Supporting Information

Comparative analysis of cleavage specificities of immobilized porcine pepsin and Nepenthesin II under HDX conditions.

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Supporting Material Figure Legends

Figure S1. Venn diagram analysis of three LC-MSMS replicates of all eleven proteins between NepII and pepsin mediated cleavage events.

Figure S2. Fasta sequence of 11 proteins.

Figure S3 P4-P4' Frequencies. Percentage of amino acid occupation for all positions P4 to P4' with pepsin (top panels) and NepII (bottom panels) for "Unique Protein Sites" (left panels) and "All Peptides Sites" (right panels). Sum of all columns in each of the 4 tables is equal to 100%.

Figure S4. The frequency at which an amino acid was found in the entire peptide was subtracted from the frequency at which it was found in the positions P4 to P4' in order to highlight amino acids that are enriched (positive numbers; red) or depleted (negative numbers; blue) at specific positions. Values near 0 suggest amino acids that appear at a position no more often than are present in the entire peptide. Data presented as in Supplementary Figure 4, pepsin (top panels) and NepII (bottom panels) for "Unique Protein Sites" (left panels) and "All Peptides Sites" (right panels).

Figure S5. Background subtracted profiles (y-axis) of amino acids (top) at different positions (P4 to P4') x-axis were grouped per protein (right) and enzyme (NepII blue, Pepsin red). Kolmogorov Smirnov Asymptotic test followed by FDR (5%) to identify amino acids that were cleaved with different rates across pepsin and NepII at each position. Differentially cleaved amino acid-position combinations are highlighted with yellow graph background.

Figure S6. Sequence coverage maps of proteins tested. The analysis for each protein with both NepII and pepsin was conducted in triplicate and merged. Unique peptides were preserved and rendered using MSTools (1) so as to visualize maximum coverage with minimal convolution. Some of these maps are necessarily large due to protein sequence length and readers are encouraged to zoom in on regions of interest. Pepsin cleaved peptides are blue and NepII cleaved peptides are red.

(1) Kavan, D. and Man, P. "MSTools - Web based application for visualization and presentation of HXMS data" Int. J. Mass Spectrom. 2011, 302: 53-58. http://dx.doi.org/10.1016/j.ijms.2010.07.030.

Figure S7. Background subtracted prevalence of amino acids present at the P1 site depending on charge state. Three different subsets from the same dataset were selected, those peptides with charge state(s) of: +1, +2 through +7, and +1 through +7. The frequency of different amino acids at the P1 site was remarkably similar for unique peptides (A) and all peptides (B) in the three different subsets regardless of digestion enzyme.

Figure S8. Sequence coverage maps for PPARg with +1, +2 through +7, and +1 through +7 charge states. unique peptides. Triplicate datasets were merged and unique peptides were preserved. Though there are many peptides in the +1 map, the visual similarity of the +2 through +7 and +1 through +7 maps highlights how the number of unique peptides is not altered significantly by adding +1 charge peptides.

	+1 to +7	+2 to +7	+1 to +7	+2 to +7
	Pepsin		Nep II	
Total peptides	16,910	15,321	27,124	24,347
Total unique peptides	1,962	1,725	2,993	2,522
Avg. length of unique peptides	16.07	17.28	14.71	16.07

Table S1. Summary statistics of peptides cleaved by pepsin or nep II with respect to charge state.

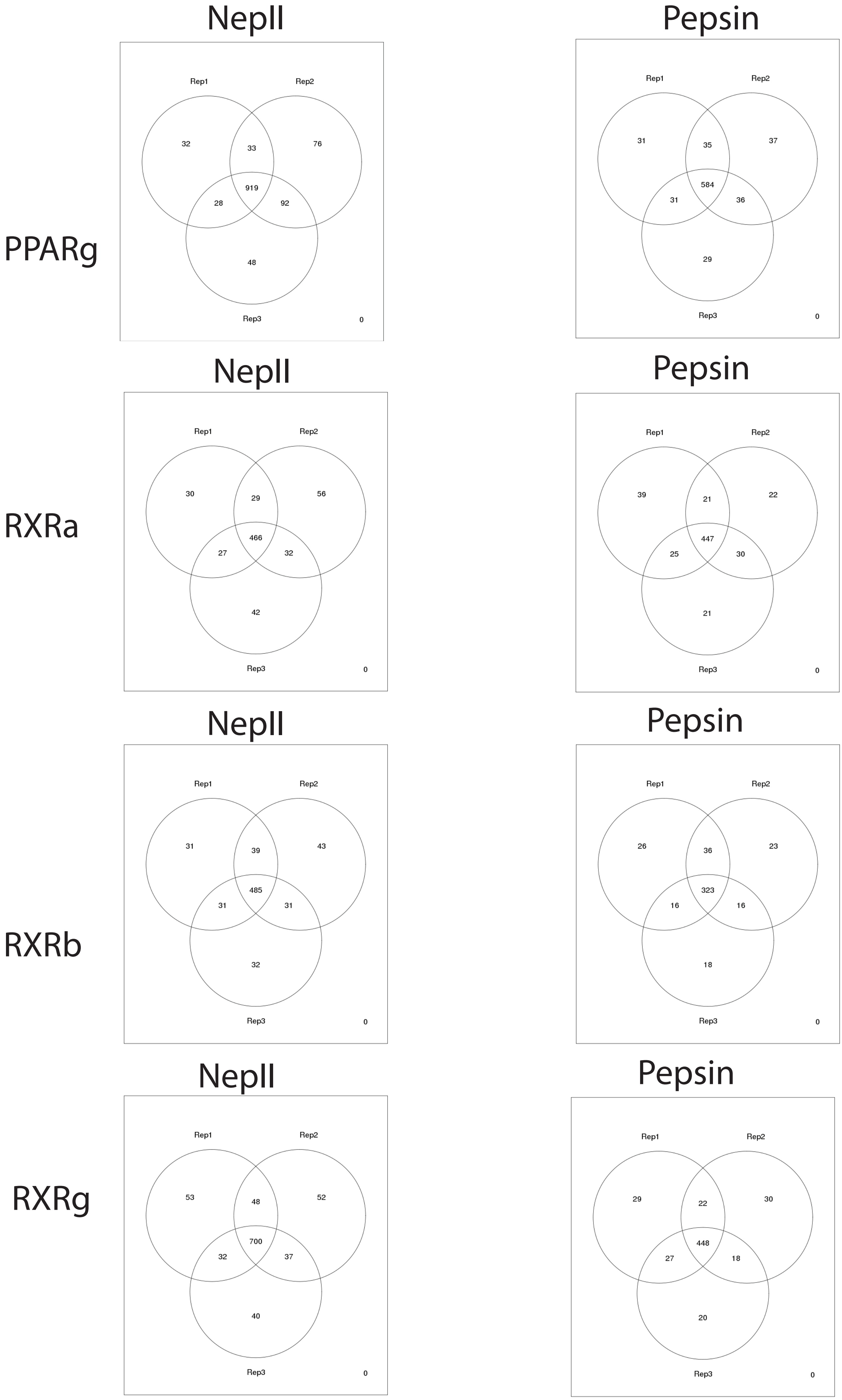
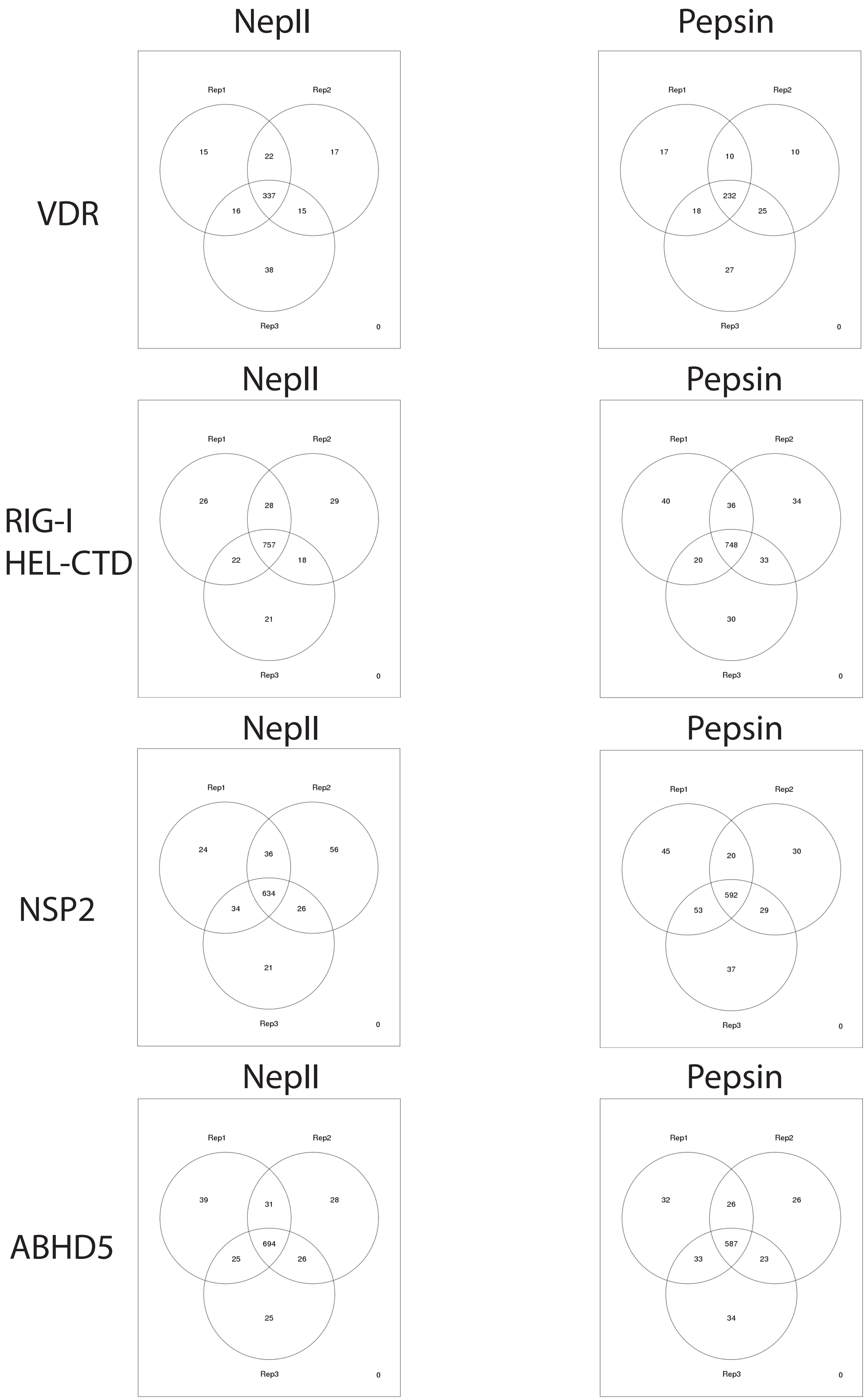

