Additional File 1 (Supplementary Figures)
This .pdf file contains the following supplementary figures: S1-S8. Legends for these figures are below.

S1 The *S. scovelli* genetic maps. a) The consensus map, which combines markers from both maps for each linkage group (LG), was used to link the scaffolds into chromosomes. b) Regional patterns of reduced recombination in males (inferred to be centromeric) and reduced recombination in females (inferred to be telomeric) were used to orient of centromeres to the top in the LGs in panel (a). Blue marks regions of relative expansion in the female map; red marks relative expansion in the male map for the markers they have in common on this example linkage group. c) On LG 1 a large block of markers (shown in red) aligning to about 17 Mb of scaffold length is non-recombining in both the male and female in this genetic cross. A possible explanation for this is that both parents carry a large inversion across this region. This is one of the two chromosomes formed by fusion of two ancestral chromosomes.

S2 Length distributions for unlinked scaffolds and for those captured by linkage groups show that the majority of large, gene-containing scaffolds are incorporated into the chromosome models. a) Boxplots and individual points reflect scaffold length distributions. Individual points (scaffolds) are coded by gene density (grading from yellow for no genes to red for high gene density). b) Scaffold length distributions in histogram form.

S3 VISTA plots suggest pipefish *dlx* clusters are missing CNEs (red arrows) that are conserved between other percomorphs and cod, a non-percomorph. The reference for the *dlx3/4a* and *3/4b* plots is stickleback (Gac) and for *dlx5/6a* is medaka. Hsa, human; Dre, zebrafish; Gmo, cod; Ssc, pipefish; Ola, medaka; Tru, pufferfish. Exons are highlighted in blue, CNEs in pink. Zebrafish has evolutionarily lost *dlx3a*. See Fig. 3 for the *dlx1/2a* VISTA comparison.

S4 Gene co-expression patterns reveal brood pouch transcriptome differences between pregnant and non-pregnant males. a) nMDS ordination of samples highlighting differences in reduced (2)-dimensional space. Orange circles represent pregnant male fish and blue boxes non-pregnant fish. b) Heatmap including all 15,253 pouch-expressed genes with sample (column) and gene (row) clustering. c) Heatmap including 70 randomly selected pouch-expressed genes with KEGG orthology (KO) assignments. d) Heatmap including the 70 pouch-expressed genes with “natural killer cell mediated cytotoxicity” KO assignments. Pink boxes highlight KO descriptions for clusters of genes showing pregnancy-depressed (above) and pregnancy-enriched (below) expression. Color keys for all heatmaps show expression values, scaled for each gene to have a mean of 0 and a standard deviation of 1, and dashed portions of clustering dendrograms represent non-pregnant males.

S5 Pathview [132] KEGG pathway renderings with scaled pregnancy-specific log_2 fold changes mapped to KOs. Blue hues represent pregnancy-depressed KOs, while orange hues represent pregnancy-enriched KOs. a) The “coagulation and complement cascades” KEGG pathway. The red asterisk marks pregnancy-enriched components of the Membrane Attack Complex (see text). b) The “cytokine-cytokine receptor interaction” KEGG map, with red asterisk marking the chemokines, of which pro-inflammatory chemokines are pregnancy-enriched.

S6 Heatmaps comparing pregnancy-specific expression patterns for an innate immunity KEGG pathway [a), “coagulation and complement cascades”] and an adaptive immunity KEGG pathway [b), “antigen processing and presentation”]. The pink box highlights pipefish genes in the coagulation and complement cascades that are distinctly pregnancy enriched. No such strong patterns are observed for antigen processing and presentation. Color keys for heatmaps show expression values, scaled for each gene to have a mean of 0 and a standard deviation of 1, and dashed portions of clustering dendrograms represent non-pregnant males.

S7 *S. scovelli* has atypical craniofacial development from early developmental stages in which cartilages can first be detected by alcian blue staining. a) Shown is a developmental series of pipefish embryos from within the brood pouch and a juvenile (one day after emergence from the pouch, at 16 days after fertilization), stained with alcian blue for cartilage and alizarin red for mineralized bone. Approximately similar developmental stages of stickleback, another percomorph, are shown. Note the upturned jaws (formed by Meckel’s and palatoquadrate cartilages), the unusually curved ethmoid cartilage, and the elongating hyosymplectic cartilage in pipefish compared to stickleback, which has less derived development and morphology. b) A ventral view of pharyngeal cartilages of an 11 day old pipefish (stained with alcian and alizarin). In all panels, anterior is to the left. m, Meckel’s cartilage; pq, palatoquadrate; et, ethmoid; ch, ceratohyal; hs, hyosymplectic.

S8 Maximum Likelihood (PhyML) tree from Fig. 7, including complete accession numbers for all amino acid sequences. Pastristacins are in purple. Clade support values are SH-aLRT, and number of bootstrap replicates (of 500 total) in which the clade was recovered. See Fig. 7 for context.

