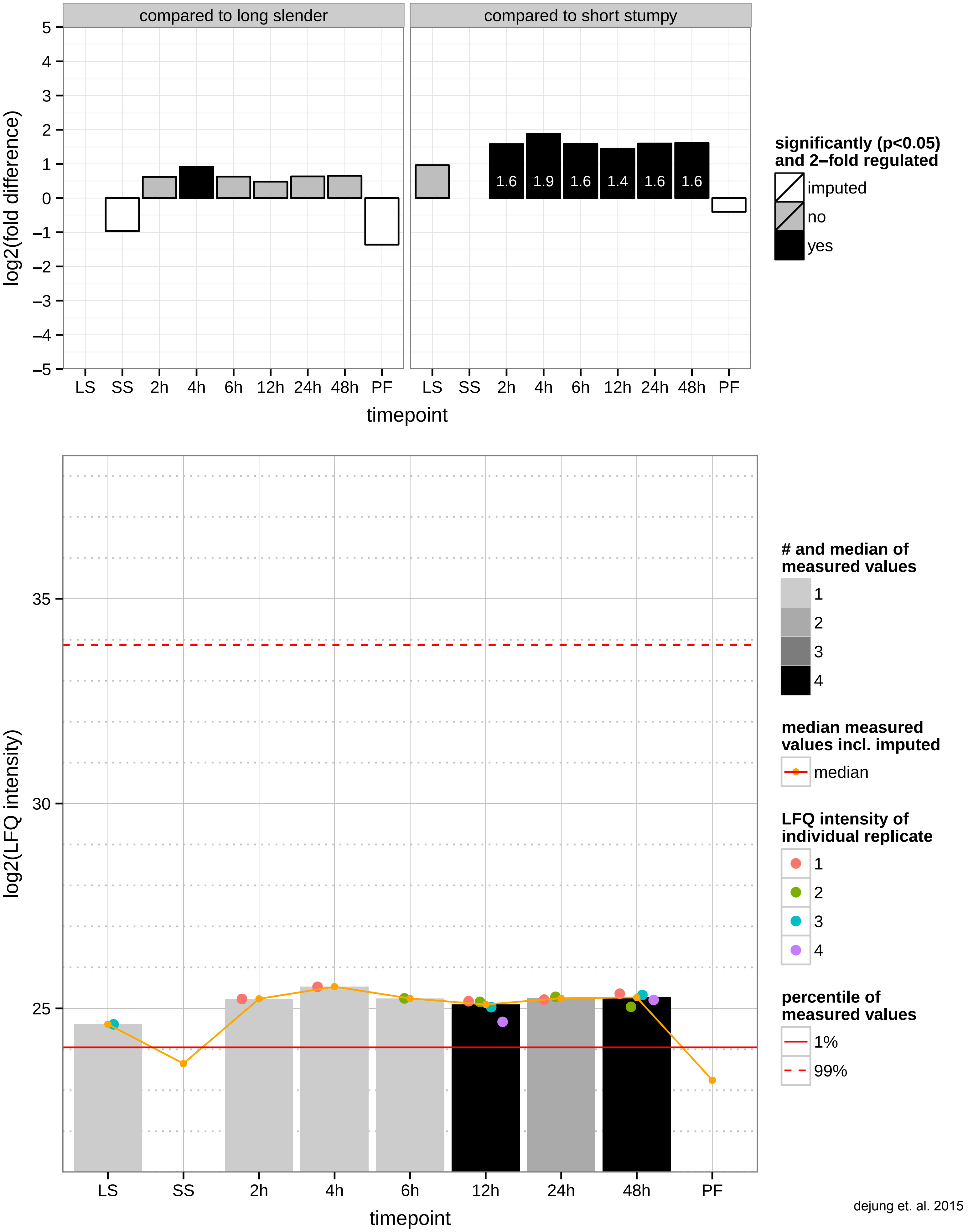
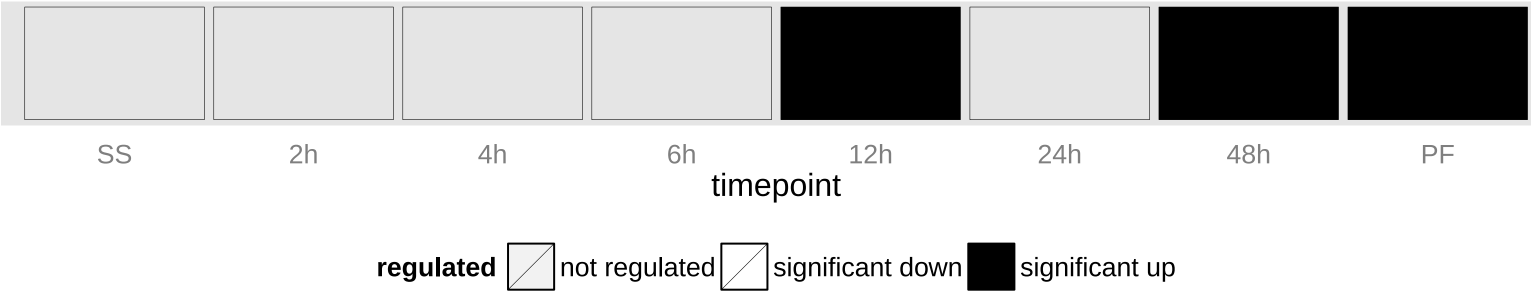
cyclophilin type peptidyl–prolyl cis–trans isomerase, putative (PPIase)
Tb927.9.11740
AGOF: peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: peptidyl–prolyl cis–trans isomerase activity
PGOC: null
PGOP: protein folding





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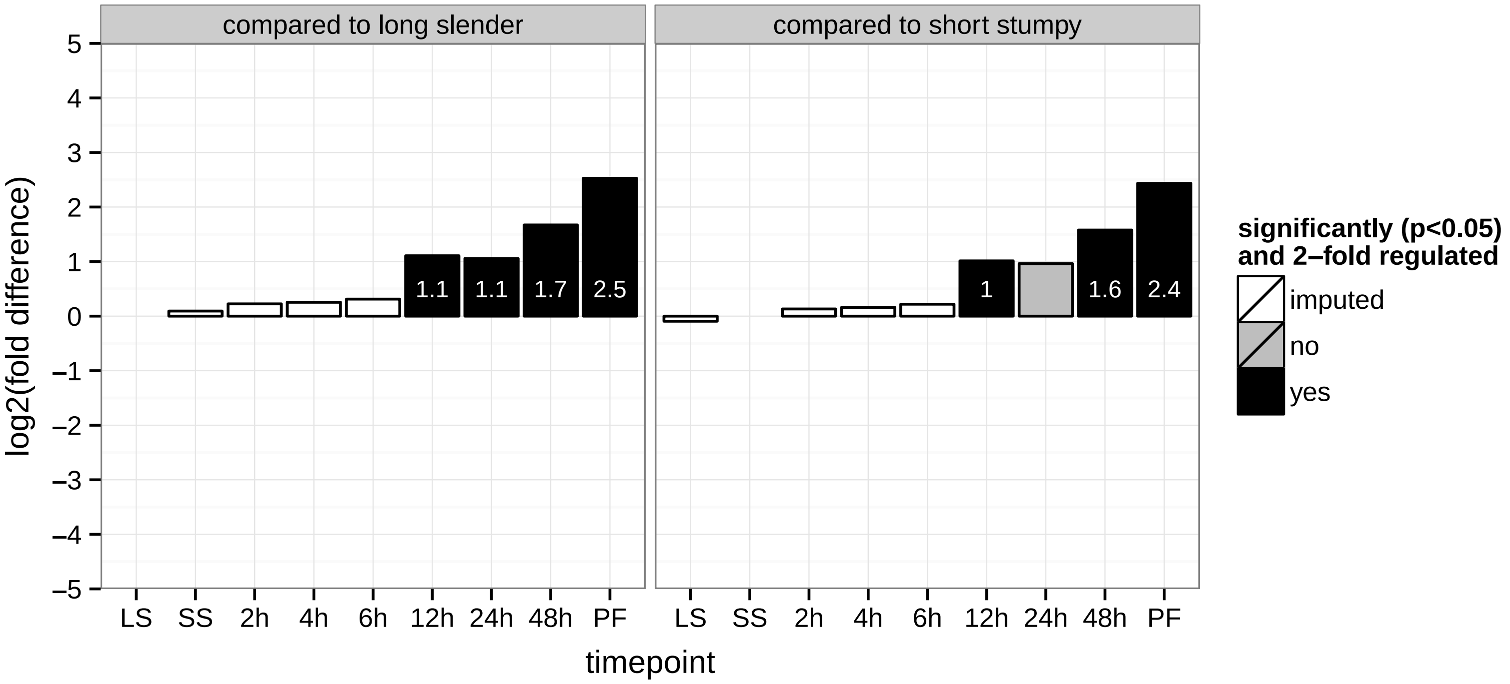
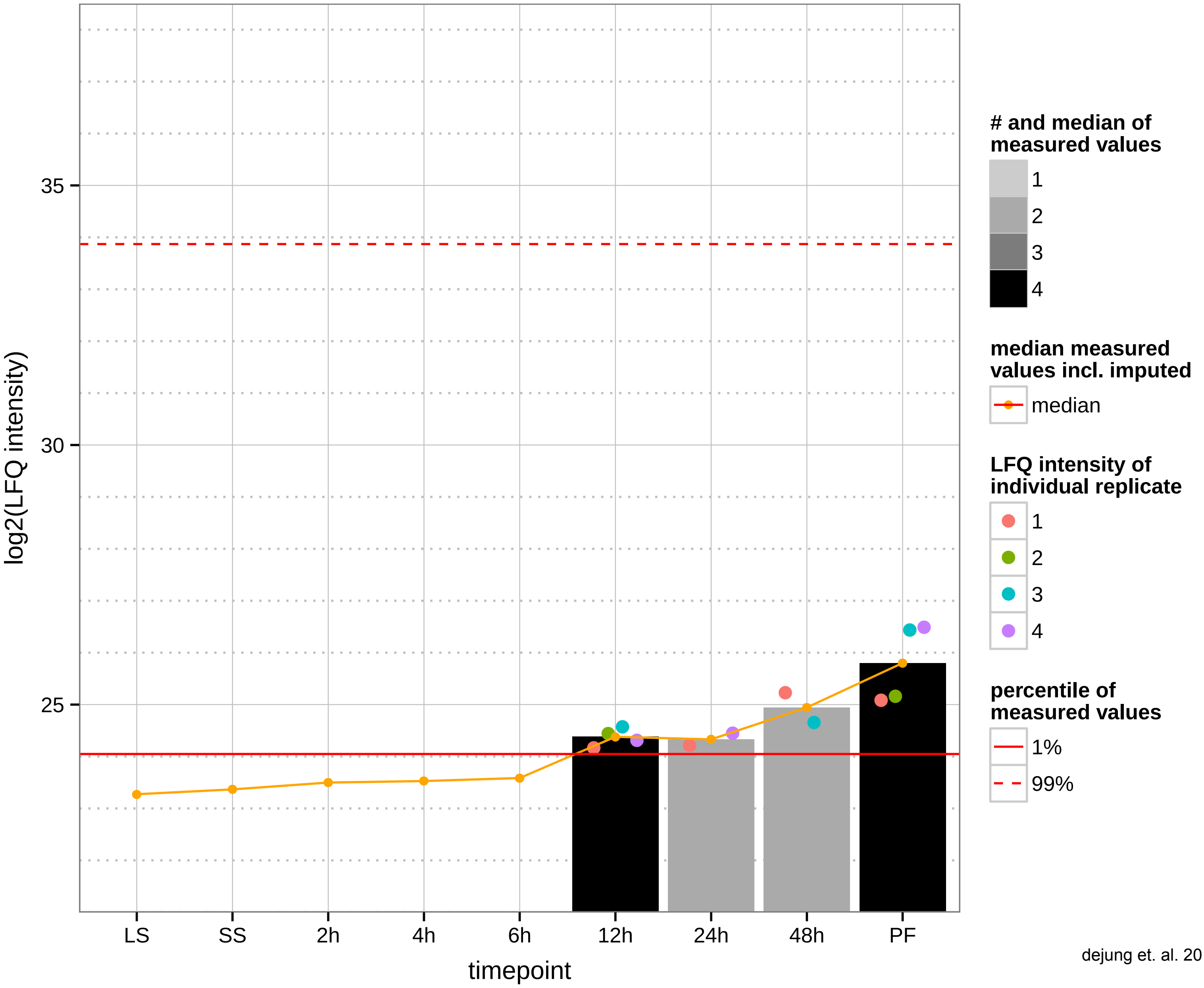
hypothetical protein, conserved
Tb927.10.1200;Tb11.v5.0487
AGOF: null
AGOC: null, cytoplasm
AGOP: null
PGOF: null
PGOC: cytoplasm
PGOP: null





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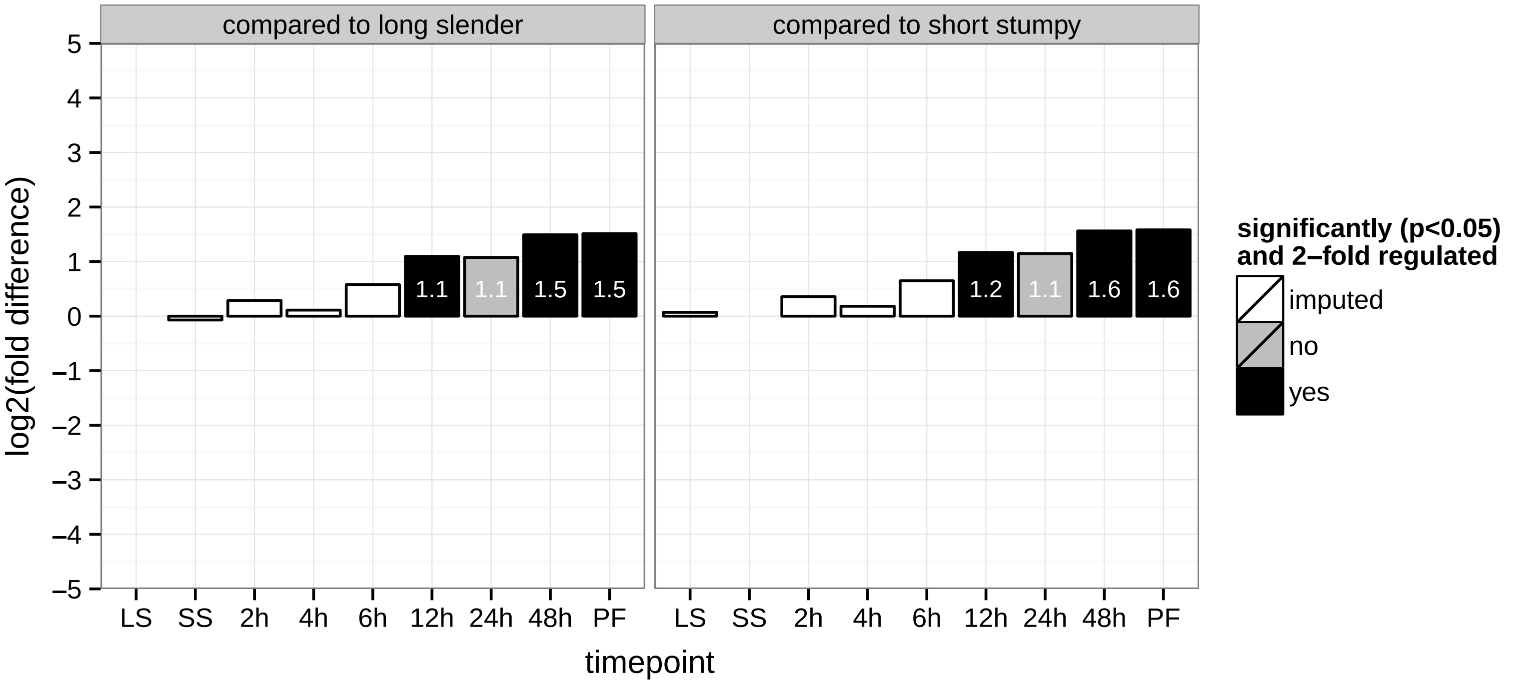
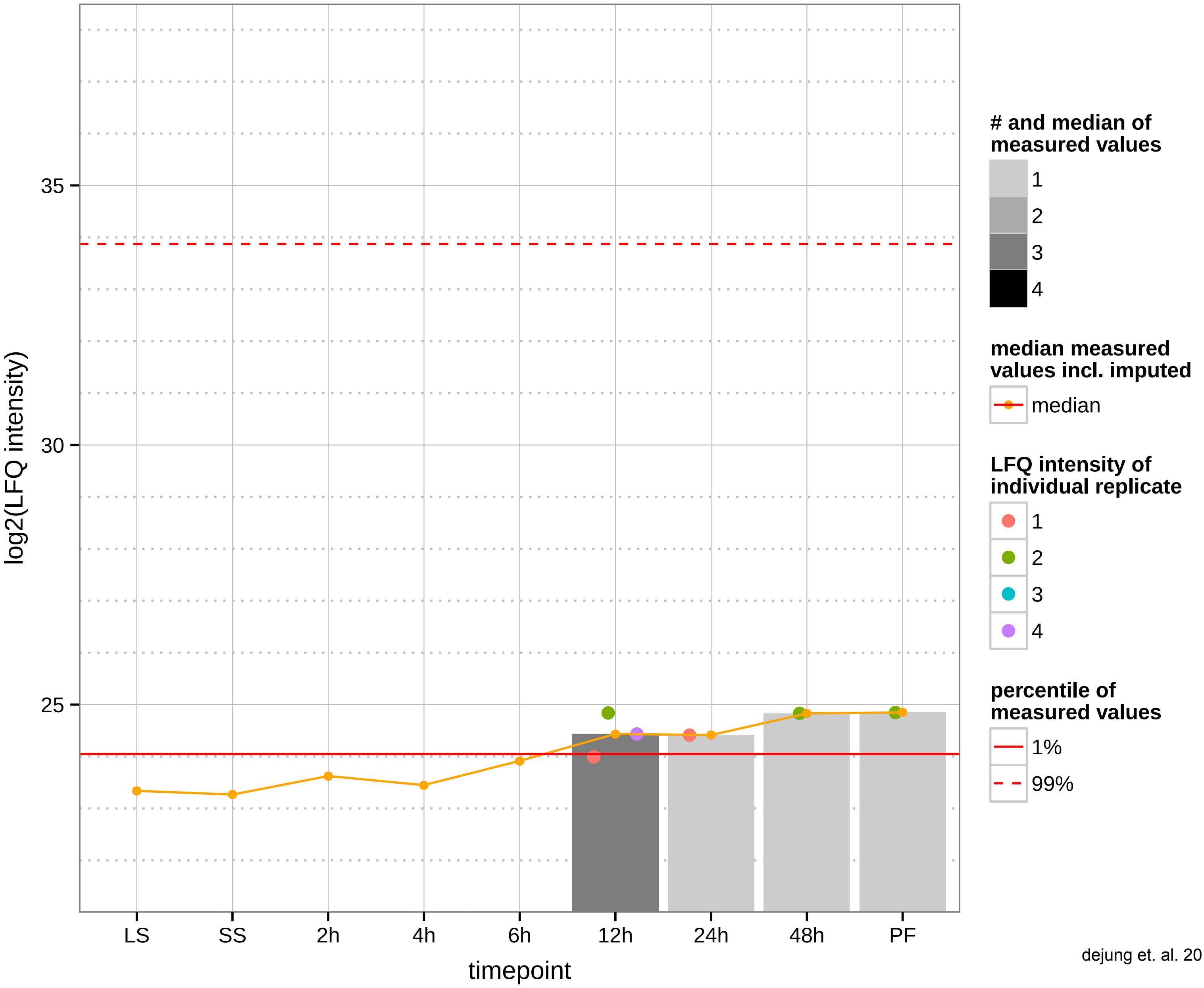
ubiquitin hydrolase, putative
Tb11.v5.0553
AGOF: null
AGOC: null
AGOP: null
PGOF: exonuclease activity, nucleic acid binding
PGOC: intracellular
PGOP: null





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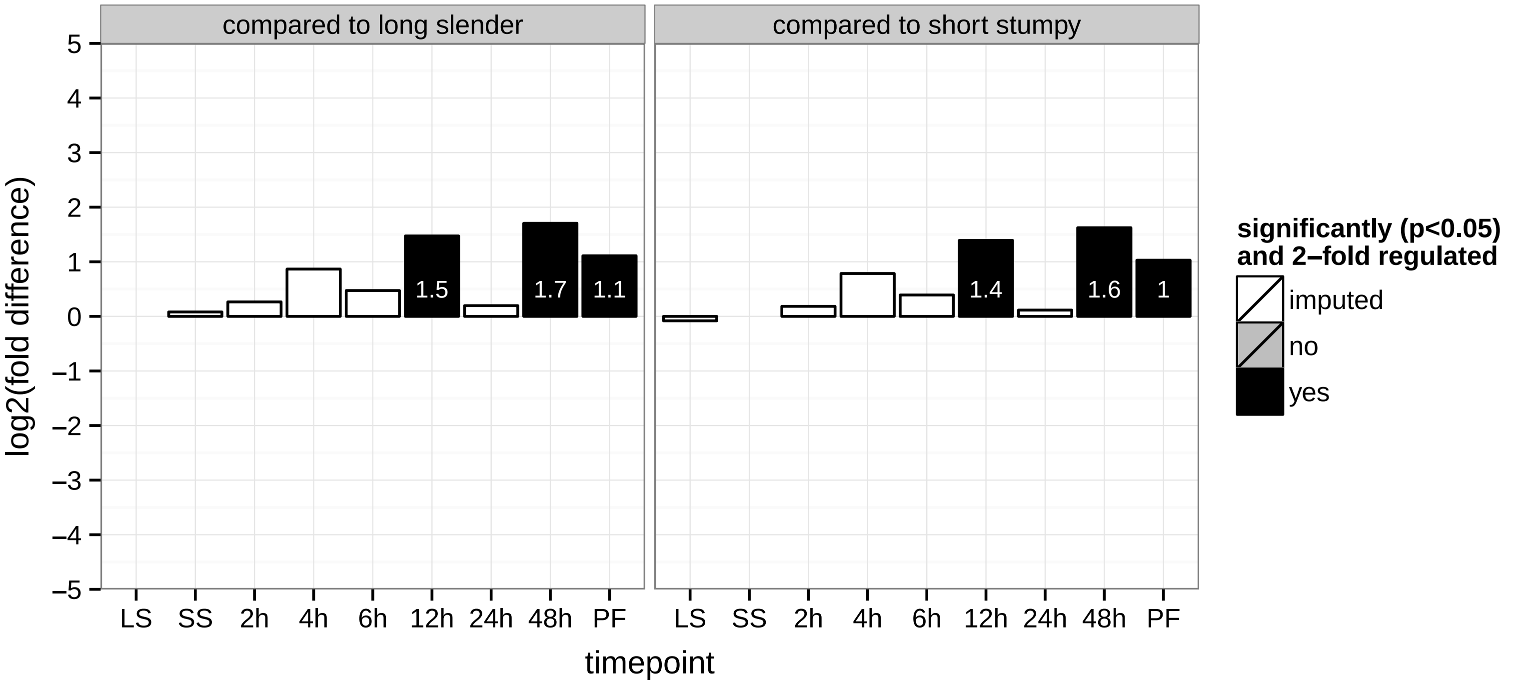
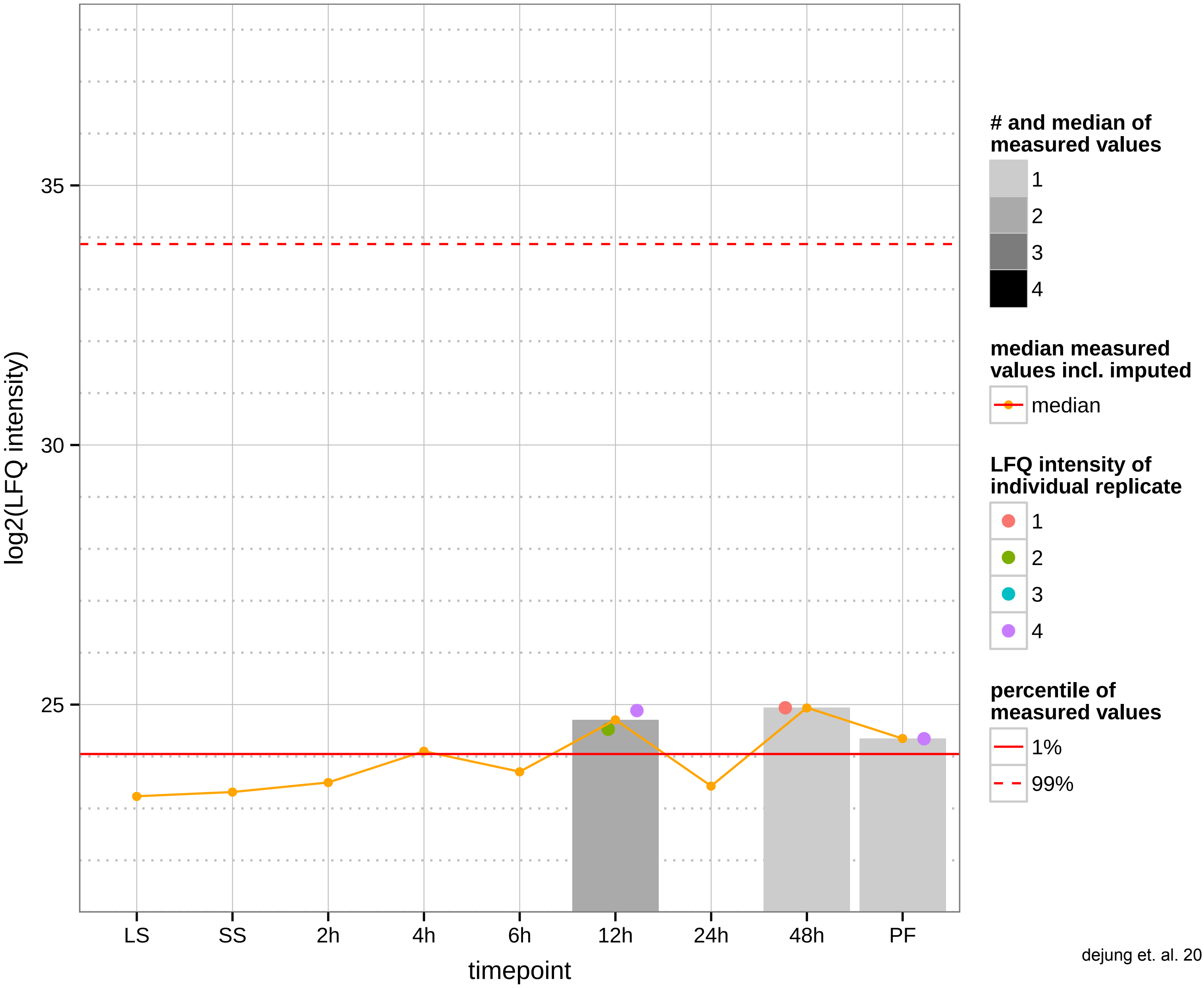
hypothetical protein, conserved
Tb927.10.11400
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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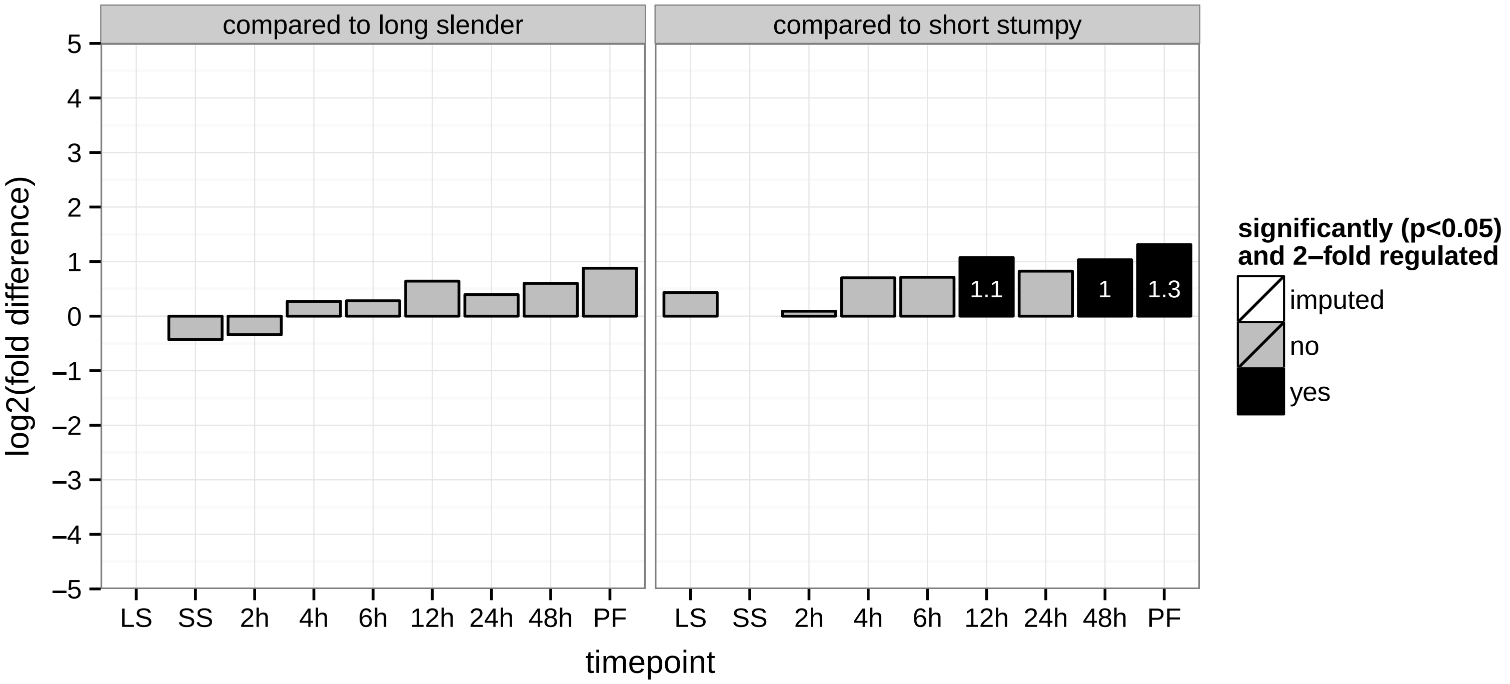
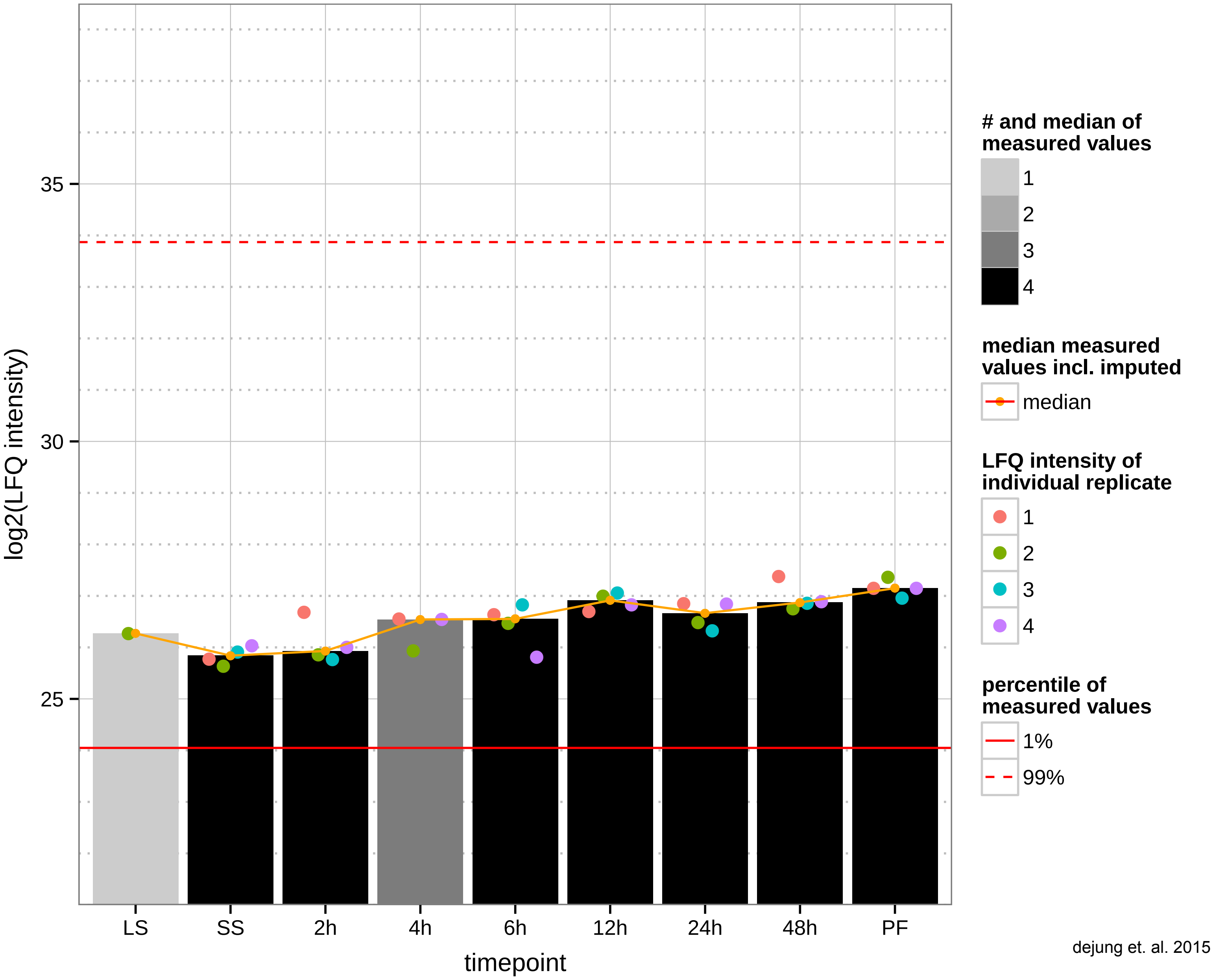
U3 small nucleolar ribonucleoprotein protein IMP3, putative
Tb927.11.13930
AGOF: RNA binding, rRNA binding
AGOC: intracellular, nucleus
AGOP: maturation of SSU−rRNA
PGOF: RNA binding
PGOC: null
PGOP: null





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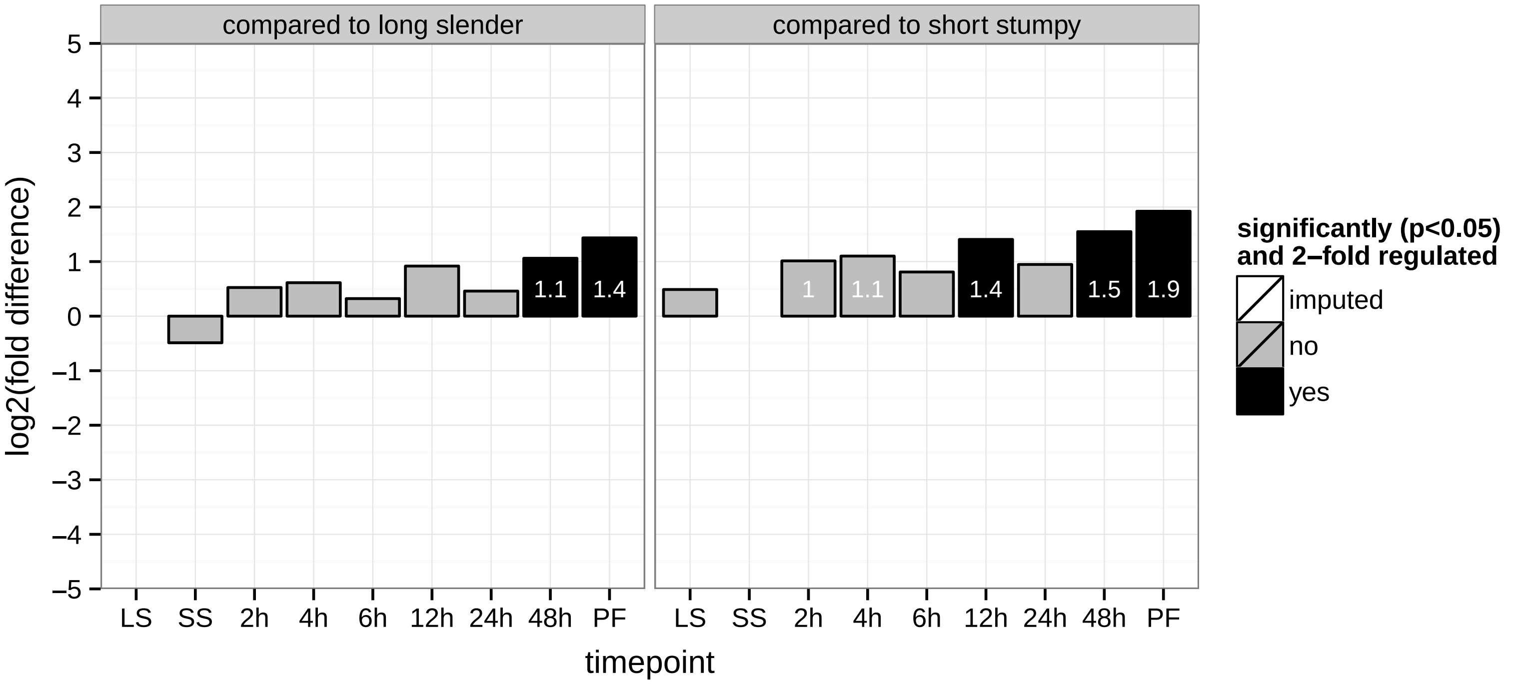
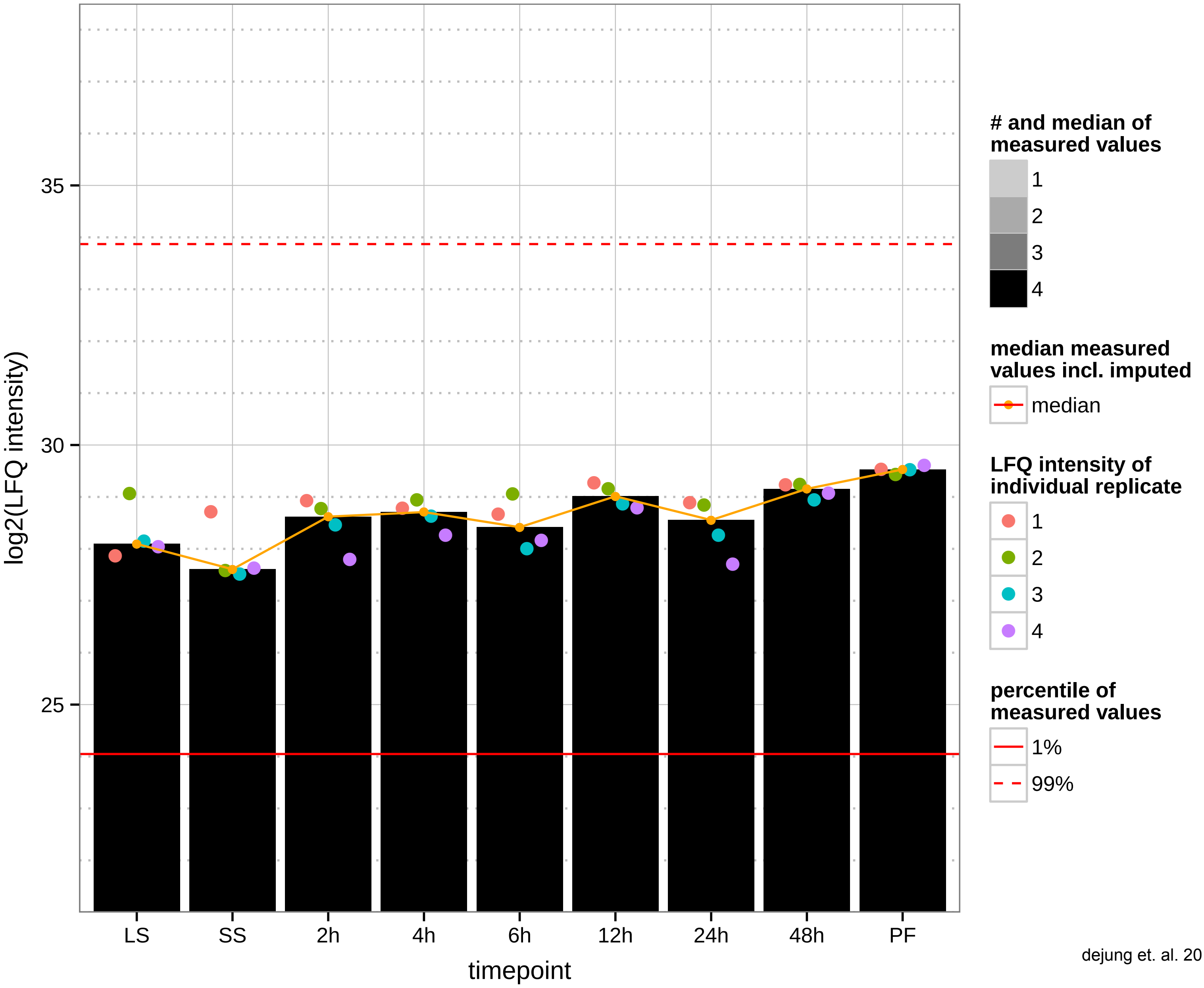
paraflagellar rod component, putative (PFC9)
Tb927.11.14880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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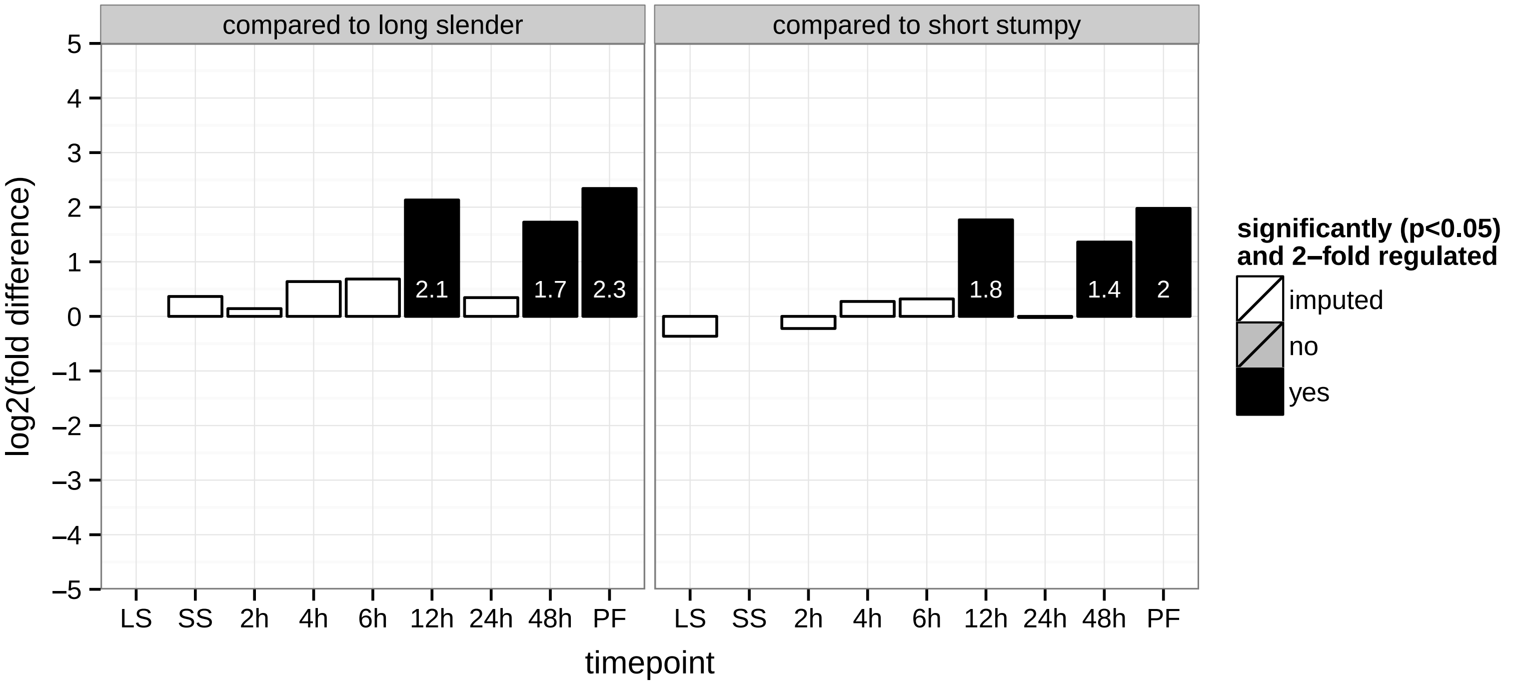
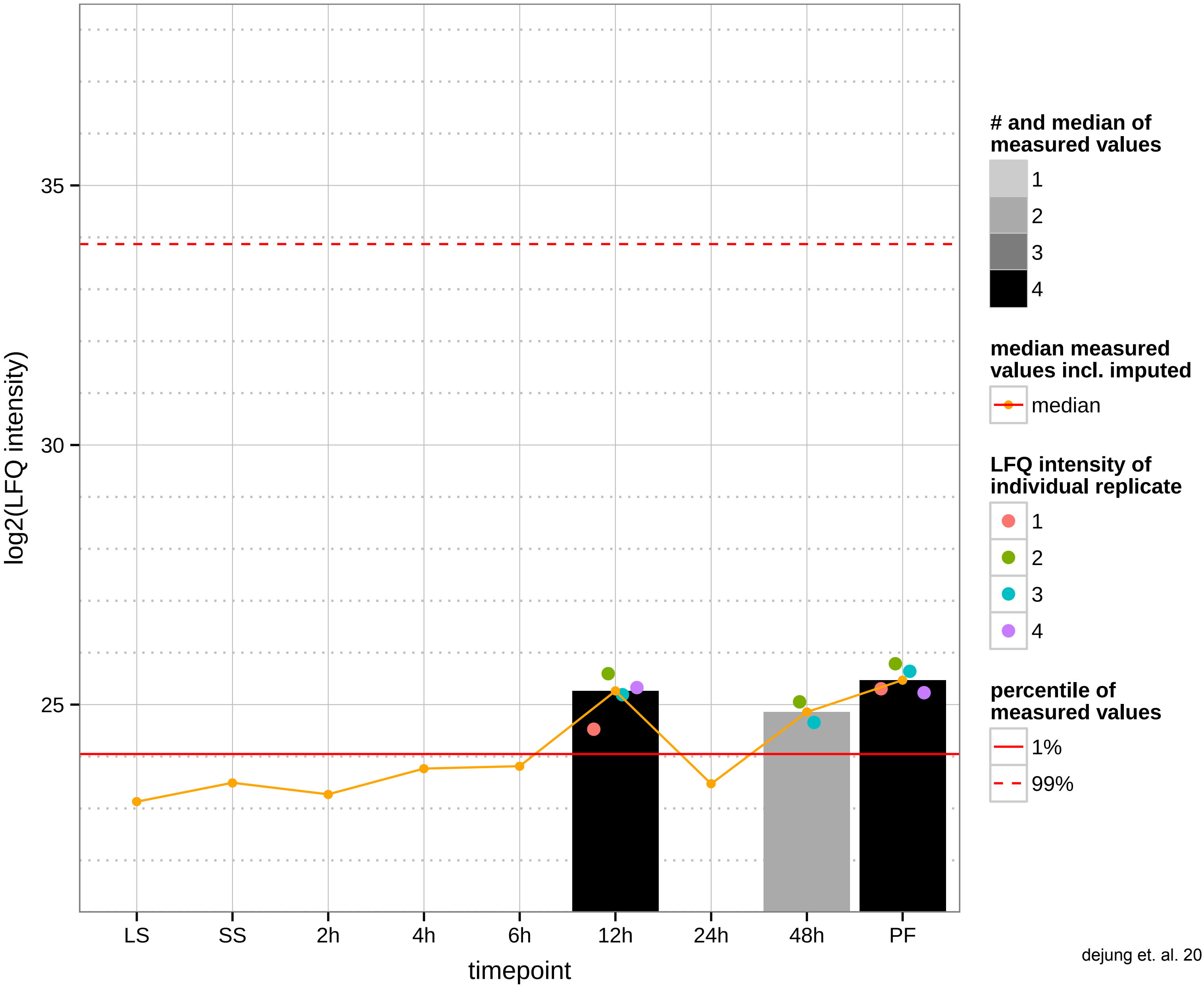
hypothetical protein, conserved
Tb927.11.1630
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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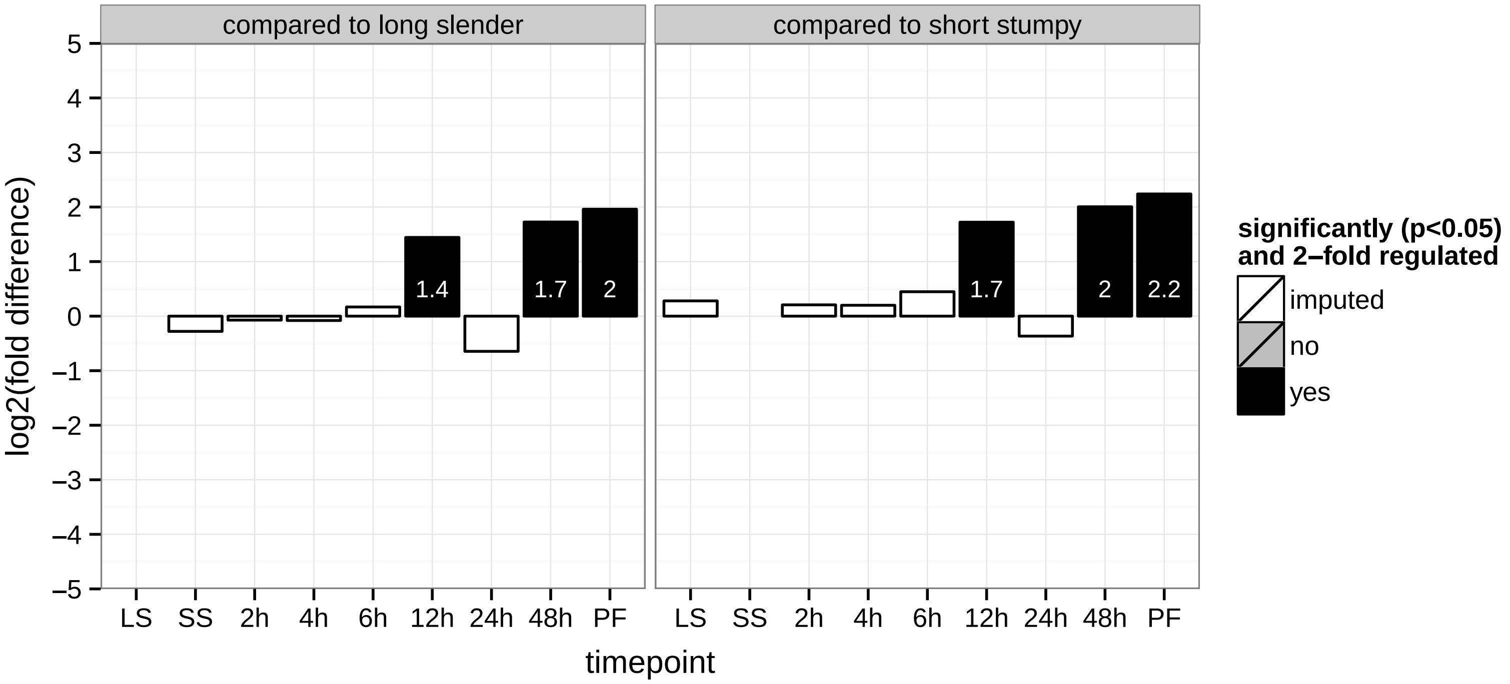
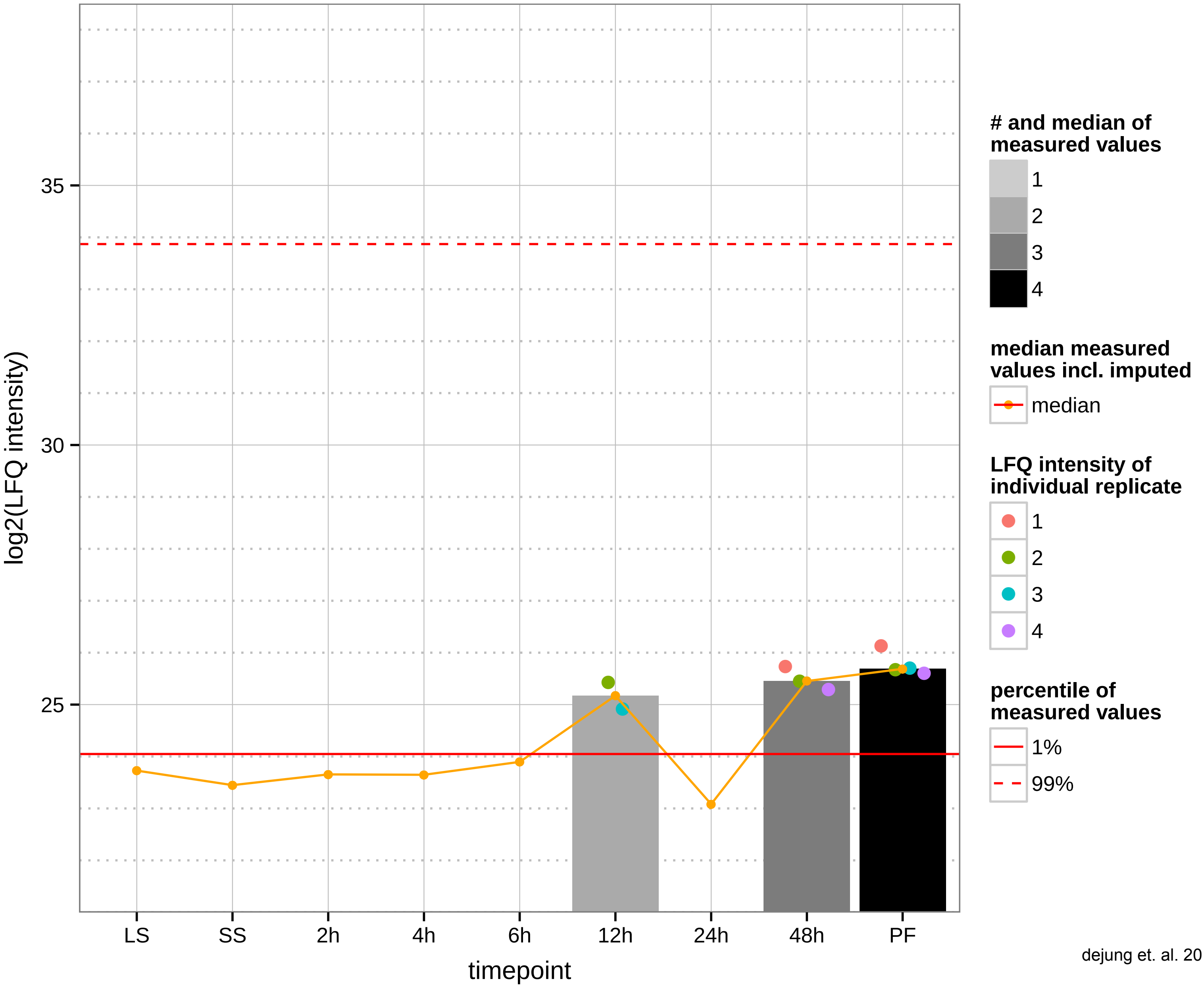
hypothetical protein, conserved
Tb927.11.8040
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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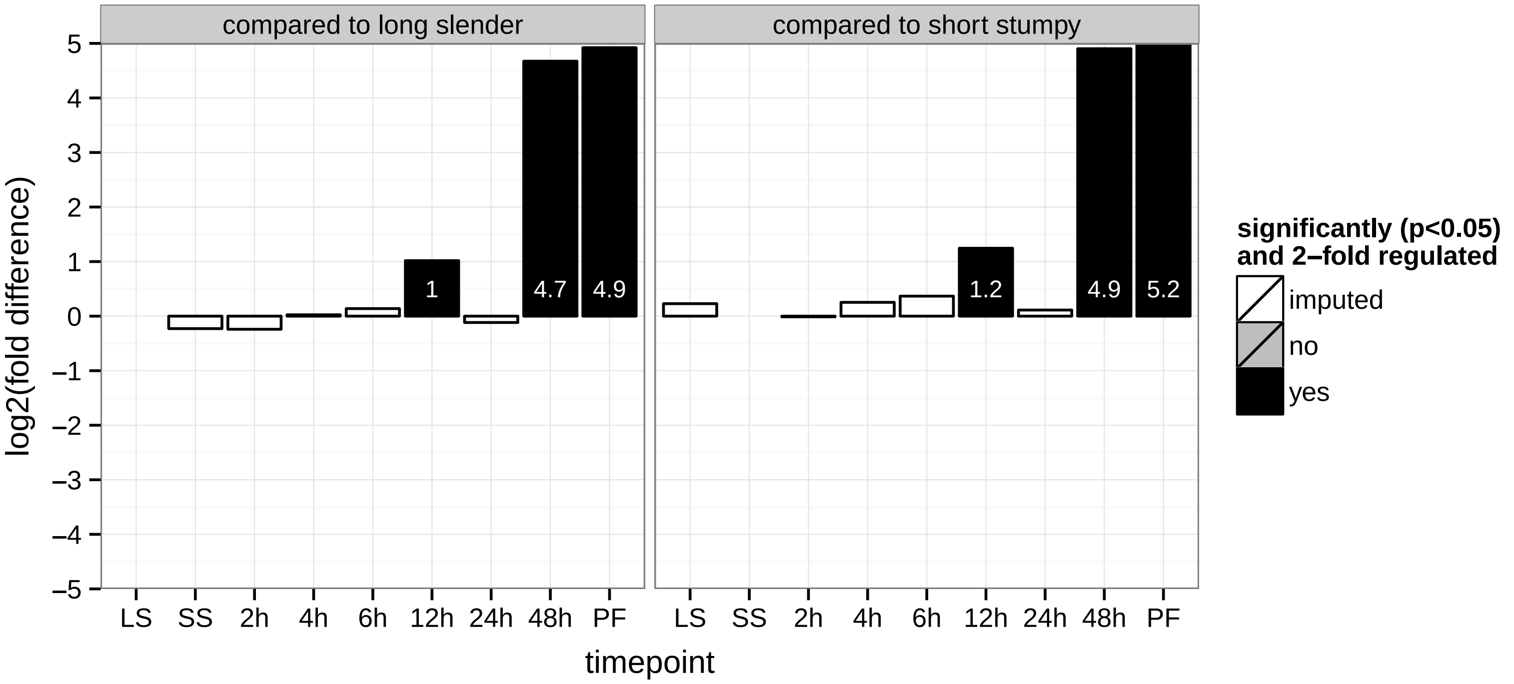
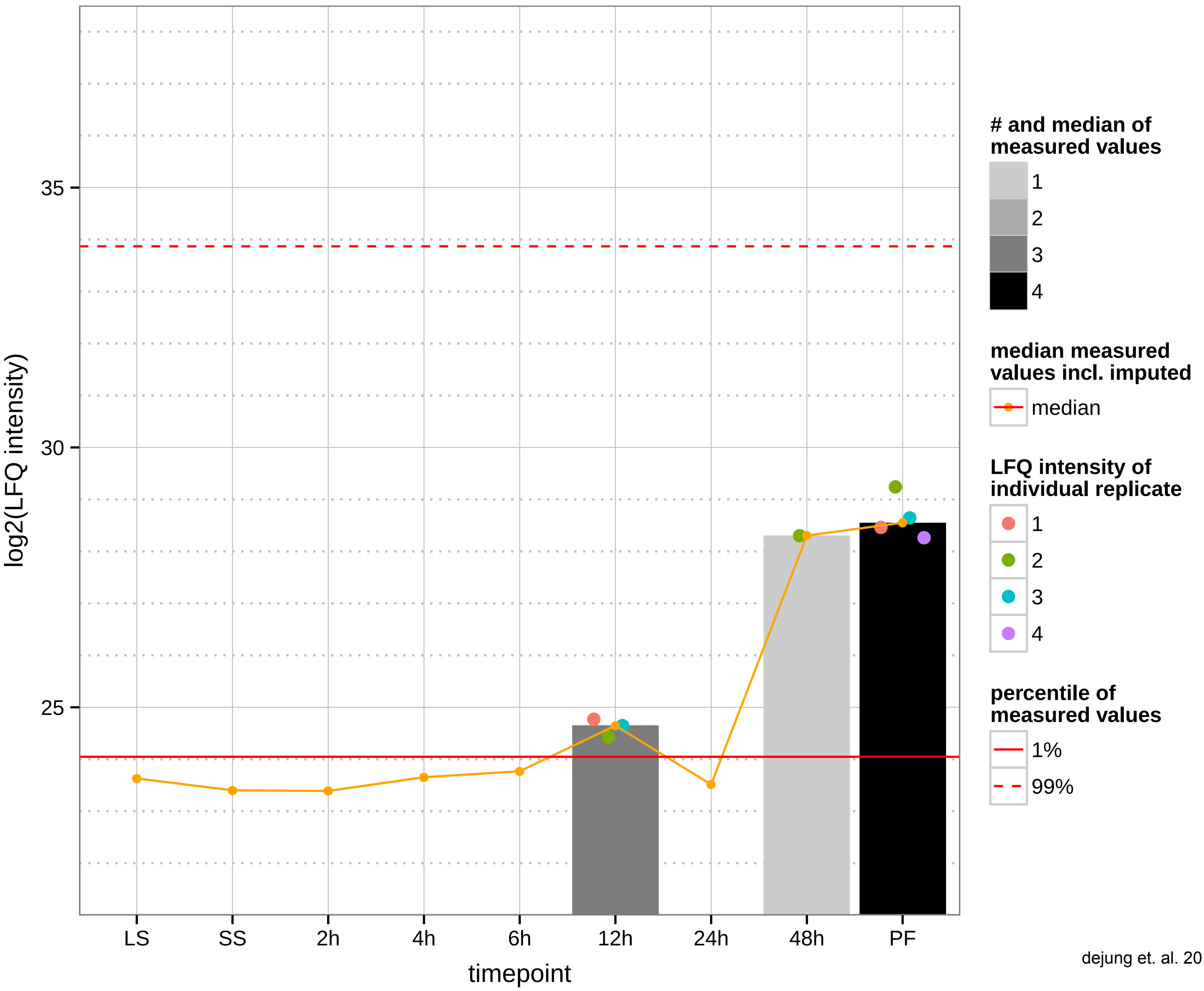
hypothetical protein, conserved
Tb927.3.700
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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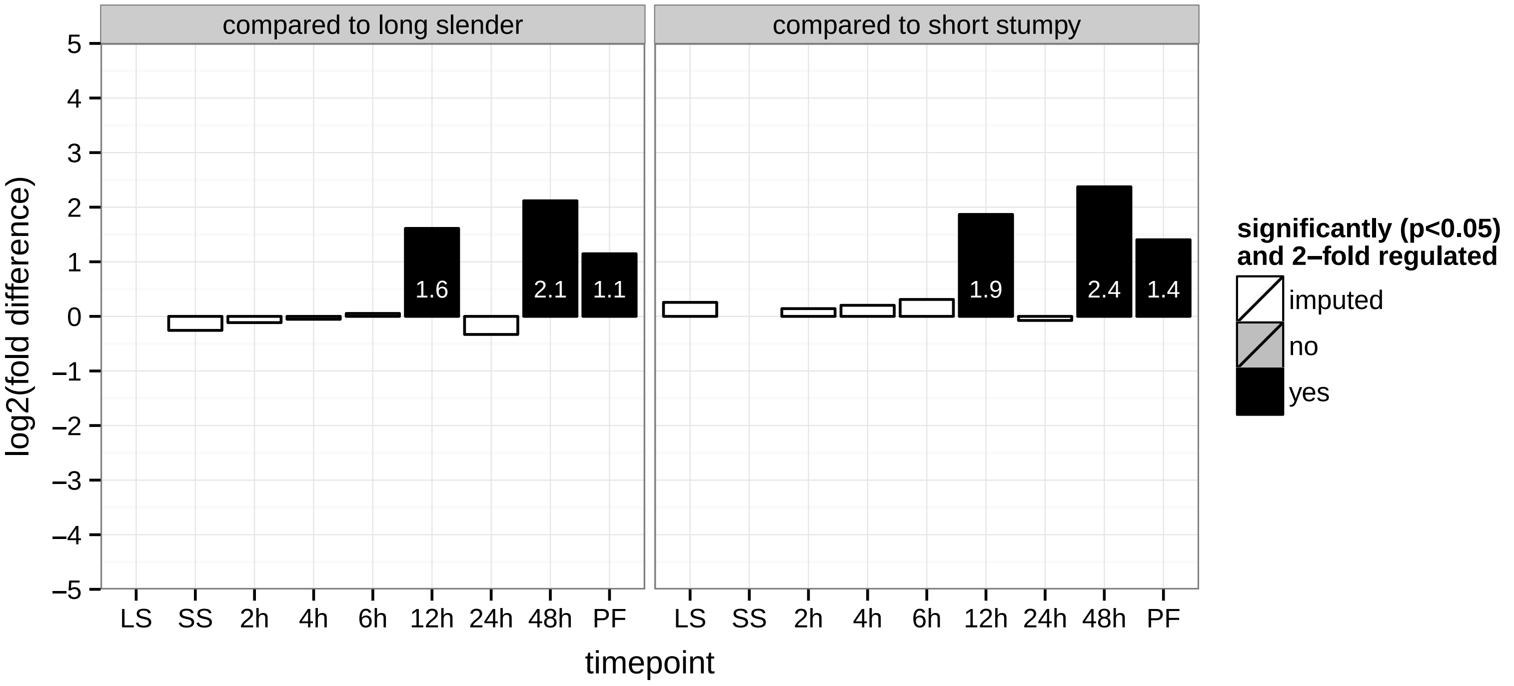
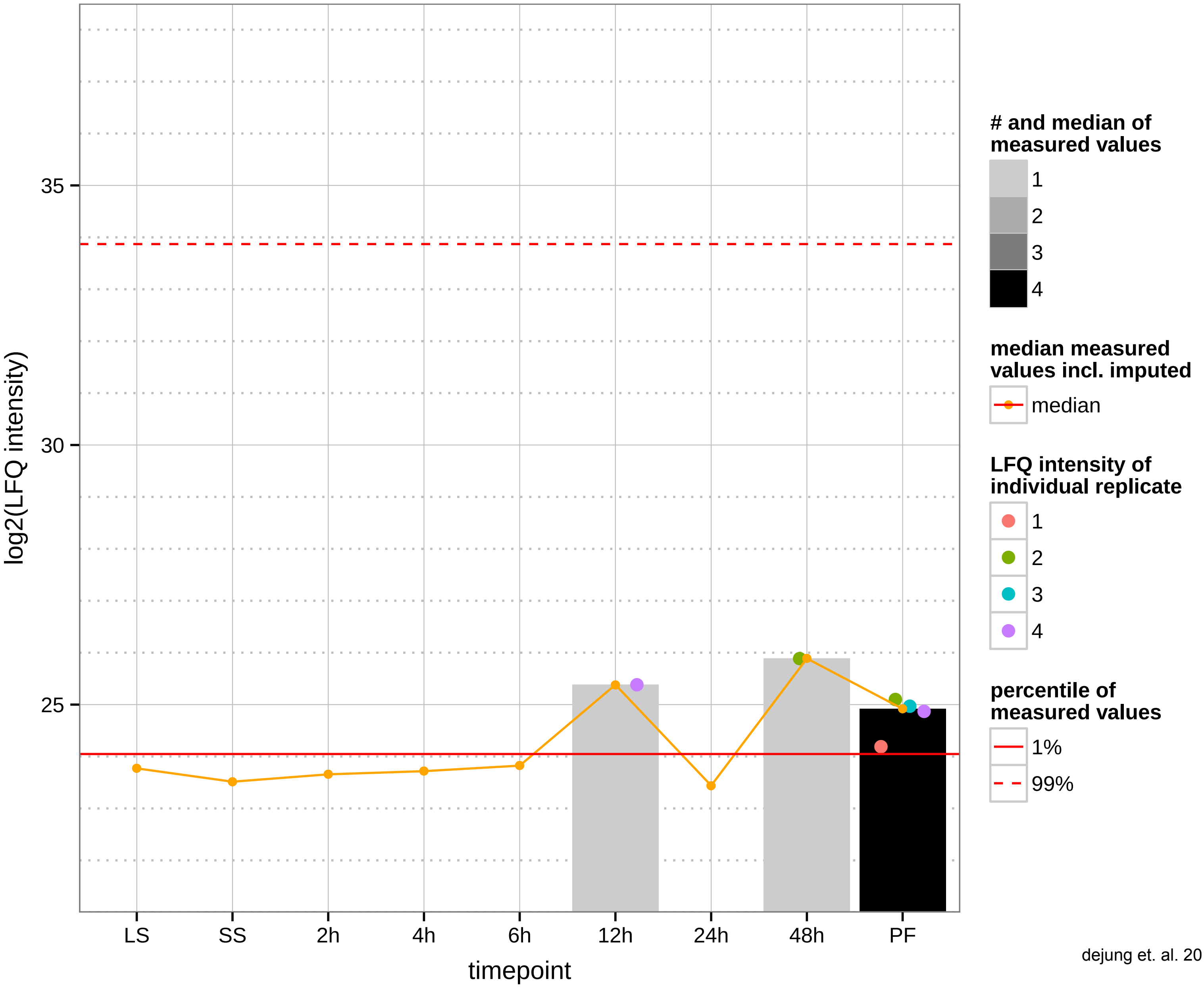
hypothetical protein, conserved
Tb927.5.2810
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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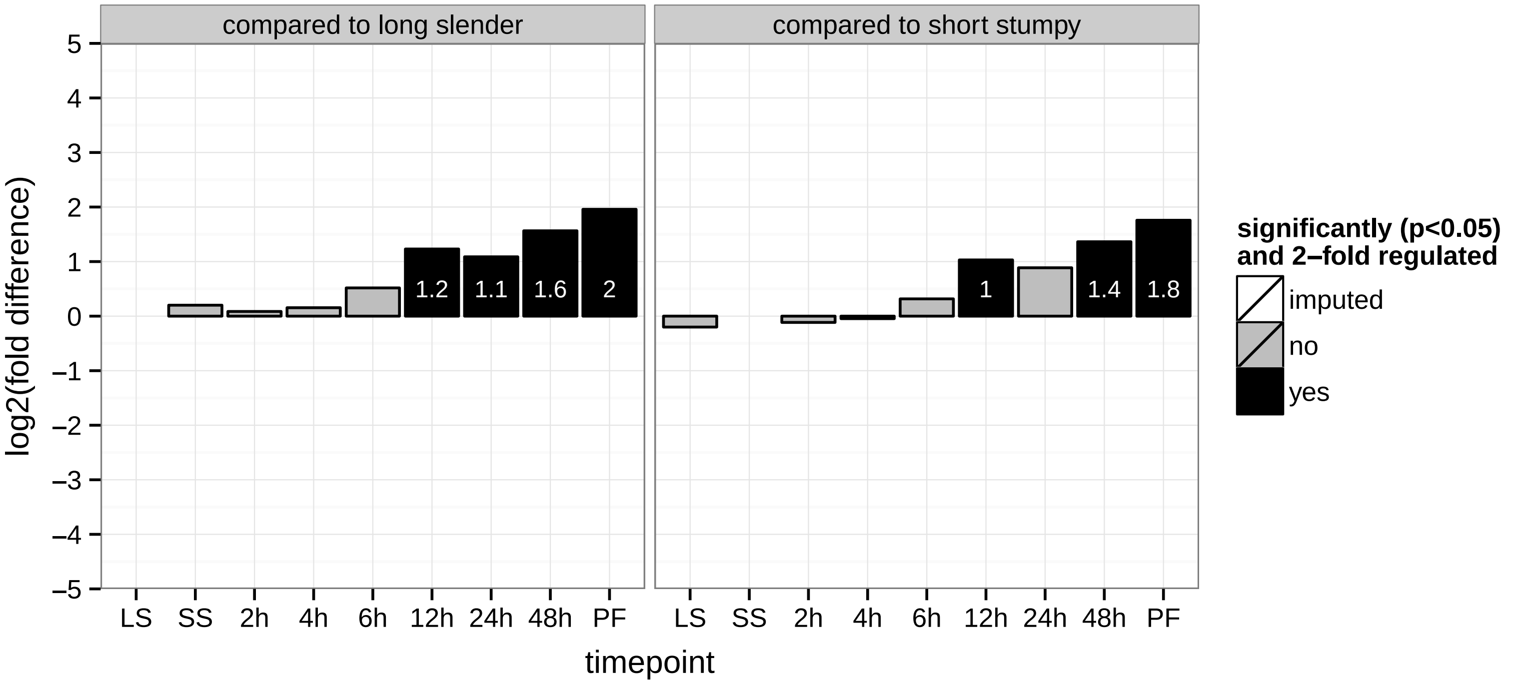
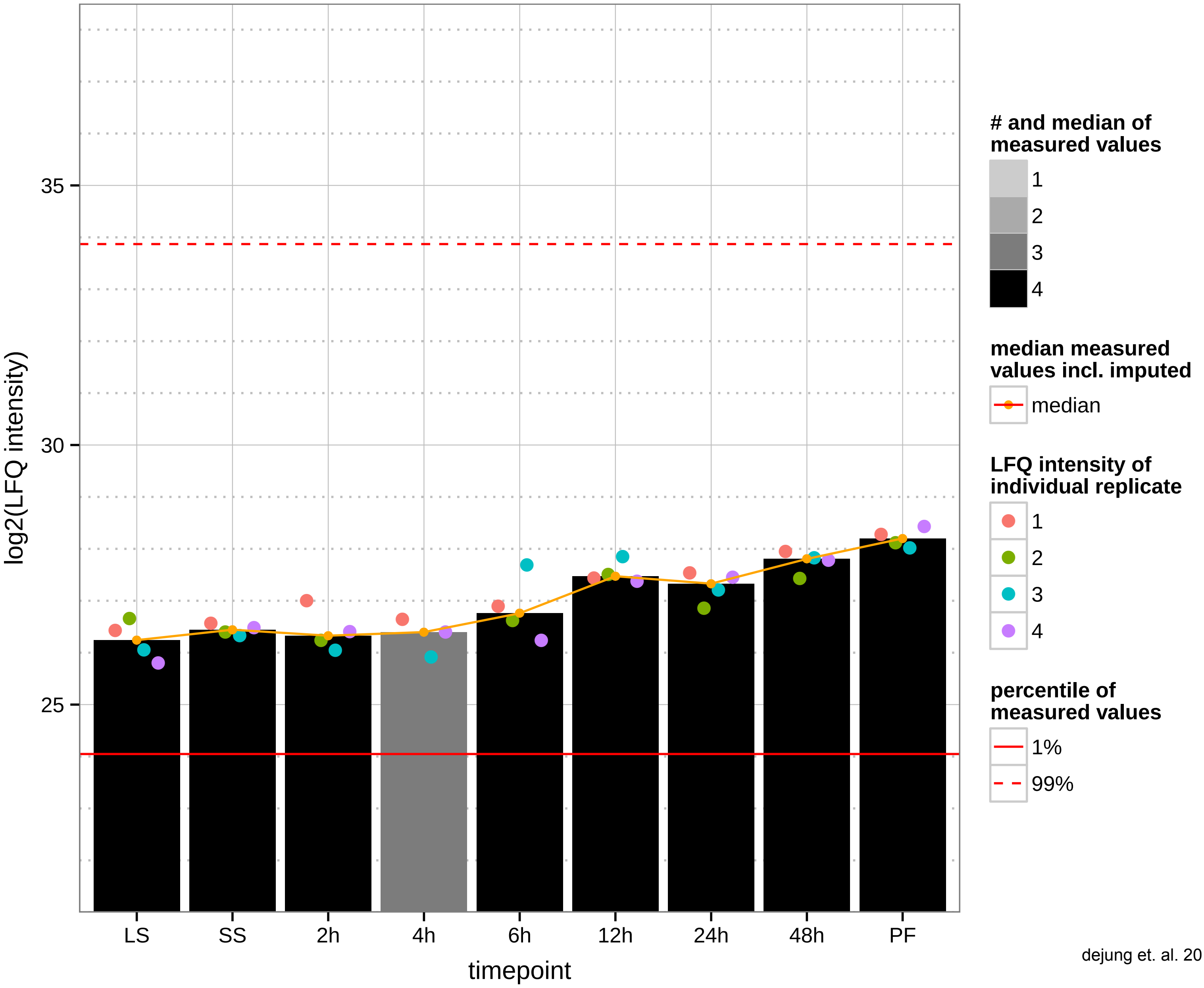
hypothetical protein, conserved
Tb927.6.630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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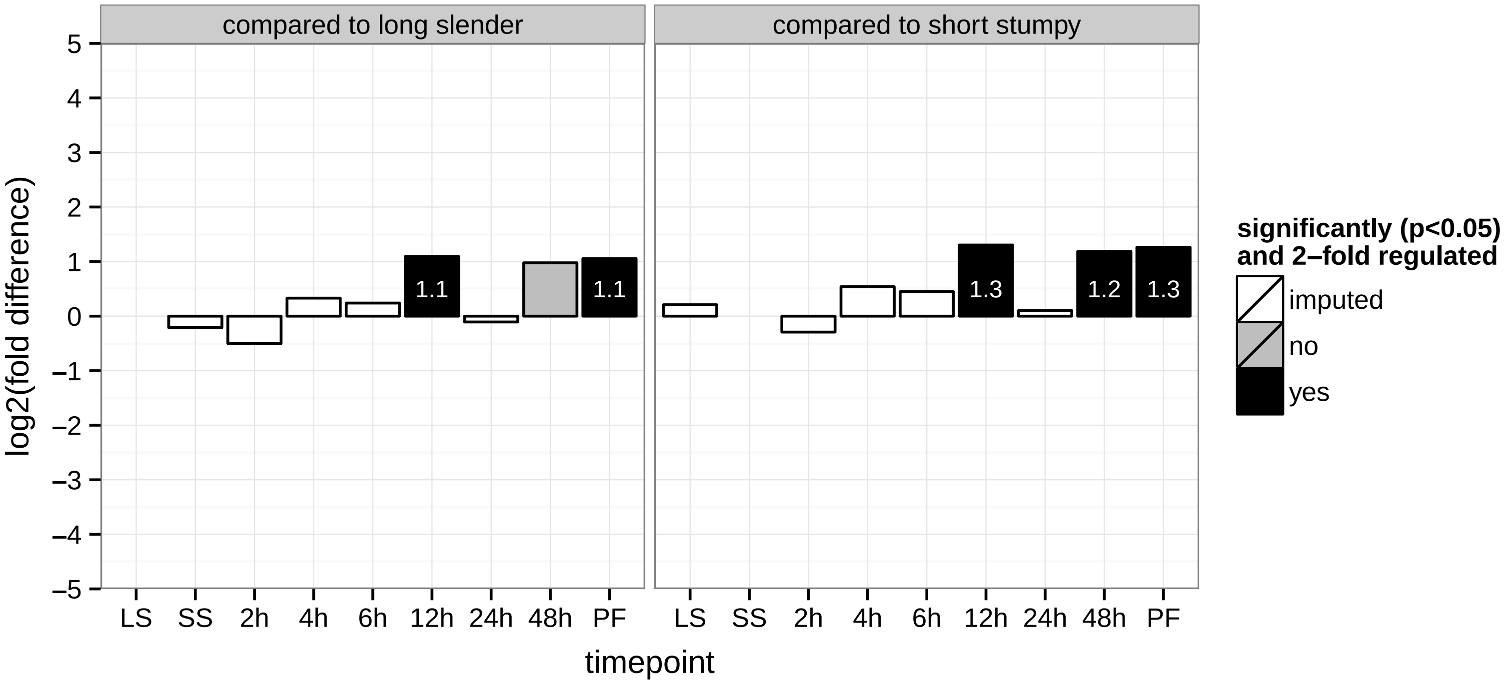
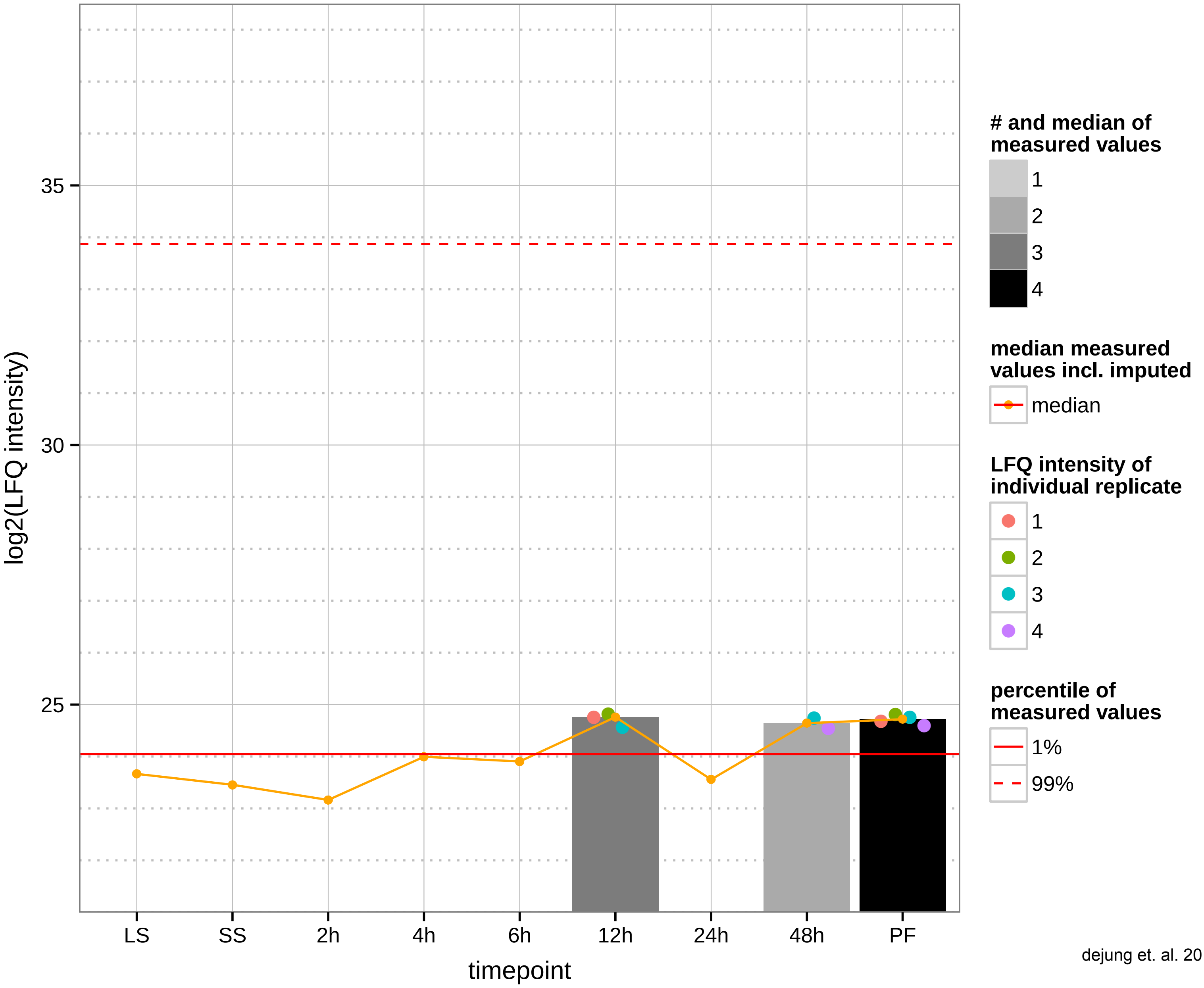
clathrin assembly sigma–adaptin protein 3, putative
Tb927.8.6680
AGOF: protein transporter activity
AGOC: AP–3 adaptor complex, clathrin vesicle coat
AGOP: intracellular protein transport, vesicle–mediated transport
PGOF: protein transporter activity
PGOC: null
PGOP: protein transport, transport





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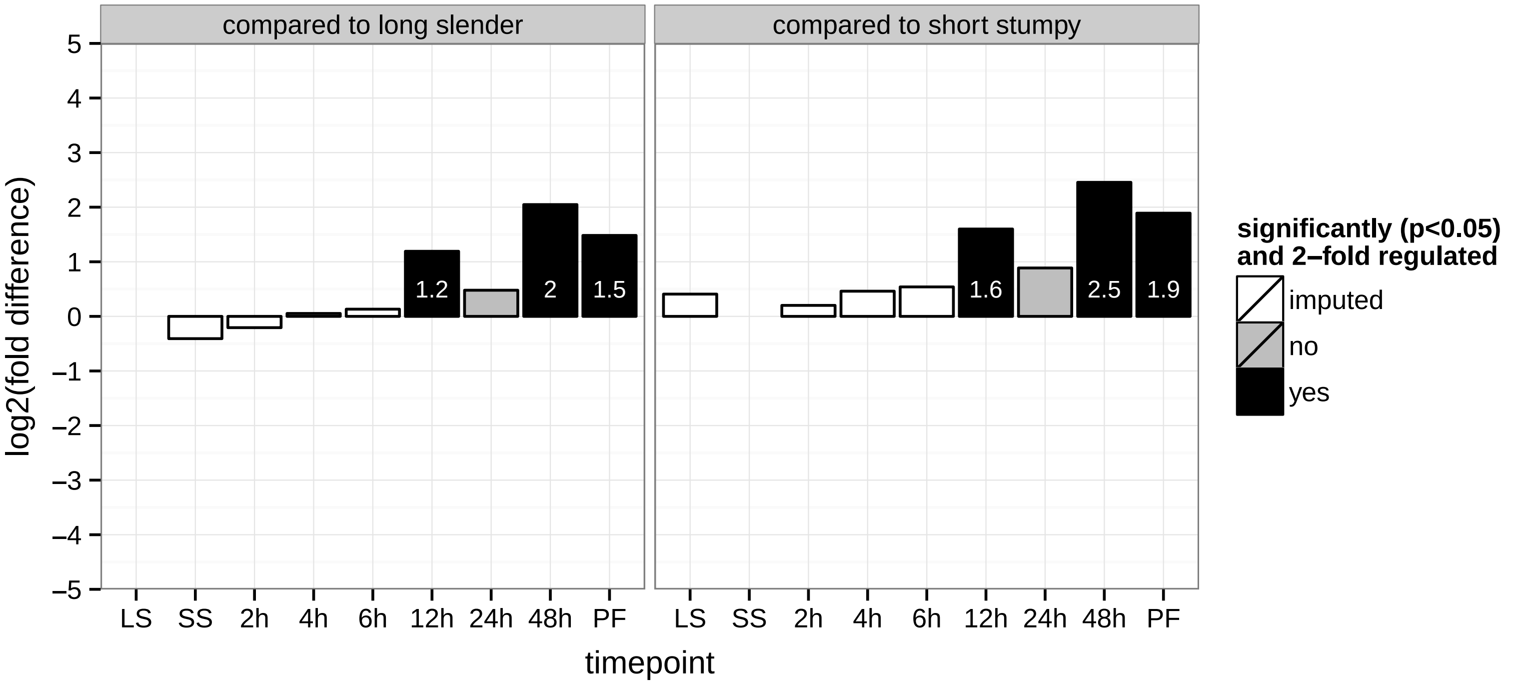
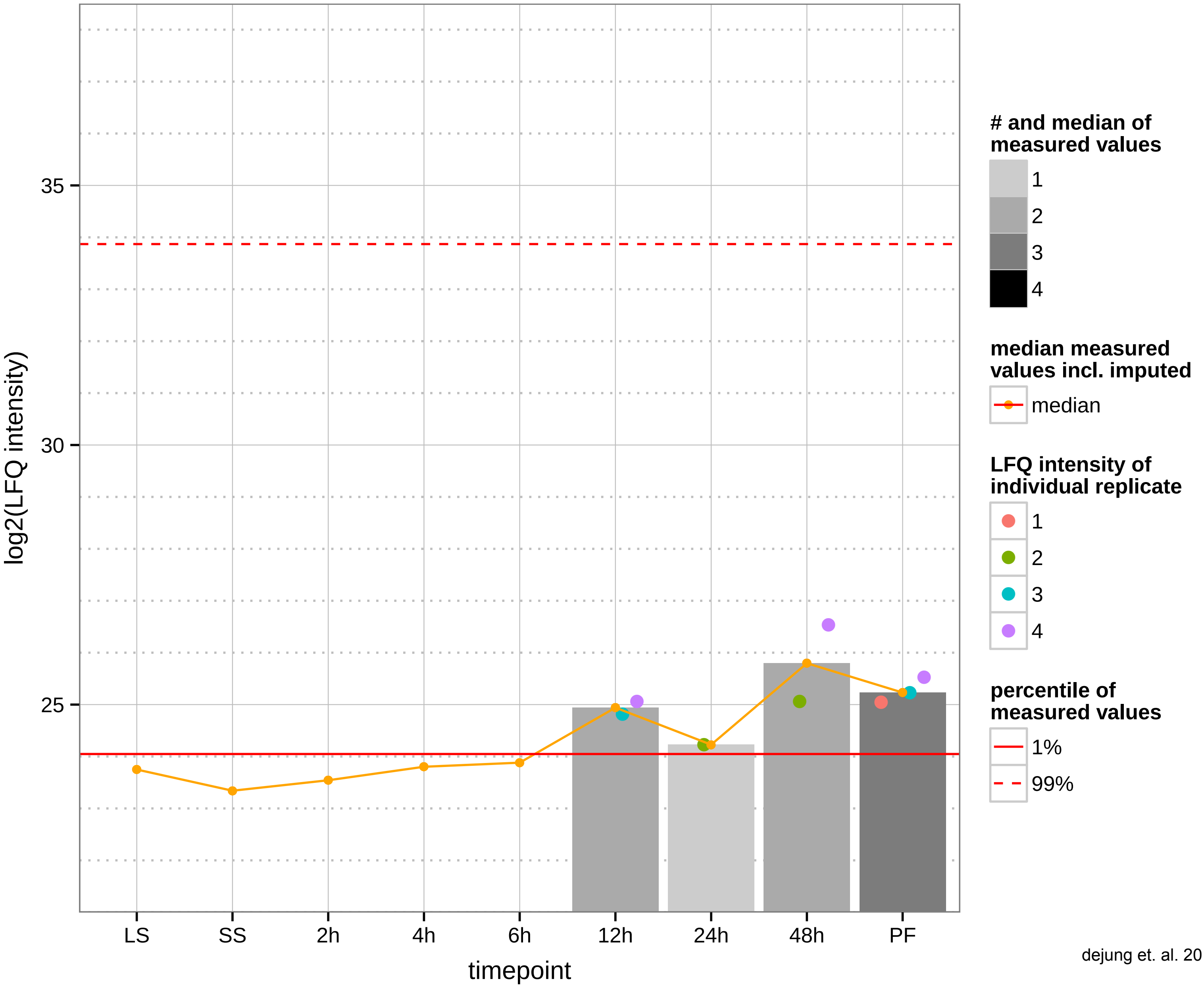
hypothetical protein, conserved
Tb927.9.9220
AGOF: antiporter activity, drug transmembrane transporter activity
AGOC: membrane
AGOP: drug transmembrane transport
PGOF: null
PGOC: null
PGOP: null





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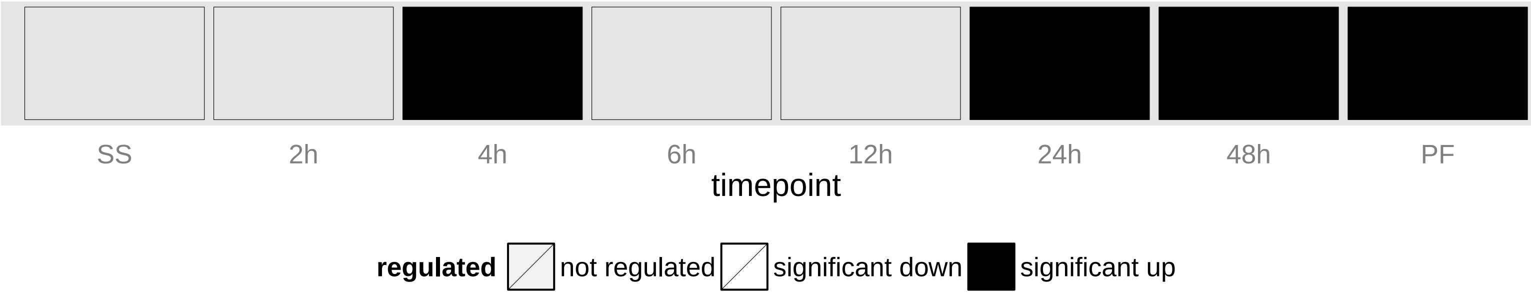

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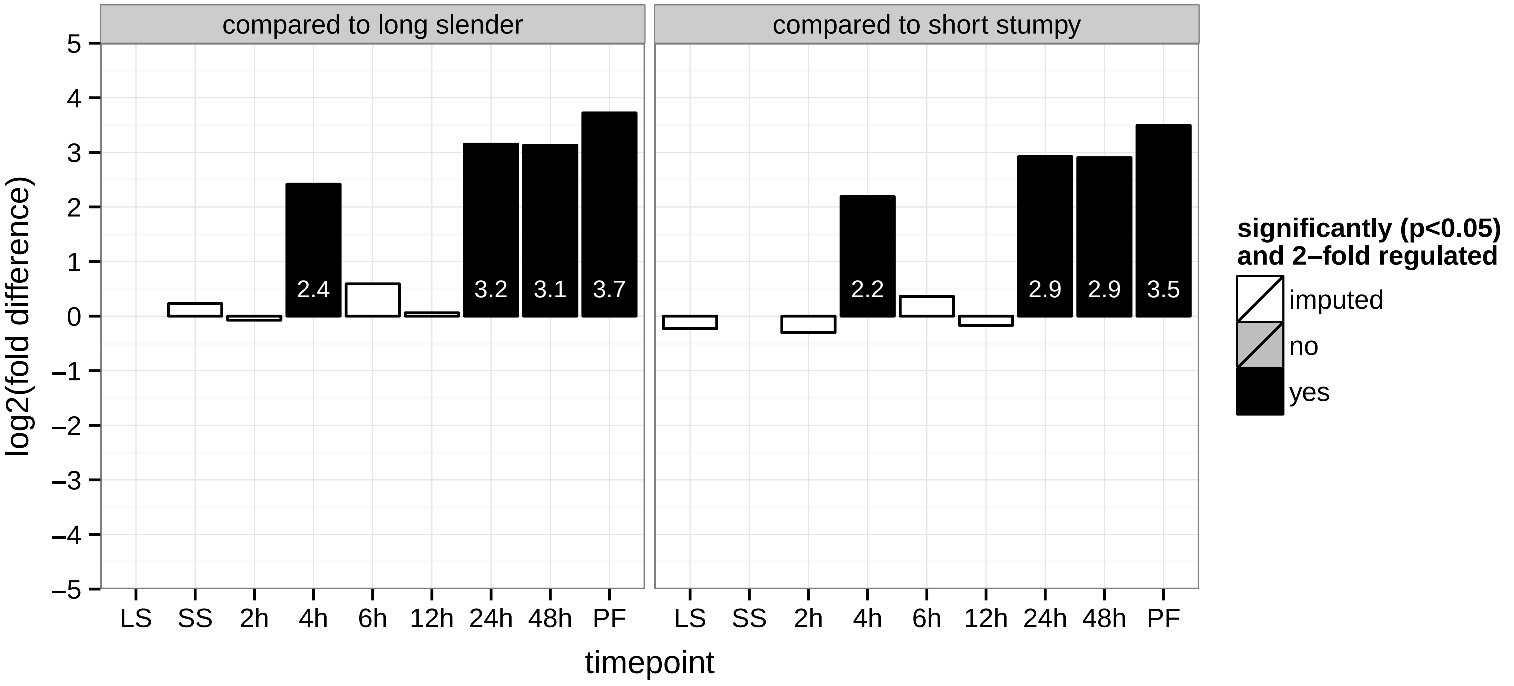
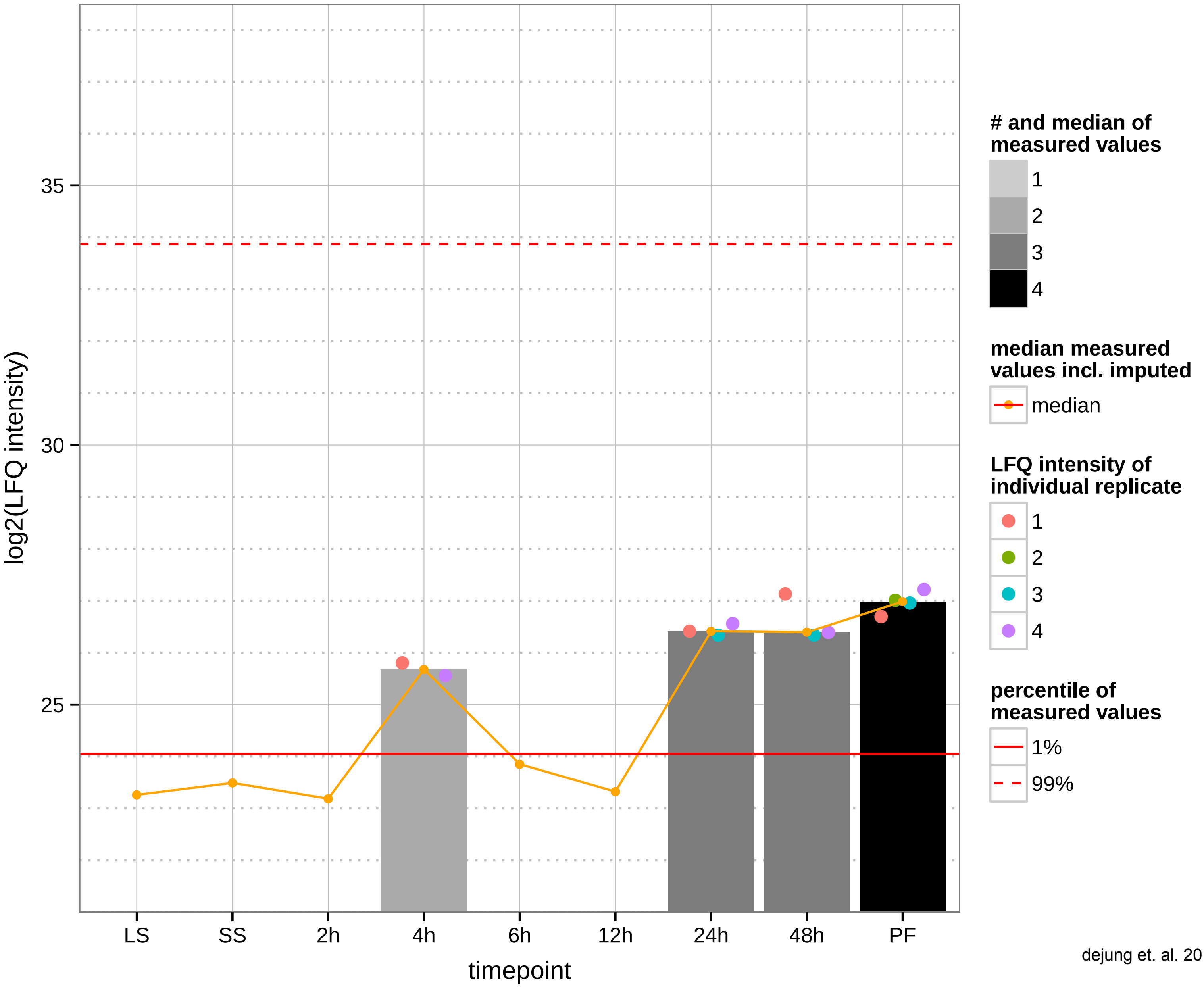
SSU ribosomal protein, mitochondrial (MRPS15)
Tb927.1.1200
AGOF: null
AGOC: mitochondrial small ribosomal subunit, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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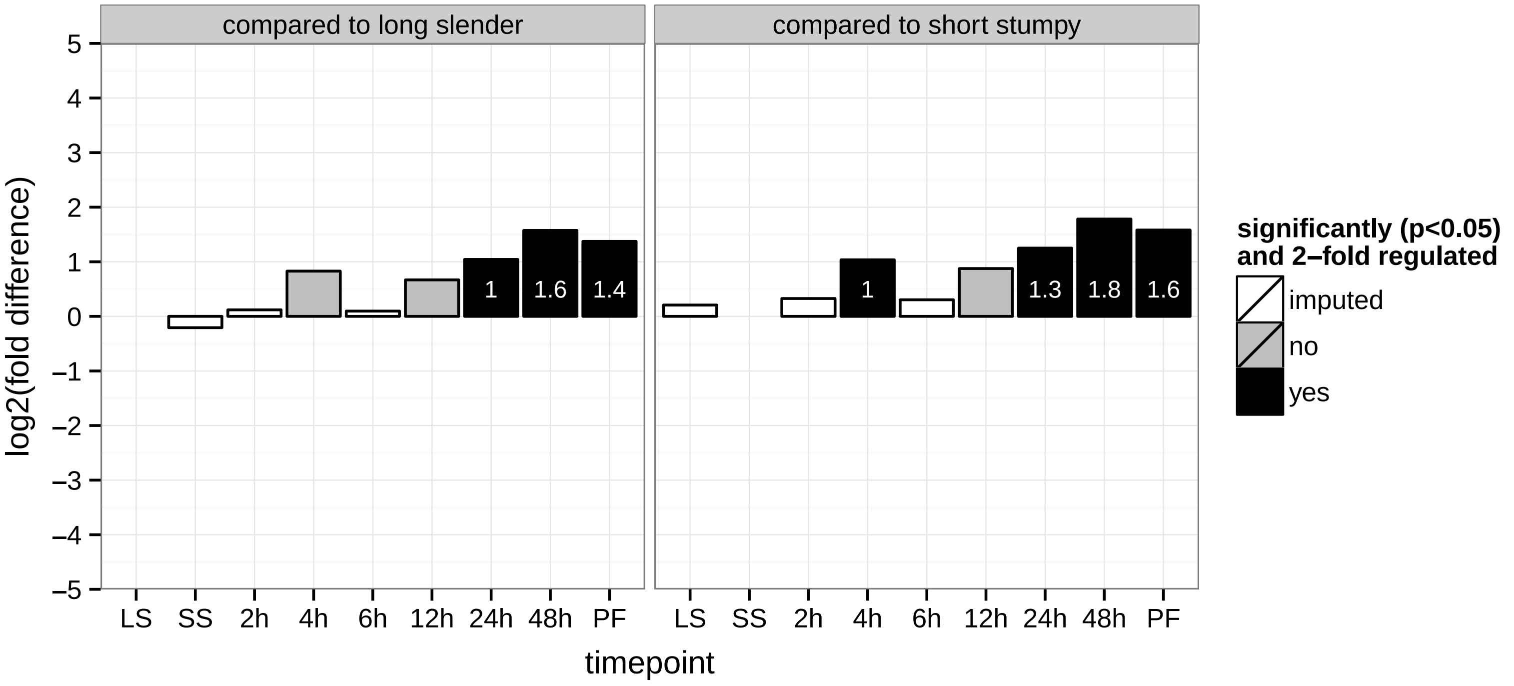
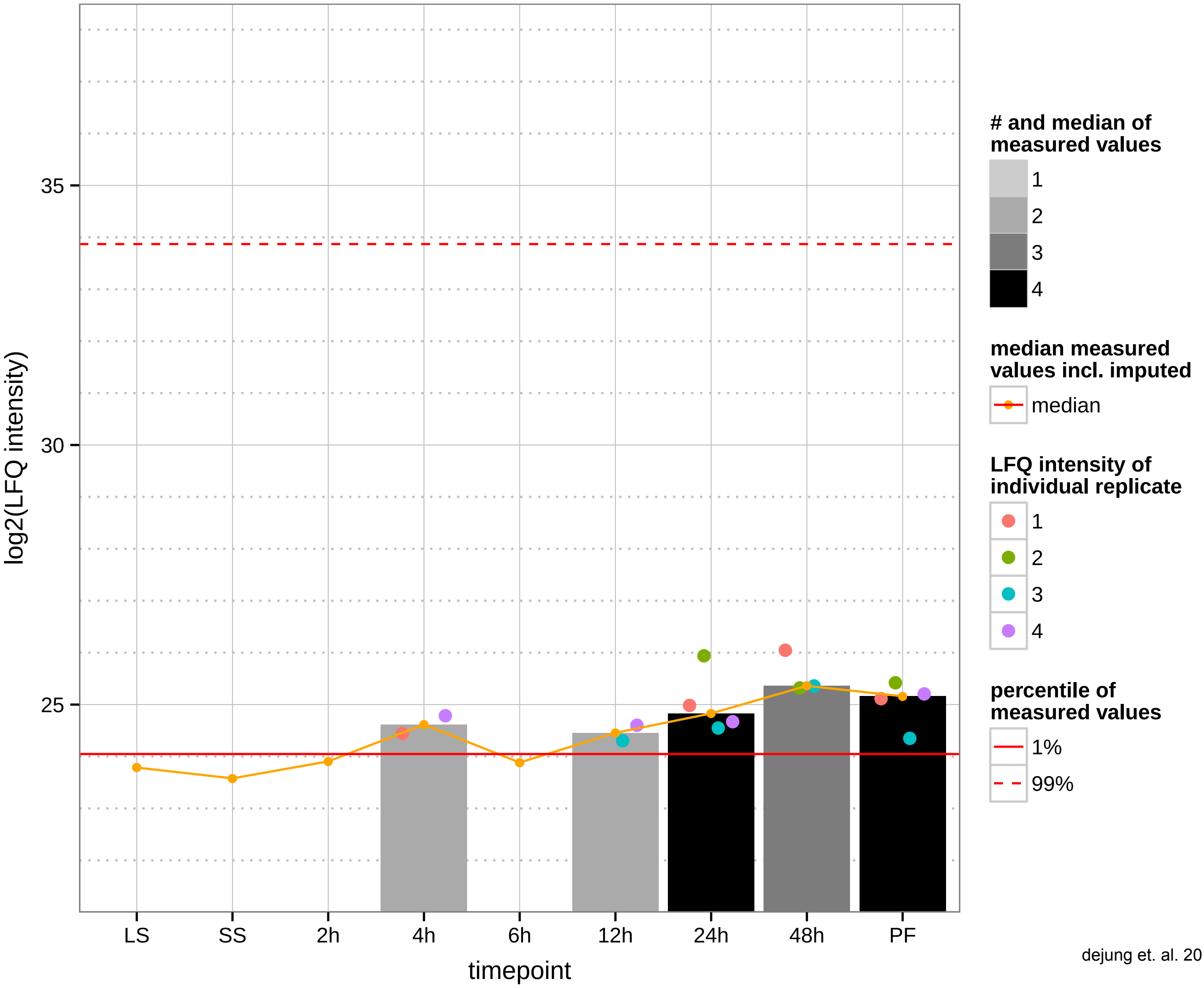
glutaredoxin, putative
Tb927.1.1770
AGOF: disulfide oxidoreductase activity, electron carrier activity, protein disulfide isomerase activity, protein disulfide oxidoredu
AGOC: null
AGOP: cell redox homeostasis
PGOF: electron carrier activity, protein disulfide oxidoreductase activity
PGOC: null
PGOP: cell redox homeostasis





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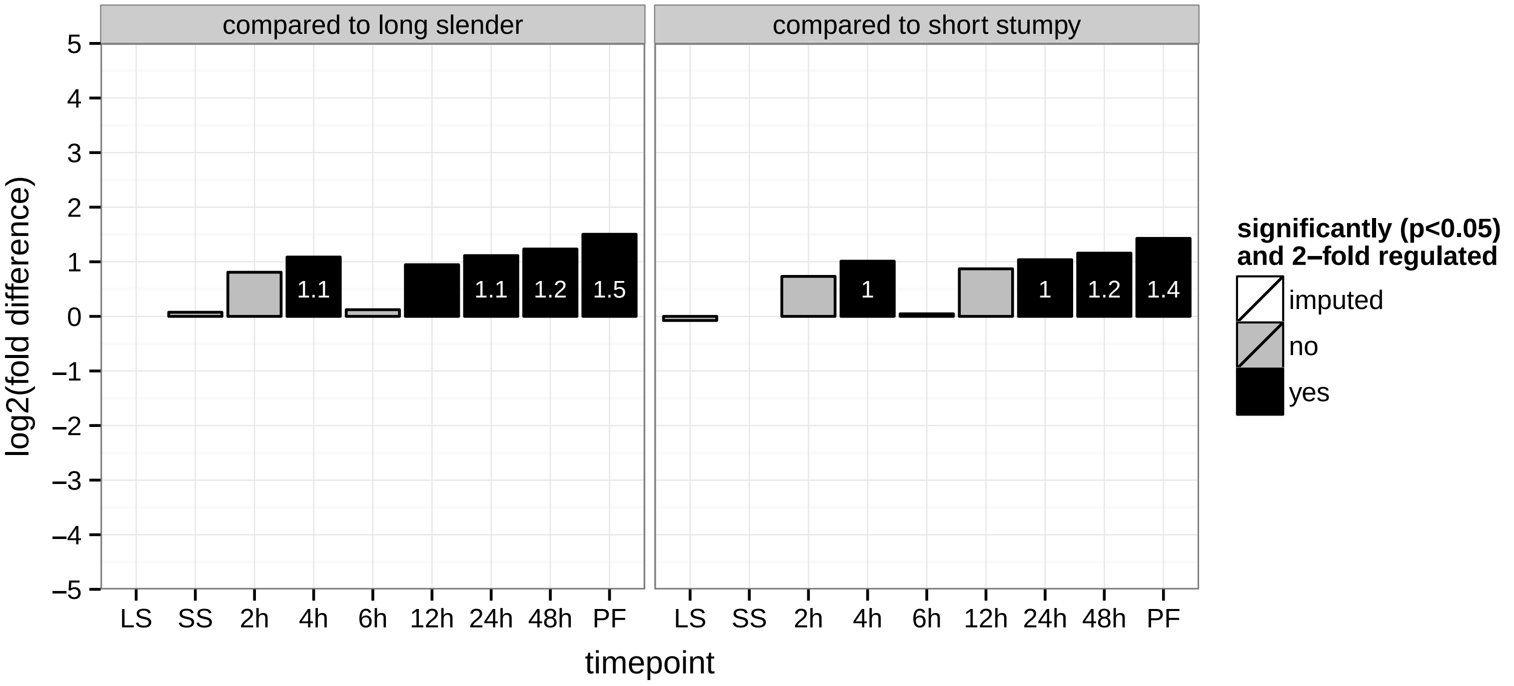
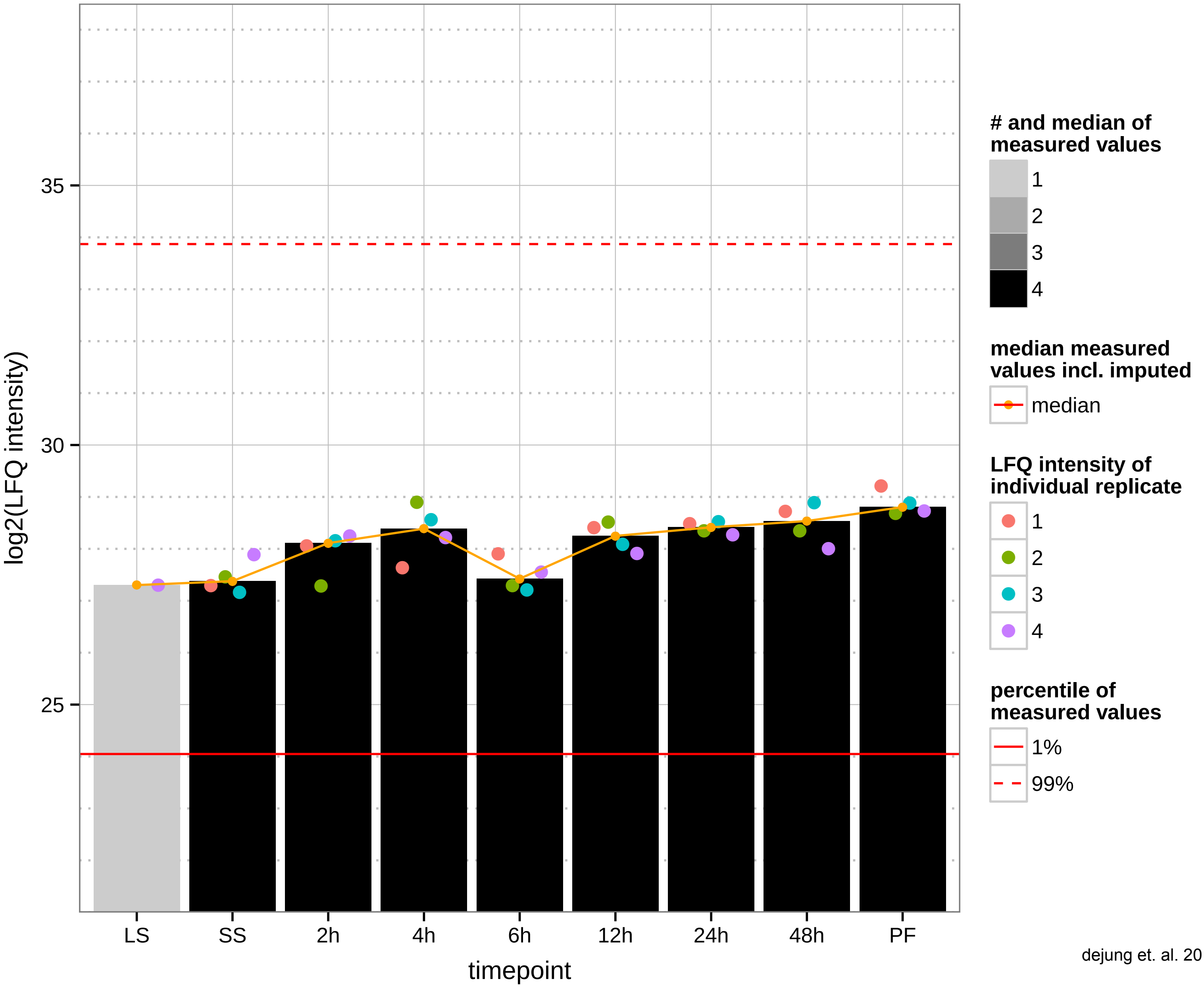
hypothetical protein, conserved
Tb927.10.9920
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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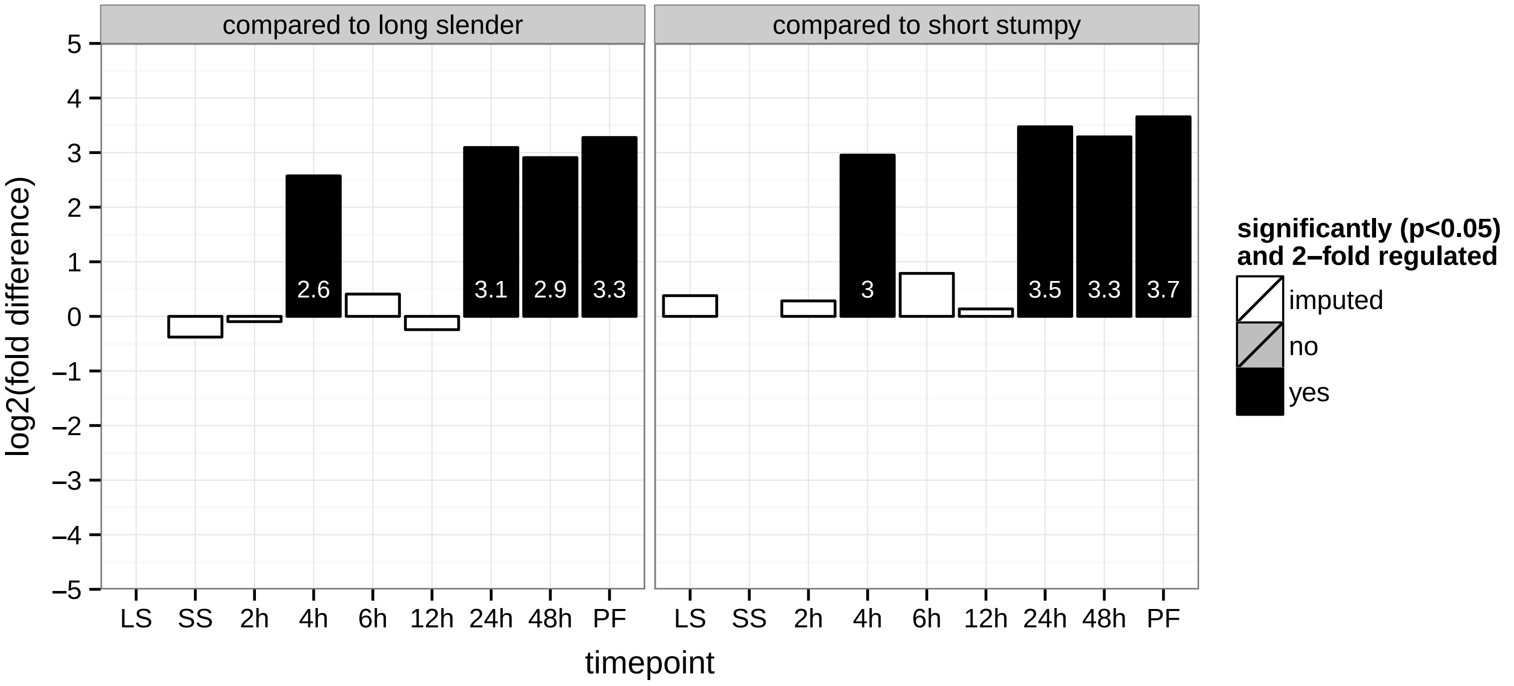
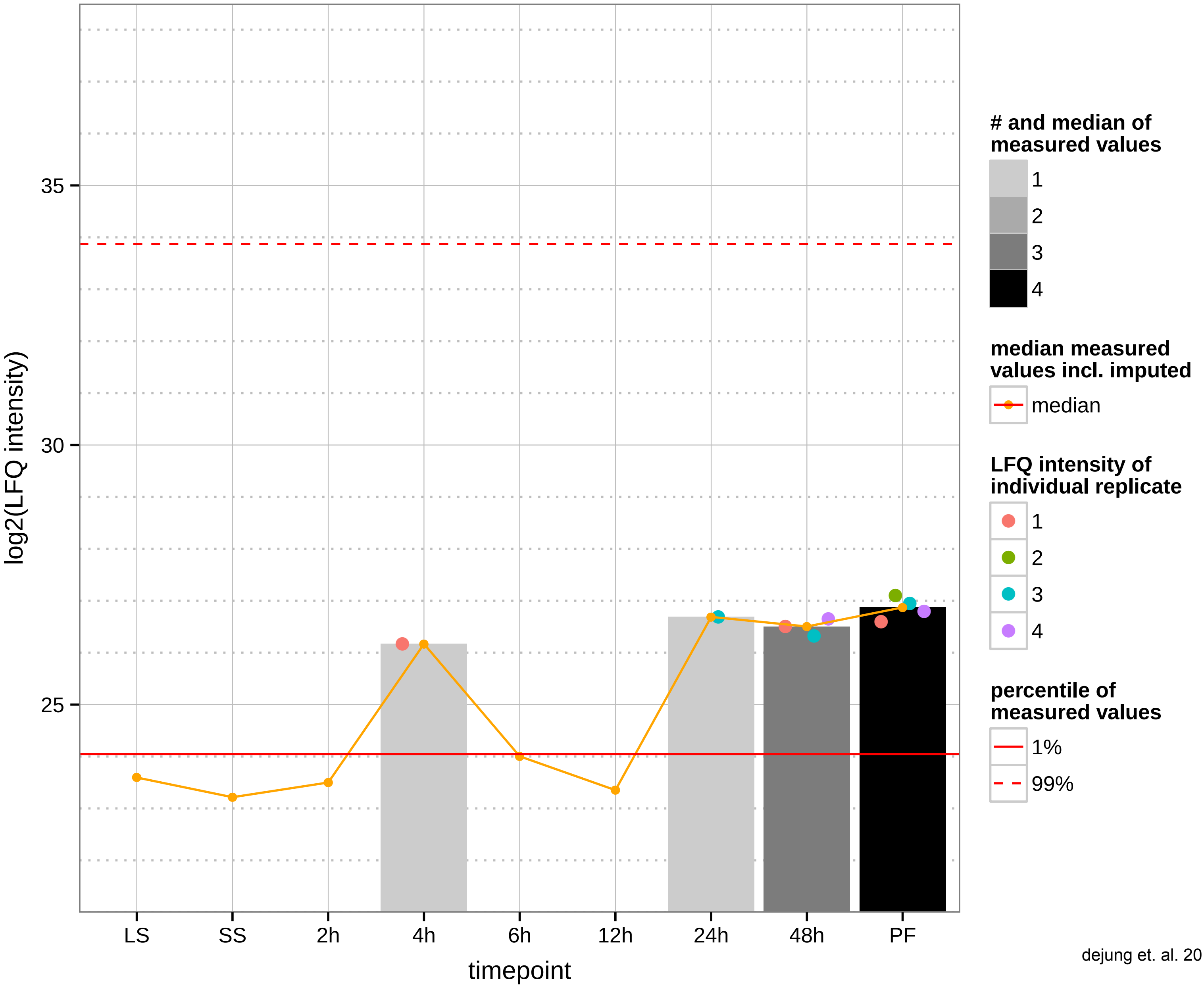
hypothetical protein, conserved
Tb927.11.11310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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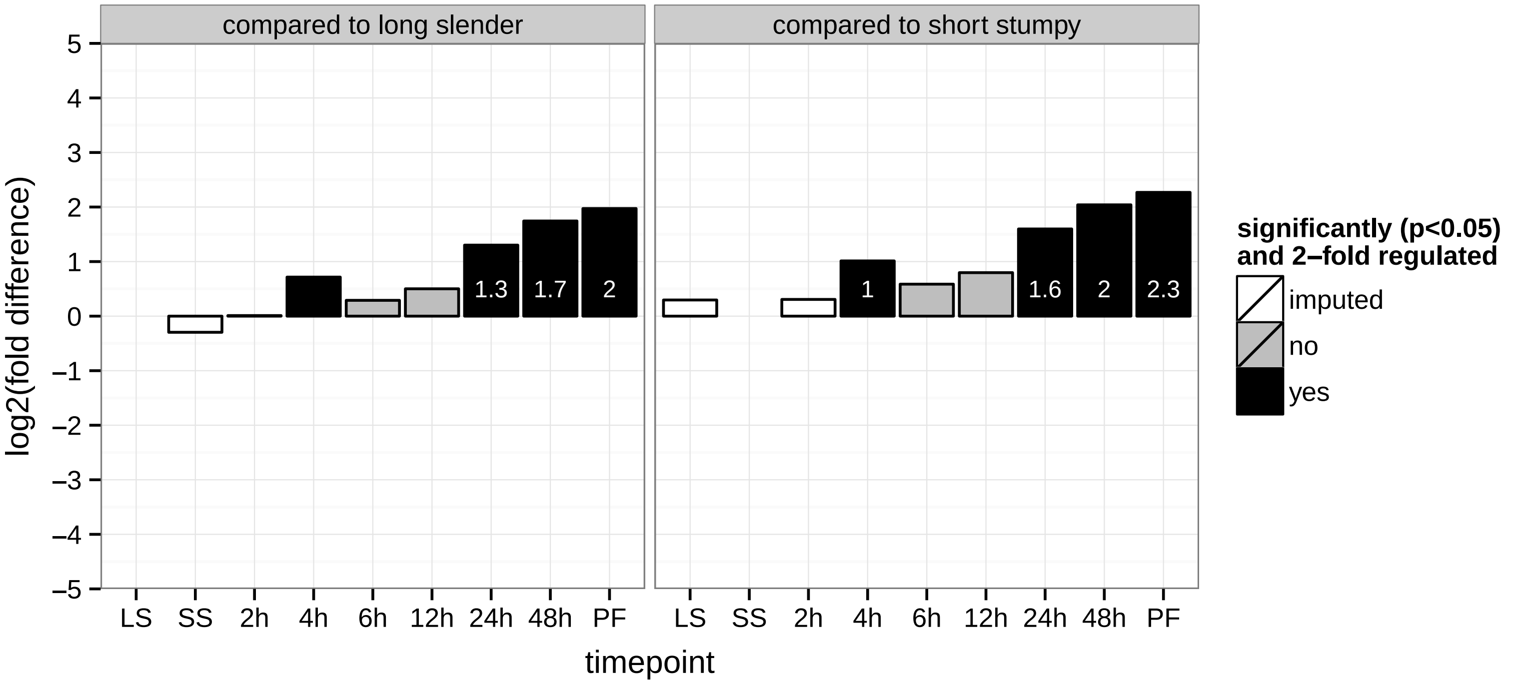
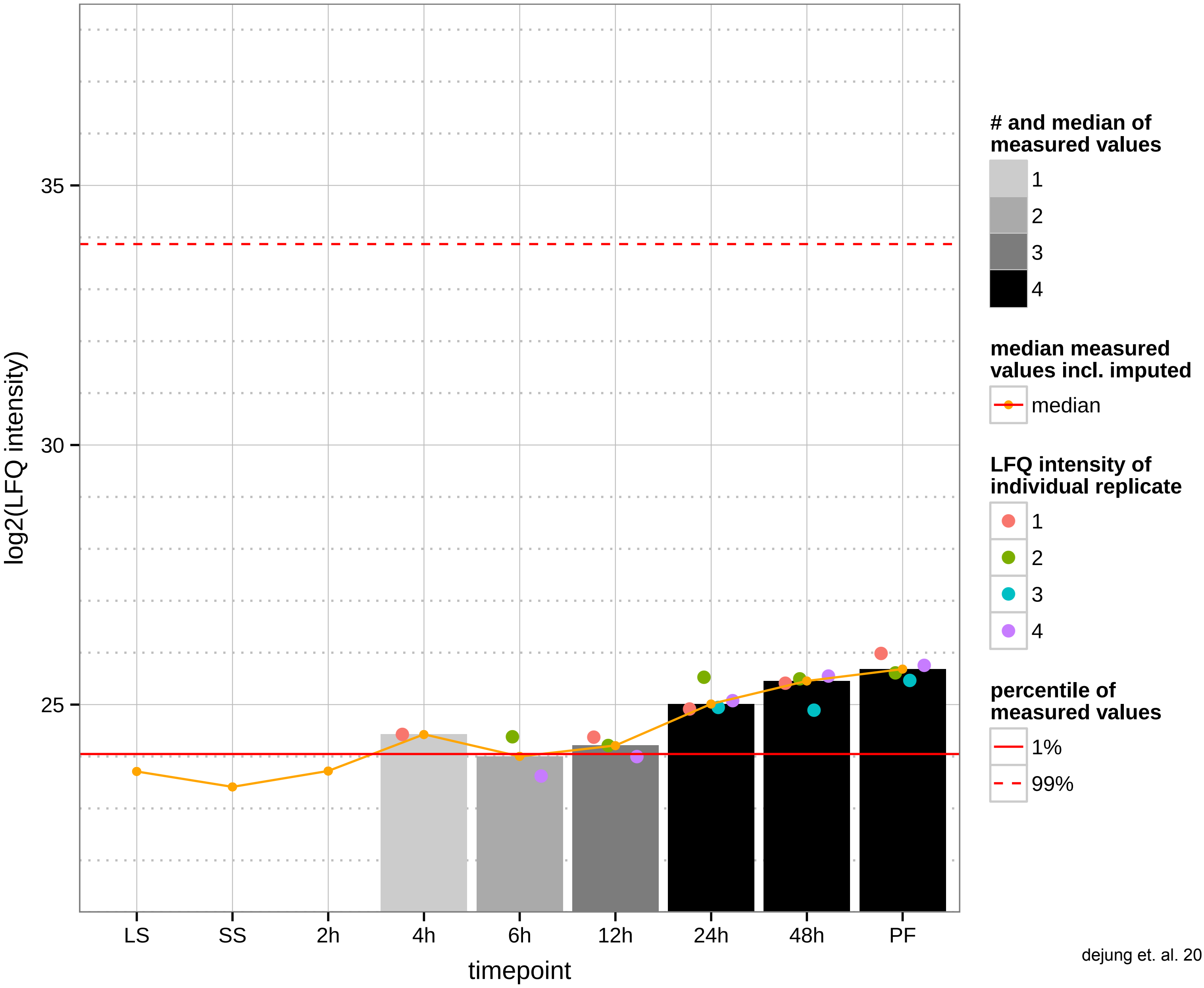
hypothetical protein, conserved
Tb927.11.12300
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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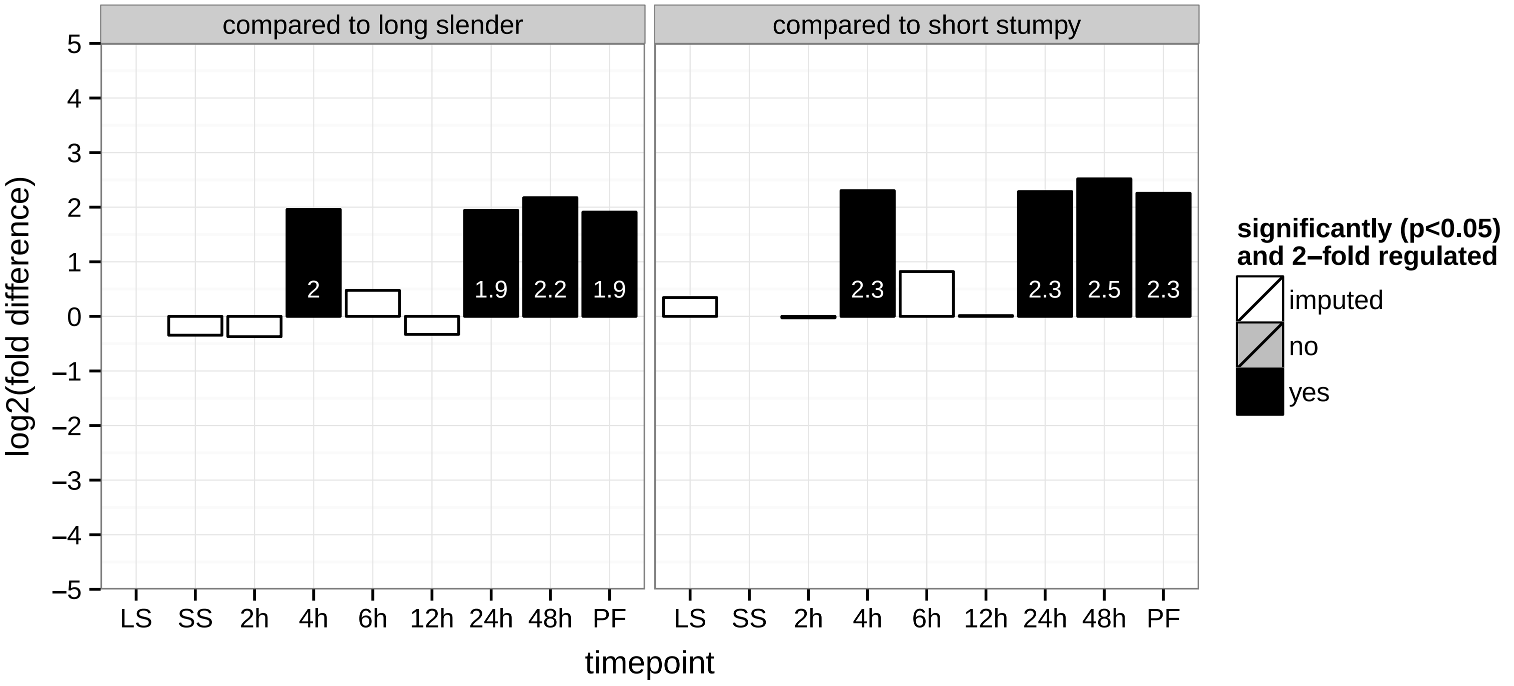
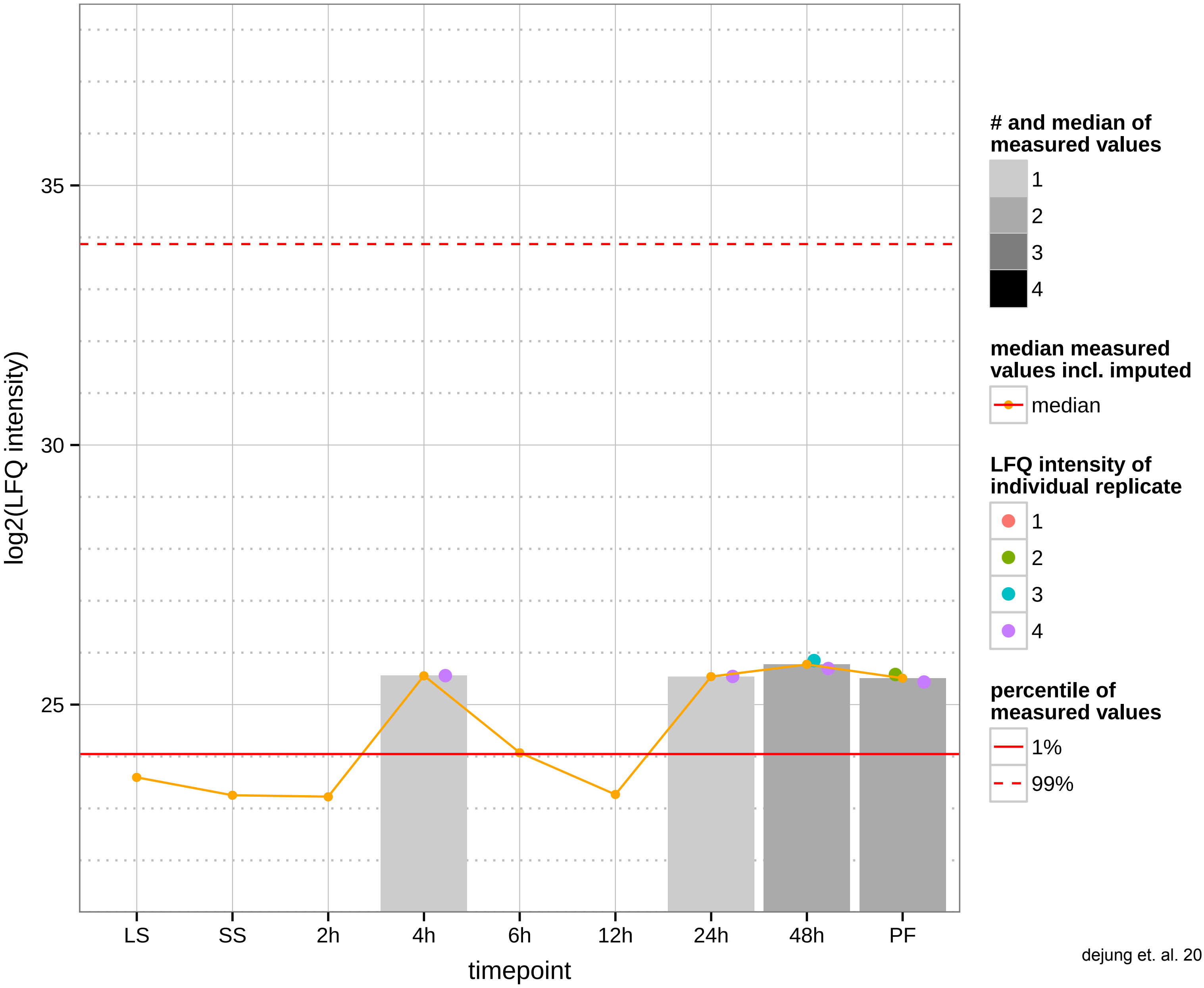
leucine–rich repeat protein 1 (LRRP1), putative, leucine–rich repeat protein (LRRP), (fragment), leucine rich repeat protein, le
Tb927.11.1500
AGOF: null
AGOC: null
AGOP: null
PGOF: null, protein binding
PGOC: null
PGOP: null





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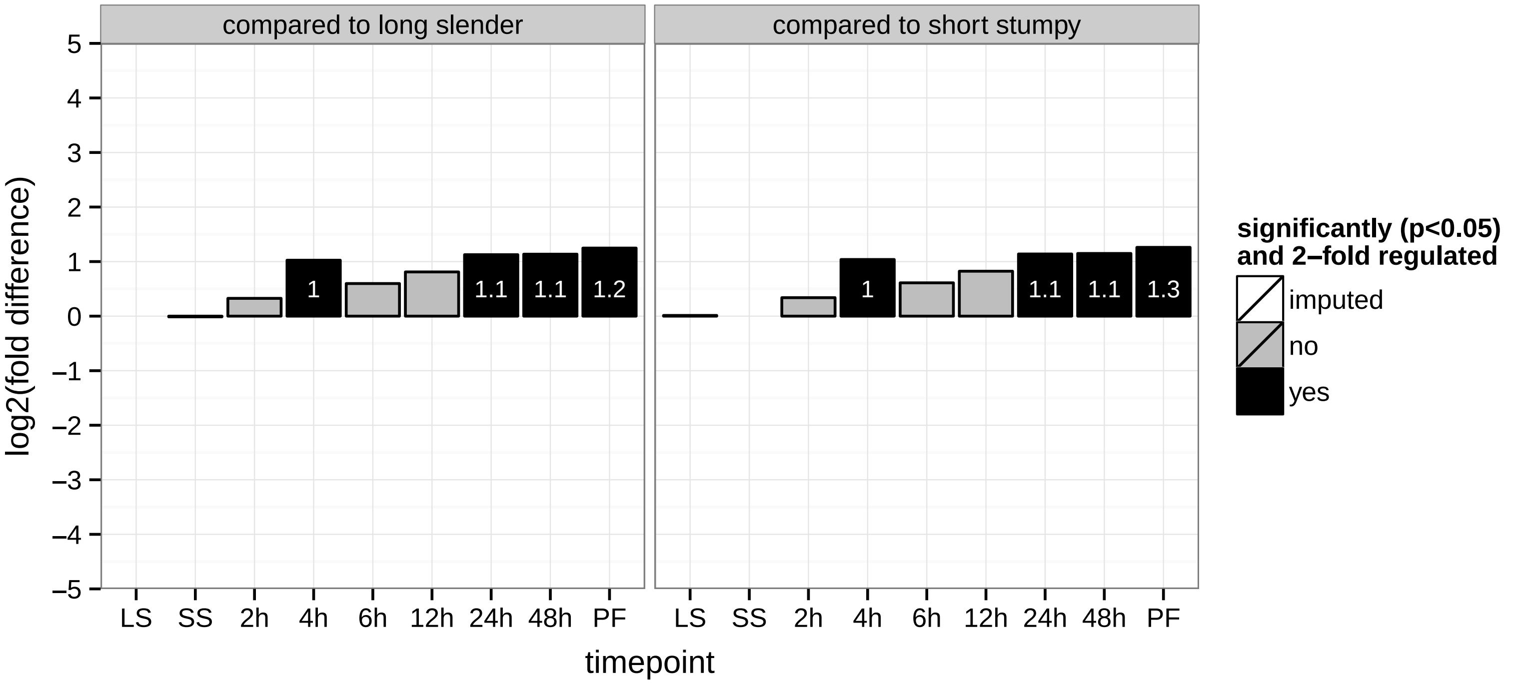
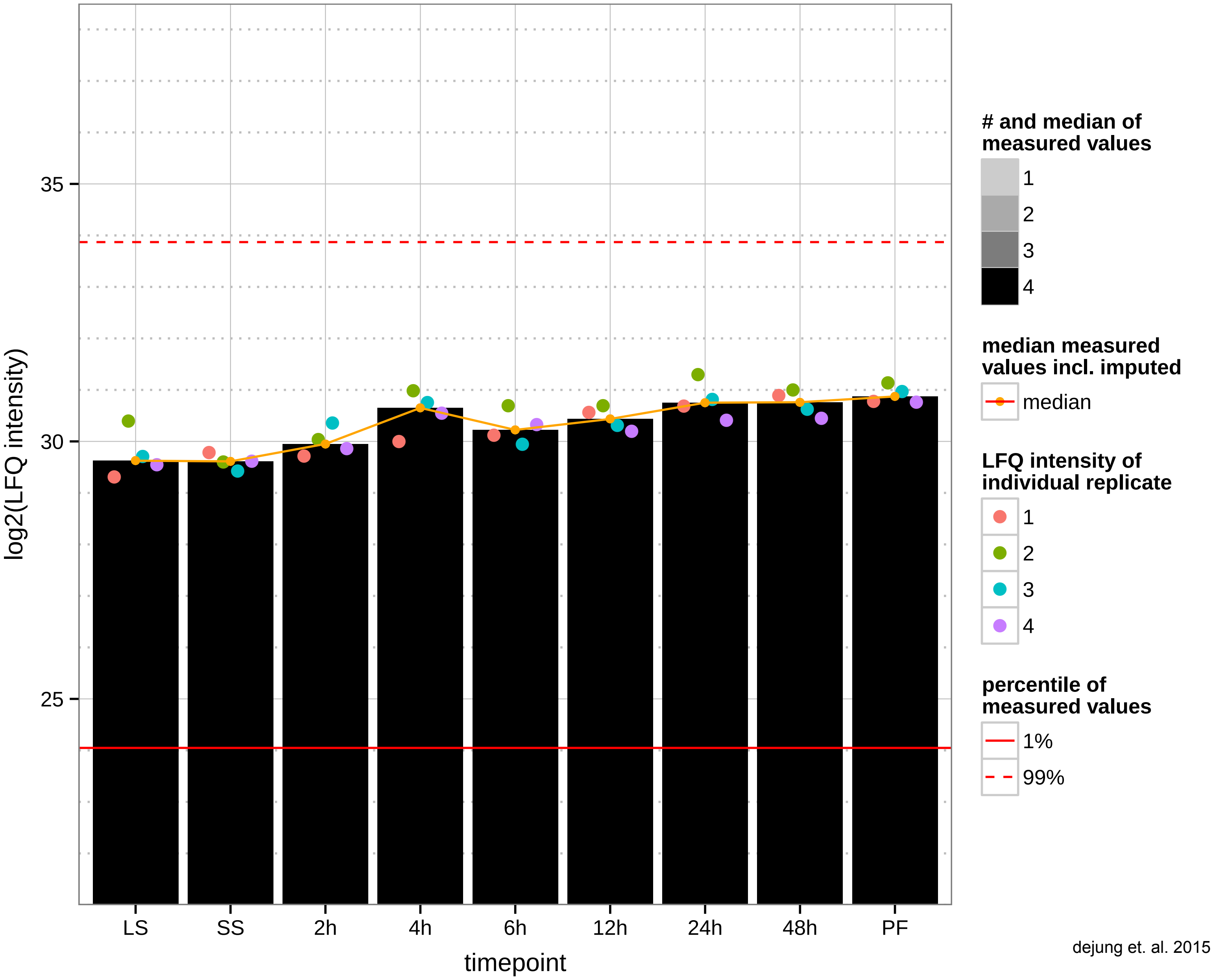
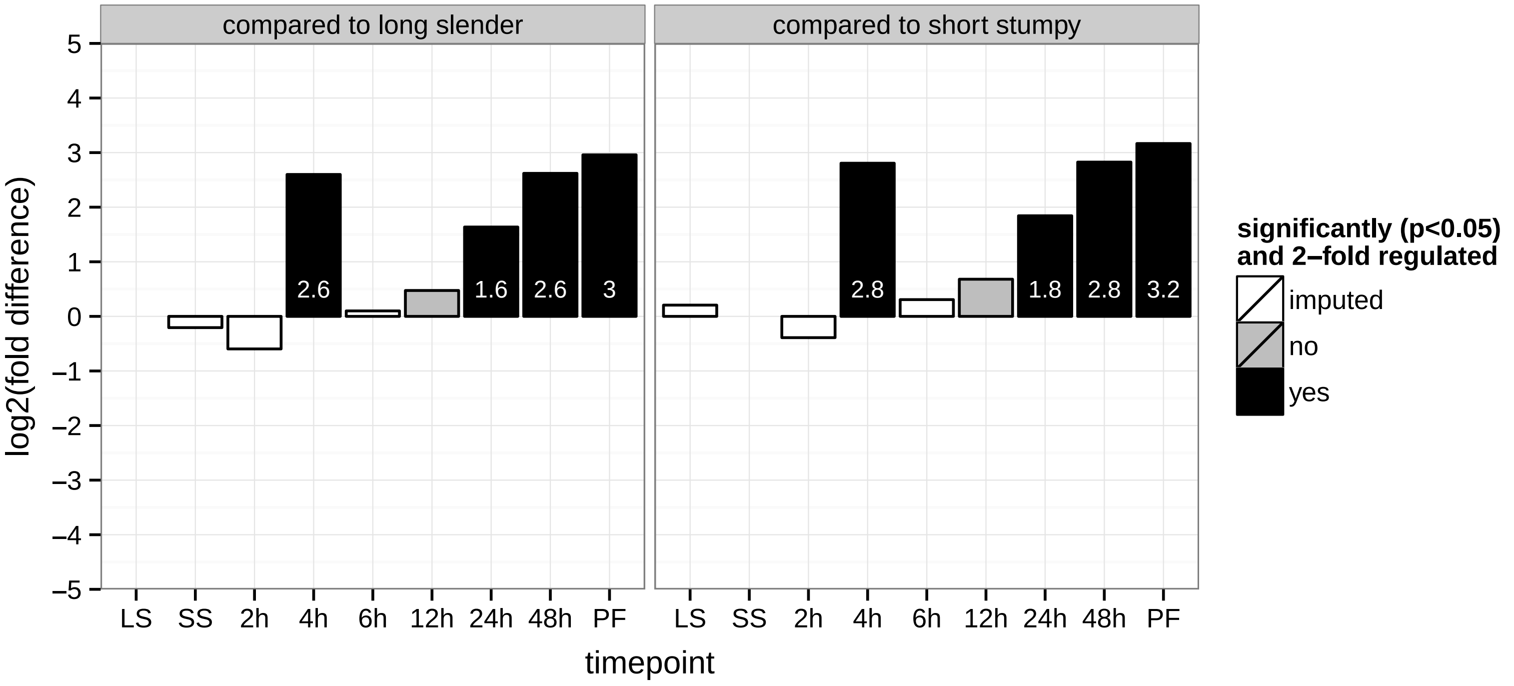
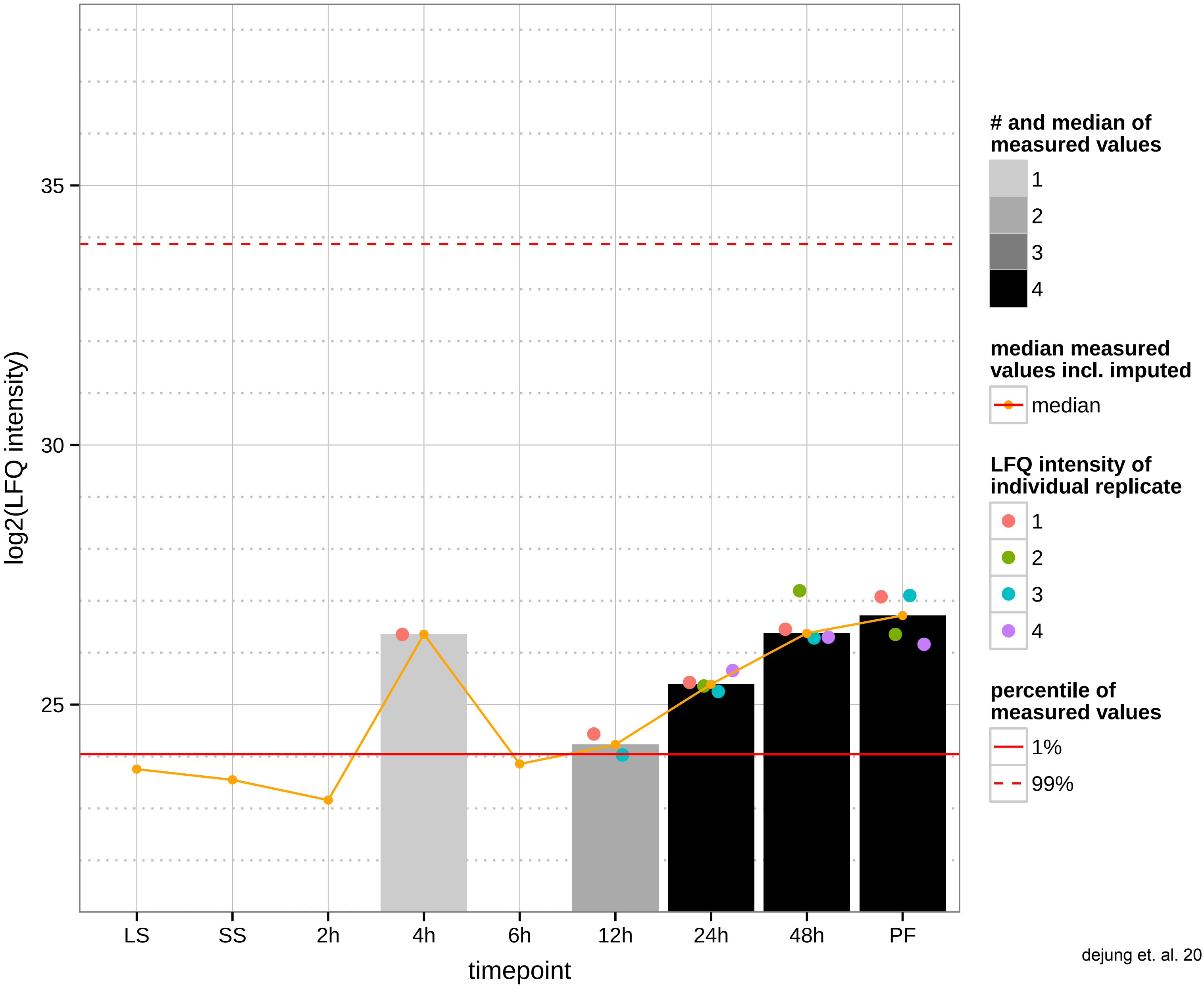
RNA–binding protein (RPB28)
Tb927.3.1030
AGOF: nucleic acid binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null





hypothetical protein, conserved
Tb927.3.3440
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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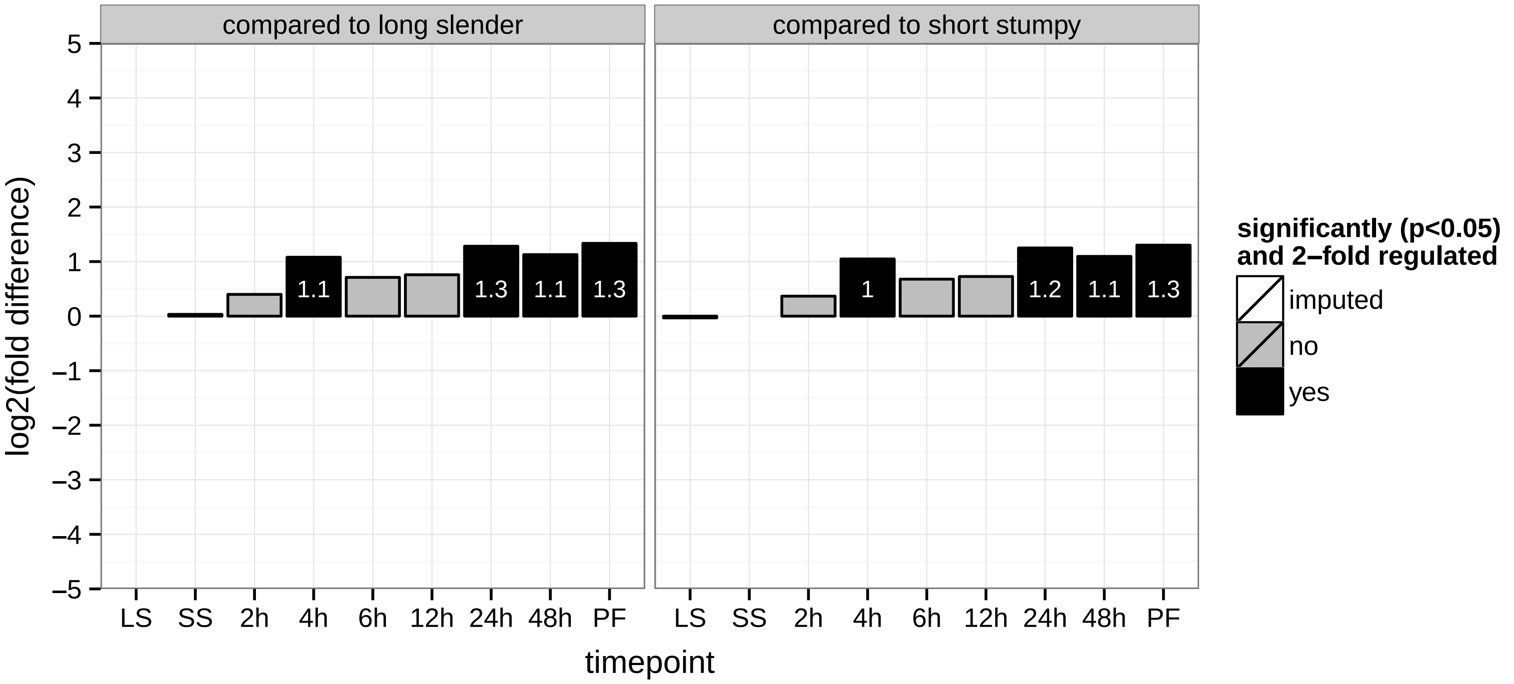
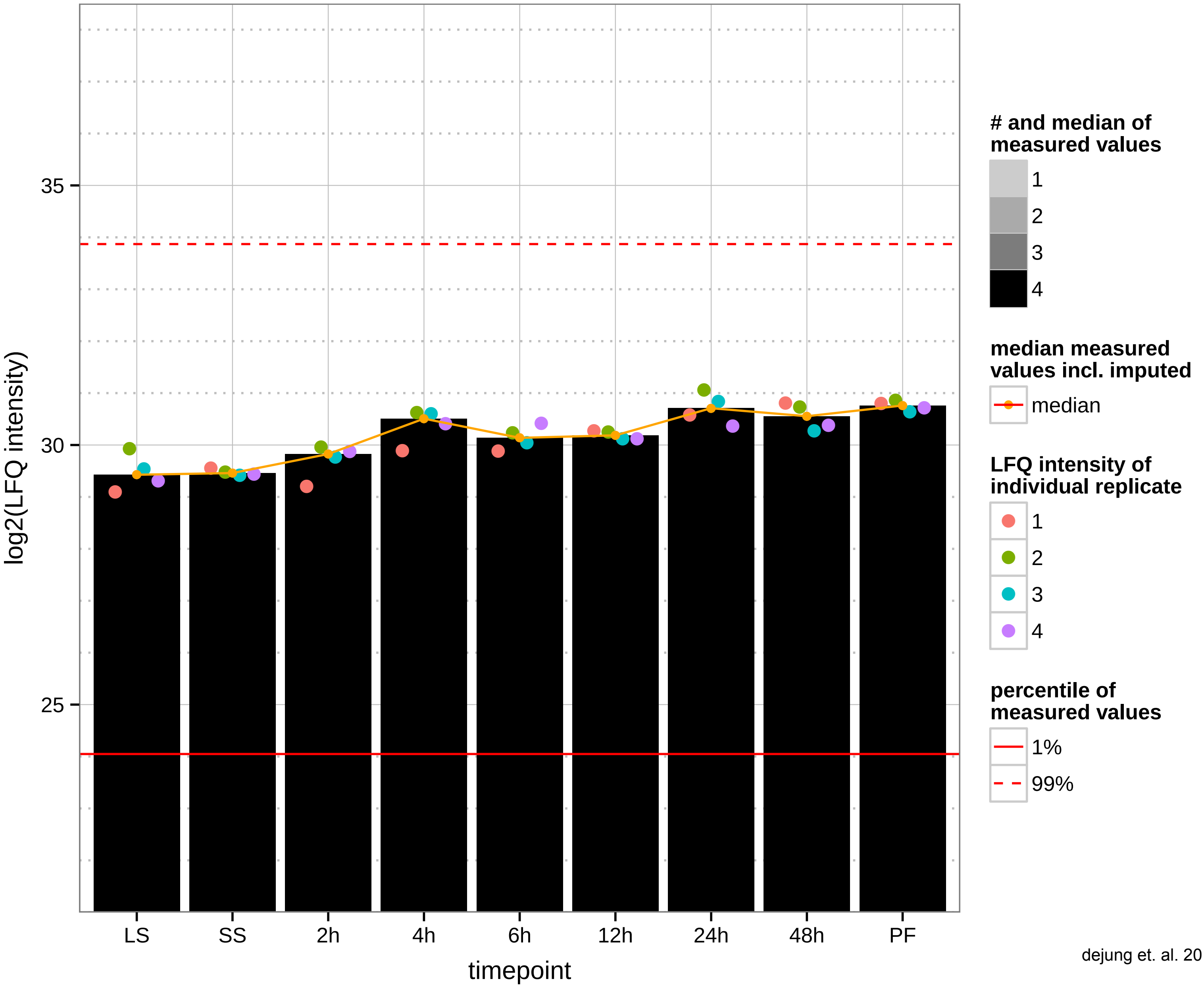
RNA–binding protein, putative (EIF3D)
Tb927.4.1930
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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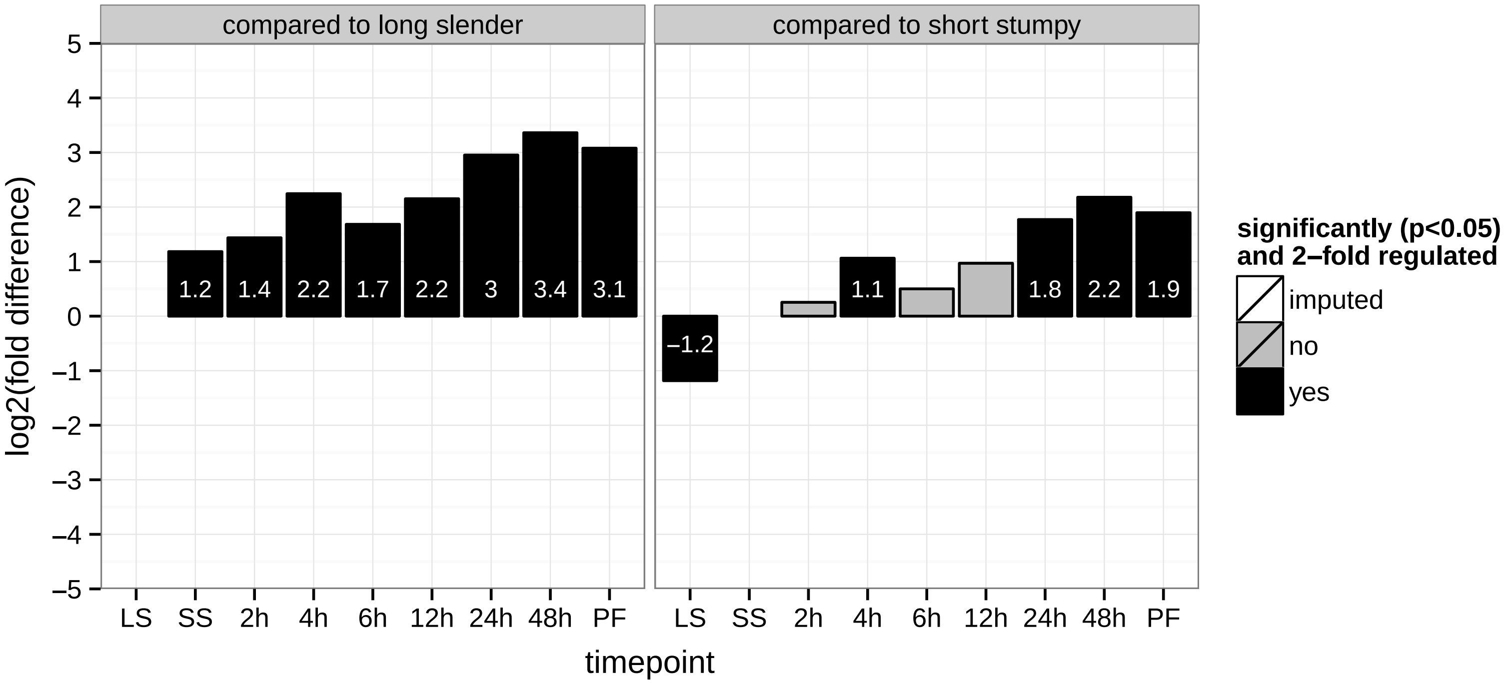
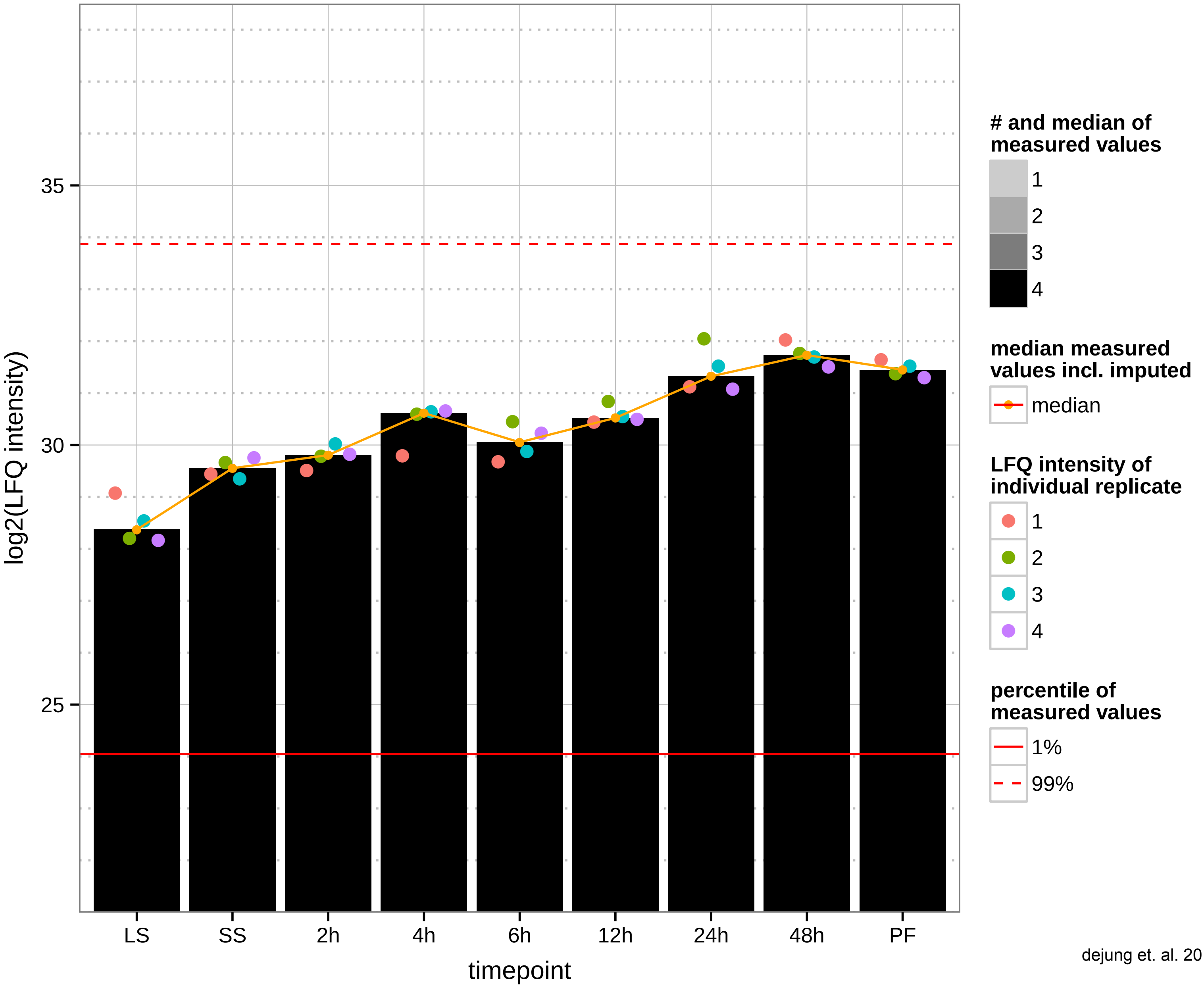
ATP synthase, epsilon chain, putative
Tb927.6.4990
AGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, proton−transporting ATPase activity
AGOC: mitochondrion, proton−transporting ATP synthase complex, catalytic core F(1)
AGOP: ATP synthesis coupled proton transport
PGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, proton−transporting ATPase activity
PGOC: proton−transporting ATP synthase complex, catalytic core F(1)
PGOP: ATP synthesis coupled proton transport





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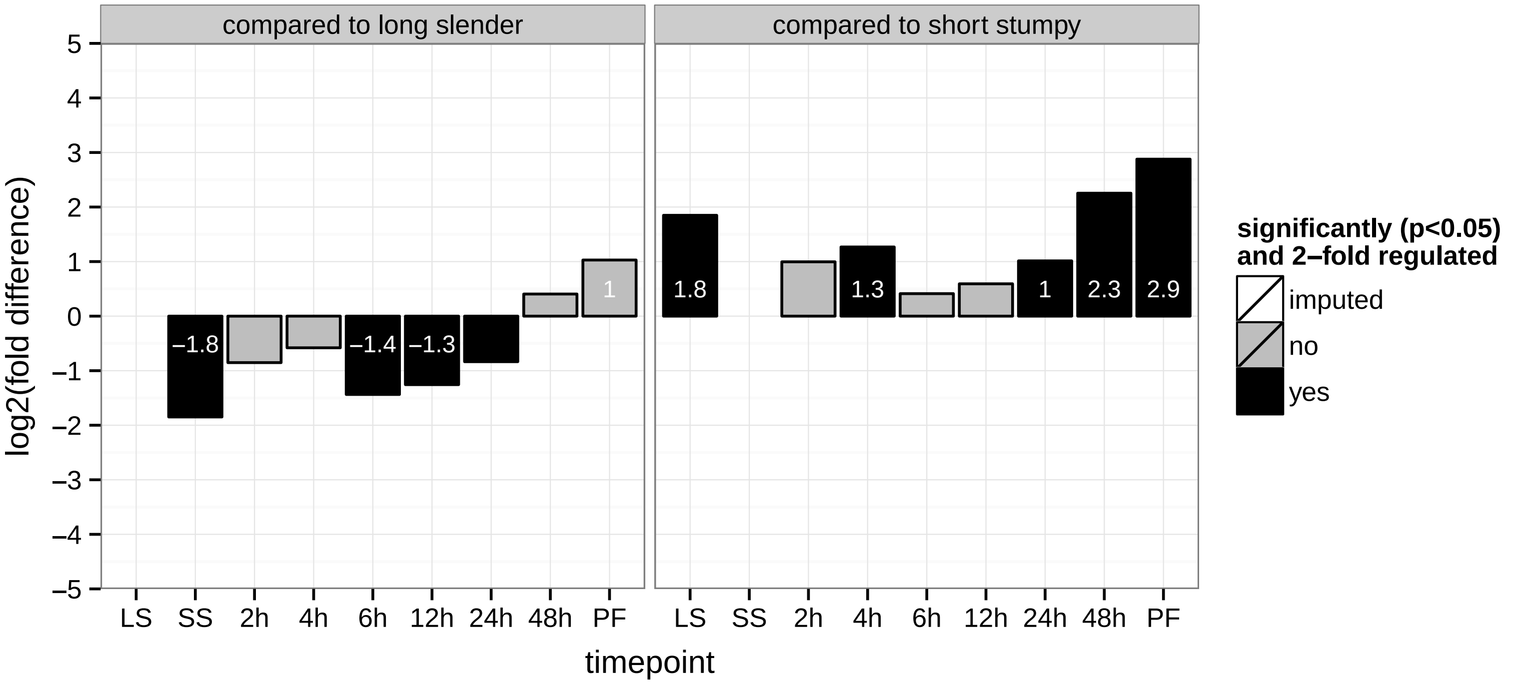
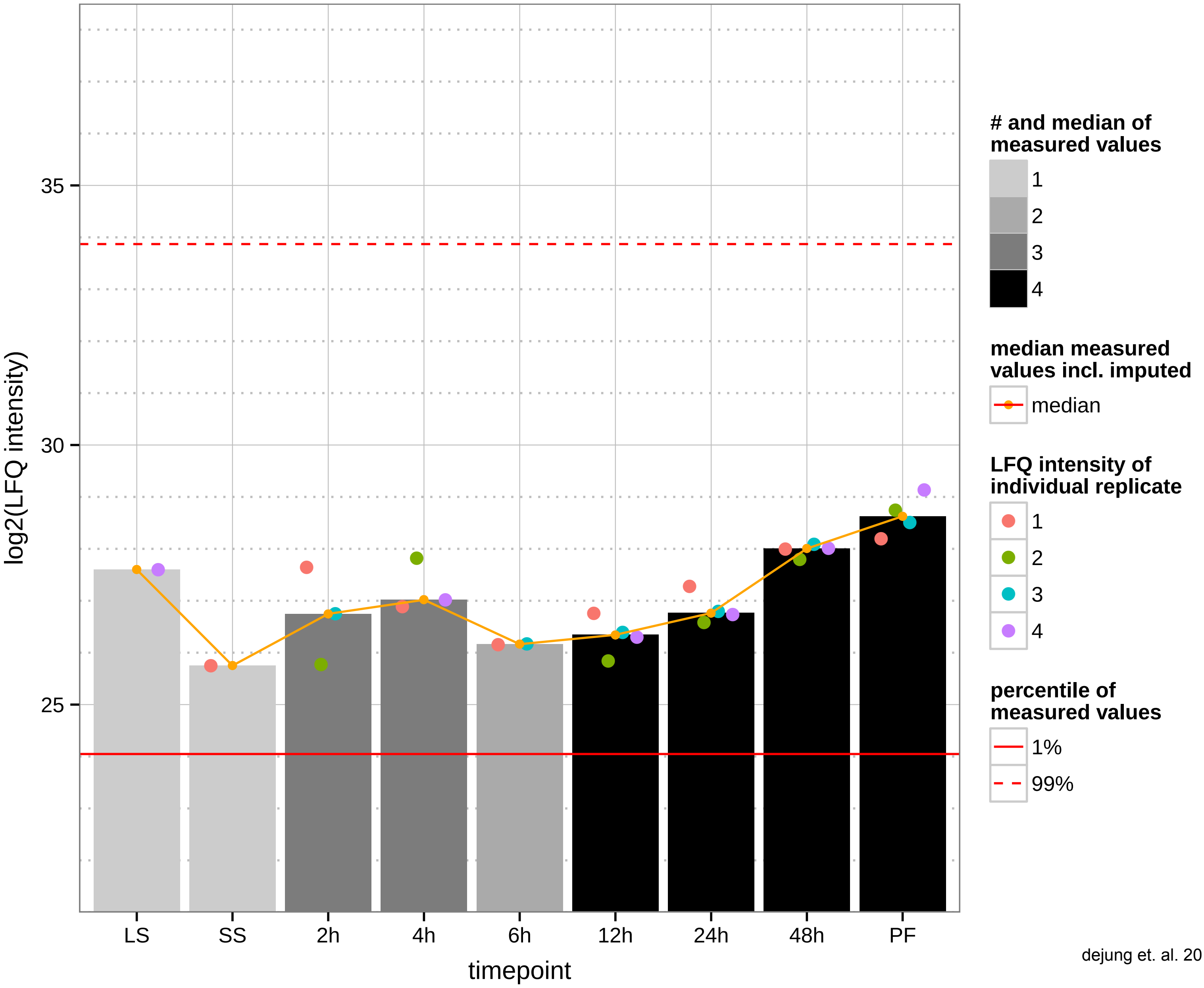
hypothetical protein, conserved
Tb927.8.1950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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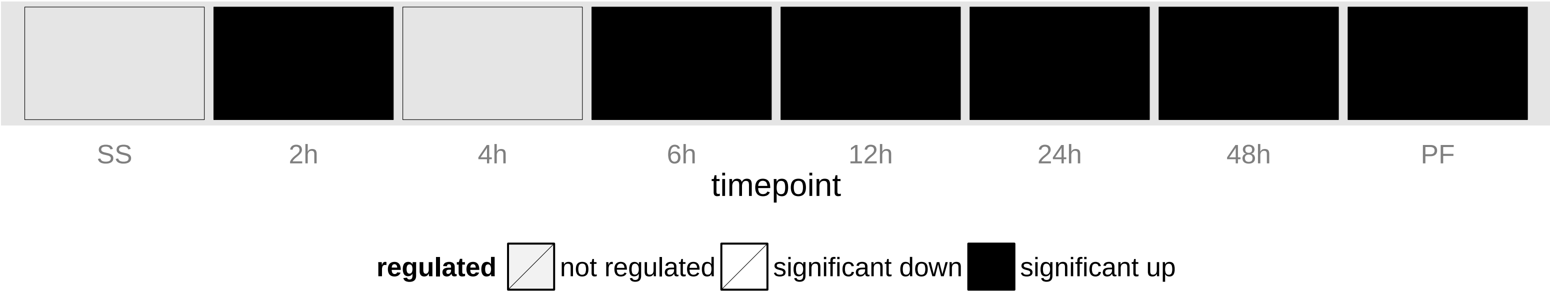

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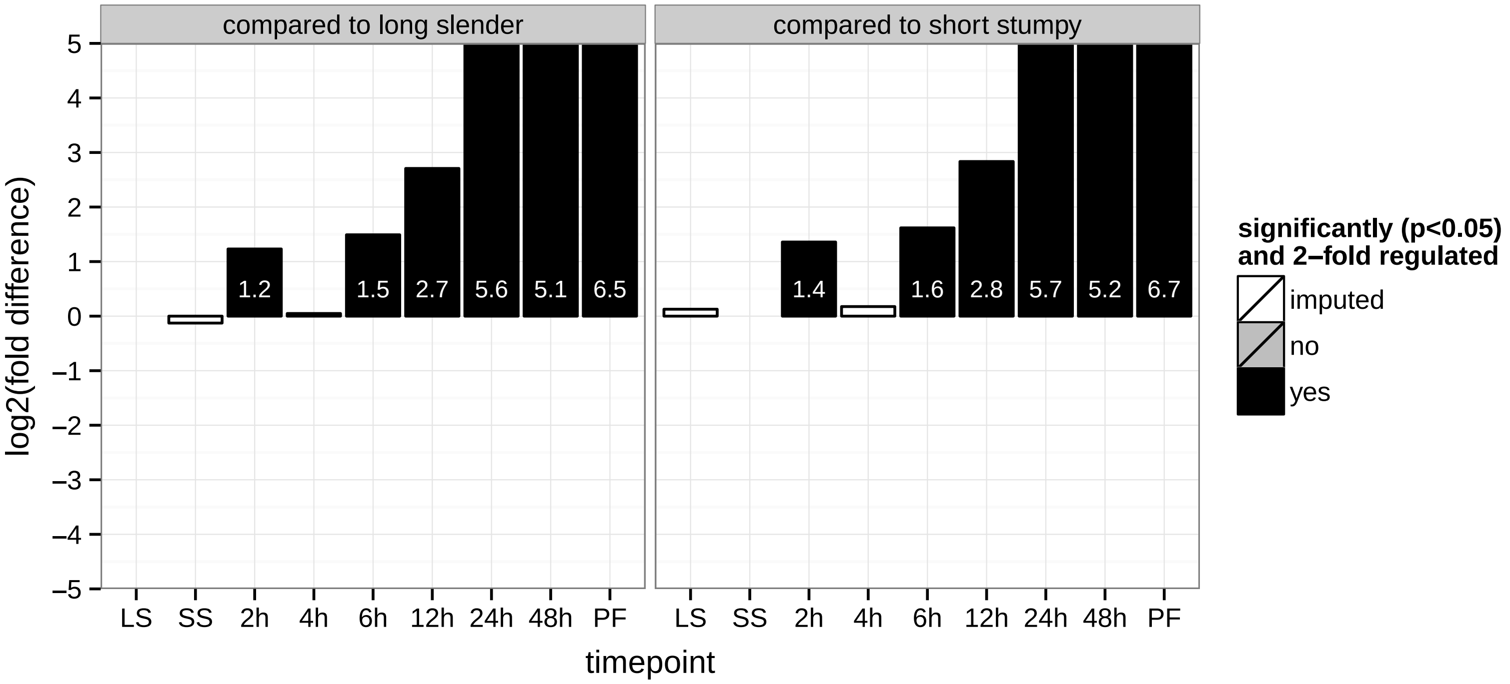
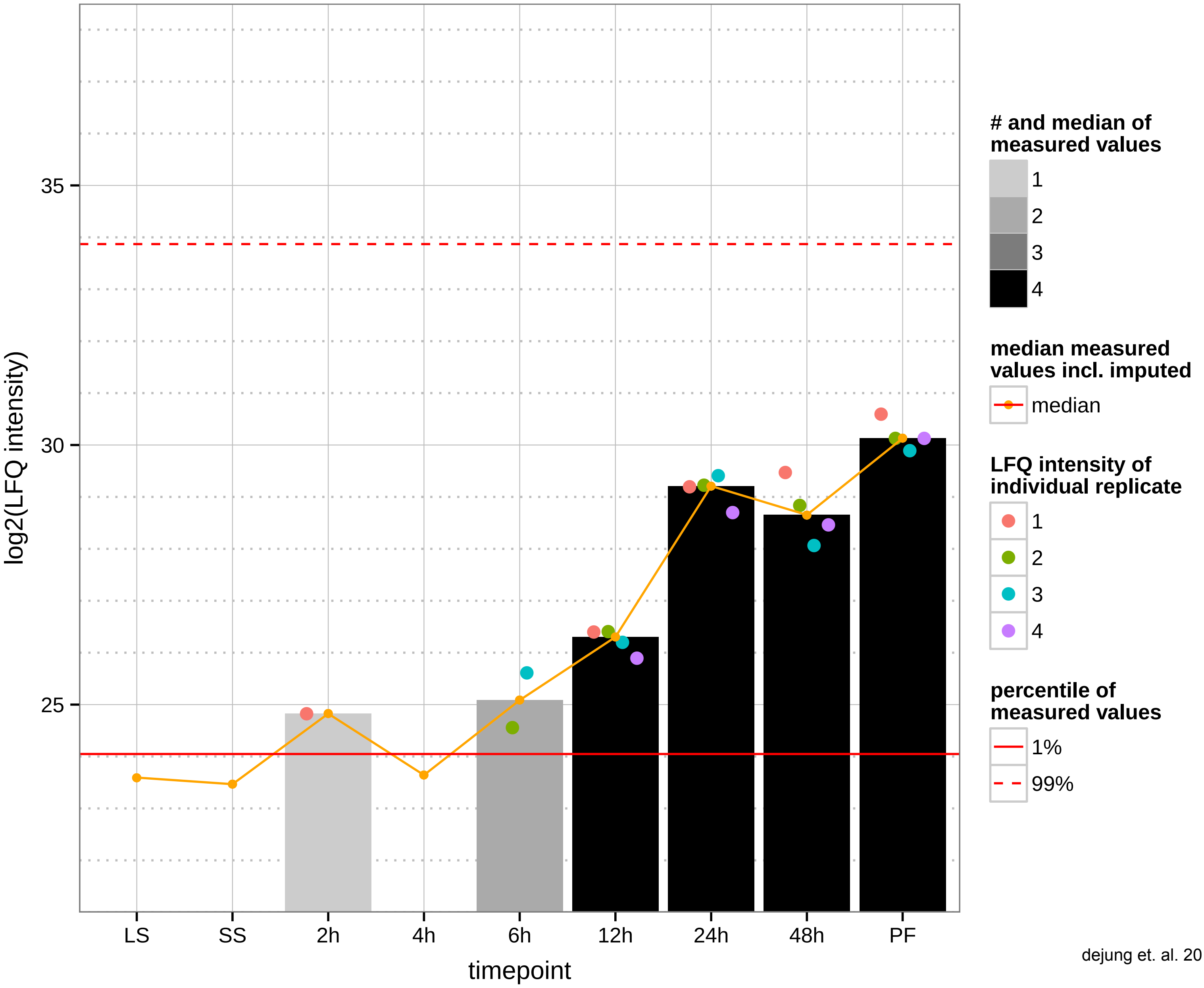
cytochrome oxidase subunit VI (COXVI)
Tb927.10.280
AGOF: cytochrome−c oxidase activity
AGOC: mitochondrion
AGOP: oxidation−reduction process
PGOF: cytochrome−c oxidase activity
PGOC: mitochondrion
PGOP: null





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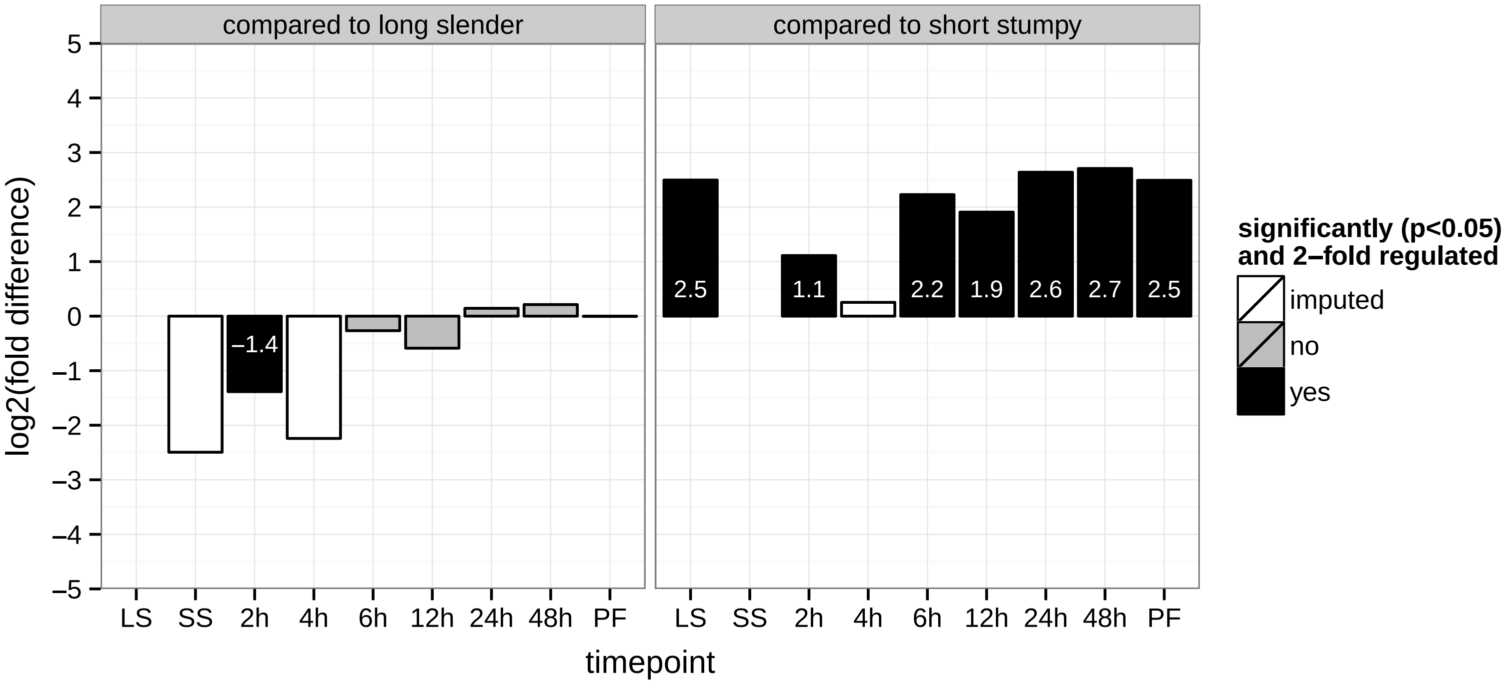
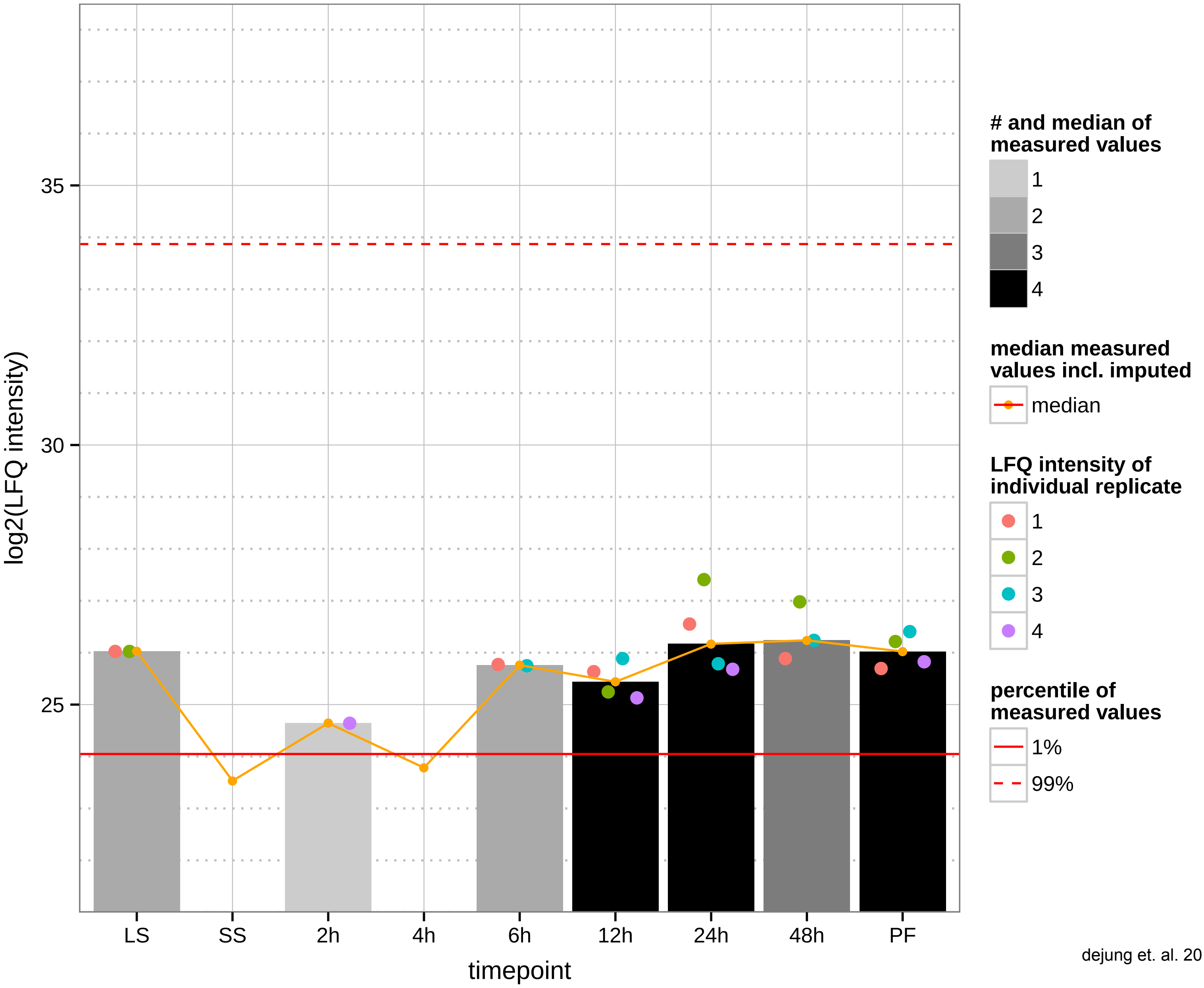
peptidyl–prolyl cis–trans isomerase, putative (PPIase)
Tb927.10.4620
AGOF: FK506 binding, peptidyl–prolyl cis–trans isomerase activity
AGOC: null
AGOP: protein folding
PGOF: null
PGOC: null
PGOP: protein folding





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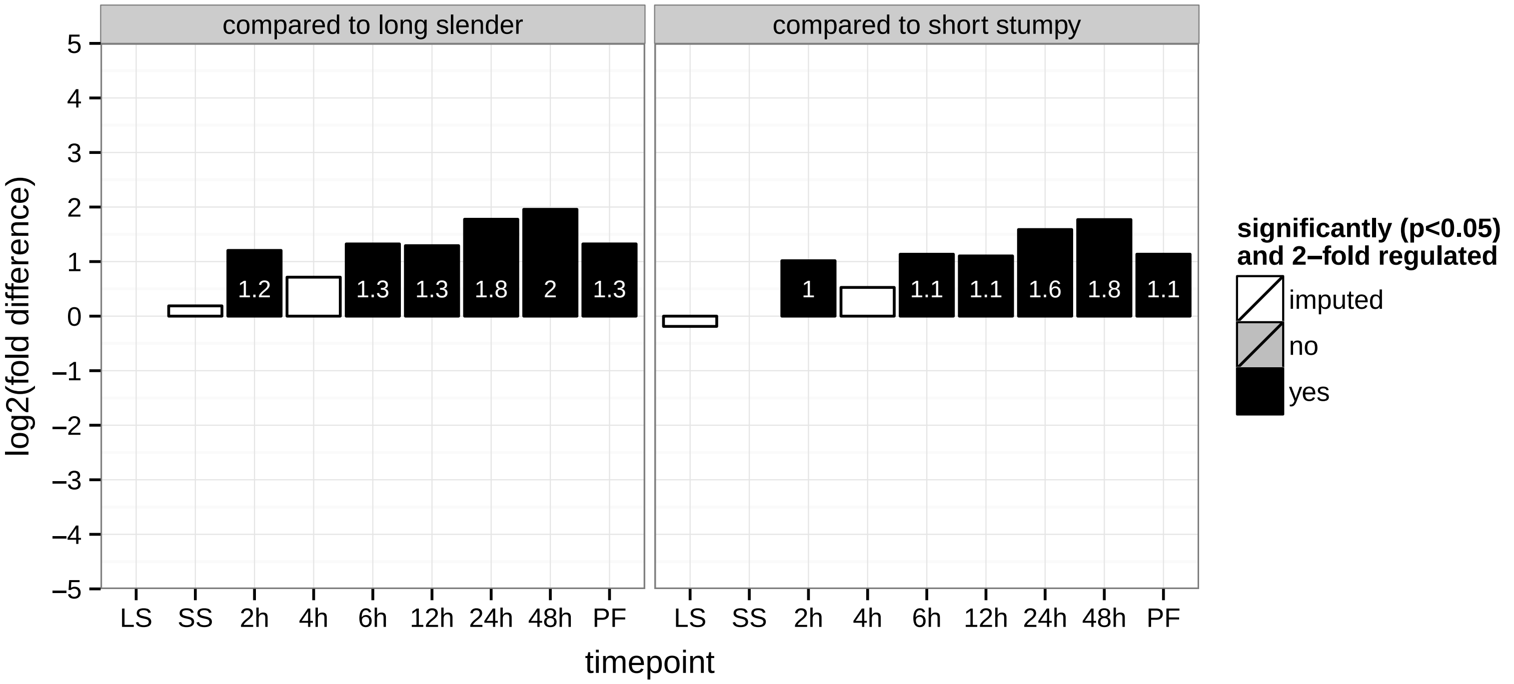
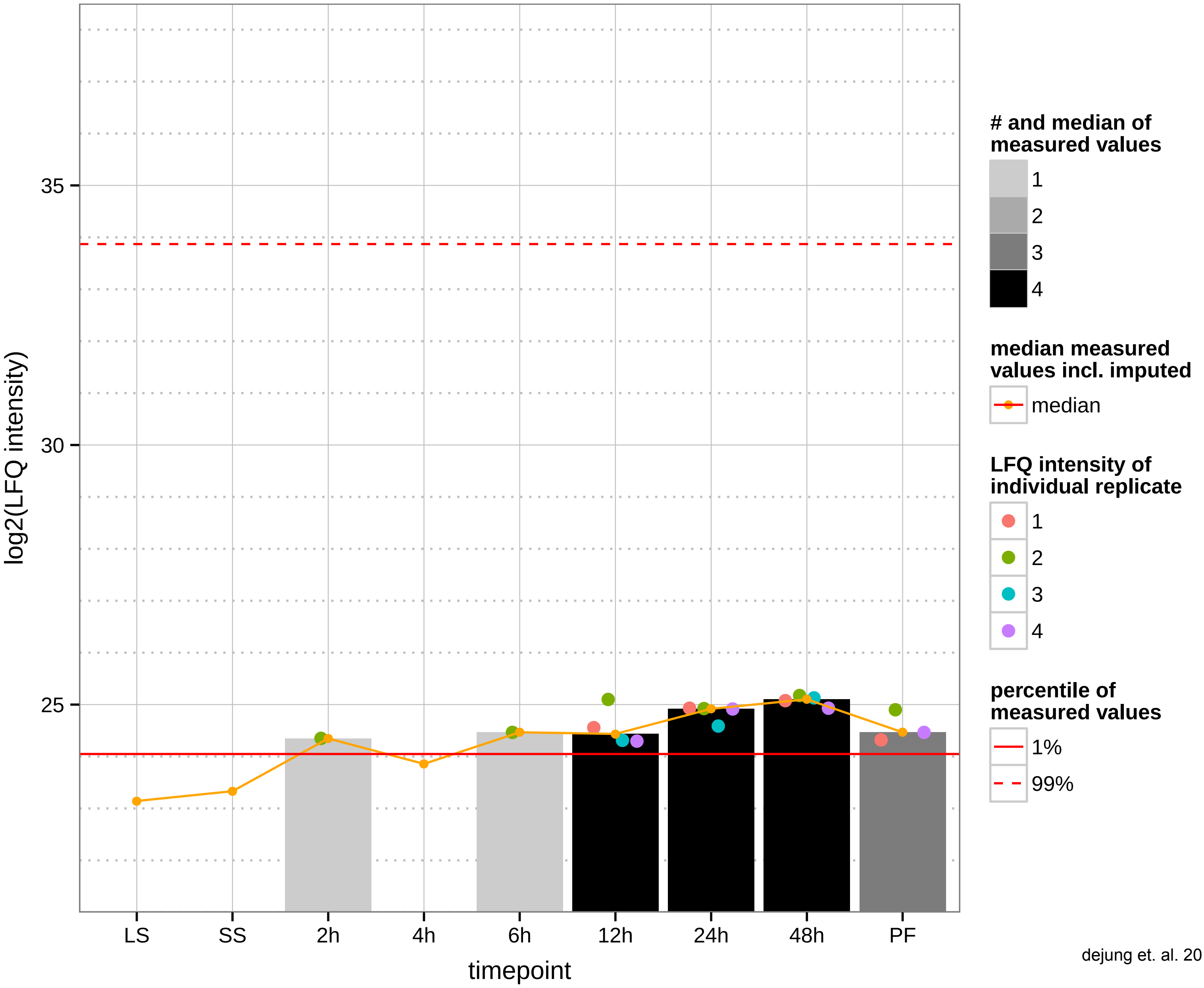
hypothetical protein, conserved
Tb927.10.7730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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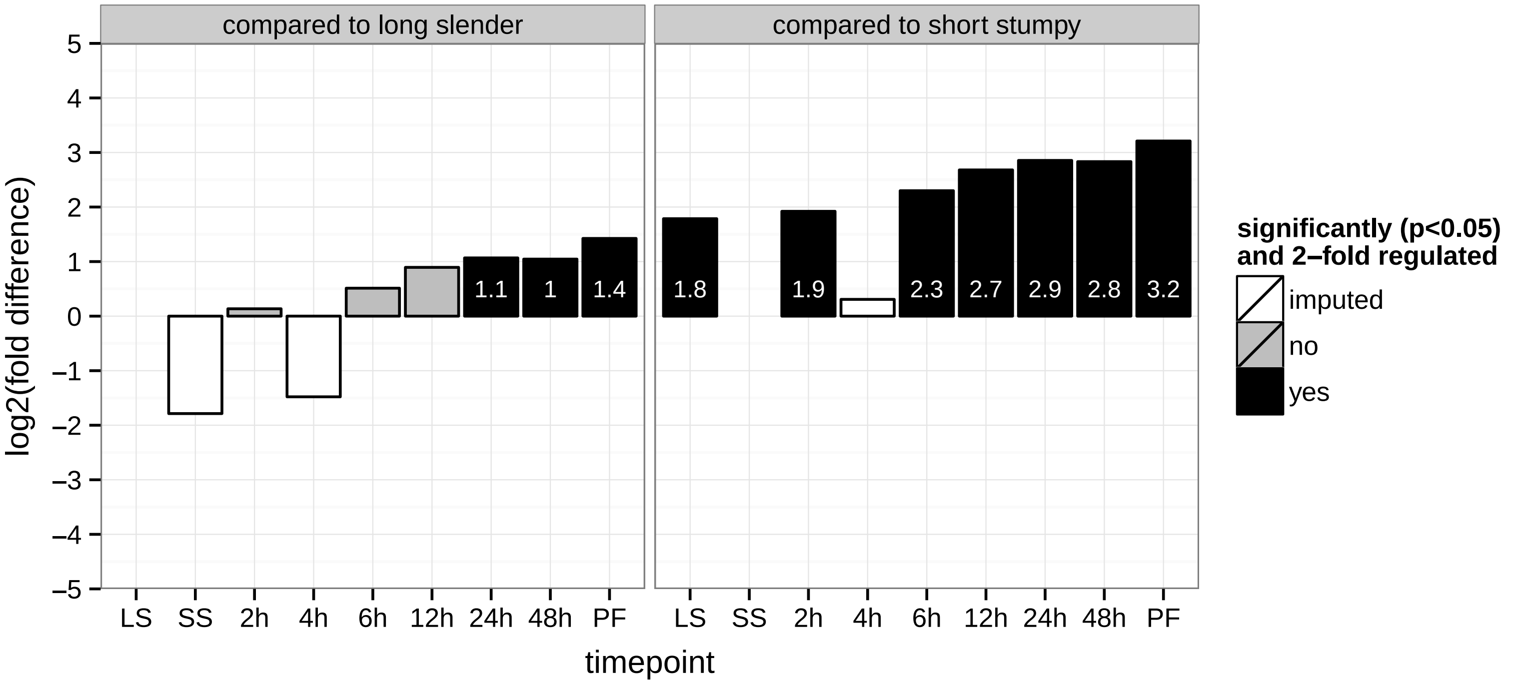
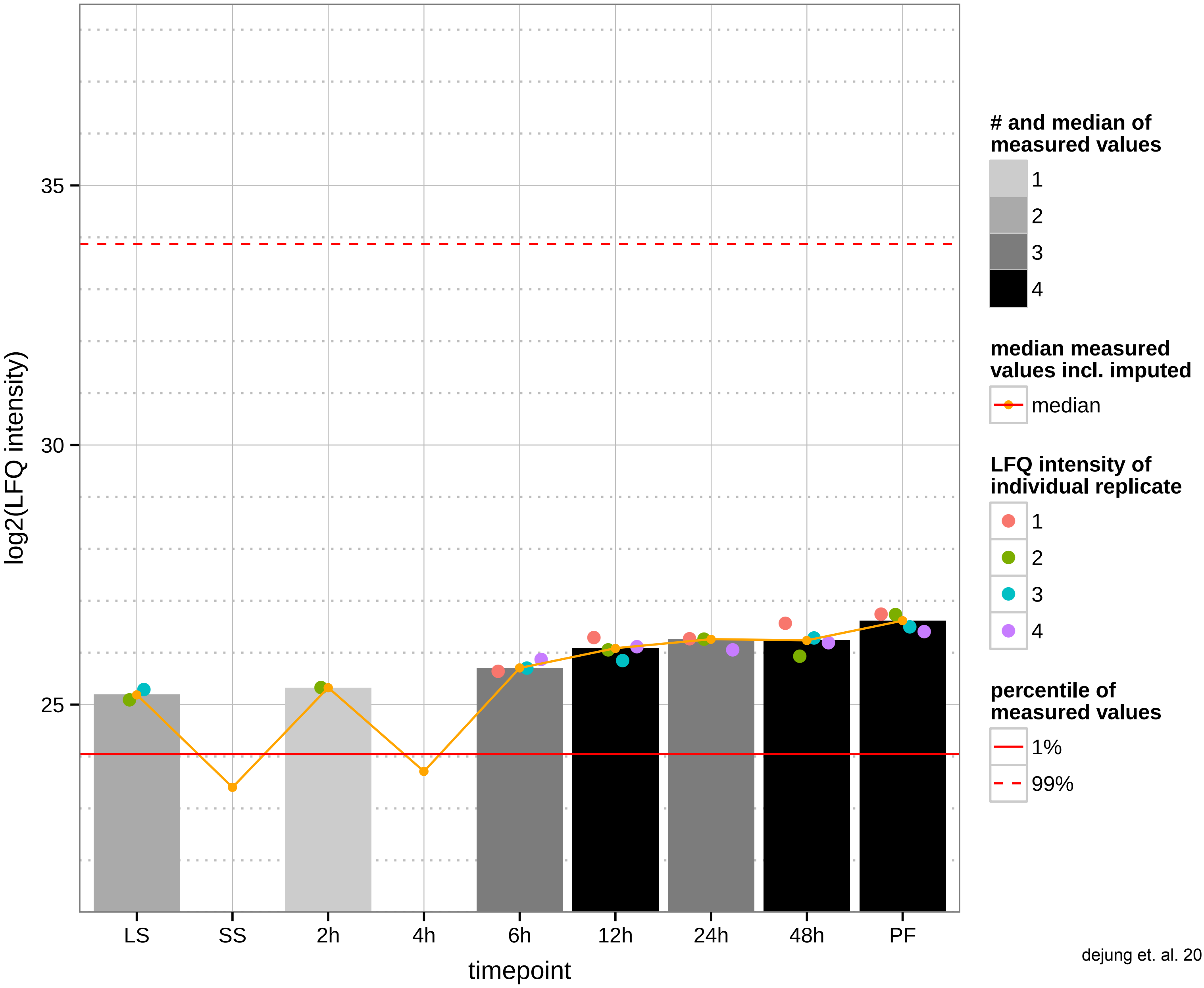
hypothetical protein, conserved
Tb927.11.11470
AGOF: null
AGOC: mitochondrion
AGOP: modulation of development of symbiont involved in interaction with host, quorum sensing involved in interaction with ho
PGOF: null
PGOC: null
PGOP: null





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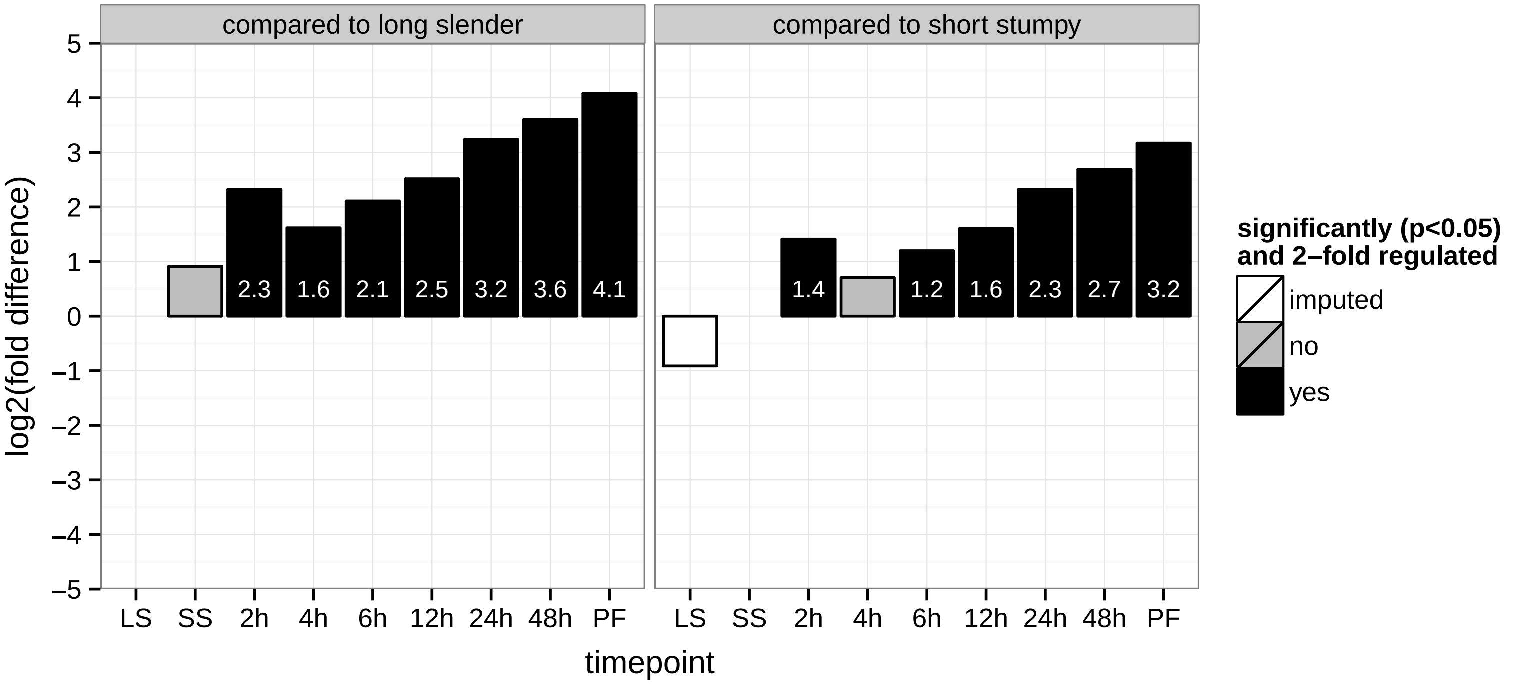
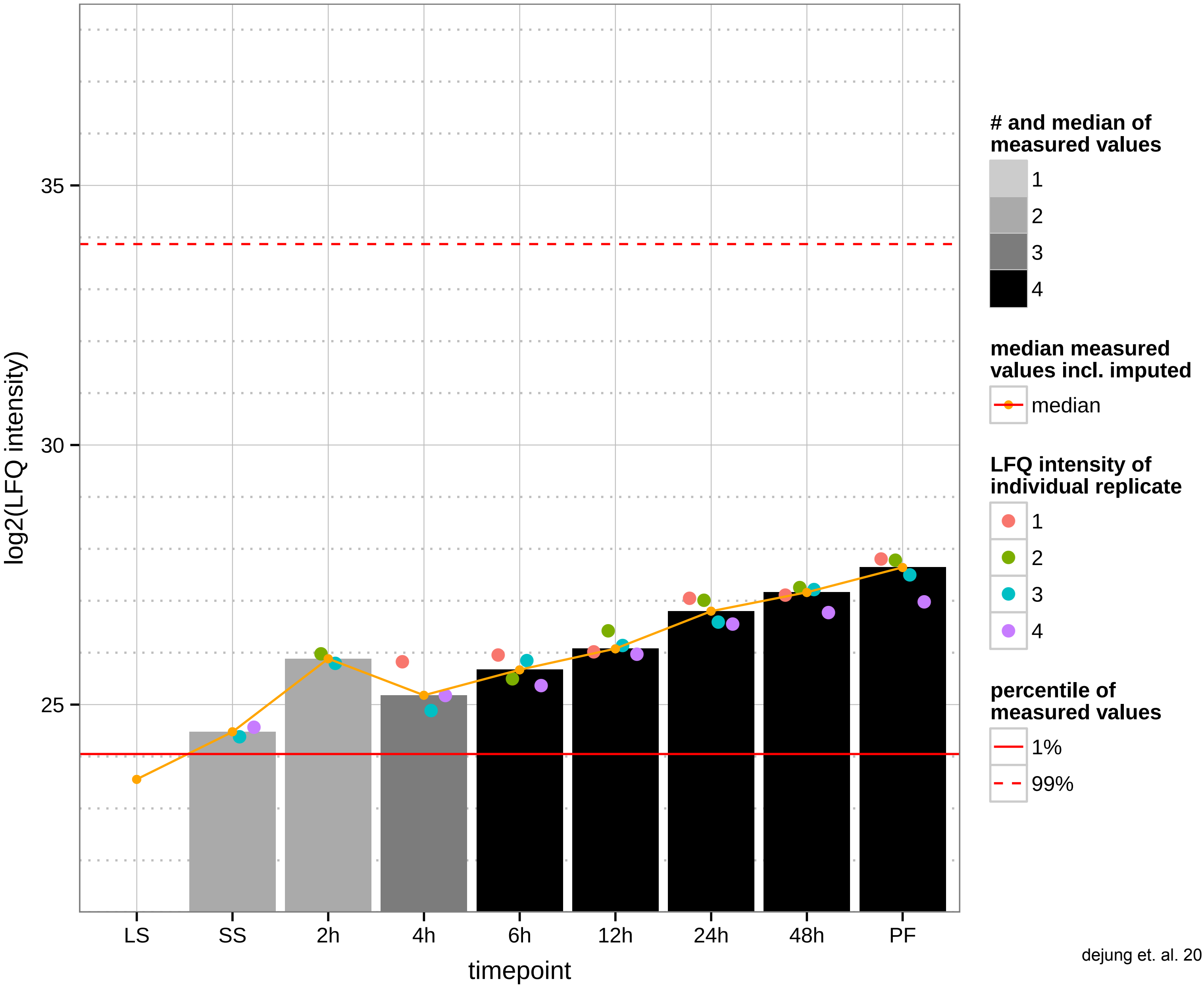
NADH–cytochrome b5 reductase, putative (B5R)
Tb927.11.3750
AGOF: cytochrome–b5 reductase activity, electron carrier activity
AGOC: integral to membrane
AGOP: oxidation–reduction process
PGOF: oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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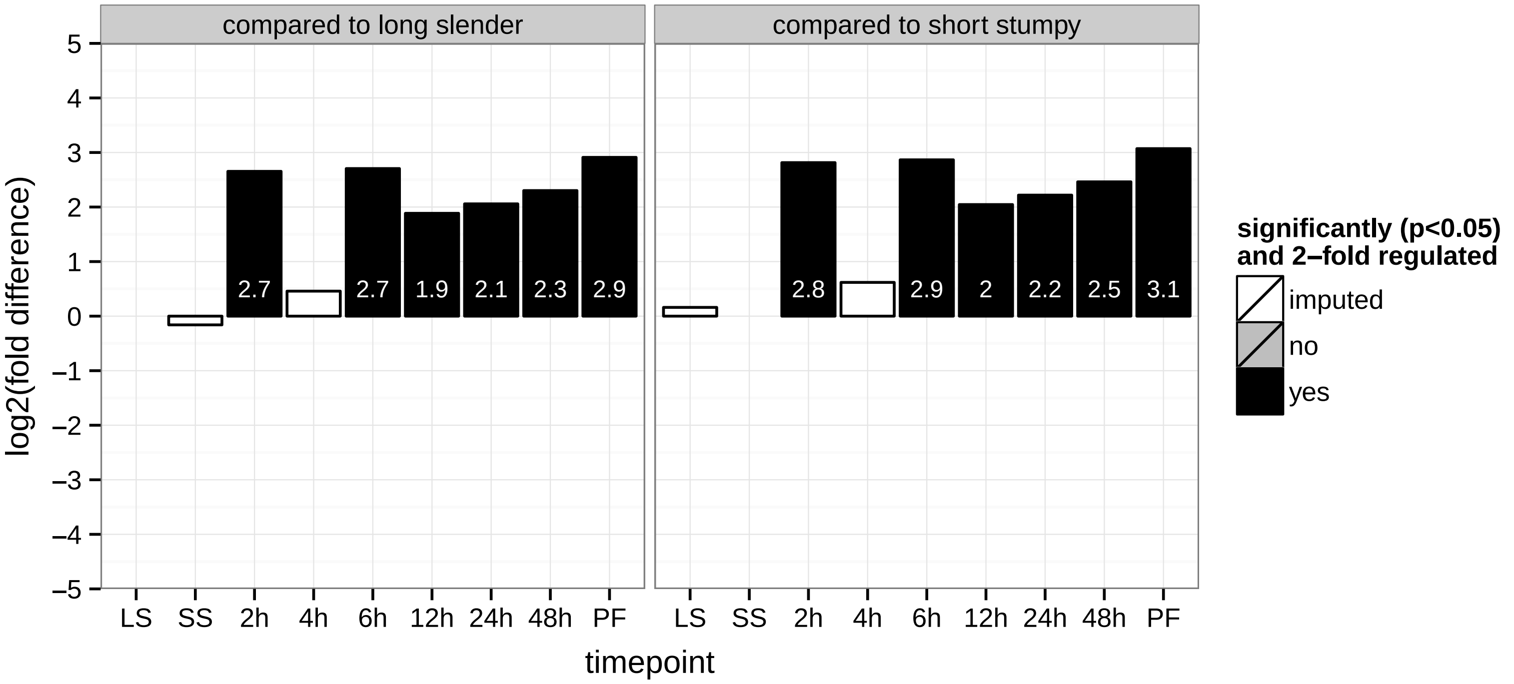
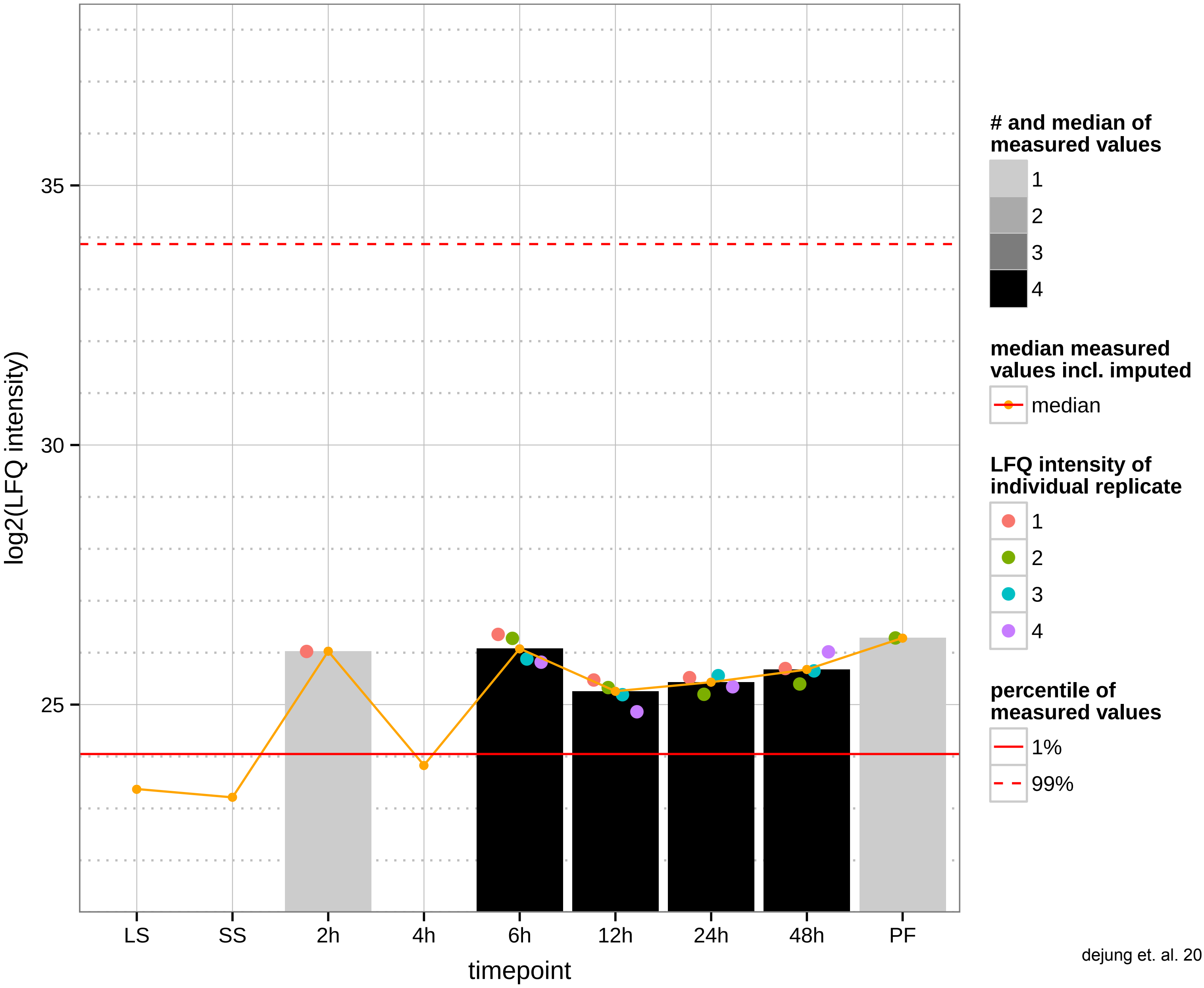
mitochondrial DNA–directed RNA polymerase (MTRNAP)
Tb927.11.5780
AGOF: DNA binding, DNA–directed RNA polymerase activity
AGOC: mitochondrion
AGOP: transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA–dependent





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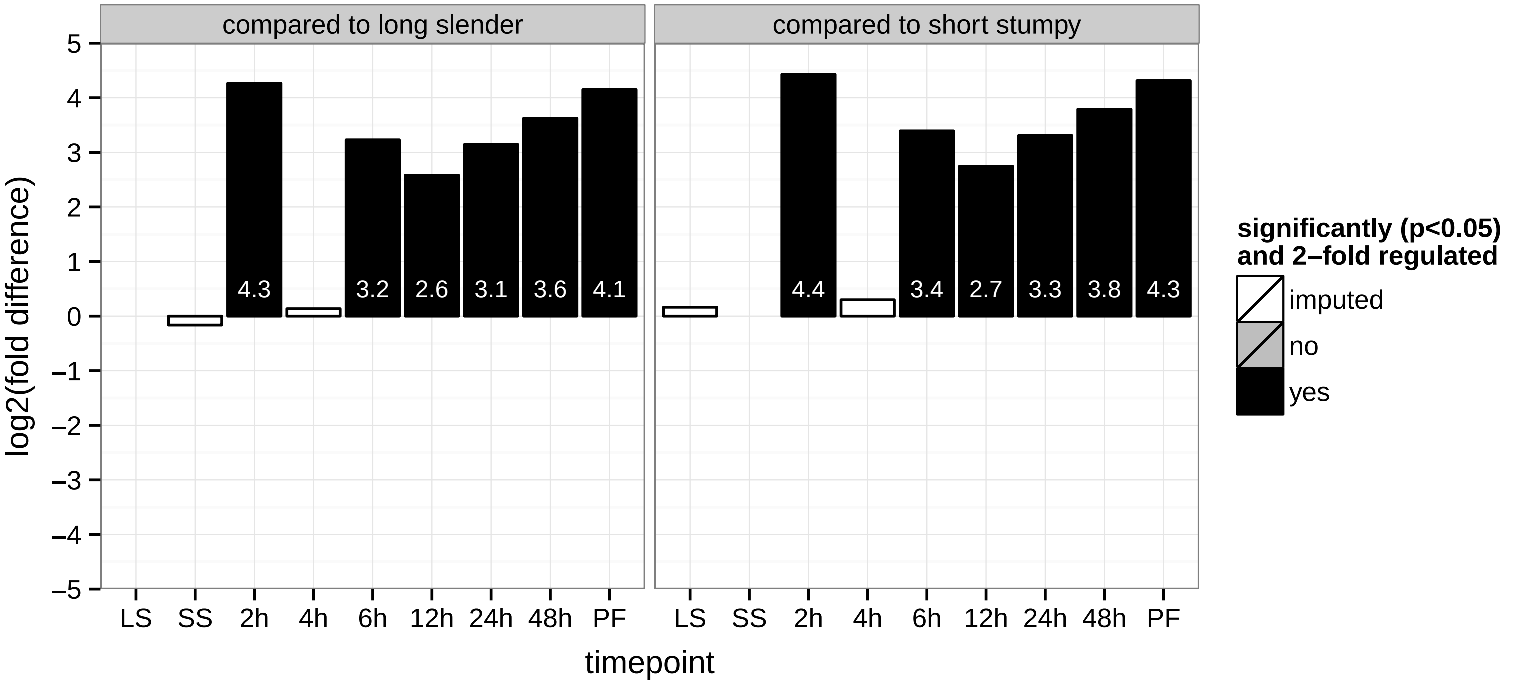
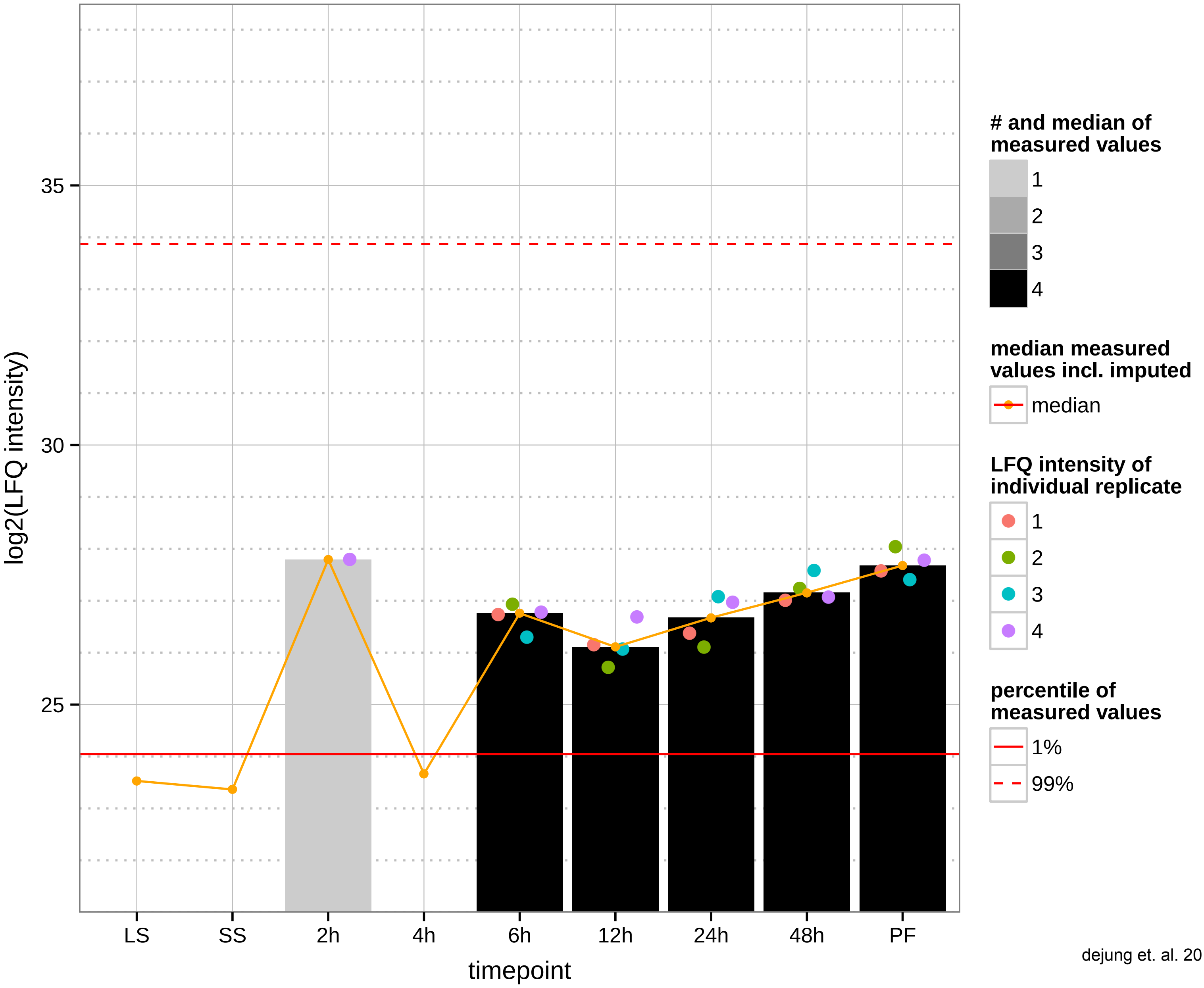
hypothetical protein, conserved
Tb927.2.2340
AGOF: glycerophosphodiester phosphodiesterase activity, phospholipase C activity
AGOC: null
AGOP: glycerol metabolic process, intracellular signal transduction, lipid metabolic process
PGOF: glycerophosphodiester phosphodiesterase activity, phospholipase C activity, phosphoric diester hydrolase activity
PGOC: null
PGOP: glycerol metabolic process, intracellular signal transduction, lipid metabolic process





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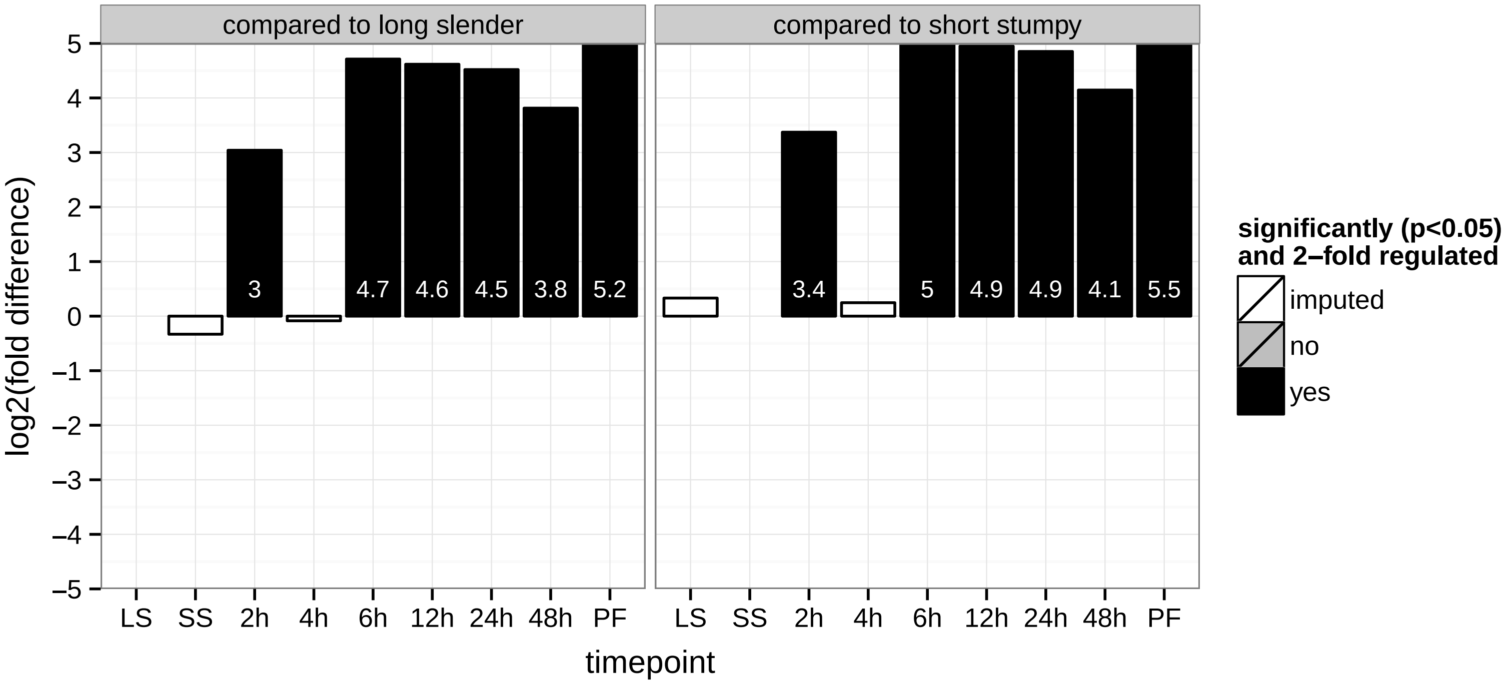
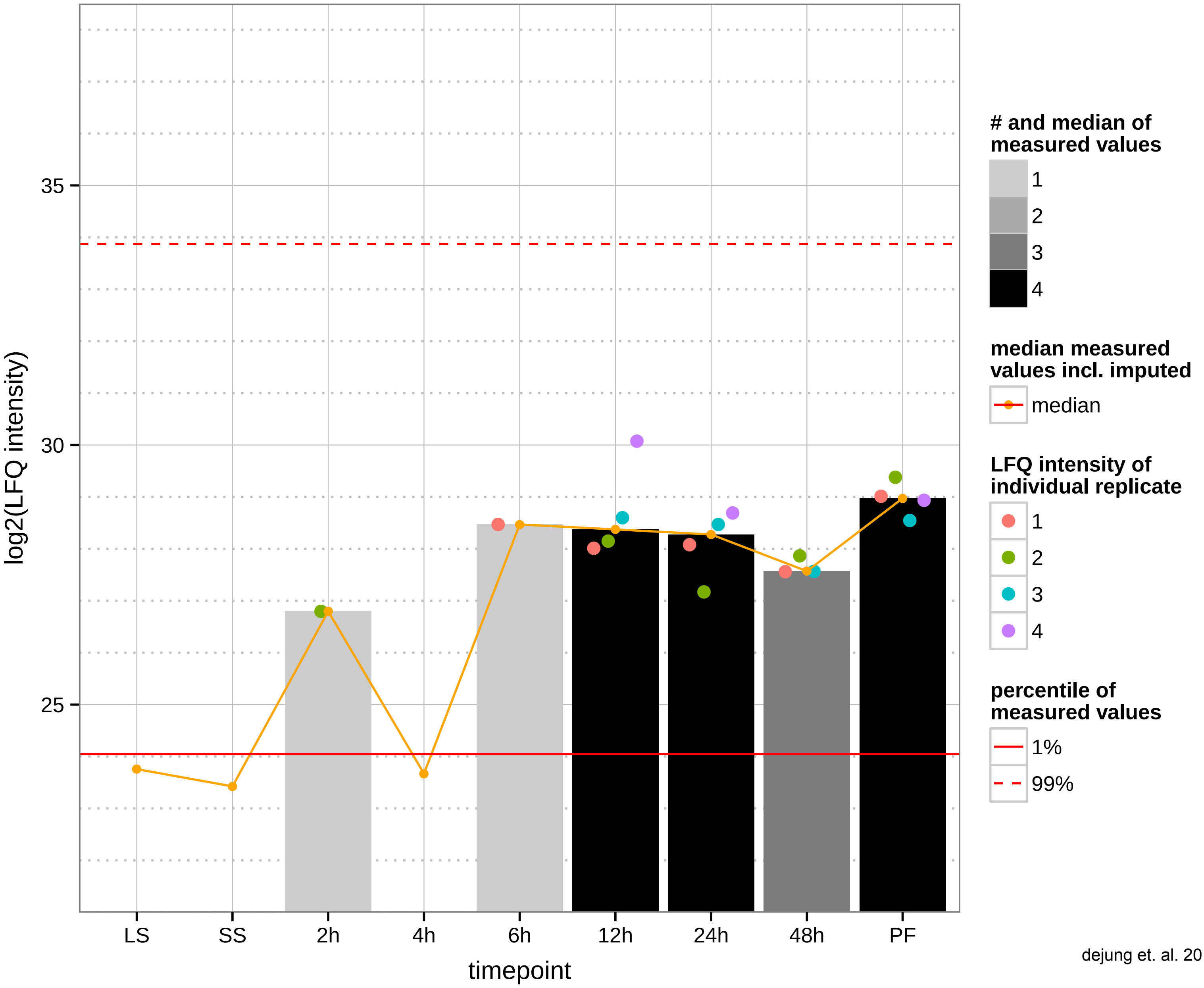
hypothetical protein, conserved
Tb927.4.3140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: ribosome biogenesis





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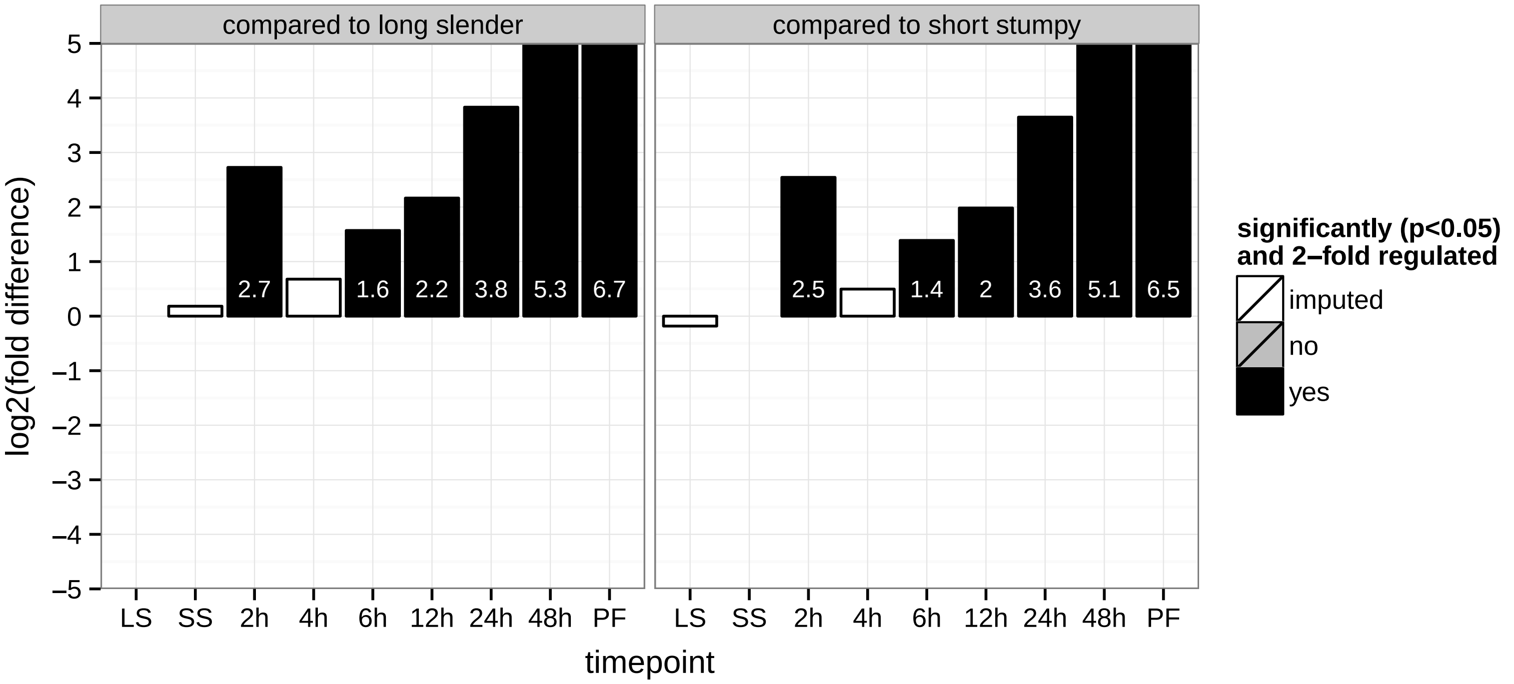
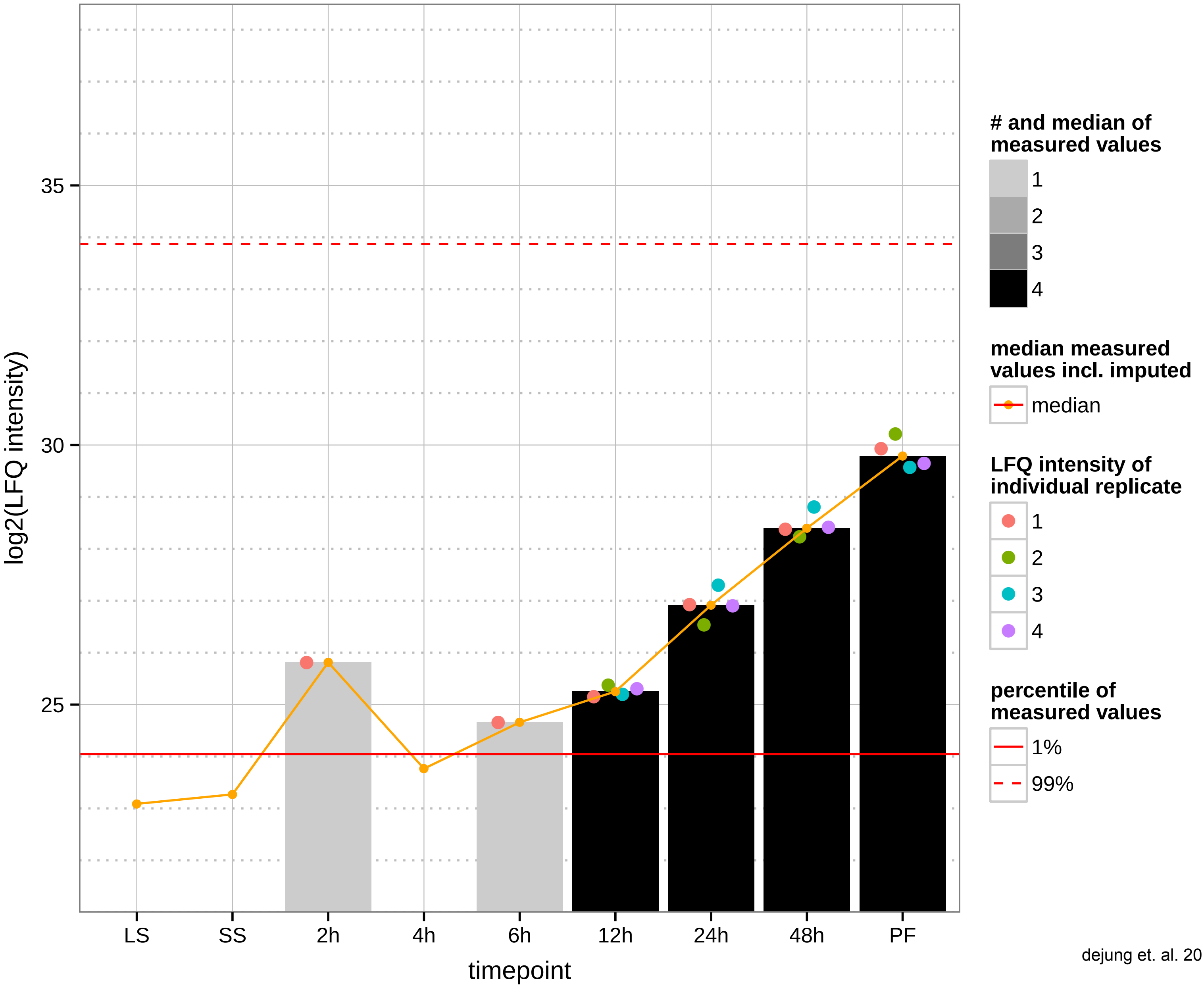
hypothetical protein, conserved, inositol 1, 4, 5–trisphosphate receptor (IP3R)
Tb927.8.2770
AGOF: null
AGOC: null, membrane
AGOP: null, ion transport
PGOF: binding, calcium channel activity, calcium channel activity, ion channel activity
PGOC: membrane
PGOP: calcium ion transmembrane transport, ion transport, transmembrane transport





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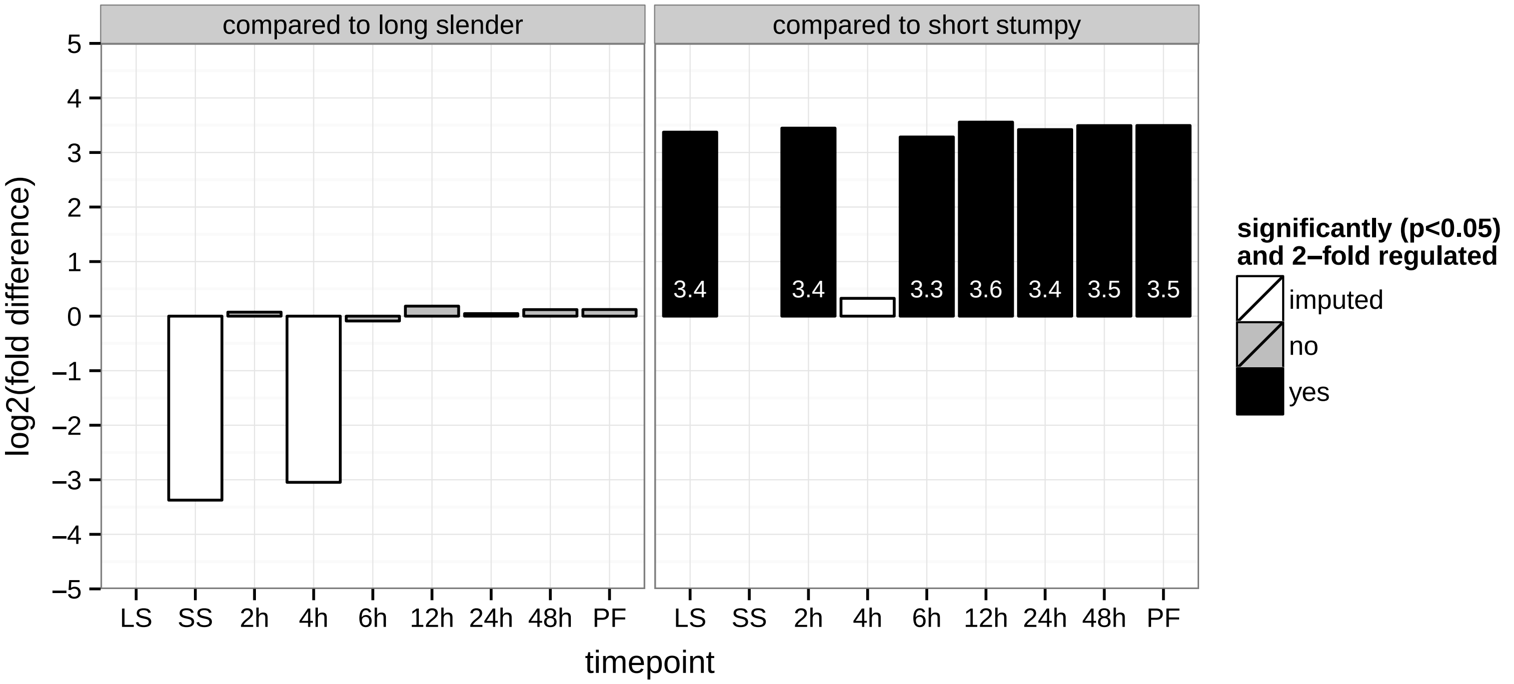
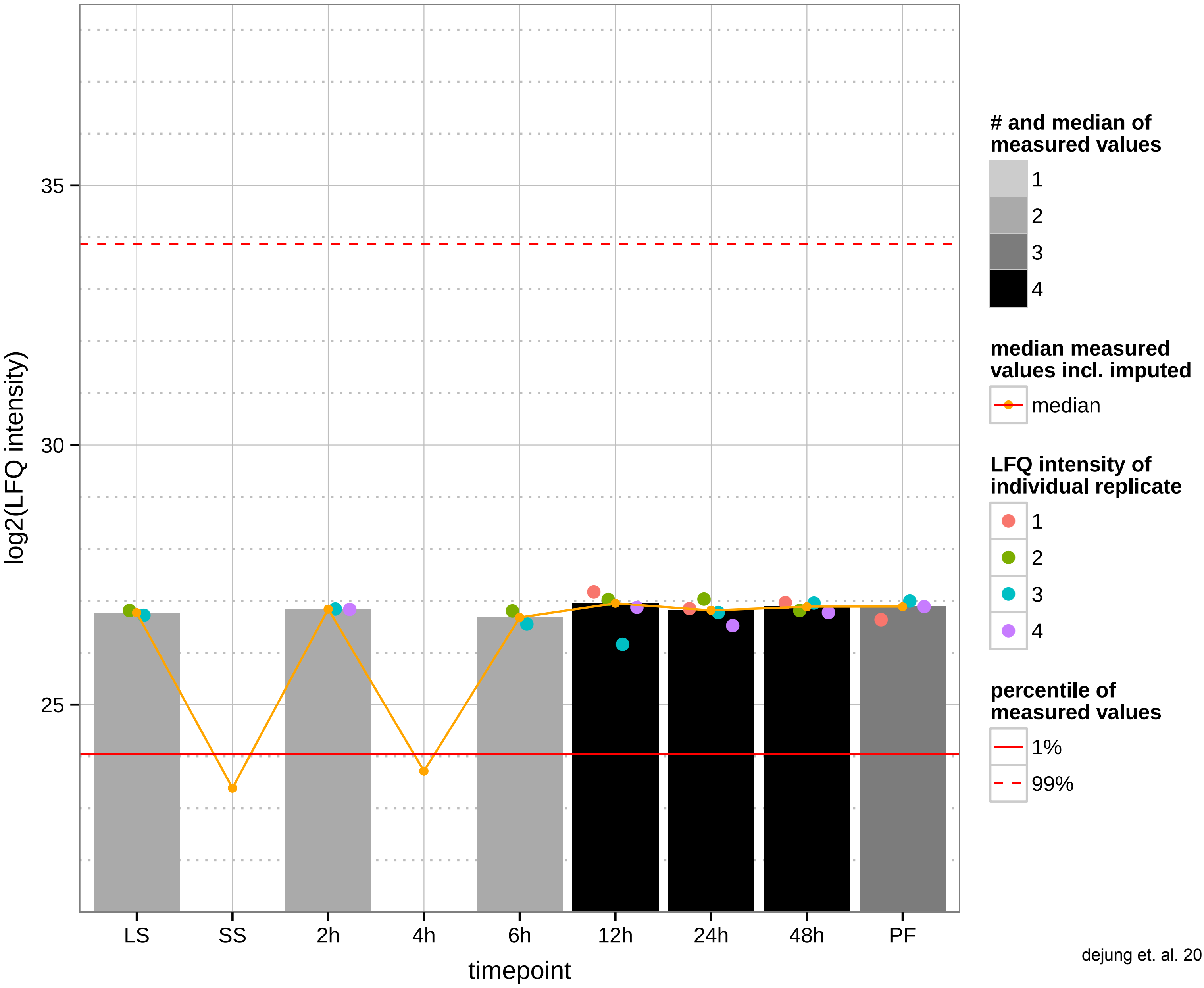
small nuclear ribonucleoprotein Sm–F (Sm–F)
Tb927.9.10250
AGOF: null
AGOC: nucleus, small nucleolar ribonucleoprotein complex
AGOP: mRNA processing, nuclear mRNA trans splicing, SL addition
PGOF: null
PGOC: null
PGOP: null





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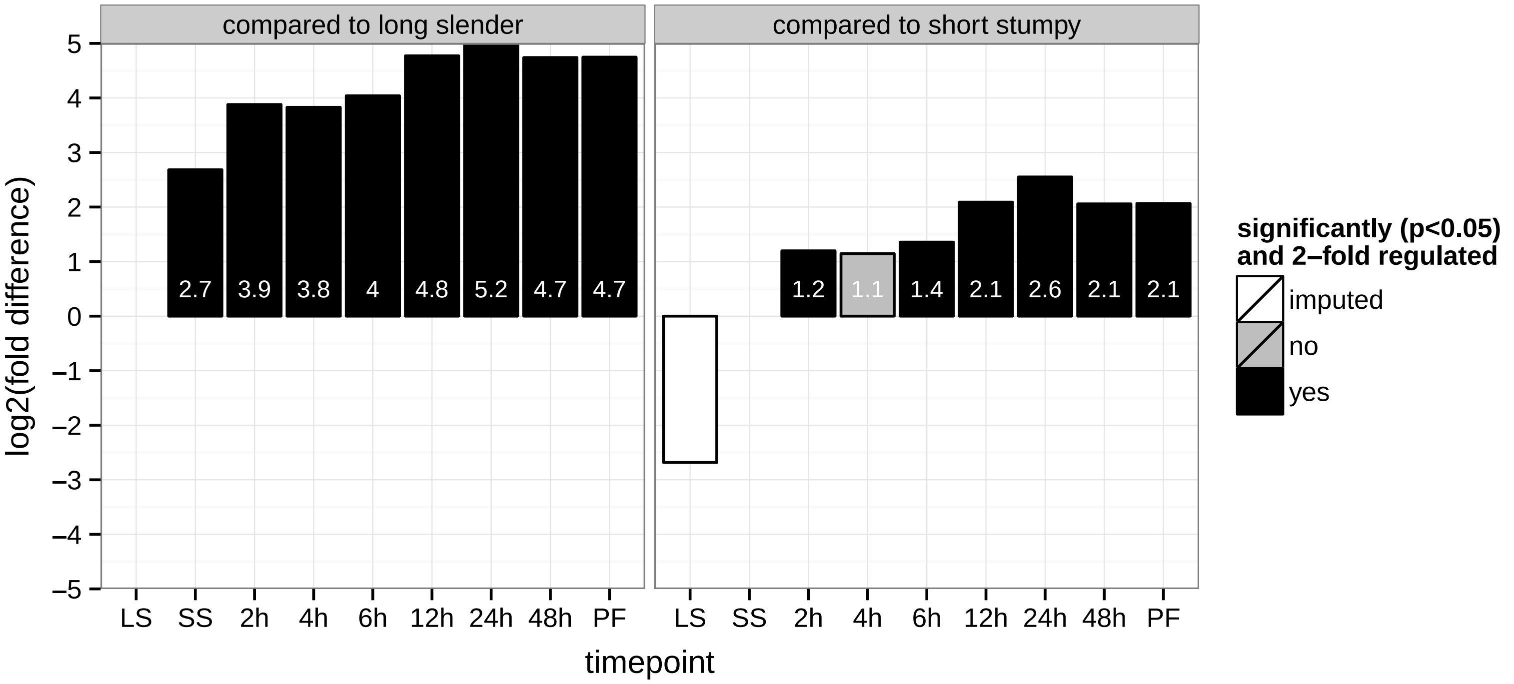
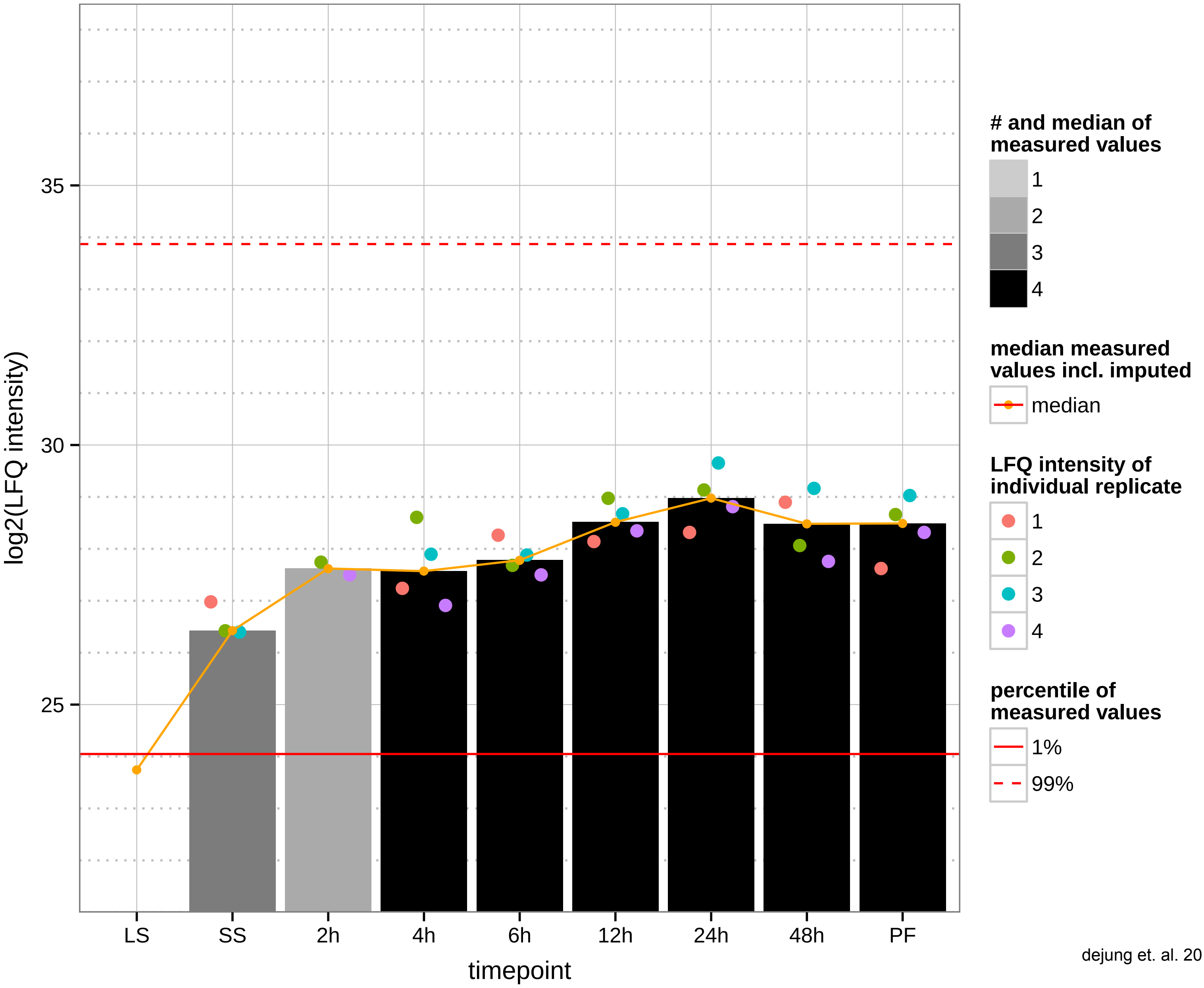
hypothetical protein, conserved
Tb927.9.10560
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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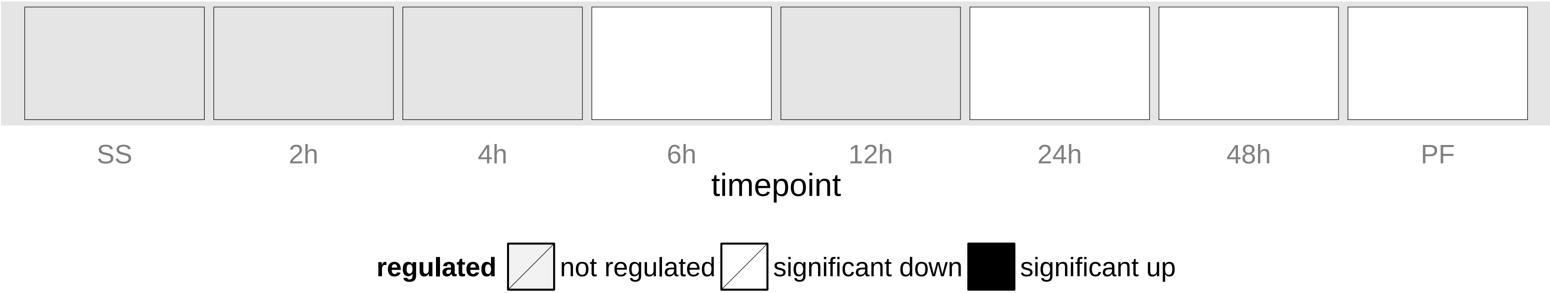

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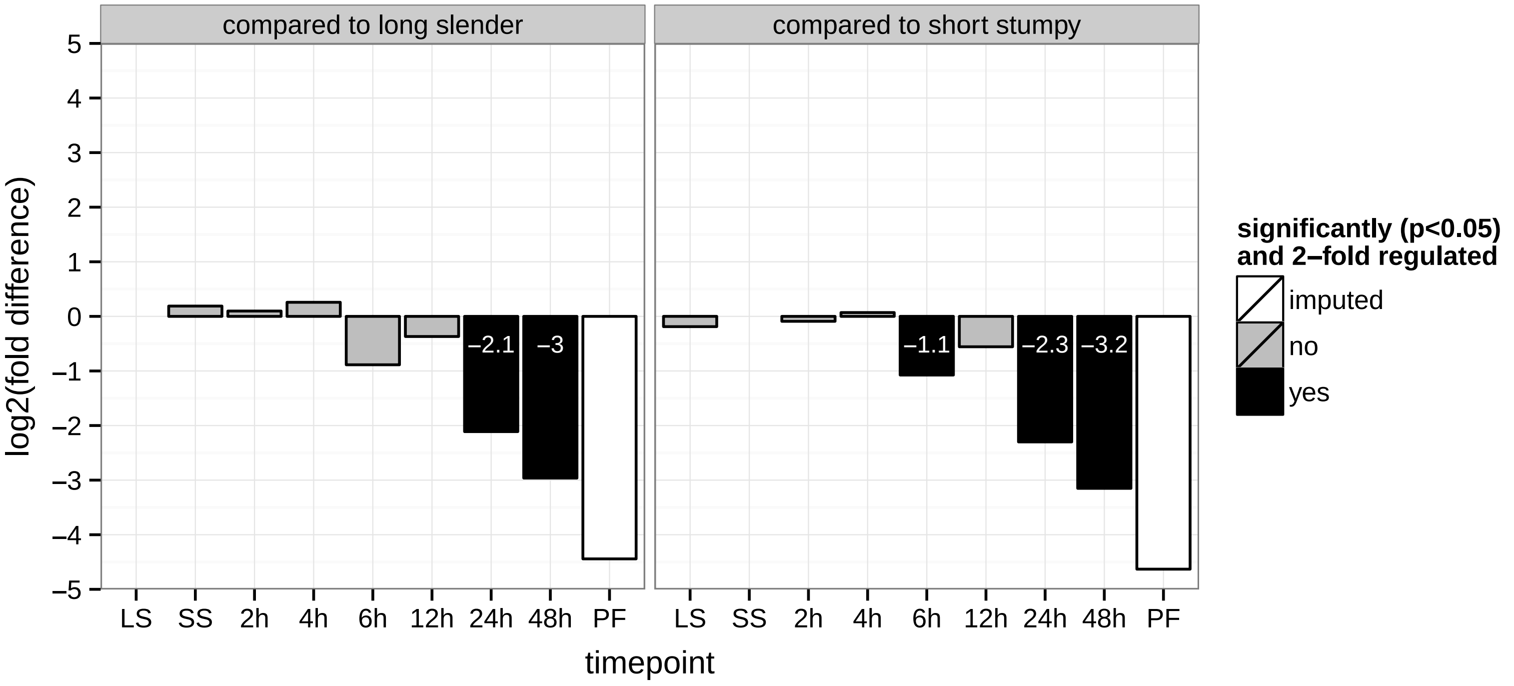
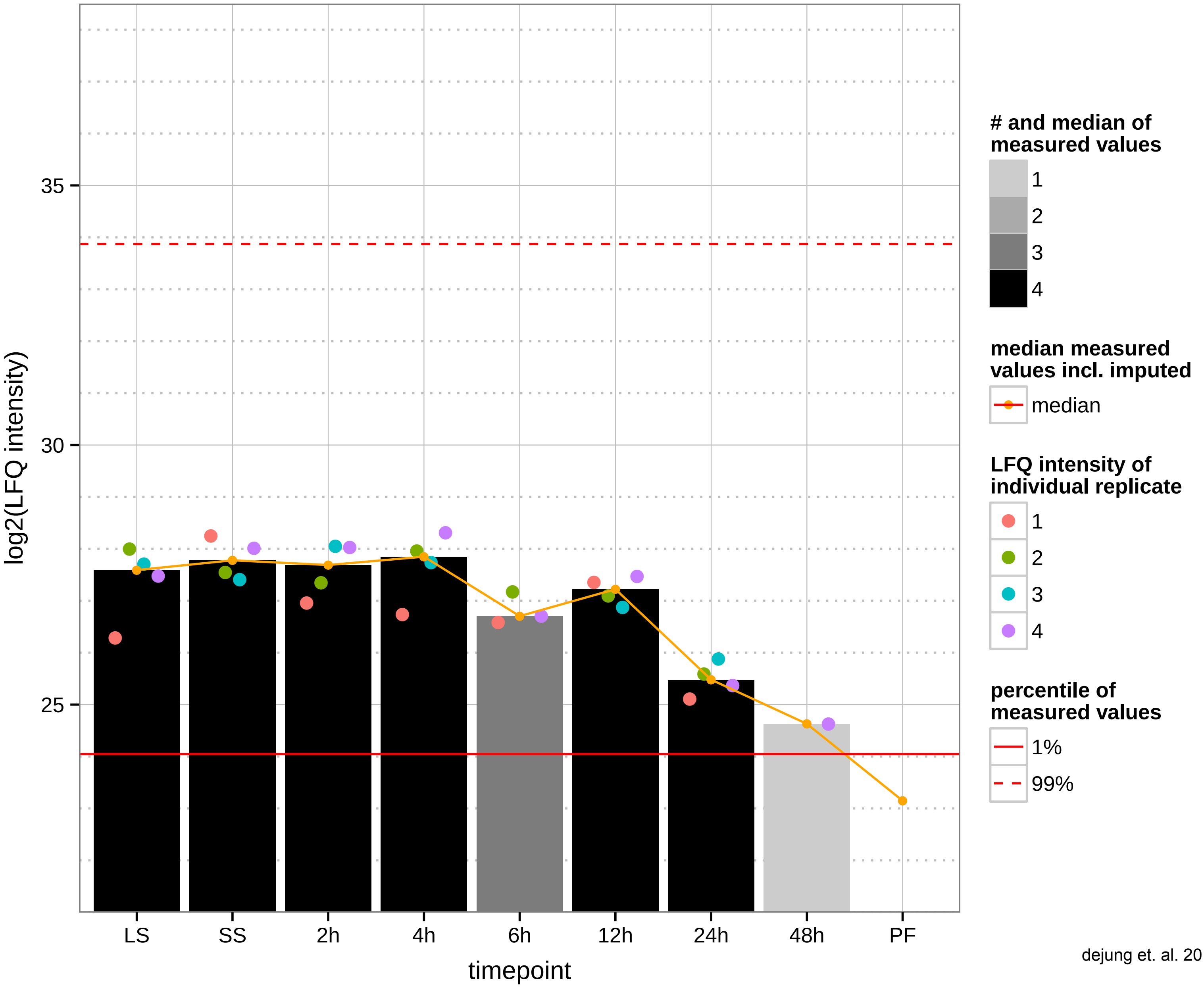
hypothetical protein, conserved
Tb927.5.309b;Tb11.v5.0216
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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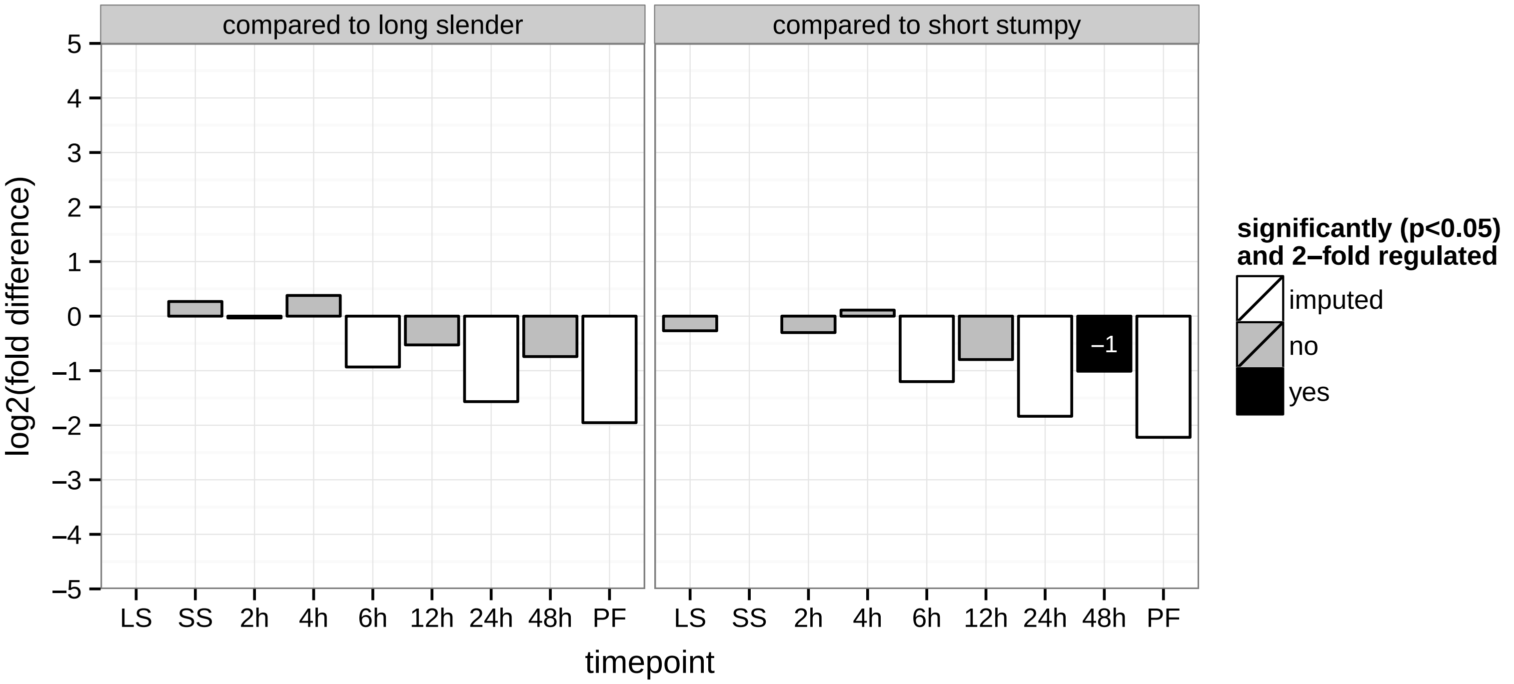
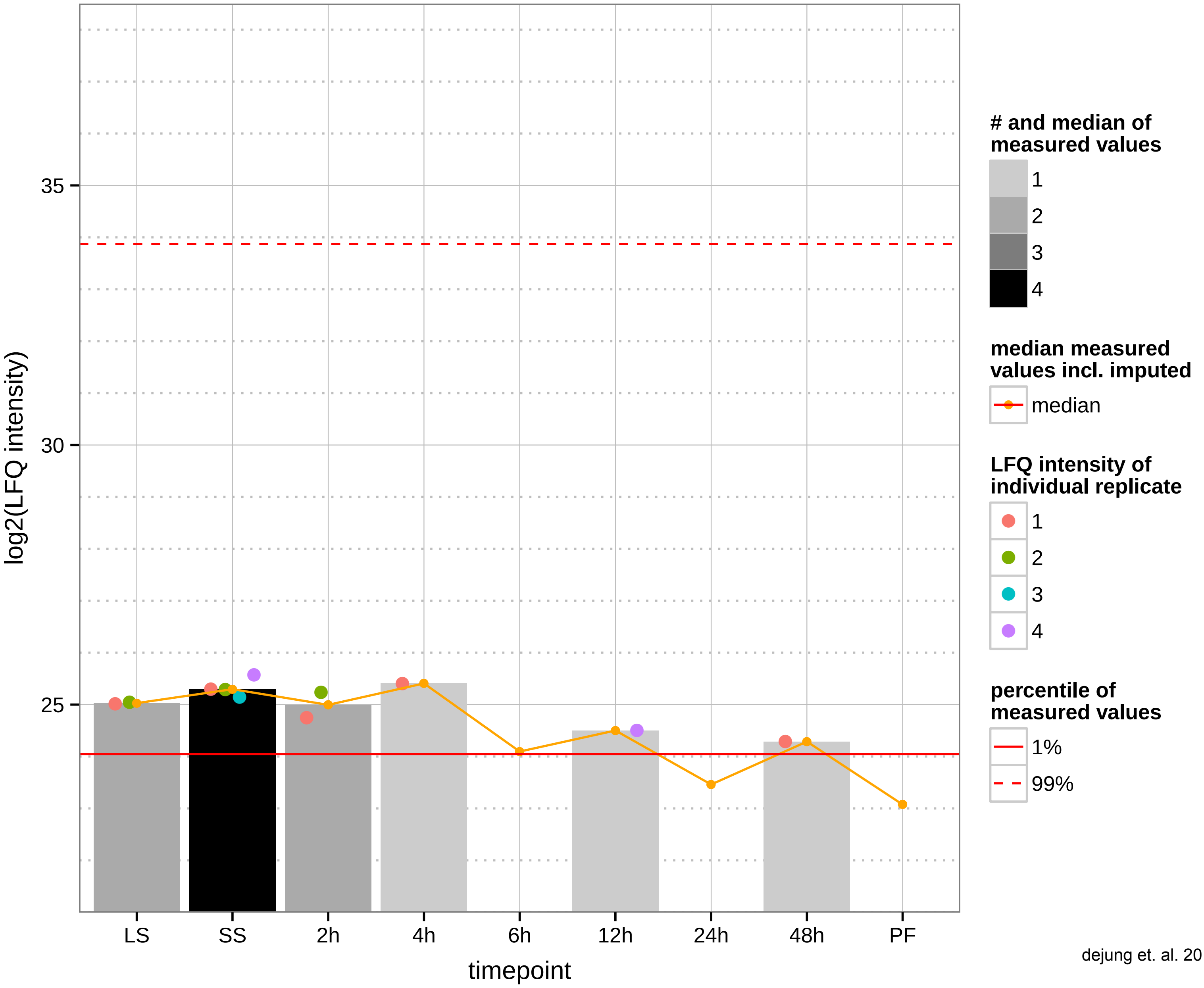
hypothetical protein, conserved
Tb927.10.10840
AGOF: null
AGOC: membrane
AGOP: null
PGOF: null
PGOC: membrane
PGOP: null





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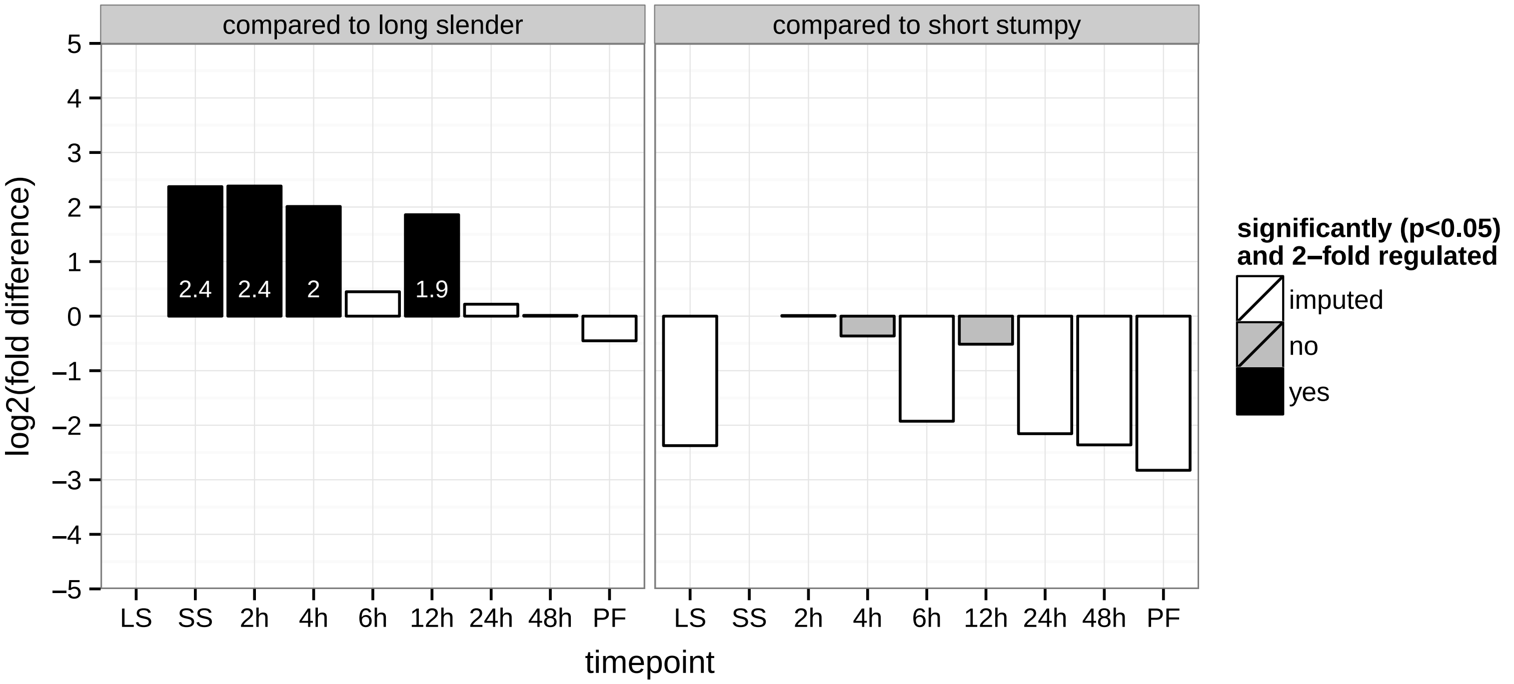
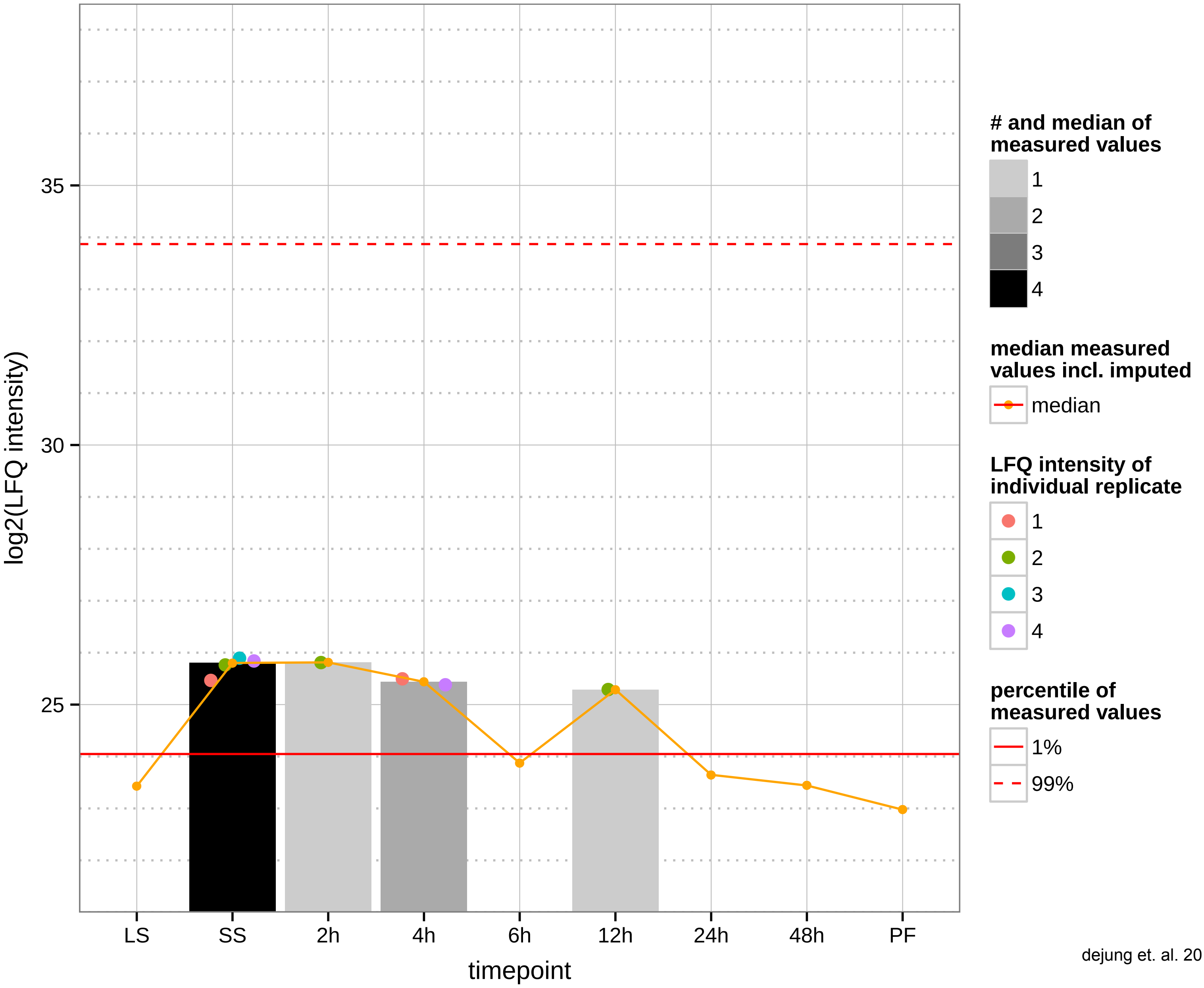
hypothetical protein, conserved
Tb927.10.3750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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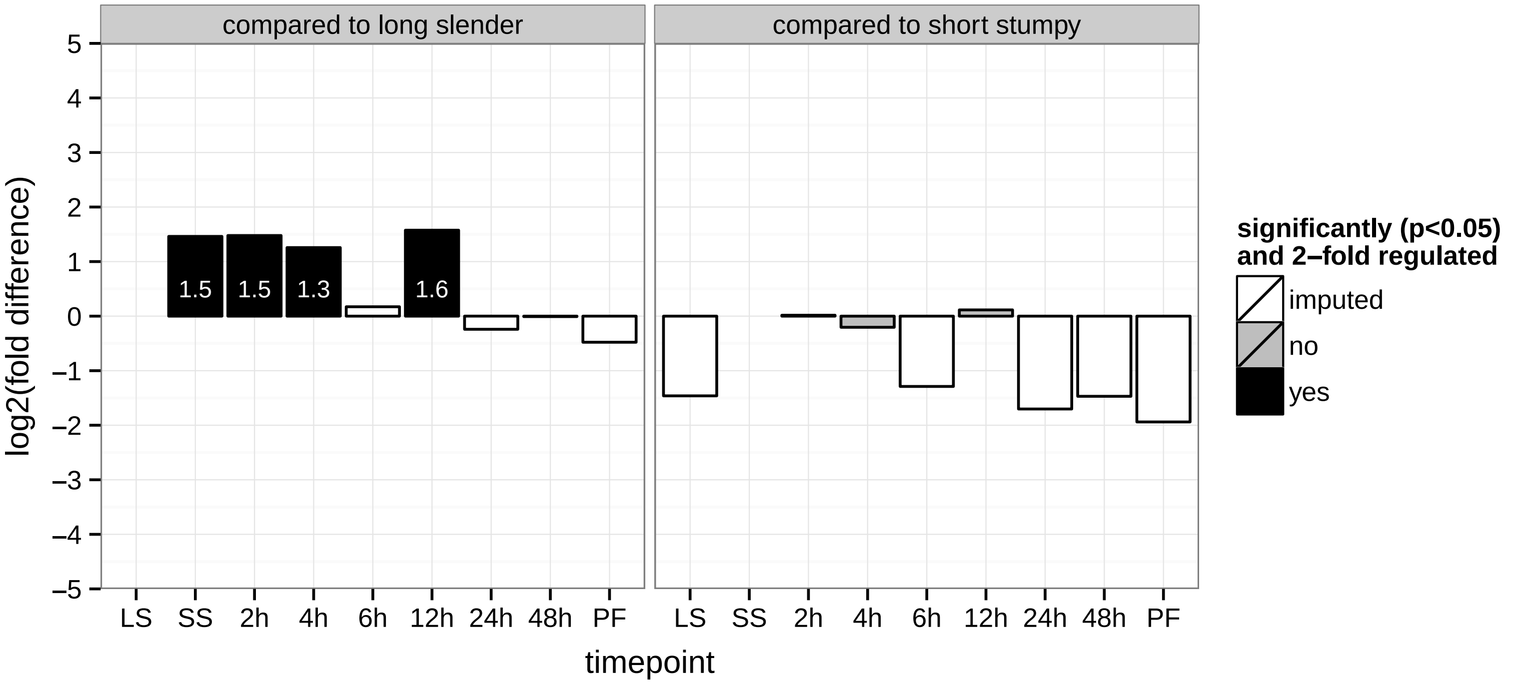
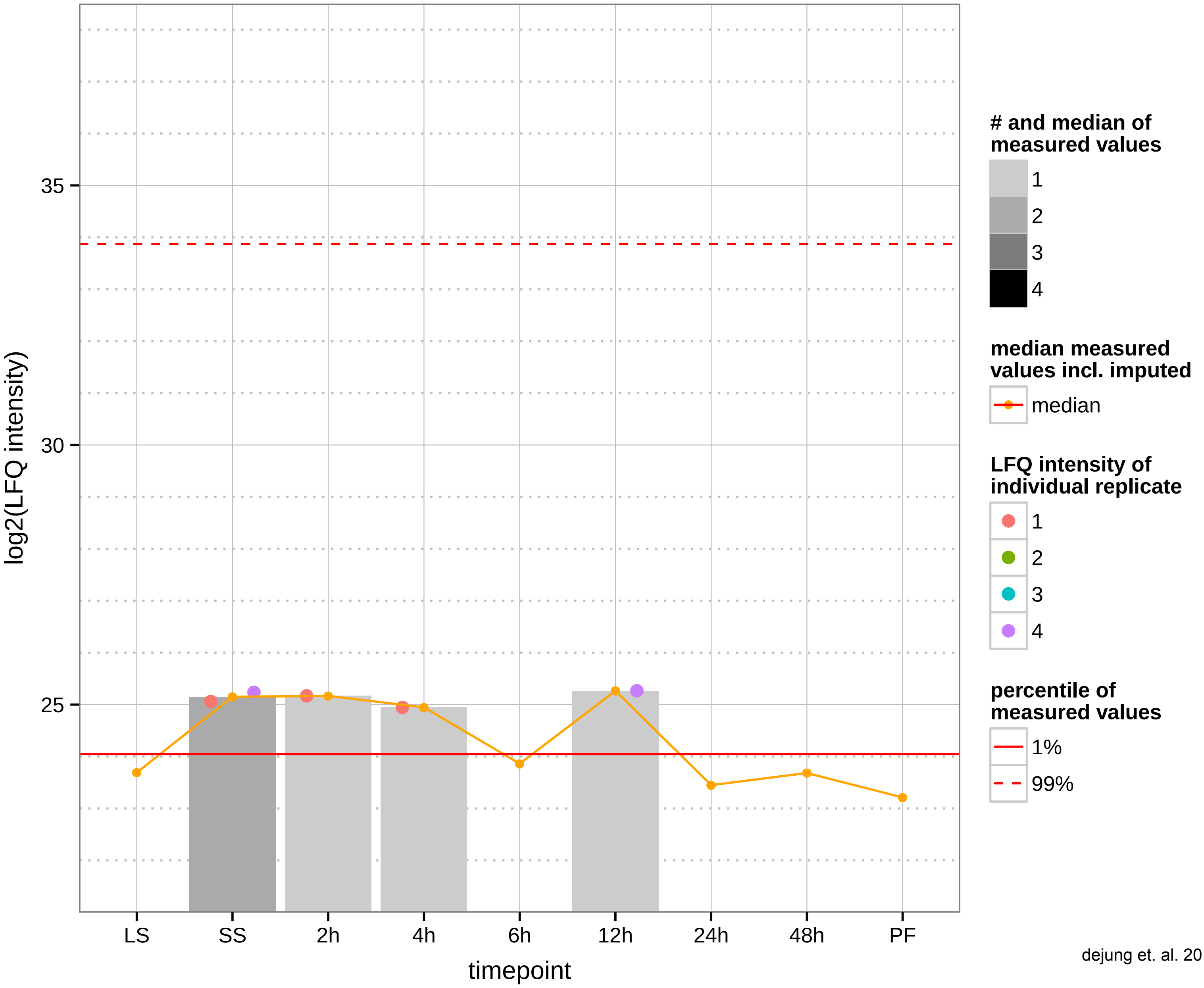
ras–like small GTPase, putative (TbRLJ)
Tb927.11.12950
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: protein transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, protein transport, signal transduction, small GTPase mediated signal transduction





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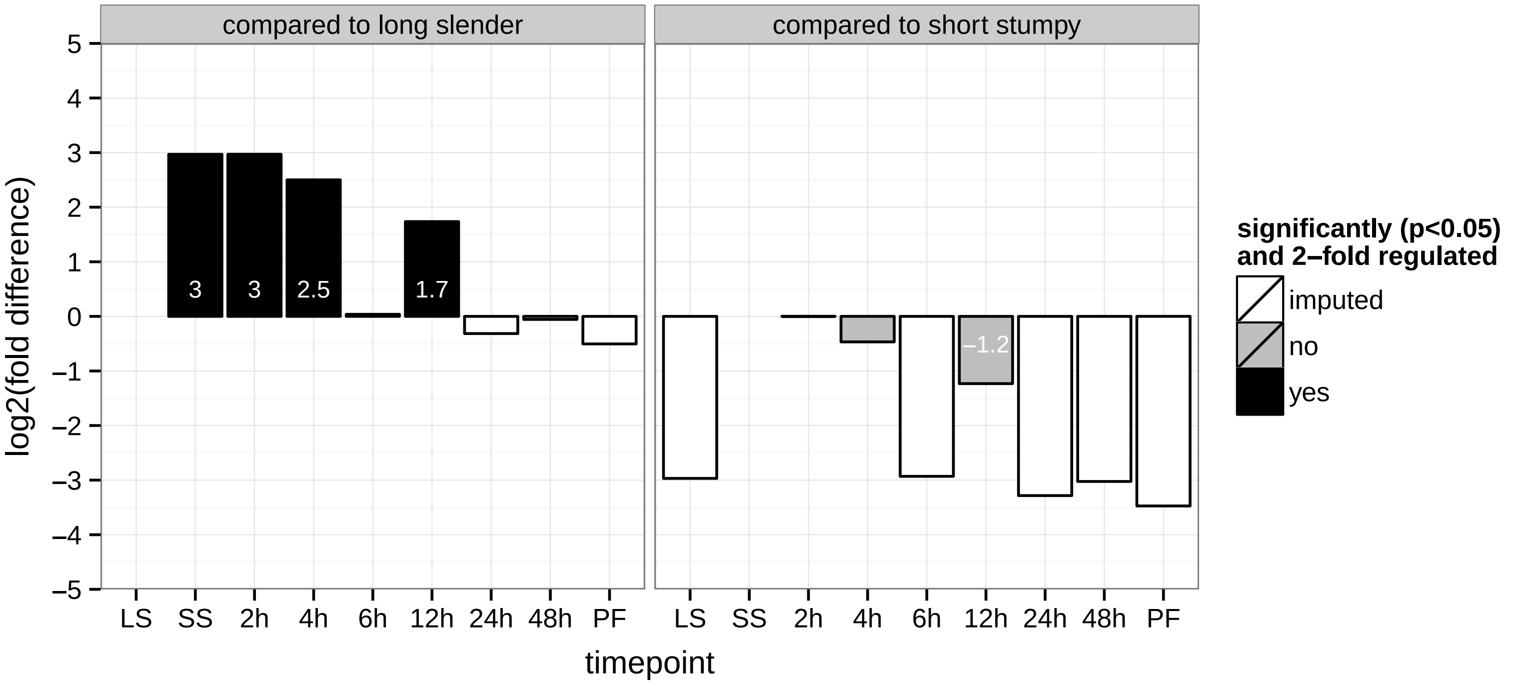
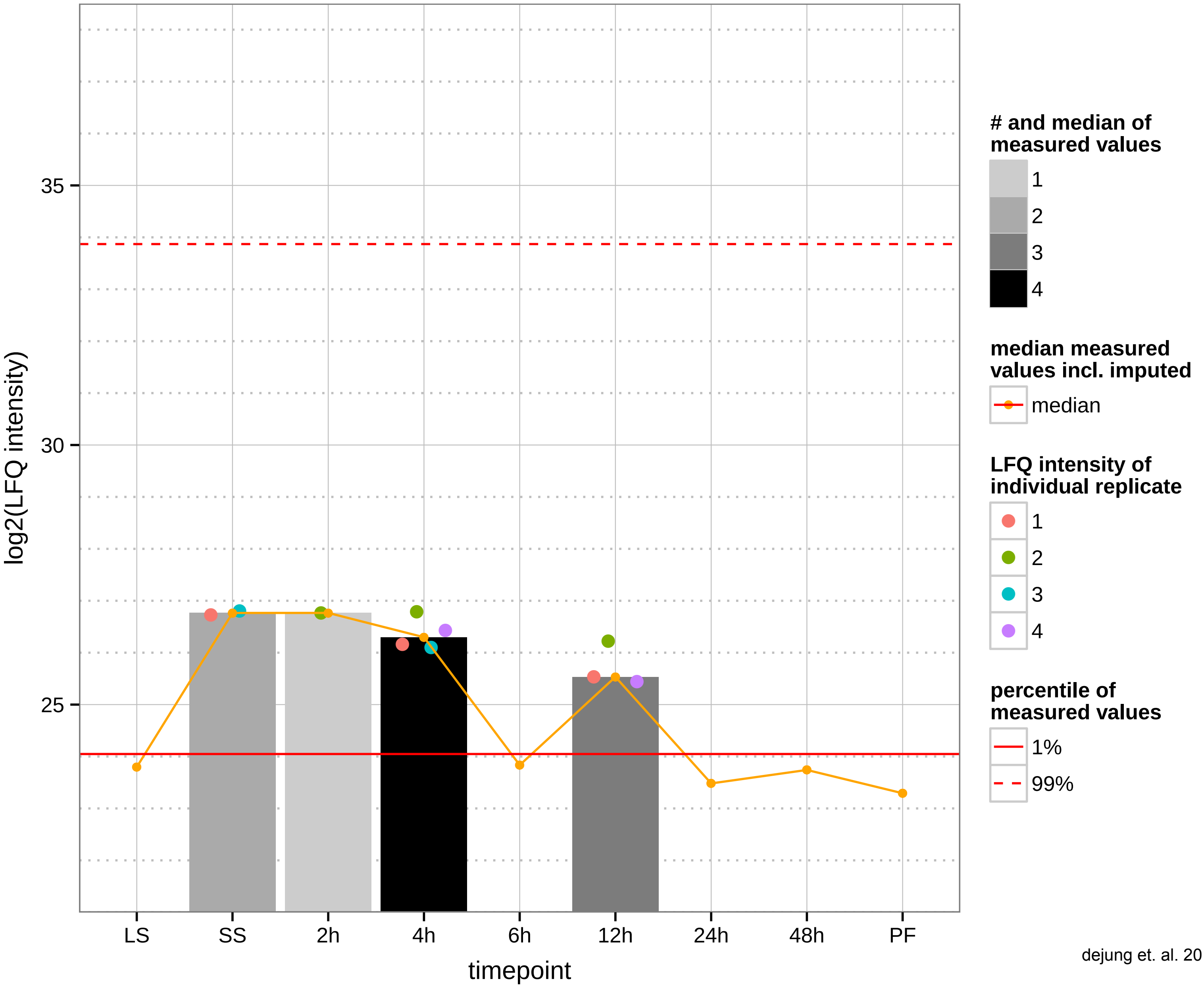
glutathionylspermidine synthetase, putative
Tb927.11.8820
AGOF: glutathionylspermidine synthase activity
AGOC: integral to membrane
AGOP: cellular biogenic amine metabolic process
PGOF: null
PGOC: null
PGOP: null





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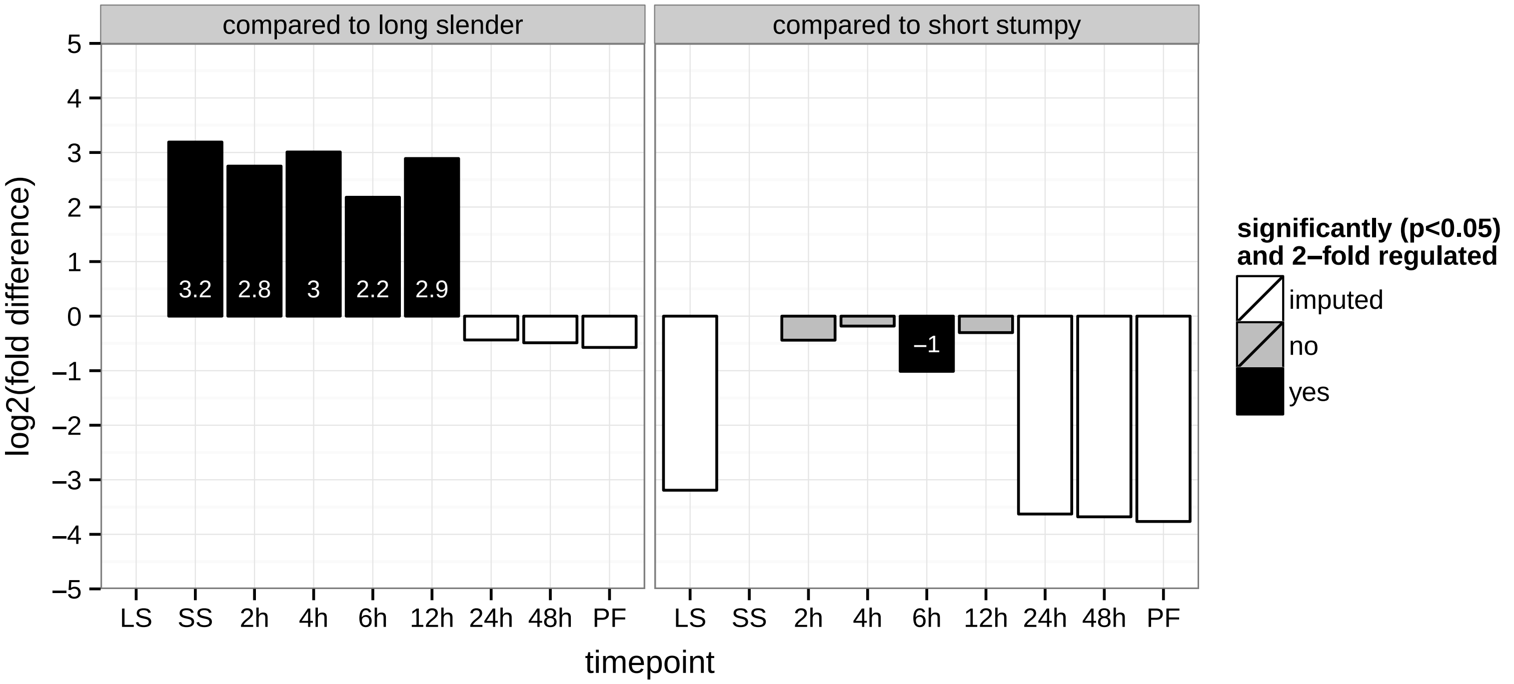
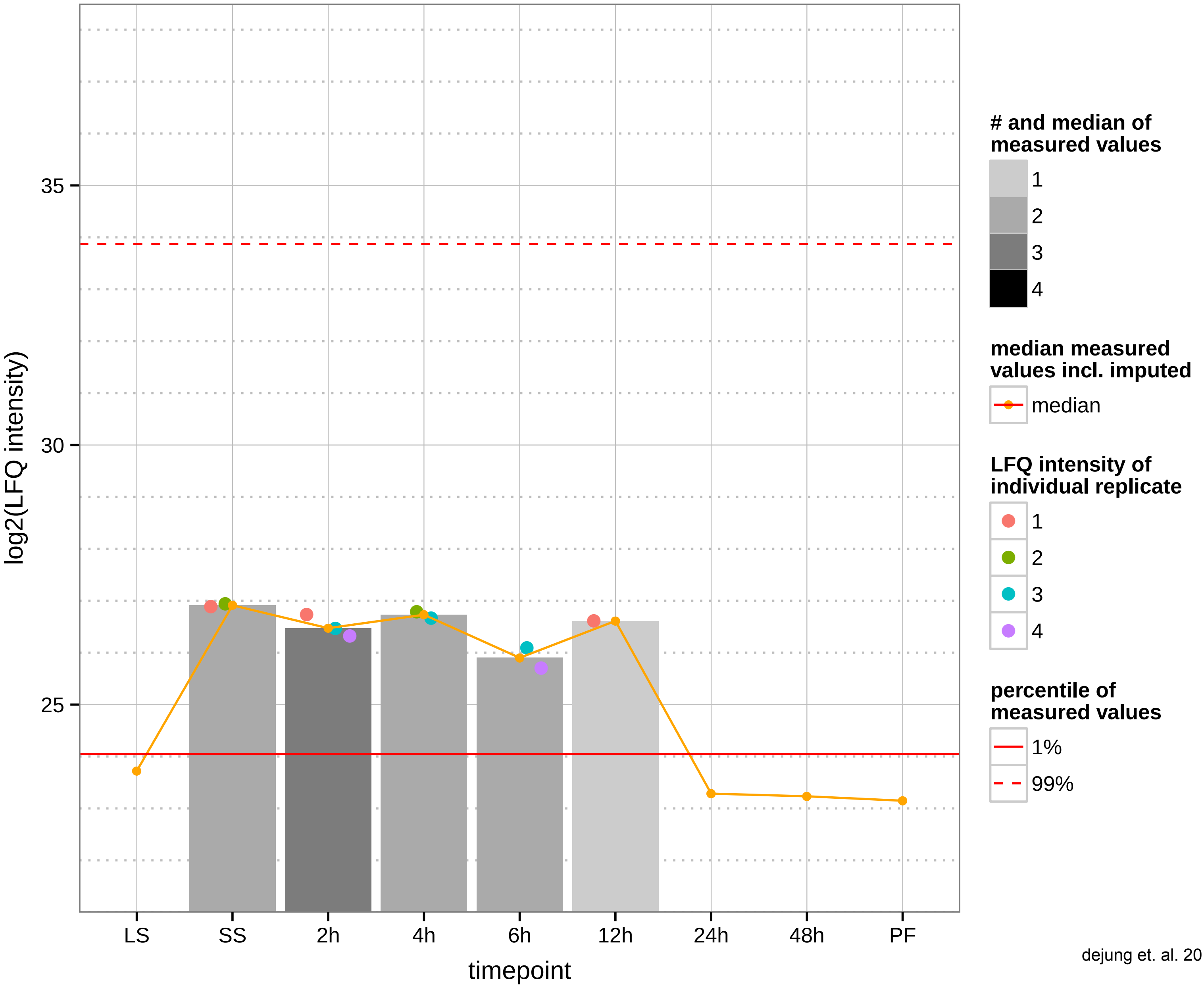
acylphosphatase, putative
Tb927.3.2030
AGOF: acylphosphatase activity
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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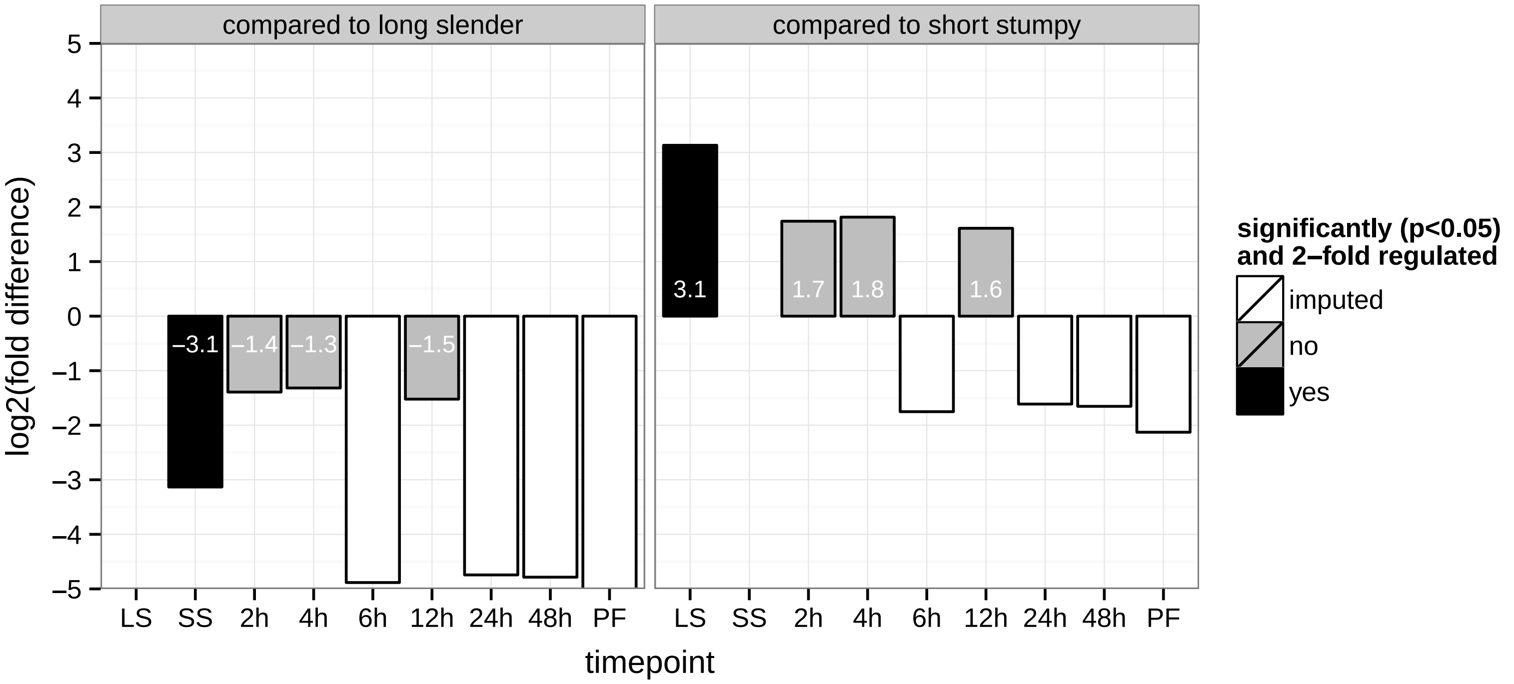
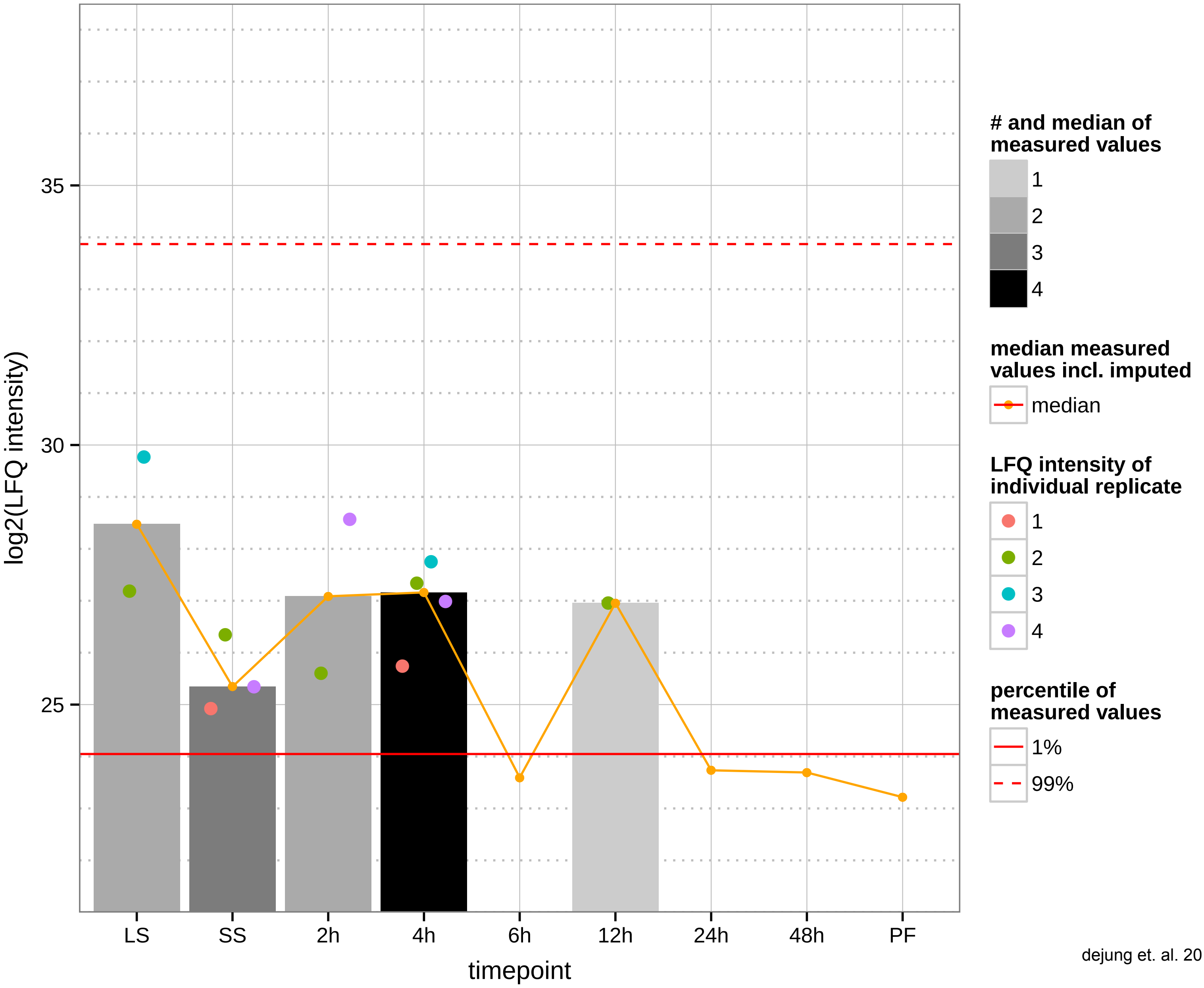
DNA–directed RNA polymerase III subunit, putative, DNA–directed rna polymerase II subunit, putative (RPB6), DNA–directed
Tb927.4.3510;Tb927.4.3490
AGOF: DNA binding, DNA–directed RNA polymerase activity
AGOC: null
AGOP: transcription, DNA–dependent
PGOF: DNA binding, DNA–directed RNA polymerase activity
PGOC: null
PGOP: transcription, DNA–dependent





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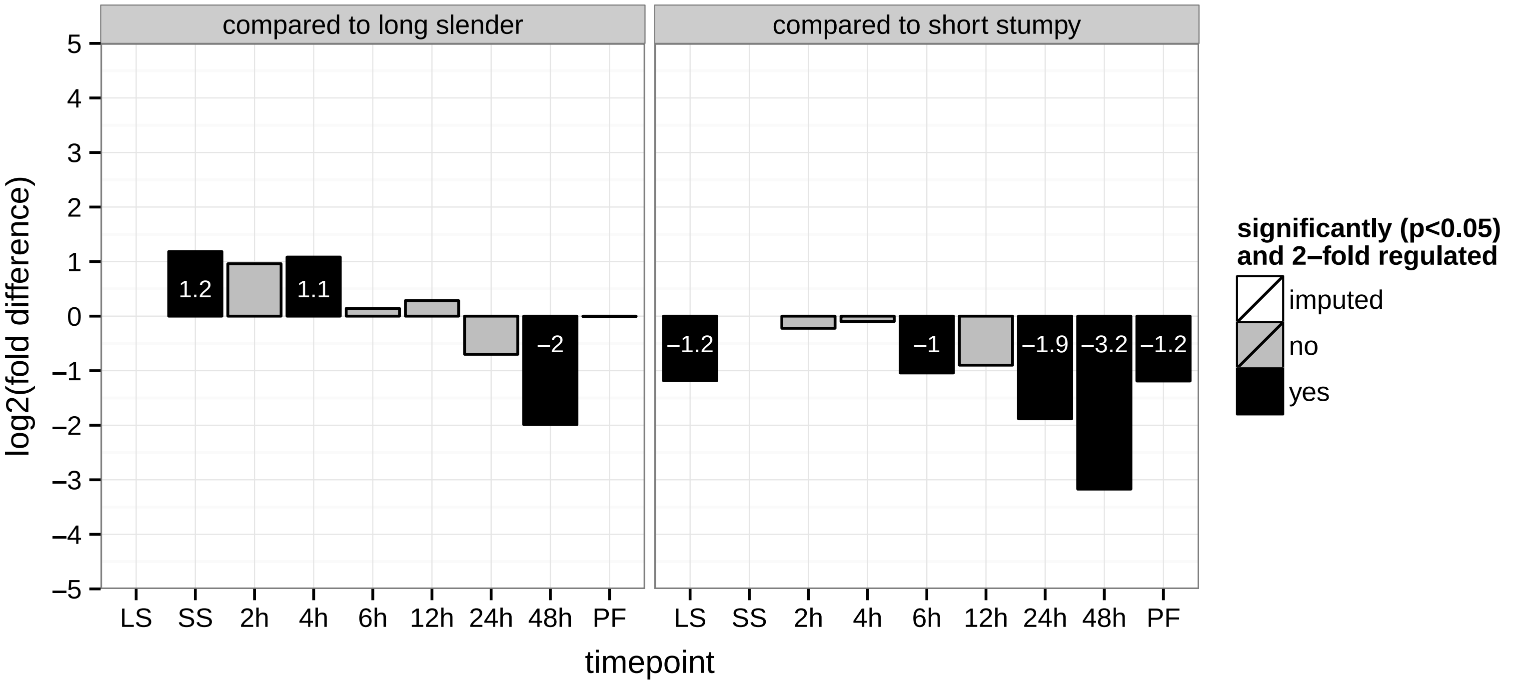
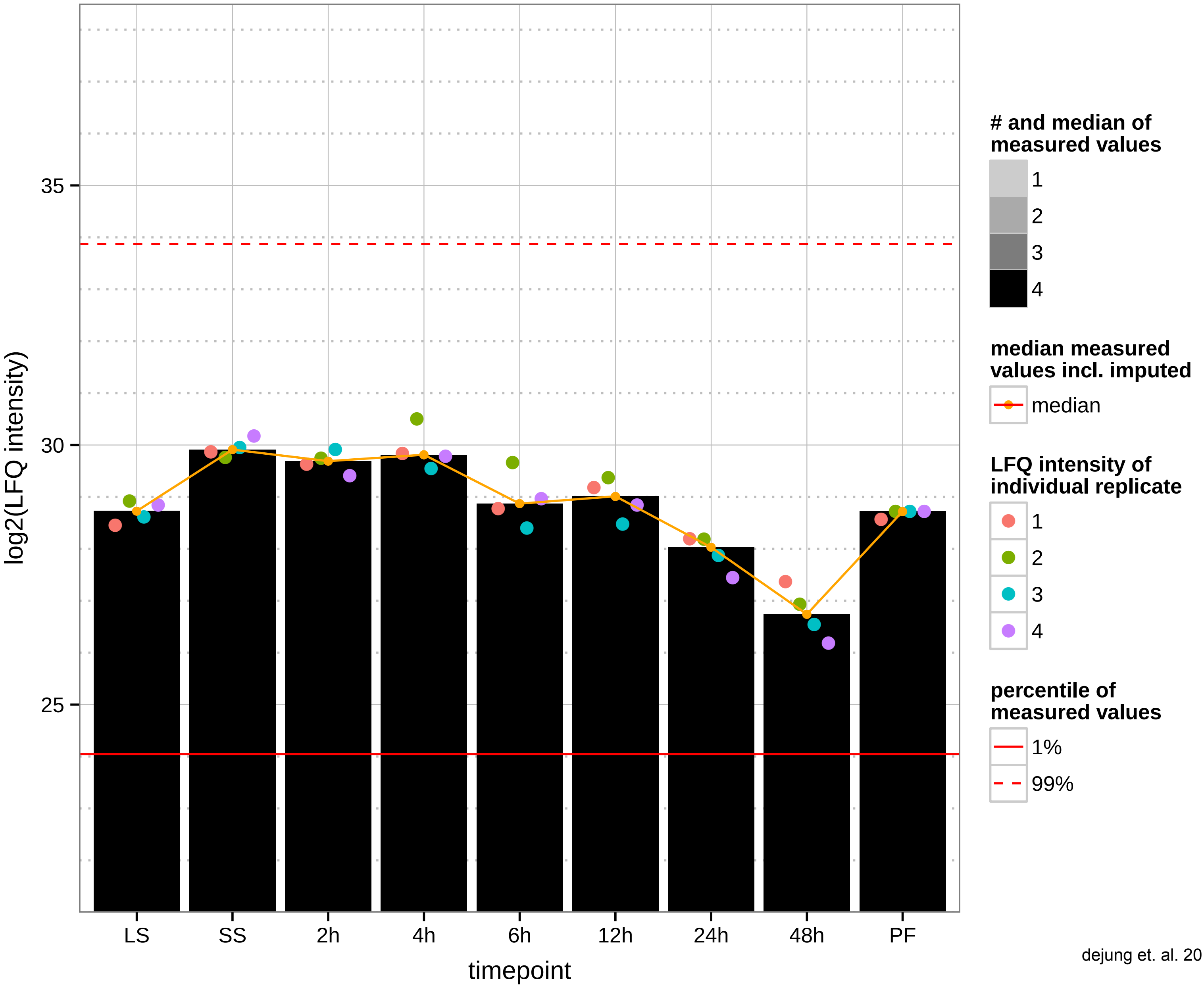
hypothetical protein, conserved
Tb927.6.3940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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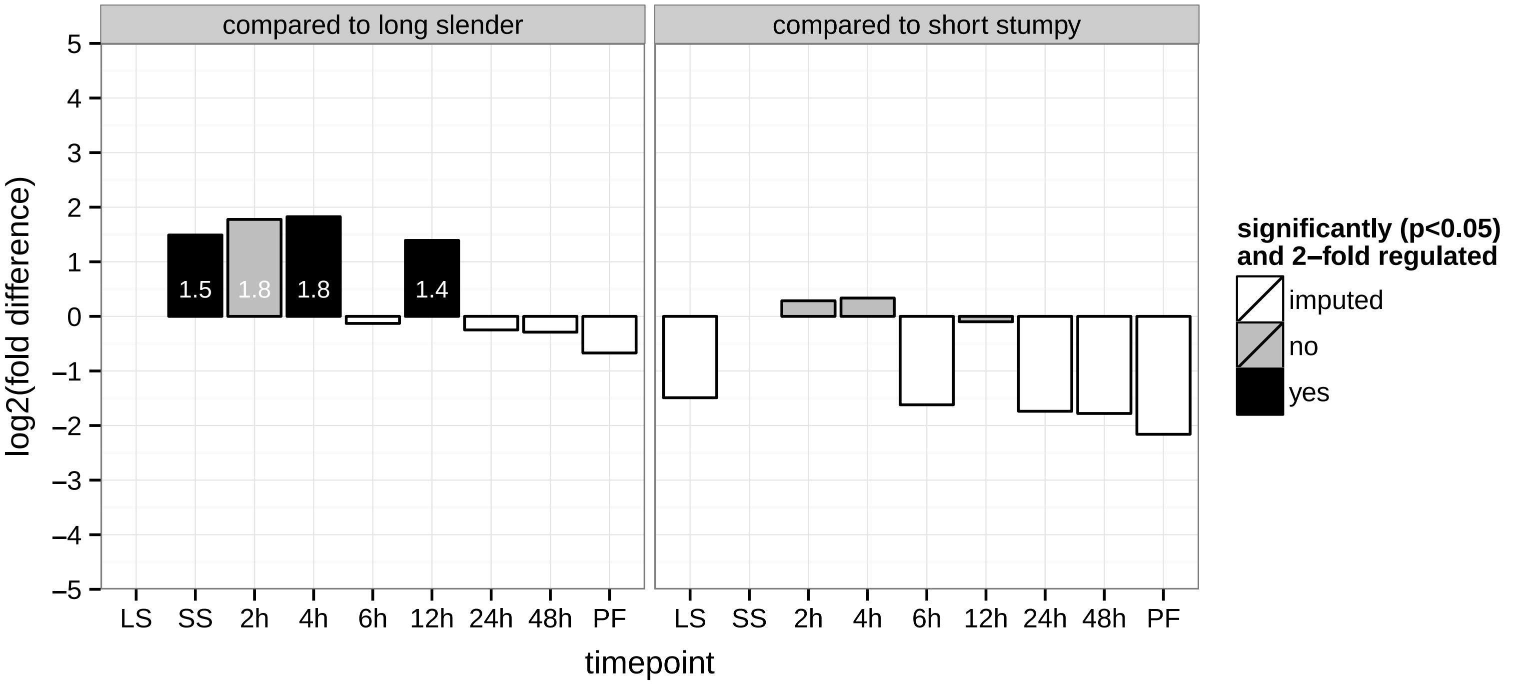
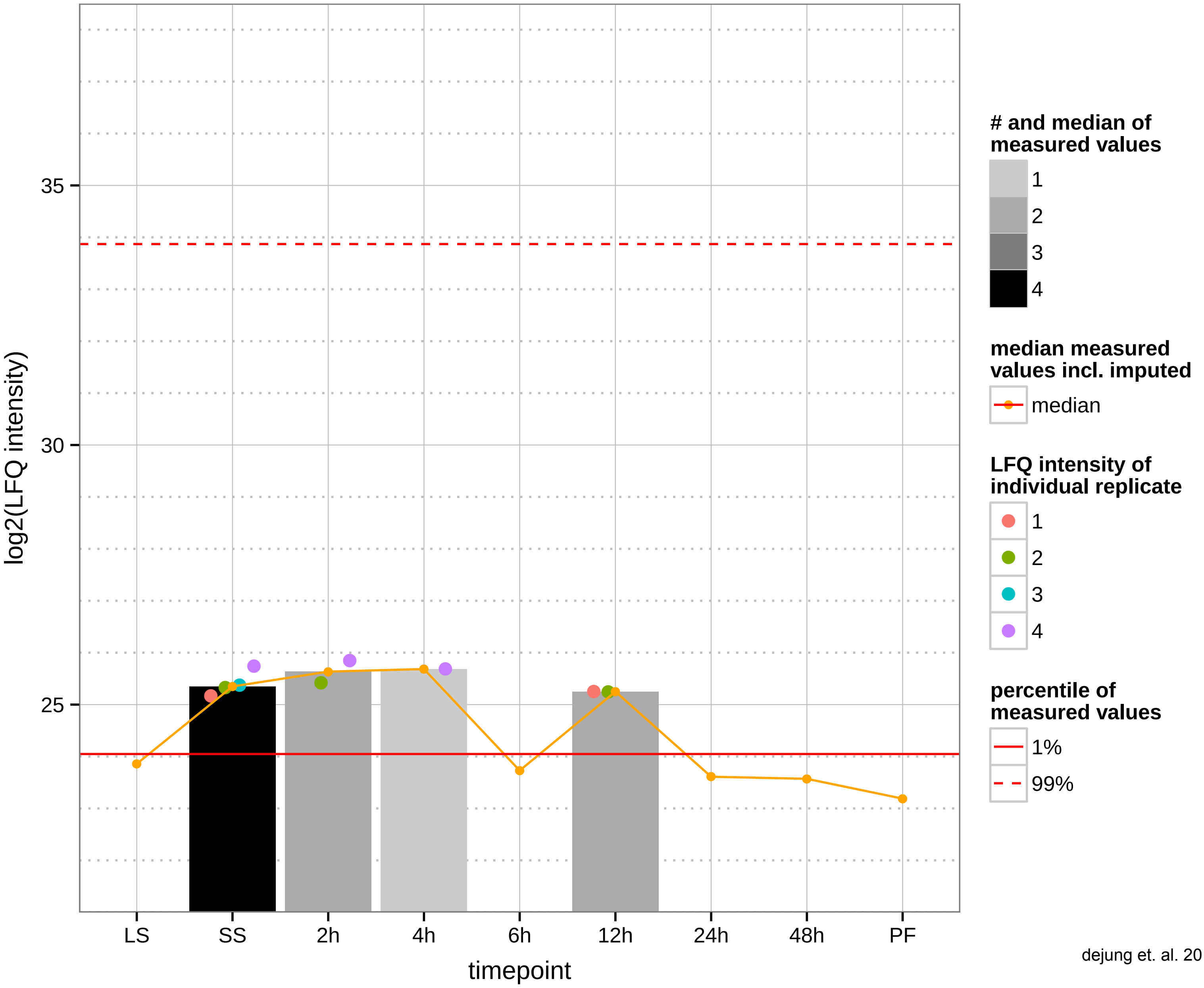
diacylglycerol kinase, putative
Tb927.8.5140
AGOF: diacylglycerol kinase activity
AGOC: cytosol, mitochondrion
AGOP: fatty acid oxidation, protein kinase C–activating G–protein coupled receptor signaling pathway
PGOF: NAD+ kinase activity, diacylglycerol kinase activity
PGOC: null
PGOP: metabolic process, protein kinase C–activating G–protein coupled receptor signaling pathway





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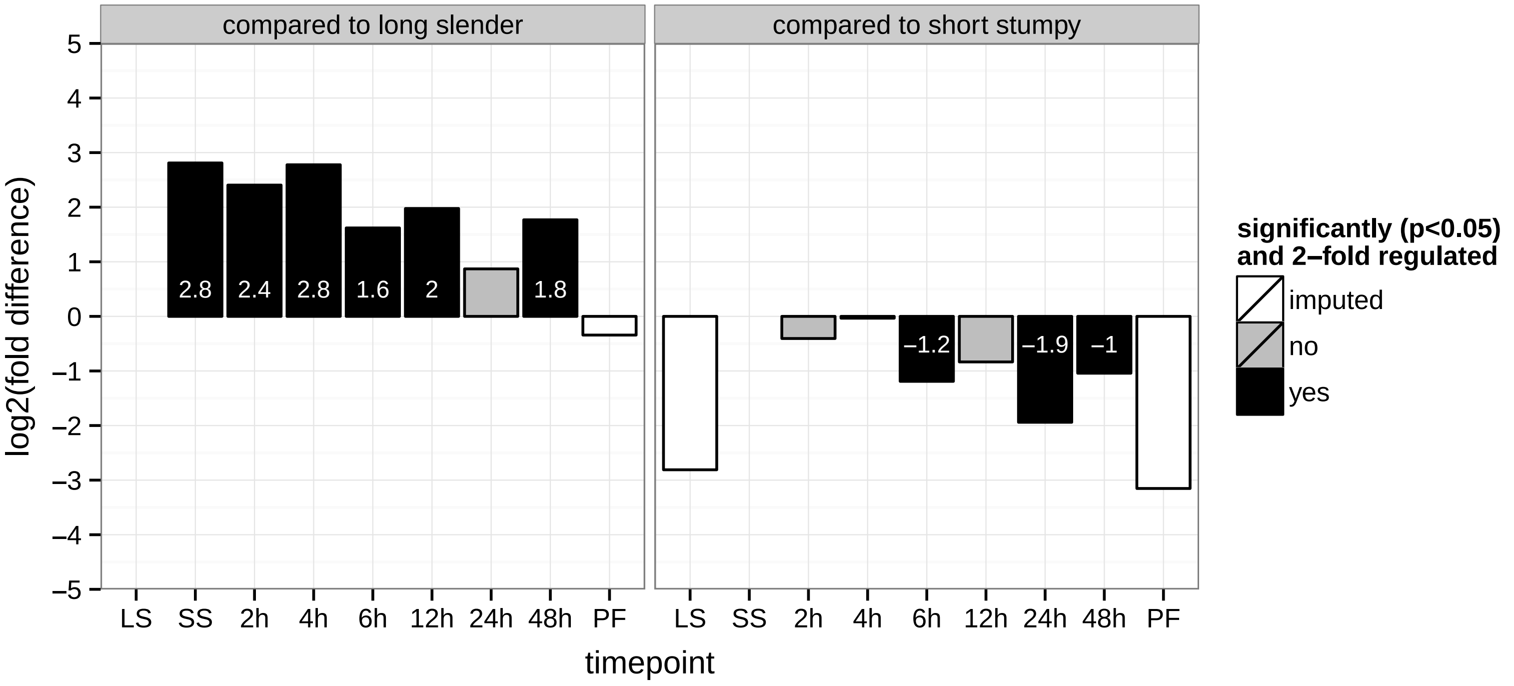
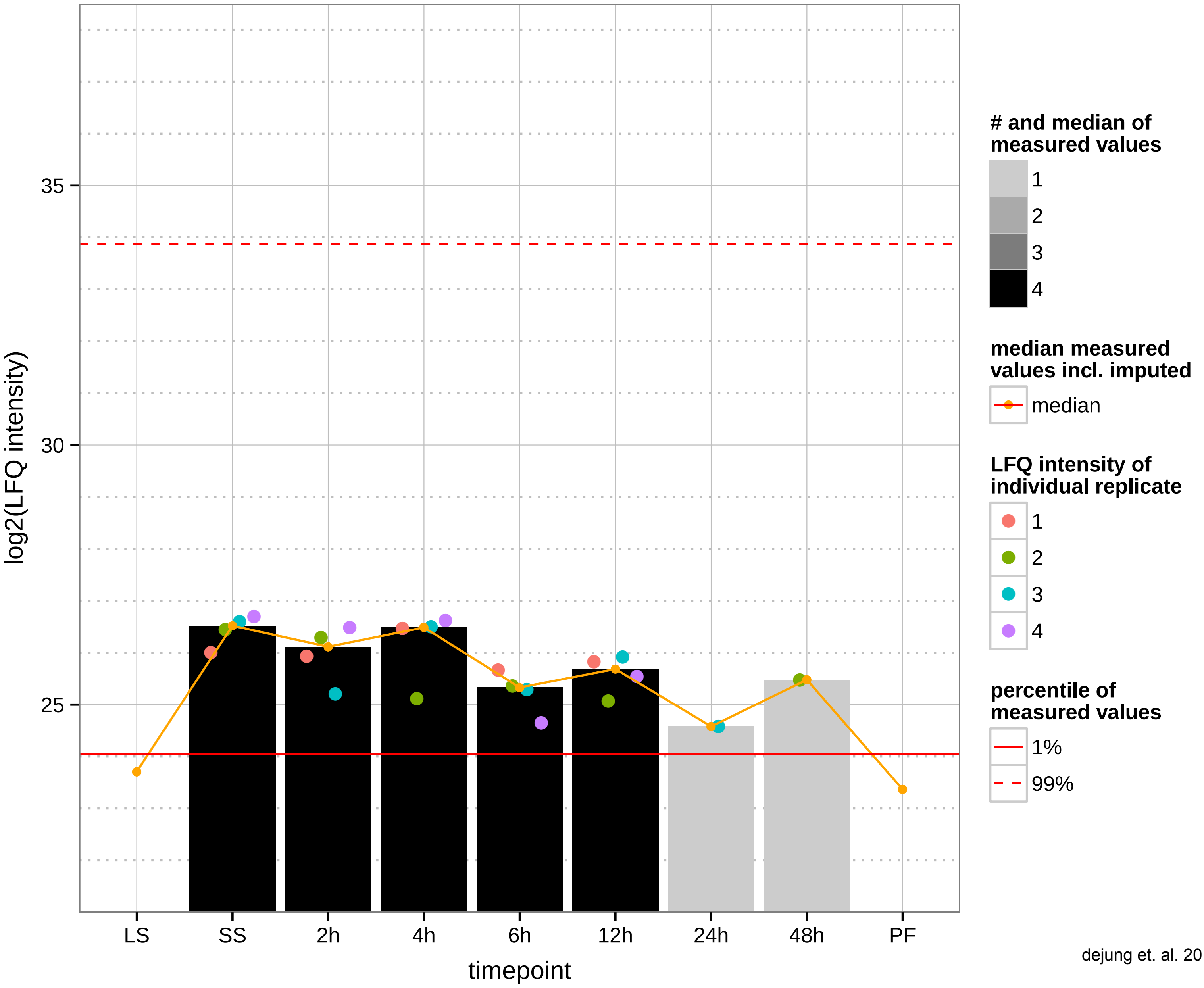
hypothetical protein, conserved
Tb927.9.12380
AGOF: ATP binding, catalytic activity
AGOC: null
AGOP: fructose 2, 6−bisphosphate metabolic process
PGOF: null
PGOC: null
PGOP: null





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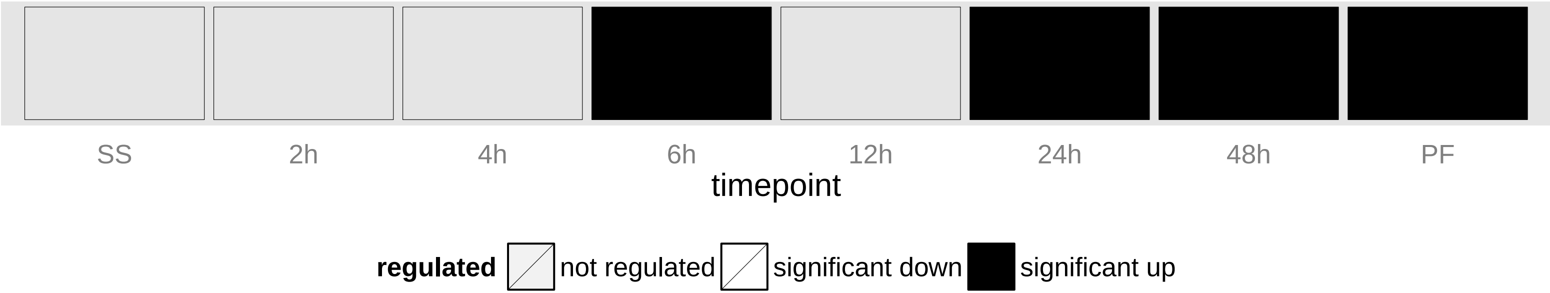
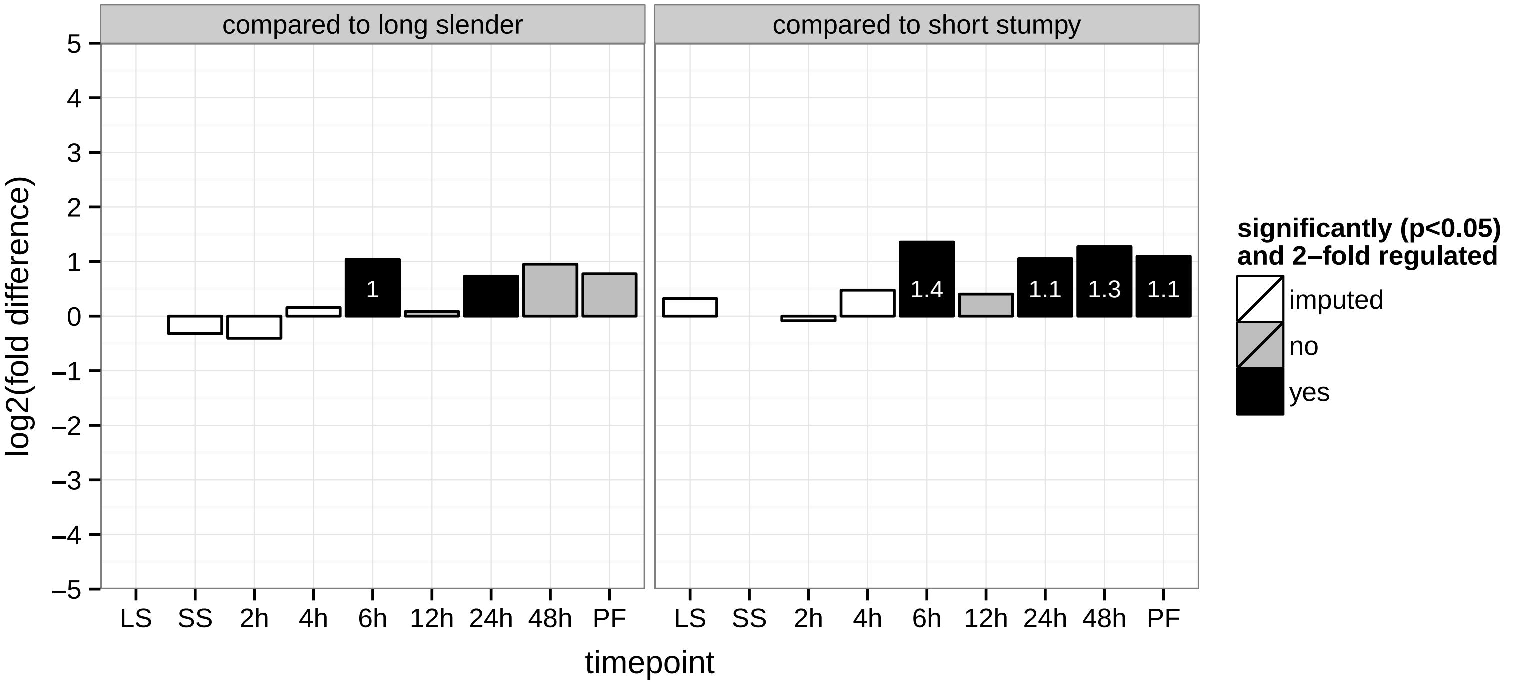
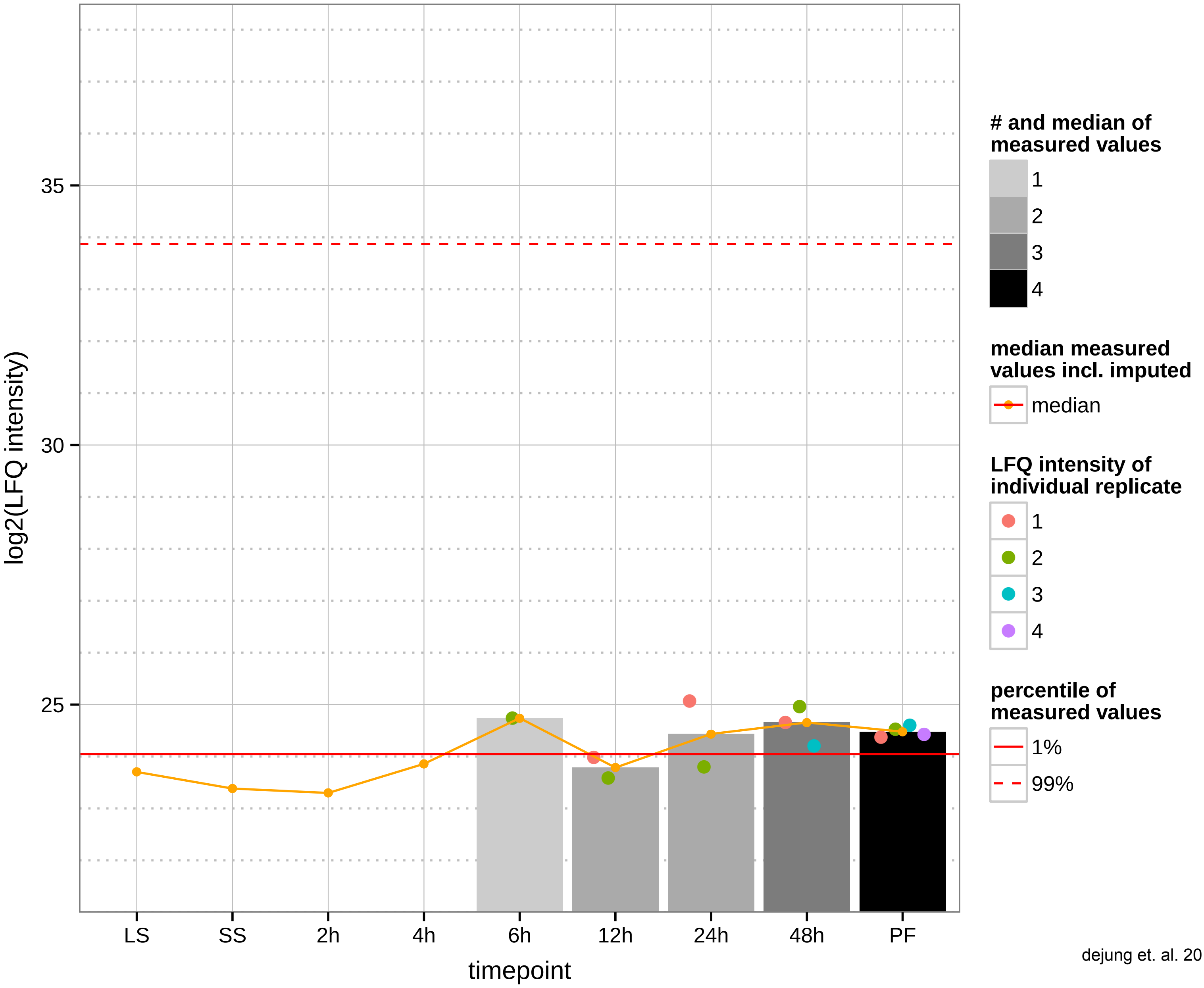


dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.11720
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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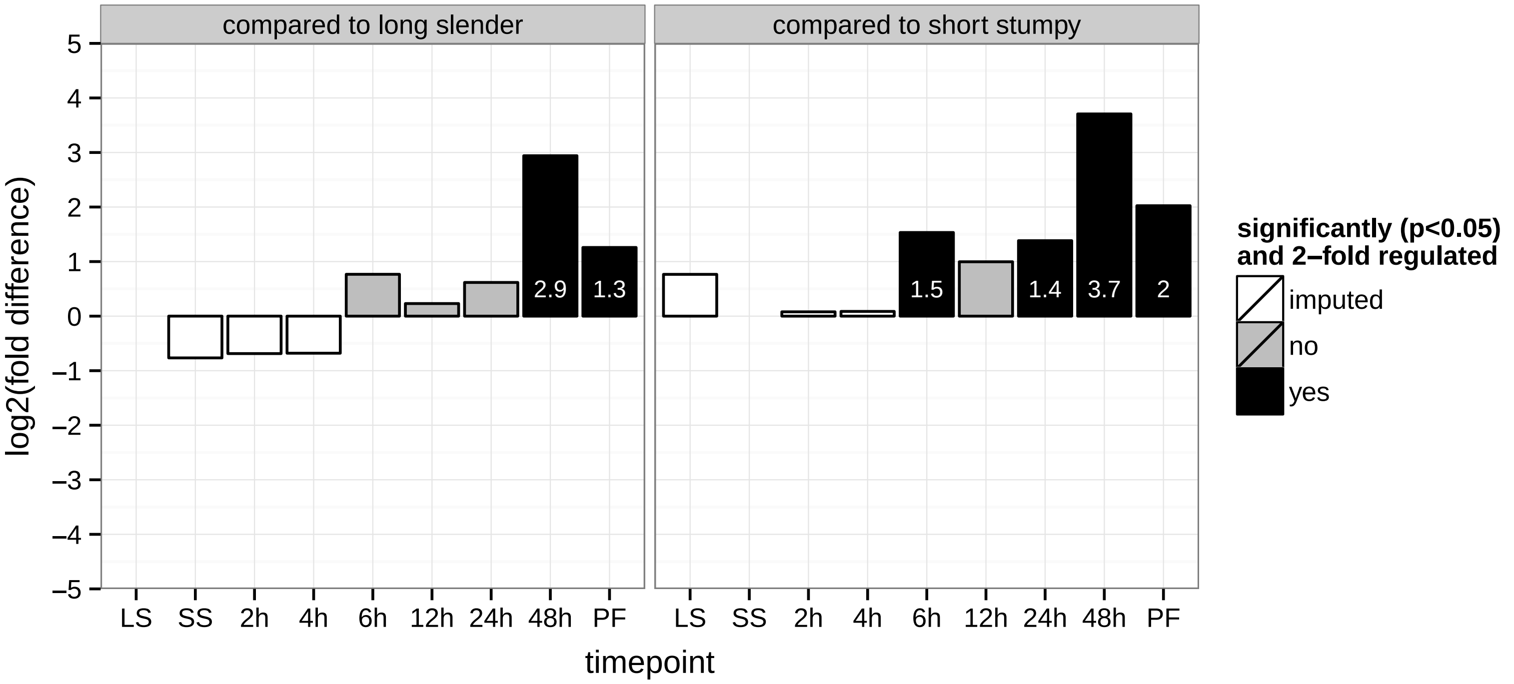
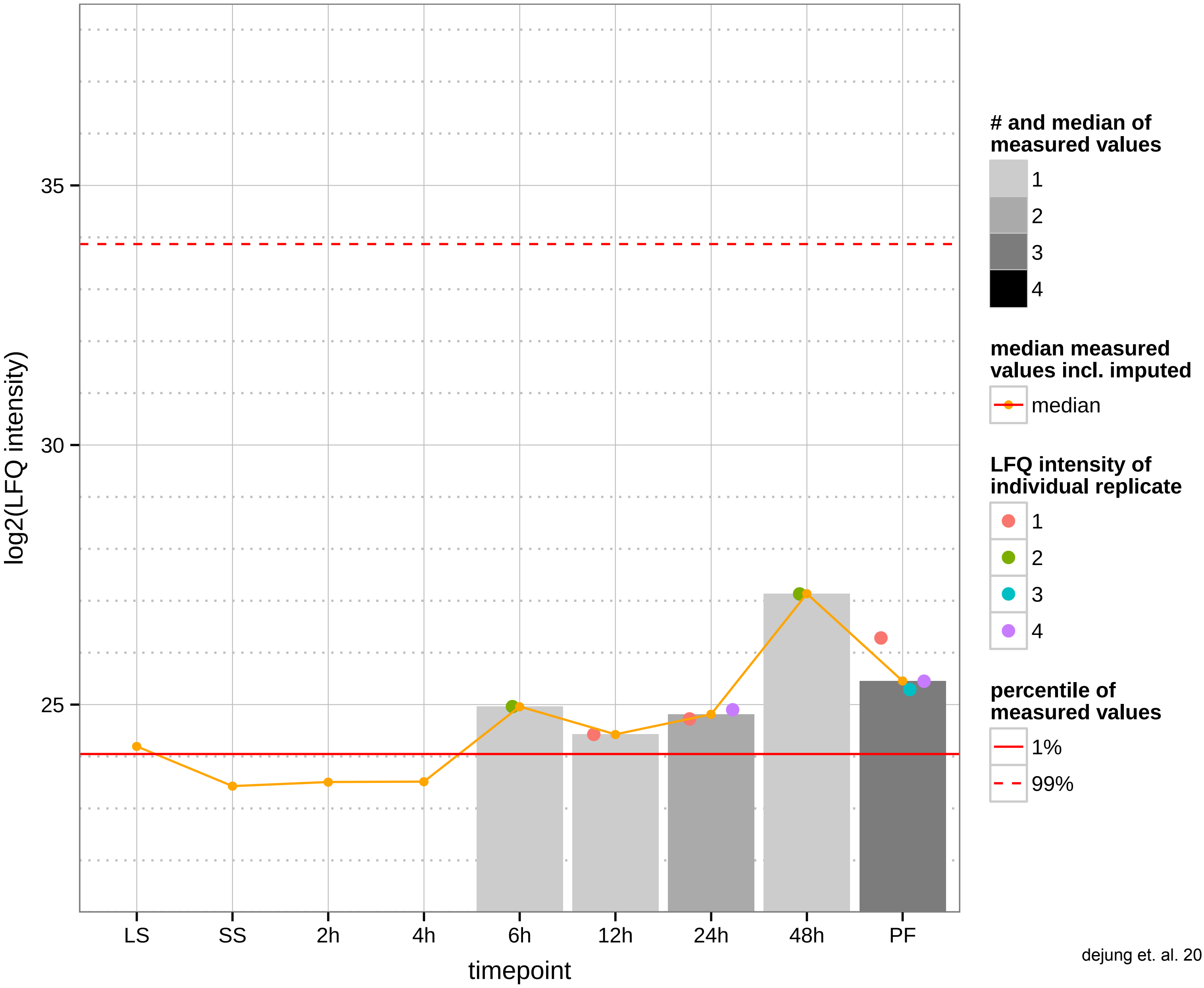
hypothetical protein, conserved
Tb927.10.7670
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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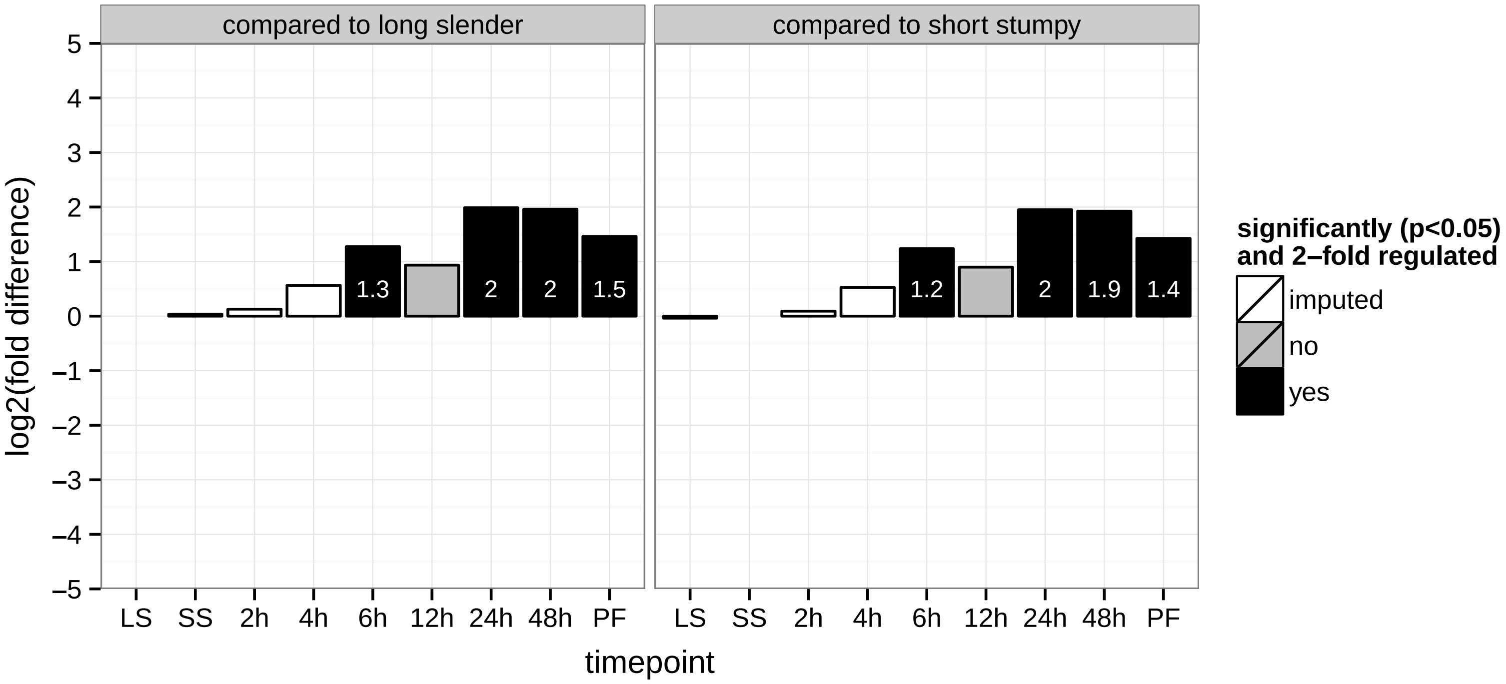
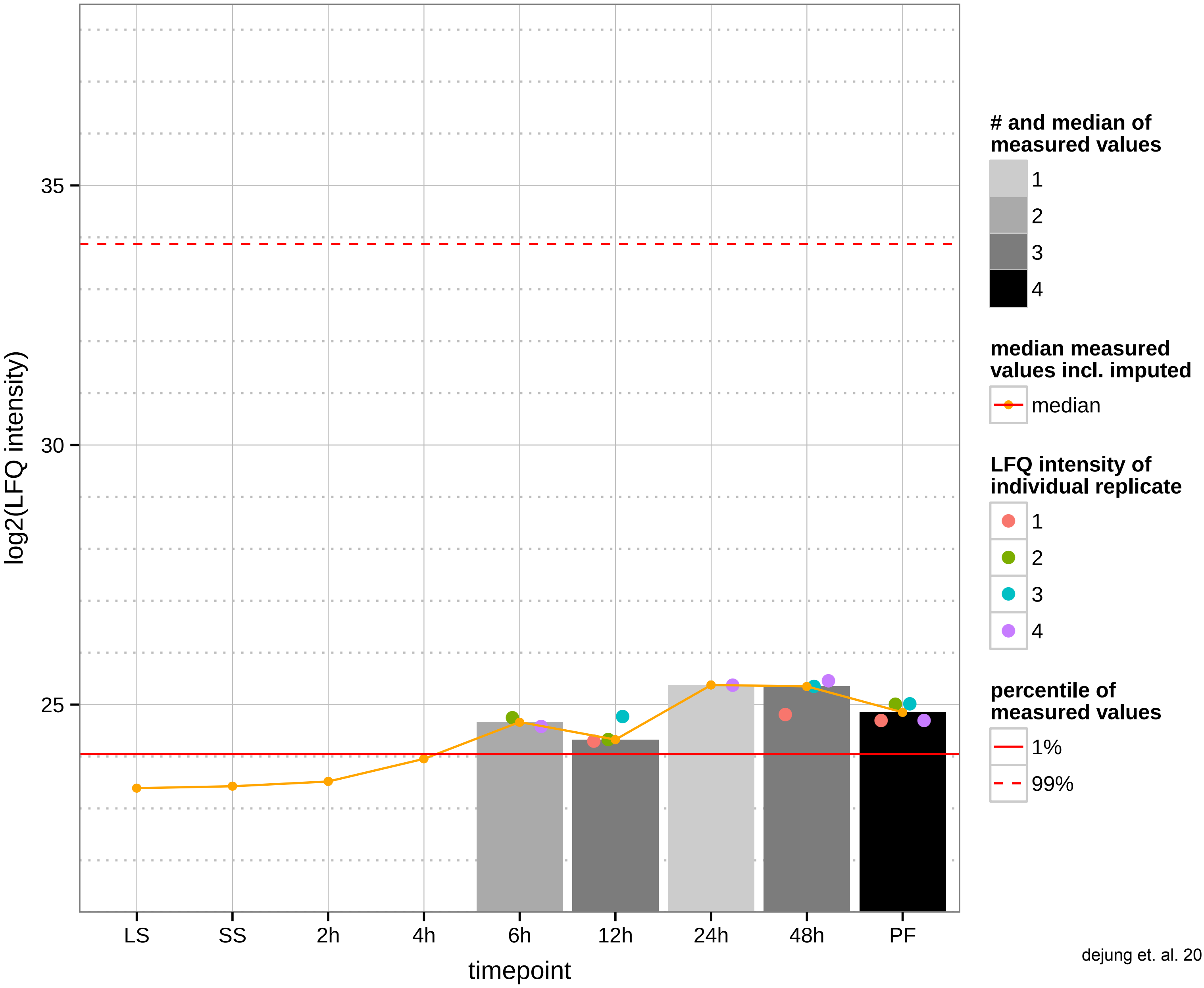
hypothetical protein, conserved
Tb927.11.16420
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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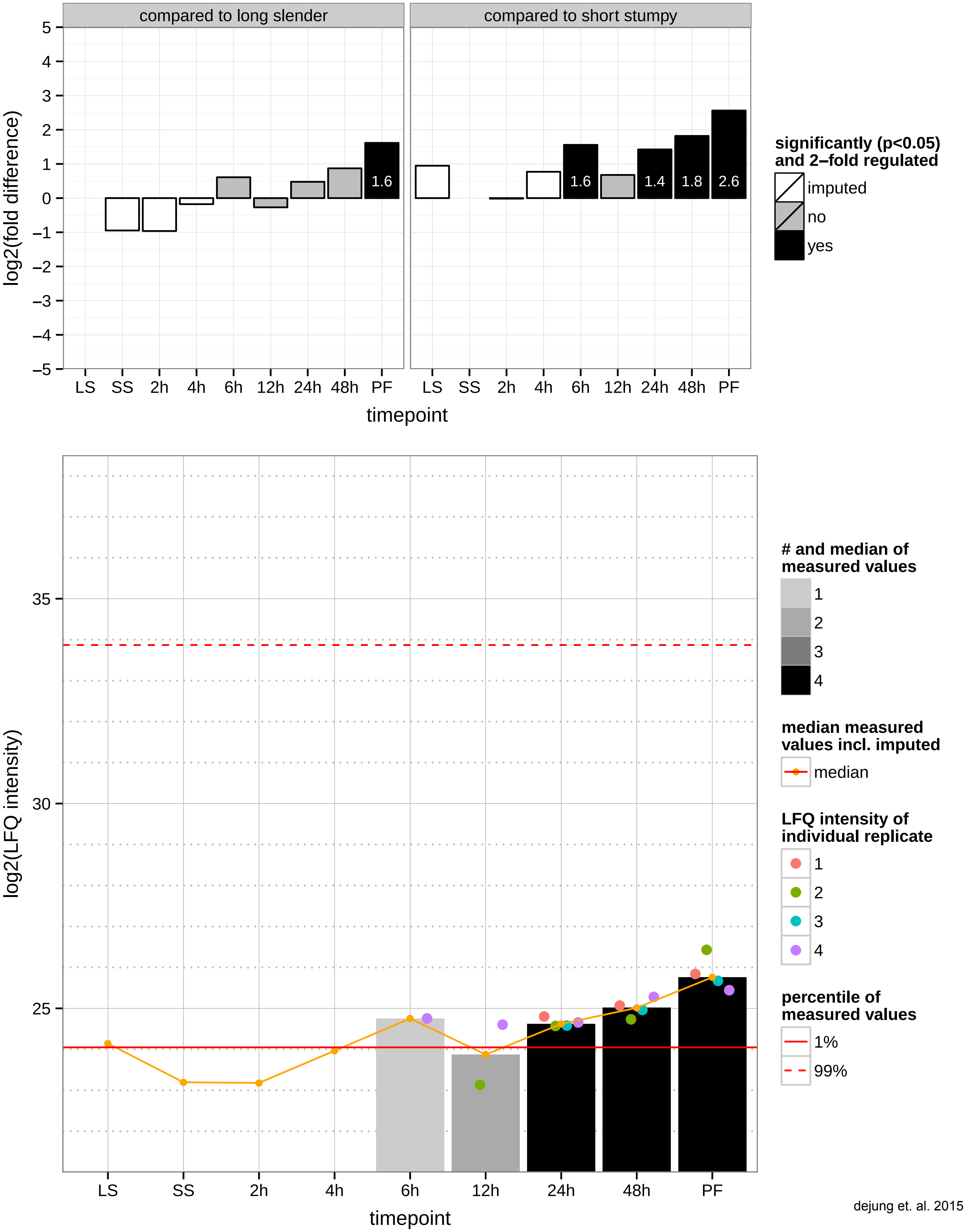
aurora B kinase (AUK1)
Tb927.11.8220
AGOF: ATP binding, protein binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: chromosome passenger complex, nucleus, spindle
AGOP: chromosome segregation, cytokinesis, histone H3–S10 phosphorylation, protein phosphorylation, regulation of mitosi
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation



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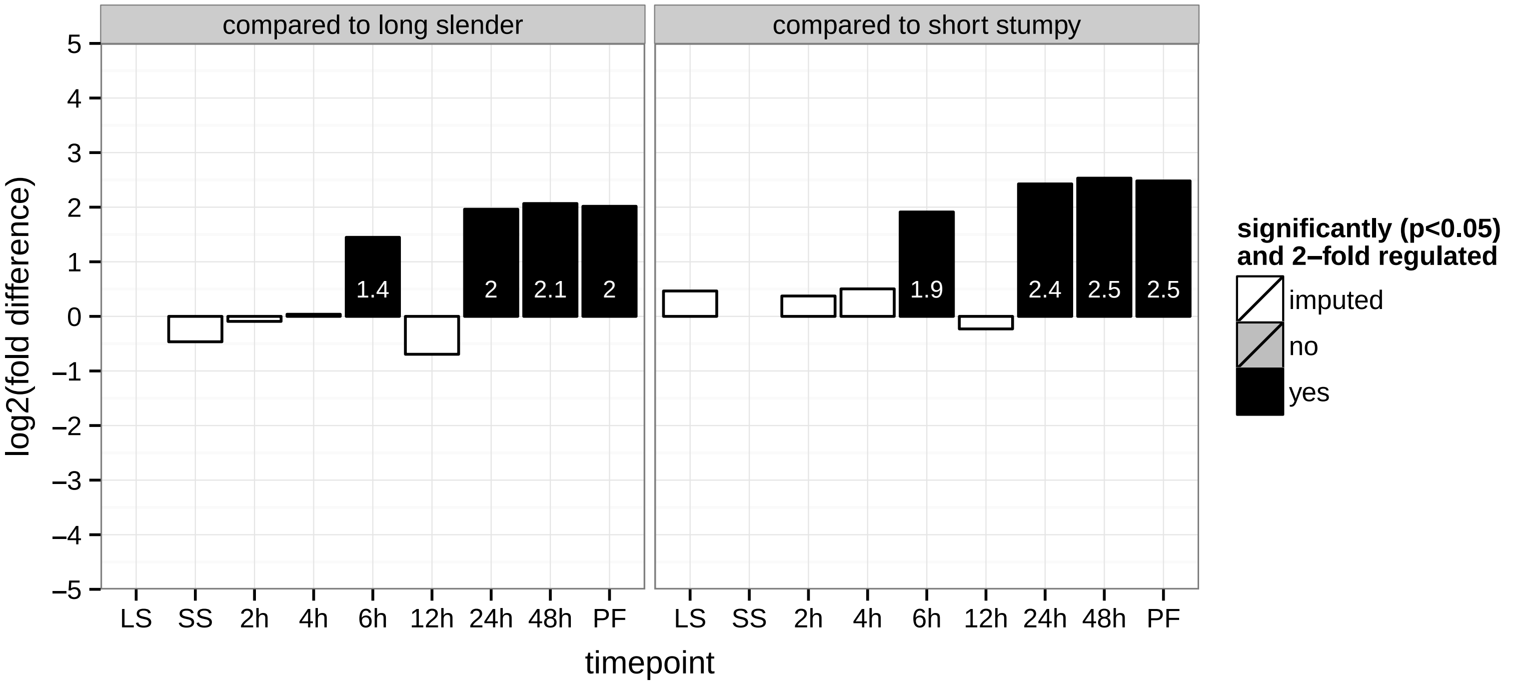
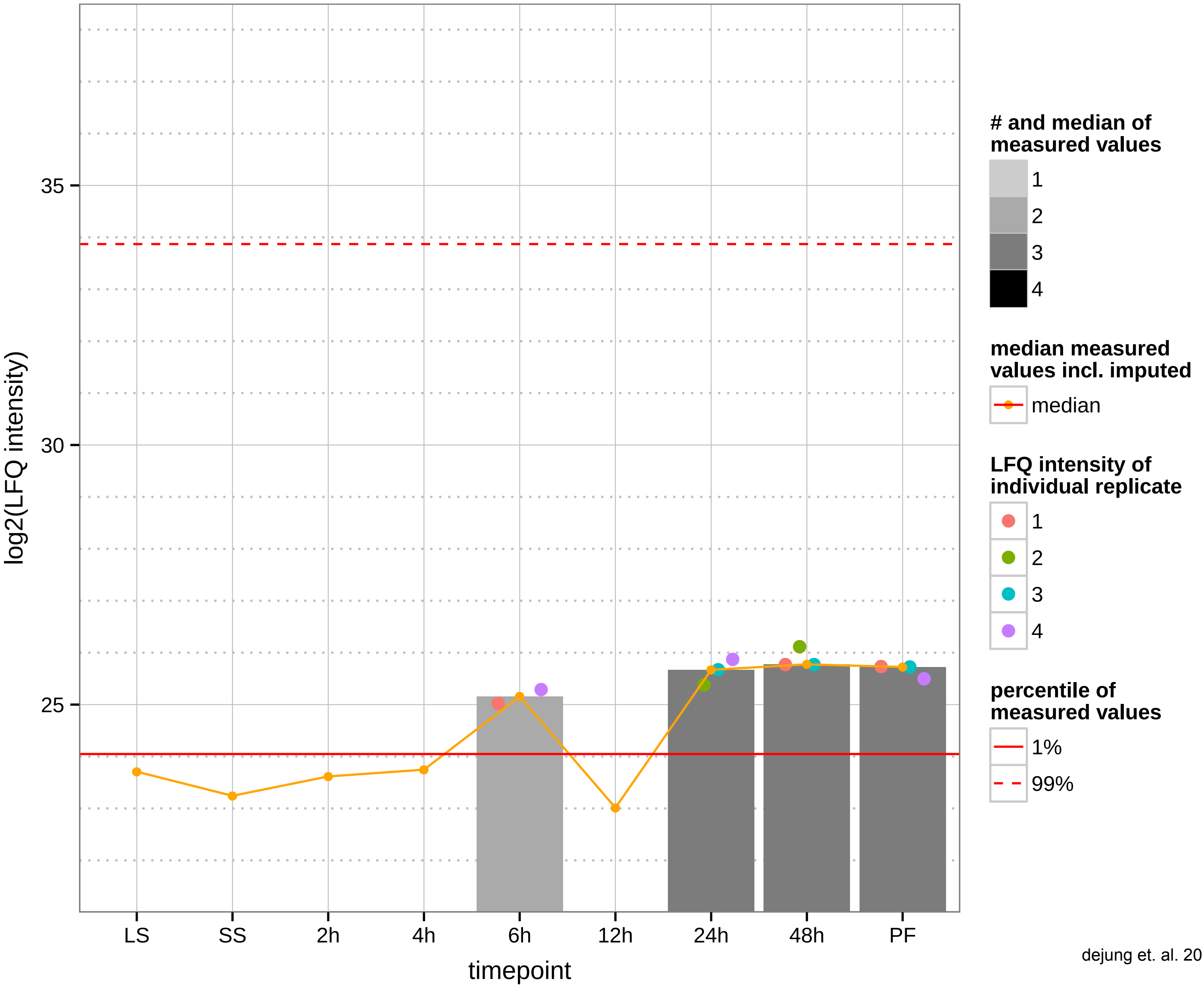
translation elongation factor EF−2, putative
Tb927.3.2170
AGOF: GTP binding, GTPase activity
AGOC: null
AGOP: mature ribosome assembly
PGOF: GTP binding, GTPase activity
PGOC: null
PGOP: null





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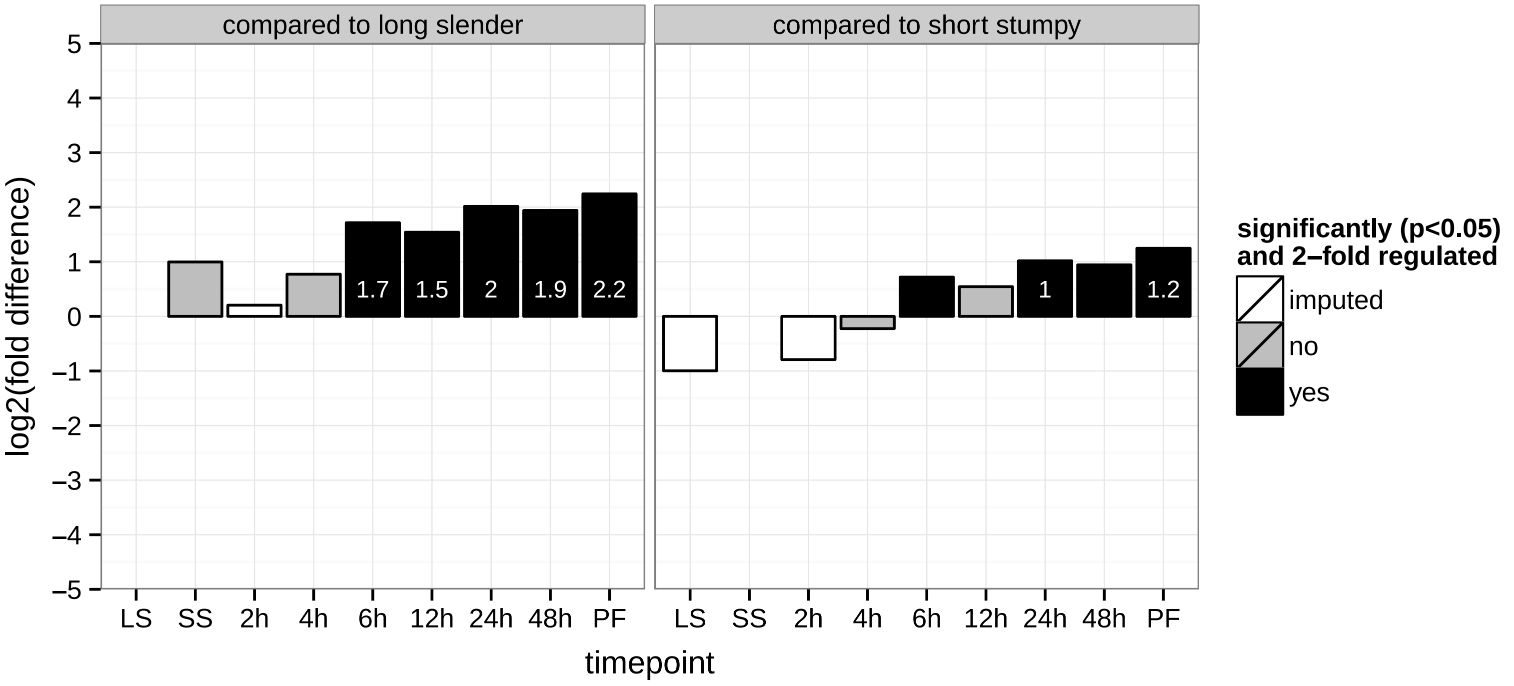
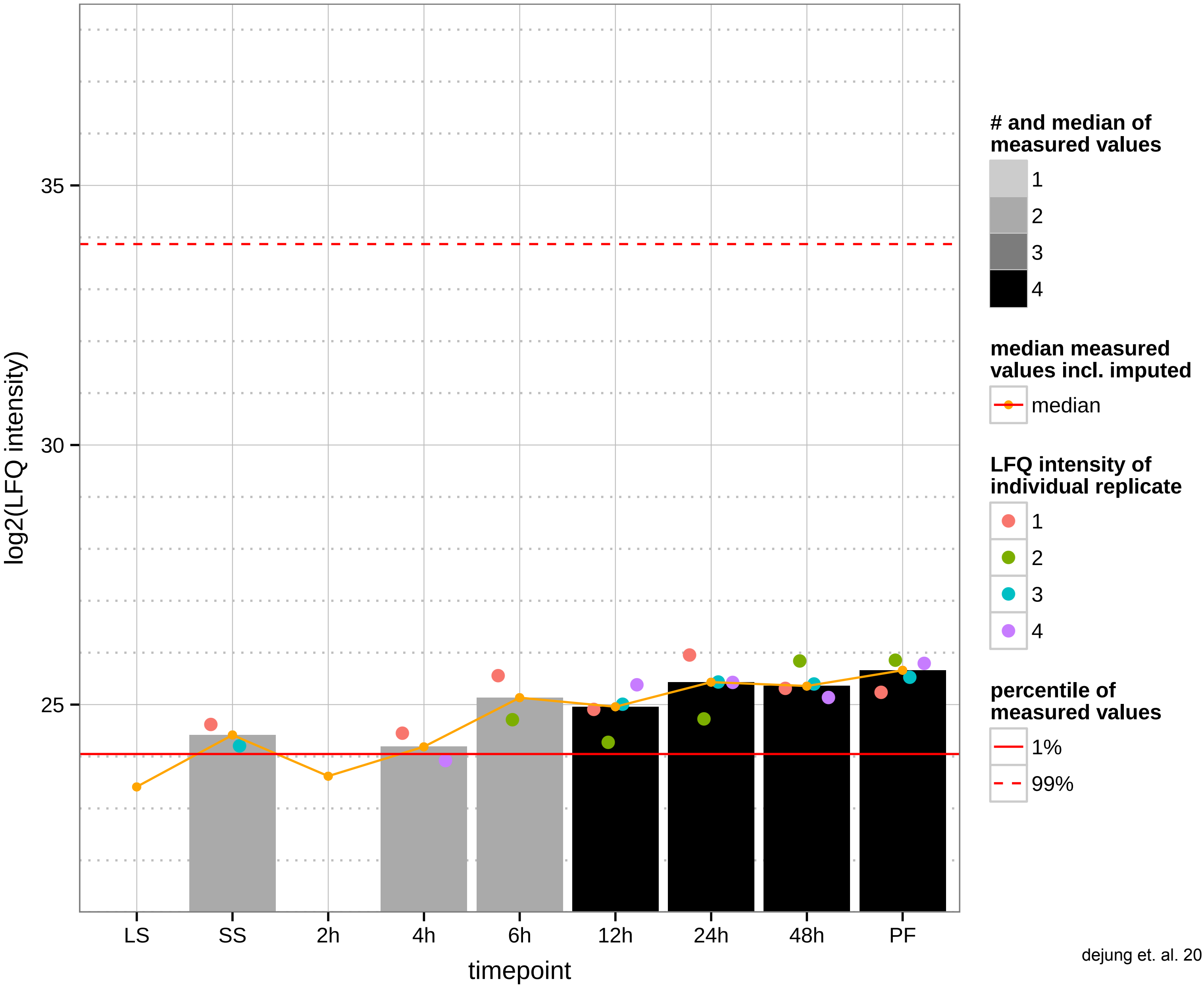
hypothetical protein, conserved
Tb927.4.2430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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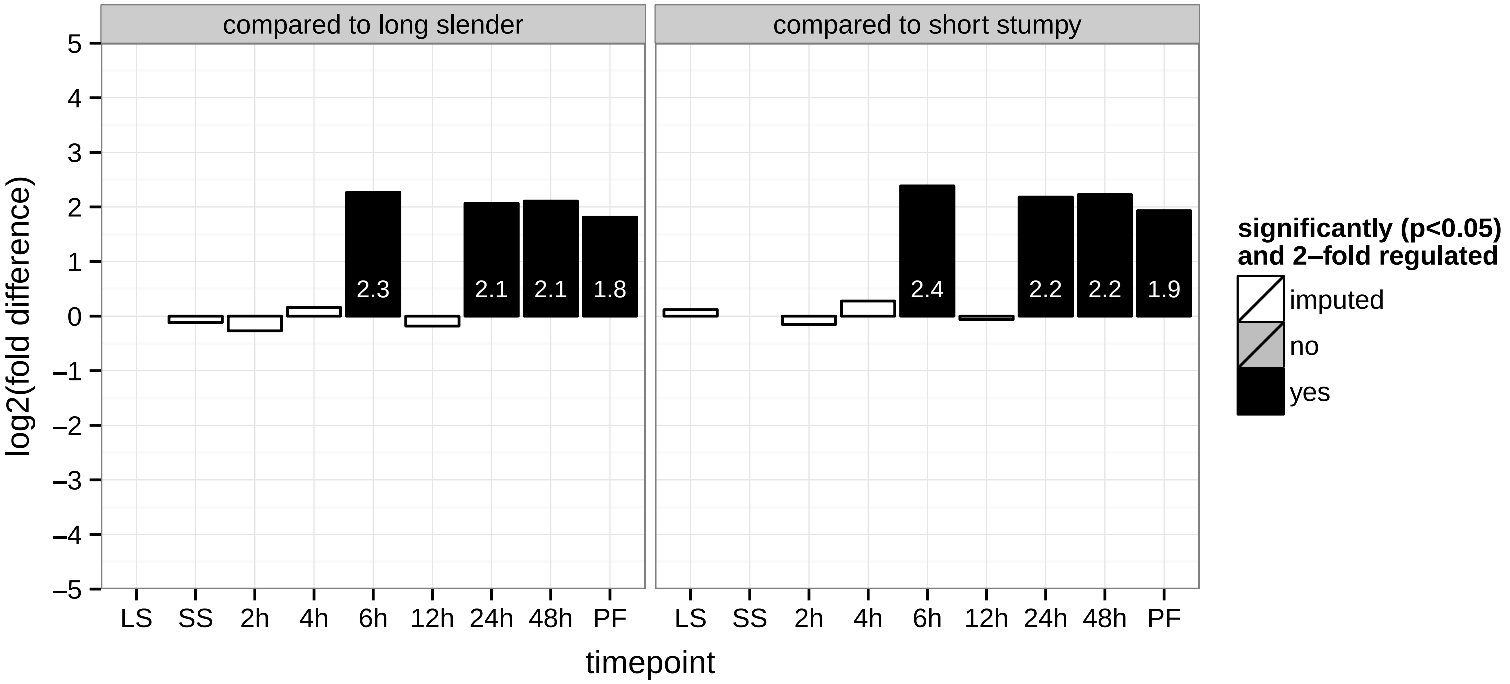
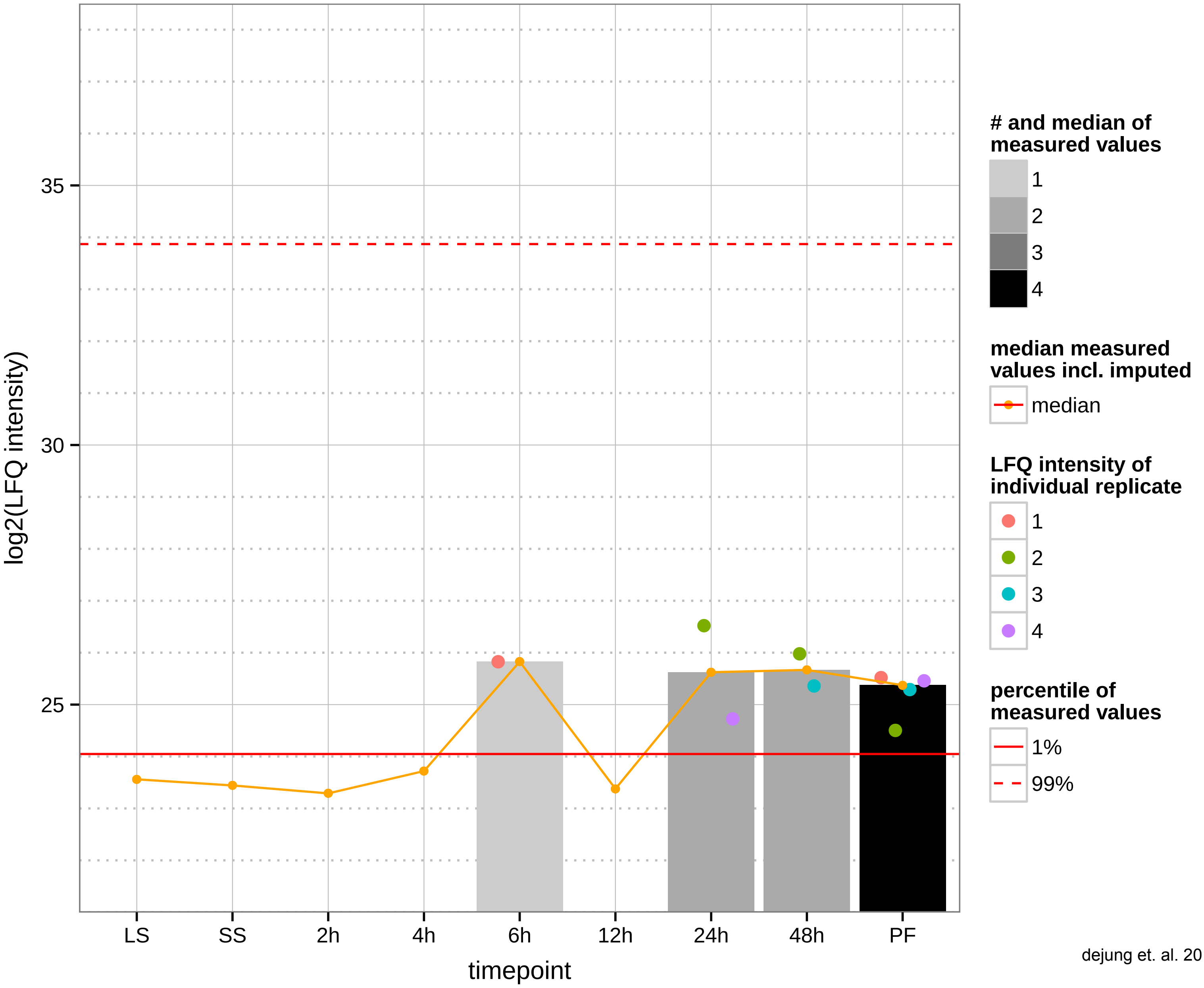
hypothetical protein, conserved
Tb927.4.2580
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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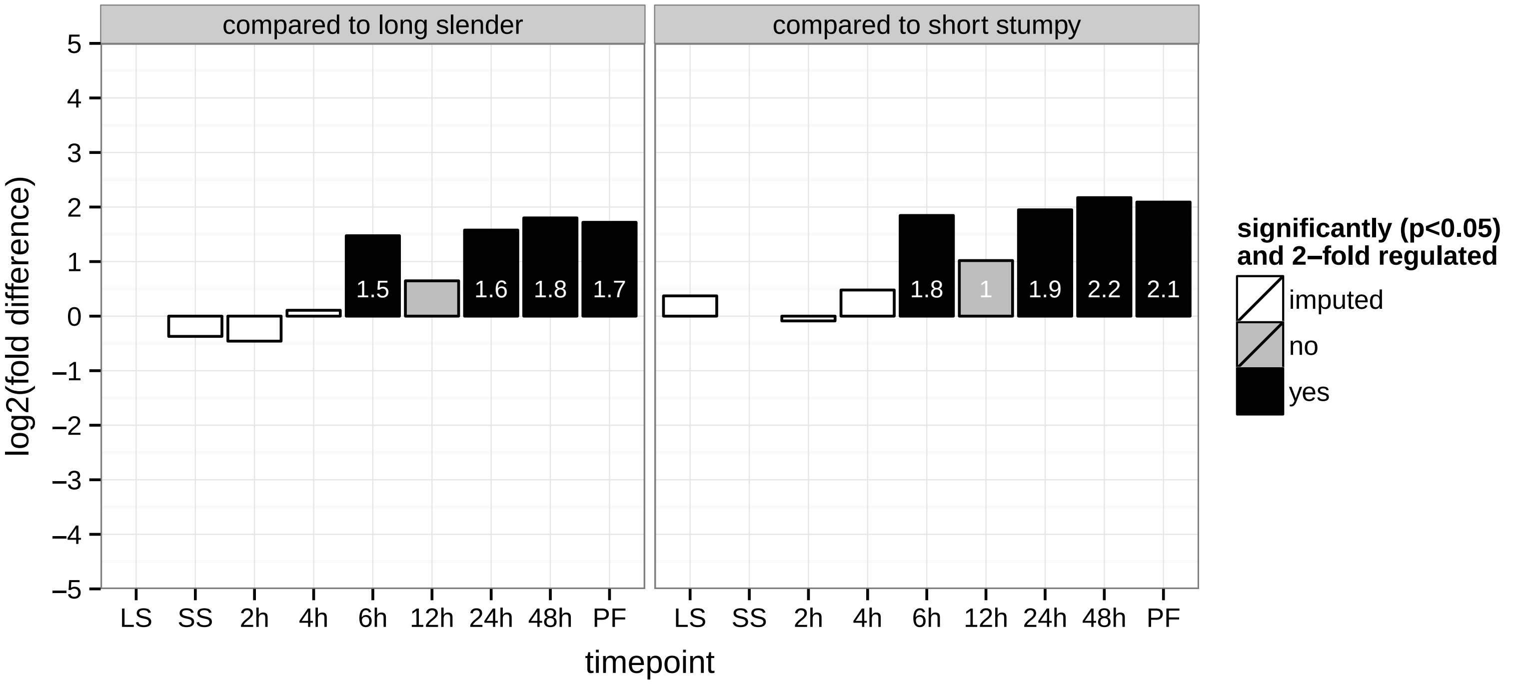
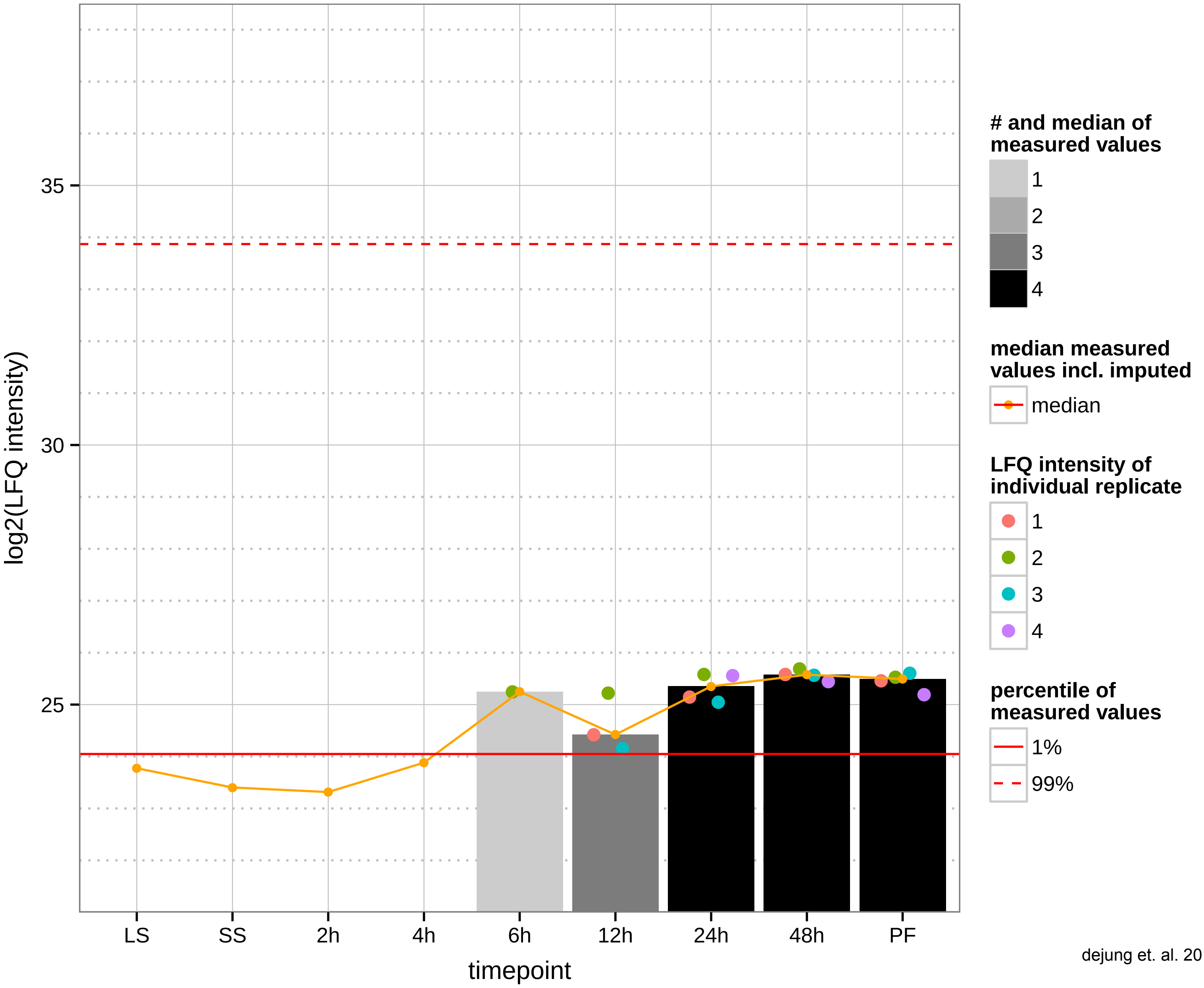
DNA primase small subunit, putative
Tb927.7.2310
AGOF: DNA primase activity
AGOC: null
AGOP: DNA replication, synthesis of RNA primer
PGOF: DNA primase activity
PGOC: null
PGOP: DNA replication, synthesis of RNA primer