NepII
Pepsin
PPARg
Rep1
Rep2
Rep3
32
33
76
919
28
92
48
0
31
35
37
584
31
36
29
0
NepII
Pepsin
RXRa
Rep1
Rep2
Rep3
30
29
56
466
27
32
42
0
39
21
22
447
25
30
21
0
NepII
Pepsin
RXRb
Rep1
Rep2
Rep3
31
39
43
485
31
31
32
0
26
36
23
323
16
16
18
0
NepII
Pepsin
RXRg
Rep1
Rep2
Rep3
53
48
52
700
32
37
40
0
29
22
30
448
27
18
20
0

Figure S1



NepII
Pepsin
VDR
Rep1
Rep2
Rep3
15
22
17
337
16
15
38
0
Rep1
Rep2
Rep3
17
10
10
232
18
25
27
0
NepII
Pepsin
RIG-I
HEL-CTD
Rep1
Rep2
Rep3
26
28
29
757
22
18
21
0
Rep1
Rep2
Rep3
40
36
34
748
20
33
30
0
NepII
Pepsin
NSP2
Rep1
Rep2
Rep3
24
36
56
634
34
26
21
0
Rep1
Rep2
Rep3
45
20
30
592
53
29
37
0
NepII
Pepsin
ABHD5
Rep1
Rep2
Rep3
39
31
28
694
25
26
25
0
Rep1
Rep2
Rep3
32
26
26
587
33
23
34
0

Figure S1

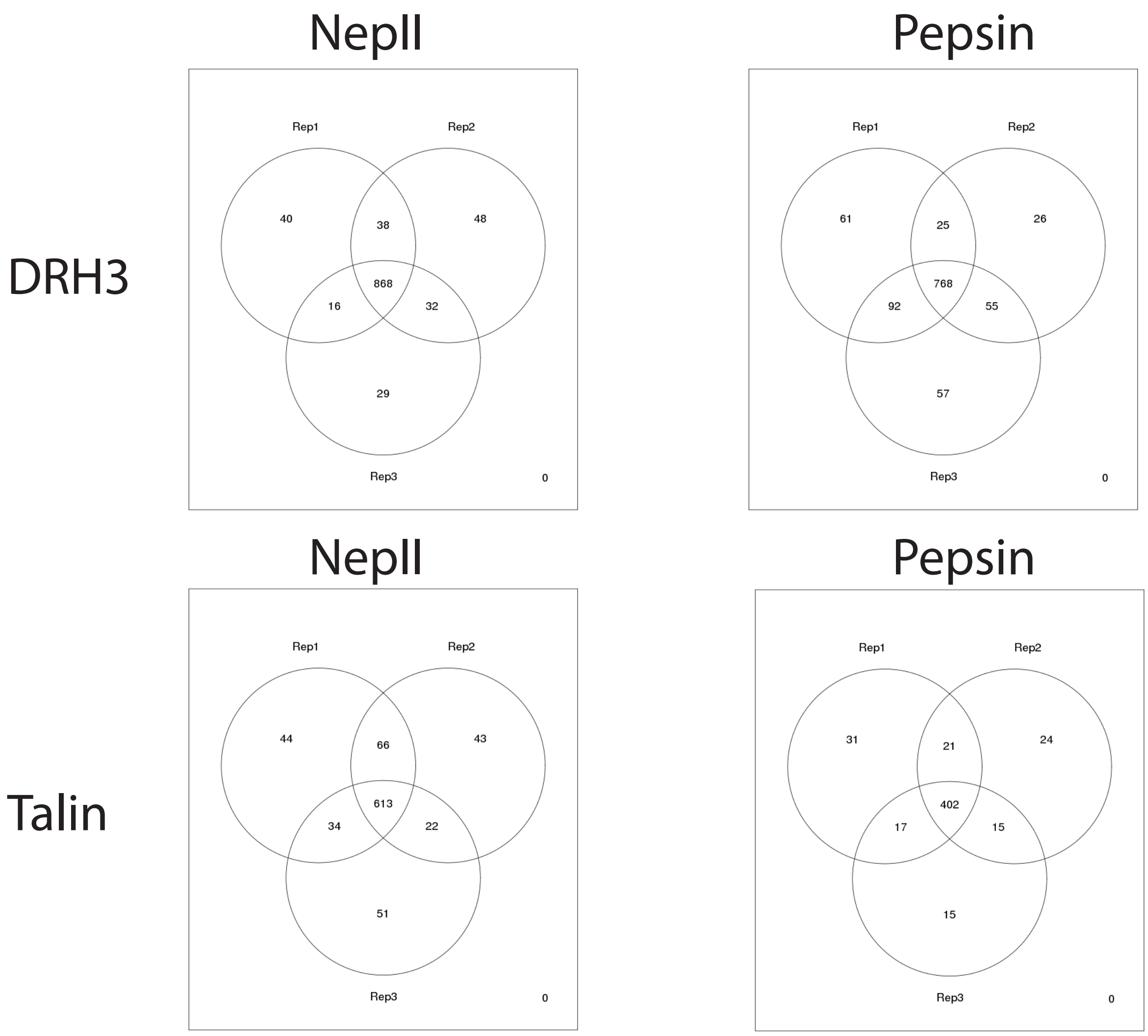

NepII
Pepsin
DRH3
Rep1
Rep2
40
38
48
868
16
32
29
Rep3
0
Rep1
Rep2
61
25
26
768
92
55
57
Rep3
0
NepII
Pepsin
Talin
Rep1
Rep2
44
66
43
613
34
22
51
Rep3
0
Rep1
Rep2
31
21
24
402
17
15
15
Rep3
0

Figure S1

>VDR

ELSQLSMLPHLADLVSYSIQKVIGFAKMIPGFRDLTSEDQIVLLKSSAIEVIMLRSNESFTMDDMS
WTCGNQDYKYRVSDVTKAGHSLELIEPLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDA
ALIEAIQDRLSNTLQTYIRCRHPPPGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECSMKL
TPLVLEVFGNEIS

>RC2

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>PPARg

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PLLQEIYKDLY

>RXRa

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NMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRIPHFSELPLDDQVILLRAGWNELLIASFSHR
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PIDTFLMEMLEAPHQMT

>RXRg

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>RXRb

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GGSGPPEDVKPPVLGVRGLHCPPPPGGPGAGKRLCAICGDRSSGKHYGVYSCEGCKGFFKR
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>RORg

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ERGKAEGRESFYSTGSQLTPDRCGLRFEEHRHPGLGELGQGPDSYGSPSFRSTPEAPYASLT
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>ABHD5