a

Additional Field 1

Fig. S1

a

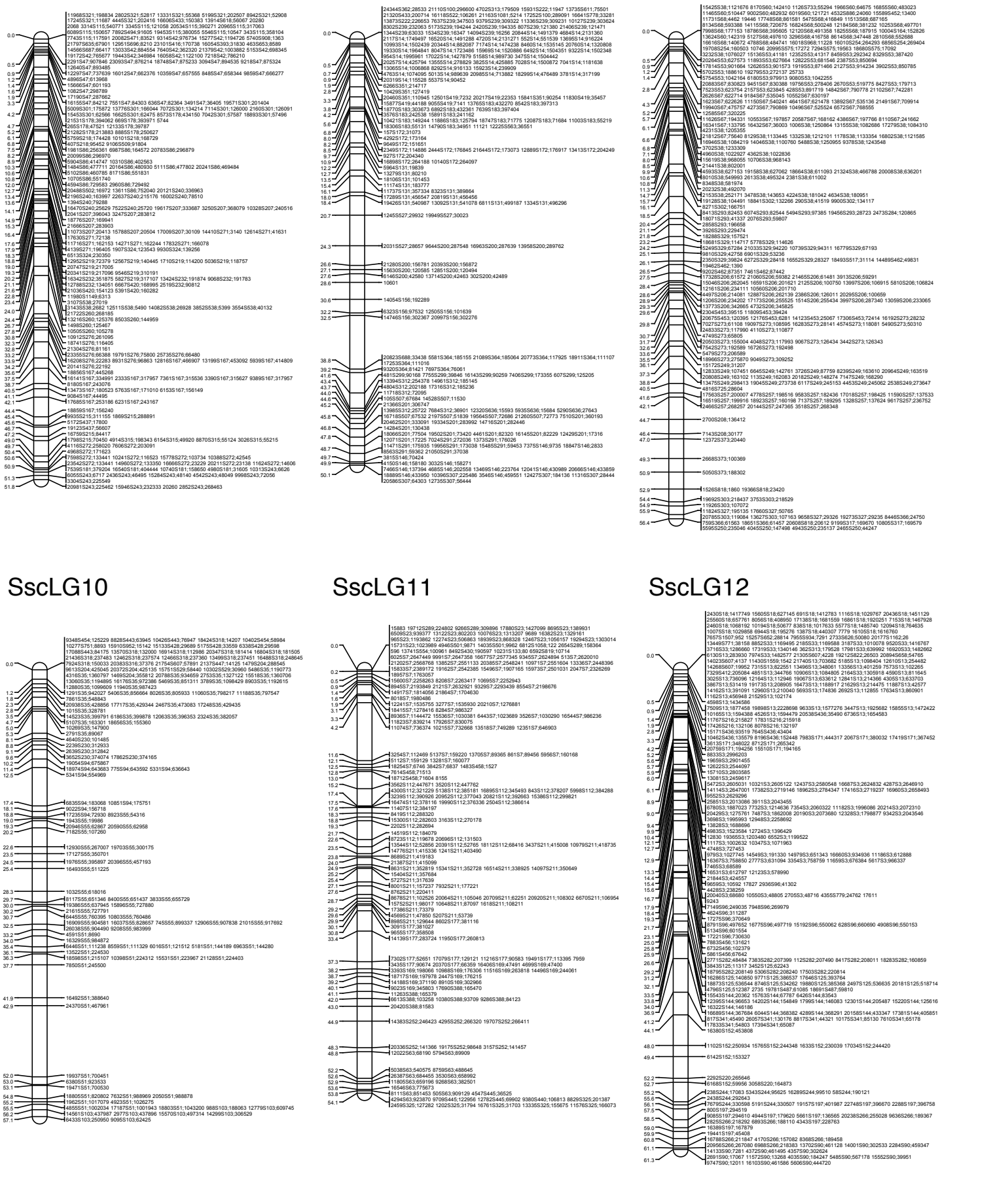

Fig. S1

a

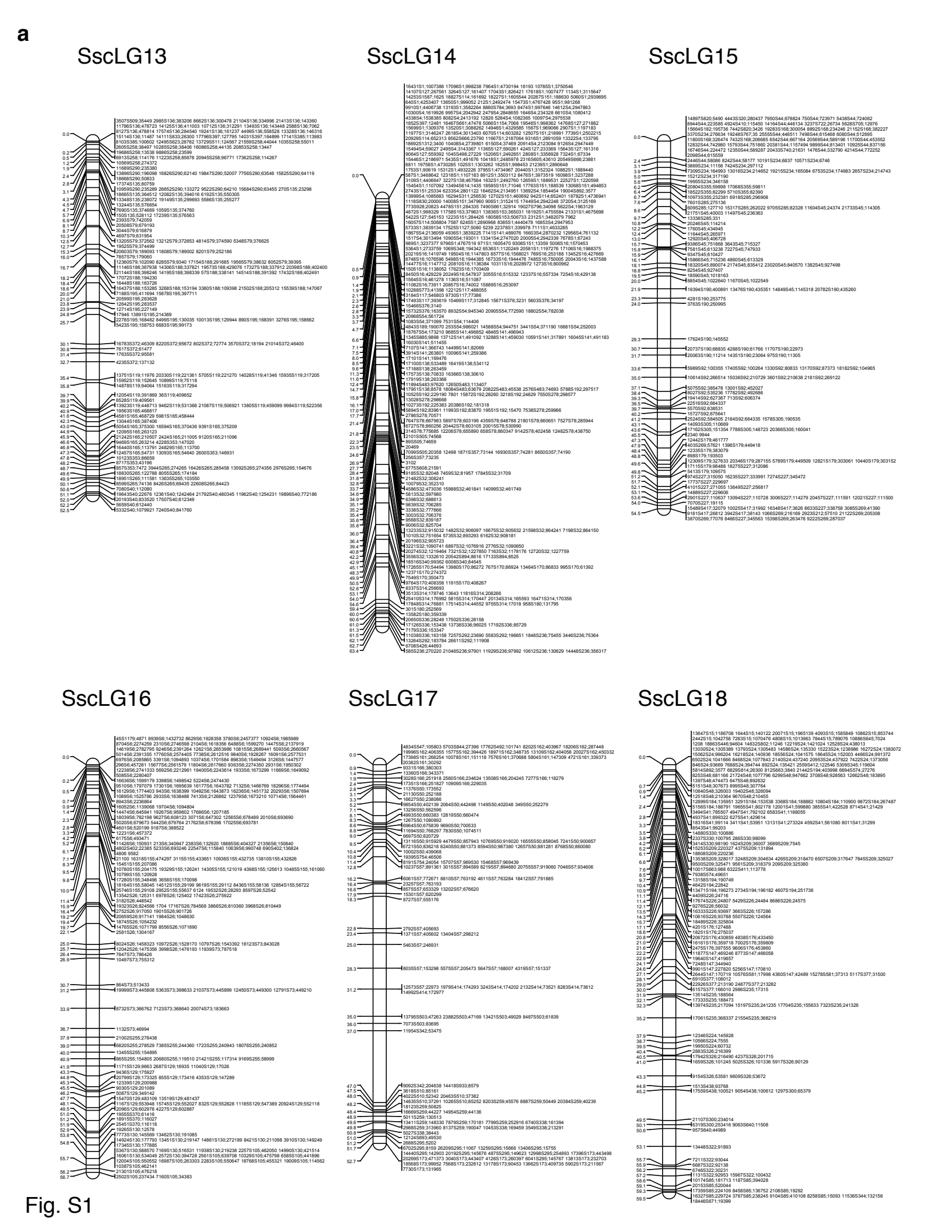

Fig. S1

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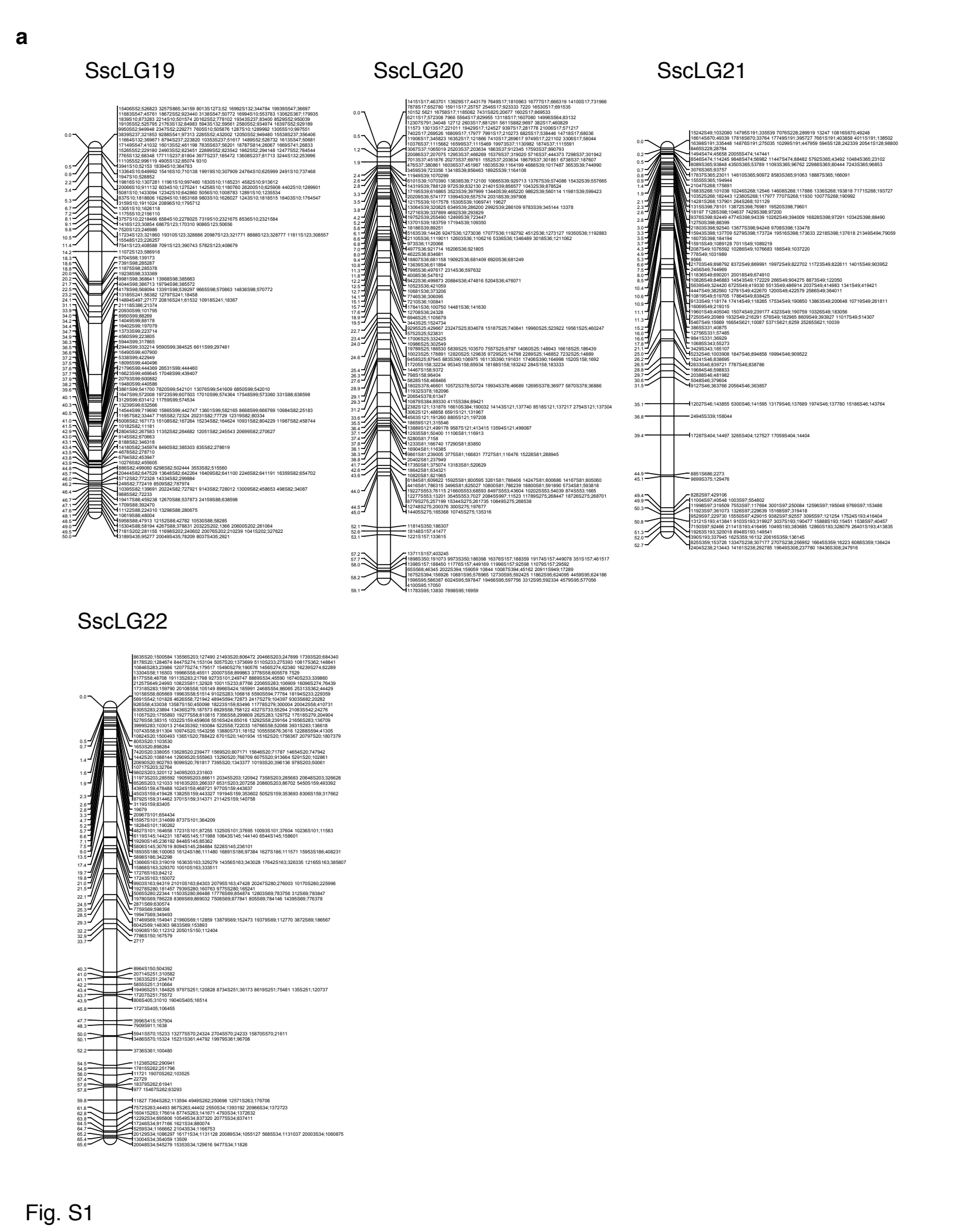