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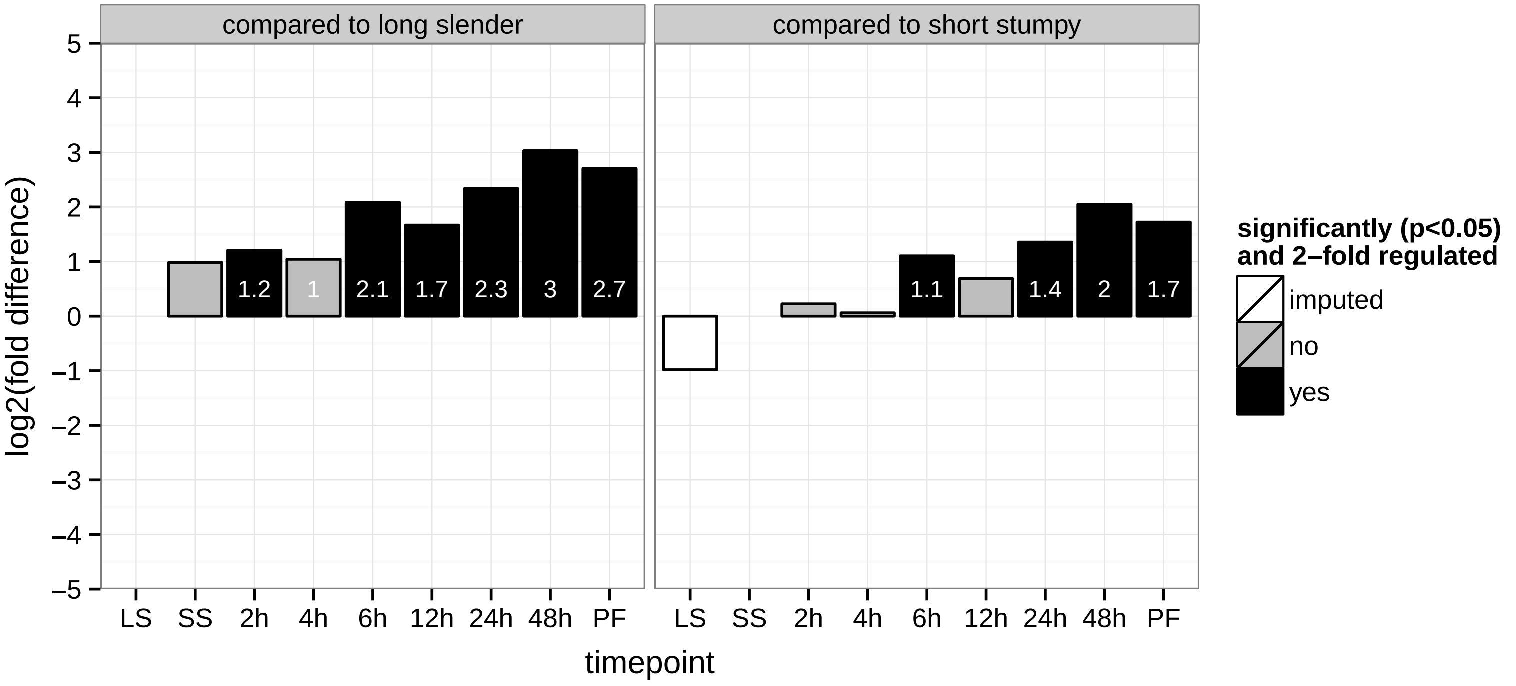
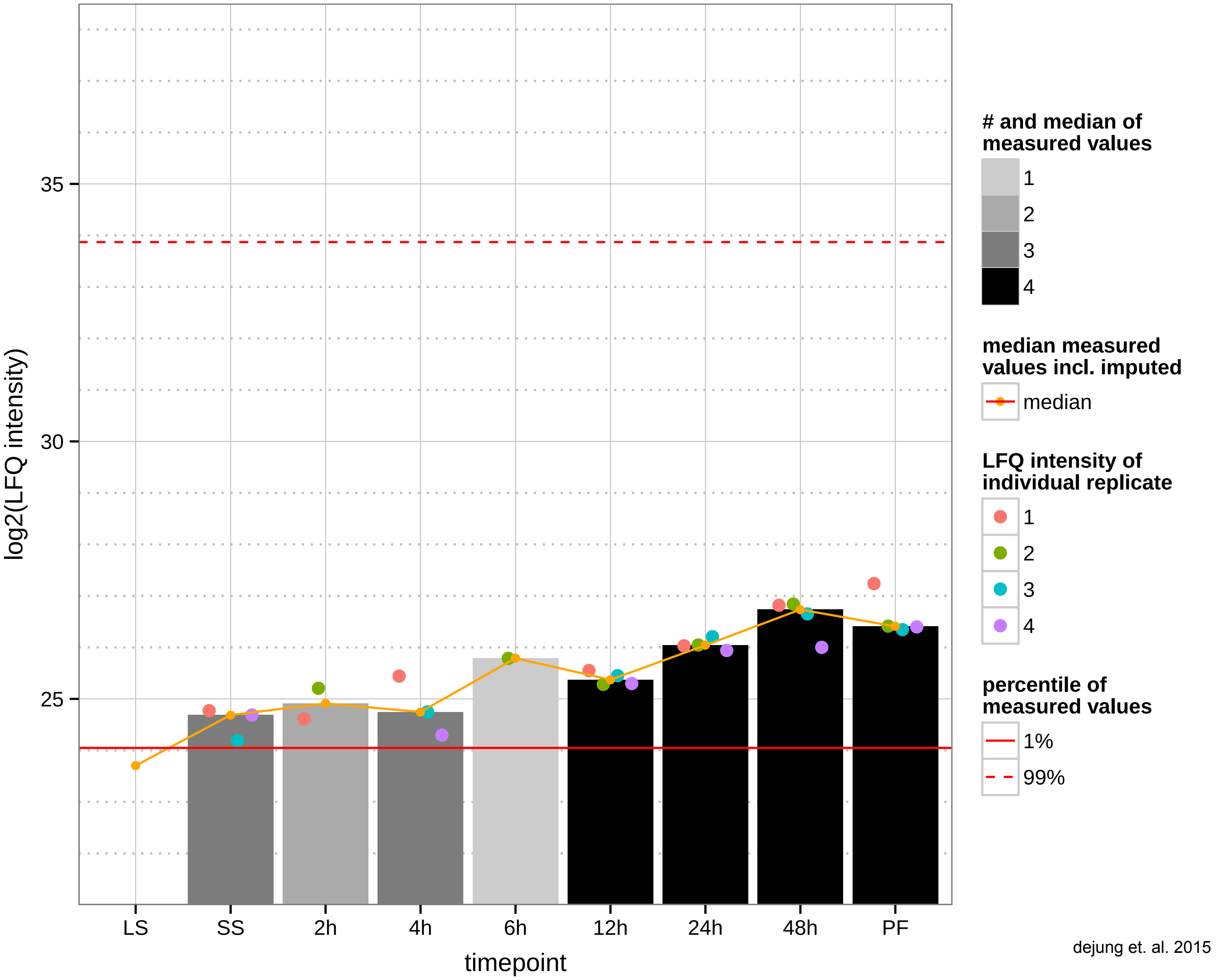
hypothetical protein, conserved
Tb927.9.11120
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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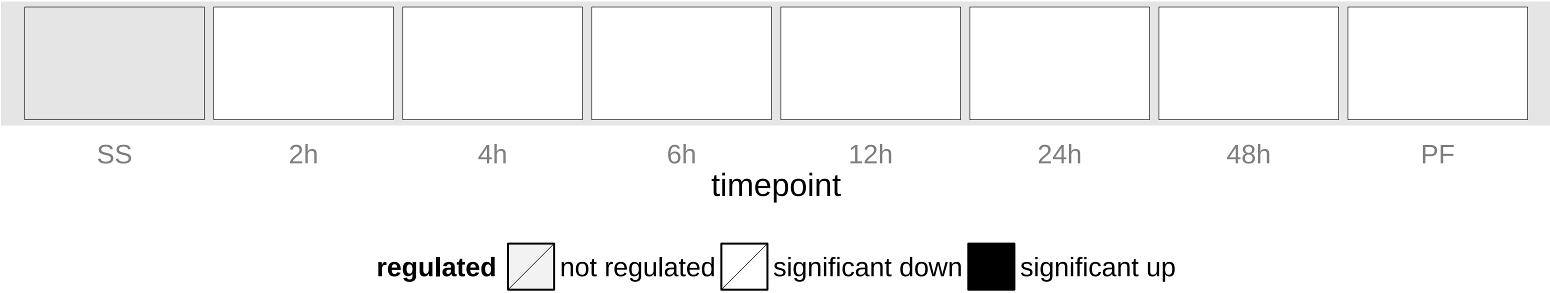

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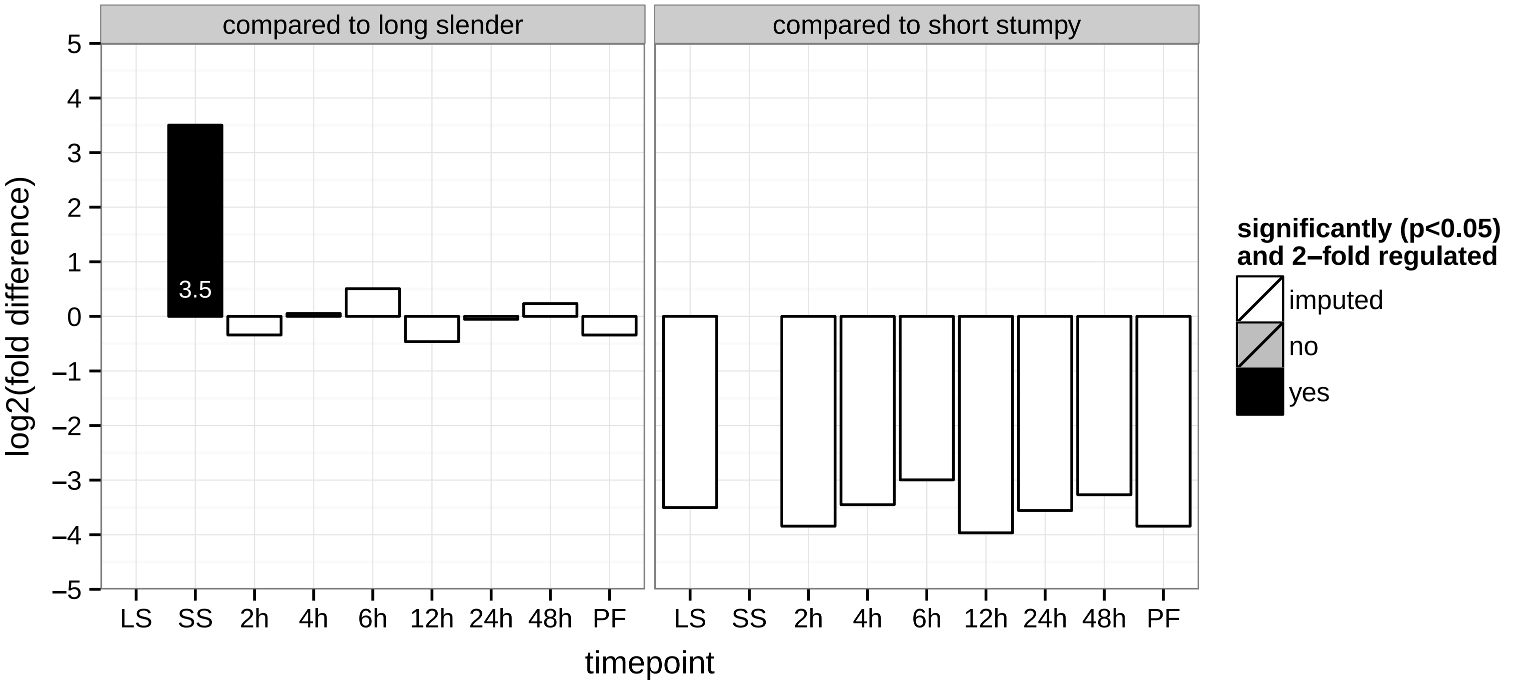
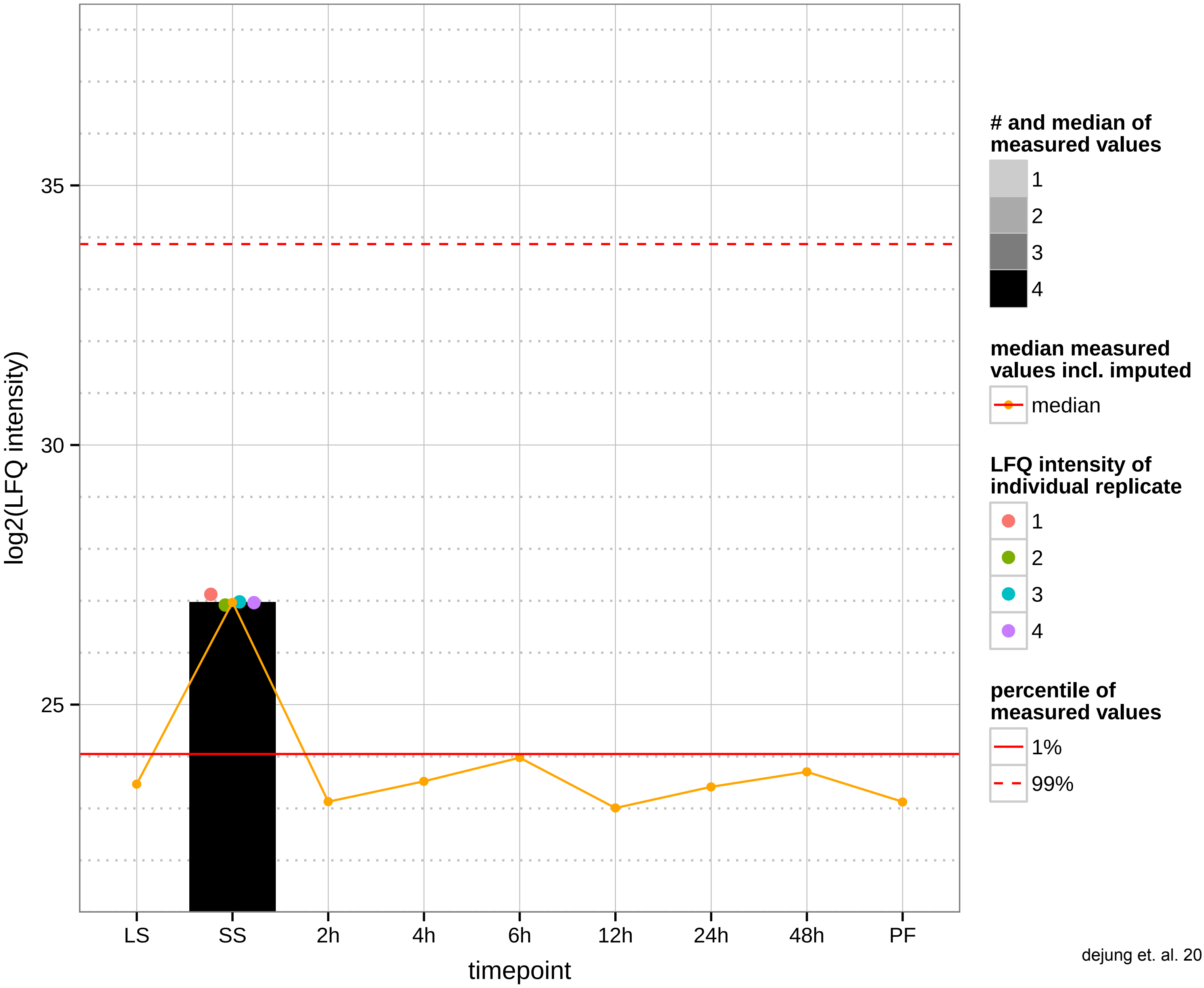
protein kinase, putative
Tb927.1.1530
AGOF: null, ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity, signal
AGOC: null
AGOP: null, protein phosphorylation, regulation of transcription, DNA–dependent, signal transduction
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups, signal transducer
PGOC: null
PGOP: protein phosphorylation, regulation of transcription, DNA–dependent, signal transduction





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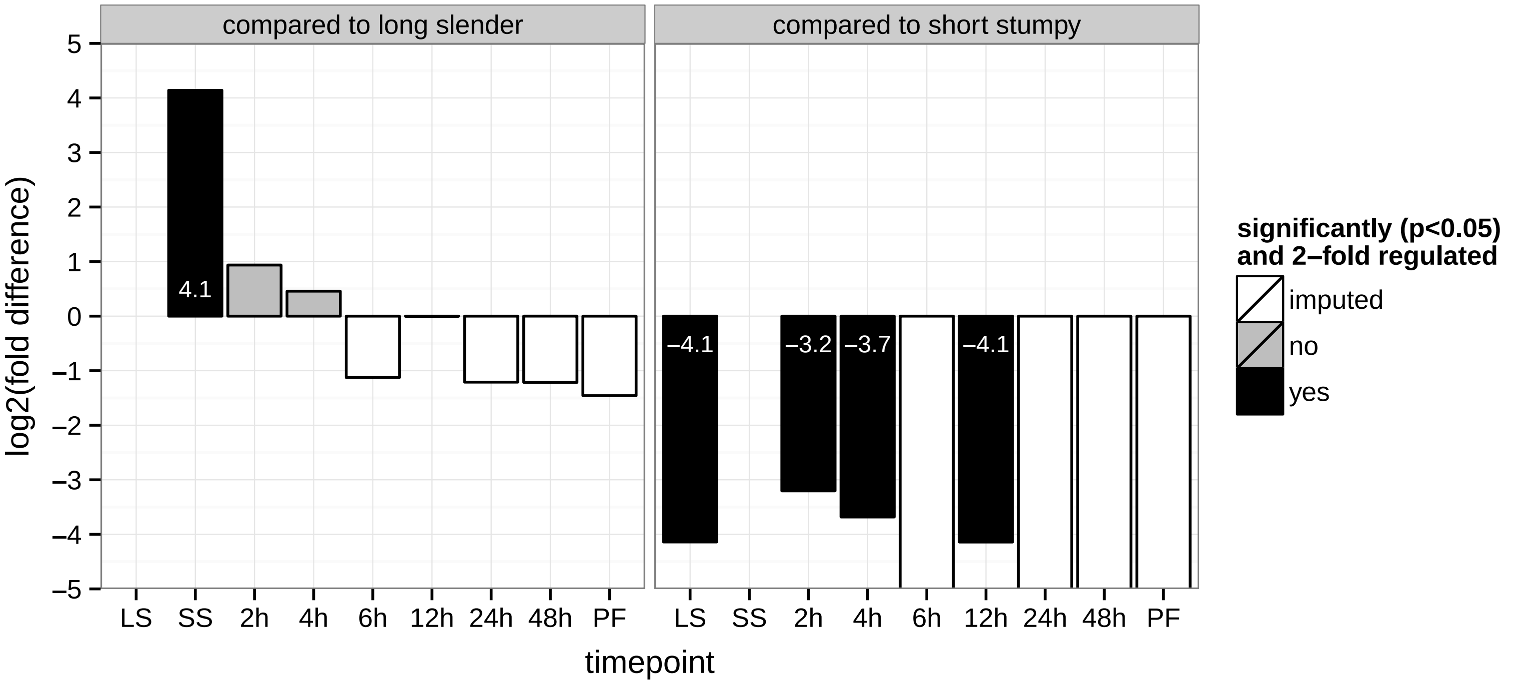
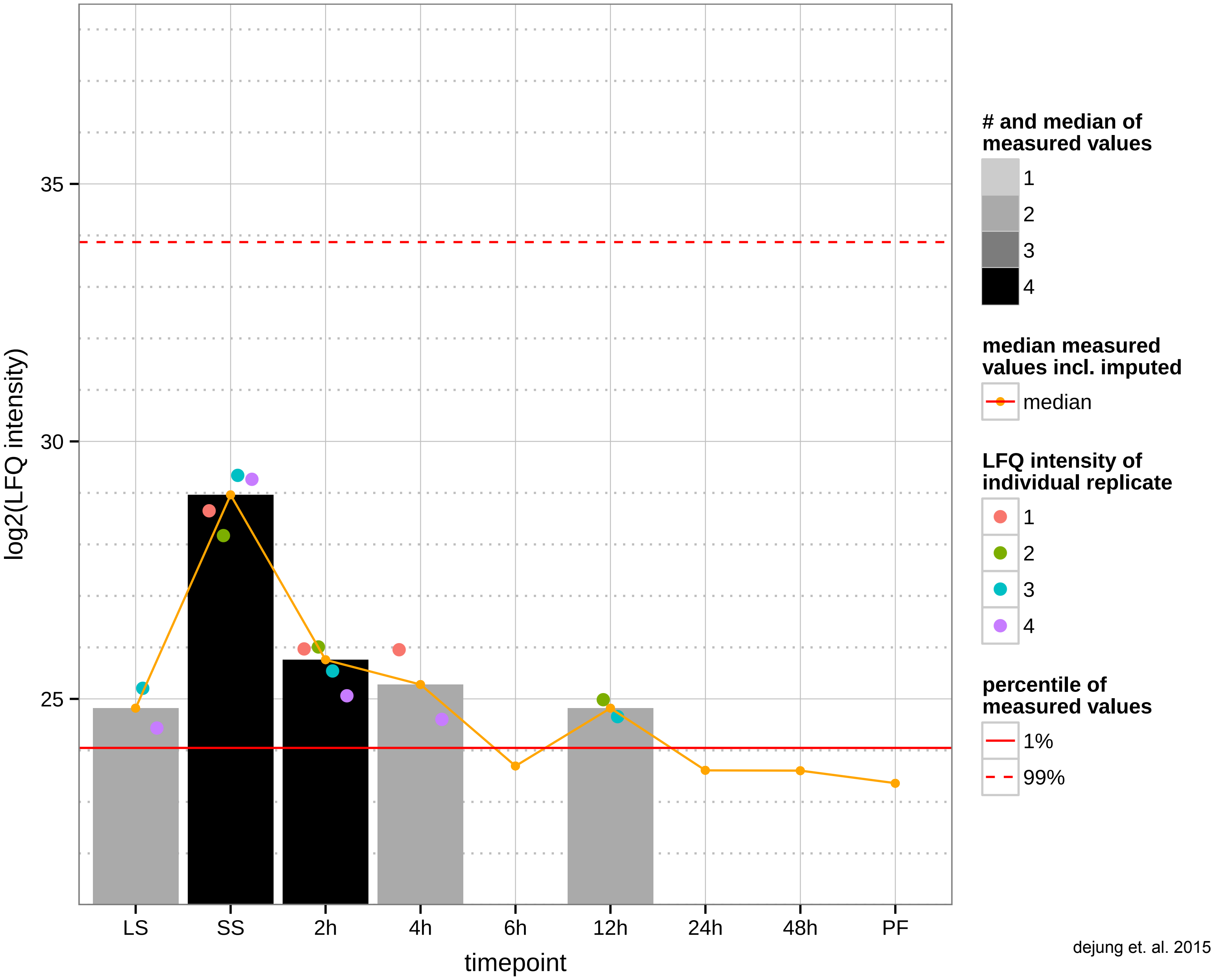
cyclin–like F–box protein 2 (CFB2)
Tb927.1.4650
AGOF: null
AGOC: null
AGOP: mitochondrial DNA replication
PGOF: protein binding
PGOC: null
PGOP: null





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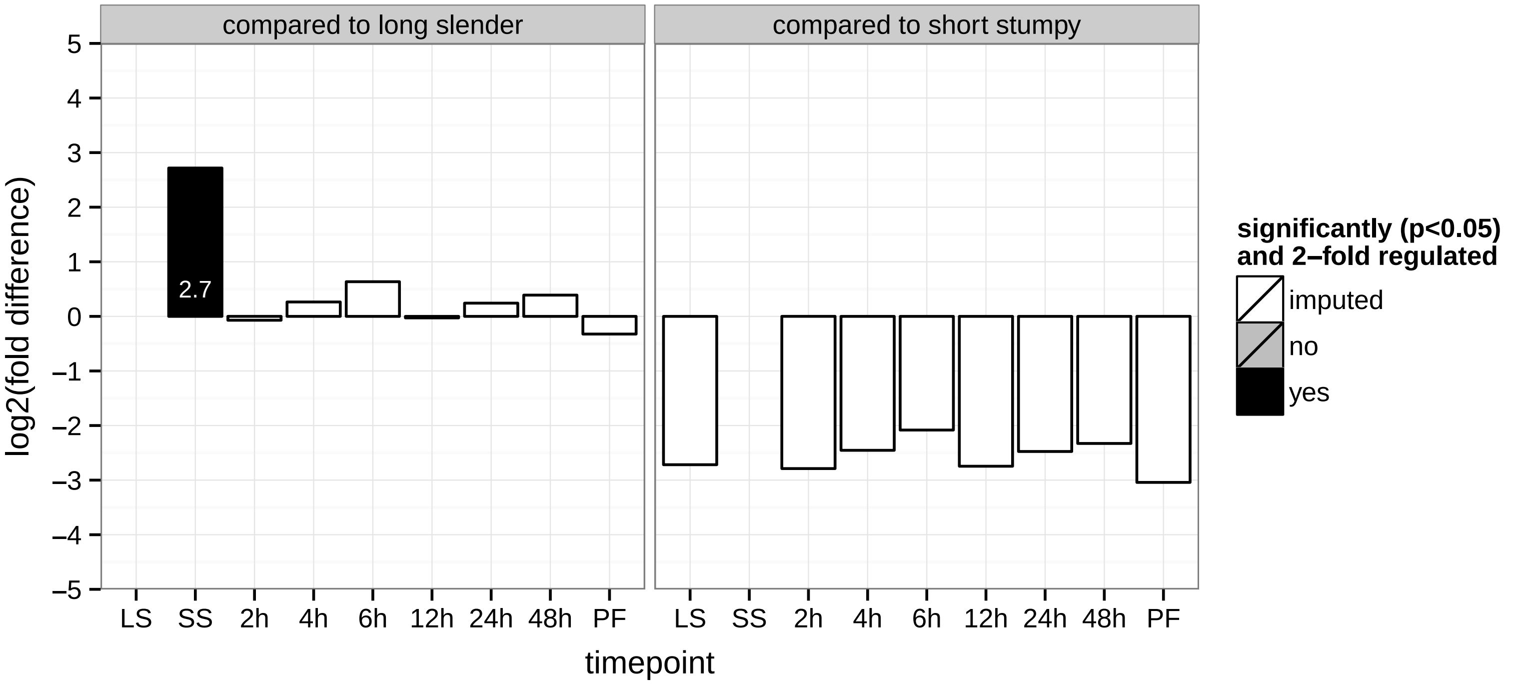
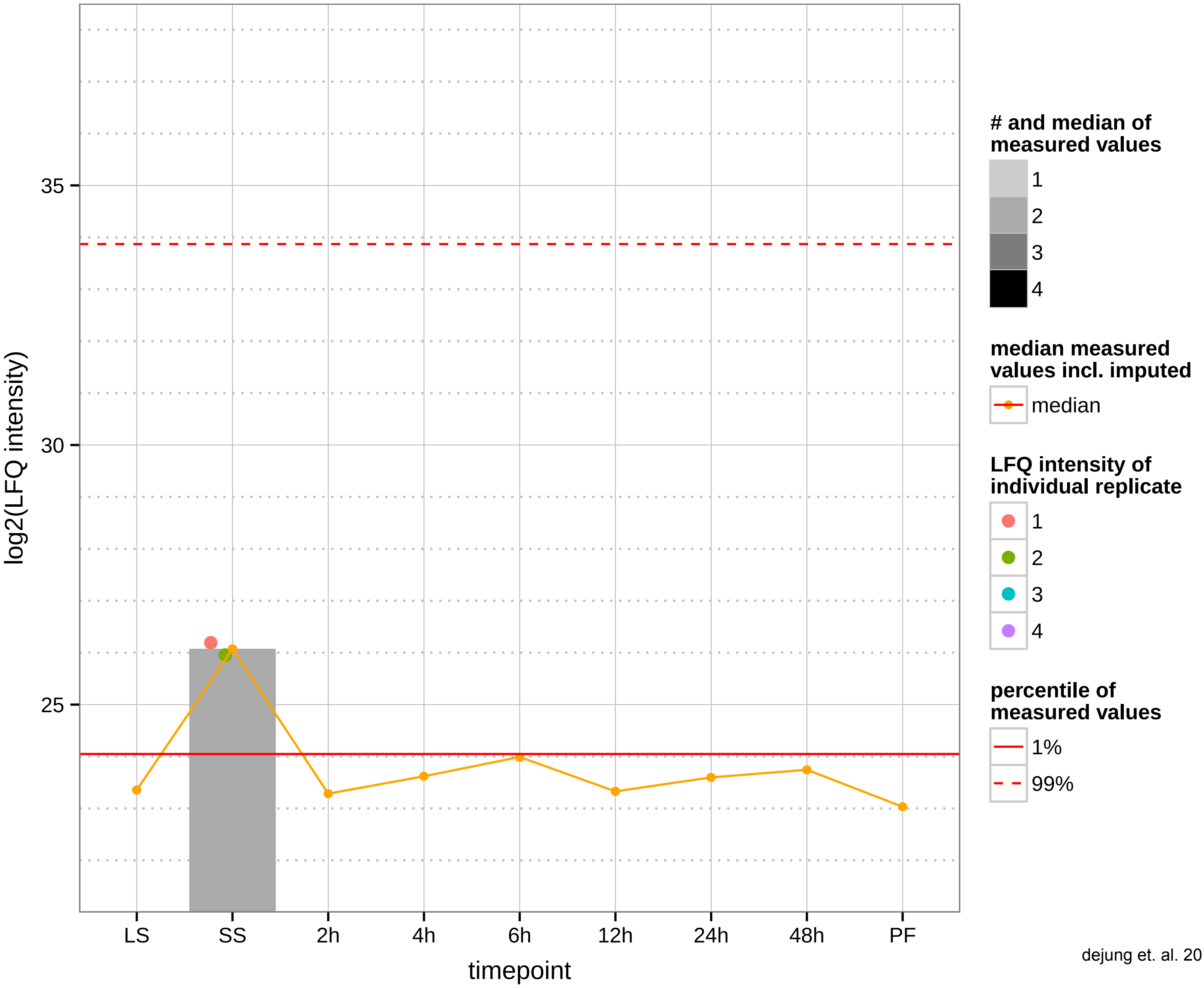
MSP–C, putative (MSP–C)
Tb927.10.2410
AGOF: metalloendopeptidase activity, zinc ion binding
AGOC: membrane
AGOP: cell adhesion, proteolysis
PGOF: metalloendopeptidase activity, zinc ion binding
PGOC: membrane
PGOP: cell adhesion, proteolysis





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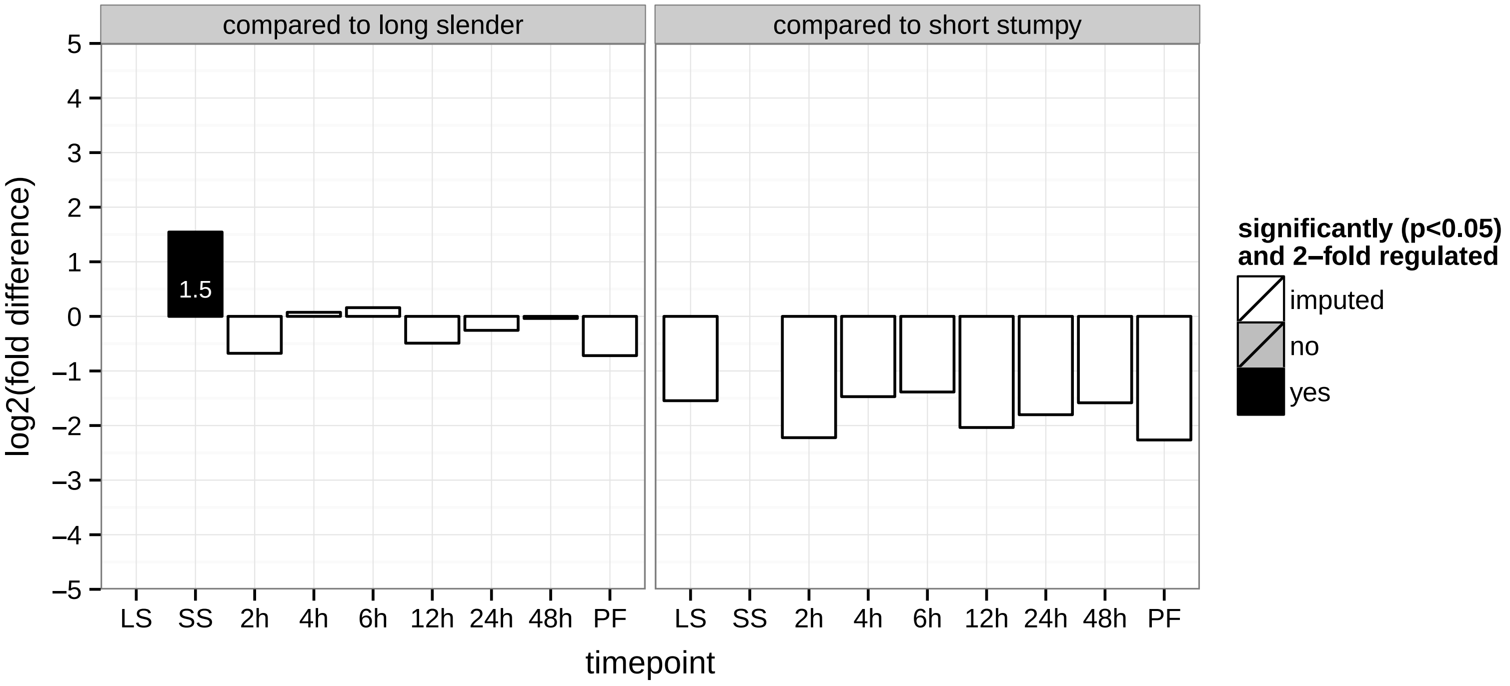
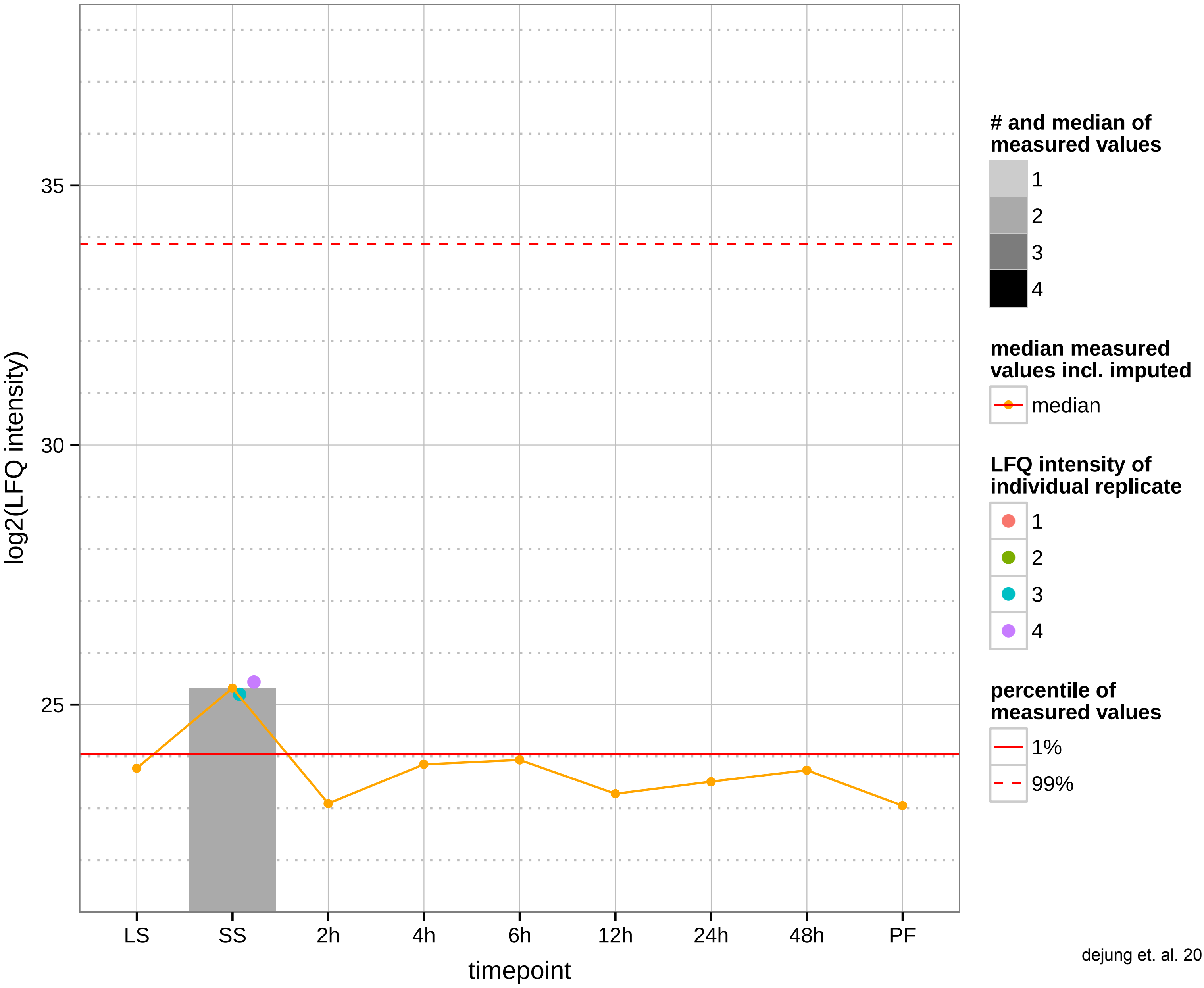
hypothetical protein
Tb927.4.1230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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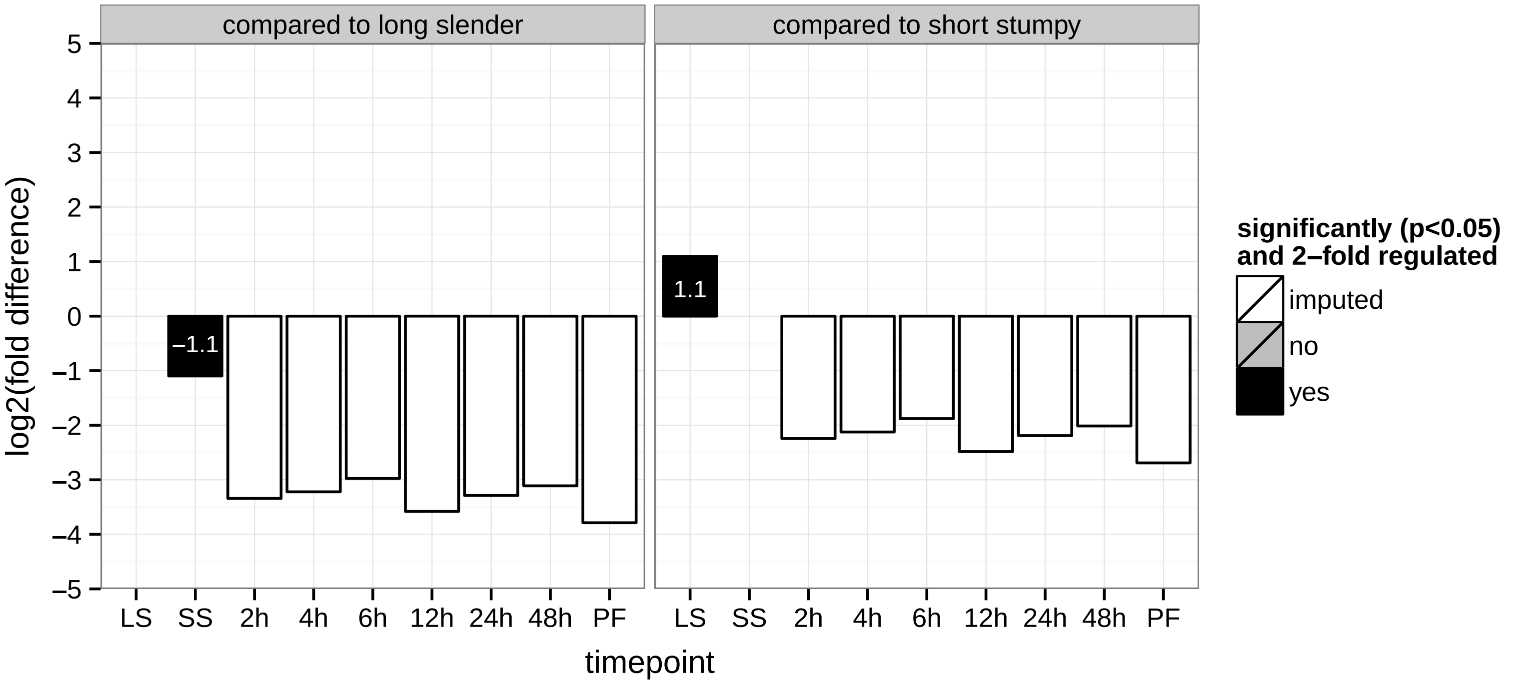
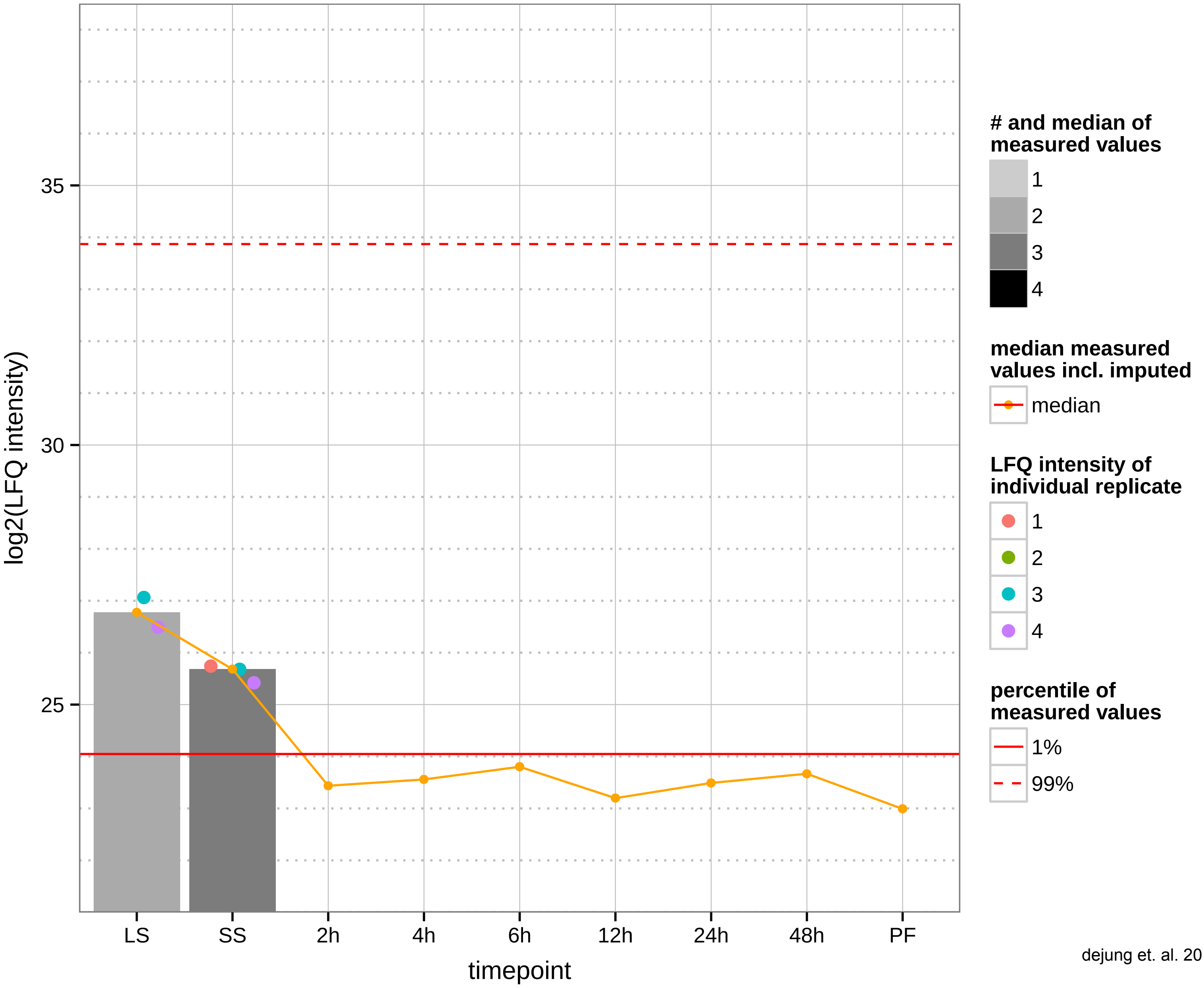
serine threonine–protein phosphatase PP1, putative (PP1–5), putative (PP1–4)
Tb927.4.3640;Tb927.4.3630
AGOF: hydrolase activity, protein serine/threonine phosphatase activity
AGOC: null
AGOP: modulation of development of symbiont involved in interaction with host, protein dephosphorylation, quorum sensing i
PGOF: hydrolase activity
PGOC: null
PGOP: null





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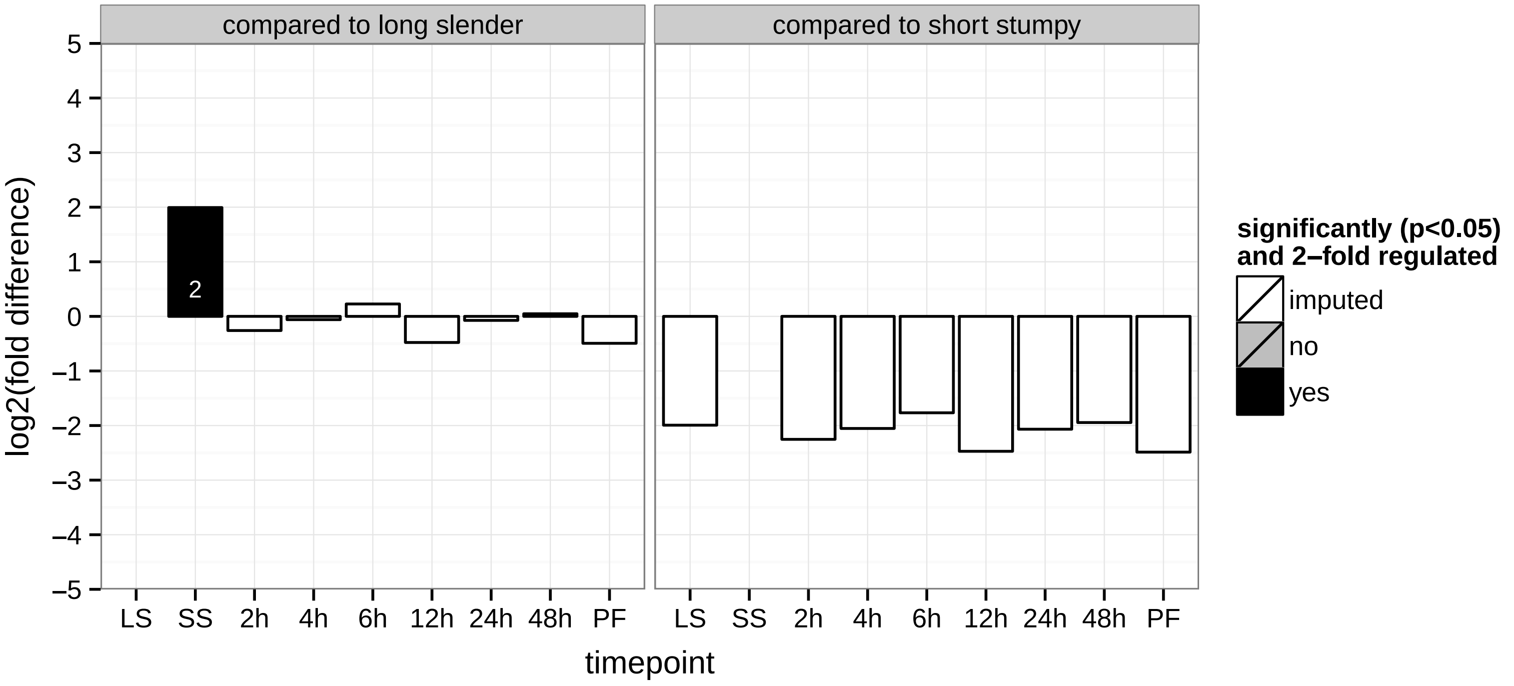
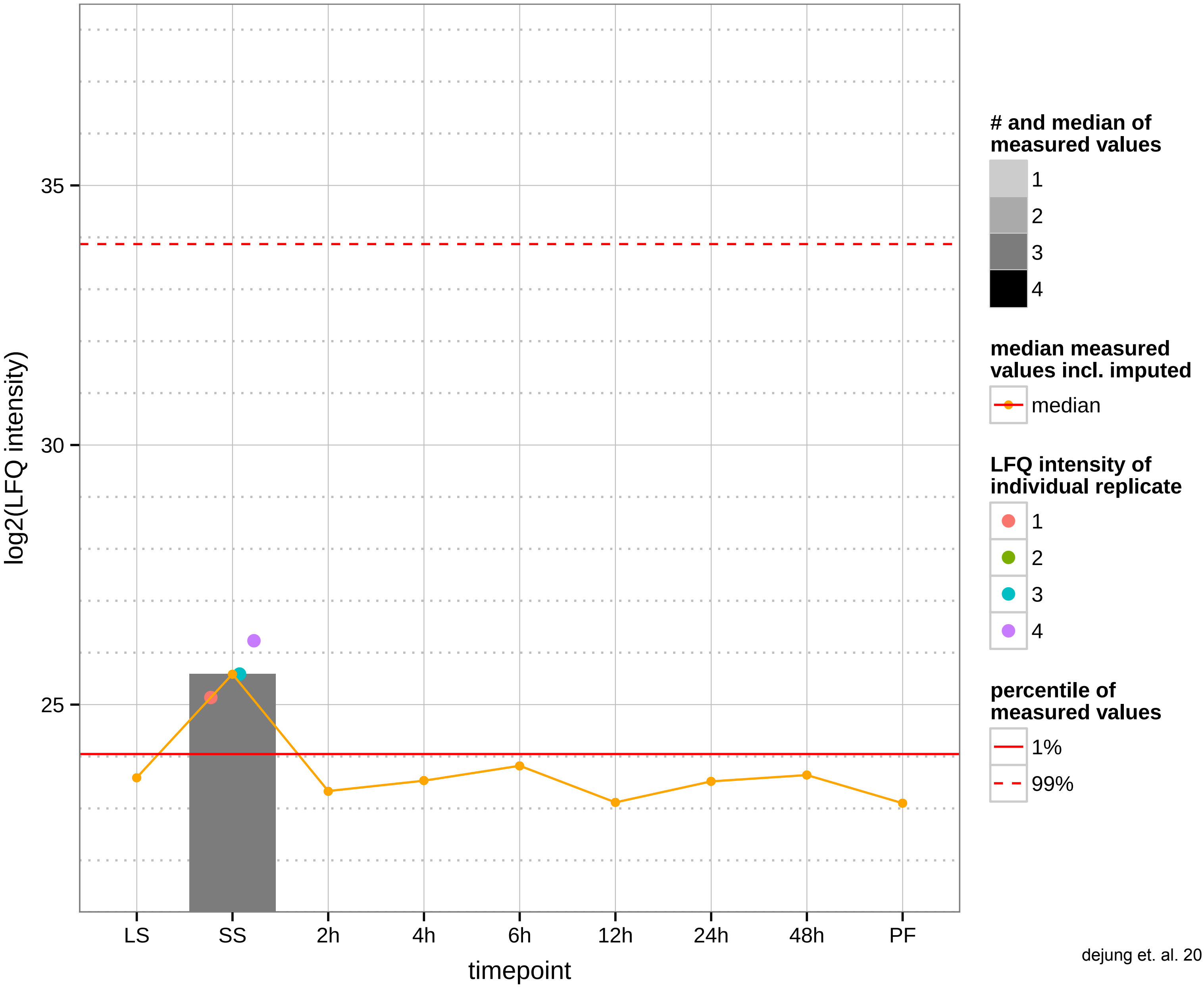
phospholipid−translocating P−type ATPase (flippase), putative
Tb927.6.3550
AGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, magnesium
AGOC: integral to membrane, membrane
AGOP: ATP biosynthetic process, phospholipid transport
PGOF: ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, hydrolase ac
PGOC: integral to membrane, membrane
PGOP: cation transport, phospholipid transport





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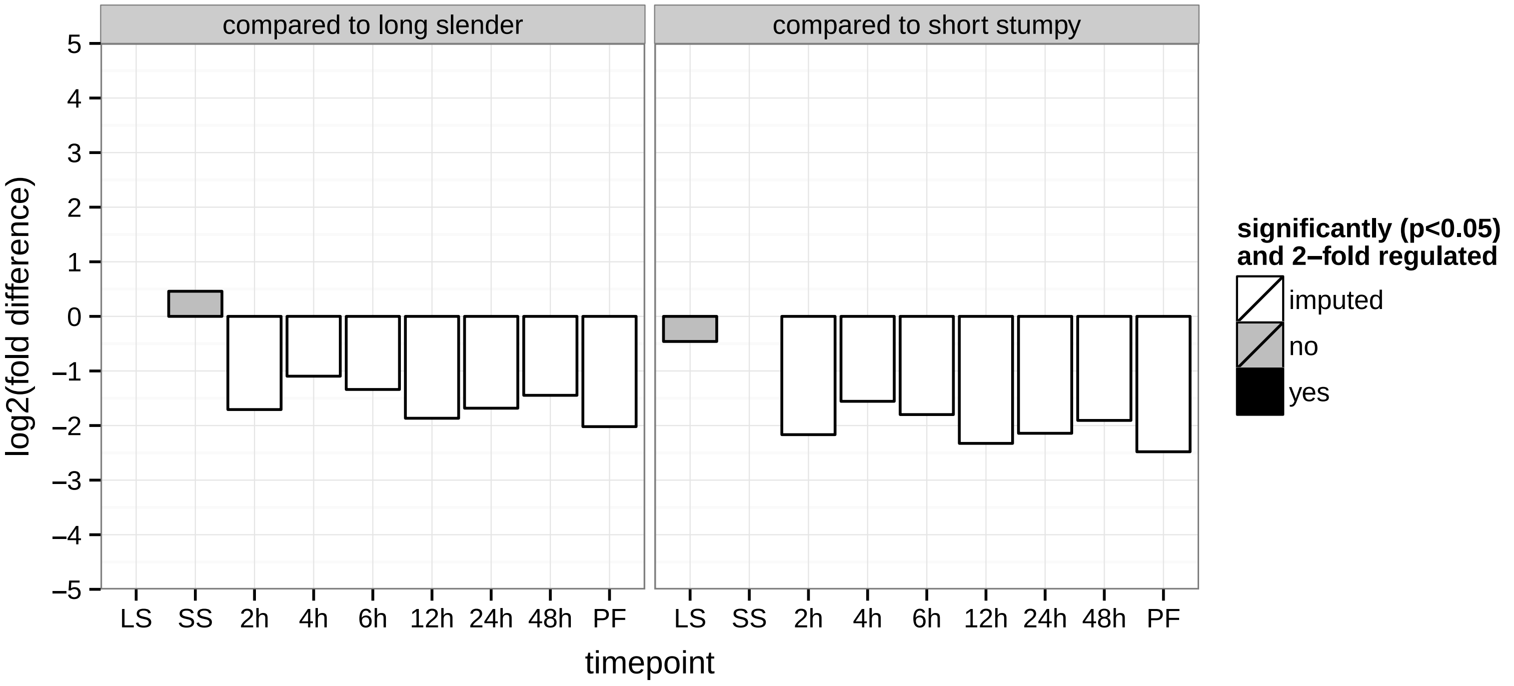
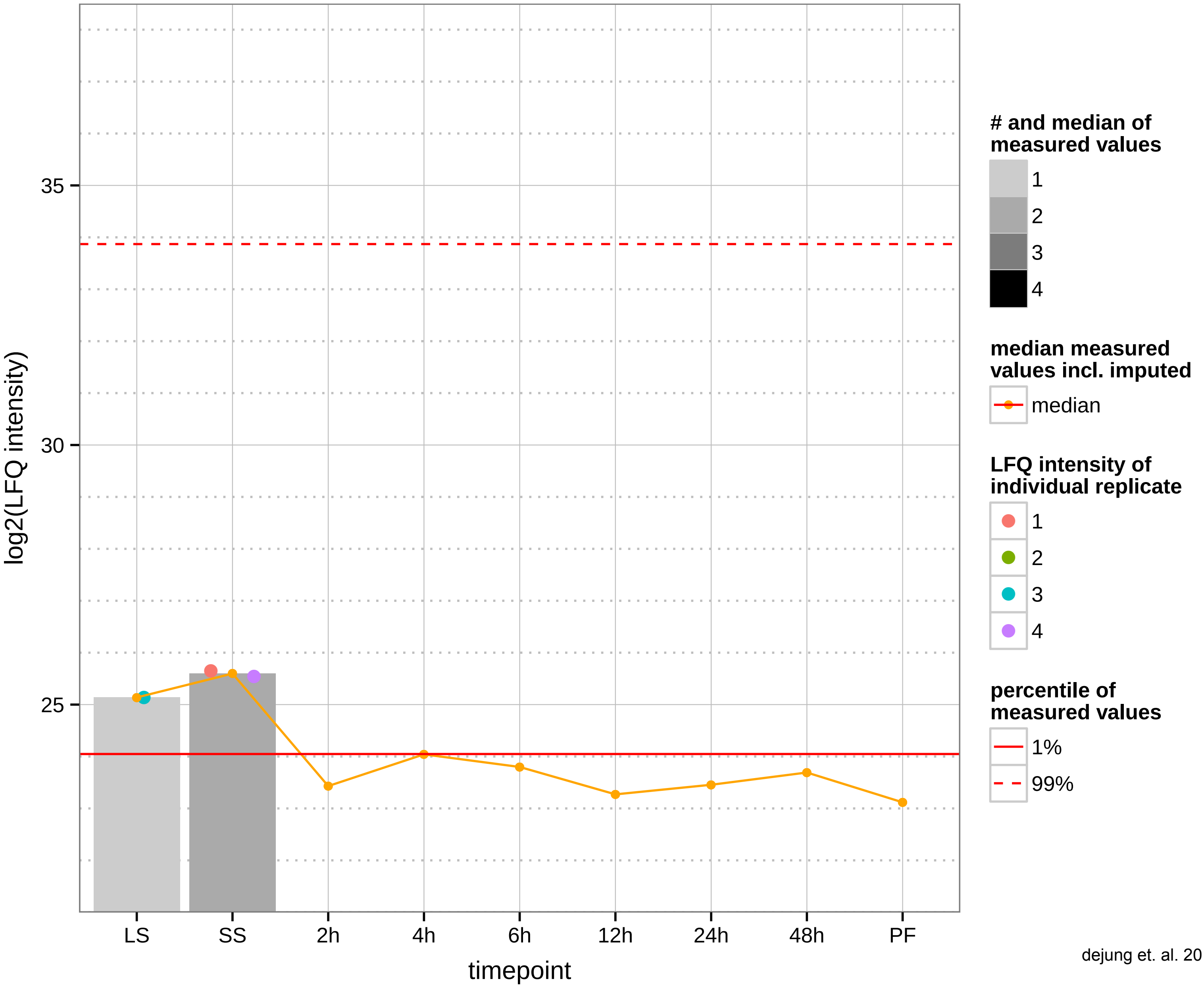
hypothetical protein, conserved
Tb927.7.6570
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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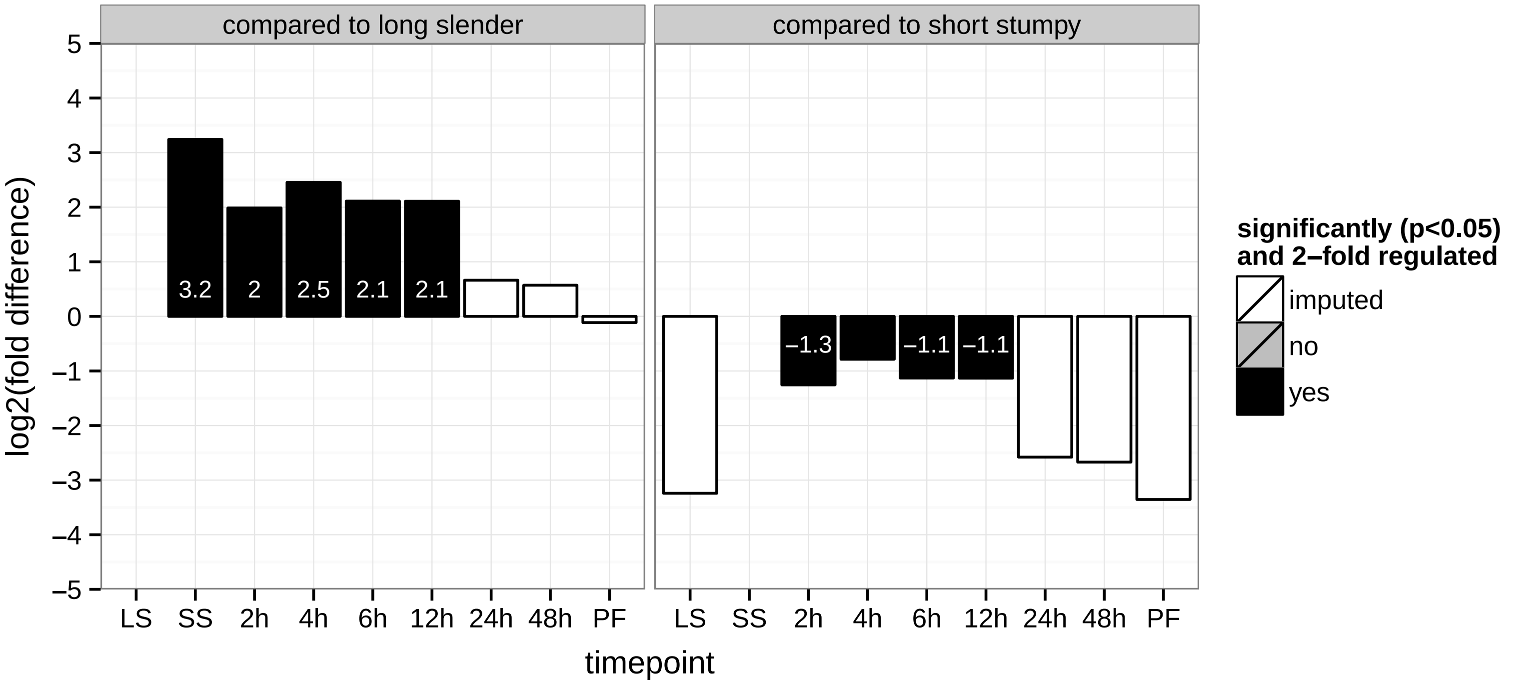
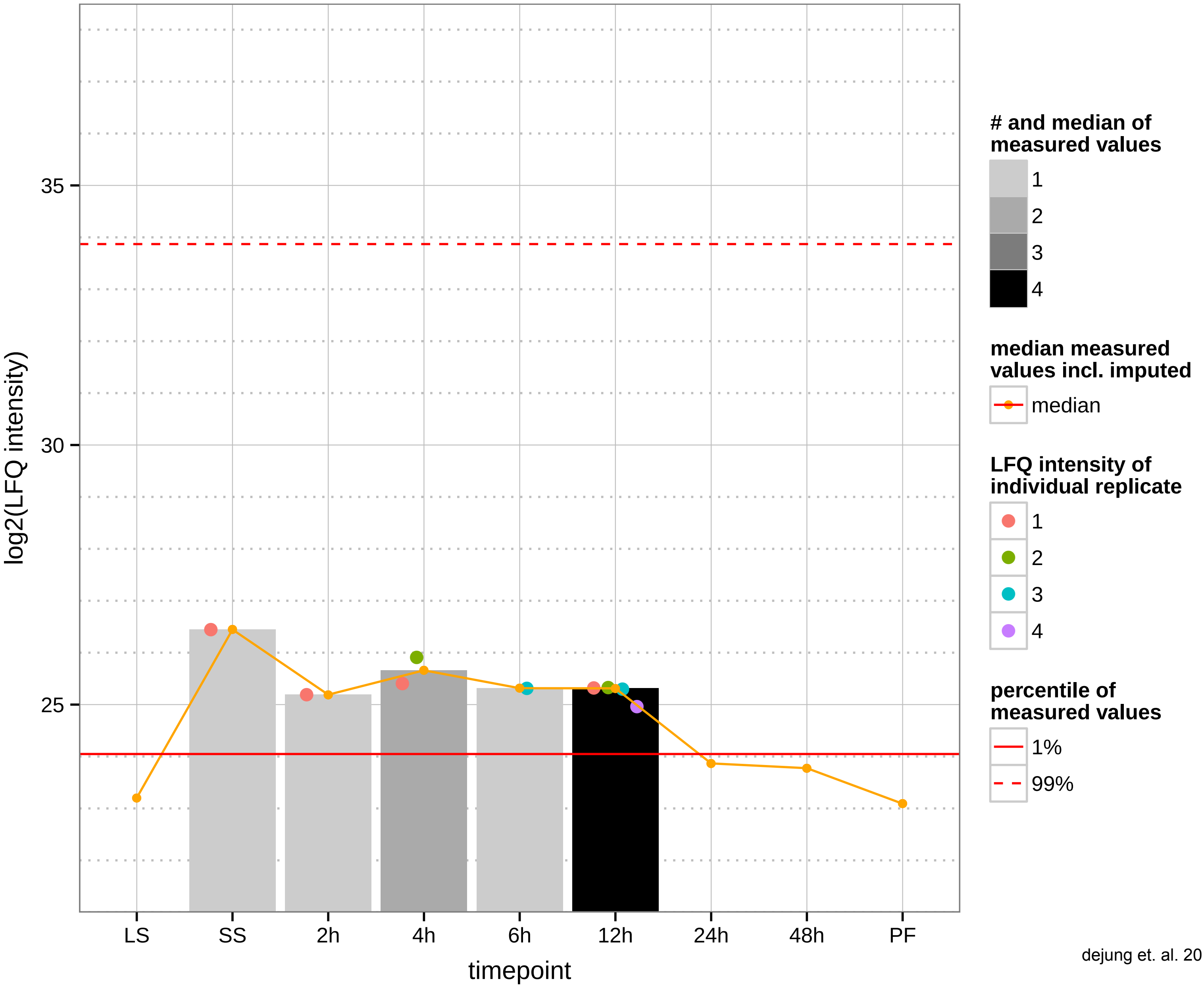
hypothetical protein, conserved
Tb927.8.2580
AGOF: null
AGOC: cytoplasm
AGOP: exocytosis, vesicle docking
PGOF: null
PGOC: cytoplasm
PGOP: exocytosis, vesicle docking





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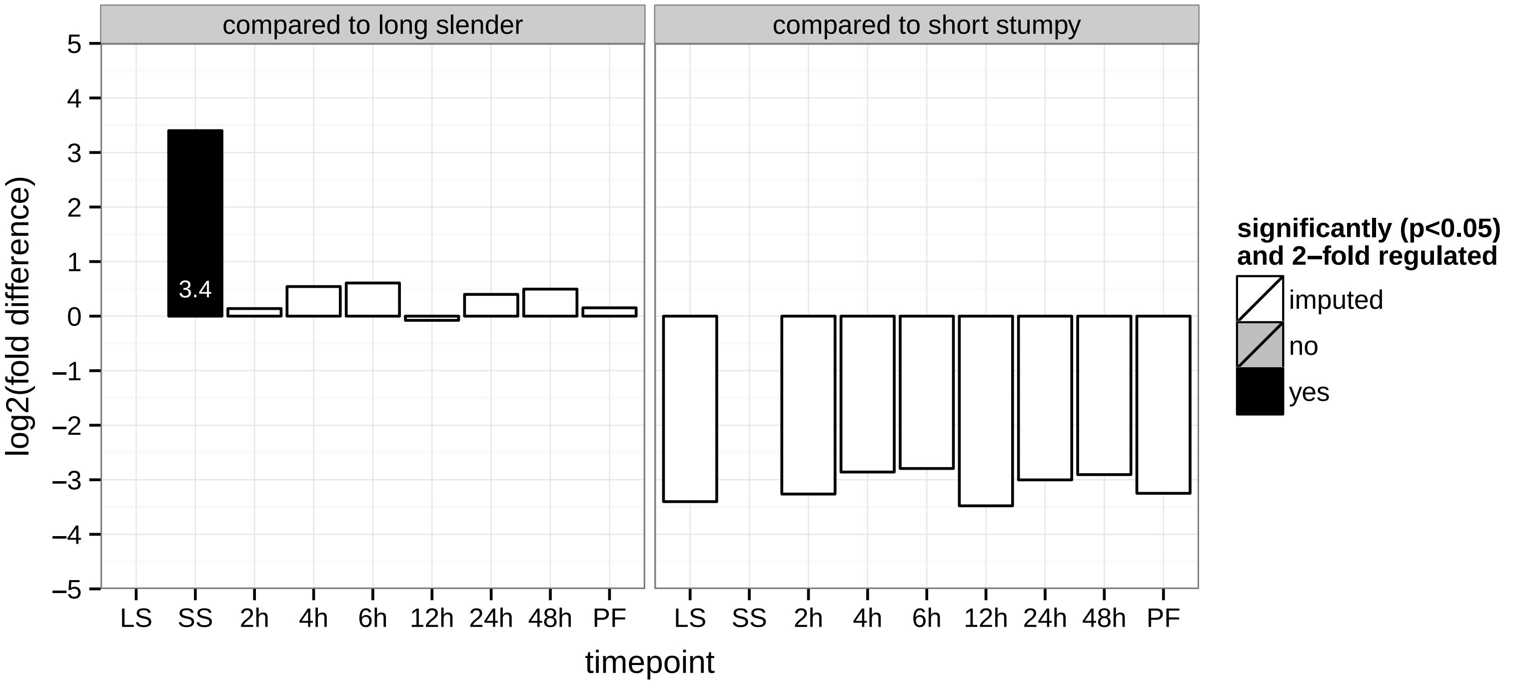
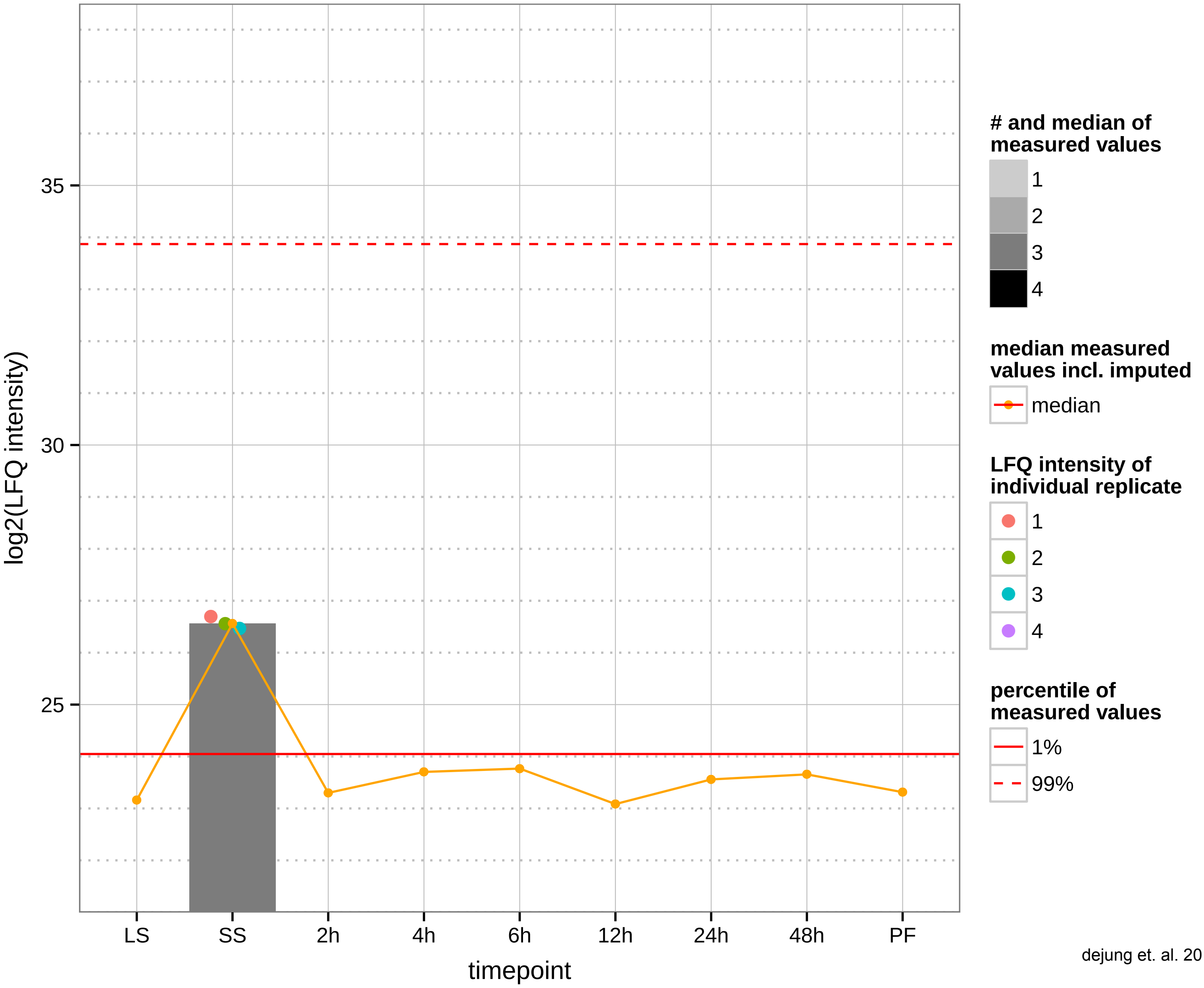
hypothetical protein, conserved
Tb927.9.5620
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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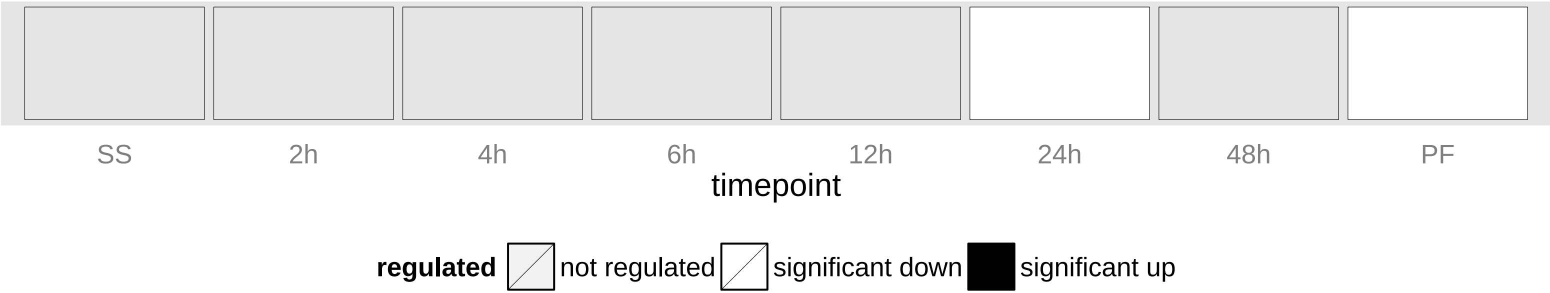

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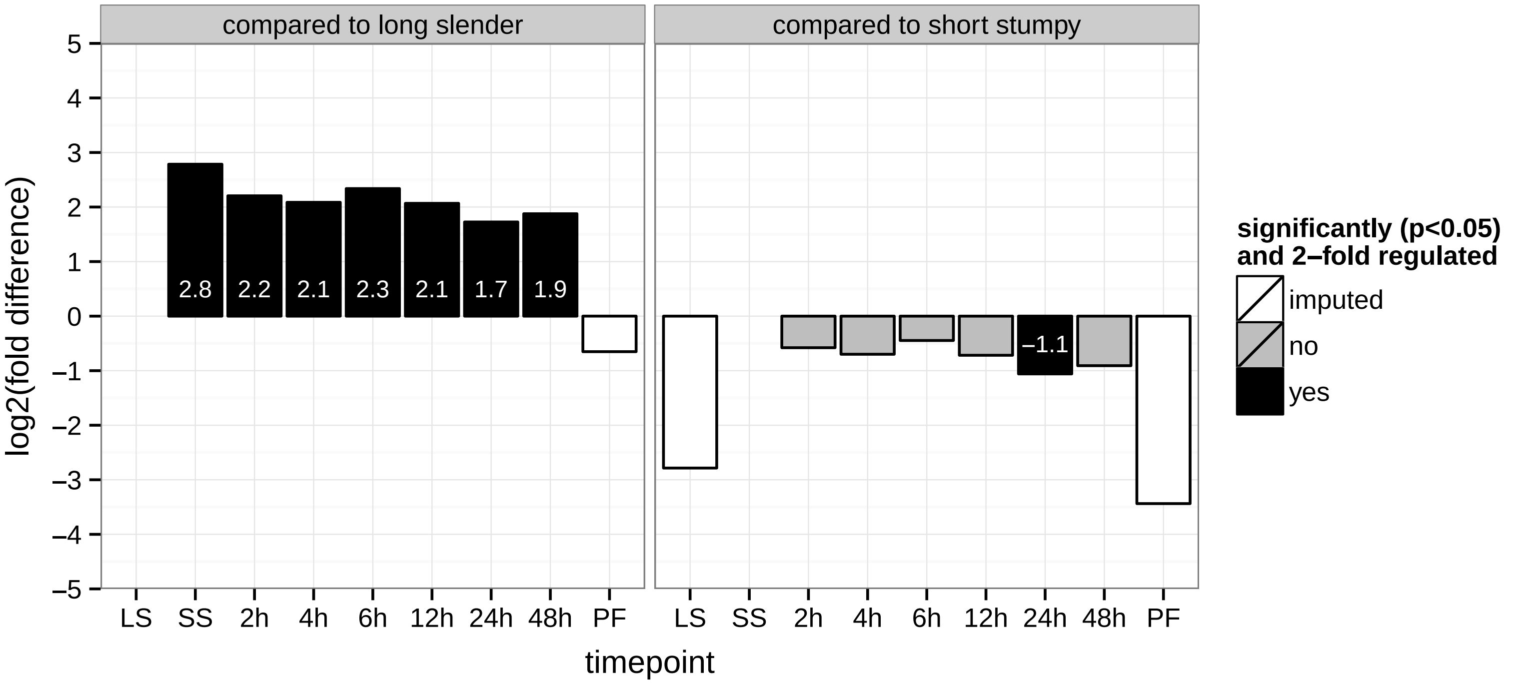
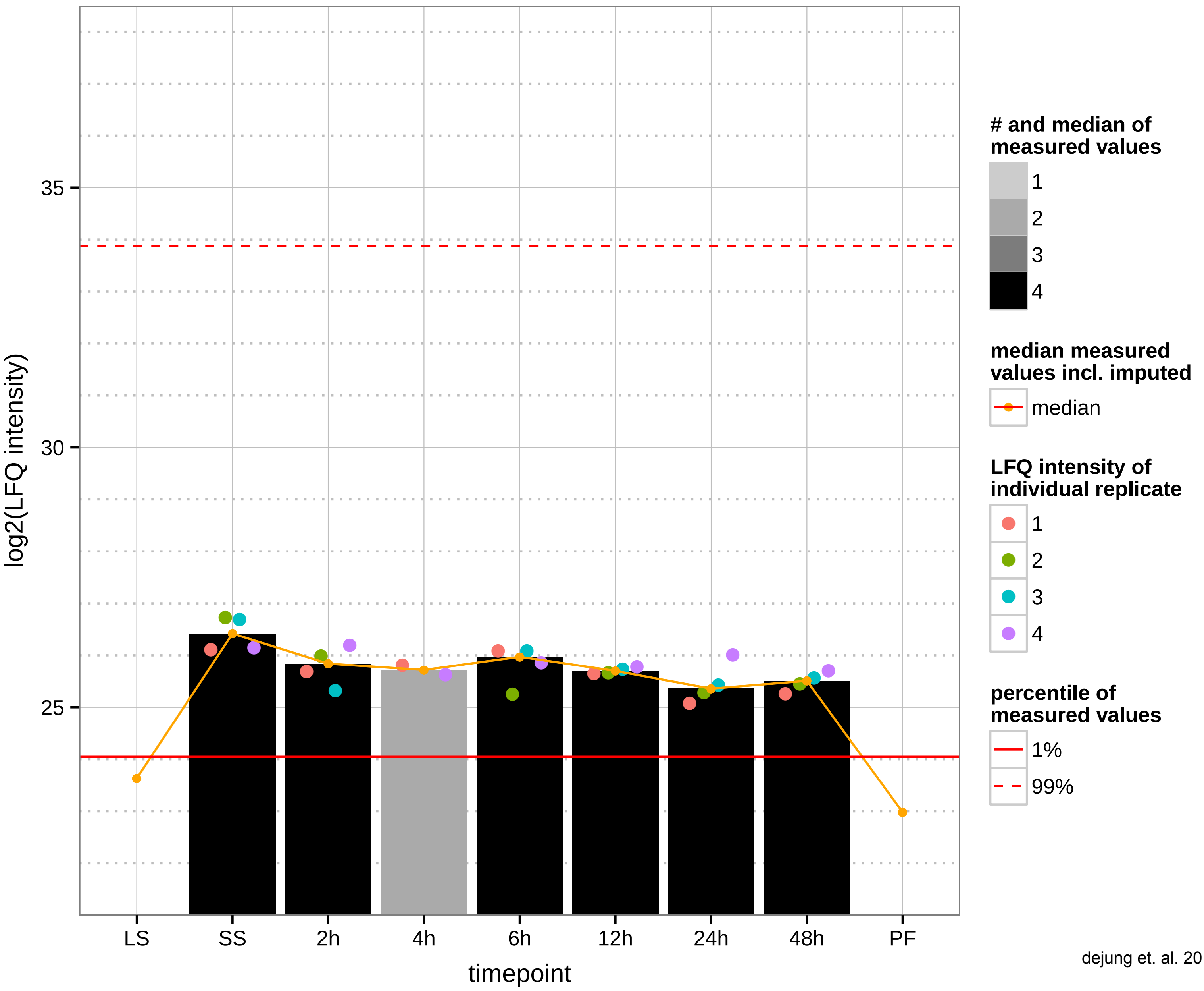
hypothetical protein, conserved
Tb927.10.11600
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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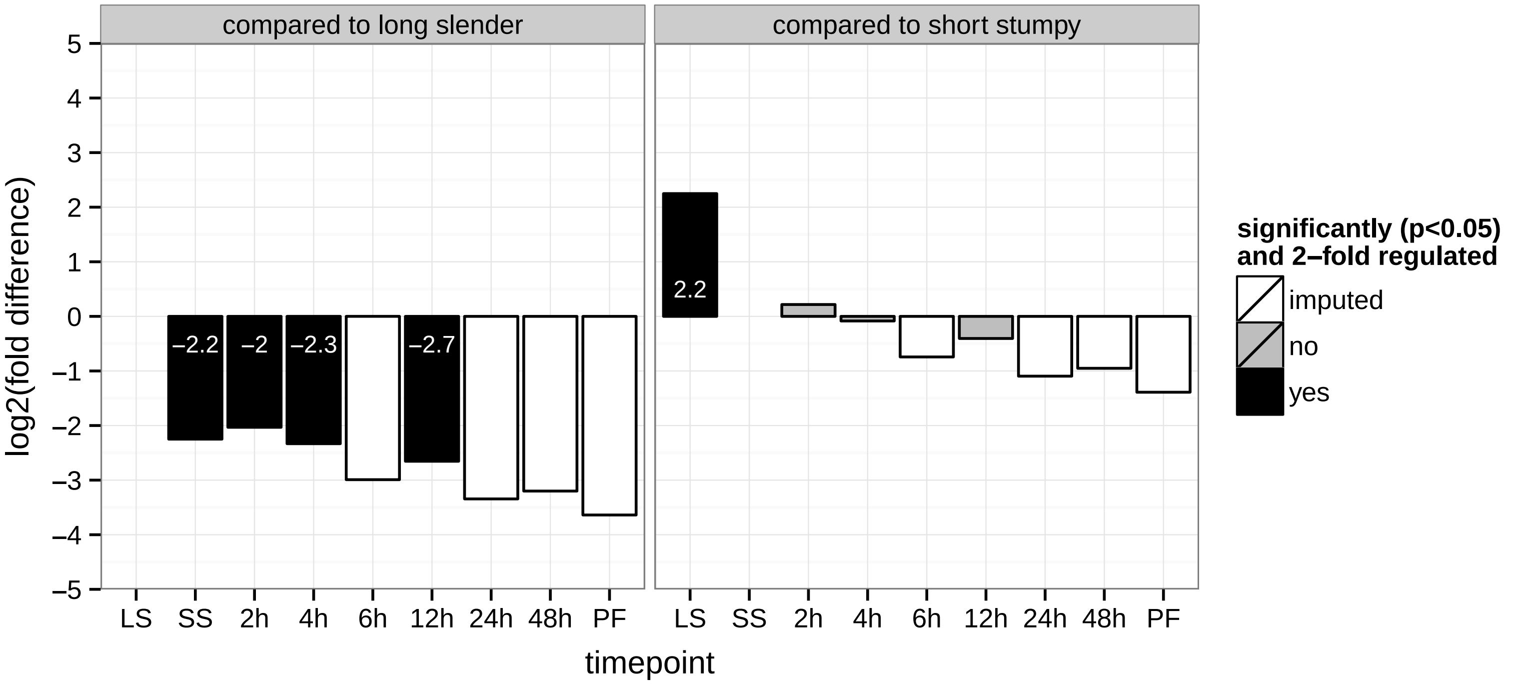
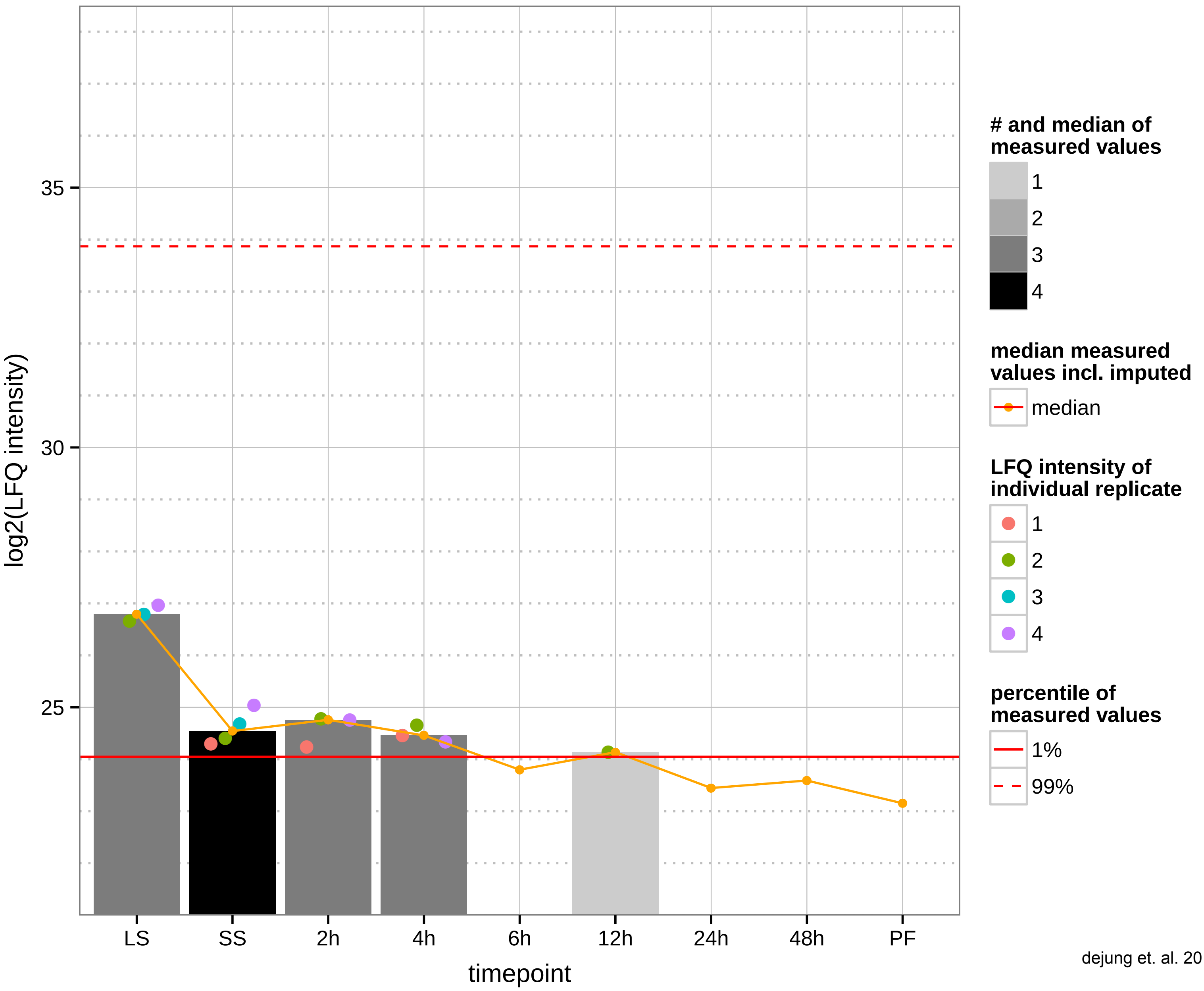
procyclin–associated gene 2 (PAG2) protein, putative
Tb927.10.5690
AGOF: null
AGOC: null
AGOP: evasion or tolerance of host immune response
PGOF: null
PGOC: null
PGOP: evasion or tolerance of host immune response





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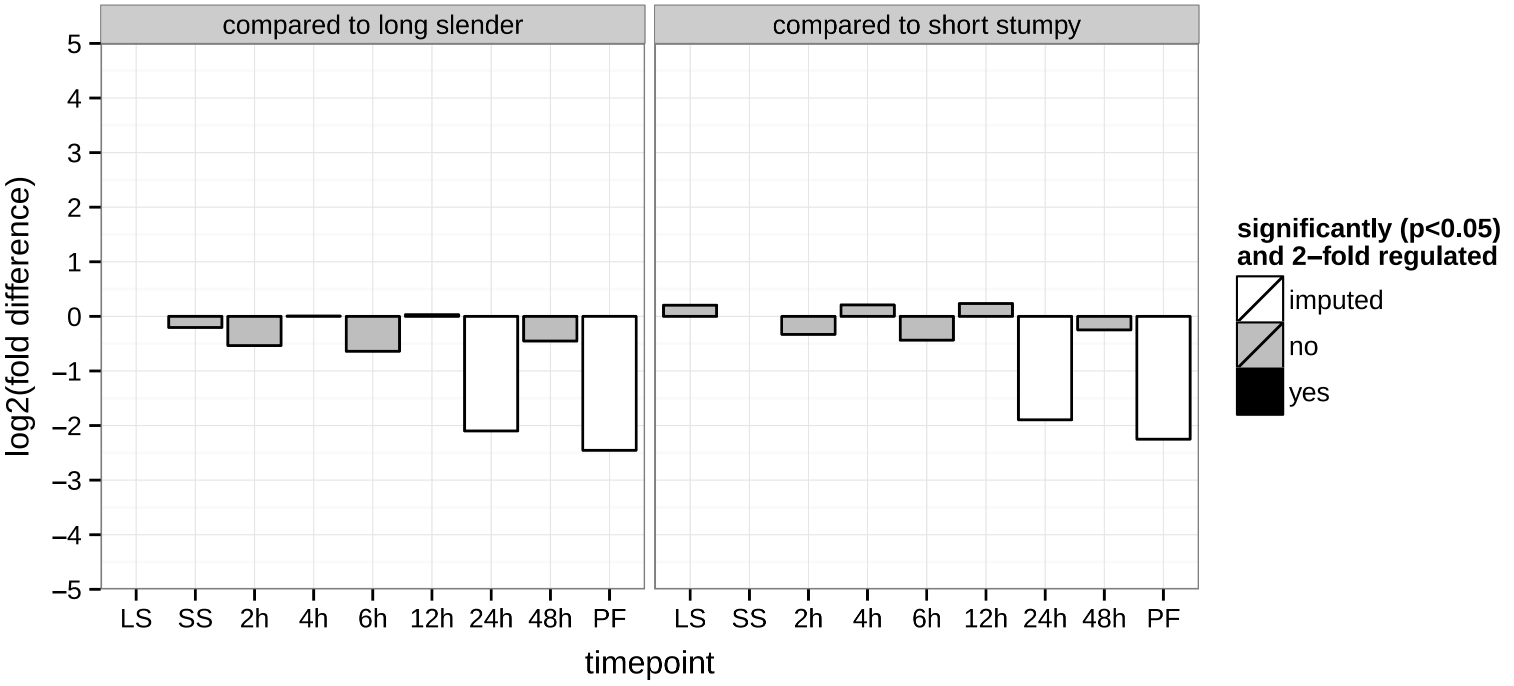
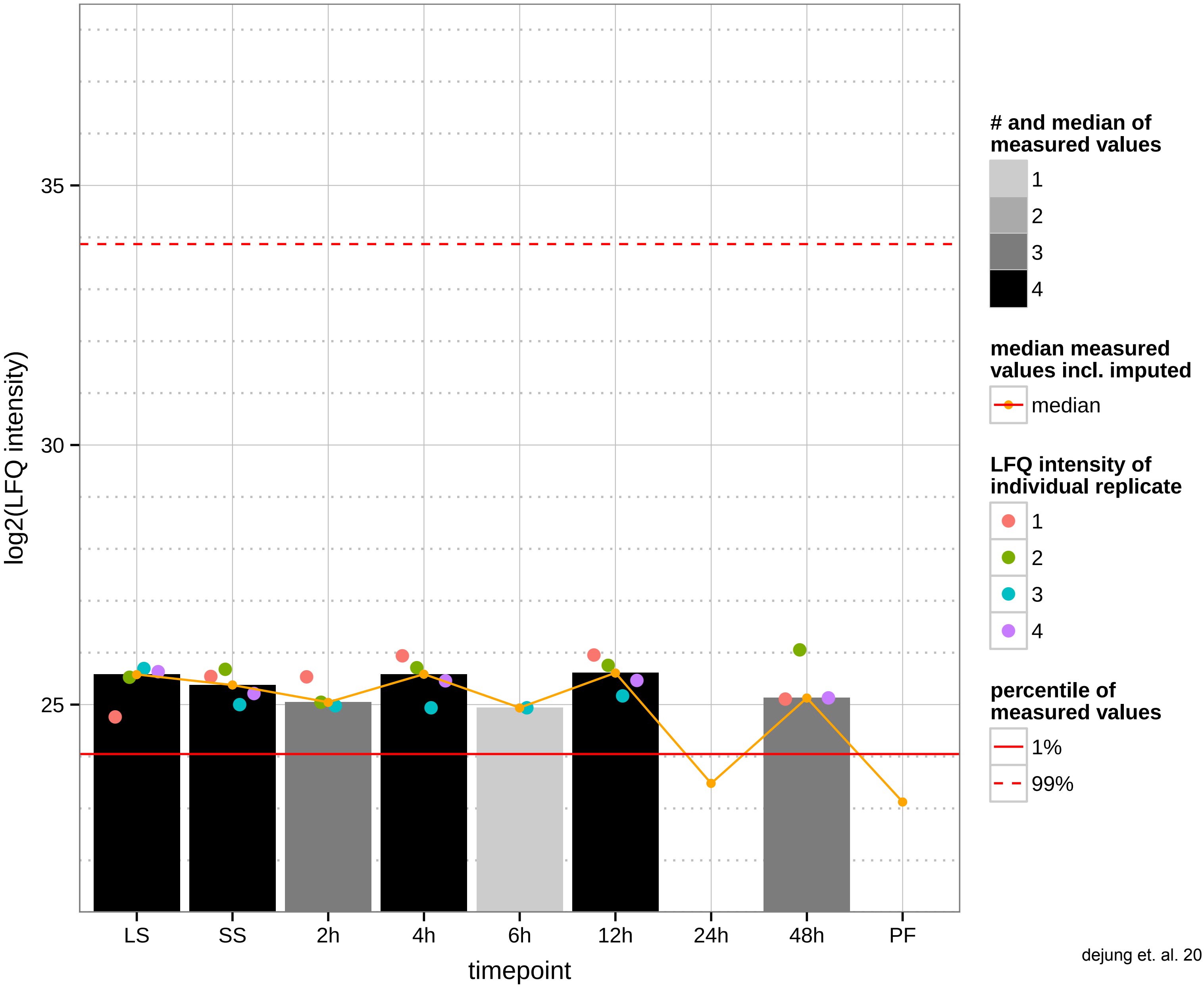
cAMP response protein, putative (CARP2a)
Tb927.11.12860.2;Tb927.11.12860.1
AGOF: null
AGOC: null
AGOP: response to drug
PGOF: null
PGOC: null
PGOP: null





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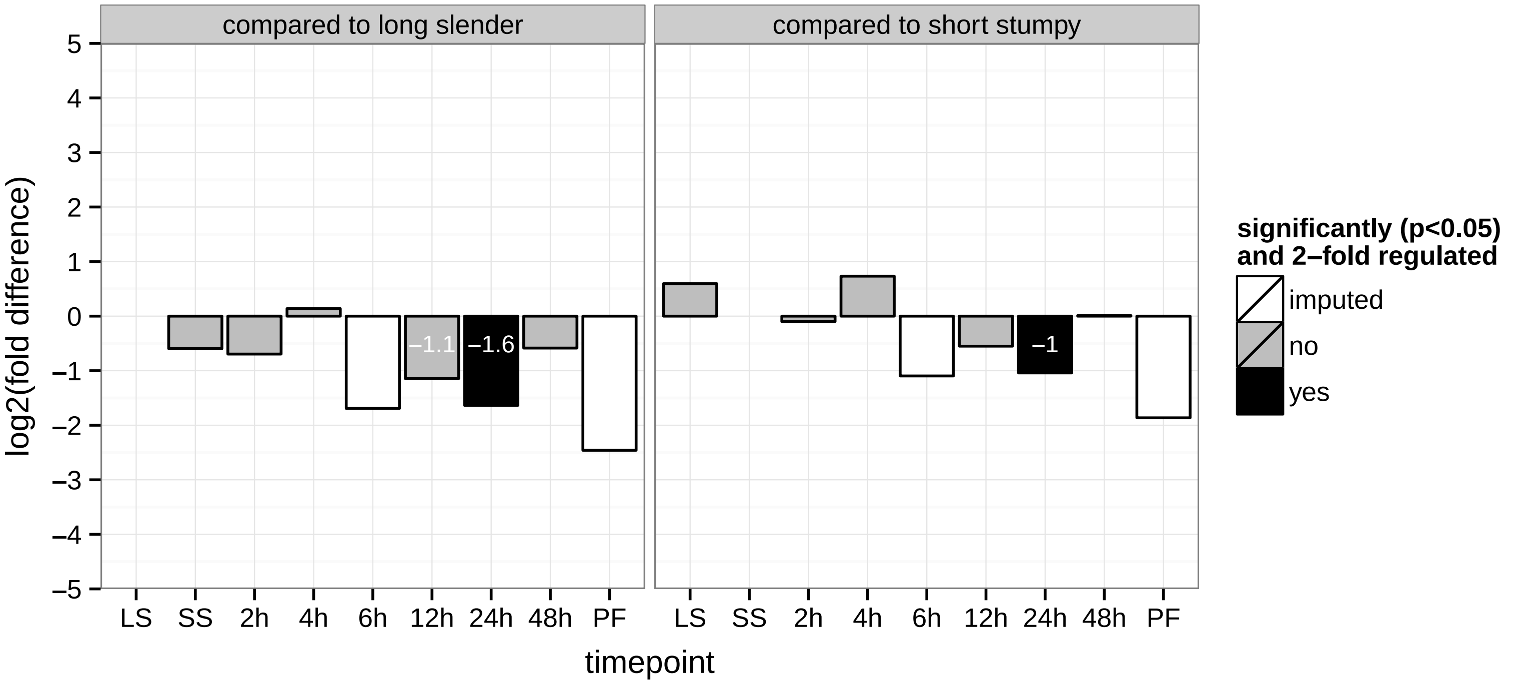
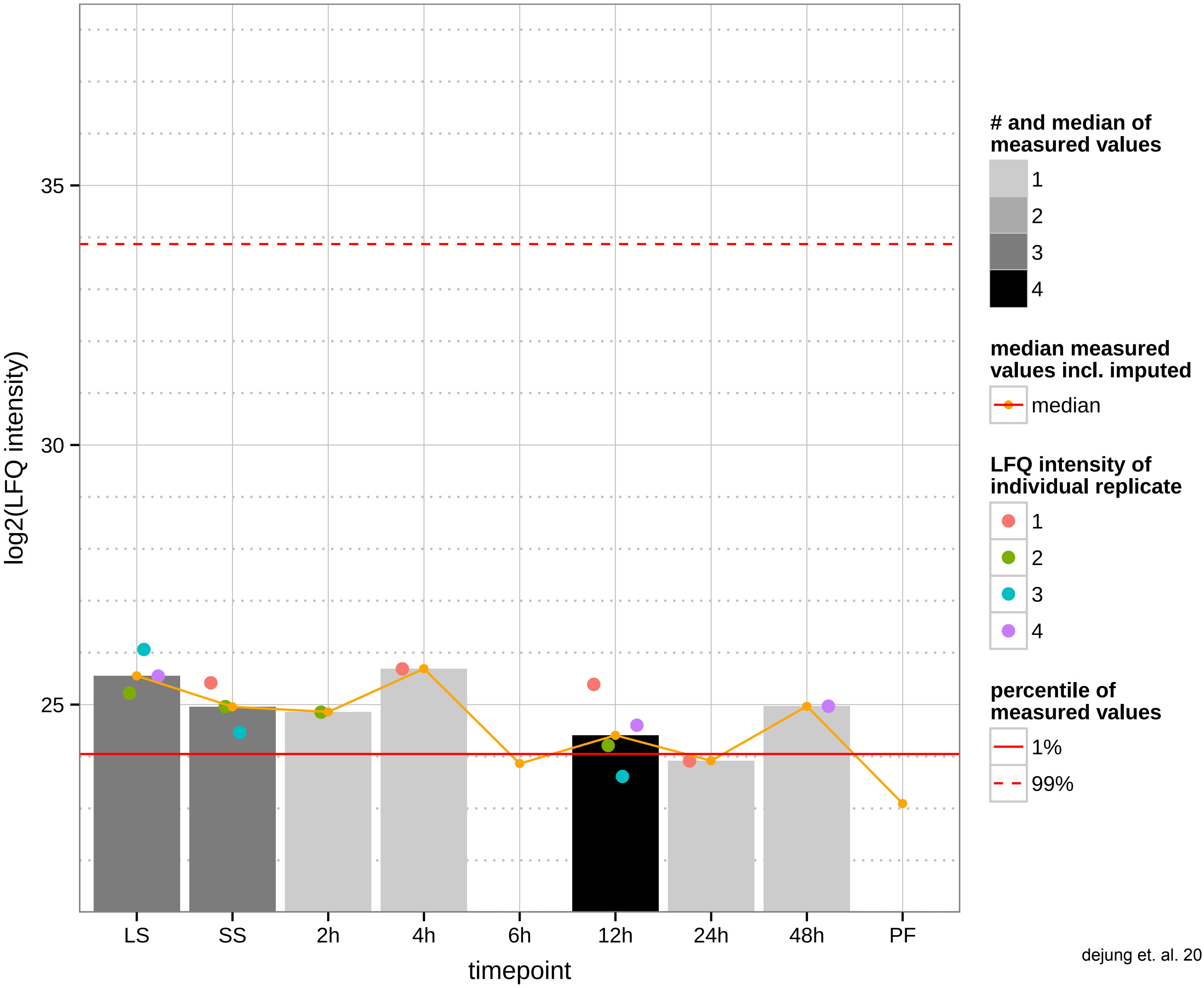
hypothetical protein, conserved
Tb927.2.1700
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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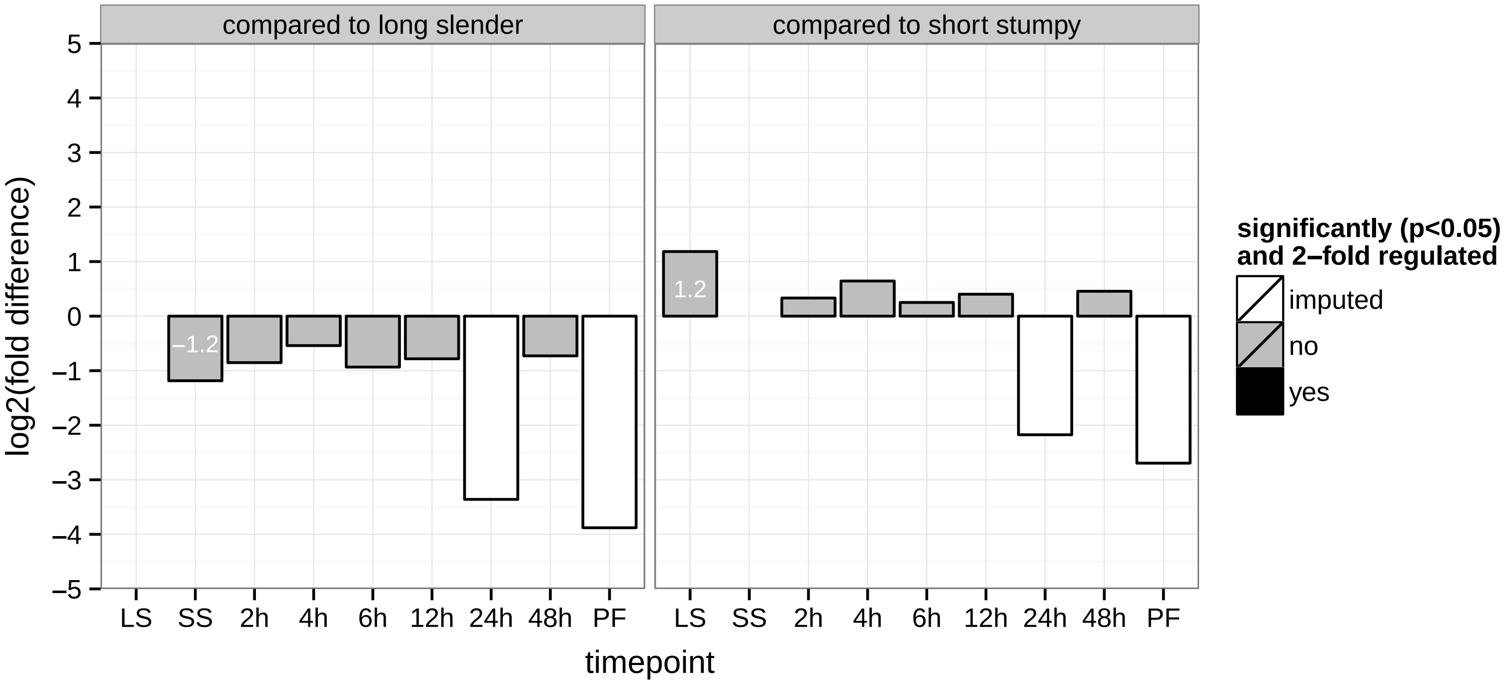
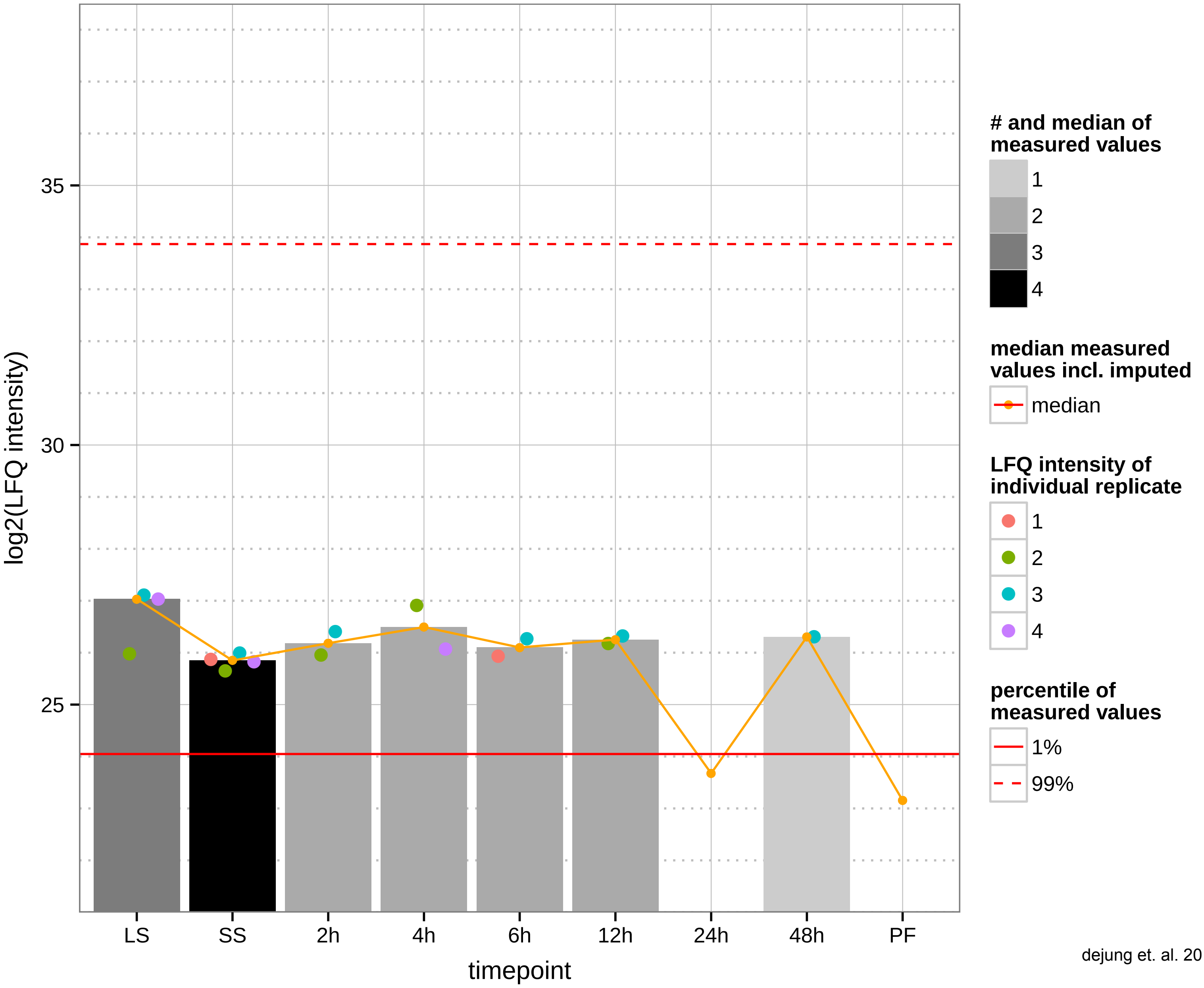
hypothetical protein, conserved
Tb927.2.1850
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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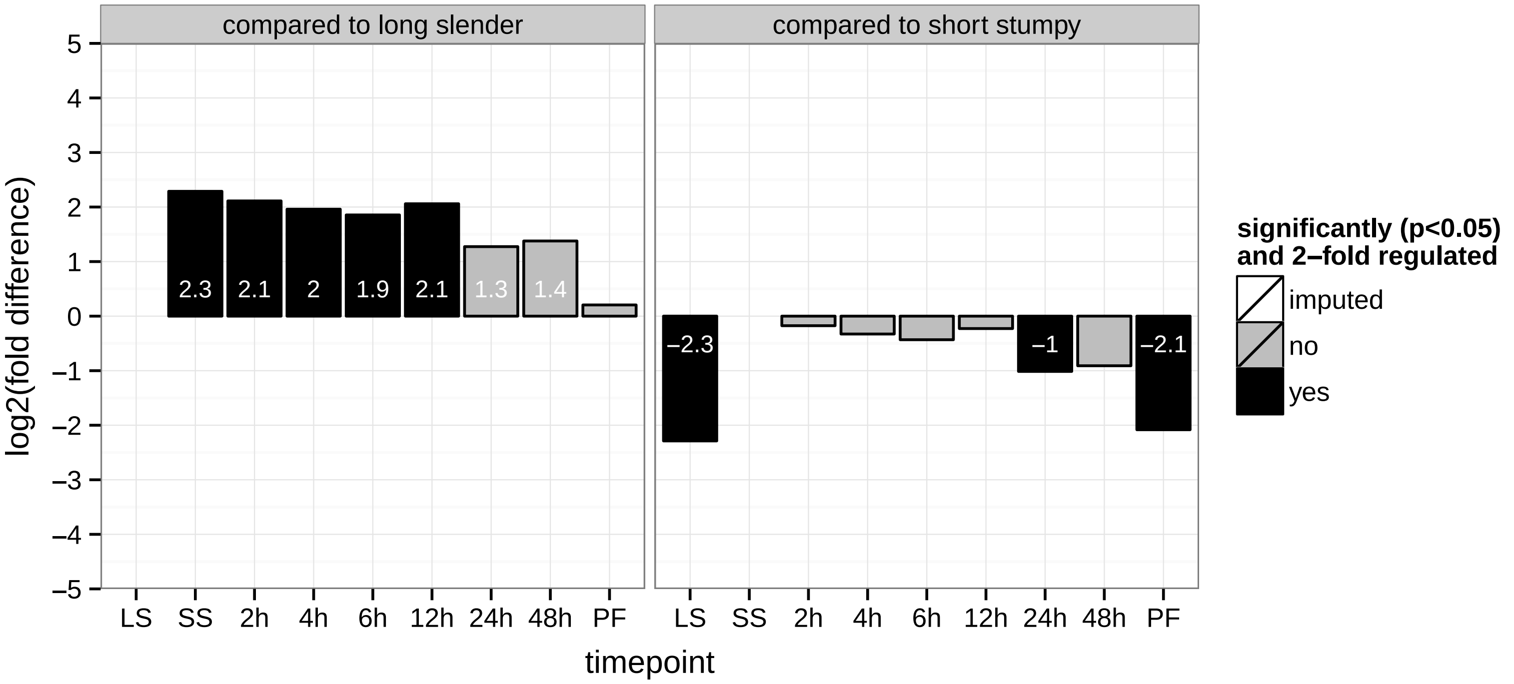
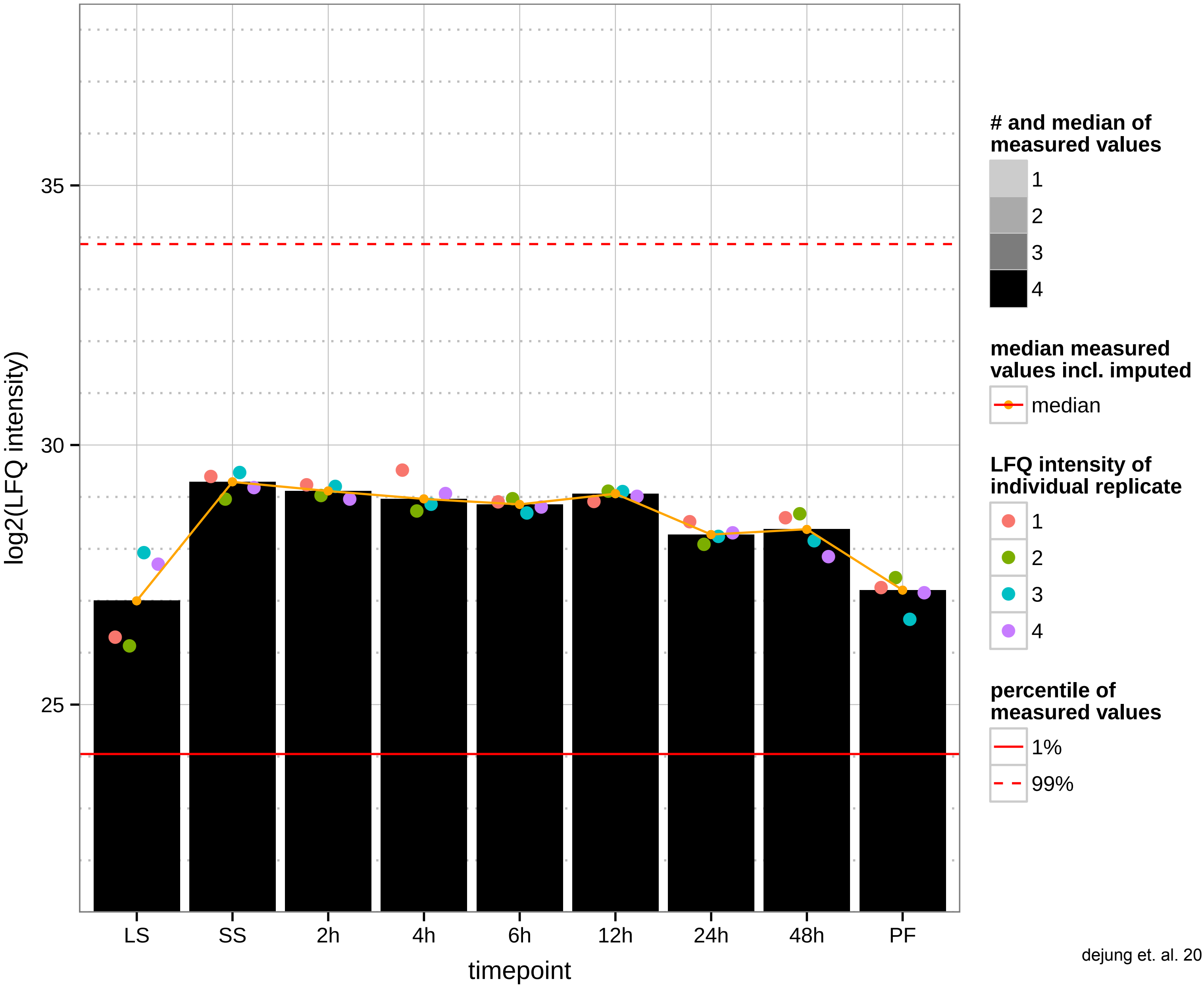
UDP–glucose:glycoprotein glucosyltransferase, putative
Tb927.3.4630
AGOF: UDP–glucose:glycoprotein glucosyltransferase activity
AGOC: endoplasmic reticulum
AGOP: protein glycosylation
PGOF: UDP–glucose:glycoprotein glucosyltransferase activity, transferase activity, transferring glycosyl groups
PGOC: null
PGOP: protein glycosylation





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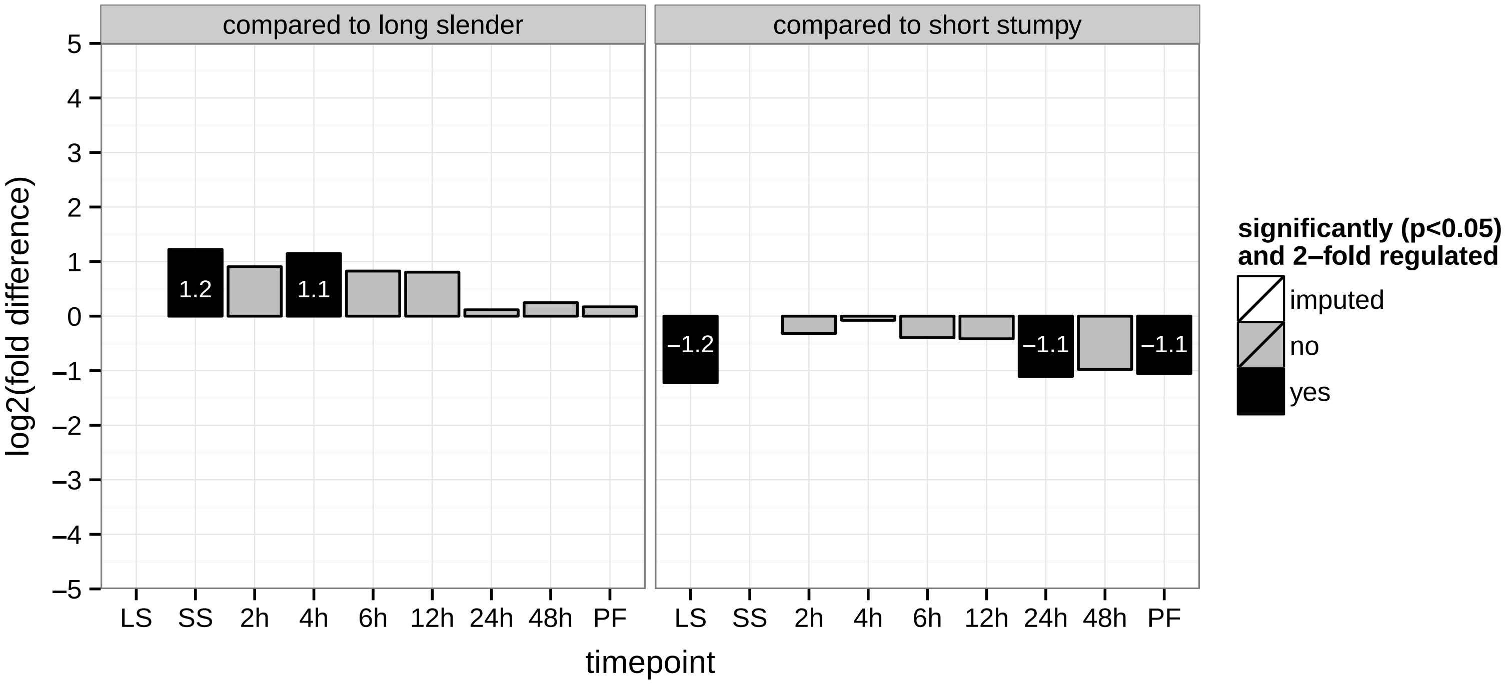
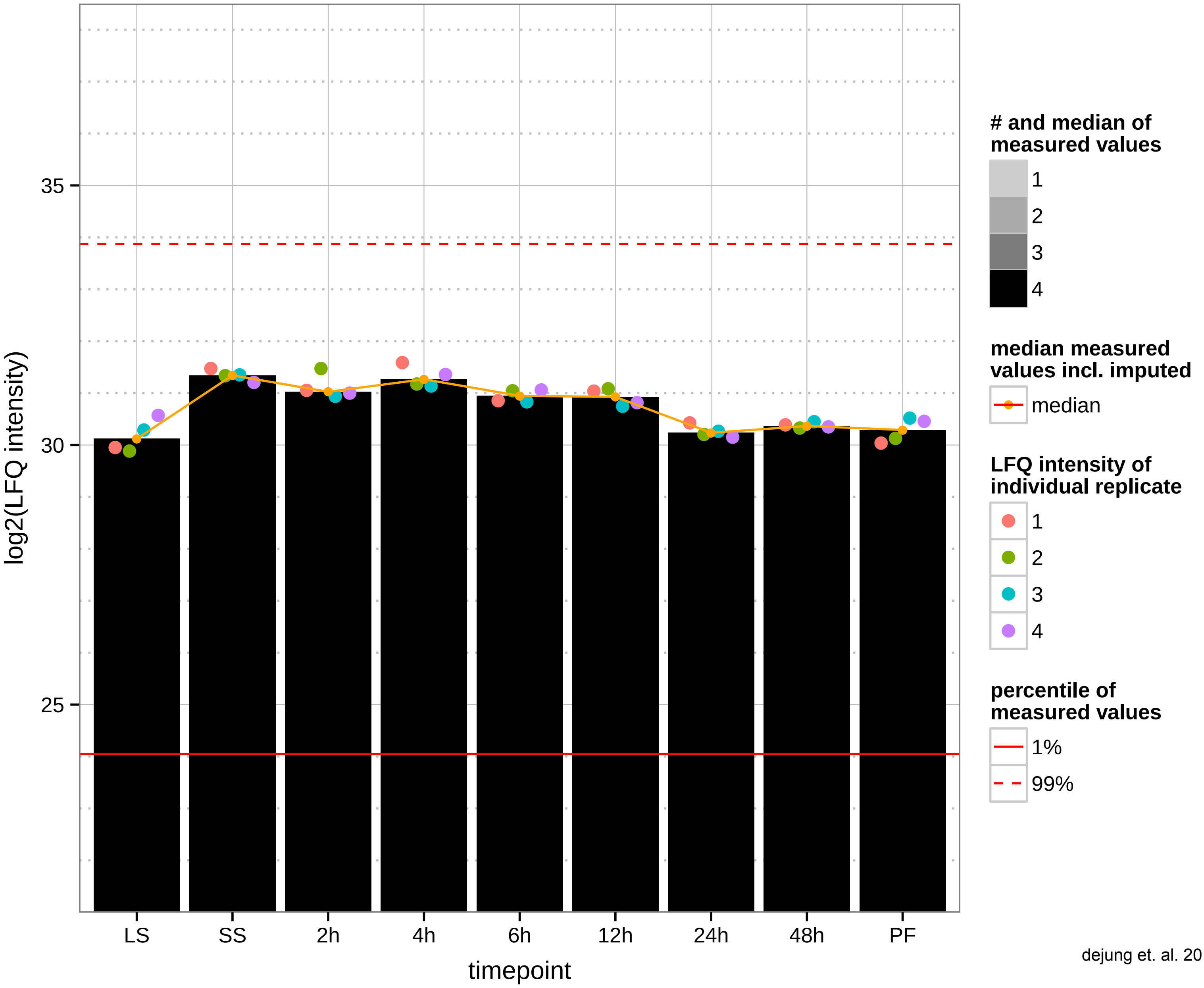
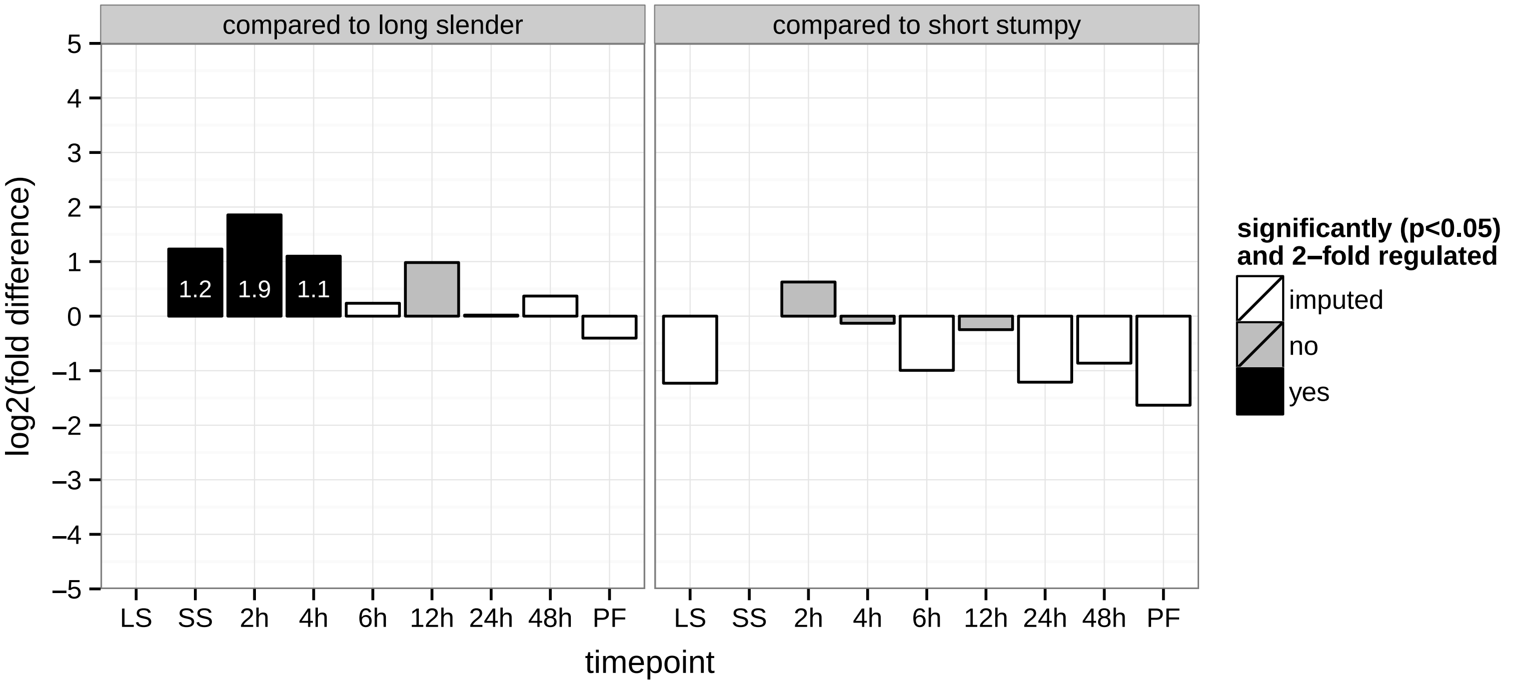
hypothetical protein, conserved
Tb927.6.2200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

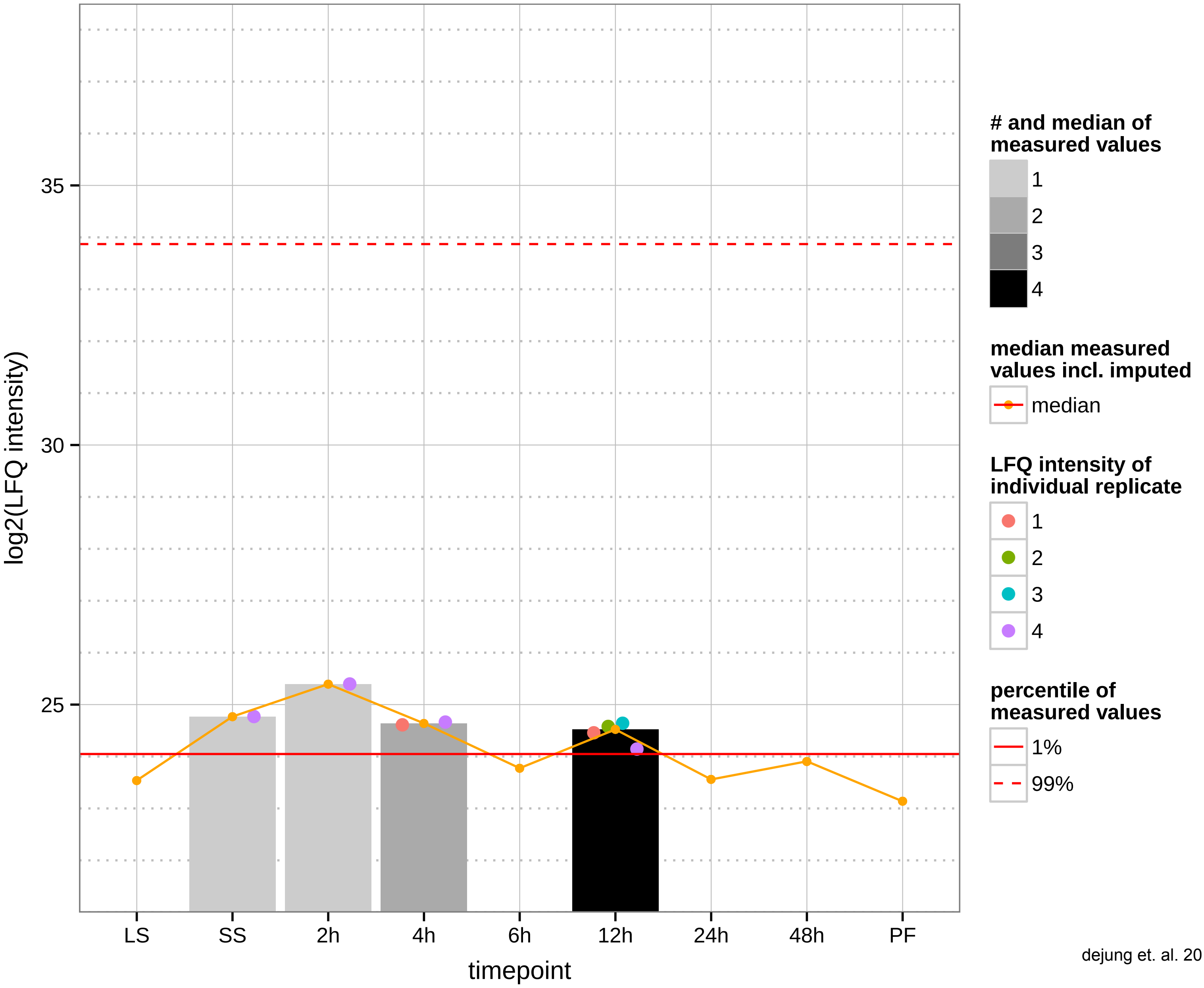




dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.5150
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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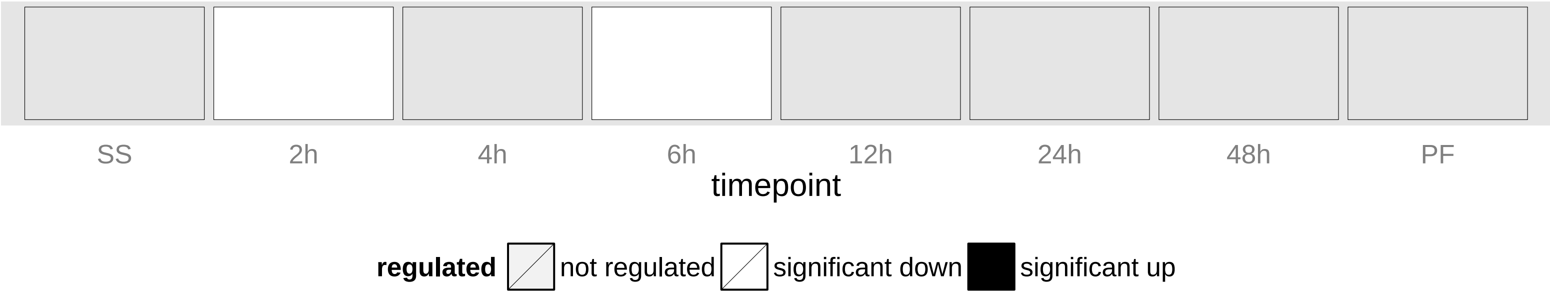

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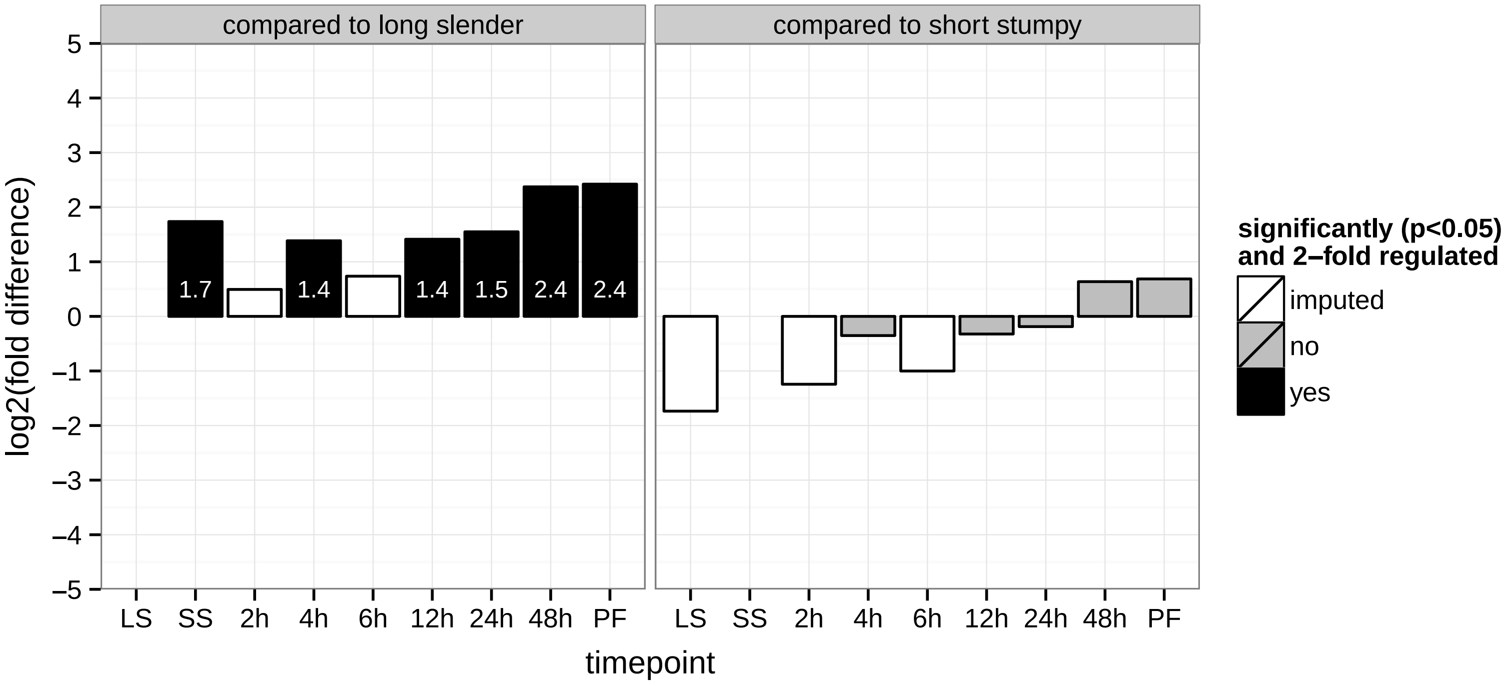
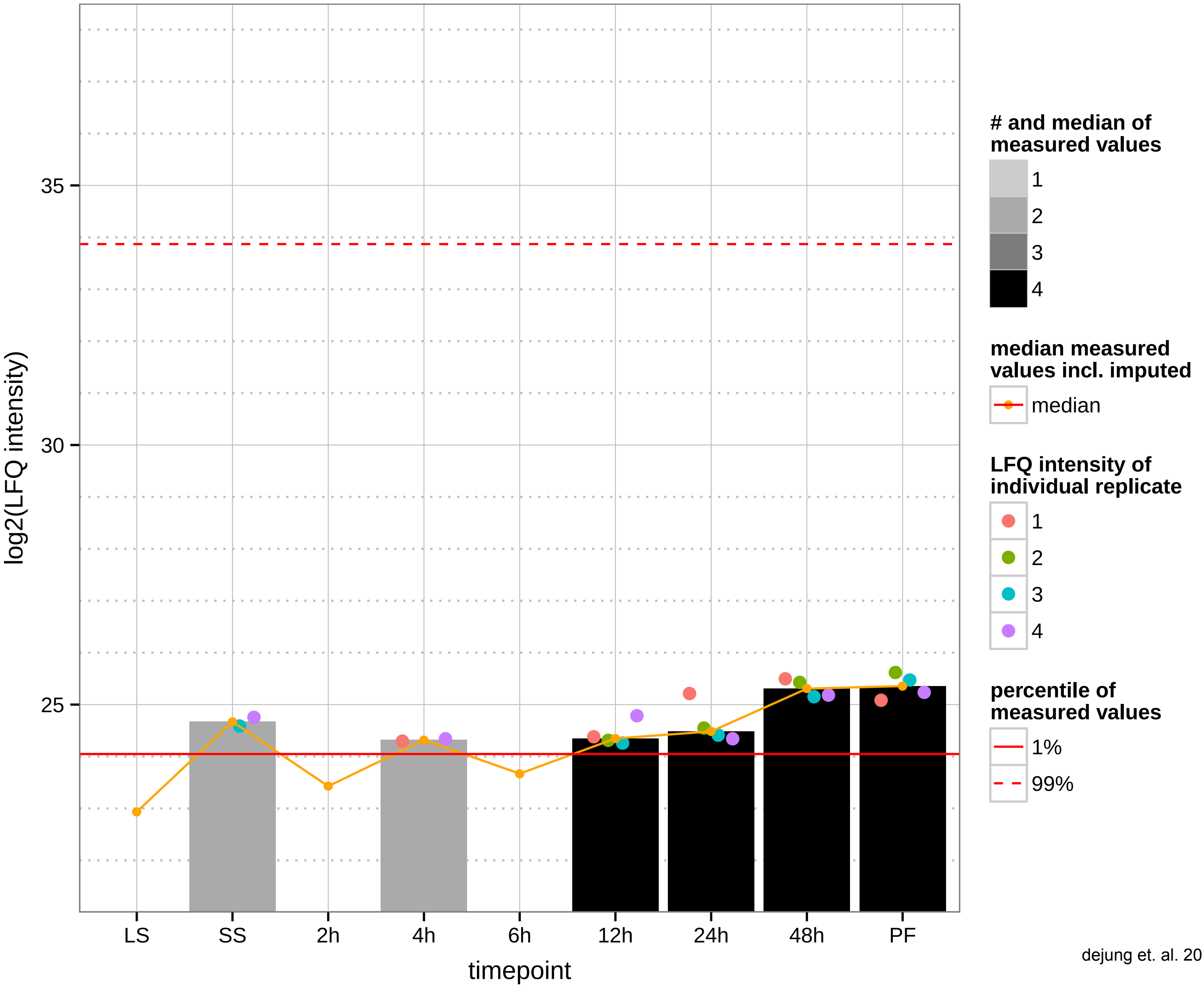
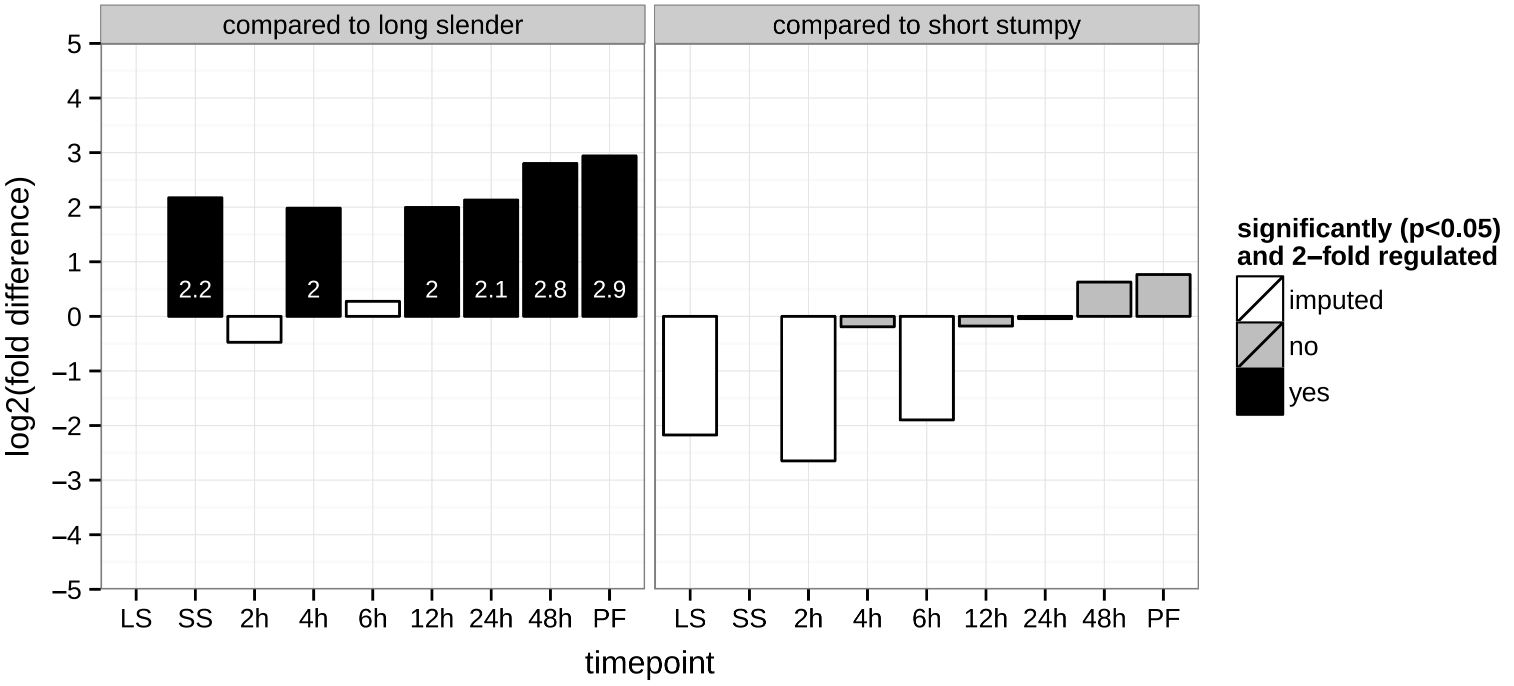
aspartyl–tRNA synthetase, putative
Tb927.10.1260
AGOF: ATP binding, asparagine–tRNA ligase activity, aspartate–tRNA ligase activity, nucleic acid binding
AGOC: cytoplasm, mitochondrion
AGOP: asparaginyl–tRNA aminoacylation, aspartyl–tRNA aminoacylation, translation
PGOF: ATP binding, aminoacyl–tRNA ligase activity, nucleic acid binding, nucleotide binding
PGOC: cytoplasm
PGOP: tRNA aminoacylation for protein translation

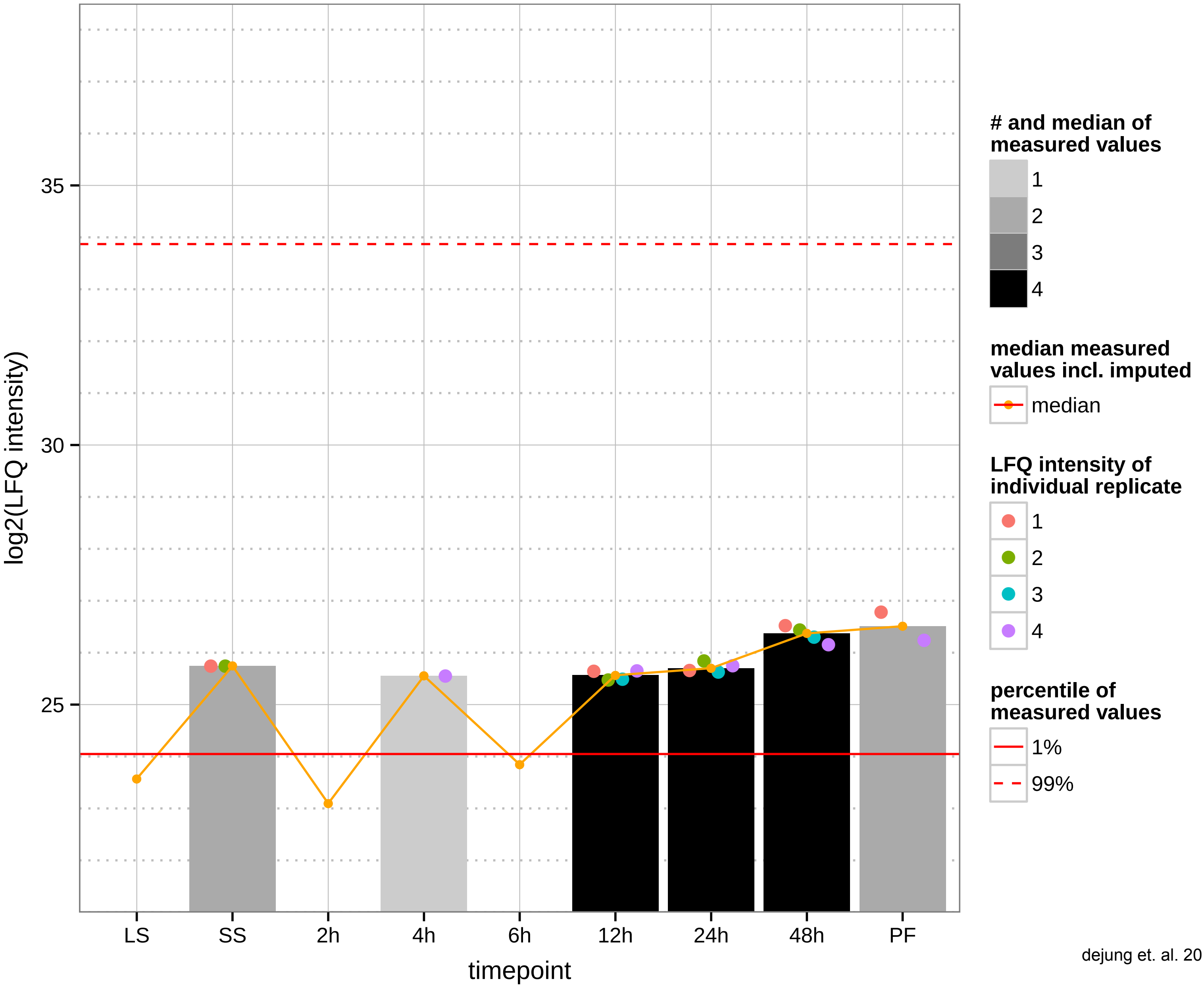




dejung et. al. 2015

hypothetical protein
Tb927.10.8880
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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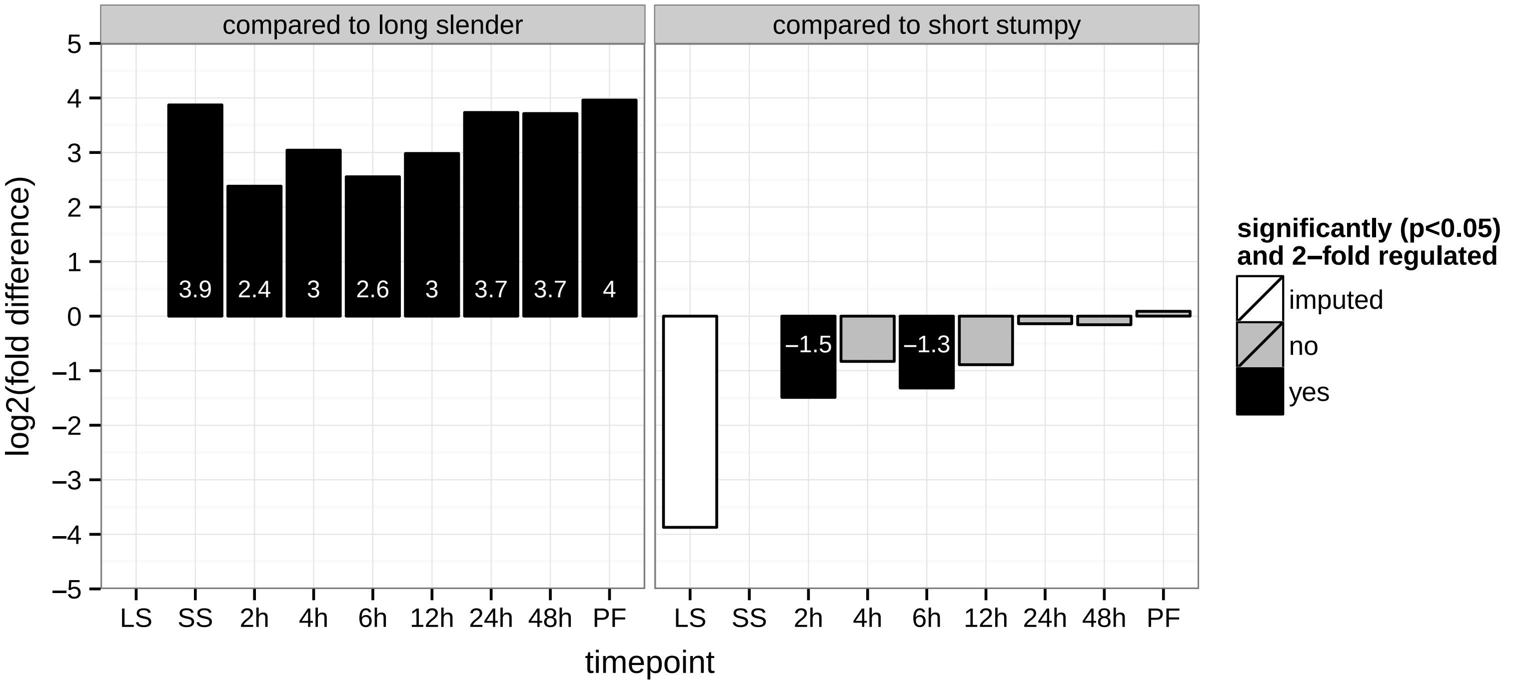
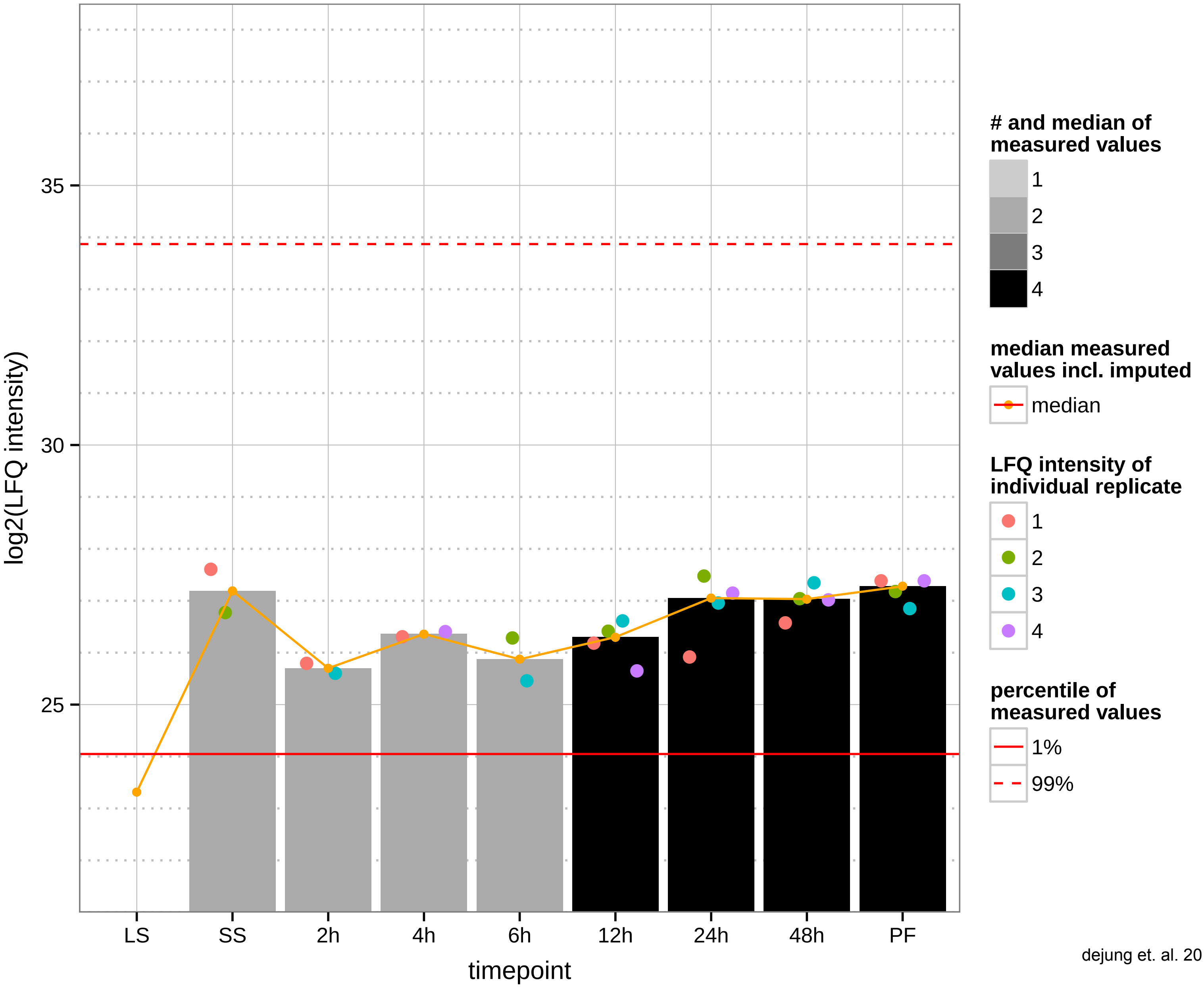
RNA–binding protein, putative
Tb927.11.350
AGOF: null
AGOC: eukaryotic translation initiation factor 4F complex
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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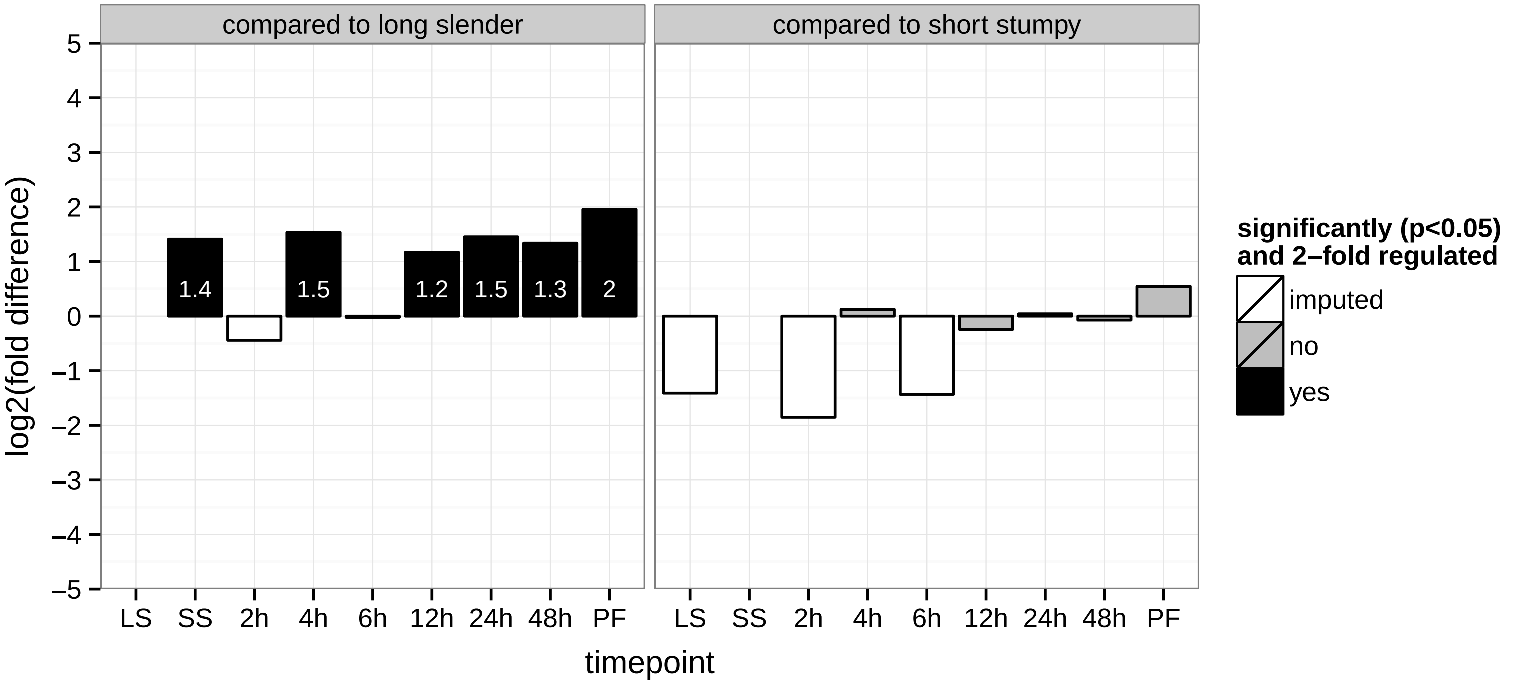
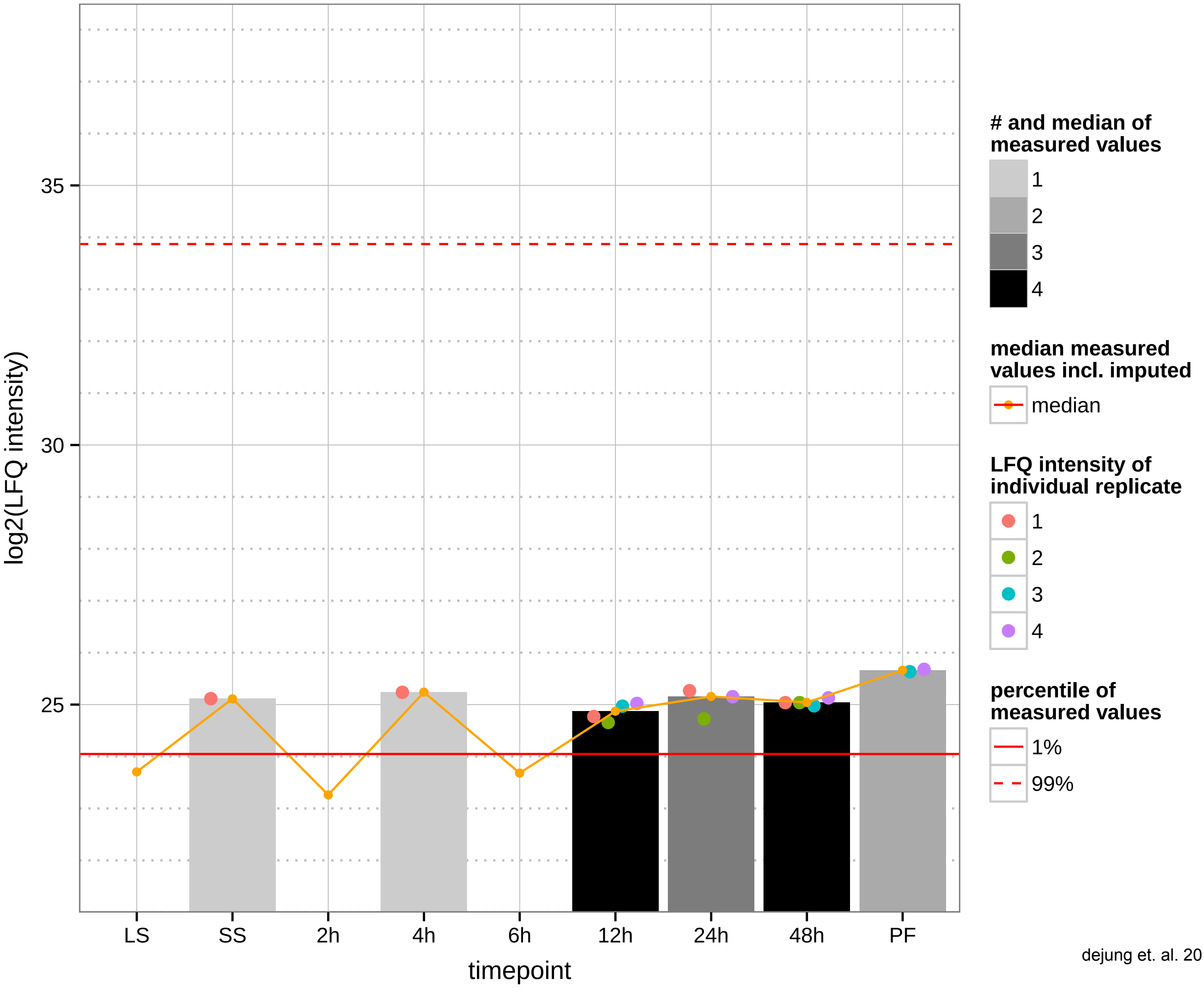
ubiquitin carboxyl–terminal hydrolase, putative, cysteine peptidase, Clan CA, family C19
Tb927.11.5270
AGOF: cysteine–type endopeptidase activity, ubiquitin thiolesterase activity
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: ubiquitin thiolesterase activity
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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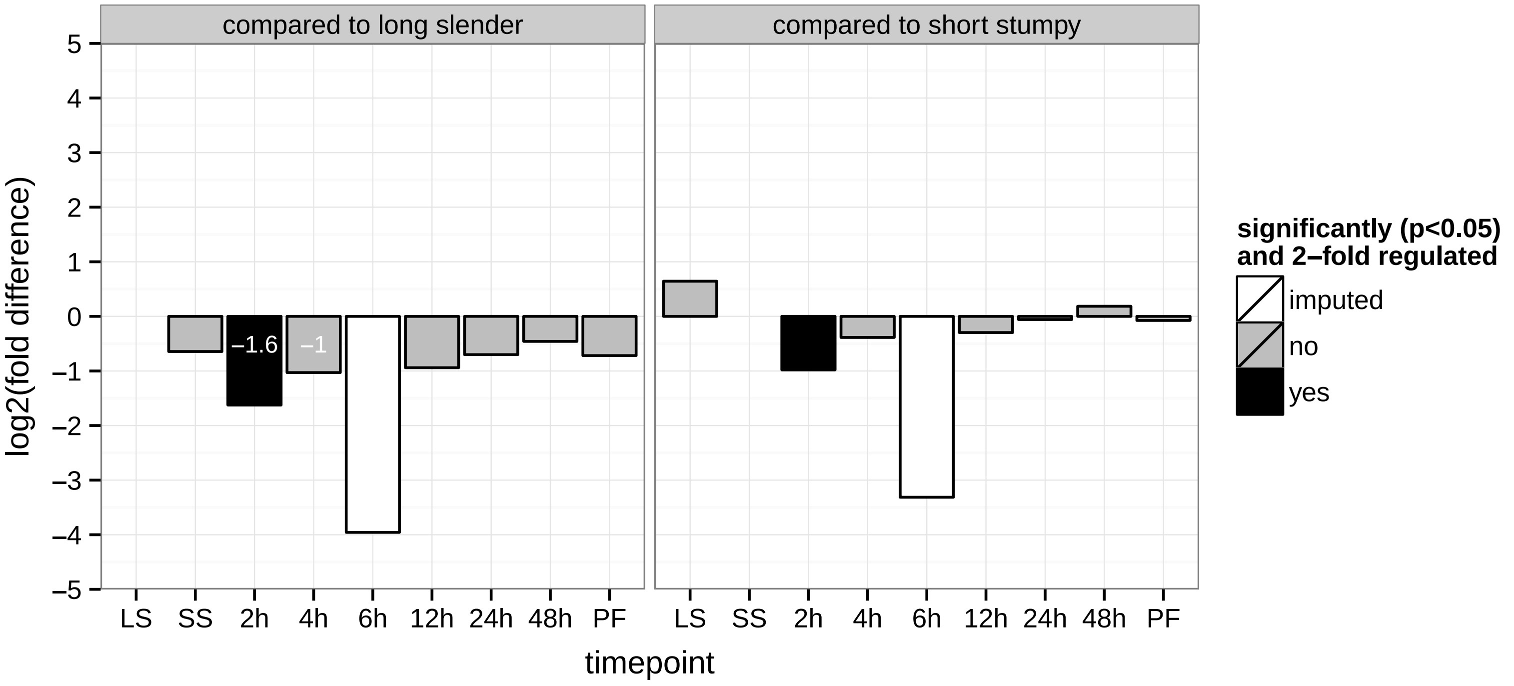
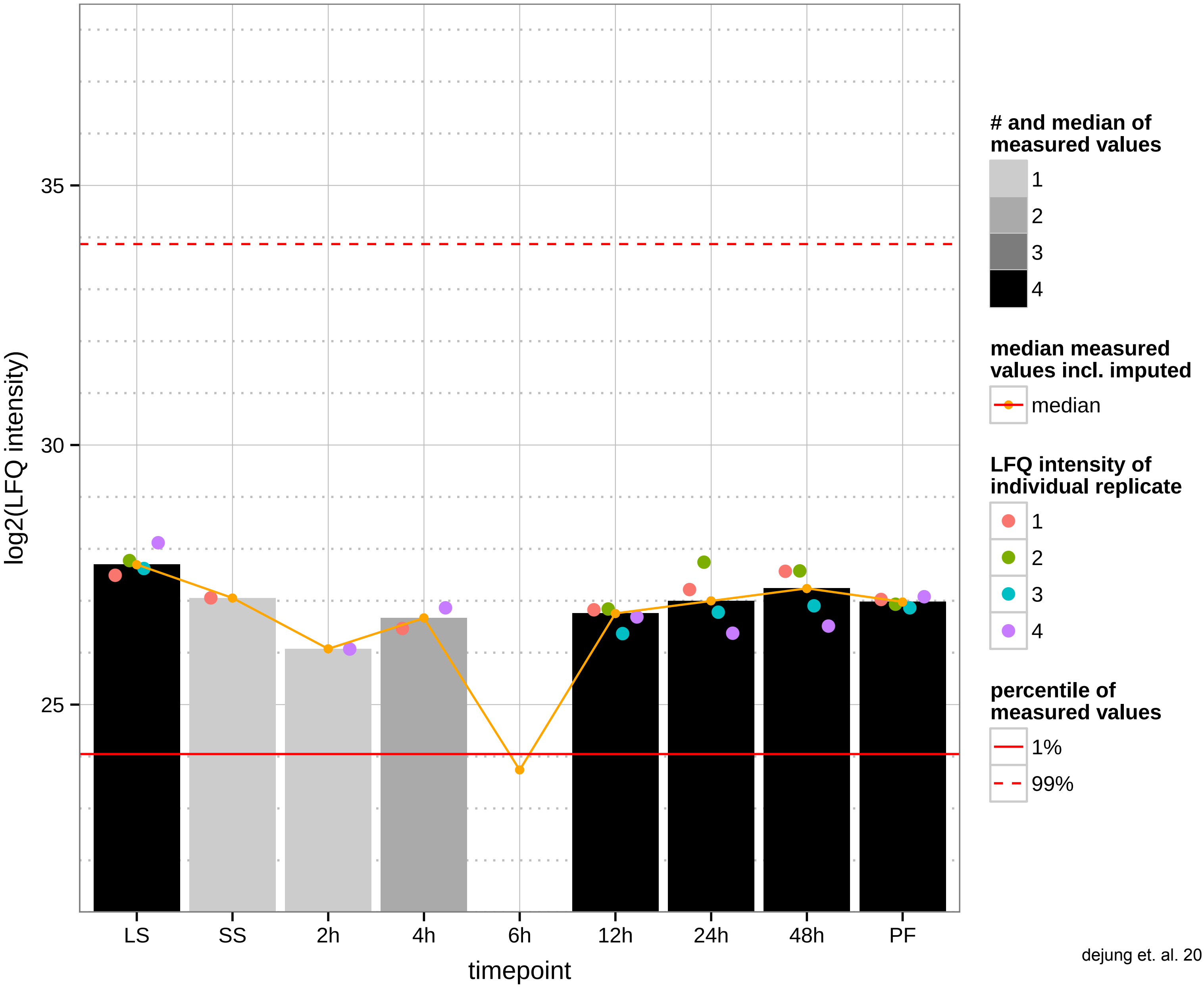
ubiquitin–conjugating enzyme E2, putative
Tb927.2.2460
AGOF: ubiquitin–protein ligase activity
AGOC: nucleus
AGOP: cellular protein modification process, post–translational protein modification, regulation of protein metabolic process
PGOF: acid–amino acid ligase activity
PGOC: null
PGOP: null





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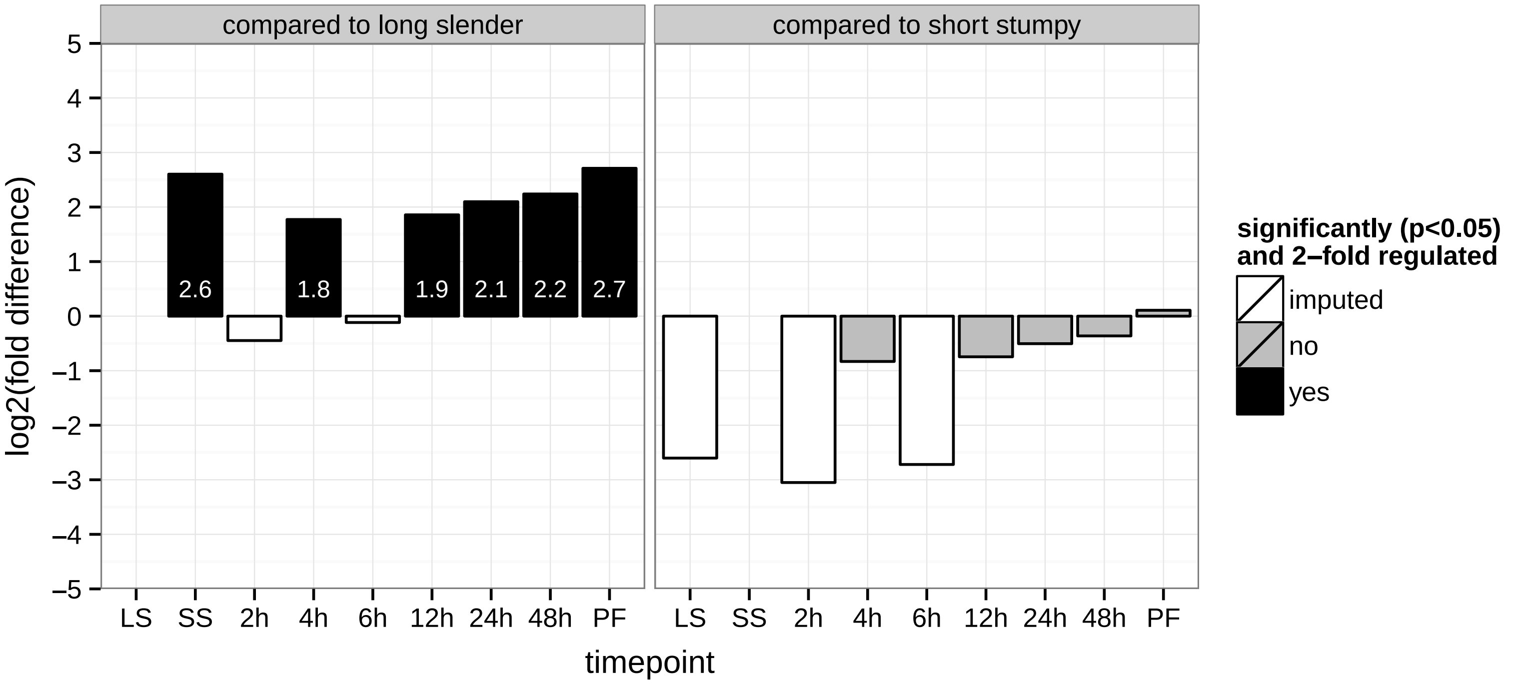
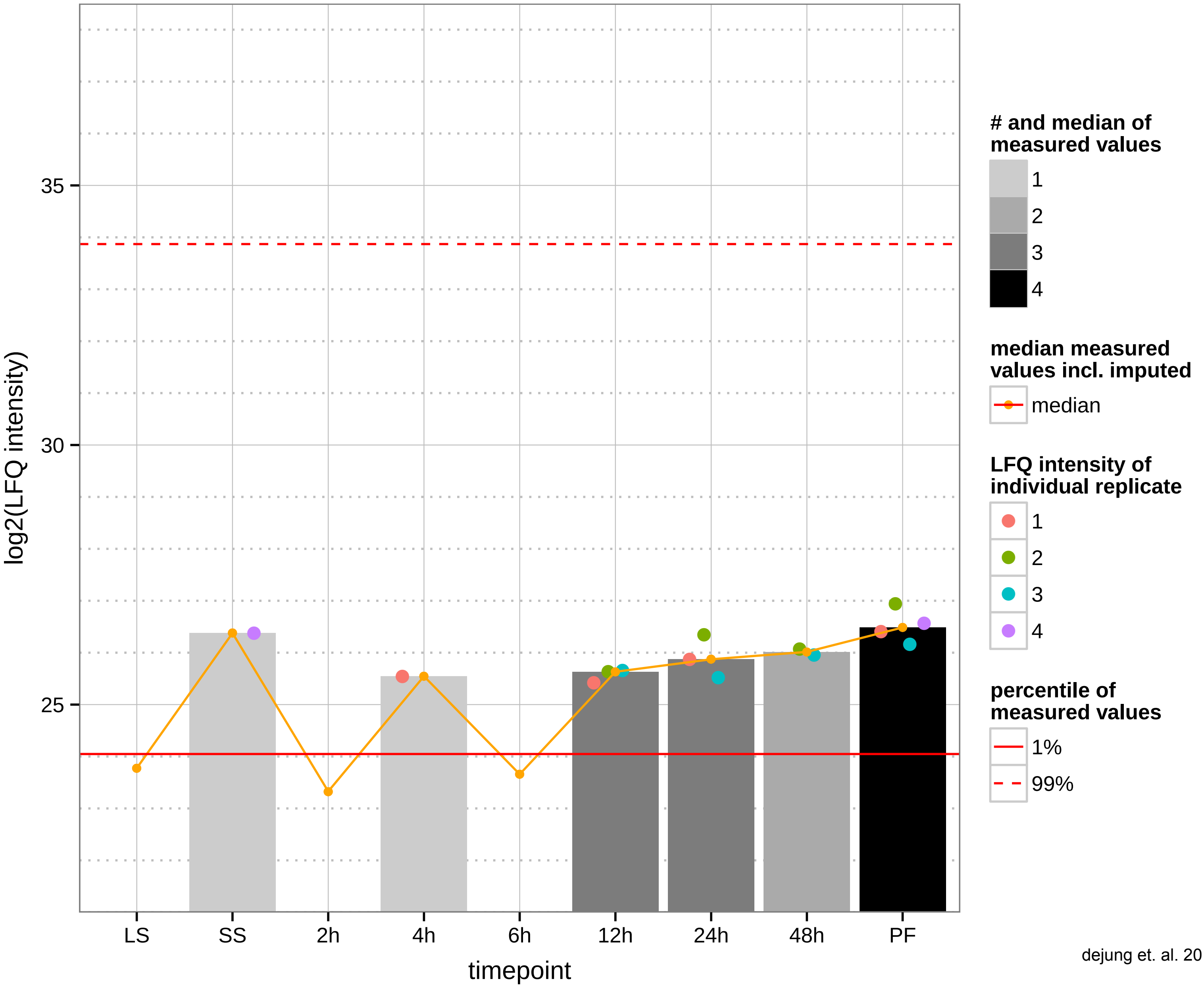
50S ribosomal protein L13, putative
Tb927.4.1070
AGOF: structural constituent of ribosome
AGOC: intracellular, mitochondrion, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: ribosome
PGOP: translation





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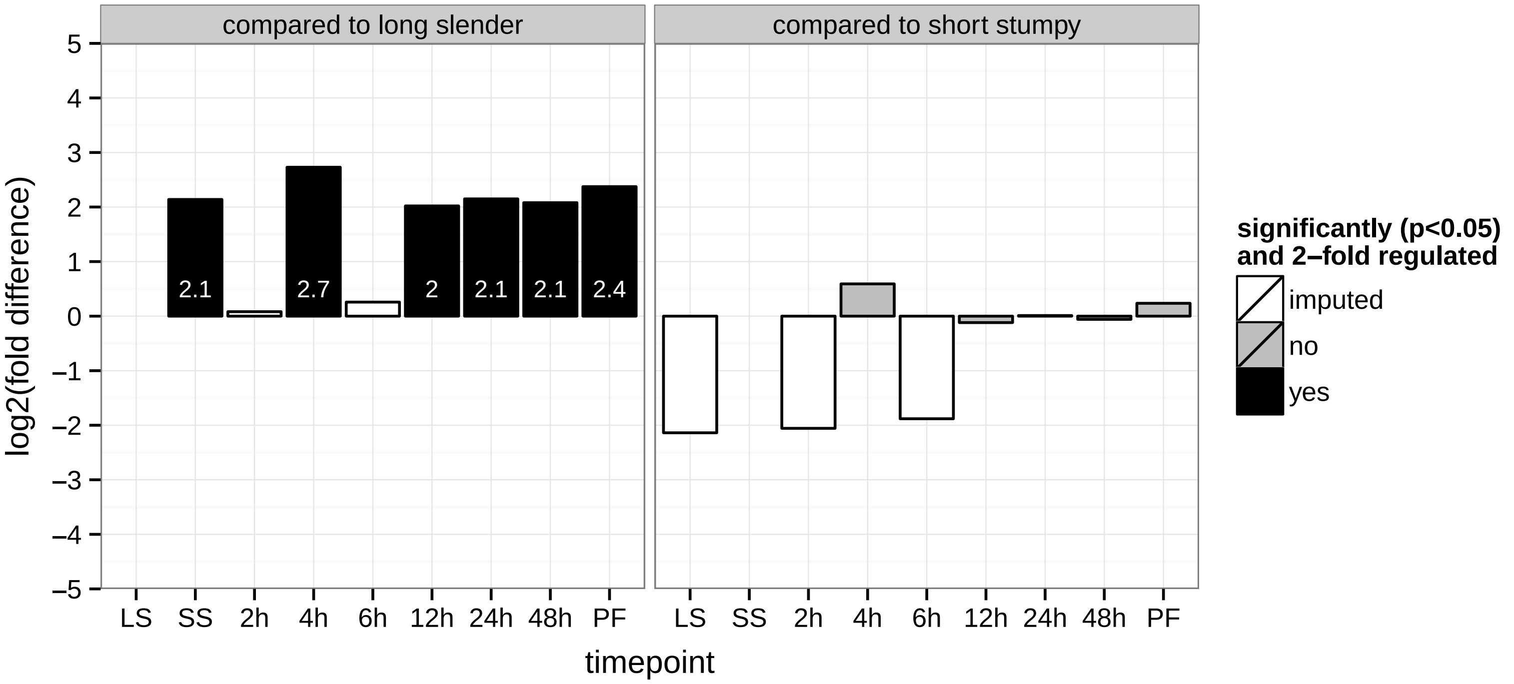
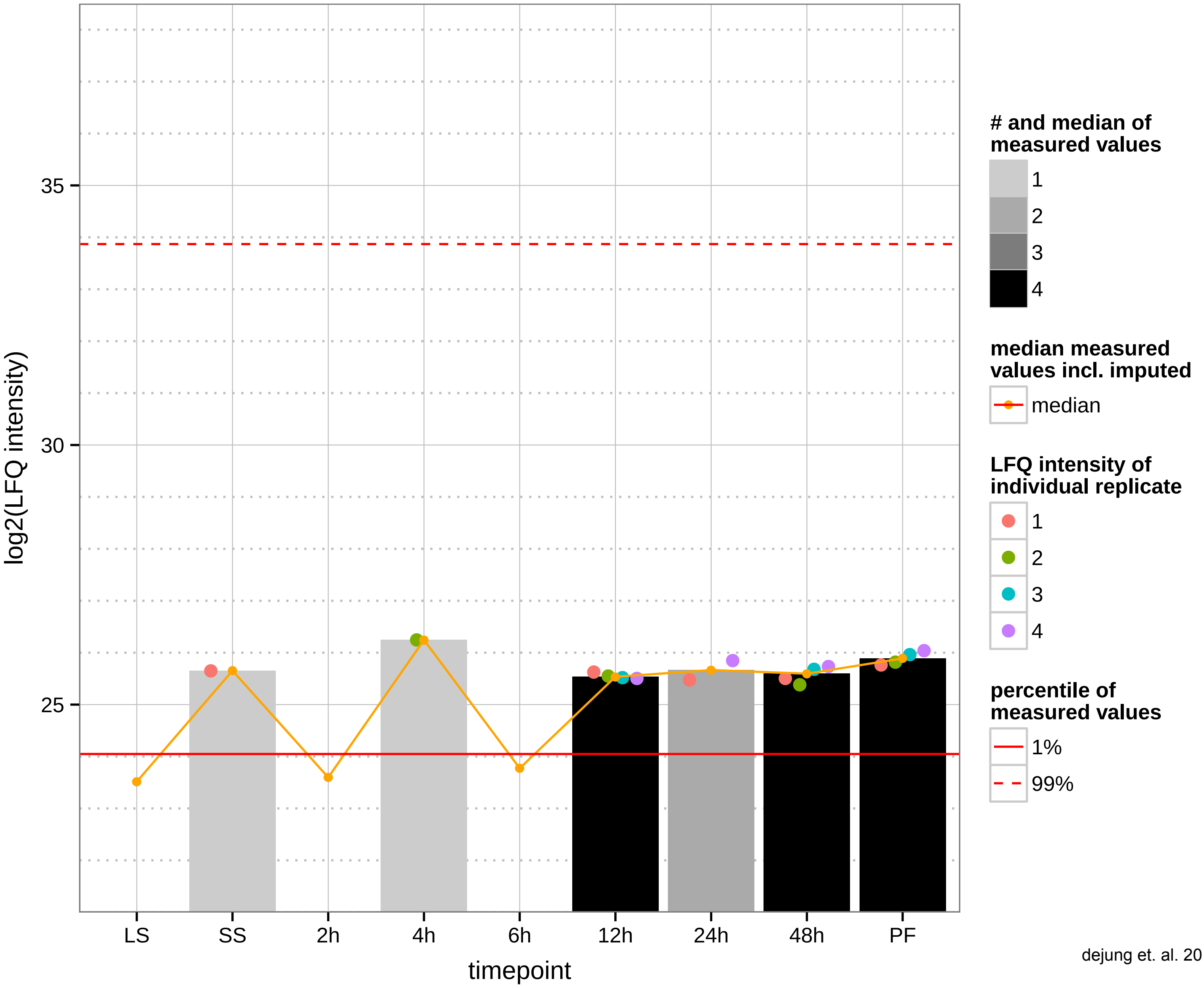
Alkylated DNA repair protein (alkB homolog), putative
Tb927.4.460
AGOF: null
AGOC: null
AGOP: null
PGOF: oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular o
PGOC: null
PGOP: oxidation−reduction process





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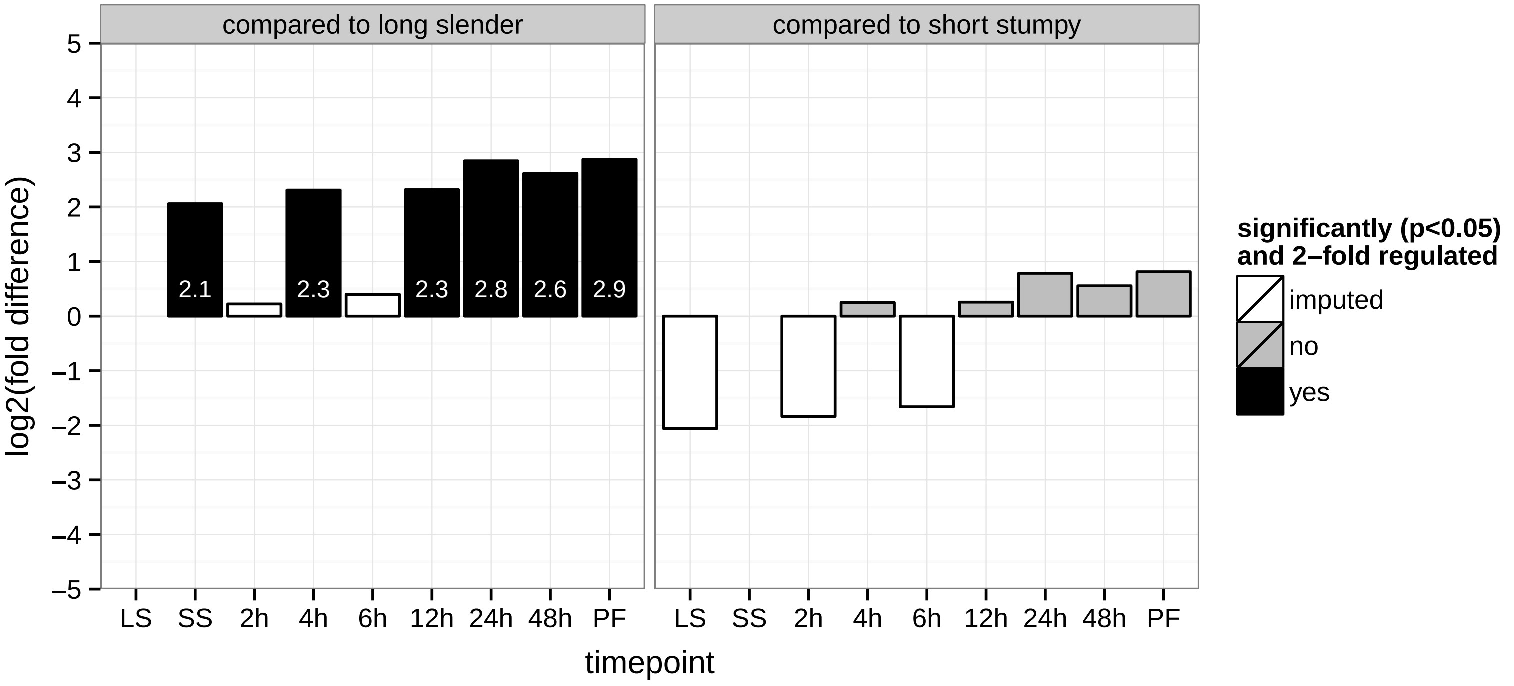
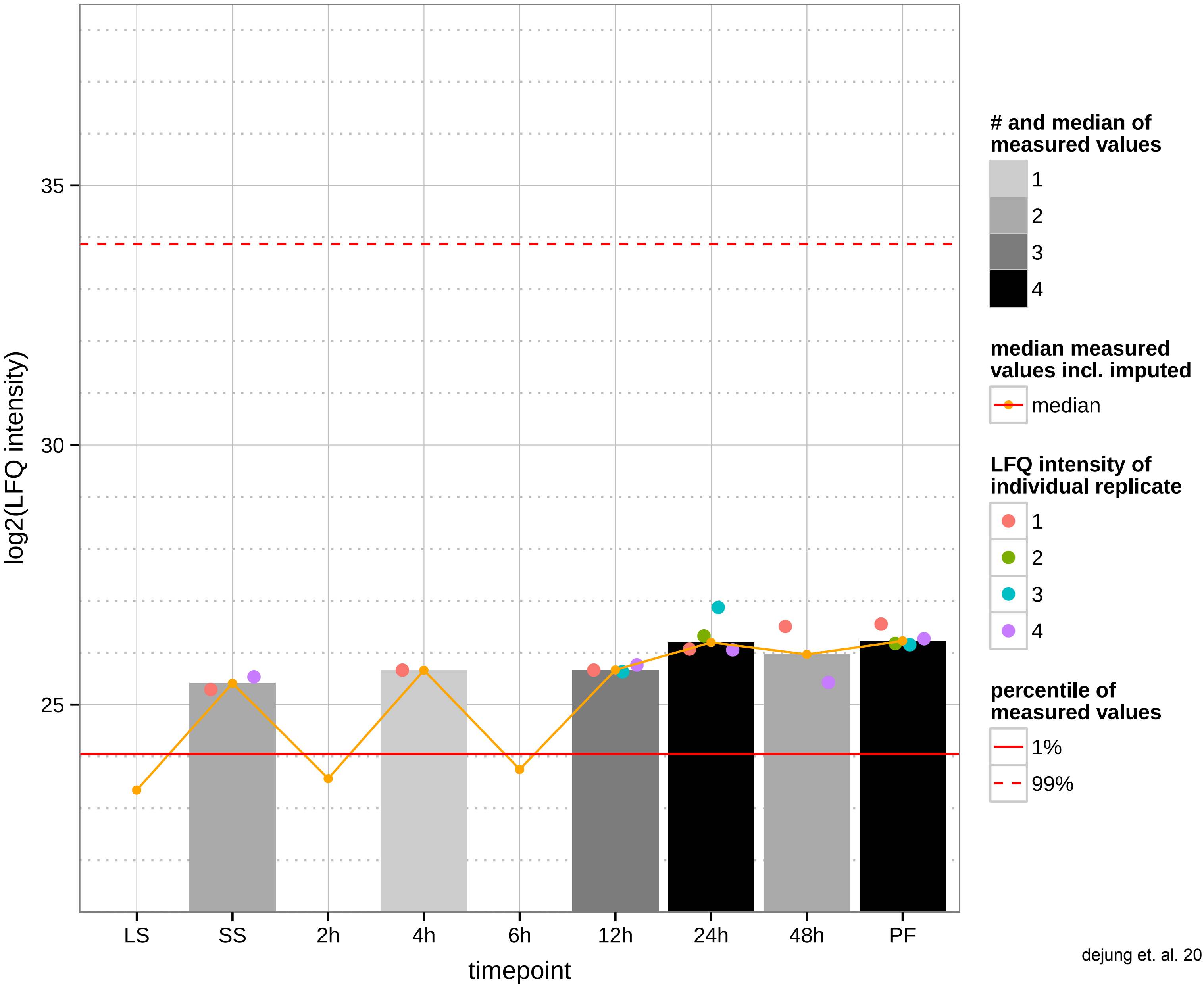
hypothetical protein, conserved
Tb927.5.3730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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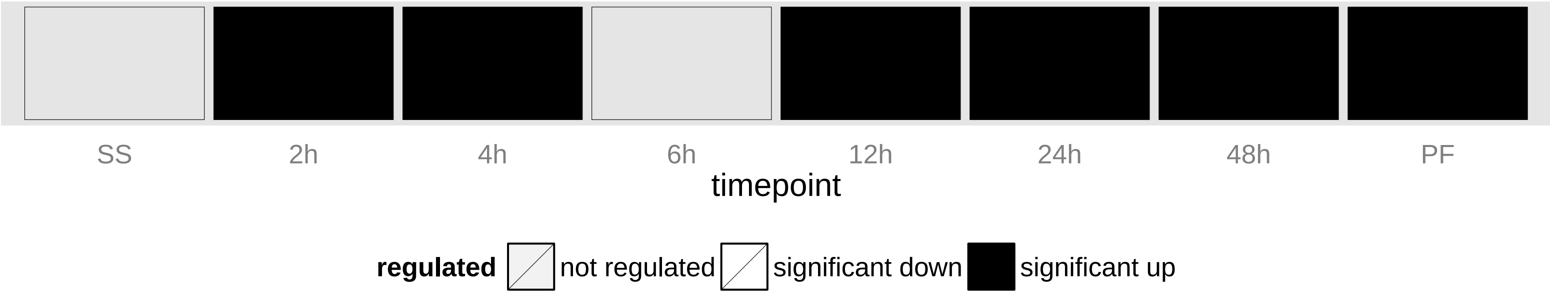

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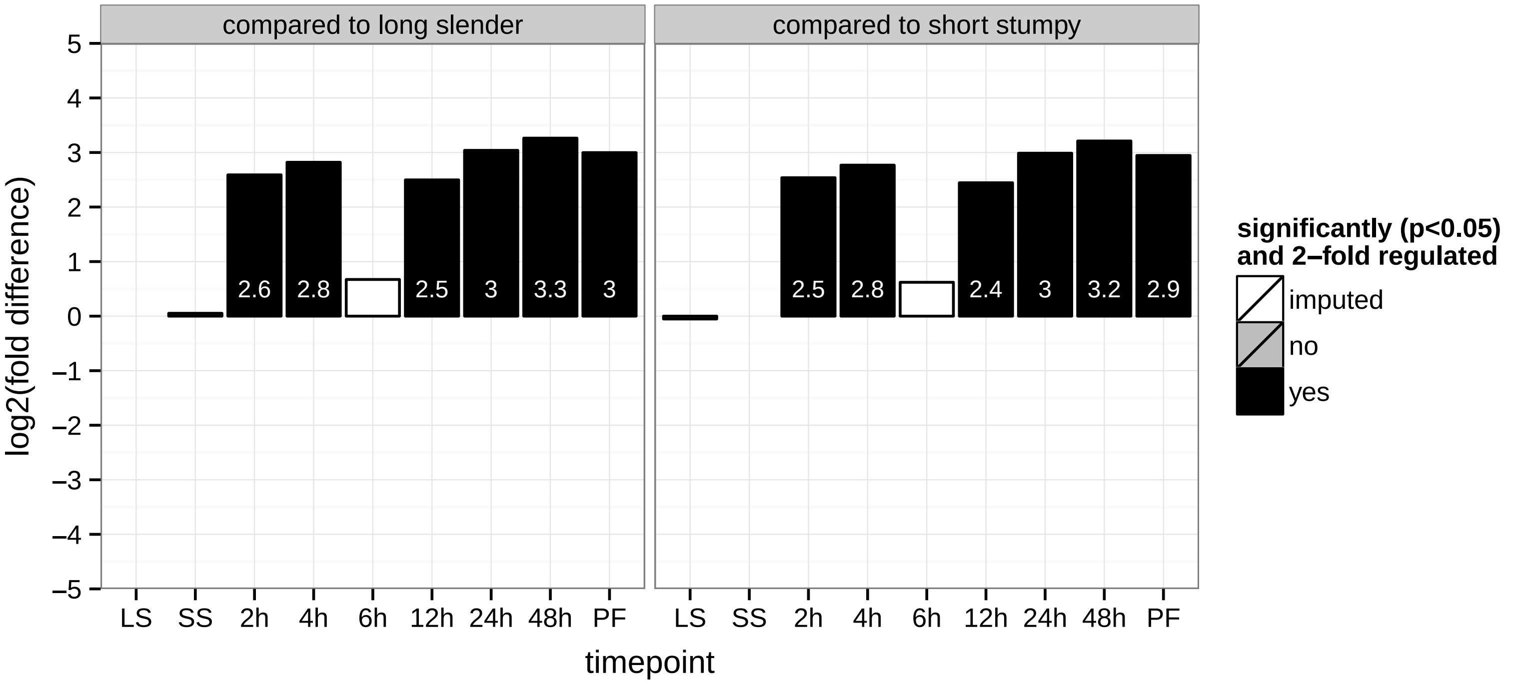
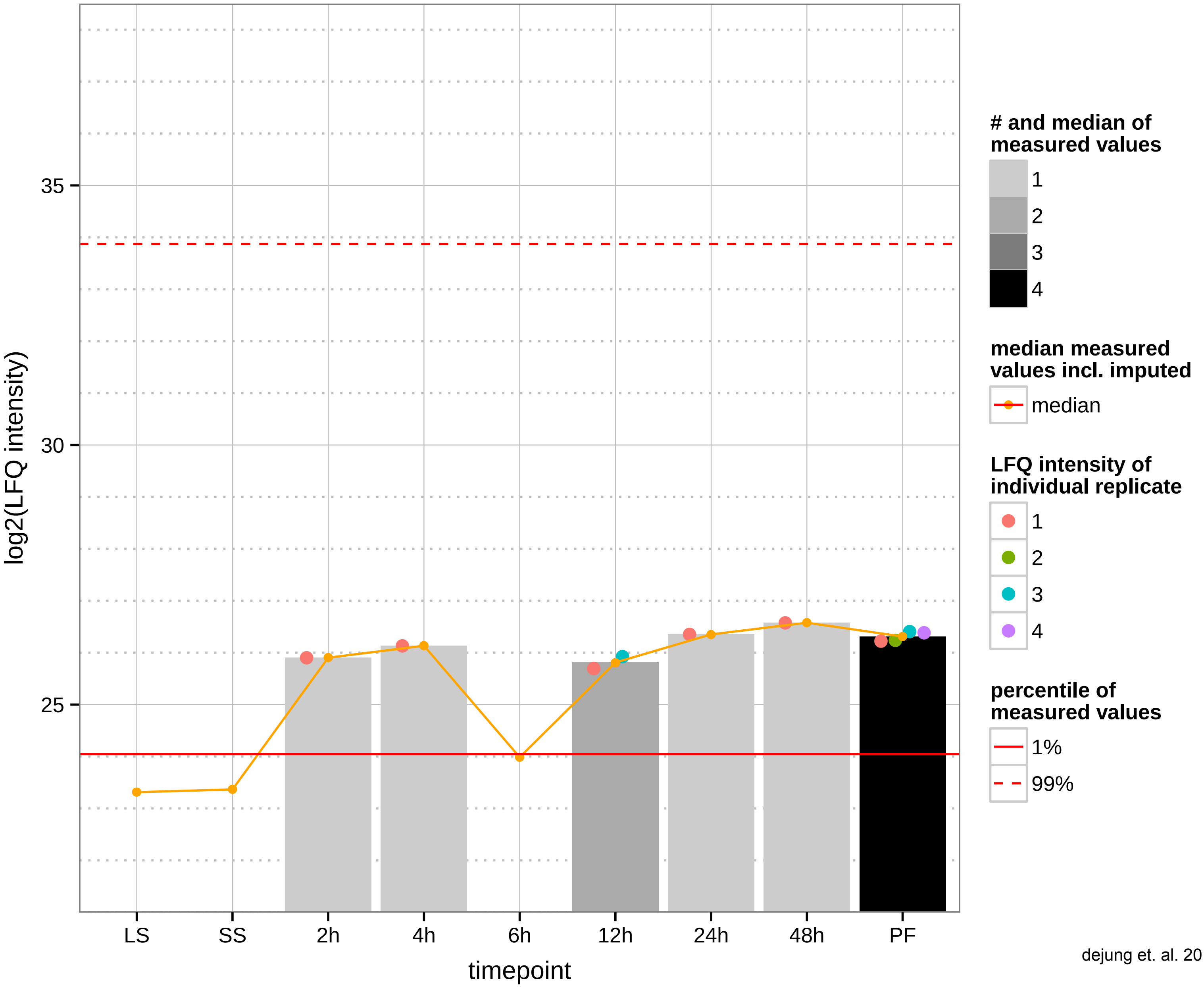
NADH−ubiquinone oxidoreductase complex I subunit, putative, ferredoxin, putative (NDUFS1)
Tb927.10.12540
AGOF: electron carrier activity, glutathione−disulfide reductase activity, iron−sulfur cluster binding
AGOC: mitochondrion
AGOP: oxidation−reduction process
PGOF: electron carrier activity, iron−sulfur cluster binding, oxidoreductase activity
PGOC: null
PGOP: oxidation−reduction process





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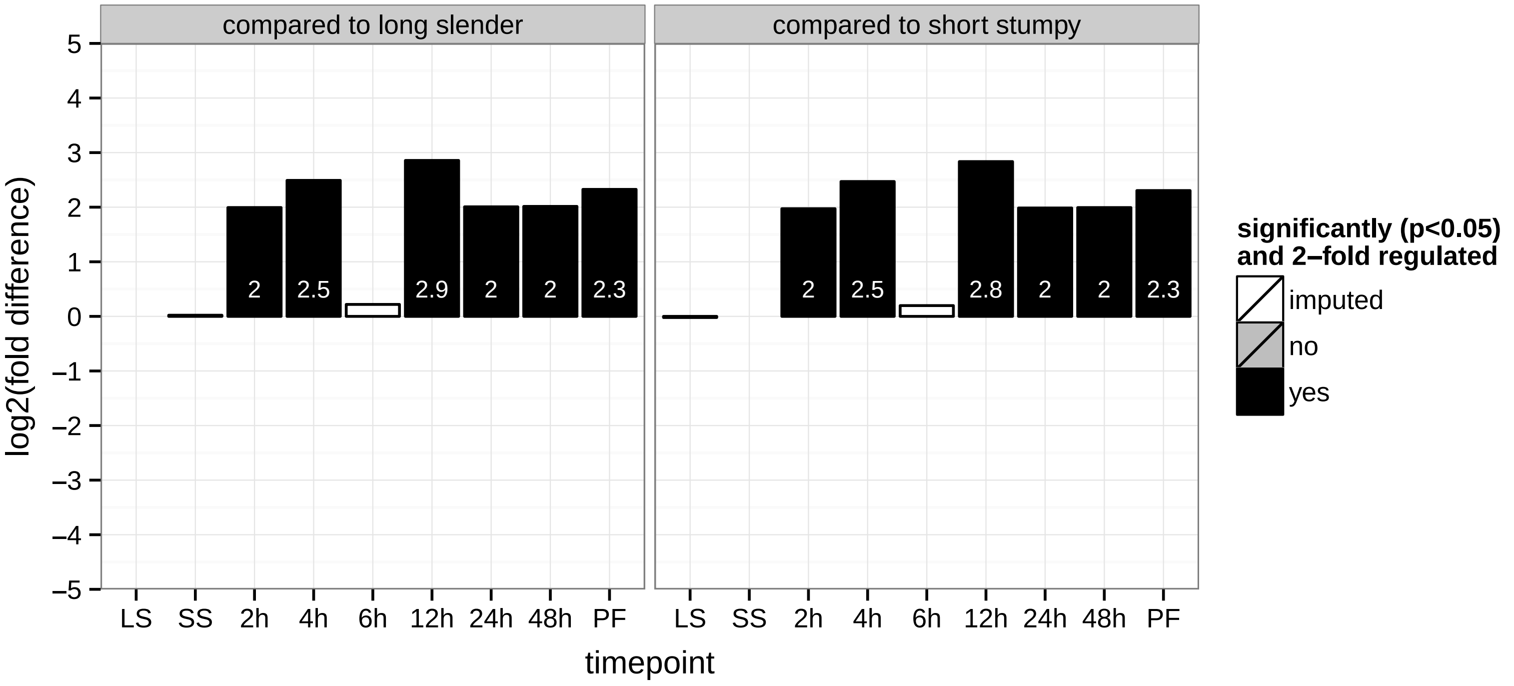
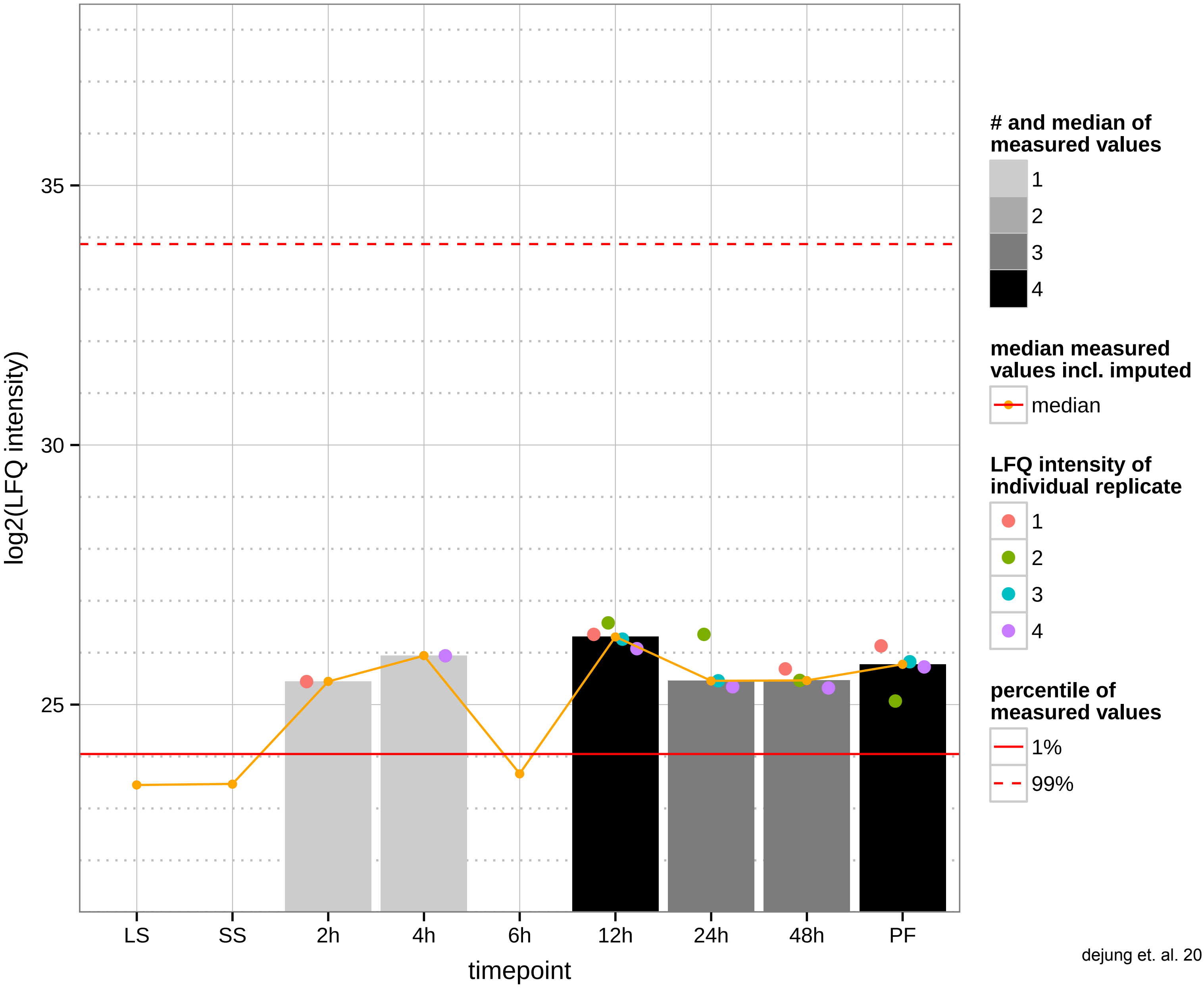
survival of motor neuron (SMN)–like protein (TbSMN)
Tb927.11.15000
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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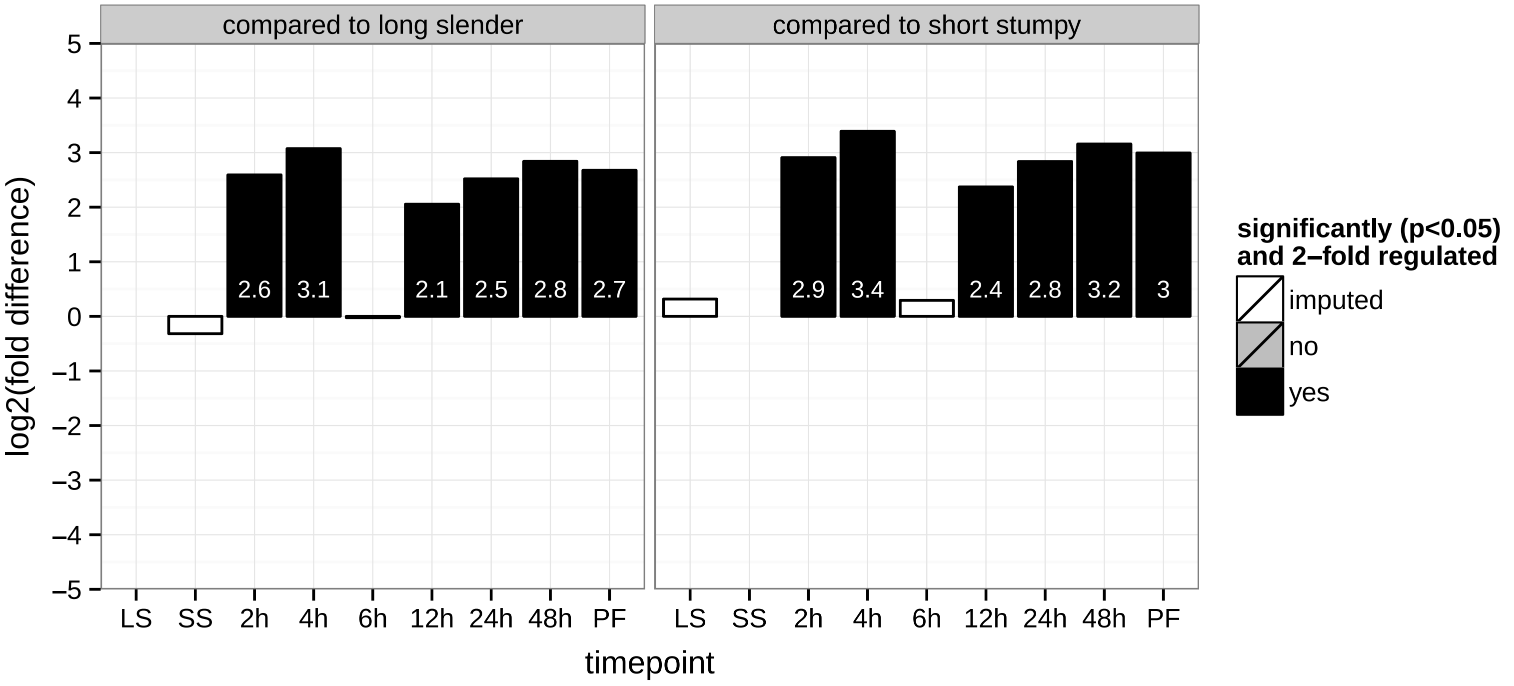
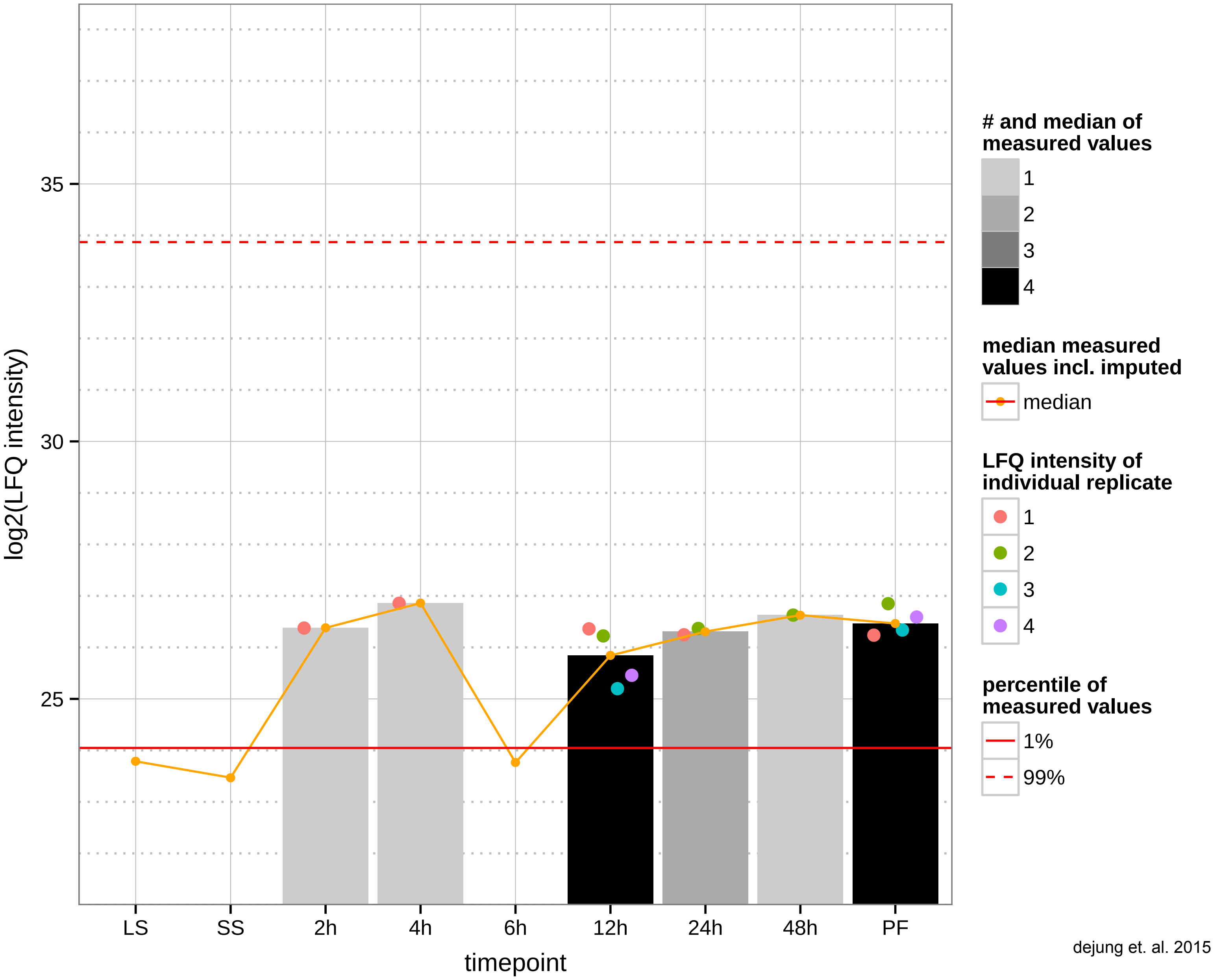
kinteoplast poly(A) polymerase complex 1 subunit
Tb927.11.15850
AGOF: RNA binding
AGOC: mitochondrion
AGOP: RNA polyadenylation, mRNA stabilization
PGOF: null
PGOC: null
PGOP: null





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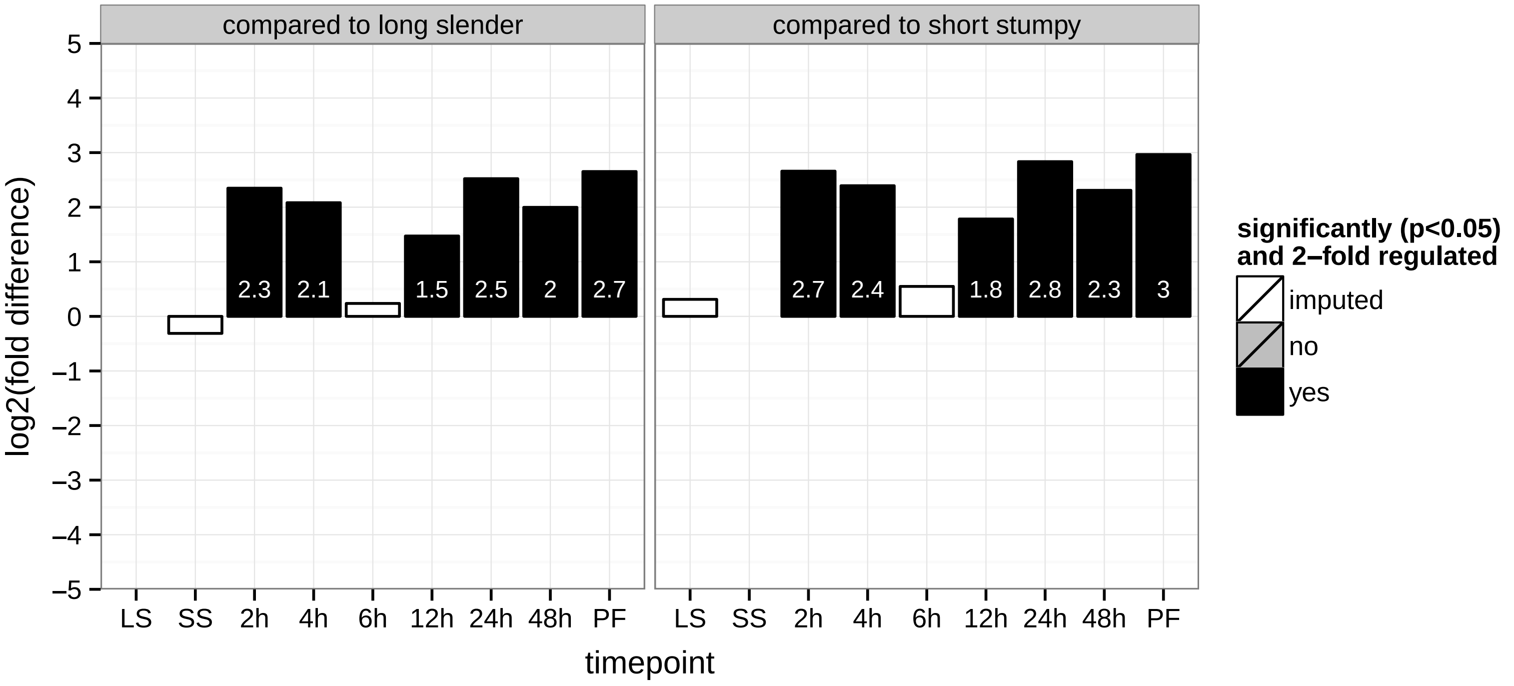
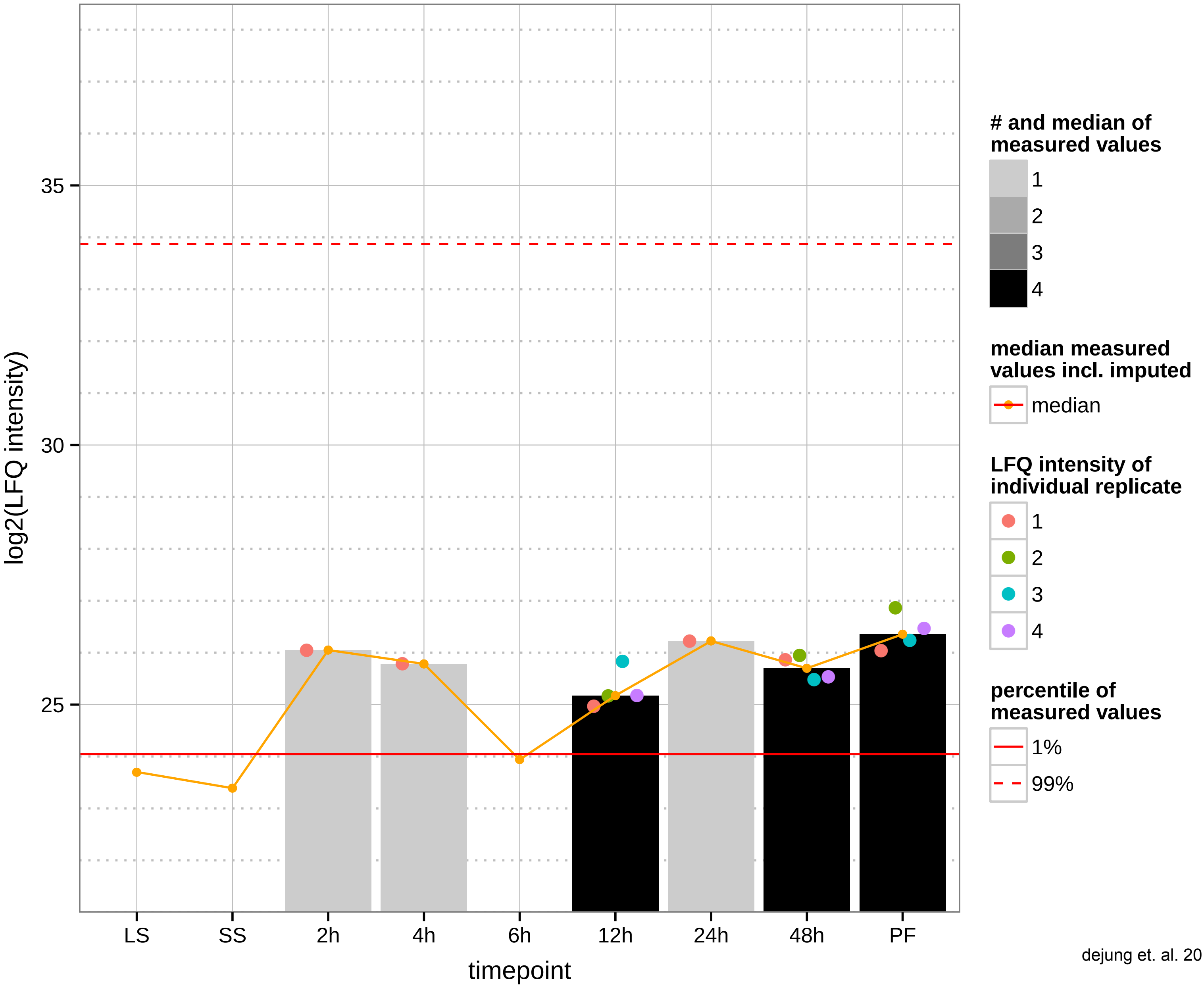
hypothetical protein, conserved
Tb927.6.2560
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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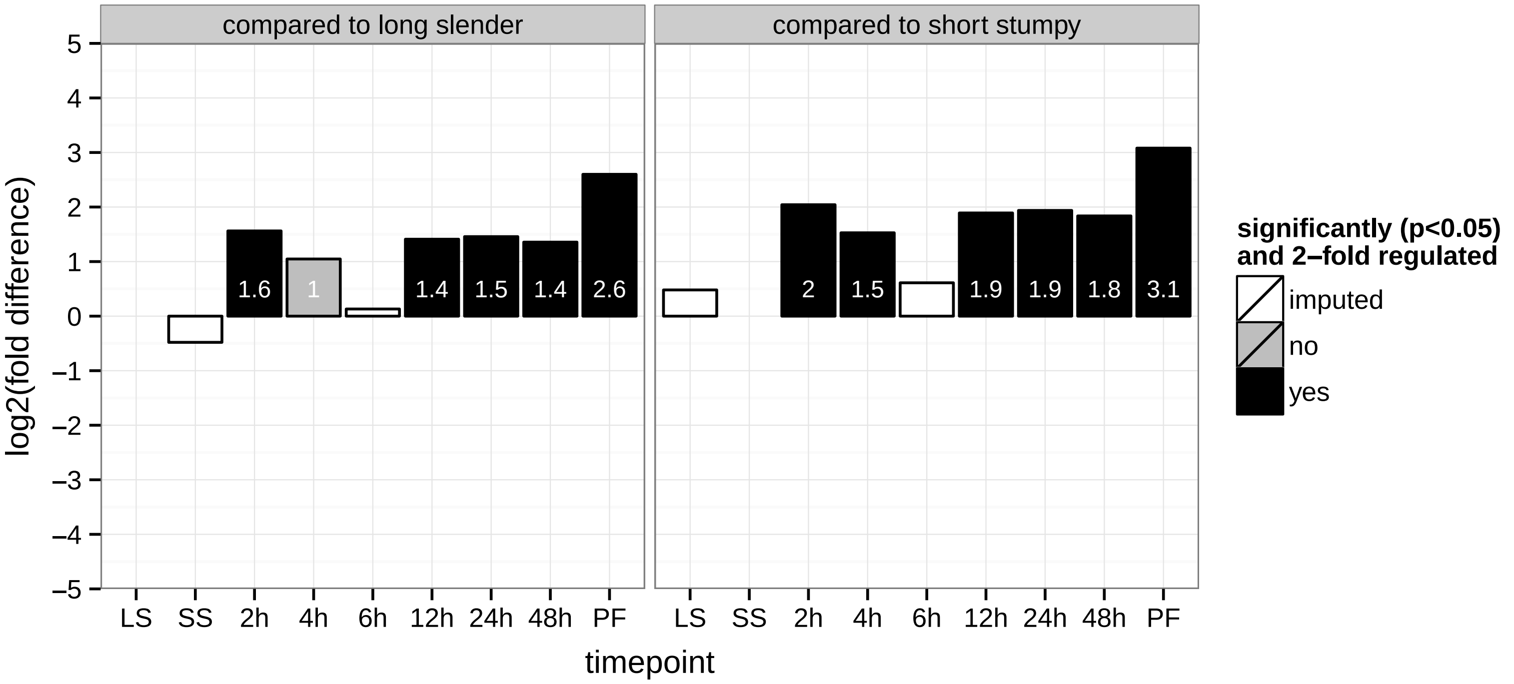
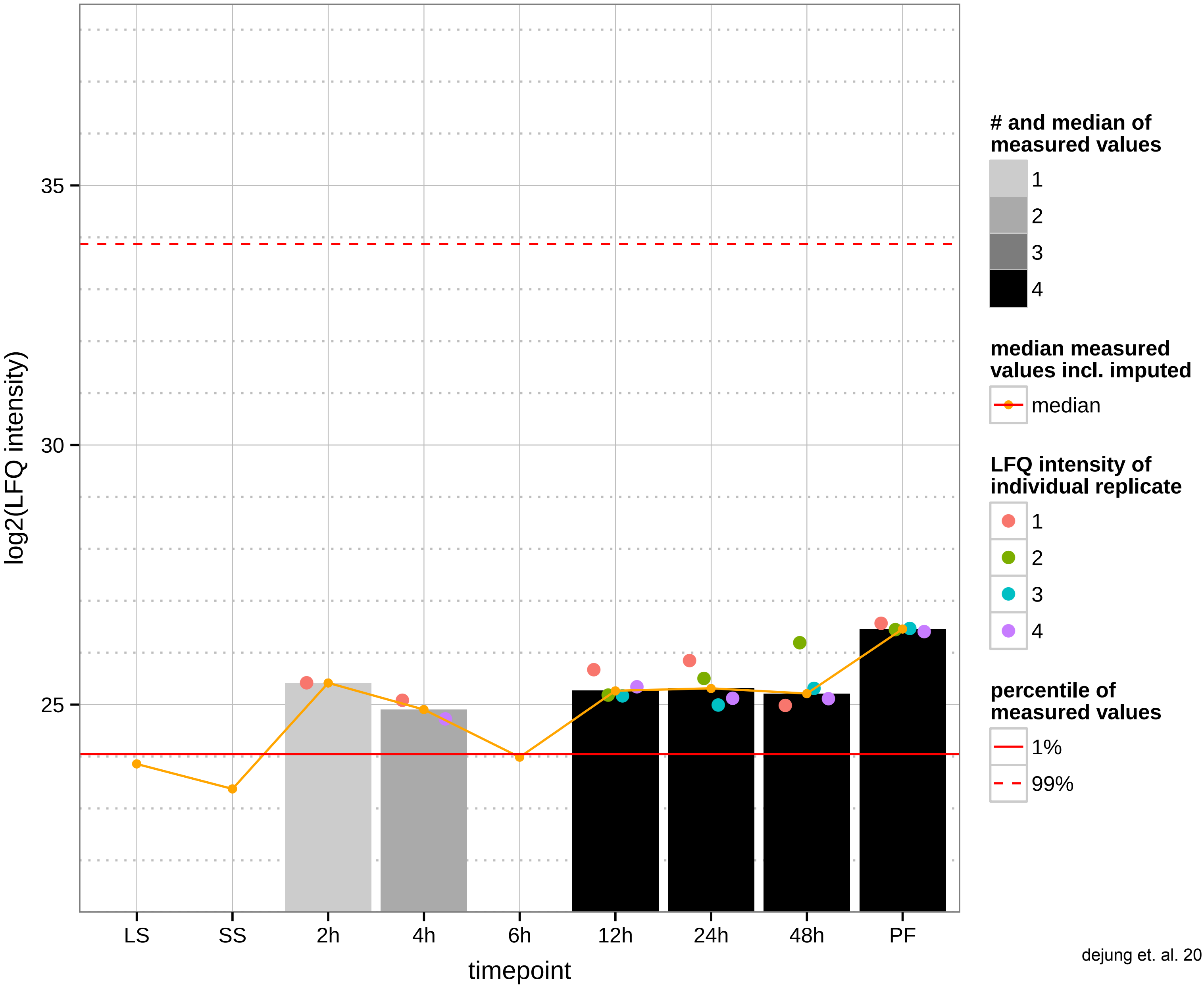
hypothetical protein, conserved
Tb927.7.4310
AGOF: flavin adenine dinucleotide binding, oxidoreductase activity
AGOC: null
AGOP: null
PGOF: flavin adenine dinucleotide binding, oxidoreductase activity
PGOC: null
PGOP: oxidation–reduction process





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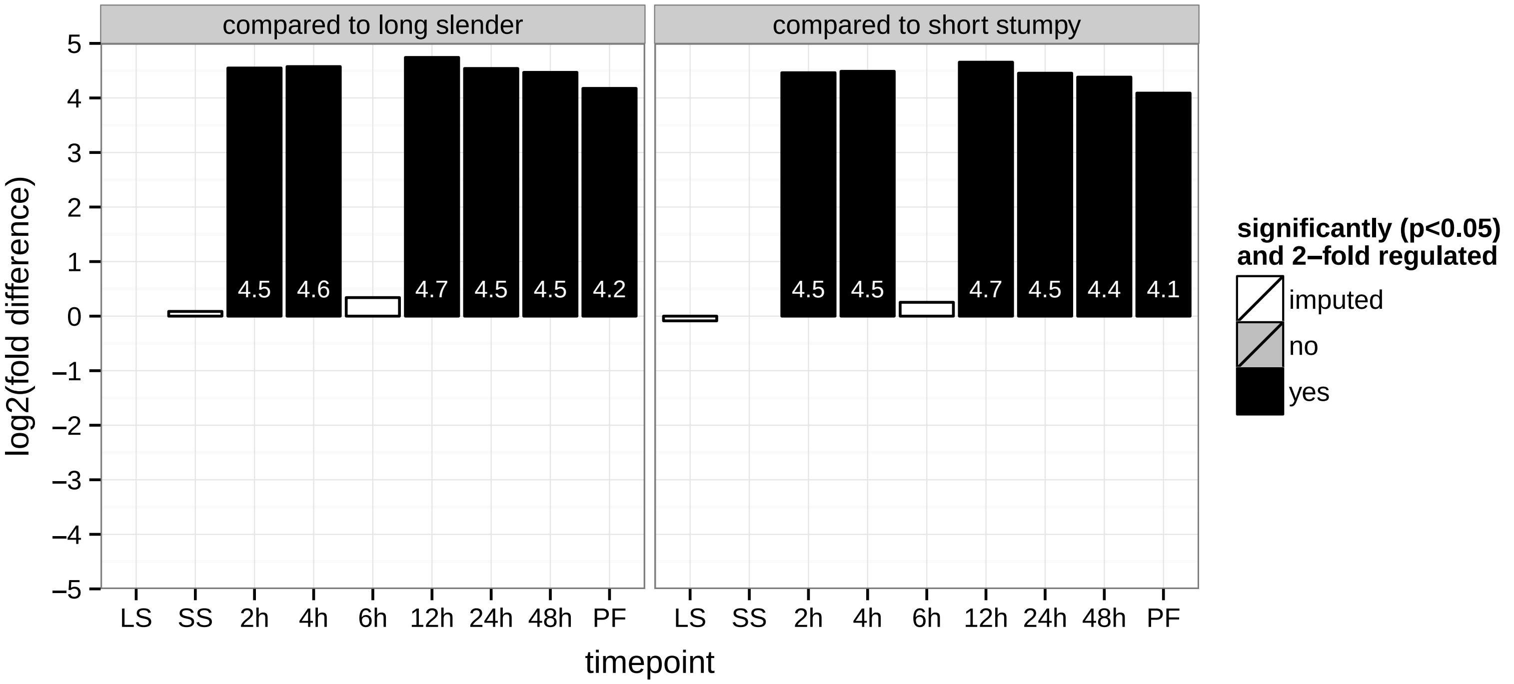
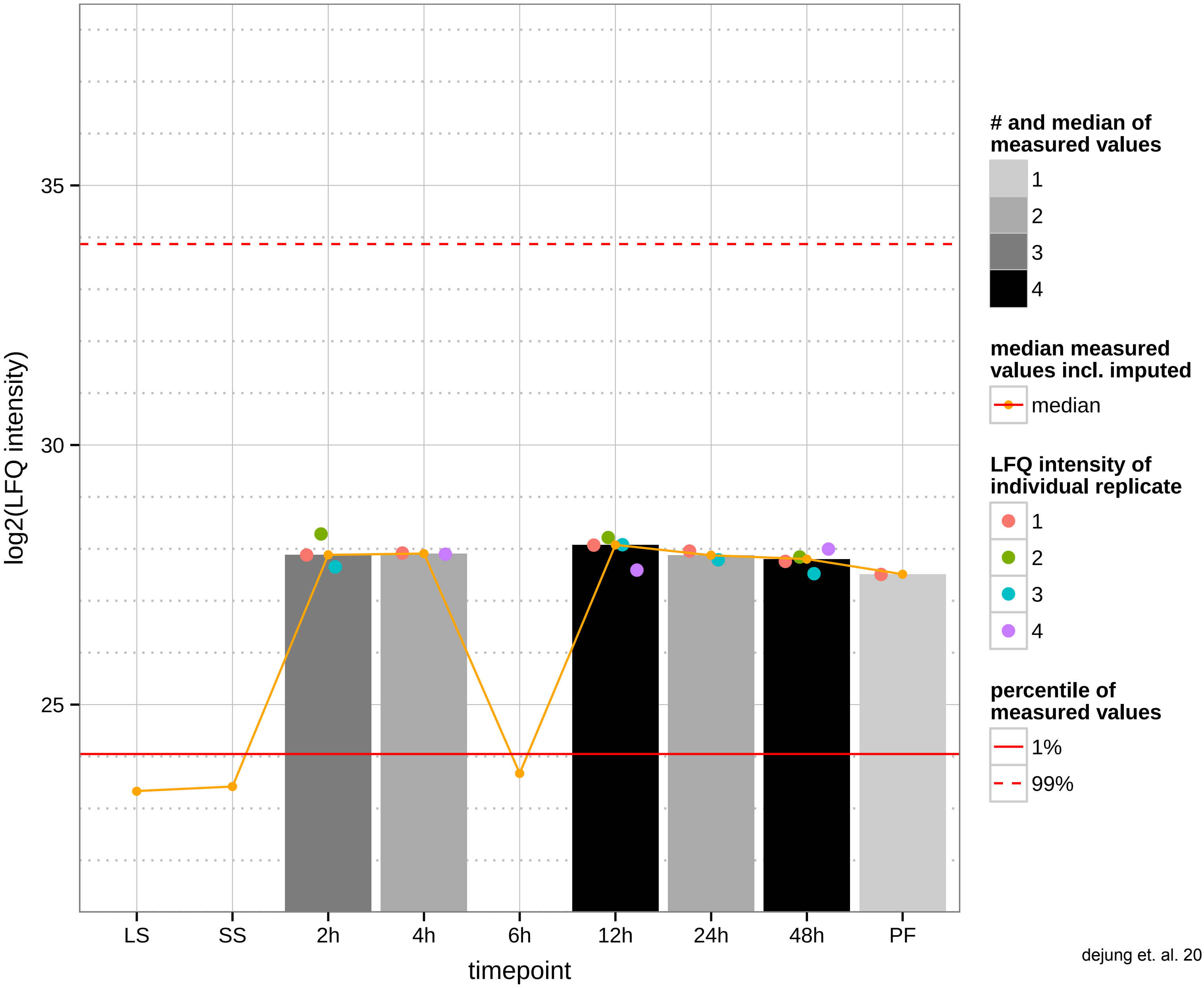
WD−repeat containing protein
Tb927.8.3860
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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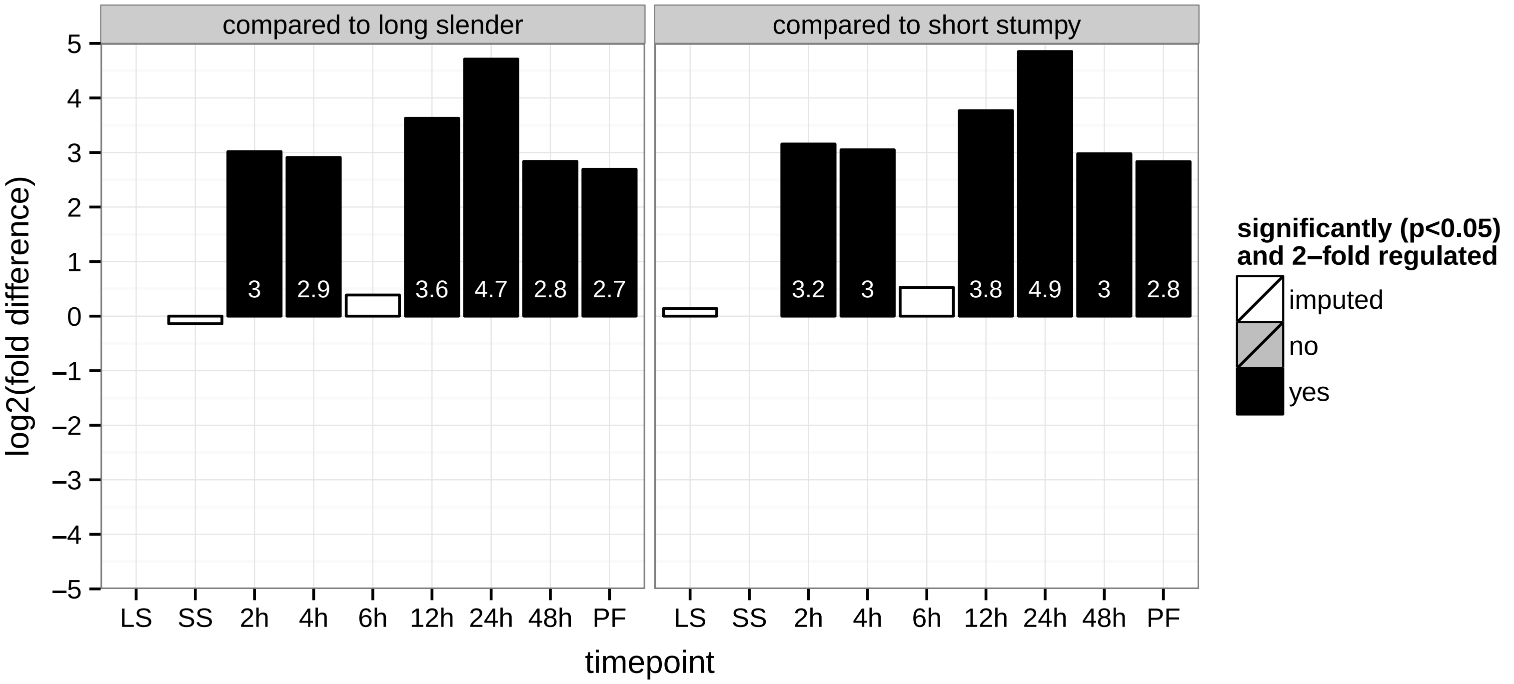
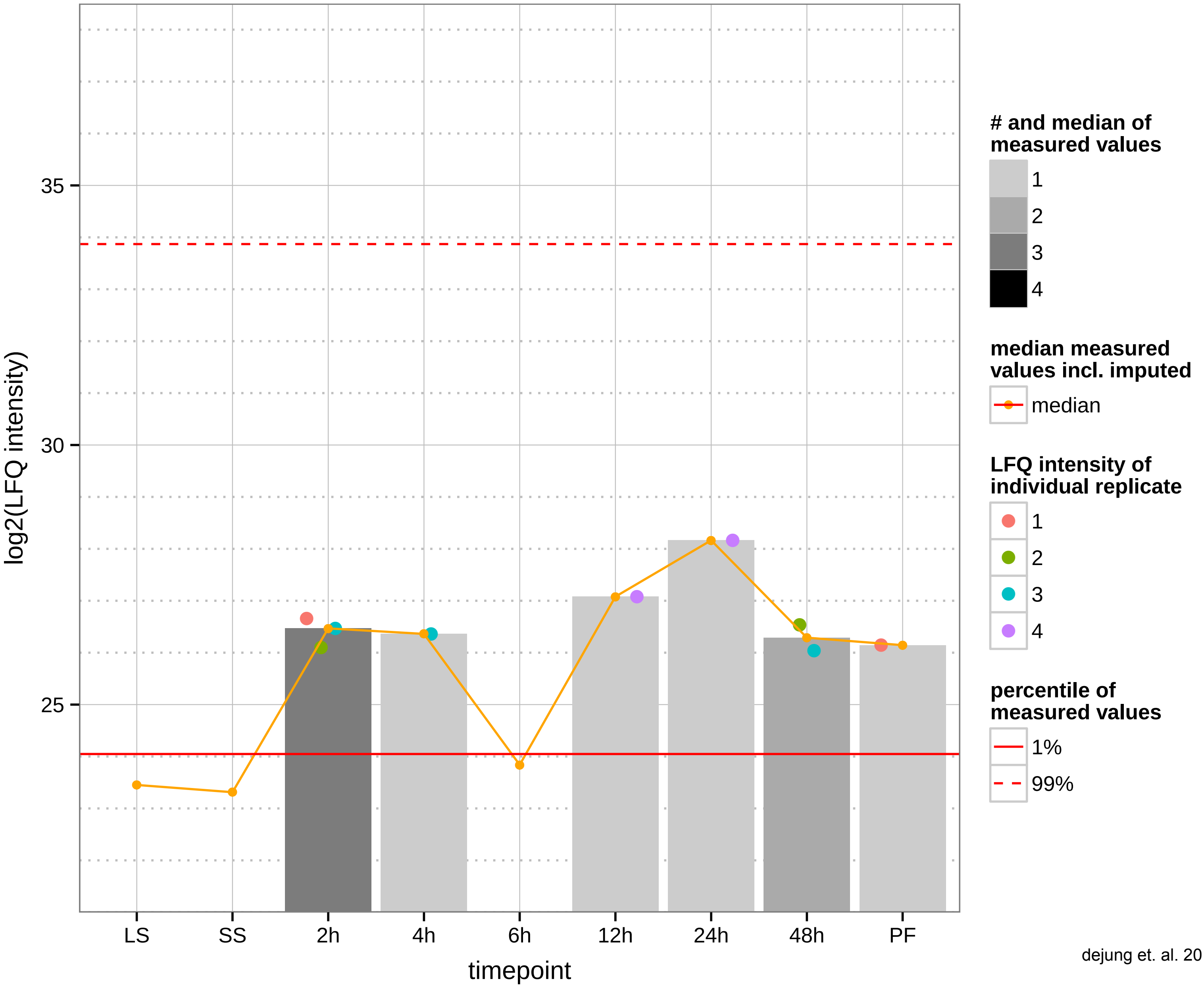
predicted zinc finger protein
Tb927.9.11070
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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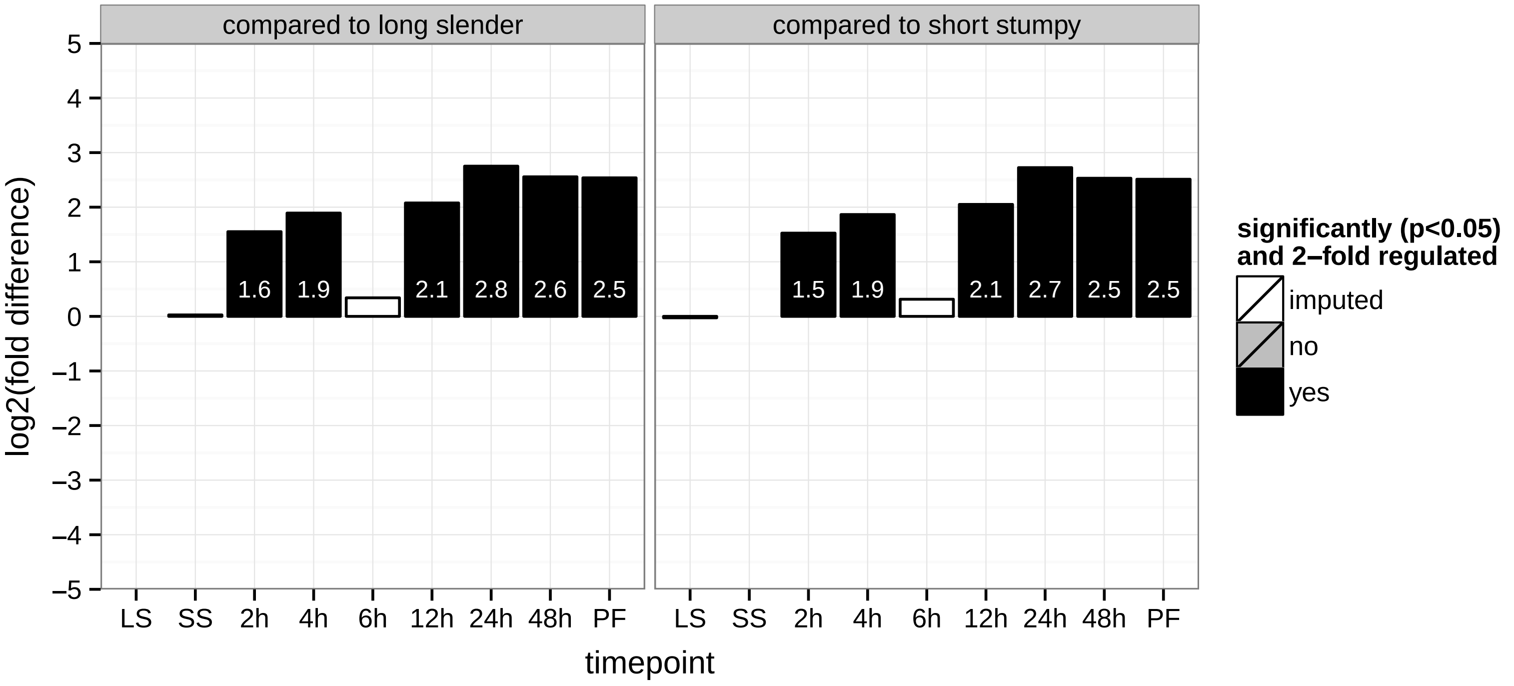
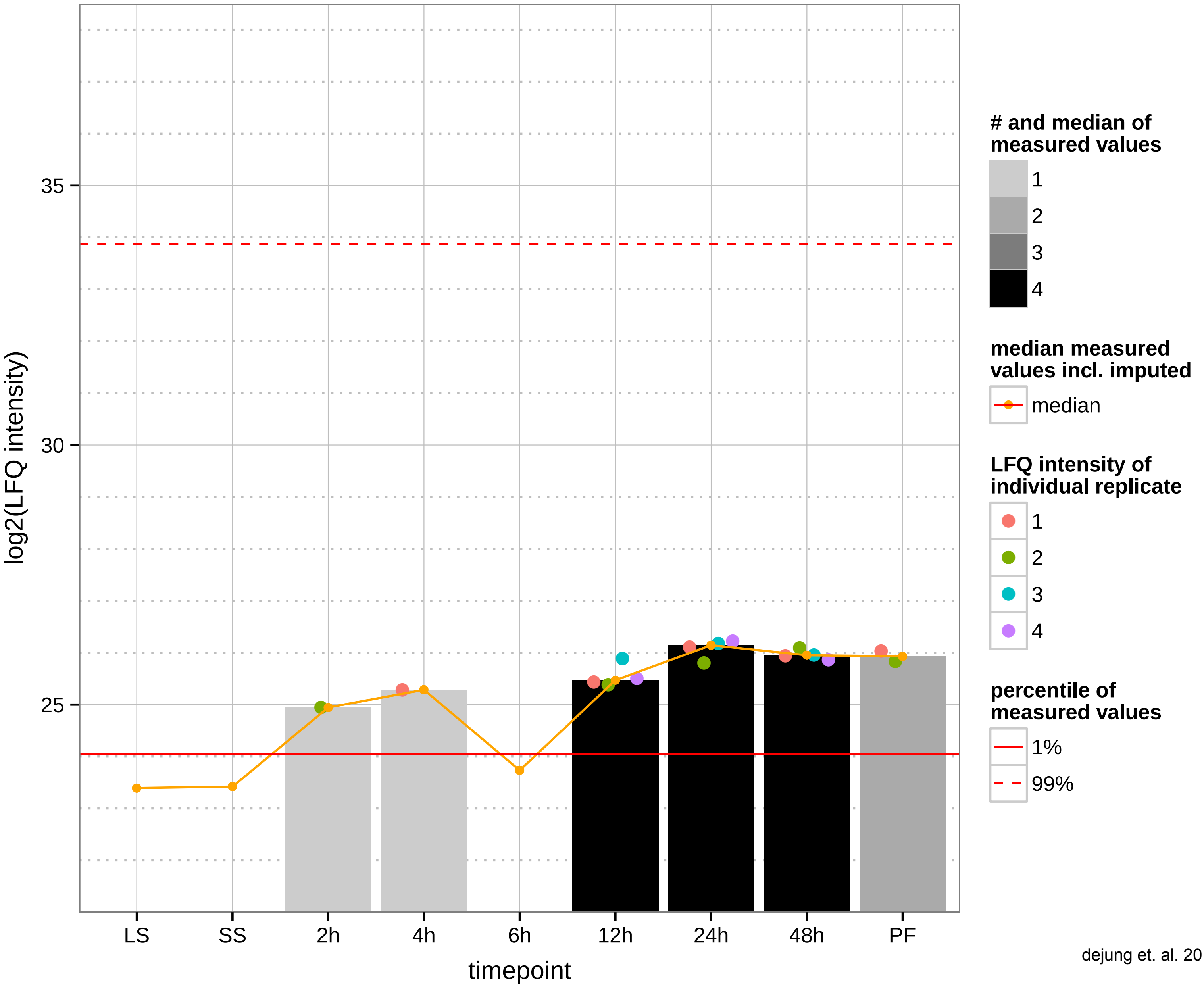
unspecified product
Tb927.9.12120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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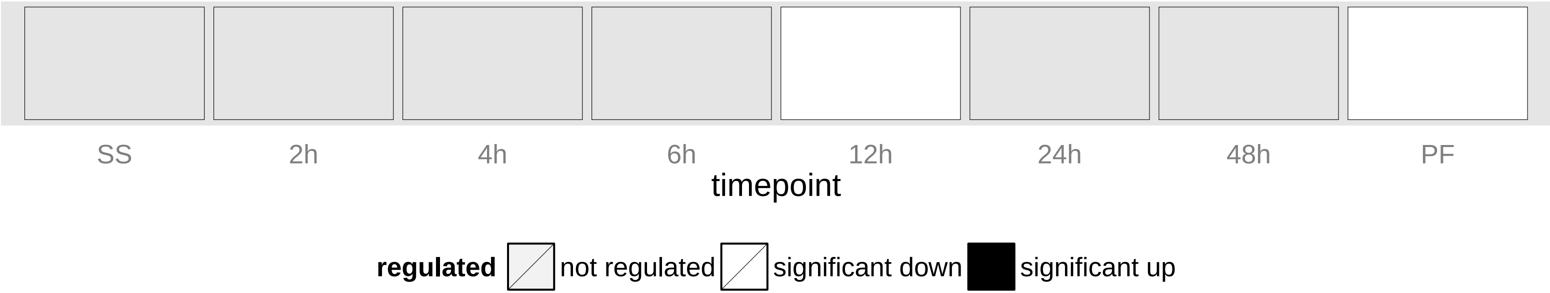

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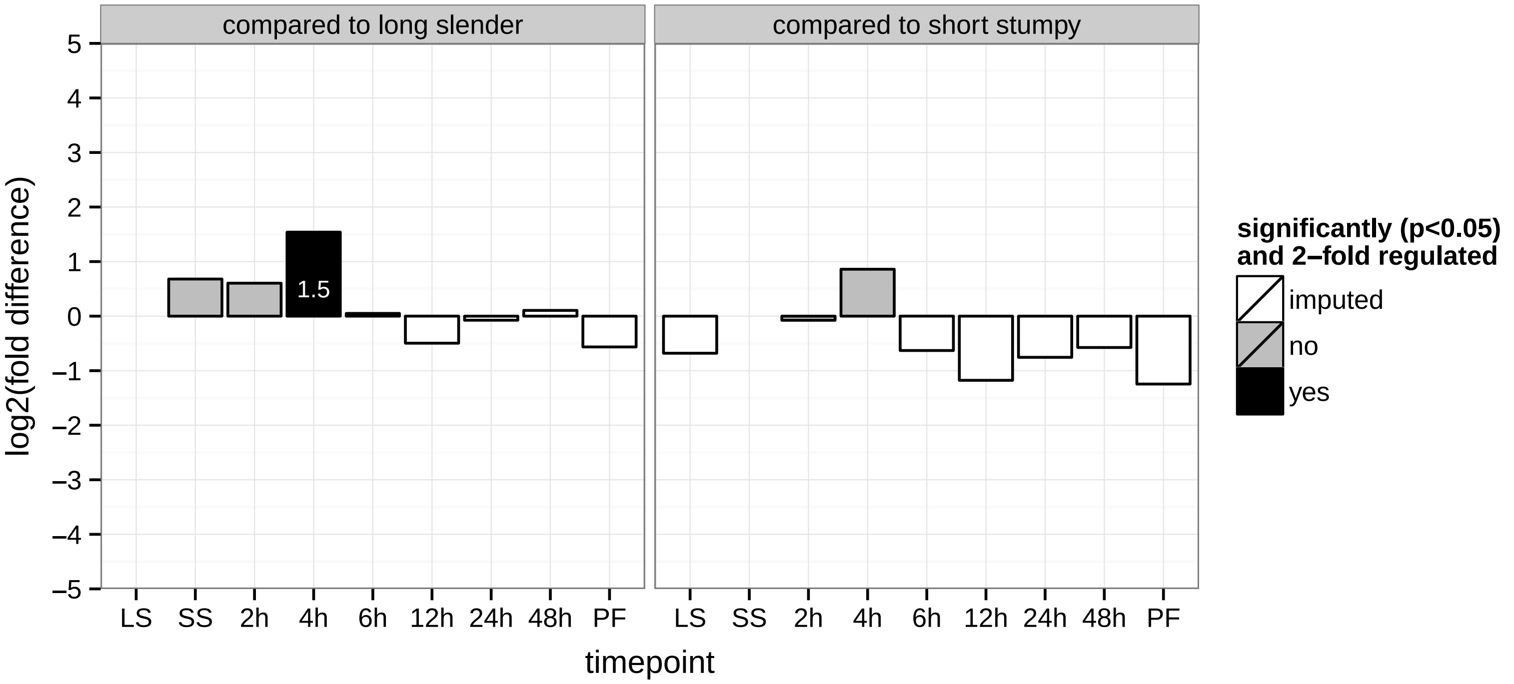
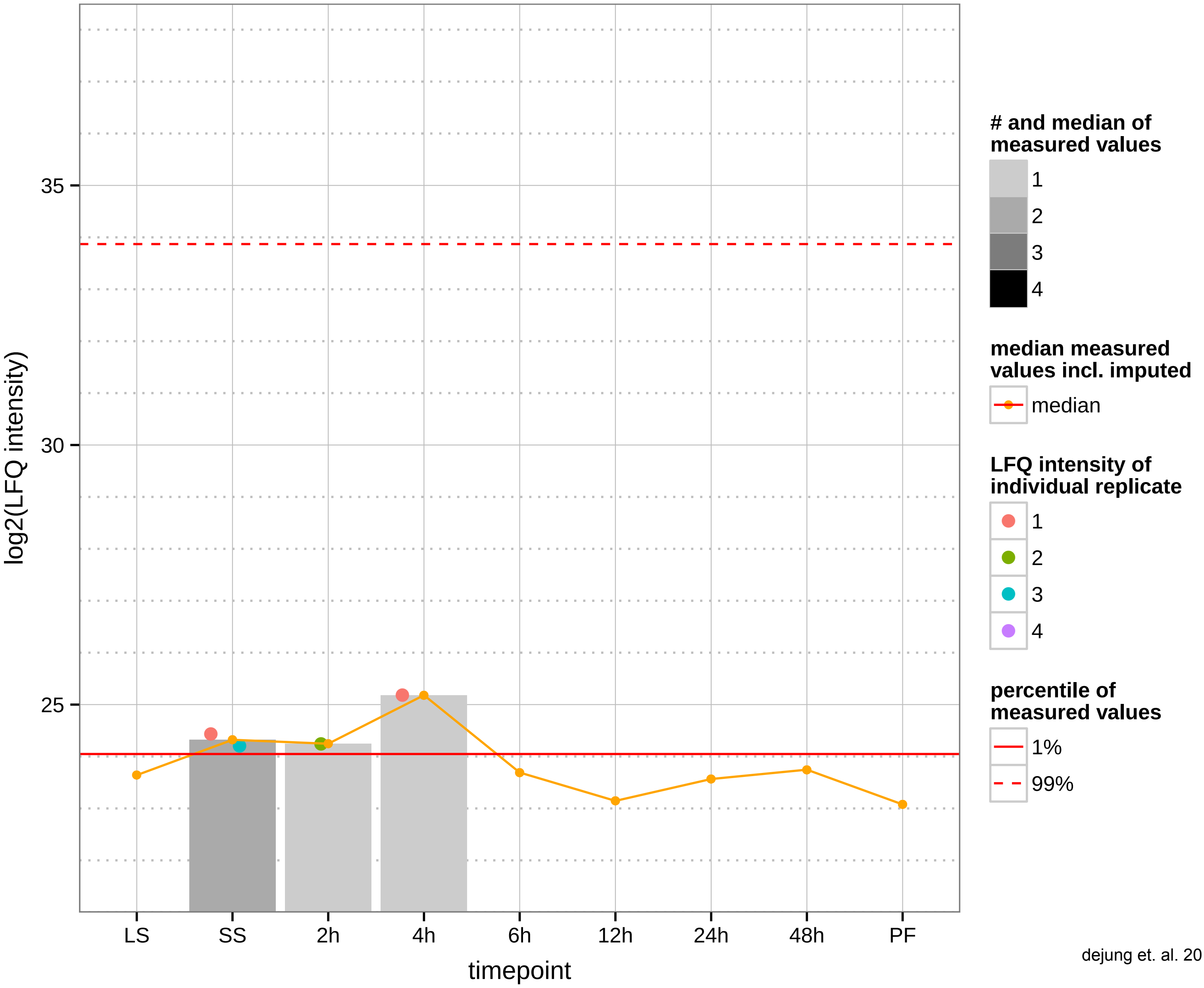
deoxyhypusine synthase, putative
Tb927.10.2750
AGOF: deoxyhypusine synthase activity
AGOC: cytosol
AGOP: peptidyl–lysine modification to hypusine, post–translational protein modification
PGOF: null
PGOC: null
PGOP: peptidyl–lysine modification to hypusine





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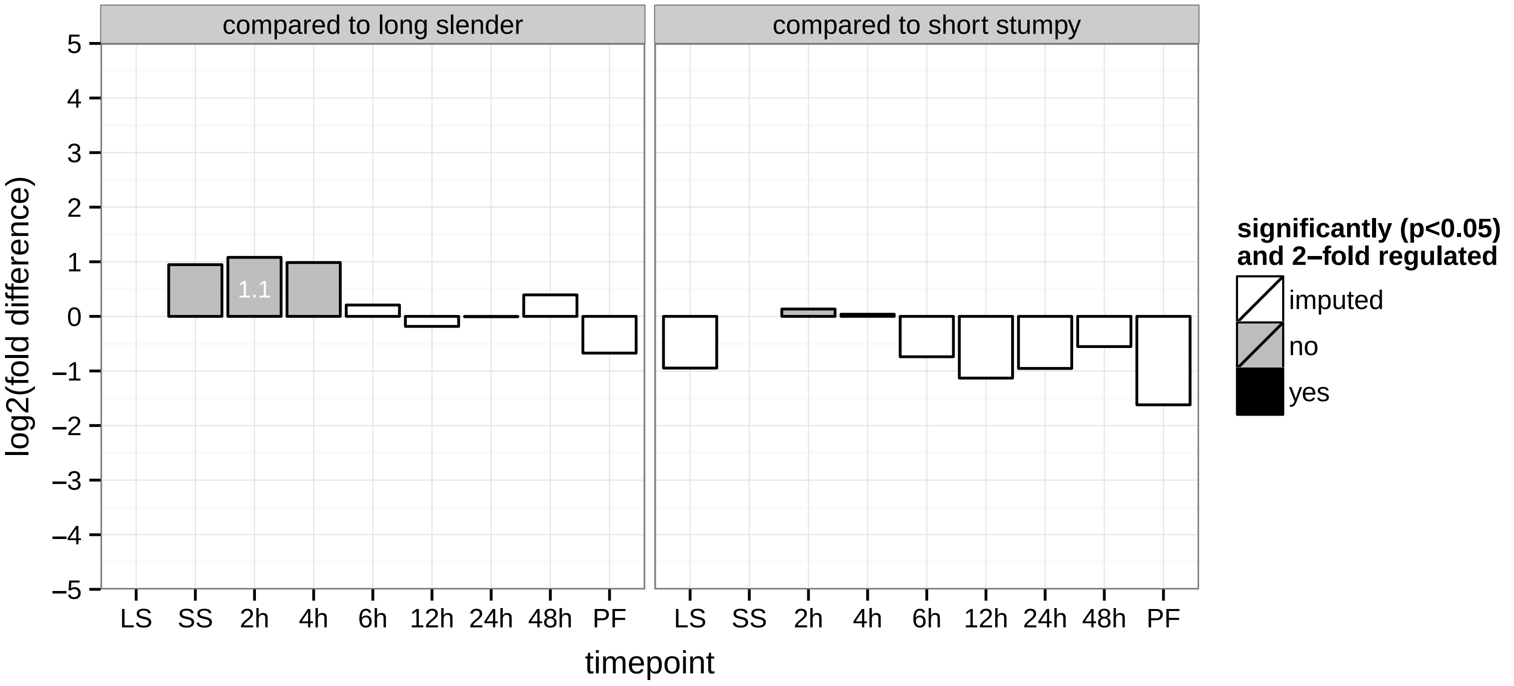
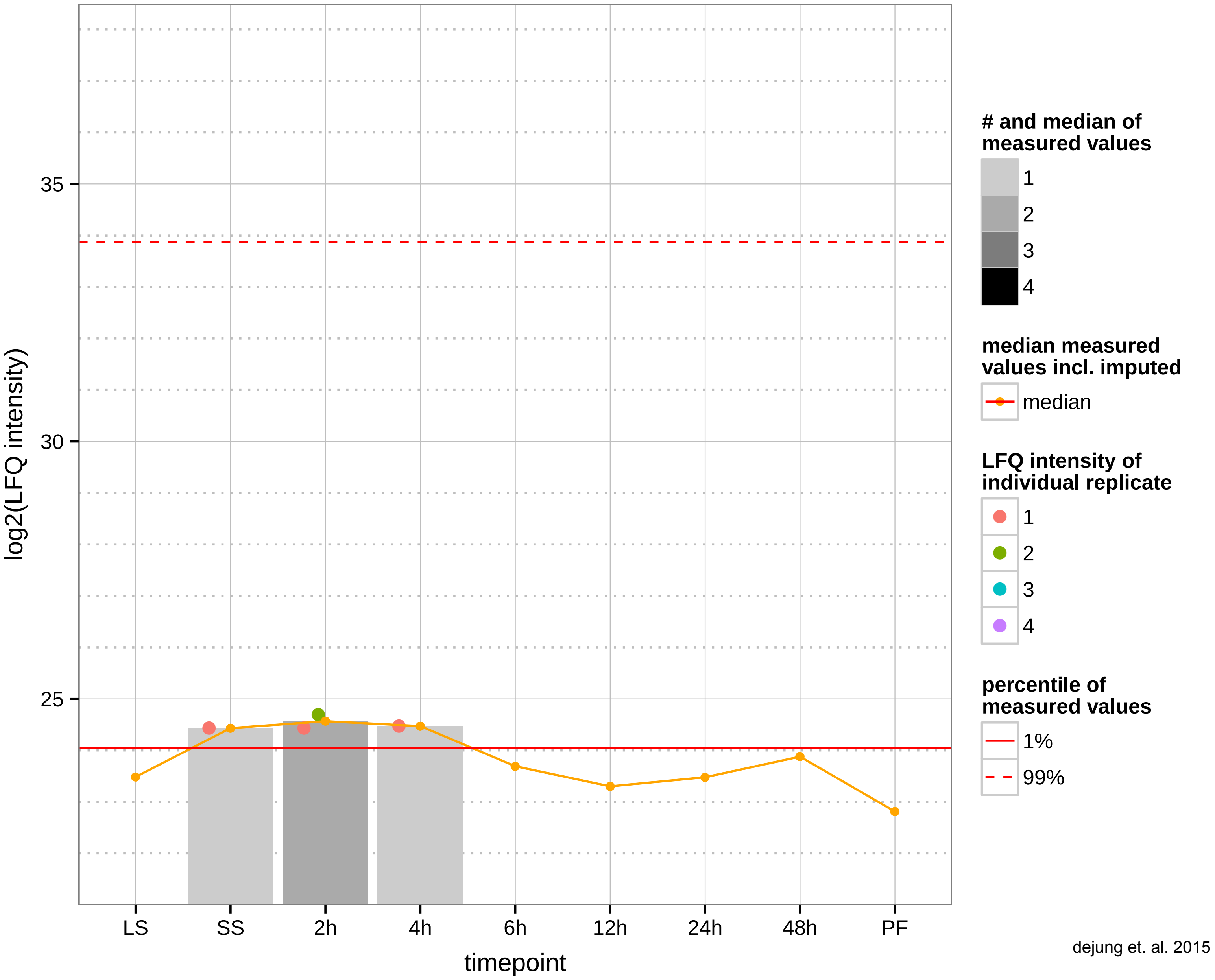
hypothetical protein, conserved
Tb927.10.420
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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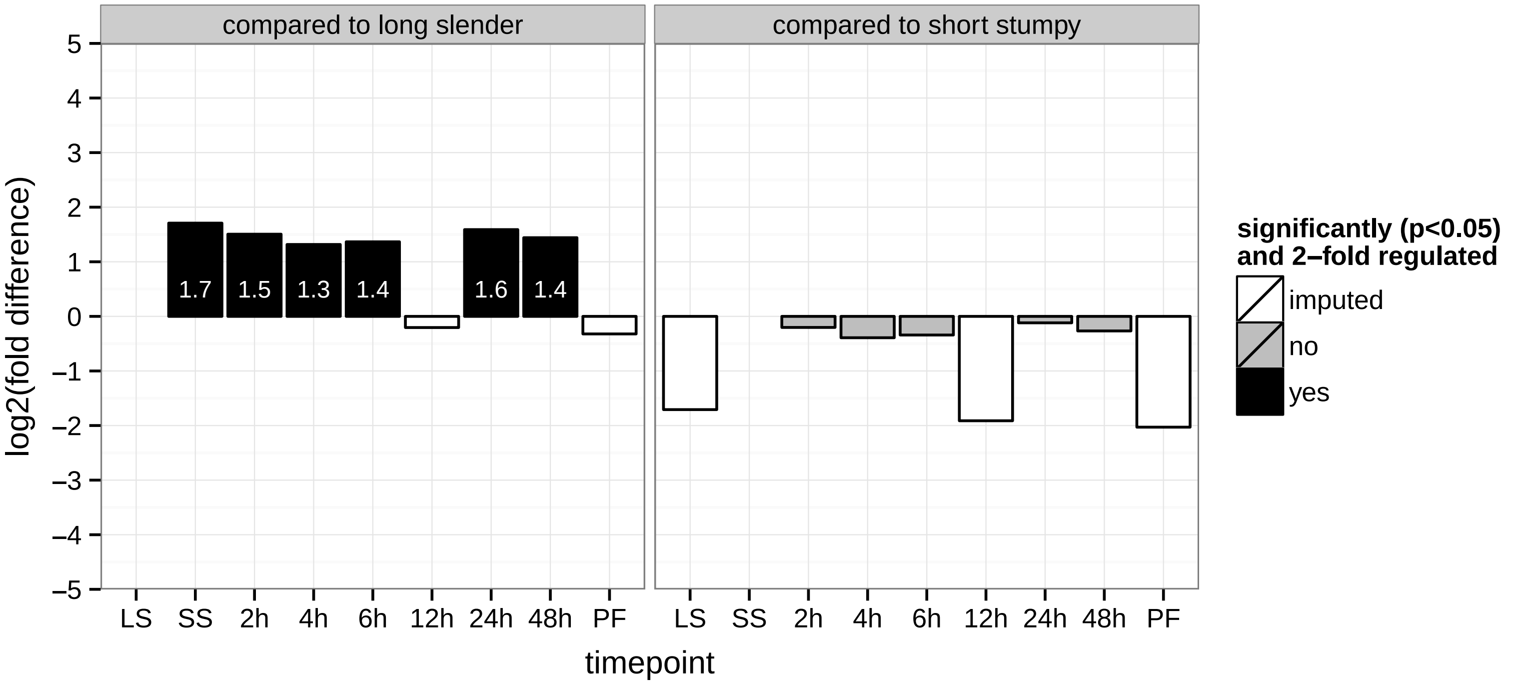
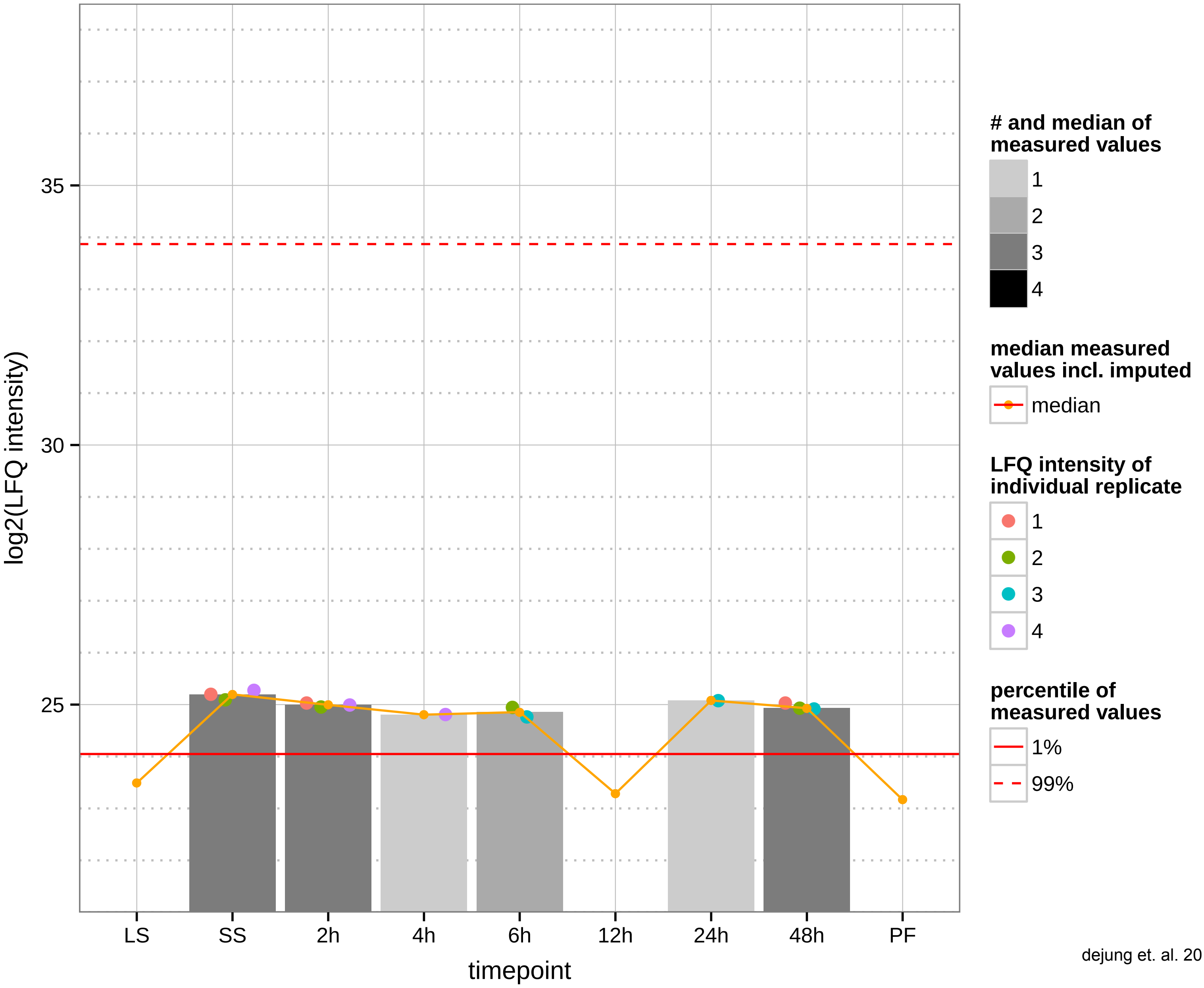
hypothetical protein, conserved
Tb927.2.4050
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: zinc ion binding
PGOC: null
PGOP: null





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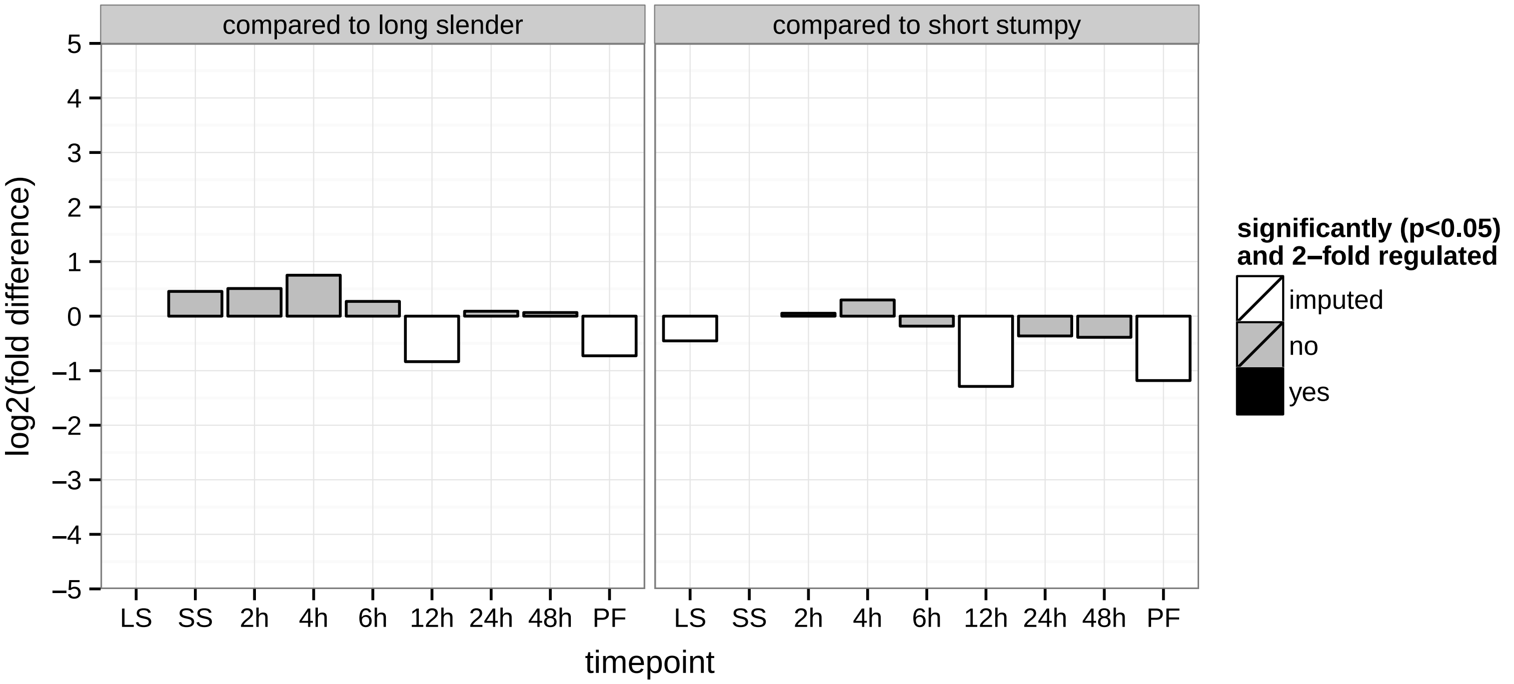
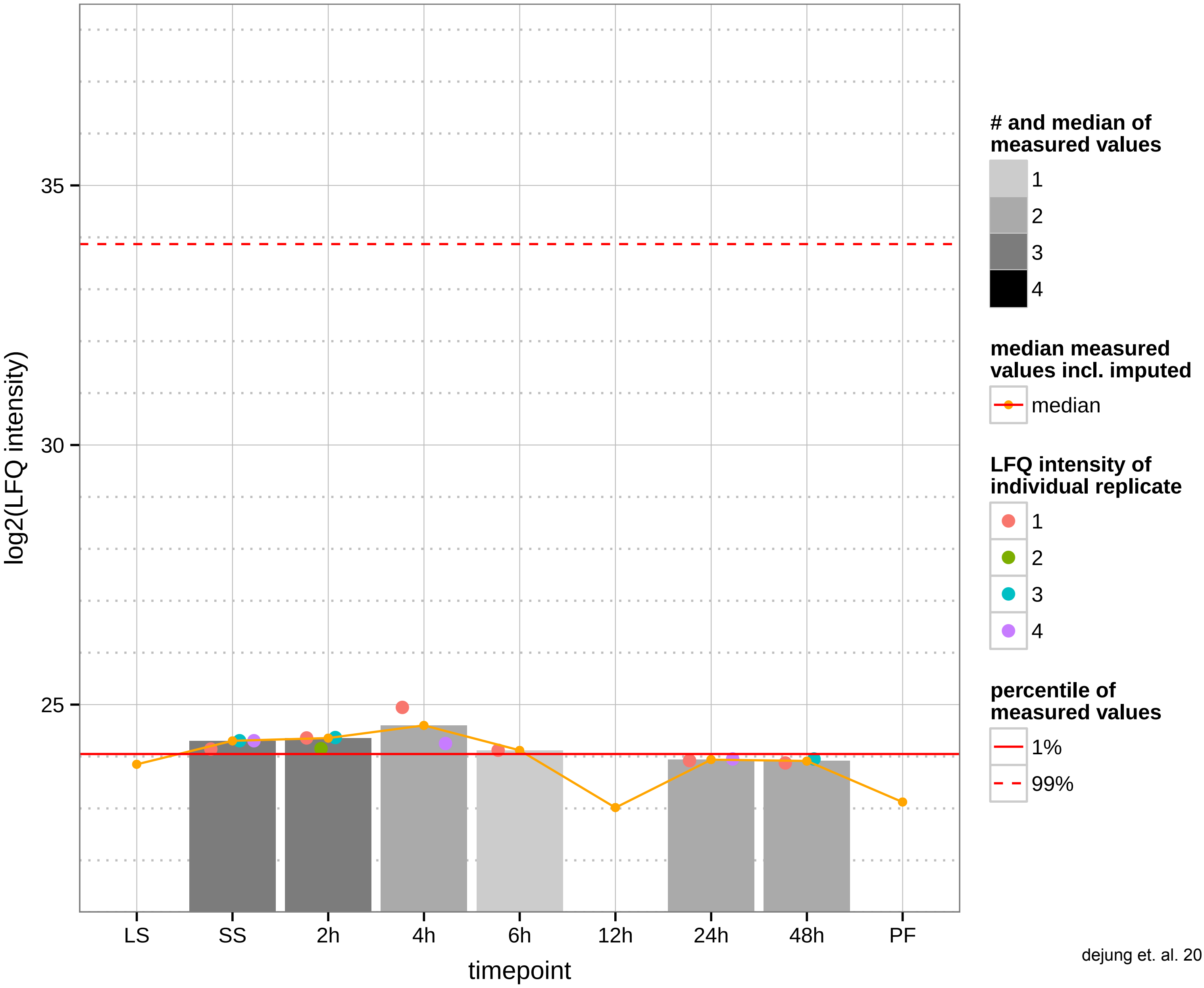
protein kinase, putative
Tb927.7.3580
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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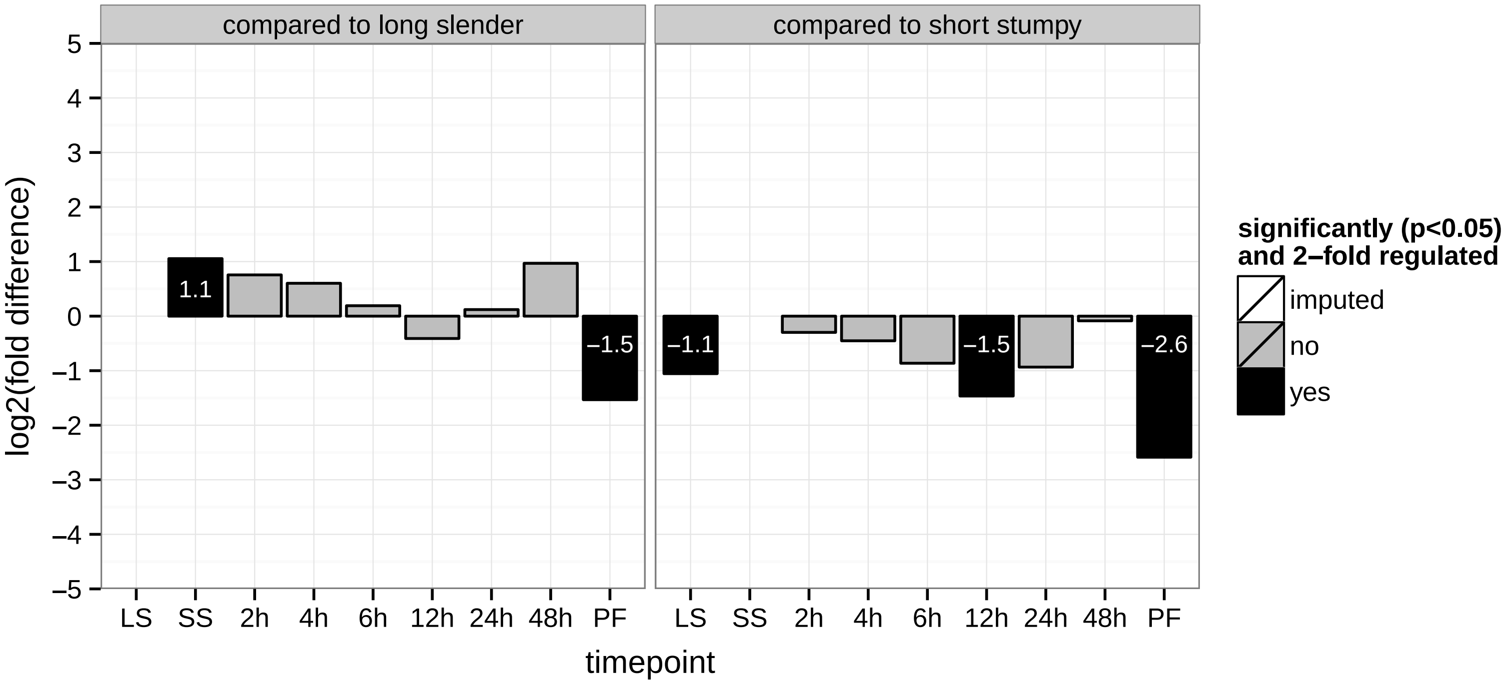
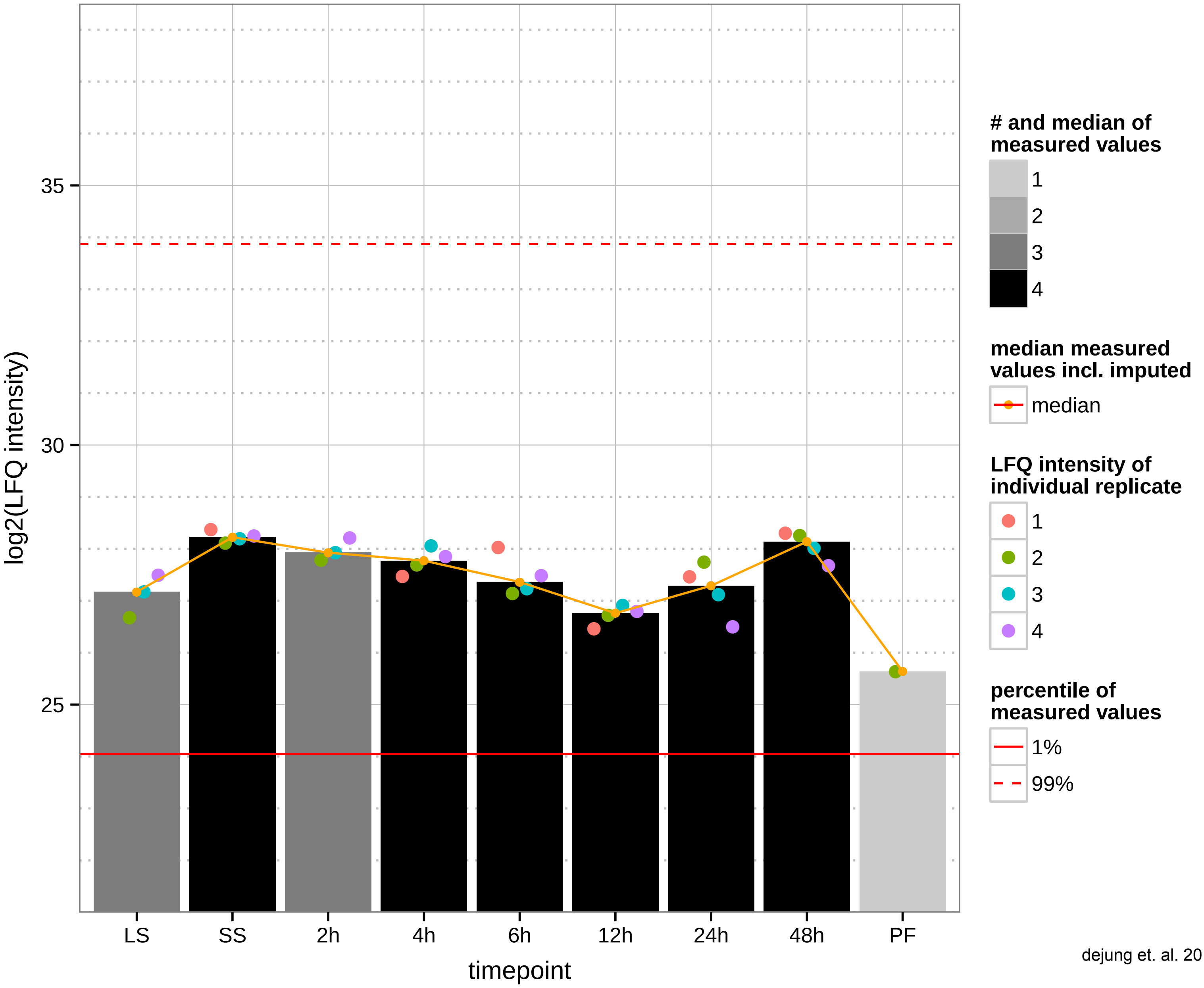
inhibitor of cysteine peptidase (ICP)
Tb927.8.6450
AGOF: endopeptidase inhibitor activity
AGOC: null
AGOP: regulation of proteolysis
PGOF: null
PGOC: null
PGOP: null





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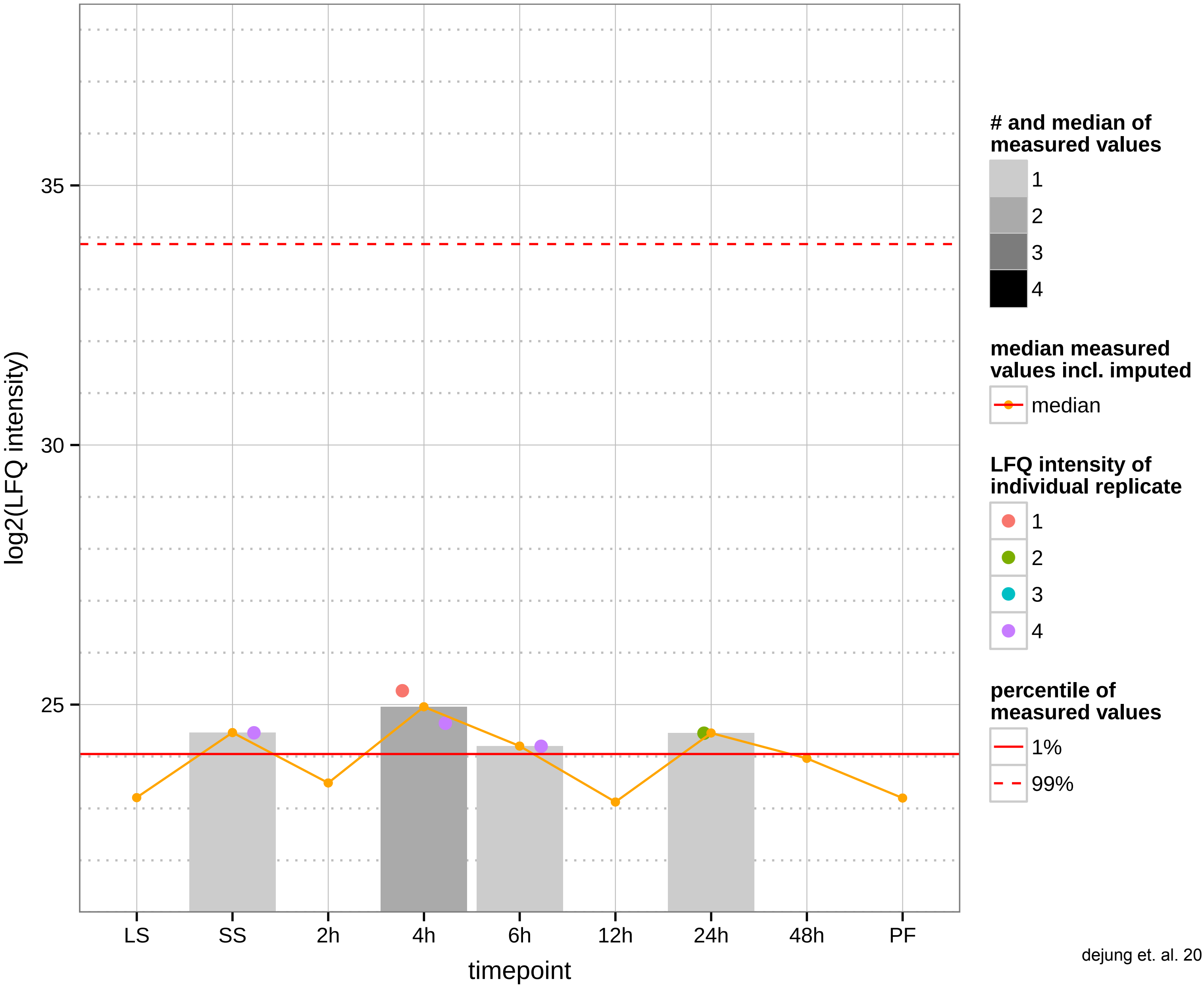
tRNA–dihydrouridine synthase 1, putative
Tb927.8.7570
AGOF: flavin adenine dinucleotide binding, tRNA dihydrouridine synthase activity
AGOC: null
AGOP: oxidation–reduction process, tRNA modification
PGOF: flavin adenine dinucleotide binding, tRNA dihydrouridine synthase activity
PGOC: null
PGOP: oxidation–reduction process, tRNA processing



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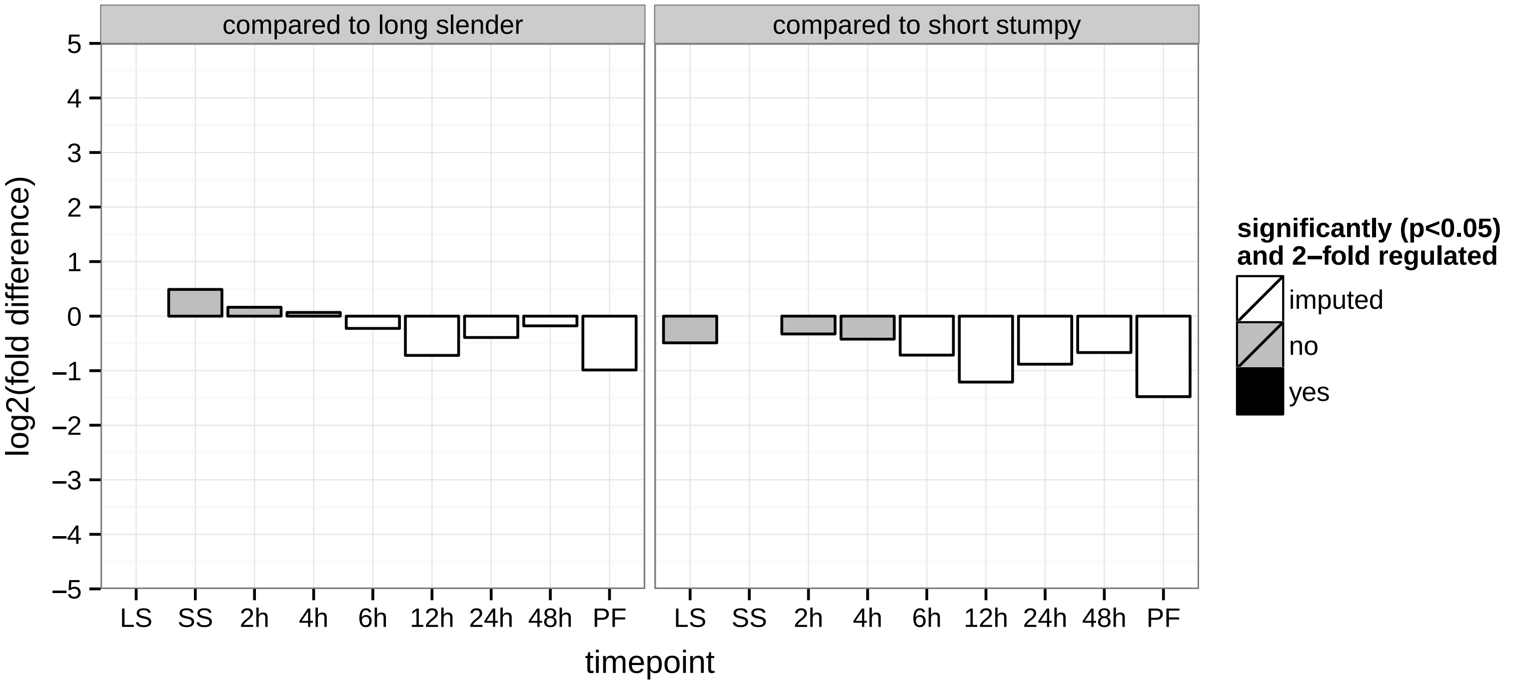
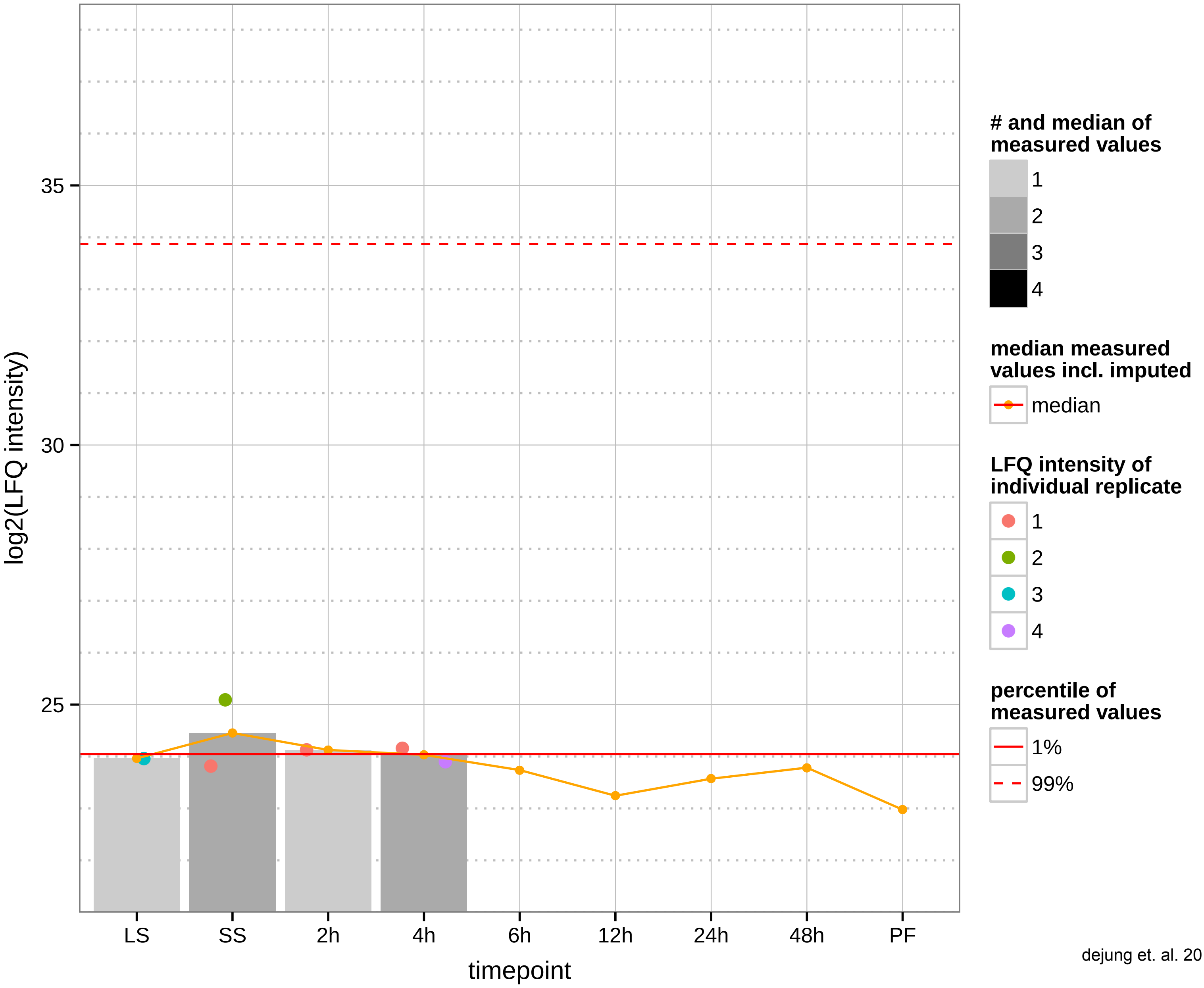
ankyrin–repeat protein, putative
Tb927.9.15400
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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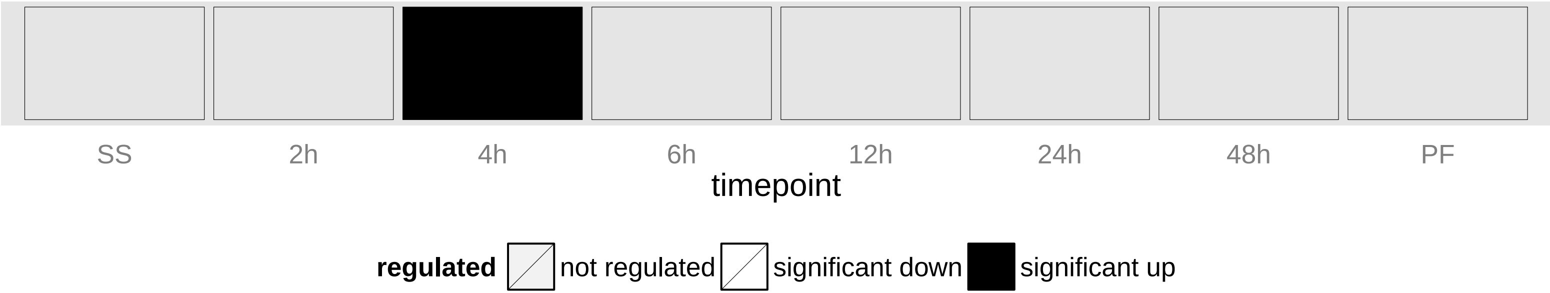

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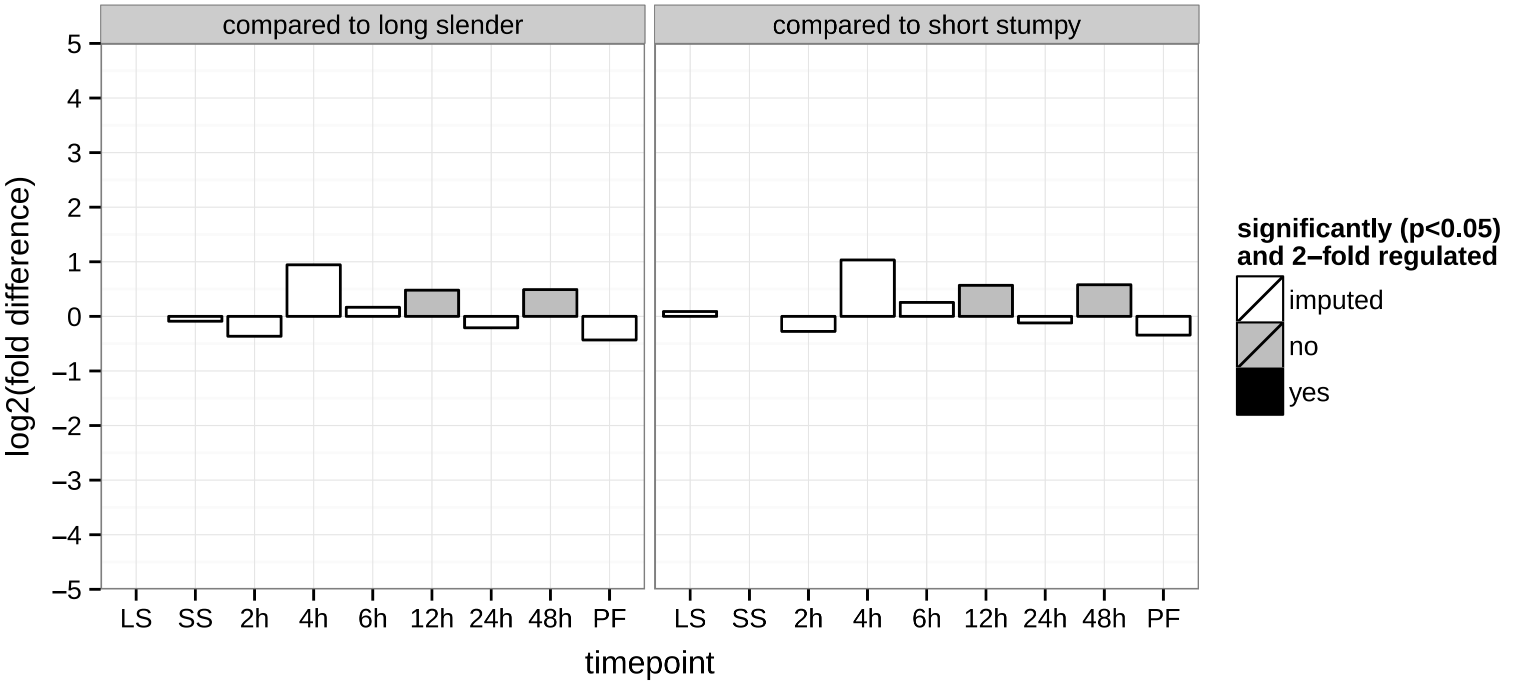
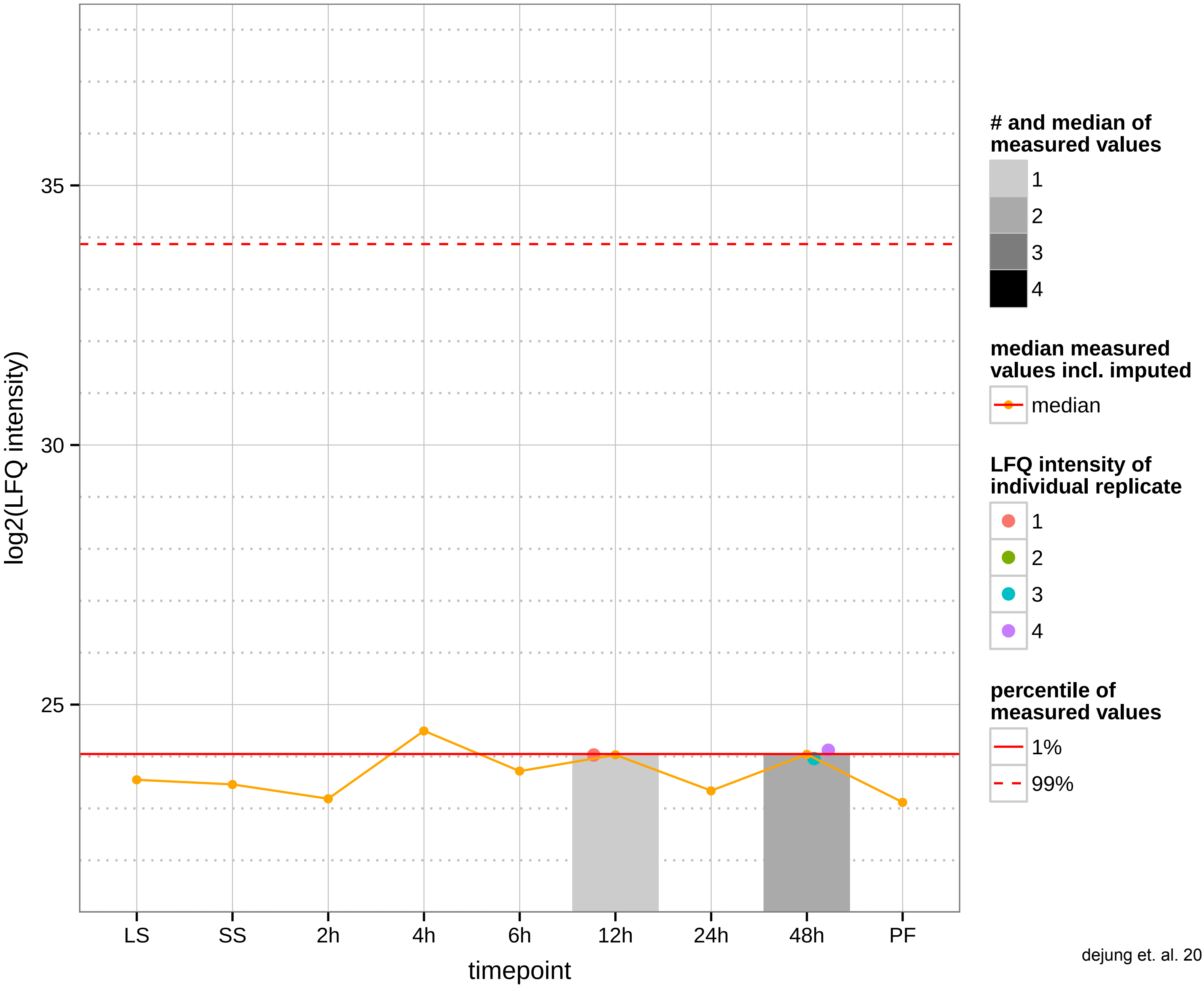
N(2), N(2)–dimethylguanosine tRNA methyltransferase, putative
Tb927.11.3890
AGOF: RNA binding, tRNA (guanine–N2–)–methyltransferase activity
AGOC: null
AGOP: tRNA processing
PGOF: RNA binding, tRNA (guanine–N2–)–methyltransferase activity
PGOC: null
PGOP: tRNA processing





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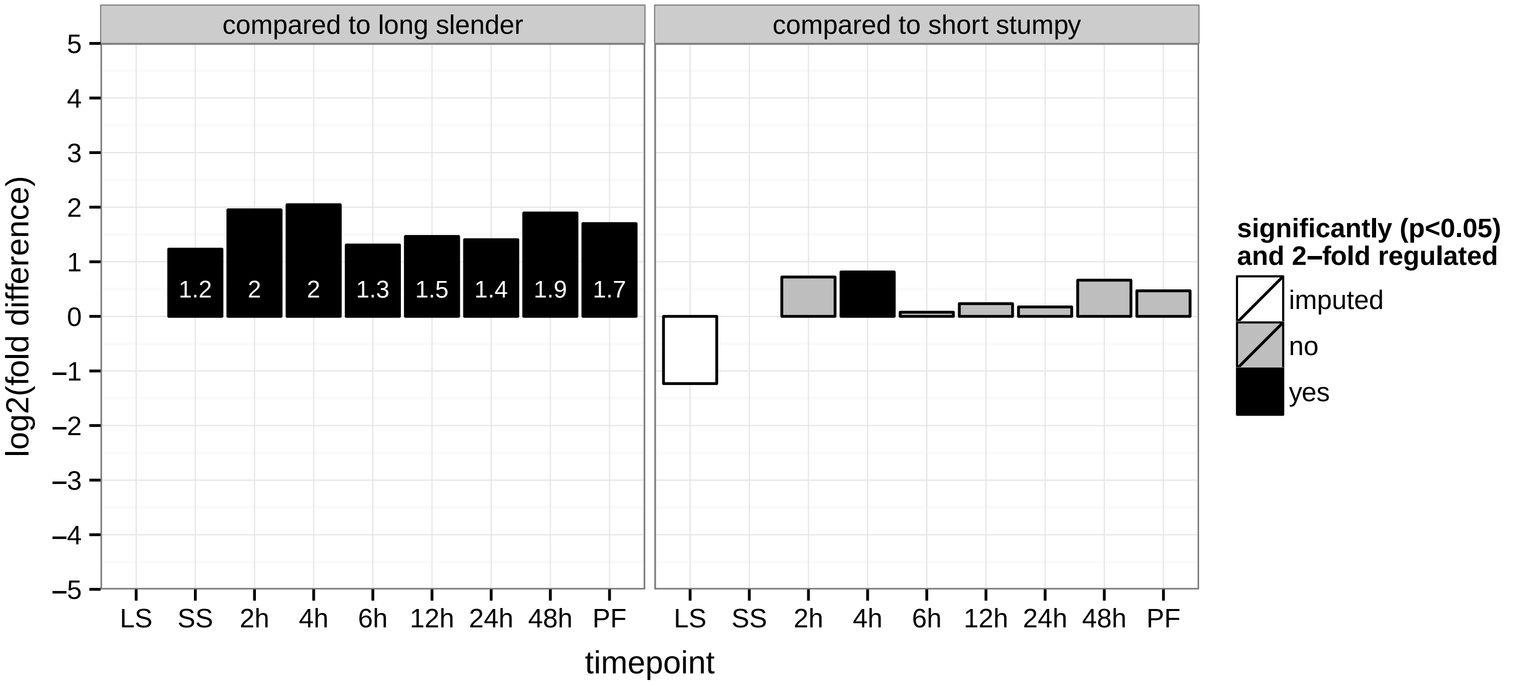
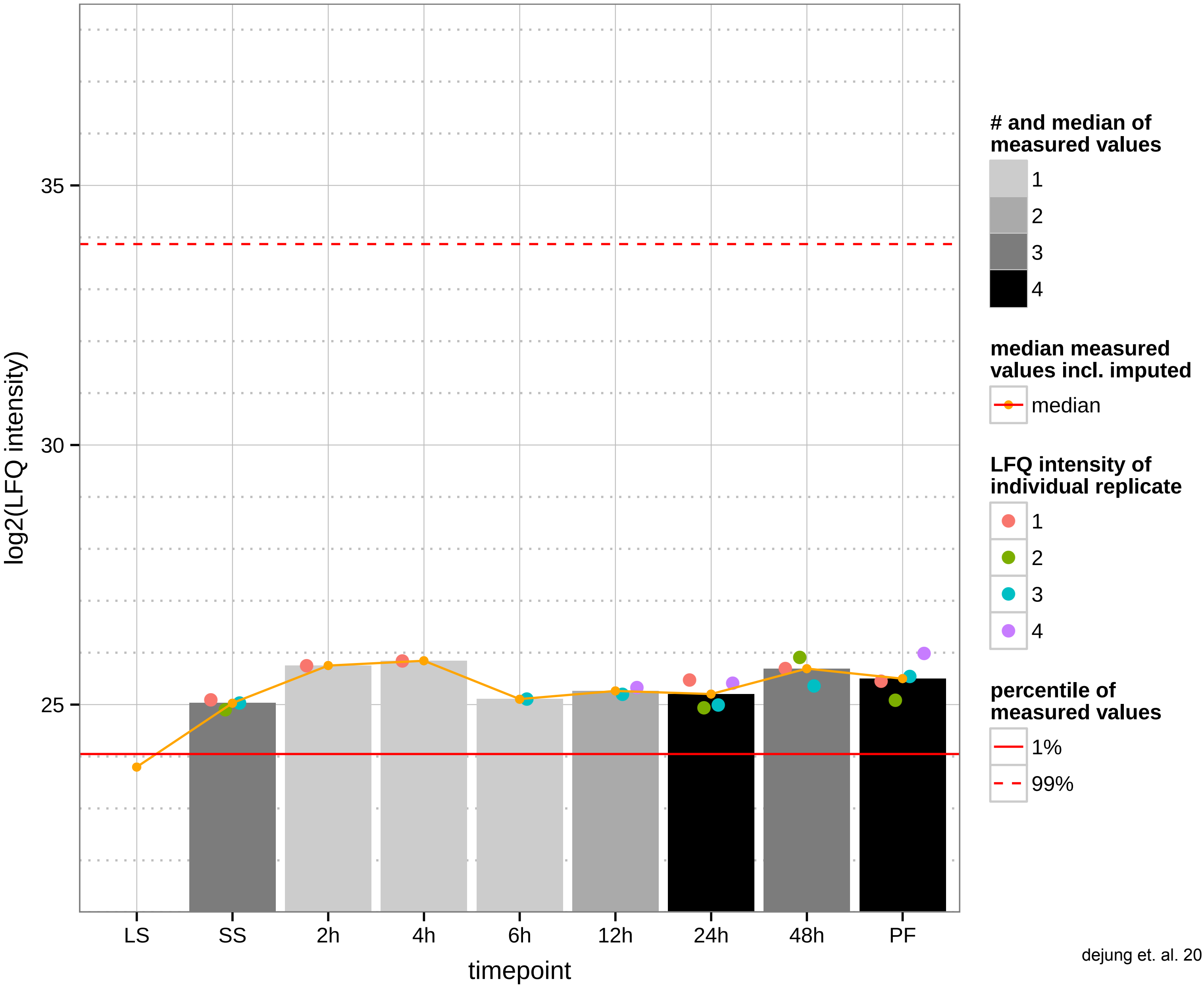
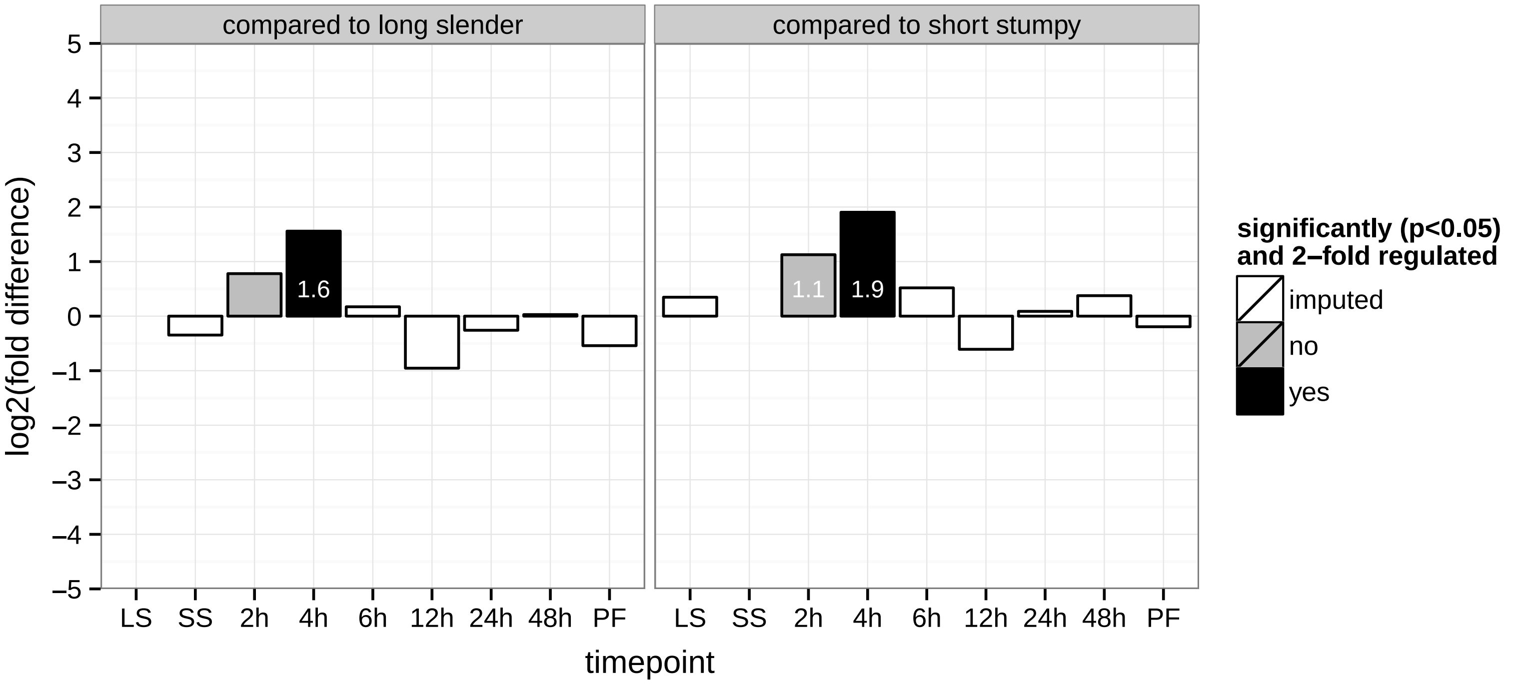
hypothetical protein, conserved
Tb927.11.4630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

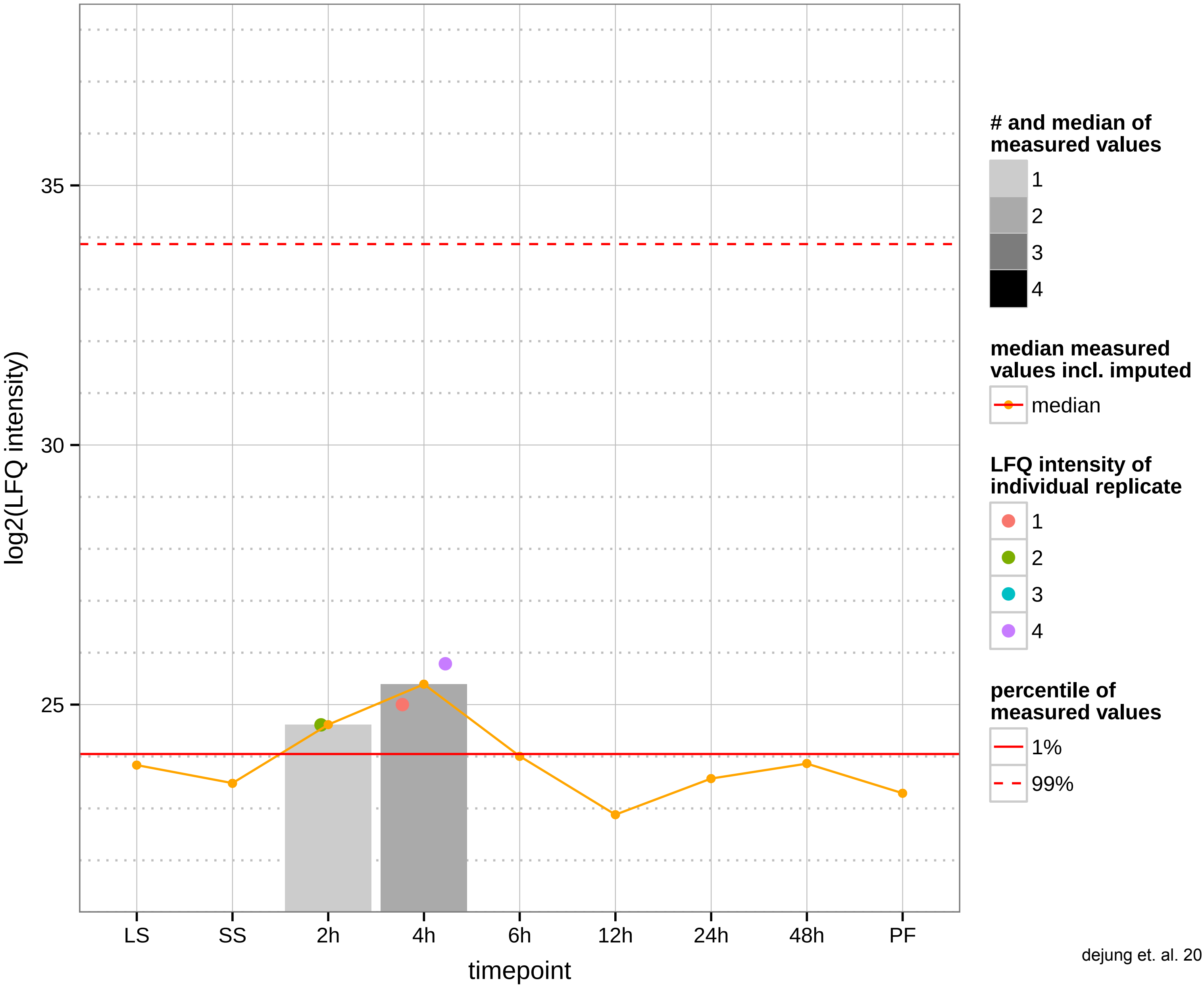




dejung et. al. 2015

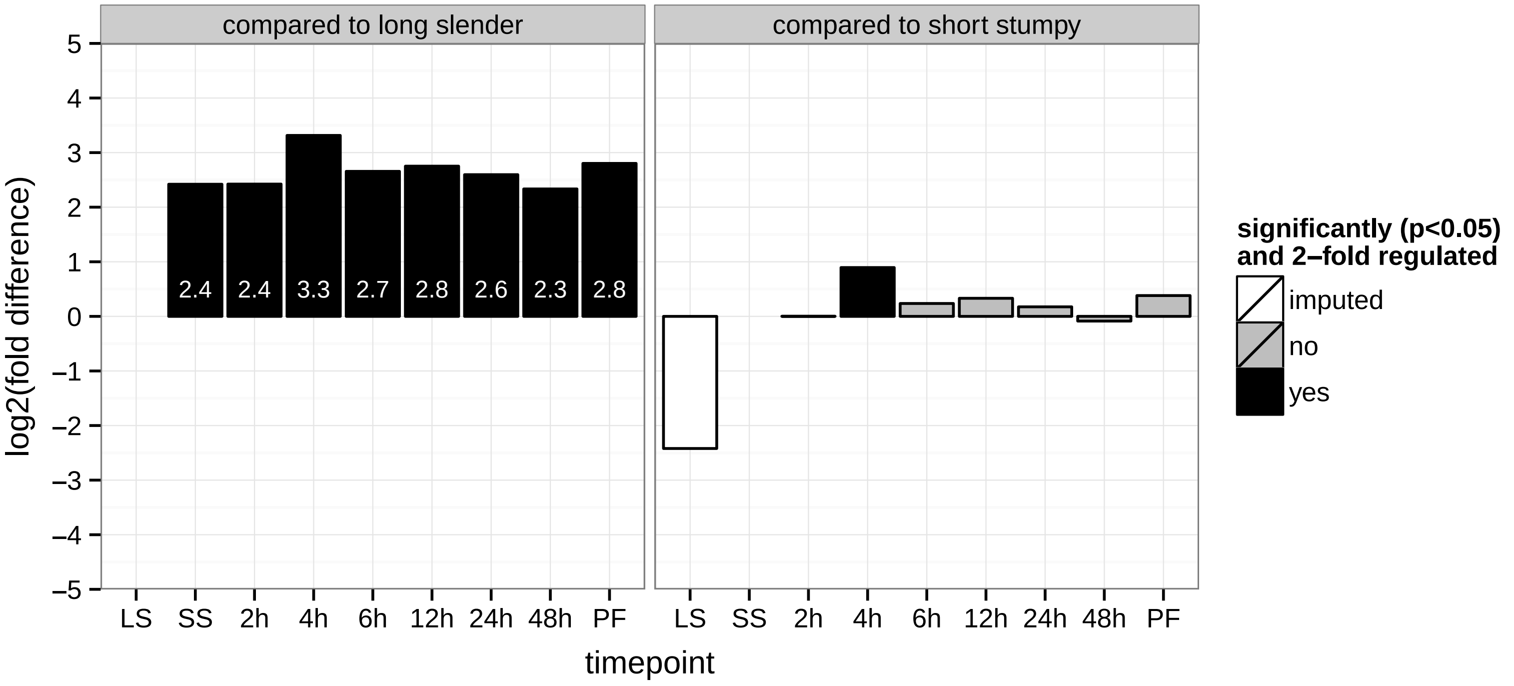
hypothetical protein, conserved
Tb927.3.5470
AGOF: null
AGOC: null
AGOP: null
PGOF: protein phosphatase inhibitor activity
PGOC: null
PGOP: regulation of phosphoprotein phosphatase activity, regulation of signal transduction

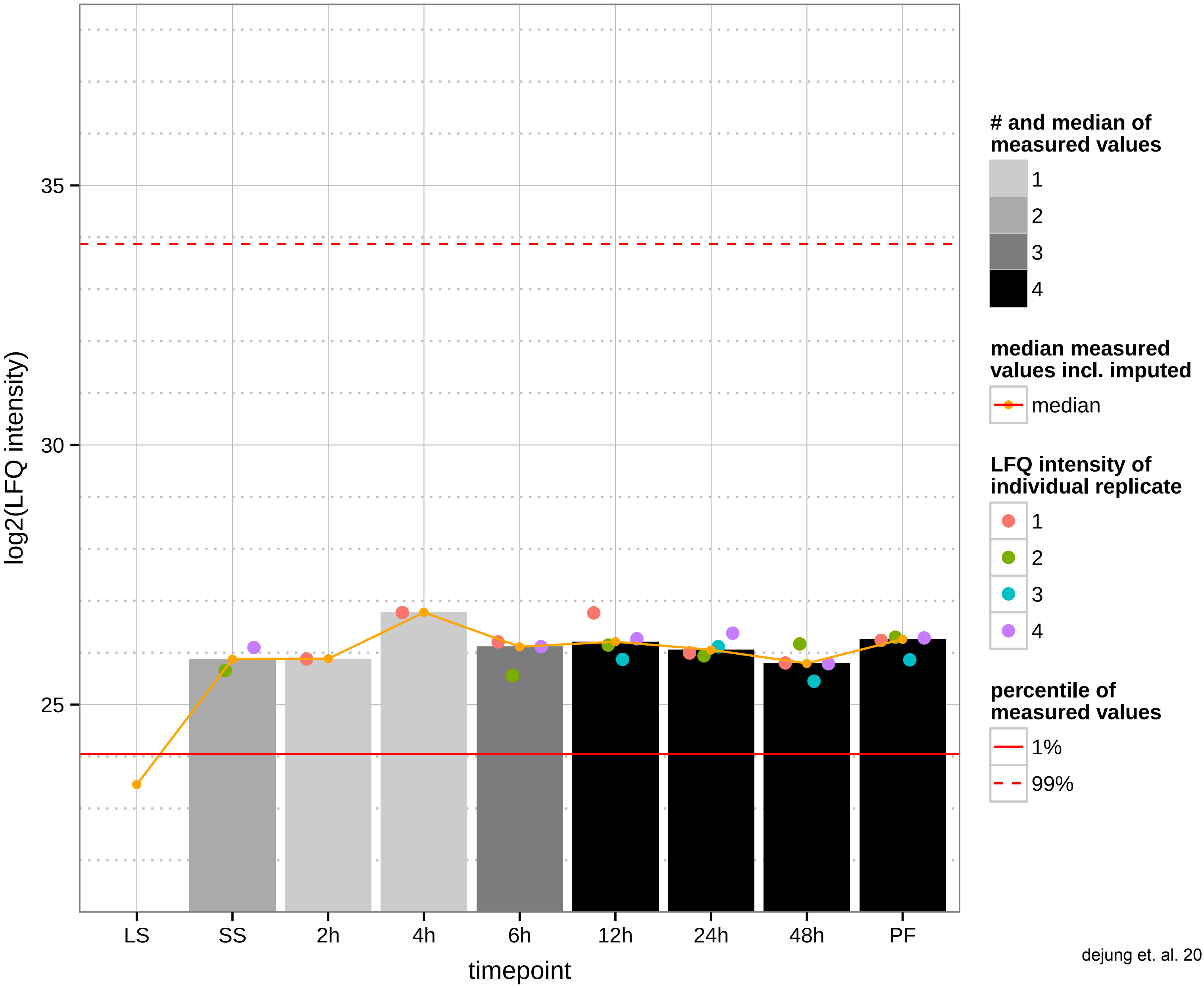




dejung et. al. 2015

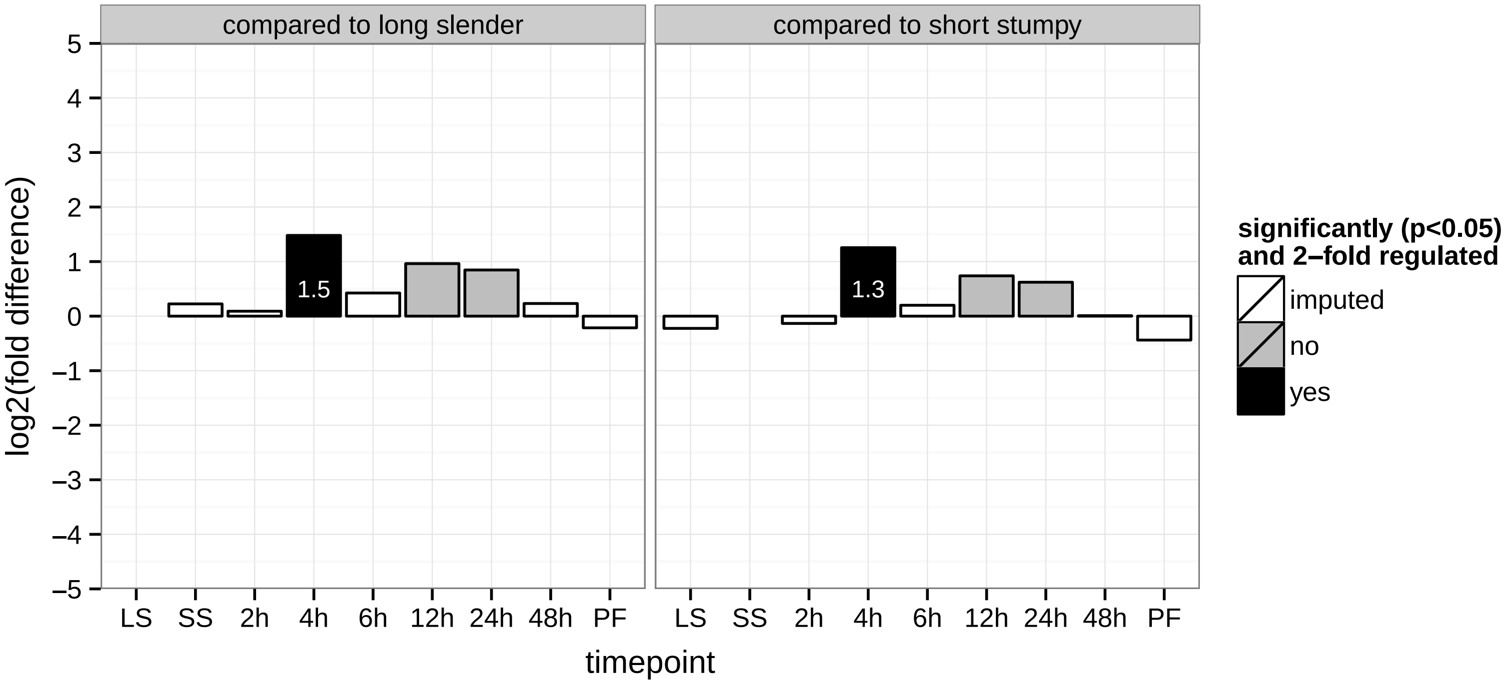
hypothetical protein, conserved
Tb927.7.4030
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

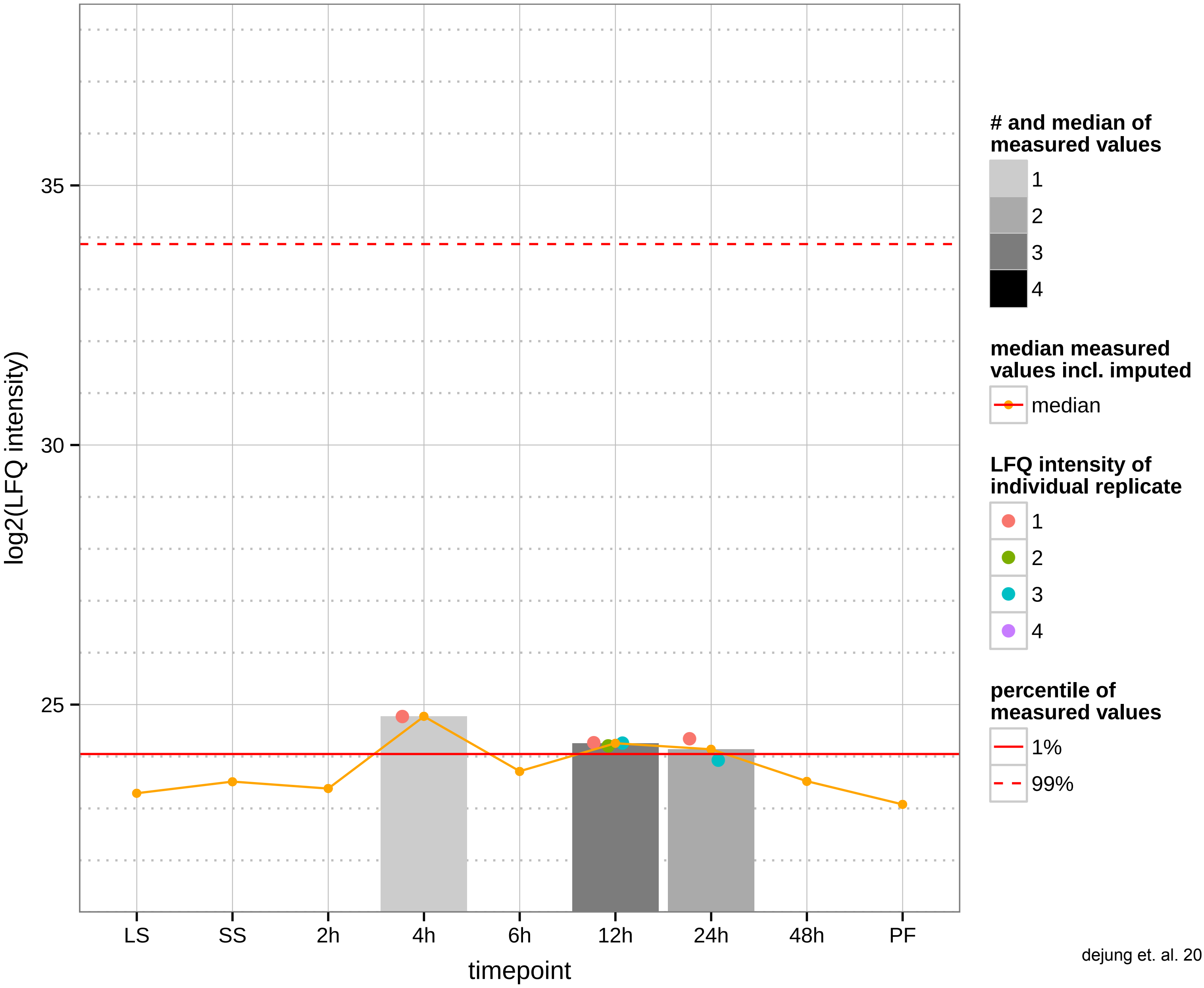




dejung et. al. 2015

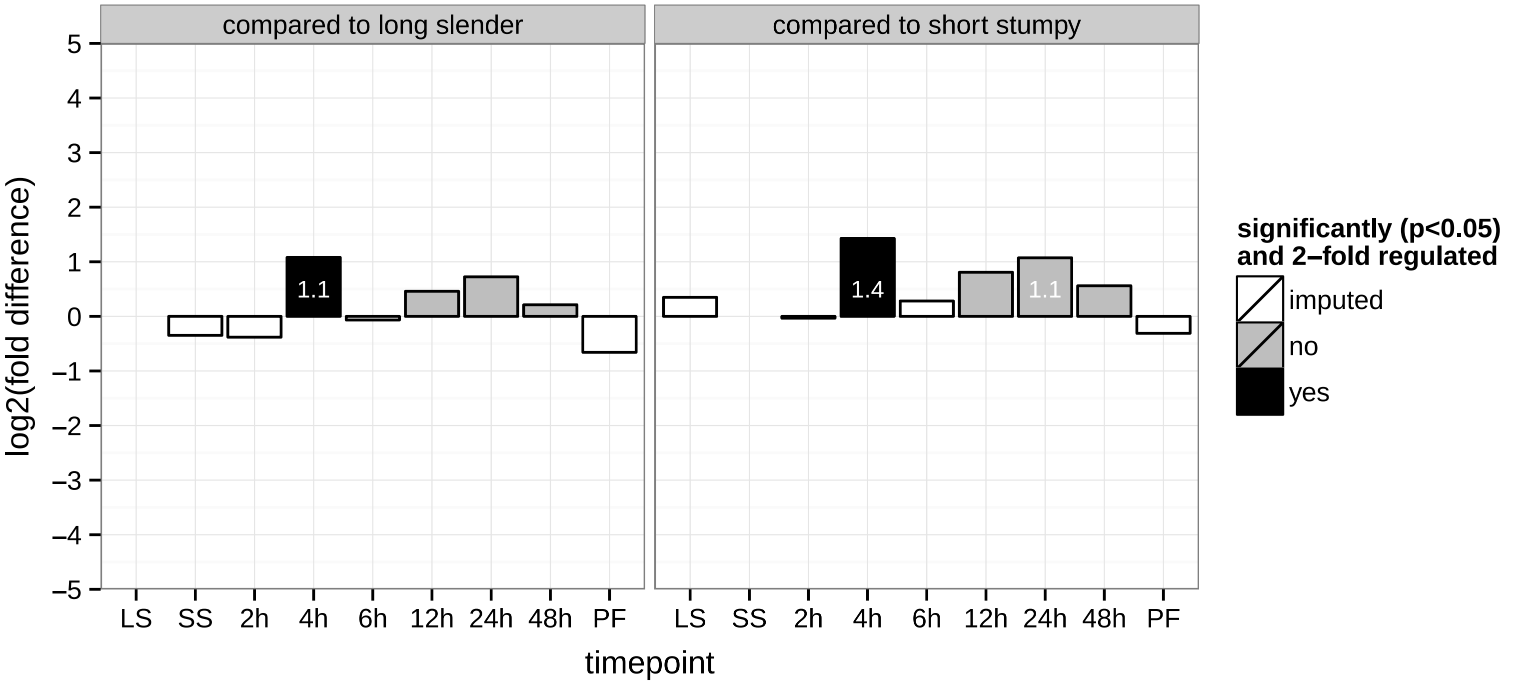
hypothetical protein, conserved
Tb927.7.6210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

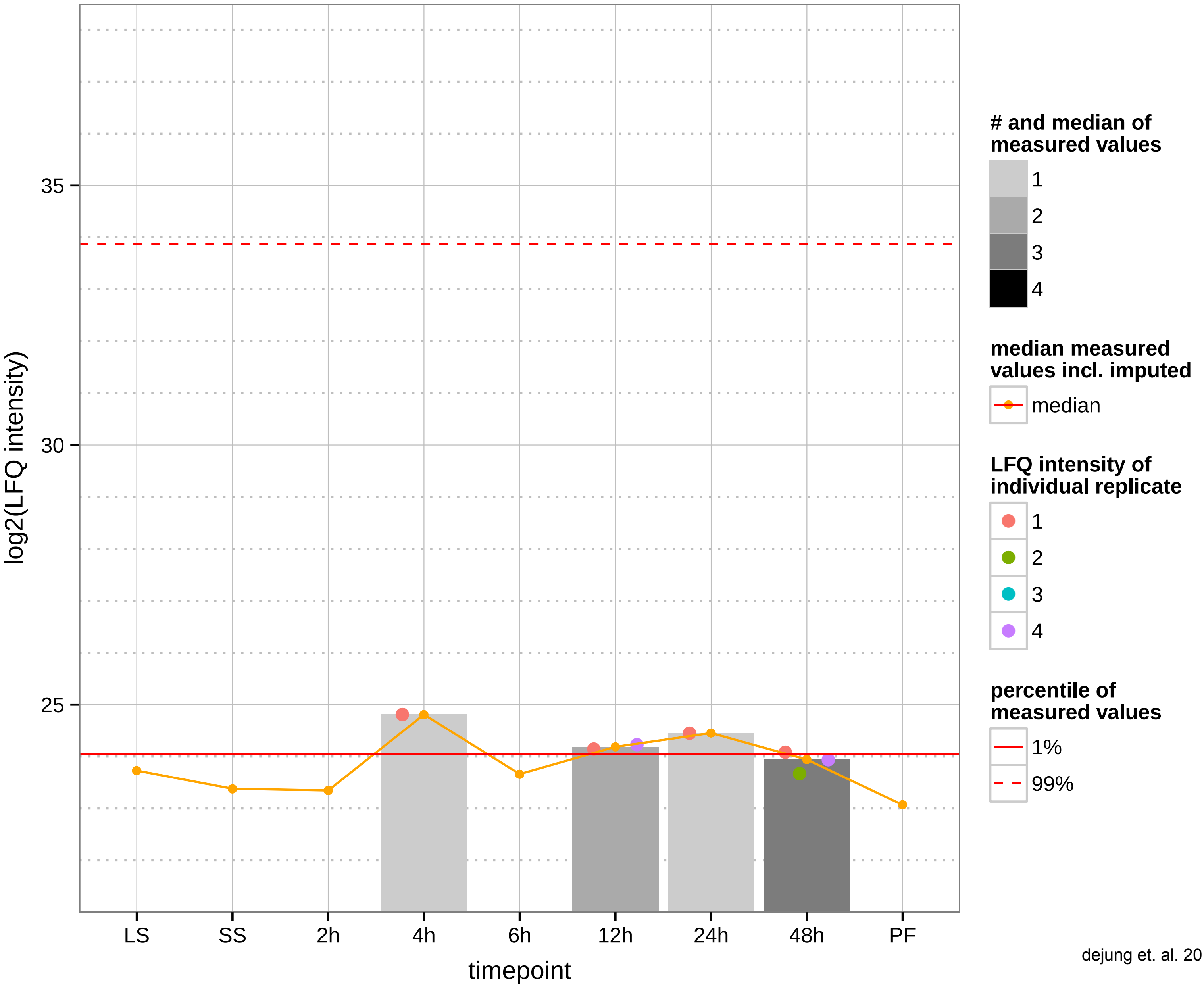




dejung et. al. 2015

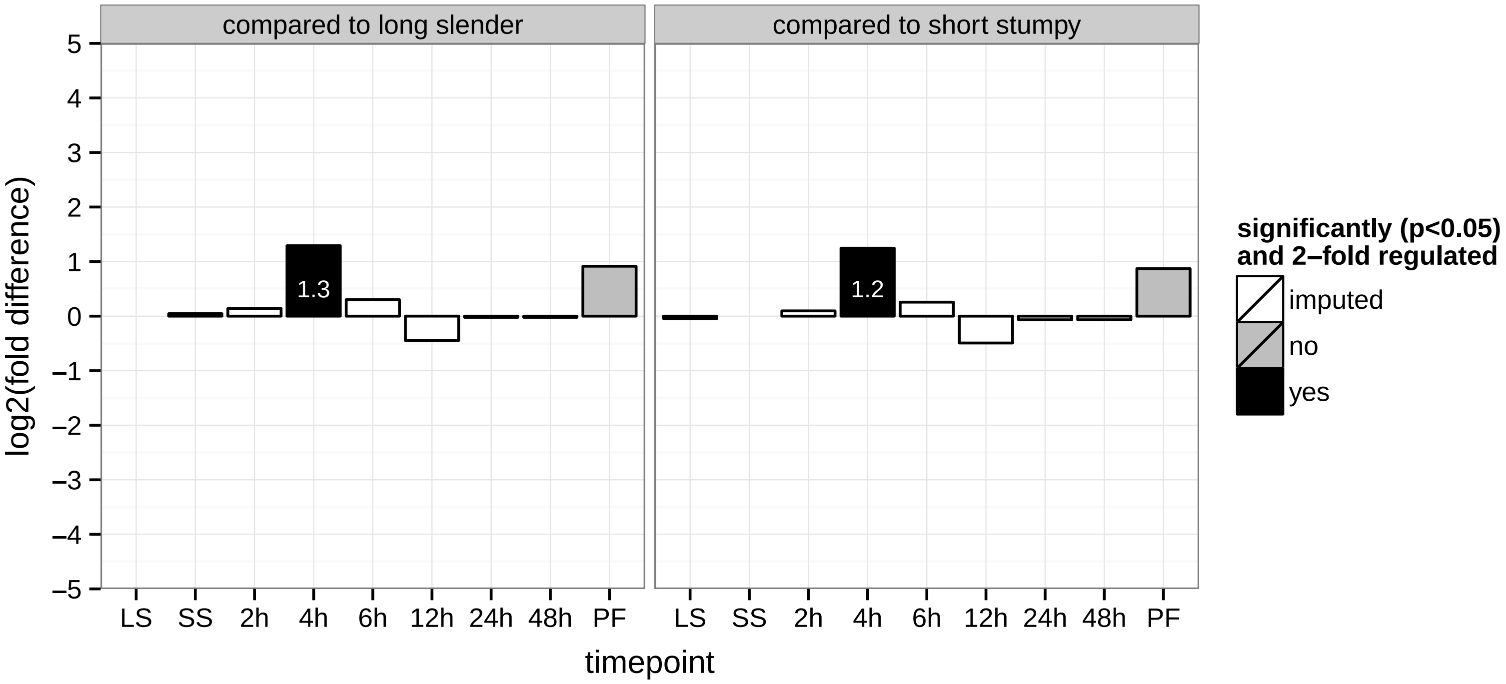
hypothetical protein, conserved
Tb927.8.2840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

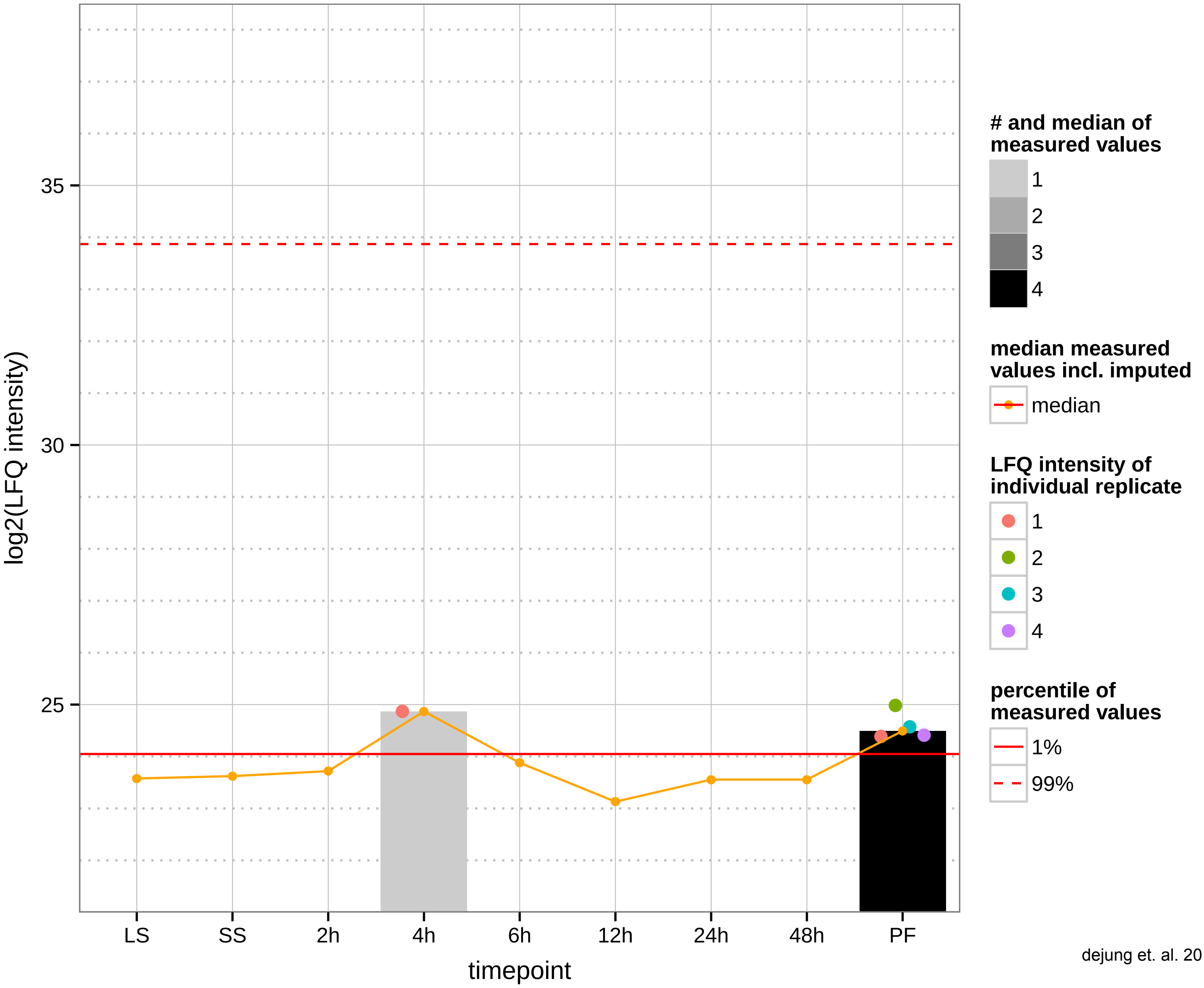




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.5720
AGOF: null
AGOC: null
AGOP: null
PGOF: transferase activity
PGOC: null
PGOP: null





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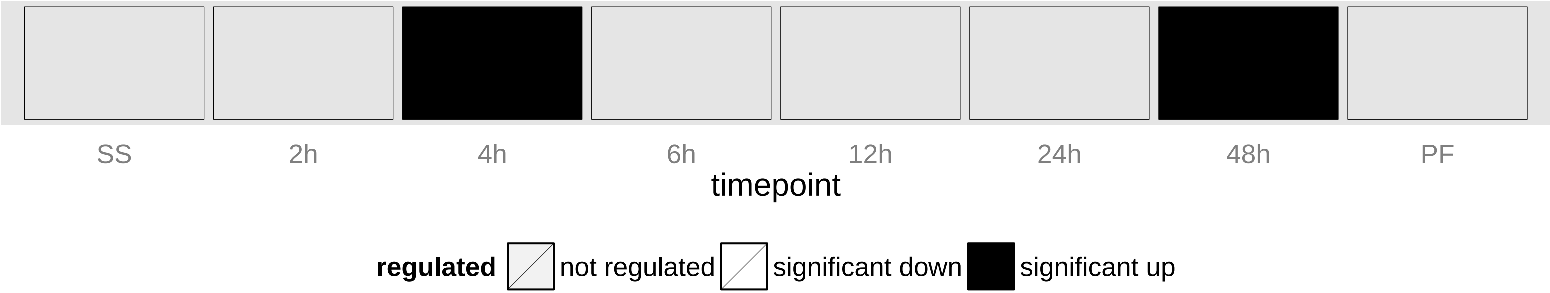

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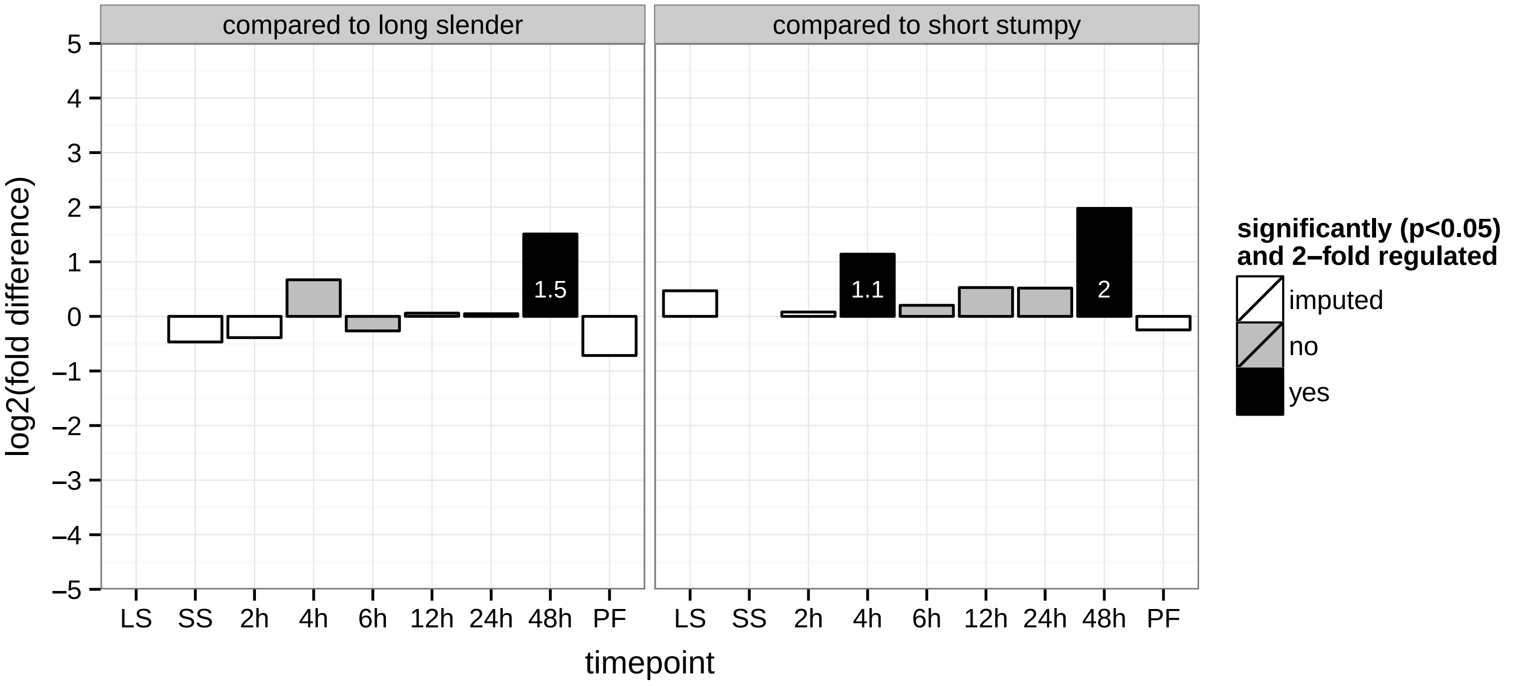
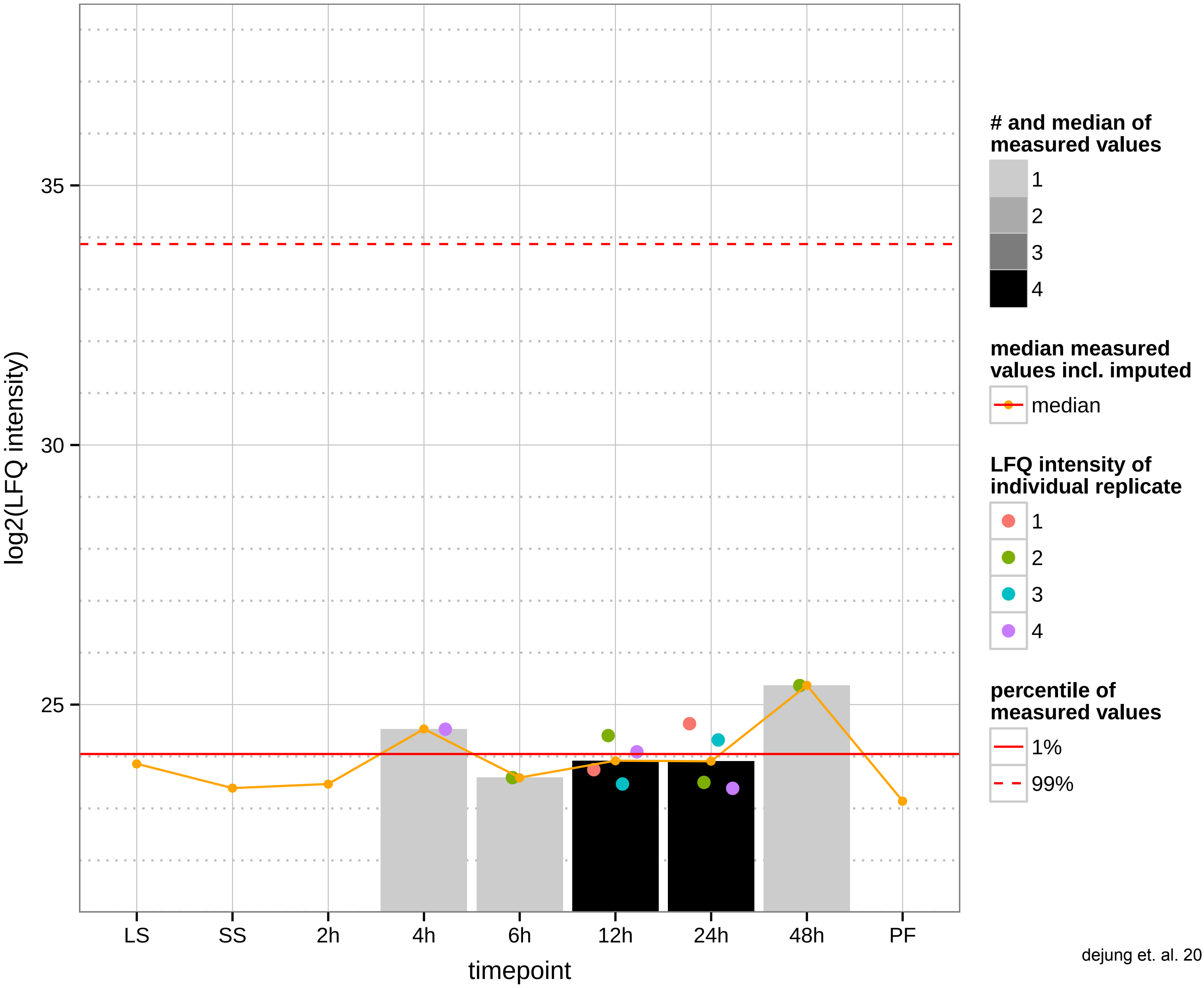
hypothetical protein, conserved
Tb927.1.1390
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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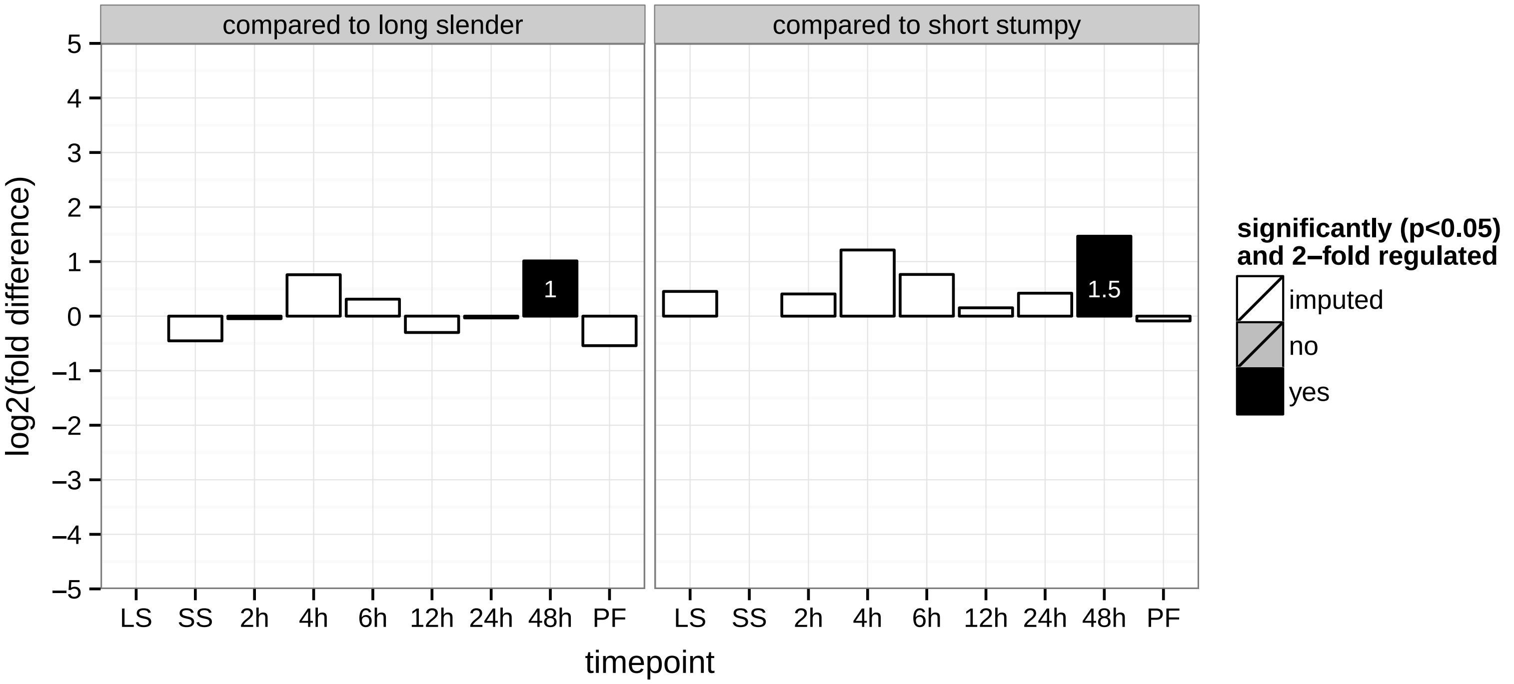
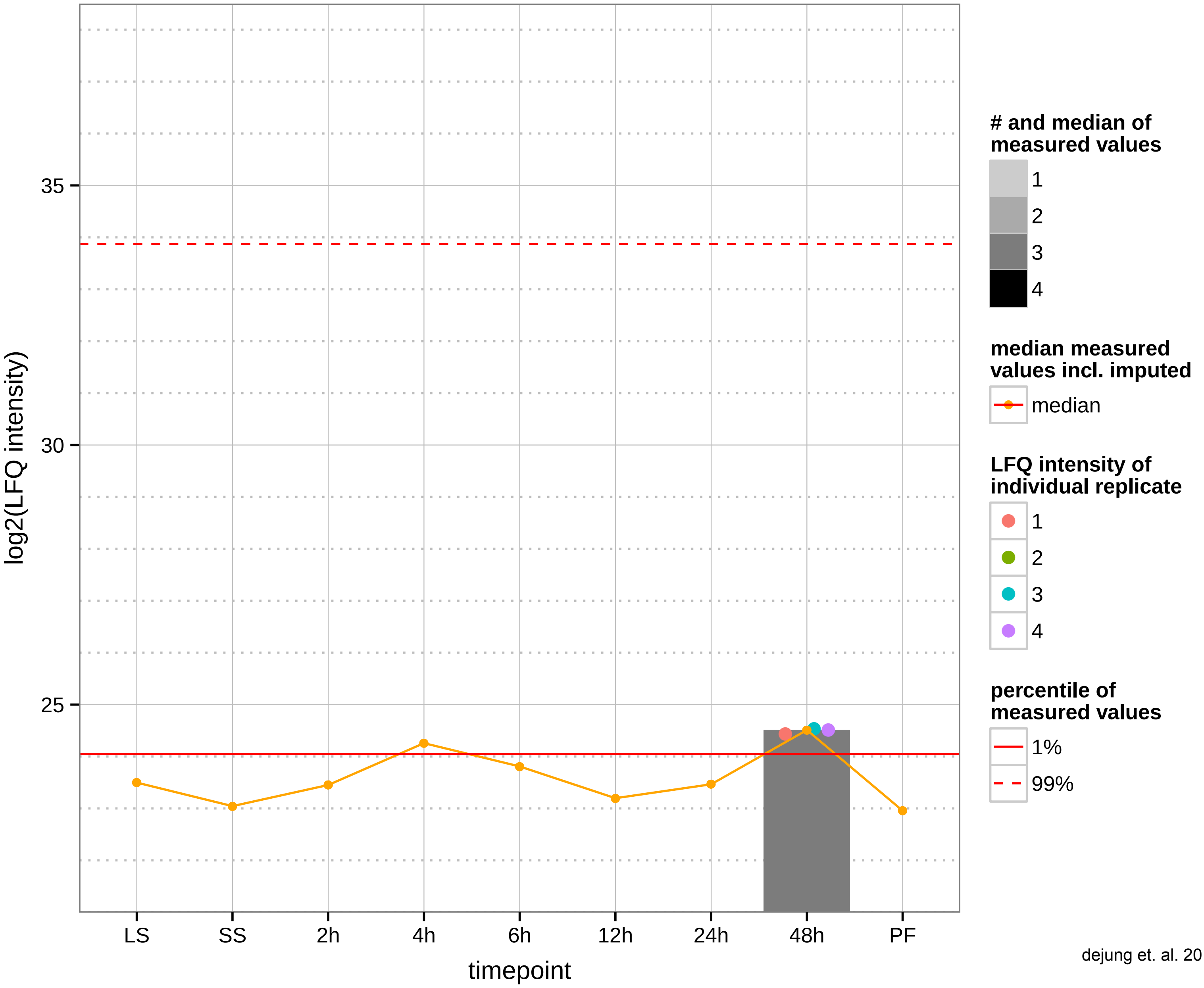
hypothetical protein, conserved
Tb927.3.1910
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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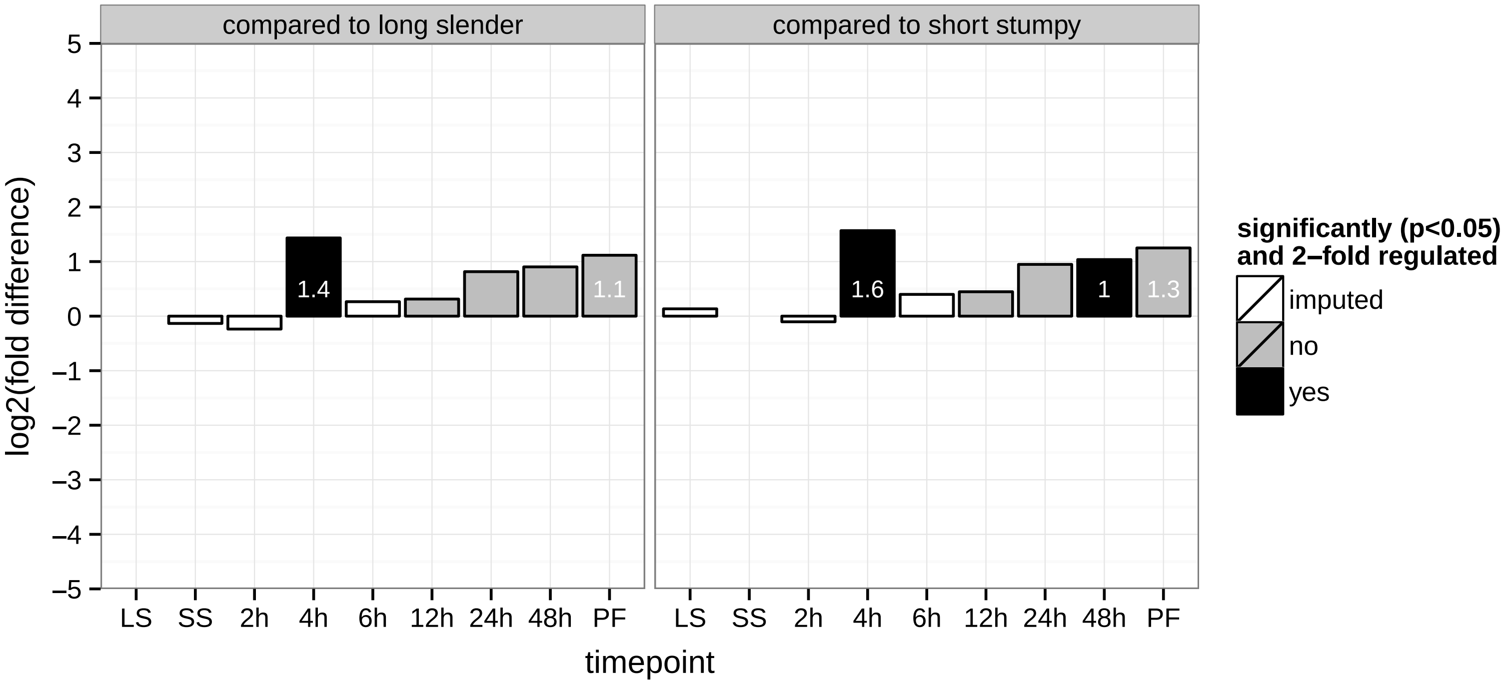
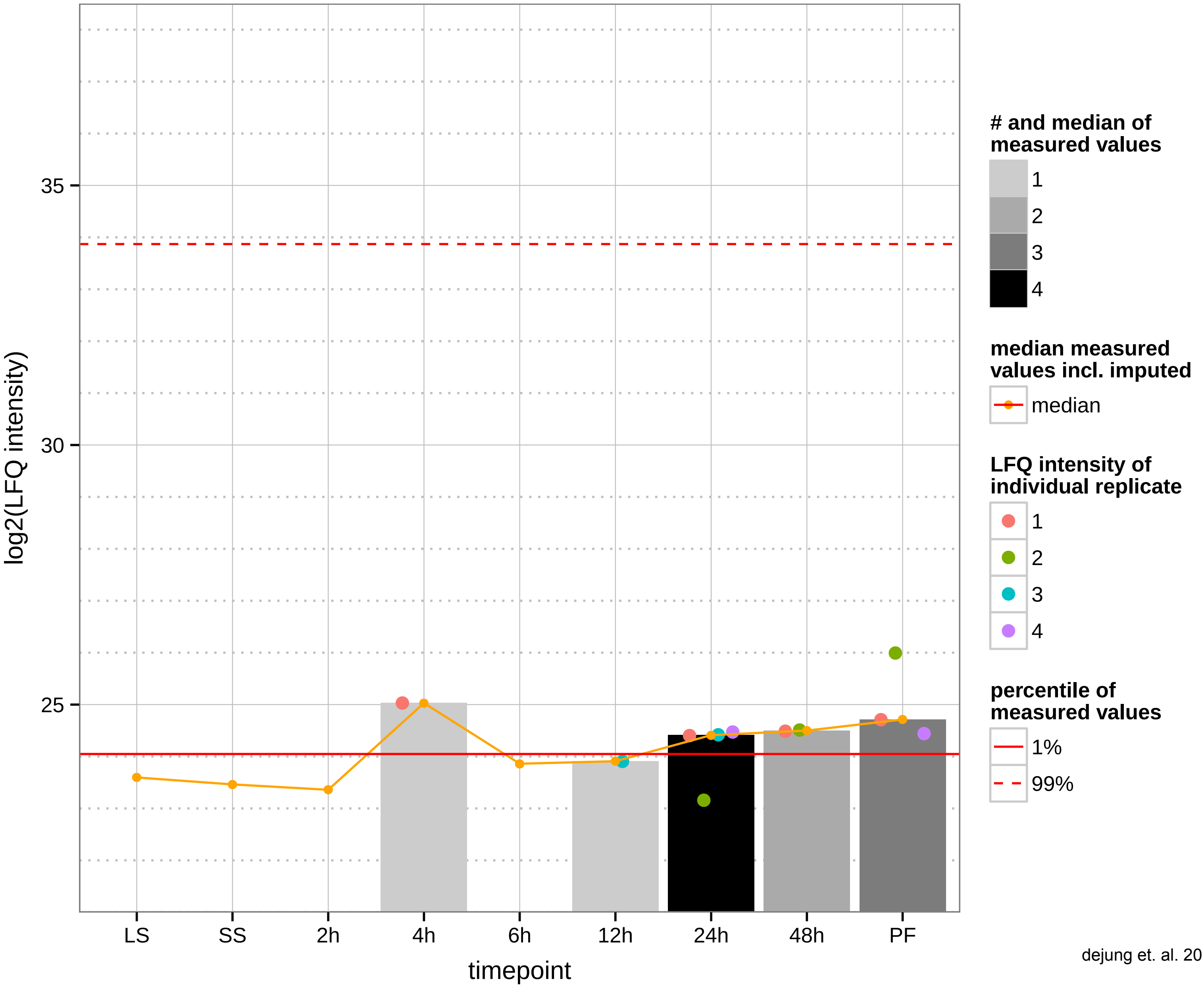
hypothetical protein, conserved
Tb927.3.1930
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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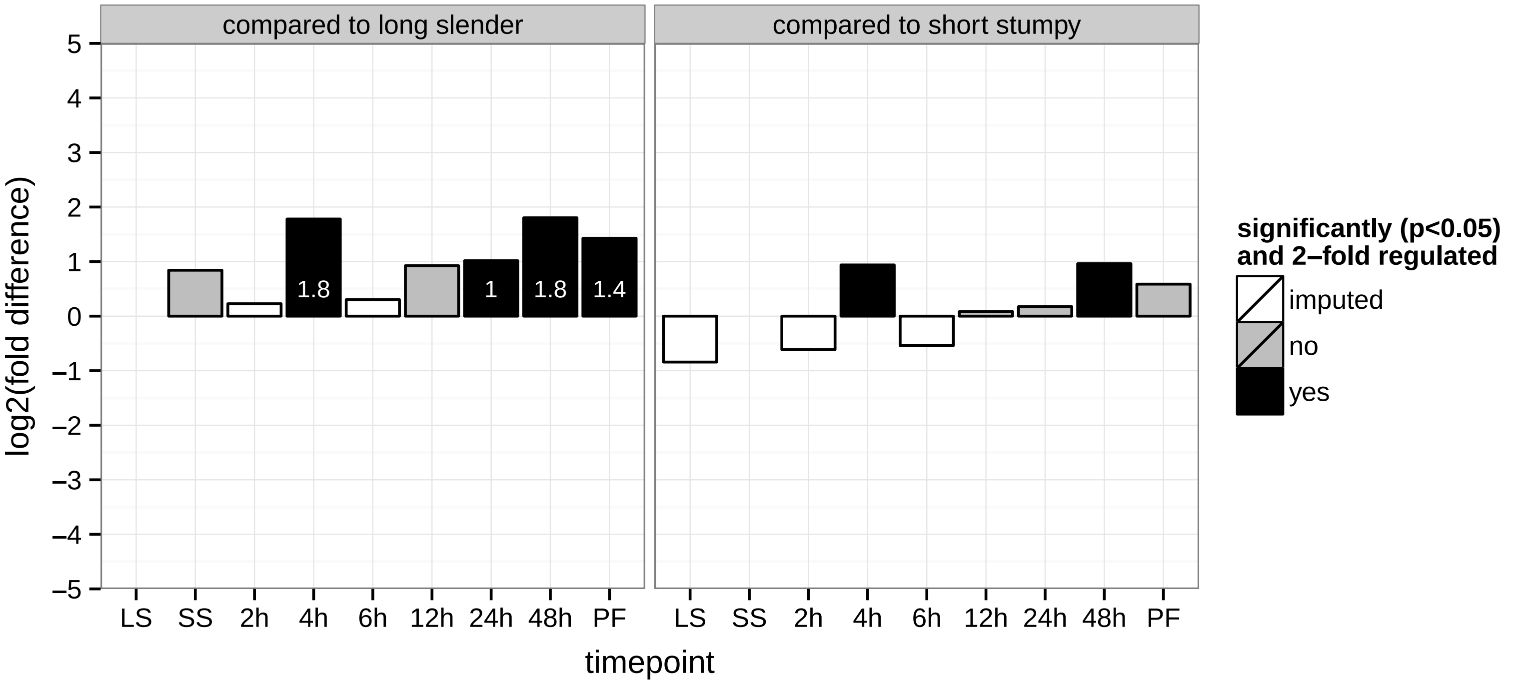
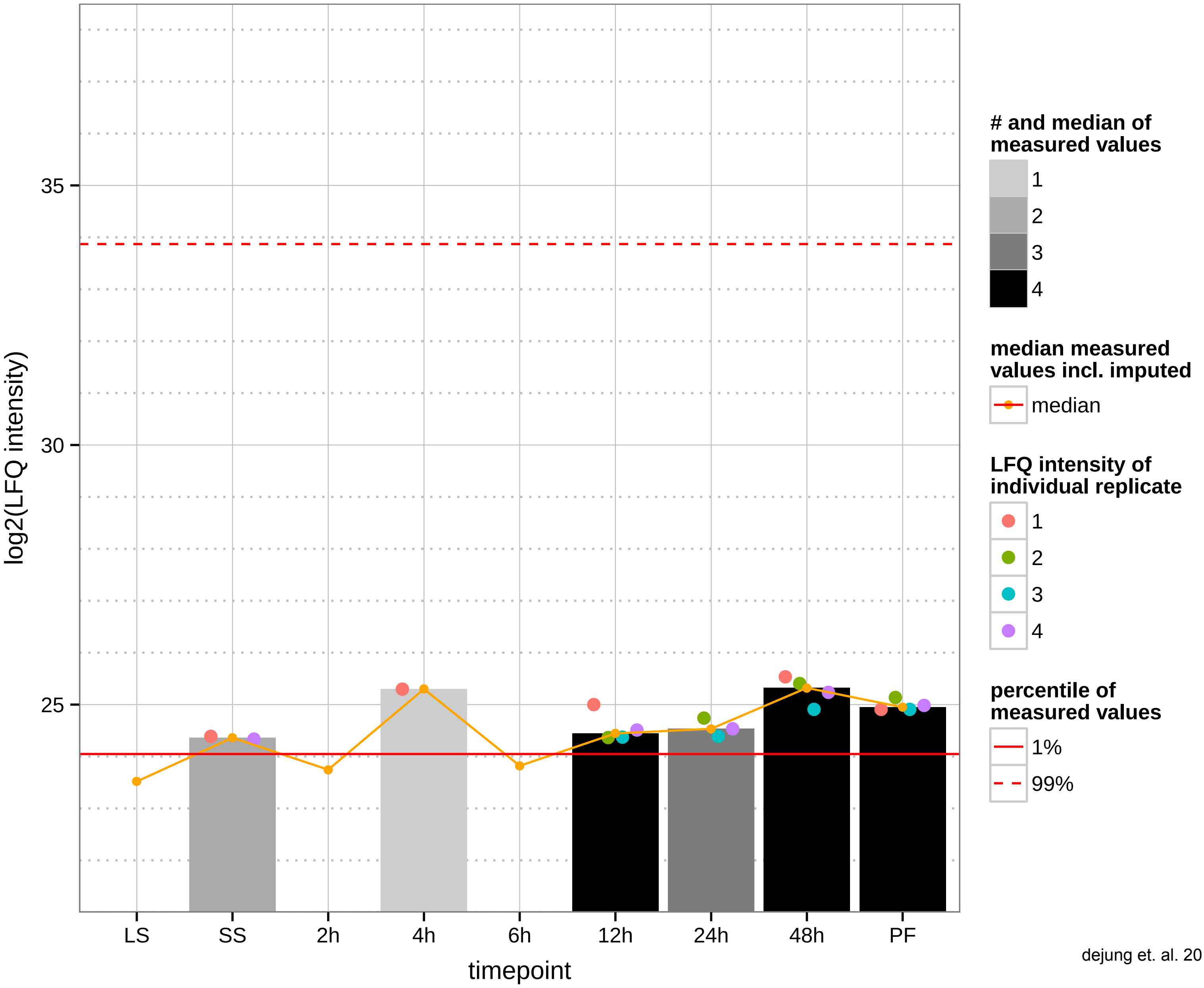
tousled–like kinase I (TLK1), tousled–like kinase II (TLK2)
Tb927.4.5180;Tb927.8.7220
AGOF: ATP binding, protein binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: nucleus, spindle pole
AGOP: DNA replication, chromosome segregation, histone H3–S10 phosphorylation, protein phosphorylation, spindle assem
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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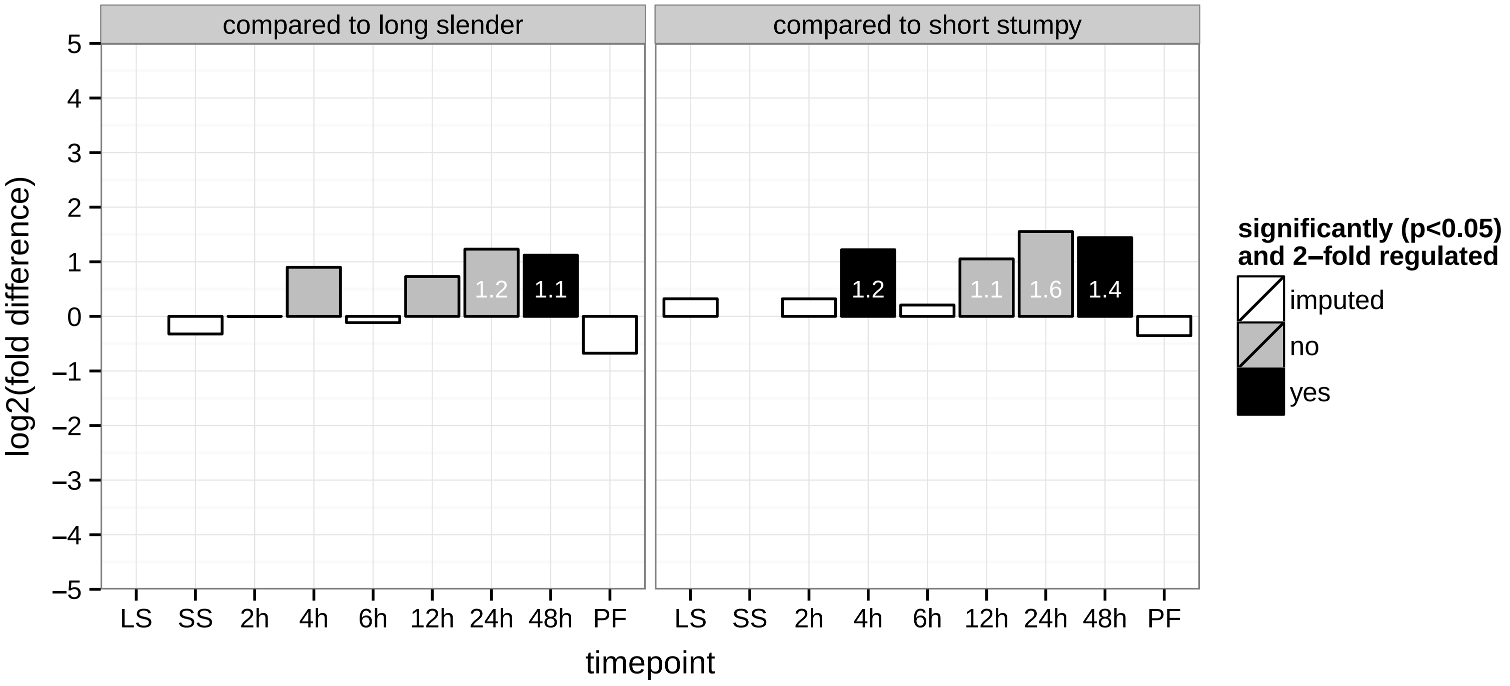
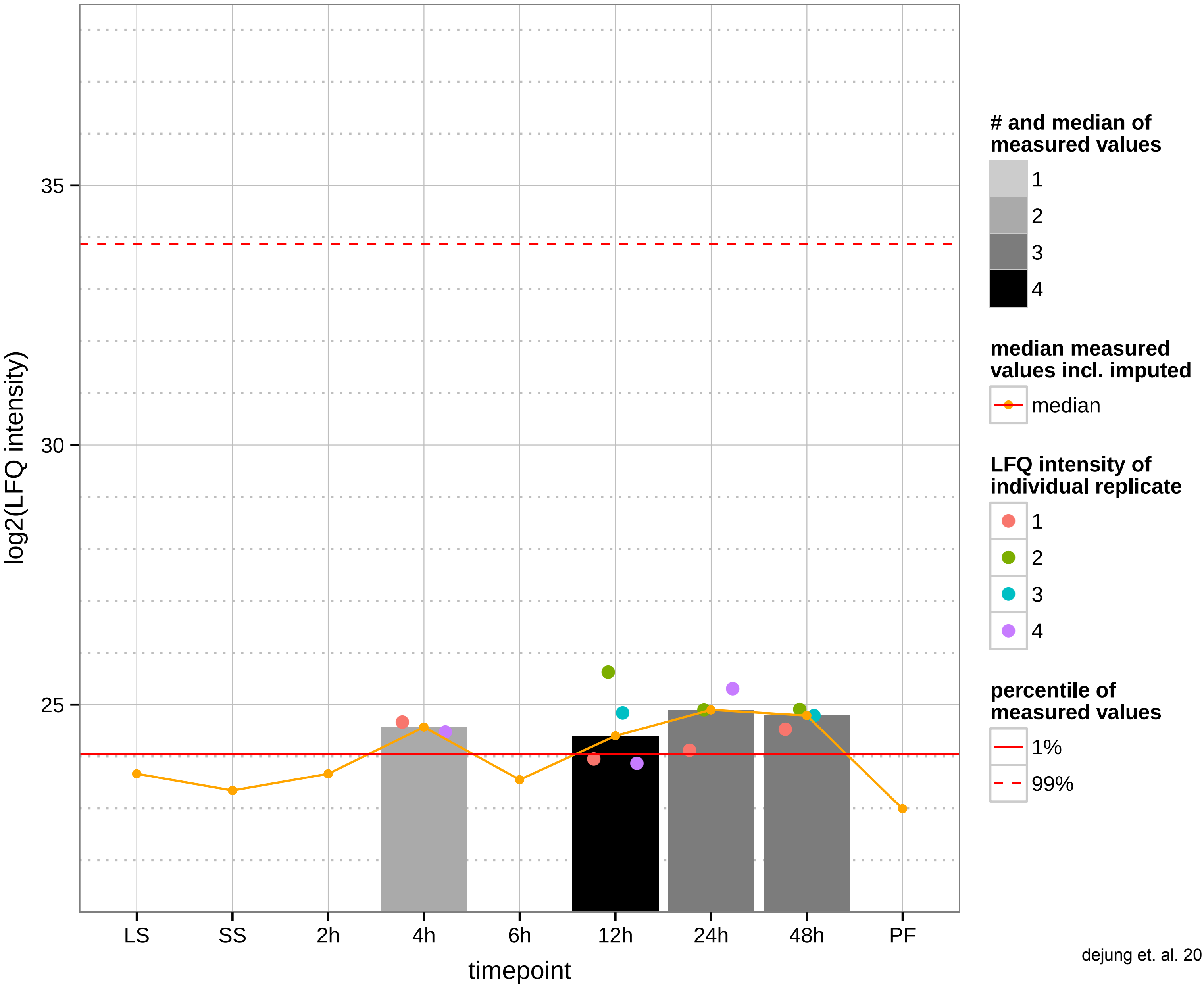
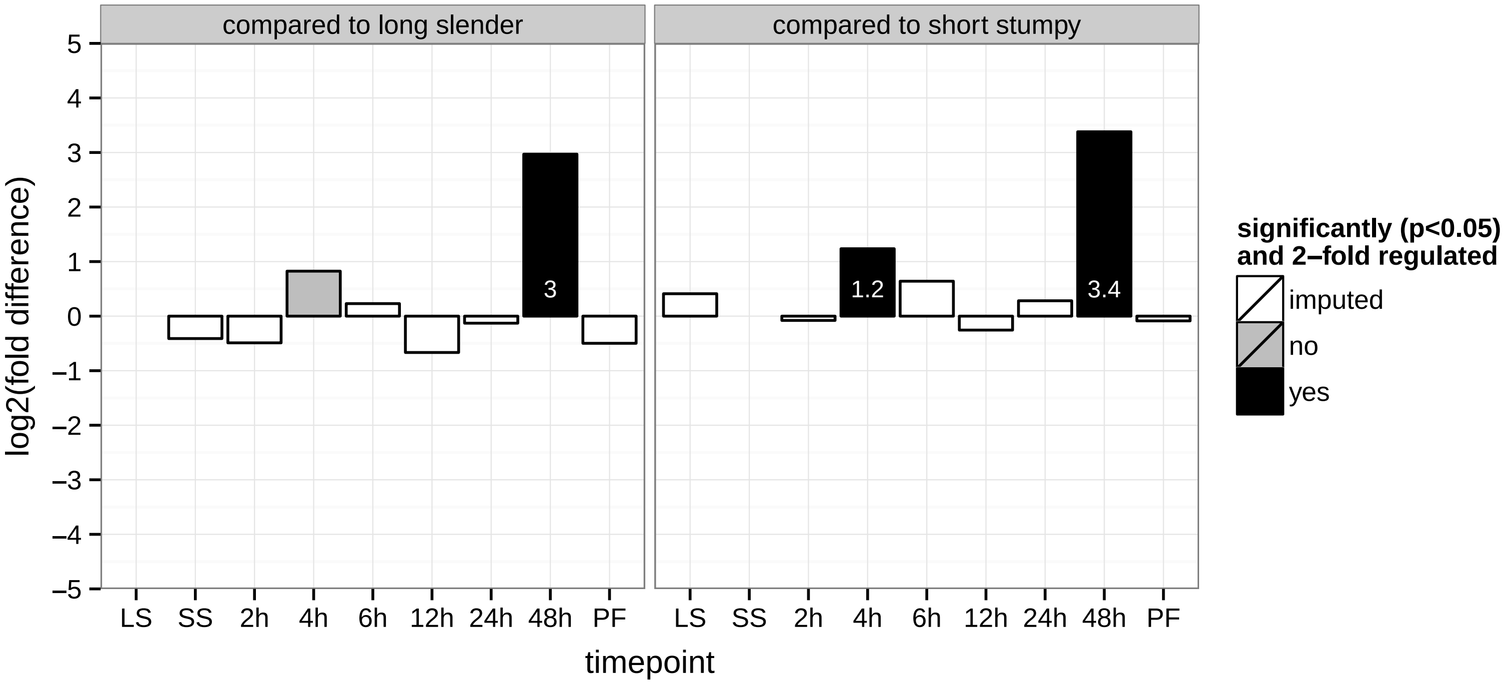
RNA–editing complex protein, RNA–editing 3' terminal uridylyl transferase 1, KRET1 (KRET1)
Tb927.7.3950
AGOF: RNA uridylyltransferase activity, nucleotide binding, polynucleotide adenylyltransferase activity
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

