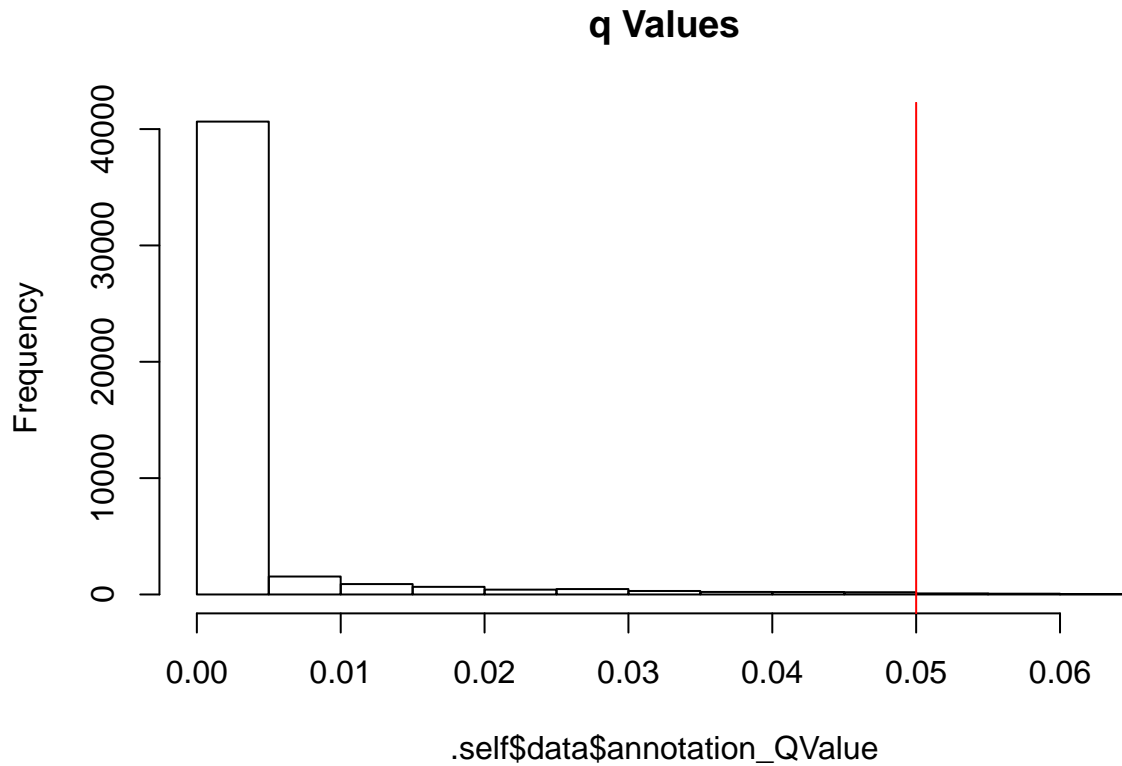# SRM

FGCZ

23 October 2017

Distribution of qValues

q Values

Histogram of qValues for all SRM assays. The red line indicates the qValue threshold - we control the False Discovery Rate (fdr) at this level.

Remove all transitions with more than X missing values

Histogram showing the number of missing values for the heavy peptides in all samples. The red line indicates the maximum of NA's allowed.

Histogram showing the number of missing values for the light peptides in all samples. The red line indicates the maximum of NA's allowed.
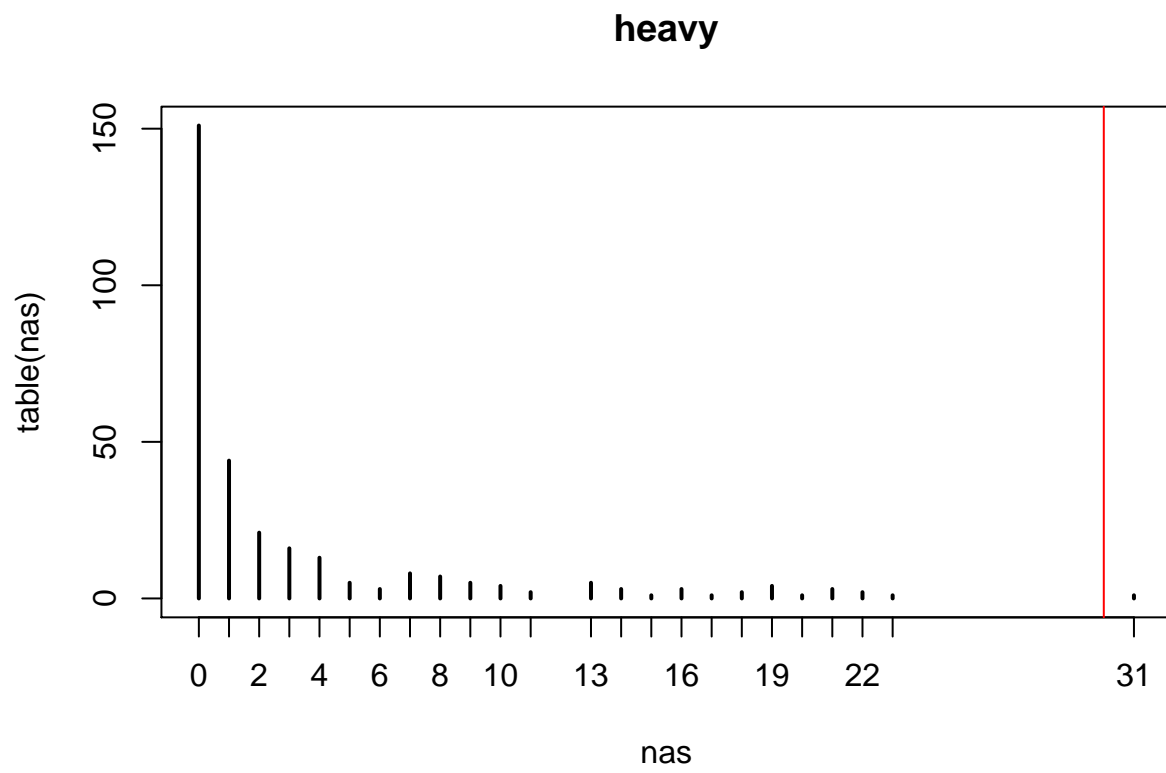
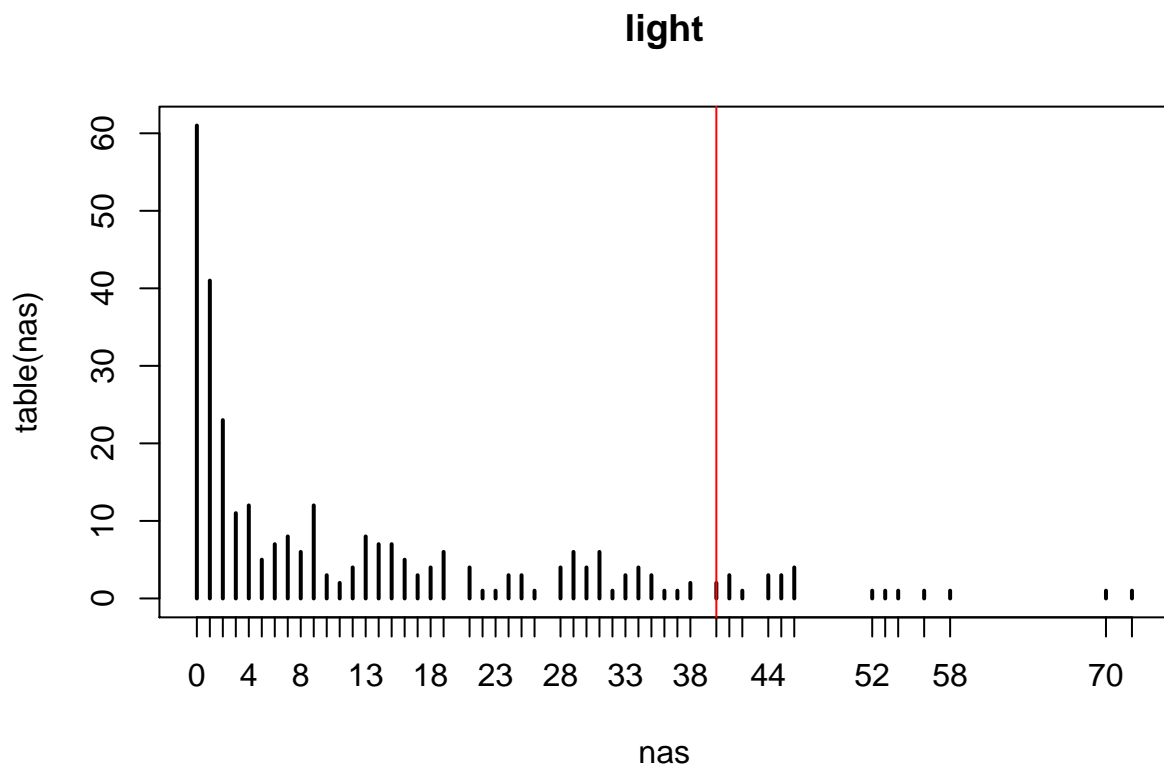Figure 1: Distribution of NA's for heavy peptides

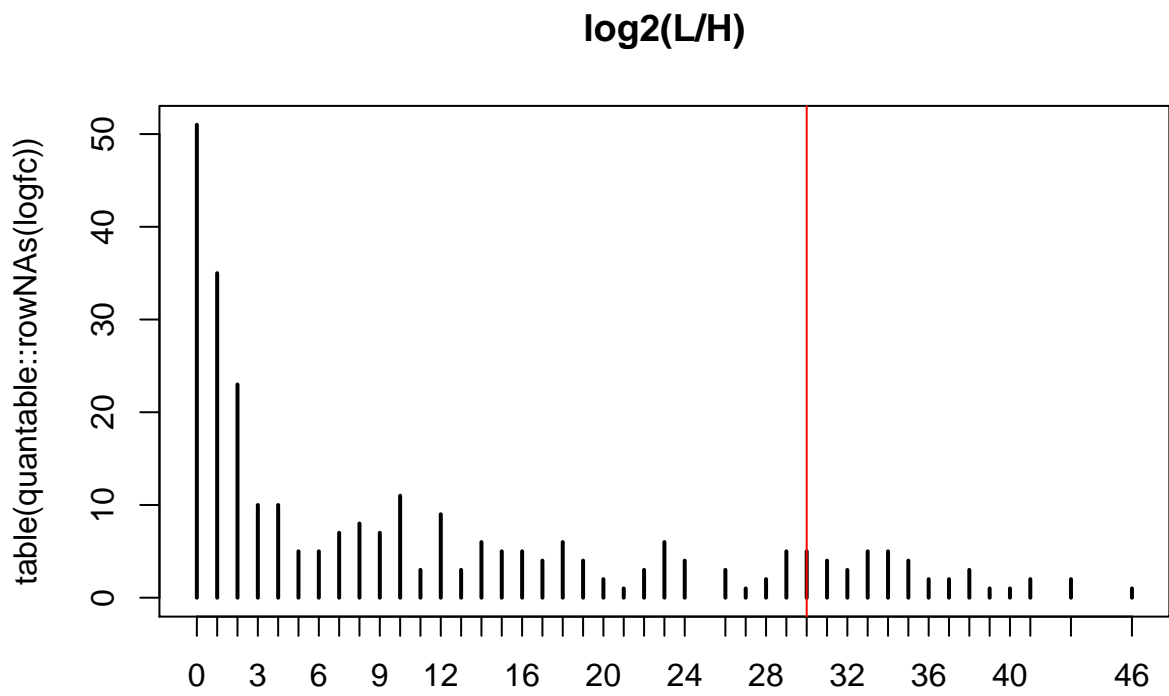Figure 2: Distribution of NA's for light peptides.

Figure 3: Missing values log2(L/H) per Transtion.

log2(L/H)

Figure 4: heatmap of log2 fold changes transtion level

Heatmap of log2(L/H)

Transitions dropped because of to many NA's in log2 fold change.

Table 1: removed transitions (to many NA's)

Peptide.Sequence	Protein.Name	Precursor.Charge	Product.Charge	Fragment.Ion
AEGAGDAK	sp|P05204|HMGN2|HUMAN	2	1	y4
AEGAGDAK	sp|P05204|HMGN2|HUMAN	2	1	y6
AEGAGDAK	sp|P05204|HMGN2|HUMAN	2	1	y7
APEQEQAAPGPAAGGEAPK	sp|P80723-1|BASP1|HUMAN	3	2	y9
CSFQDLDLCPLDGGIQLR	sp|P01584|IL1B|HUMAN	3	1	y7
CSFQDLDLCPLDGGIQLR	sp|P01584|IL1B|HUMAN	3	1	y9
CSFQDLDLCPLDGGIQLR	sp|P01584|IL1B|HUMAN	3	2	y9
DDKPTLQLESVDPK	sp|P01584|IL1B|HUMAN	3	1	y5
DDKPTLQLESVDPK	sp|P01584|IL1B|HUMAN	3	1	y6
DDKPTLQLESVDPK	sp|P01584|IL1B|HUMAN	3	1	y7
DPAFTALLTTQTQVQR	sp|P54108|CRIS3|HUMAN	2	1	y7
FALITWIGENVSGLQR	sp|Q14019|COTL1|HUMAN	3	1	y5
FALITWIGENVSGLQR	sp|Q14019|COTL1|HUMAN	3	1	y7
FYQLPSNQYQSTR	sp|P22894|MMP8|HUMAN	2	1	b4
FYQLPSNQYQSTR	sp|P22894|MMP8|HUMAN	2	1	y5
FYQLPSNQYQSTR	sp|P22894|MMP8|HUMAN	2	1	y6
FYQLPSNQYQSTR	sp|P22894|MMP8|HUMAN	2	2	y9
GFSGTPGSNENSTQNVYK	sp|Q9NP99-1|TREM1|HUMAN	2	1	b5
GFSGTPGSNENSTQNVYK	sp|Q9NP99-1|TREM1|HUMAN	2	1	y2
GFSGTPGSNENSTQNVYK	sp|Q9NP99-1|TREM1|HUMAN	2	1	y4
GFSGTPGSNENSTQNVYK	sp|Q9NP99-1|TREM1|HUMAN	2	2	y13
GNFHAVYR	sp|P05109|S10A8|HUMAN	2	1	y2
GNFHAVYR	sp|P05109|S10A8|HUMAN	2	1	y5
GNFHAVYR	sp|P05109|S10A8|HUMAN	2	2	y5
GNPTVEVDLFTSK	sp|P06733-1|ENOA|HUMAN	2	1	y3
GNPTVEVDLFTSK	sp|P06733-1|ENOA|HUMAN	2	1	y6
GNPTVEVDLFTSK	sp|P06733-1|ENOA|HUMAN	2	1	y8
IILEDYHDHGLLR	sp|Q9NP99-1|TREM1|HUMAN	3	2	y11
IQNLLPDDSVDSTTR	sp|P48595|SPB10|HUMAN	2	1	y7
LGNGVQCLAMGWGLLGR	sp|P08246|ELNE|HUMAN	2	1	y8
NLYLSCVLK	sp|P01584|IL1B|HUMAN	2	1	y6
NLYLSCVLK	sp|P01584|IL1B|HUMAN	2	1	y7
NSHPVQVGR	sp|Q9NP99-1|TREM1|HUMAN	2	1	b3
NSHPVQVGR	sp|Q9NP99-1|TREM1|HUMAN	2	1	y6
NSHPVQVGR	sp|Q9NP99-1|TREM1|HUMAN	2	2	y6
NSHPVQVGR	sp|Q9NP99-1|TREM1|HUMAN	2	2	y7
NYPENTYYSNFISHLANIK	sp|P23280|CAH6|HUMAN	2	1	y7
QGNMTAALQAALK	sp|O15511-1|ARPC5|HUMAN	2	2	y10
TYFPHFDLSHGSAQVK	sp|P69905|HBA|HUMAN	2	2	y12
TYLFLQEYLDAIK	sp|P29508-1|SPB3|HUMAN	2	1	y7
TYLFLQEYLDAIK	sp|P29508-1|SPB3|HUMAN	2	1	y8
VDVDEYDENK	sp|O15511-1|ARPC5|HUMAN	2	1	y5
VDVDEYDENK	sp|O15511-1|ARPC5|HUMAN	2	1	y6
VDVDEYDENK	sp|O15511-1|ARPC5|HUMAN	2	1	y7
VDVVLGPIQLQTPPR	sp|Q9UGM3-1|DMBT1|HUMAN	2	1	b3
VDVVLGPIQLQTPPR	sp|Q9UGM3-1|DMBT1|HUMAN	2	1	b4

Peptide.Sequence	Protein.Name	Precursor.Charge	Product.Charge	Fragment.Ion
VDVVLGPIQLQTPPR	sp|Q9UGM3-1|DMBT1|HUMAN	2	1	b5
VDVVLGPIQLQTPPR	sp|Q9UGM3-1|DMBT1|HUMAN	2	2	y11
VFDEFKPLVEEPQNLIK	sp|P02768-1|ALBU|HUMAN	3	2	y5
VPAQSESVR	sp|P50552|VASP|HUMAN	2	1	y6
VPAQSESVR	sp|P50552|VASP|HUMAN	2	1	y7
VPAQSESVR	sp|P50552|VASP|HUMAN	2	2	y8
VQIYHNPTANSFR	sp|P50552|VASP|HUMAN	2	1	b6
VQIYHNPTANSFR	sp|P50552|VASP|HUMAN	2	1	y7
VQIYHNPTANSFR	sp|P50552|VASP|HUMAN	2	1	y8
VQIYHNPTANSFR	sp|P50552|VASP|HUMAN	2	2	y11
VTIAQGGVLPNIQAVLLPK	sp|P0C0S8|H2A1|HUMAN	2	2	y10

Peptide Quantification

The following plots show Log2(H/L) of peptides belonging to the same proteins (y axis) given samples (x axis). These fold changes will be used to compute the fold H/L fold change of the protein in a sample.

Remove all peptides with only one transition.

Table 2: peptides removed since only a single valid transition

Peptide.Sequence	Protein.Name	Precursor.Charge	Product.Charge	Fragment.Ion
FALITWIGENVSGLQR	sp|Q14019|COTL1|HUMAN	3	1	y4
FYQLPSNQYQSTR	sp|P22894|MMP8|HUMAN	2	1	b3
TYLFLQEYLDAIK	sp|P29508-1|SPB3|HUMAN	2	1	b3
VDVVLGPIQLQTPPR	sp|Q9UGM3-1|DMBT1|HUMAN	2	1	y3

Removing decorrelated

List of peptides removed

Peptides might have been removed since there were no quantified transtions, only a single transition was quantified or the transition were uncorrelated.

Table 3: All removed peptides.

Protein.Name	Peptide.Sequence	Precursor.Charge
sp|P05204|HMGN2|HUMAN	AEGAGDAK	2
sp|P80723-1|BASP1|HUMAN	APEQEQAAPGPAAGGEAPK	3
sp|P01584|IL1B|HUMAN	CSFQDLDLCPLDGGIQLR	3
sp|P01584|IL1B|HUMAN	DDKPTLQLESVDPK	3
sp|Q14019|COTL1|HUMAN	FALITWIGENVSGLQR	3
sp|P22894|MMP8|HUMAN	FYQLPSNQYQSTR	2
sp|Q9NP99-1|TREM1|HUMAN	GFSGTPGSNENSTQNVYK	2
sp|P05109|S10A8|HUMAN	GNFHAVYR	2
sp|P06733-1|ENOA|HUMAN	GNPTVEVDLFTSK	2
sp|P01584|IL1B|HUMAN	NLYLSCVLK	2
sp|Q9NP99-1|TREM1|HUMAN	NSHPVQVGR	2
sp|O15511-1|ARPC5|HUMAN	QGNMTAALQAALK	2
sp|P29508-1|SPB3|HUMAN	TYLFLQEYLDAIK	2
sp|O15511-1|ARPC5|HUMAN	VDVDEYDENK	2
sp|Q9UGM3-1|DMBT1|HUMAN	VDVVLGPIQLQTPPR	2
sp|P50552|VASP|HUMAN	VPAQSESVR	2
sp|P50552|VASP|HUMAN	VQIYHNPTANSFR	2

List of peptides used for quantification

Table 4: Peptides Still available and Nr of transitions per peptide. Columns charge state.

	2	3
AAQVTIQSSGTFSSK	3	0
AAYNLVR	3	0
AGFAGDDAPR	3	0
AGLQFPVGR	3	0
ALAAGGVGSIVR	3	0
ALDFAVGEYNK	3	0
ALNSIIDVYHK	3	0
ALQVVR	3	0
ALTGHLEEVVLALLK	0	3
APEPHVEEDDDDELDSK	0	4
APNVVVTR	3	0
ASNDMYHSR	3	0
ASSIIDELFQDR	3	0
AVFPSIVGRPR	3	0
AVGLQLYYK	3	0
CVWDIEVQNNYR	4	0
DGAGDVAFIR	3	0
DNENVVNEYSSELEK	5	0
DPAFTALLTTQTQVQR	3	0
EDGGGWWYNR	3	0
EILSVDCSTNNPSQAK	3	0
ELLALIQLER	3	0
ESEPQAAAEPAEAK	3	0
ETPAATEAPSSTPK	3	0
FCEAEFSVK	3	0
FFADLLDYIK	3	0
FGNADGAACHFPFIFEGR	0	3
FLASVSTVLTSK	3	0
FQNALLVR	3	0
GEELSCEER	3	0
GLGTDEDTLIEILASR	3	0
GVDEATIIDILTK	3	0
HLQLAIR	3	0
HVIEIHIVHYNSK	0	3
IGAEVYHNLK	3	0
IILEDYHDHGLLR	0	2
INLGFSNLK	3	0
IQNLLPDDSVDSTTR	4	0
LENSLLDHR	3	0
LFAFVR	3	0
LFDSDPITVTVPVEVSR	4	0
LGNGVQCLAMGWGLLGR	2	0
LLETECPQYIR	3	0
LSAKPAPPKPEPKPK	0	3
LTFINDLCGPR	3	0
NLFLSNVFHK	3	0
NLLFNDNTECLAR	3	0

	2	3
NQGNTWLTAFVLK	3	0
NYPENTYYSNFISHLANIK	2	0
QDGSVDFGR	4	0
QGHNSVFLIK	0	3
QLAEEYLYR	3	0
QNCELFEQLGEYK	3	0
QSTLVLFPGDLR	3	0
QYTSFHFASLEDVQAK	0	3
SGAQATWTELPWPHEK	0	3
SISGAFPGIESK	3	0
SNLCALCIGDEQGENK	3	0
SNVCTLVR	3	0
SYELPDGQVITIGNER	3	0
TLLGDGPVVTDPK	3	0
TYFPHFDLSHGSAQVK	2	0
VFDEFKPLVEEPQNLIK	0	2
VGAHAGEYGAEALER	0	3
VIGGDDLSTLTGK	3	0
VLHFDQVTENTTGK	0	3
VLSSIEQK	3	0
VSVQLEASPAFLAVPVEK	4	0
VTIAQGGVLPNIQAVLLPK	5	0
VVLGAHNLSR	0	3
VWVYPPEK	3	0
WANQCNYR	3	0
YISPDQLADLYK	4	0
YLAEVATGDDK	3	0
YNQATPNFHQWR	0	3
YYAFDLIAQR	3	0
YYYVCQYCPAGNWANR	5	0

Peptide Intensities

log2(L/H)
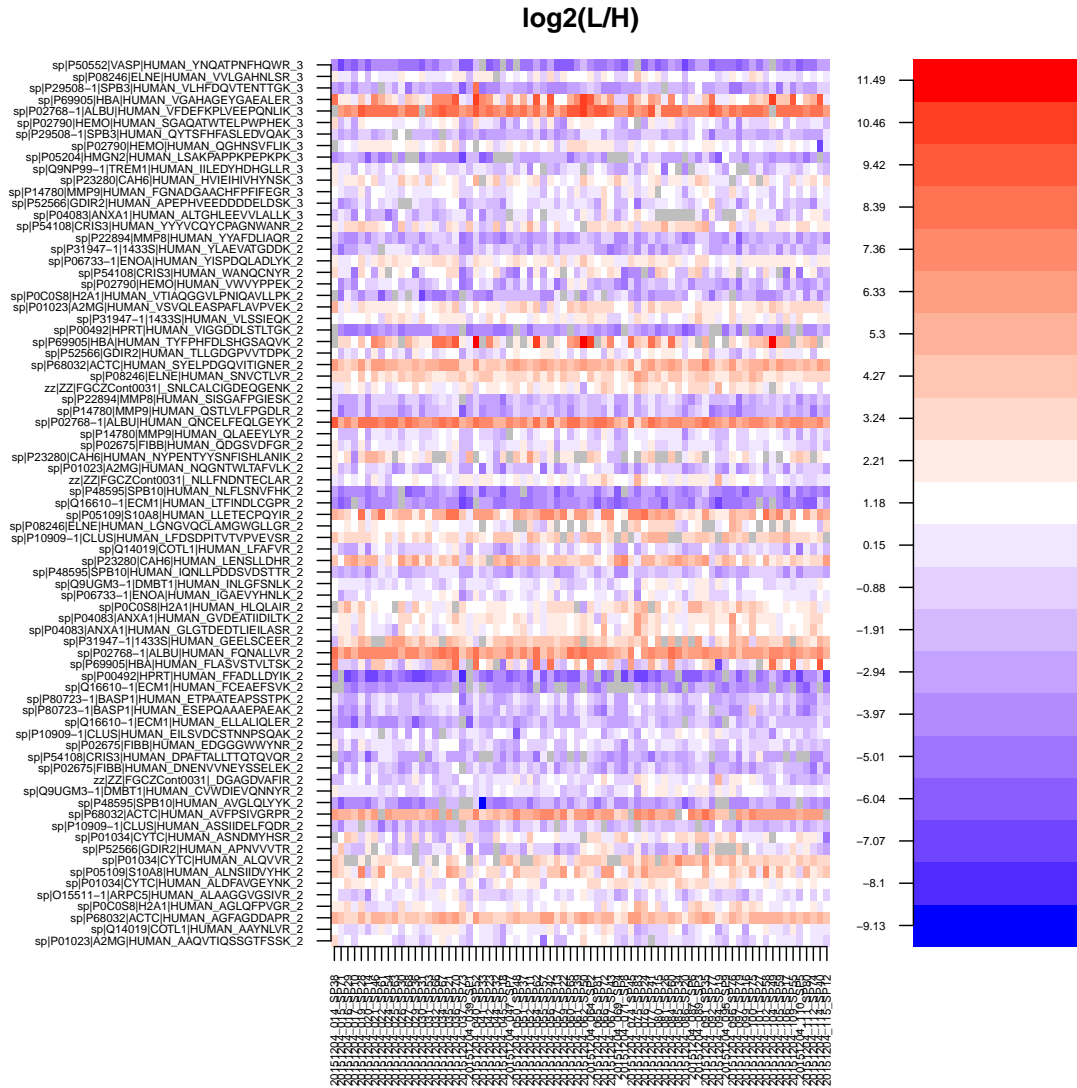
Protein Intensities

log2(L/H)
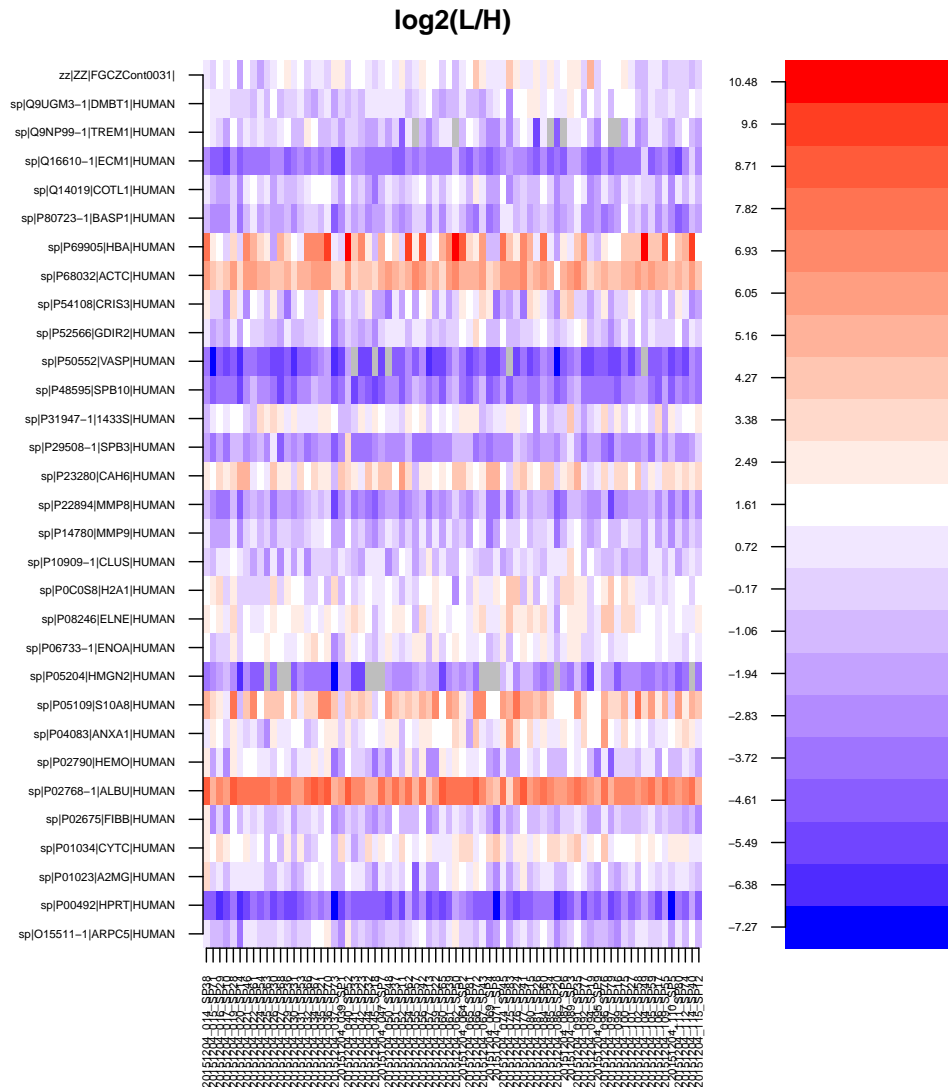
List of quantified proteins

Table 5: Quantified proteins with number of peptides used for quantification

Portein	NrPeptides
sp|O15511-1|ARPC5|HUMAN	1
sp|P00492|HPRT|HUMAN	2
sp|P01023|A2MG|HUMAN	3
sp|P01034|CYTC|HUMAN	3
sp|P02675|FIBB|HUMAN	3
sp|P02768-1|ALBU|HUMAN	3
sp|P02790|HEMO|HUMAN	3
sp|P04083|ANXA1|HUMAN	3
sp|P05109|S10A8|HUMAN	2
sp|P05204|HMGN2|HUMAN	1
sp|P06733-1|ENOA|HUMAN	2
sp|P08246|ELNE|HUMAN	3
sp|P0C0S8|H2A1|HUMAN	3
sp|P10909-1|CLUS|HUMAN	3
sp|P14780|MMP9|HUMAN	3
sp|P22894|MMP8|HUMAN	2
sp|P23280|CAH6|HUMAN	3
sp|P29508-1|SPB3|HUMAN	2
sp|P31947-1|1433S|HUMAN	3
sp|P48595|SPB10|HUMAN	3
sp|P50552|VASP|HUMAN	1
sp|P52566|GDIR2|HUMAN	3
sp|P54108|CRIS3|HUMAN	3
sp|P68032|ACTC|HUMAN	3
sp|P69905|HBA|HUMAN	3
sp|P80723-1|BASP1|HUMAN	2
sp|Q14019|COTL1|HUMAN	2
sp|Q16610-1|ECM1|HUMAN	3
sp|Q9NP99-1|TREM1|HUMAN	1
sp|Q9UGM3-1|DMBT1|HUMAN	2
zz|ZZ|FGCZCont0031|	3