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>NSP2FL

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SGCSLALPTKRVTWVAPLGVRGADYTYNLELGLPATLGRYDLVVINIHTPFRIHHYQQCVDHAM
KLQMLGGDSLRLLKPGGSLLIRAYGYADRTSERVICVLGRKFRSSRALKPPCVTSNTEMFFLFS
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>Talin

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>DRH3

MQPTAIRLEDYDKSKLRLPFESPYFPAYFRLLKWKFLDVCVESTRNNDIGYFKLFESLFPPGKLE
EIARMIIDEPTPVSHDPDMIKIRNADLDVKIRKQAETYVTLRHAHQQKVQRRRFSECFLNTVLFD
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QLSVKALTFVQESDYSSMTKAKWSDVEQDLFYISEAIEDDFRIMLNALSDTEENIEKKIVLDLDS
RQHNKQLEMKRFHIQQEPPTKGVAPEAQ

Figure S2

Unique peptides in triple overlap - pepsin

	P4	P3	P2	P1	P1'	P2'	P3'	P4'
A	6.48	7.32	6.58	8.7	7.72	9.1	5.69	5.79
R	4.75	0.49	5	0.49	4.75	6.33	5.34	5.74
N	4.2	3.07	4.45	2.42	3.41	2.67	3.26	4.1
D	6.33	4.85	5.69	6.08	4.4	4.6	5.79	5.14
C	1.88	2.92	2.87	3.07	2.03	2.77	2.37	2.52
Q	4.3	3.61	5.24	4.45	2.82	4.01	4.25	3.91
E	7.27	7.37	8.95	11.03	5.98	7.96	7.17	7.17
G	4.95	6.63	4.06	4.15	2.42	4.65	4.5	6.78
H	3.07	0.89	2.13	0.54	2.52	1.29	2.32	3.02
I	6.33	7.96	6.78	2.42	8.16	6.68	7.32	4.95
L	8.7	14.14	9.64	21.61	12.46	8.26	12.22	10.14
K	7.12	2.57	6.23	0.3	5.39	7.91	8.9	7.32
M	2.27	3.07	2.57	5.14	3.76	2.52	3.56	2.77
F	4.2	2.77	3.66	8.85	6.97	2.92	3.26	3.36
P	5.89	6.38	0.59	0.45	3.46	2.32	2.67	6.58
S	5.39	9.1	8.36	4.75	6.38	7.37	6.82	6.48
T	5.04	5.89	5.64	5.24	4.15	5.54	5.29	5
W	0.94	0.64	0.64	1.24	1.19	0.35	0.69	1.04
Y	4.8	2.67	2.47	5	4.95	3.17	3.31	2.77
V	6.08	7.67	8.46	4.06	7.07	9.59	5.24	5.44

All peptides in triple overlap - pepsin

	P4	P3	P2	P1	P1'	P2'	P3'	P4'
A	5.97	9.31	6.32	7.58	7.77	11.26	5.77	4.83
R	5.08	0.09	4.72	0.09	4.51	7.66	7.07	4.95
N	3.99	3.29	5.2	1.26	2.54	2.29	1.89	3.62
D	6.91	3.36	6.44	4.49	4.22	3.45	5.66	5.59
C	1.15	2.79	2.93	2.65	1.5	2.4	1.38	3.21
Q	4.43	2.49	6.15	3.1	2.57	3.03	3.51	3.76
E	6	5.77	8.74	10.48	4.26	8.67	8.57	6.37
G	4.82	7.61	4.38	2.18	1.72	4.87	3.11	9.56
H	3.33	0.54	1.94	0.18	1.99	0.49	2.13	2.69
I	5.36	10.22	9.52	0.57	10.19	7.77	8.17	5.21
L	7.89	14.98	7.46	31.51	15.06	6.24	13.41	9.79
K	8.22	1.62	6.98	0.07	3.92	8.18	9.36	6.91
M	2.2	2.92	1.99	6.29	2.73	1.73	2.89	2.03
F	4.09	2.08	3.07	13.02	8.88	1.85	3.18	3.2
P	7.92	6.74	0.12	0.06	1.94	0.69	1.97	8.36
S	4.83	9.11	9.72	2.88	4.43	9.08	6.16	6.06
T	5.38	6.74	4.65	5.84	3.74	5.48	6.26	5.78
W	1.3	0.4	0.34	1.04	1.47	0.16	1.08	1.43
Y	5.27	2.5	1.25	4.1	7.27	2.73	2.72	2.02
V	5.86	7.44	8.09	2.6	9.28	11.98	5.71	4.65

Unique peptides in triple overlap - nepII

	P4	P3	P2	P1	P1'	P2'	P3'	P4'
A	4.74	5.97	6.53	7.57	7.93	9.52	6.81	5.06
R	5.38	5.66	5.66	5.66	4.1	4.5	6.13	5.62
N	3.9	3.82	3.31	3.7	4.82	3.11	3.58	4.54
D	5.3	4.34	5.58	7.25	5.89	3.31	6.37	5.62
C	2.23	2.99	2.95	3.07	2.79	2.99	2.59	2.31
Q	4.18	4.42	5.26	3.03	3.07	4.46	4.78	4.18
E	6.49	7.37	9.2	6.97	5.93	8.2	7.61	7.37
G	5.69	5.42	3.98	2.55	2.99	5.93	4.9	6.25
H	2.87	3.19	1.31	1.83	1.55	2.59	3.11	3.35
I	7.09	5.26	9.32	1.43	7.73	4.06	5.89	5.5
L	11.11	11.63	10.27	19.28	11.07	8.28	9.28	10.55
K	5.46	7.73	8.24	12.11	3.82	7.49	7.93	7.01
M	3.19	3.07	3.27	4.5	3.5	2.51	2.67	3.03
F	5.06	4.46	1.99	5.81	6.57	4.66	3.35	3.54
P	4.58	3.98	0.52	0.2	3.58	2.71	3.27	6.09
S	5.69	5.77	7.33	2.51	6.53	8.44	7.01	6.01
T	5.66	3.58	5.1	3.27	5.22	5.18	5.18	4.58
W	1.12	1.08	0.44	0.56	1	1.15	1	0.92
Y	4.34	4.3	1.23	5.58	4.9	3.5	2.83	2.87
V	5.93	5.97	8.52	3.15	7.01	7.41	5.73	5.62

All peptides in triple overlap - nepII

	P4	P3	P2	P1	P1'	P2'	P3'	P4'
A	3.88	7.22	5.24	5.74	7.63	13.95	7.25	4.68
R	4.05	6.04	4.96	6.92	4.74	4.74	7.21	4.25
N	3.53	4.26	2.09	2.76	4.43	2.76	2.79	3.69
D	7.35	4.48	4.52	6.2	6.31	1.78	6.12	5.73
C	1.89	1.82	3.7	2.79	3.08	2.41	1.92	1.94
Q	3.19	4.3	7.09	2.61	1.87	4.58	4.91	3.79
E	5.55	6.99	9.91	5.45	5.08	8.01	6.95	6.67
G	5.1	7.04	3.52	1.34	1.45	9.03	5.63	7.63
H	3.35	4.09	0.52	0.79	0.8	1.94	3.09	3.91
I	6.96	3.65	15.82	0.4	10.04	3.33	6.55	5.15
L	12.8	12.57	9.09	30.92	12.65	6.91	10.12	11.19
K	4.82	8.61	6.41	14.81	1.91	6.4	8.52	5.58
M	3.1	2.23	2.69	3.85	3.47	1.88	1.73	3.96
F	5.77	4.4	1.18	5.07	8.93	4.19	2.41	2.9
P	5.82	3.23	0.19	0.02	2.16	1.46	2.61	8.32
S	5.3	6.87	6.48	1.03	6.23	9.74	7.53	5.62
T	5.99	2.89	5.31	1.83	5.75	4.84	5.23	4.96
W	1.07	1.15	0.37	0.3	0.6	1.02	0.93	0.69
Y	4.72	3.88	0.57	5.65	4.8	3.31	2.13	2.62
V	5.74	4.27	10.35	1.52	8.08	7.73	6.38	6.71