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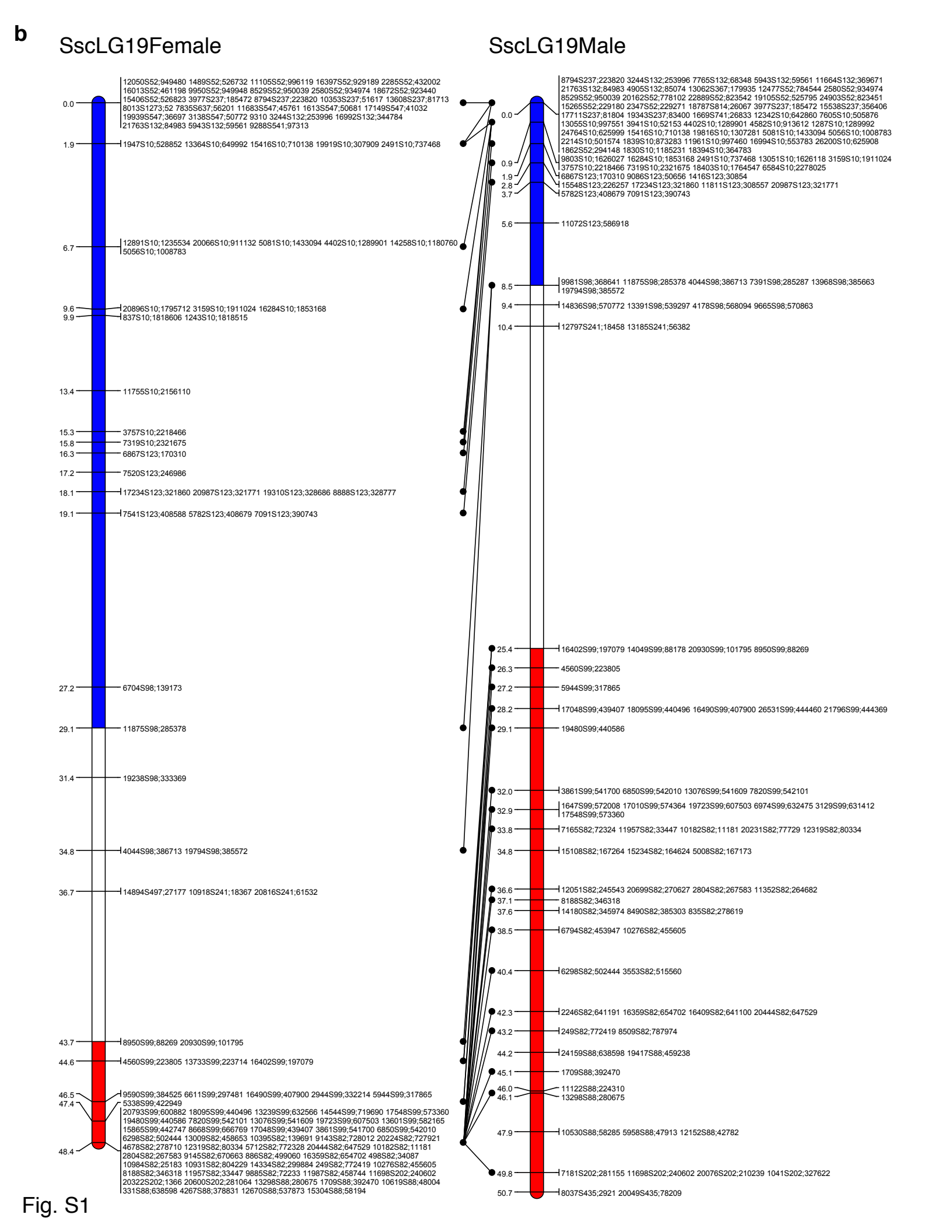
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Fig. S1

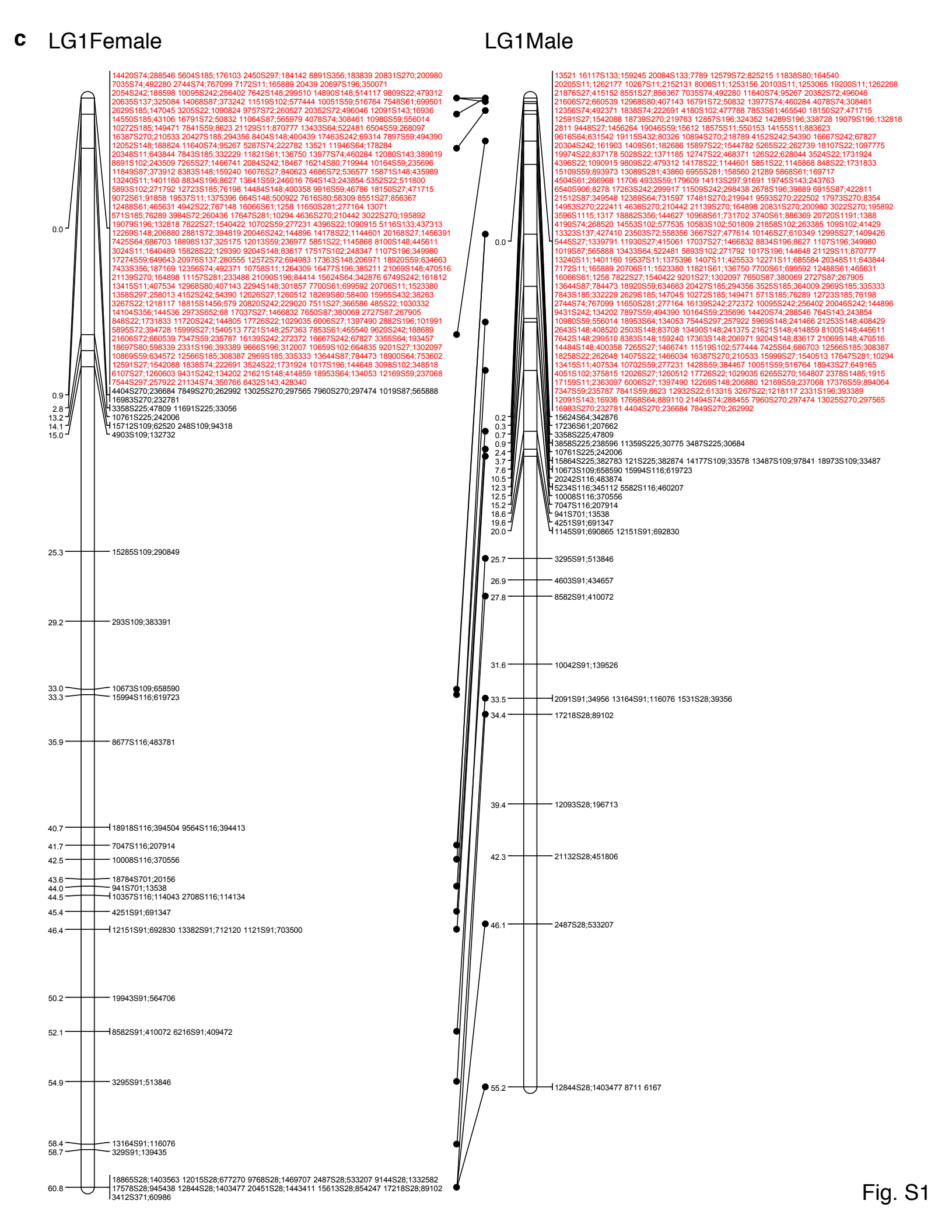
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Fig. S1