List of proteins not quantified

proteins
sp|P01584|IL1B|HUMAN

Peptide profiles per Protein

sp|O15511−1|ARPC5|HUMAN
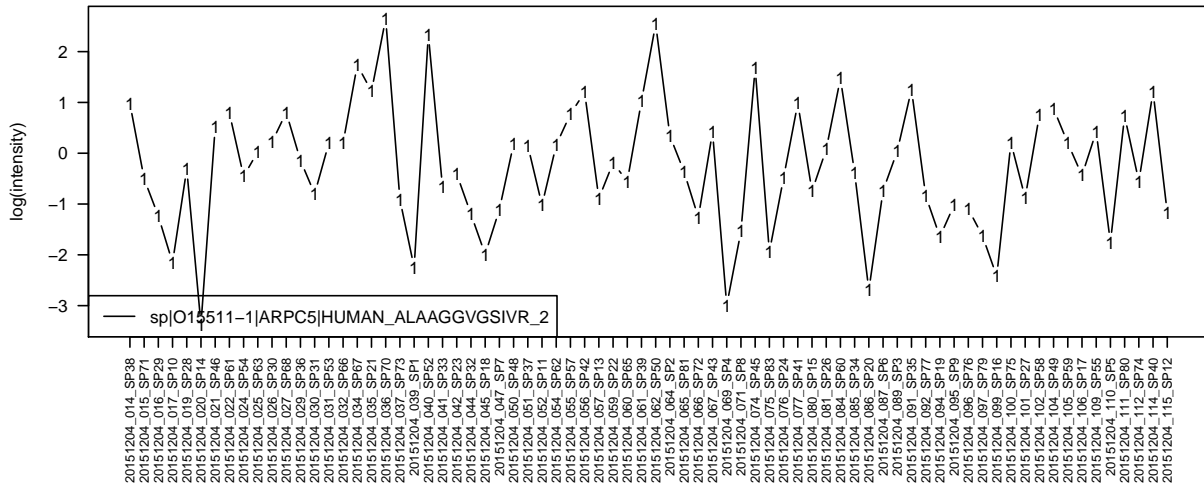
sp|P00492|HPRT|HUMAN

sp|P01023|A2MG|HUMAN

Legend:
- sp|P01023|A2MG|HUMAN_AAQVTIQSSGTFSSK_2
- sp|P01023|A2MG|HUMAN_NQGNTWLTAFVLK_2
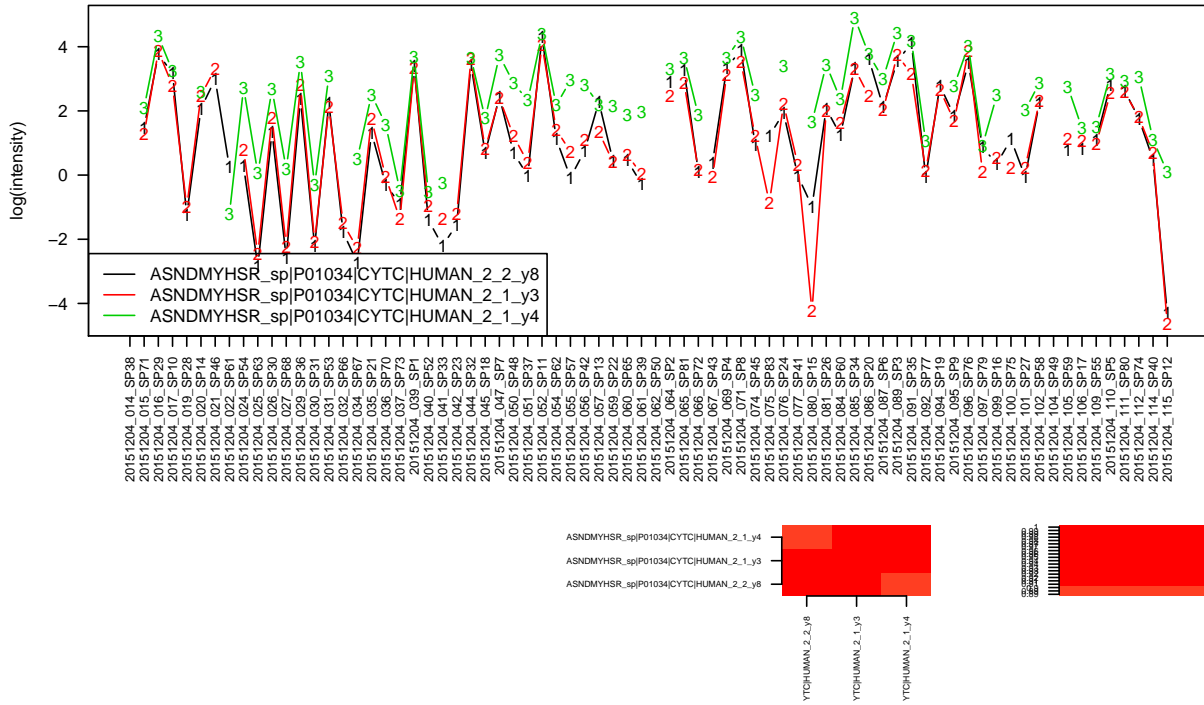- sp|P01023|A2MG|HUMAN_VSVQLEASPAFLAVPVEK_2

sp|P01034|CYTC|HUMAN

Legend:
- sp|P01034|CYTC|HUMAN_ALDFAVGEYNK_2
- sp|P01034|CYTC|HUMAN_ALQVVR_2
- sp|P01034|CYTC|HUMAN_ASNDMYHSR_2

17
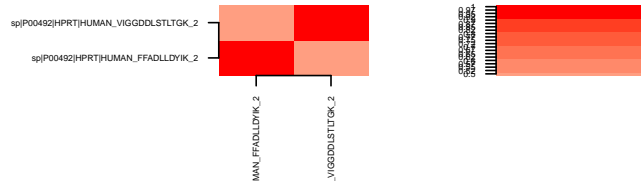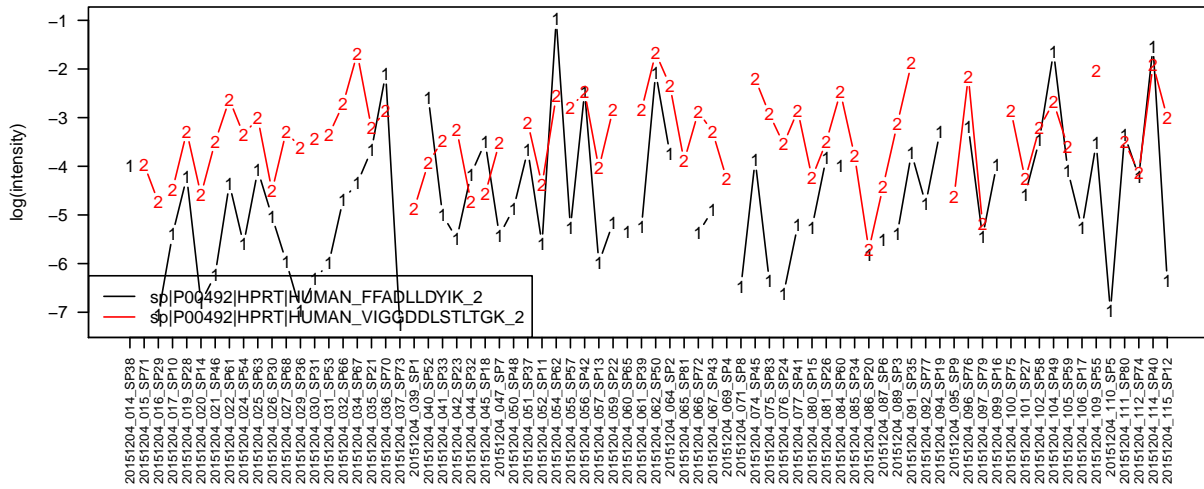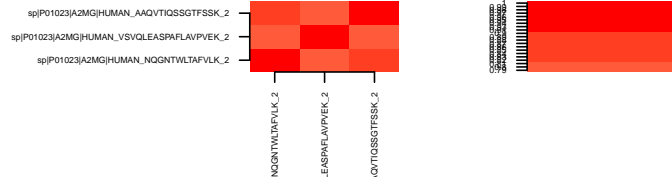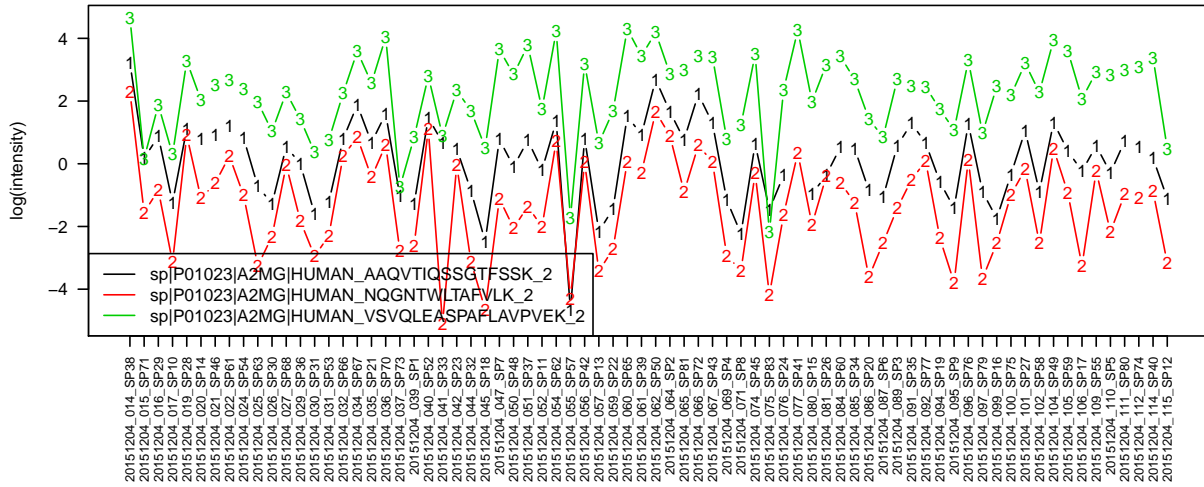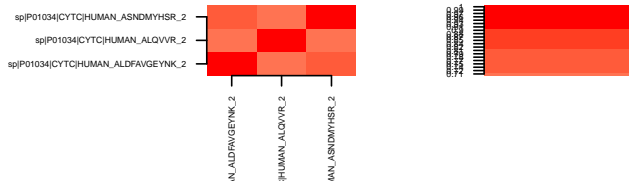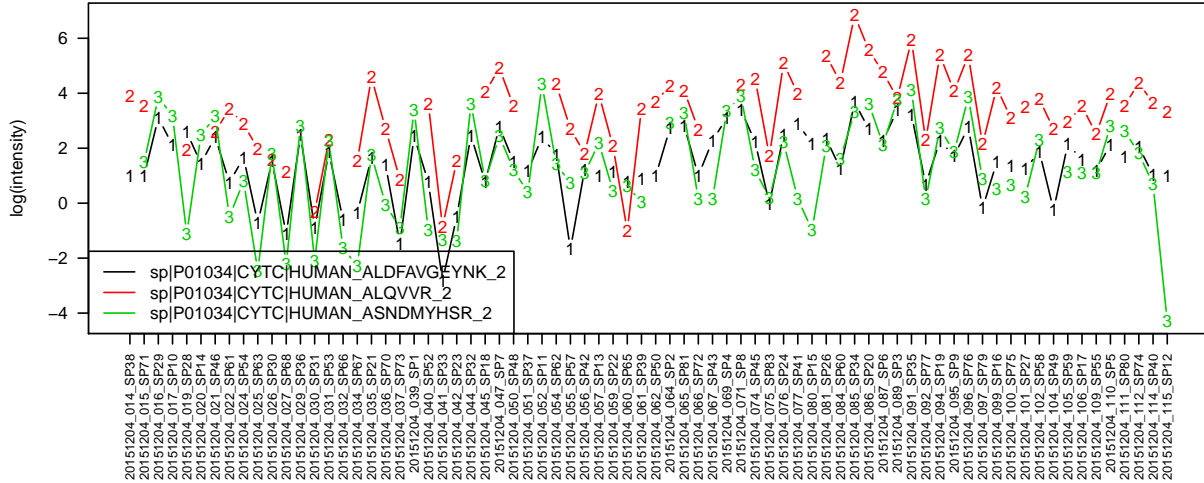
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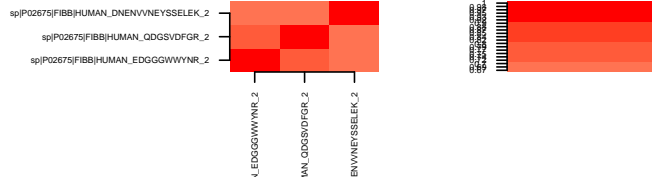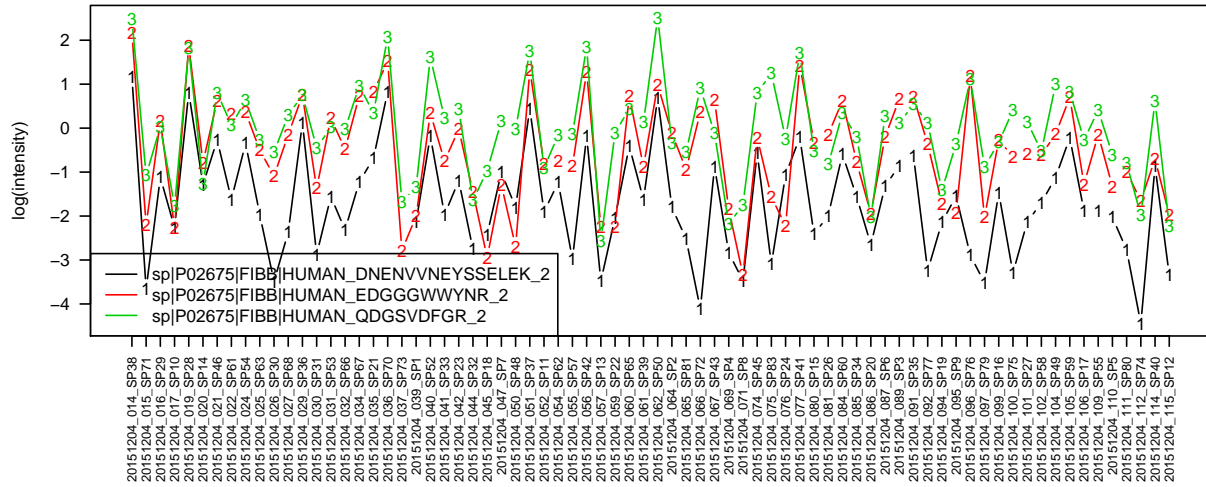
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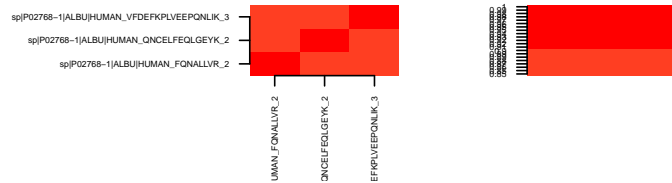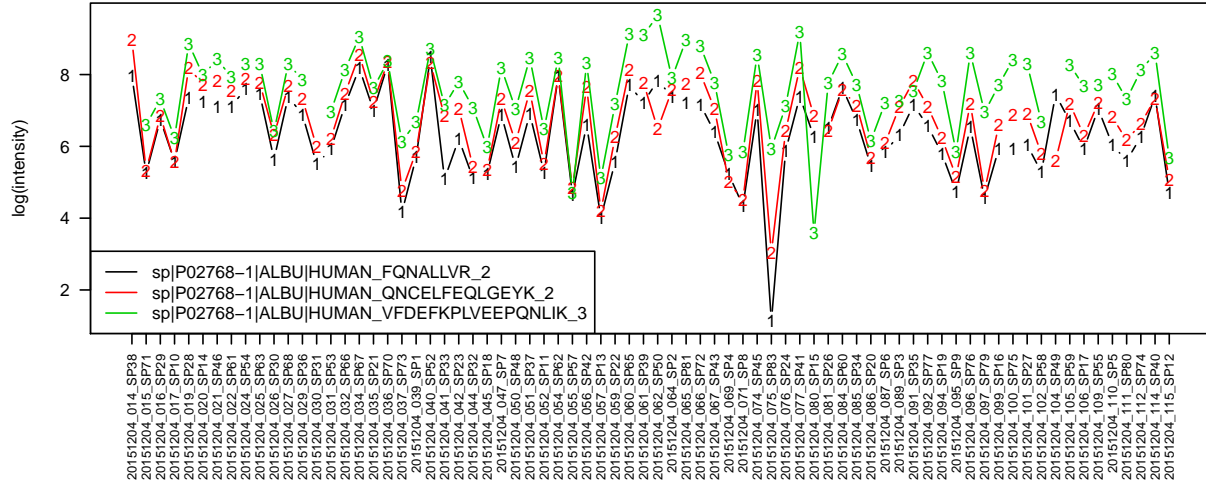
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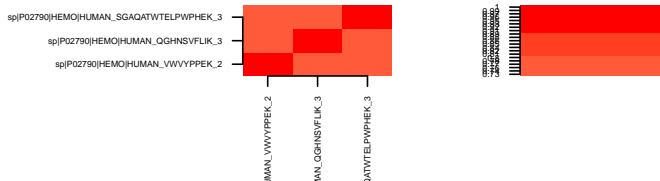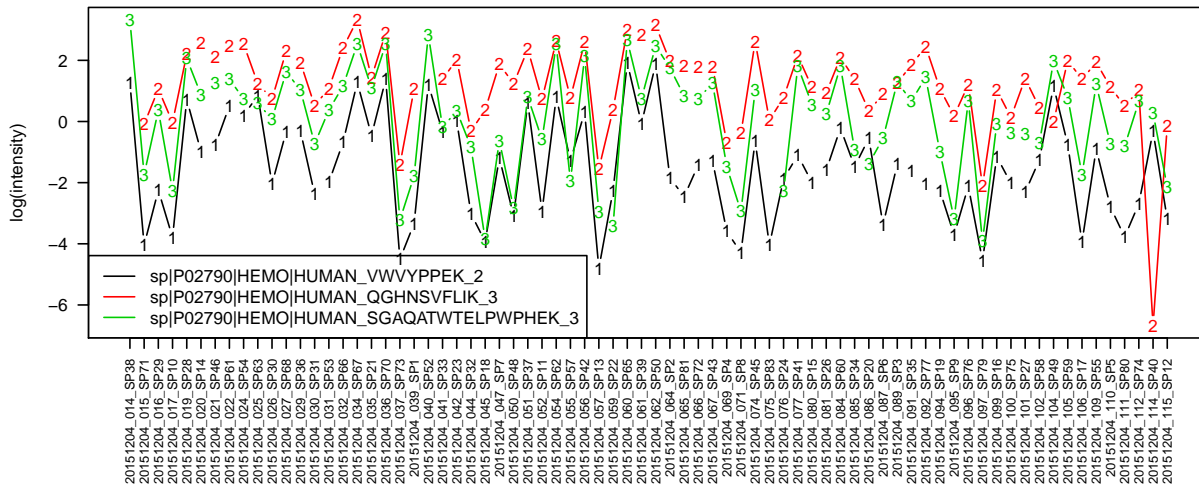
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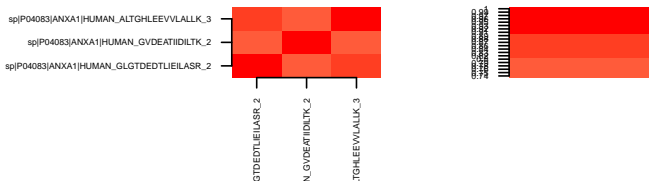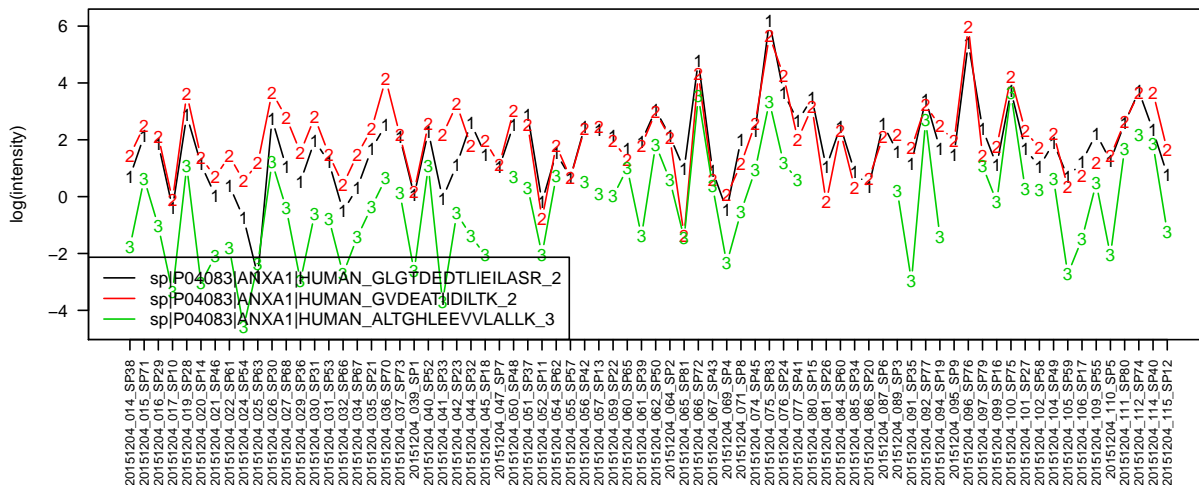
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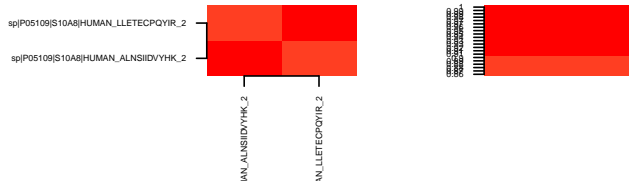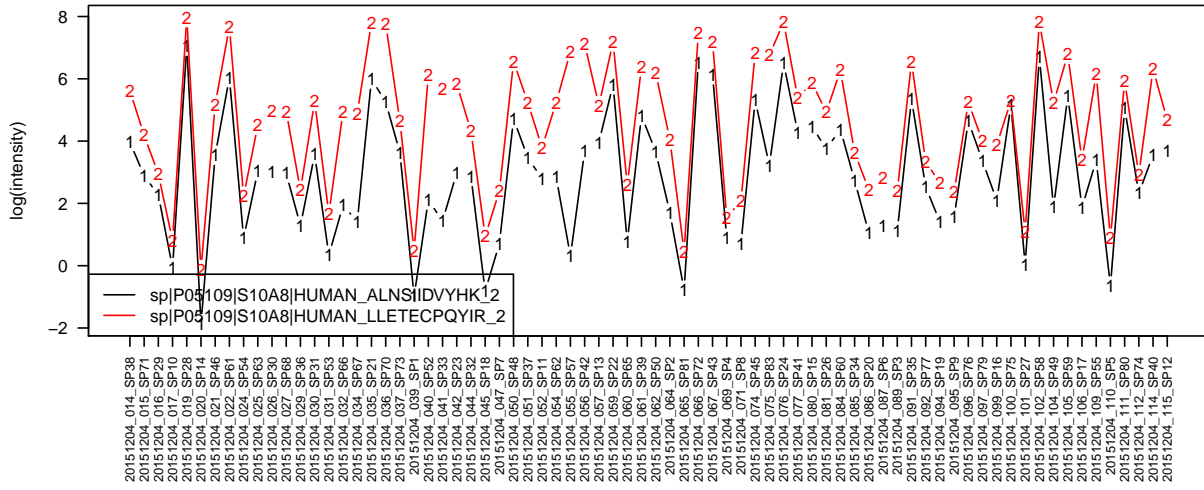
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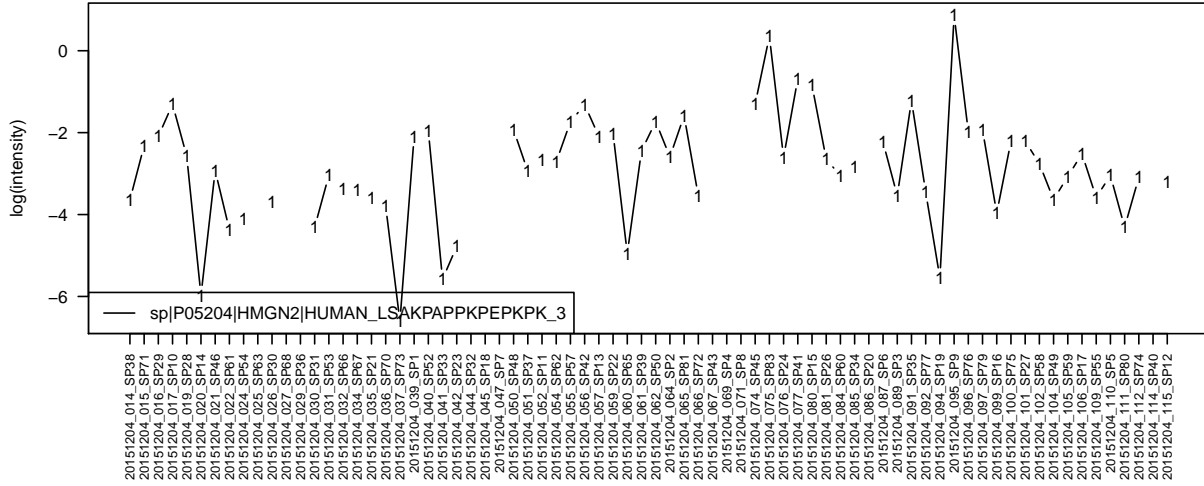
sp|P06733−1|ENOA|HUMAN

sp|P08246|ELNE|HUMAN

21
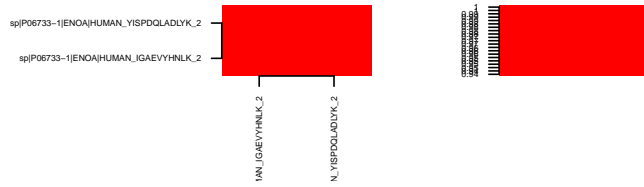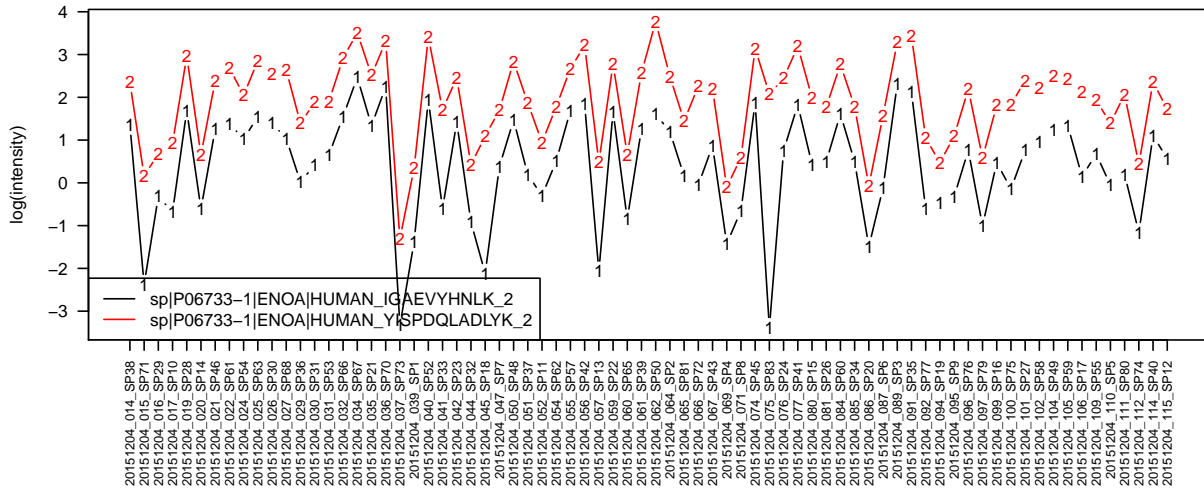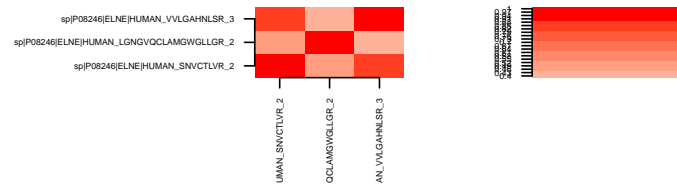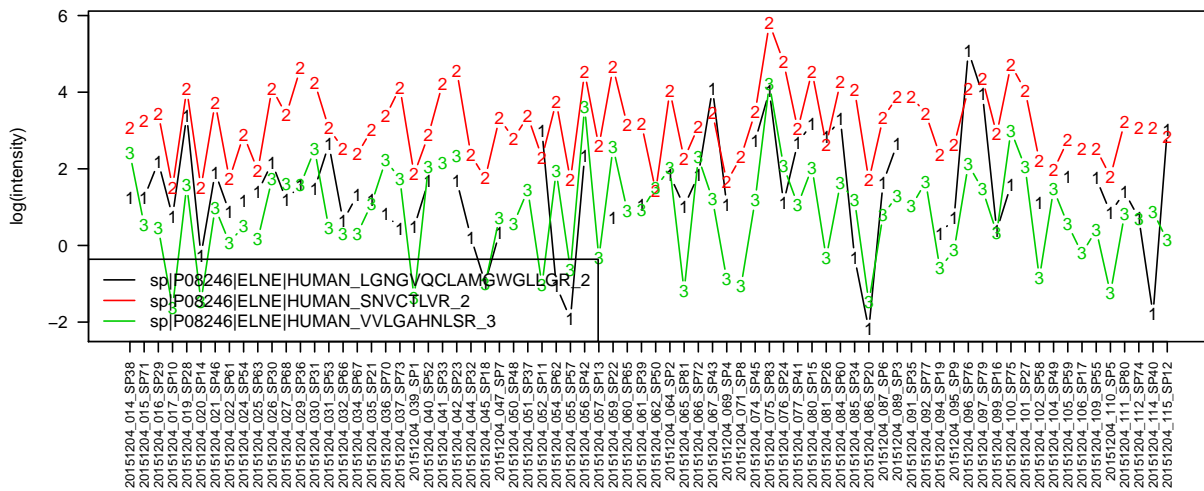
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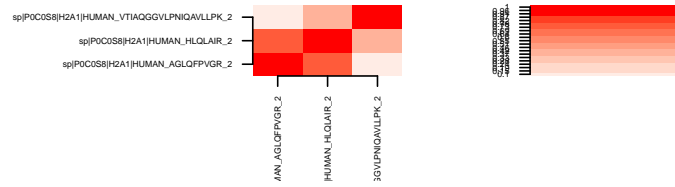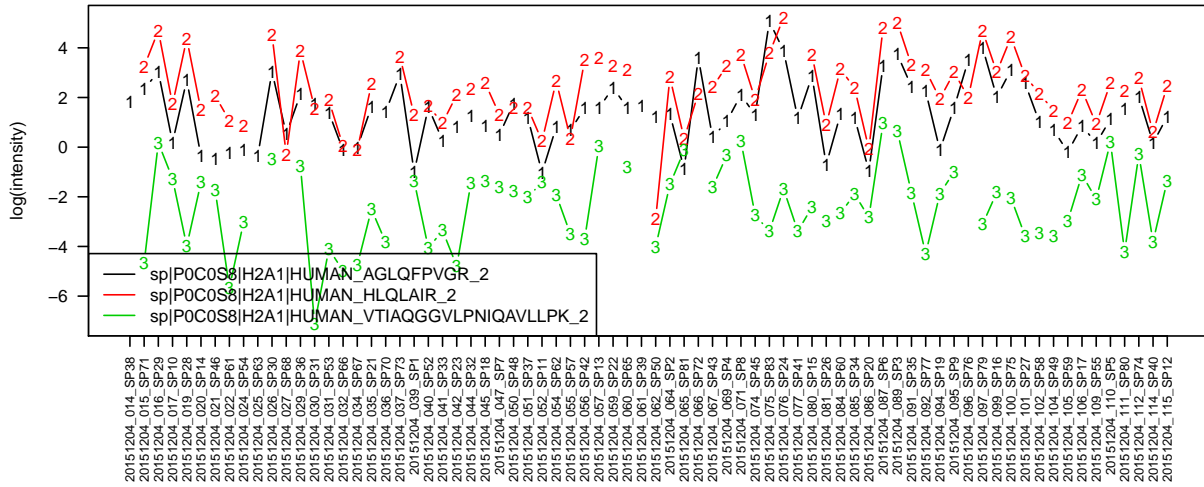
sp|P10909−1|CLUS|HUMAN
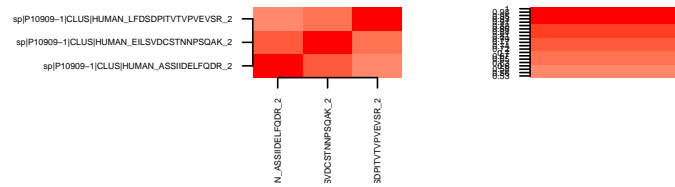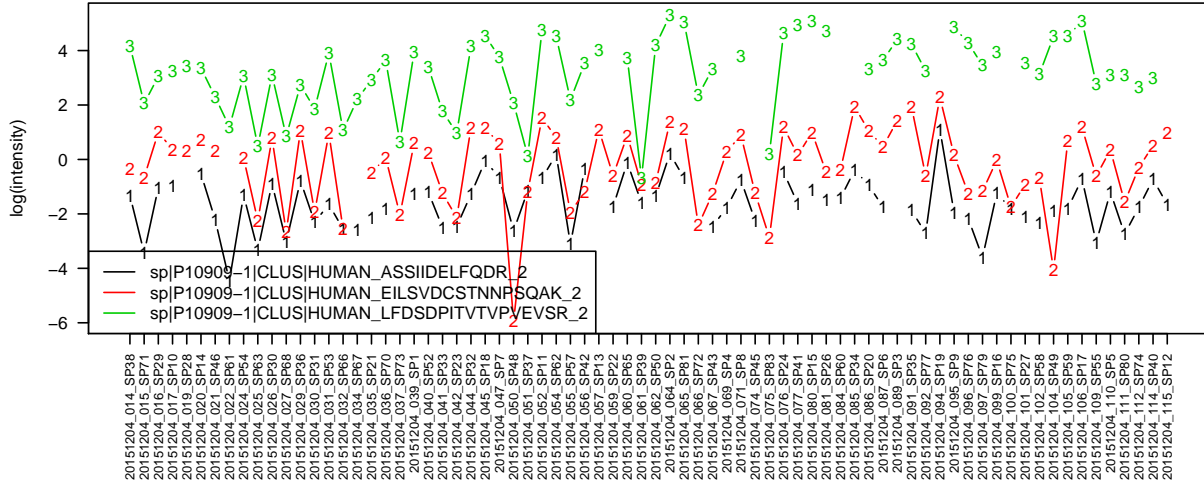
sp|P14780|MMP9|HUMAN

sp|P22894|MMP8|HUMAN

23
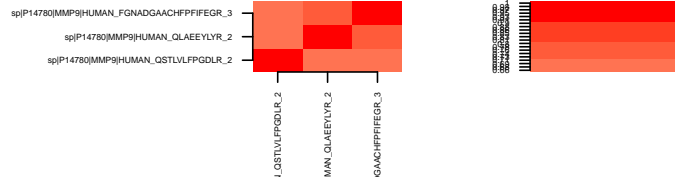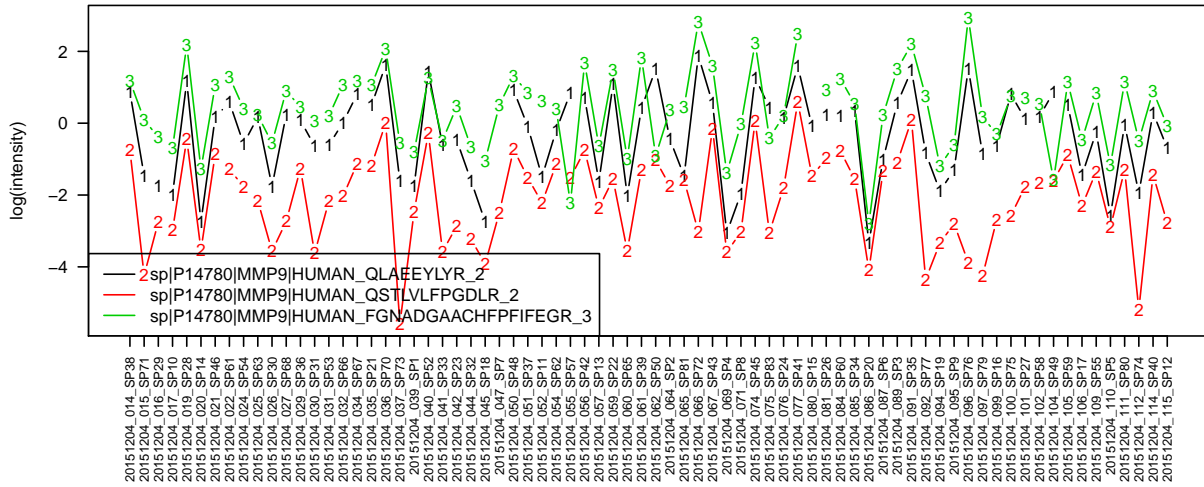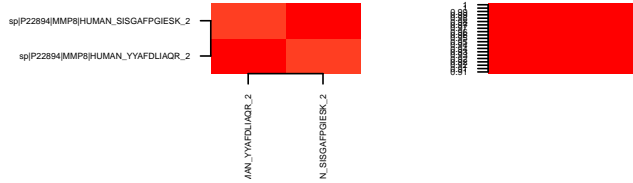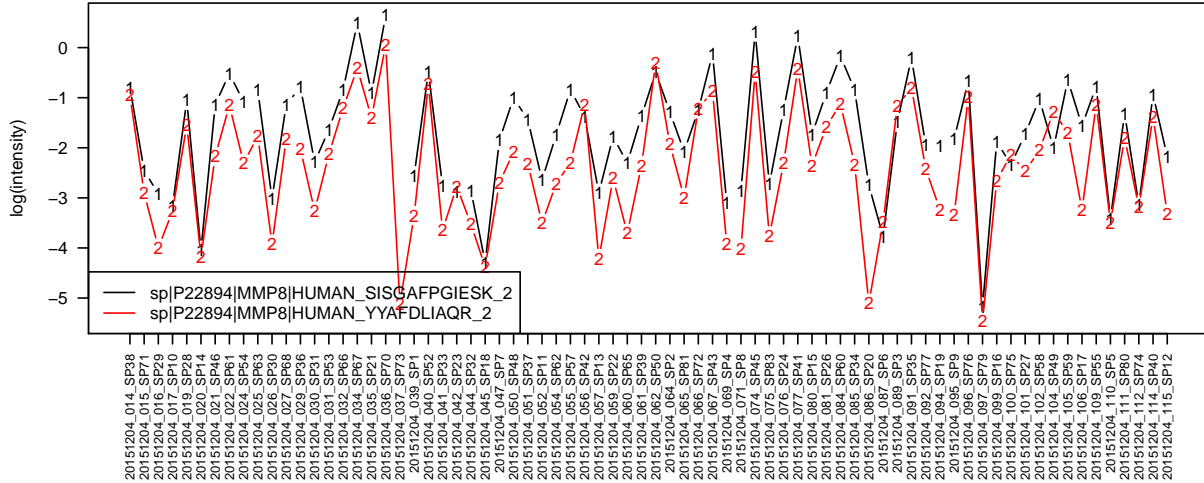
sp|P23280|CAH6|HUMAN
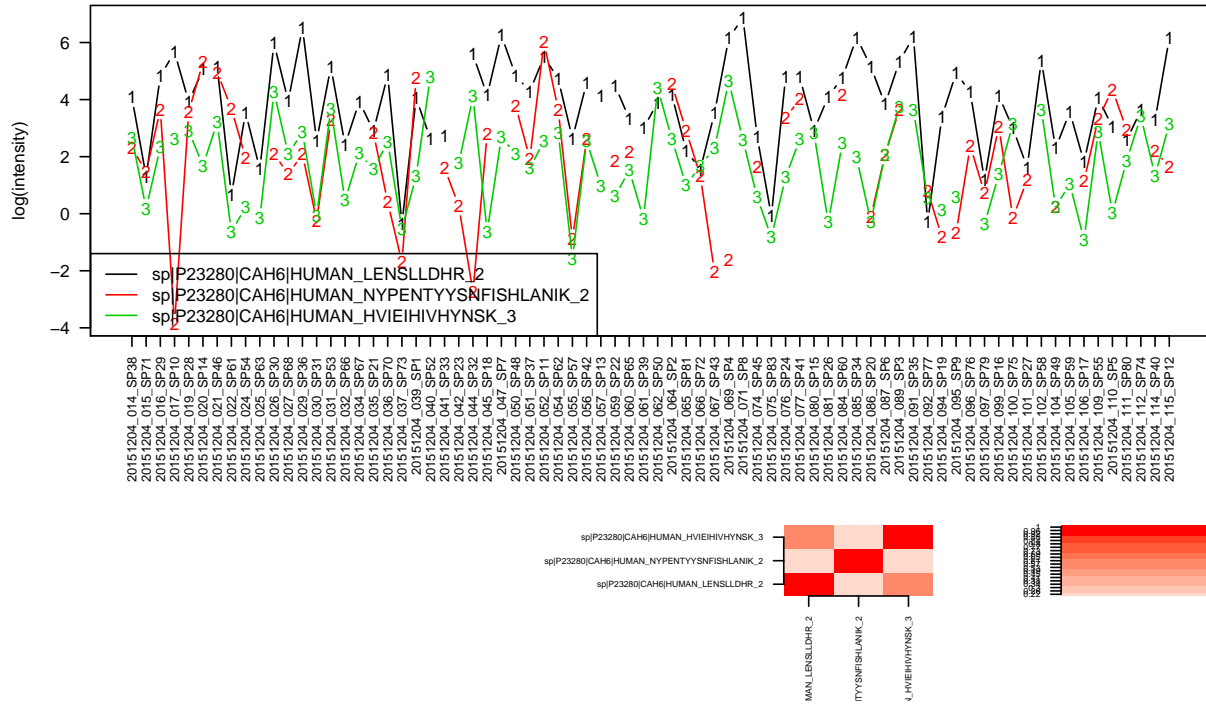
sp|P29508−1|SPB3|HUMAN
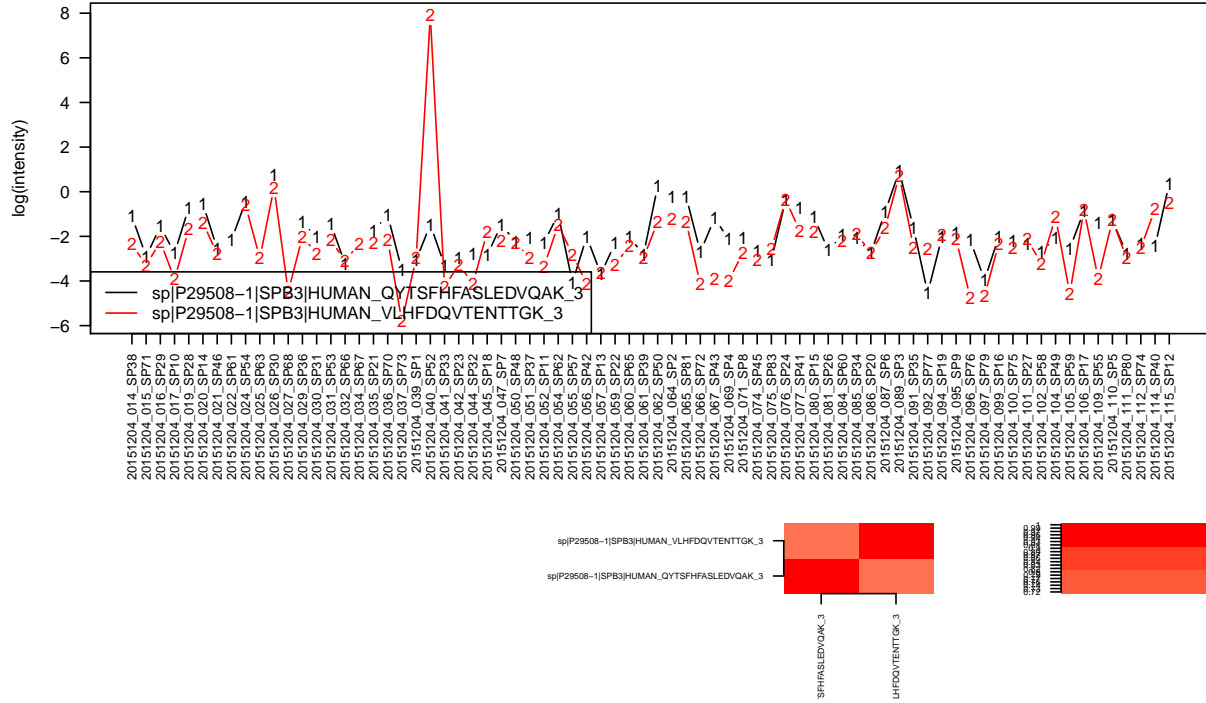
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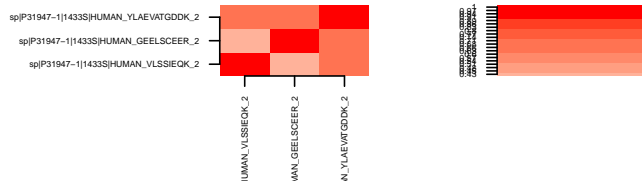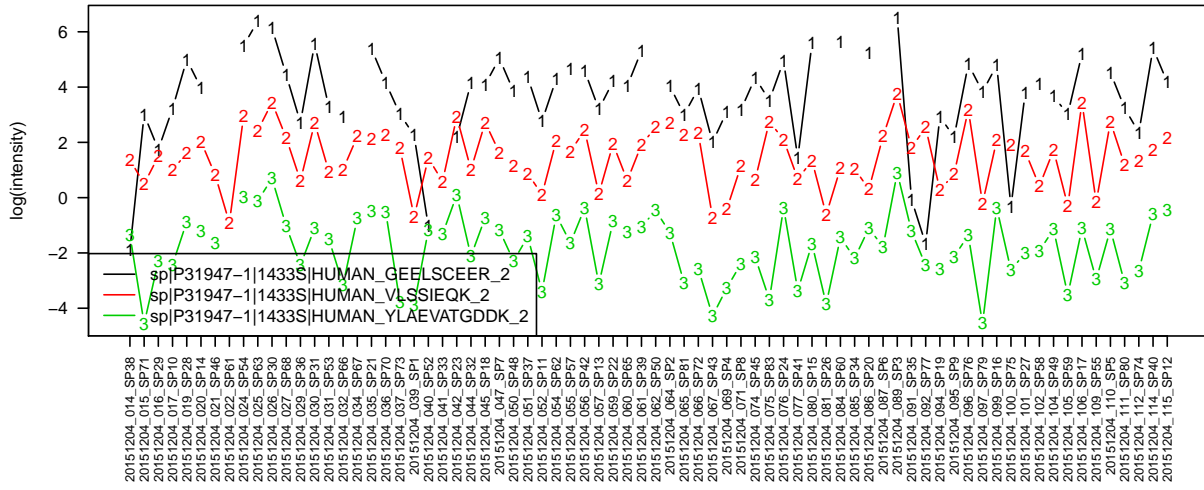
sp|P48595|SPB10|HUMAN
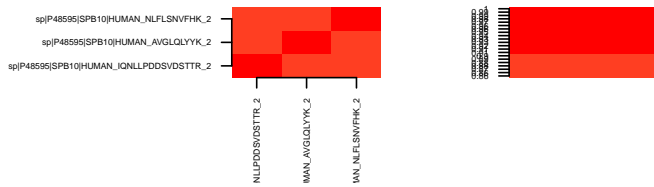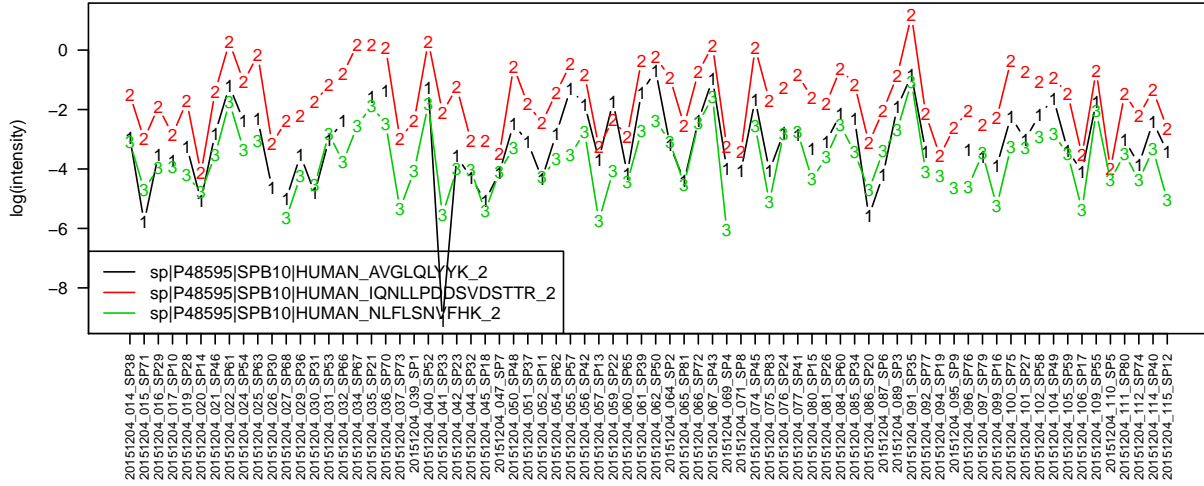
sp|P50552|VASP|HUMAN