Figure S3

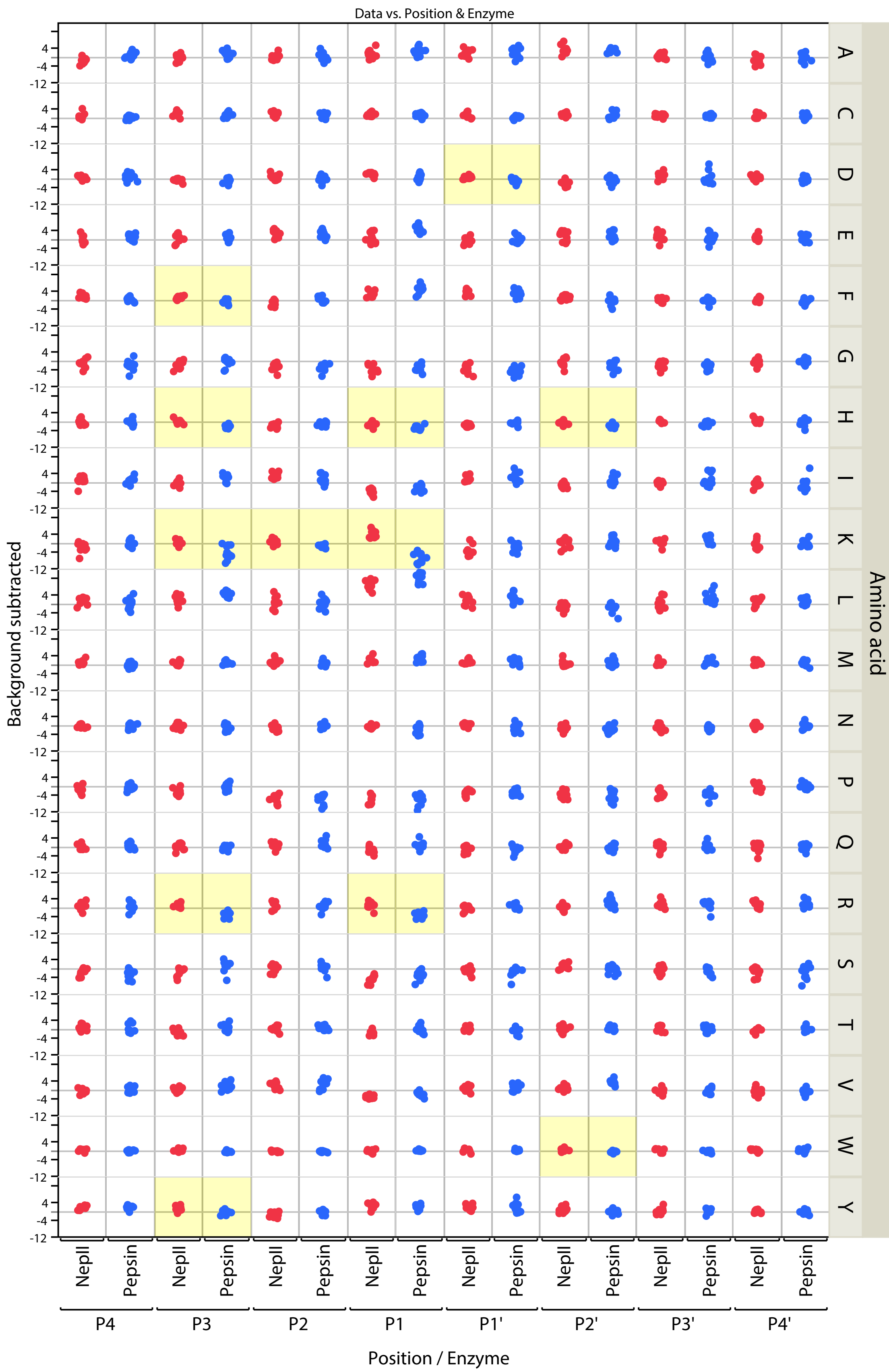
	Unique peptides in triple overlap - pepsin							
	P4	**P3**	**P2**	**P1**	**P1'**	**P2'**	**P3'**	**P4'**
A	0.38	1.22	0.48	2.61	1.62	3	-0.41	-0.31
R	0.74	-3.51	0.99	-3.51	0.74	2.33	1.34	1.73
N	-0.46	-1.59	-0.21	-2.24	-1.25	-1.99	-1.4	-0.56
D	0.96	-0.52	0.32	0.71	-0.97	-0.77	0.42	-0.23
C	0.22	1.26	1.21	1.4	0.37	1.11	0.71	0.86
Q	0.37	-0.32	1.31	0.52	-1.11	0.07	0.32	-0.02
E	1.08	1.18	2.76	4.84	-0.21	1.77	0.98	0.98
G	-2.06	-0.38	-2.95	-2.85	-4.58	-2.35	-2.5	-0.23
H	-0.12	-2.29	-1.06	-2.64	-0.66	-1.9	-0.86	-0.17
I	0.59	2.22	1.04	-3.32	2.42	0.94	1.58	-0.79
L	-0.85	4.59	0.09	12.06	2.91	-1.3	2.66	0.58
K	-0.17	-4.72	-1.07	-7	-1.91	0.62	1.61	0.02
M	0.04	0.83	0.33	2.91	1.52	0.28	1.32	0.53
F	0.58	-0.86	0.03	5.22	3.35	-0.71	-0.36	-0.27
P	-0.75	-0.25	-6.04	-6.19	-3.17	-4.31	-3.96	-0.05
S	-2.44	1.26	0.52	-3.09	-1.46	-0.47	-1.01	-1.36
T	-0.19	0.65	0.4	0	-1.08	0.3	0.05	-0.24
W	-0.12	-0.42	-0.42	0.17	0.12	-0.72	-0.37	-0.02
Y	1.92	-0.21	-0.41	2.11	2.06	0.28	0.43	-0.11
V	0.3	1.88	2.67	-1.73	1.28	3.81	-0.55	-0.35

	All peptides in triple overlap - pepsin							
	P4	**P3**	**P2**	**P1**	**P1'**	**P2'**	**P3'**	**P4'**
A	-0.03	3.3	0.31	1.57	1.76	5.25	-0.23	-1.18
R	1.27	-3.72	0.92	-3.71	0.71	3.85	3.26	1.14
N	-0.65	-1.34	0.56	-3.37	-2.1	-2.35	-2.74	-1.02
D	1.82	-1.73	1.35	-0.6	-0.87	-1.64	0.57	0.5
C	-0.27	1.37	1.52	1.24	0.09	0.99	-0.03	1.8
Q	0.58	-1.36	2.3	-0.75	-1.28	-0.82	-0.34	-0.09
E	0.15	-0.07	2.9	4.64	-1.59	2.83	2.72	0.52
G	-2.23	0.56	-2.68	-4.88	-5.34	-2.19	-3.94	2.5
H	0.25	-2.54	-1.14	-2.91	-1.09	-2.6	-0.96	-0.39
I	-0.86	4	3.3	-5.65	3.97	1.55	1.95	-1.01
L	-1.92	5.17	-2.36	21.7	5.25	-3.58	3.6	-0.02
K	1.28	-5.31	0.05	-6.86	-3.01	1.25	2.43	-0.02
M	-0.07	0.65	-0.28	4.02	0.46	-0.54	0.62	-0.24
F	0.32	-1.69	-0.69	9.25	5.11	-1.91	-0.59	-0.56
P	0.68	-0.49	-7.12	-7.17	-5.29	-6.54	-5.26	1.12
S	-3.38	0.89	1.51	-5.34	-3.78	0.87	-2.05	-2.16
T	0.05	1.4	-0.69	0.51	-1.6	0.14	0.92	0.44
W	0.24	-0.67	-0.73	-0.02	0.41	-0.9	0.02	0.37
Y	2.62	-0.15	-1.4	1.45	4.63	0.08	0.07	-0.63
V	0.13	1.72	2.36	-3.12	3.55	6.25	-0.02	-1.08

	Unique peptides in triple overlap - nepII							
	P4	**P3**	**P2**	**P1**	**P1'**	**P2'**	**P3'**	**P4'**
A	-1.58	-0.34	0.22	1.25	1.61	3.2	0.49	-1.26
R	0.94	1.22	1.22	1.22	-0.34	0.06	1.69	1.18
N	-0.31	-0.39	-0.91	-0.51	0.61	-1.11	-0.63	0.33
D	-0.01	-0.97	0.27	1.94	0.59	-2	1.06	0.31
C	0.64	1.39	1.35	1.47	1.2	1.39	1	0.72
Q	-0.01	0.23	1.06	-1.17	-1.13	0.27	0.58	-0.01
E	0.16	1.04	2.87	0.64	-0.39	1.88	1.28	1.04
G	-1.21	-1.48	-2.92	-4.35	-3.91	-0.97	-2	-0.65
H	-0.23	0.08	-1.79	-1.27	-1.55	-0.51	0.01	0.24
I	1.18	-0.65	3.41	-4.47	1.82	-1.84	-0.01	-0.41
L	1.39	1.91	0.56	9.56	1.35	-1.44	-0.44	0.83
K	-2	0.27	0.79	4.65	-3.63	0.03	0.47	-0.44
M	0.82	0.7	0.9	2.14	1.14	0.15	0.31	0.66
F	1.85	1.26	-1.21	2.61	3.37	1.45	0.14	0.34
P	-2.05	-2.64	-6.11	-6.43	-3.04	-3.92	-3.36	-0.53
S	-2.06	-1.98	-0.43	-5.25	-1.23	0.69	-0.75	-1.74
T	0.59	-1.48	0.03	-1.8	0.15	0.11	0.11	-0.49
W	0.4	0.36	-0.28	-0.16	0.28	0.44	0.28	0.2
Y	1.64	1.6	-1.46	2.88	2.2	0.81	0.13	0.17
V	-0.17	-0.13	2.42	-2.95	0.91	1.31	-0.37	-0.48