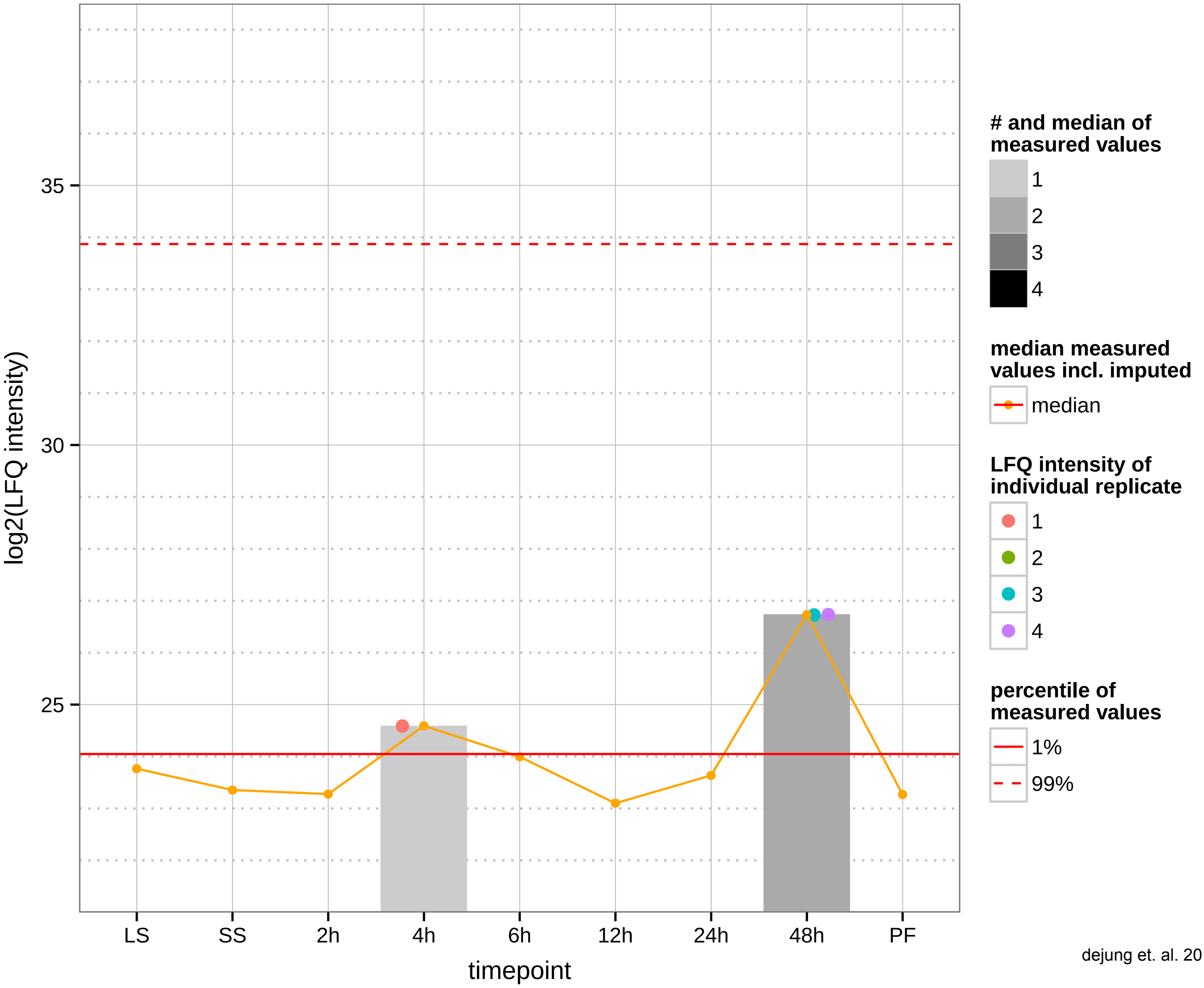




dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.2430
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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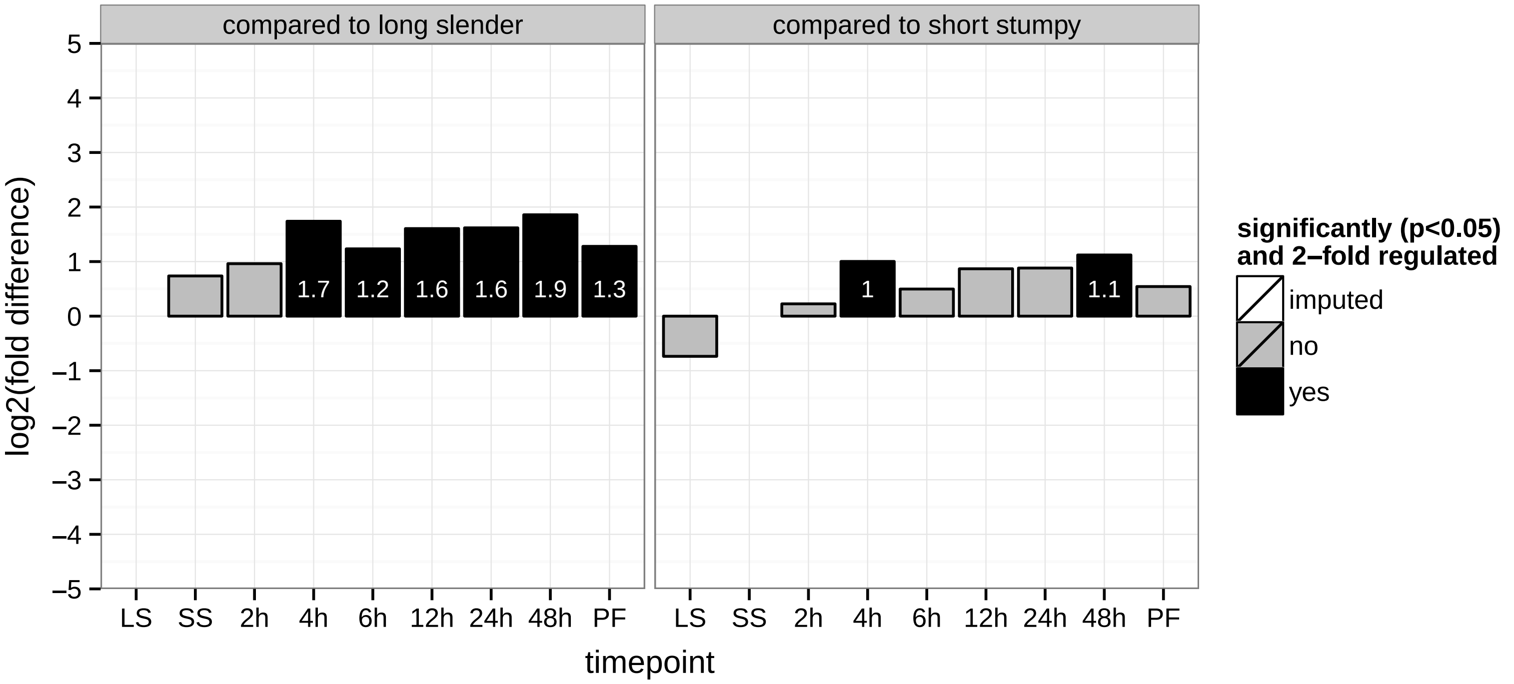
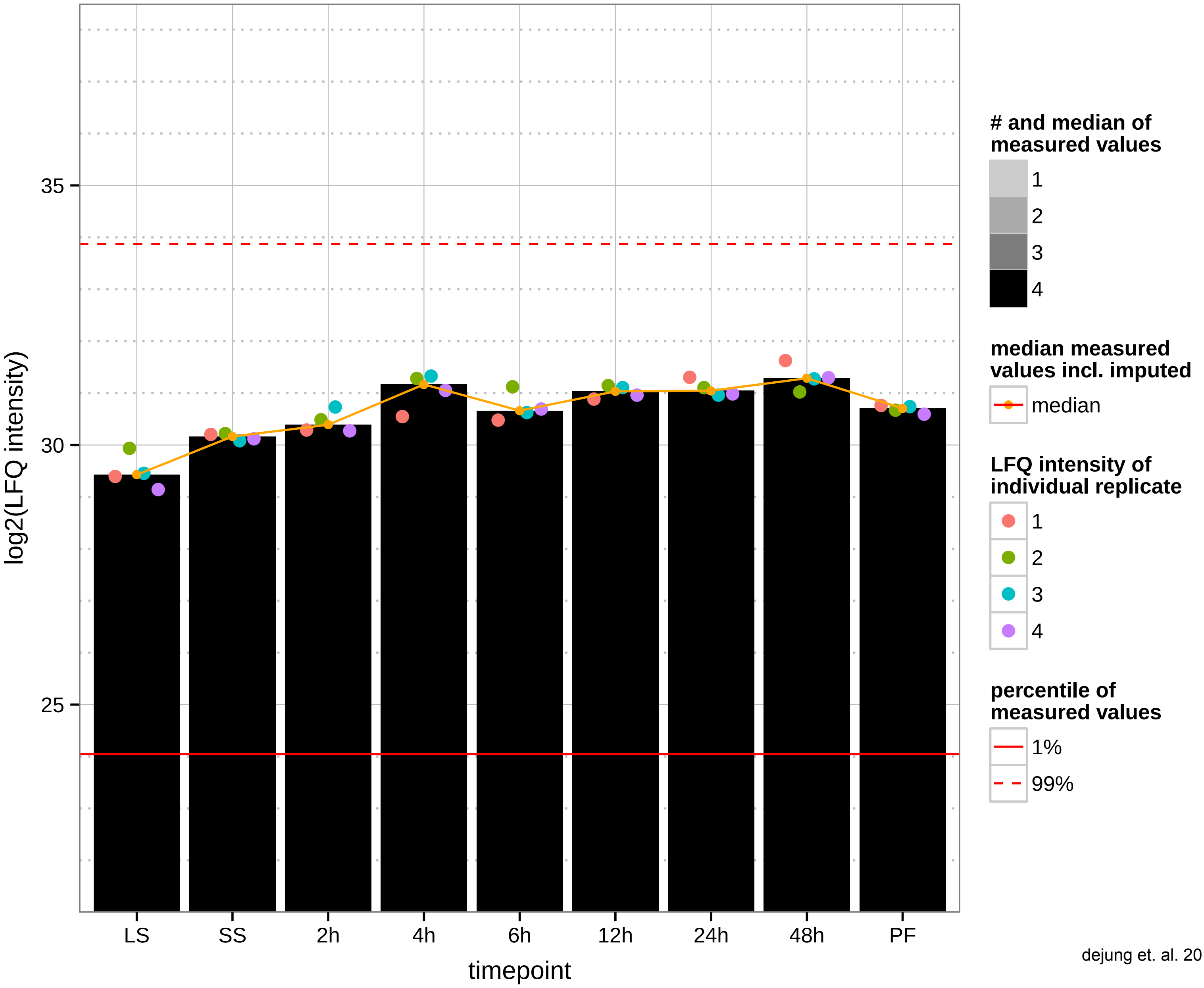
nucleosome assembly protein–like protein
Tb927.9.5730
AGOF: histone binding
AGOC: nucleus
AGOP: nucleosome assembly
PGOF: null
PGOC: nucleus
PGOP: nucleosome assembly





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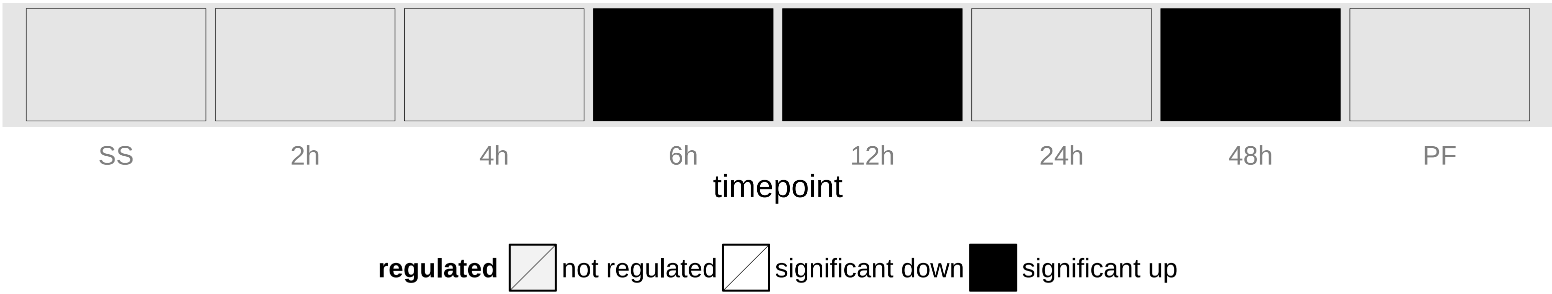

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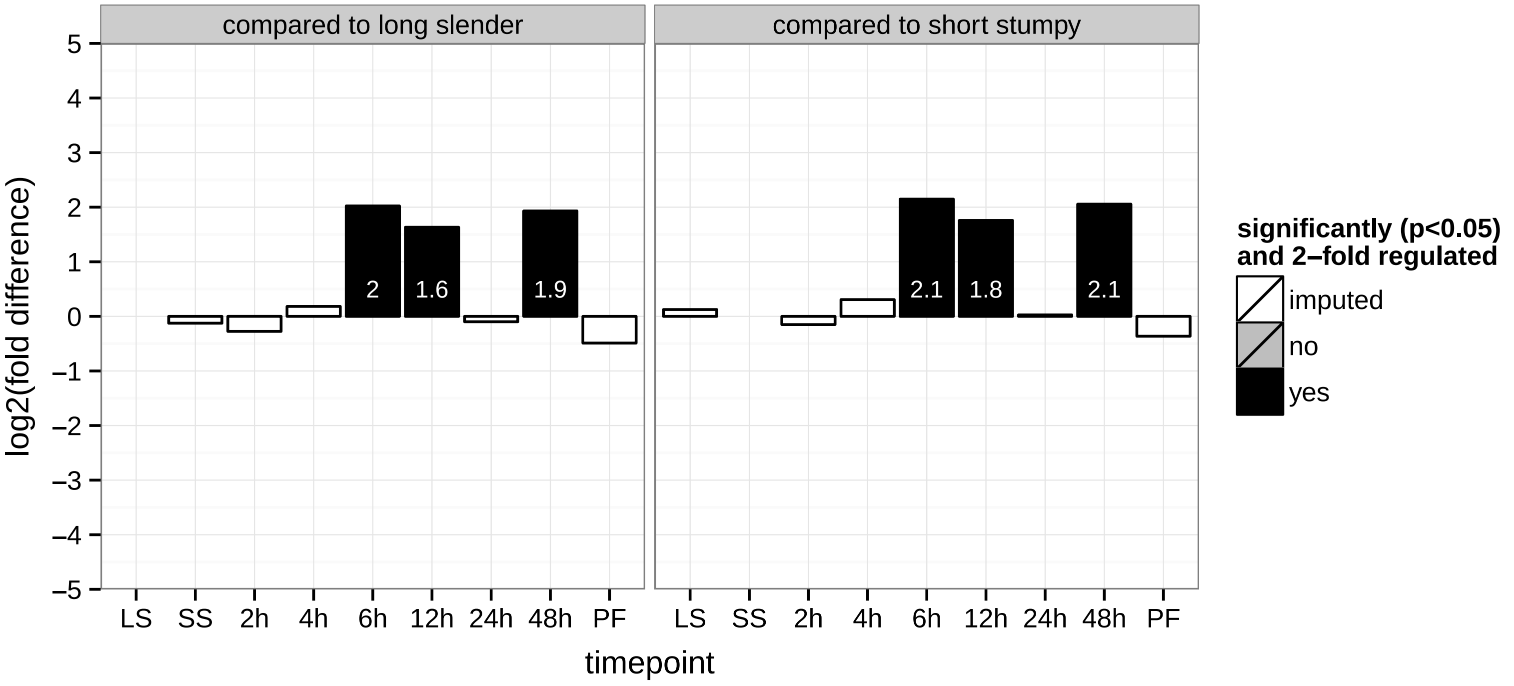
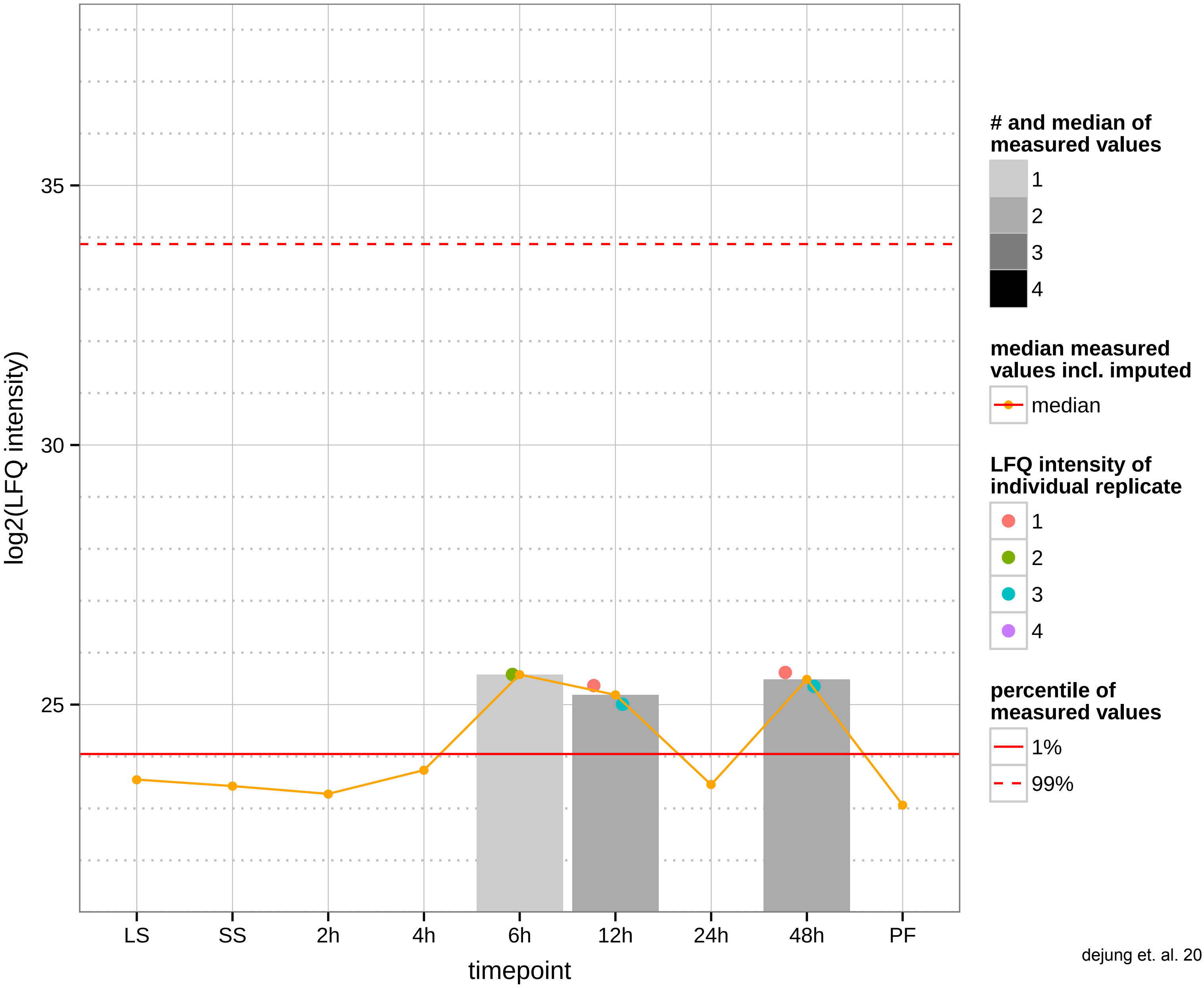
kinetoplastid kinetochore protein 19, protein kinase, putative (kkt19)
Tb927.11.12420
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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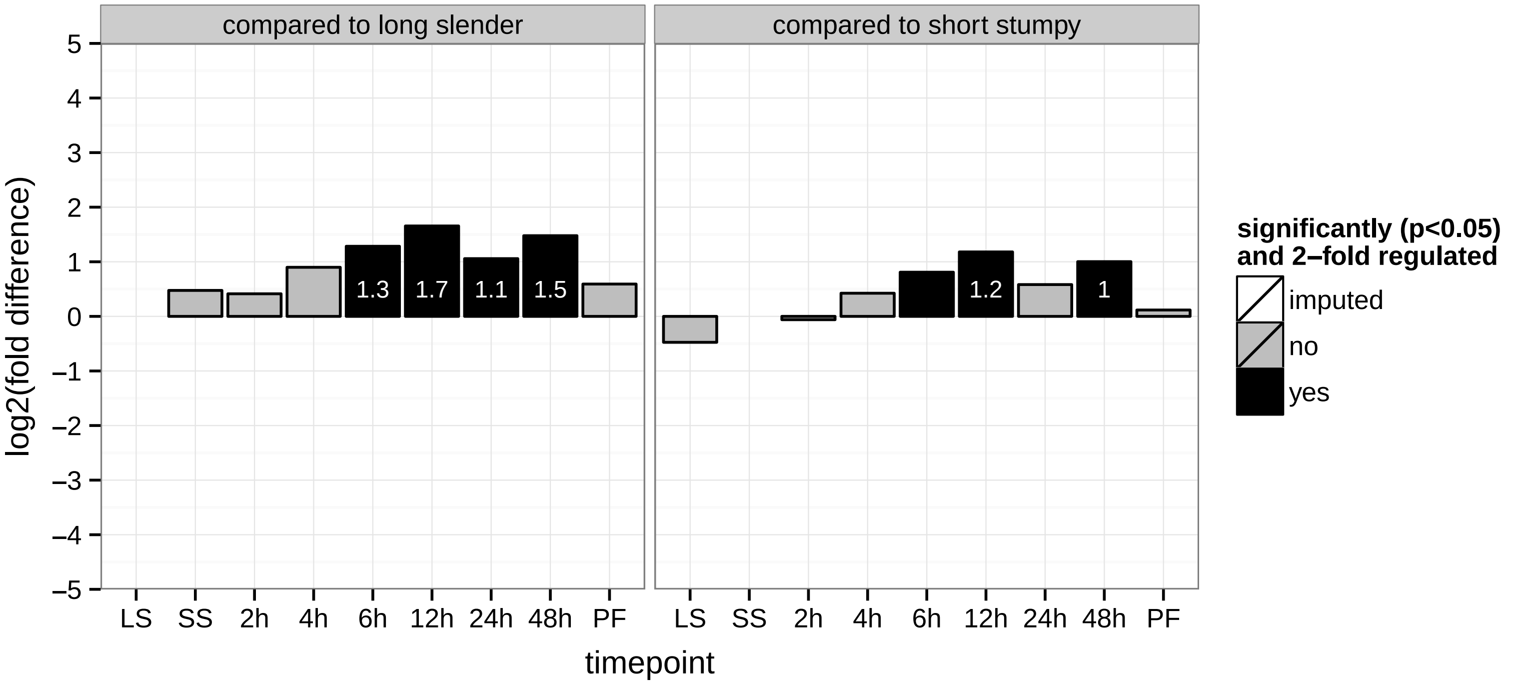
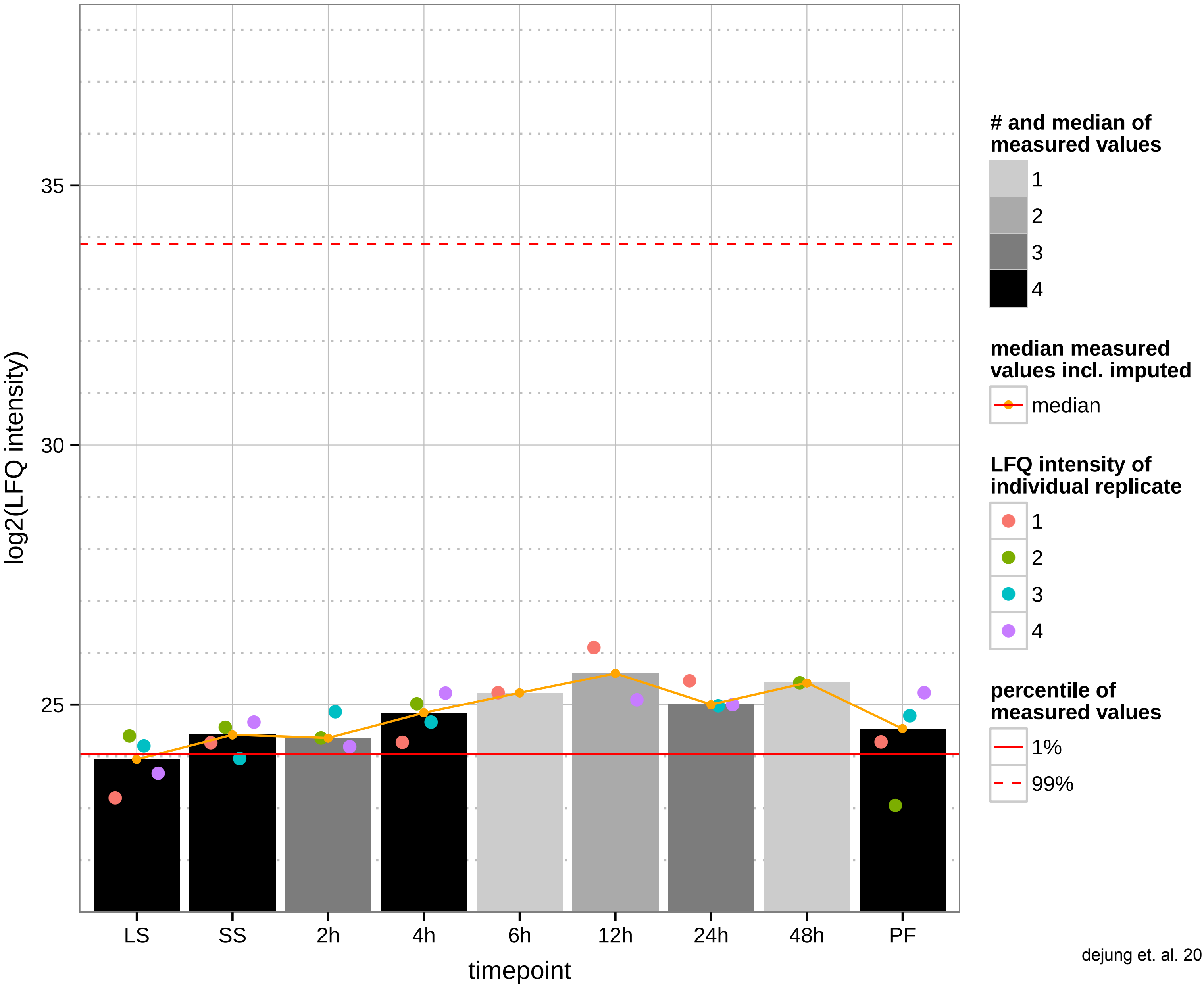
hypothetical protein, conserved
Tb927.2.2540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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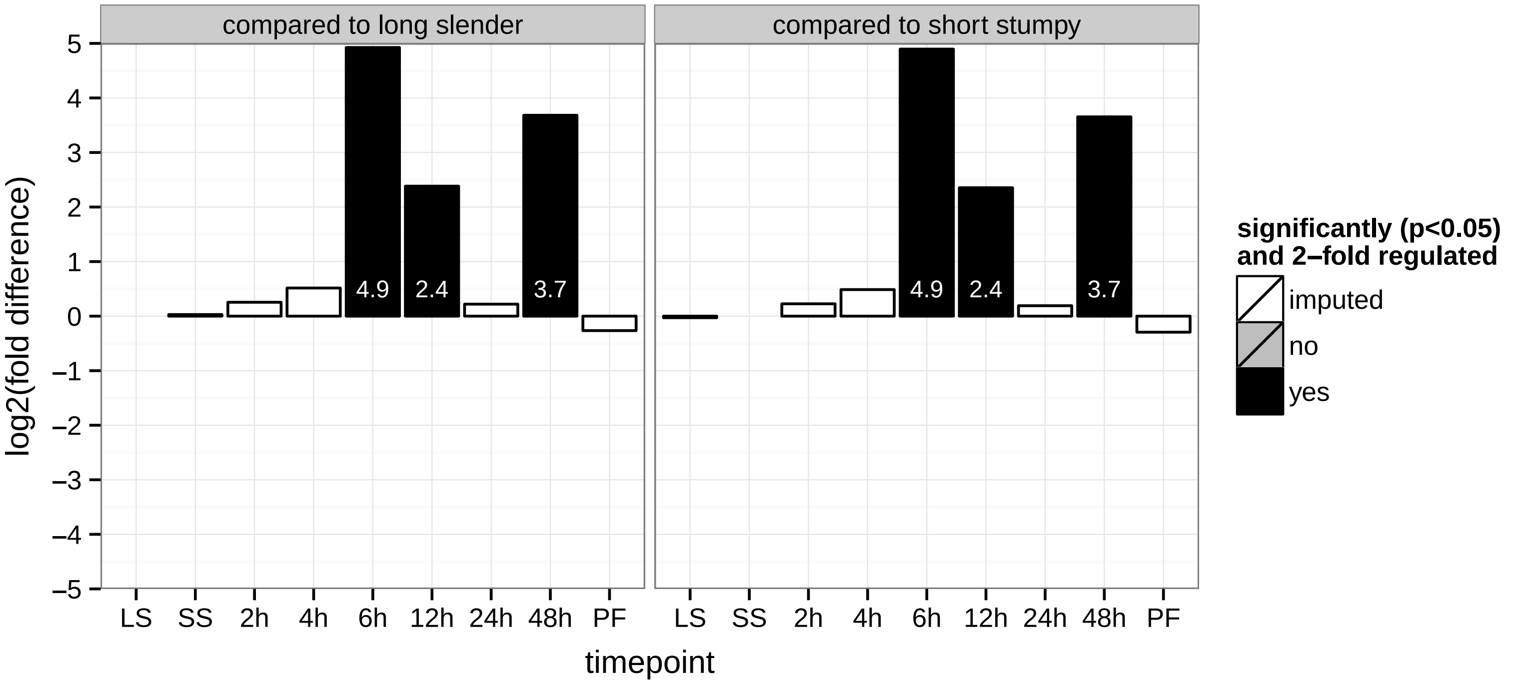
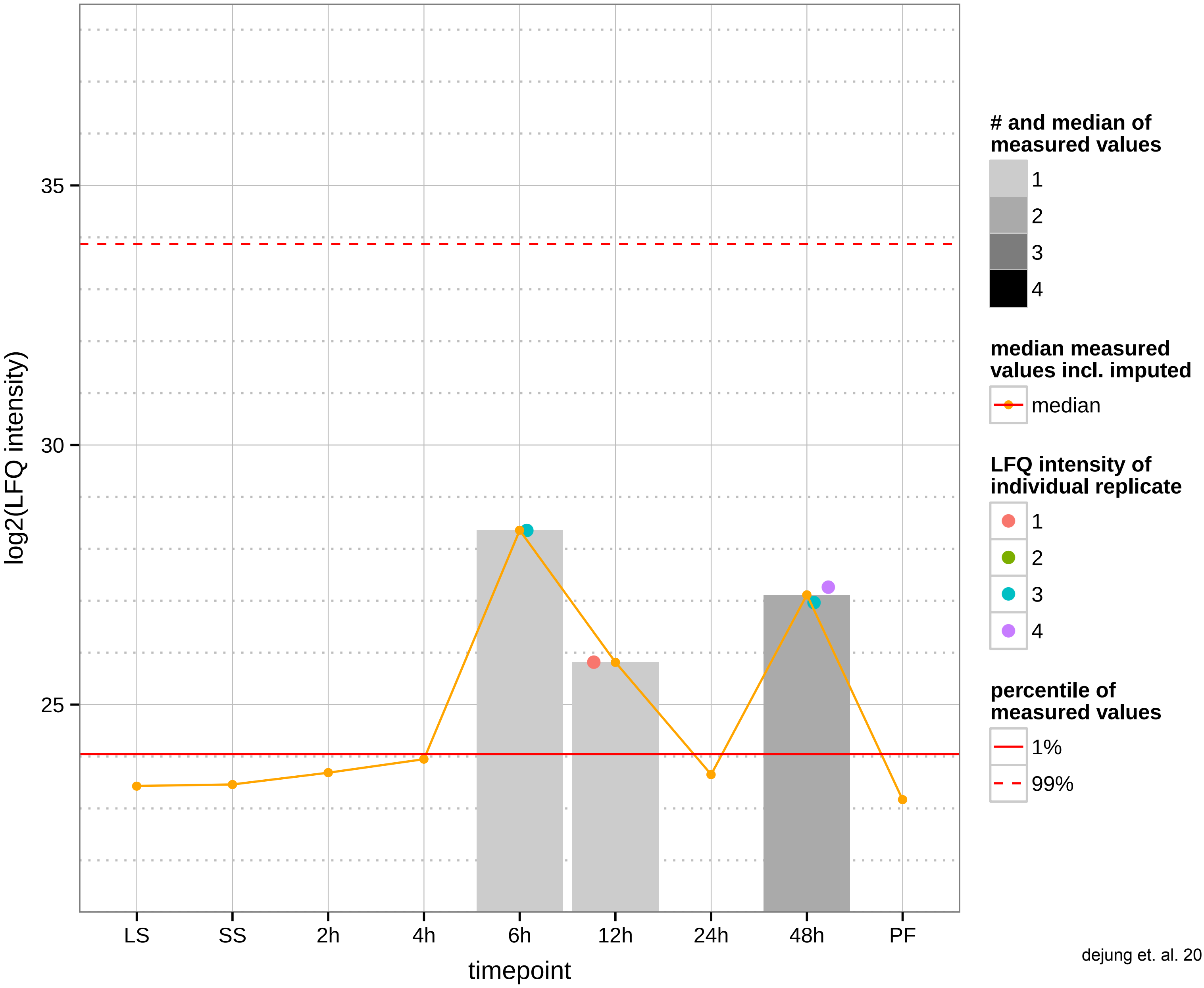
hypothetical protein, conserved
Tb927.3.4210
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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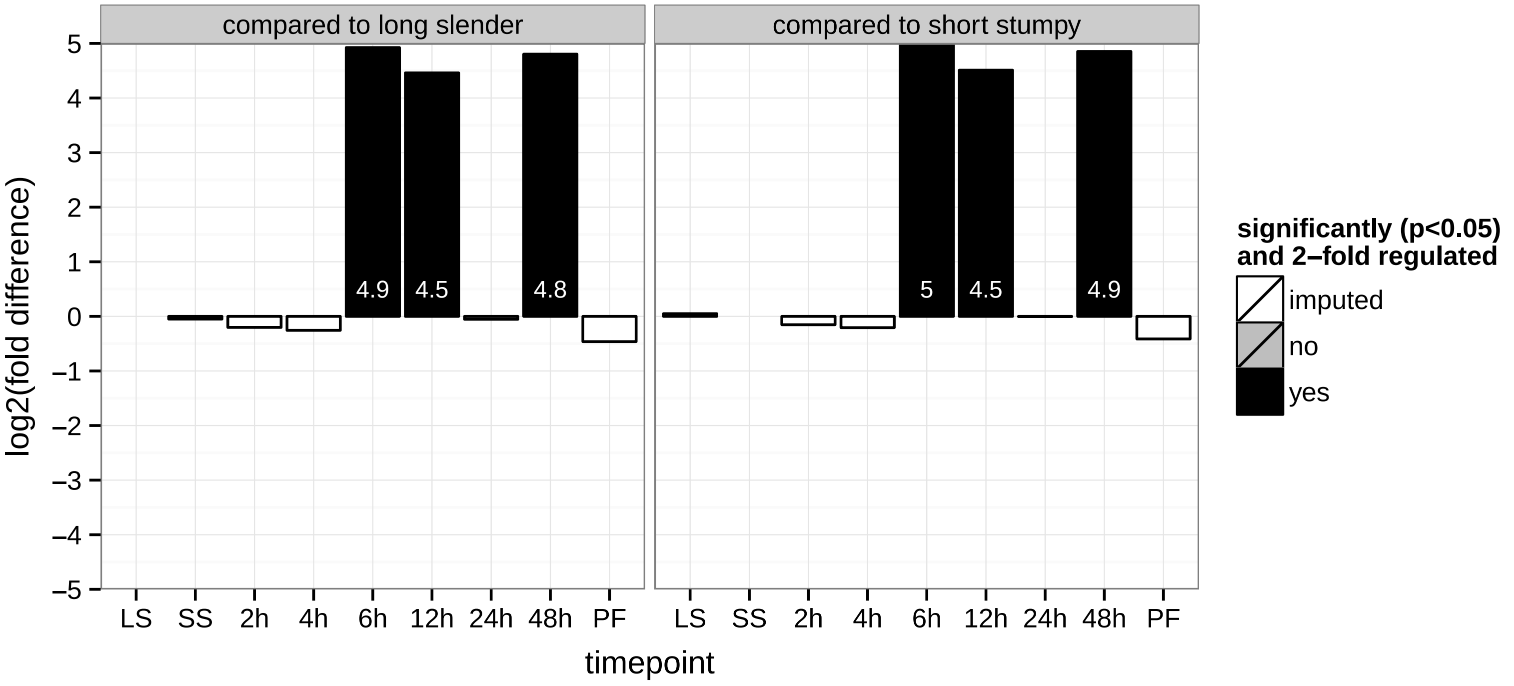
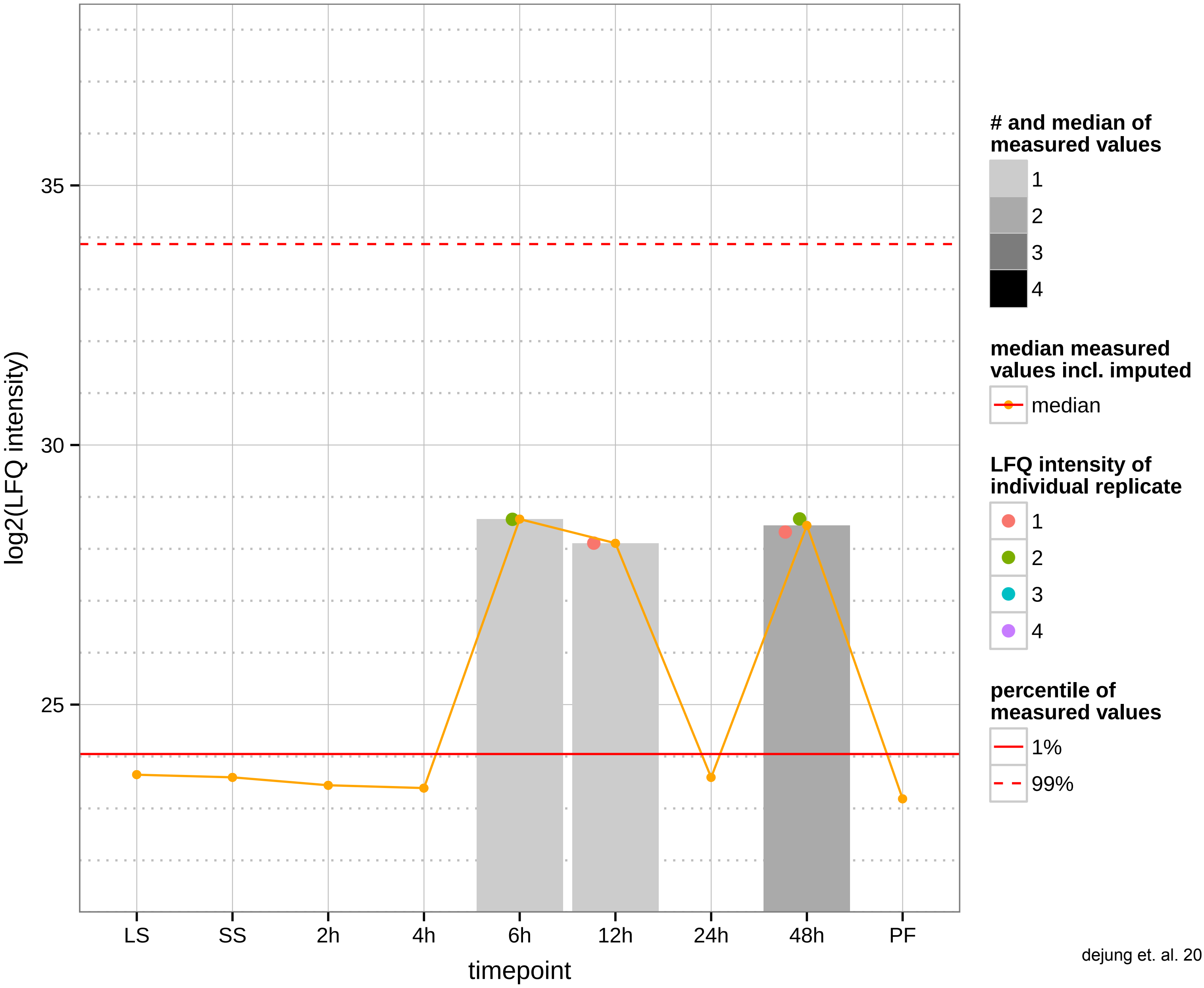
hypothetical protein, conserved
Tb927.7.3060
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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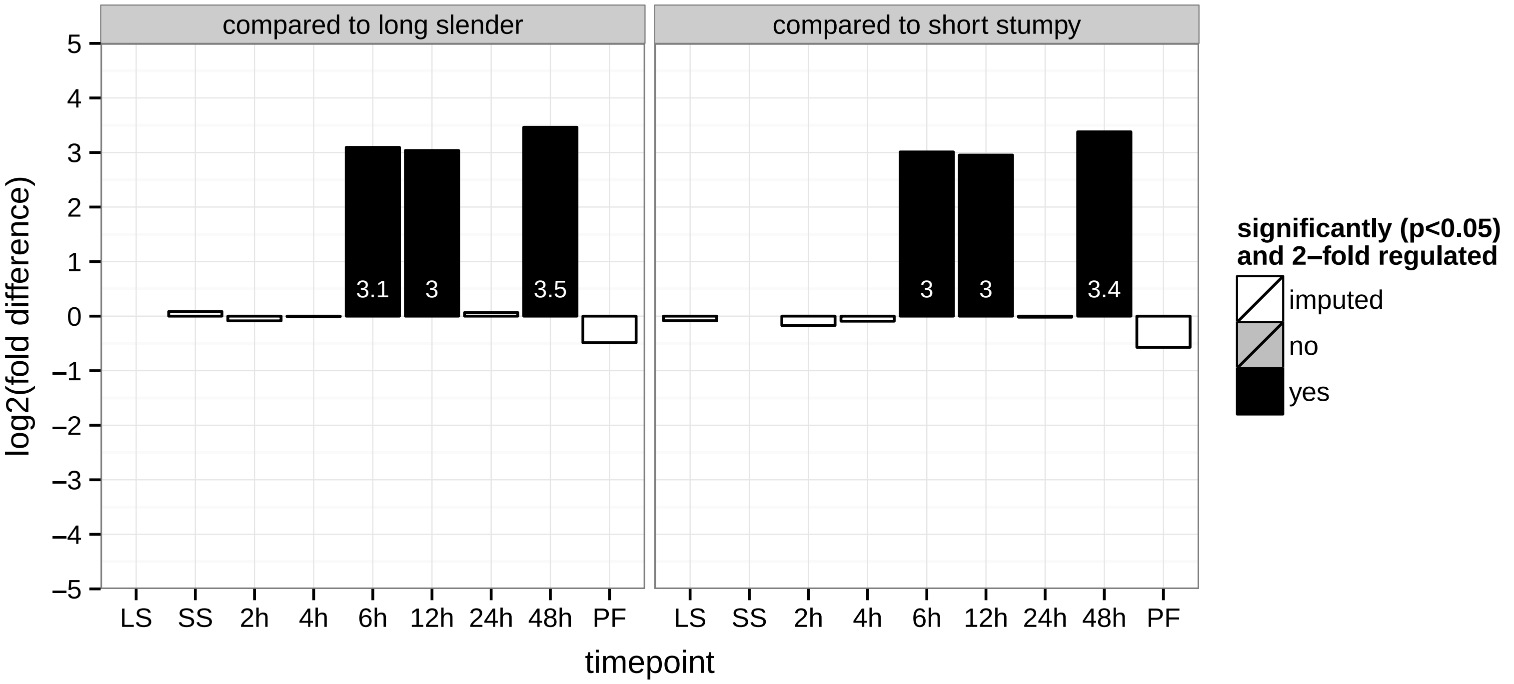
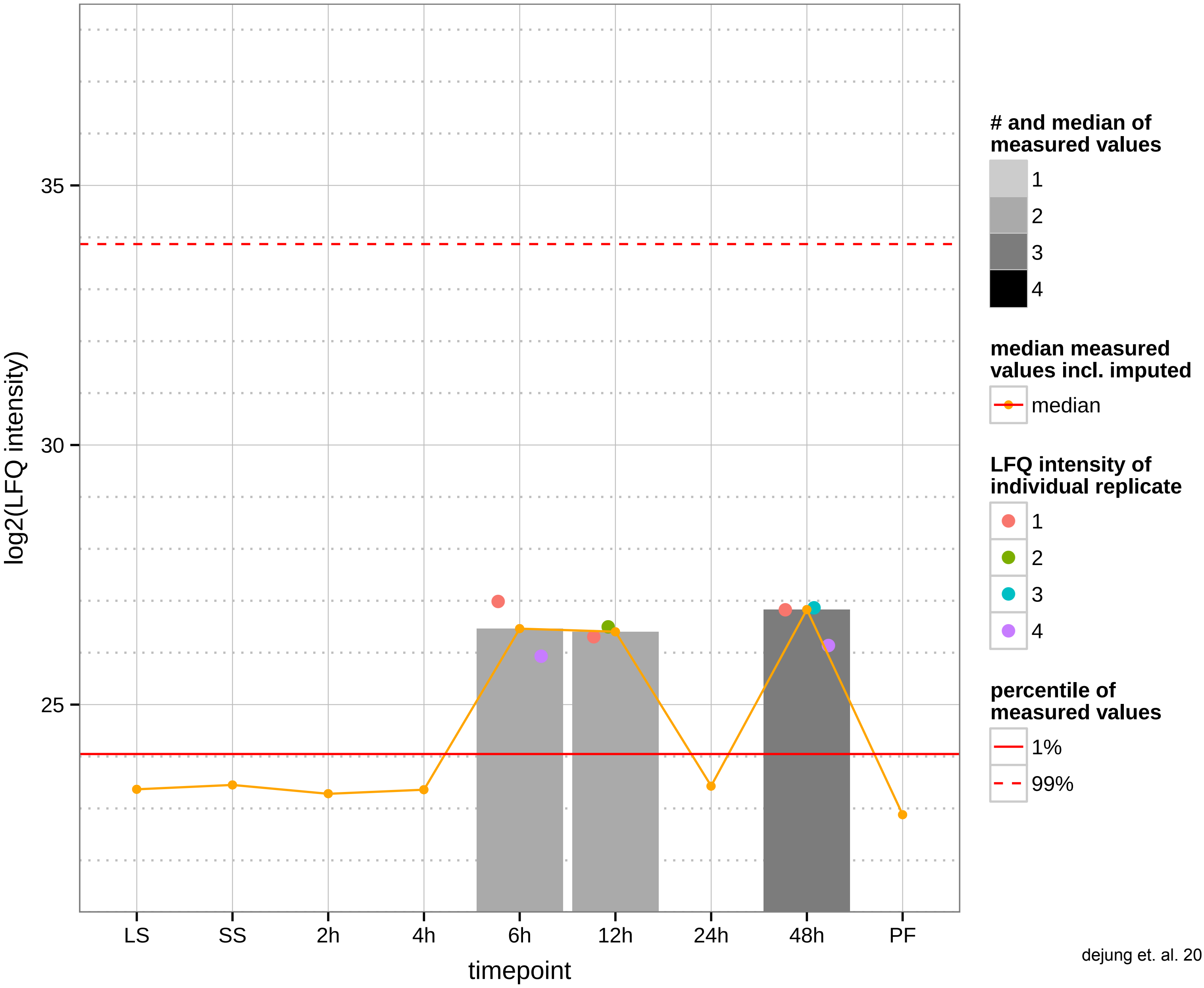
hypothetical protein, conserved
Tb927.7.660
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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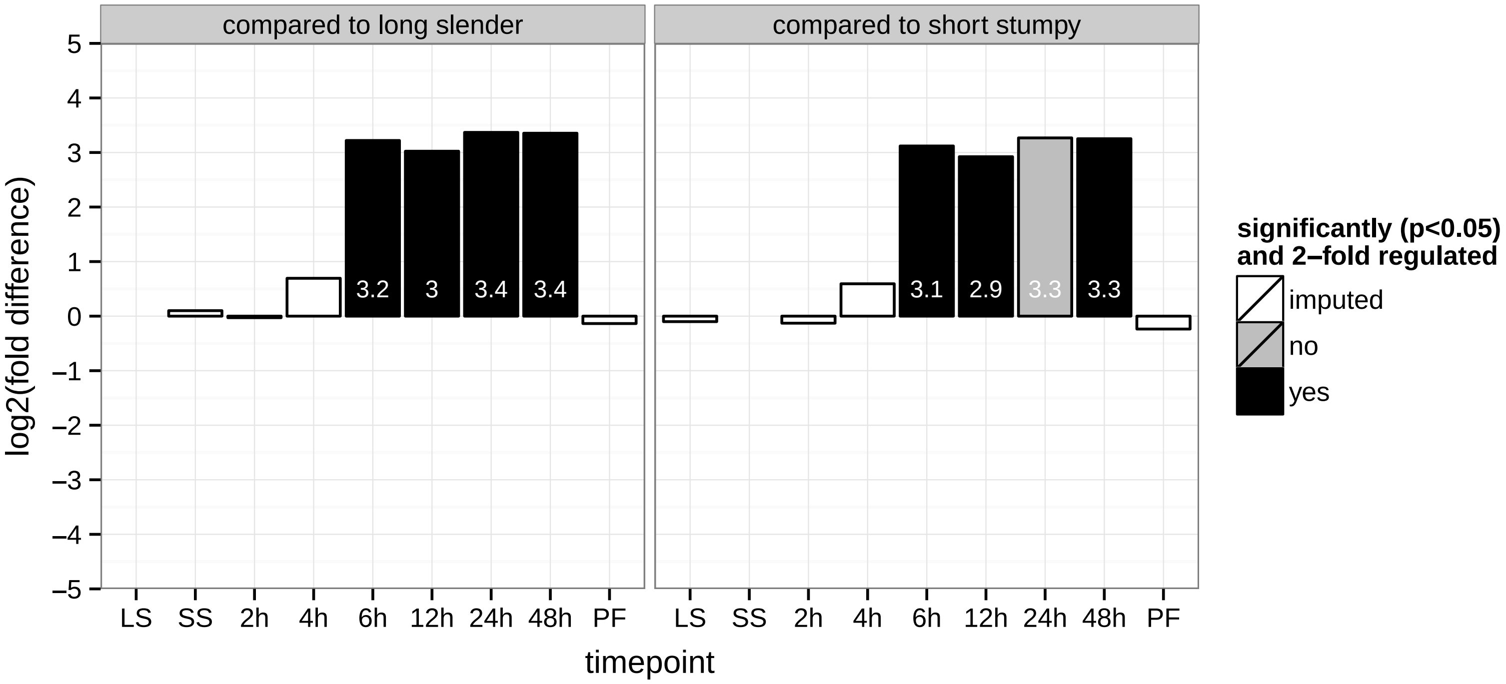
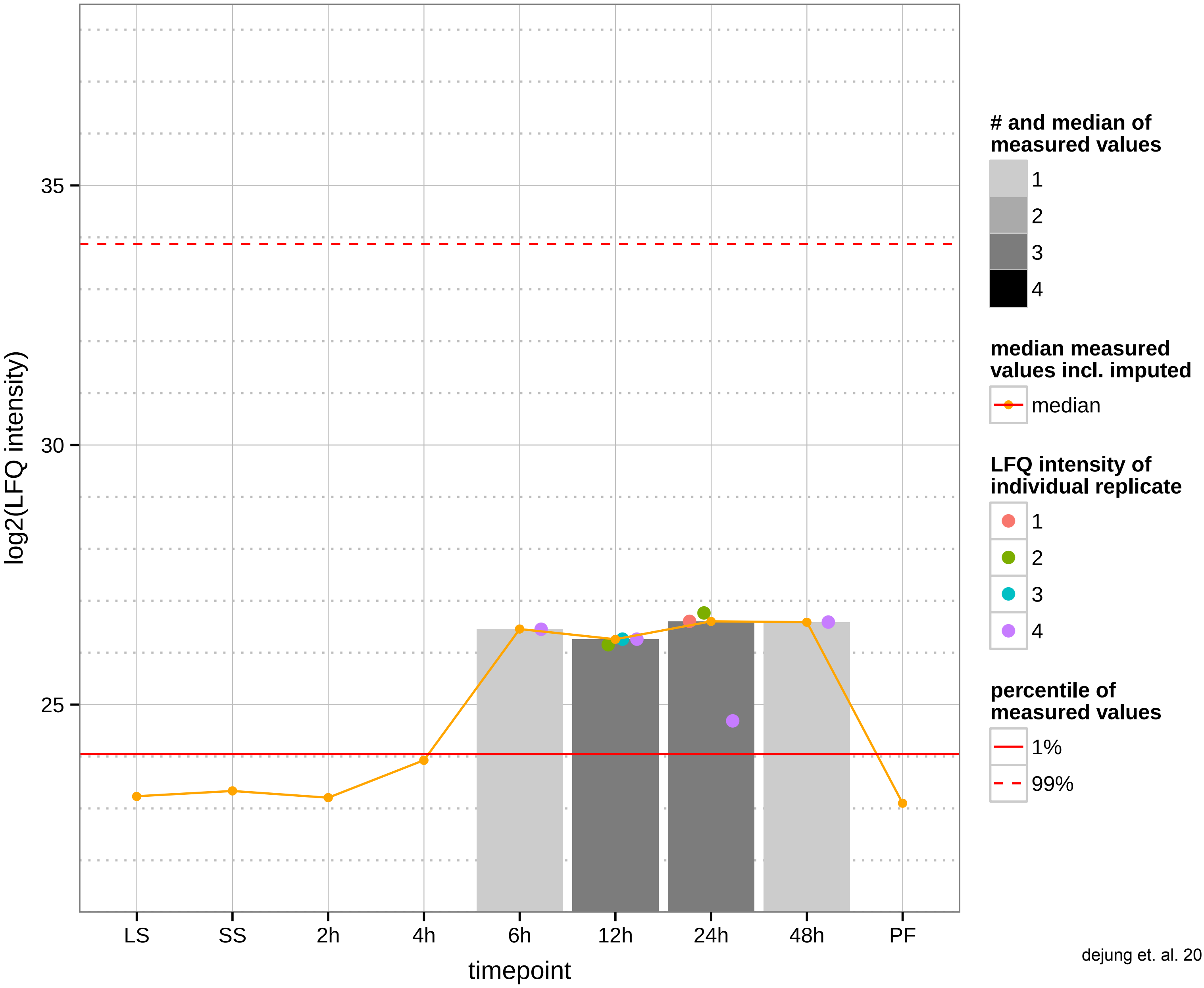
hypothetical protein, conserved
Tb927.8.7080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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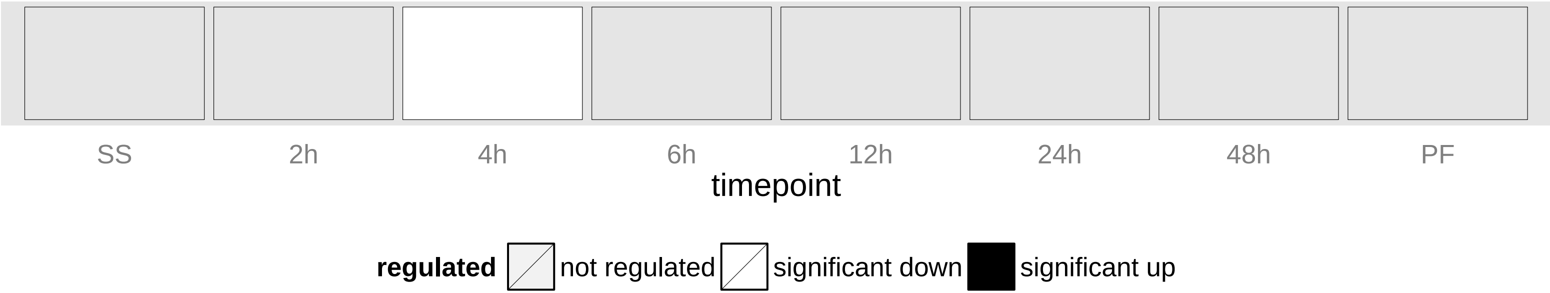

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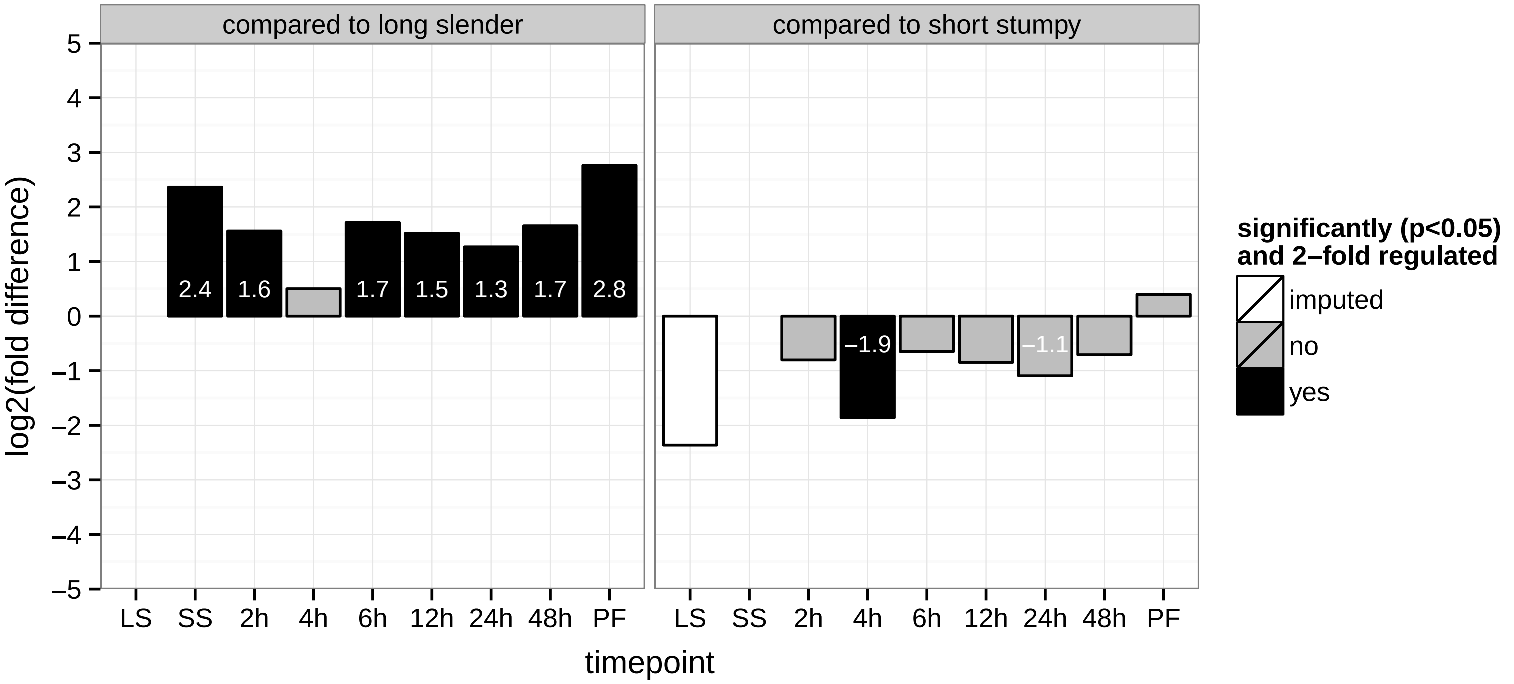
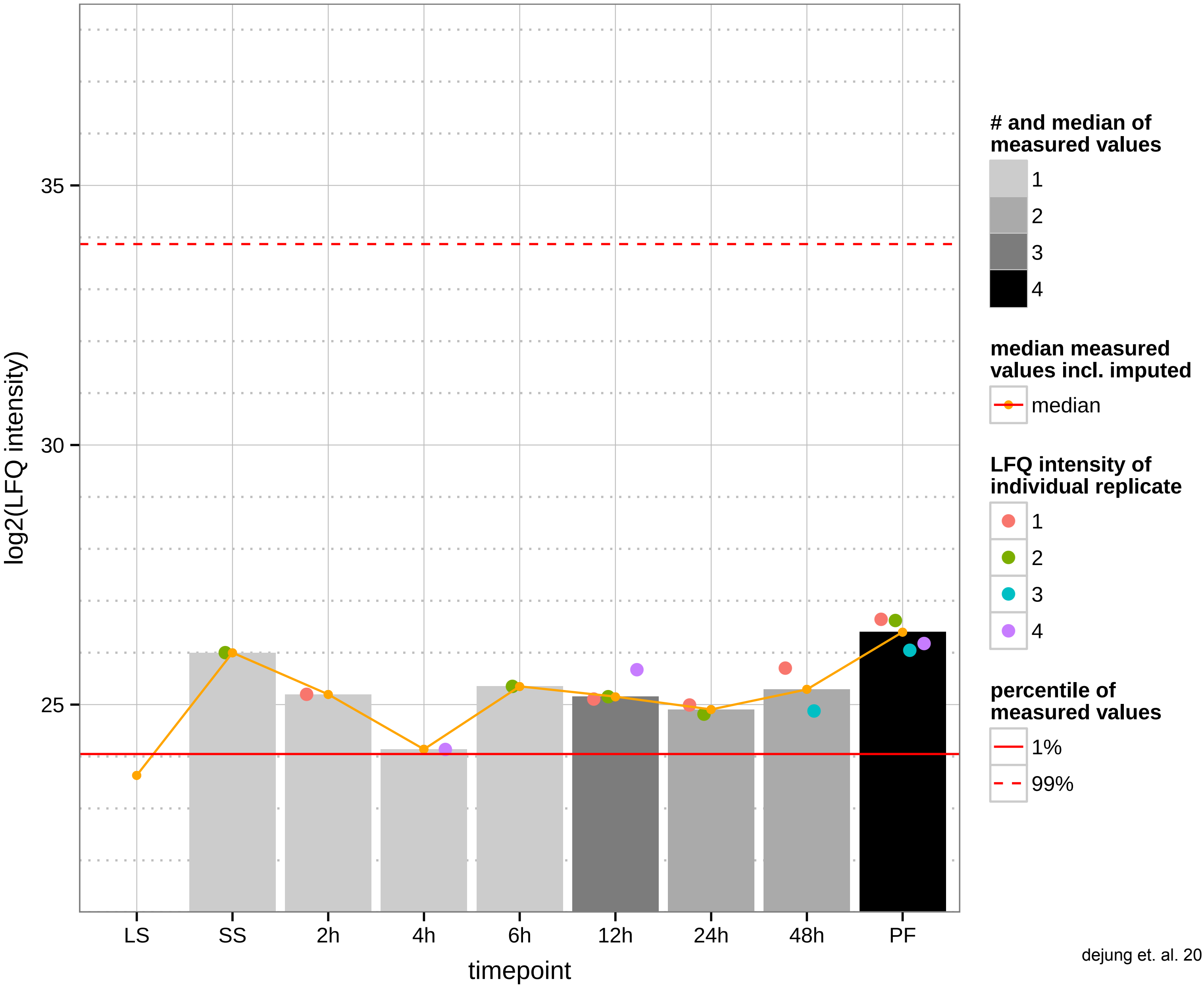
protein kinase A catalytic subunit, putative, protein kinase A catalytic subunit (PKAC3)
Tb927.10.13010;Tb11.v5.0671
AGOF: null, ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null, protein phosphorylation
PGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity, transferring phosphoru
PGOC: null
PGOP: protein phosphorylation





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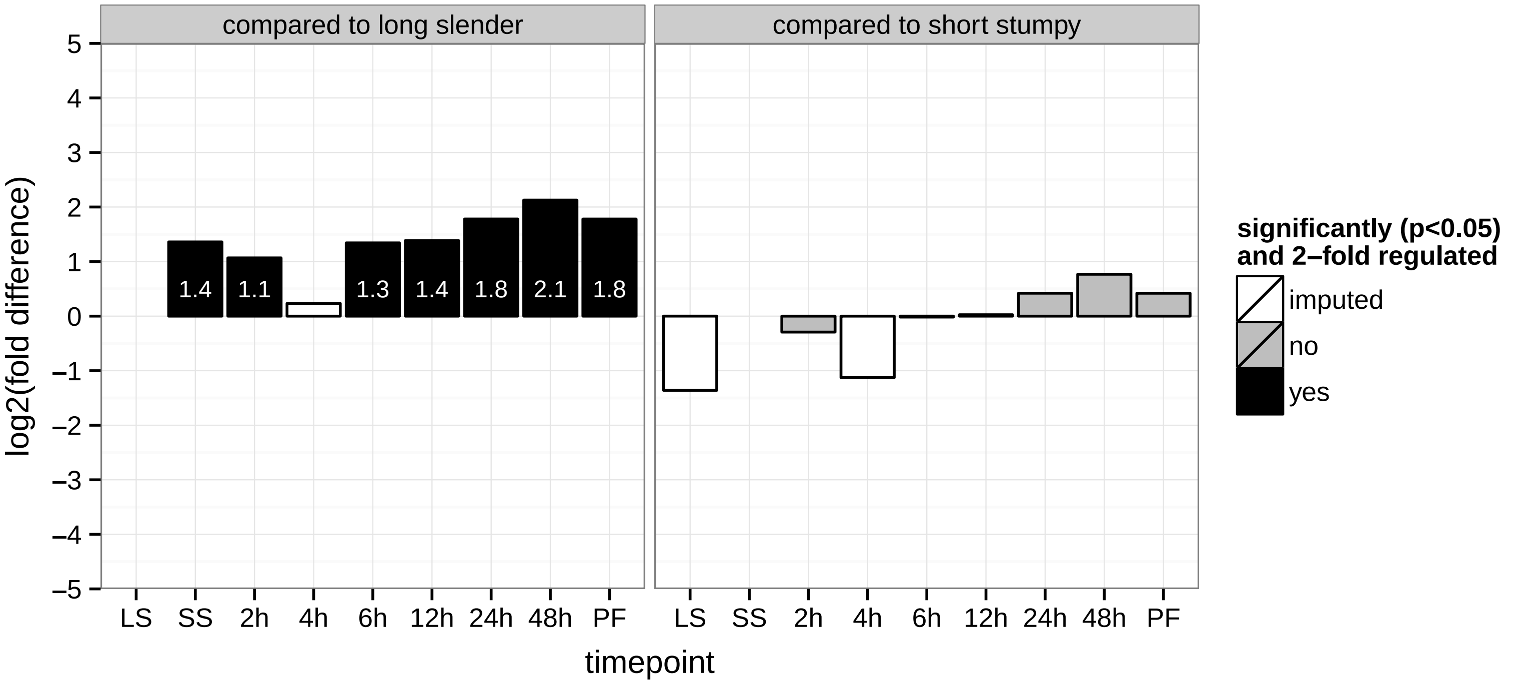
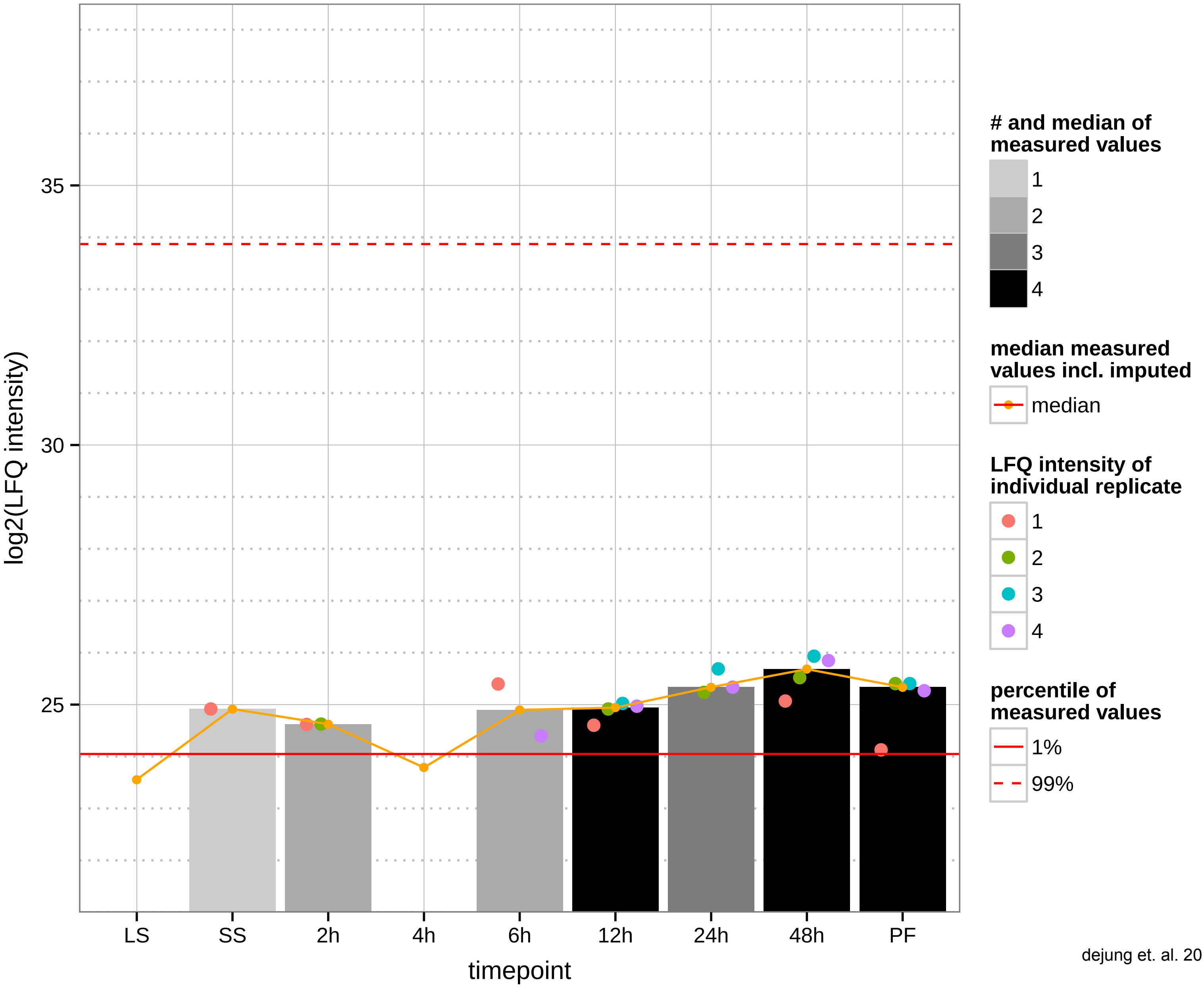
Protein C21orf2 homolog, putative
Tb927.10.5130
AGOF: null
AGOC: mitochondrion
AGOP: cilium morphogenesis, cytoskeleton organization, regulation of cell shape
PGOF: null
PGOC: null
PGOP: null





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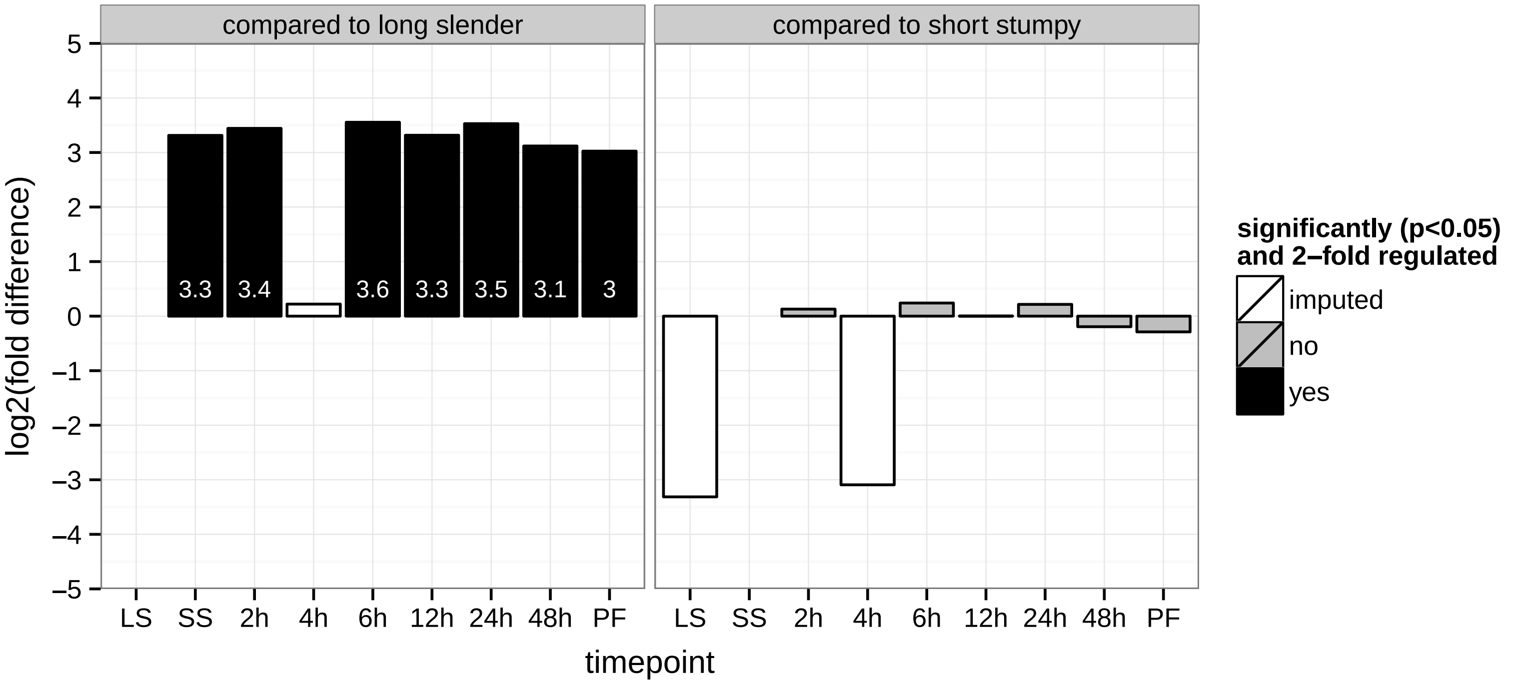
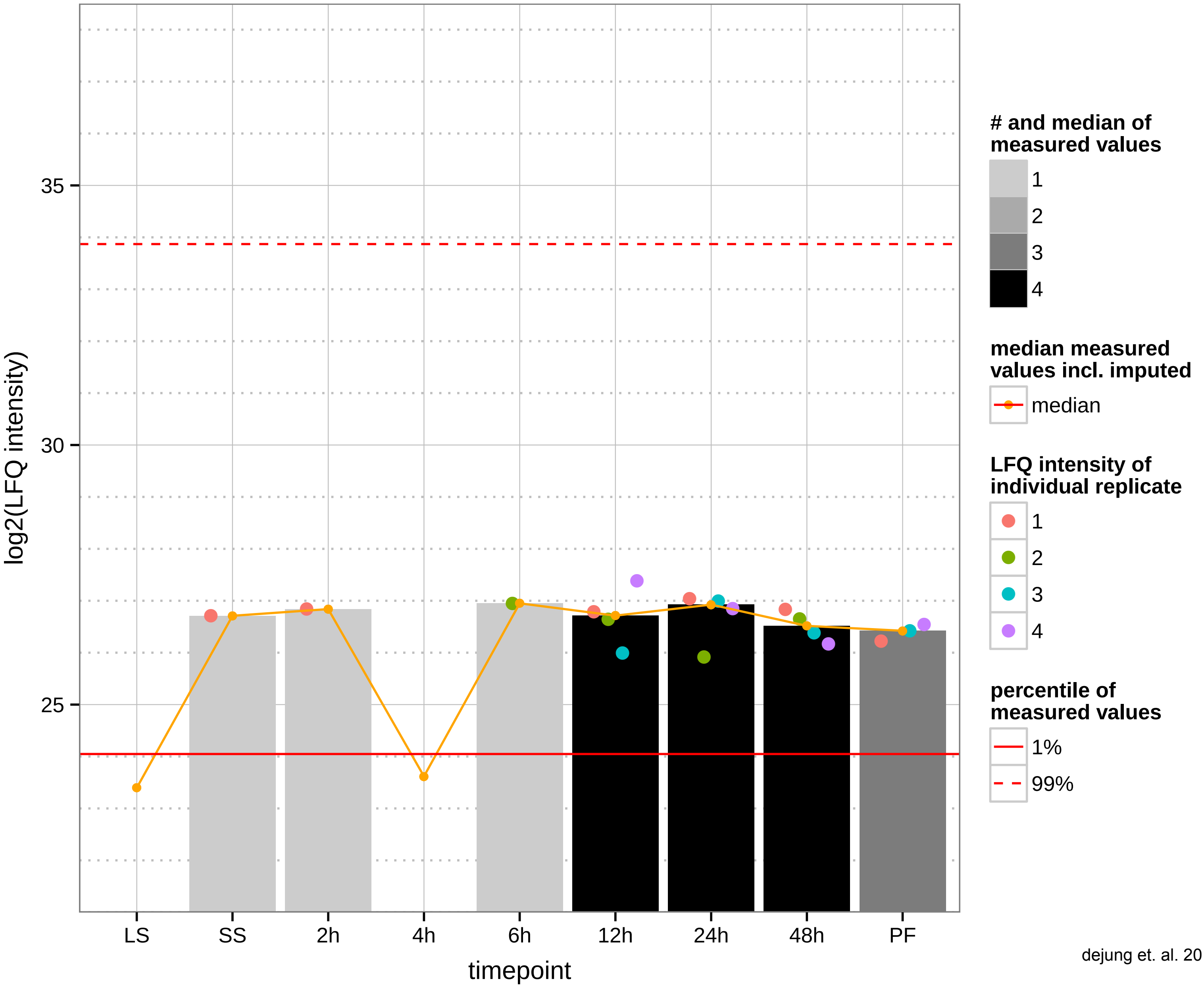
hypothetical protein, conserved
Tb927.6.2920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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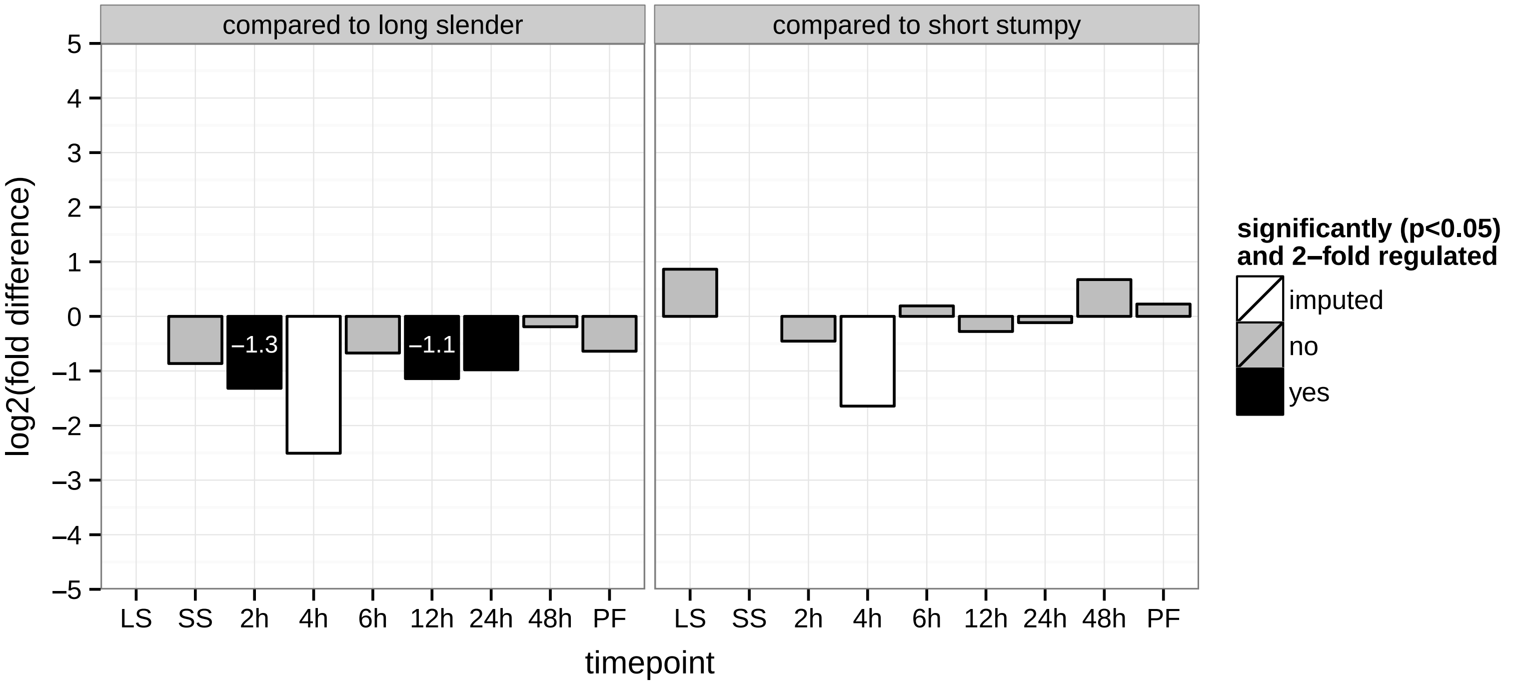
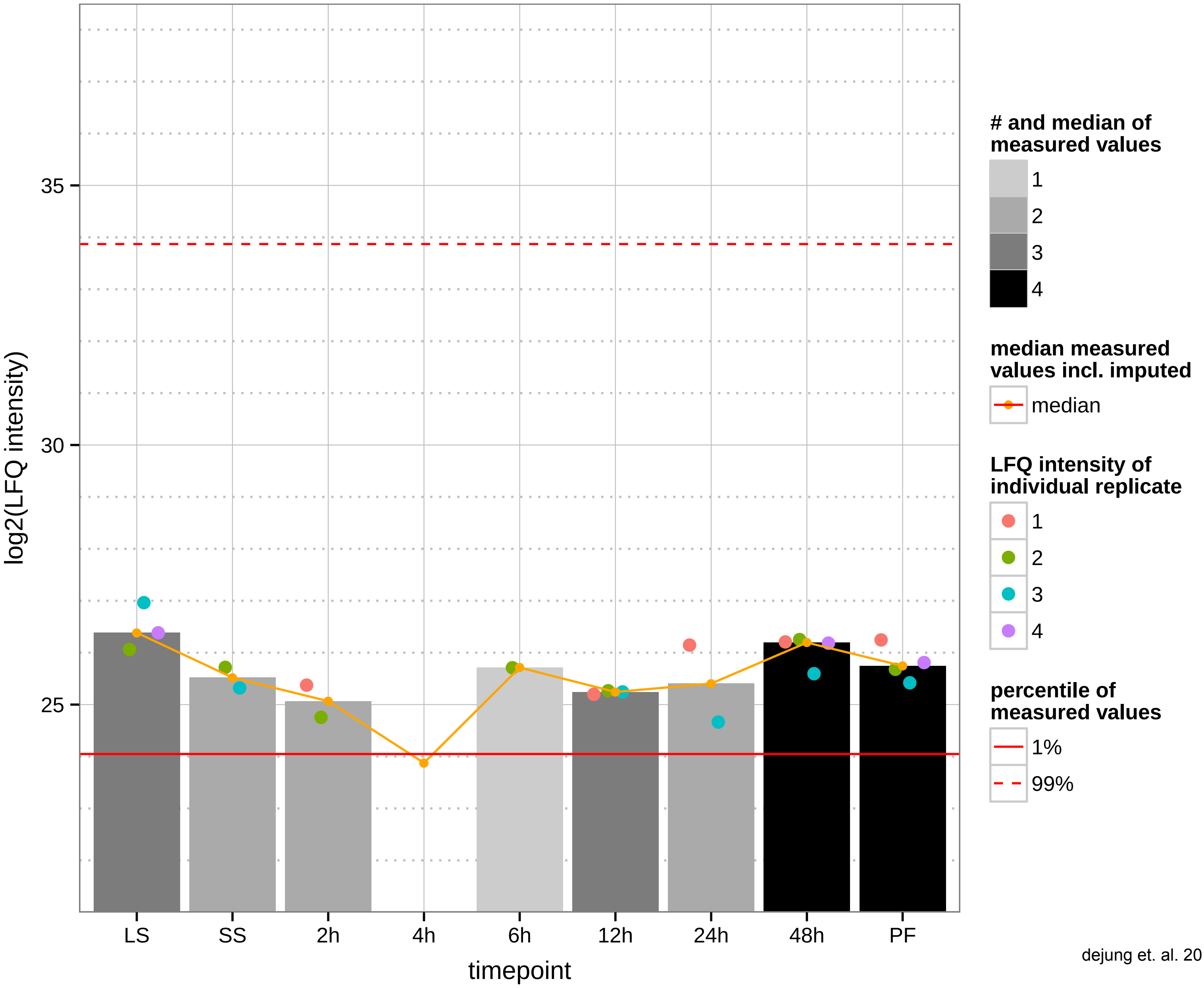
hypothetical protein, conserved
Tb927.7.6610
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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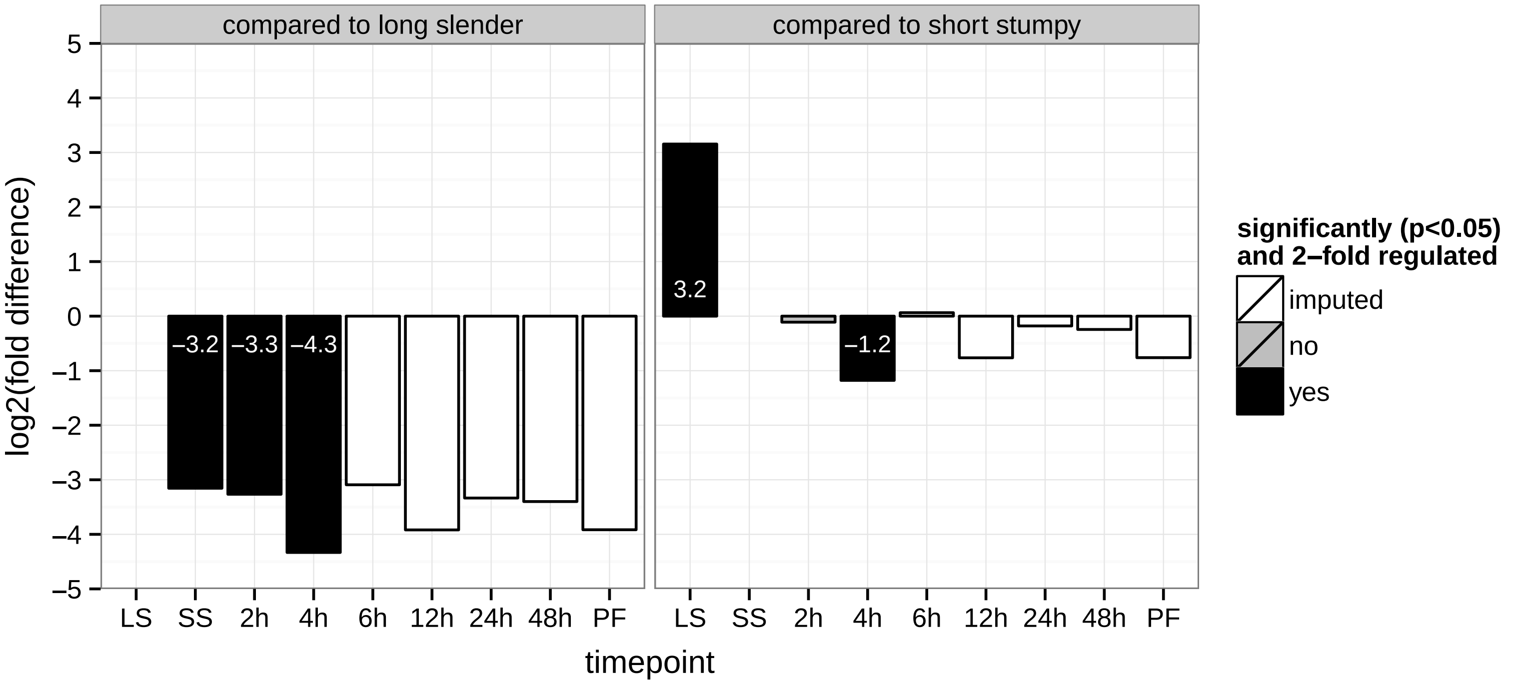
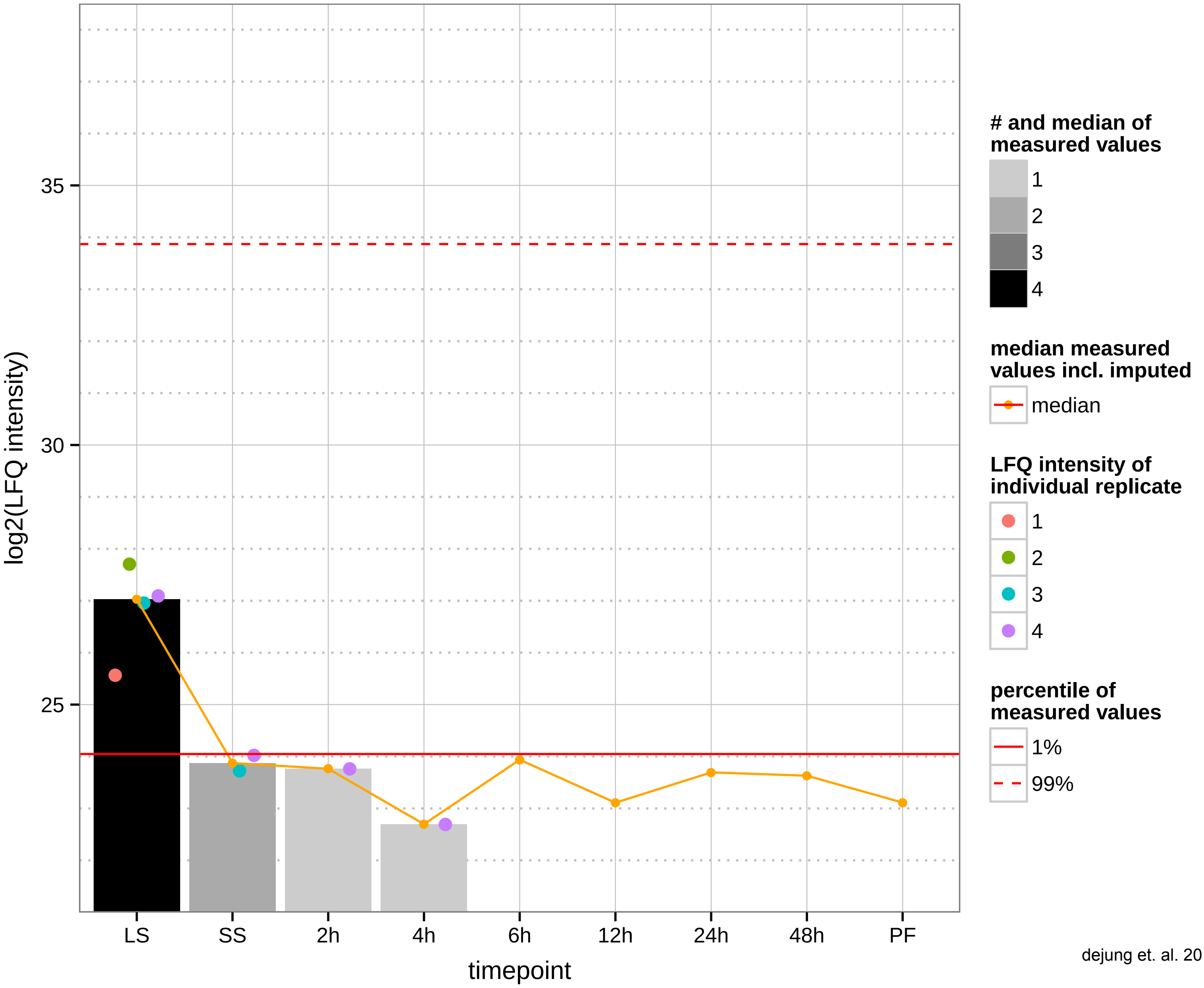
hypothetical protein, conserved
Tb927.8.6730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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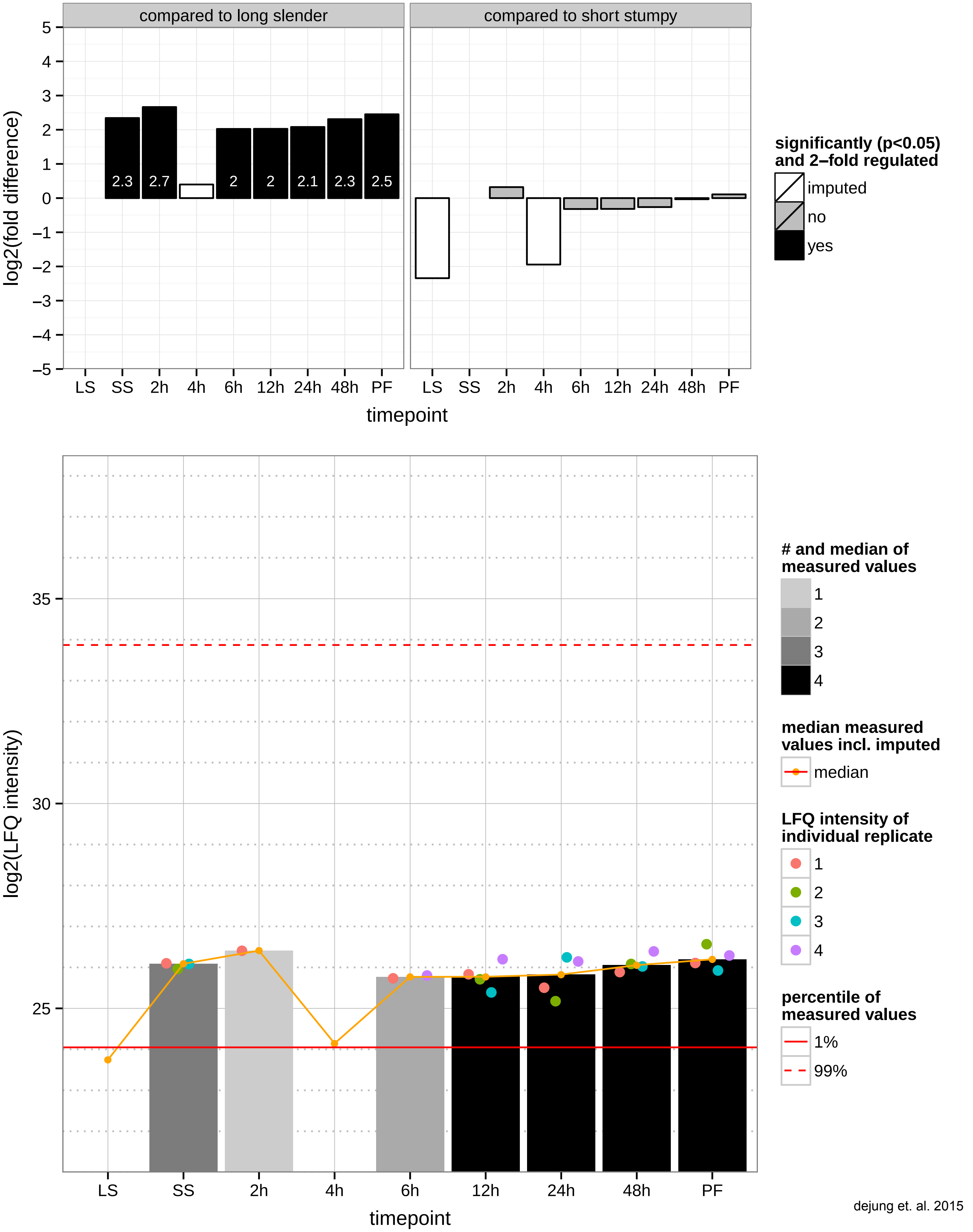
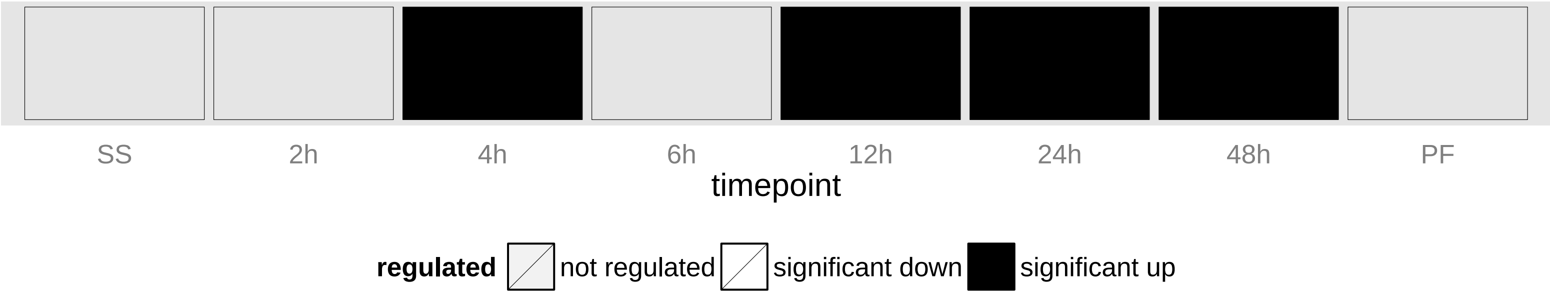
hypothetical protein, conserved
Tb927.9.8350
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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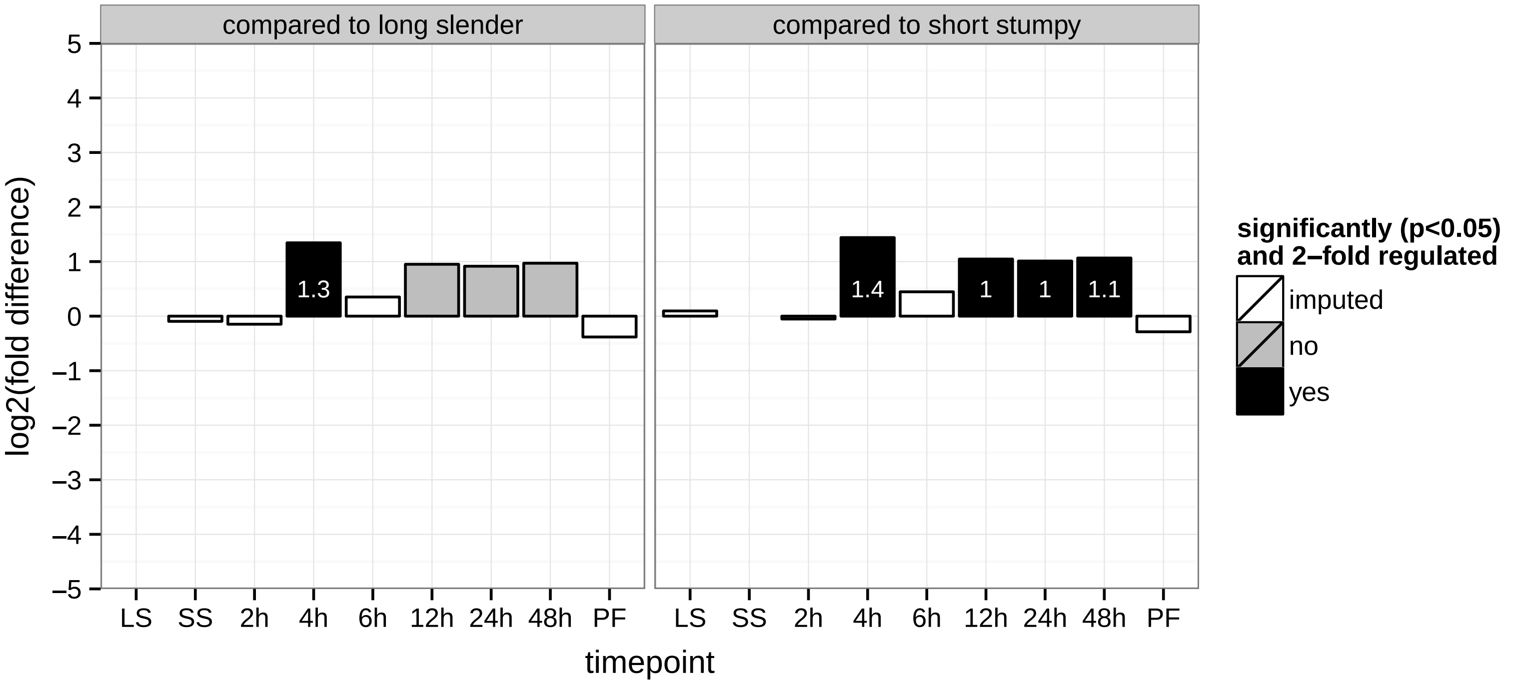
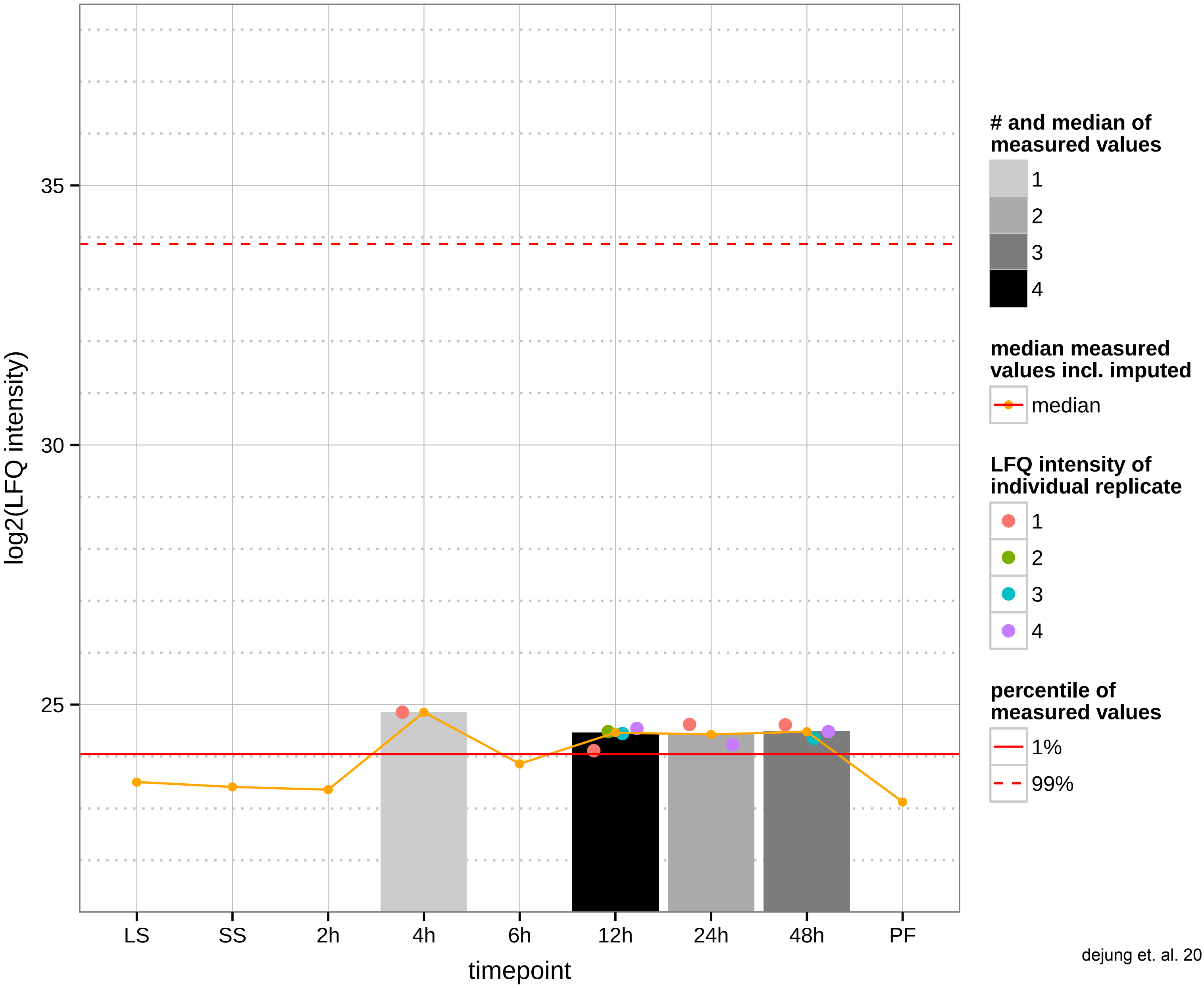
Cell cycle checkpoint protein RAD1–like, putative
Tb927.1.1060
AGOF: exodeoxyribonuclease activity
AGOC: null
AGOP: DNA repair
PGOF: damaged DNA binding
PGOC: nucleus
PGOP: DNA repair





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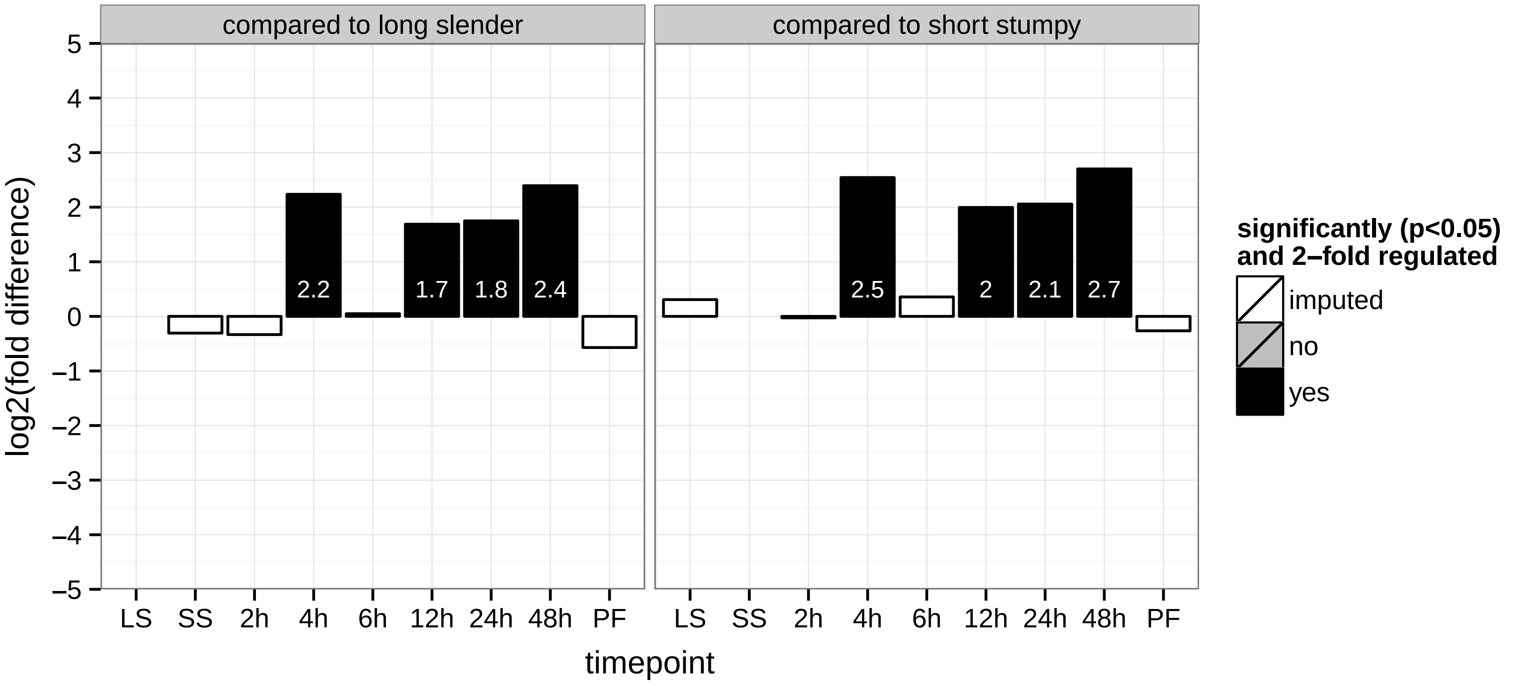
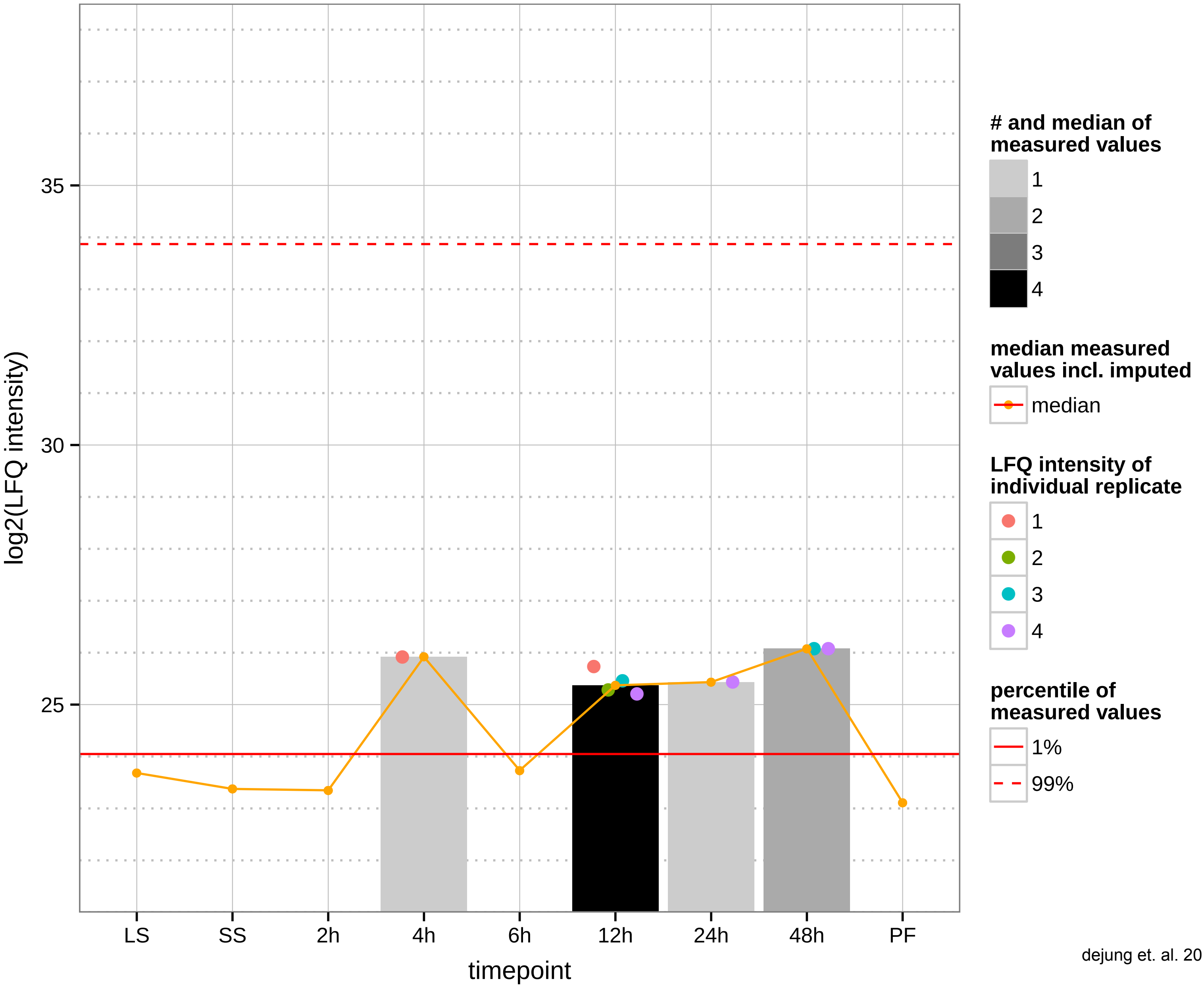
hypothetical protein, conserved
Tb927.11.6540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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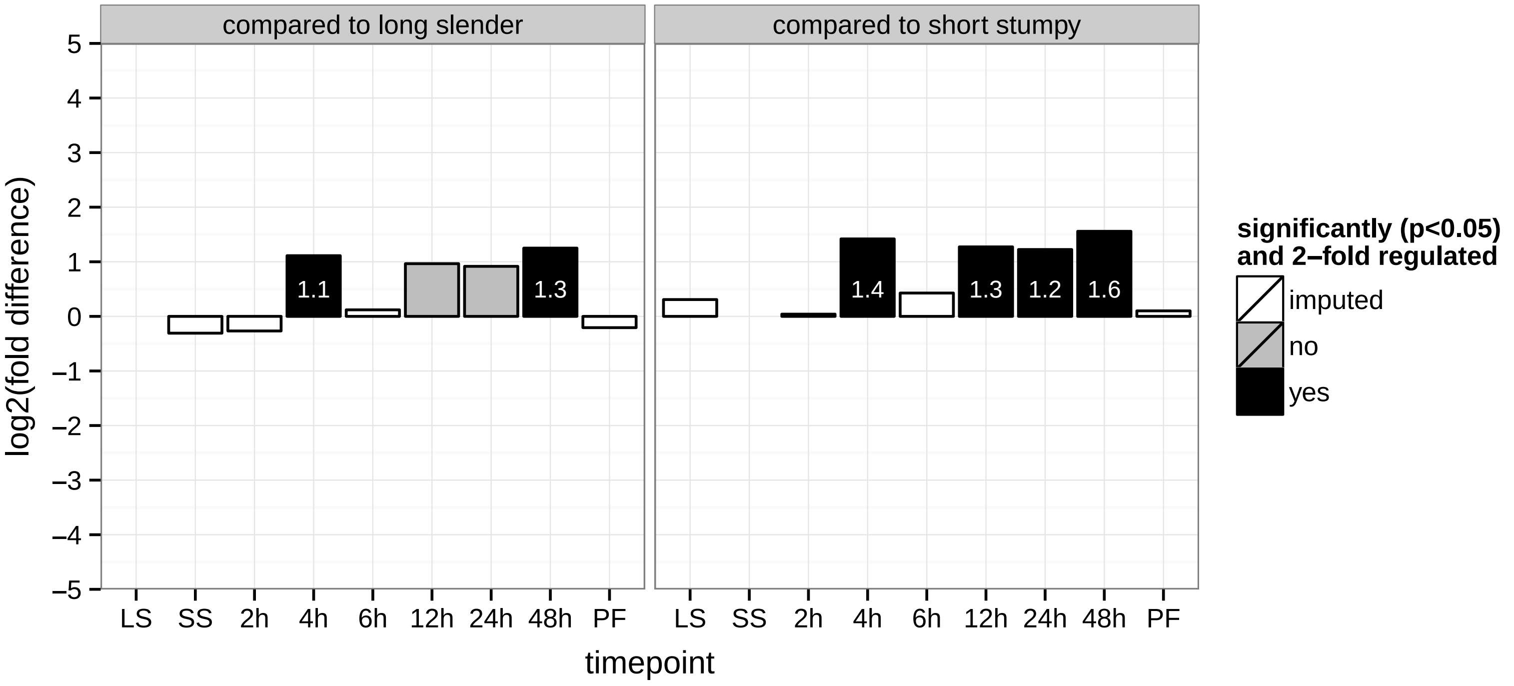
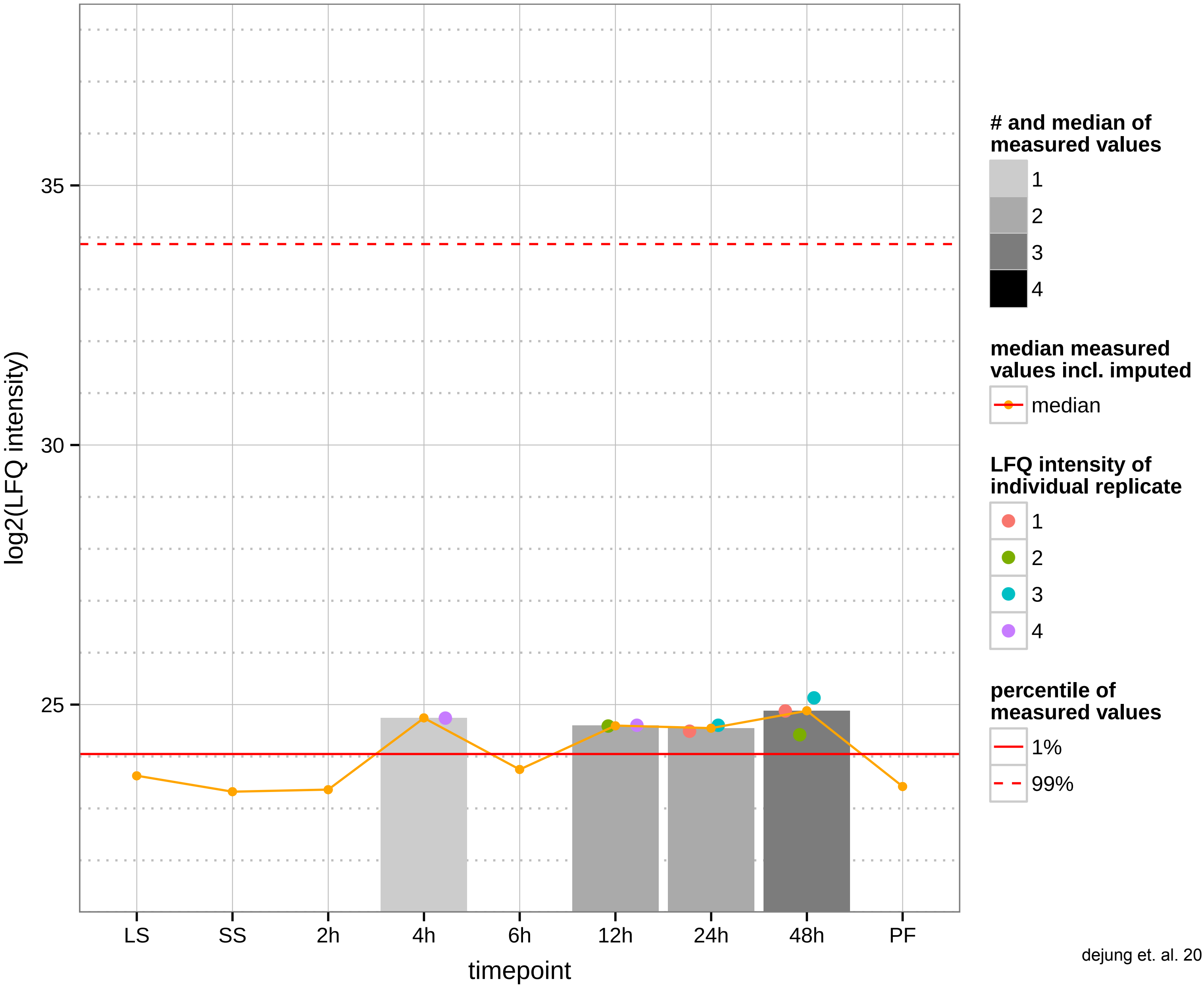
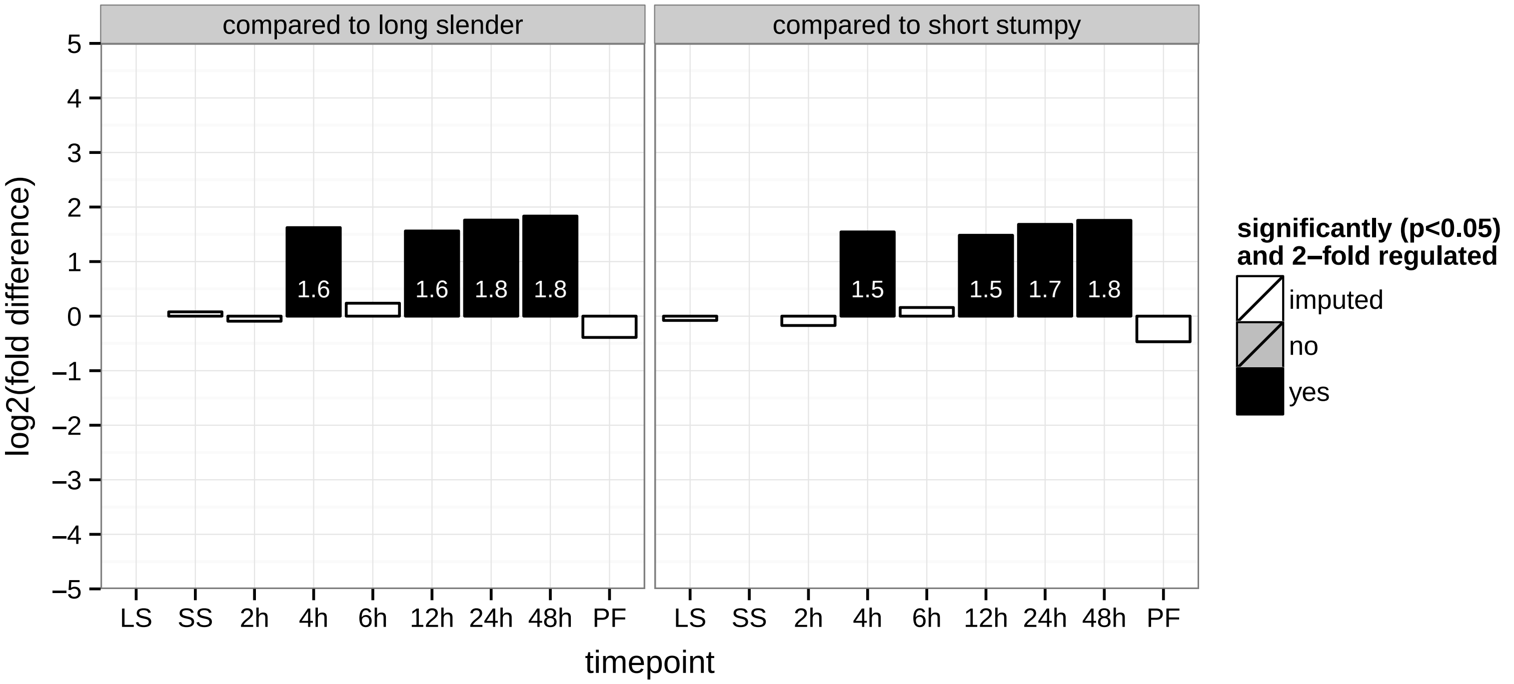
small nuclear RNA (snRNA) U1 (TbU1–24K)
Tb927.3.1090
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

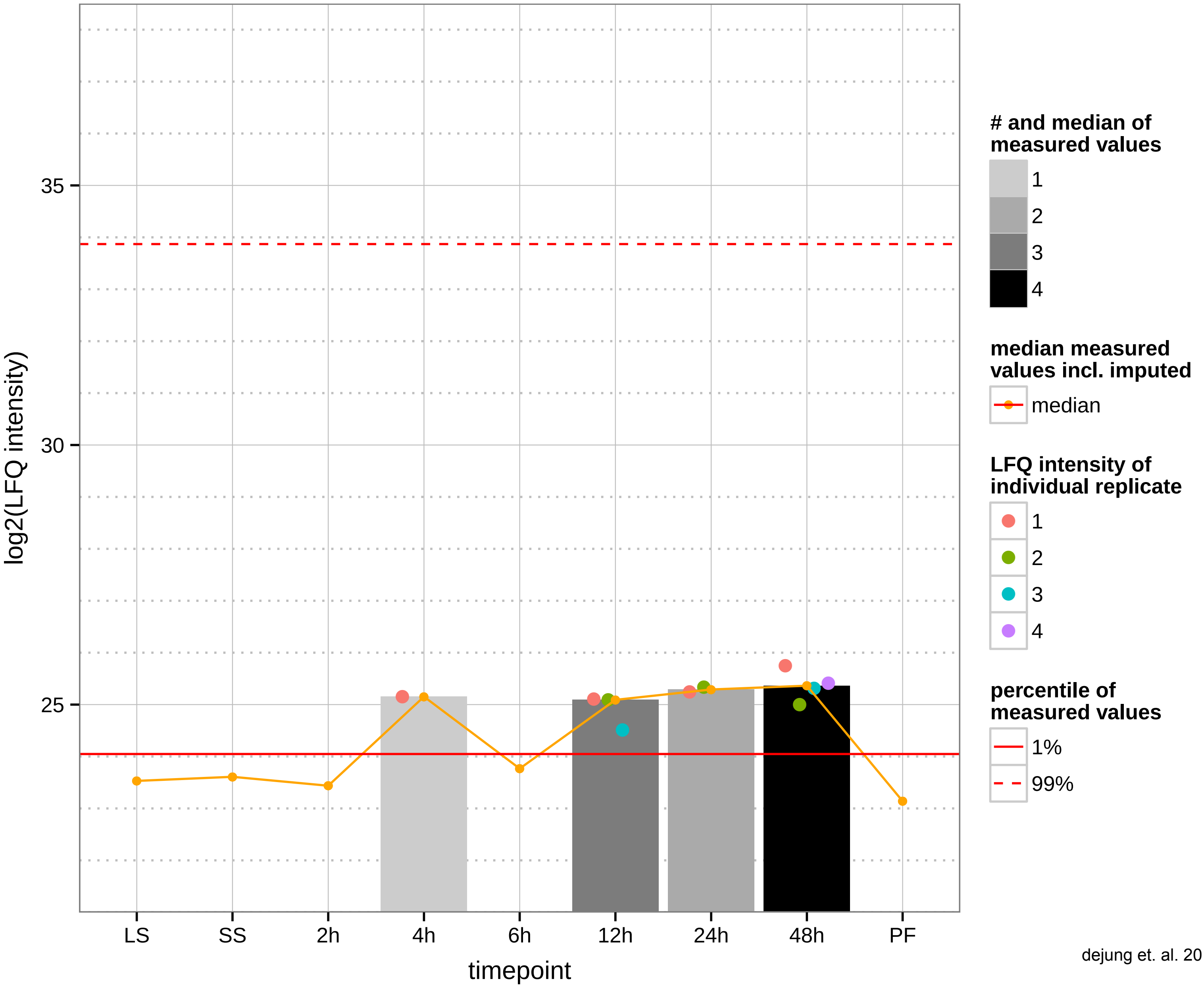




dejung et. al. 2015

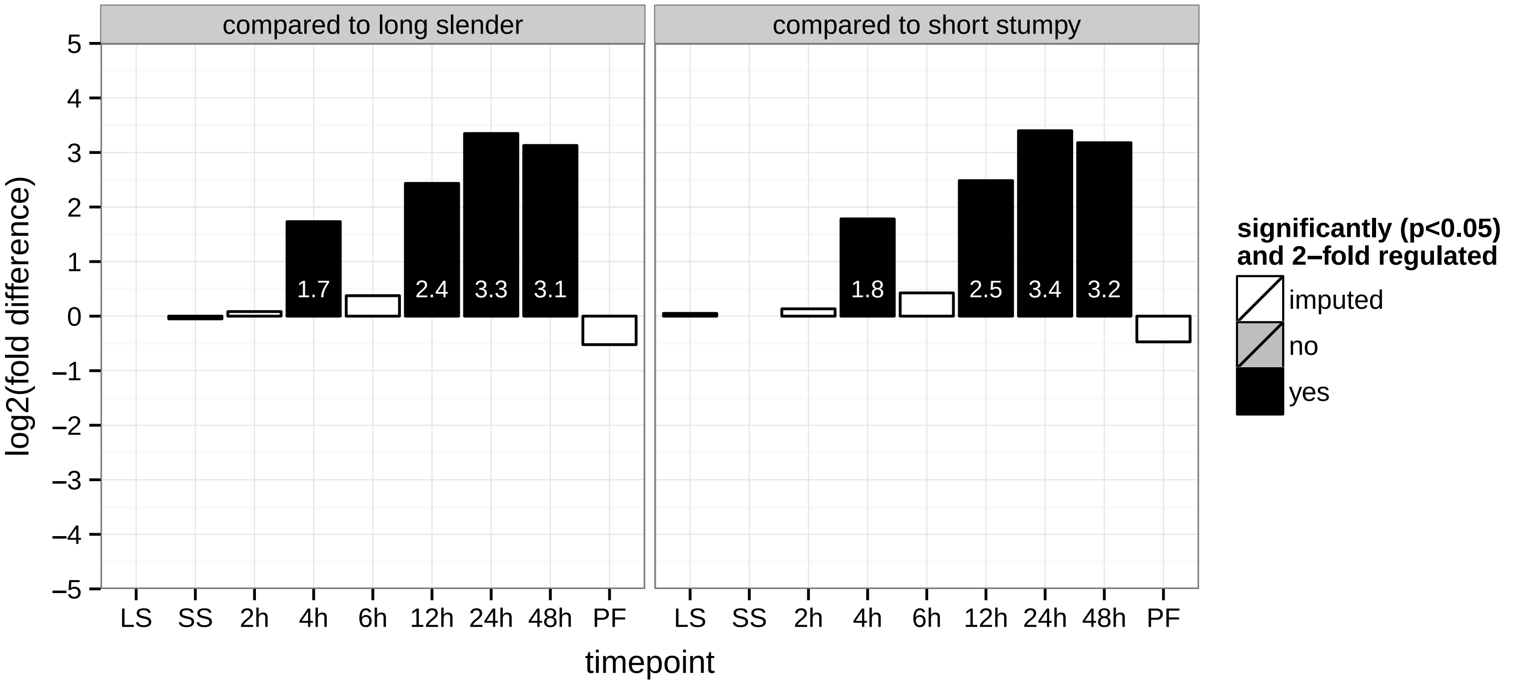
hypothetical protein, conserved
Tb927.7.3800
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

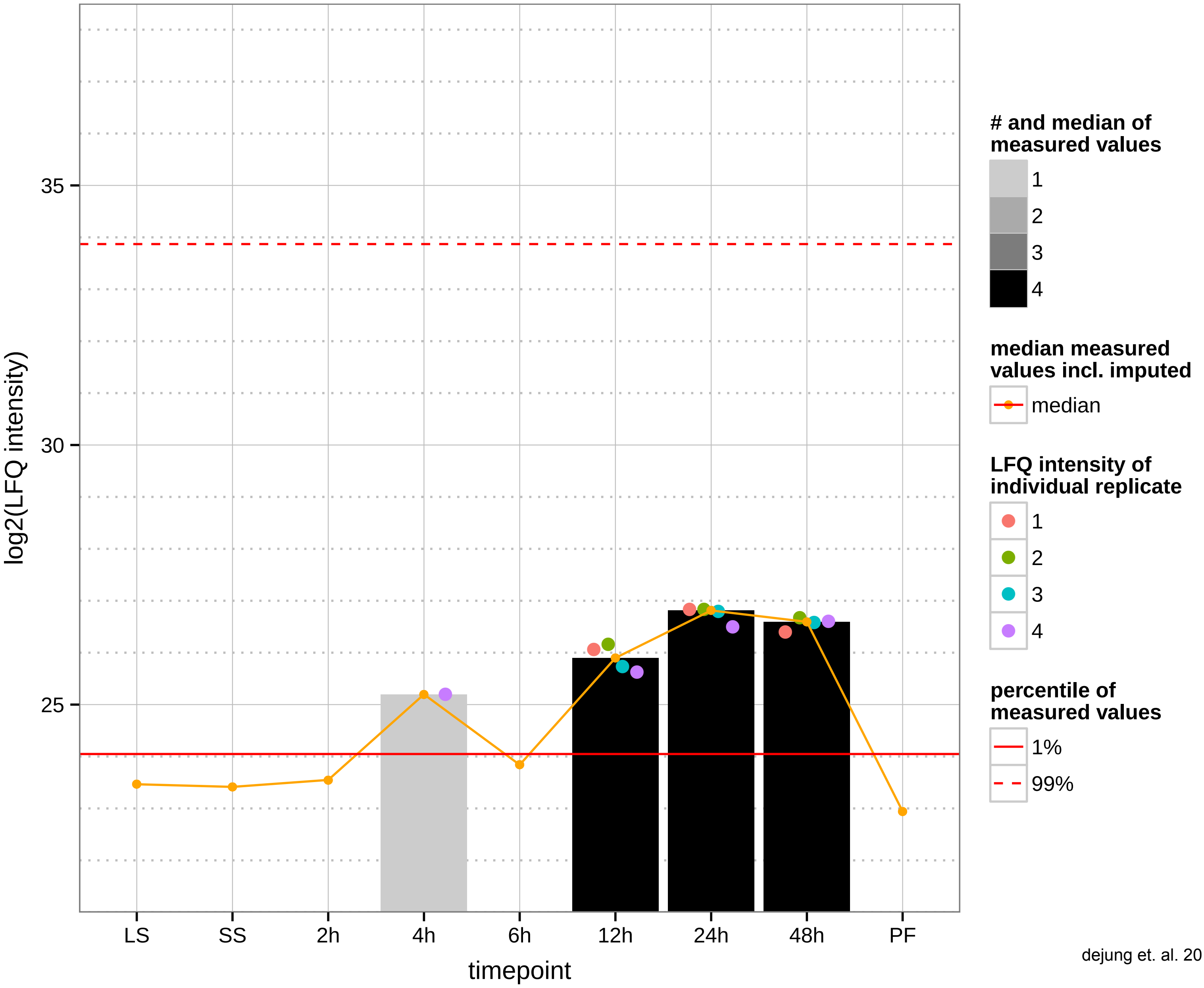




dejung et. al. 2015

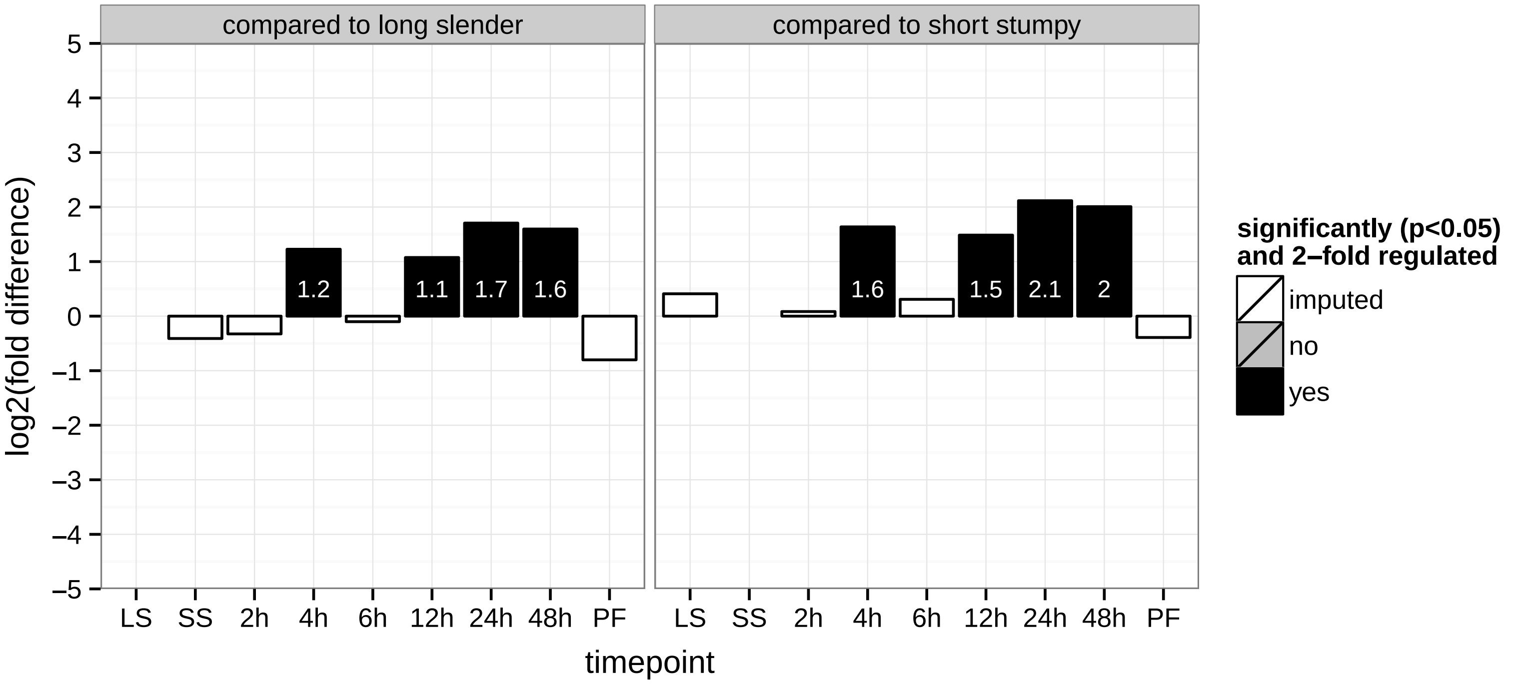
chaperone protein DNAj, putative
Tb927.7.6660
AGOF: heat shock protein binding, unfolded protein binding
AGOC: integral to membrane, mitochondrion
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null

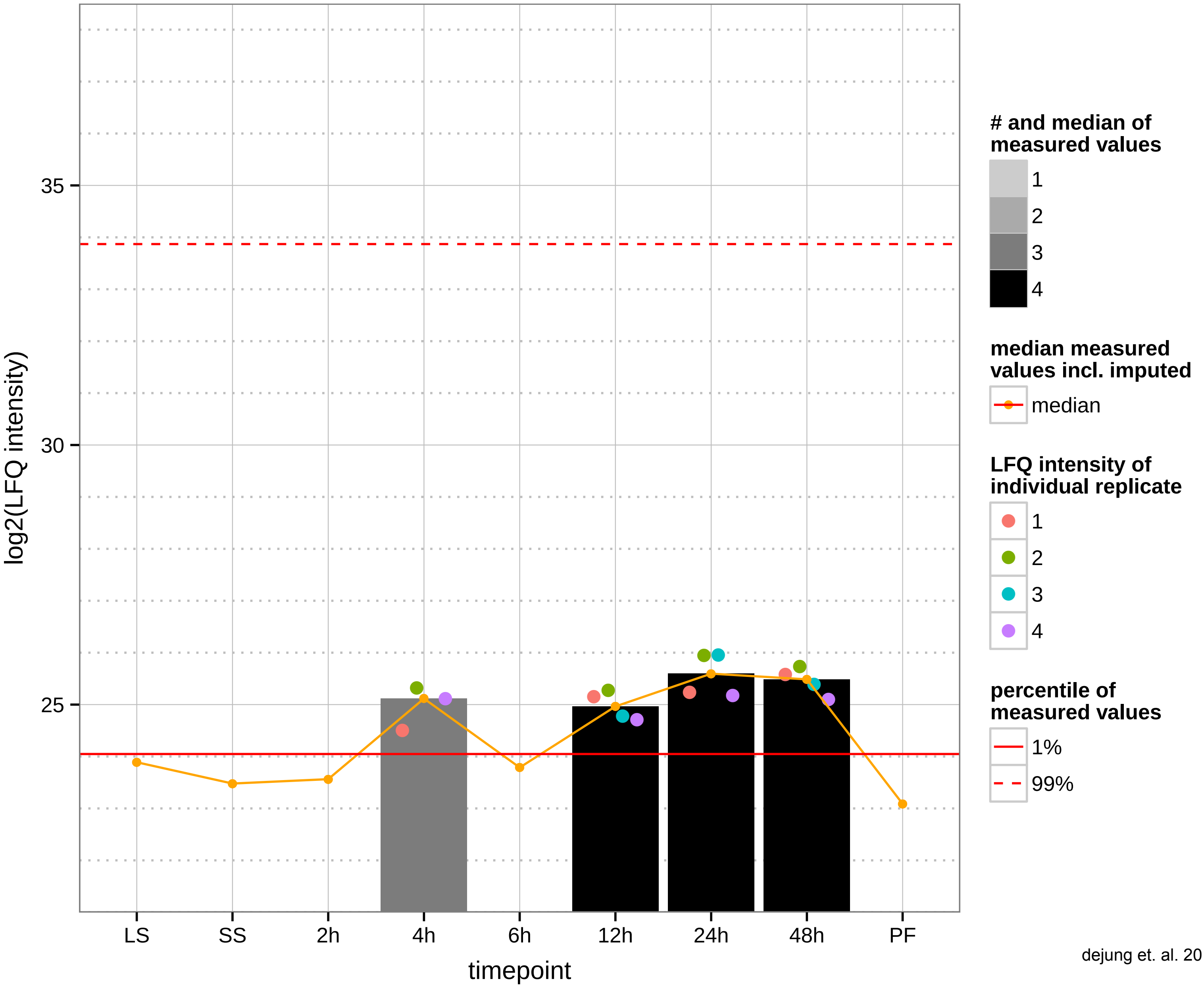




dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.7010
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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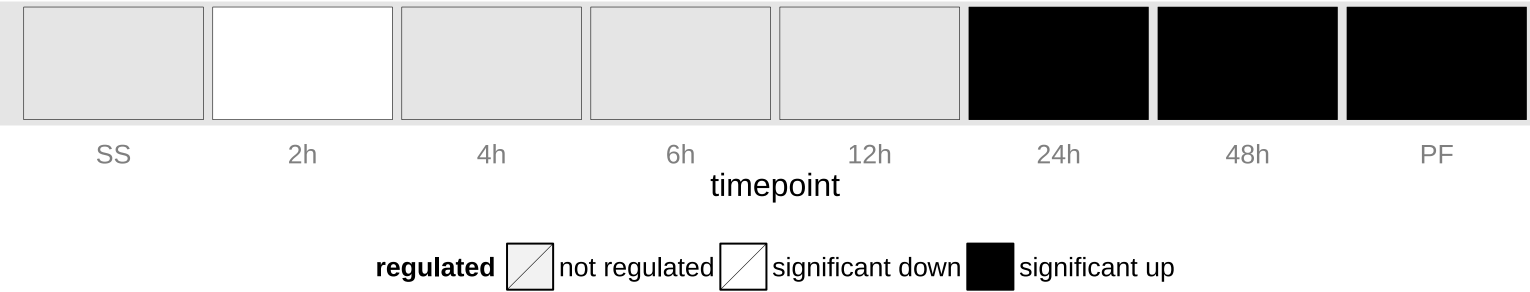

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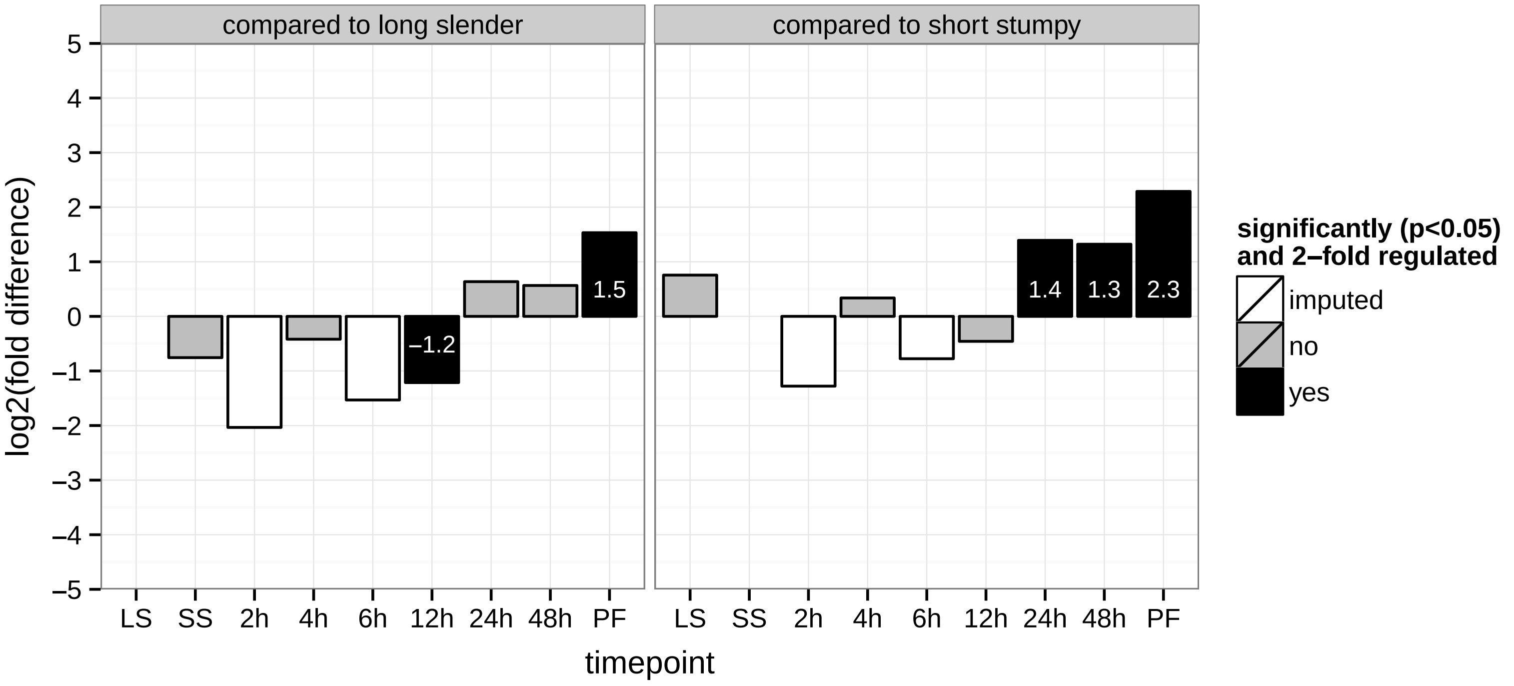
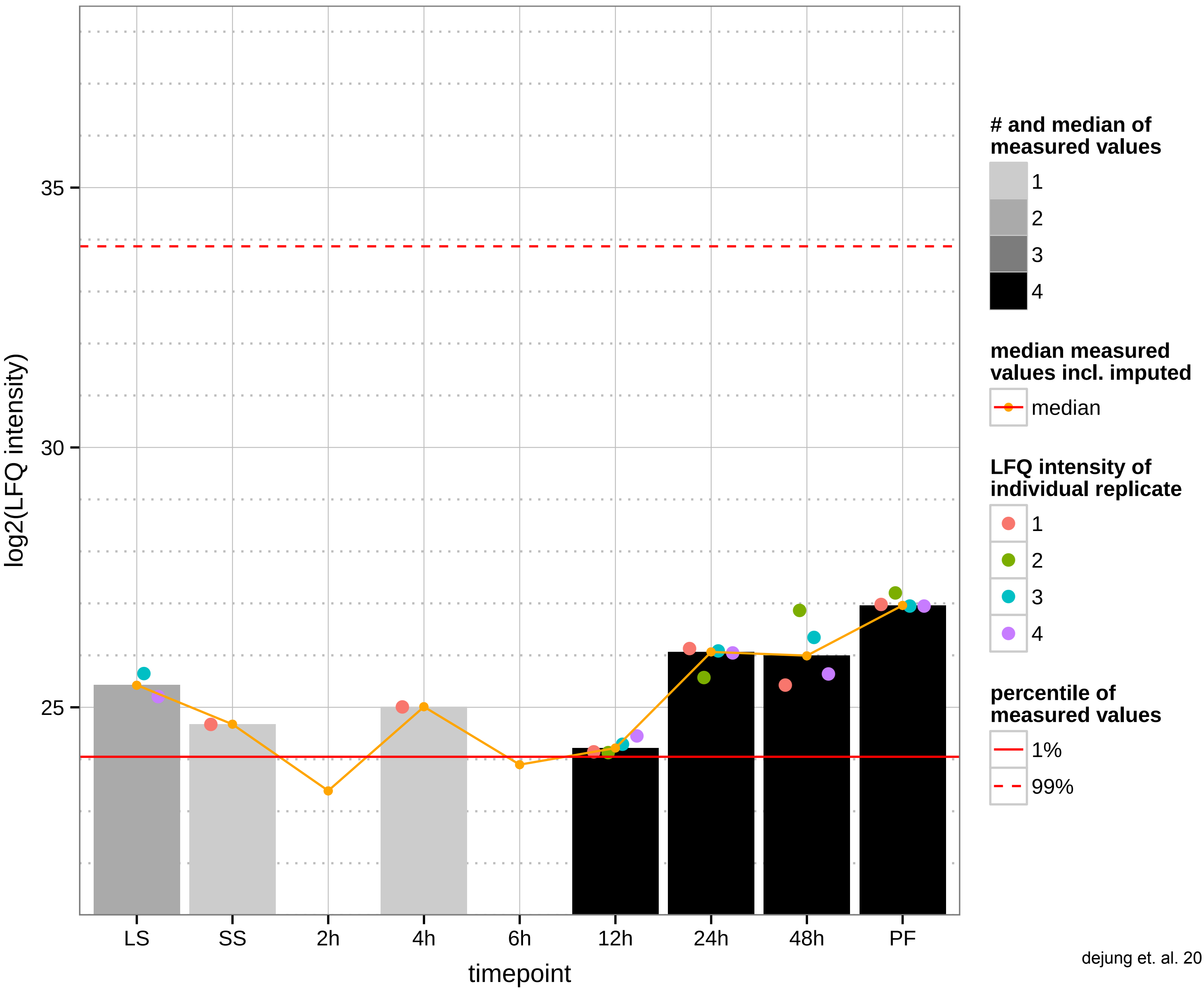
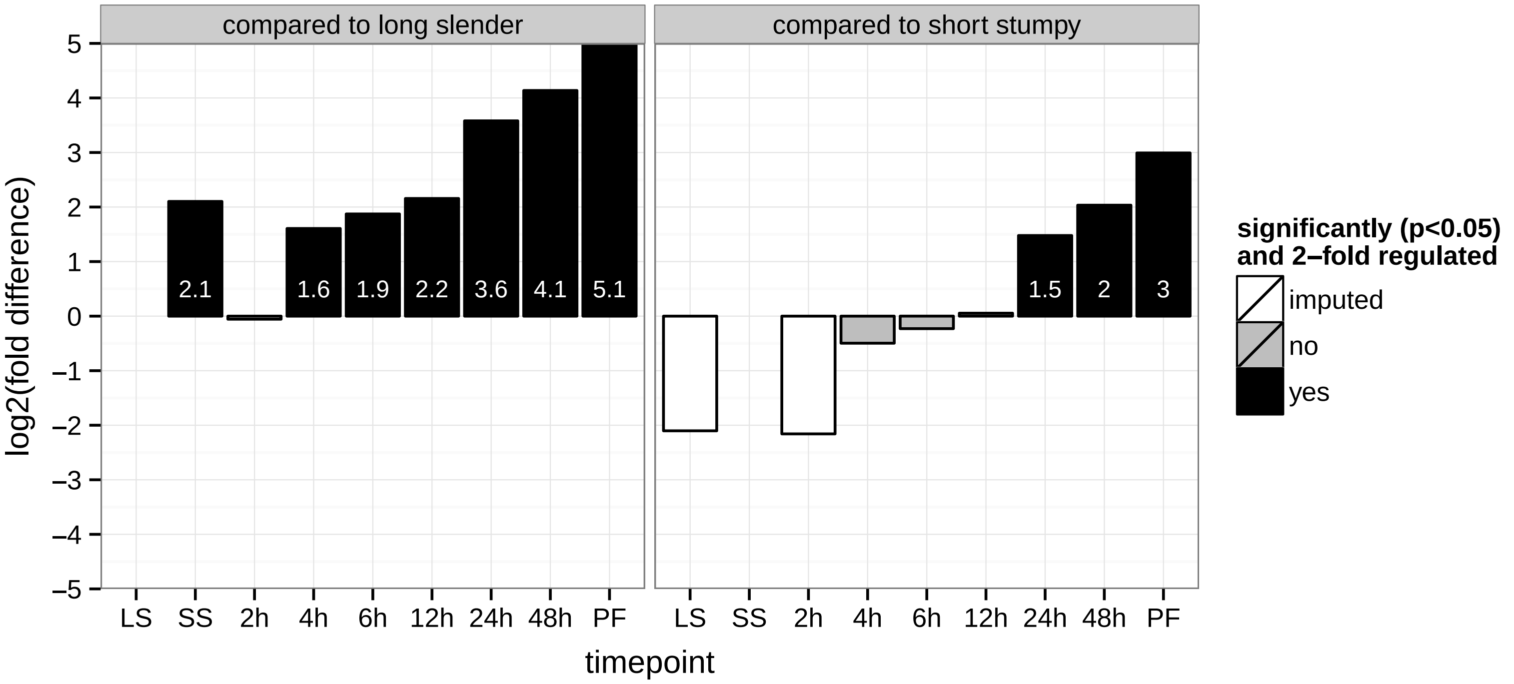
DNA mismatch repair protein, putative, DNA mismatch repair protein MSH2, MutS protein homolog 2, putative (MSH2)
Tb927.10.11020
AGOF: null, ATP binding, damaged DNA binding, mismatched DNA binding
AGOC: null, MutSalpha complex, MutSbeta complex
AGOP: null, DNA metabolic process, mismatch repair
PGOF: ATP binding, mismatched DNA binding
PGOC: null, MutSalpha complex, MutSbeta complex
PGOP: mismatch repair

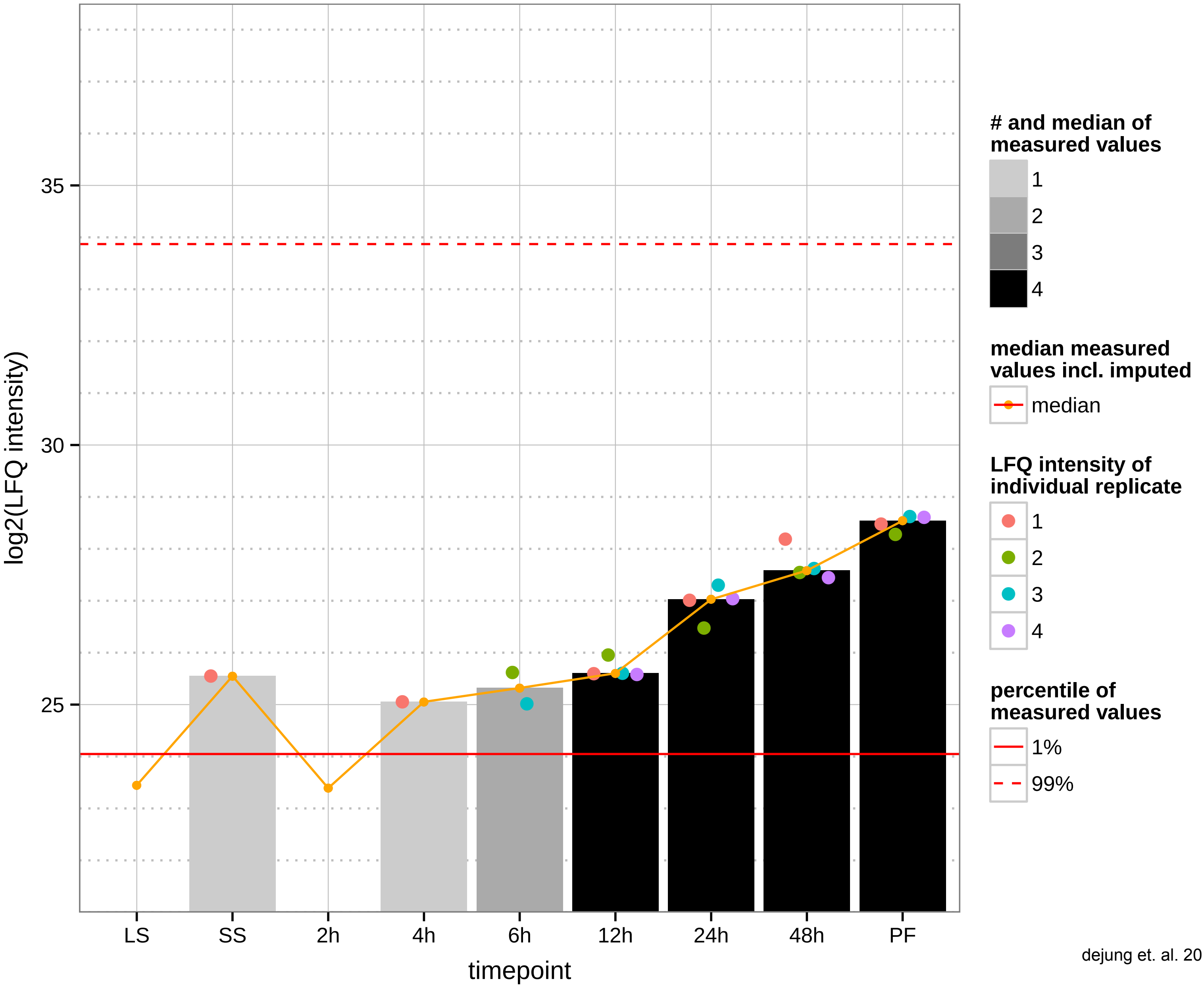




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.11380
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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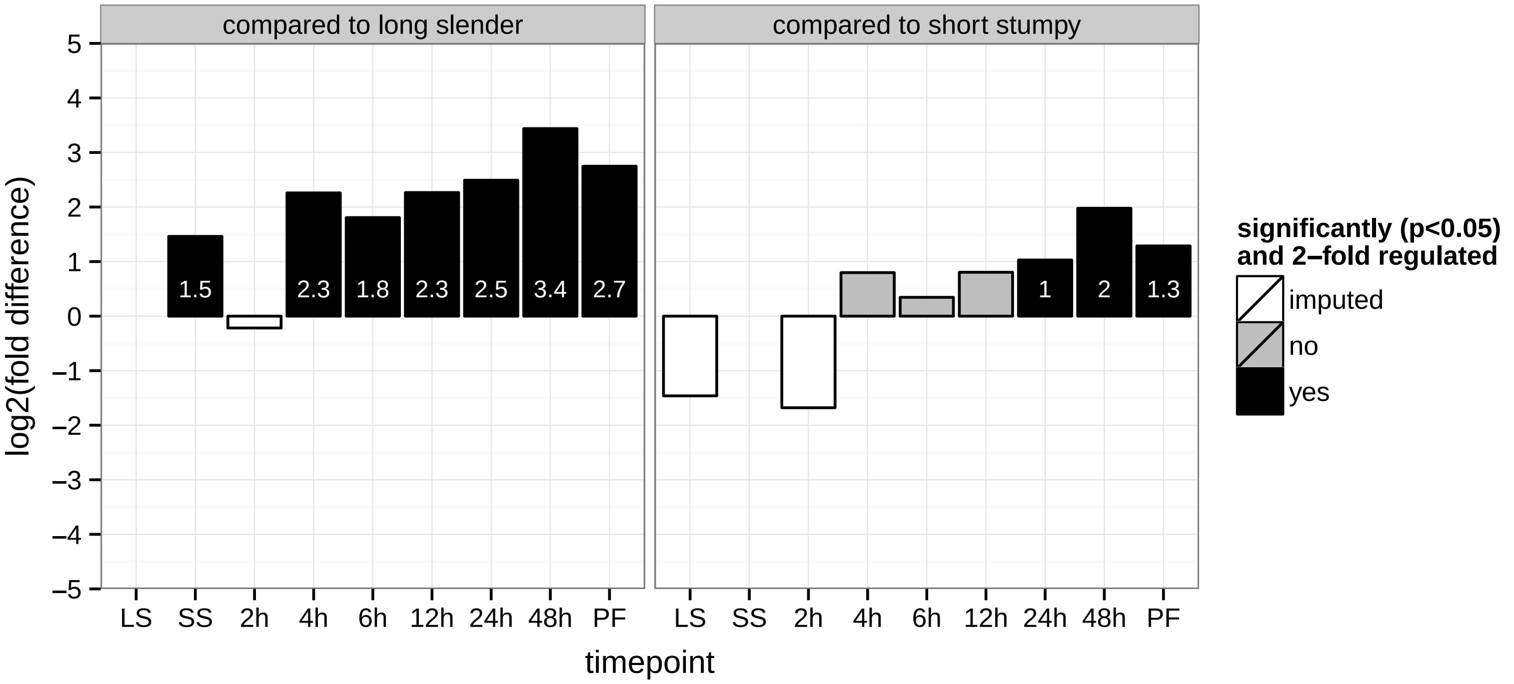
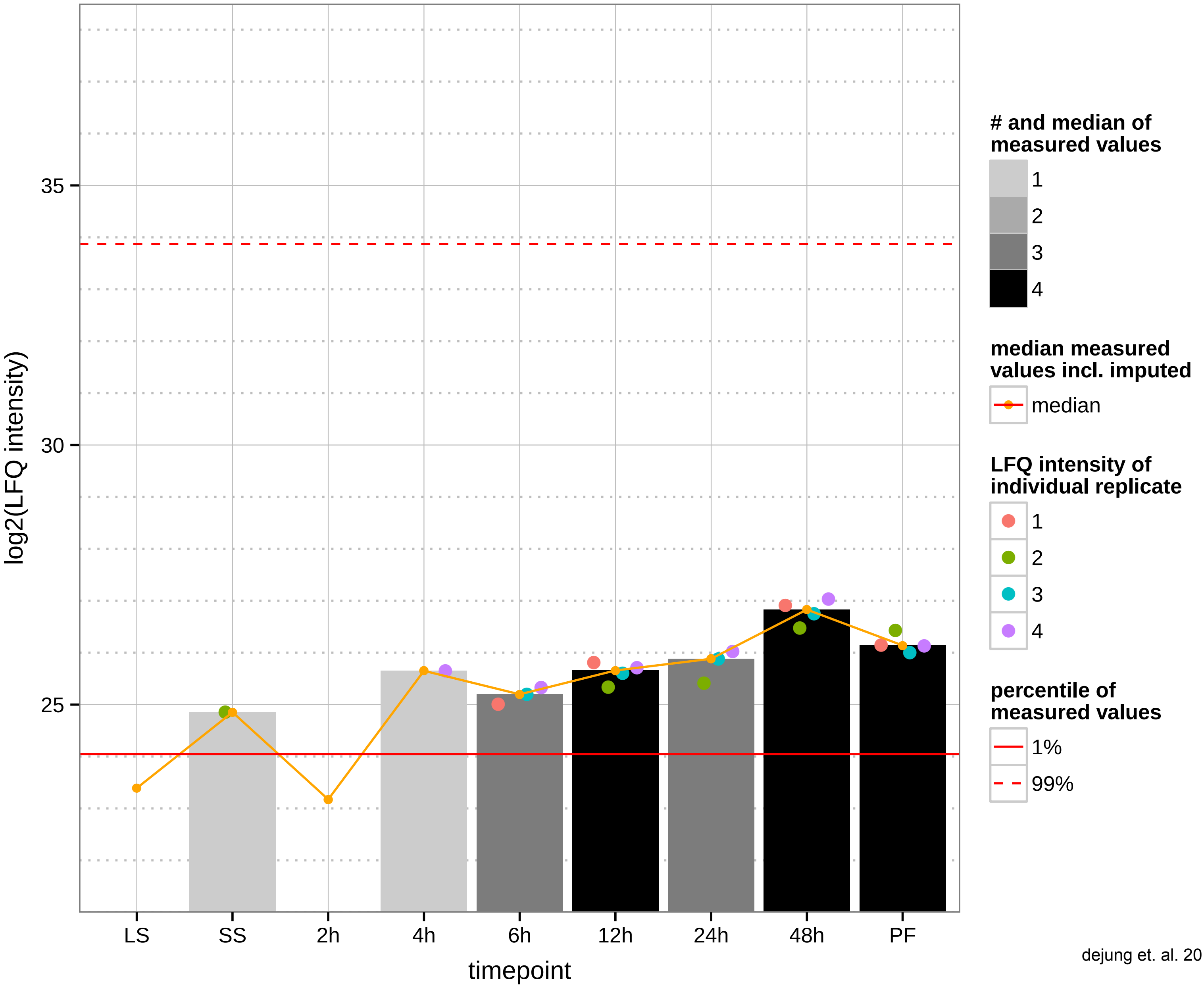
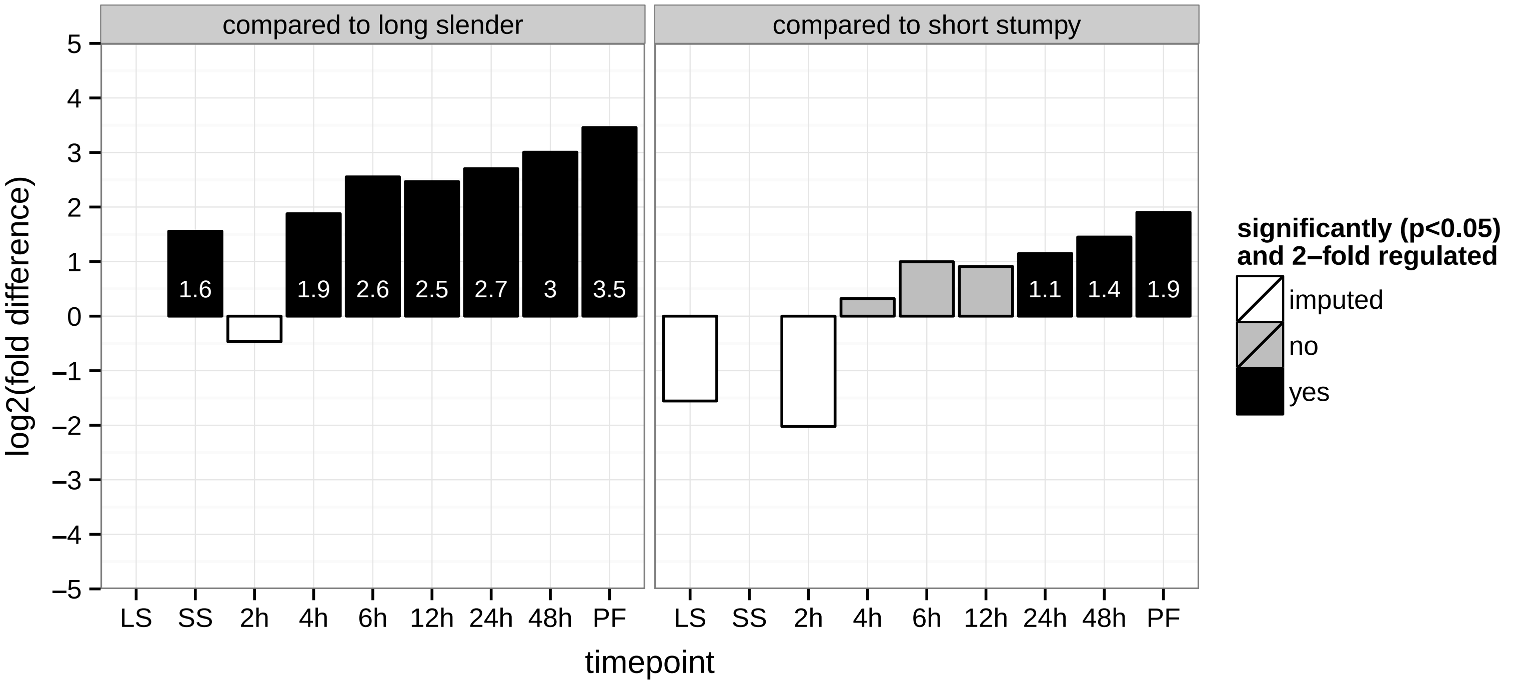
ribosomal protein L11, putative
Tb927.2.4890;Tb927.2.4740
AGOF: structural constituent of ribosome
AGOC: intracellular, mitochondrion, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: ribosome
PGOP: translation

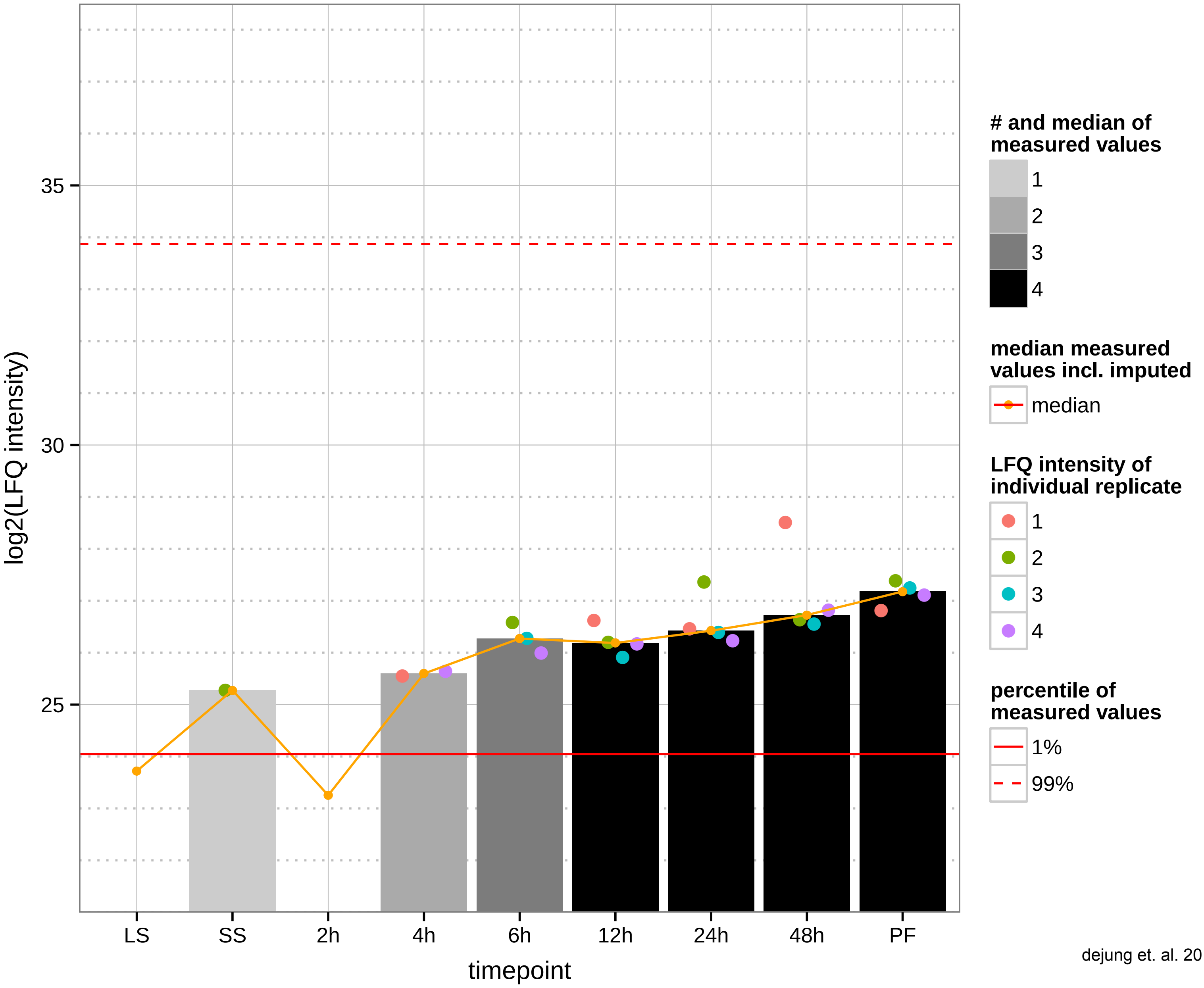




dejung et. al. 2015

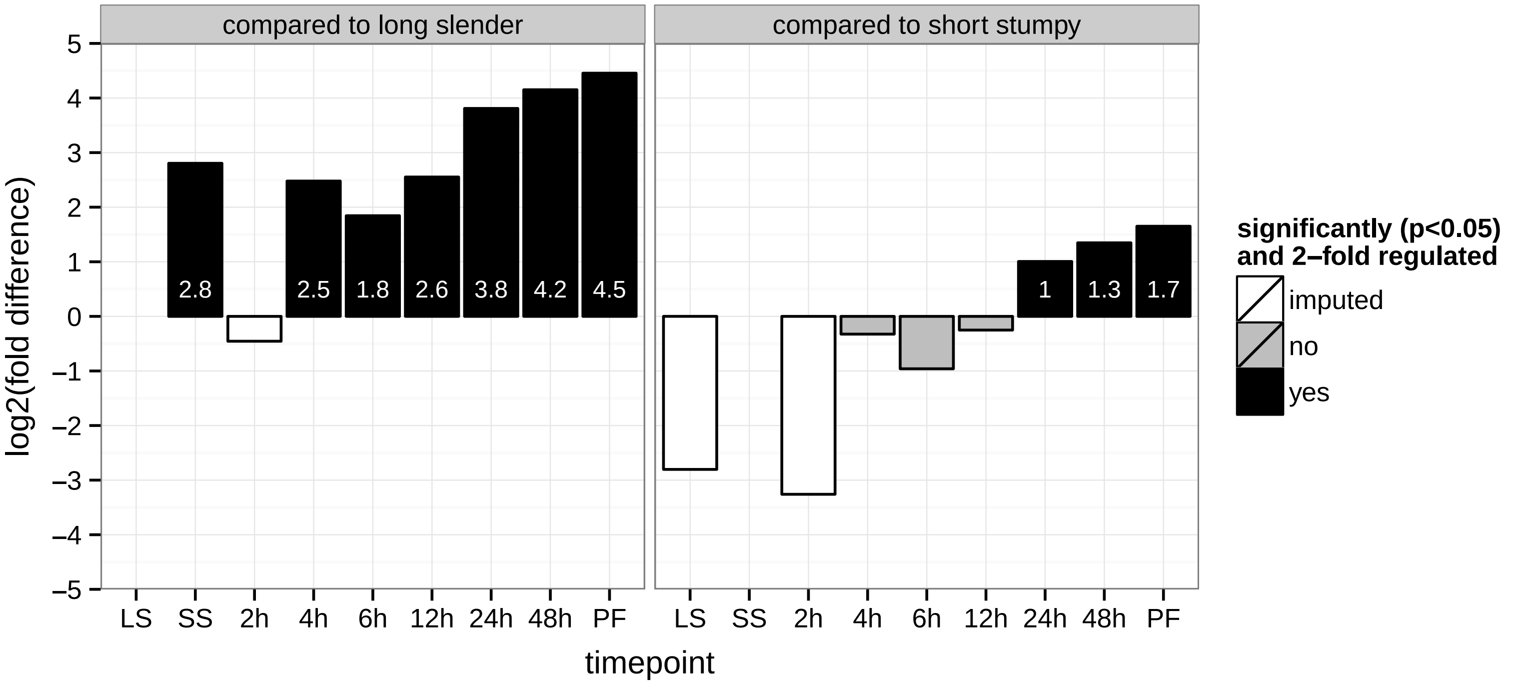
hypothetical protein, conserved
Tb927.5.3410
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

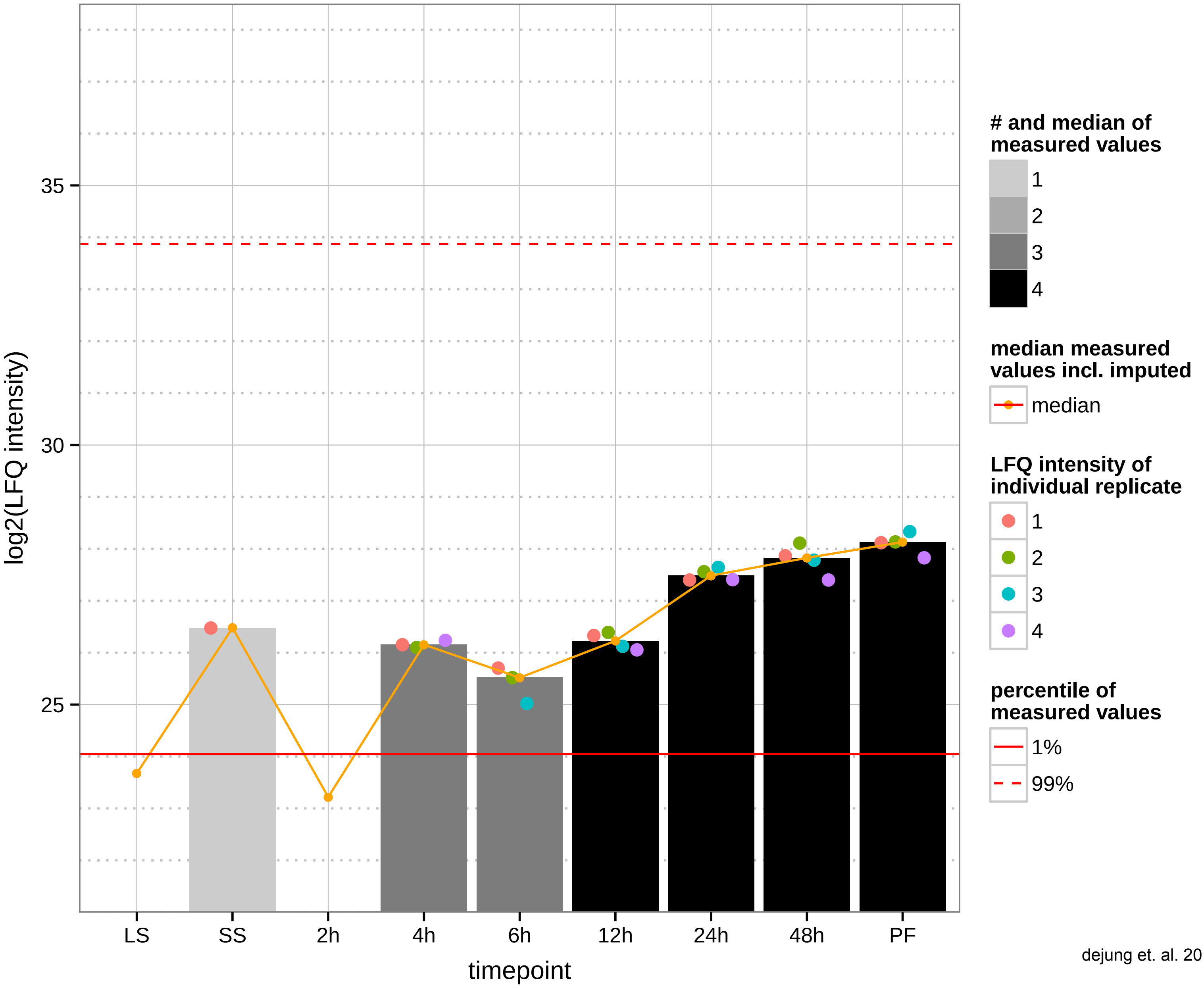




dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.4130
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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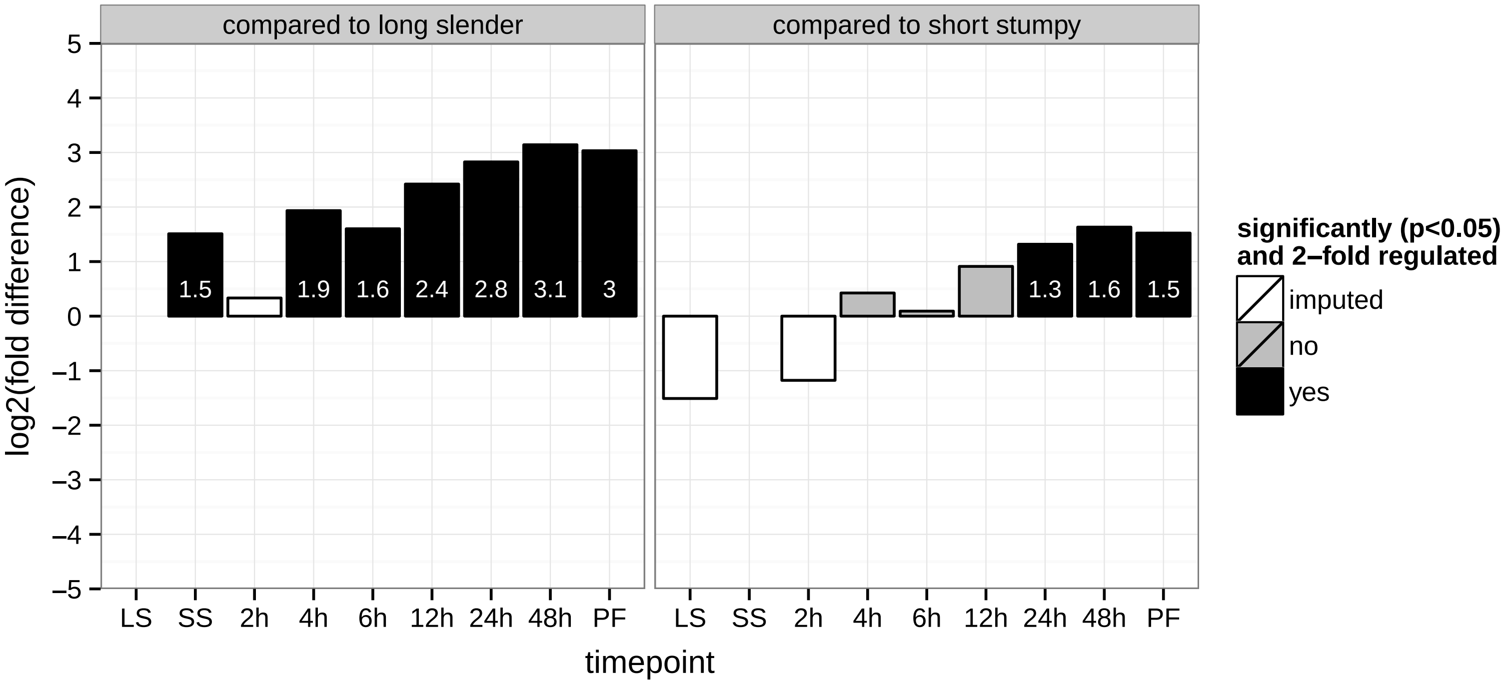
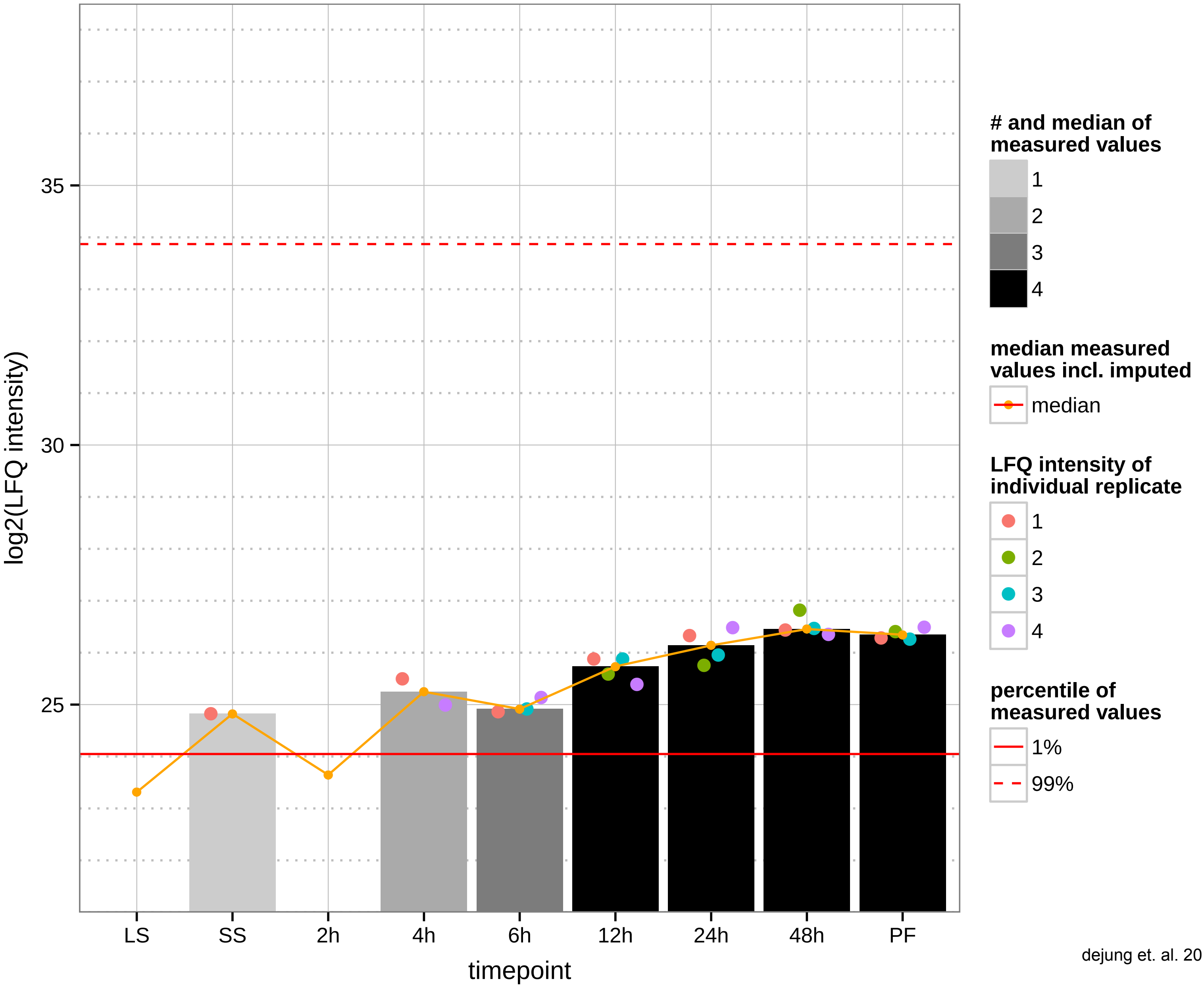
hypothetical protein, conserved
Tb927.8.3300
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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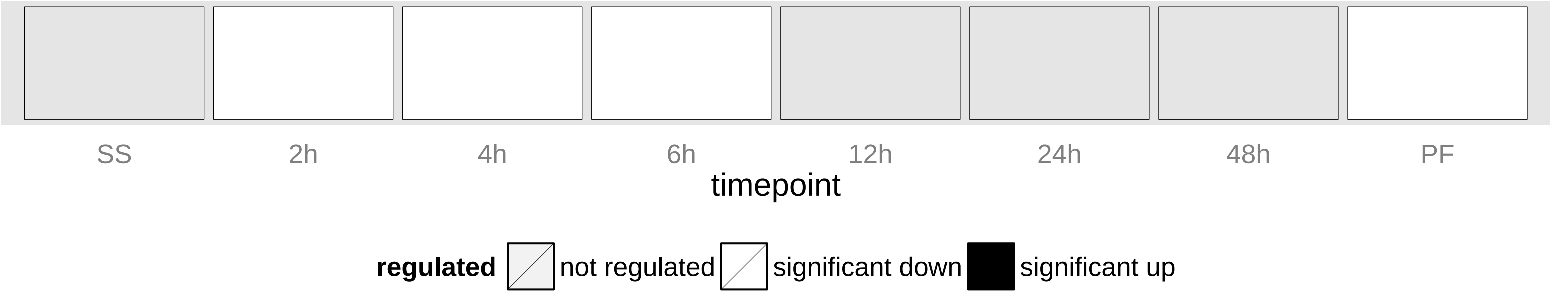

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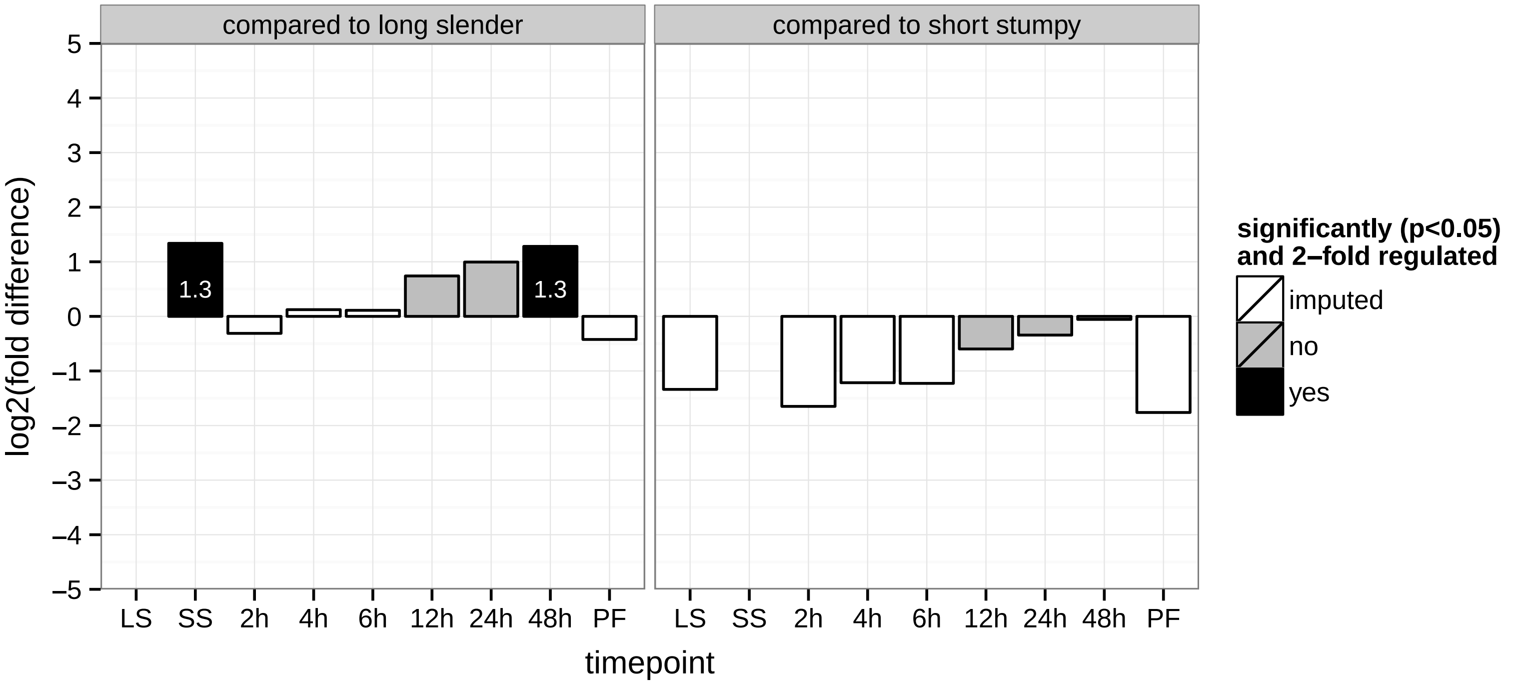
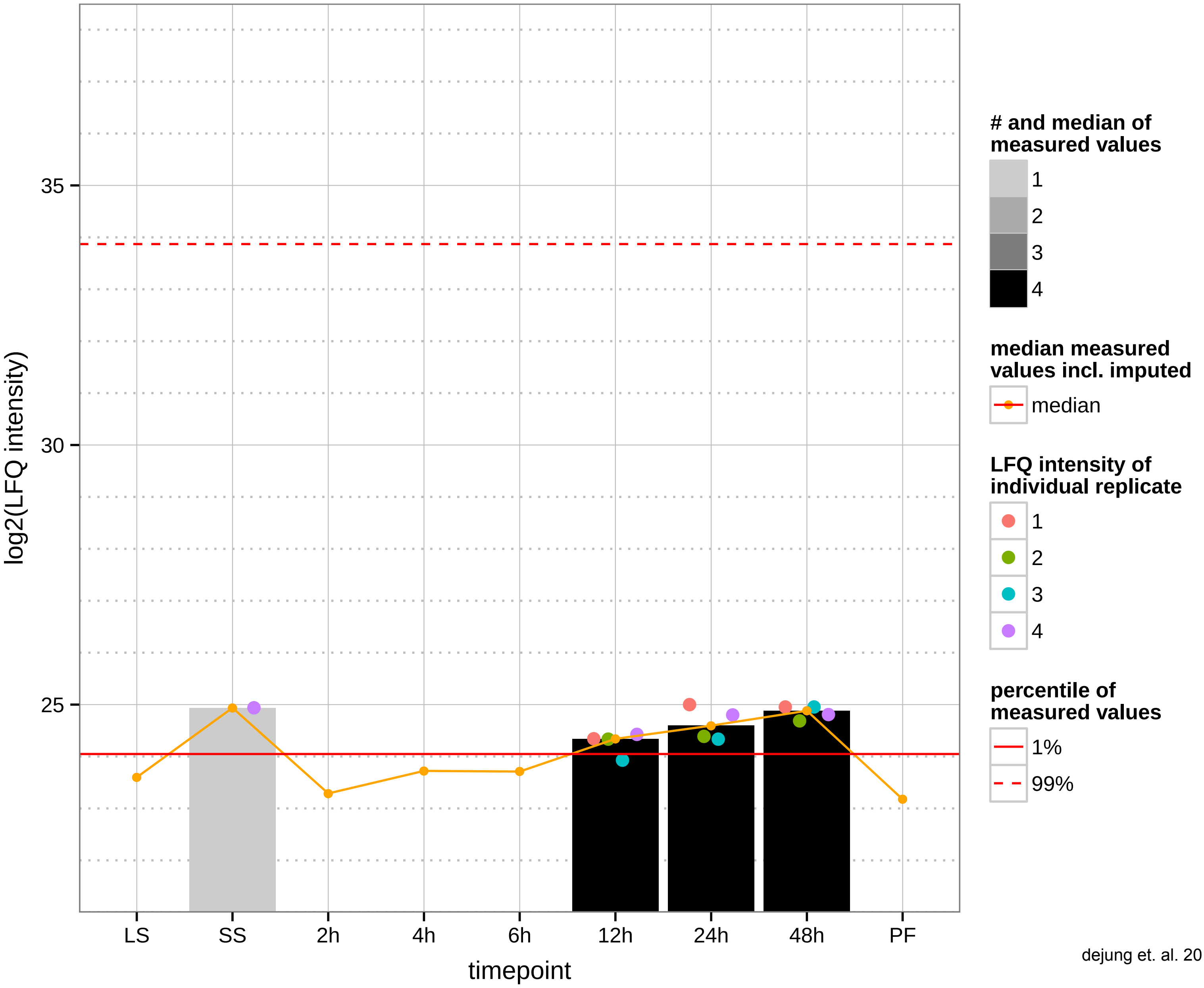
ATP−dependent DEAH−box RNA helicase, putative
Tb927.4.3020;Tb11.v5.0965
AGOF: null, ATP binding, double−stranded RNA binding, helicase activity
AGOC: null, intracellular
AGOP: null
PGOF: helicase activity, ATP binding, ATP−dependent helicase activity, double−stranded RNA binding, helicase activity, nucle
PGOC: null, intracellular
PGOP: null





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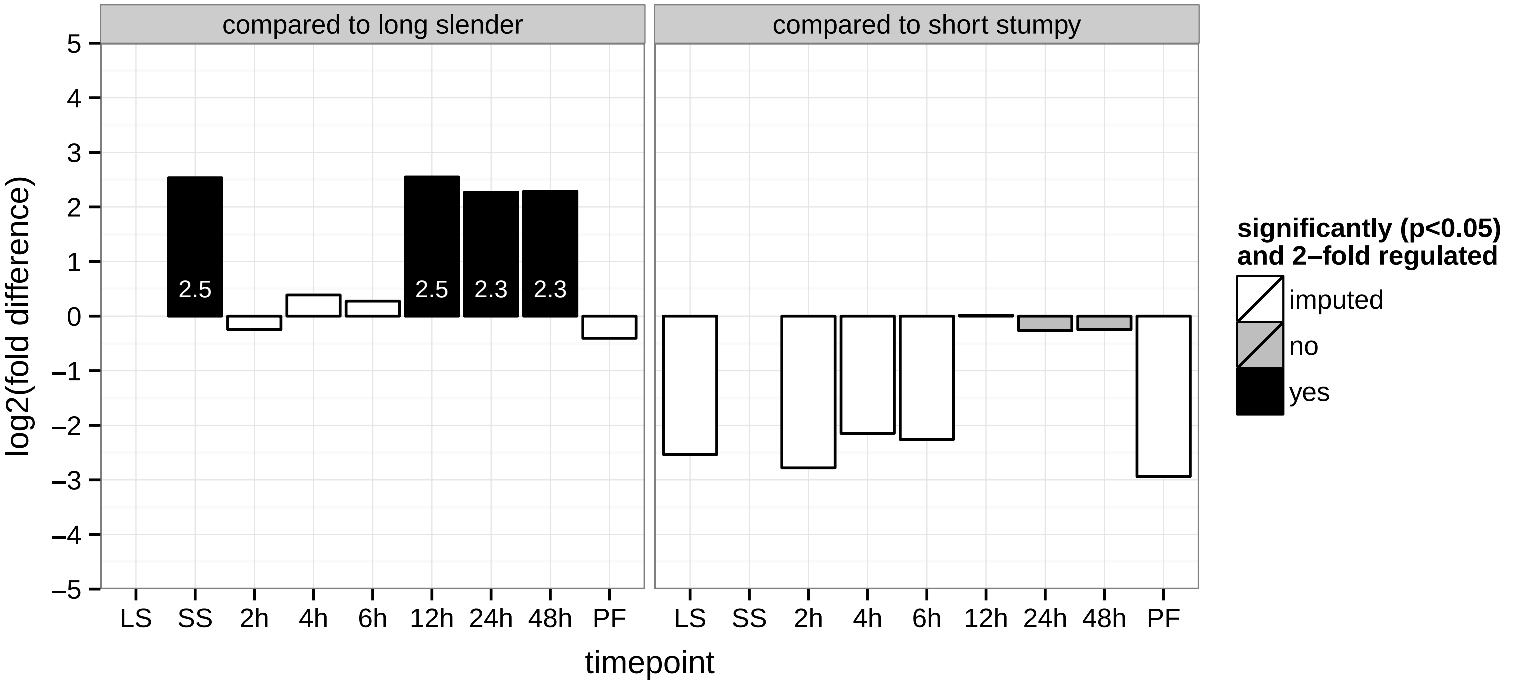
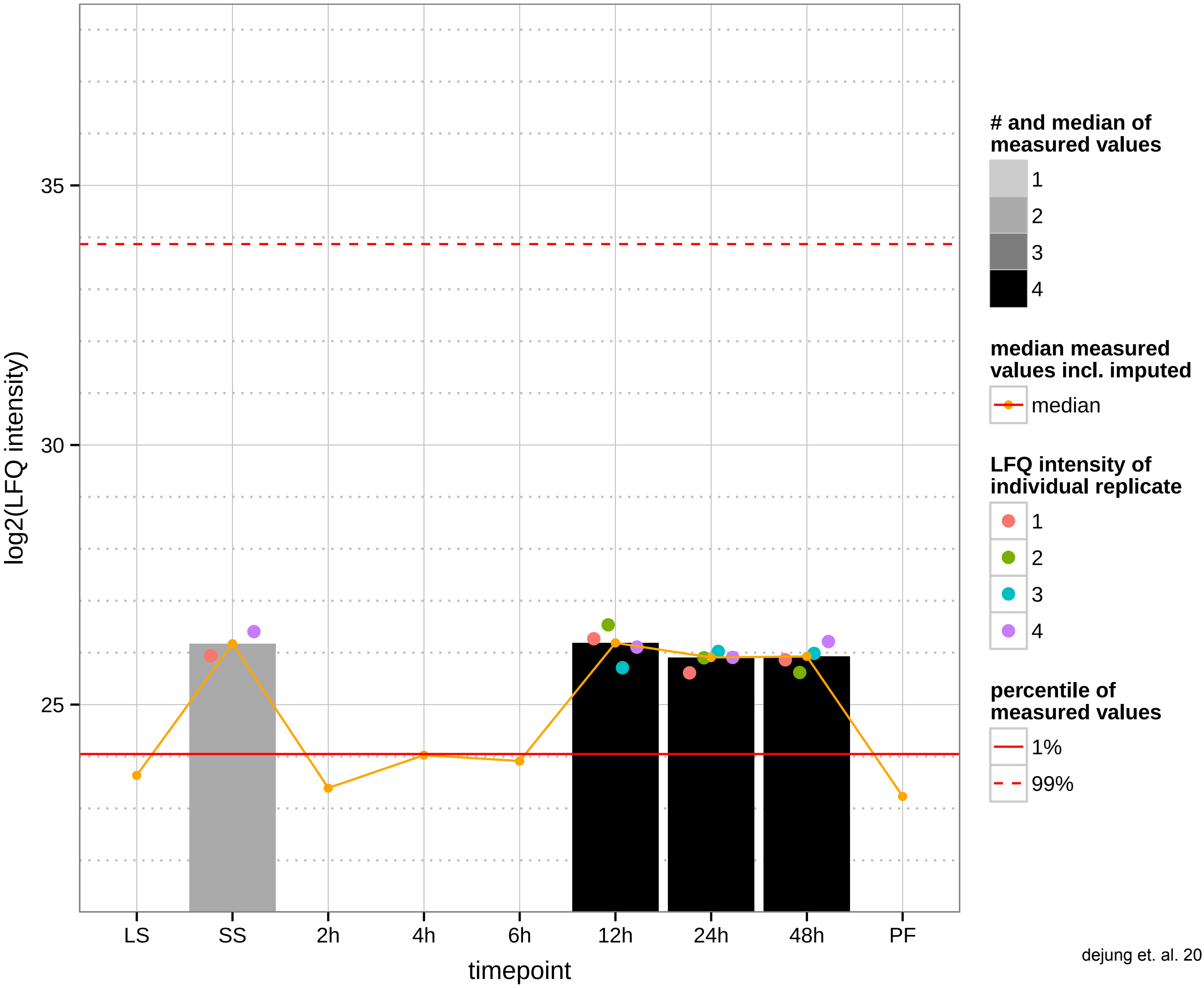
coatomer subunit zeta, putative
Tb927.10.4270
AGOF: null
AGOC: membrane coat
AGOP: intracellular protein transport, vesicle−mediated transport
PGOF: null
PGOC: null
PGOP: transport





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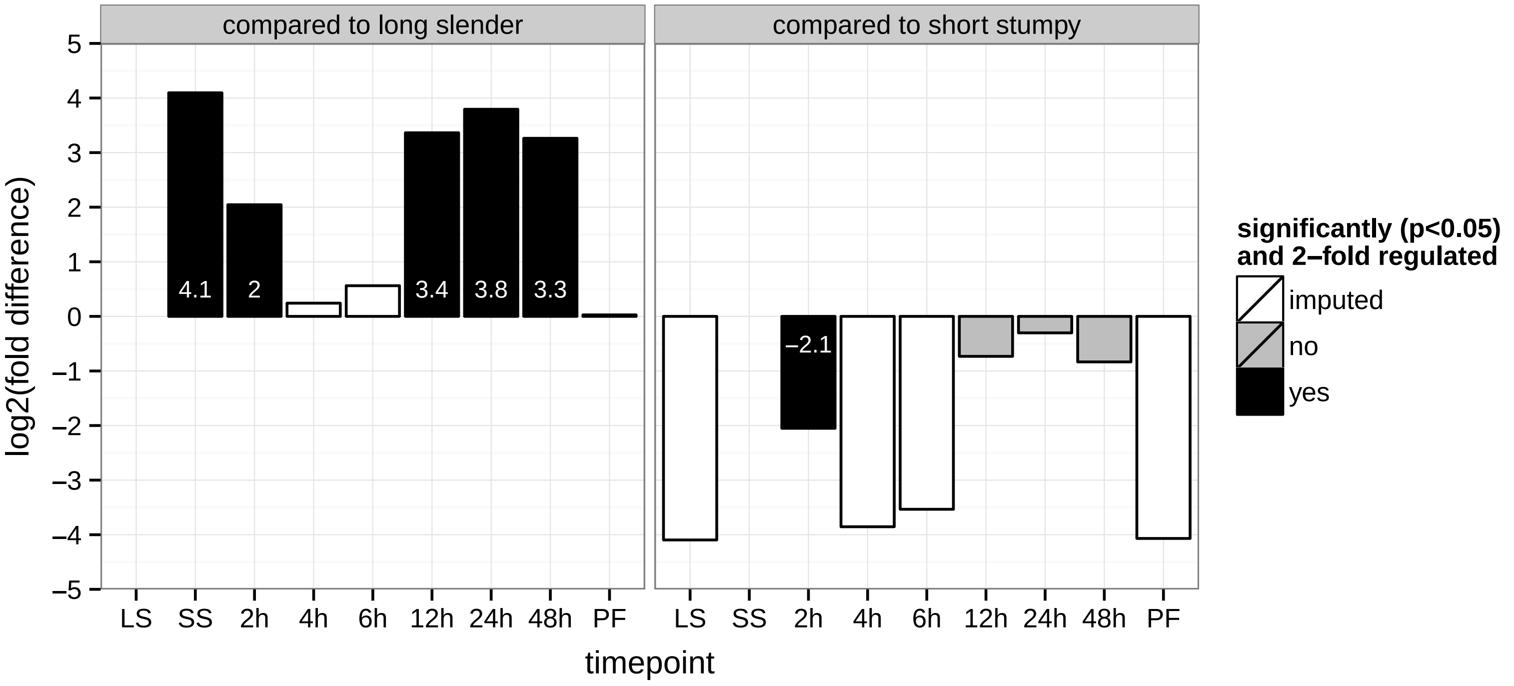
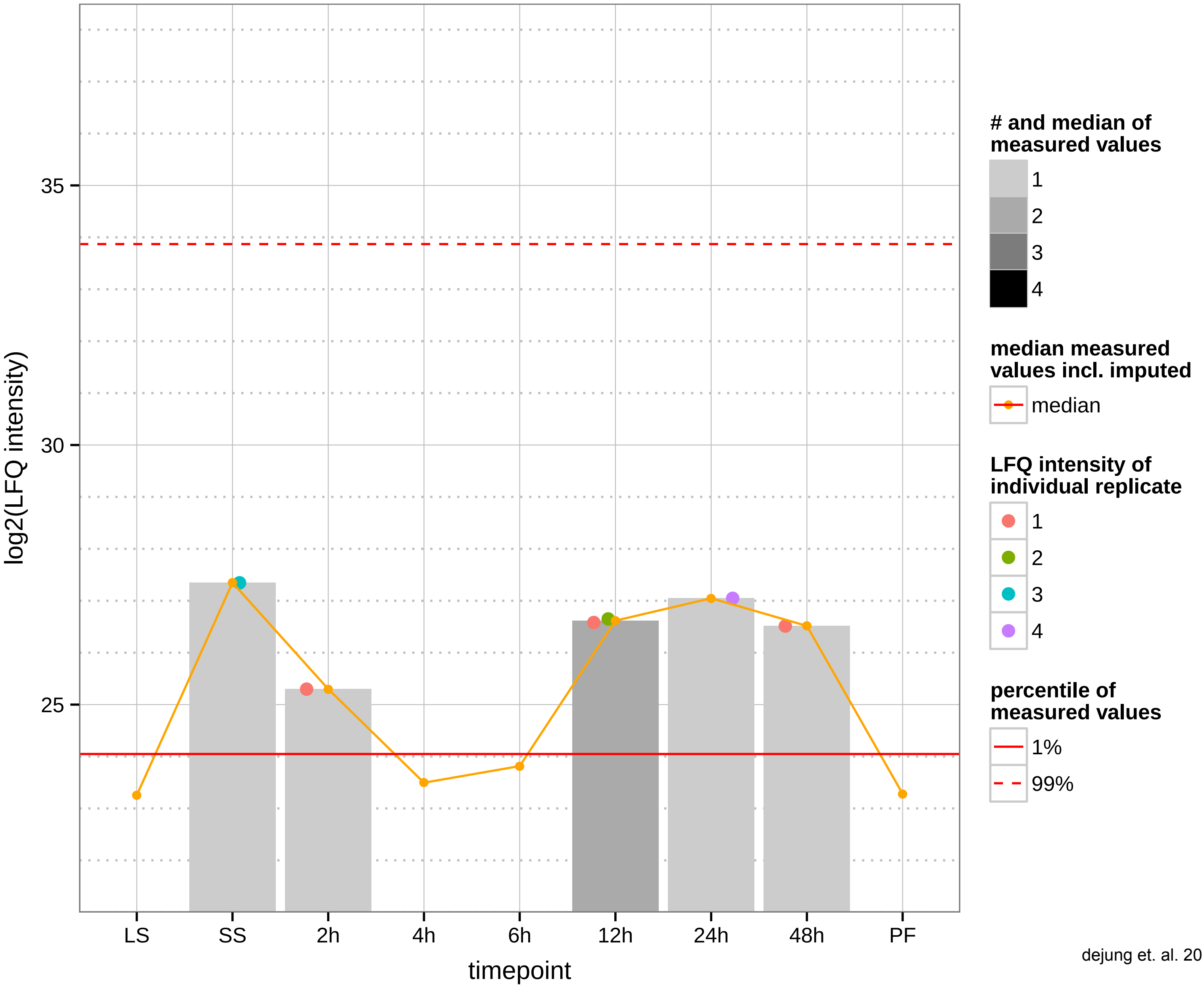
intergrin alpha chain protein, putative, FG−GAP repeat protein
Tb927.3.3640
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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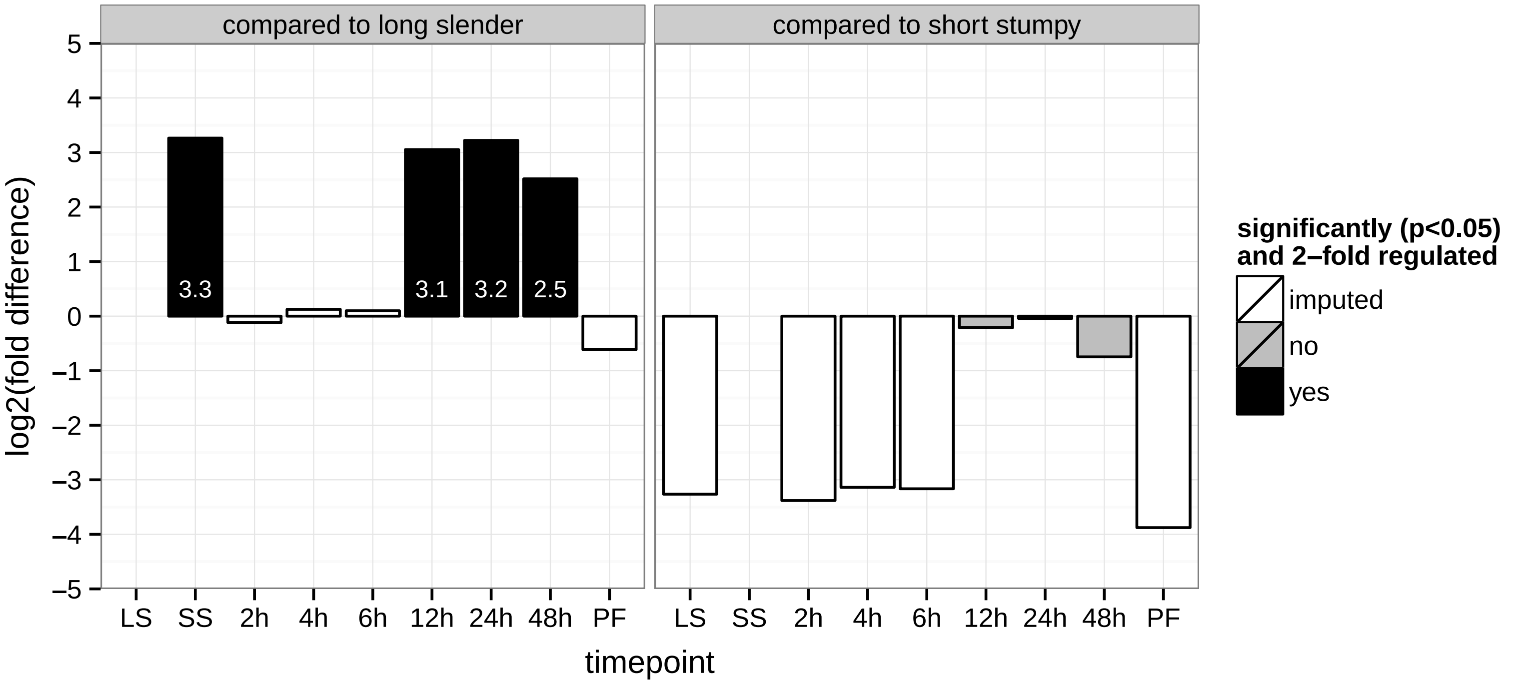
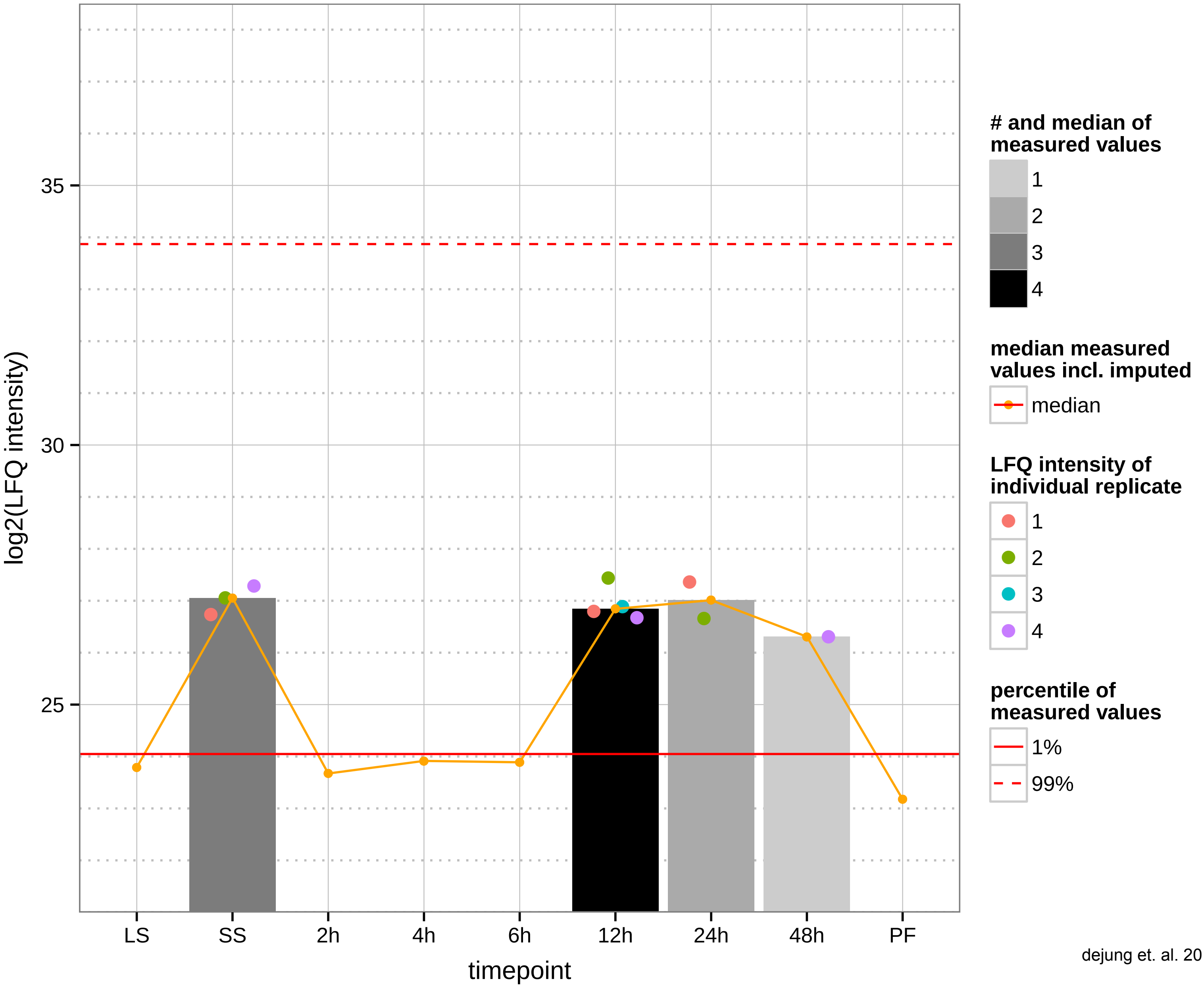
glycosyltransferase family 28 protein, putative
Tb927.6.1960
AGOF: carbohydrate binding, transferase activity, transferring hexosyl groups
AGOC: null
AGOP: carbohydrate metabolic process, lipid glycosylation
PGOF: carbohydrate binding, transferase activity, transferring hexosyl groups
PGOC: null
PGOP: carbohydrate metabolic process, lipid glycosylation





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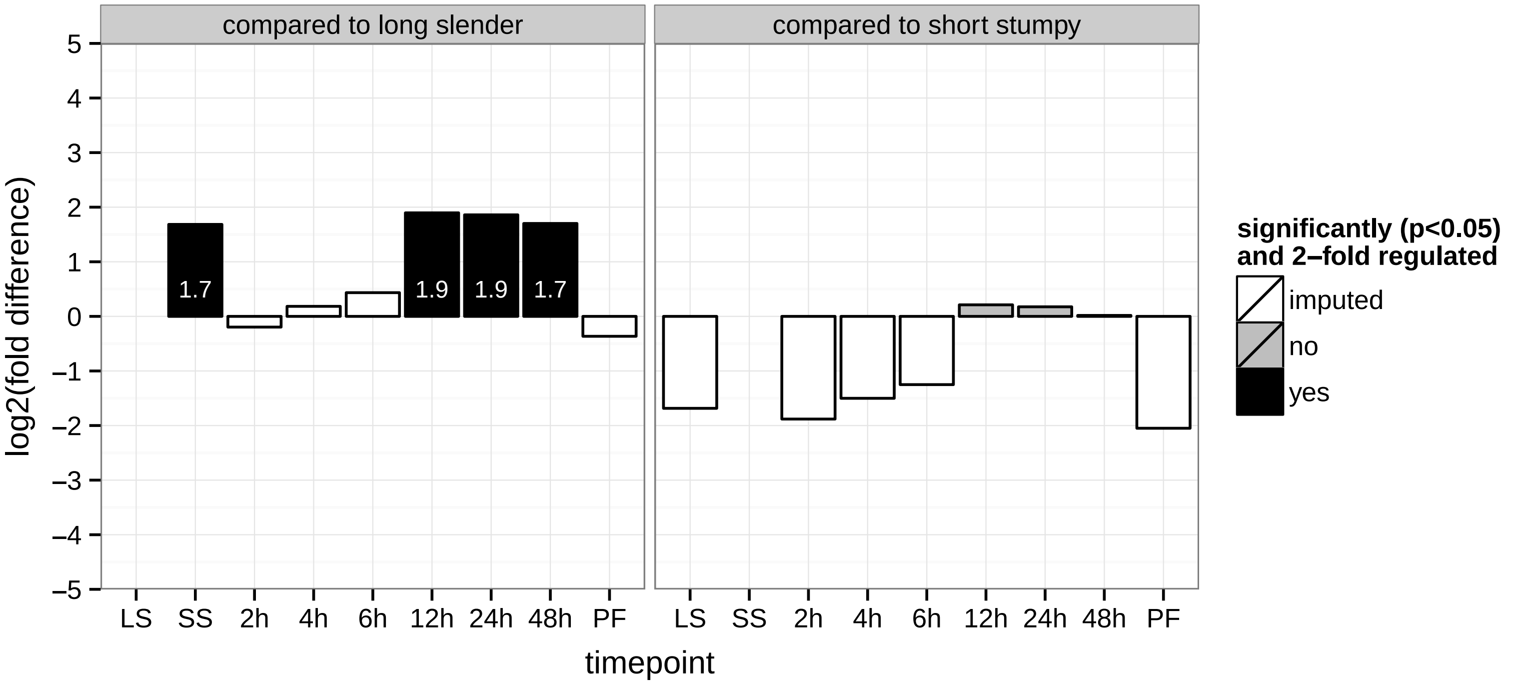
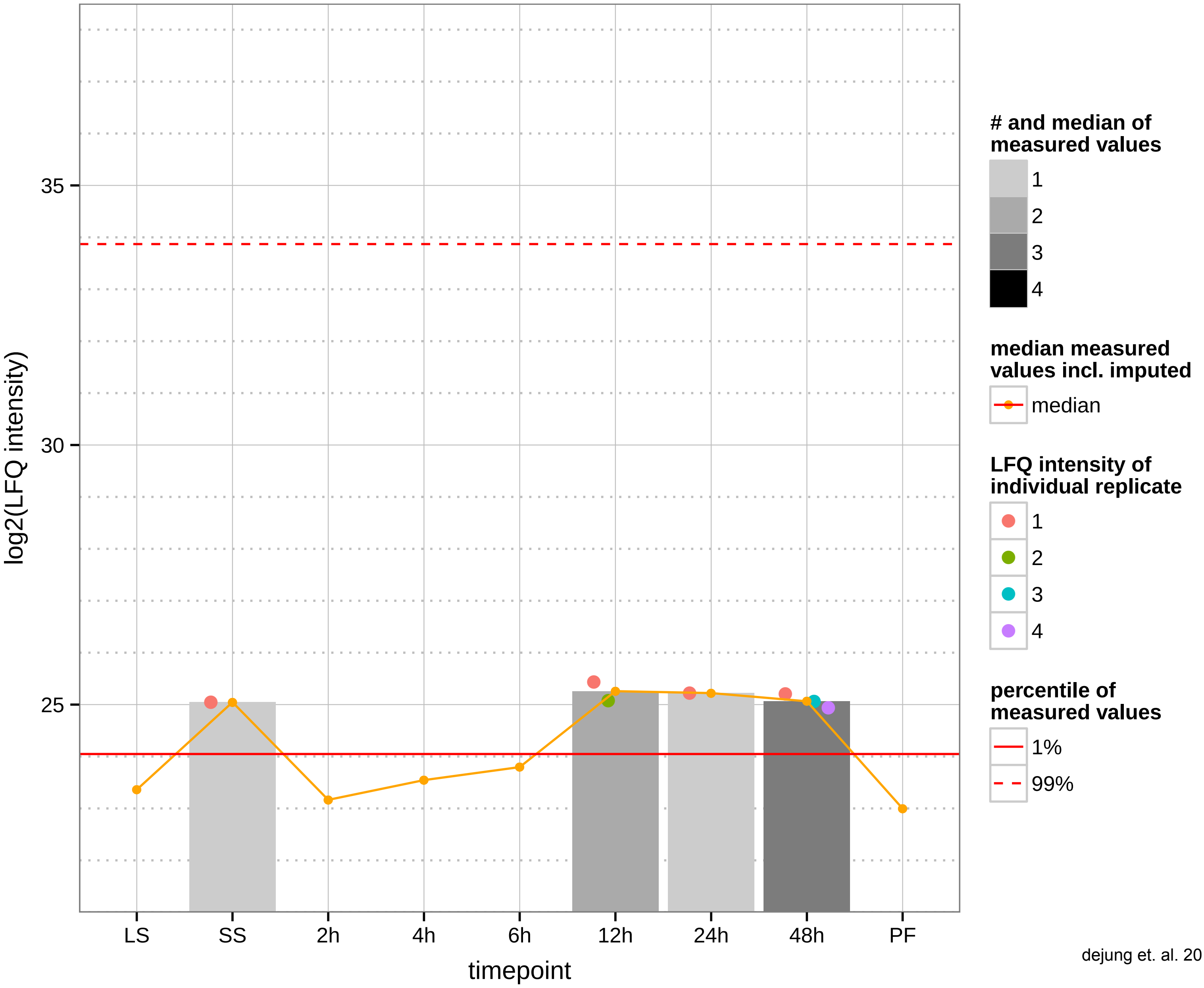
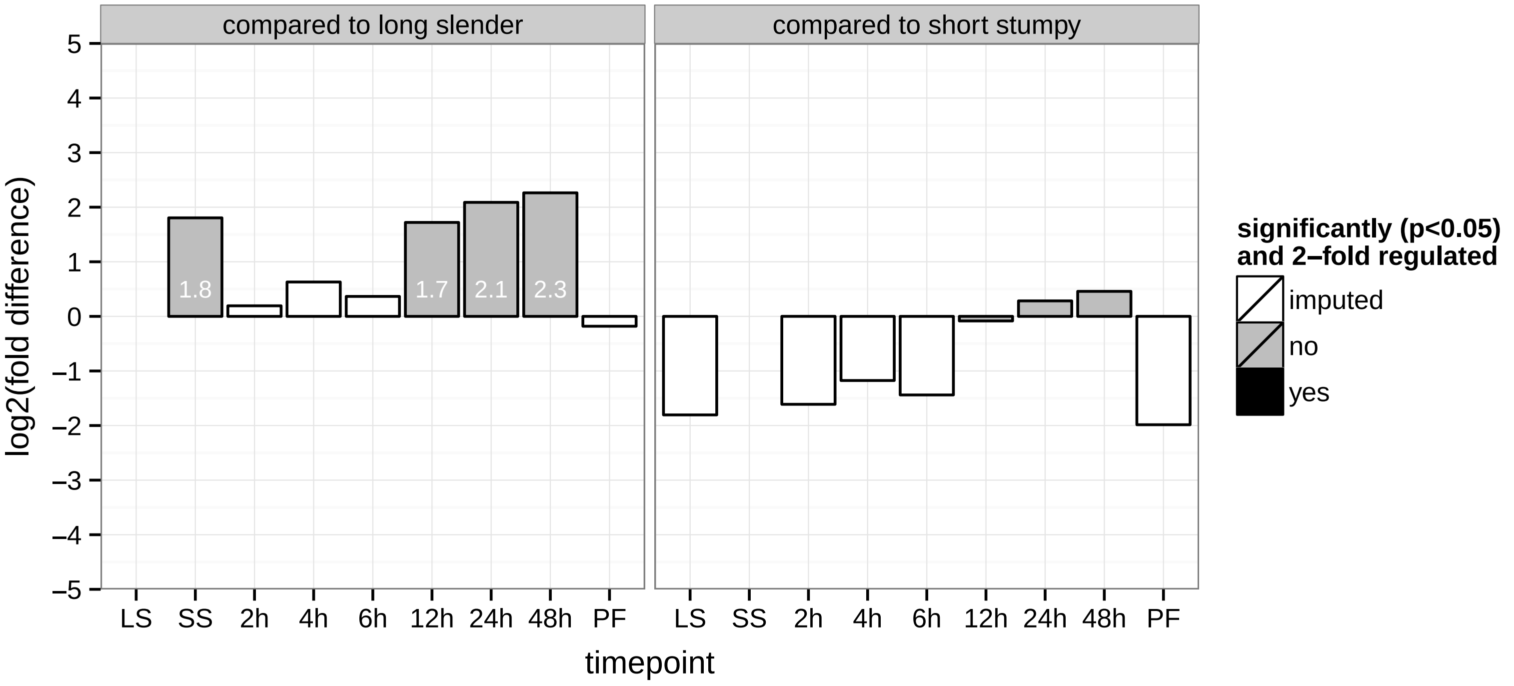
intergrin alpha chain protein, putative, FG−GAP repeat protein
Tb927.6.2020
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null

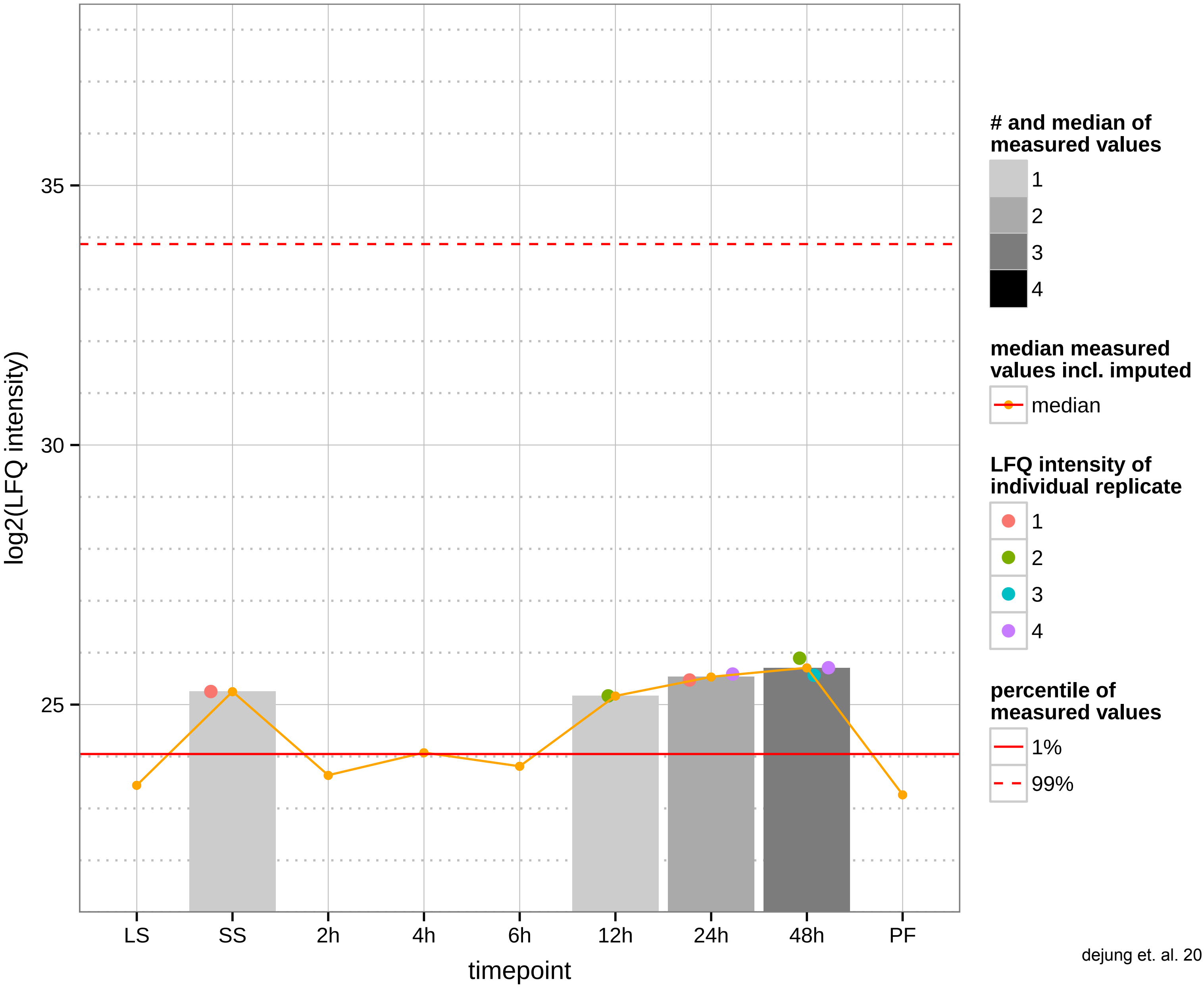




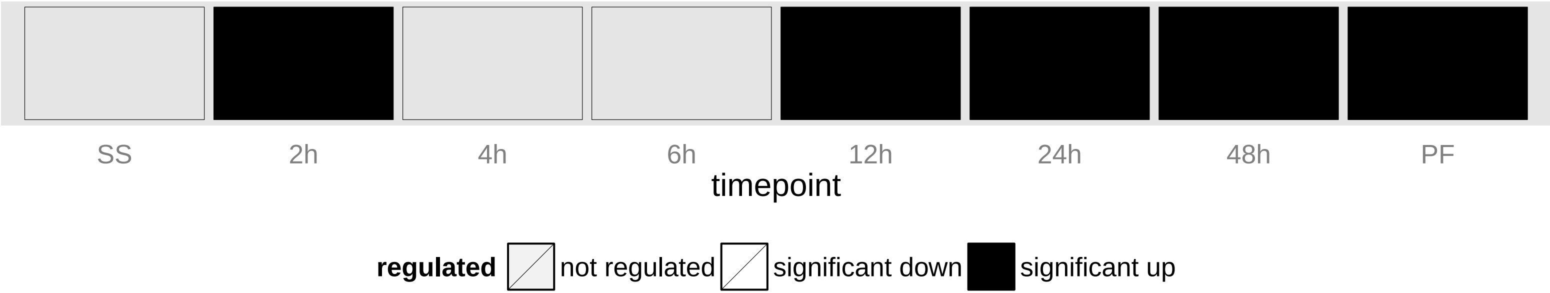
dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.2040
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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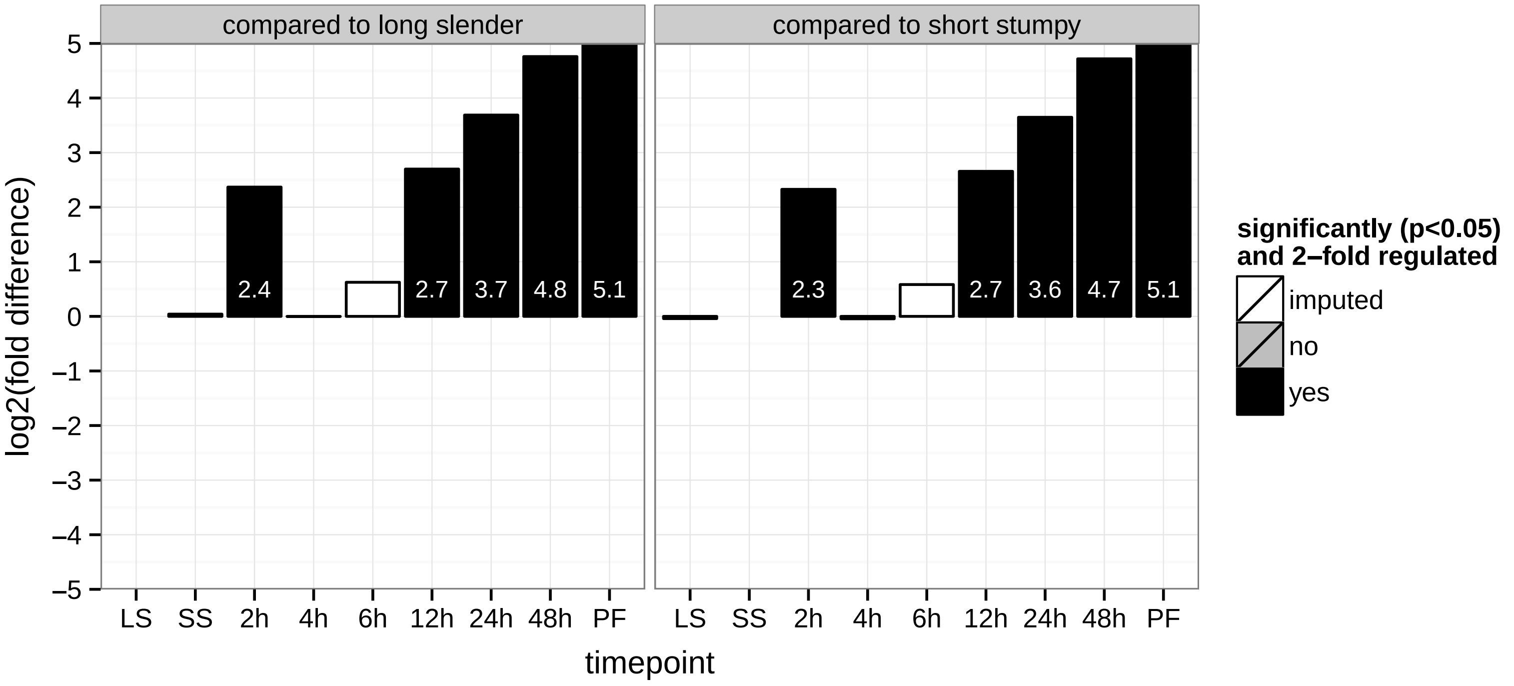
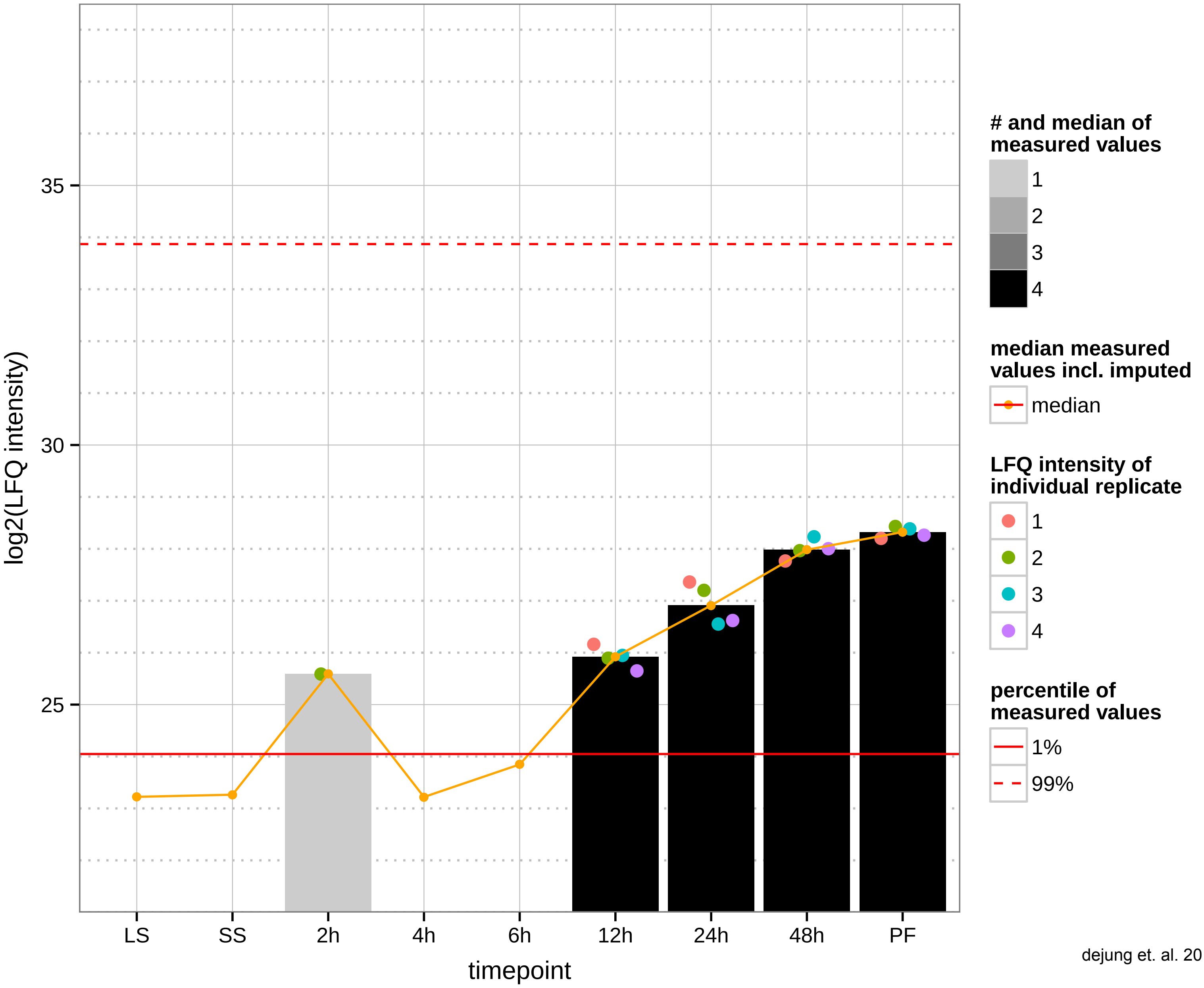
beta–D–hydroxybutyrate dehydrogenase
Tb927.10.11930
AGOF: 3–hydroxybutyrate dehydrogenase activity
AGOC: mitochondrion
AGOP: ketone body biosynthetic process
PGOF: 3–hydroxybutyrate dehydrogenase activity, oxidoreductase activity
PGOC: null
PGOP: metabolic process, oxidation–reduction process





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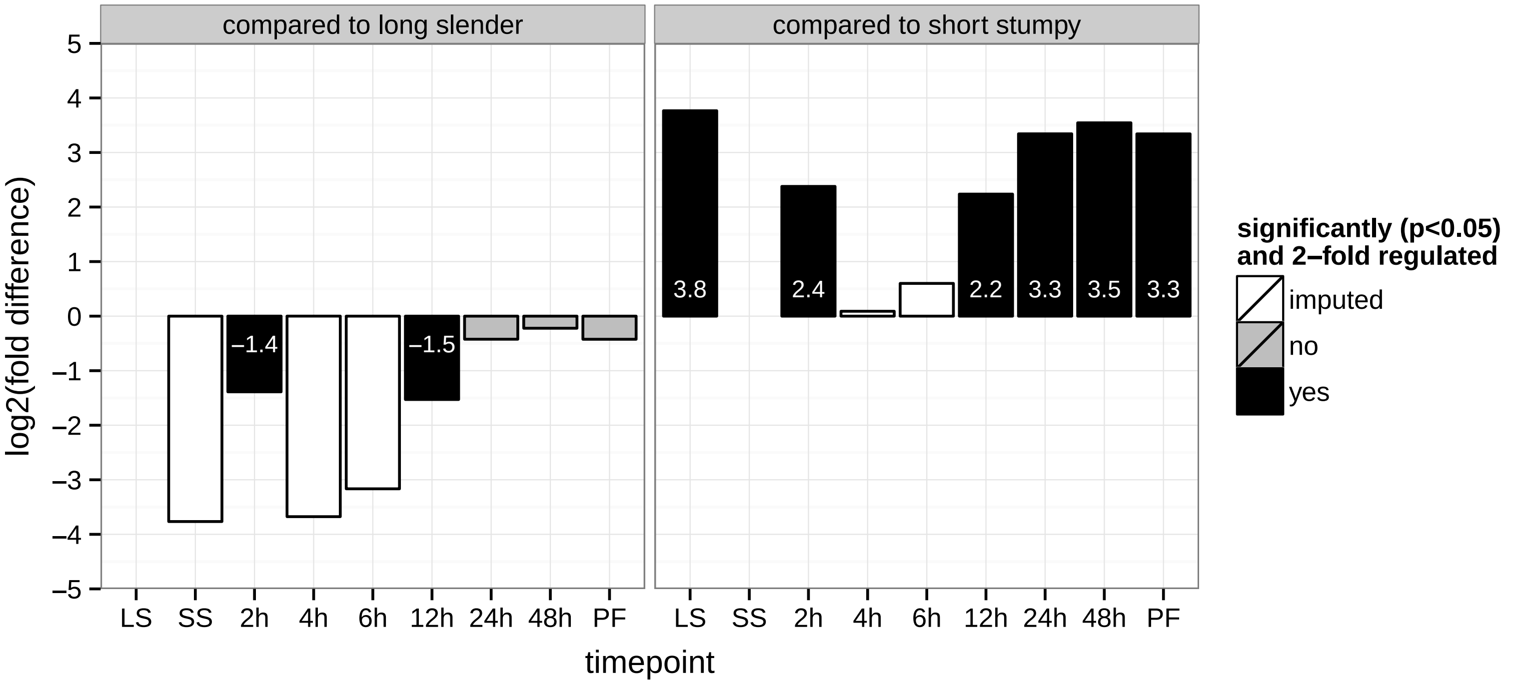
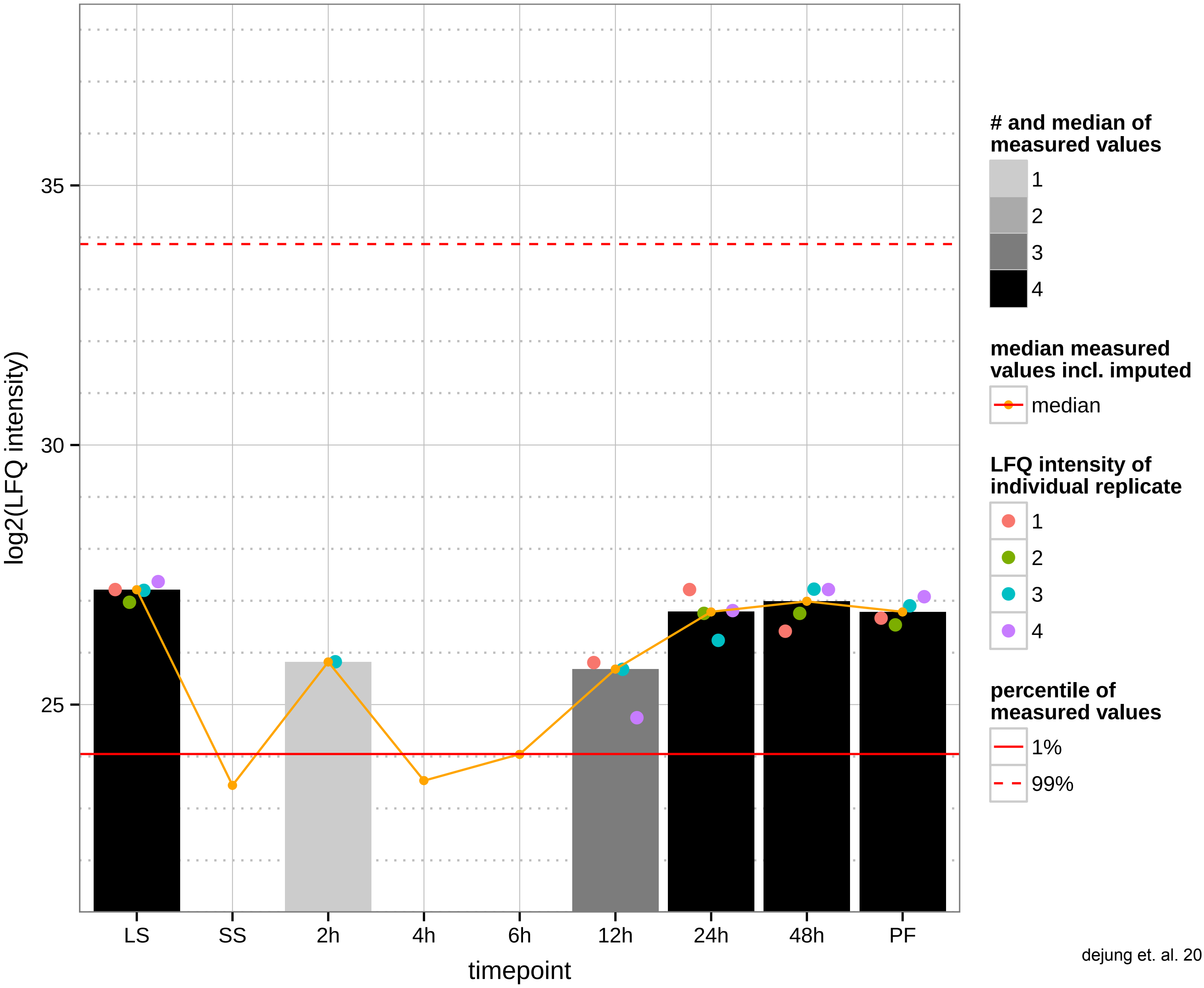
hypothetical protein, conserved
Tb927.11.14750
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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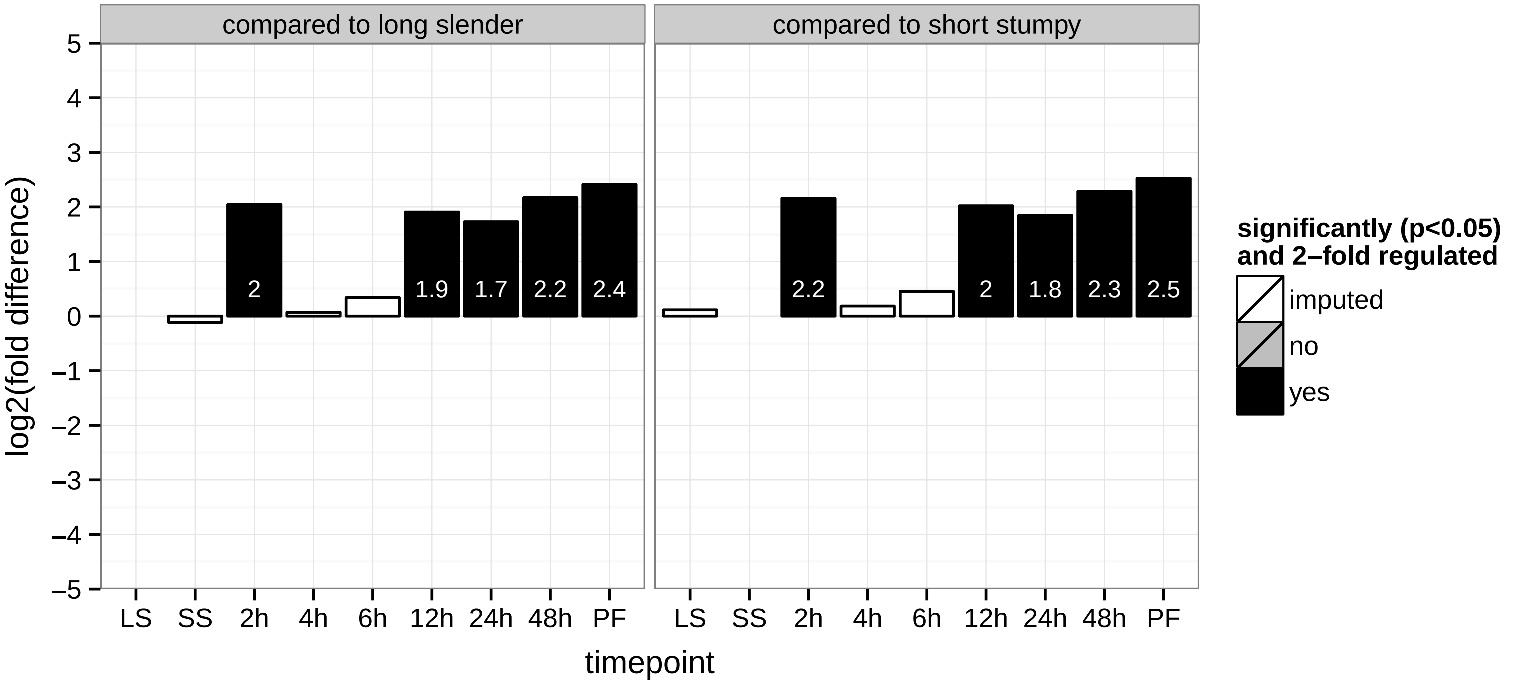
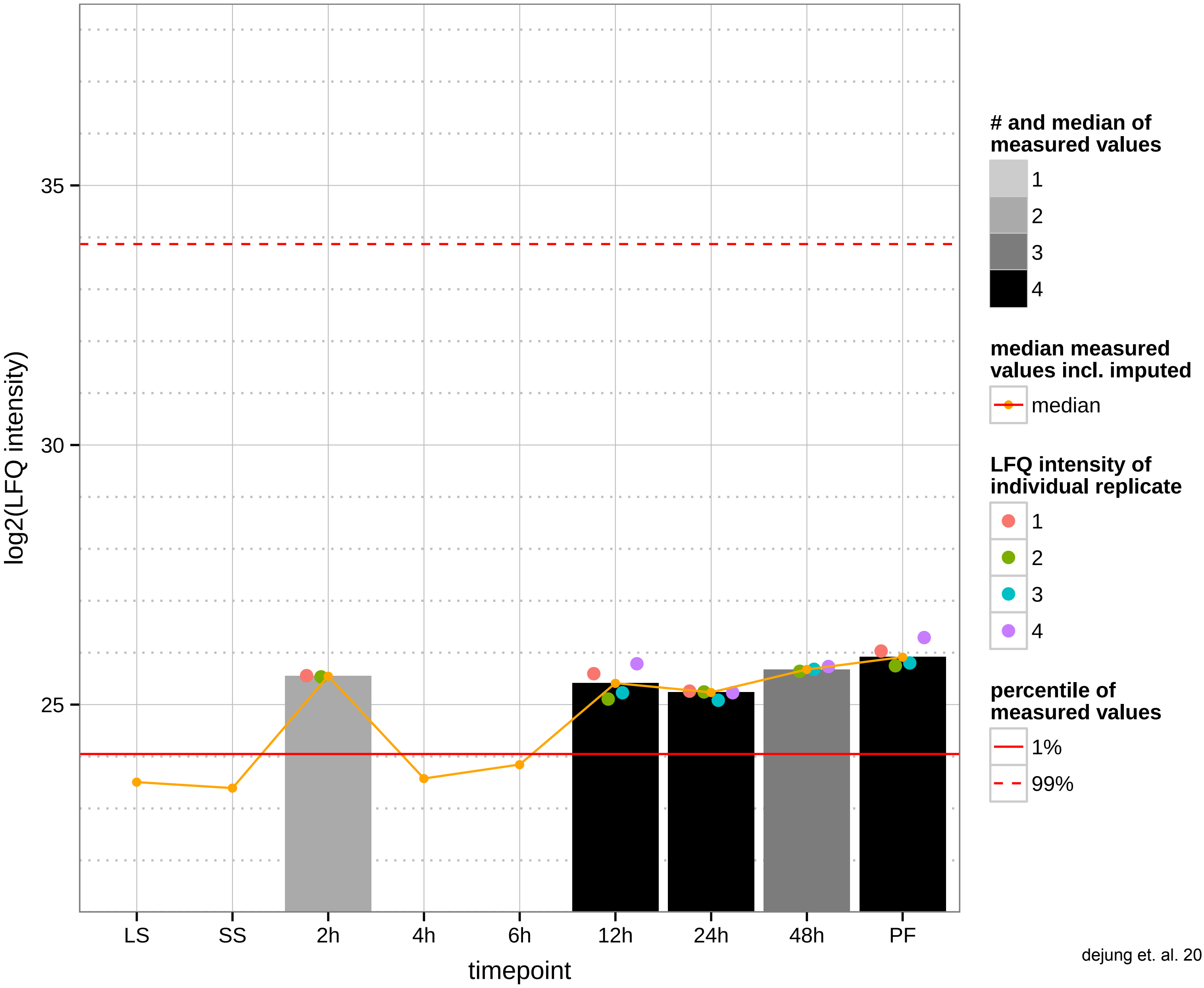
hypothetical protein, conserved
Tb927.5.530
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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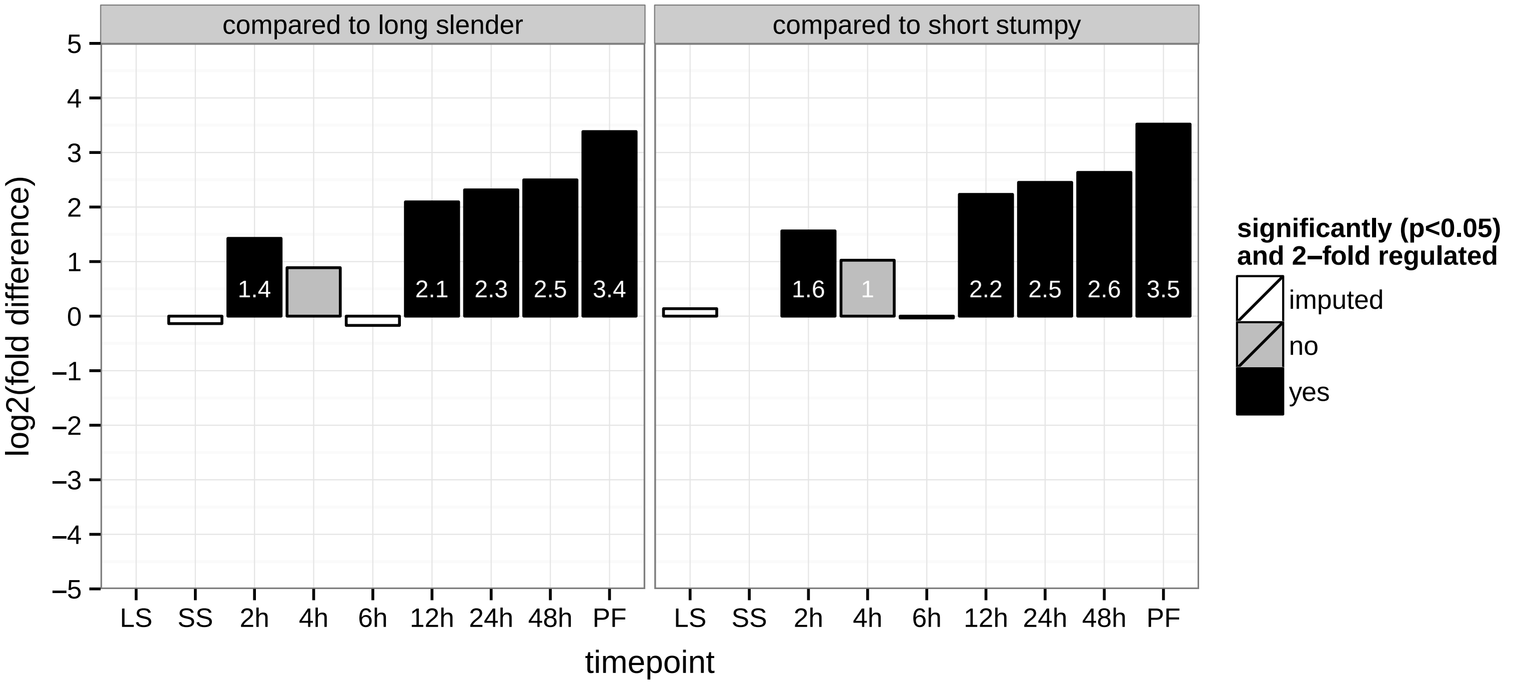
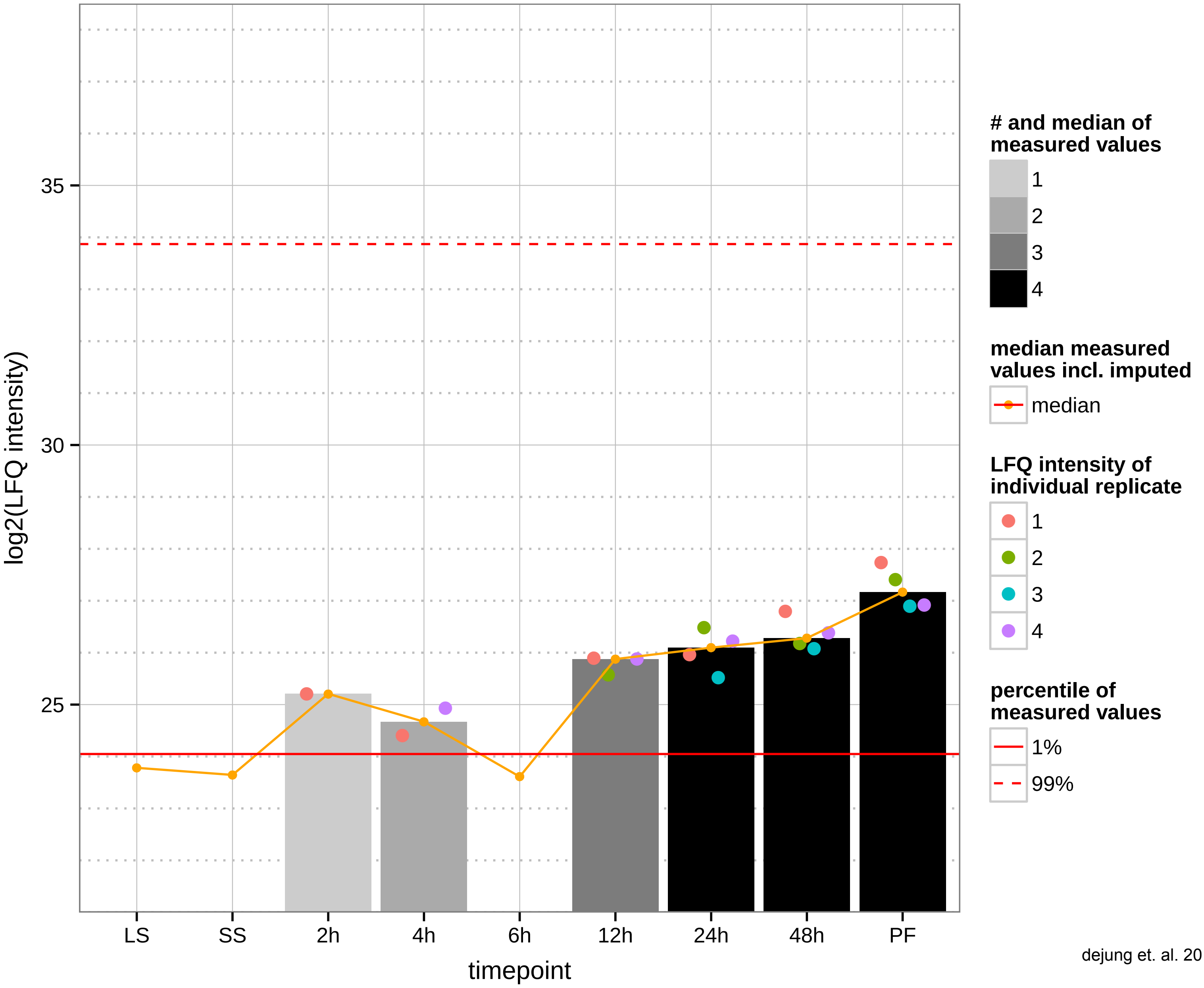
ribosomal RNA adenine dimethylase family protein, conserved
Tb927.6.1610
AGOF: rRNA (adenine–N6, N6–)–dimethyltransferase activity
AGOC: null
AGOP: rRNA modification
PGOF: rRNA (adenine) methyltransferase activity, rRNA (adenine–N6, N6–)–dimethyltransferase activity, rRNA methyltransfer
PGOC: null
PGOP: rRNA modification, rRNA processing





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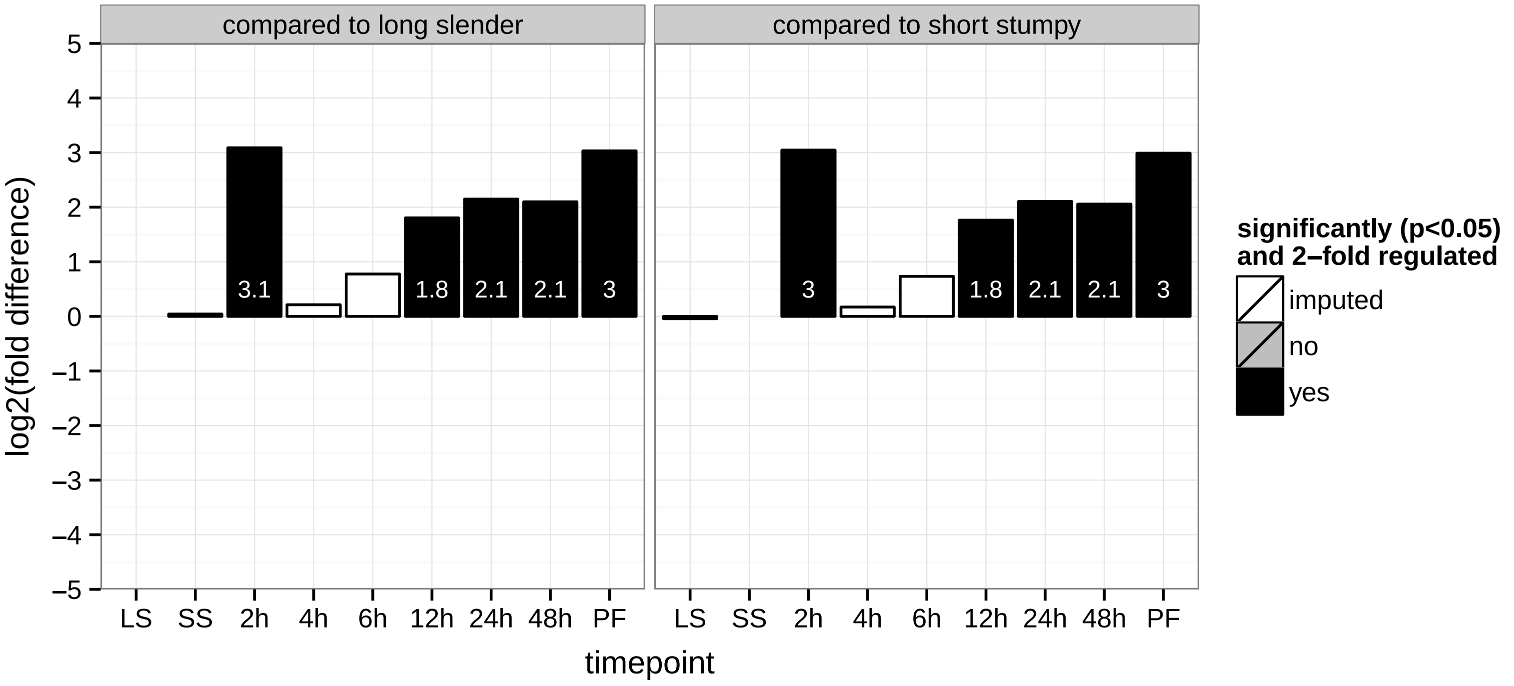
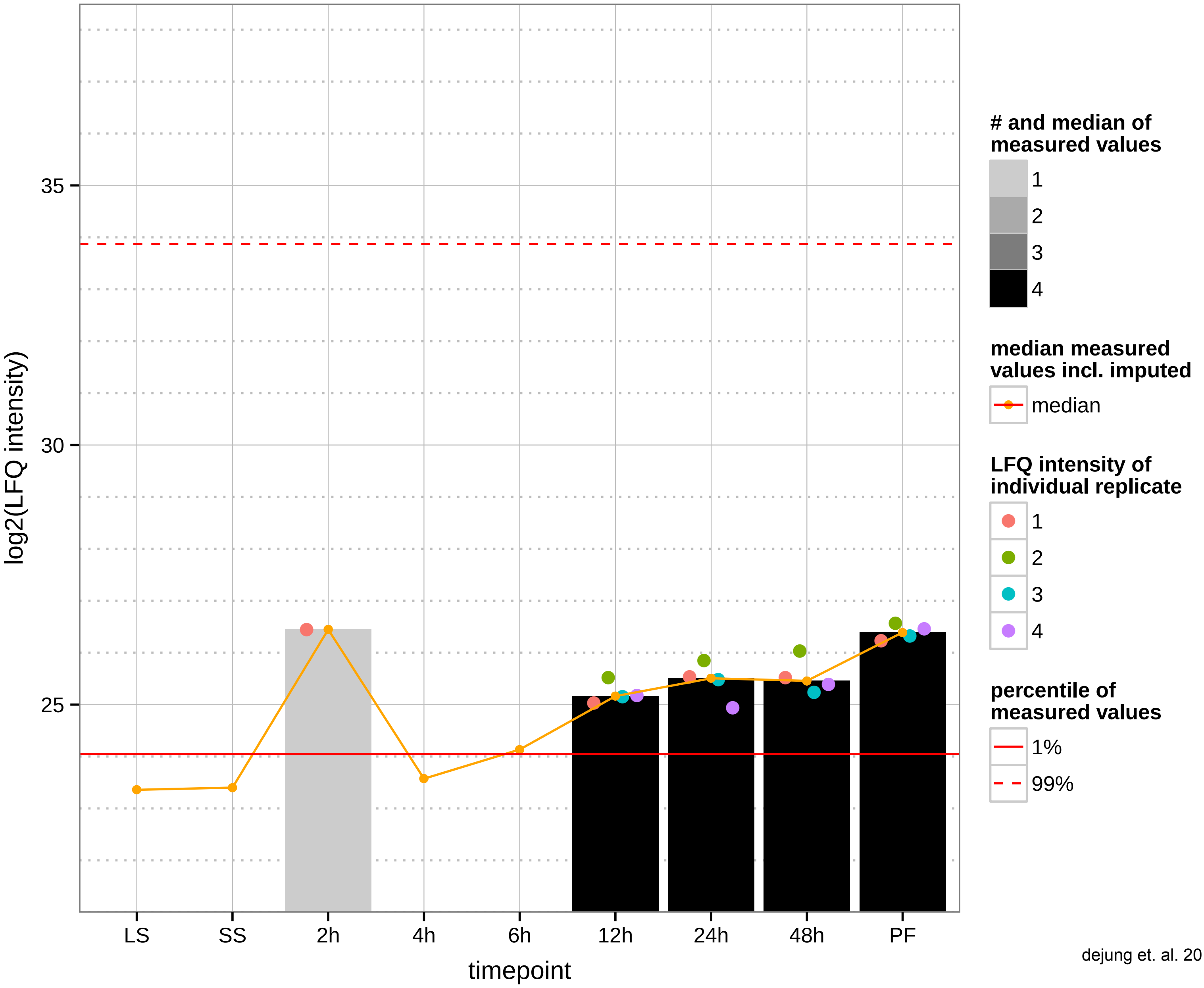
hypothetical protein, conserved
Tb927.7.4710
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: hydrolase activity
PGOC: null
PGOP: null





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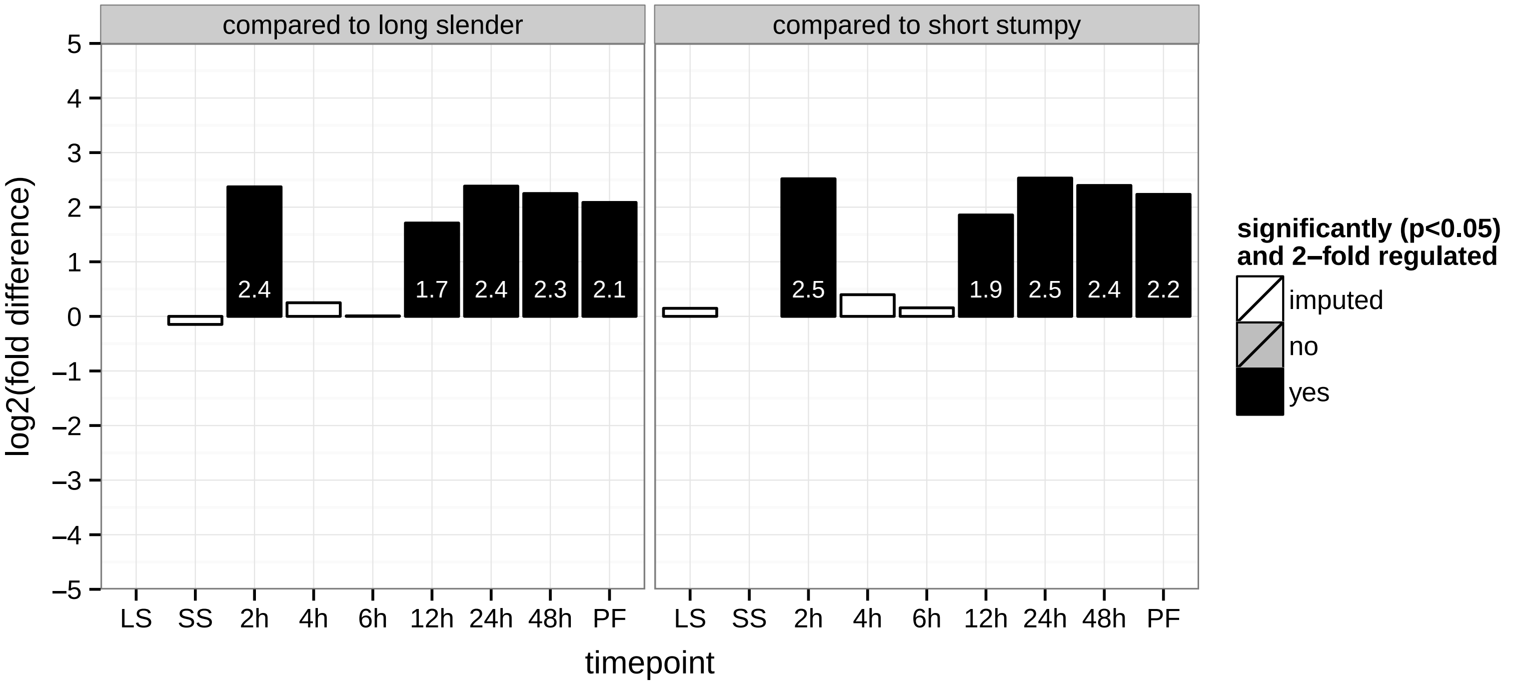
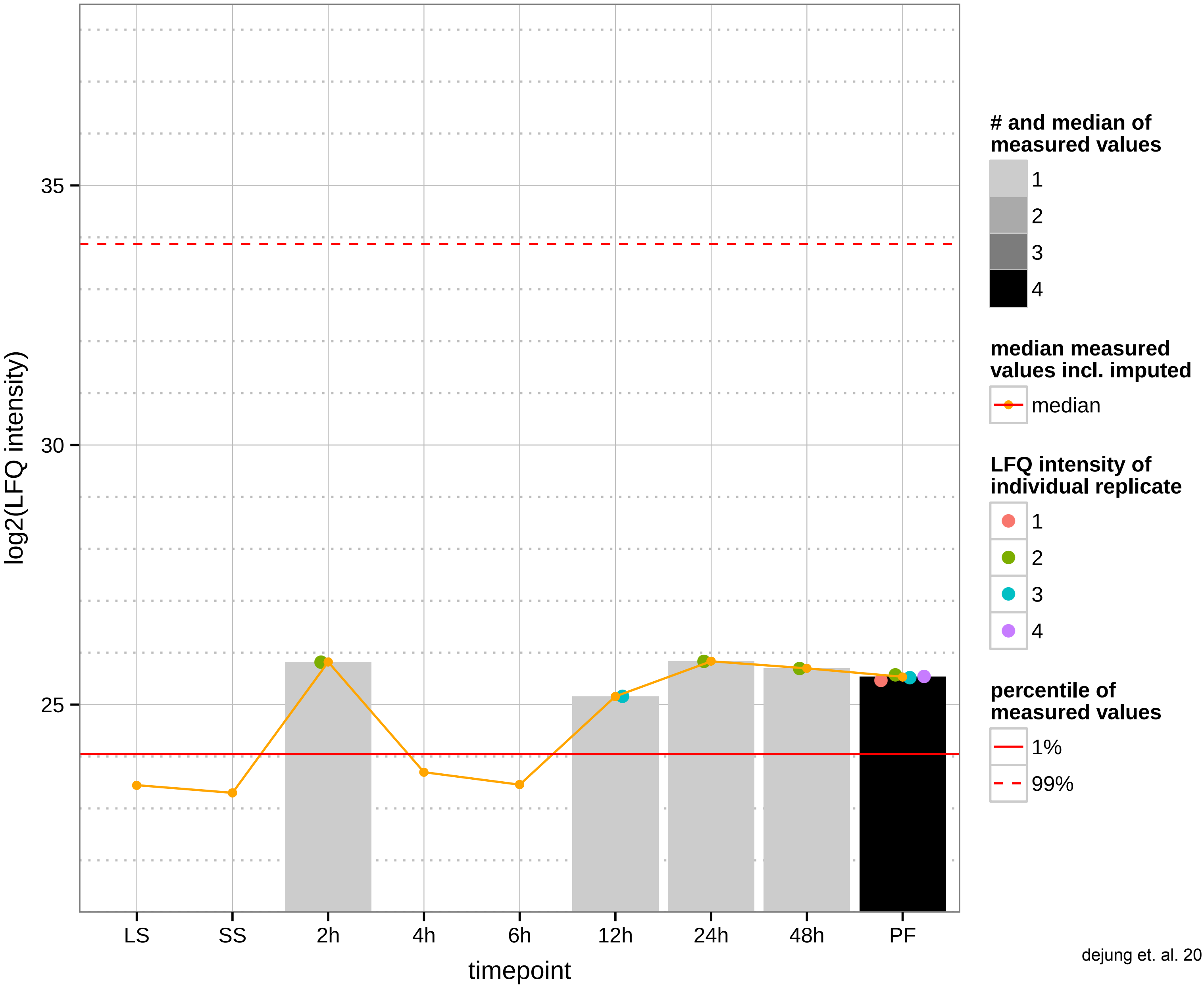
KREPA3, RNA−editing complex protein MP42 (KREPA3)
Tb927.8.620
AGOF: 3'−5'−exoribonuclease activity, endoribonuclease activity, producing 5'−phosphomonoesters, zinc ion binding
AGOC: intracellular, mitochondrial mRNA editing complex, mitochondrion
AGOP: mRNA modification, response to metal ion
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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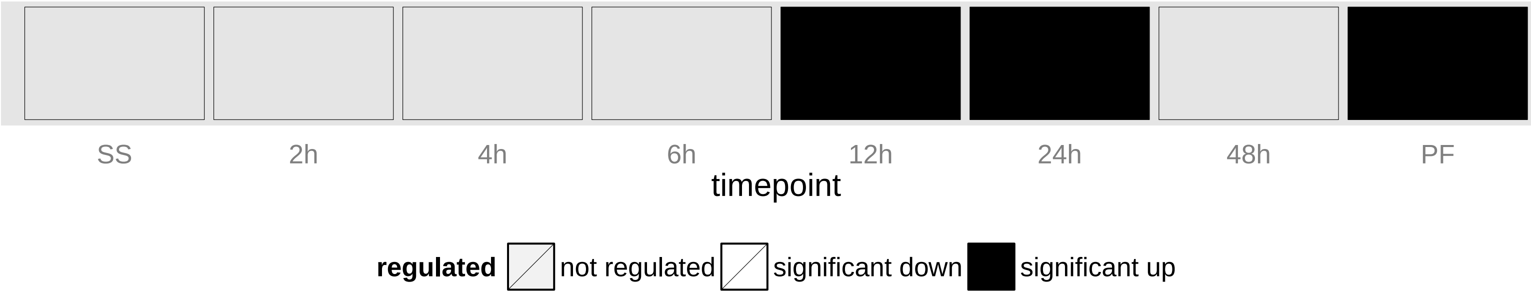

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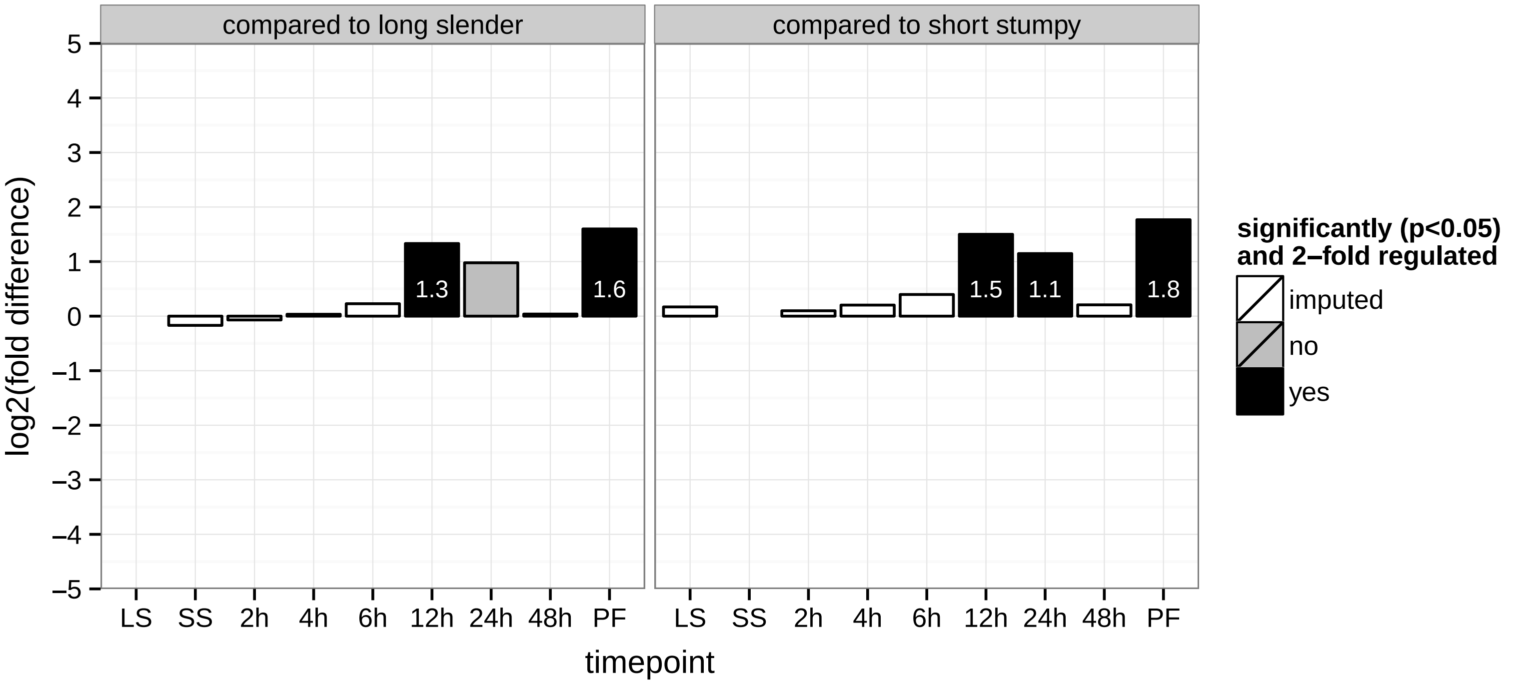
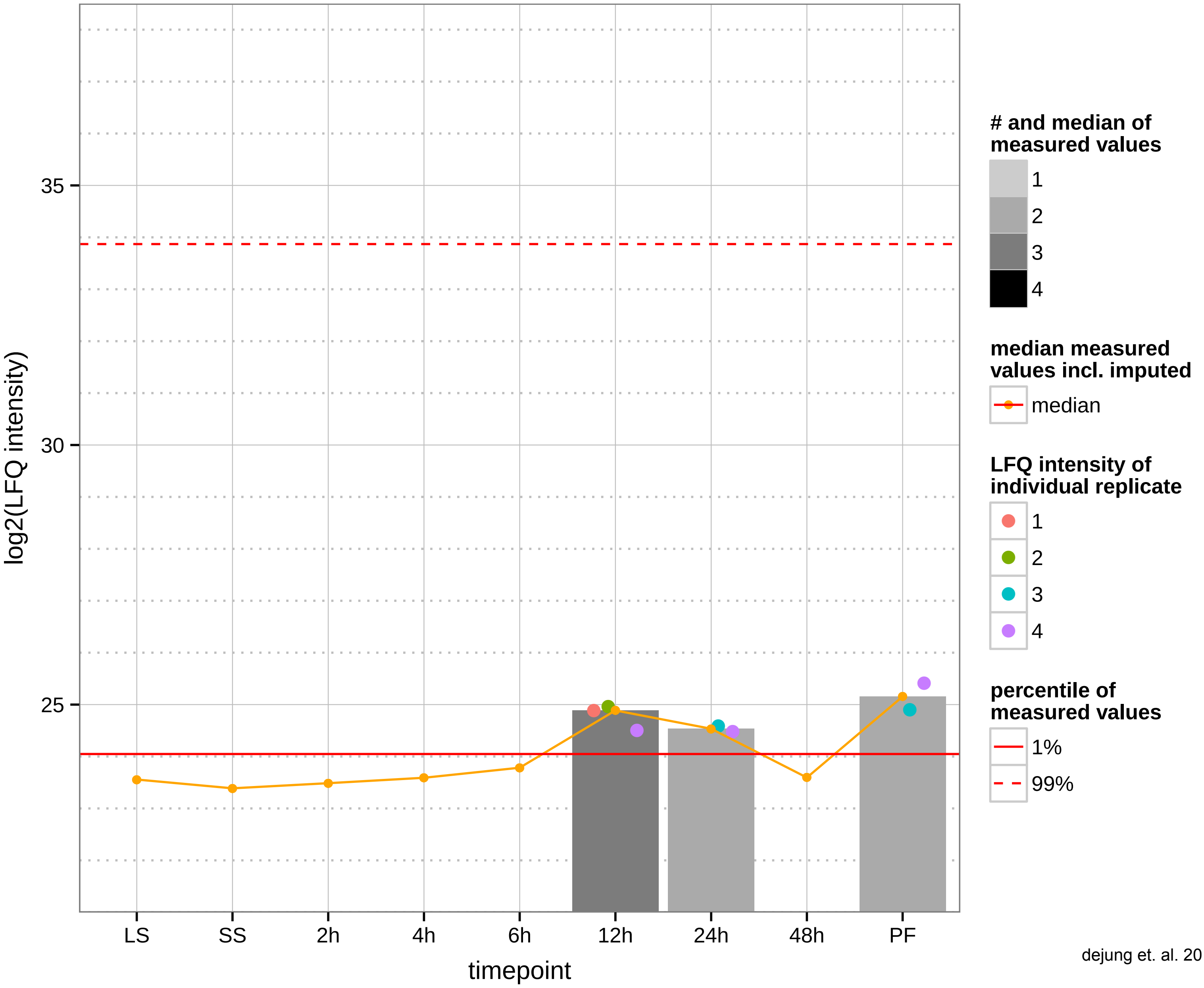
septum formation protein MAF homologue, putative
Tb927.1.3280
AGOF: null
AGOC: cytoplasm
AGOP: null
PGOF: null
PGOC: cytoplasm
PGOP: null





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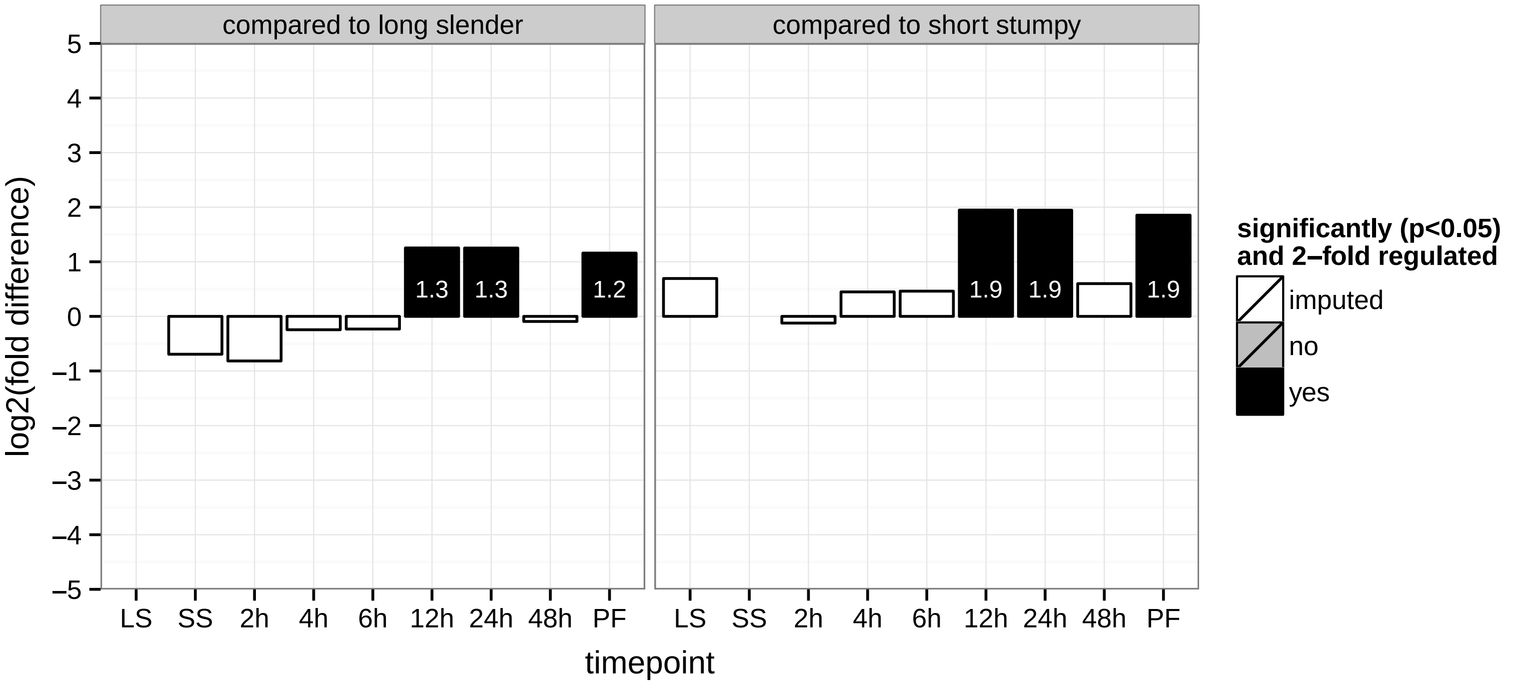
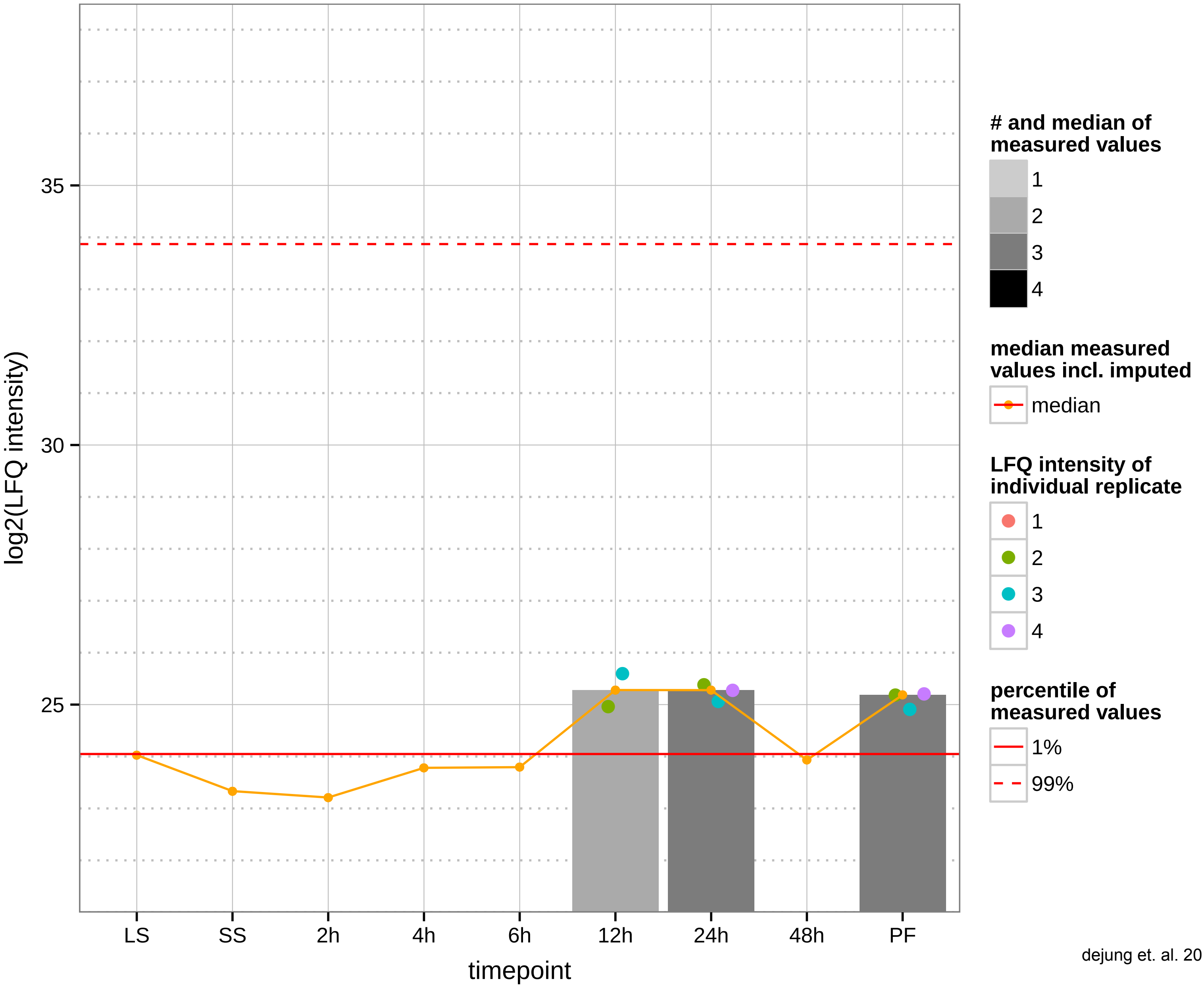
cullin, putative
Tb927.10.7490
AGOF: ubiquitin protein ligase binding
AGOC: cullin–RING ubiquitin ligase complex
AGOP: cell cycle, ubiquitin–dependent protein catabolic process
PGOF: ubiquitin protein ligase binding
PGOC: cullin–RING ubiquitin ligase complex
PGOP: ubiquitin–dependent protein catabolic process





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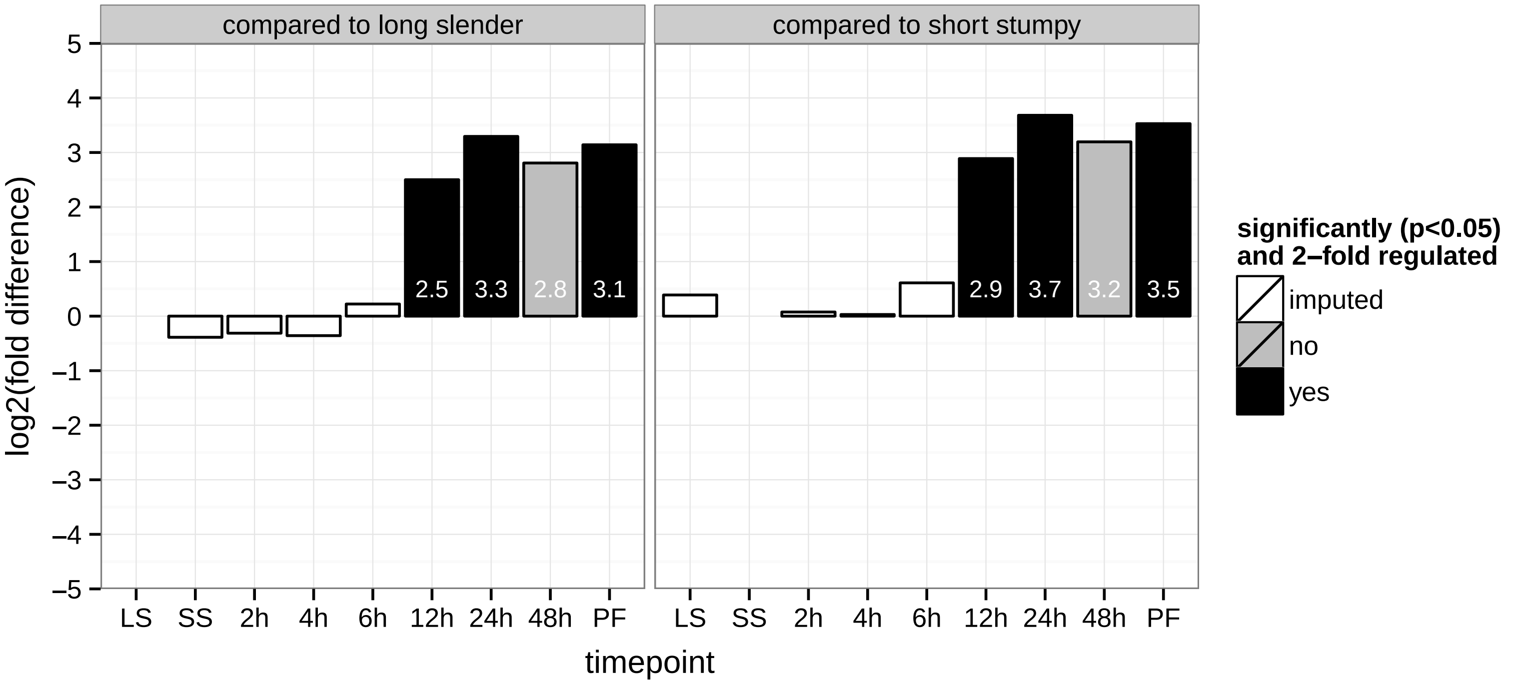
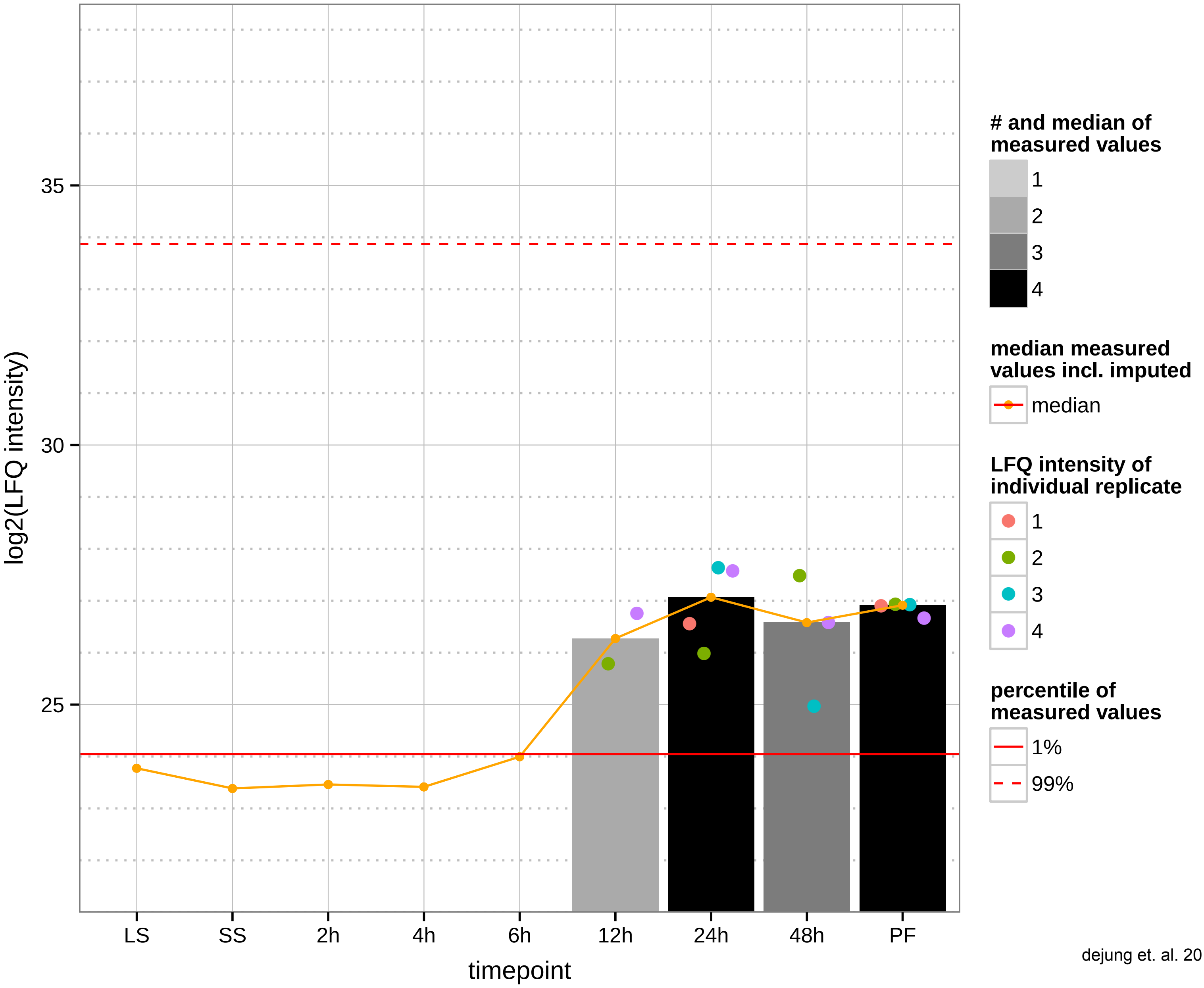
hypothetical protein, conserved
Tb927.11.15080
AGOF: null
AGOC: membrane
AGOP: null
PGOF: null
PGOC: membrane
PGOP: null





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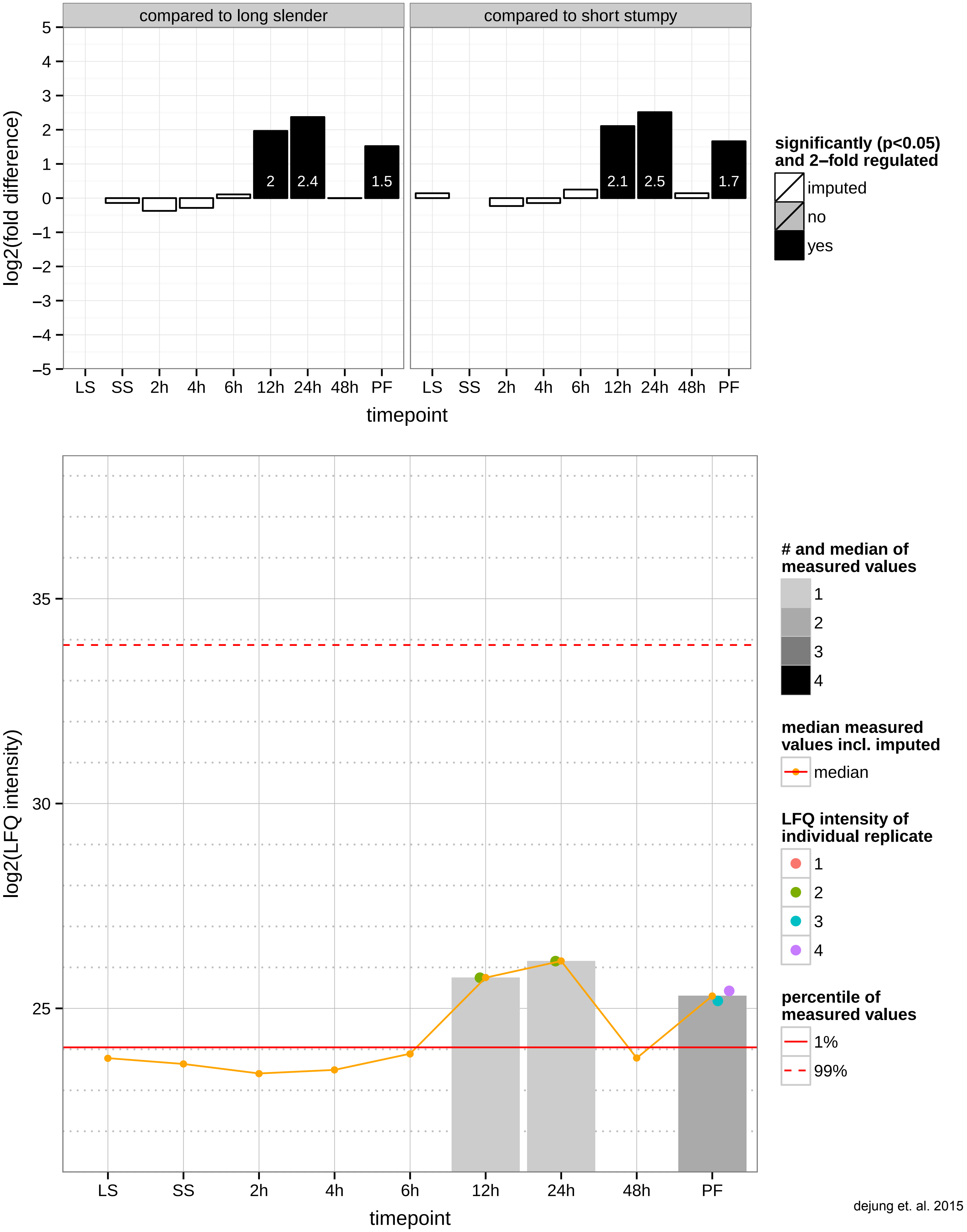
hypothetical protein, conserved
Tb927.8.4690
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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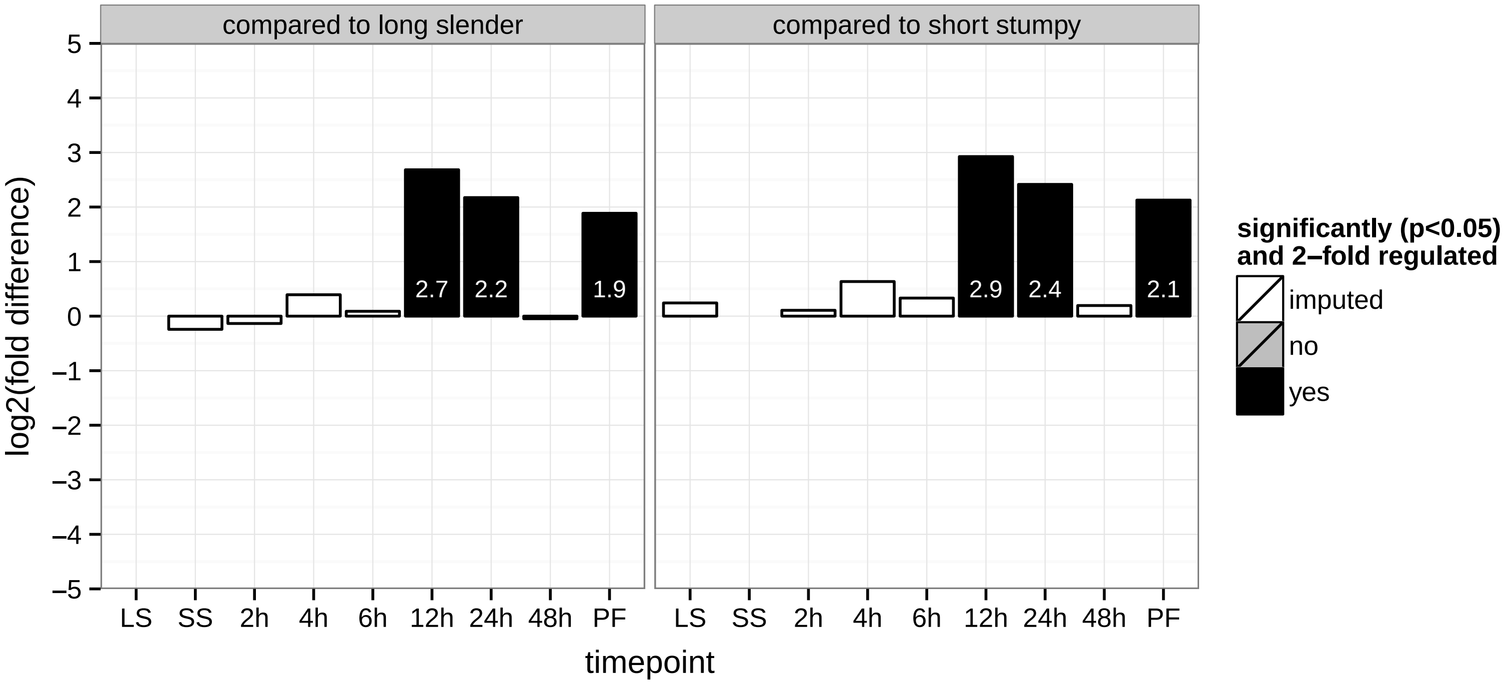
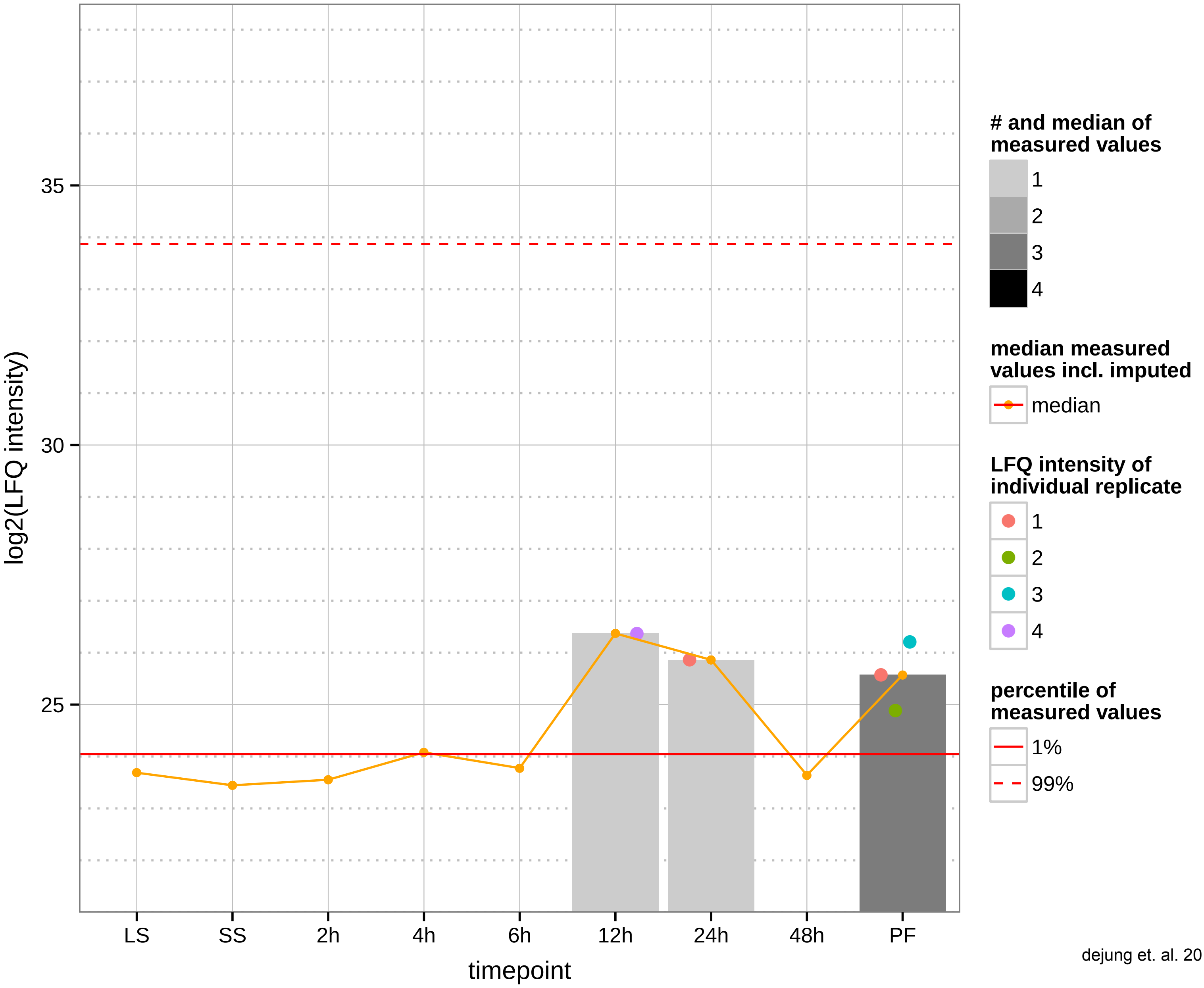
flavoprotein monooxygenase, putative
Tb927.9.6710
AGOF: monooxygenase activity
AGOC: mitochondrion
AGOP: cellular aromatic compound metabolic process
PGOF: null
PGOC: null
PGOP: null





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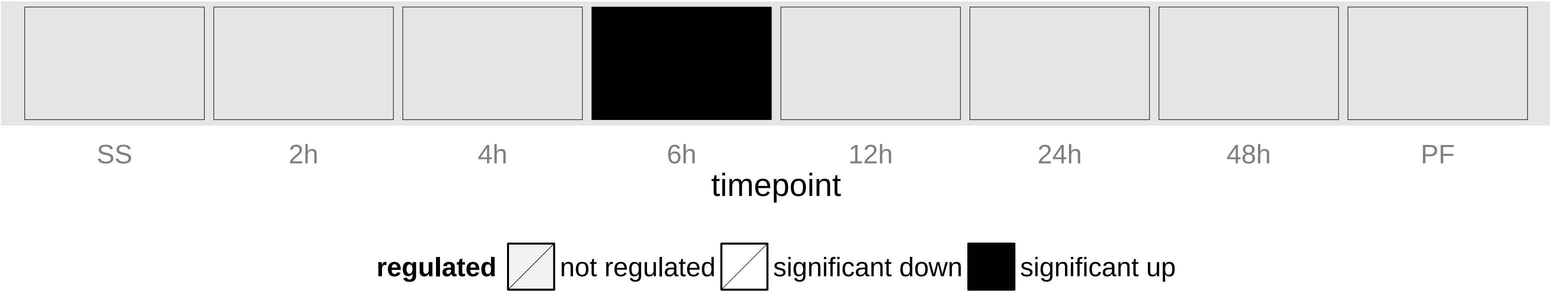

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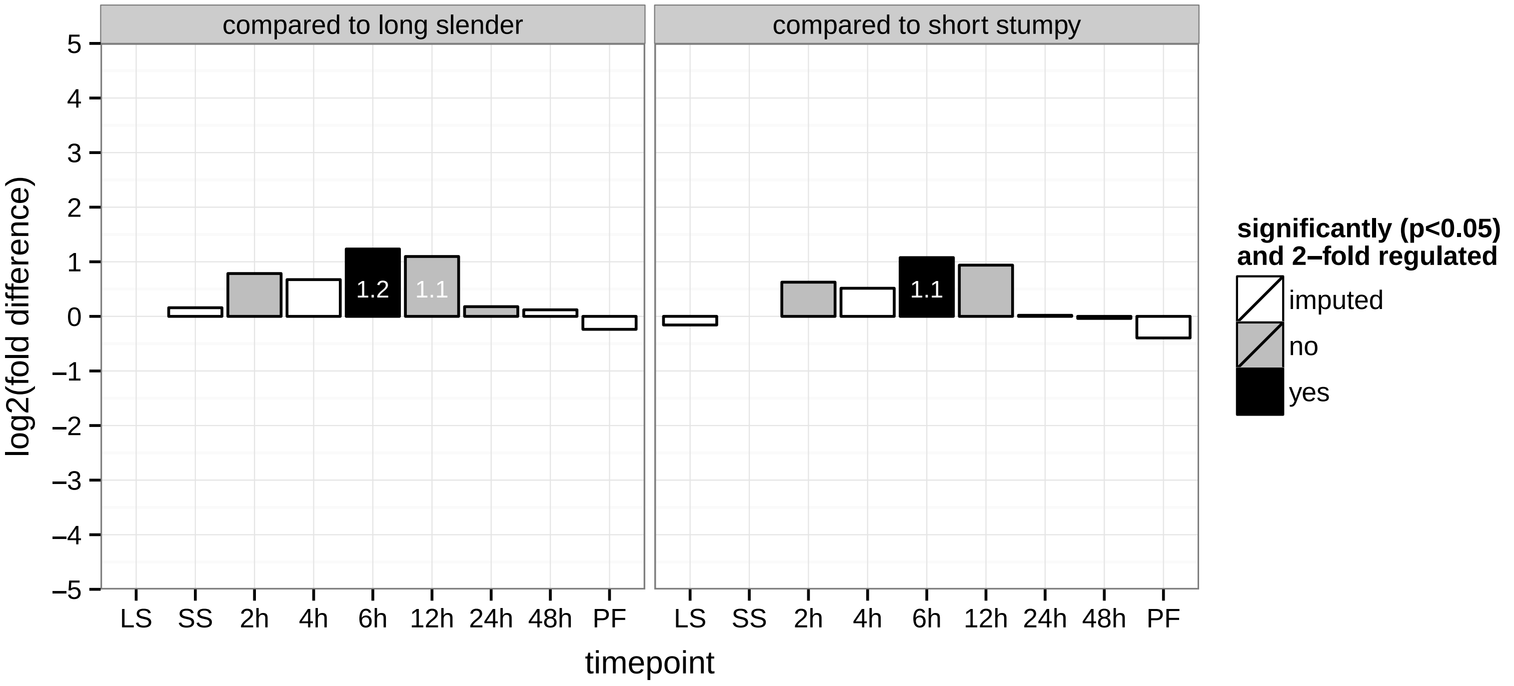
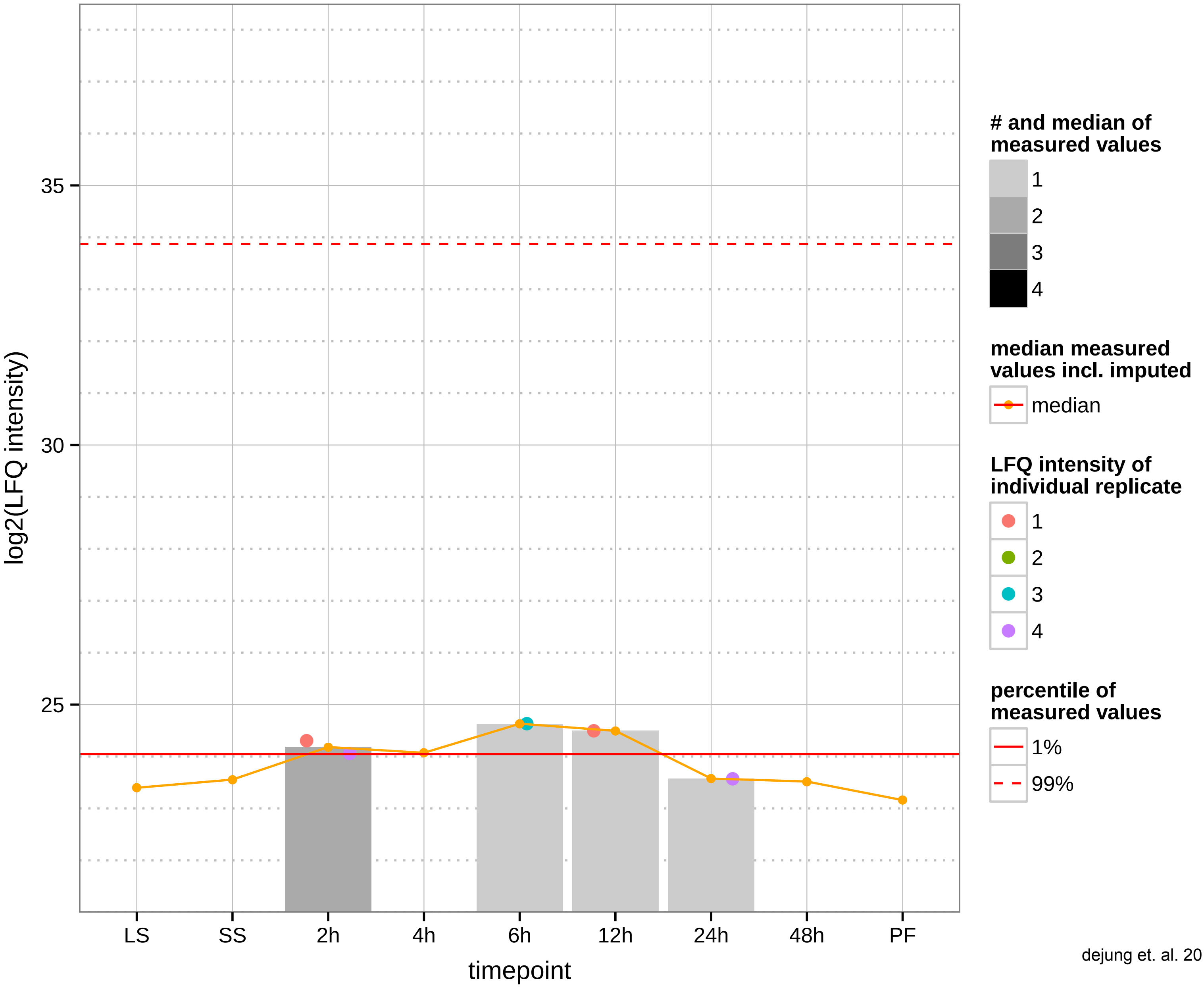
protein kinase, putative
Tb927.3.3290;Tb11.v5.0474
AGOF: null, ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: null, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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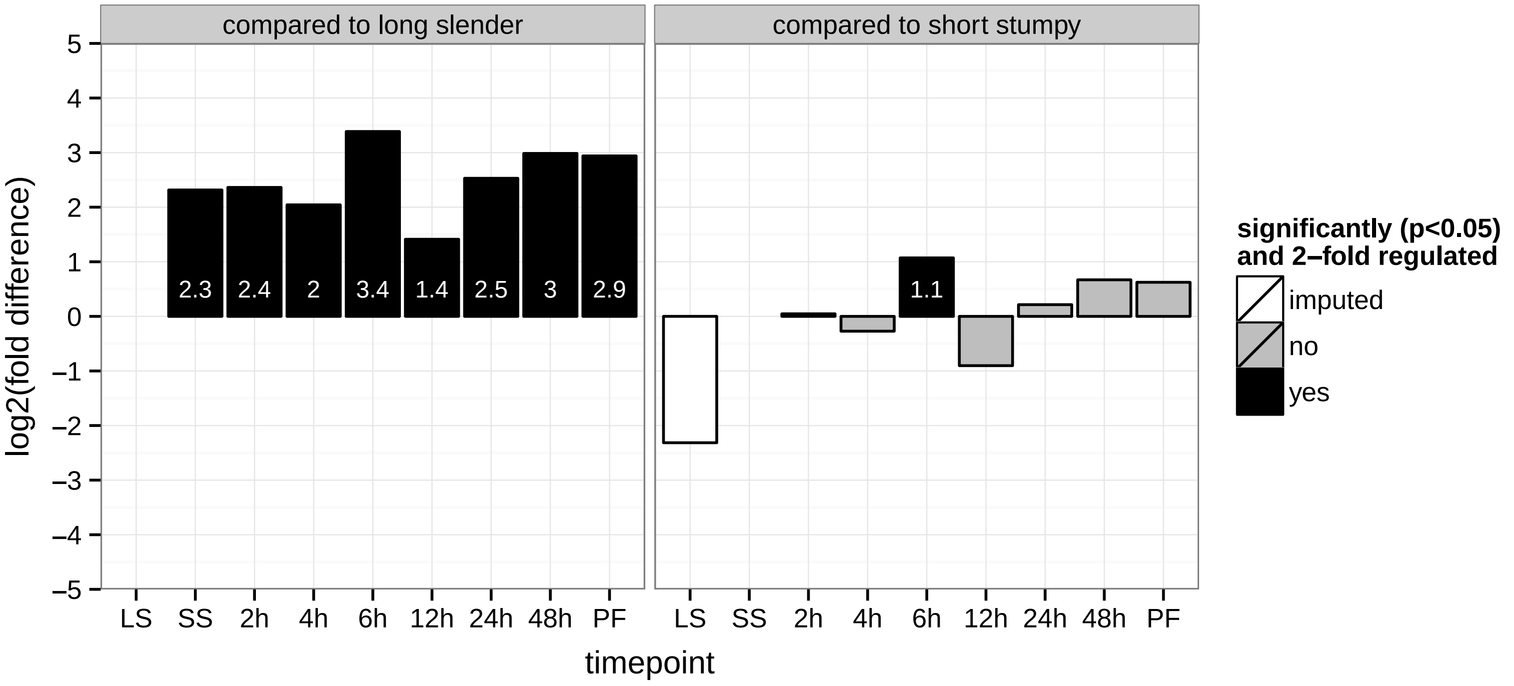
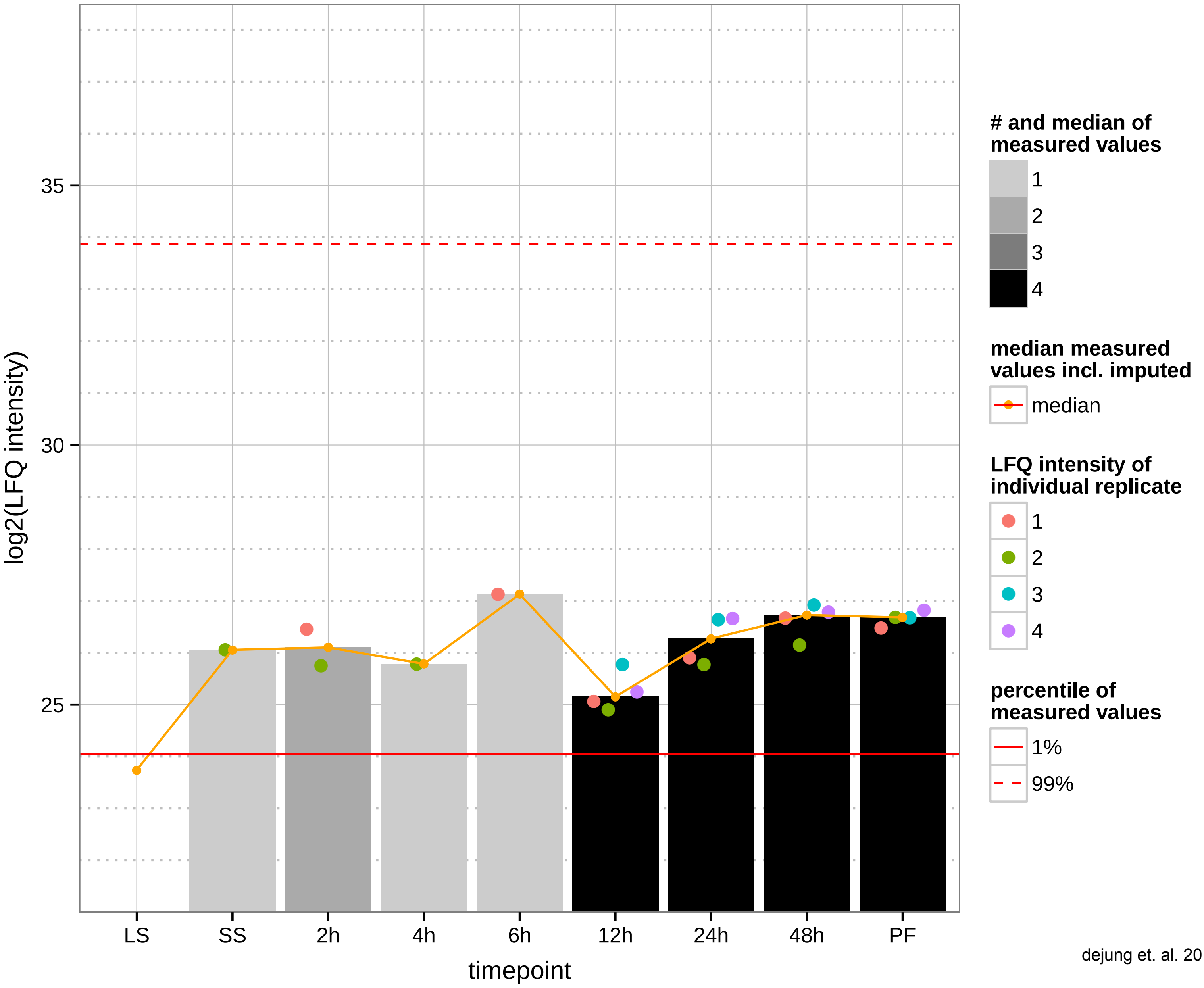
histone deacetylase 4, histone deacetylase−like protein HDO4 (HDAC4)
Tb927.5.2900
AGOF: histone deacetylase activity
AGOC: cytoplasm, nucleus
AGOP: cell cycle, histone deacetylation
PGOF: null
PGOC: null
PGOP: null





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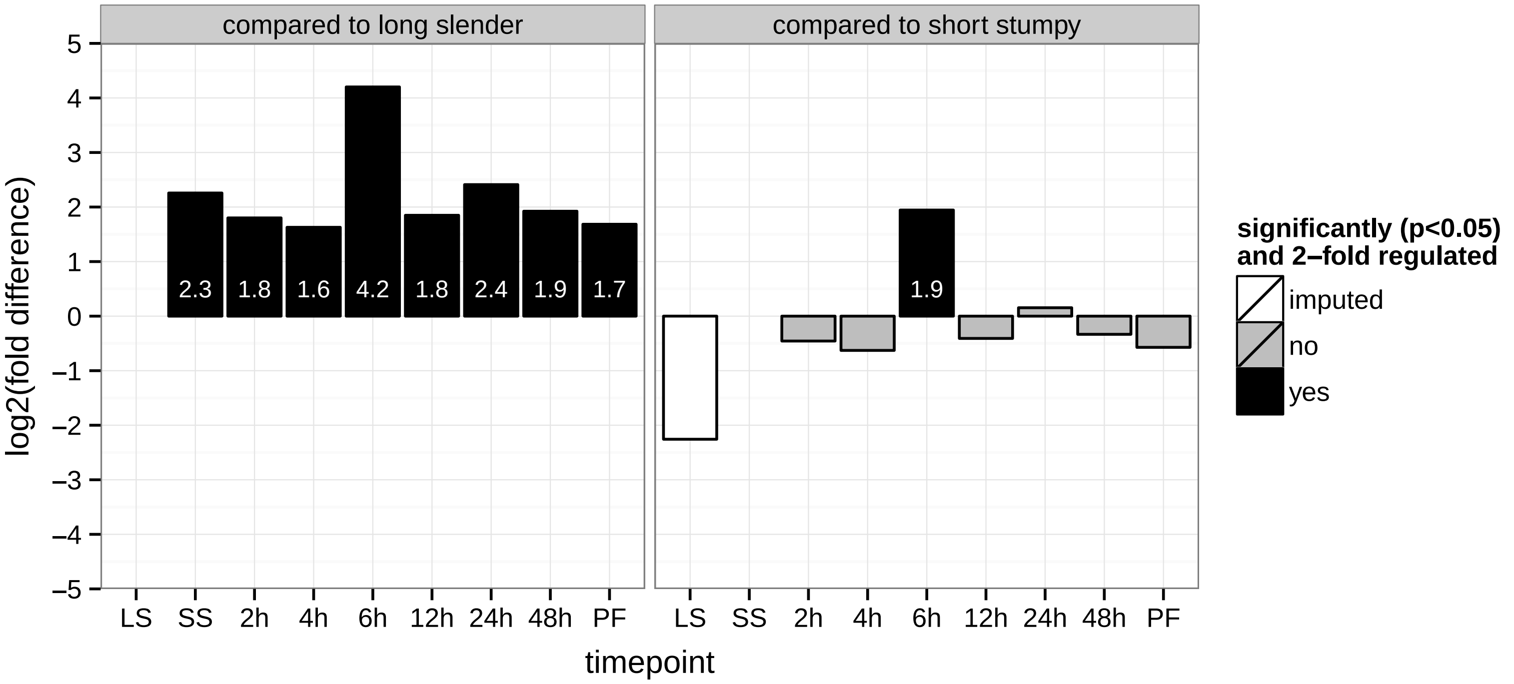
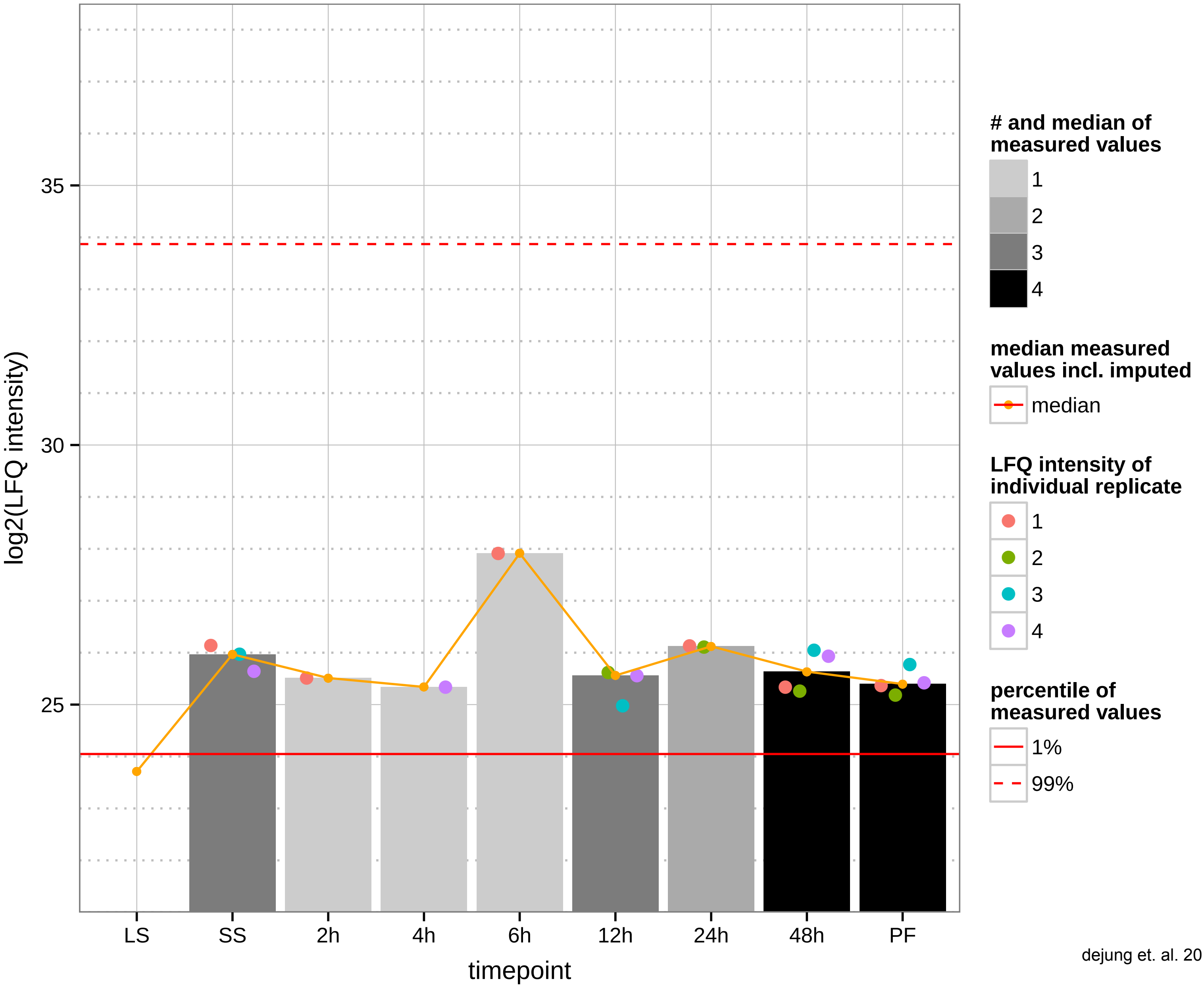
ubiquitin hydrolase, pseudogene, putative, cysteine peptidase, Clan CA, family C19, frameshift, frameshift (PAN2)
Tb927.6.1670
AGOF: ubiquitin thiolesterase activity
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: protein binding
PGOC: null
PGOP: null





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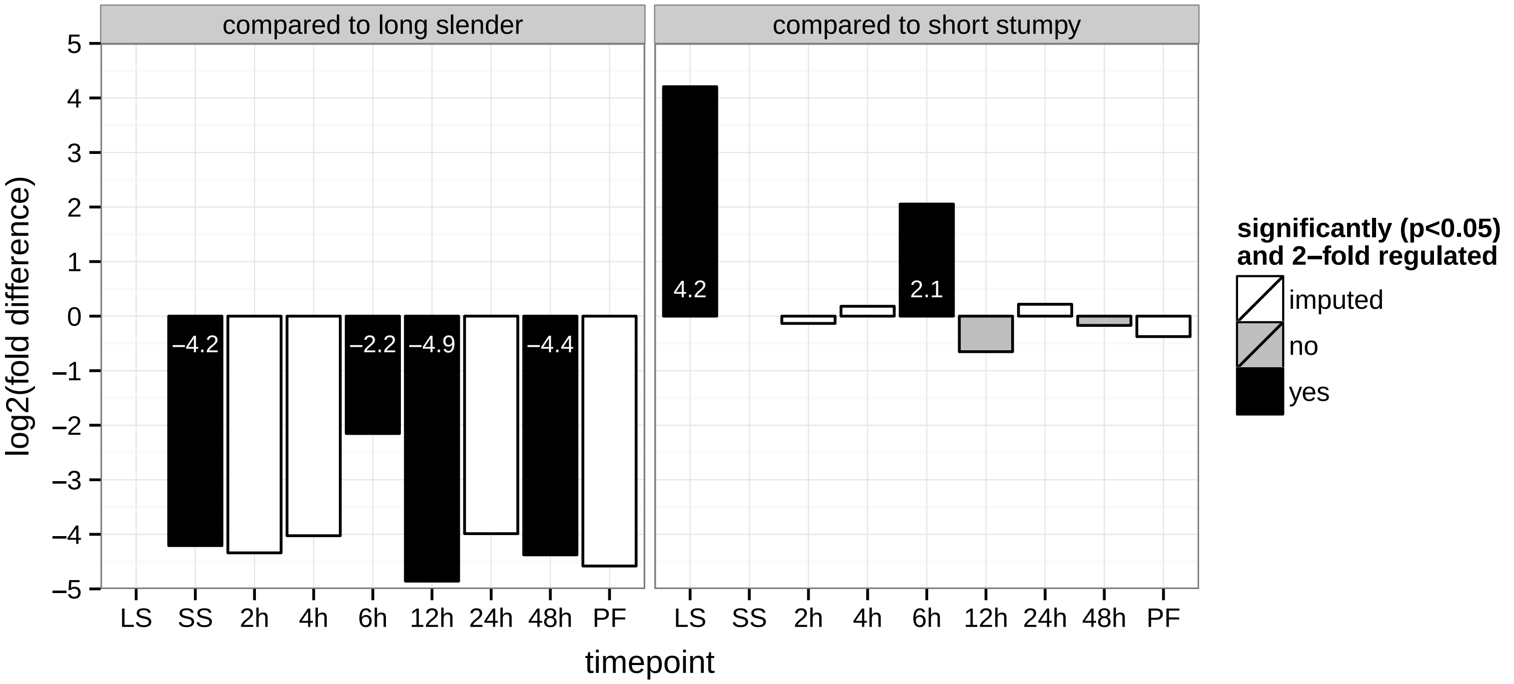
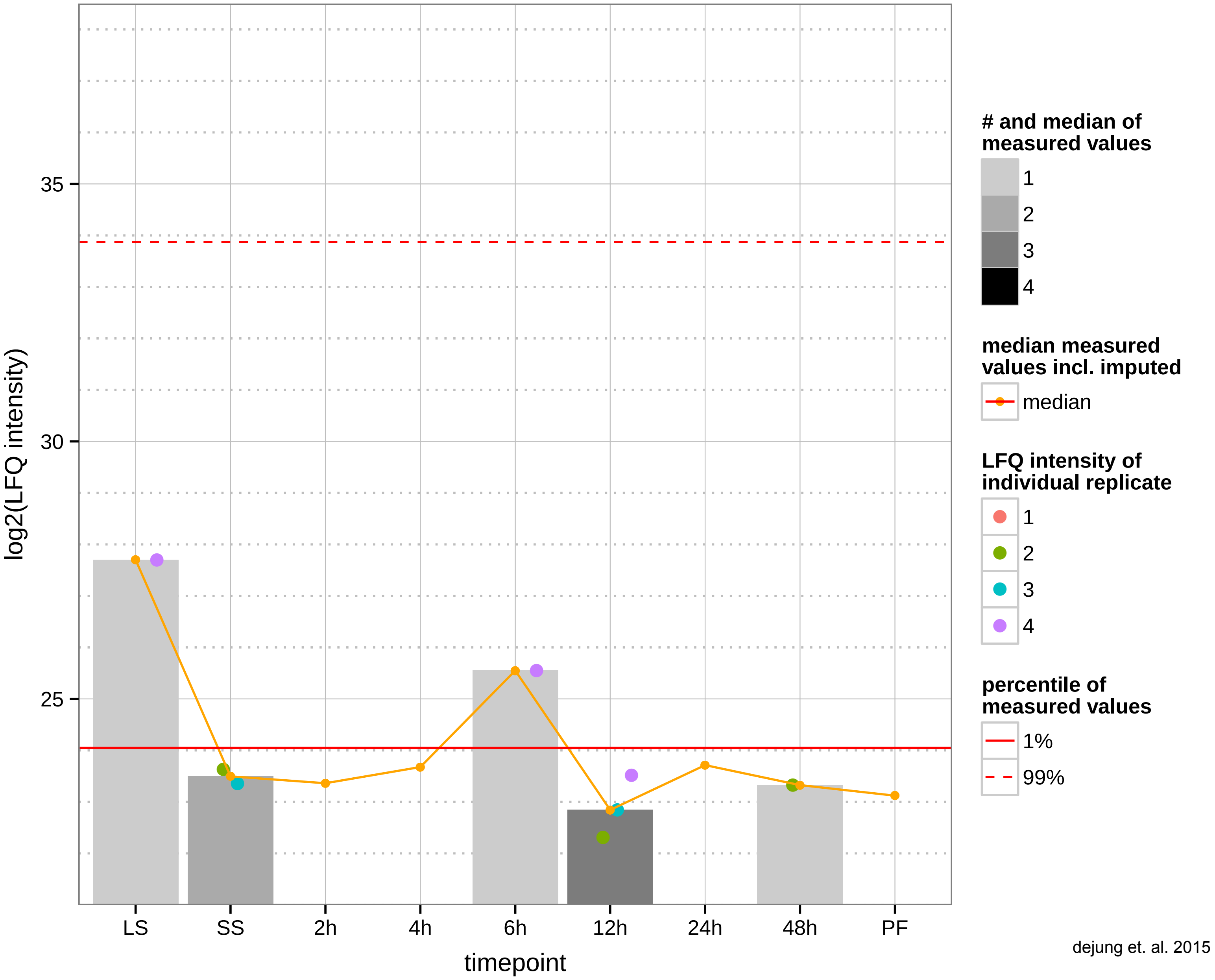
ABC transporter, putative
Tb927.6.2810
AGOF: ATP binding, ATPase activity
AGOC: integral to membrane
AGOP: transport
PGOF: ATP binding, ATPase activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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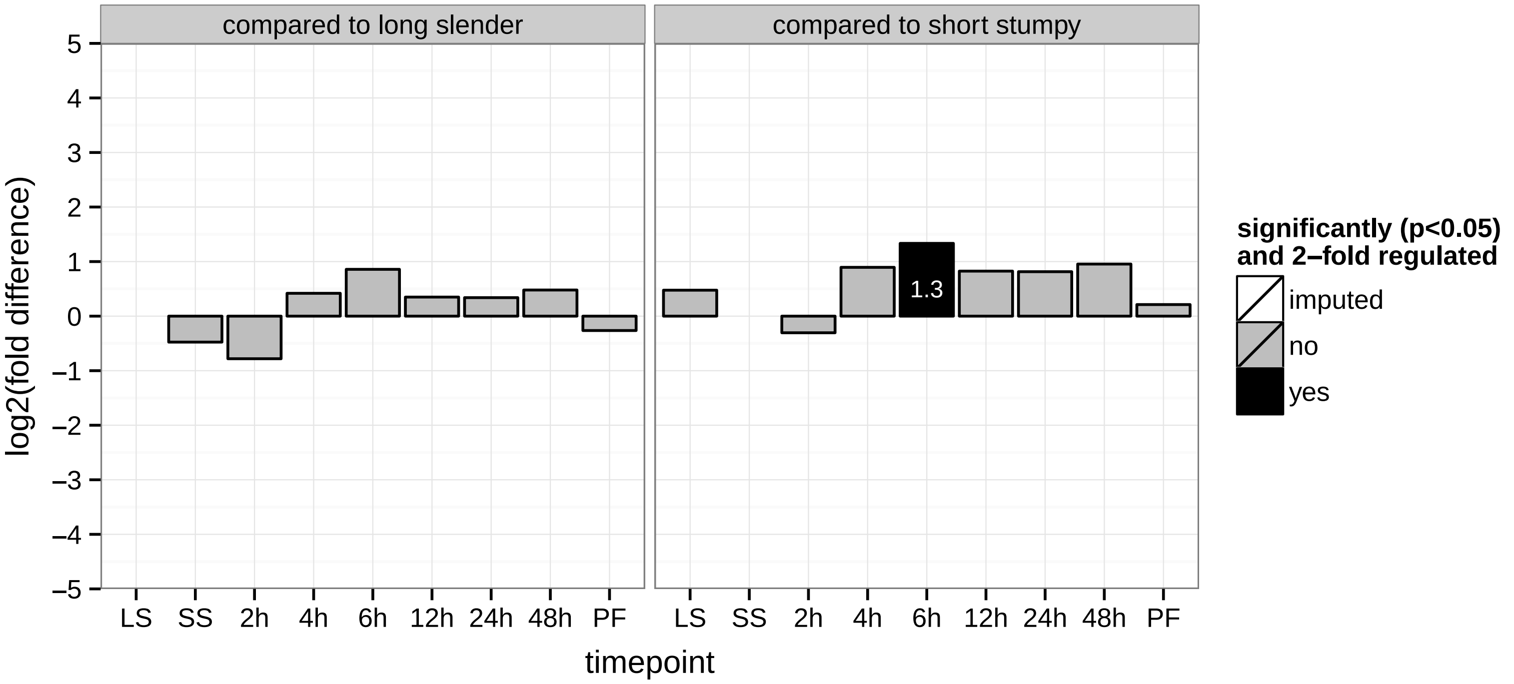
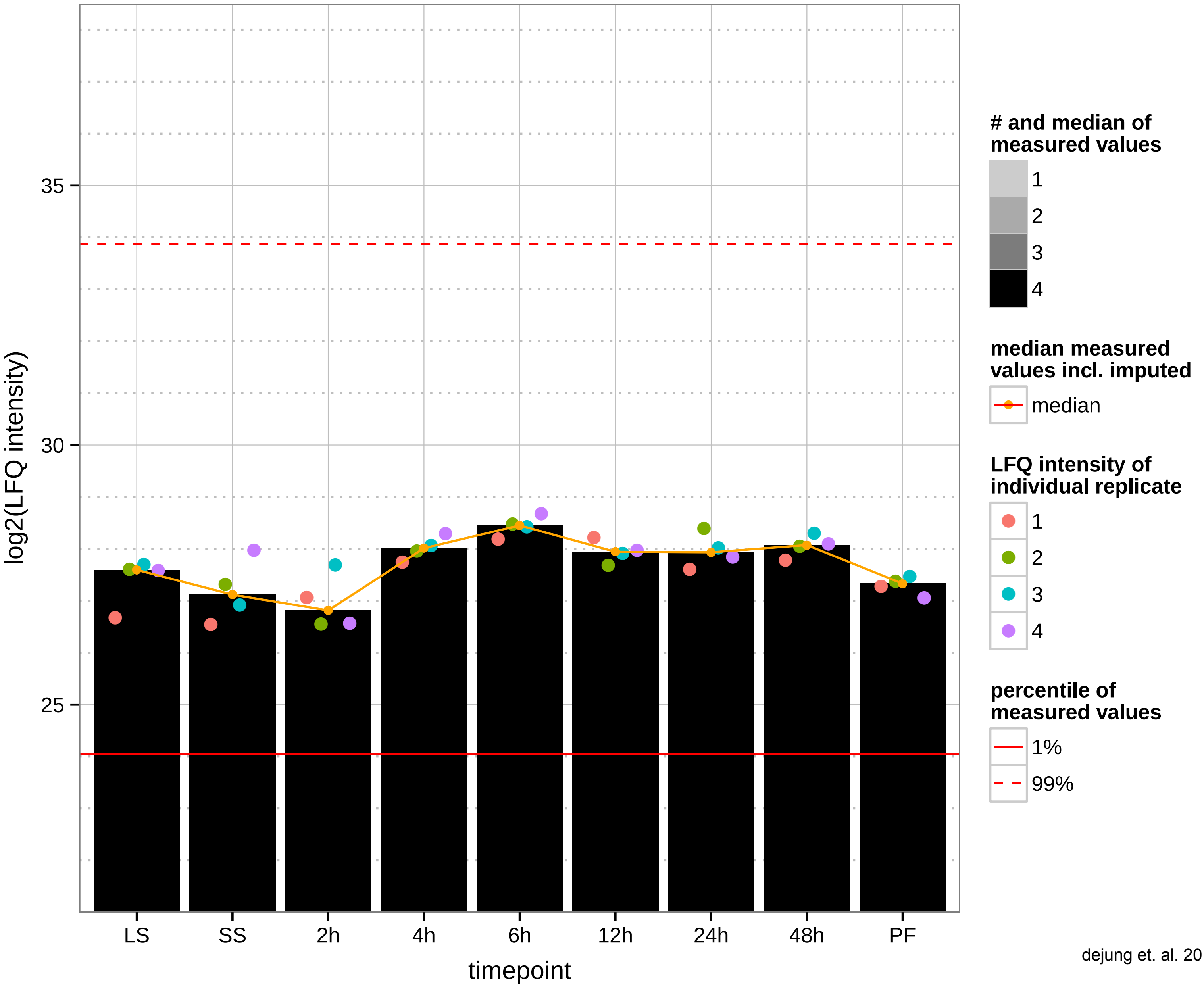
hypothetical protein, conserved
Tb927.9.7080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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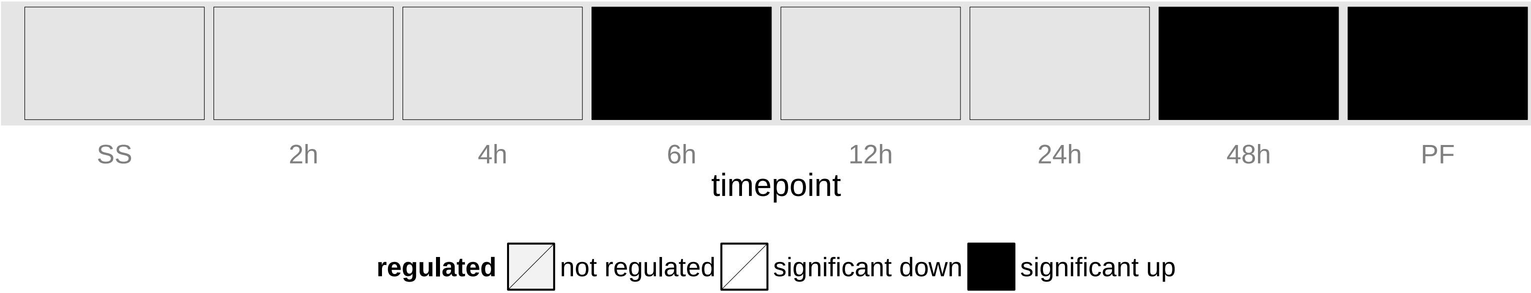

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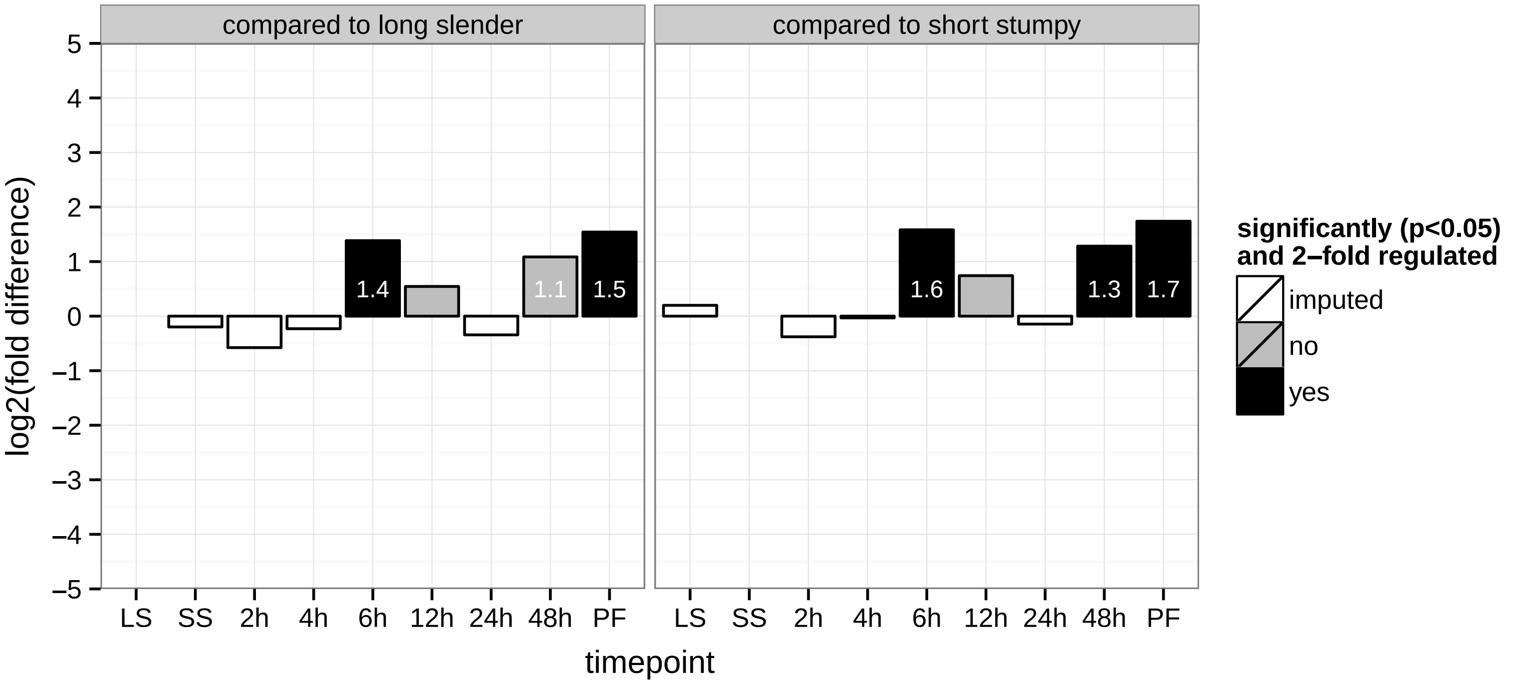
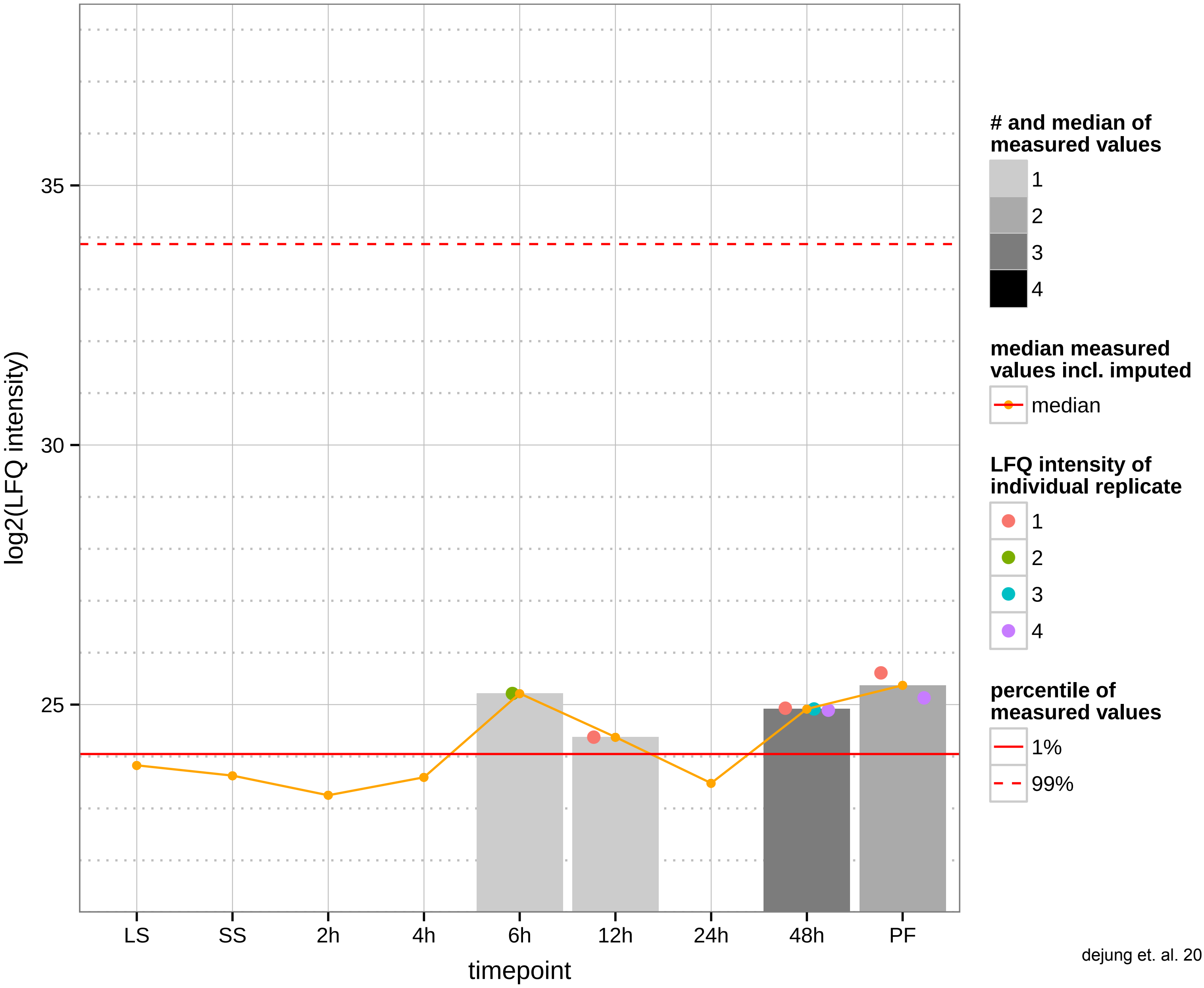
DNA replication licensing factor MCM4, putative (MCM4)
Tb927.11.12250
AGOF: ATP binding, DNA binding
AGOC: PCNA complex, nucleus
AGOP: DNA replication, DNA–dependent DNA replication initiation
PGOF: ATP binding, DNA binding
PGOC: null
PGOP: DNA replication





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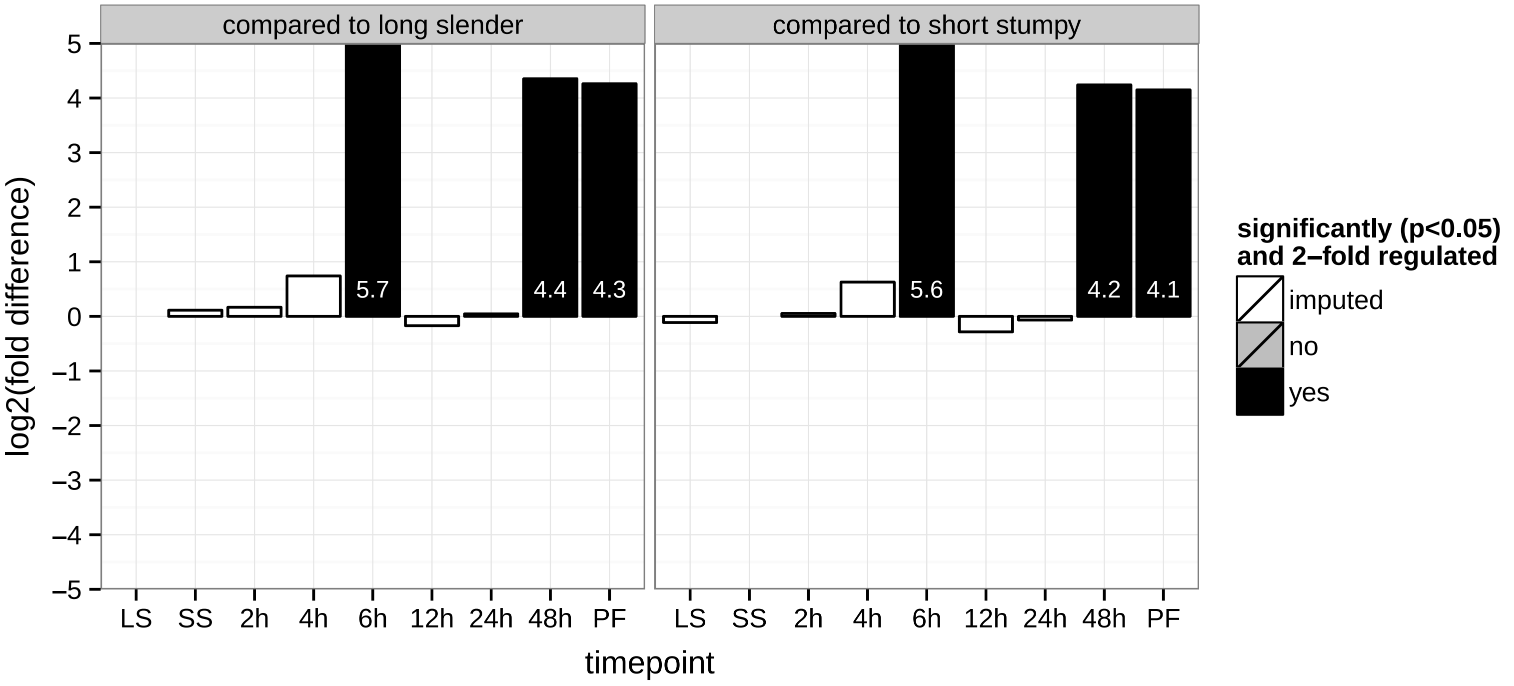
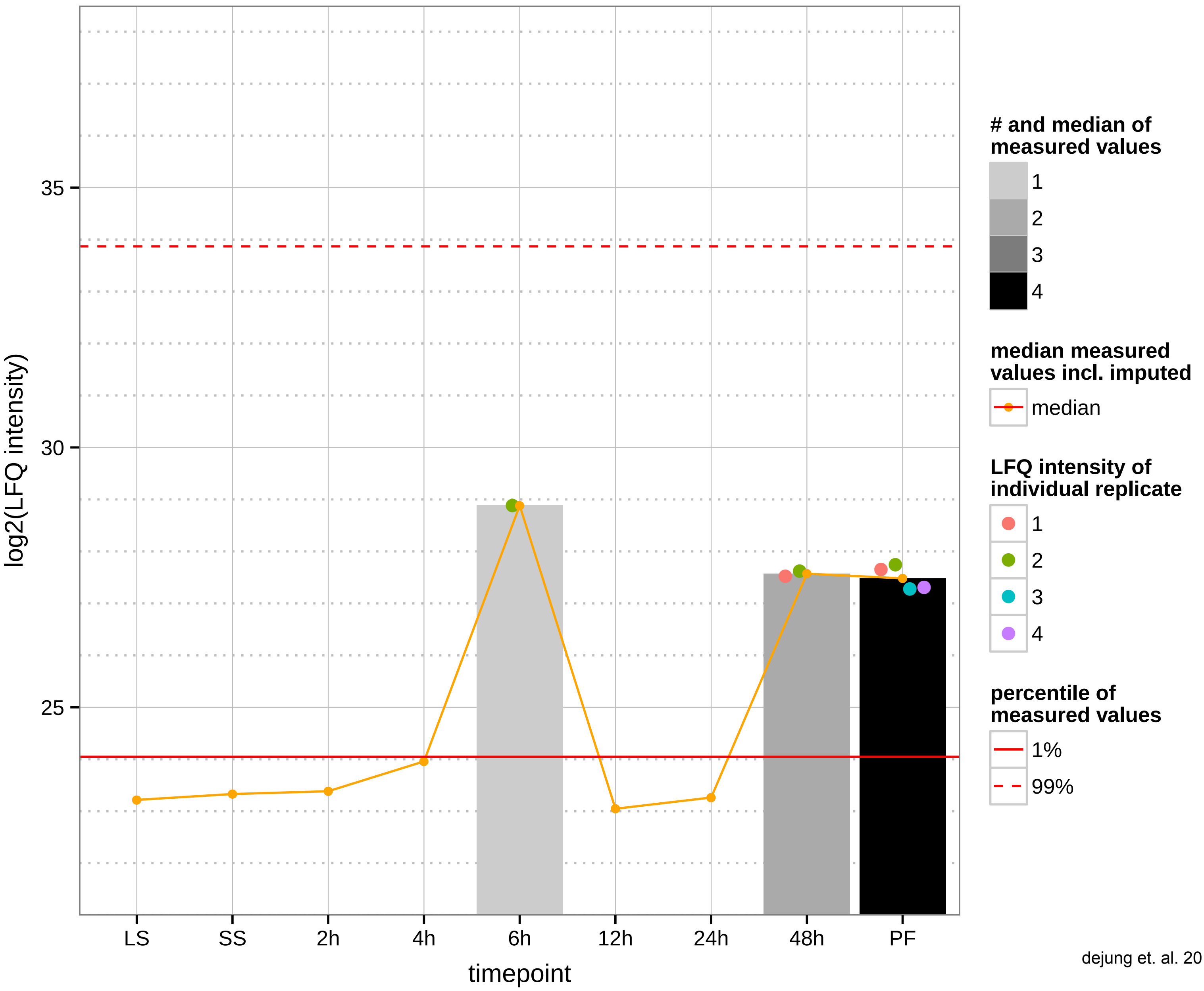
hypothetical protein, conserved
Tb927.11.5820
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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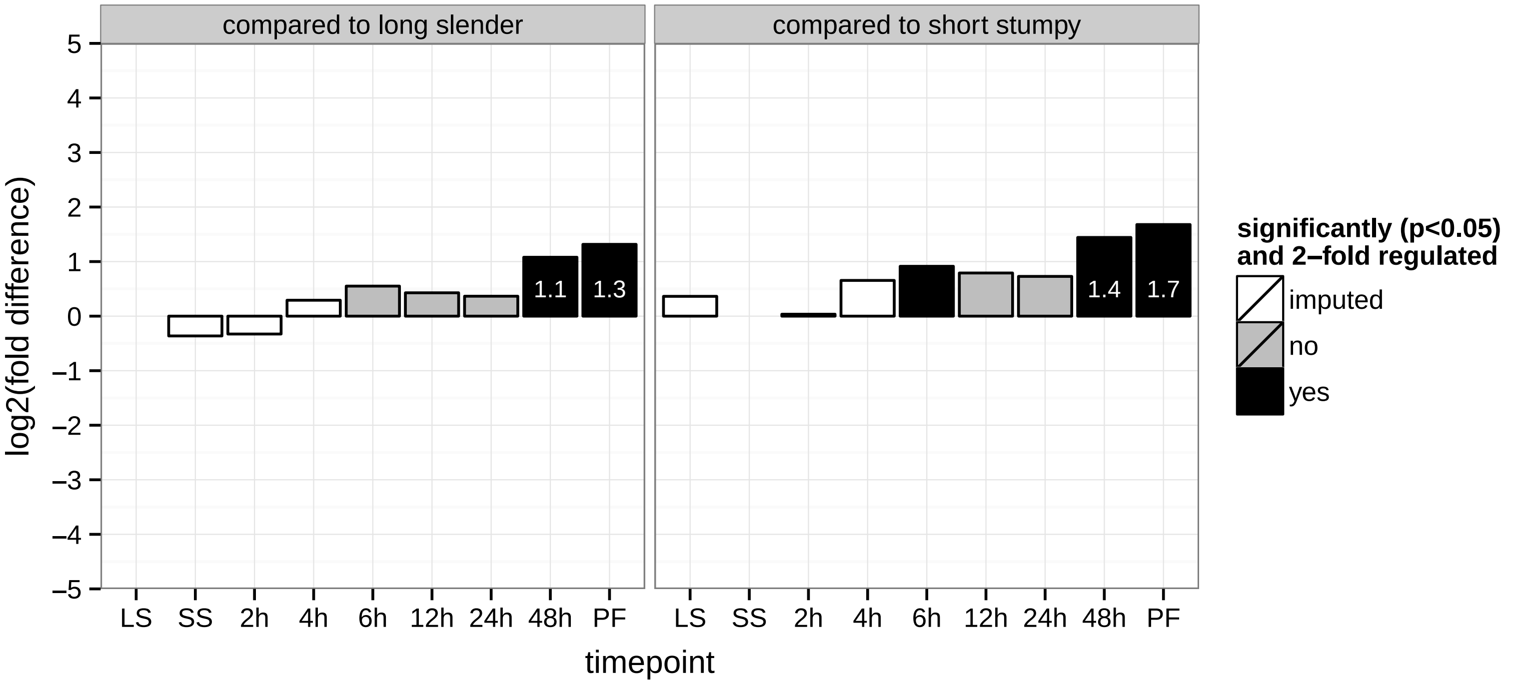
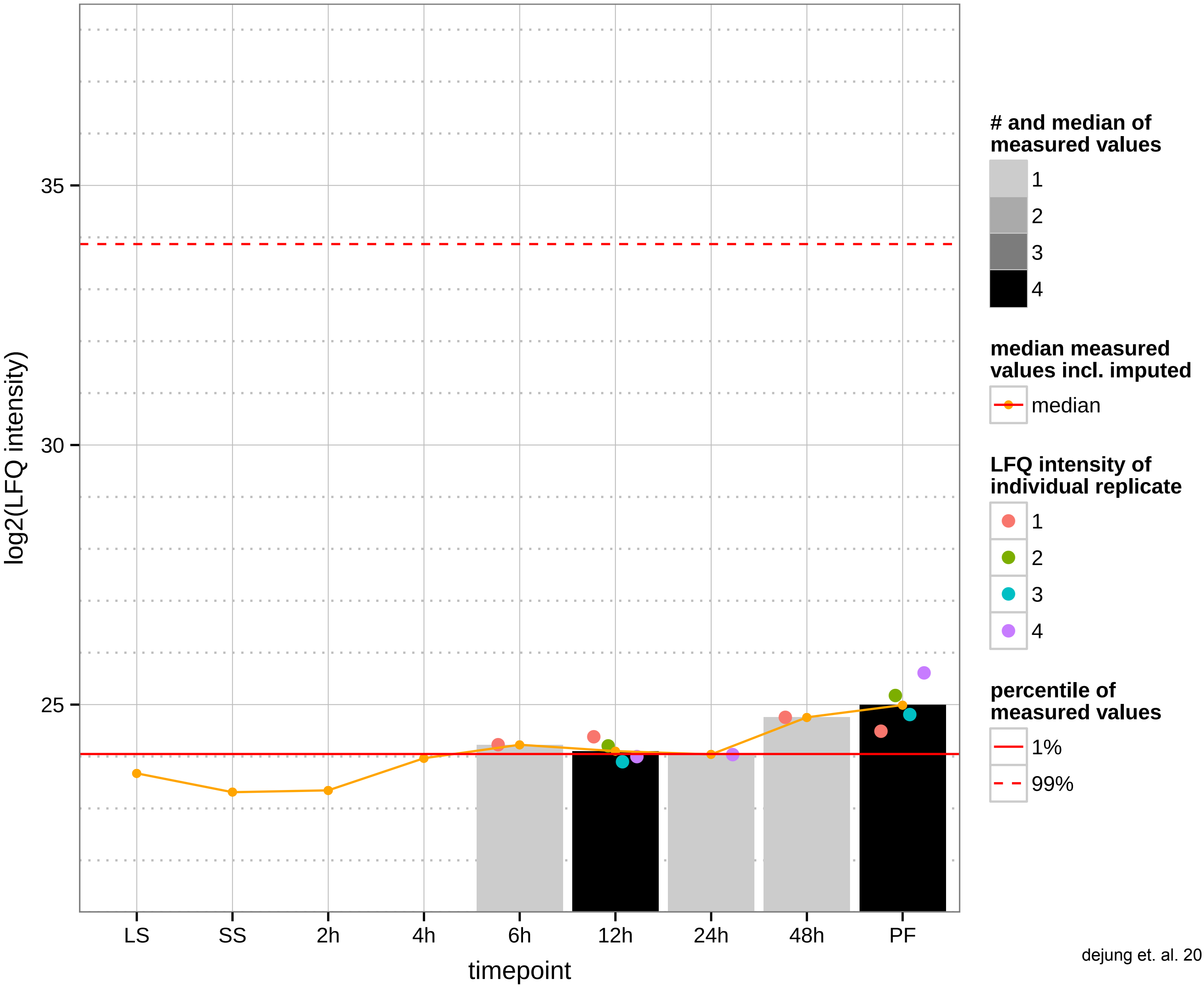
hypothetical protein, conserved
Tb927.4.4300
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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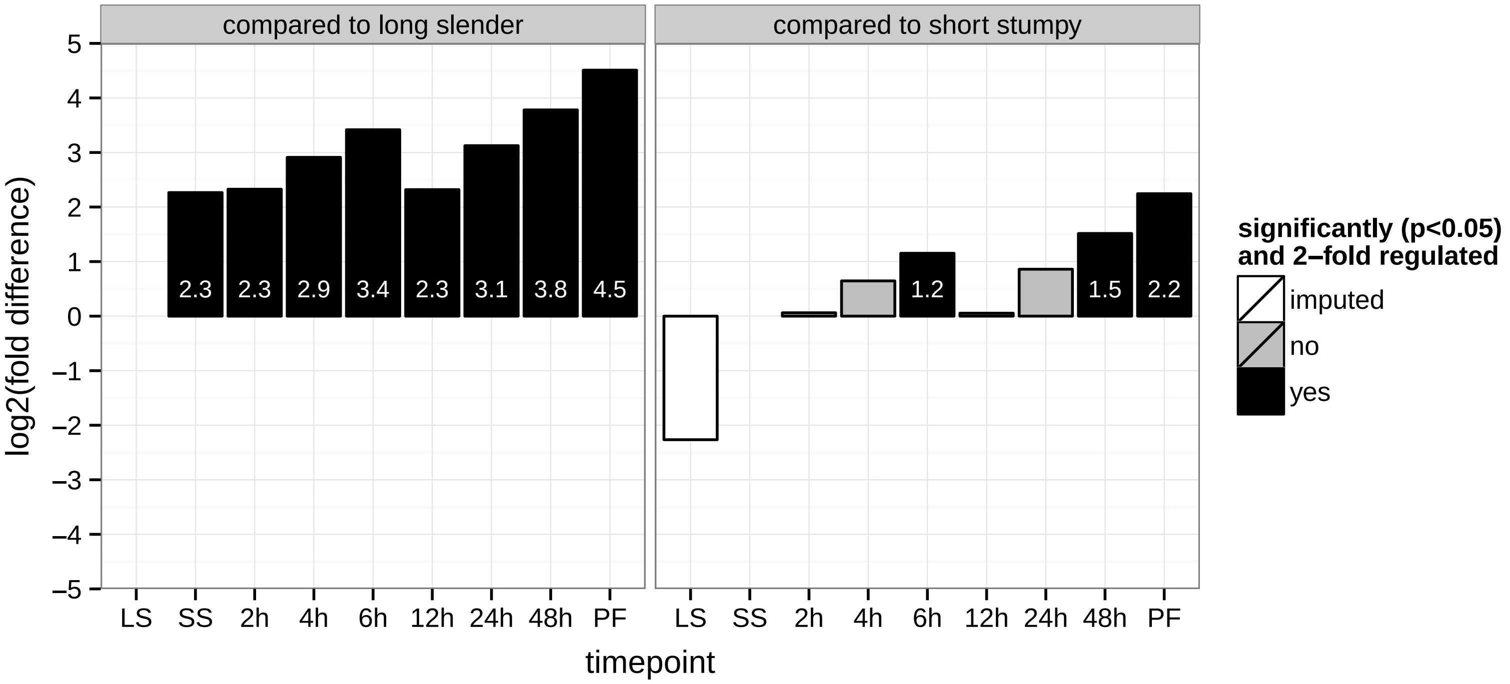
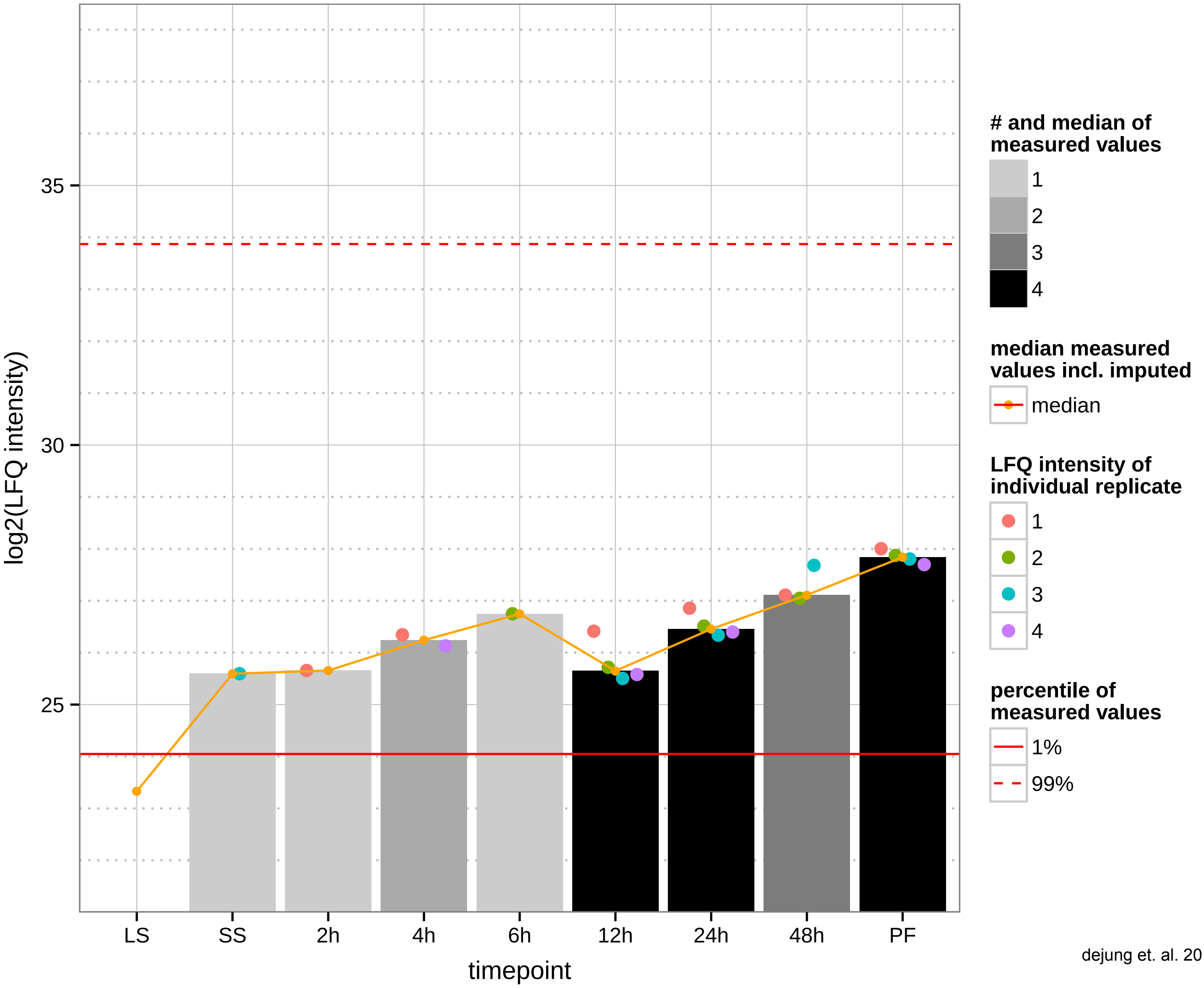
disulfide isomerase, putative
Tb927.5.1020
AGOF: null
AGOC: null
AGOP: cell redox homeostasis
PGOF: null
PGOC: null
PGOP: cell redox homeostasis





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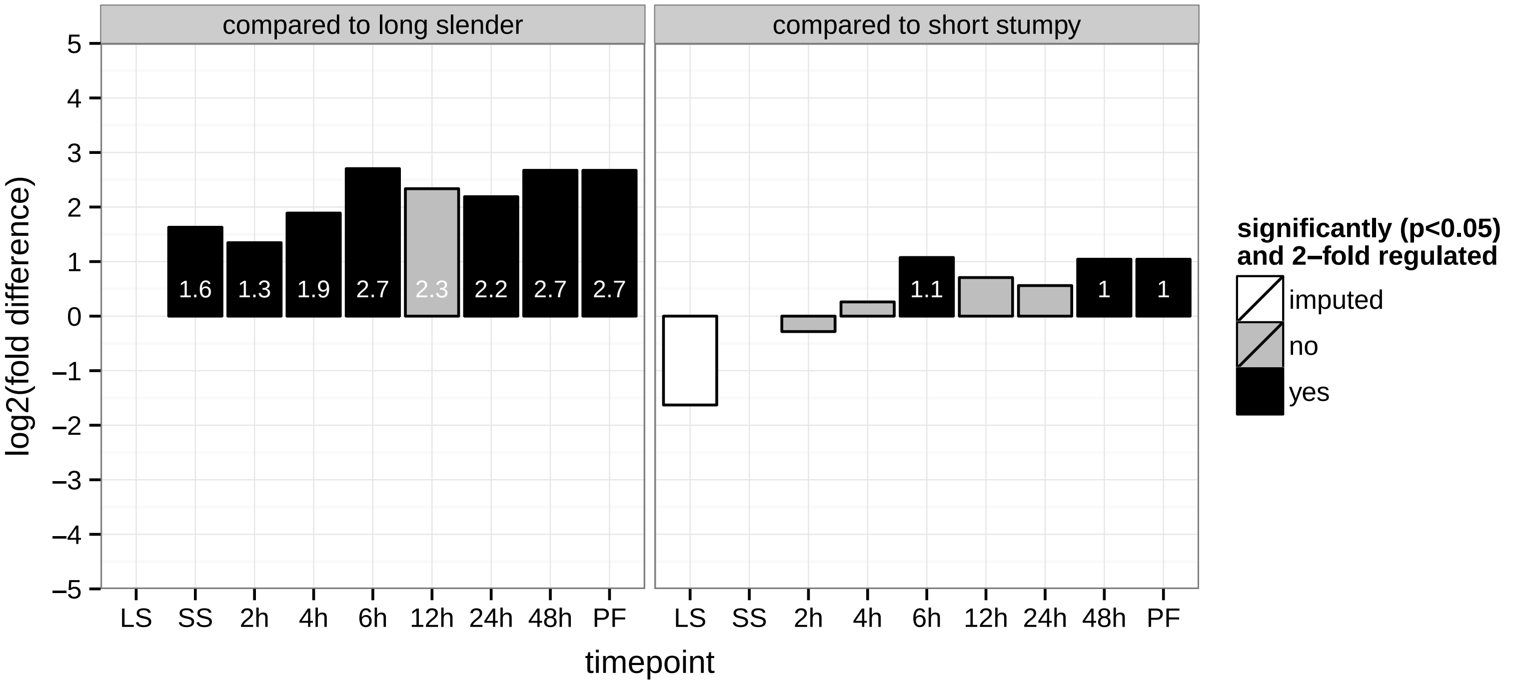
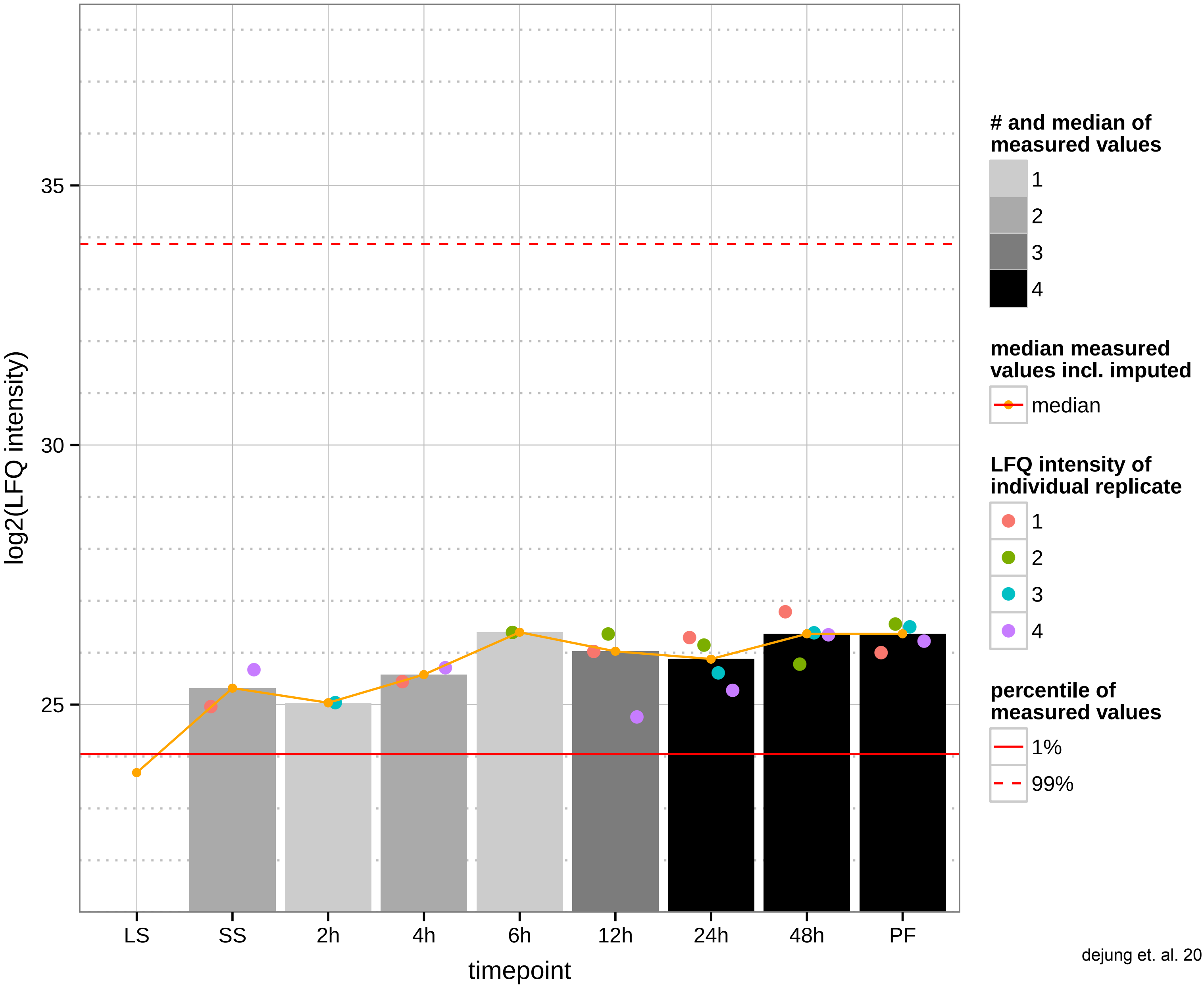
ubiquitin–conjugating enzyme E2, putative, ubiquitin carrier protein, ubiquitin–protein ligase
Tb927.7.2540
AGOF: ubiquitin–protein ligase activity
AGOC: null
AGOP: cellular protein modification process, post–translational protein modification, regulation of protein metabolic process
PGOF: acid–amino acid ligase activity
PGOC: null
PGOP: null