sp|P52566|GDIR2|HUMAN

26
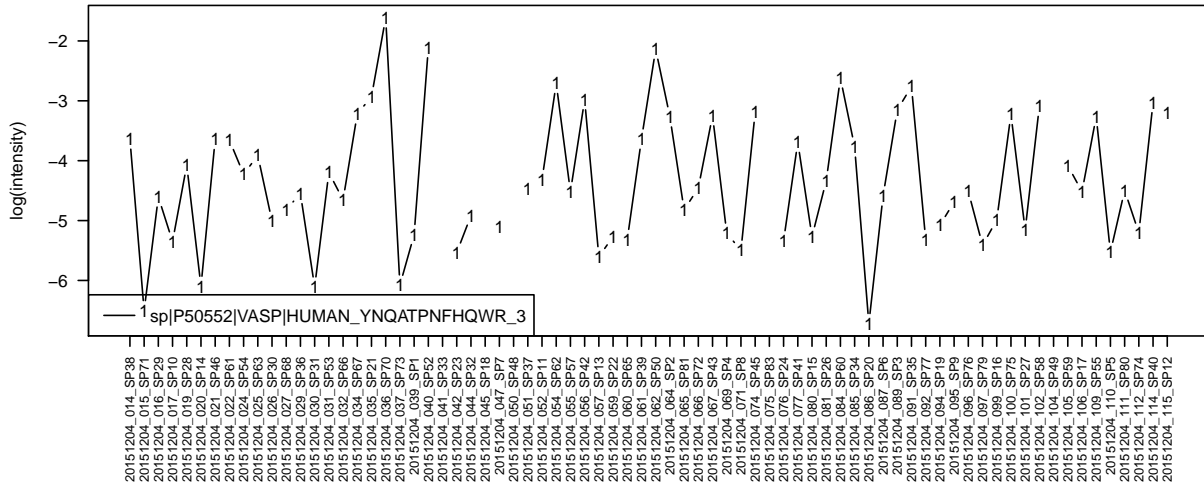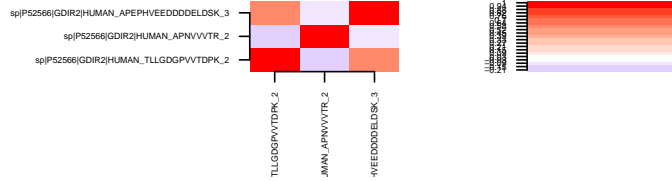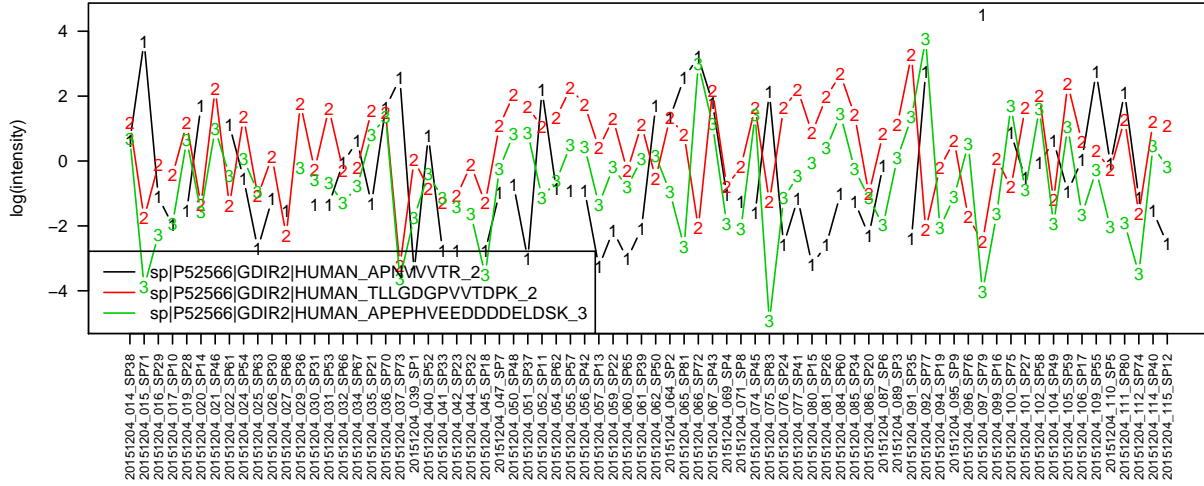
sp|P54108|CRIS3|HUMAN

sp|P68032|ACTC|HUMAN

27
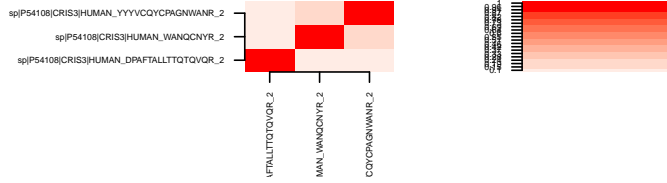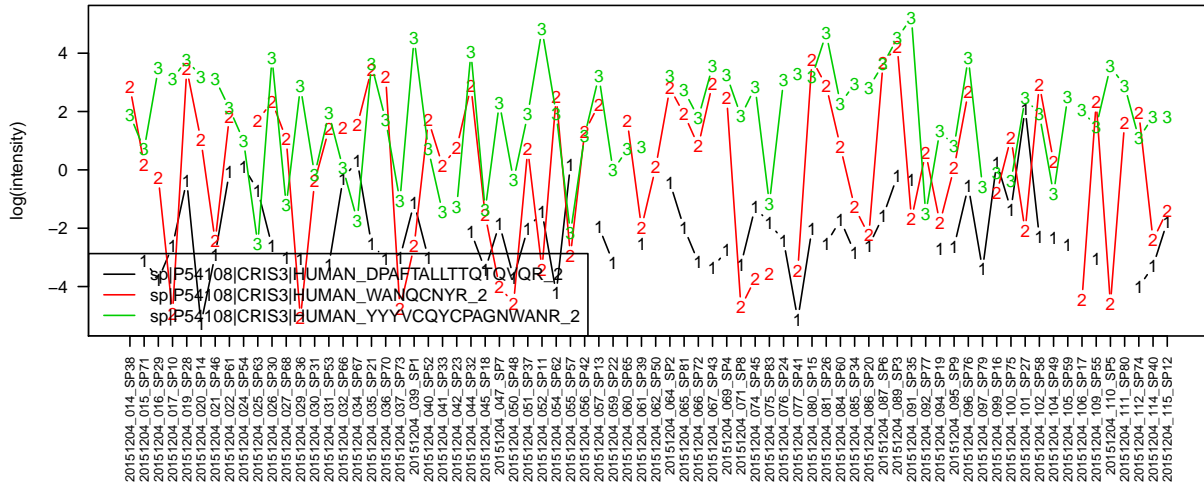
sp|P69905|HBA|HUMAN

sp|P69905|HBA|HUMAN_FLASVSTVLTSK_2
sp|P69905|HBA|HUMAN_TYFPHFDLSHGSAQVK_2
sp|P69905|HBA|HUMAN_VGAHAGEYGAEALER_3
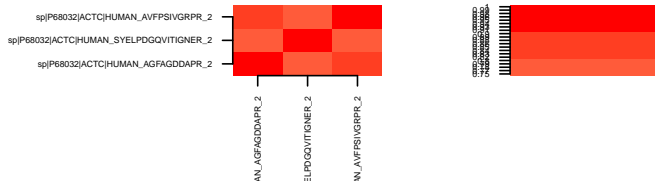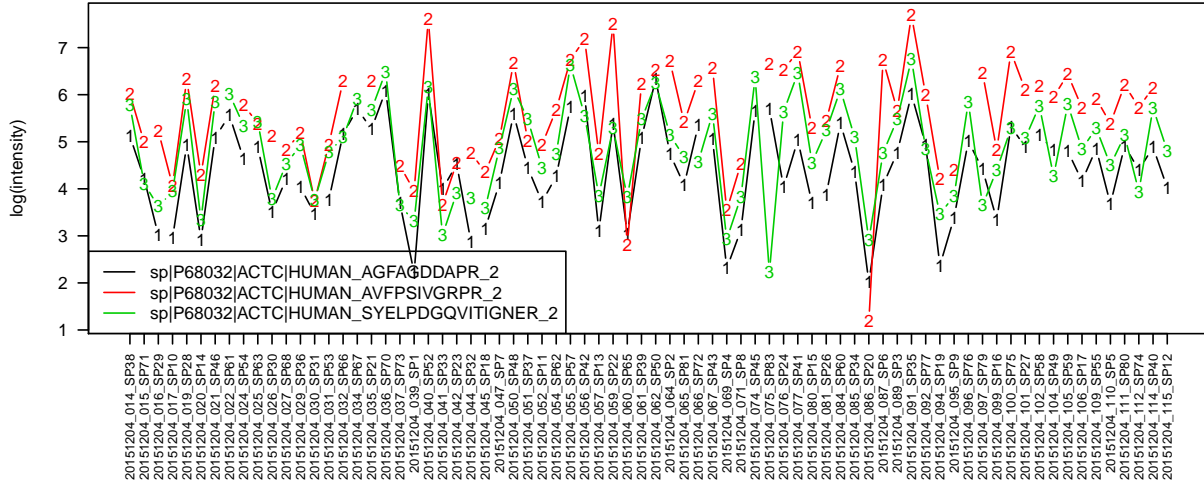
sp|P80723−1|BASP1|HUMAN

sp|P80723−1|BASP1|HUMAN_ESEPQAAAEPAEAK_2
sp|P80723−1|BASP1|HUMAN_ETPAATEAPSSTPK_2
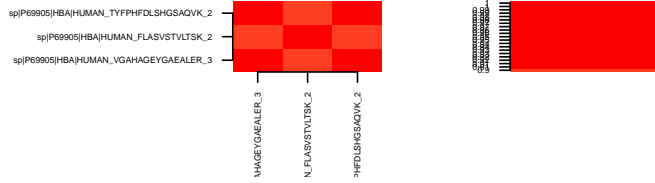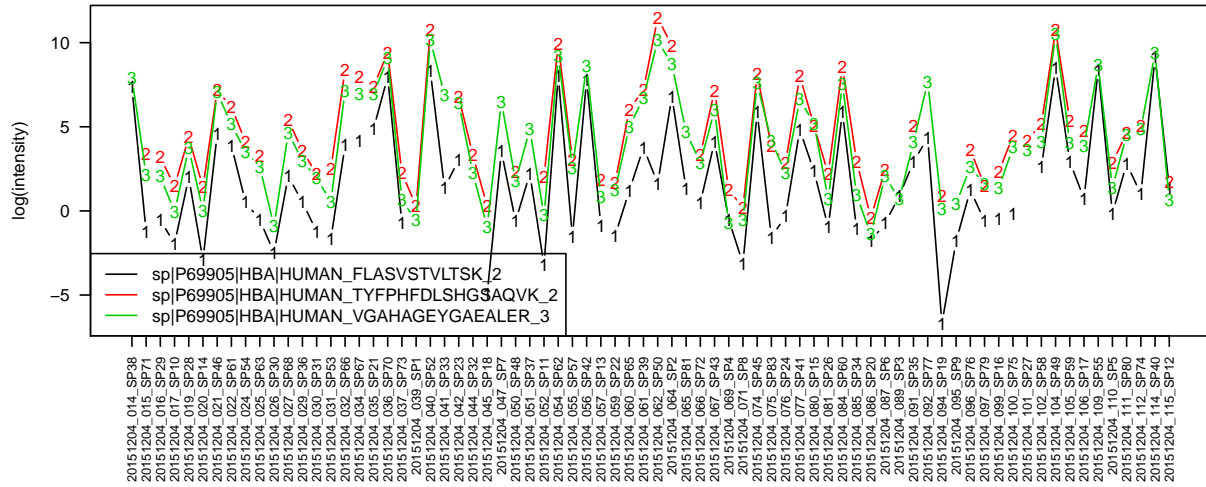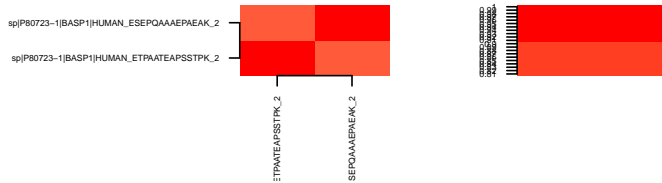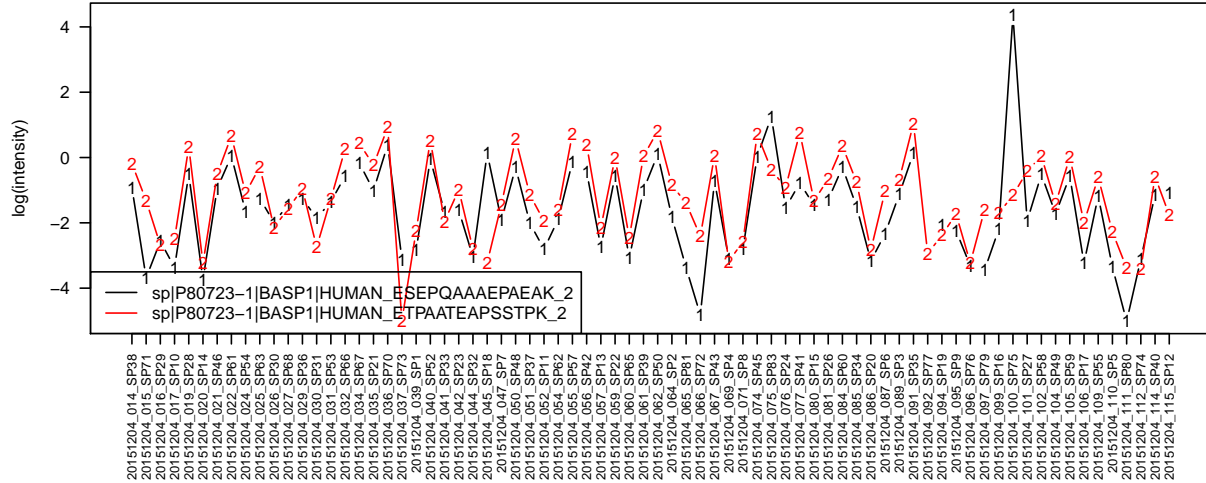
sp|Q14019|COTL1|HUMAN
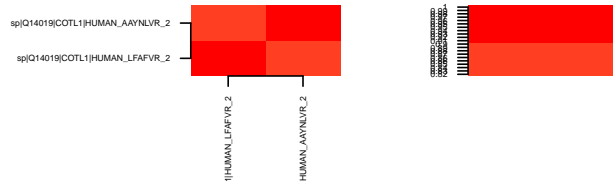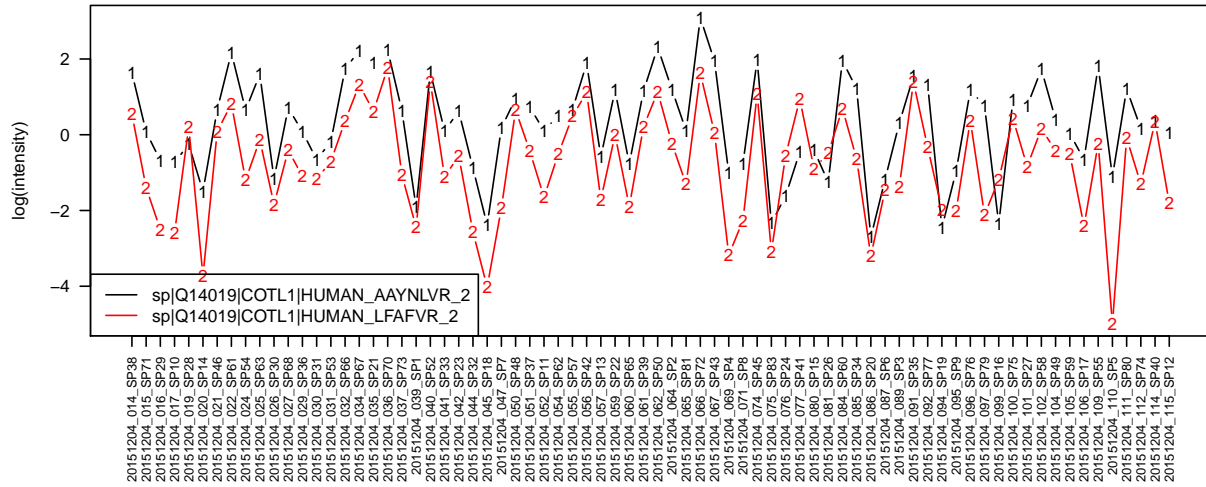
sp|Q16610−1|ECM1|HUMAN
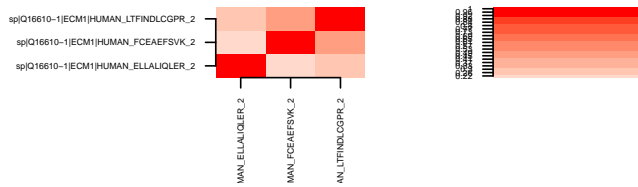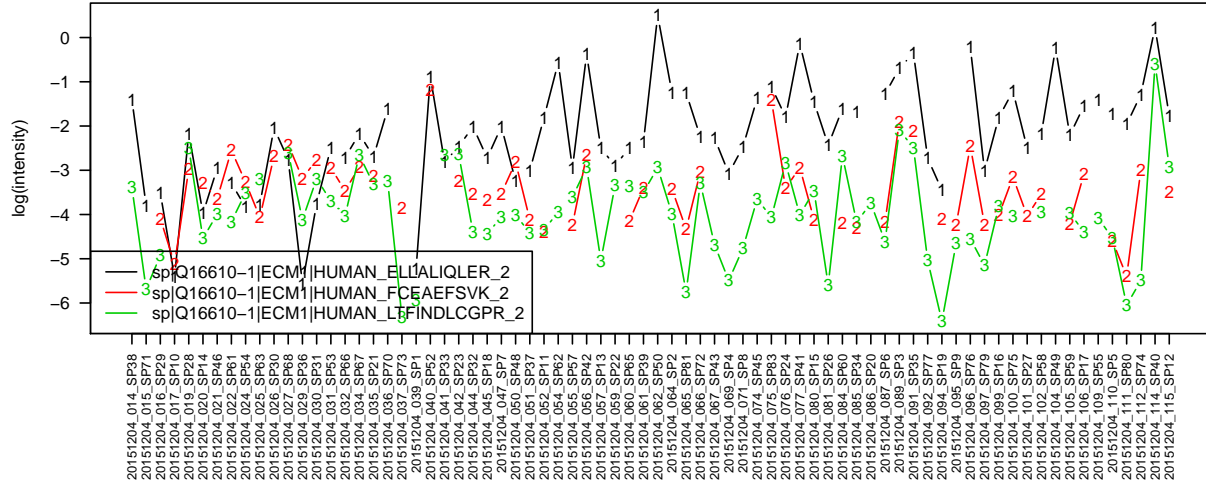
sp|Q9NP99−1|TREM1|HUMAN
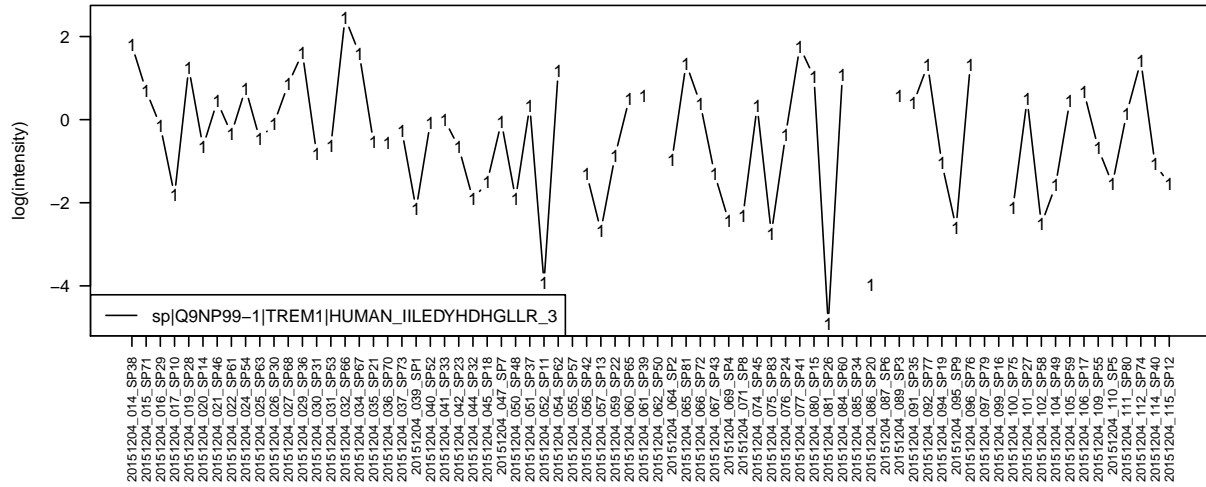
sp|Q9UGM3−1|DMBT1|HUMAN
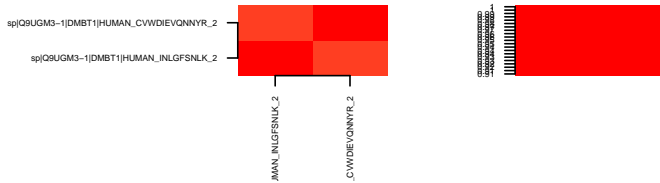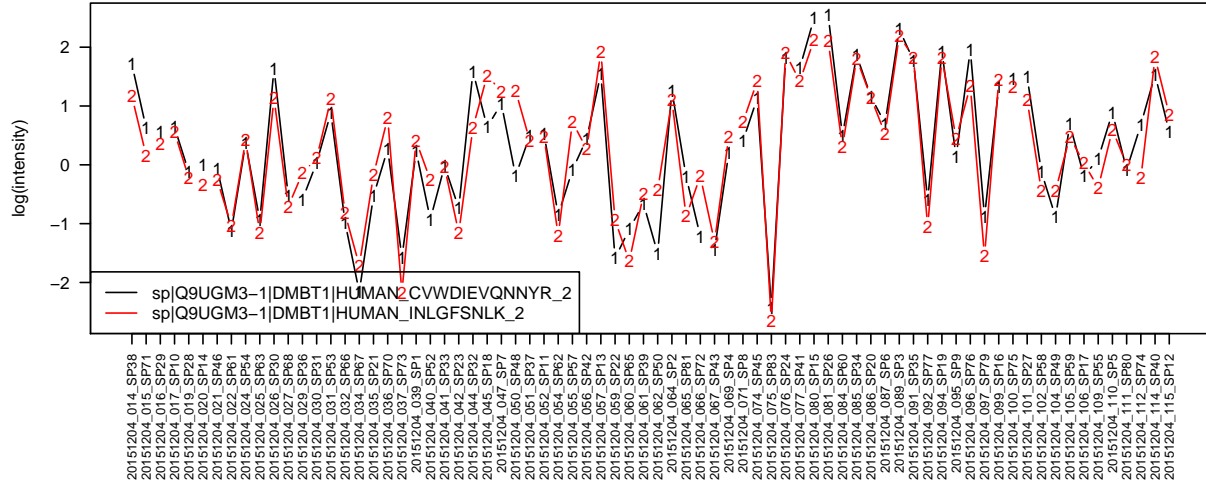
zz|ZZ|FGCZCont0031|
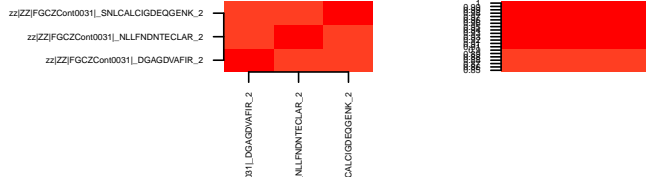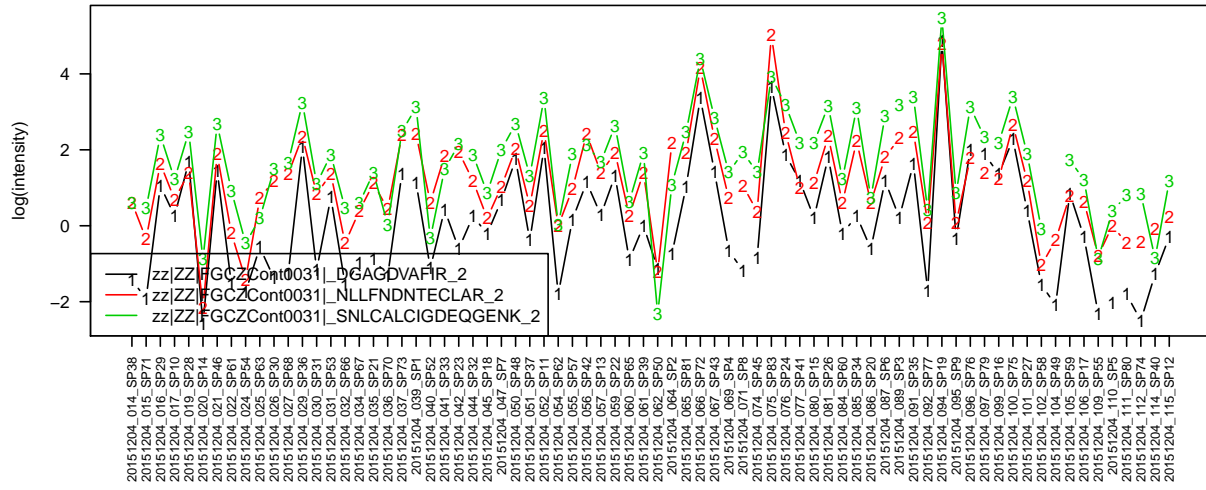
Peptides used for quantification and their transitions

sp|O15511−1|ARPC5|HUMAN_ALAAGGVGSIVR_2

sp|P00492|HPRT|HUMAN_FFADLLDYIK_2
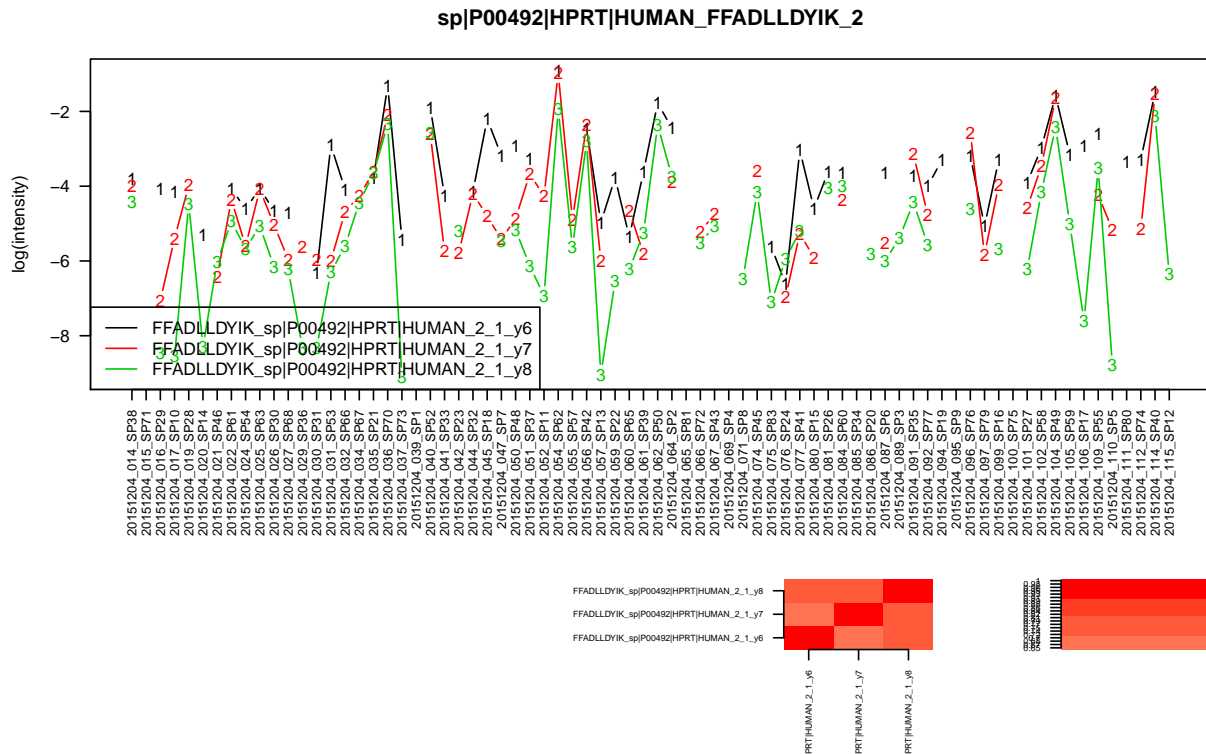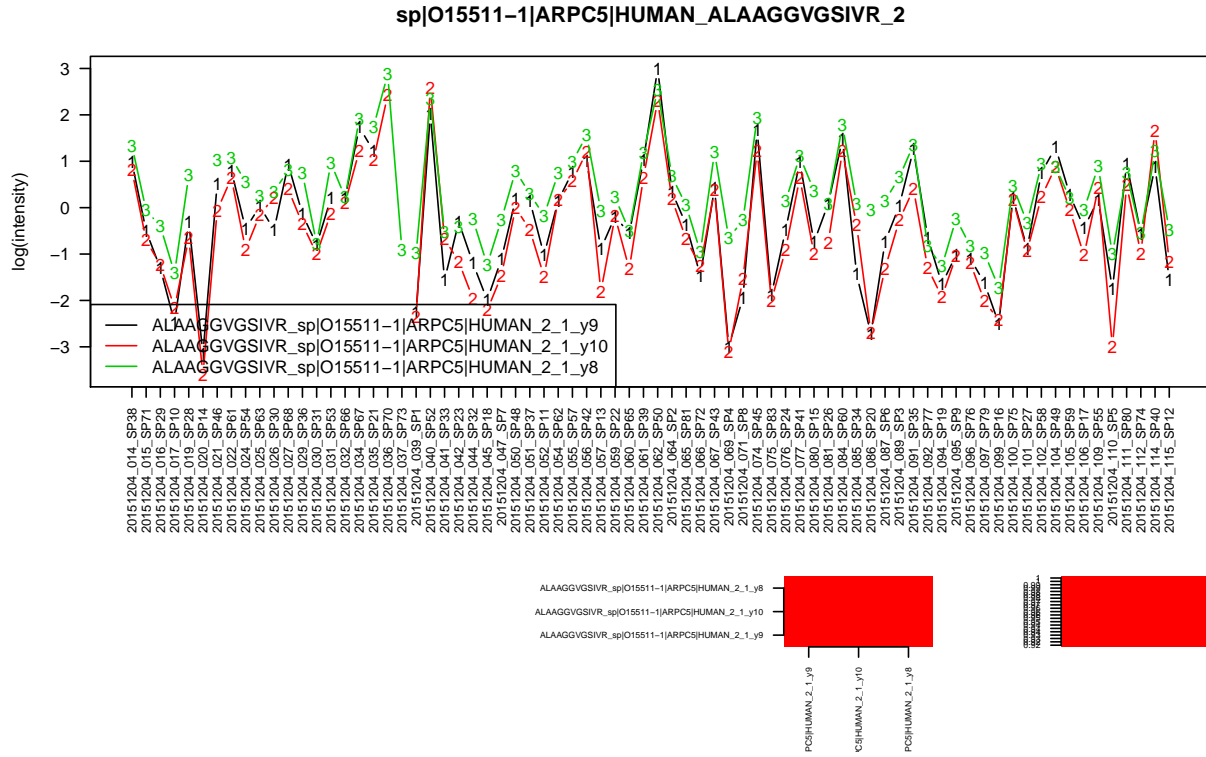
sp|P00492|HPRT|HUMAN_VIGGDDLSTLTGK_2