	All peptides in triple overlap - nepII							
	P4	**P3**	**P2**	**P1**	**P1'**	**P2'**	**P3'**	**P4'**
A	-2.65	0.68	-1.3	-0.8	1.09	7.41	0.72	-1.86
R	-0.19	1.8	0.72	2.68	0.5	0.5	2.96	0.01
N	-0.57	0.16	-2.02	-1.35	0.32	-1.35	-1.32	-0.41
D	2.22	-0.65	-0.62	1.07	1.17	-3.35	0.99	0.6
C	0.49	0.42	2.3	1.39	1.68	1.01	0.51	0.54
Q	-0.89	0.22	3.01	-1.47	-2.21	0.5	0.83	-0.29
E	-0.37	1.07	3.99	-0.47	-0.84	2.09	1.03	0.75
G	-2.19	-0.25	-3.78	-5.96	-5.84	1.73	-1.66	0.33
H	0.28	1.02	-2.55	-2.28	-2.28	-1.13	0.01	0.83
I	0.71	-2.6	9.57	-5.85	3.79	-2.92	0.31	-1.1
L	2.85	2.63	-0.85	20.98	2.7	-3.03	0.17	1.24
K	-2.09	1.7	-0.51	7.9	-5	-0.51	1.61	-1.33
M	0.91	0.03	0.5	1.65	1.28	-0.32	-0.46	1.77
F	2.58	1.21	-2.01	1.87	5.74	0.99	-0.78	-0.29
P	-1.51	-4.1	-7.14	-7.3	-5.17	-5.87	-4.72	0.99
S	-2.87	-1.3	-1.68	-7.14	-1.94	1.57	-0.64	-2.54
T	1.08	-2.02	0.4	-3.07	0.85	-0.06	0.32	0.05
W	0.38	0.46	-0.32	-0.39	-0.09	0.34	0.24	0
Y	2.2	1.36	-1.95	3.13	2.27	0.79	-0.39	0.1
V	-0.38	-1.85	4.23	-4.6	1.96	1.6	0.26	0.59

Figure S4



Data vs. Position & Enzyme
Background subtracted
4
-4
-12
A
C
D
E
F
G
H
I
K
L
M
N
P
Q
R
S
T
V
W
Y
Amino acid
NepII
Pepsin
P4
P3
P2
P1
P1'
P2'
P3'
P4'
Position / Enzyme