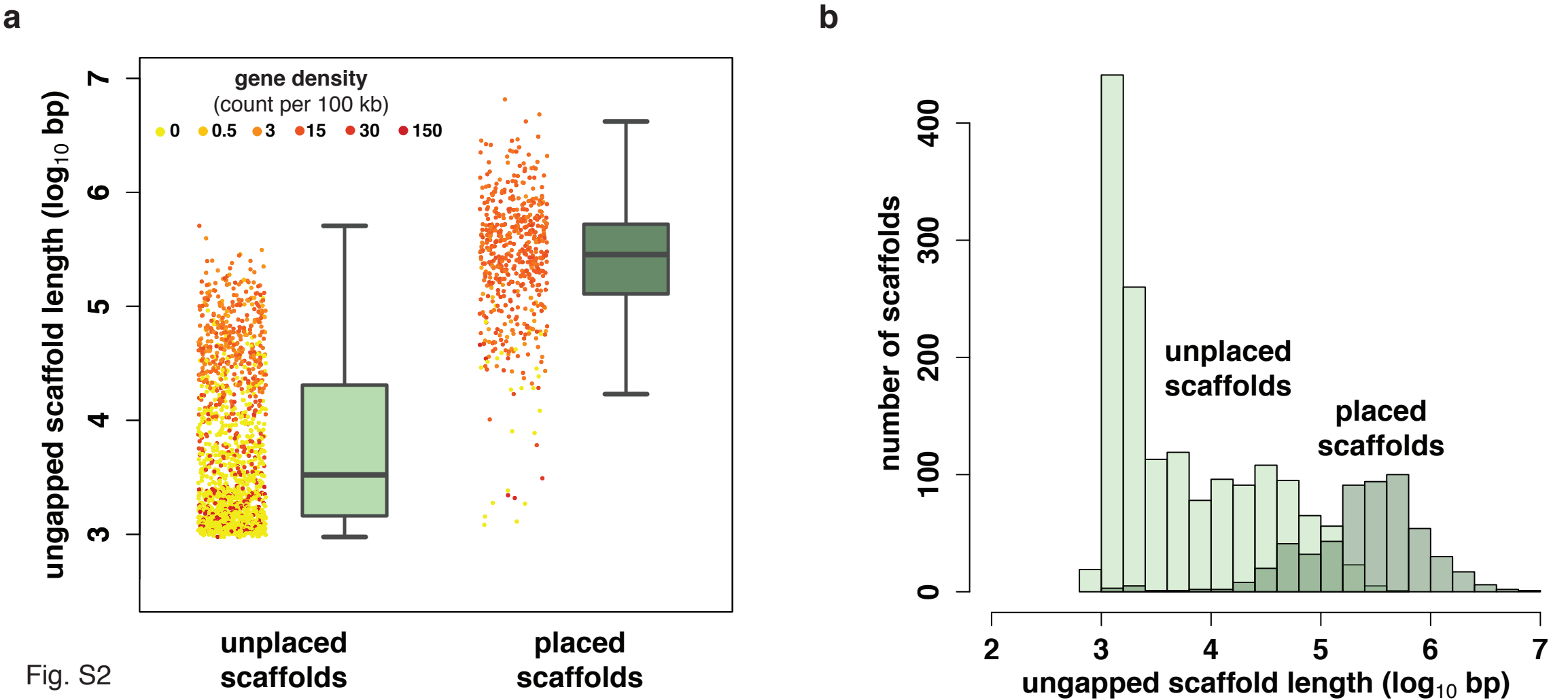
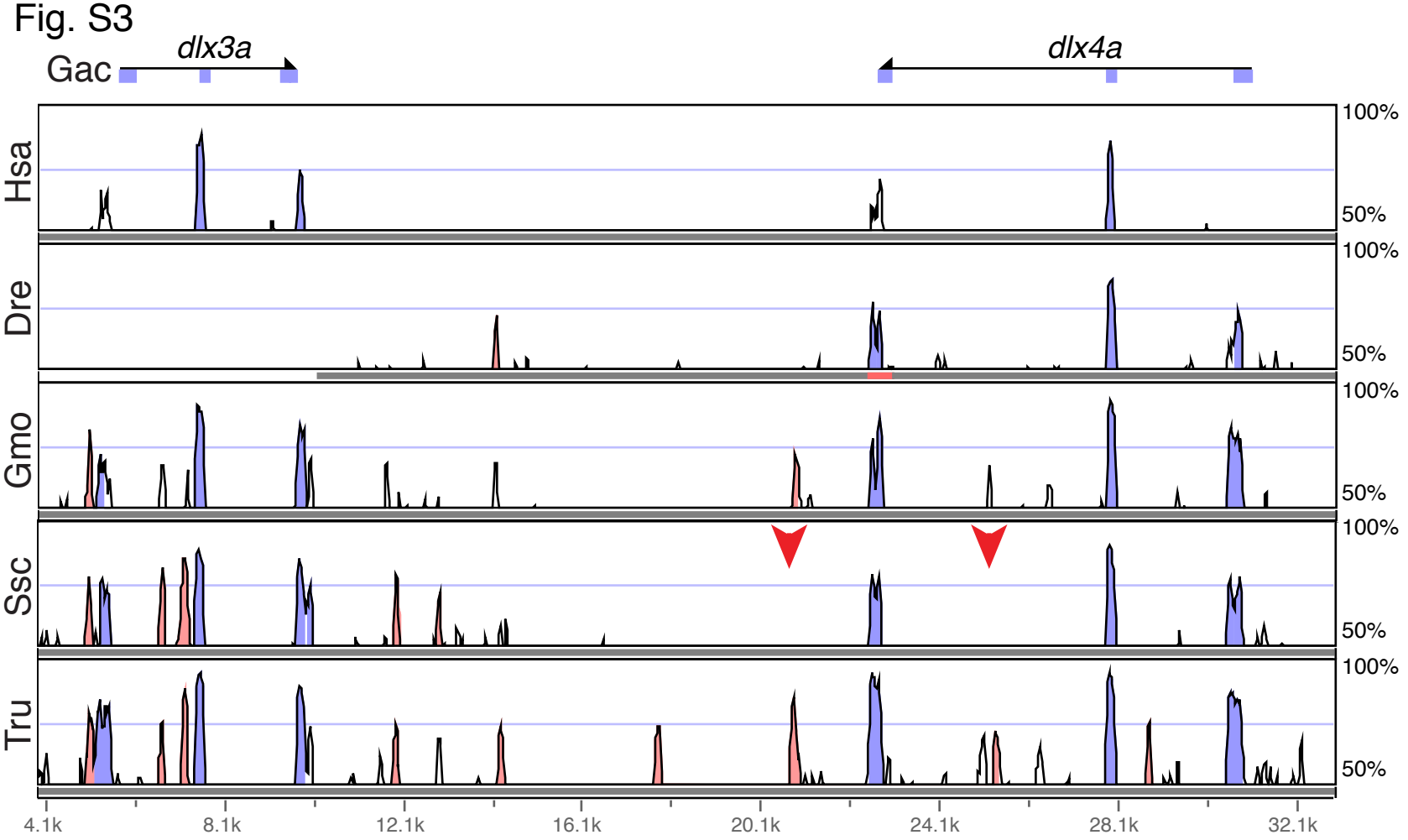
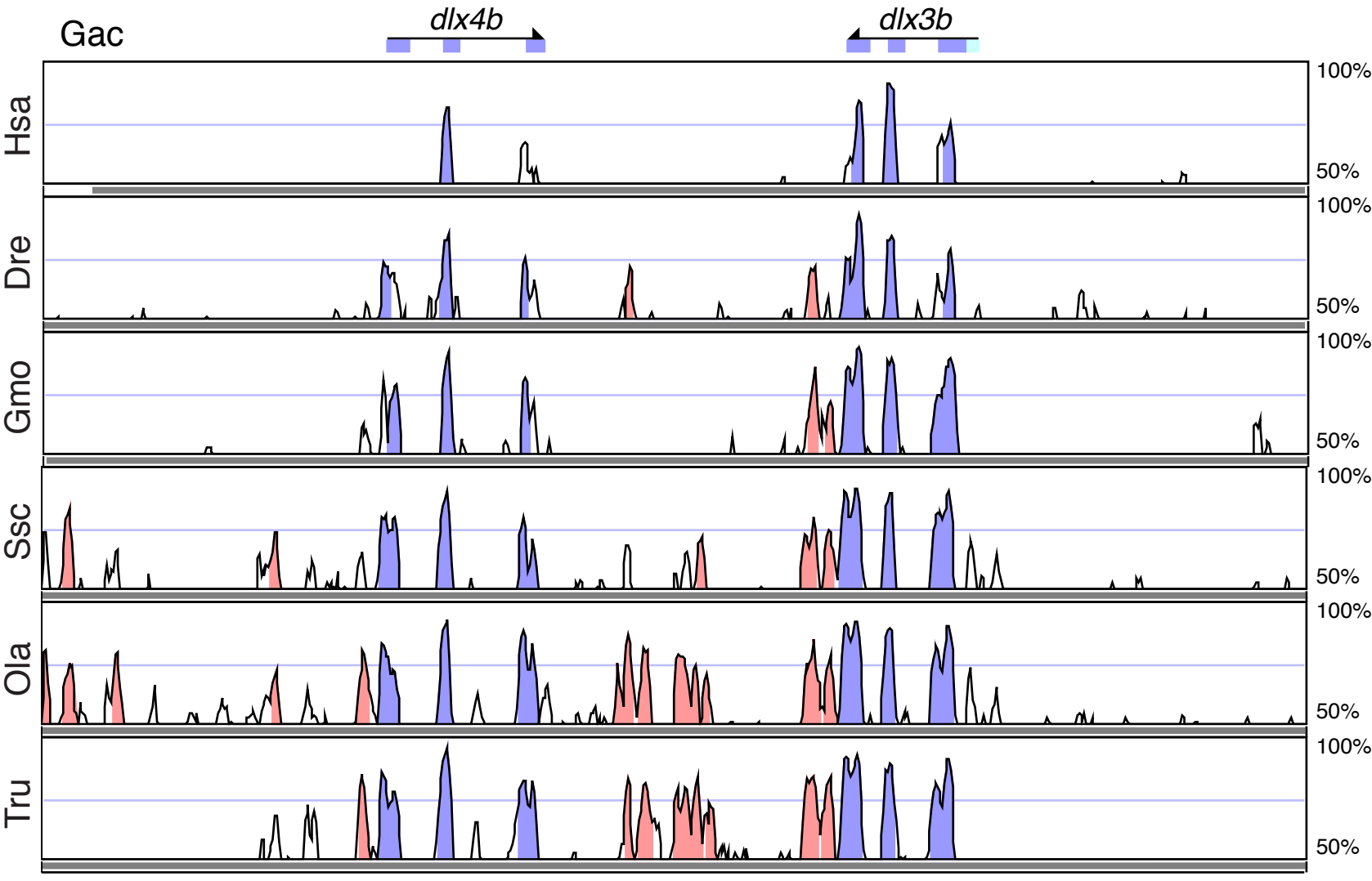
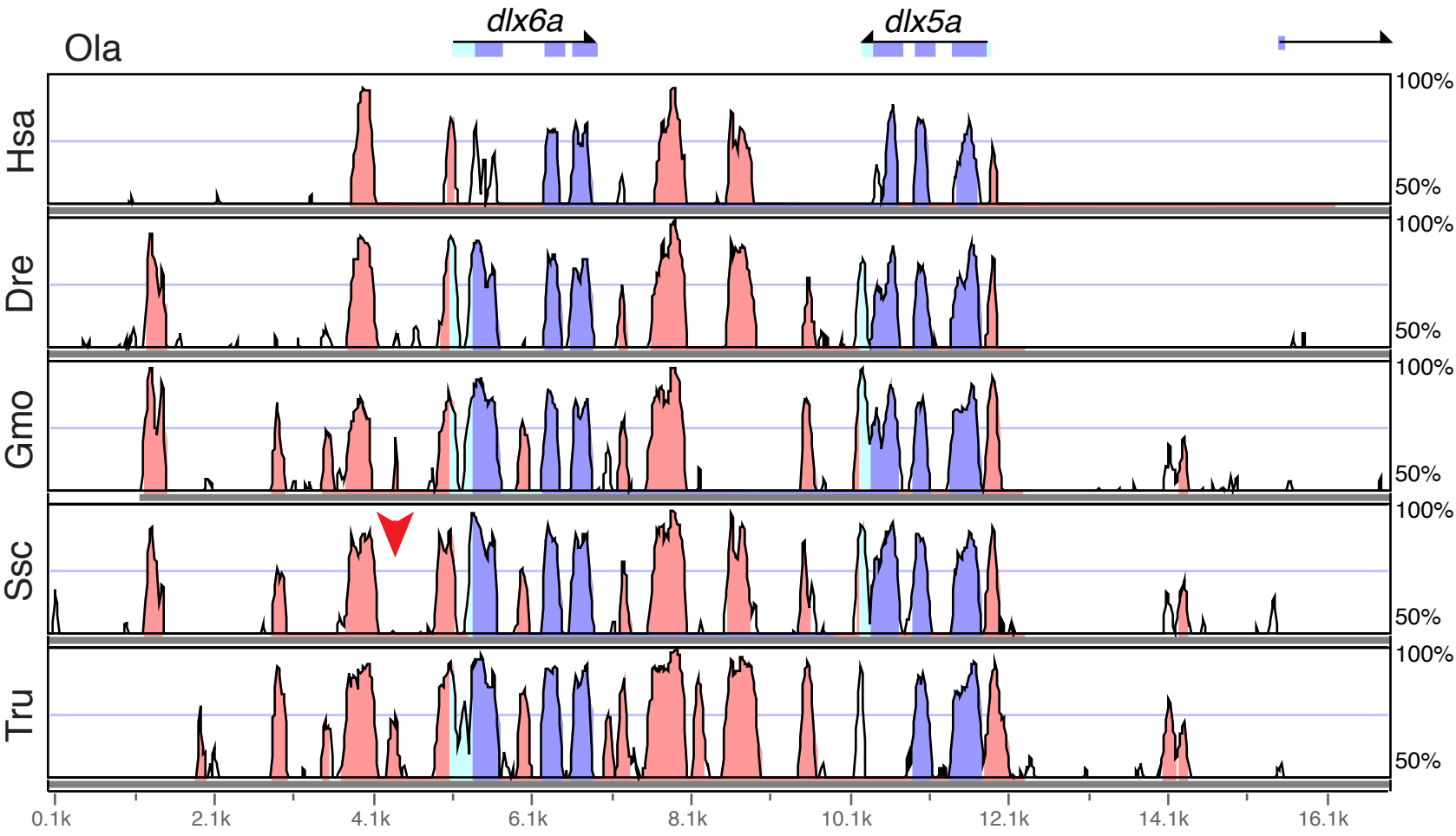