sp|P01023|A2MG|HUMAN_AAQVTIQSSGTFSSK_2

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sp|P01023|A2MG|HUMAN_NQGNTWLTAFVLK_2

sp|P01023|A2MG|HUMAN_VSVQLEASPAFLAVPVEK_2

sp|P01034|CYTC|HUMAN_ALDFAVGEYNK_2

sp|P01034|CYTC|HUMAN_ALQVVR_2

35

sp|P01034|CYTC|HUMAN_ASNDMYHSR_2

sp|P02675|FIBB|HUMAN_DNENVVNEYSSELEK_2

36
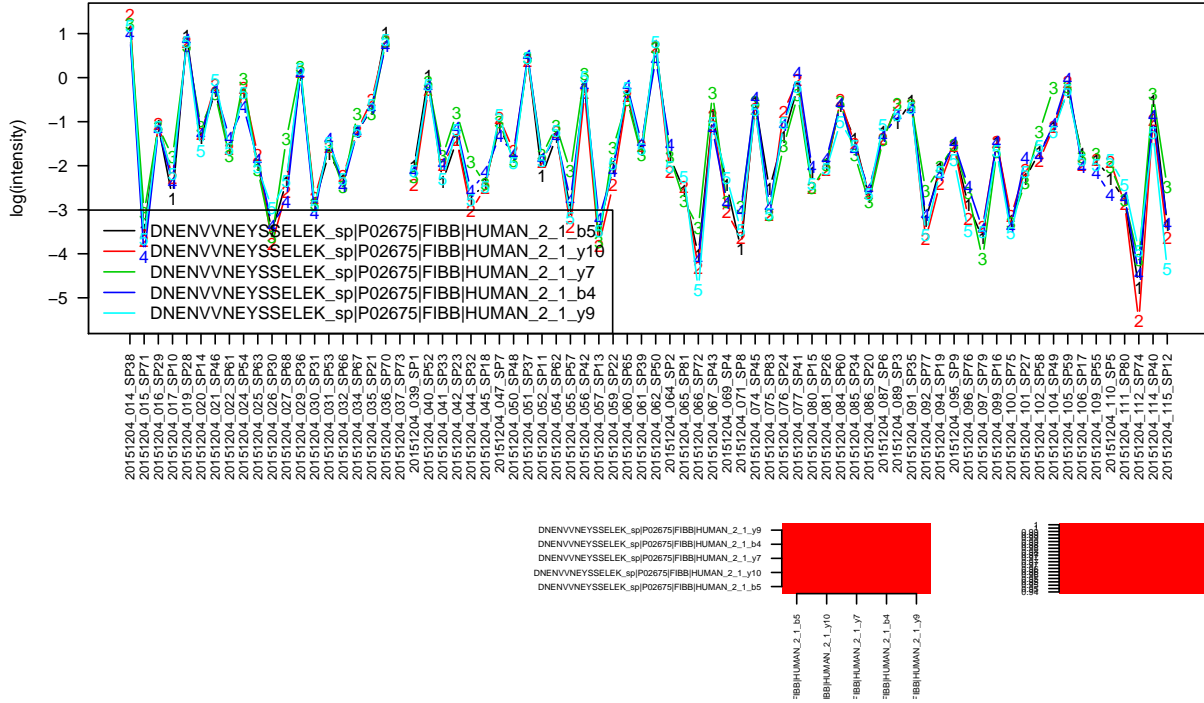
sp|P02675|FIBB|HUMAN_EDGGGWWYNR_2
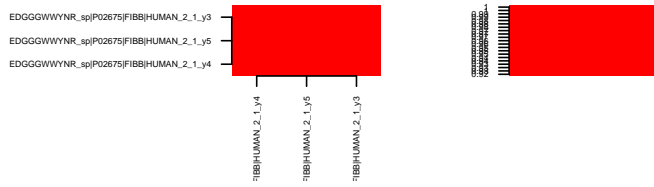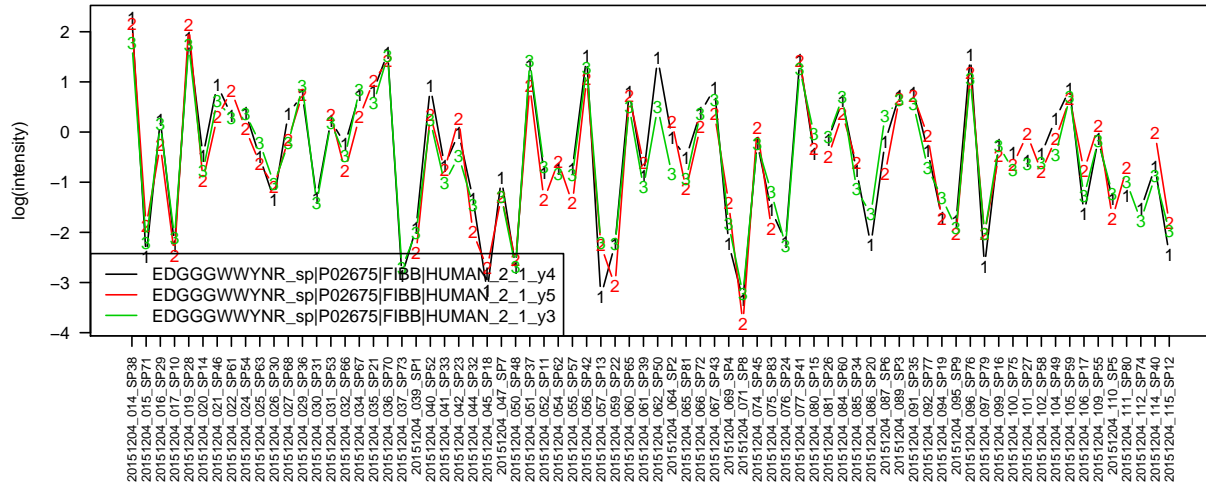
sp|P02675|FIBB|HUMAN_QDGSVDFGR_2

37
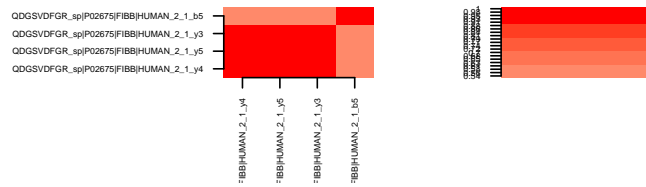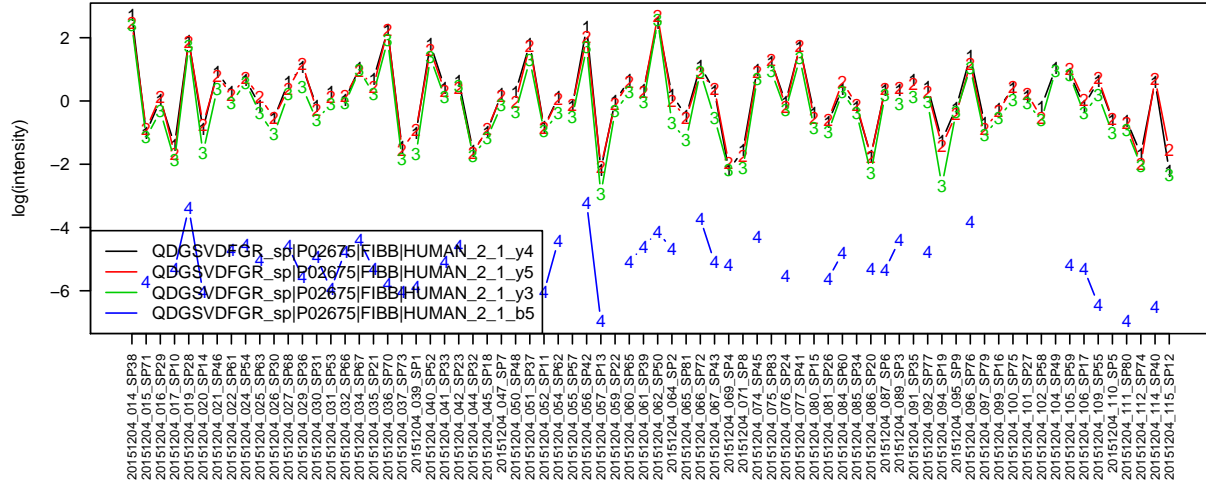
sp|P02768−1|ALBU|HUMAN_FQNALLVR_2
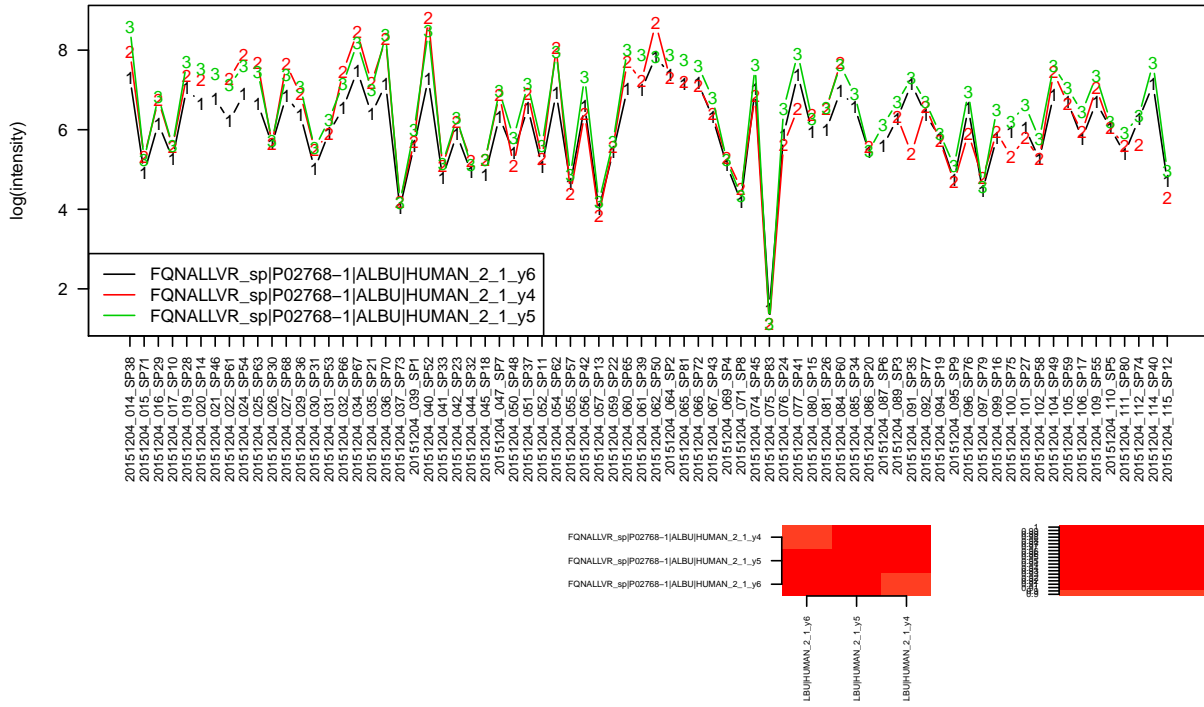
sp|P02768−1|ALBU|HUMAN_QNCELFEQLGEYK_2
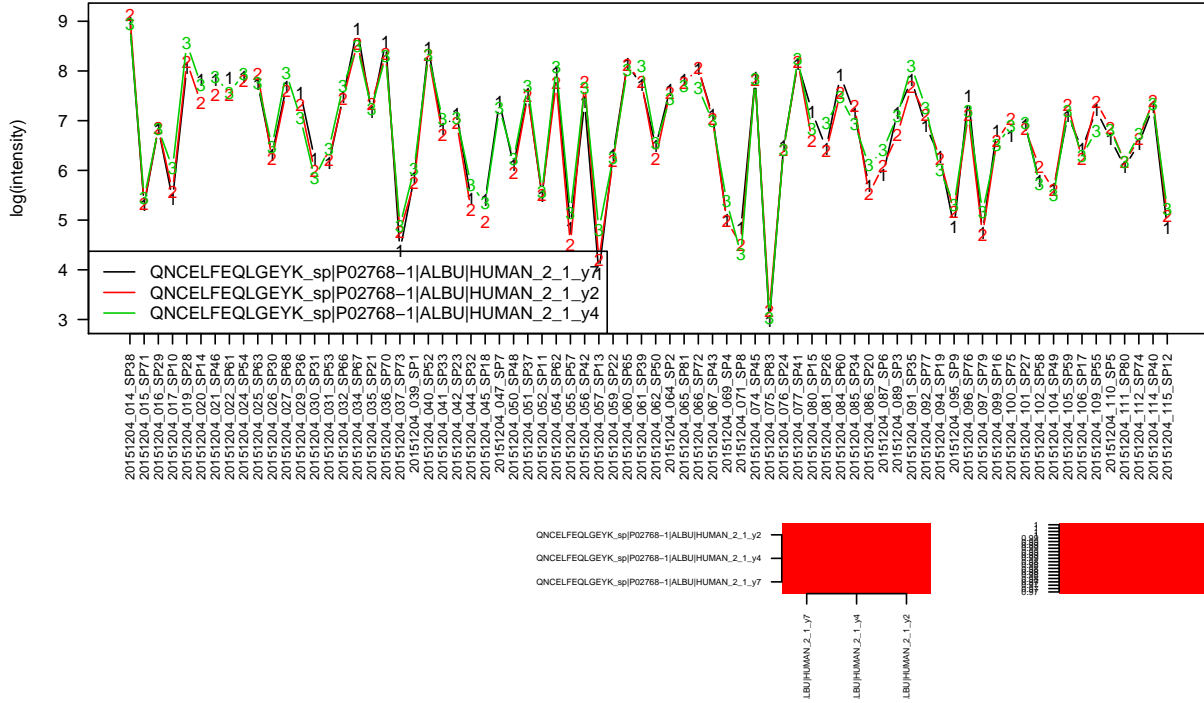
sp|P02768−1|ALBU|HUMAN_VFDEFKPLVEEPQNLIK_3

Legend:
- VFDEFKPLVEEPQNLIK_sp|P02768−1|ALBU|HUMAN_3_2_y13
- VFDEFKPLVEEPQNLIK_sp|P02768−1|ALBU|HUMAN_3_1_y6
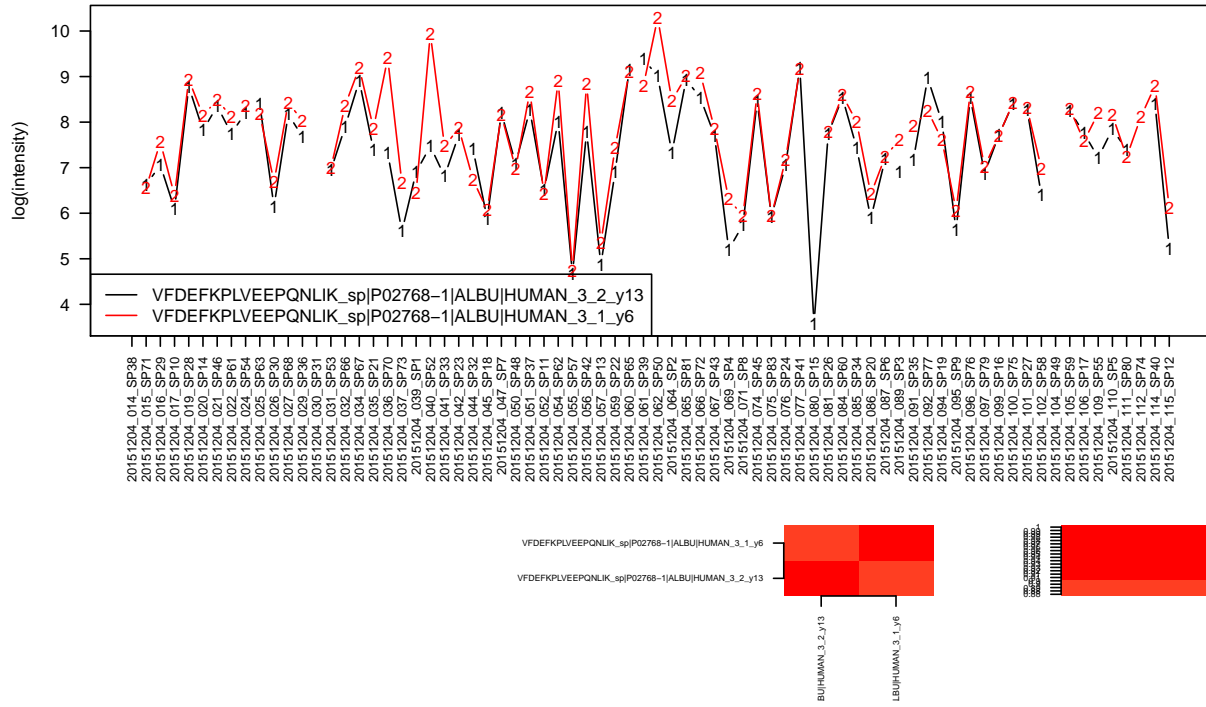
sp|P02790|HEMO|HUMAN_QGHNSVFLIK_3

Legend:
- QGHNSVFLIK_sp|P02790|HEMO|HUMAN_3_1_y4
- QGHNSVFLIK_sp|P02790|HEMO|HUMAN_3_2_y9
- QGHNSVFLIK_sp|P02790|HEMO|HUMAN_3_1_y3
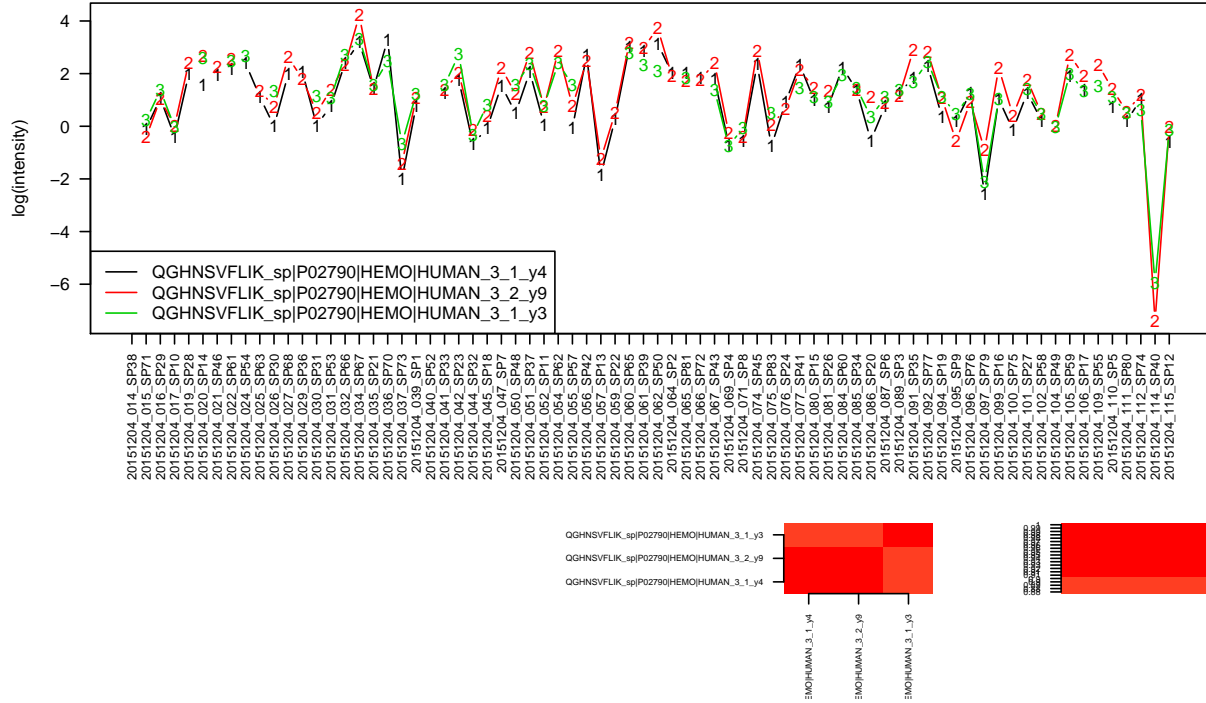
sp|P02790|HEMO|HUMAN_SGAQATWTELPWPHEK_3
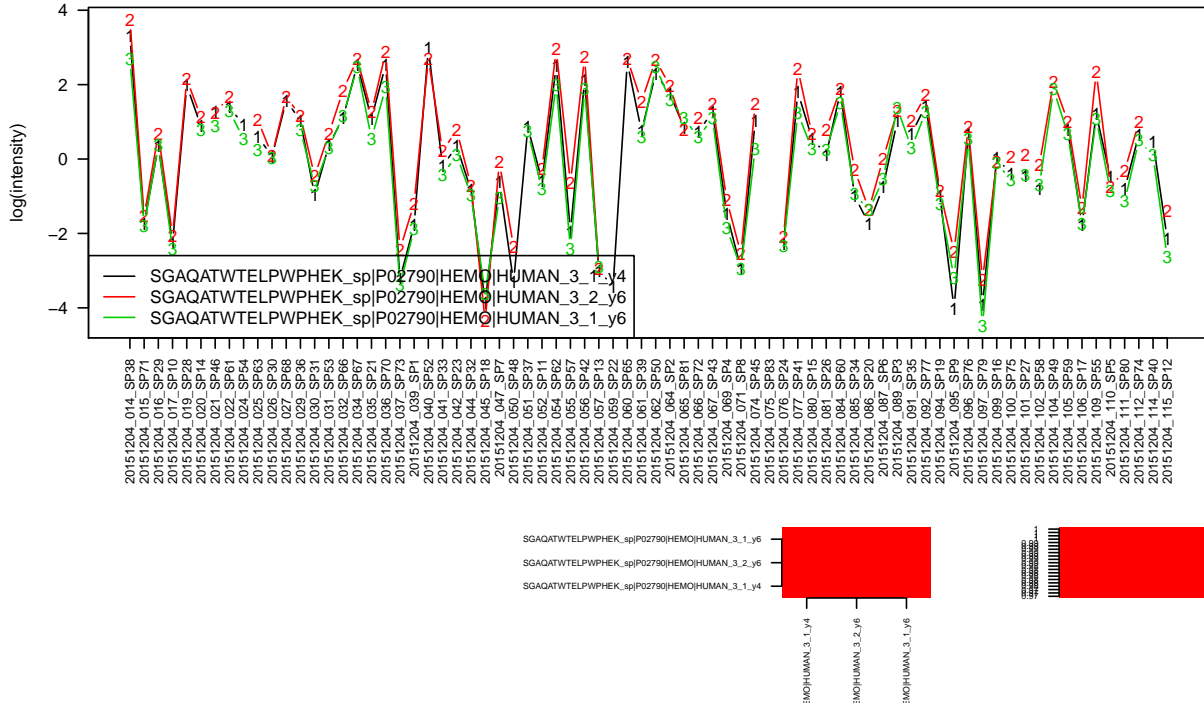
sp|P02790|HEMO|HUMAN_VWVYPPEK_2
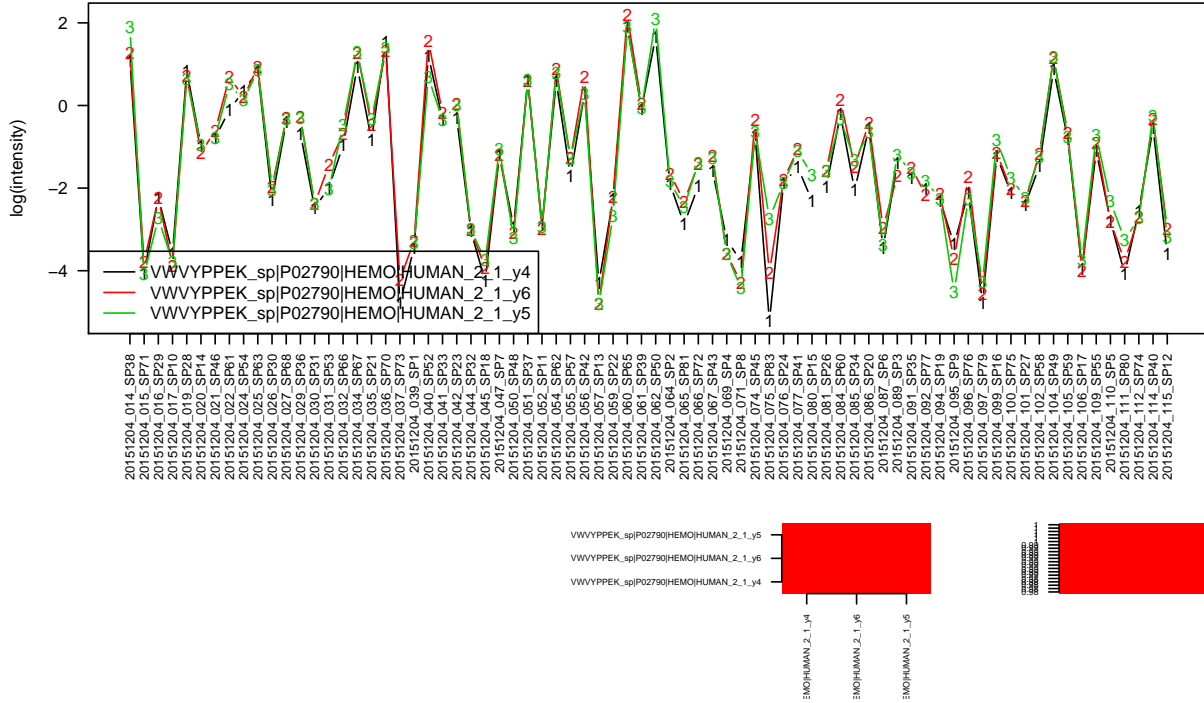
sp|P04083|ANXA1|HUMAN_ALTGHLEEVVLALLK_3
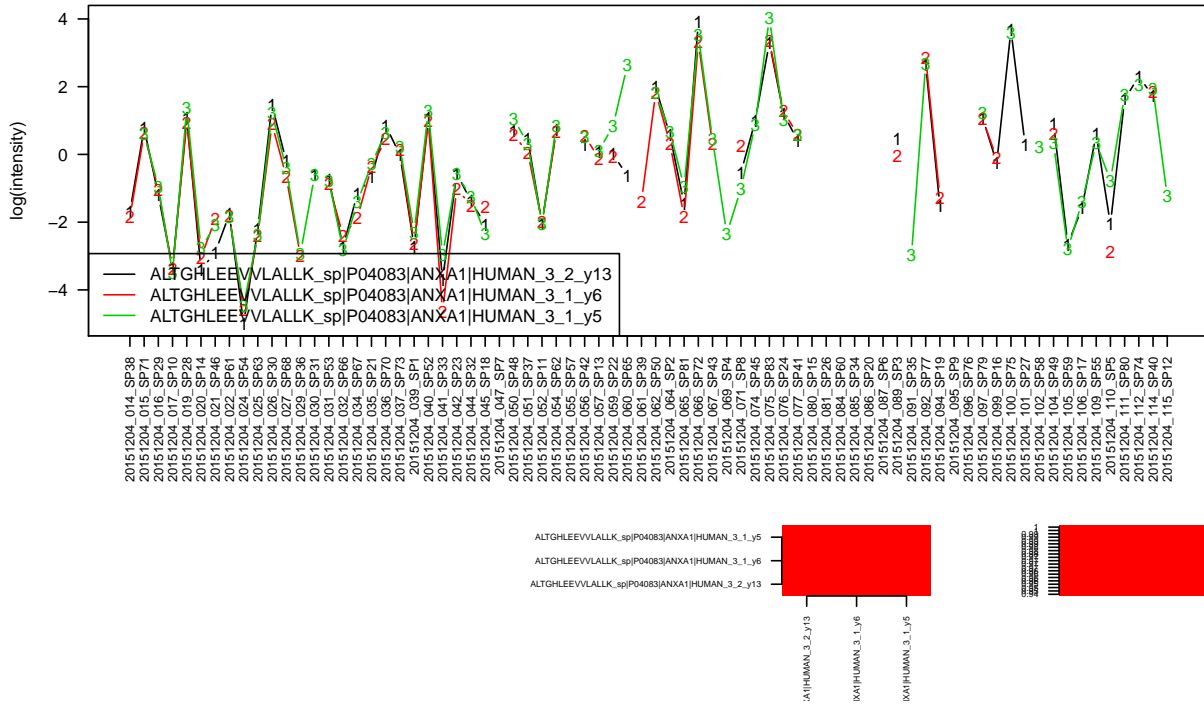
sp|P04083|ANXA1|HUMAN_GLGTDEDTLIEILASR_2
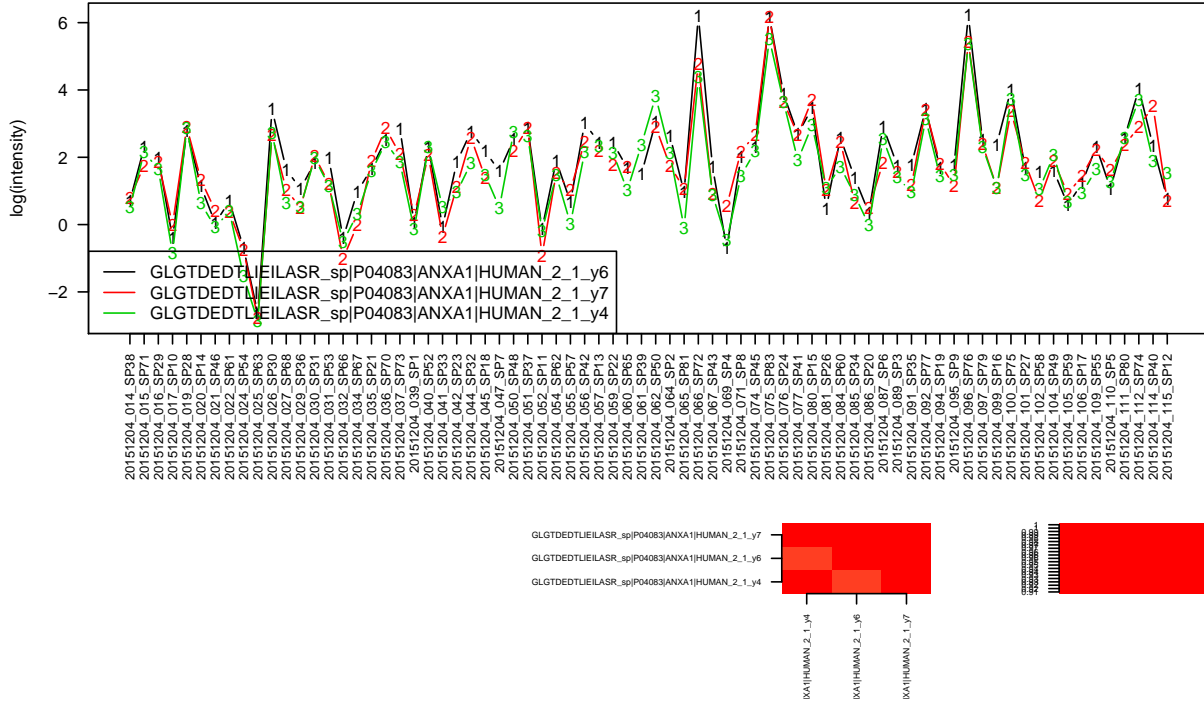
sp|P04083|ANXA1|HUMAN_GVDEATIIDILTK_2
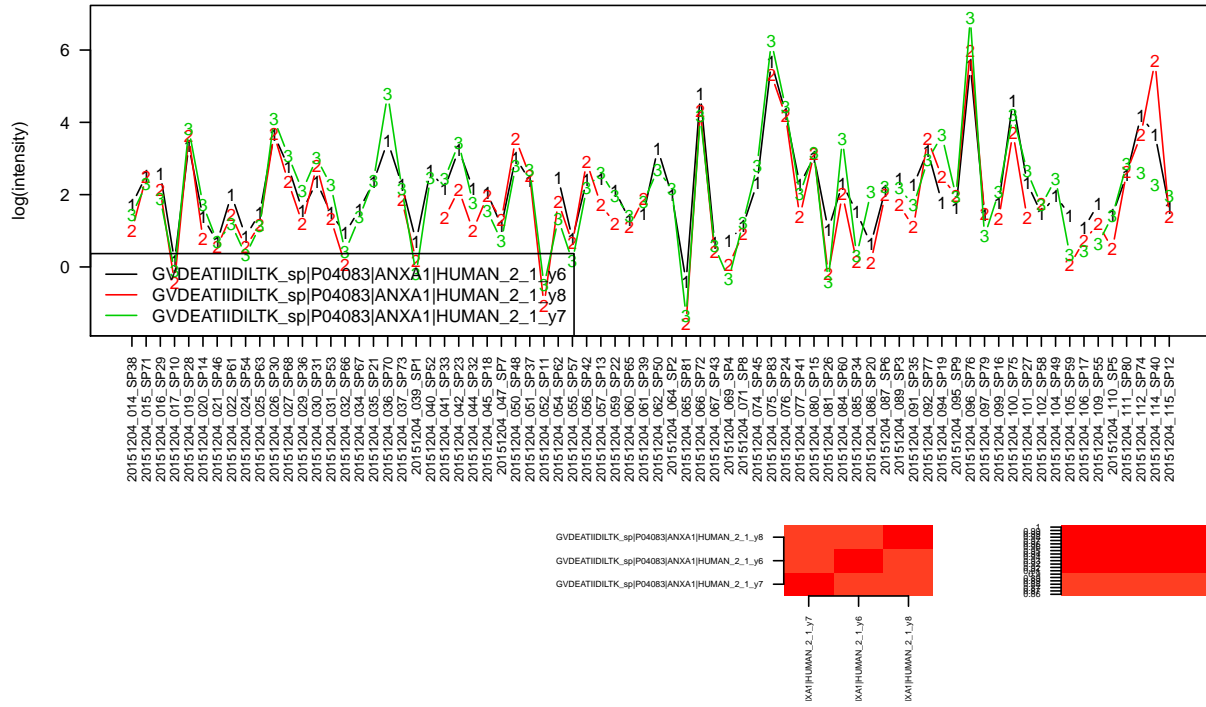
sp|P05109|S10A8|HUMAN_ALNSIIDVYHK_2
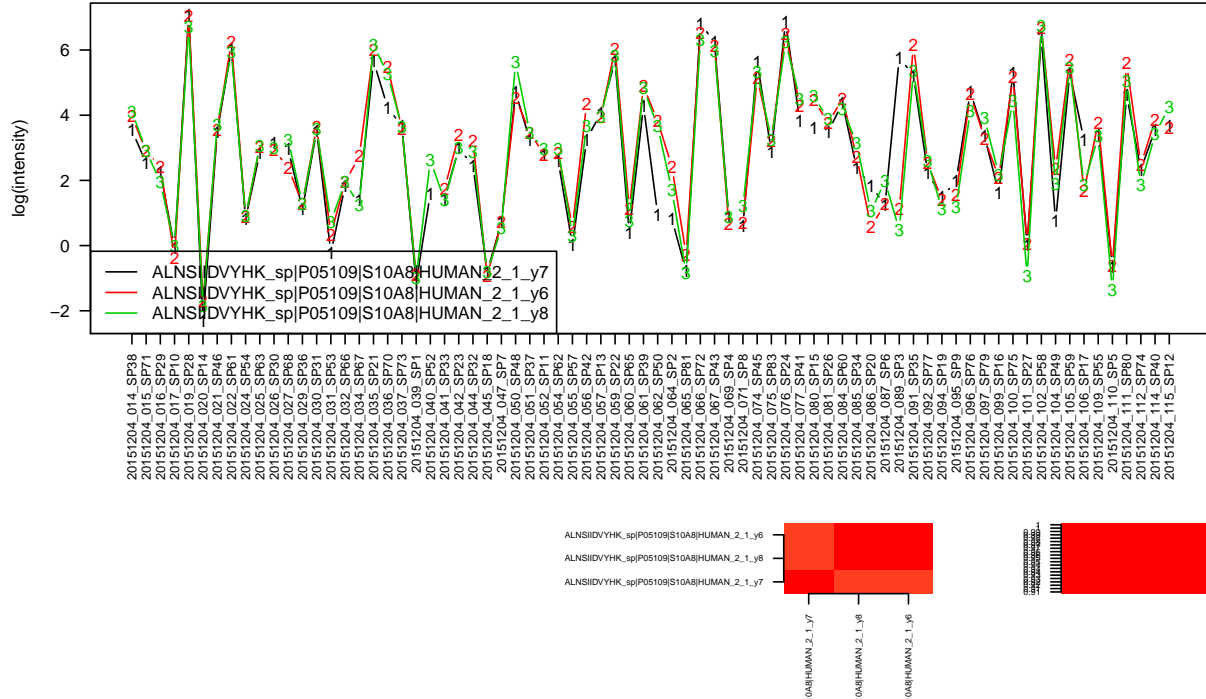
sp|P05109|S10A8|HUMAN_LLETECPQYIR_2