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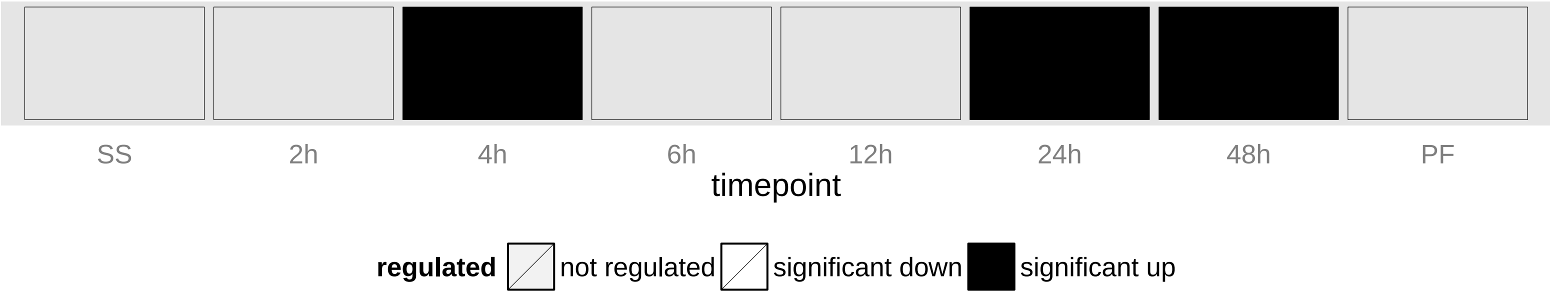

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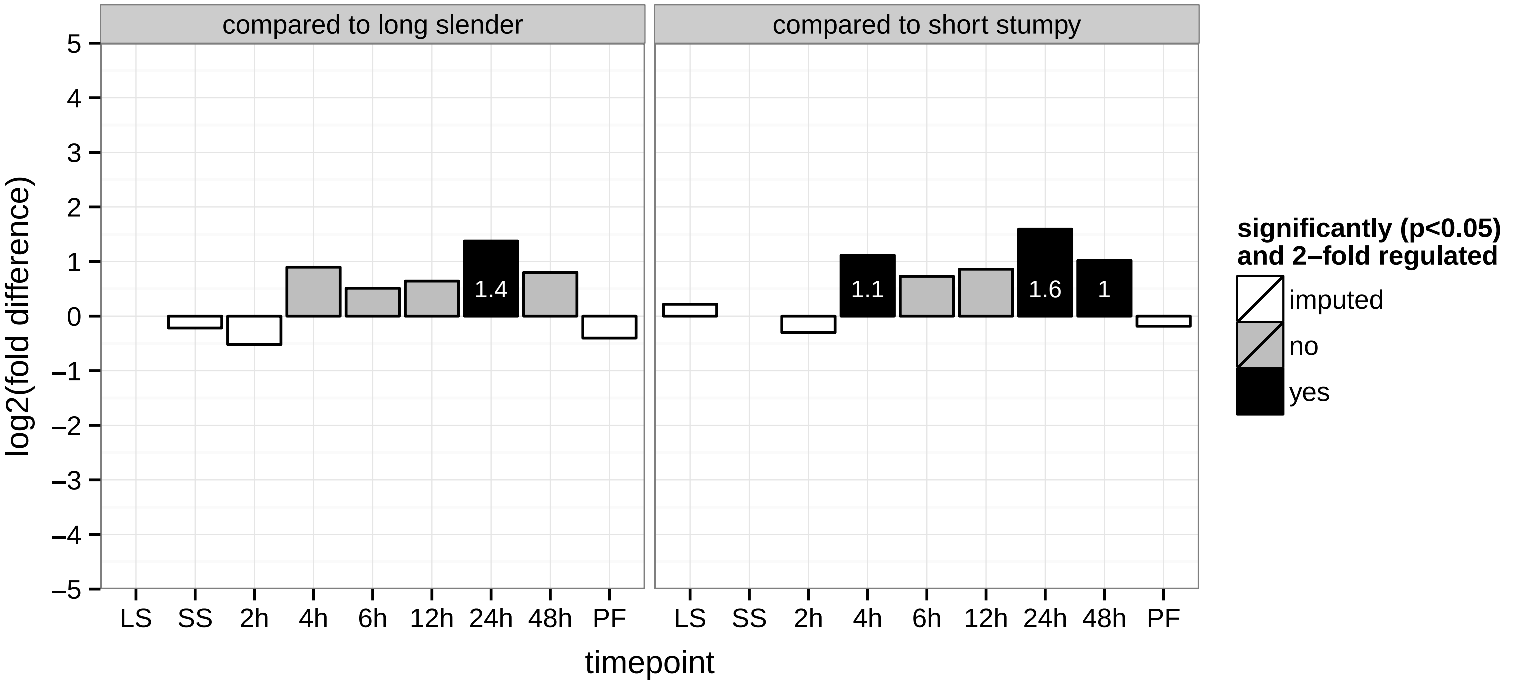
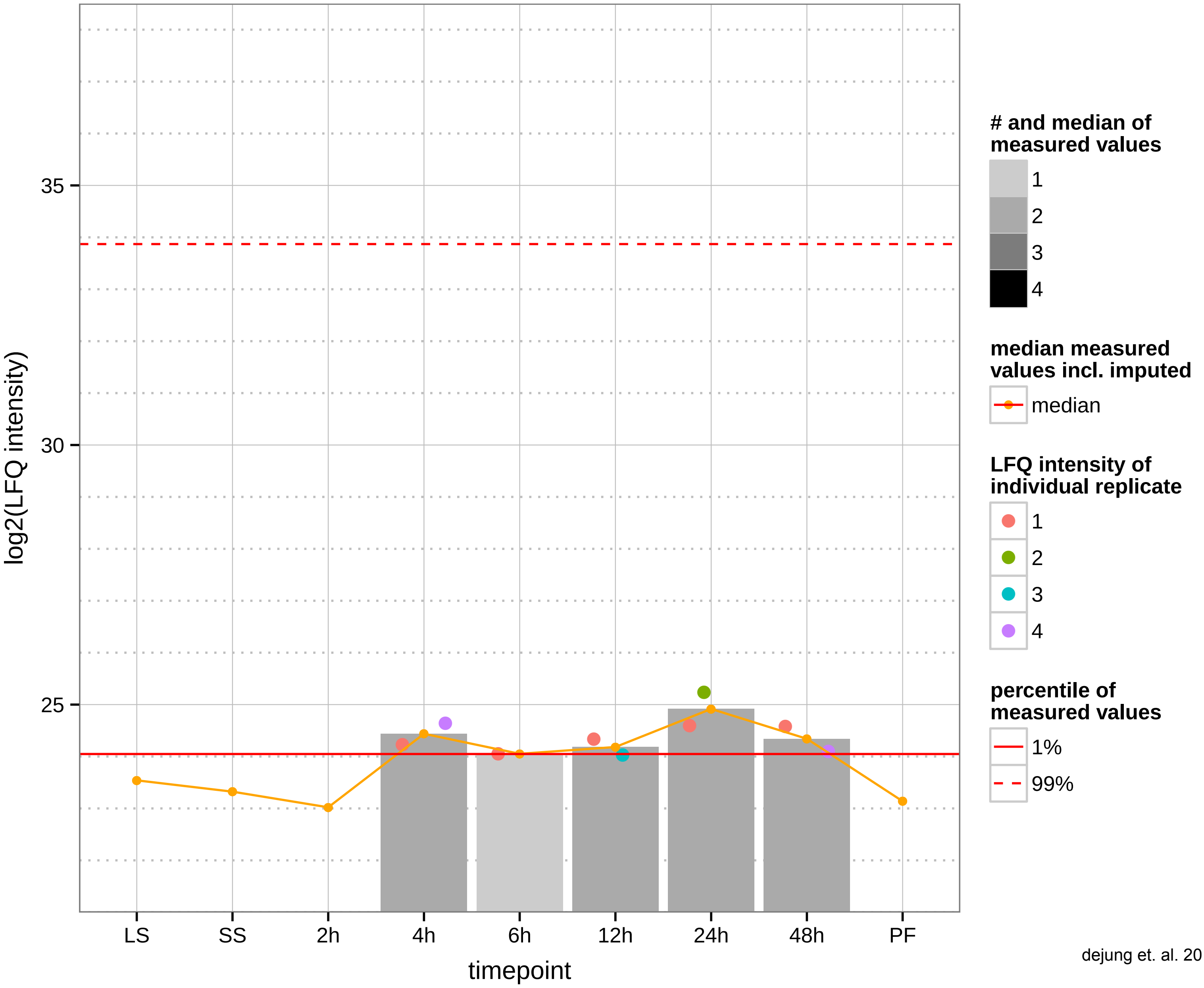
hypothetical protein, conserved
Tb927.11.10950
AGOF: heat shock protein binding
AGOC: null
AGOP: null
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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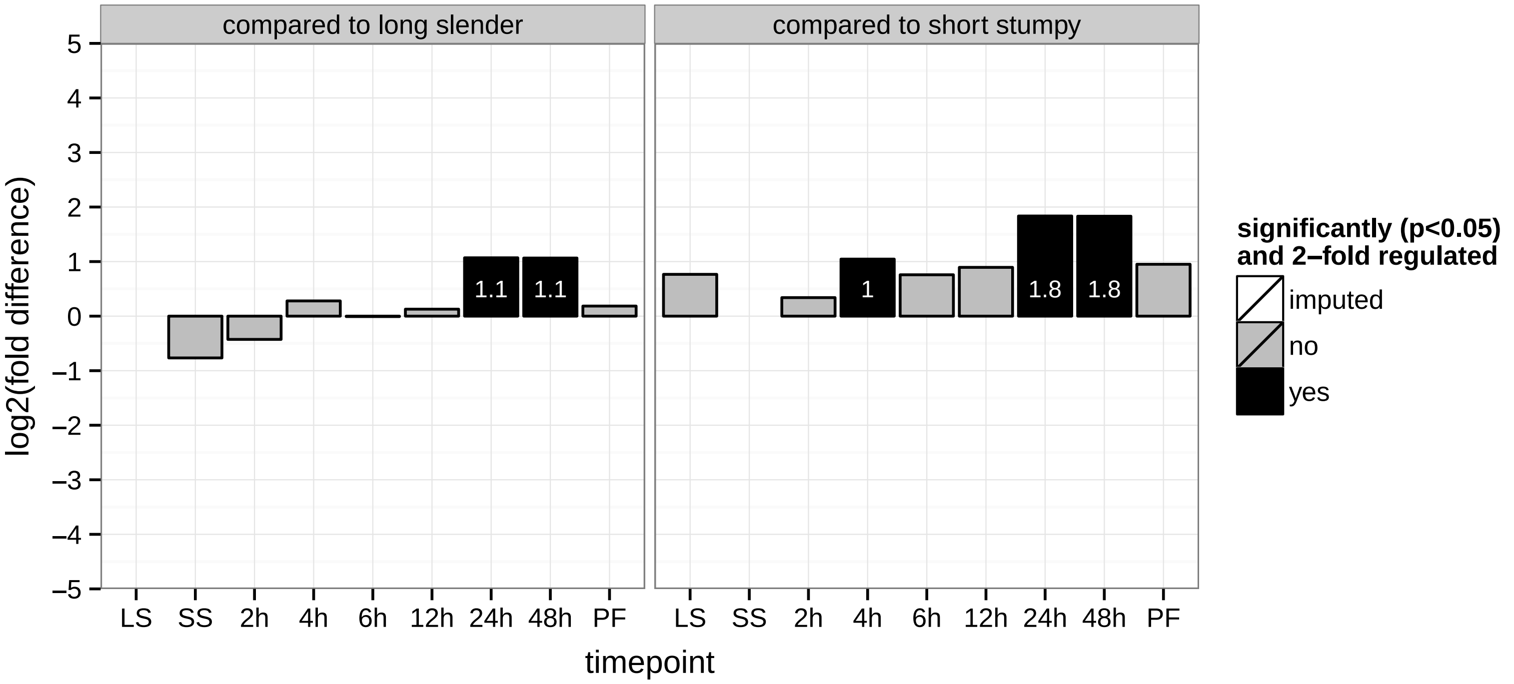
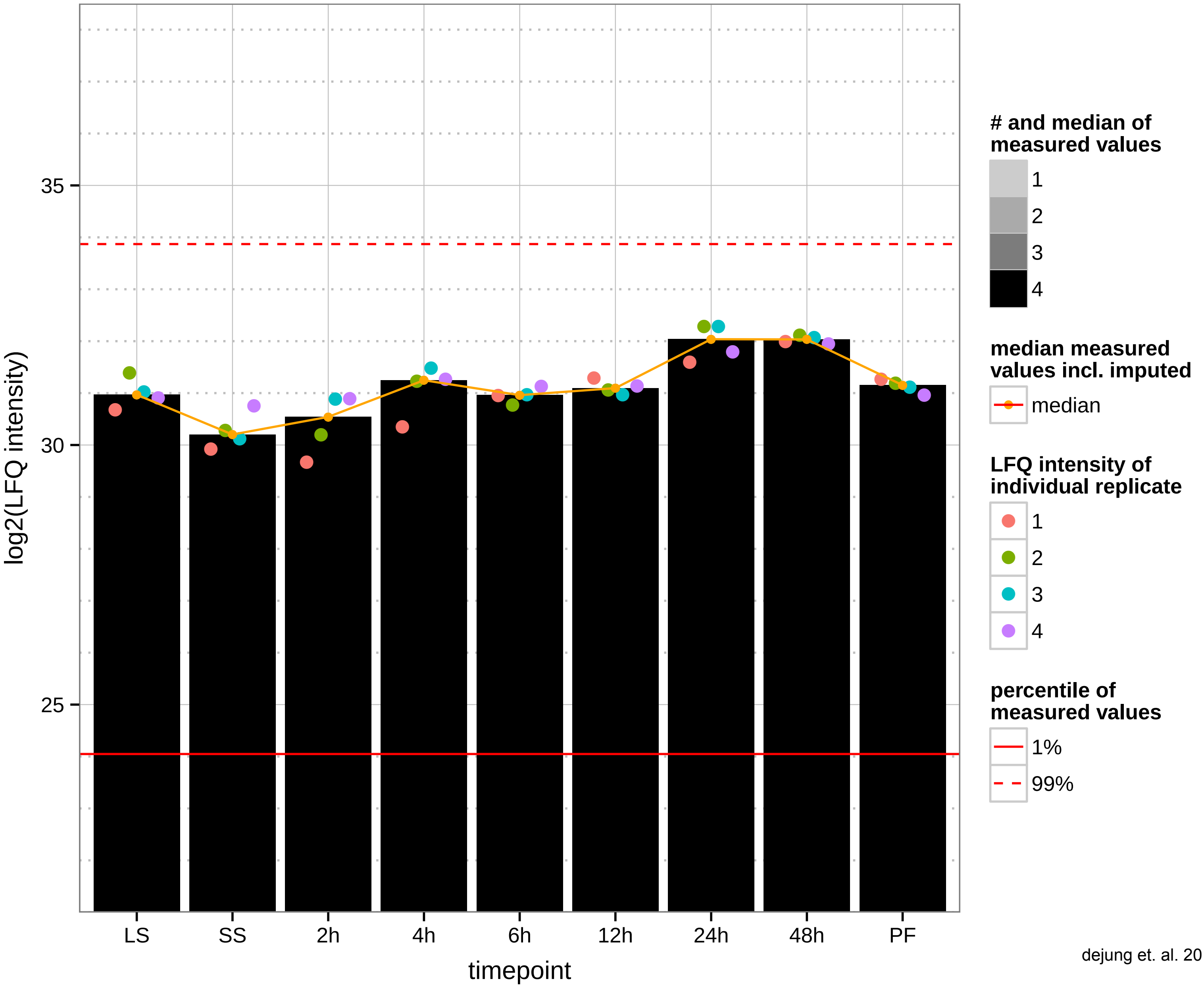
nascent polypeptide associated complex alpha subunit, putative
Tb927.11.9700
AGOF: sequence−specific DNA binding transcription factor activity
AGOC: nascent polypeptide−associated complex
AGOP: positive regulation of growth rate
PGOF: null
PGOC: null
PGOP: null





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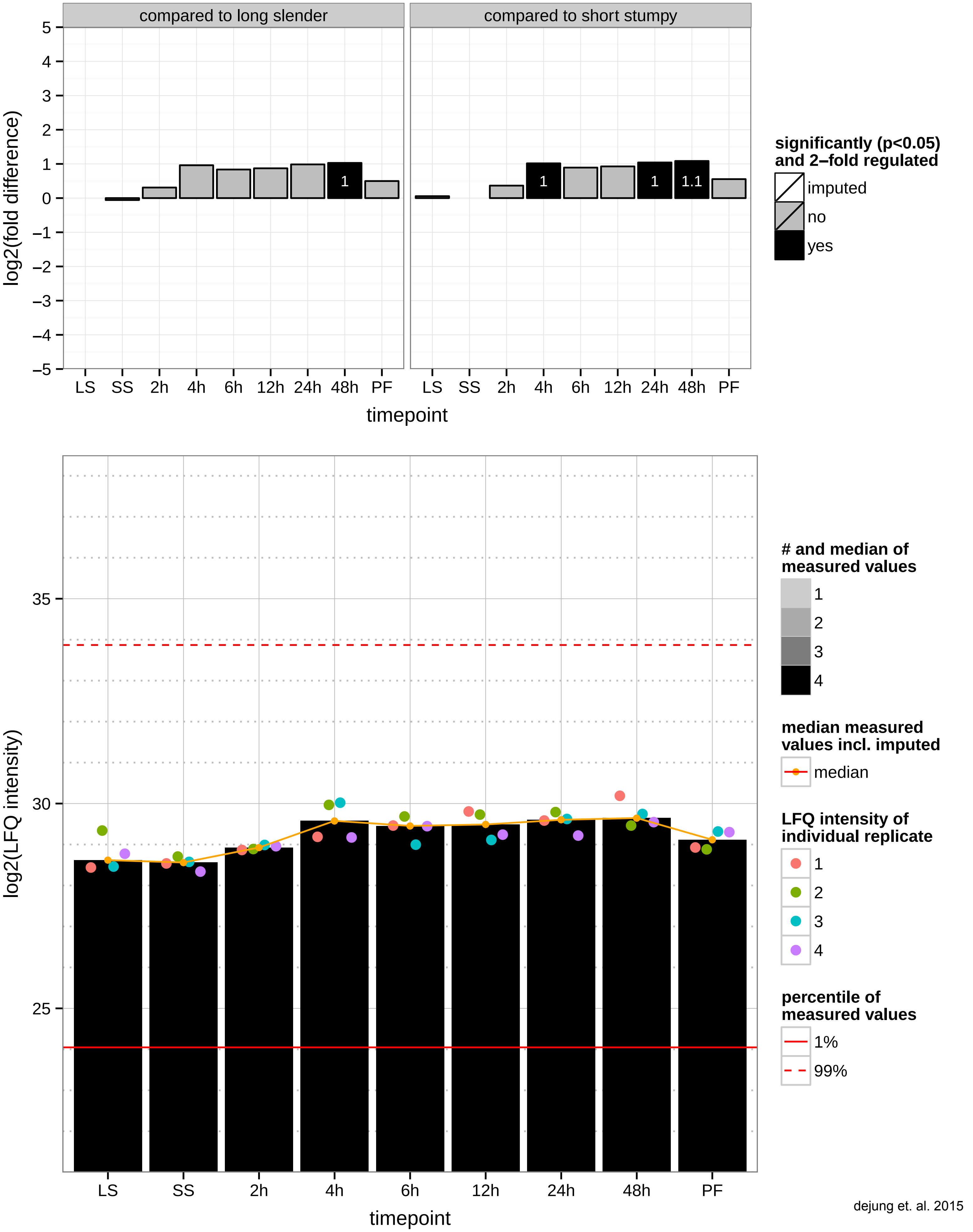
hypothetical protein, conserved
Tb927.11.9910
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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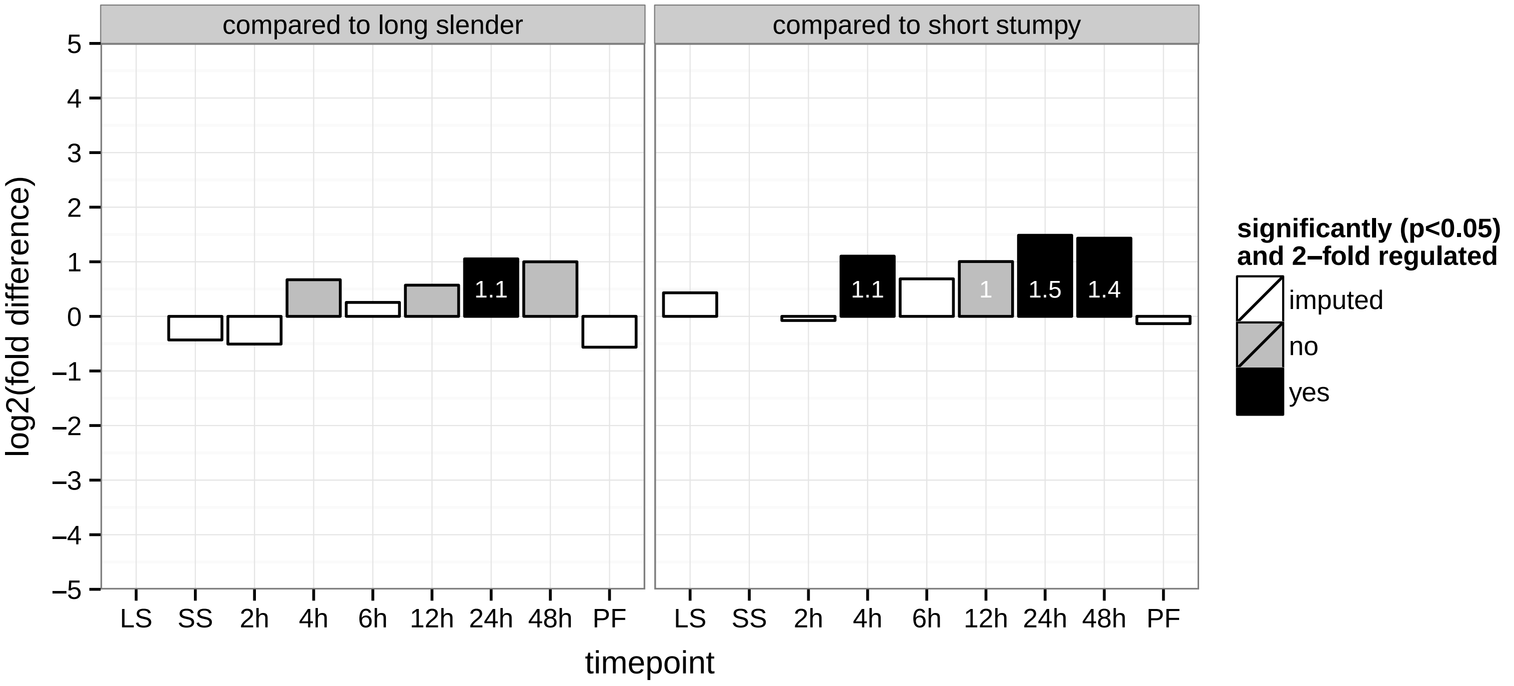
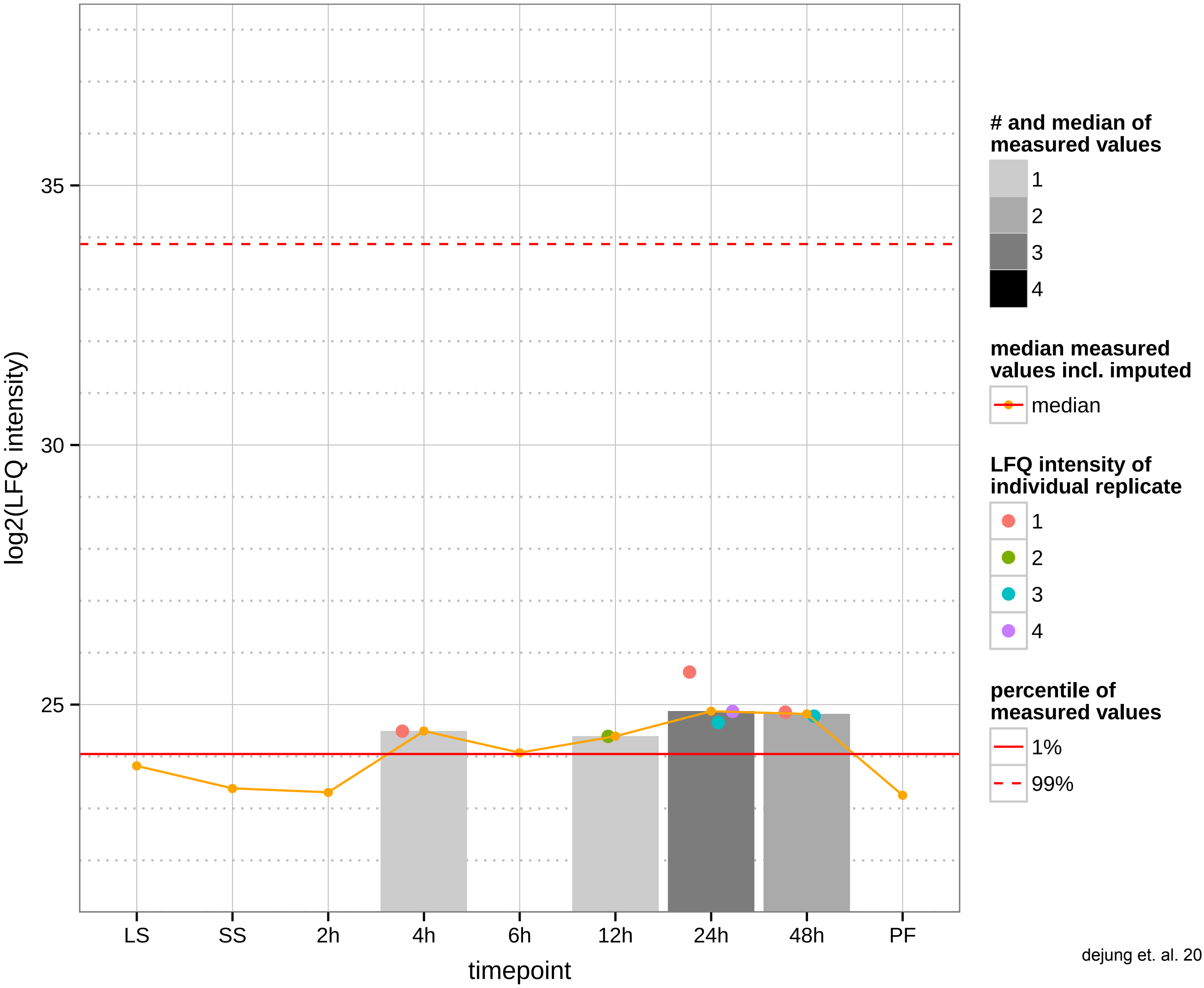
hypothetical protein, conserved
Tb927.4.3070
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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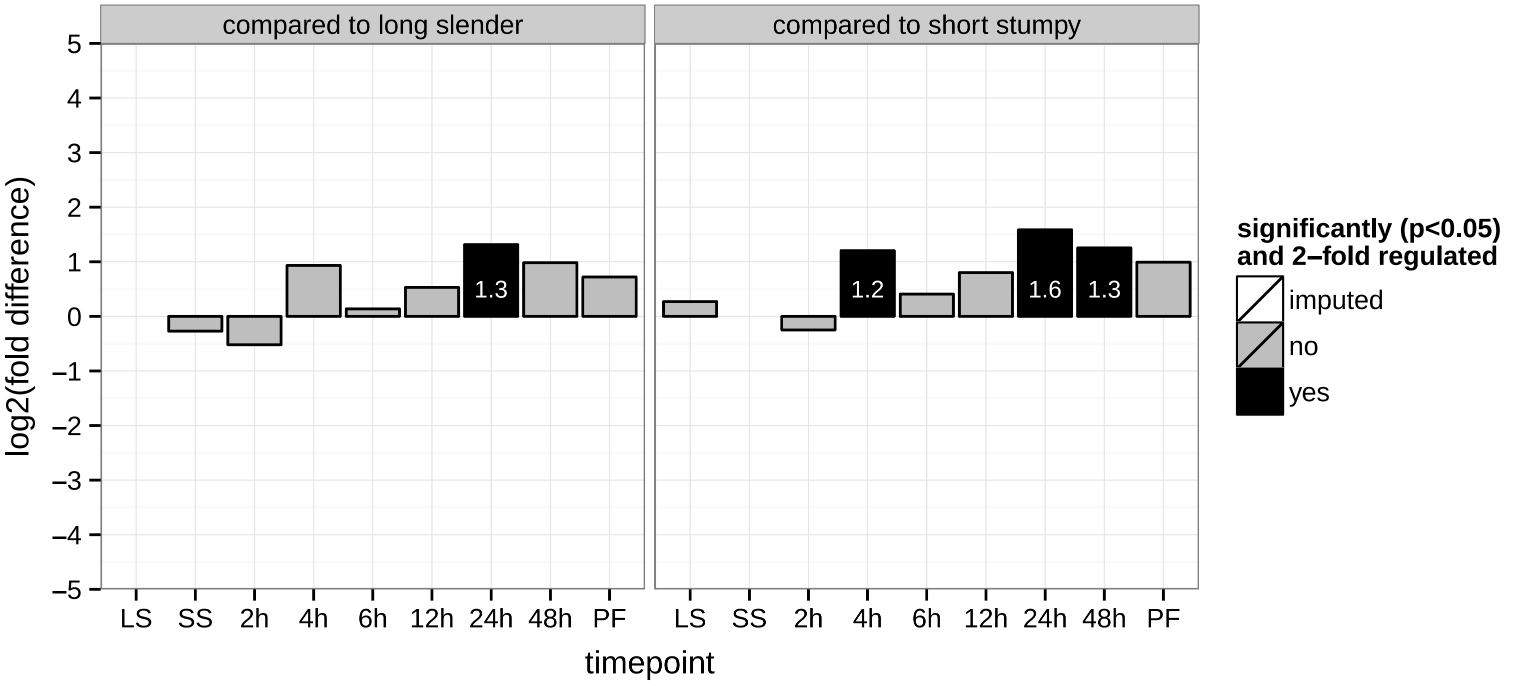
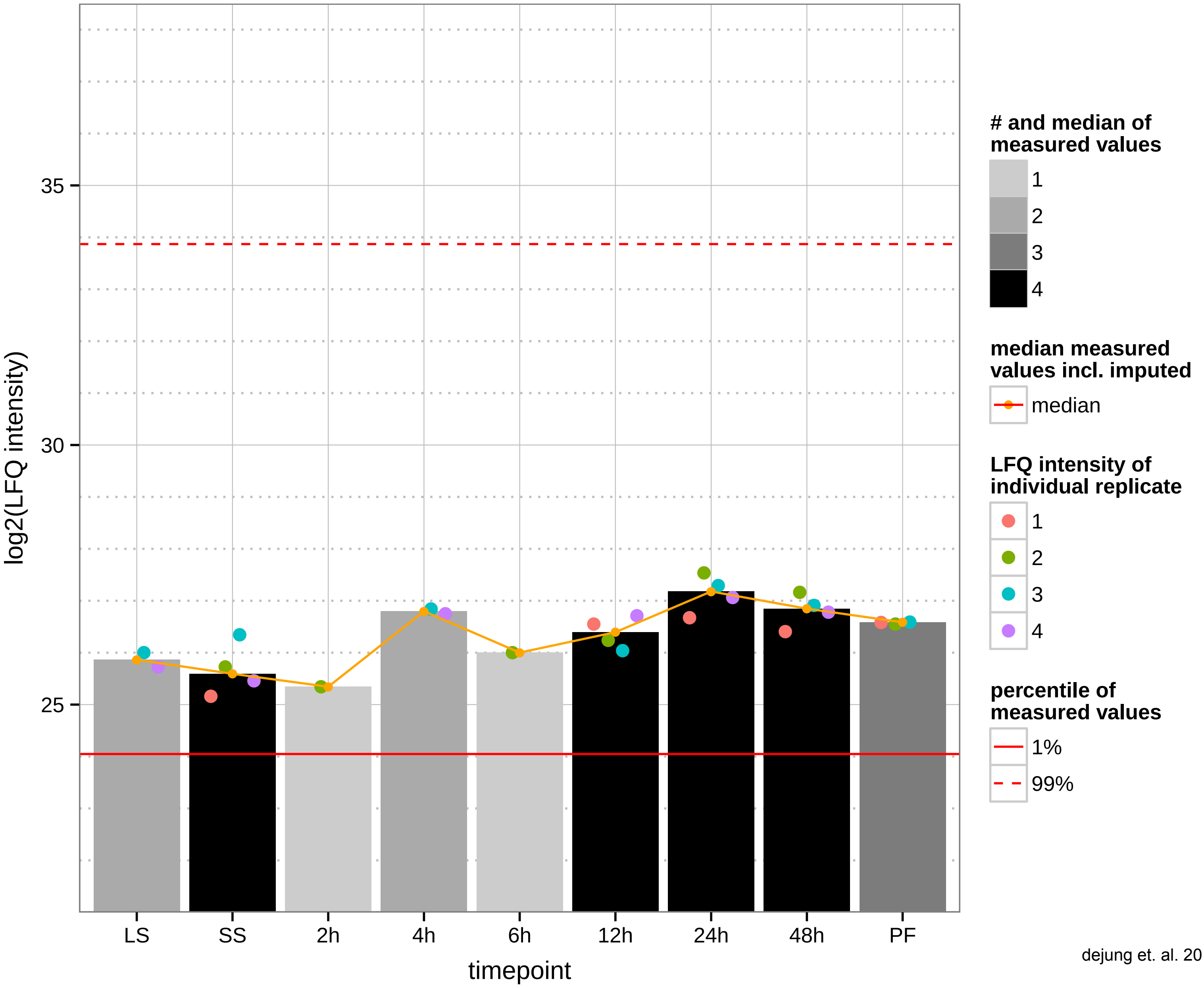
hypothetical protein, conserved
Tb927.7.2200
AGOF: null
AGOC: mitochondrial intermembrane space protein transporter complex, mitochondrion
AGOP: protein import into mitochondrial inner membrane
PGOF: null
PGOC: mitochondrial intermembrane space protein transporter complex
PGOP: protein import into mitochondrial inner membrane, protein targeting to mitochondrion





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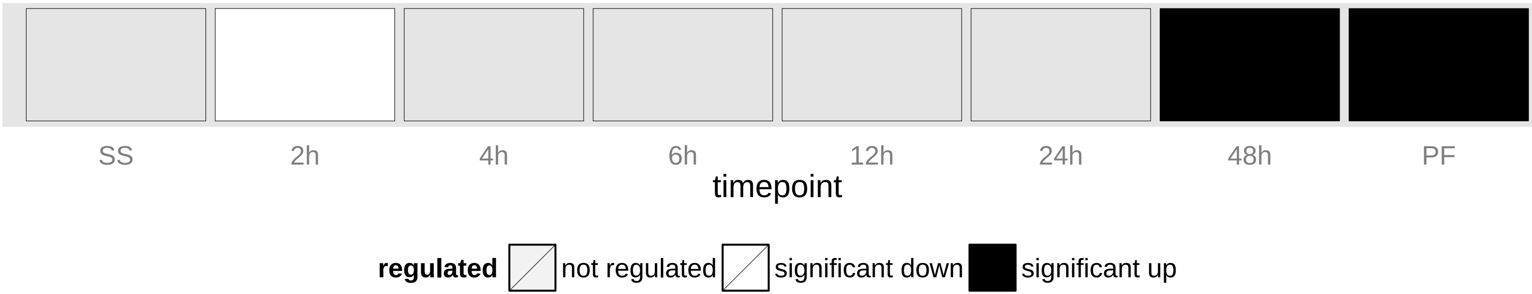

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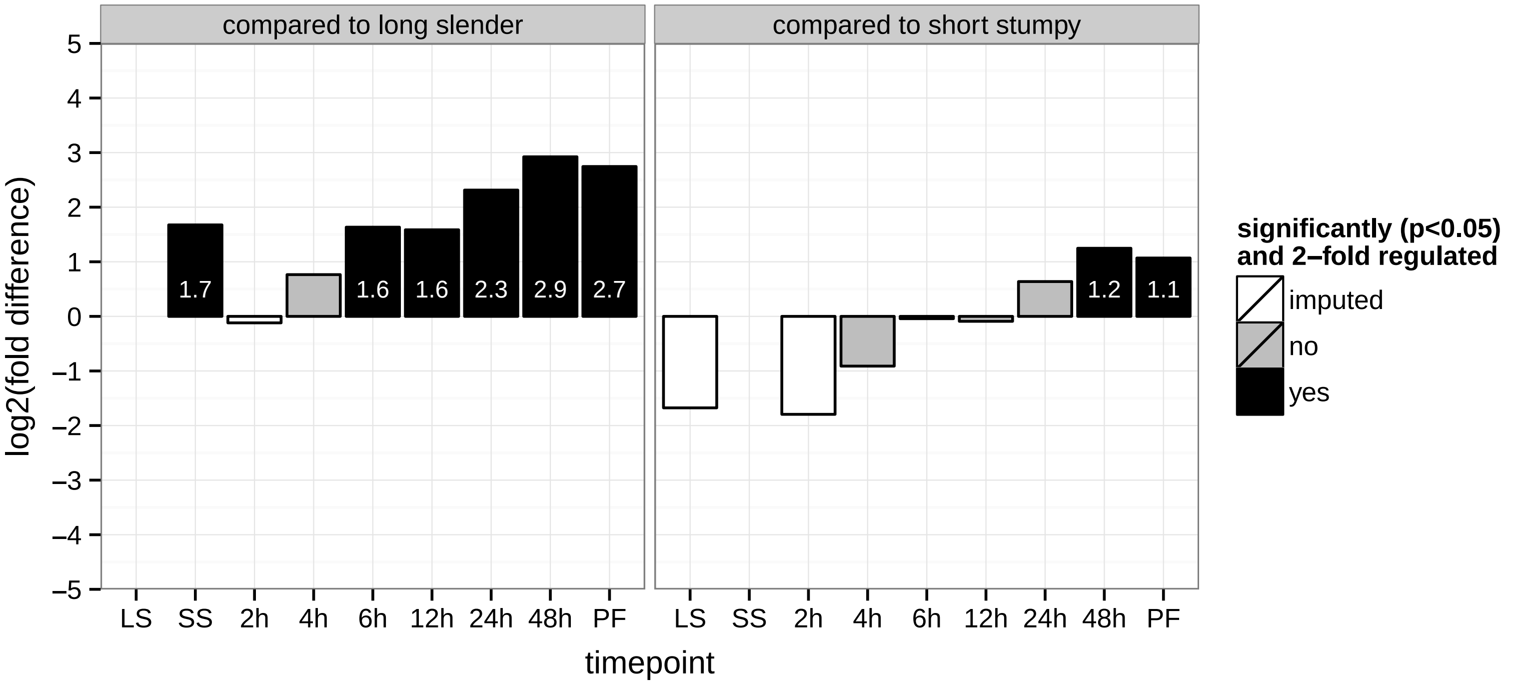
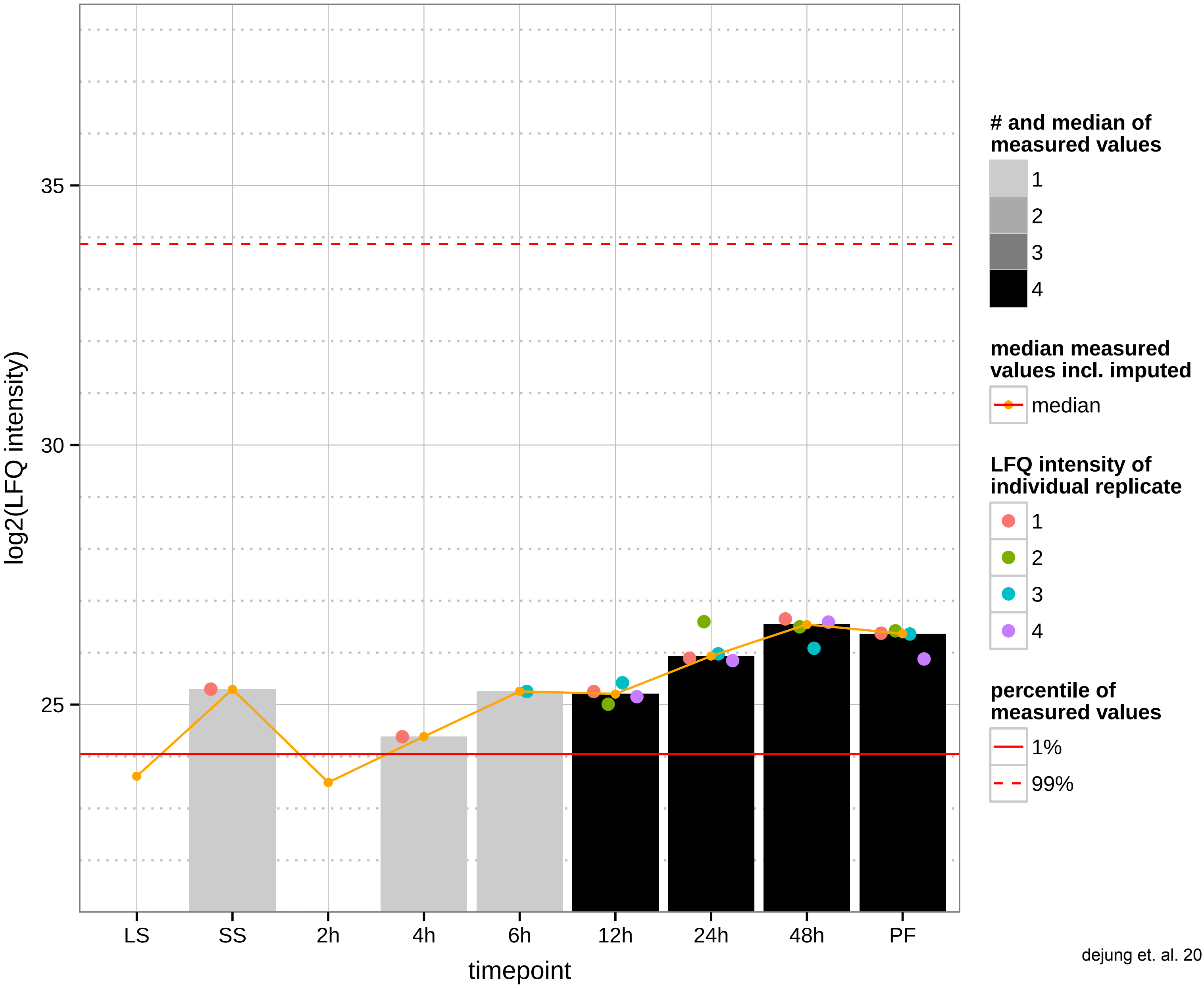
hypothetical protein, conserved
Tb927.10.6300;Tb11.v5.0276
AGOF: null, structural constituent of ribosome
AGOC: null, intracellular, mitochondrion, ribosome
AGOP: null, translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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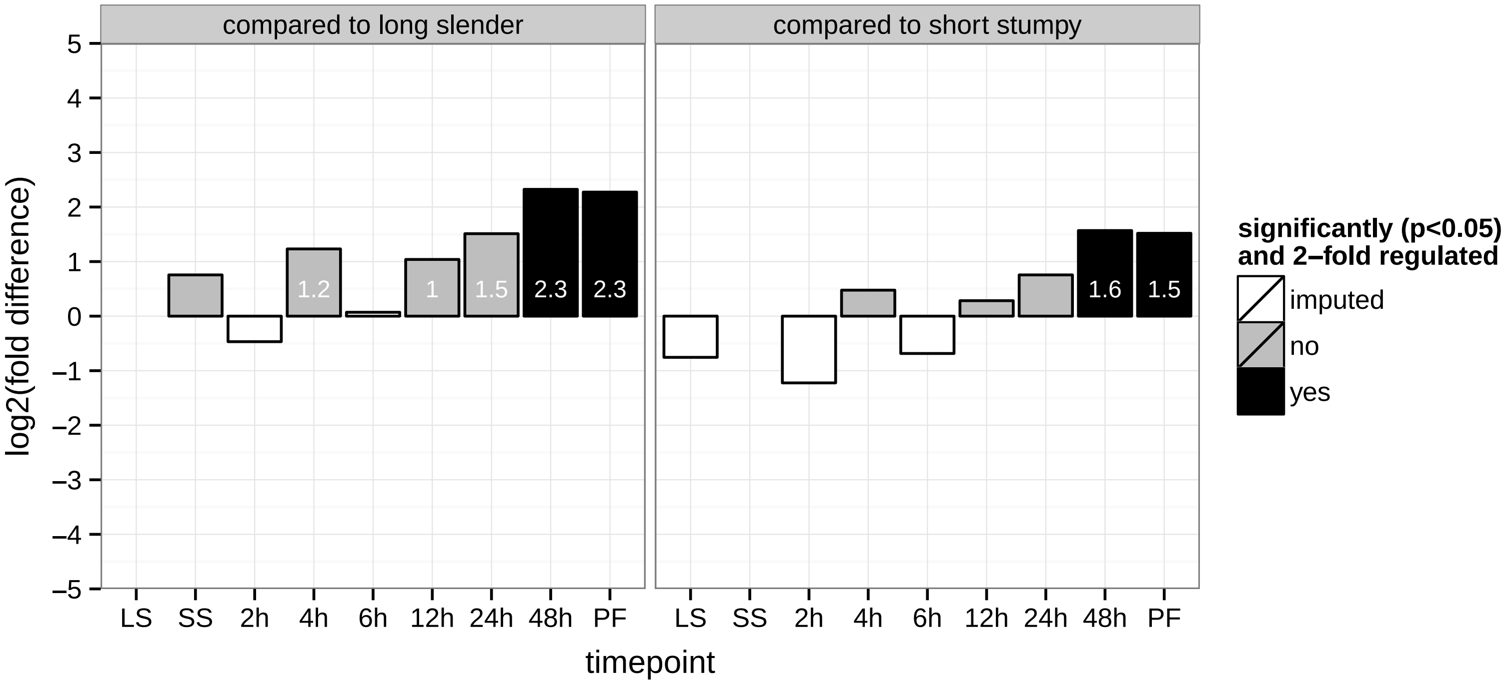
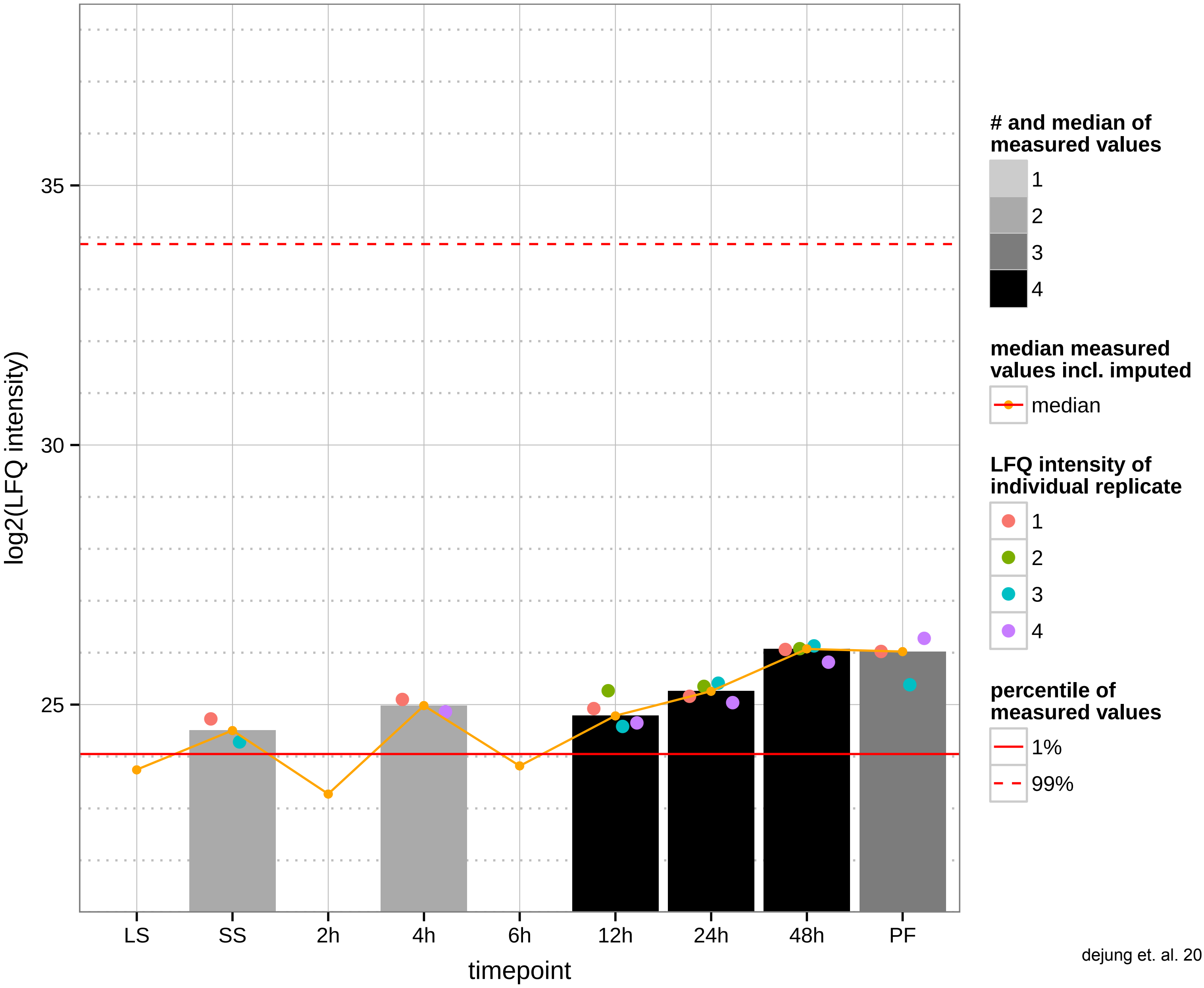
hypothetical protein, conserved
Tb927.4.4340
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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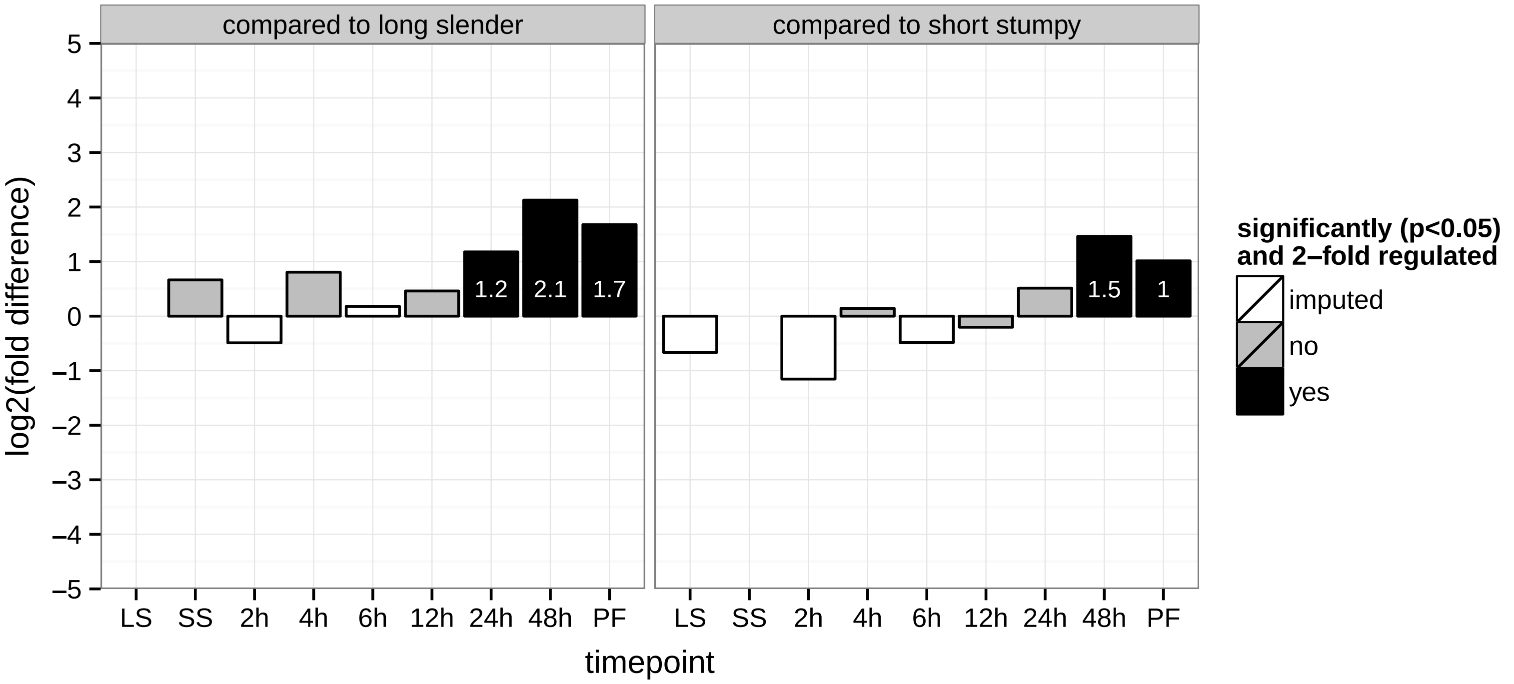
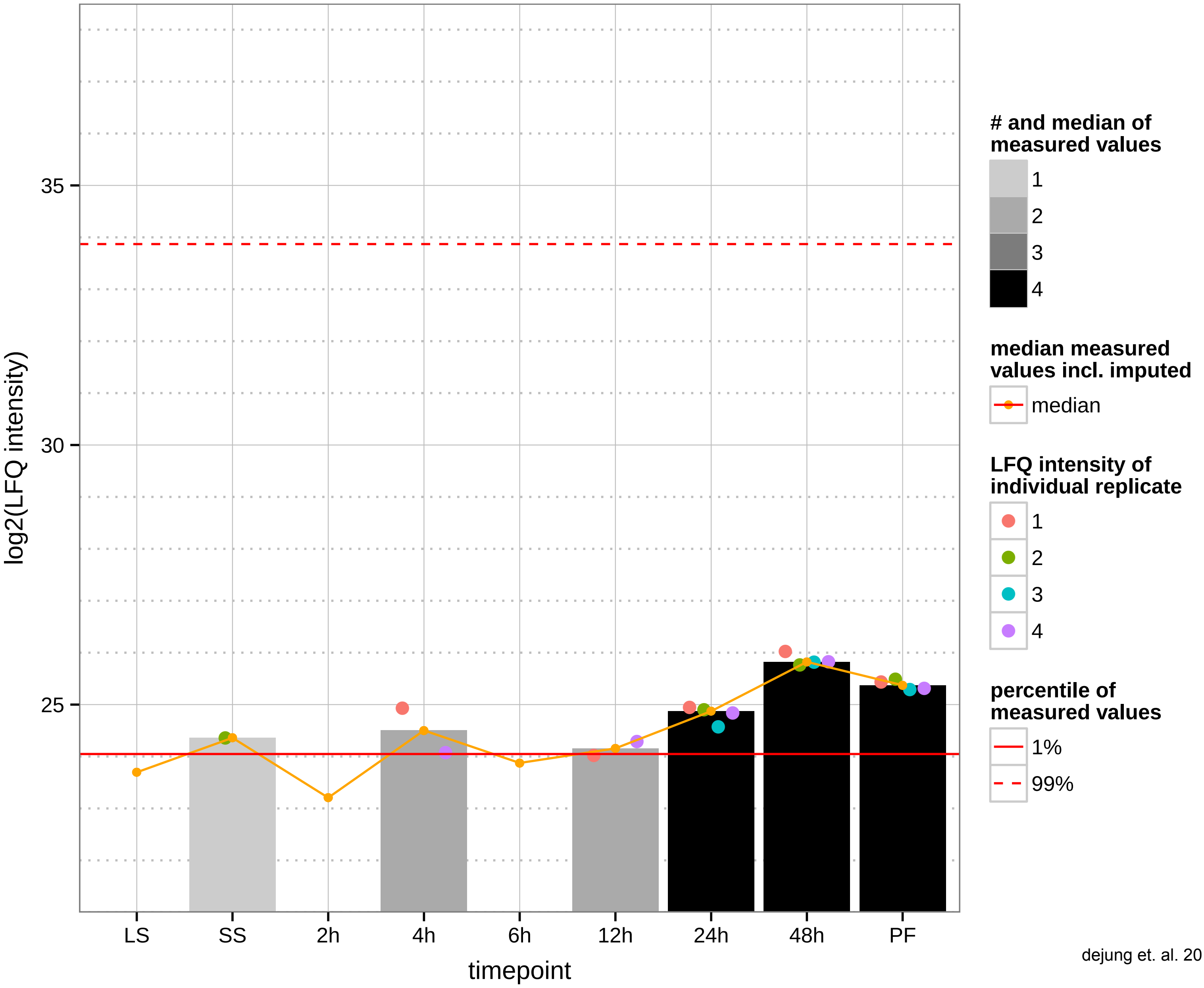
hypothetical protein, conserved, BAC from homologous region on chr5
Tb927.5.4360;Tb05.5K5.20
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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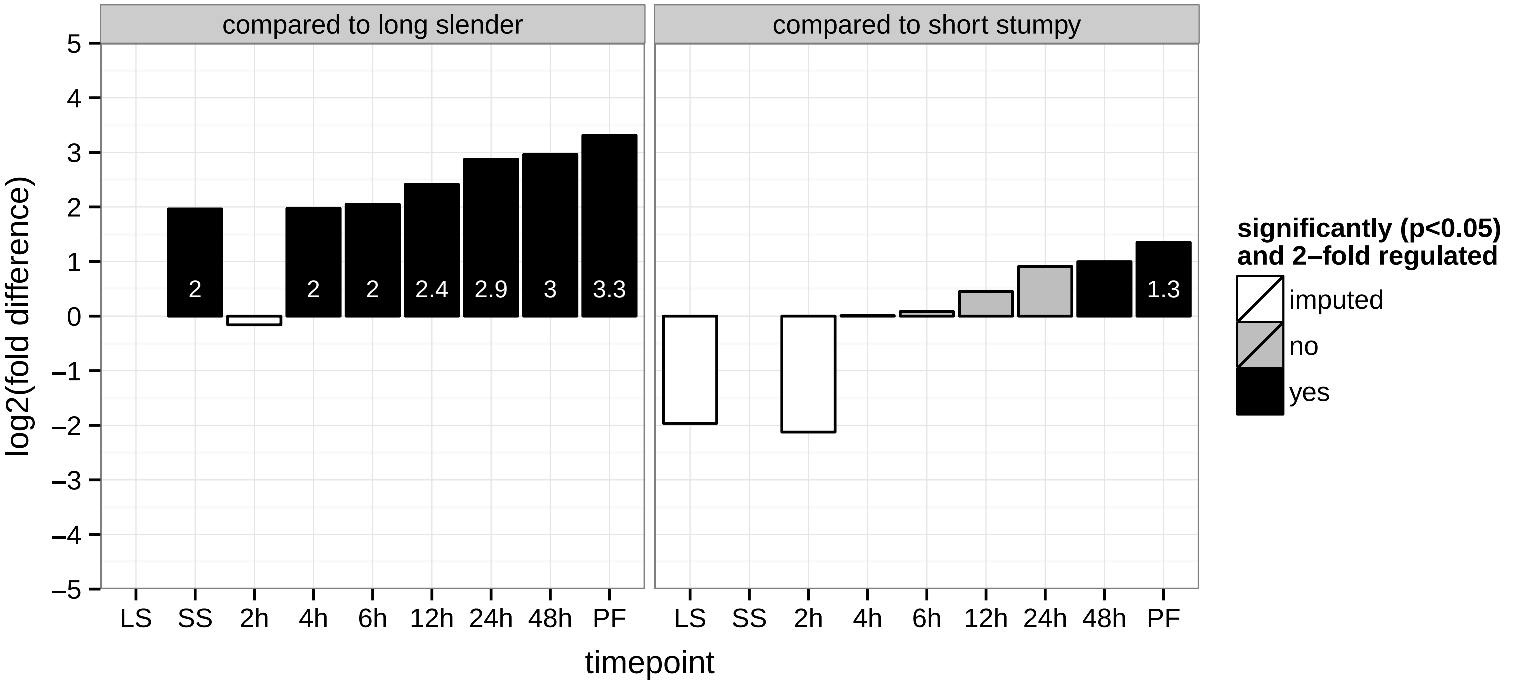
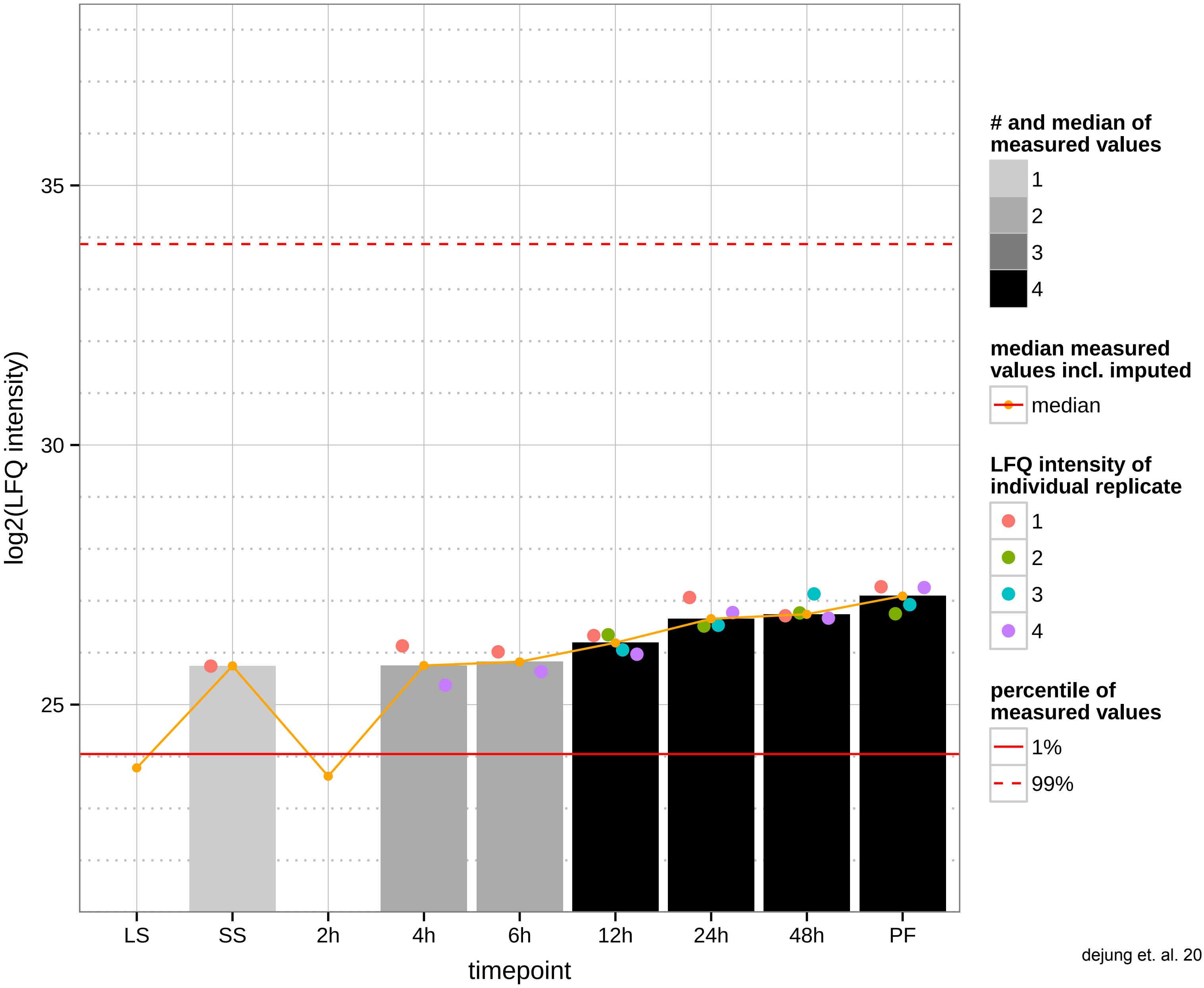
hypothetical protein, conserved
Tb927.8.6770
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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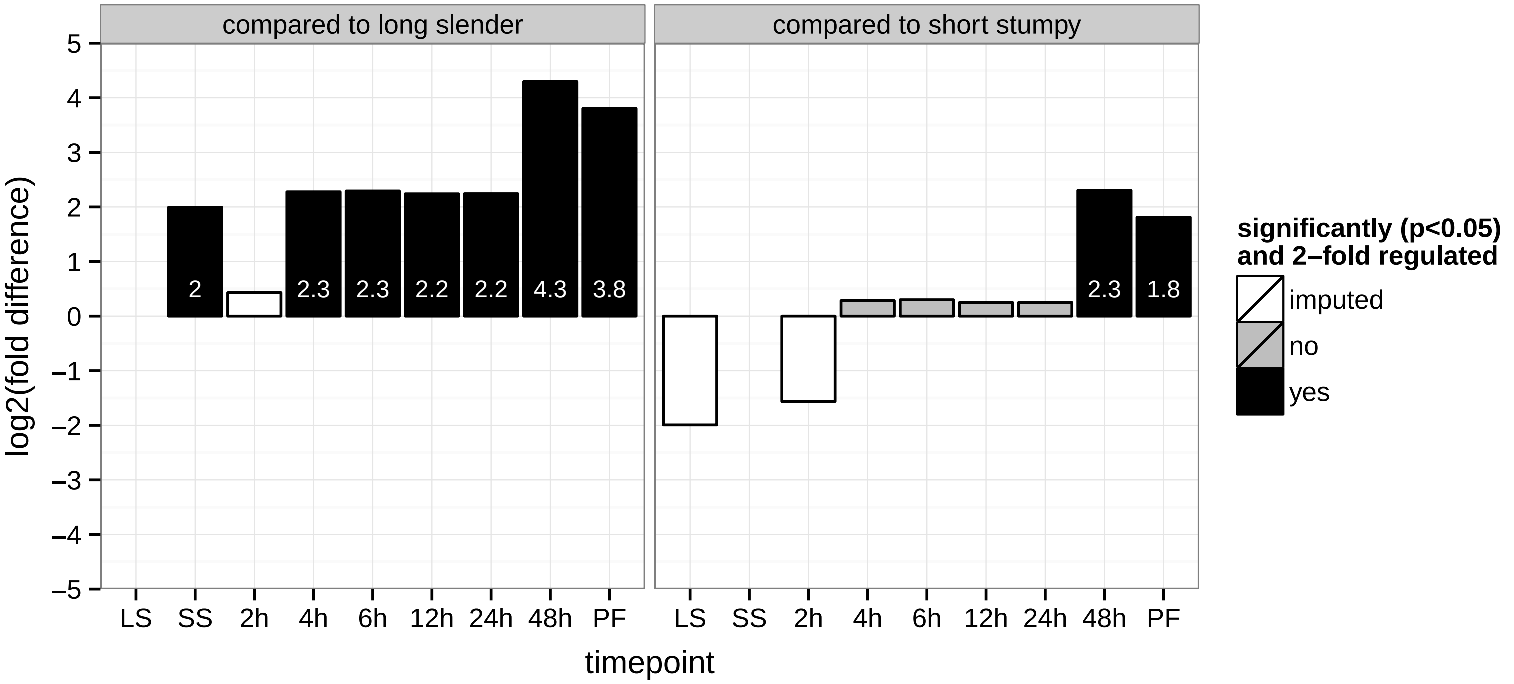
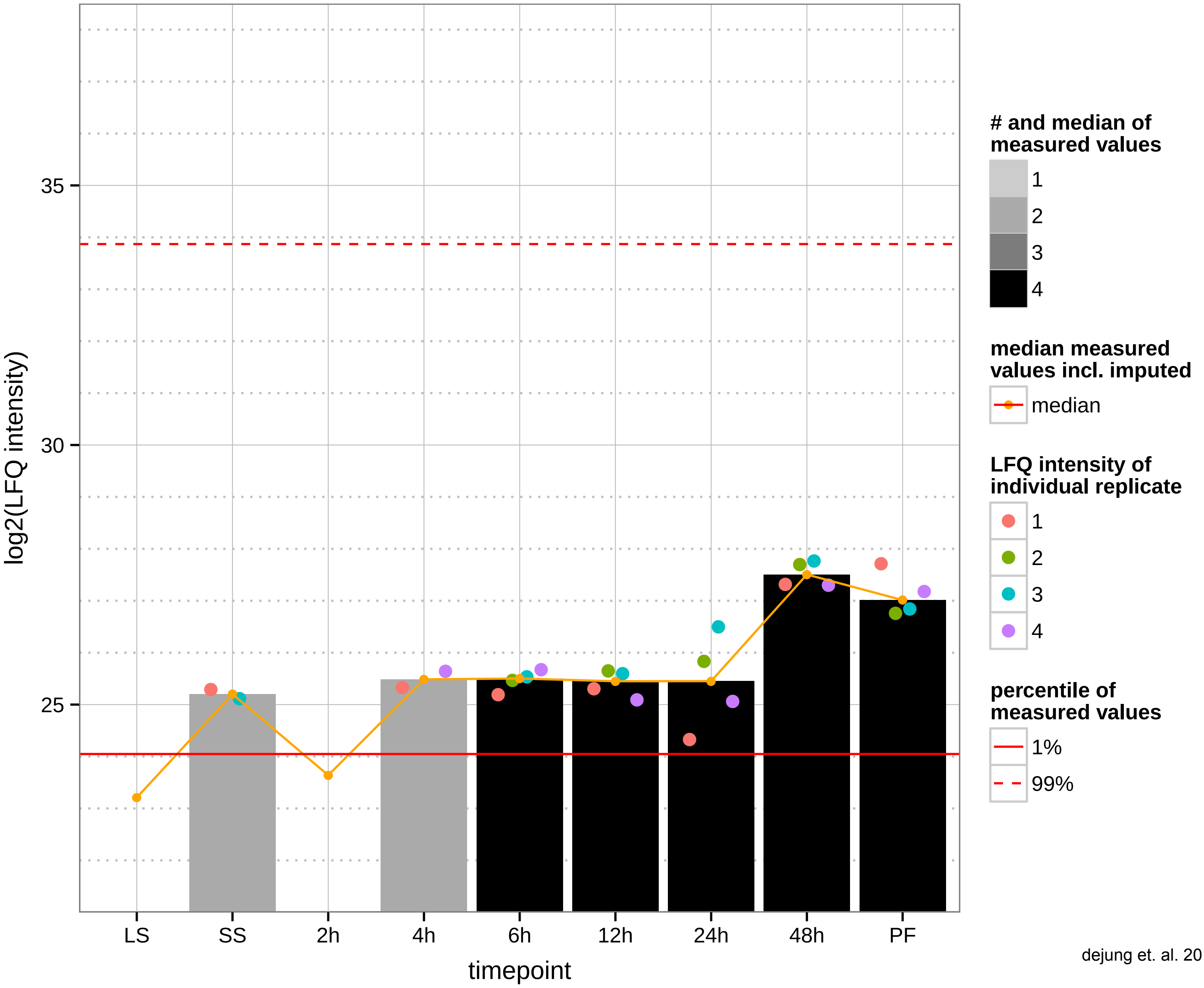
trans−sialidase, putative, neuraminidase
Tb927.8.7340
AGOF: exo−alpha−sialidase activity
AGOC: null
AGOP: pathogenesis
PGOF: null
PGOC: null
PGOP: null





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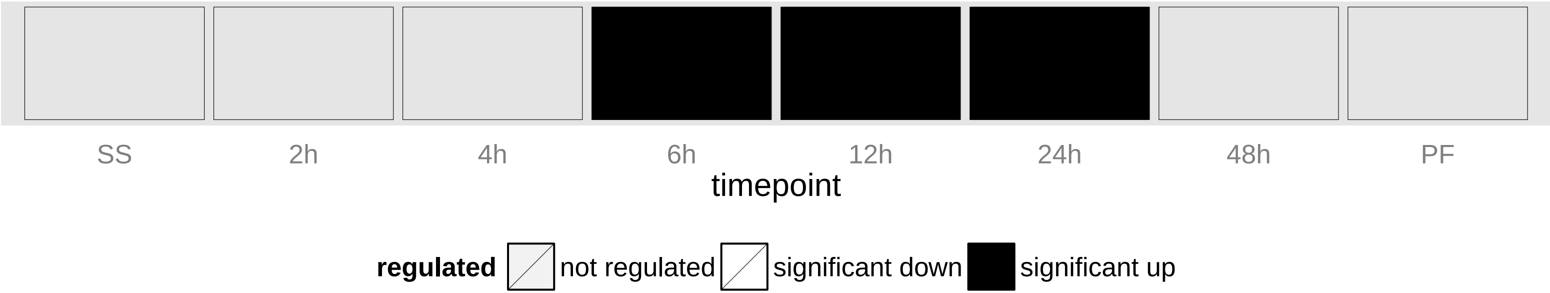

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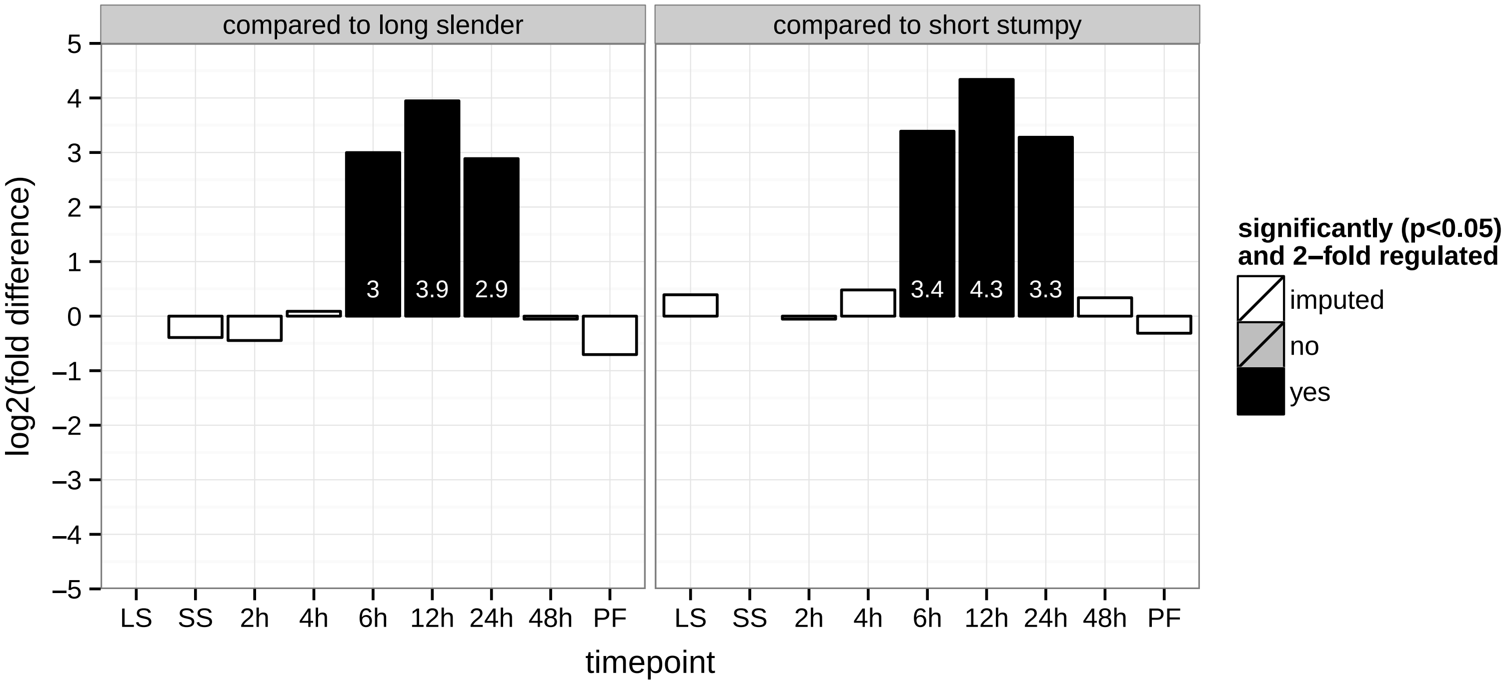
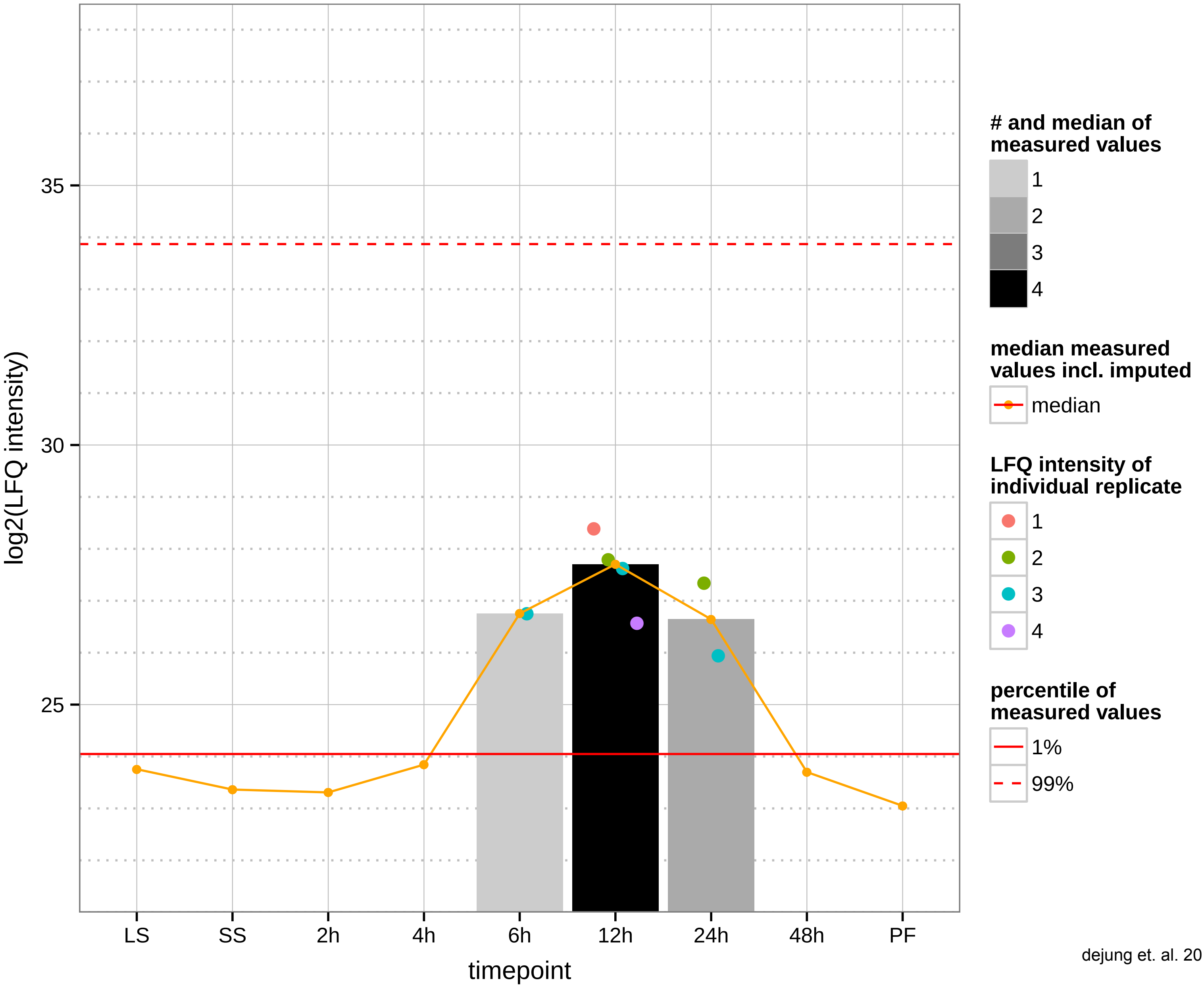
GPI inositol deacylase precursor (GPIdeAc)
Tb927.10.4780
AGOF: phosphatidylinositol deacylase activity
AGOC: membrane
AGOP: GPI anchor biosynthetic process
PGOF: null
PGOC: null
PGOP: null





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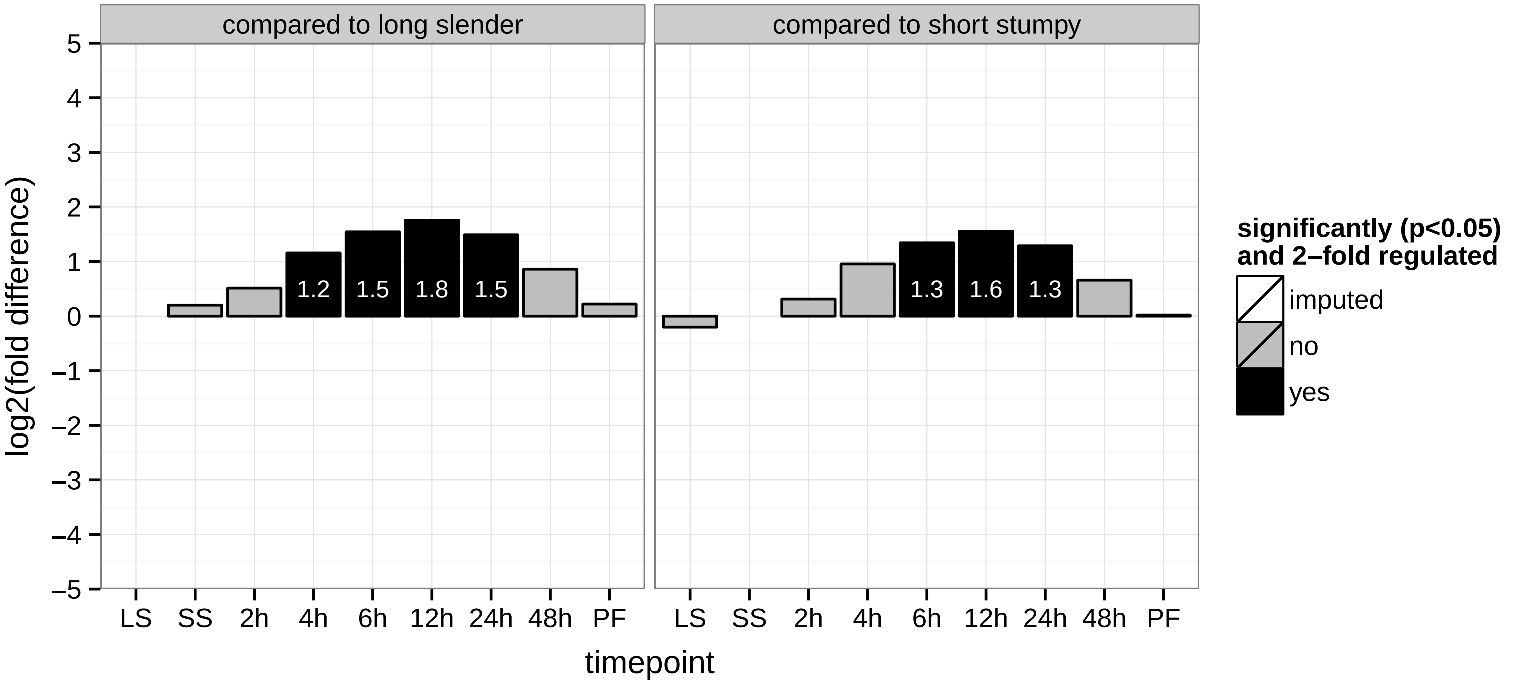
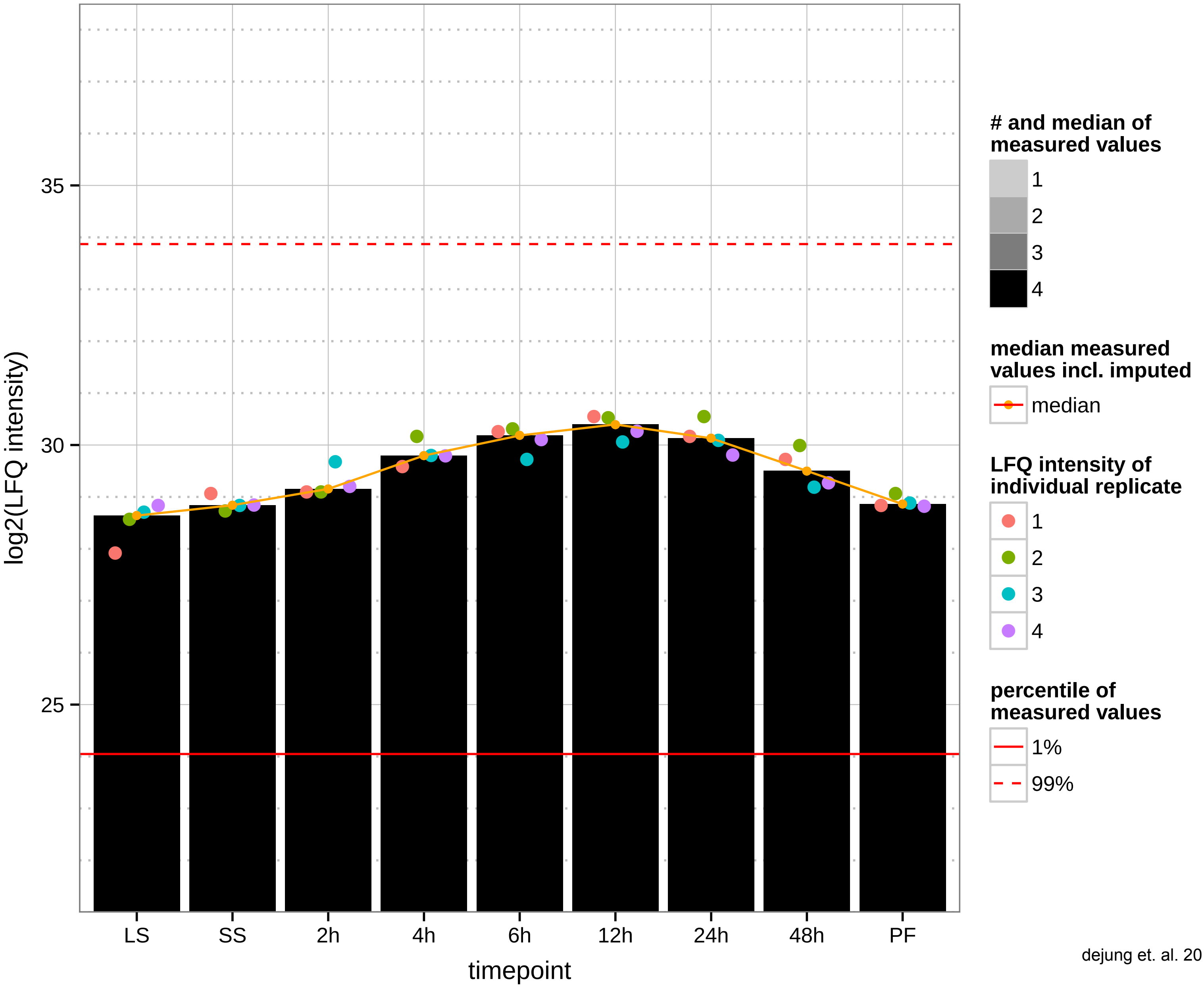
hypothetical protein, conserved
Tb927.10.6730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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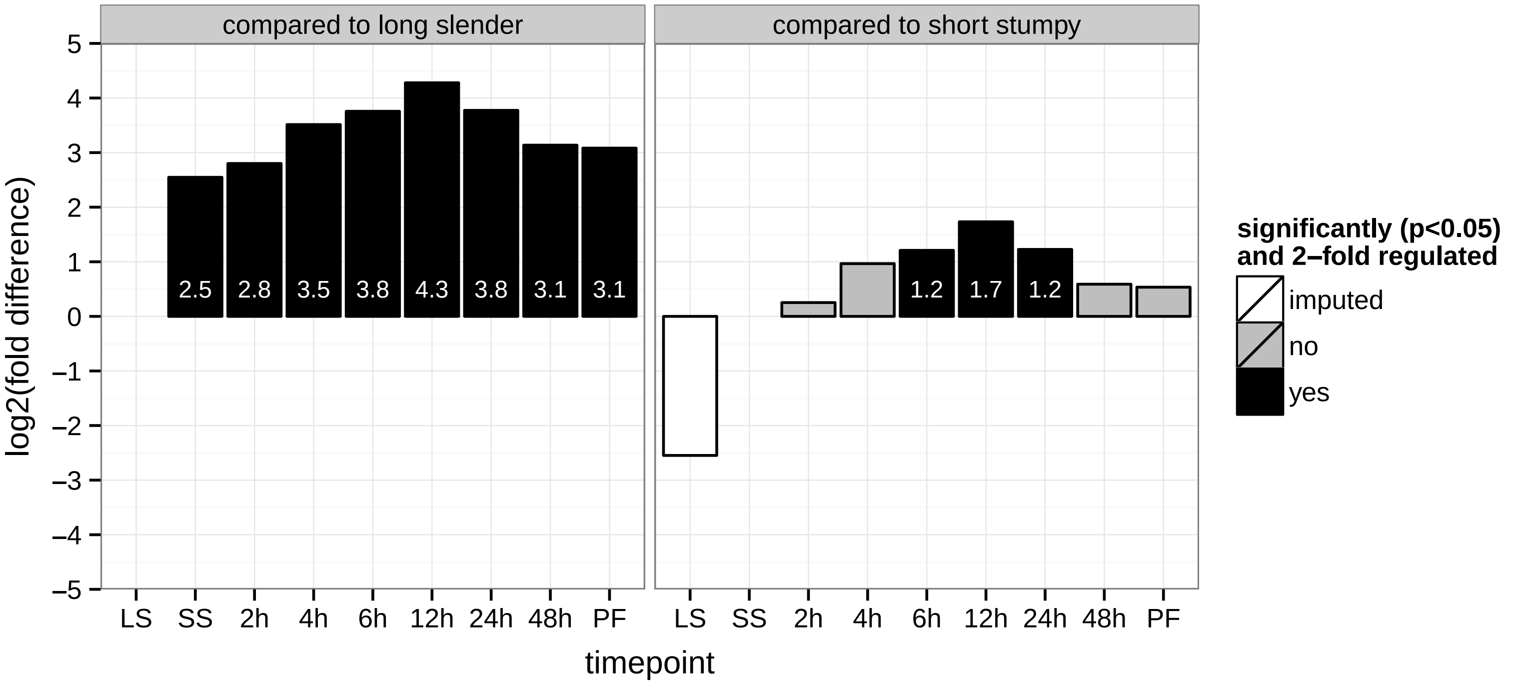
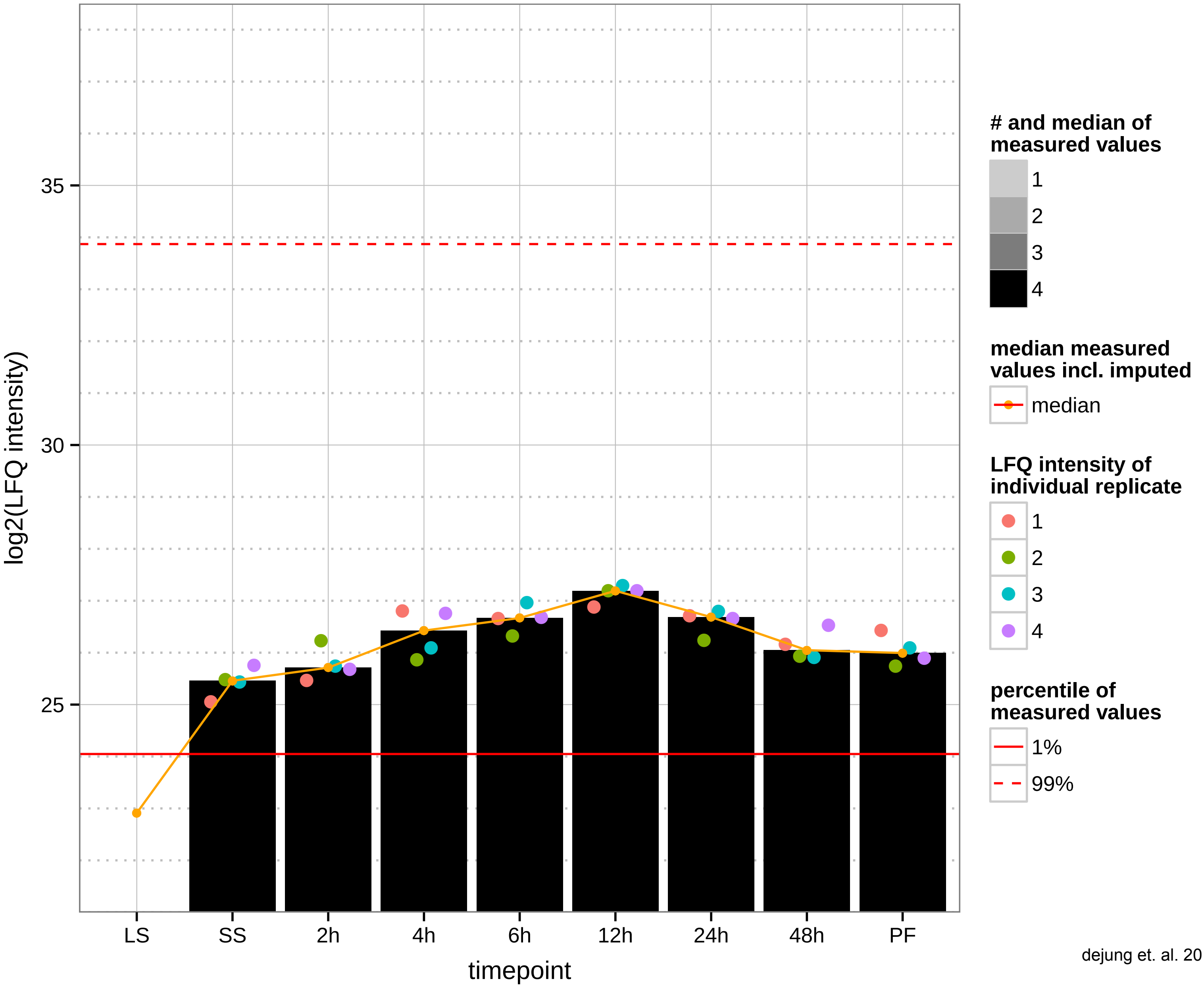
hypothetical protein, conserved
Tb927.7.4360
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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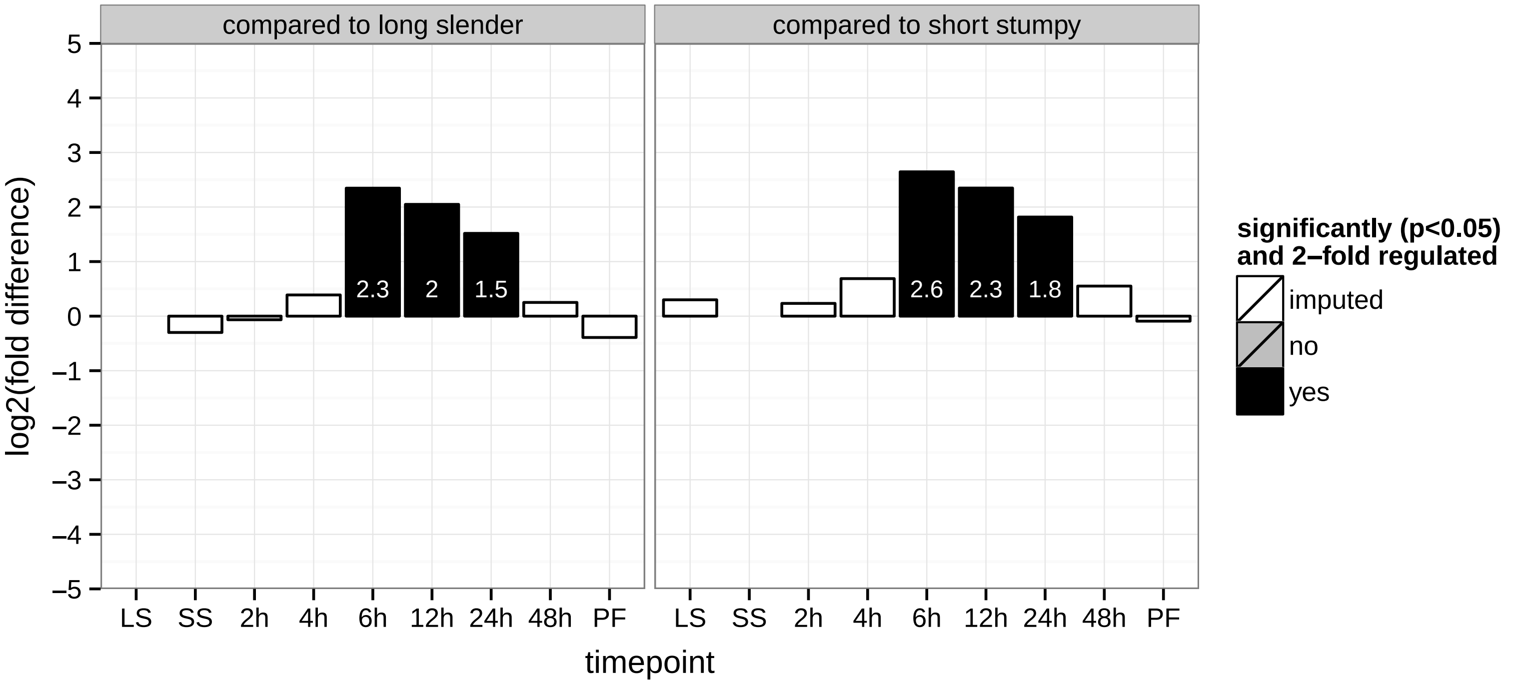
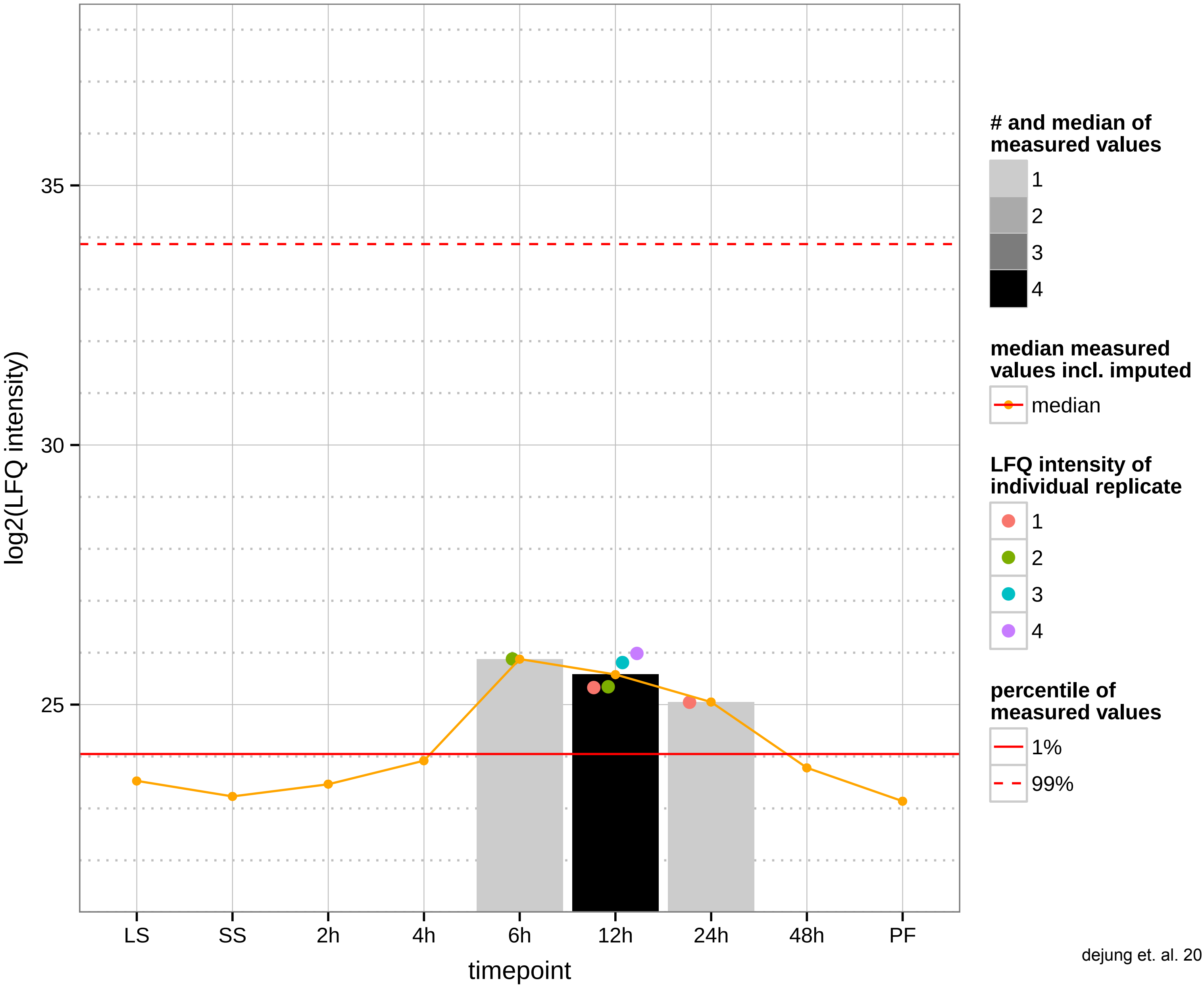
hypothetical protein
Tb927.8.6630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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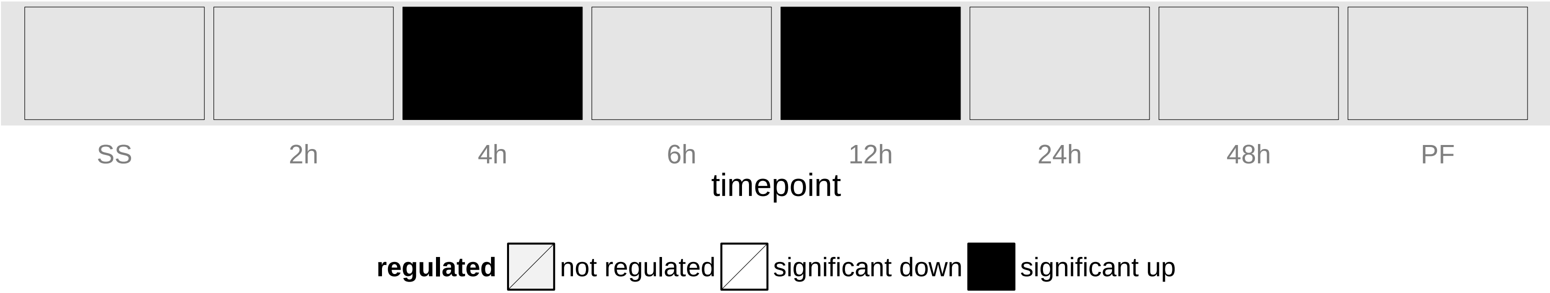

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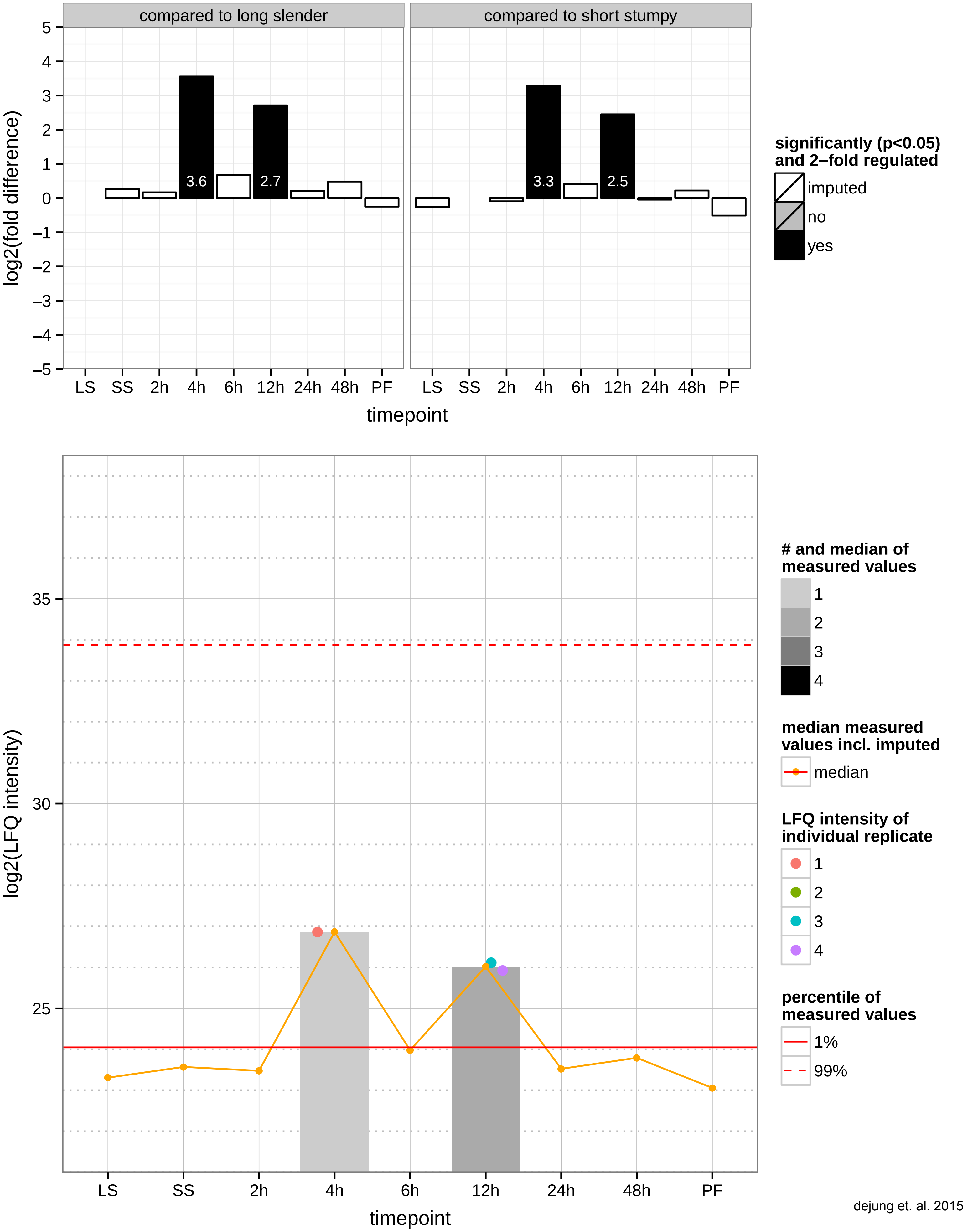
hypothetical protein, conserved
Tb927.11.1380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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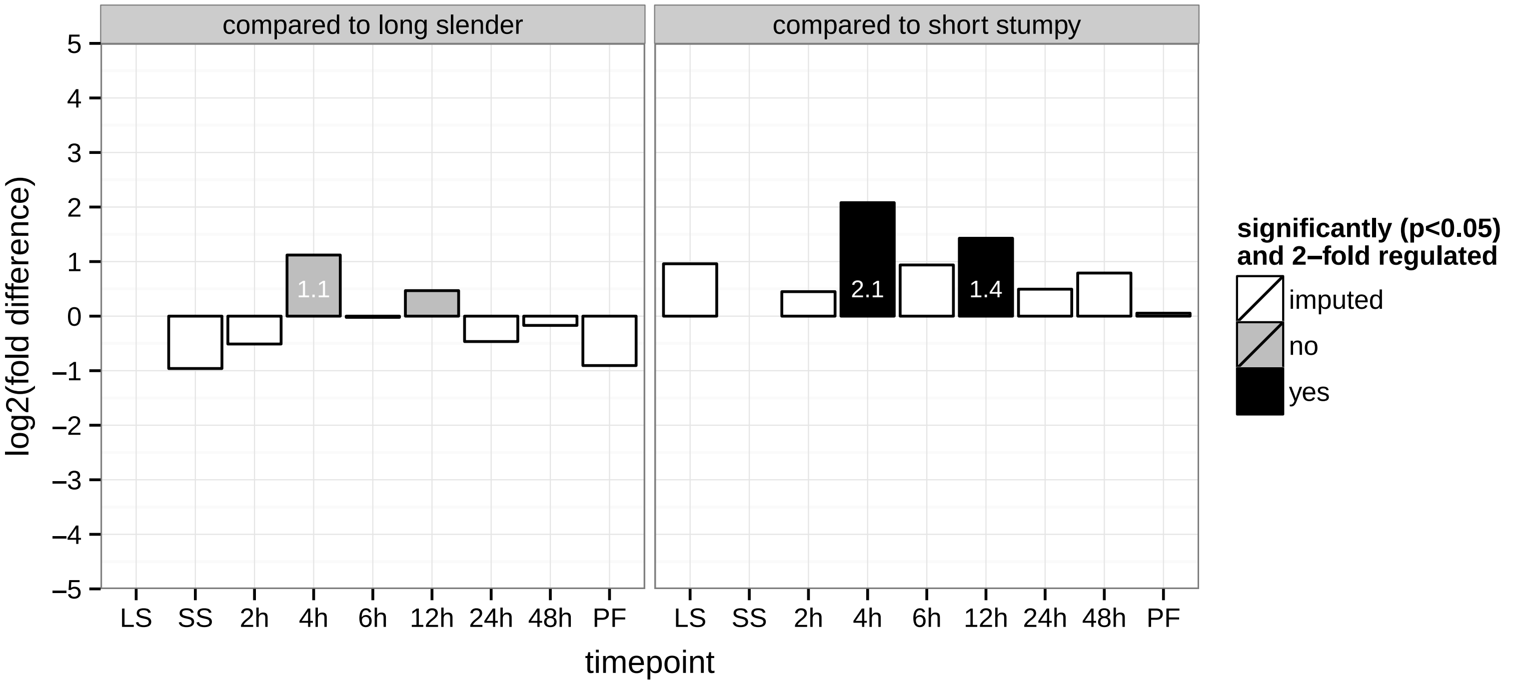
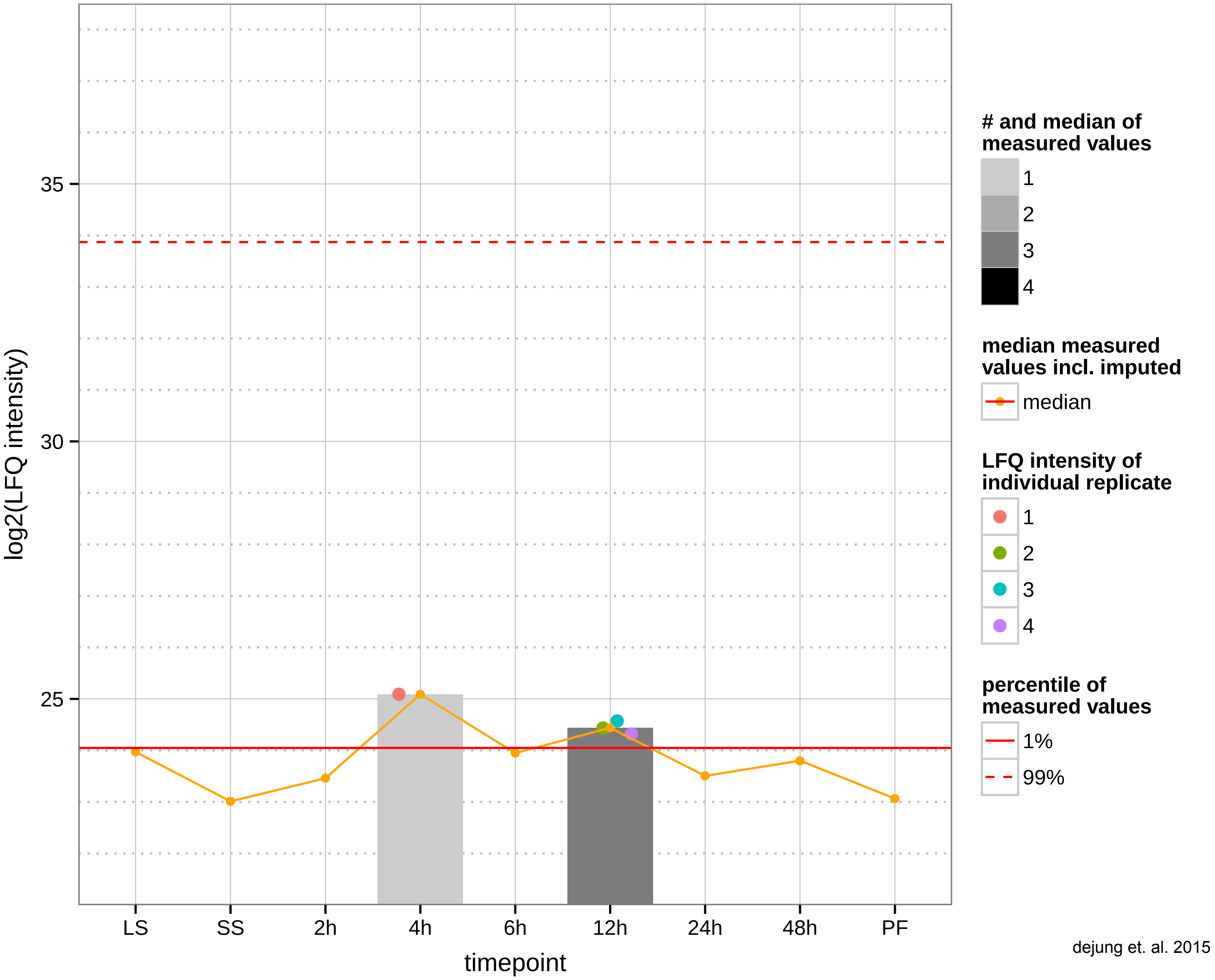
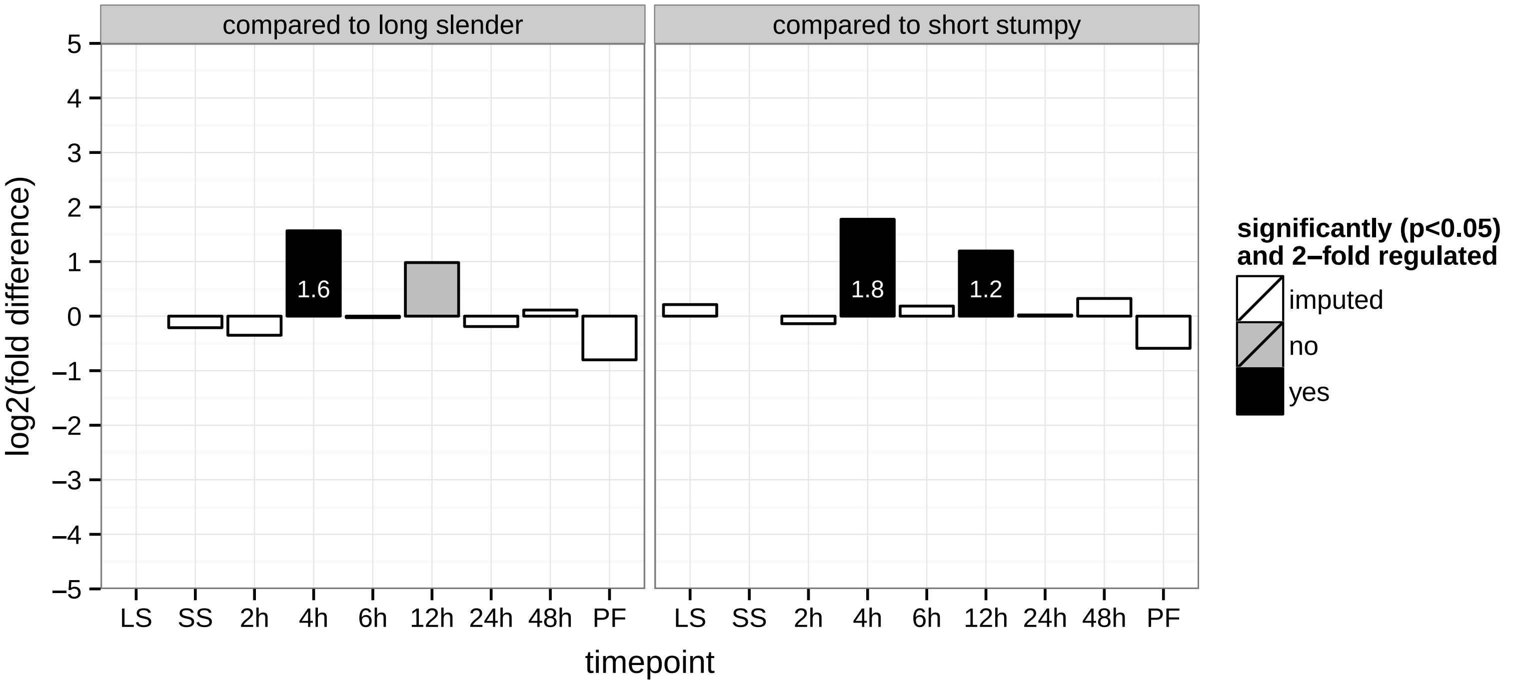
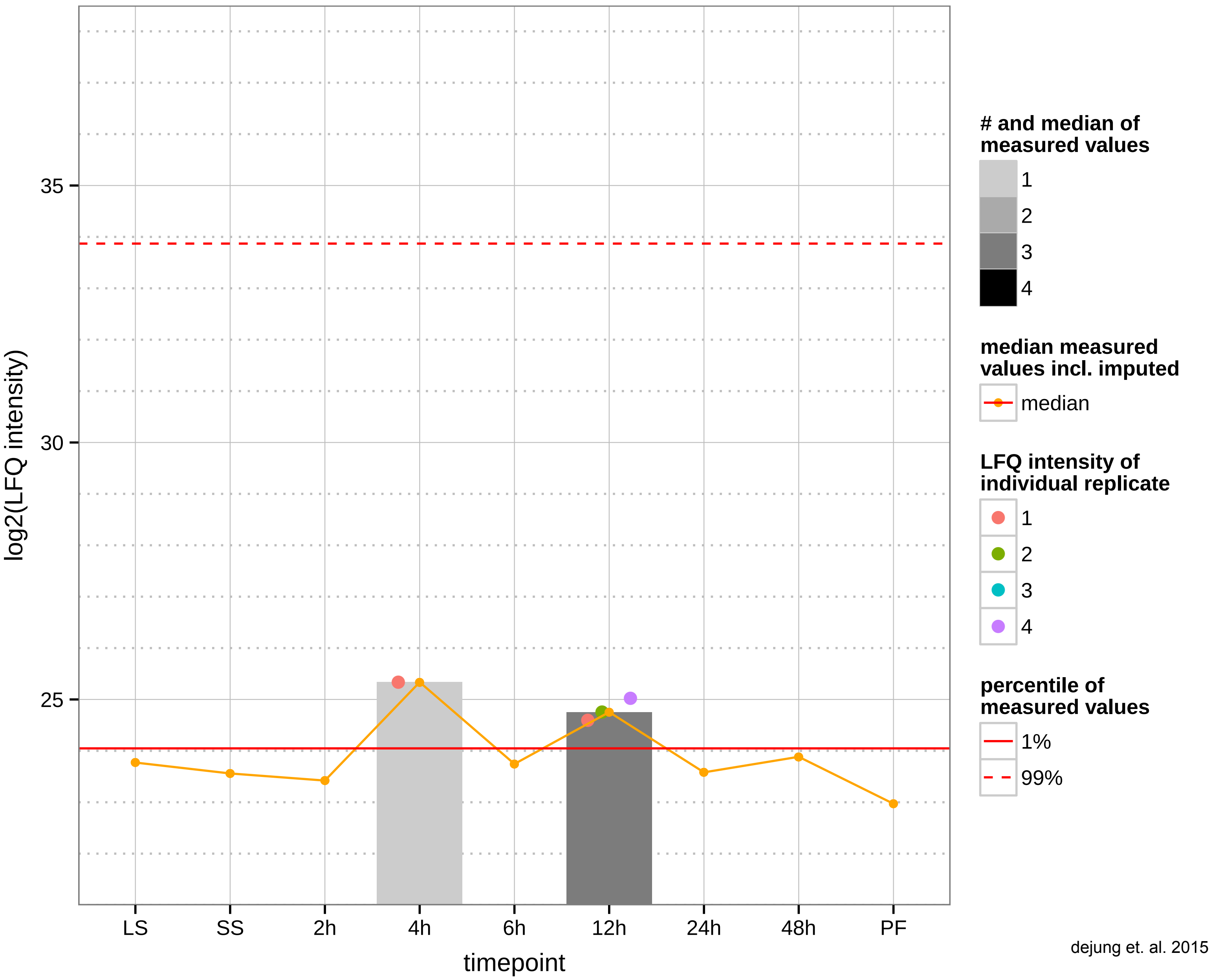
hypothetical protein, conserved
Tb927.11.1610
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





carnitine O−palmitoyltransferase II, putative
Tb927.7.2250
AGOF: transferase activity, transferring acyl groups
AGOC: null
AGOP: null
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: null





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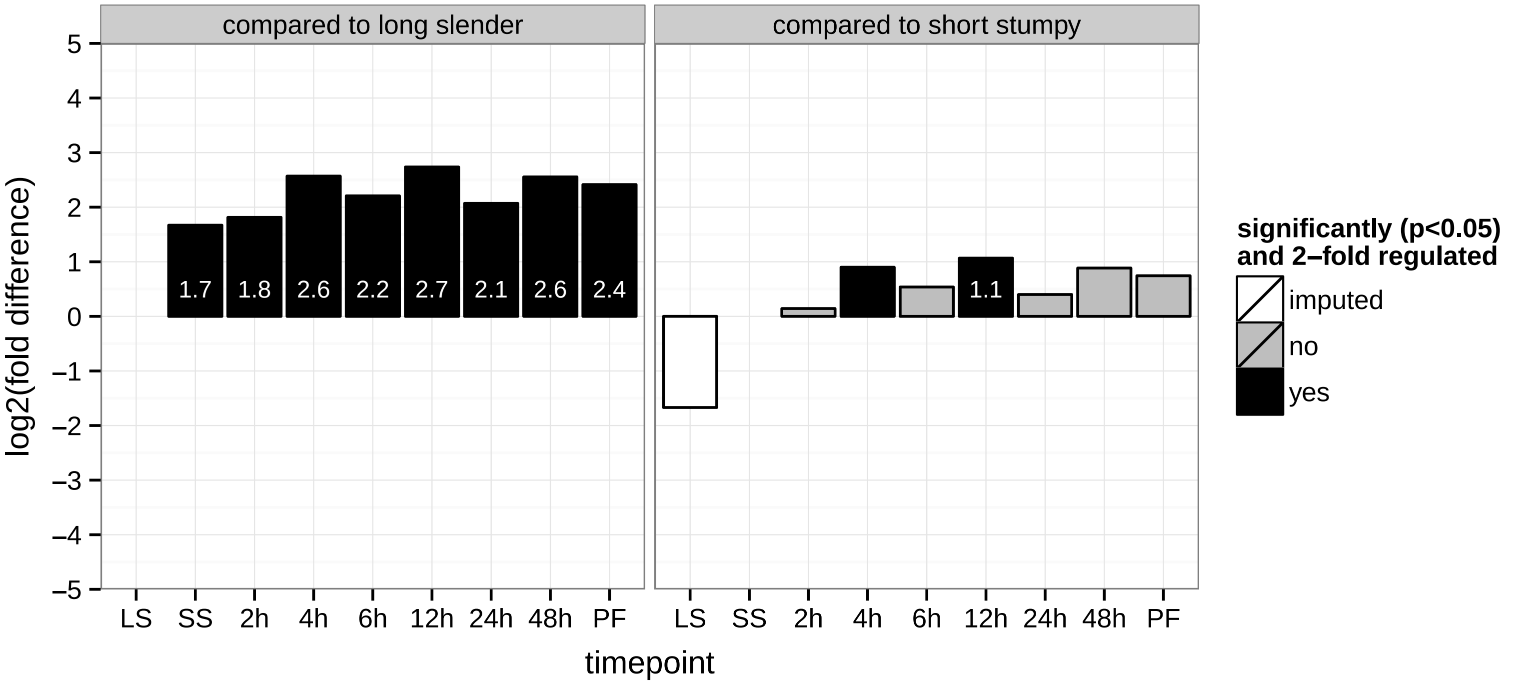
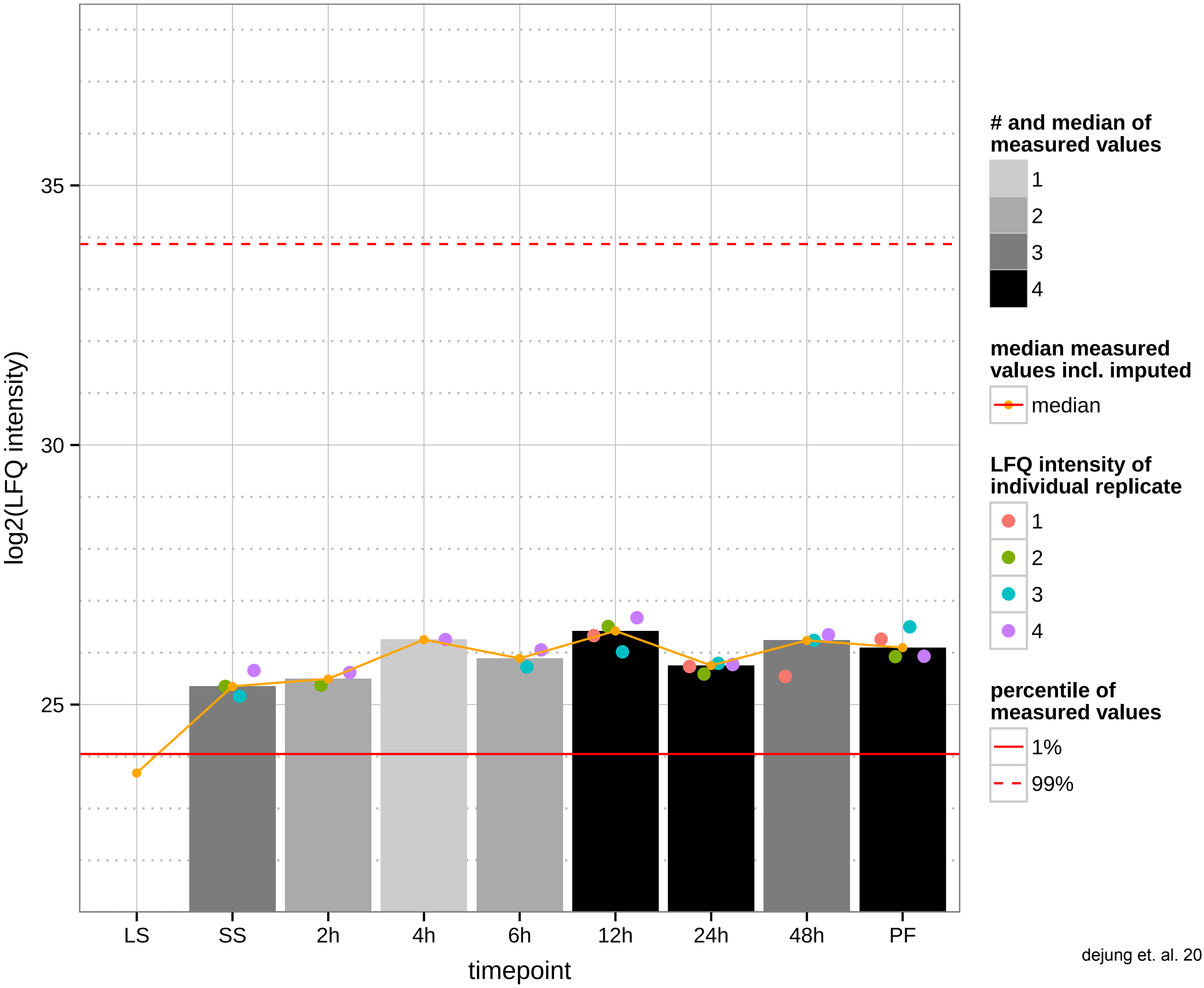
CDP–diacylglycerol––inositol 3–phosphatidyltransferase, putative, phosphatidyltransferase
Tb927.9.1610
AGOF: CDP–diacylglycerol–inositol 3–phosphatidyltransferase activity, phosphatidylinositol transporter activity
AGOC: Golgi apparatus, endoplasmic reticulum, membrane
AGOP: phospholipid biosynthetic process
PGOF: phosphotransferase activity, for other substituted phosphate groups
PGOC: membrane
PGOP: phospholipid biosynthetic process





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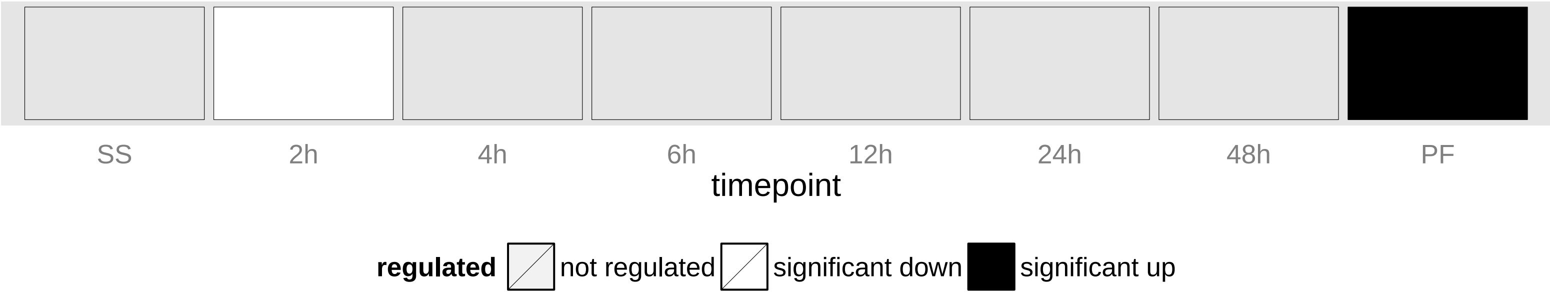
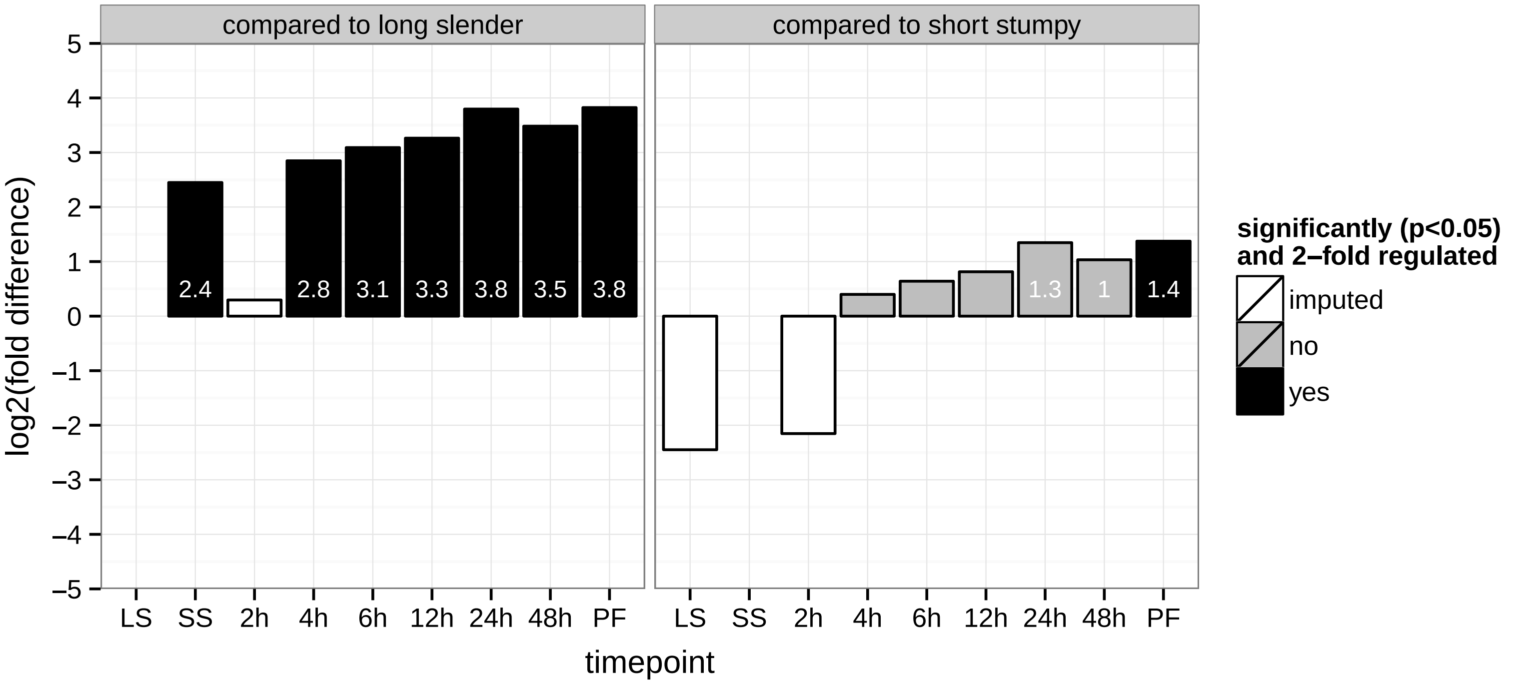
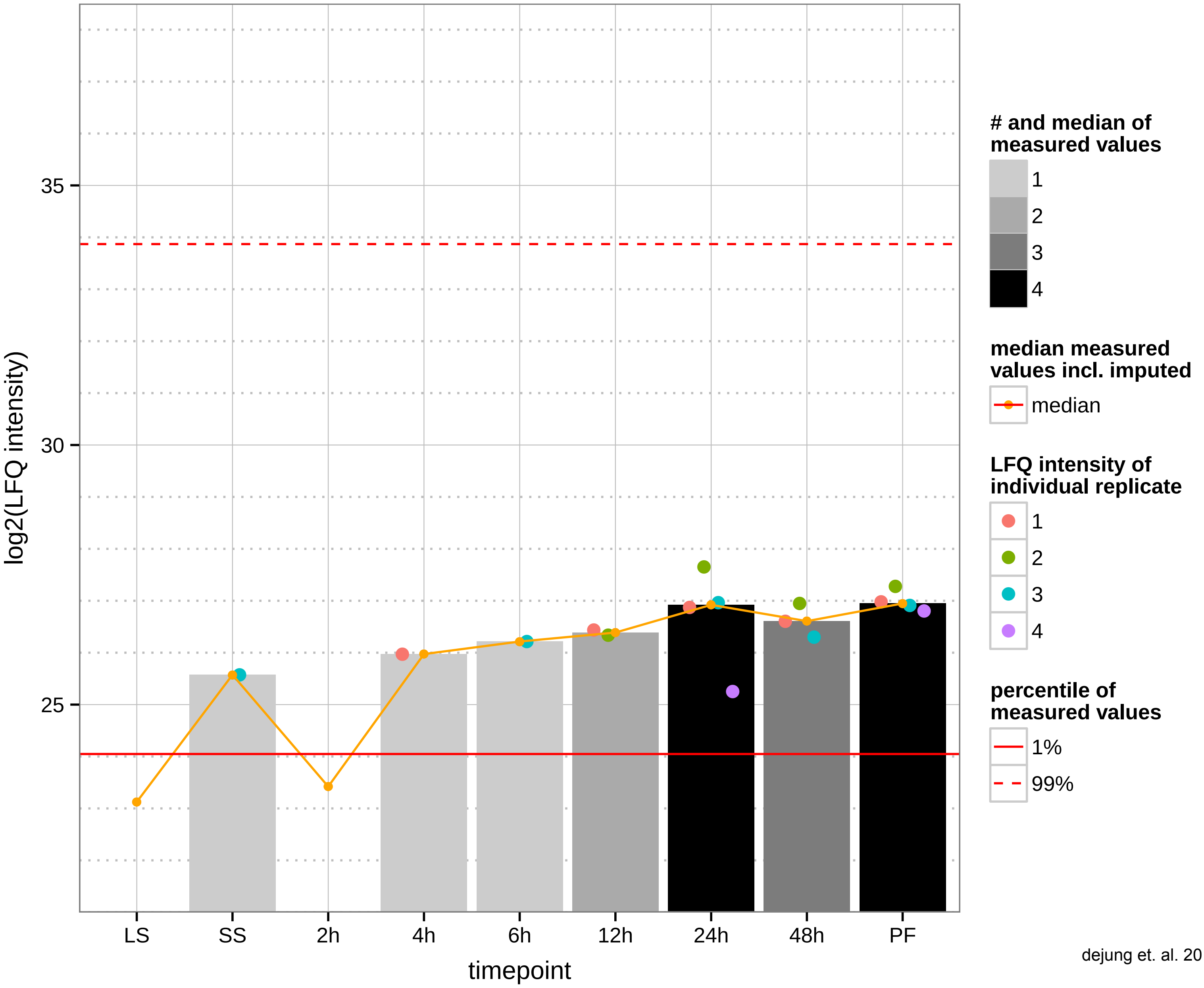


dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.1660
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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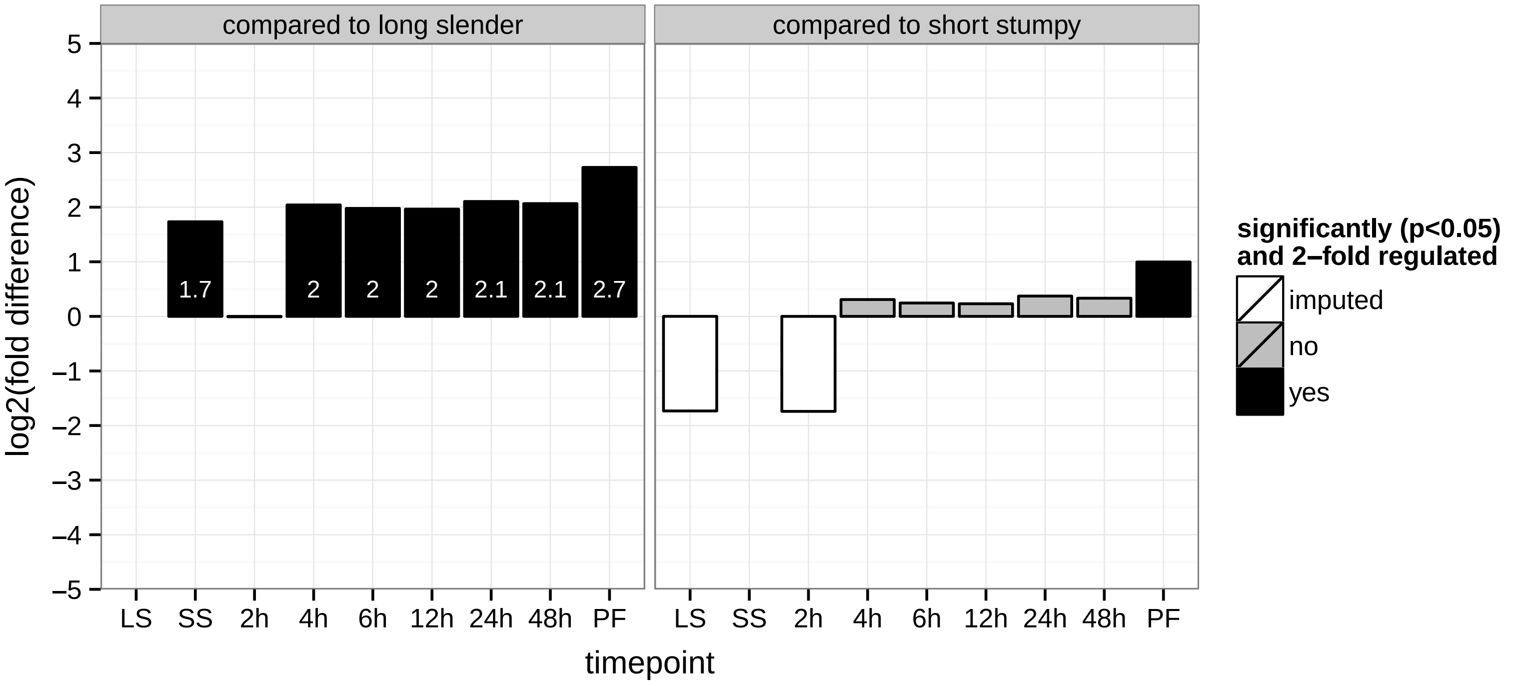
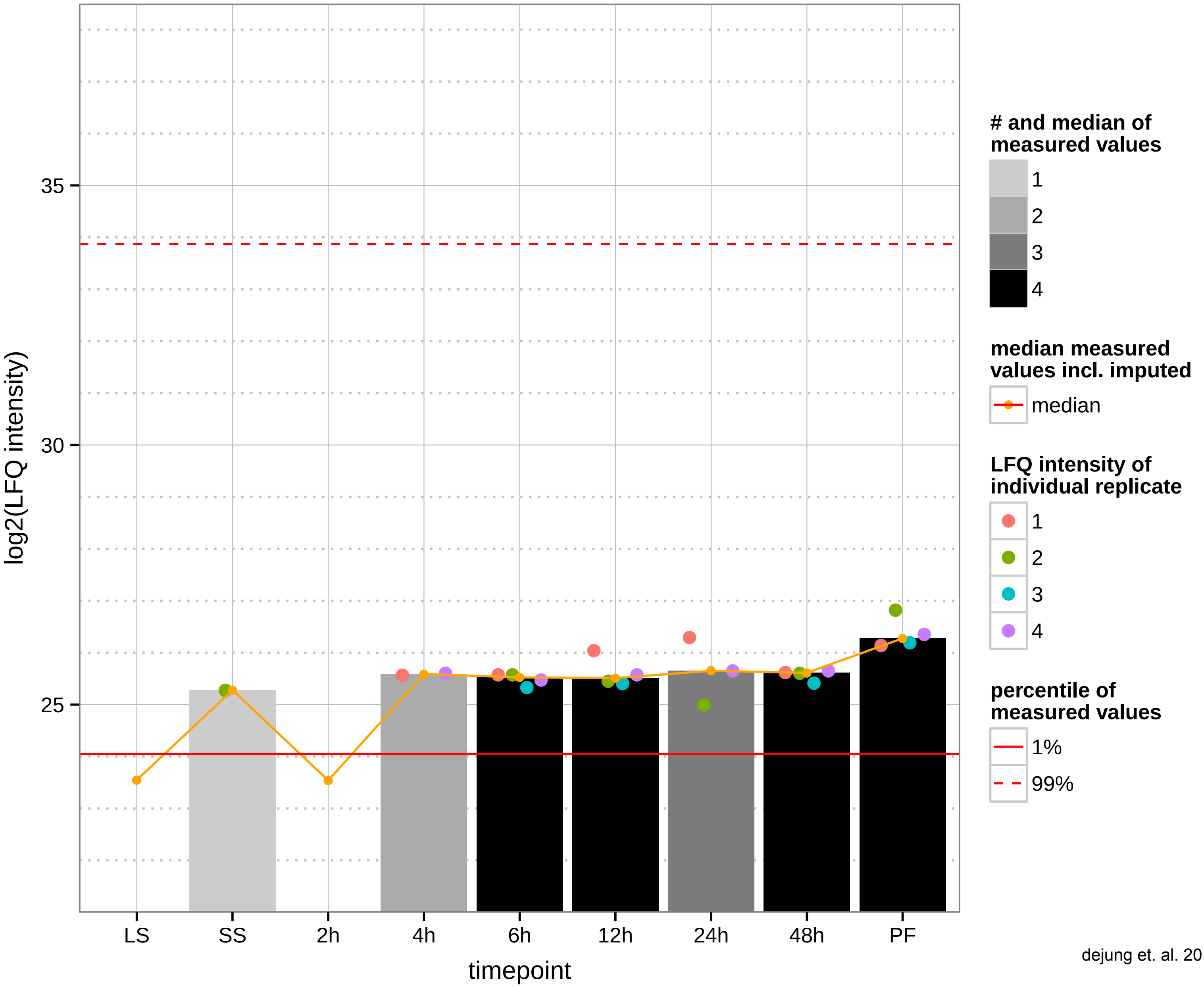
kinetoplastid–specific dual specificity phosphatase, putative
Tb927.2.4280
AGOF: protein tyrosine/serine/threonine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: phosphatase activity, protein tyrosine/serine/threonine phosphatase activity
PGOC: null
PGOP: dephosphorylation, protein dephosphorylation





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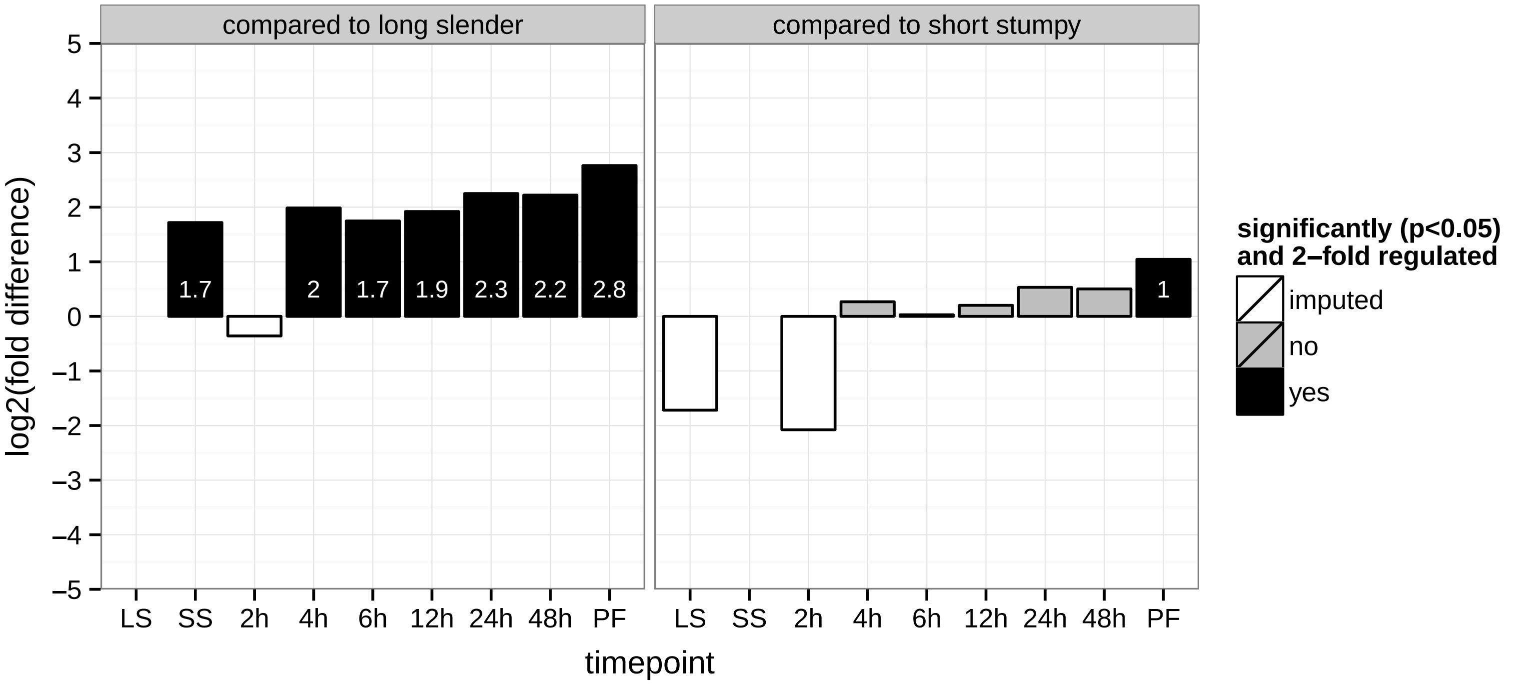
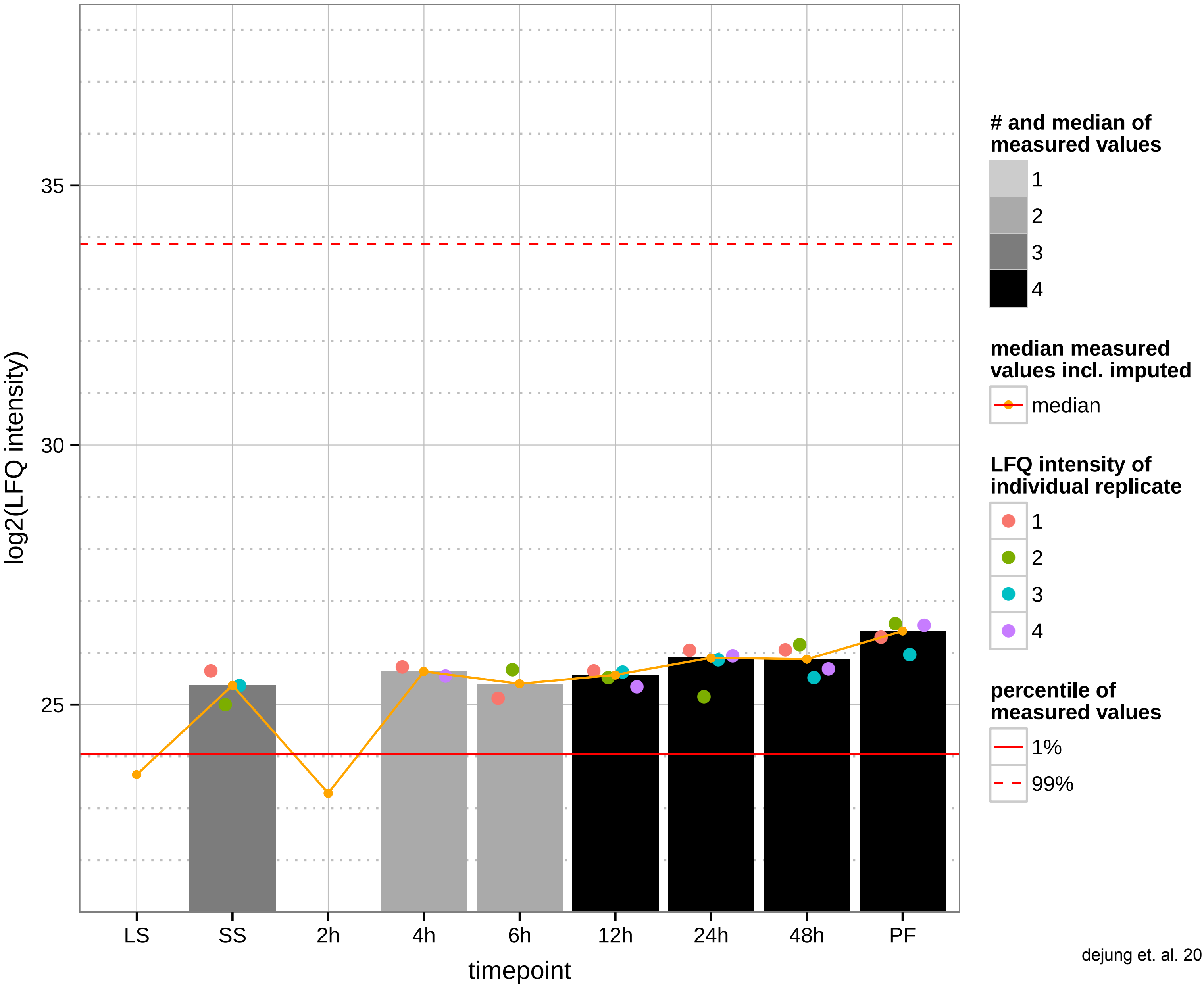
ribosomal protein L3 mitochondrial, putative
Tb927.3.5610
AGOF: structural constituent of ribosome
AGOC: intracellular, mitochondrion, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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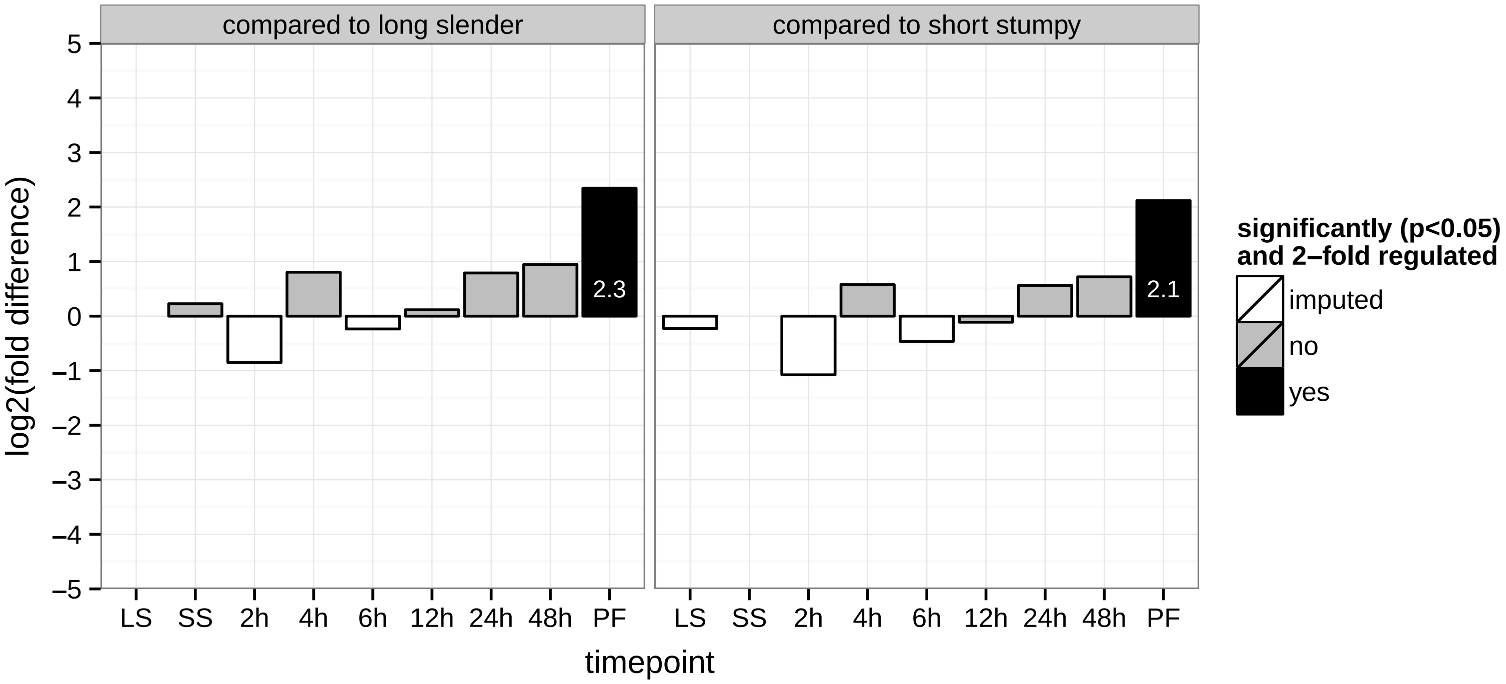
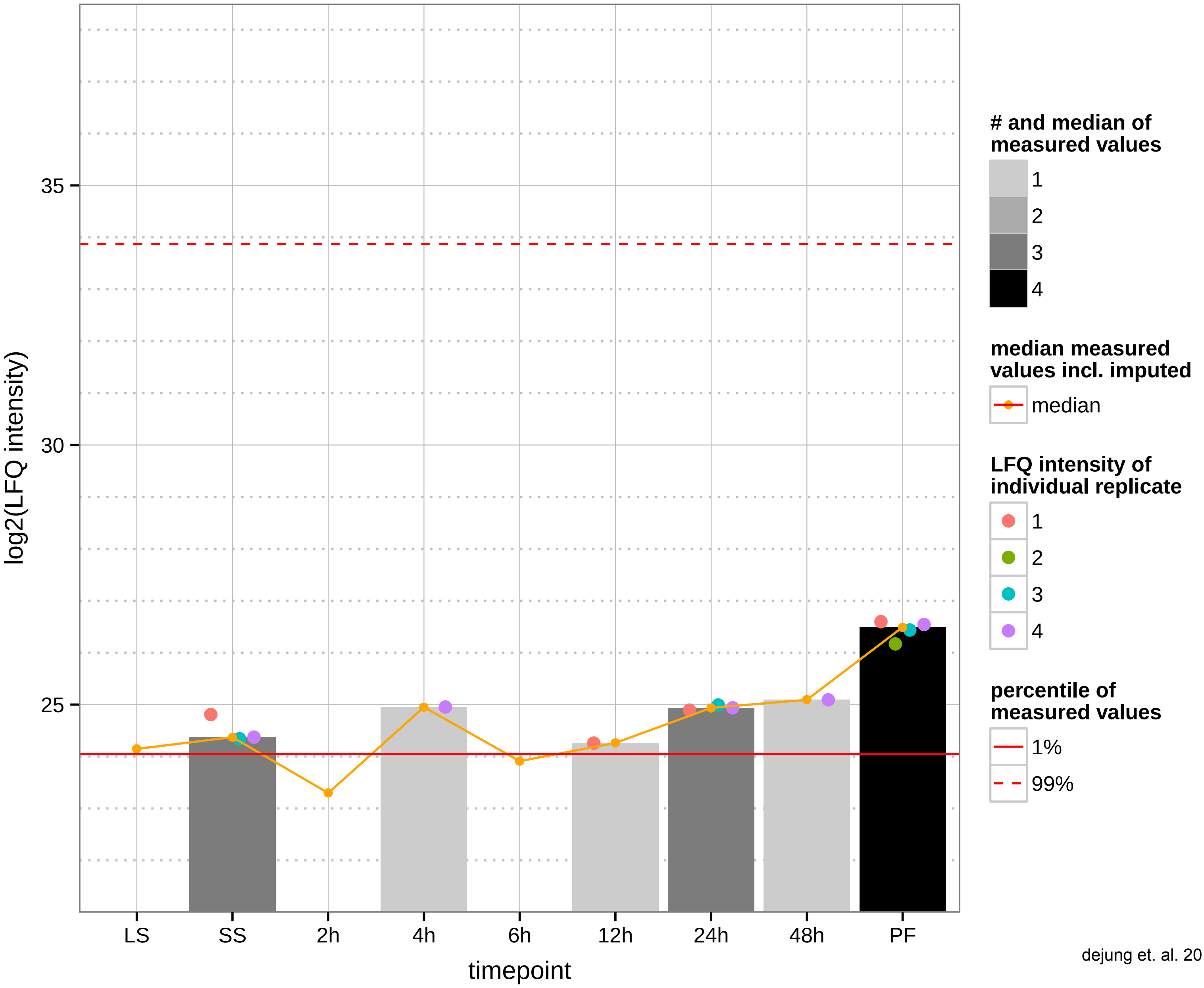
hypothetical protein, conserved
Tb927.4.1900
AGOF: methyltransferase activity
AGOC: null
AGOP: metabolic process
PGOF: null
PGOC: null
PGOP: null





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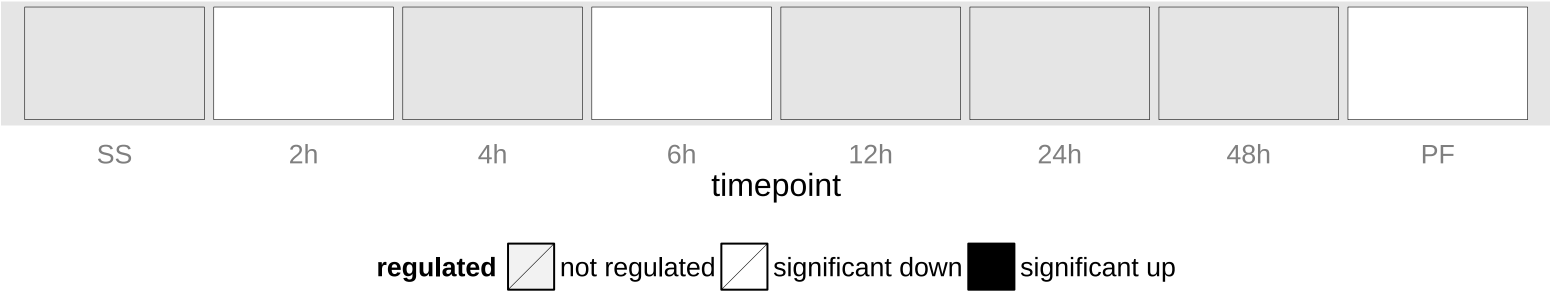

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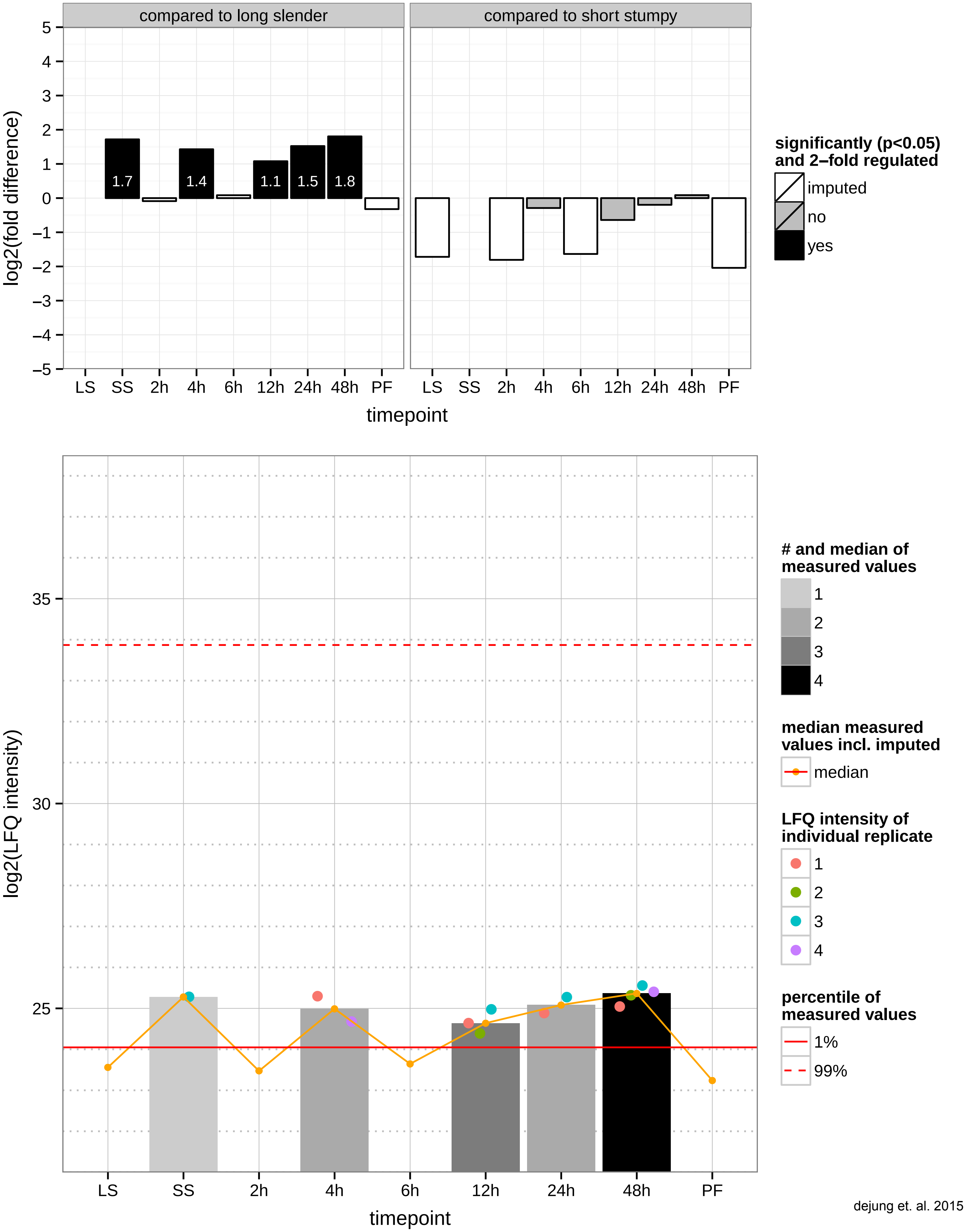
hypothetical protein, conserved
Tb927.10.15730
AGOF: null
AGOC: null
AGOP: null
PGOF: null, protein binding
PGOC: null
PGOP: null



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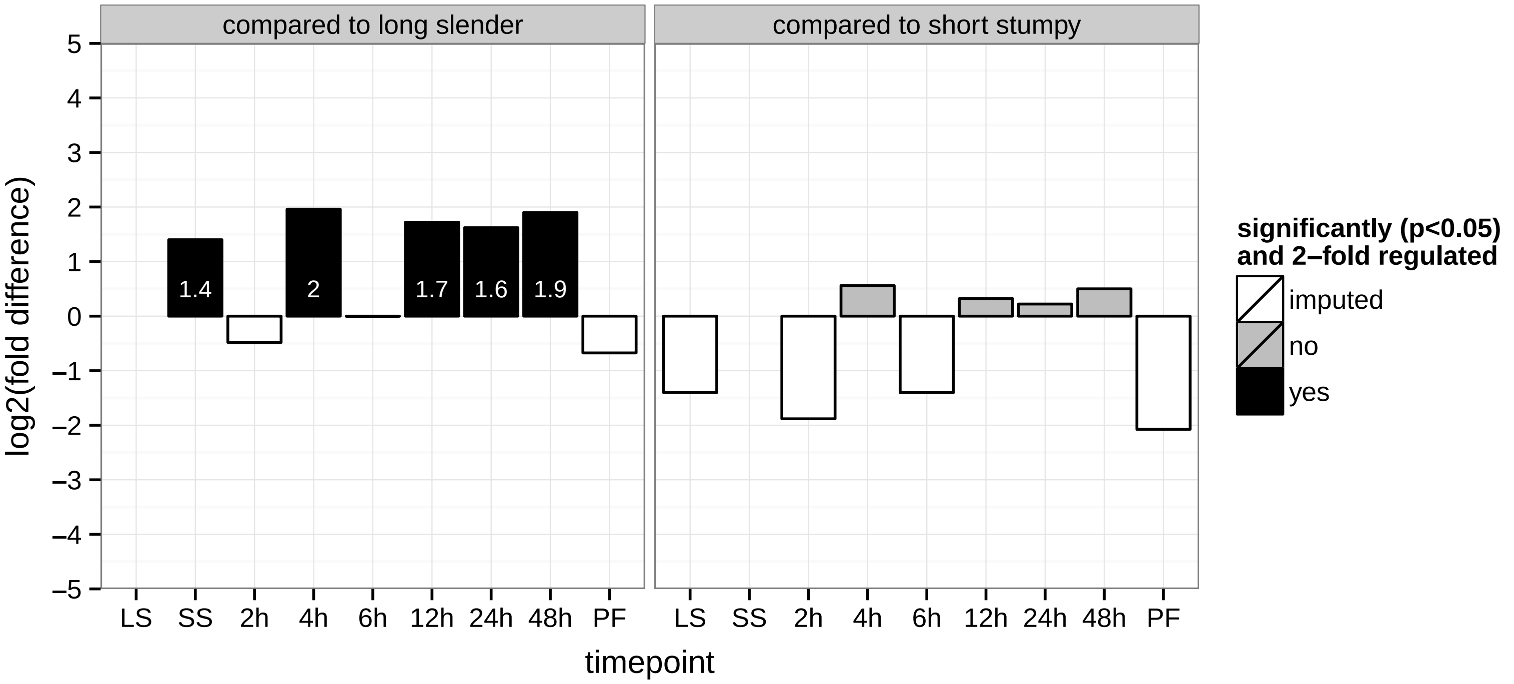
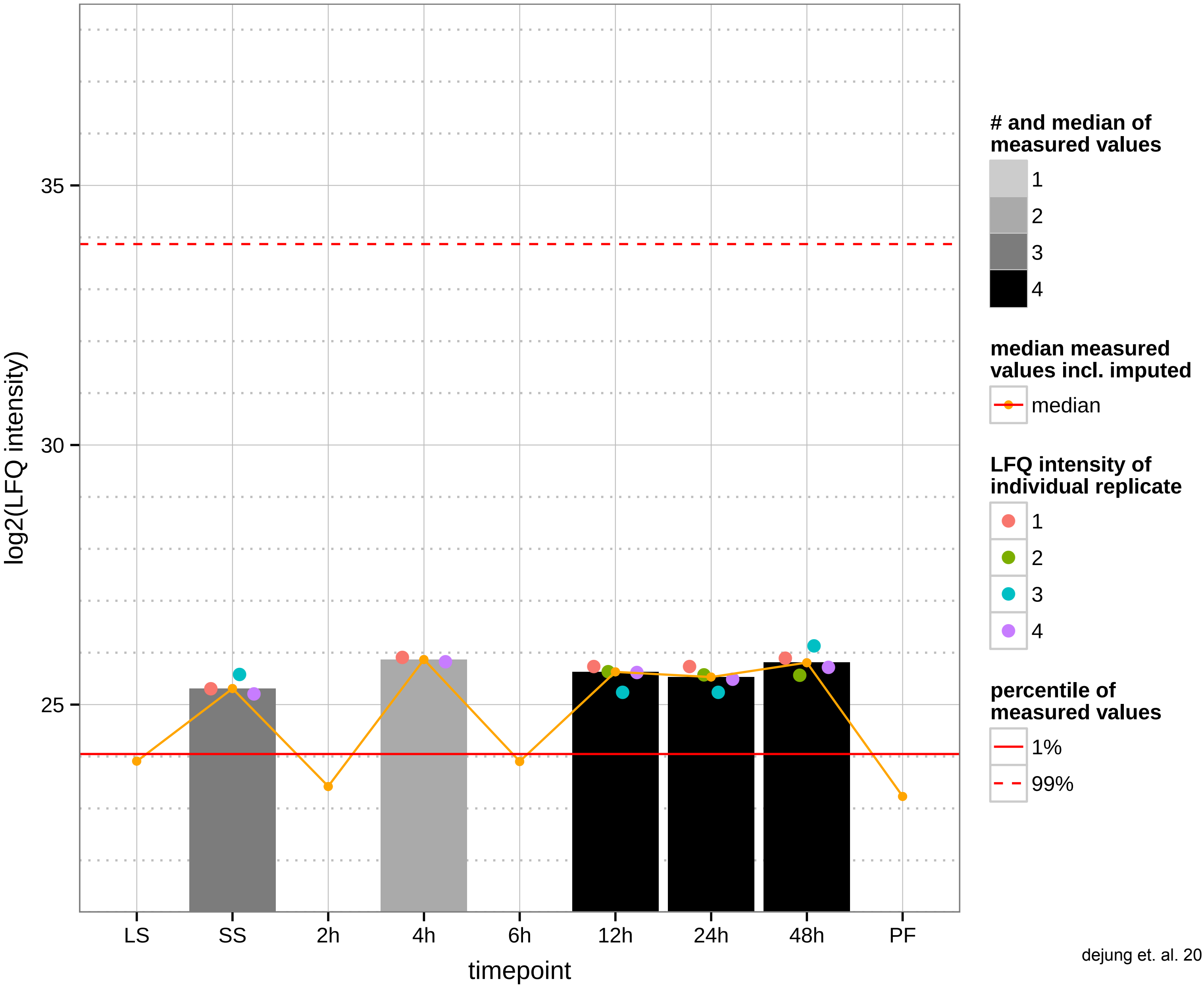
protein phosphatase 2A, putative
Tb927.11.11940
AGOF: hydrolase activity
AGOC: null
AGOP: null
PGOF: hydrolase activity
PGOC: null
PGOP: null





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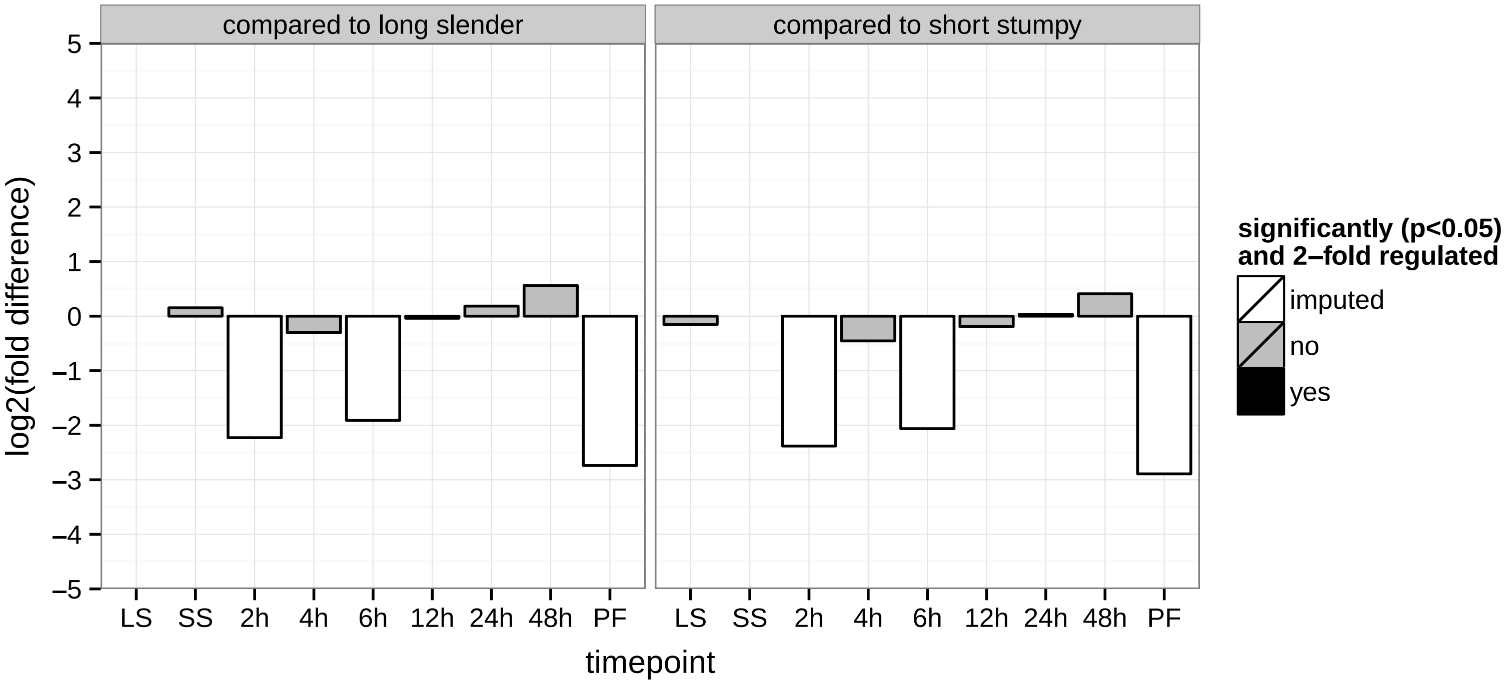
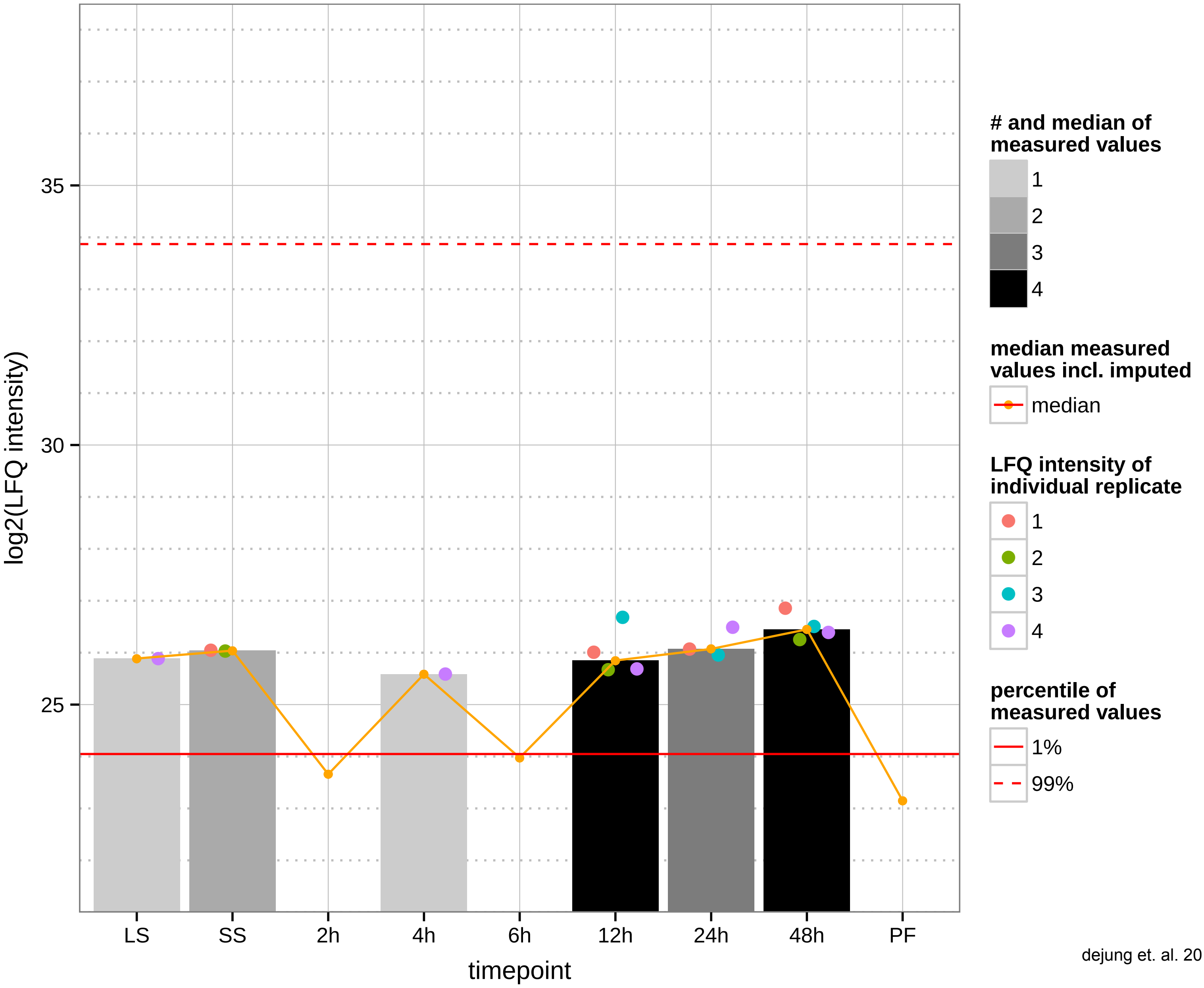
ATP−dependent DEAD/H RNA helicase, putative
Tb927.11.15460
AGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
AGOC: null
AGOP: nucleobase−containing compound metabolic process
PGOF: ATP binding, ATP−dependent helicase activity, helicase activity, nucleic acid binding
PGOC: null
PGOP: null





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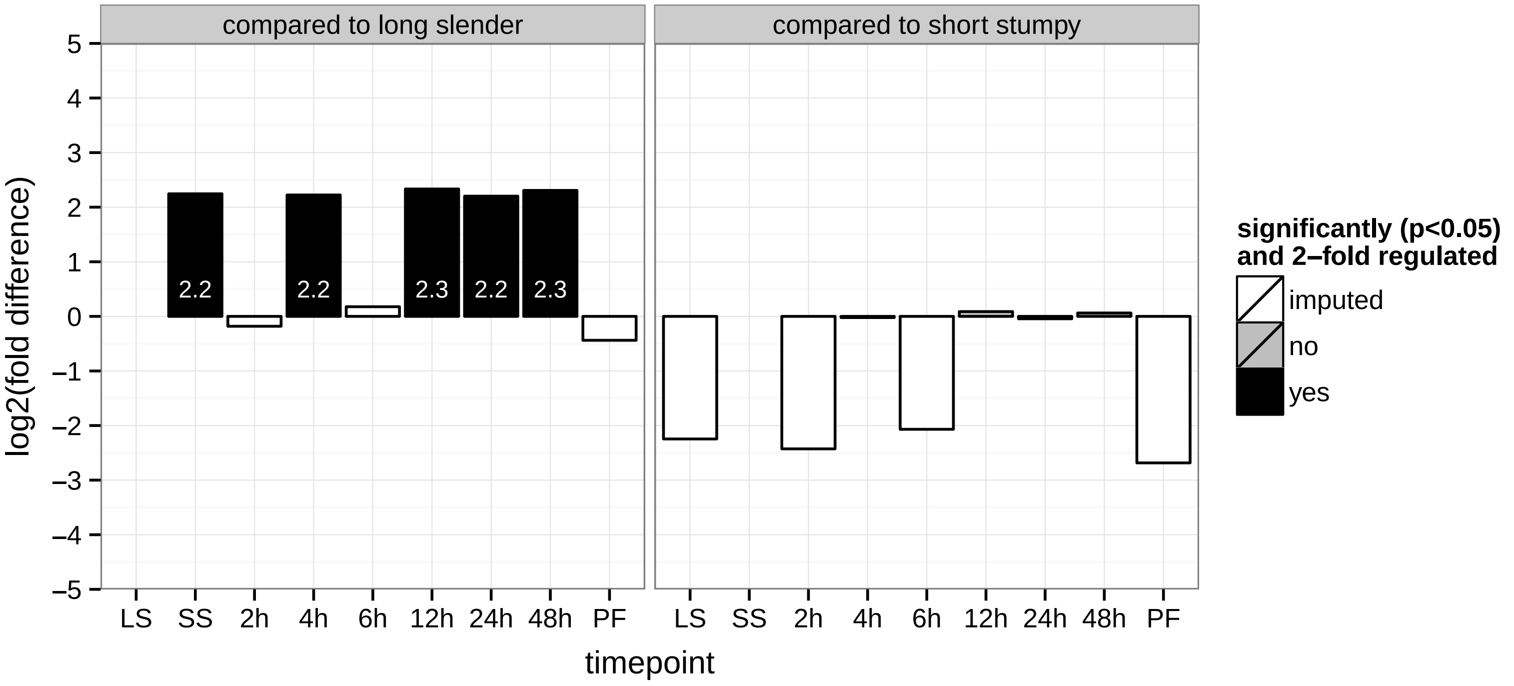
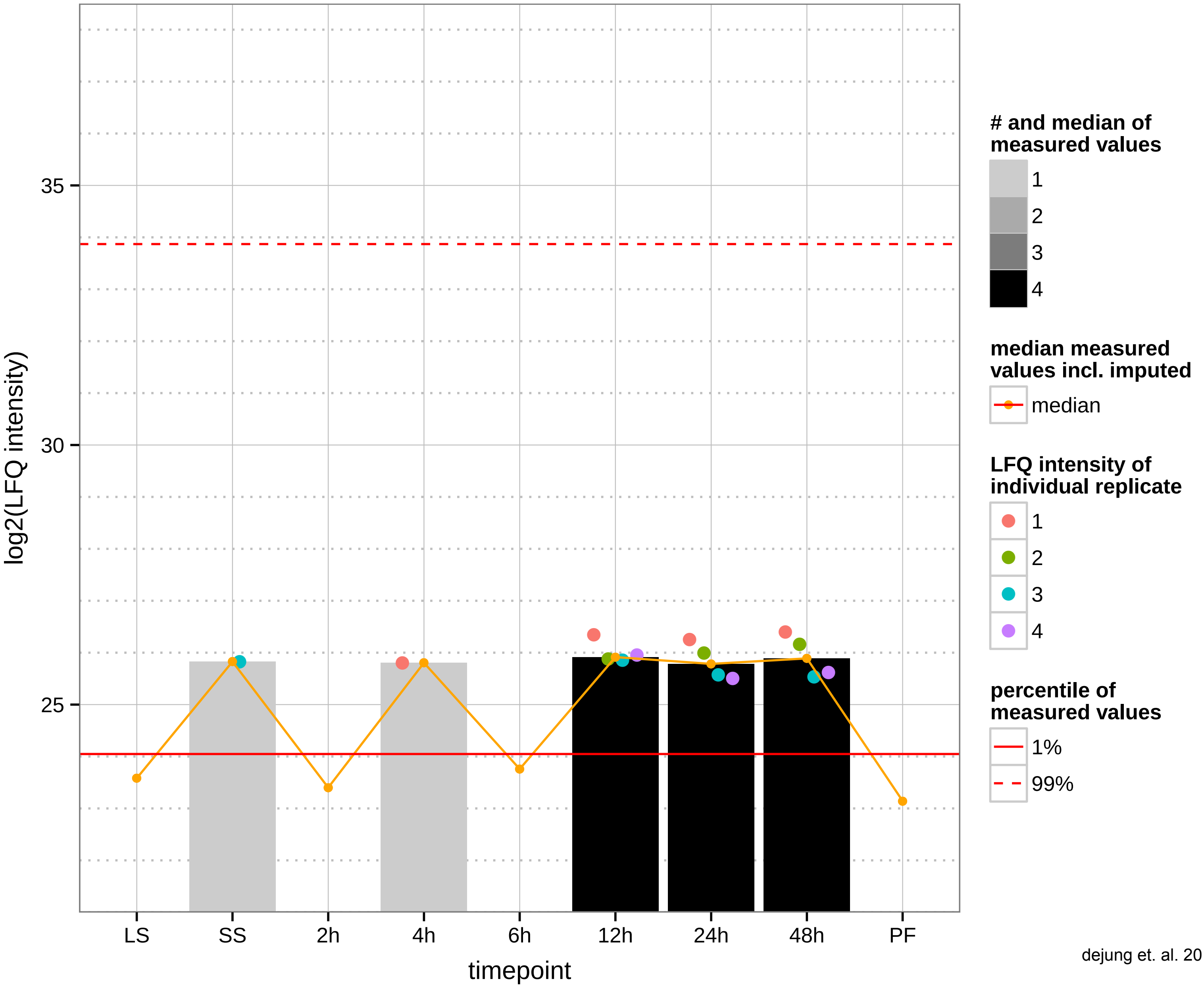
unspecified product
Tb927.9.11280
AGOF: null
AGOC: null
AGOP: null
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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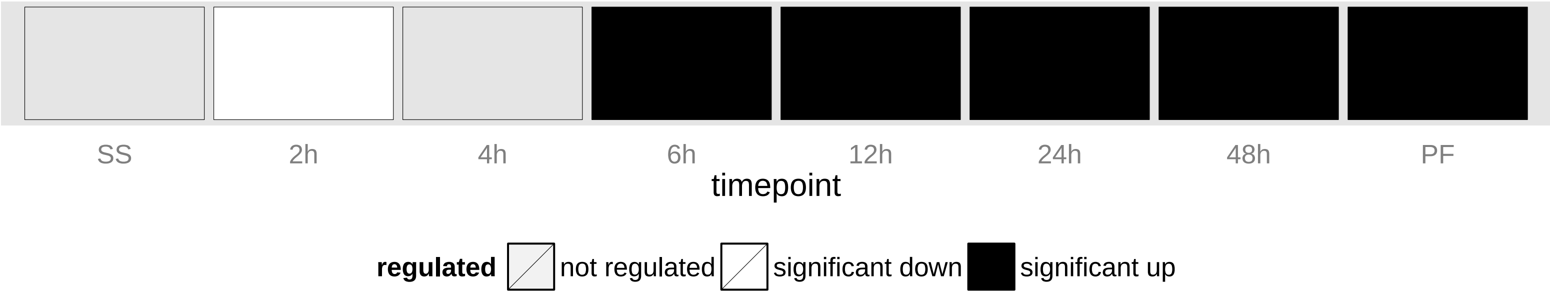

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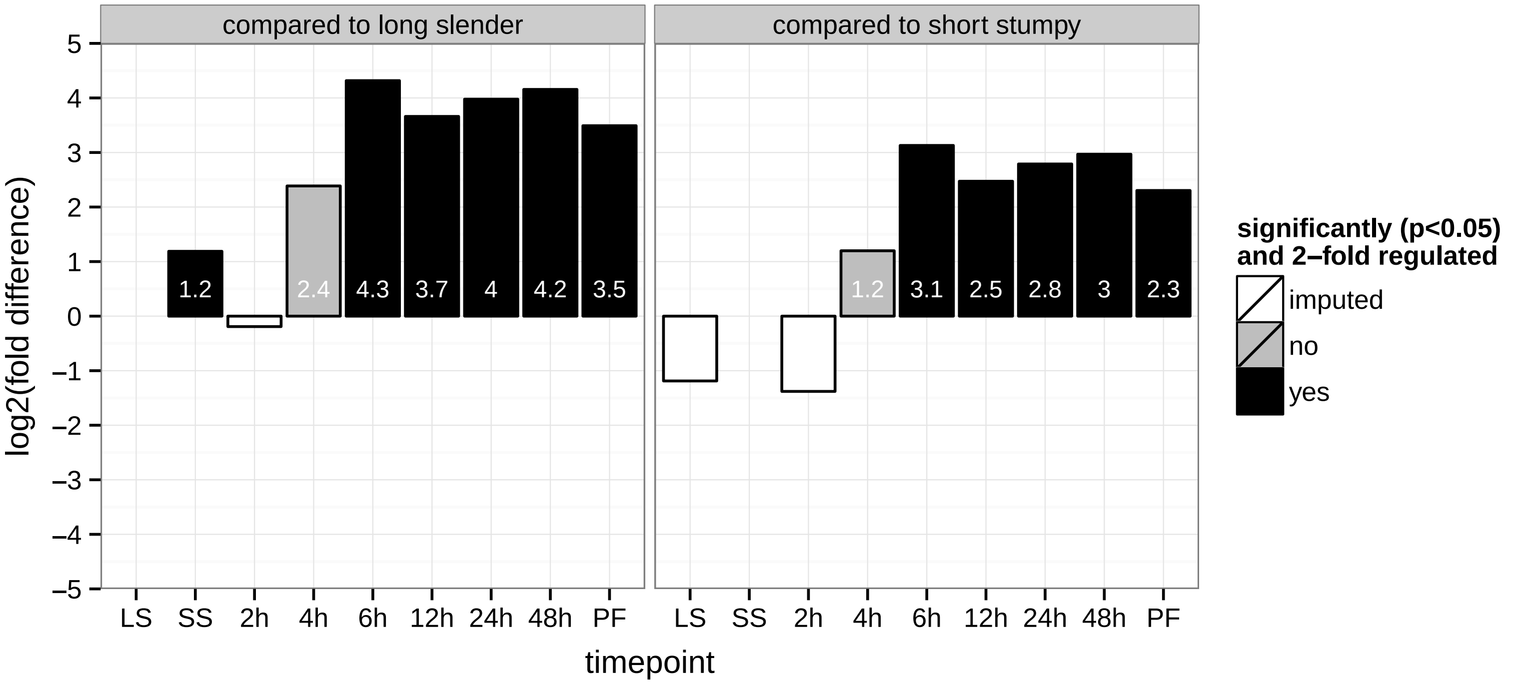
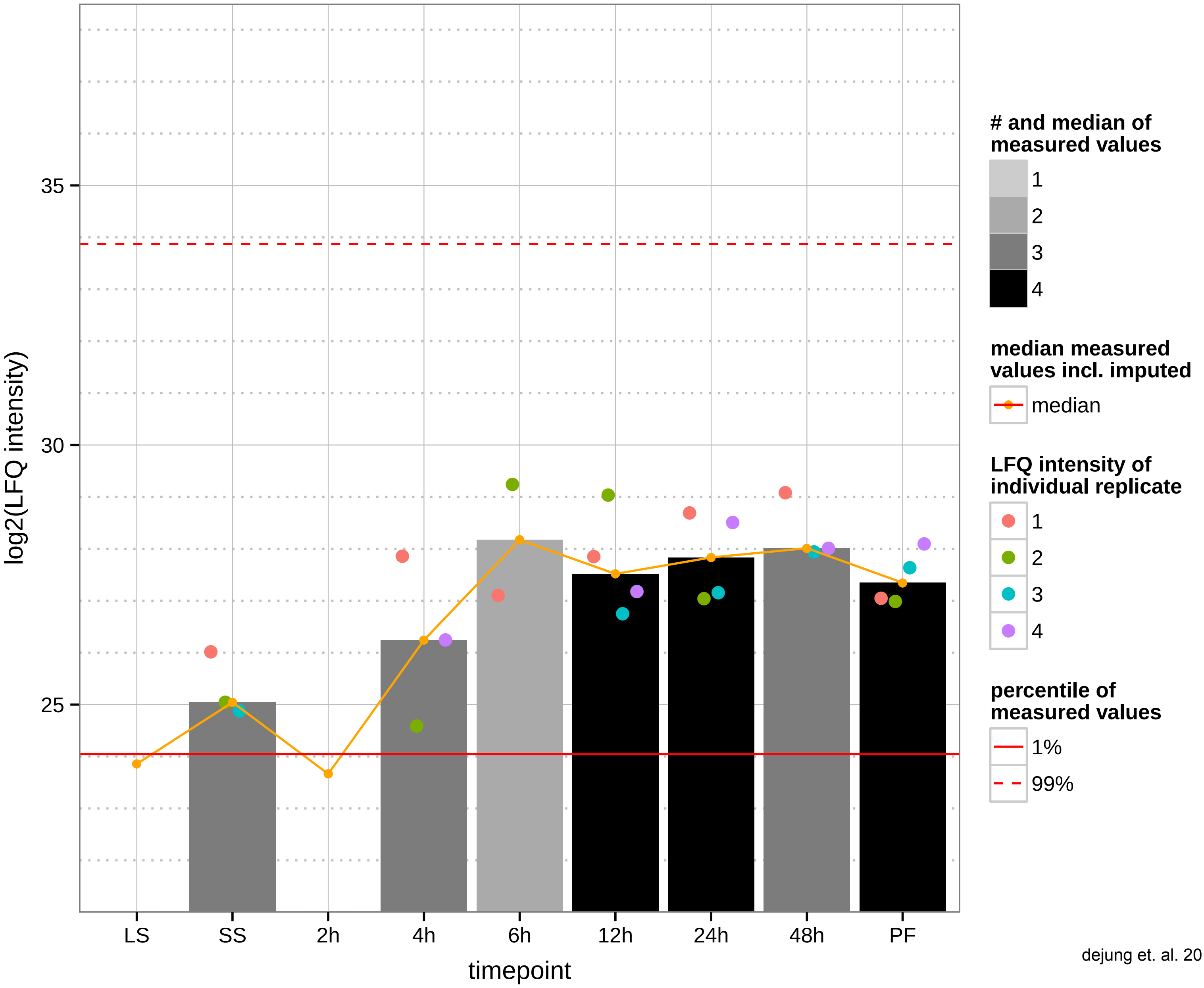
hypothetical protein, conserved
Tb927.11.240
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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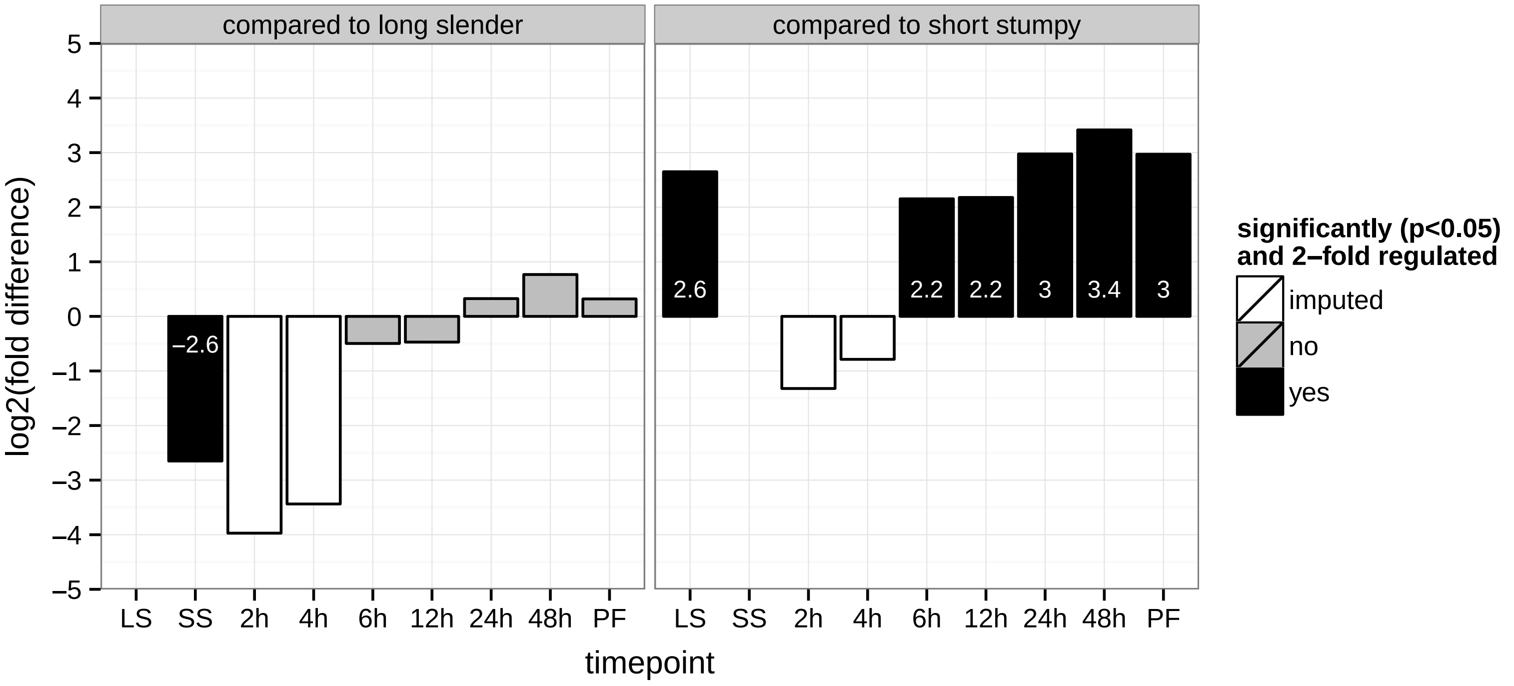
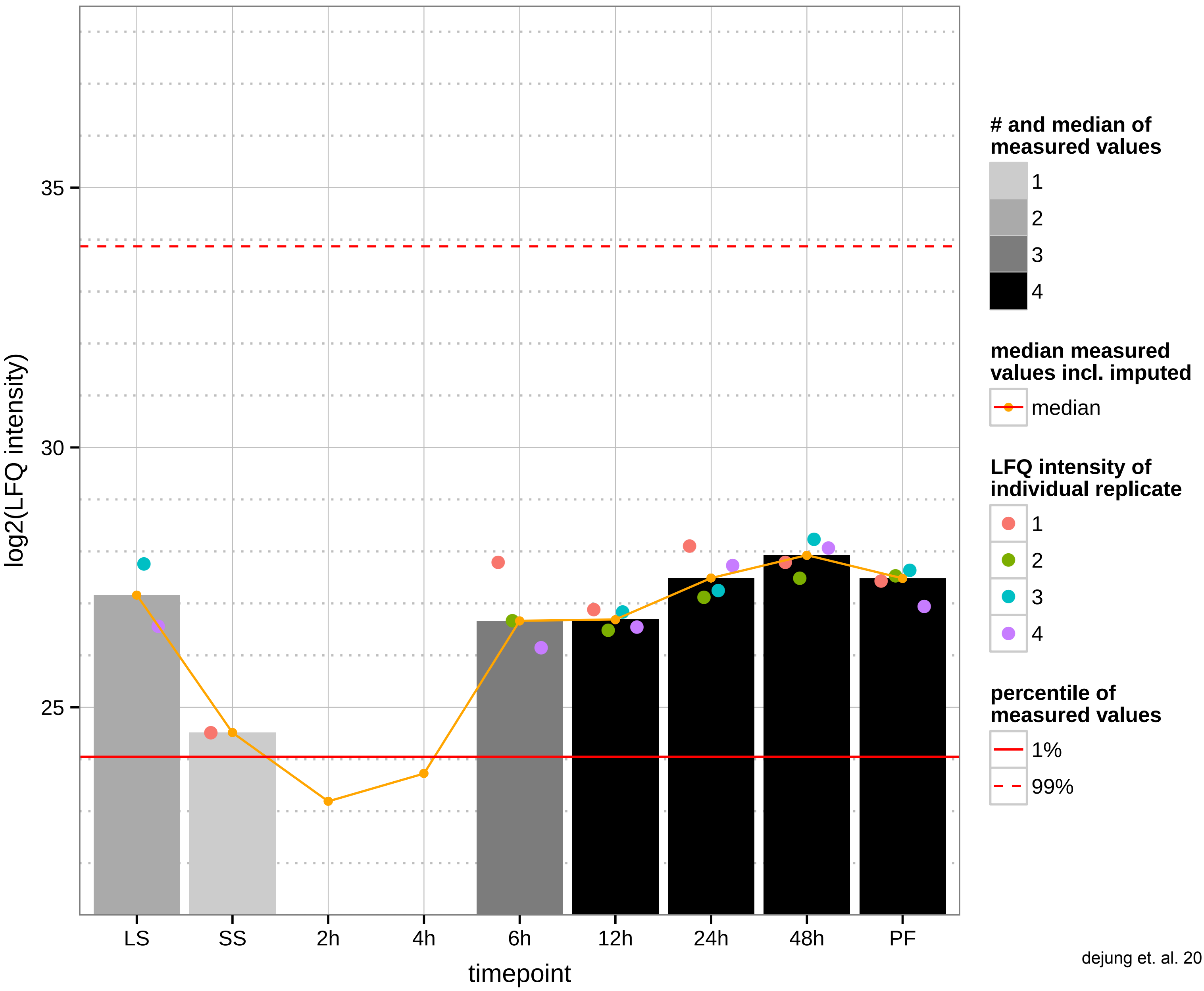
hypothetical protein, conserved
Tb927.4.3370
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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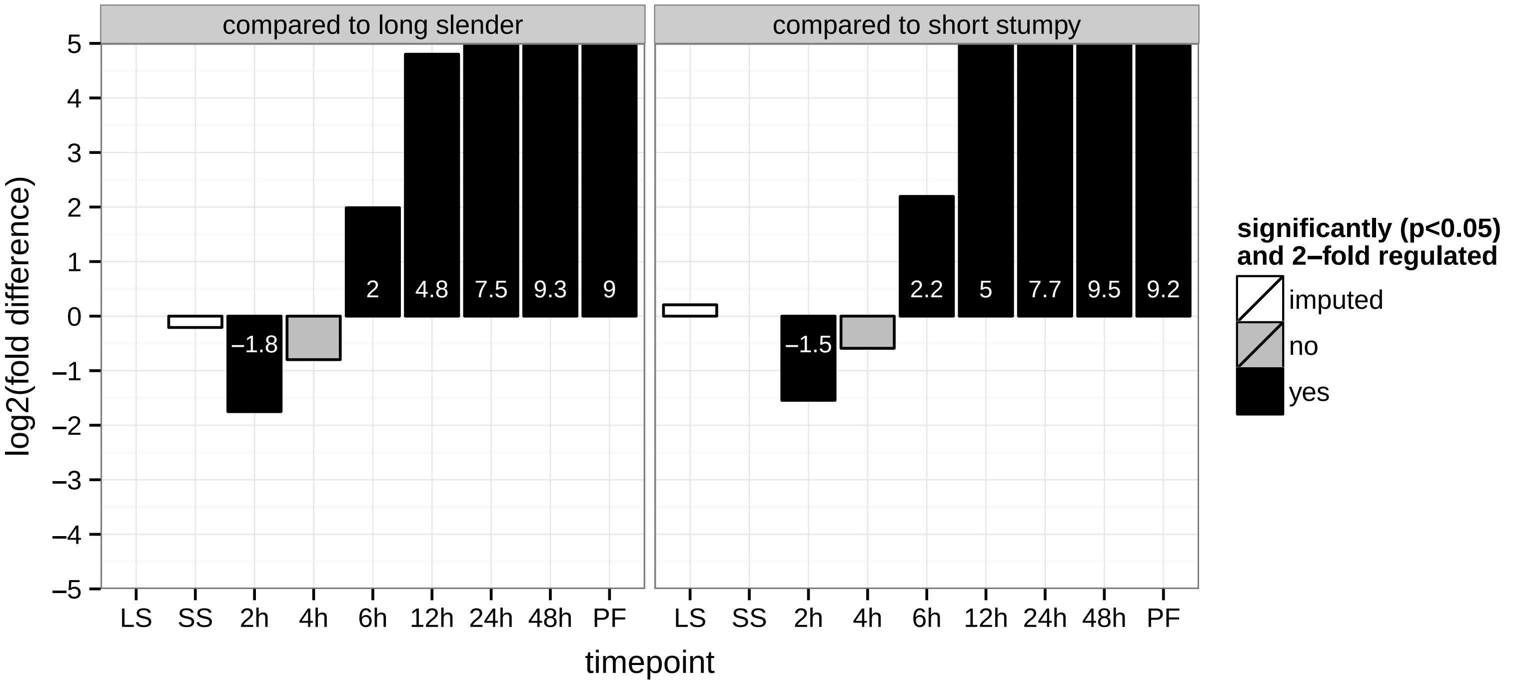
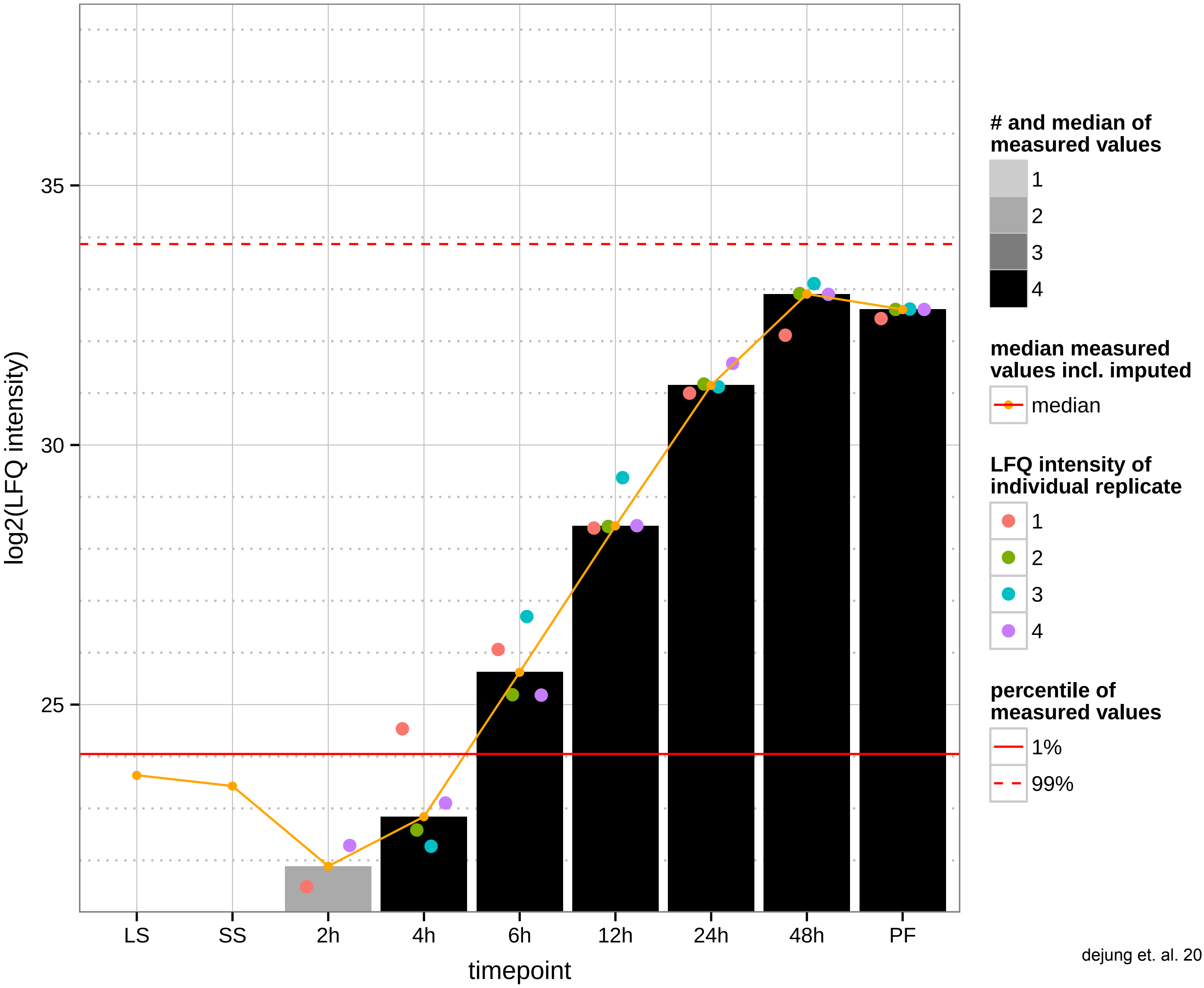
mitochondrial processing peptidase, beta subunit, putative, metallo−peptidase, Clan ME, Family M16
Tb927.5.1060
AGOF: catalytic activity, metalloendopeptidase activity, zinc ion binding
AGOC: mitochondrion
AGOP: proteolysis
PGOF: catalytic activity, metal ion binding, metalloendopeptidase activity, zinc ion binding
PGOC: null
PGOP: proteolysis





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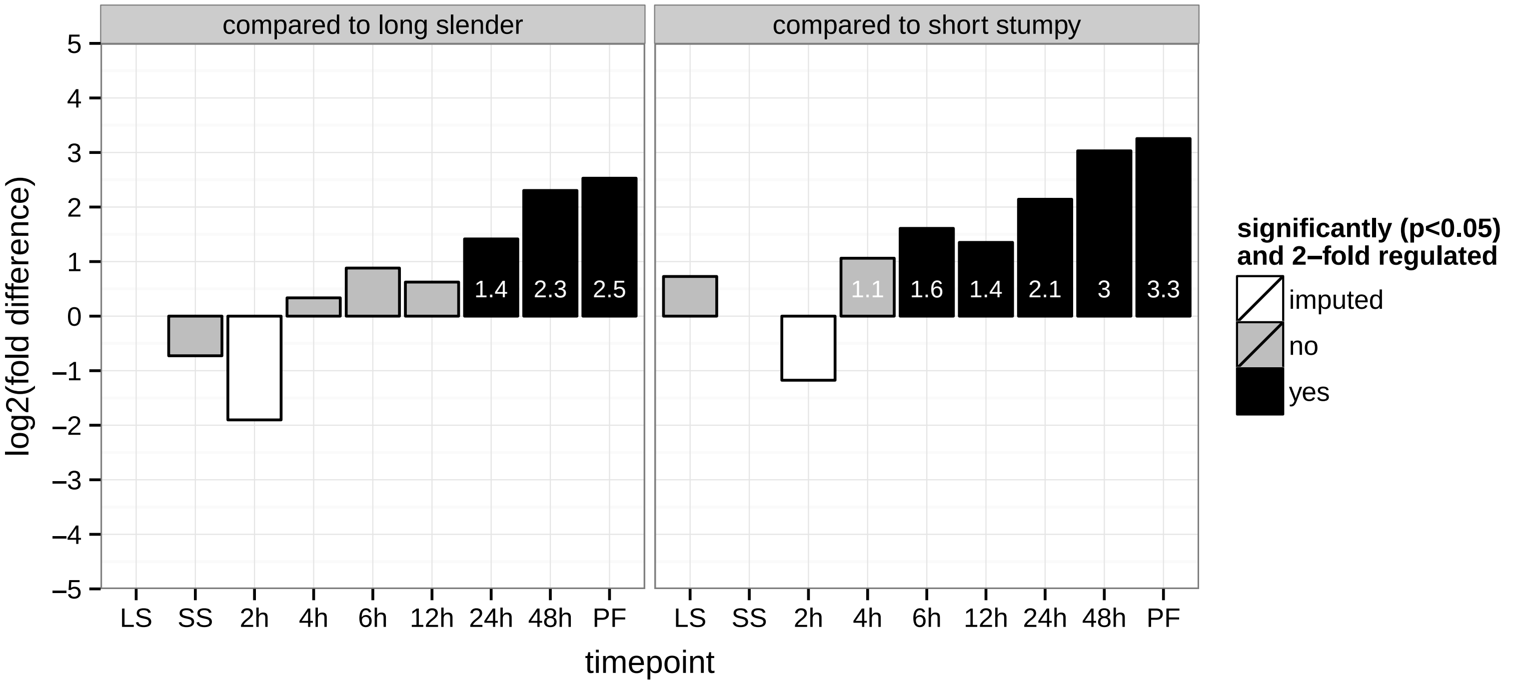
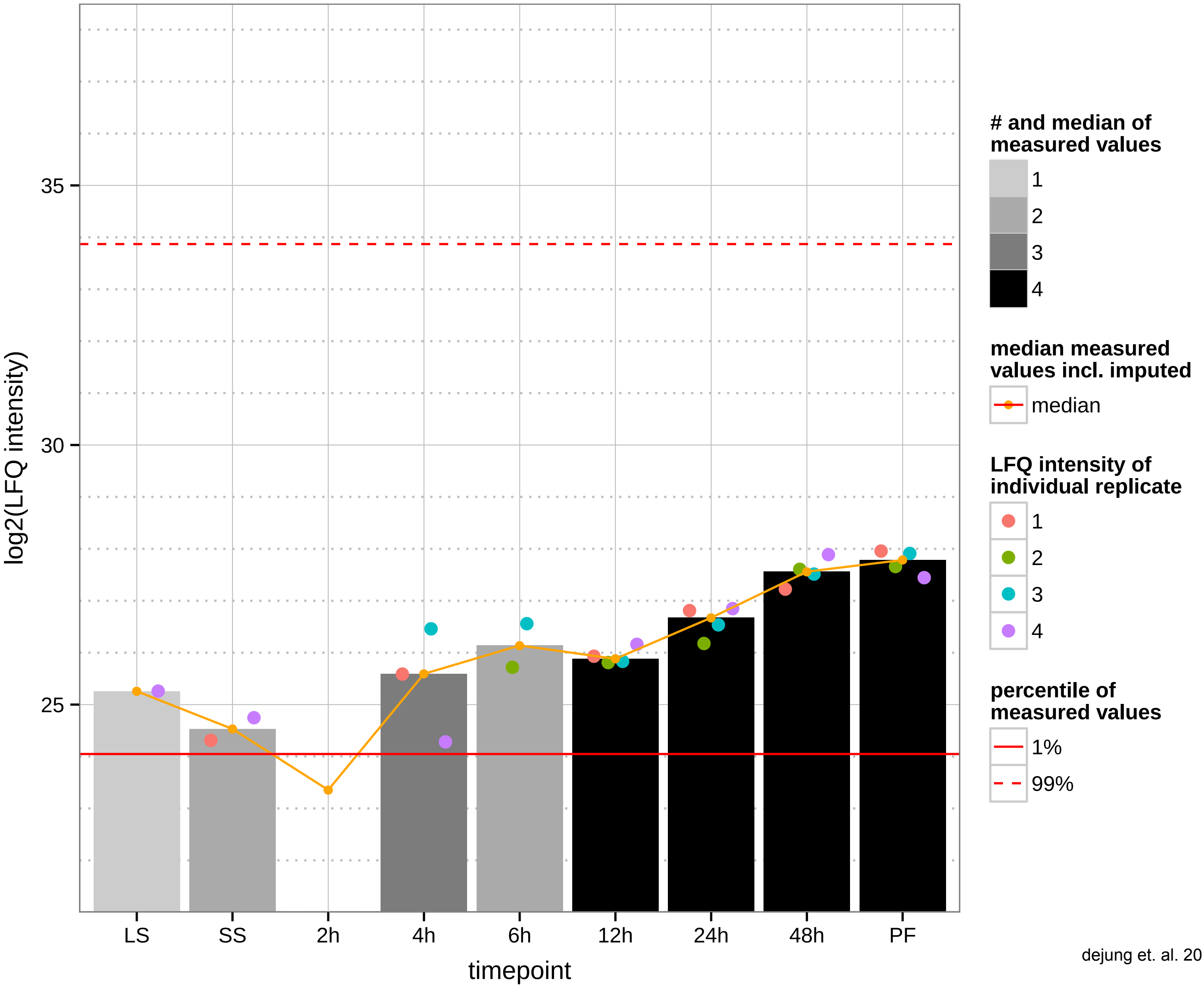
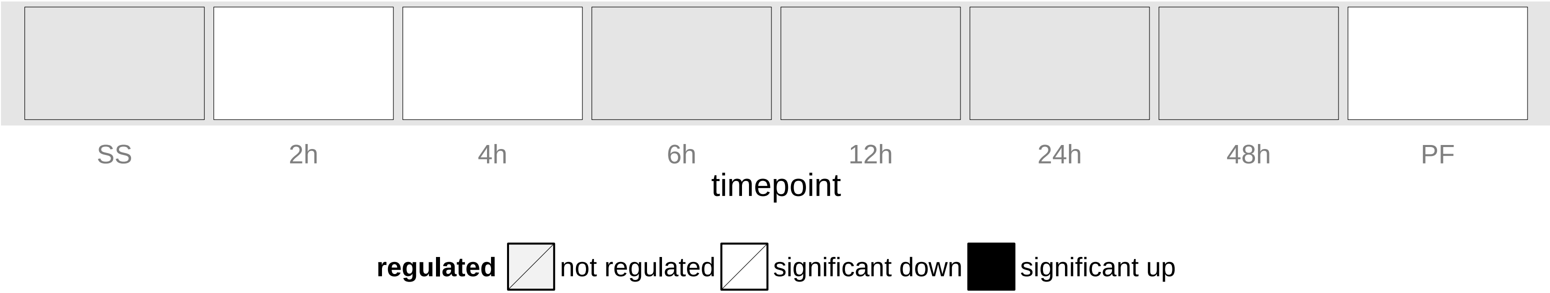
hypothetical protein, conserved
Tb927.8.5200
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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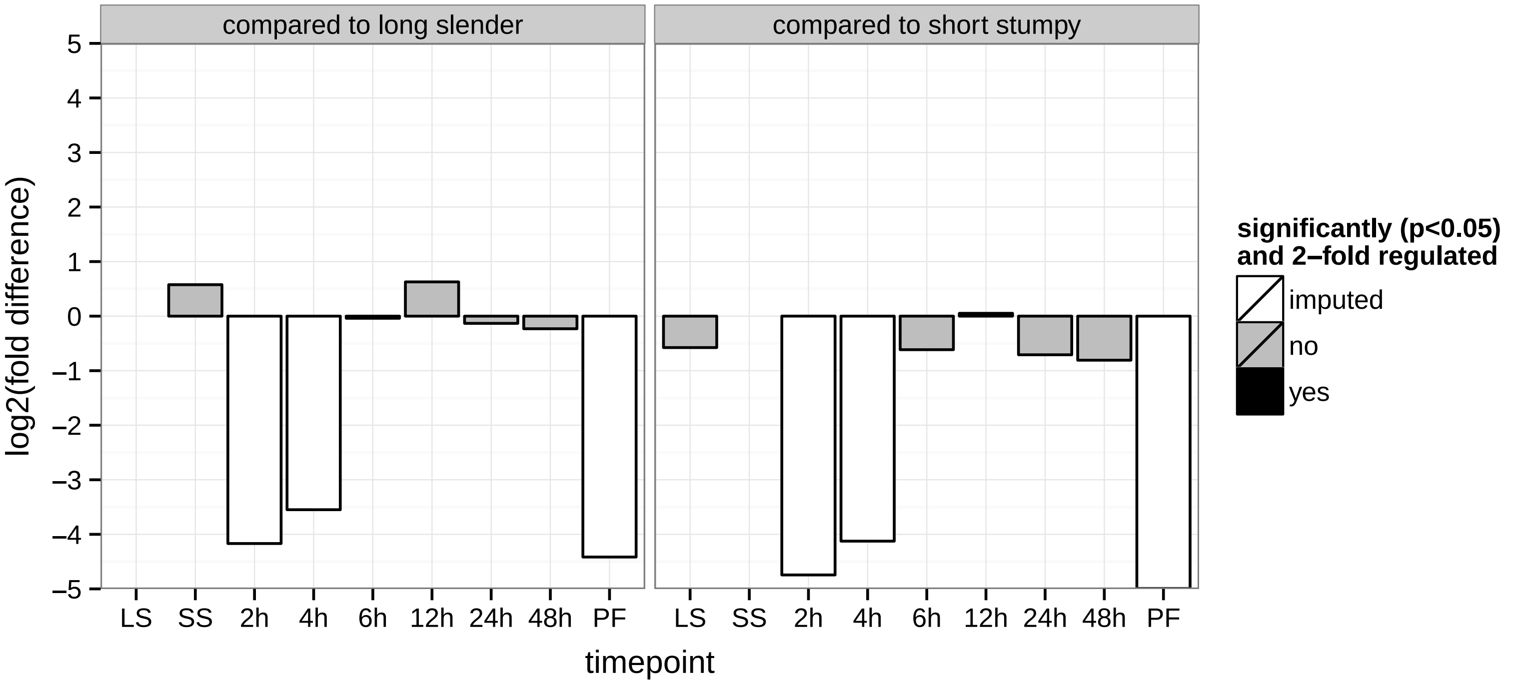
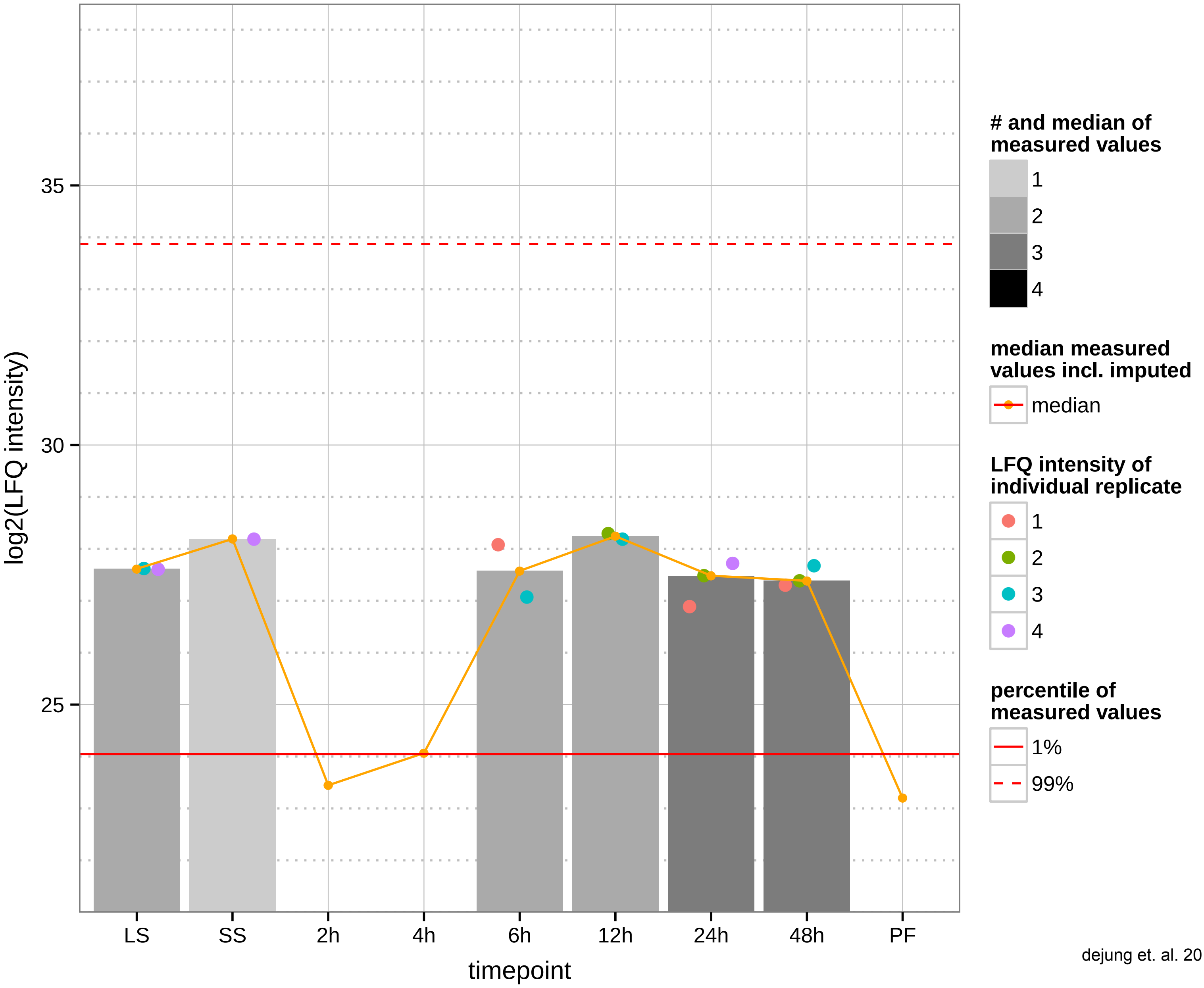
hypothetical protein, conserved
Tb927.10.14760
AGOF: structural molecule activity
AGOC: clathrin coat of coated pit, clathrin coat of trans–Golgi network vesicle
AGOP: intracellular protein transport, vesicle–mediated transport
PGOF: structural molecule activity
PGOC: clathrin coat of coated pit, clathrin coat of trans–Golgi network vesicle
PGOP: intracellular protein transport, vesicle–mediated transport





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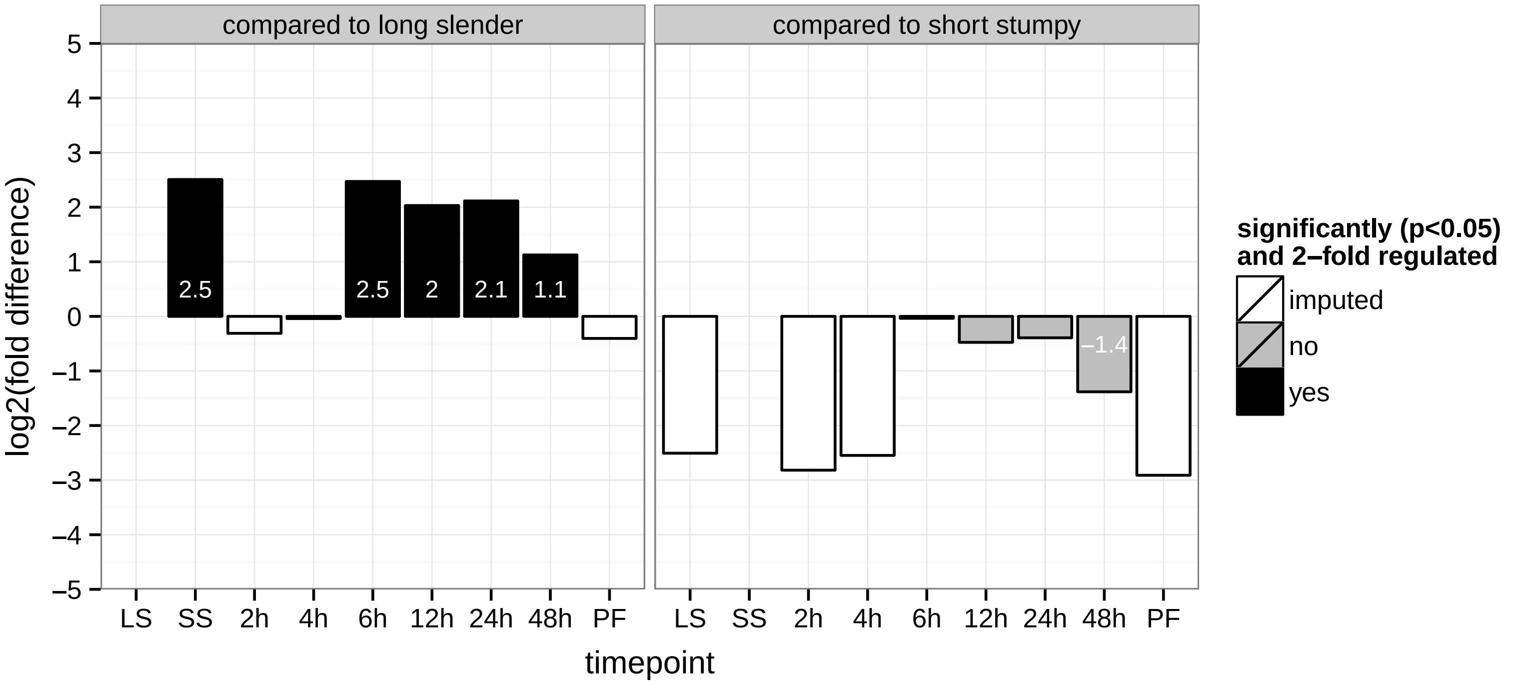
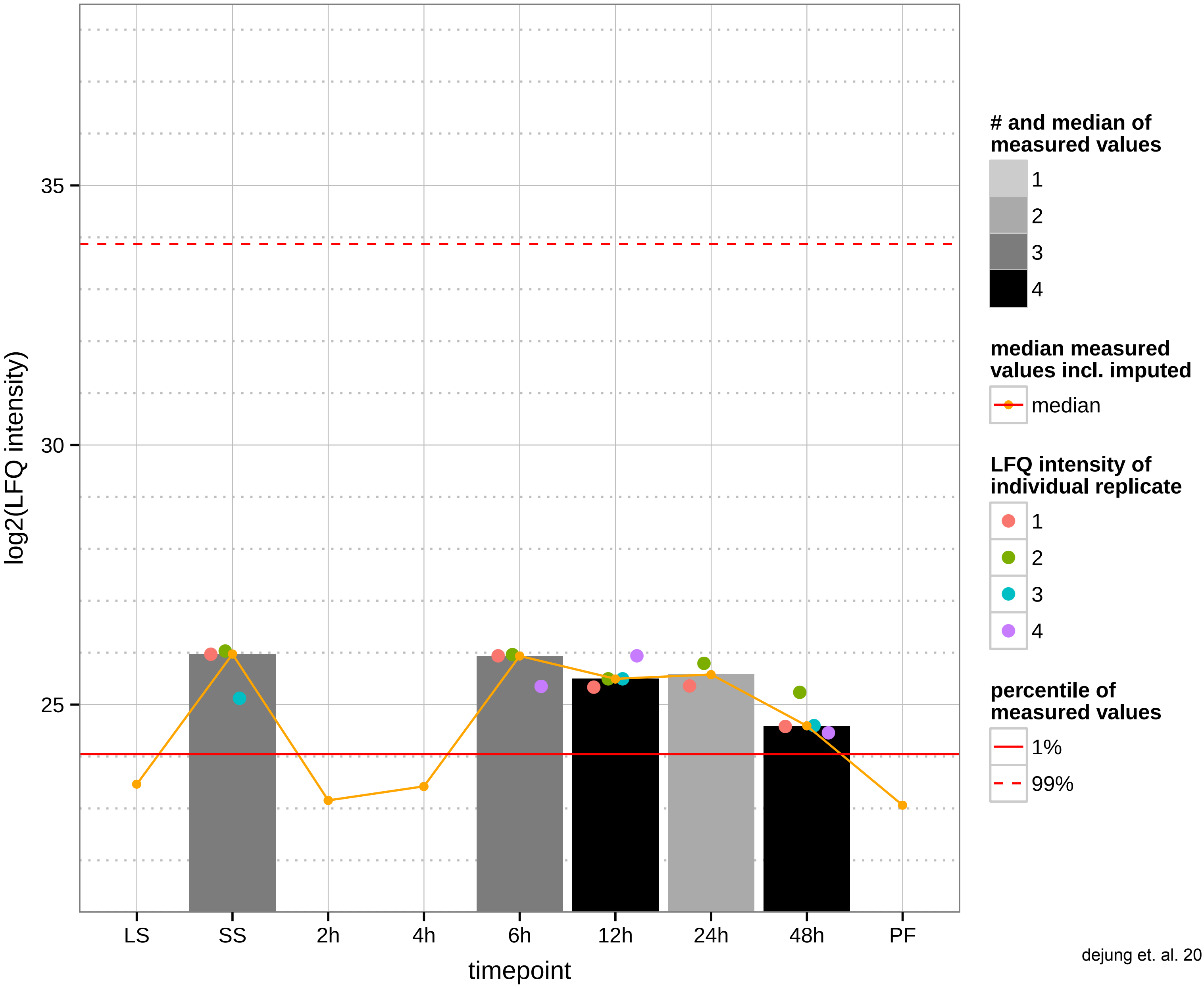
hypothetical protein, conserved
Tb927.10.2130
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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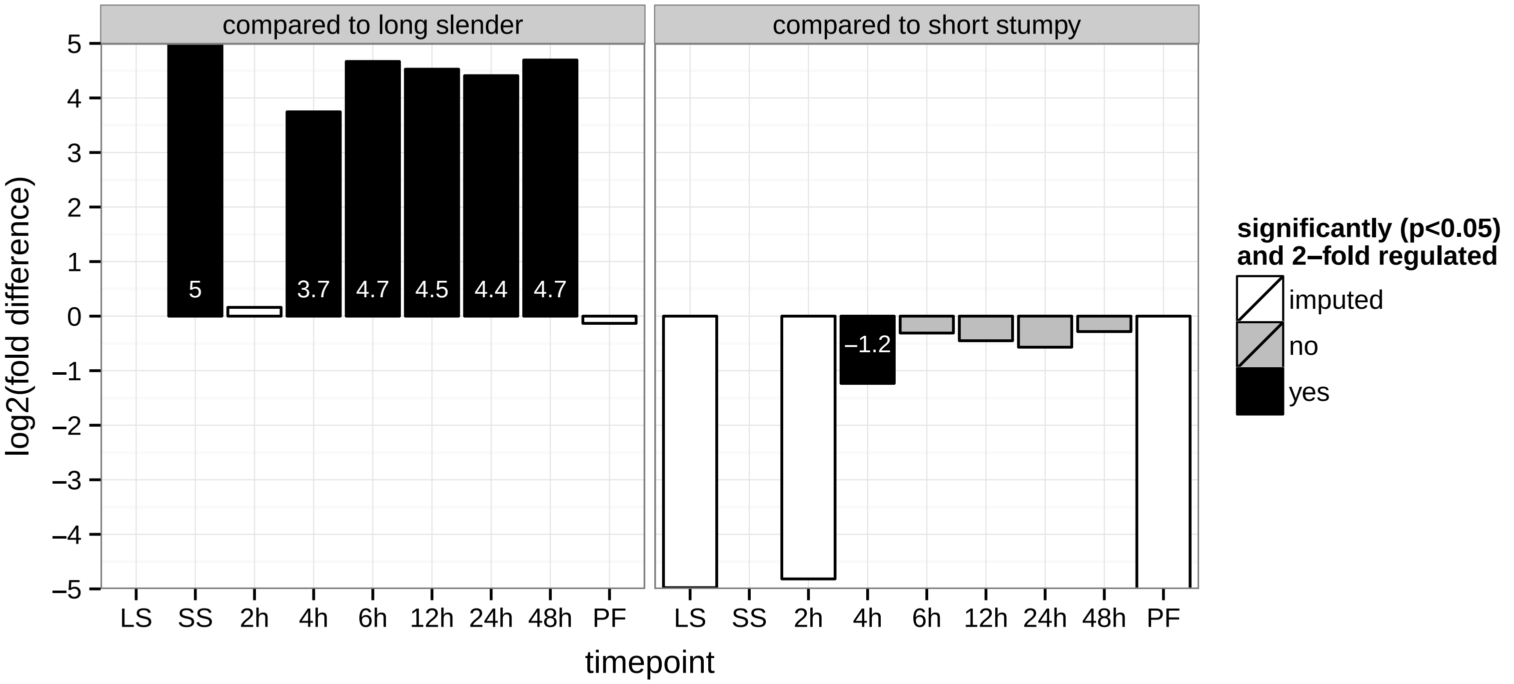
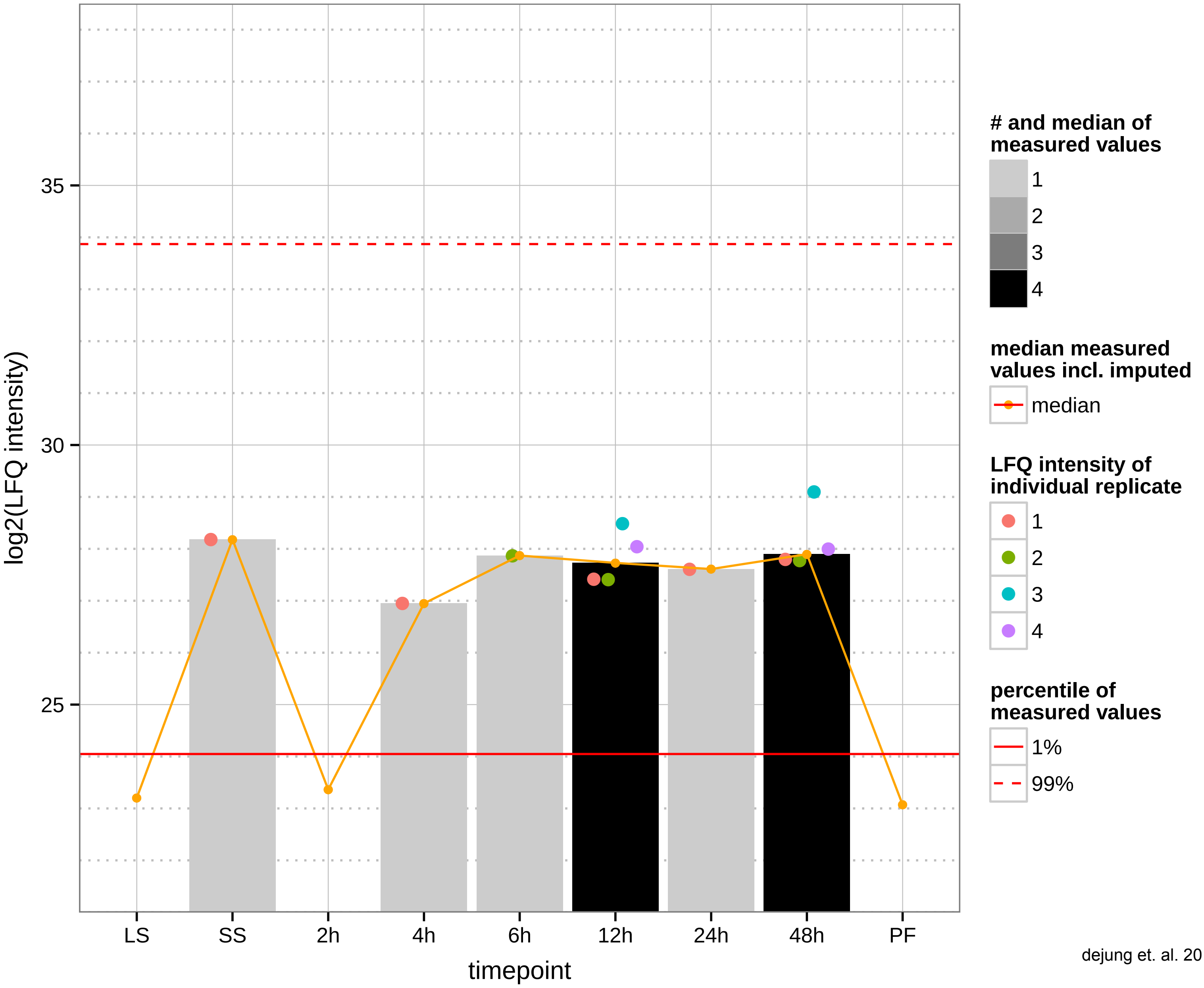
TOR–like 1 (TOR–like 1)
Tb927.4.800
AGOF: phosphotransferase activity, alcohol group as acceptor
AGOC: cytosol
AGOP: cellular response to glucose starvation, regulation of response to osmotic stress
PGOF: binding, phosphotransferase activity, alcohol group as acceptor, protein binding, transferase activity, transferring phosp
PGOC: null
PGOP: null





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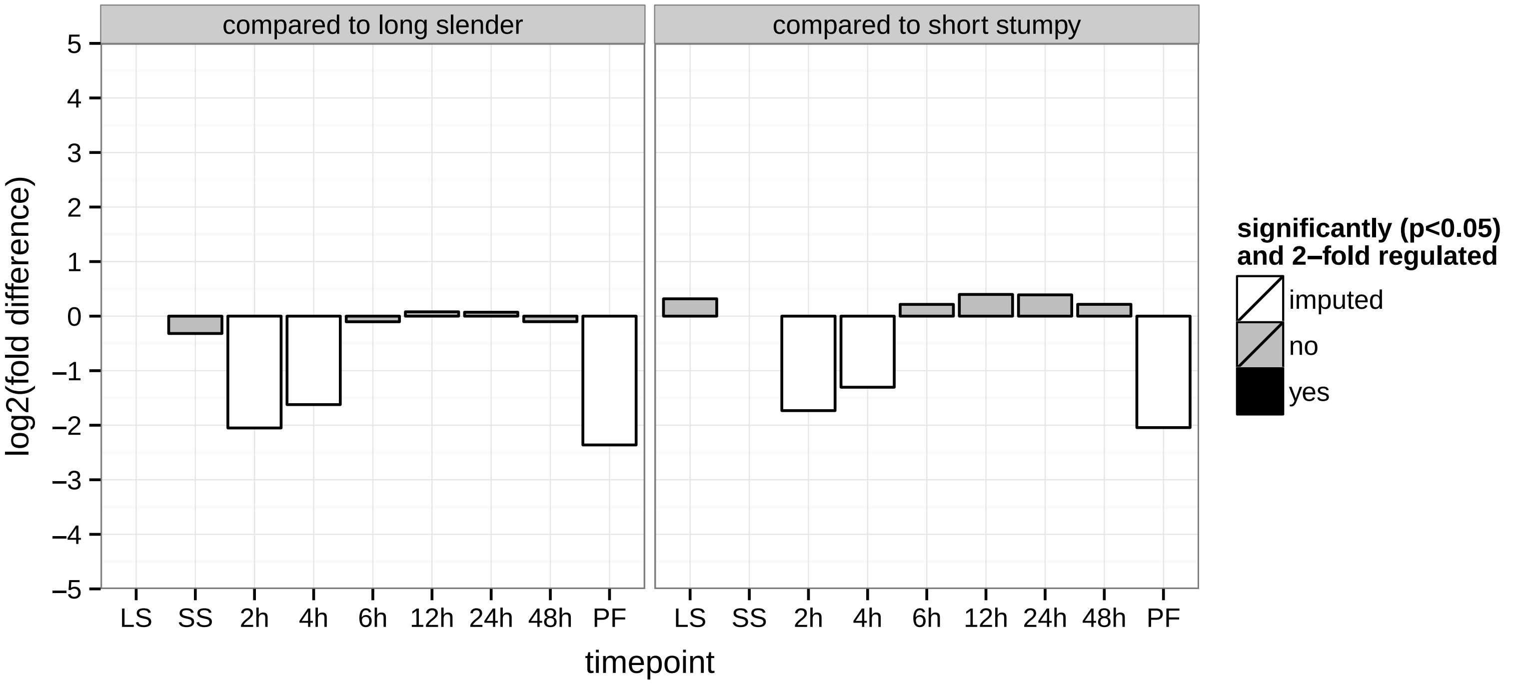
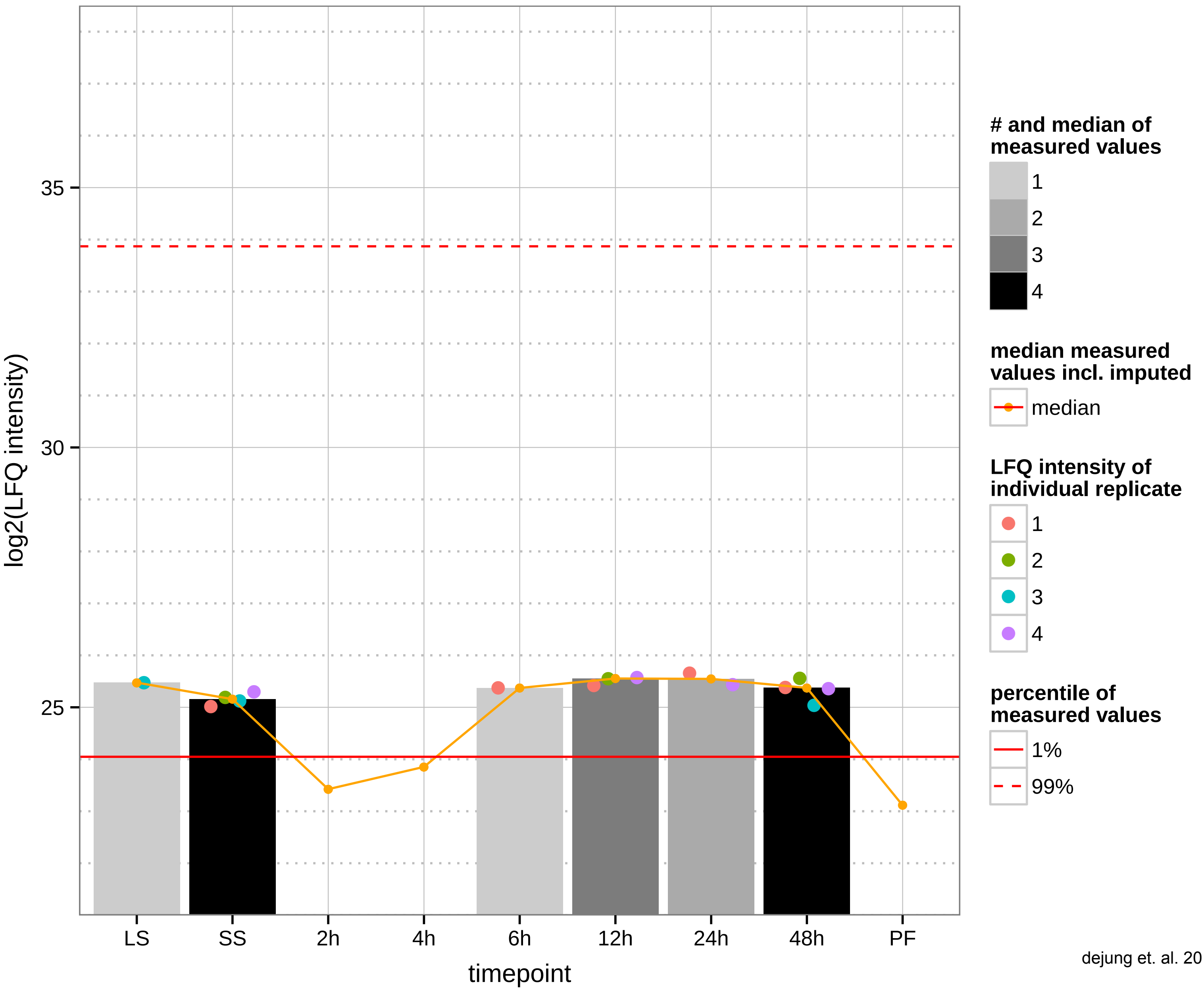
hypothetical protein, conserved
Tb927.9.12780
AGOF: protein C−terminal carboxyl O−methyltransferase activity
AGOC: null
AGOP: cellular protein modification process
PGOF: methyltransferase activity, protein binding
PGOC: null
PGOP: null





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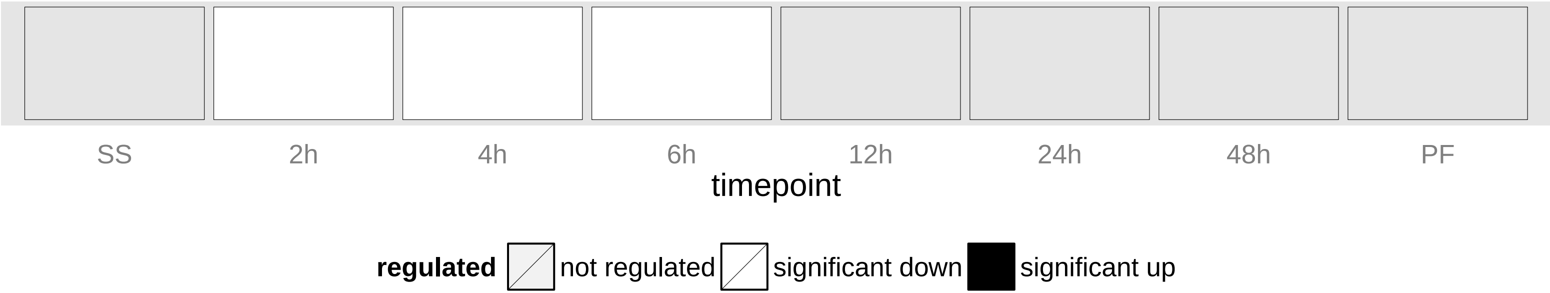

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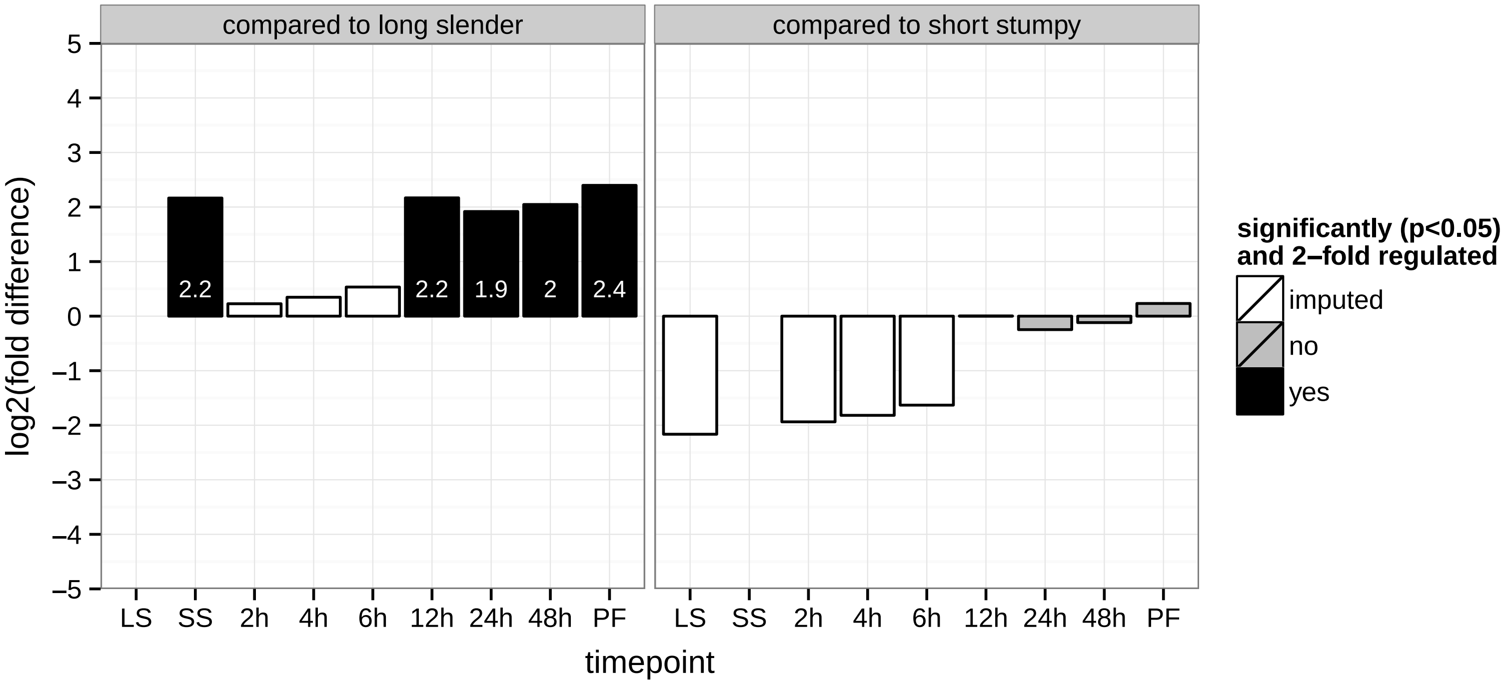
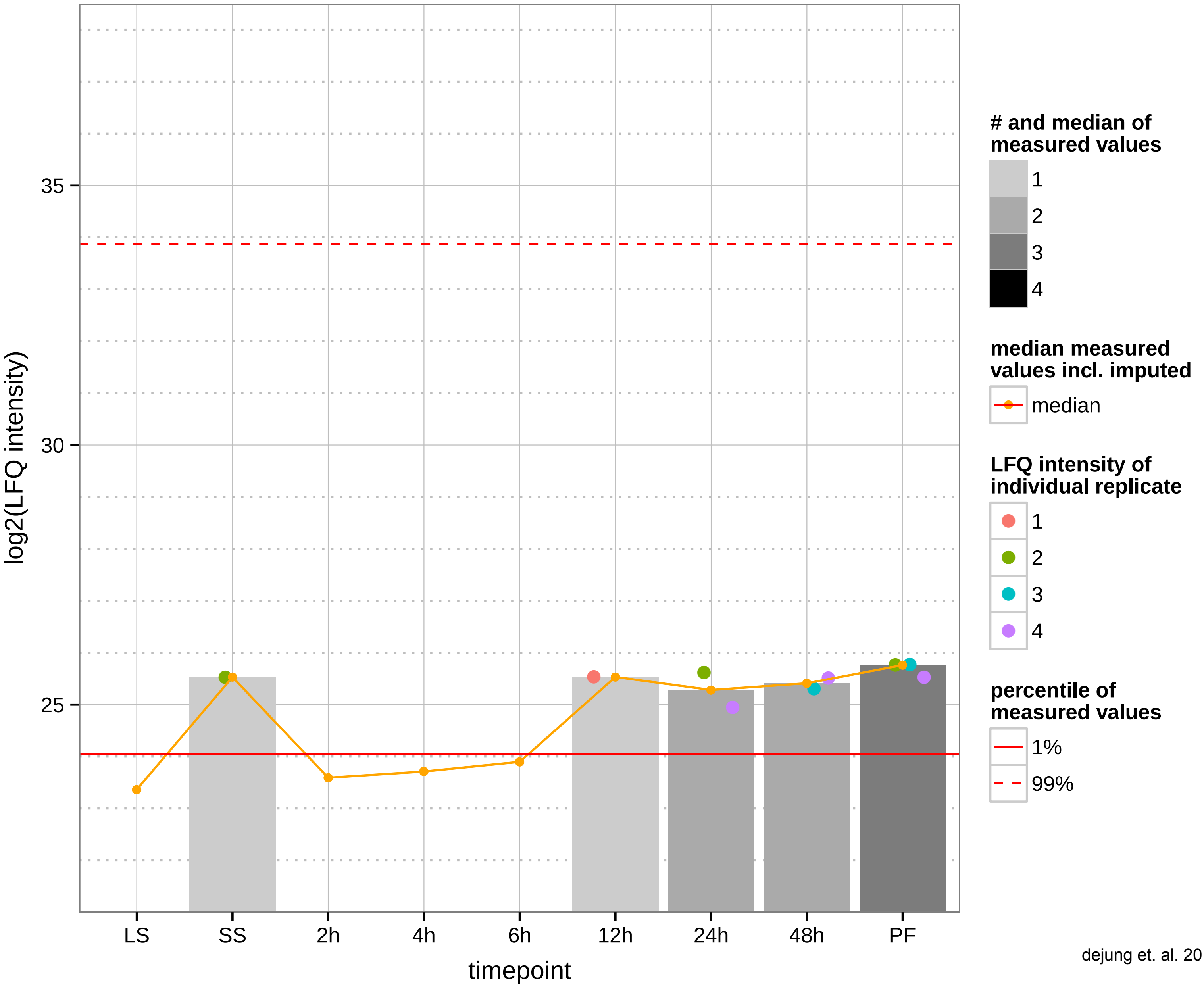
hypothetical protein, conserved
Tb927.3.3680
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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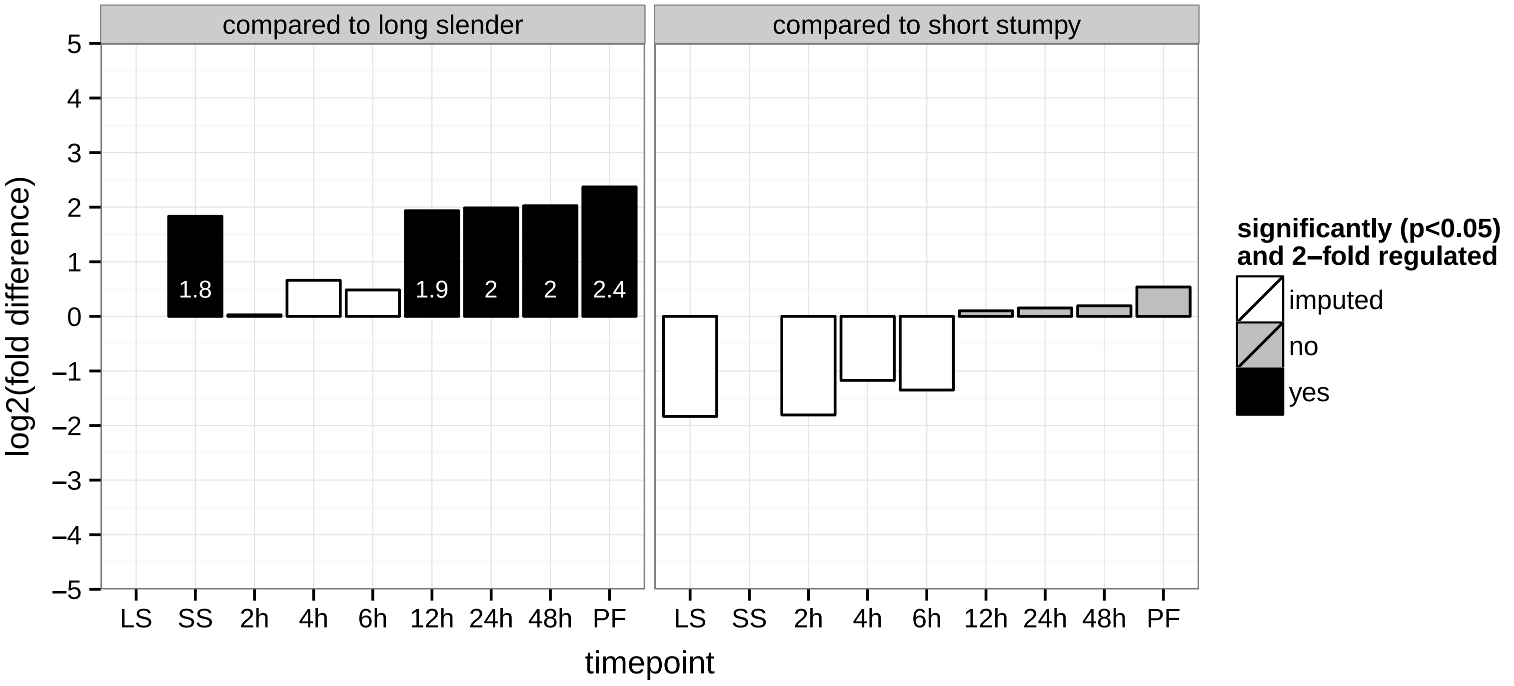
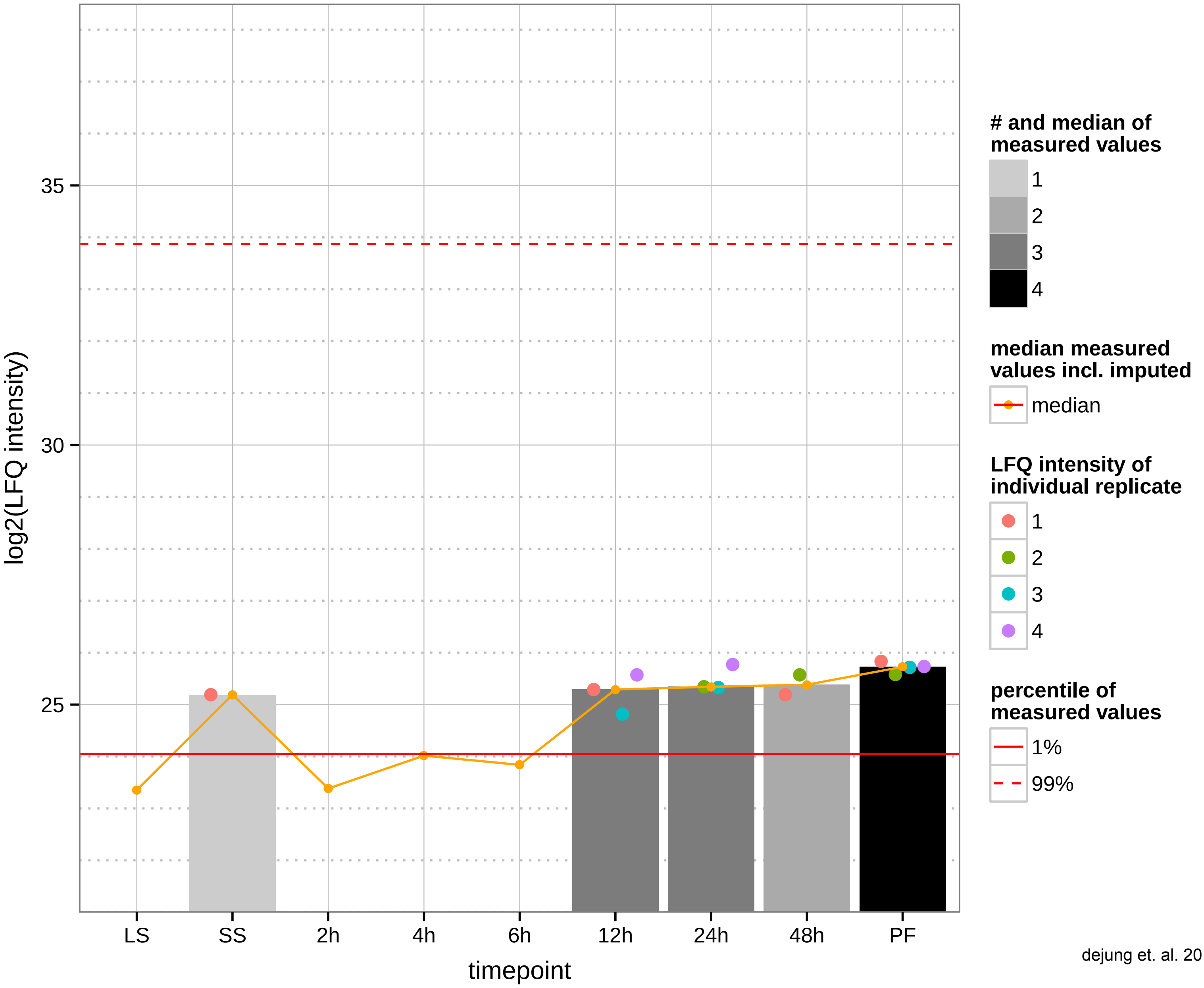
hypothetical protein, conserved
Tb927.7.2760
AGOF: structural constituent of ribosome
AGOC: intracellular, mitochondrion, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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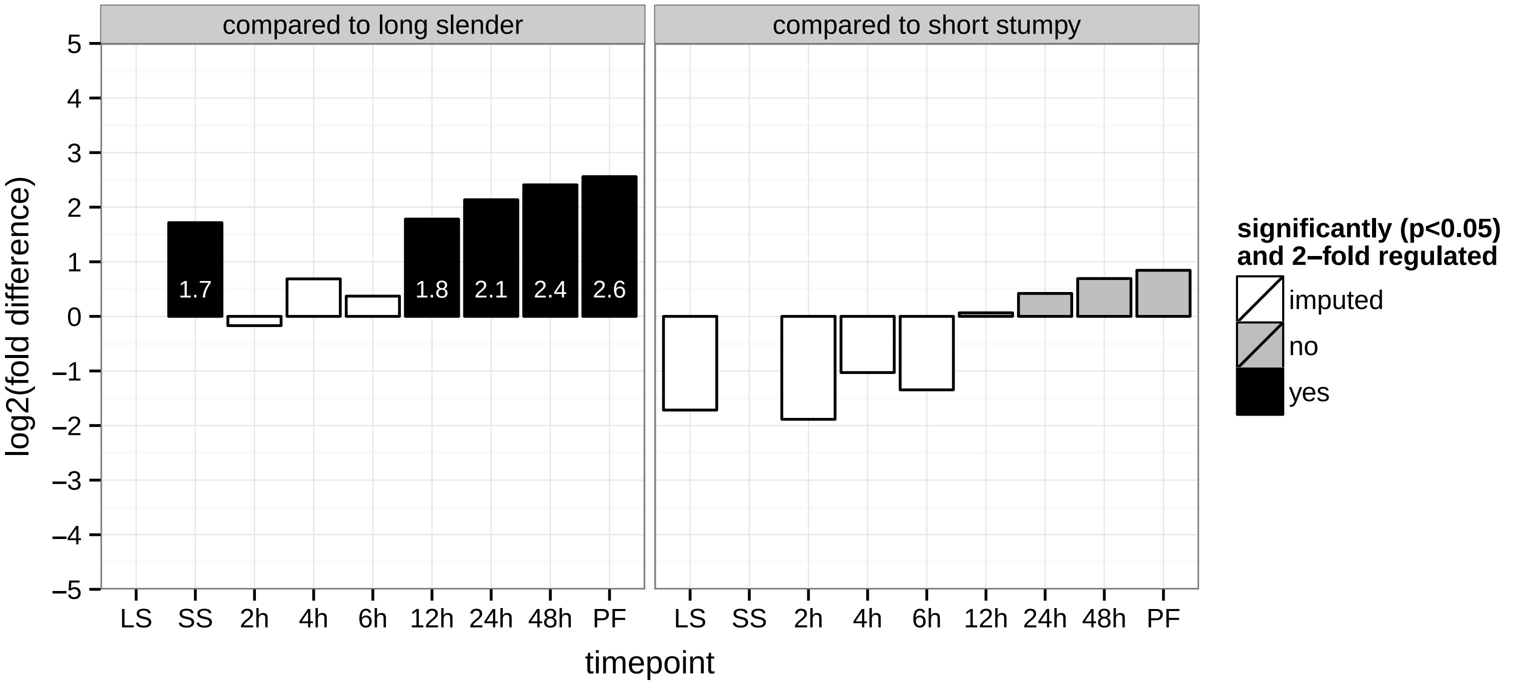
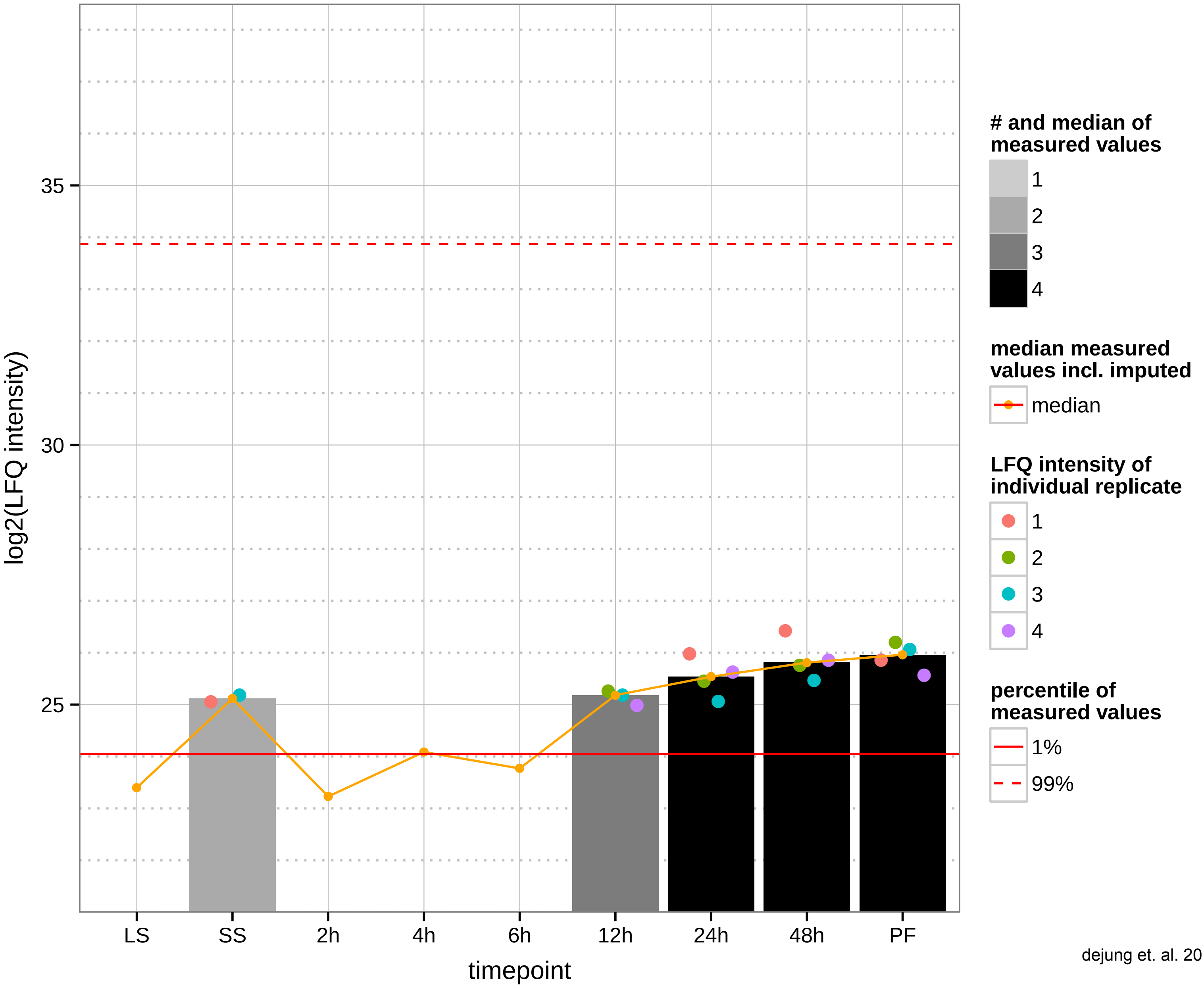
hypothetical protein, conserved
Tb927.8.6480
AGOF: aminomethyltransferase activity
AGOC: cytoplasm, extracellular region
AGOP: glycine decarboxylation via glycine cleavage system
PGOF: aminomethyltransferase activity
PGOC: cytoplasm
PGOP: glycine catabolic process





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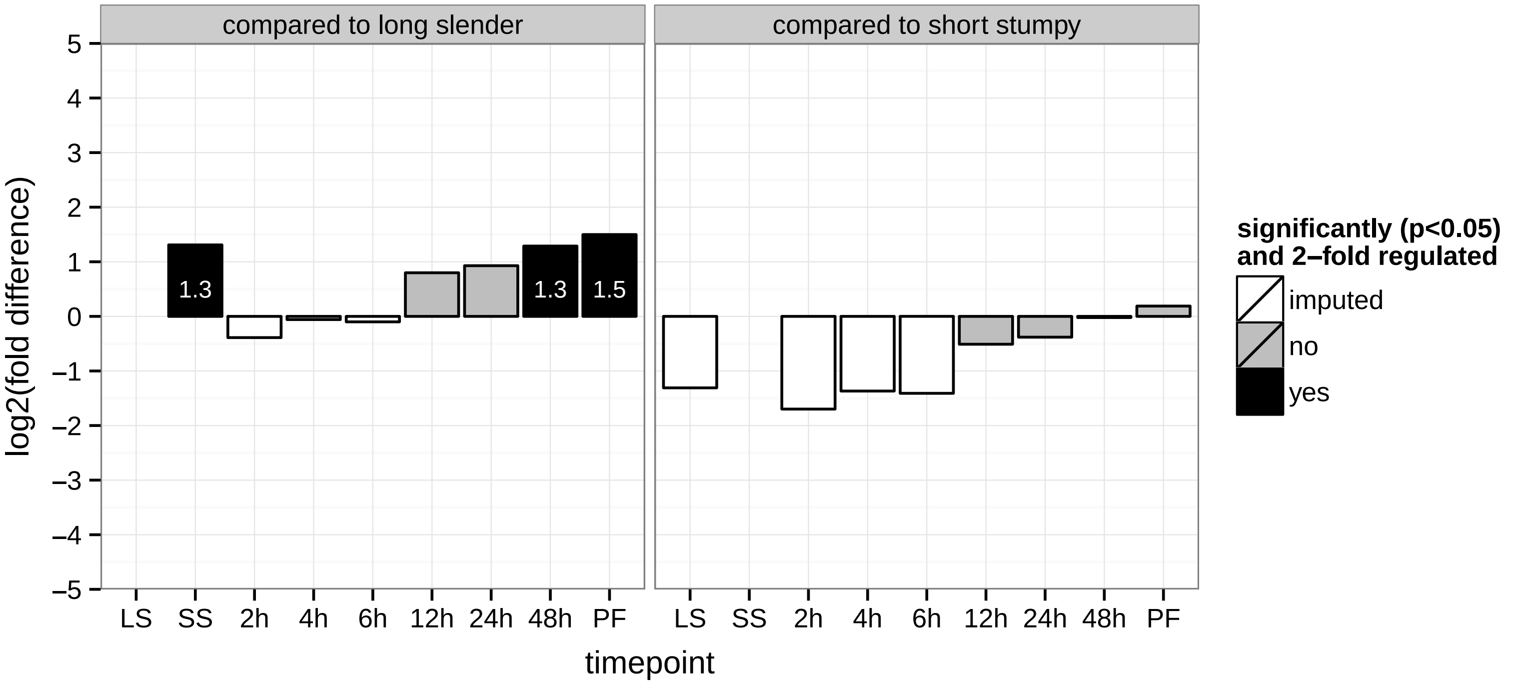
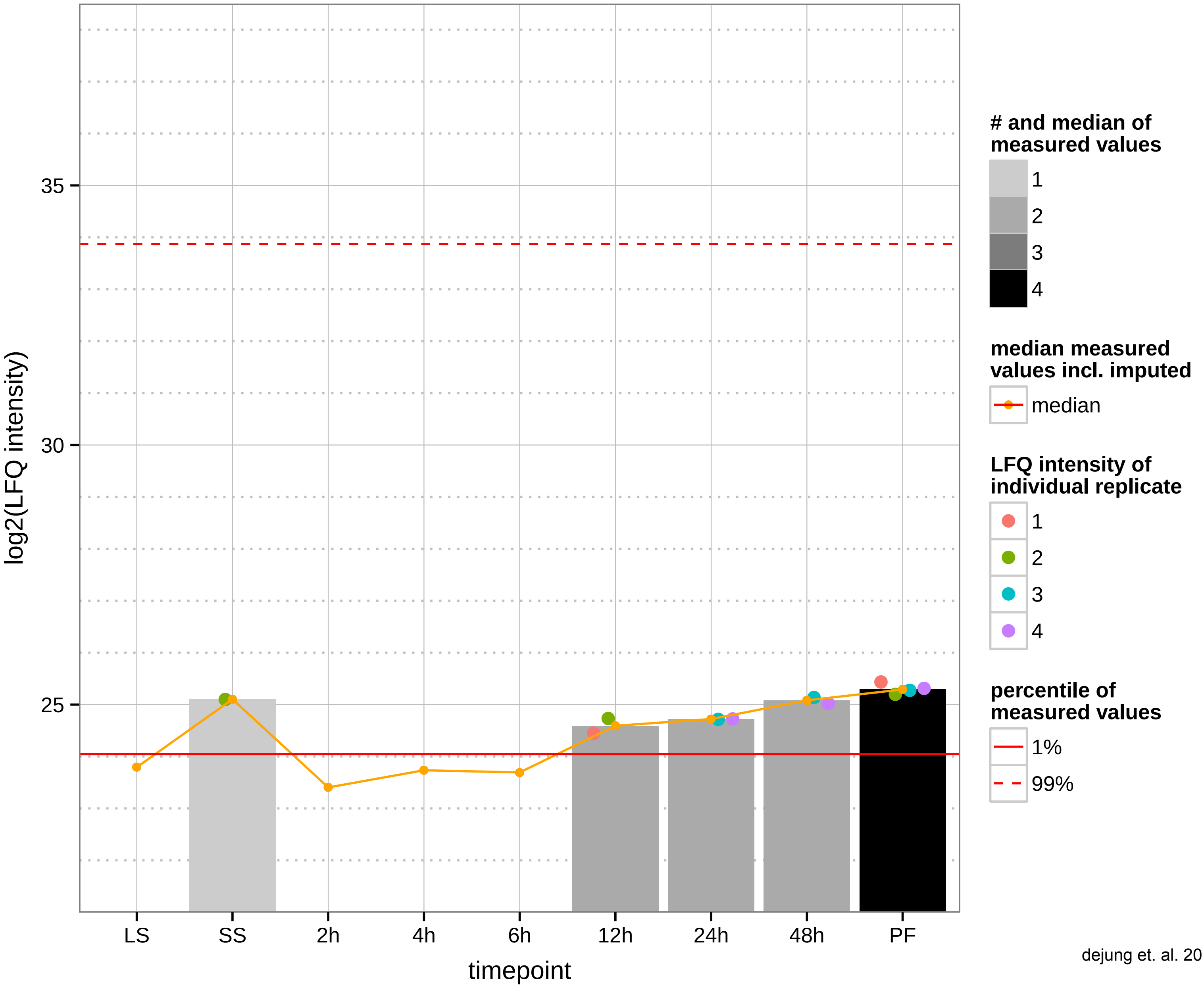
hypothetical protein, conserved
Tb927.9.3560
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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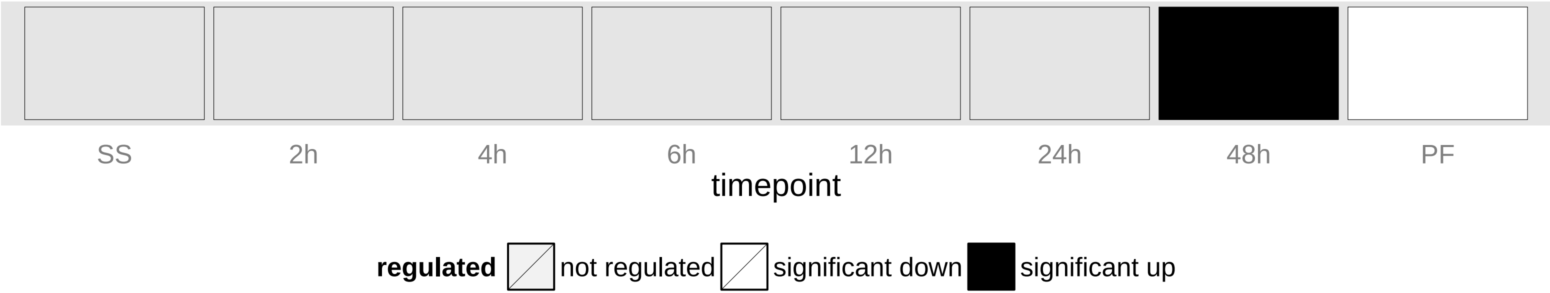

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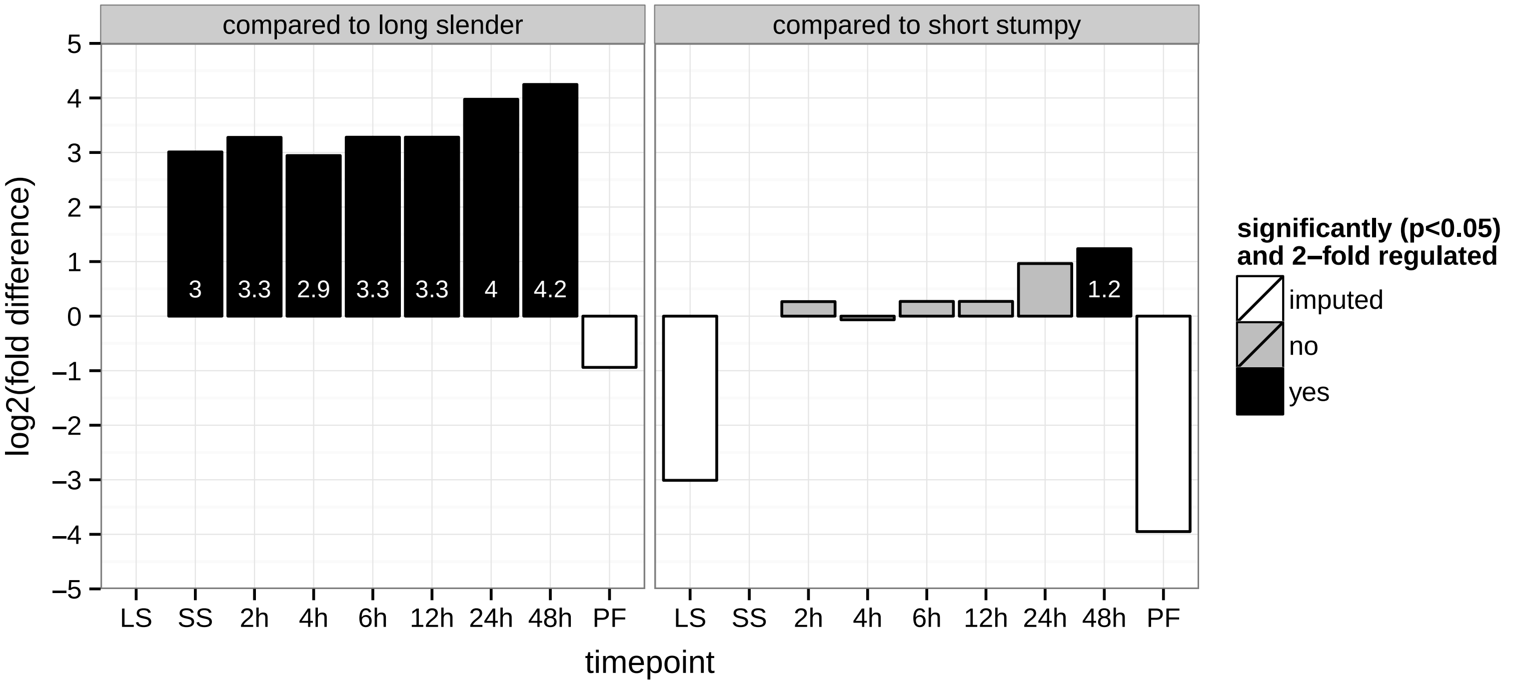
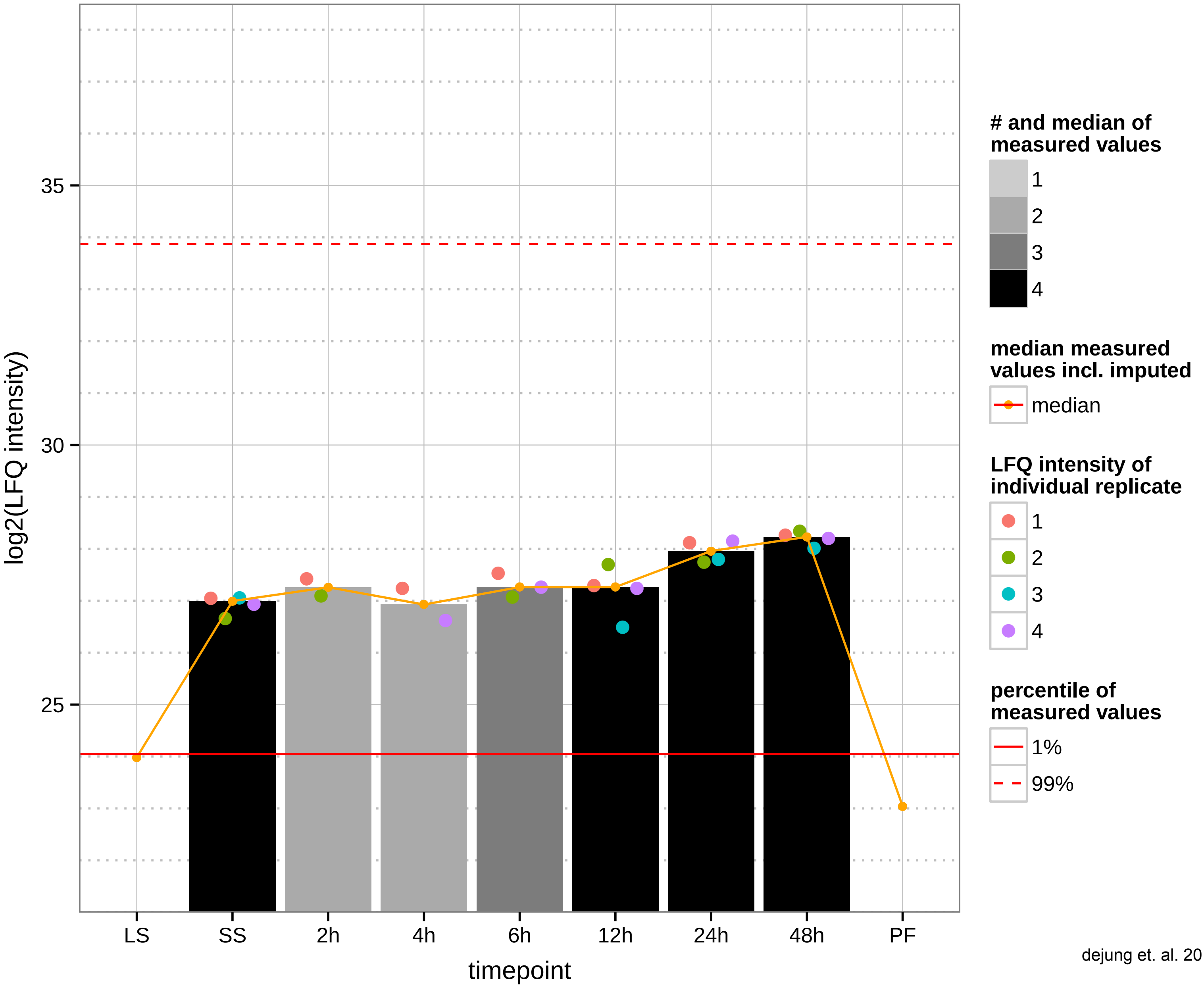
retrotransposon hot spot (RHS) protein, putative
Tb11.v5.0326
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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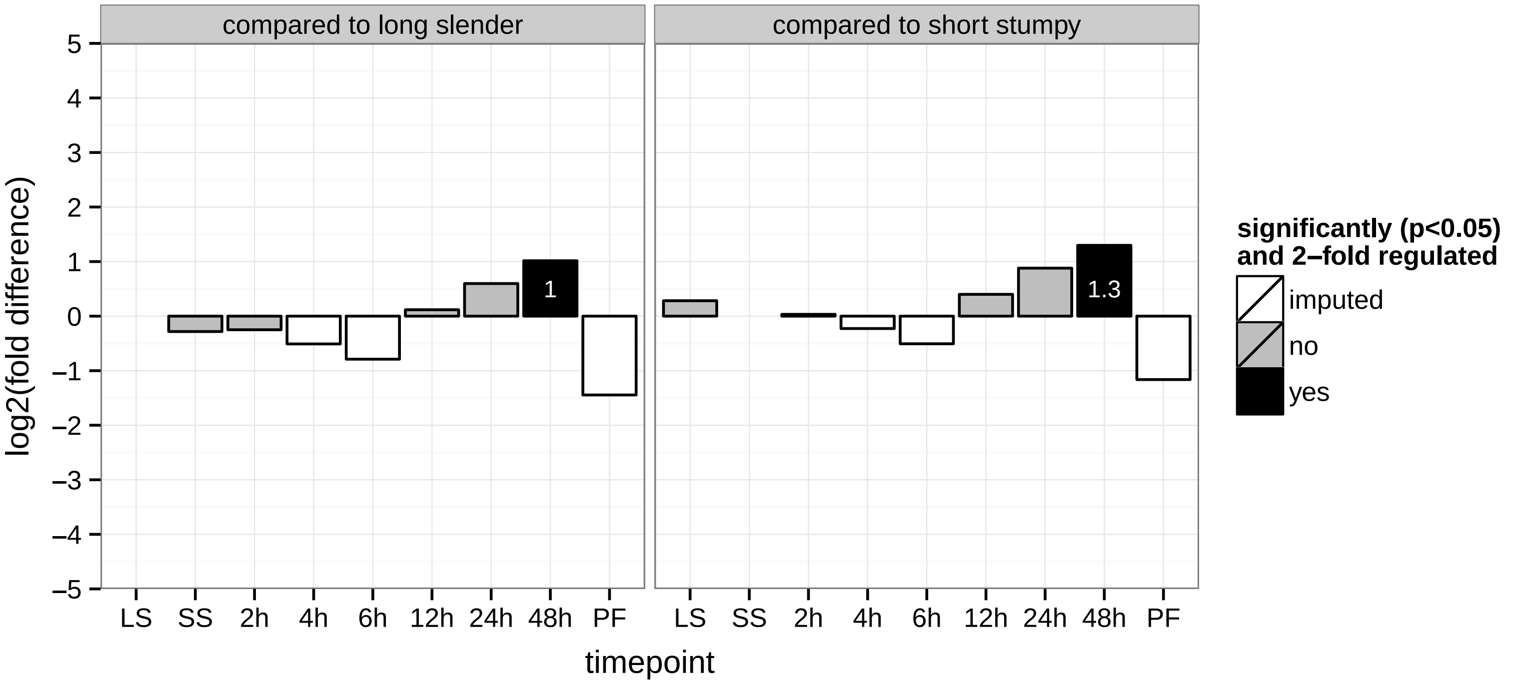
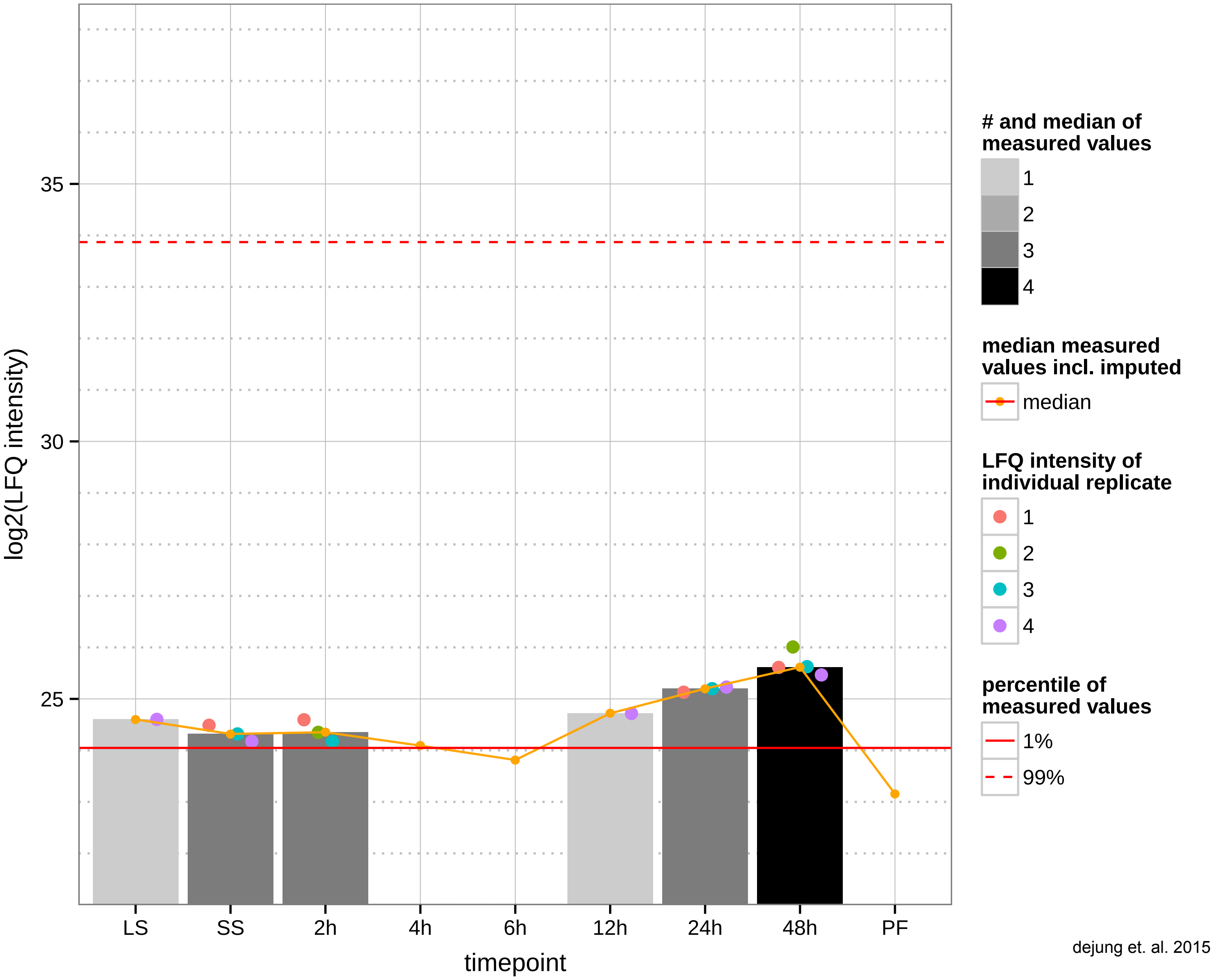
hypothetical protein, conserved
Tb927.10.8850
AGOF: RNA binding, catalytic activity
AGOC: null
AGOP: null
PGOF: catalytic activity
PGOC: null
PGOP: null





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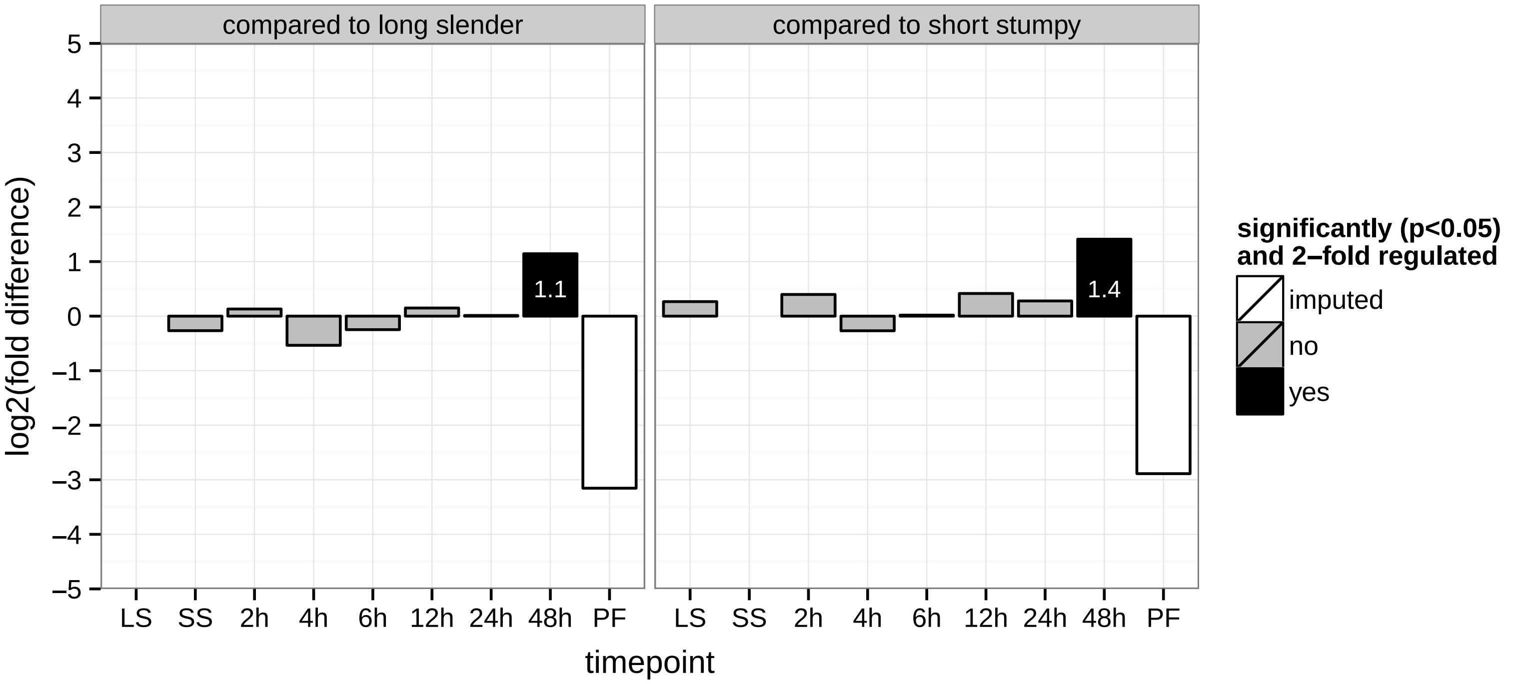
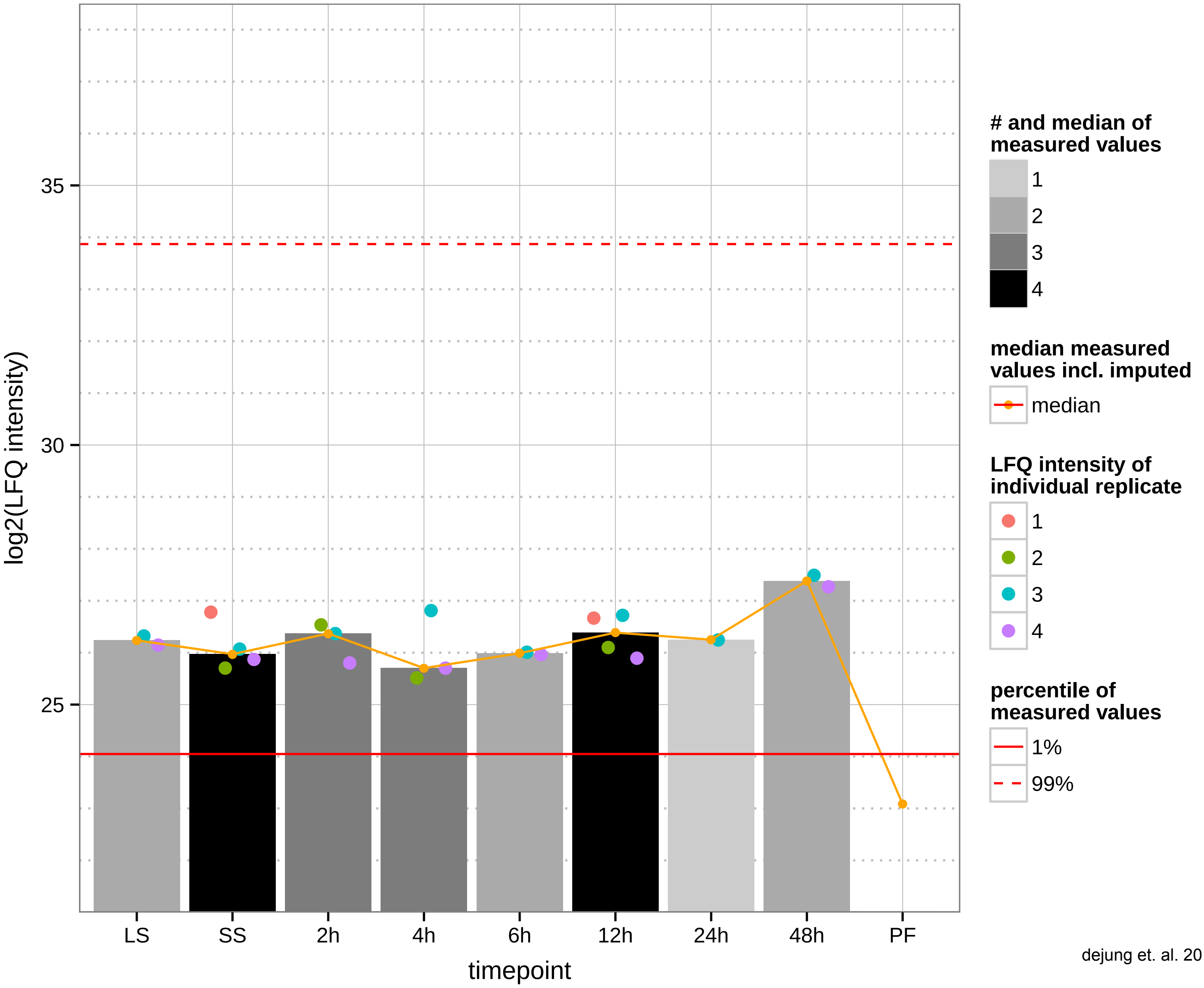
hypothetical protein, conserved
Tb927.7.2330
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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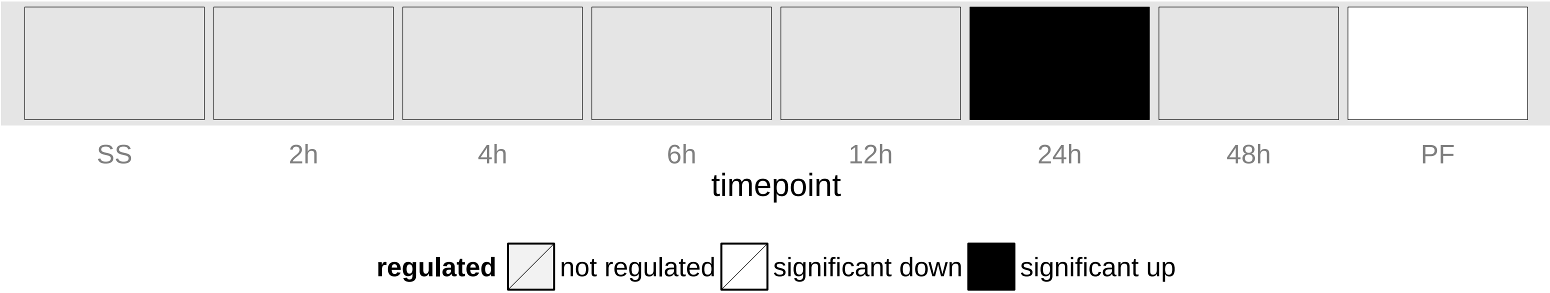
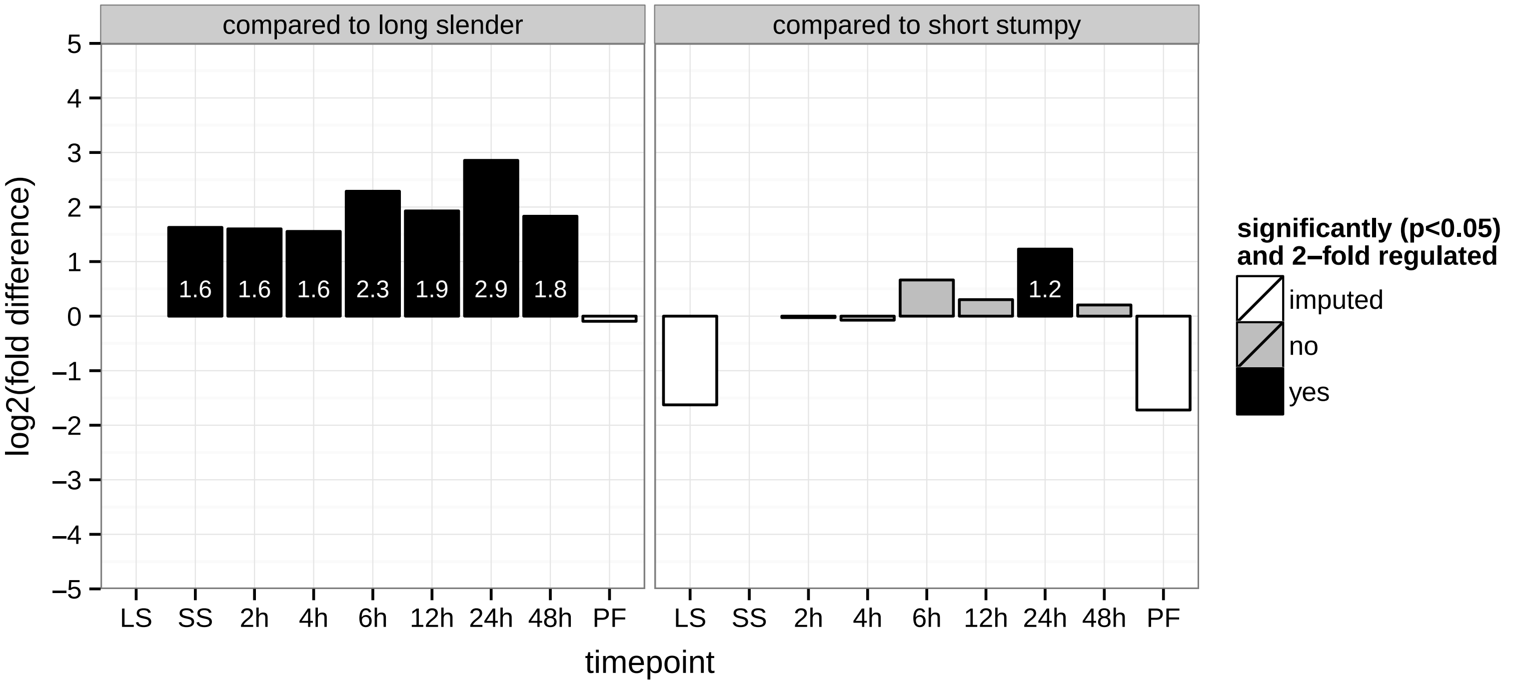
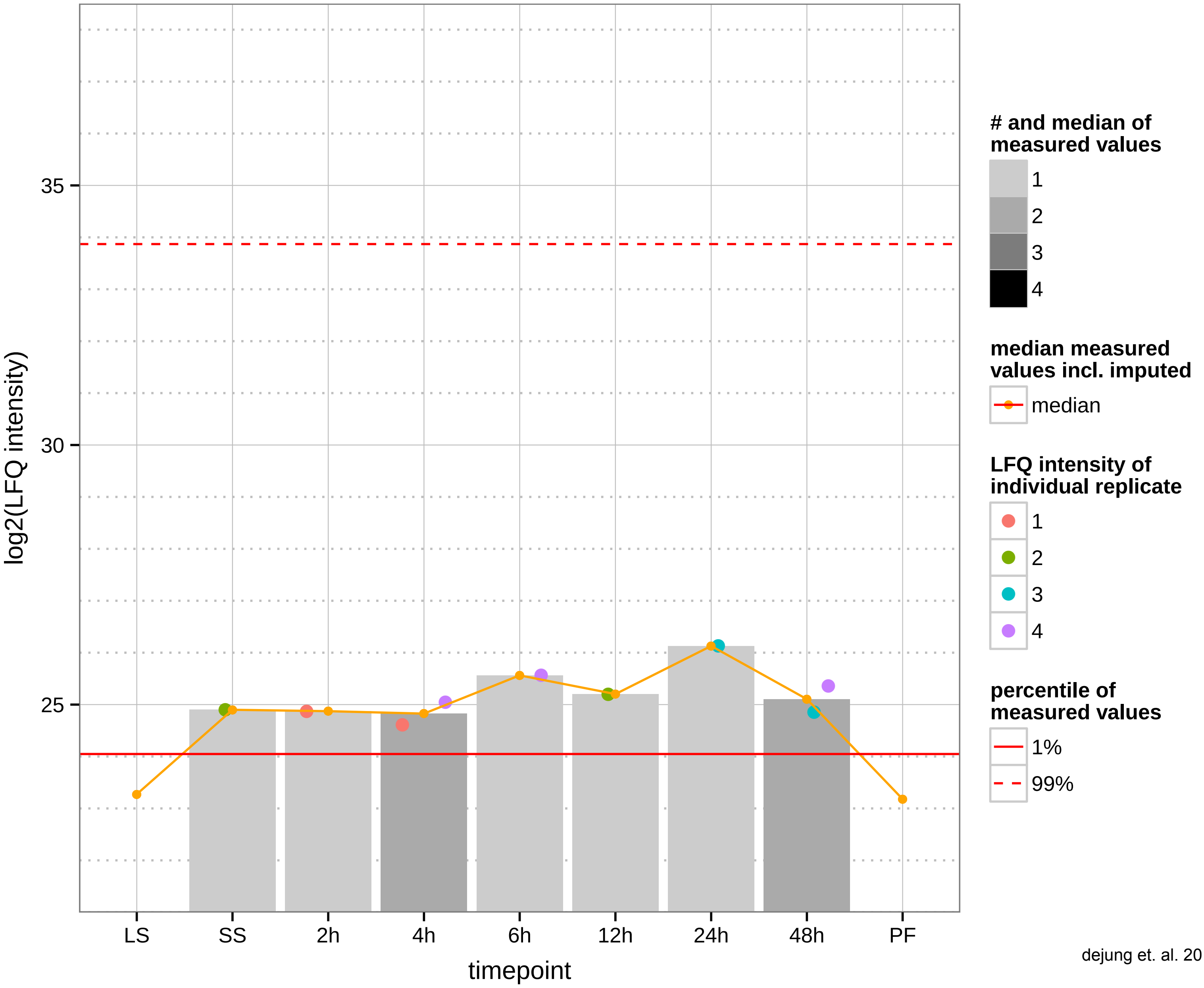


dejung et. al. 2015

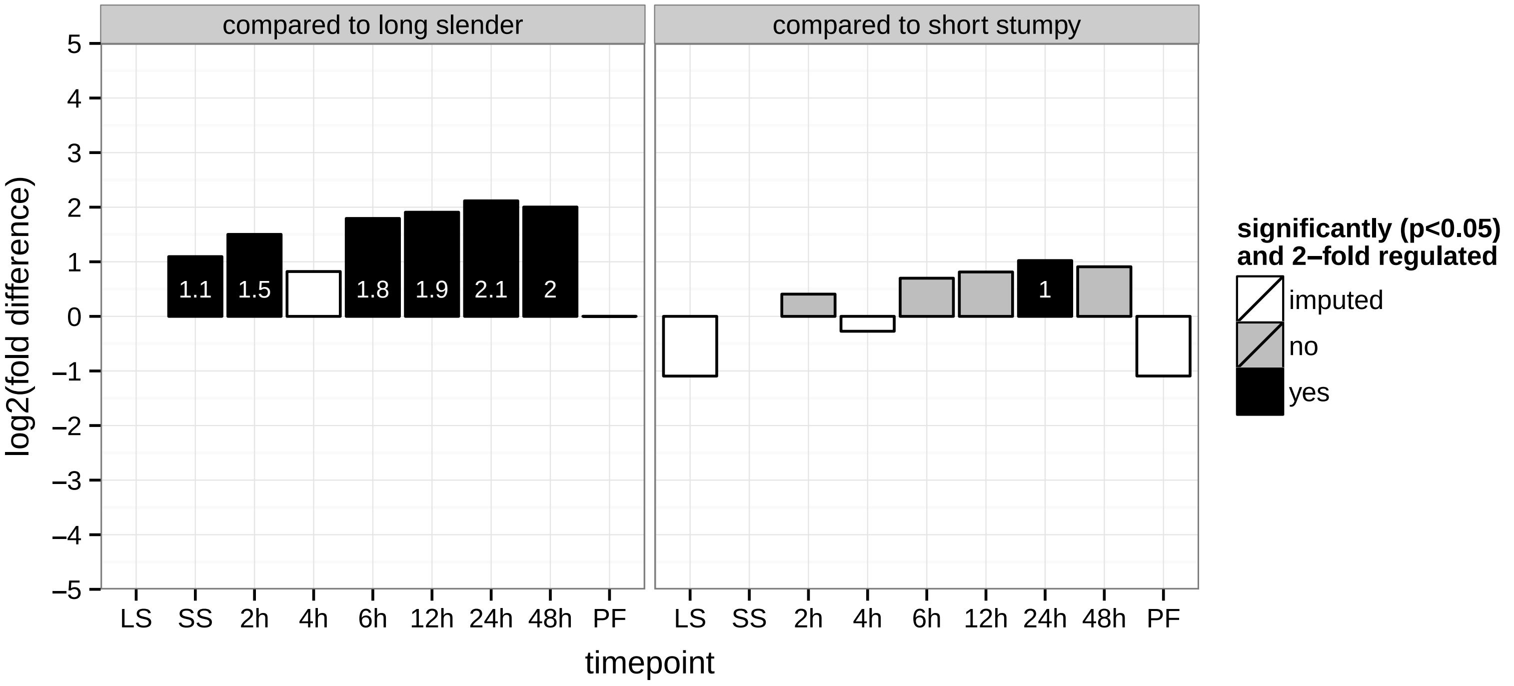
hypothetical protein, conserved
Tb927.10.2580
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

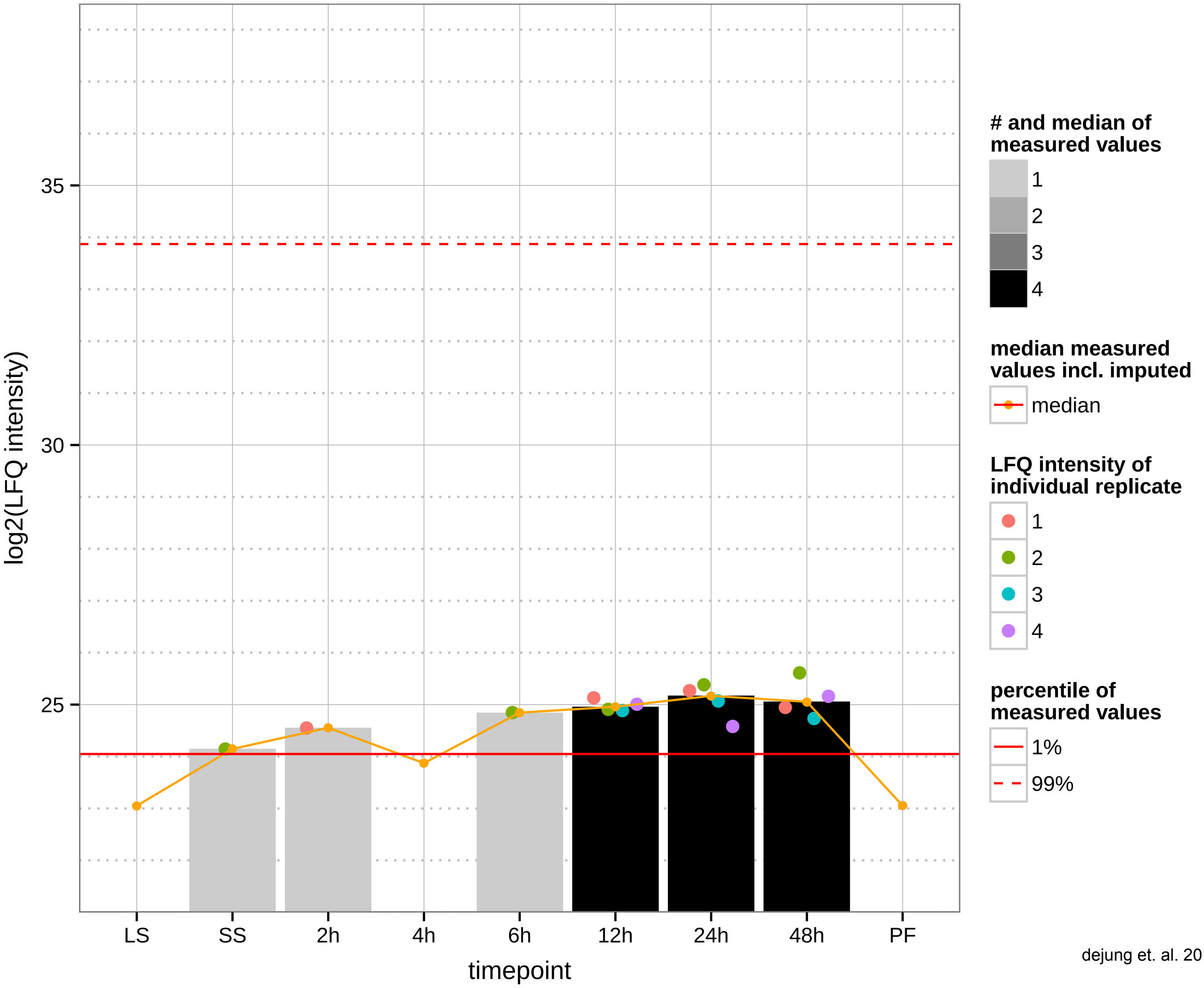




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.10170
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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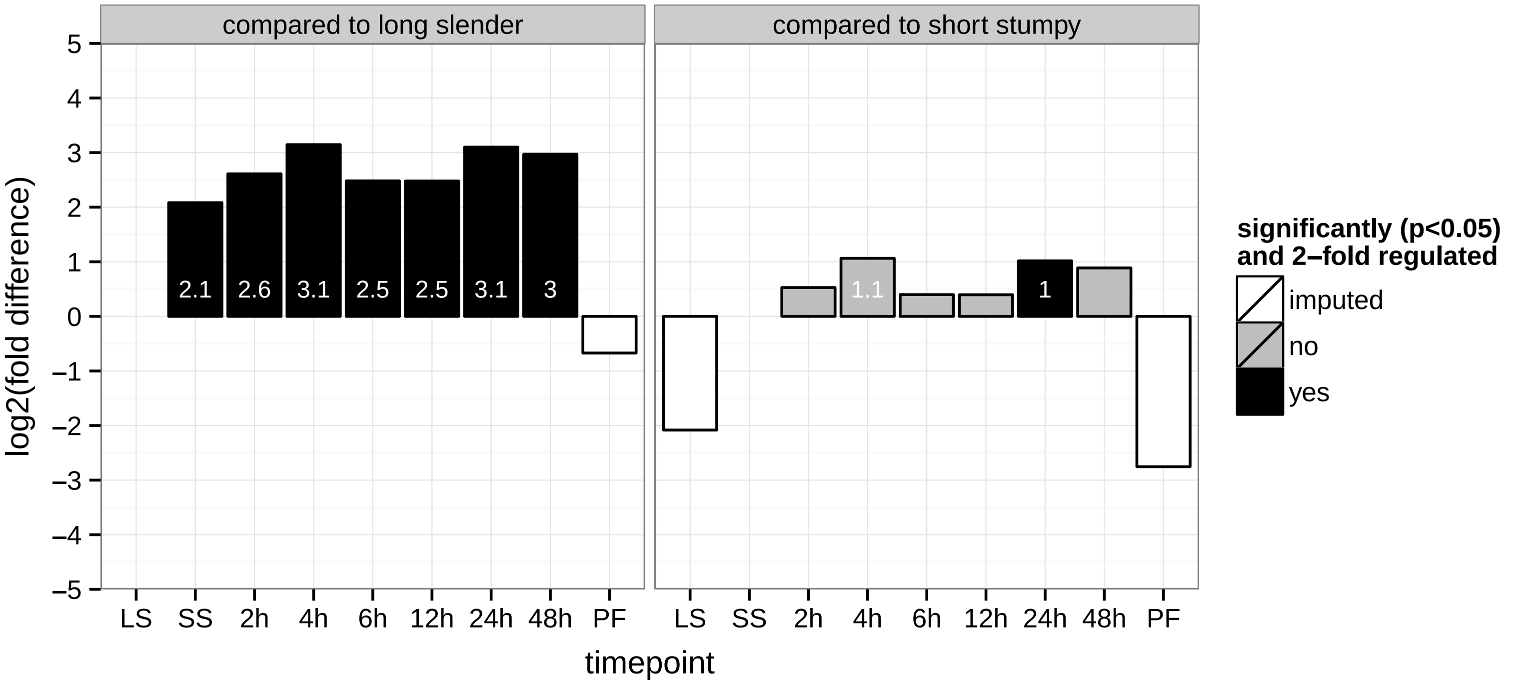
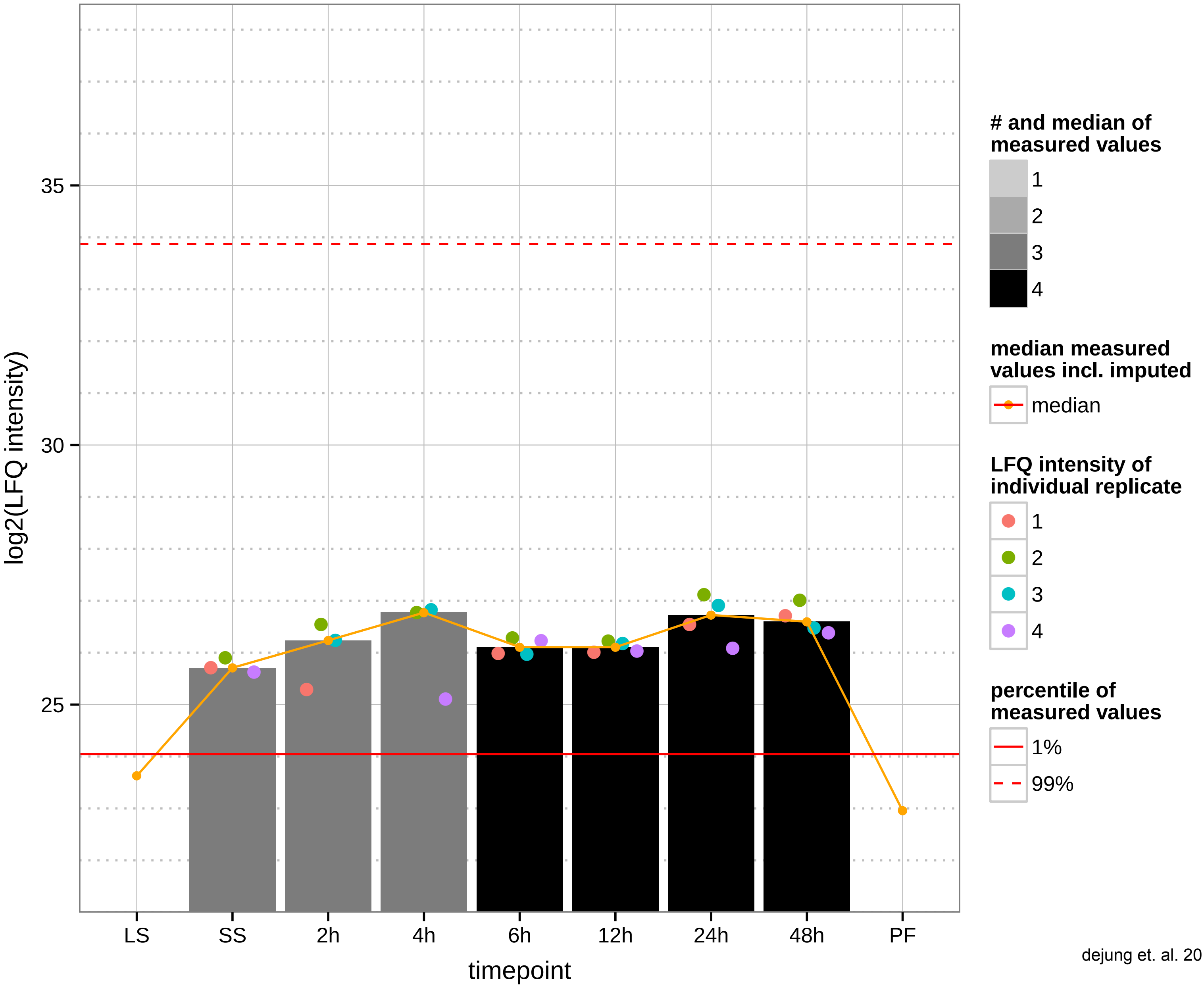
conserved protein
Tb927.6.1860
AGOF: null
AGOC: mitochondrion
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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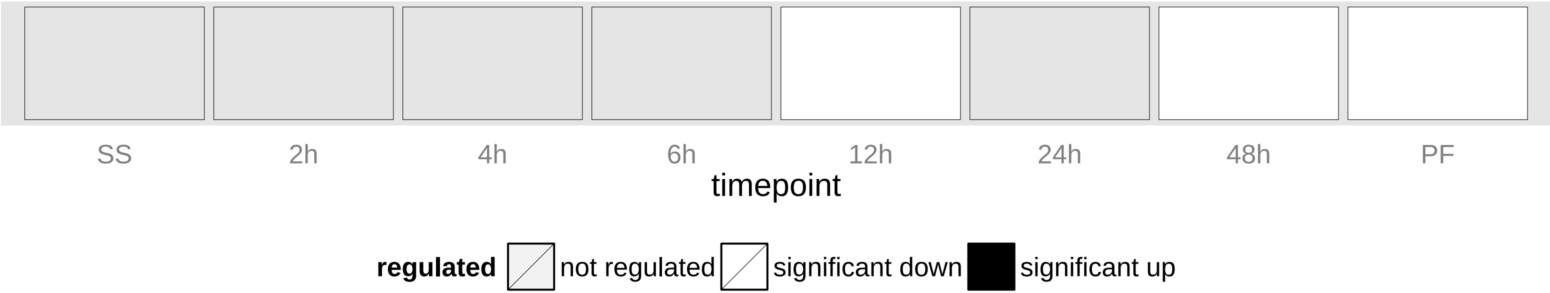
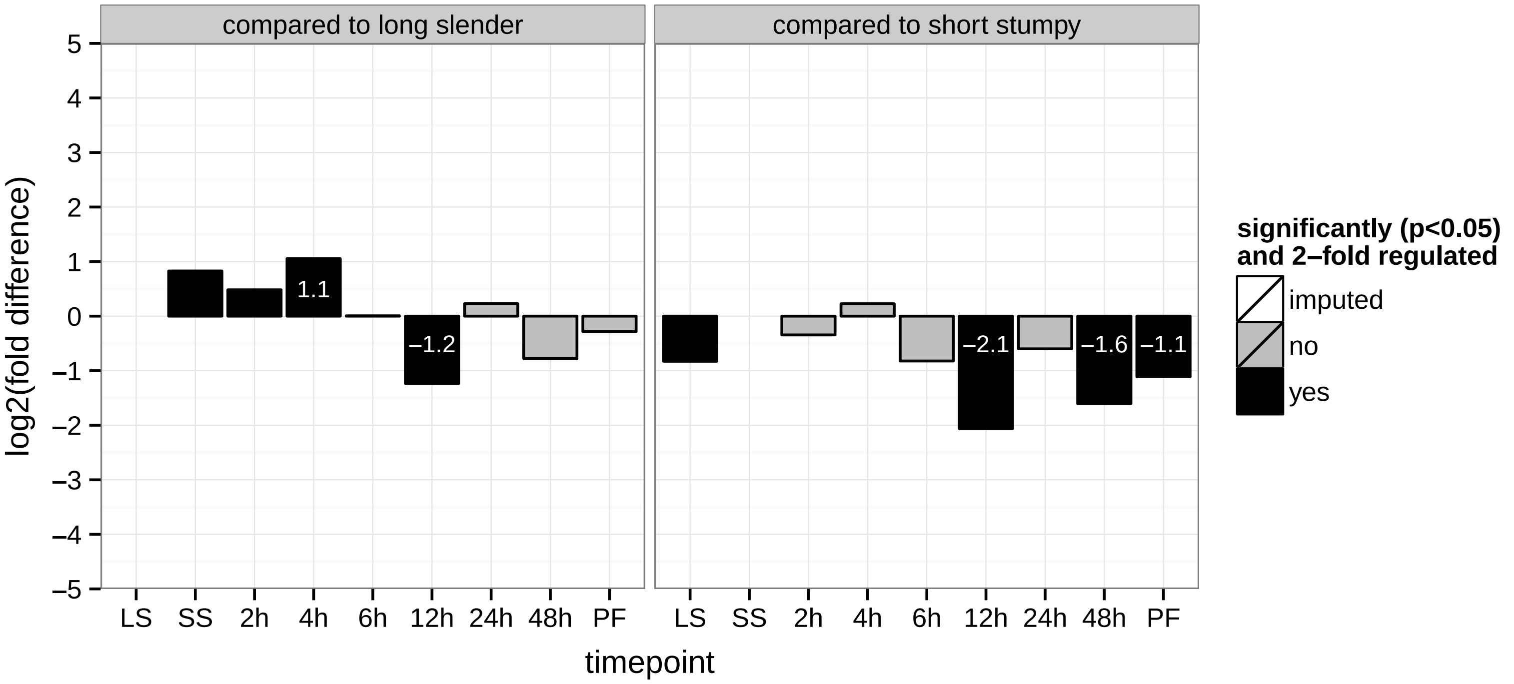
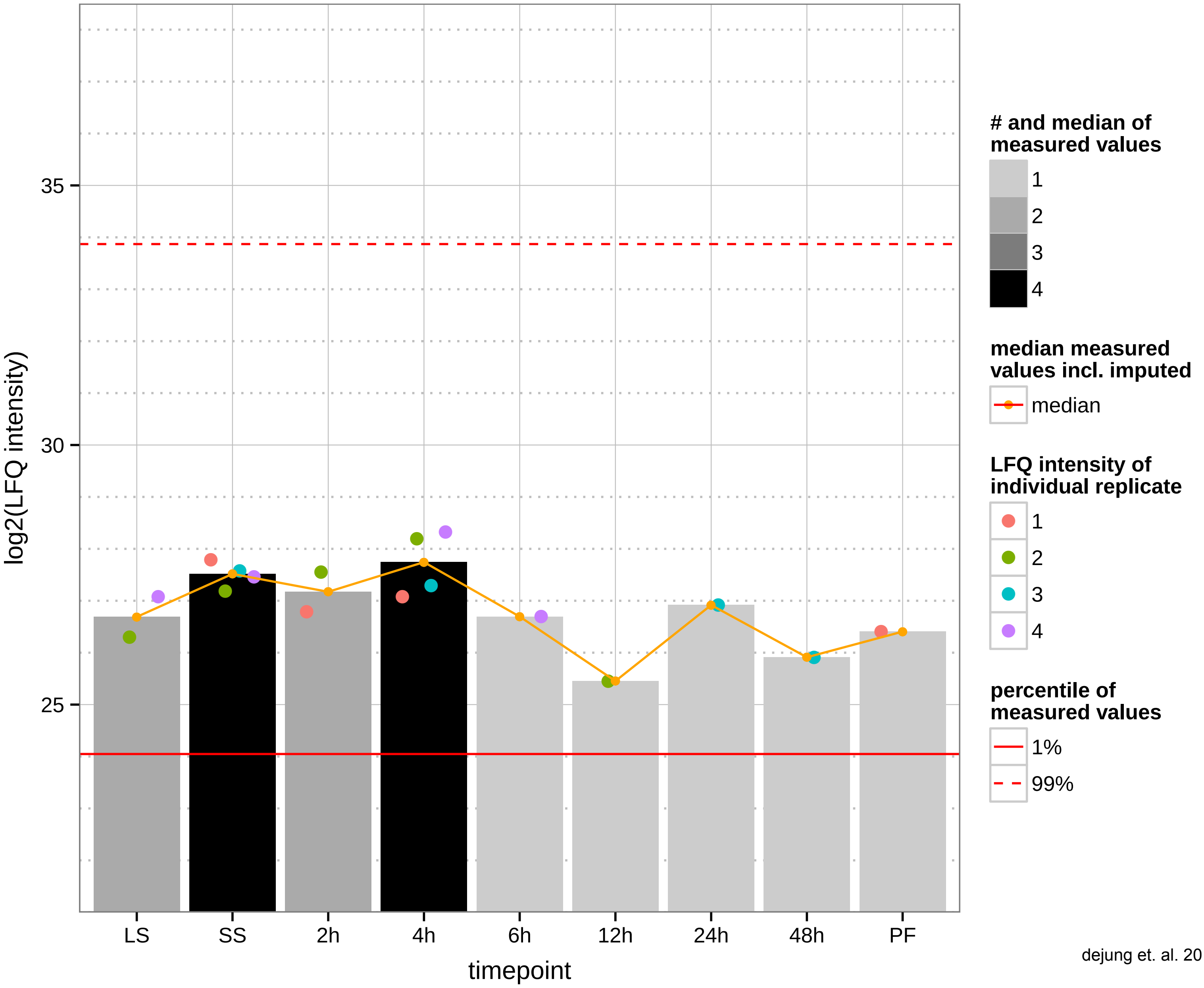


dejung et. al. 2015

hypothetical protein, conserved
Tb927.2.4410
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: integral to membrane
PGOP: null





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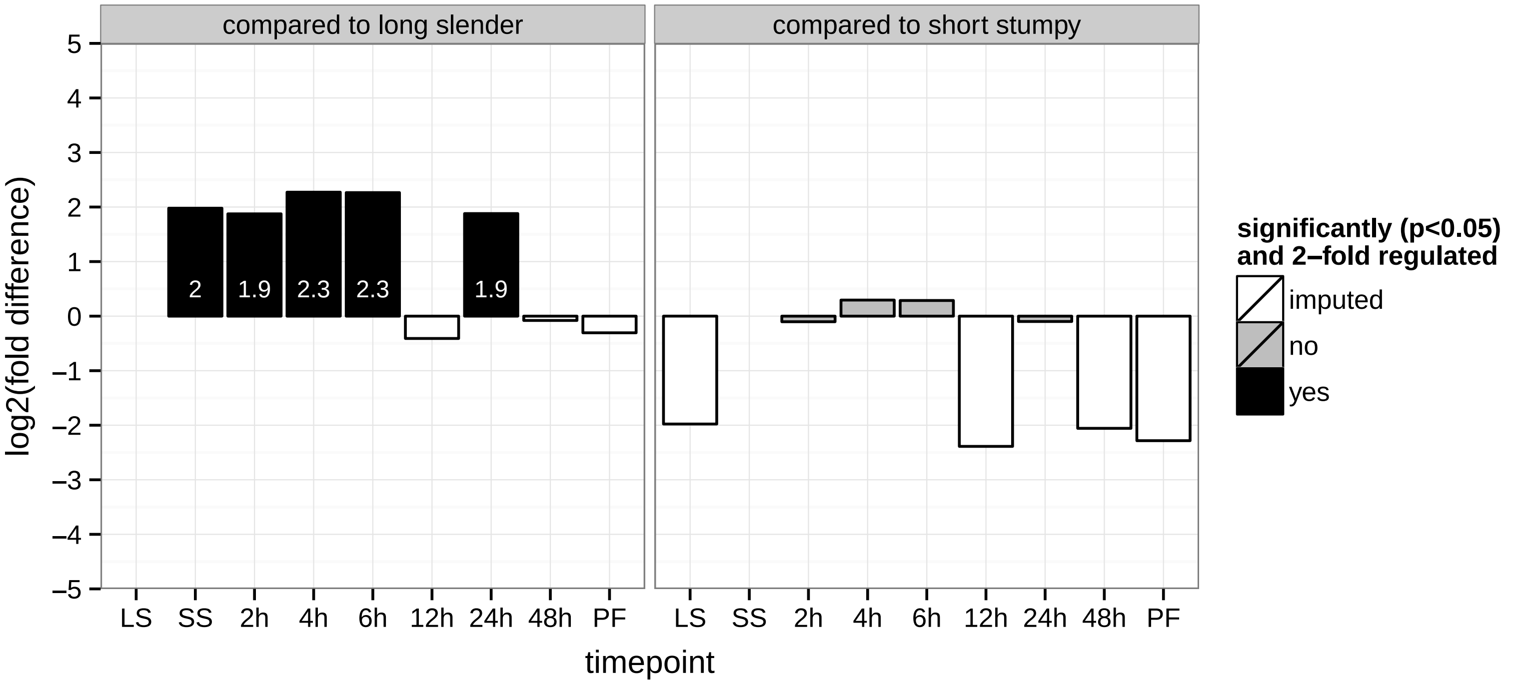
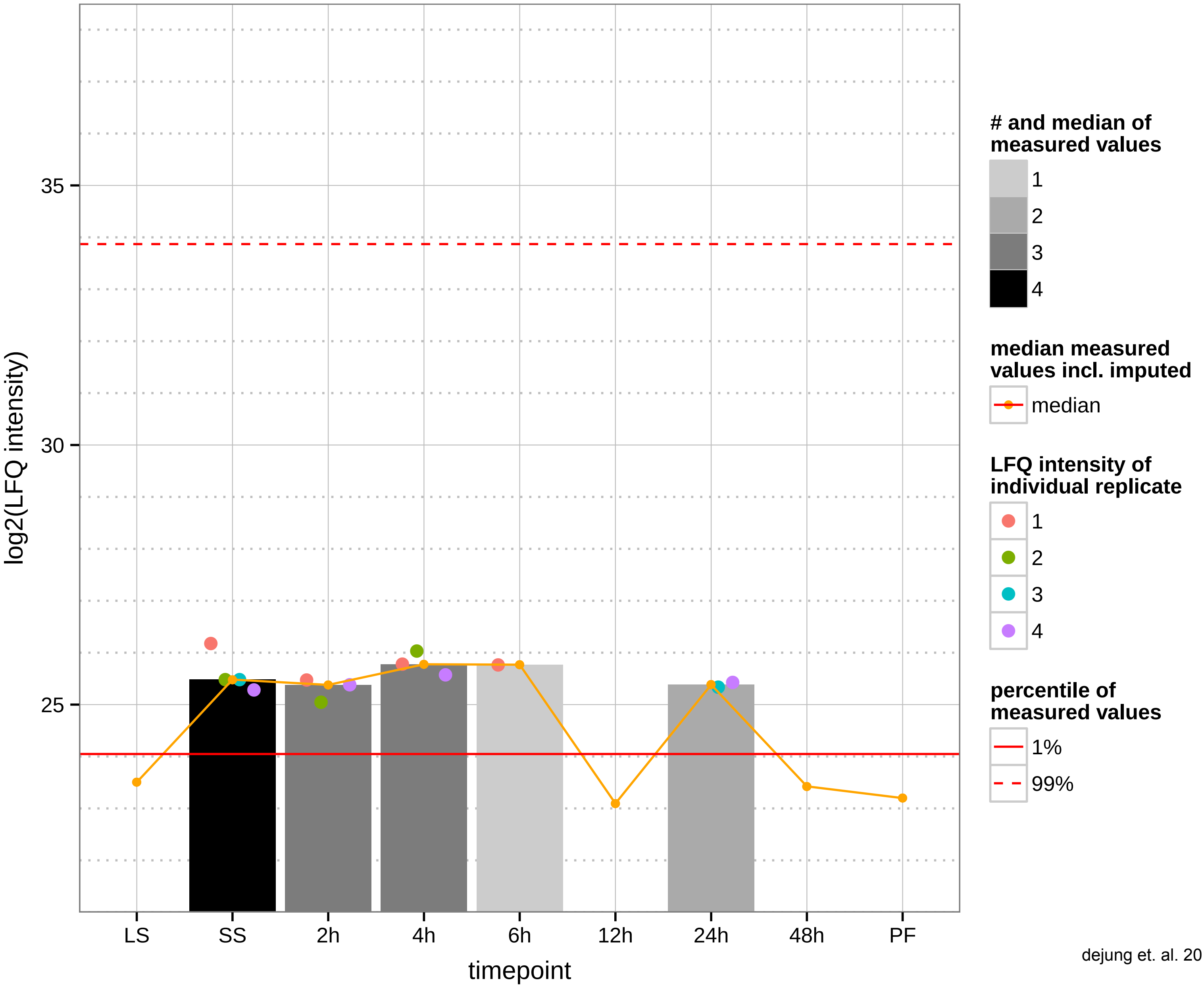
p22 protein precursor, putative
Tb927.7.3470
AGOF: null
AGOC: mitochondrial matrix, mitochondrion
AGOP: null
PGOF: null
PGOC: mitochondrial matrix
PGOP: null





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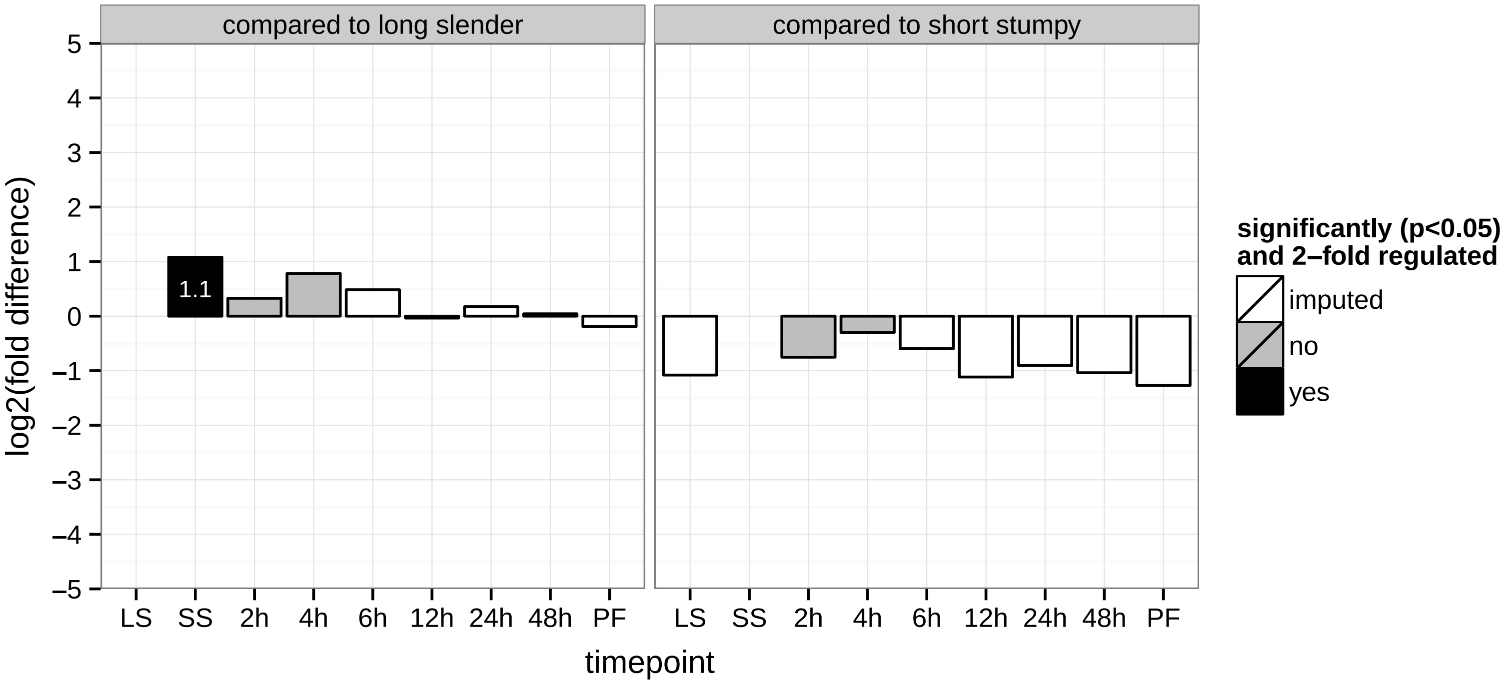
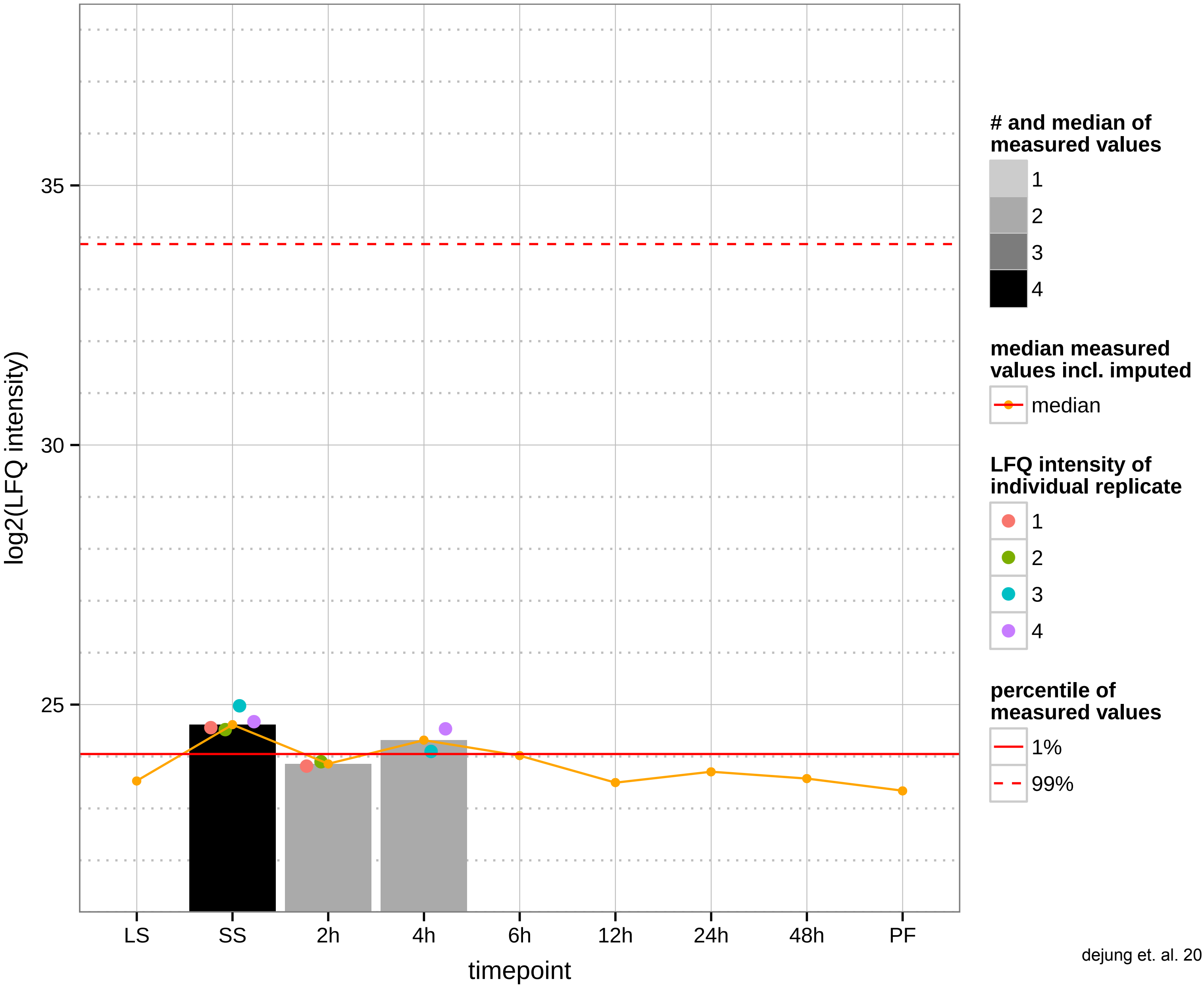
hypothetical protein, conserved
Tb927.8.7760
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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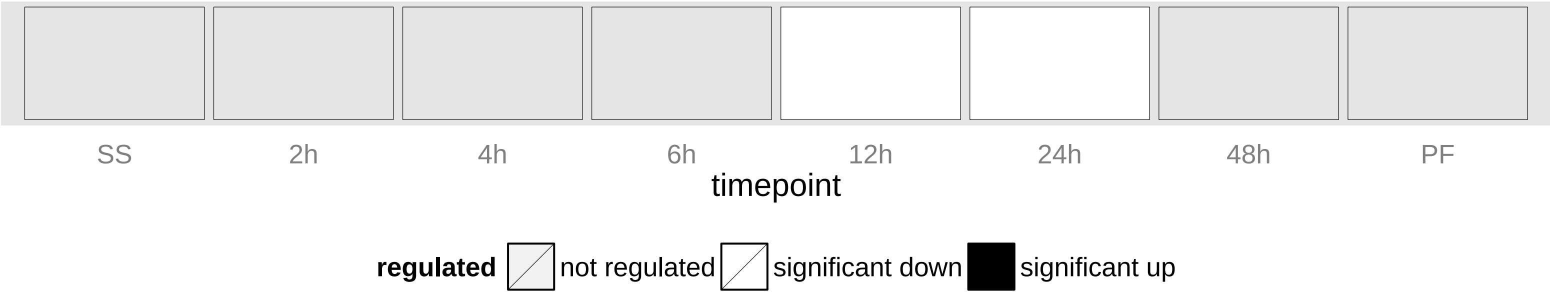

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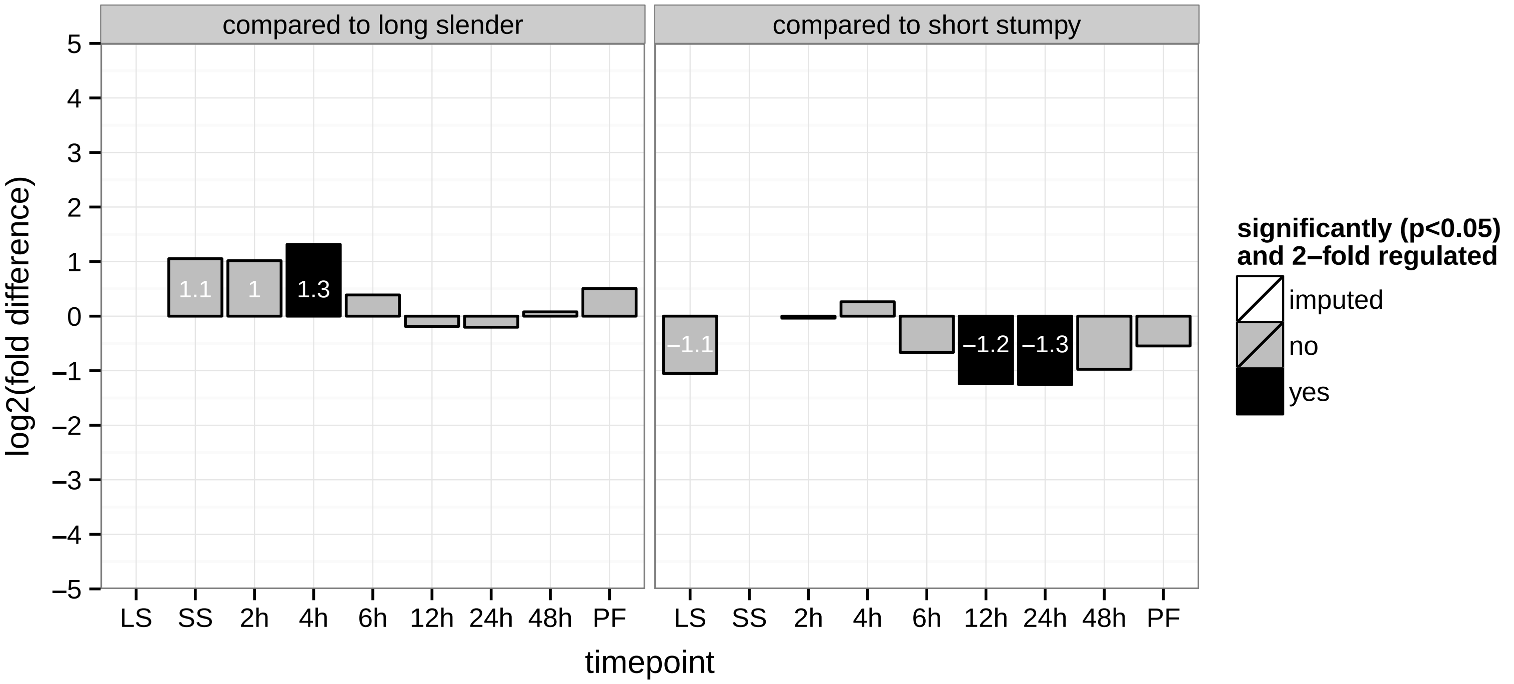
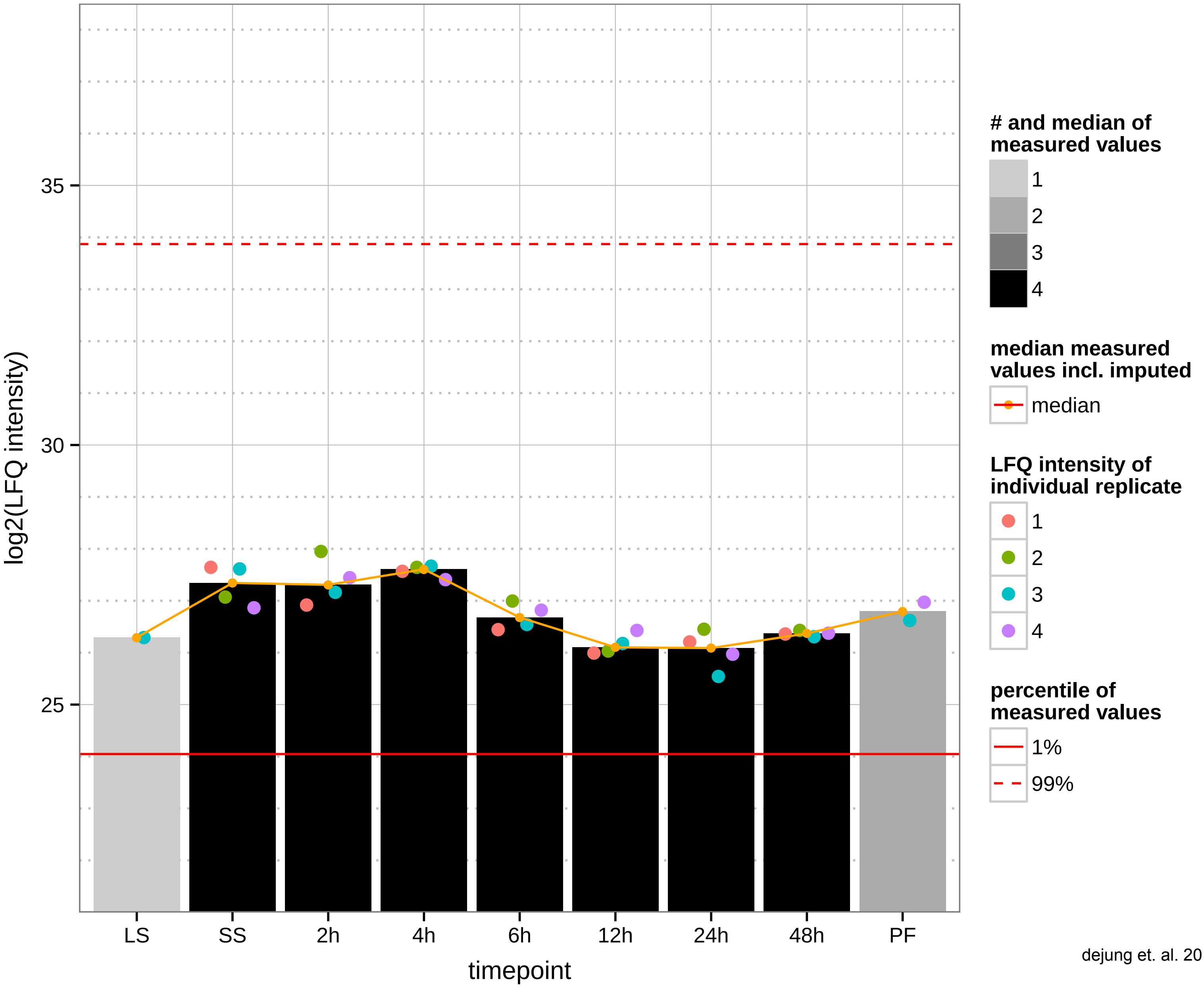
Dynein light chain Tctex−type, putative
Tb927.10.10320
AGOF: microtubule motor activity
AGOC: microtubule associated complex
AGOP: microtubule−based process
PGOF: null
PGOC: null
PGOP: null





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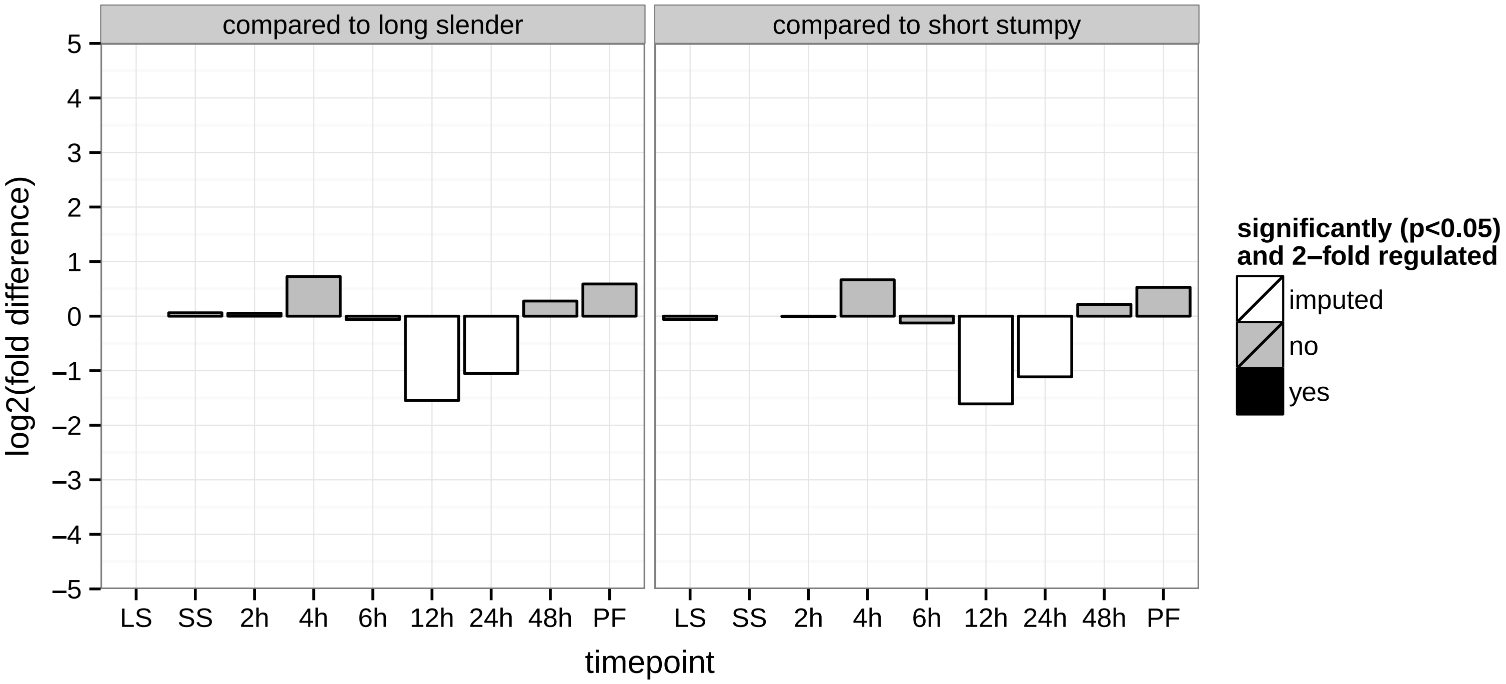
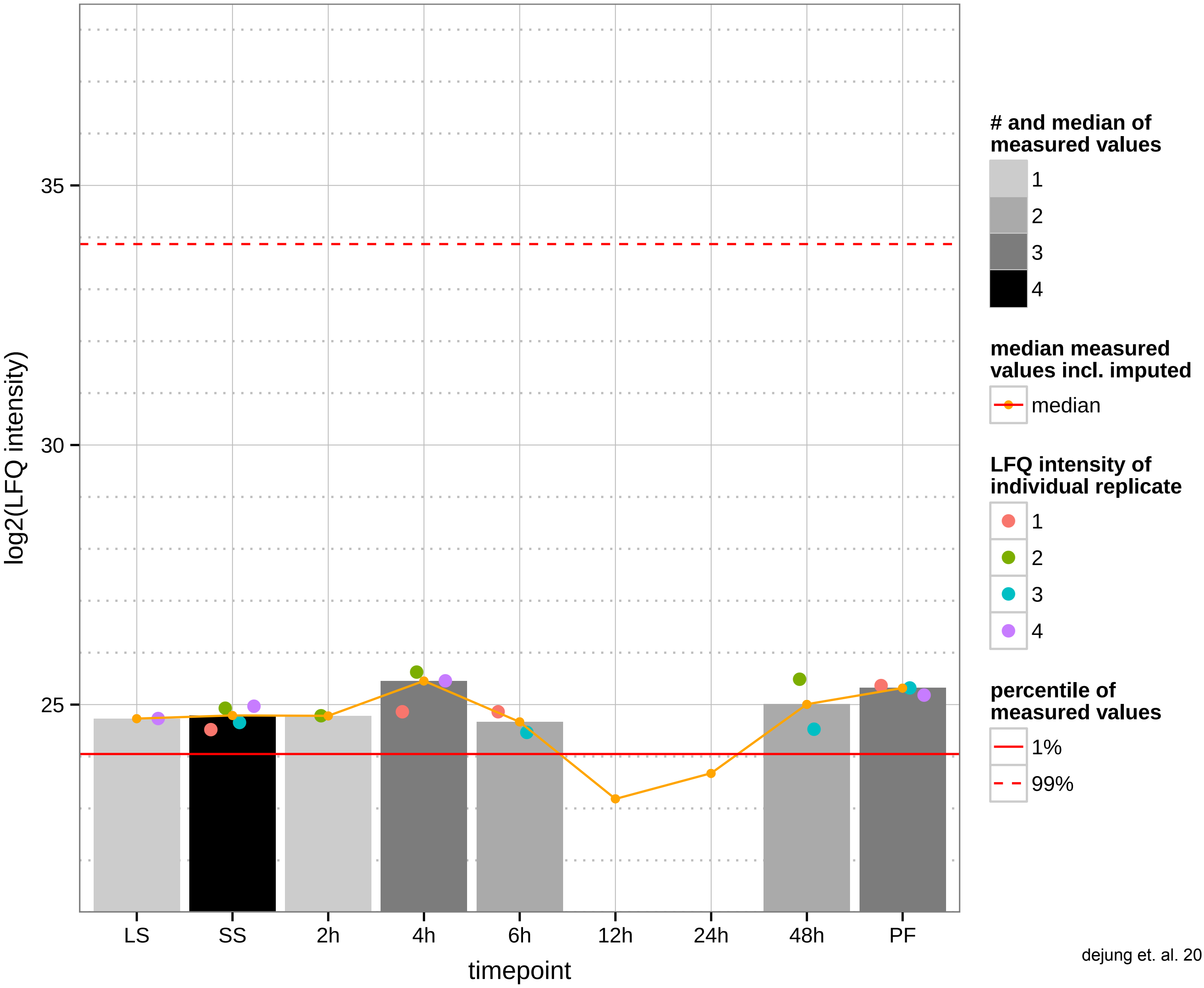
RNA–binding protein, putative (RBP39)
Tb927.11.15350
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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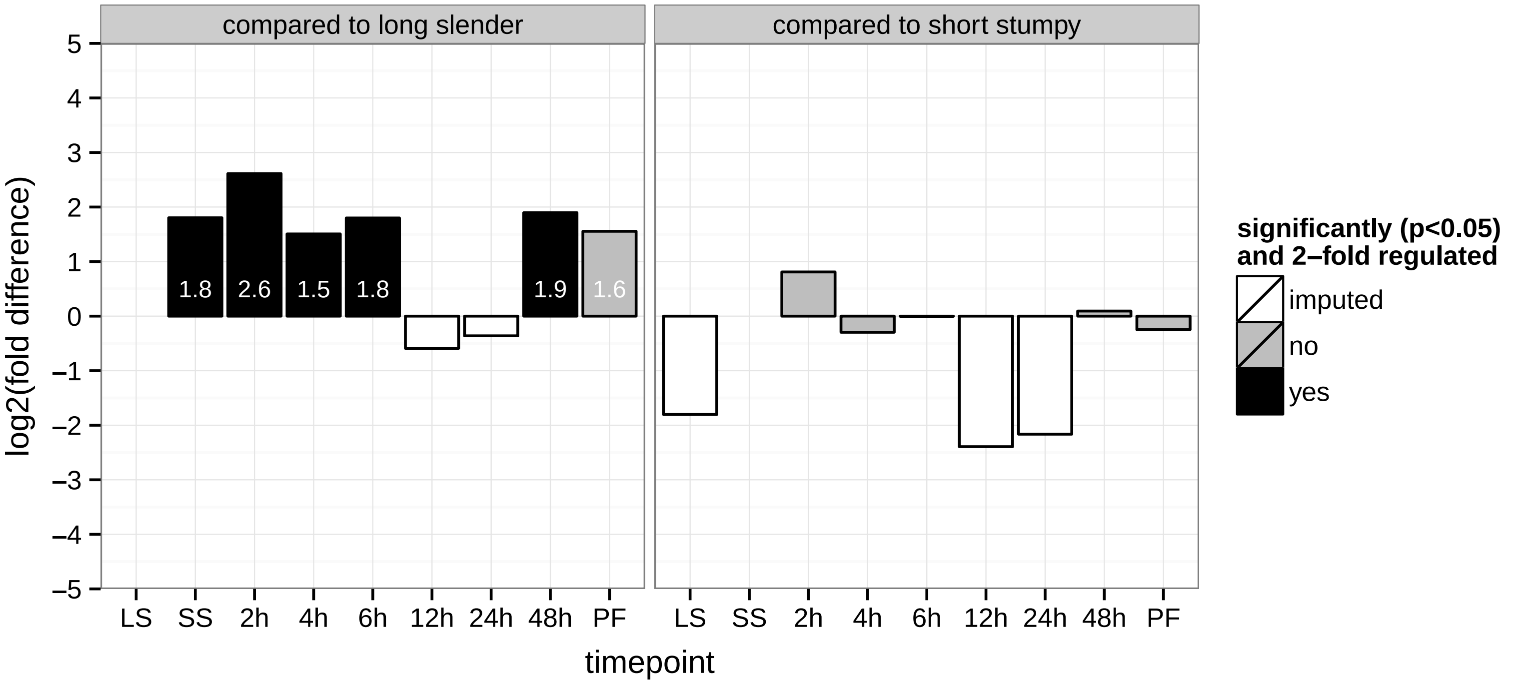
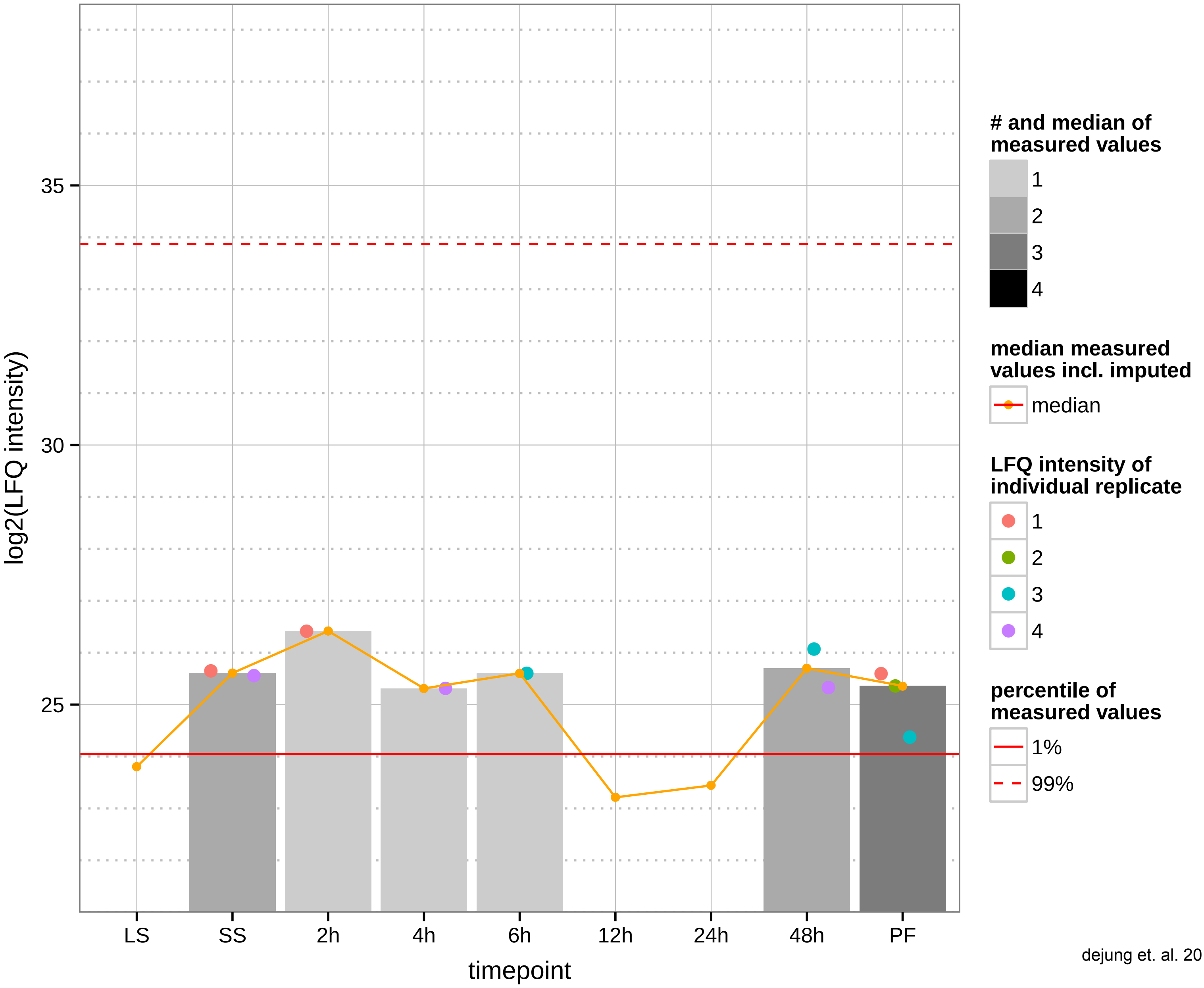
ADP–ribosylation factor GTPase activating protein, putative
Tb927.9.15490
AGOF: ARF GTPase activator activity, DNA binding, zinc ion binding
AGOC: nucleus
AGOP: regulation of ARF GTPase activity
PGOF: ARF GTPase activator activity, zinc ion binding
PGOC: null
PGOP: regulation of ARF GTPase activity





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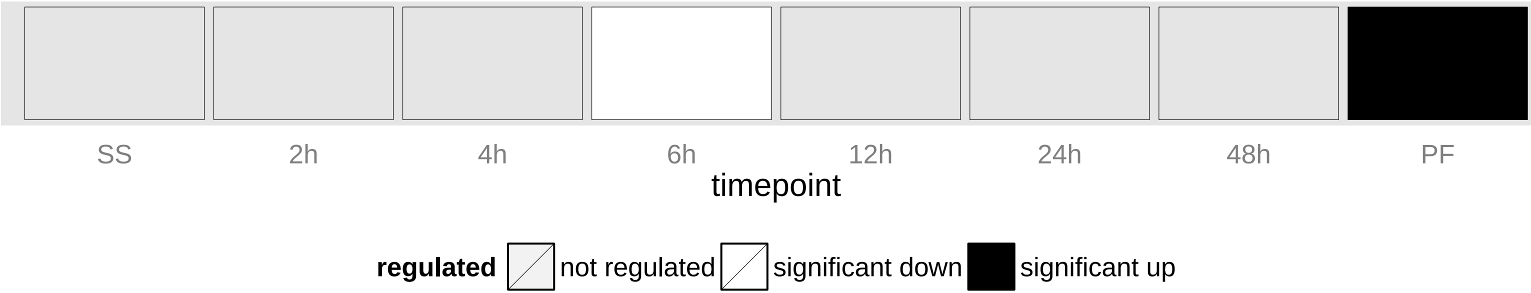

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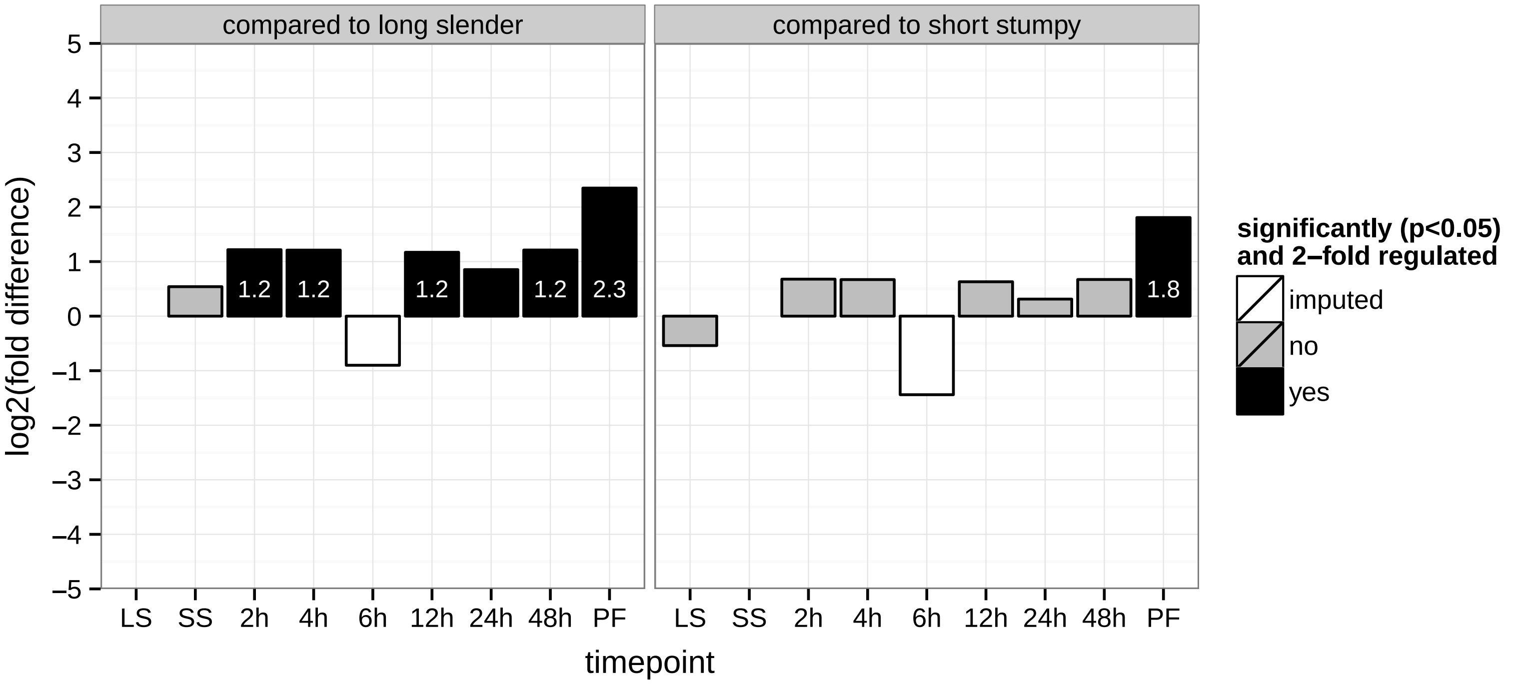
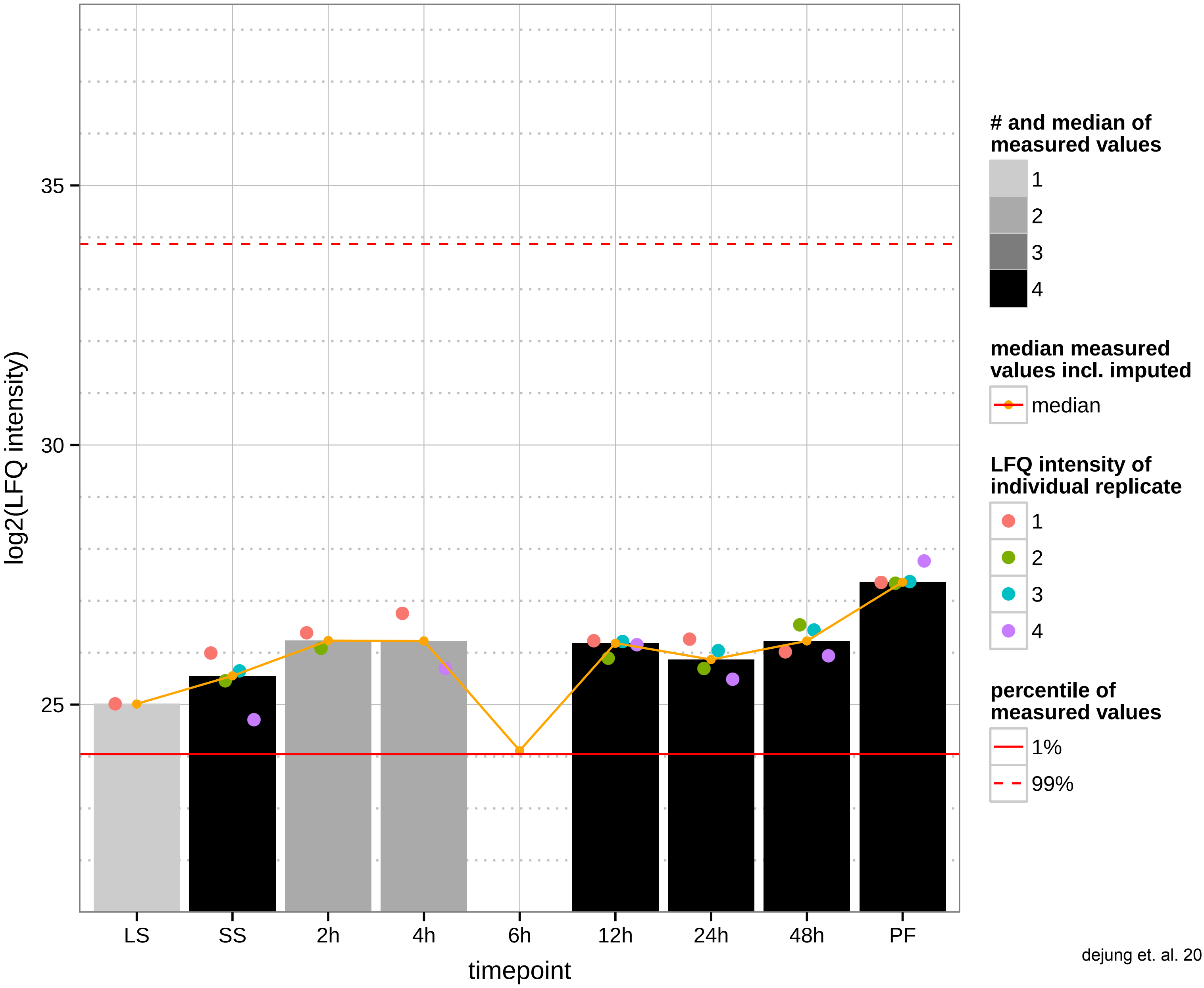
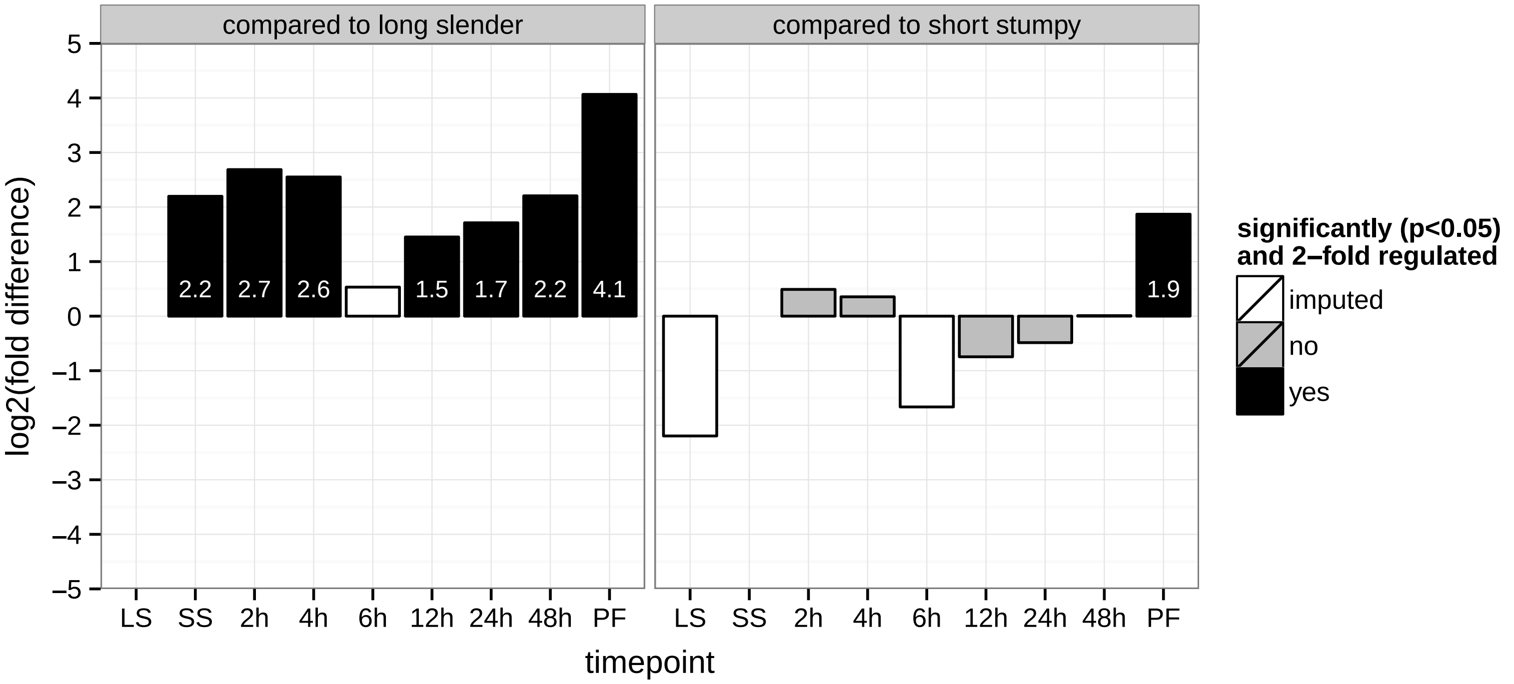
dihydrolipoamide dehydrogenase, putative (GCVL−1)
Tb927.3.4390
AGOF: dihydrolipoyl dehydrogenase activity, flavin adenine dinucleotide binding
AGOC: cytoplasm
AGOP: cell redox homeostasis
PGOF: flavin adenine dinucleotide binding, oxidoreductase activity
PGOC: cytoplasm
PGOP: cell redox homeostasis, oxidation−reduction process

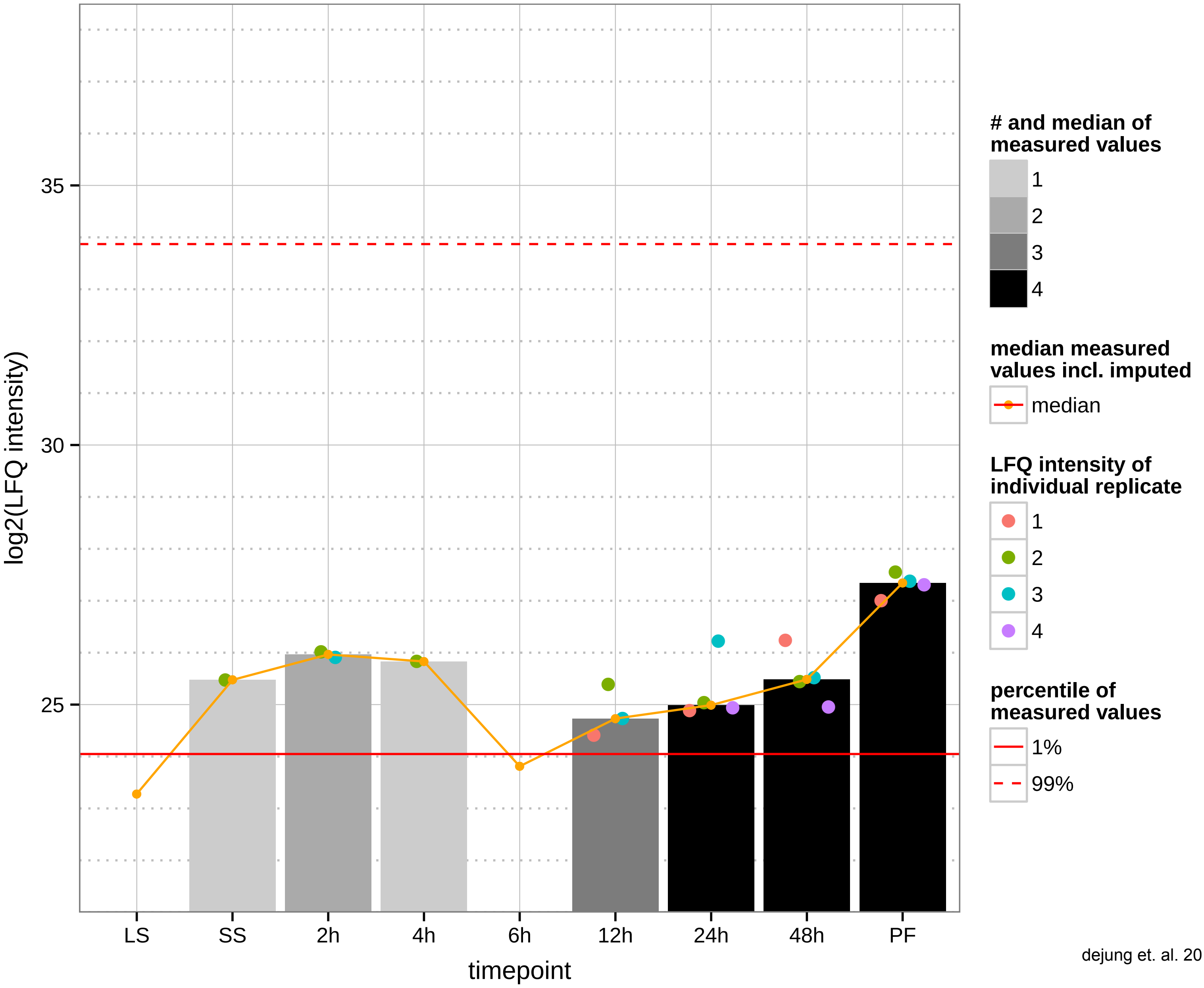




dejung et. al. 2015

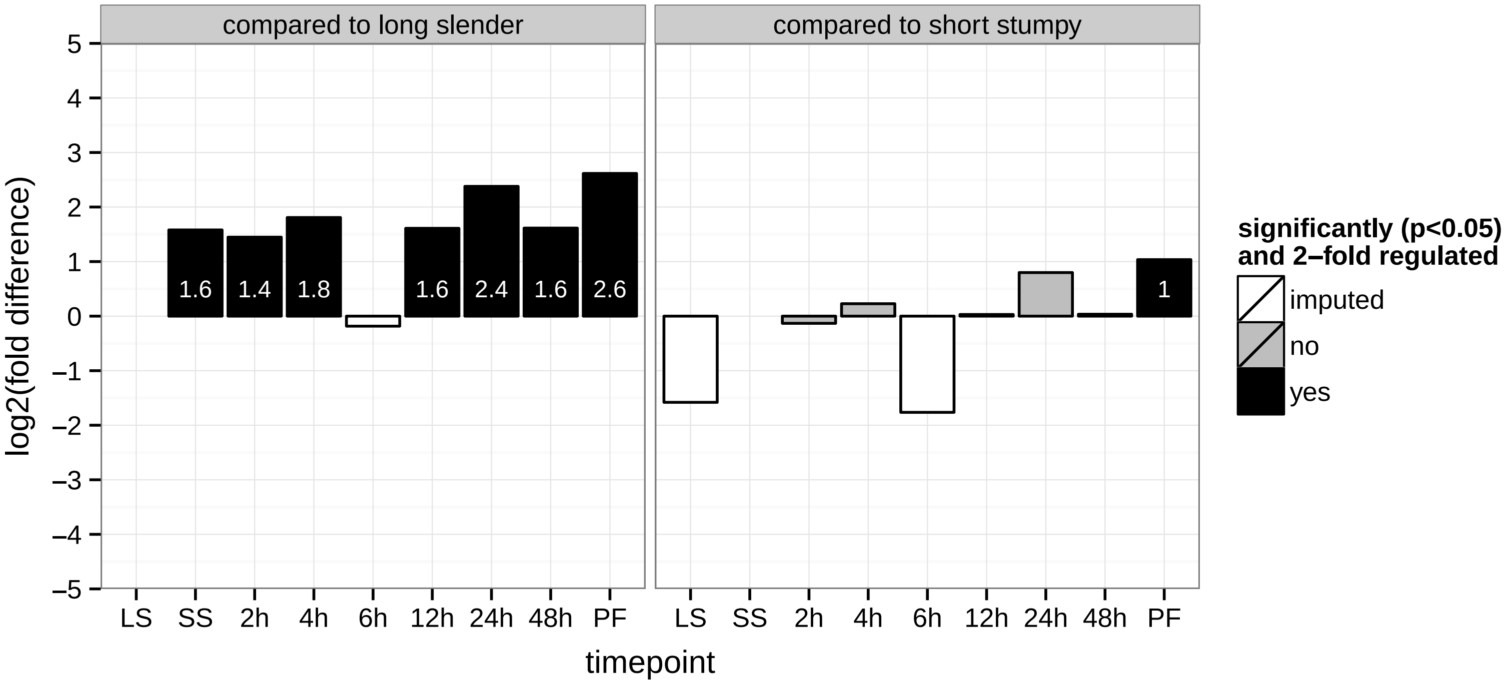
hypothetical protein, conserved
Tb927.4.2360
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