Figure S5

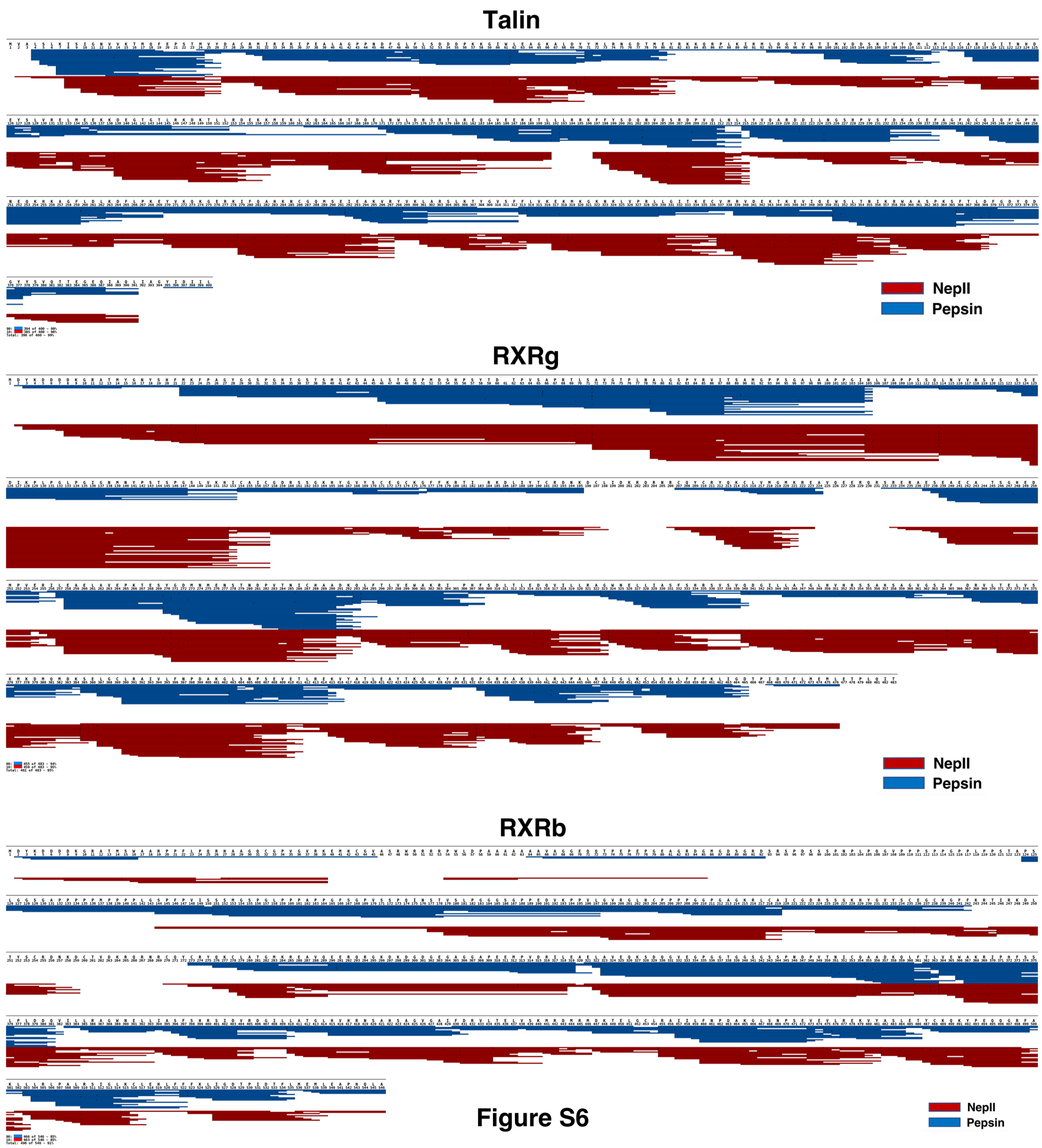


Figure S6

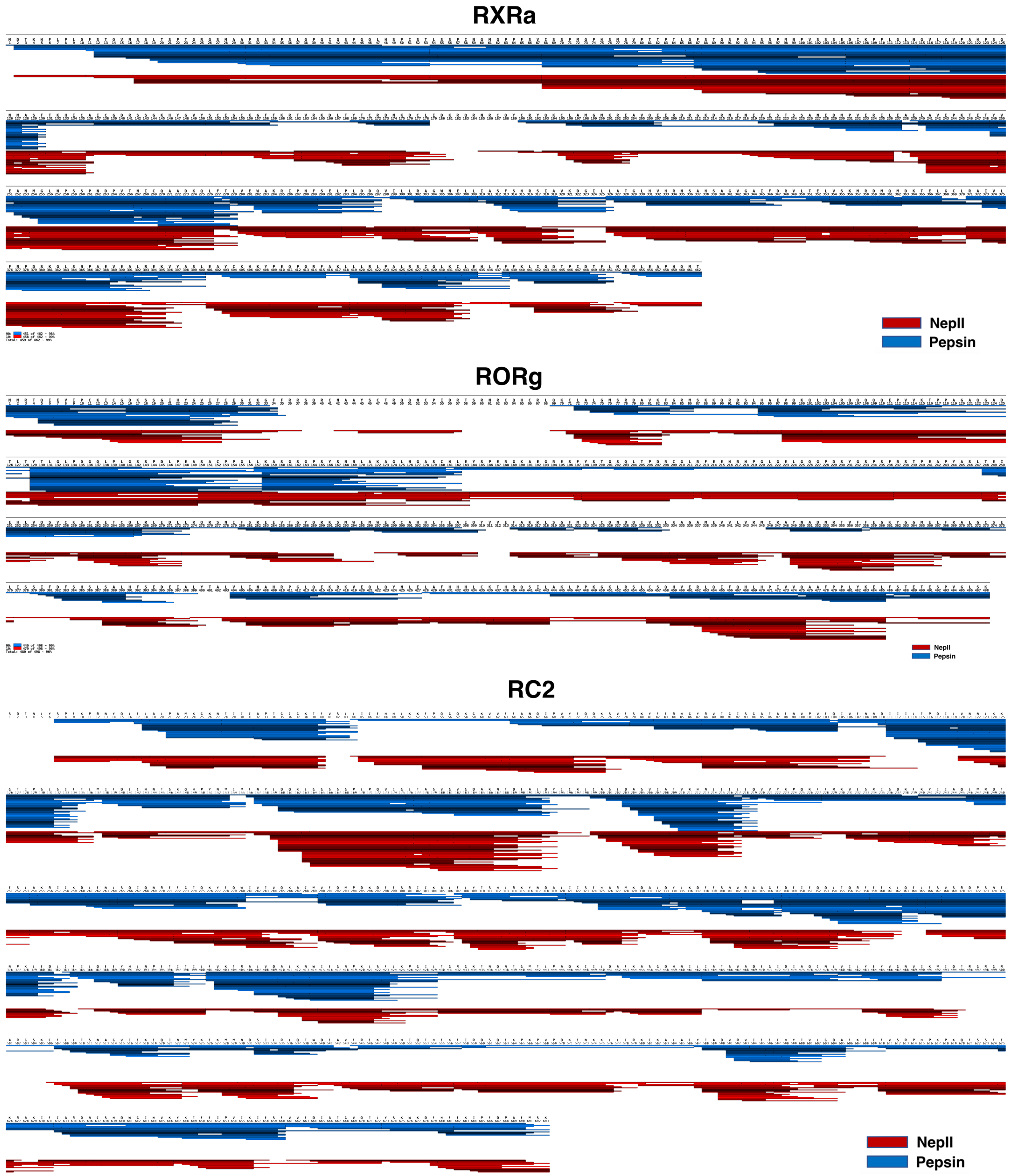
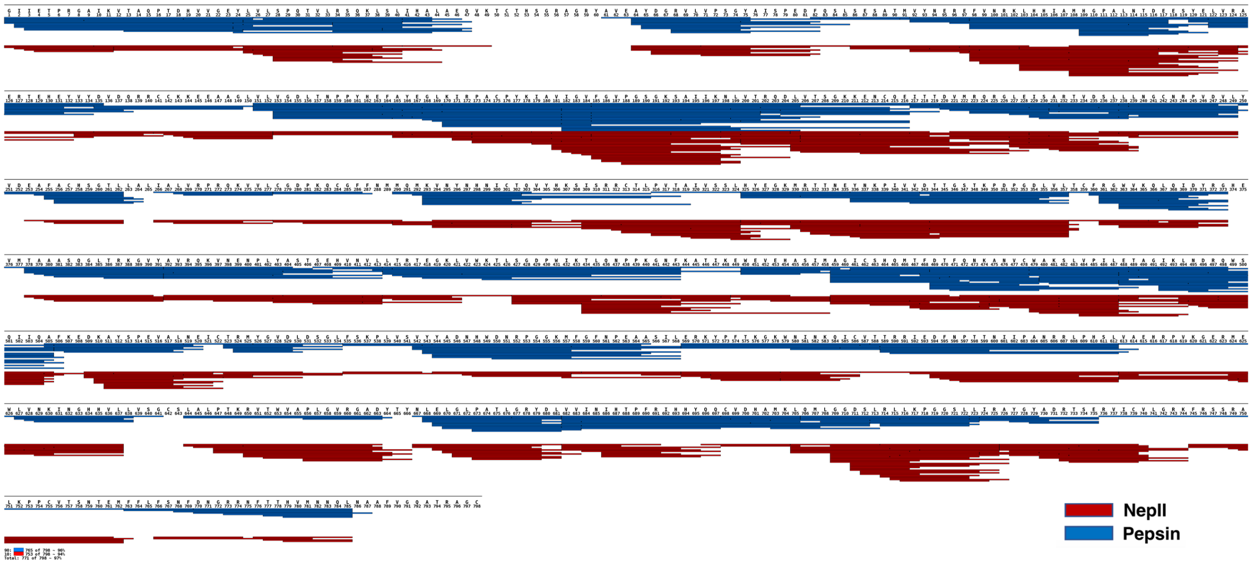


Figure S6

NSP2



DRH3

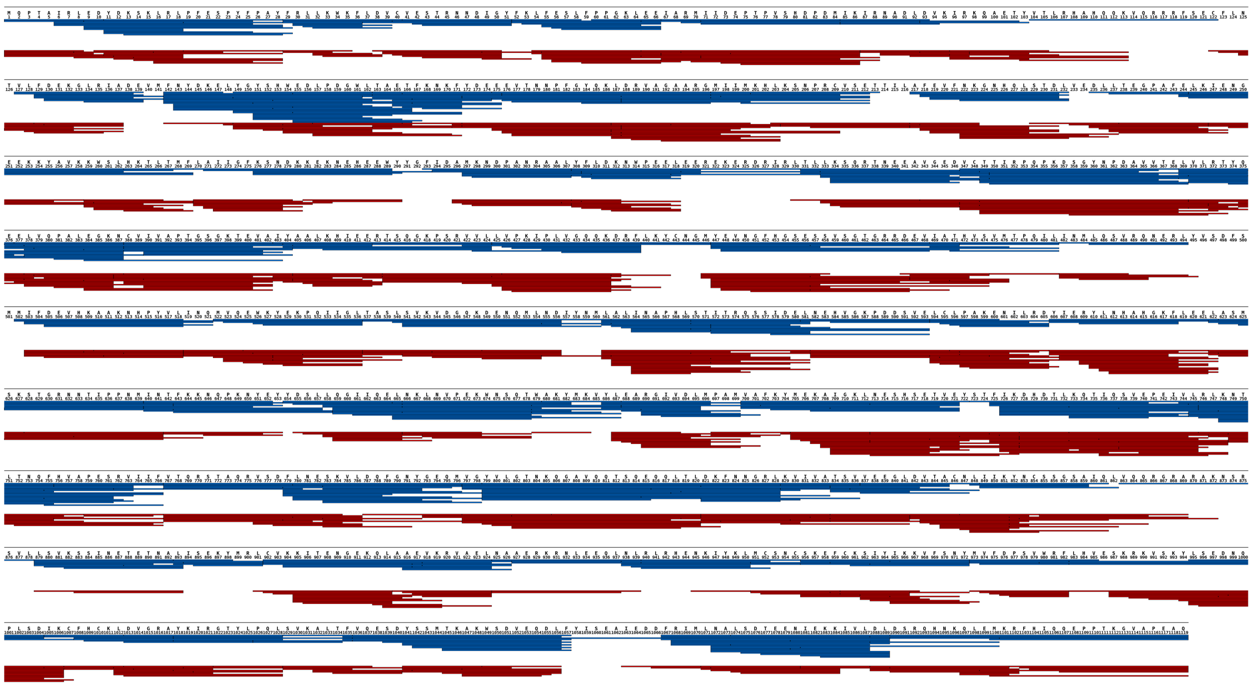
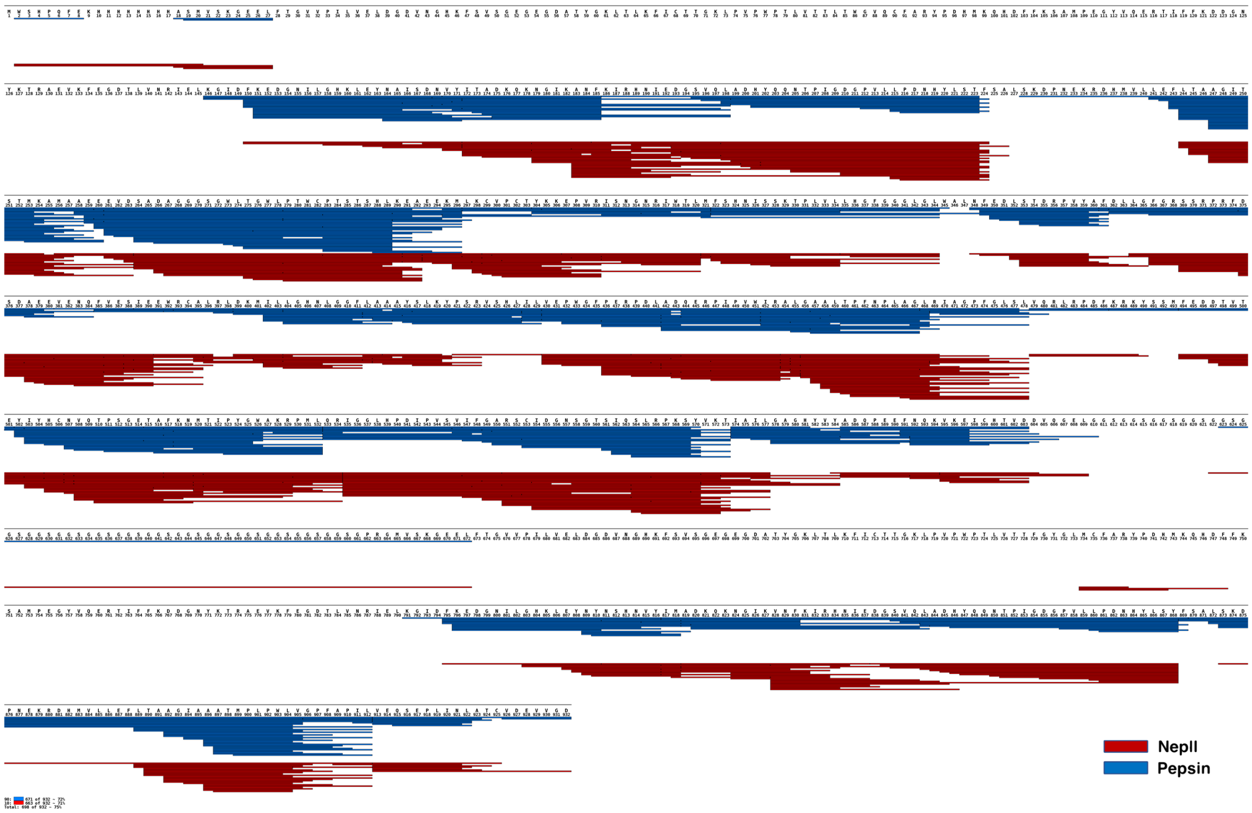