Legend:
- LLETECPQYIR_sp|P05109|S10A8|HUMAN_2_1_y5
- LLETECPQYIR_sp|P05109|S10A8|HUMAN_2_1_y6
- LLETECPQYIR_sp|P05109|S10A8|HUMAN_2_1_y7
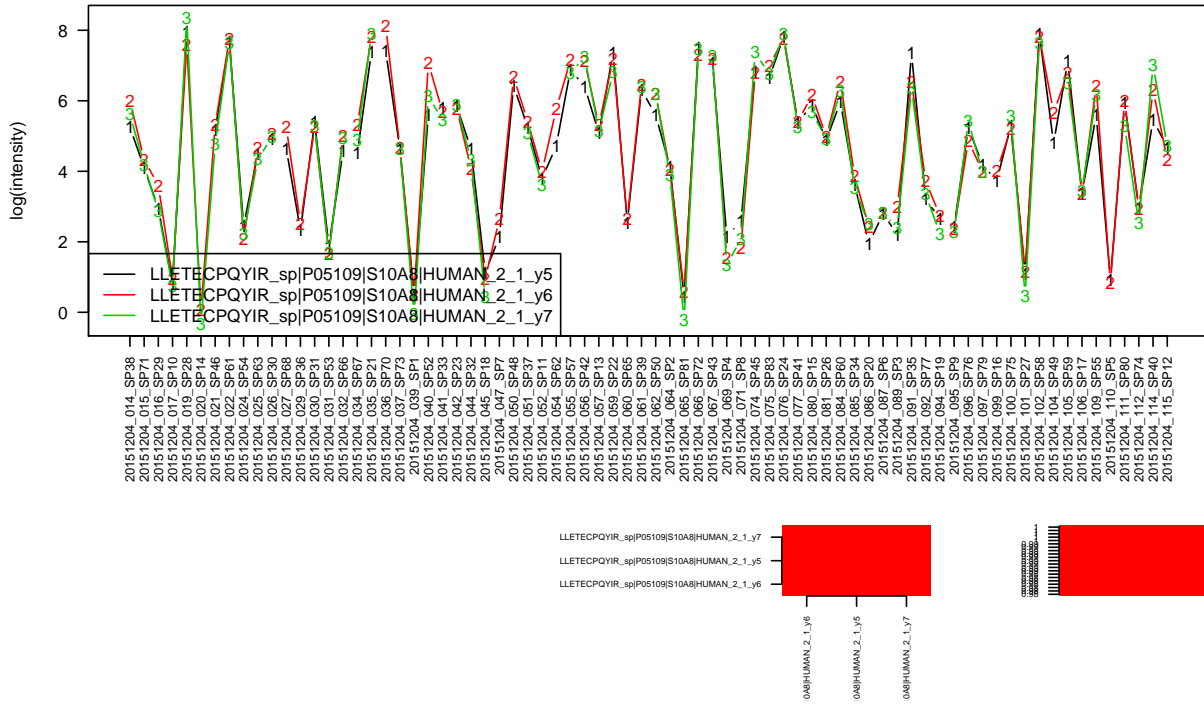
sp|P05204|HMGN2|HUMAN_LSAKPAPPKPEPKPK_3

Legend:
- LSAKPAPPKPEPKPK_sp|P05204|HMGN2|HUMAN_3_2_y9
- LSAKPAPPKPEPKPK_sp|P05204|HMGN2|HUMAN_3_1_y4
- LSAKPAPPKPEPKPK_sp|P05204|HMGN2|HUMAN_3_1_y6

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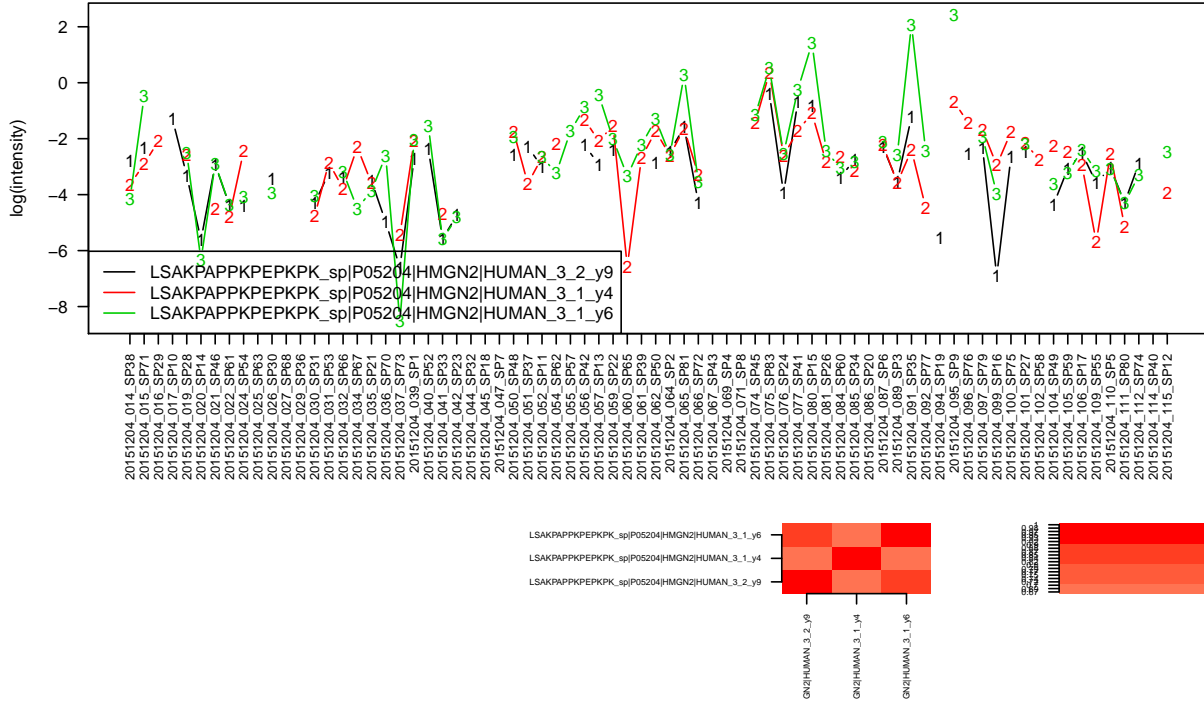
sp|P06733−1|ENOA|HUMAN_IGAEVYHNLK_2

Legend:
- IGAEVYHNLK_sp|P06733−1|ENOA|HUMAN_2_2_y9
- IGAEVYHNLK_sp|P06733−1|ENOA|HUMAN_2_1_y5
- IGAEVYHNLK_sp|P06733−1|ENOA|HUMAN_2_2_y8
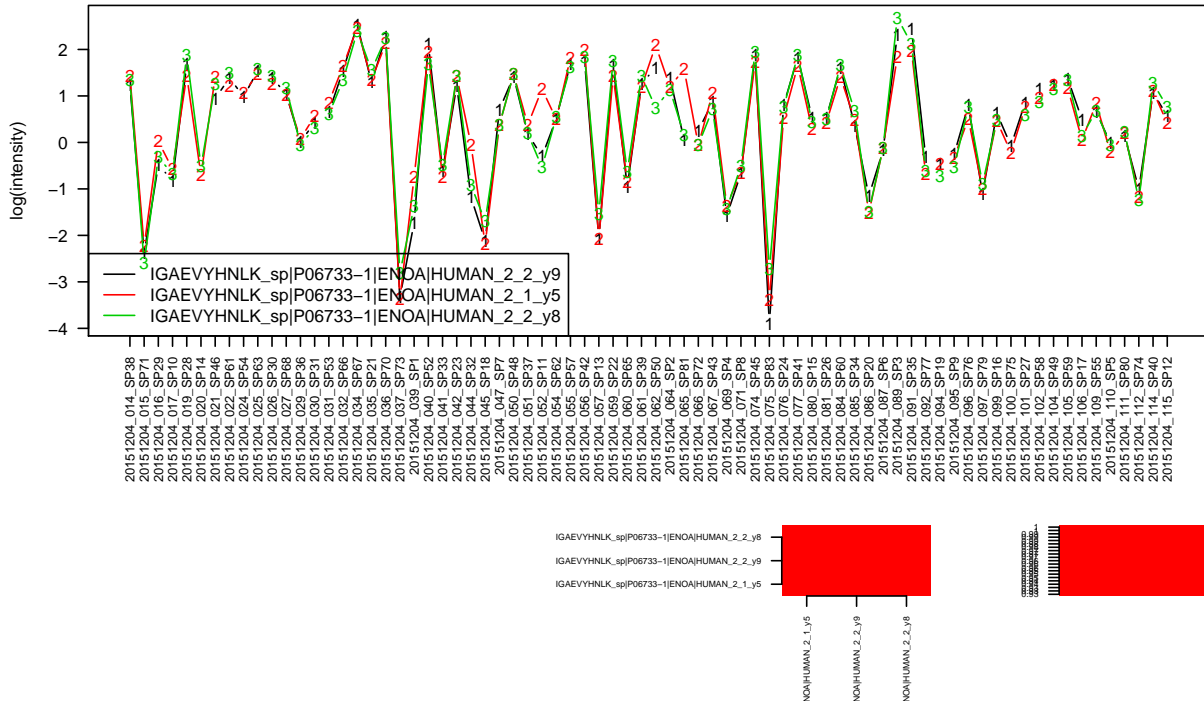
sp|P06733−1|ENOA|HUMAN_YISPDQLADLYK_2

Legend:
- YISPDQLADLYK_sp|P06733−1|ENOA|HUMAN_2_1_y5
- YISPDQLADLYK_sp|P06733−1|ENOA|HUMAN_2_1_b3
- YISPDQLADLYK_sp|P06733−1|ENOA|HUMAN_2_2_y10
- YISPDQLADLYK_sp|P06733−1|ENOA|HUMAN_2_2_y9
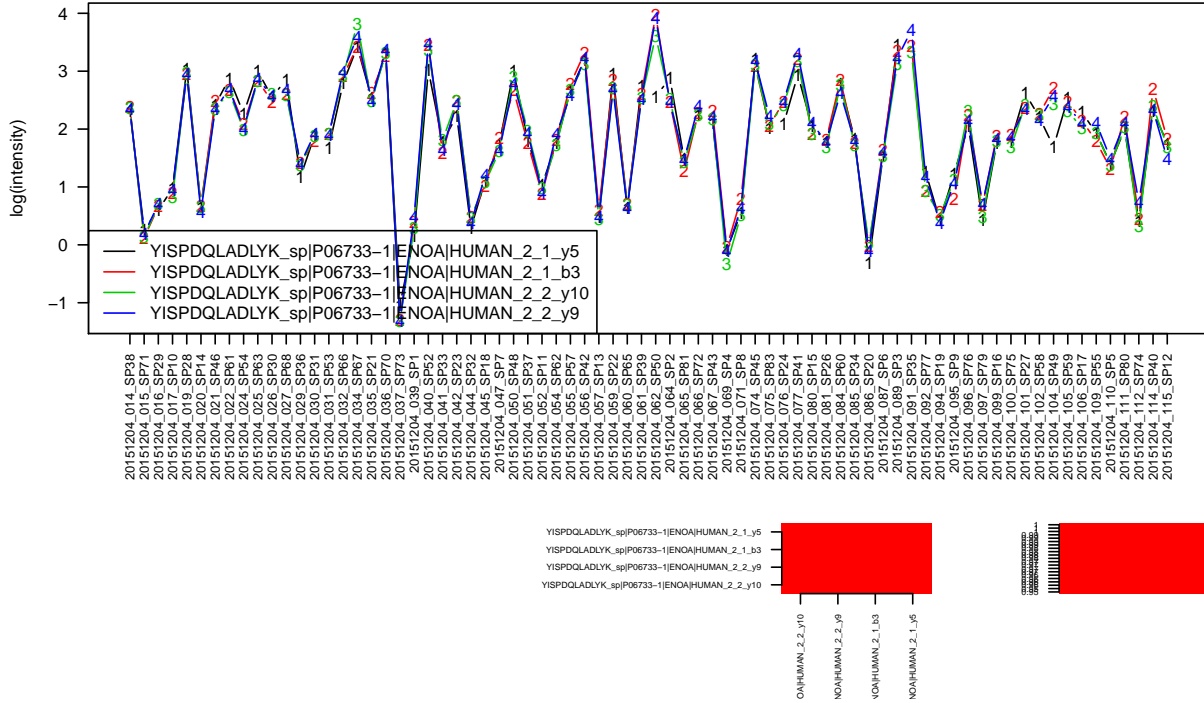
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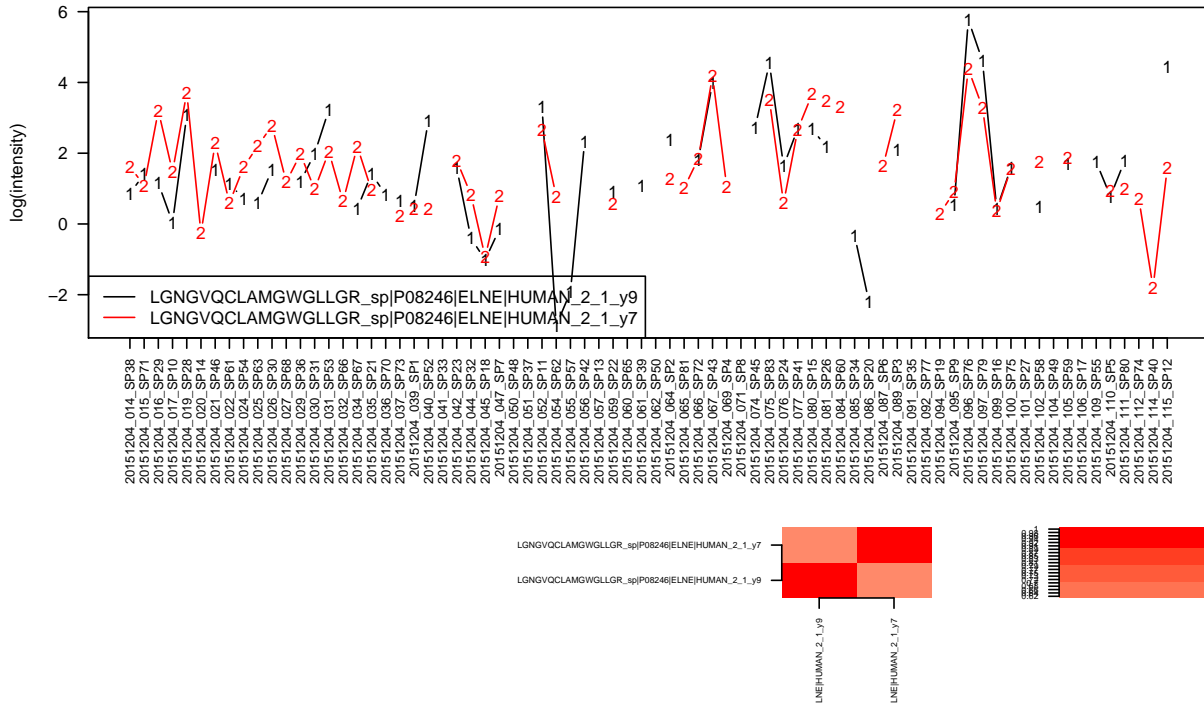
sp|P08246|ELNE|HUMAN_SNVCTLVR_2
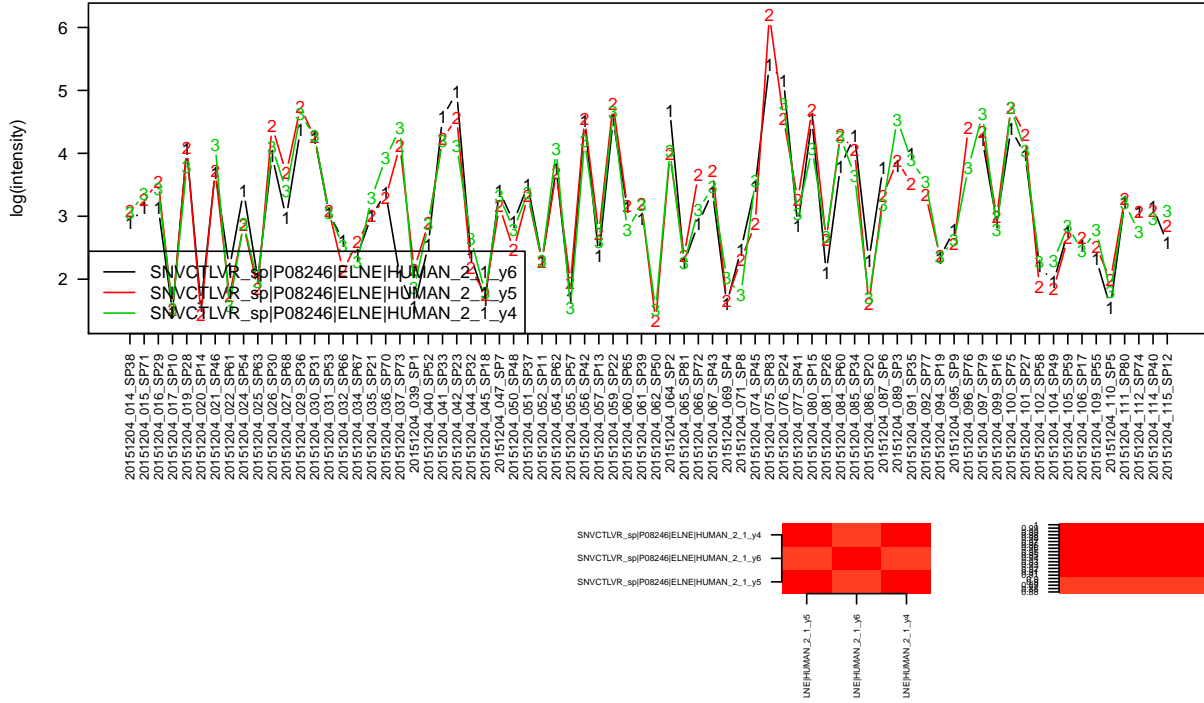
sp|P08246|ELNE|HUMAN_VVLGAHNLSR_3
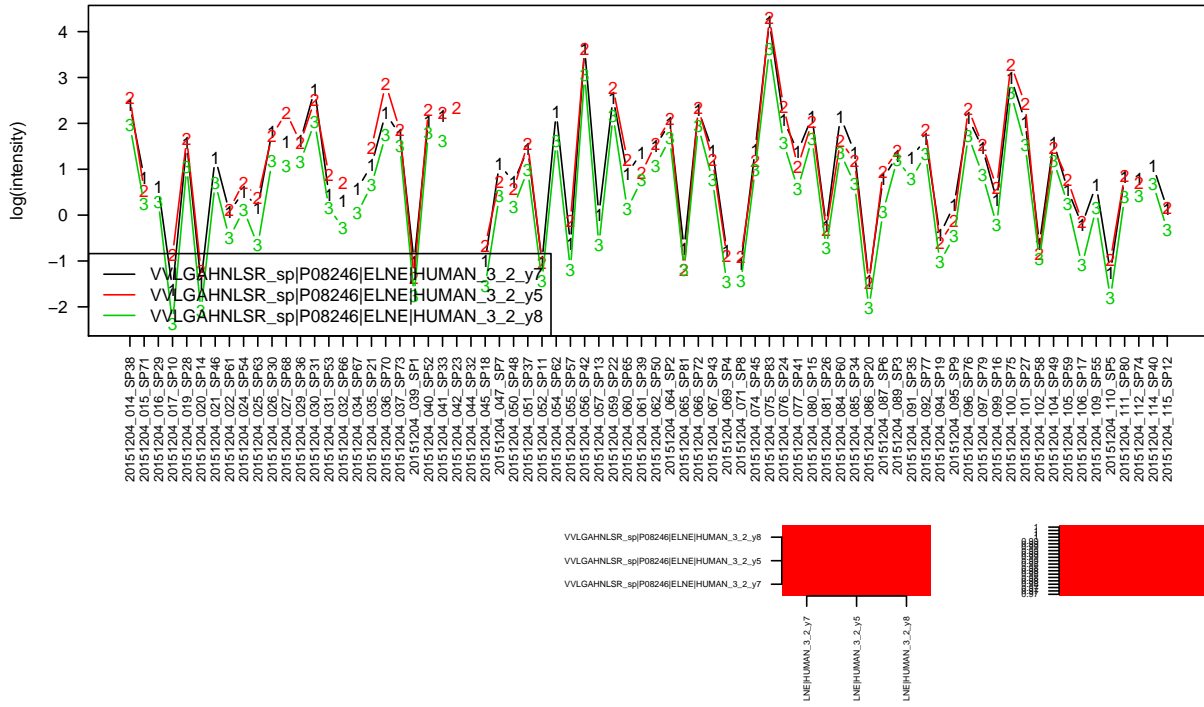
sp|P0C0S8|H2A1|HUMAN_AGLQFPVGR_2
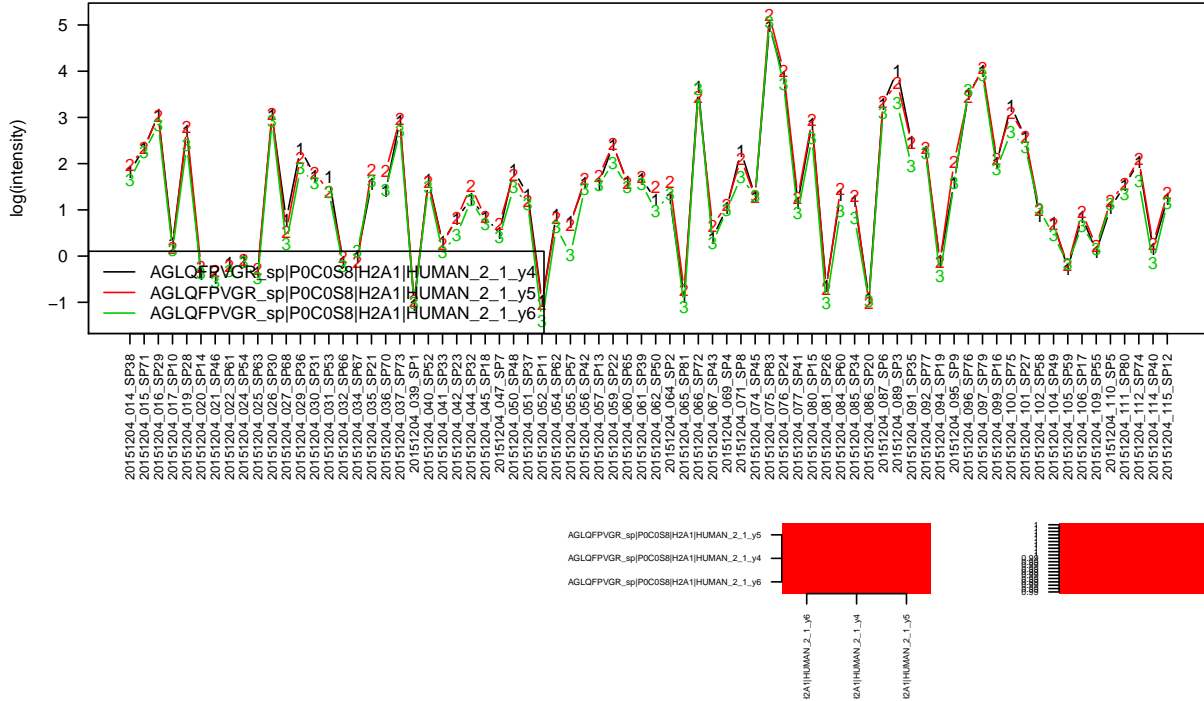
sp|P0C0S8|H2A1|HUMAN_HLQLAIR_2
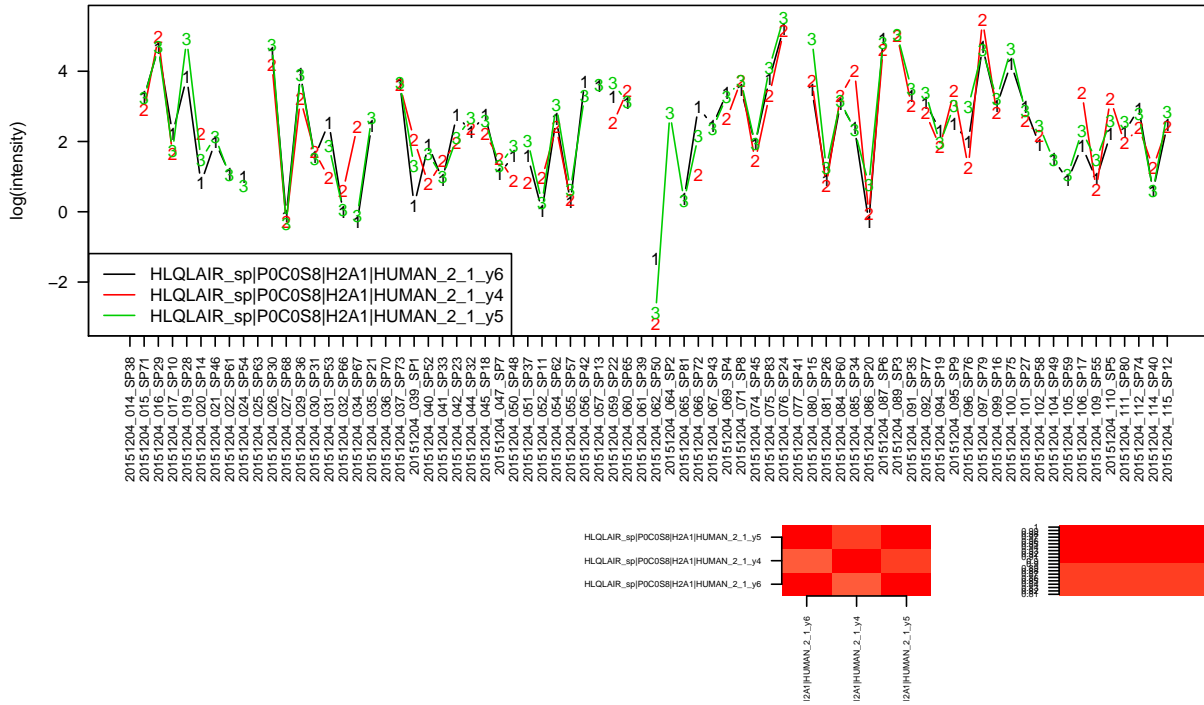
sp|P0C0S8|H2A1|HUMAN_VTIAQGGVLPNIQAVLLPK_2
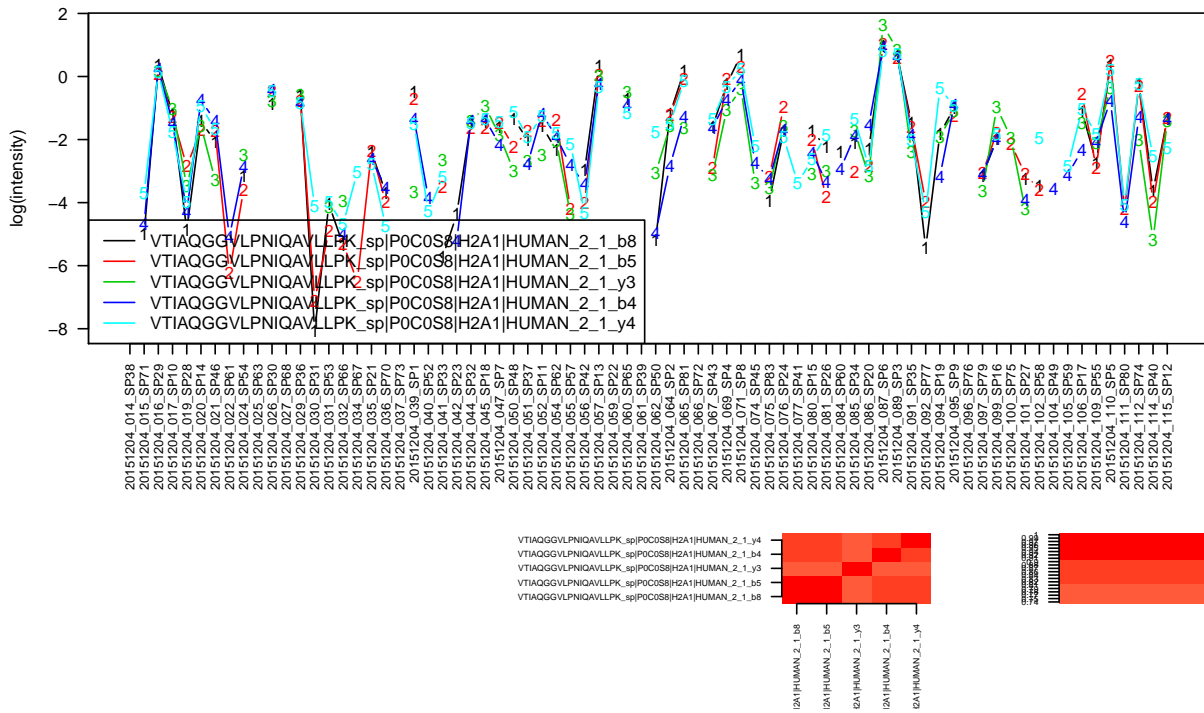
sp|P10909−1|CLUS|HUMAN_ASSIIDELFQDR_2
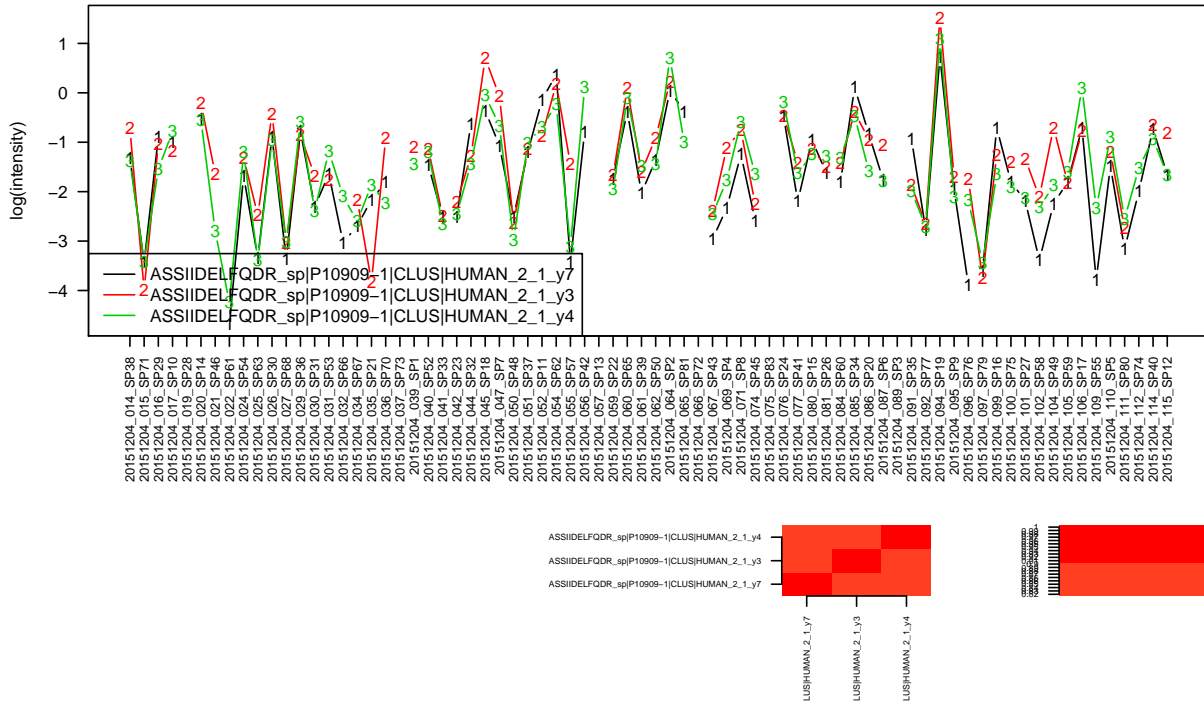
sp|P10909−1|CLUS|HUMAN_EILSVDCSTNNPSQAK_2
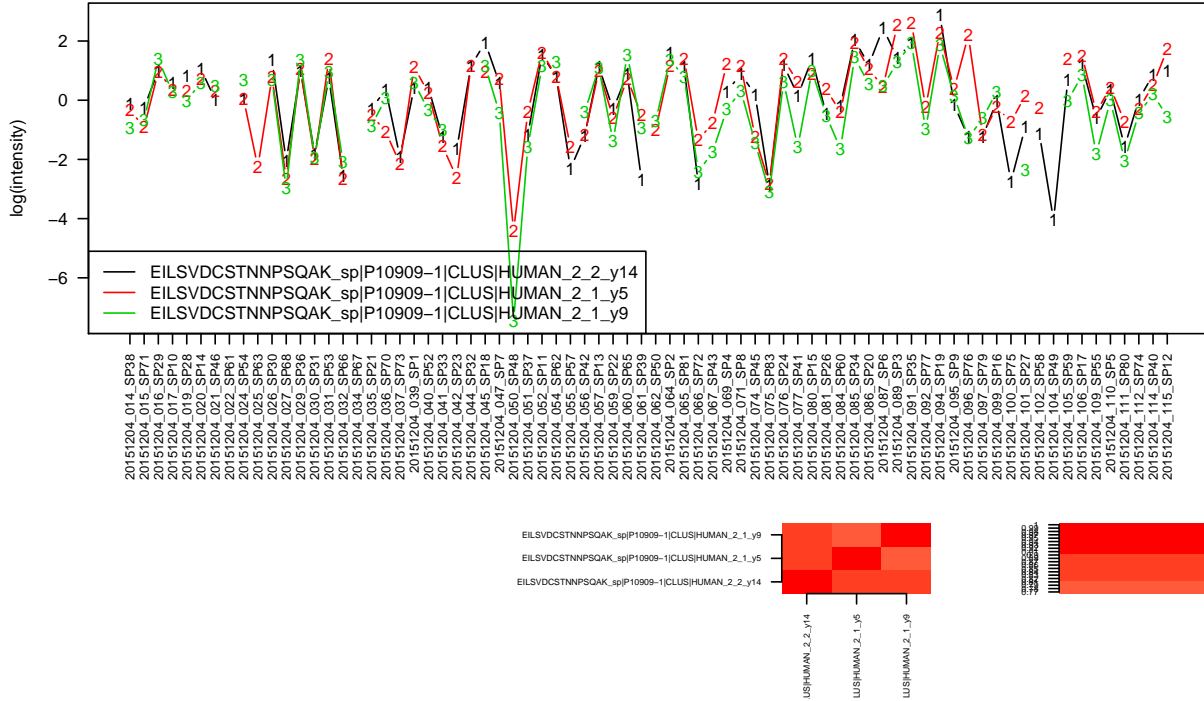
sp|P10909−1|CLUS|HUMAN_LFDSDPITVTVPVEVSR_2
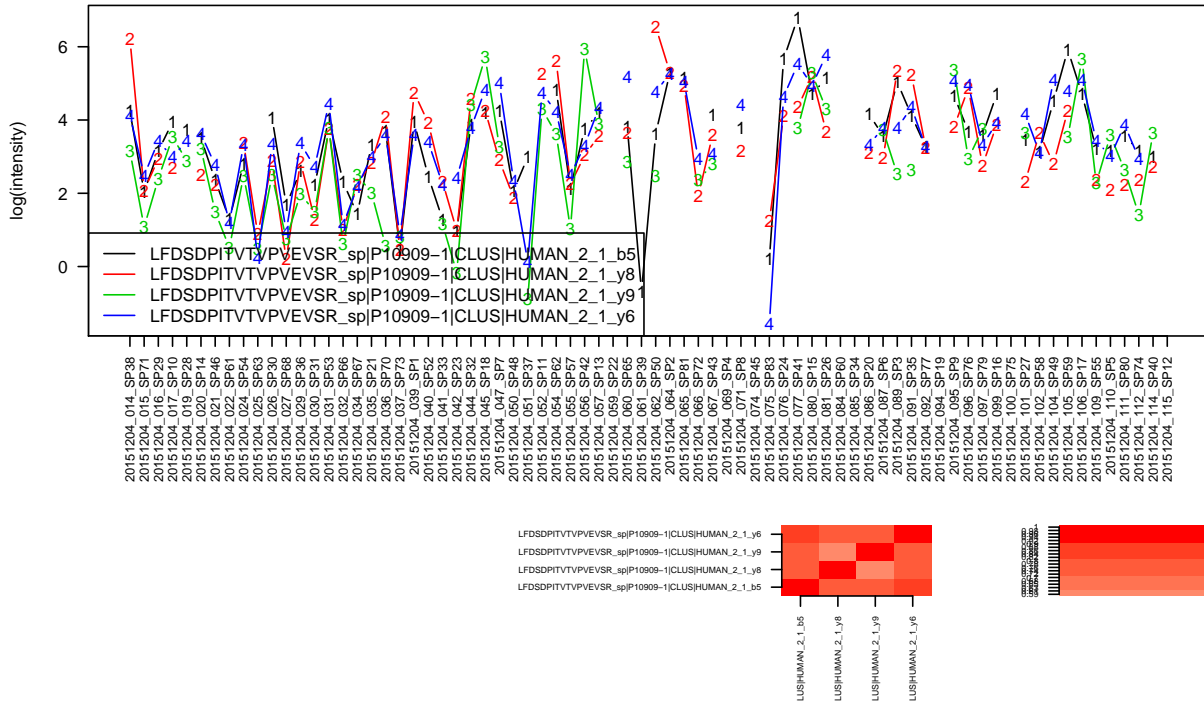
sp|P14780|MMP9|HUMAN_FGNADGAACHFPFIFEGR_3