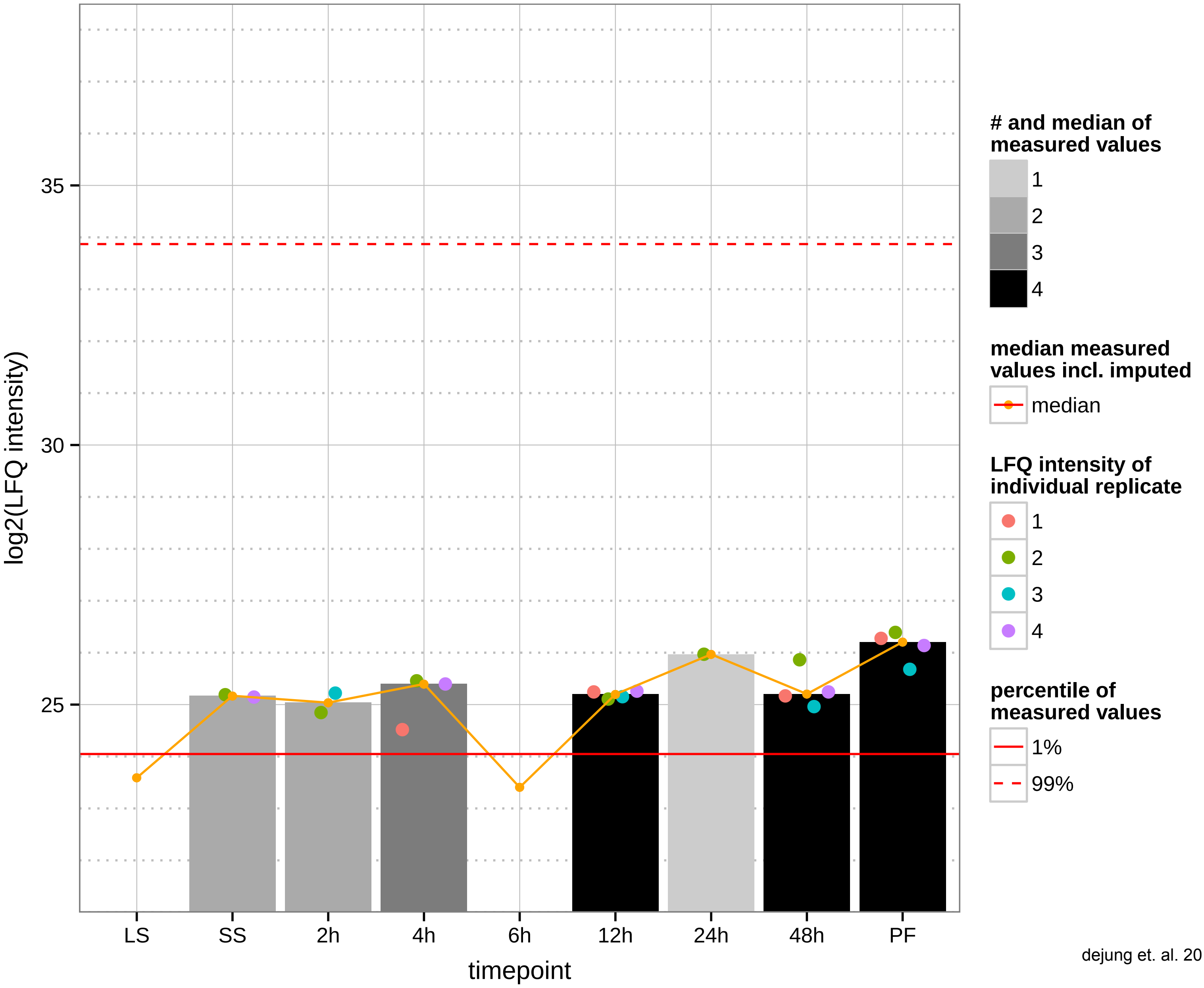




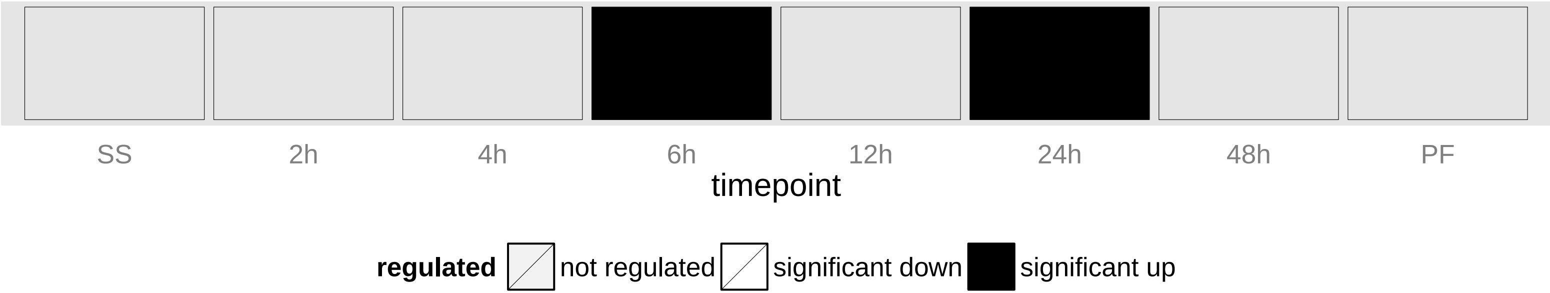
dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.3210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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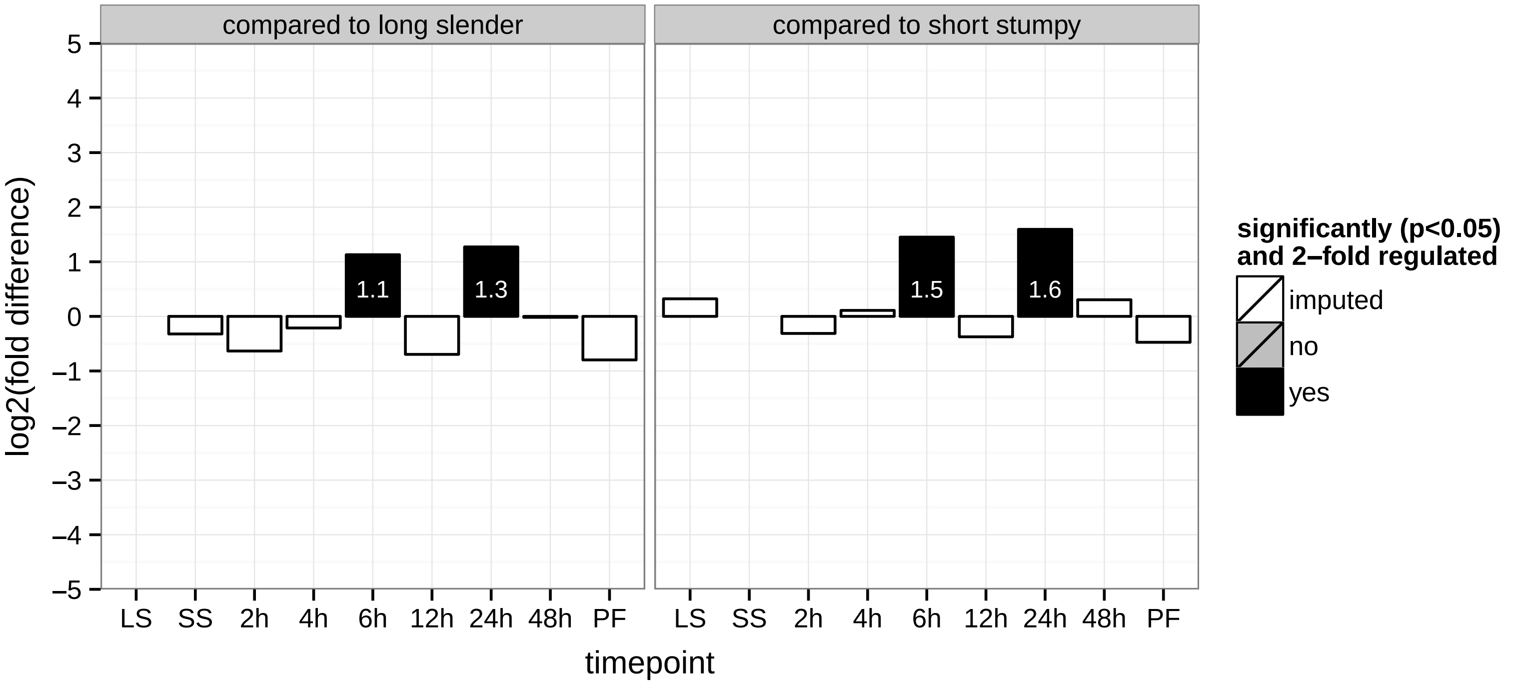
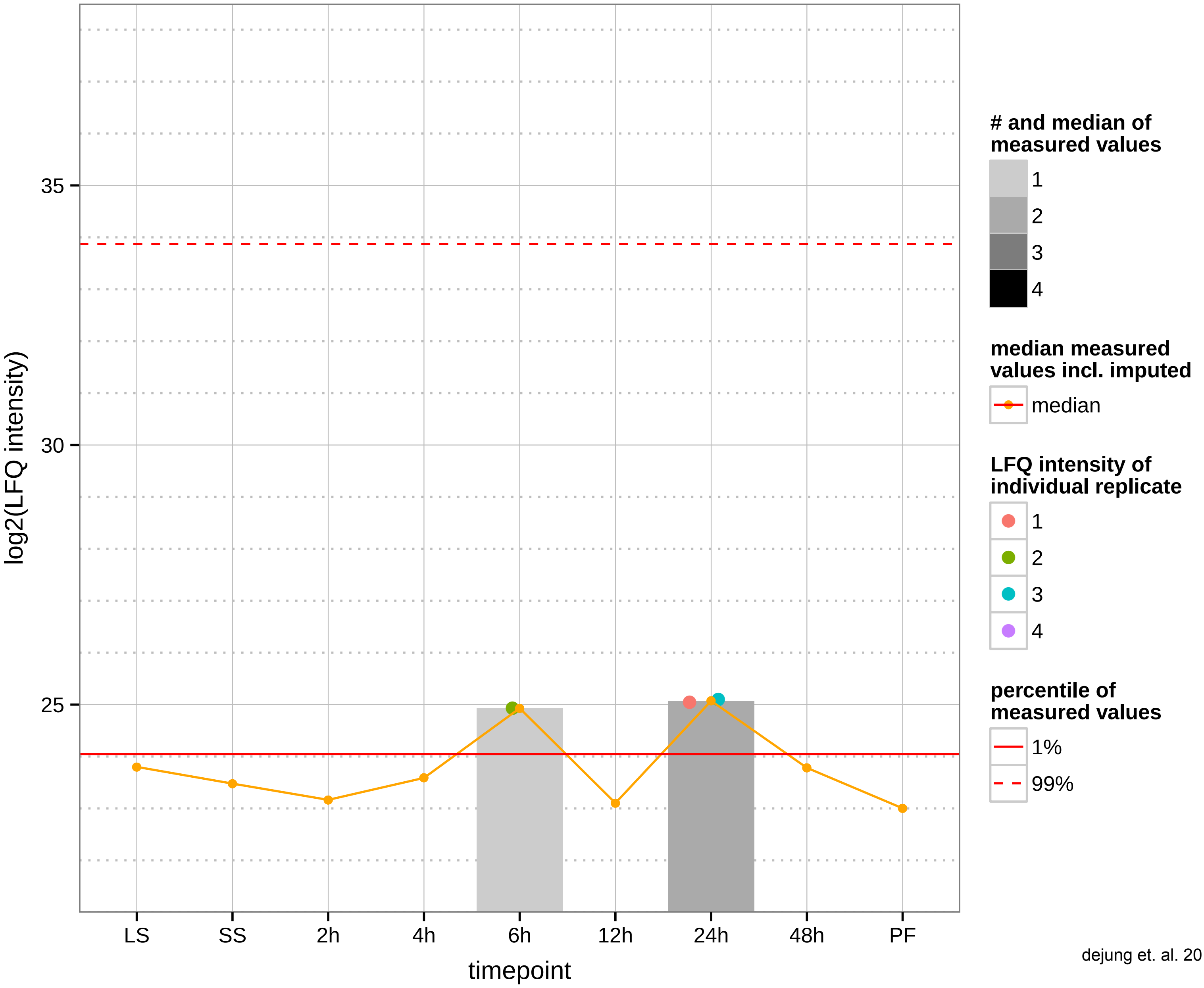
mitochondrial carrier protein (MCP14)
Tb927.10.13120
AGOF: null
AGOC: membrane, mitochondrial part
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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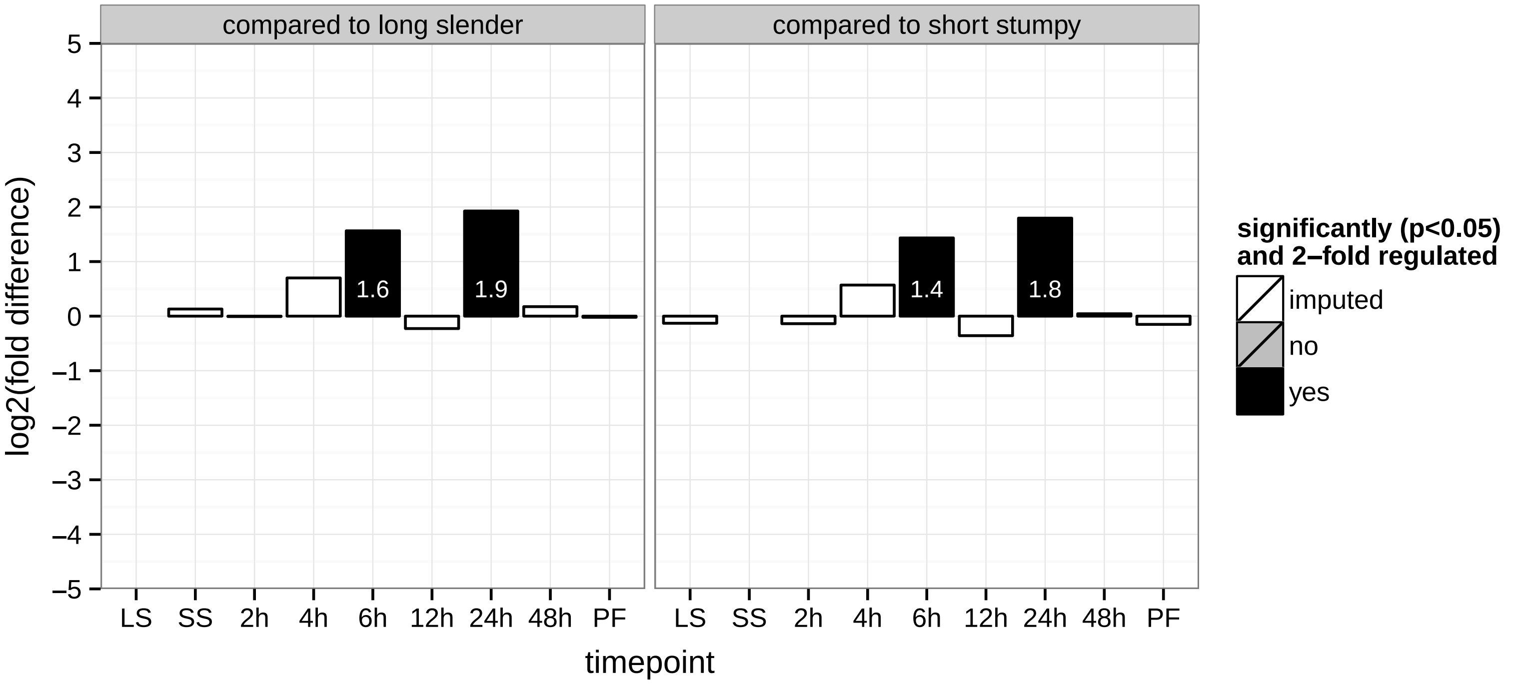
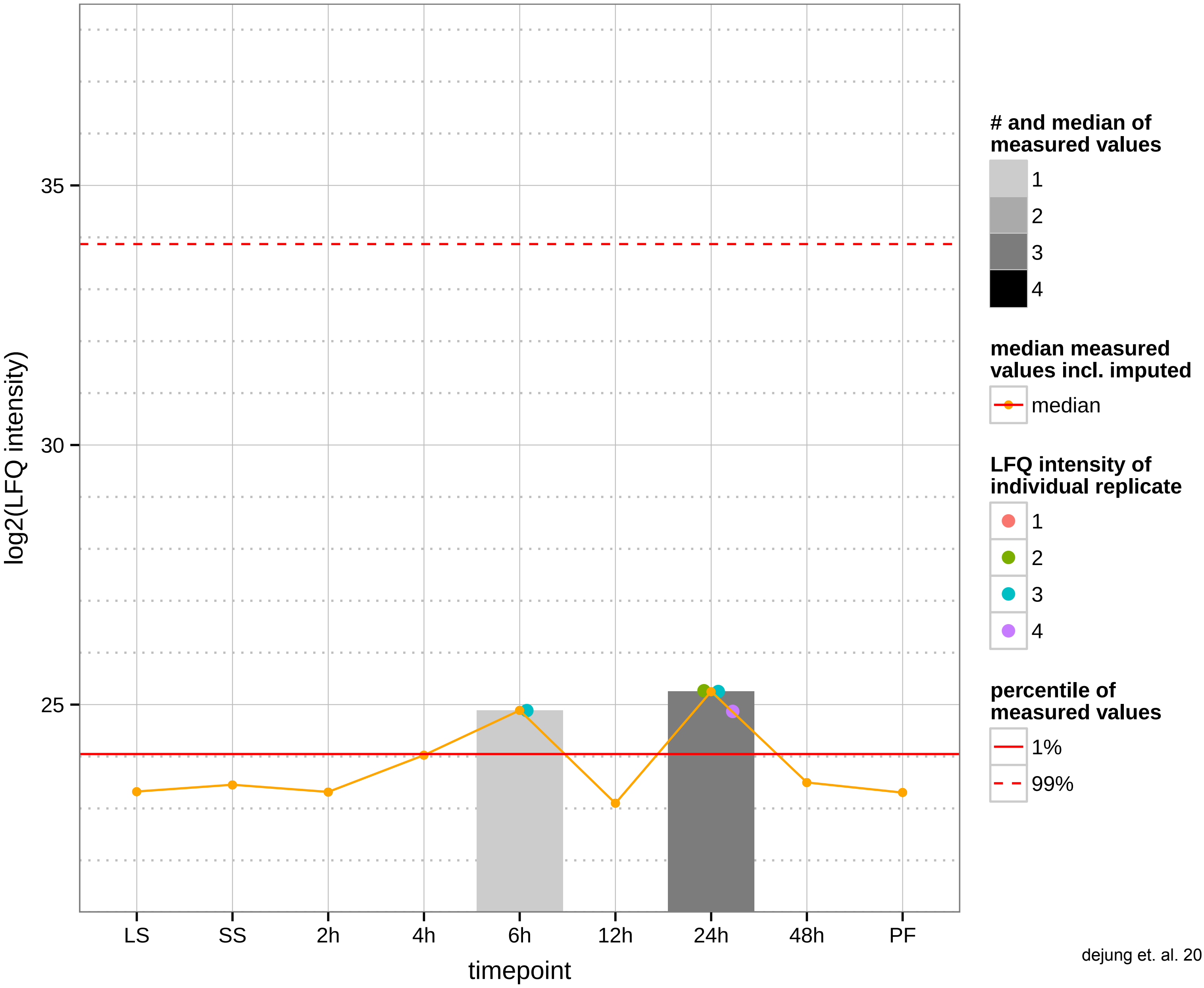
hypothetical protein, conserved
Tb927.10.2510;Tb11.v5.0623
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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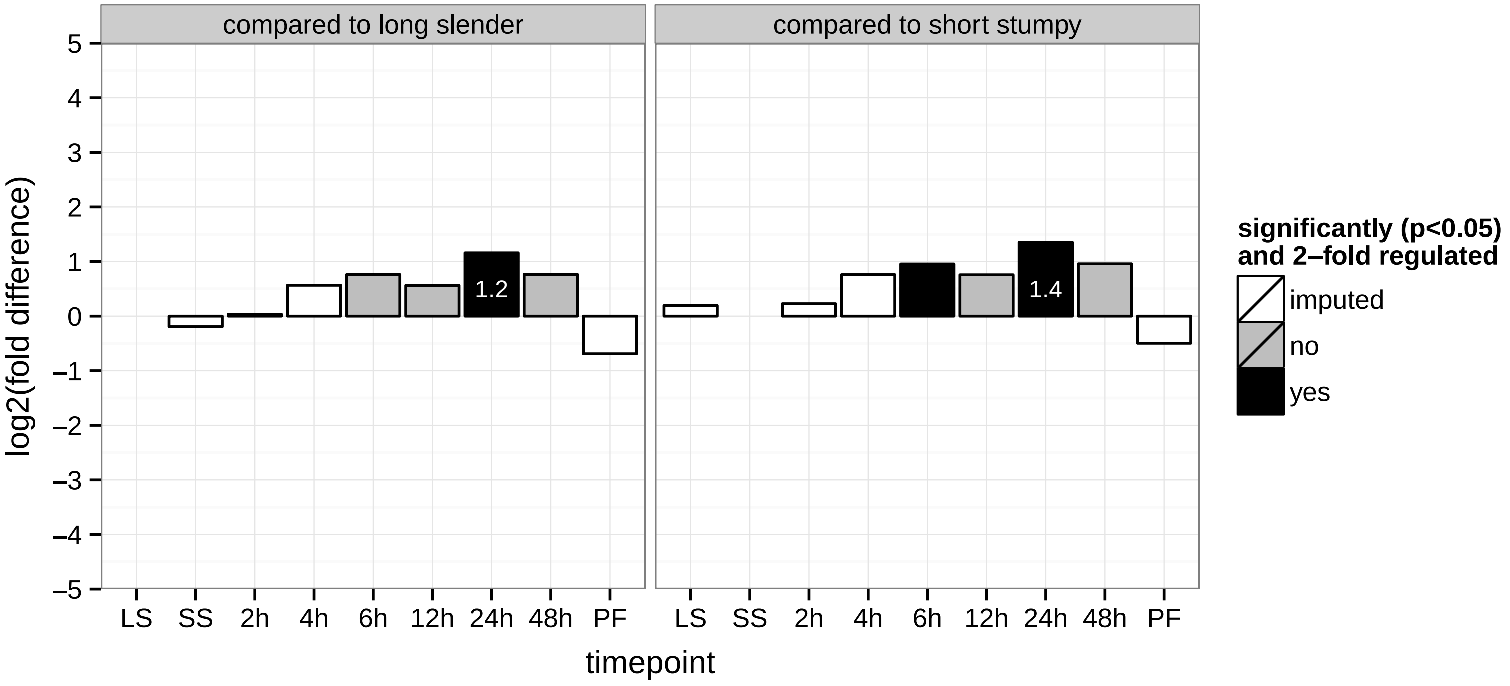
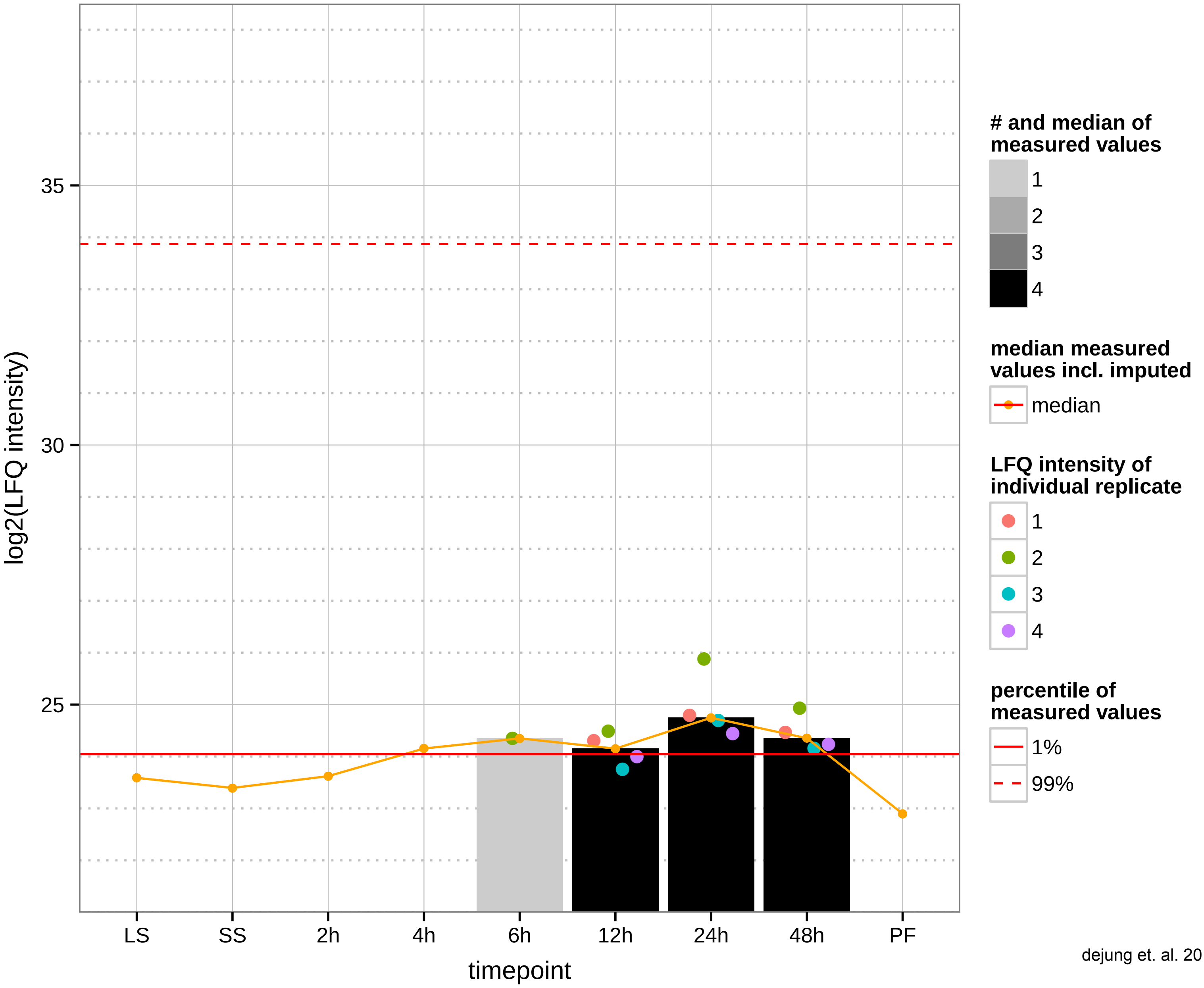
centrin, putative
Tb927.10.8710
AGOF: calcium ion binding
AGOC: null
AGOP: null
PGOF: calcium ion binding
PGOC: null
PGOP: null





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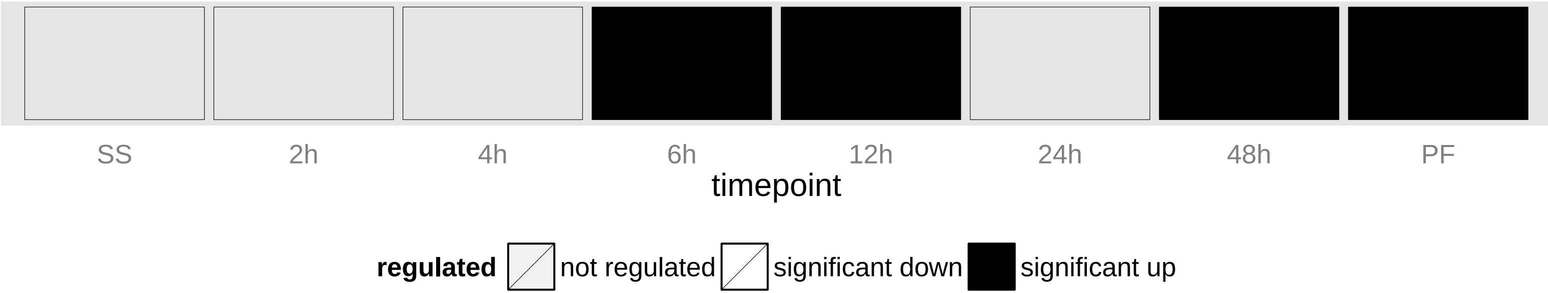

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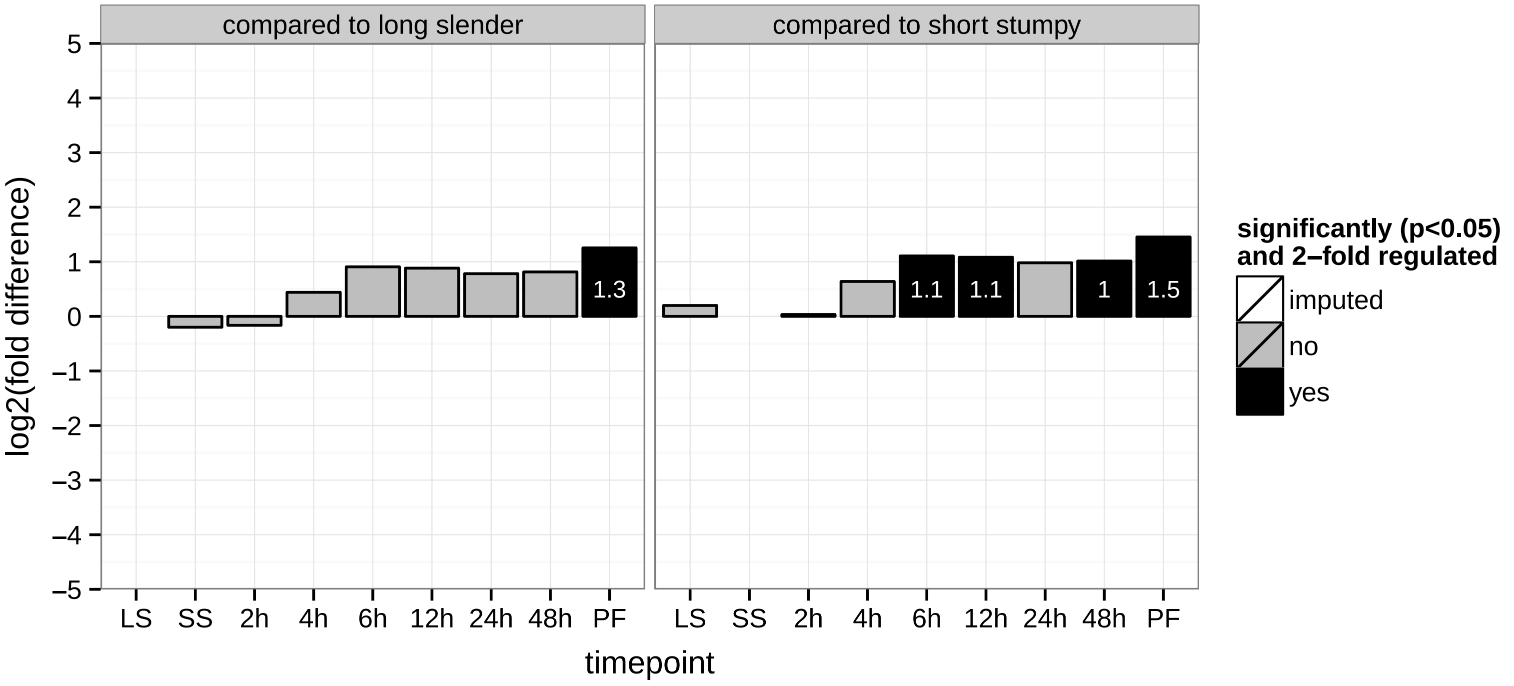
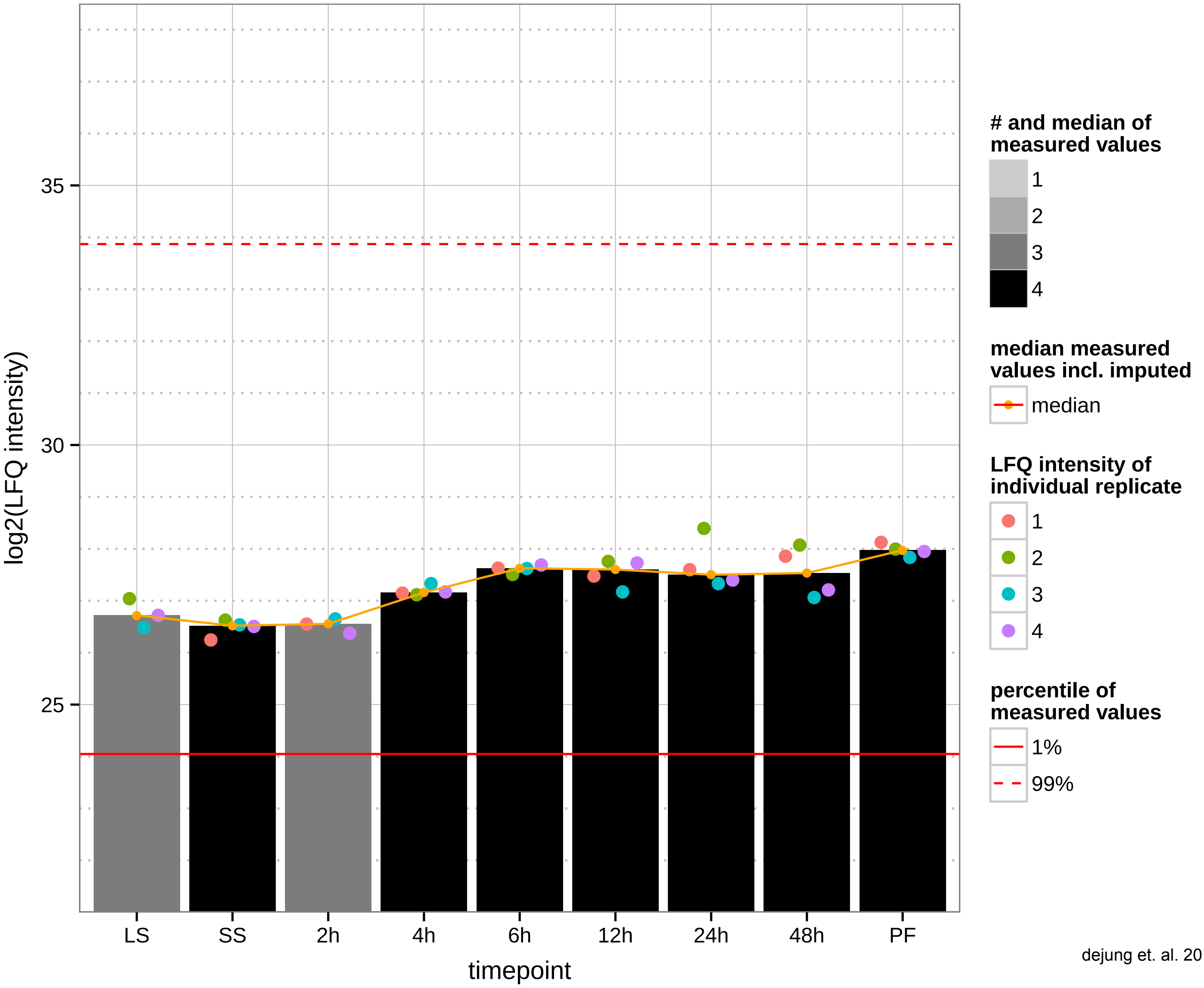
transmembrane protein, putative
Tb927.1.860
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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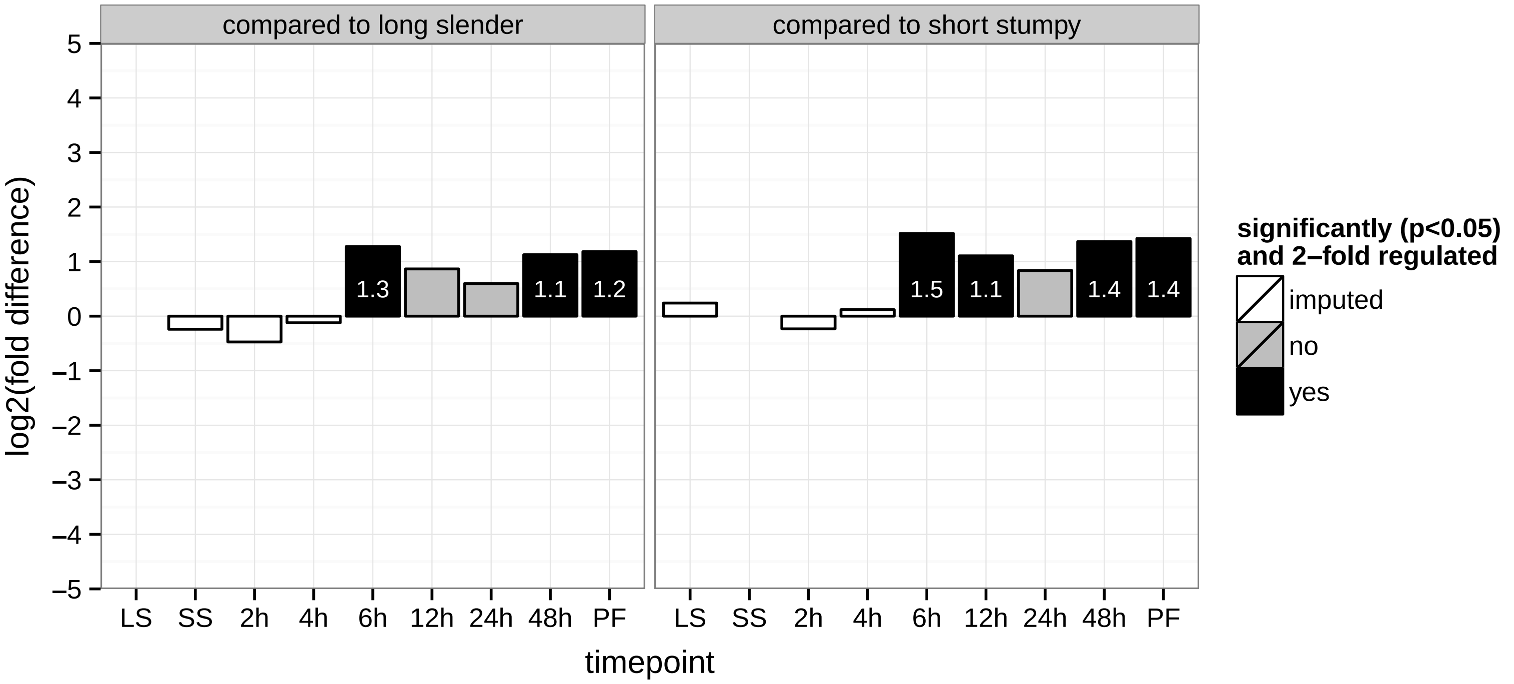
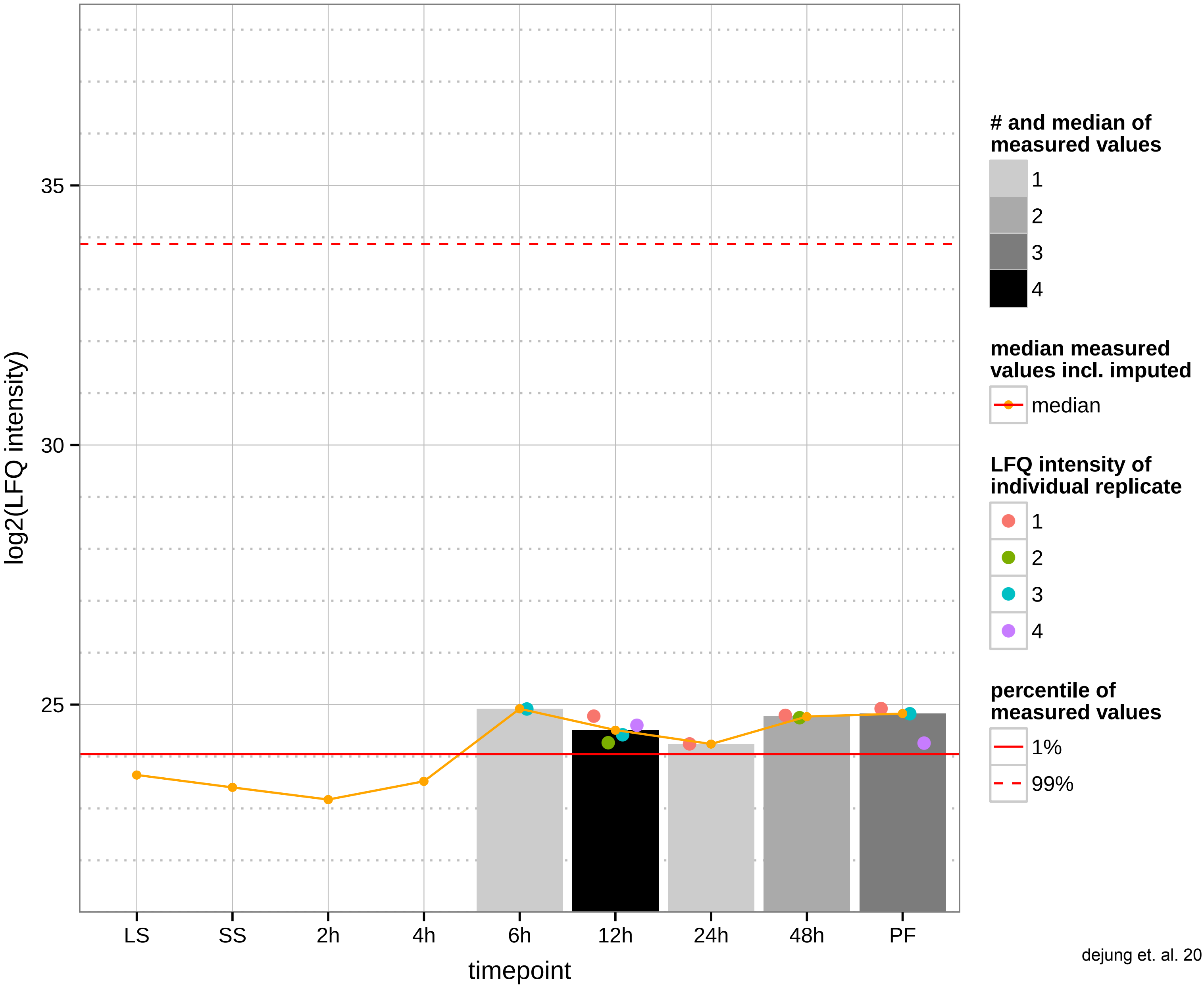
hypothetical protein, conserved
Tb927.10.13550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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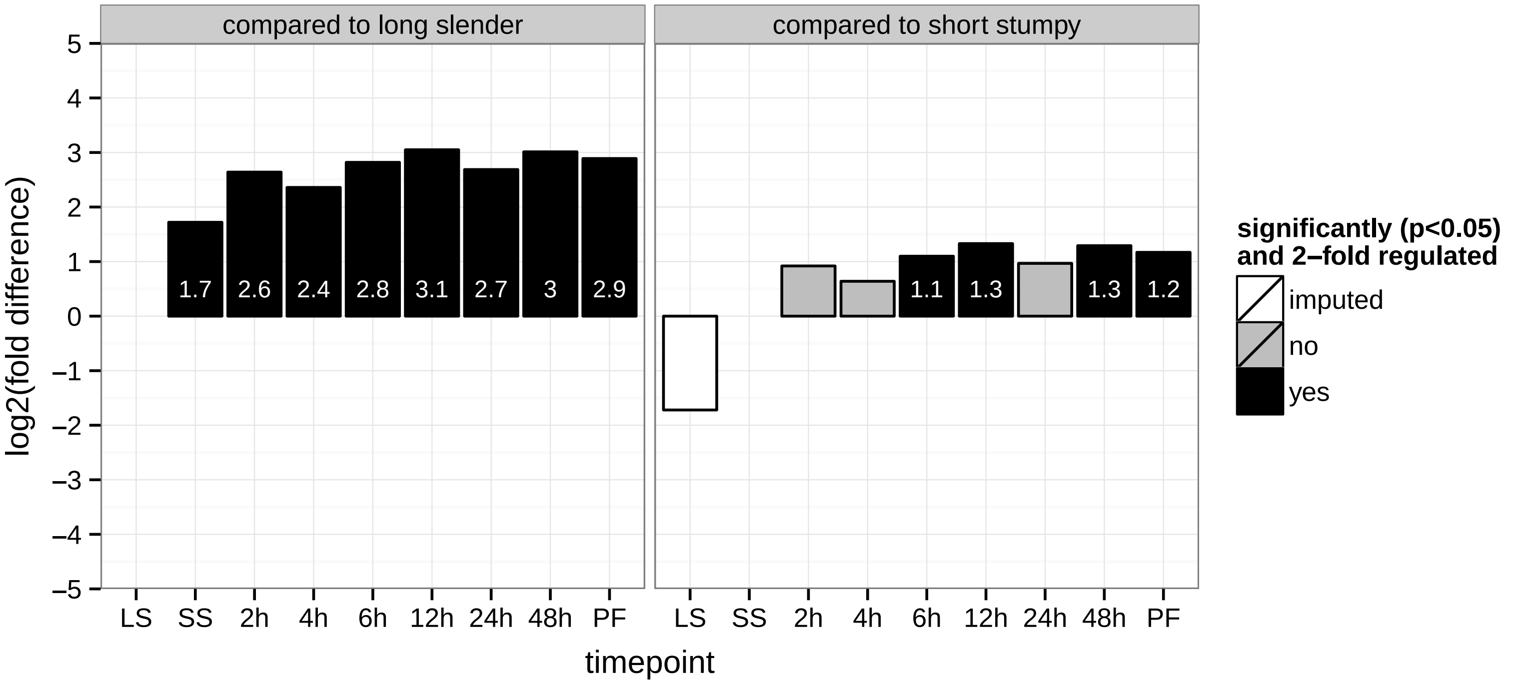
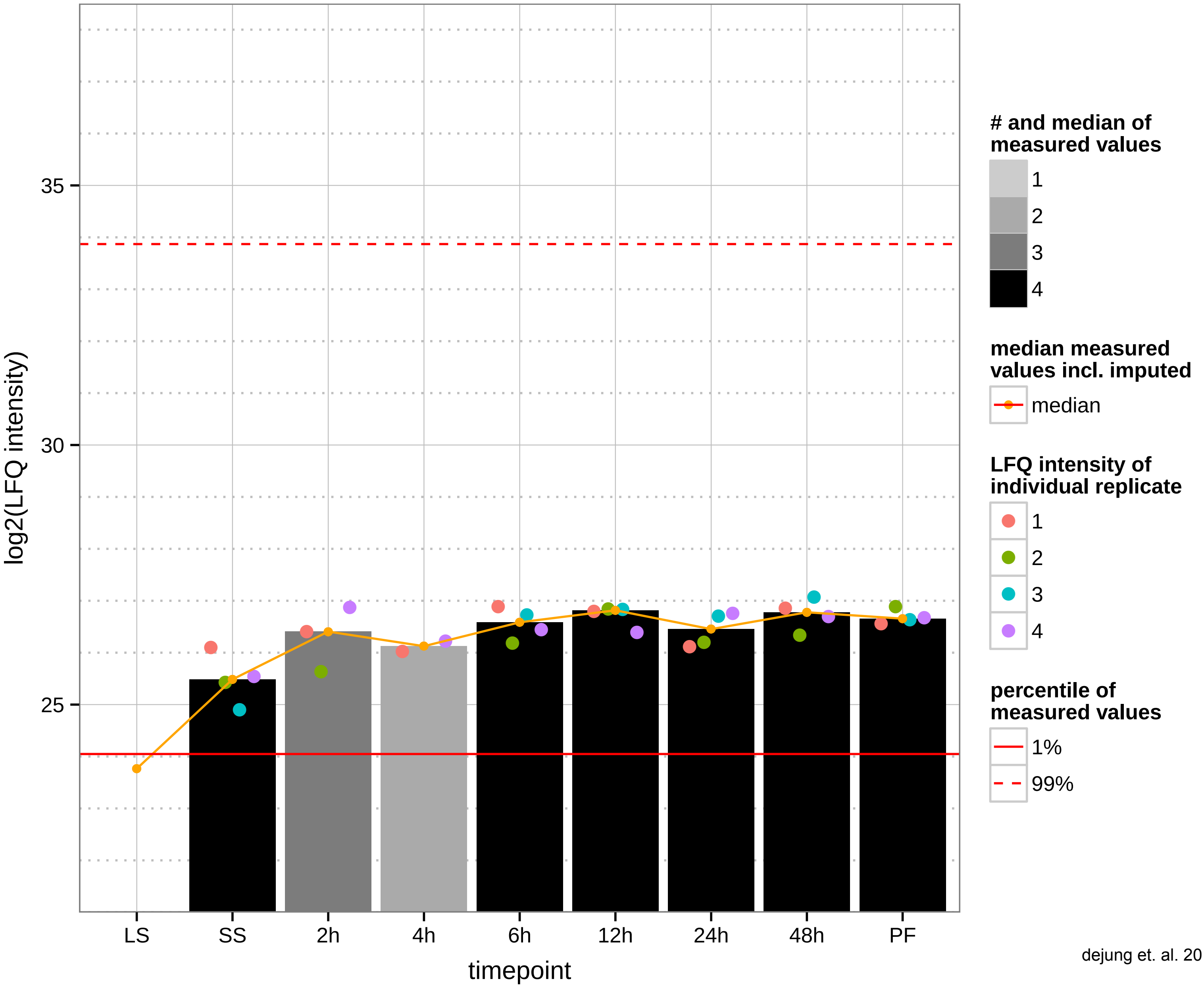
zinc–finger protein, conserved
Tb927.6.3540
AGOF: zinc ion binding
AGOC: intracellular
AGOP: null
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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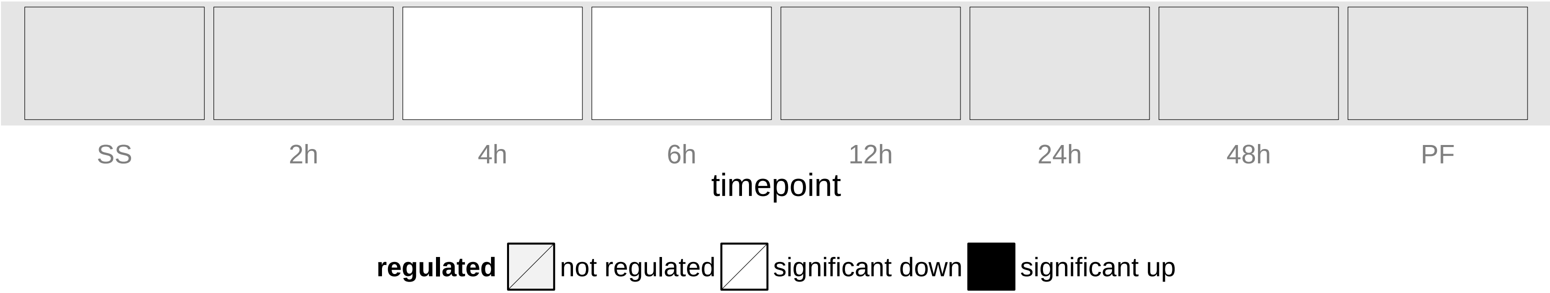

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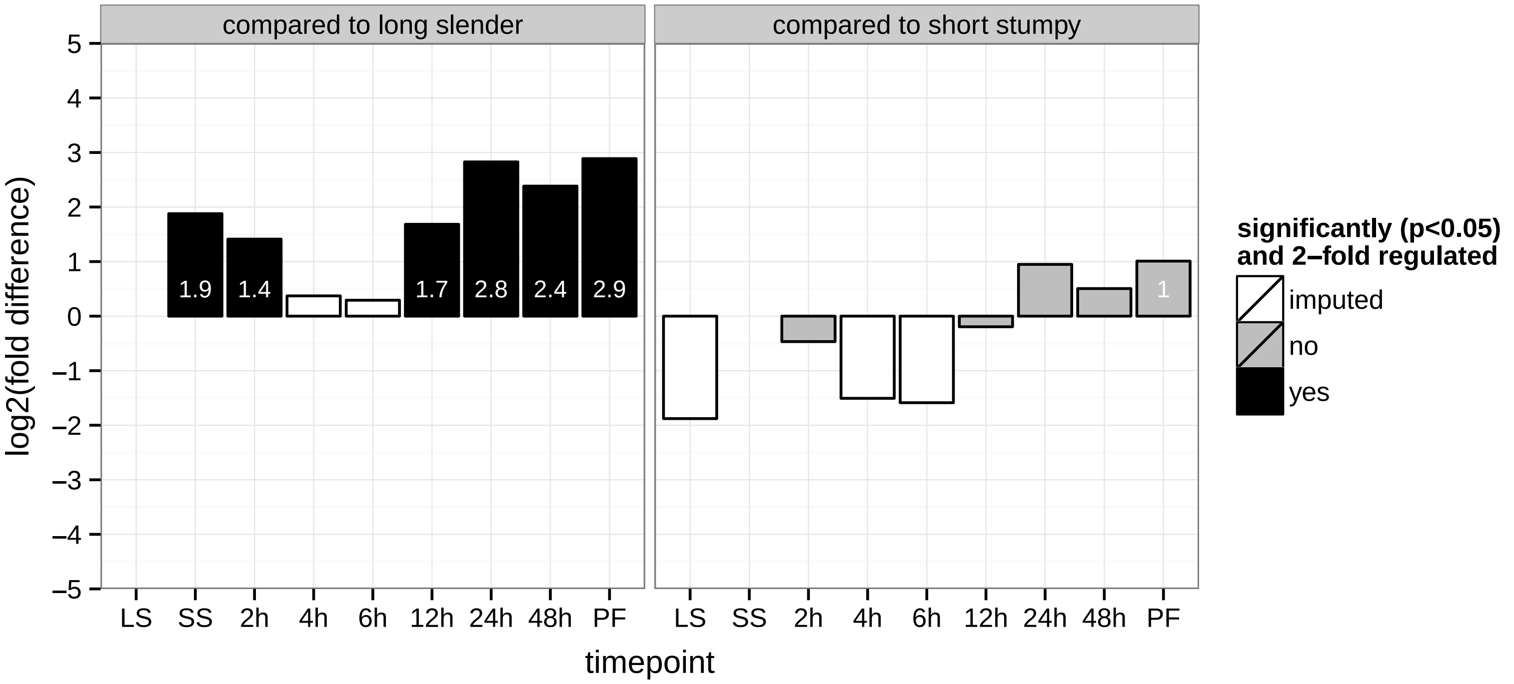
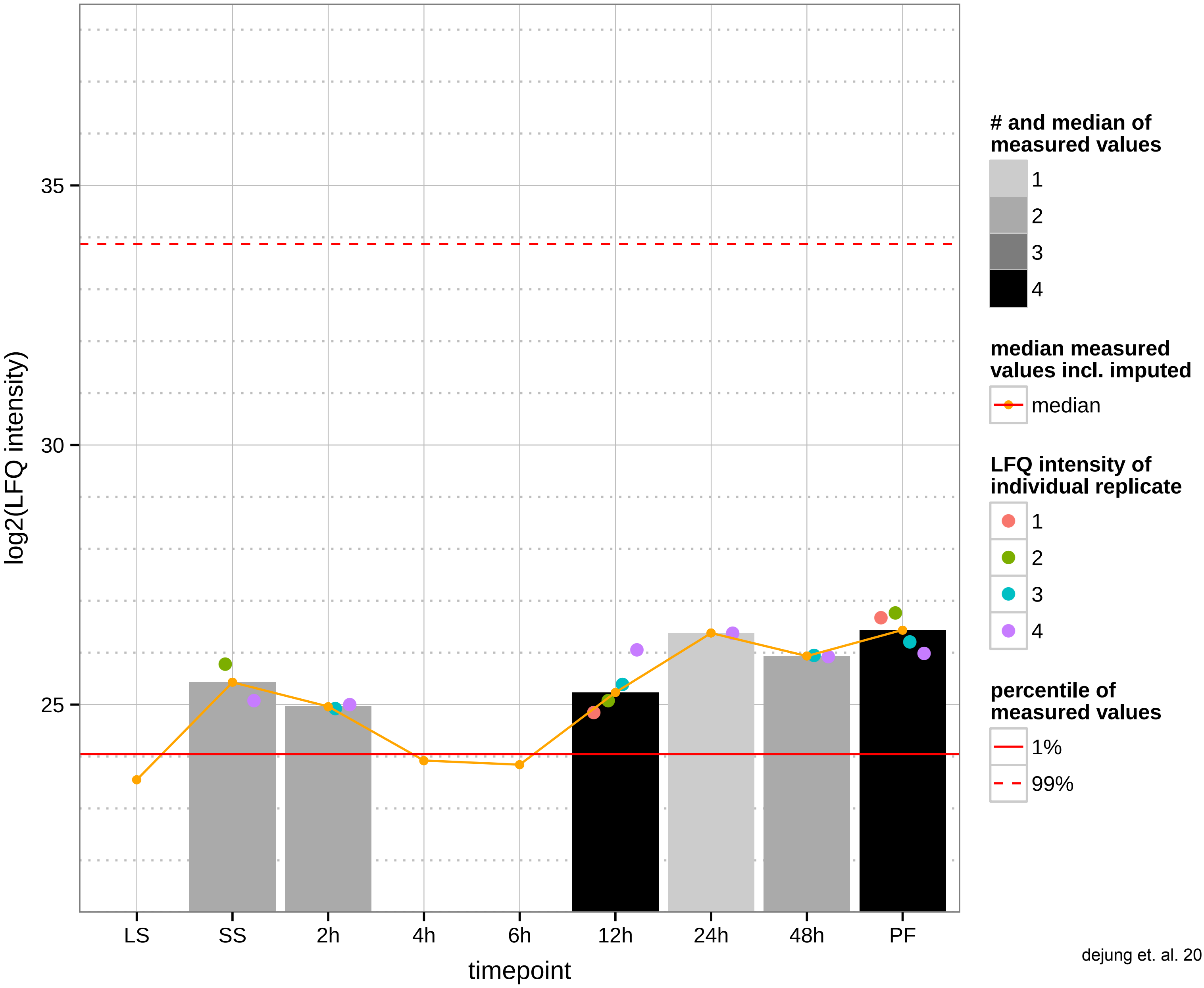
mitochondrial RNA binding complex 1 subunit (MRB6070)
Tb927.2.6070
AGOF: RNA binding, zinc ion binding
AGOC: intracellular, mitochondrion
AGOP: cytidine to uridine editing, mRNA stabilization
PGOF: zinc ion binding
PGOC: intracellular
PGOP: null





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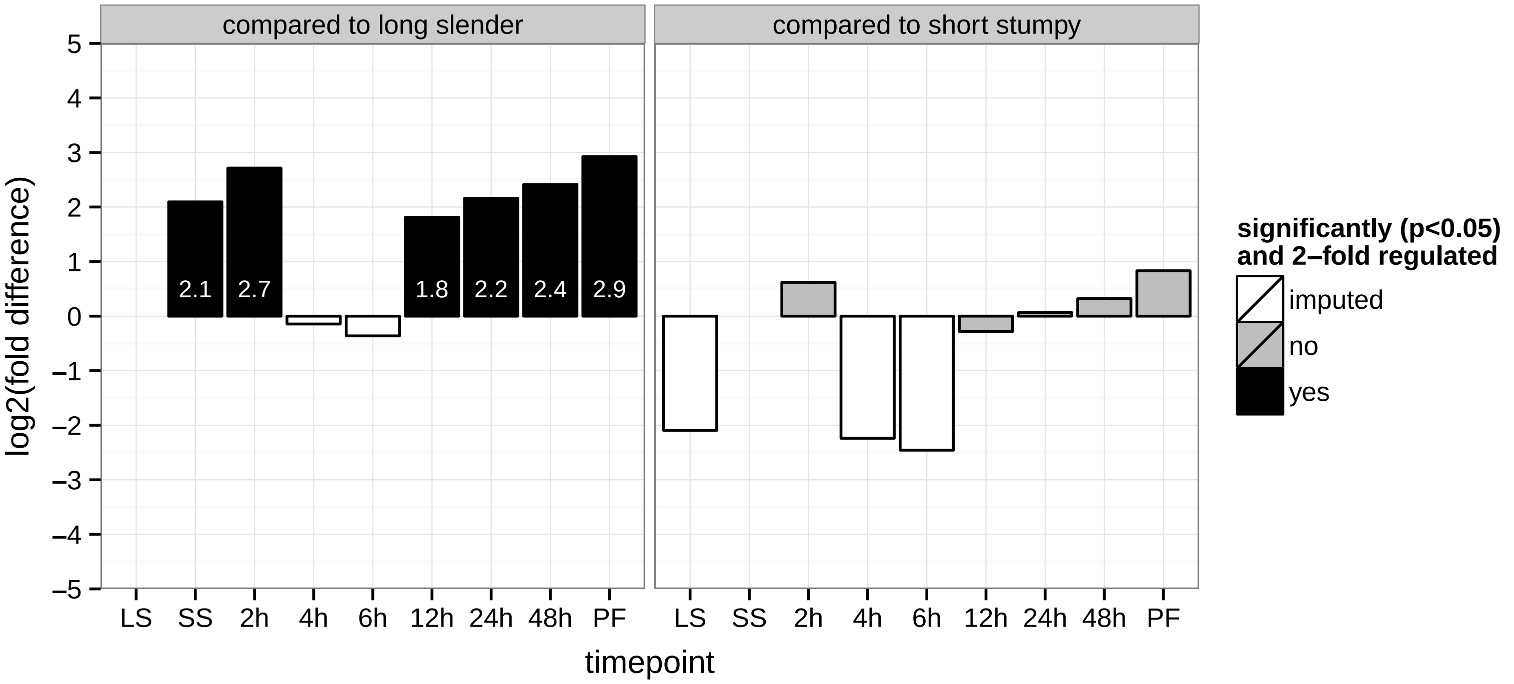
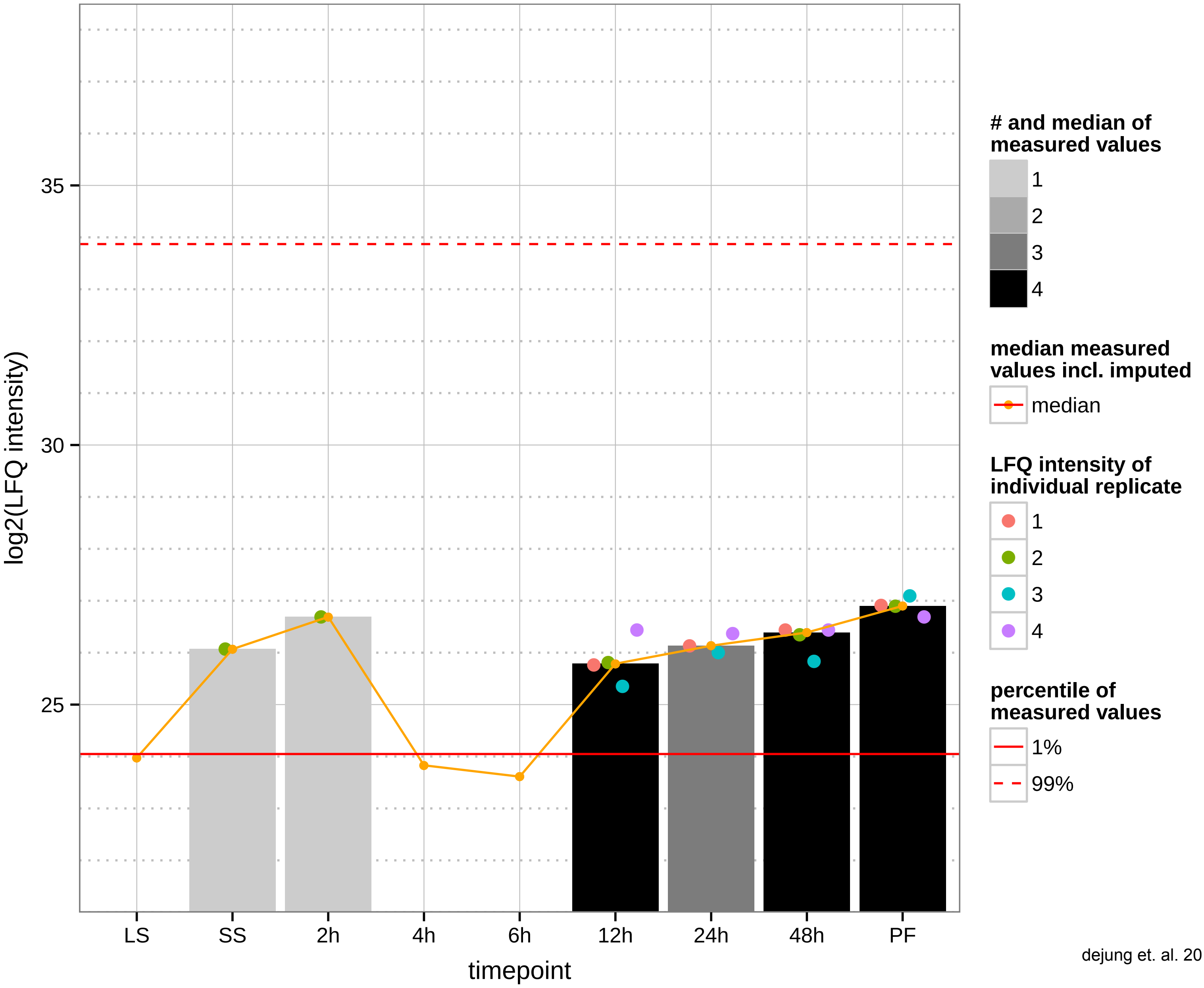
hypothetical protein, conserved
Tb927.3.5240
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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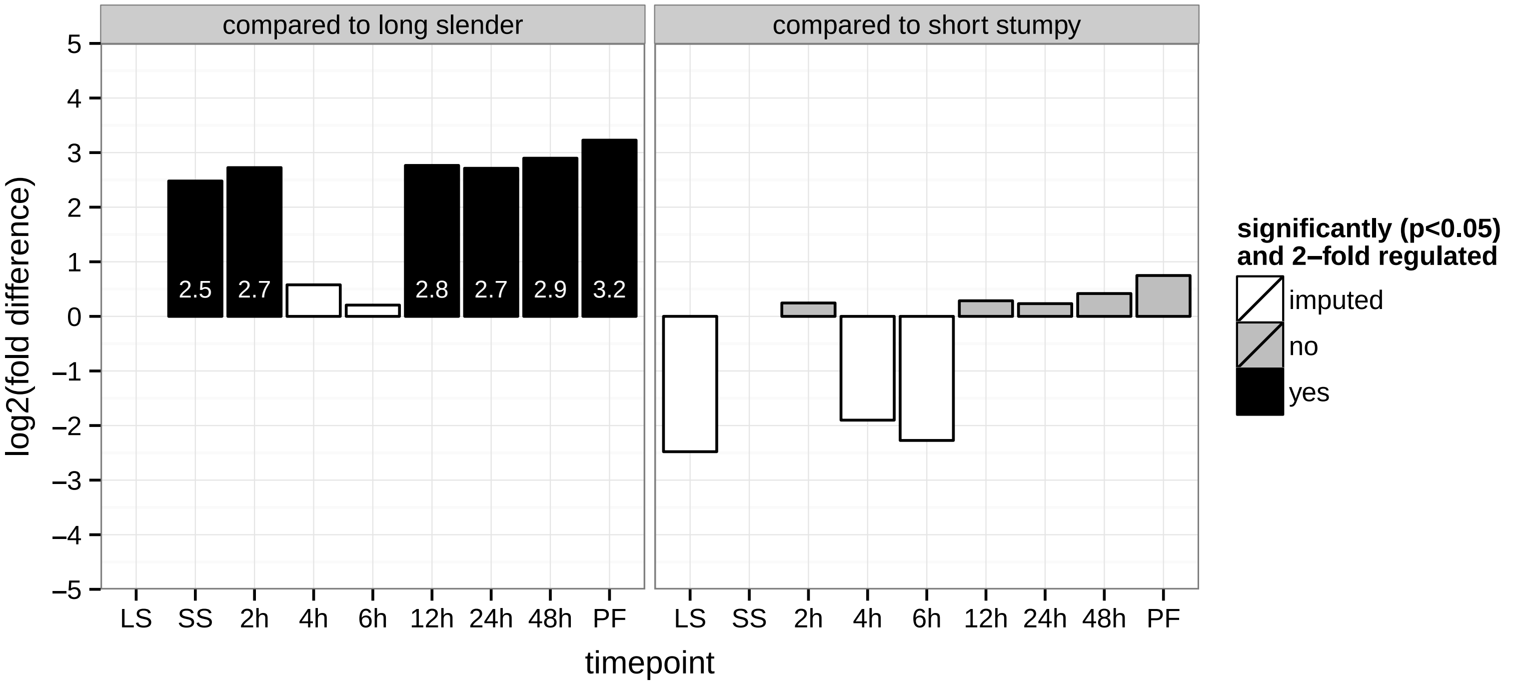
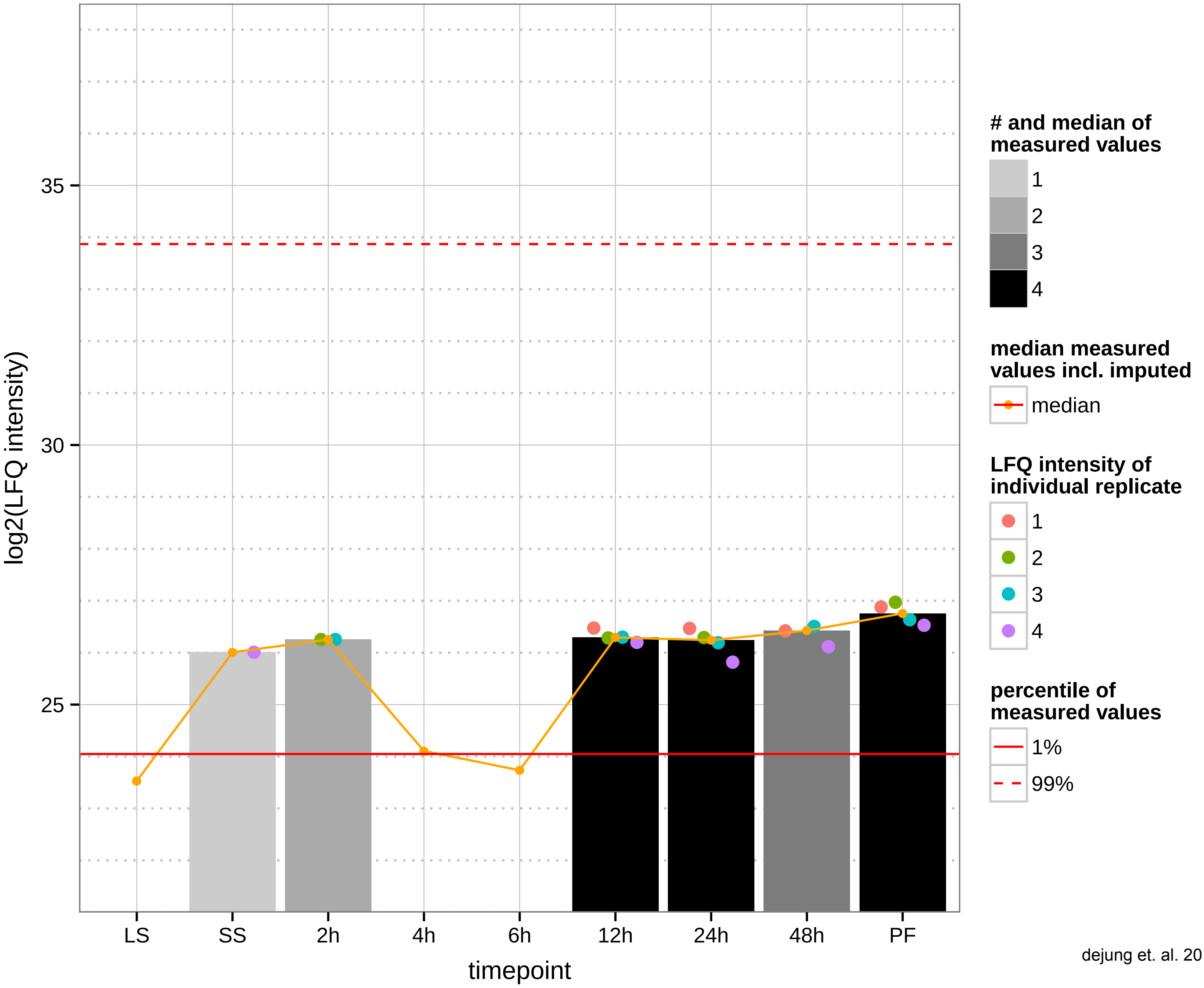
hypothetical protein, conserved
Tb927.4.730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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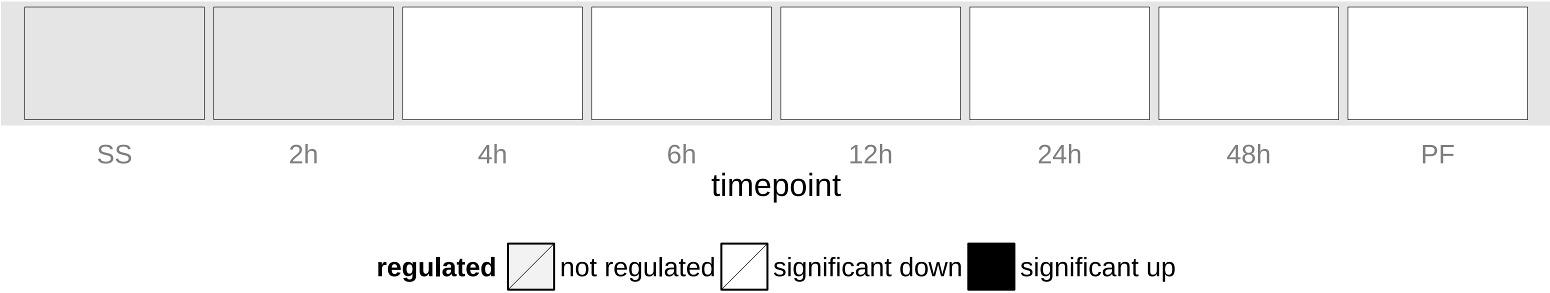

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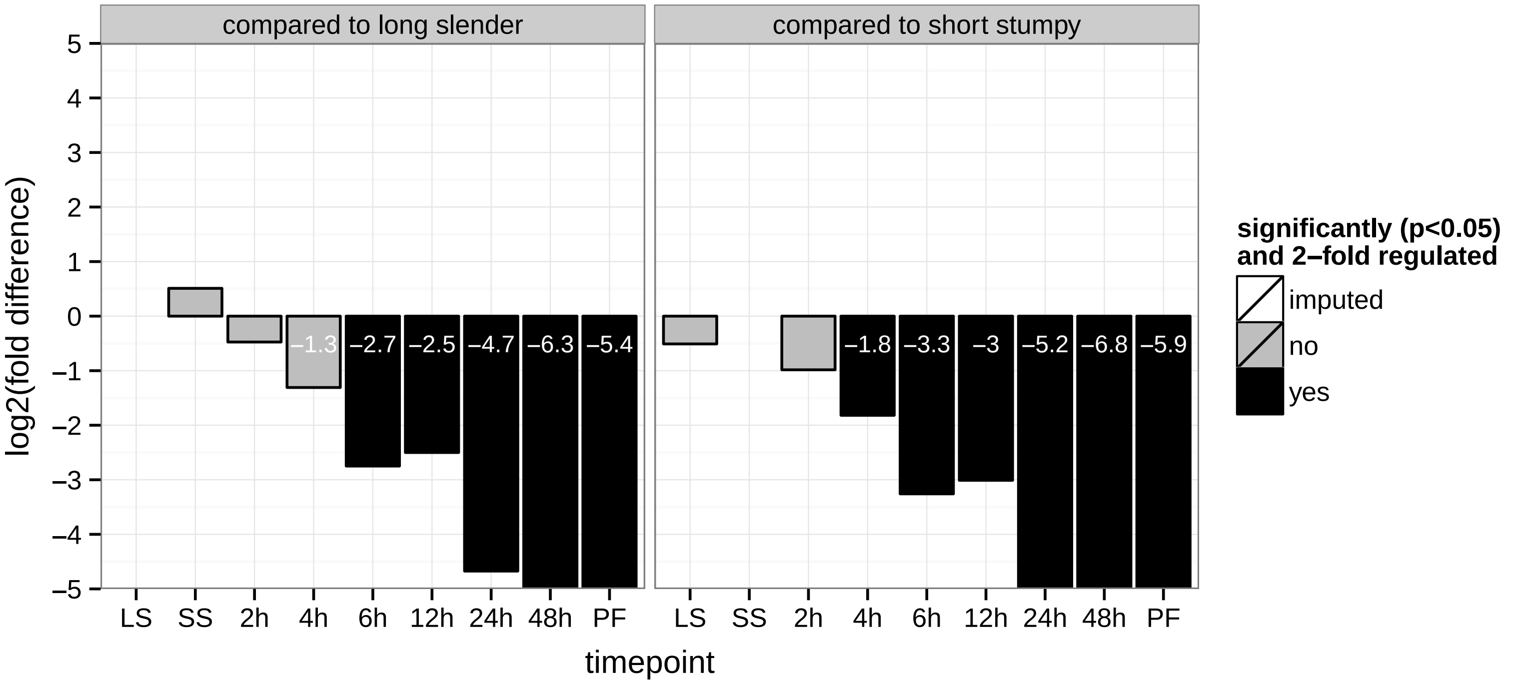
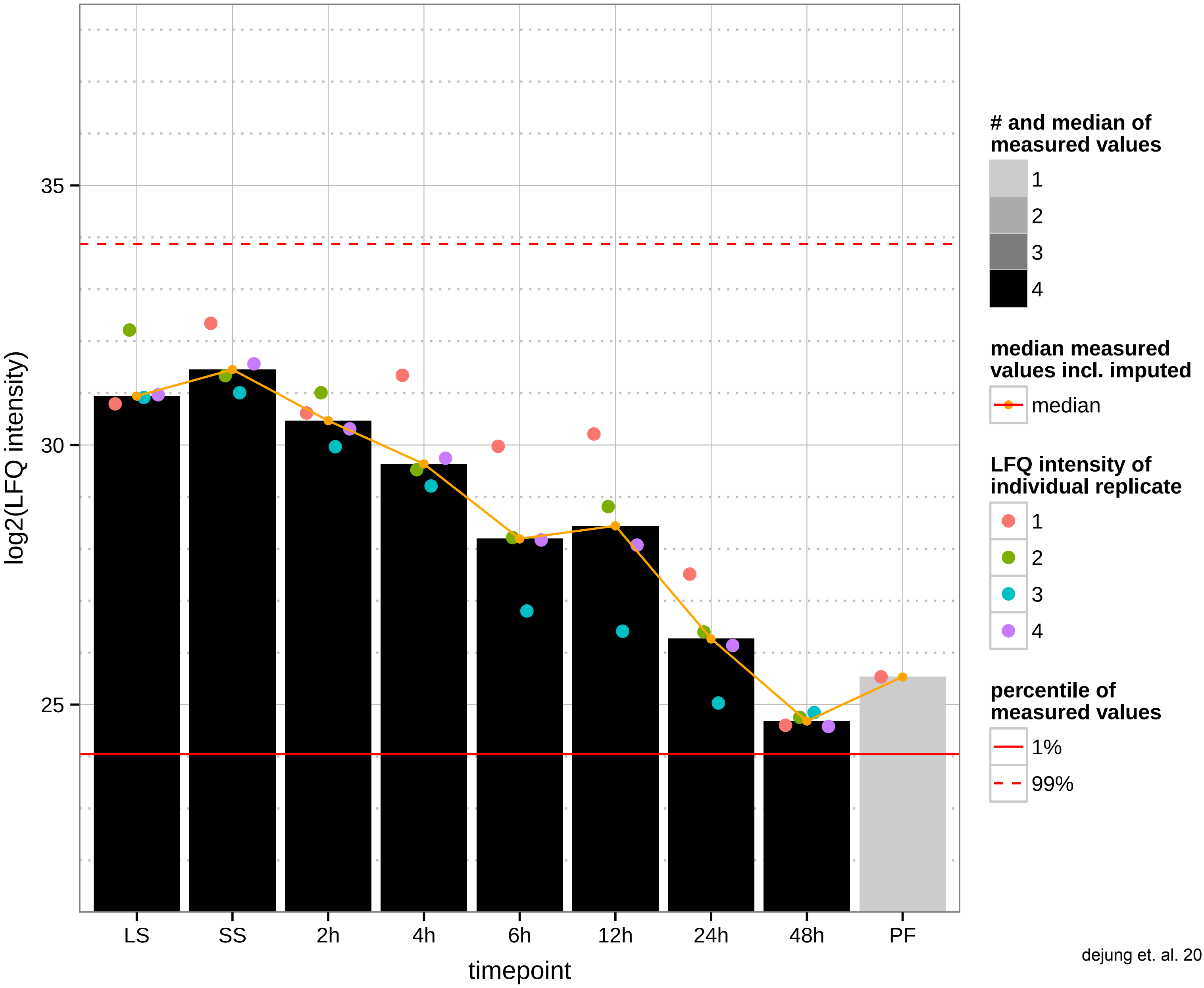
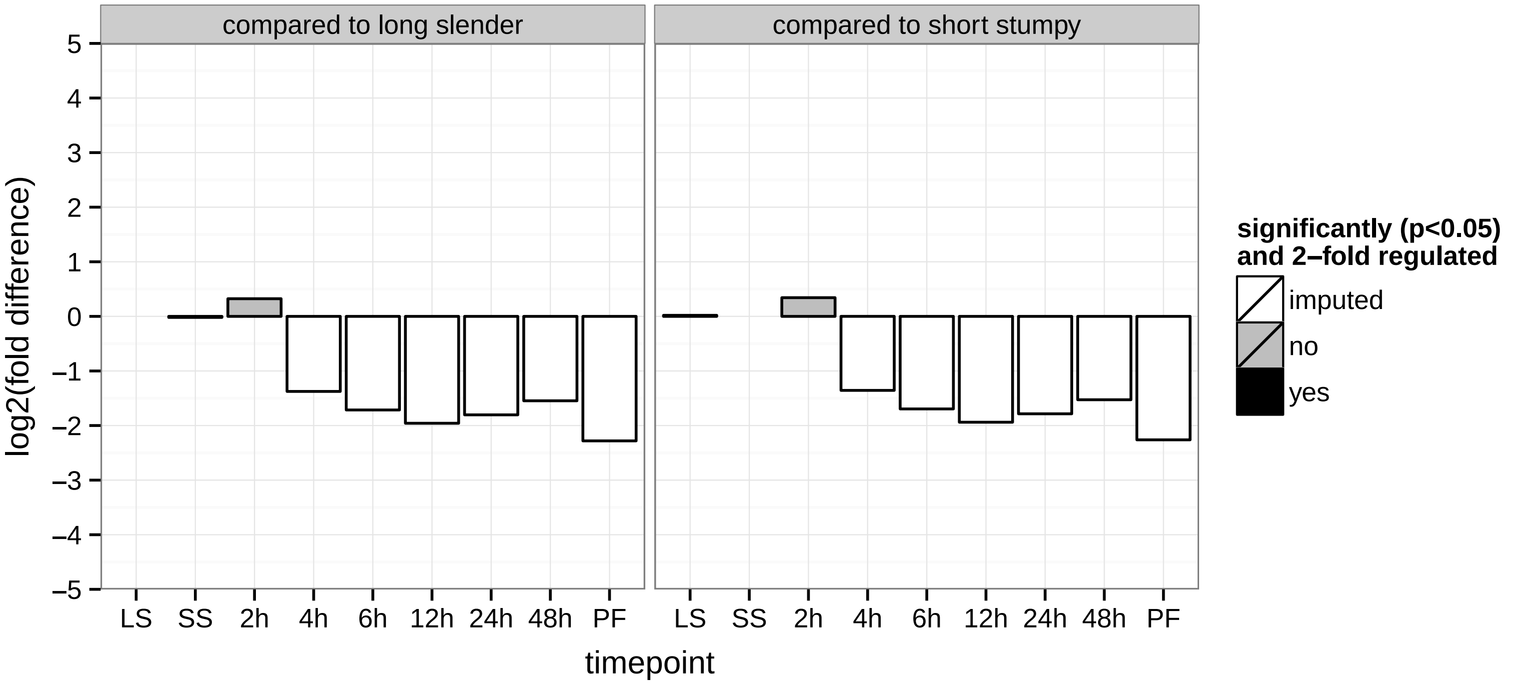
75 kDa invariant surface glycoprotein, putative
Tb927.5.390;Tb11.v5.0228
AGOF: null
AGOC: null, plasma membrane
AGOP: null
PGOF: null
PGOC: null
PGOP: null

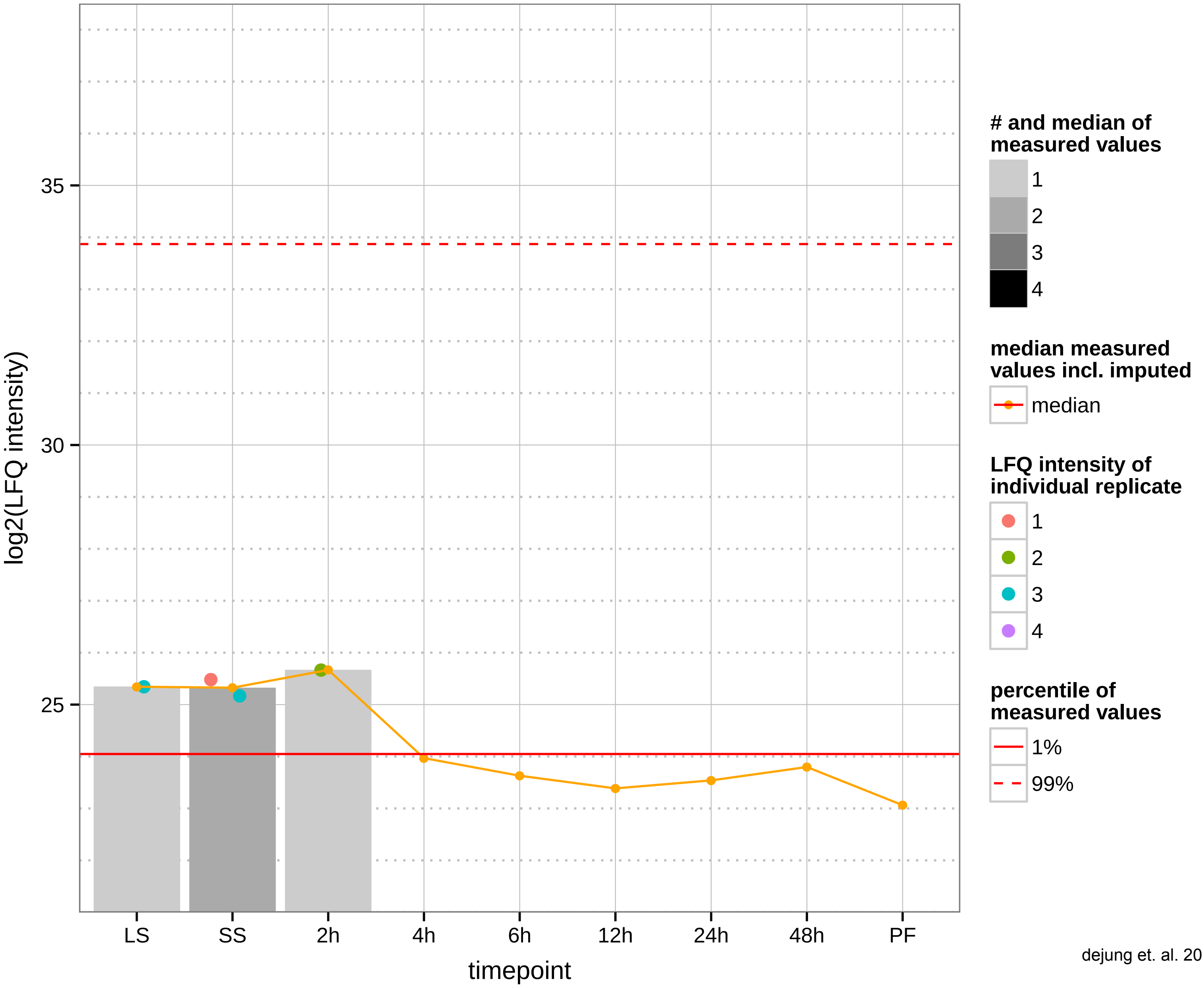




dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.2080
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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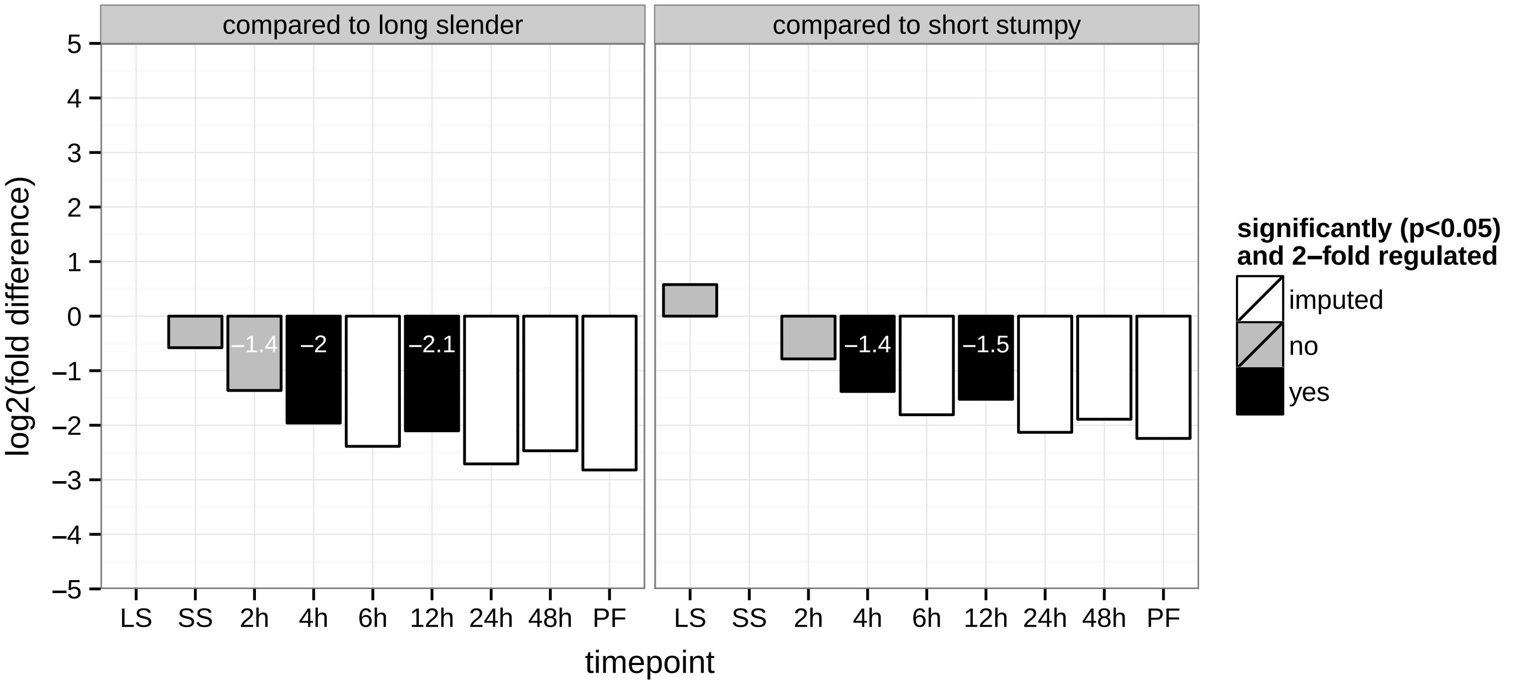
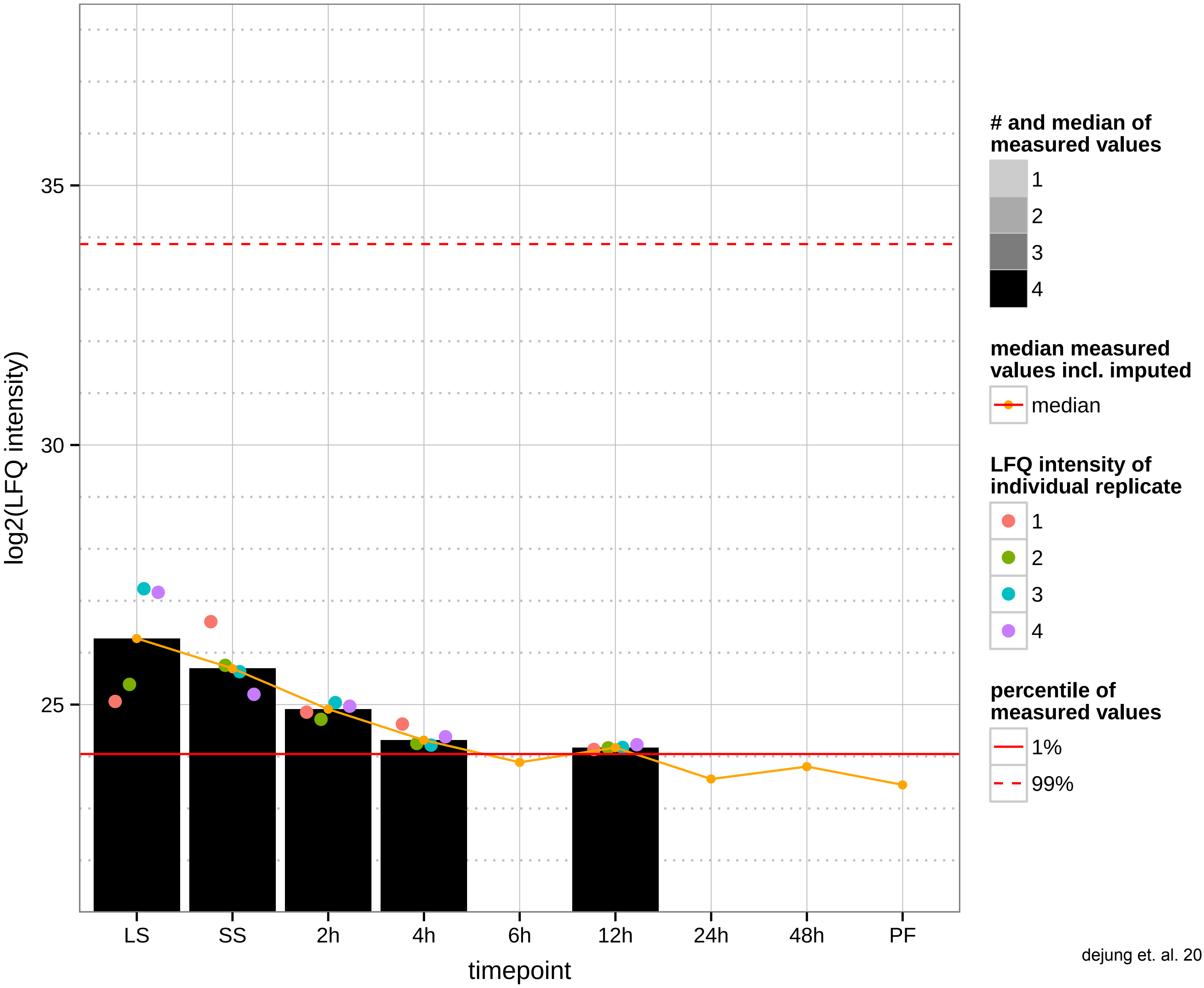
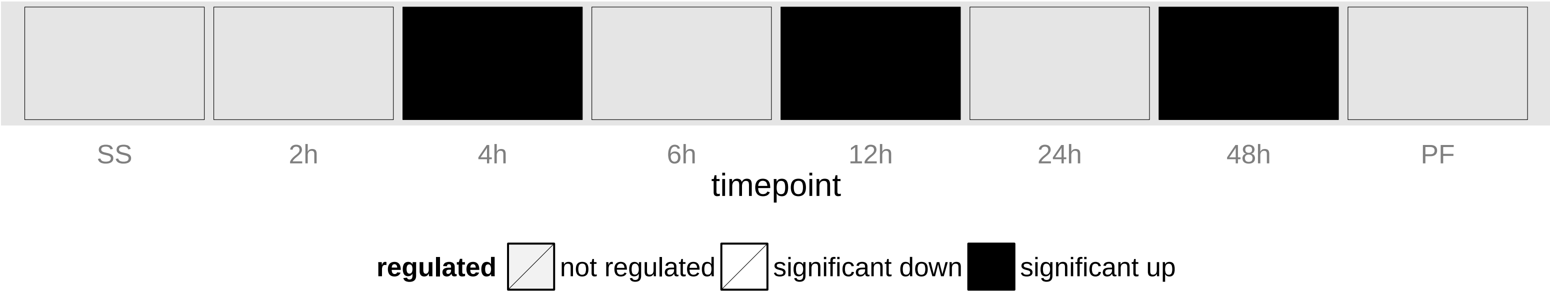
UDP−GlcNAc:alpha3−D−mannoside beta−1, 2−N−acetylglucosaminyltransferase I, N−Acetylglucosaminyltransferase I (GnTI)
Tb927.3.5660
AGOF: UDP−glycosyltransferase activity, alpha−1, 3−mannosylglycoprotein 2−beta−N−acetylglucosaminyltransferase activity
AGOC: Golgi apparatus, integral to membrane
AGOP: GPI anchor biosynthetic process, N−glycan processing, cell proliferation, pathogenesis
PGOF: null
PGOC: null
PGOP: null



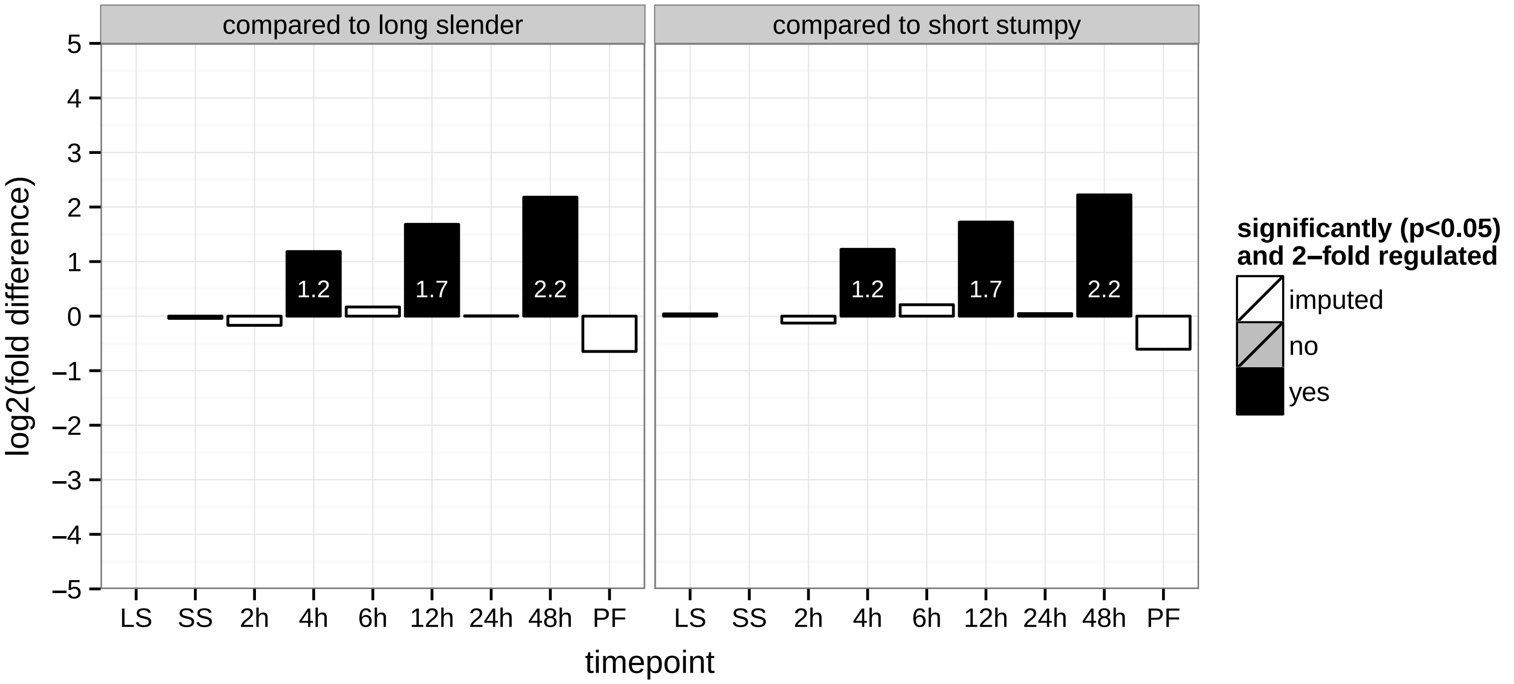


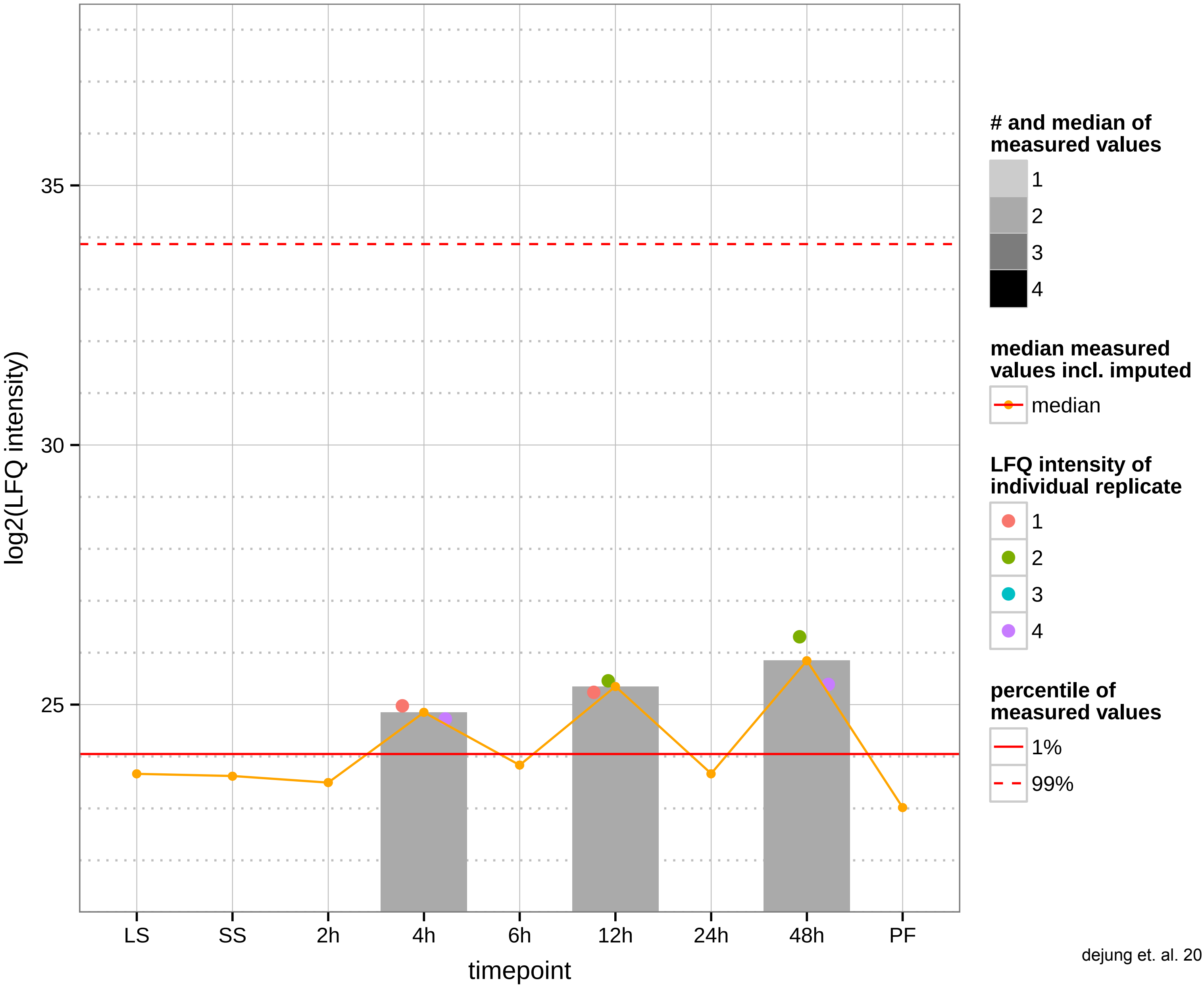
dejung et. al. 2015



dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.9630
AGOF: null
AGOC: null
AGOP: protein transport, vesicle–mediated transport
PGOF: null
PGOC: null
PGOP: protein transport





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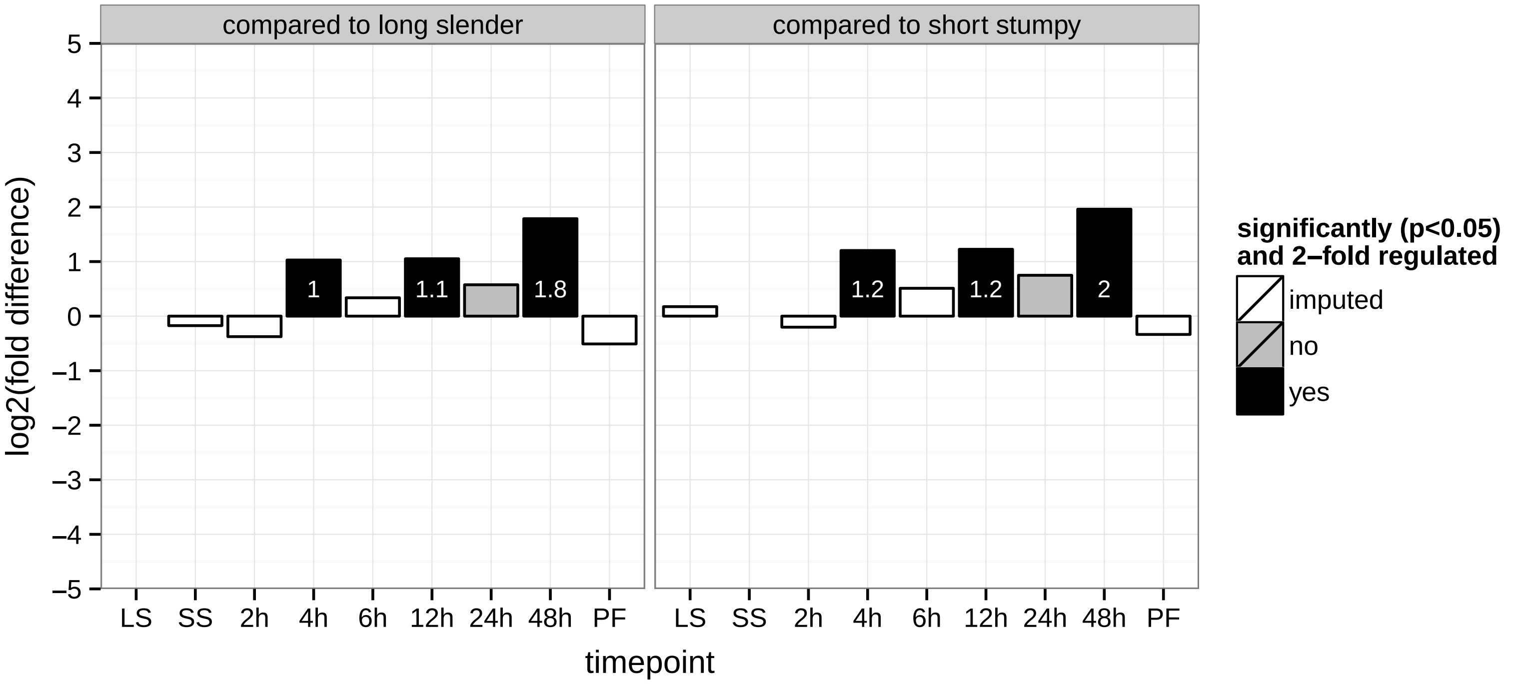
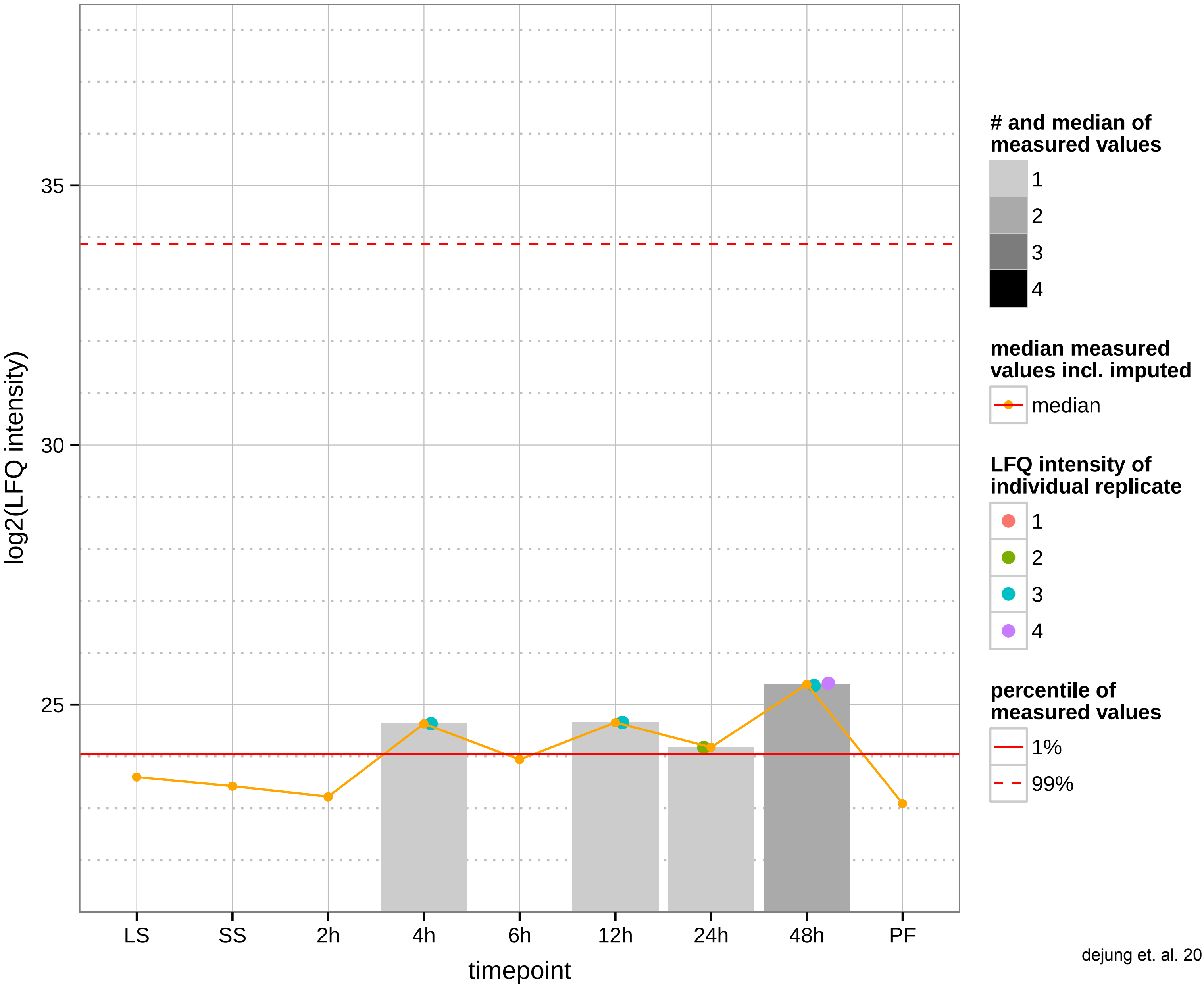
peroxisome assembly protein, putative
Tb927.3.2410
AGOF: zinc ion binding
AGOC: peroxisomal membrane
AGOP: peroxisome organization
PGOF: protein binding, zinc ion binding
PGOC: null
PGOP: null





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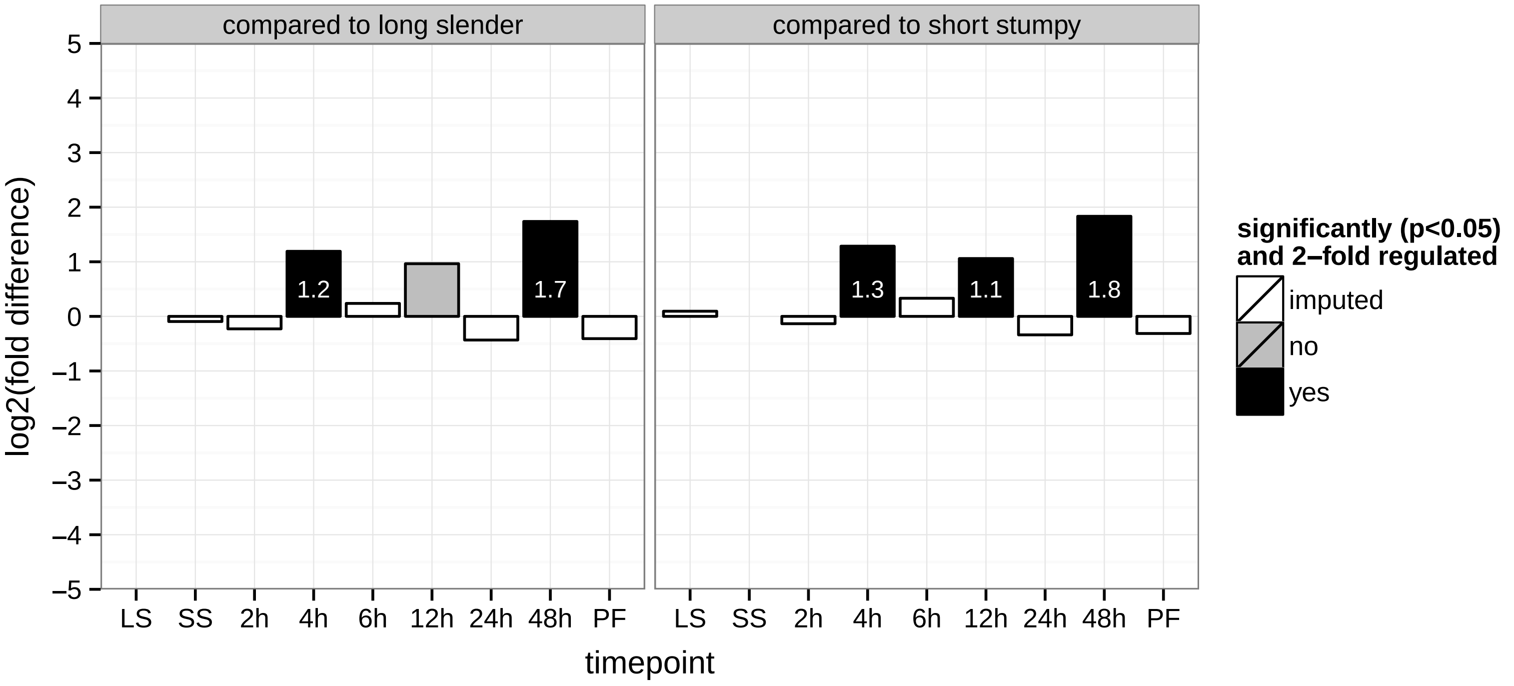
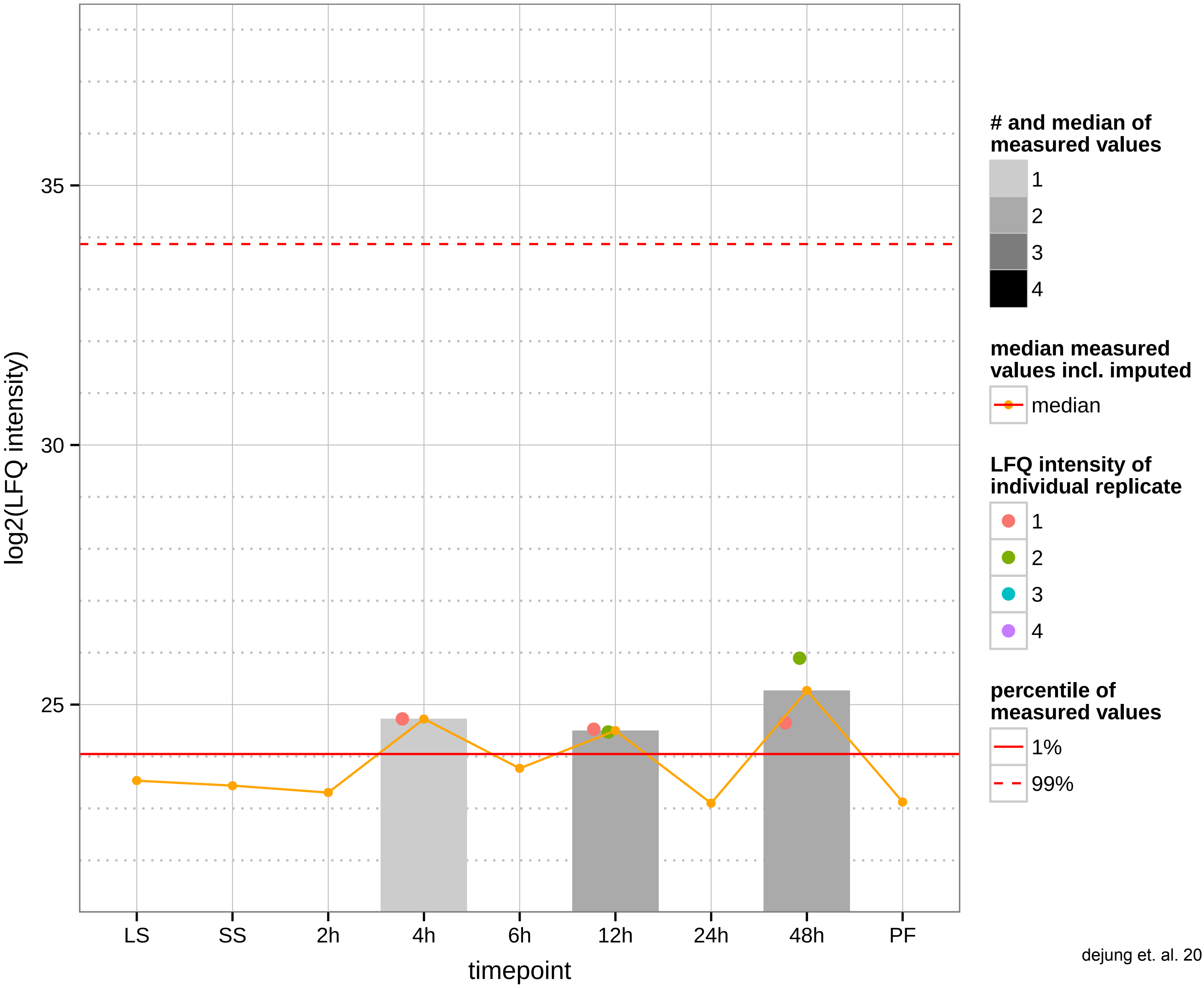
hypothetical protein, conserved
Tb927.9.11660
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity
PGOC: mitochondrion
PGOP: null





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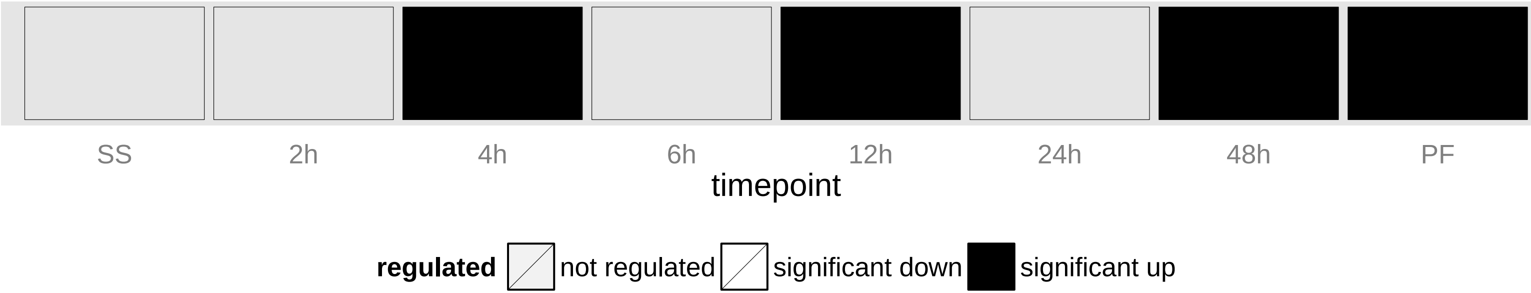

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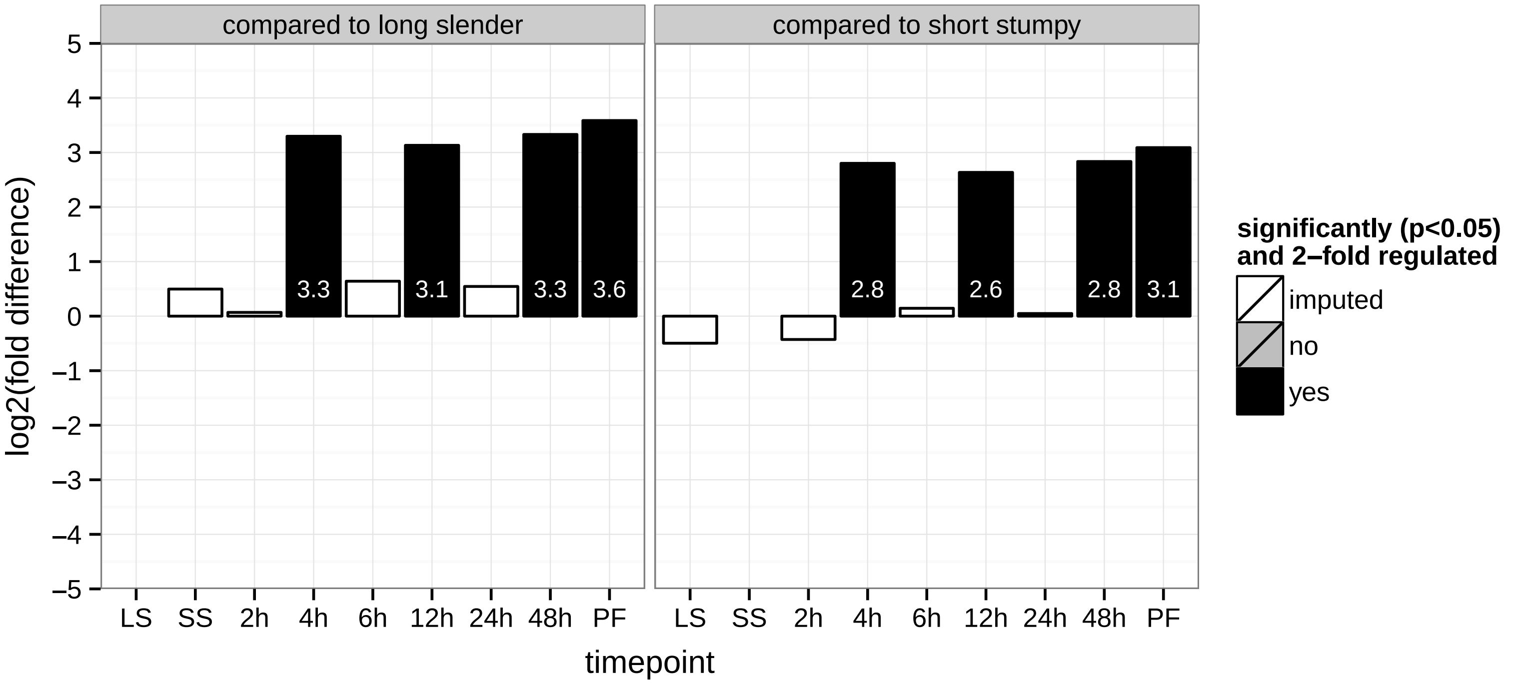
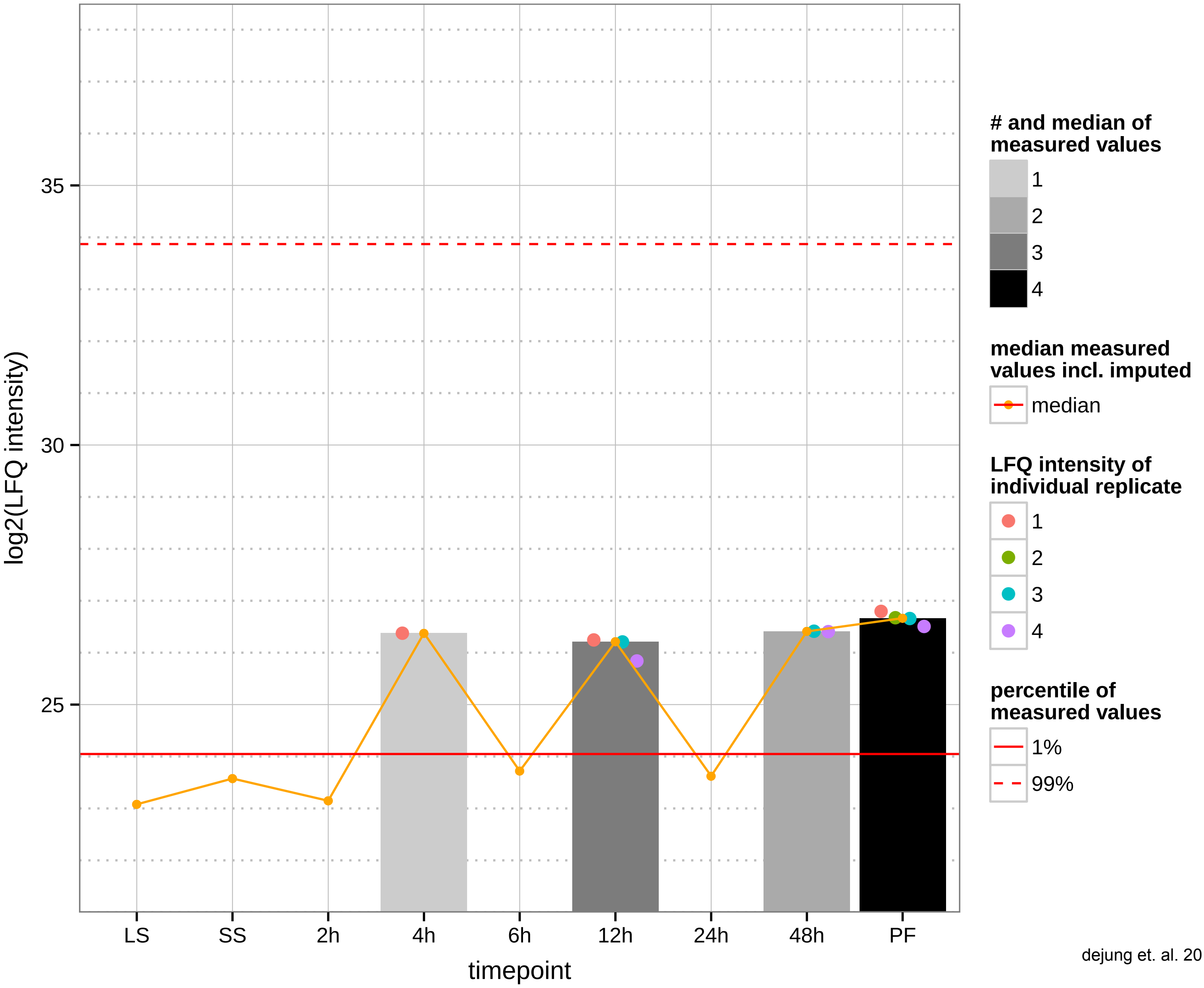
hypothetical protein, conserved
Tb927.10.1980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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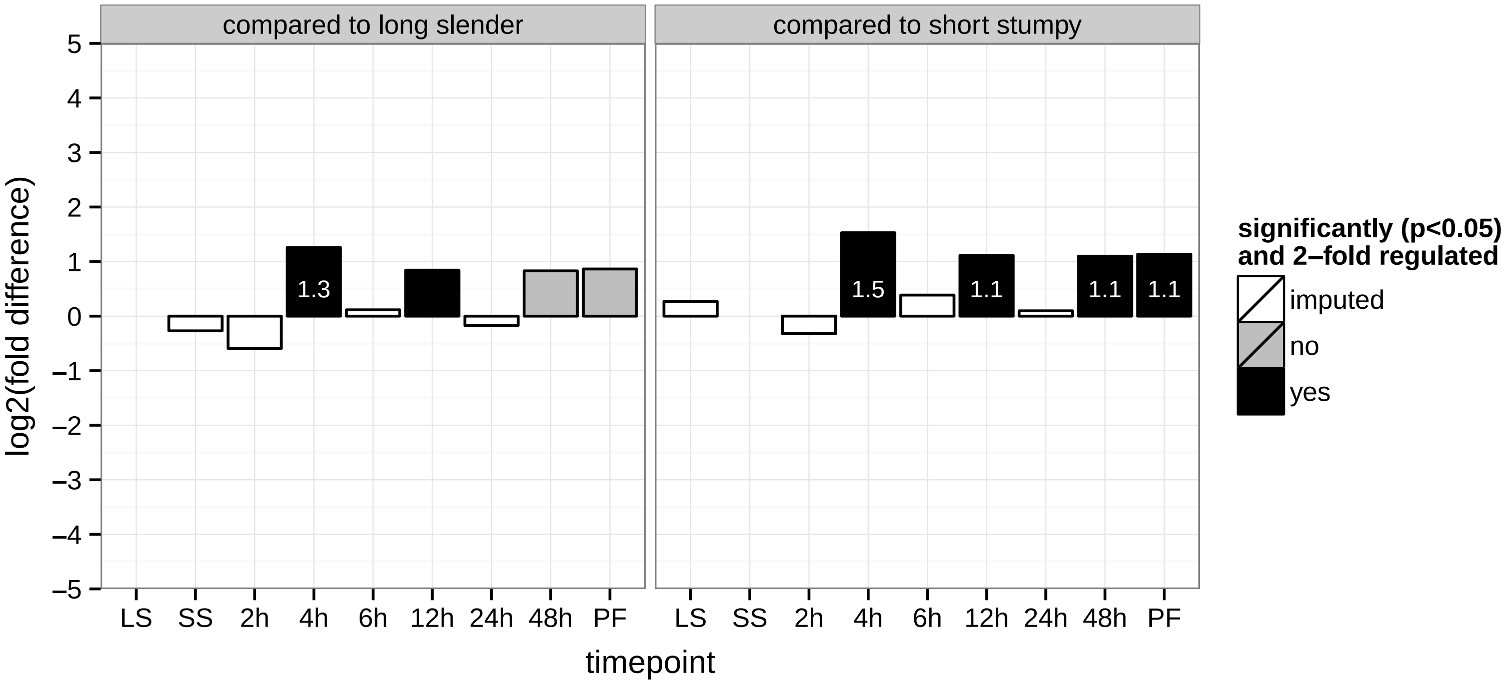
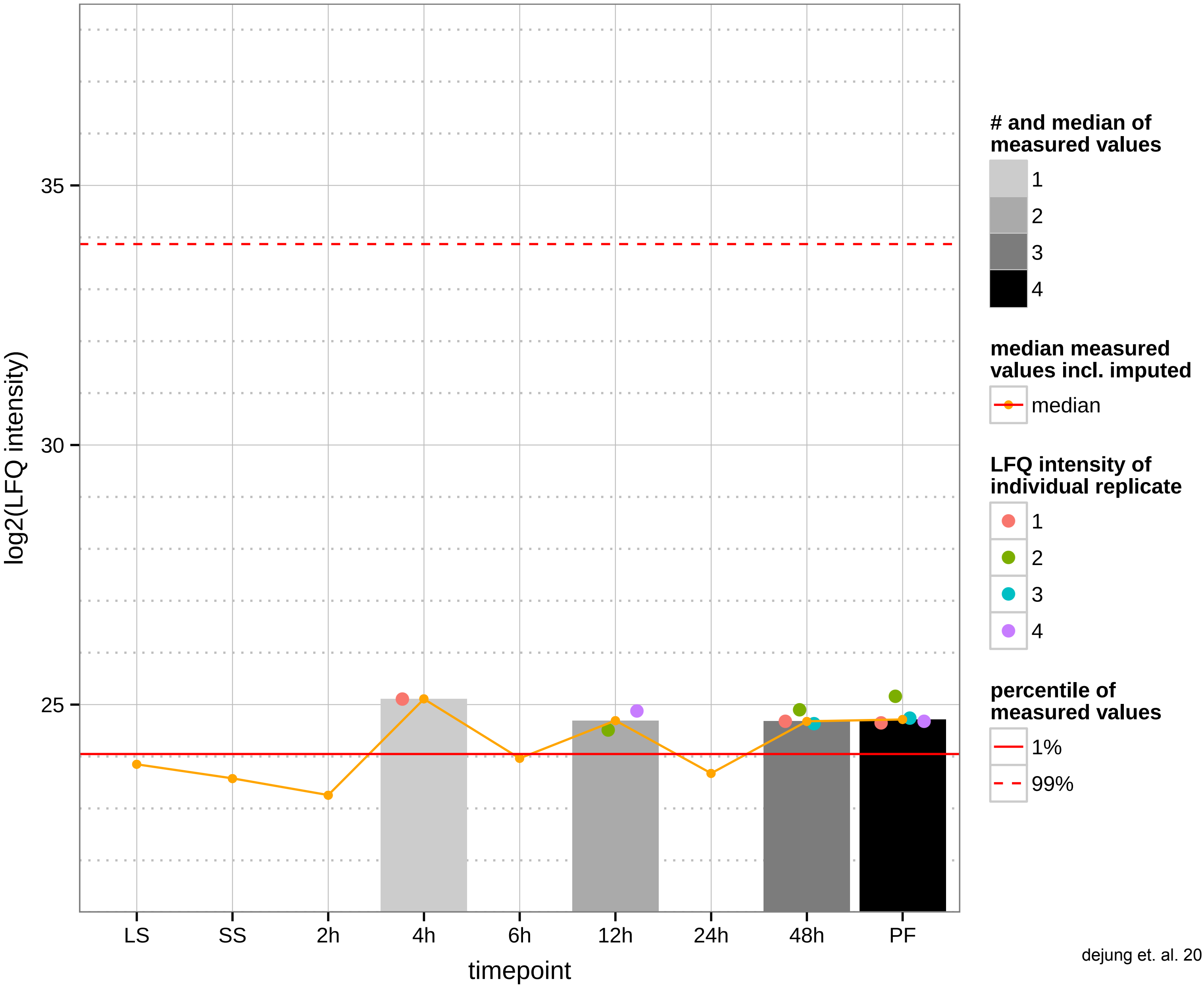
hypothetical protein, conserved
Tb927.11.1200
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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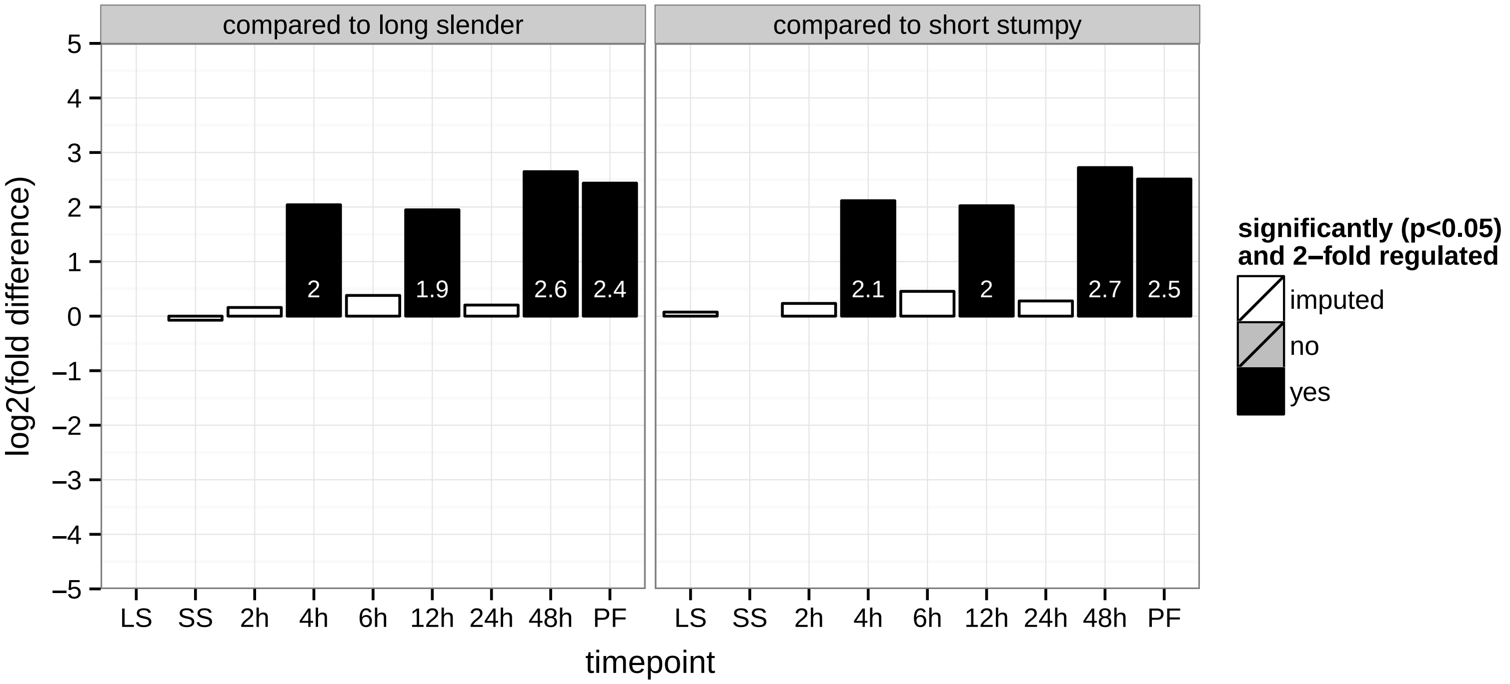
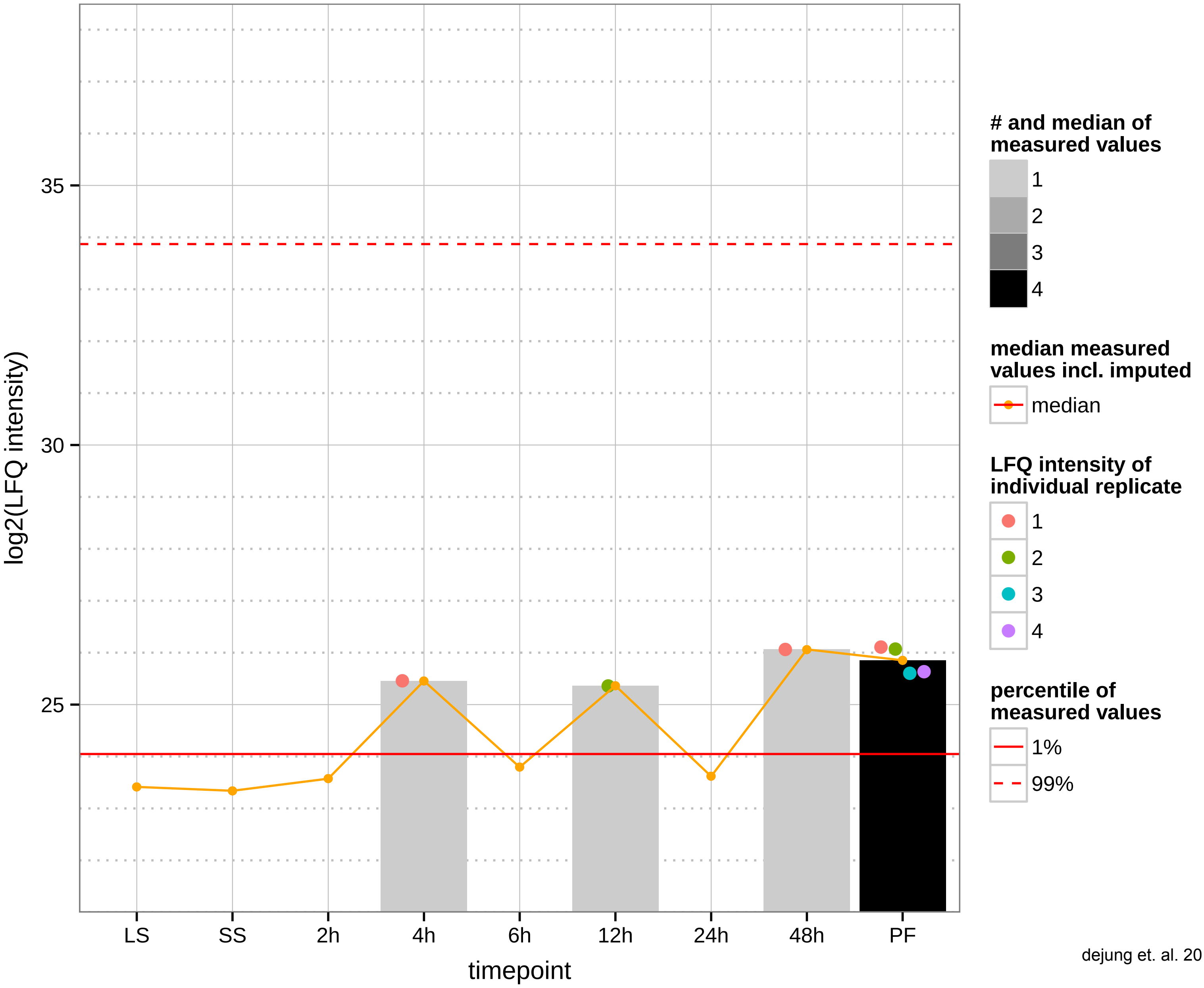
hypothetical protein, conserved
Tb927.3.2260
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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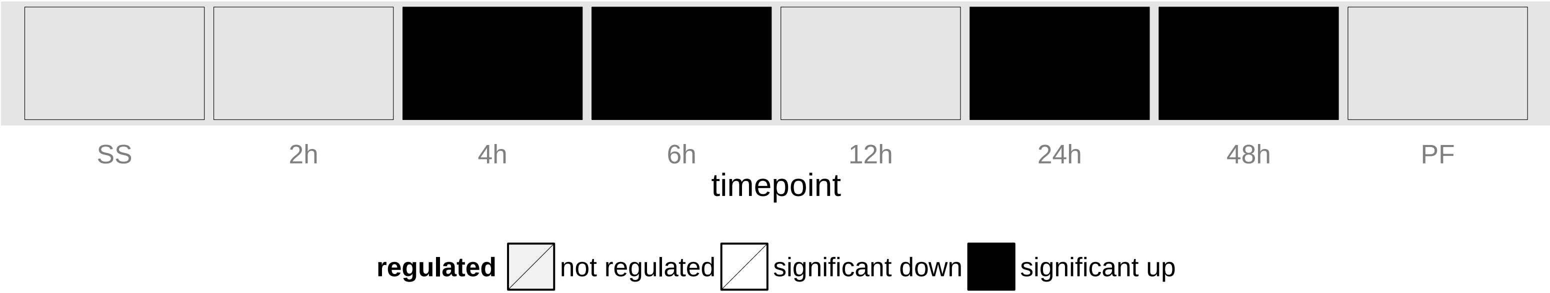

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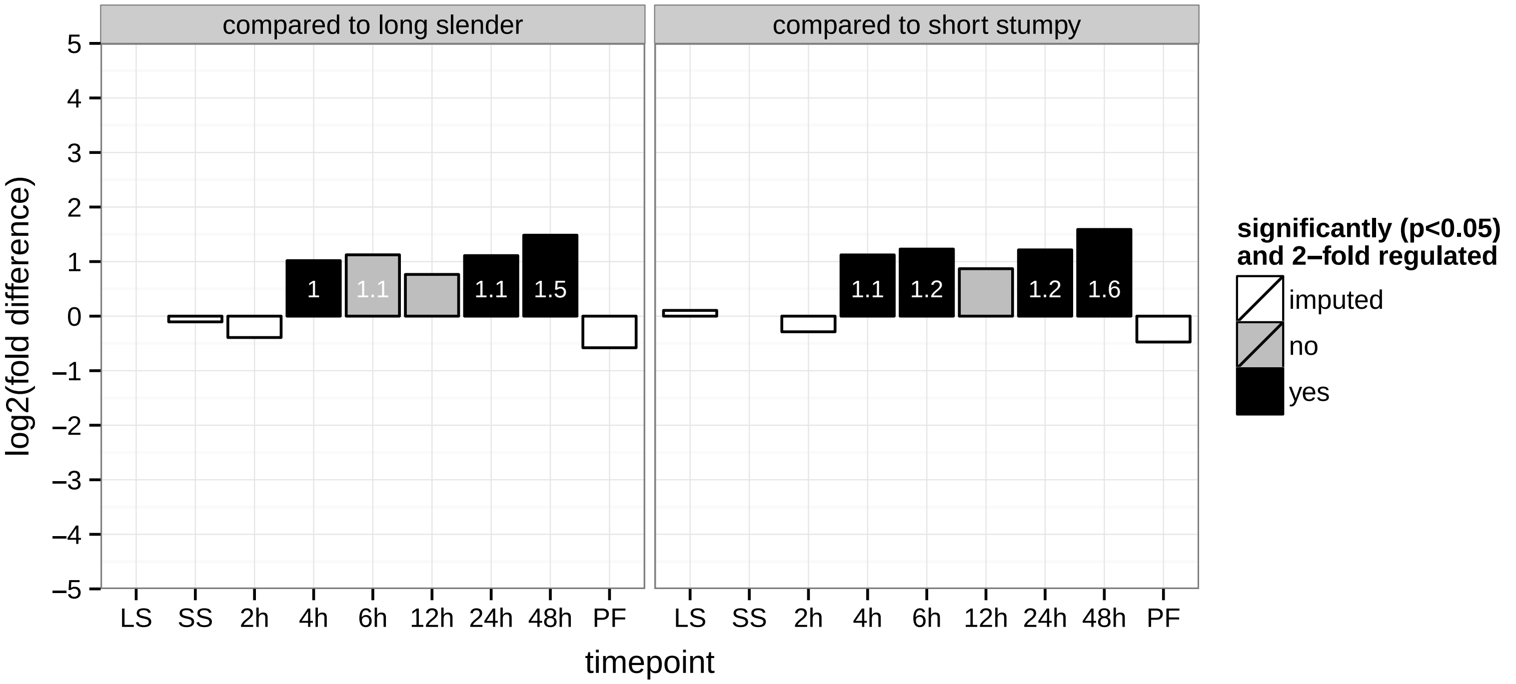
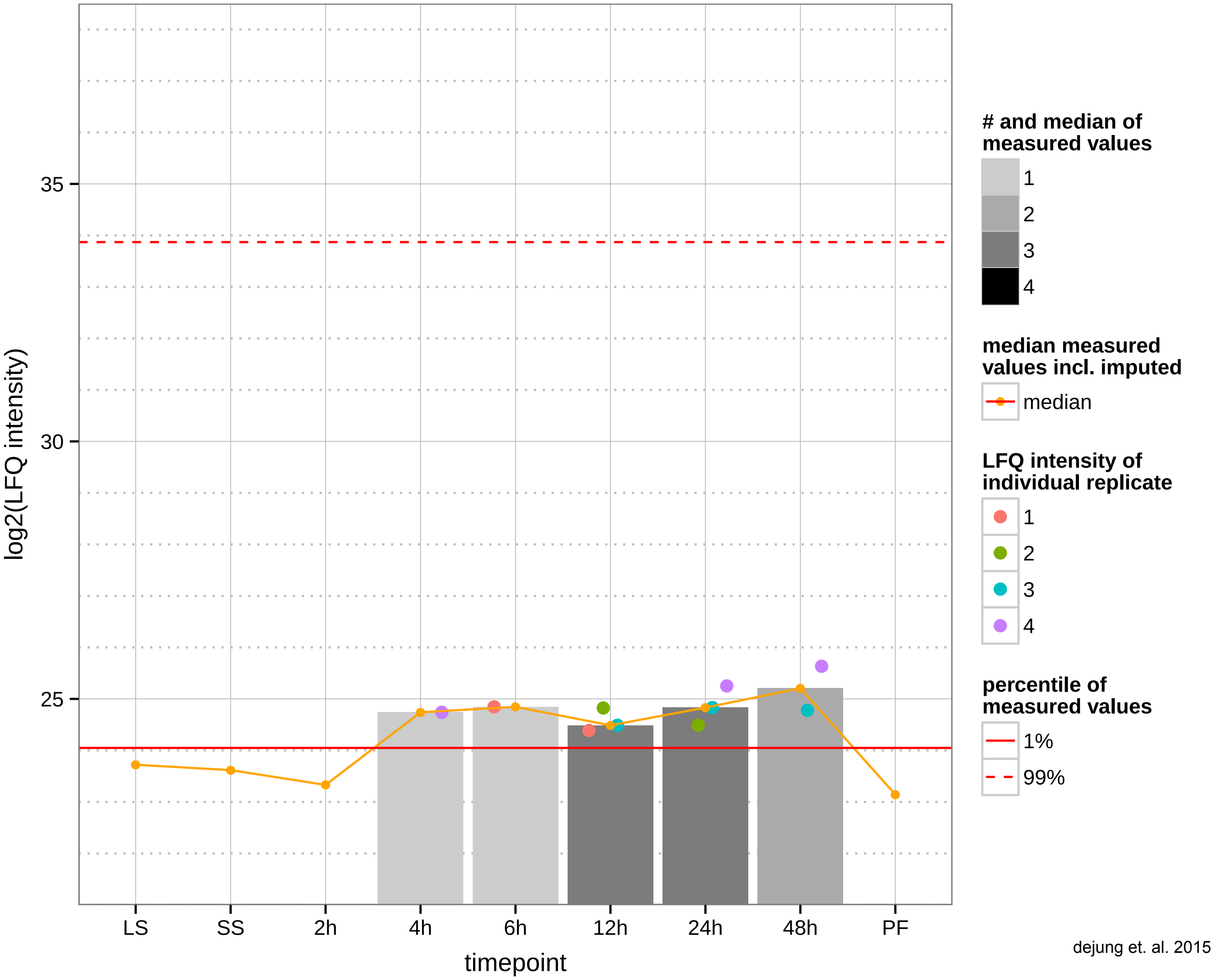
hypothetical protein, conserved
Tb927.11.11050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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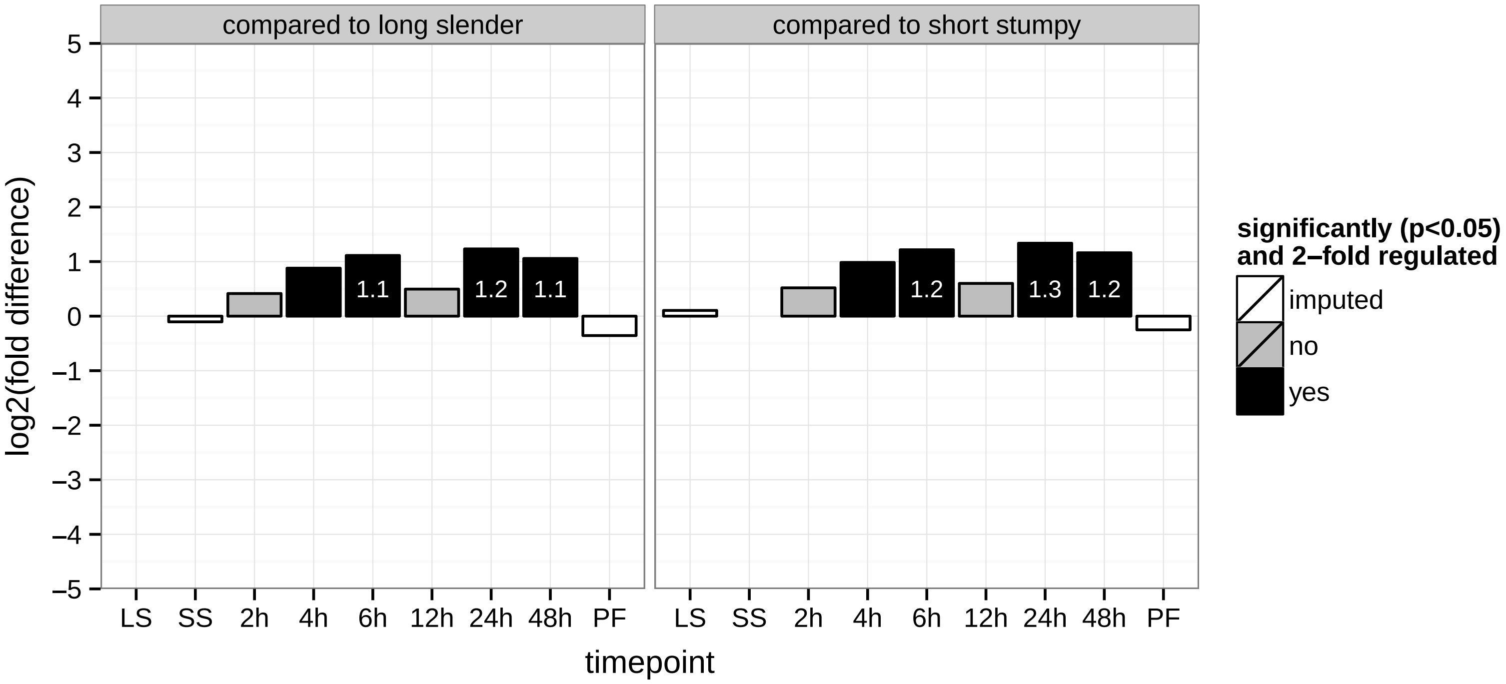
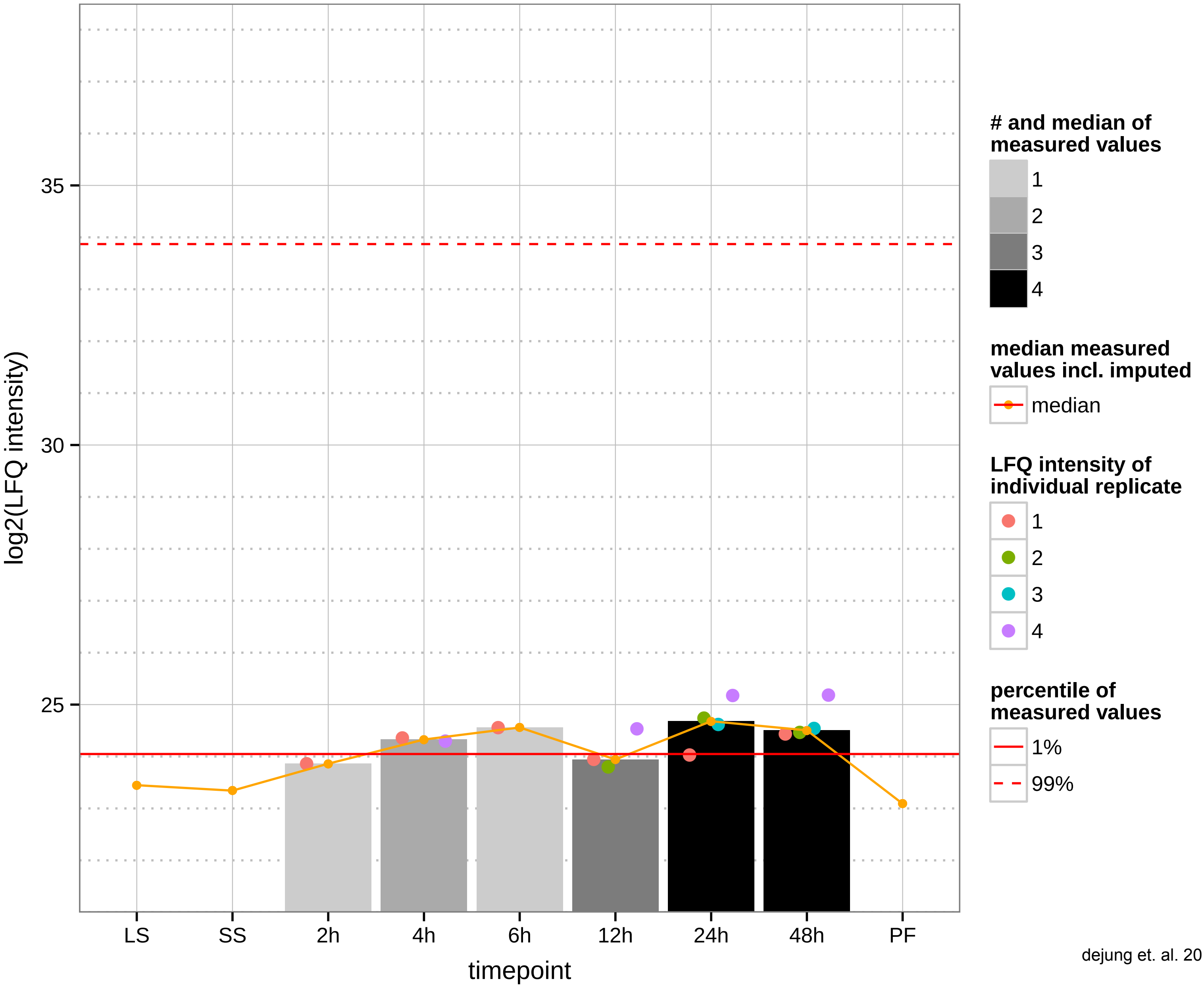
hypothetical protein, conserved
Tb927.11.14990
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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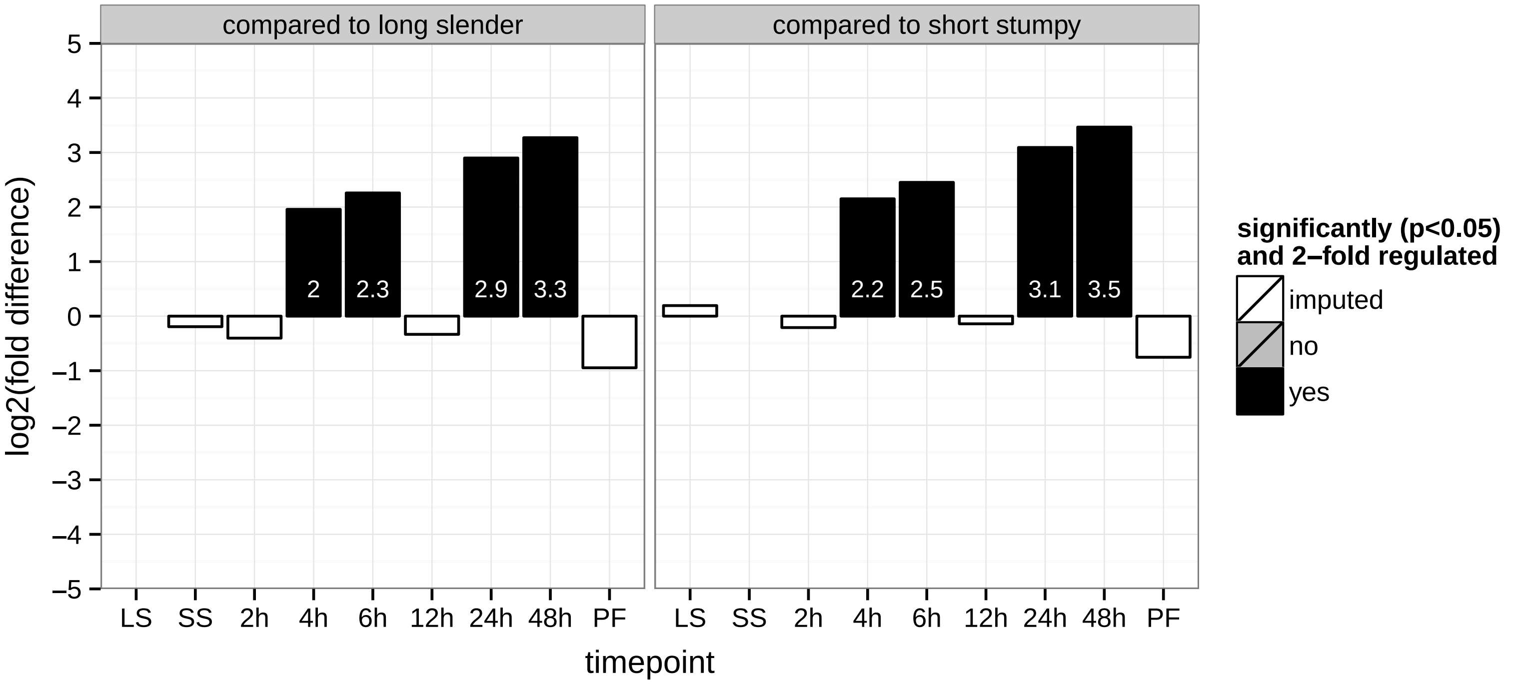
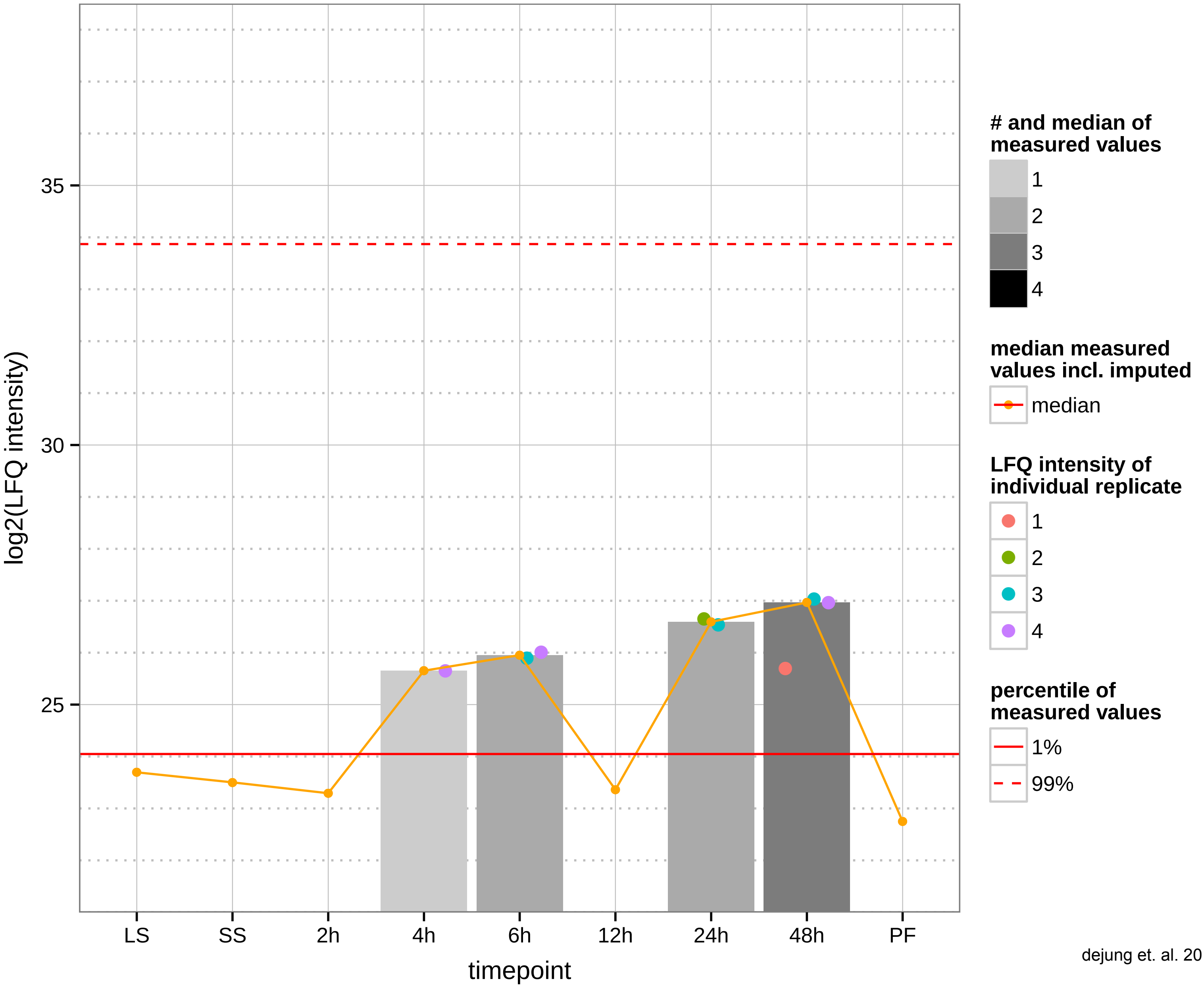
L–Lysine transport protein, putative
Tb927.11.15860;Tb927.11.15840
AGOF: L–lysine transmembrane transporter activity, amine transmembrane transporter activity
AGOC: flagellar pocket, integral to membrane, kinetoplast, nucleus, plasma membrane
AGOP: lysine transport, amino acid transport, lysine transport
PGOF: null
PGOC: null
PGOP: null





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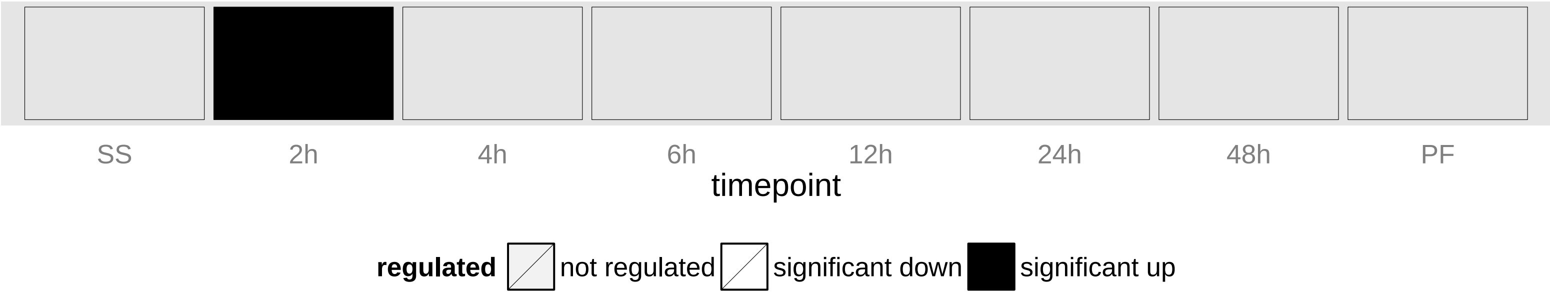

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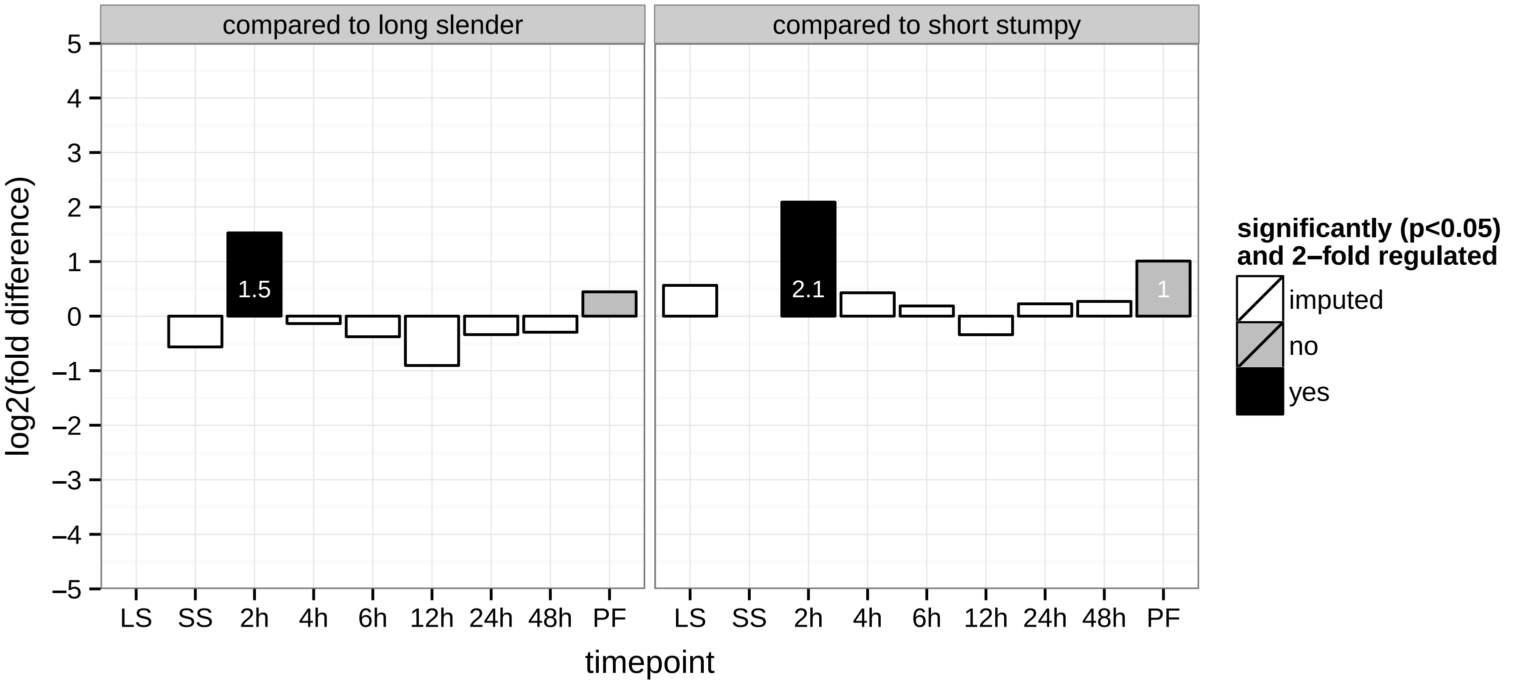
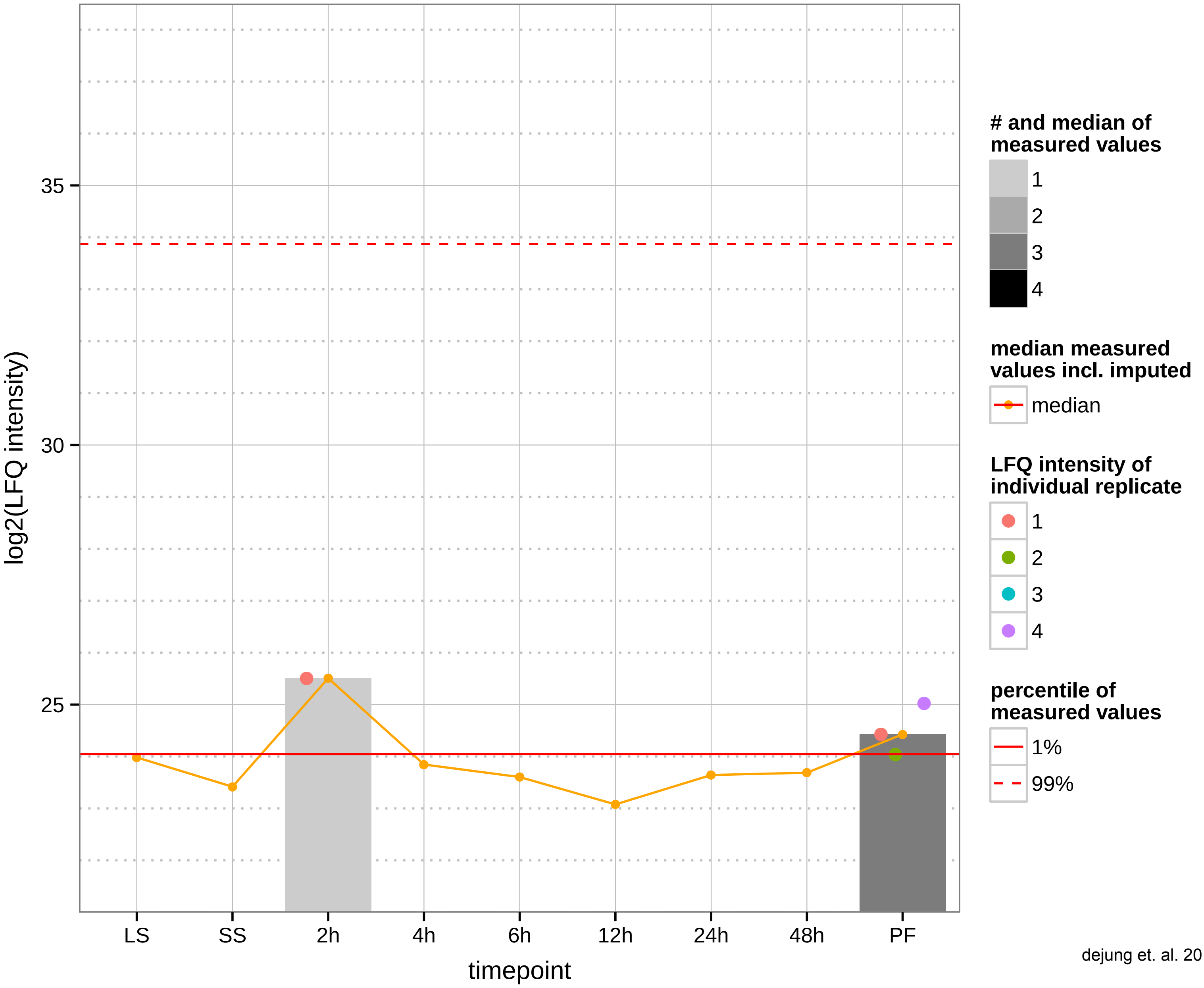
hypothetical protein, conserved
Tb927.11.9290
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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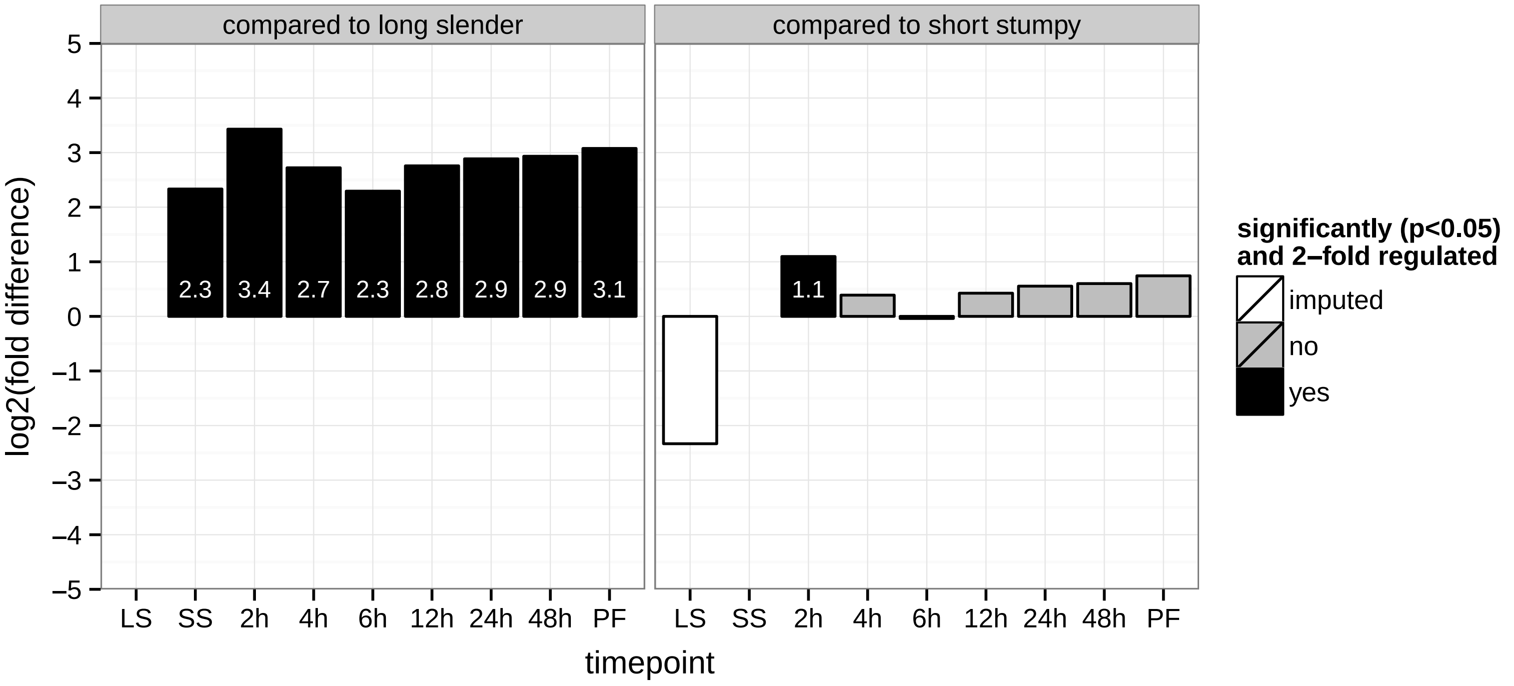
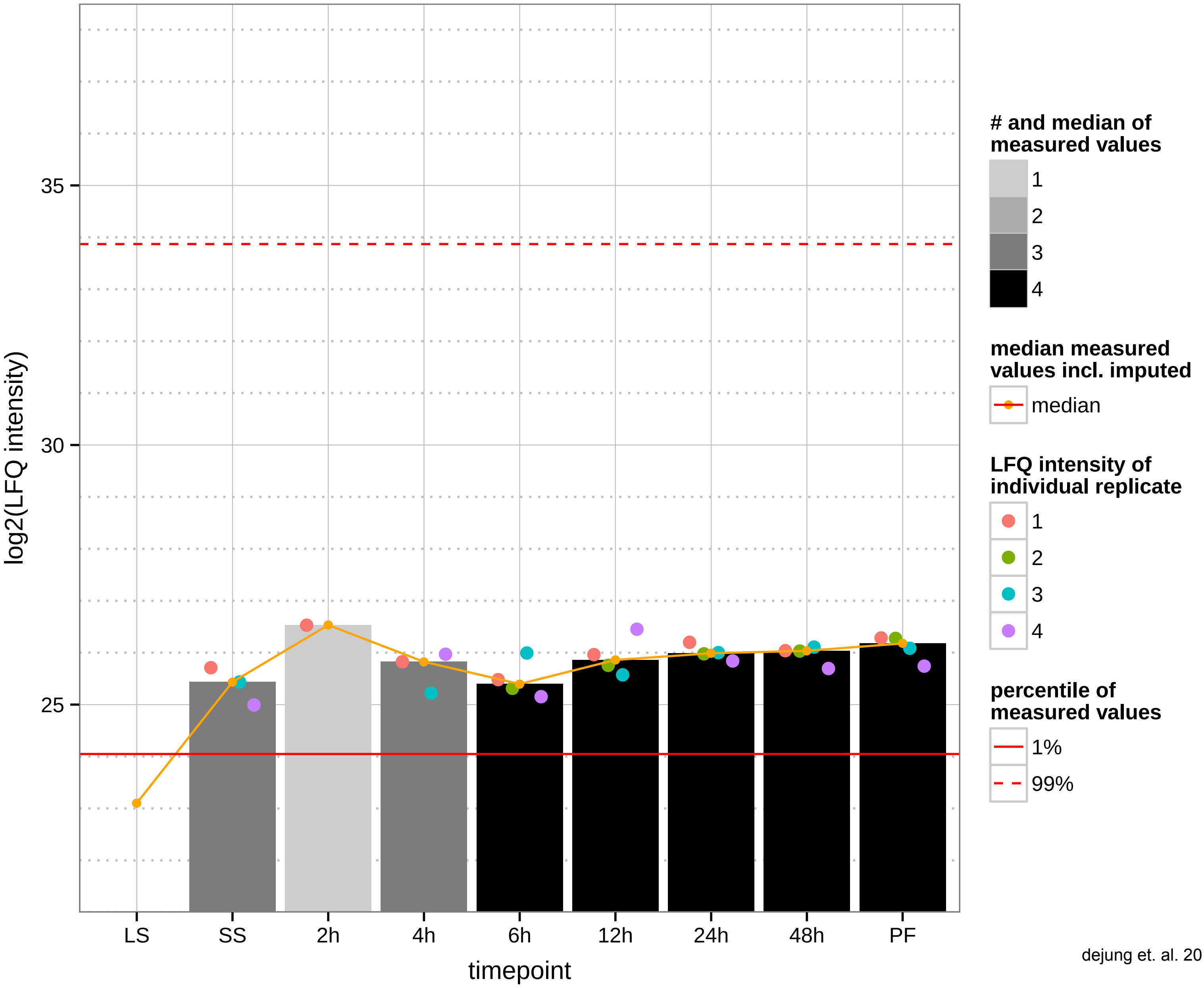
hypothetical protein, conserved
Tb927.5.2150
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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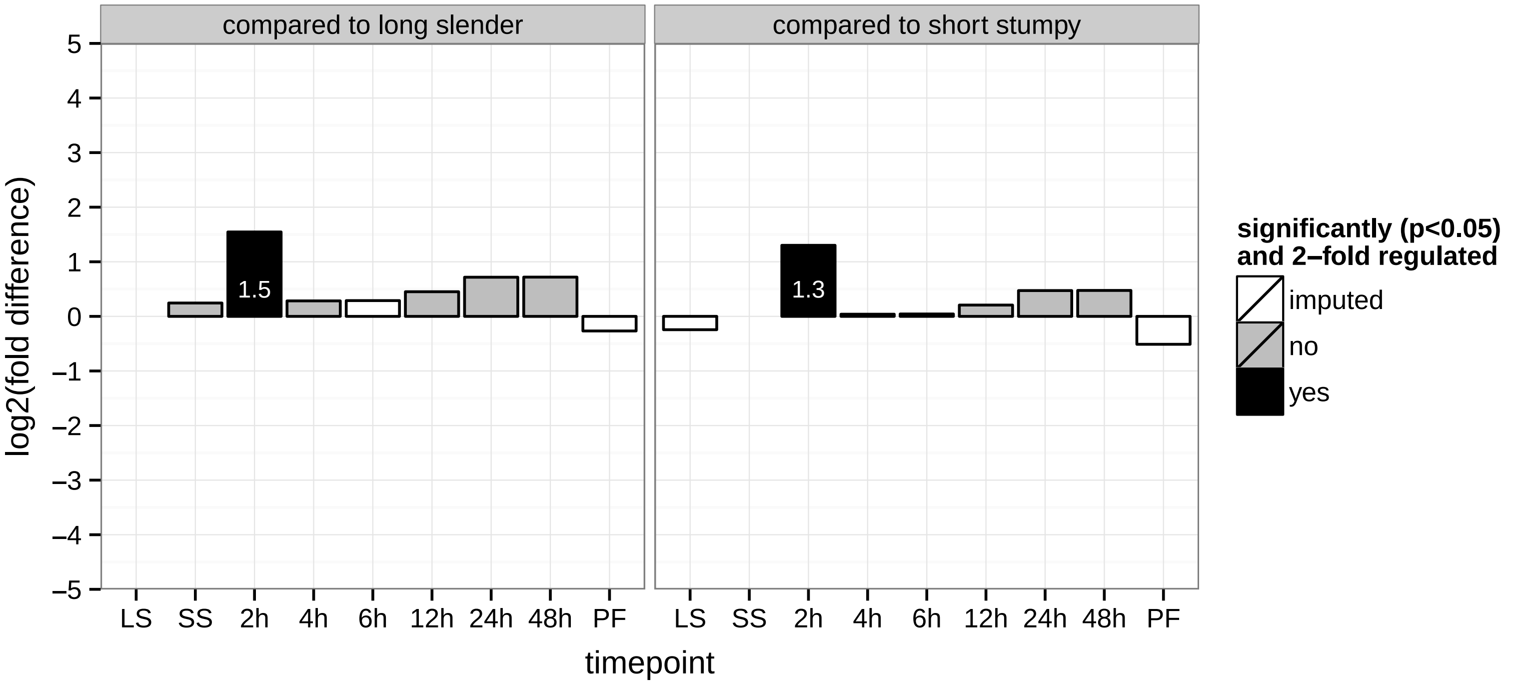
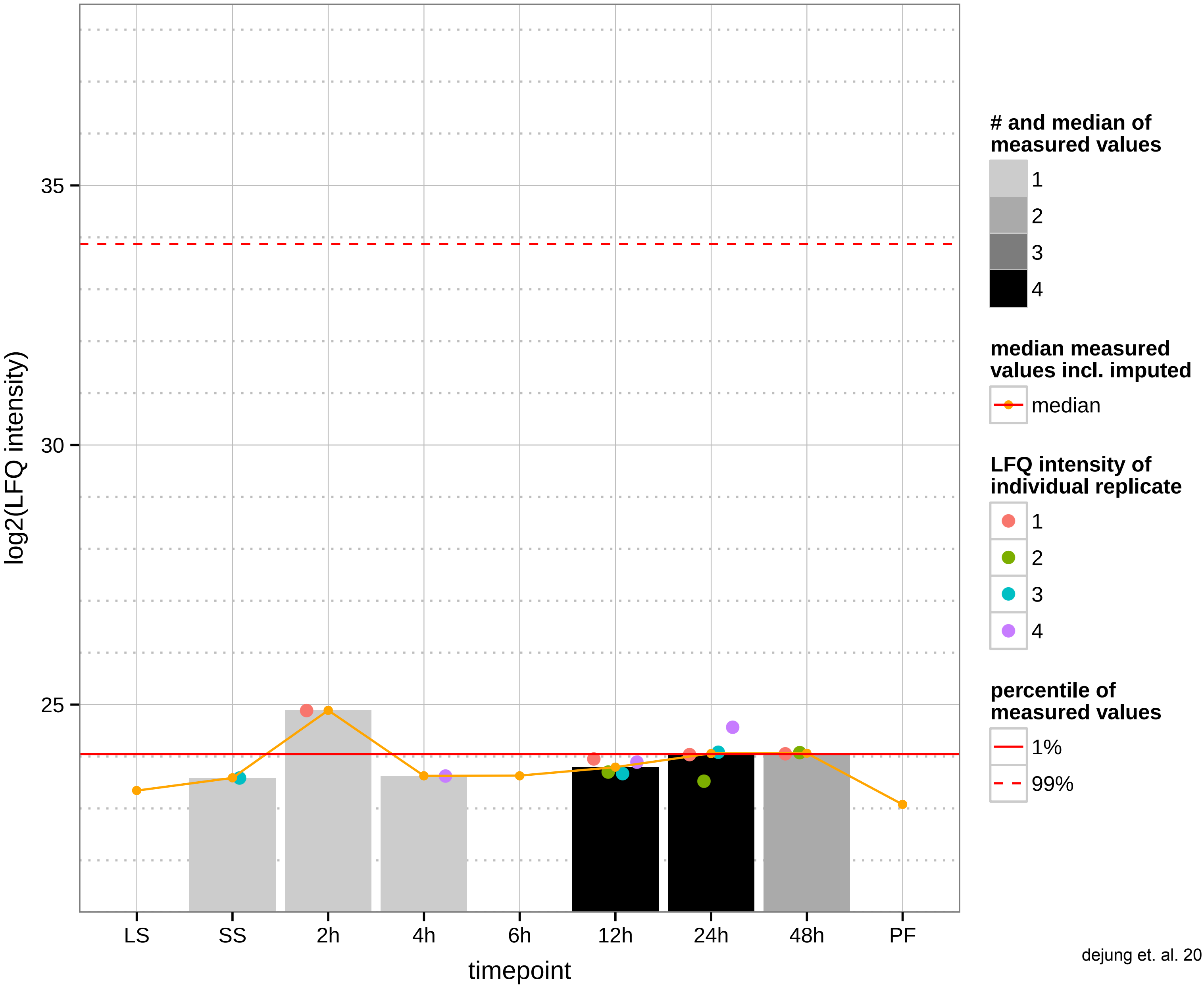
hypothetical protein, conserved
Tb927.9.13470
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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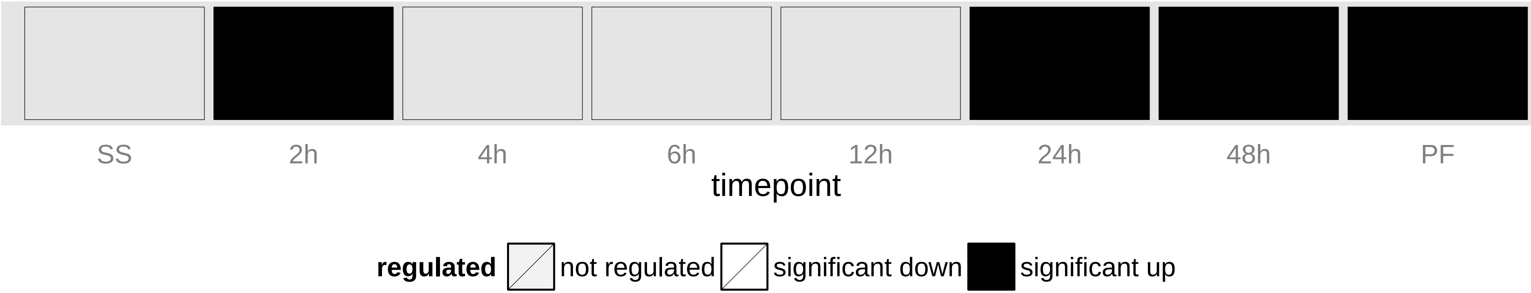

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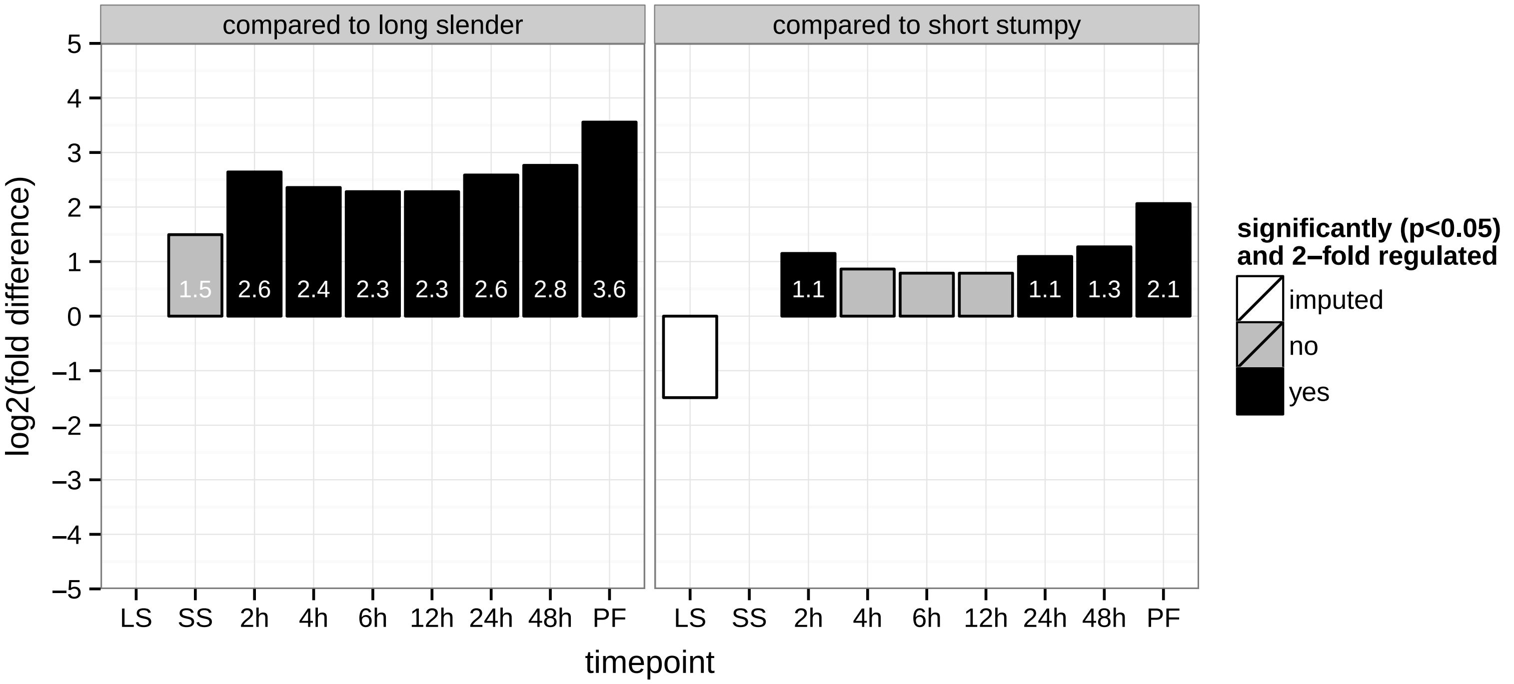
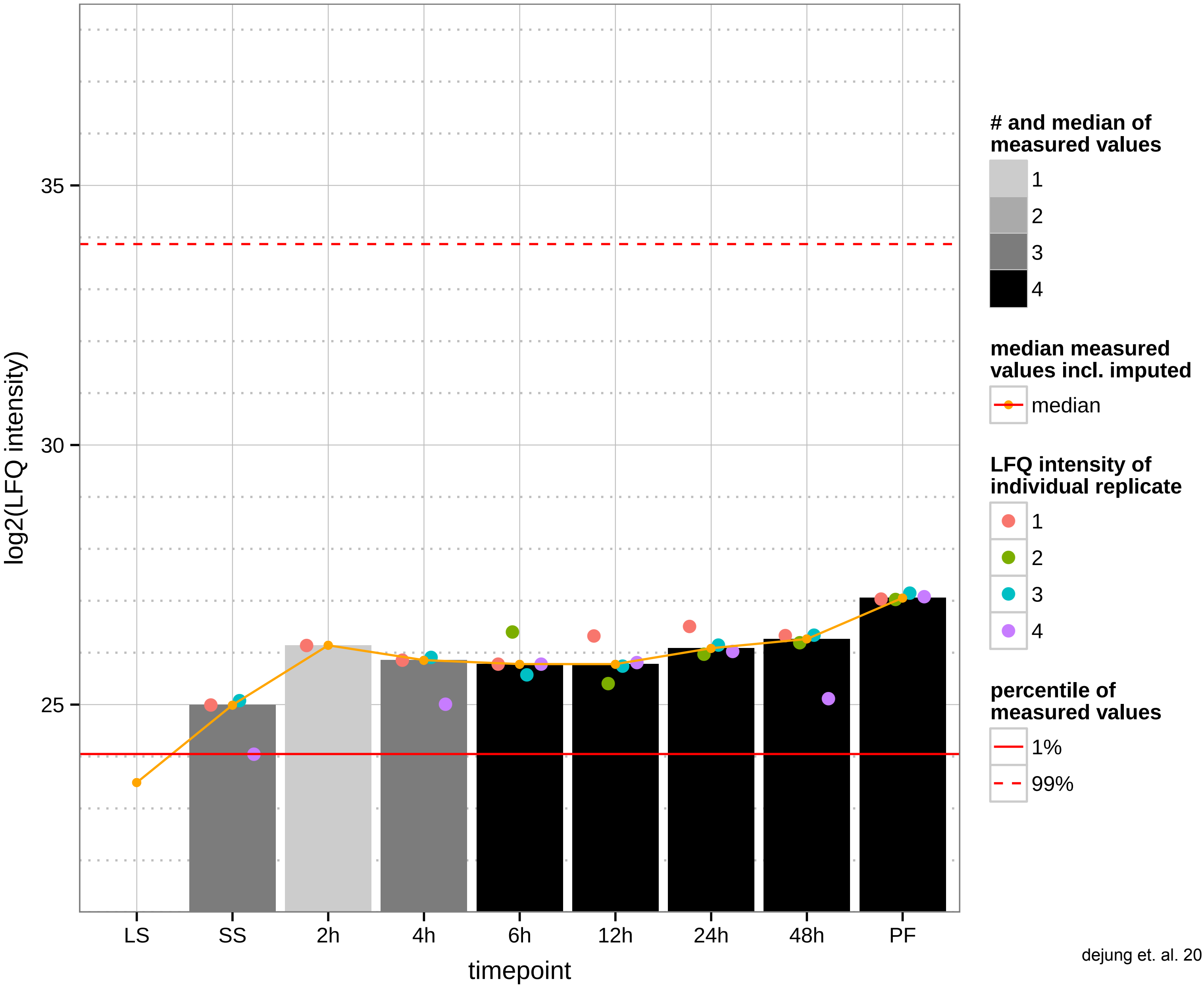
acetyltransferase, putative
Tb927.5.2280
AGOF: transferase activity, transferring acyl groups
AGOC: null
AGOP: metabolic process
PGOF: transferase activity, transferring acyl groups
PGOC: null
PGOP: metabolic process





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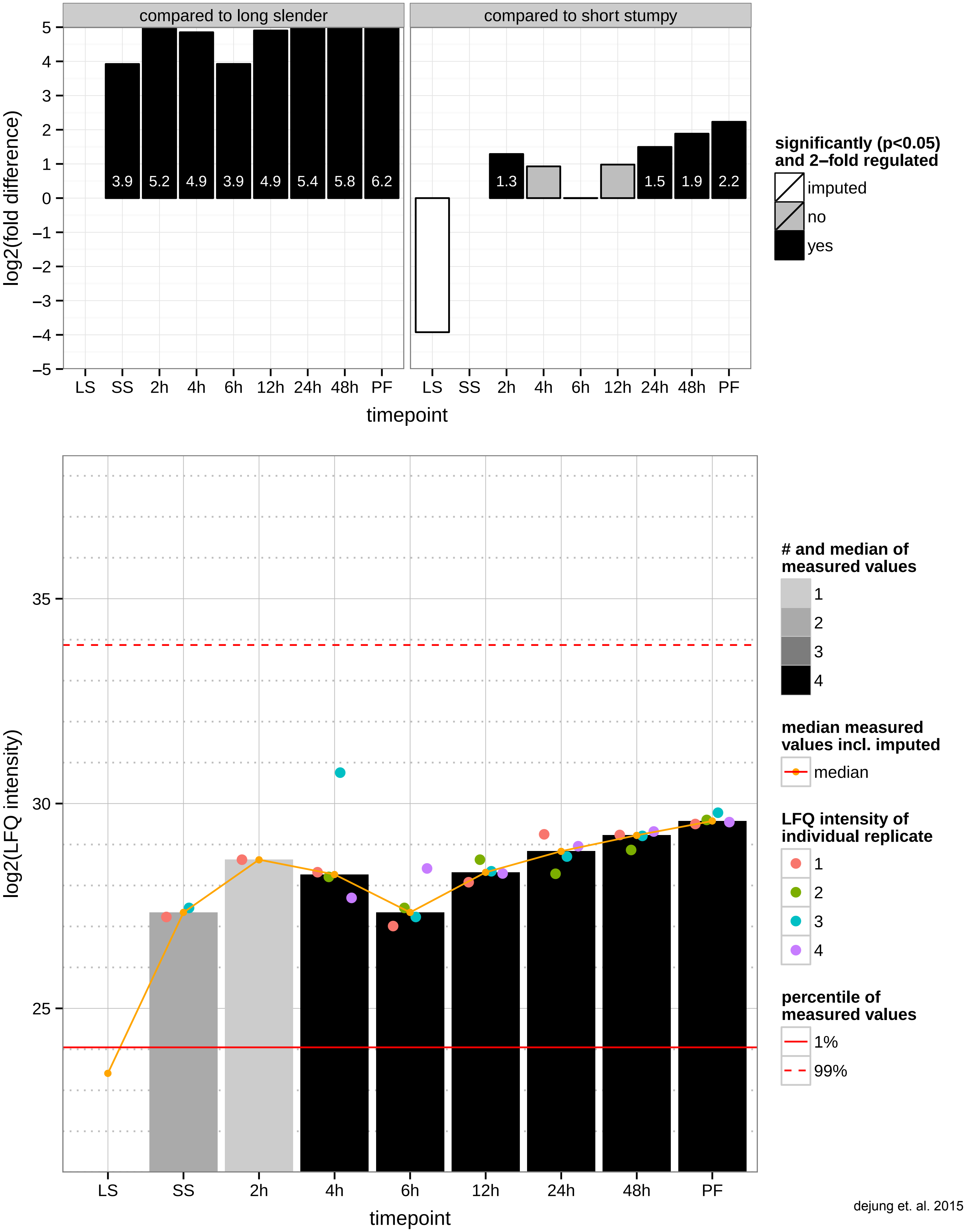
hypothetical protein, conserved
Tb927.5.2520
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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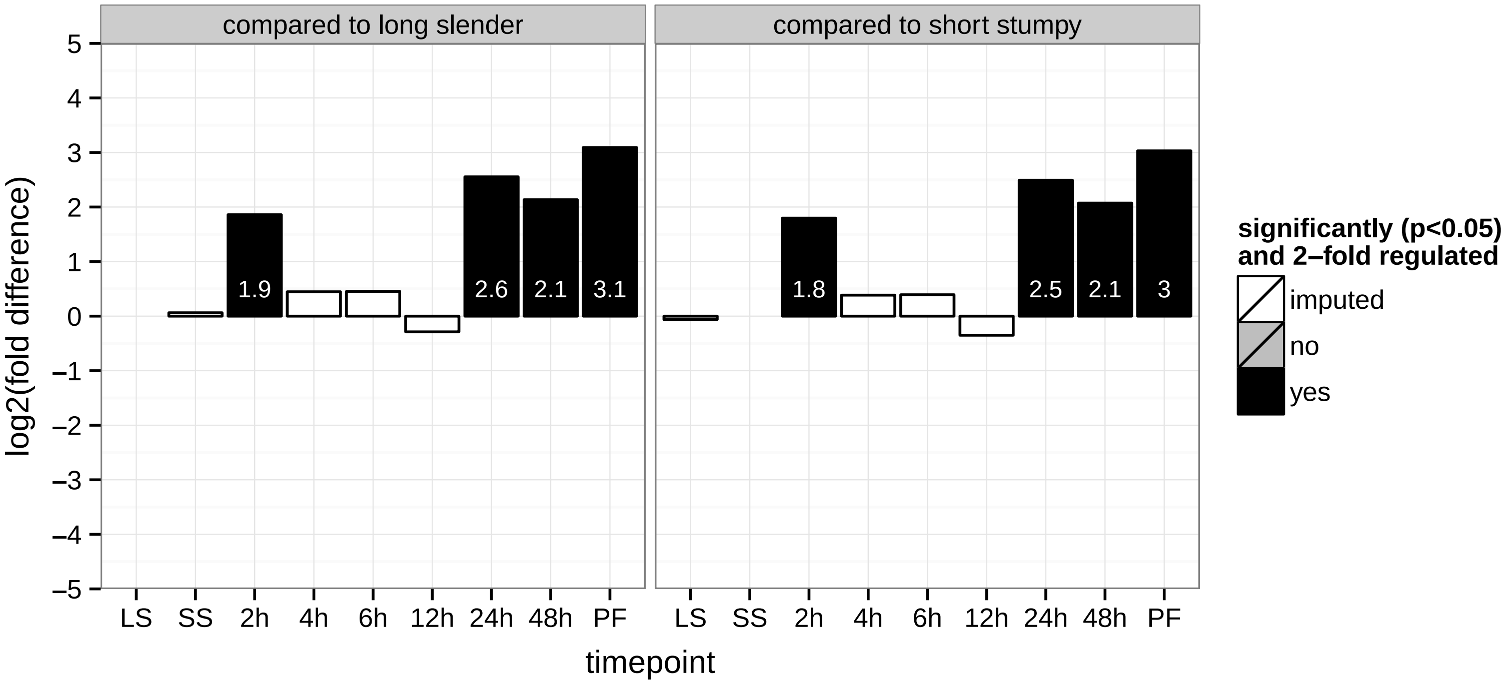
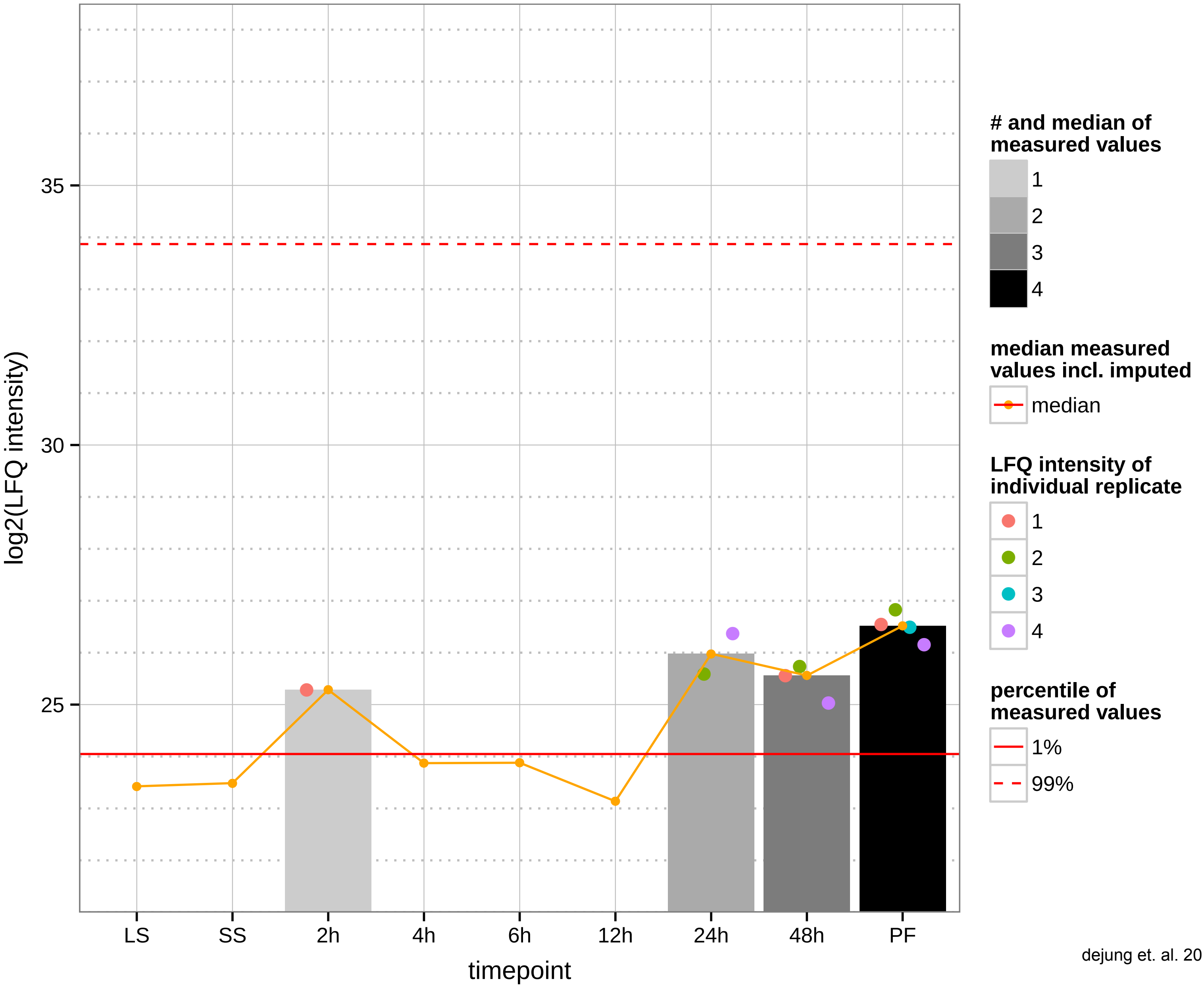
thiosulfate sulfurtransferase, mitochondrial, putative
Tb927.6.4930
AGOF: null
AGOC: mitochondrial small ribosomal subunit, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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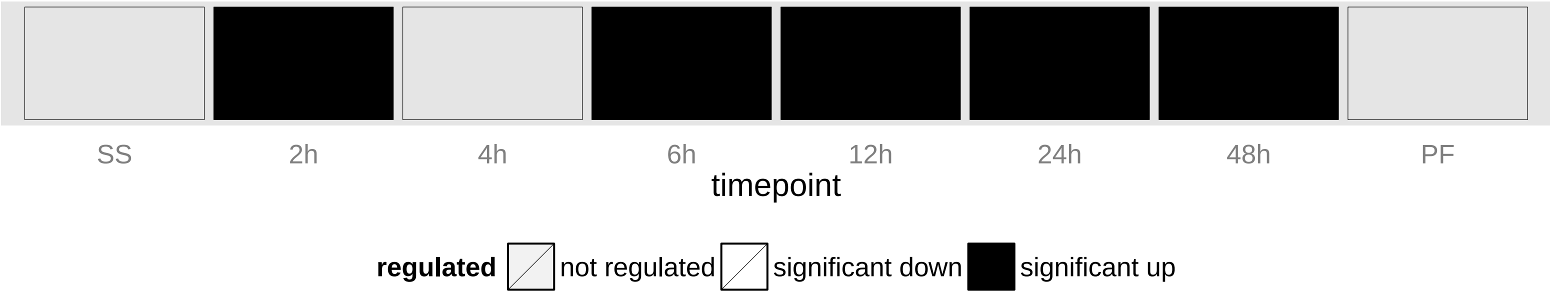

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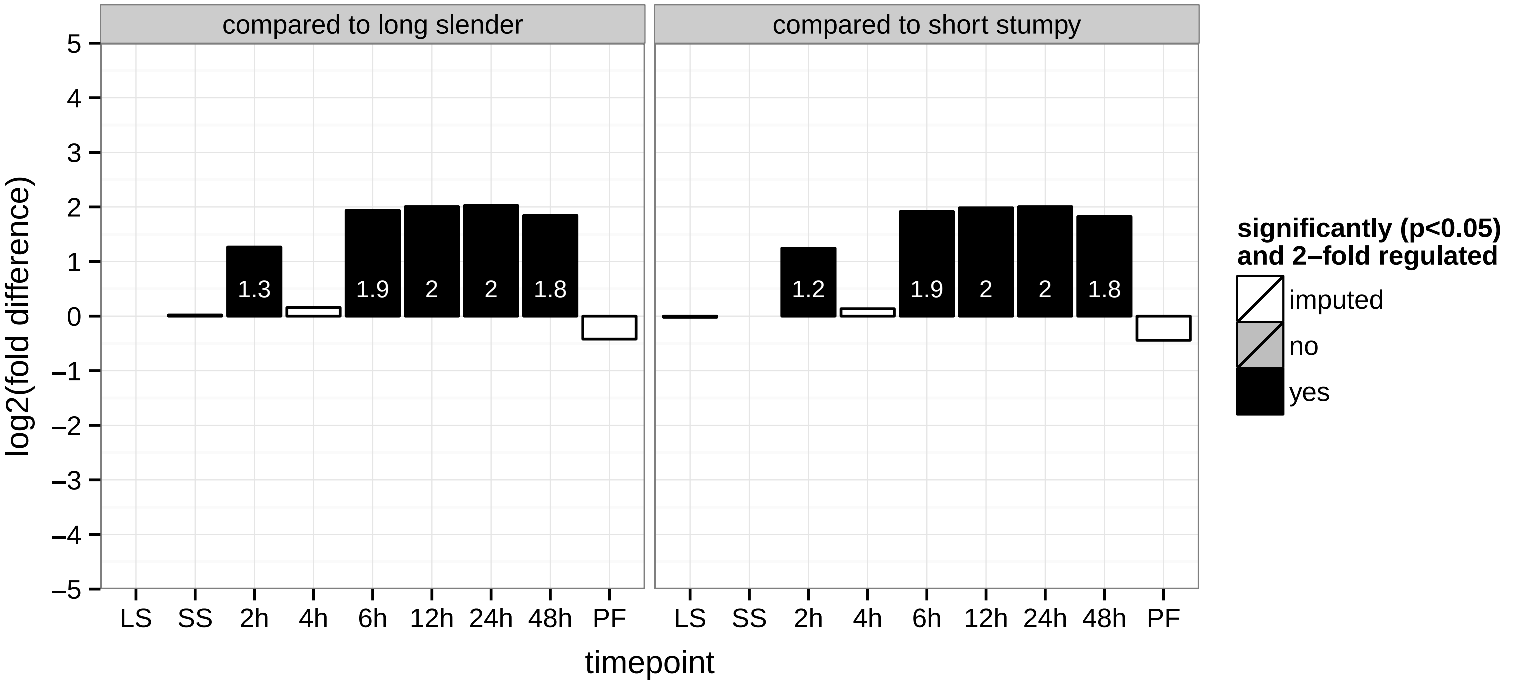
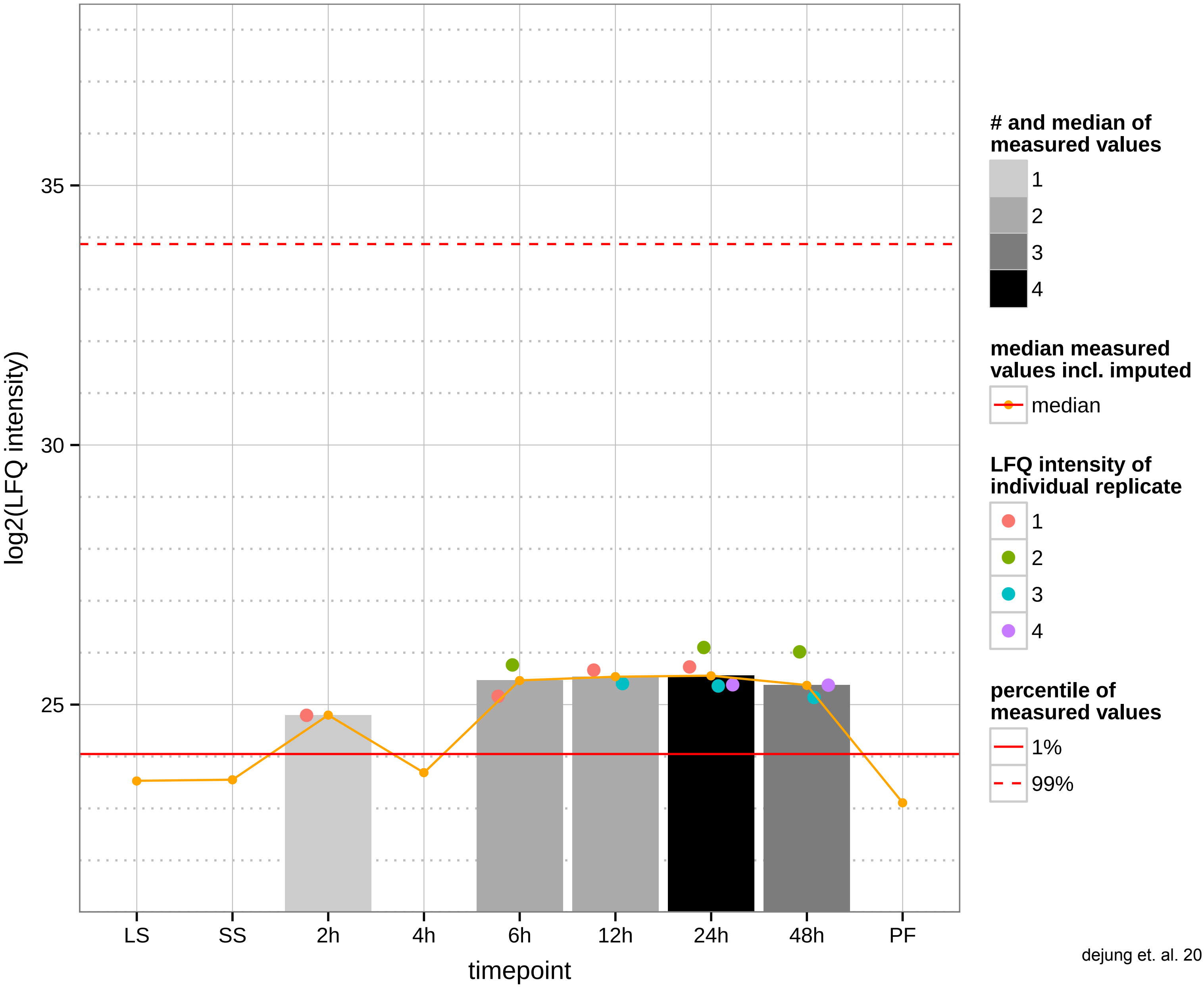
RNA–binding protein, putative (RBP15)
Tb927.10.7470
AGOF: RNA binding
AGOC: null
AGOP: RNA processing
PGOF: nucleic acid binding
PGOC: null
PGOP: null





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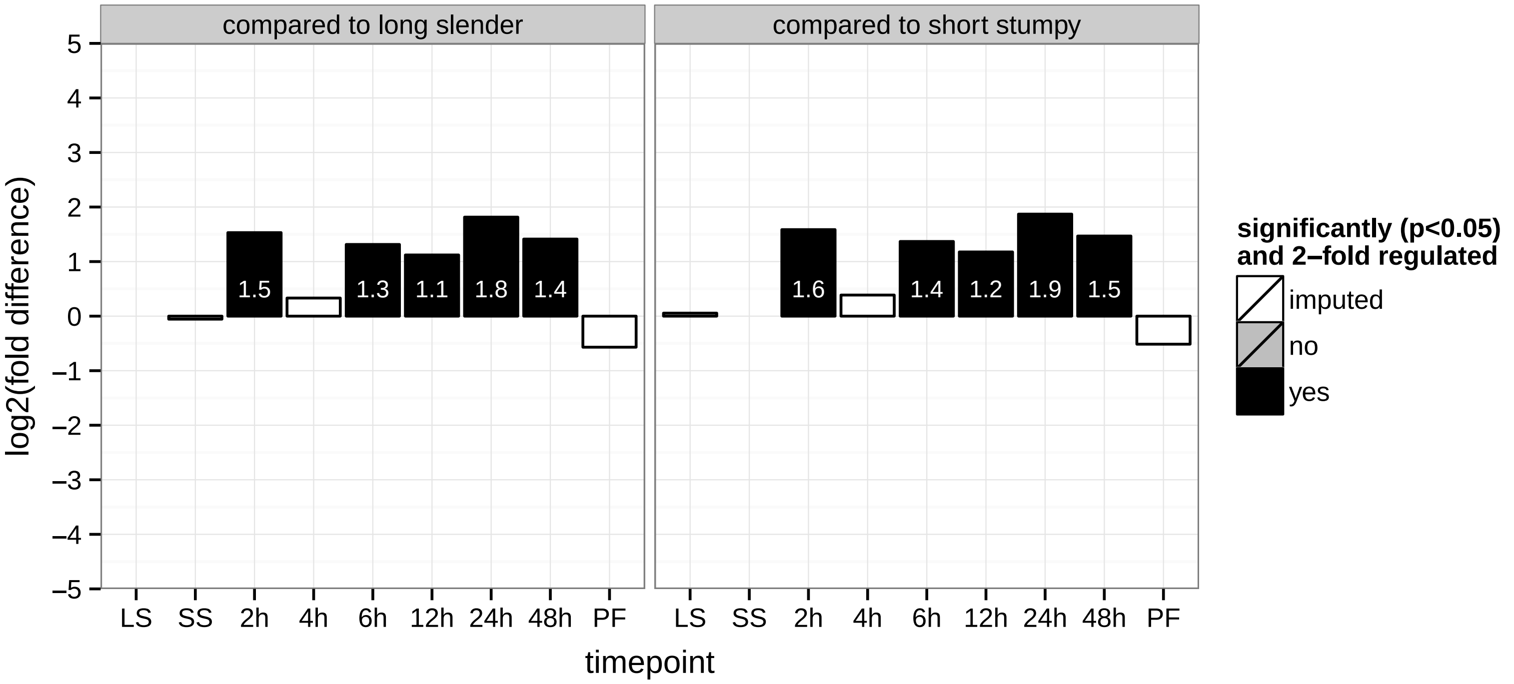
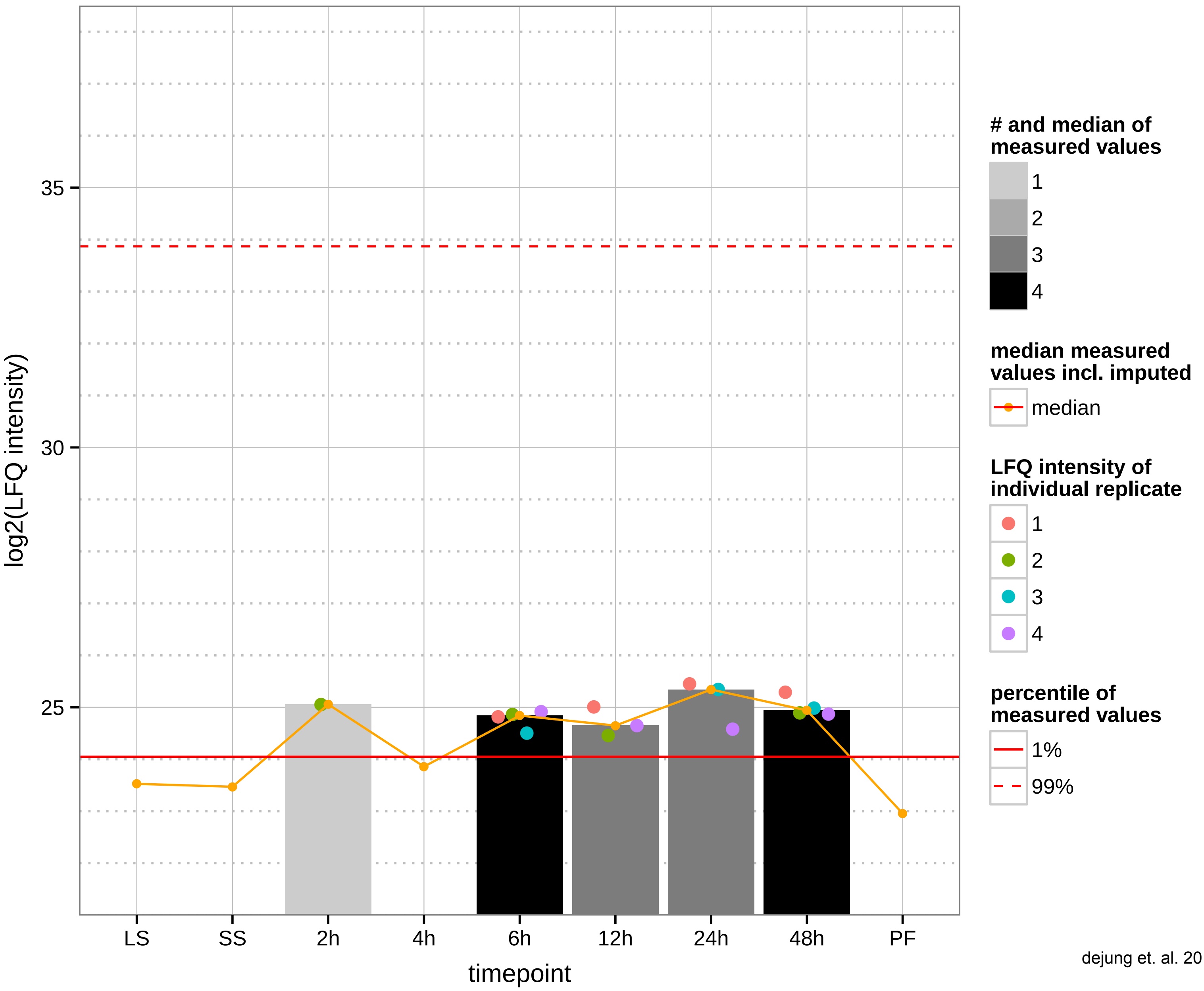
hypothetical protein, conserved
Tb927.3.1560
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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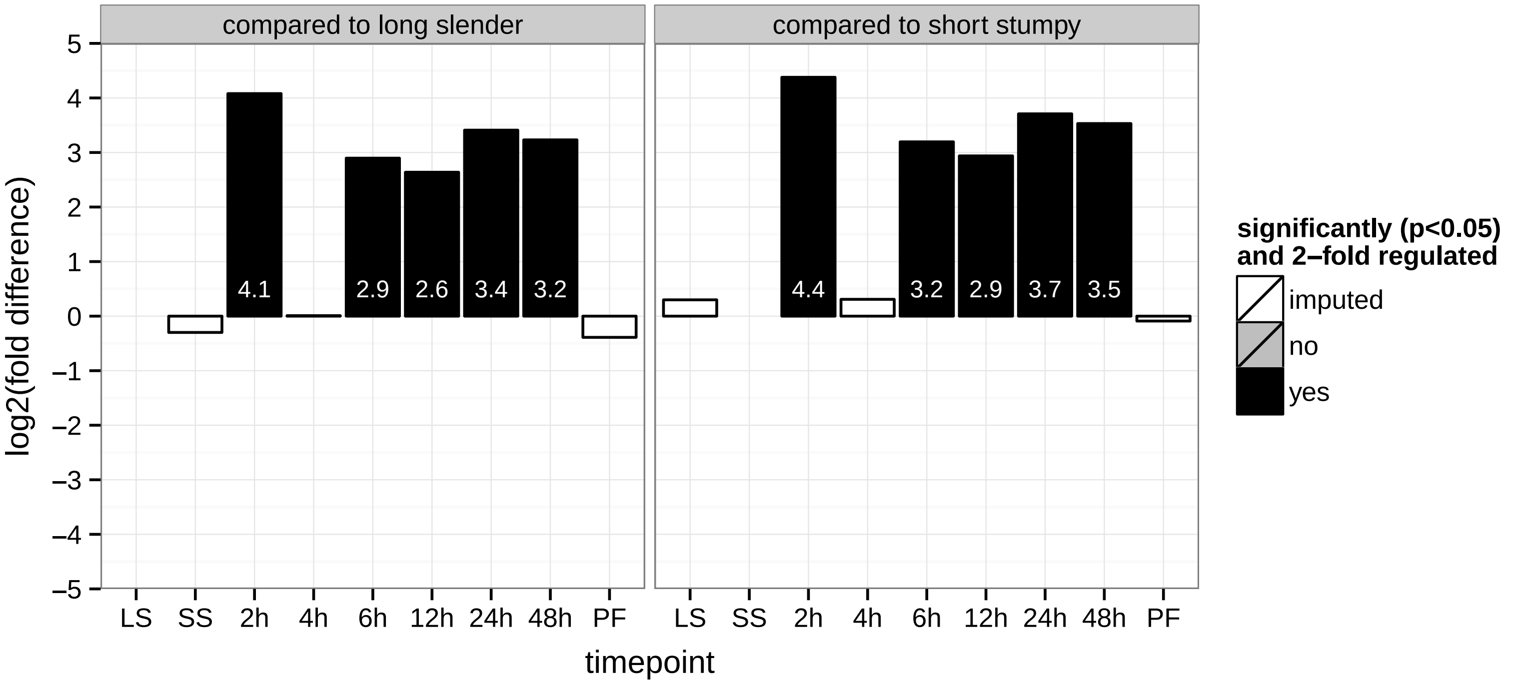
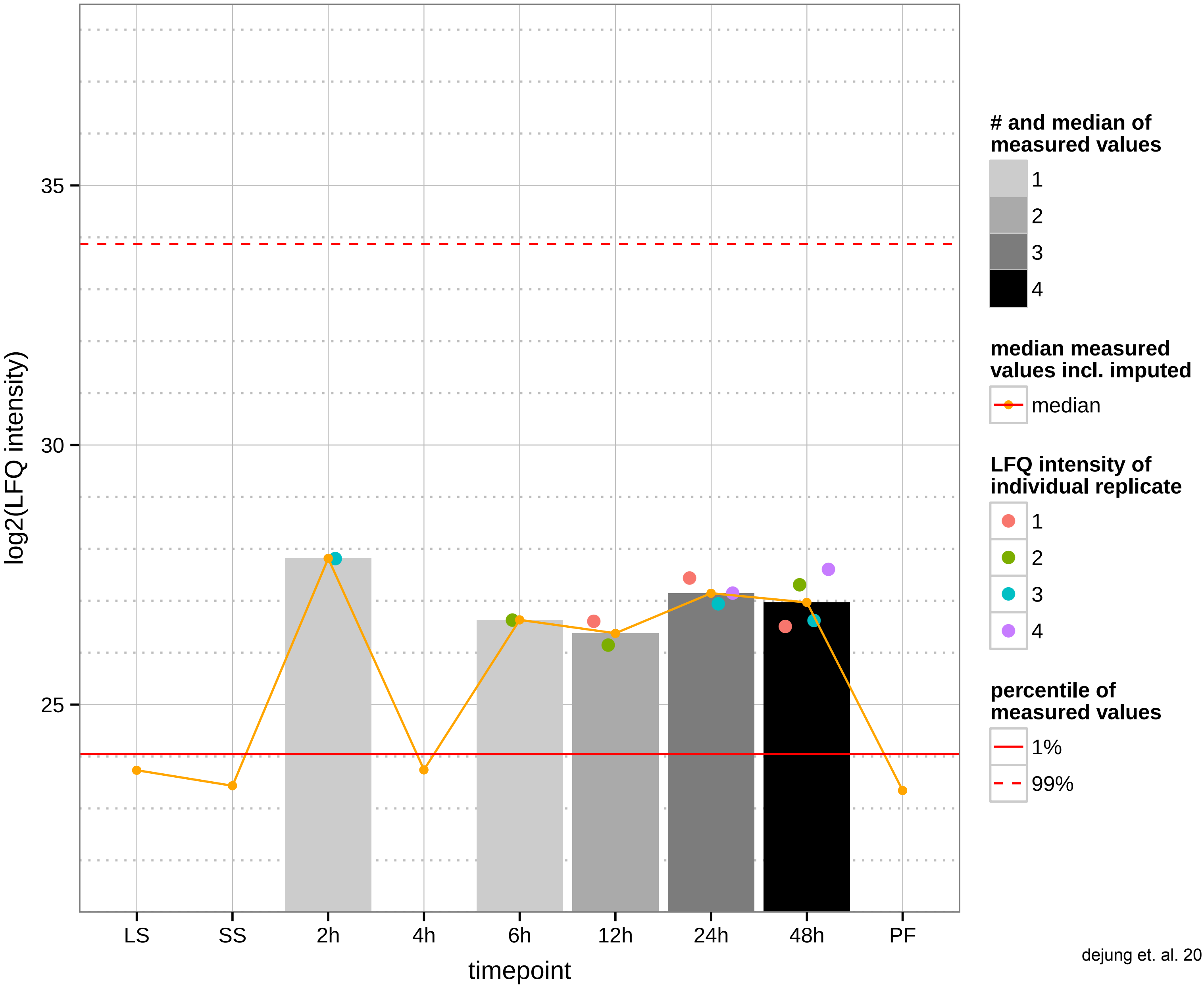
hypothetical protein, conserved
Tb927.7.3270
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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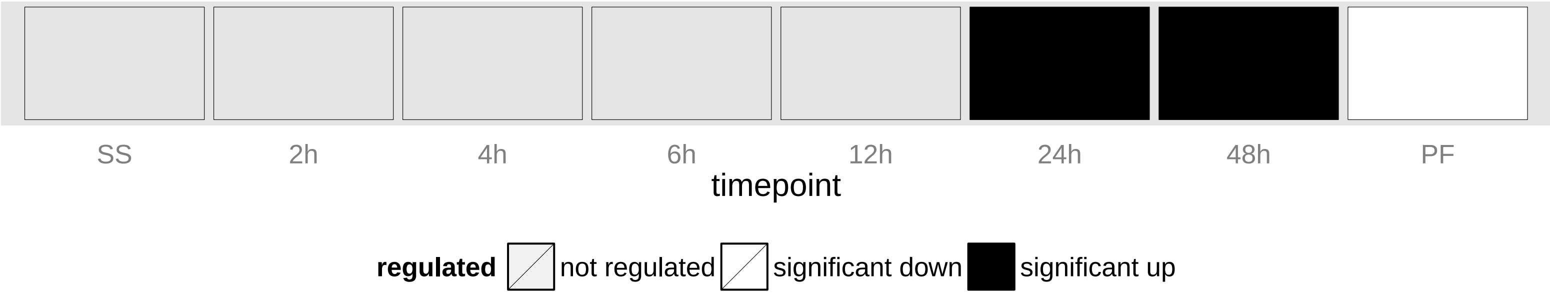

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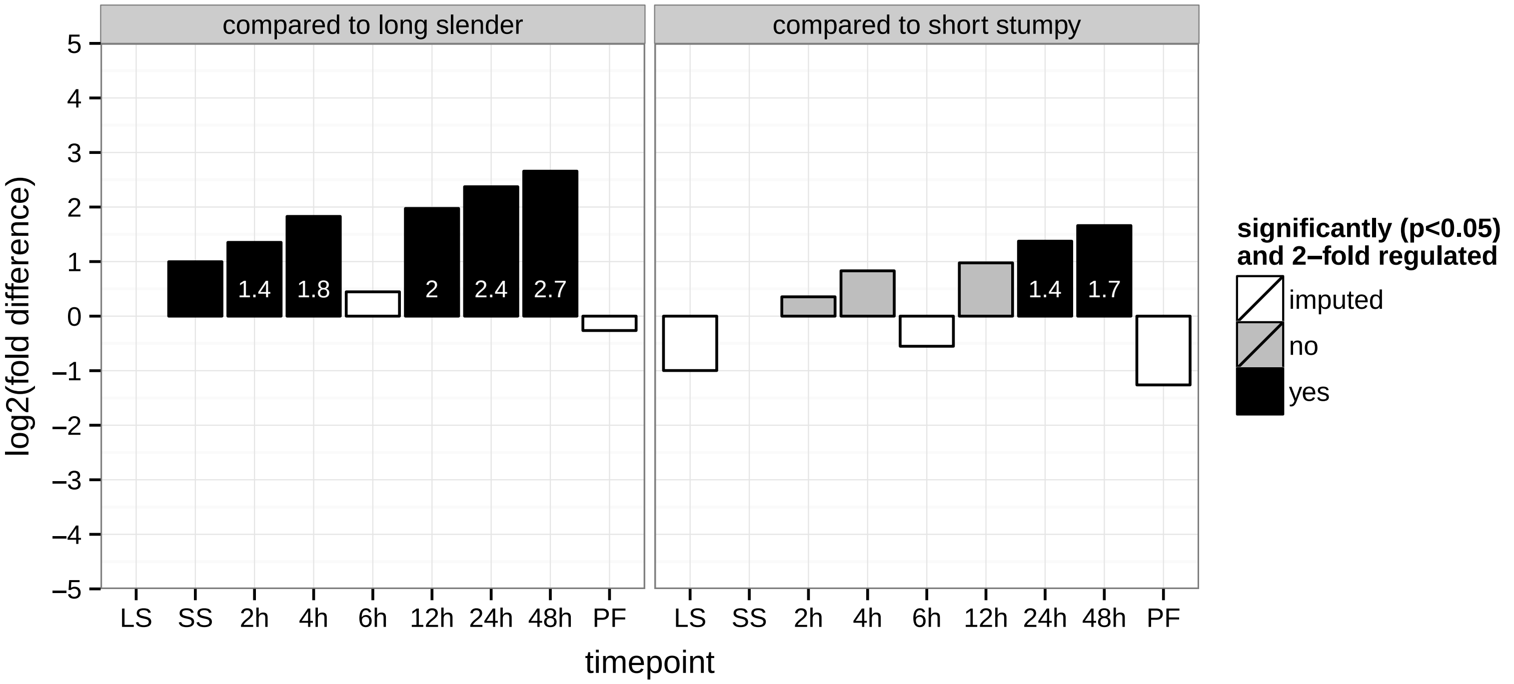
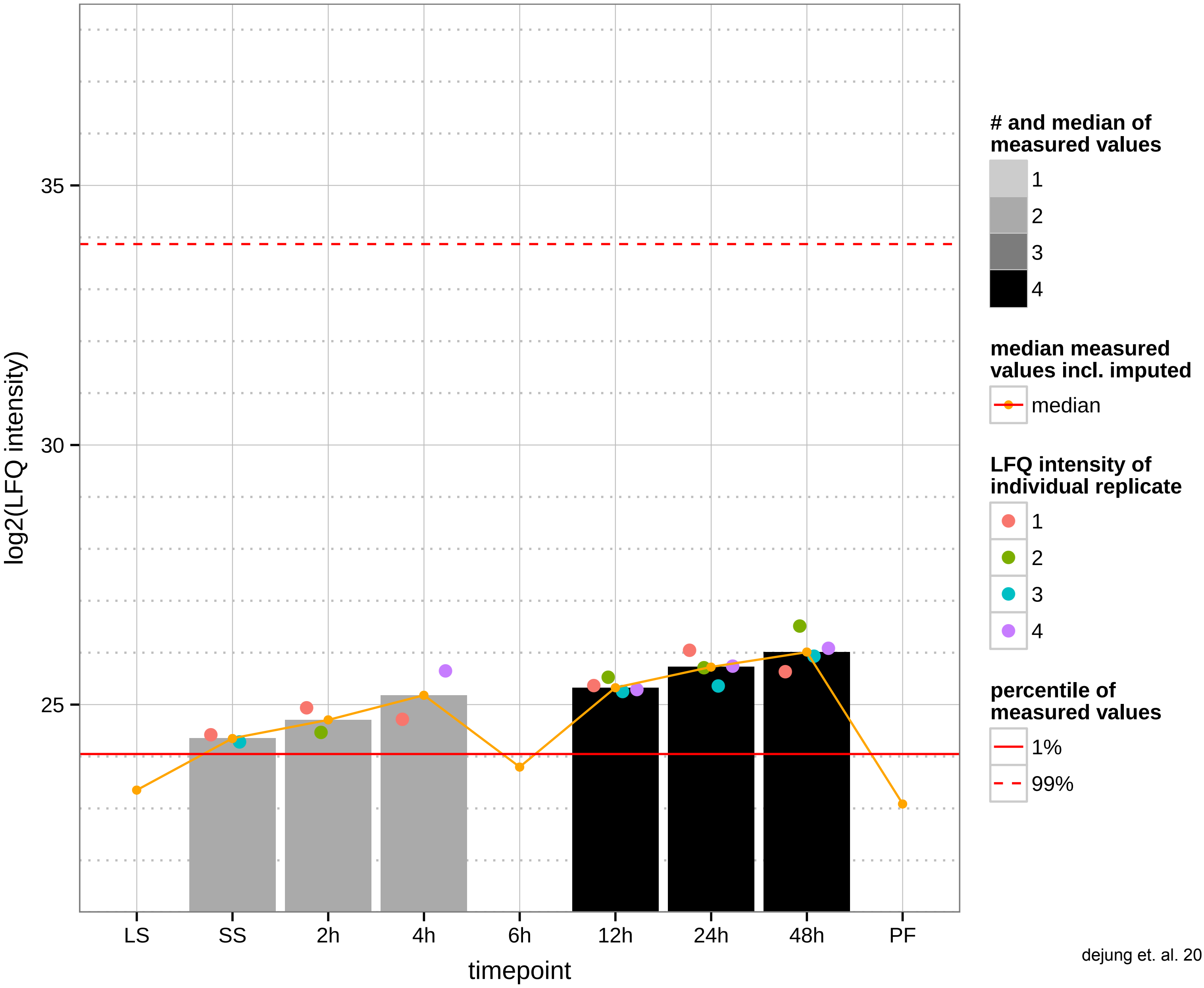
hypothetical protein, conserved
Tb927.10.15830
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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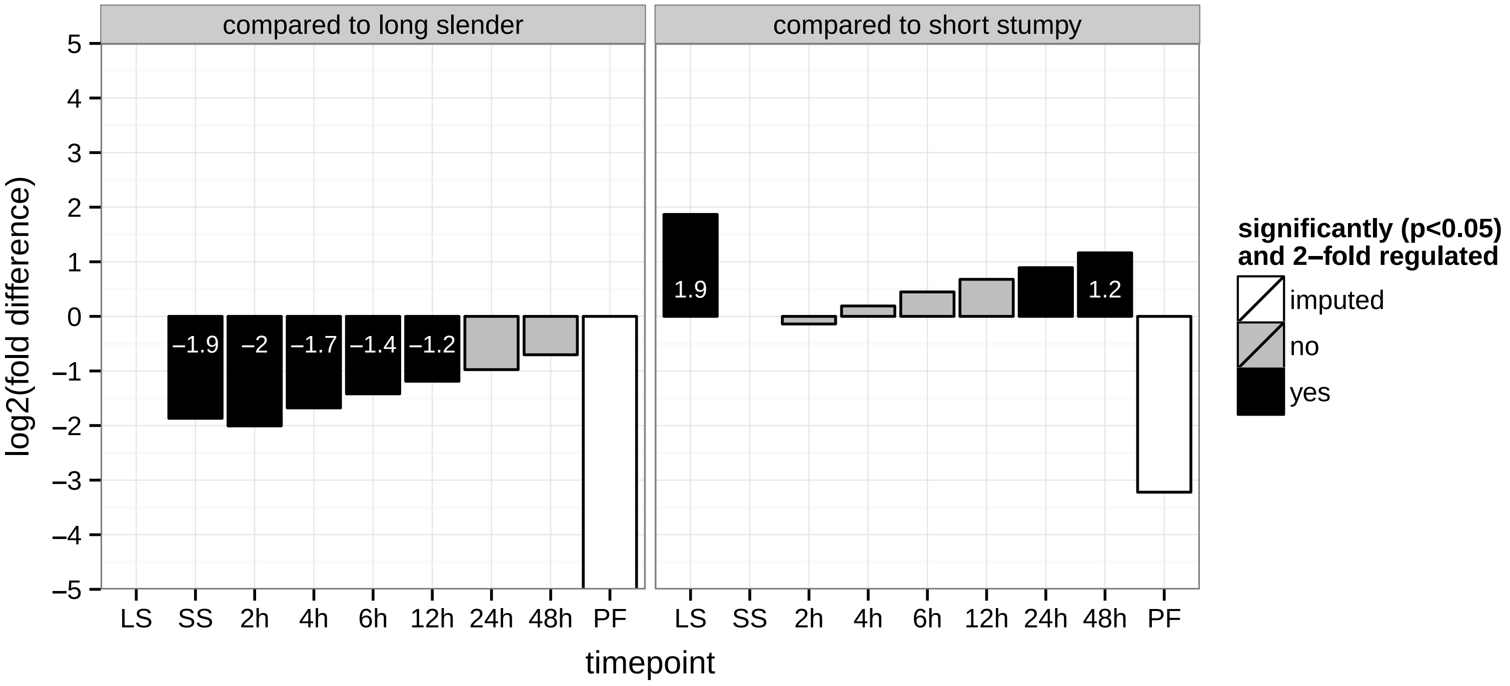
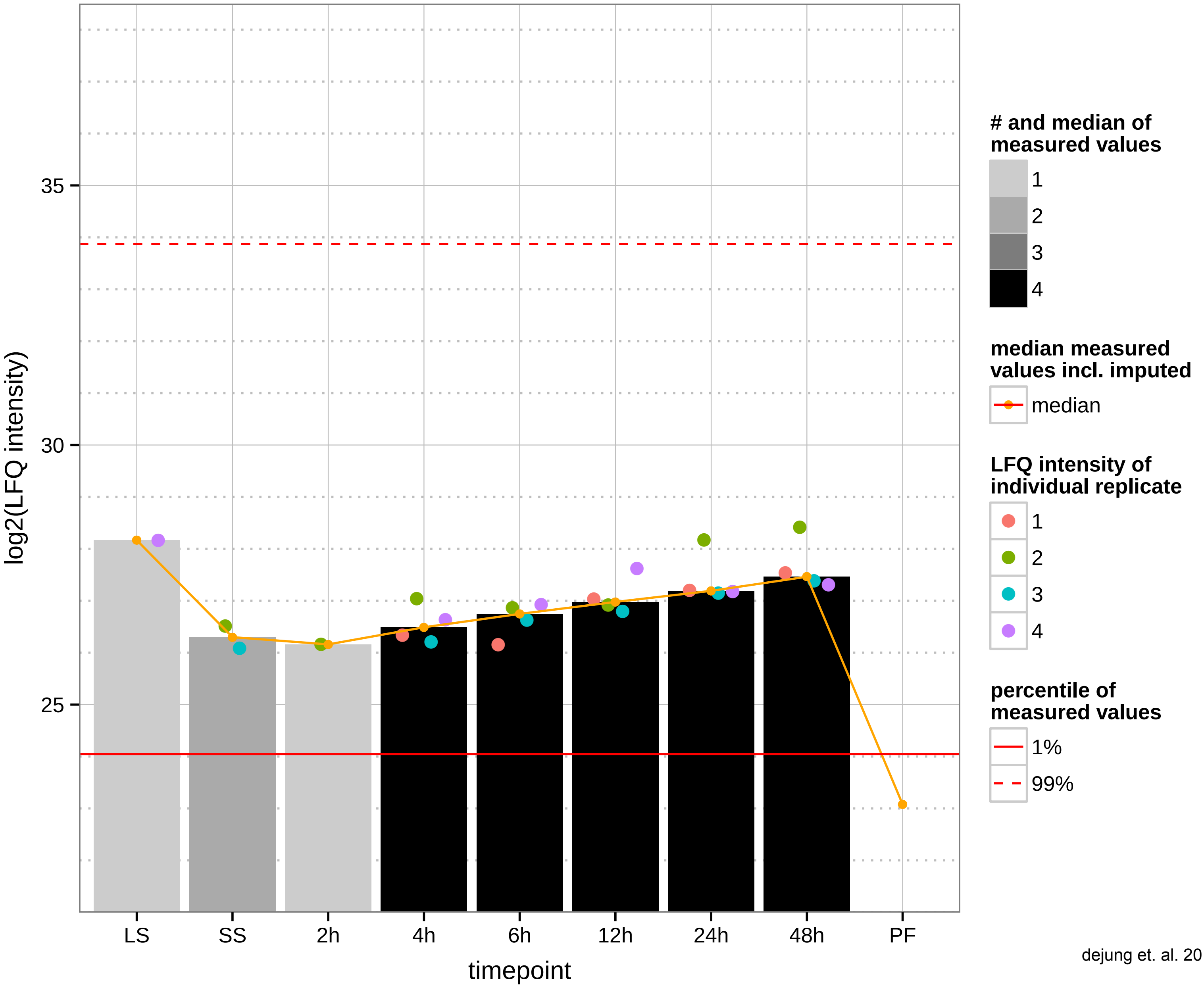
hypothetical protein, conserved
Tb927.5.1510
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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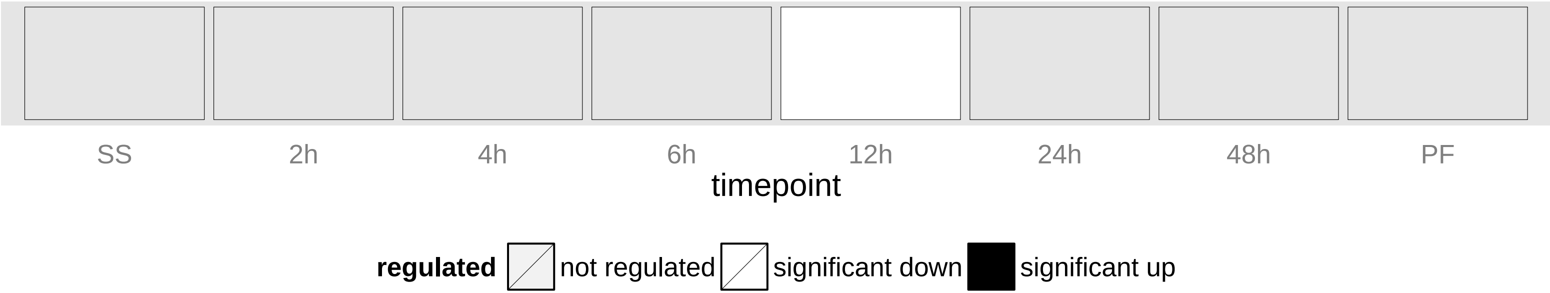

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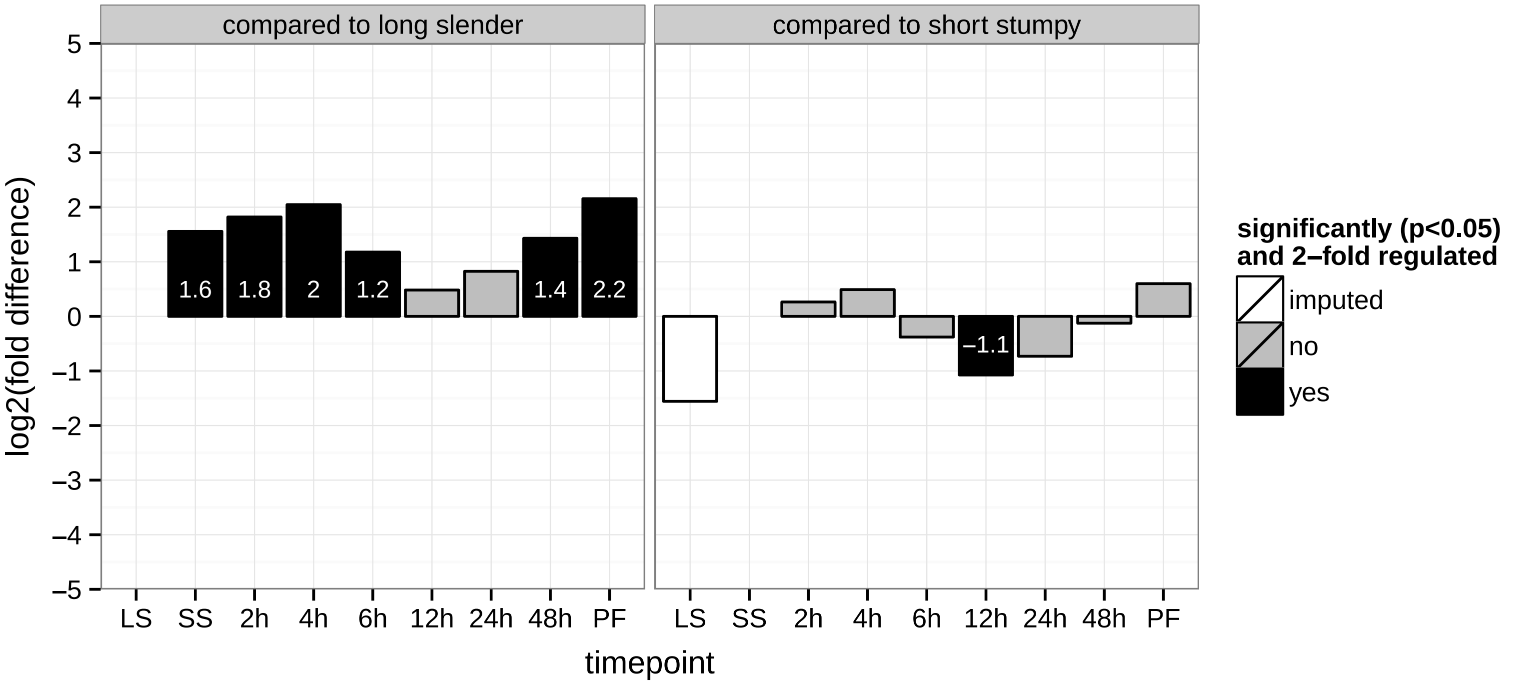
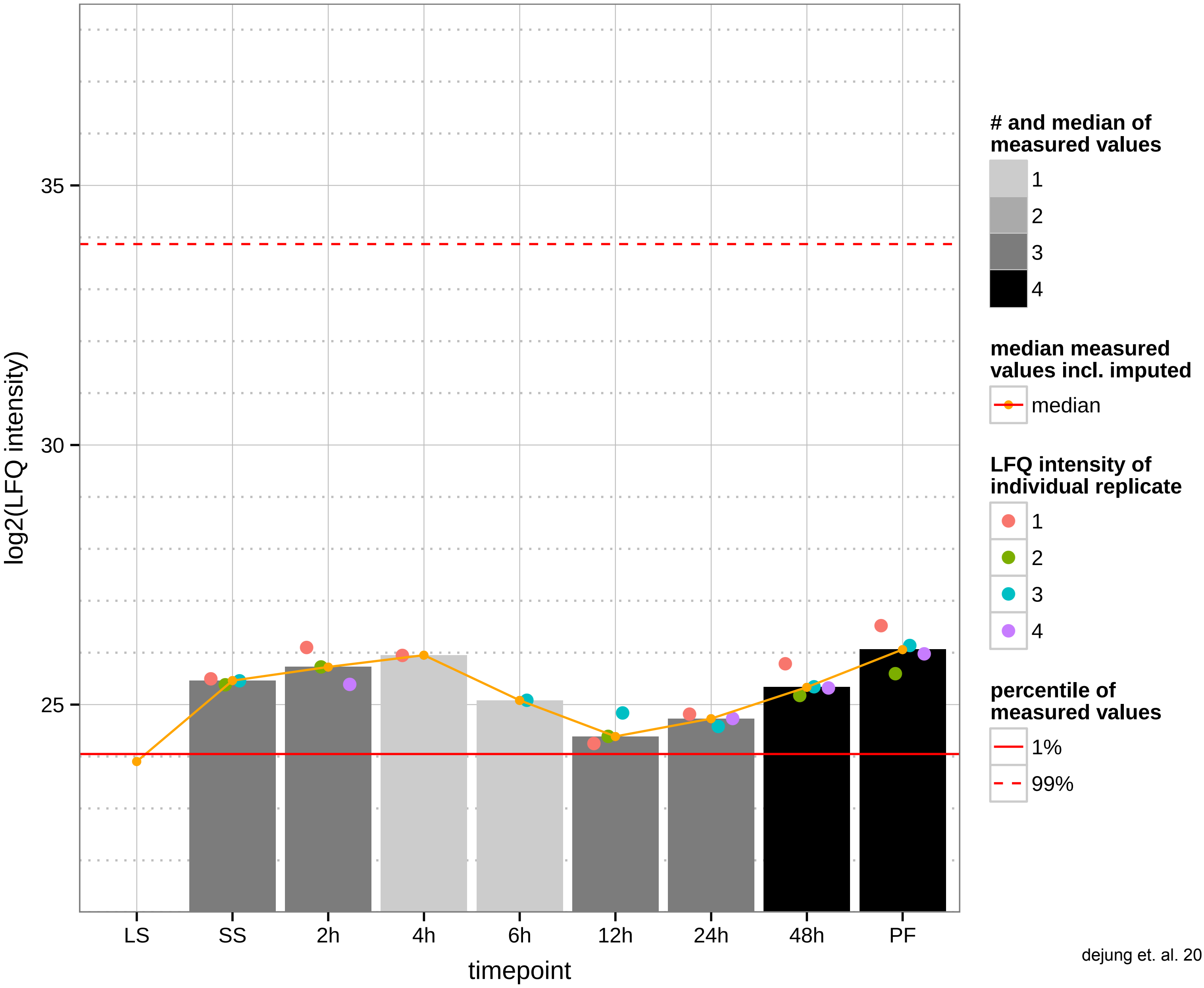
hypothetical protein, conserved
Tb927.10.12130
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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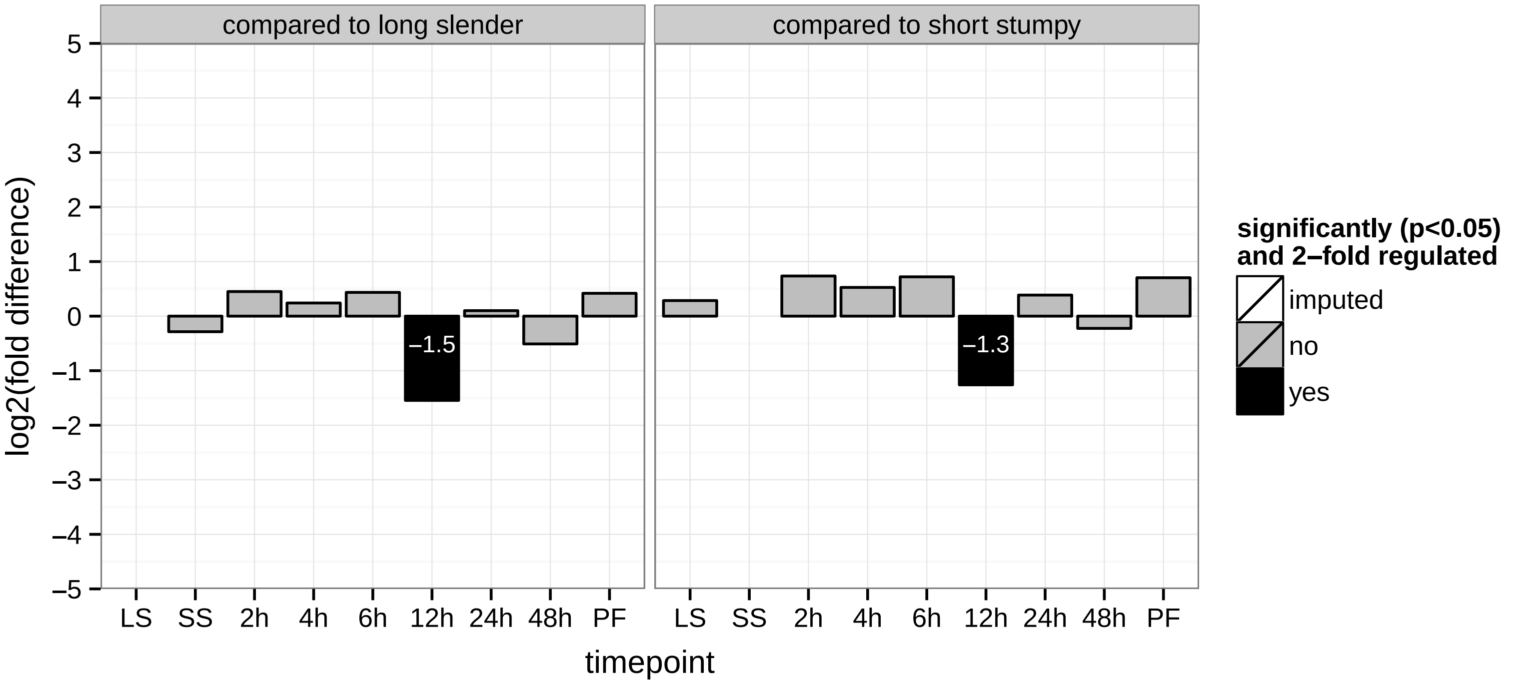
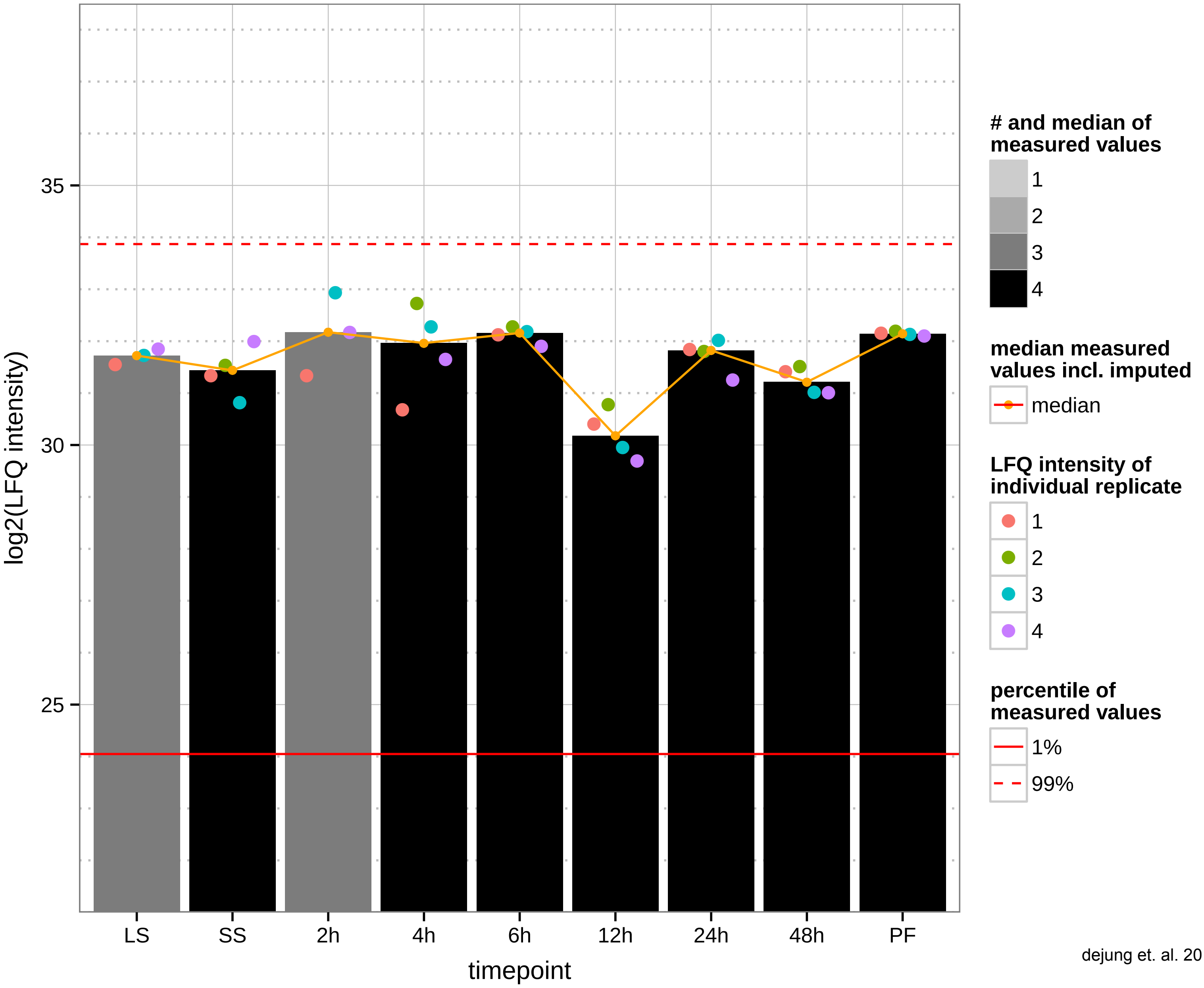
thymidylate kinase, putative
Tb927.8.3510;Tb927.8.3910;Tb11.v5.0738
AGOF: null, ATP binding, thymidylate kinase activity
AGOC: null
AGOP: null, TTP biosynthetic process, dTDP biosynthetic process, pyrimidine–containing compound salvage
PGOF: null
PGOC: null
PGOP: null





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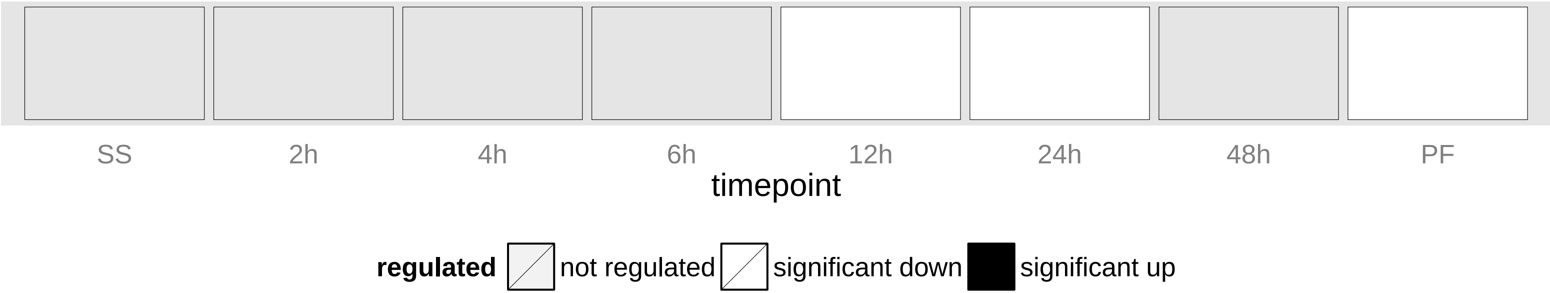

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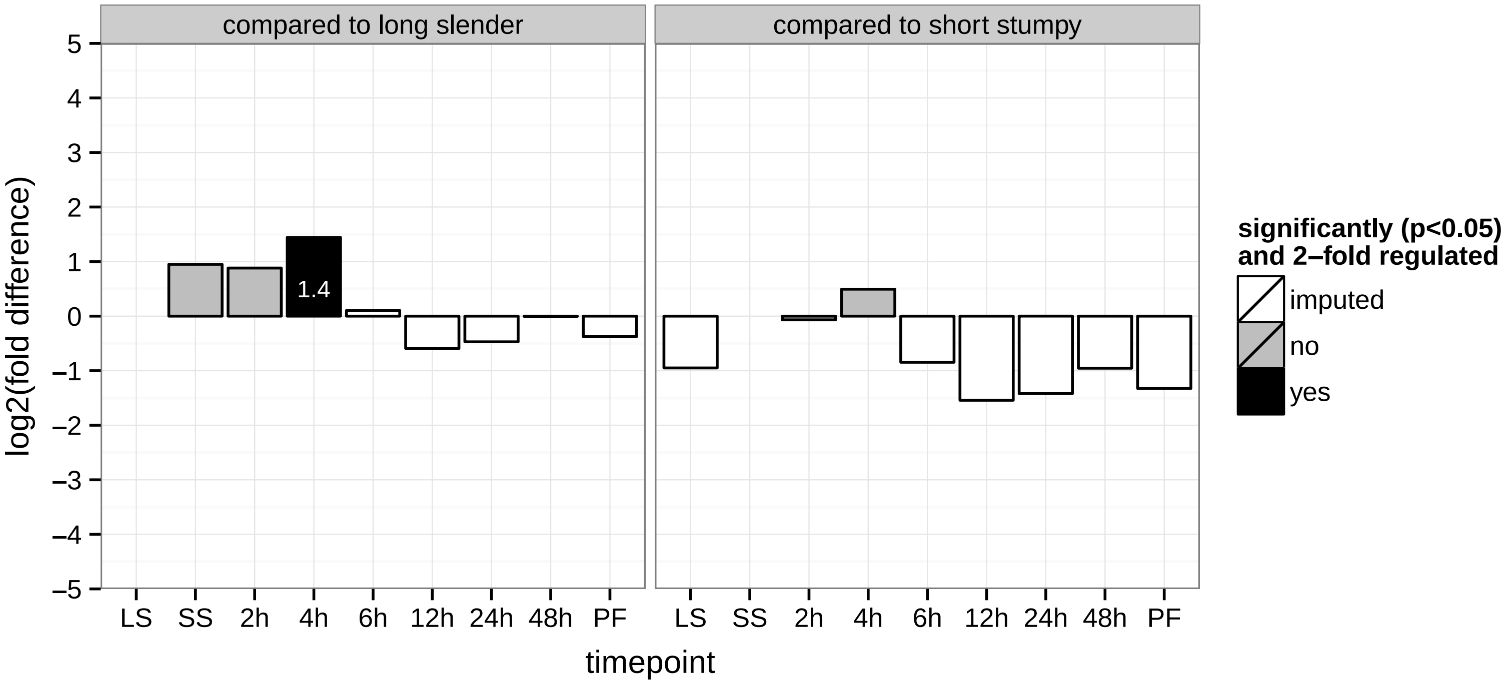
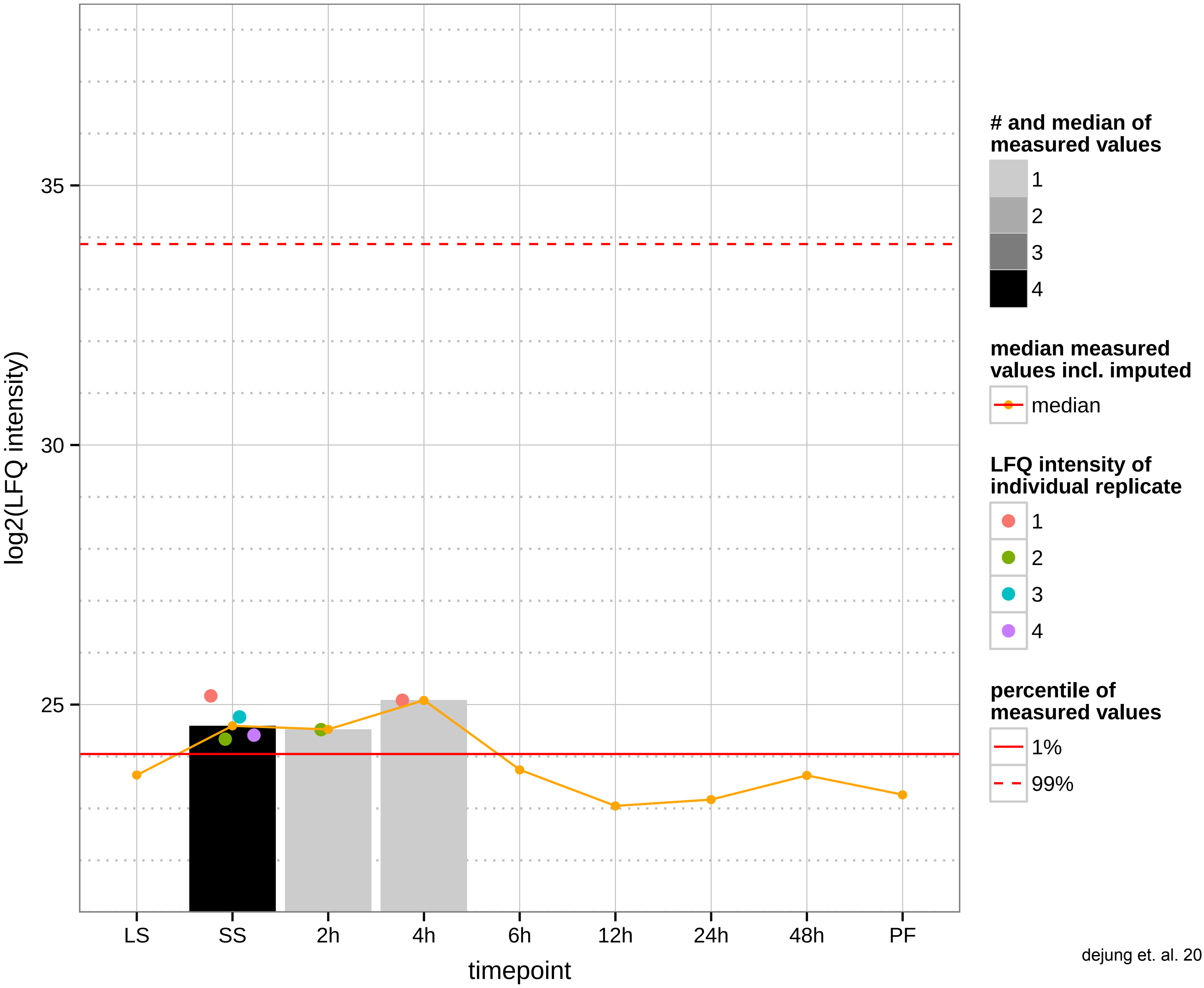
mitochondrial carrier protein (MCP20)
Tb927.10.14280
AGOF: null
AGOC: membrane, mitochondrion
AGOP: transport
PGOF: null
PGOC: null
PGOP: null





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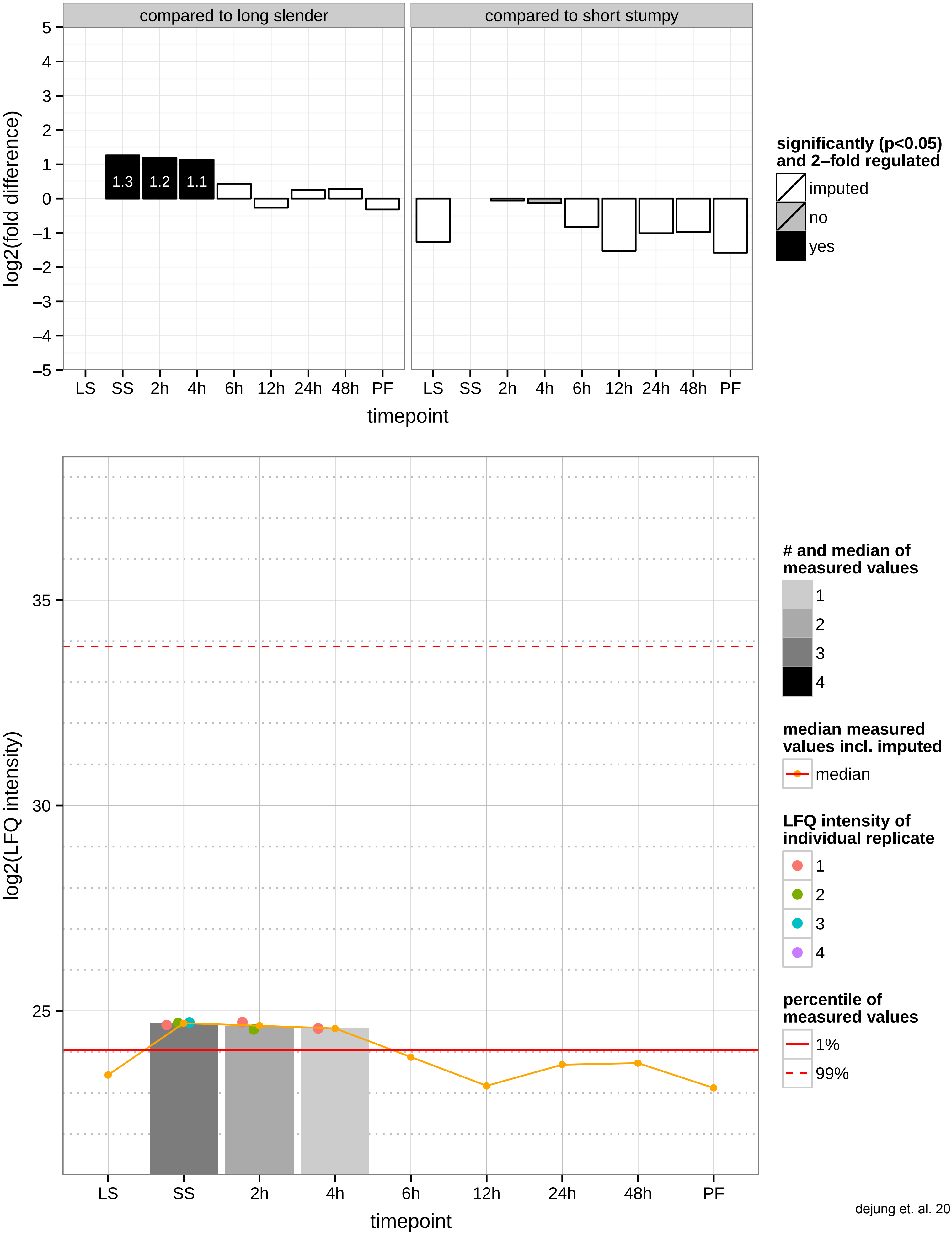
hypothetical protein, conserved
Tb927.11.5770
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



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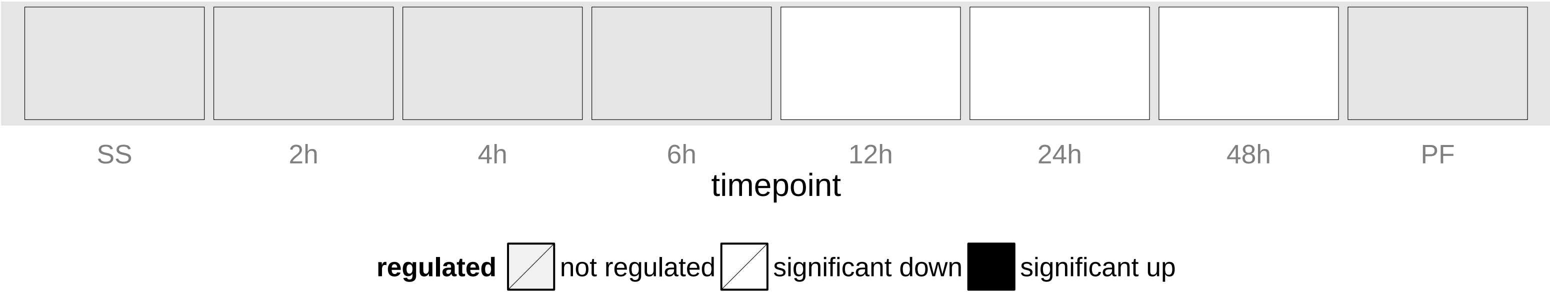

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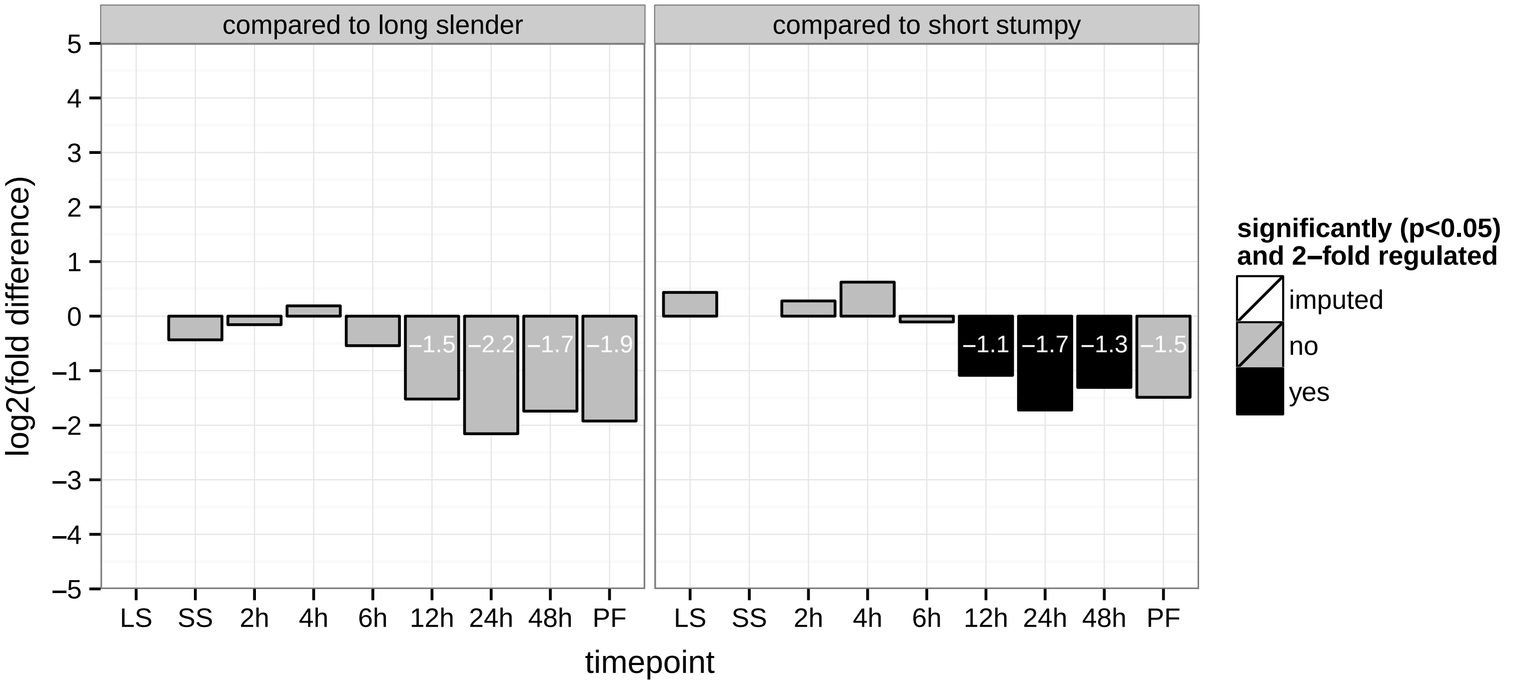
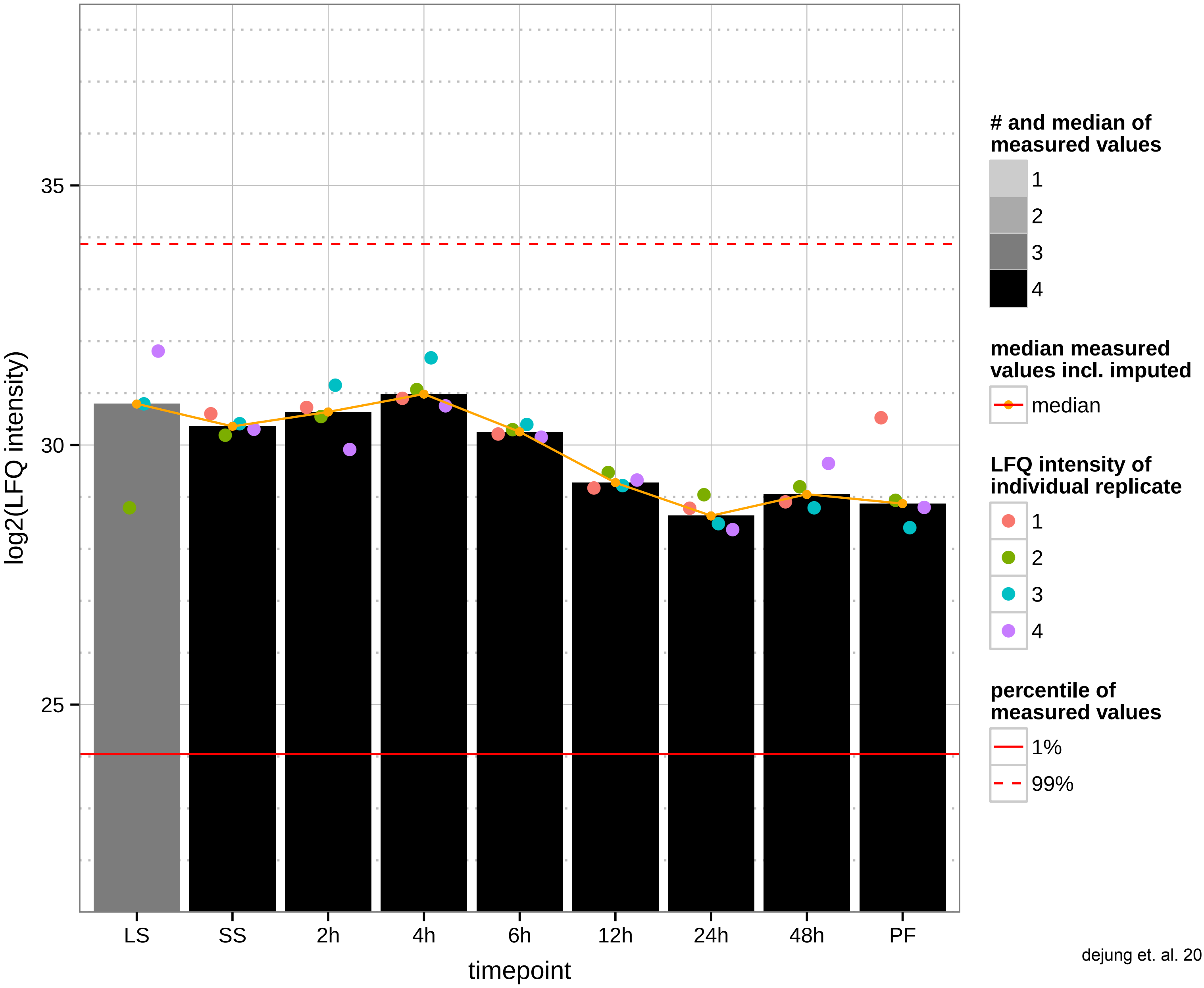
vacuolar protein sorting–associated protein 45, putative (VPS45)
Tb927.10.6780
AGOF: SNARE binding
AGOC: null
AGOP: vesicle docking involved in exocytosis, vesicle–mediated transport
PGOF: null
PGOC: null
PGOP: vesicle docking involved in exocytosis, vesicle–mediated transport





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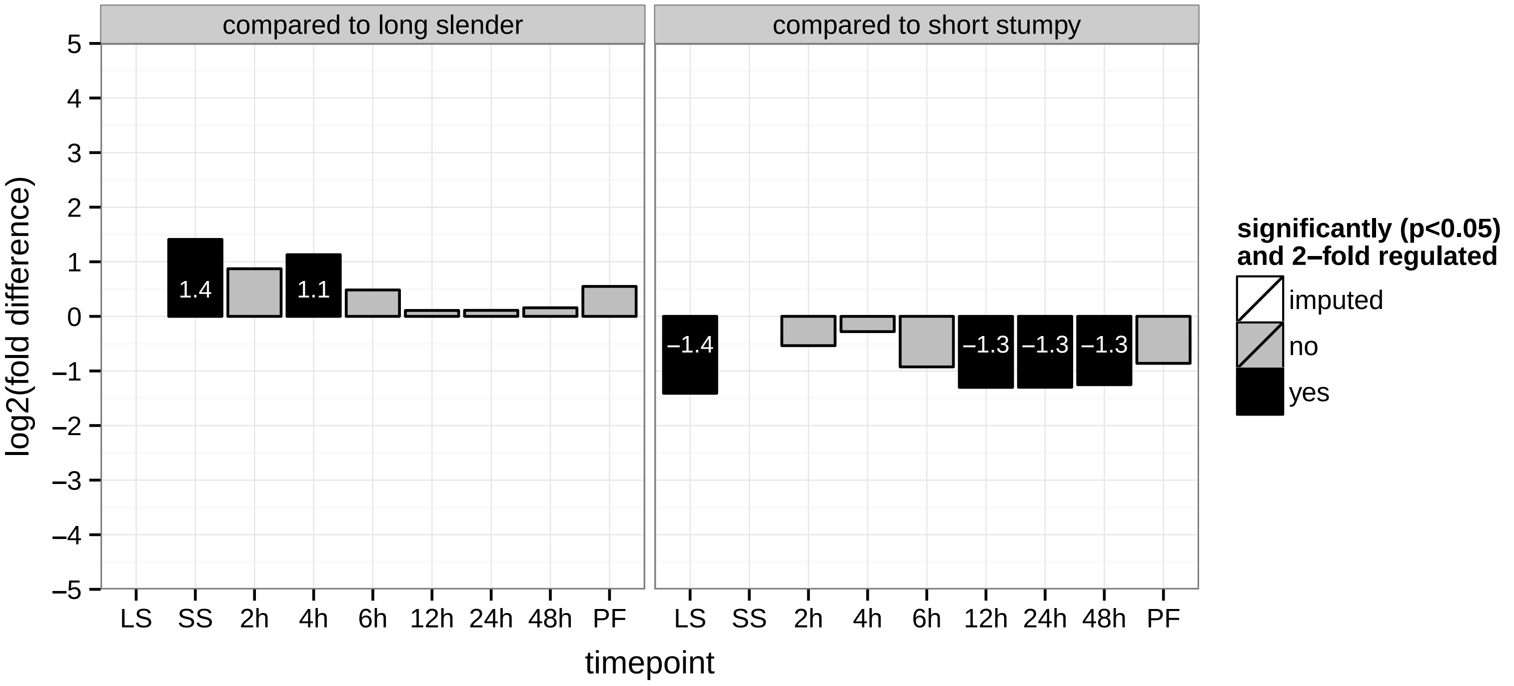
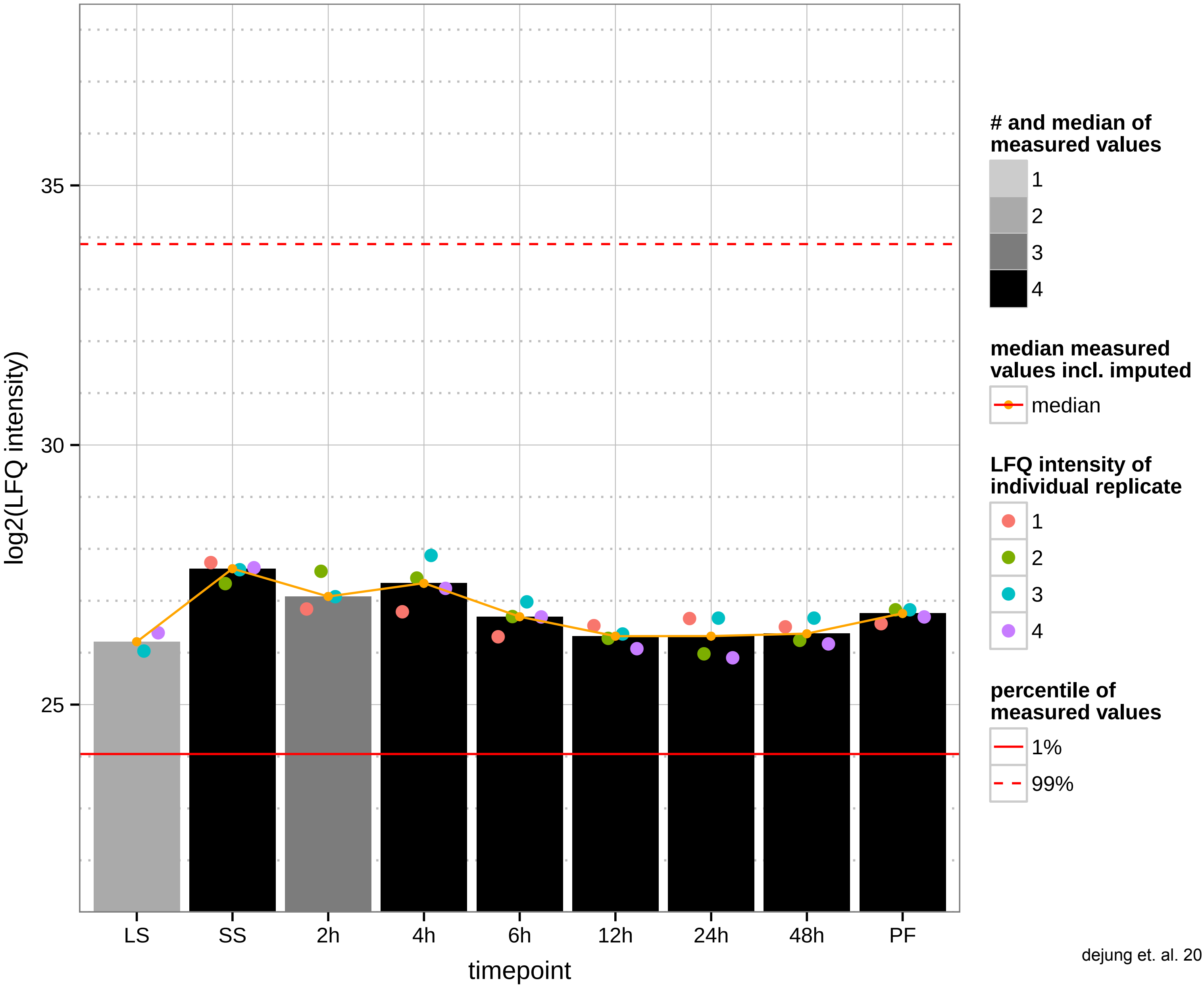
engulfment and cell motility domain 2, putative
Tb927.9.2670
AGOF: null
AGOC: cytoskeleton
AGOP: phagocytosis
PGOF: null
PGOC: cytoskeleton
PGOP: phagocytosis





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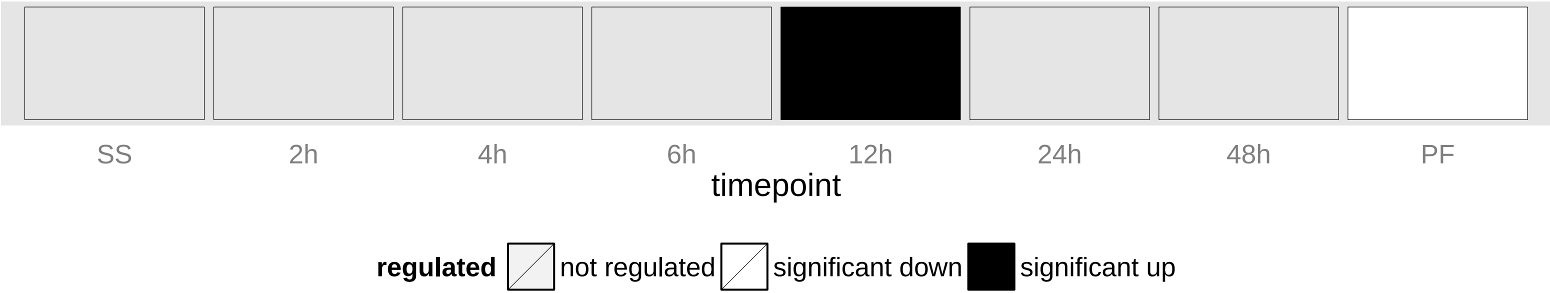

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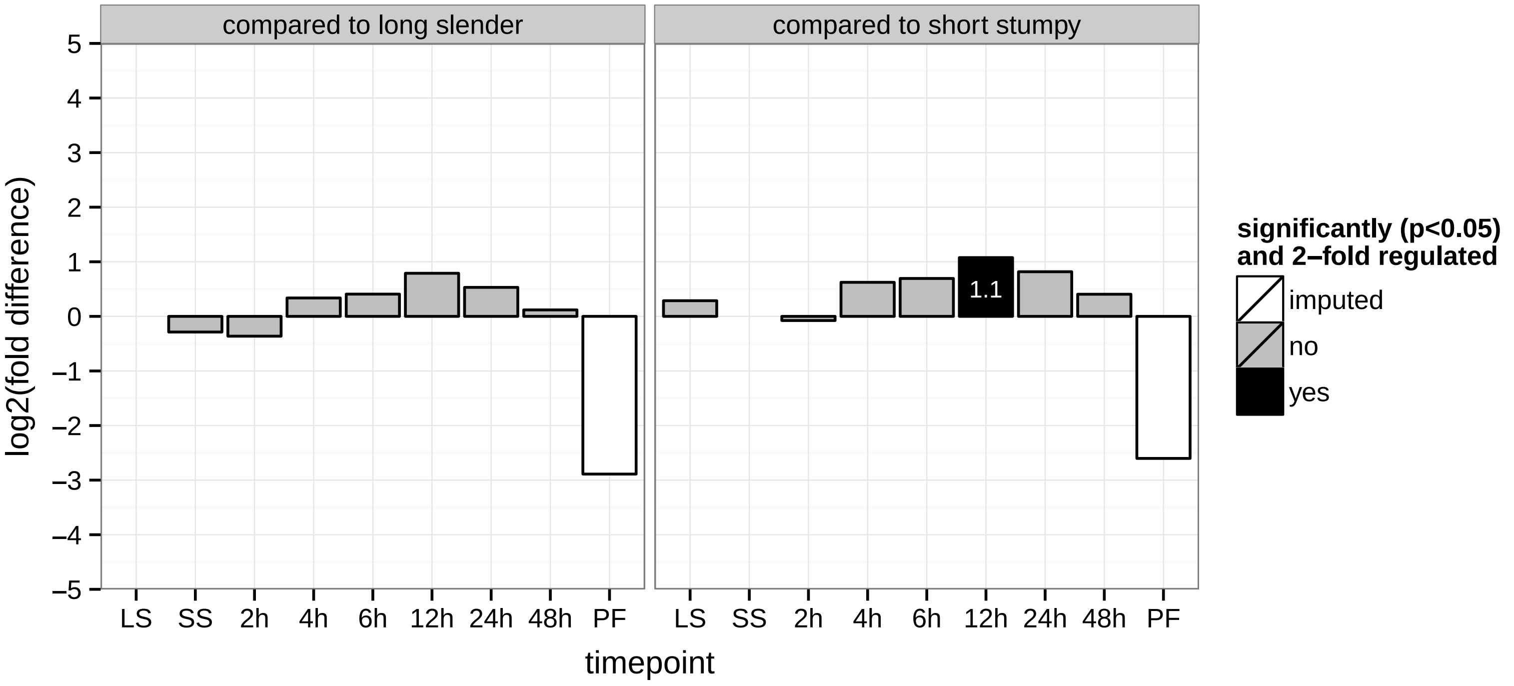
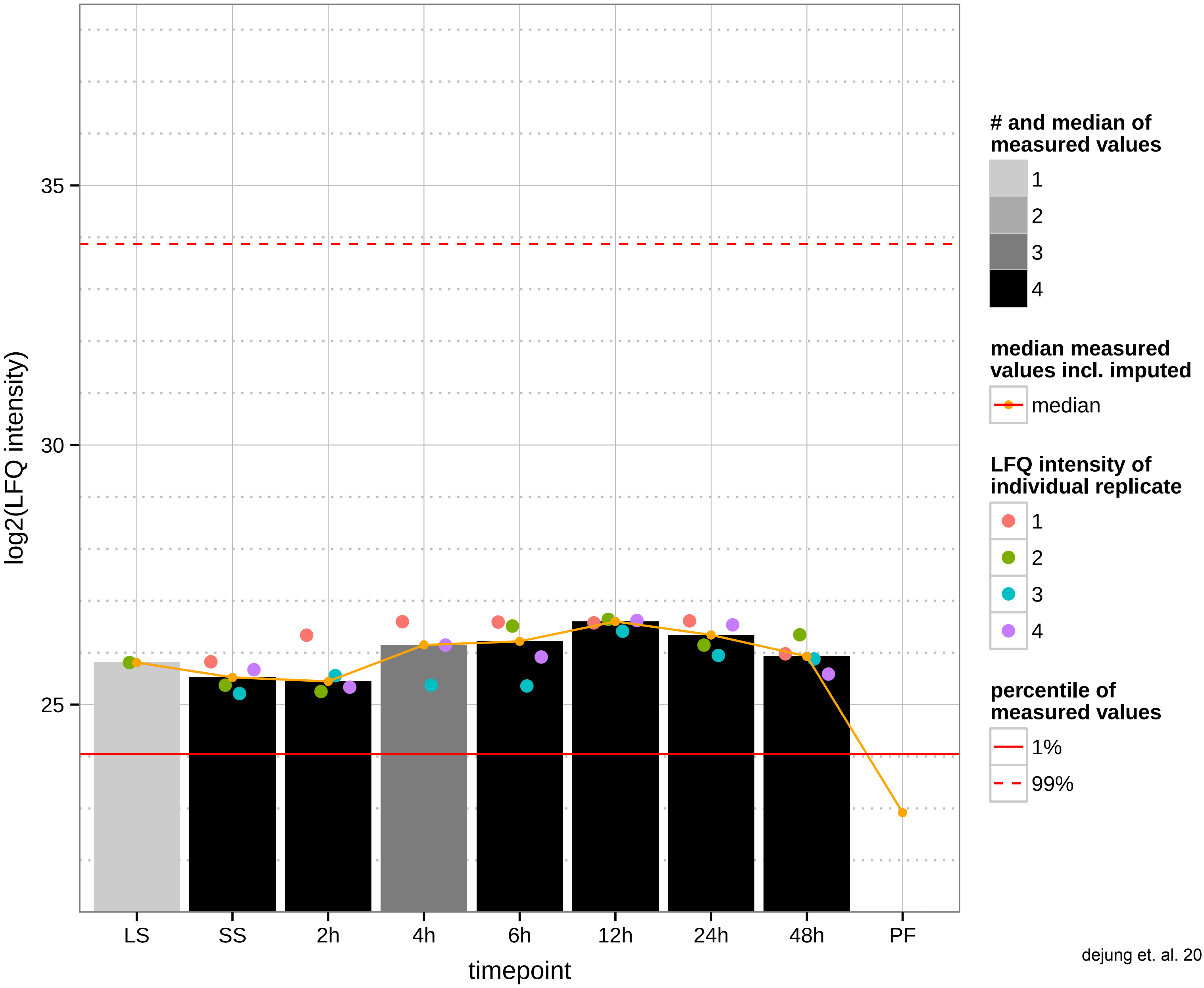
Ribosomal RNA–processing protein 8, putative (RRP8)
Tb927.1.1120
AGOF: methyltransferase activity
AGOC: null
AGOP: null
PGOF: methyltransferase activity
PGOC: null
PGOP: null





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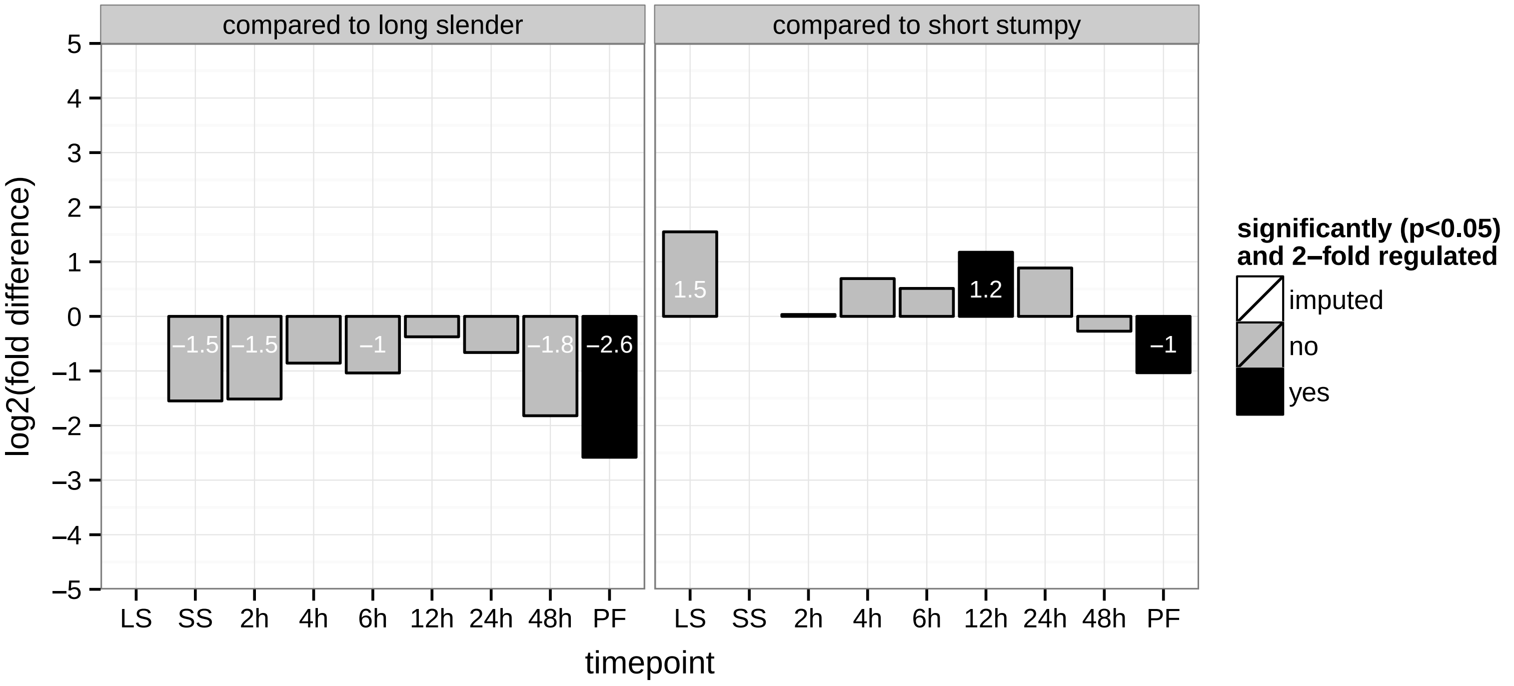
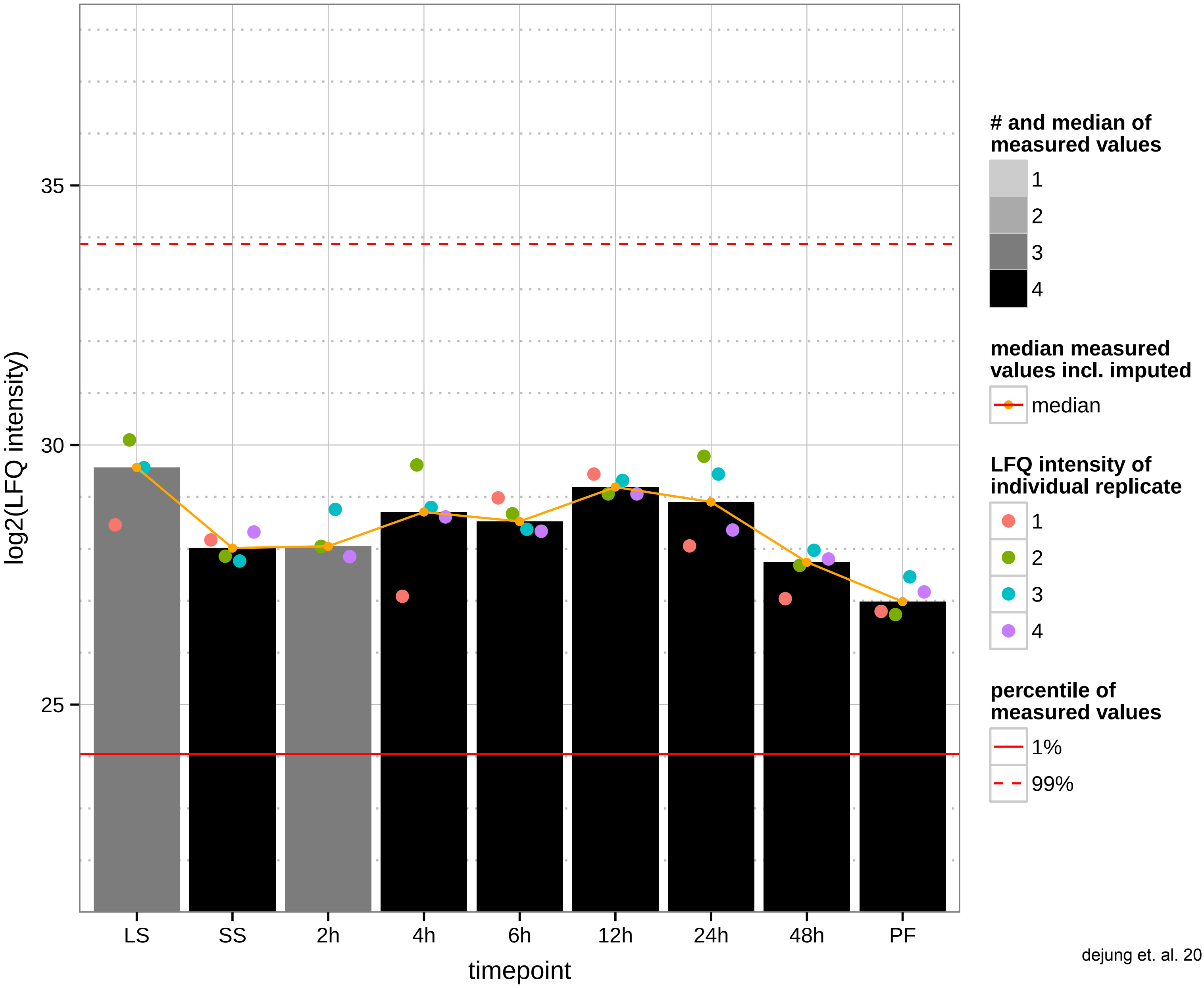
IgE−dependent histamine−releasing factor, putative
Tb927.8.6760
AGOF: null
AGOC: cytoplasm
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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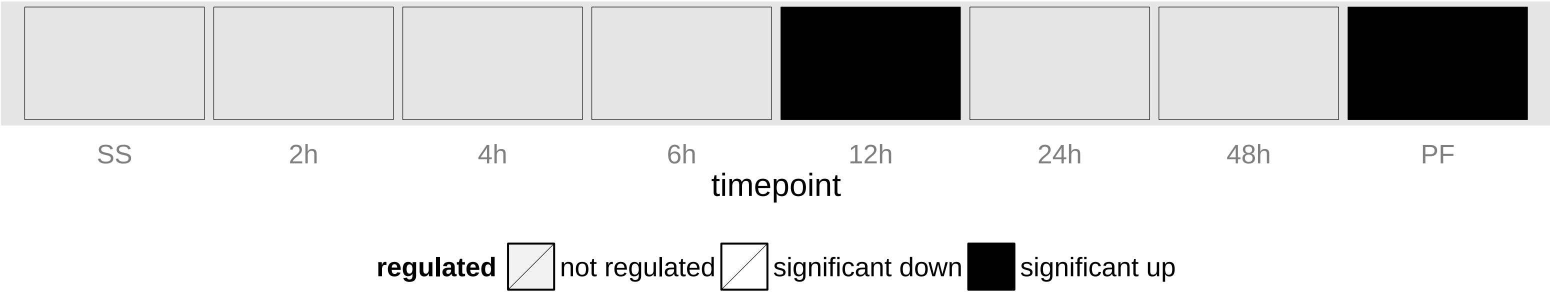

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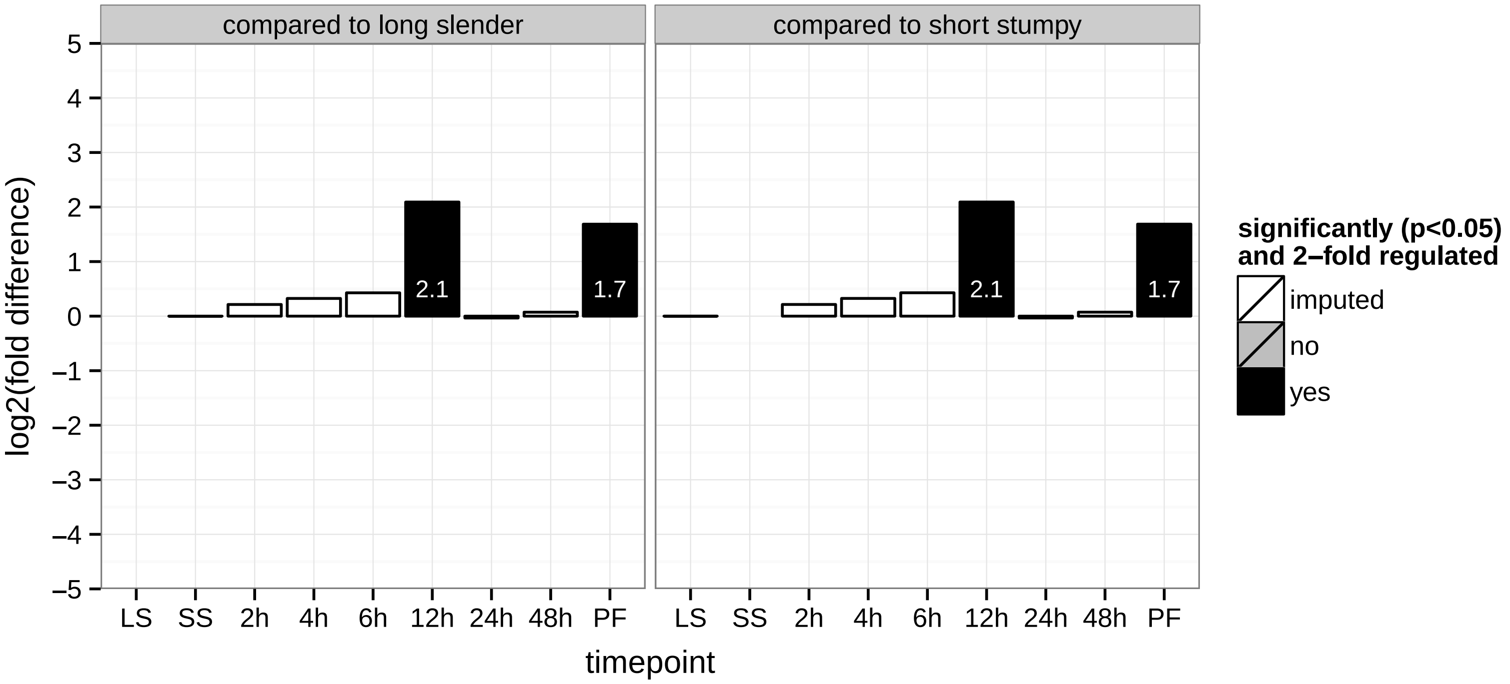
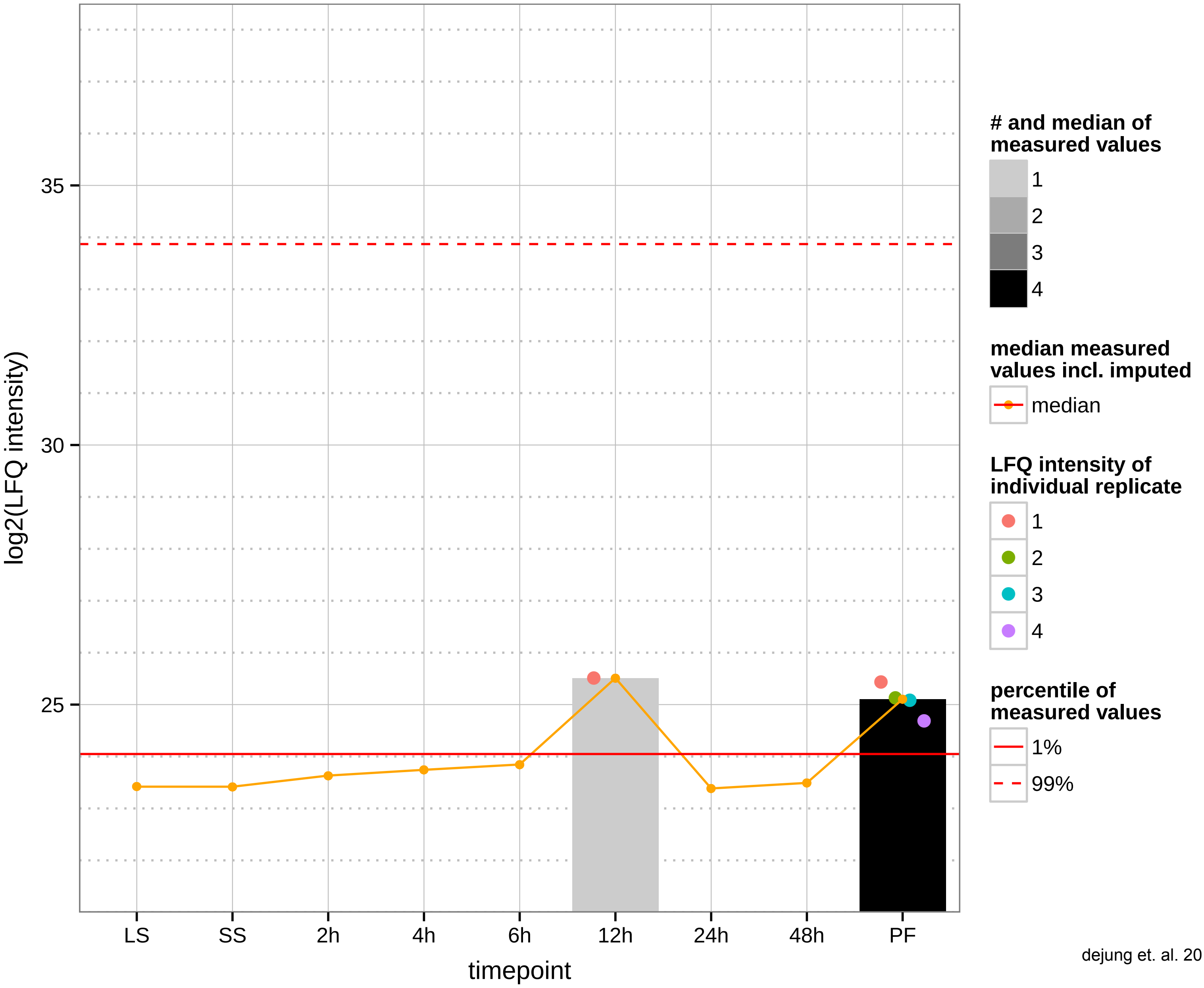
chaperone protein DNAj, putative
Tb11.v5.0778;Tb927.7.680
AGOF: null, heat shock protein binding, unfolded protein binding
AGOC: null
AGOP: null, protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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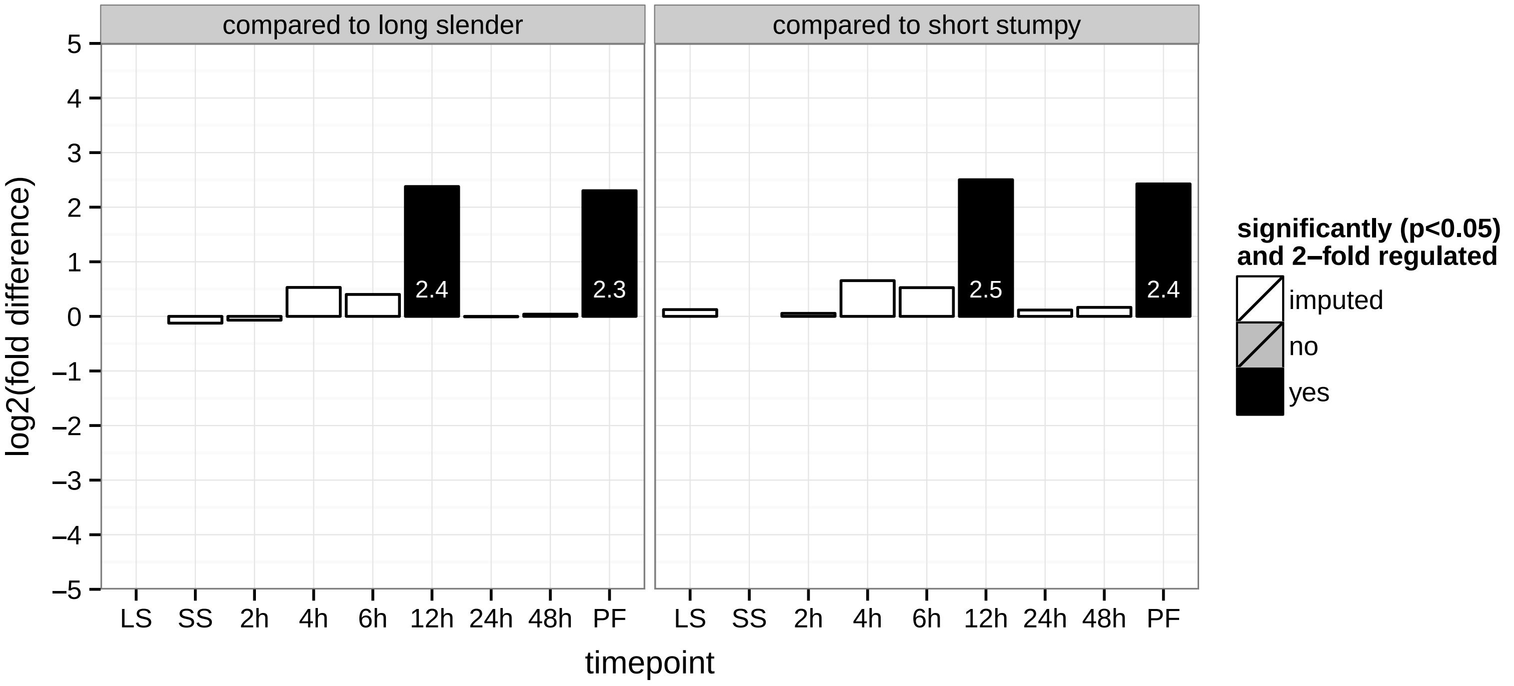
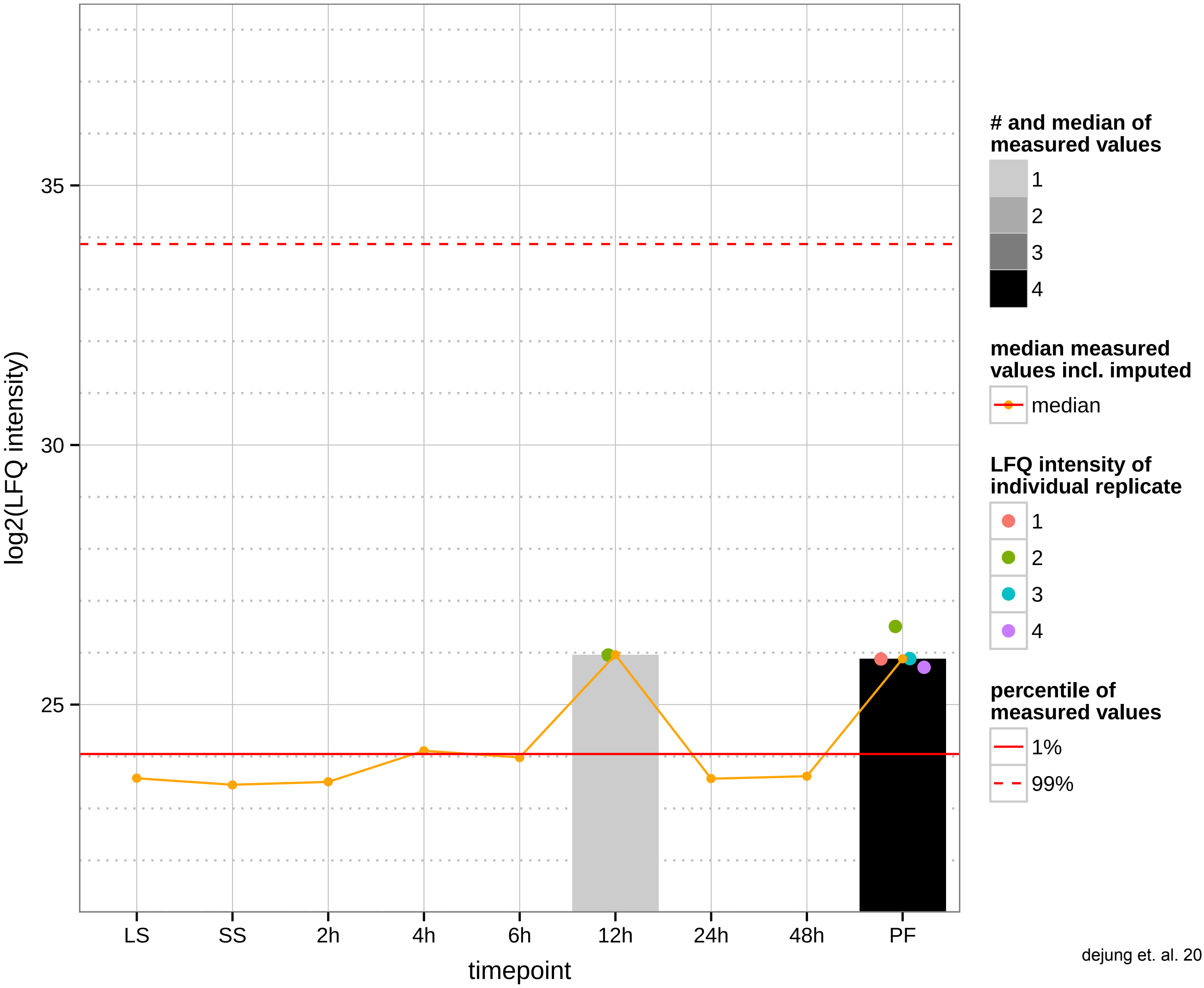
hypothetical protein, conserved
Tb927.11.13660
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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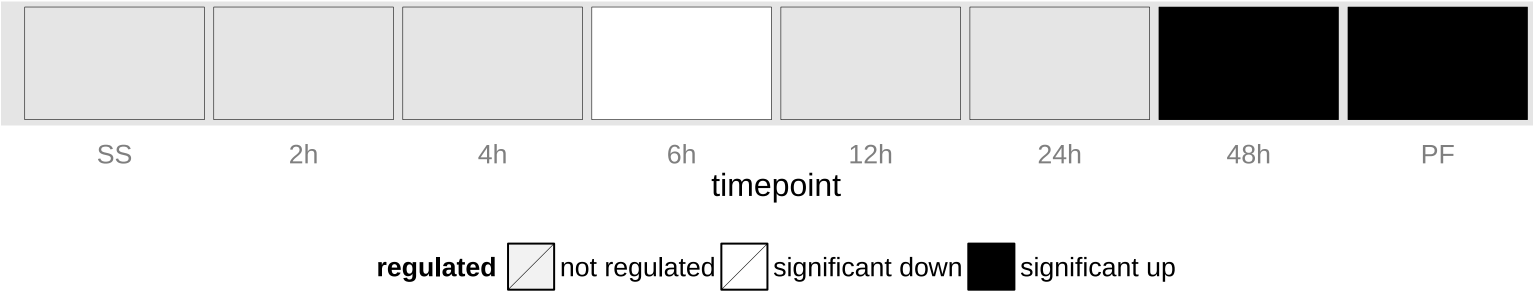

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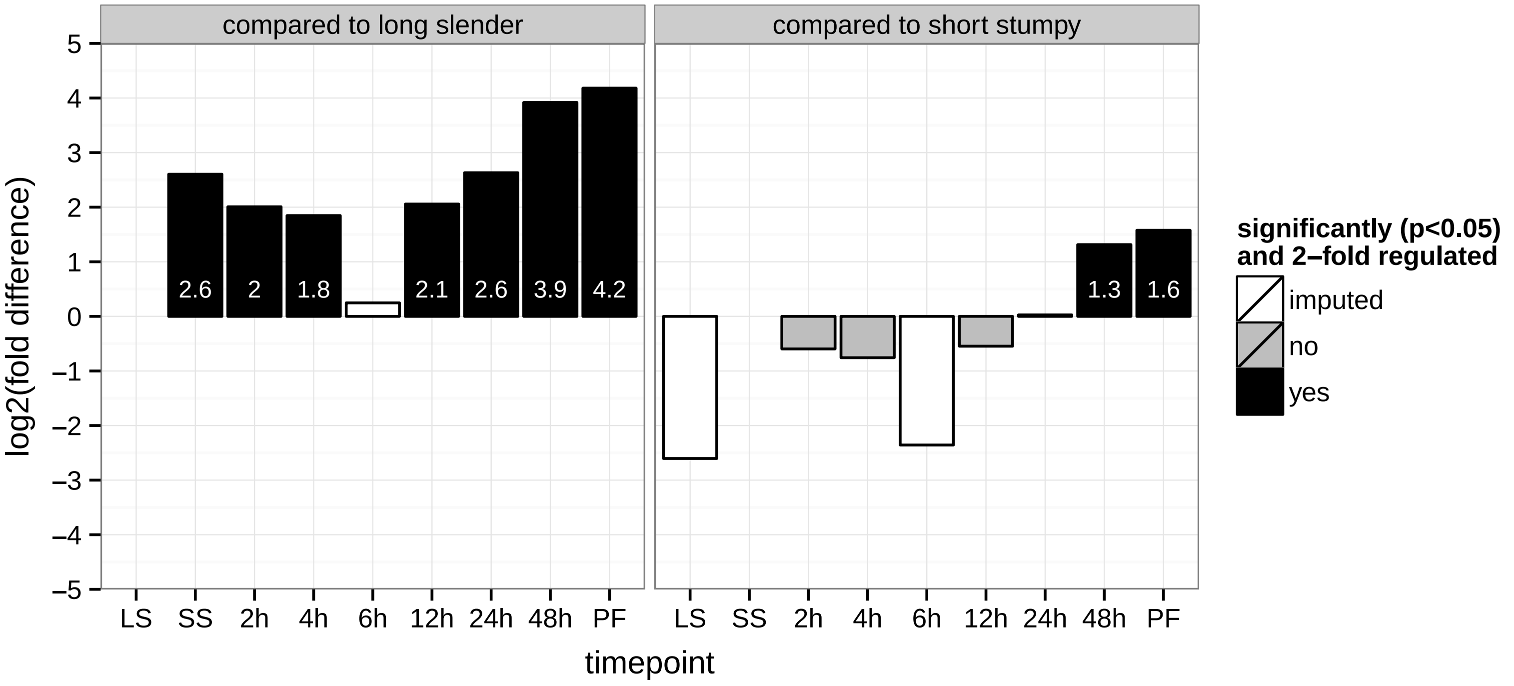
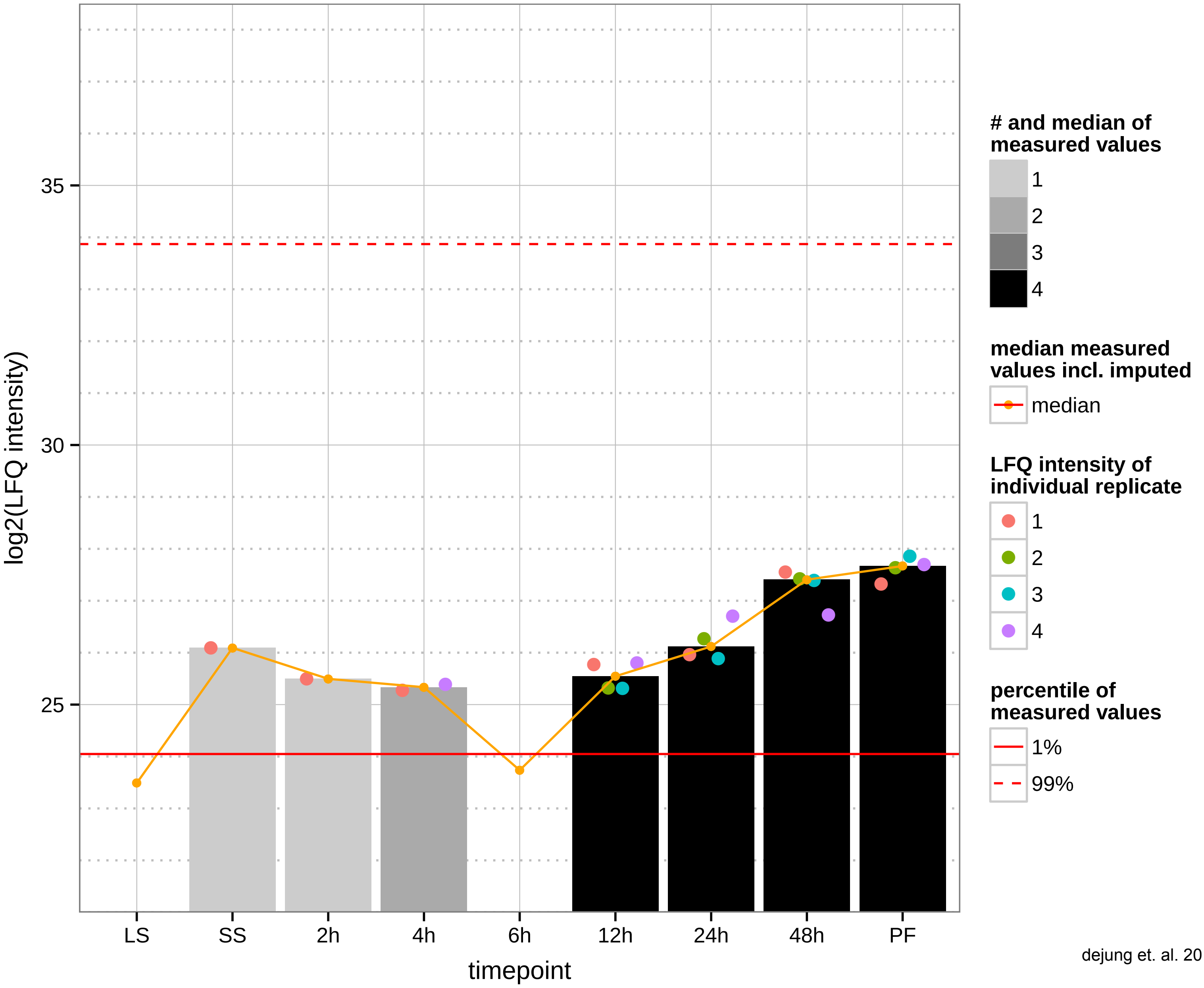
conserved protein, unknown function
Tb927.1.1420
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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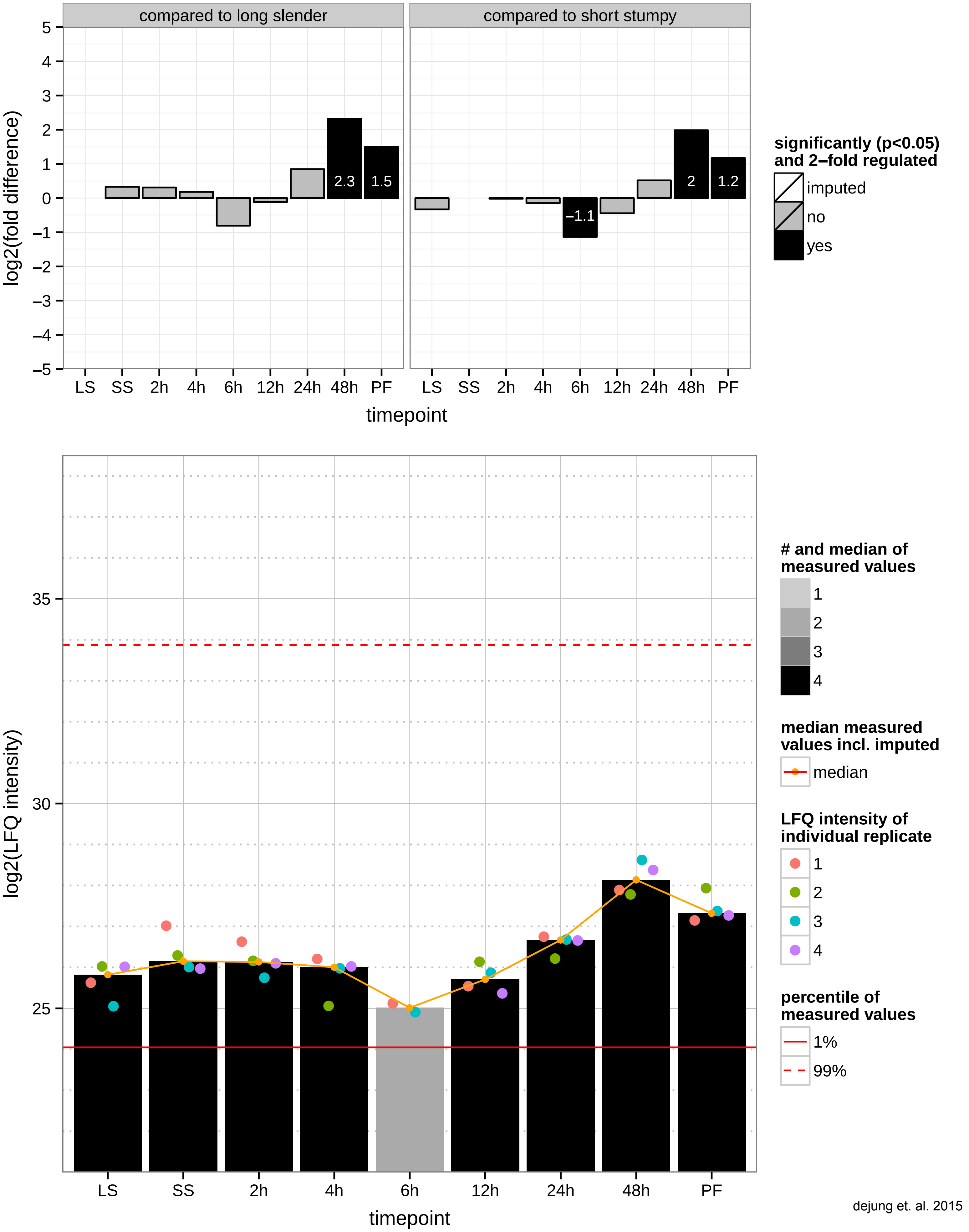
fatty acid desaturase, putative, oleate desaturase
Tb927.2.3080
AGOF: oxidoreductase activity
AGOC: null
AGOP: fatty acid biosynthetic process
PGOF: null
PGOC: null
PGOP: lipid metabolic process



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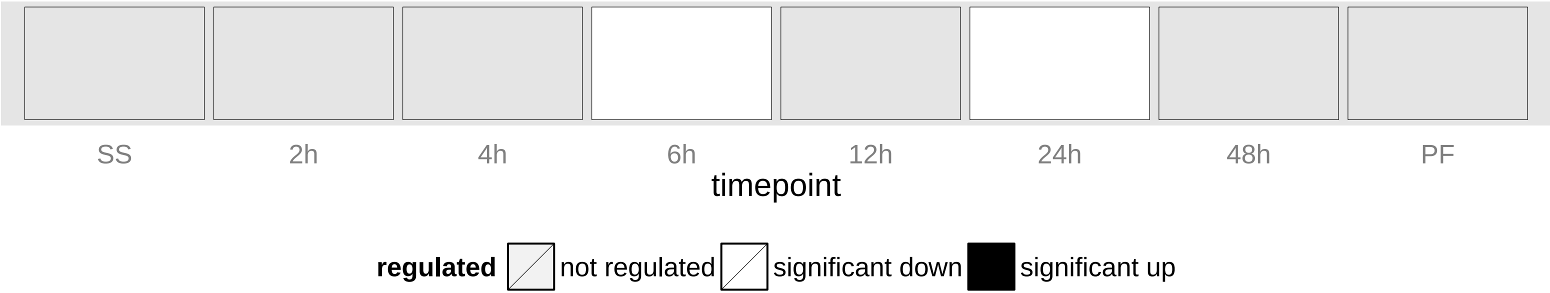

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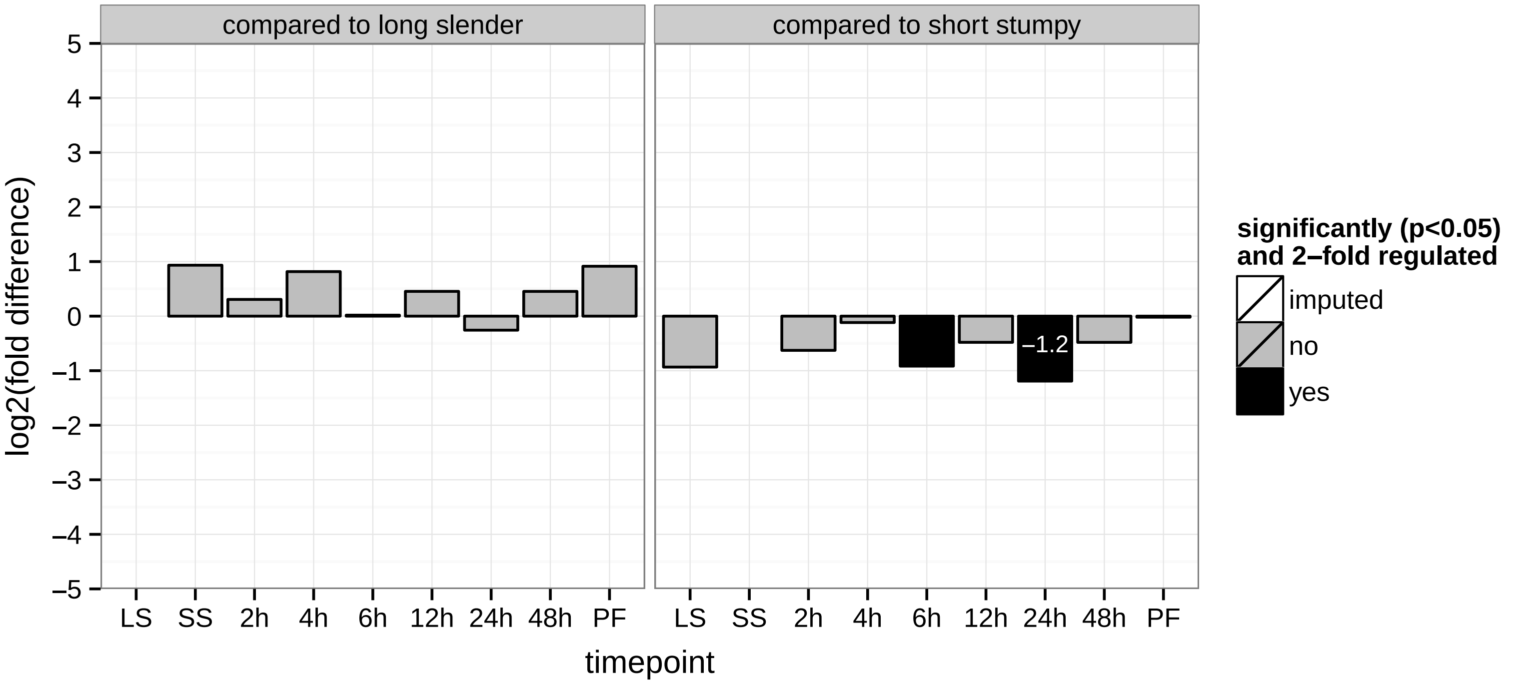
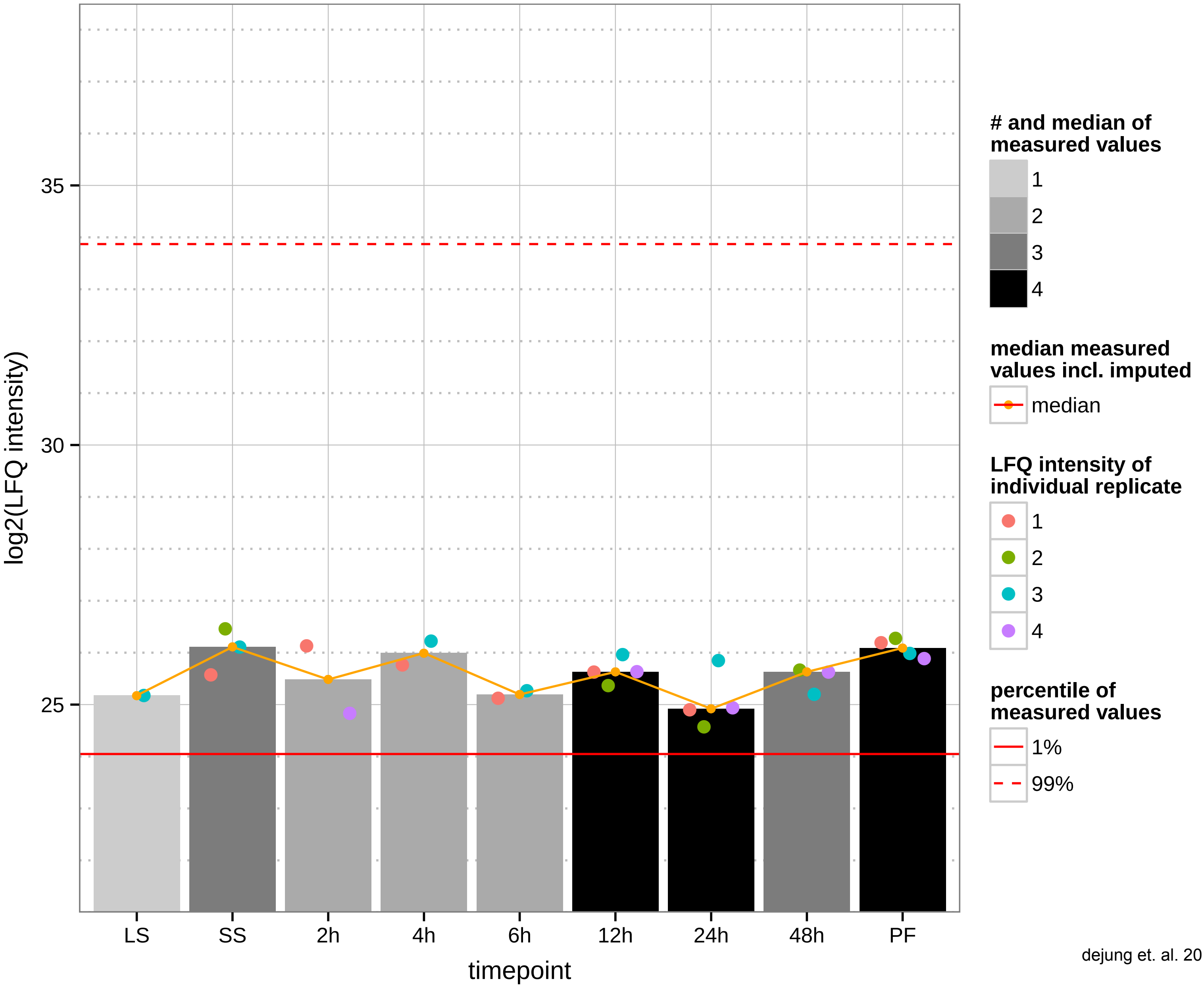
short–chain dehydrogenase, putative
Tb927.10.6870
AGOF: oxidoreductase activity
AGOC: null
AGOP: metabolic process
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process





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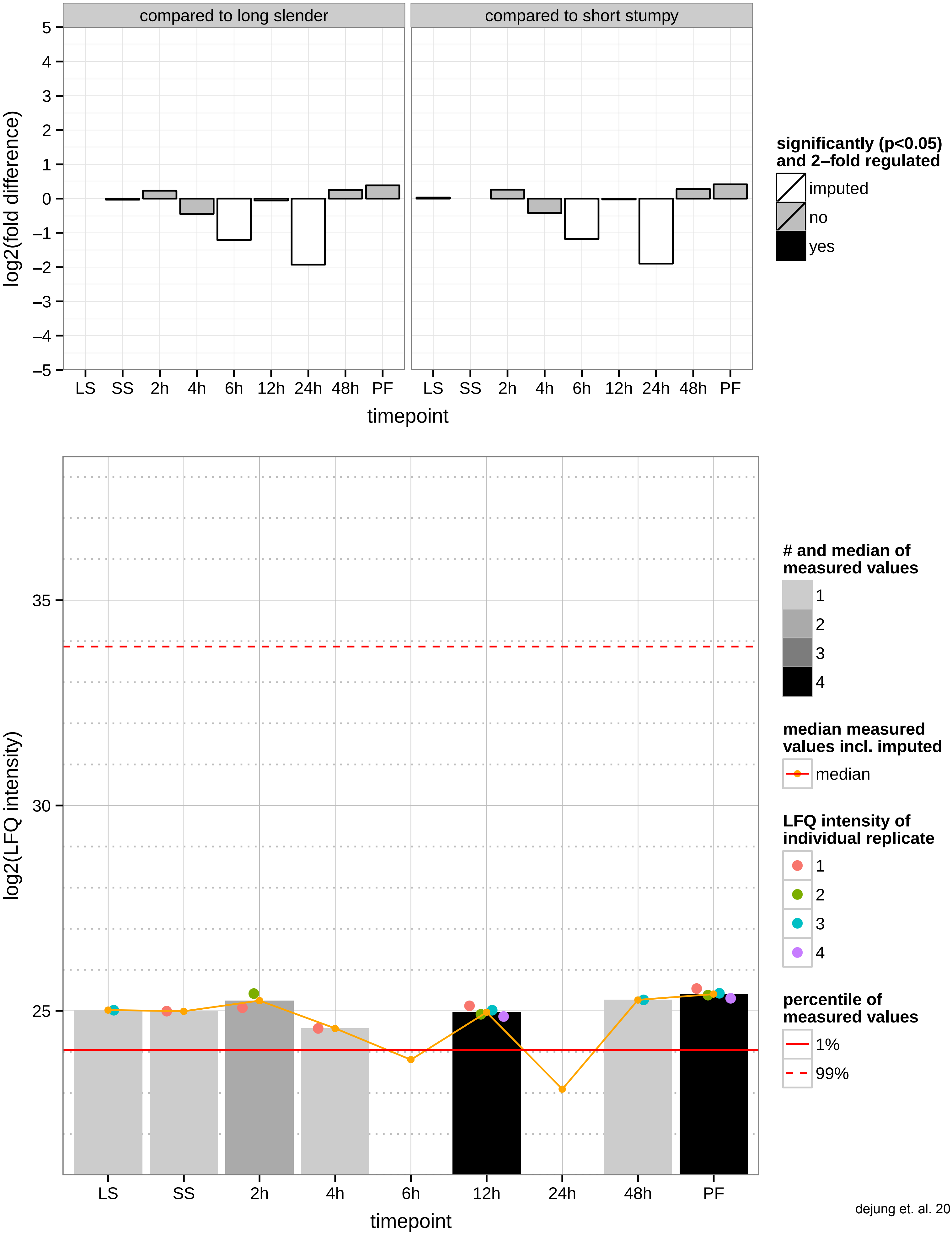
enolase, putative
Tb927.11.16410
AGOF: phosphopyruvate hydratase activity
AGOC: phosphopyruvate hydratase complex
AGOP: glycolysis
PGOF: magnesium ion binding, phosphopyruvate hydratase activity
PGOC: phosphopyruvate hydratase complex
PGOP: glycolysis



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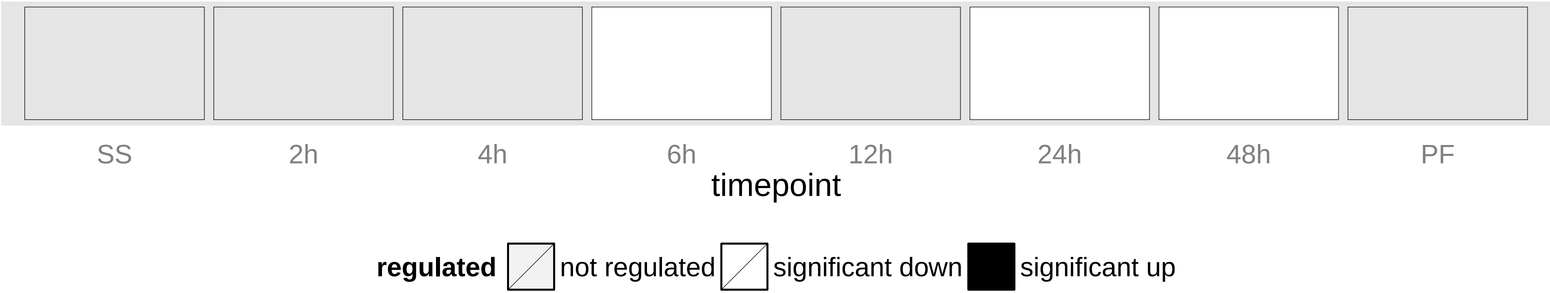

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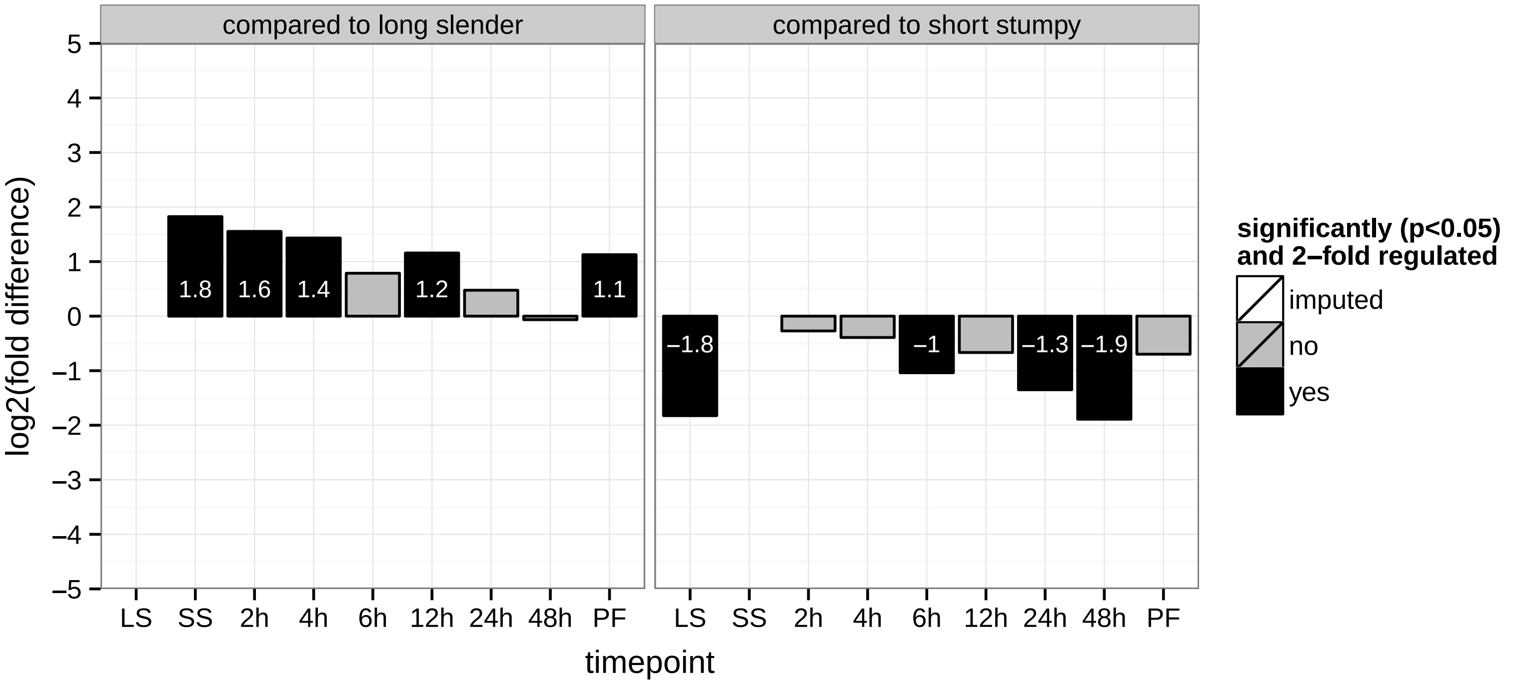
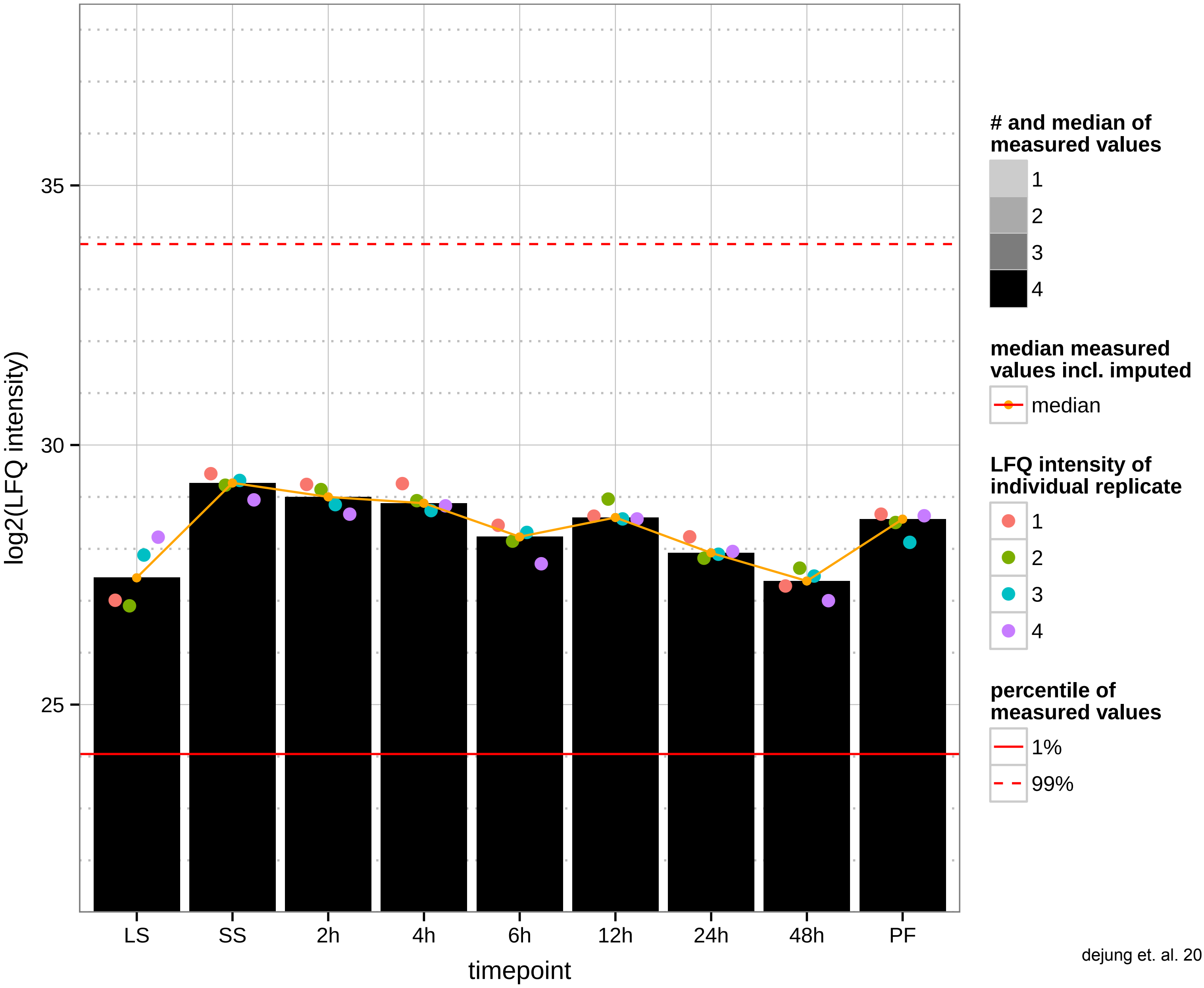
vacuolar ATP synthase, putative
Tb927.5.550
AGOF: hydrogen ion transmembrane transporter activity
AGOC: proton−transporting V−type ATPase, V0 domain
AGOP: ATP synthesis coupled proton transport
PGOF: hydrogen ion transmembrane transporter activity
PGOC: proton−transporting V−type ATPase, V0 domain, proton−transporting two−sector ATPase complex, proton−transportin
PGOP: ATP hydrolysis coupled proton transport





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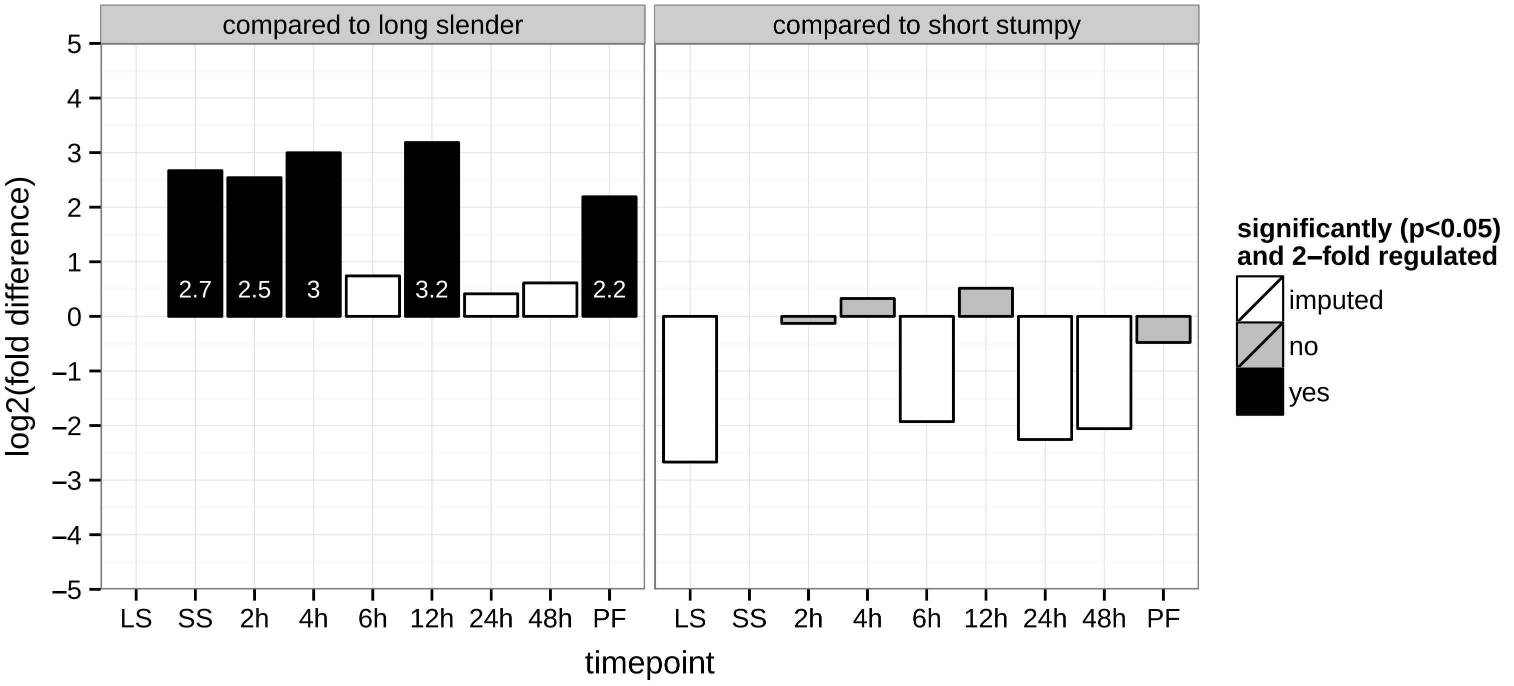
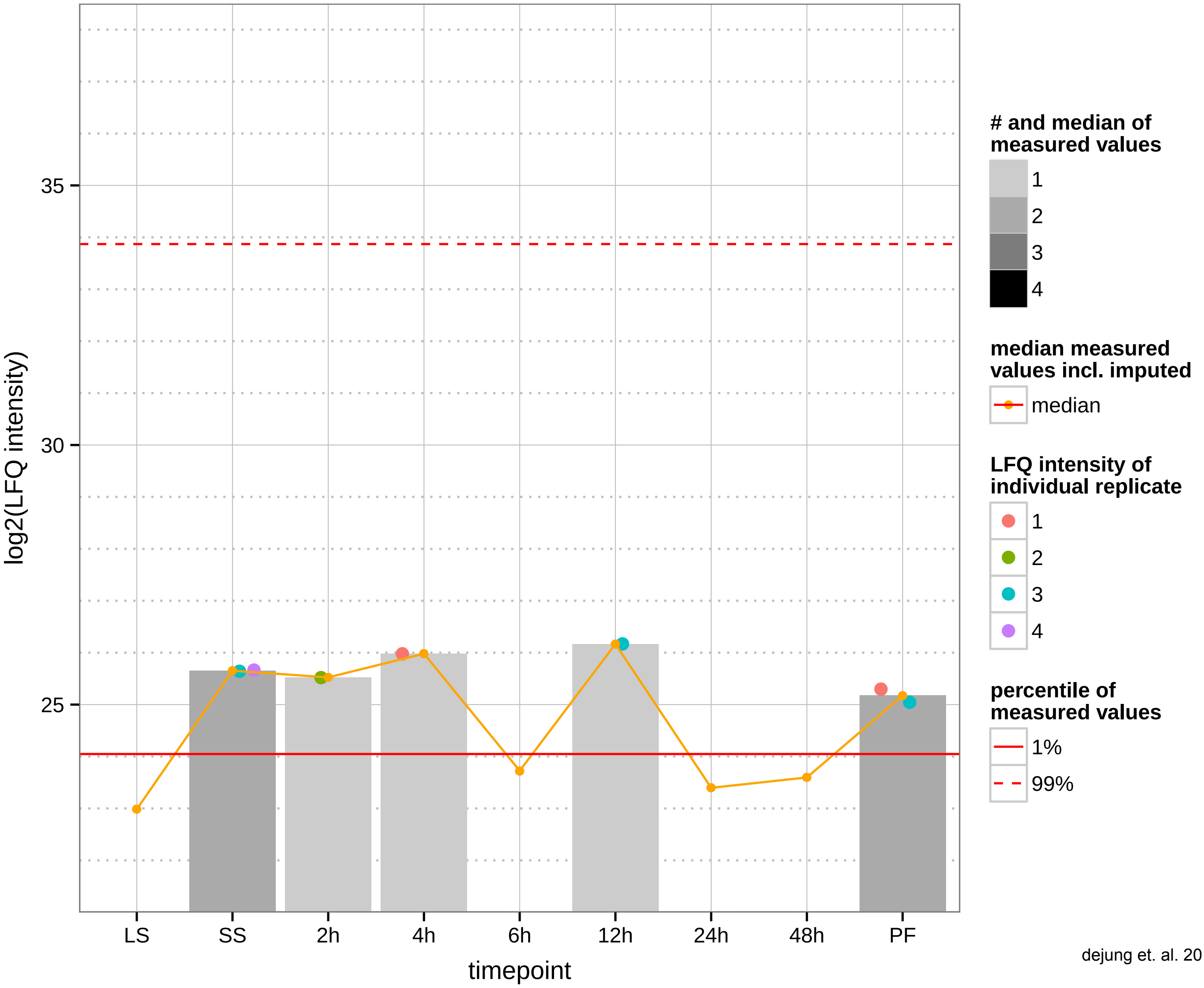
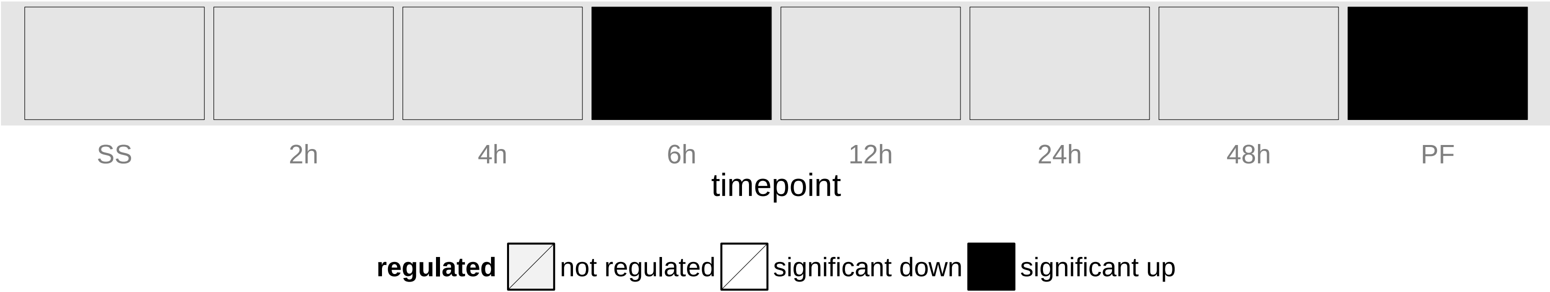
hypothetical protein, conserved
Tb927.8.7200
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: binding, protein binding, zinc ion binding
PGOC: null
PGOP: intracellular protein transport, vesicle−mediated transport





dejung et. al. 2015



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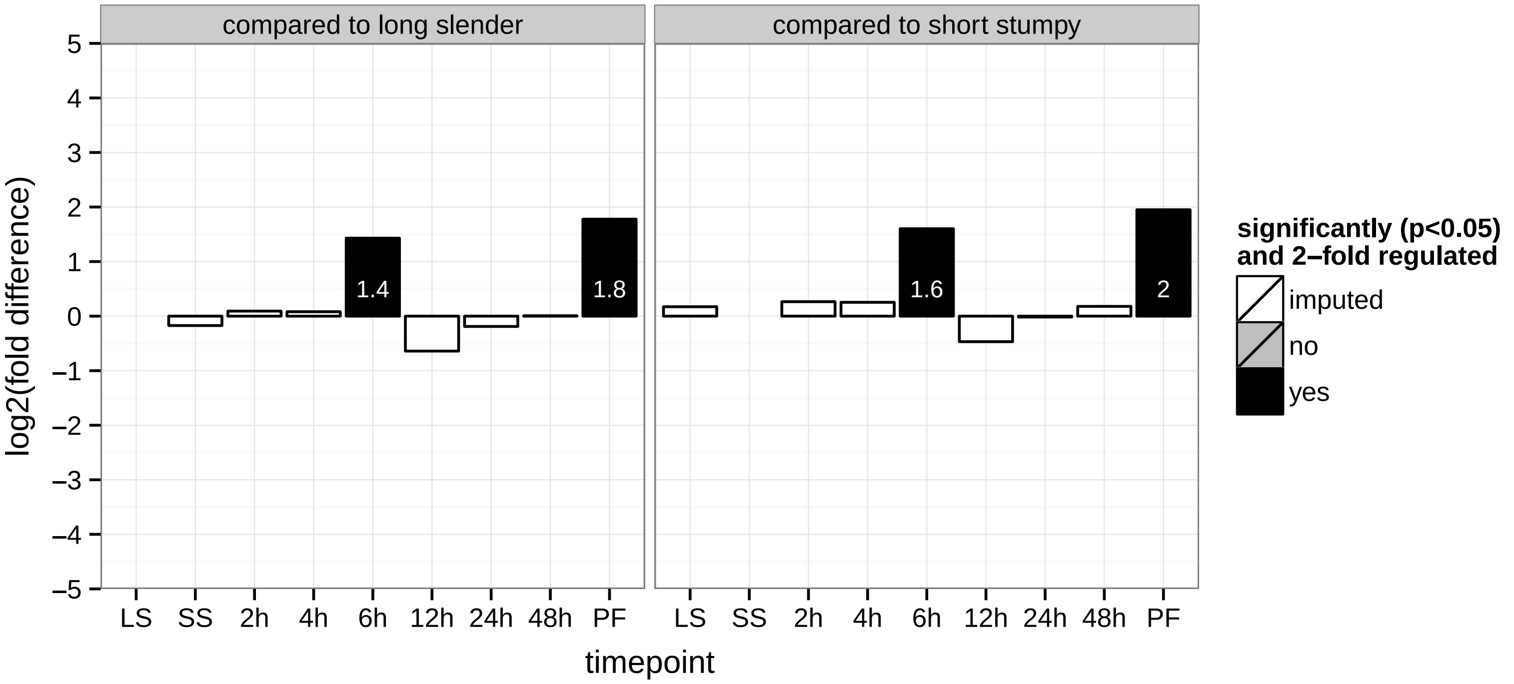
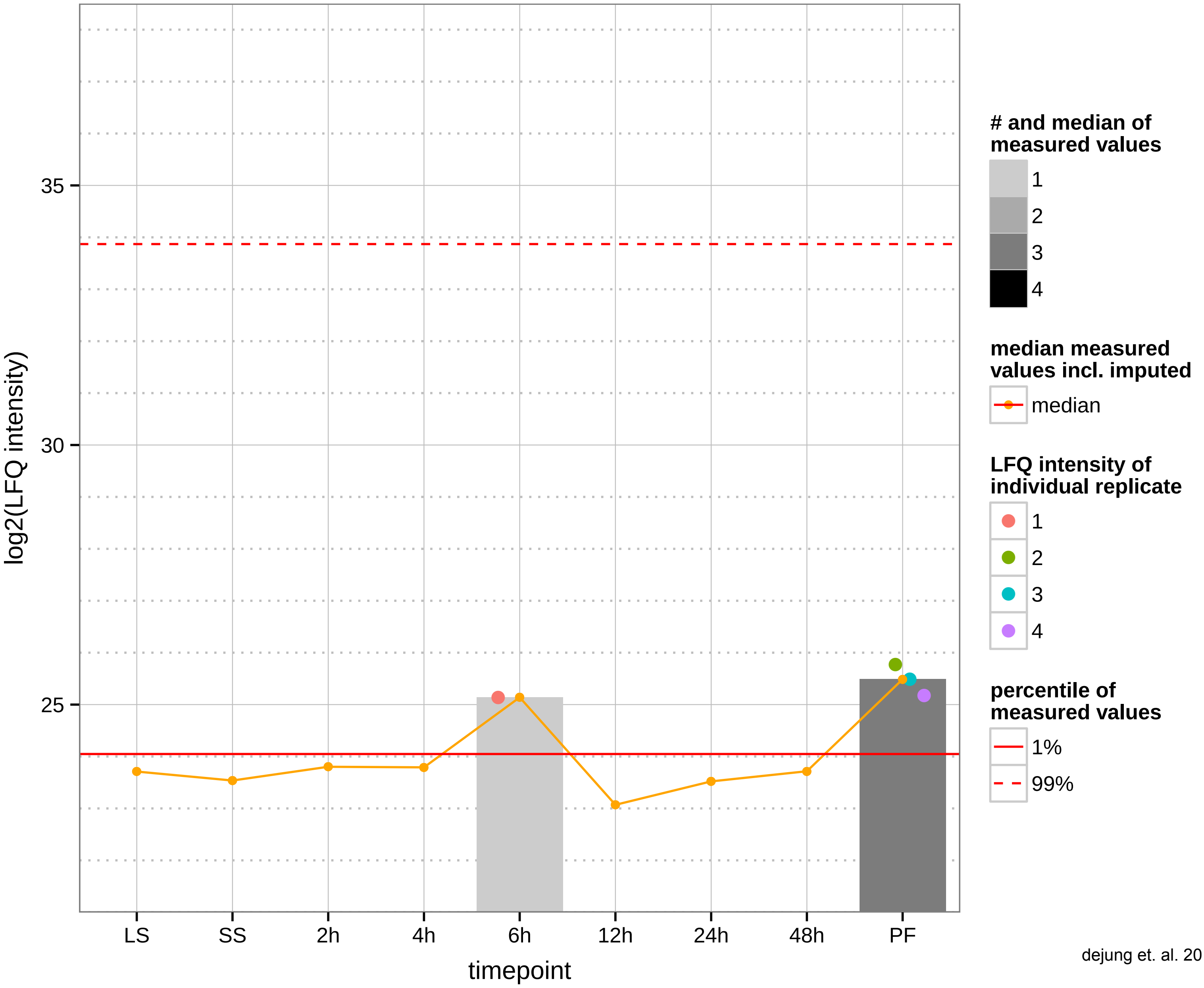
glycosyltransferase, putative, dolichyl−P−Man:GDP−ManGlcNAc2−PP−dolichyl beta−1, 4−mannosyltransferase
Tb927.10.13210;Tb11.v5.0694
AGOF: null, dolichyl−phosphate beta−D−mannosyltransferase activity
AGOC: null, endoplasmic reticulum membrane
AGOP: null, protein mannosylation
PGOF: null
PGOC: null
PGOP: null





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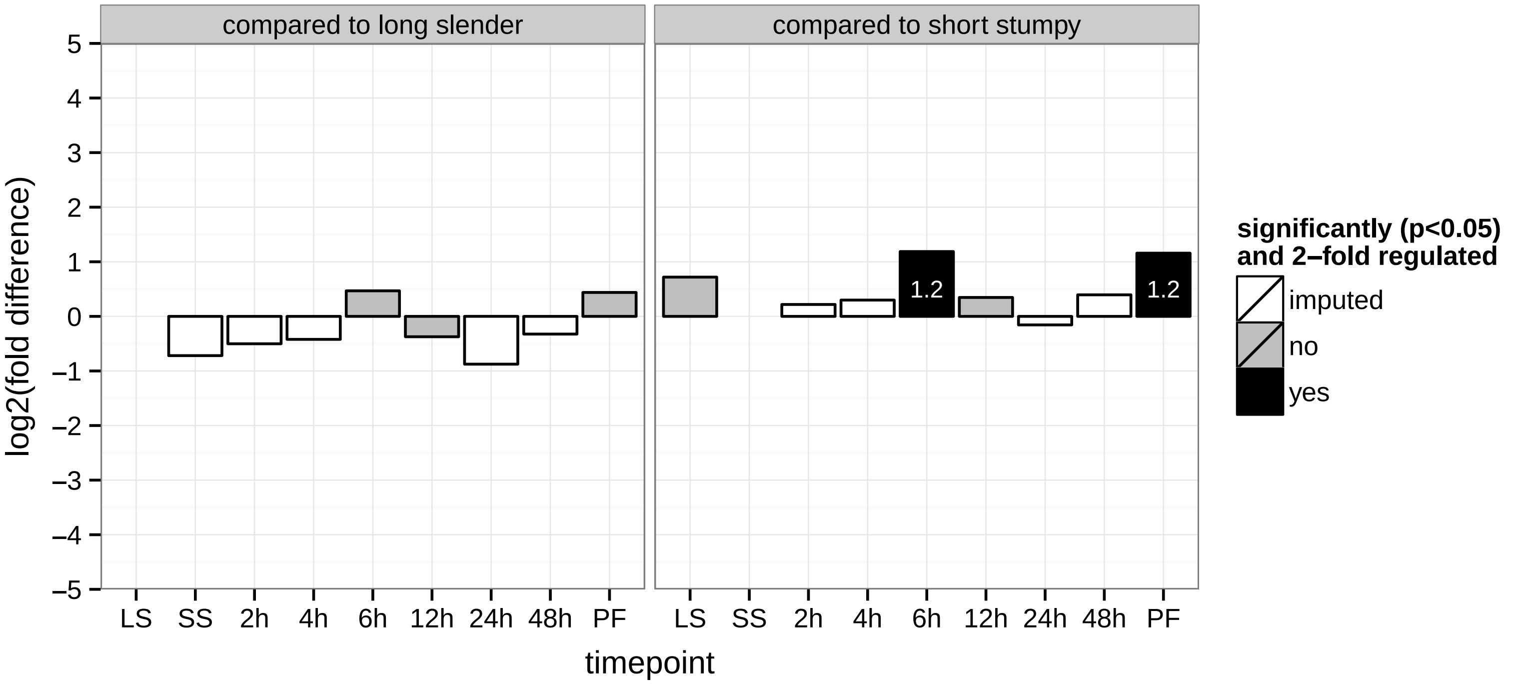
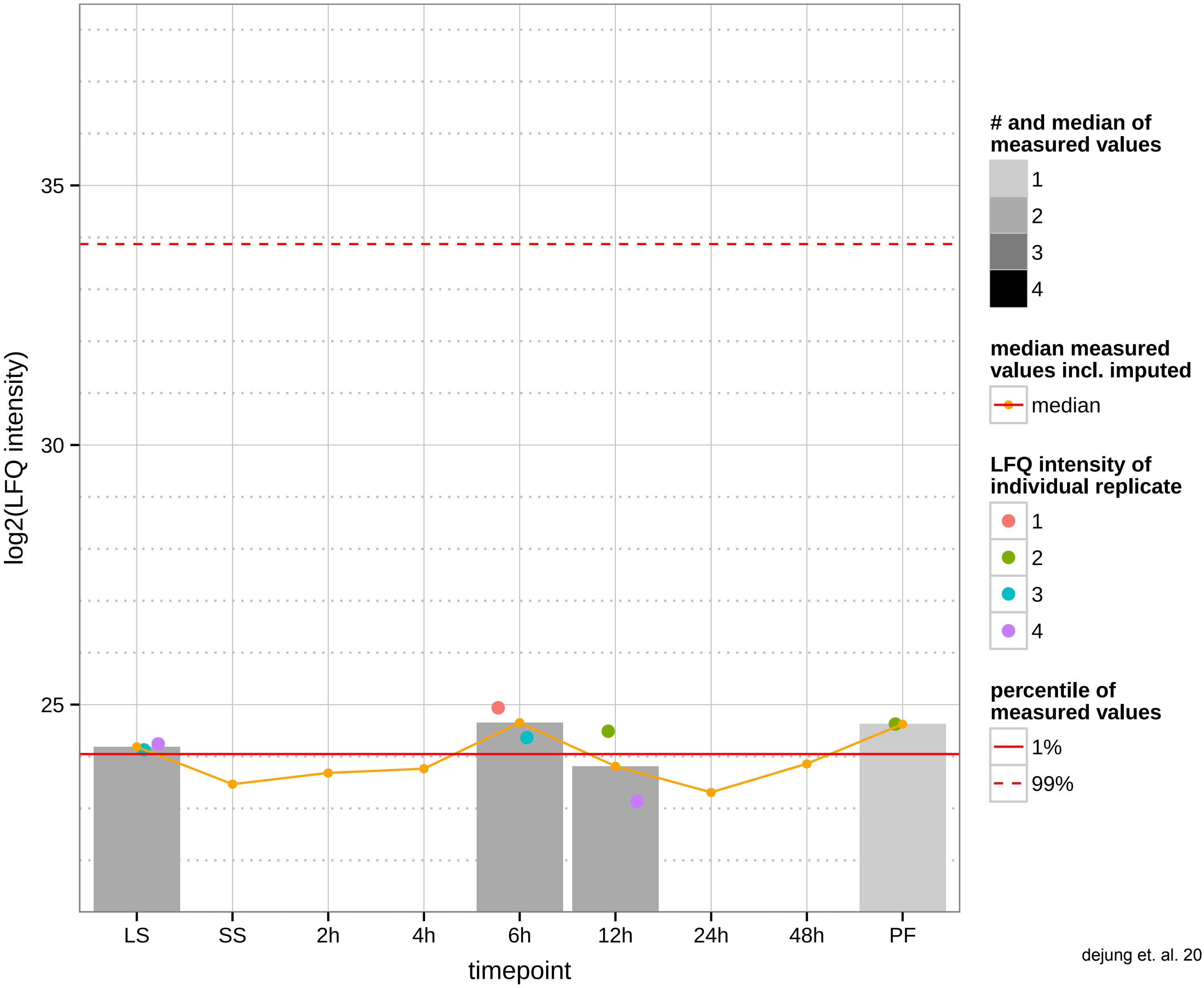
hypothetical protein, conserved
Tb927.11.7180
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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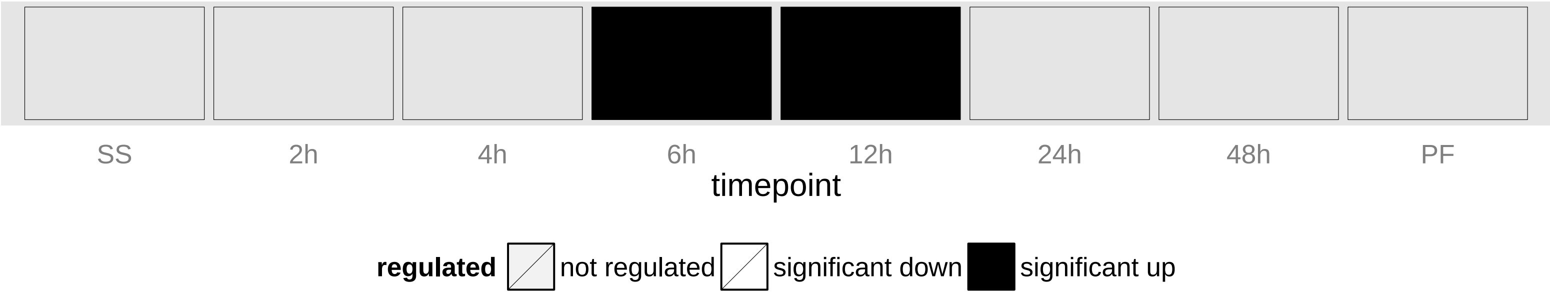