a
gene density
(count per 100 kb)
0
0.5
3
15
30
150
ungapped scaffold length (log10 bp)
3
4
5
6
7
unplaced scaffolds
placed scaffolds
b
number of scaffolds
0
100
200
300
400
unplaced scaffolds
placed scaffolds
2
3
4
5
6
7
ungapped scaffold length (log10 bp)

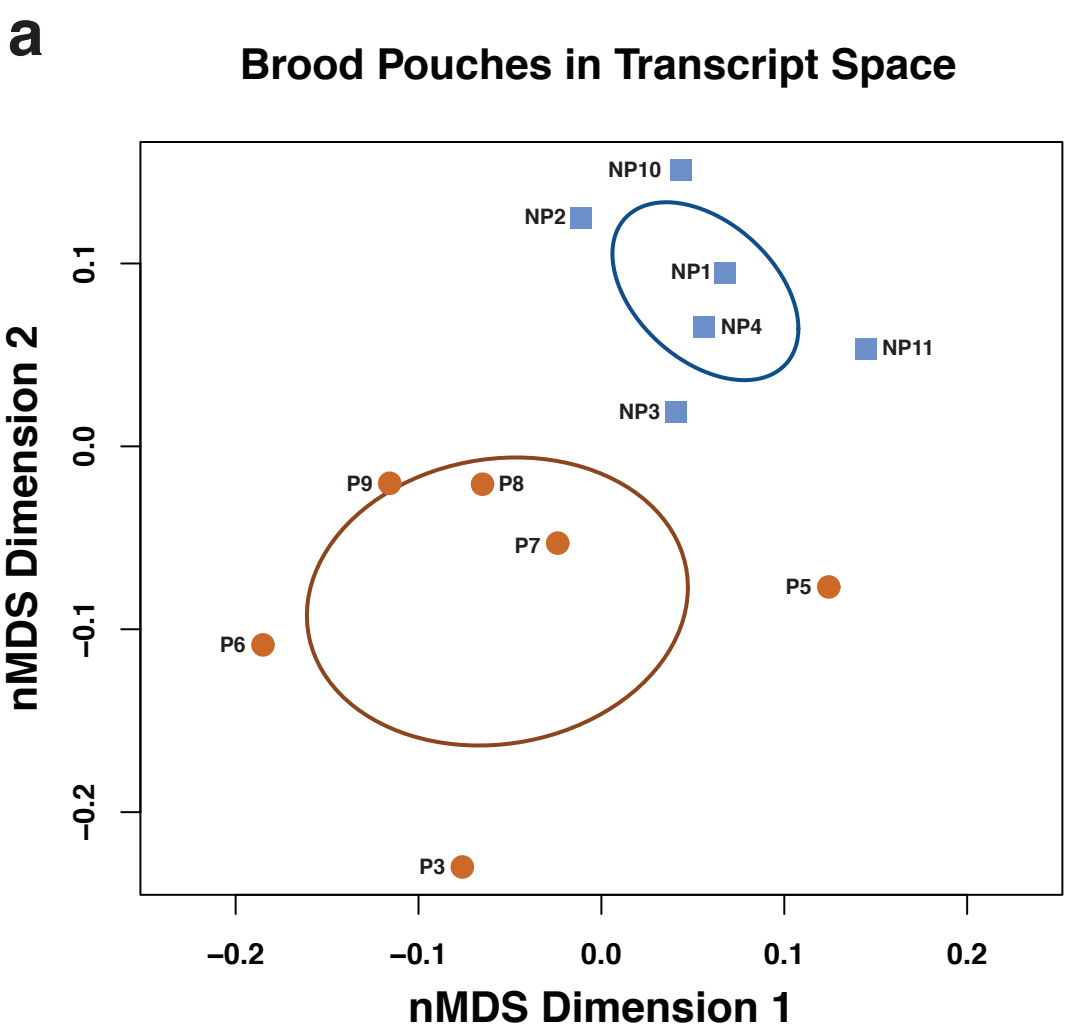
Fig. S2

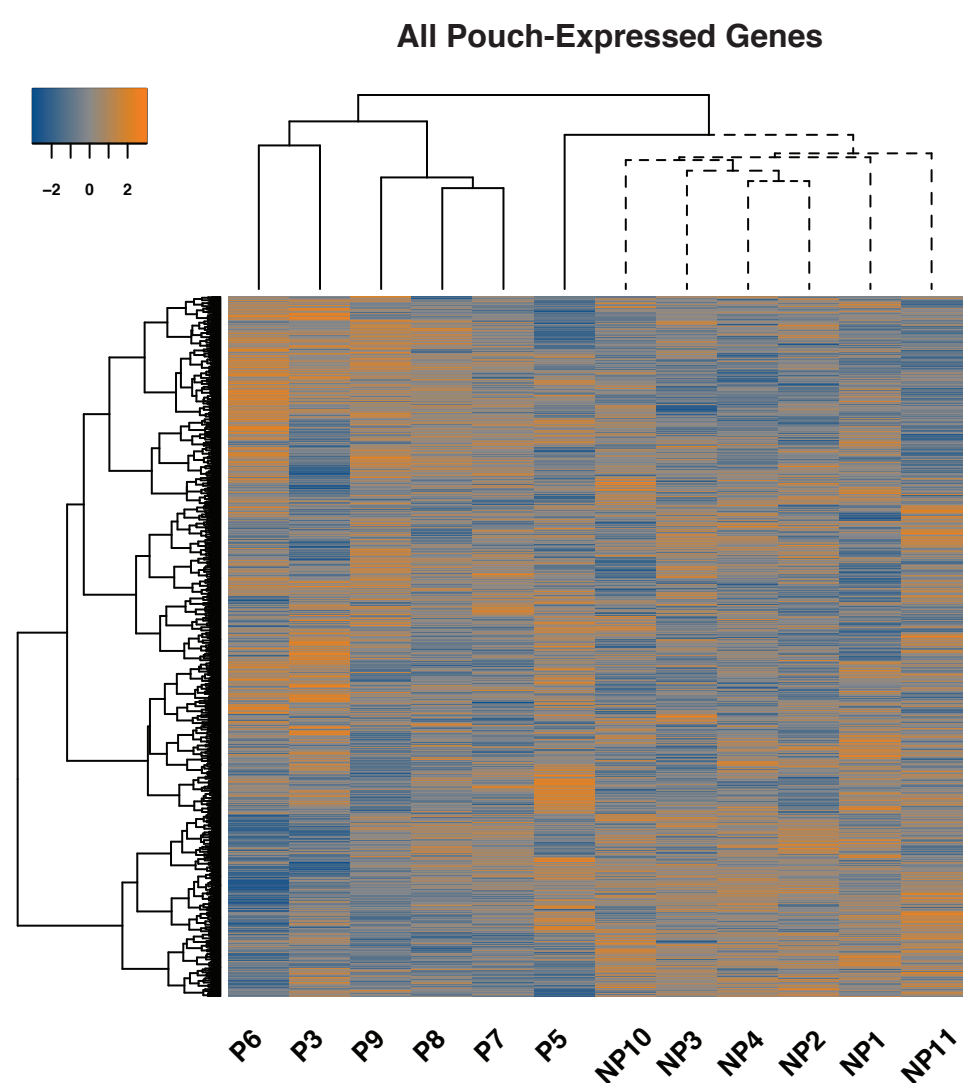
Fig. S3

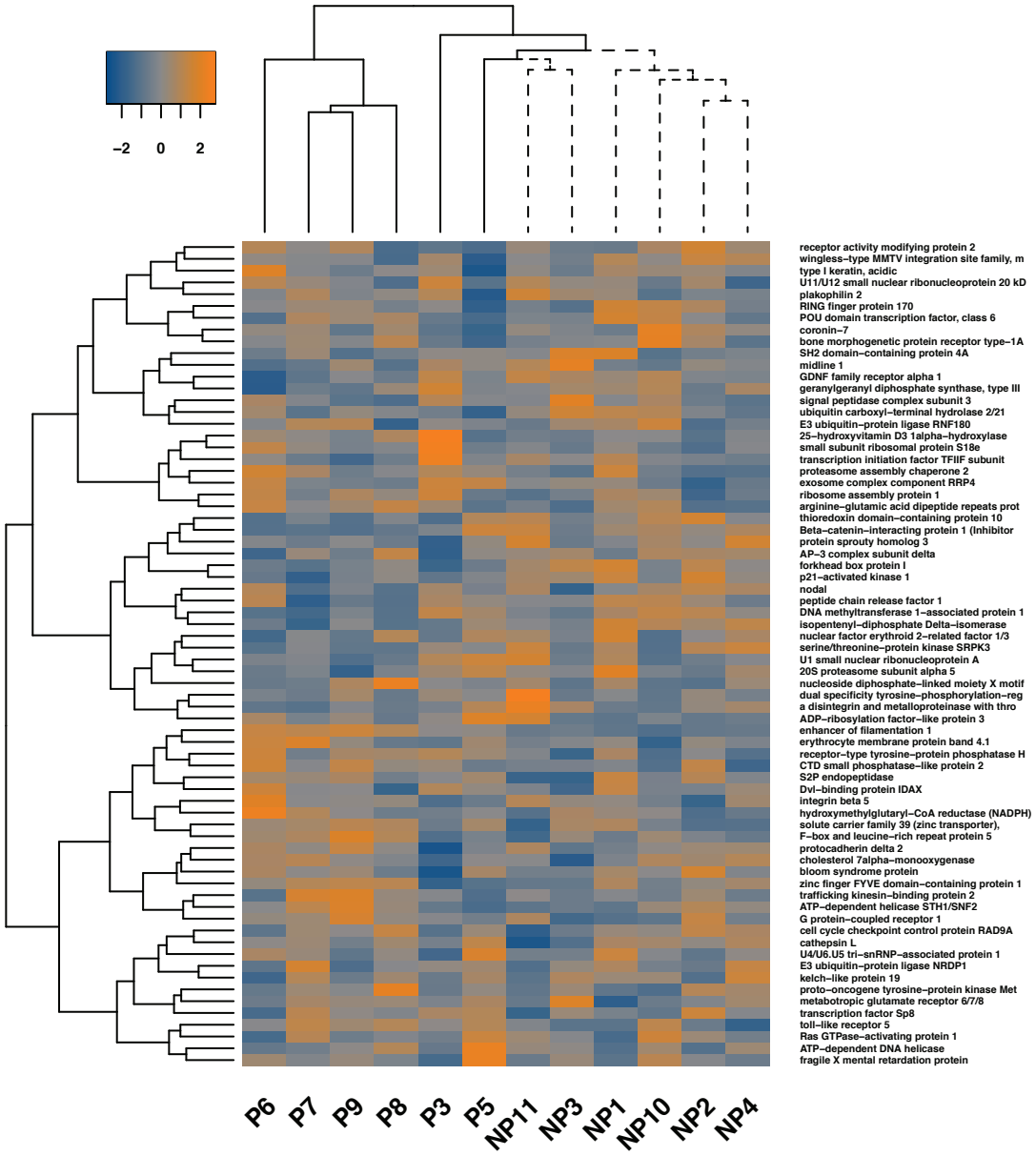

Gac
dlx3a
dlx4a
Hsa
Dre
Gmo
Ssc
Tru
100%
50%
4.1k
8.1k
12.1k
16.1k
20.1k
24.1k
28.1k
32.1k


Gac
dlx4b
dlx3b
Hsa
Dre
Gmo
Ssc
Ola
Tru
100%
50%


Ola
dlx6a
dlx5a
Hsa
Dre
Gmo
Ssc
Tru
100%
50%
0.1k
2.1k
4.1k
6.1k
8.1k
10.1k
12.1k
14.1k
16.1k


a
Brood Pouches in Transcript Space
NP10
NP2
NP1
NP4
NP11
NP3
P9
P8
P7
P5
P6
P3
nMDS Dimension 2
nMDS Dimension 1
0.1
0.0
−0.1
−0.2
−0.2
−0.1
0.0
0.1
0.2


b
All Pouch-Expressed Genes
−2
0
2
P6
P3
P9
P8
P7
P5
NP10
NP3
NP4
NP2
NP1
NP11


c
Randomly Selected
−2
0
2
receptor activity modifying protein 2
wingless−type MMTV integration site family, m
type I keratin, acidic
U11/U12 small nuclear ribonucleoprotein 20 kD
plakophilin 2
RING finger protein 170
POU domain transcription factor, class 6
coronin−7
bone morphogenetic protein receptor type−1A
SH2 domain−containing protein 4A
midline 1
GDNF family receptor alpha 1
geranylgeranyl diphosphate synthase, type III
signal peptidase complex subunit 3
ubiquitin carboxyl−terminal hydrolase 2/21
E3 ubiquitin−protein ligase RNF180
25−hydroxyvitamin D3 1alpha−hydroxylase
small subunit ribosomal protein S18e
transcription initiation factor TFIIF subunit
proteasome assembly chaperone 2
exosome complex component RRP4
ribosome assembly protein 1
arginine−glutamic acid dipeptide repeats prot
thioredoxin domain−containing protein 10
Beta−catenin−interacting protein 1 (Inhibitor
protein sprouty homolog 3
AP−3 complex subunit delta
forkhead box protein I
p21−activated kinase 1
nodal
peptide chain release factor 1
DNA methyltransferase 1−associated protein 1
isopentenyl−diphosphate Delta−isomerase
nuclear factor erythroid 2−related factor 1/3
serine/threonine−protein kinase SRPK3
U1 small nuclear ribonucleoprotein A
20S proteasome subunit alpha 5
nucleoside diphosphate−linked moiety X motif
dual specificity tyrosine−phosphorylation−reg
a disintegrin and metalloproteinase with thro
ADP−ribosylation factor−like protein 3
enhancer of filamentation 1
erythrocyte membrane protein band 4.1
receptor−type tyrosine−protein phosphatase H
CTD small phosphatase−like protein 2
S2P endopeptidase
Dvl−binding protein IDAX
integrin beta 5
hydroxymethylglutaryl−CoA reductase (NADPH)
solute carrier family 39 (zinc transporter),
F−box and leucine−rich repeat protein 5
protocadherin delta 2
cholesterol 7alpha−monooxygenase
bloom syndrome protein
zinc finger FYVE domain−containing protein 1
trafficking kinesin−binding protein 2
ATP−dependent helicase STH1/SNF2
G protein−coupled receptor 1
cell cycle checkpoint control protein RAD9A
cathepsin L
U4/U6.U5 tri−snRNP−associated protein 1
E3 ubiquitin−protein ligase NRDP1
kelch−like protein 19
proto−oncogene tyrosine−protein kinase Met
metabotropic glutamate receptor 6/7/8
transcription factor Sp8
toll−like receptor 5
Ras GTPase−activating protein 1
ATP−dependent DNA helicase
fragile X mental retardation protein
P6
P7
P9
P8
P3
P5
NP11
NP3
NP1
NP10
NP2
NP4