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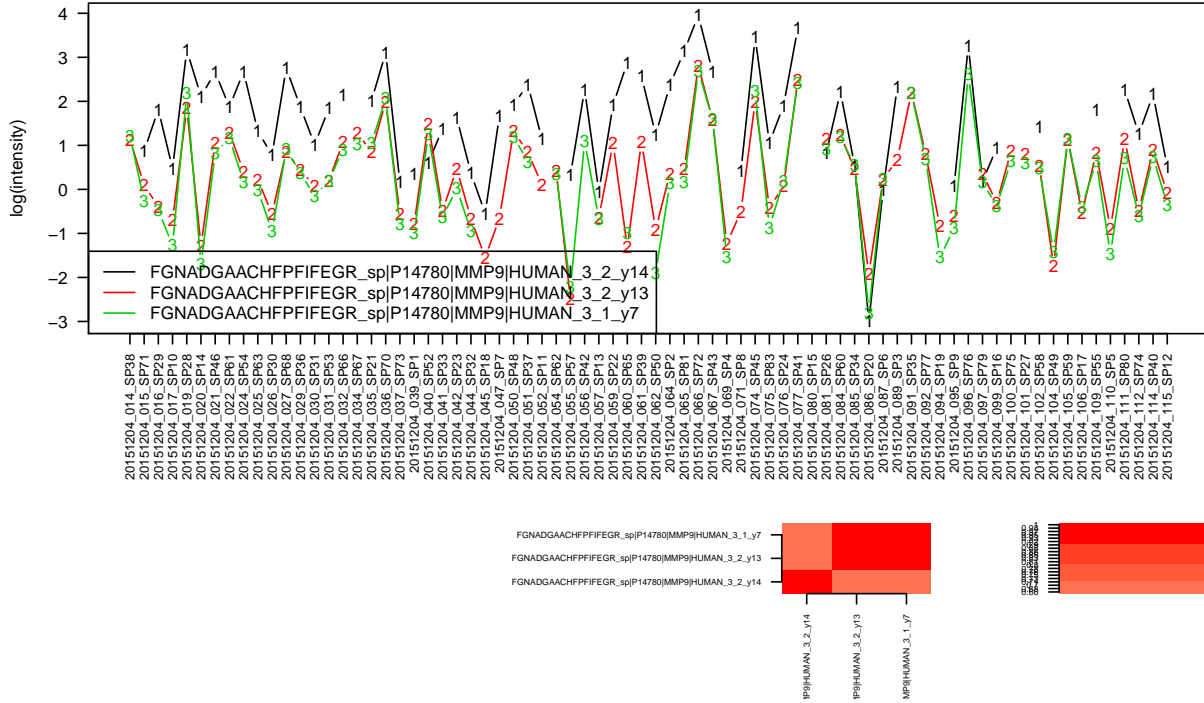
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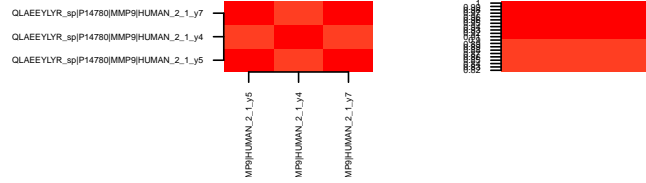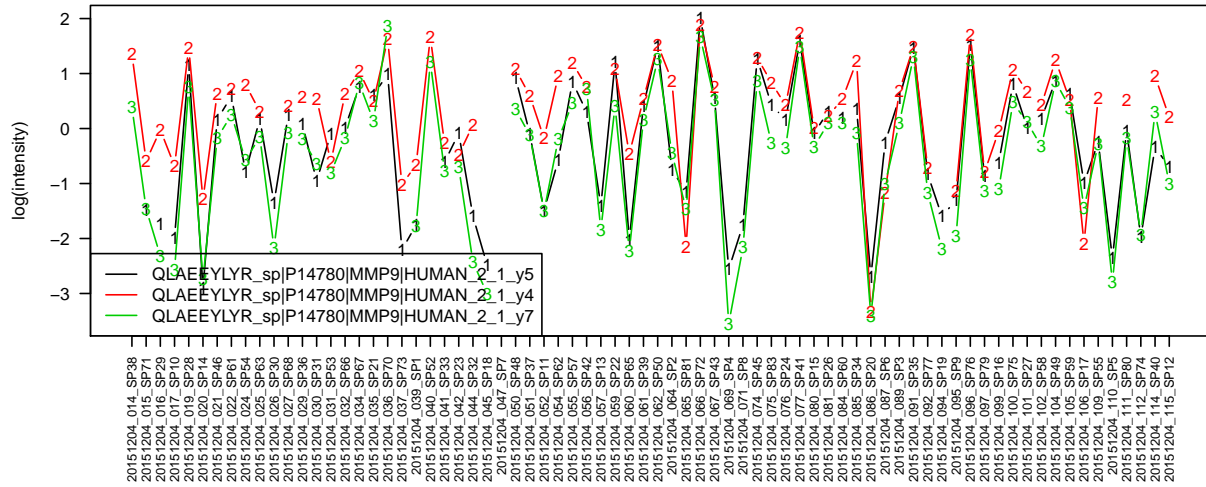
sp|P14780|MMP9|HUMAN_QSTLVLFPGDLR_2
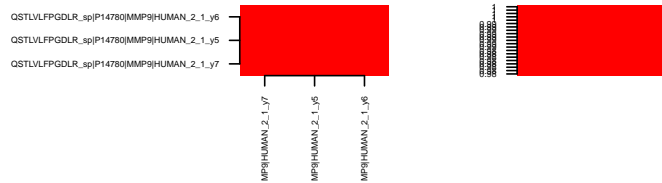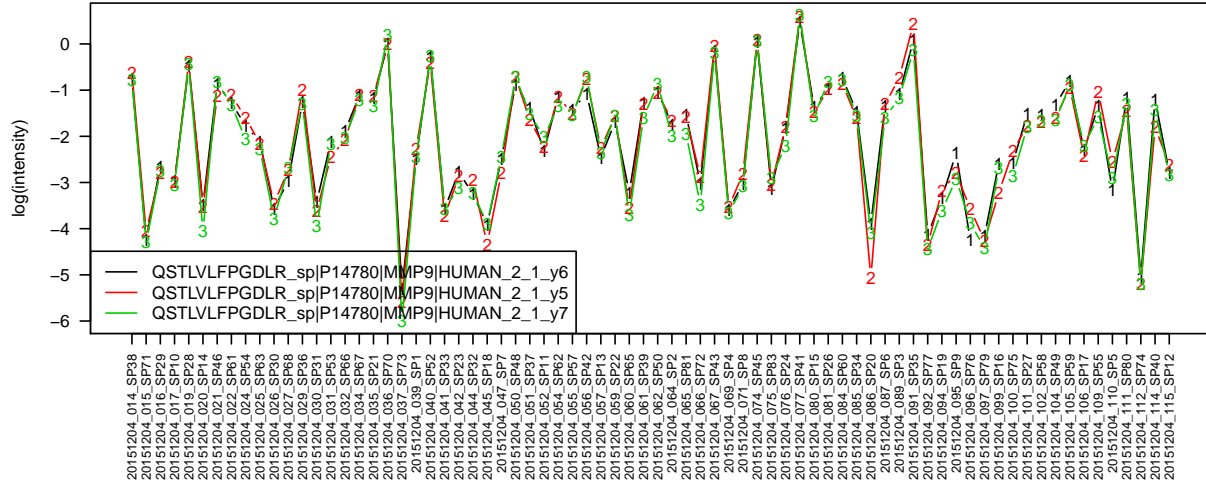
sp|P22894|MMP8|HUMAN_SISGAFPGIESK_2
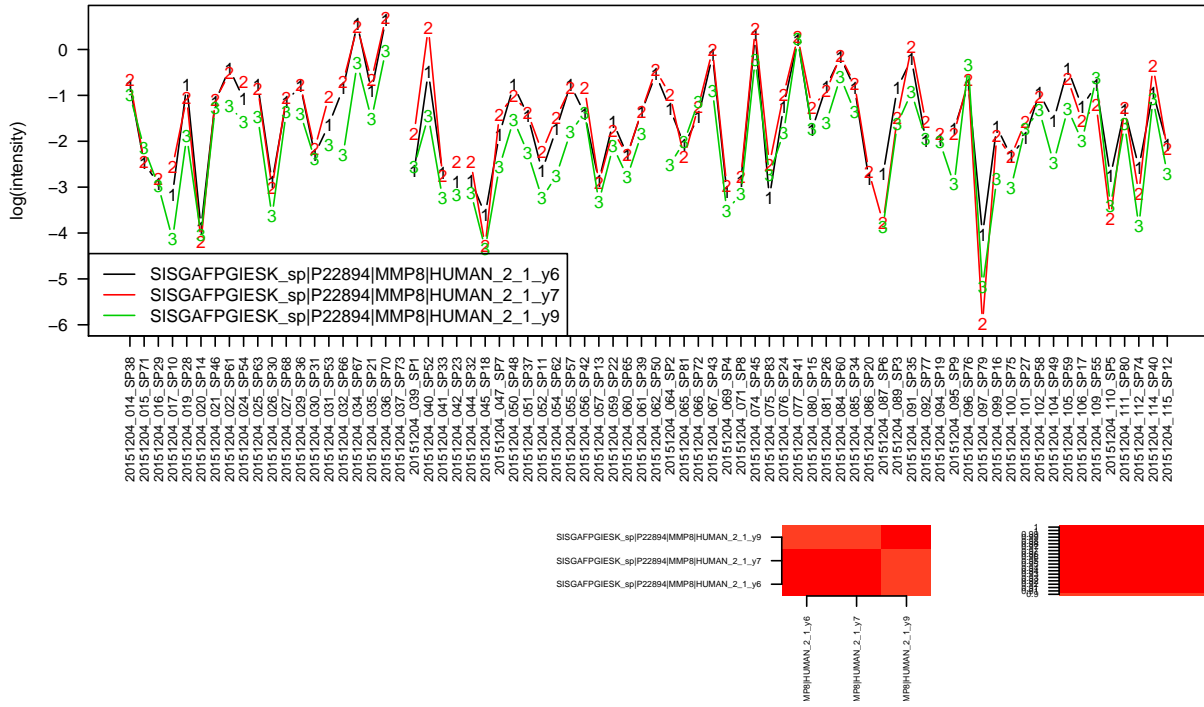
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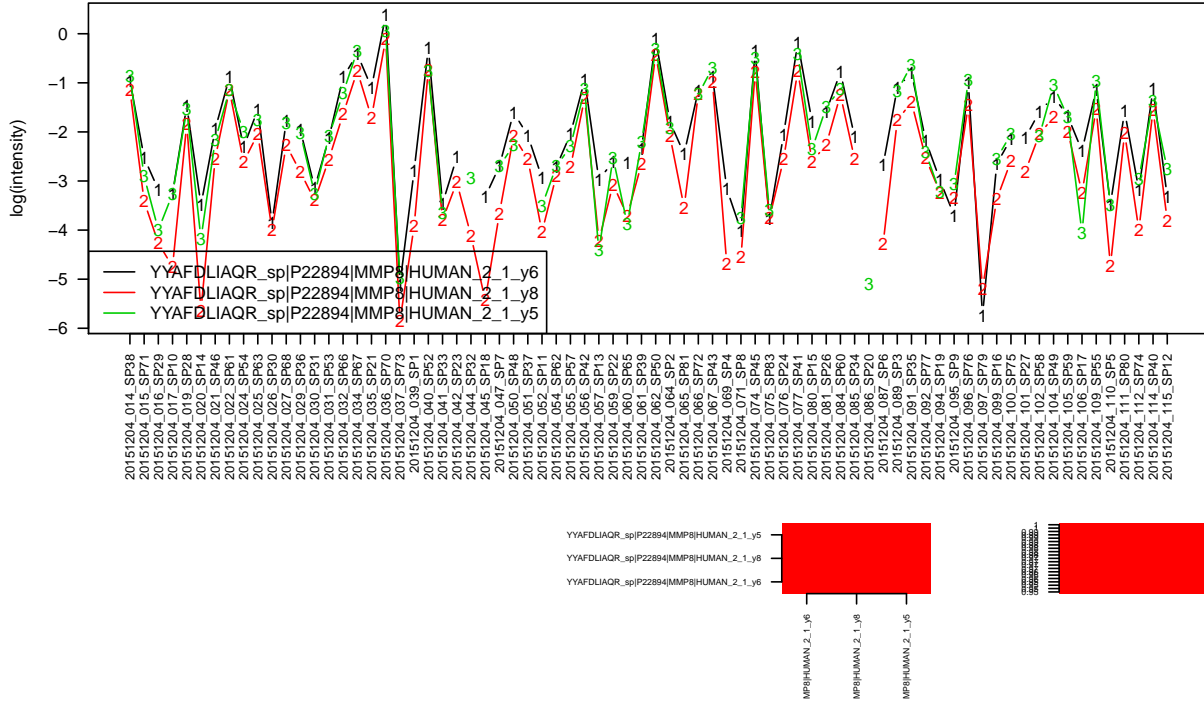
sp|P23280|CAH6|HUMAN_HVIEIHIVHYNSK_3
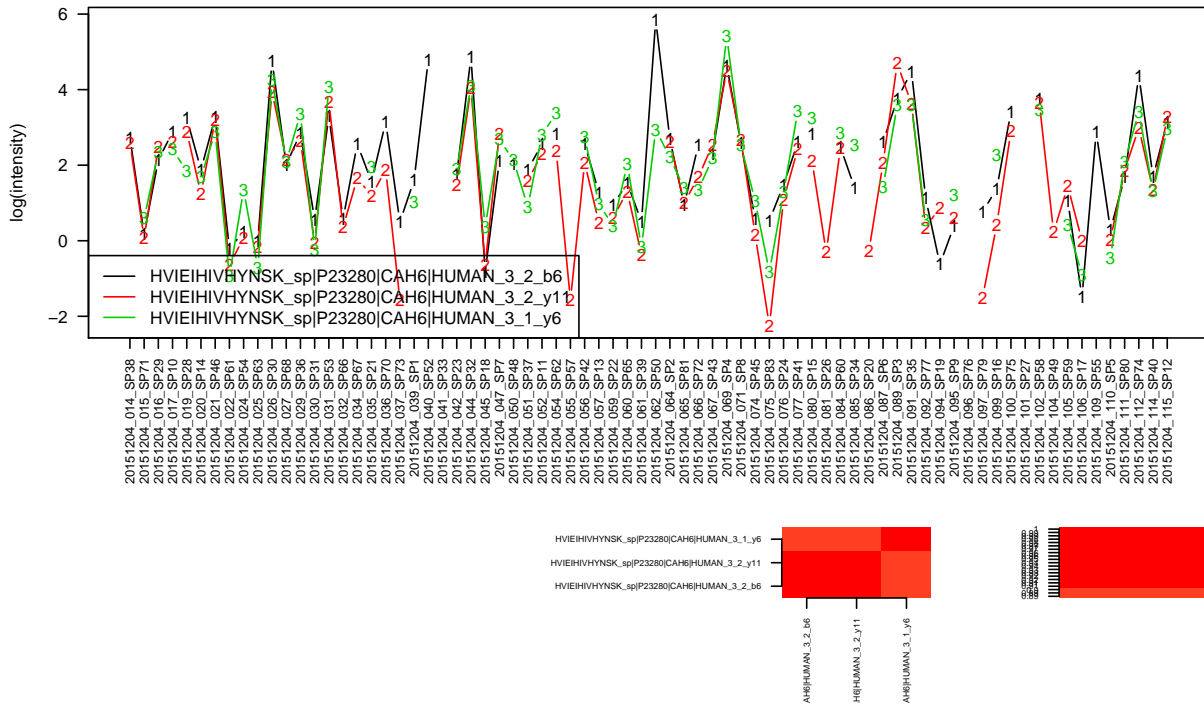
sp|P23280|CAH6|HUMAN_LENSLLDHR_2
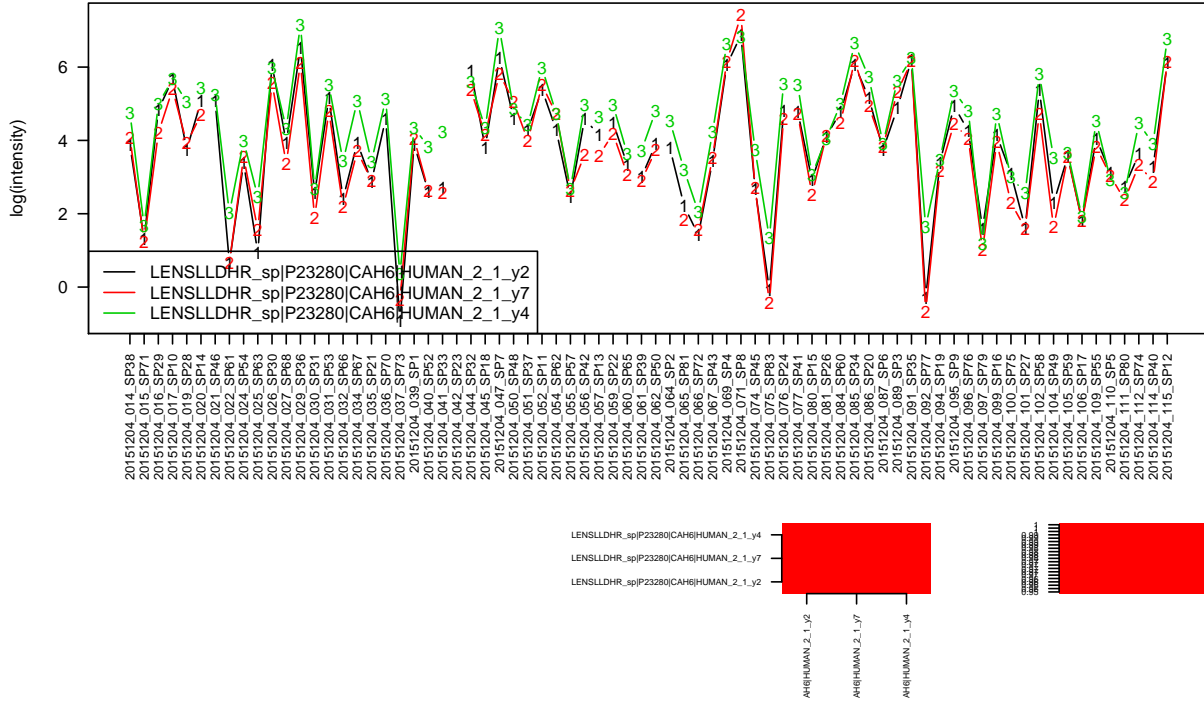
sp|P23280|CAH6|HUMAN_NYPENTYYSNFISHLANIK_2
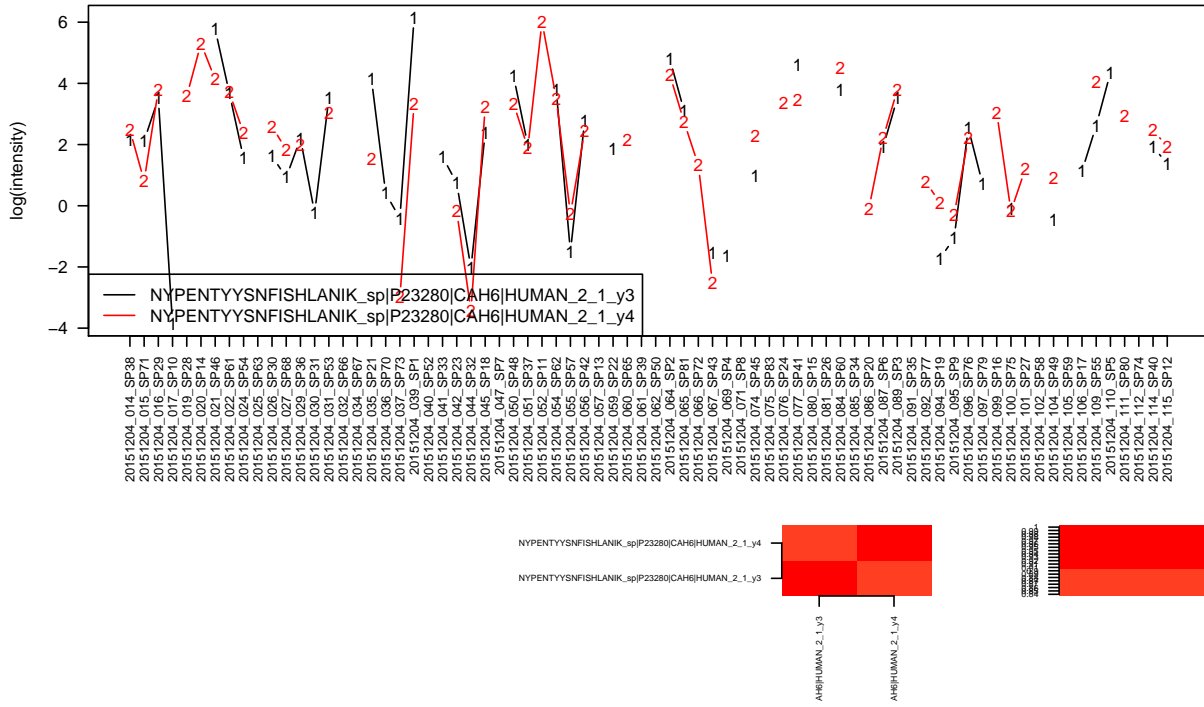
sp|P29508−1|SPB3|HUMAN_QYTSFHFASLEDVQAK_3
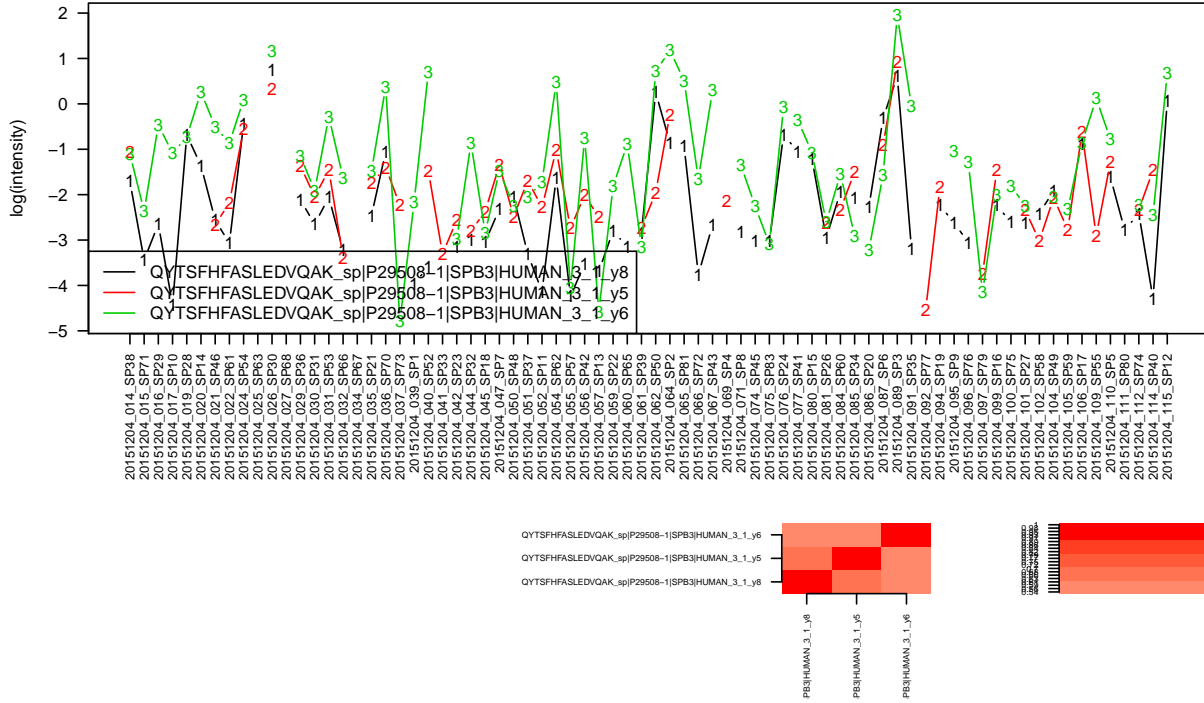
sp|P29508−1|SPB3|HUMAN_VLHFDQVTENTTGK_3
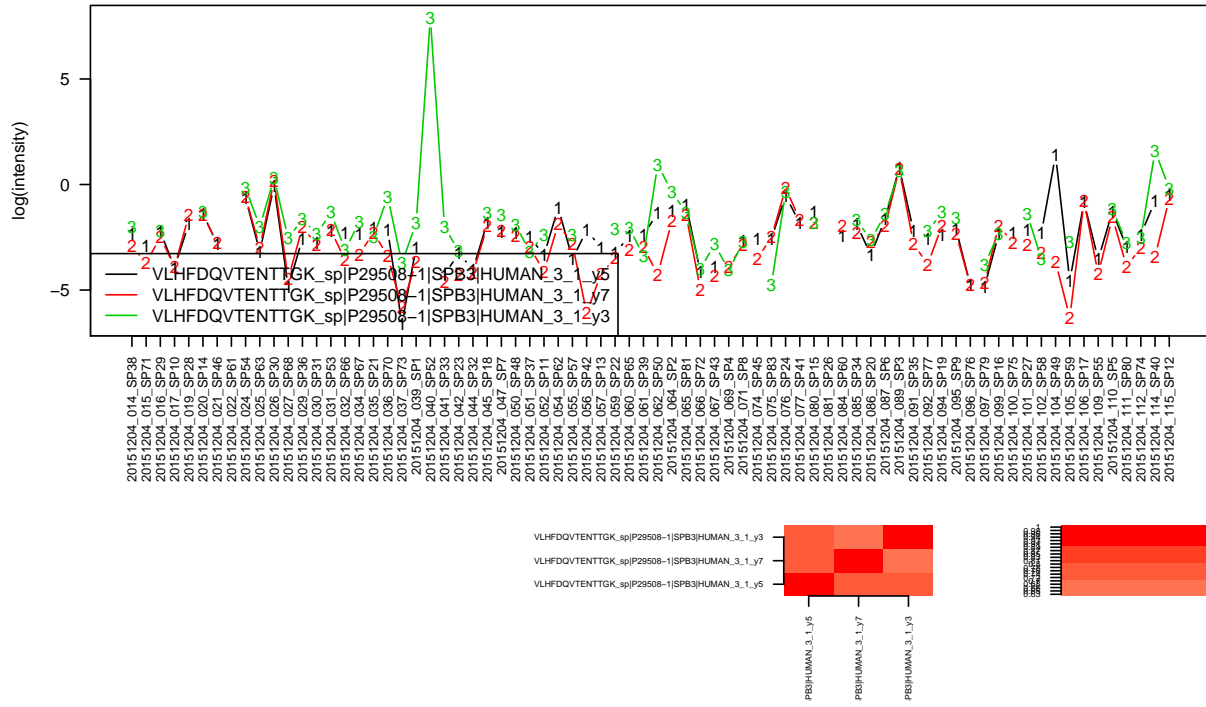
sp|P31947−1|1433S|HUMAN_GEELSCEER_2

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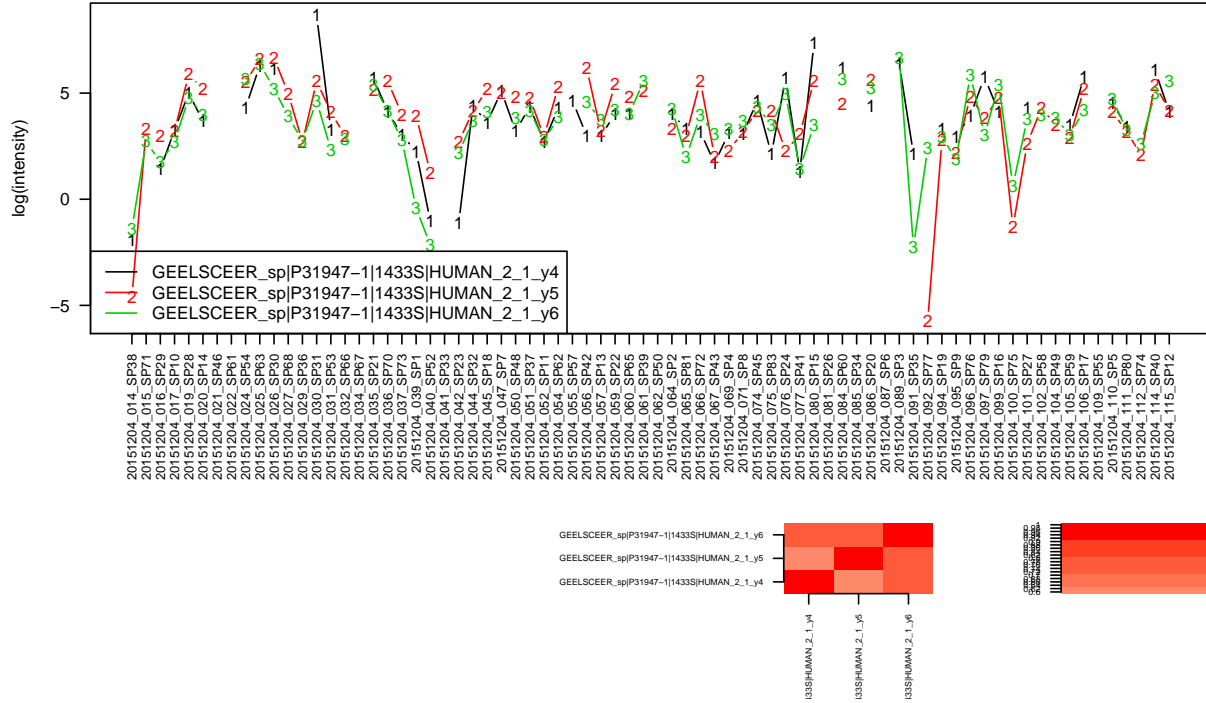
sp|P31947−1|1433S|HUMAN_VLSSIEQK_2
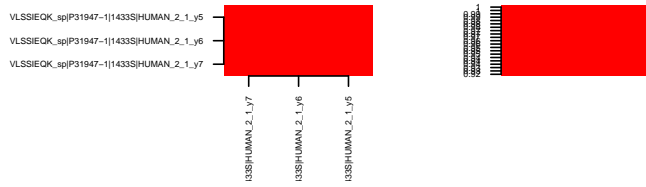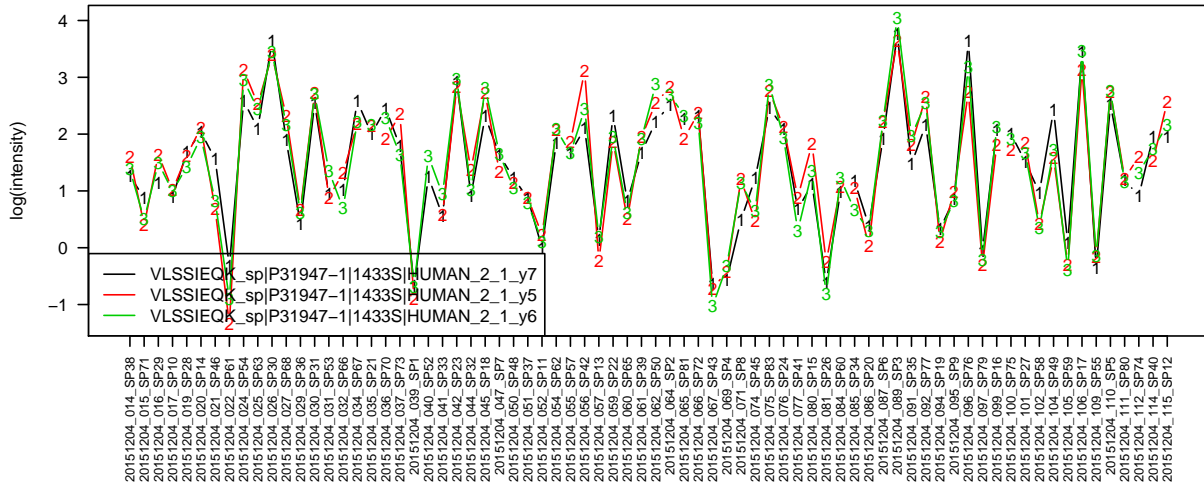
sp|P31947−1|1433S|HUMAN_YLAEVATGDDK_2
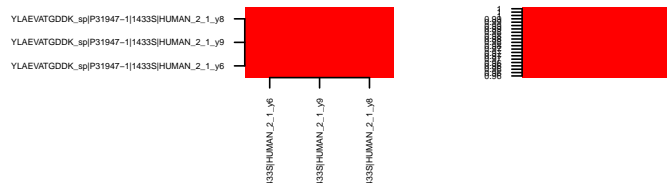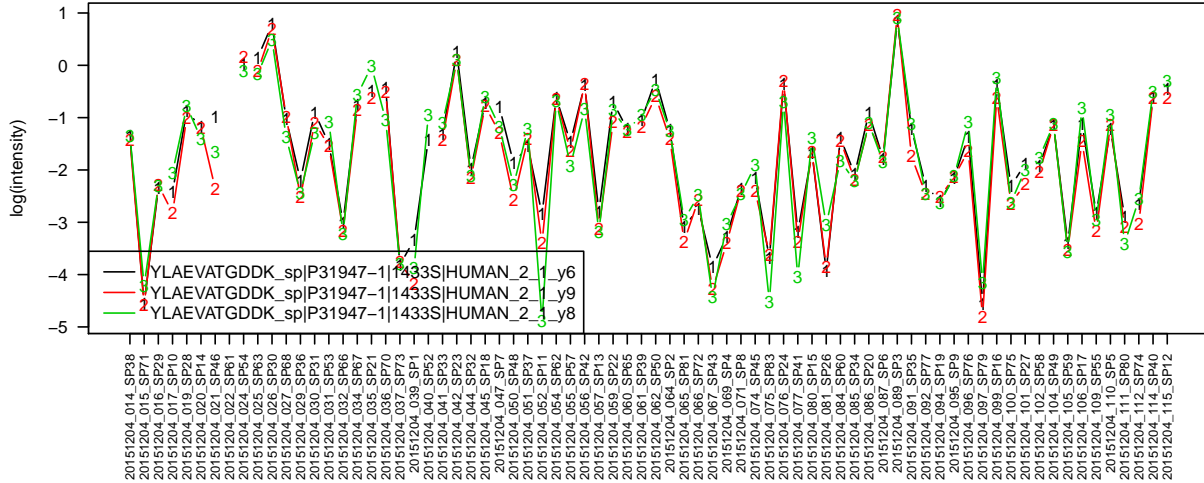
sp|P48595|SPB10|HUMAN_AVGLQLYYK_2
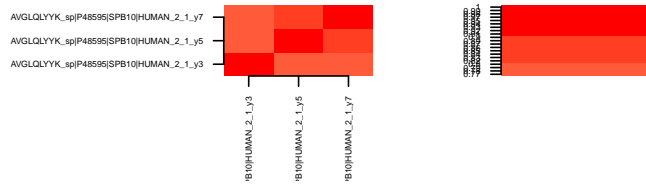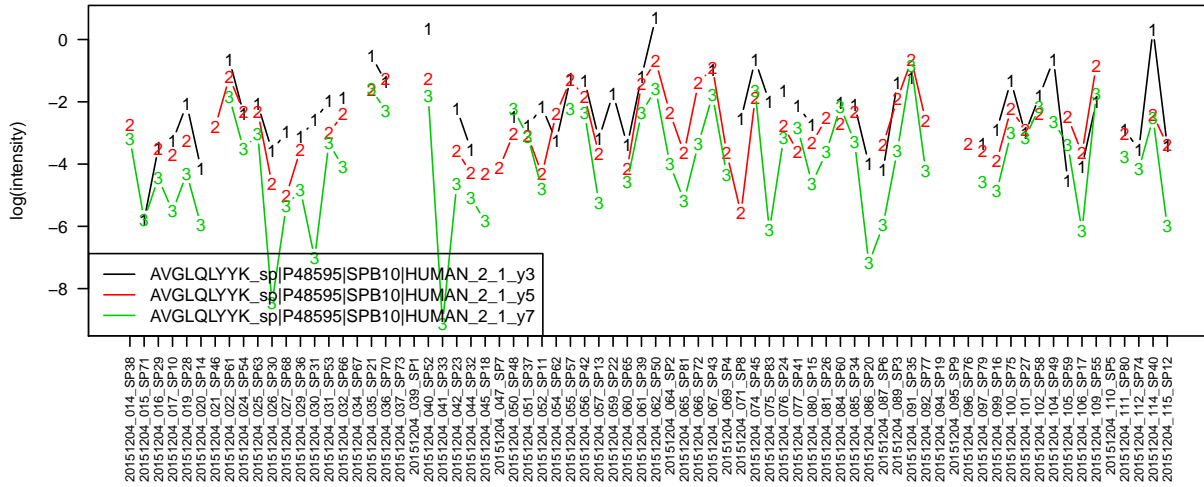
sp|P48595|SPB10|HUMAN_IQNLLPDDSVDSTTR_2
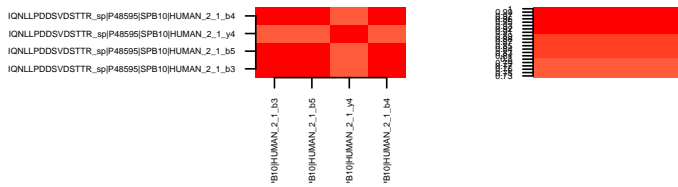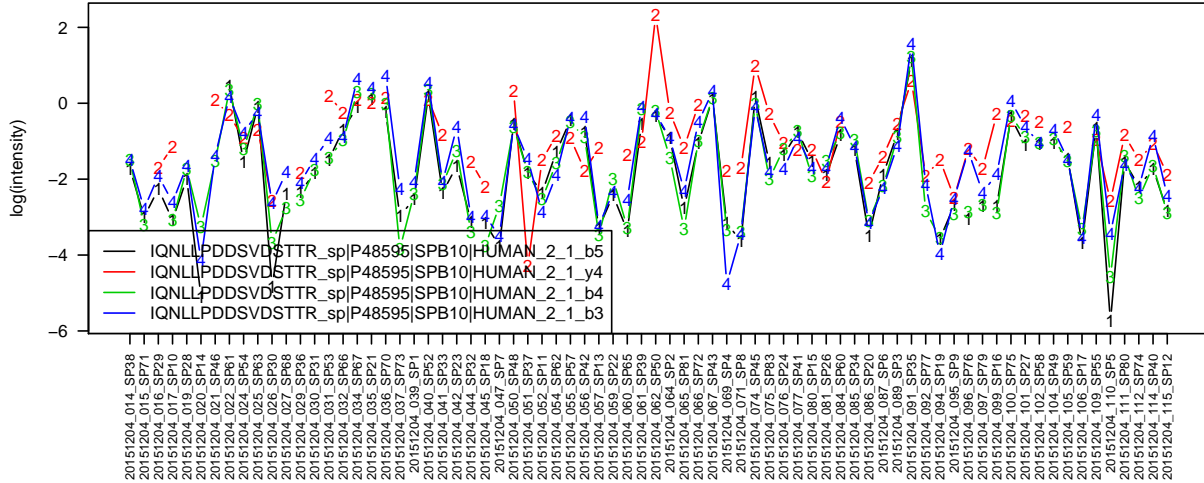
sp|P48595|SPB10|HUMAN_NLFLSNVFHK_2