Figure S6

ABHD5



PPARg

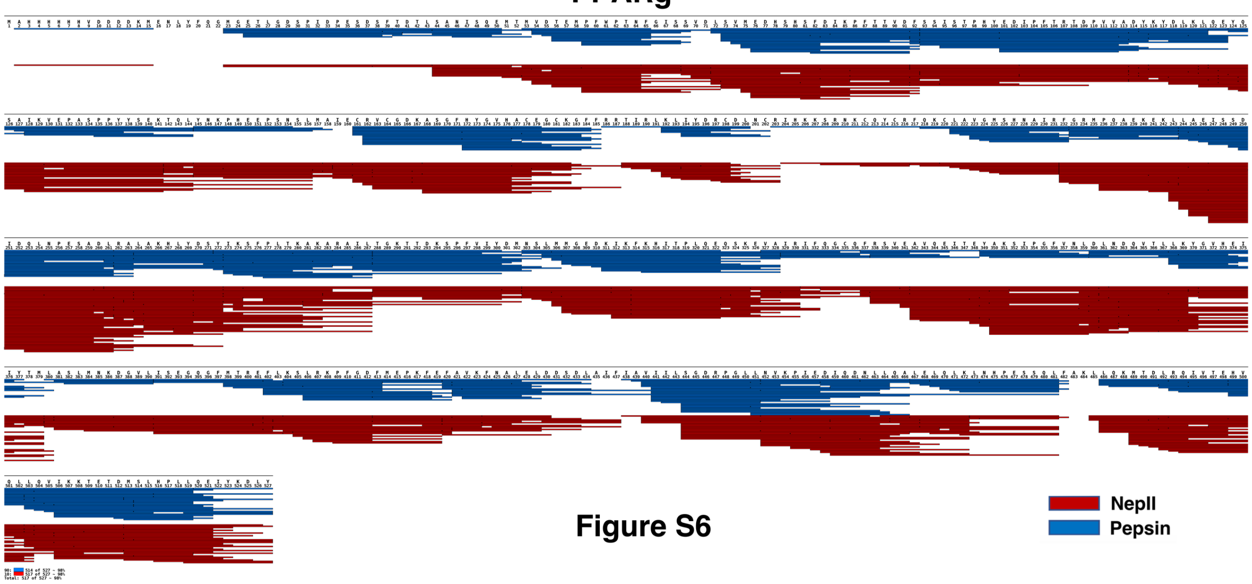


Figure S6

VDR

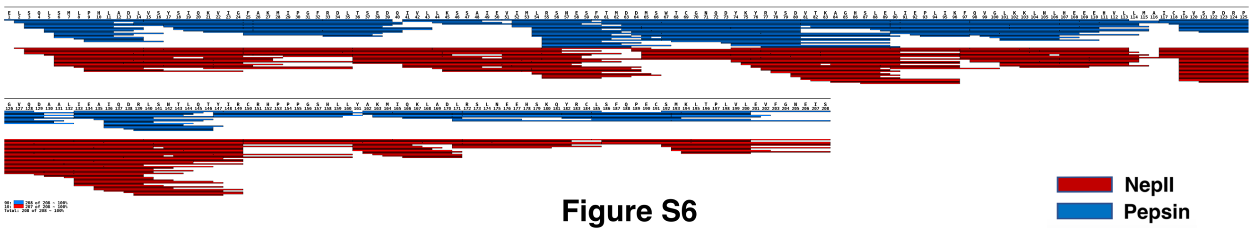


Figure S6

A

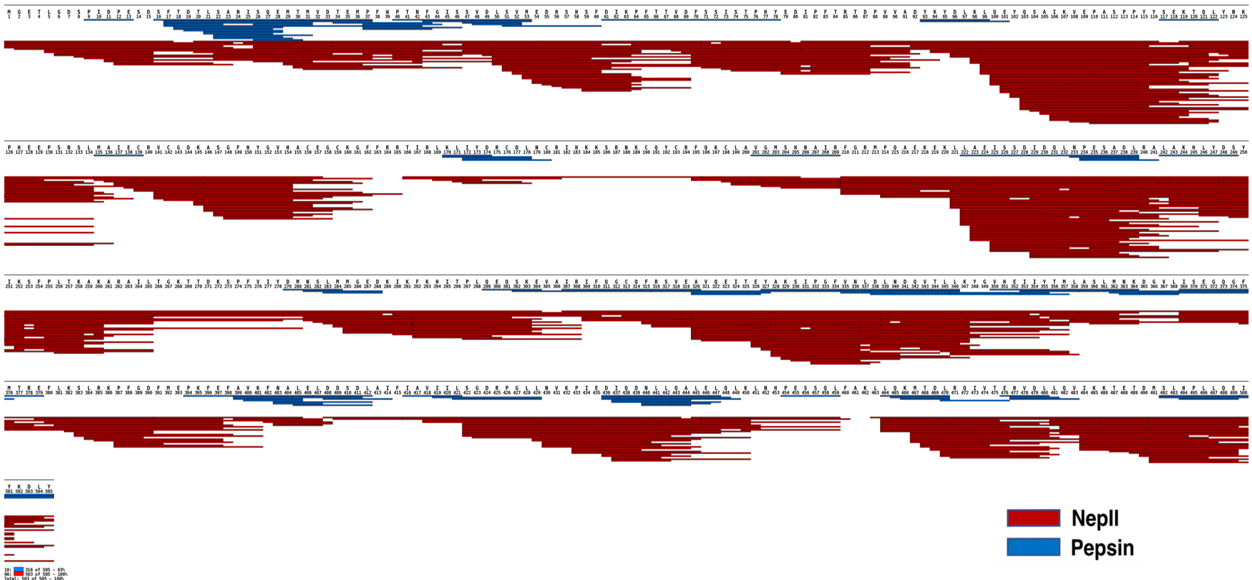
	1	2-7	1-7	1	2-7	1-7
		pepsin			nep II	
	P1	P1	P1	P1	P1	P1
A	1.57	2.4	2.25	0.37	0.74	0.94
R	-1.35	-3.99	-3.88	3.16	1.22	1.44
N	-2.27	-2.06	-1.66	-0.97	-0.2	-0.29
D	2.3	2.86	3.09	1.79	2.72	2.4
C	-0.29	0.36	0.57	-0.2	1.42	1.12
Q	-0.35	1.06	1	-1.17	-1.56	-1.34
E	5.77	3.58	3.45	0.46	1.54	1.23
G	-1.96	-1.96	-1.81	-2.43	-3.51	-3.07
H	-2.56	-3.14	-3.12	-0.69	-1.14	-1.09
I	-4.84	-4.33	-3.84	-5.48	-4.33	-3.82
L	13.17	12.29	11.4	9.89	7.91	6.73
K	-3.04	-6.25	-5.97	7.49	4.48	3.96
M	2.86	3.31	3.23	1.24	1.69	1.69
F	5.67	5.83	5.05	1.14	2.36	2.45
P	-4.49	-5.22	-5.07	-4.82	-6.15	-5.8
S	-4.79	-2.55	-2.6	-4.89	-3.89	-3.74
T	-1.33	-0.85	-0.88	-2.04	-1.84	-1.78
W	0.05	0.11	0.21	-0.1	-0.06	0
Y	0.06	1.01	0.95	1.41	1.69	1.63
V	-4.16	-2.46	-2.37	-4.15	-3.1	-2.66