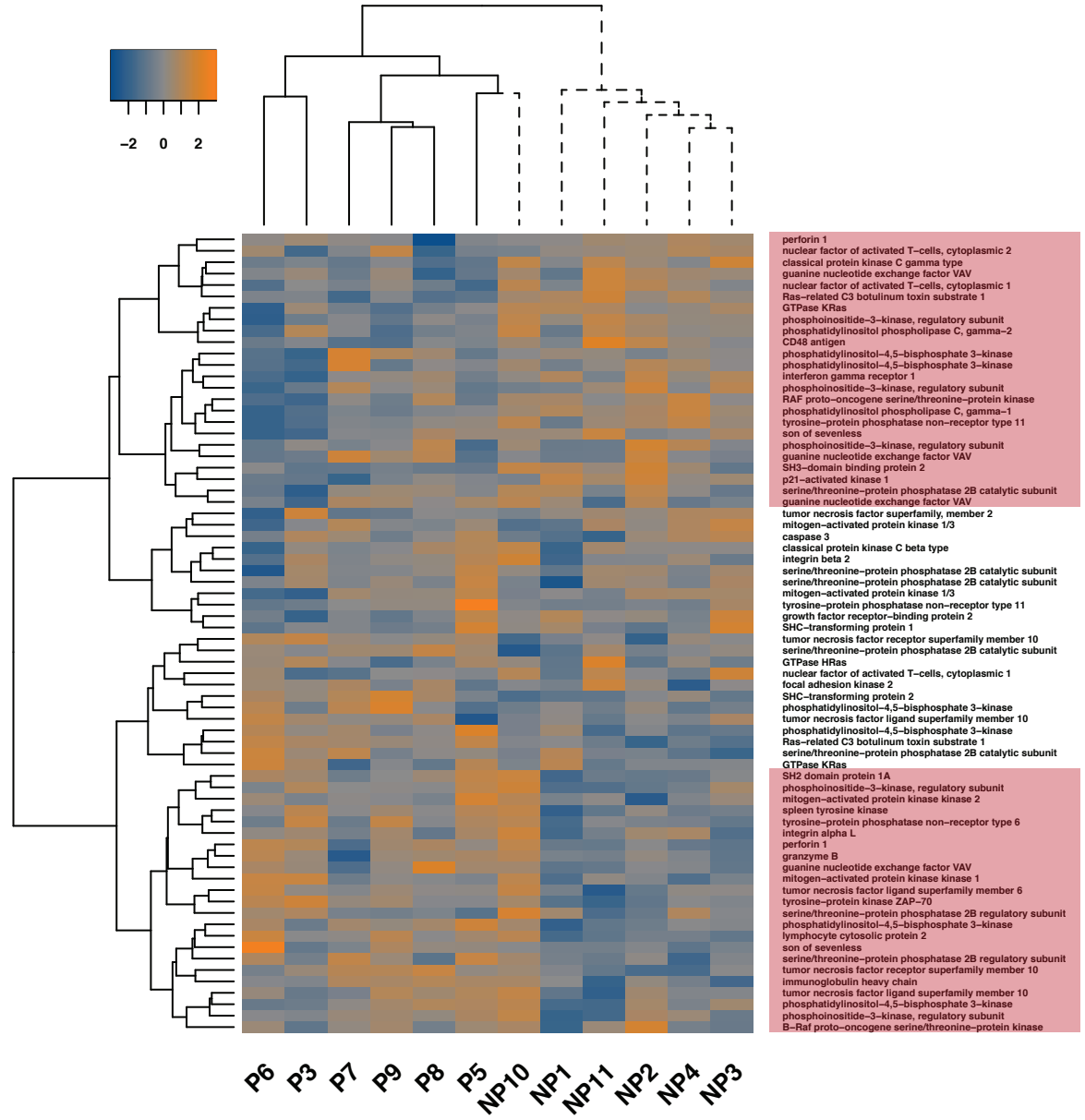
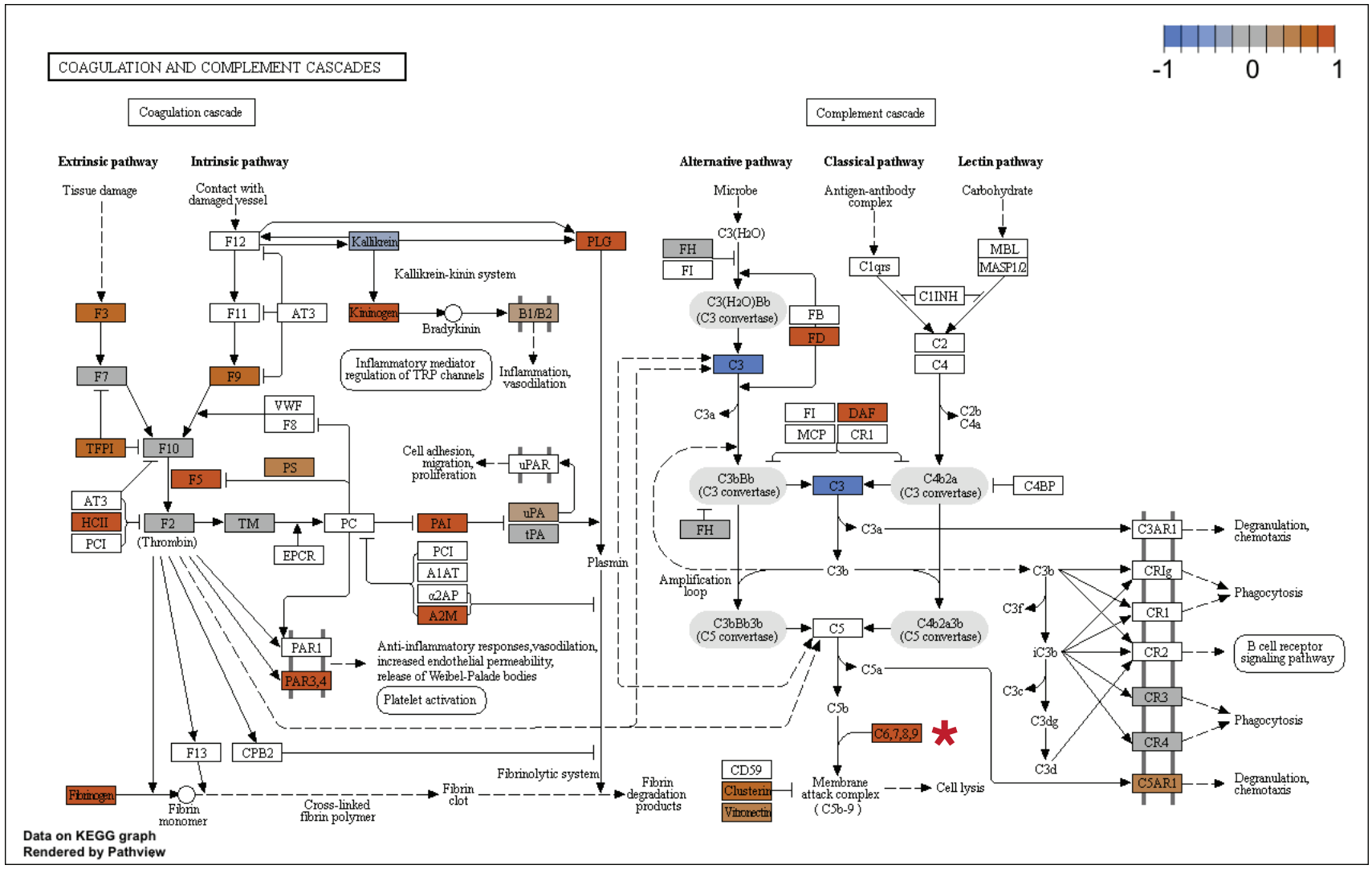

d
“Natural Killer Cell Mediated Cytotoxicity”
−2
0
2
perforin 1
nuclear factor of activated T−cells, cytoplasmic 2
classical protein kinase C gamma type
guanine nucleotide exchange factor VAV
nuclear factor of activated T−cells, cytoplasmic 1
Ras−related C3 botulinum toxin substrate 1
GTPase KRas
phosphoinositide−3−kinase, regulatory subunit
phosphatidylinositol phospholipase C, gamma−2
CD48 antigen
phosphatidylinositol−4,5−bisphosphate 3−kinase
phosphatidylinositol−4,5−bisphosphate 3−kinase
interferon gamma receptor 1
phosphoinositide−3−kinase, regulatory subunit
RAF proto−oncogene serine/threonine−protein kinase
phosphatidylinositol phospholipase C, gamma−1
tyrosine−protein phosphatase non−receptor type 11
son of sevenless
phosphoinositide−3−kinase, regulatory subunit
guanine nucleotide exchange factor VAV
SH3−domain binding protein 2
p21−activated kinase 1
serine/threonine−protein phosphatase 2B catalytic subunit
guanine nucleotide exchange factor VAV
tumor necrosis factor superfamily, member 2
mitogen−activated protein kinase 1/3
caspase 3
classical protein kinase C beta type
integrin beta 2
serine/threonine−protein phosphatase 2B catalytic subunit
serine/threonine−protein phosphatase 2B catalytic subunit
mitogen−activated protein kinase 1/3
tyrosine−protein phosphatase non−receptor type 11
growth factor receptor−binding protein 2
SHC−transforming protein 1
tumor necrosis factor receptor superfamily member 10
serine/threonine−protein phosphatase 2B catalytic subunit
GTPase HRas
nuclear factor of activated T−cells, cytoplasmic 1
focal adhesion kinase 2
SHC−transforming protein 2
phosphatidylinositol−4,5−bisphosphate 3−kinase
tumor necrosis factor ligand superfamily member 10
phosphatidylinositol−4,5−bisphosphate 3−kinase
Ras−related C3 botulinum toxin substrate 1
serine/threonine−protein phosphatase 2B catalytic subunit
GTPase KRas
SH2 domain protein 1A
phosphoinositide−3−kinase, regulatory subunit
mitogen−activated protein kinase kinase 2
spleen tyrosine kinase
tyrosine−protein phosphatase non−receptor type 6
integrin alpha L
perforin 1
granzyme B
guanine nucleotide exchange factor VAV
mitogen−activated protein kinase kinase 1
tumor necrosis factor ligand superfamily member 6
tyrosine−protein kinase ZAP−70
serine/threonine−protein phosphatase 2B regulatory subunit
phosphatidylinositol−4,5−bisphosphate 3−kinase
lymphocyte cytosolic protein 2
son of sevenless
serine/threonine−protein phosphatase 2B regulatory subunit
tumor necrosis factor receptor superfamily member 10
immunoglobulin heavy chain
tumor necrosis factor ligand superfamily member 10
phosphatidylinositol−4,5−bisphosphate 3−kinase
phosphoinositide−3−kinase, regulatory subunit
B−Raf proto−oncogene serine/threonine−protein kinase
P6
P3
P7
P9
P8
P5
NP10
NP1
NP11
NP2
NP4
NP3

Fig . S4

a


COAGULATION AND COMPLEMENT CASCADES
-1
0
1
Coagulation cascade
Complement cascade
Extrinsic pathway
Intrinsic pathway
Alternative pathway
Classical pathway
Lectin pathway
Tissue damage
Contact with damaged vessel
Microbe
Antigen-antibody complex
Carbohydrate
F12
Kallikrein
PLG
Kallikrein-kinin system
F3
F11
AT3
Kininogen
Bradykinin
B1/B2
FH
FI
C3(H2O)
C1qrs
MBL
MASP1/2
C3(H2O)Bb (C3 convertase)
FB
FD
C1INH
C2
C4
F7
F9
Inflammatory mediator regulation of TRP channels
Inflammation, vasodilation
C3
VWF
F8
C3a
FI
DAF
MCP
CR1
C2b
C4a
TFPI
F10
Cell adhesion, migration, proliferation
uPAR
F5
PS
C3bBb (C3 convertase)
C3
C4b2a (C3 convertase)
C4BP
AT3
HCII
PCI
F2
(Thrombin)
TM
PC
PAI
uPA
tPA
EPCR
FH
C3a
C3AR1
Degranulation, chemotaxis
Plasmin
PCI
A1AT
α2AP
A2M
Amplification loop
C3b
CRIg
Phagocytosis
C3f
CR1
PAR1
PAR3,4
Anti-inflammatory responses,vasodilation, increased endothelial permeability, release of Weibel-Palade bodies
Platelet activation
C3bBb3b (C5 convertase)
C5
C4b2a3b (C5 convertase)
iC3b
CR2
B cell receptor signaling pathway
C5a
C3c
CR3
C5b
C6,7,8,9
C3dg
Phagocytosis
CR4
F13
CPB2
Fibrinolytic system
C3d
C5AR1
Degranulation, chemotaxis
Fibrinogen
Fibrin monomer
Cross-linked fibrin polymer
Fibrin clot
Fibrin degradation products
CD59
Clusterin
Vitronectin
Membrane attack complex (C5b-9)
Cell lysis
Data on KEGG graph
Rendered by Pathview