Legend:
- NLFLSNVFHK_sp|P48595|SPB10|HUMAN_2_1_y8
- NLFLSNVFHK_sp|P48595|SPB10|HUMAN_2_1_y6
- NLFLSNVFHK_sp|P48595|SPB10|HUMAN_2_1_b3
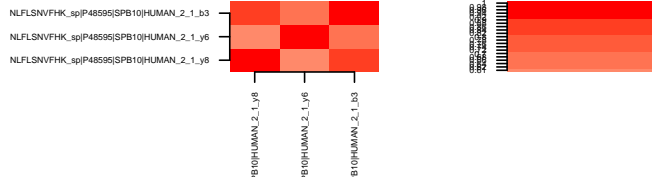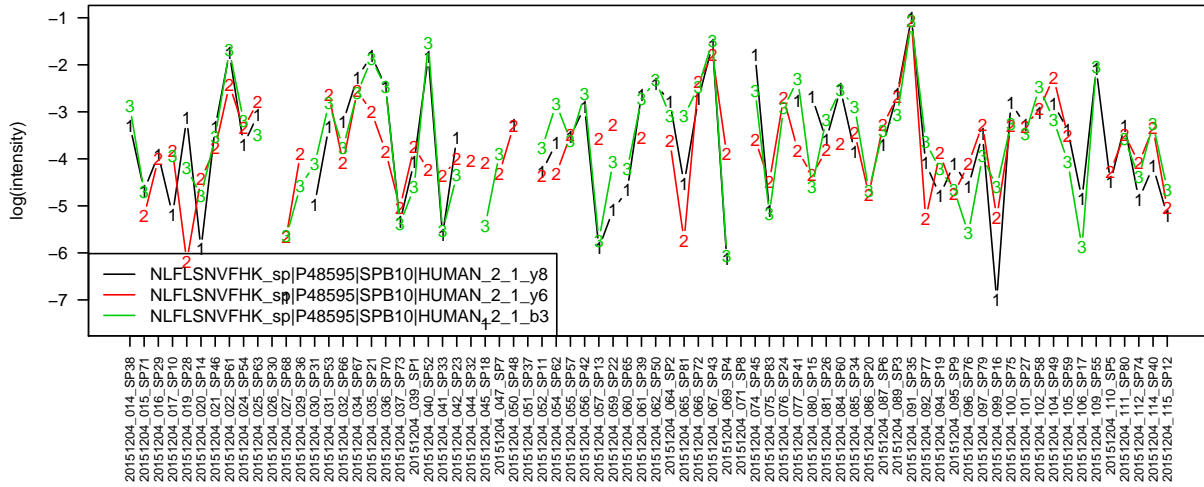
sp|P50552|VASP|HUMAN_YNQATPNFHQWR_3

Legend:
- YNQATPNFHQWR_sp|P50552|VASP|HUMAN_3_1_y7
- YNQATPNFHQWR_sp|P50552|VASP|HUMAN_3_2_y7
- YNQATPNFHQWR_sp|P50552|VASP|HUMAN_3_2_y8
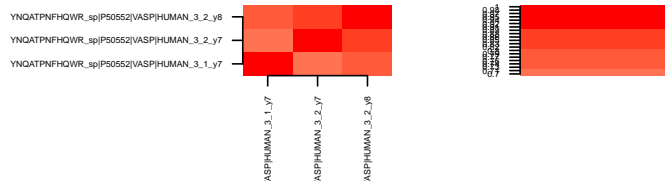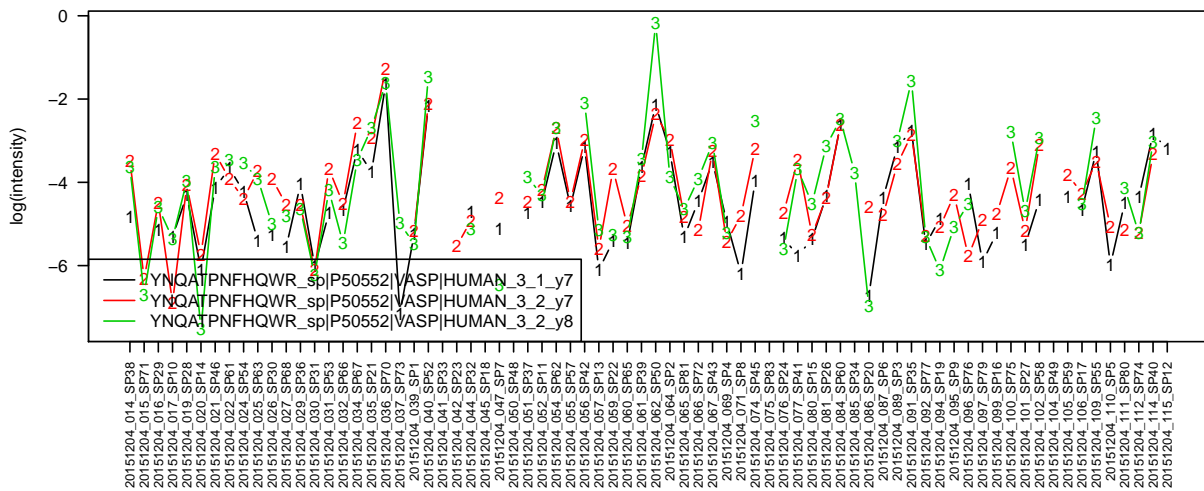
sp|P52566|GDIR2|HUMAN_APEPHVEEDDDDELDSK_3
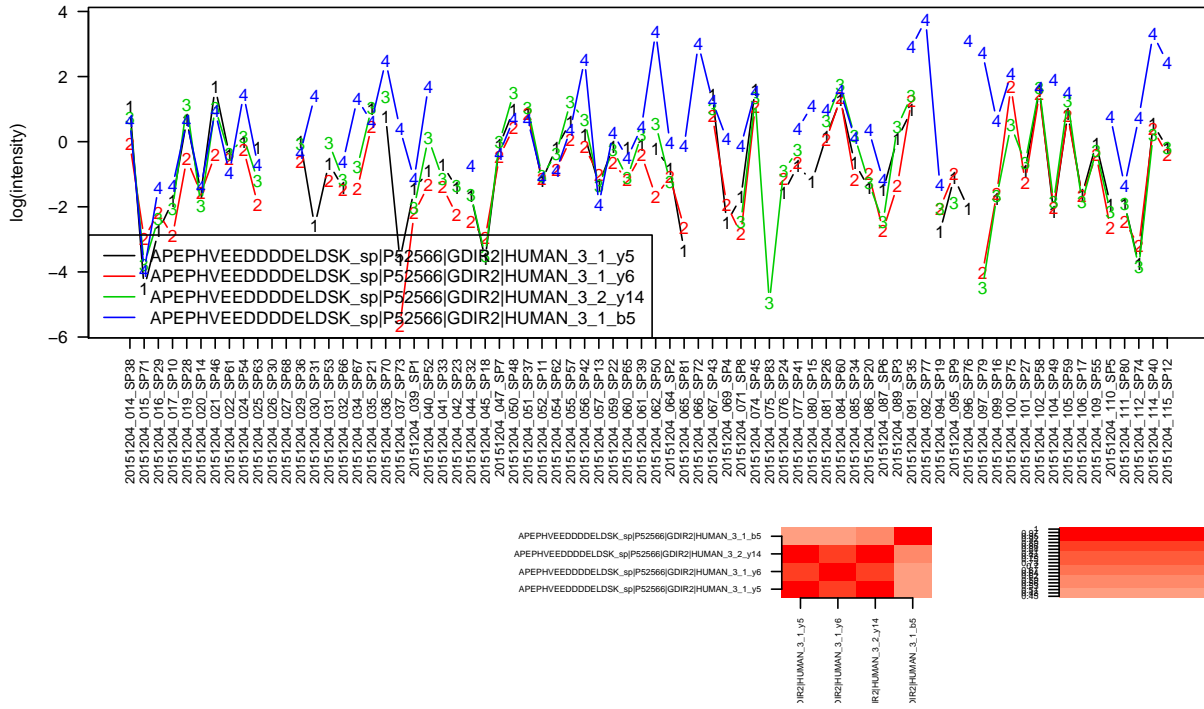
sp|P52566|GDIR2|HUMAN_APNVVVTR_2
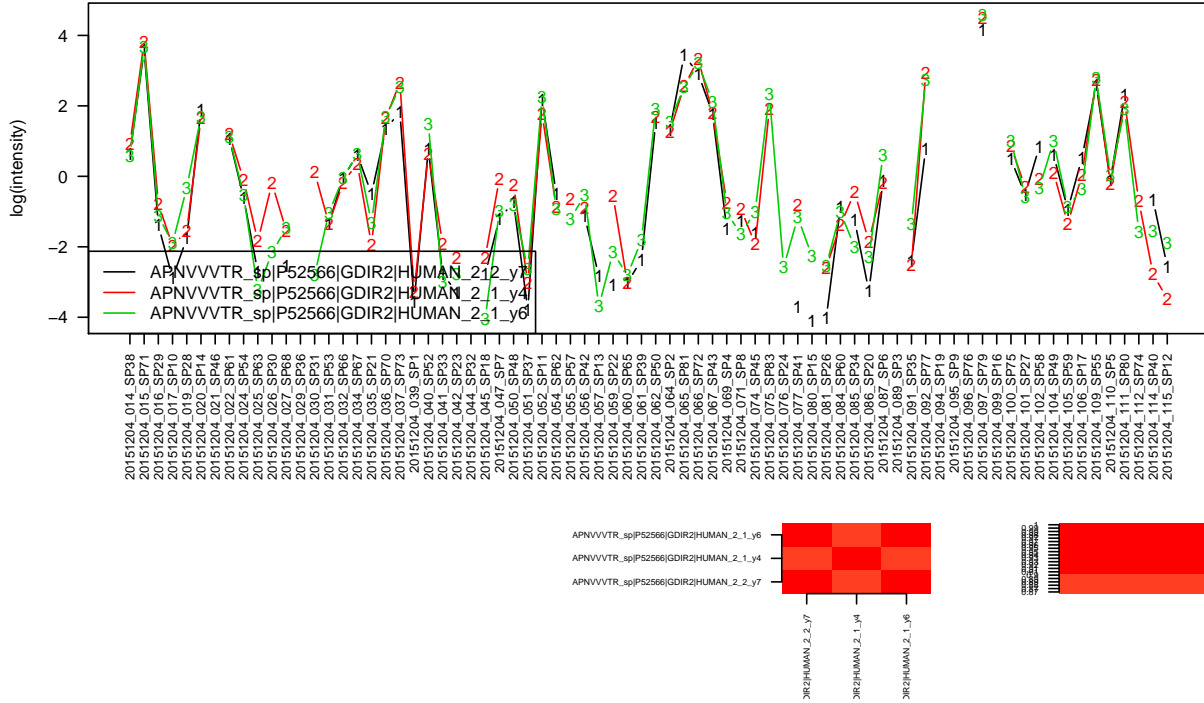
sp|P52566|GDIR2|HUMAN_TLLGDGPVVTDPK_2
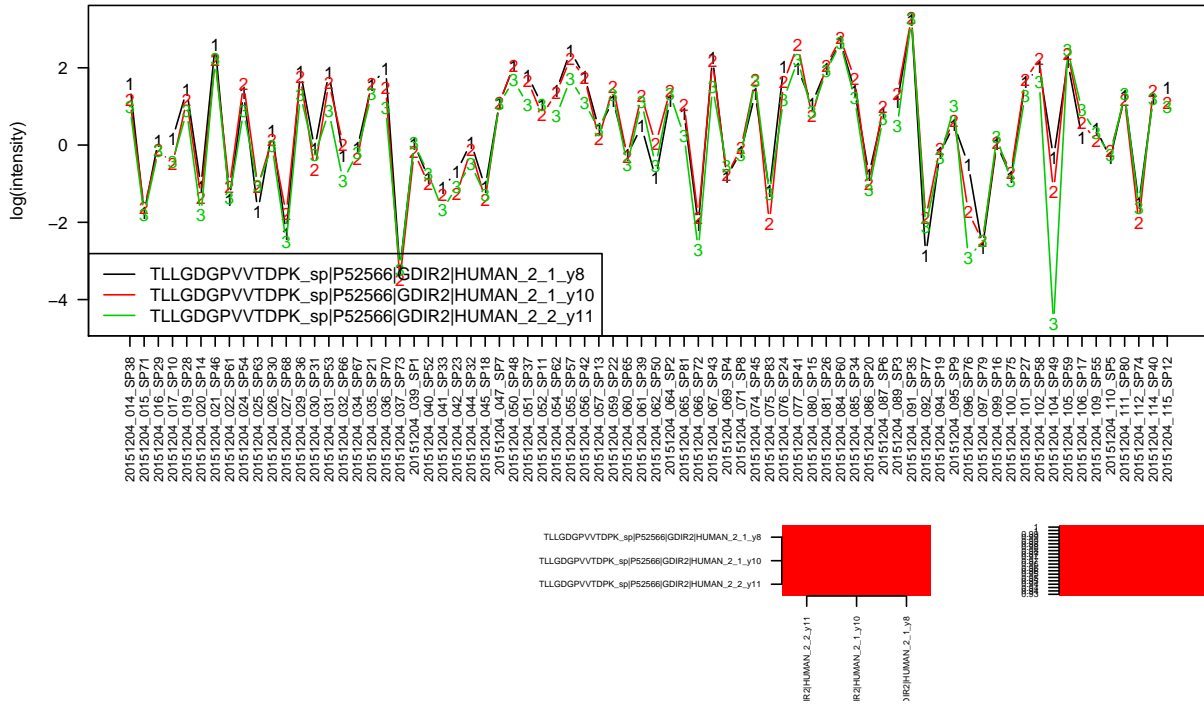
sp|P54108|CRIS3|HUMAN_DPAFTALLTTQTQVQR_2
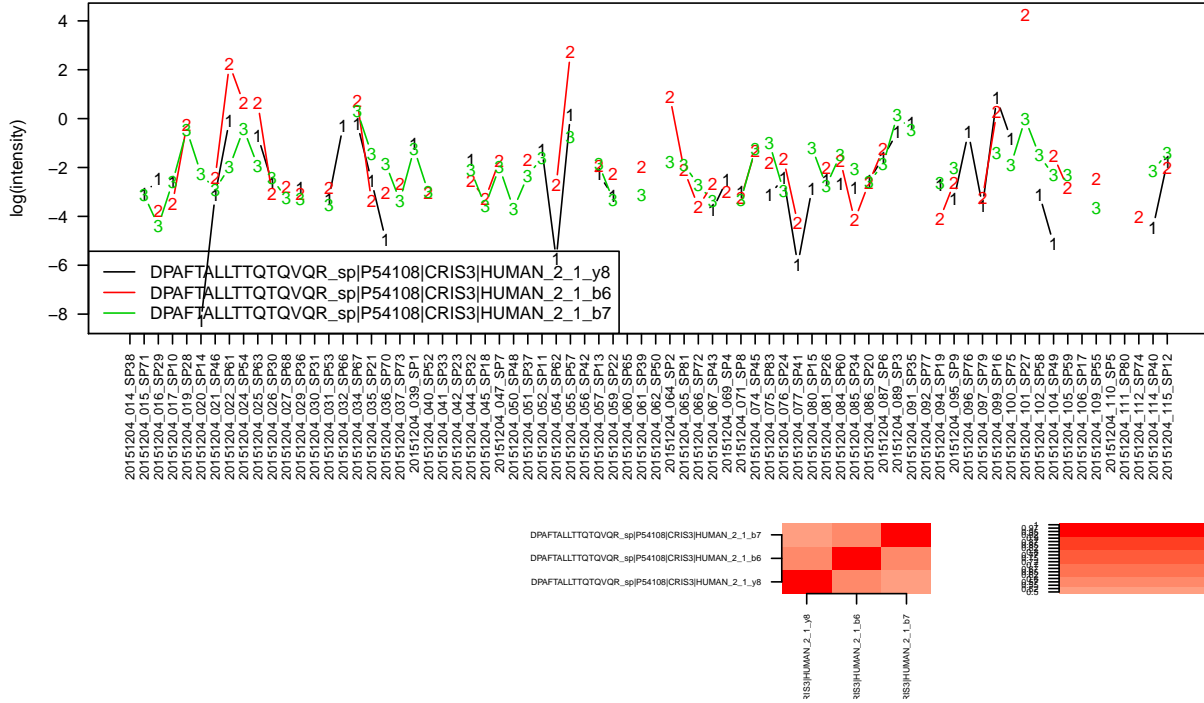
sp|P54108|CRIS3|HUMAN_WANQCNYR_2
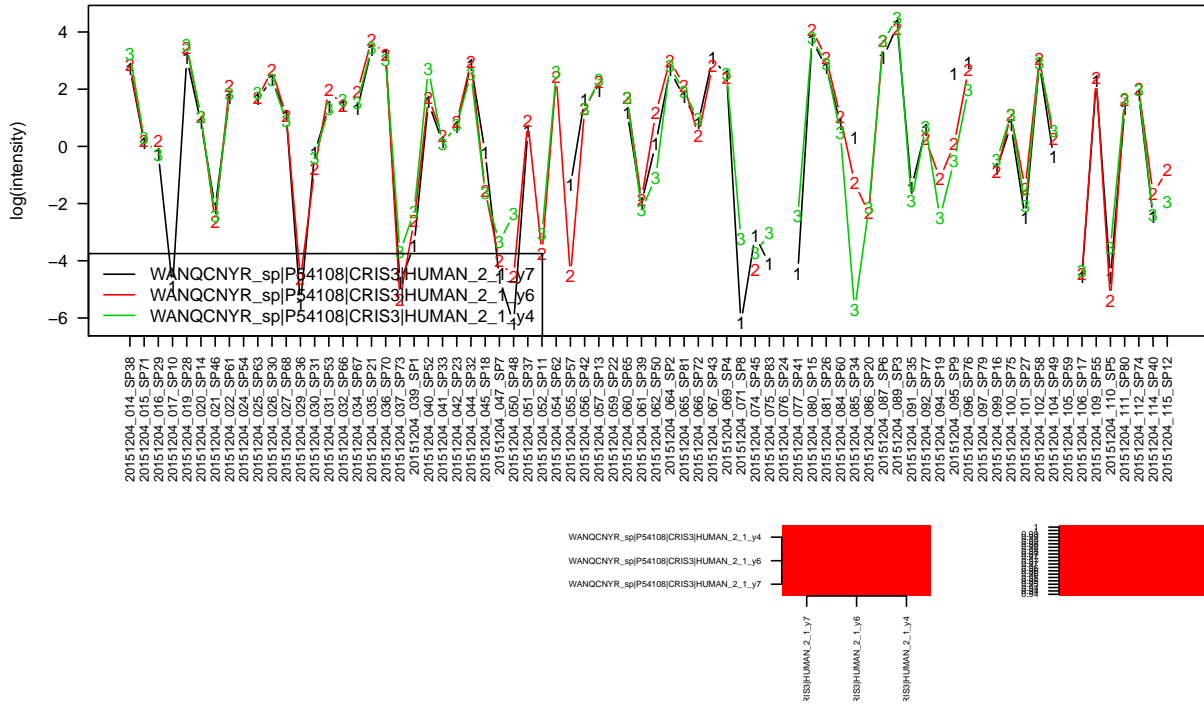
sp|P54108|CRIS3|HUMAN_YYYVCQYCPAGNWANR_2

60
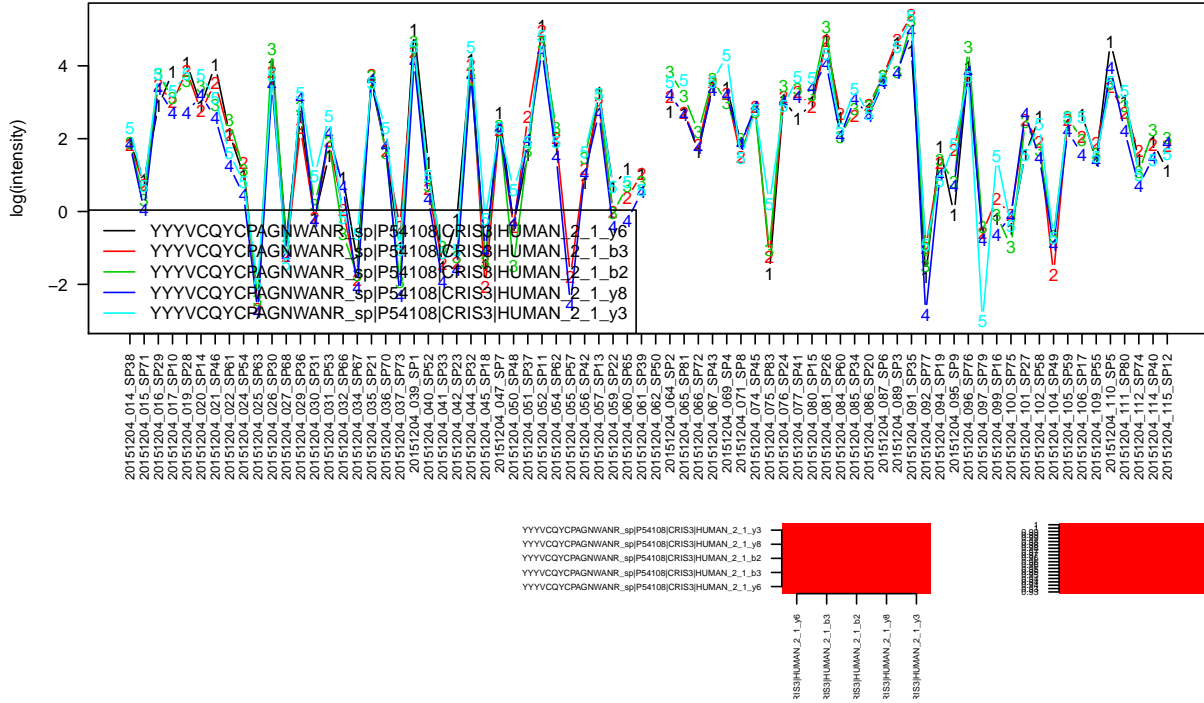
sp|P68032|ACTC|HUMAN_AGFAGDDAPR_2

Legend:
- AGFAGDDAPR_sp|P68032|ACTC|HUMAN_2_1_y6
- AGFAGDDAPR_sp|P68032|ACTC|HUMAN_2_1_y7
- AGFAGDDAPR_sp|P68032|ACTC|HUMAN_2_2_y8
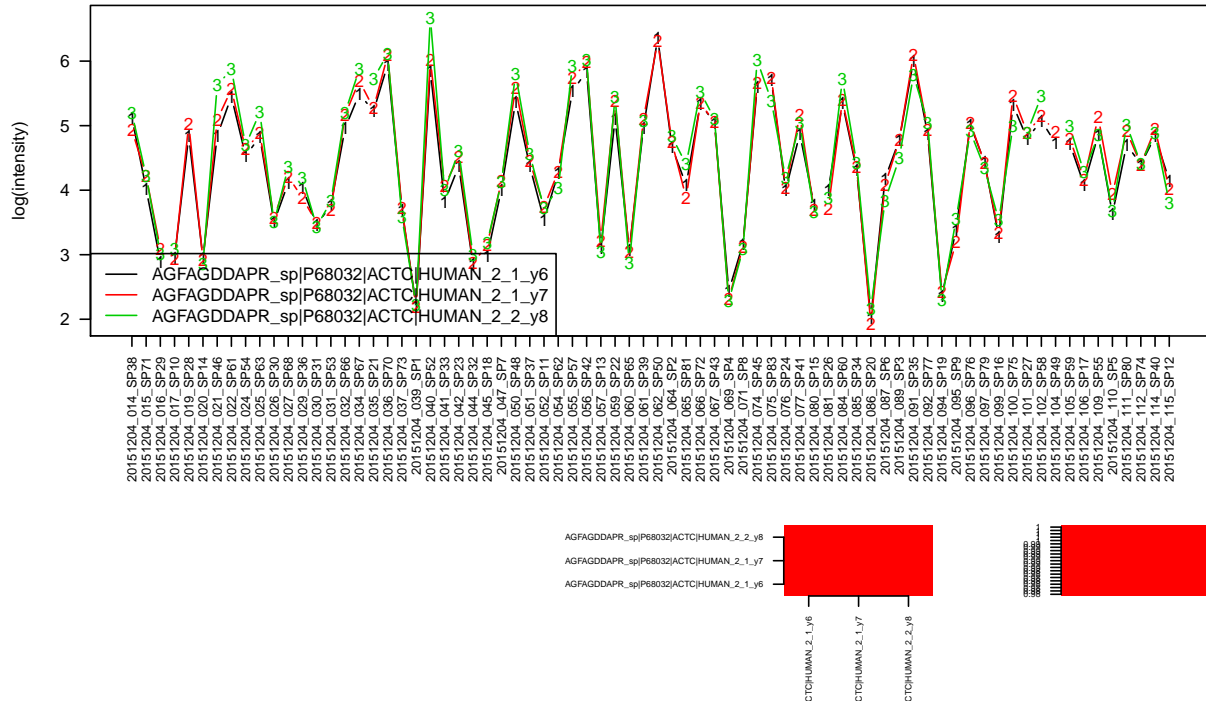
sp|P68032|ACTC|HUMAN_AVFPSIVGRPR_2

Legend:
- AVFPSIVGRPR_sp|P68032|ACTC|HUMAN_2_1_y8
- AVFPSIVGRPR_sp|P68032|ACTC|HUMAN_2_2_y8
- AVFPSIVGRPR_sp|P68032|ACTC|HUMAN_2_2_y9
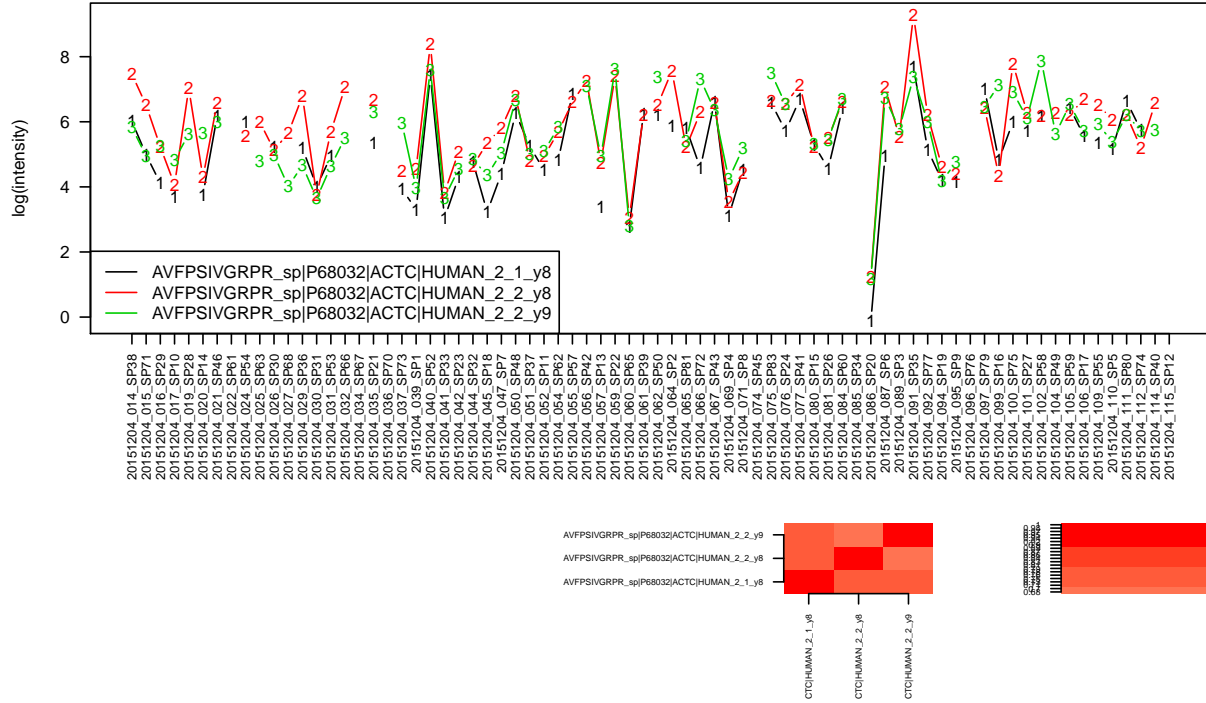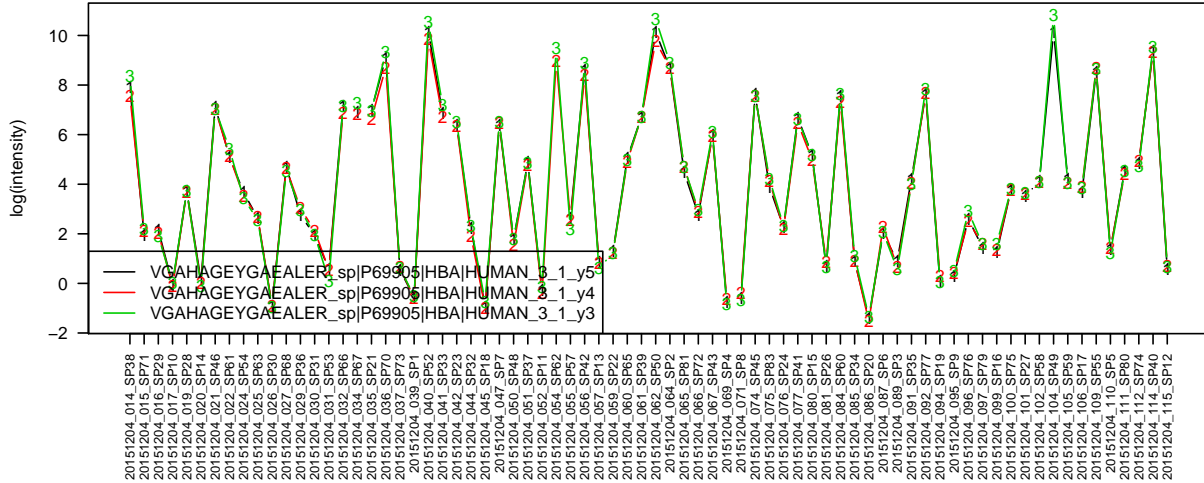
sp|P68032|ACTC|HUMAN_SYELPDGQVITIGNER_2
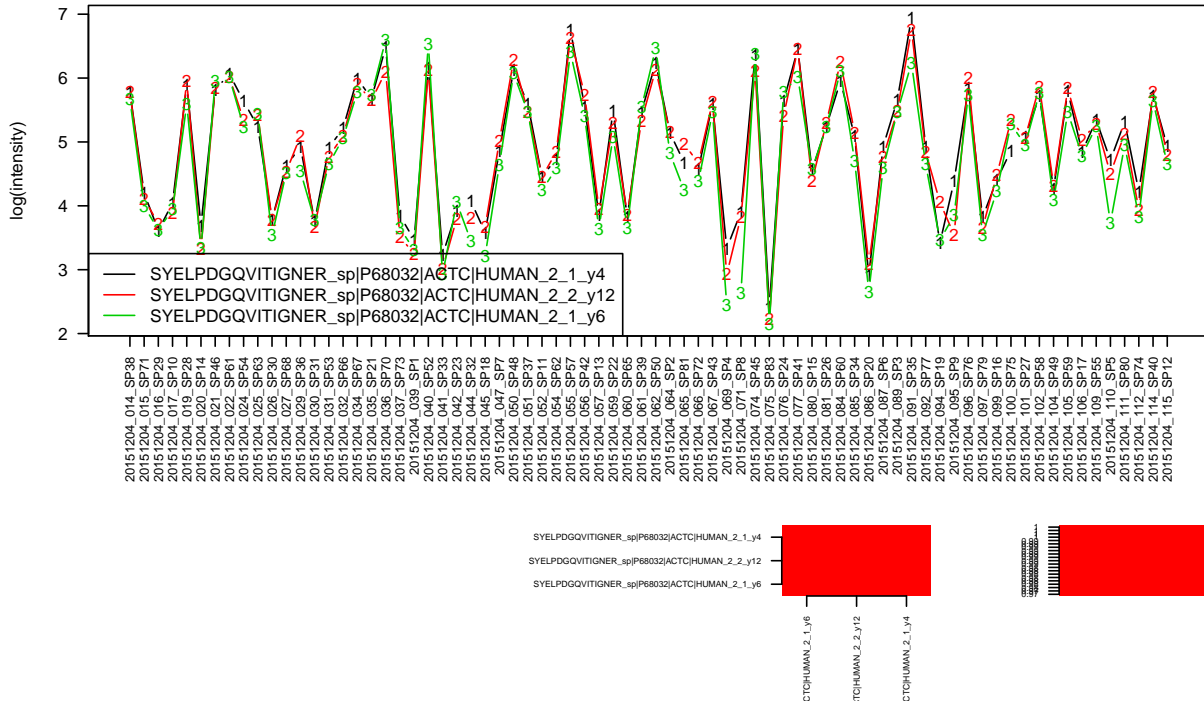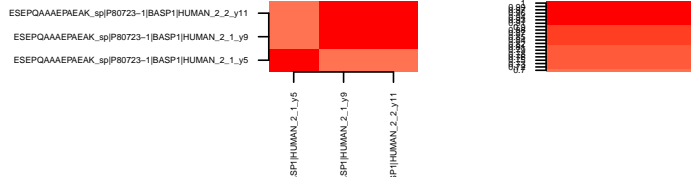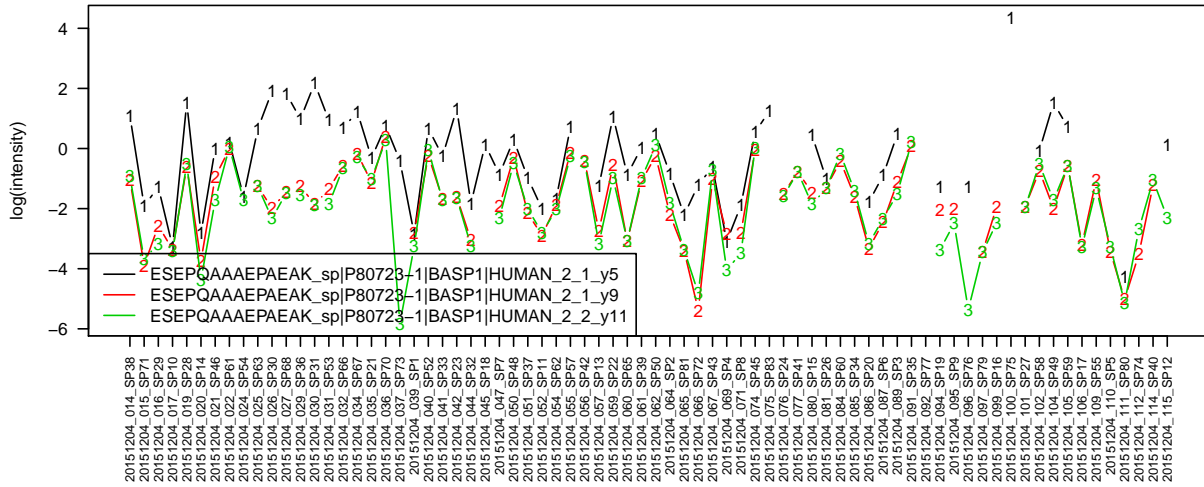