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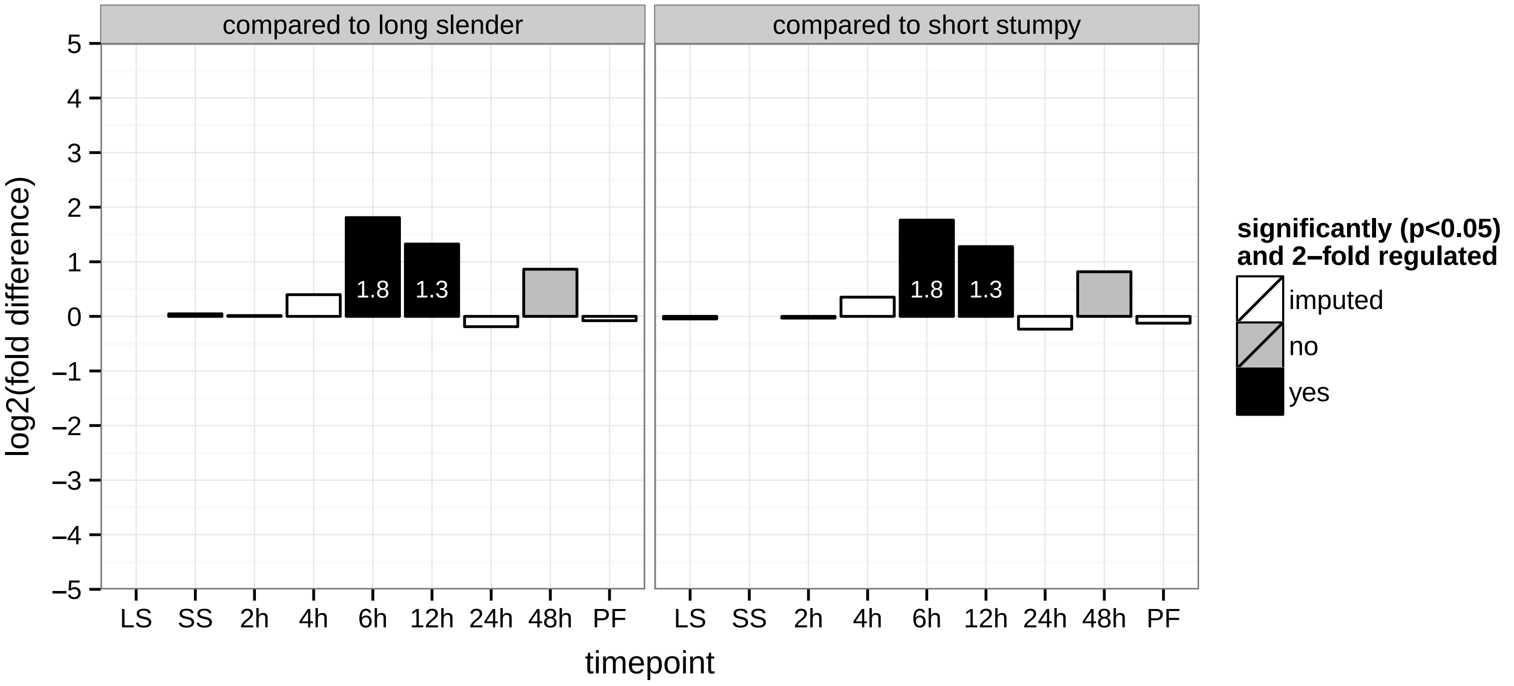
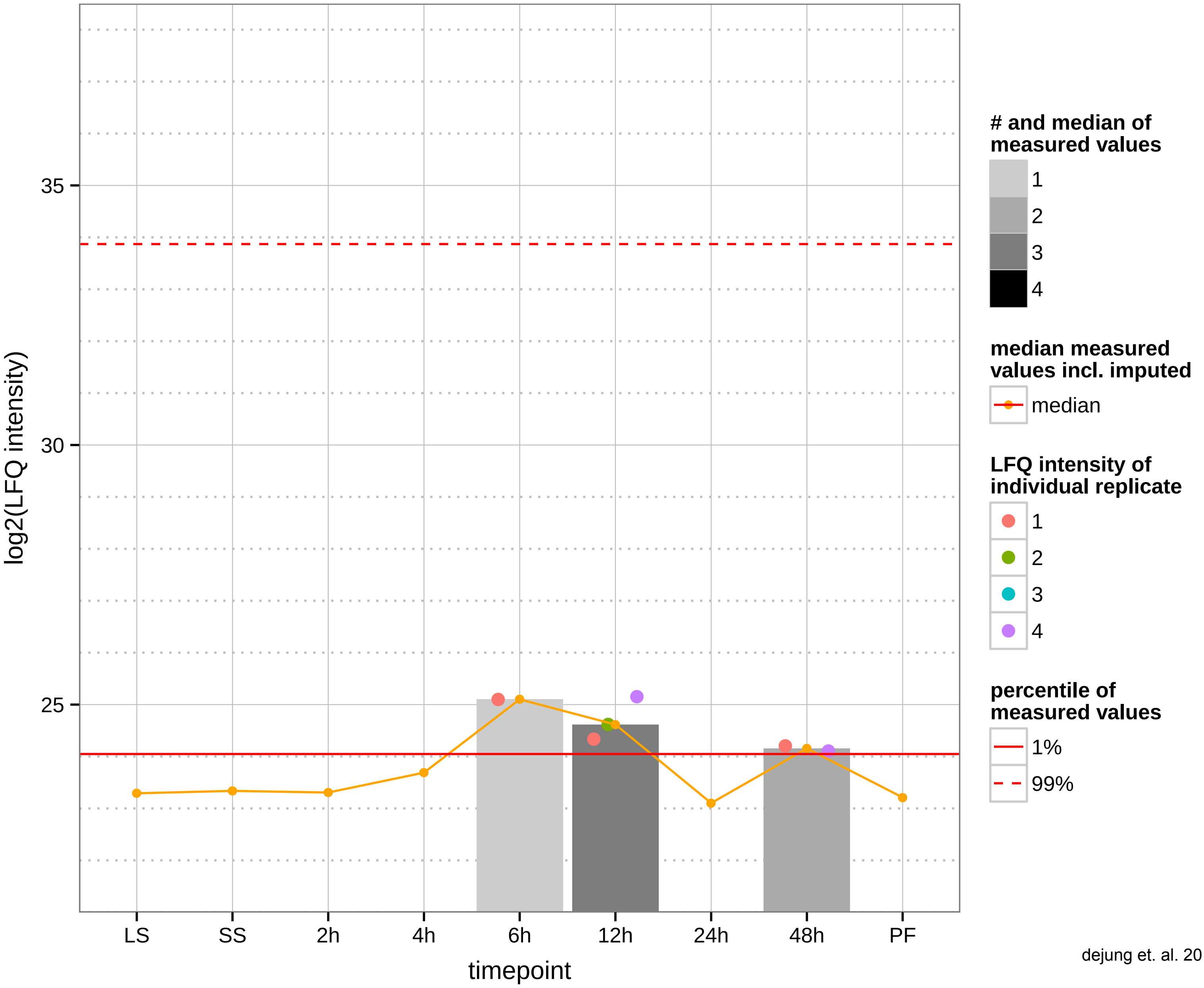
hypothetical protein, conserved
Tb927.3.4510
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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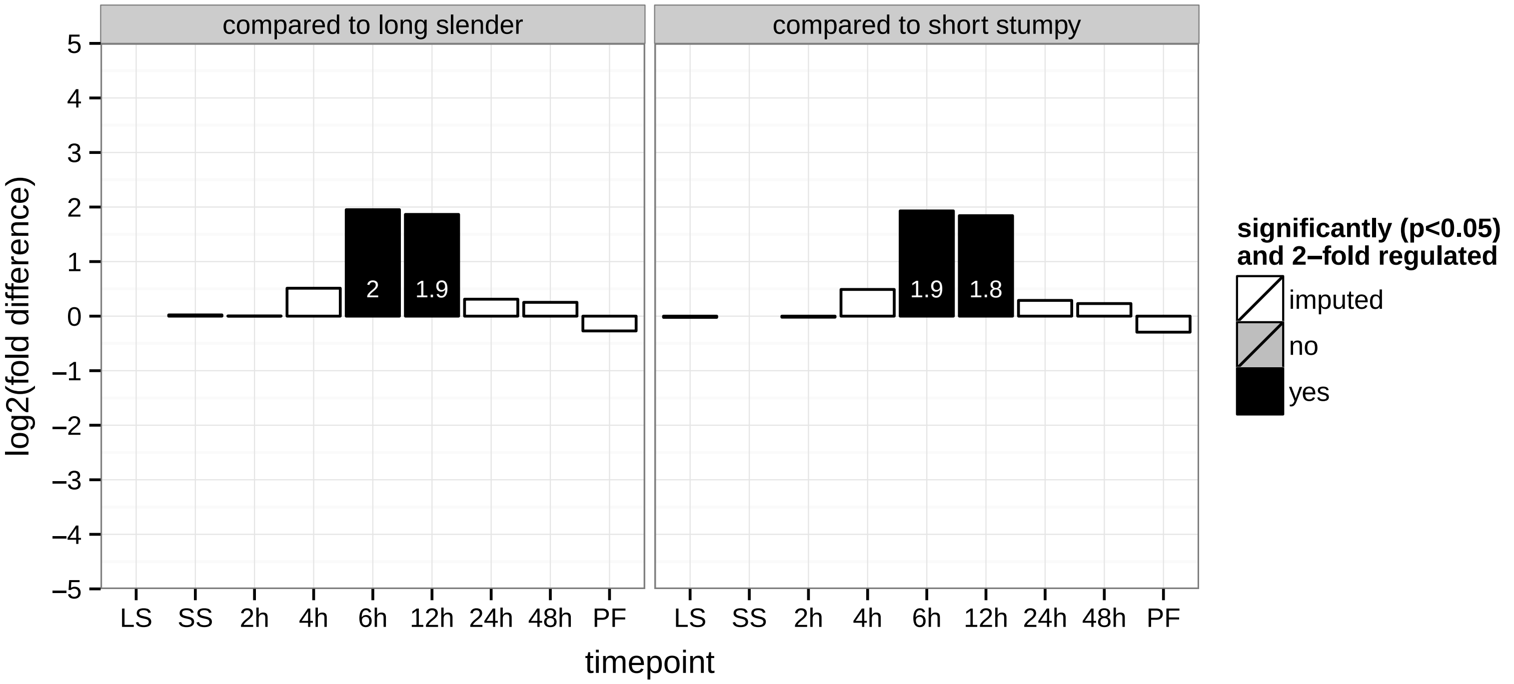
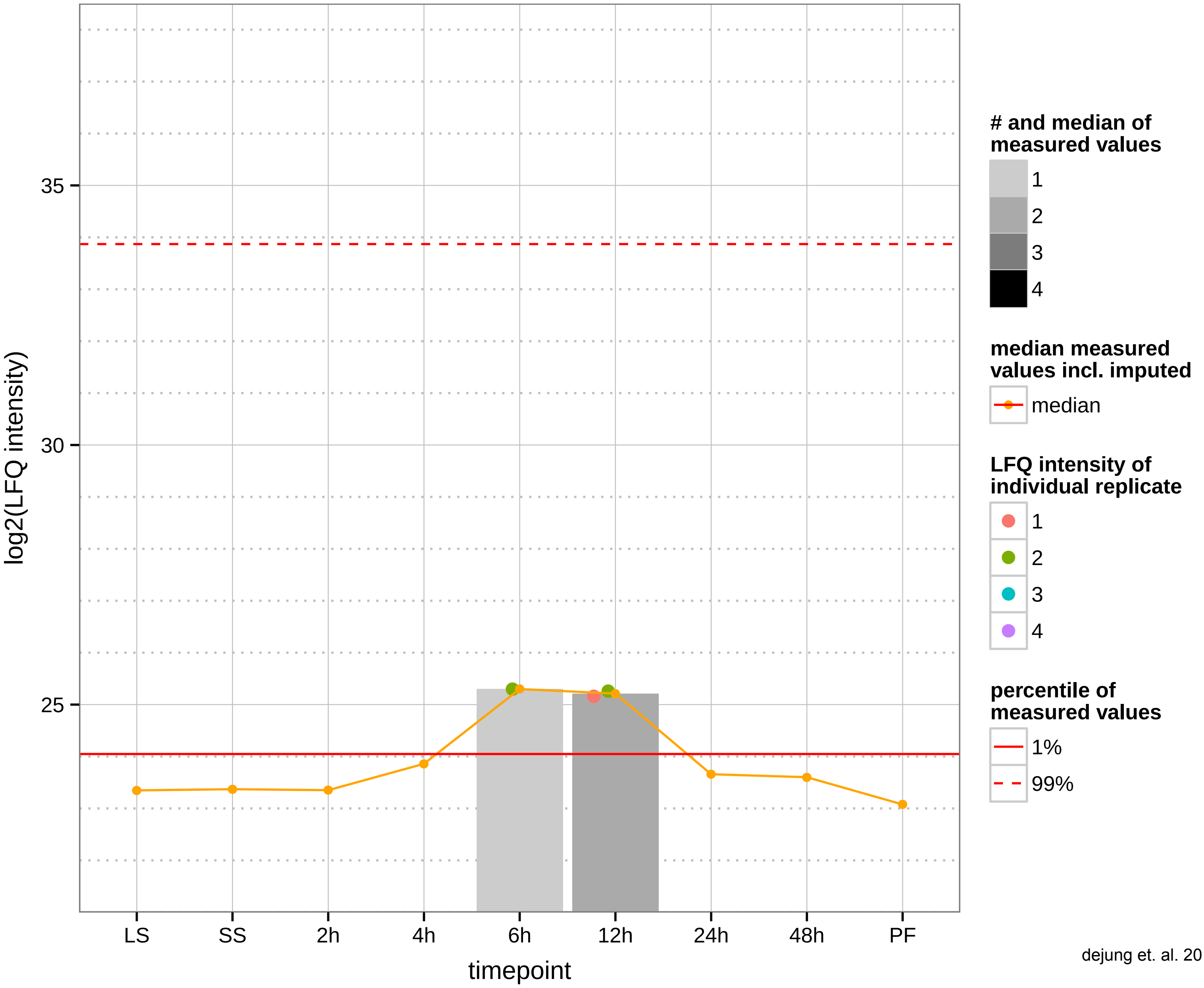
hypothetical protein, conserved
Tb927.9.10140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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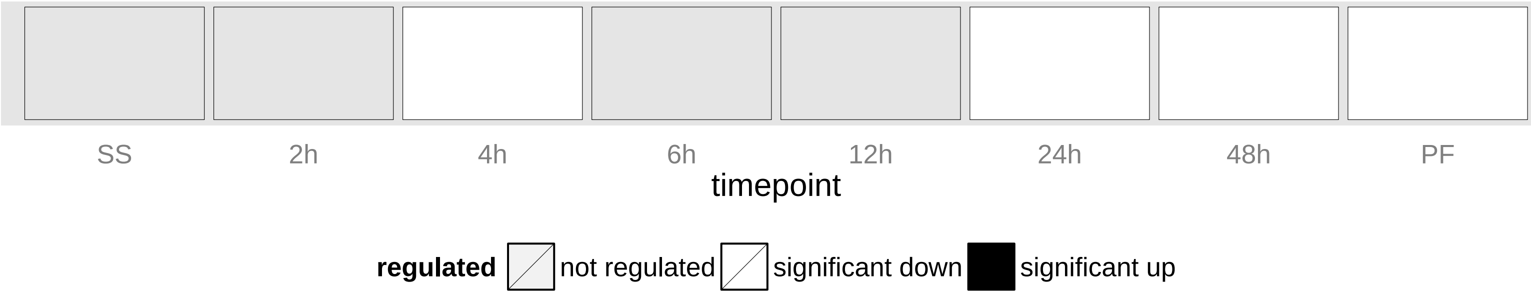

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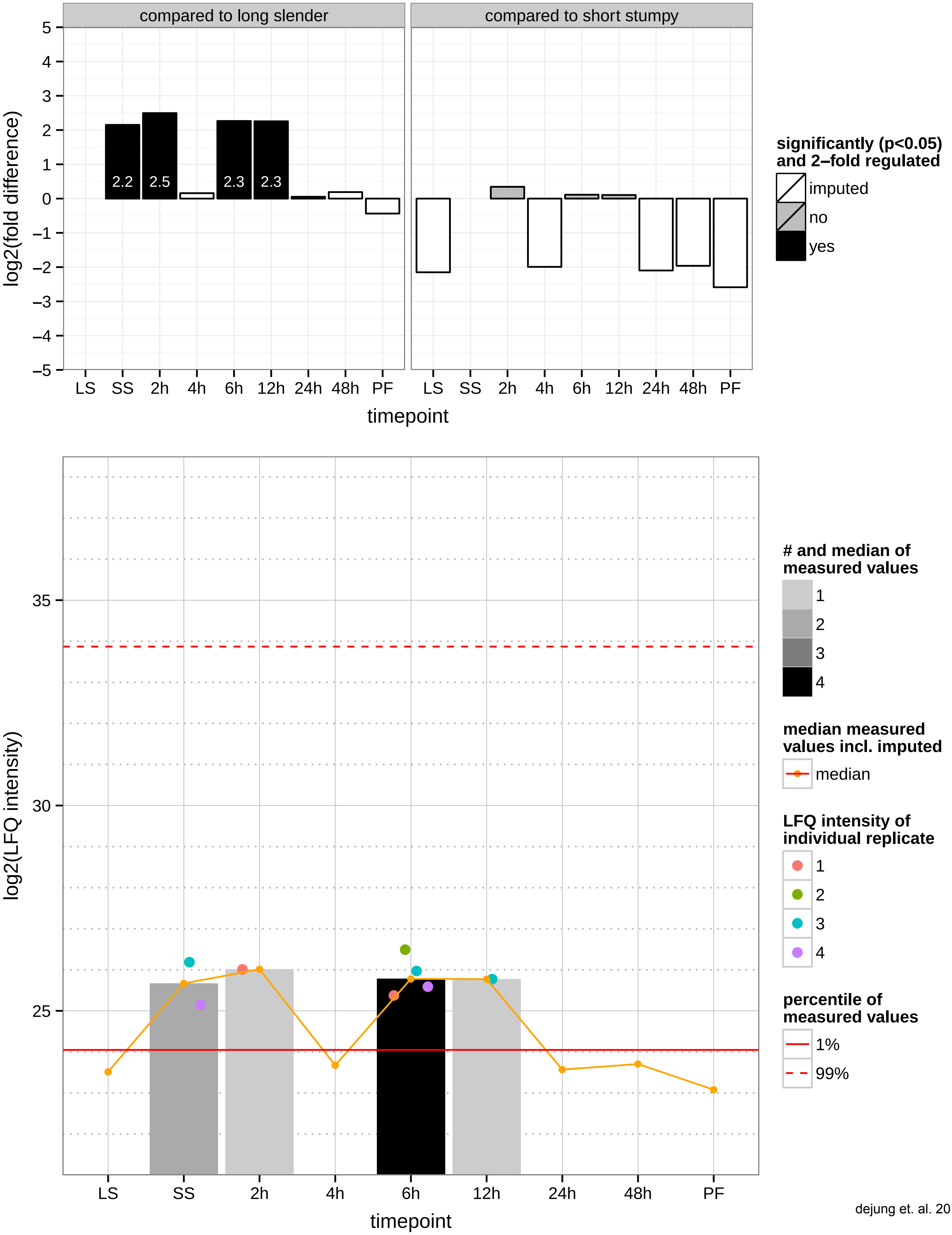
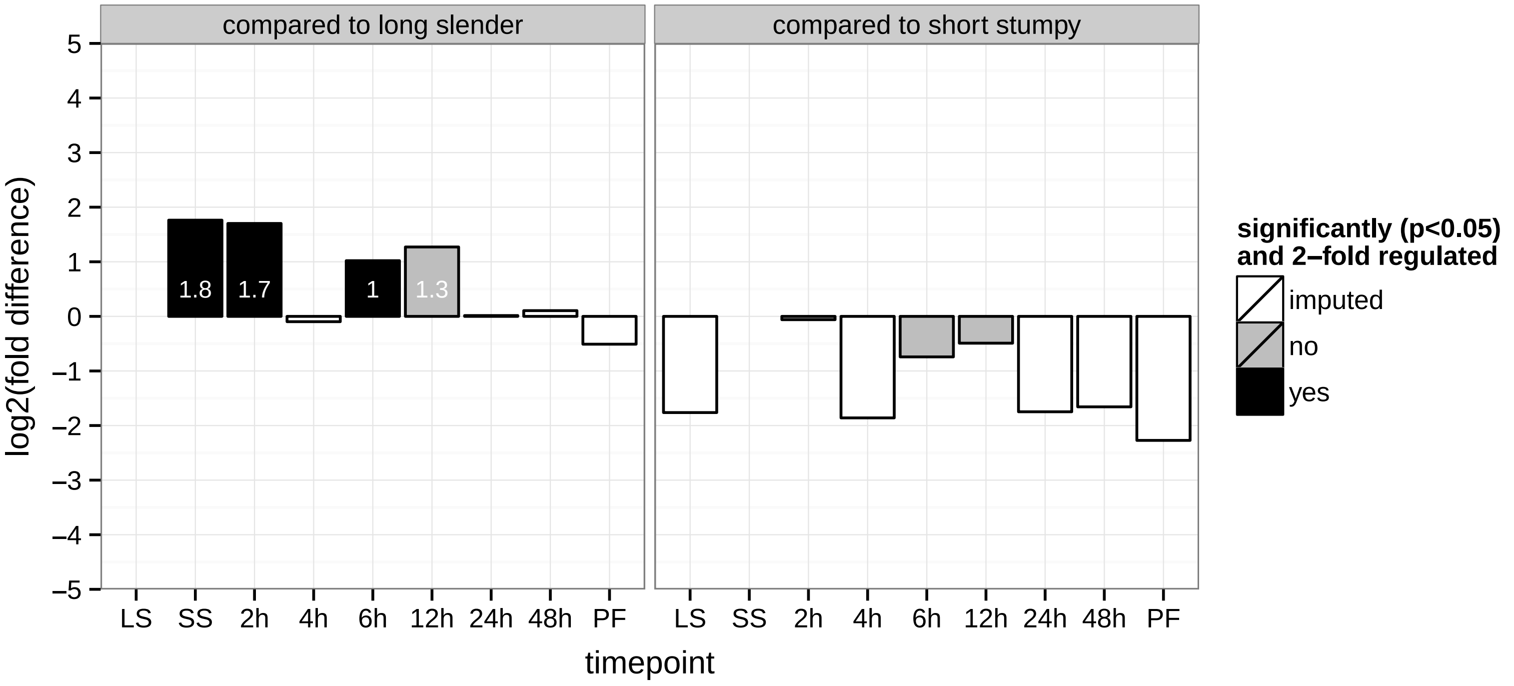
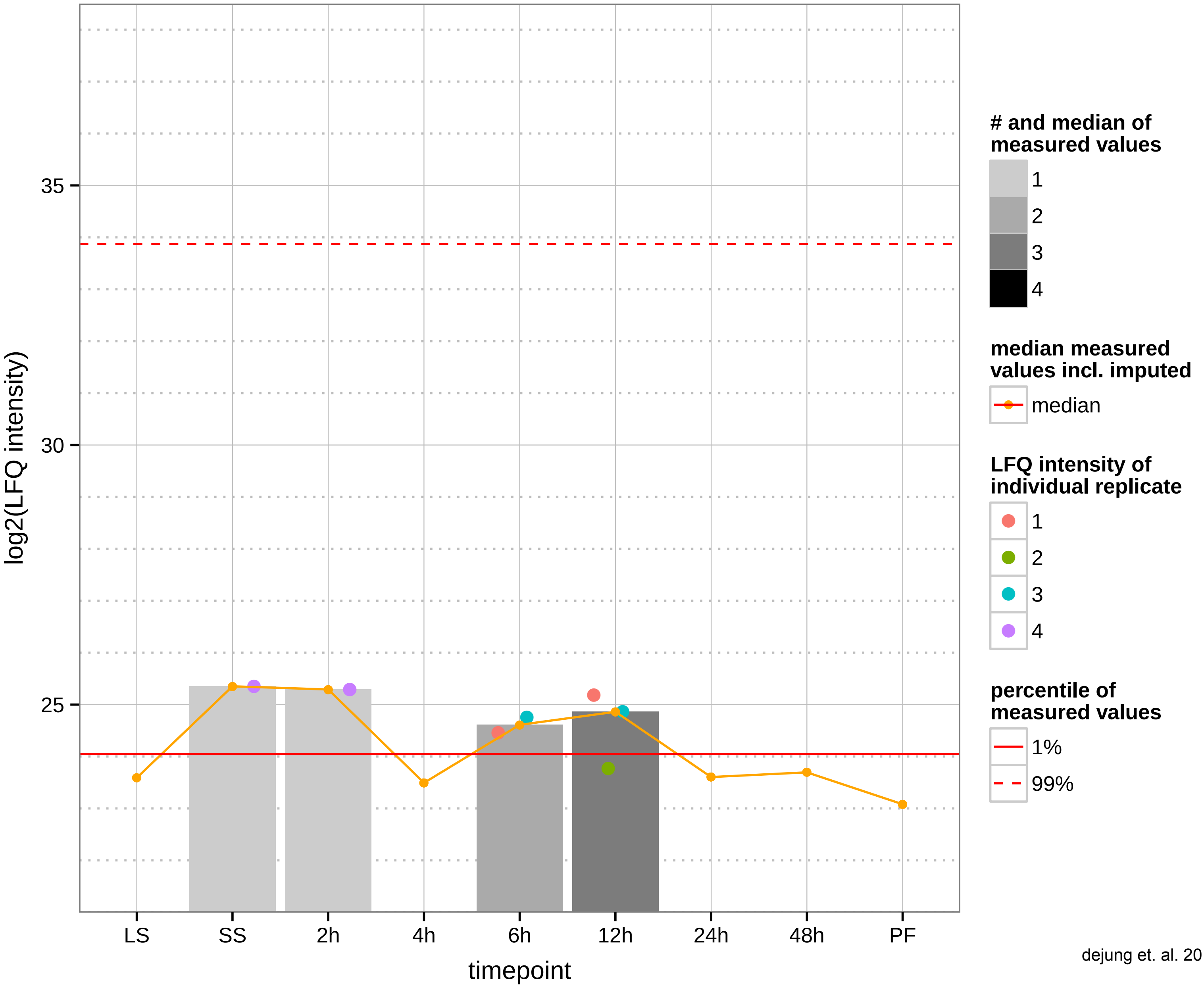
leucine−rich repeat−containing protein
Tb927.1.1020
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.6020
AGOF: nucleoside–triphosphatase activity, nucleotide binding
AGOC: null
AGOP: null
PGOF: nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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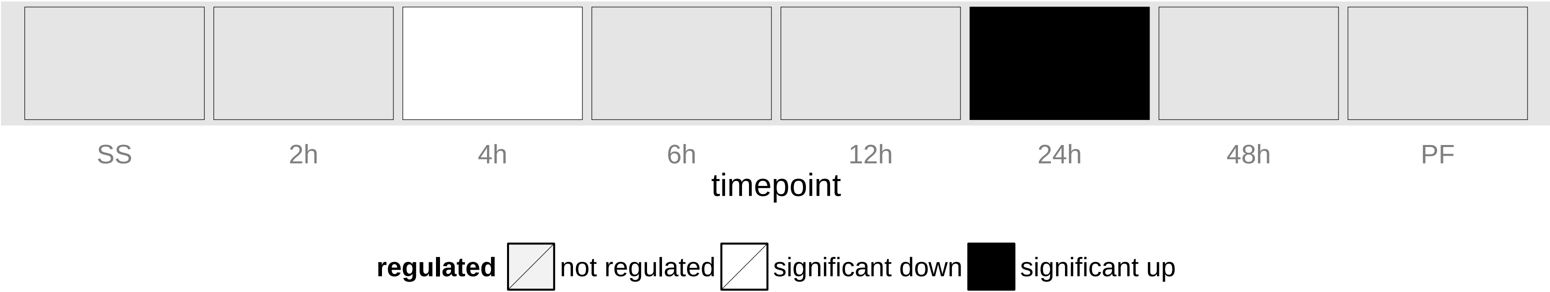

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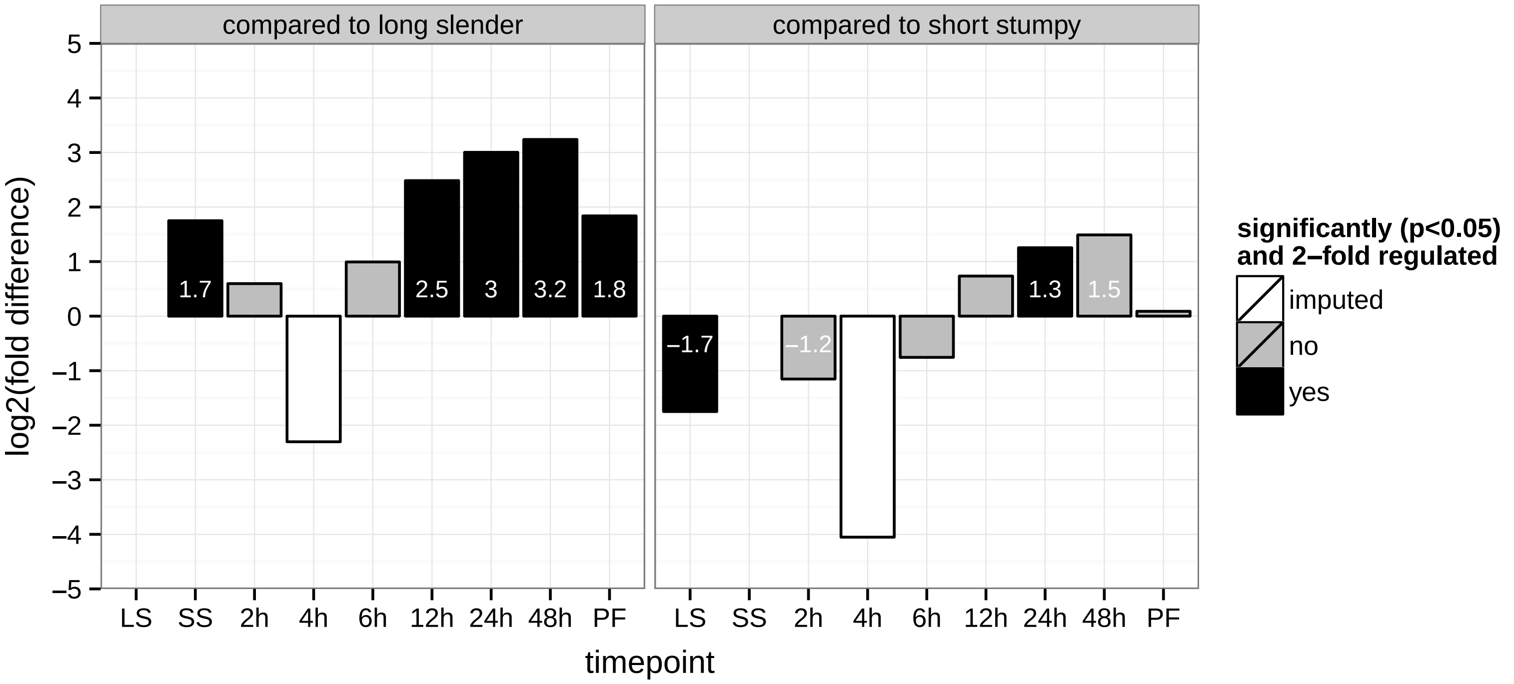
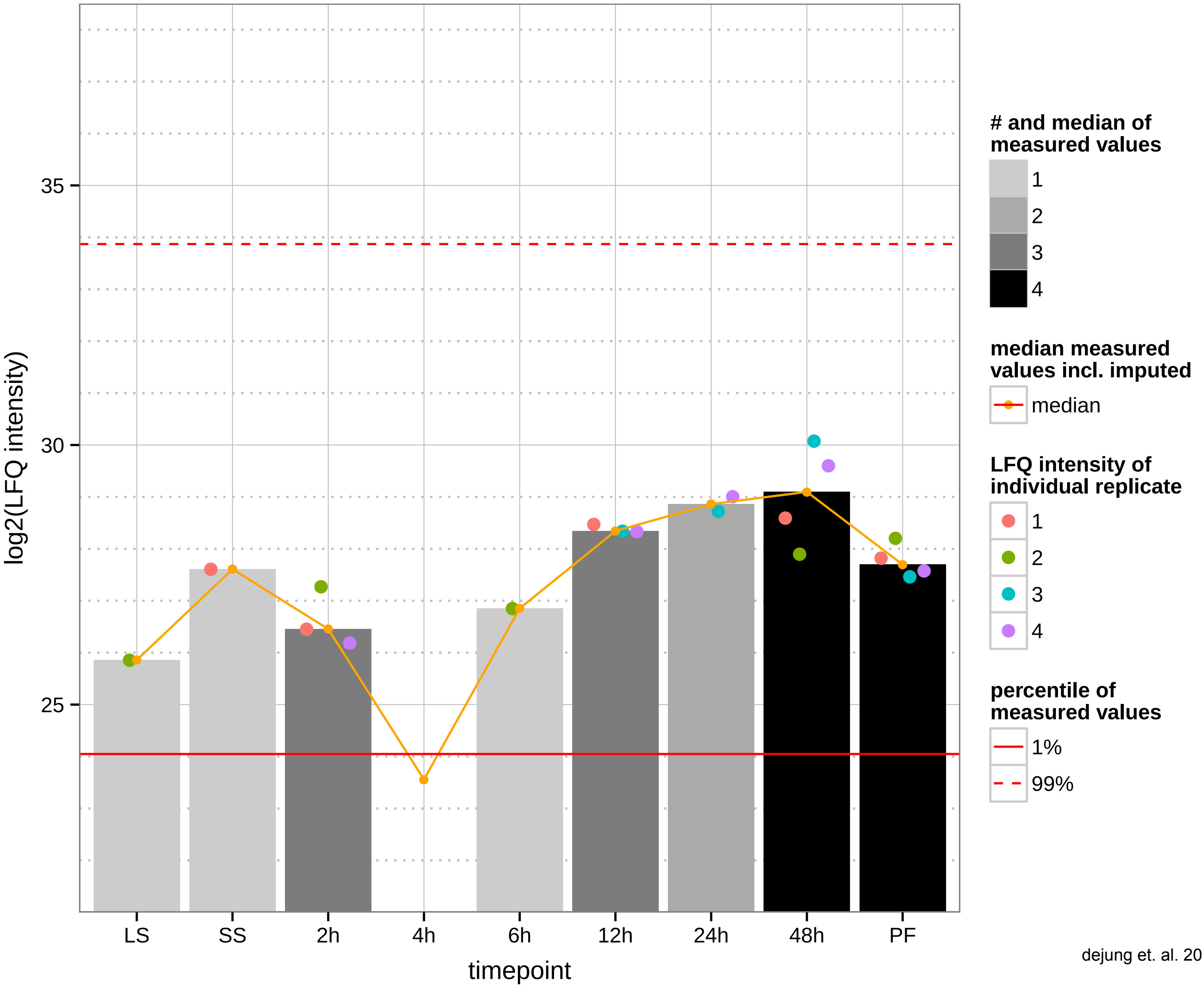
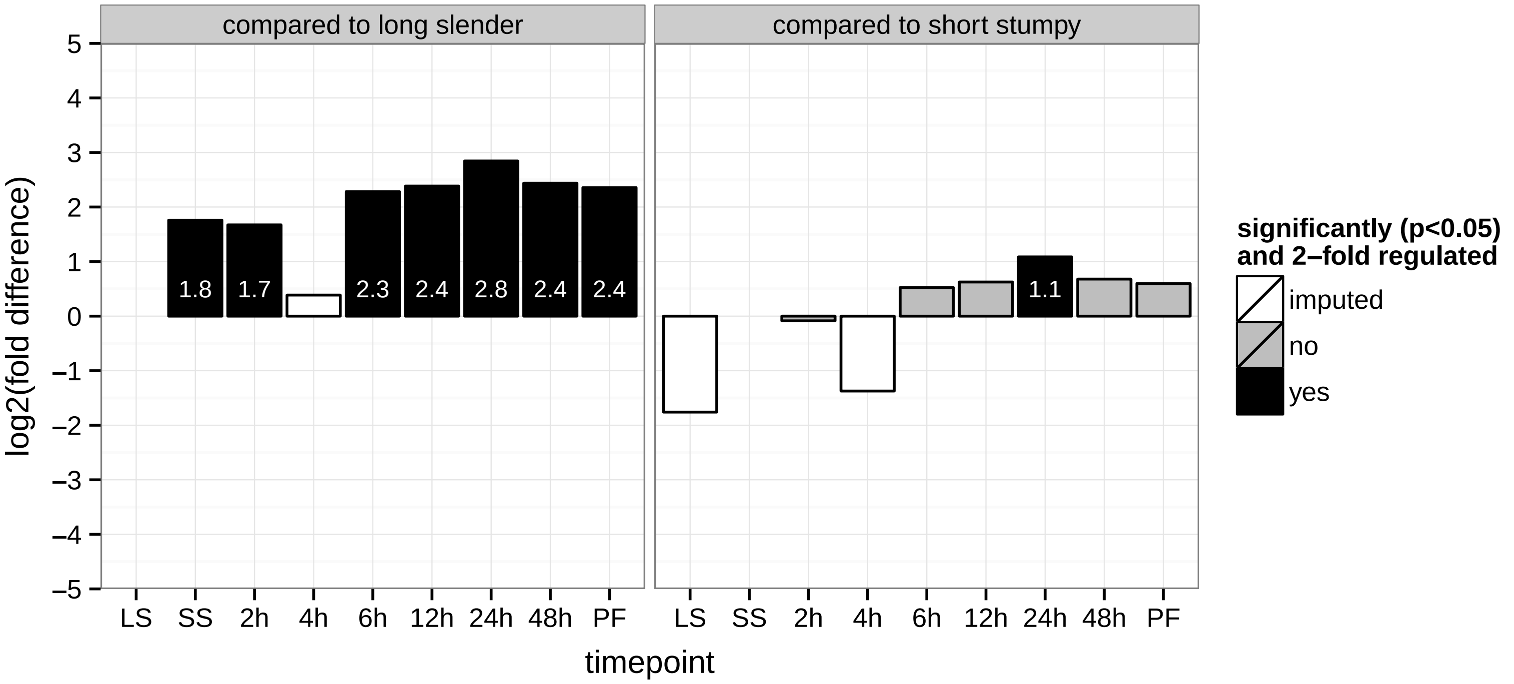
retrotransposon hot spot protein 5 (RHS5), putative
Tb927.1.420
AGOF: null
AGOC: nucleus
AGOP: null
PGOF: null
PGOC: null
PGOP: null

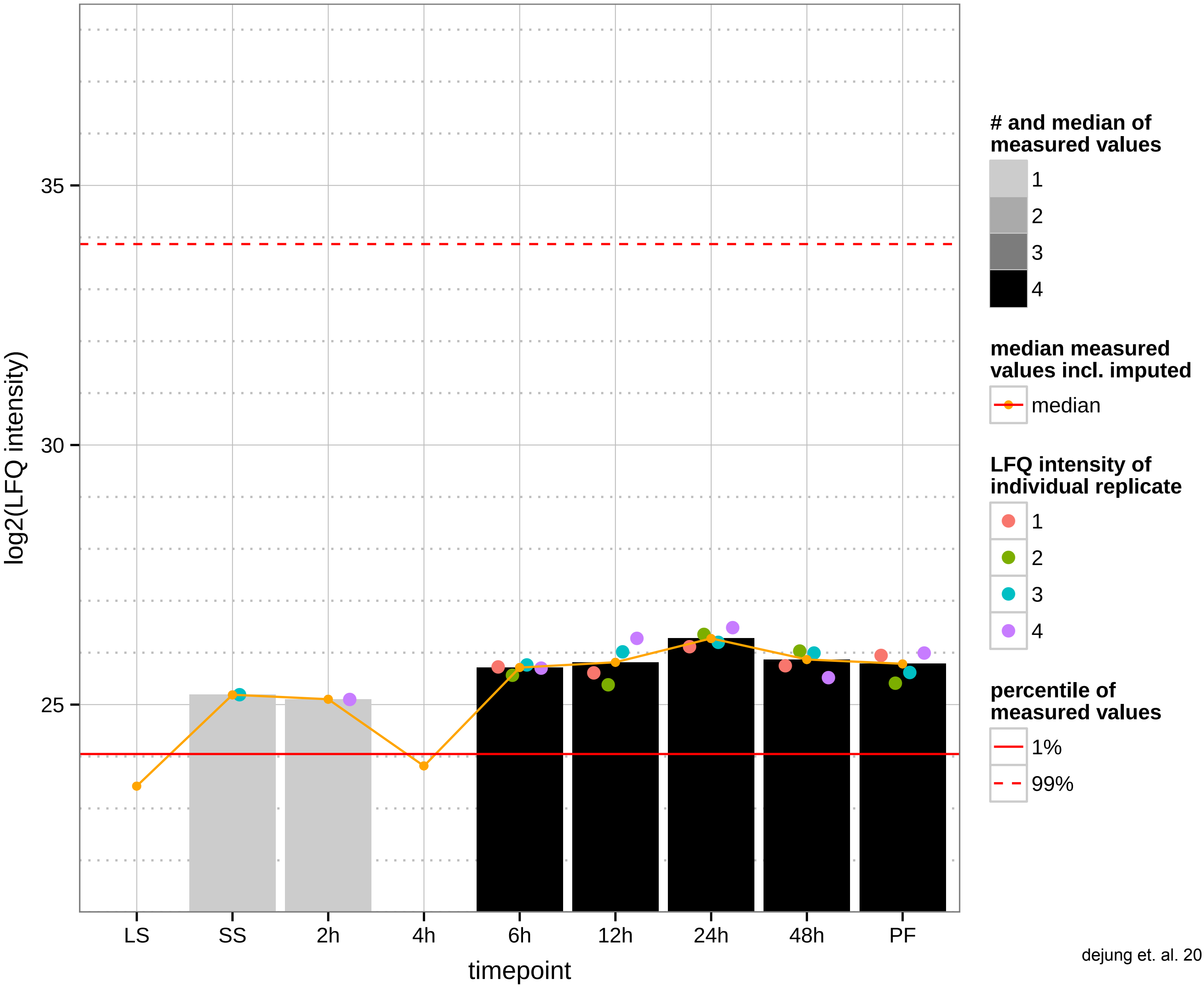




dejung et. al. 2015

hypothetical protein, conserved
Tb927.4.3540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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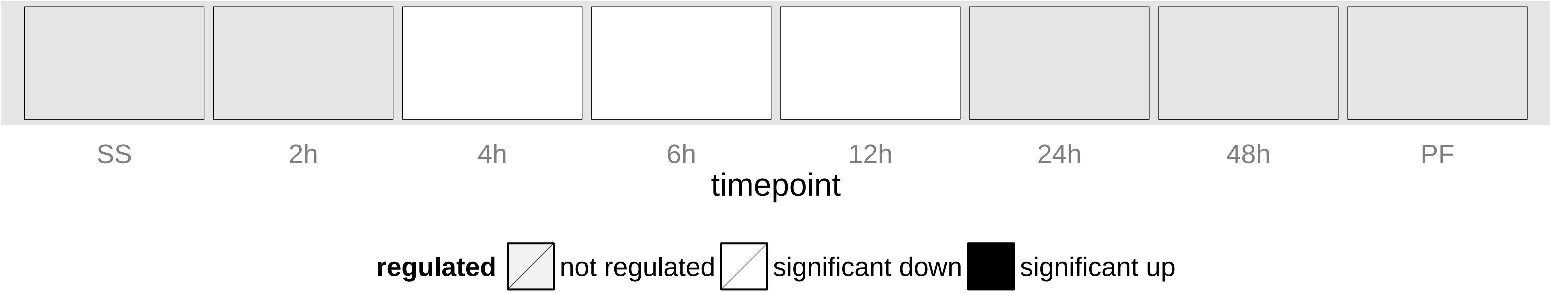

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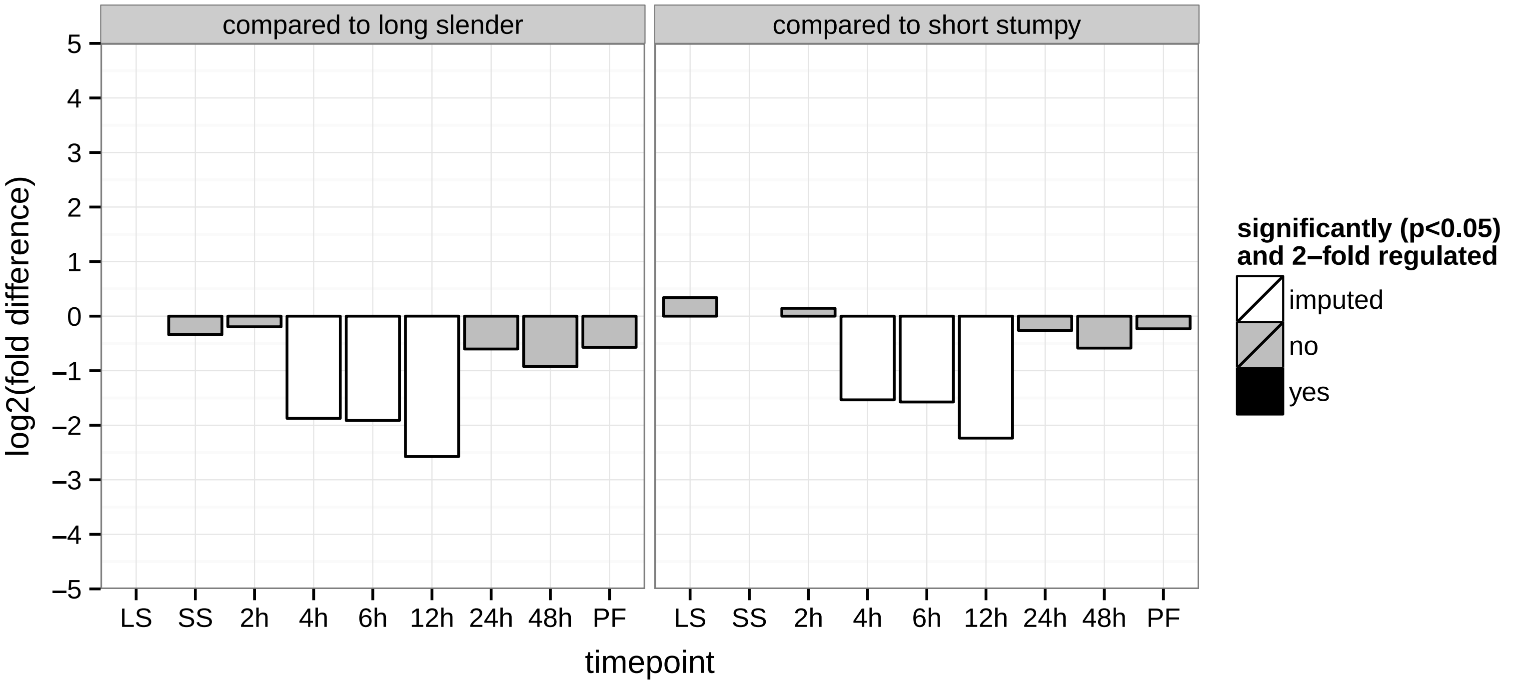
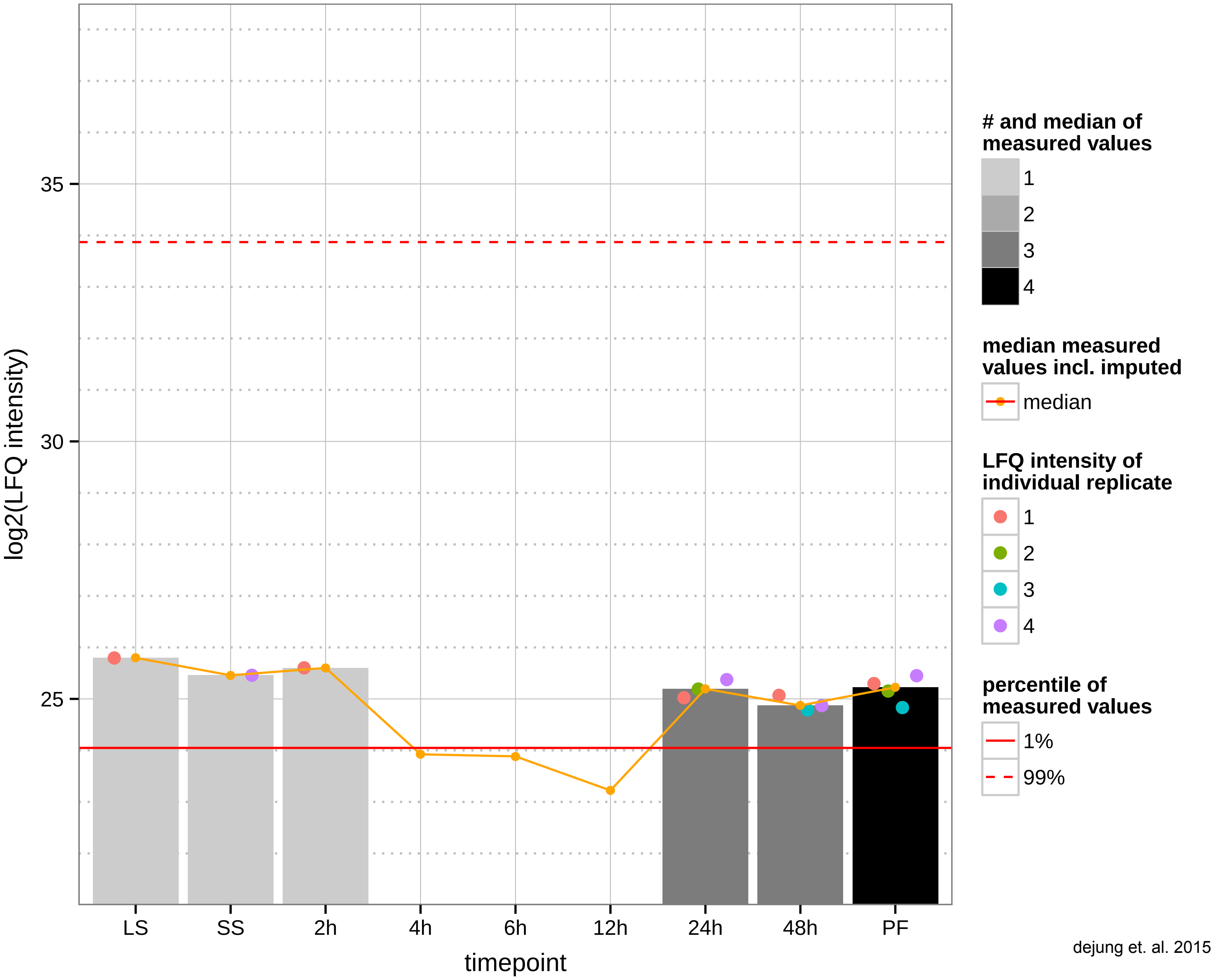
NADH–ubiquinone oxidoreductase, mitochondrial, putative, putative (NUBM)
Tb927.5.450;Tb11.v5.0222
AGOF: null, 4 iron, 4 sulfur cluster binding, FMN binding, NAD binding, oxidoreductase activity, acting on NADH or NADPH
AGOC: null, mitochondrion, respiratory chain complex I
AGOP: null, oxidation–reduction process
PGOF: 4 iron, 4 sulfur cluster binding, FMN binding, NAD binding, oxidoreductase activity, acting on NADH or NADPH
PGOC: null
PGOP: oxidation–reduction process





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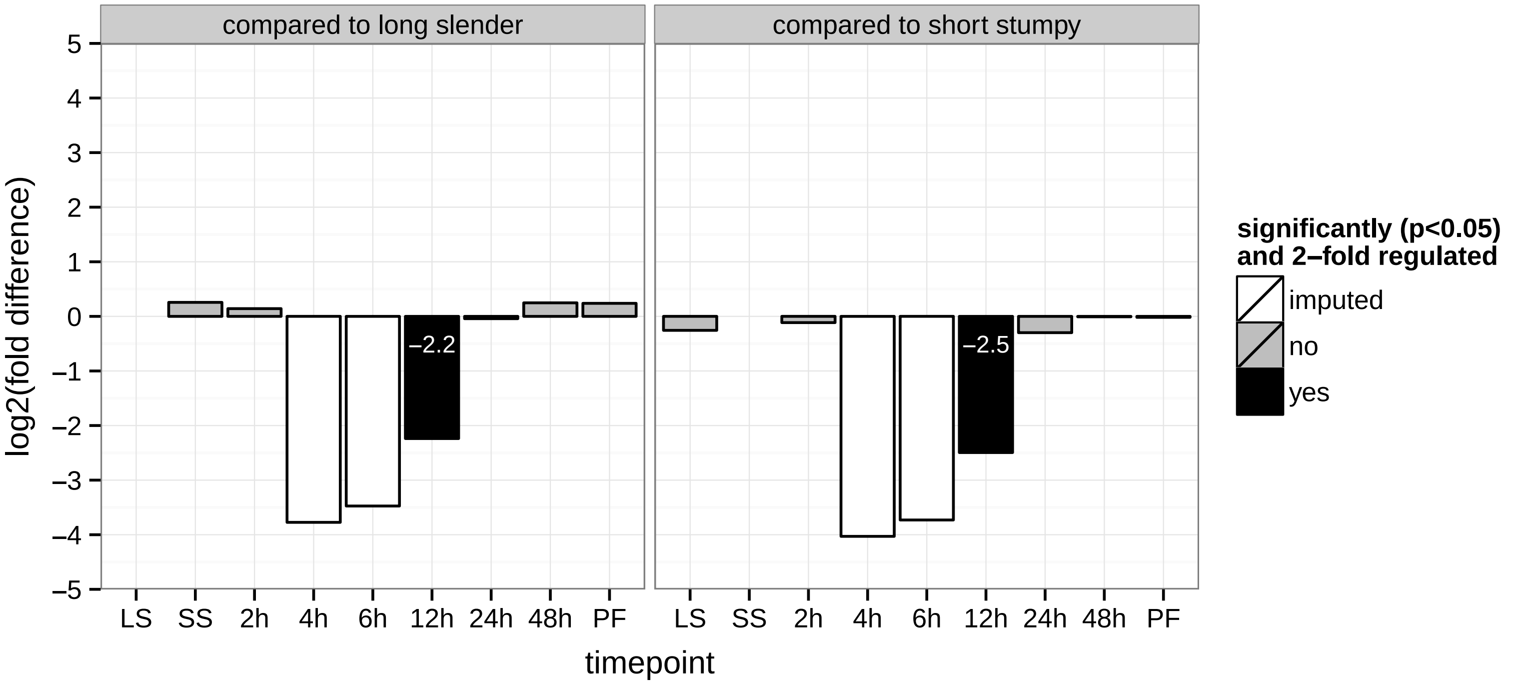
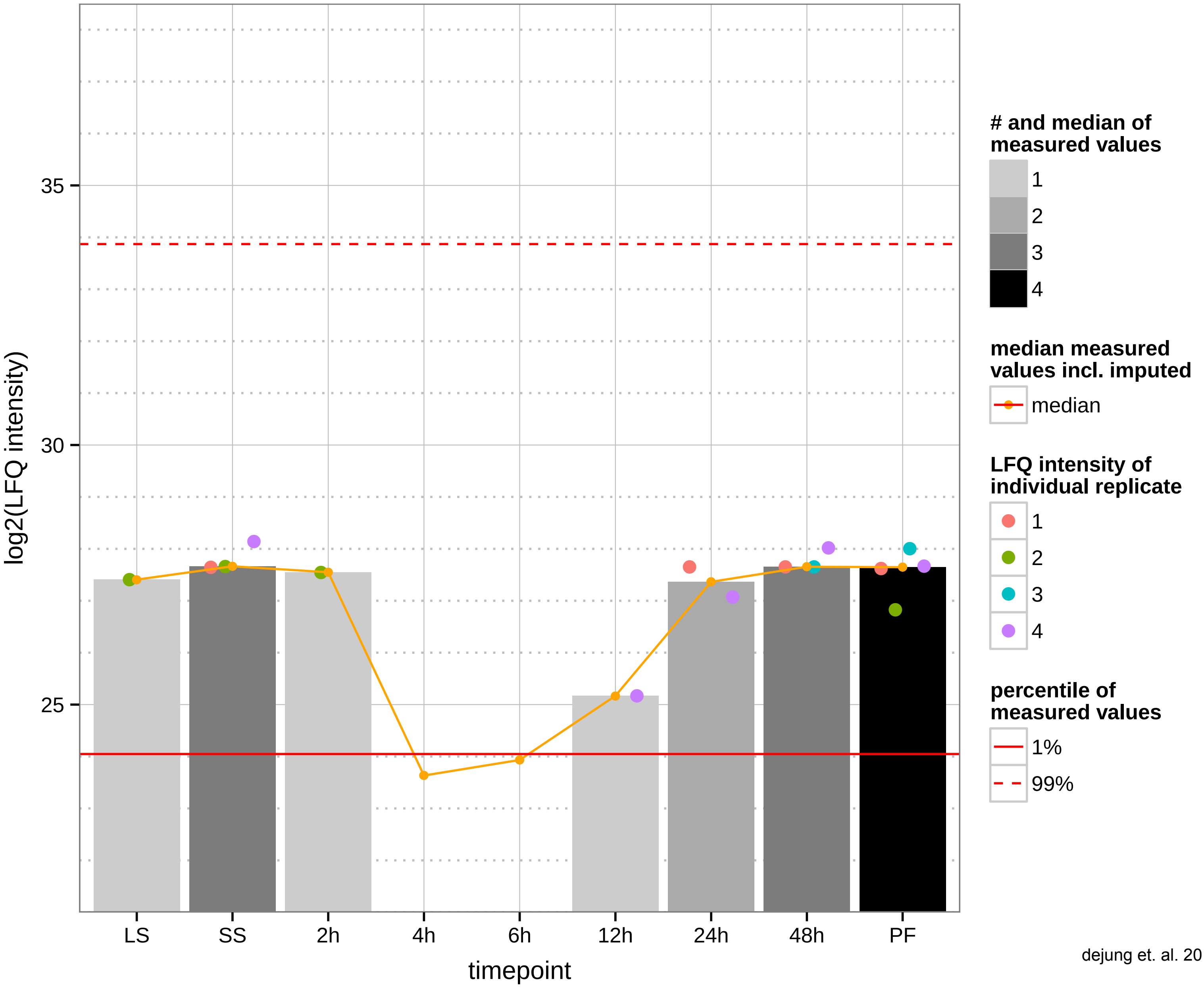
hypothetical protein, conserved
Tb927.10.3810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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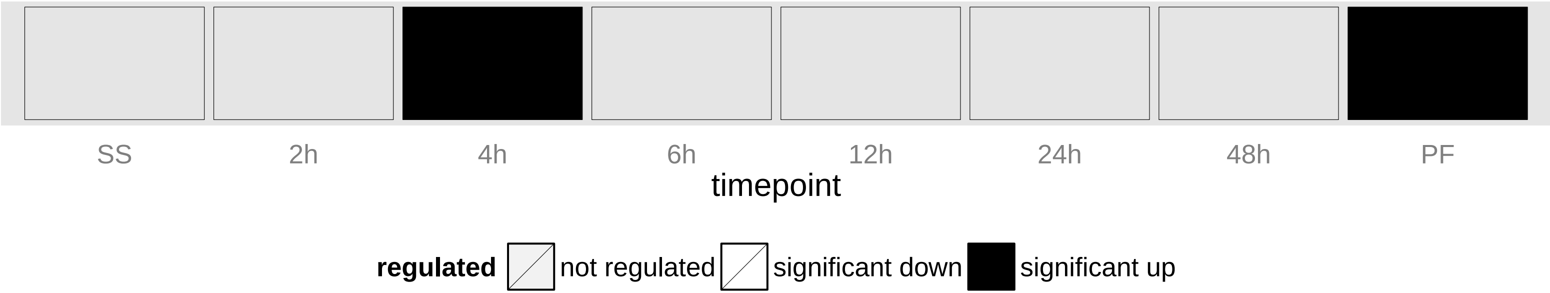

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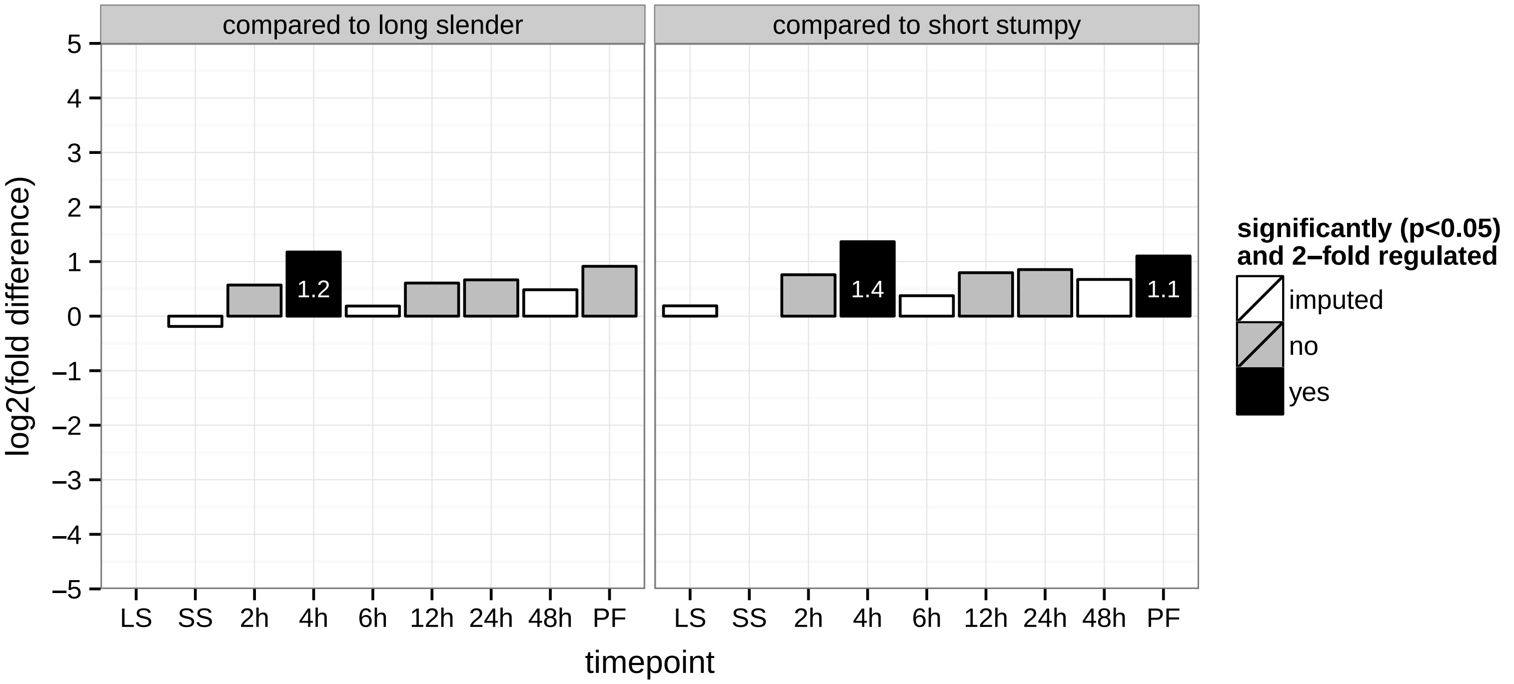
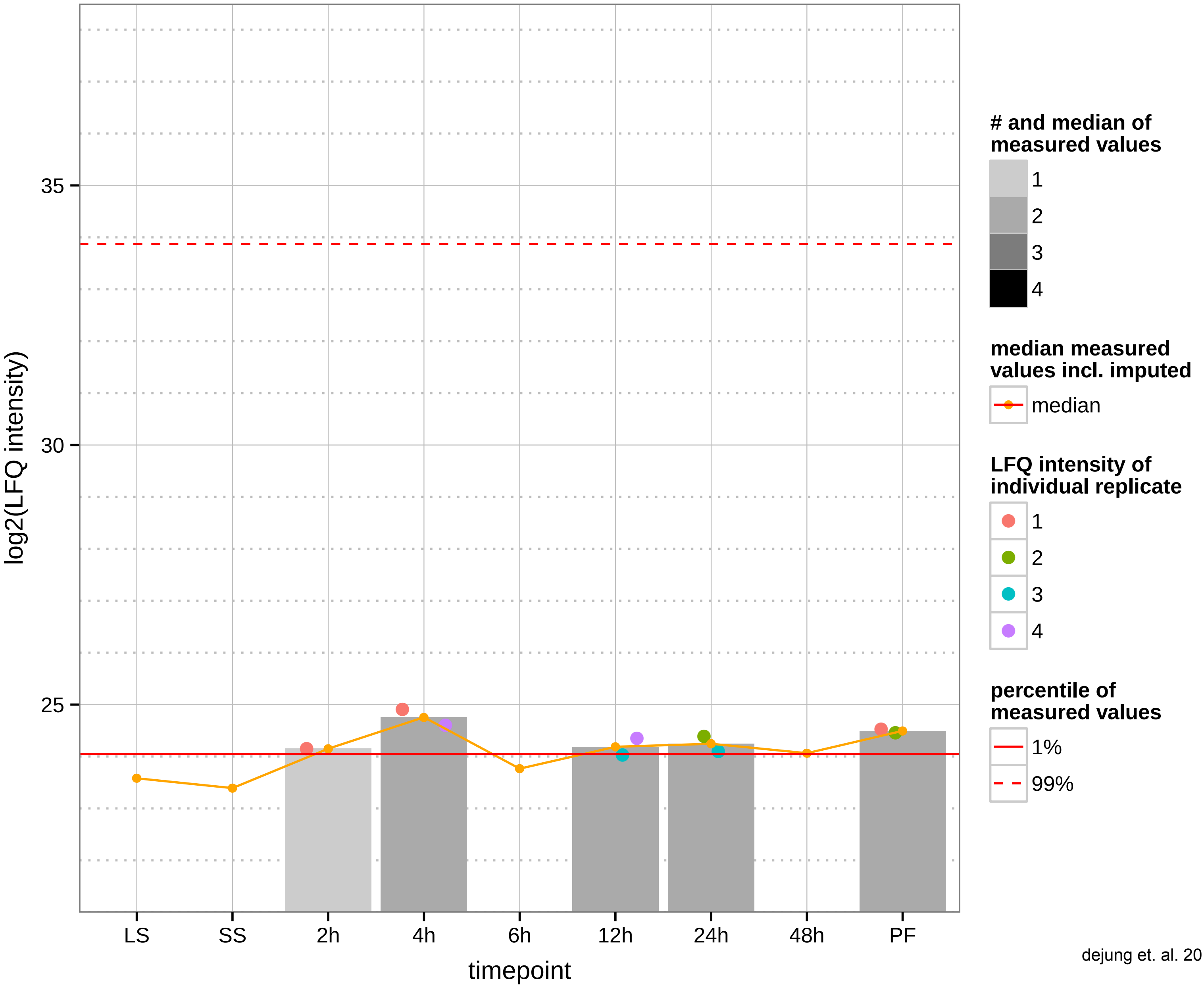
hypothetical protein, conserved
Tb927.11.2220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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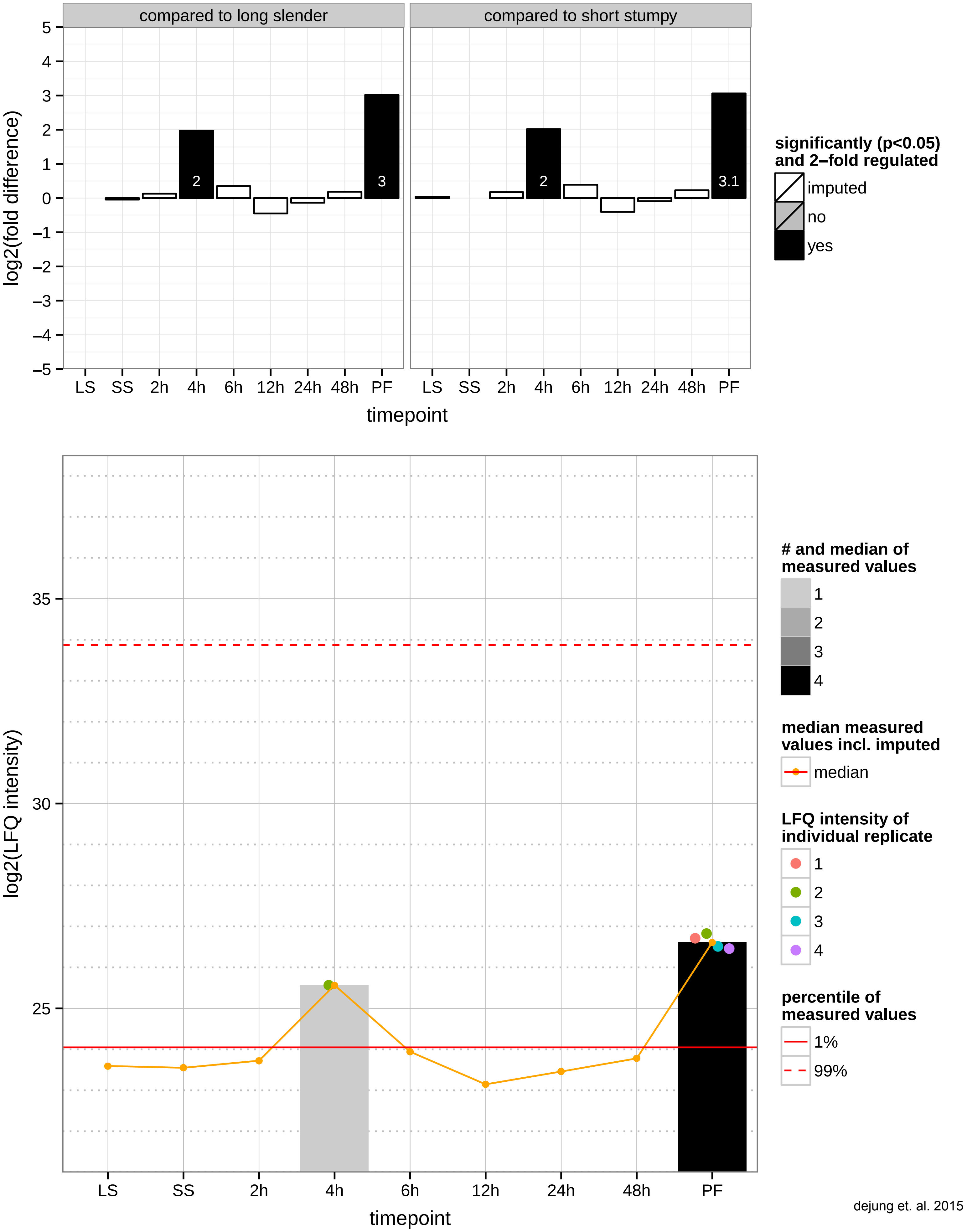
retrotransposon hot spot protein 1 (RHS1), putative
Tb927.6.160
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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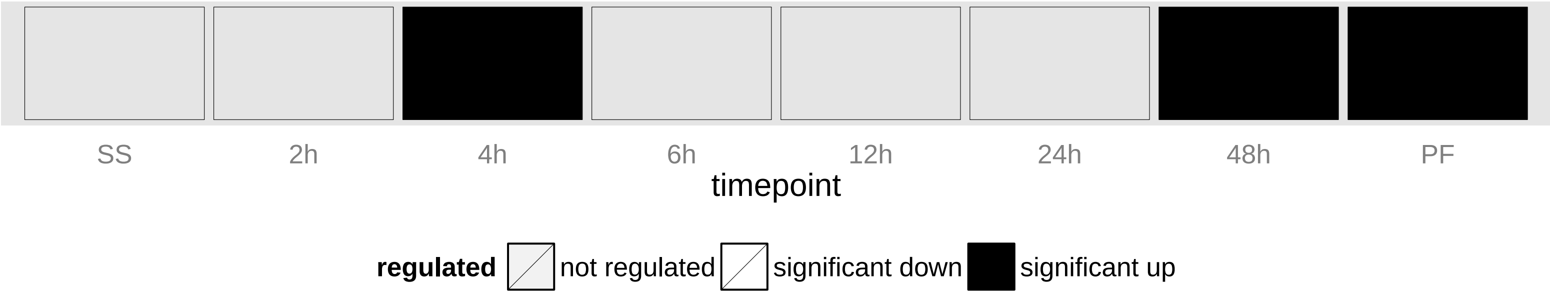

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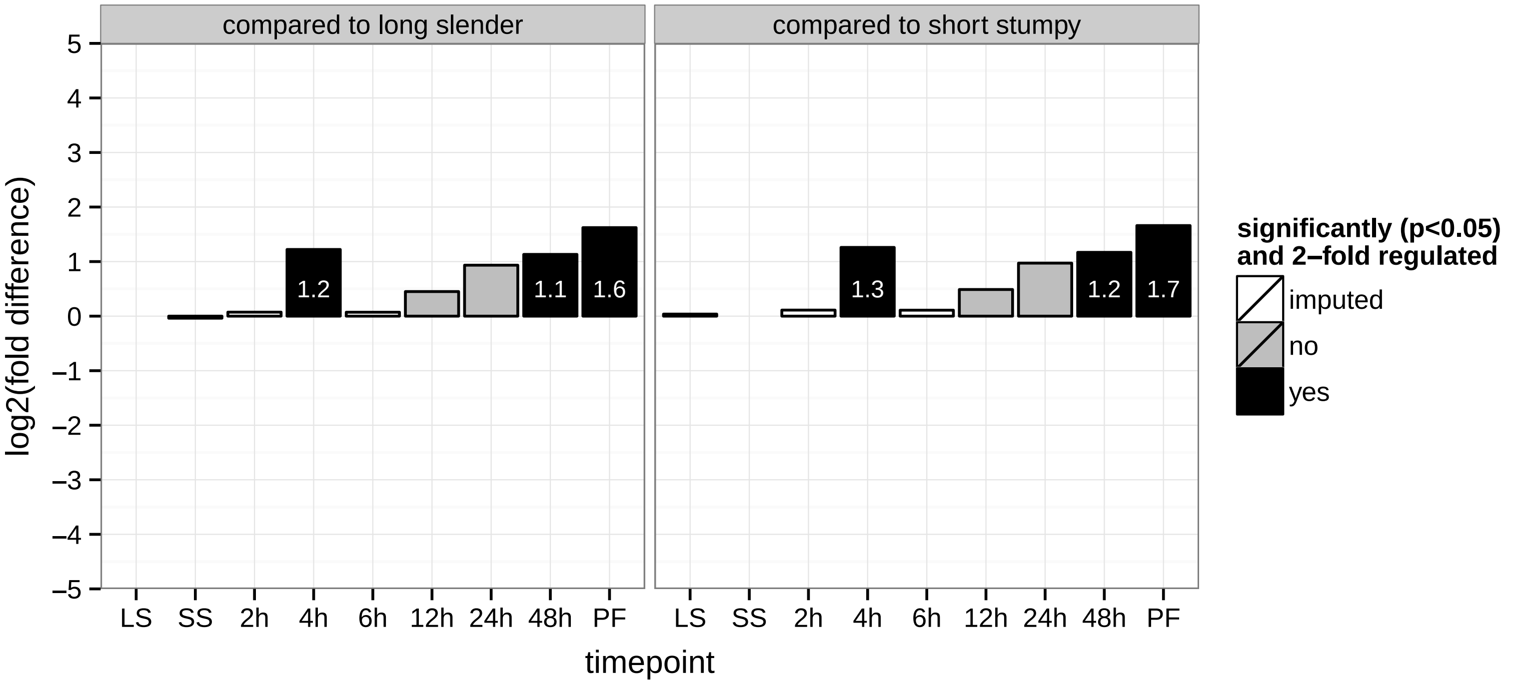
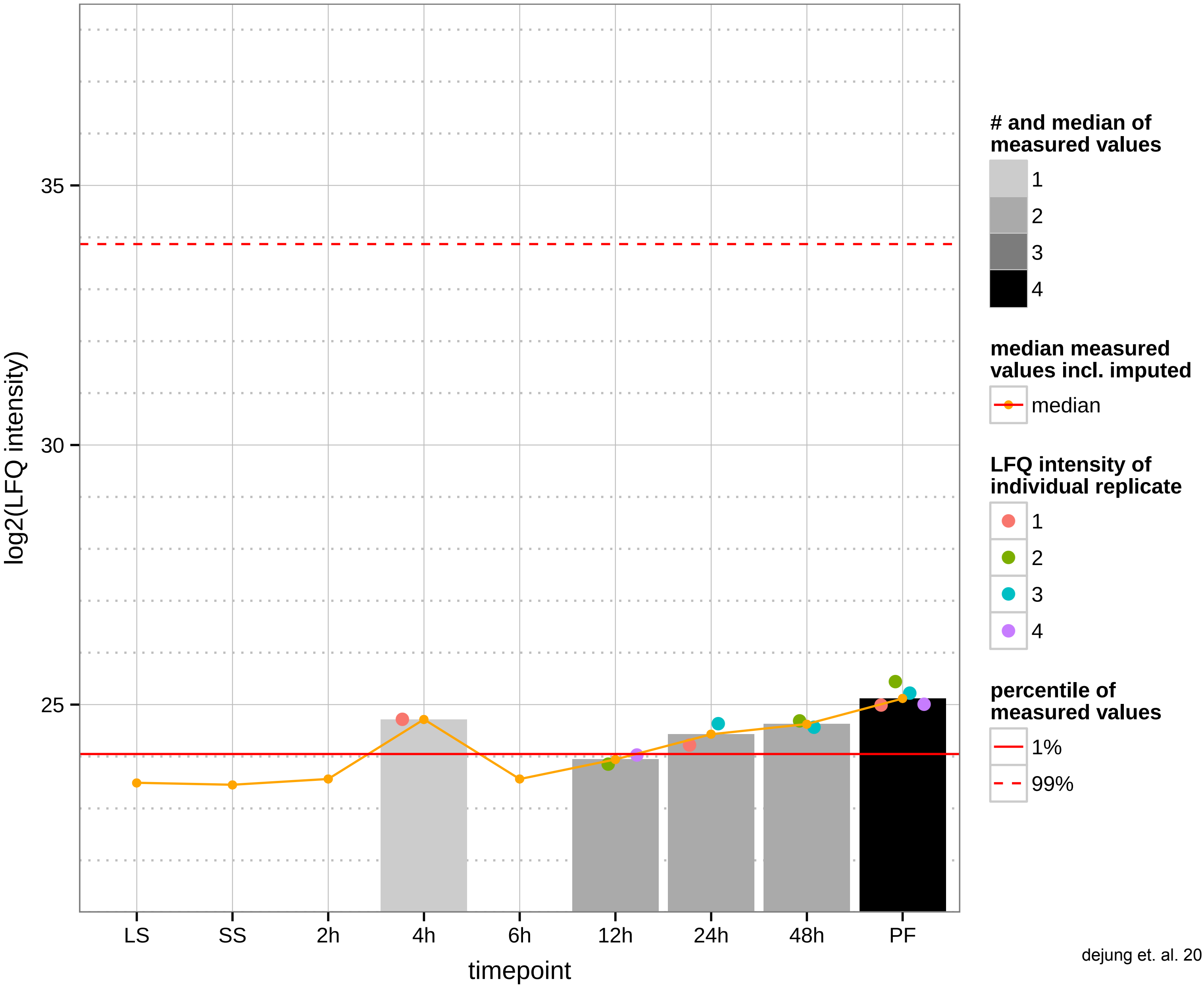
tubulin tyrosine ligase protein, putative
Tb927.10.13870
AGOF: tubulin–tyrosine ligase activity
AGOC: null
AGOP: cellular protein modification process
PGOF: tubulin–tyrosine ligase activity
PGOC: null
PGOP: cellular protein modification process





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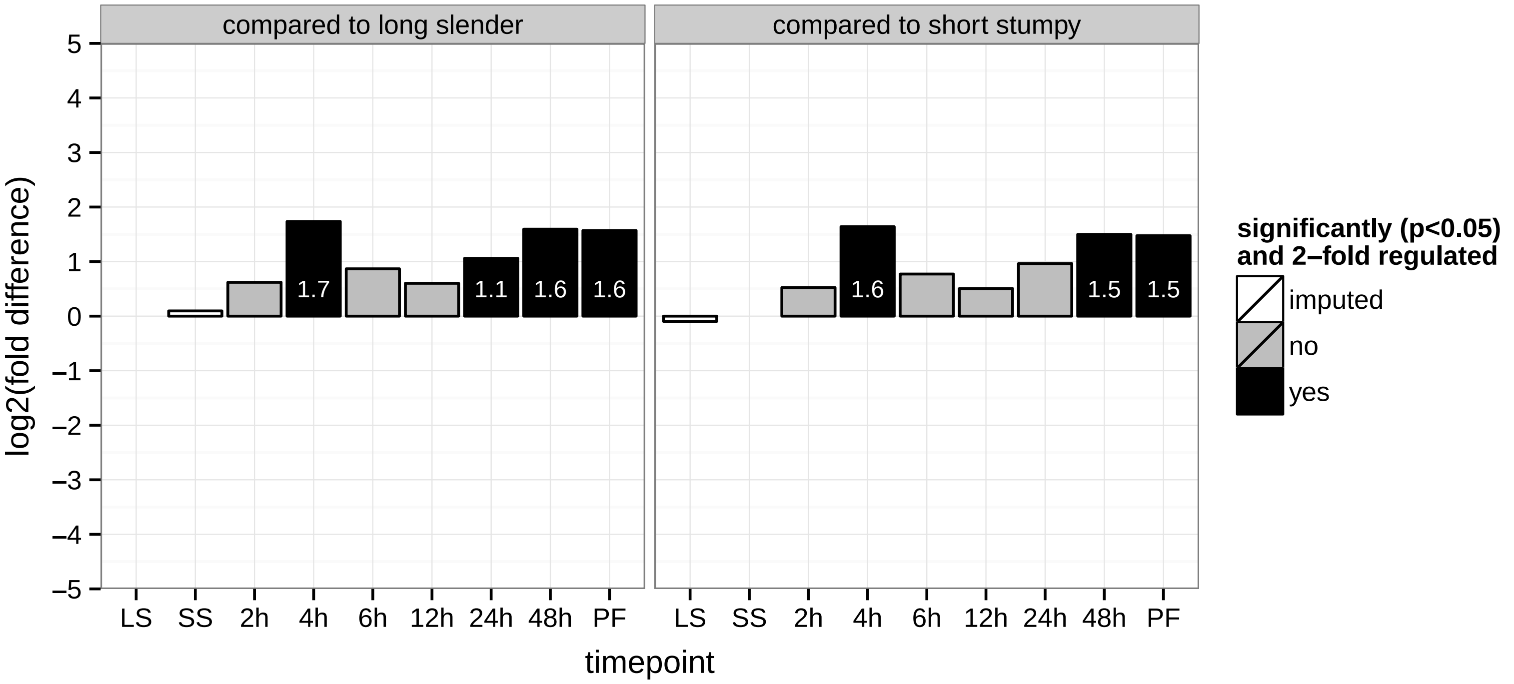
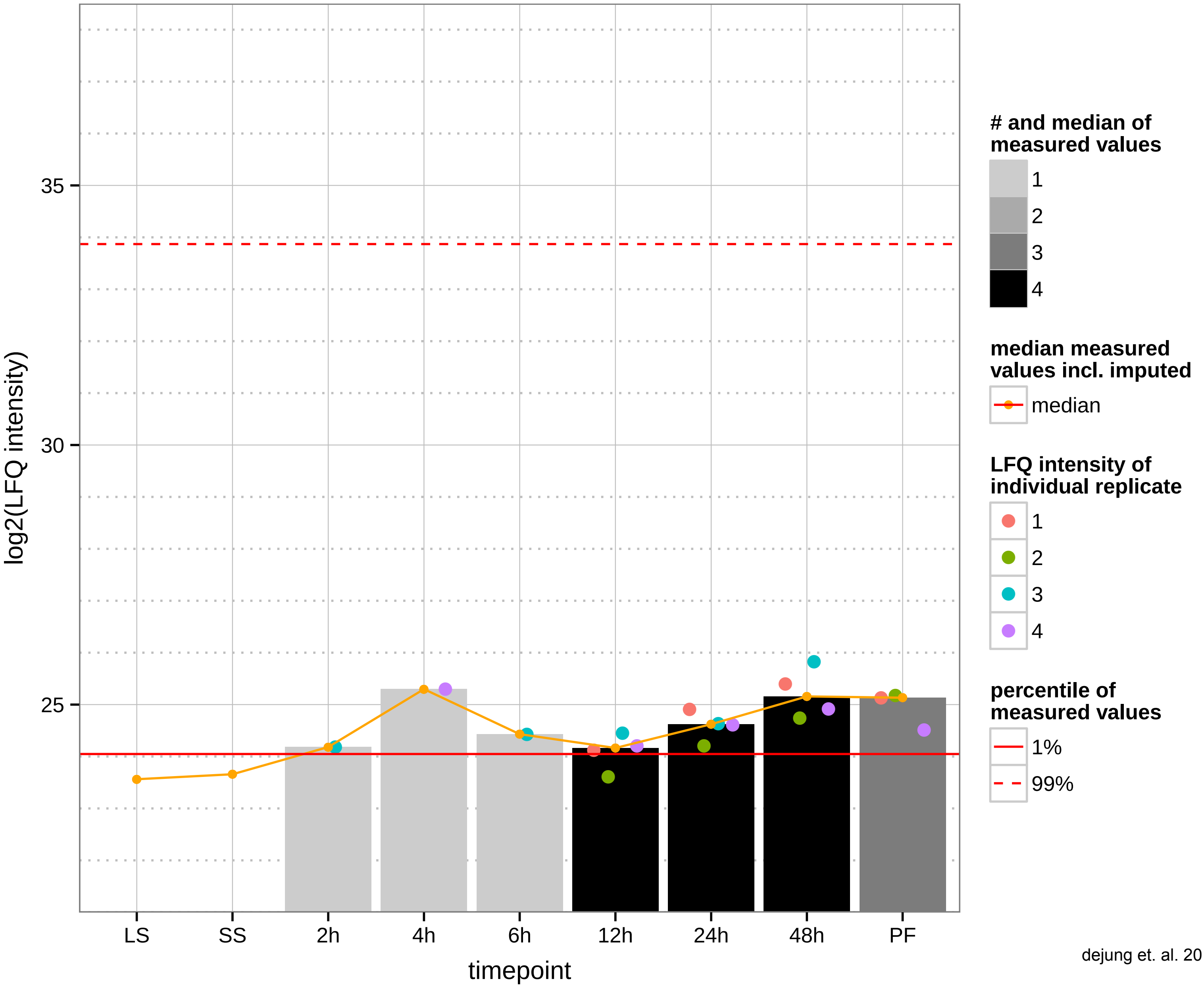
hydrolase, alpha/beta fold family, putative
Tb927.5.2370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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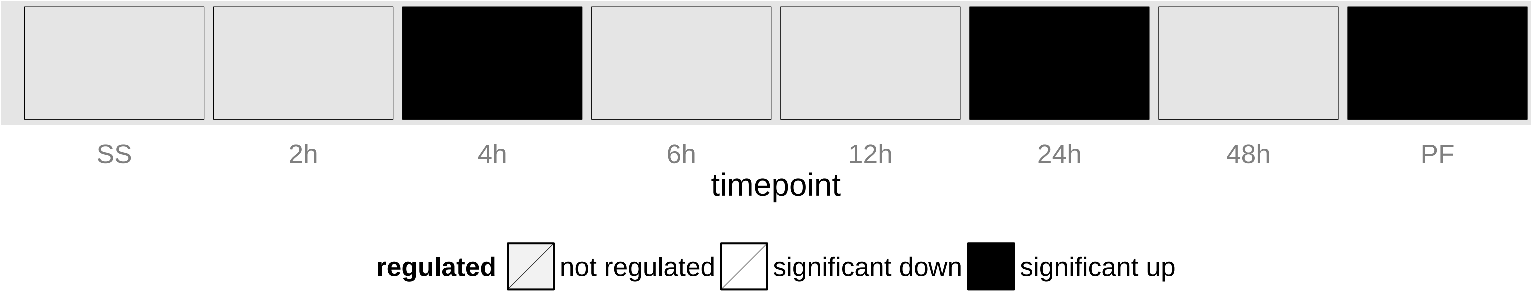
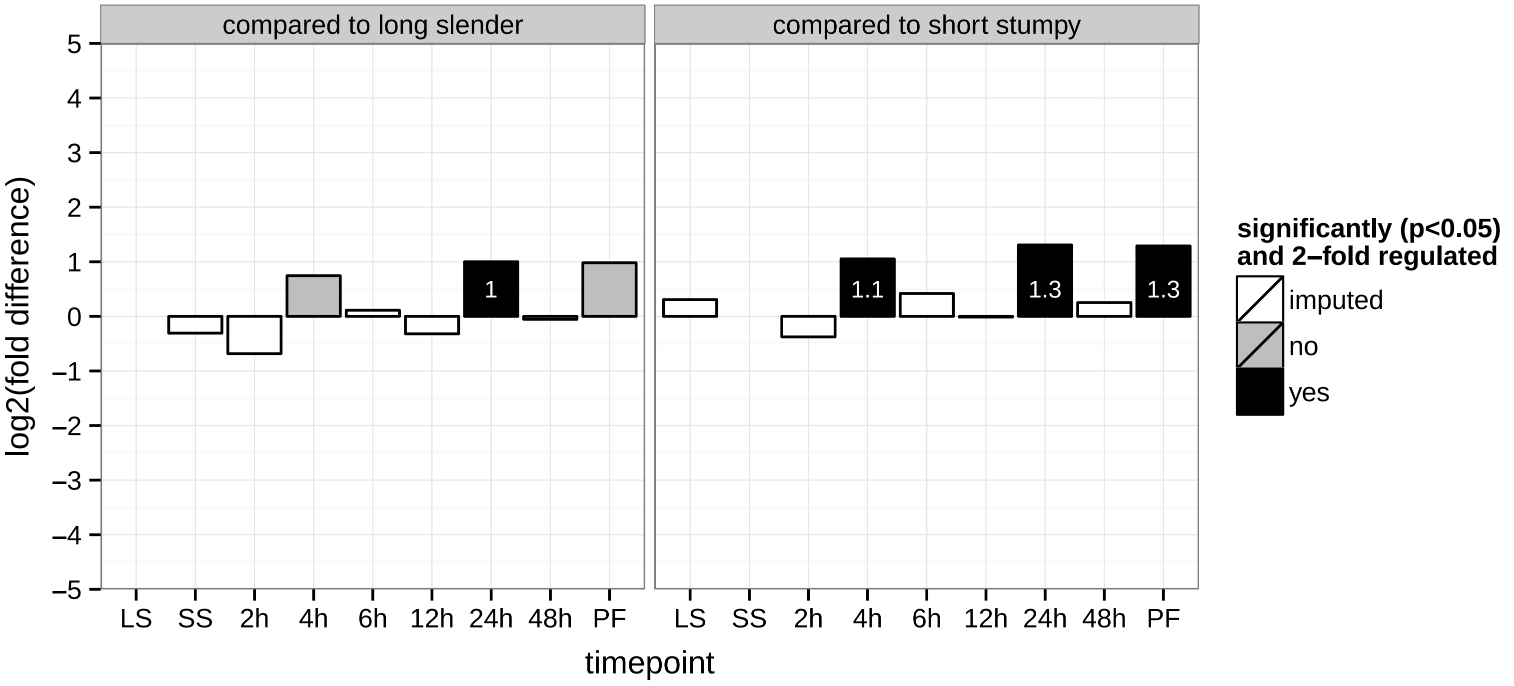
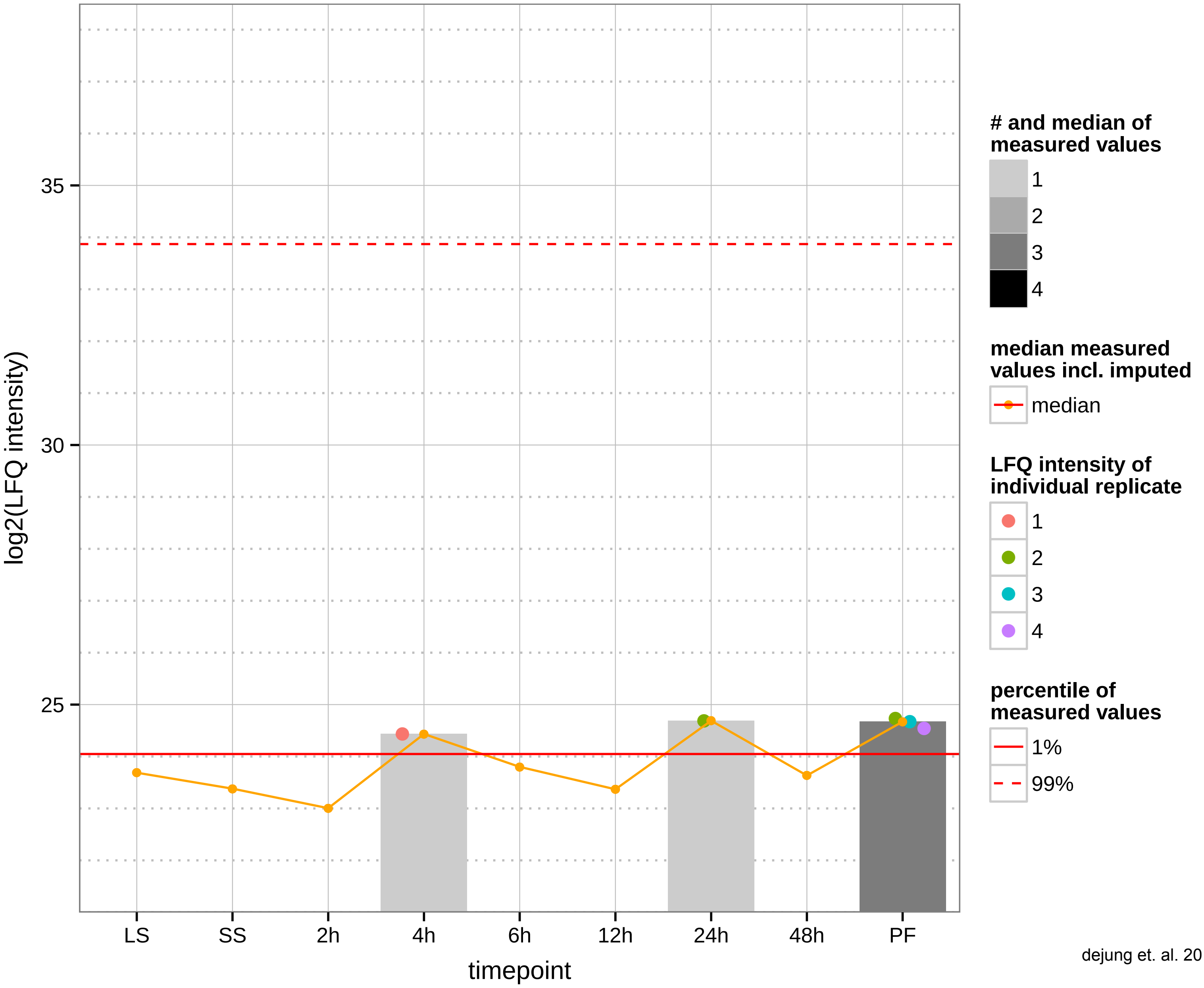


dejung et. al. 2015

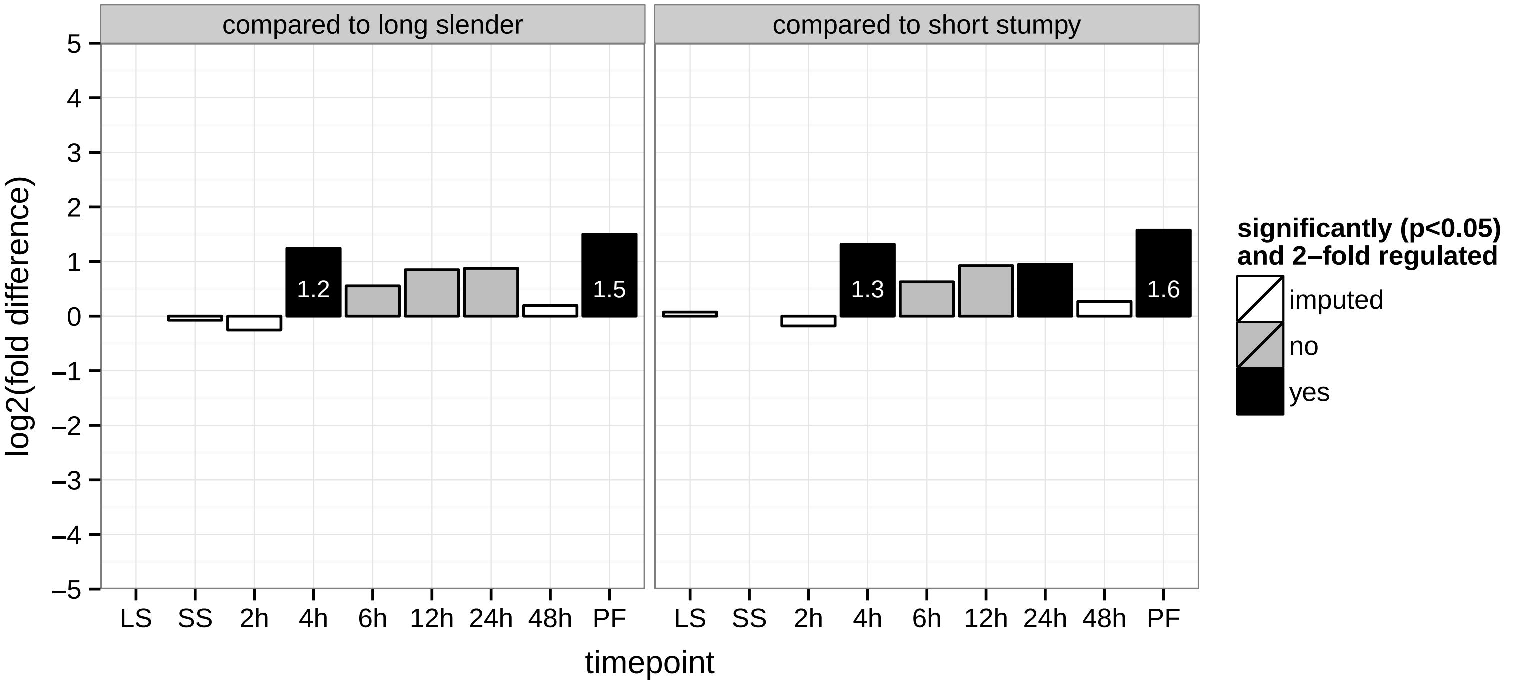
hypothetical protein, conserved
Tb927.10.4550
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

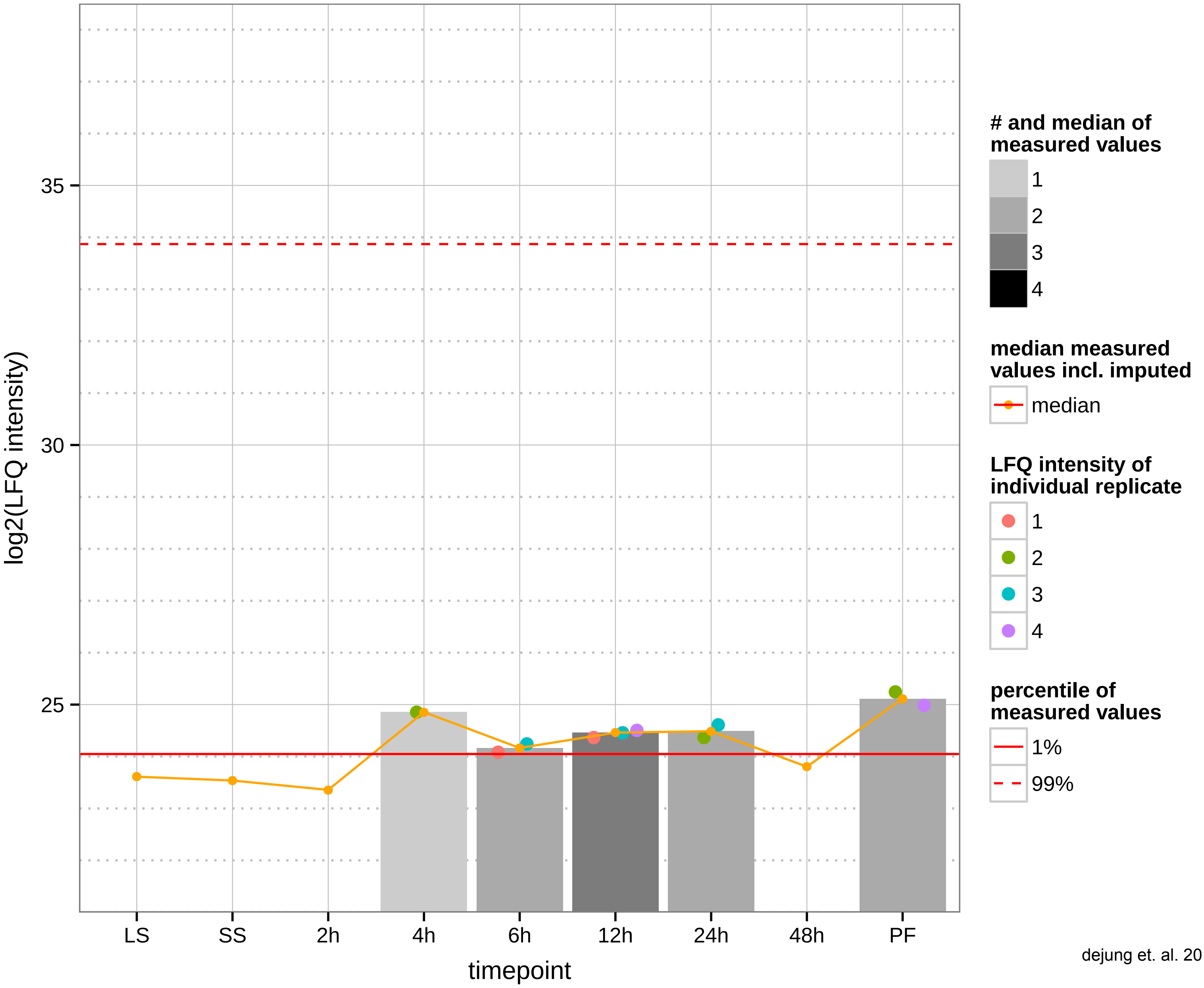




dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.9580.1;Tb927.11.9580.2
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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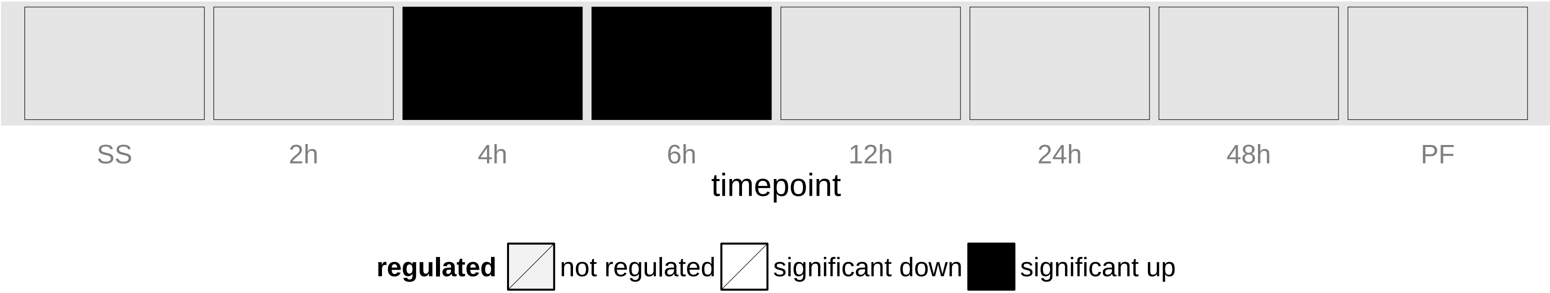

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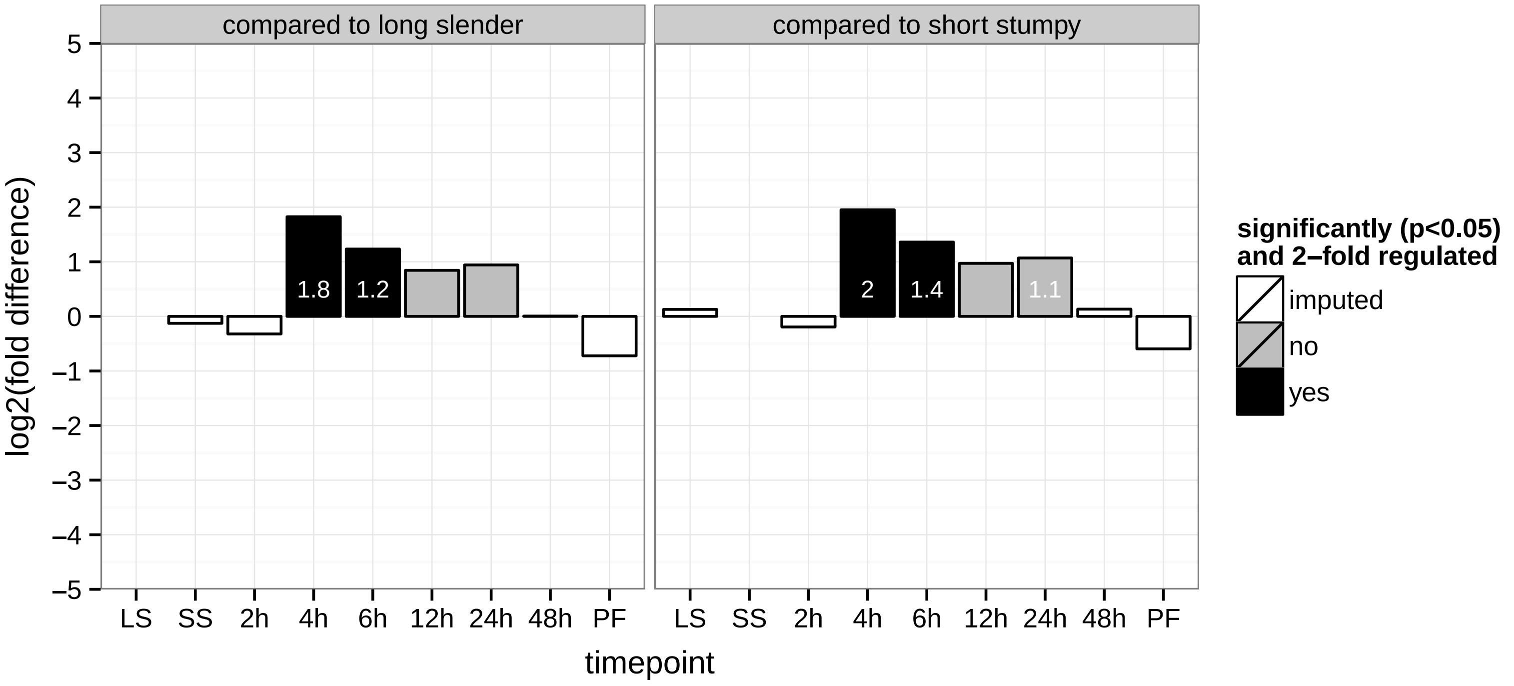
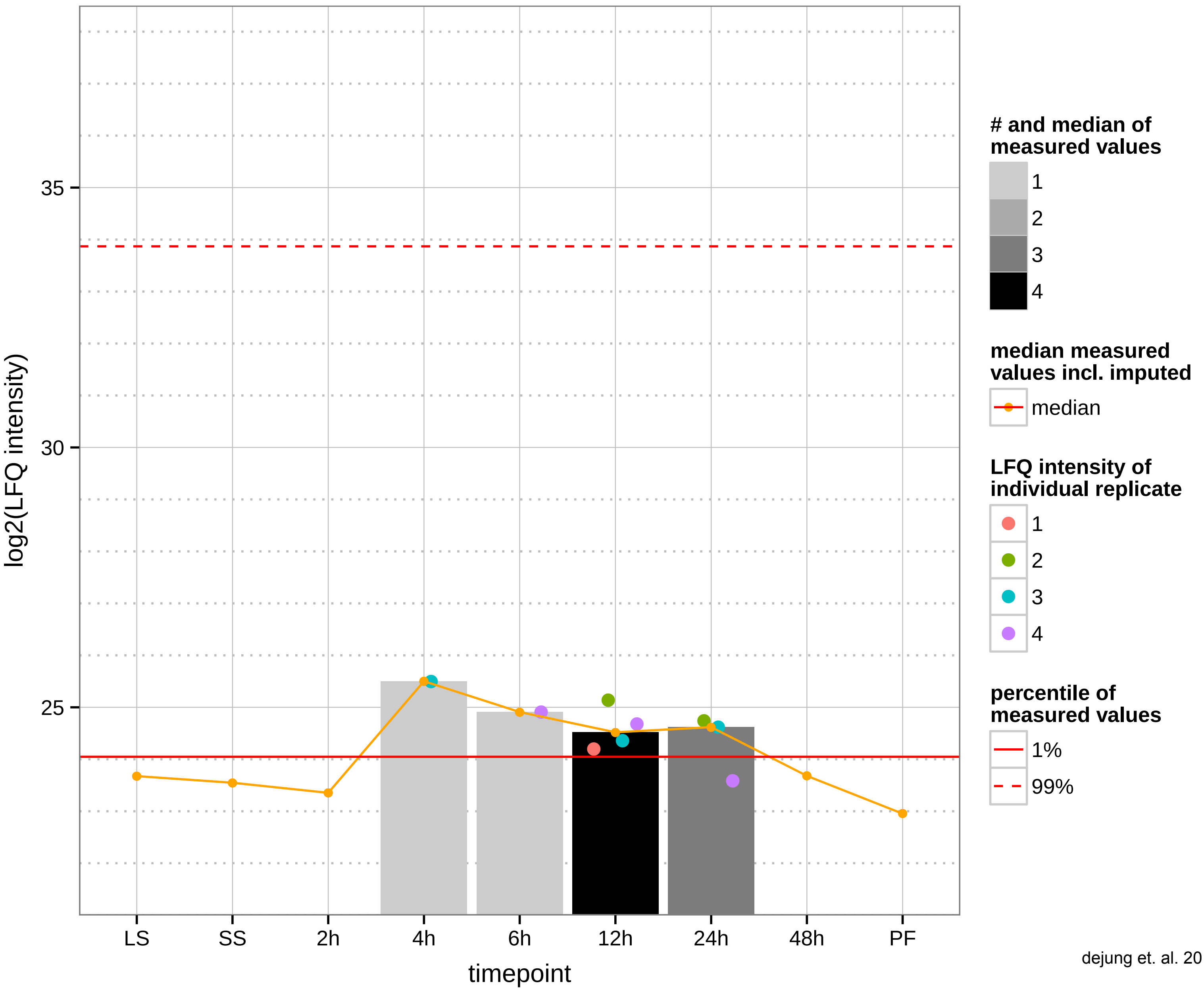
ATP synthase subunit, putative
Tb927.1.3820
AGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, proton−transporting ATPase activity
AGOC: proton−transporting V−type ATPase, V1 domain
AGOP: ATP hydrolysis coupled proton transport
PGOF: hydrogen ion transporting ATP synthase activity, rotational mechanism, proton−transporting ATPase activity
PGOC: proton−transporting V−type ATPase, V1 domain, proton−transporting two−sector ATPase complex, catalytic domain
PGOP: ATP hydrolysis coupled proton transport





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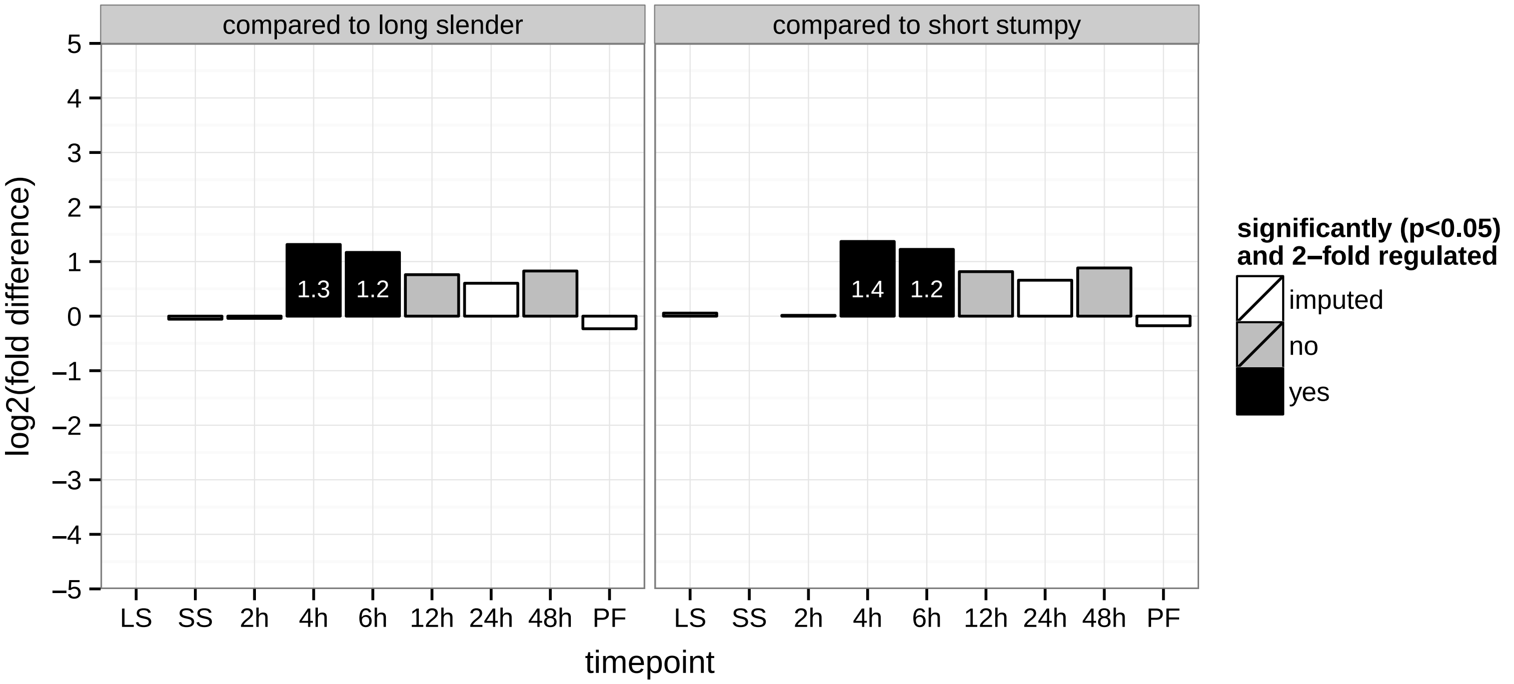
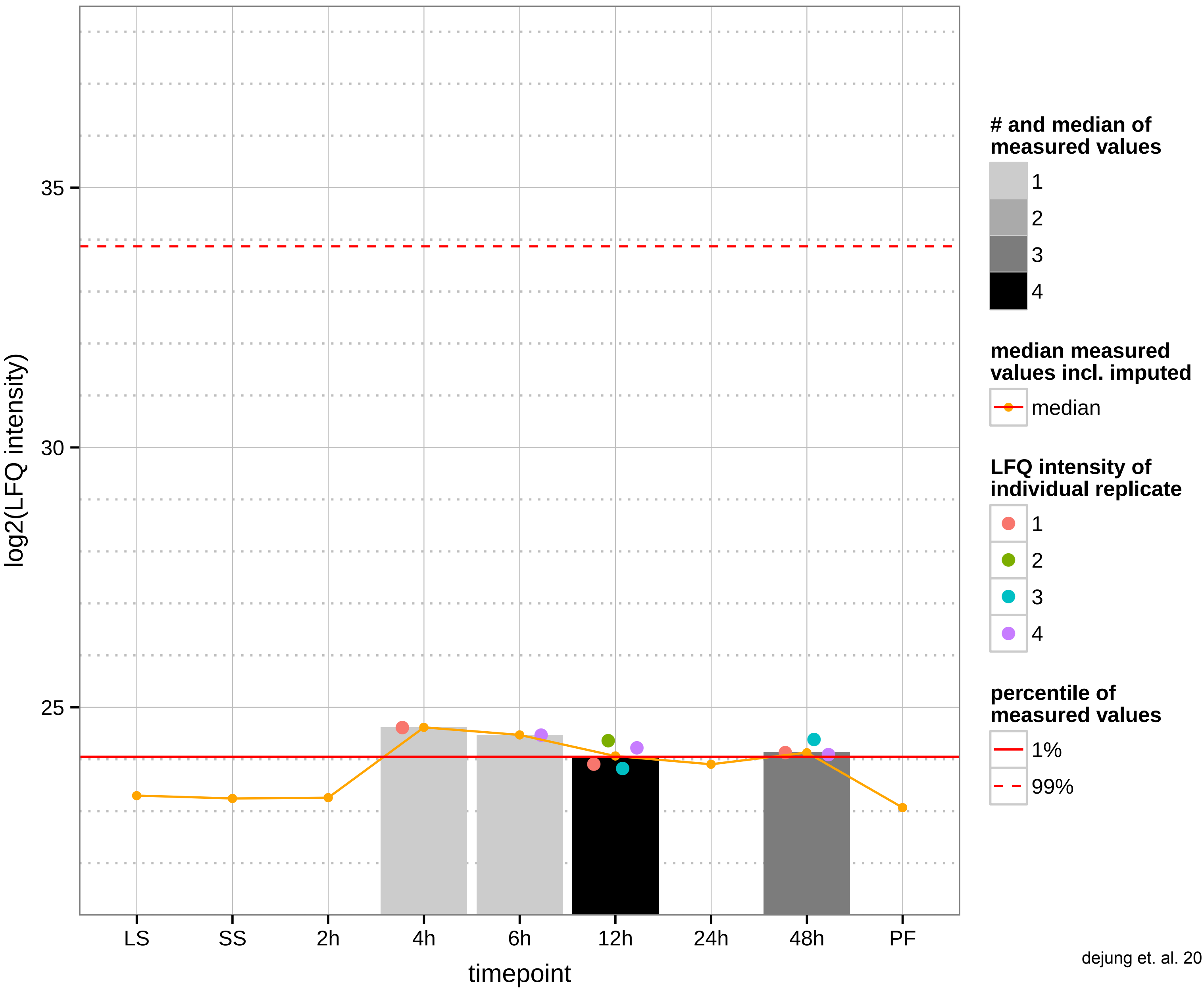
hypothetical protein, conserved
Tb927.9.8050
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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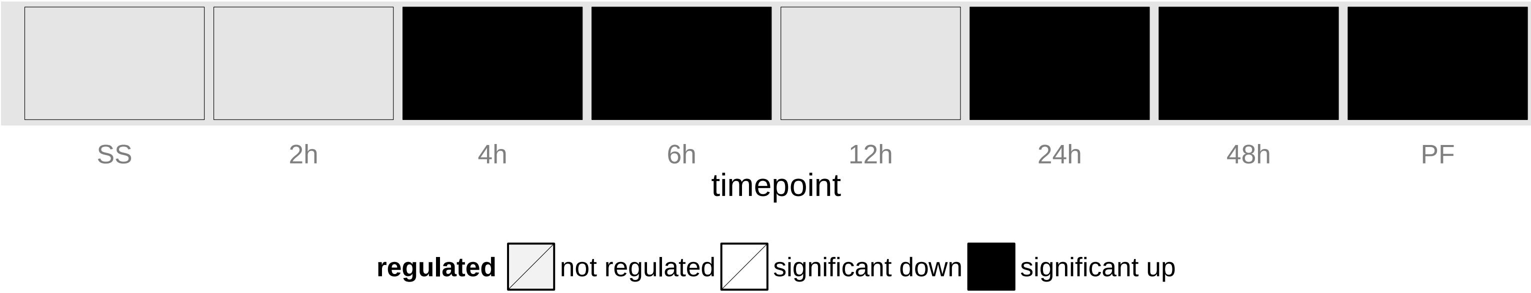
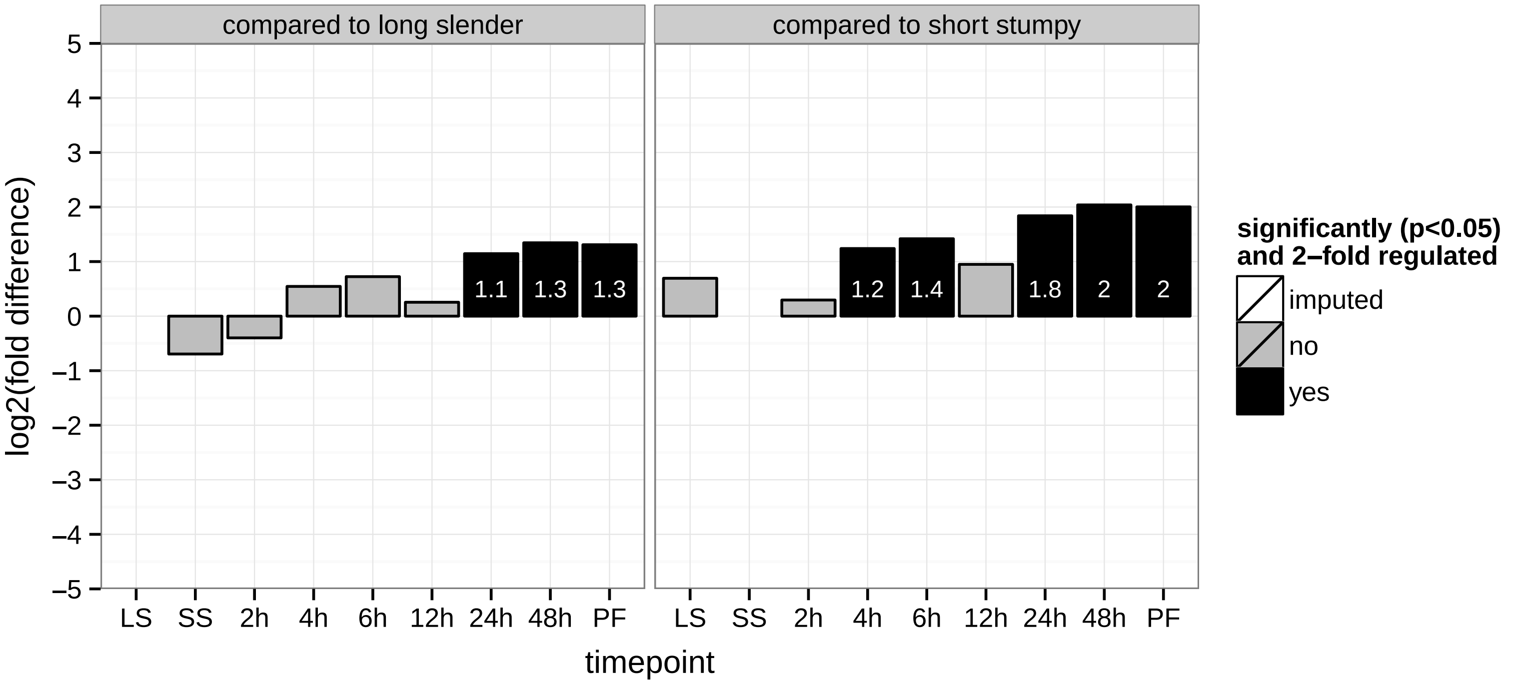
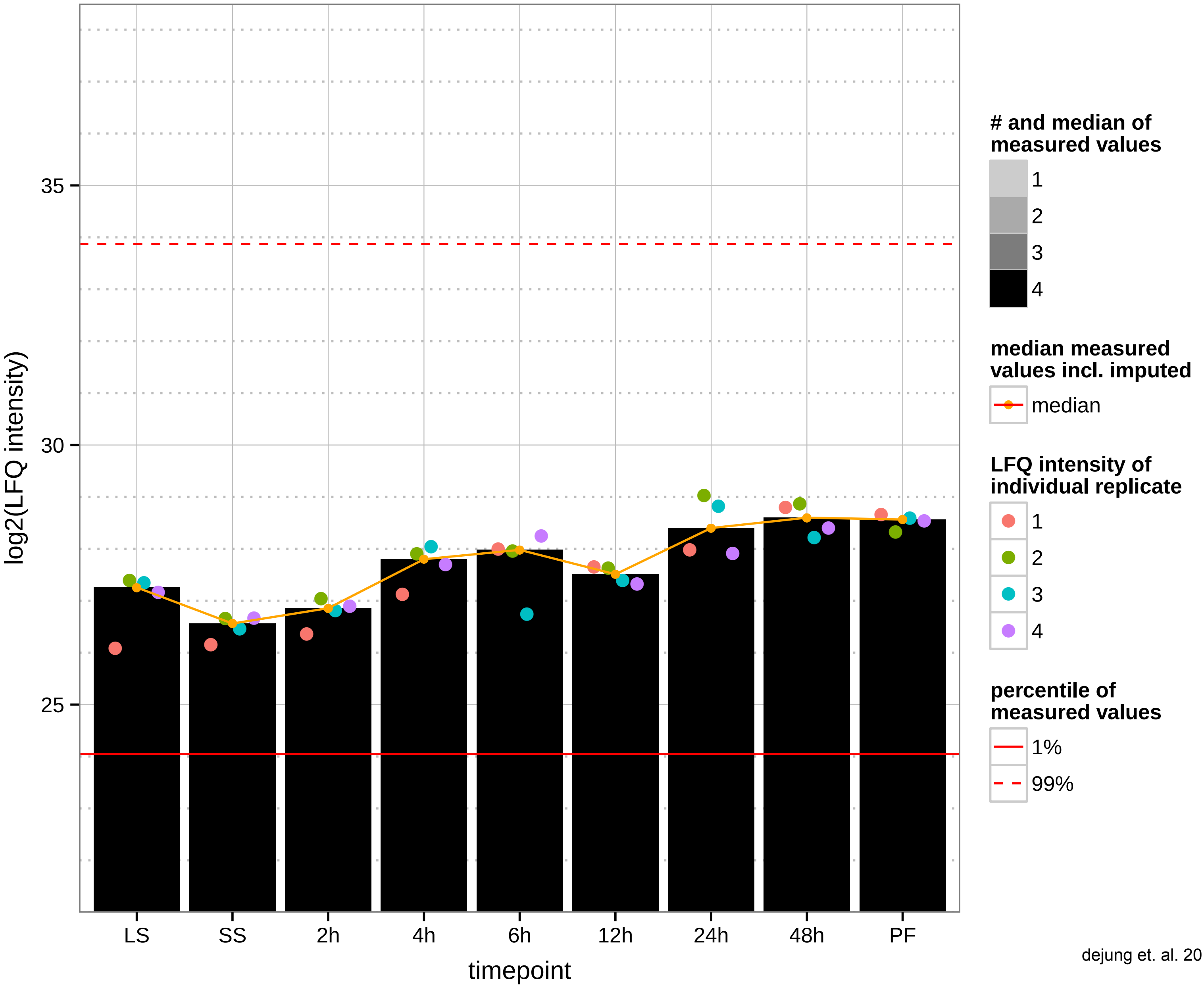


dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.16080
AGOF: null
AGOC: Golgi apparatus, endoplasmic reticulum
AGOP: intracellular protein transport
PGOF: null
PGOC: null
PGOP: null





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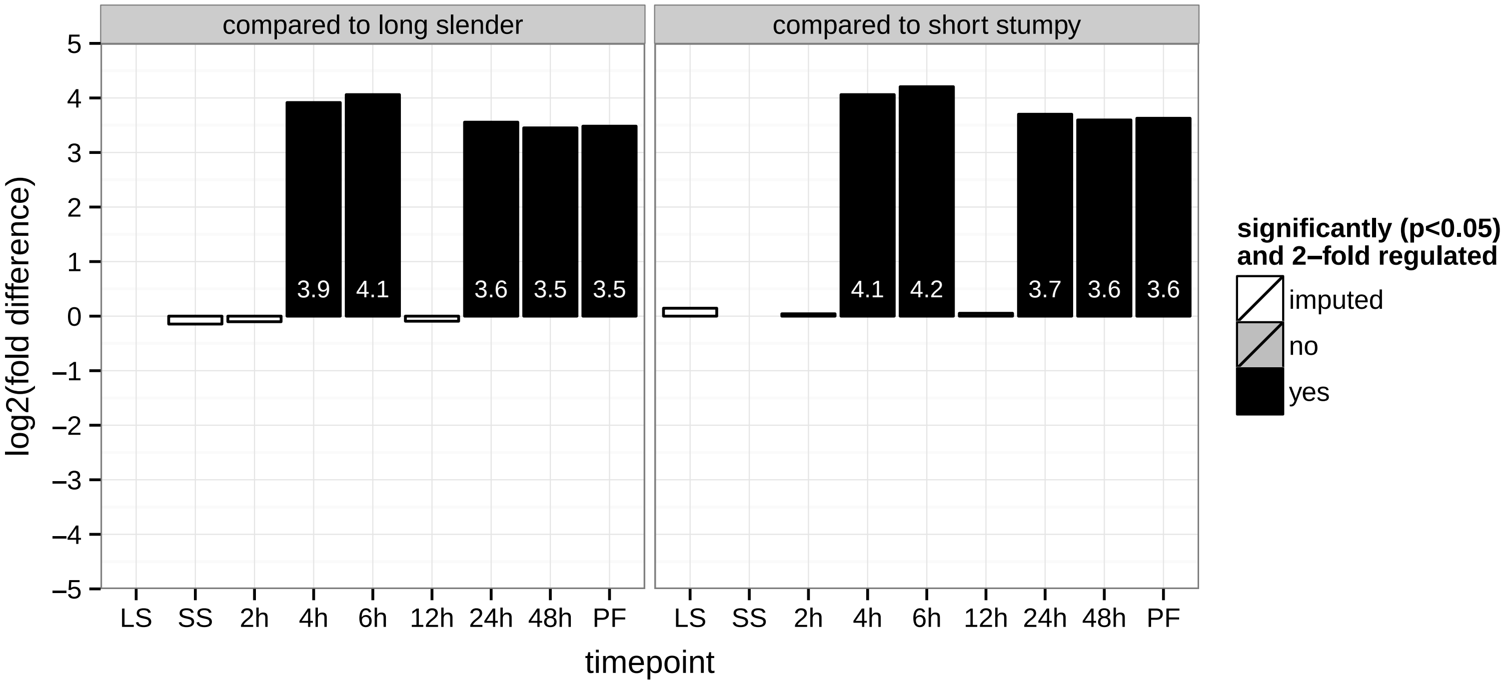
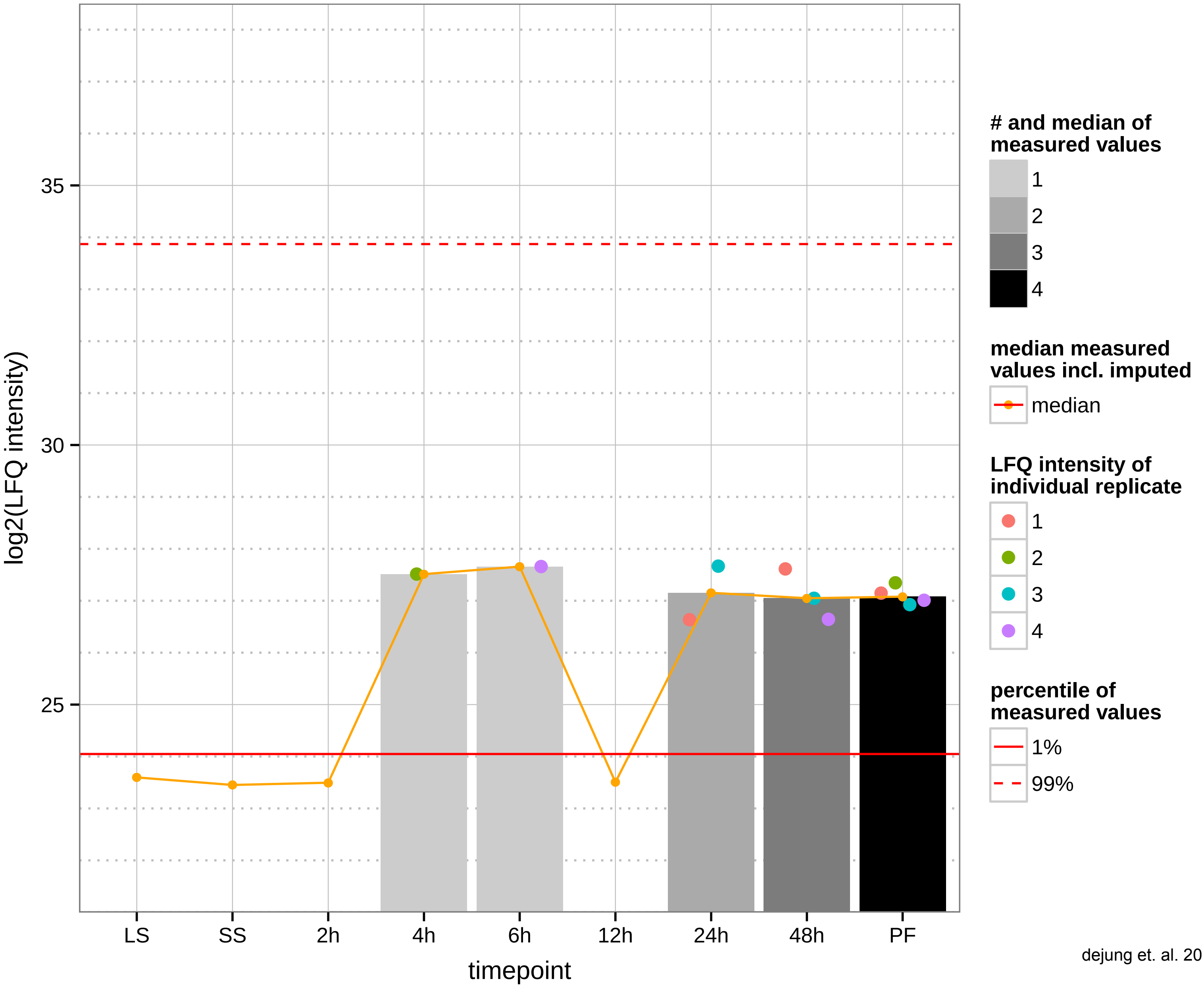
ATP–dependent chaperone, putative, mitochondrial chaperone BCS1
Tb927.8.3580
AGOF: ATP binding, nucleoside–triphosphatase activity
AGOC: mitochondrion
AGOP: aerobic respiration
PGOF: ATP binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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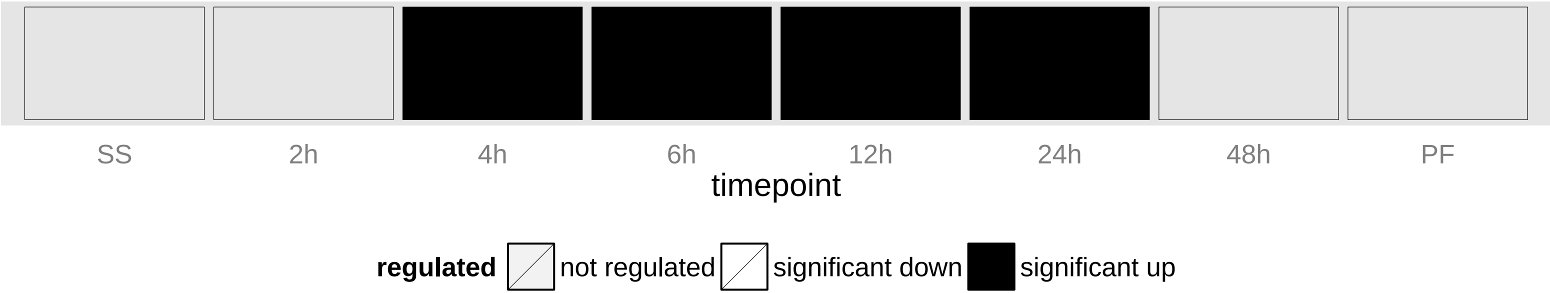
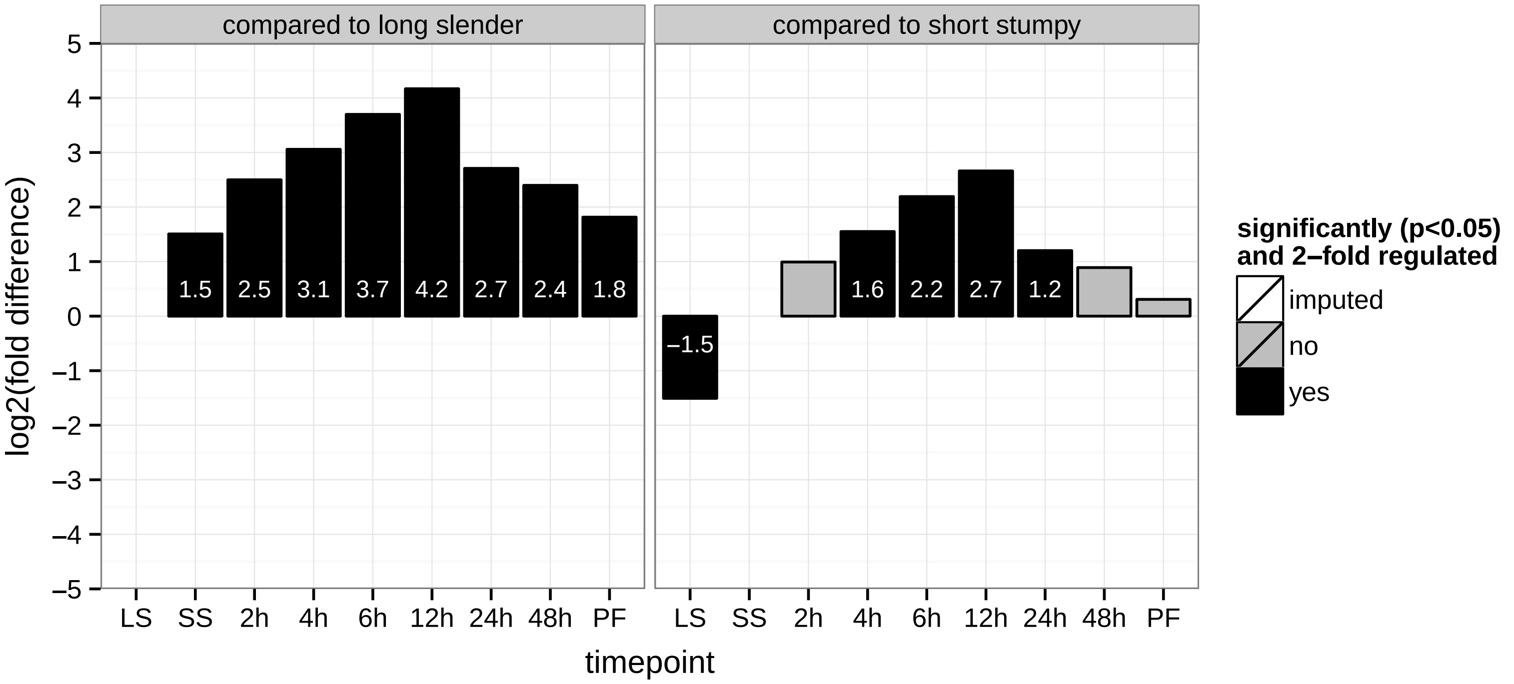
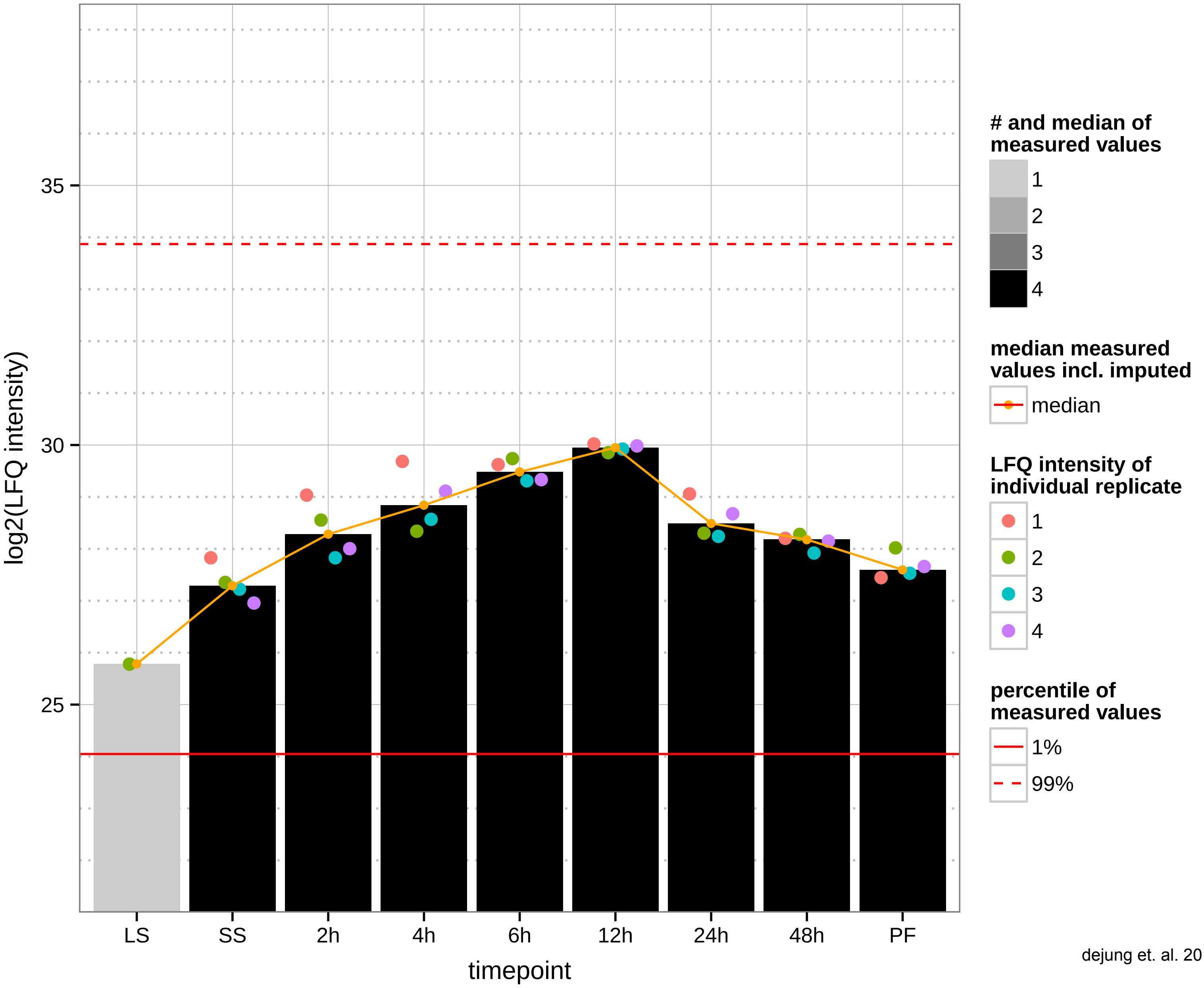


dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.7290
AGOF: null
AGOC: null
AGOP: null
PGOF: glutathione gamma–glutamylcysteinyltransferase activity, metal ion binding
PGOC: null
PGOP: phytochelatin biosynthetic process, response to metal ion





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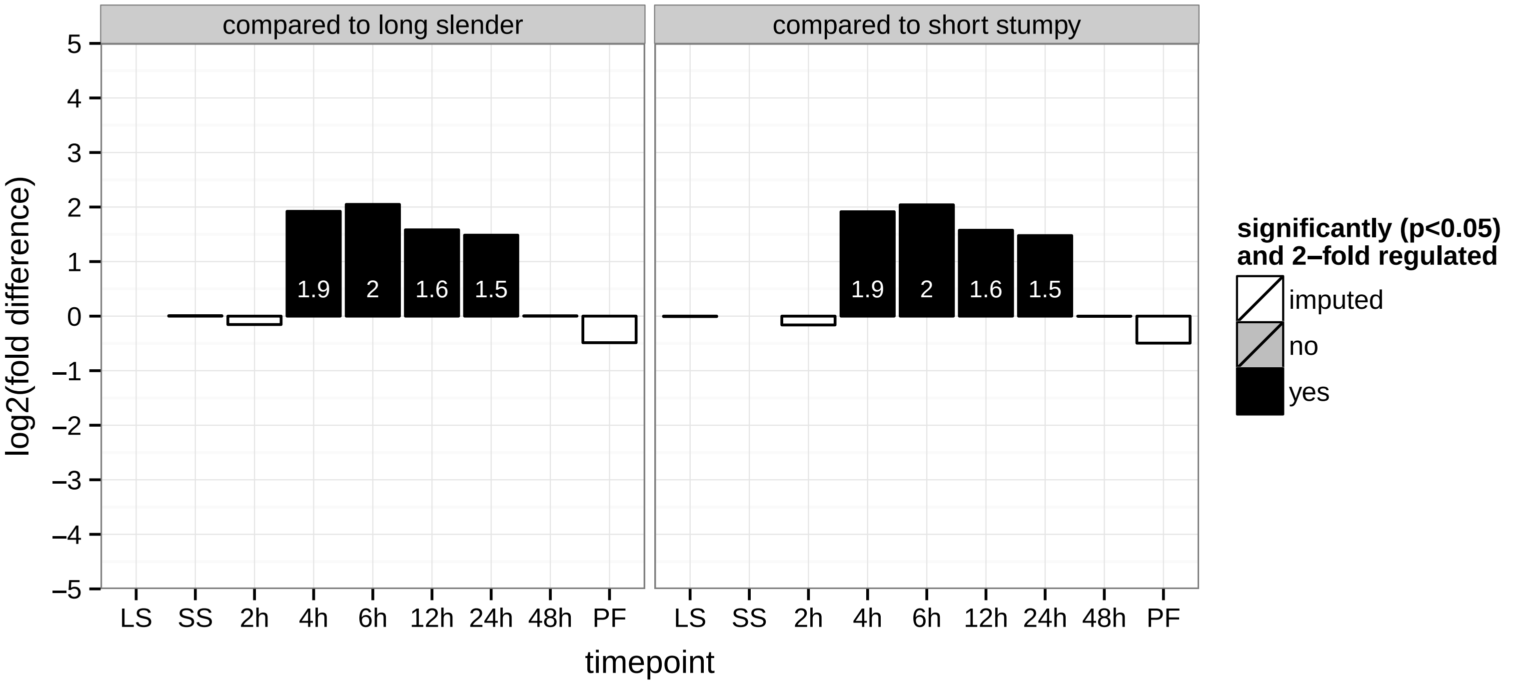
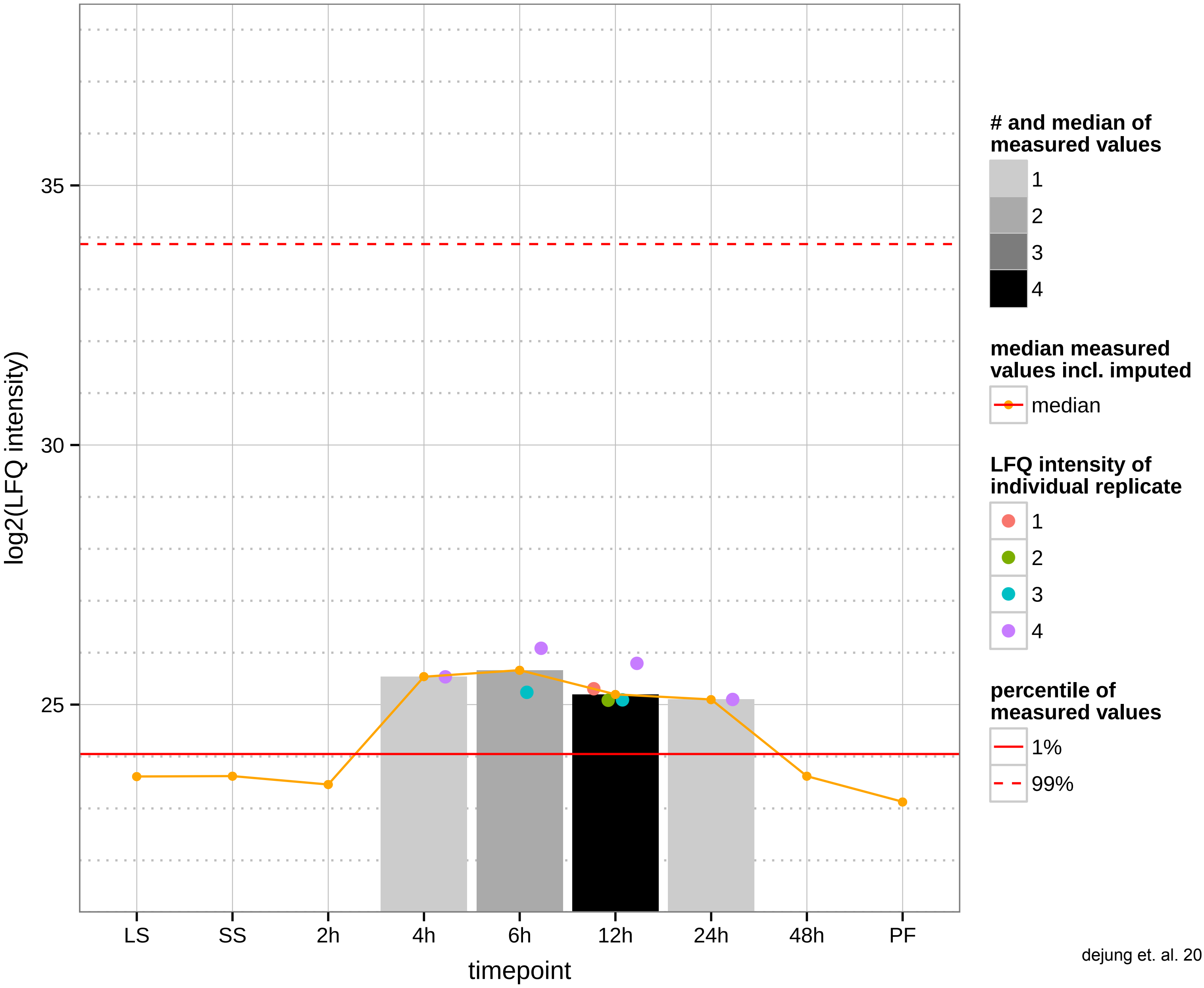
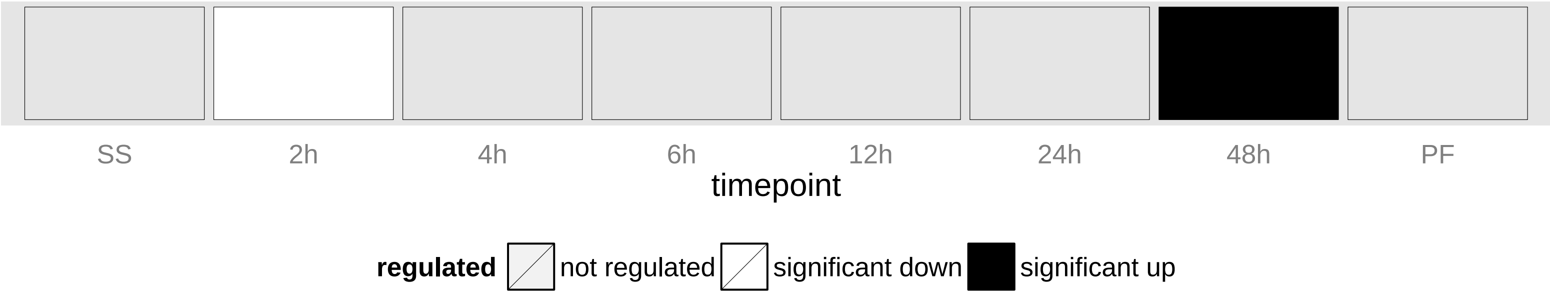
hypothetical protein, conserved
Tb927.4.4540
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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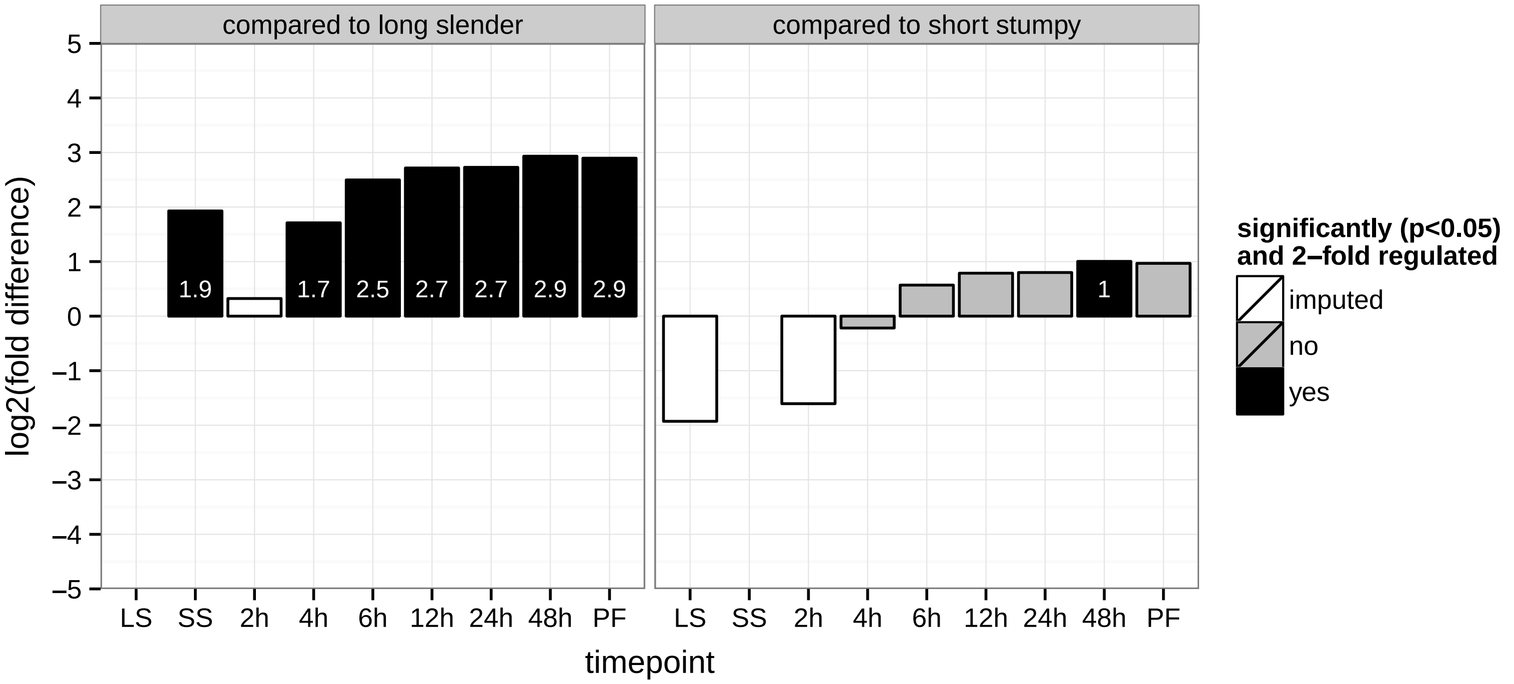
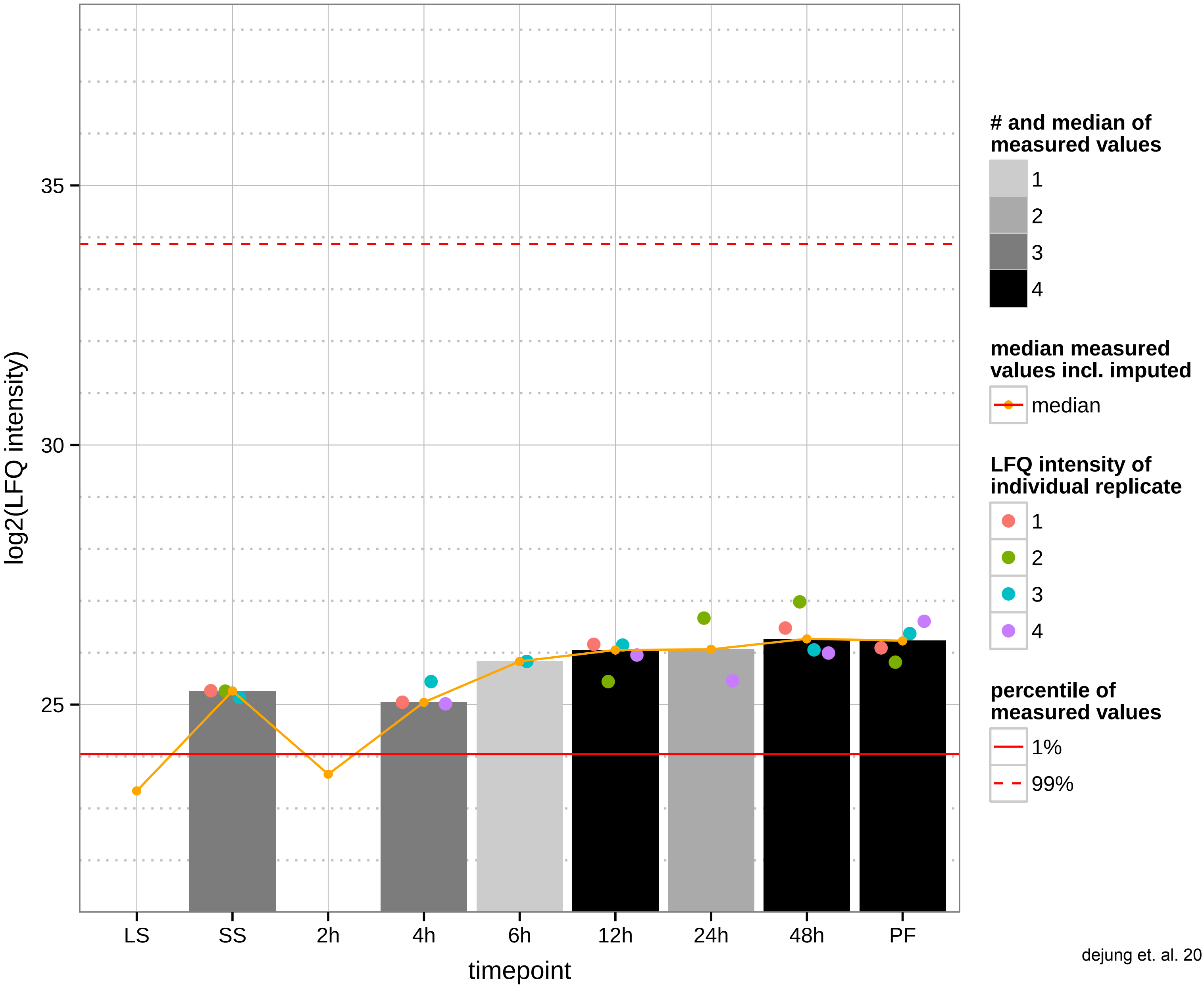
hypothetical protein, conserved
Tb927.7.7030
AGOF: zinc ion binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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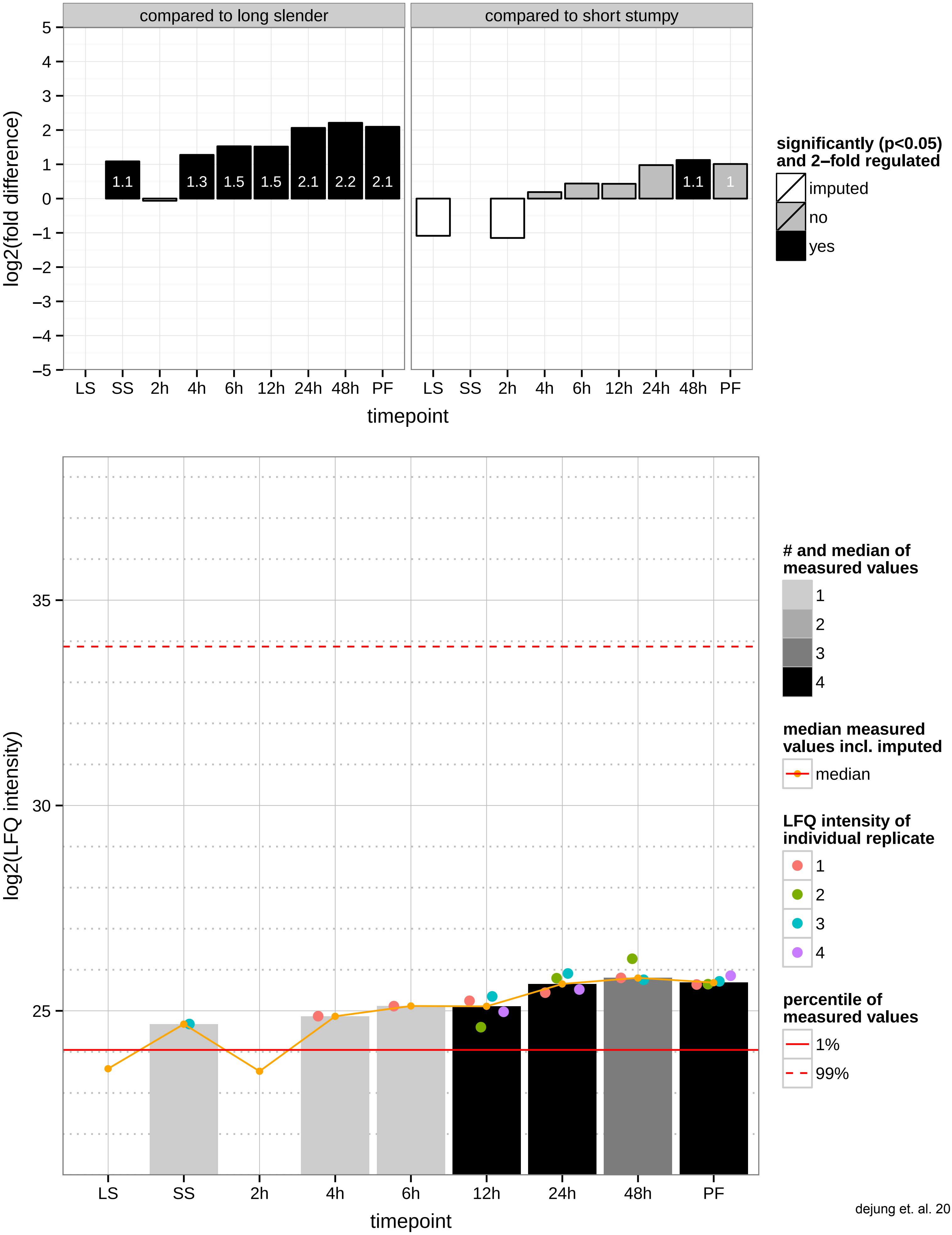
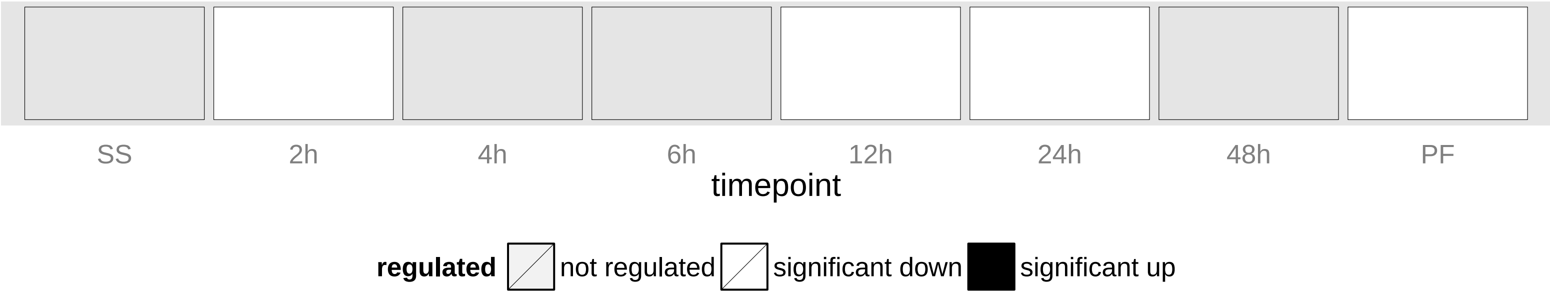
general transcription factor IIB (tf2b)
Tb927.9.5710
AGOF: null
AGOC: null
AGOP: transcription from RNA polymerase II promoter, transcription, DNA–dependent
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015



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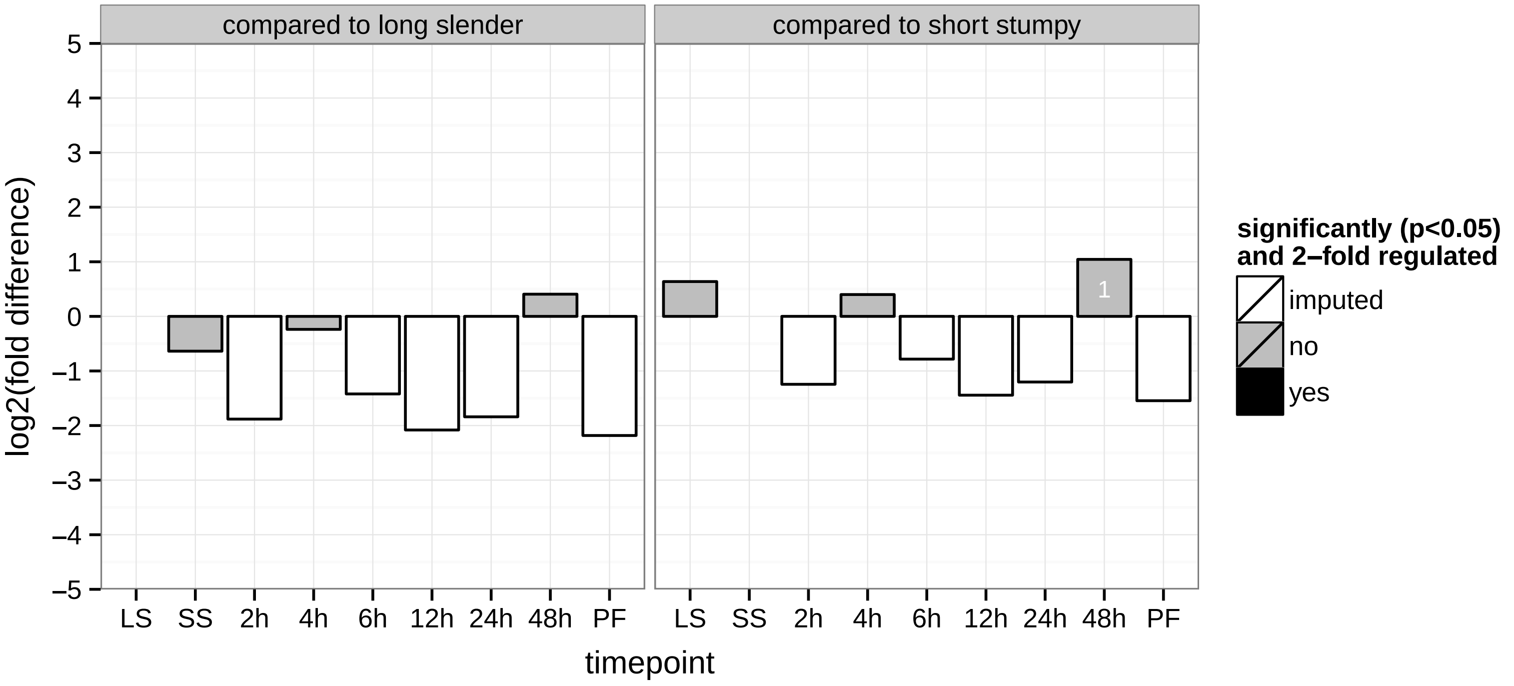
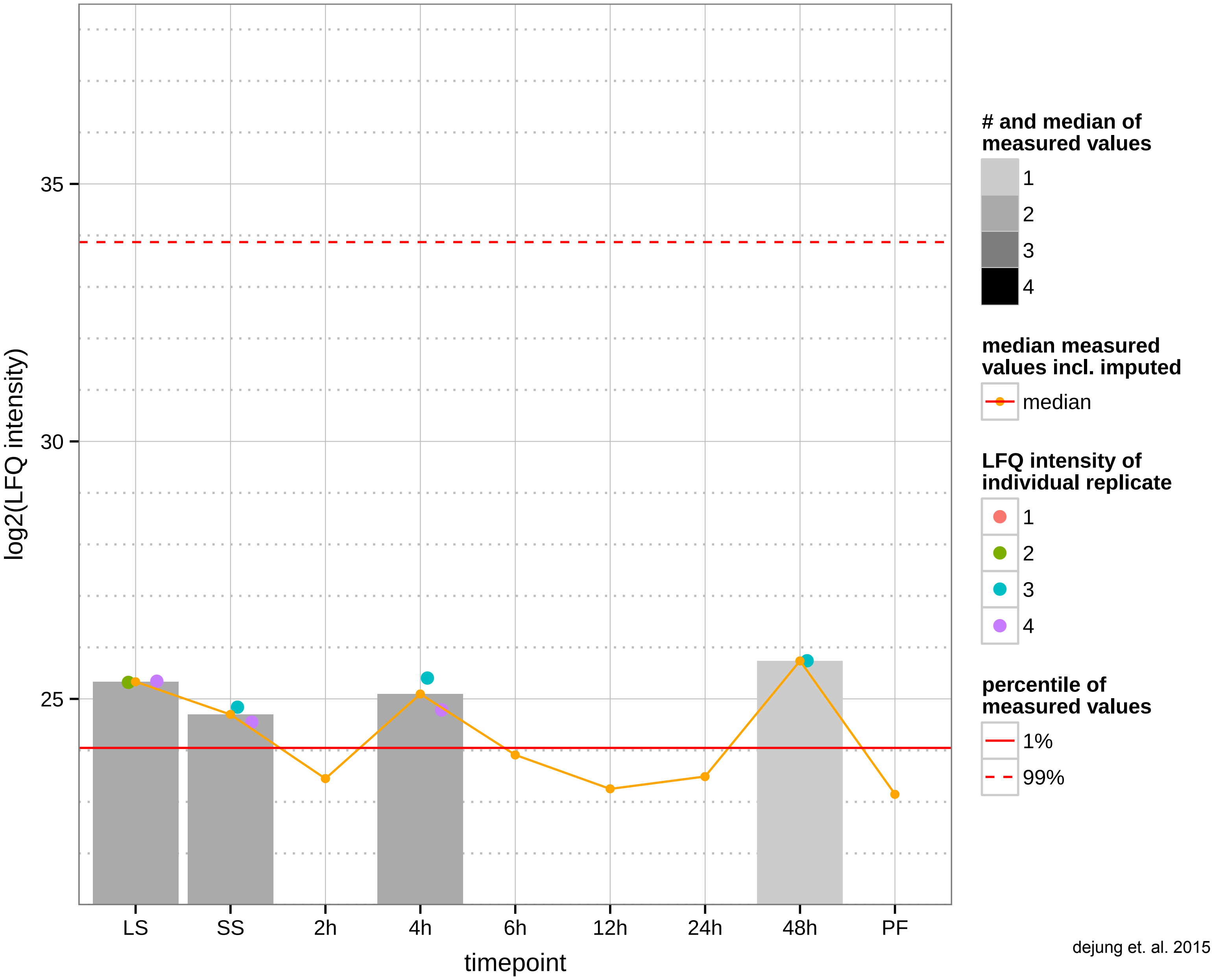
hypothetical protein, conserved
Tb927.10.5000
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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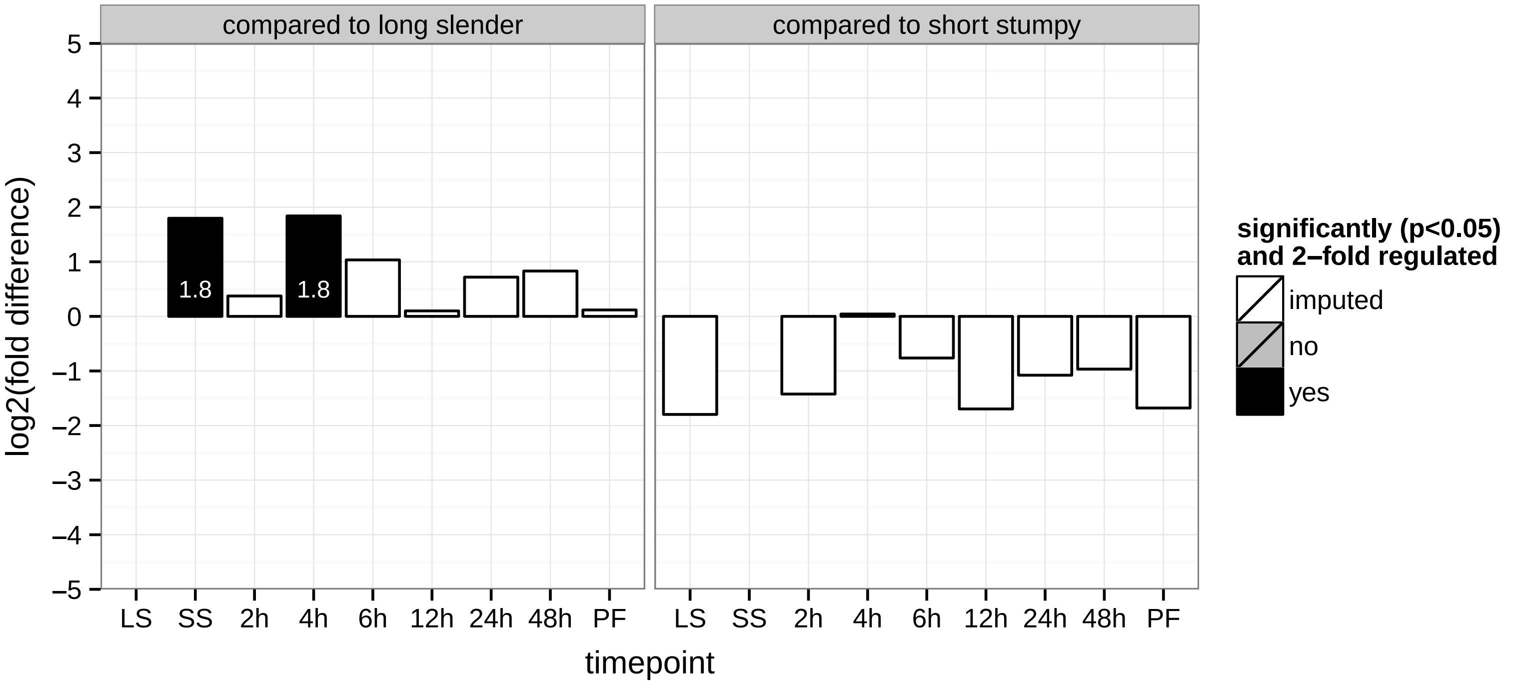
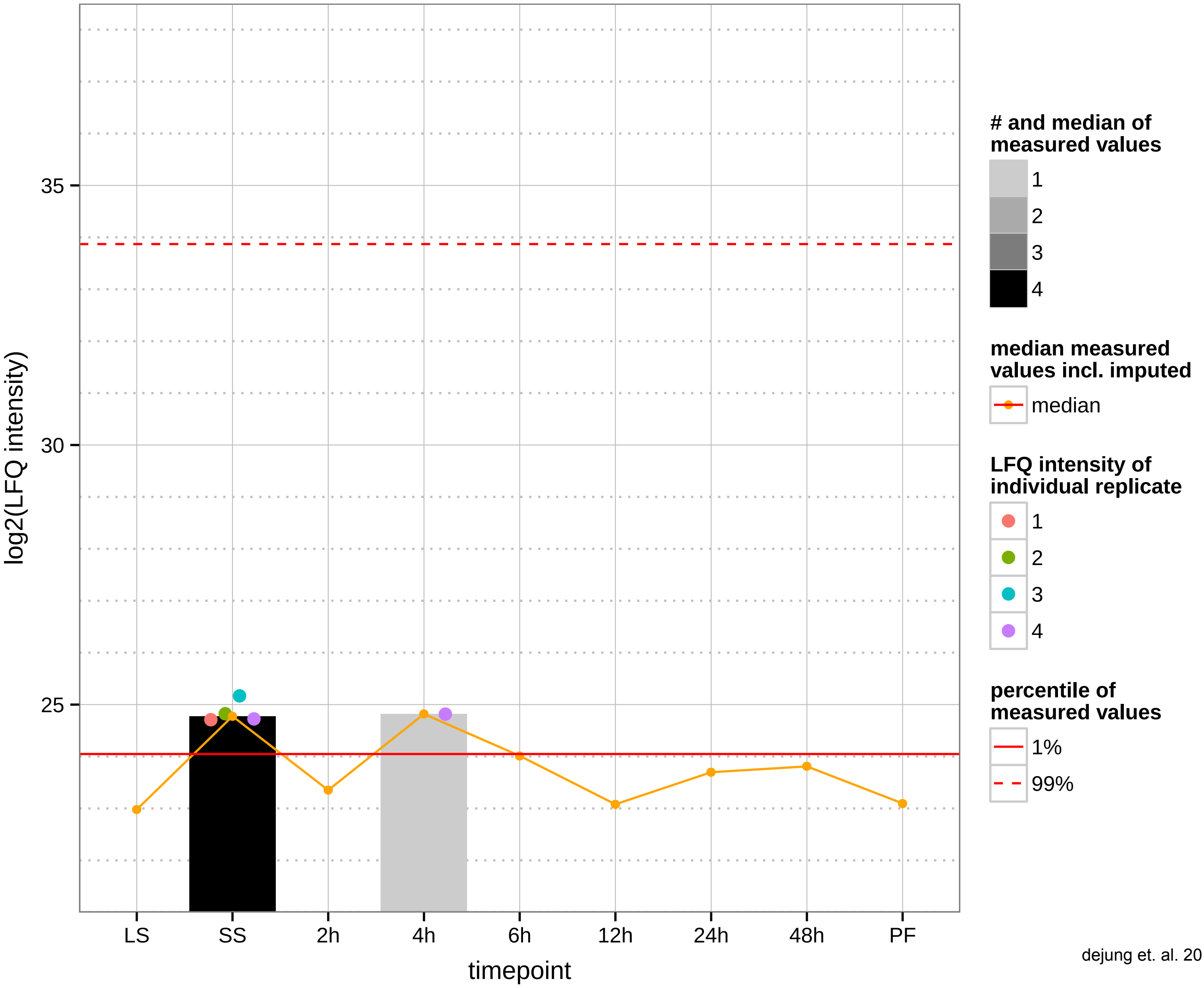
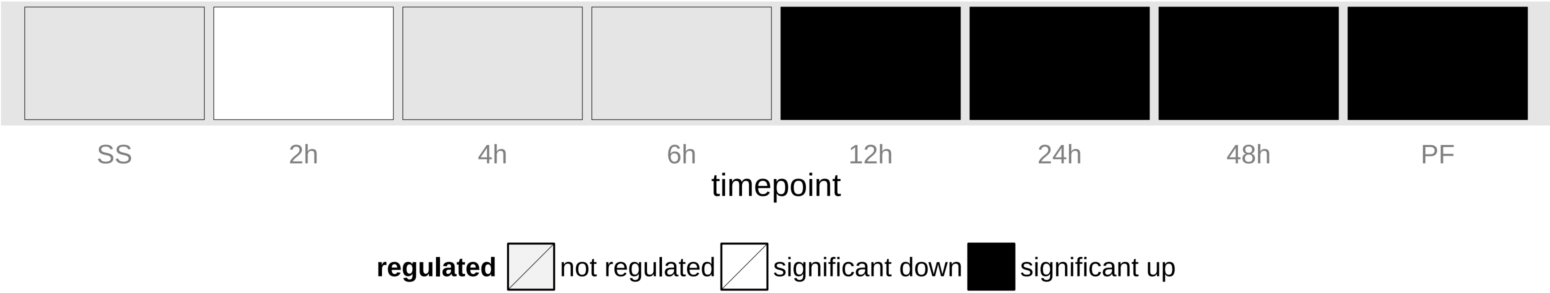
hypothetical protein, conserved
Tb927.11.9950
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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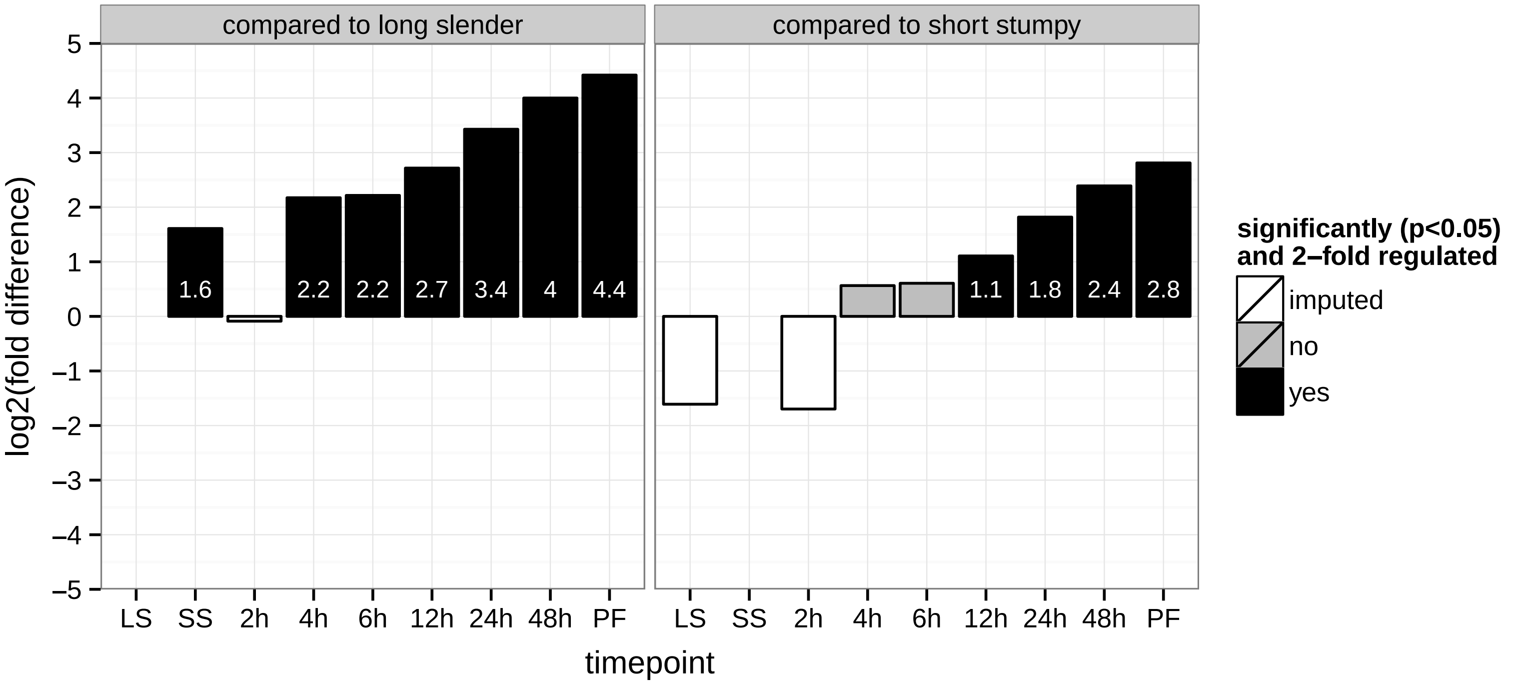
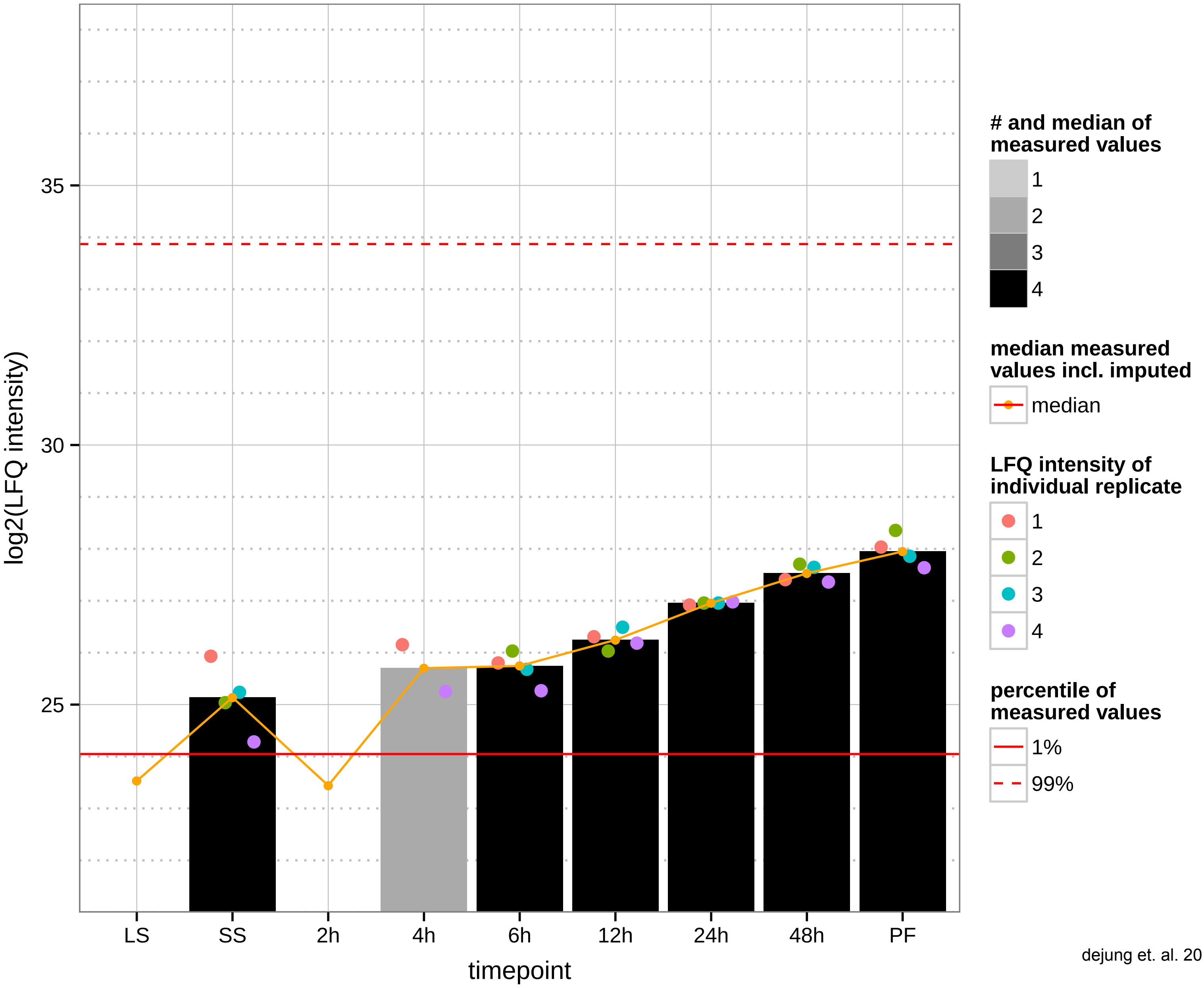
hypothetical protein, conserved
Tb927.11.3860
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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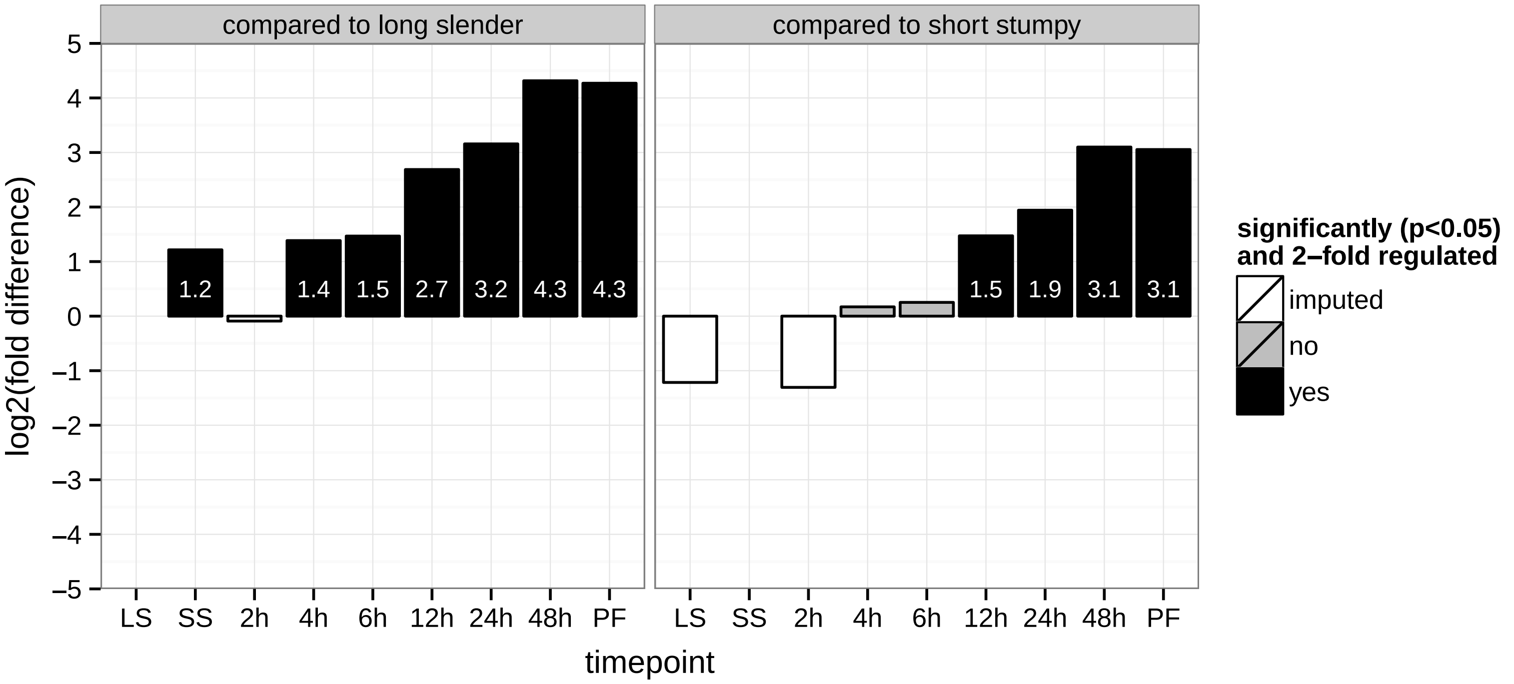
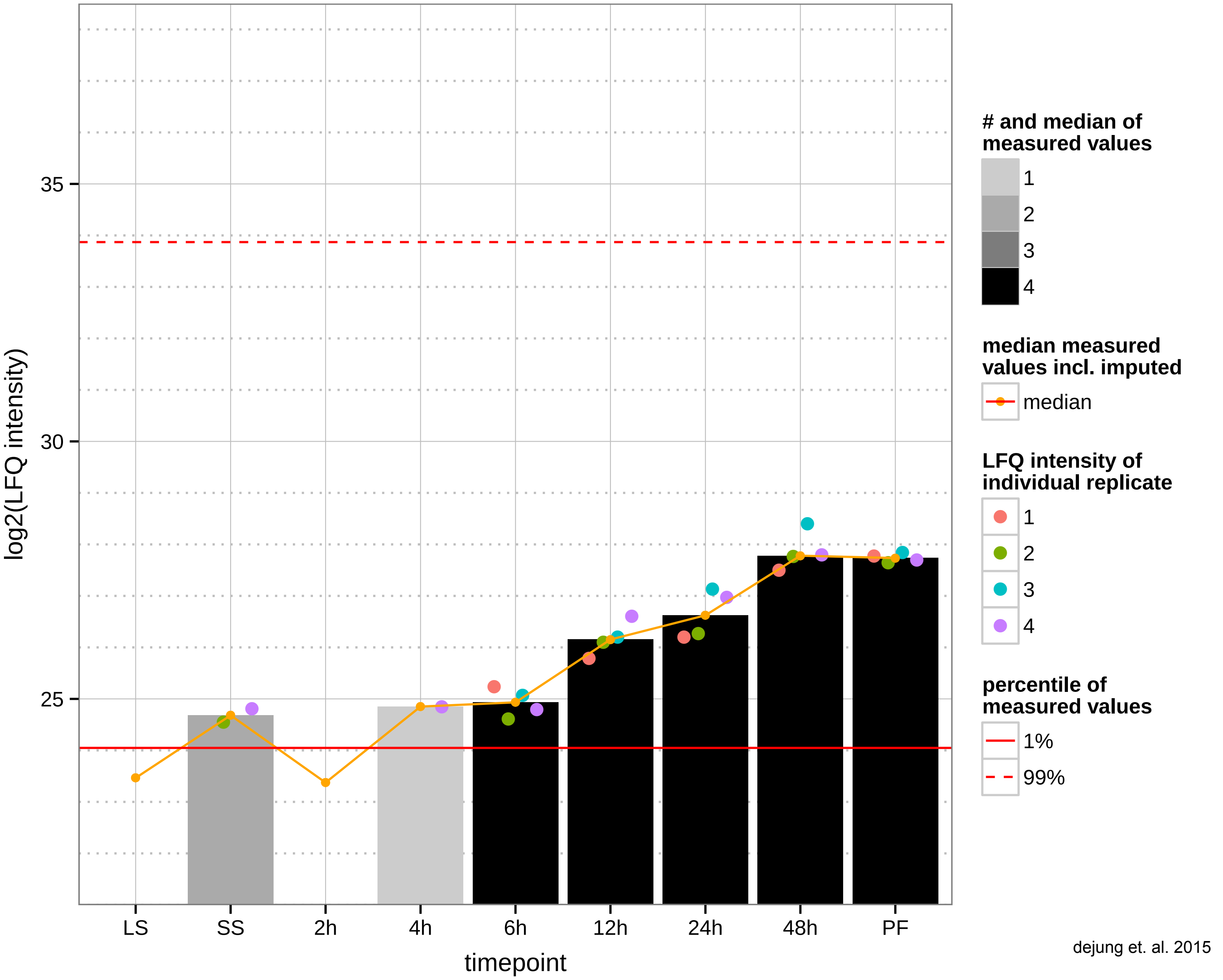
cytochrome P450, putative
Tb927.3.680
AGOF: electron carrier activity, heme binding, iron ion binding, monooxygenase activity
AGOC: null
AGOP: null
PGOF: electron carrier activity, heme binding, iron ion binding, oxidoreductase activity, acting on paired donors, with incorpora
PGOC: null
PGOP: oxidation−reduction process





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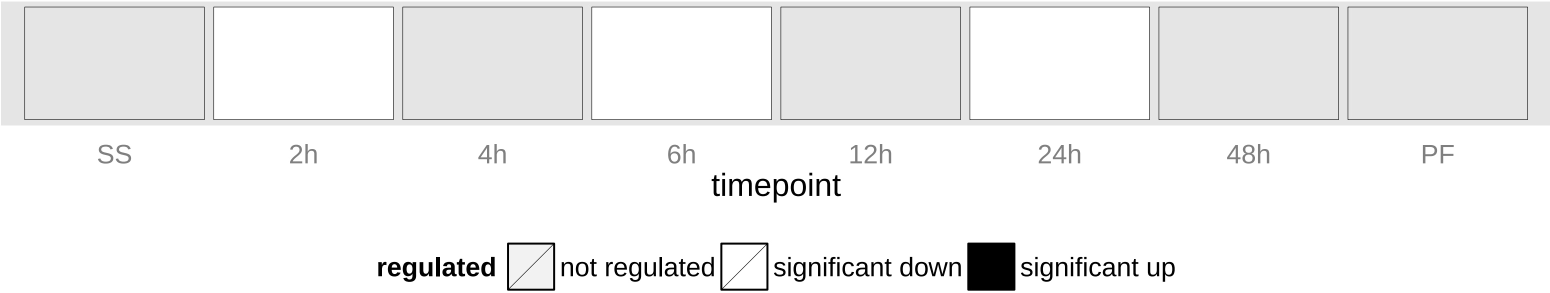

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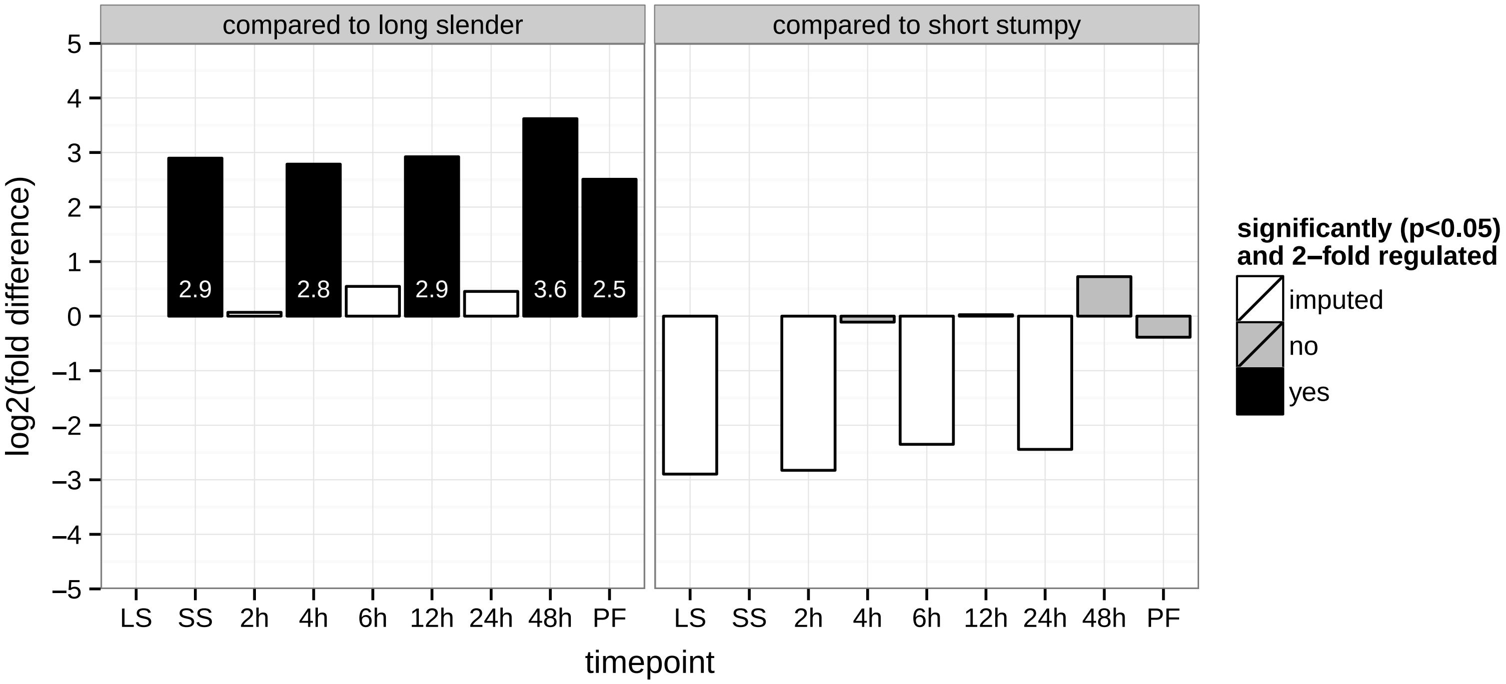
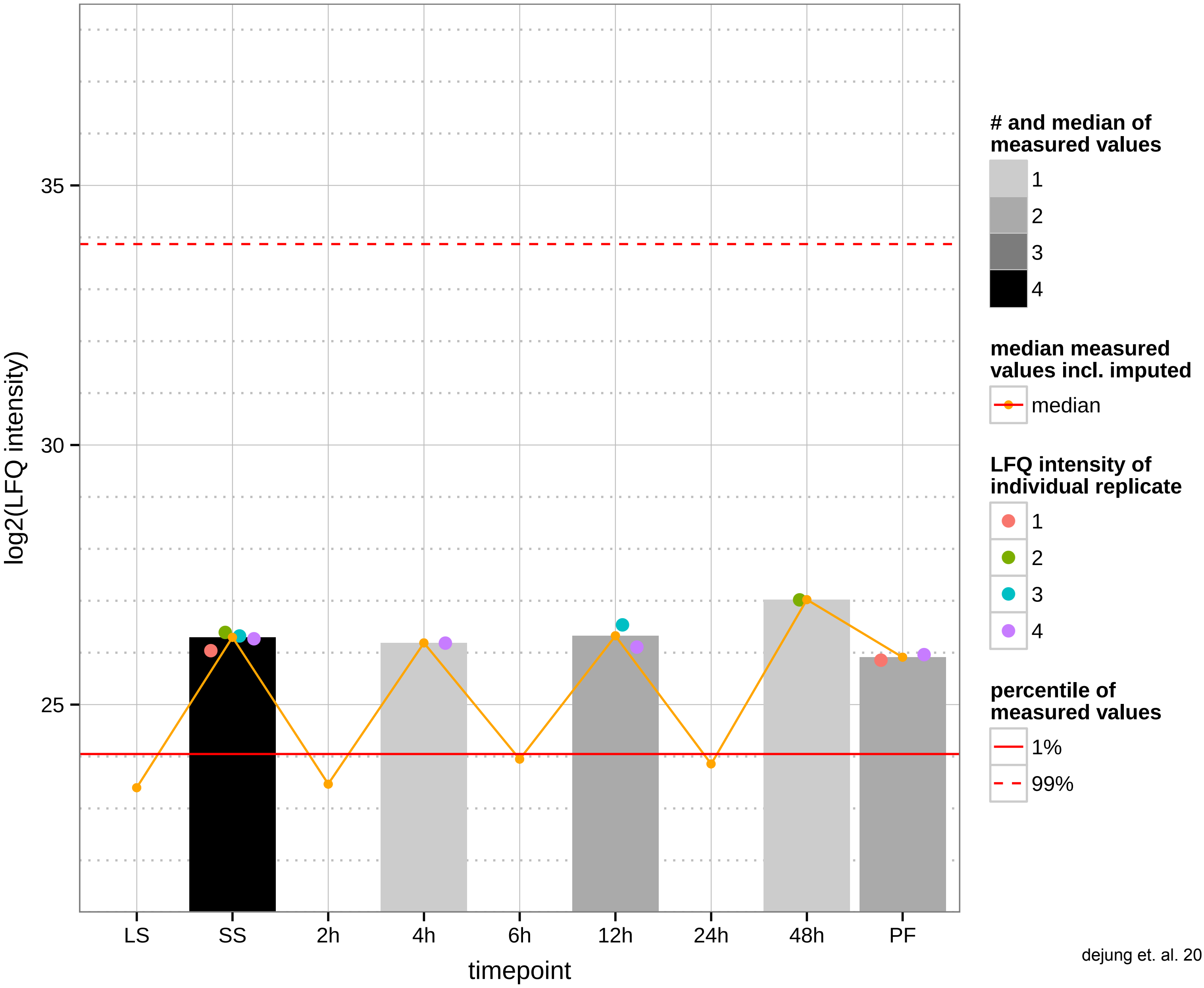
hypothetical protein, conserved
Tb927.11.12720;Tb11.v5.0433
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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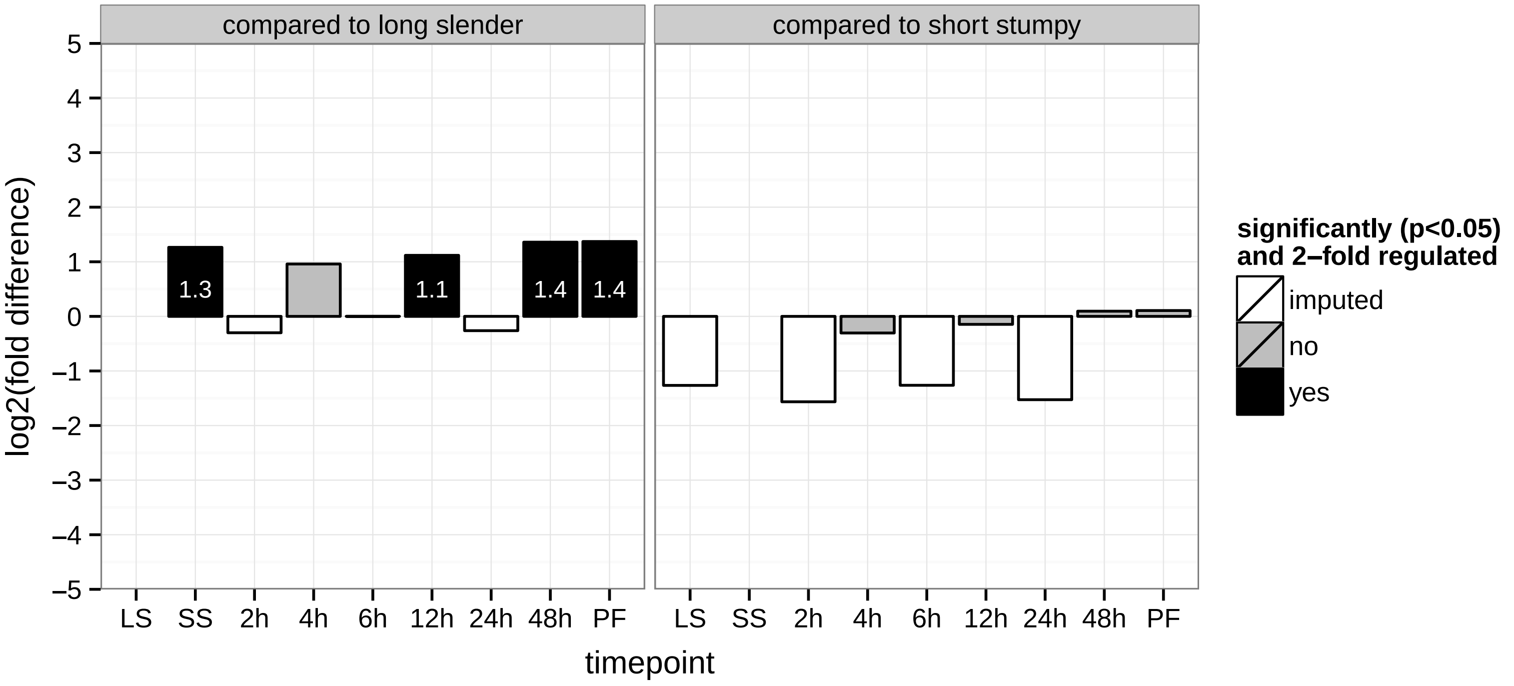
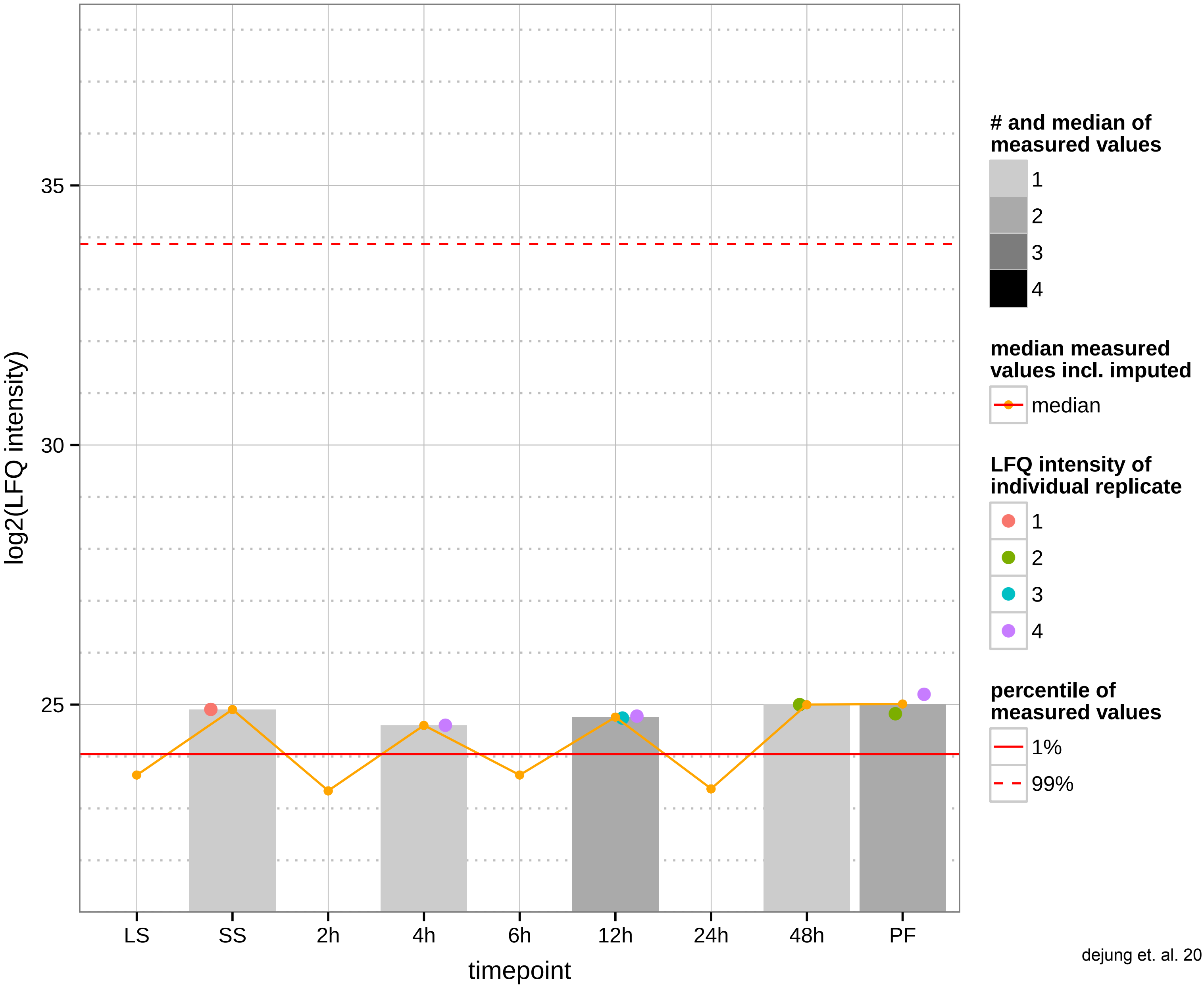
hypothetical protein, conserved
Tb927.4.2920
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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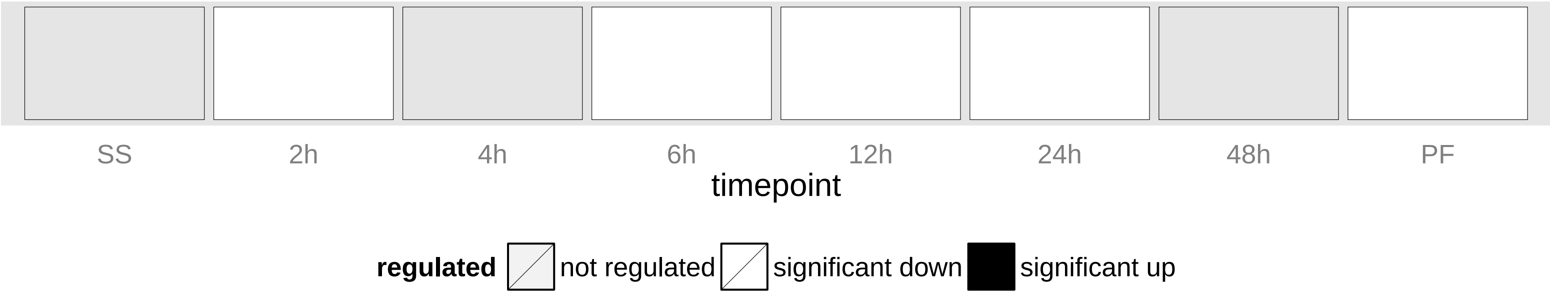

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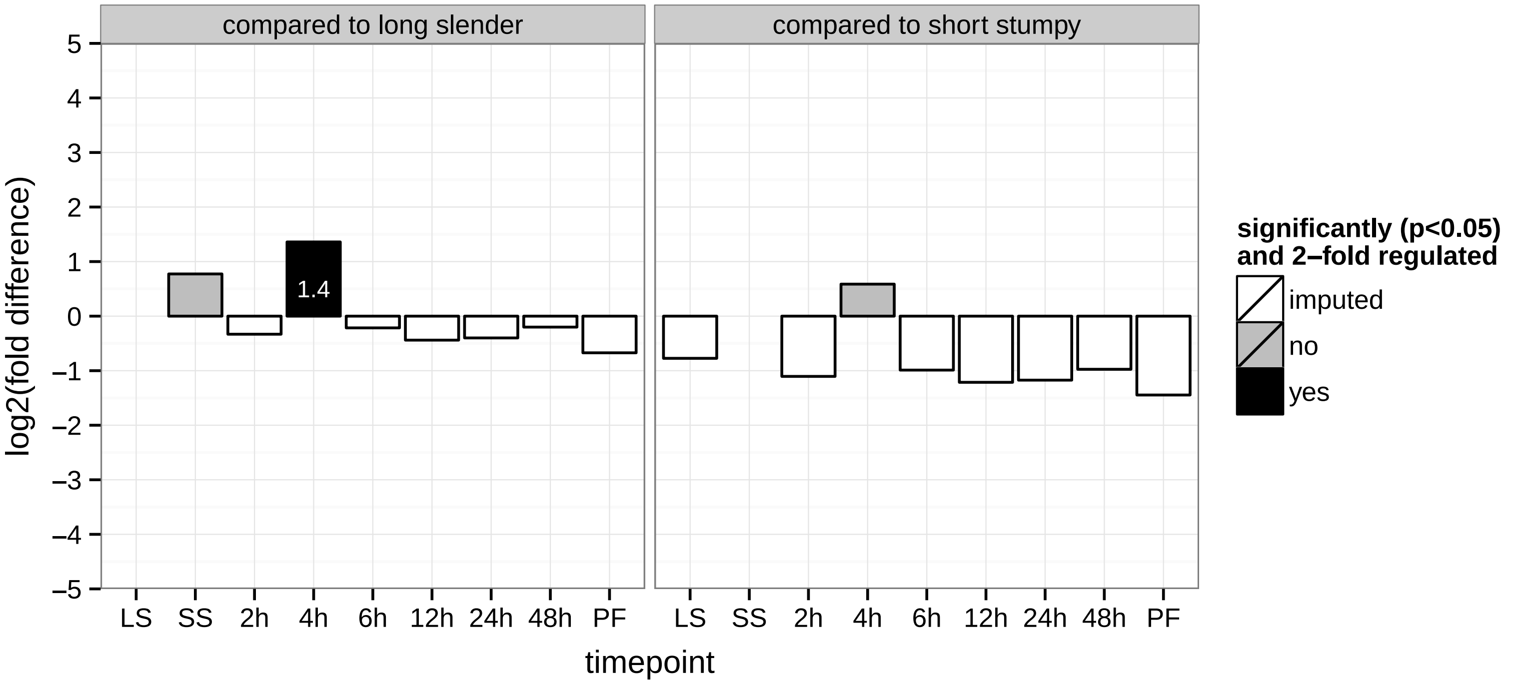
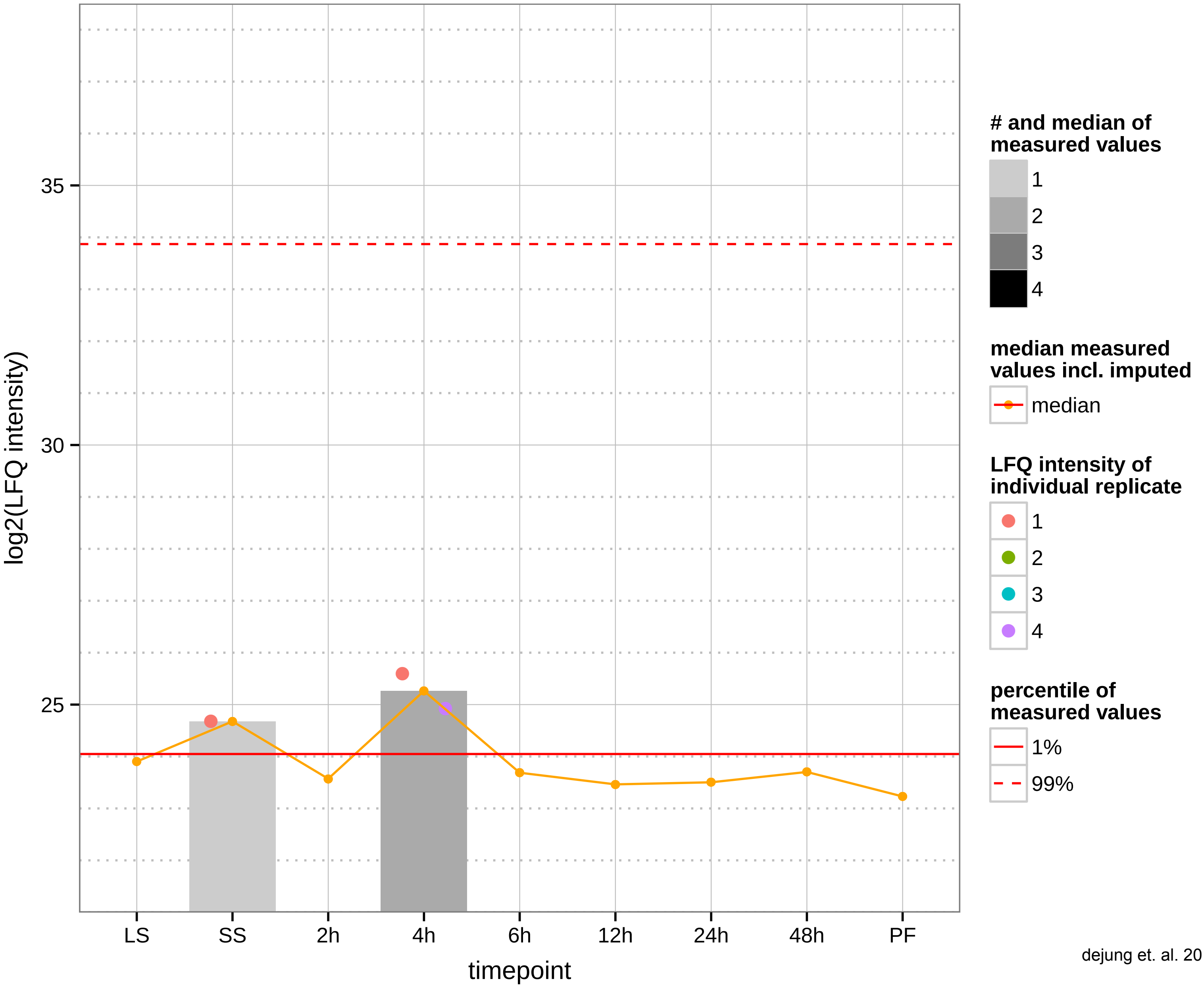
hypothetical protein, conserved
Tb927.3.5190
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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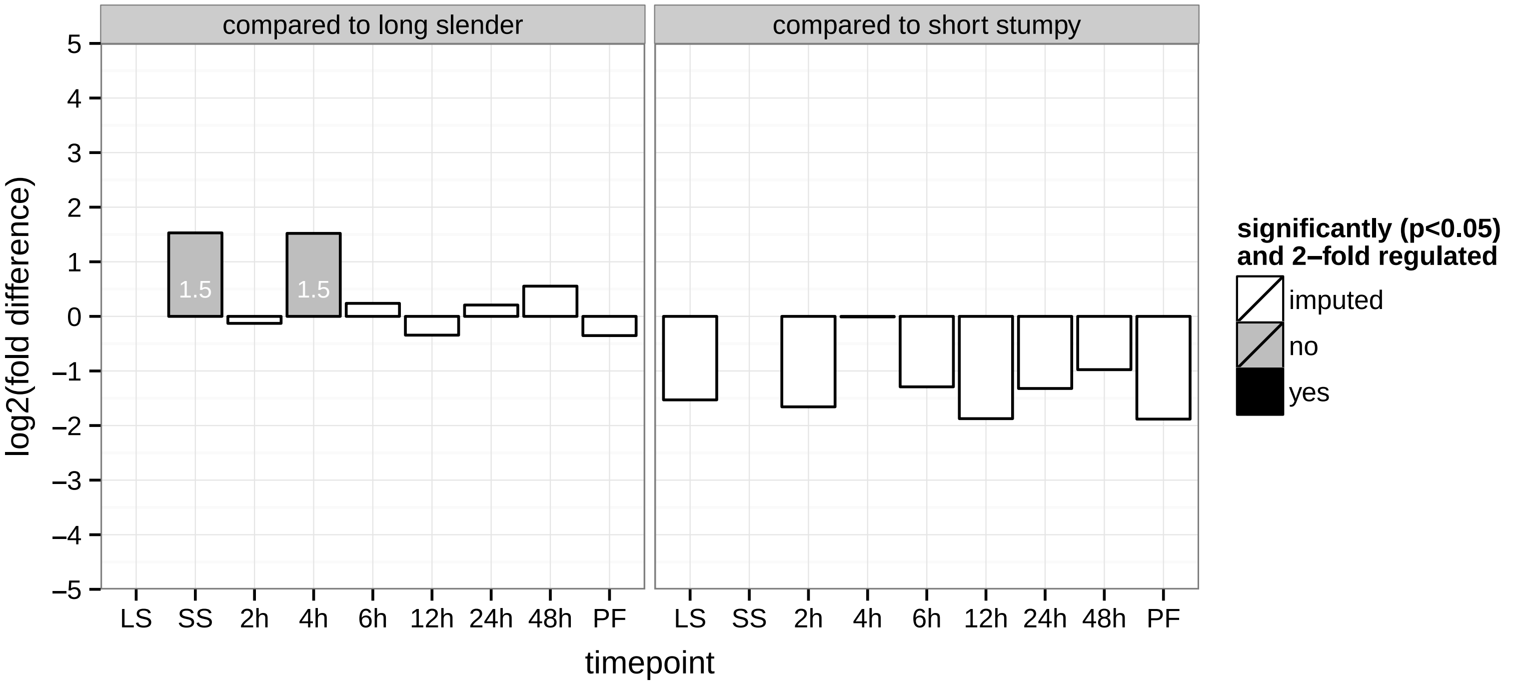
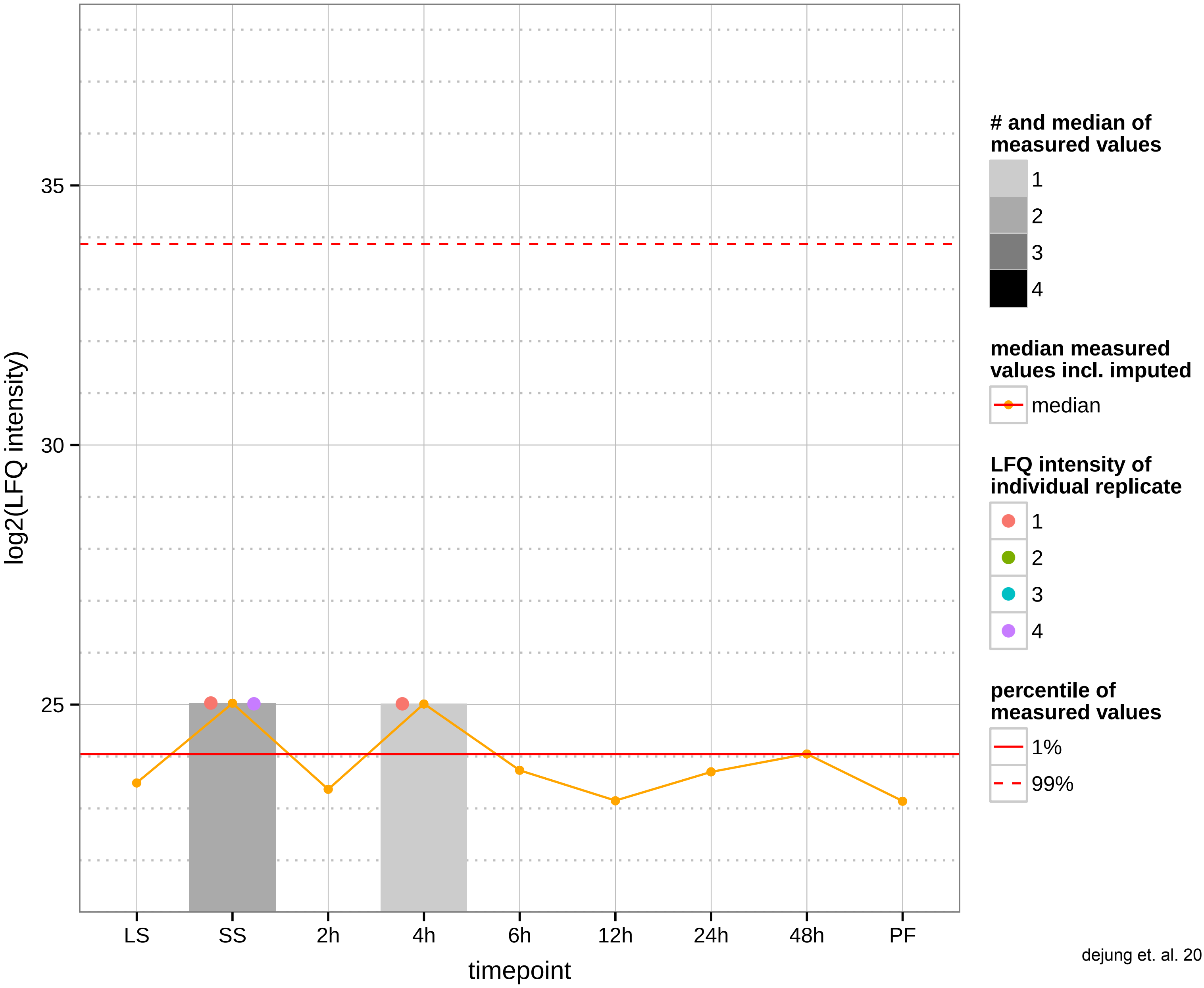
hypothetical protein, conserved
Tb927.8.3930
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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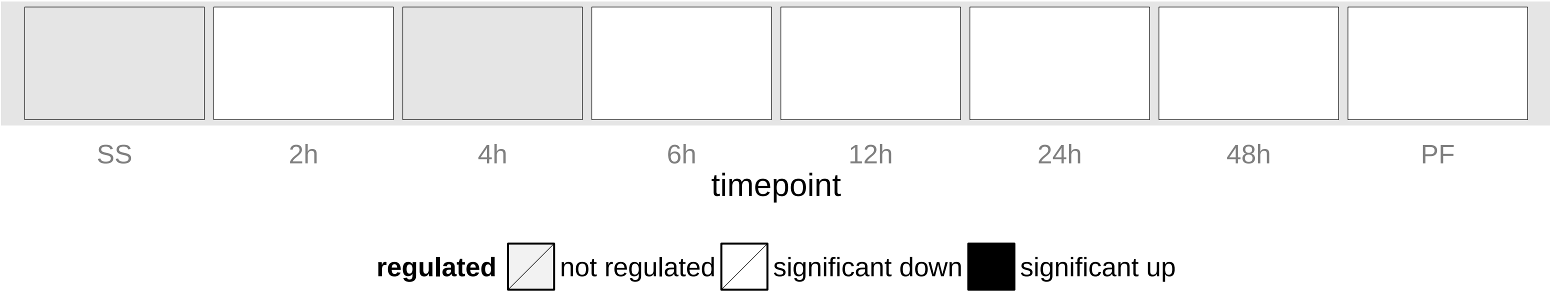

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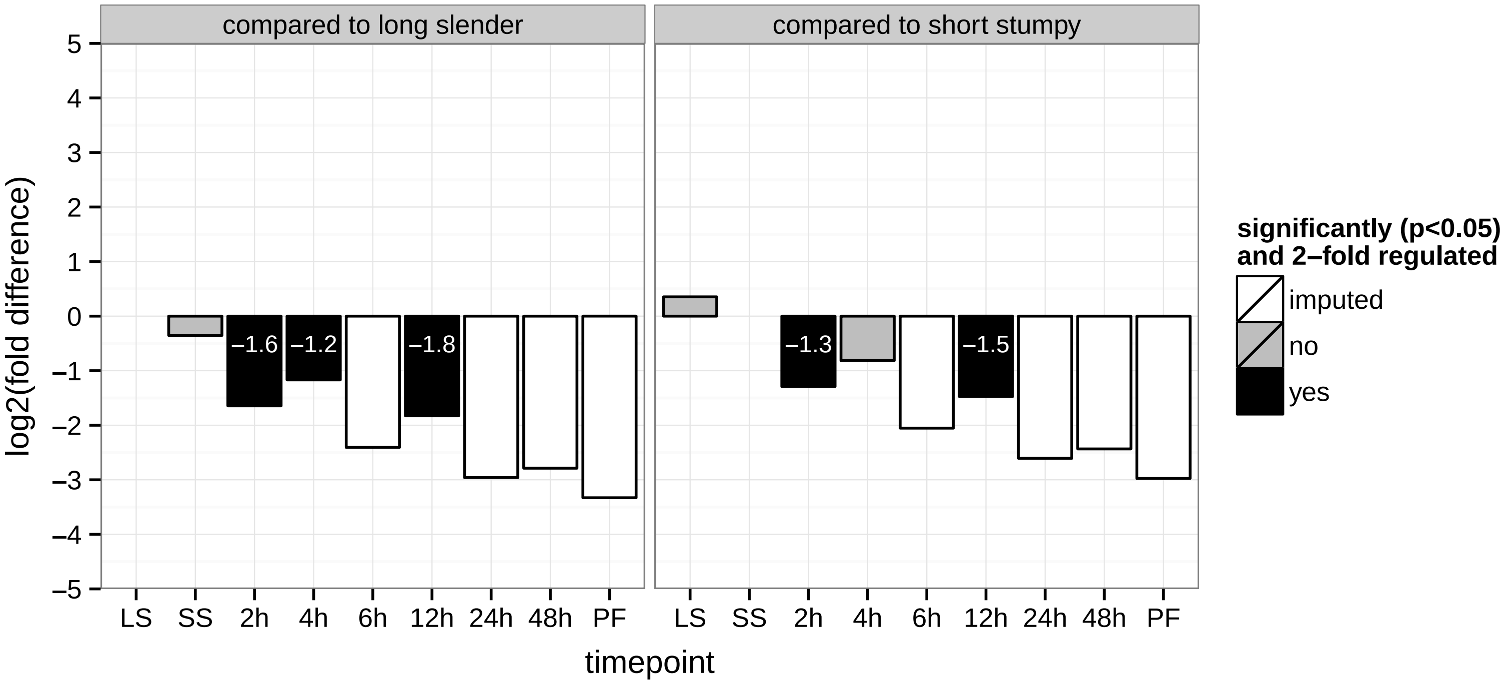
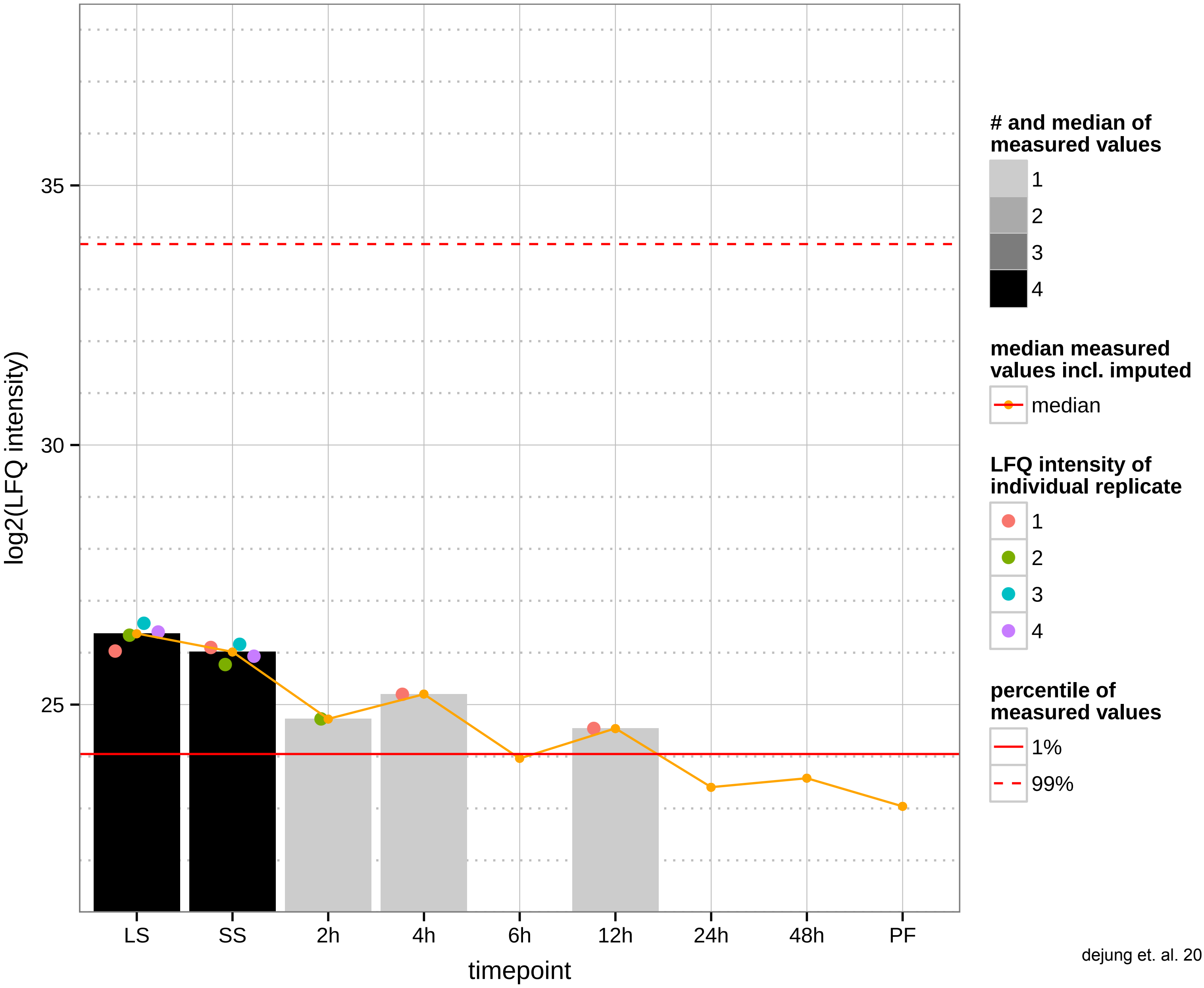
conserved protein, unknown function
Tb927.1.1500
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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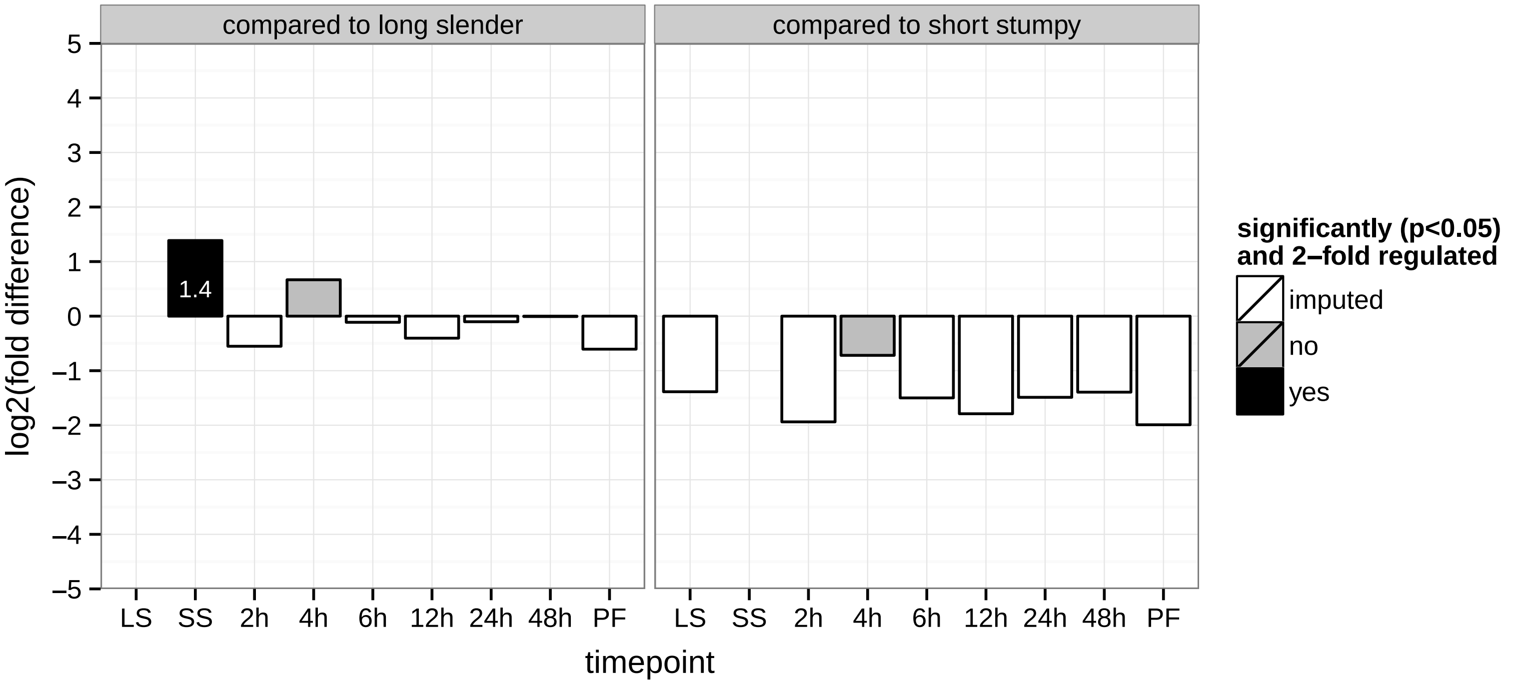
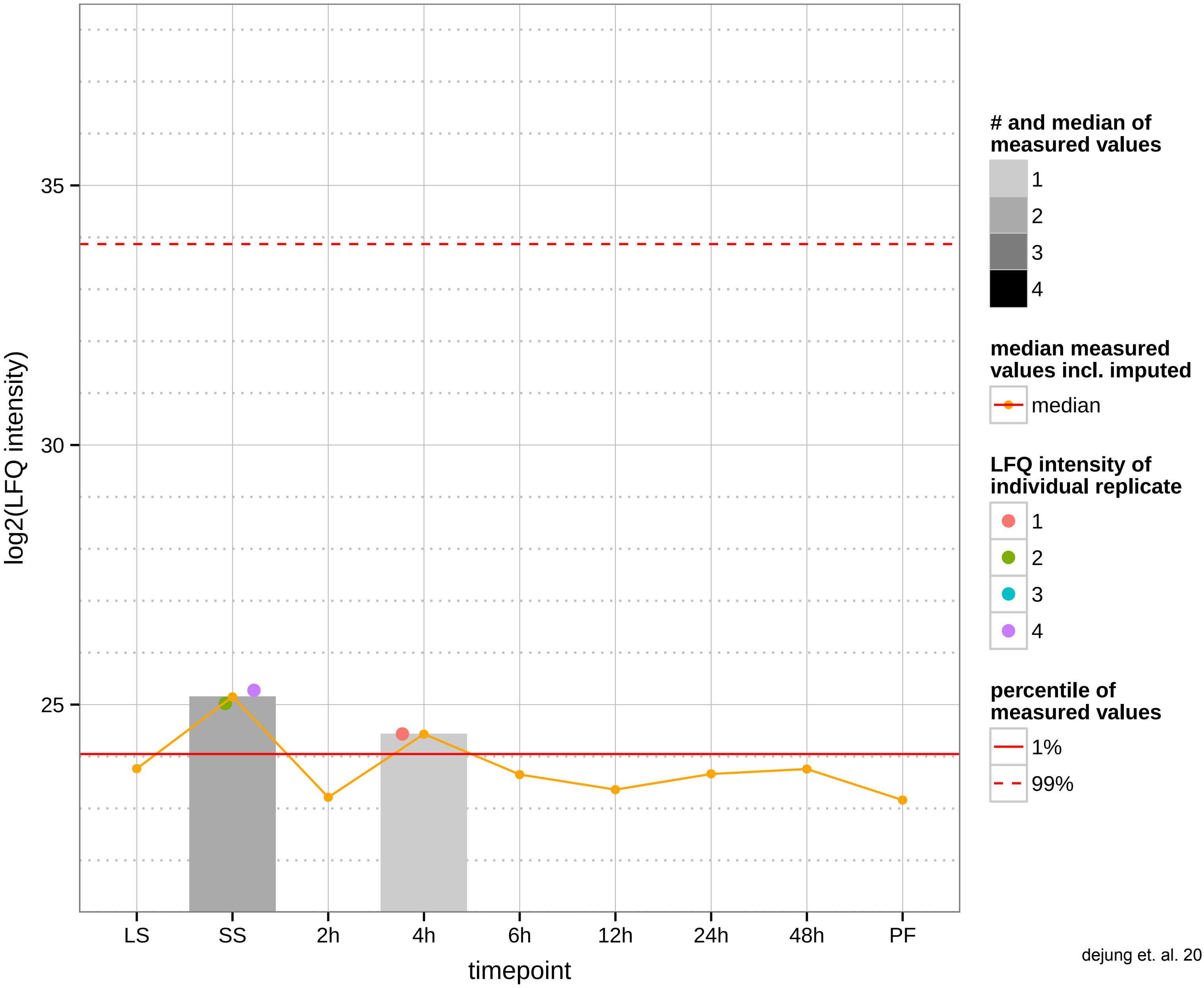
hypothetical PIN domain–containing protein
Tb927.1.1820
AGOF: RNA binding
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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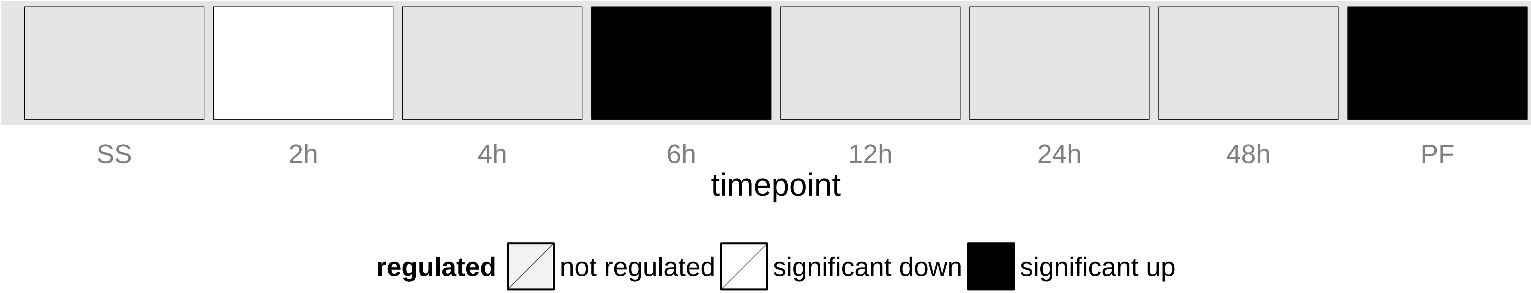

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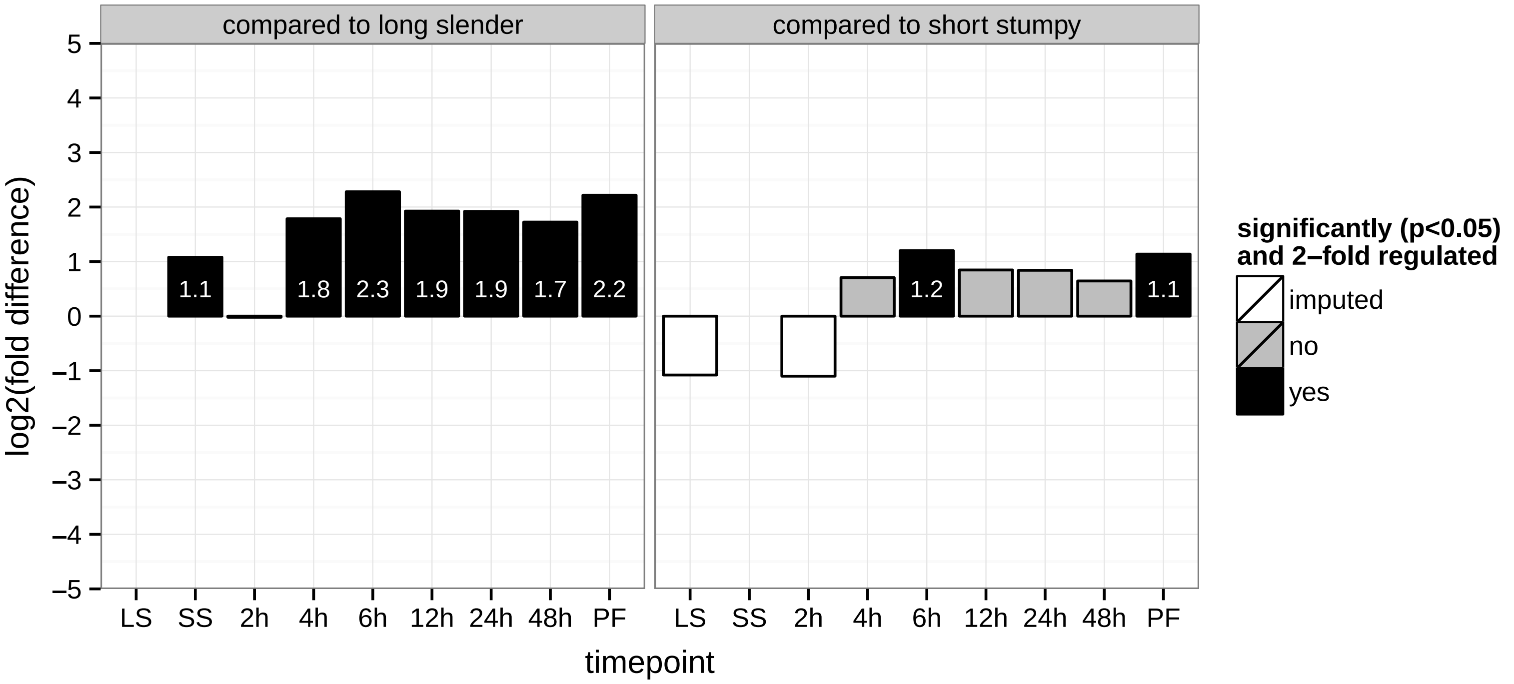
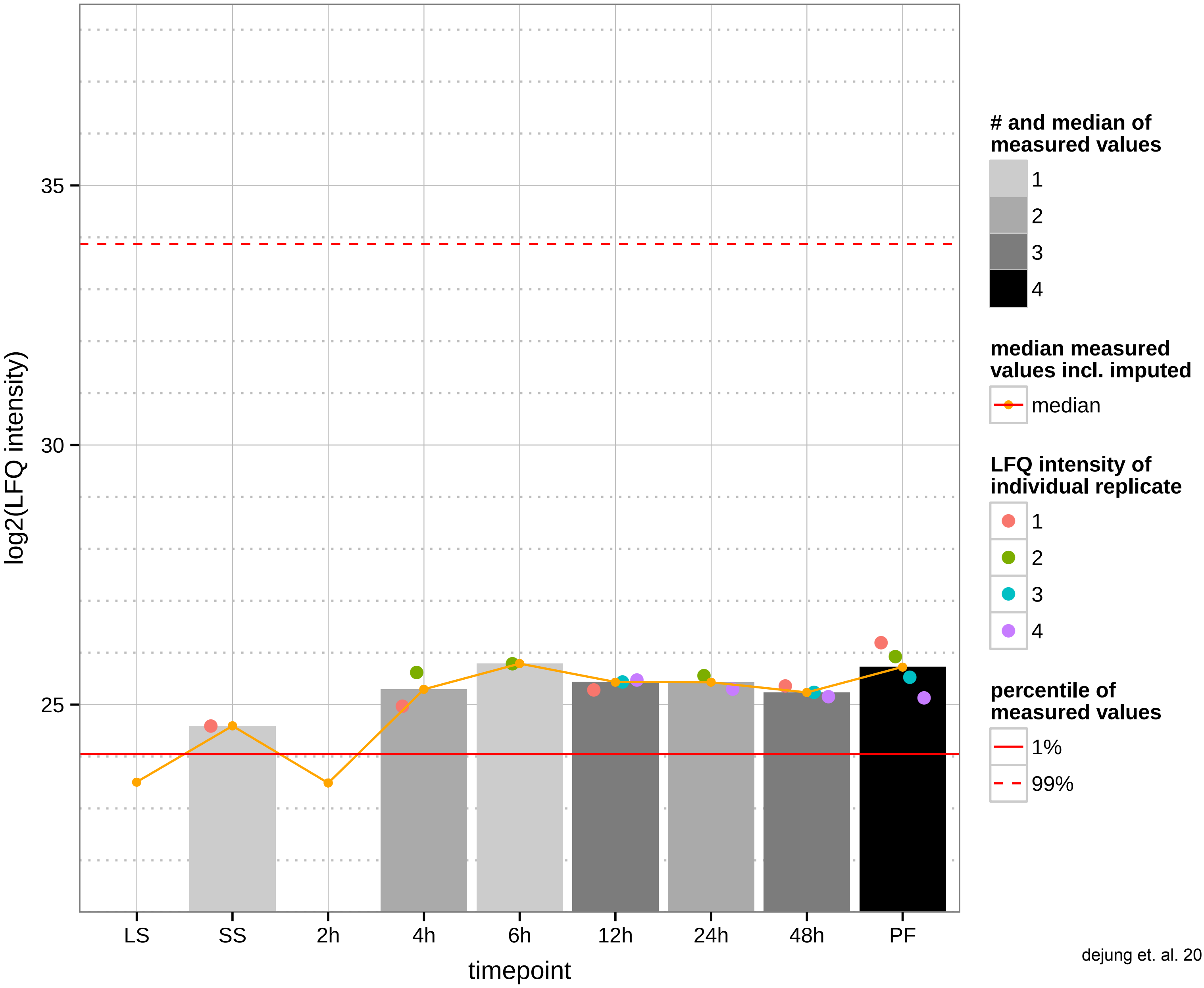
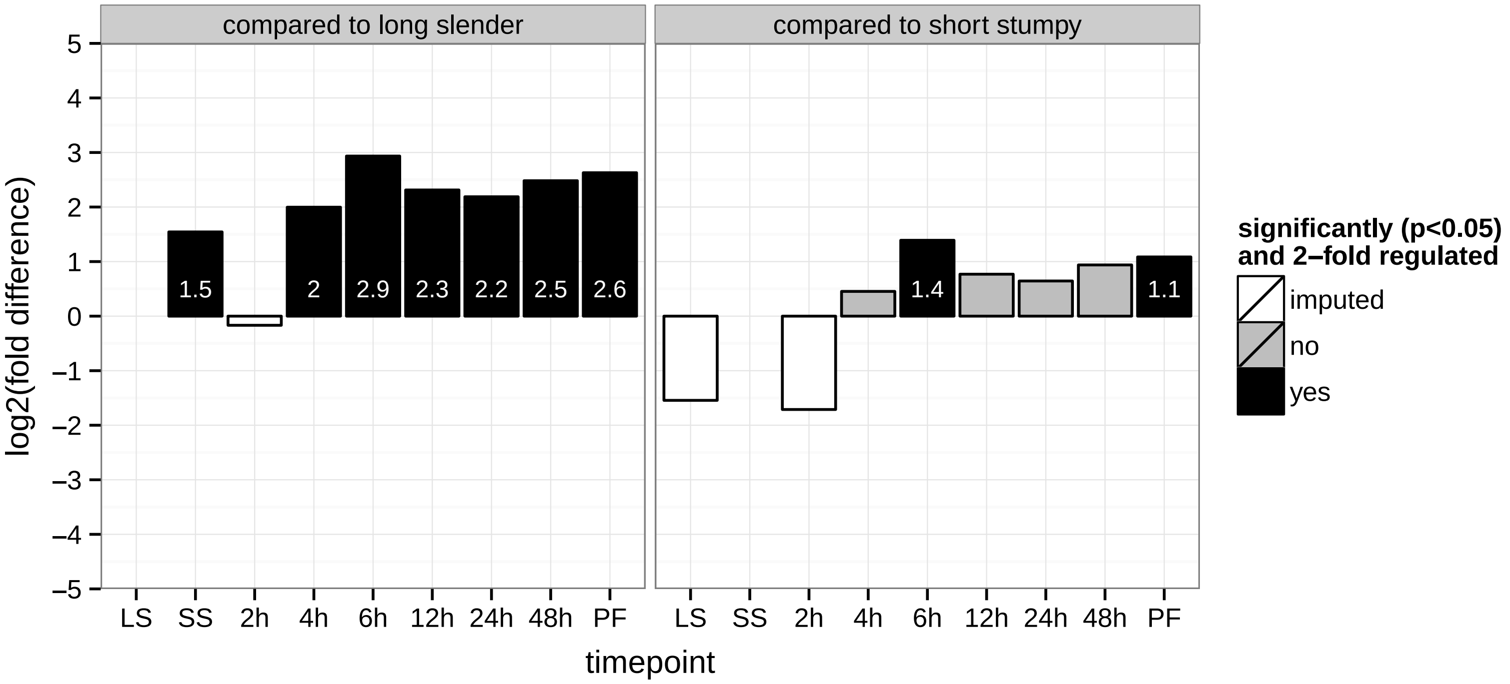
zinc finger protein family member, putative (FIP1)
Tb927.5.4320
AGOF: RNA binding, zinc ion binding
AGOC: null
AGOP: null
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: null

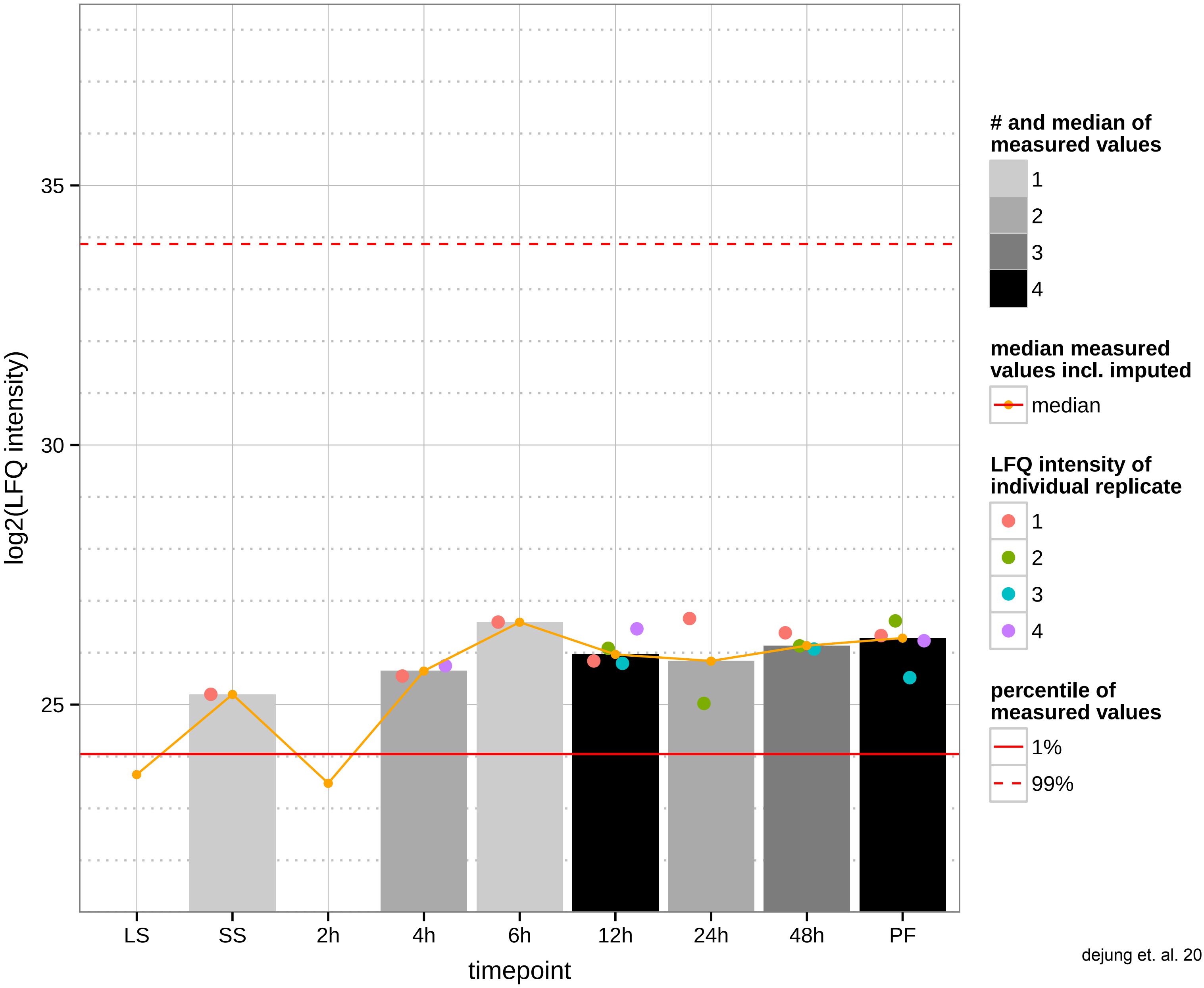




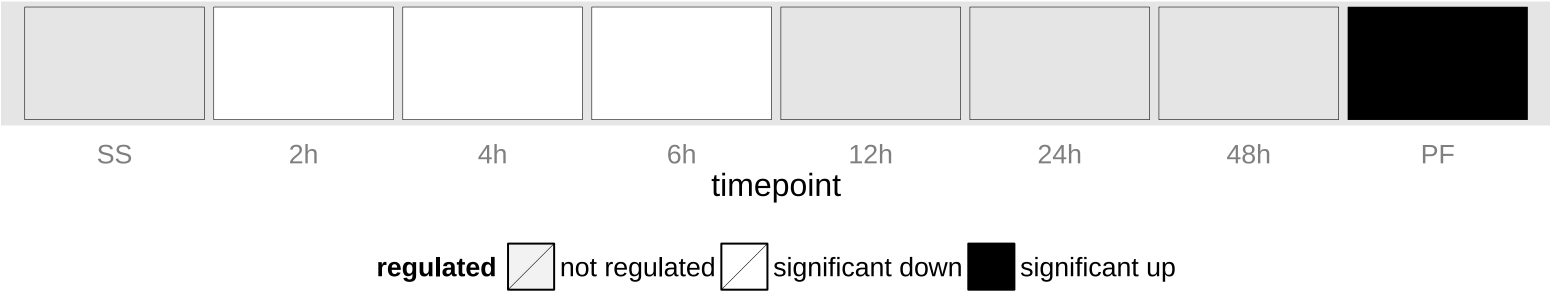
dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.3960
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



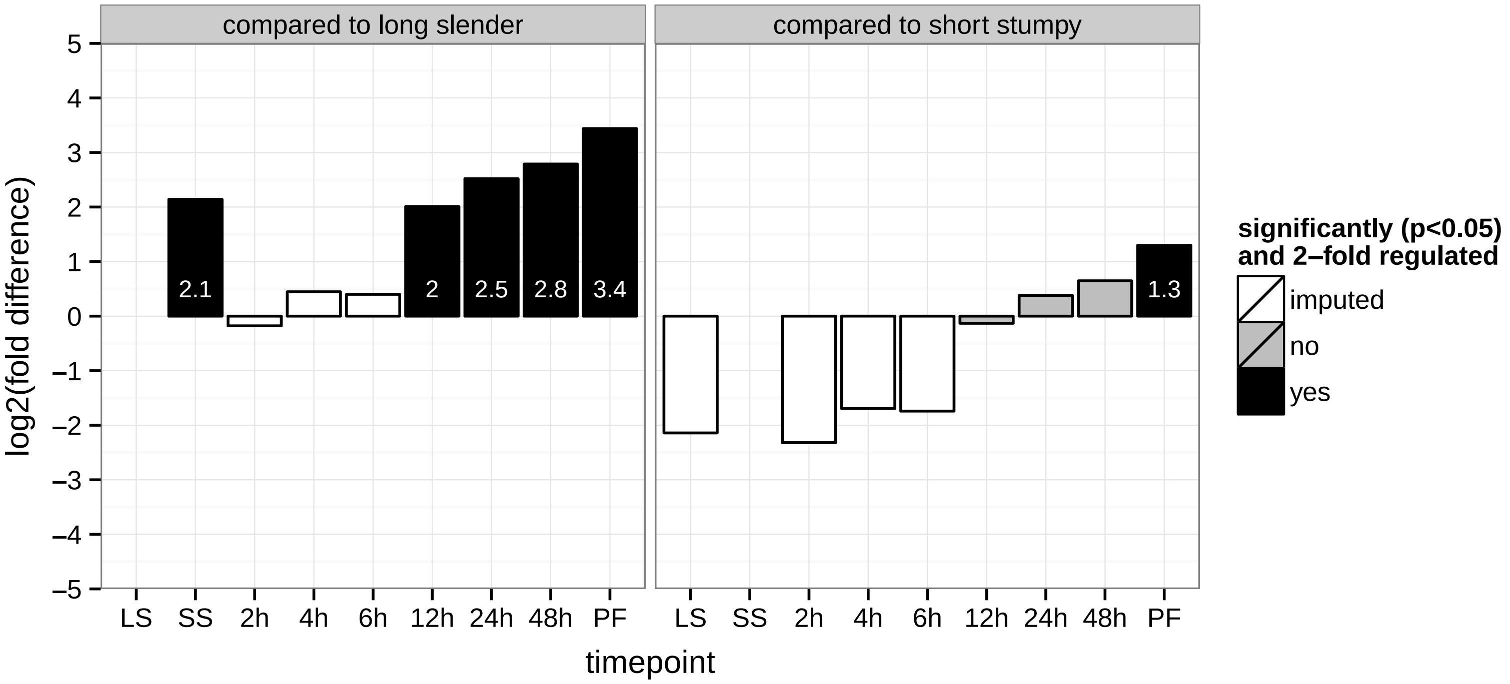


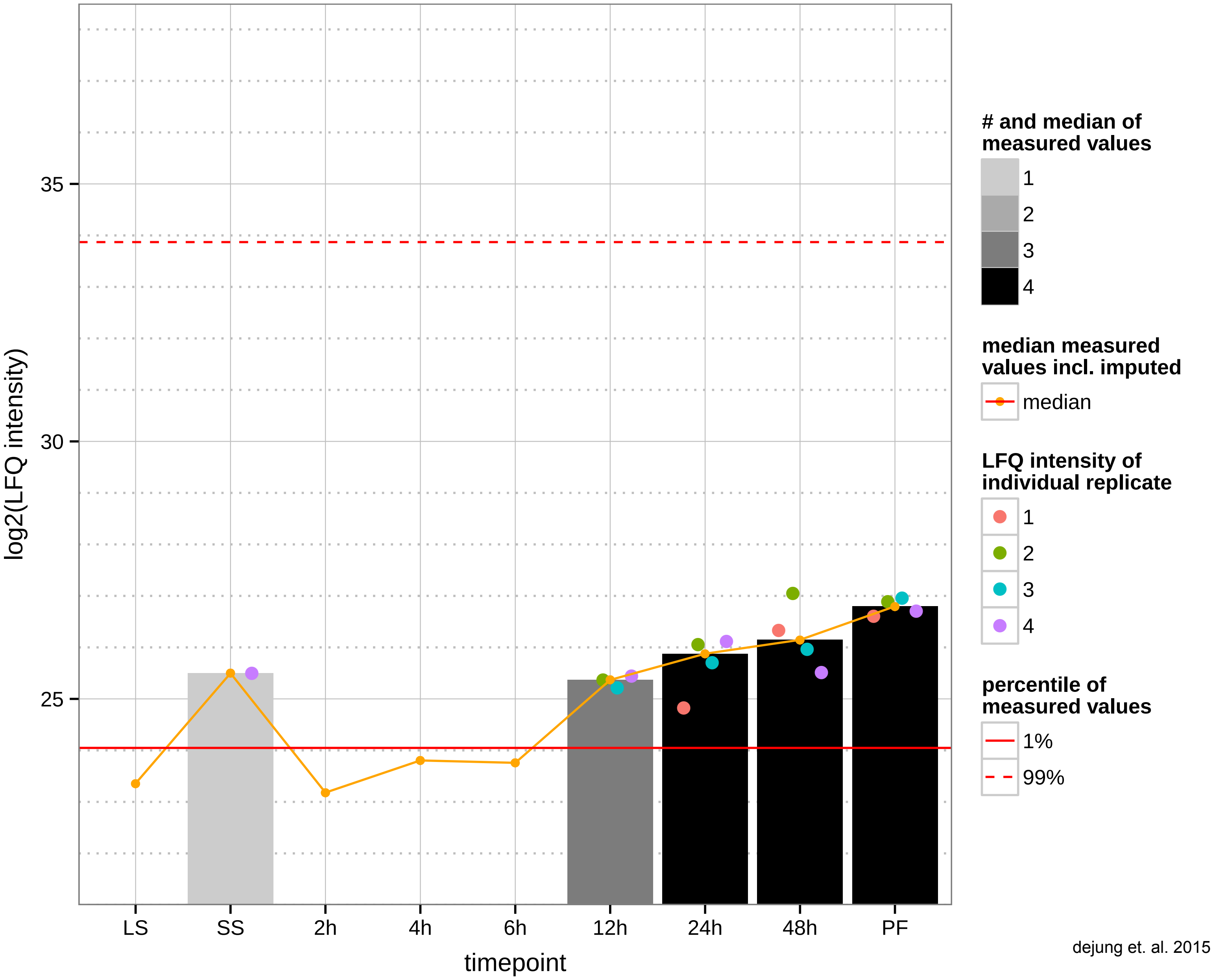
dejung et. al. 2015



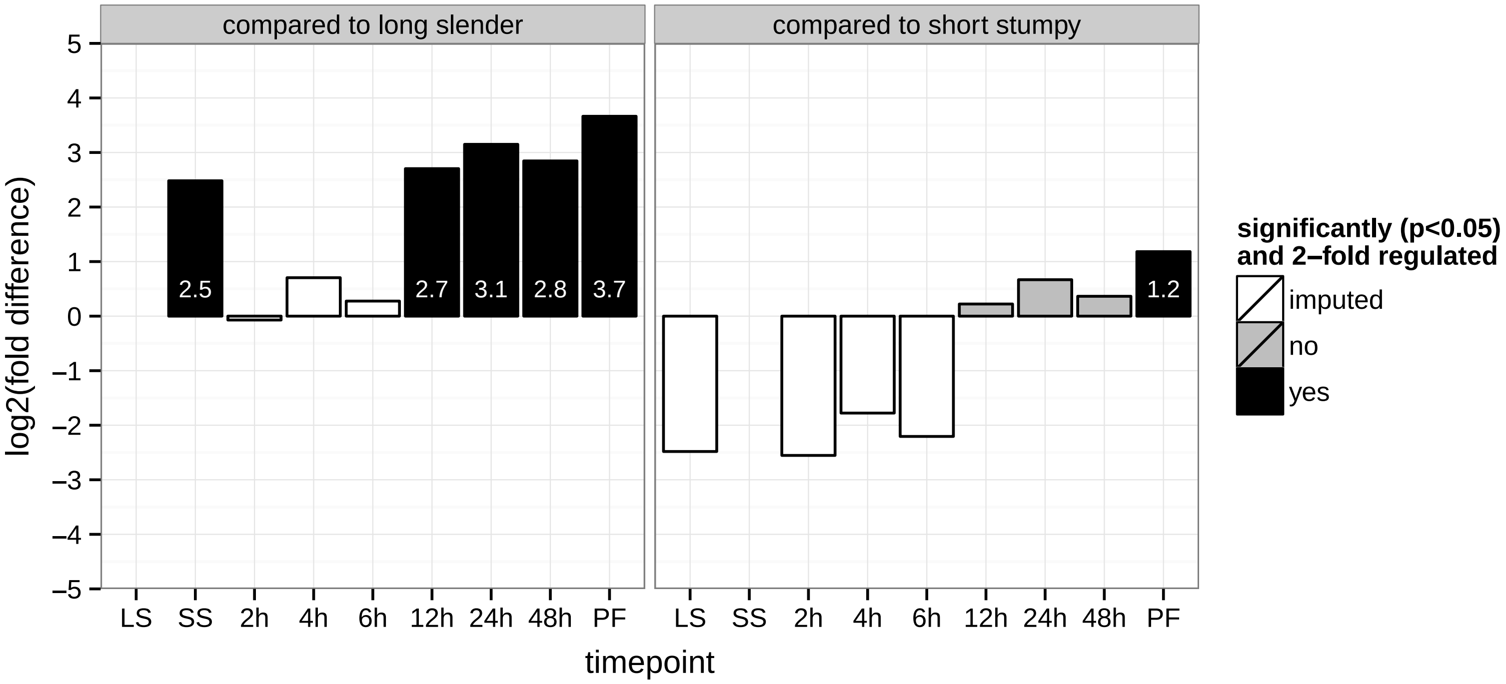
dejung et. al. 2015

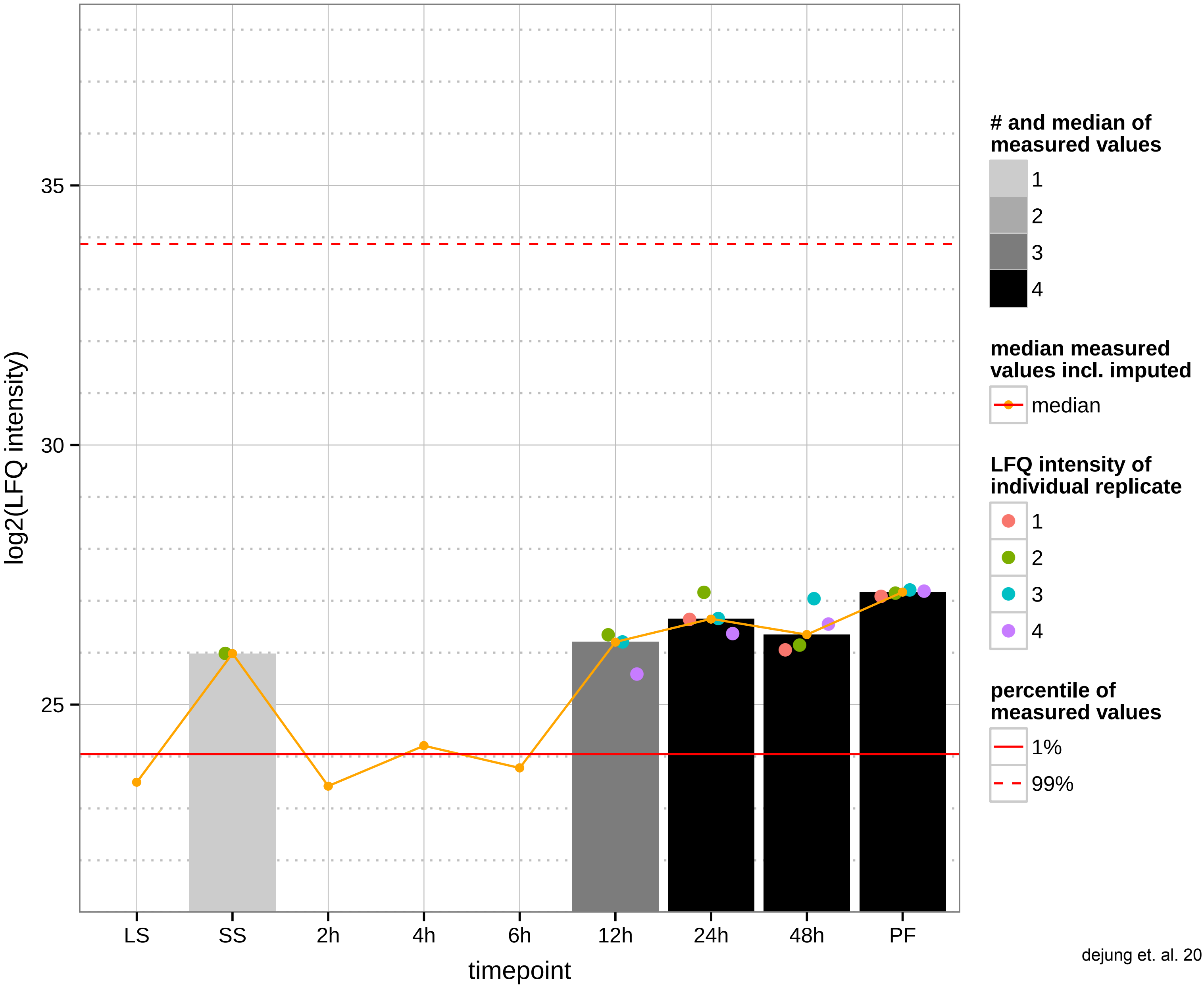
hypothetical protein, conserved
Tb927.5.2540;Tb11.v5.0574
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





hypothetical protein, conserved
Tb927.1.3170
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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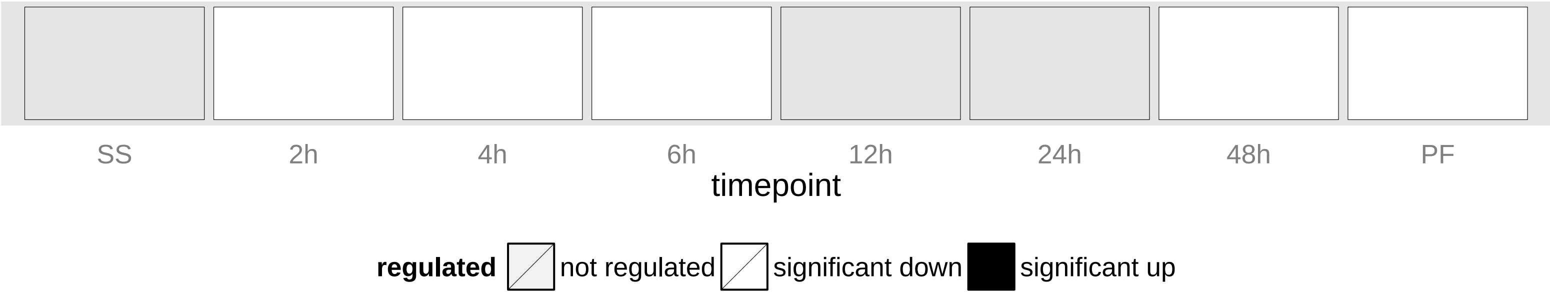
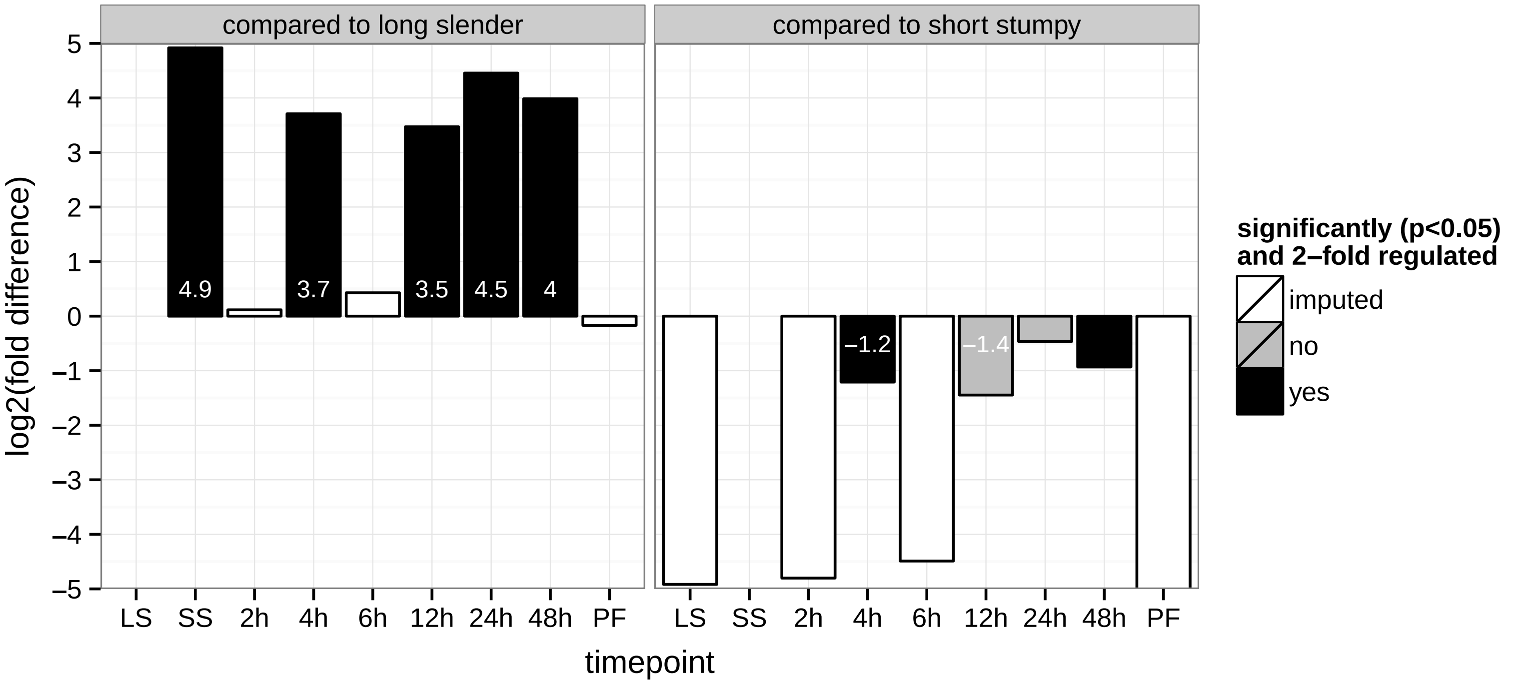
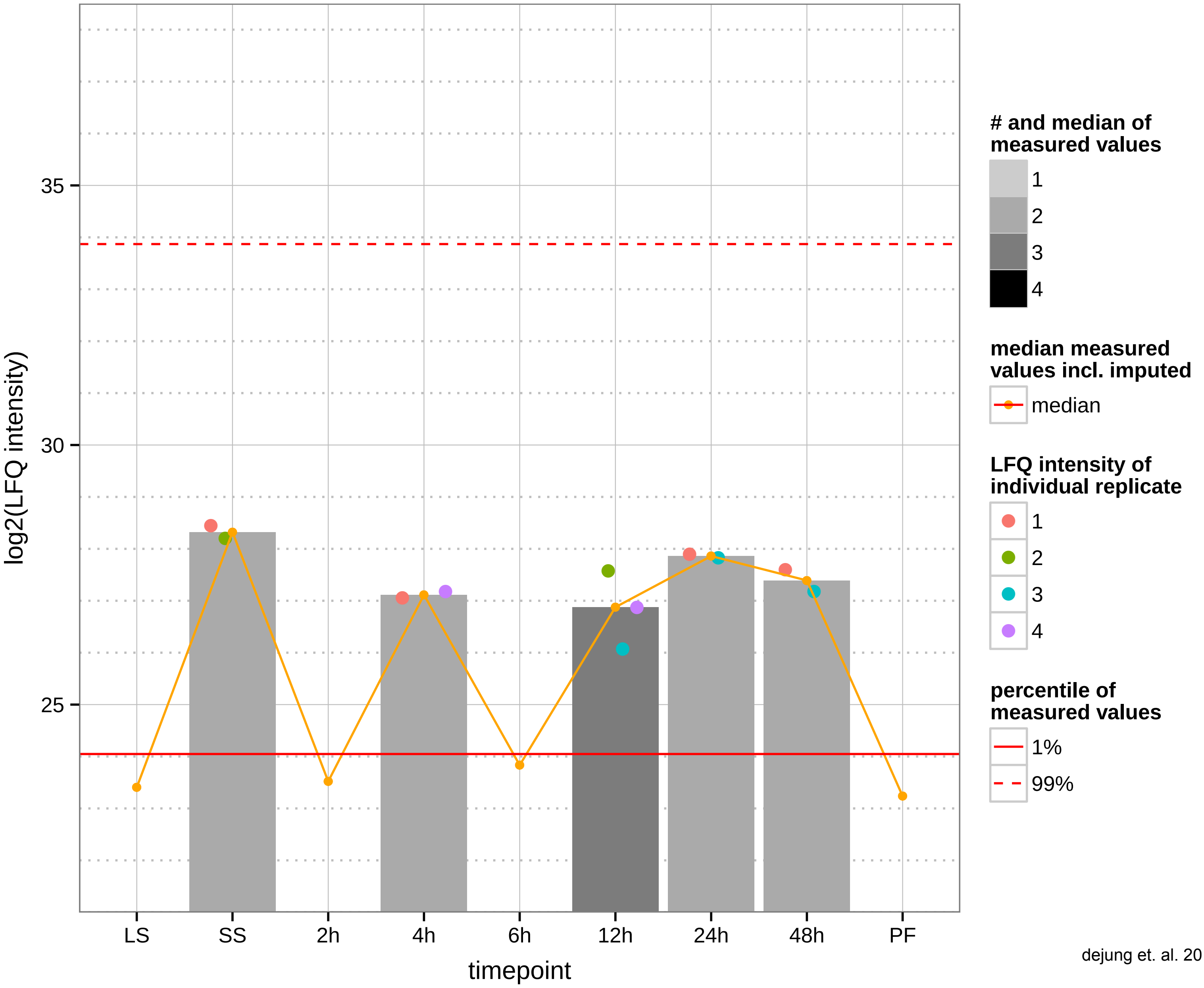


dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.1740
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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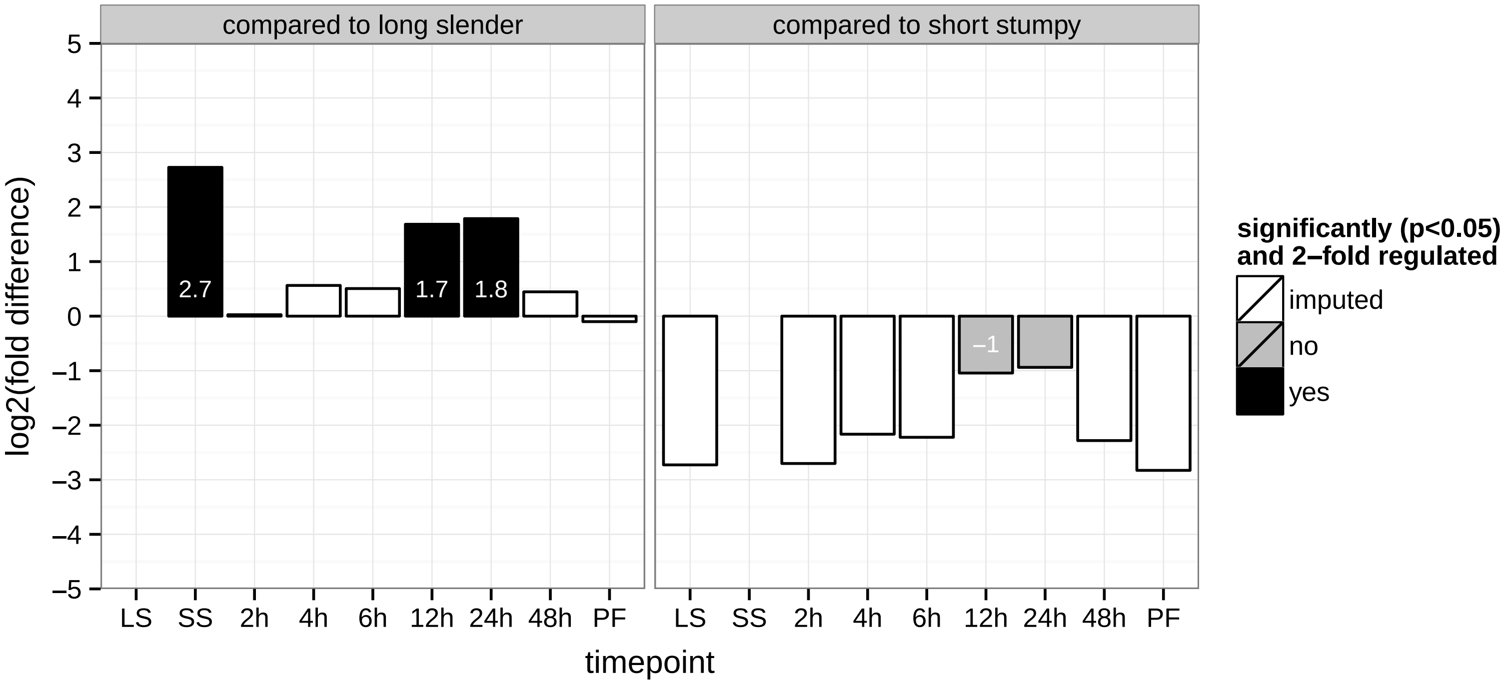
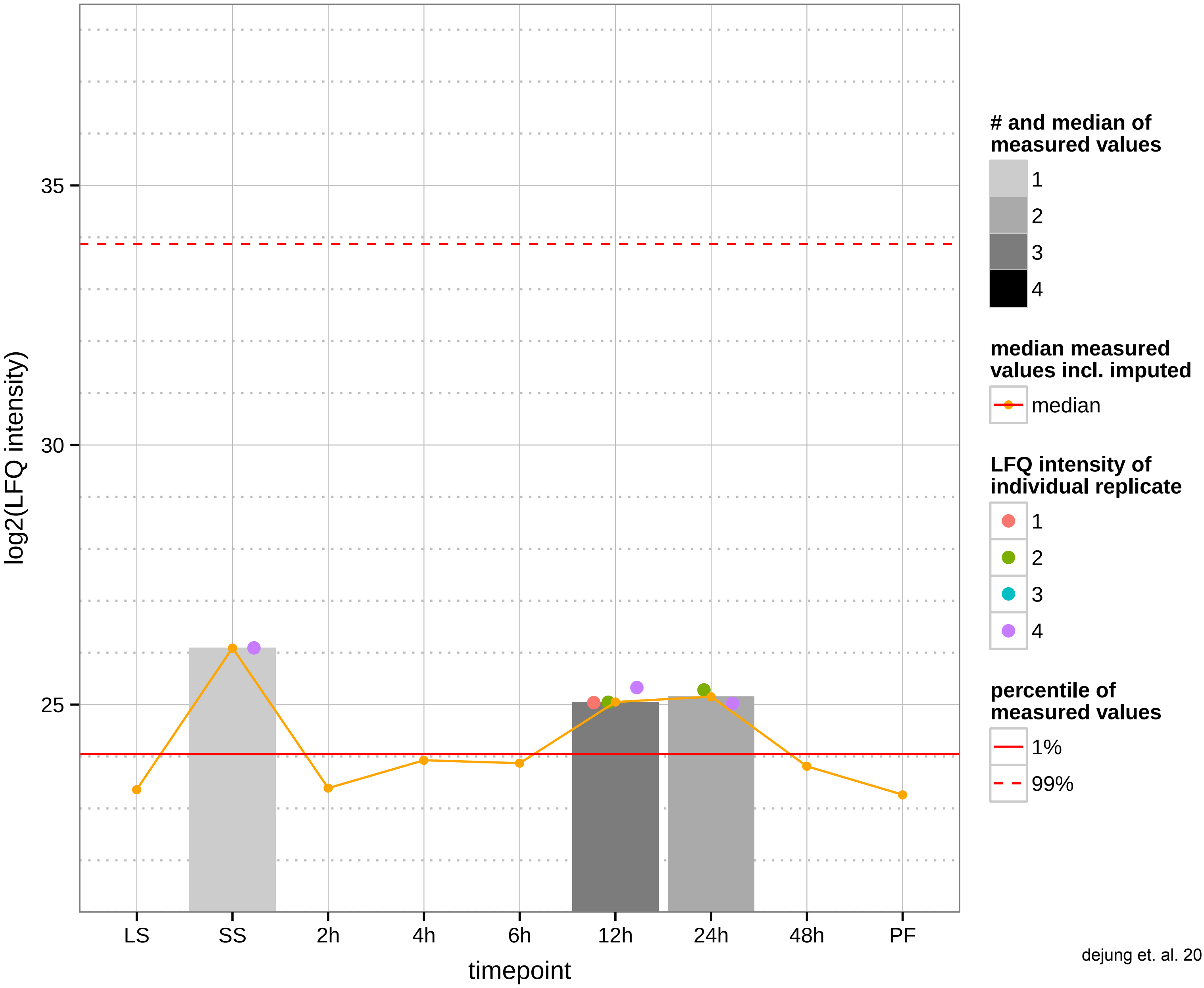
hypothetical protein, conserved
Tb927.10.8380
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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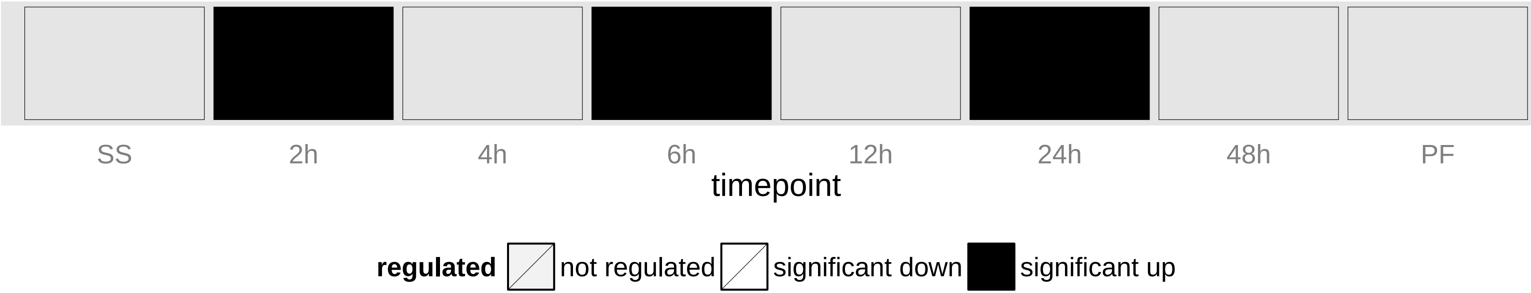
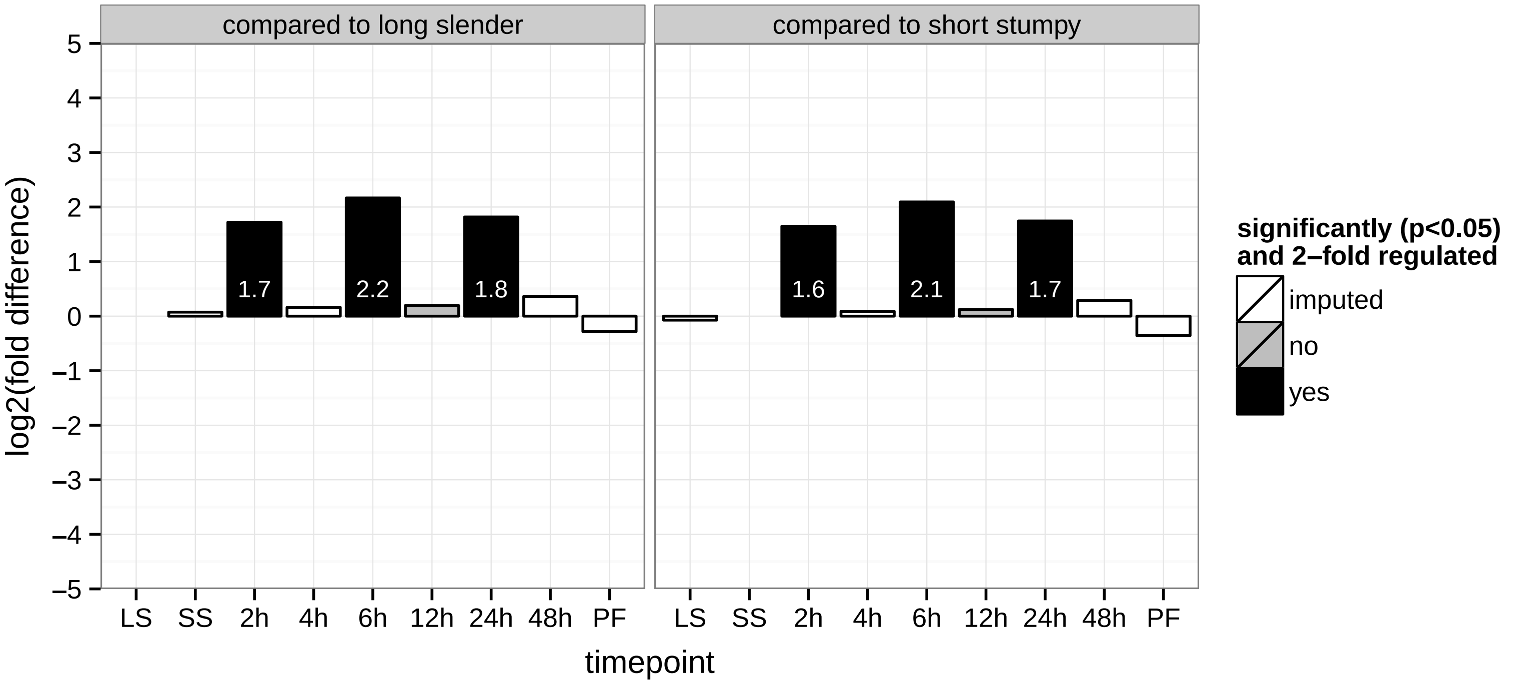
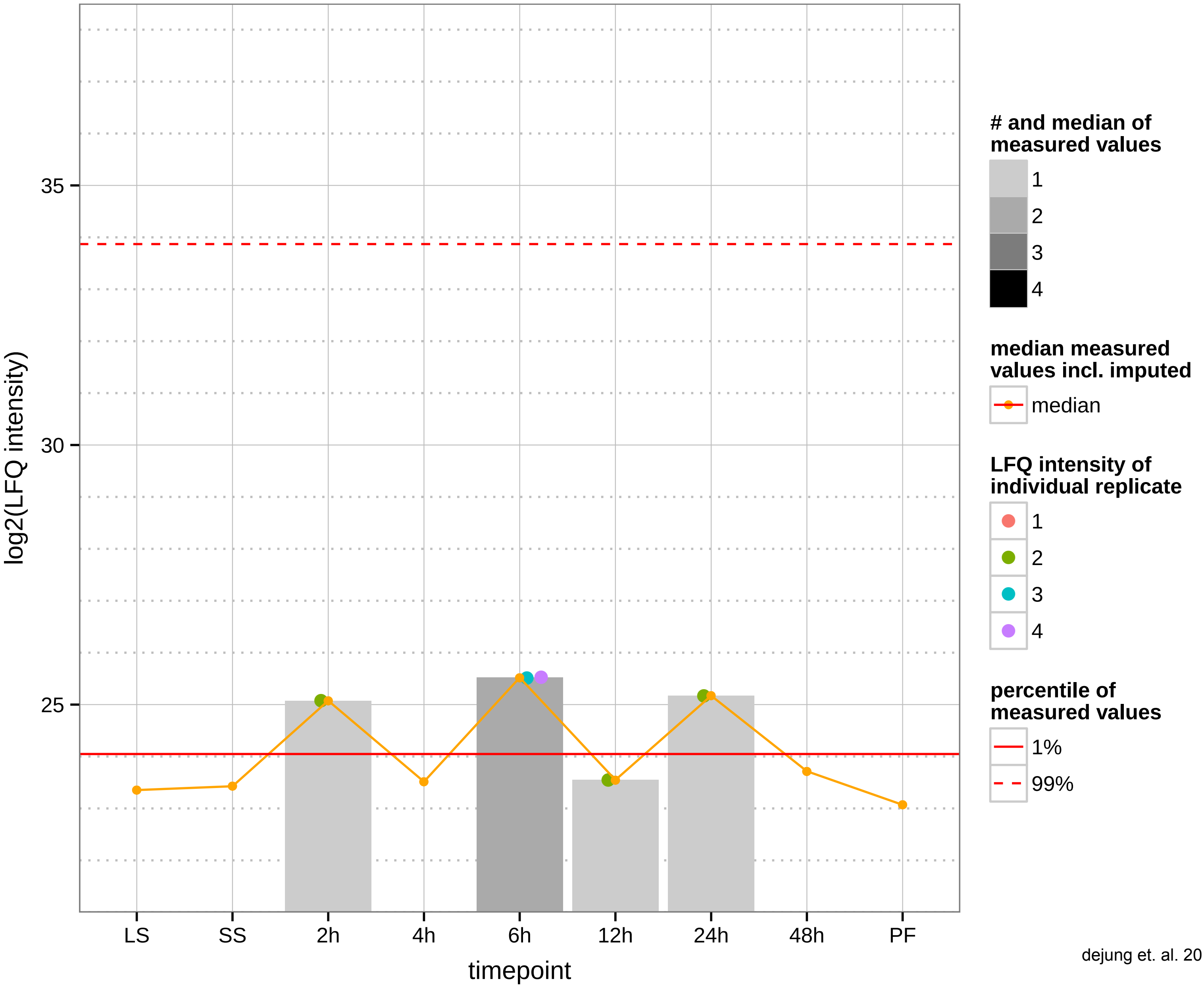


dejung et. al. 2015

hypothetical protein, conserved
Tb927.10.4070
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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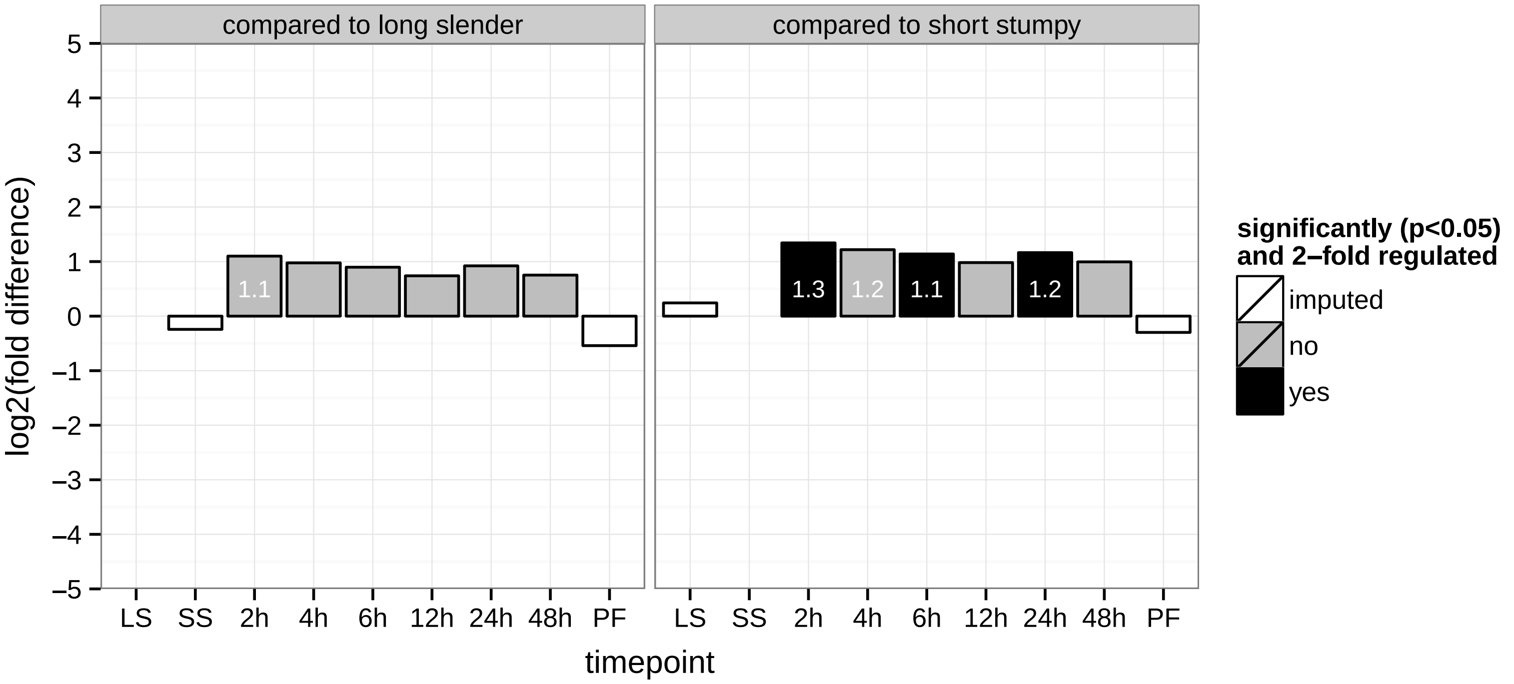
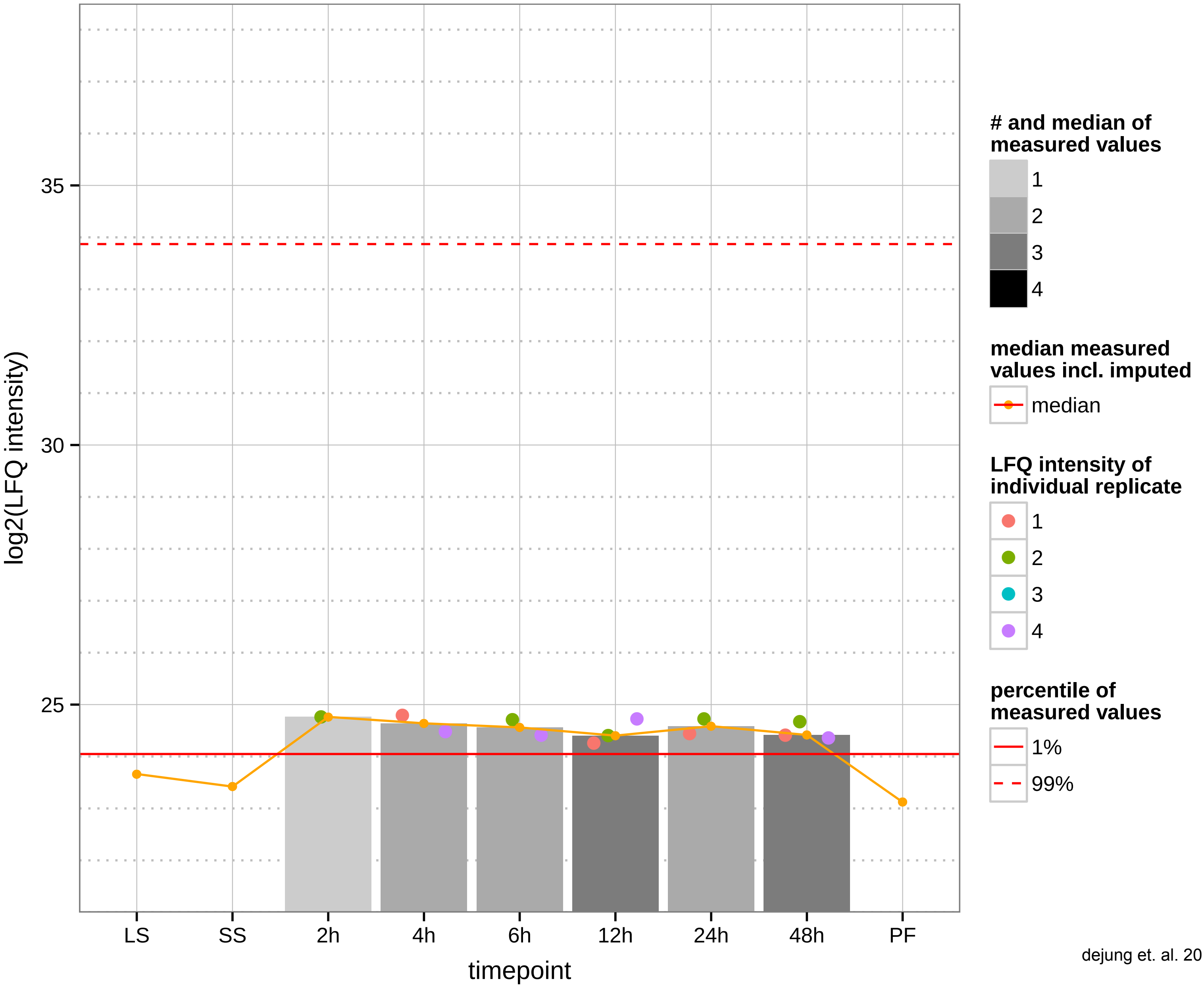
transcription elongation factor s–II, putative (TFIIS1)
Tb927.11.4960
AGOF: DNA binding, sequence−specific DNA binding transcription factor activity, zinc ion binding
AGOC: null
AGOP: DNA−dependent transcription, elongation, regulation of transcription, DNA−dependent, transcription
PGOF: nucleic acid binding, zinc ion binding
PGOC: null
PGOP: transcription, DNA−dependent





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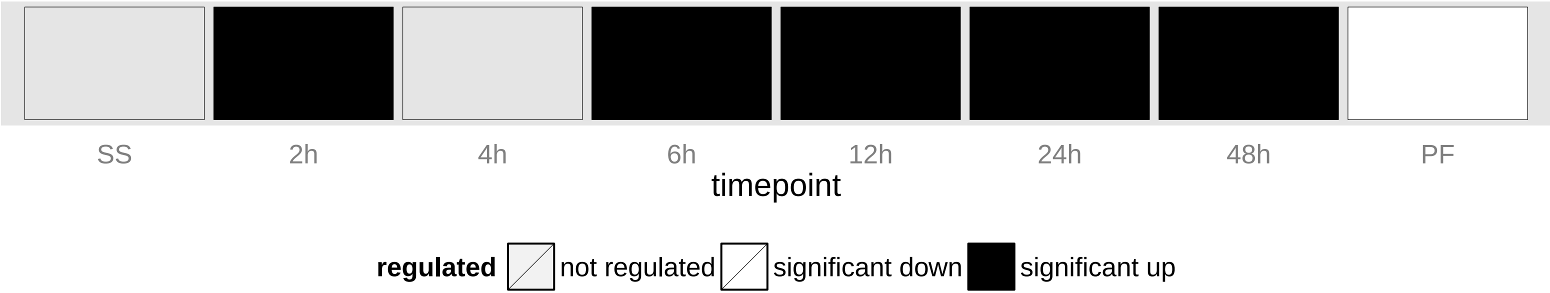

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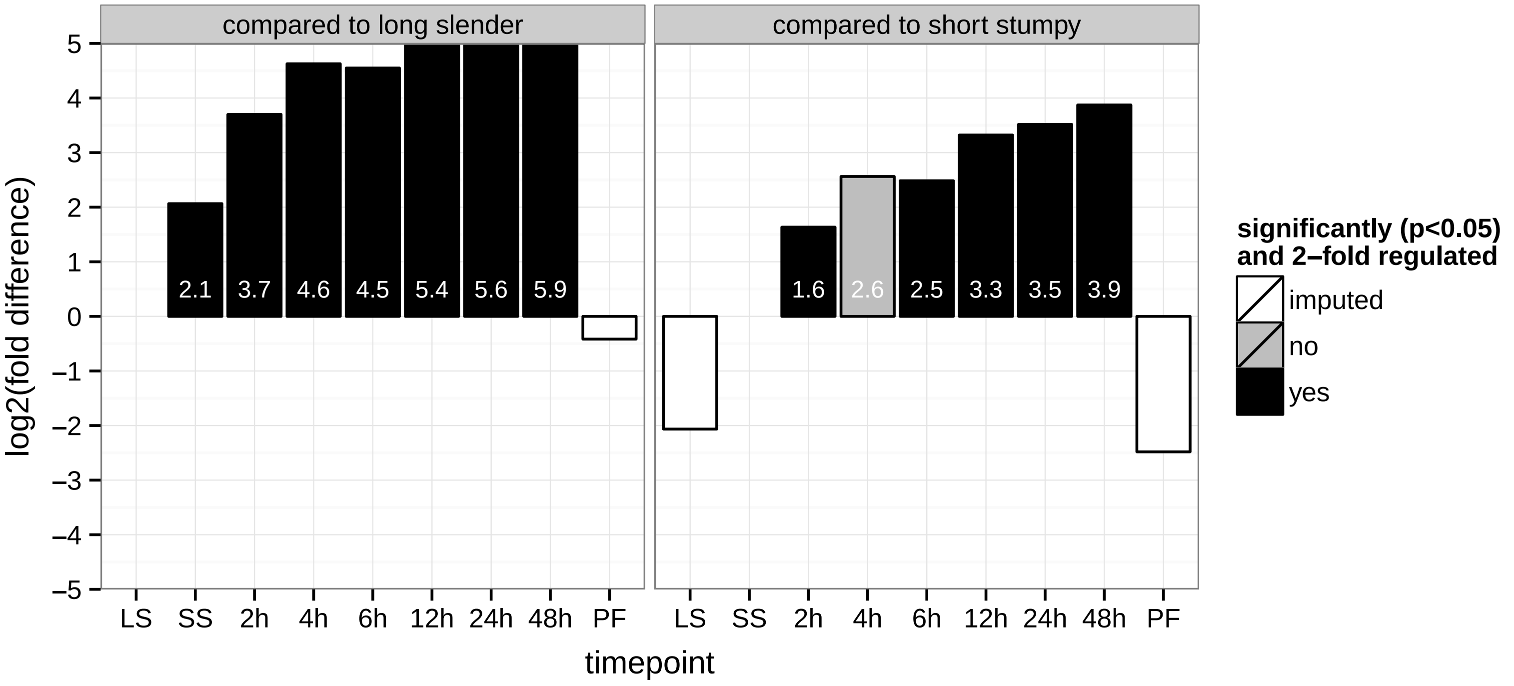
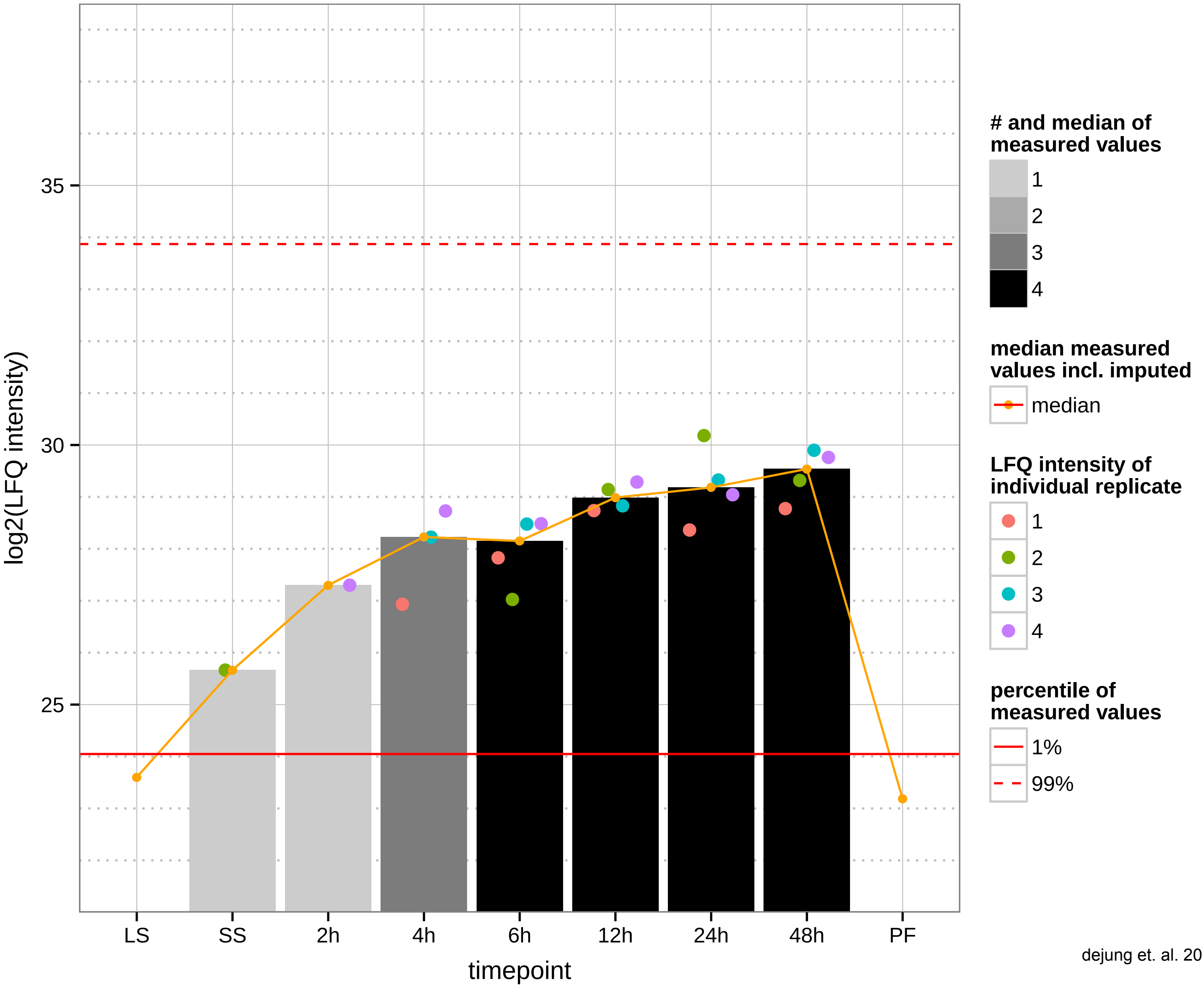
calpain–like protein fragment, putative
Tb927.1.2230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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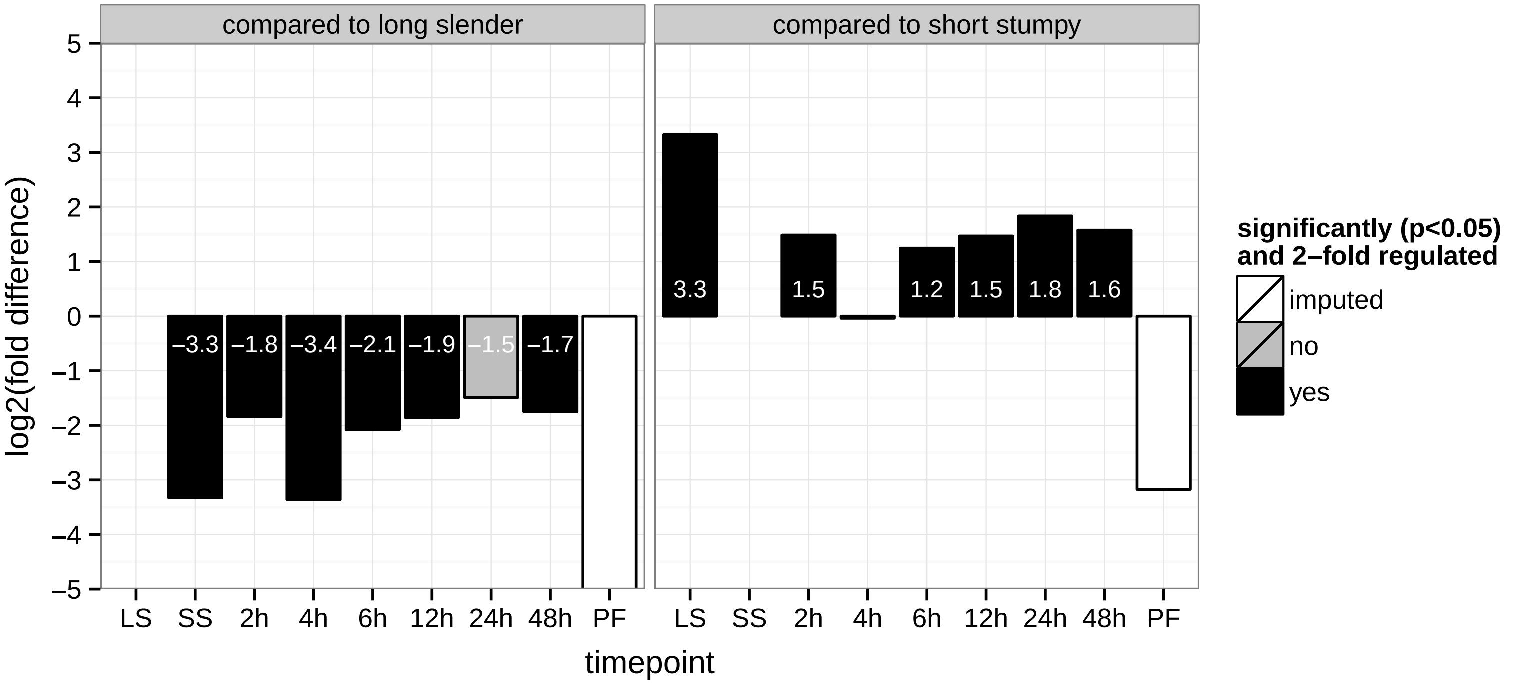
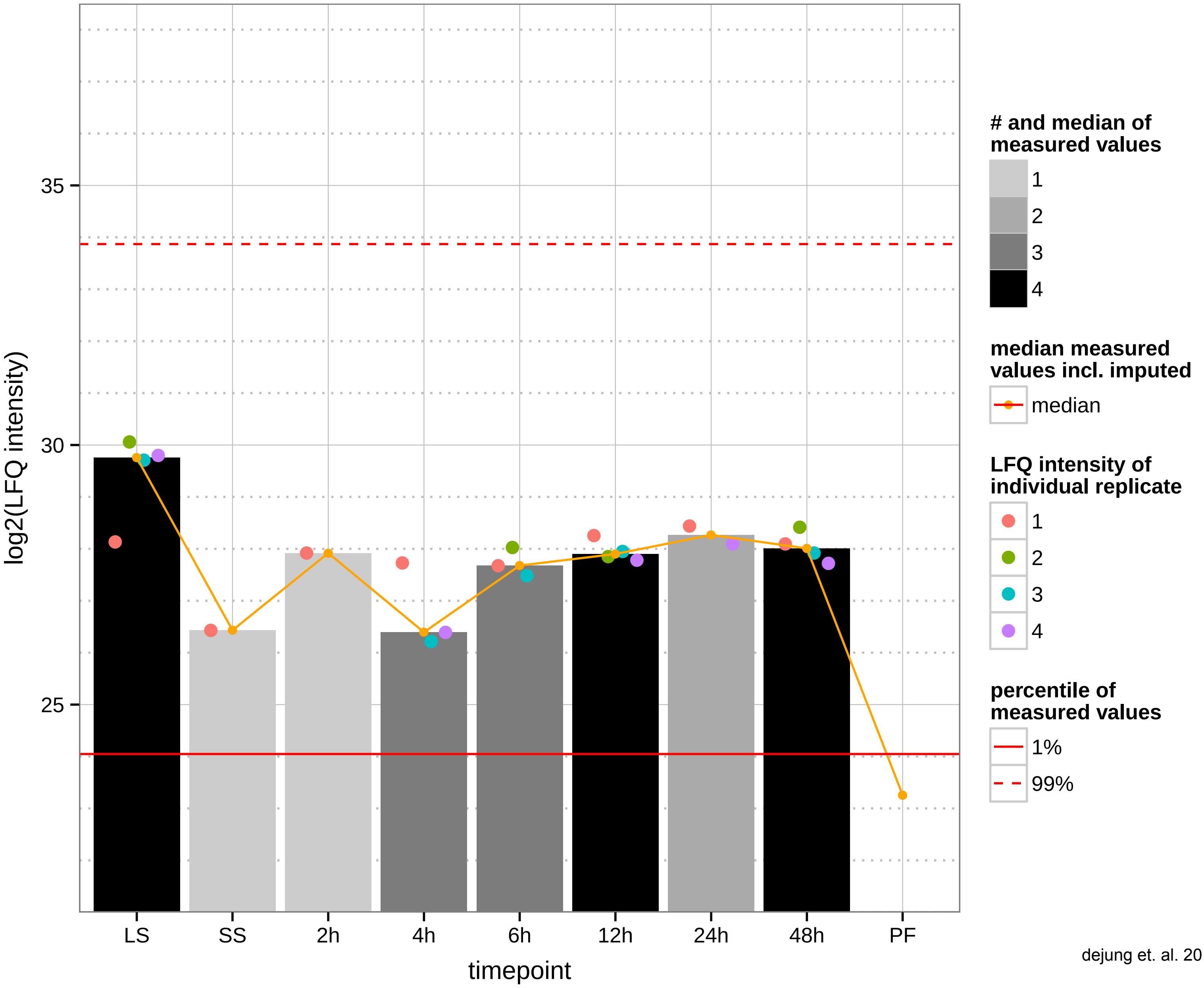
dynein heavy chain, cytosolic, putative, Cytoplasmic dynein 1 heavy chain (DYNC1H1)
Tb927.7.3160
AGOF: null, ATP binding, ATPase activity, microtubule motor activity
AGOC: null, dynein complex
AGOP: null, chromosome segregation, microtubule−based movement, minus−end−directed vesicle transport along microtubul
PGOF: null, ATP binding, ATPase activity, microtubule motor activity, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null, dynein complex
PGOP: null, microtubule−based movement





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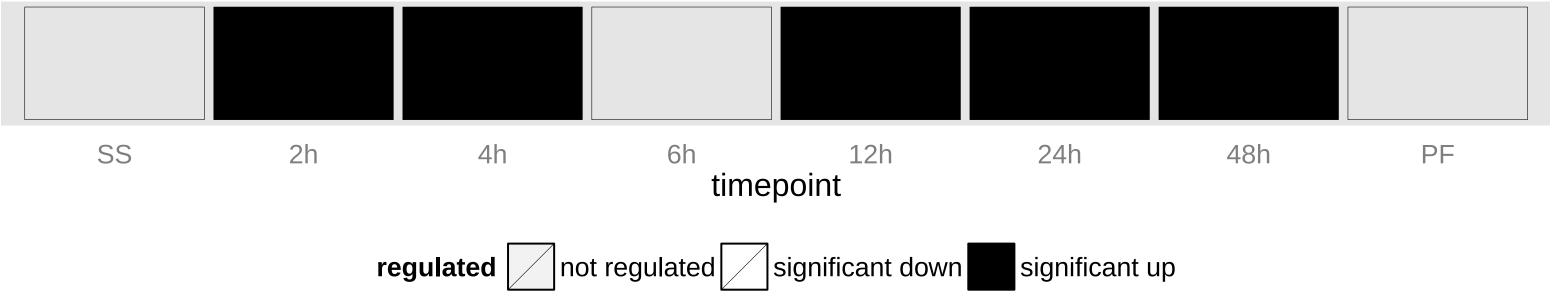

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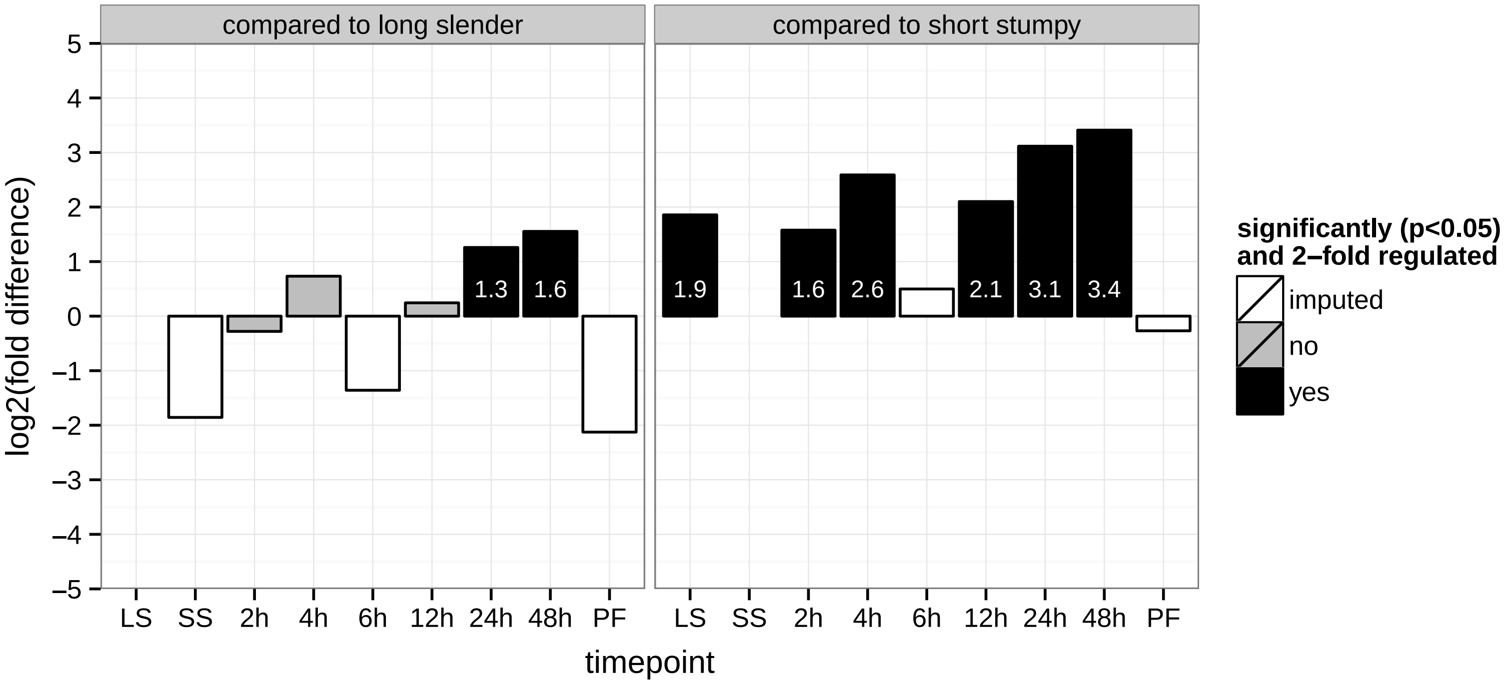
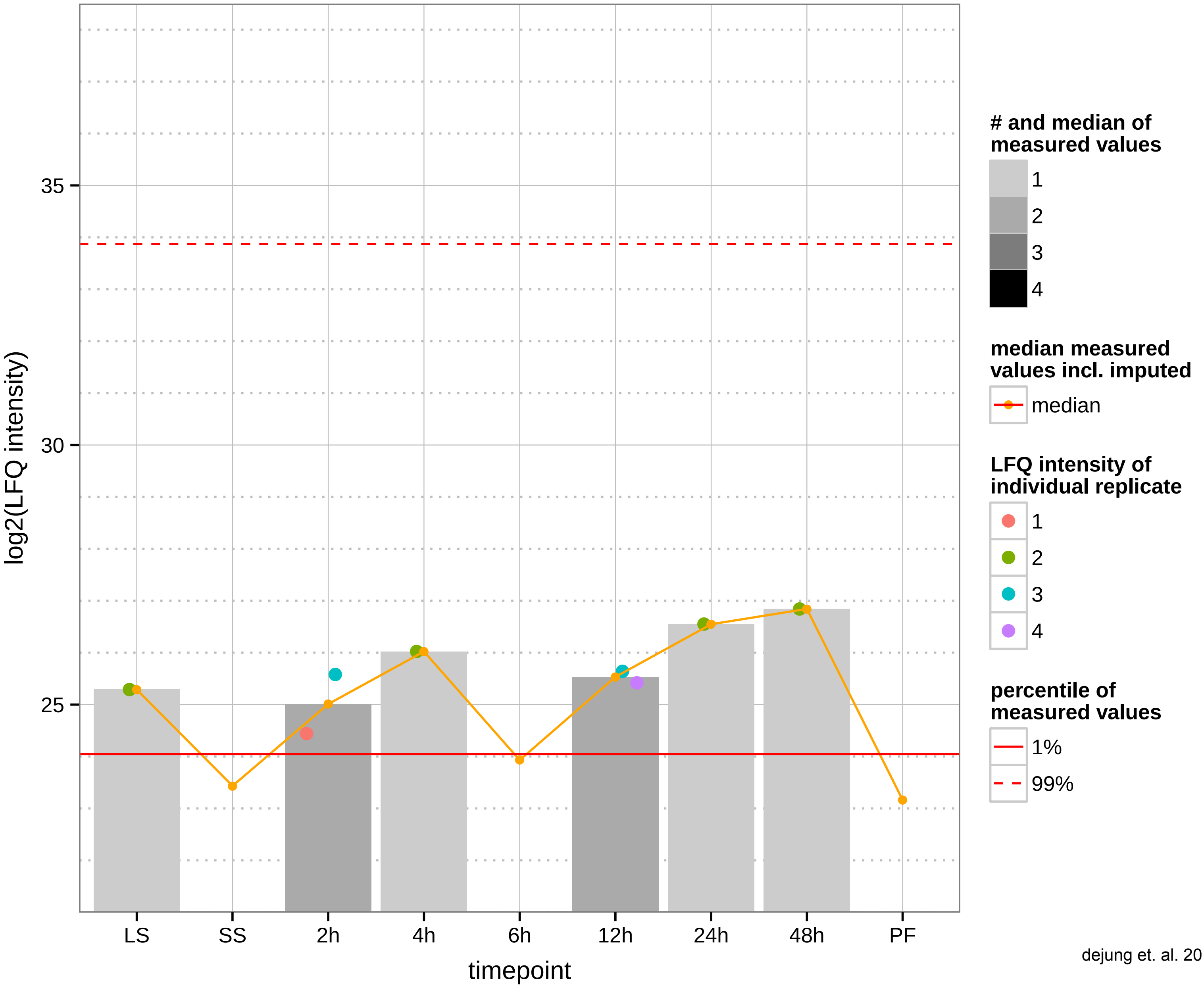
iron–sulfur cluster assembly protein, putative
Tb927.10.12000
AGOF: iron–sulfur cluster binding
AGOC: cytoplasm, mitochondrion
AGOP: tRNA thio–modification
PGOF: null
PGOC: null
PGOP: null





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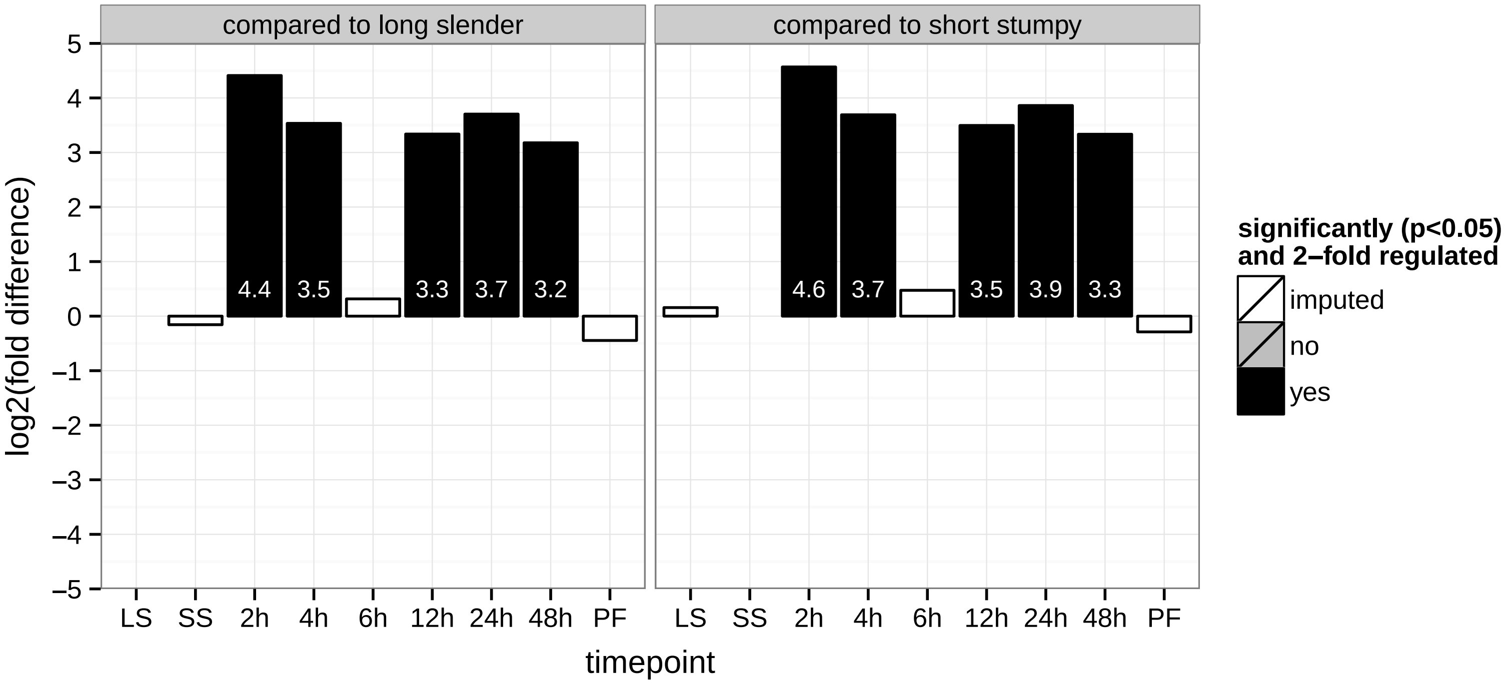
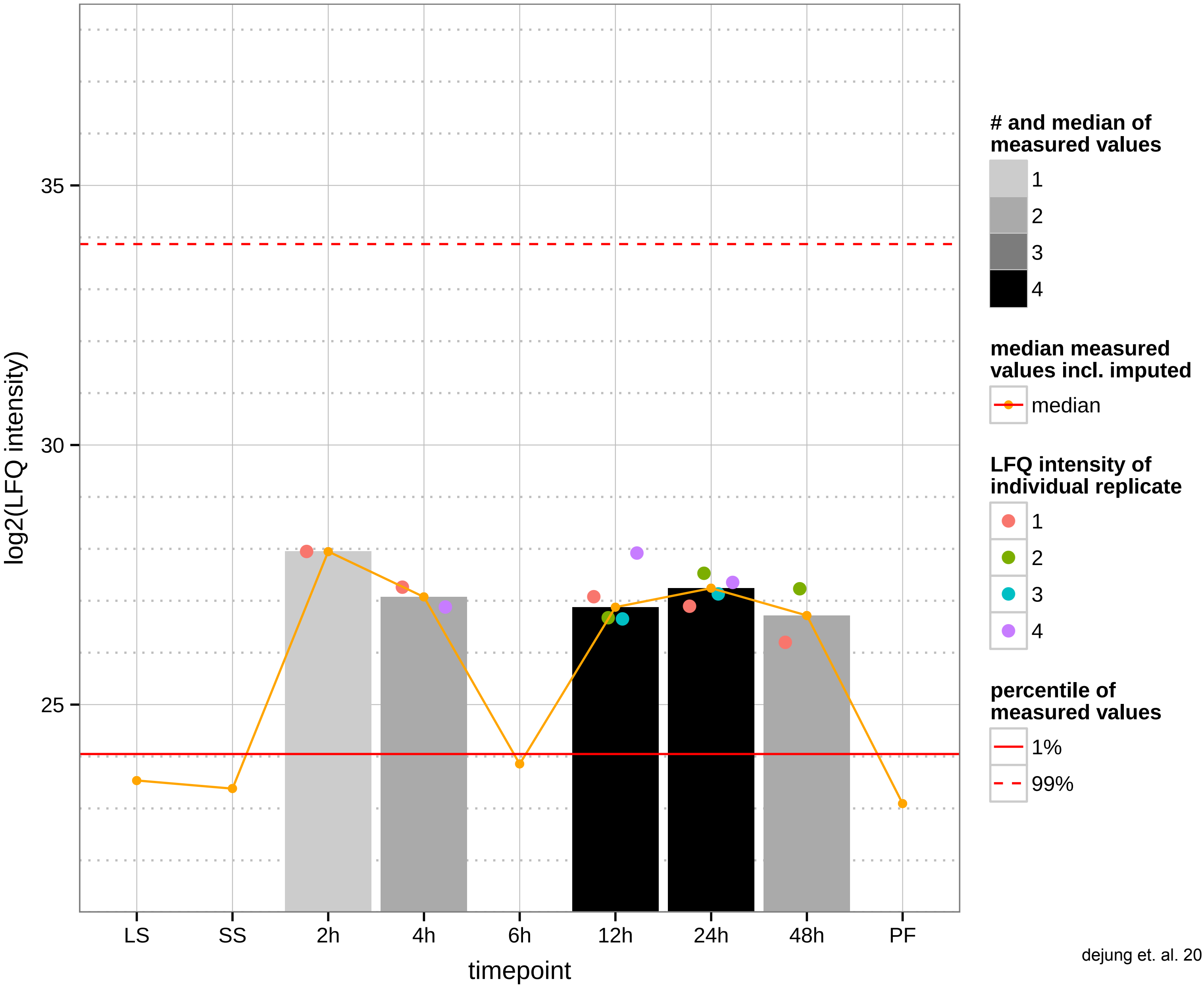
DNA–directed RNA polymerases II subunit, putative (RPB4)
Tb927.3.5270
AGOF: DNA–directed RNA polymerase activity, protein binding
AGOC: null
AGOP: transcription, DNA–dependent
PGOF: DNA–directed RNA polymerase activity, catalytic activity, nucleotide binding
PGOC: null
PGOP: cellular metabolic process, transcription, DNA–dependent





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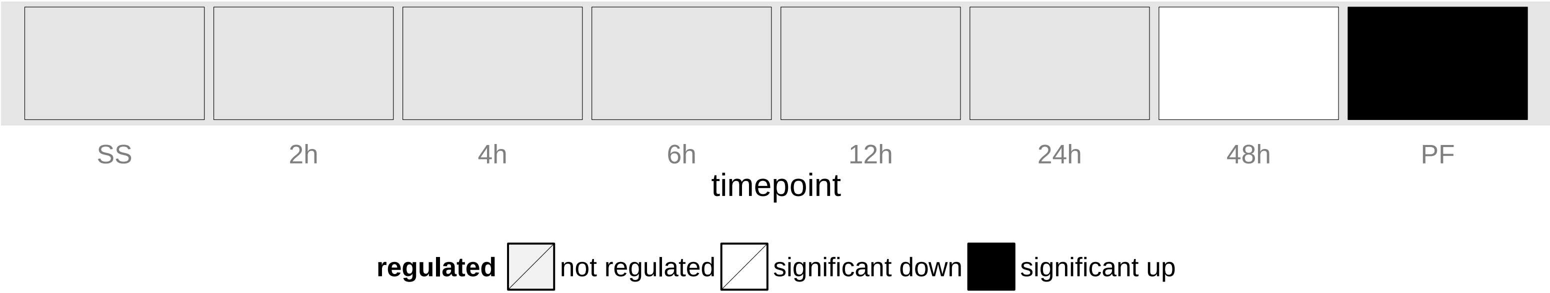

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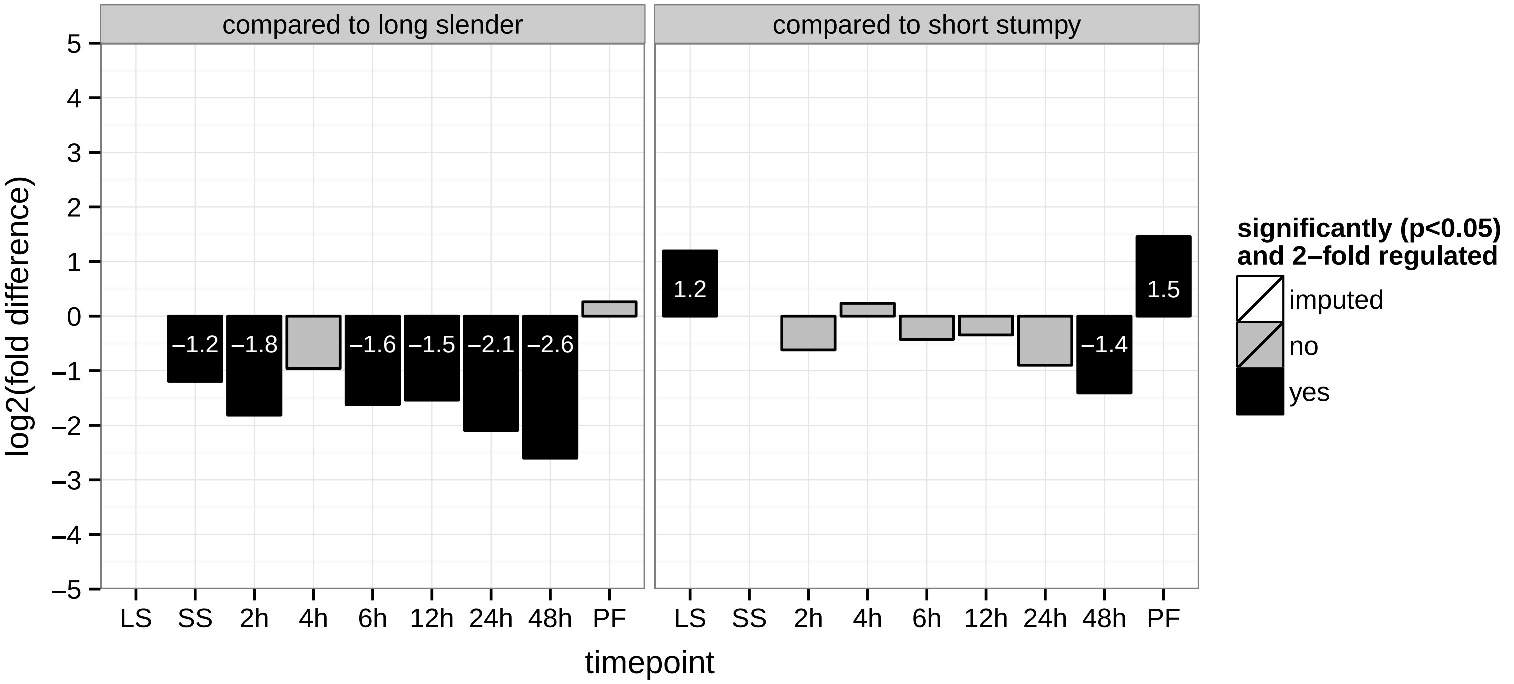
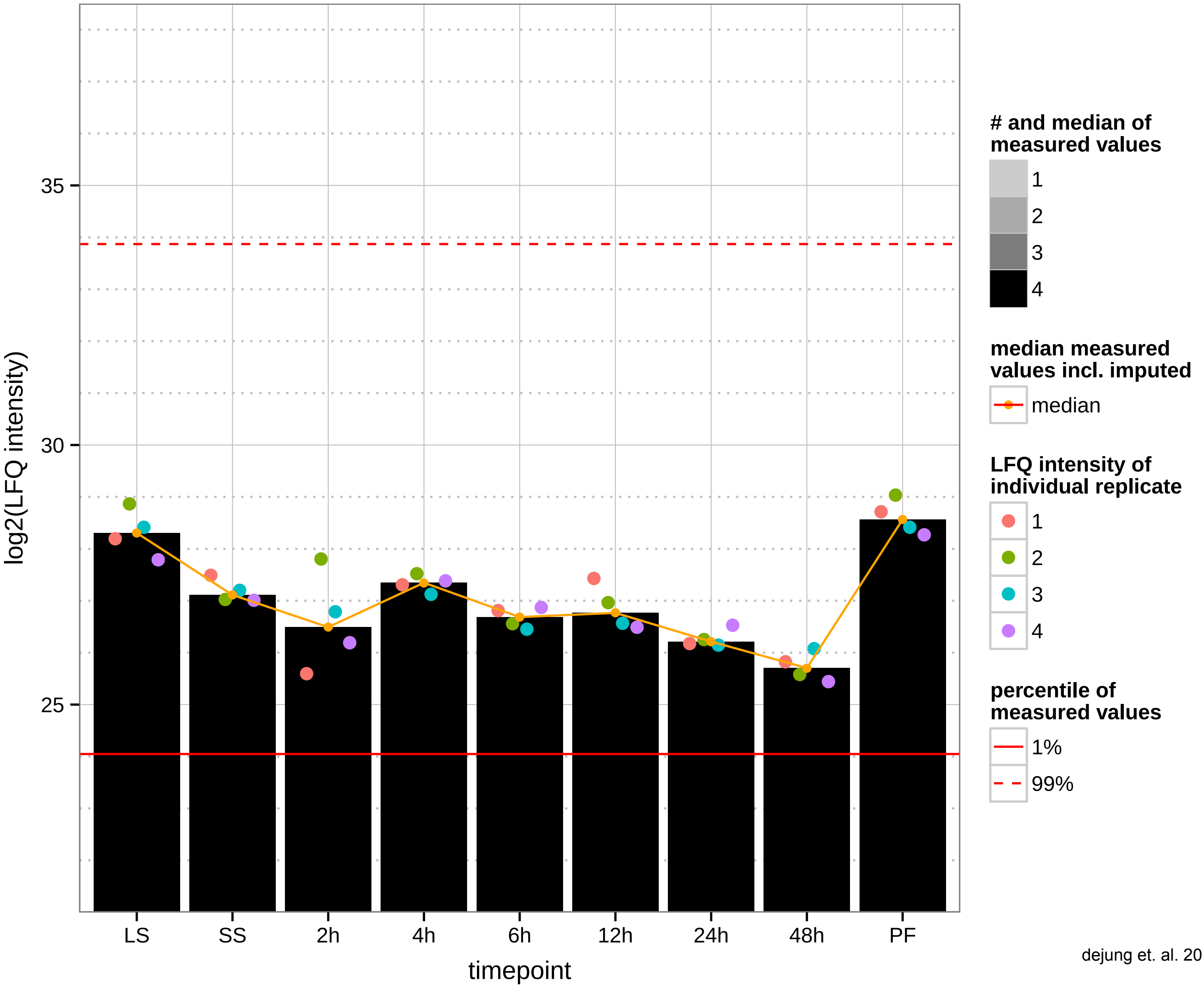
hypothetical protein, conserved
Tb927.11.10690
AGOF: null
AGOC: endoplasmic reticulum
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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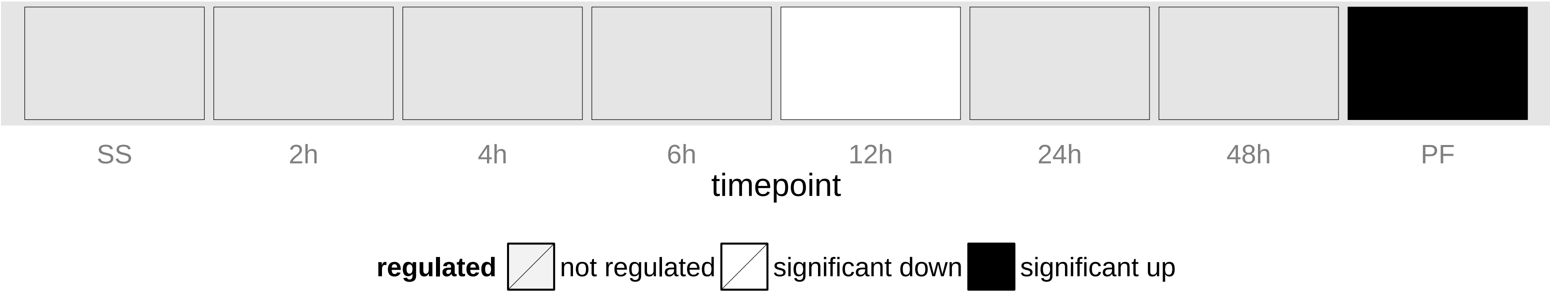

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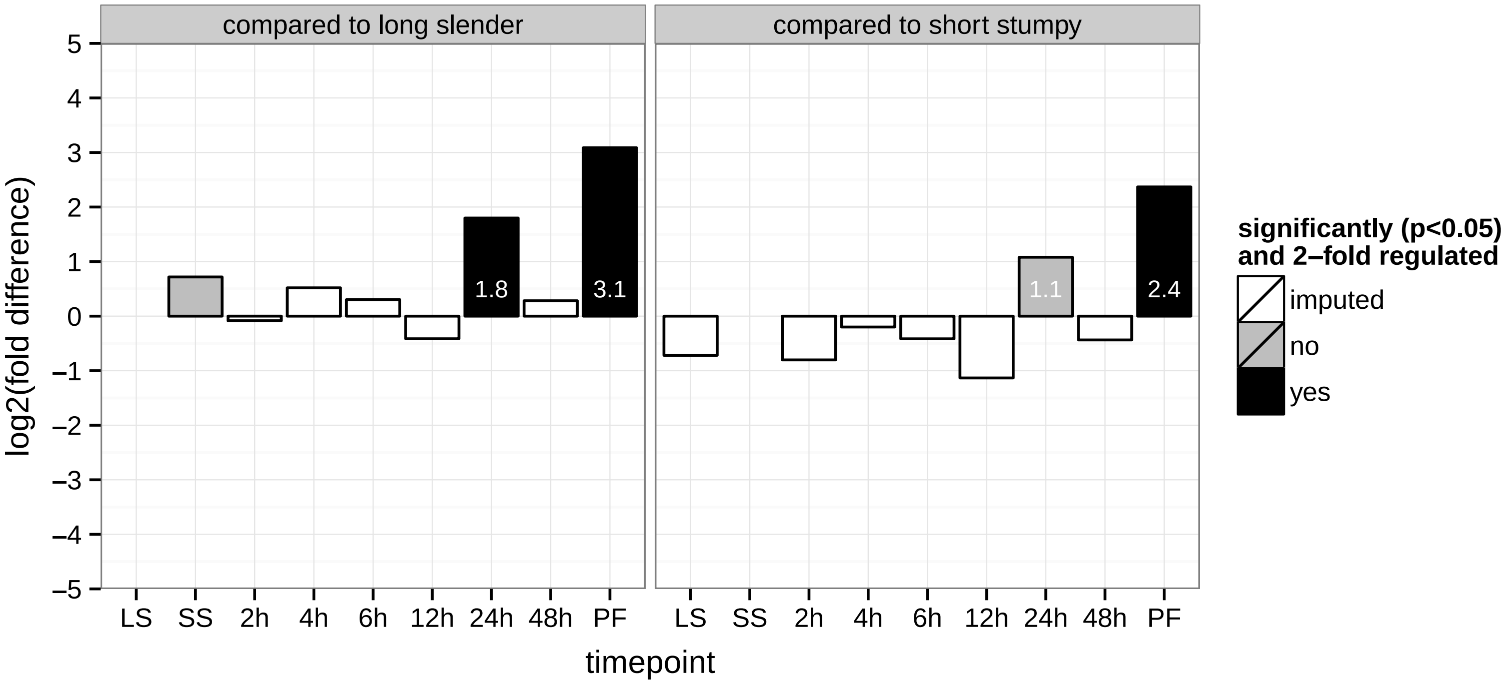
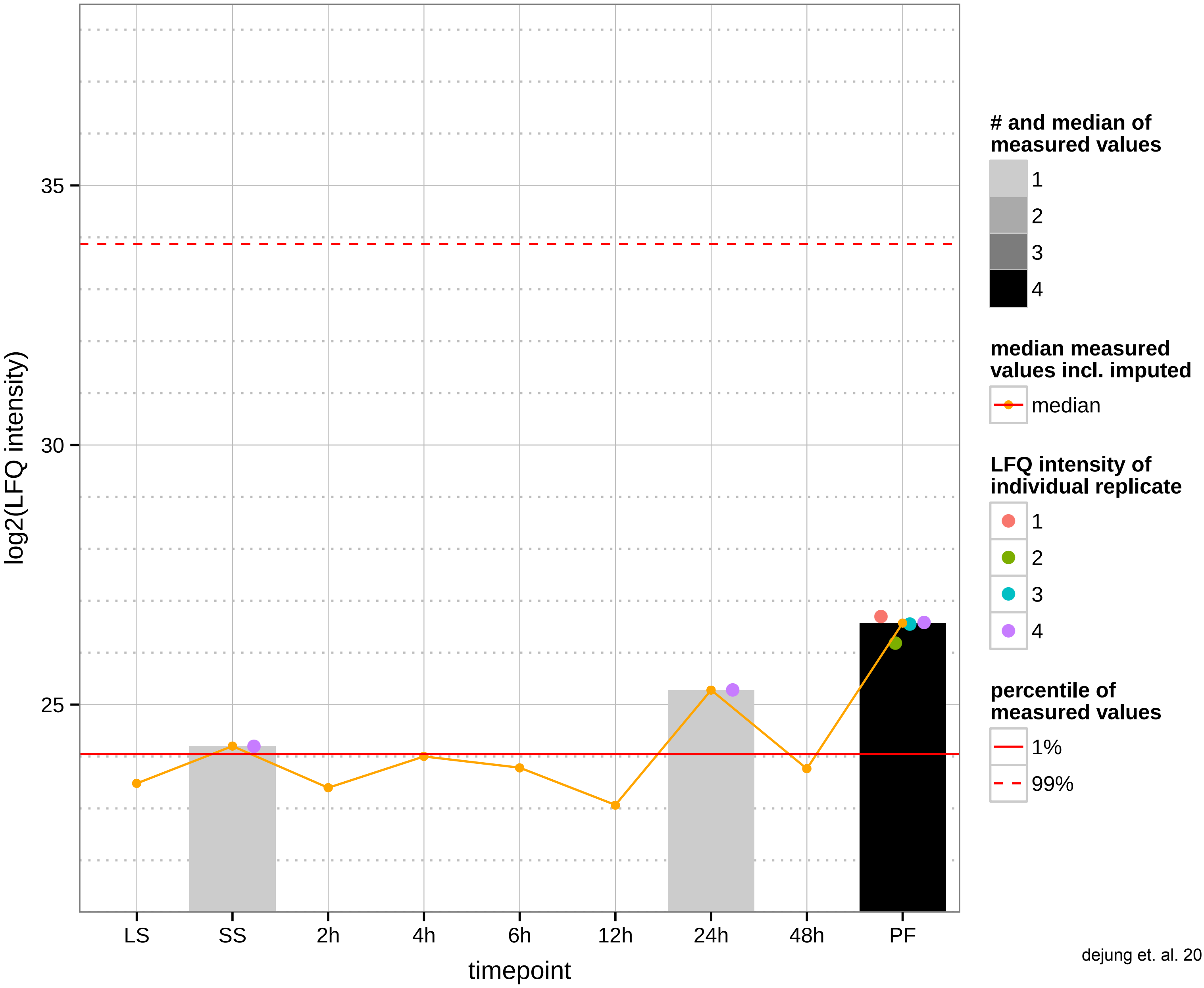
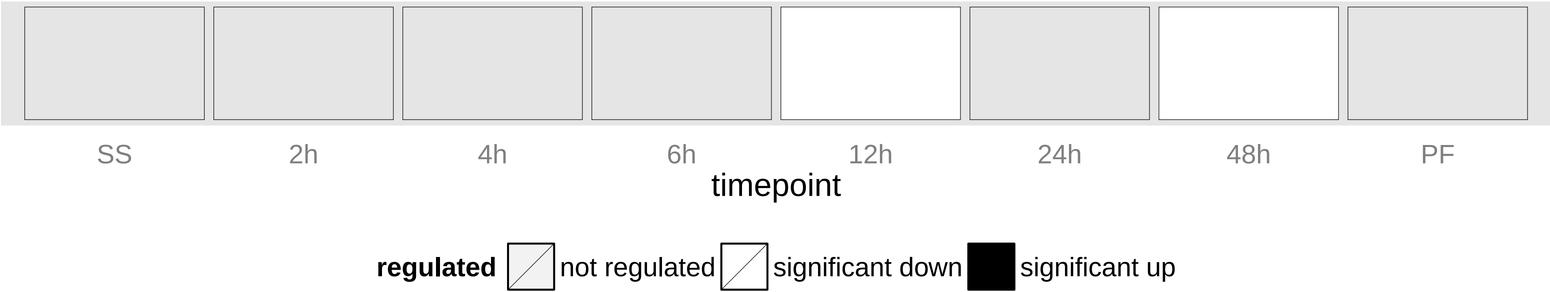
hypothetical protein, conserved
Tb927.11.14700
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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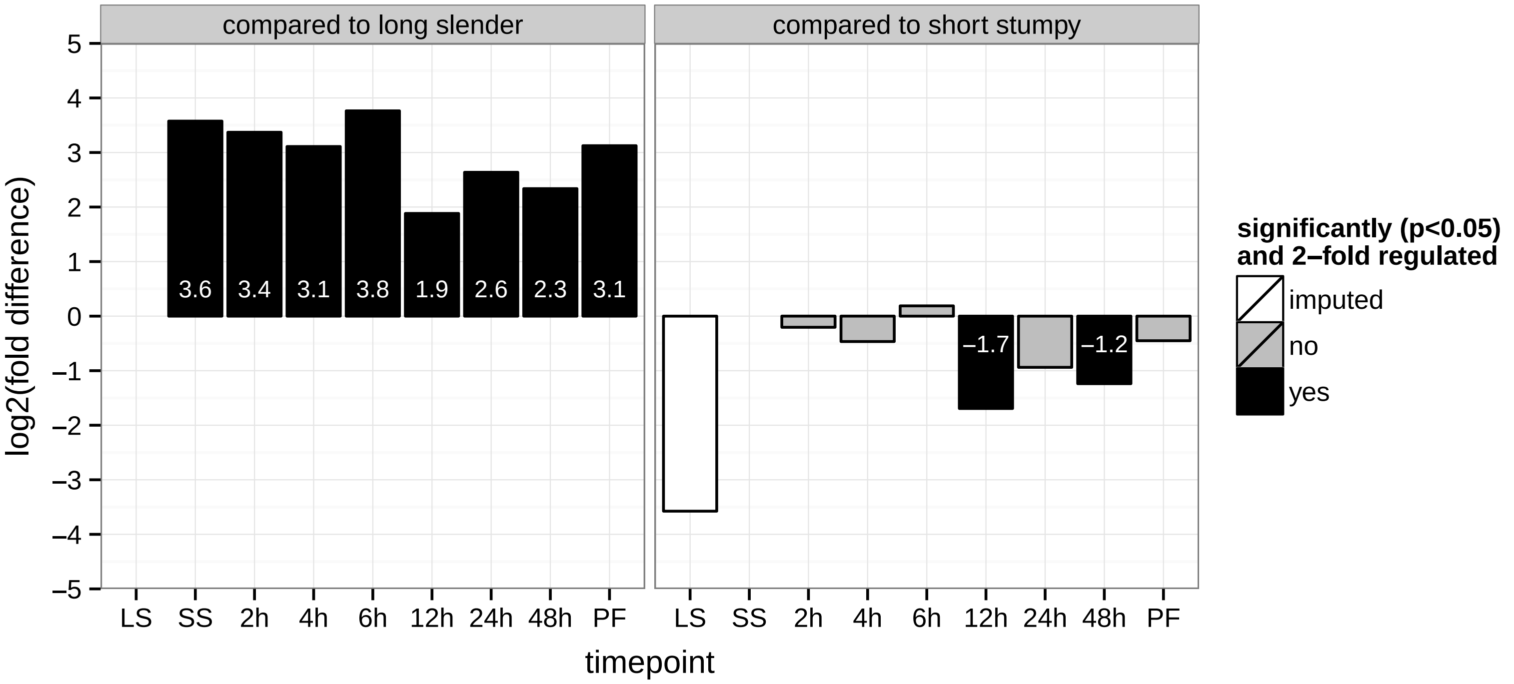
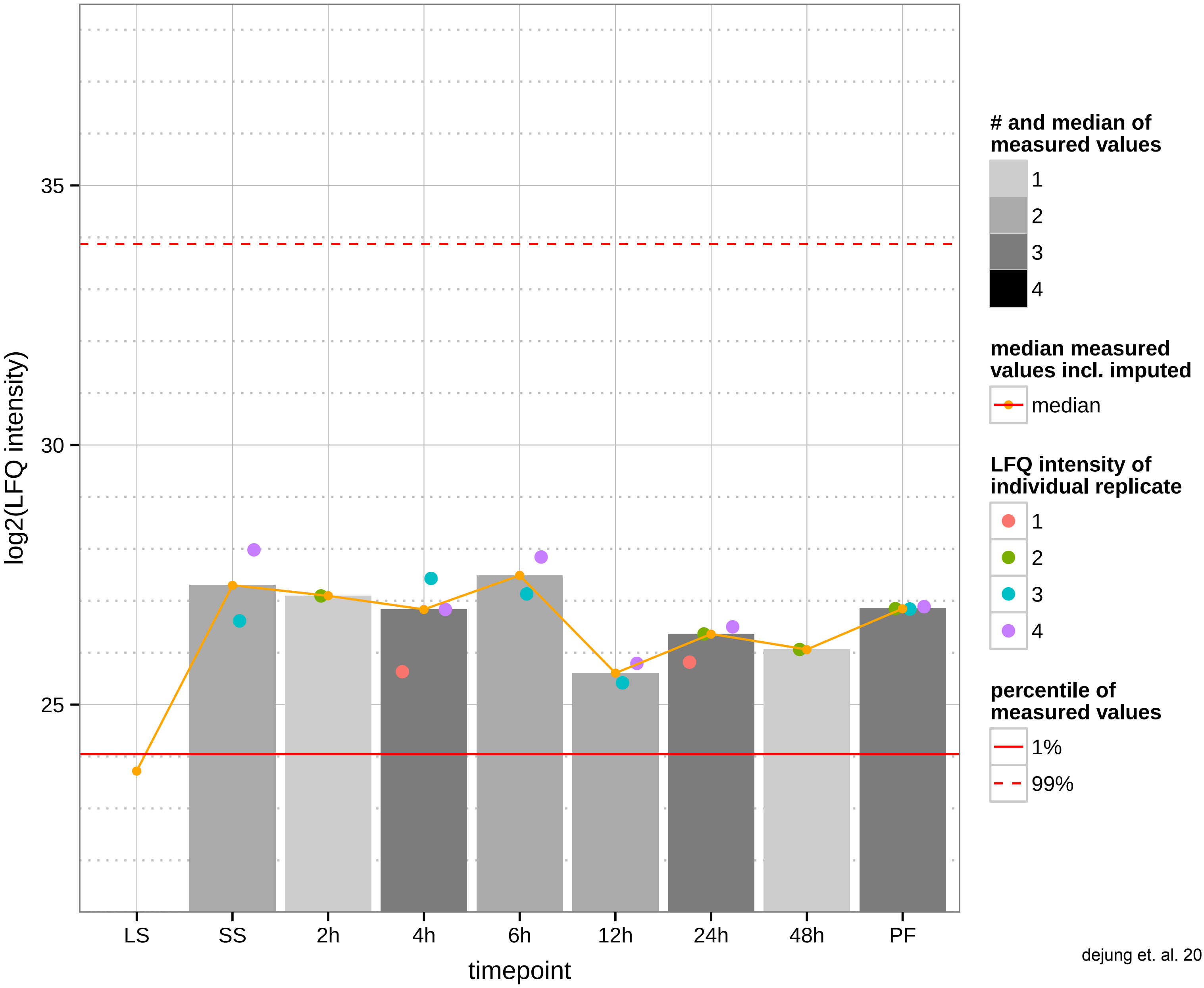
ATP–binding protein, putative
Tb927.11.360
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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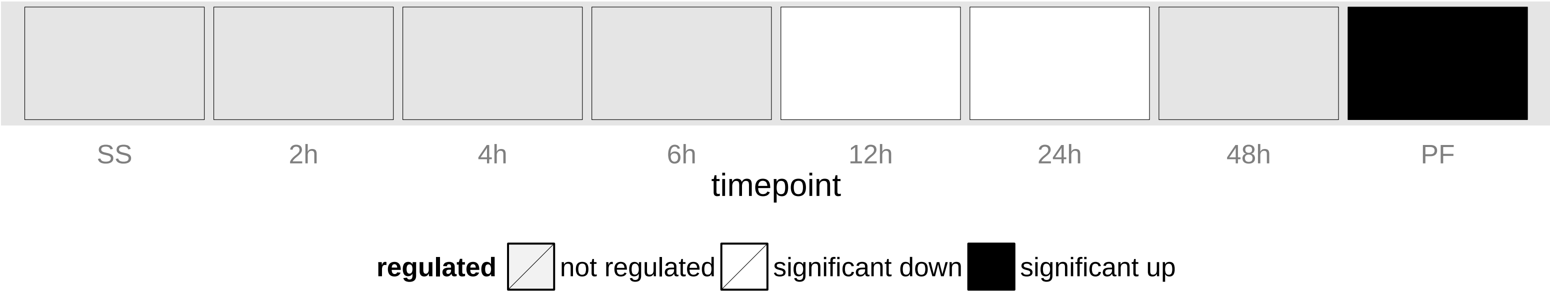

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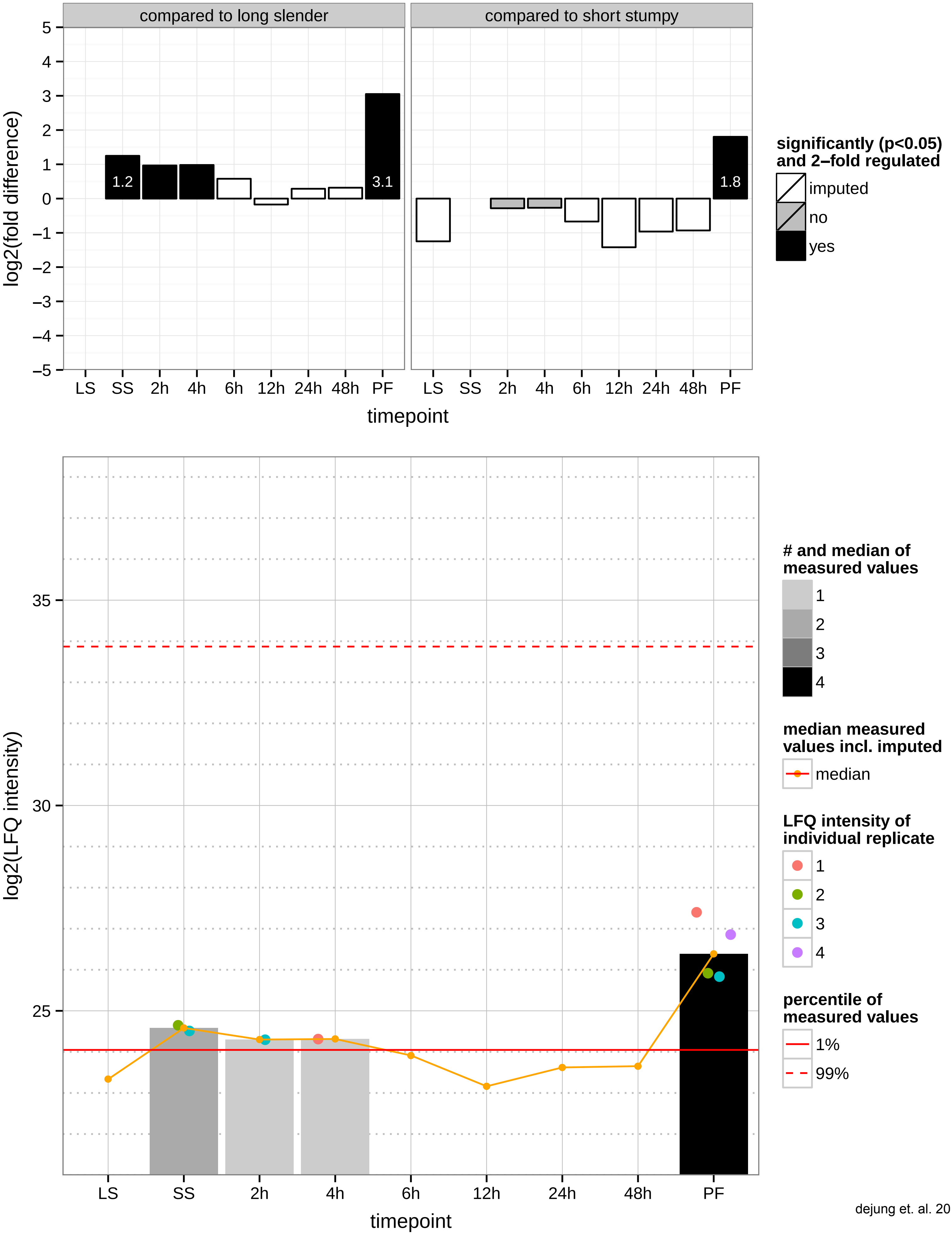
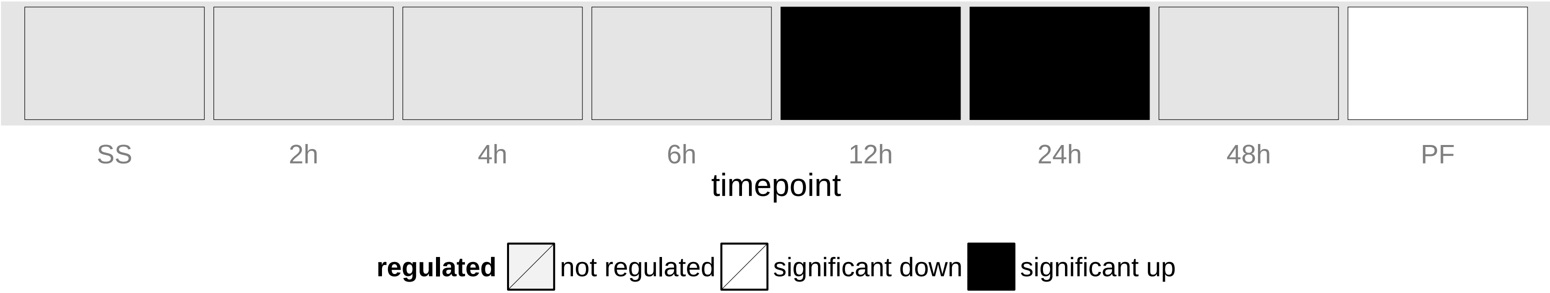
hypothetical protein, conserved
Tb927.7.3860
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null

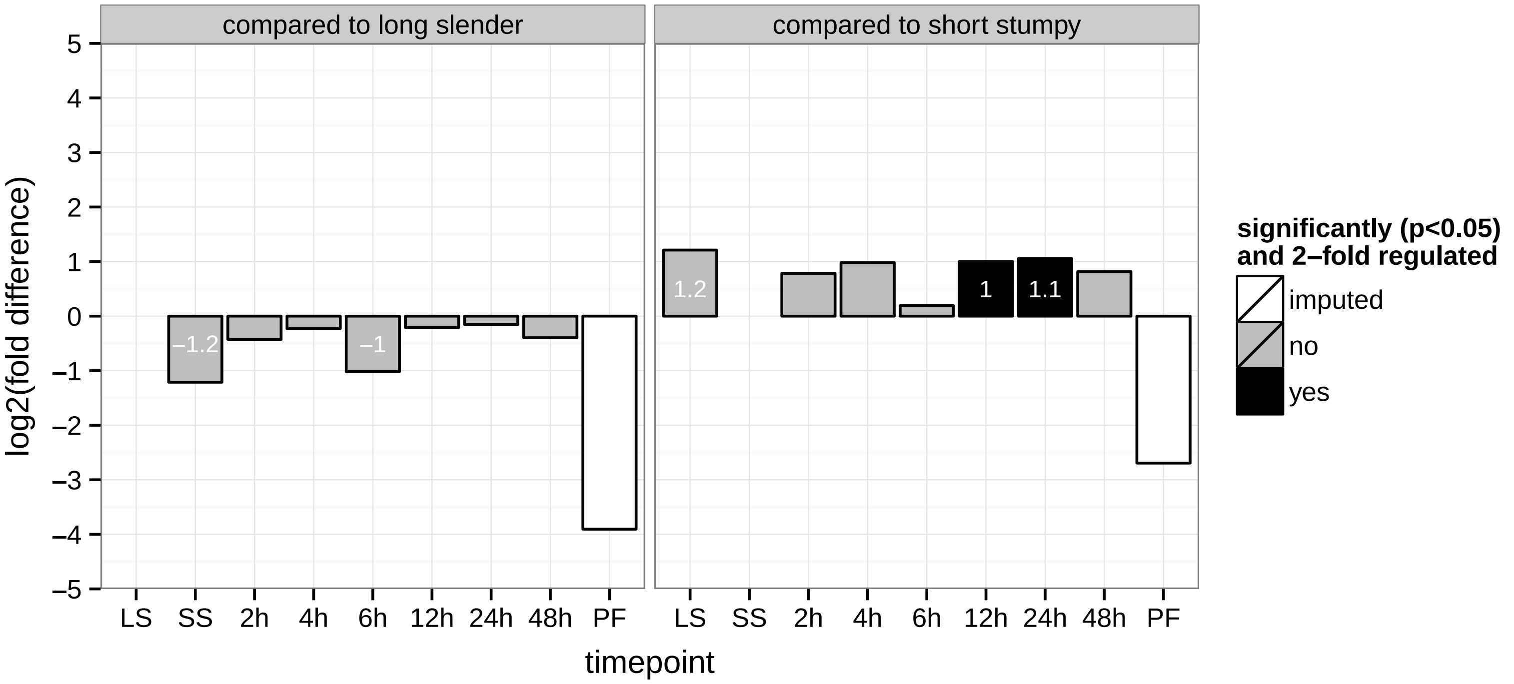


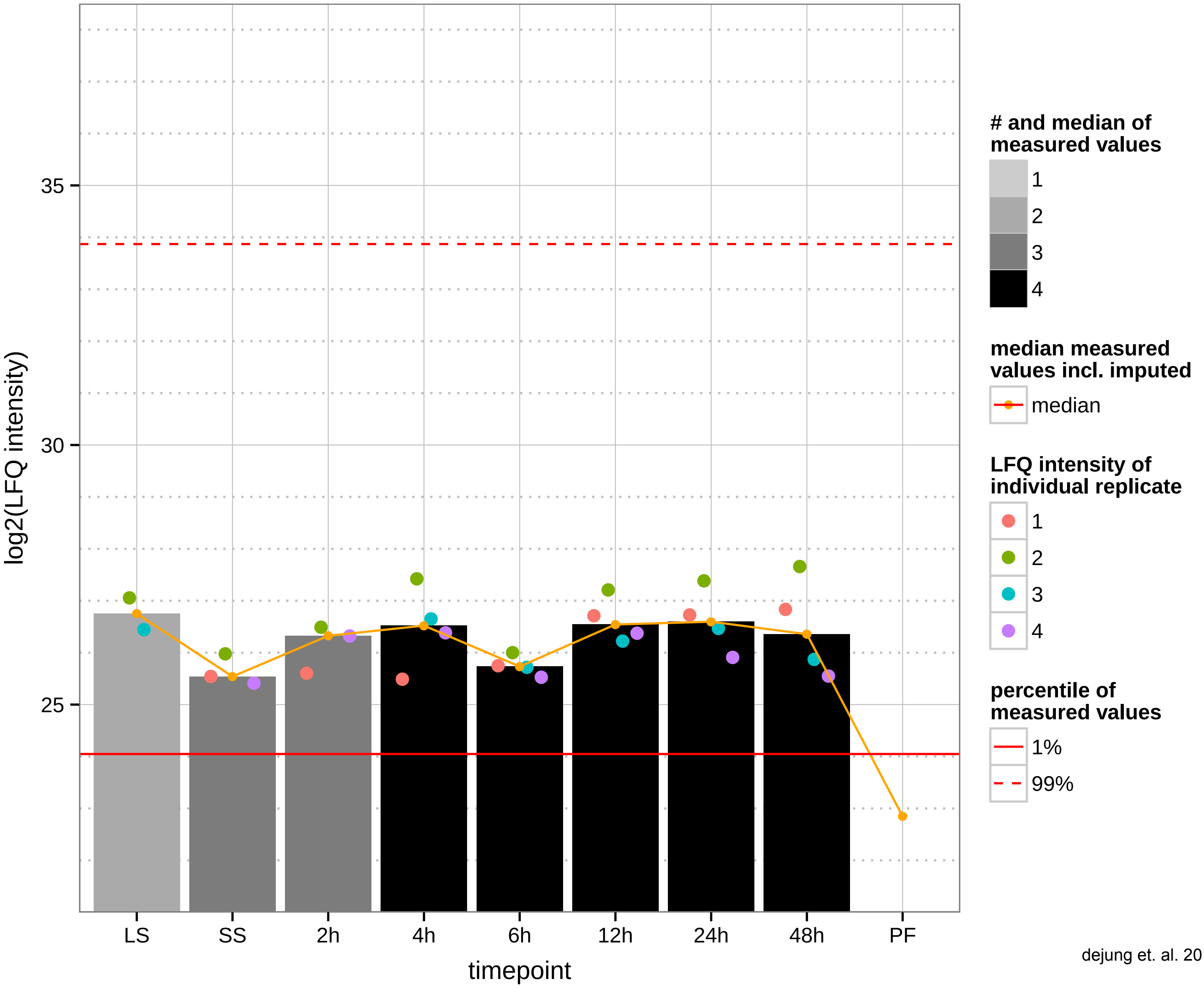
dejung et. al. 2015



dejung et. al. 2015

hypothetical protein, conserved
Tb927.6.2220
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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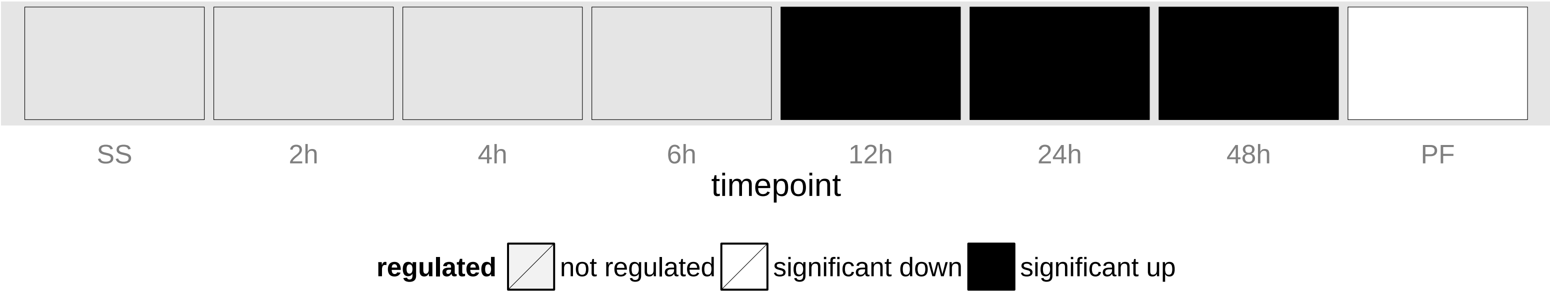

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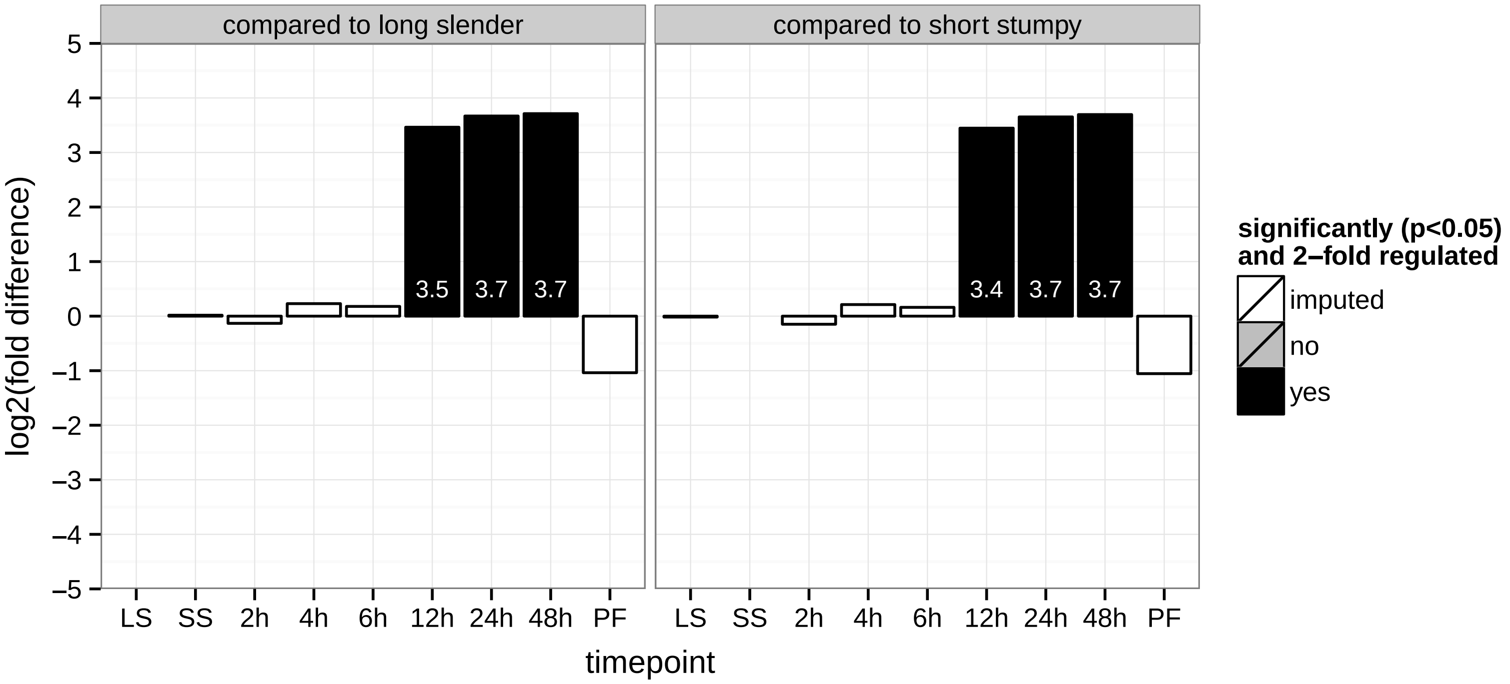
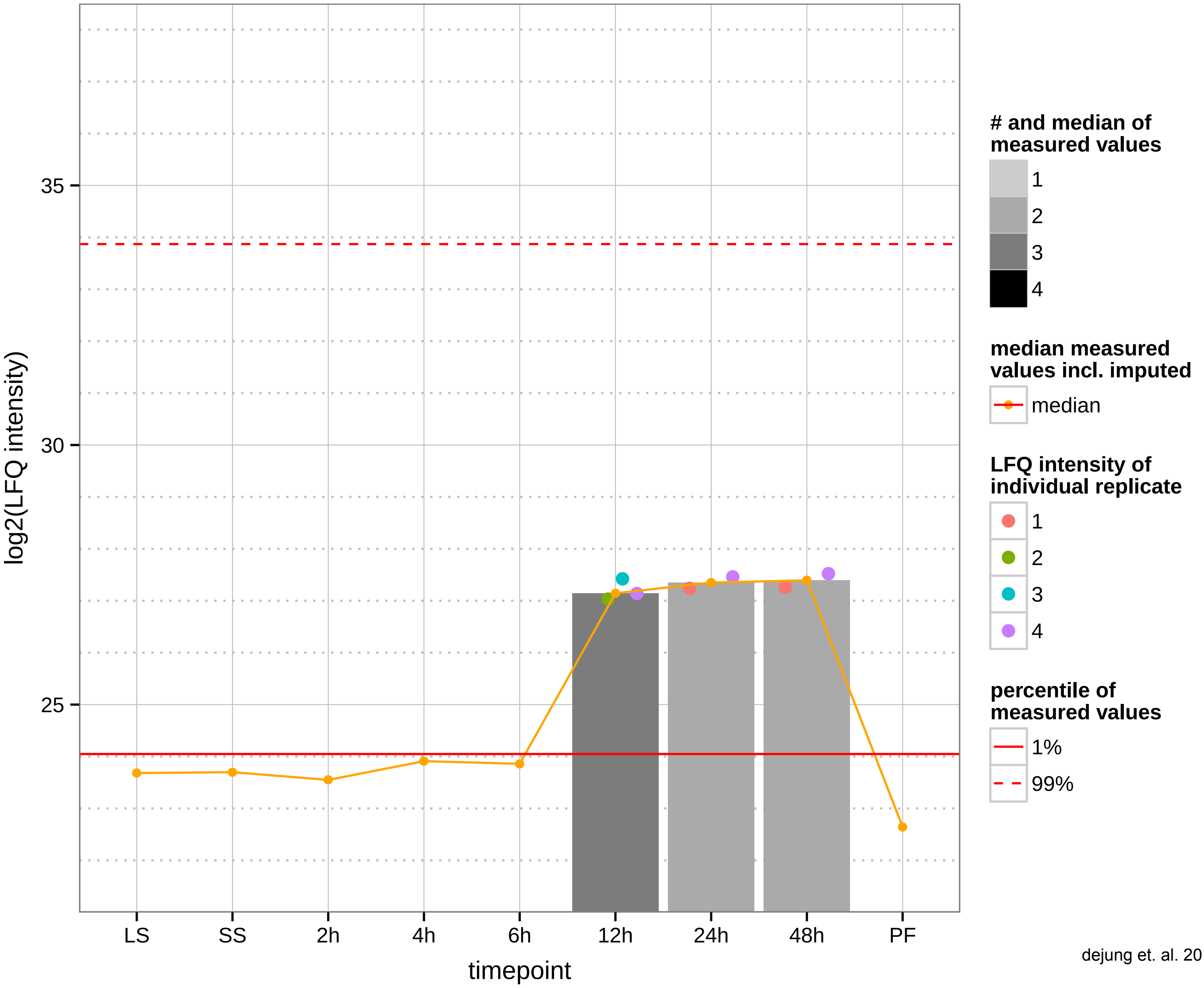
hypothetical protein, conserved
Tb927.11.12840
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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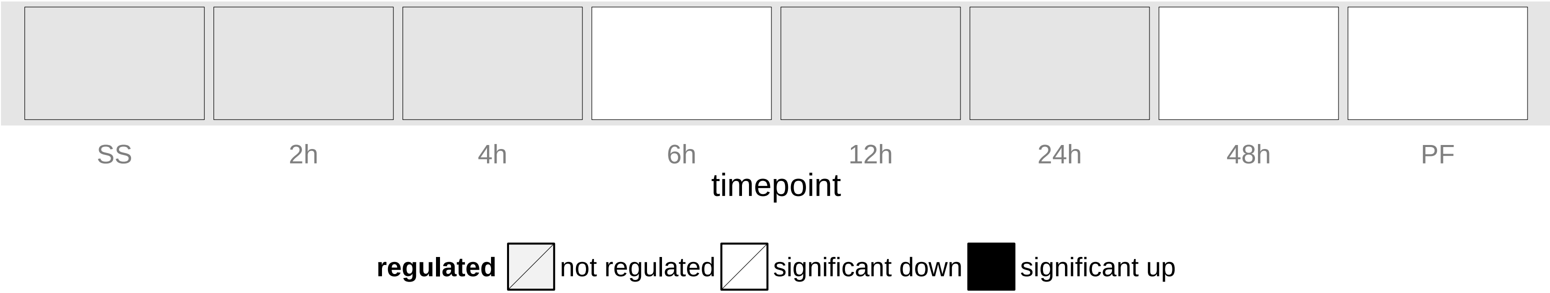

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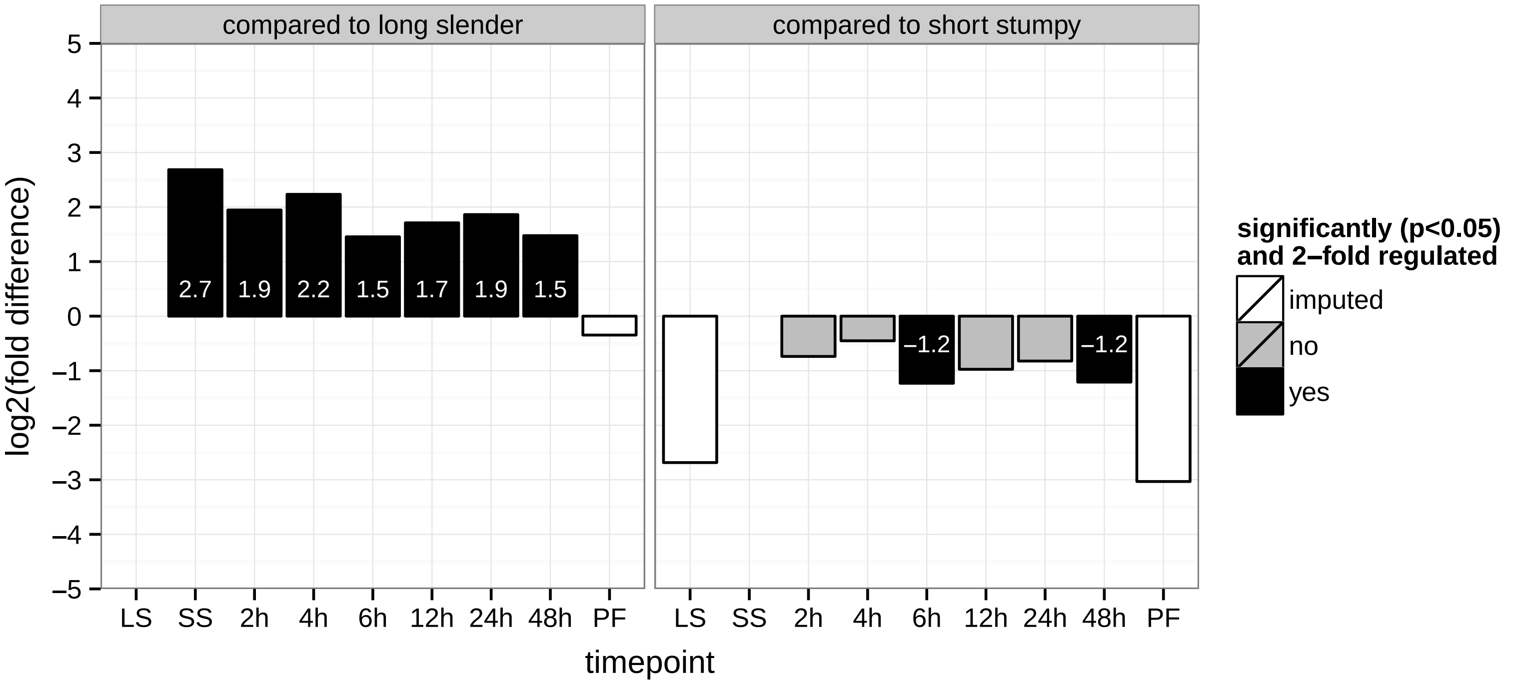
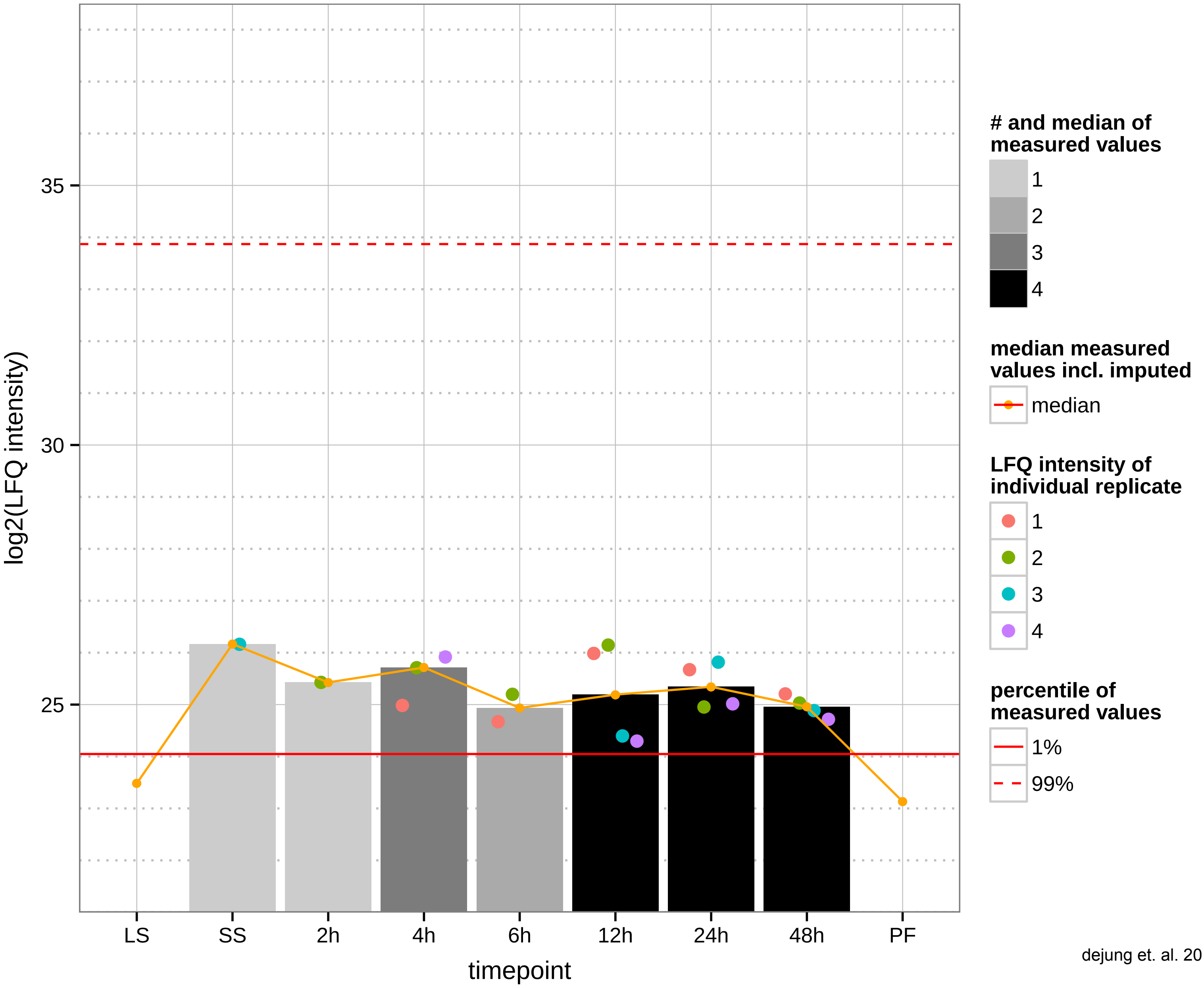
hypothetical protein, conserved
Tb927.9.10060
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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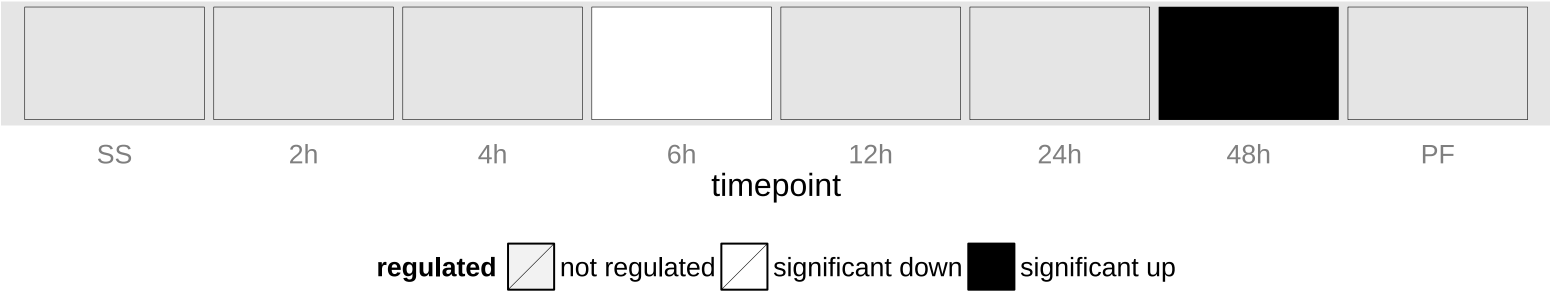