b

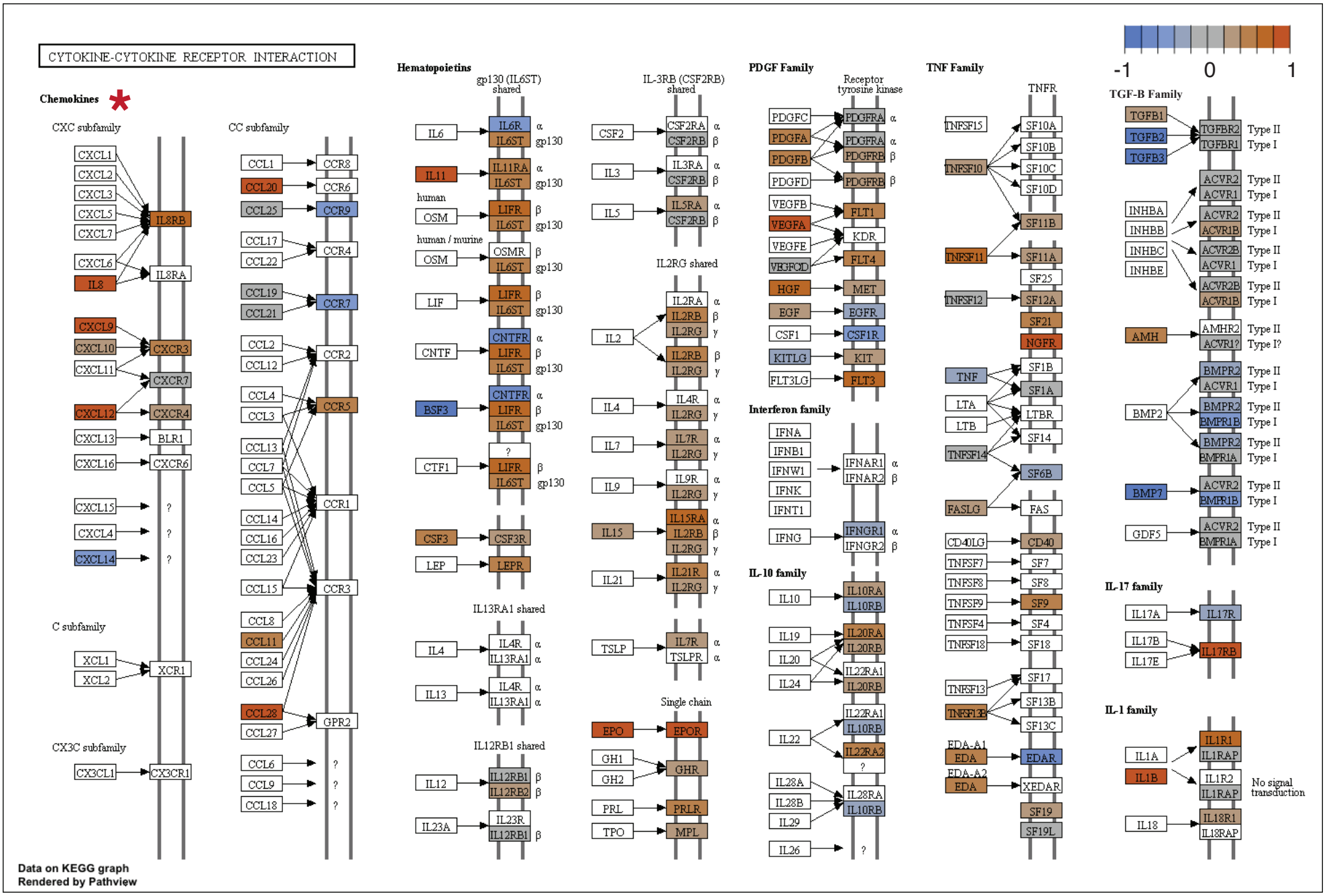

CYTOKINE-CYTOKINE RECEPTOR INTERACTION
-1
0
1
Chemokines
CXC subfamily
CC subfamily
CXCL1
CXCL2
CXCL3
CXCL5
CXCL7
CXCL6
IL8
CXCL9
CXCL10
CXCL11
CXCL12
CXCL13
CXCL16
CXCL15
CXCL4
CXCL14
IL8RB
IL8RA
CXCR3
CXCR7
CXCR4
BLR1
CXCR6
?
C subfamily
XCL1
XCL2
XCR1
CX3C subfamily
CX3CL1
CX3CR1
CCL1
CCL20
CCL25
CCL17
CCL22
CCL19
CCL21
CCL2
CCL12
CCL4
CCL3
CCL13
CCL7
CCL5
CCL14
CCL16
CCL23
CCL15
CCL8
CCL11
CCL24
CCL26
CCL28
CCL27
CCL6
CCL9
CCL18
CCR8
CCR6
CCR9
CCR4
CCR7
CCR2
CCR5
CCR1
CCR3
GPR2
Hematopoietins
gp130 (IL6ST) shared
IL6
IL11
human
OSM
human / murine
OSM
LIF
CNTF
BSF3
CTF1
CSF3
LEP
IL6R
IL6ST
IL11RA
LIFR
OSMR
CNTFR
?
CSF3R
LEPR
α
β
gp130
IL13RA1 shared
IL4
IL13
IL4R
IL13RA1
IL12RB1 shared
IL12
IL23A
IL12RB1
IL12RB2
IL23R
IL-3RB (CSF2RB) shared
CSF2
IL3
IL5
CSF2RA
IL3RA
IL5RA
CSF2RB
IL2RG shared
IL2
IL4
IL7
IL9
IL15
IL21
TSLP
IL2RA
IL2RB
IL2RG
IL4R
IL7R
IL9R
IL15RA
IL21R
TSLPR
γ
Single chain
EPO
GH1
GH2
PRL
TPO
EPOR
GHR
PRLR
MPL
PDGF Family
Receptor tyrosine kinase
PDGFC
PDGFA
PDGFB
PDGFD
VEGFB
VEGFA
VEGFE
VEGFOD
HGF
EGF
CSF1
KITLG
FLT3LG
PDGFRA
PDGFRB
FLT1
KDR
FLT4
MET
EGFR
CSF1R
KIT
FLT3
Interferon family
IFNA
IFNB1
IFNW1
IFNK
IFNT1
IFNG
IFNAR1
IFNAR2
IFNGR1
IFNGR2
IL-10 family
IL10
IL19
IL20
IL24
IL22
IL28A
IL28B
IL29
IL26
IL10RA
IL10RB
IL20RA
IL20RB
IL22RA1
IL22RA2
IL28RA
TNF Family
TNFR
TNFSF15
TNFSF10
TNFSF11
TNFSF12
TNF
LTA
LTB
TNFSF14
FASLG
CD40LG
TNFSF7
TNFSF8
TNFSF9
TNFSF4
TNFSF18
TNFSF13
TNFSF13B
EDA-A1
EDA
EDA-A2
EDA
SF10A
SF10B
SF10C
SF10D
SF11B
SF11A
SF25
SF12A
SF21
NGFR
SF1B
SF1A
LTBR
SF14
SF6B
FAS
CD40
SF7
SF8
SF9
SF4
SF18
SF17
SF13B
SF13C
EDAR
XEDAR
SF19
SF19L
TGF-B Family
TGFB1
TGFB2
TGFB3
INHBA
INHBB
INHBC
INHBE
AMH
BMP2
BMP7
GDF5
TGFBR2
TGFBR1
ACVR2
ACVR1
ACVR2B
ACVR1B
AMHR2
ACVR1?
BMPR2
BMPR1B
BMPR1A
Type II
Type I
Type I?
IL-17 family
IL17A
IL17B
IL17E
IL17R
IL17RB
IL-1 family
IL1A
IL1B
IL18
IL1R1
IL1RAP
IL1R2
IL1RAP
IL18R1
IL18RAP
No signal transduction
Data on KEGG graph
Rendered by Pathview

Fig. S5

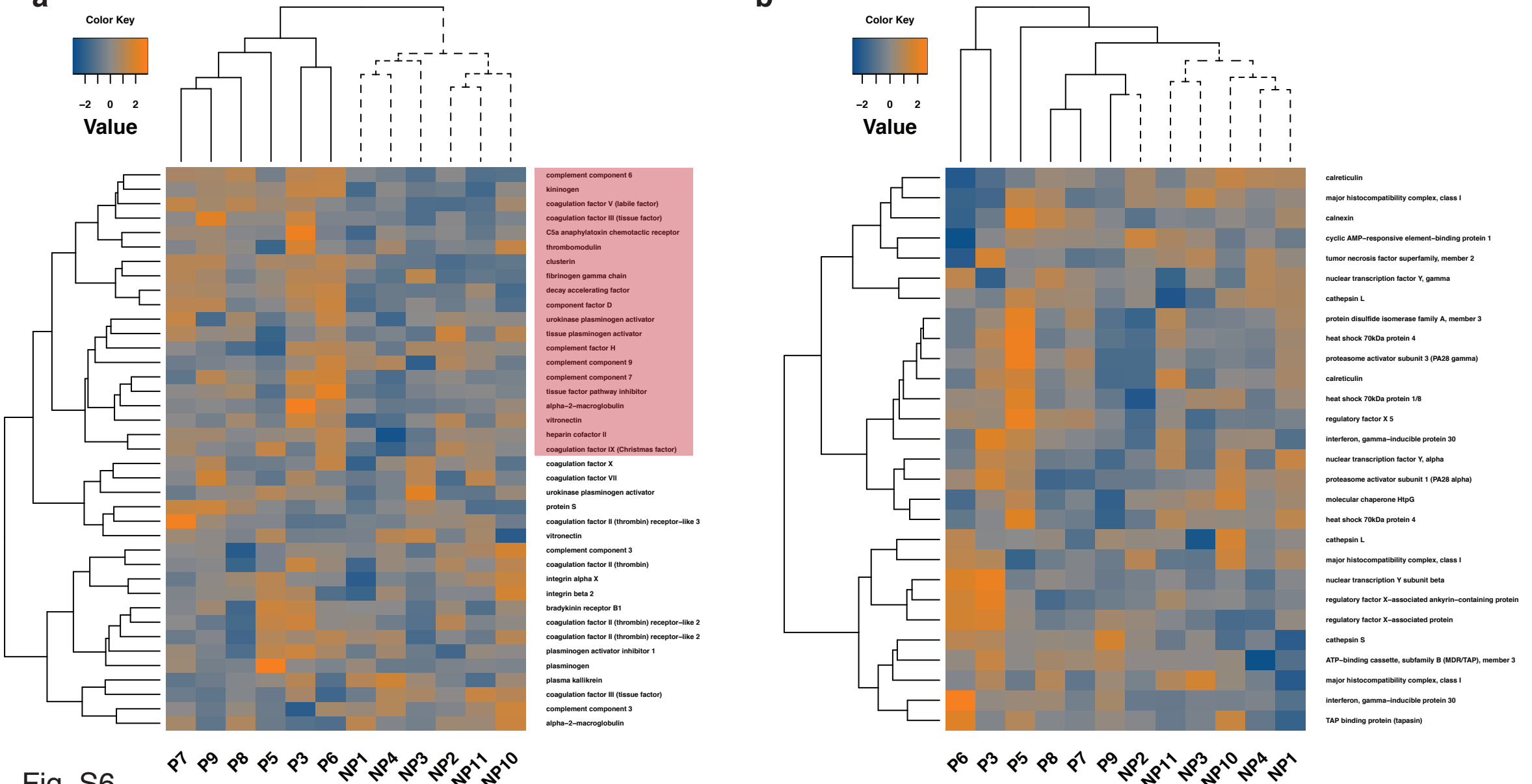
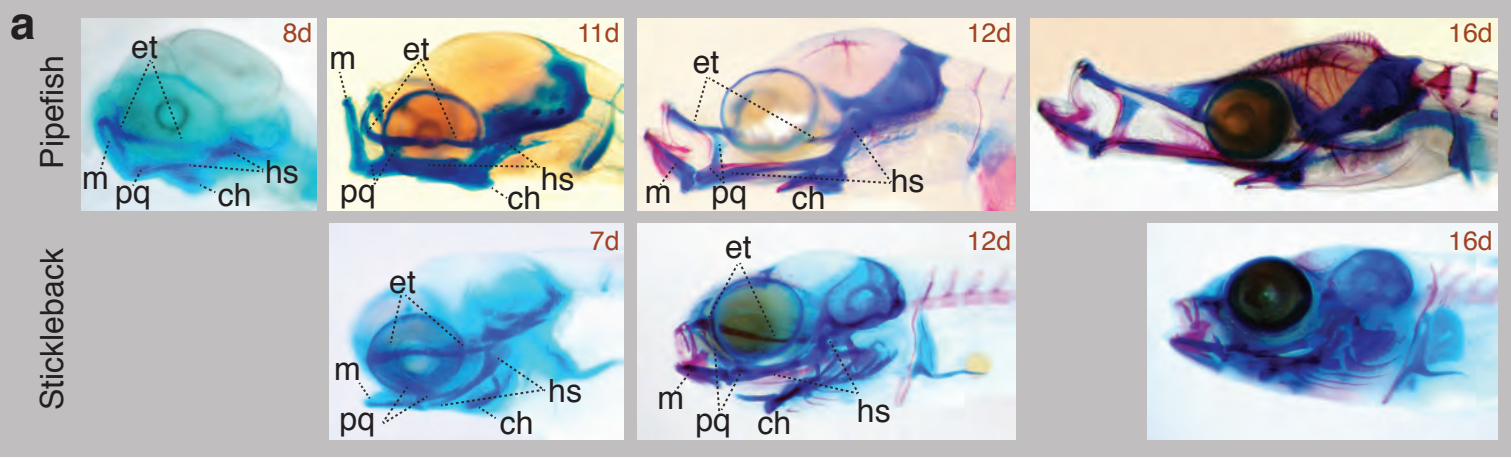