B

	1	2-7	1-7	1	2-7	1-7
		pepsin			nep II	
	P1	P1	P1	P1	P1	P1
A	0.97	1.23	1.29	-0.88	-2.39	-2.2
R	-1.29	-4.44	-4.33	2.69	4.4	4.07
N	-2.98	-3.03	-3.01	-1.19	-2.1	-2
D	0.21	-0.09	0.09	2.94	2.29	2.43
C	-0.65	0.21	0.11	-0.38	0.58	0.47
Q	-2.07	-0.84	-0.95	-1.61	-1.88	-1.89
E	5.62	4.41	4.5	-1.7	-0.17	-0.29
G	-2.32	-4.36	-4.31	-3.04	-5.07	-4.96
H	-2.33	-4.55	-4.47	-1.11	-3.3	-3.16
I	-6.38	-5.06	-5.05	-6.14	-5.87	-5.8
L	20.65	20.9	21.24	17.07	17.13	17.36
K	-2.85	-5.91	-5.91	11.17	13.09	12.79
M	2.52	6.34	6.05	1.1	2.3	2.21
F	7.89	9.71	9.66	0.81	1.52	1.53
P	-4.67	-5.87	-5.83	-5.78	-6.59	-6.54
S	-4.96	-4.31	-4.28	-6.01	-6.73	-6.66
T	-1.62	-1.49	-1.6	-2.83	-4.24	-4.16
W	-0.06	-0.83	-0.79	-0.42	-0.24	-0.24
Y	-0.56	1.95	1.68	-0.1	2.45	2.16
V	-5.1	-4	-4.08	-4.58	-5.17	-5.12

Figure S7

PPARγ +1



PPARγ +2 through +7

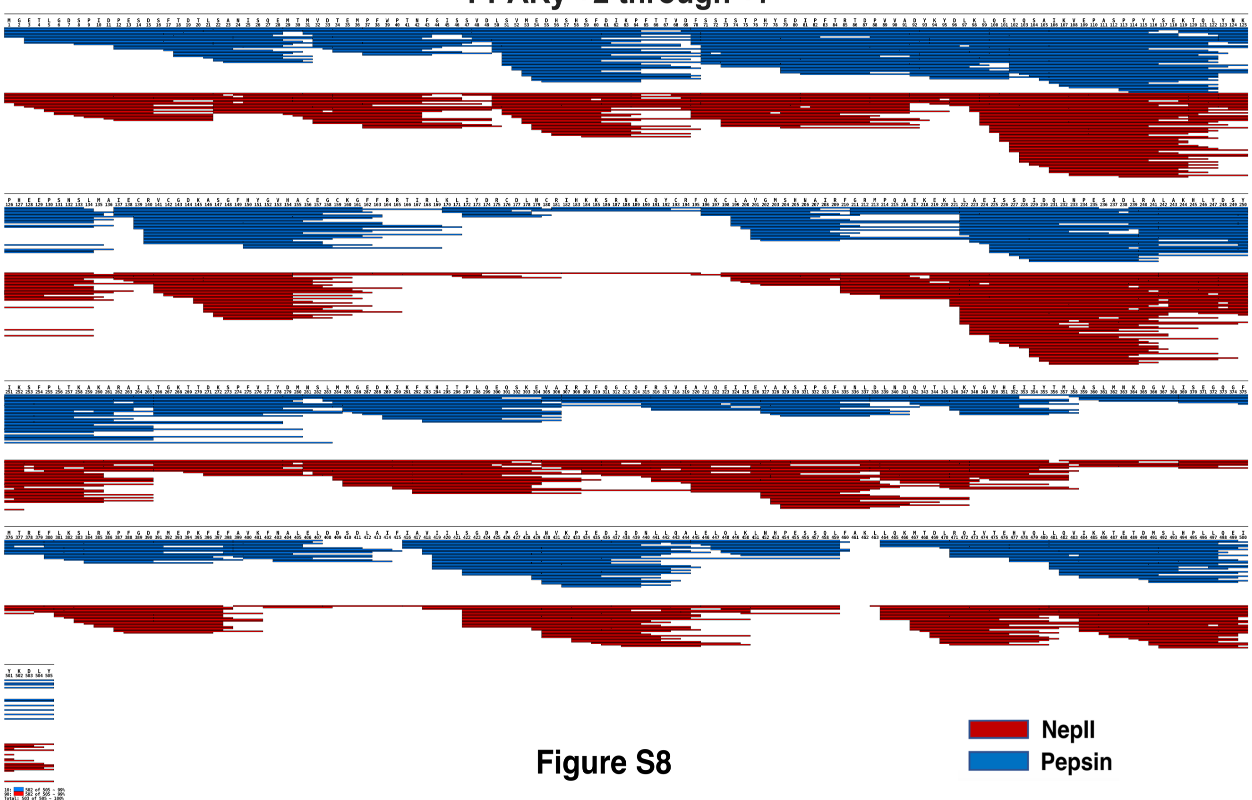


Figure S8

PPARy +1 through +7

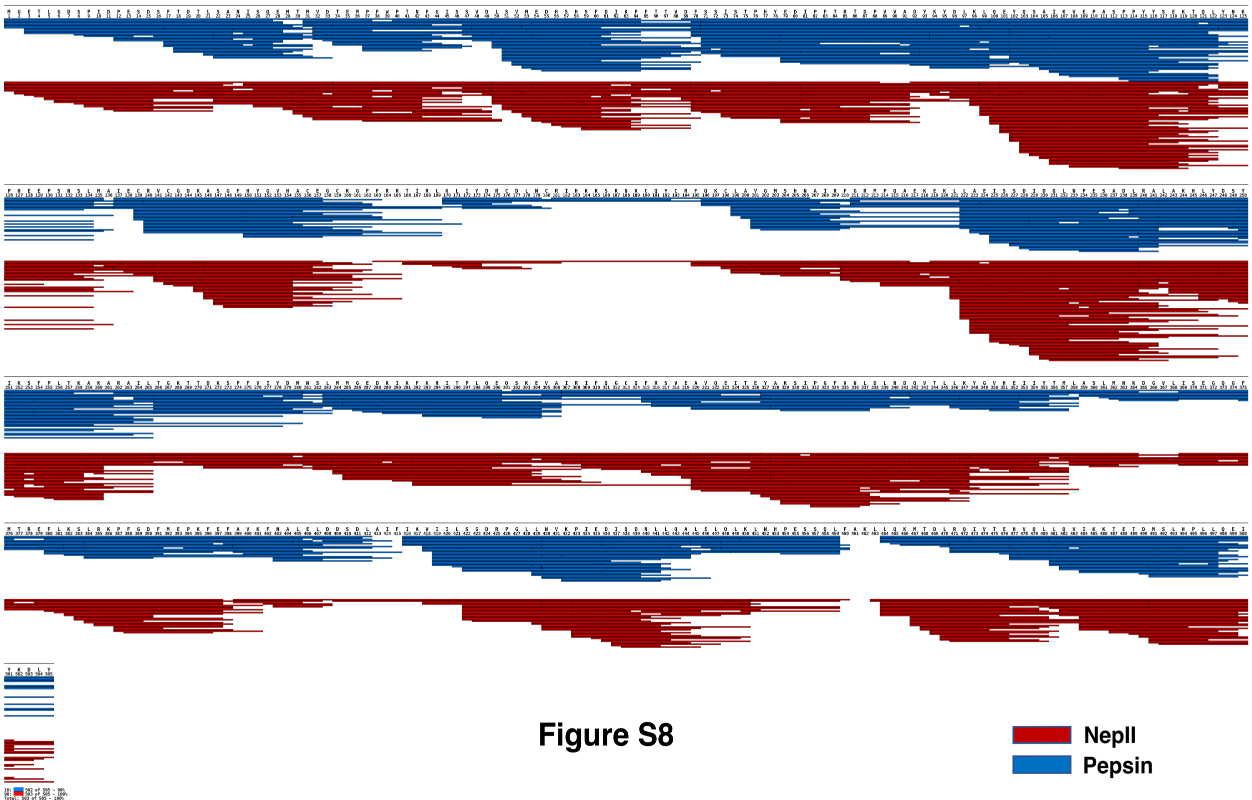


Figure S8