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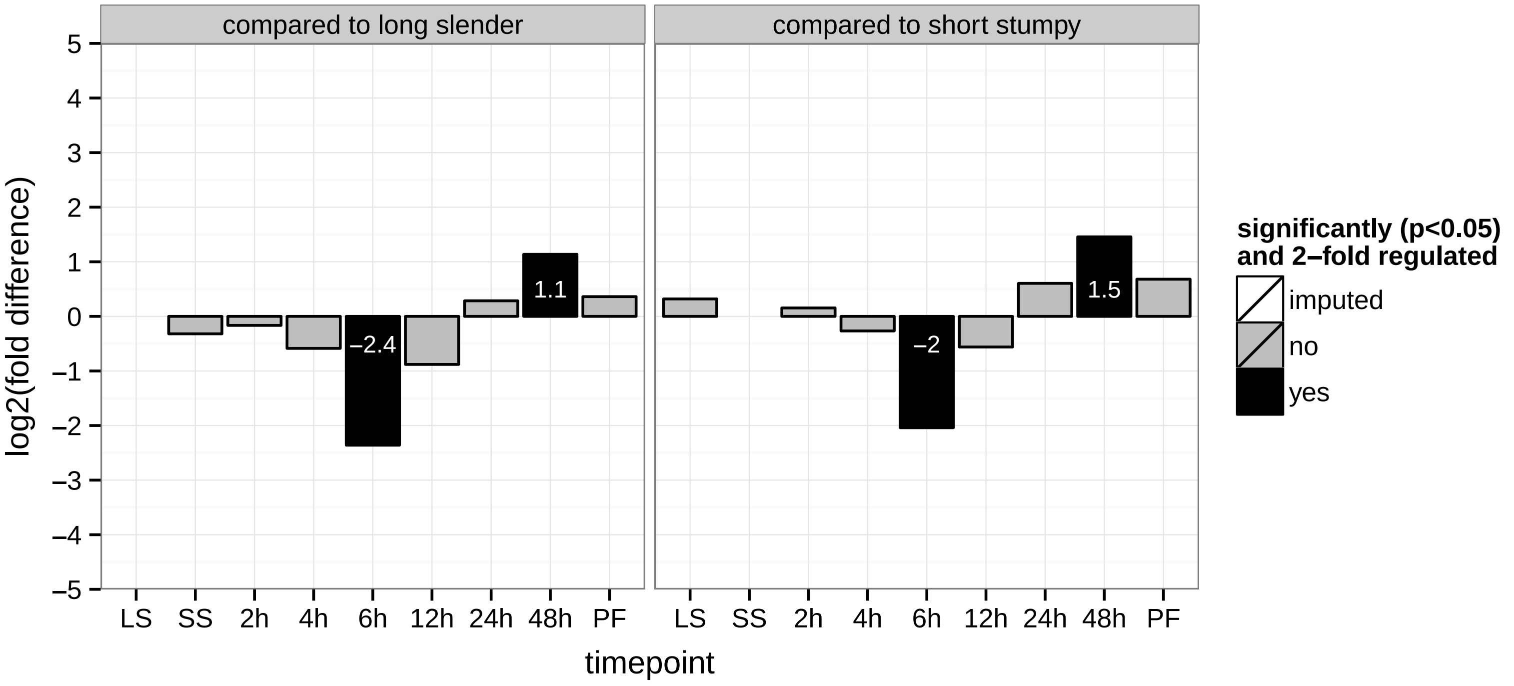
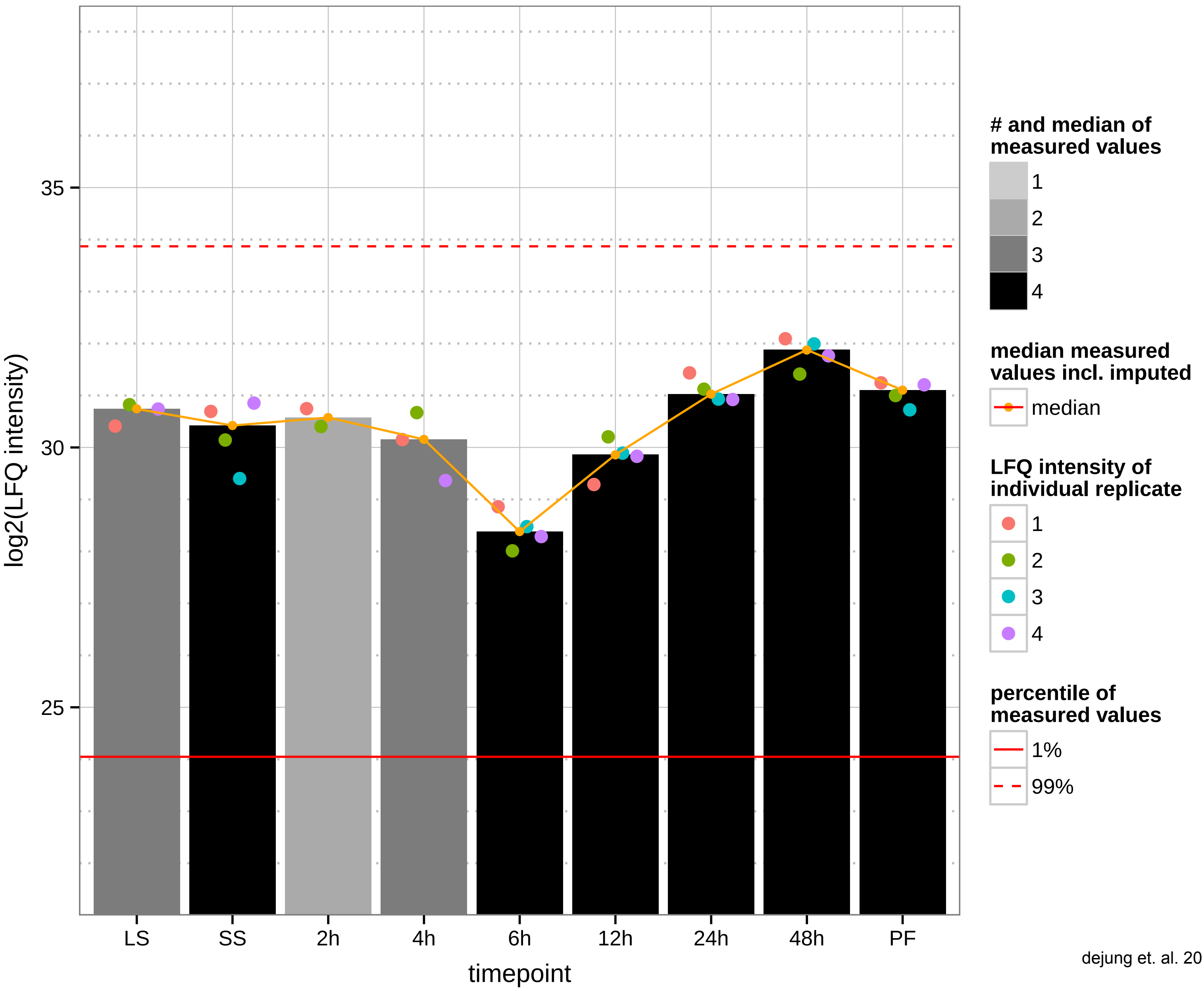
phosphoglycerate kinase (PGKB)
Tb927.1.710
AGOF: phosphoglycerate kinase activity
AGOC: cytoplasm
AGOP: glycolysis
PGOF: phosphoglycerate kinase activity
PGOC: null
PGOP: glycolysis





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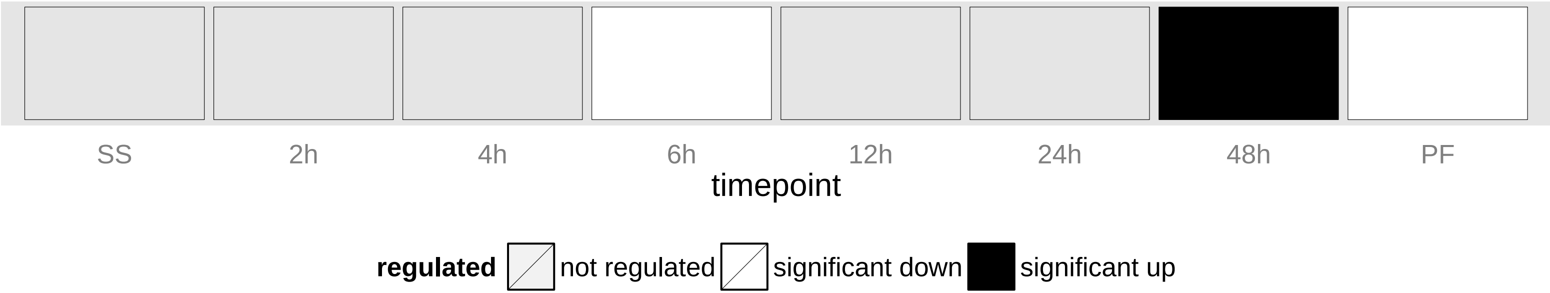

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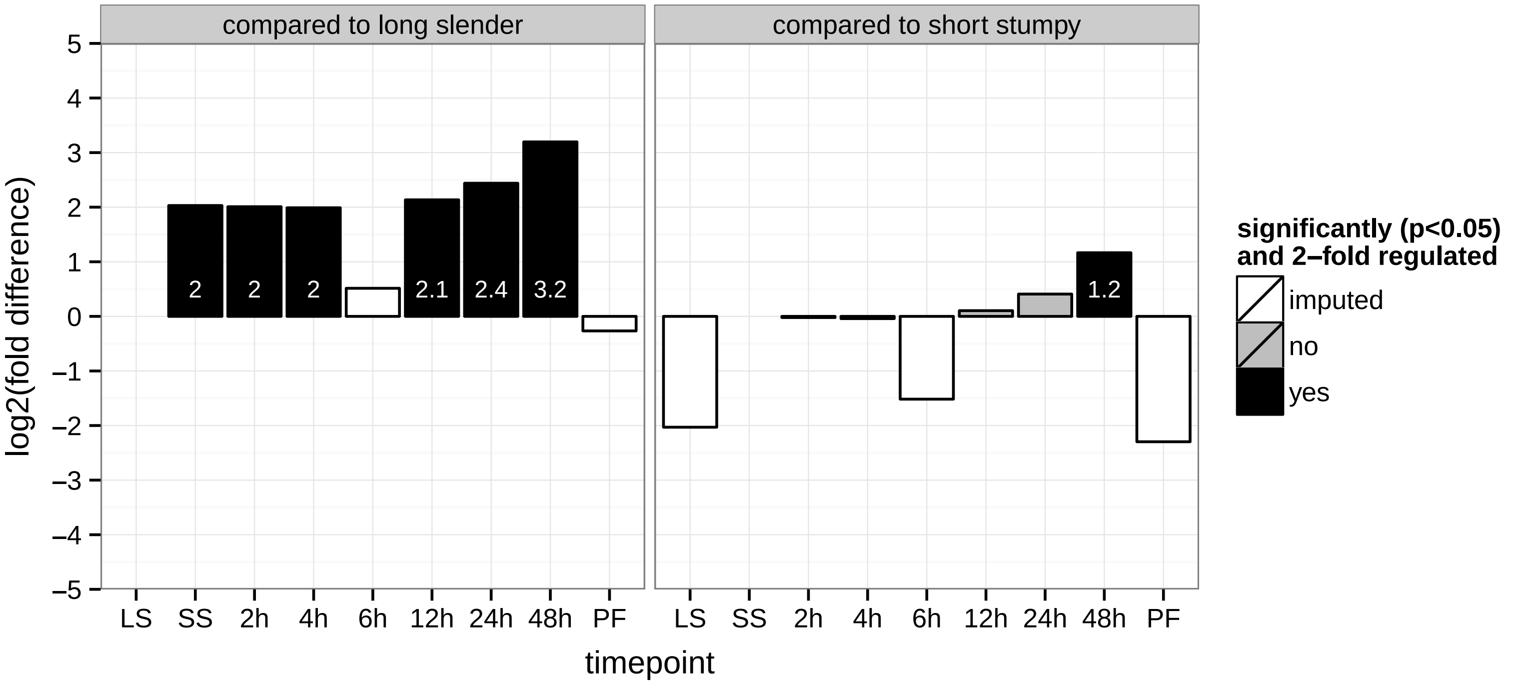
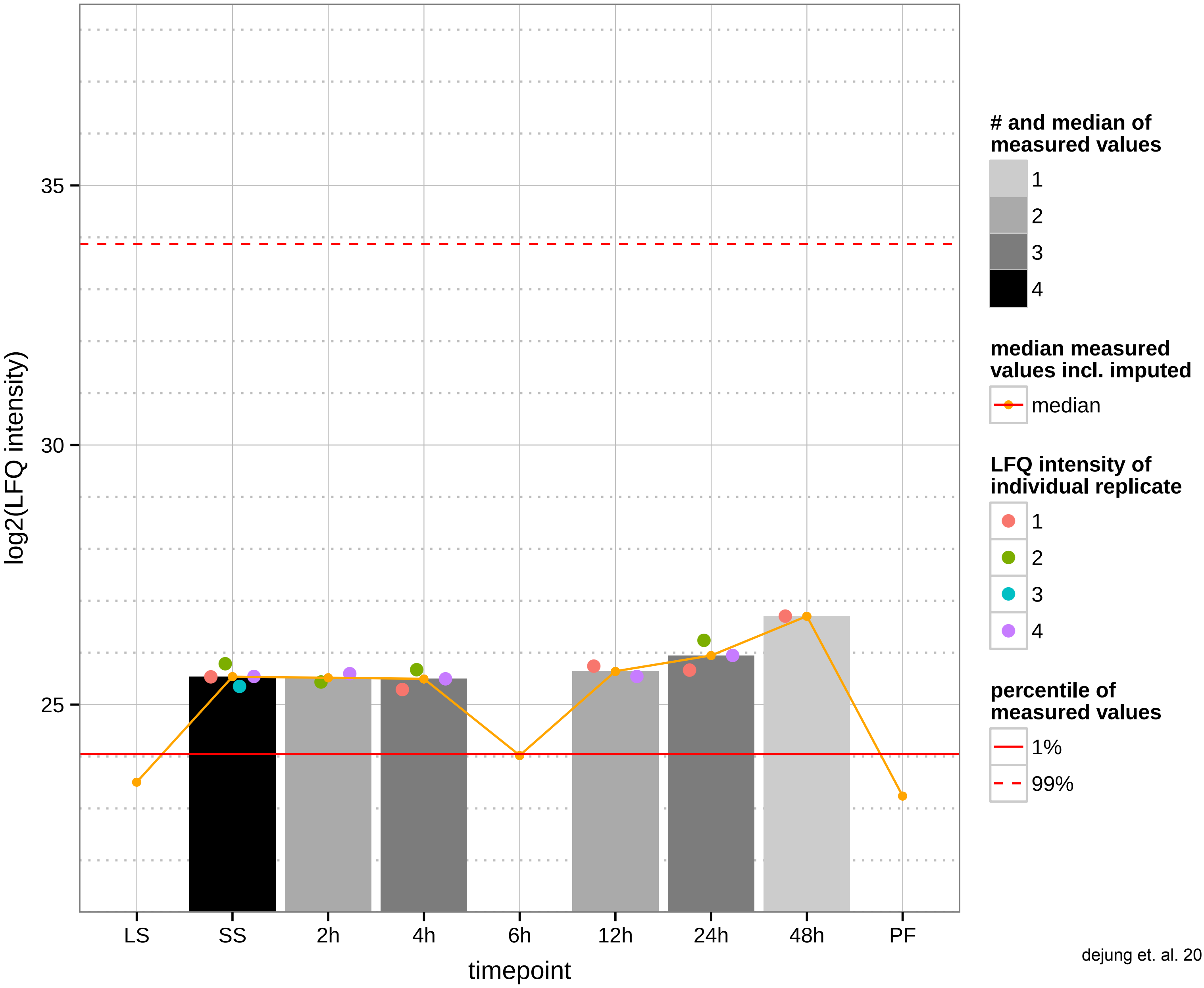
chrX additional, unordered contigs, hypothetical protein, conserved
Tb927.10.1160;Tb11.0550
AGOF: null
AGOC: null, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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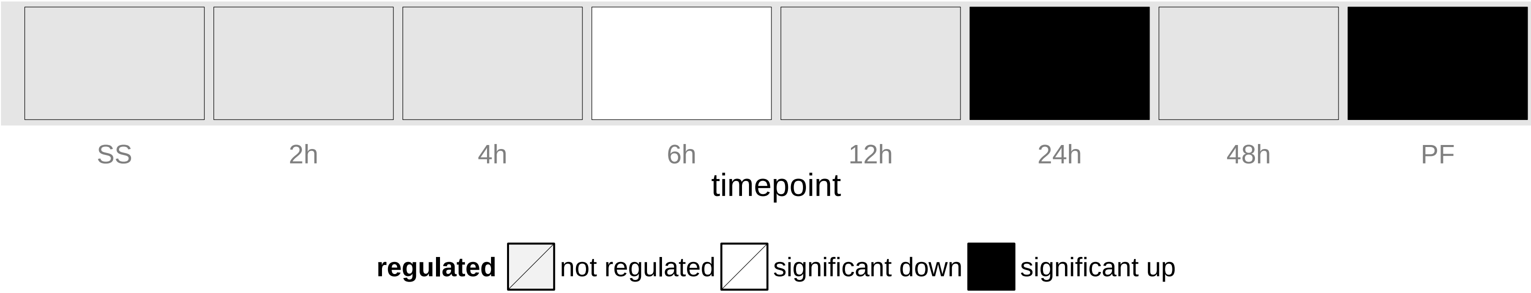
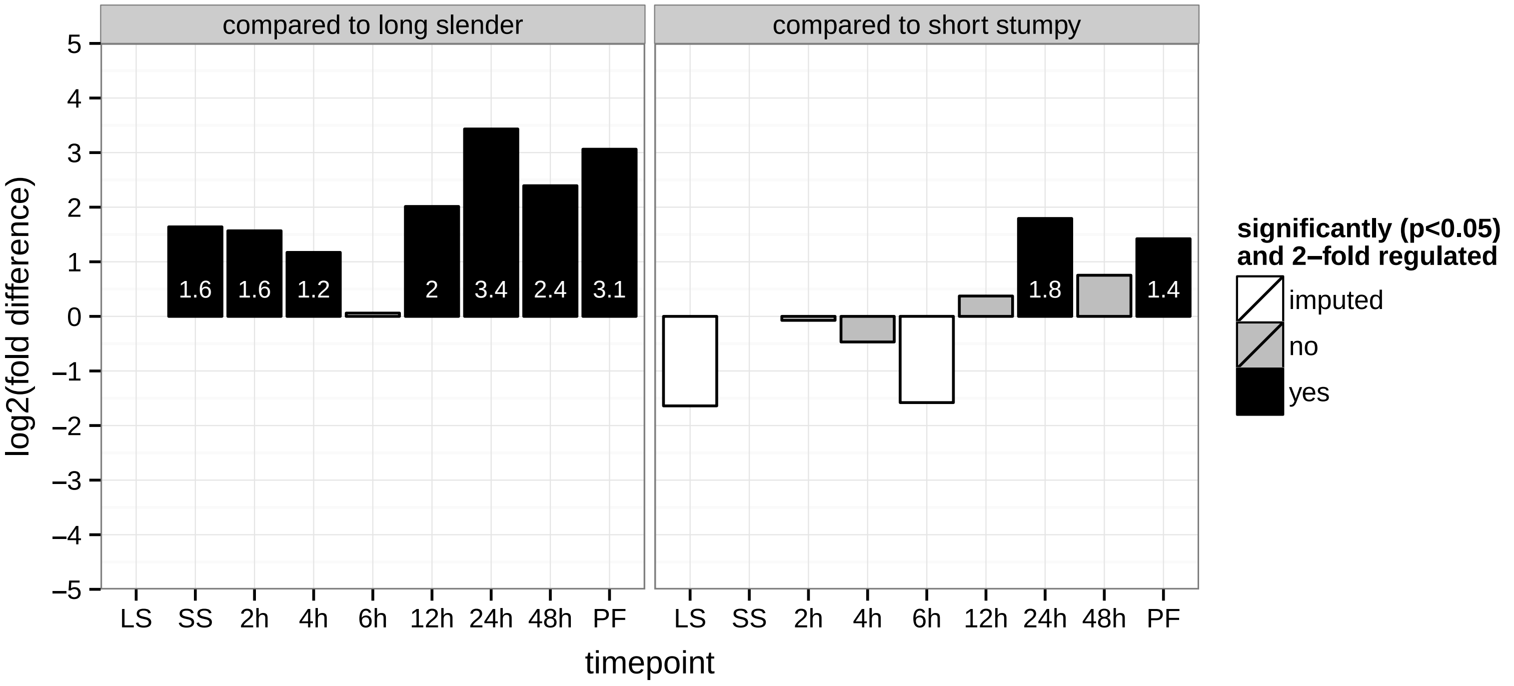
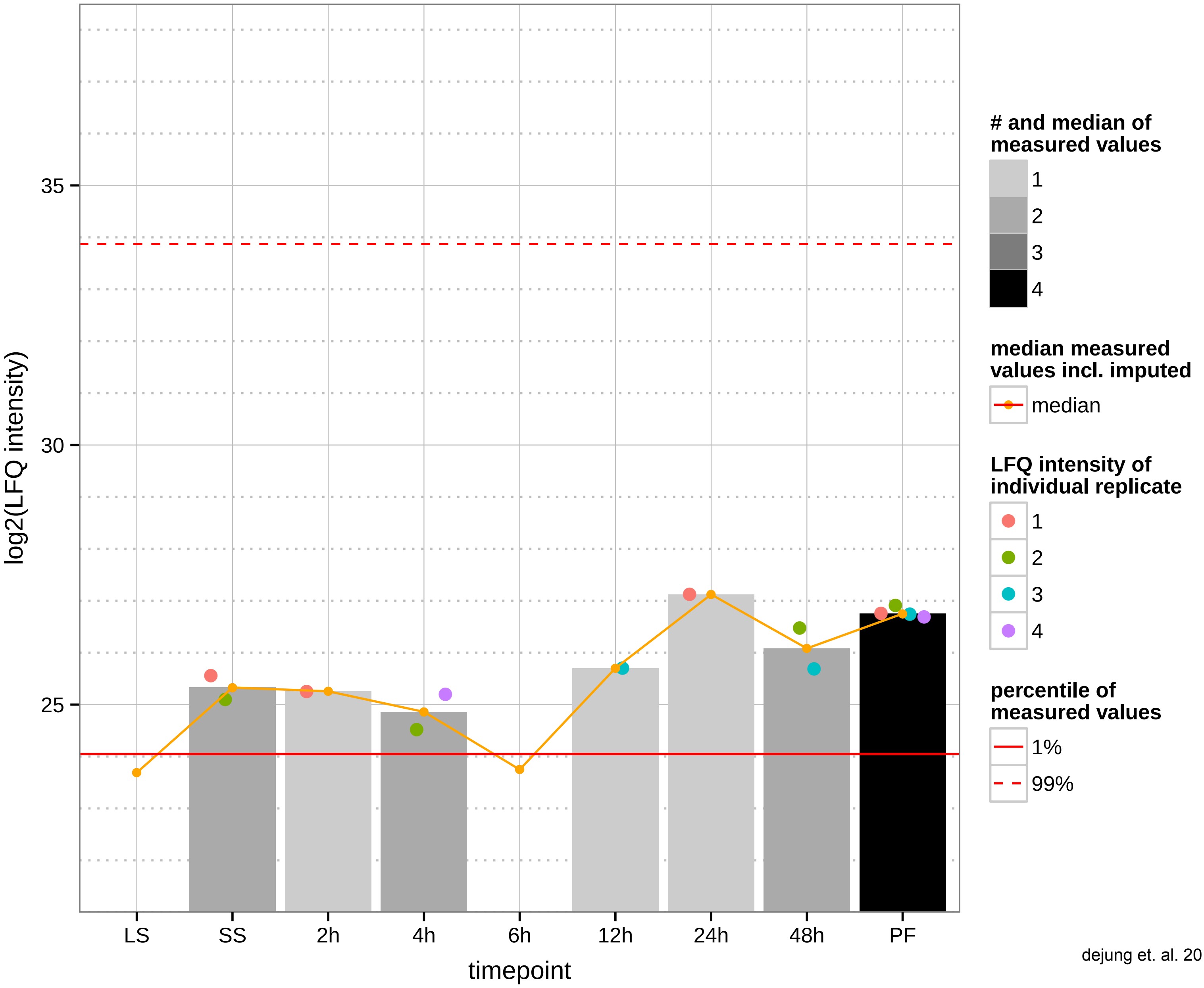


dejung et. al. 2015

hypothetical protein, conserved
Tb927.3.820
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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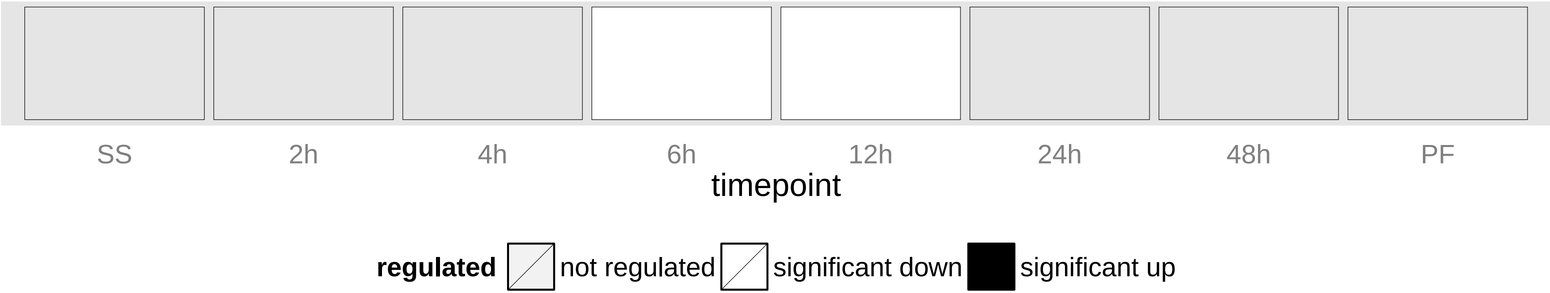

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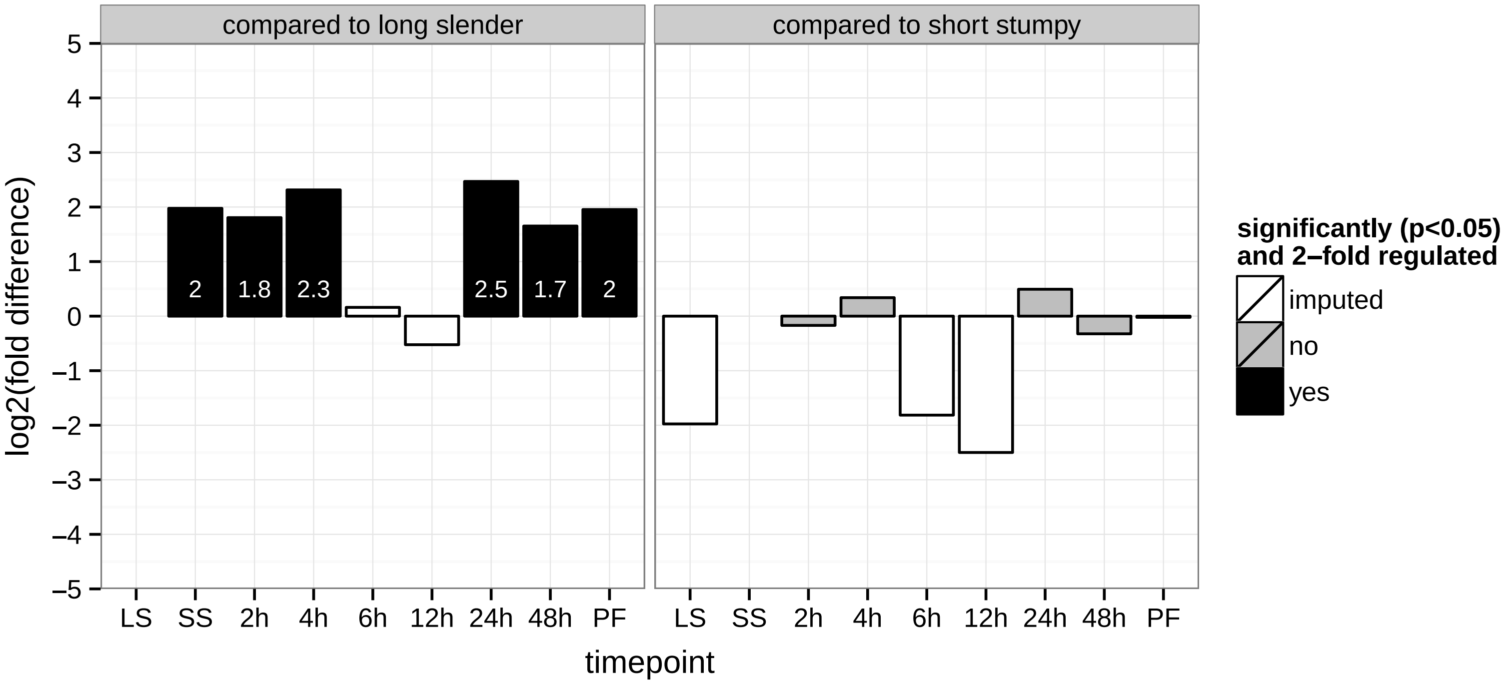
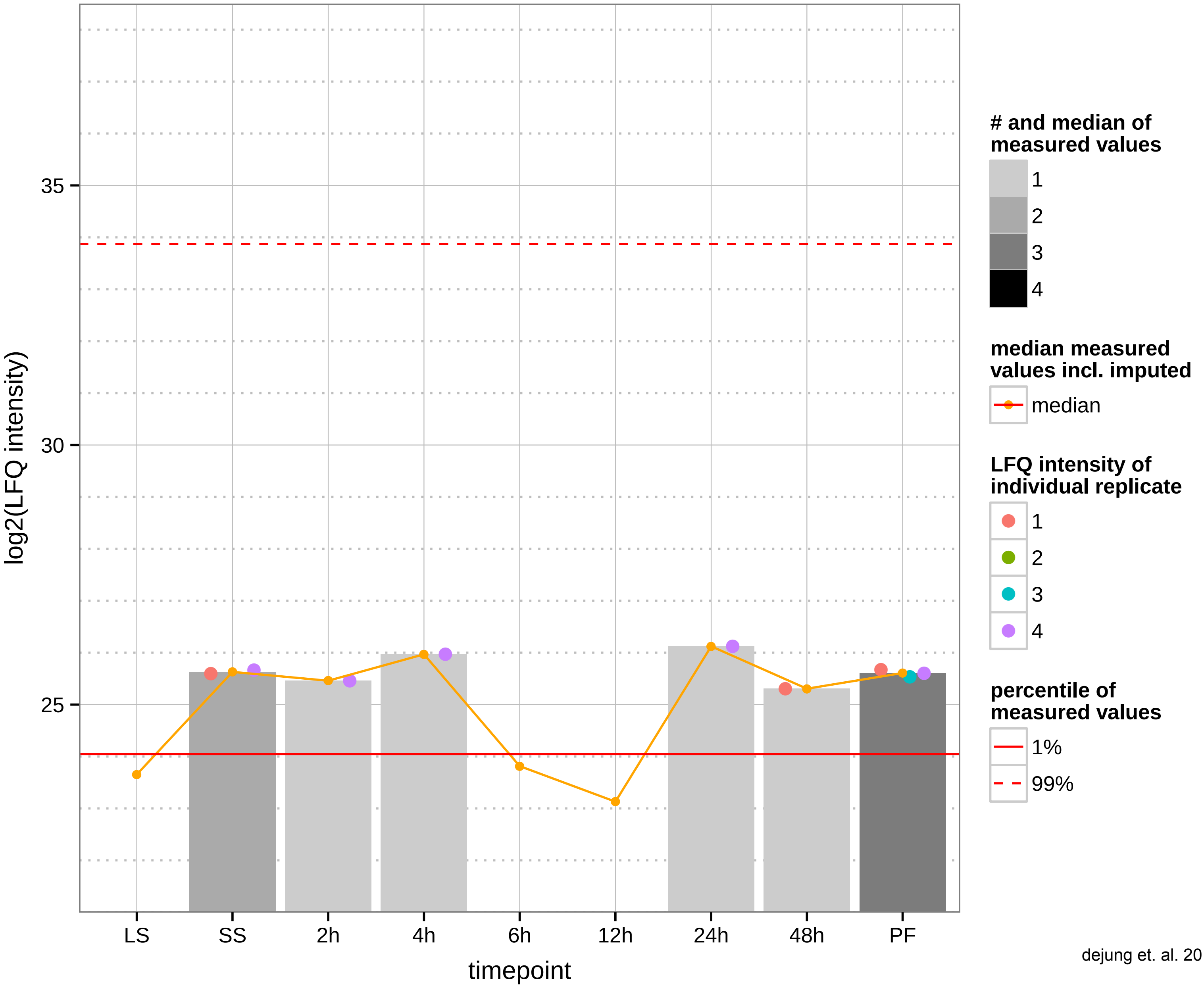
class I transcription factor A, subunit 6 (CITFA−6)
Tb927.5.970
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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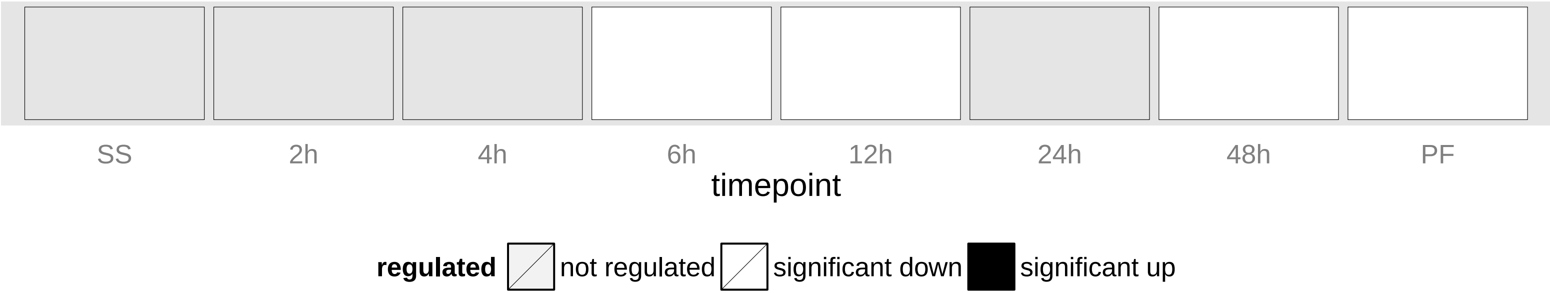

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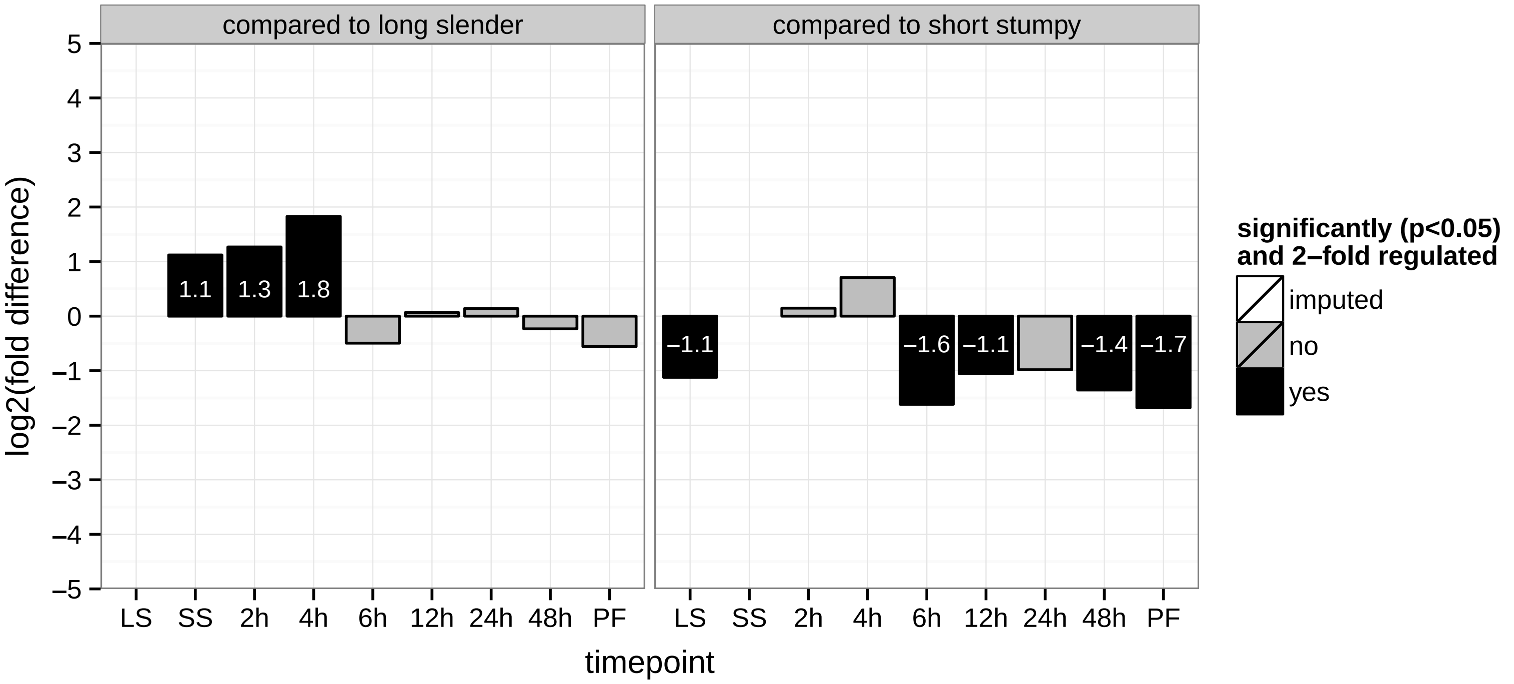
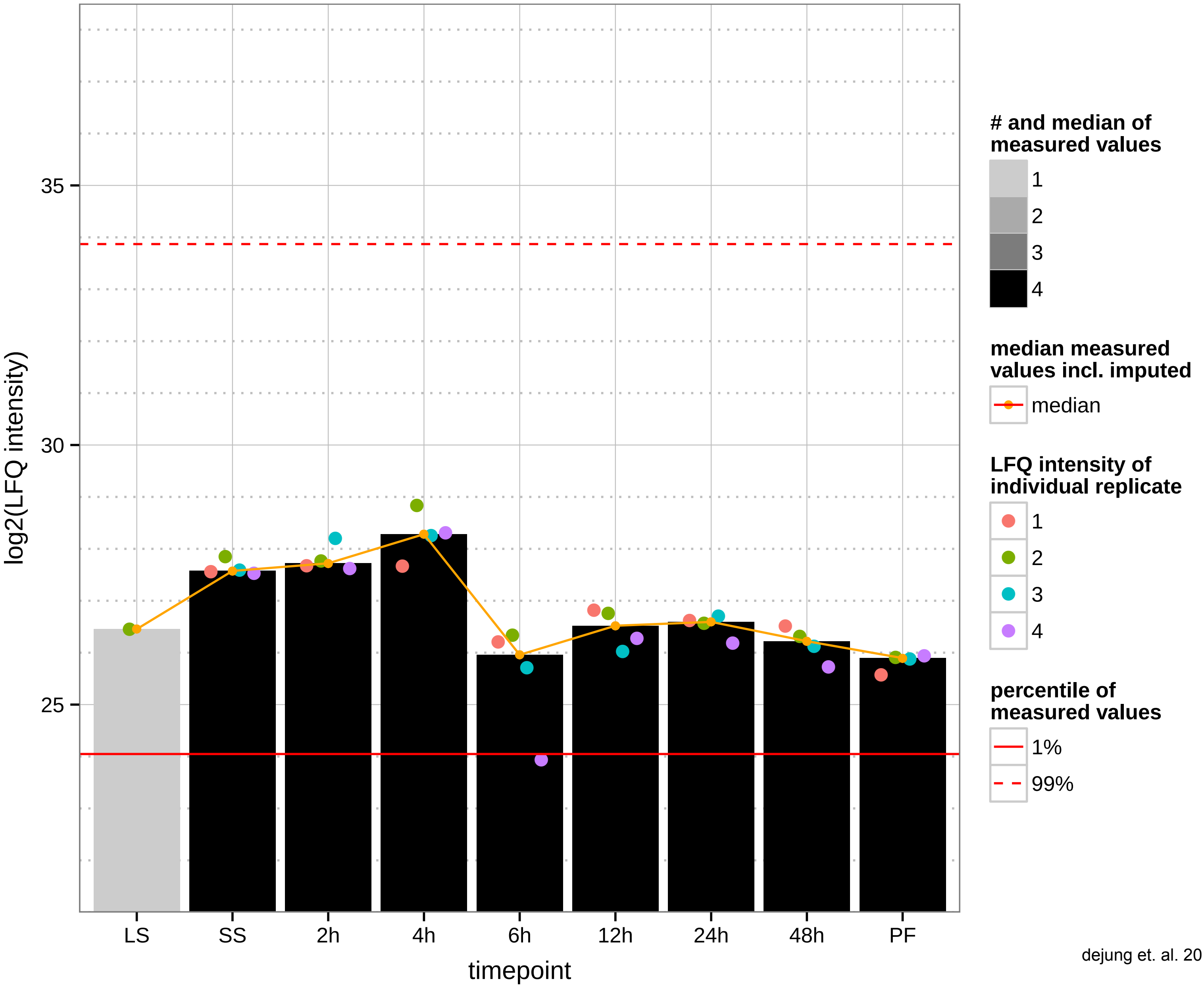
ATG8/AUT7/APG8/PAZ2, putative, ubiquitin–like protein (ATG8A), ubiquitin–like protein (ATG8B)
Tb927.7.5910;Tb927.7.5900
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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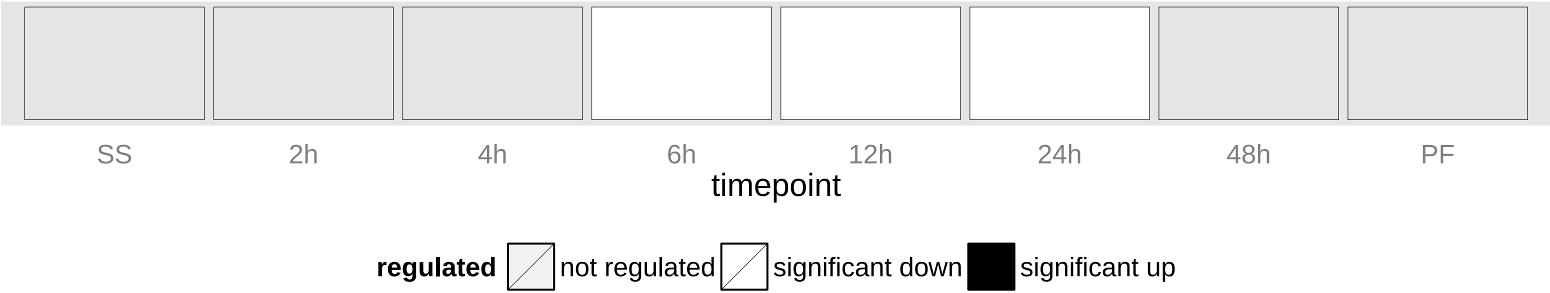
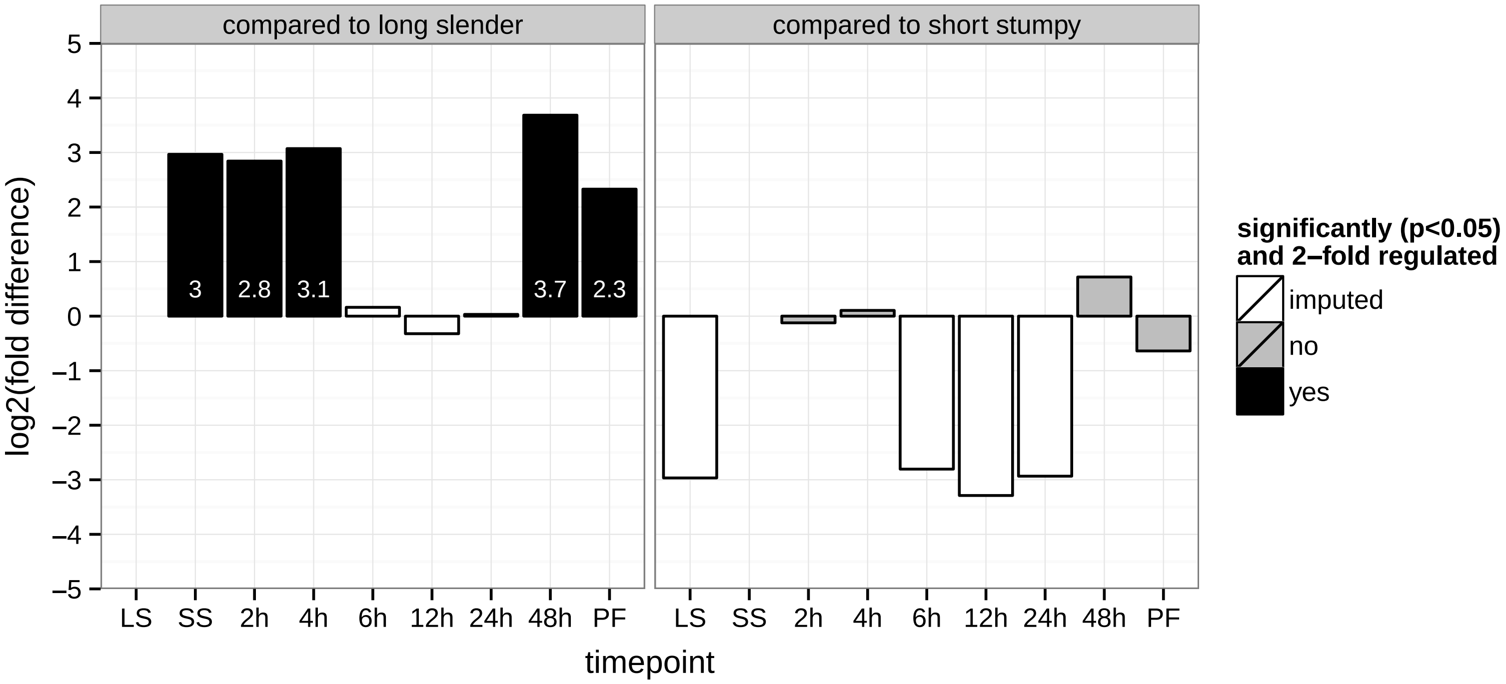
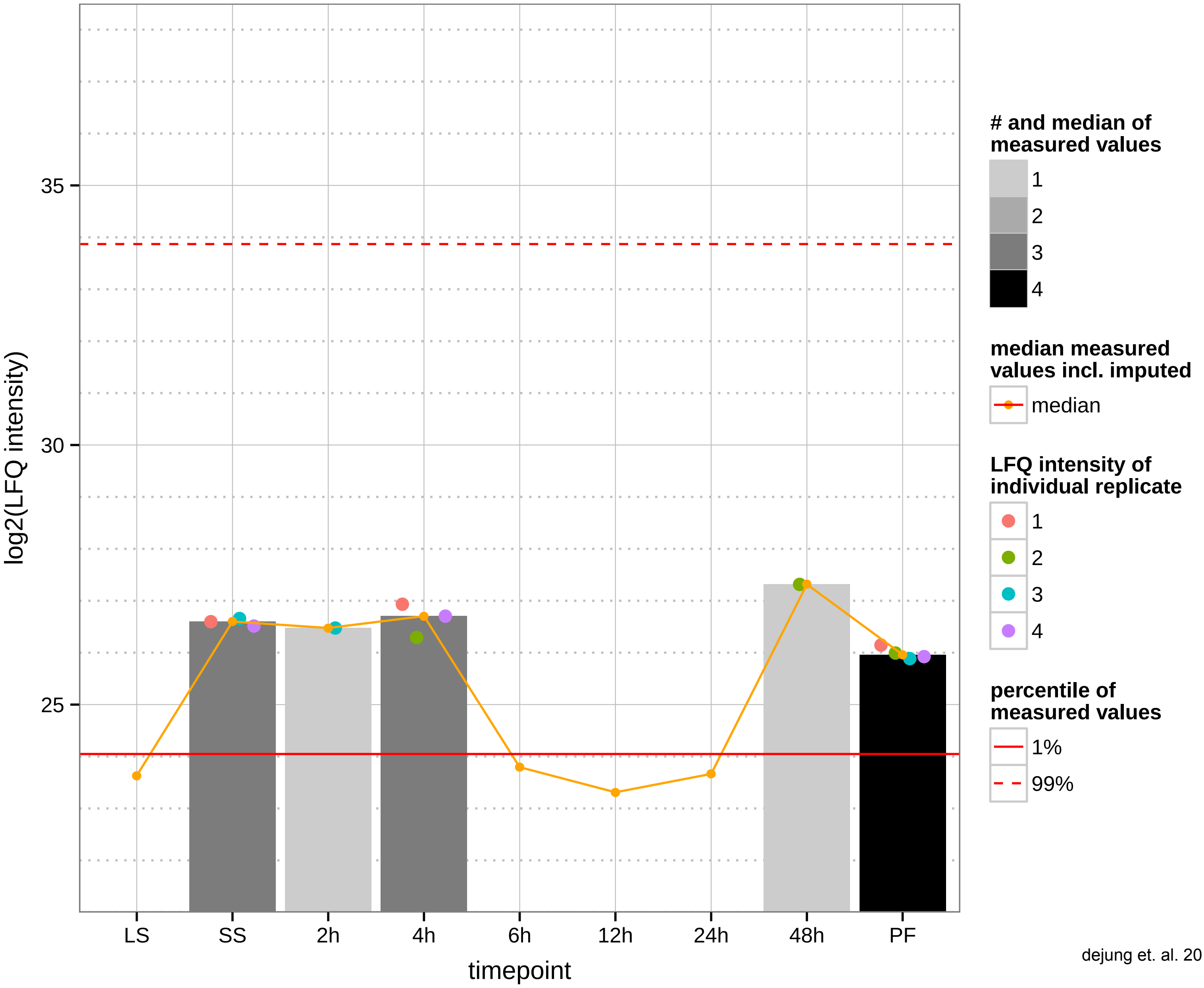


dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.4910
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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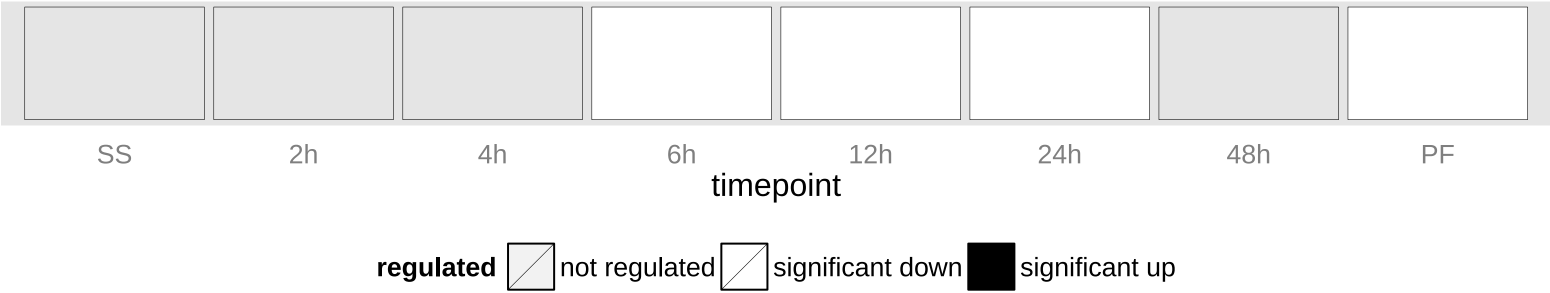
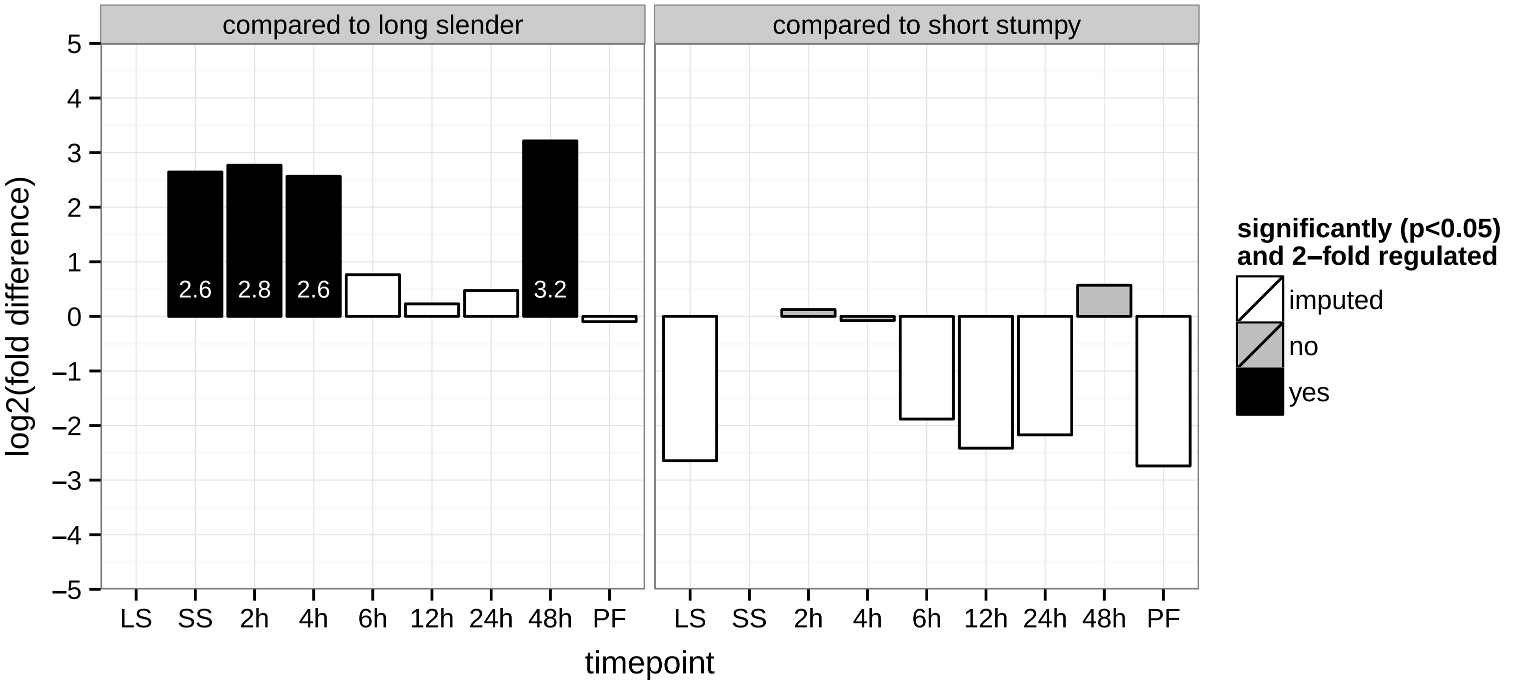
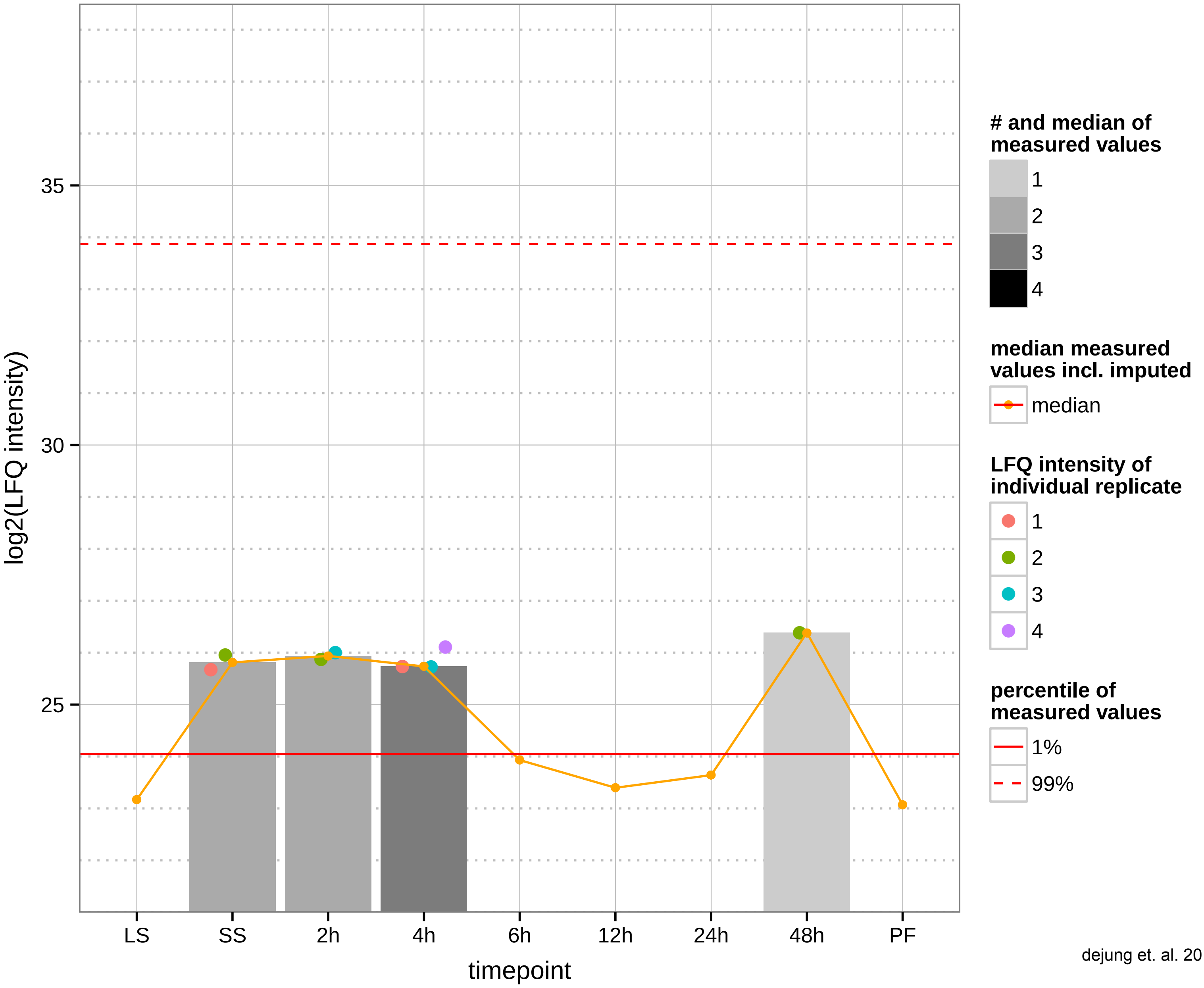


dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.4550
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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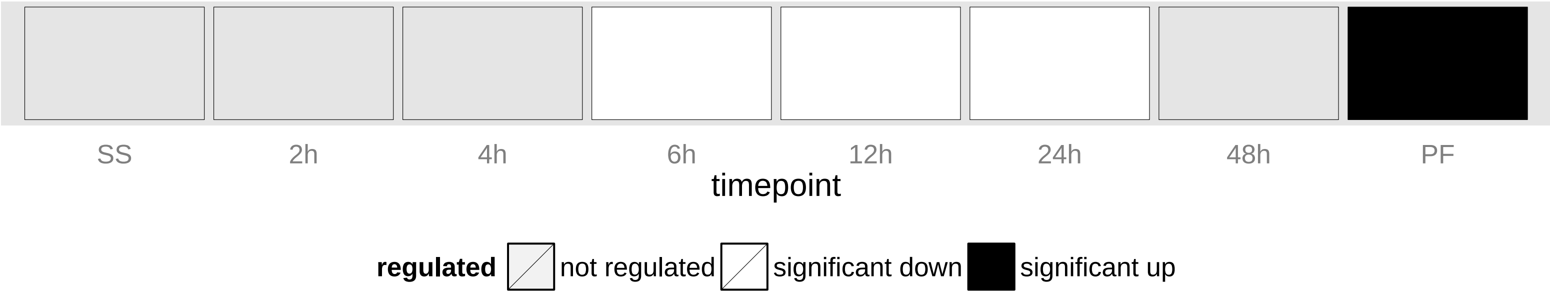
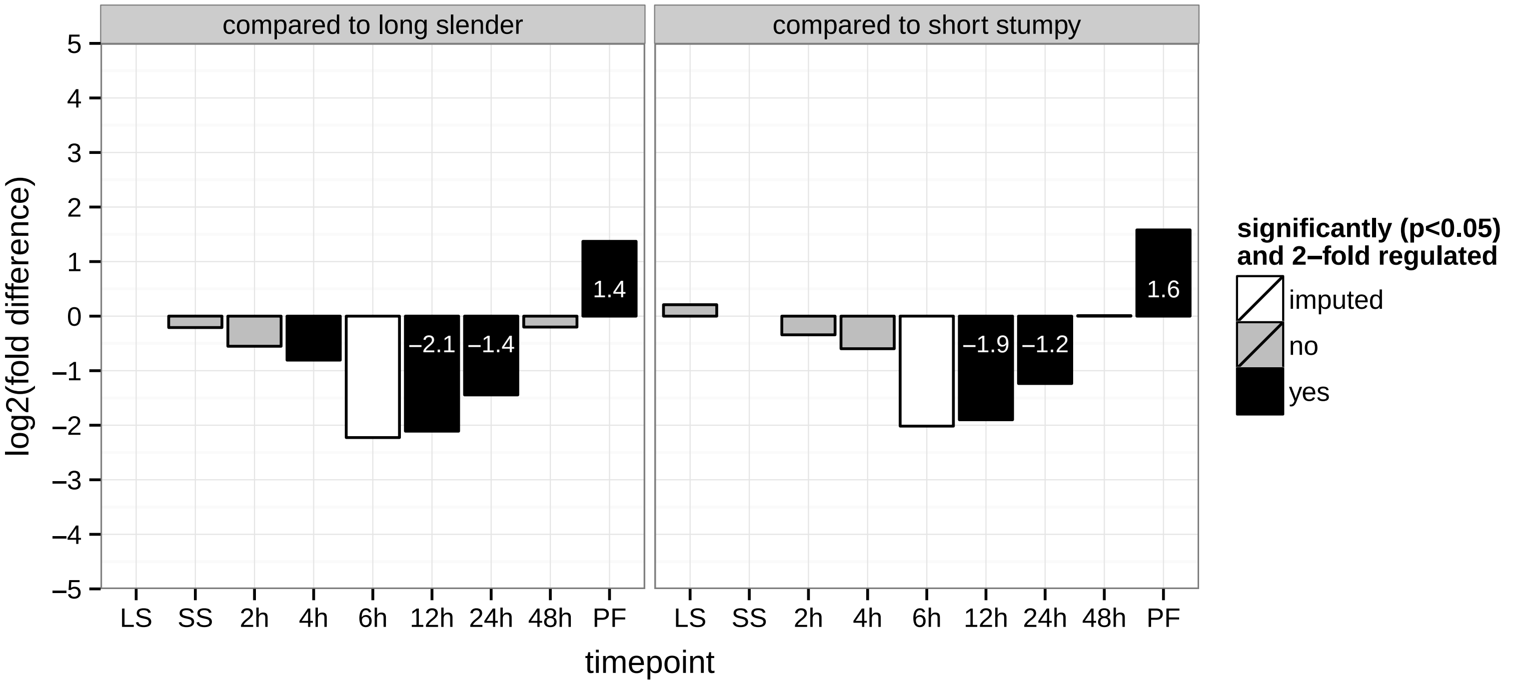
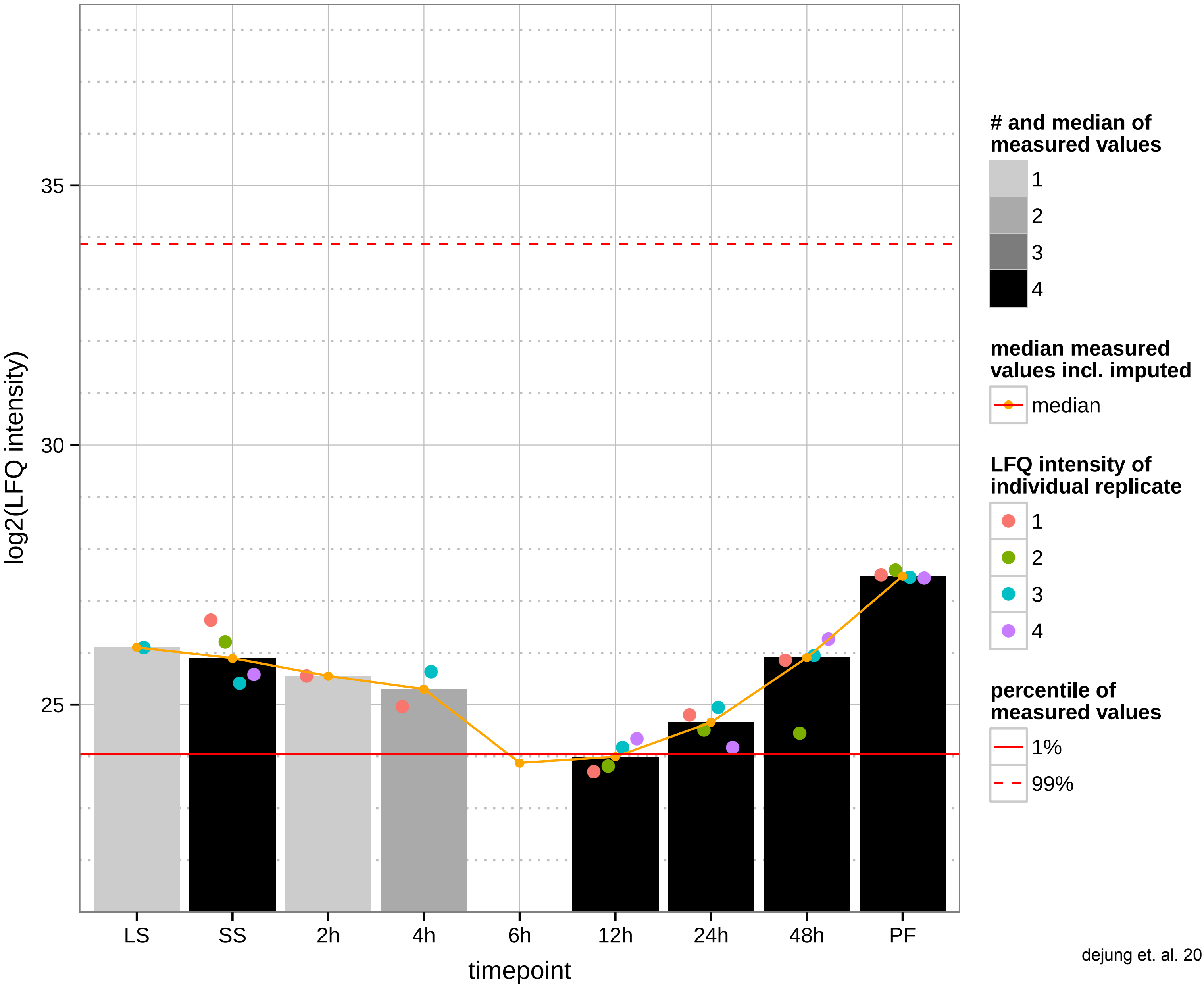


dejung et. al. 2015

endosomal integral membrane protein, putative
Tb927.8.1940
AGOF: null
AGOC: integral to membrane
AGOP: null
PGOF: null
PGOC: integral to membrane
PGOP: null





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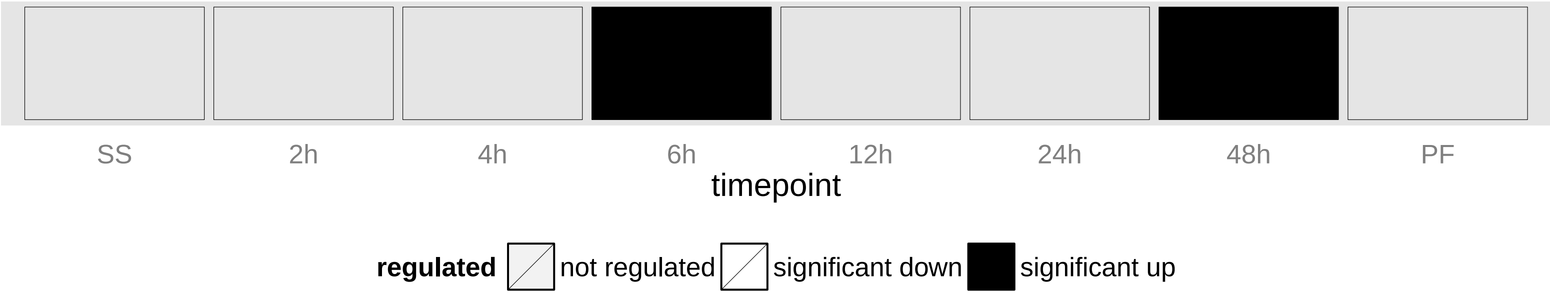
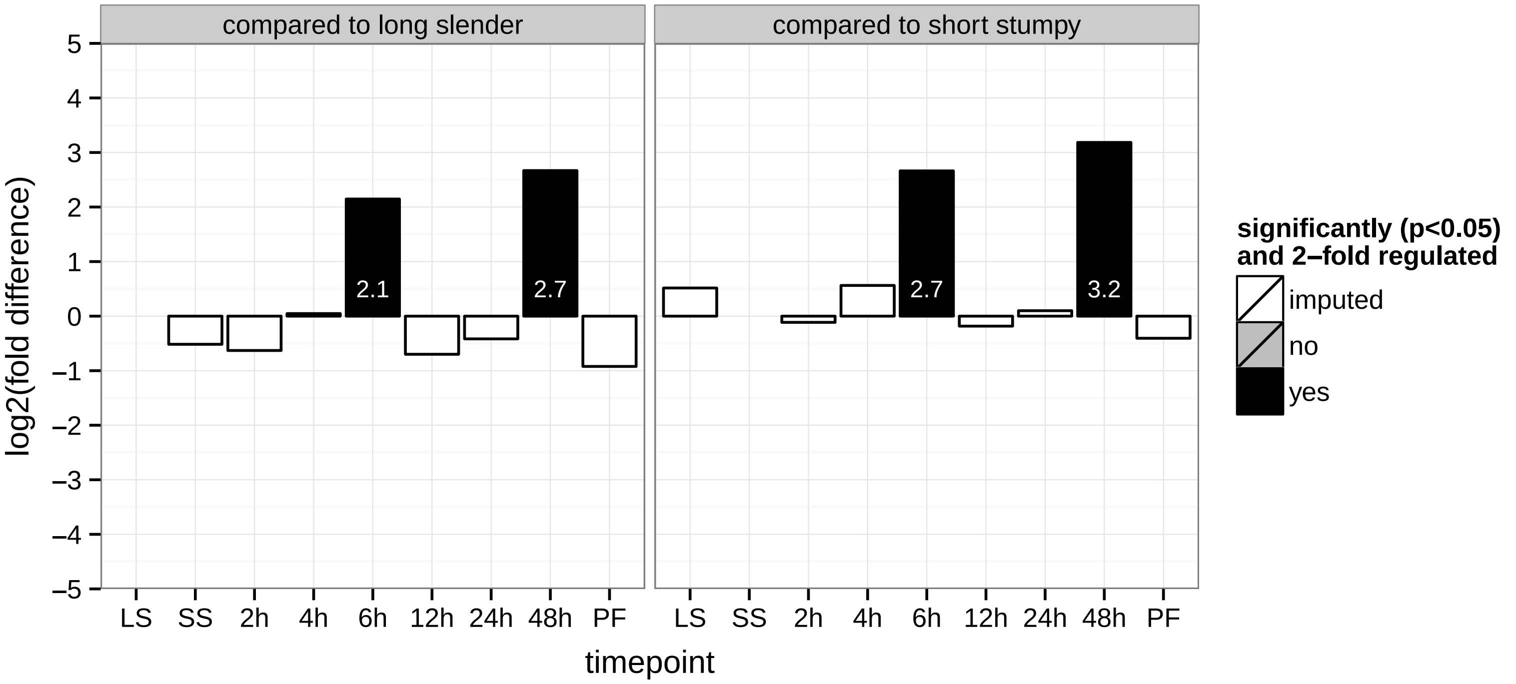
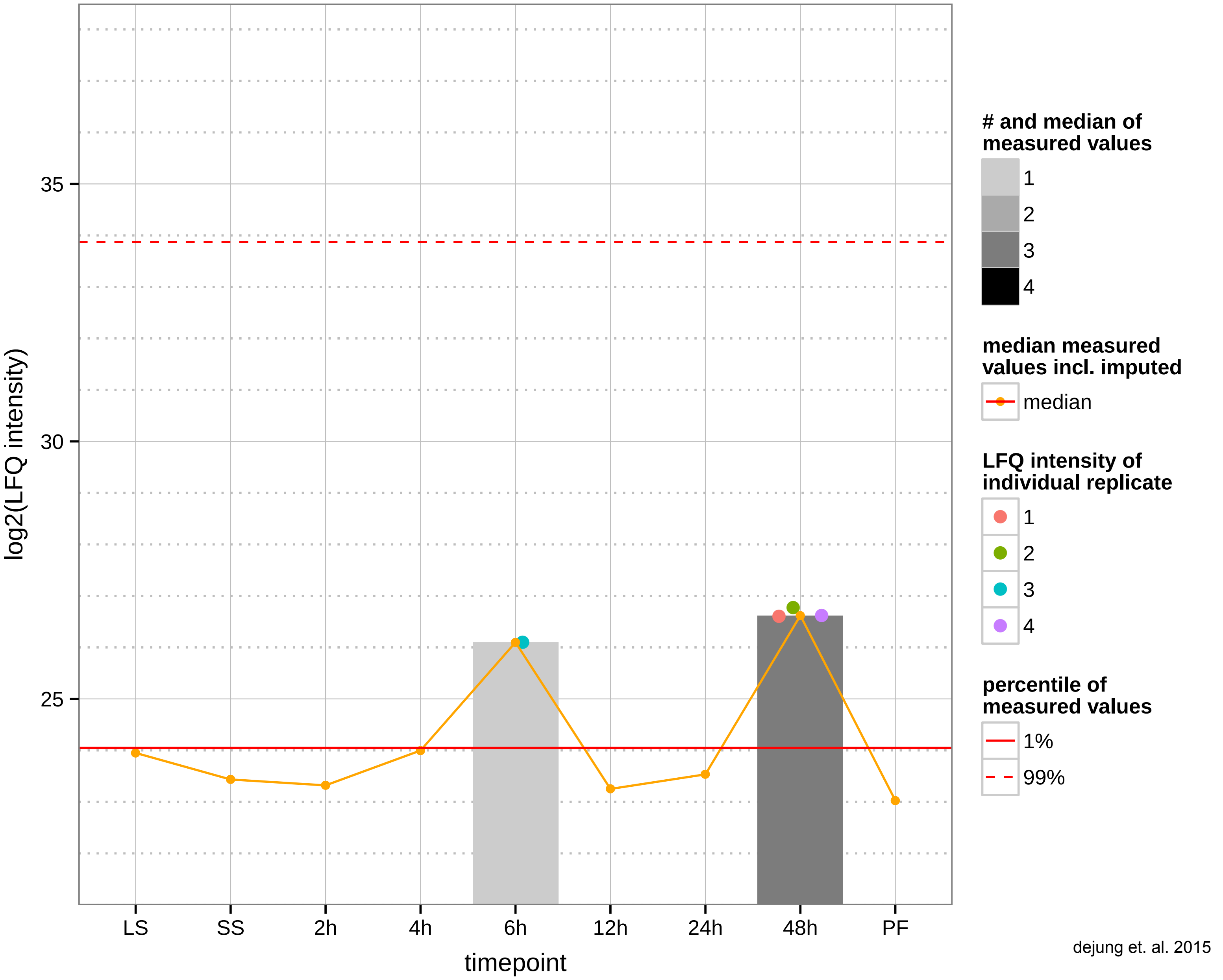


dejung et. al. 2015

expression site−associated gene (ESAG, pseudogene), putative, expression site−associated gene 4 (ESAG4), degenerate
Tb927.2.1260
AGOF: phosphorus−oxygen lyase activity
AGOC: null
AGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction
PGOF: phosphorus−oxygen lyase activity
PGOC: null
PGOP: cyclic nucleotide biosynthetic process, intracellular signal transduction





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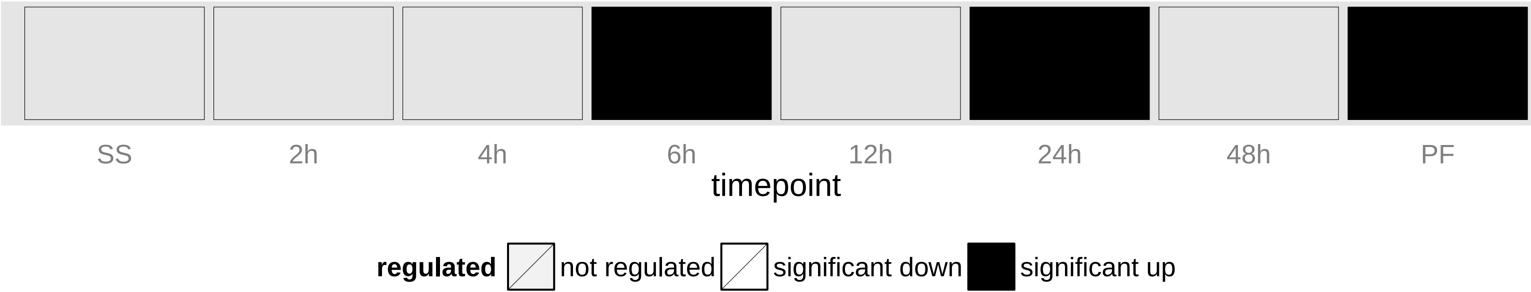
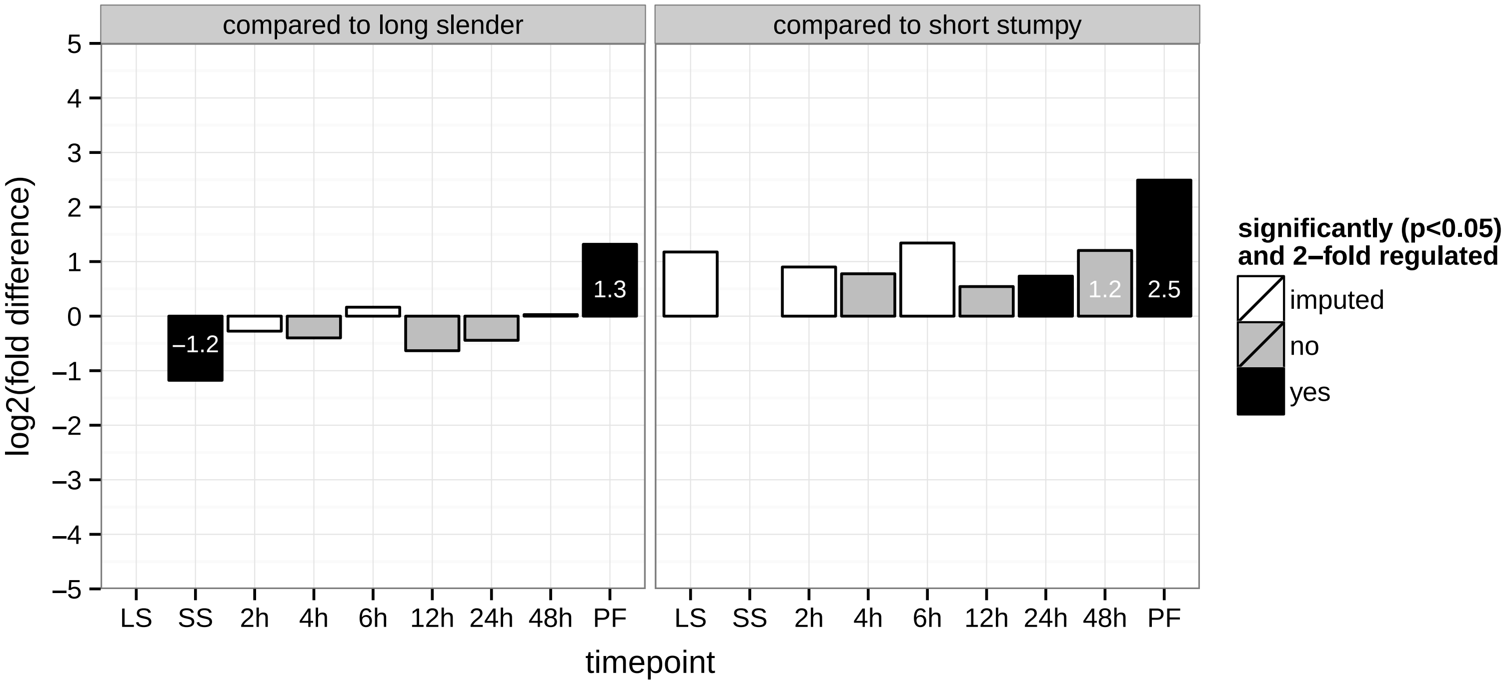
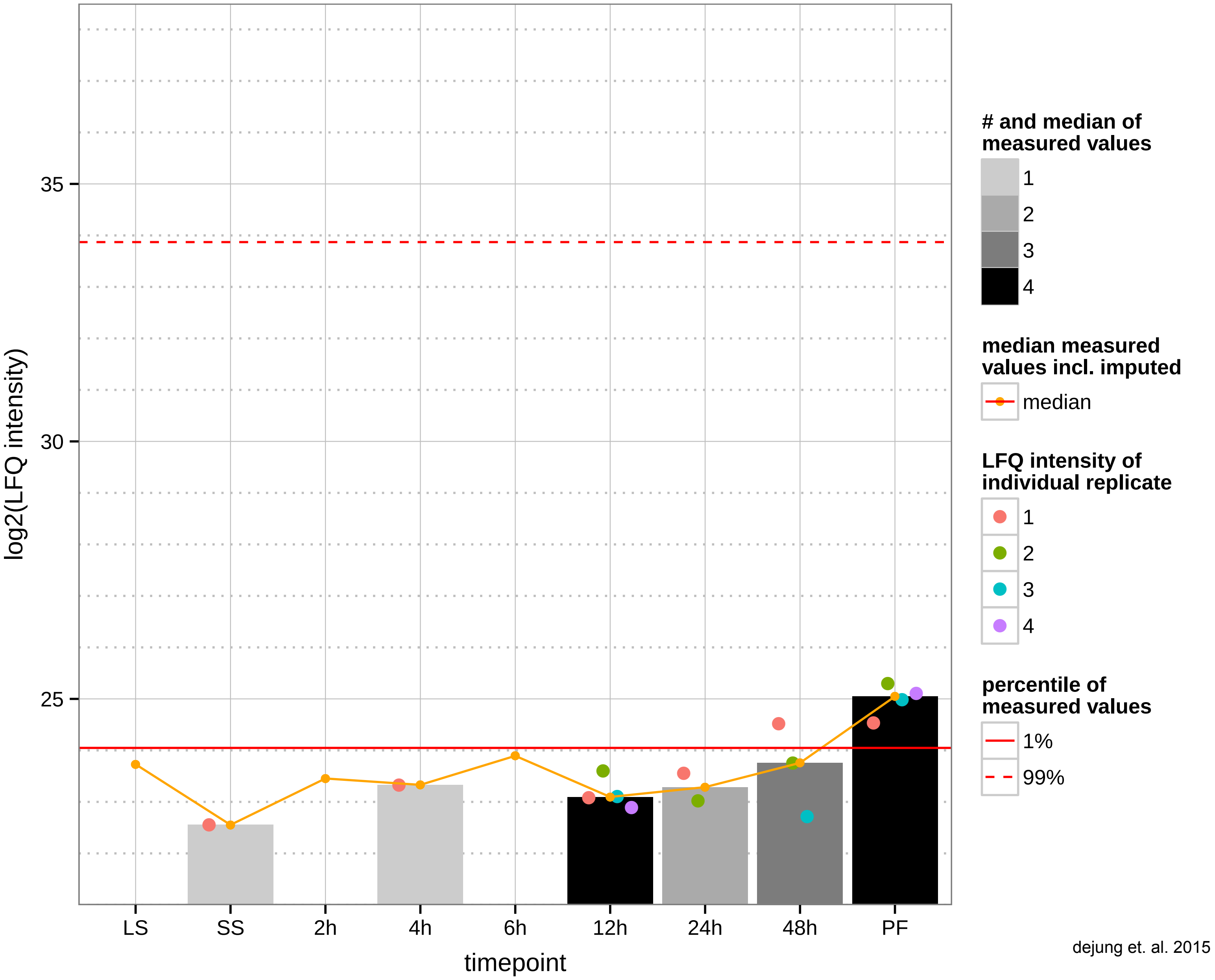


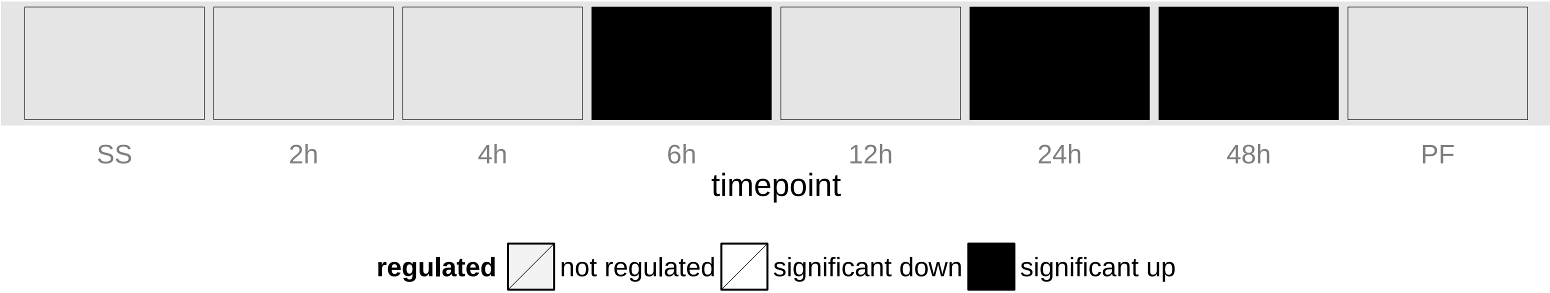
dejung et. al. 2015

COP9 signalosome complex subunit 5, putative, JAB−MPN domain protein
Tb927.8.5530
AGOF: null
AGOC: signalosome
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null



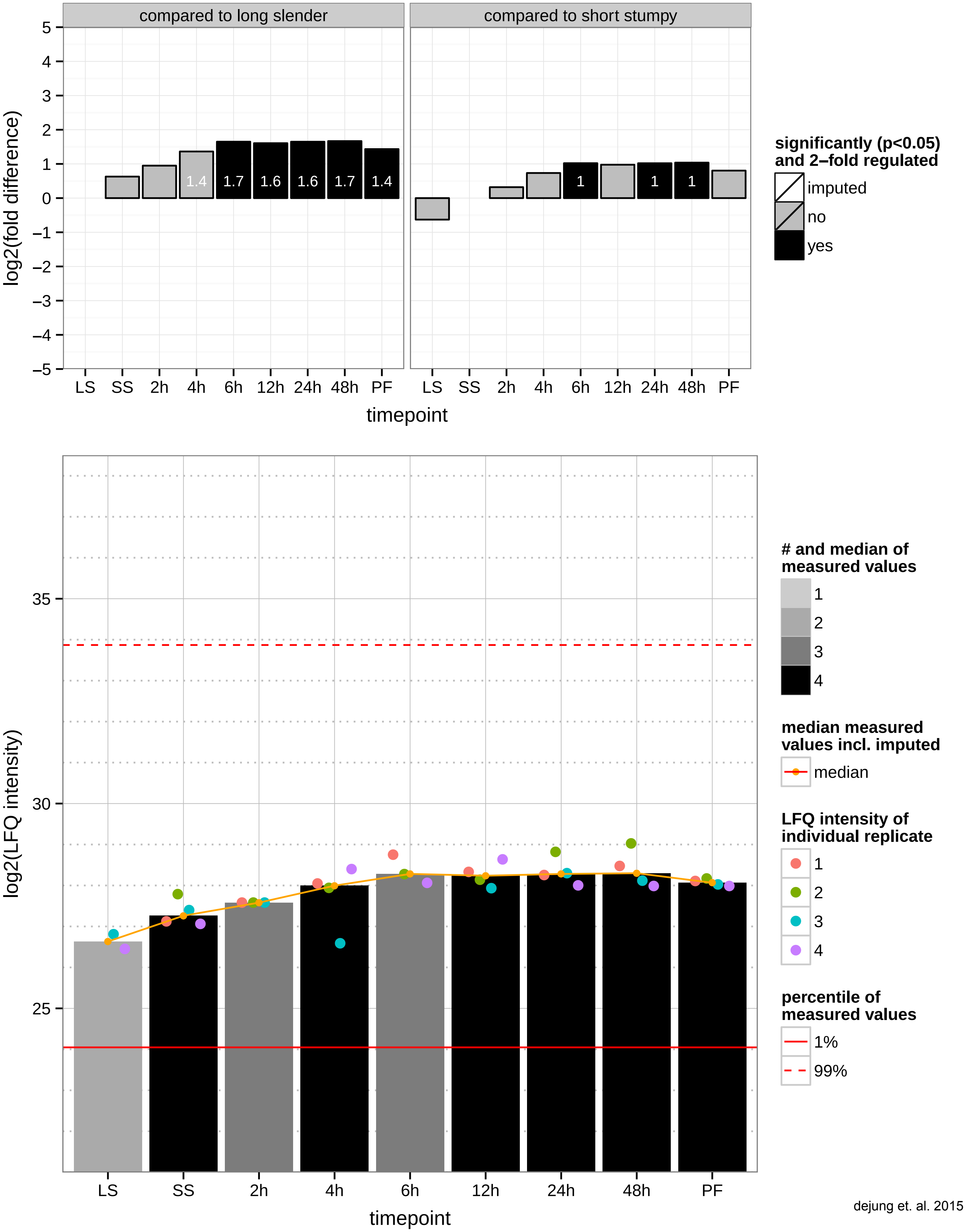


dejung et. al. 2015

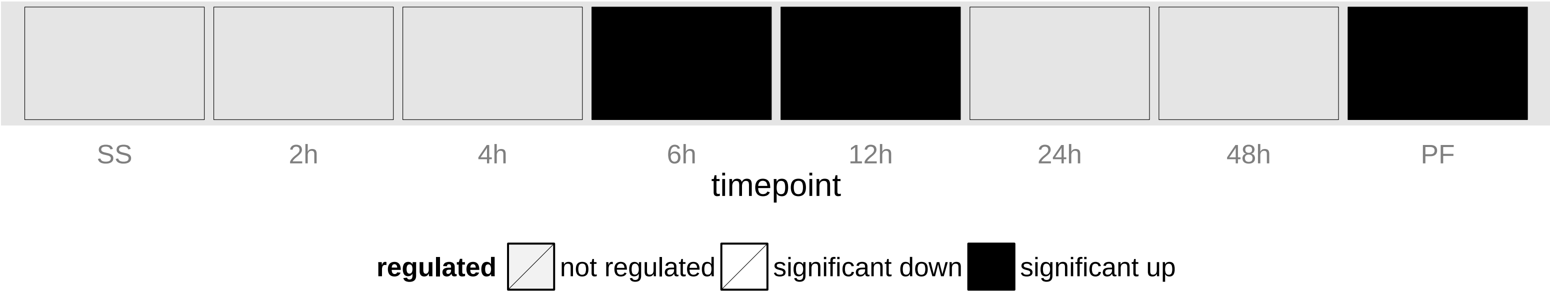


dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.11940
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null

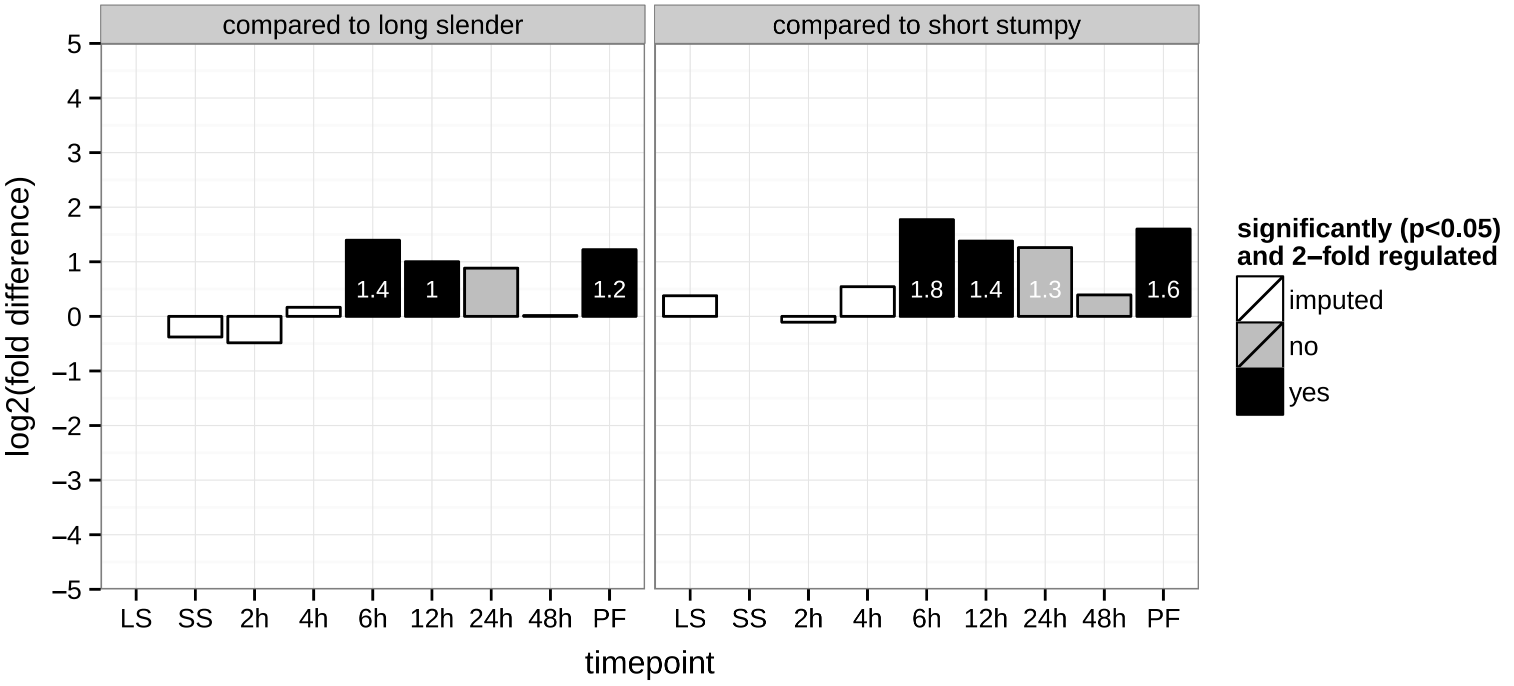


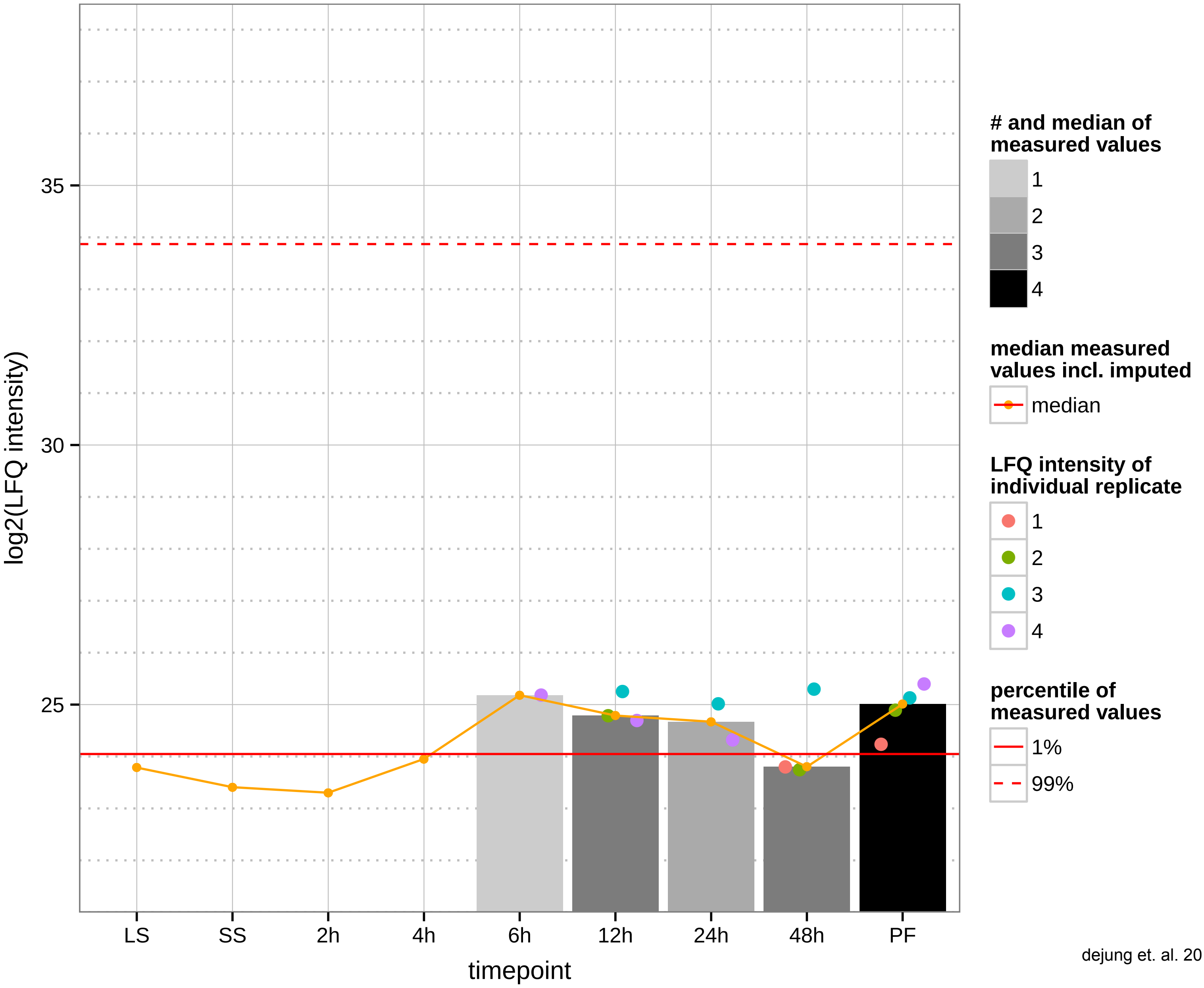
dejung et. al. 2015



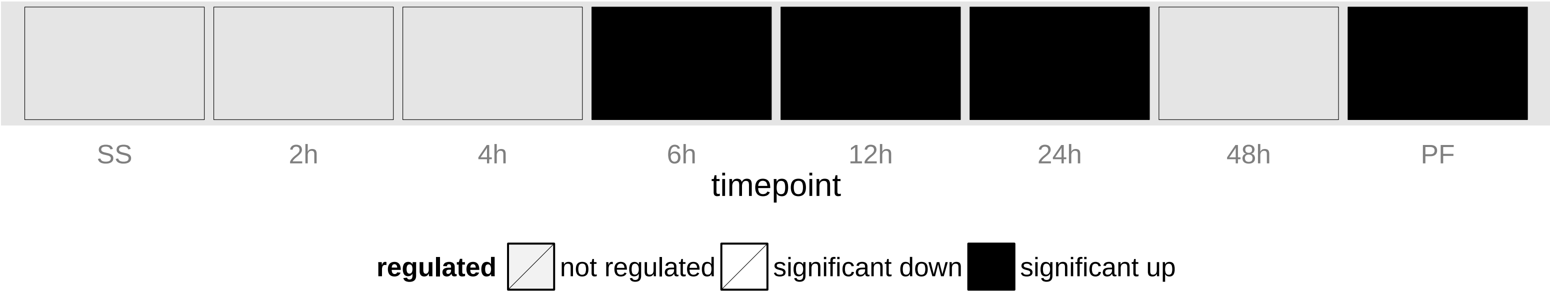
dejung et. al. 2015

hypothetical protein, conserved
Tb927.8.3810
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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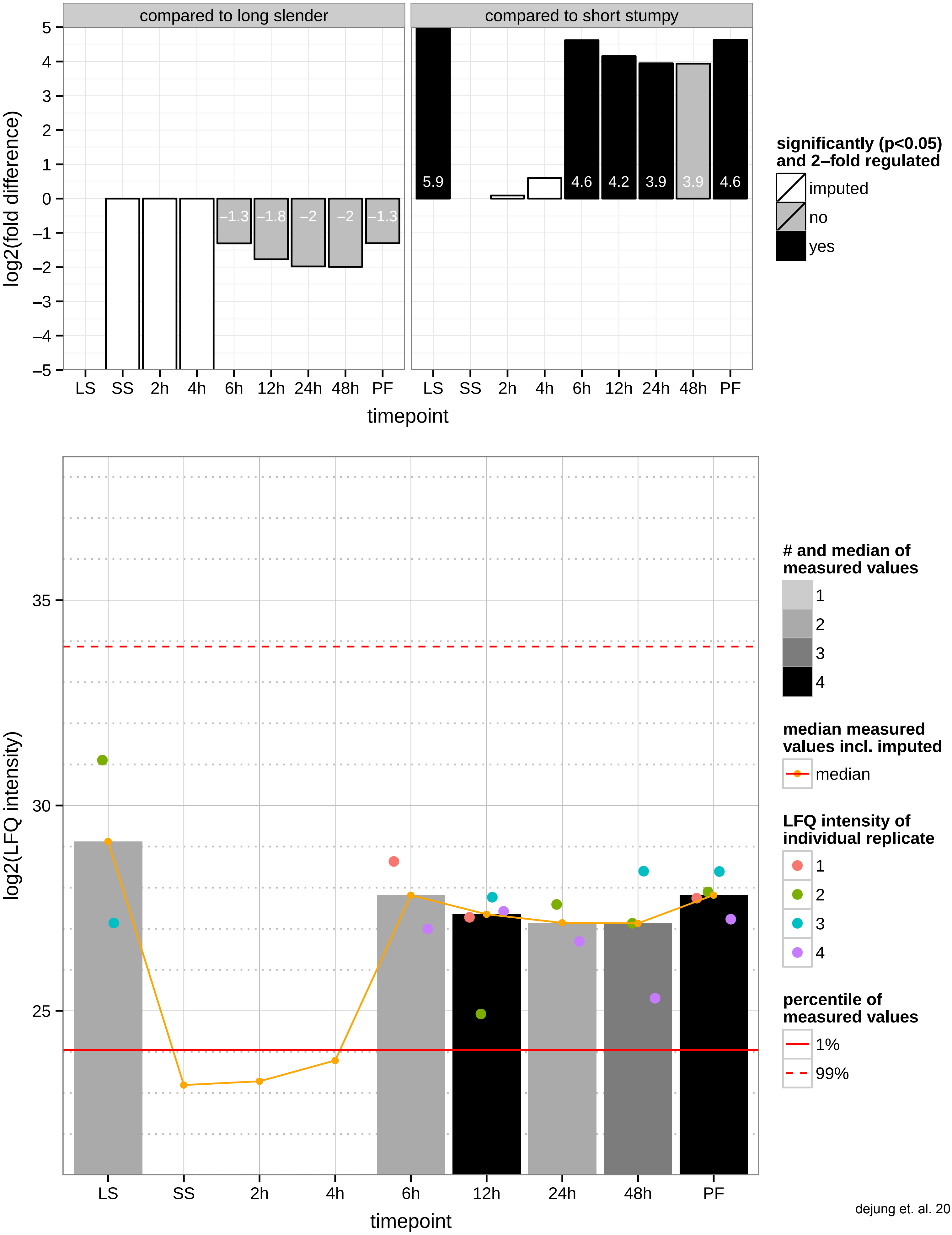
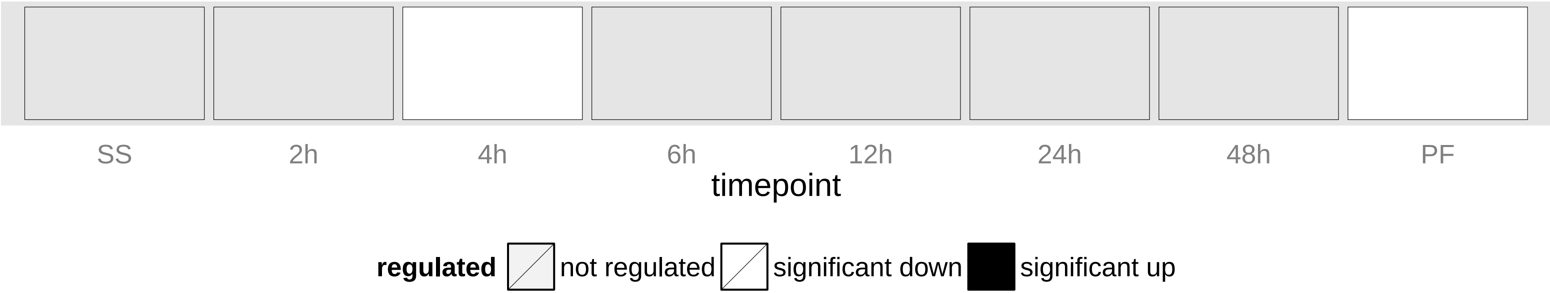
beta–ketoacyl–ACP reductase 2 (KAR2)
Tb927.8.6420
AGOF: 3–oxoacyl–[acyl–carrier–protein] reductase (NADPH) activity
AGOC: mitochondrion
AGOP: fatty acid elongation
PGOF: oxidoreductase activity
PGOC: null
PGOP: metabolic process

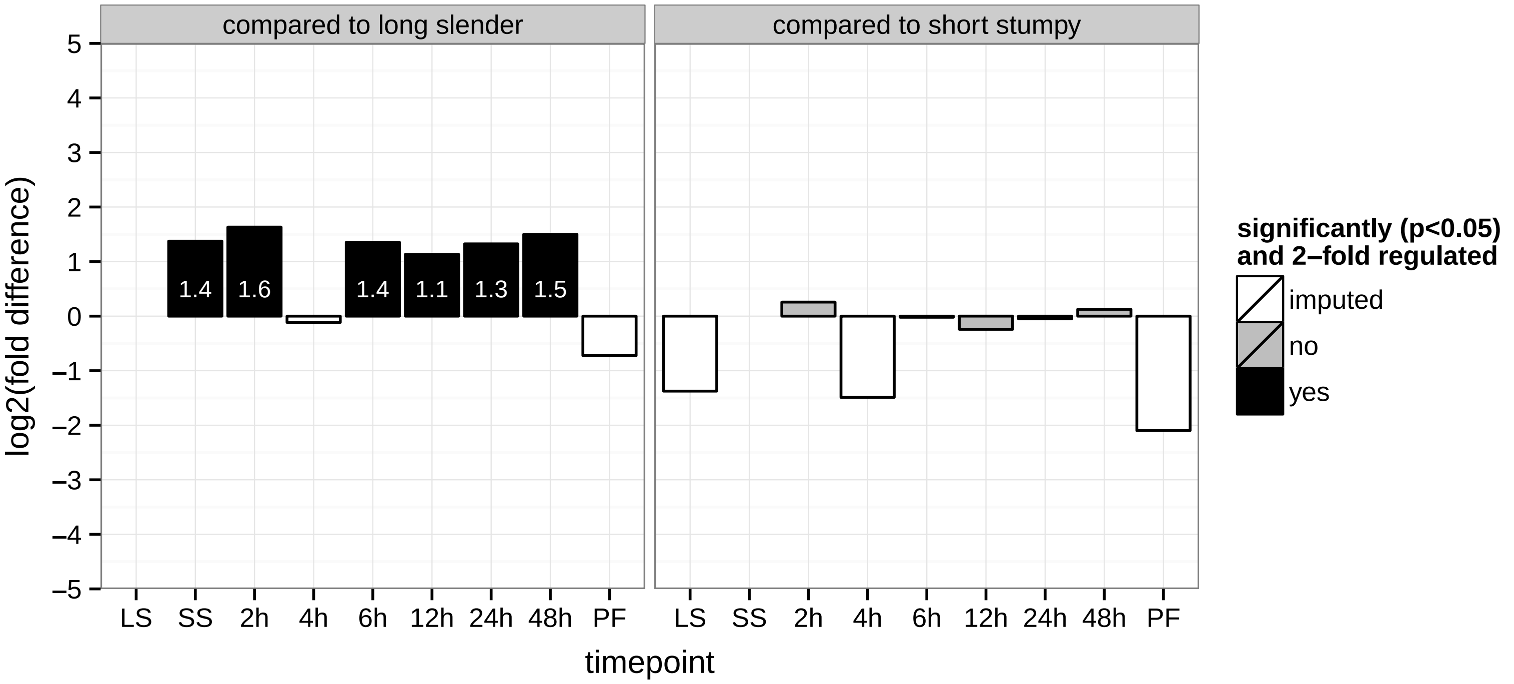


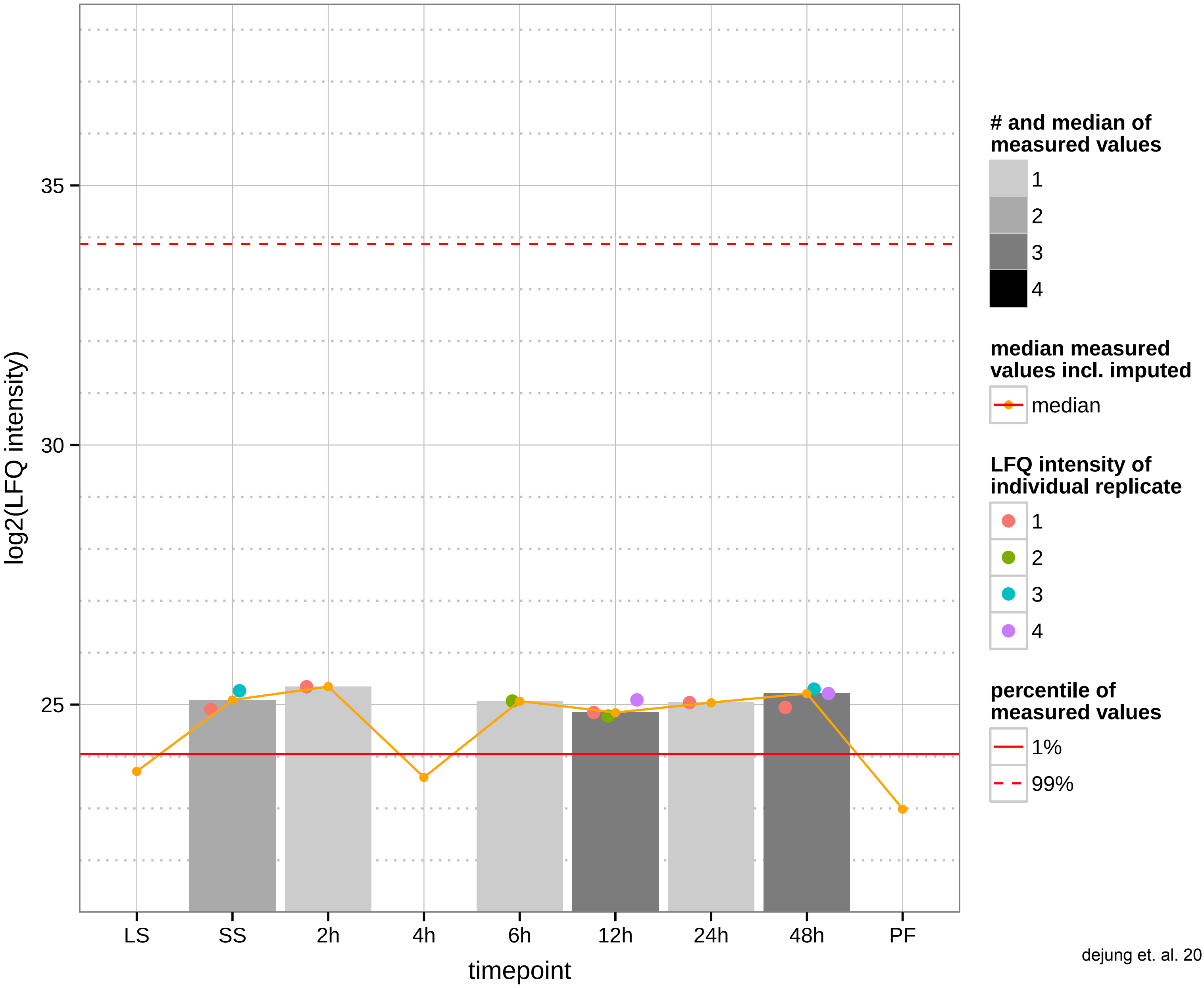
dejung et. al. 2015



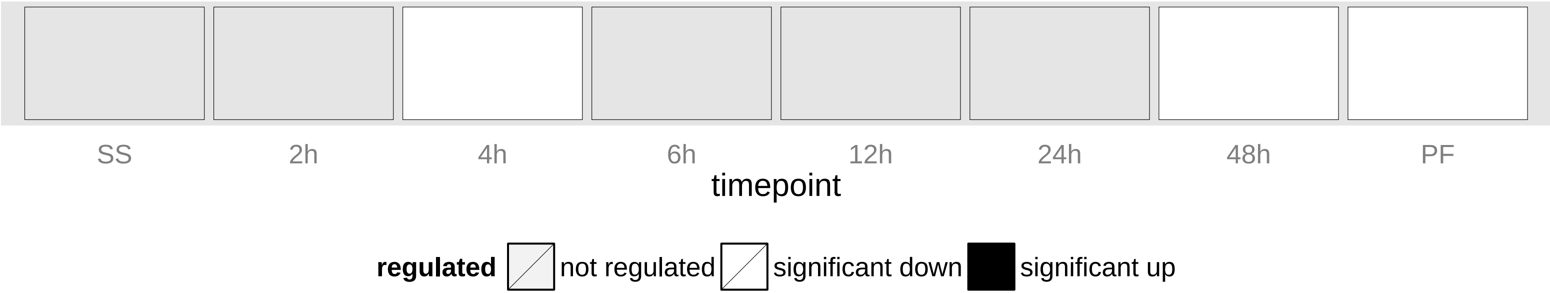
dejung et. al. 2015

hypothetical protein, conserved
Tb927.9.2940
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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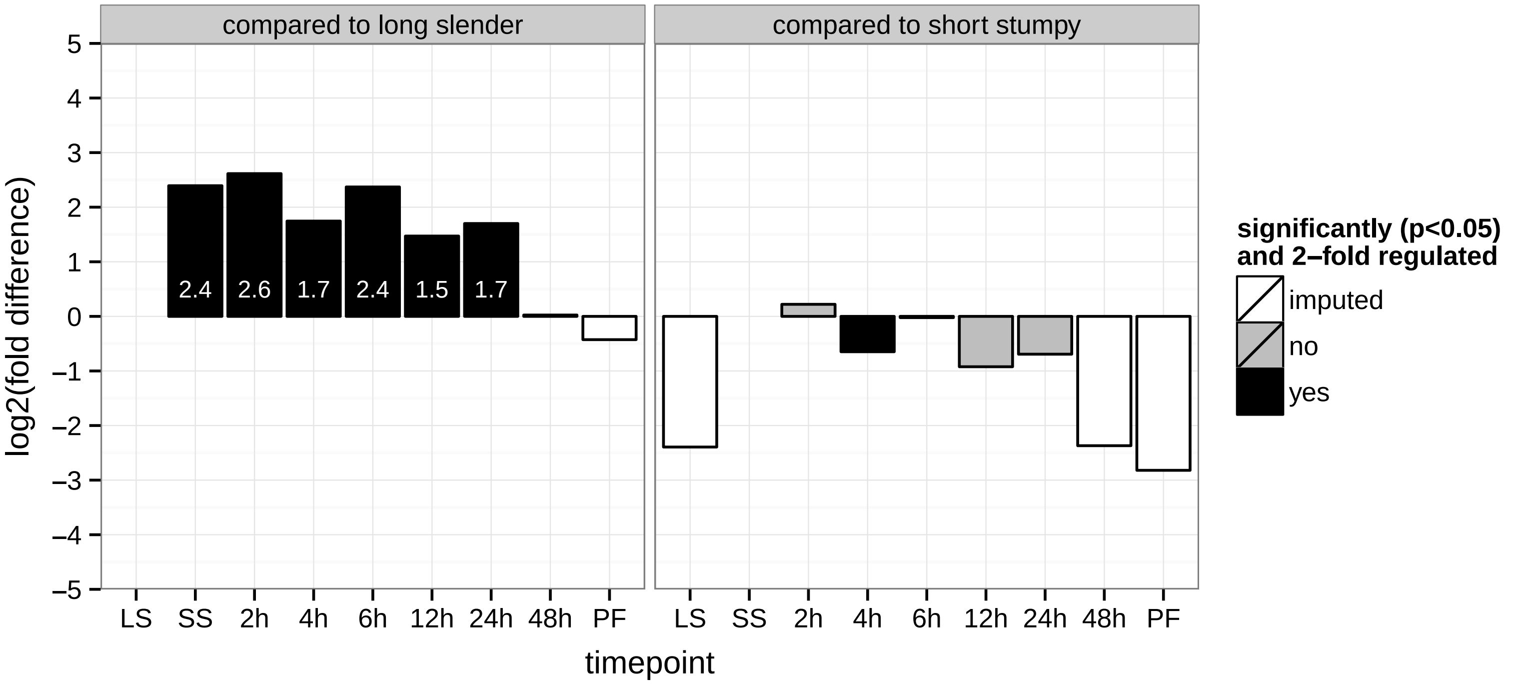
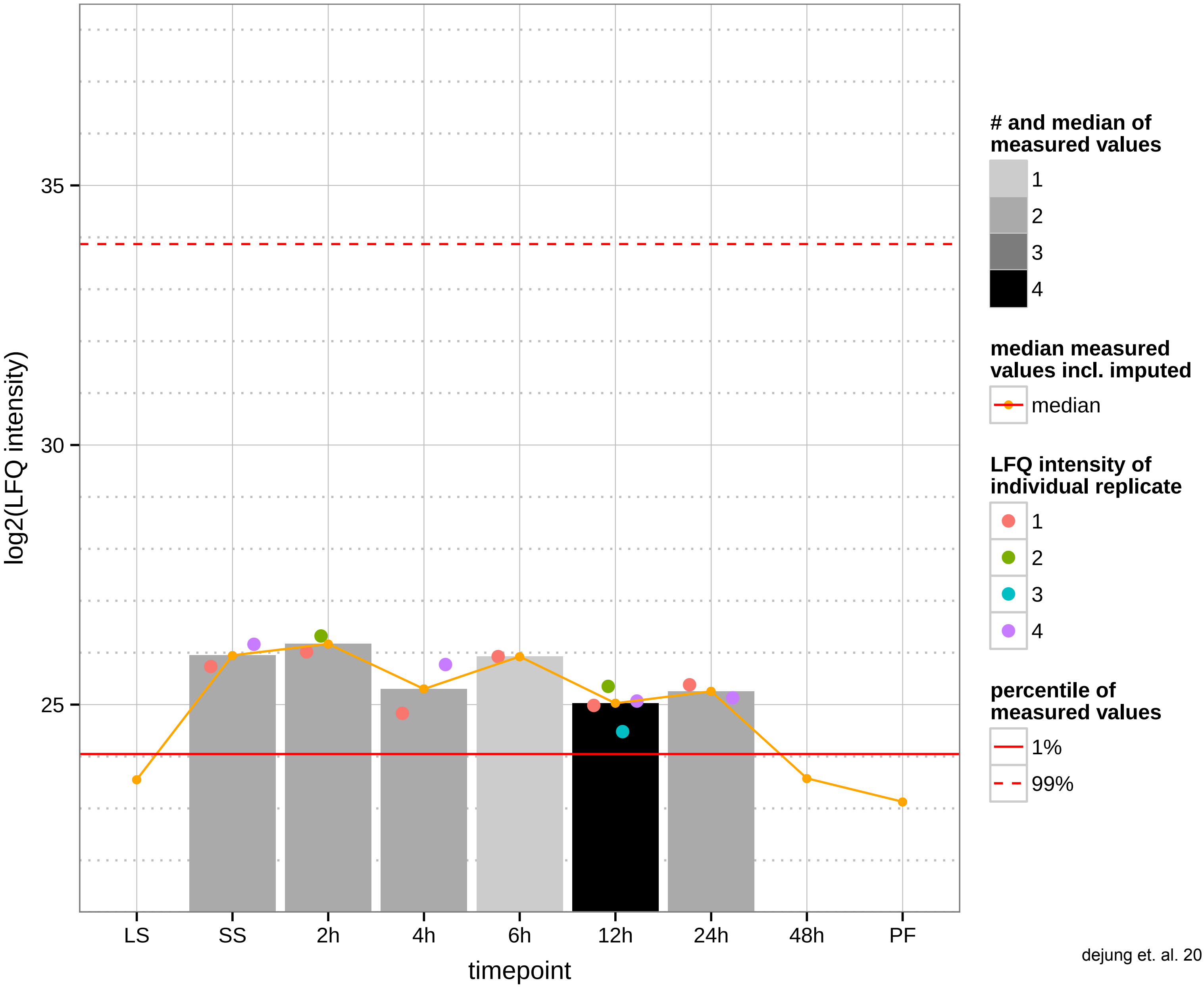
cdc2–related kinase, putative, cell division control protein, putative (CRK10)
Tb927.3.4670
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: cell cycle, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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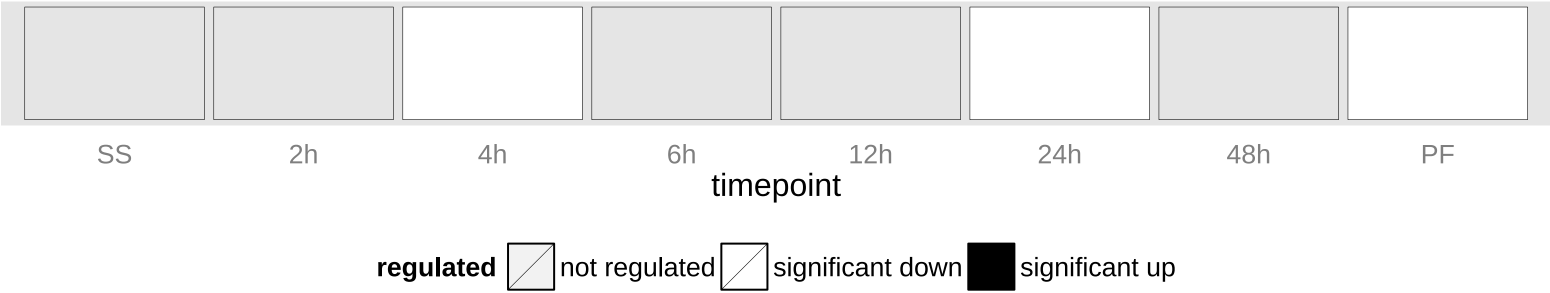

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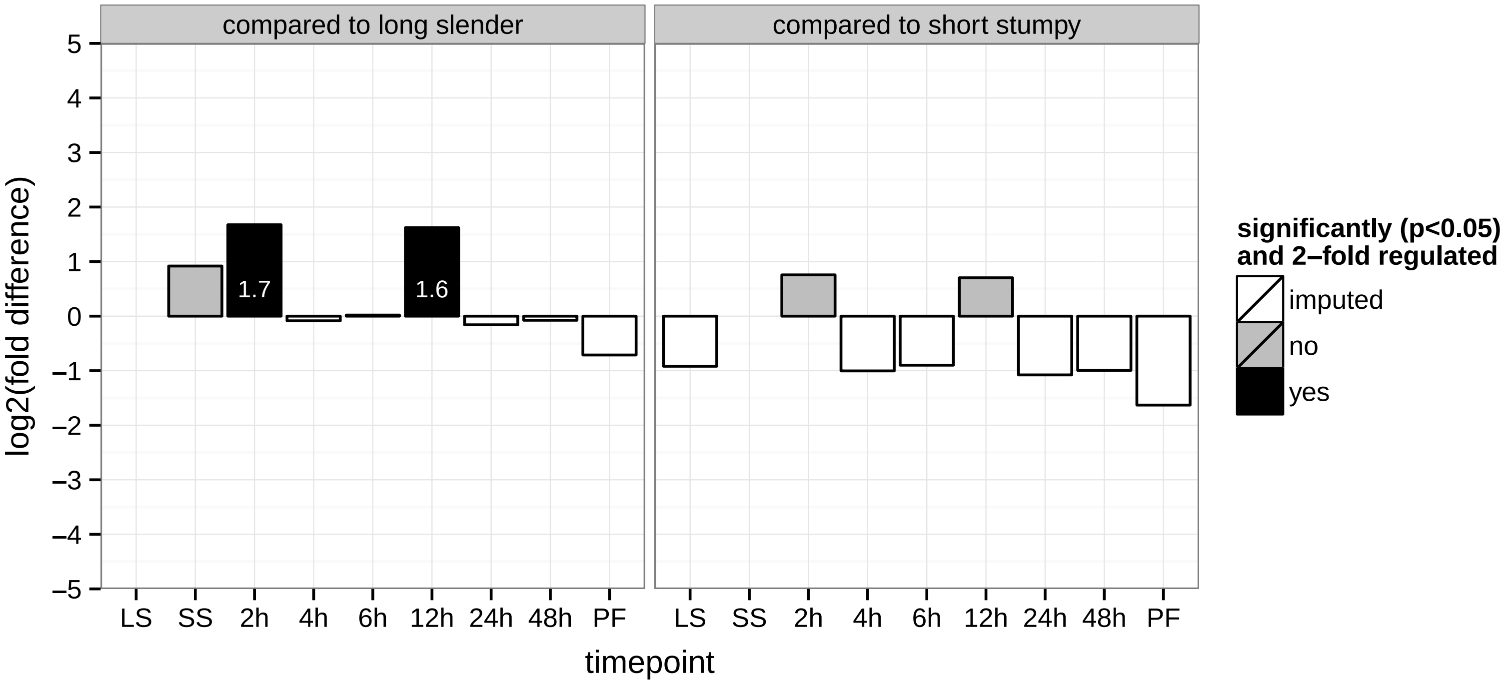
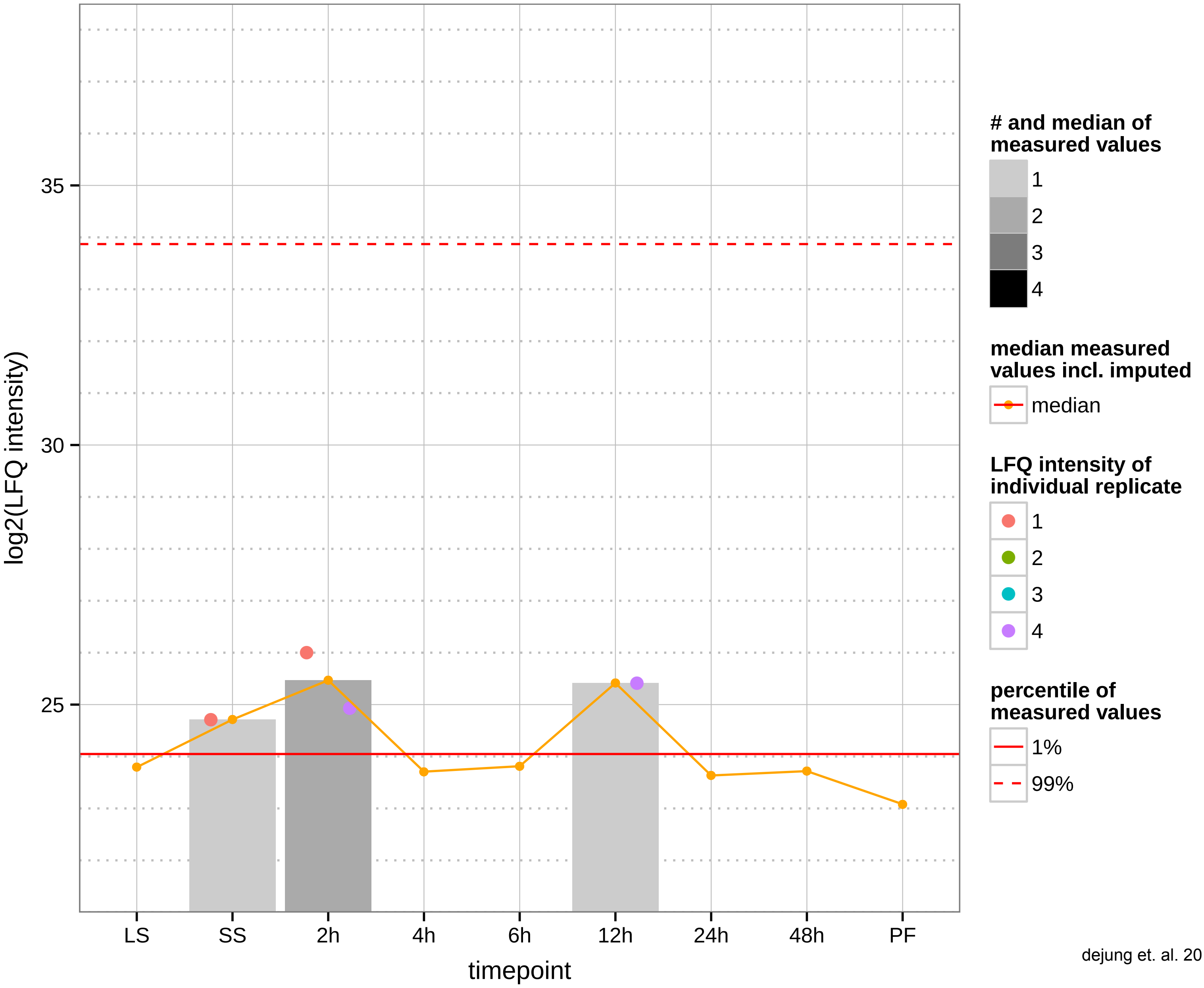
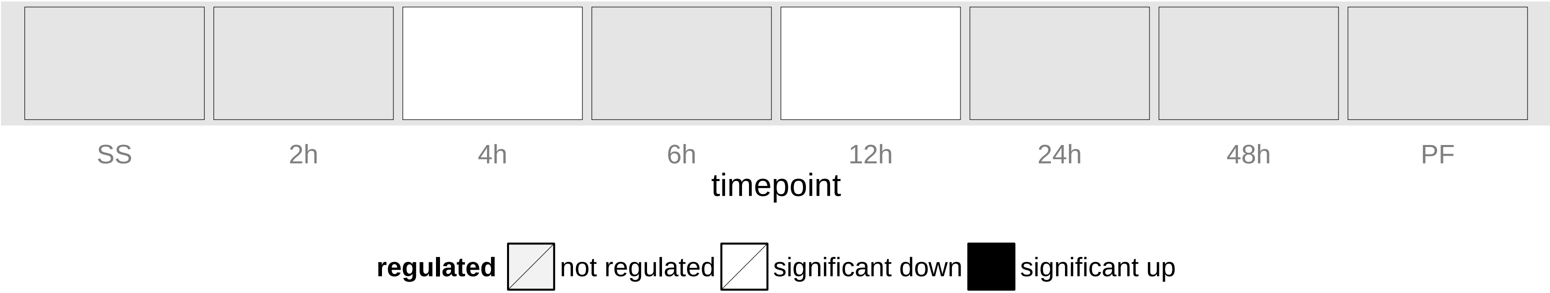
hypothetical protein, conserved
Tb927.10.14310
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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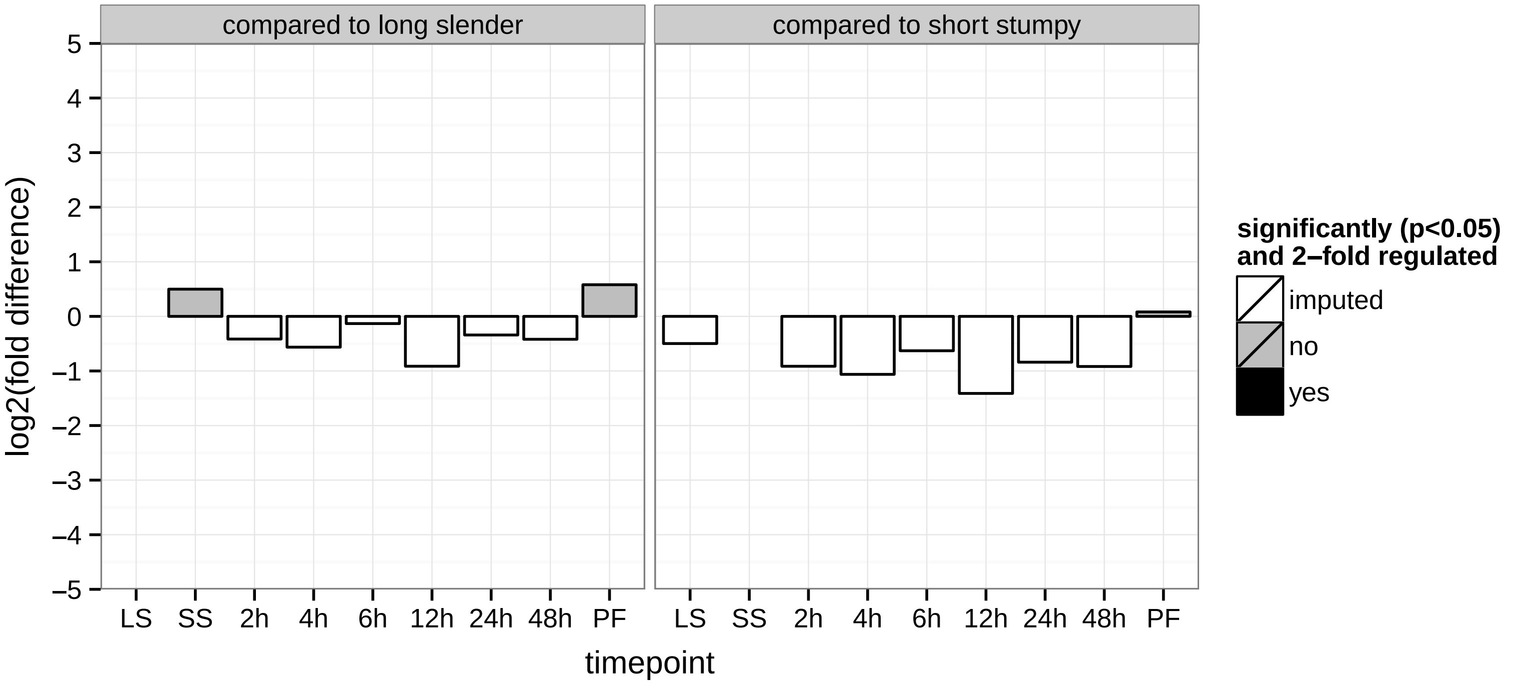
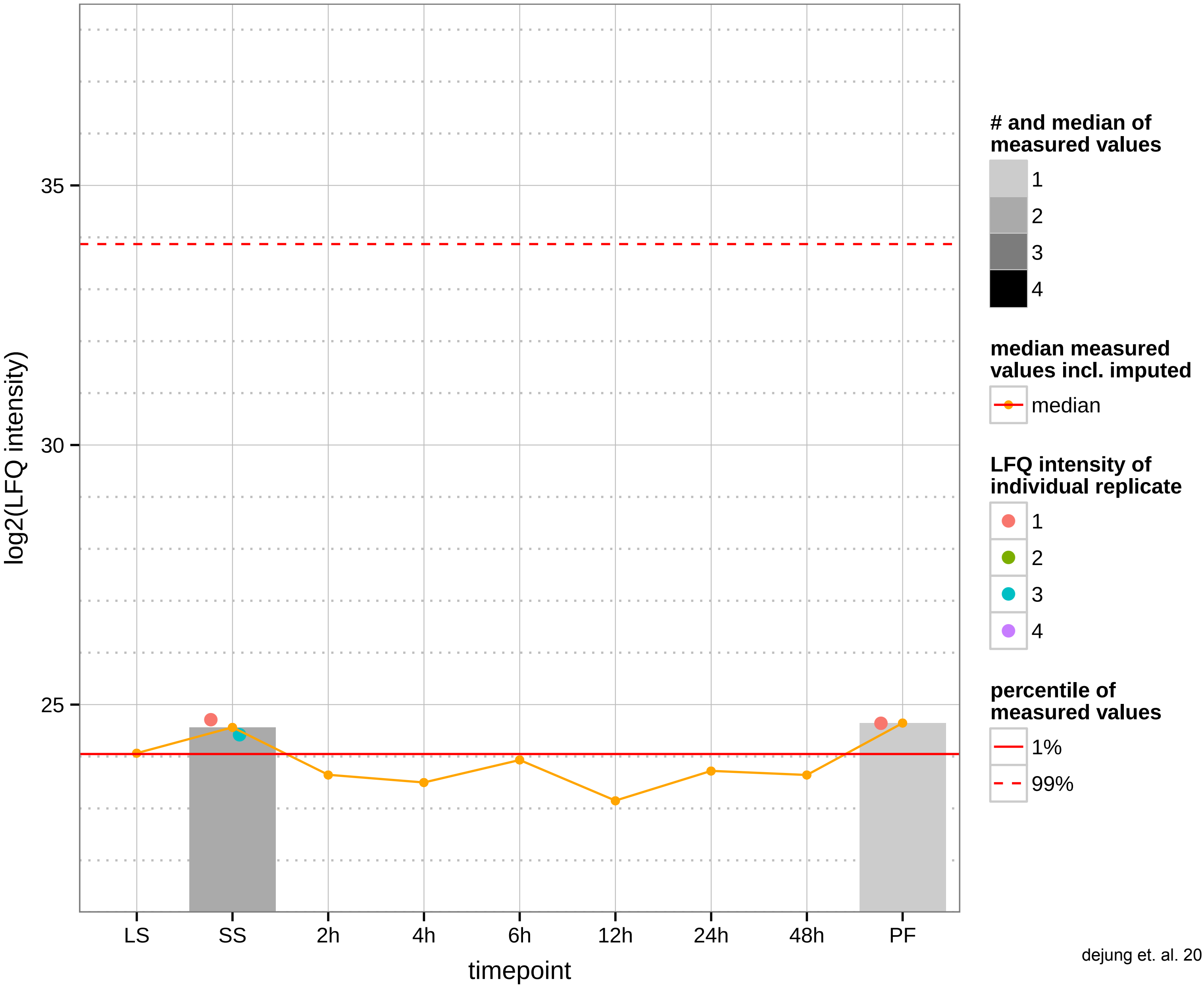
hypothetical protein, conserved
Tb927.9.15260
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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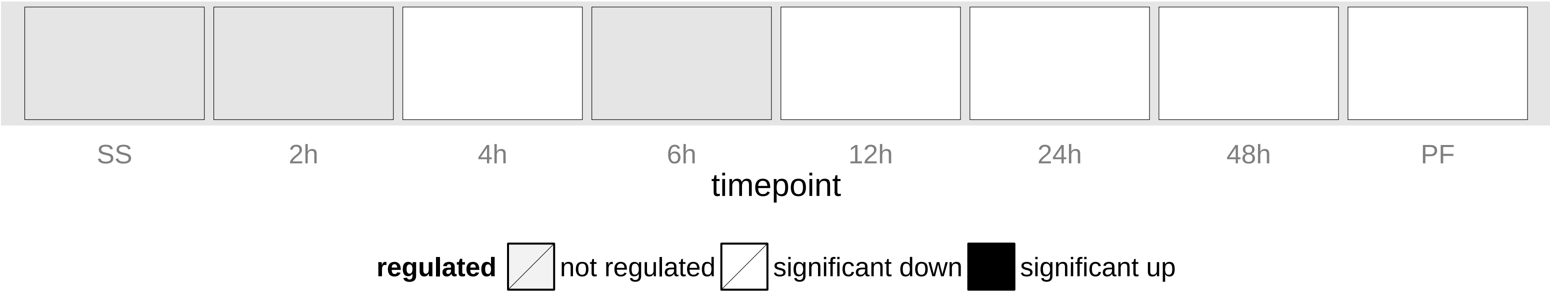

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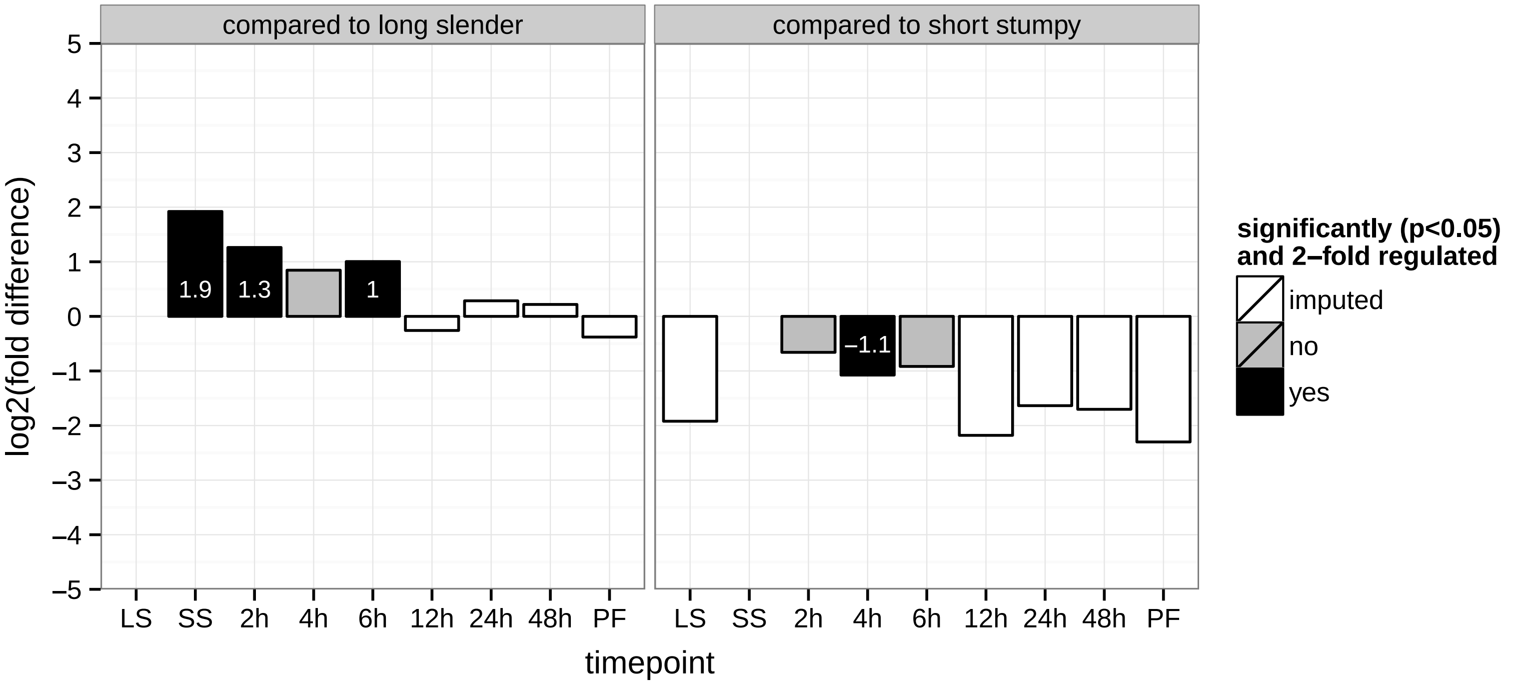
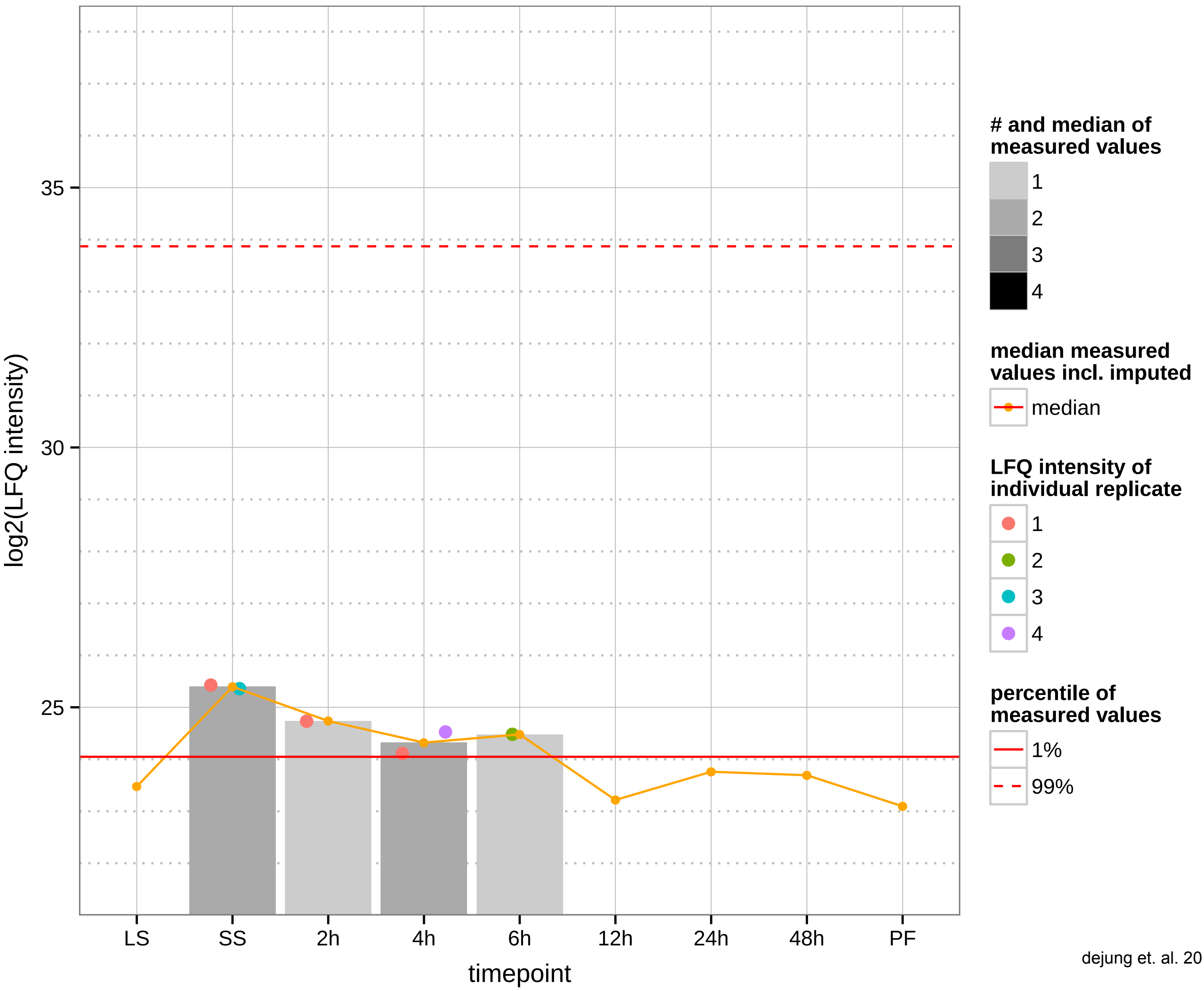
ubiquitin–protein ligase, putative (upl3)
Tb927.9.13360
AGOF: ubiquitin–protein ligase activity
AGOC: intracellular
AGOP: cellular protein modification process
PGOF: acid–amino acid ligase activity
PGOC: intracellular
PGOP: cellular protein modification process





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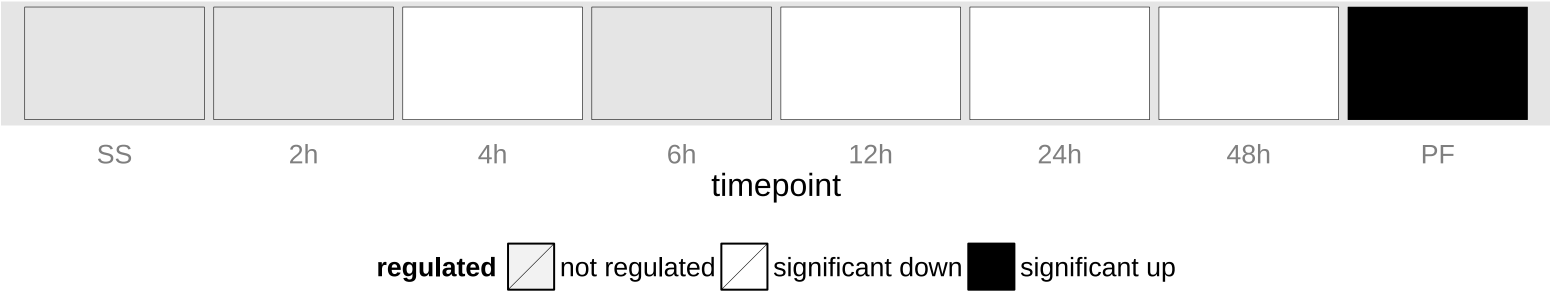

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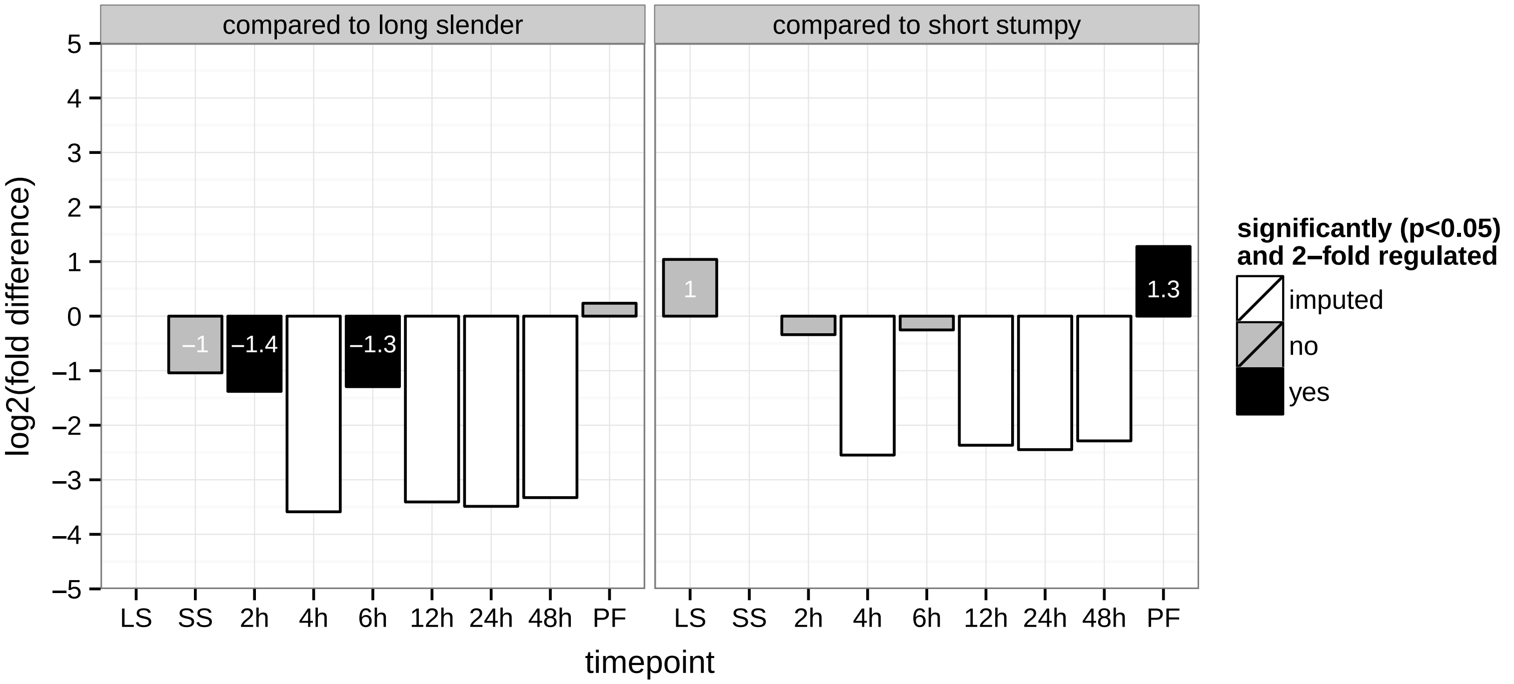
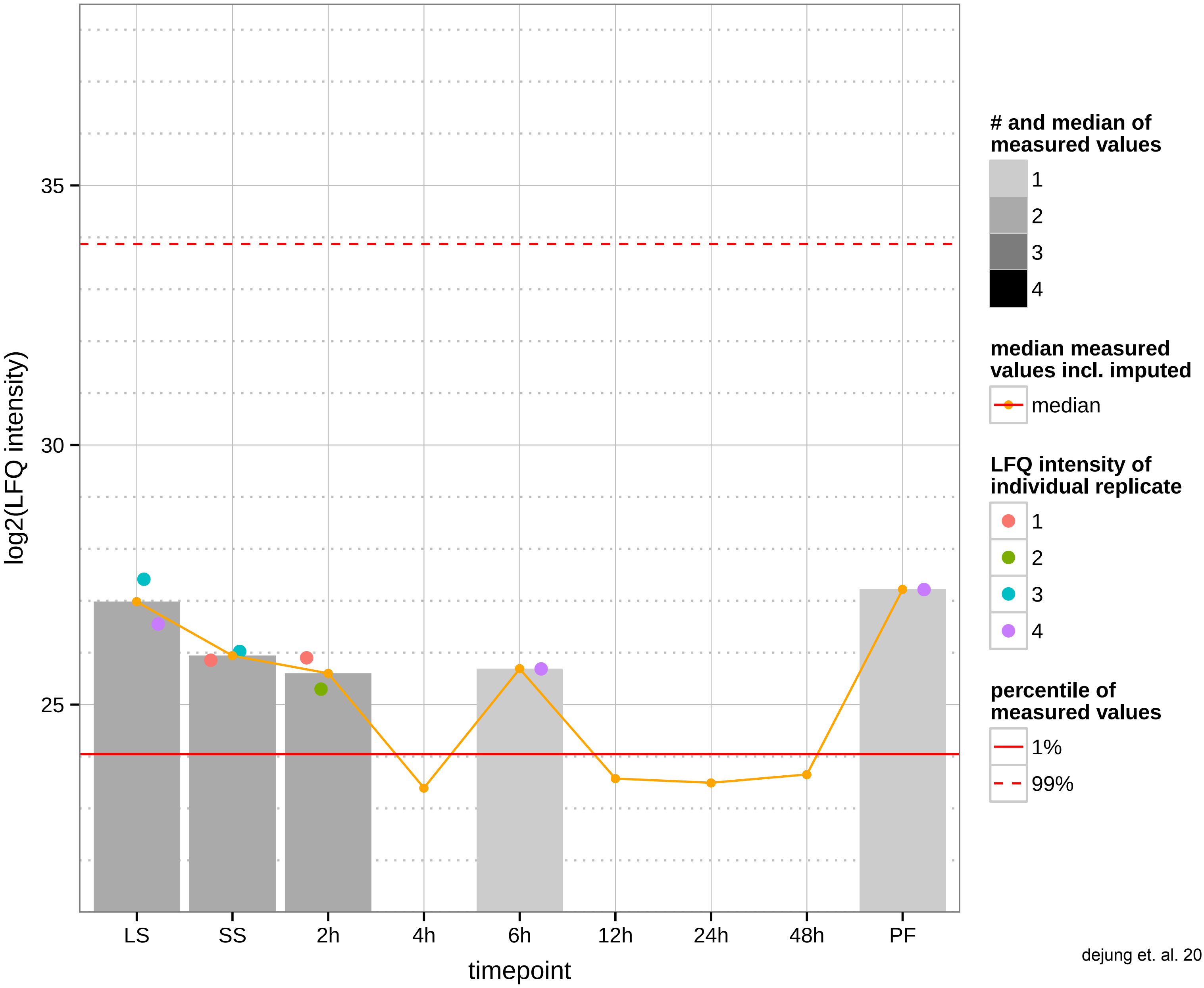
amino acid transporter 8, putative, amino acid transporter 10, putative (AATP10), amino acid transporter 7, putative (AATP7),
Tb927.4.4860;Tb11.v5.0540;Tb927.4.4840;Tb927.4.4820
AGOF: null, amine transmembrane transporter activity
AGOC: null, membrane
AGOP: null, amino acid transport
PGOF: null
PGOC: null
PGOP: null





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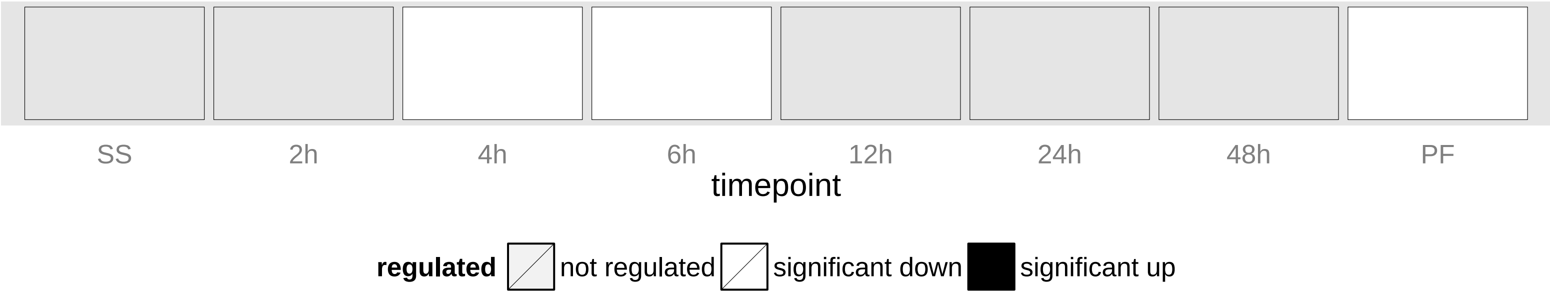

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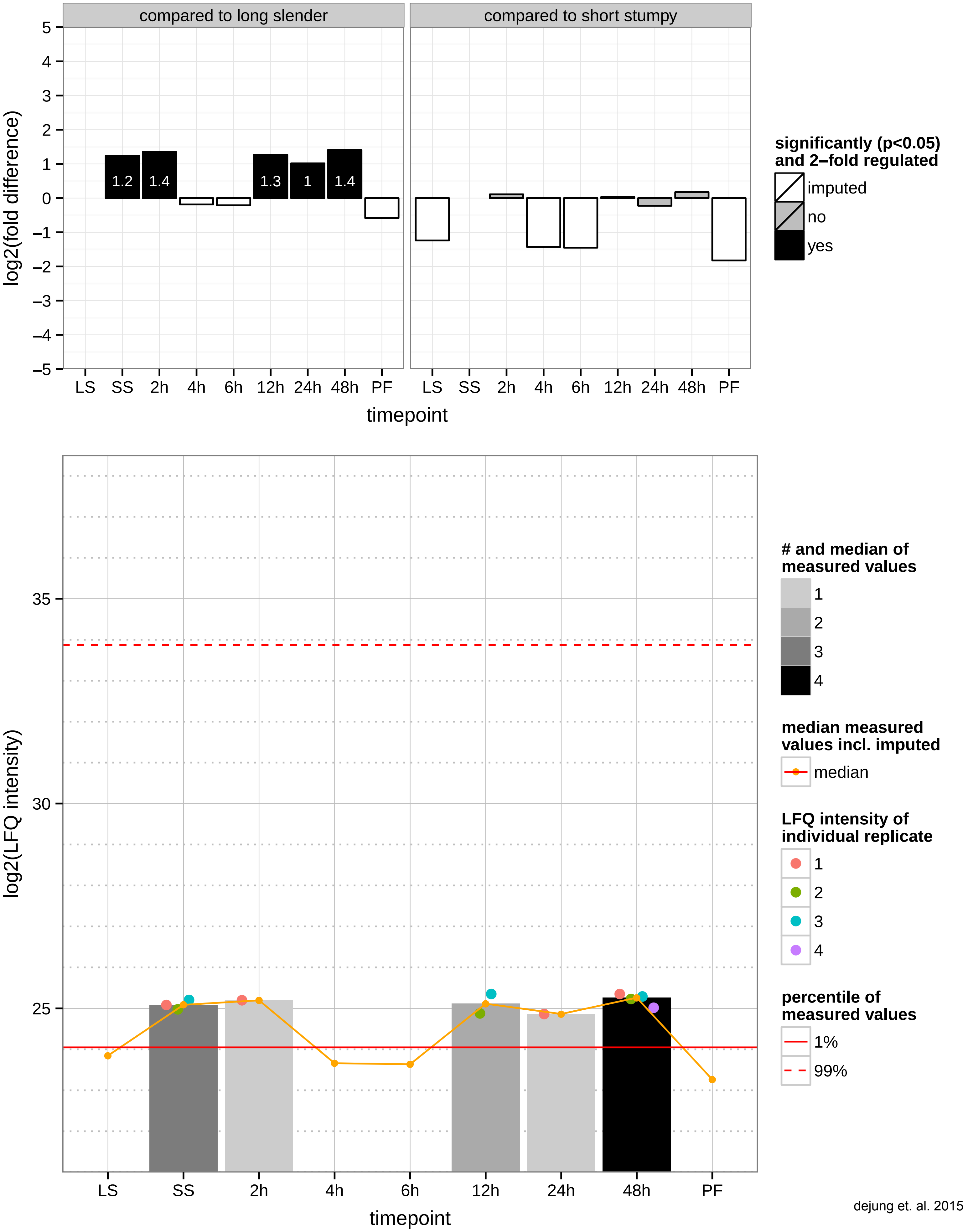
hypothetical protein, conserved
Tb927.11.10120
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



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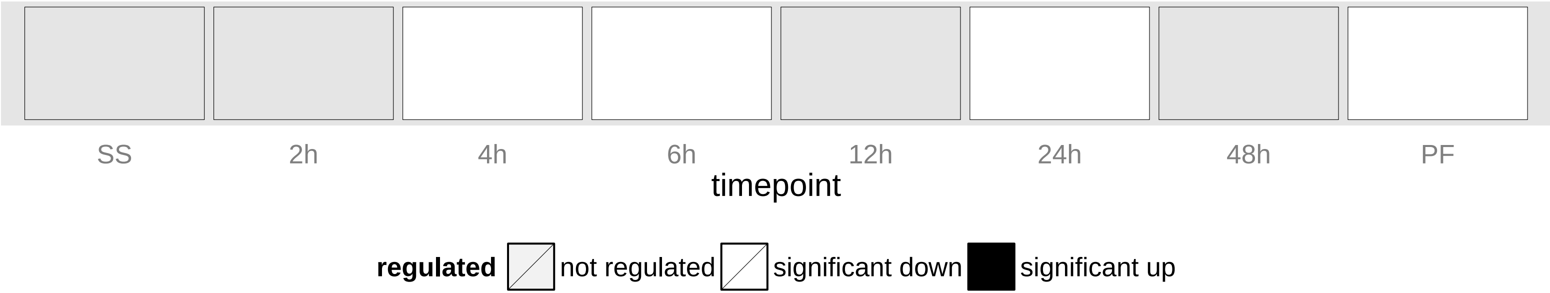
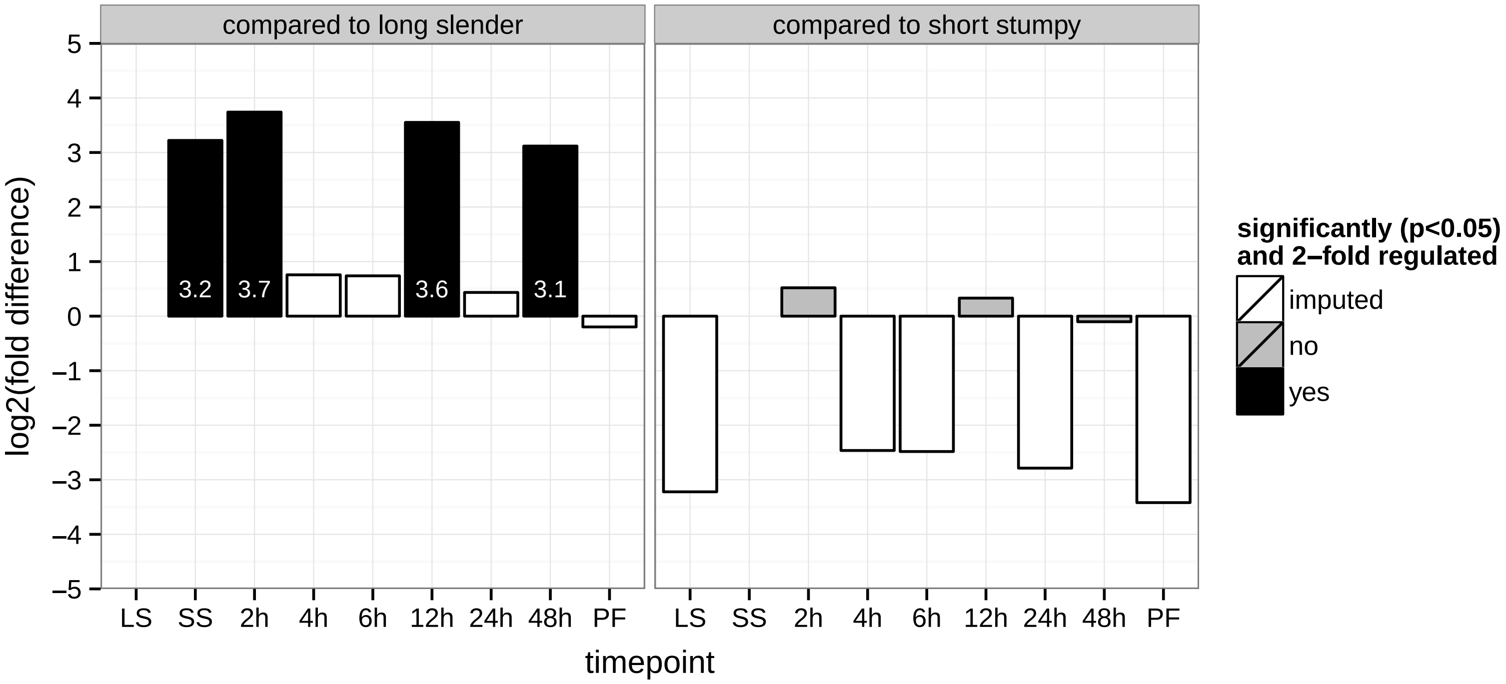
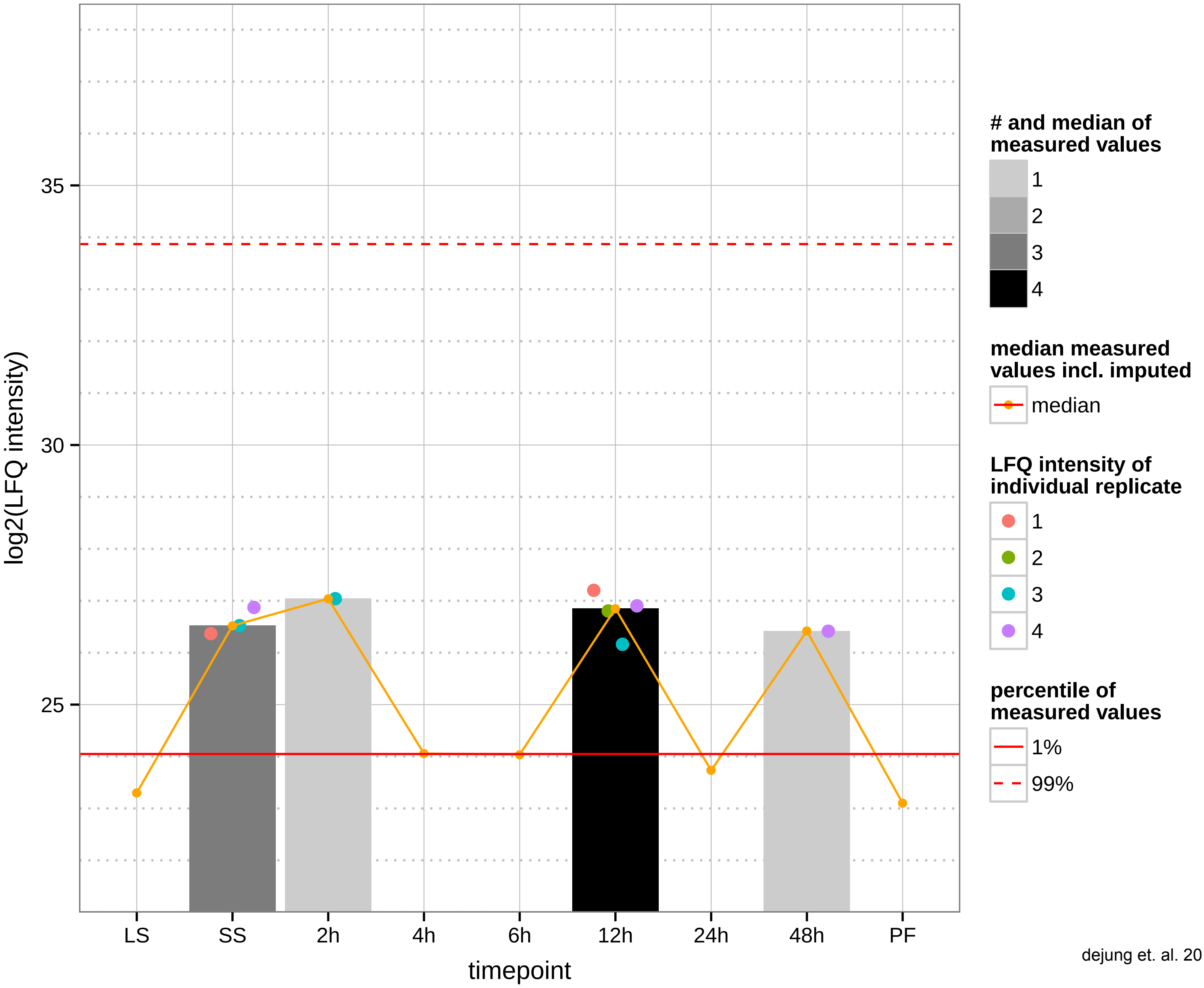


dejung et. al. 2015

hypothetical protein, conserved
Tb927.7.2520
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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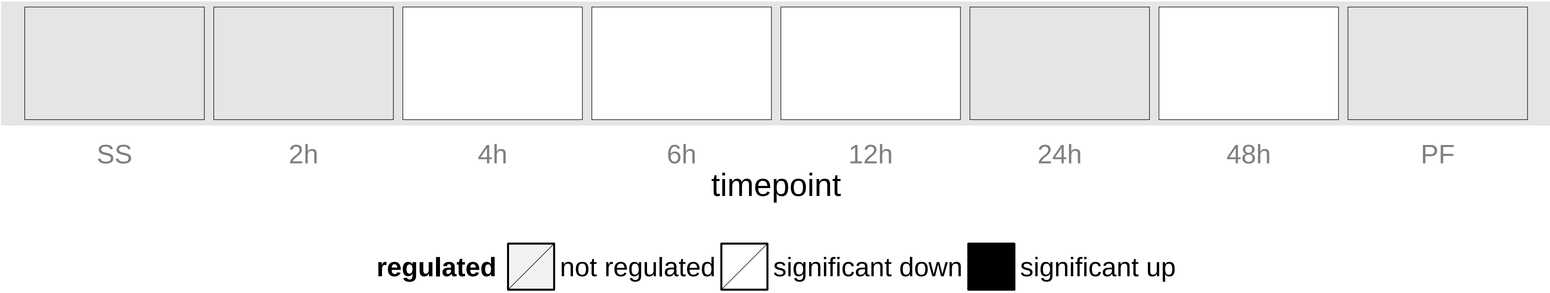

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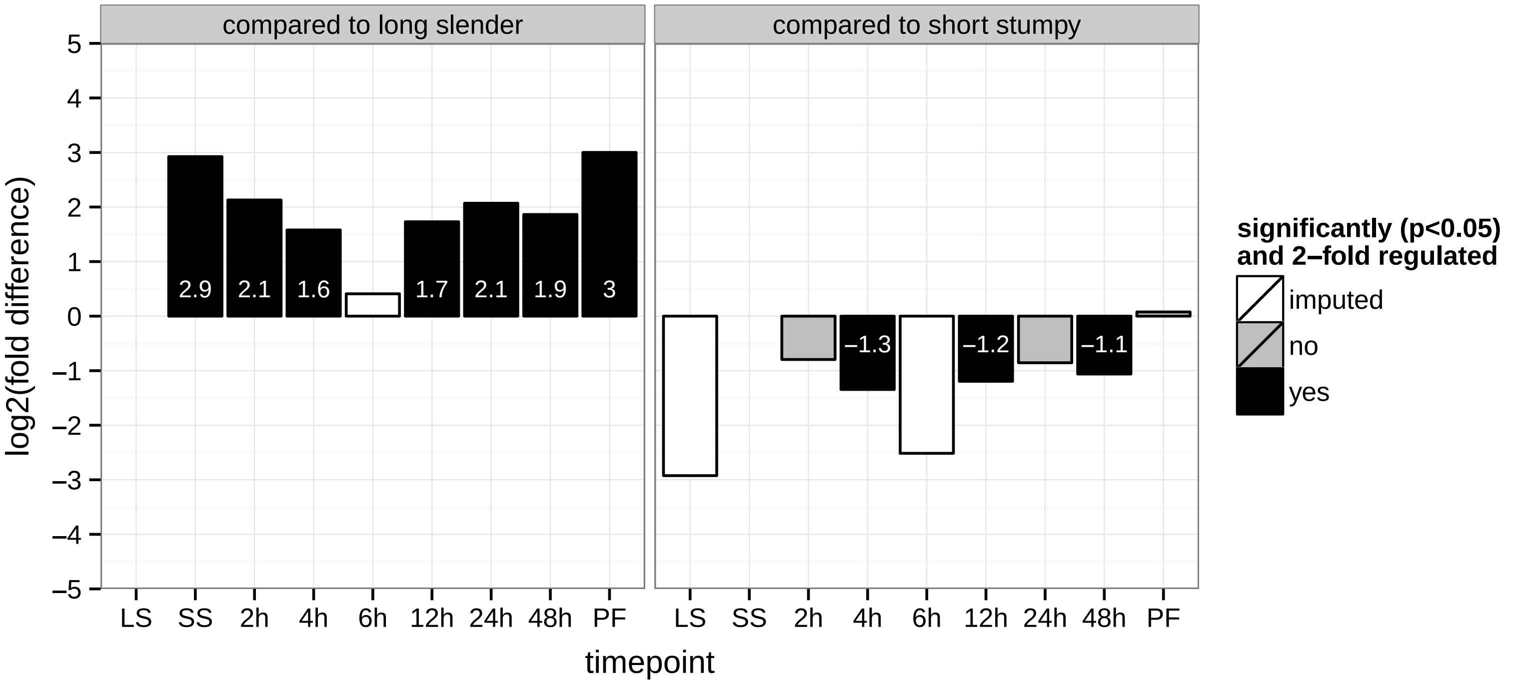
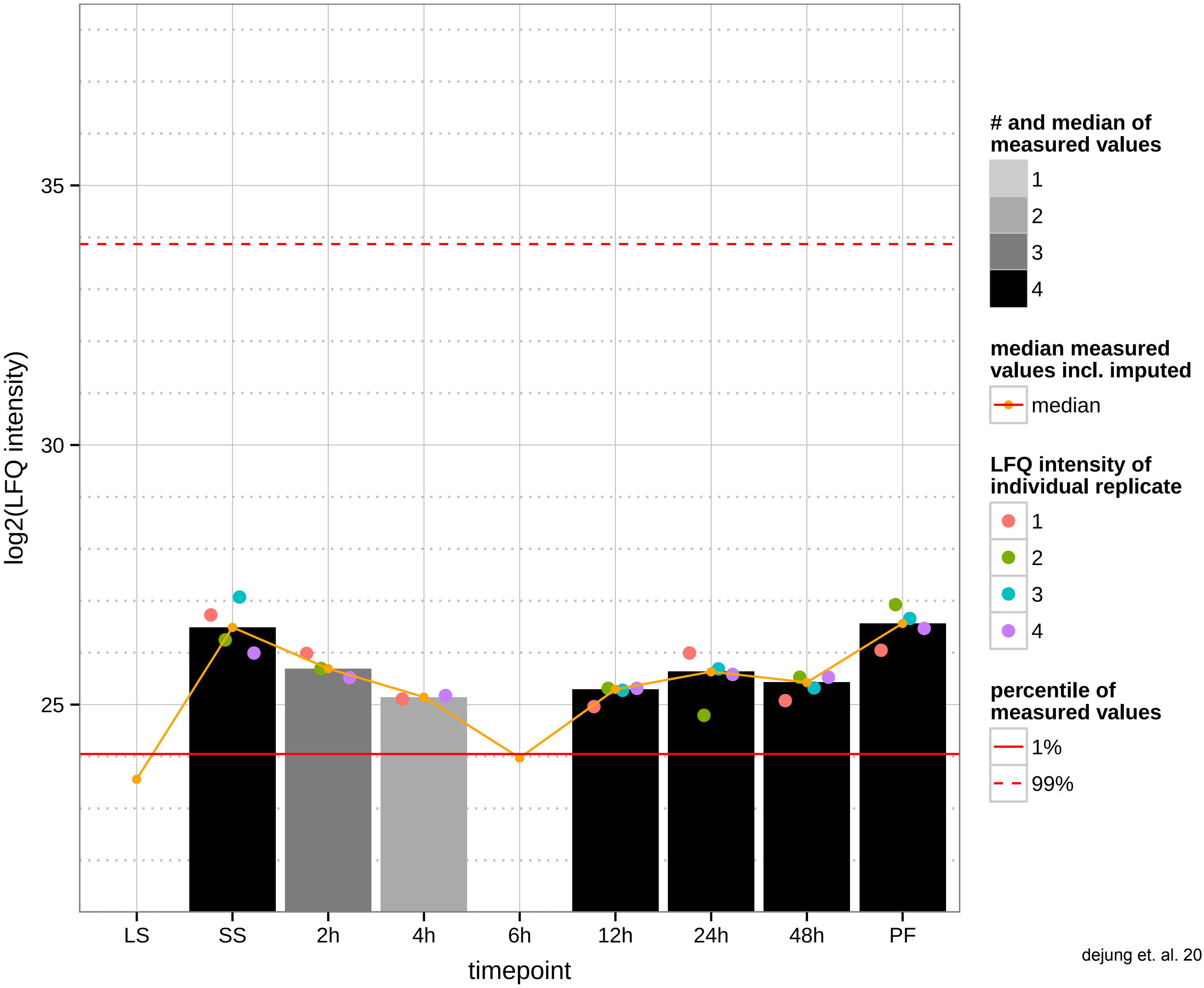
Nuclear Dbf2–related kinase, PK53 (PK53)
Tb927.7.5770
AGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: cytosol
AGOP: cell proliferation, cytokinesis, protein phosphorylation, regulation of cell cycle
PGOF: ATP binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity, transferring phosphoru
PGOC: null
PGOP: protein phosphorylation





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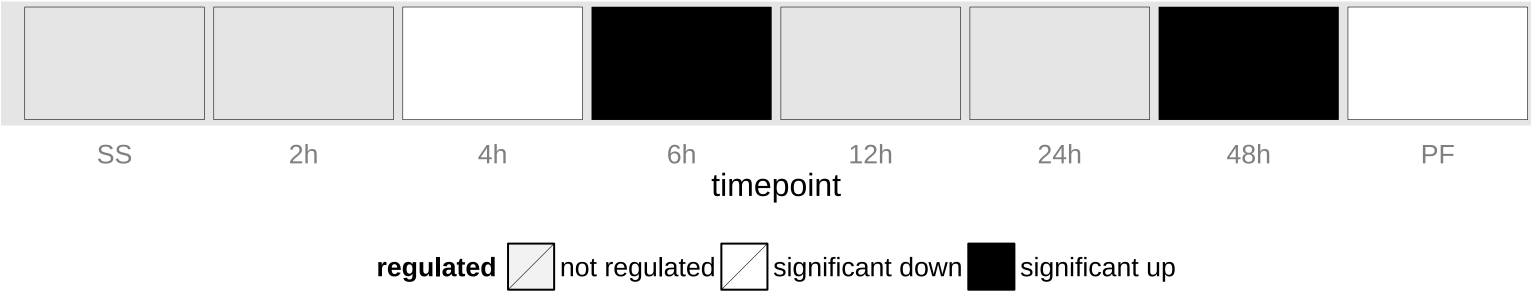

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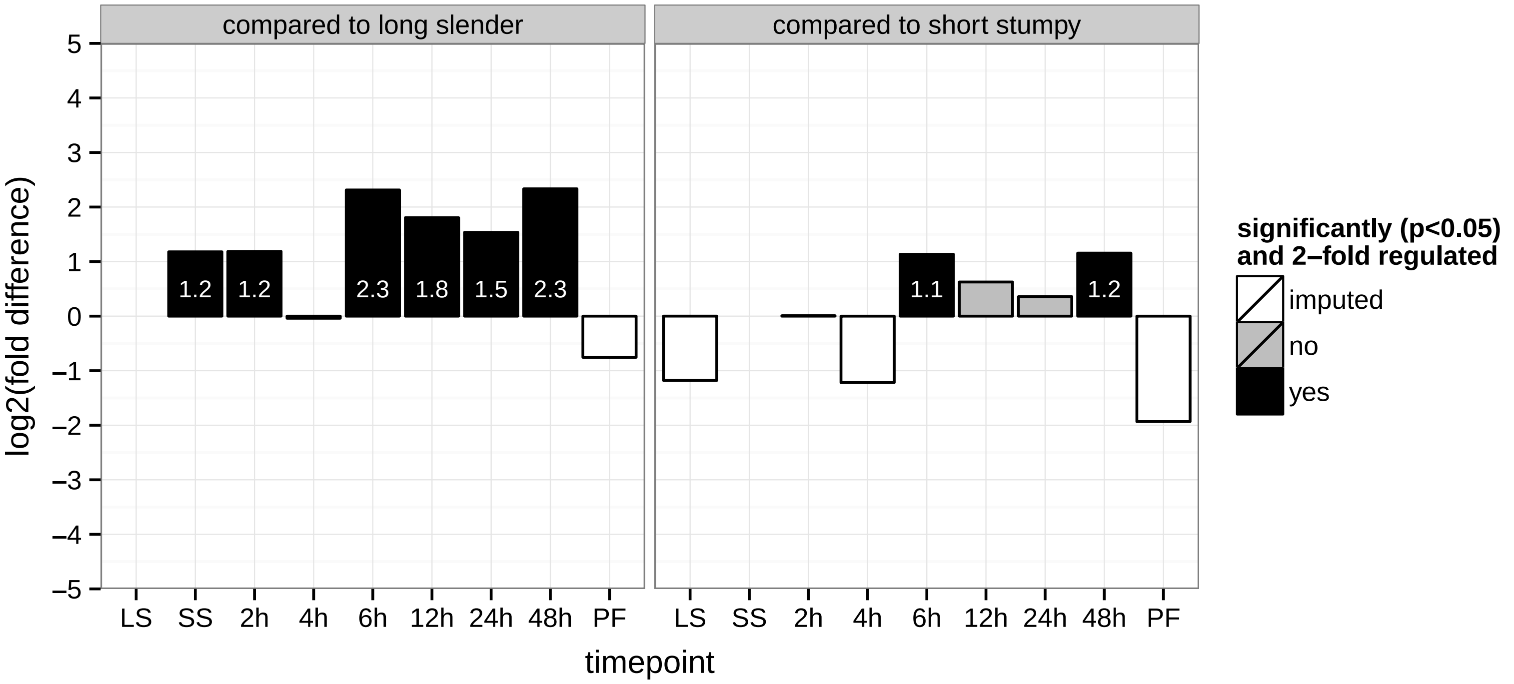
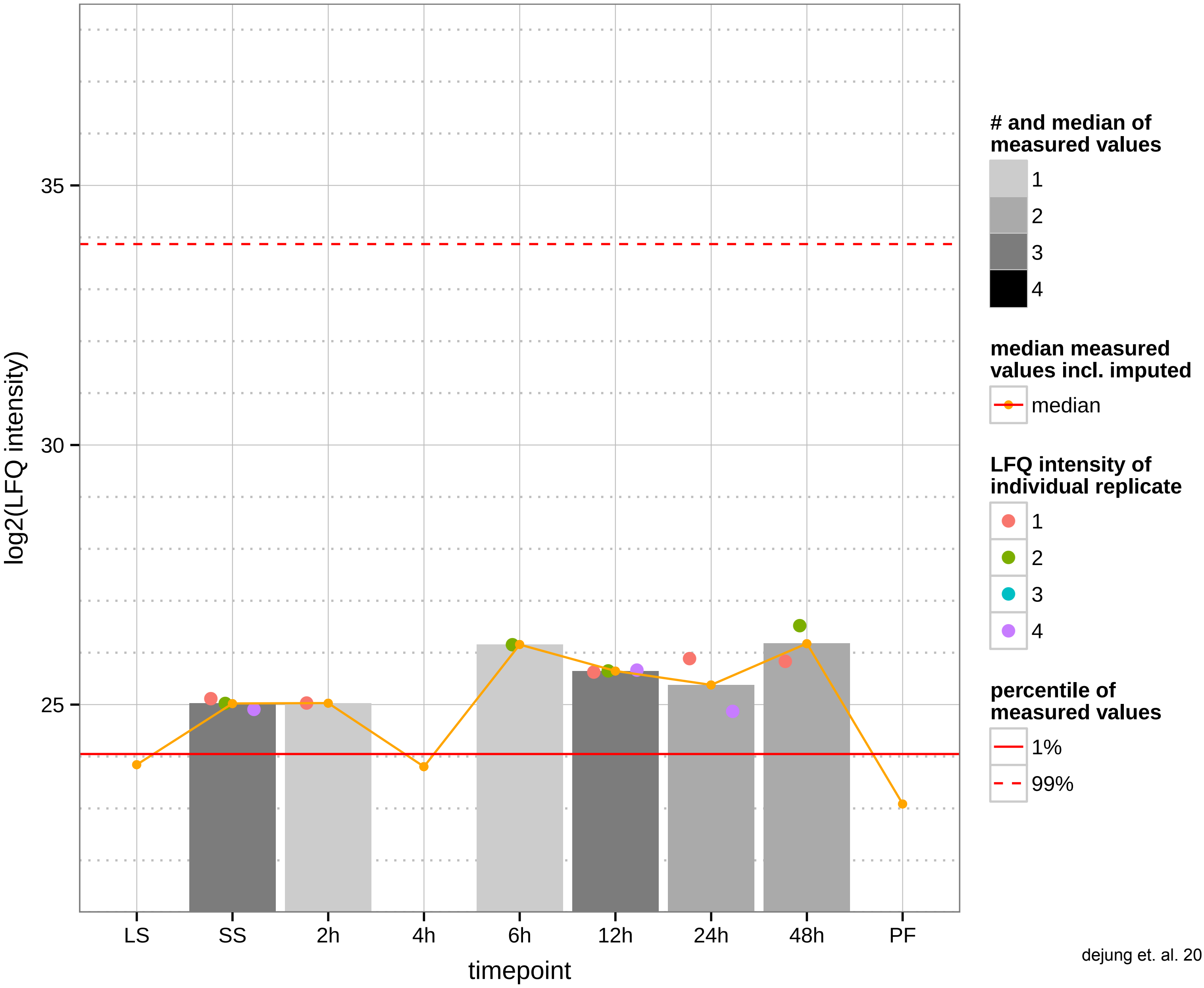
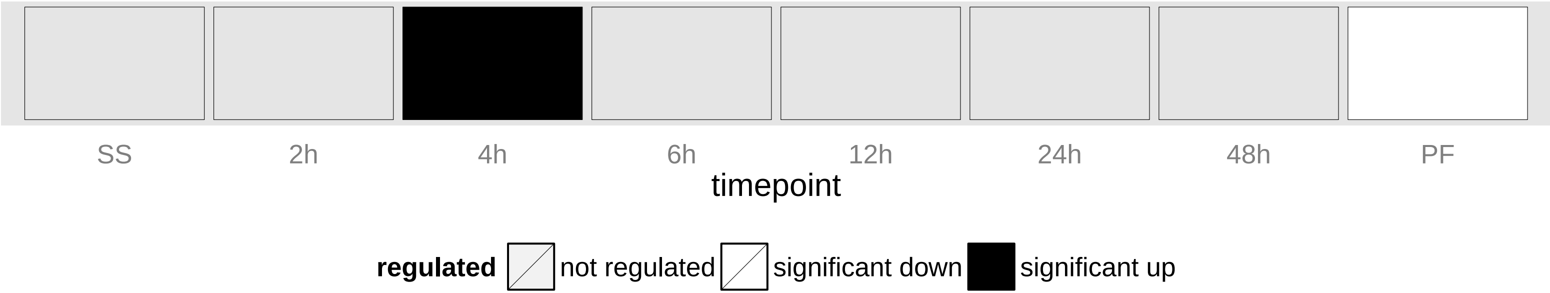
hypothetical protein, conserved
Tb927.11.11170
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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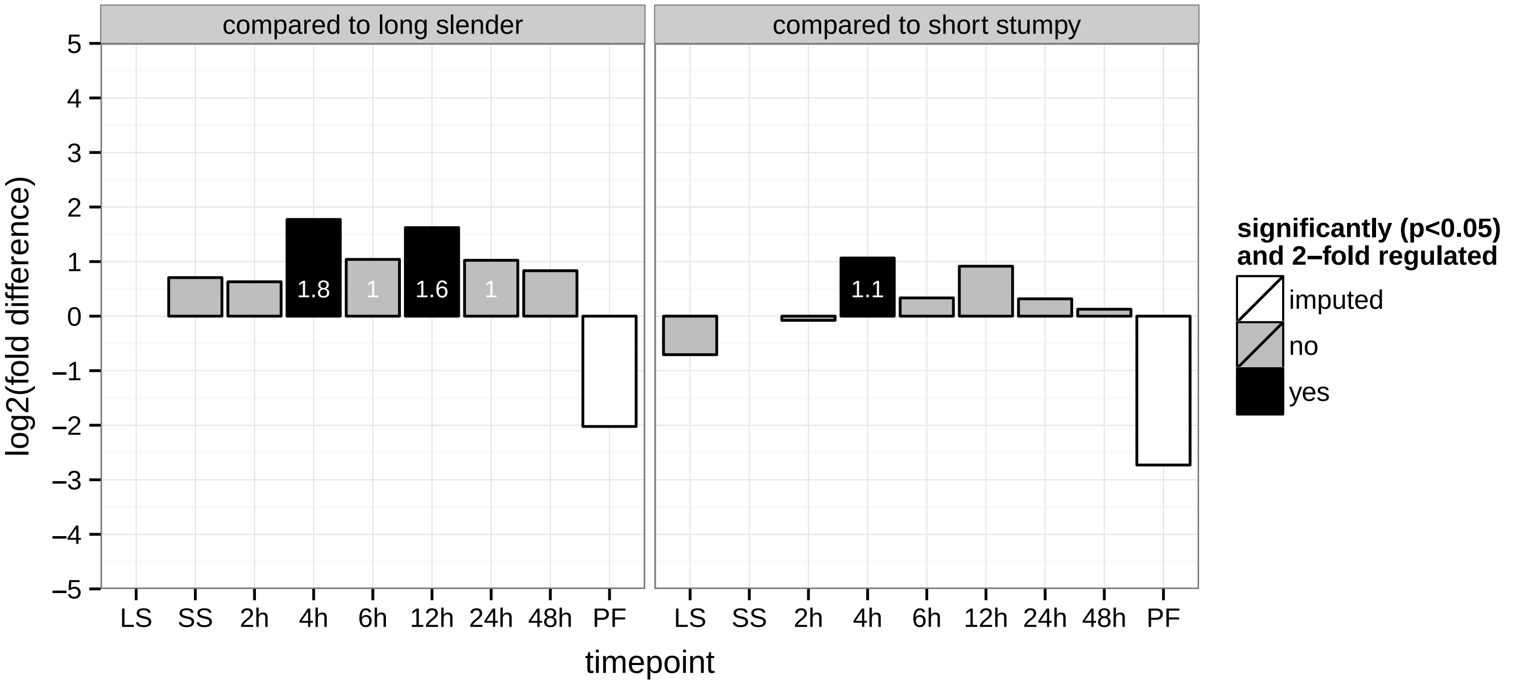
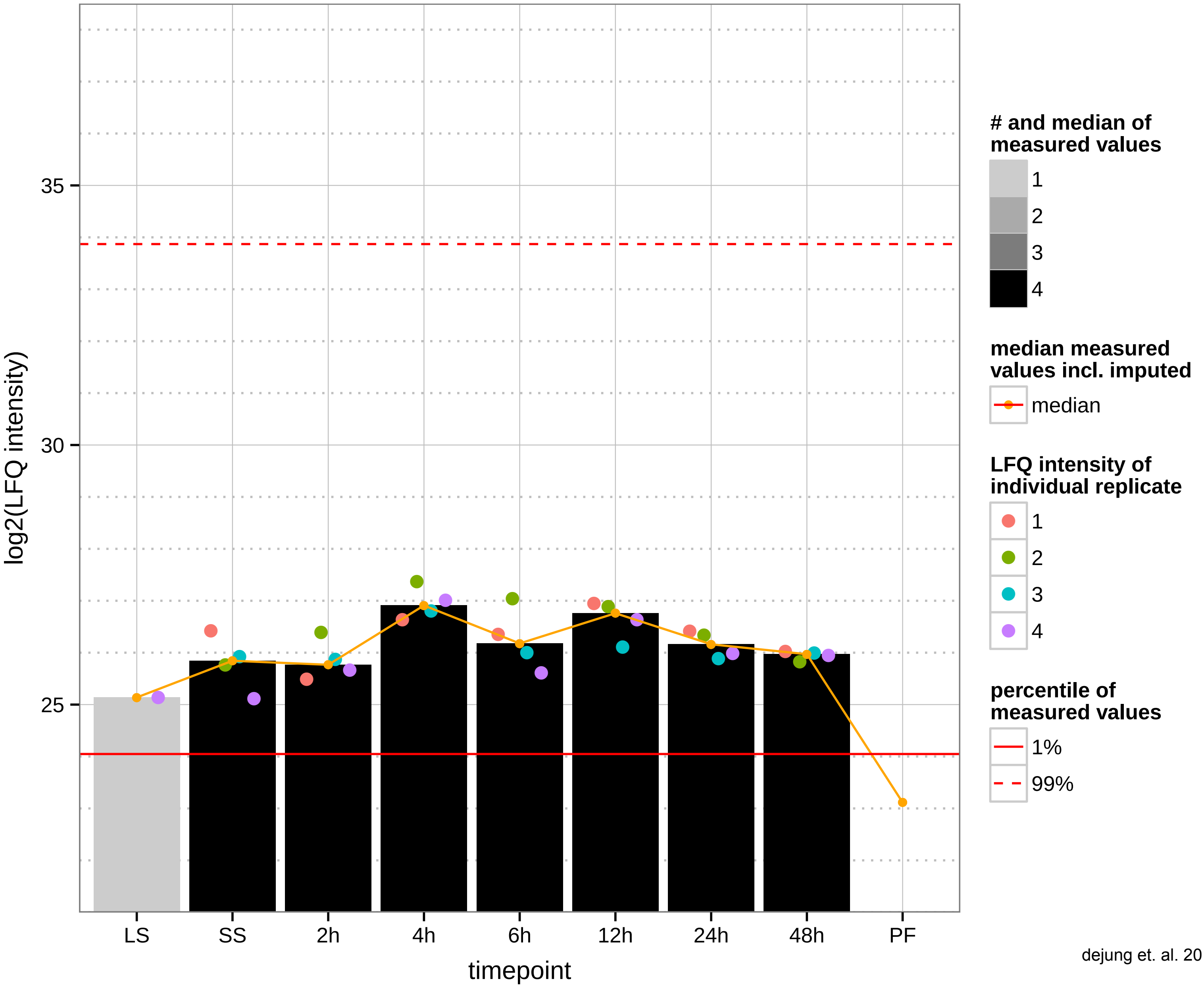
SKP1–like protein
Tb927.10.11610
AGOF: null
AGOC: null
AGOP: ubiquitin–dependent protein catabolic process
PGOF: null
PGOC: null
PGOP: ubiquitin–dependent protein catabolic process





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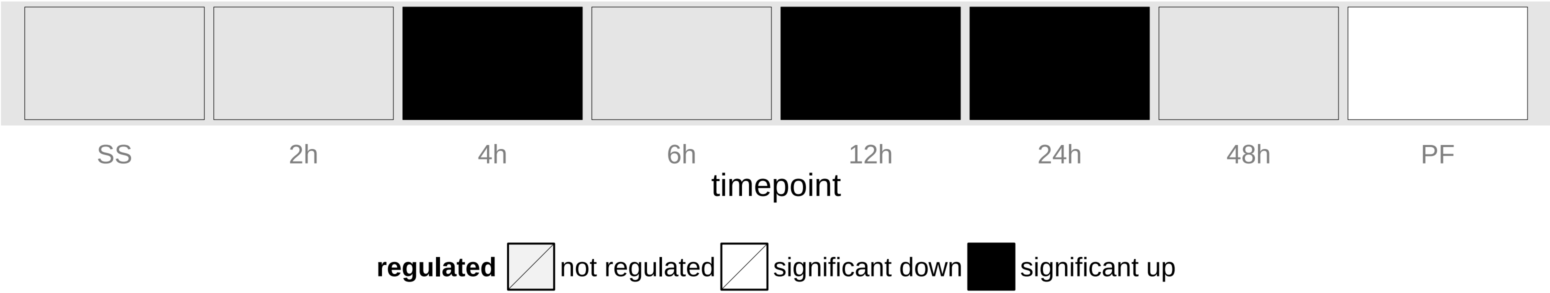

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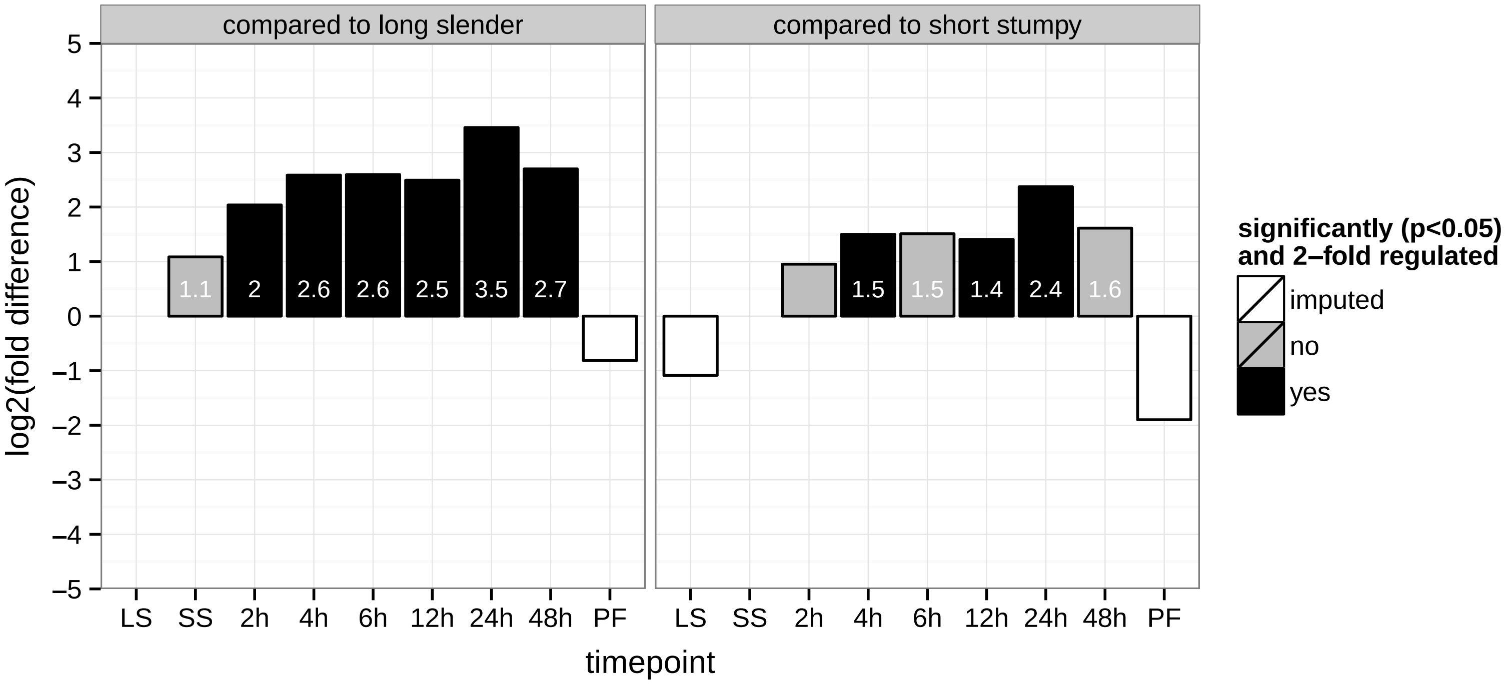
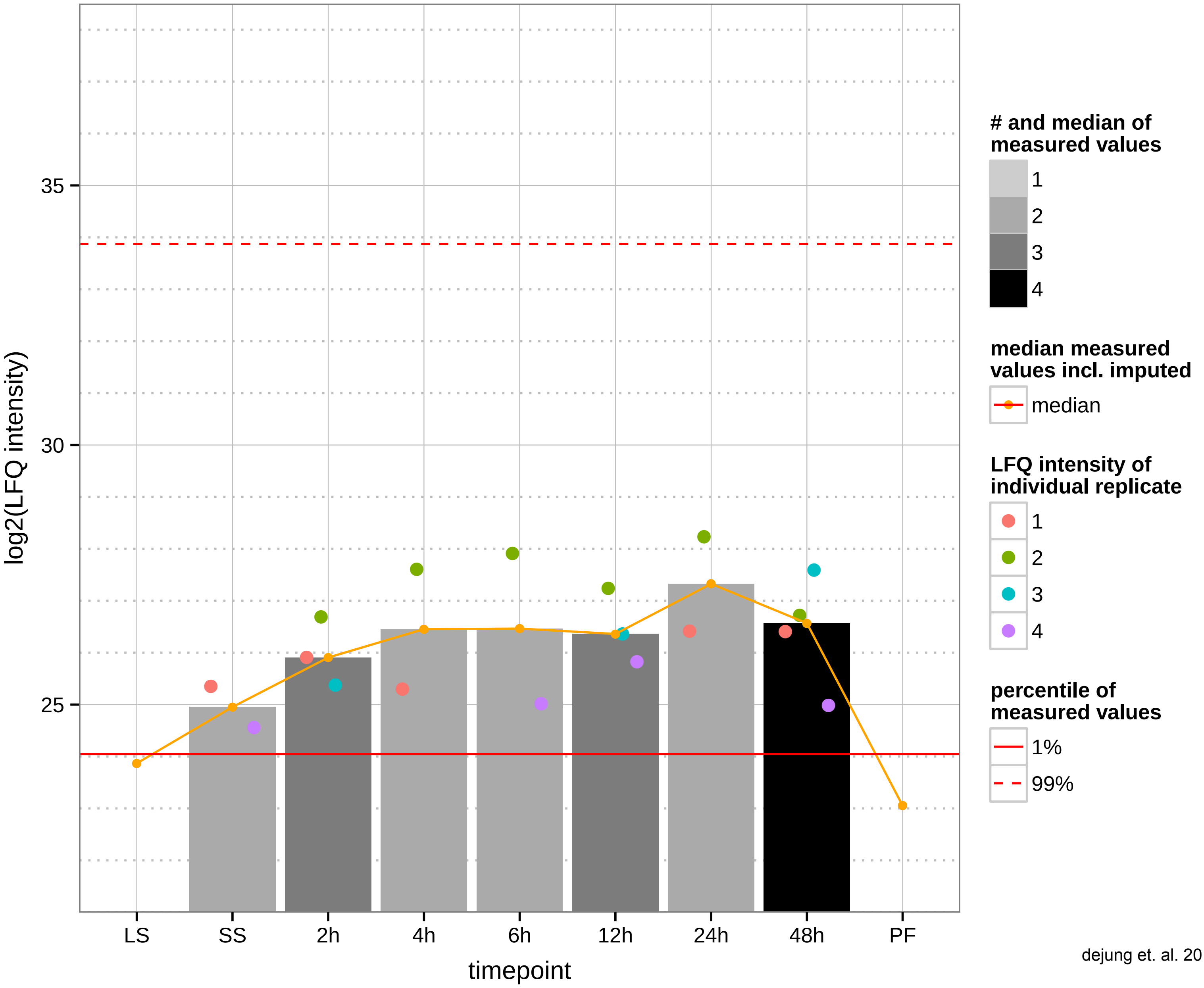
prefoldin subunit, putative
Tb927.5.580
AGOF: unfolded protein binding
AGOC: prefoldin complex
AGOP: protein folding
PGOF: unfolded protein binding
PGOC: prefoldin complex
PGOP: protein folding





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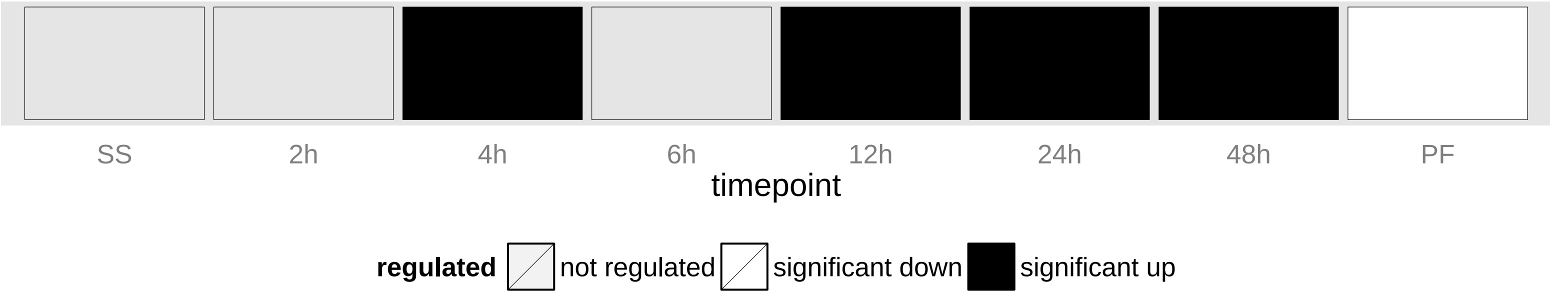
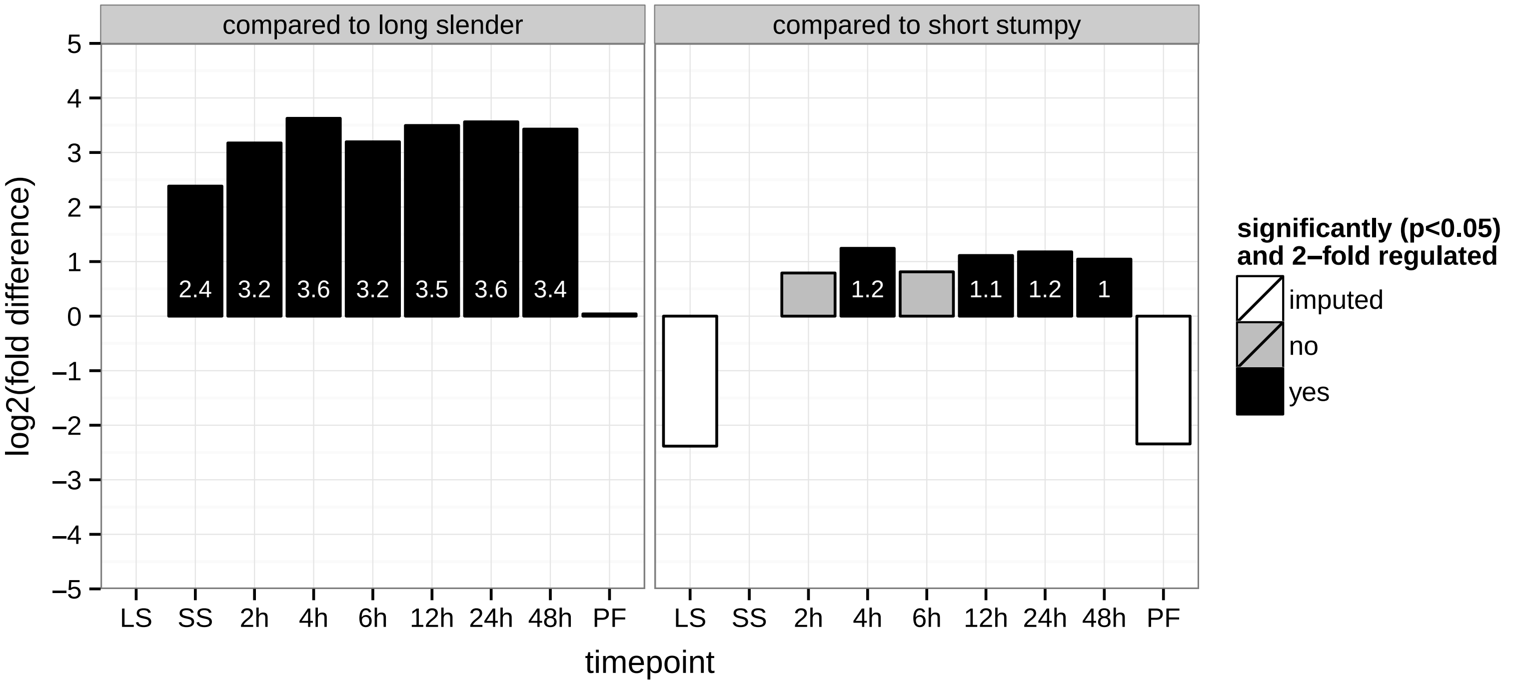
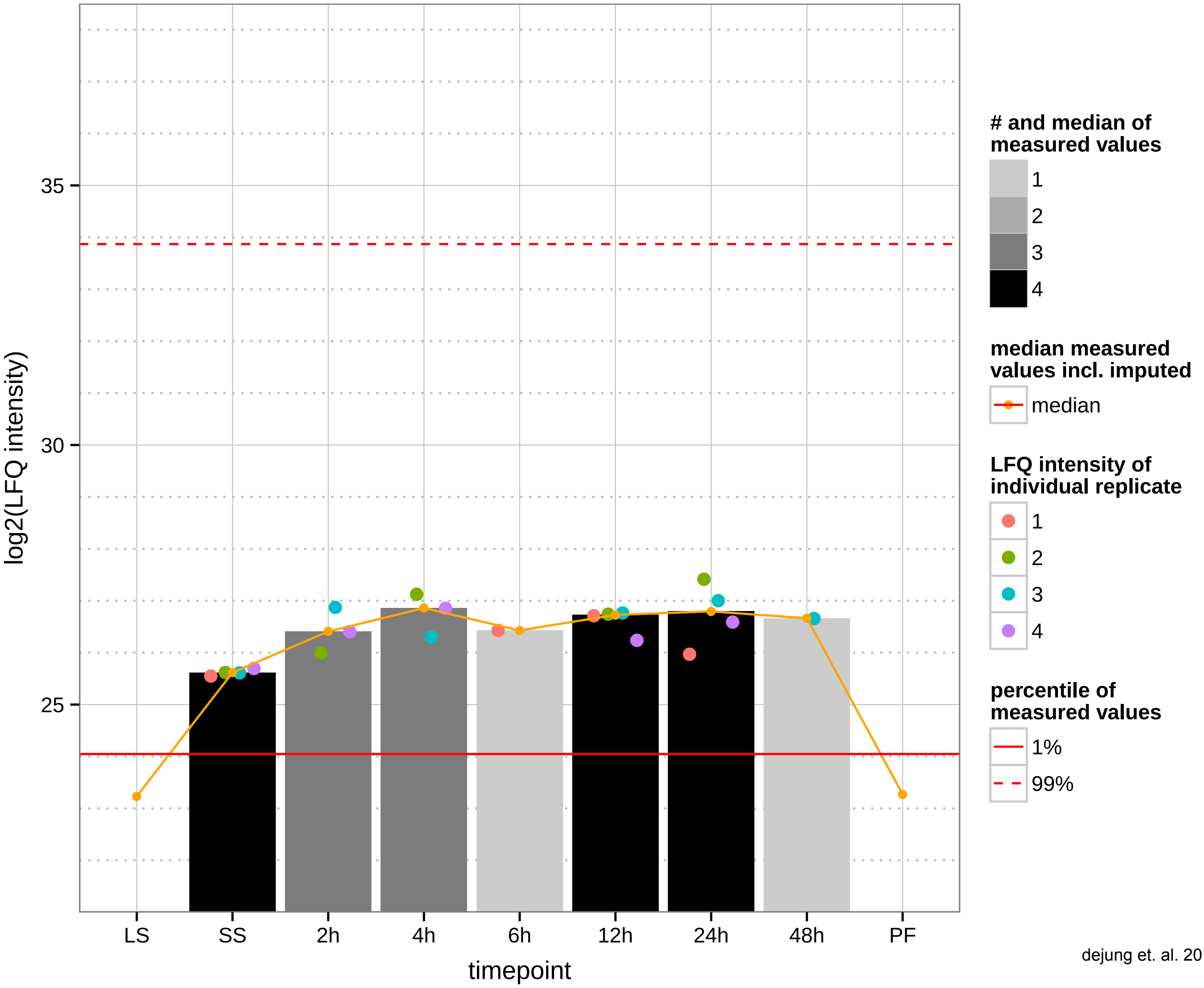


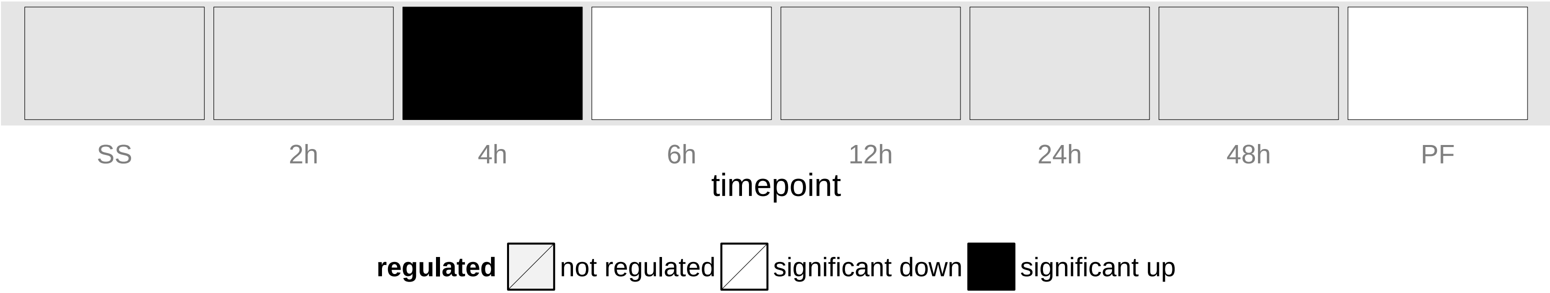
dejung et. al. 2015

hypothetical protein, conserved
Tb927.2.4445
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null



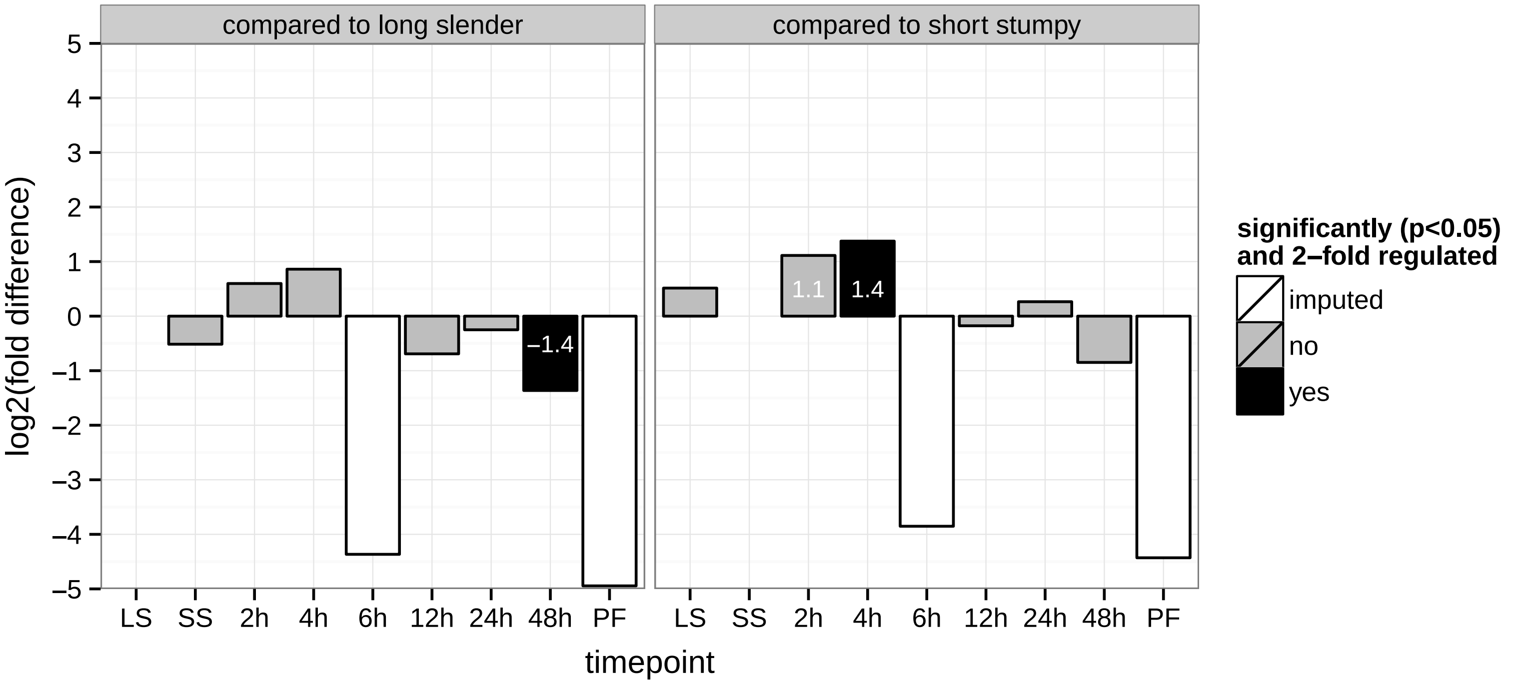


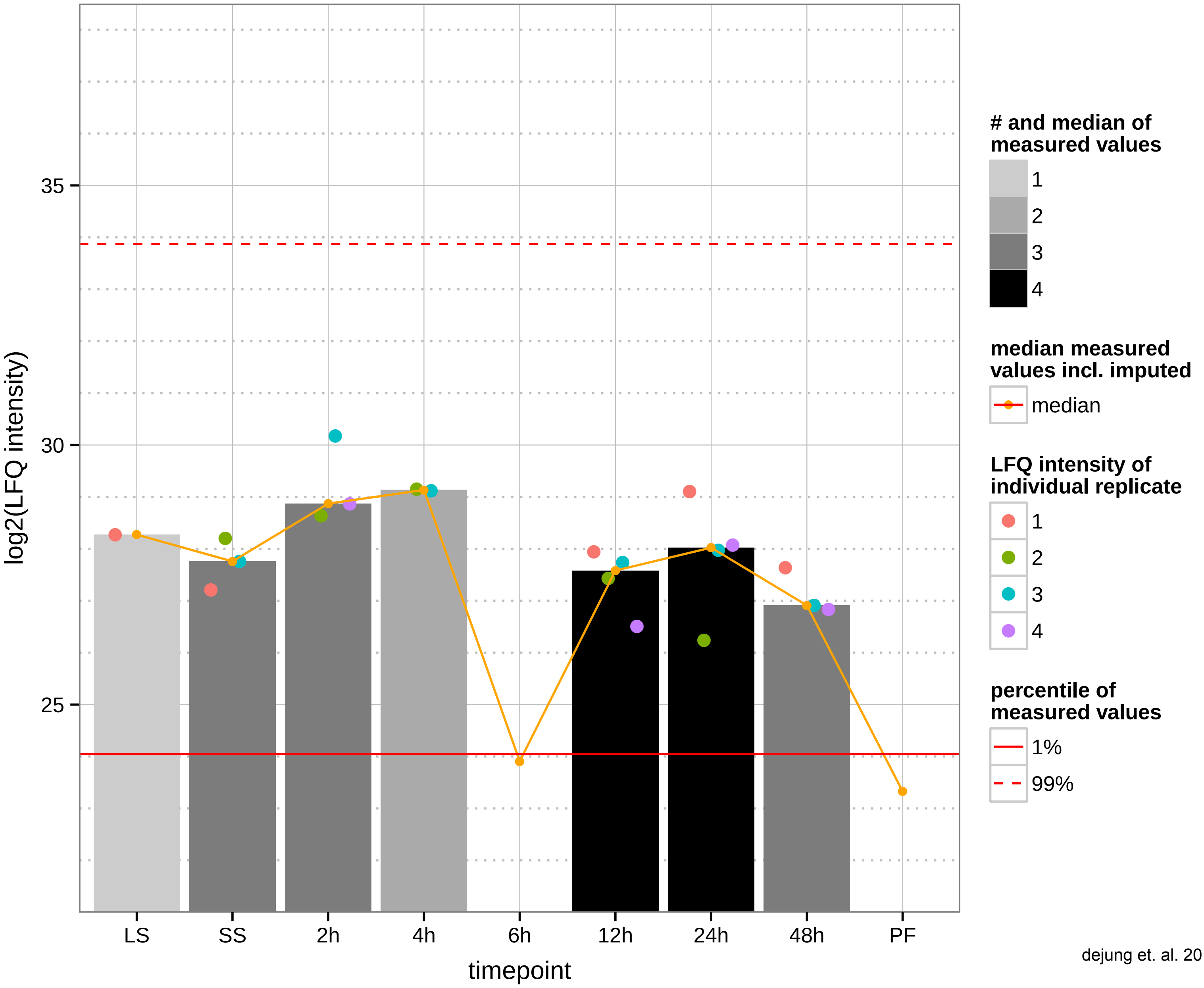
dejung et. al. 2015



dejung et. al. 2015

hypothetical protein, conserved
Tb927.5.3950
AGOF: L−ascorbic acid binding, iron ion binding, oxidoreductase activity, acting on paired donors, with incorporation or reduct
AGOC: null
AGOP: oxidation−reduction process
PGOF: L−ascorbic acid binding, iron ion binding, oxidoreductase activity, acting on paired donors, with incorporation or reduct
PGOC: null
PGOP: oxidation−reduction process





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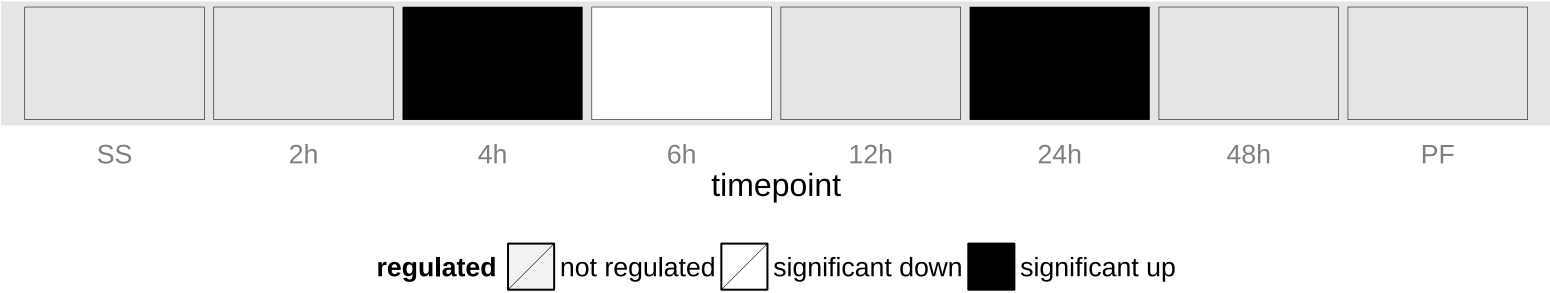

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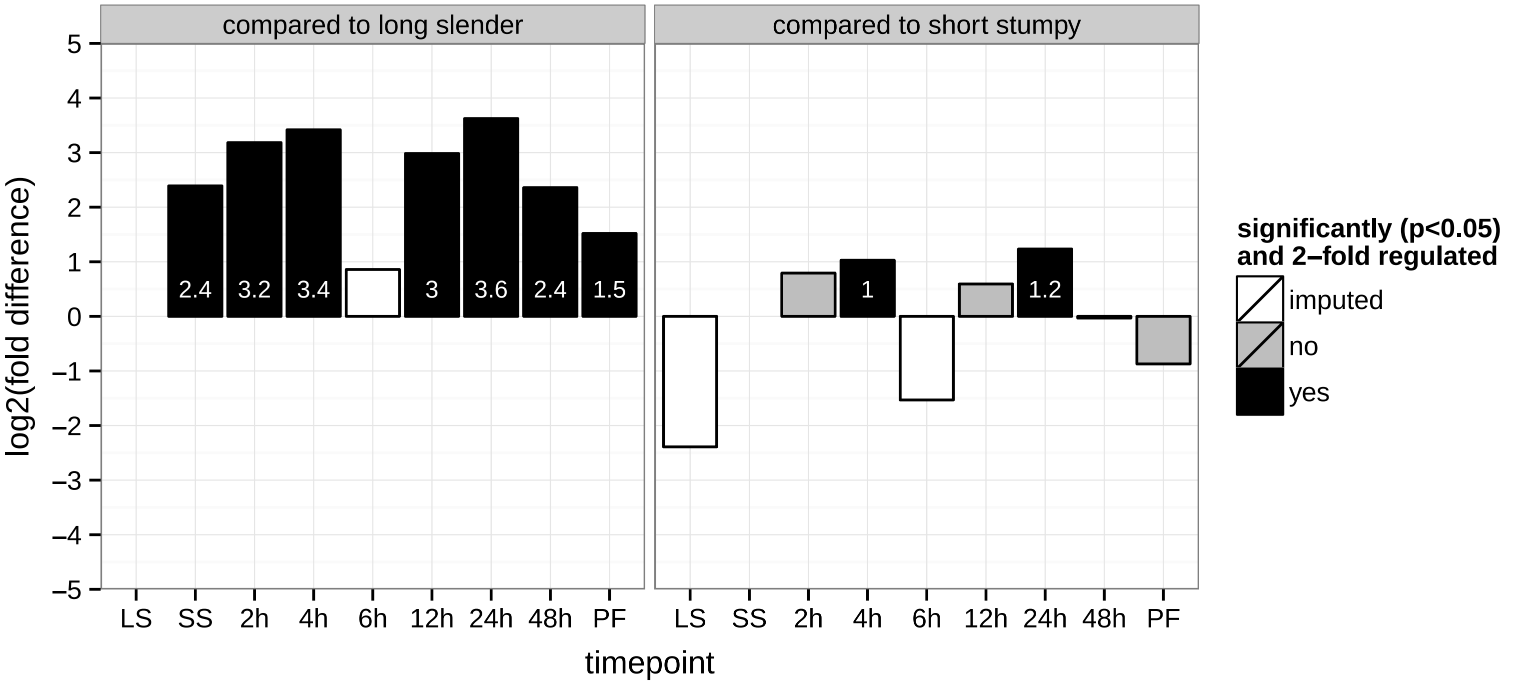
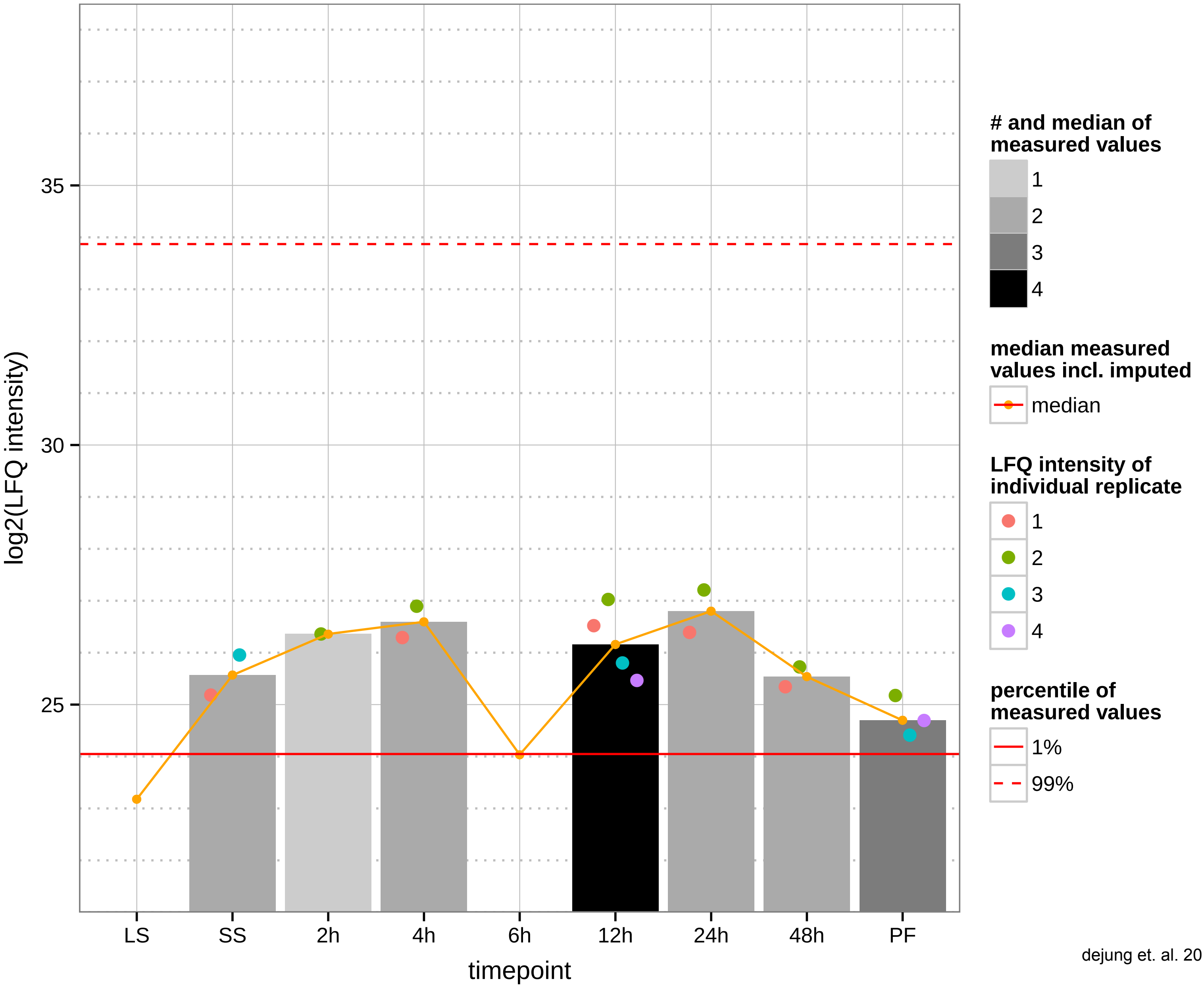
hypothetical protein, conserved
Tb927.10.2340
AGOF: null
AGOC: null
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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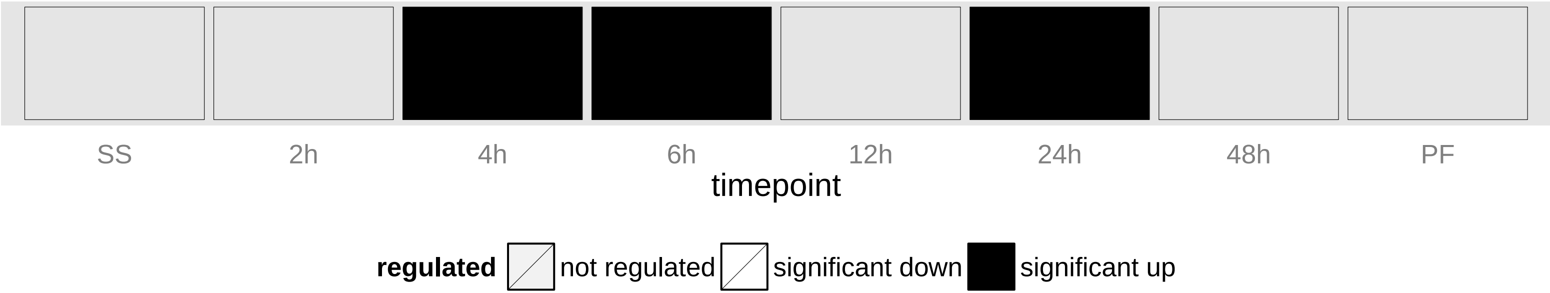

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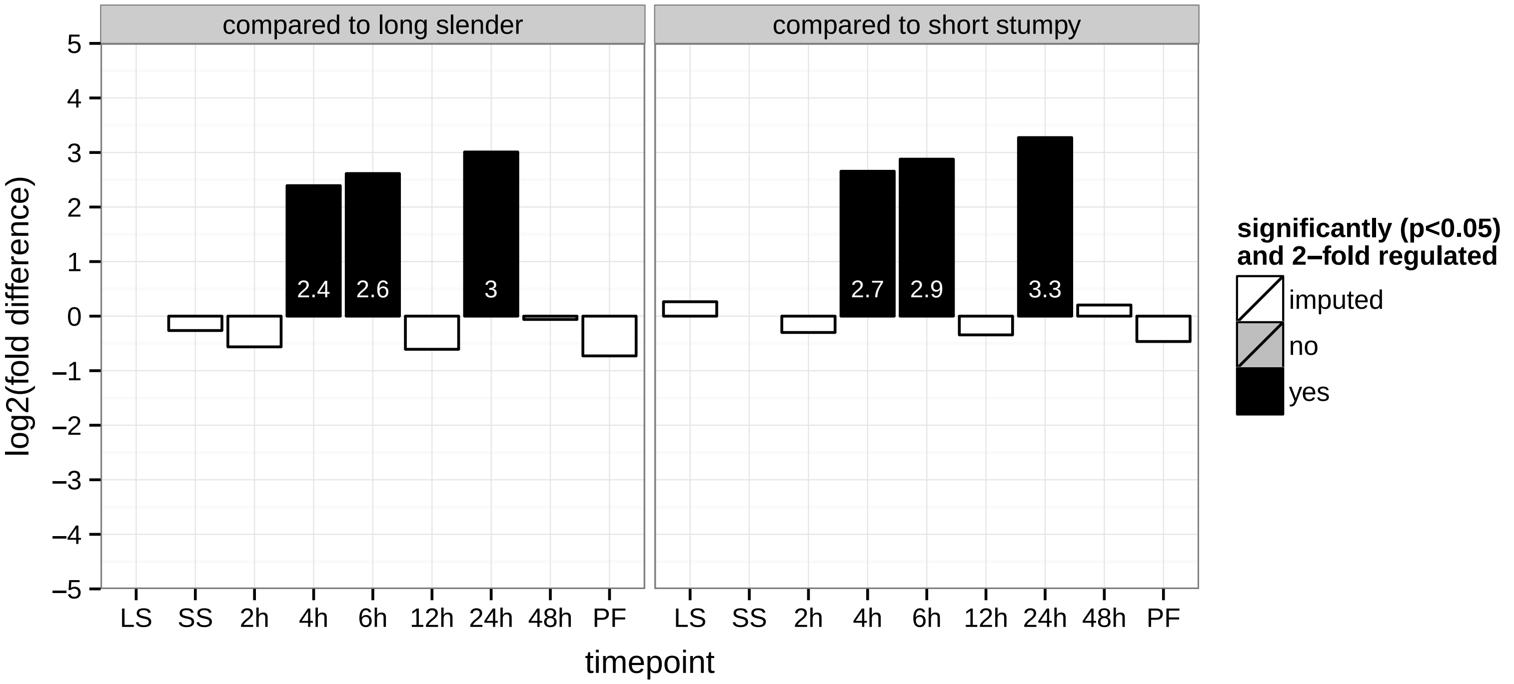
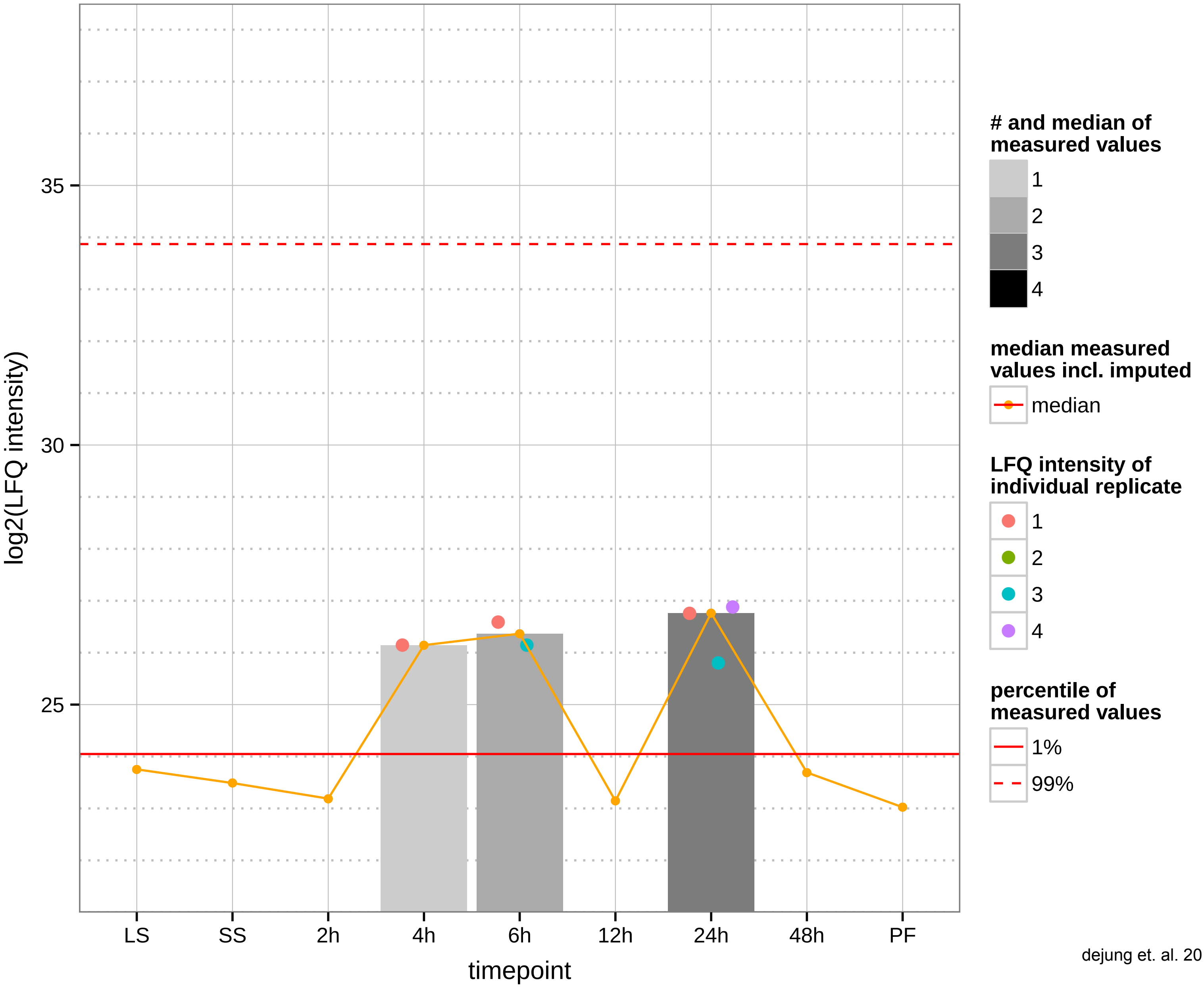
hypothetical protein, conserved
Tb927.9.8290
AGOF: structural constituent of ribosome
AGOC: mitochondrion, ribosome
AGOP: translation
PGOF: null
PGOC: null
PGOP: null





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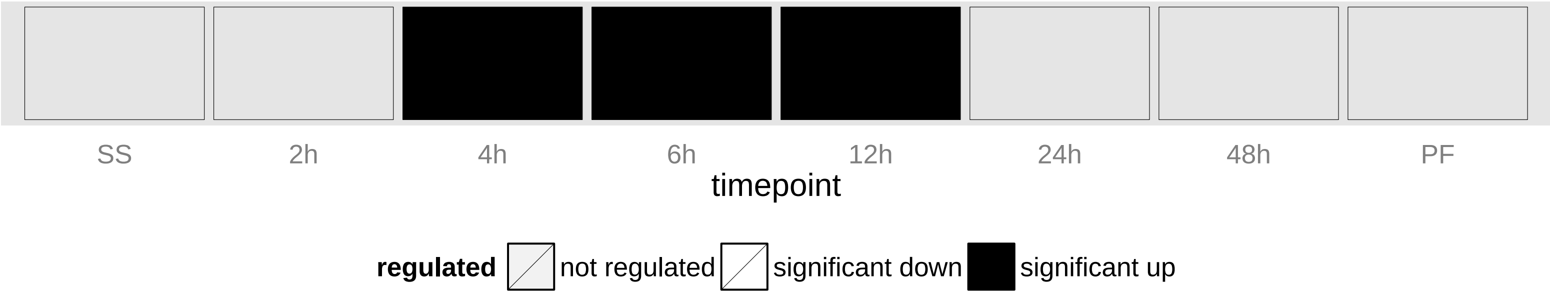

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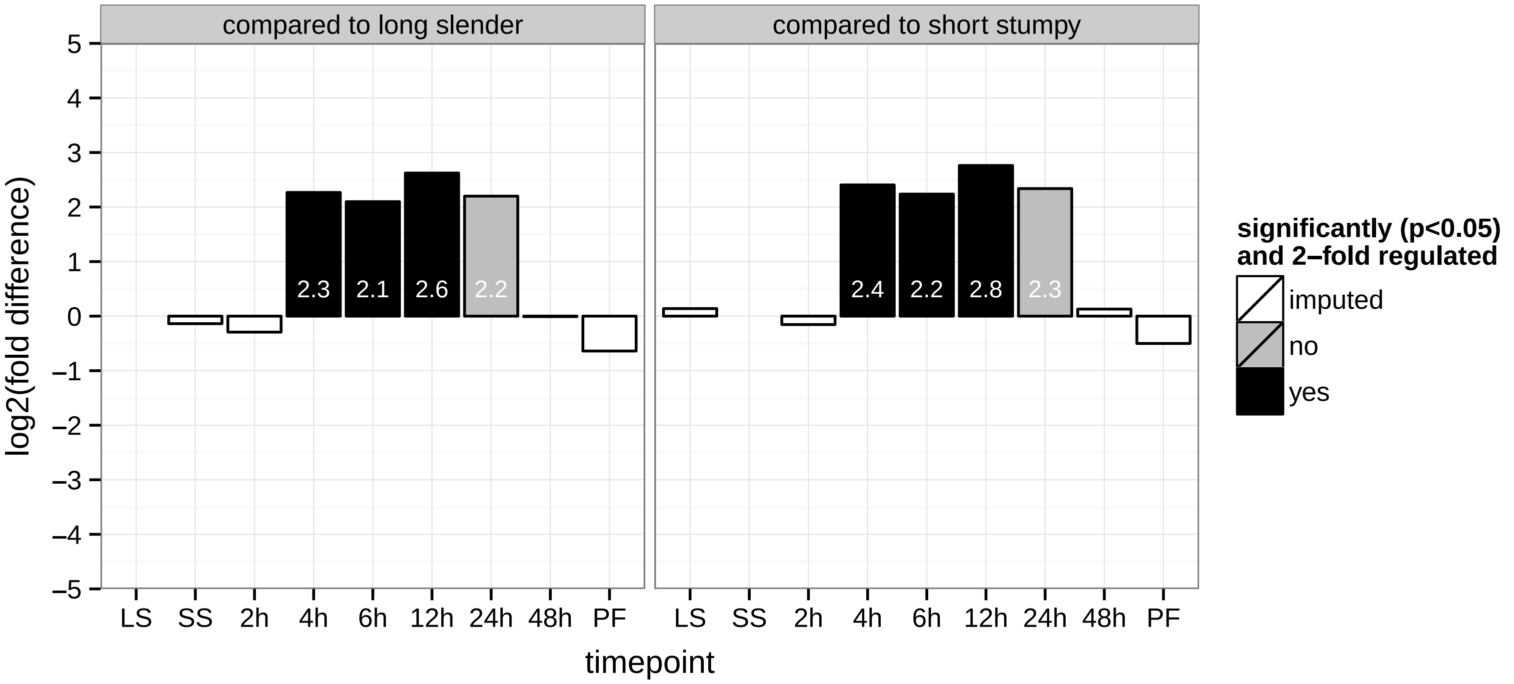
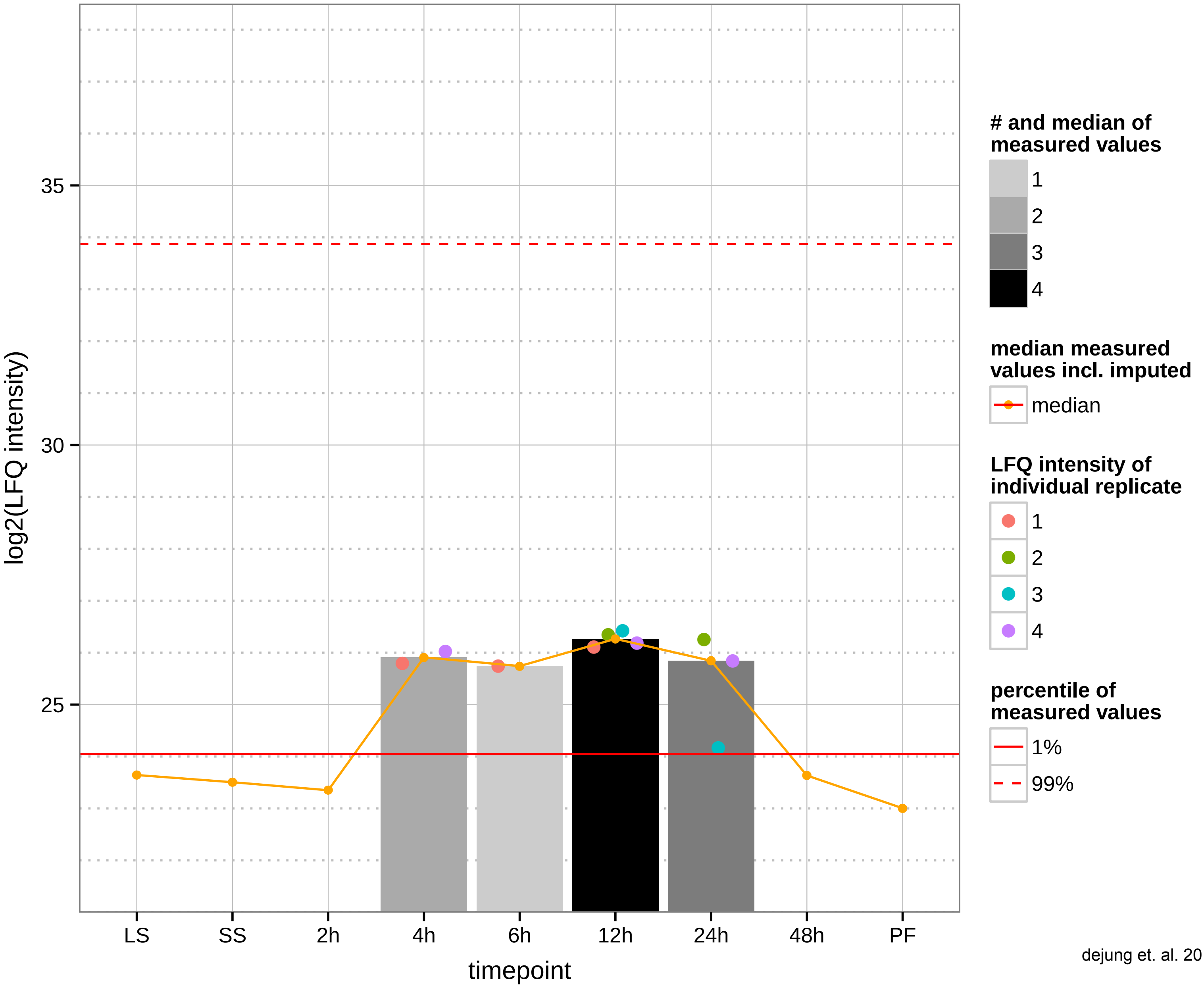
ubiquitin−conjugating enzyme E2, putative, ubiquitin carrier protein, ubiquitin−protein ligase
Tb927.4.2710
AGOF: ubiquitin−protein ligase activity
AGOC: null
AGOP: cellular protein modification process, post−translational protein modification, regulation of protein metabolic process
PGOF: acid−amino acid ligase activity
PGOC: null
PGOP: null





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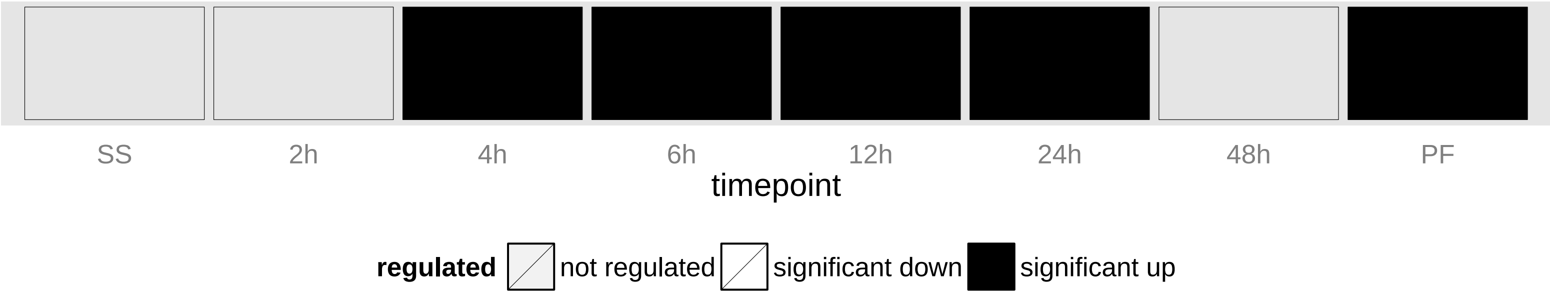

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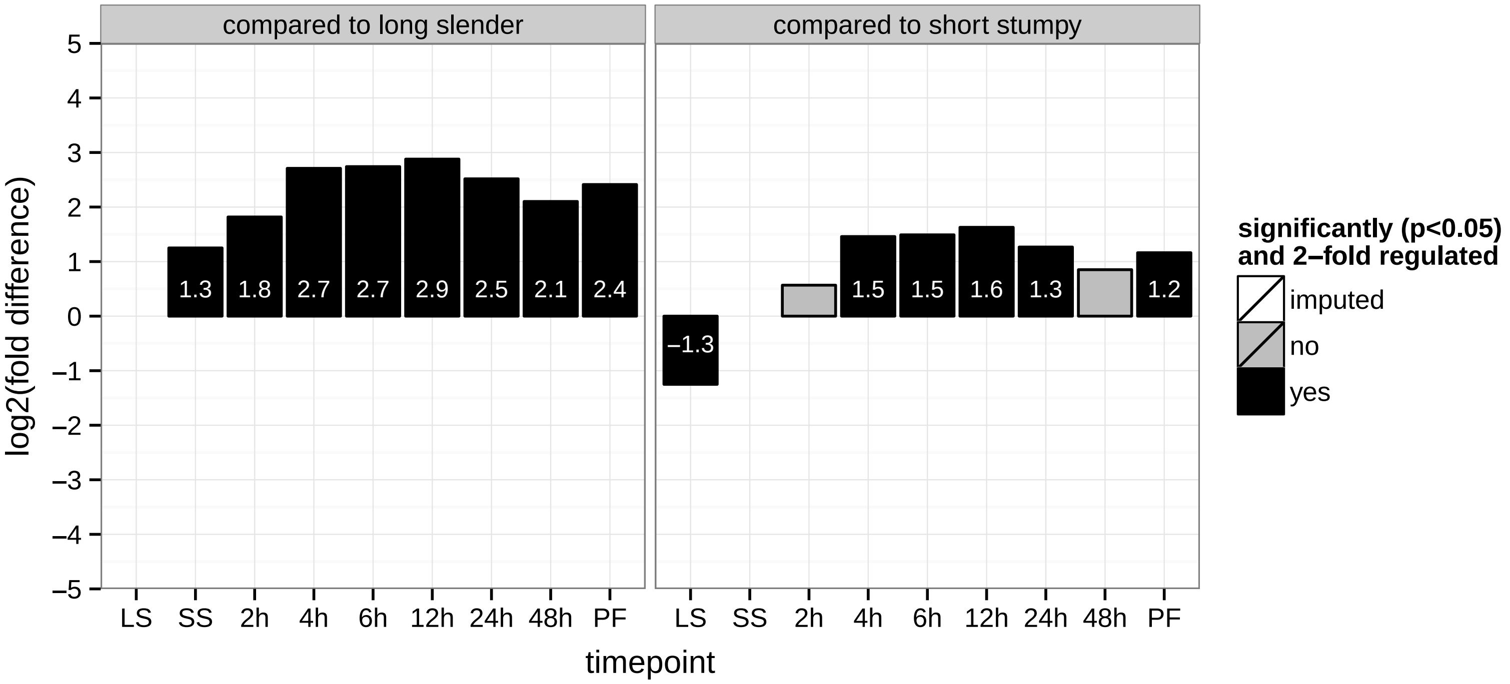
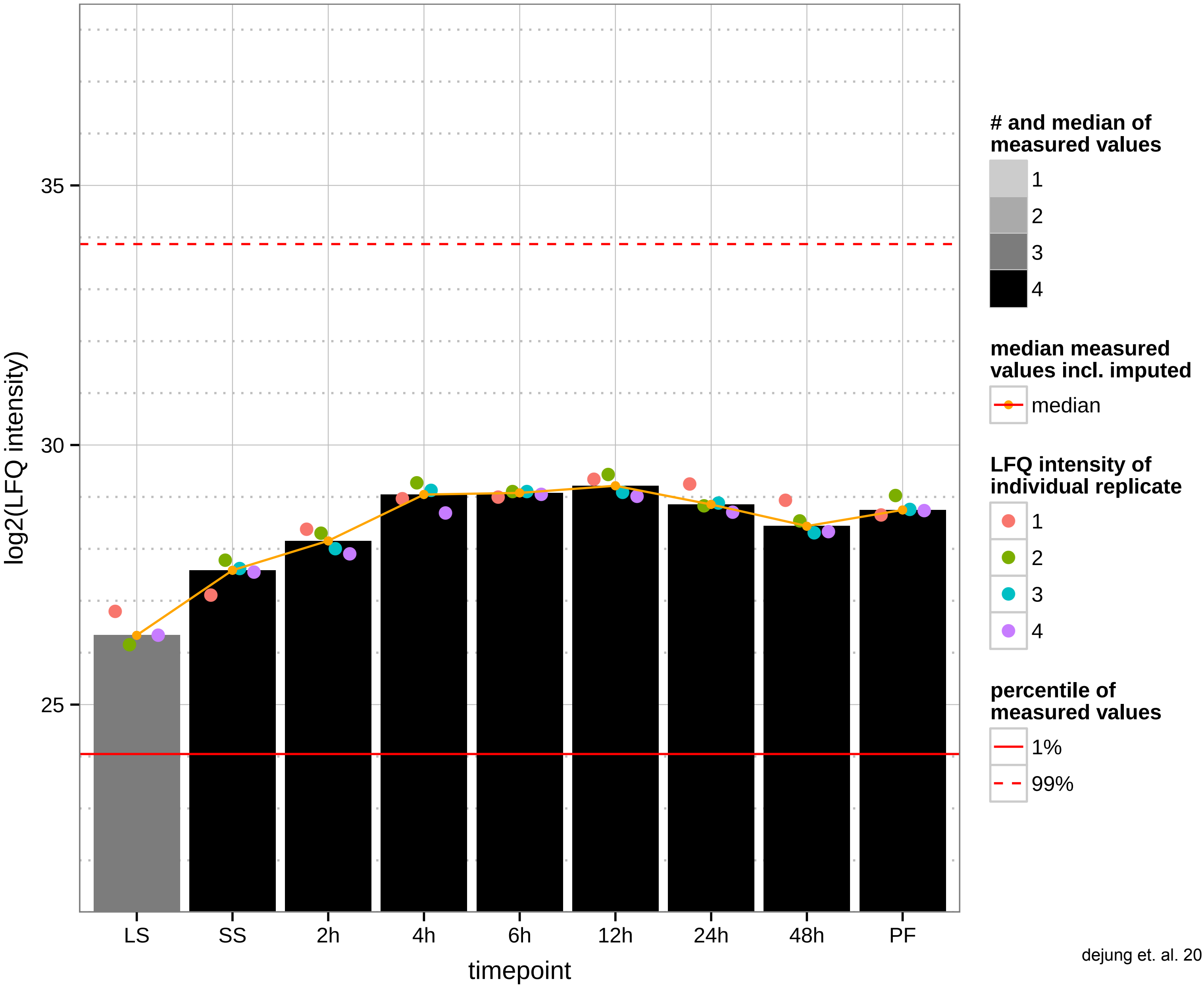
chaperone protein DNAj, putative
Tb927.9.8160
AGOF: heat shock protein binding, unfolded protein binding
AGOC: integral to membrane
AGOP: protein folding
PGOF: heat shock protein binding
PGOC: null
PGOP: null





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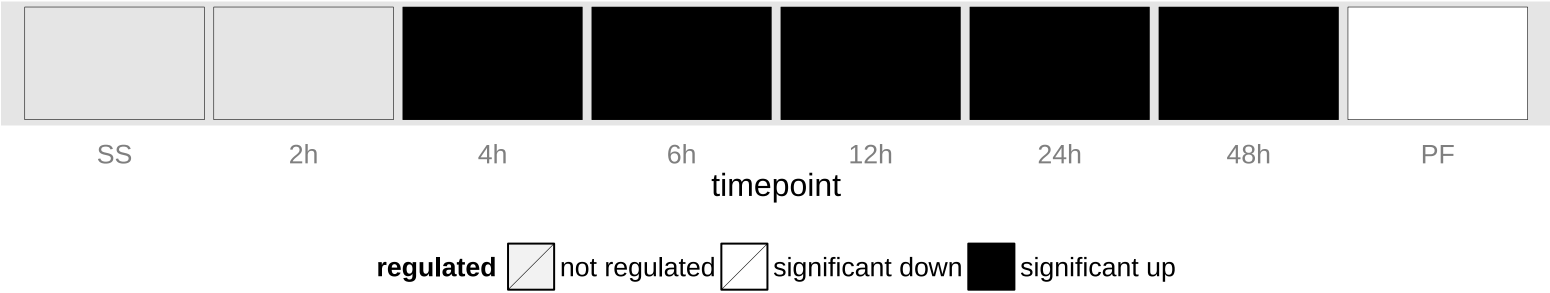

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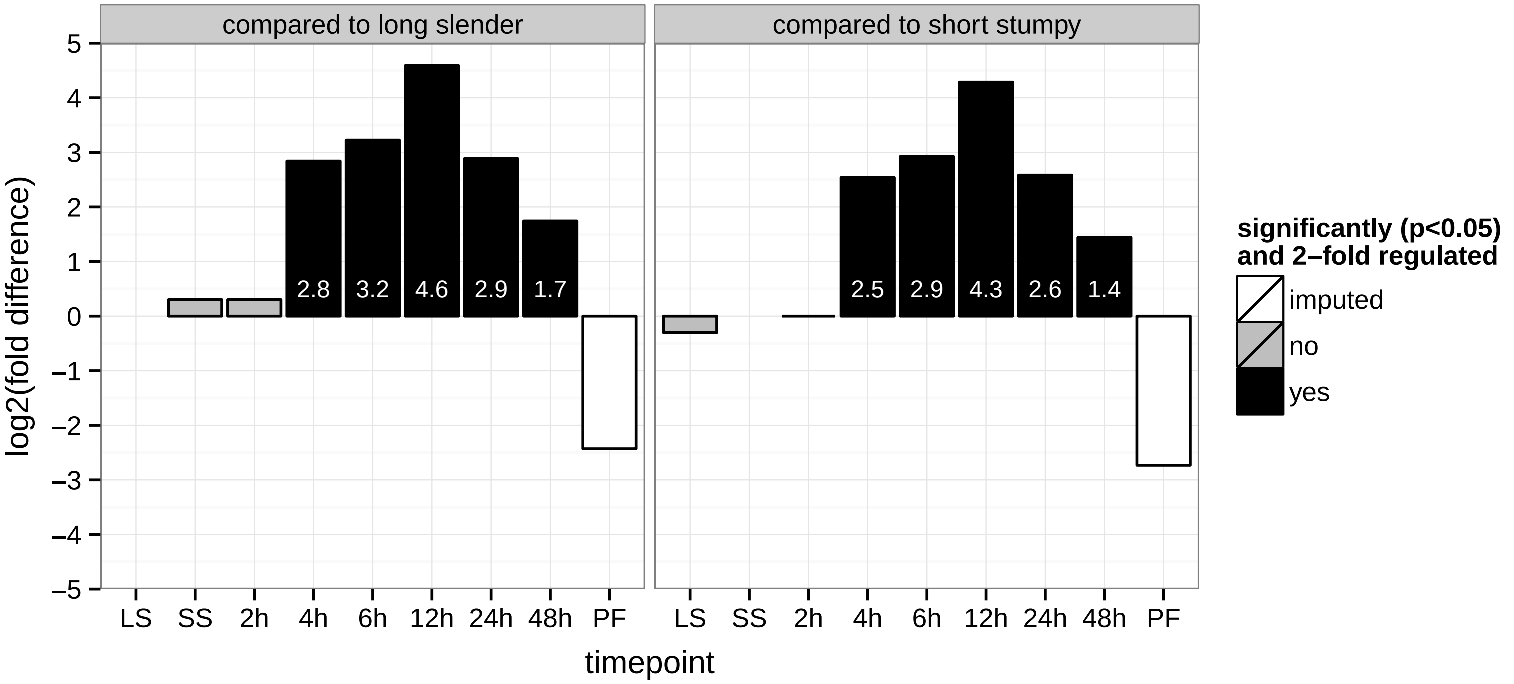
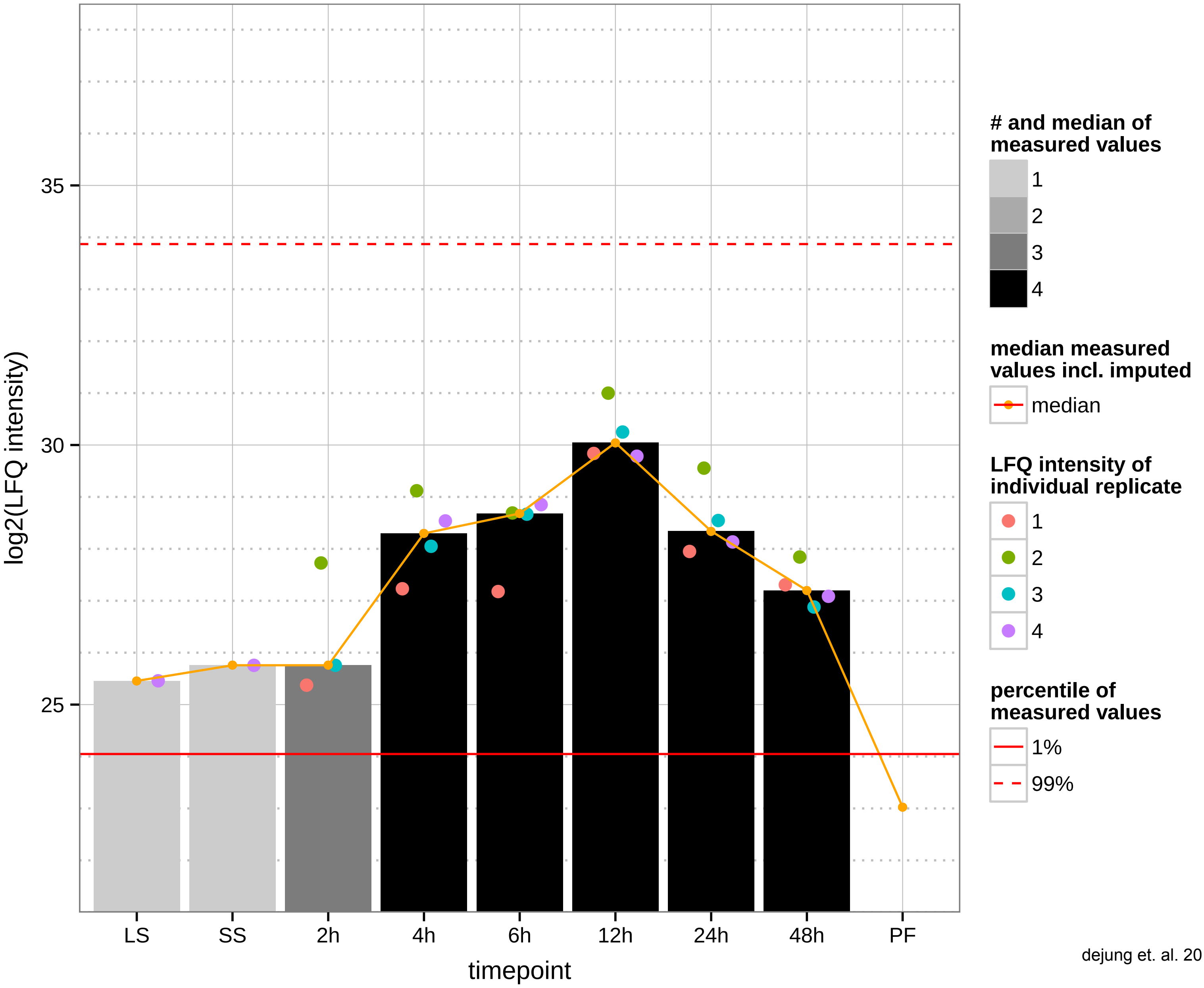
hypothetical protein
Tb927.5.4020
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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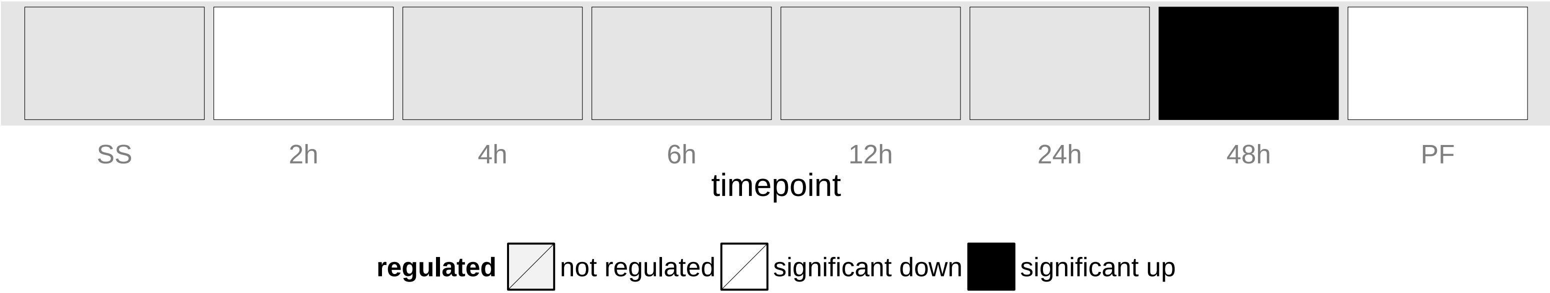

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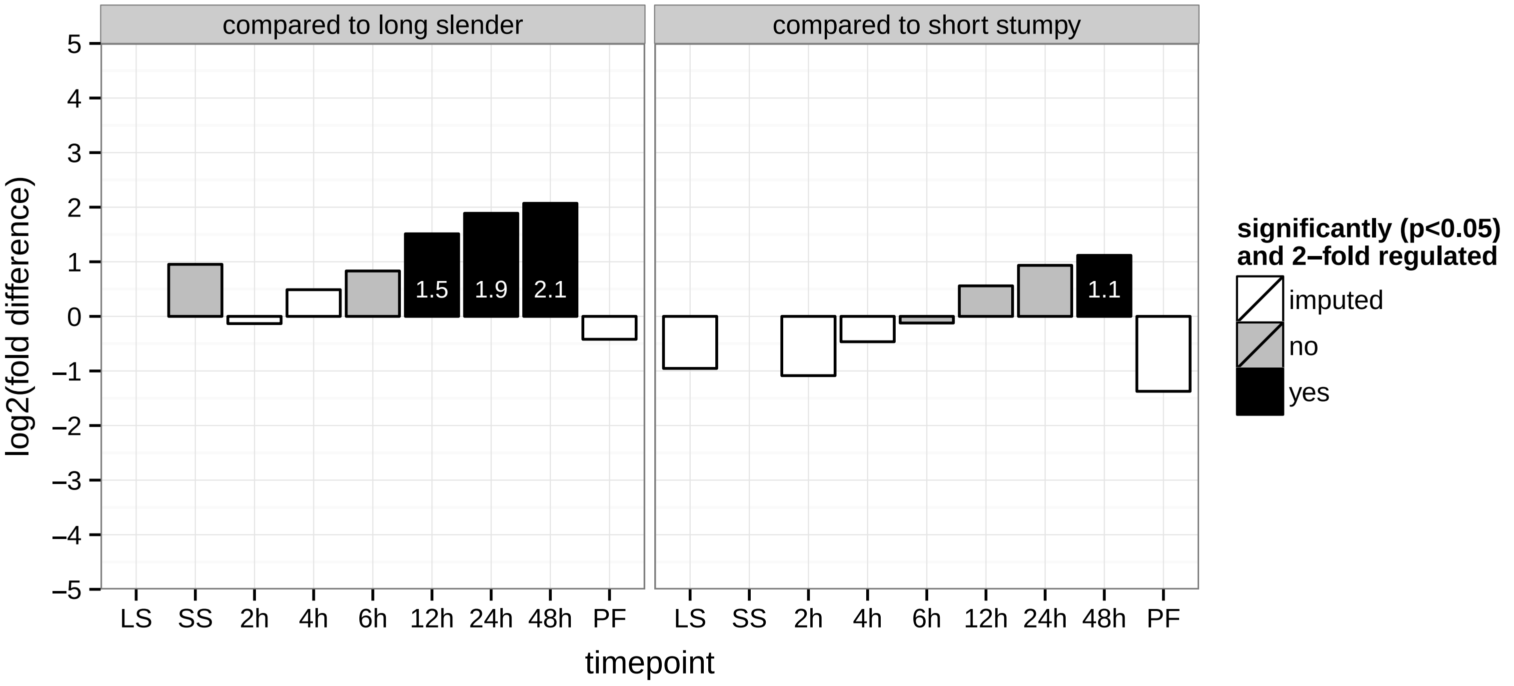
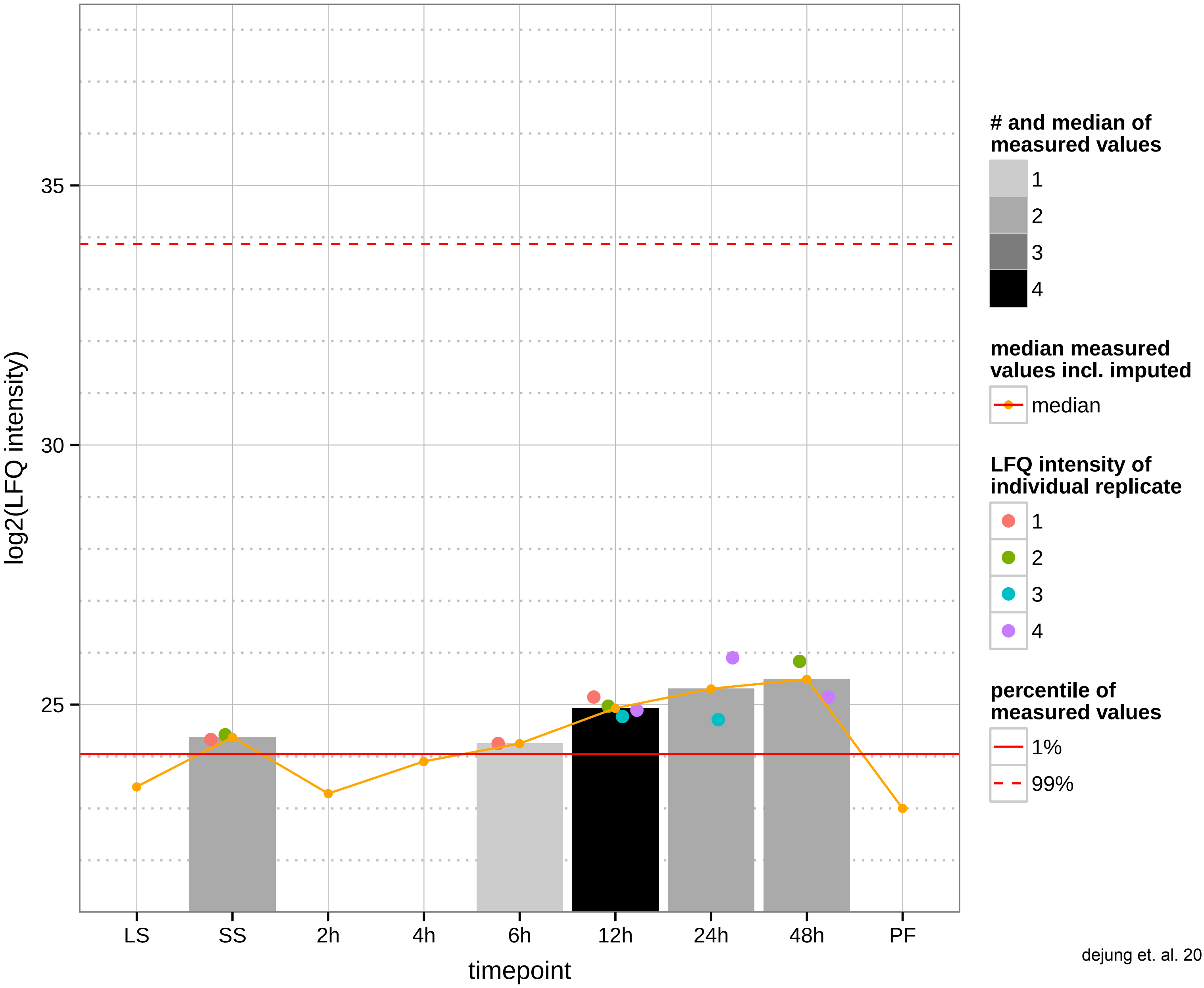
hypothetical protein, conserved
Tb927.8.3980
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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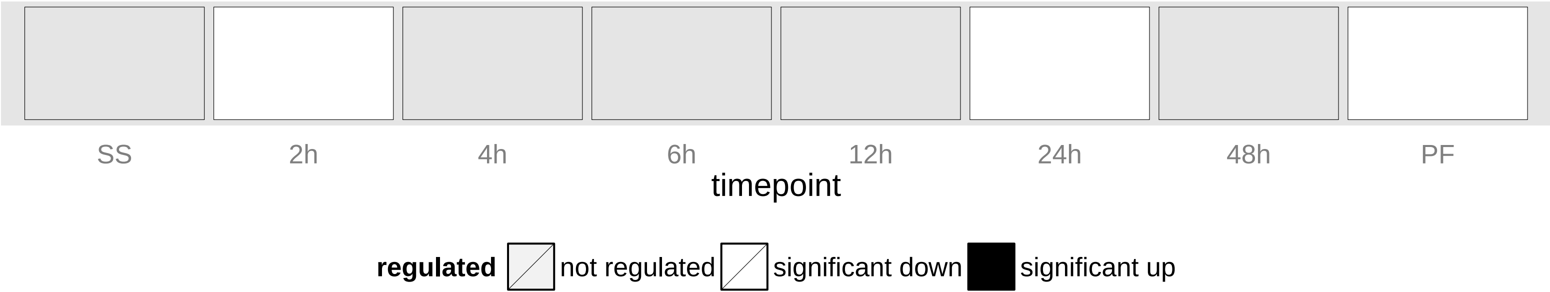

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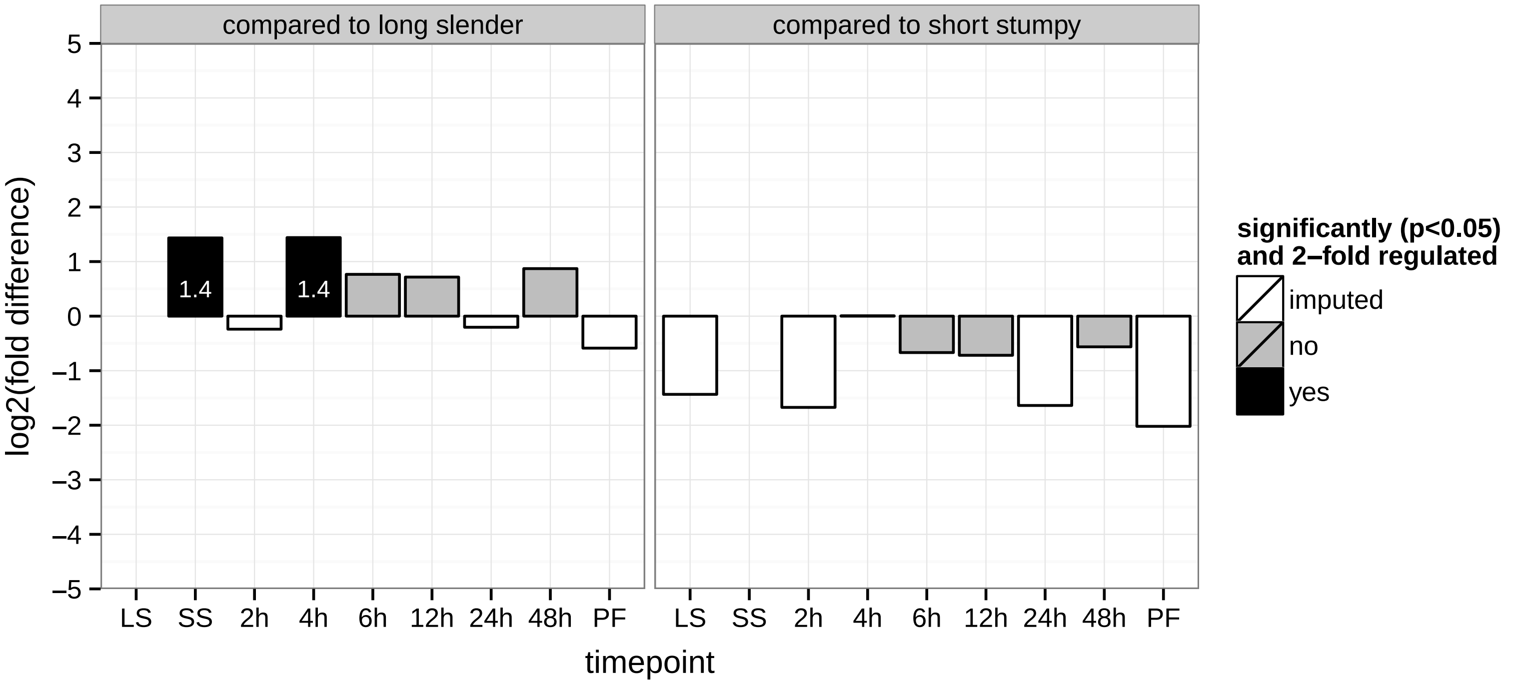
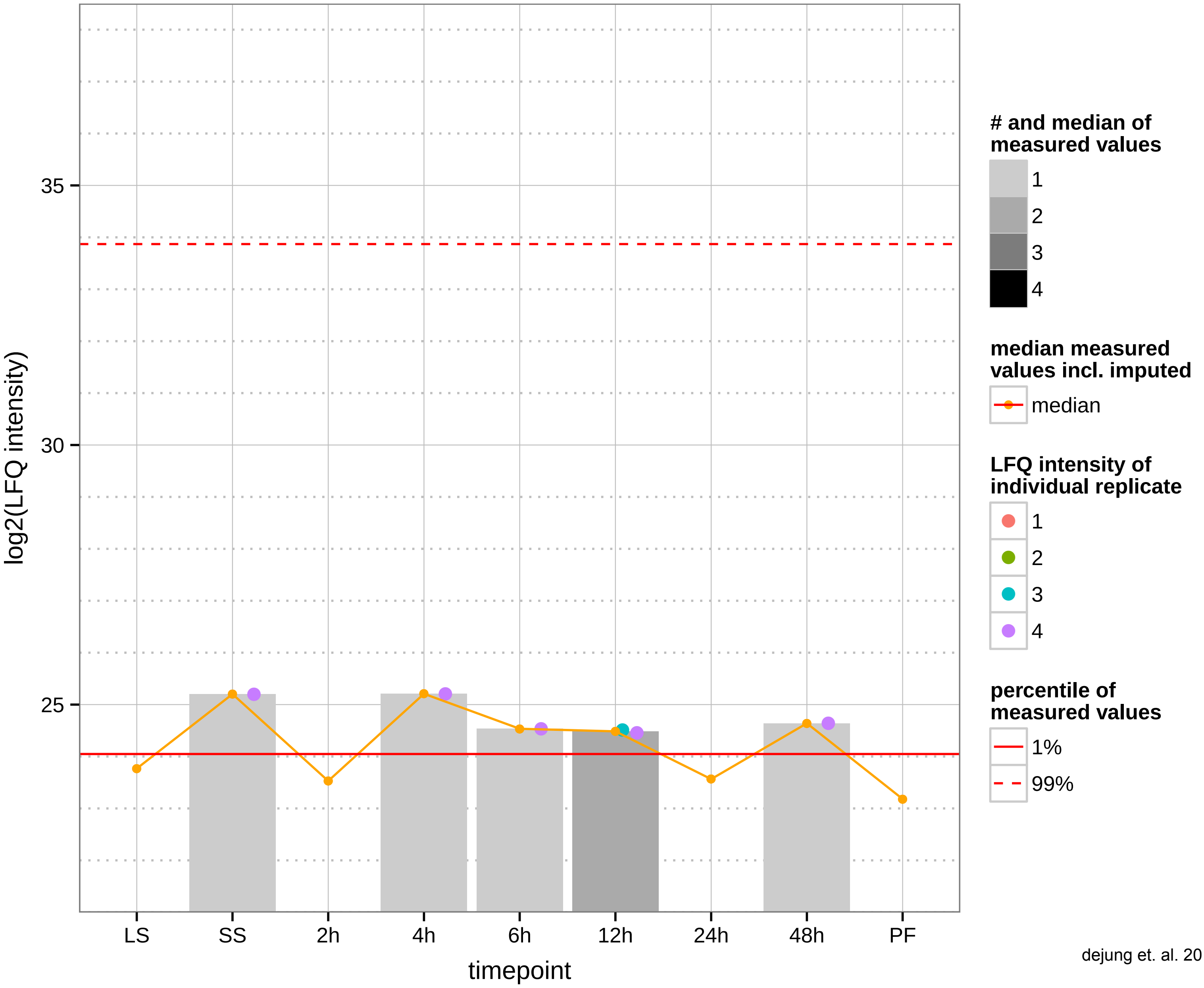
hypothetical protein, conserved, class I transcription factor A, subunit 5a (CITFA–5a)
Tb927.8.4080;Tb927.8.4030;Tb11.v5.0861
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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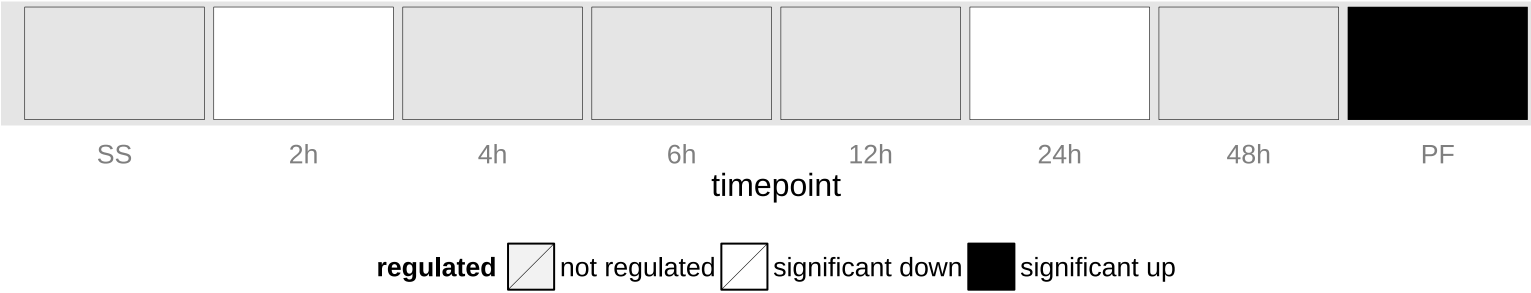

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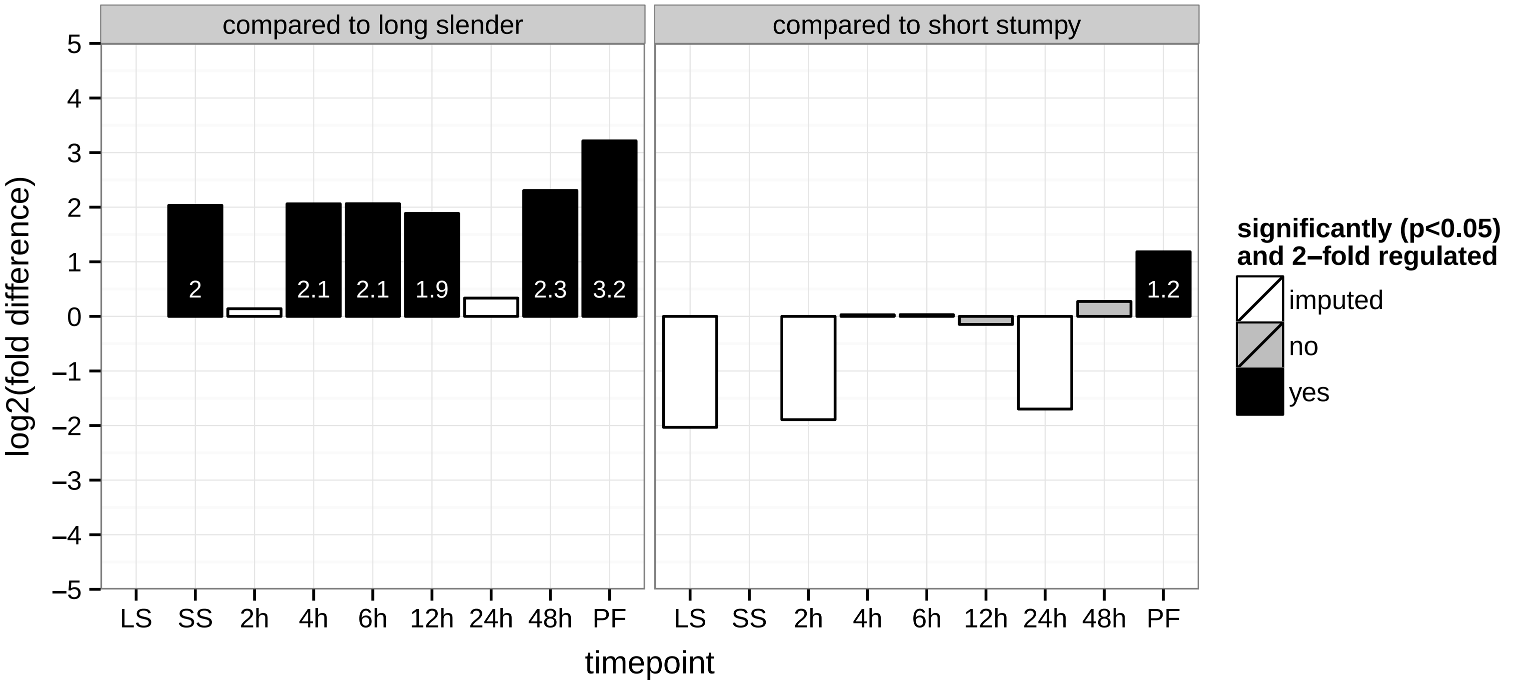
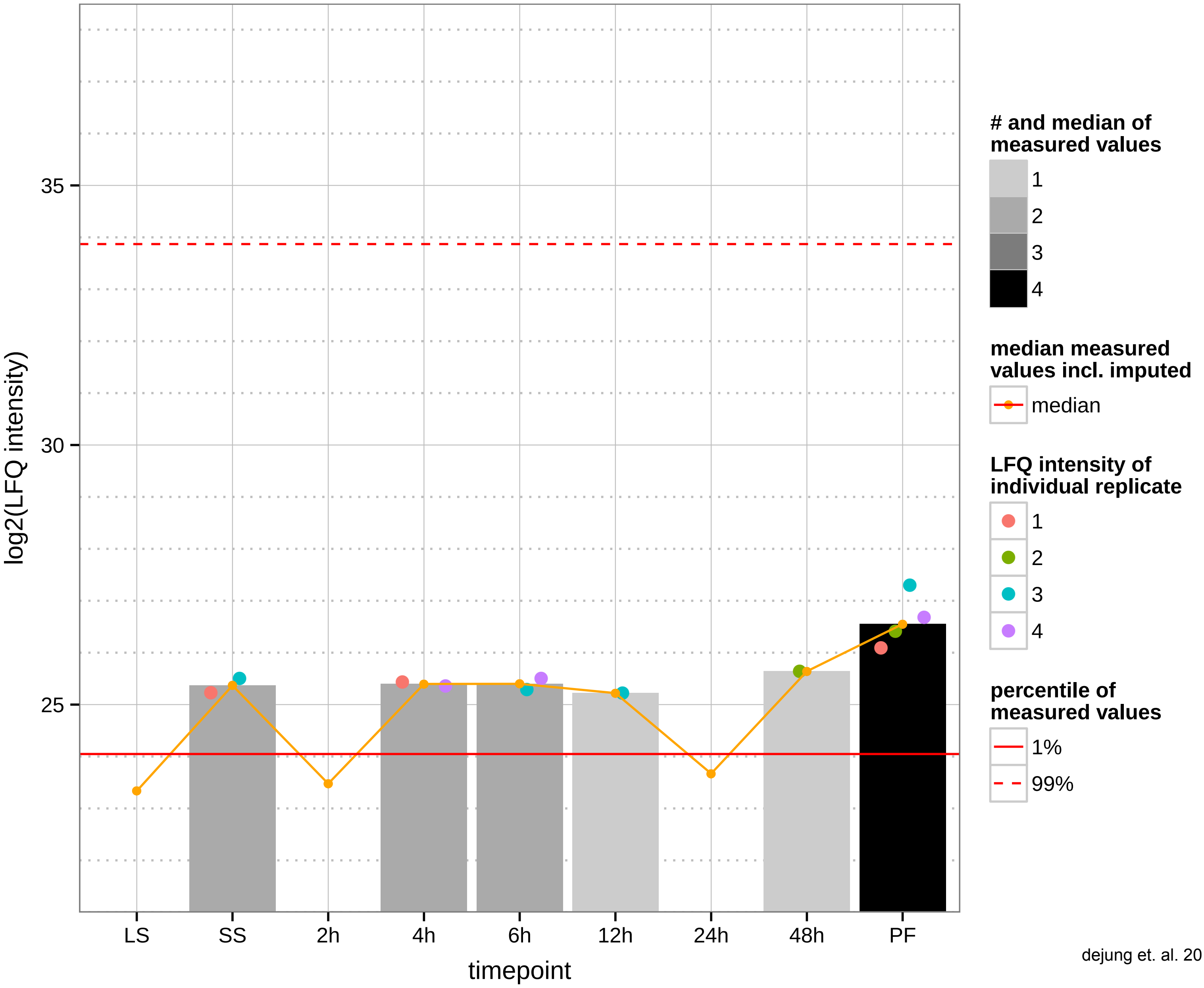
hypothetical protein, conserved
Tb927.10.2200
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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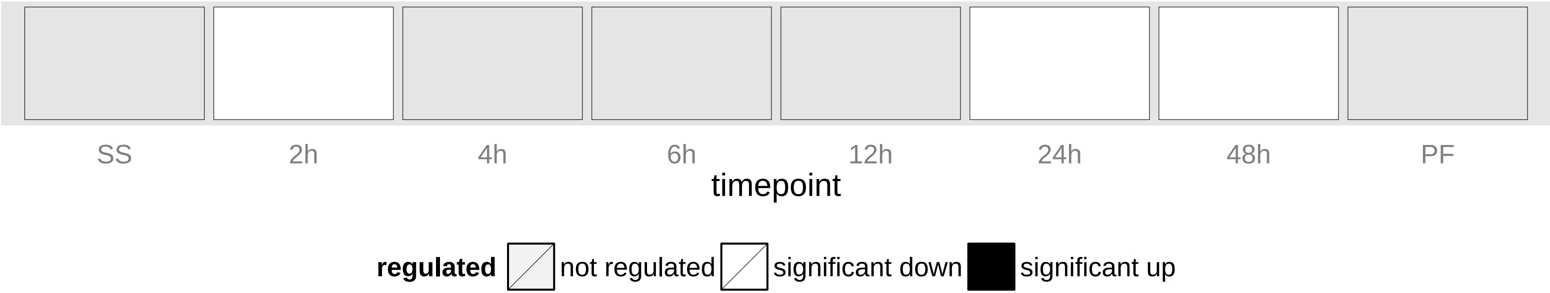

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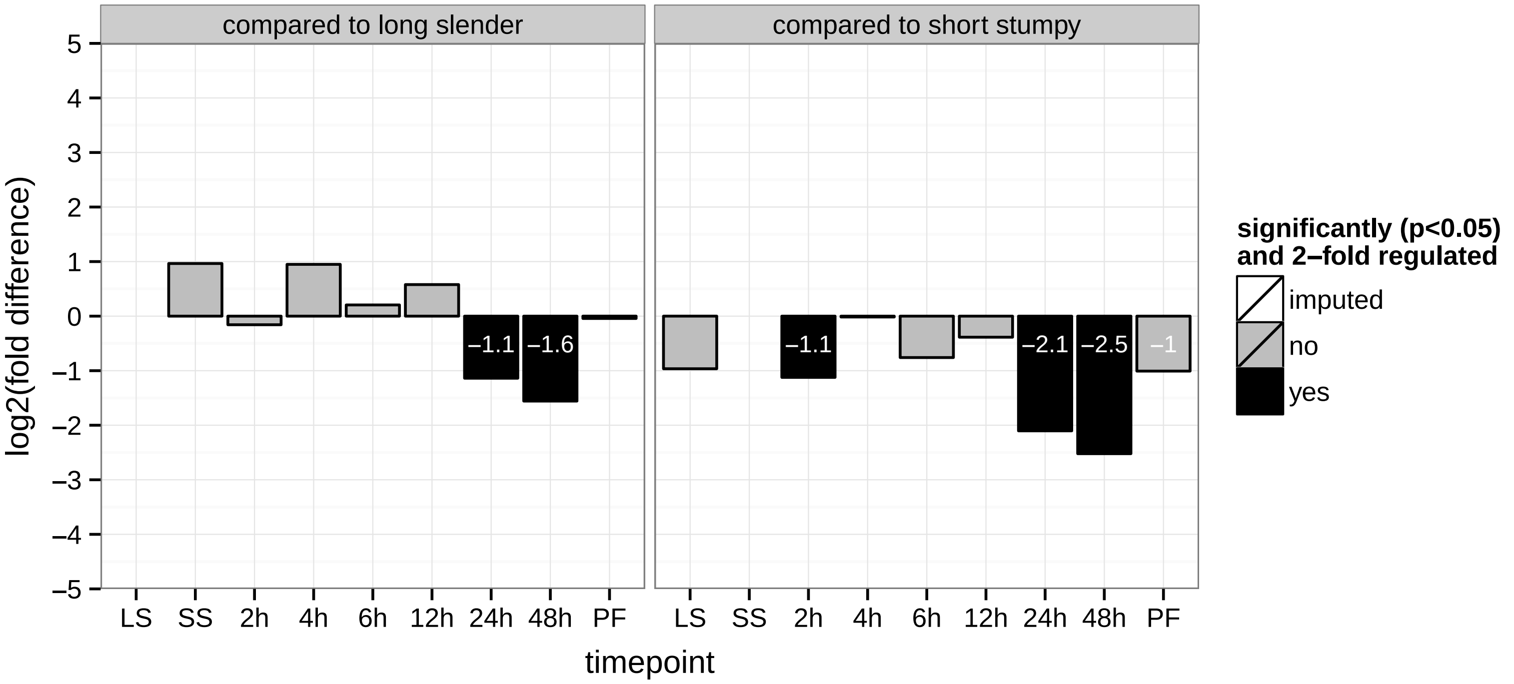
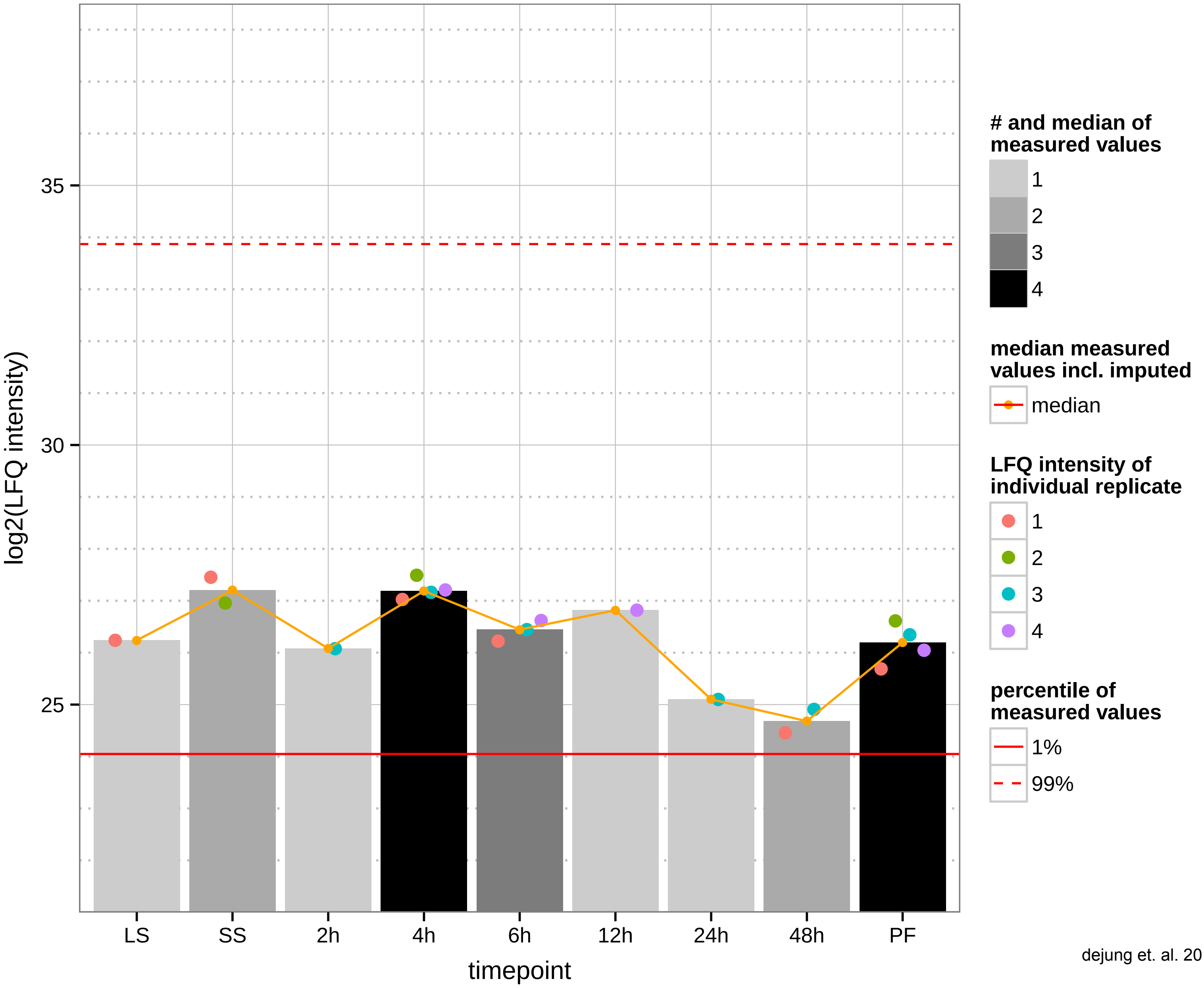
trypanothione/tryparedoxin dependent peroxidase 1, cytosolic, glutathione peroxidase–like protein 1 (TDPX1)
Tb927.7.1120
AGOF: glutathione peroxidase activity
AGOC: null
AGOP: response to oxidative stress
PGOF: glutathione peroxidase activity
PGOC: null
PGOP: oxidation–reduction process, response to oxidative stress





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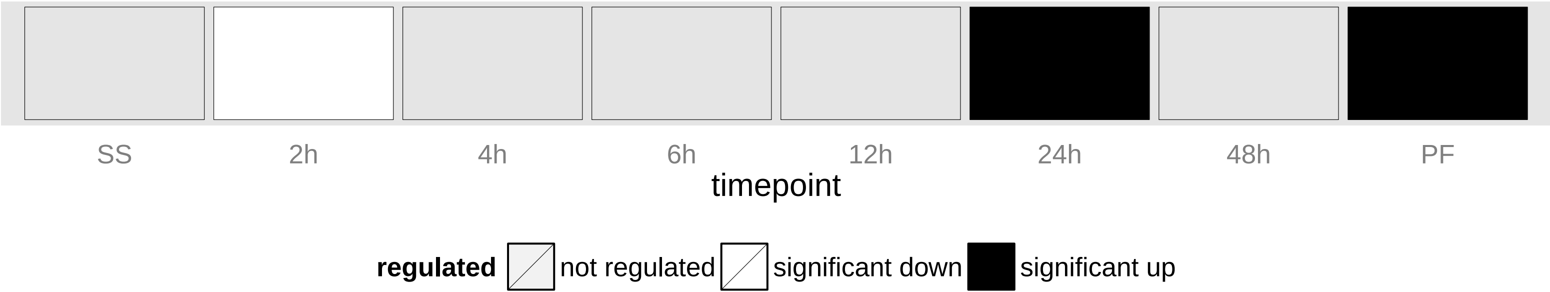

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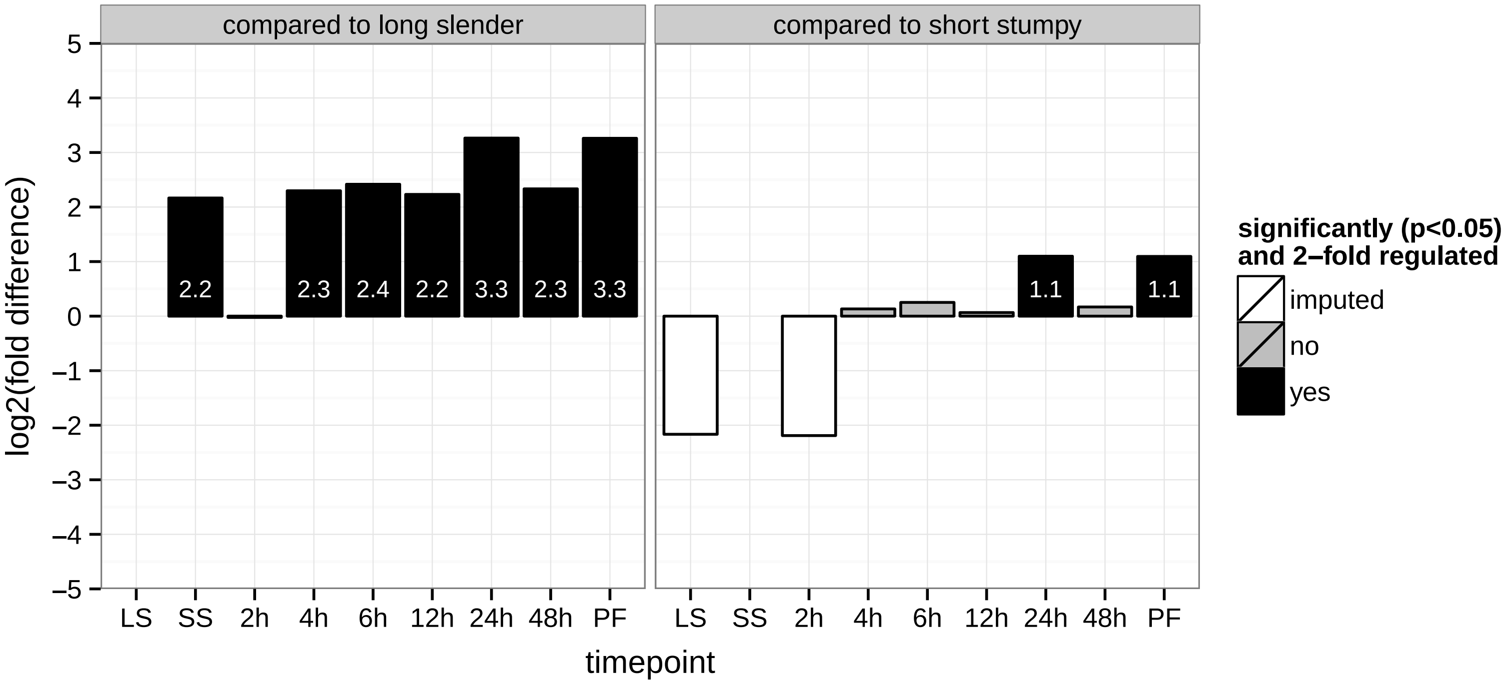
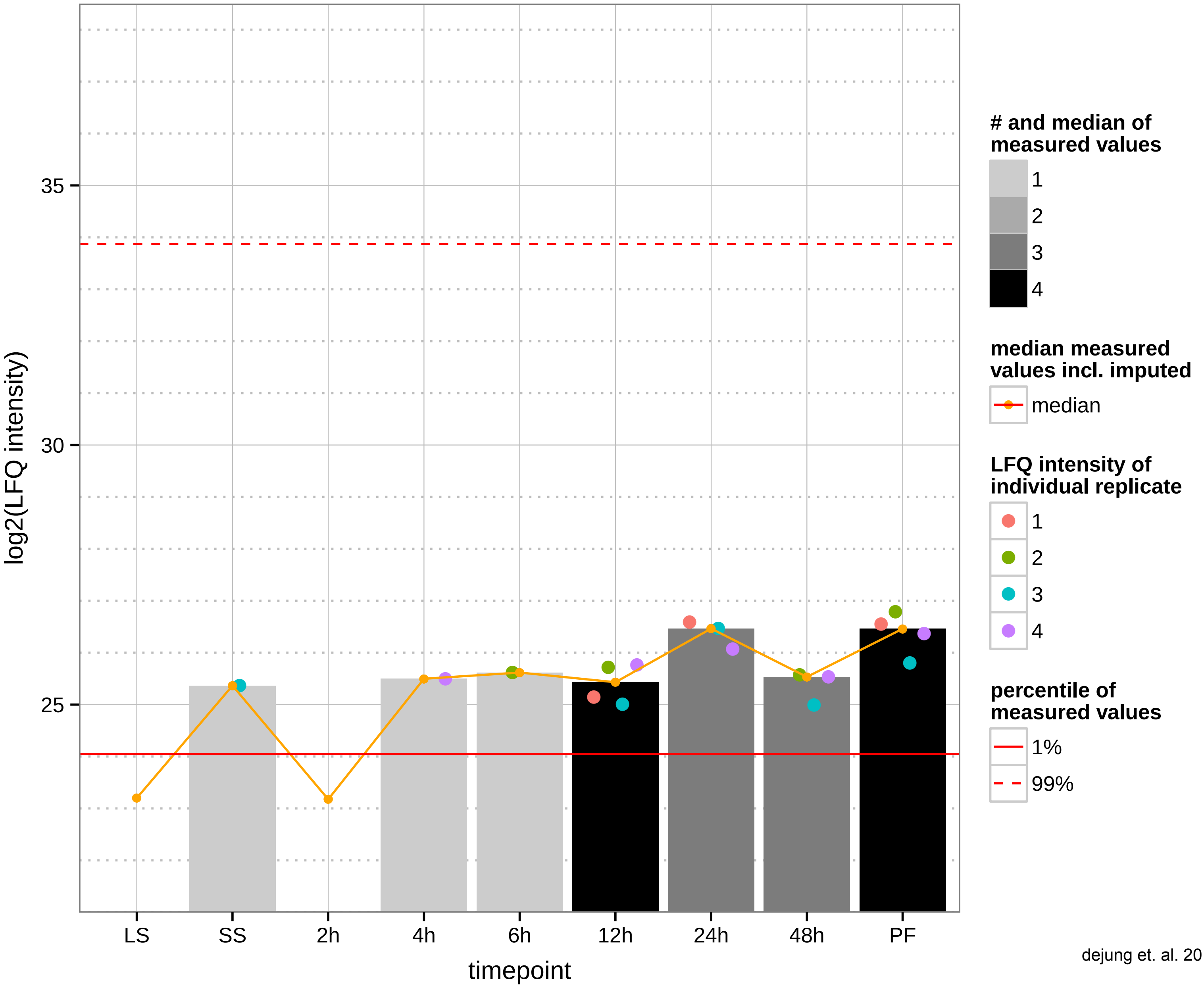
hypothetical protein, conserved
Tb927.8.2570
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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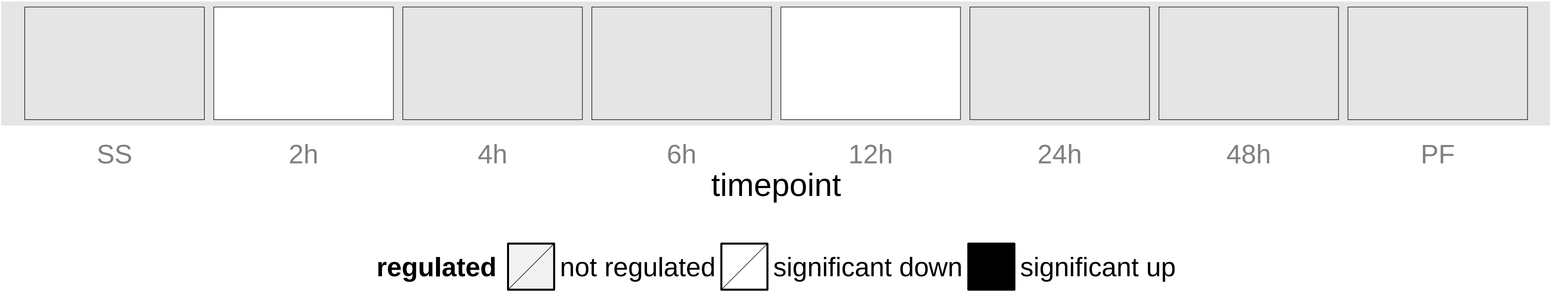

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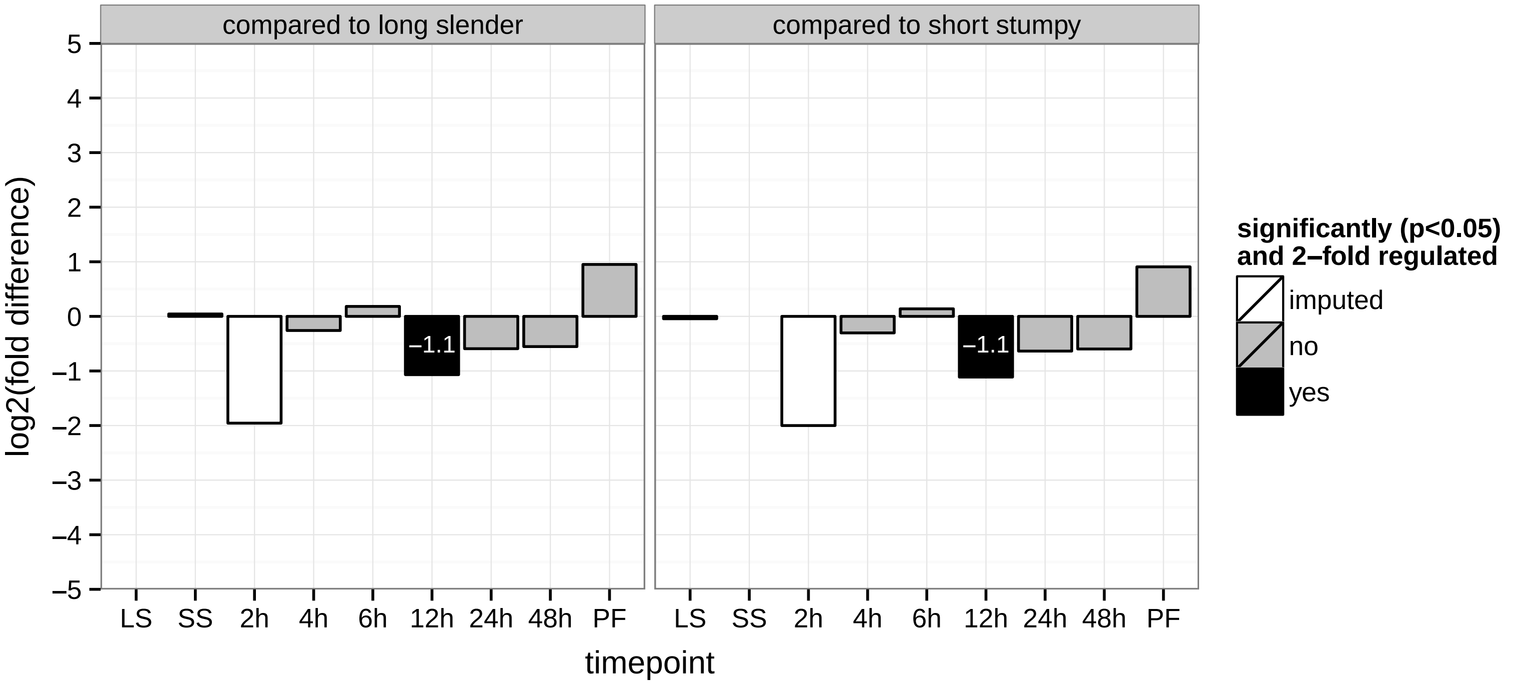
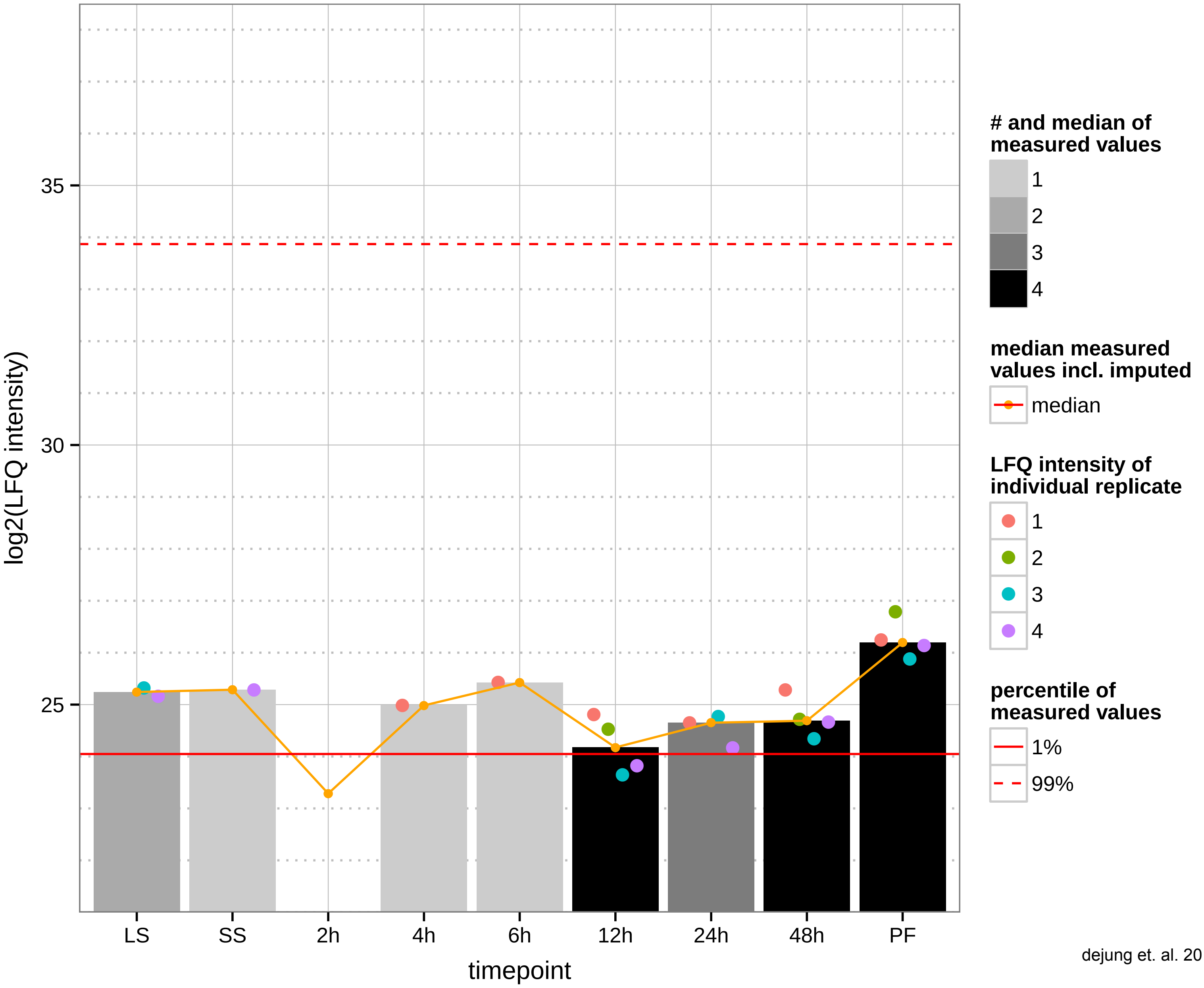
hypothetical protein, conserved
Tb927.9.6010
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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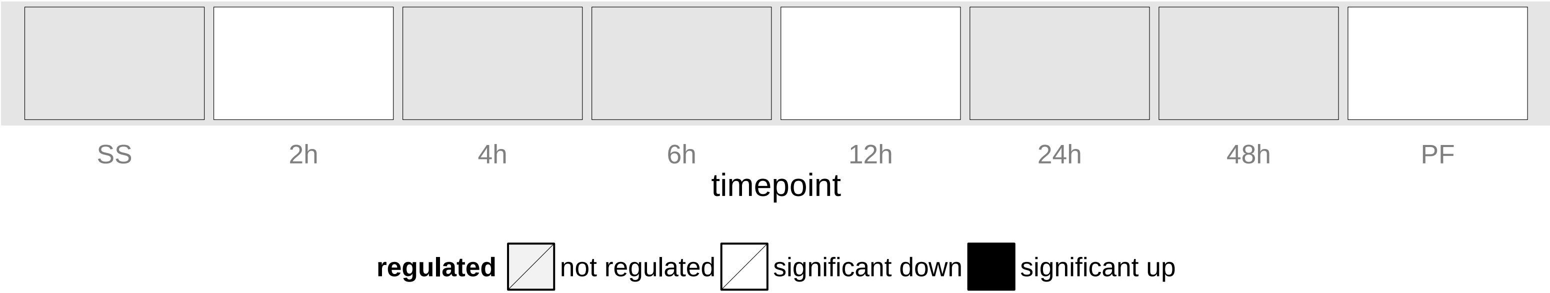

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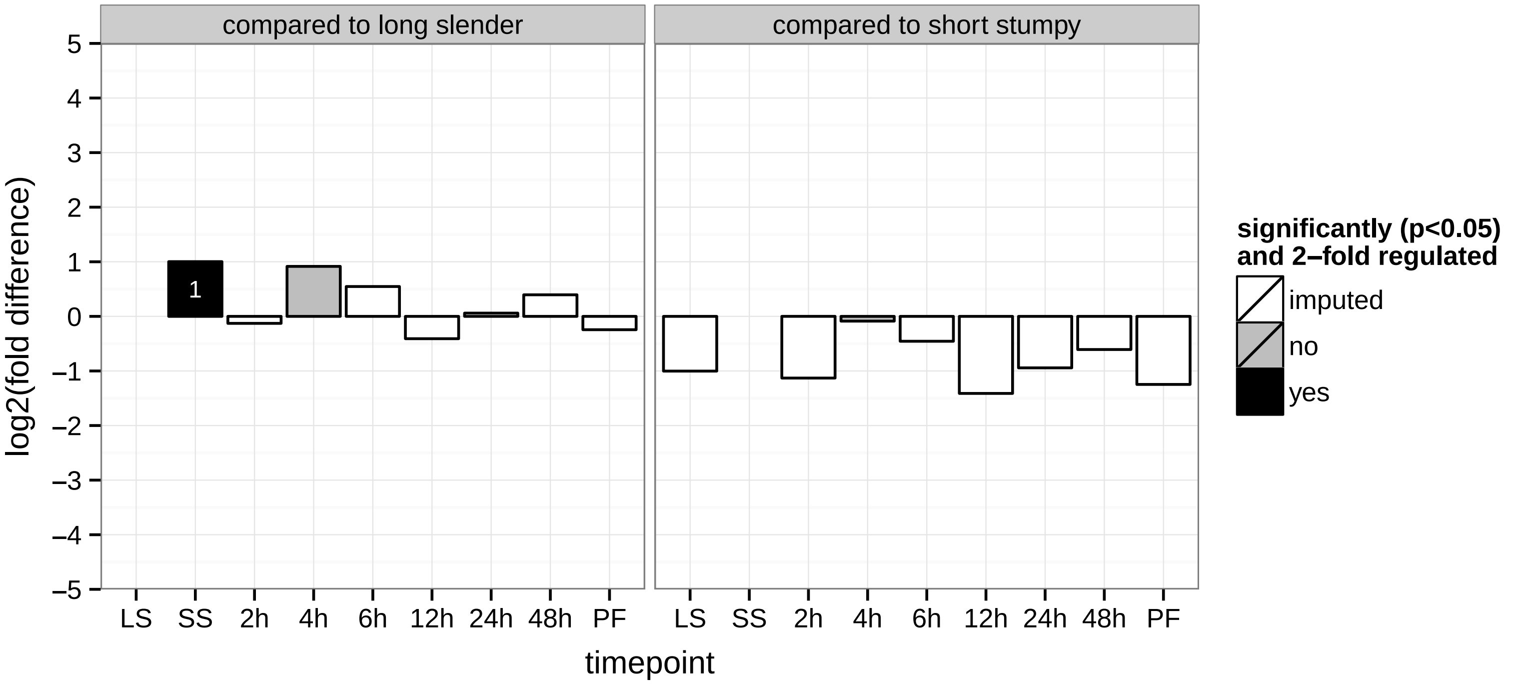
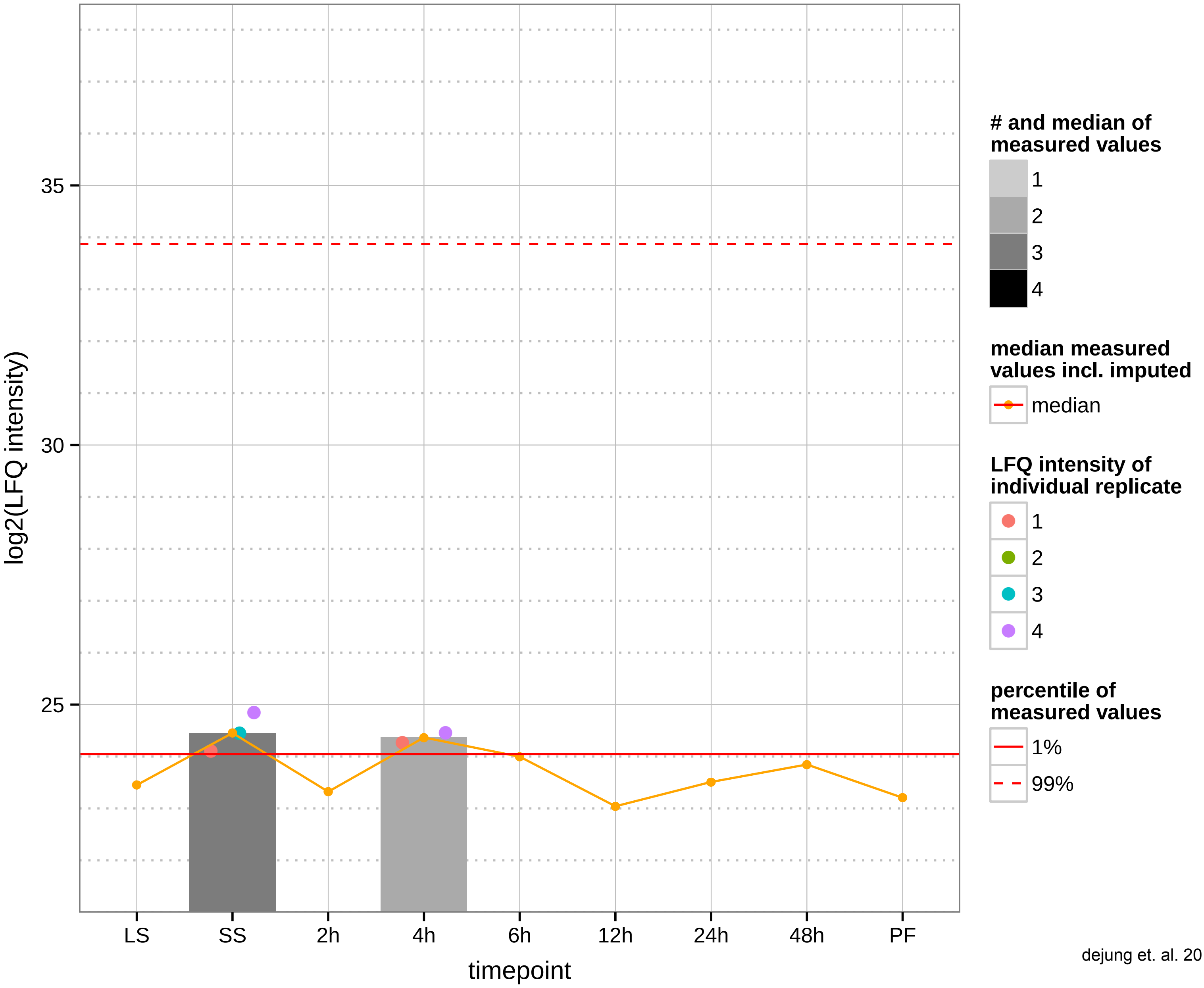
5–methyltetrahydropteroyltriglutamate–homocysteine S–methyltransferase, putative, cobalamin–independent methionine synt
Tb927.8.2610
AGOF: 5–methyltetrahydropteroyltriglutamate–homocysteine S–methyltransferase activity, zinc ion binding
AGOC: null
AGOP: methionine biosynthetic process
PGOF: 5–methyltetrahydropteroyltriglutamate–homocysteine S–methyltransferase activity, zinc ion binding
PGOC: null
PGOP: cellular amino acid biosynthetic process, methionine biosynthetic process





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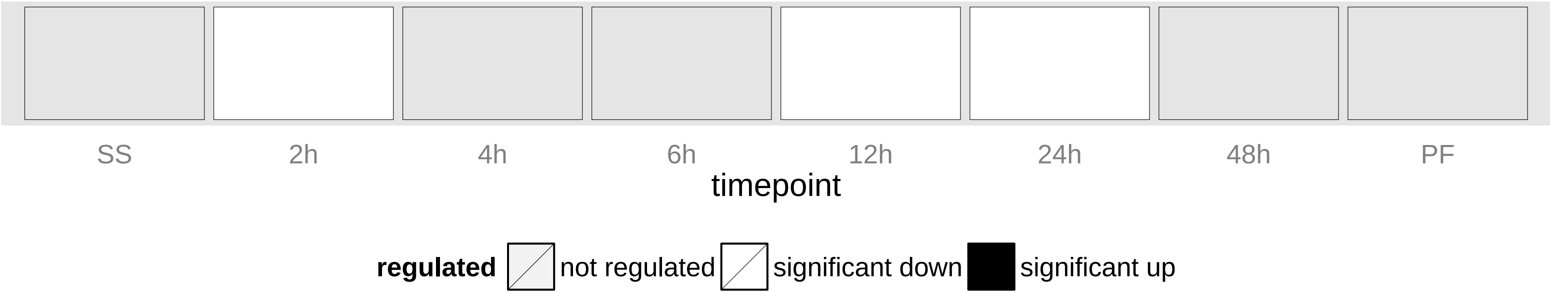

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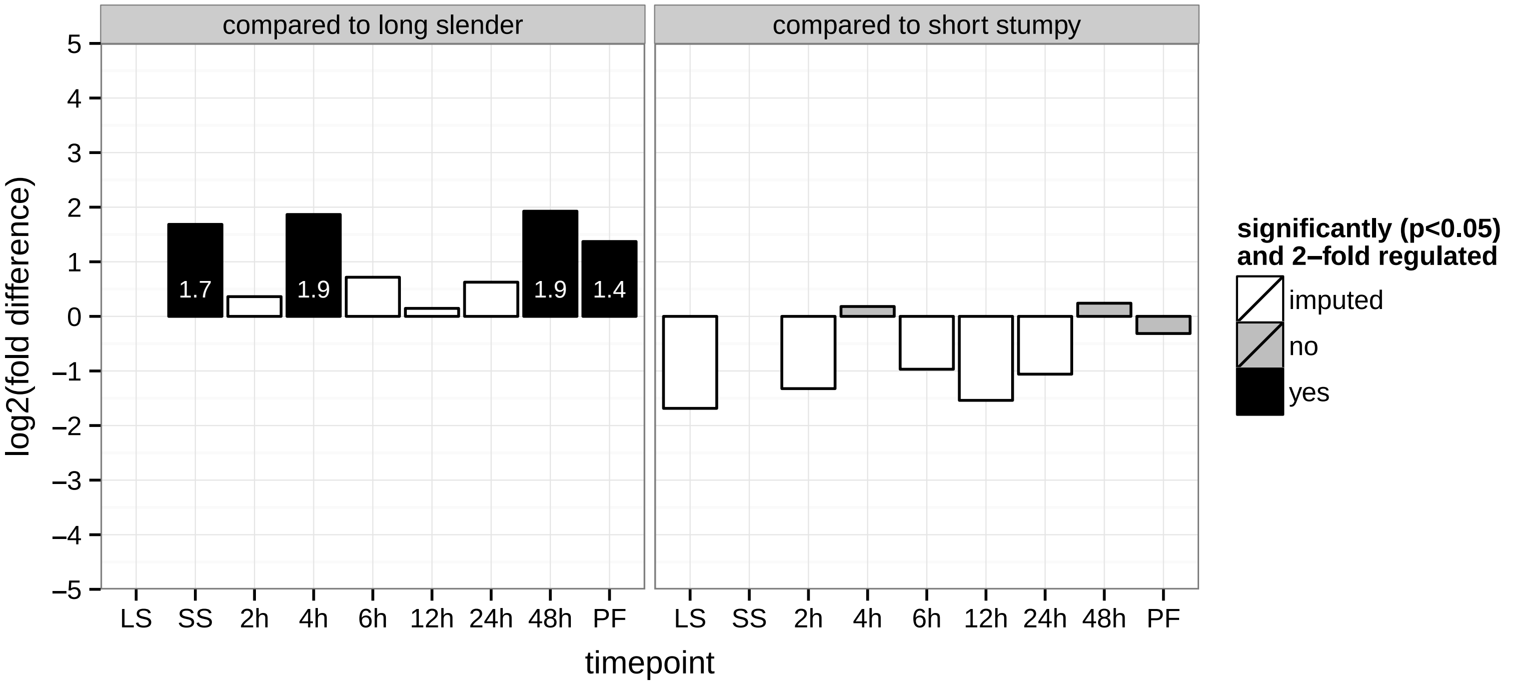
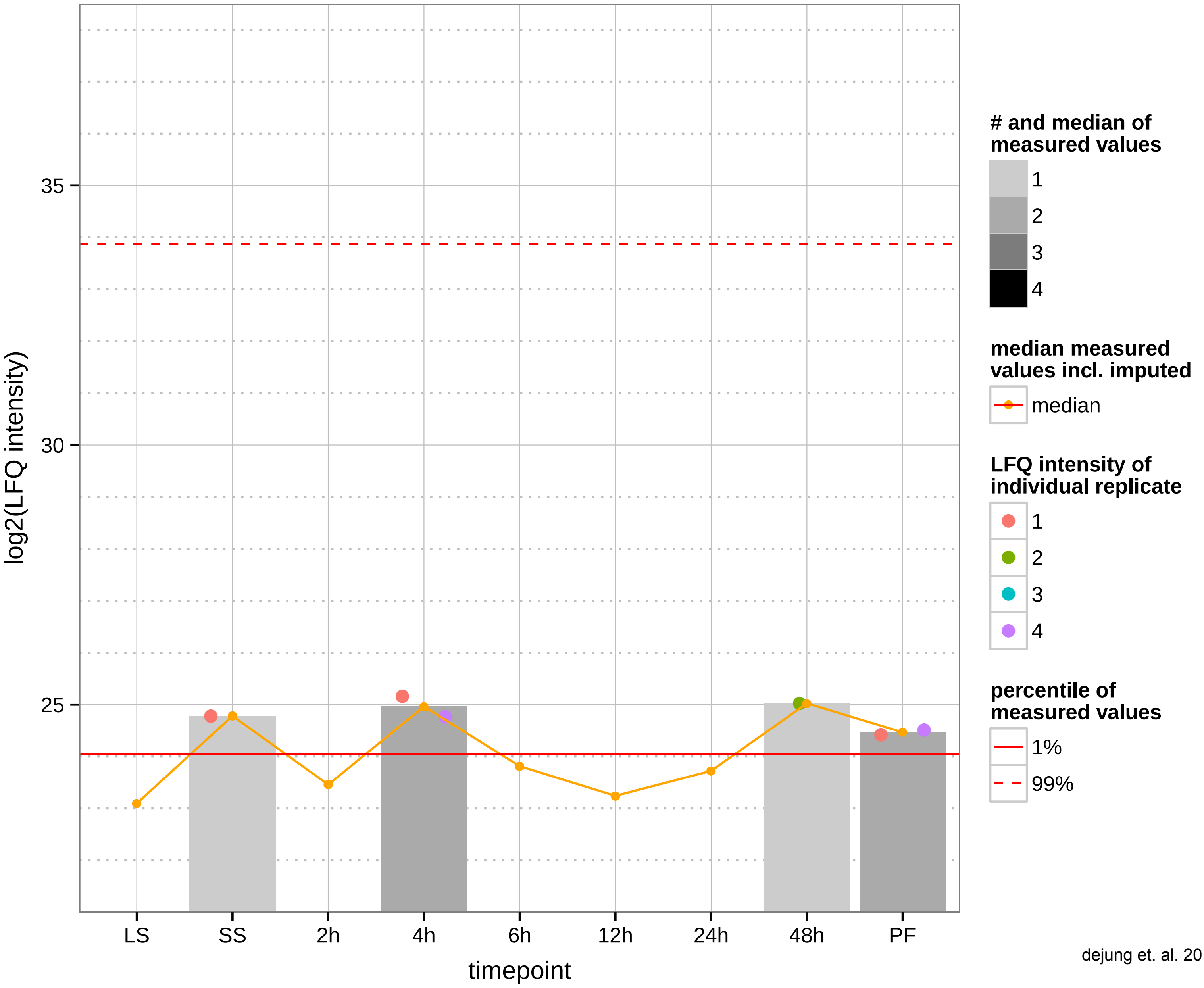
kinetoplastid kinetochore protein 4 (kkt4)
Tb927.8.3680
AGOF: null
AGOC: intracellular, kinetochore
AGOP: chromosome segregation
PGOF: null
PGOC: null
PGOP: null





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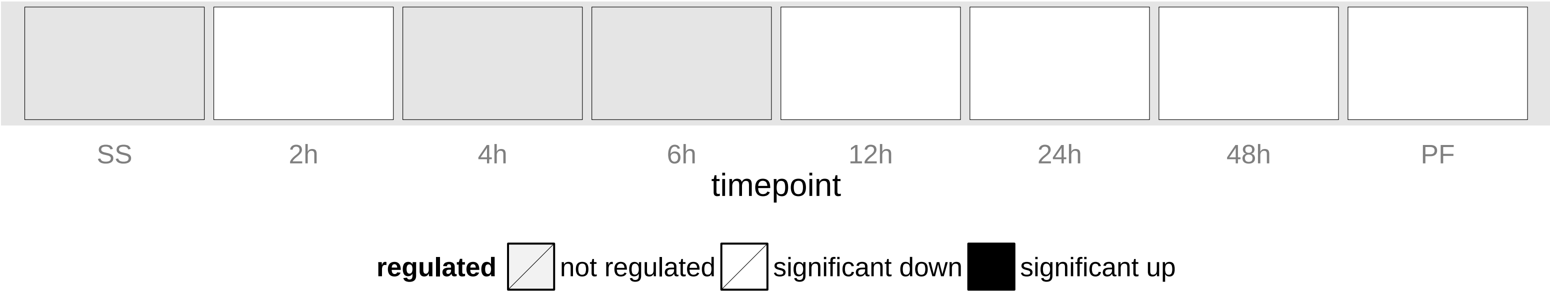

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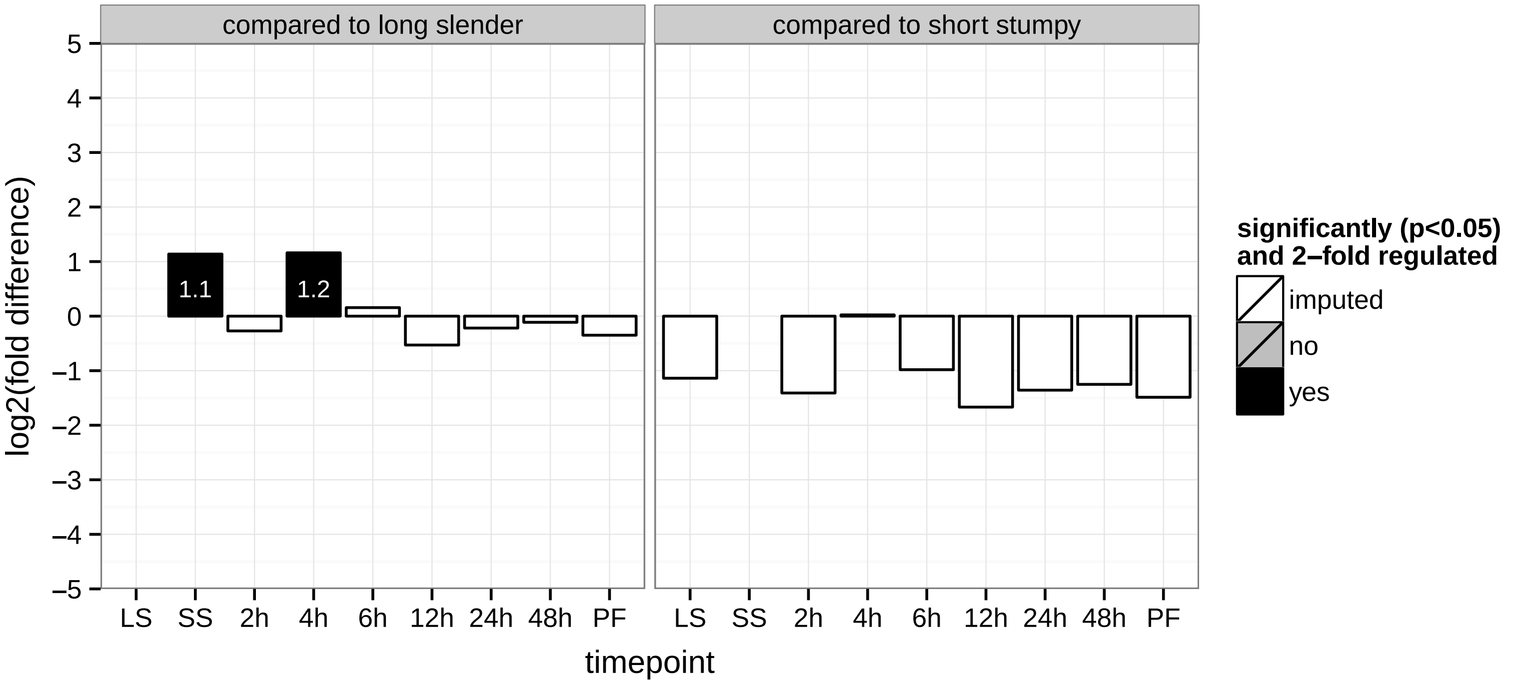
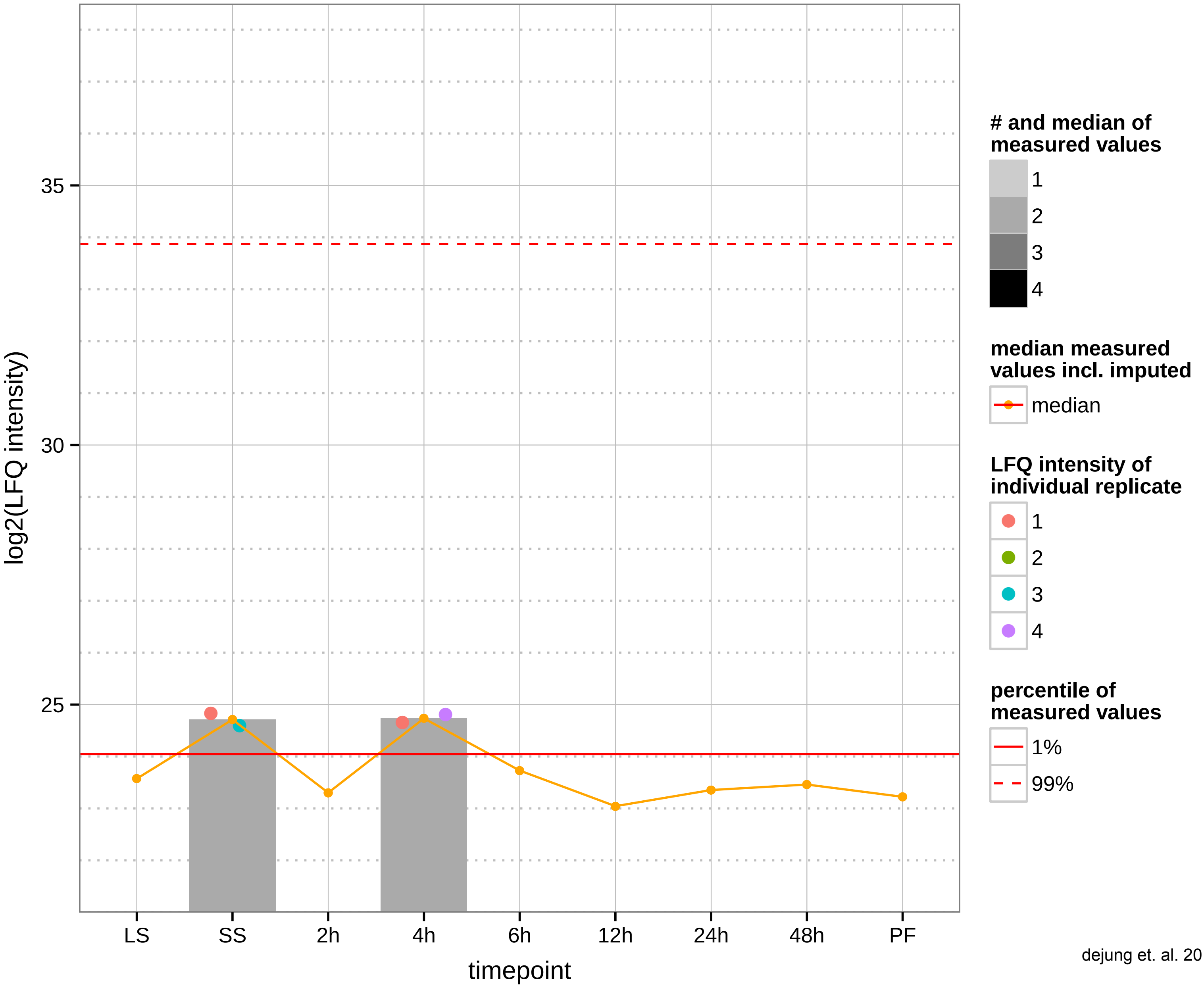
hypothetical protein, conserved
Tb927.10.2760
AGOF: ATP binding, nucleoside−triphosphatase activity
AGOC: null
AGOP: null
PGOF: ATP binding, nucleoside−triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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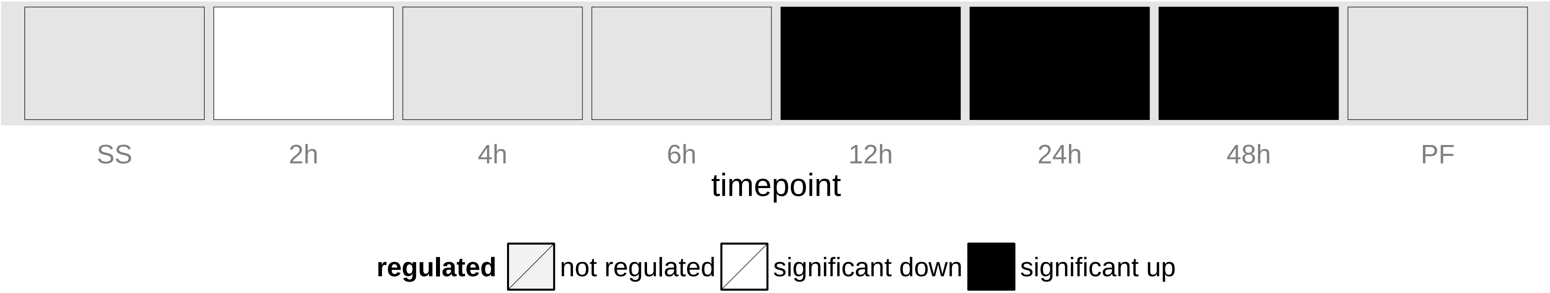

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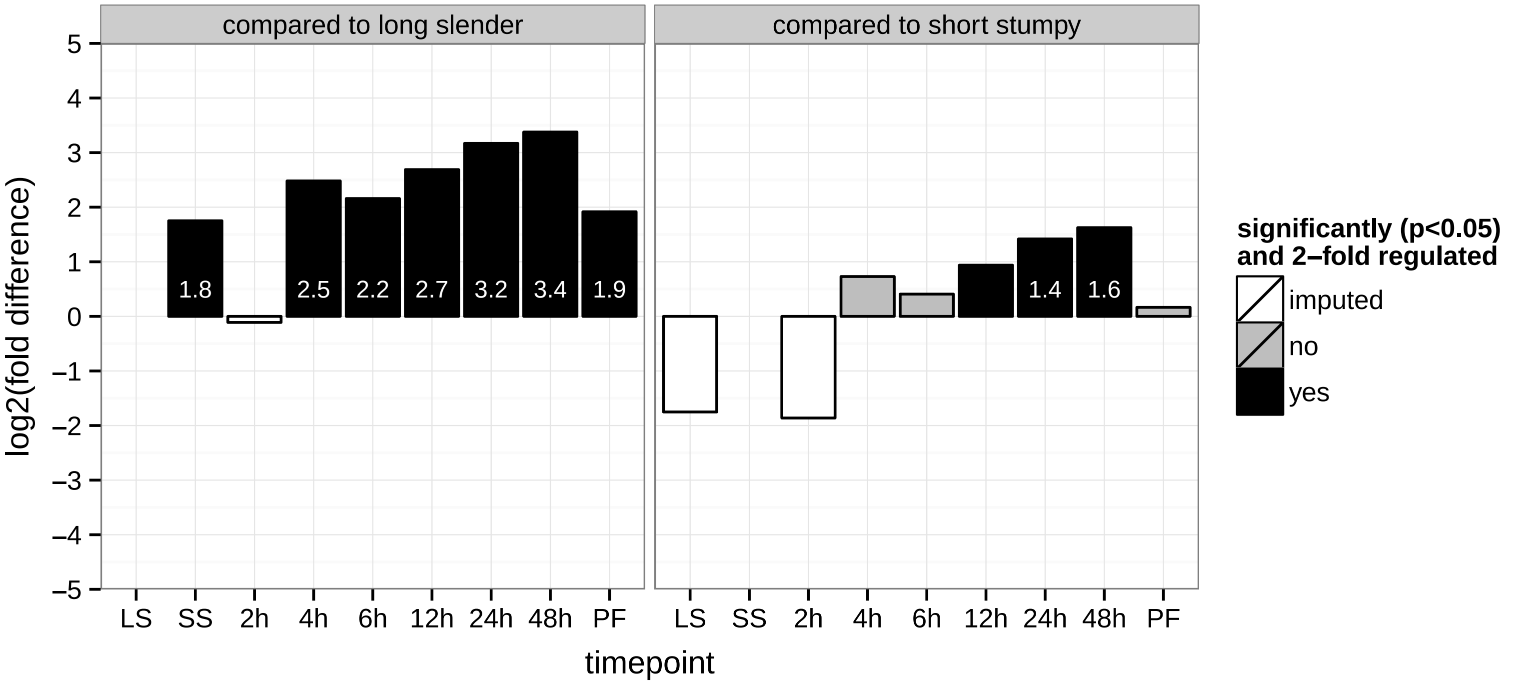
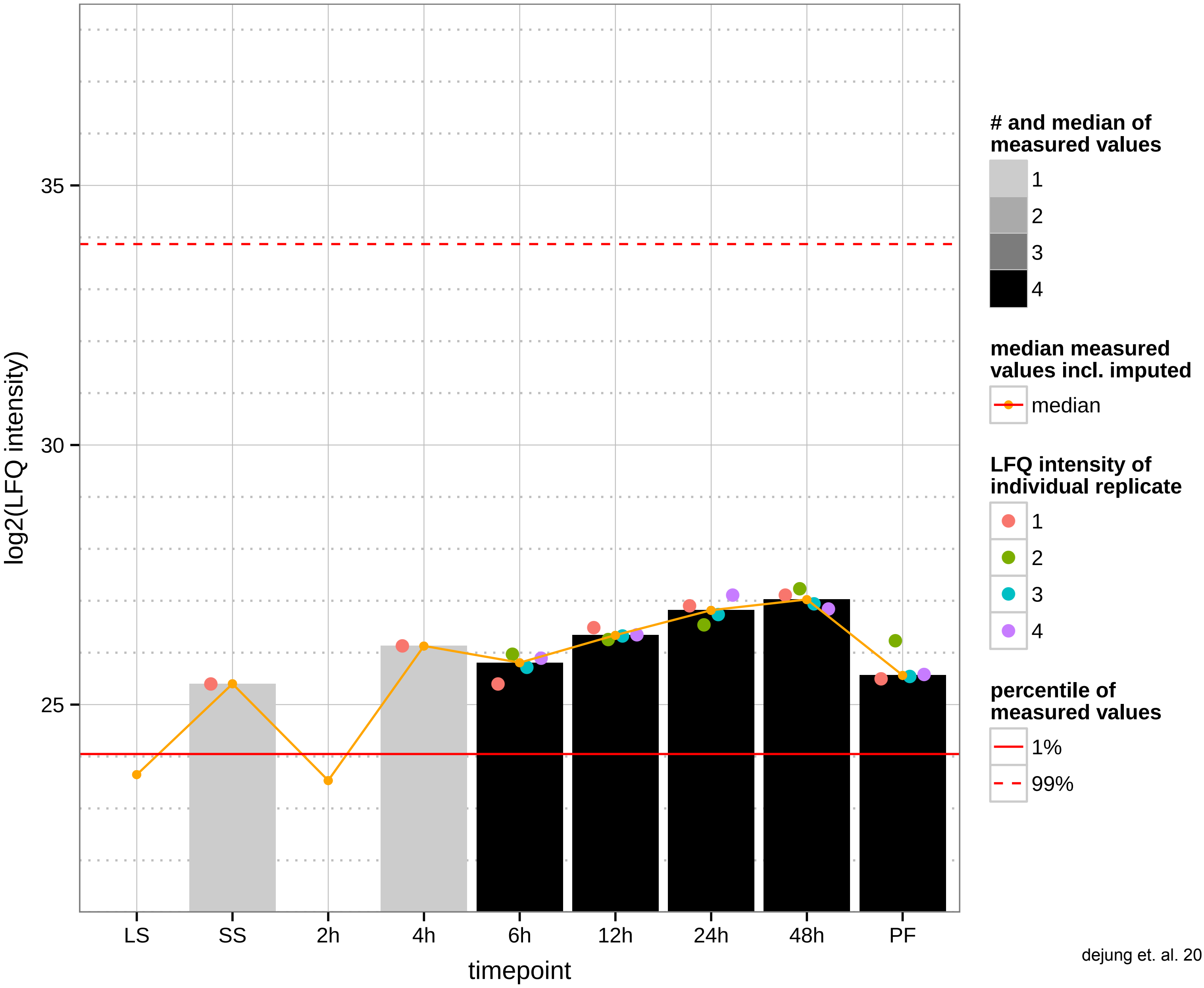
hypothetical protein, conserved
Tb927.11.2630
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: cytoplasm
PGOP: peptidyl–diphthamide biosynthetic process from peptidyl–histidine





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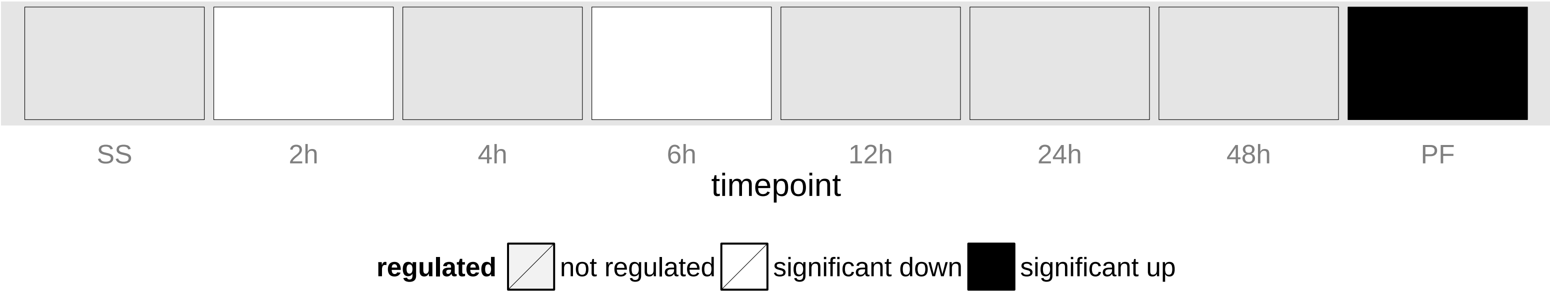

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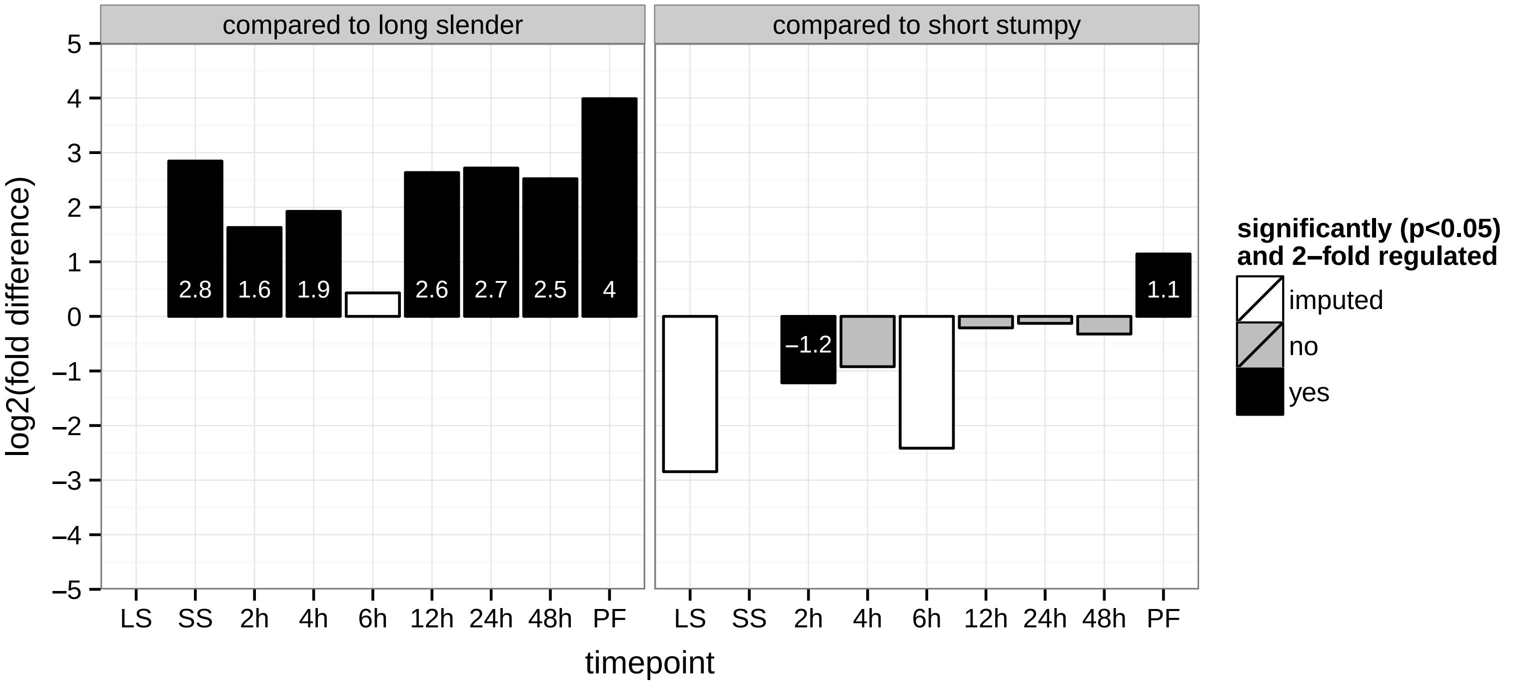
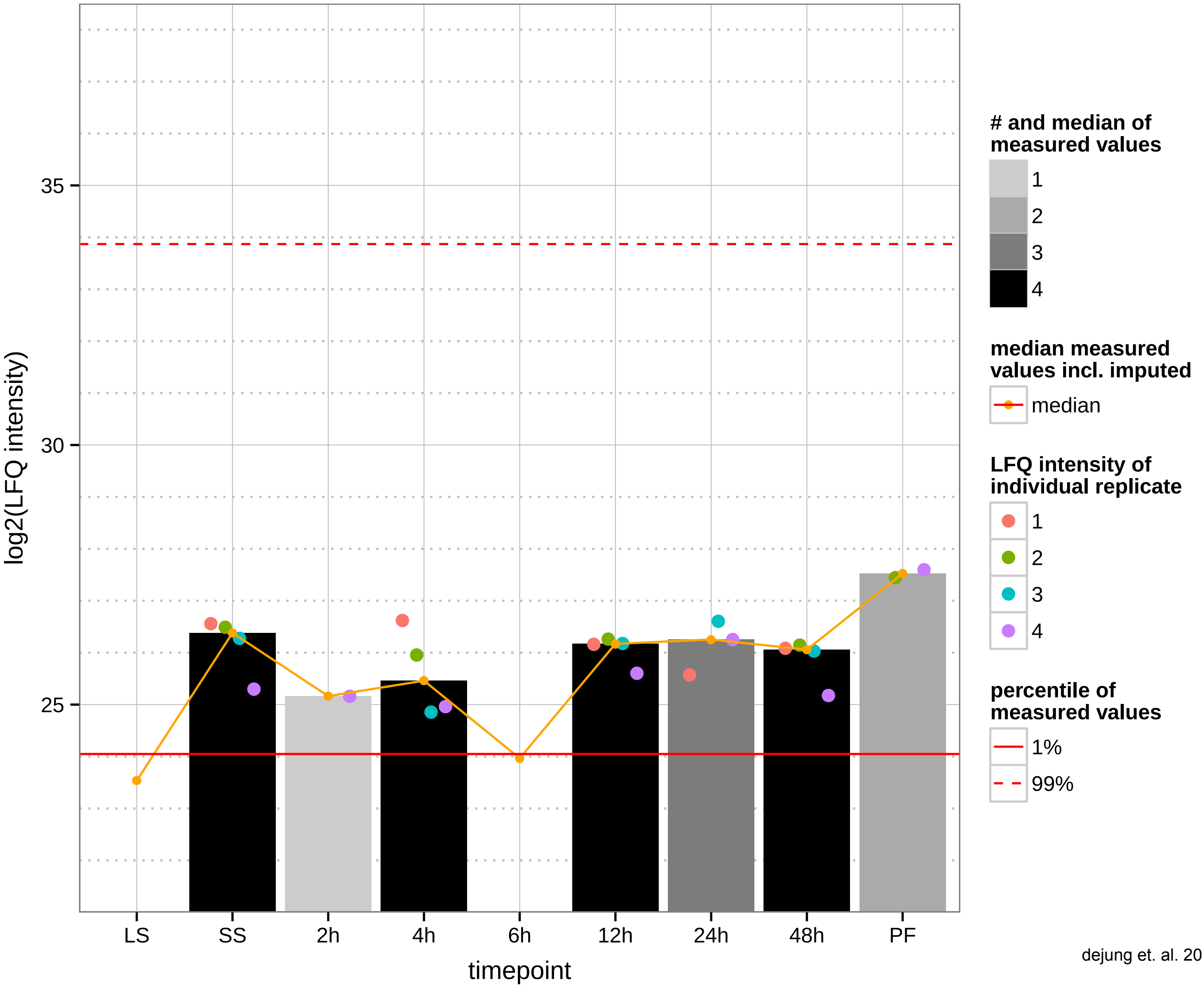
retrotransposon hot spot (RHS) protein, putative, retrotransposon hot spot protein 5 (RHS5)
Tb11.v5.0567;Tb927.6.140
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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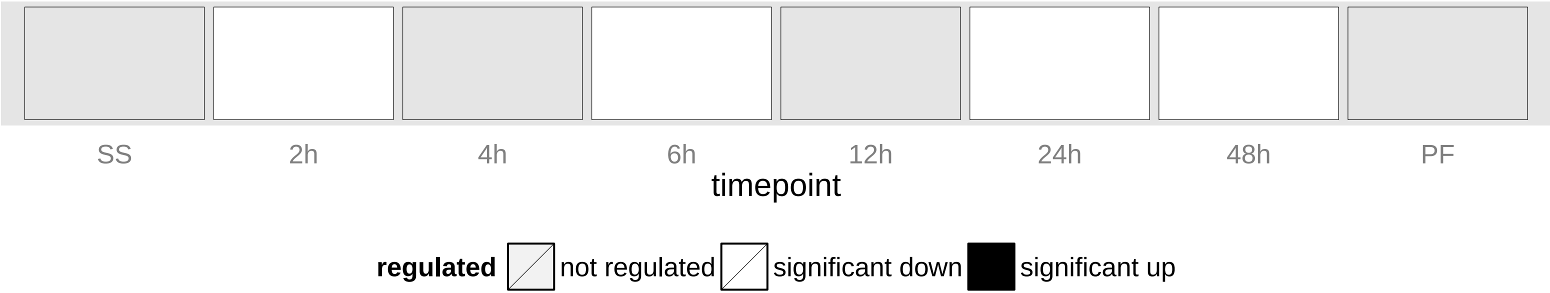

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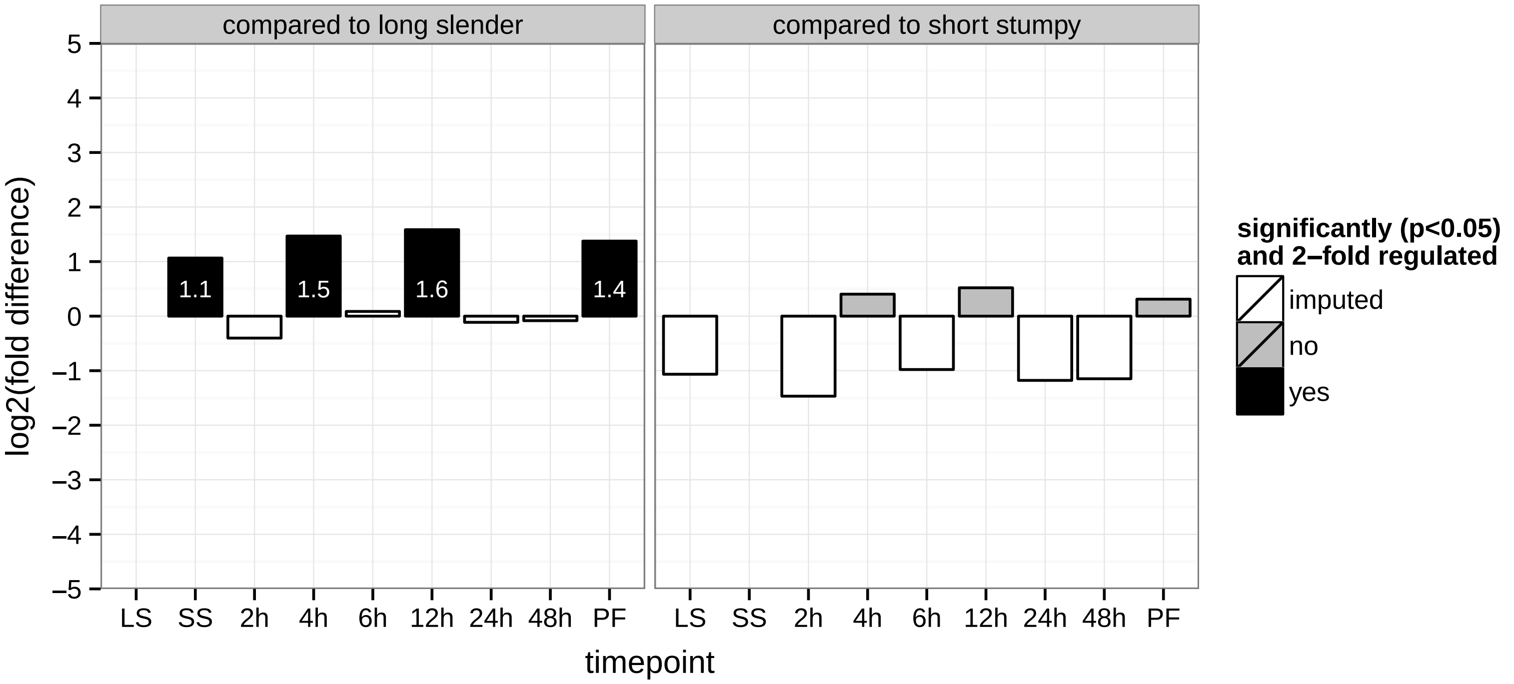
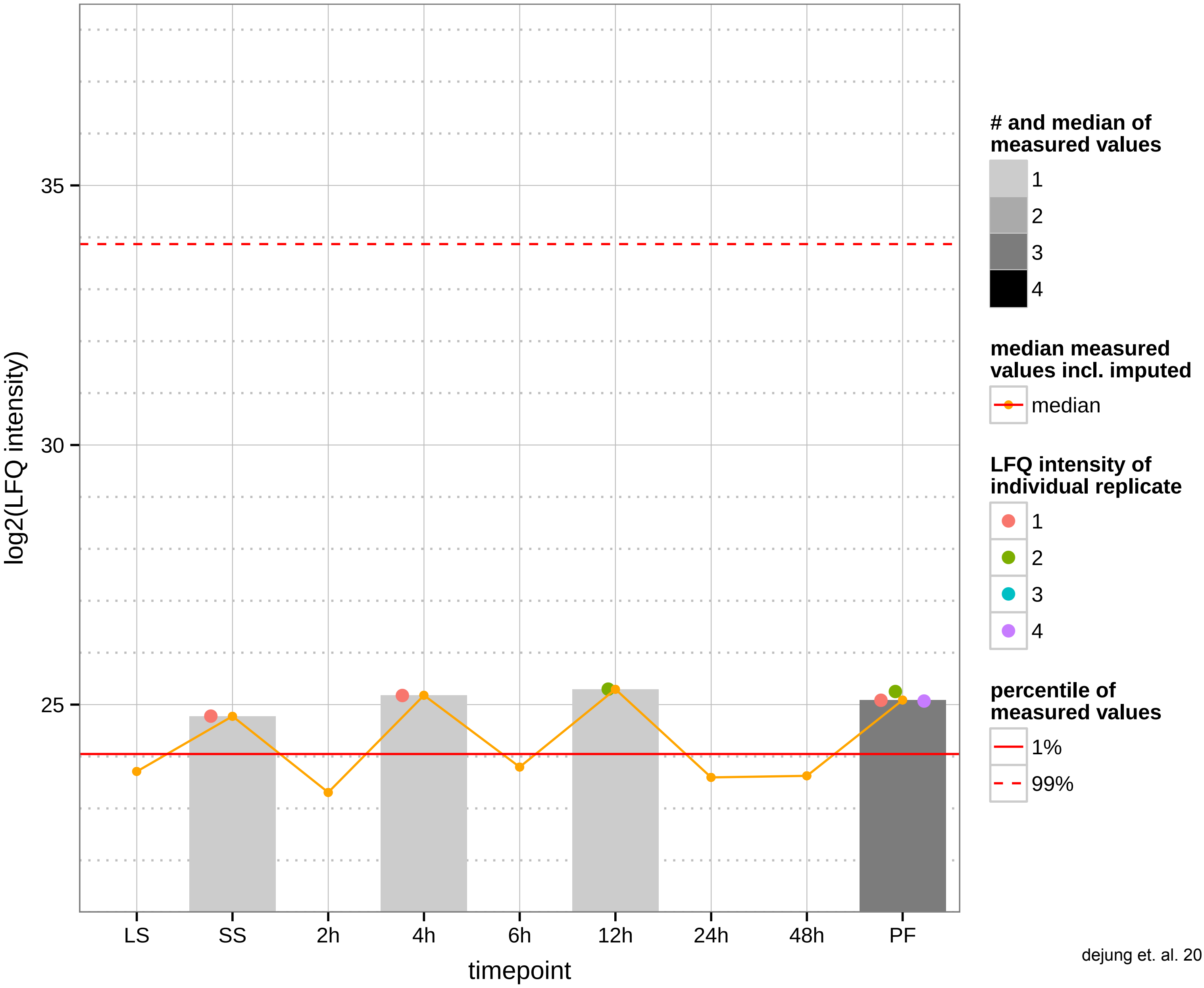
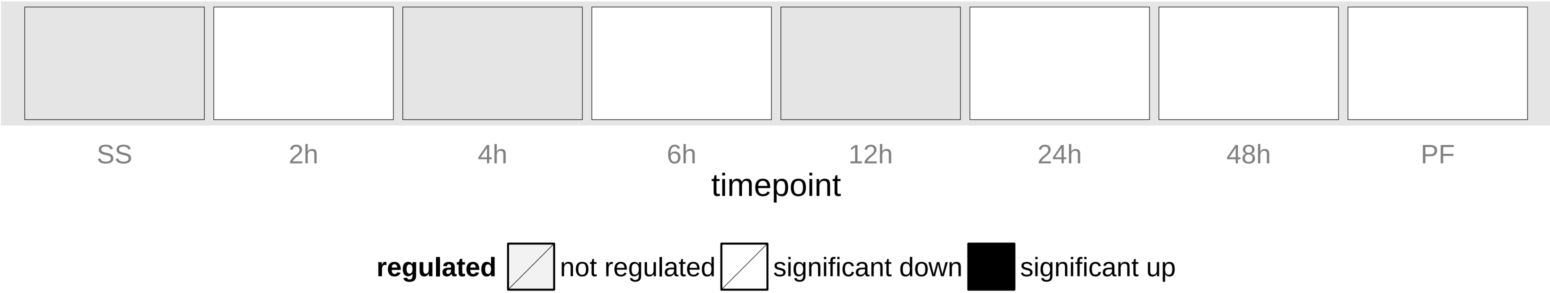
hypothetical protein, conserved
Tb927.11.12500
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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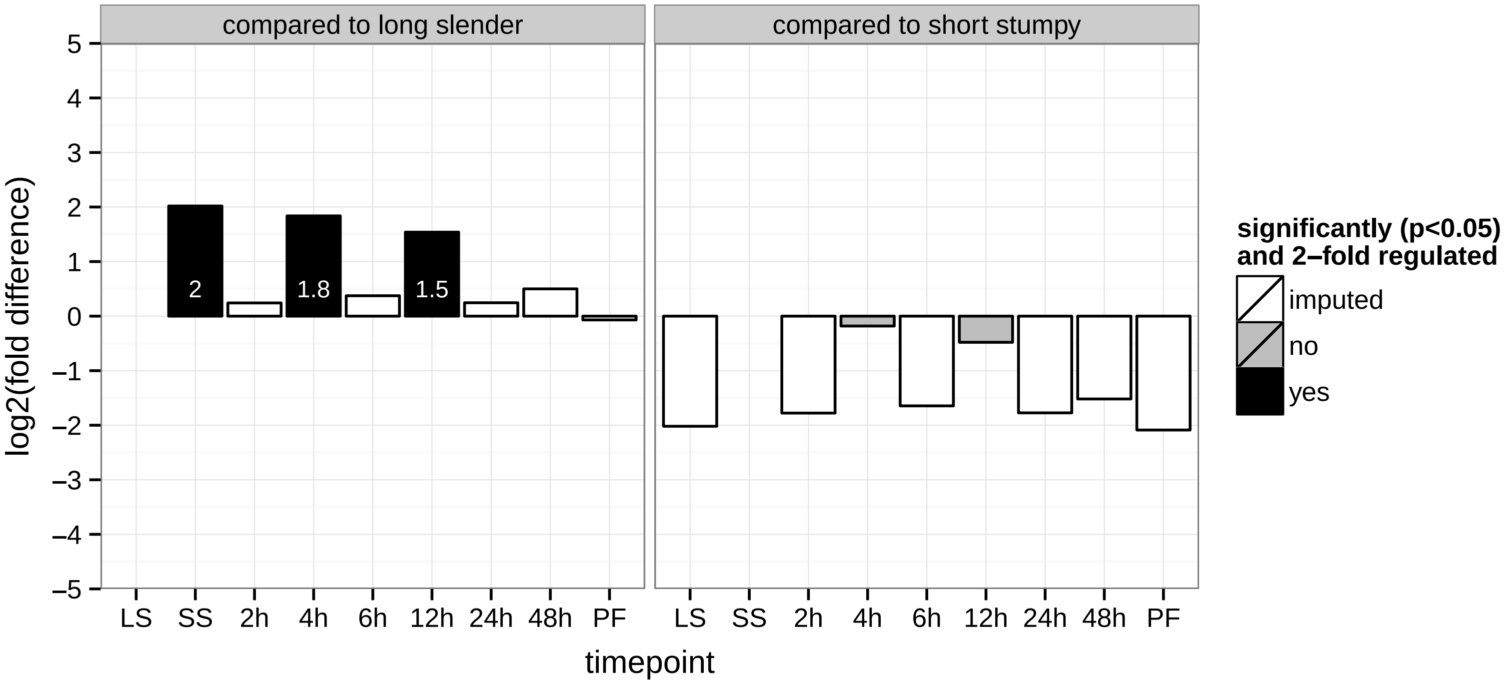
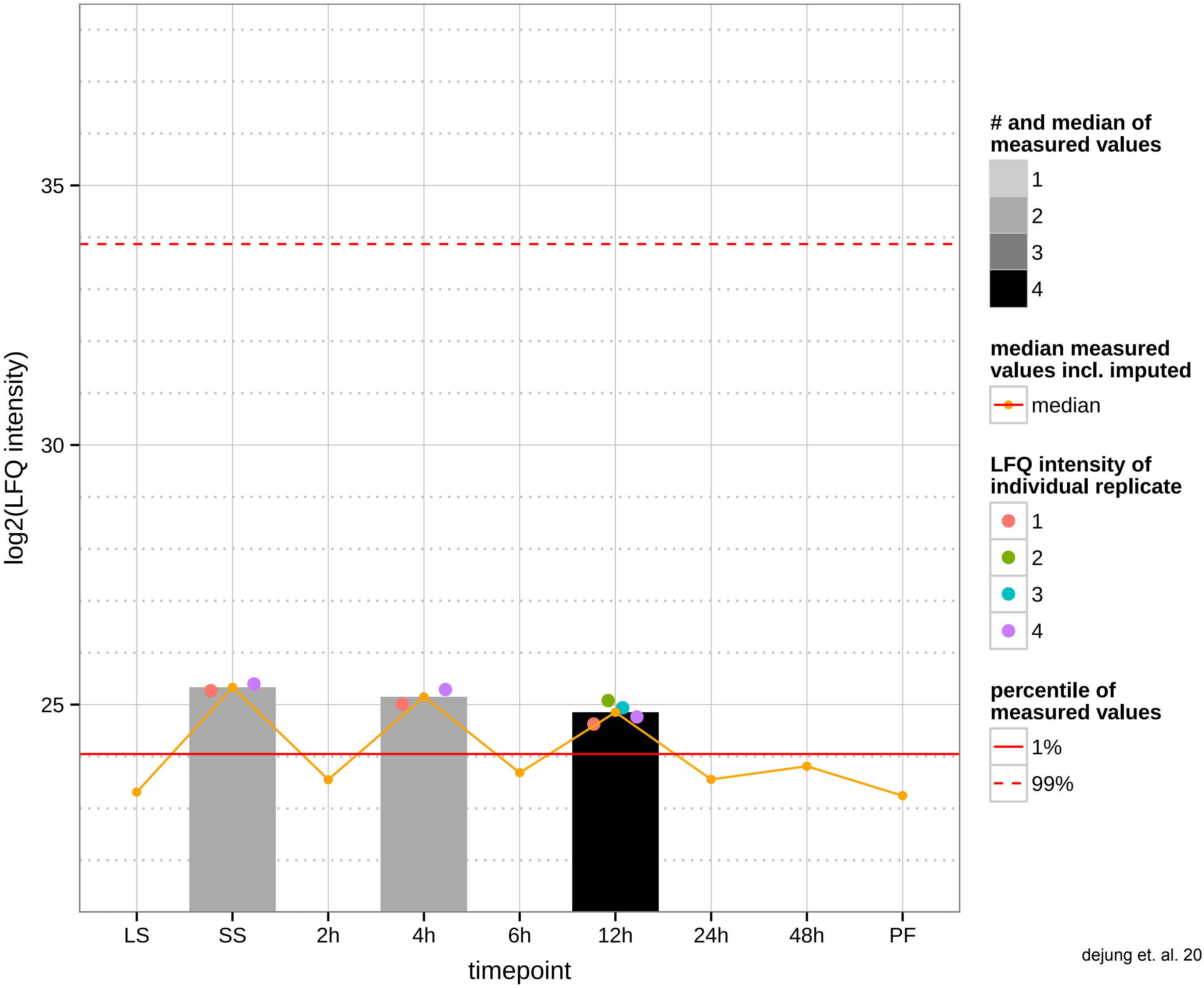
hypothetical protein, chrIX additional, unordered contigs
Tb927.9.15850;Tb09.v4.0110;Tb09.v4.0014
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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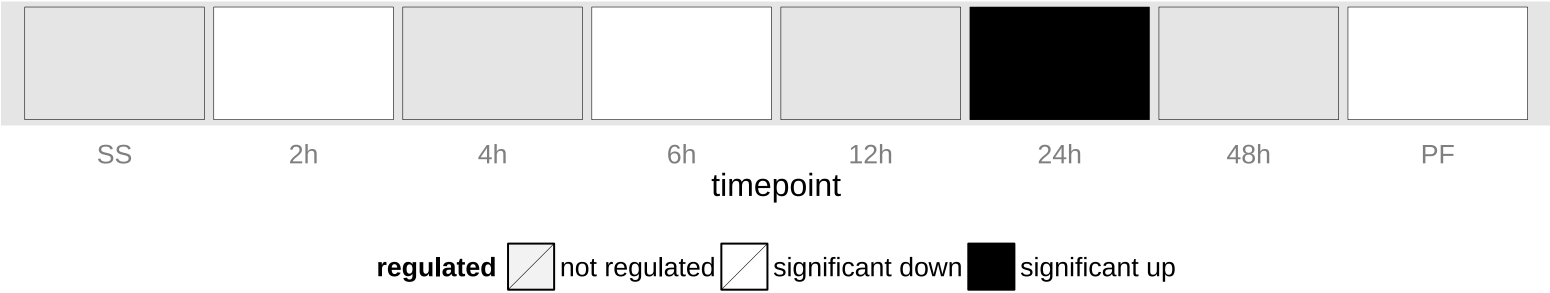