a
coagulation and complement cascades
Color Key
−2 0 2
Value
complement component 6
kininogen
coagulation factor V (labile factor)
coagulation factor III (tissue factor)
C5a anaphylatoxin chemotactic receptor
thrombomodulin
clusterin
fibrinogen gamma chain
decay accelerating factor
component factor D
urokinase plasminogen activator
tissue plasminogen activator
complement factor H
complement component 9
complement component 7
tissue factor pathway inhibitor
alpha−2−macroglobulin
vitronectin
heparin cofactor II
coagulation factor IX (Christmas factor)
coagulation factor X
coagulation factor VII
urokinase plasminogen activator
protein S
coagulation factor II (thrombin) receptor−like 3
vitronectin
complement component 3
coagulation factor II (thrombin)
integrin alpha X
integrin beta 2
bradykinin receptor B1
coagulation factor II (thrombin) receptor−like 2
coagulation factor II (thrombin) receptor−like 2
plasminogen activator inhibitor 1
plasminogen
plasma kallikrein
coagulation factor III (tissue factor)
complement component 3
alpha−2−macroglobulin
P7 P9 P8 P5 P3 P6 NP1 NP4 NP3 NP2 NP11 NP10
b
antigen processing and presentation
Color Key
−2 0 2
Value
calreticulin
major histocompatibility complex, class I
calnexin
cyclic AMP−responsive element−binding protein 1
tumor necrosis factor superfamily, member 2
nuclear transcription factor Y, gamma
cathepsin L
protein disulfide isomerase family A, member 3
heat shock 70kDa protein 4
proteasome activator subunit 3 (PA28 gamma)
calreticulin
heat shock 70kDa protein 1/8
regulatory factor X 5
interferon, gamma−inducible protein 30
nuclear transcription factor Y, alpha
proteasome activator subunit 1 (PA28 alpha)
molecular chaperone HtpG
heat shock 70kDa protein 4
cathepsin L
major histocompatibility complex, class I
nuclear transcription Y subunit beta
regulatory factor X−associated ankyrin−containing protein
regulatory factor X−associated protein
cathepsin S
ATP−binding cassette, subfamily B (MDR/TAP), member 3
major histocompatibility complex, class I
interferon, gamma−inducible protein 30
TAP binding protein (tapasin)
P6 P3 P5 P8 P7 P9 NP2 NP11 NP3 NP10 NP4 NP1

Fig. S6


a
Pipefish
Stickleback
8d
11d
12d
16d
7d
16d
et
m
pq
ch
hs

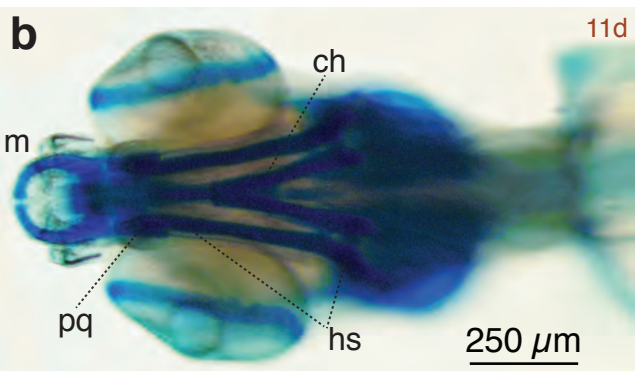

b
11d
ch
m
pq
hs
250 μm

Fig. S7

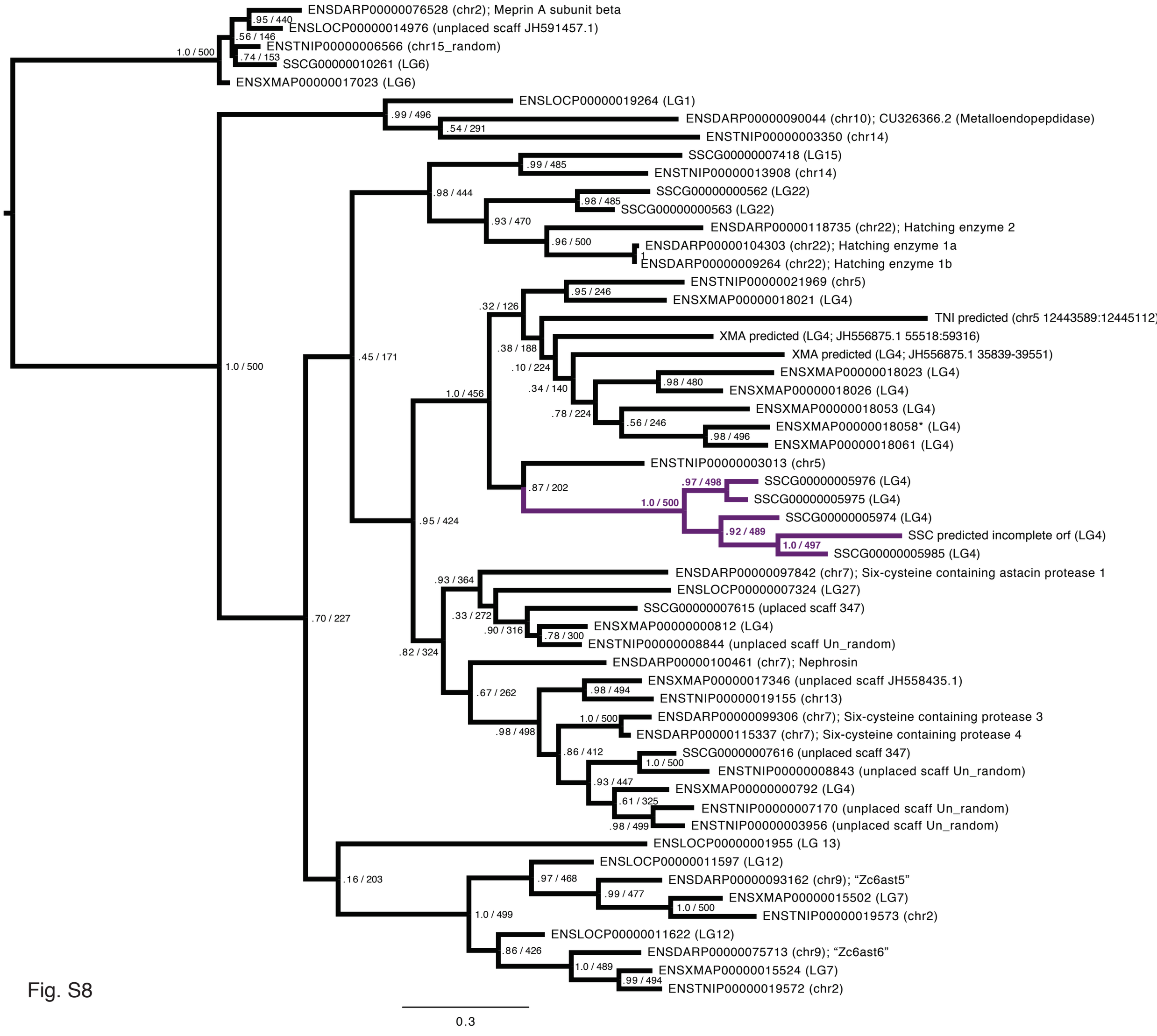

ENSDARP00000076528 (chr2); Meprin A subunit beta
.95 / 440
ENSLOCP00000014976 (unplaced scaff JH591457.1)
.56 / 146
ENSTNIP00000006566 (chr15_random)
1.0 / 500
.74 / 153
SSCG00000010261 (LG6)
ENSXMAP00000017023 (LG6)
ENSLOCP00000019264 (LG1)
.99 / 496
ENSDARP00000090044 (chr10); CU326366.2 (Metalloendopepdidase)
.54 / 291
ENSTNIP00000003350 (chr14)
SSCG00000007418 (LG15)
.99 / 485
ENSTNIP00000013908 (chr14)
.98 / 444
SSCG00000000562 (LG22)
.98 / 485
SSCG00000000563 (LG22)
.93 / 470
ENSDARP00000118735 (chr22); Hatching enzyme 2
.96 / 500
ENSDARP00000104303 (chr22); Hatching enzyme 1a
1
ENSDARP00000009264 (chr22); Hatching enzyme 1b
ENSTNIP00000021969 (chr5)
.95 / 246
ENSXMAP00000018021 (LG4)
.32 / 126
TNI predicted (chr5 12443589:12445112)
XMA predicted (LG4; JH556875.1 55518:59316)
.38 / 188
XMA predicted (LG4; JH556875.1 35839-39551)
.10 / 224
ENSXMAP00000018023 (LG4)
.98 / 480
.34 / 140
ENSXMAP00000018026 (LG4)
1.0 / 456
ENSXMAP00000018053 (LG4)
.78 / 224
.56 / 246
ENSXMAP00000018058* (LG4)
.98 / 496
ENSXMAP00000018061 (LG4)
ENSTNIP00000003013 (chr5)
.87 / 202
.97 / 498
SSCG00000005976 (LG4)
1.0 / 500
SSCG00000005975 (LG4)
SSCG00000005974 (LG4)
.92 / 489
SSC predicted incomplete orf (LG4)
1.0 / 497
SSCG00000005985 (LG4)
.45 / 171
1.0 / 500
.95 / 424
ENSDARP00000097842 (chr7); Six-cysteine containing astacin protease 1
.93 / 364
ENSLOCP00000007324 (LG27)
SSCG00000007615 (uplaced scaff 347)
.33 / 272
ENSXMAP00000000812 (LG4)
.90 / 316
.78 / 300
ENSTNIP00000008844 (unplaced scaff Un_random)
.82 / 324
ENSDARP00000100461 (chr7); Nephrosin
ENSXMAP00000017346 (unplaced scaff JH558435.1)
.67 / 262
.98 / 494
ENSTNIP00000019155 (chr13)
1.0 / 500
ENSDARP00000099306 (chr7); Six-cysteine containing protease 3
.98 / 498
ENSDARP00000115337 (chr7); Six-cysteine containing protease 4
.86 / 412
SSCG00000007616 (unplaced scaff 347)
1.0 / 500
ENSTNIP00000008843 (unplaced scaff Un_random)
.93 / 447
ENSXMAP00000000792 (LG4)
.61 / 325
ENSTNIP00000007170 (unplaced scaff Un_random)
.98 / 499
ENSTNIP00000003956 (unplaced scaff Un_random)
.70 / 227
ENSLOCP00000001955 (LG 13)
ENSLOCP00000011597 (LG12)
.16 / 203
.97 / 468
ENSDARP00000093162 (chr9); “Zc6ast5”
.99 / 477
ENSXMAP00000015502 (LG7)
1.0 / 500
ENSTNIP00000019573 (chr2)
1.0 / 499
ENSLOCP00000011622 (LG12)
.86 / 426
ENSDARP00000075713 (chr9); “Zc6ast6”
1.0 / 489
ENSXMAP00000015524 (LG7)
.99 / 494
ENSTNIP00000019572 (chr2)
0.3

Fig. S8