sp|P69905|HBA|HUMAN_FLASVSTVLTSK_2
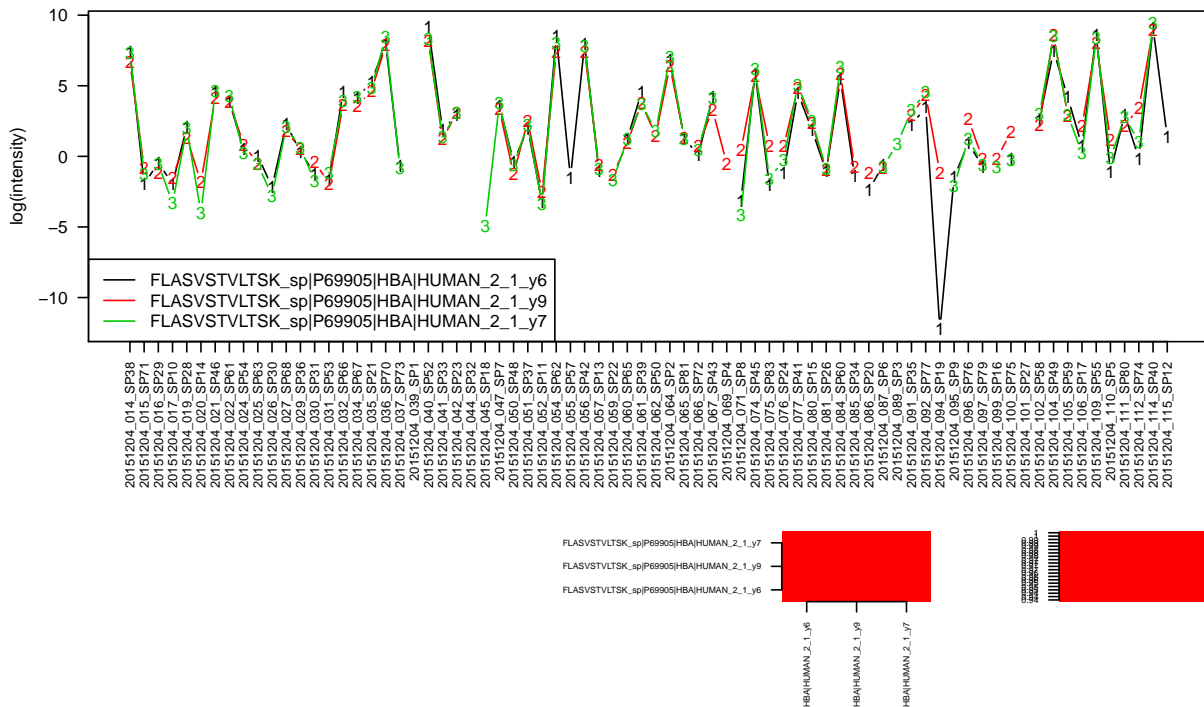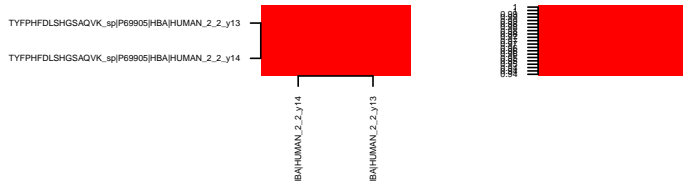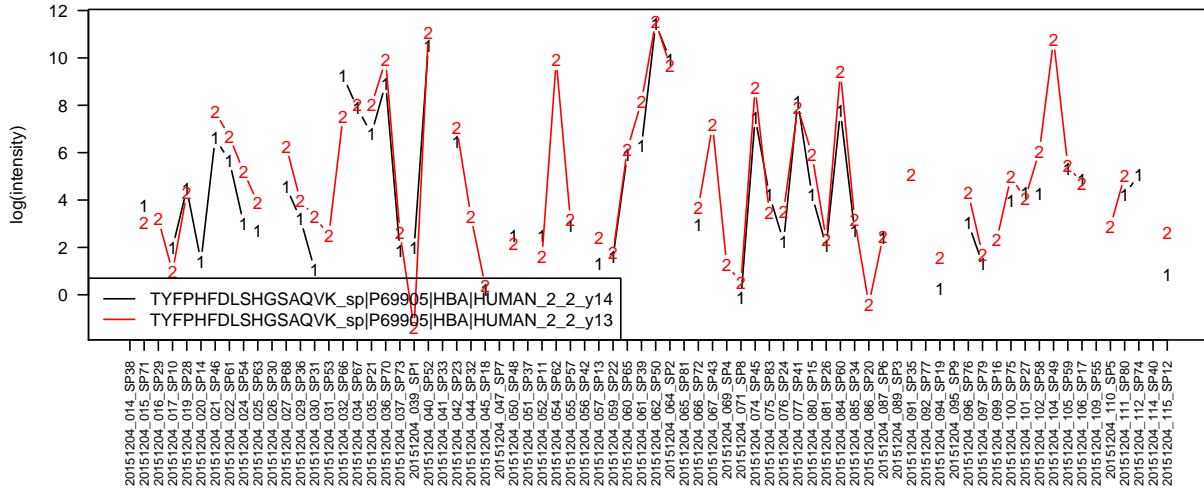
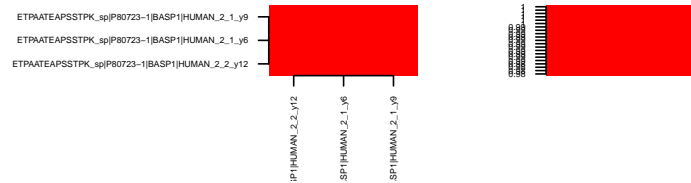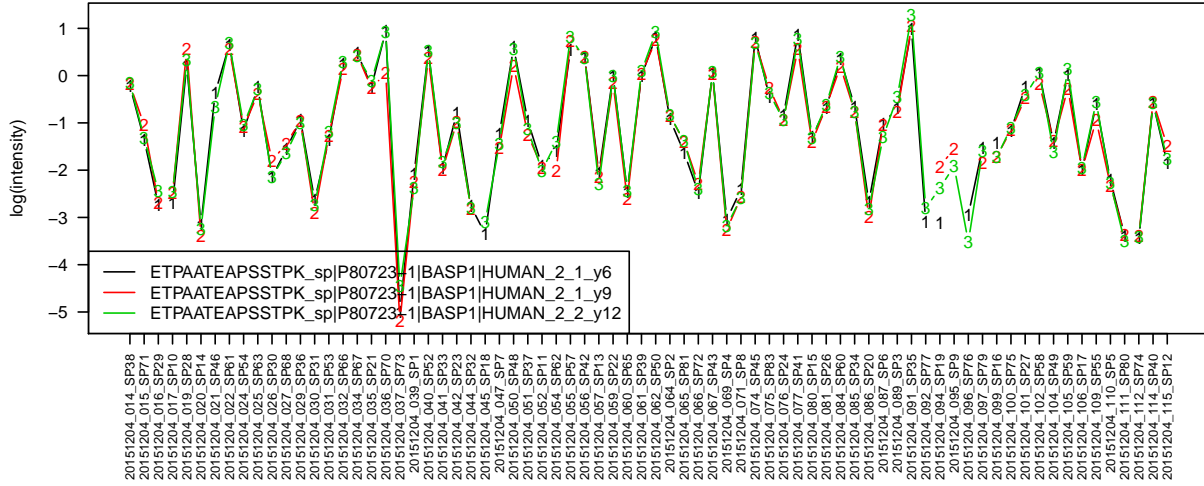# sp|P69905|HBA|HUMAN_TYFPHFDLSHGSAQVK_2

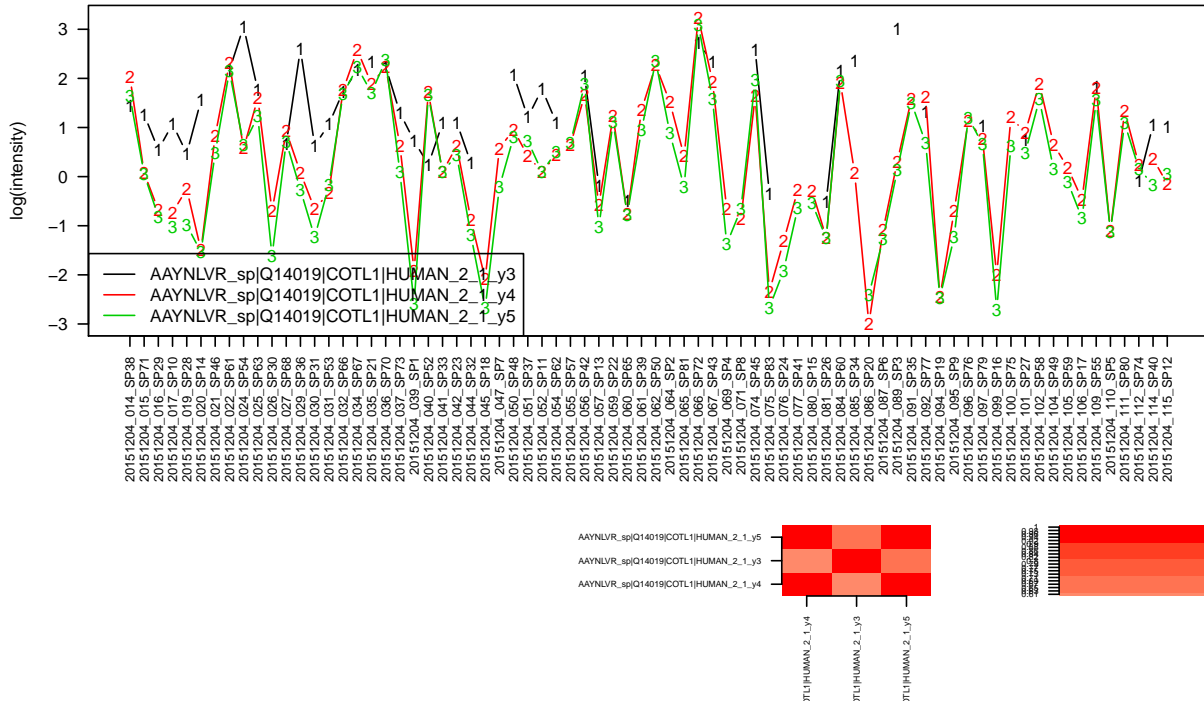# sp|P69905|HBA|HUMAN_VGAHAGEYGAEALER_3

sp|P80723−1|BASP1|HUMAN_ESEPQAAAEPAEAK_2

- ESEPQAAAEPAEAK_sp|P80723−1|BASP1|HUMAN_2_1_y5
- ESEPQAAAEPAEAK_sp|P80723−1|BASP1|HUMAN_2_1_y9
- ESEPQAAAEPAEAK_sp|P80723−1|BASP1|HUMAN_2_2_y11

sp|P80723−1|BASP1|HUMAN_ETPAATEAPSSTPK_2

- ETPAATEAPSSTPK_sp|P80723−1|BASP1|HUMAN_2_1_y6
- ETPAATEAPSSTPK_sp|P80723−1|BASP1|HUMAN_2_1_y9
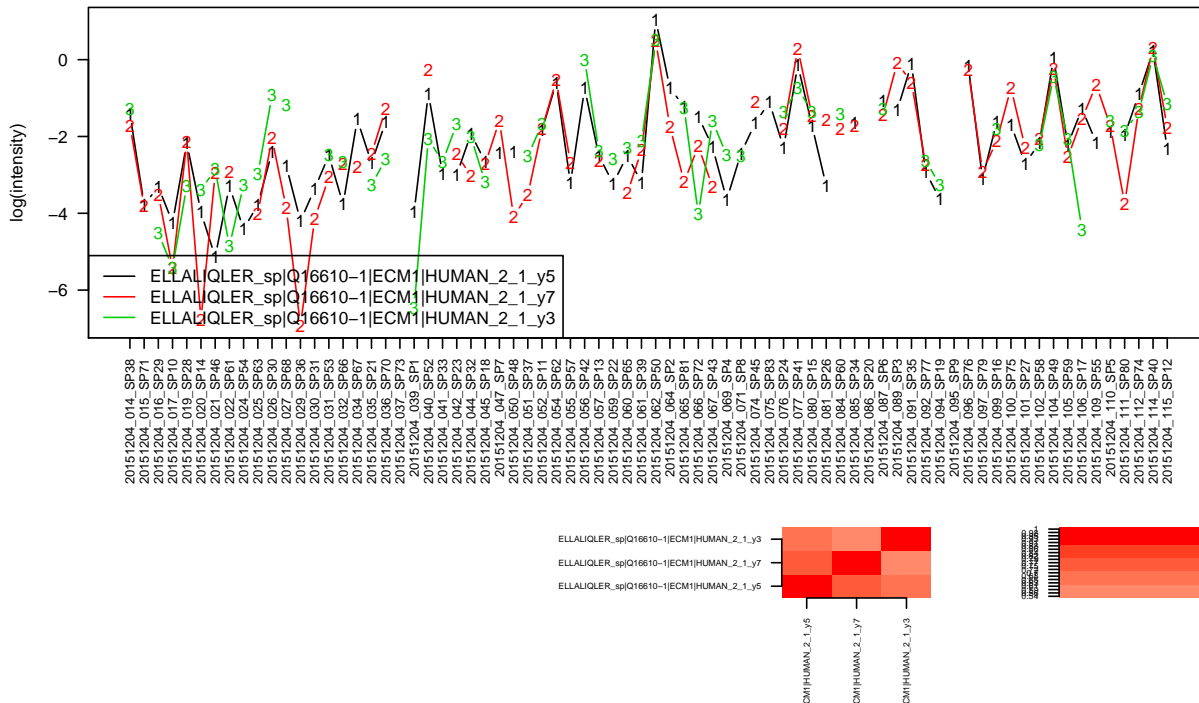- ETPAATEAPSSTPK_sp|P80723−1|BASP1|HUMAN_2_2_y12
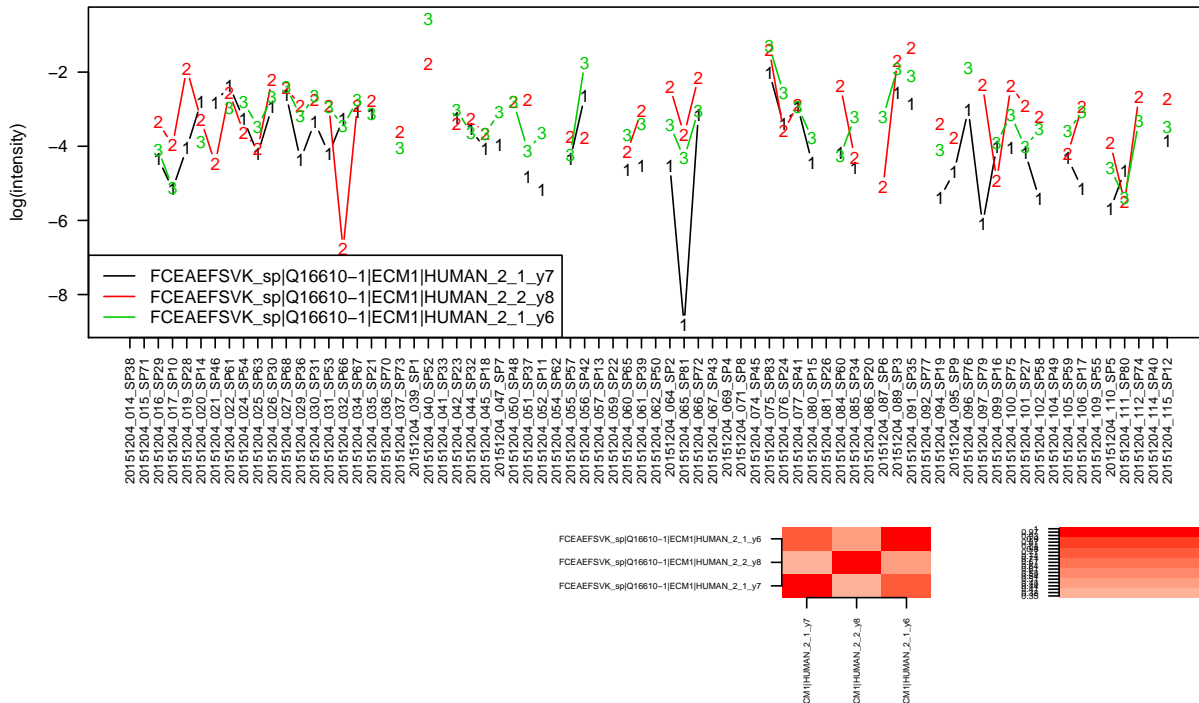
64
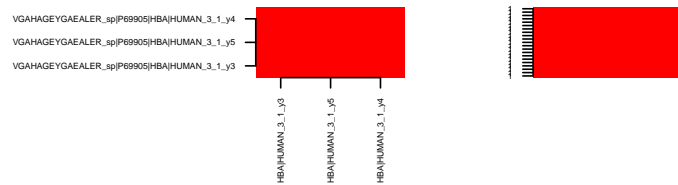
sp|Q14019|COTL1|HUMAN_AAYNLVR_2
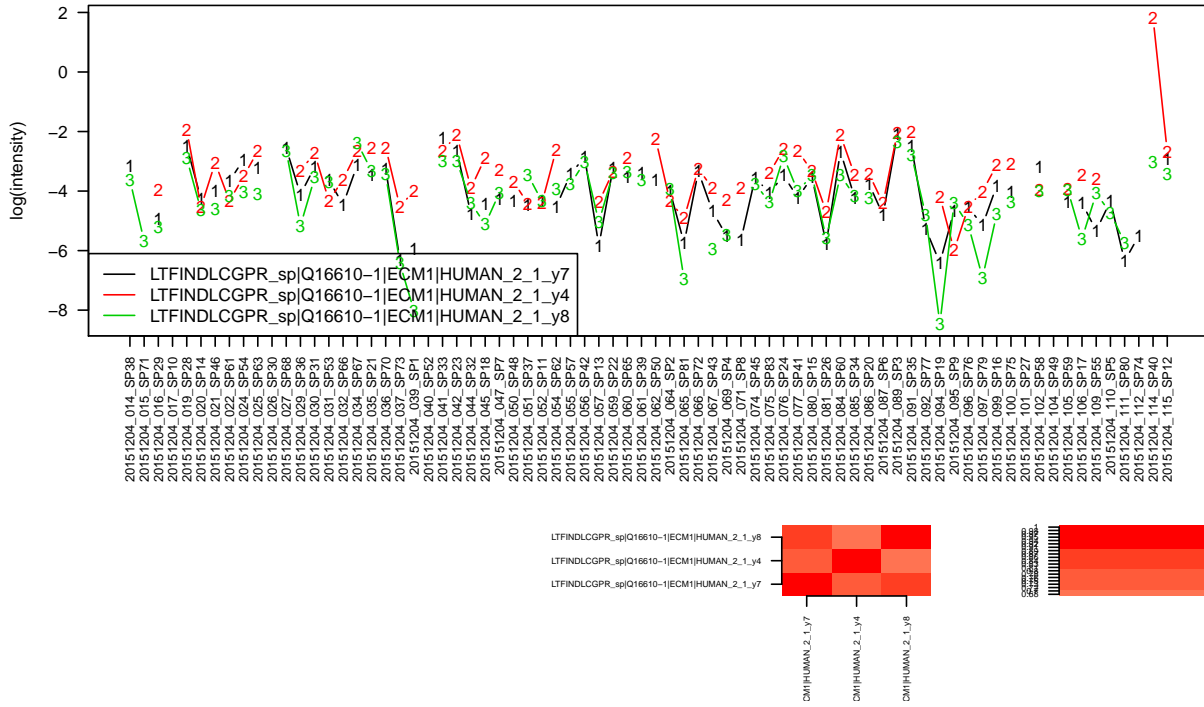

sp|Q14019|COTL1|HUMAN_LFAFVR_2
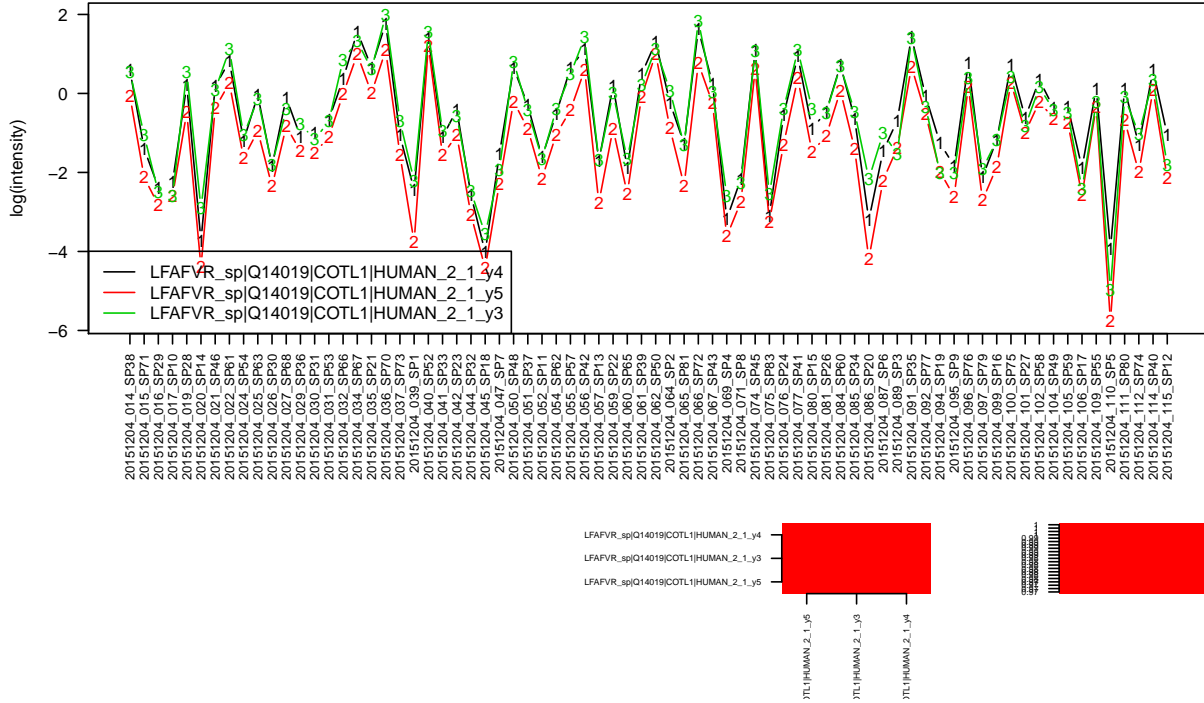
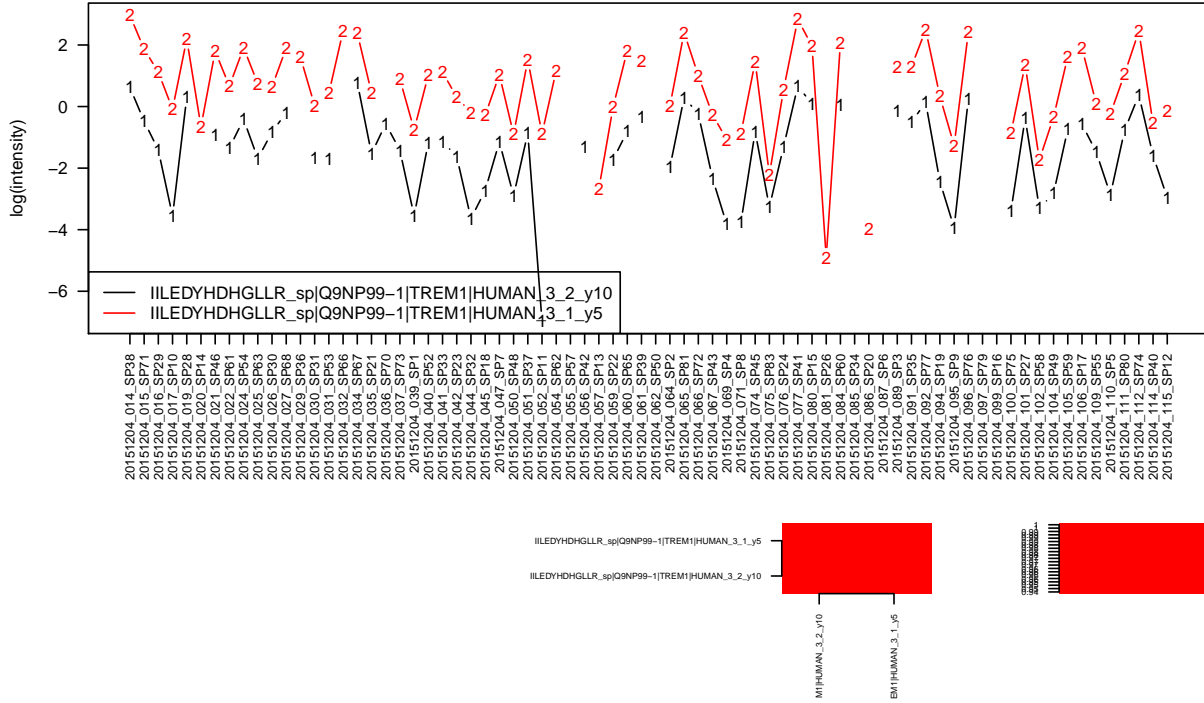**sp|Q16610−1|ECM1|HUMAN_ELLALIQLER_2**
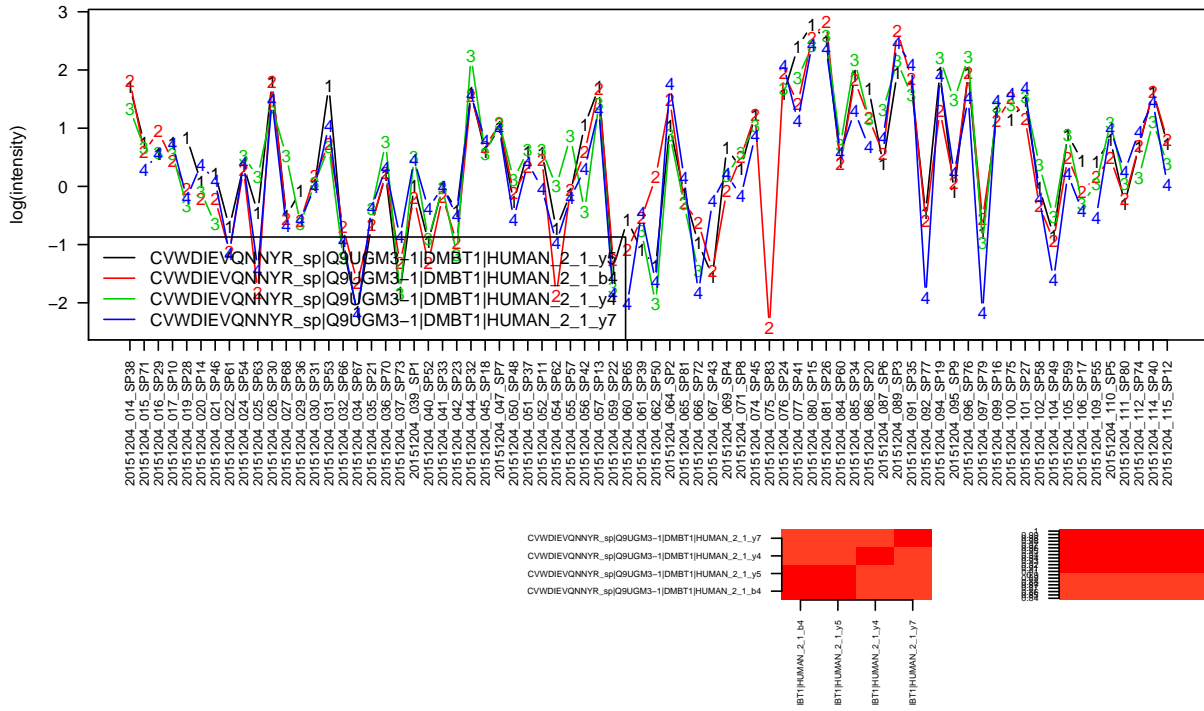

sp|Q16610−1|ECM1|HUMAN_FCEAEFSVK_2

sp|Q16610−1|ECM1|HUMAN_LTFINDLCGPR_2
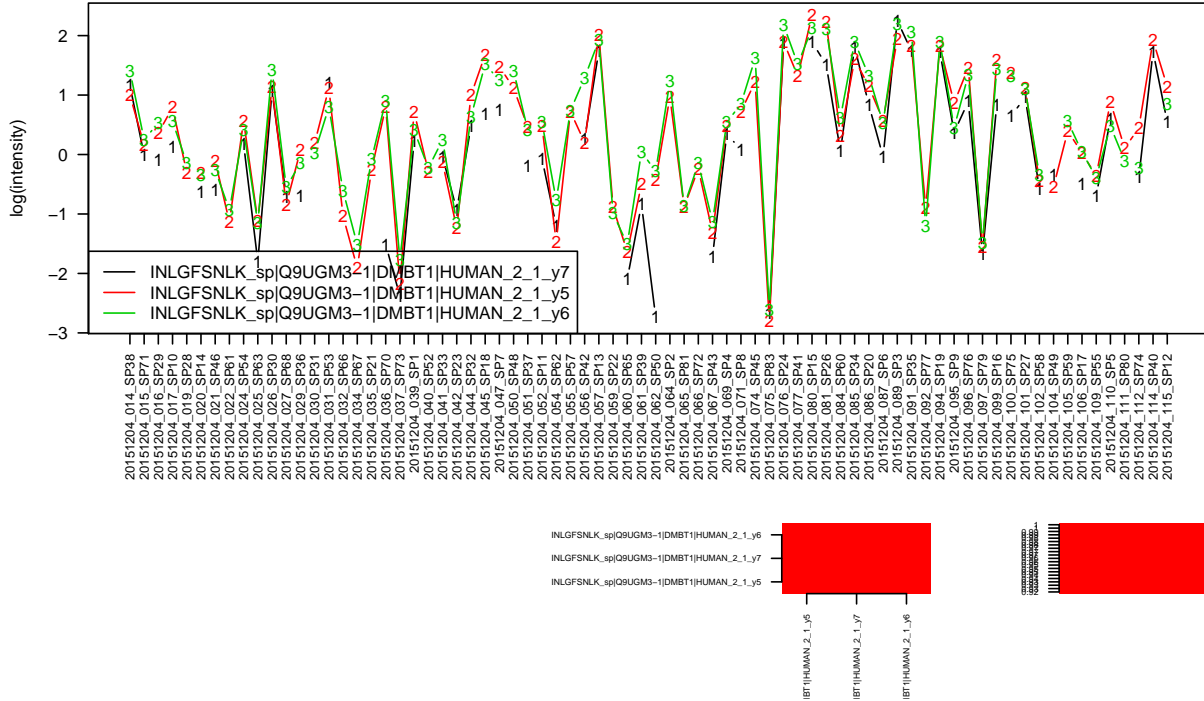

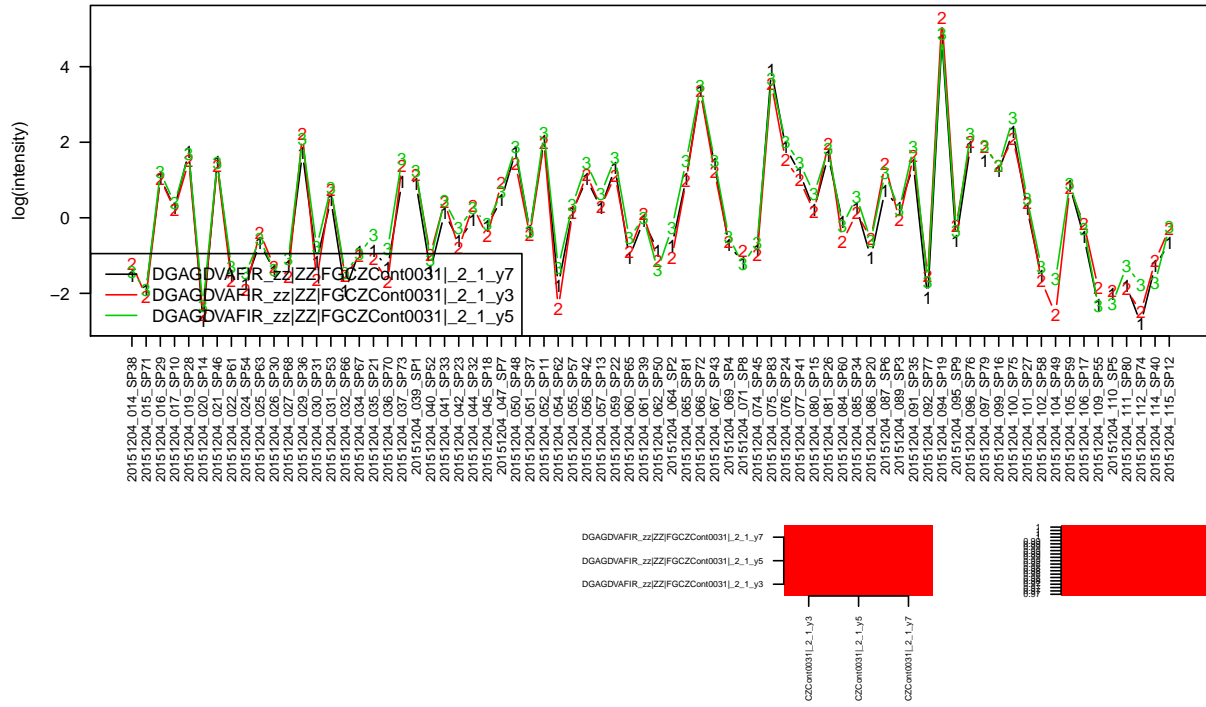**sp|Q9NP99−1|TREM1|HUMAN_IILEDYHDHGLLR_3**

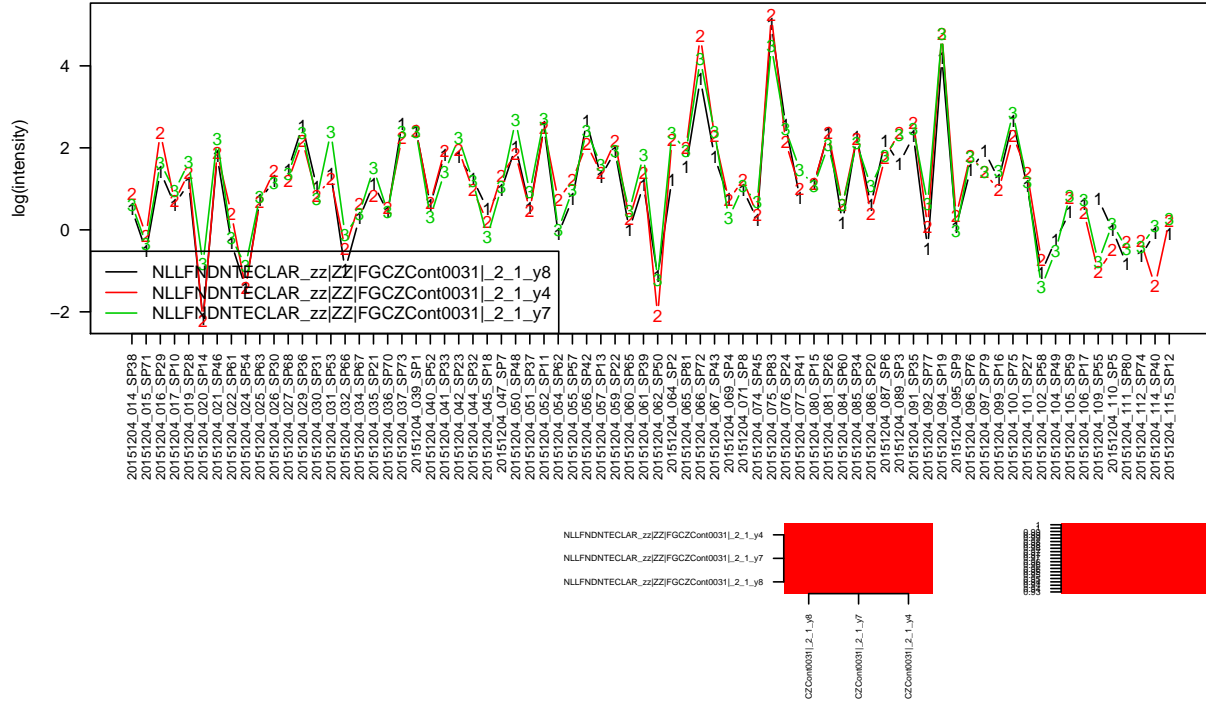**sp|Q9UGM3−1|DMBT1|HUMAN_CVWDIEVQNNYR_2**

sp|Q9UGM3−1|DMBT1|HUMAN_INLGFSNLK_2

zz|ZZ|FGCZCont0031|_DGAGDVAFIR_2

zz|ZZ|FGCZCont0031|_NLLFNDNTECLAR_2

zz|ZZ|FGCZCont0031|_SNLCALCIGDEQGENK_2