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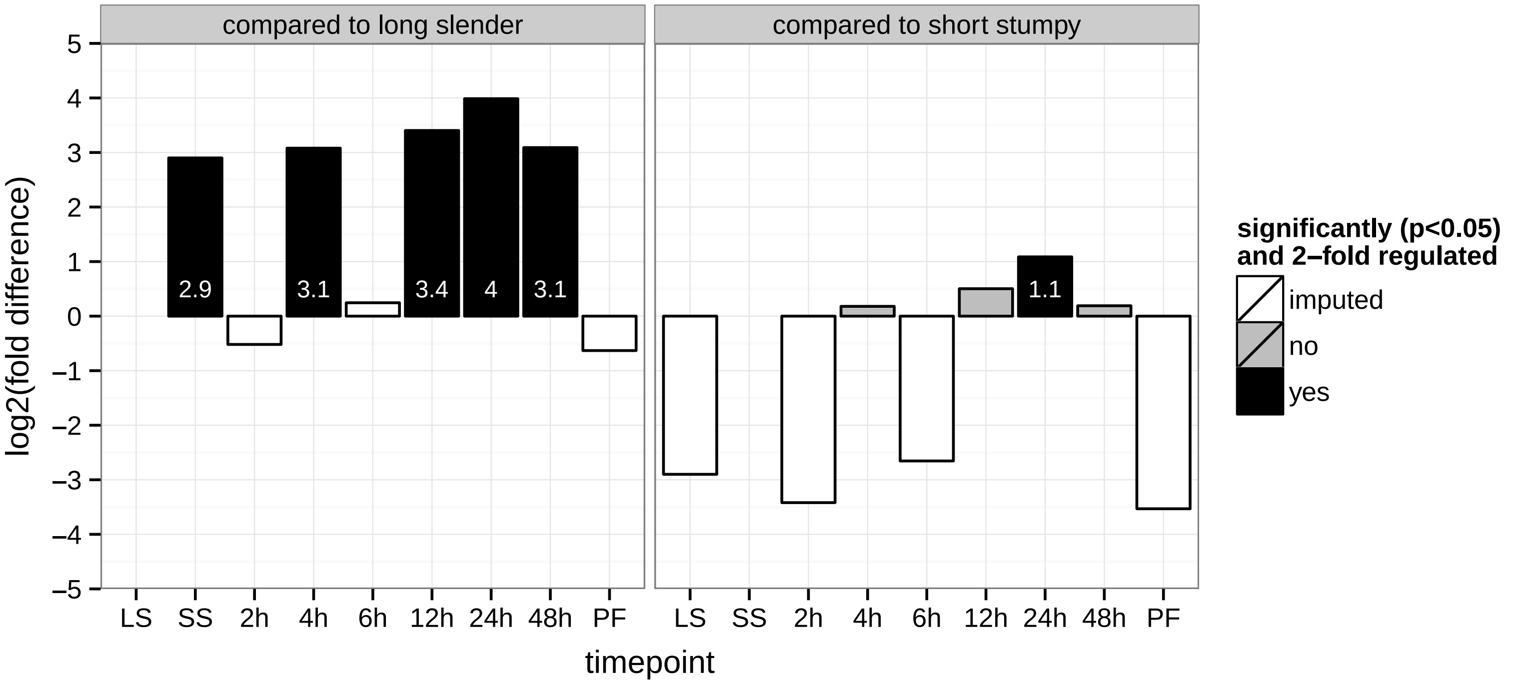
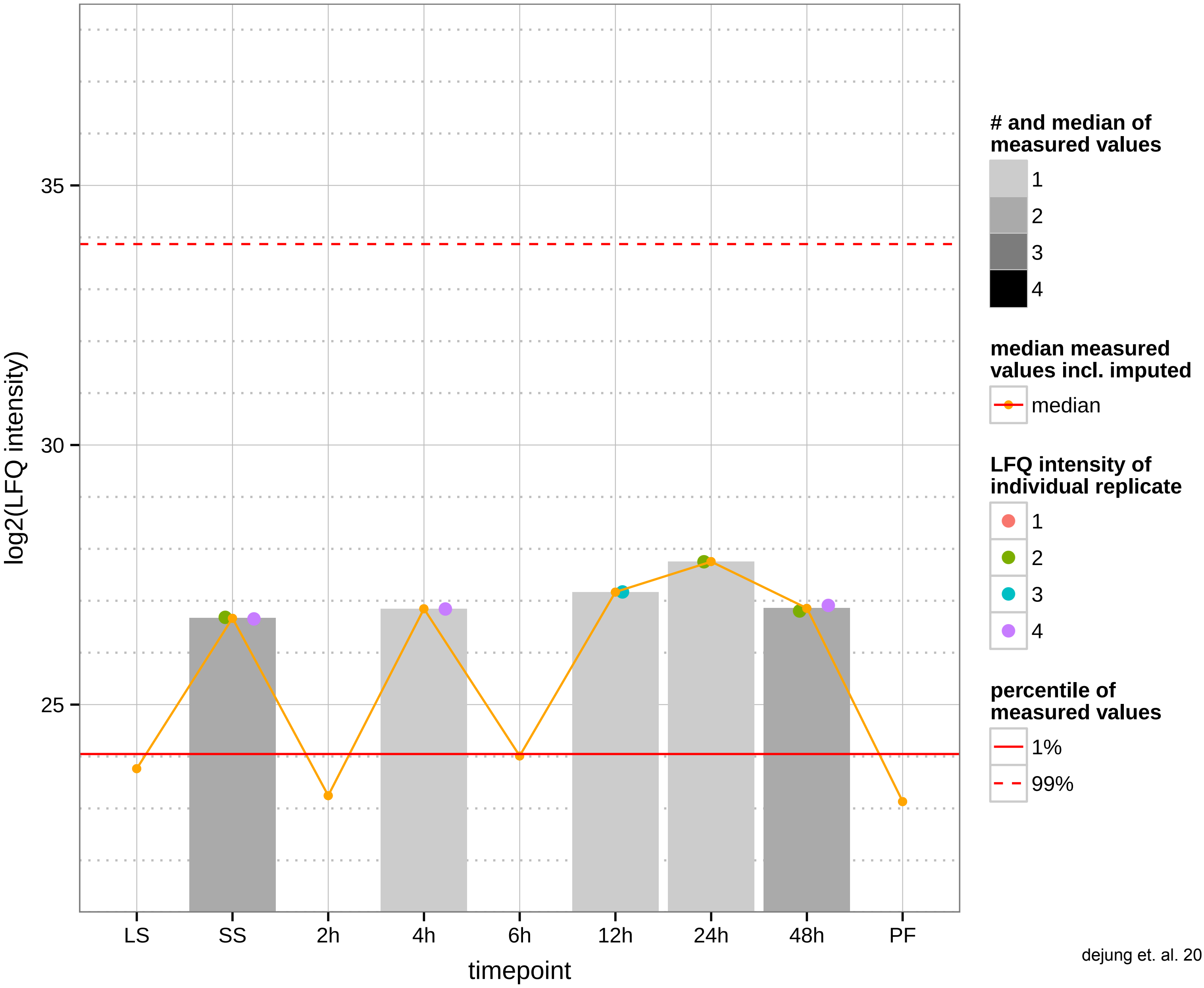
hypothetical protein, conserved
Tb927.11.13570
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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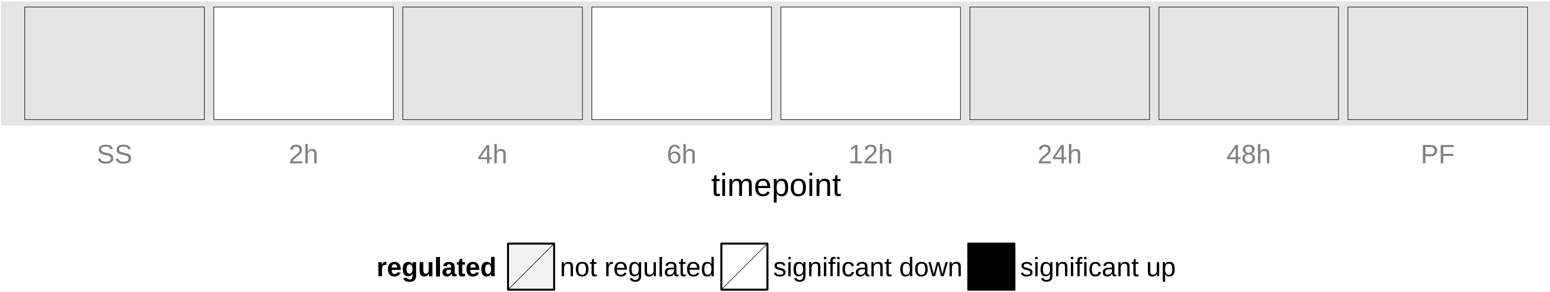
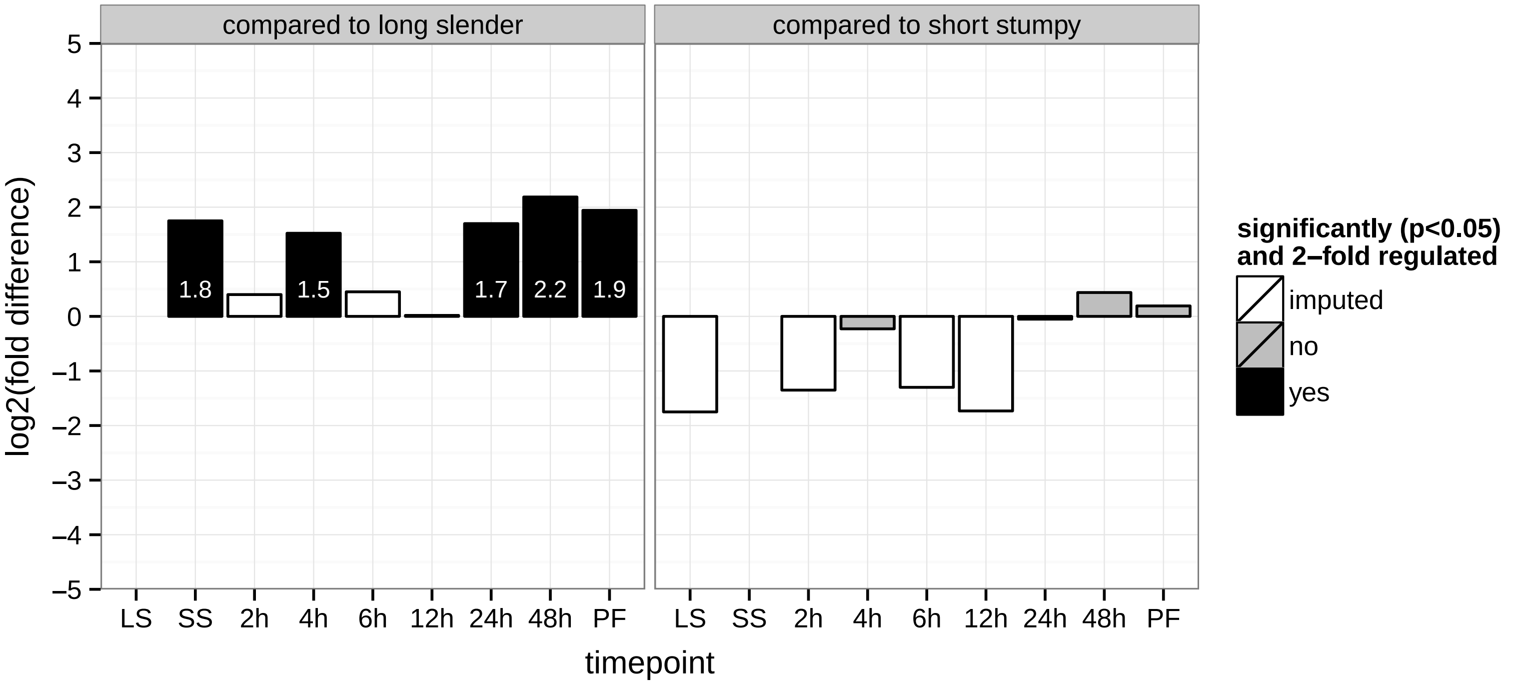
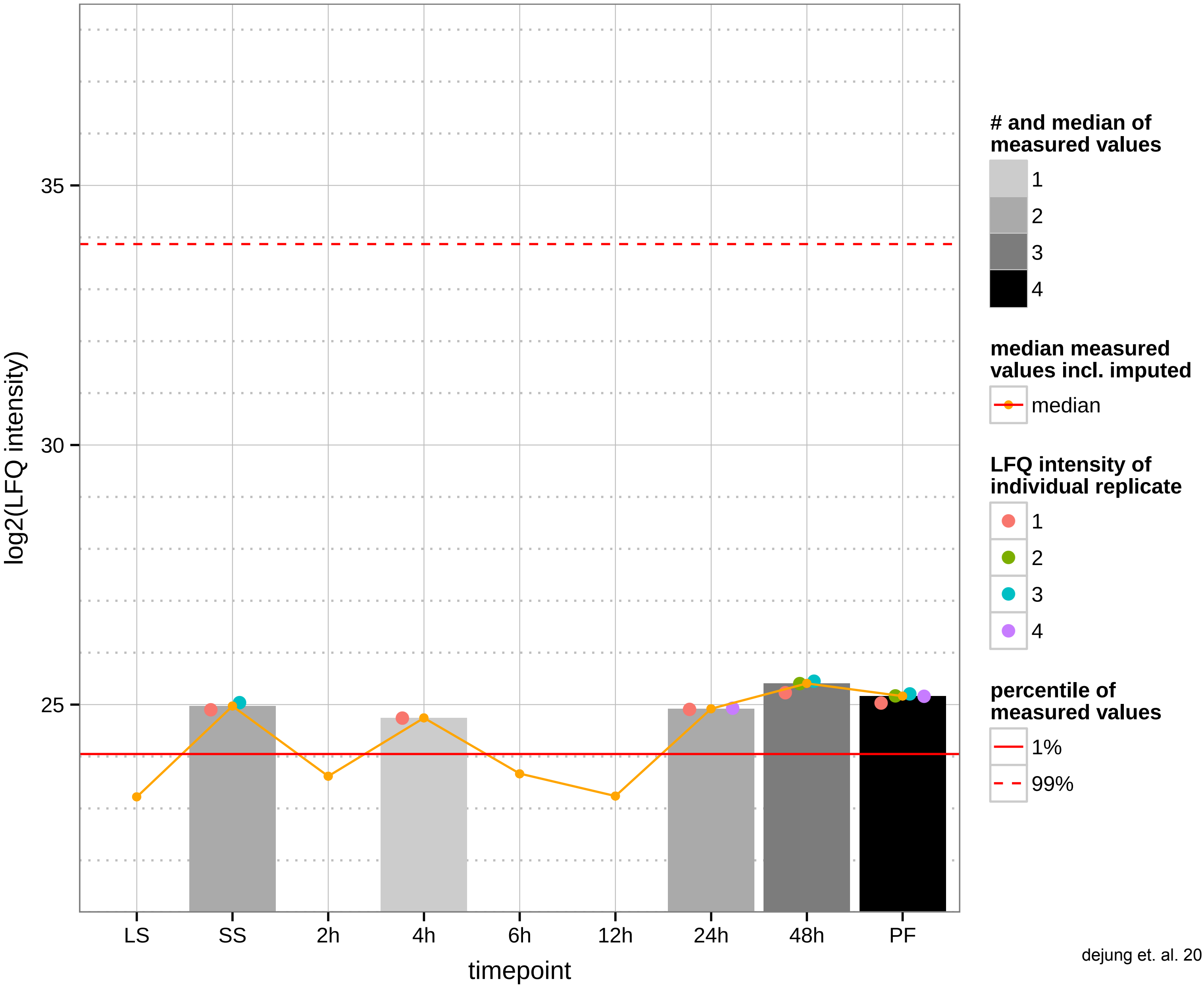


dejung et. al. 2015

hypothetical protein, conserved
Tb927.11.2010
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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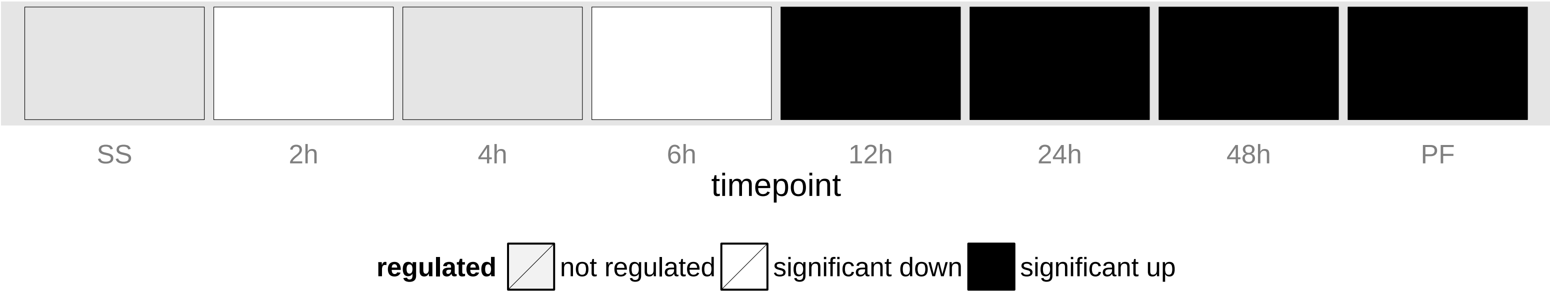

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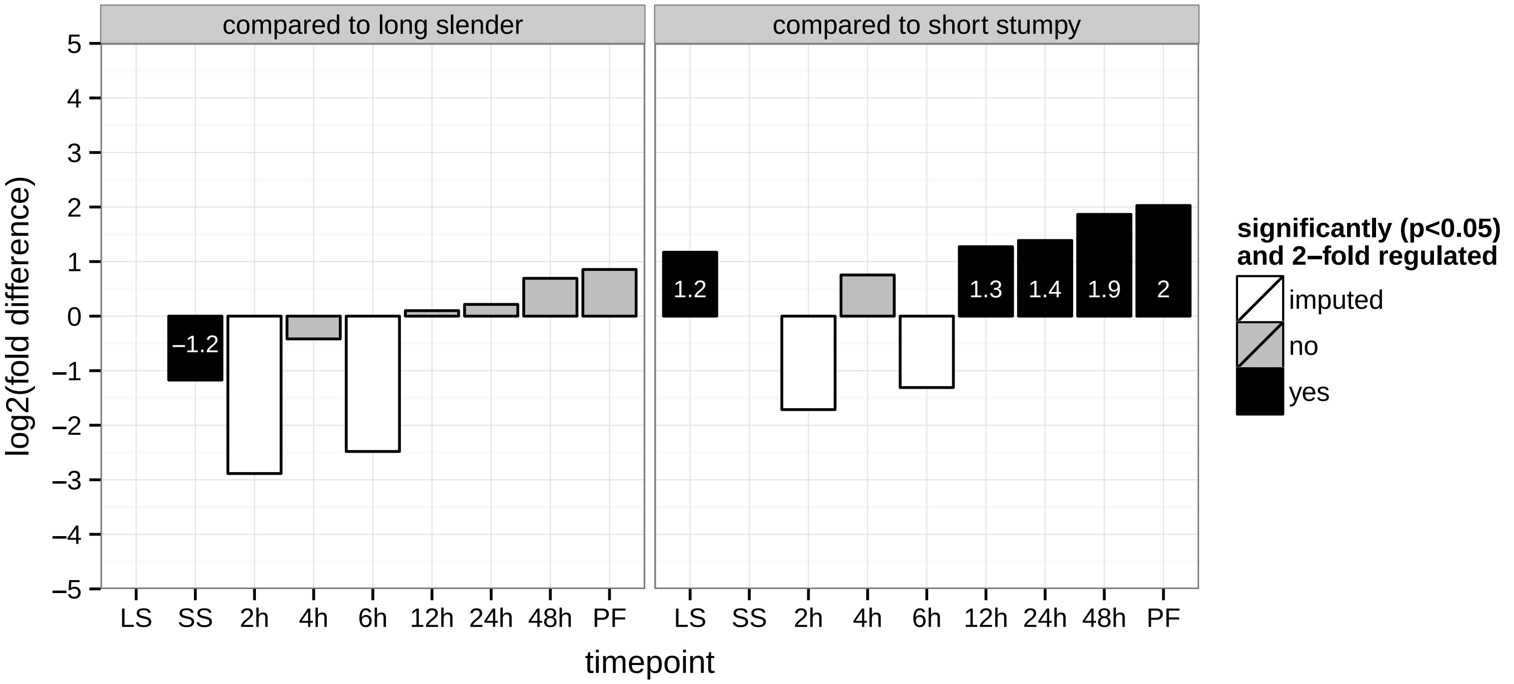
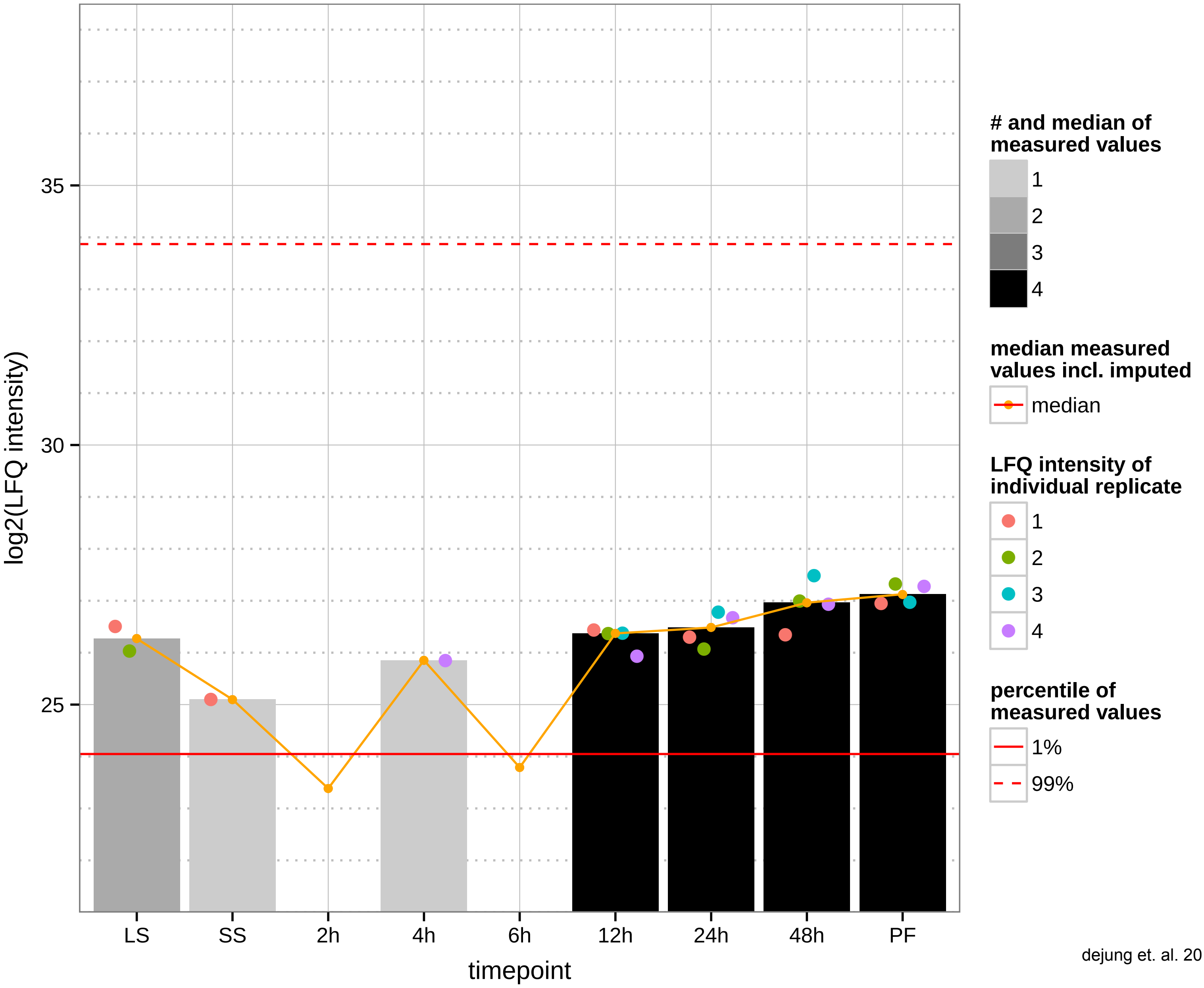
cyclin 1, serine peptidase family S51, peptidase E, putative
Tb927.11.12610
AGOF: null
AGOC: null
AGOP: null
PGOF: serine–type peptidase activity
PGOC: null
PGOP: proteolysis





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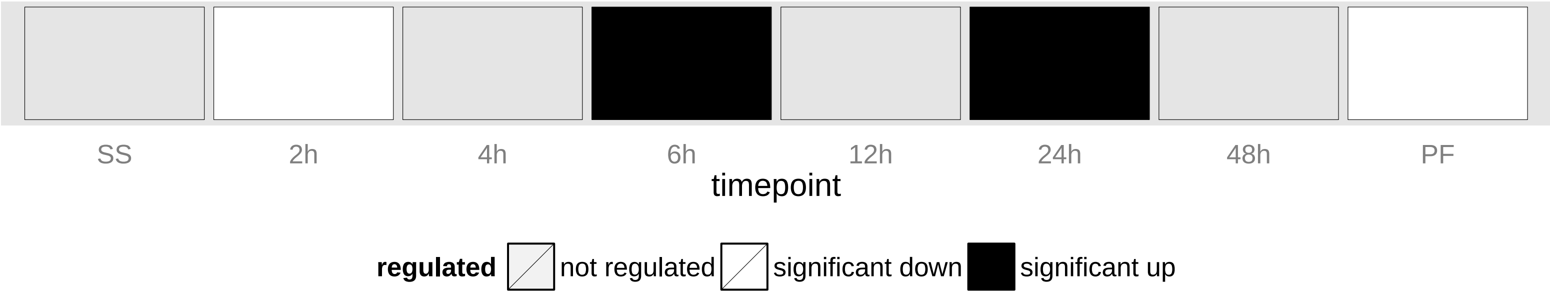

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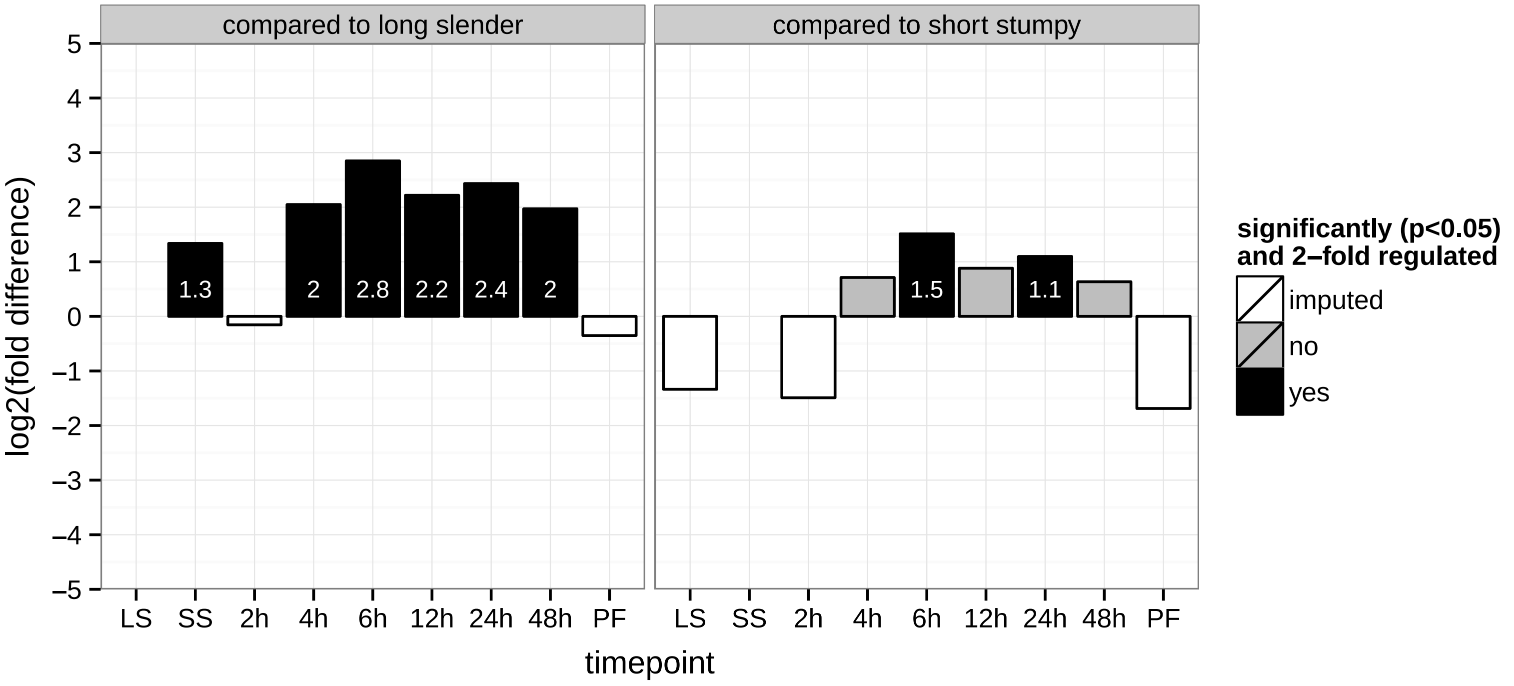
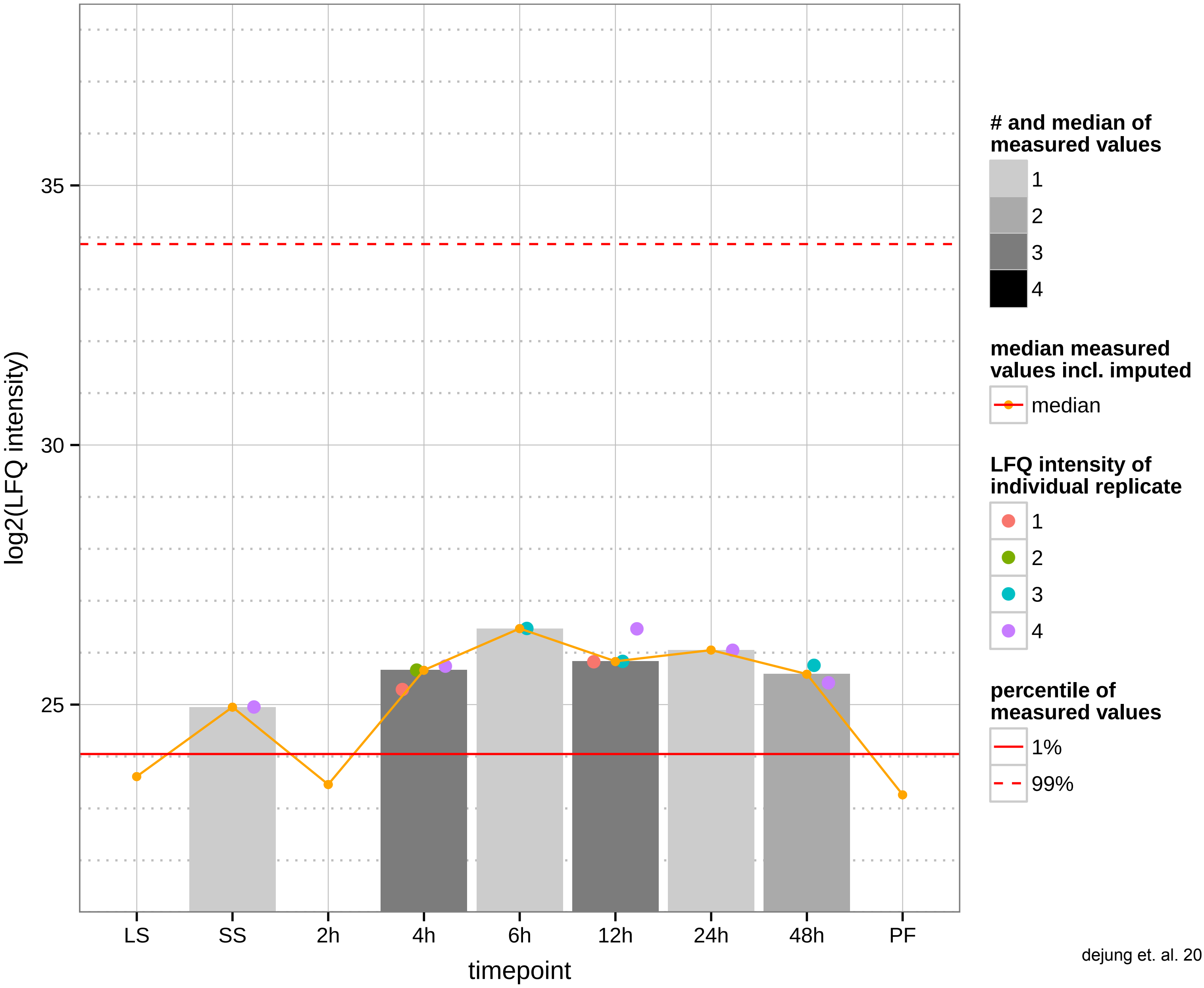
small GTP–binding protein Rab7, putative (Trab7)
Tb927.8.4620
AGOF: GTP binding, GTPase activity
AGOC: intracellular
AGOP: intracellular protein transport, nucleocytoplasmic transport, small GTPase mediated signal transduction
PGOF: GTP binding, GTPase activity
PGOC: intracellular, membrane
PGOP: GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, protein transport, signal transducti





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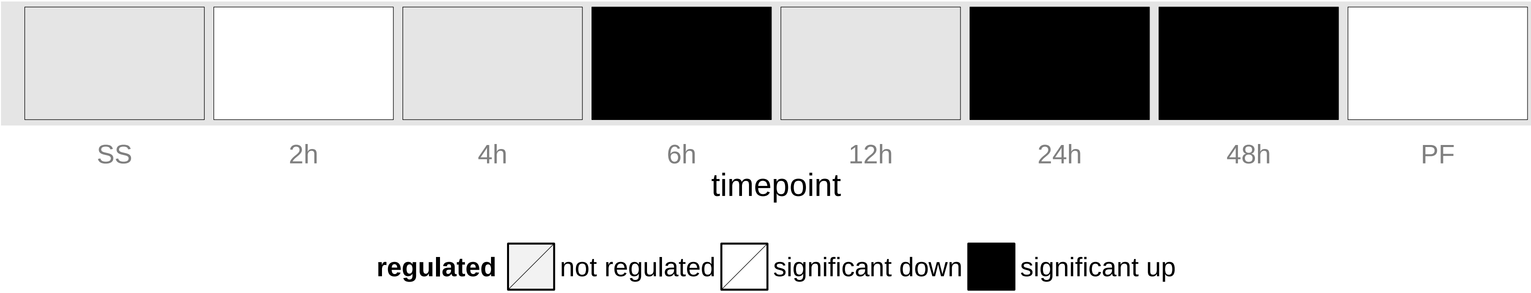

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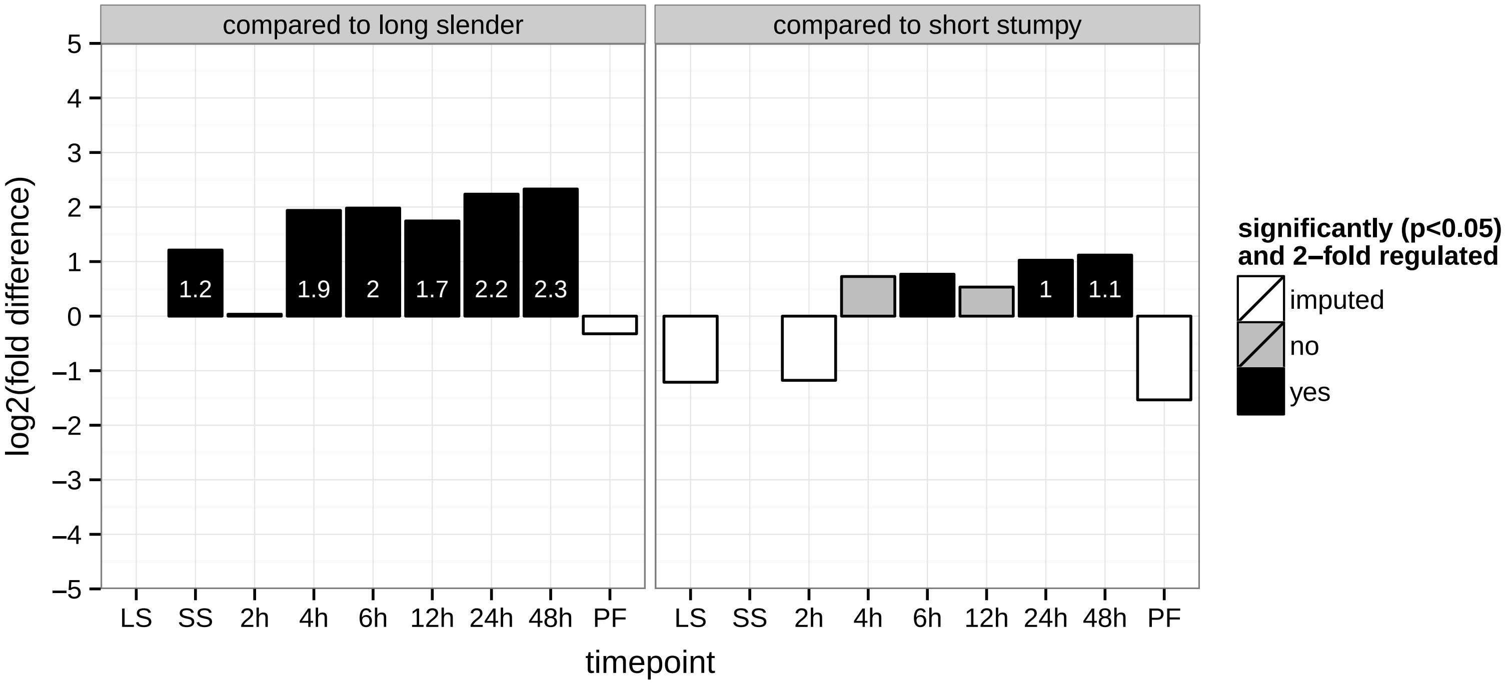
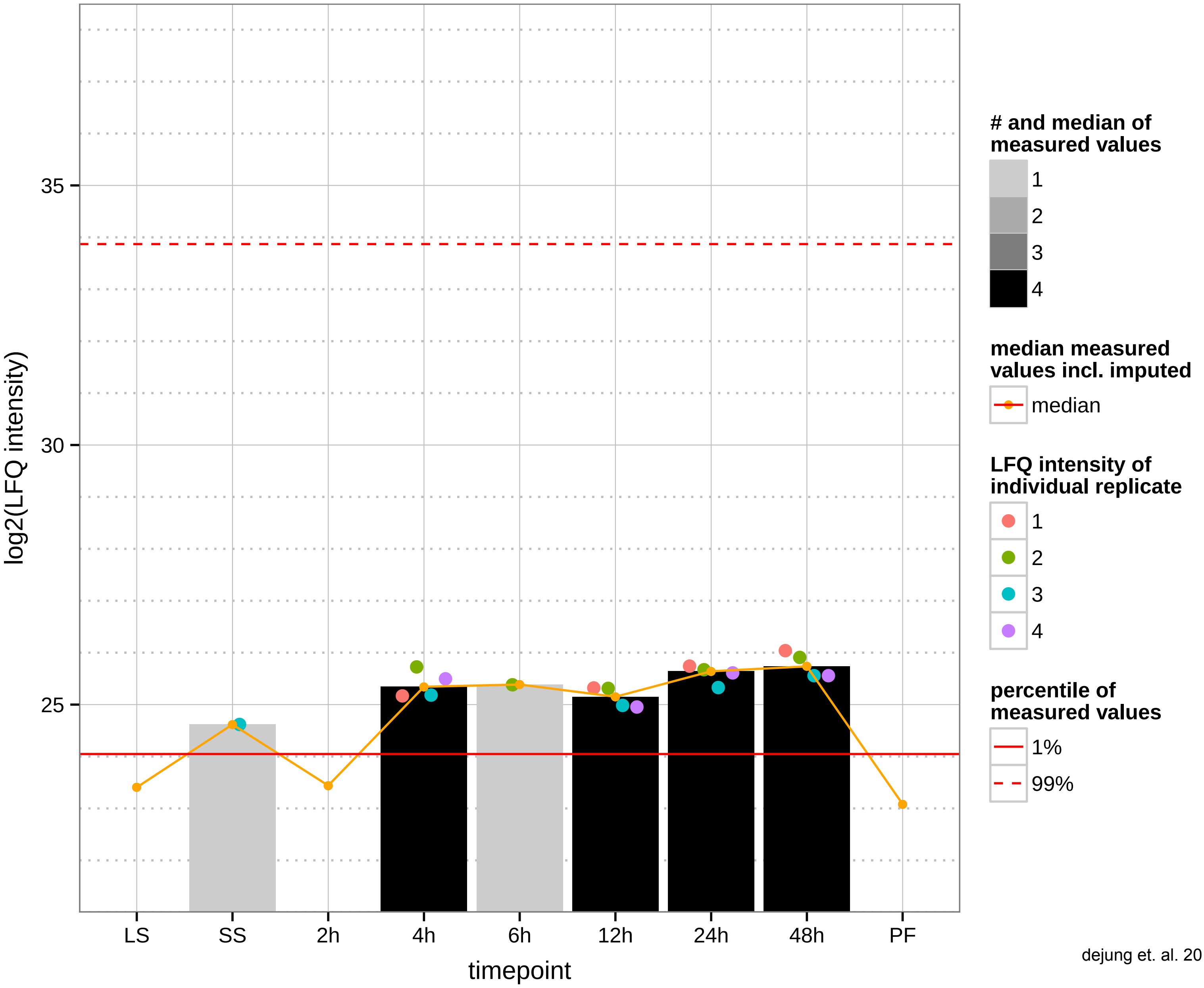
hypothetical protein, conserved
Tb927.10.13980
AGOF: voltage−gated potassium channel activity
AGOC: membrane, voltage−gated potassium channel complex
AGOP: potassium ion transport
PGOF: protein binding
PGOC: null
PGOP: protein homooligomerization





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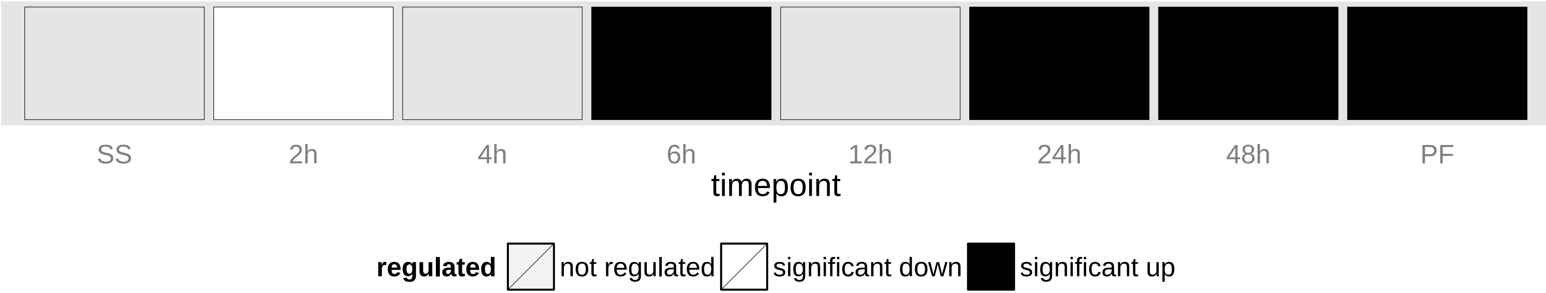

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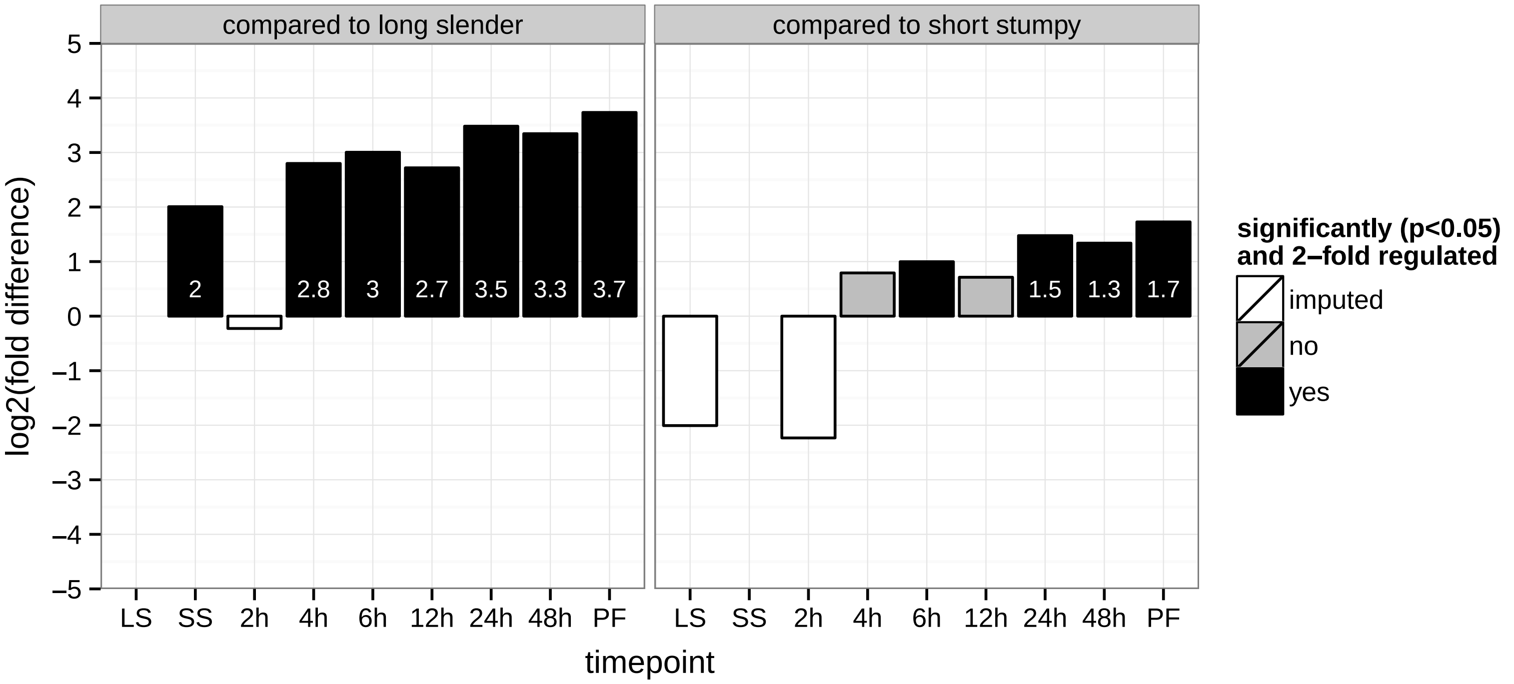
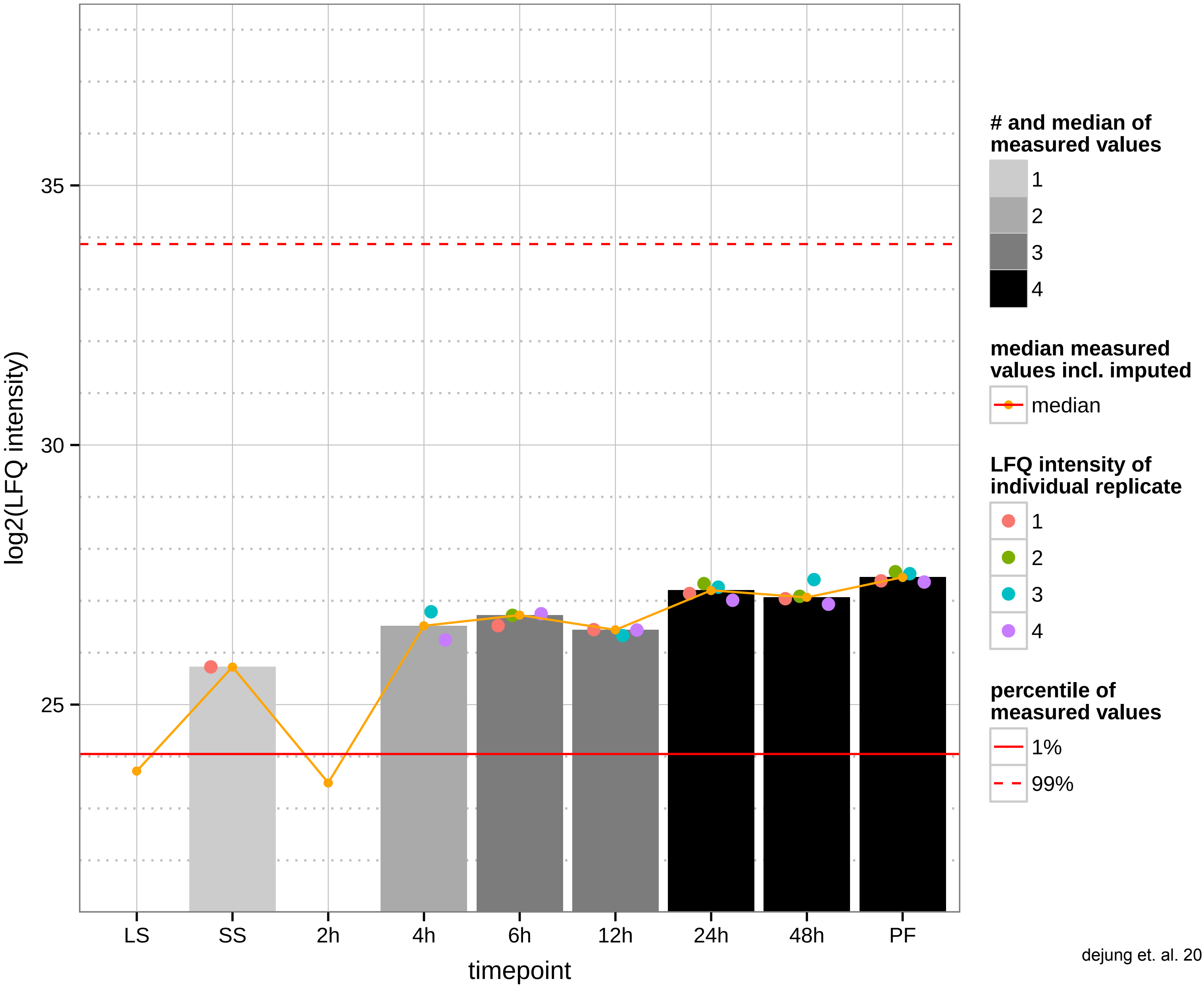
60S ribosomal protein–like, putative
Tb927.7.4550;Tb11.v5.0268
AGOF: null, structural constituent of ribosome
AGOC: null, intracellular, ribosome
AGOP: null, translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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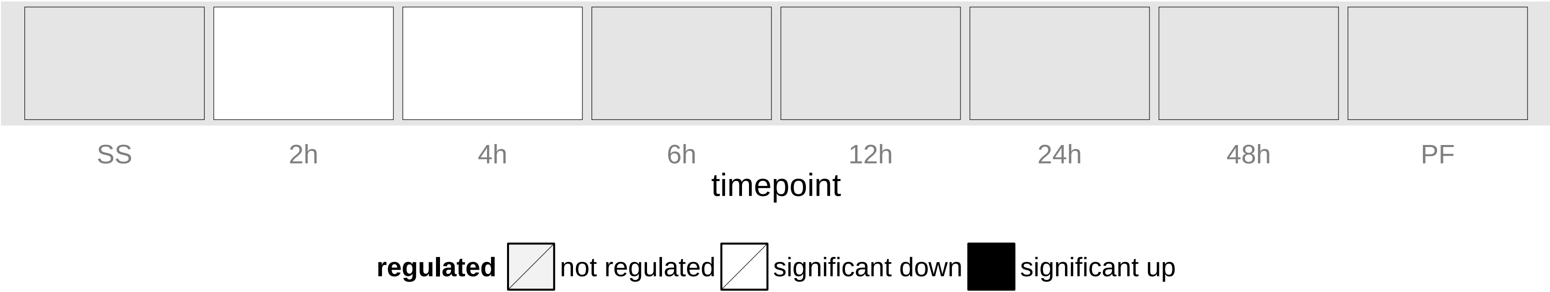

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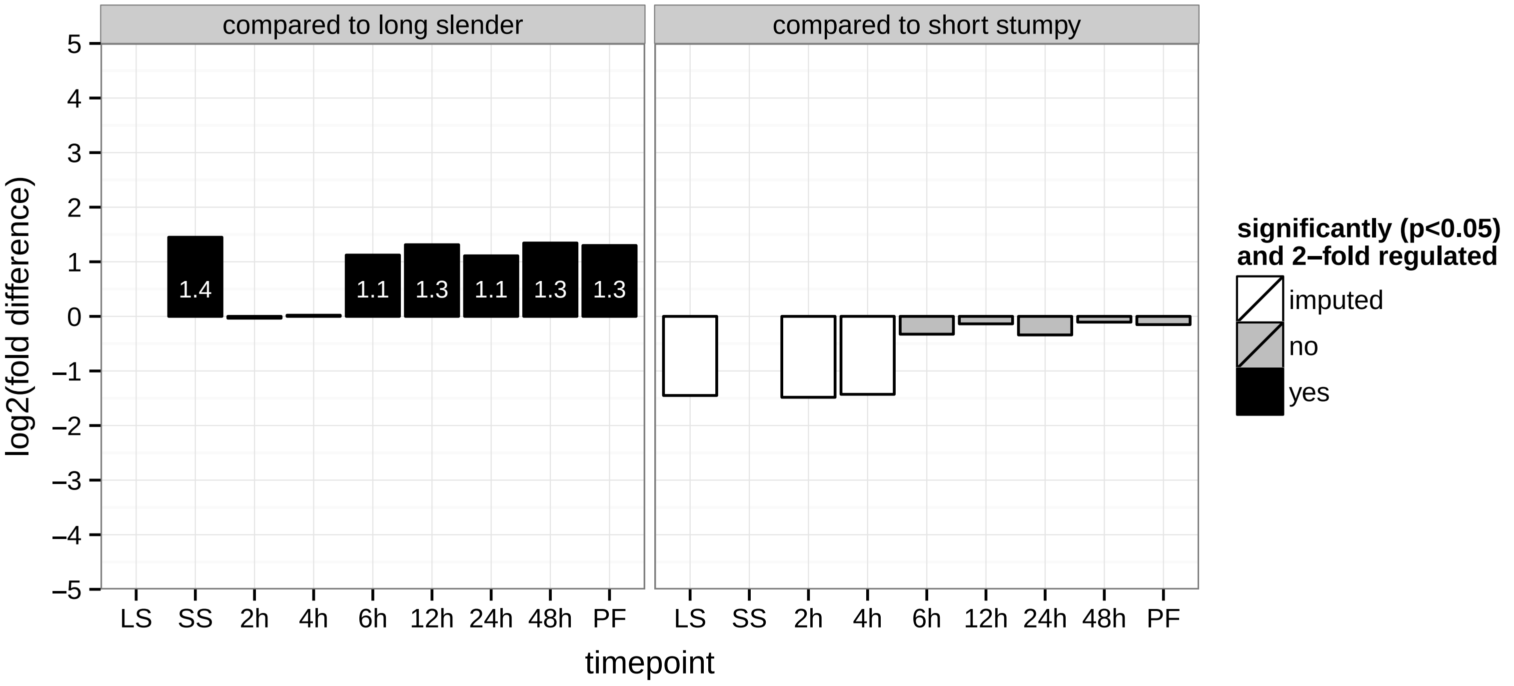
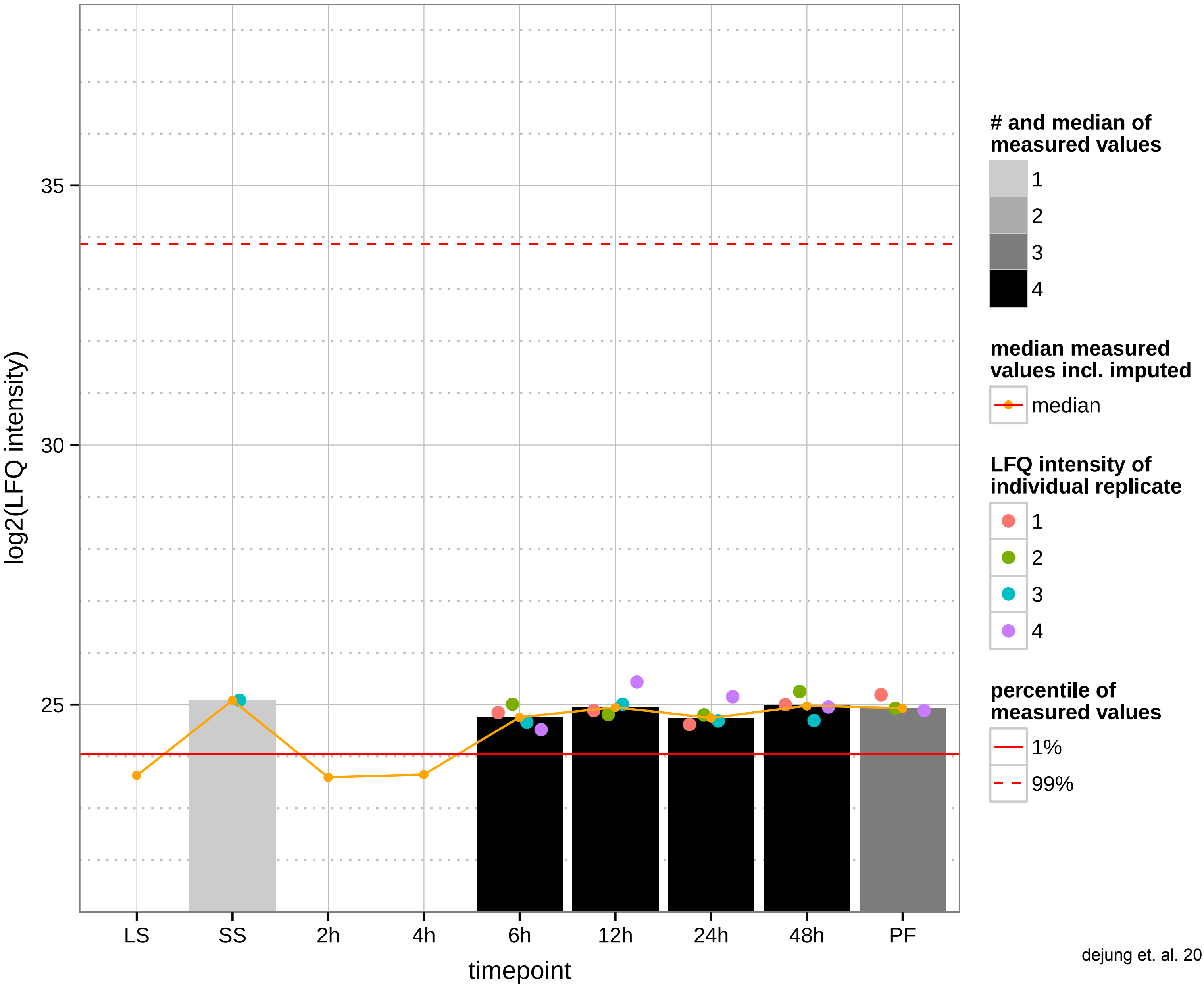
hypothetical protein, conserved
Tb927.8.6800
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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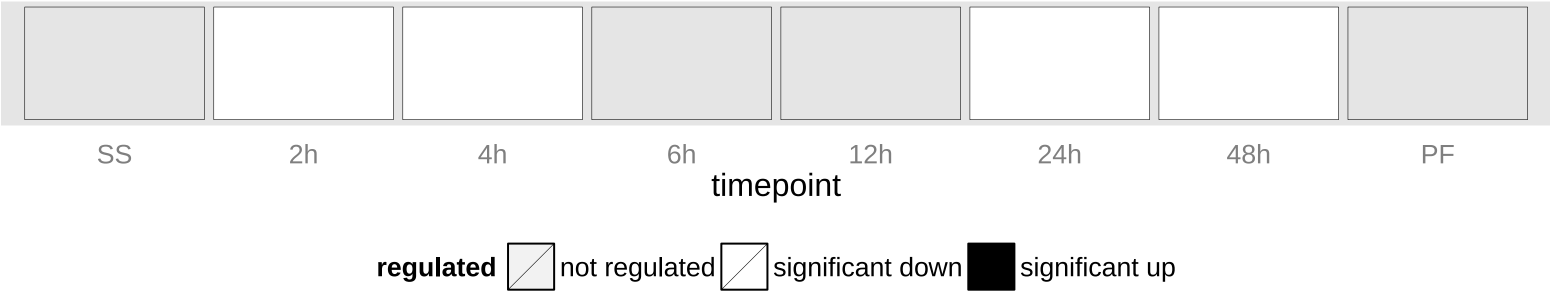

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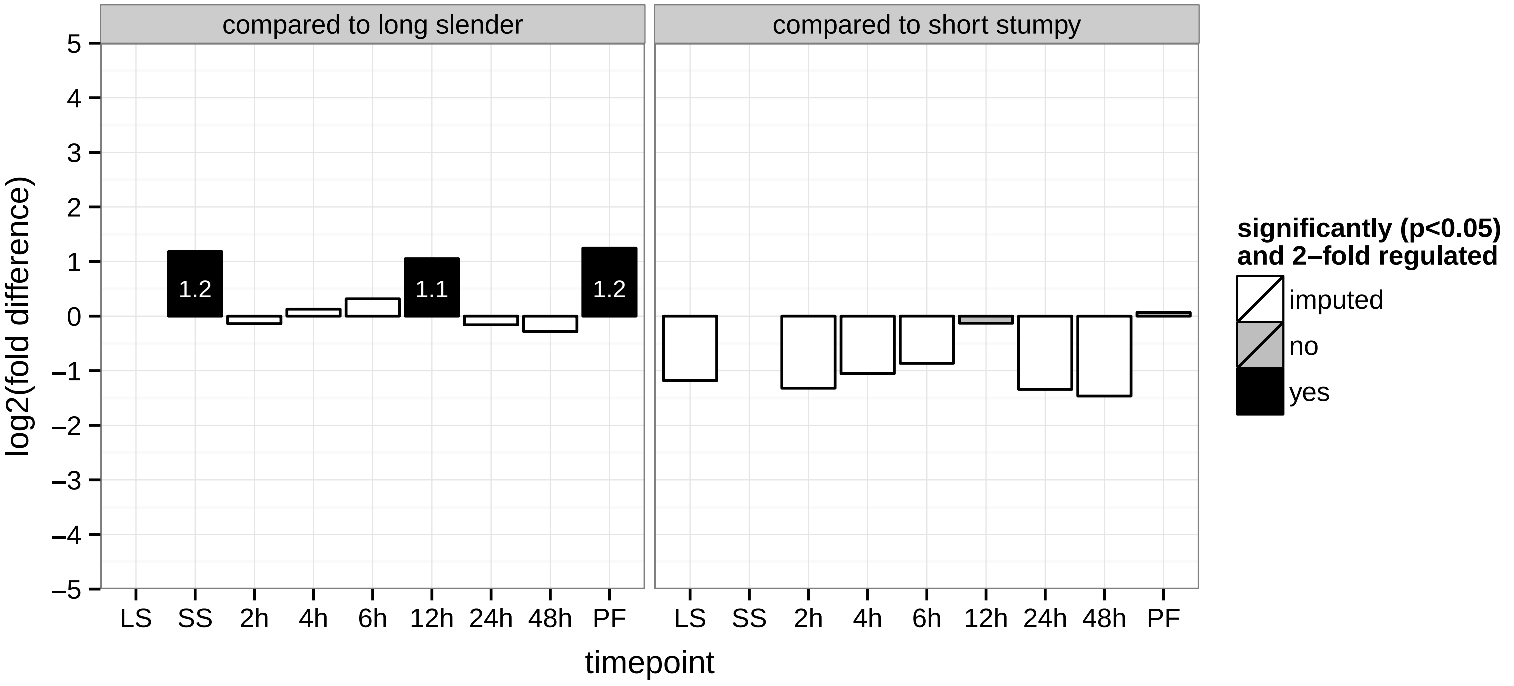
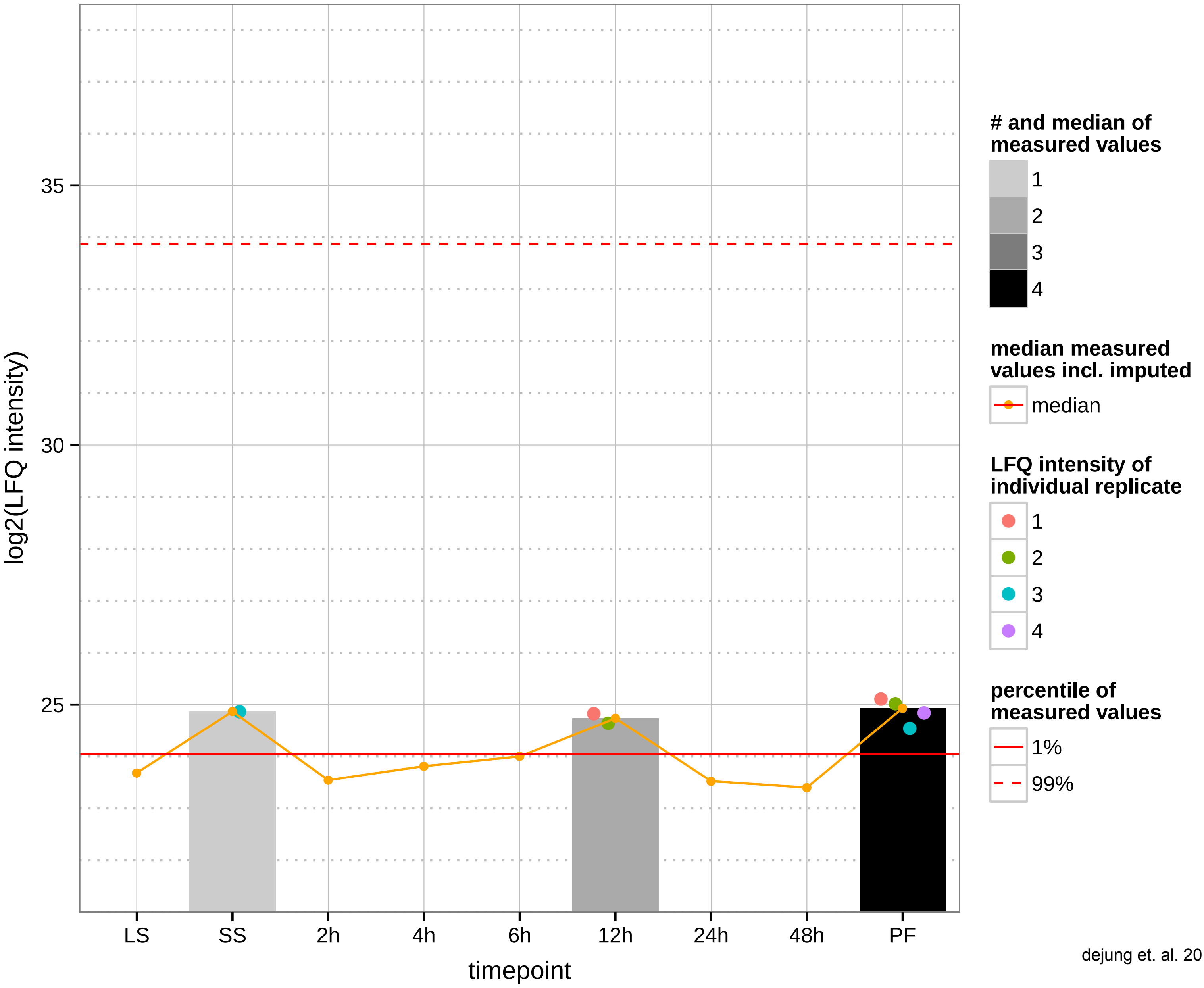
GPI alpha–mannosyltransferase III, GPI10 (GPI10)
Tb927.10.5560
AGOF: mannosyltransferase activity
AGOC: integral to membrane, intrinsic to endoplasmic reticulum membrane
AGOP: GPI anchor biosynthetic process, growth
PGOF: transferase activity, transferring glycosyl groups
PGOC: intrinsic to endoplasmic reticulum membrane
PGOP: GPI anchor biosynthetic process





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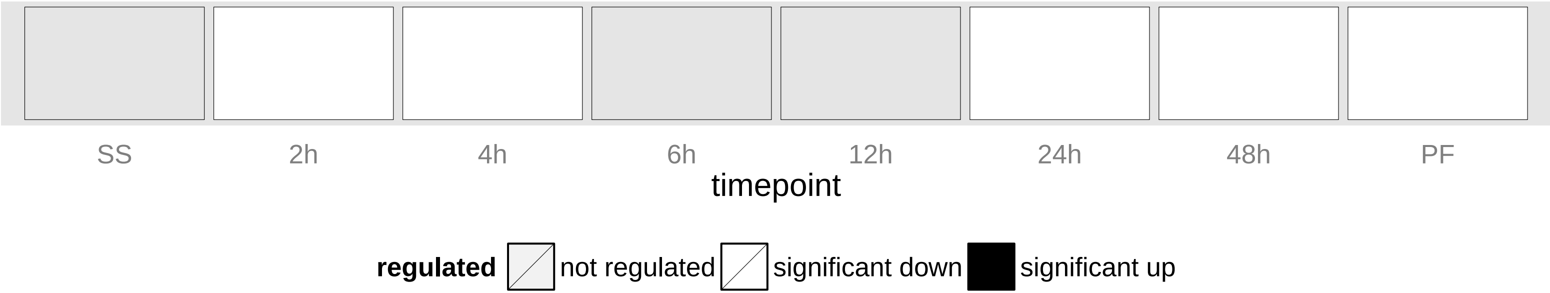

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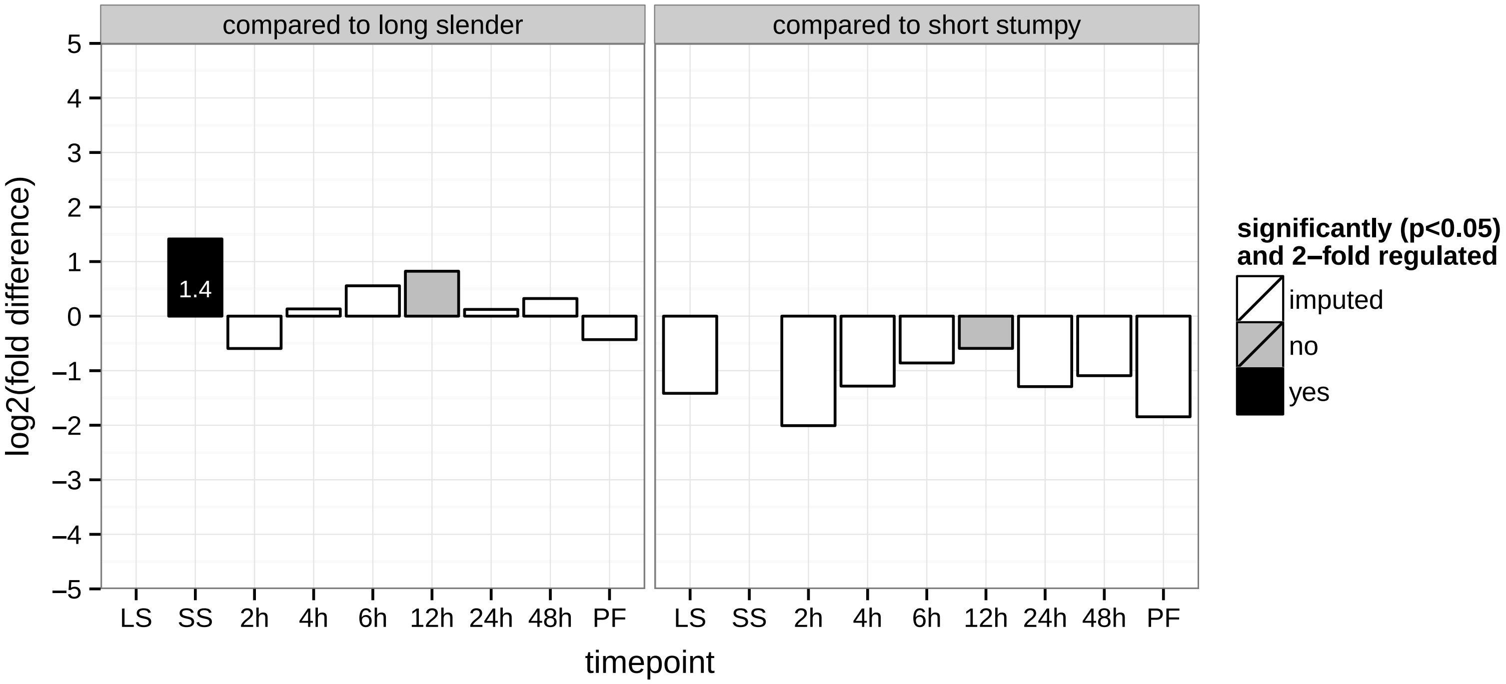
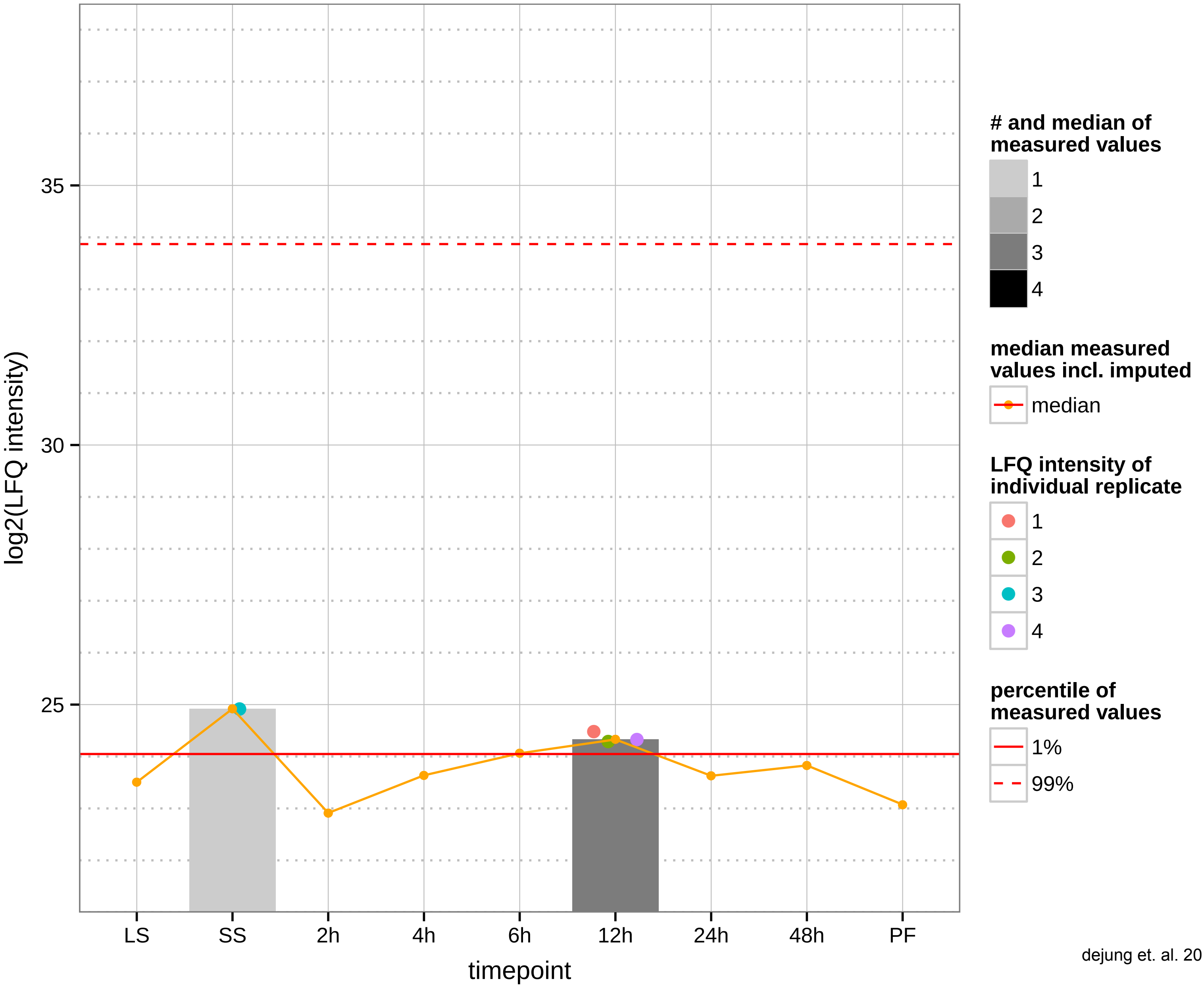
variant surface glycoprotein, fragment, hypothetical protein, conserved, chrX additional, unordered contigs, predicted SAP dor
Tb927.10.4440;Tb10.v4.0034
AGOF: null, nucleic acid binding
AGOC: null
AGOP: null
PGOF: null, nucleic acid binding
PGOC: null
PGOP: evasion or tolerance of host immune response, null





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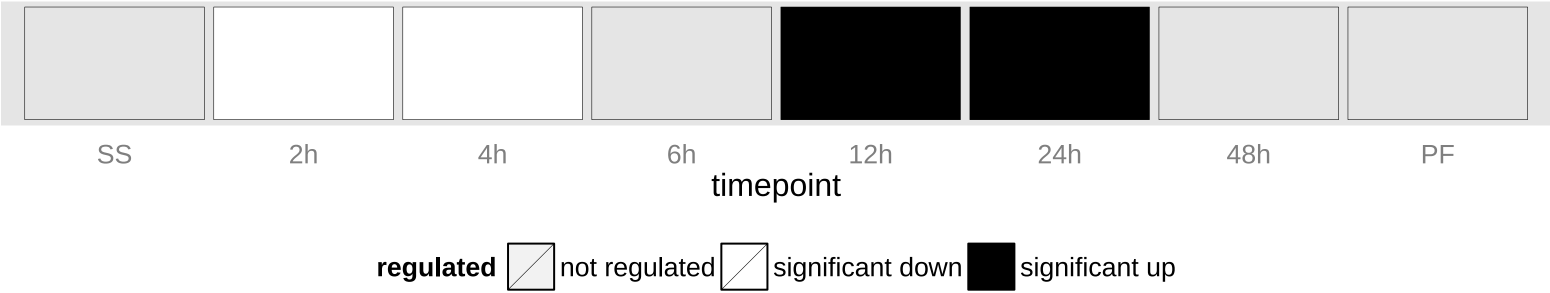

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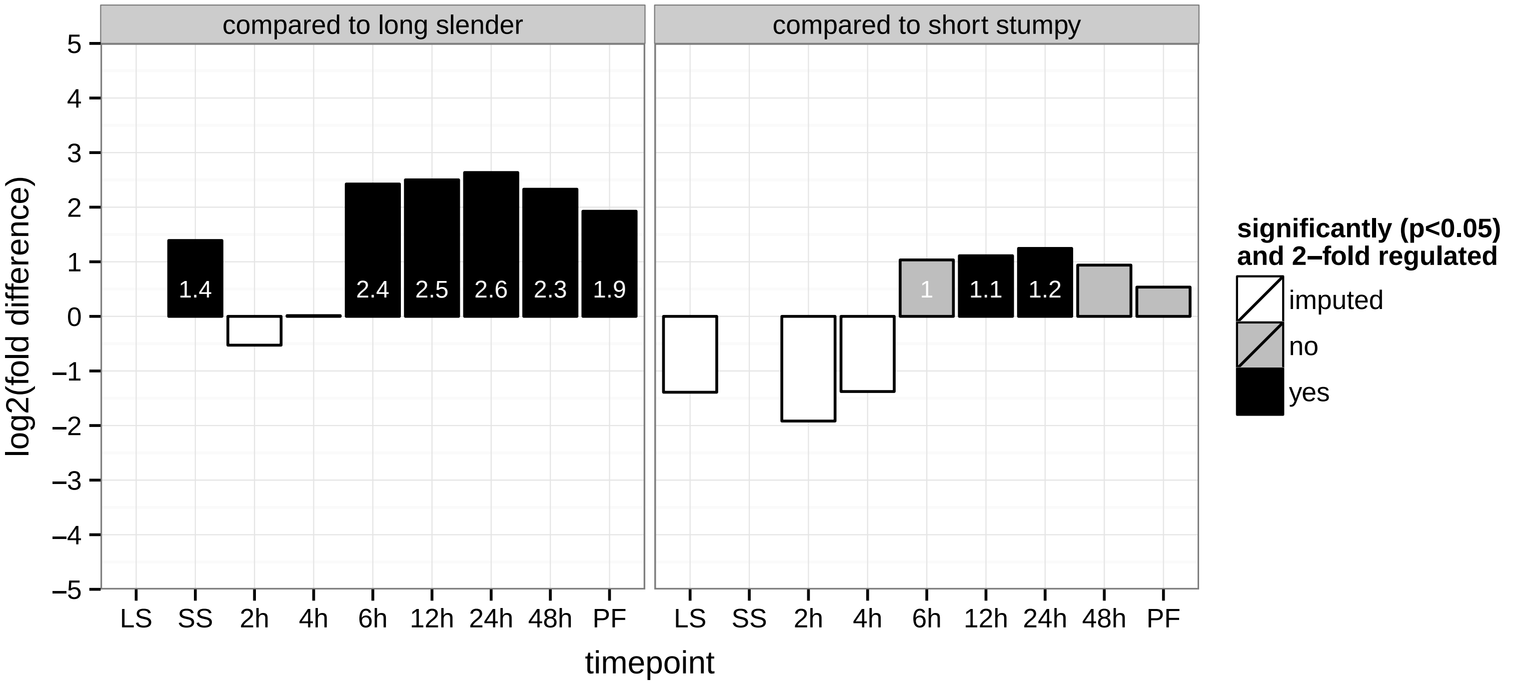
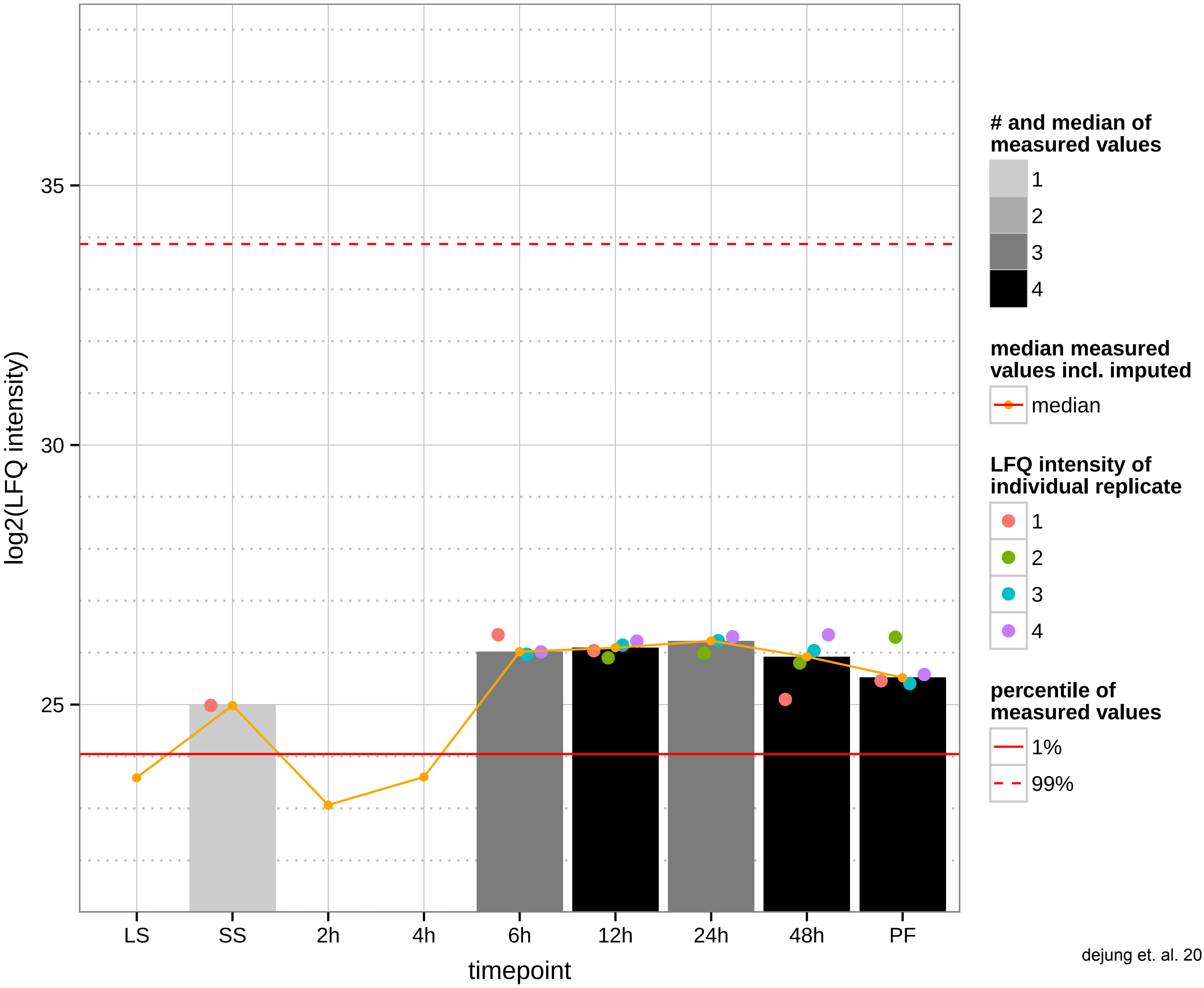
hypothetical protein, conserved
Tb927.10.15810
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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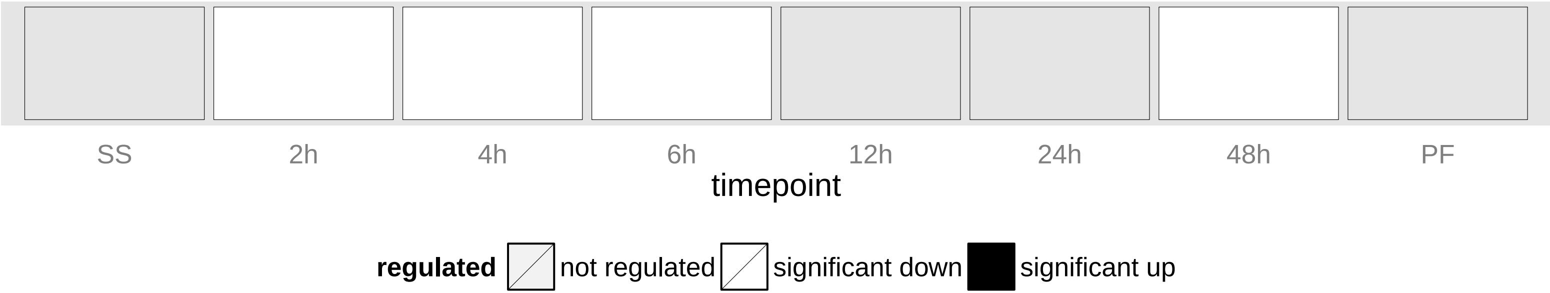

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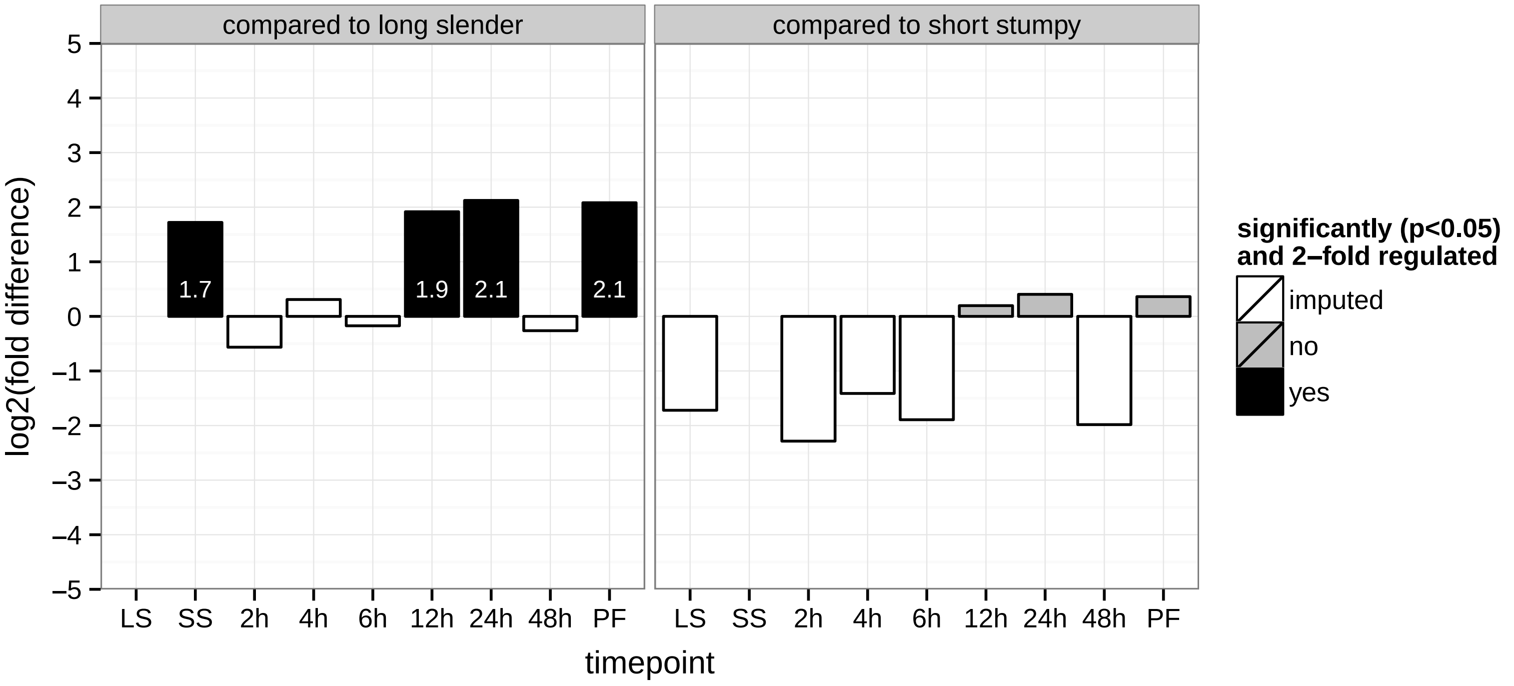
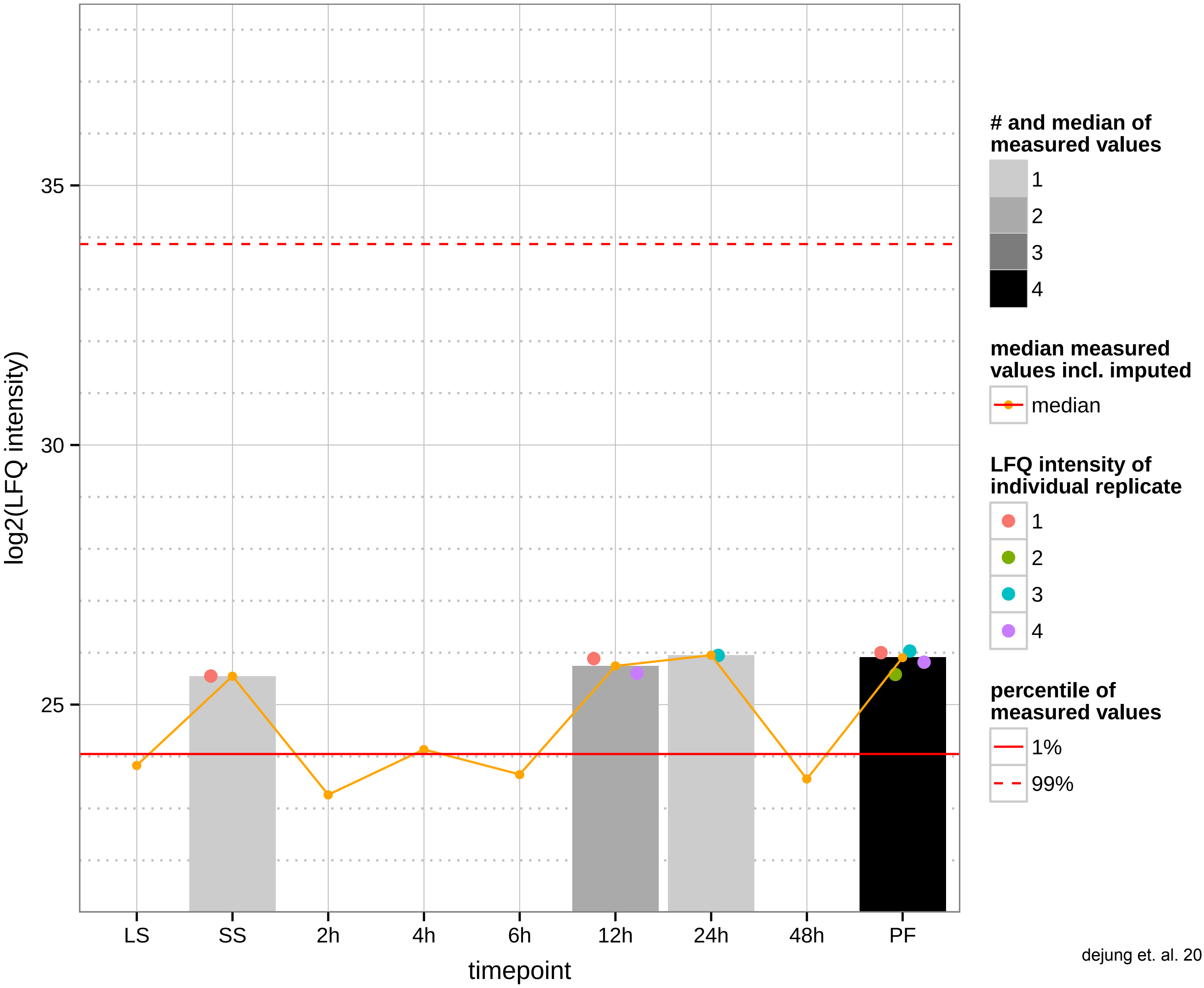
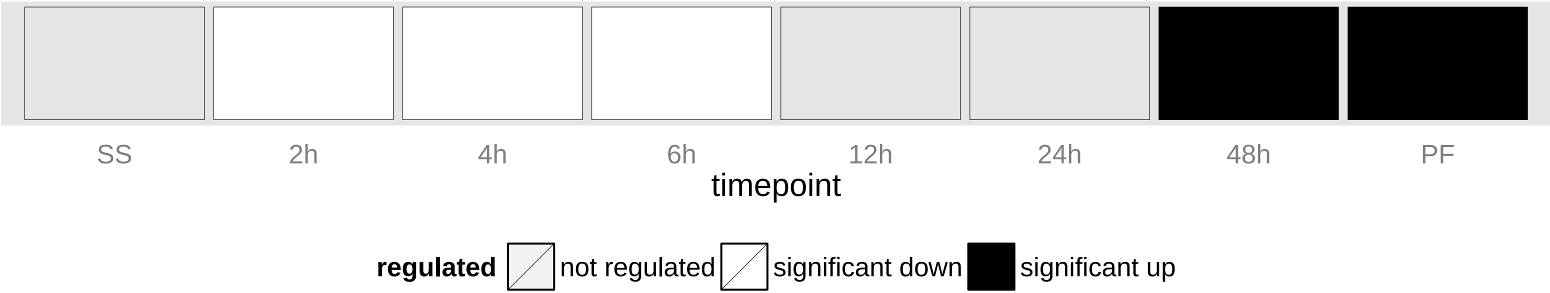
hypothetical protein, conserved
Tb927.11.14230
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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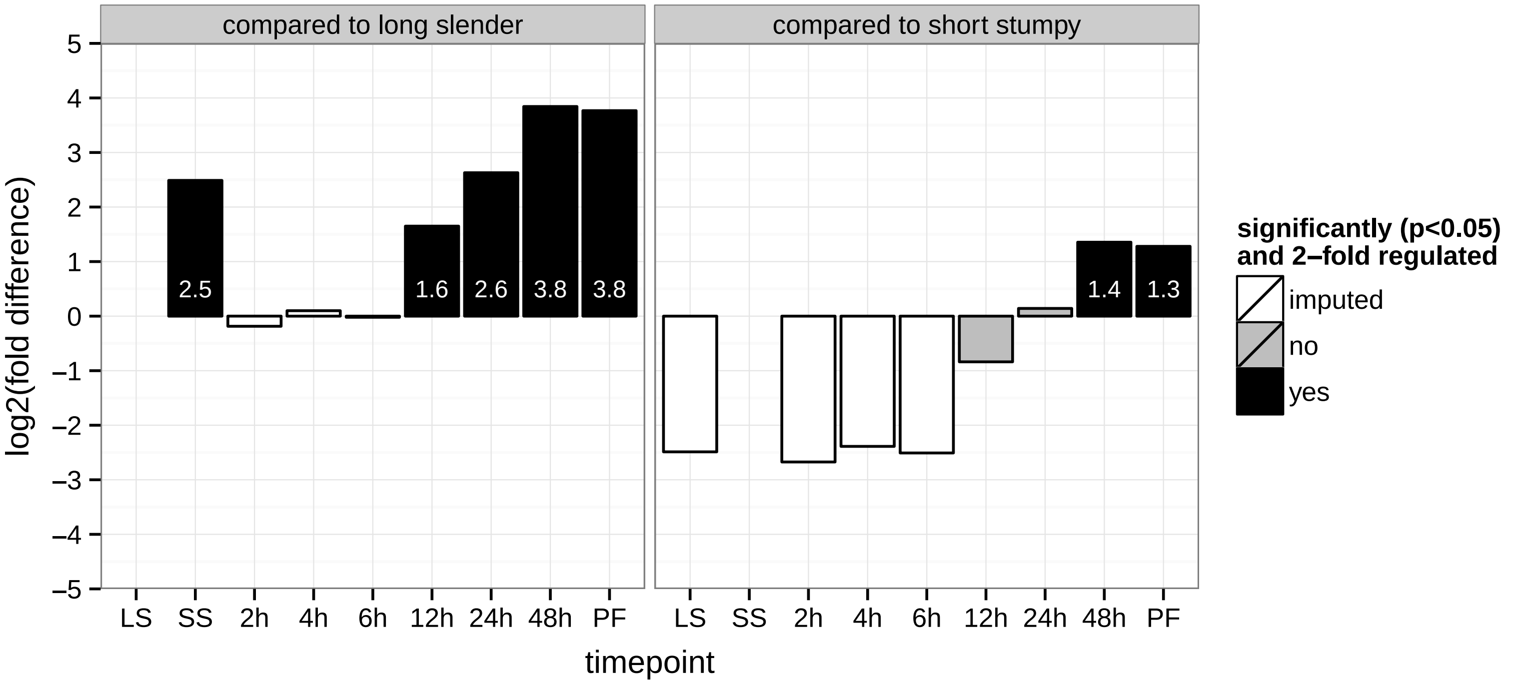
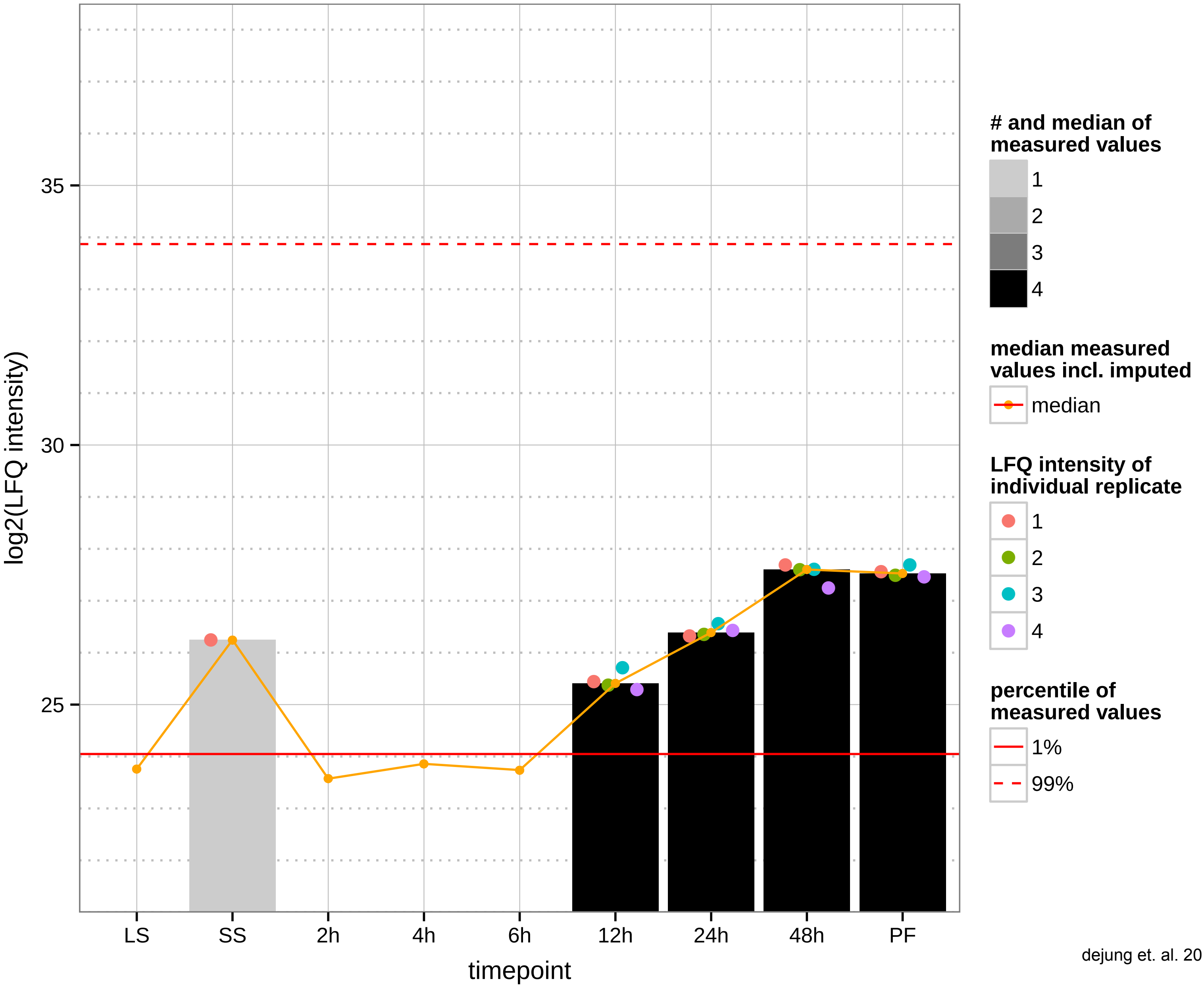
hypothetical protein, conserved
Tb927.5.1780
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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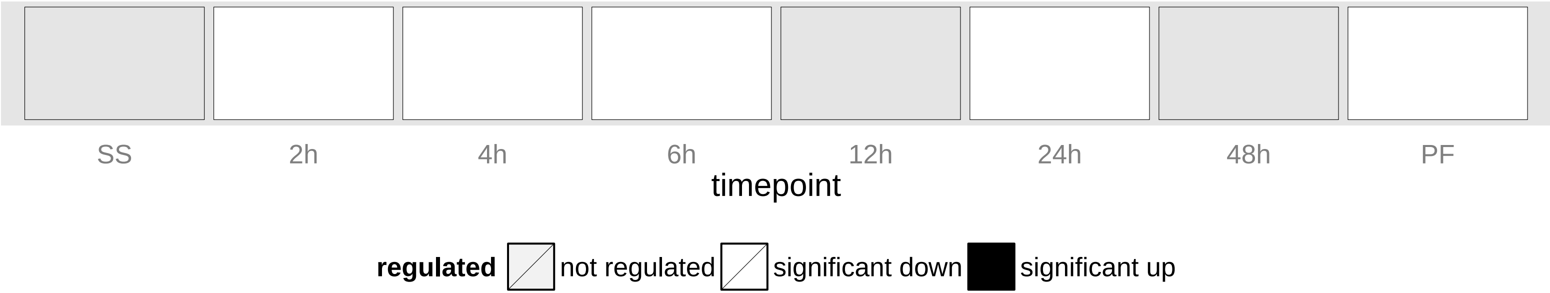

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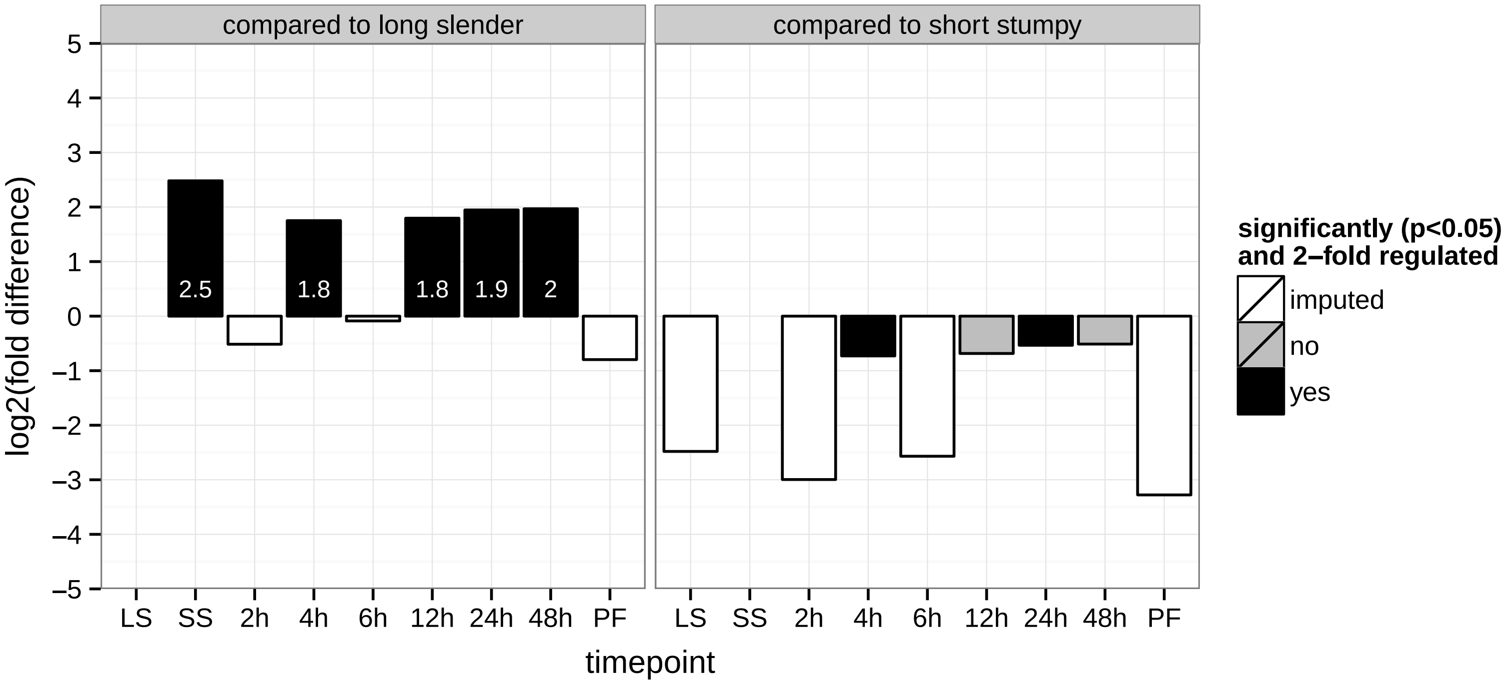
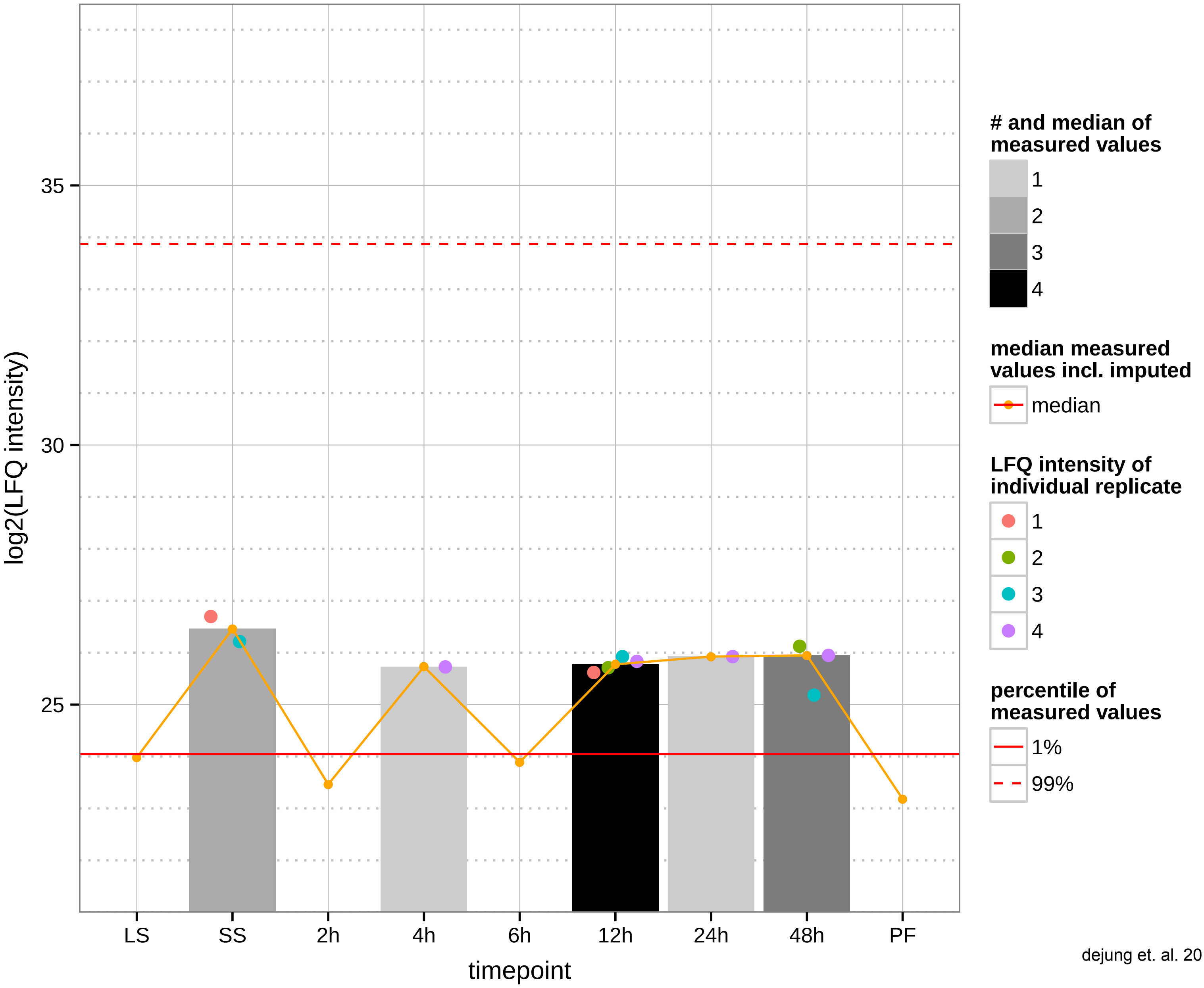
hypothetical protein, conserved
Tb927.2.2530
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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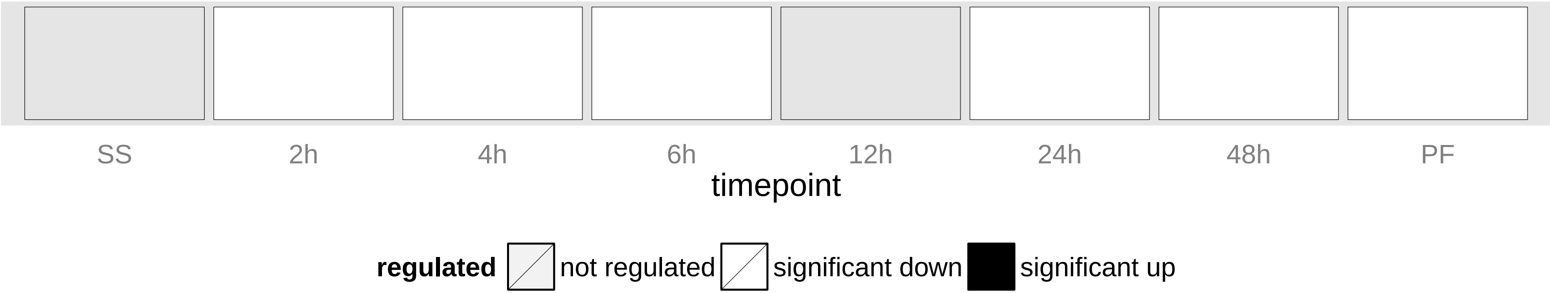

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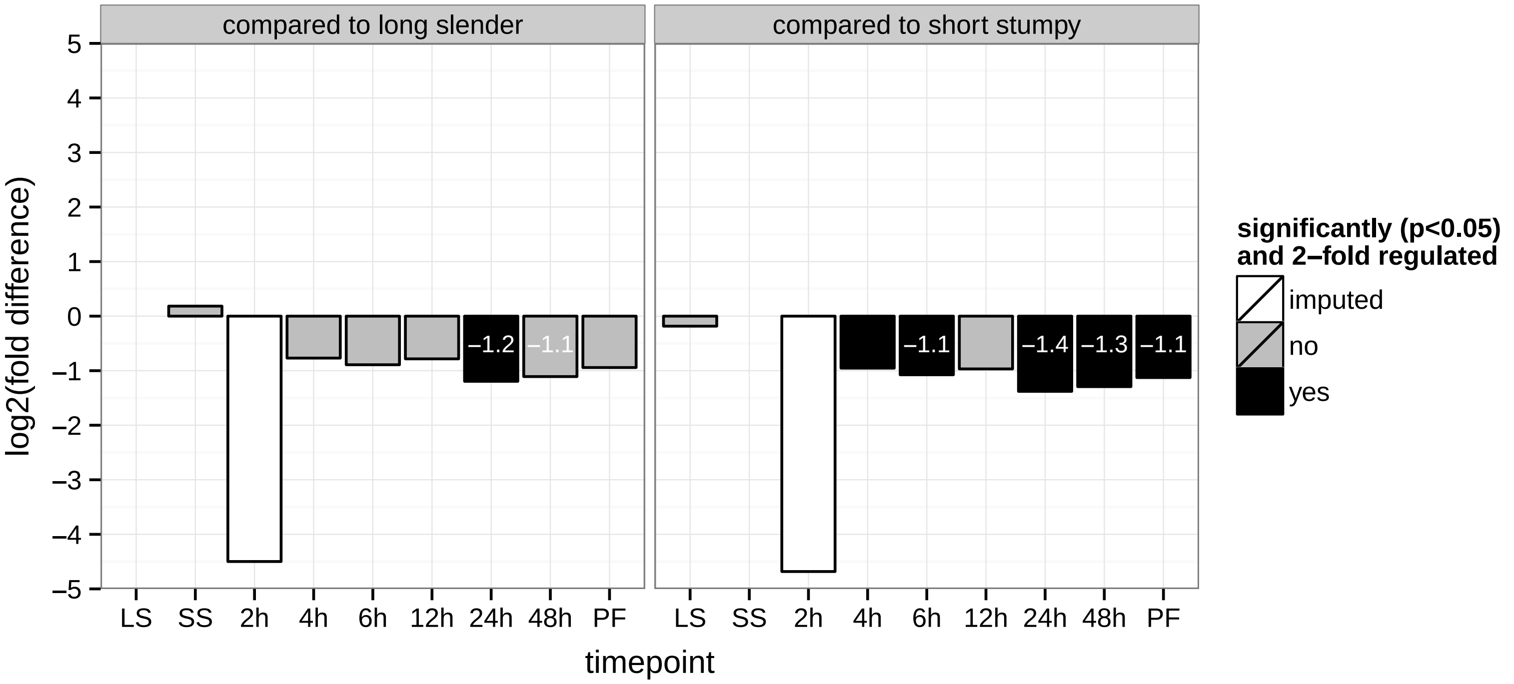
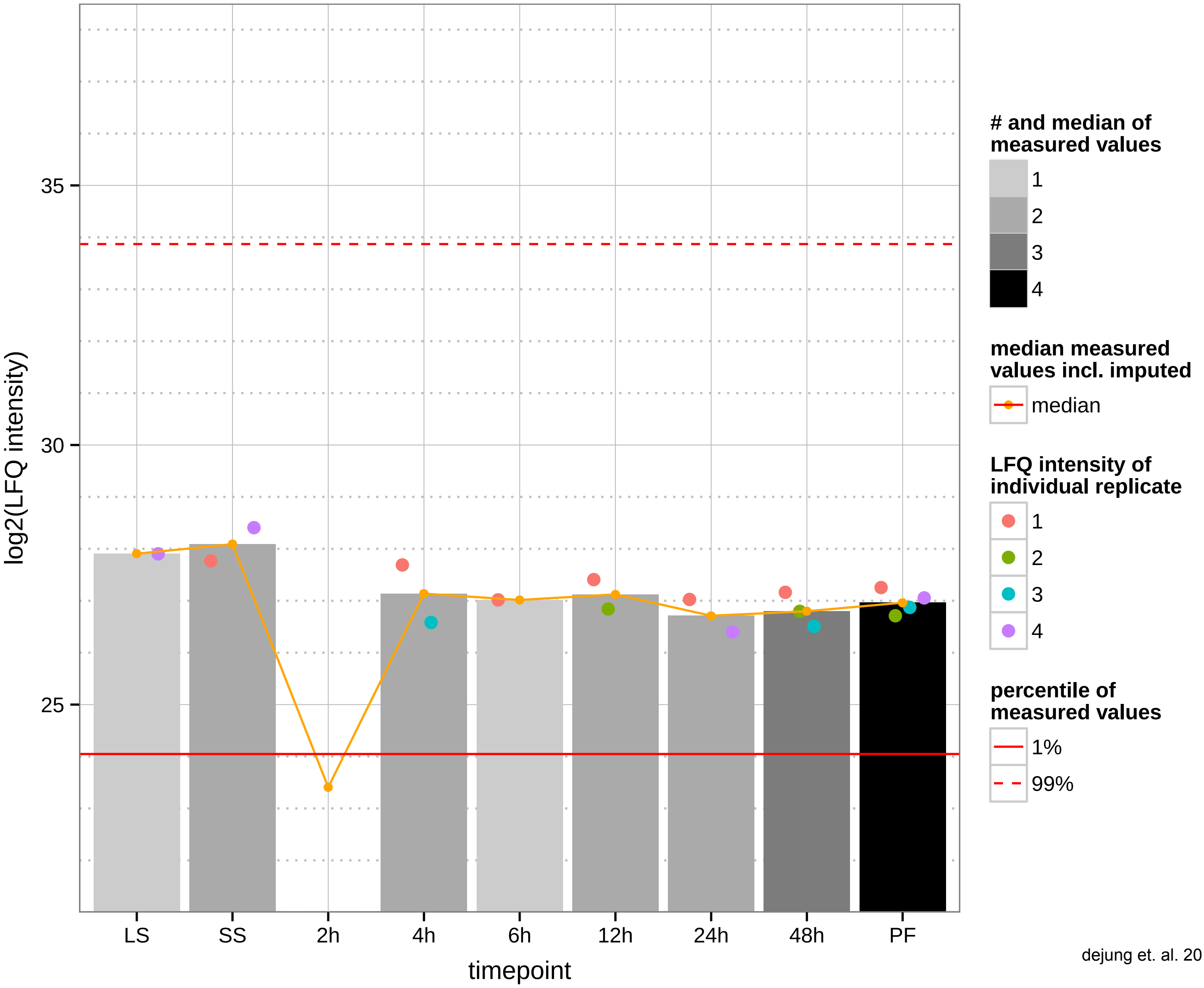
AAA ATPase, putative
Tb927.11.6350
AGOF: ATP binding, ATPase activity
AGOC: null
AGOP: protein metabolic process
PGOF: ATP binding, nucleoside–triphosphatase activity, nucleotide binding
PGOC: null
PGOP: null





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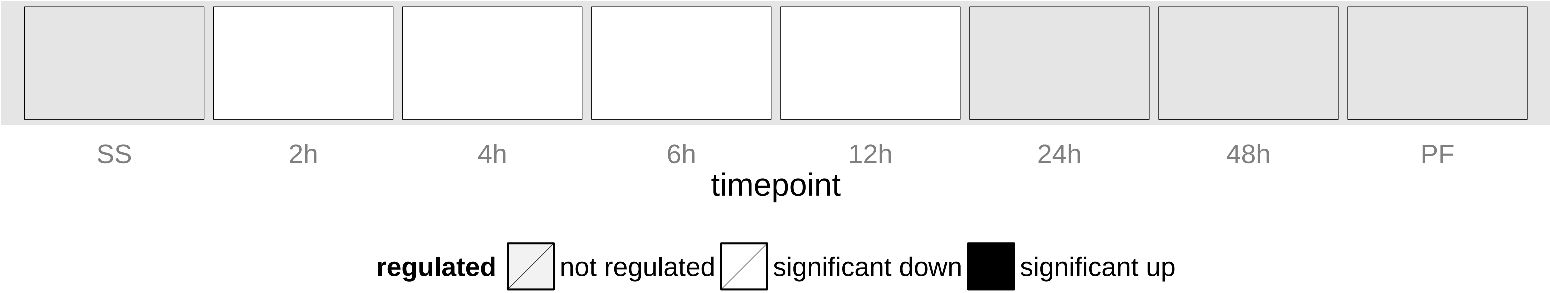

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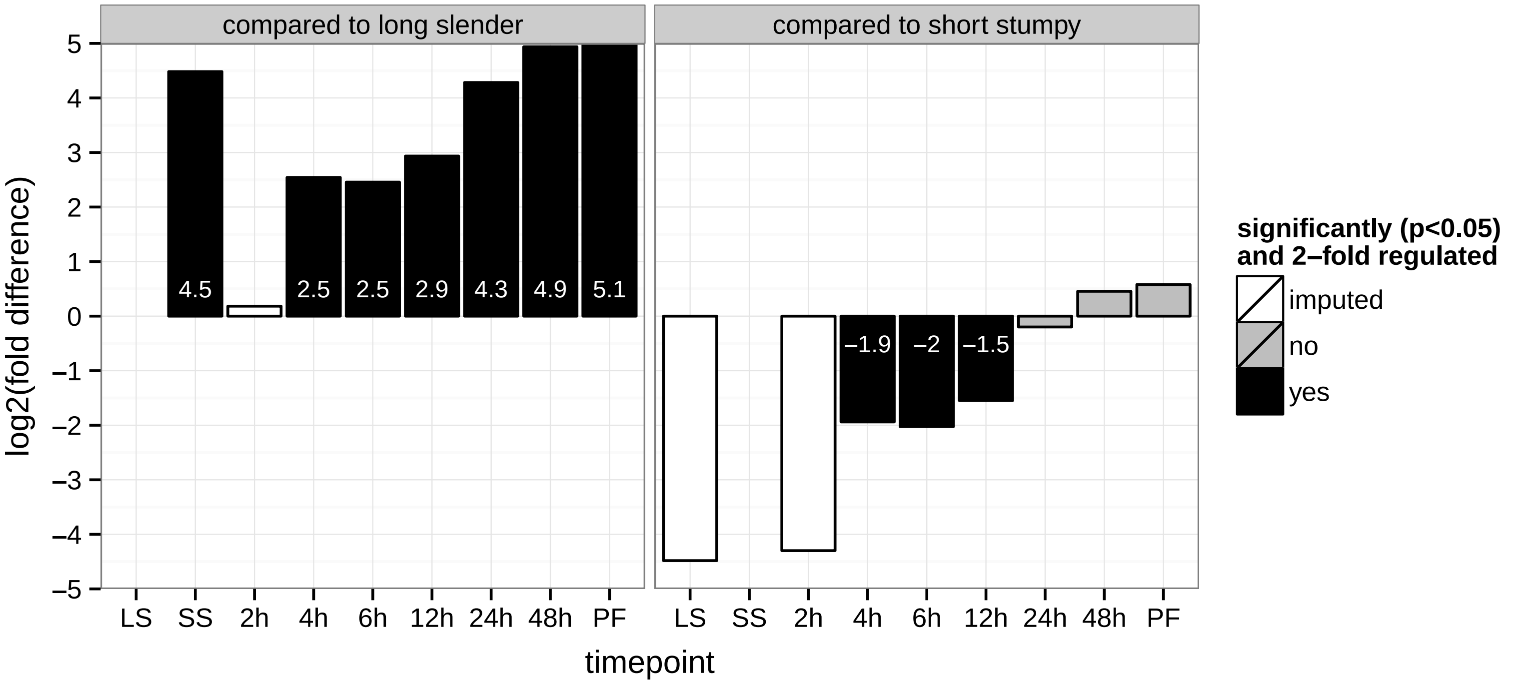
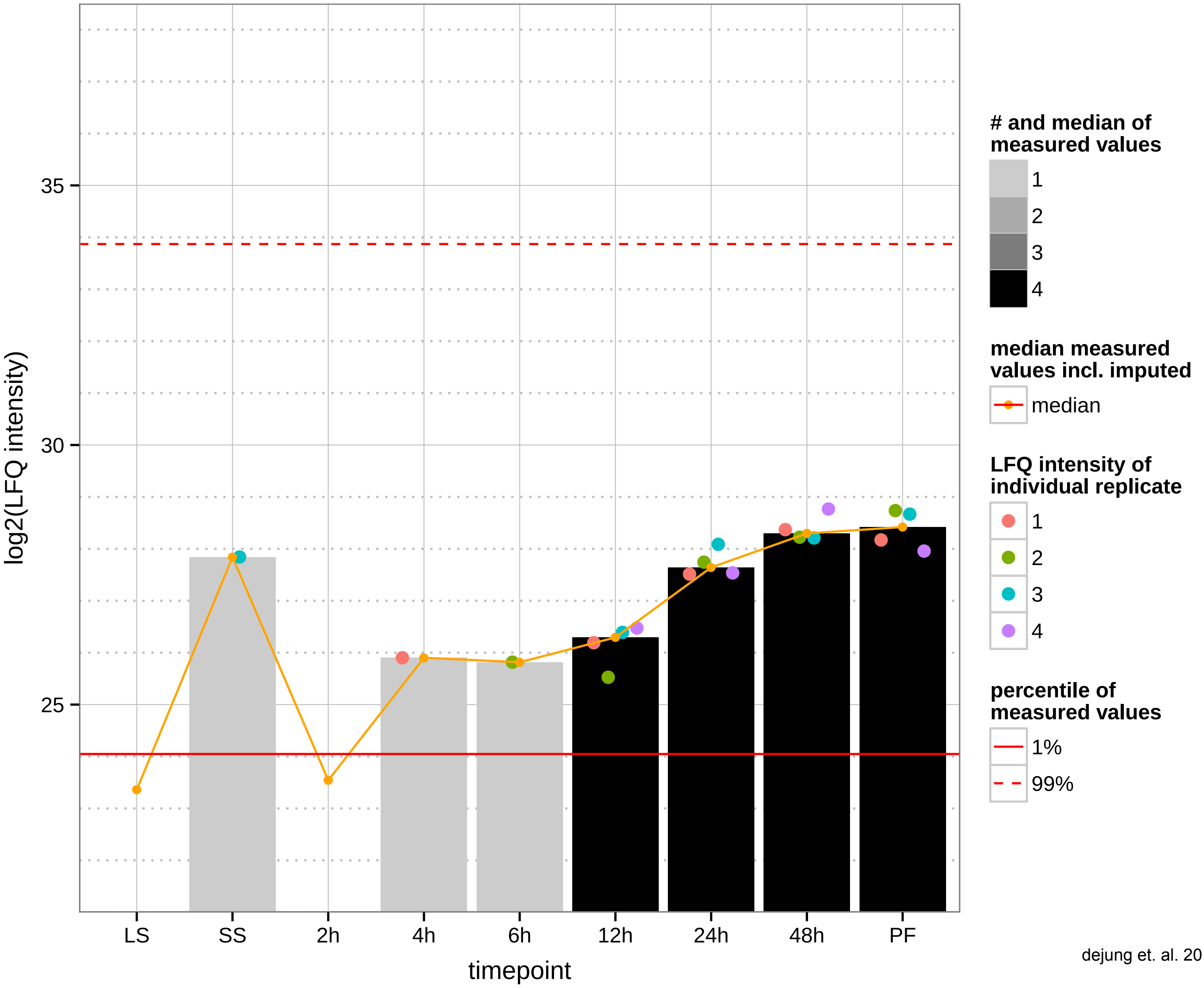
amino acid transporter, putative (AATP11), putative
Tb927.4.4730;Tb927.8.7740
AGOF: amine transmembrane transporter activity
AGOC: null
AGOP: amino acid transport
PGOF: null
PGOC: null
PGOP: null





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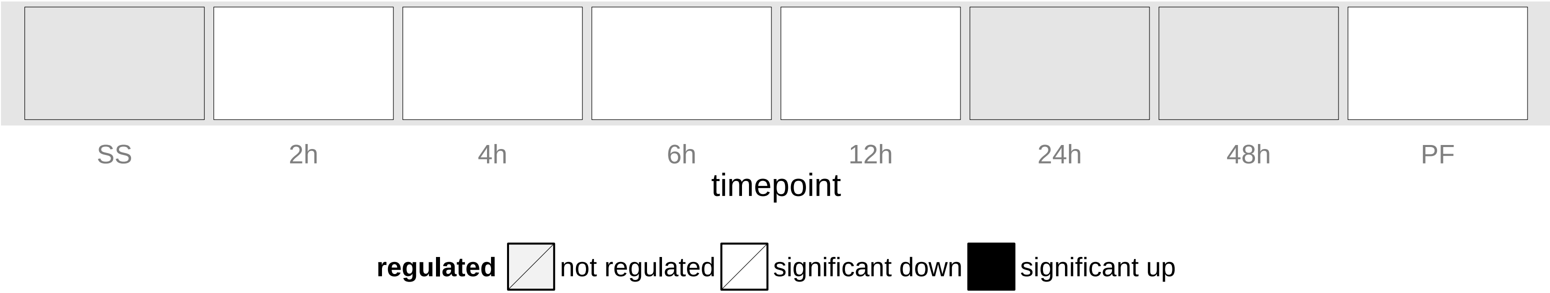

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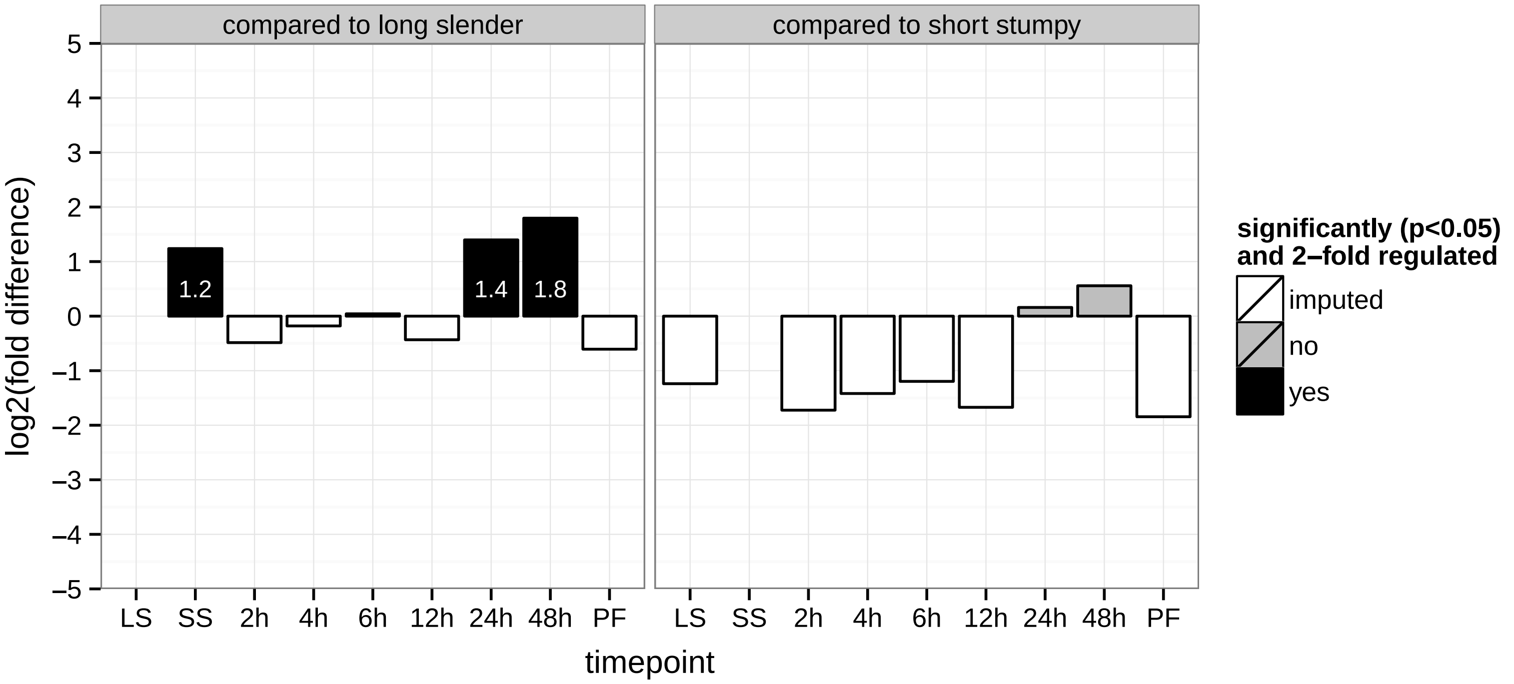
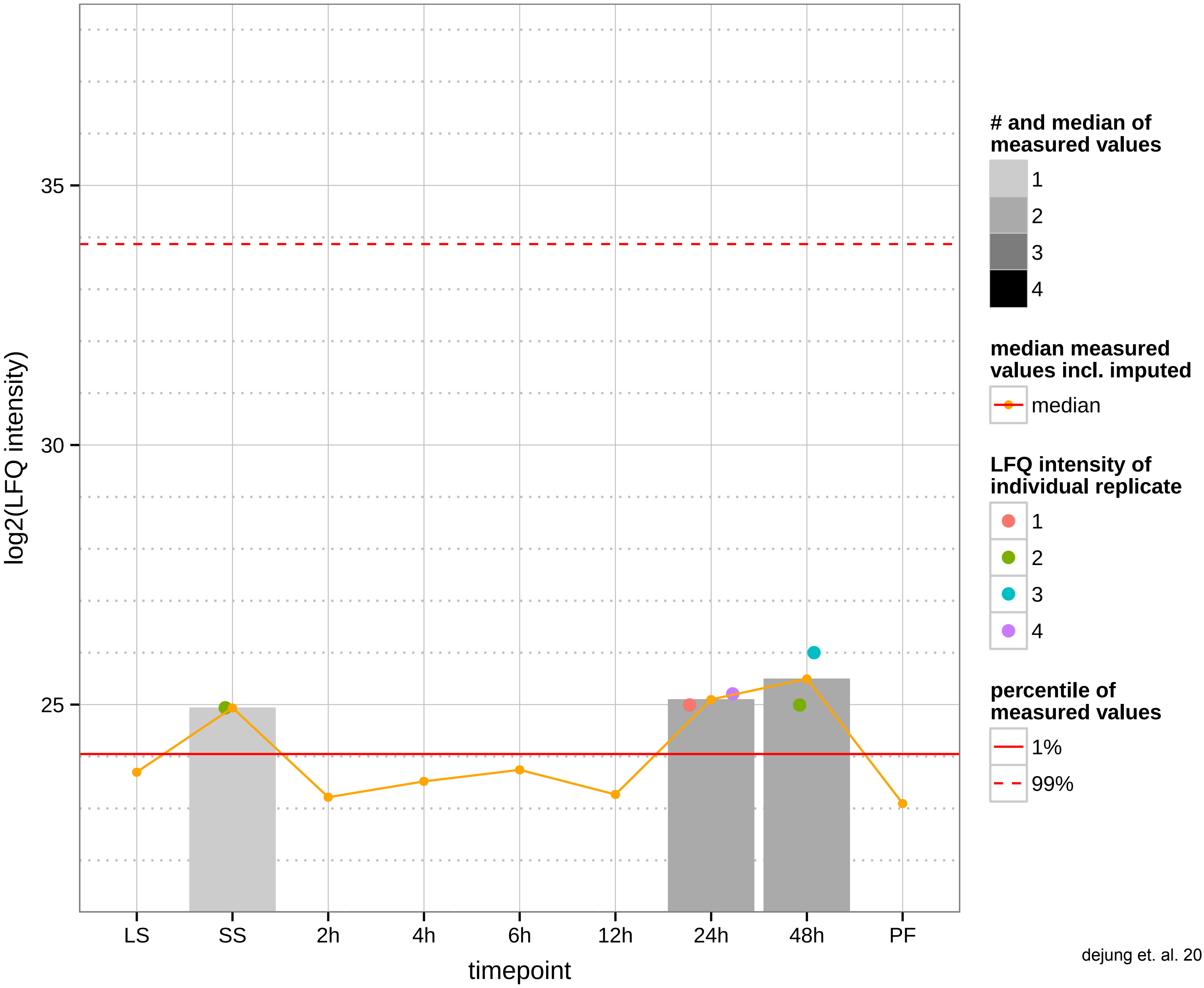
mitochondrial RNA binding protein (MRB4160)
Tb927.4.4160
AGOF: RNA binding
AGOC: mitochondrion
AGOP: RNA metabolic process
PGOF: null
PGOC: null
PGOP: null





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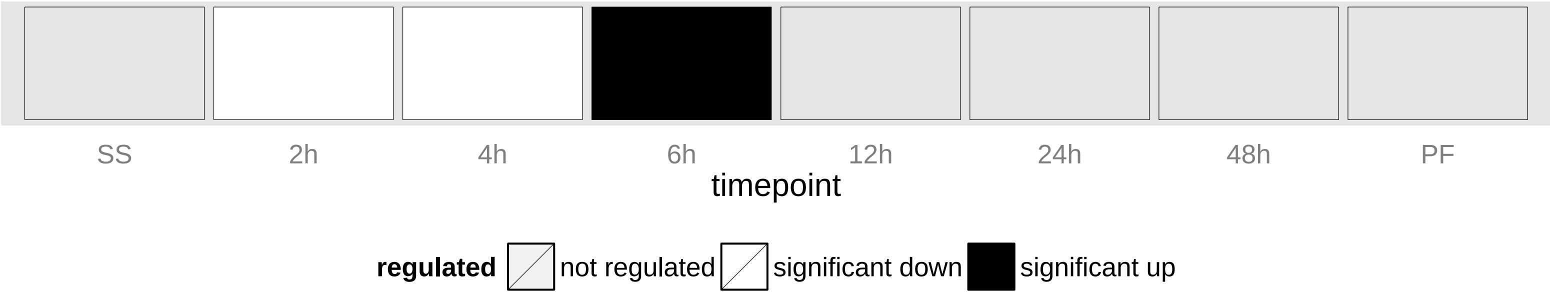

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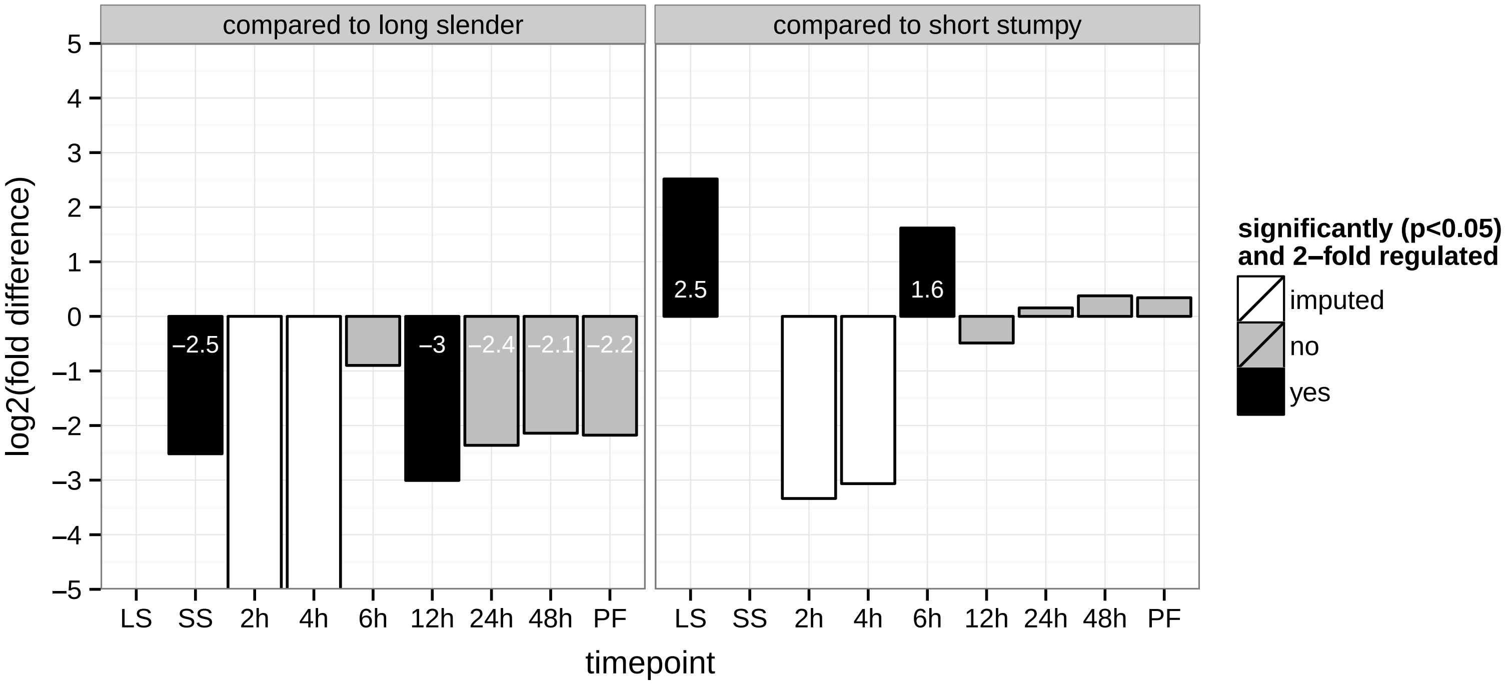
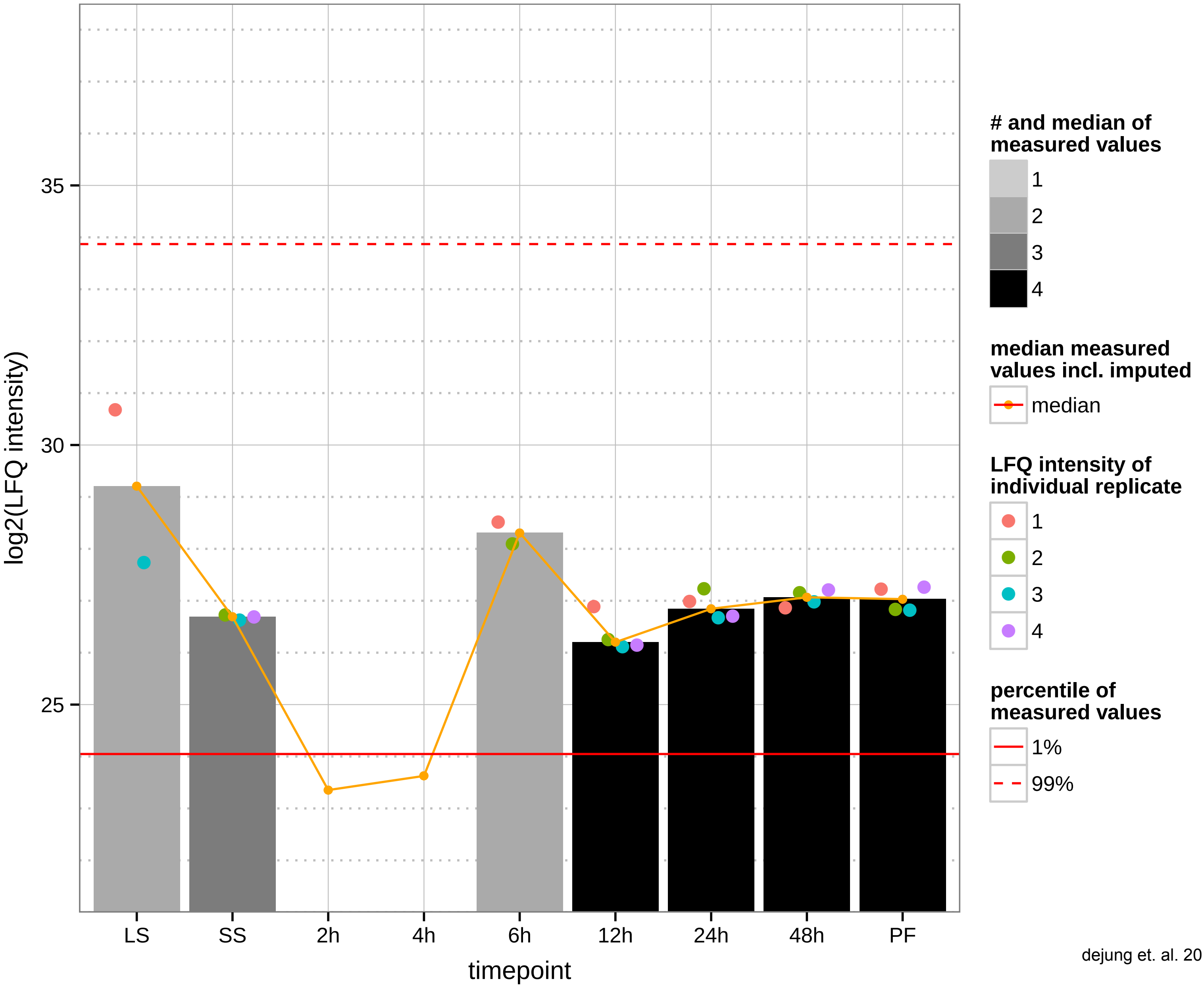
TPR–repeat–containing chaperone protein DNAJ, putative
Tb927.4.2220
AGOF: heat shock protein binding
AGOC: null
AGOP: null
PGOF: heat shock protein binding, protein binding
PGOC: null
PGOP: null





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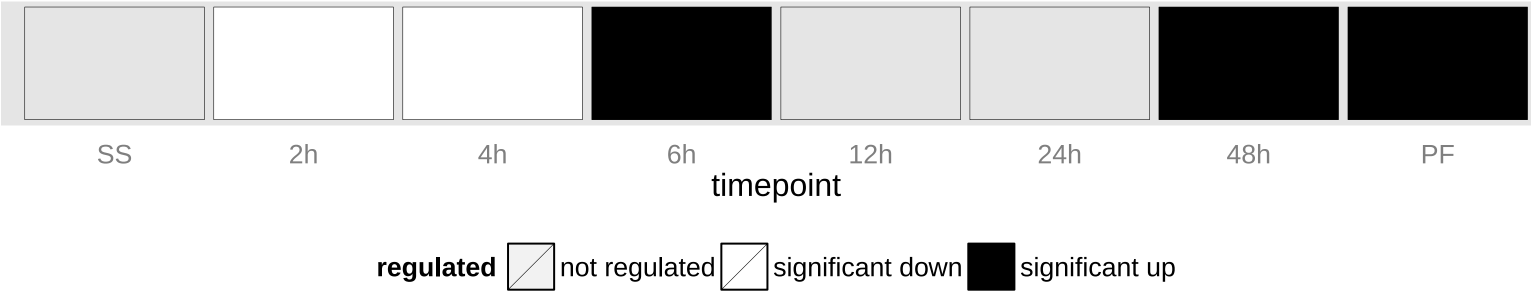

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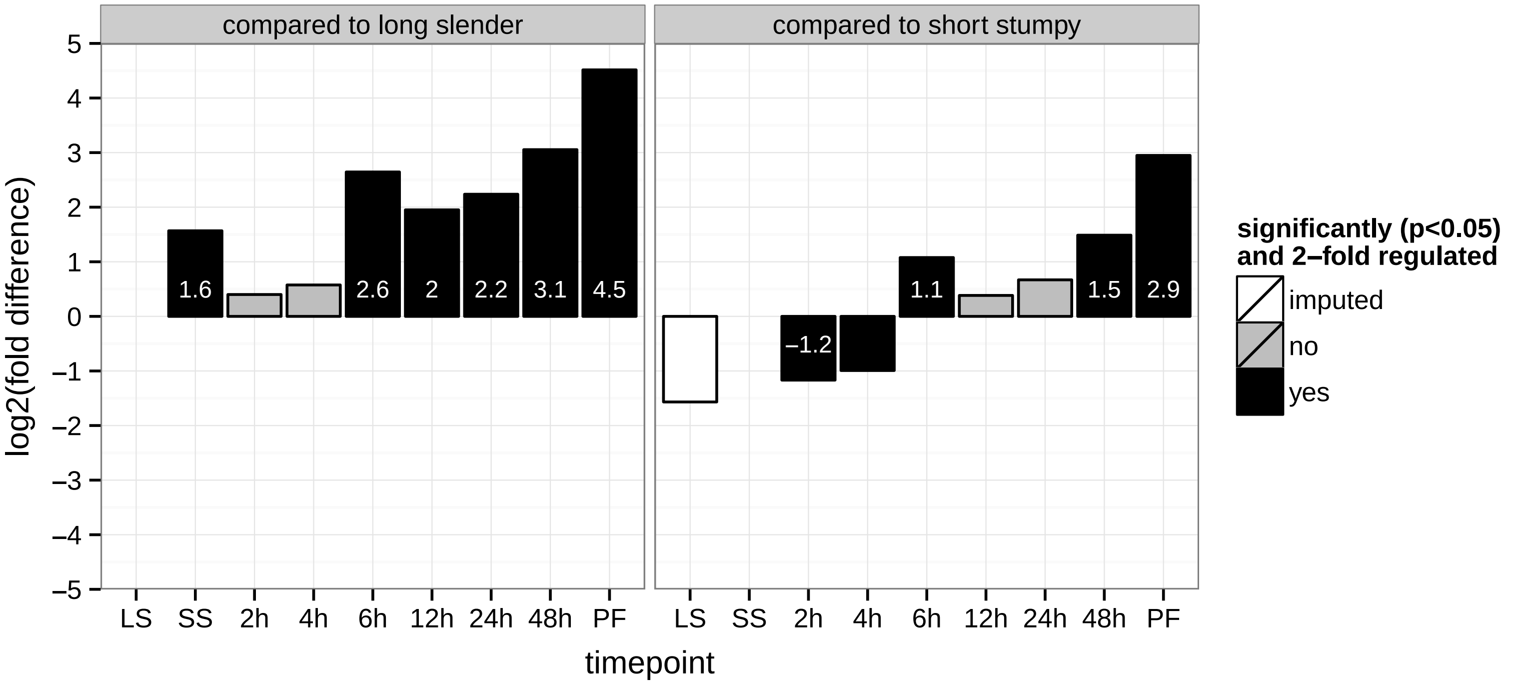
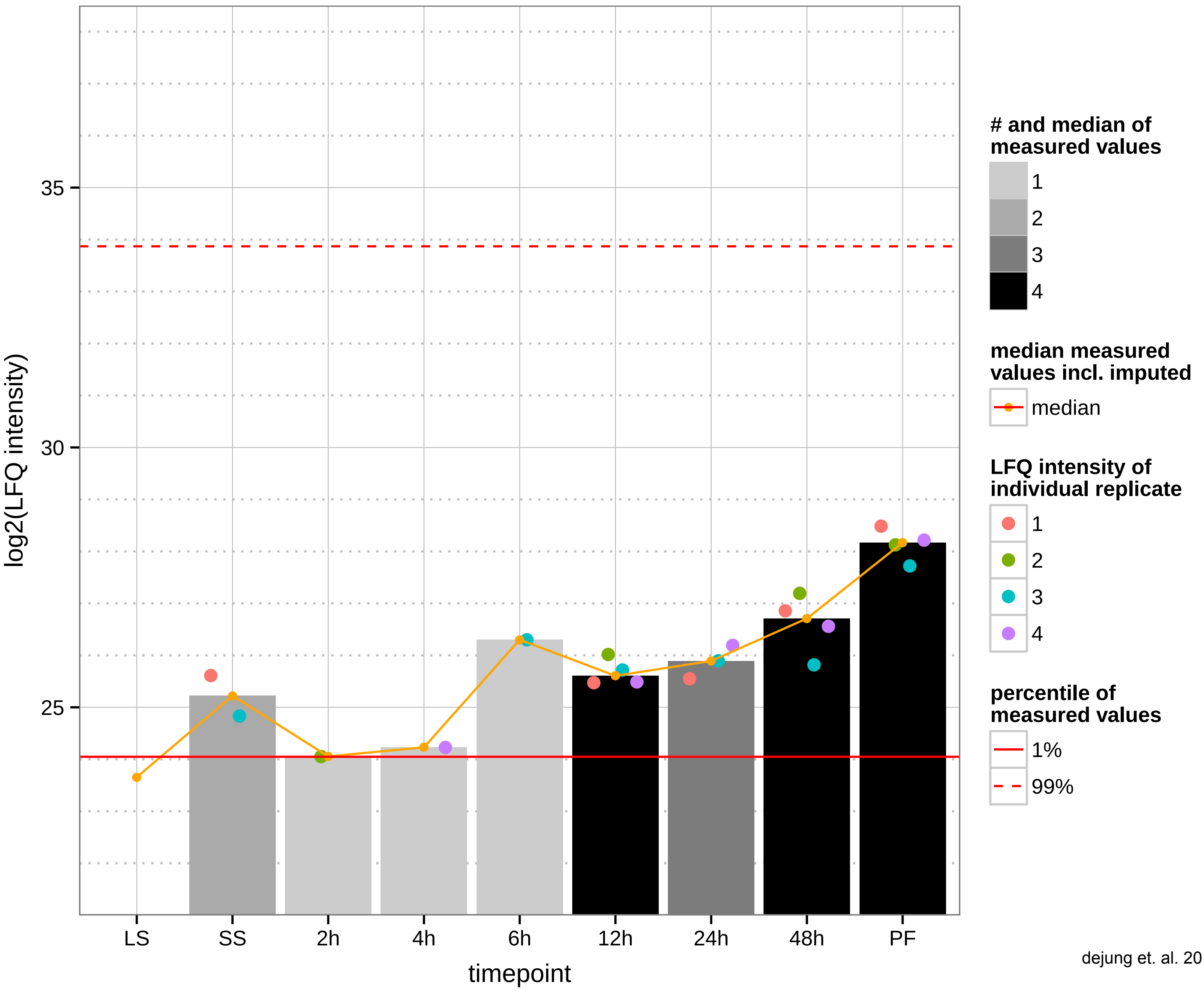
metacaspase 5, putative (MCA5)
Tb927.9.14220
AGOF: cysteine–type endopeptidase activity
AGOC: null
AGOP: apoptotic process, cellular response to hydrogen peroxide, induction of apoptosis by oxidative stress, protein autoproc
PGOF: cysteine–type endopeptidase activity
PGOC: null
PGOP: proteolysis





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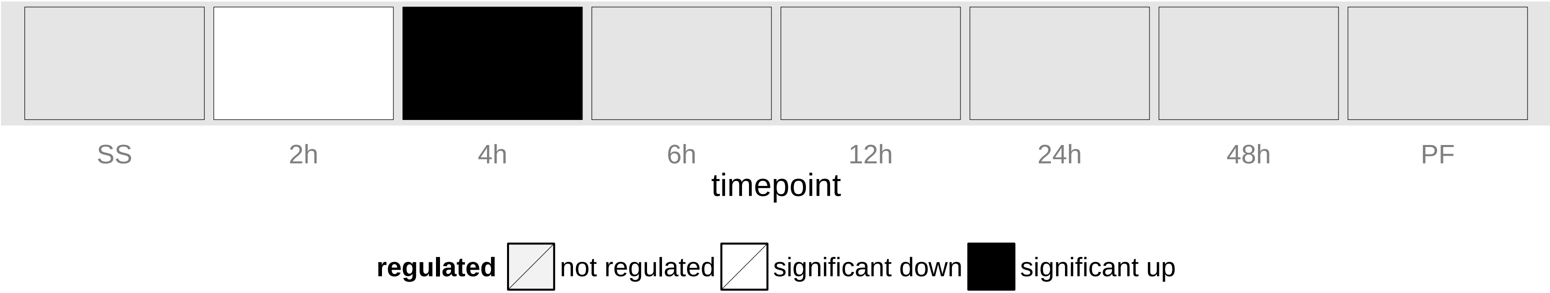

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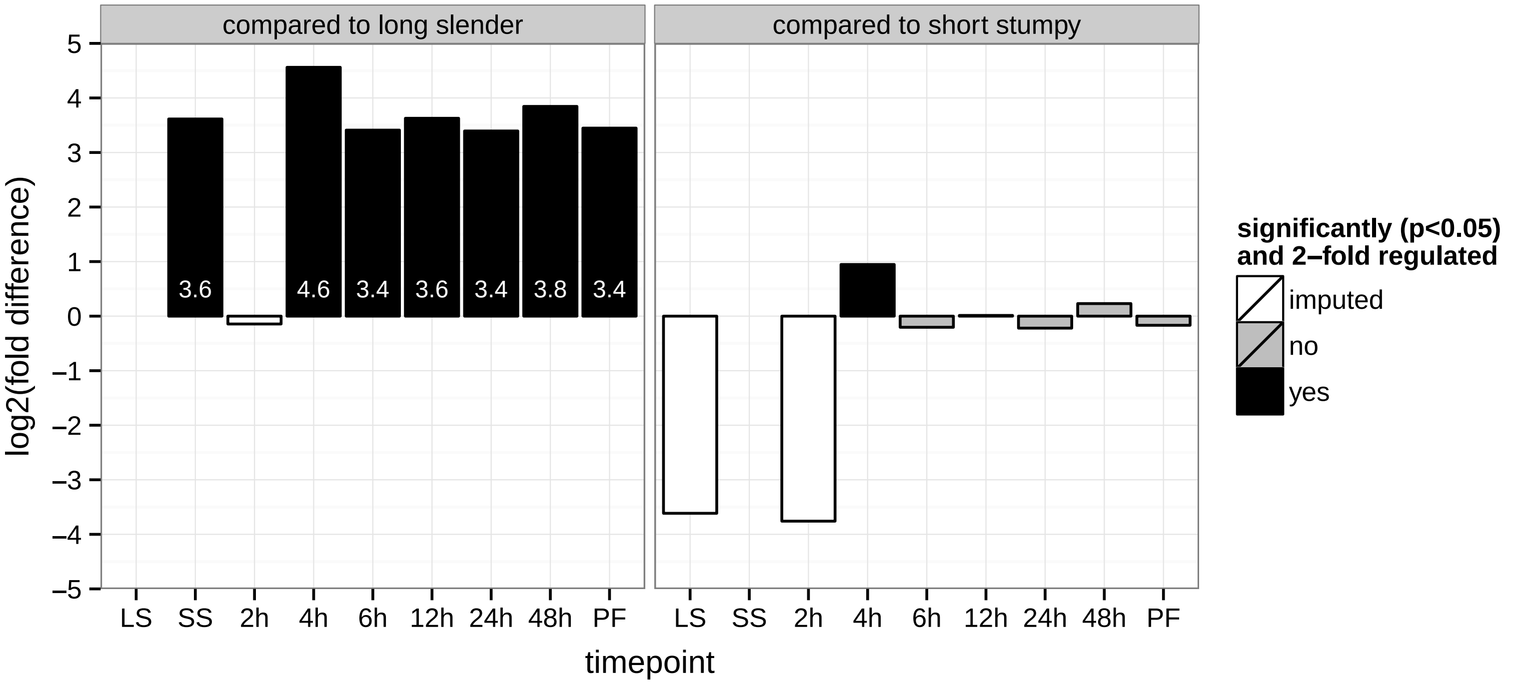
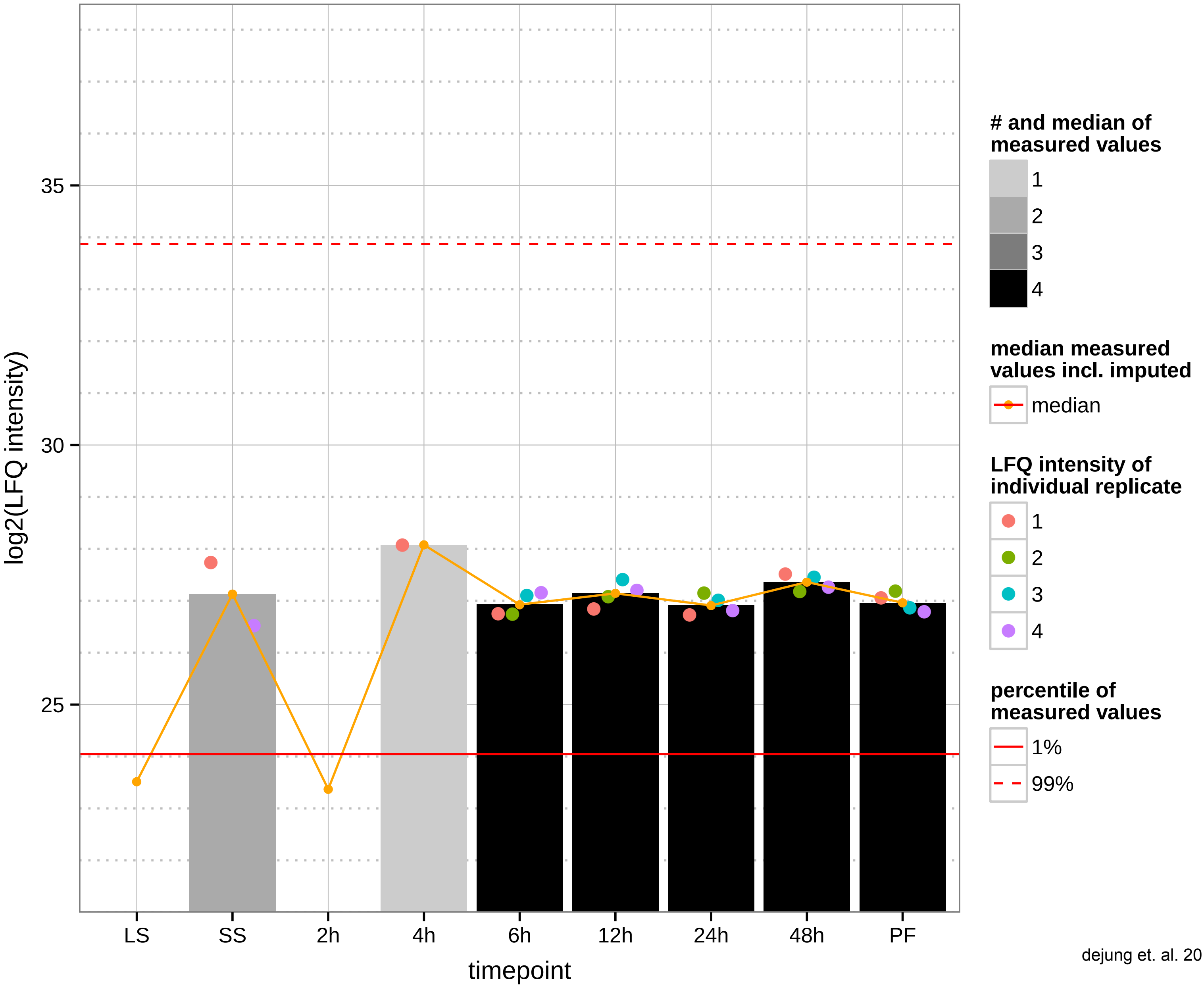
Golgi reassembly stacking protein (GRASP homologue), putative
Tb927.11.2660
AGOF: null
AGOC: Golgi stack
AGOP: Golgi organization
PGOF: protein binding
PGOC: null
PGOP: null





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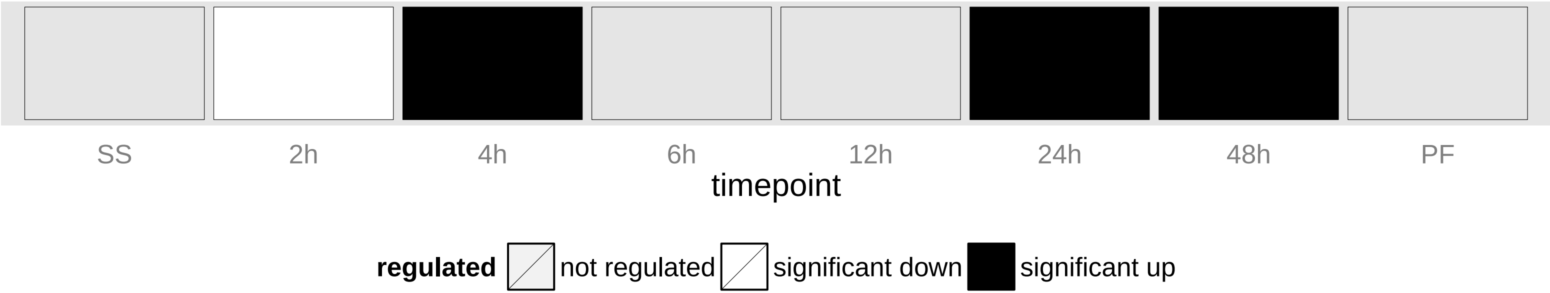

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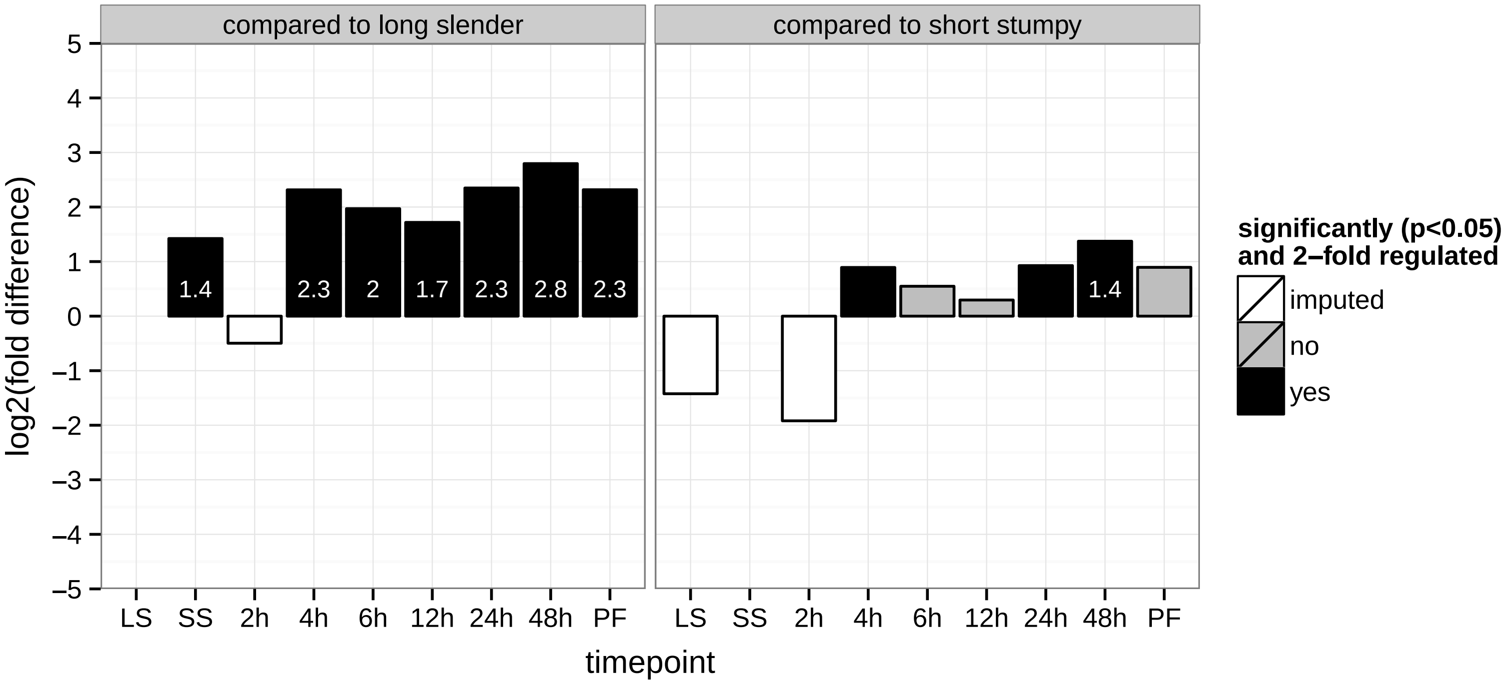
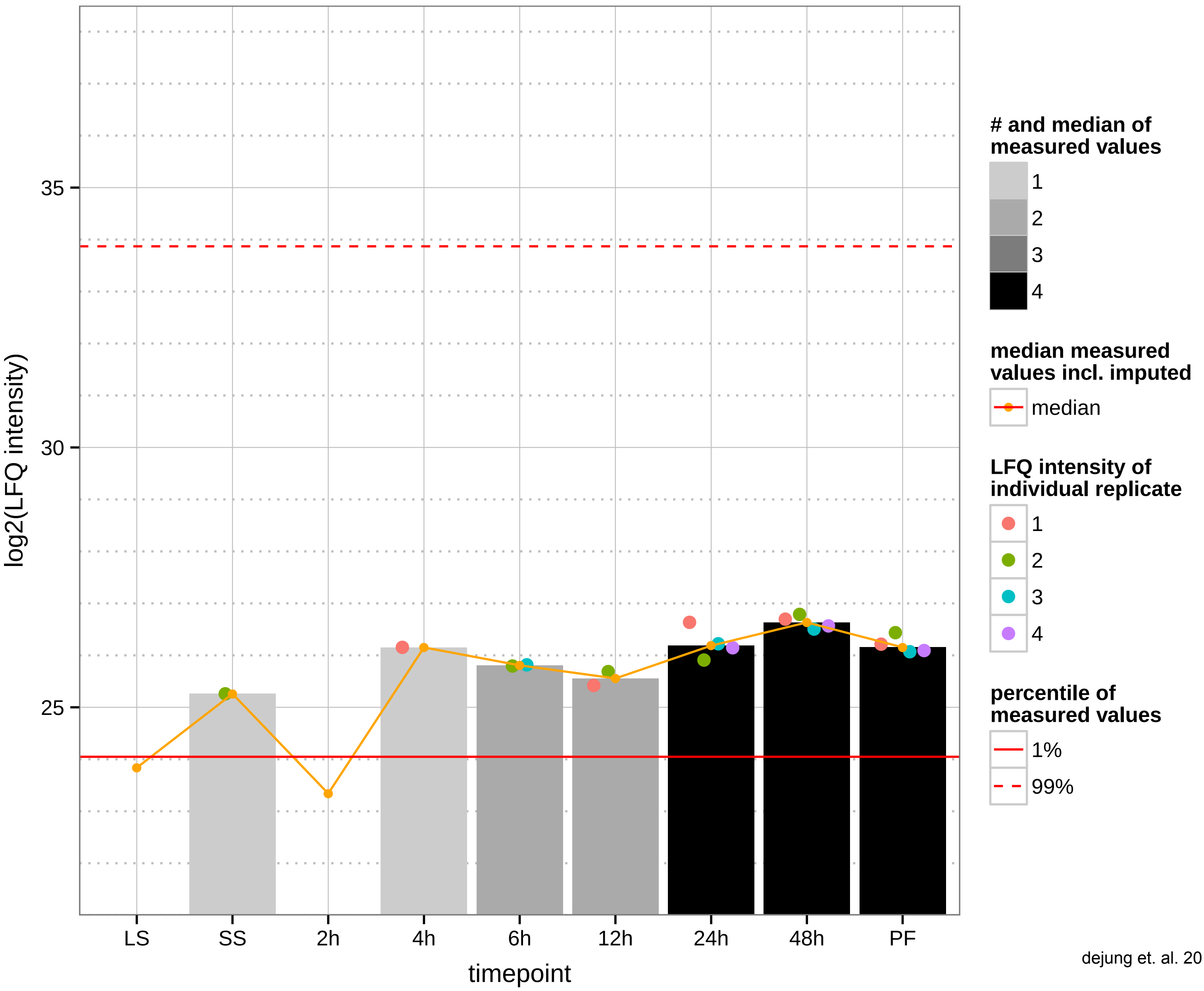
hypothetical protein, conserved
Tb927.3.3110
AGOF: null
AGOC: null
AGOP: null
PGOF: binding
PGOC: null
PGOP: null





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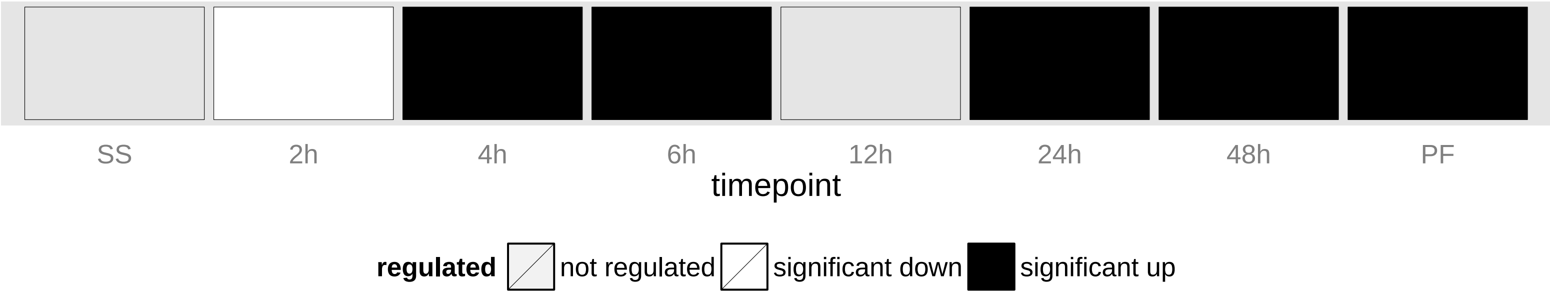

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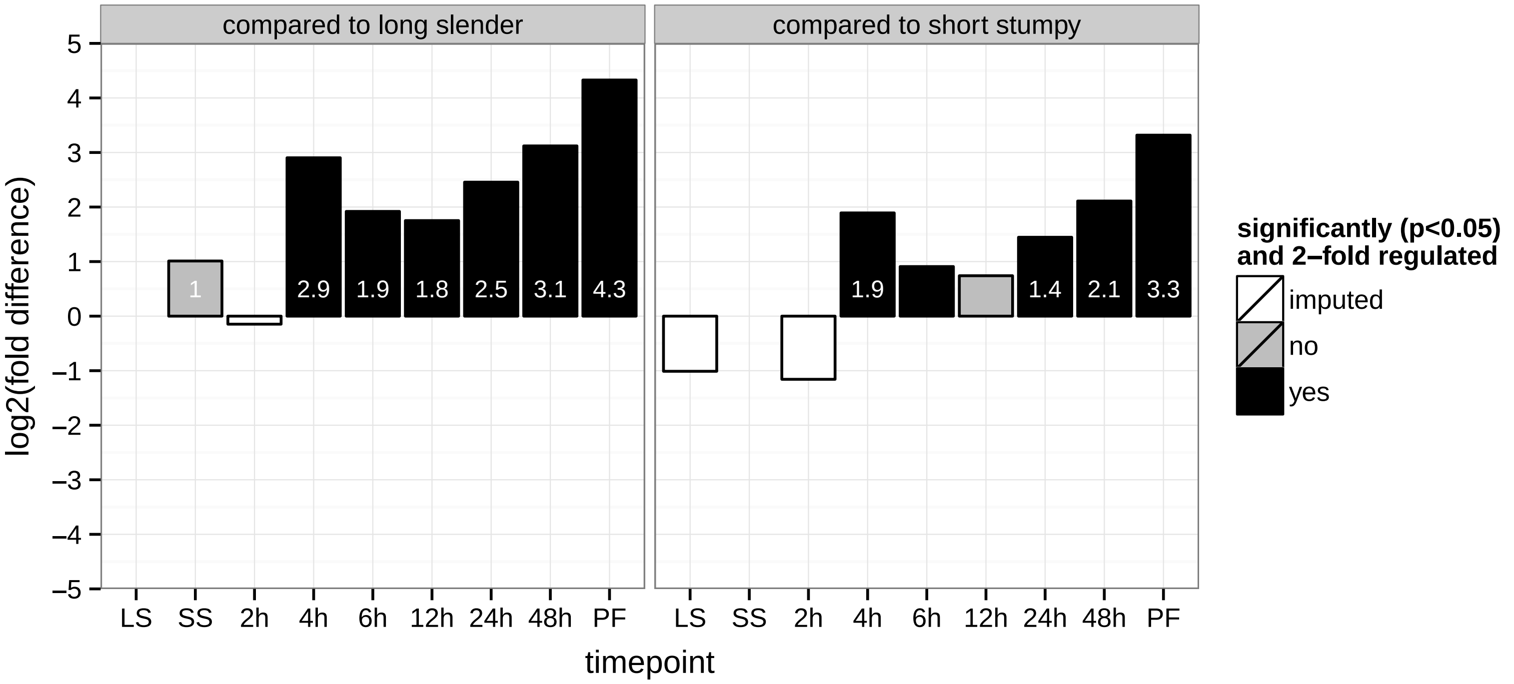
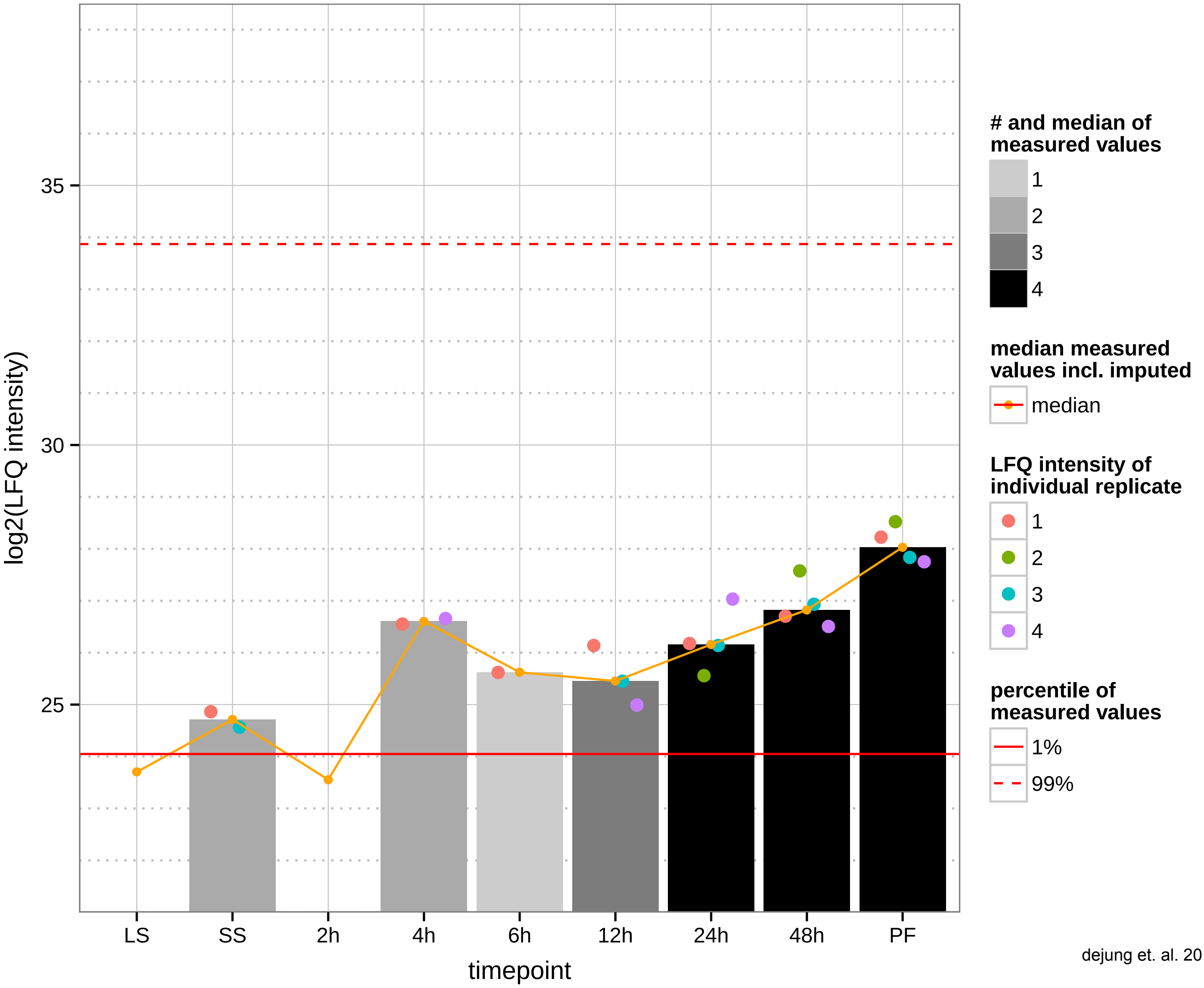
hypothetical protein, conserved
Tb927.4.4370
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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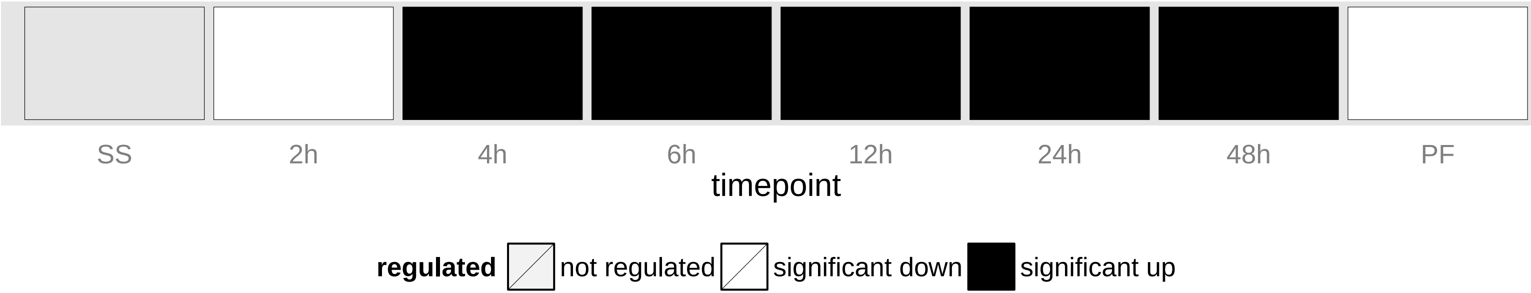

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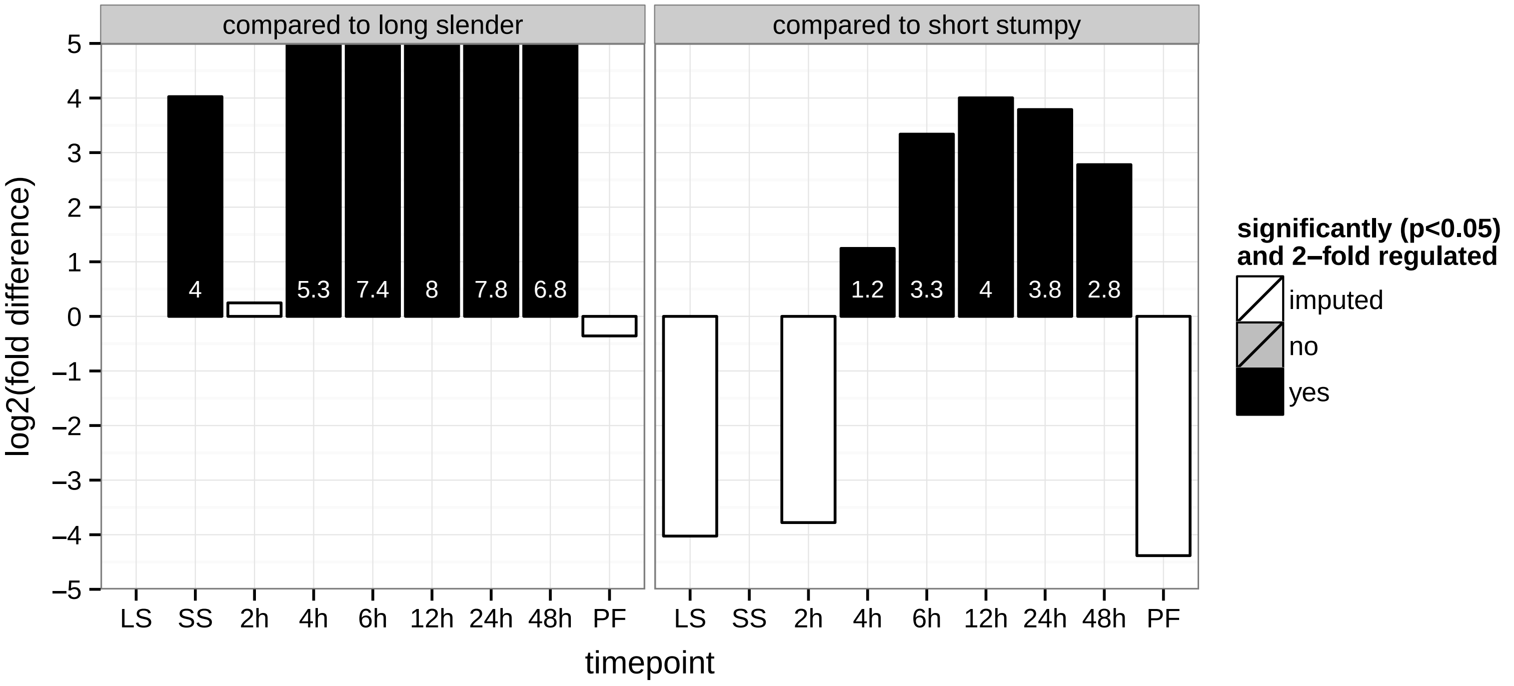
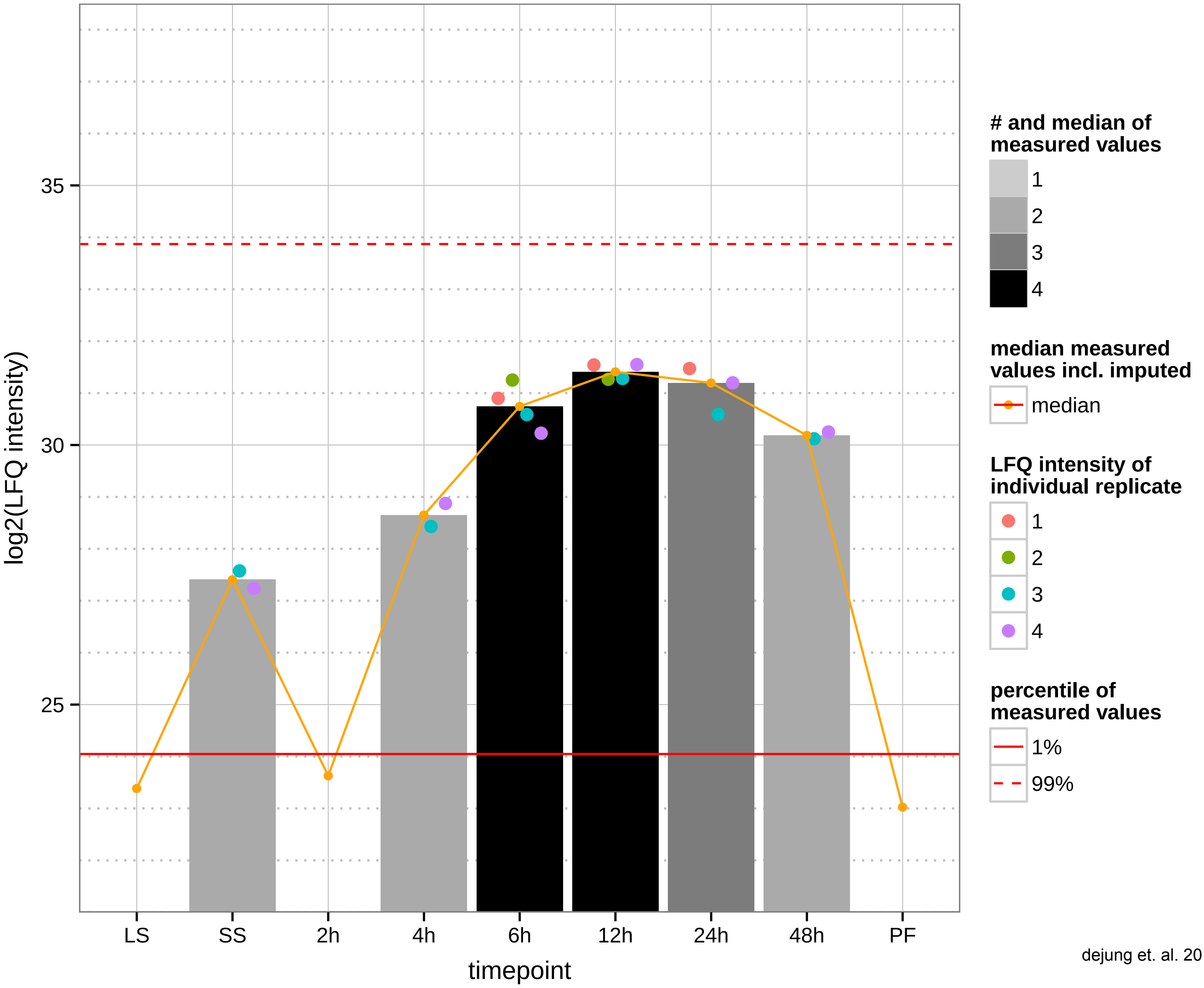
TFIIF−stimulated CTD phosphatase, putative
Tb927.9.6100
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: protein binding
PGOC: null
PGOP: null





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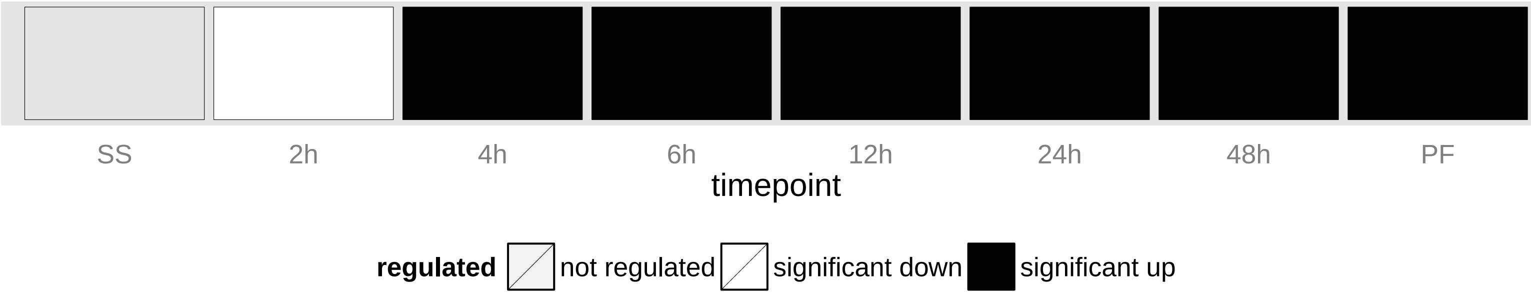

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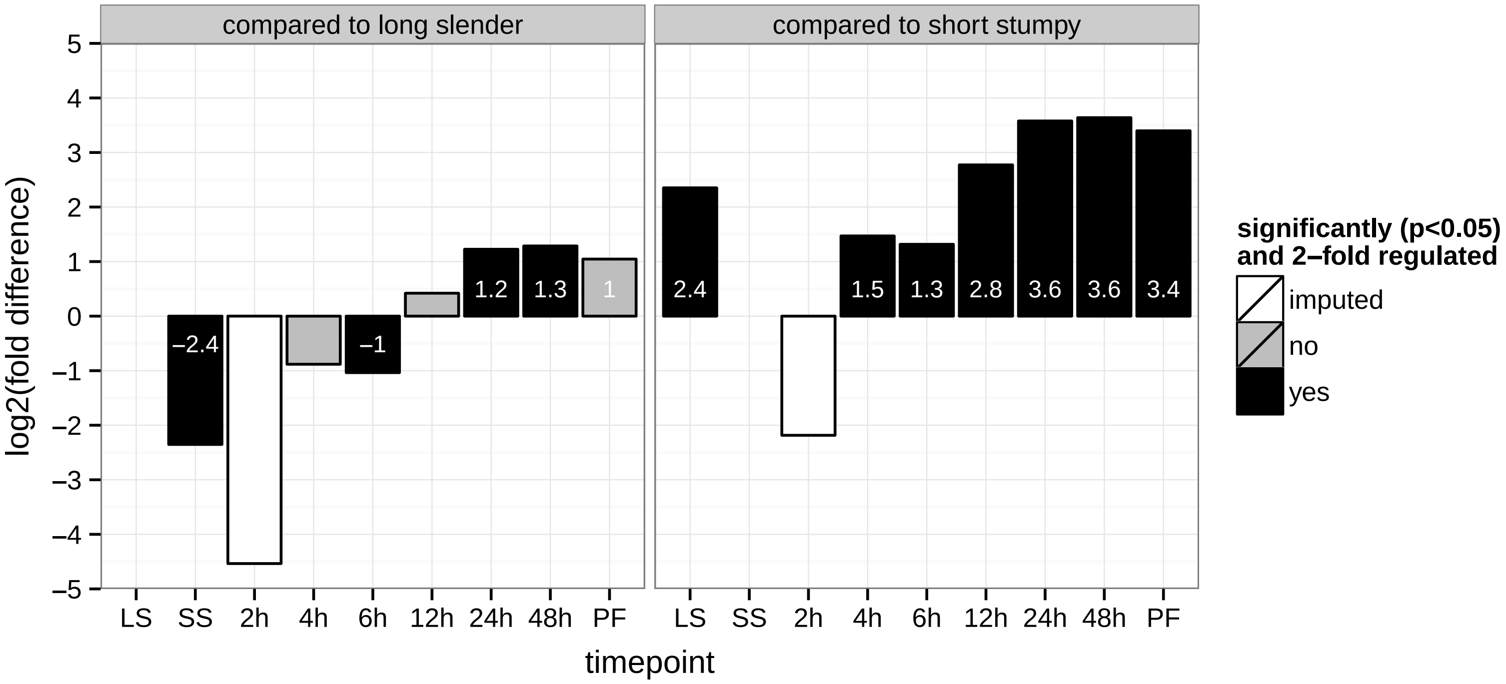
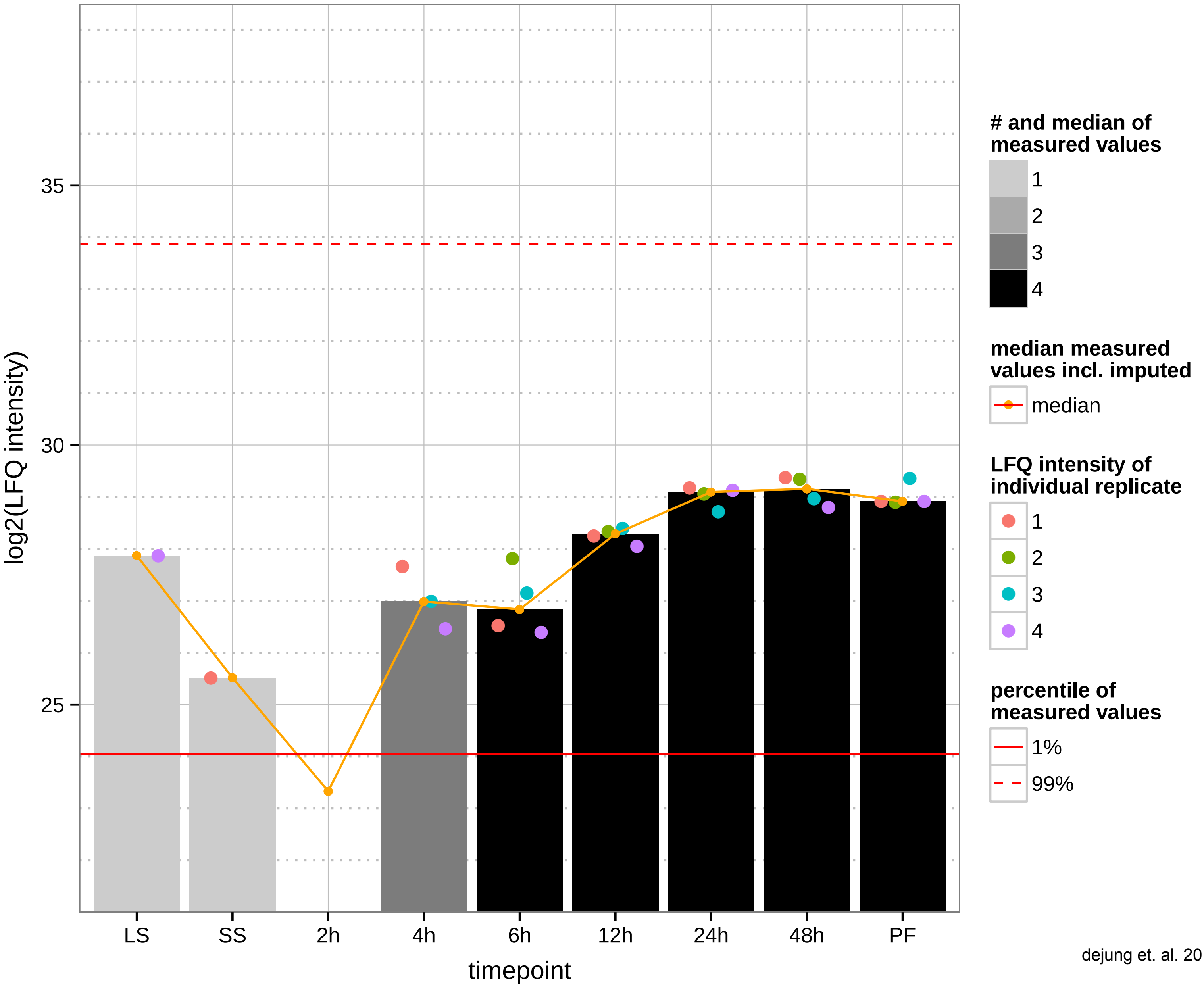
gamma–glutamylcysteine synthetase (GCS)
Tb927.10.12370
AGOF: glutamate–cysteine ligase activity
AGOC: null
AGOP: glutathione biosynthetic process, response to reactive oxygen species, trypanothione biosynthetic process
PGOF: glutamate–cysteine ligase activity
PGOC: null
PGOP: glutathione biosynthetic process





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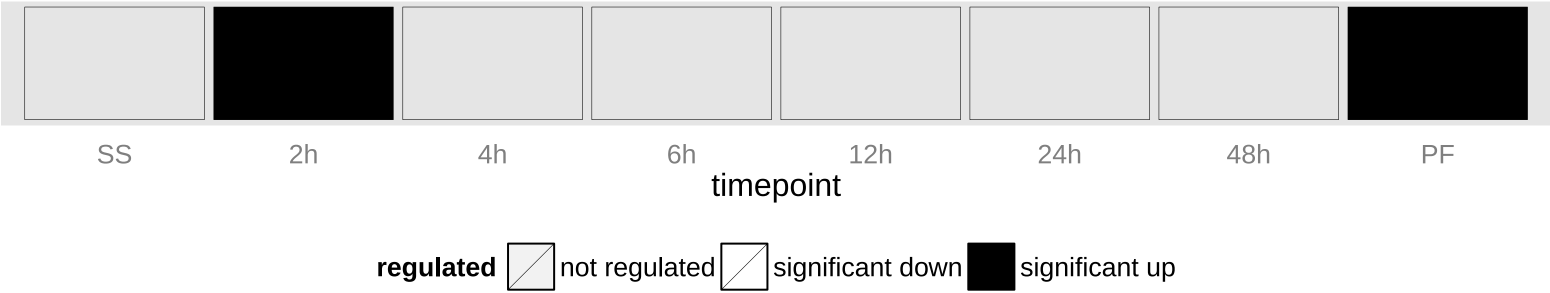

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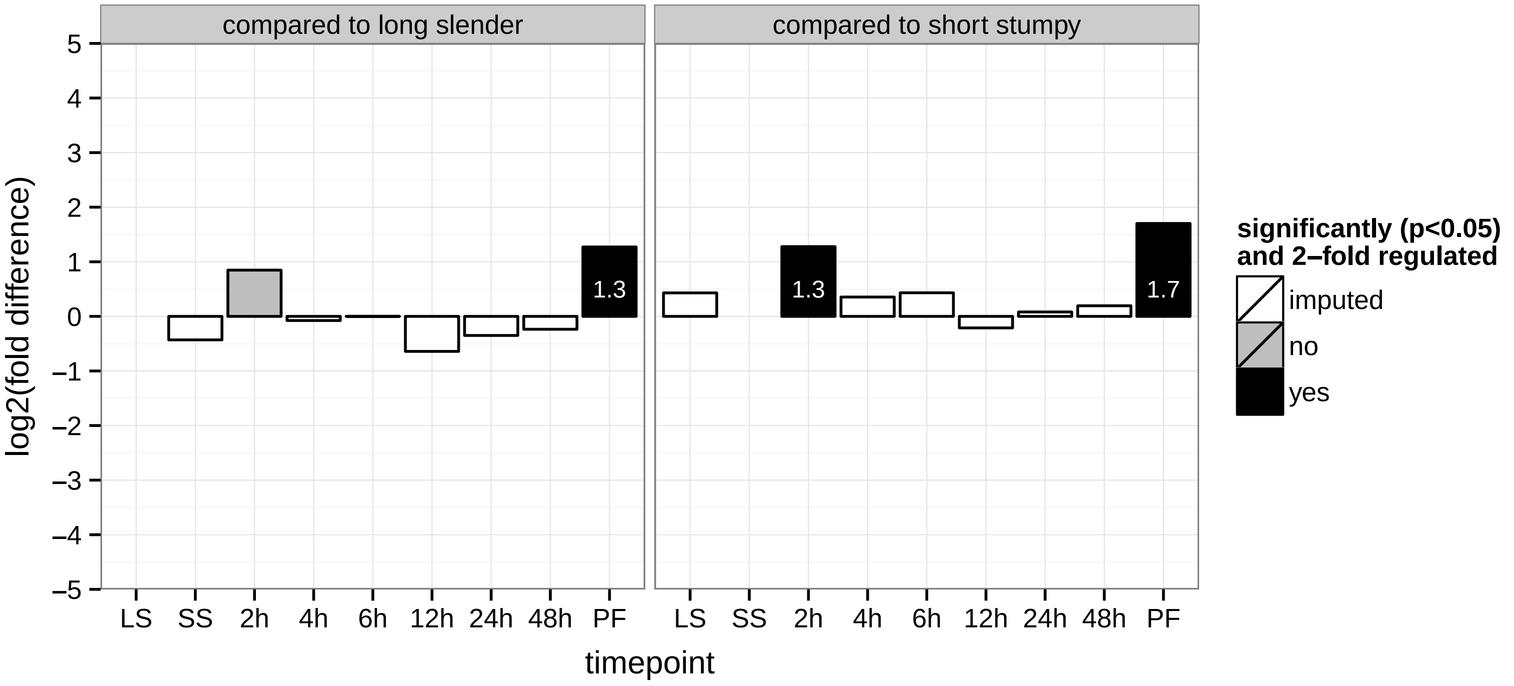
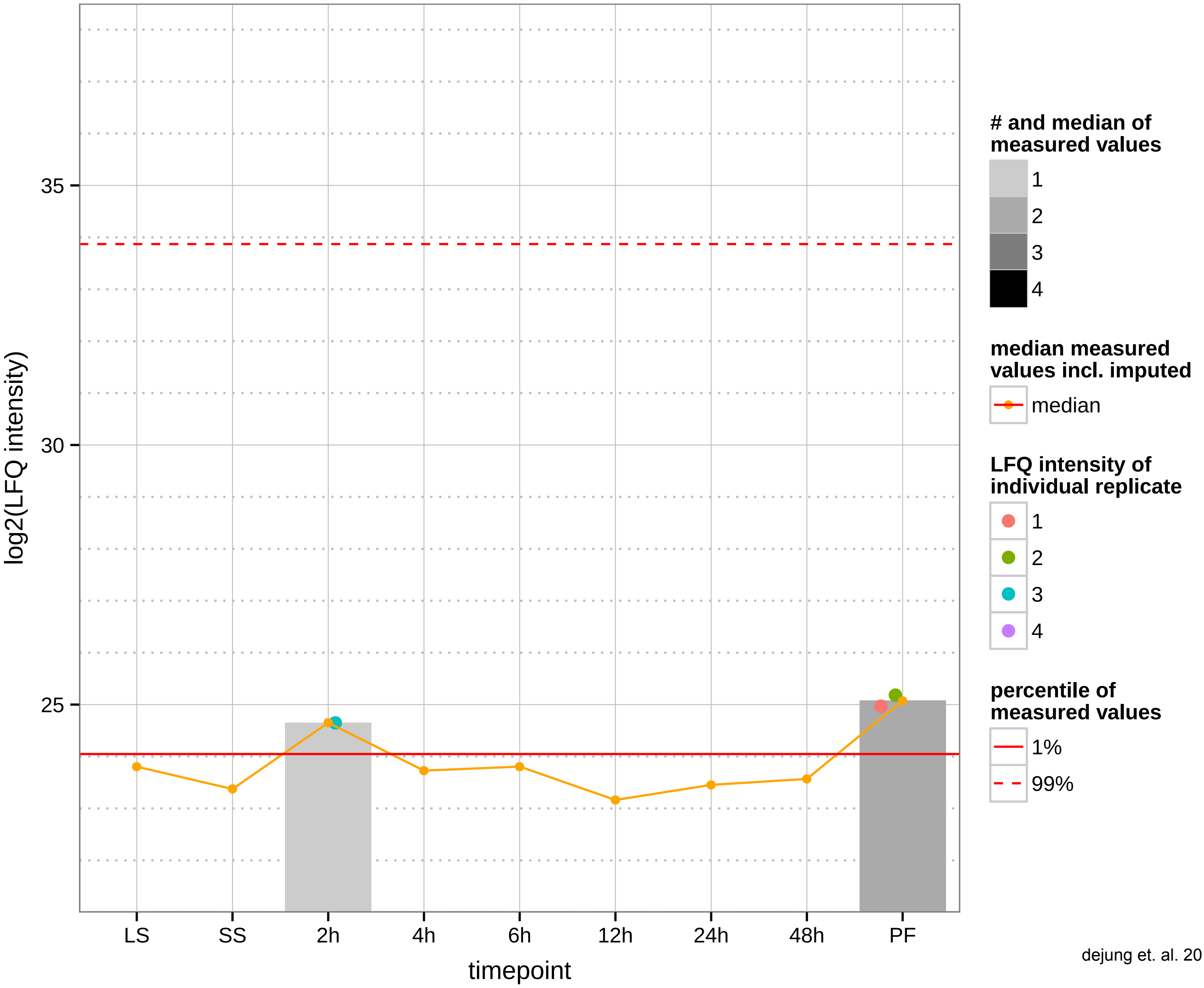
hypothetical protein, conserved
Tb927.3.3500
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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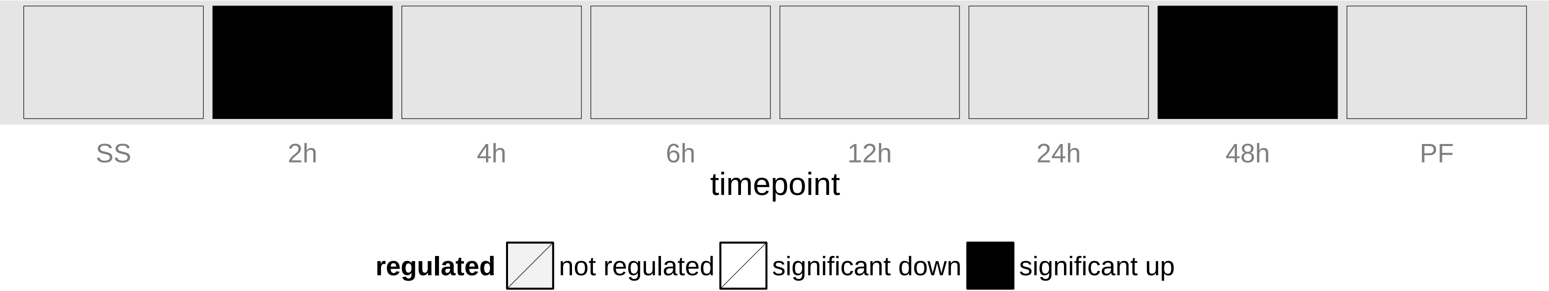

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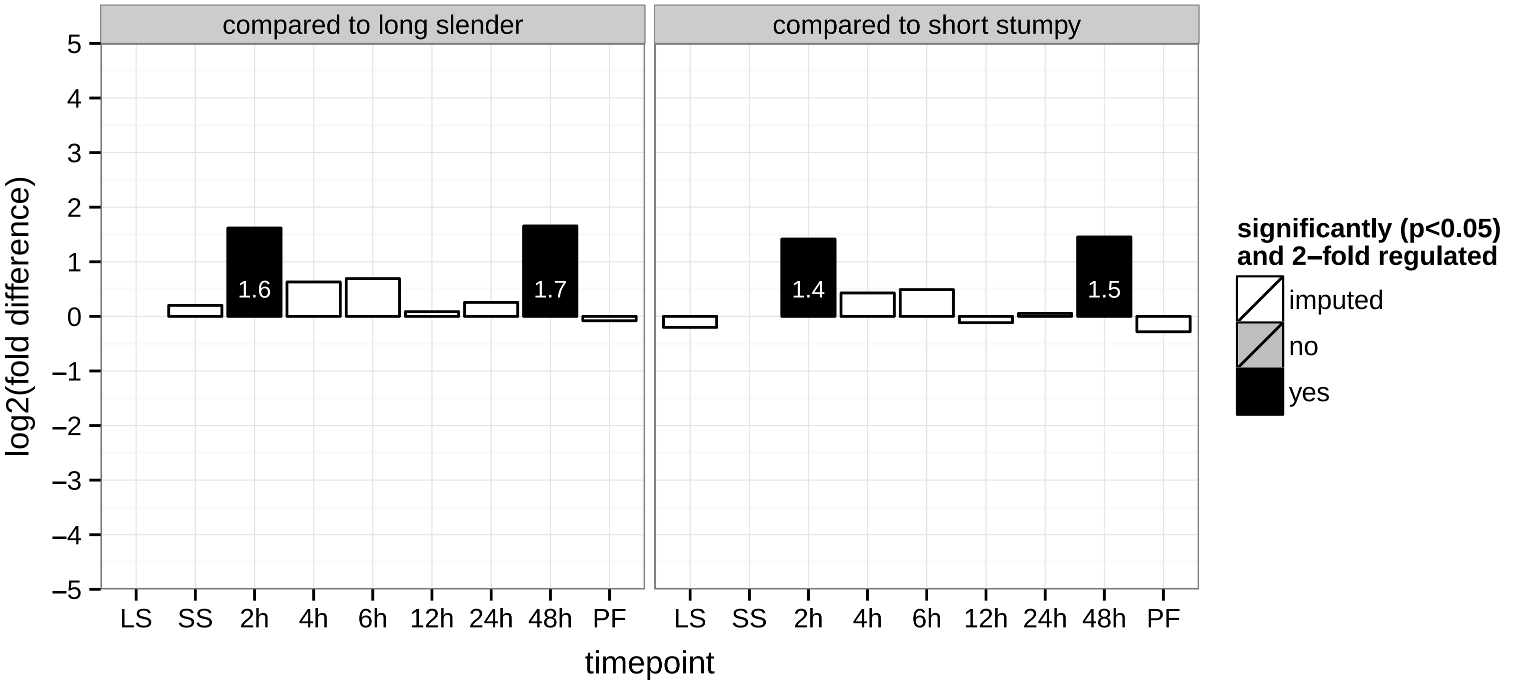
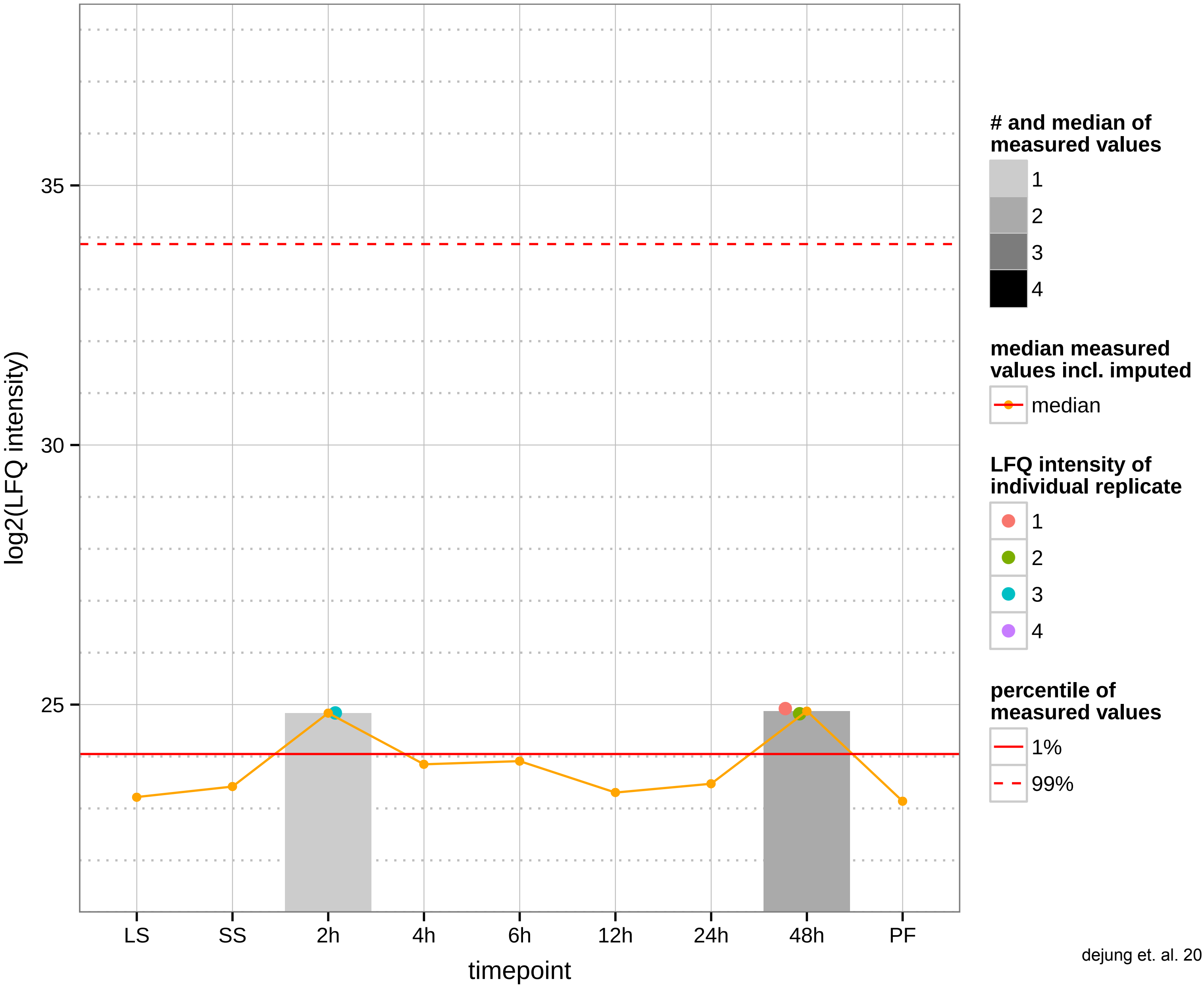
hypothetical protein, conserved
Tb927.8.5170
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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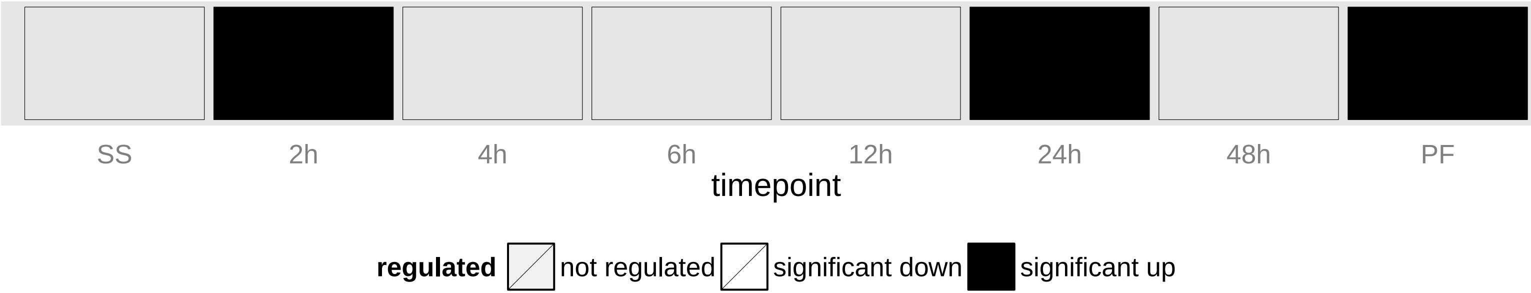

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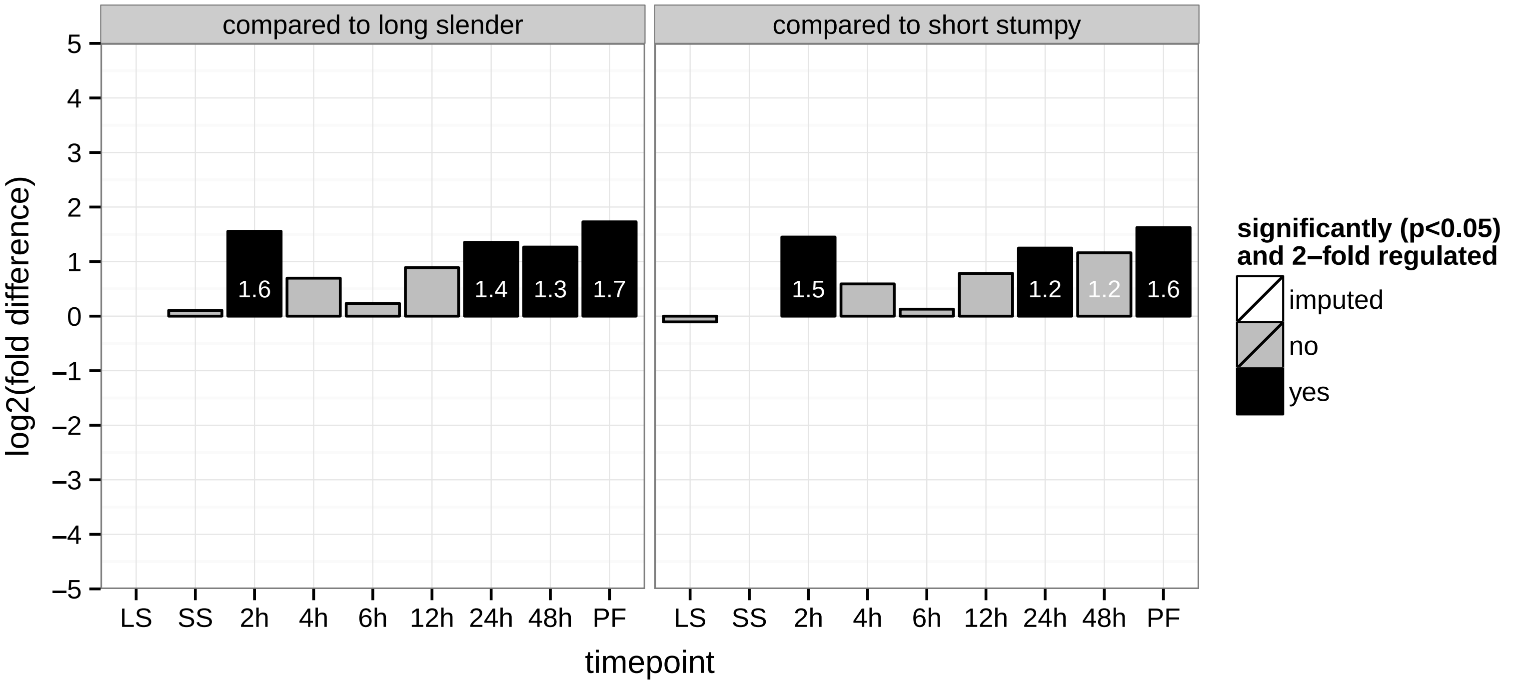
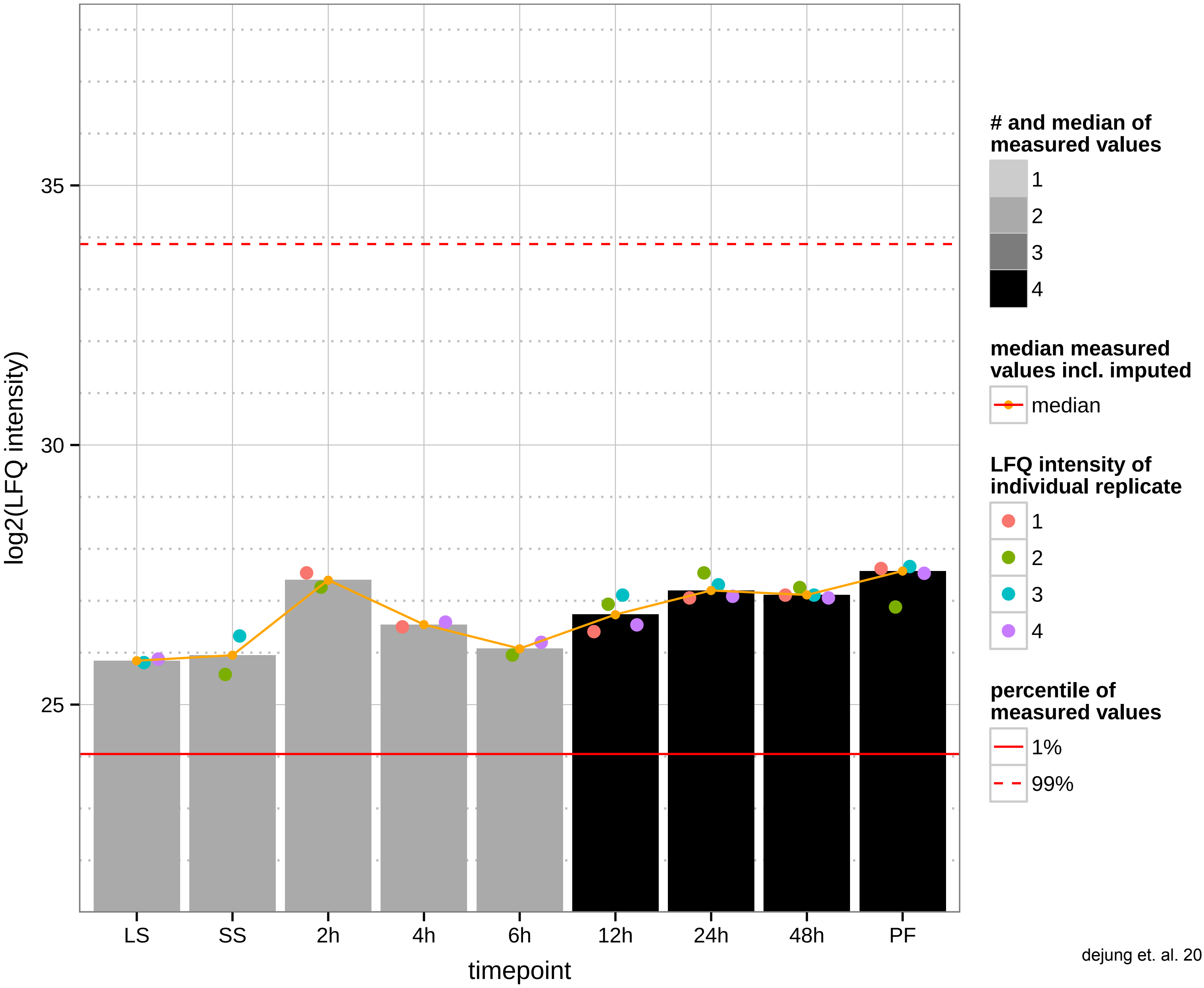
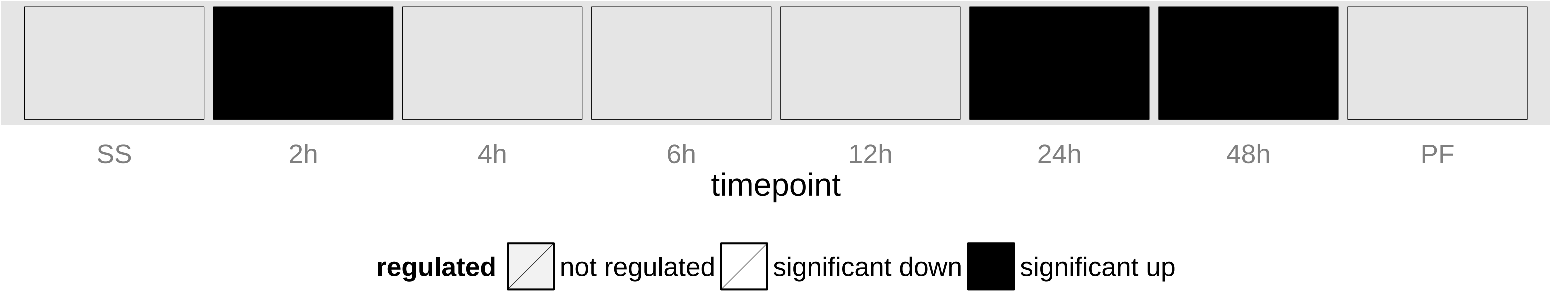
cyclosome subunit 1, putative
Tb927.6.3280
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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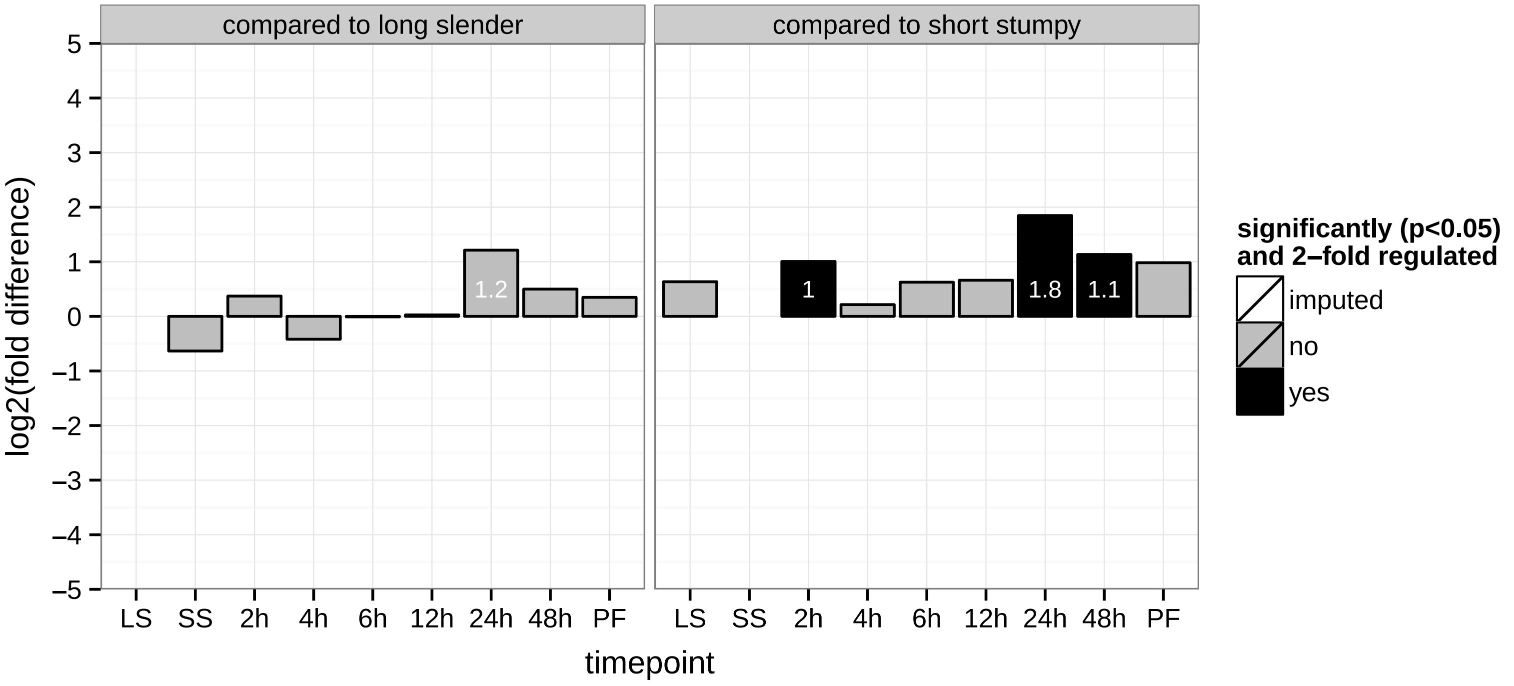
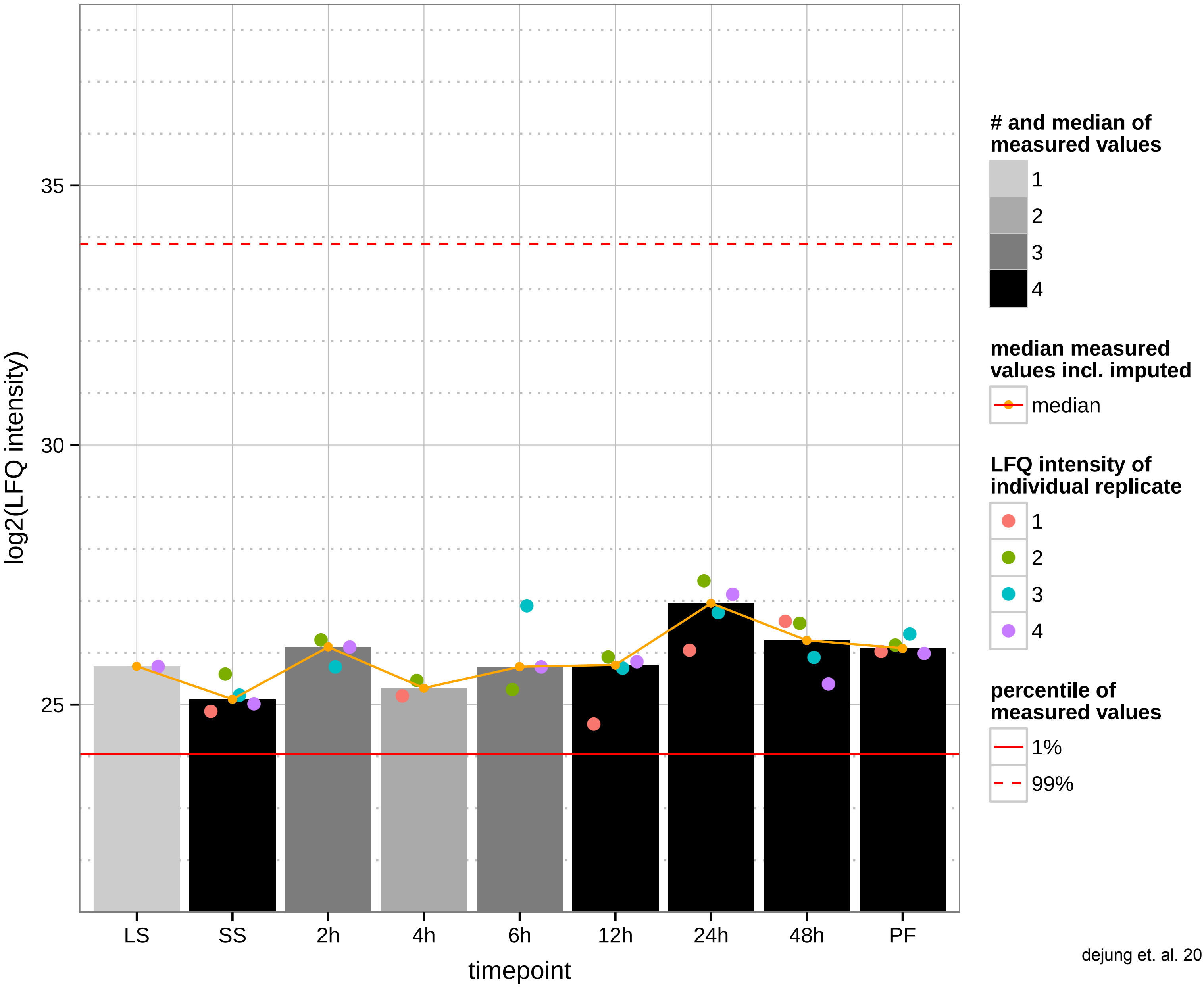
peptide methionine sulfoxide reductase, putative, peptide Met(O) reductase, methionine−S−sulfoxide reductase
Tb927.8.550
AGOF: peptide−methionine−(S)−S−oxide reductase activity
AGOC: null
AGOP: cellular protein modification process, oxidation−reduction process
PGOF: oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor
PGOC: null
PGOP: oxidation−reduction process, protein metabolic process





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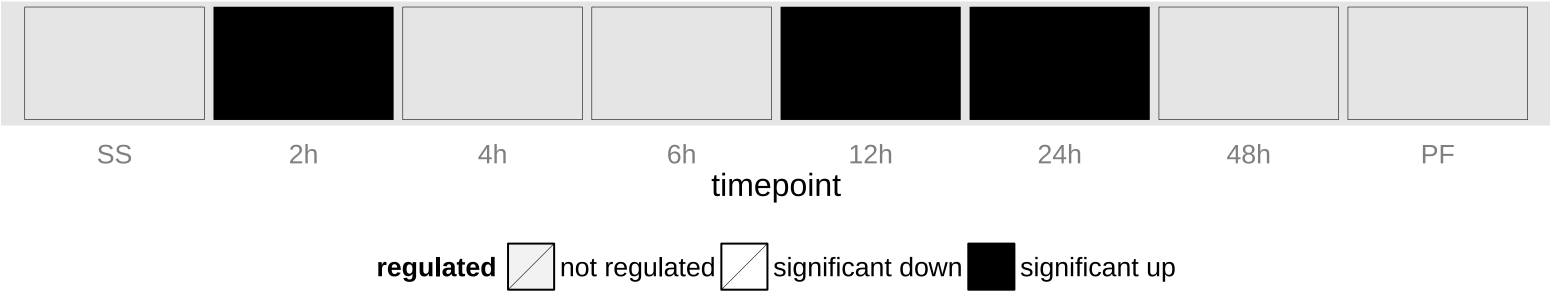

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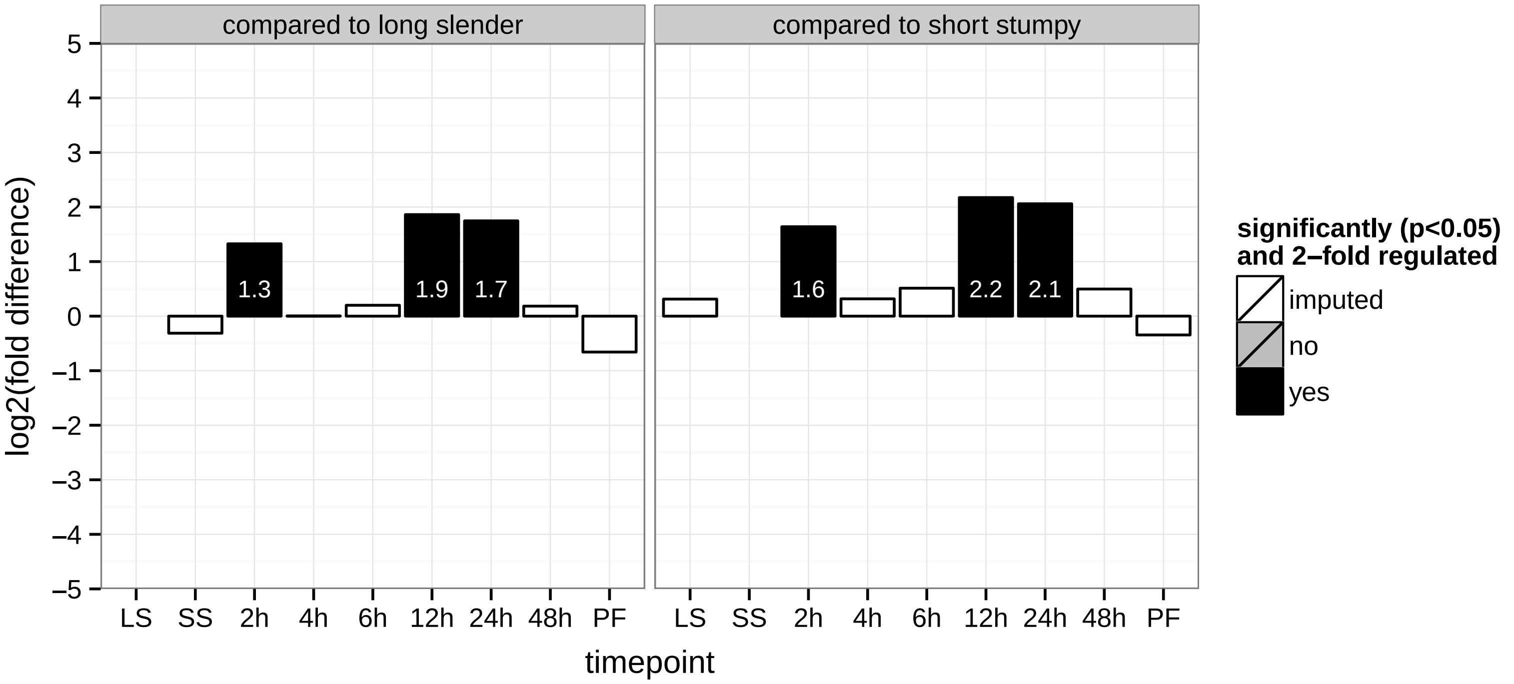
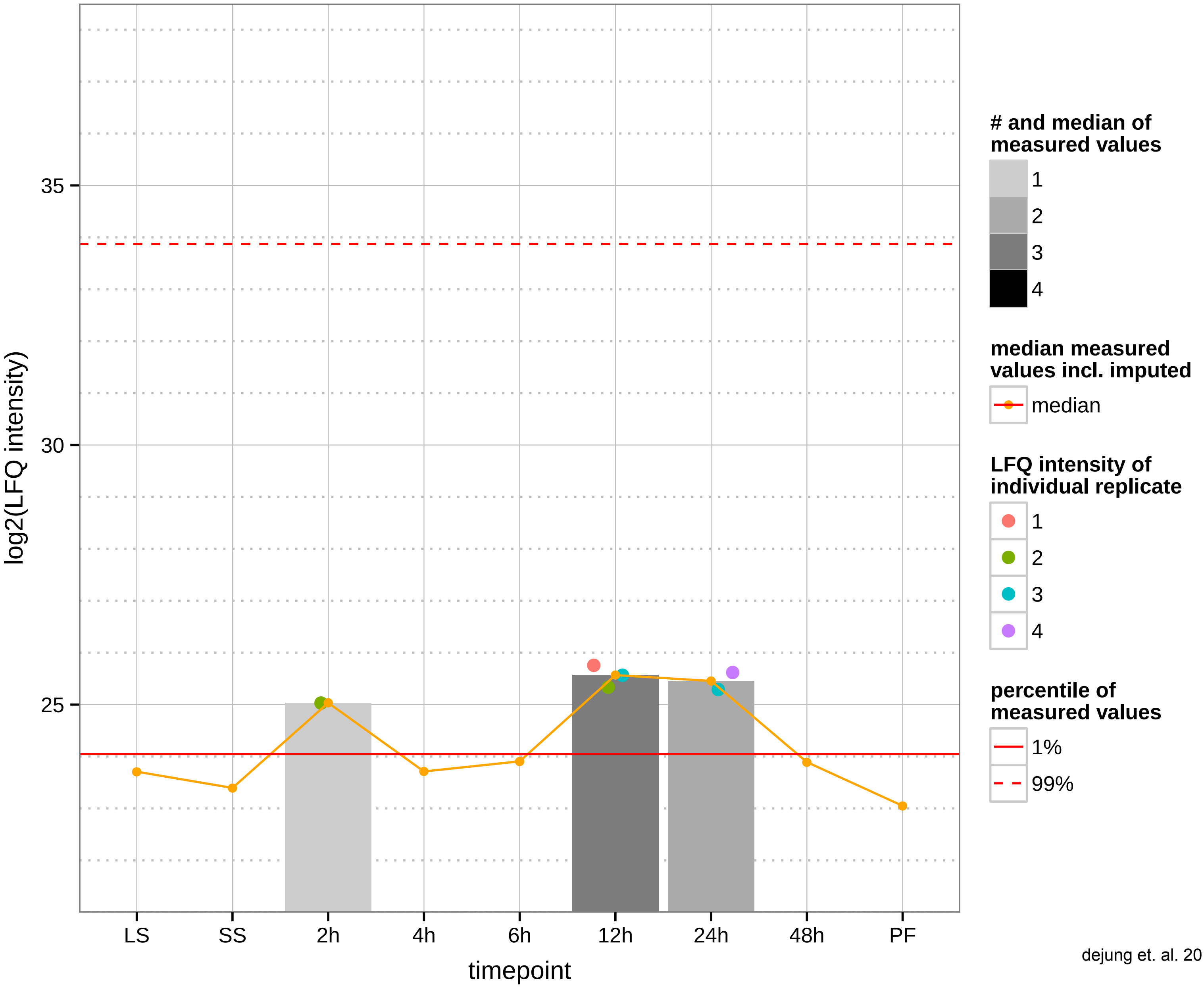
kinesin, putative
Tb927.10.12490
AGOF: ATP binding, microtubule motor activity, motor activity
AGOC: microtubule associated complex
AGOP: microtubule–based movement
PGOF: ATP binding, microtubule motor activity
PGOC: null
PGOP: microtubule–based movement





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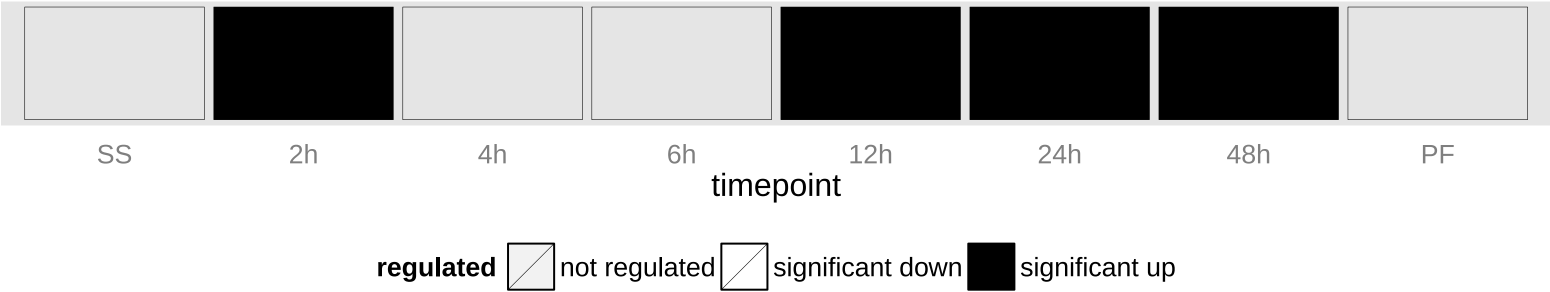

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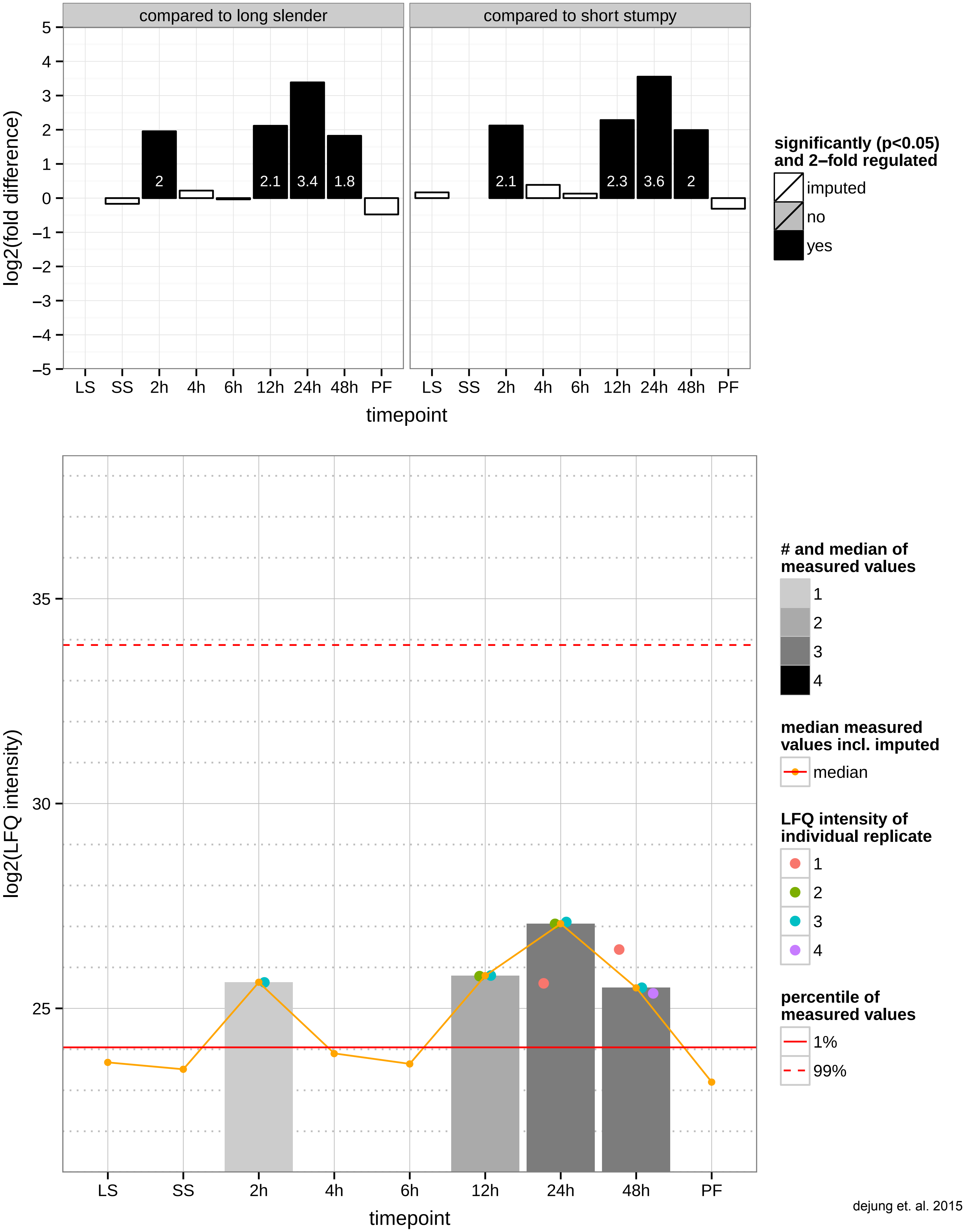
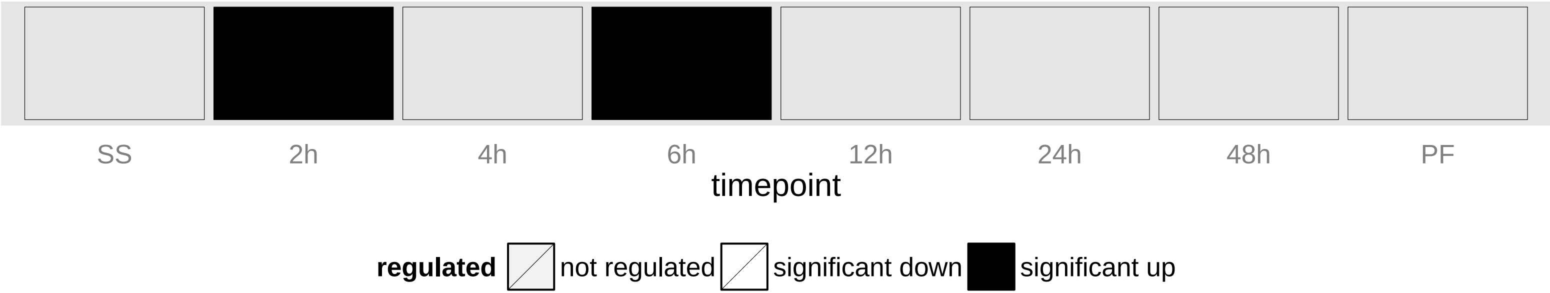
hypothetical protein, conserved
Tb927.5.510
AGOF: null
AGOC: mitochondrial membrane, mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015



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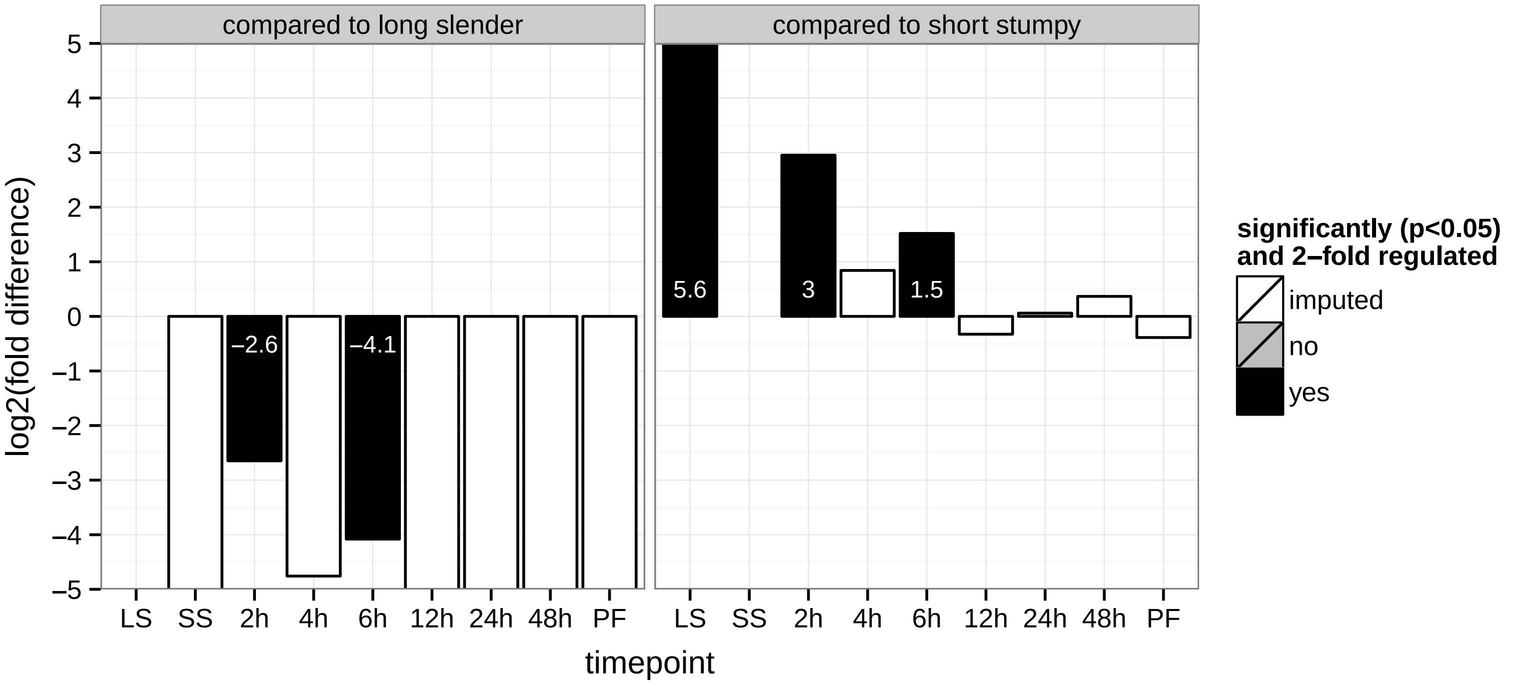
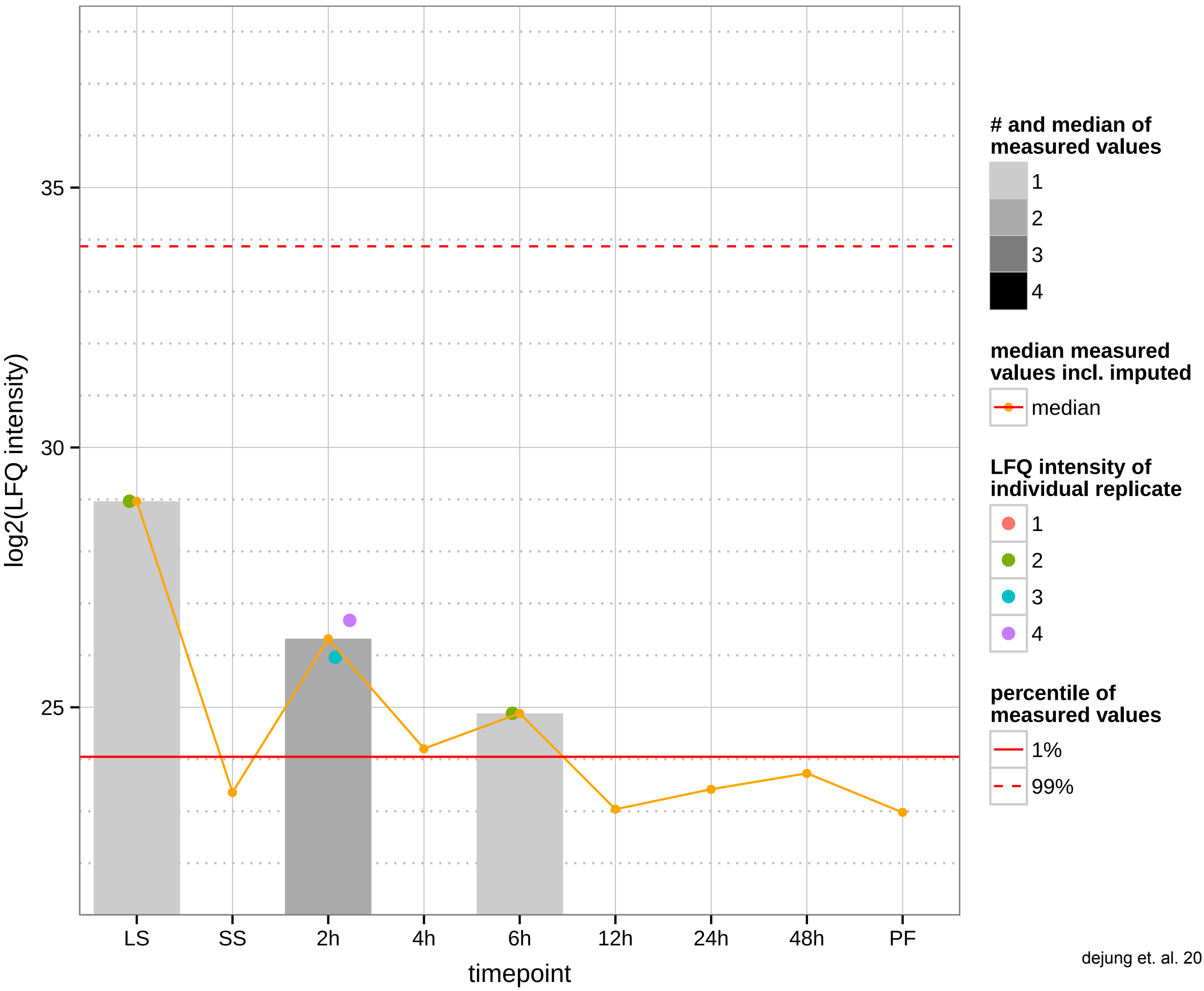
65 kDa invariant surface glycoprotein
Tb927.2.3310;Tb927.2.3300;Tb927.2.3290;Tb927.2.3280
AGOF: null
AGOC: plasma membrane
AGOP: plasma membrane organization
PGOF: null
PGOC: null
PGOP: null





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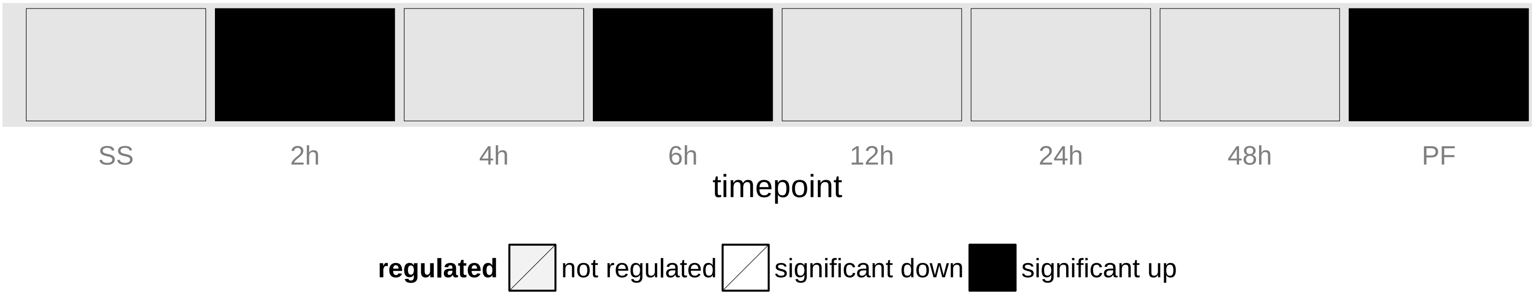

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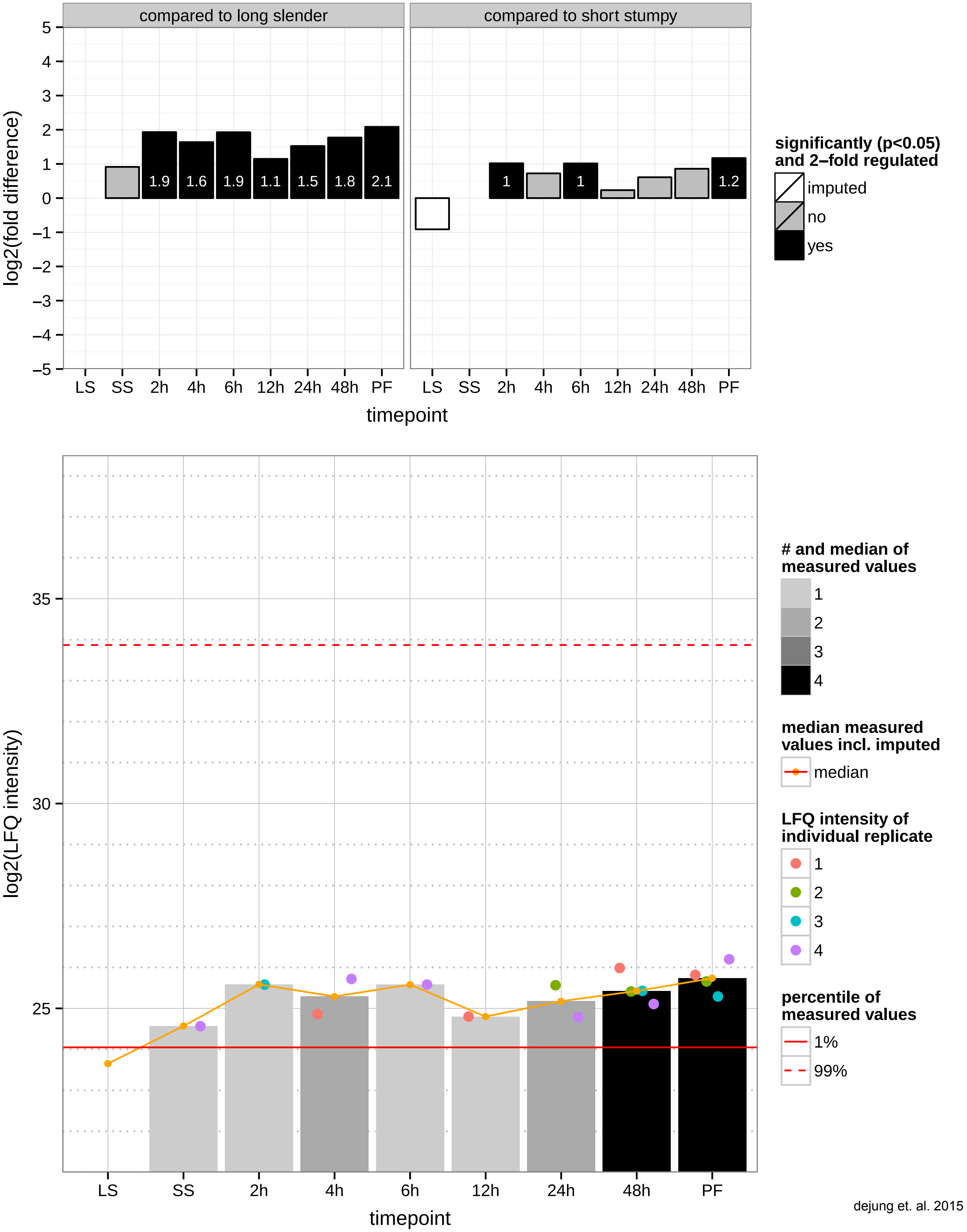
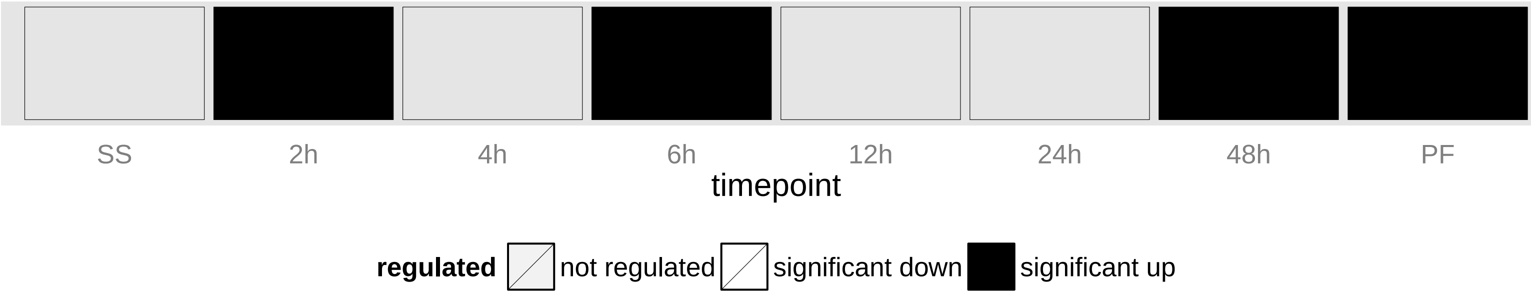
hypothetical protein, conserved
Tb927.8.5280
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null



dejung et. al. 2015



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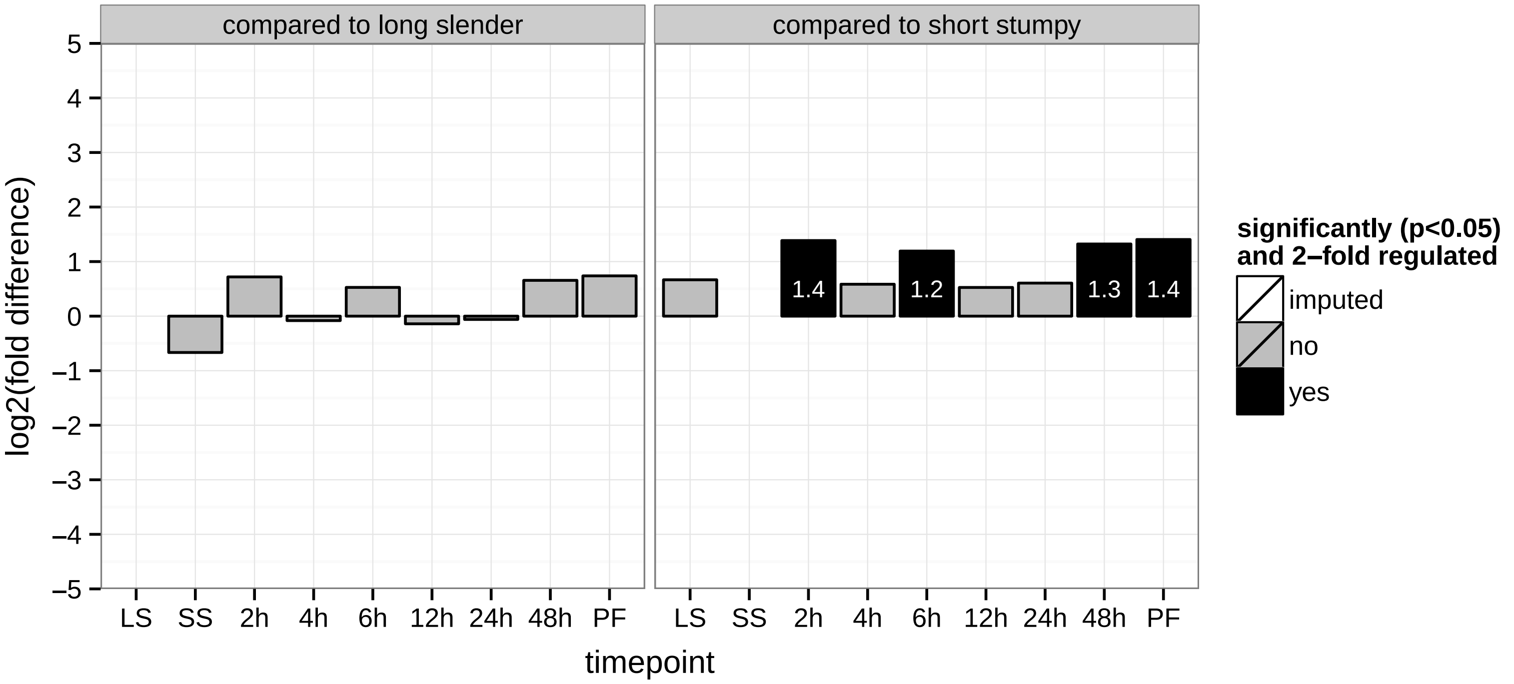
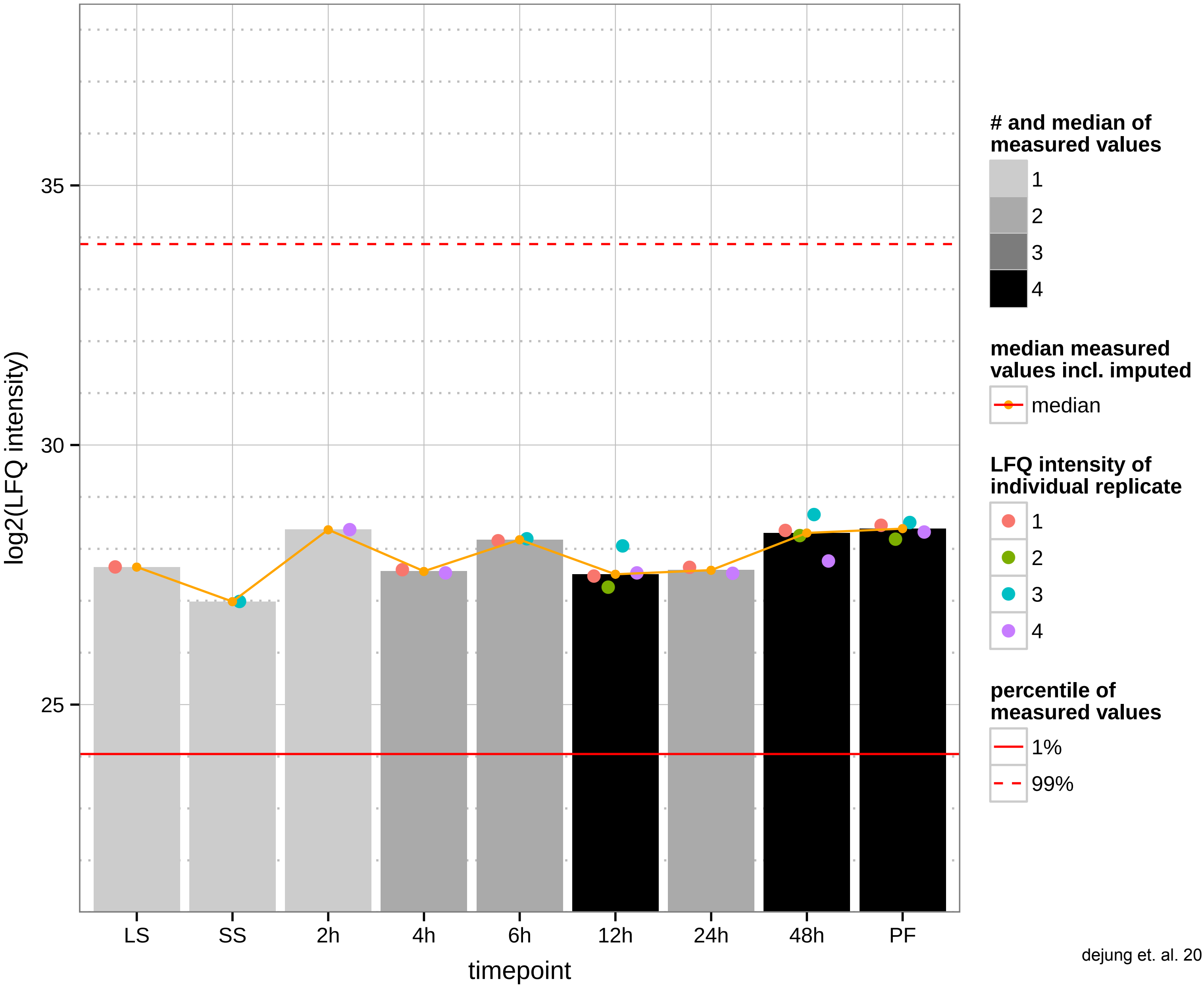
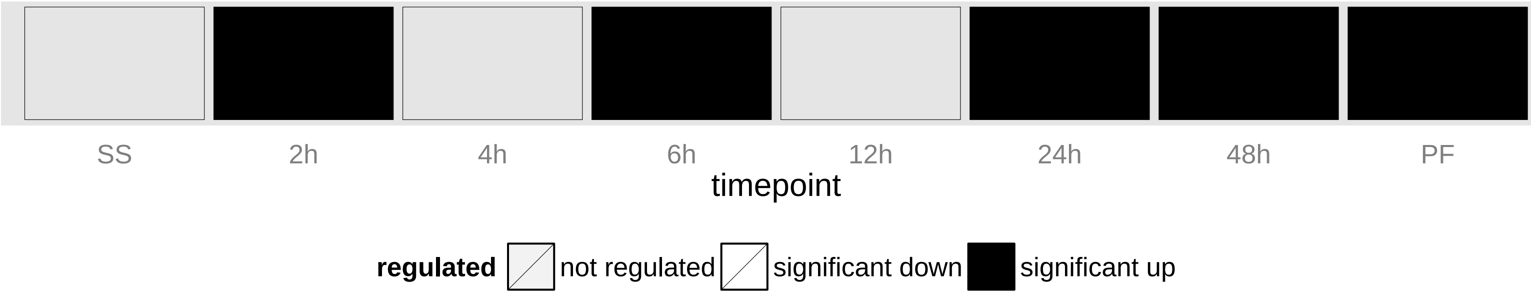
RNA Interference Factor 5 (RIF5)
Tb927.10.10730
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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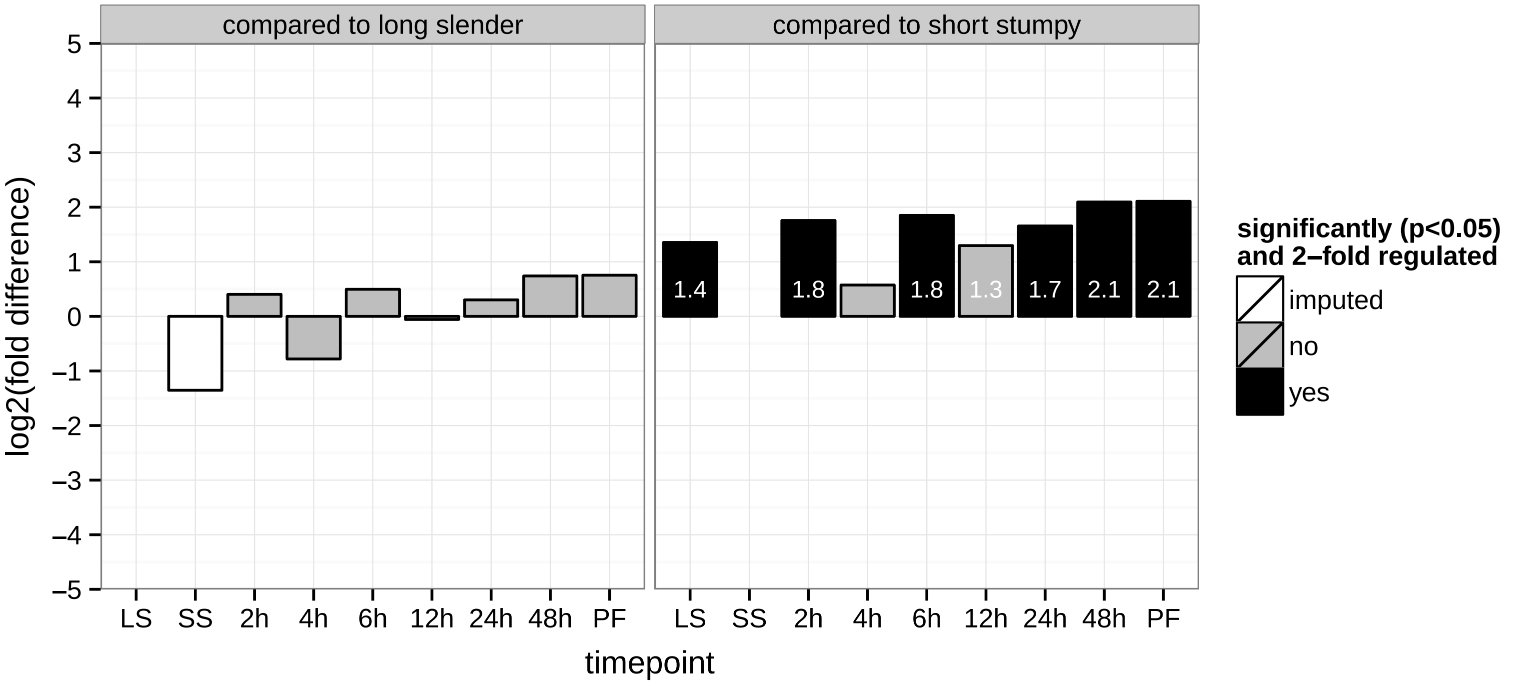
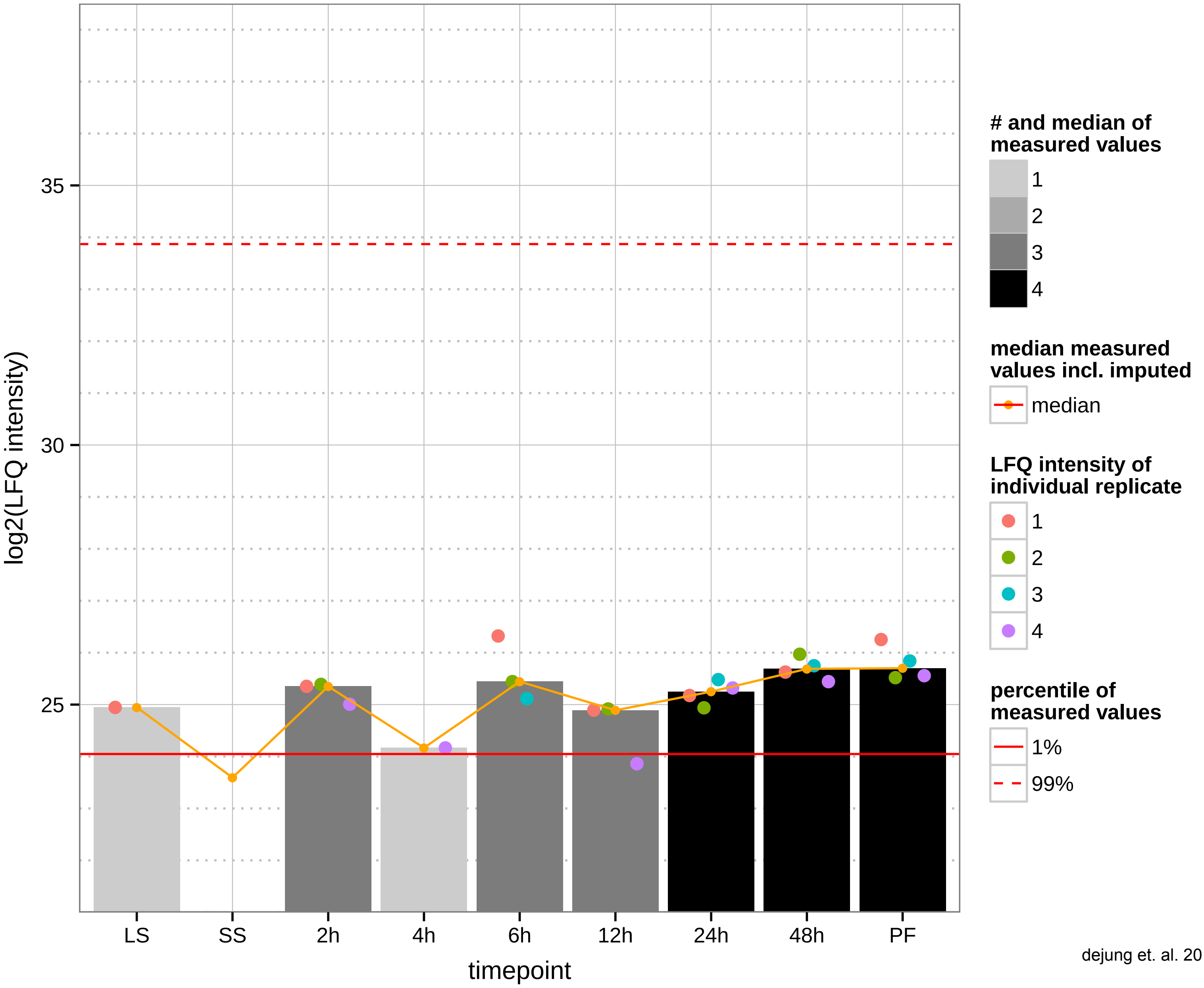
protein kinase, putative
Tb927.3.690
AGOF: ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity
AGOC: null
AGOP: cytokinesis after mitosis, protein phosphorylation
PGOF: ATP binding, protein kinase activity, transferase activity, transferring phosphorus–containing groups
PGOC: null
PGOP: protein phosphorylation





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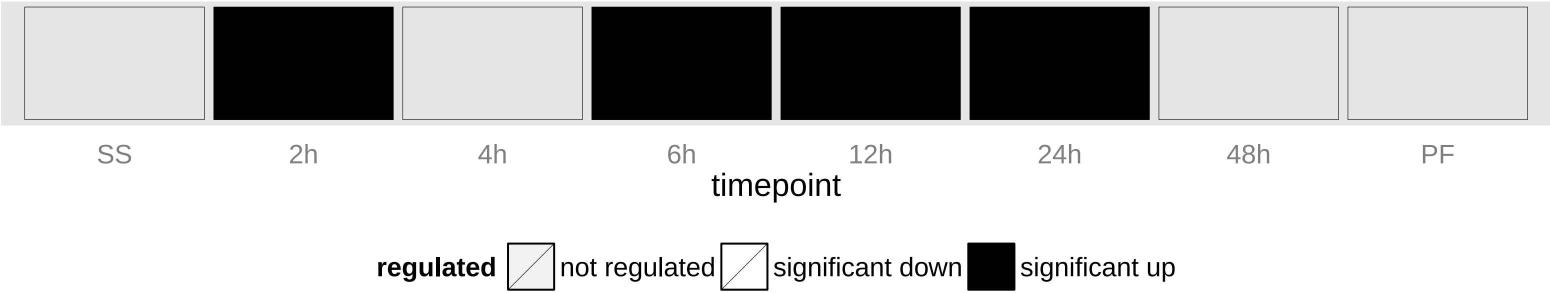

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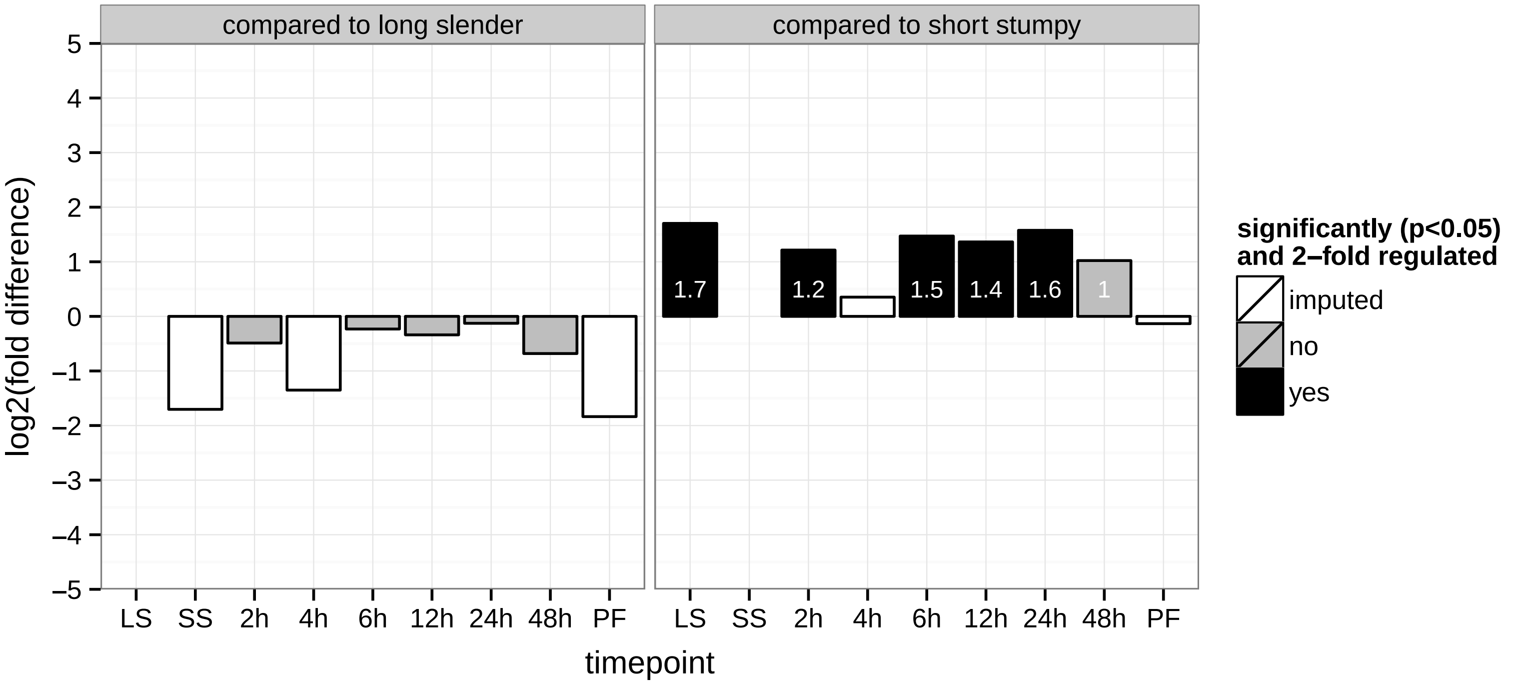
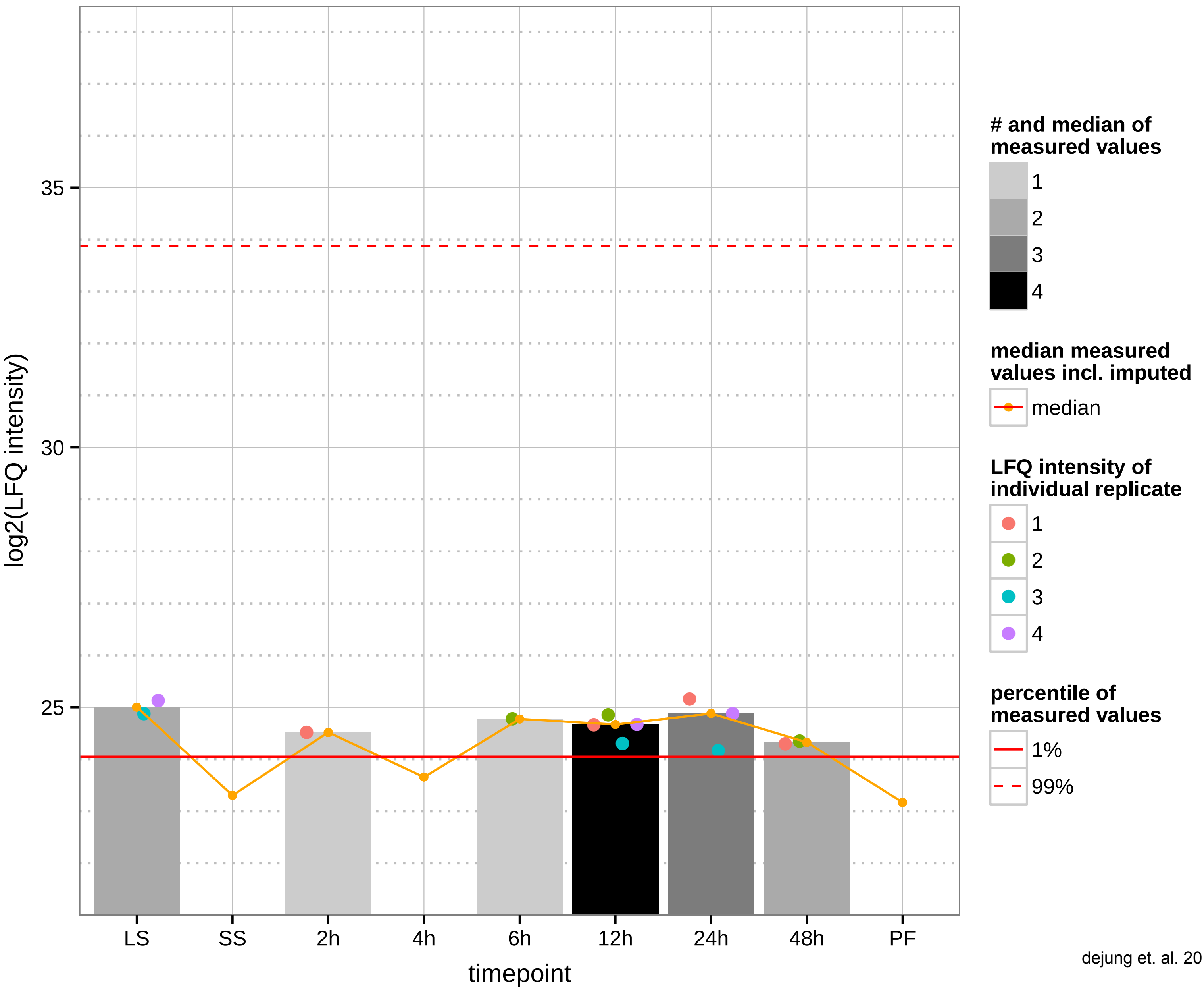
kinetoplastid–specific phospho–protein phosphatase, putative
Tb927.4.1870
AGOF: protein serine/threonine phosphatase activity
AGOC: null
AGOP: protein dephosphorylation
PGOF: hydrolase activity
PGOC: null
PGOP: null





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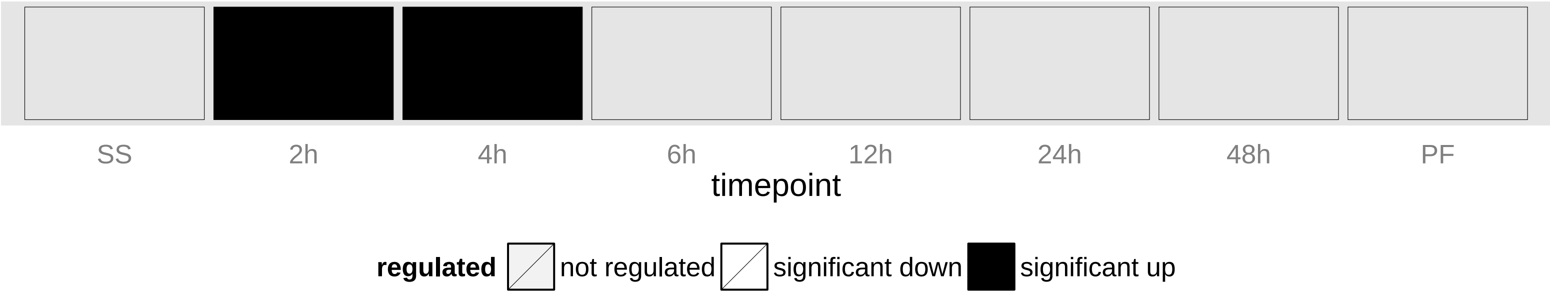

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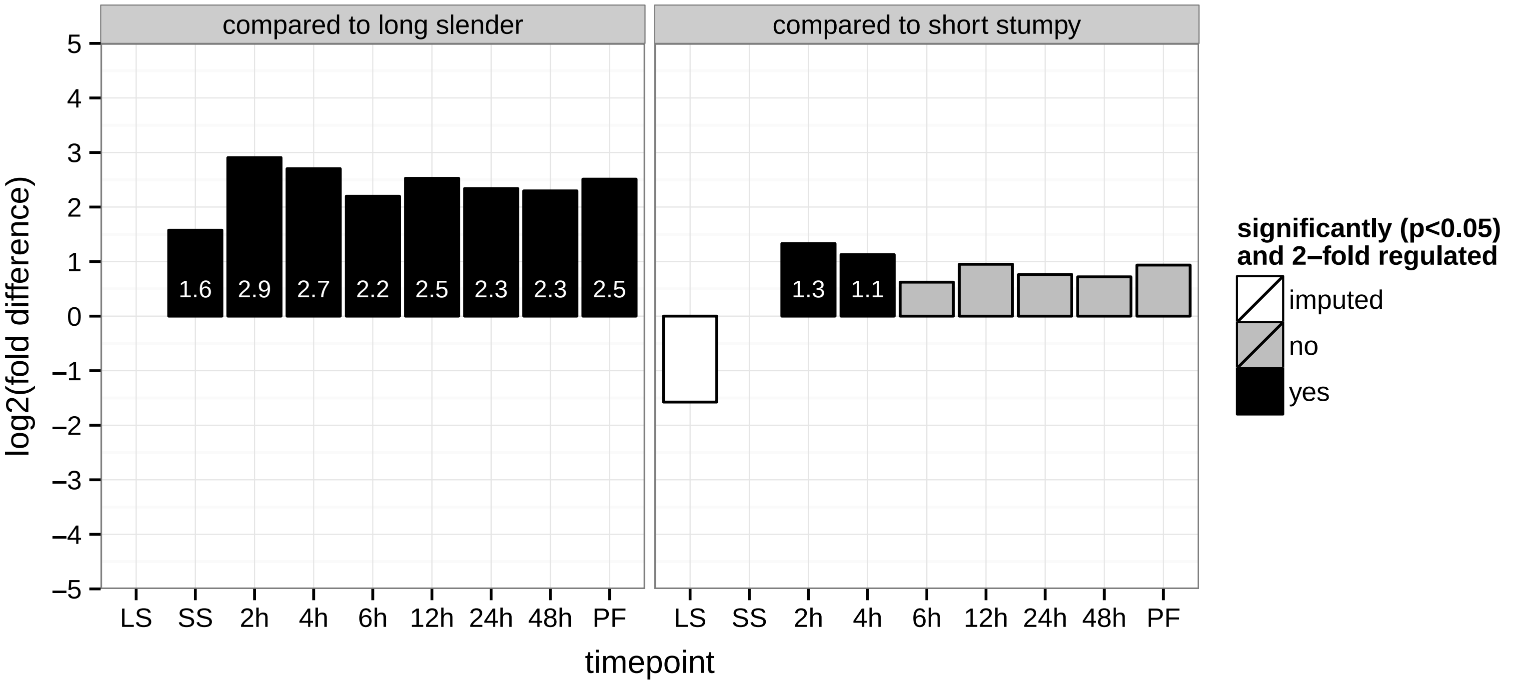
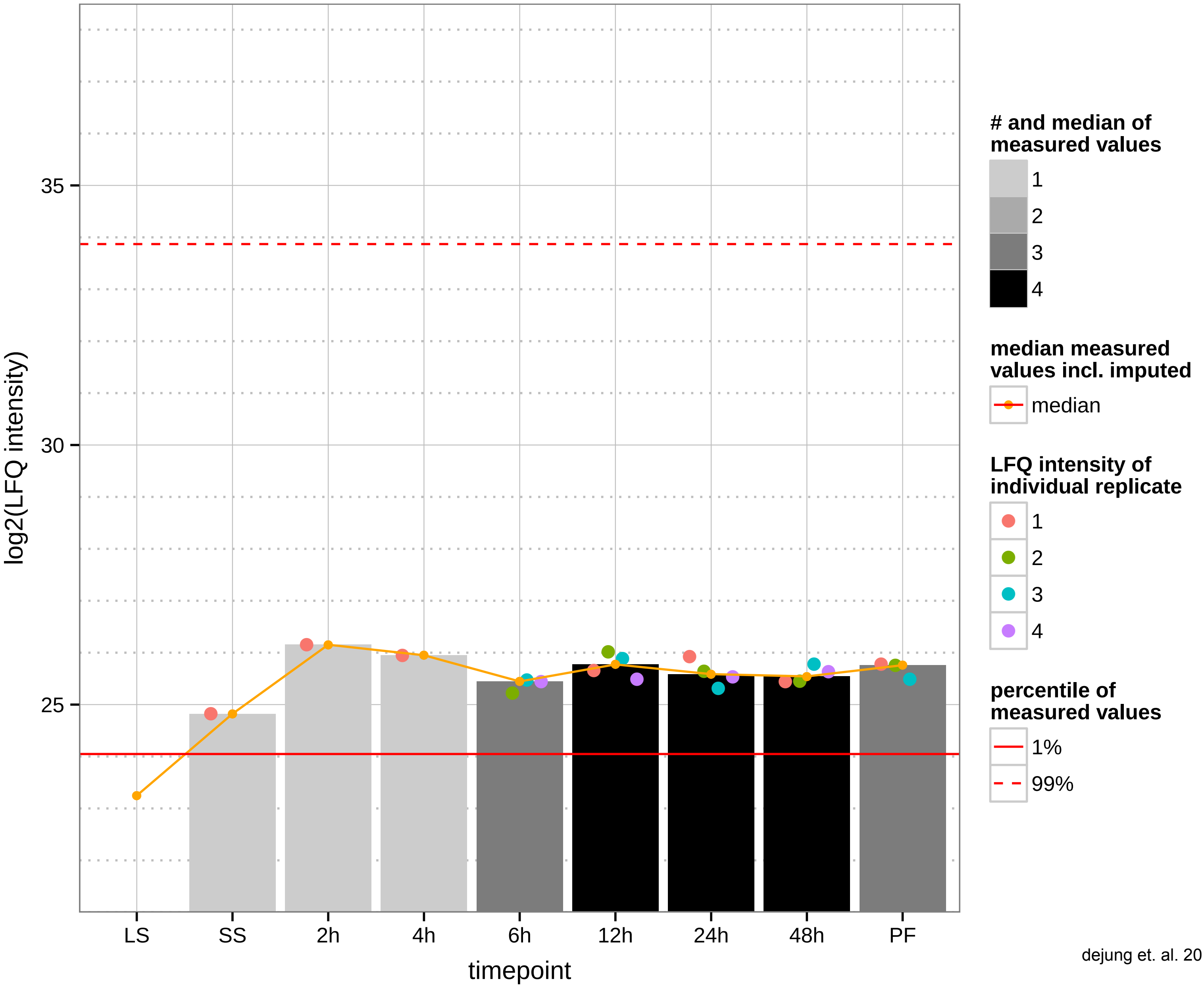
double−strand−break repair protein rad21 homolog, putative
Tb927.7.6900
AGOF: null
AGOC: nuclear chromosome
AGOP: null
PGOF: protein binding
PGOC: nuclear chromosome
PGOP: null





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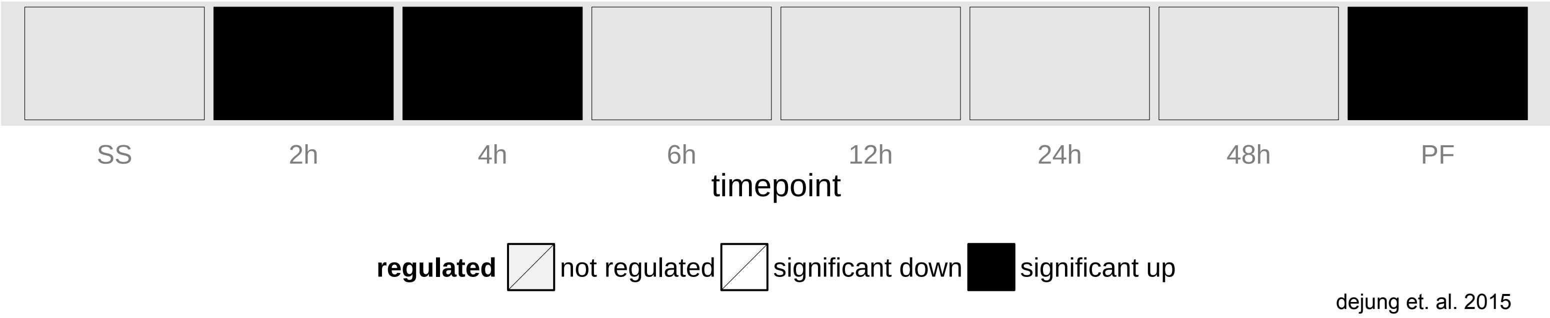
SS
2h
4h
6h
12h
24h
48h
PF
timepoint
regulated
not regulated
significant down
significant up
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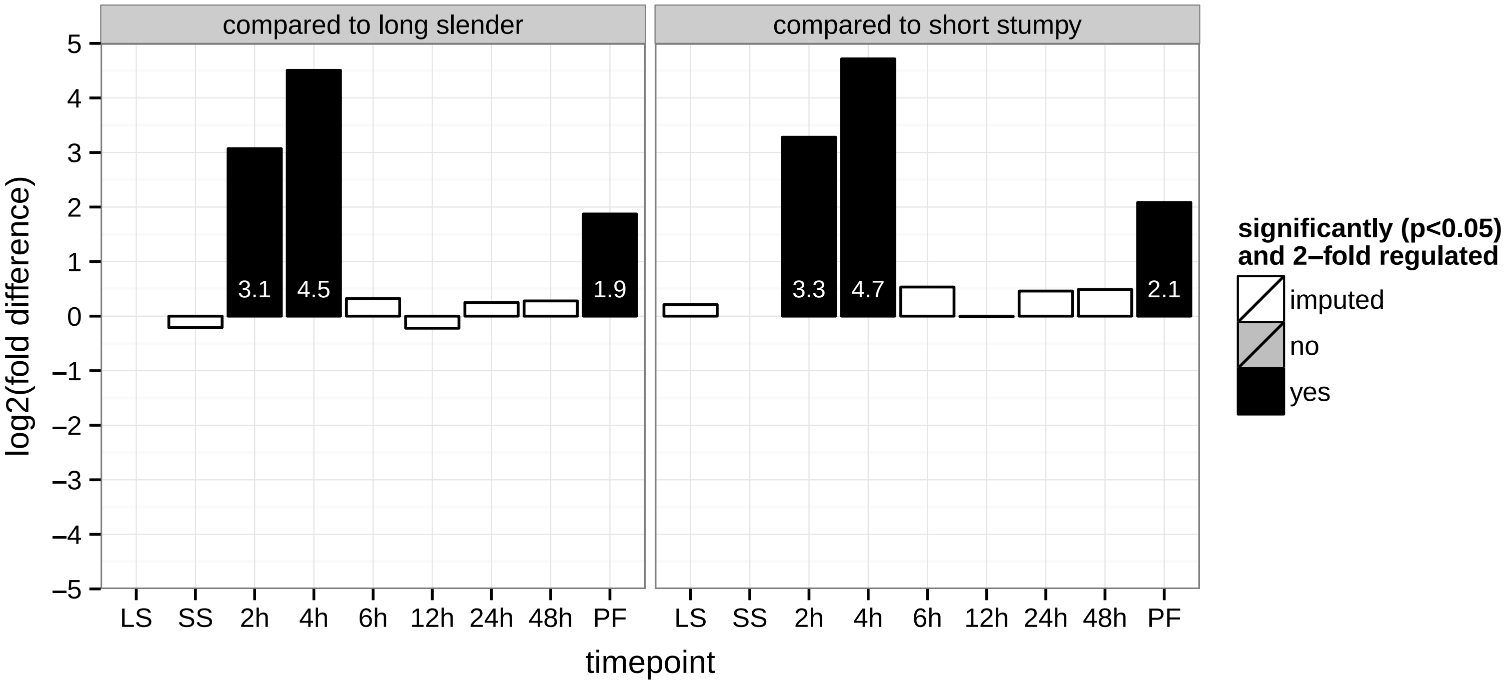
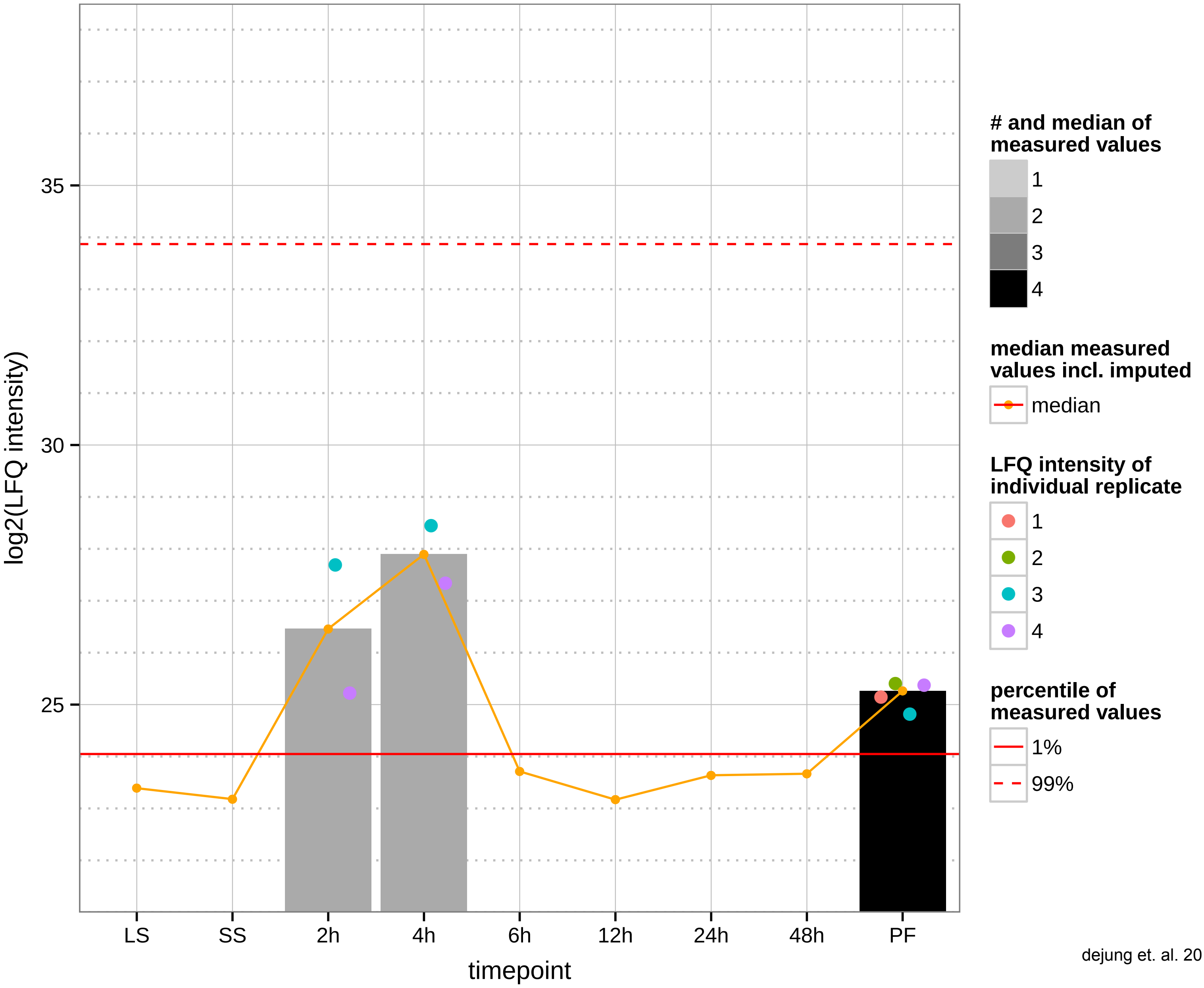
hypothetical protein, conserved
Tb927.8.3890;Tb927.8.3900;Tb927.8.3880
AGOF: null, structural constituent of cell wall
AGOC: integral to membrane
AGOP: null, plant–type cell wall organization
PGOF: null
PGOC: null
PGOP: null





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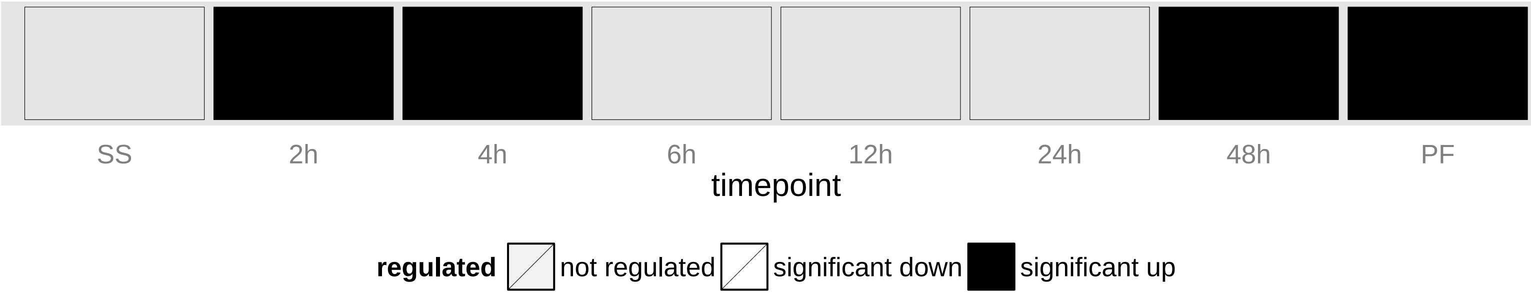

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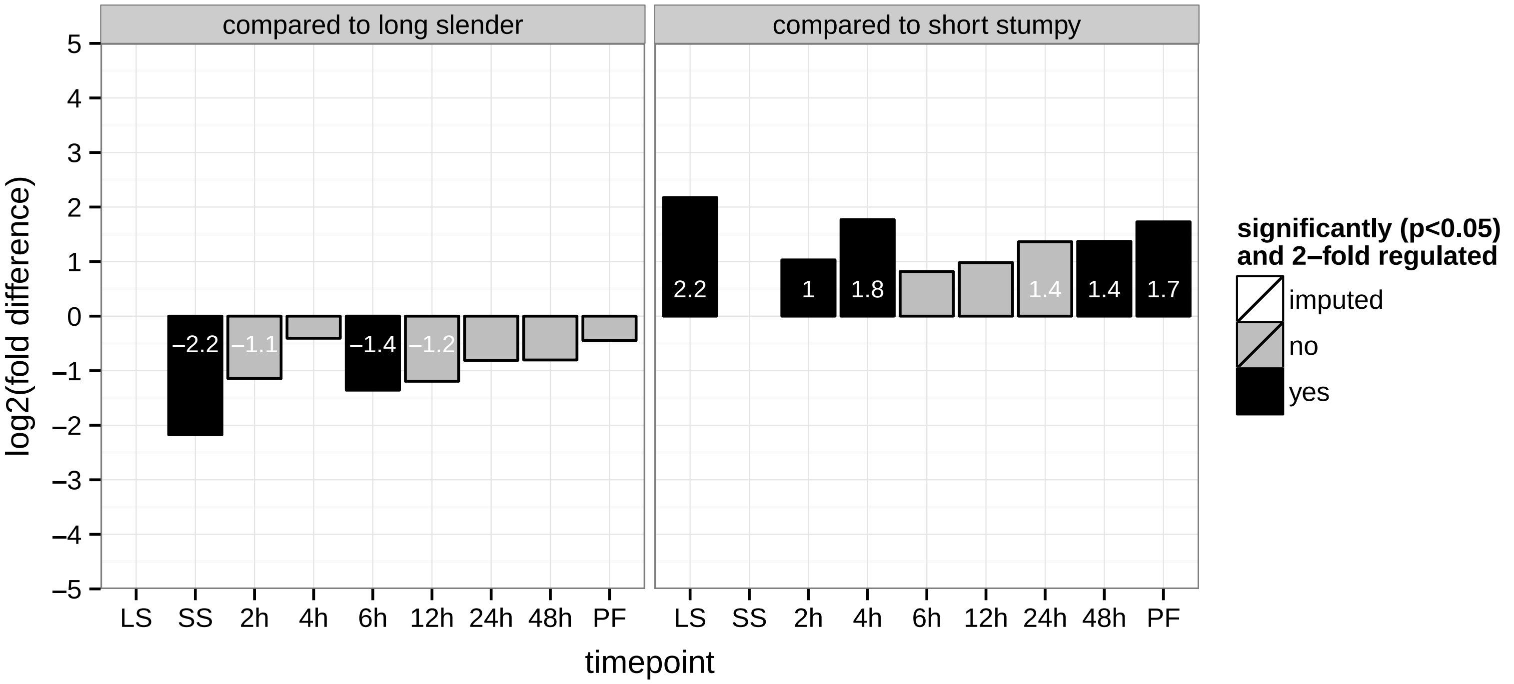
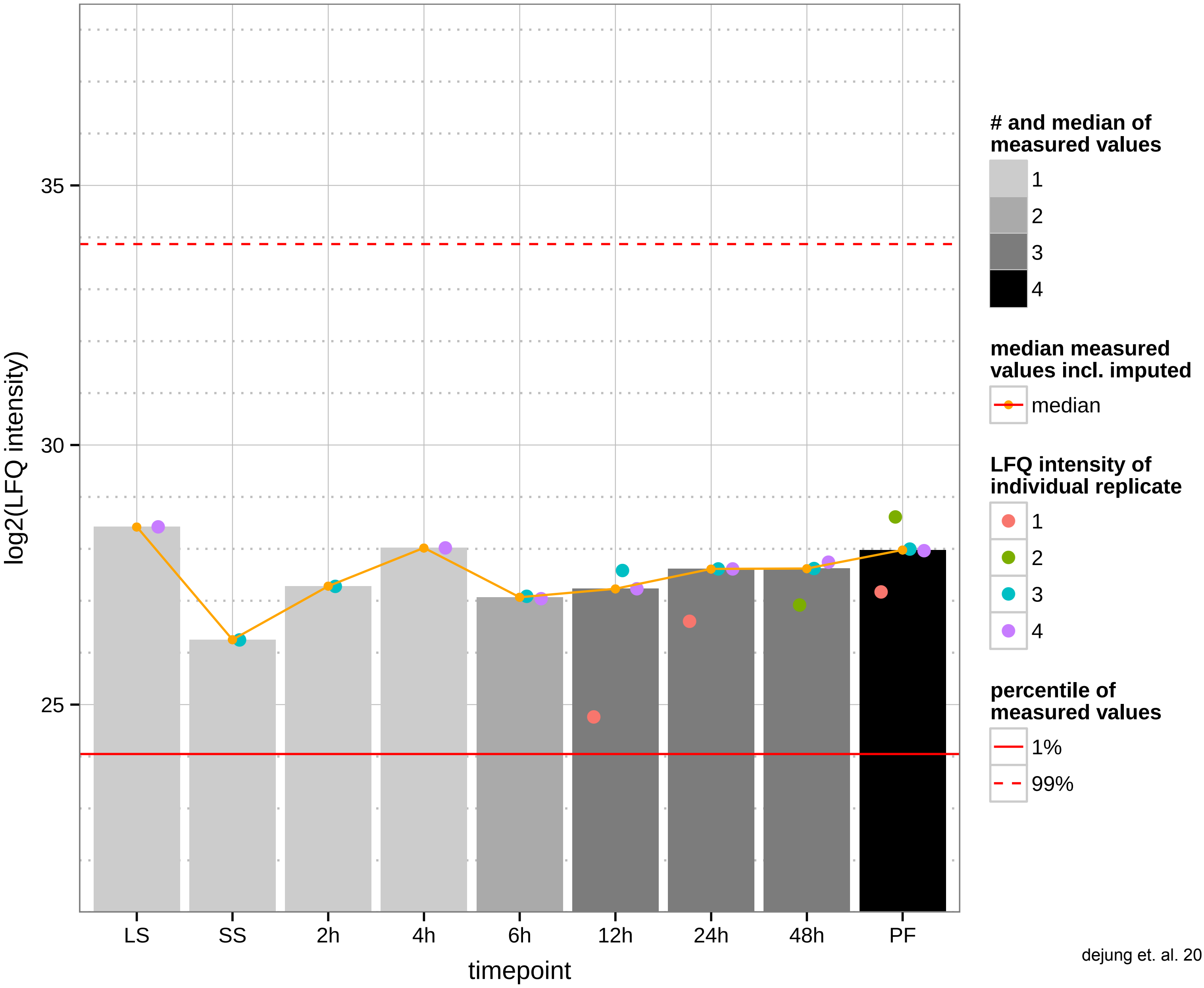
60S ribosomal protein L39, putative
Tb927.8.5260
AGOF: structural constituent of ribosome
AGOC: intracellular, ribosome
AGOP: translation
PGOF: structural constituent of ribosome
PGOC: intracellular, ribosome
PGOP: translation





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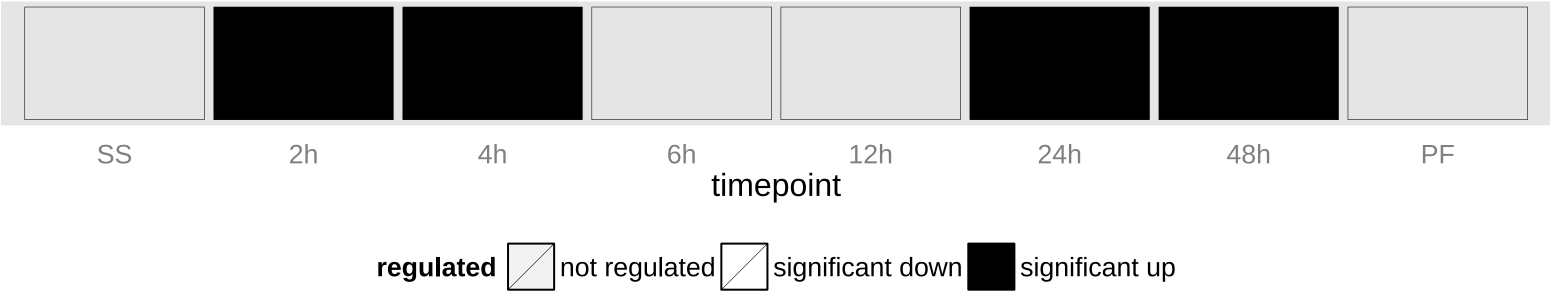

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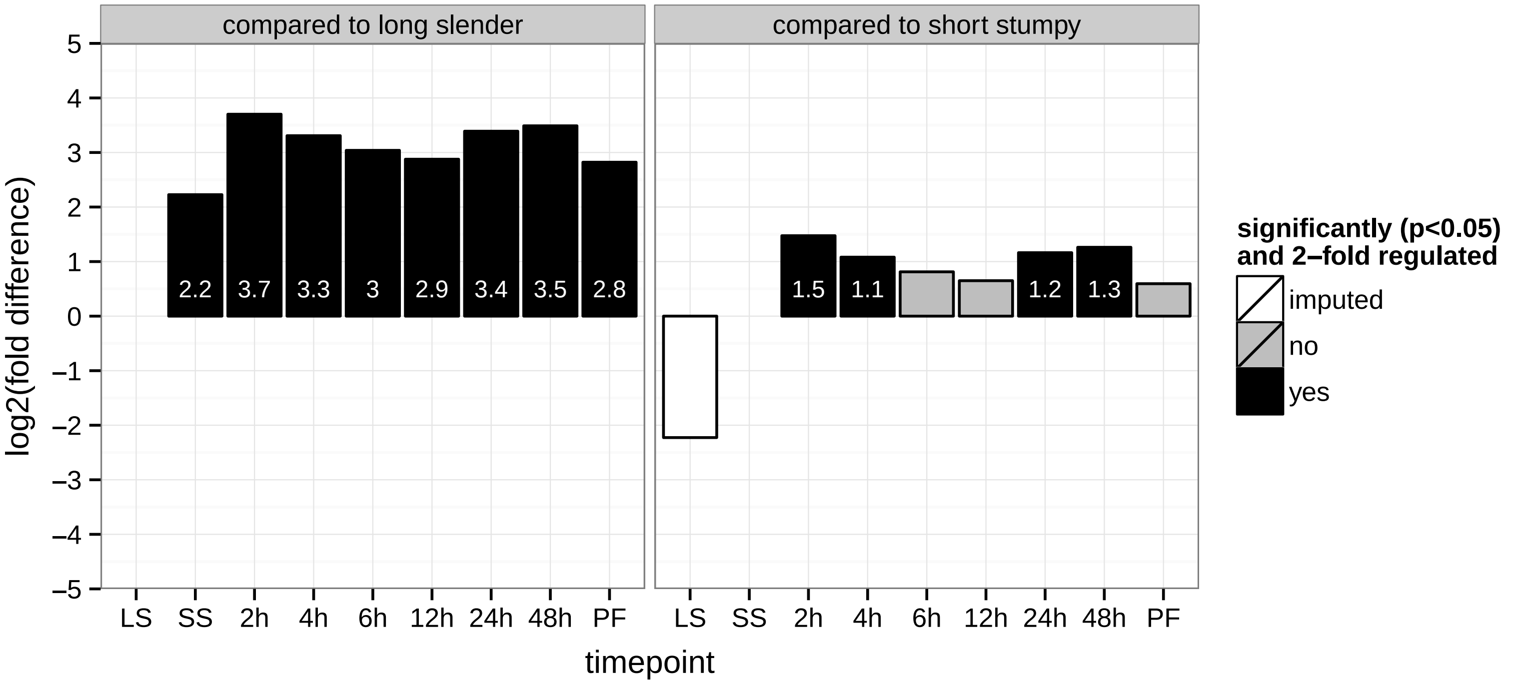
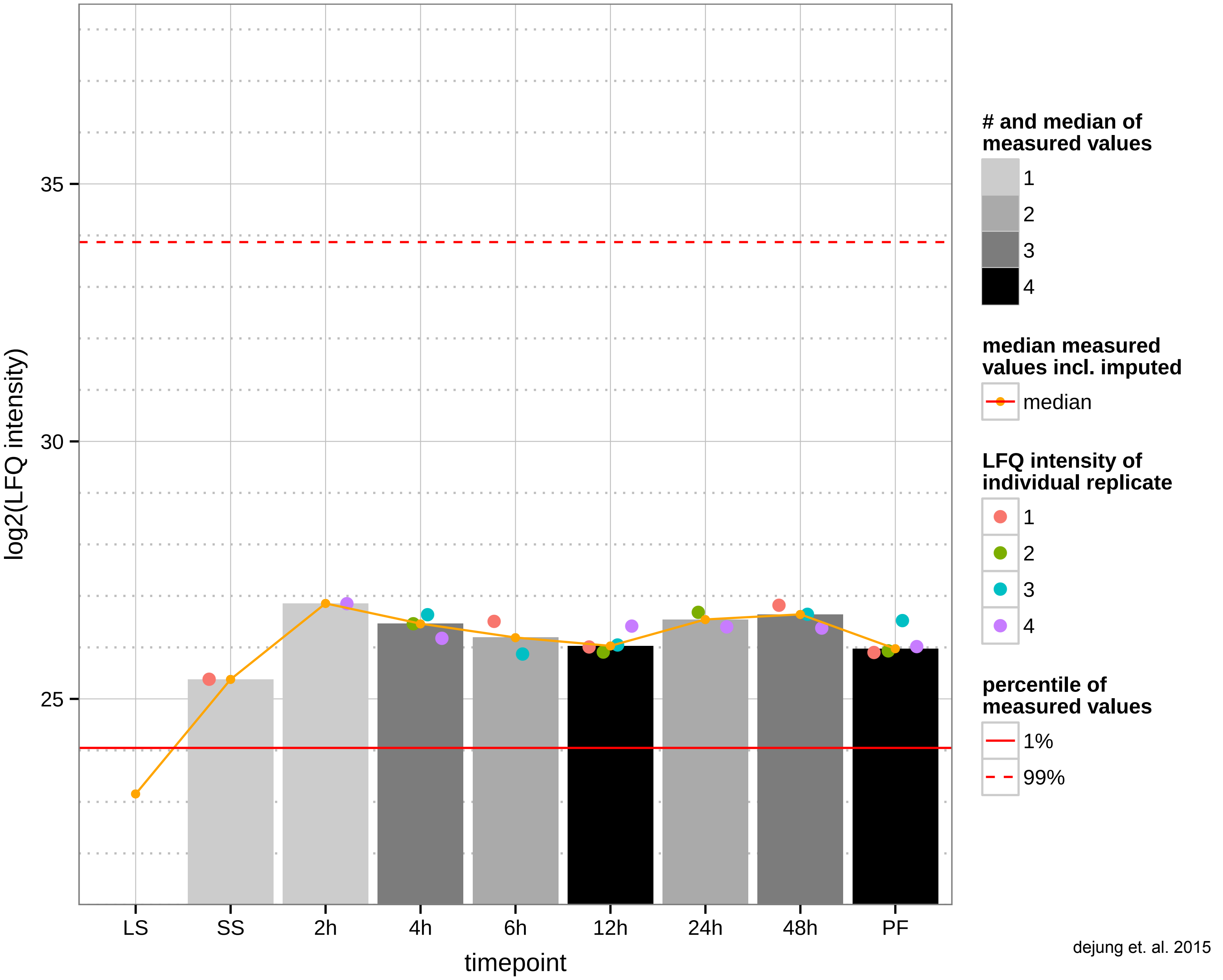
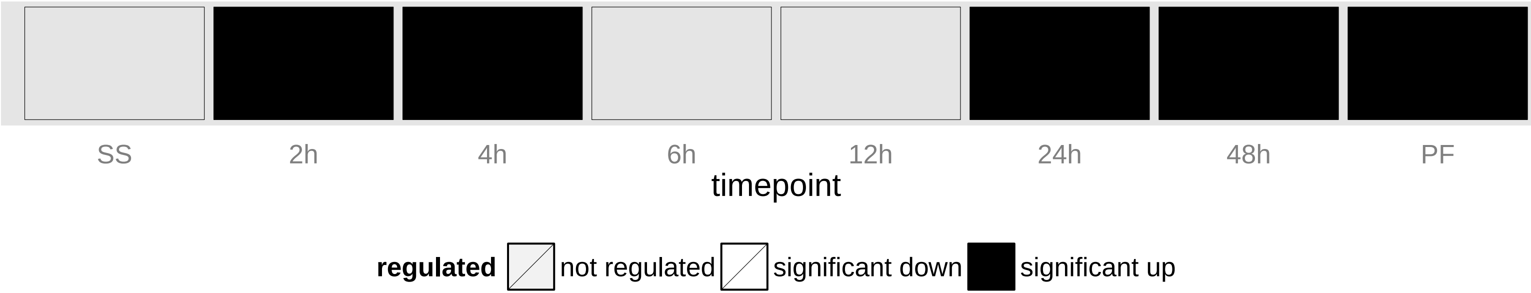
ribulose−5−phosphate 3−epimerase, putative
Tb927.10.12210
AGOF: ribulose−phosphate 3−epimerase activity
AGOC: null
AGOP: pentose−phosphate shunt
PGOF: catalytic activity, racemase and epimerase activity, acting on carbohydrates and derivatives, ribulose−phosphate 3−epi
PGOC: null
PGOP: carbohydrate metabolic process, metabolic process, pentose−phosphate shunt





dejung et. al. 2015



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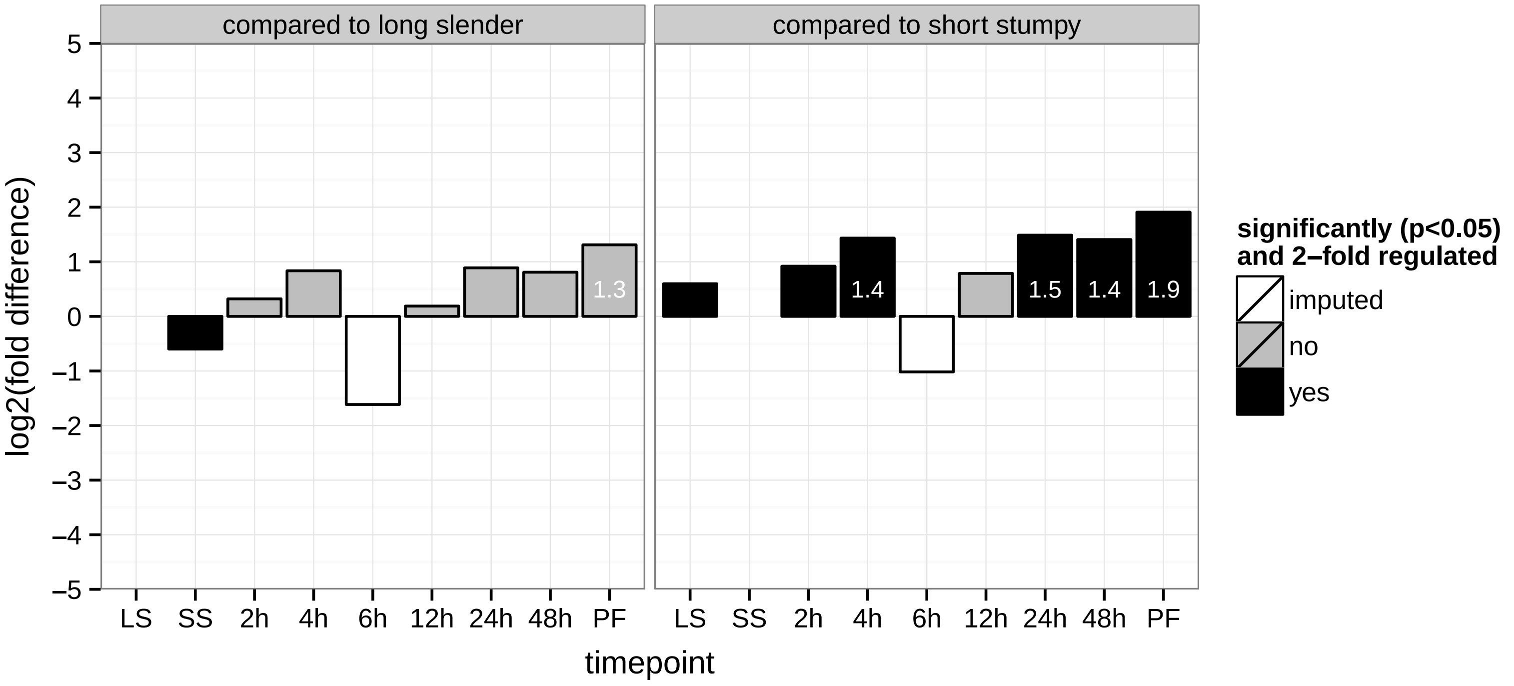
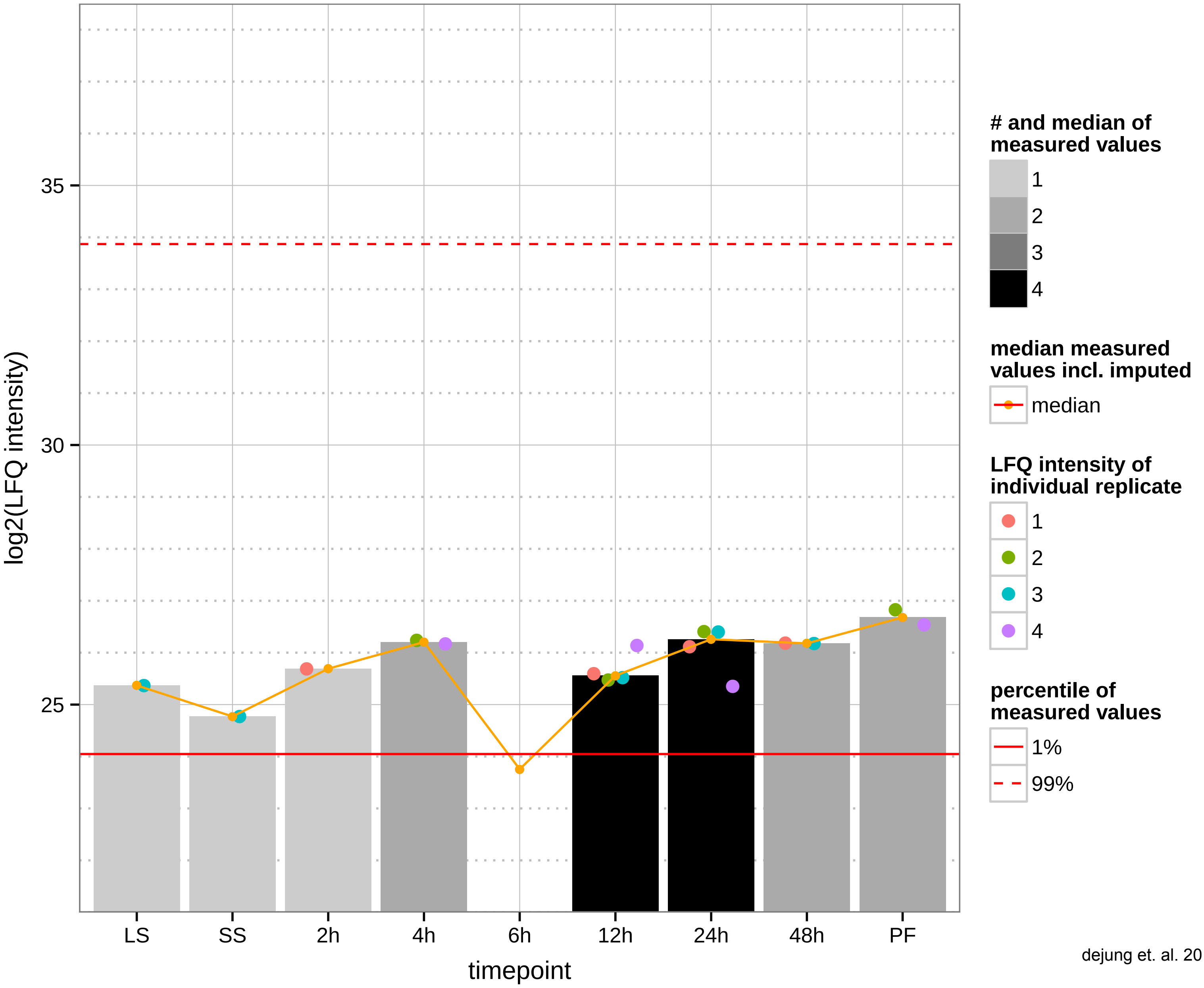
hypothetical protein, conserved
Tb927.10.11520
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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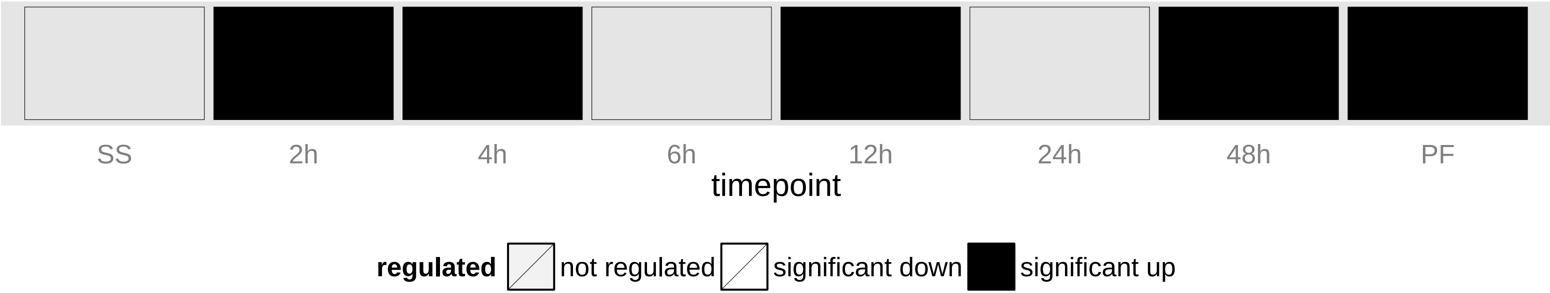

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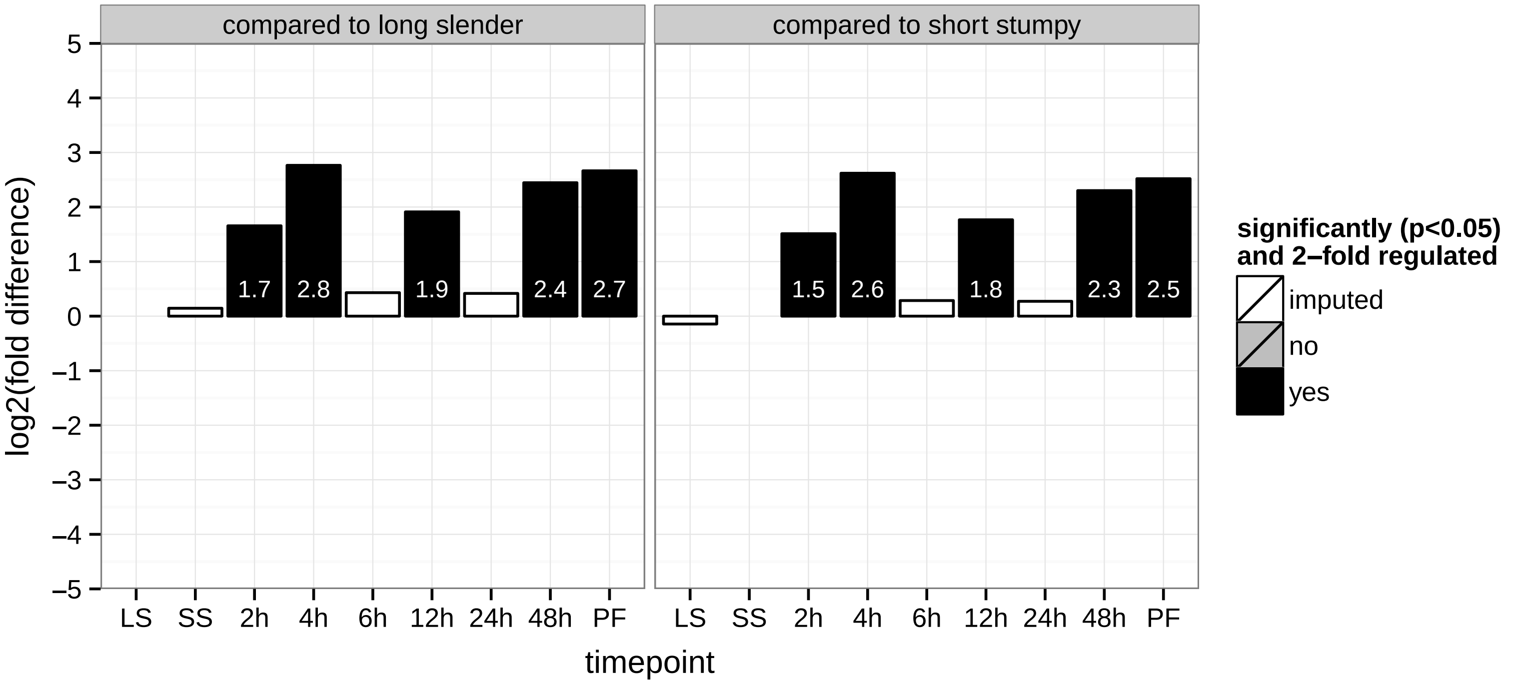
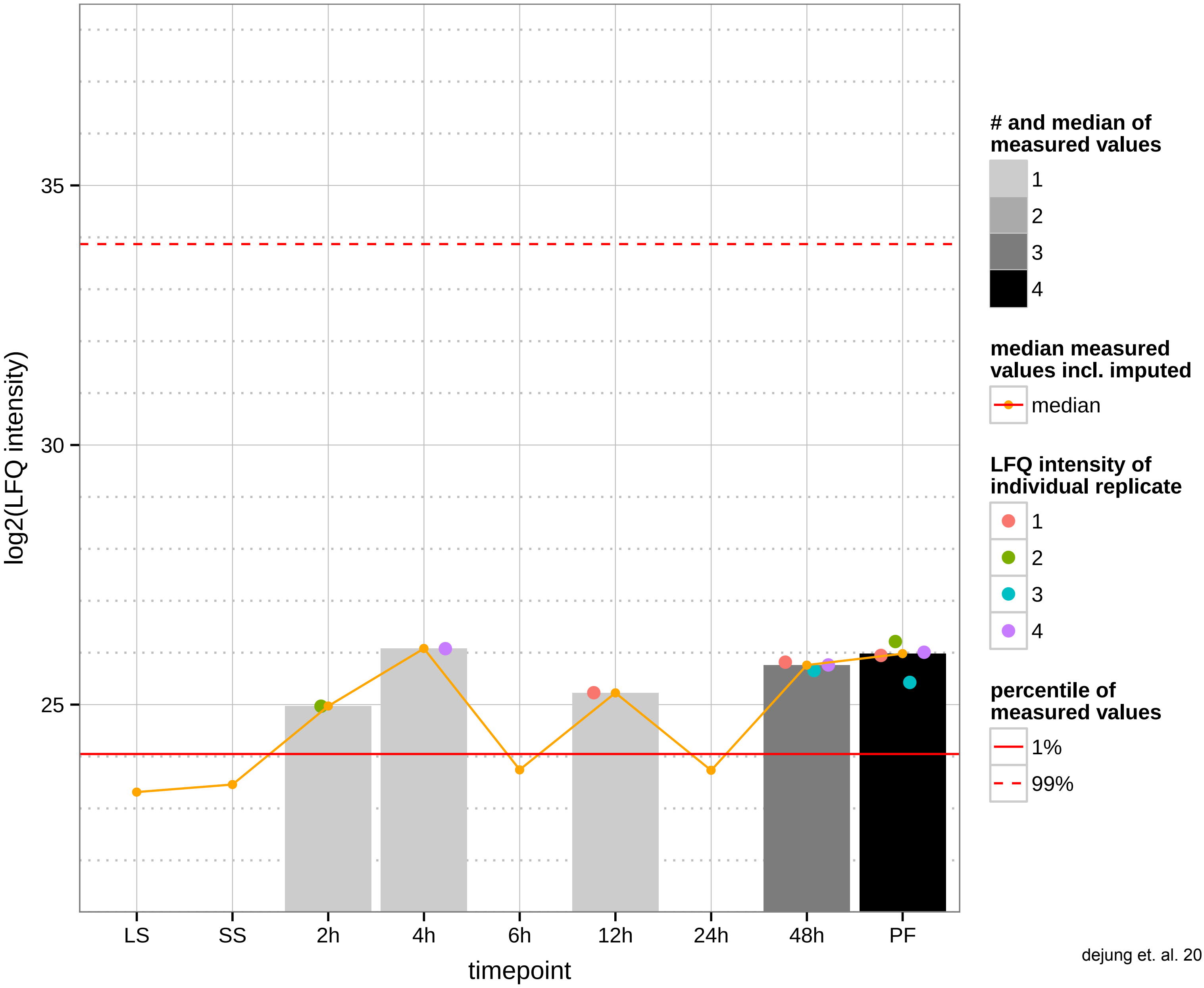
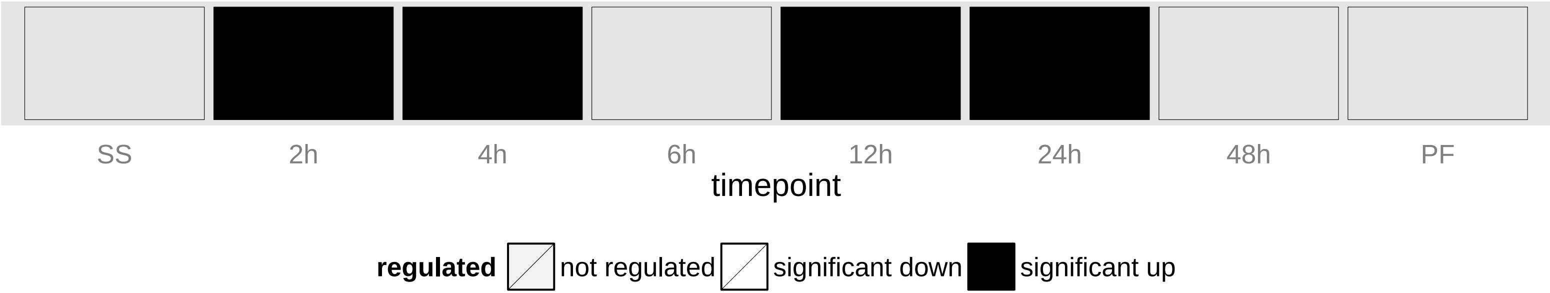
hypothetical protein, conserved
Tb927.5.4120
AGOF: null
AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
PGOP: null





dejung et. al. 2015



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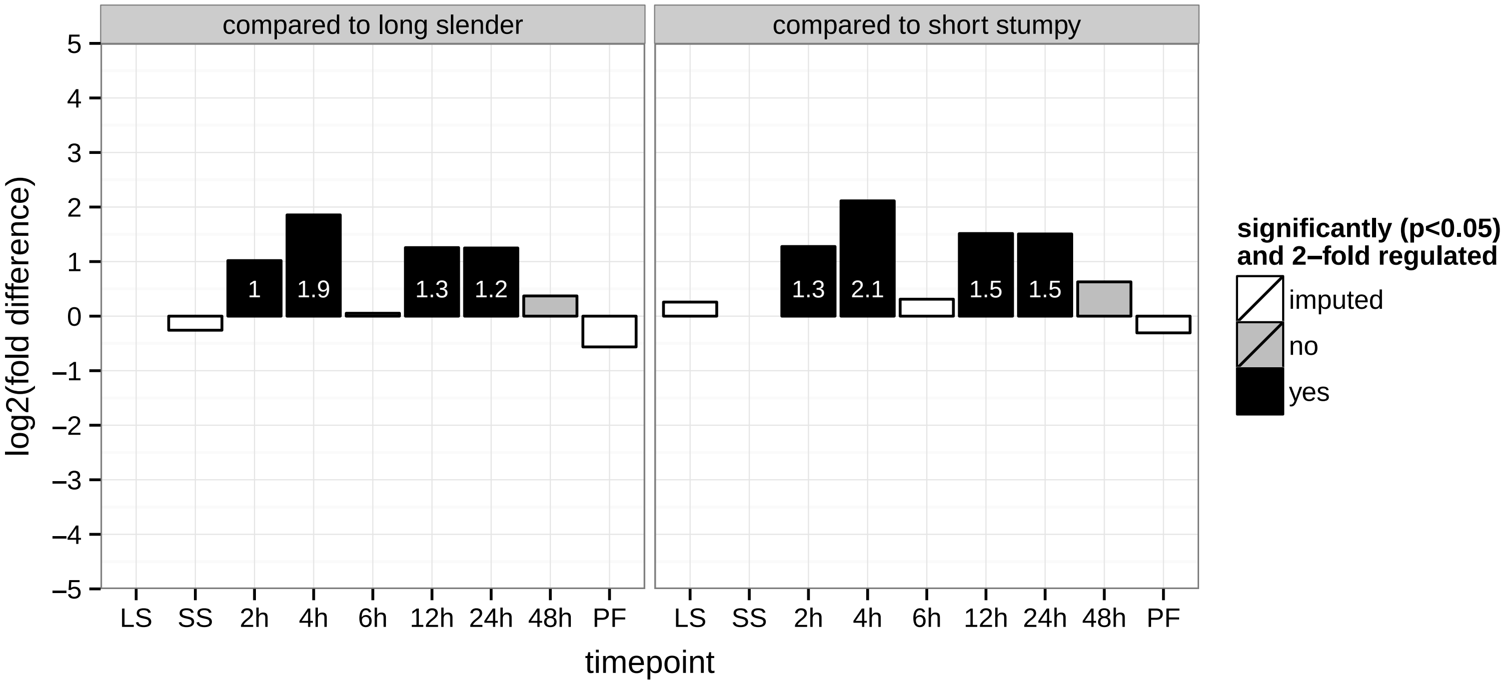
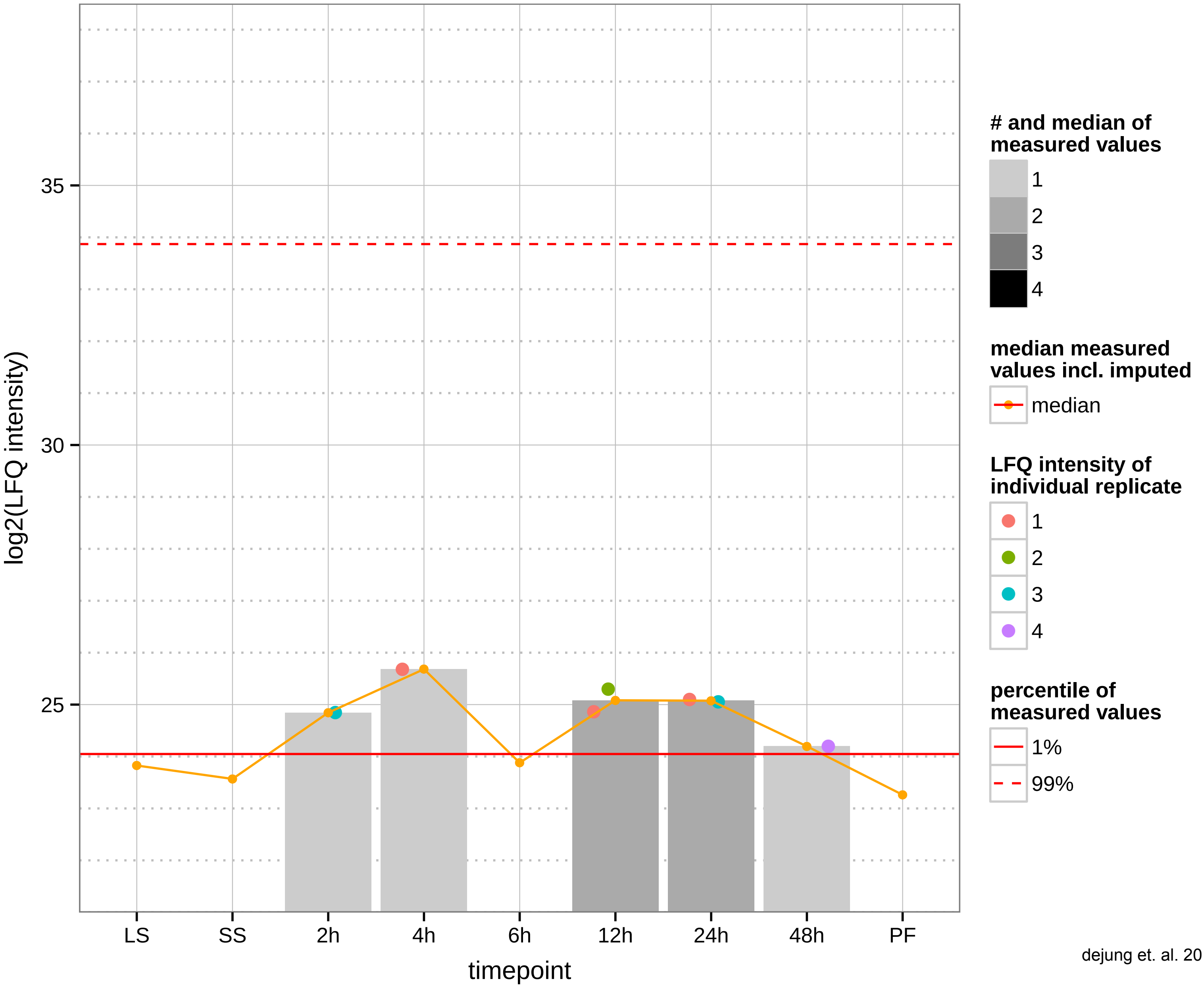
hypothetical protein, conserved
Tb927.11.15210
AGOF: null
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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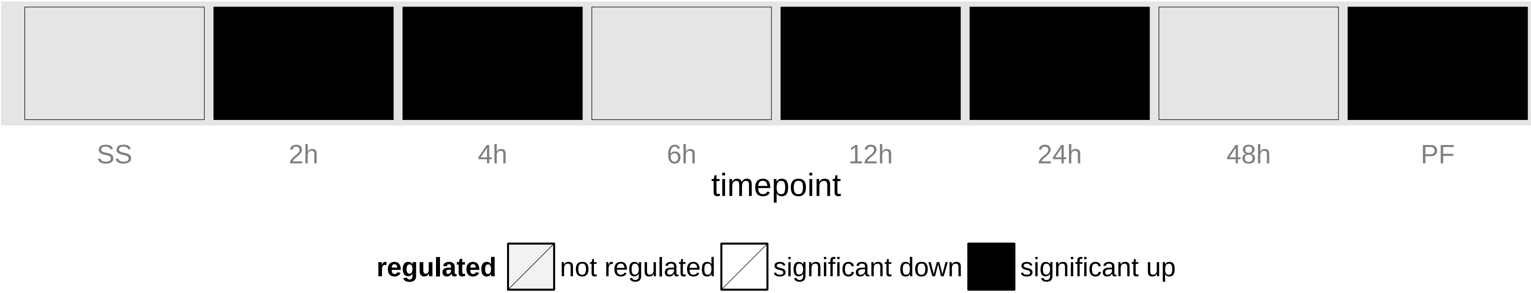

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hypothetical protein, conserved
Tb927.10.11890
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AGOC: mitochondrion
AGOP: null
PGOF: null
PGOC: null
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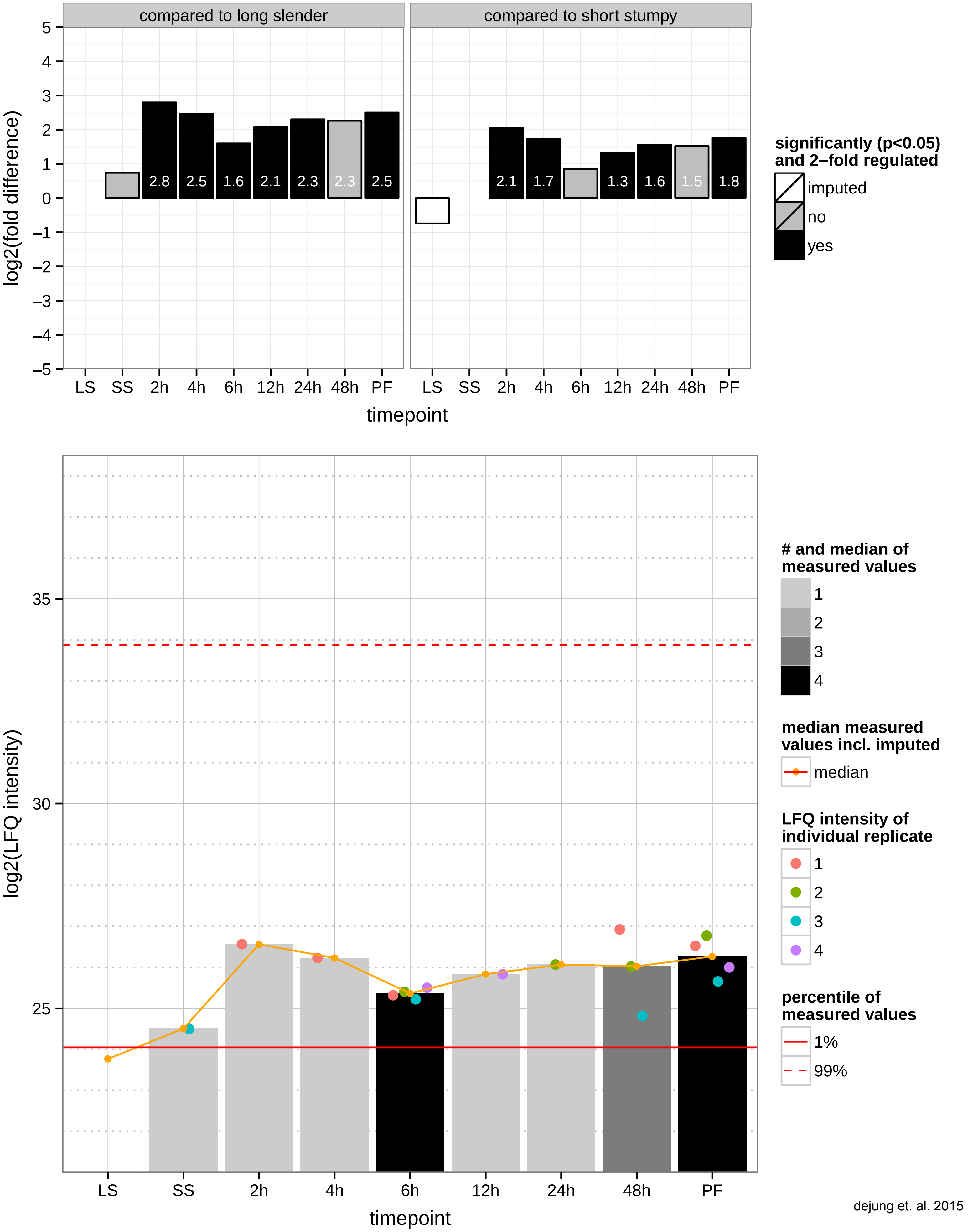

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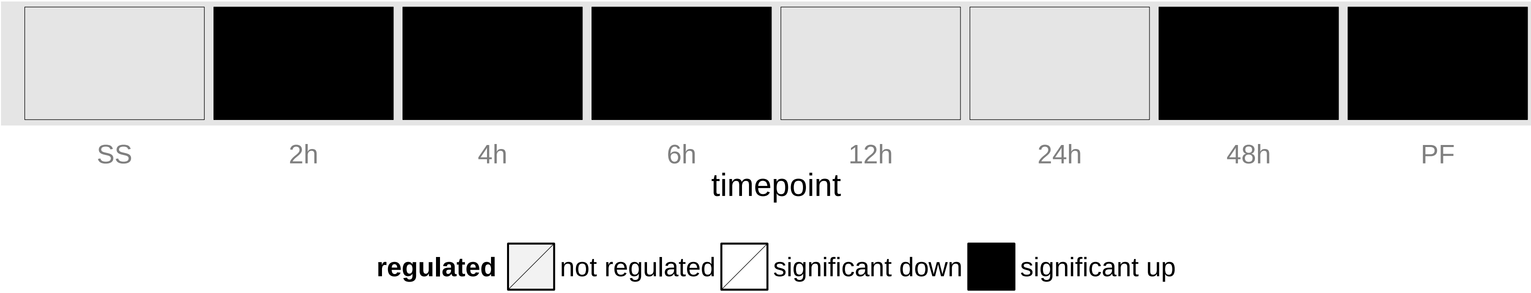

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hypothetical protein, conserved
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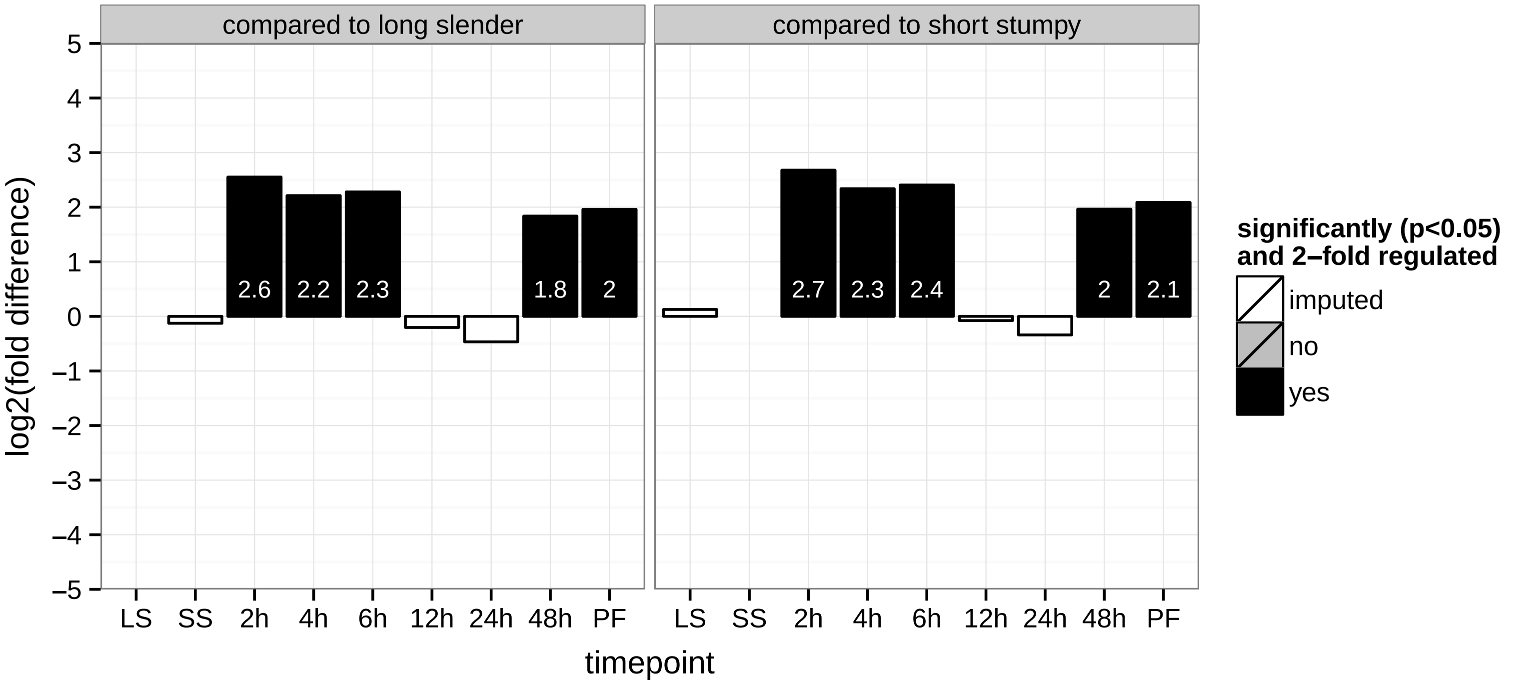
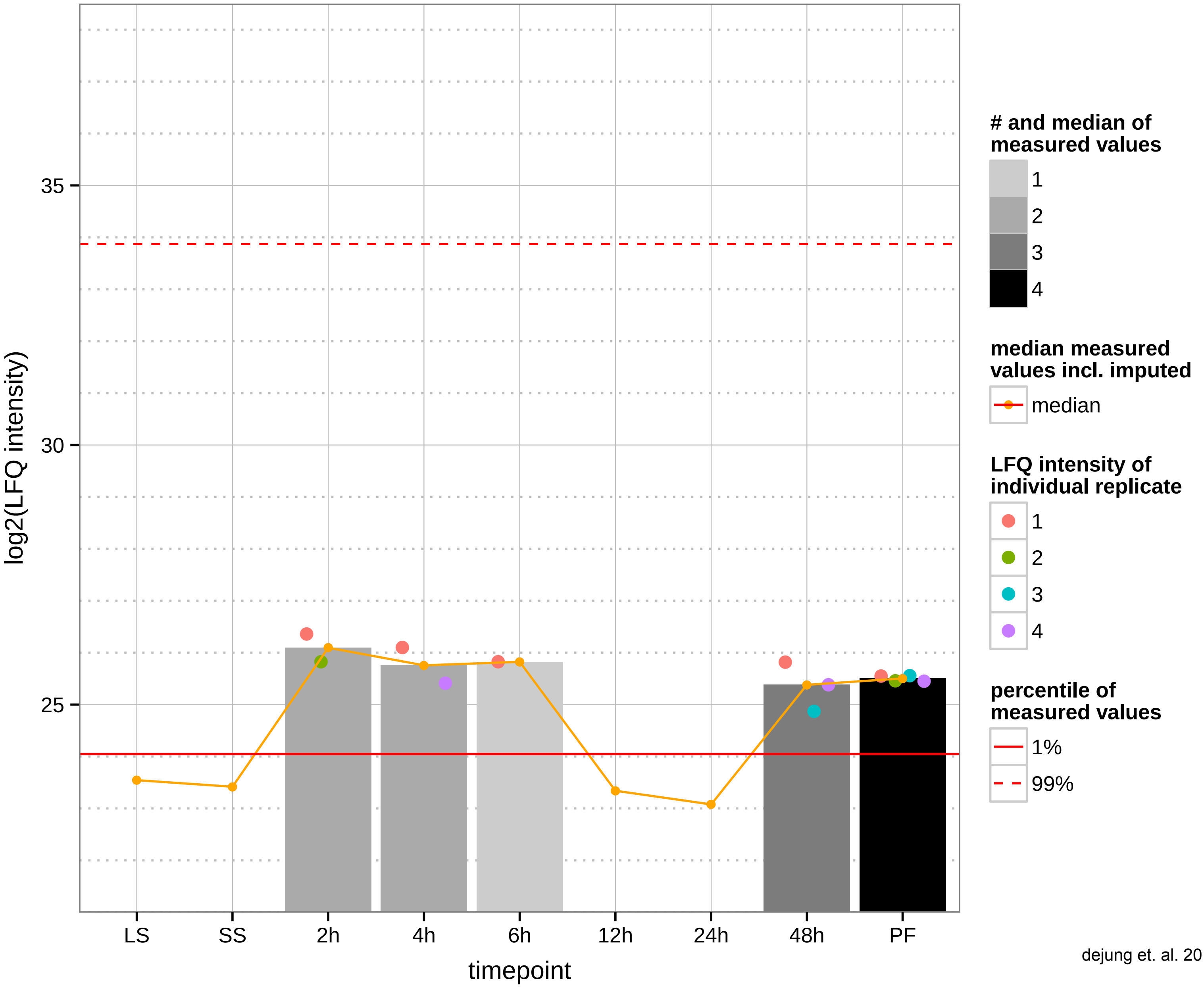
PGOF: null
PGOC: null
PGOP: null





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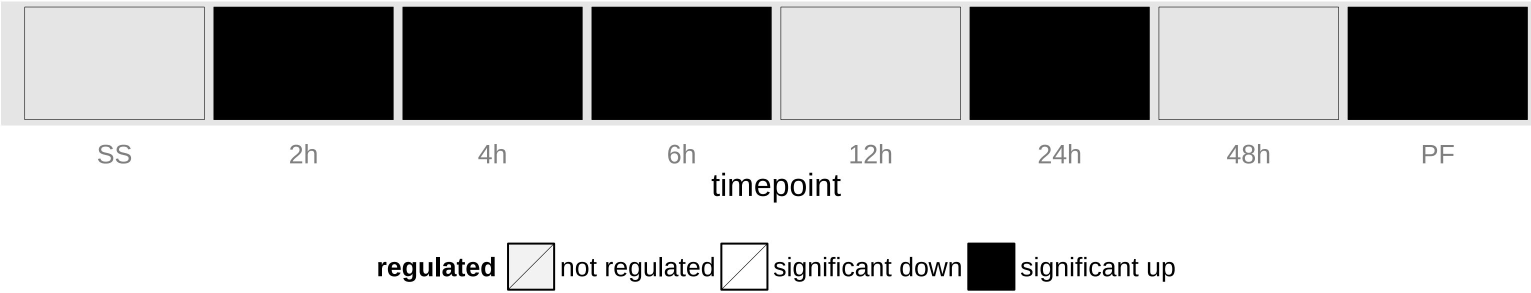

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hypothetical protein, conserved
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AGOC: null
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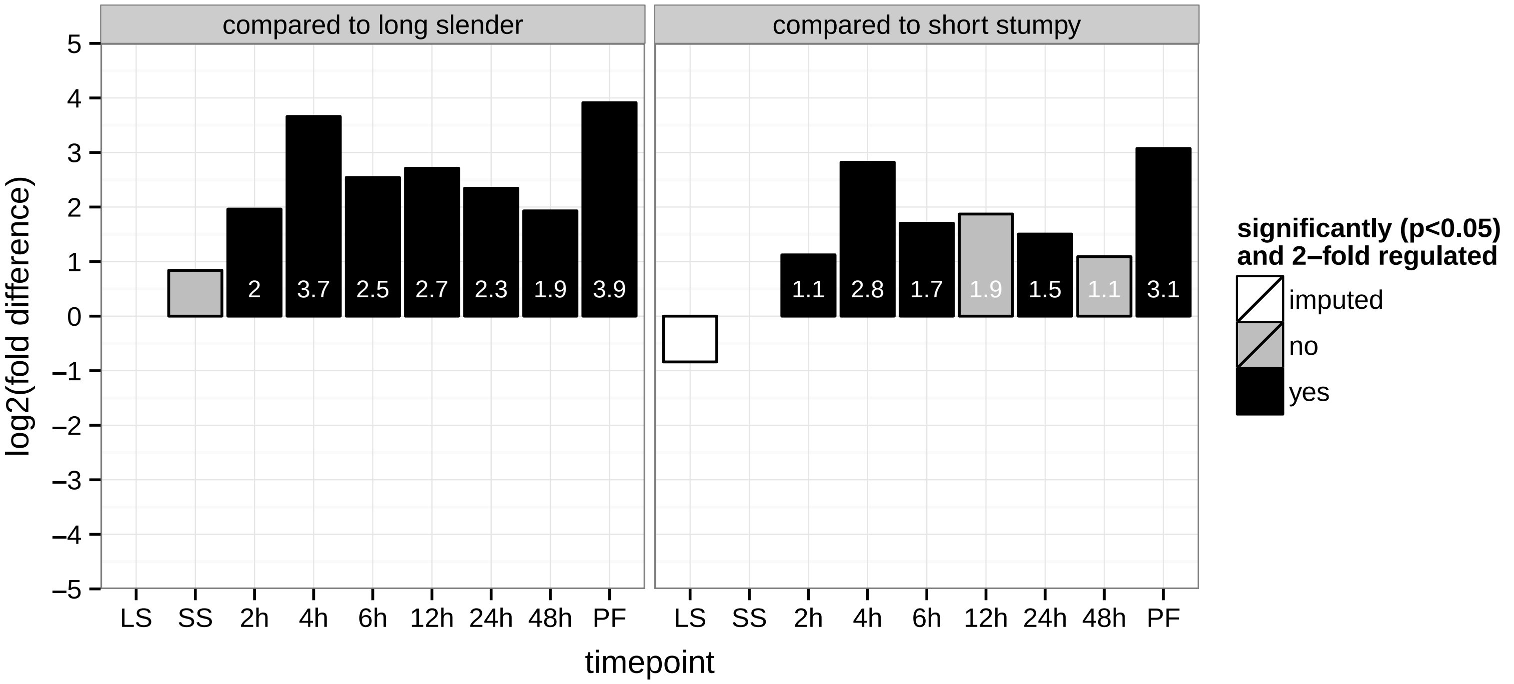

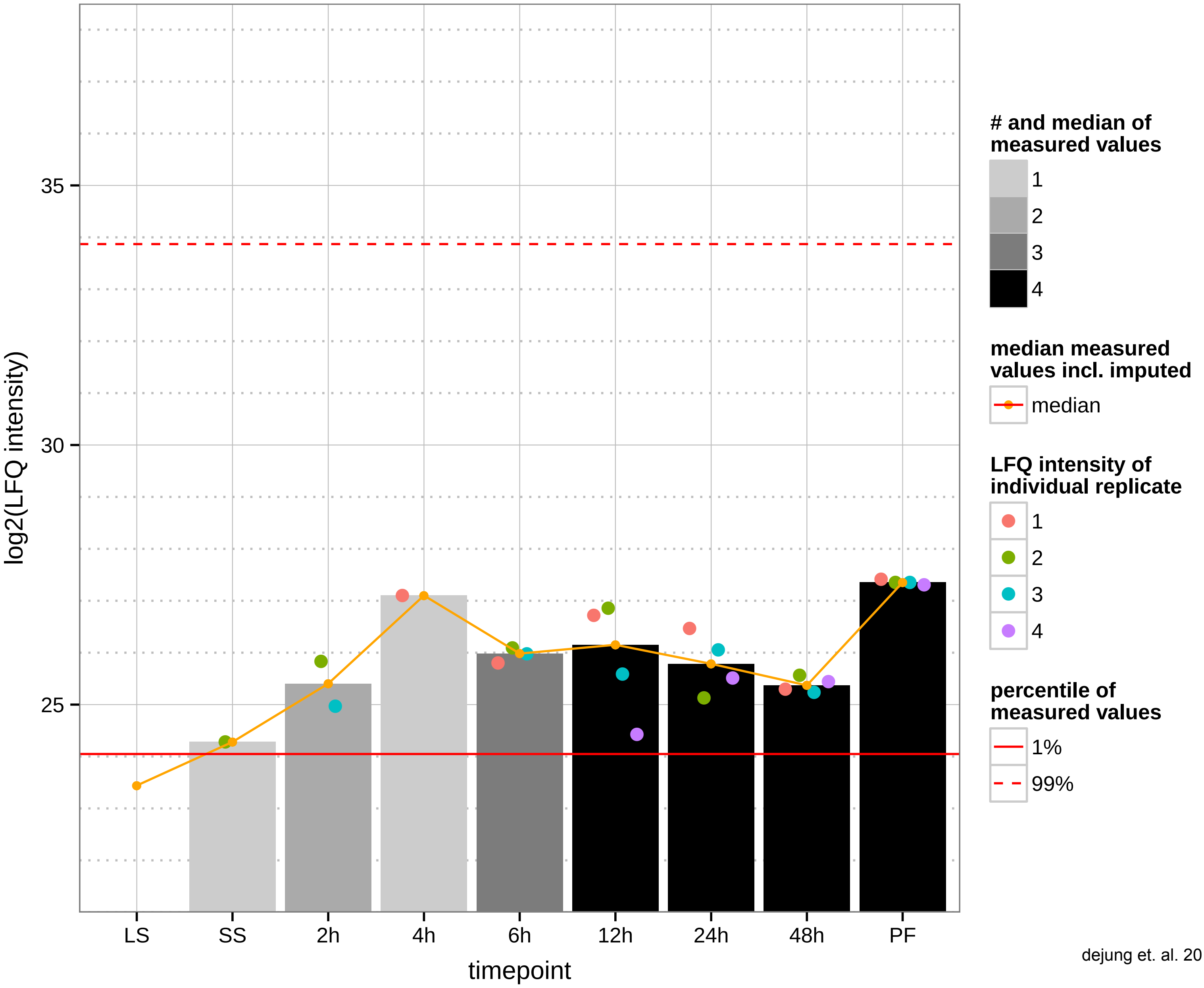

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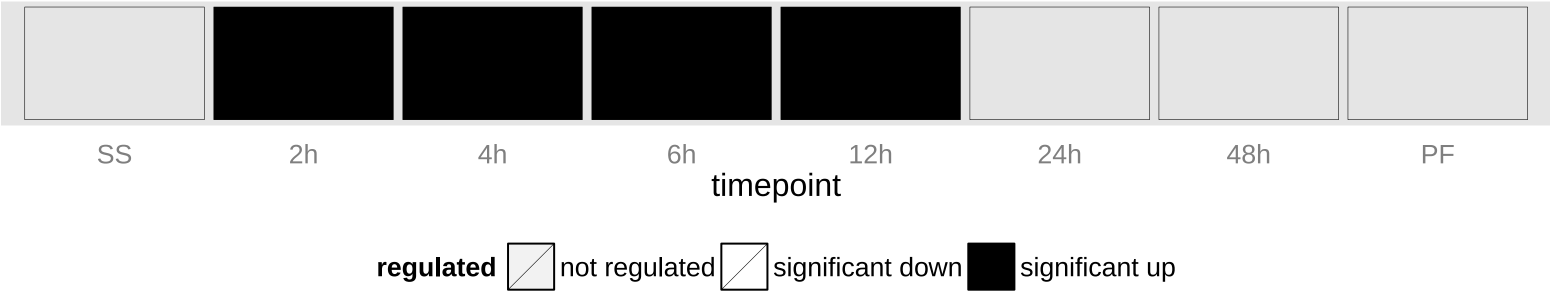

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hypothetical protein, conserved
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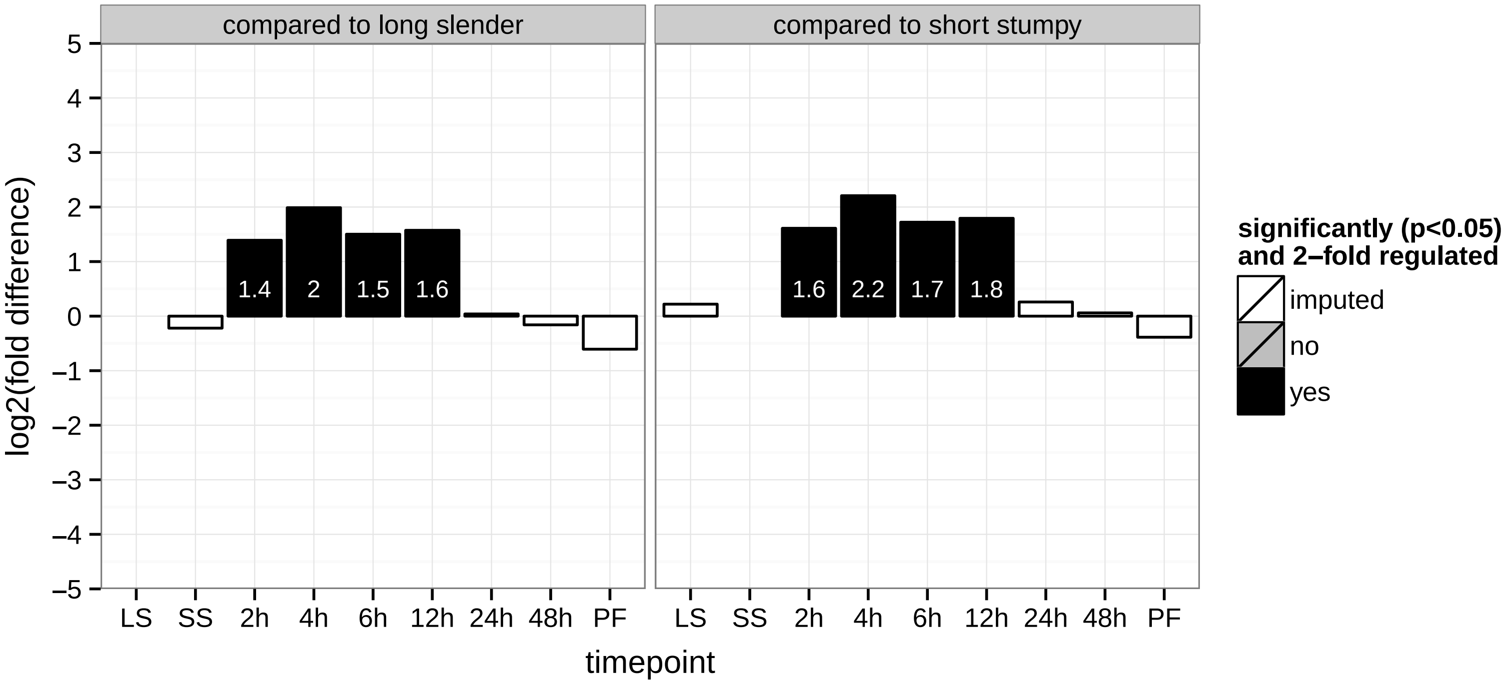
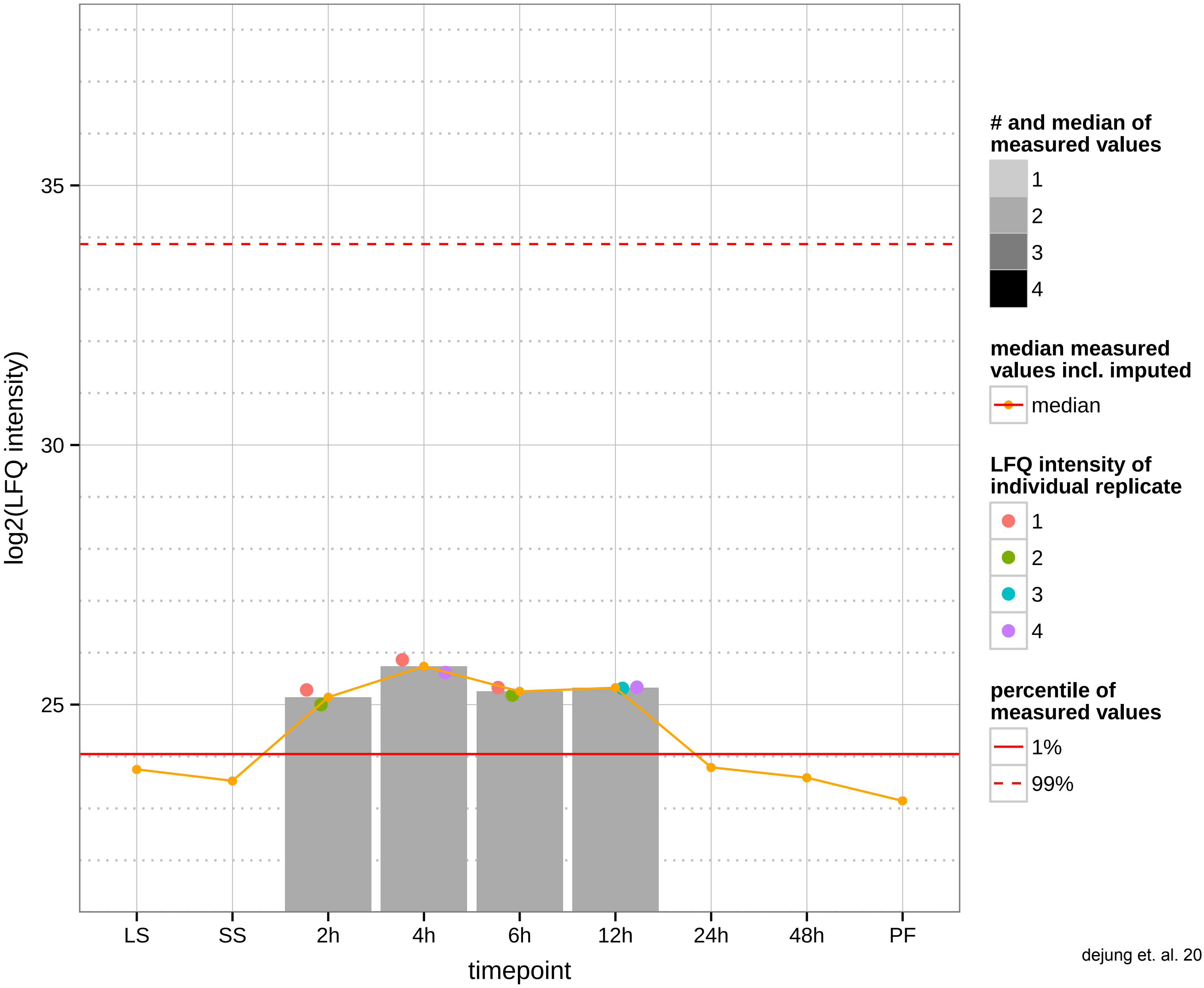
PGOC: null
PGOP: null





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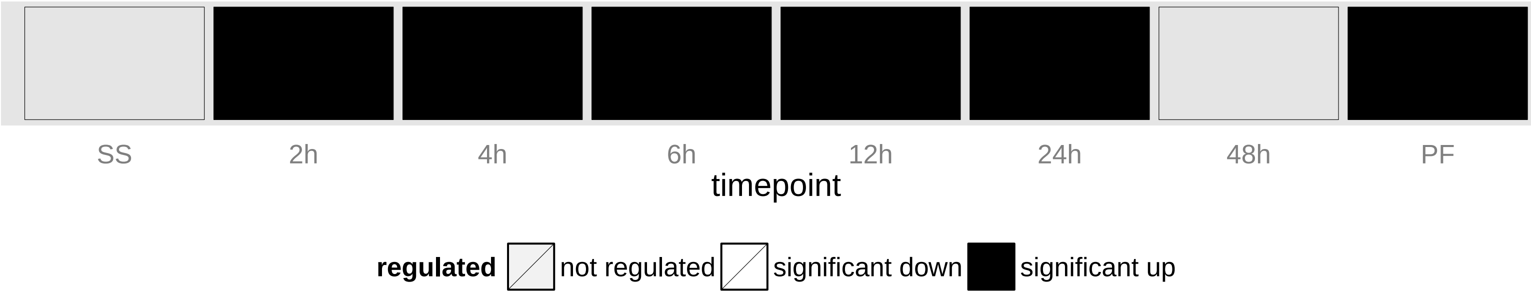

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hypothetical protein, conserved
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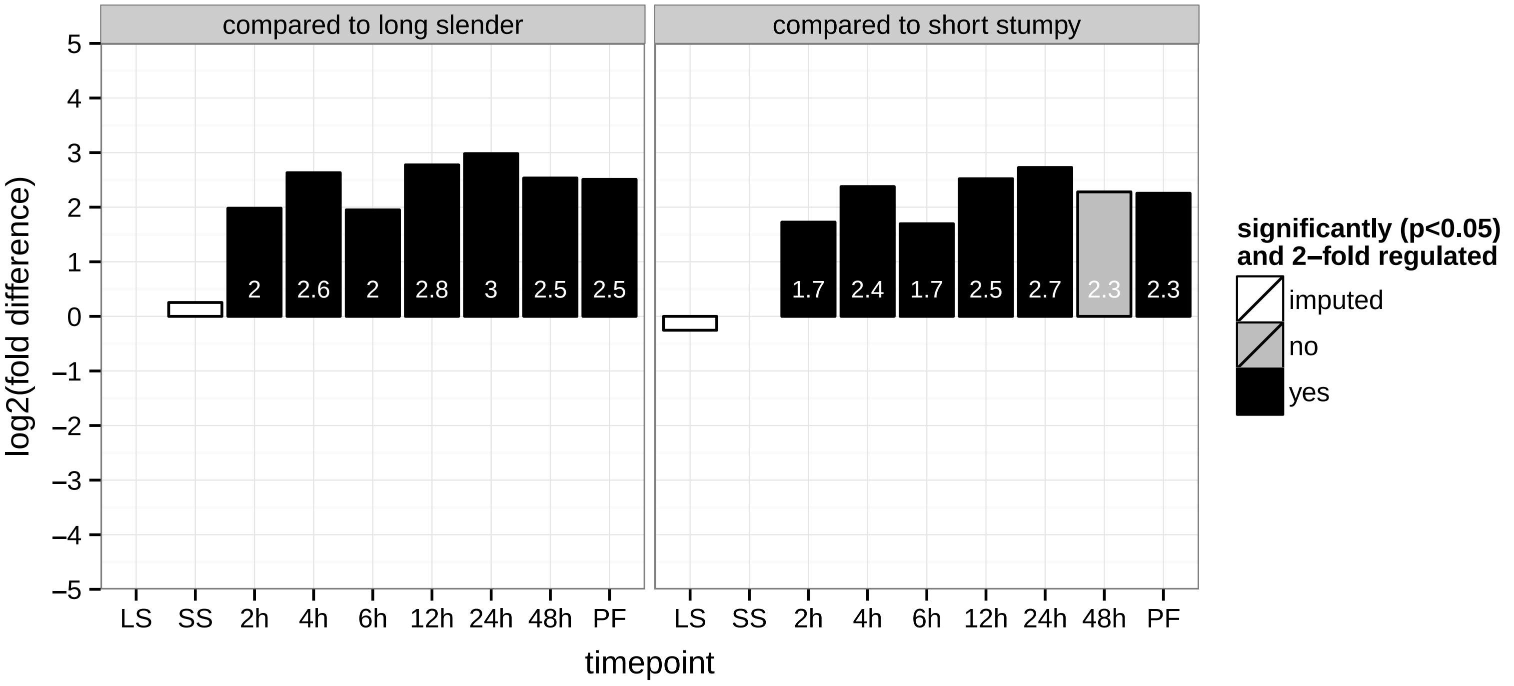
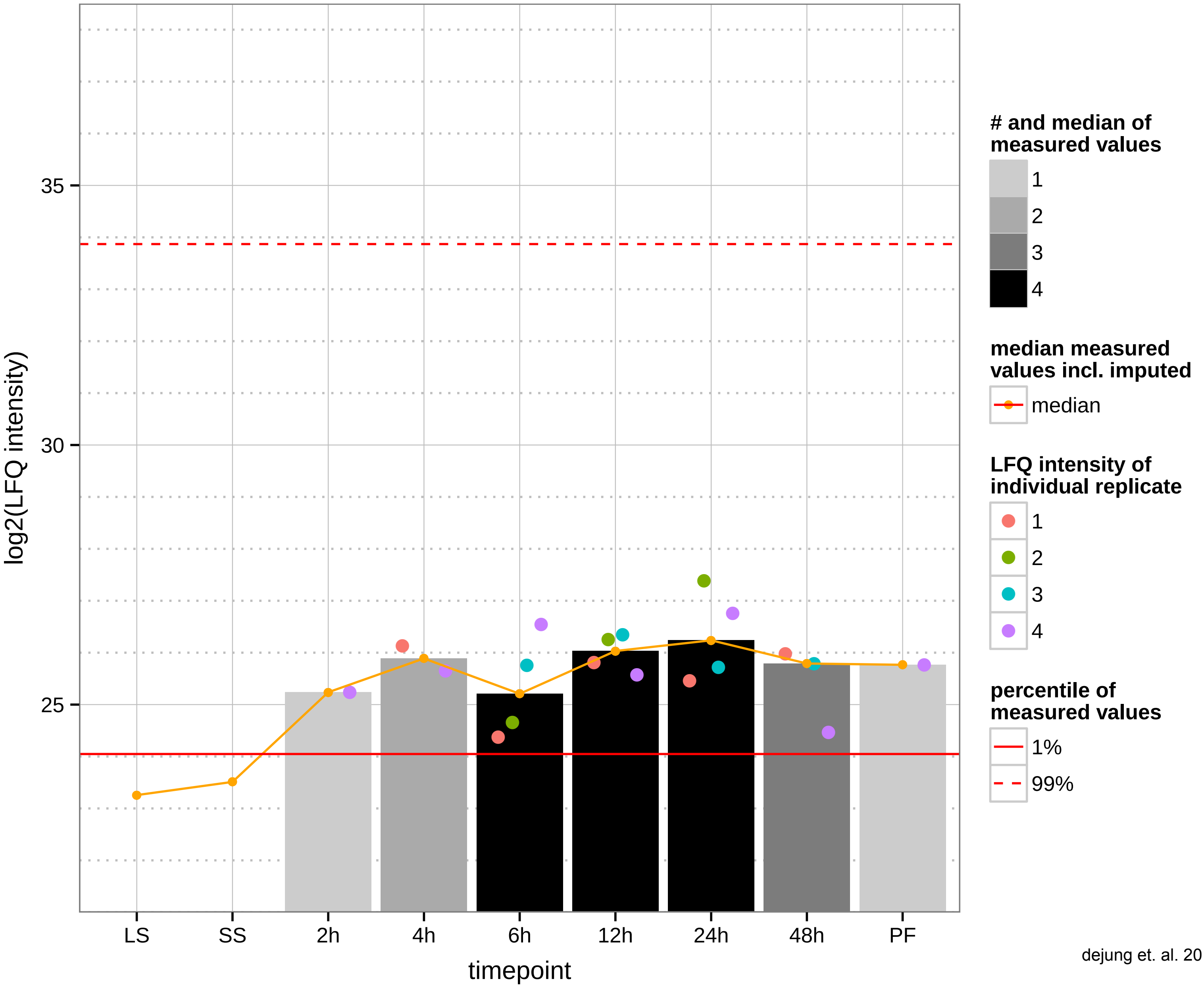
AGOC: null
AGOP: null
PGOF: null
PGOC: null
PGOP: null





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