Supporting Information

A peptide resource for the analysis of *Staphylococcus aureus* in host–pathogen interaction studies

[c]

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Supplemental Material S1: Details of LC-MS/MS analysis and database search

strong cationic exchange chromatography (SCX)	
instrument	Ultimate 3000 RSLC (Dionex, Idstein, Germany)
SCX column	nano column (Poros 10S, 300 µm x 10 cm, nanoViper, SCX, 10 µm)
buffer system	binary buffer system consisting of 5 mM Na_2HPO_4 pH 3, 5% ACN in water (SCX buffer A) and 1 M NaCl, 5 mM Na_2HPO_4 pH 3, 5% ACN in water (SCX buffer B)
flow rate	loading: 5 µl/min elution: 300 nl/min
method	2D salt steps; 7 different concentrations of NaCl
salt step volume	12 µl
salt step concentrations	2 mM, 10 mM, 20 mM, 50 mM, 100 mM, 200 mM, 500 mM
column oven temperature	40°C

reversed phase liquid chromatography (RPLC)	
instrument	Ultimate 3000 RSLC (Dionex, Idstein, Germany)
trap column	75 µm inner diameter, packed with 3 µm C18 particles (Acclaim PepMap100, Thermo Scientific)
analytical column	*for SCX and off-gel prefractionated samples and non-fractionated samples (standard method):* 15 cm analytical column packed with 2 µm C18 particles (Acclaim PepMap RSLC, Thermo Scientific) *for samples from cell culture infection model:* 25 cm analytical column packed with 2 µm C18 particles (Acclaim PepMap RSLC, Thermo Scientific)
buffer system	binary buffer system consisting of 0.1% acetic acid, 2% ACN (buffer A) and 0.1% acetic acid in 100% ACN in (buffer B)
flow rate	300 nl/min
gradient	linear gradient of buffer B from 2% up to 25%
gradient duration	30 min *for SCX pre-fractionated samples* 30 min *for off-gel pre-fractionated samples* 100 min *for non-fractionated samples (standard method)* 120 min *for samples from cell culture infection model*
column oven temperature	40°C

mass spectrometry (MS)	
instrument	Q Exactive mass spectrometer (Thermo Scientific)
electrospray	via TriVersa NanoMate (Advion Biosciences, Norwich, UK)
operation mode	data-dependent
MS scan resolution	70,000
MS ion target value	3e6
maximum ion injection time for the MS scan	250 ms *for SCX pre-fractionated, off-gel pre-fractionated, and non-fractionated samples (standard method)* 120 ms *for samples from cell culture infection model*
selection for MS/MS	10 most abundant isotope patterns with charge ≥2 from the survey scan
isolation window	3 *m/z*
dissociation mode	higher energy collisional dissociation (HCD)
normalized collision energy	27.5%
maximum ion injection time for the MS/MS scans	120 ms
MS/MS ion target value	2e5
dynamic exclusion	40 s *for SCX pre-fractionated, off-gel pre-fractionated, and non-fractionated samples (standard method)* 30 s *for samples from cell culture infection model*
MS/MS operation mode	profile mode, peptide match: on *for SCX pre-fractionated, off-gel pre-fractionated, and non-fractionated samples (standard method)* centroid mode, peptide match: preferred *for samples from cell culture infection model*

database search and analysis

SEARCH PARAMETERS AND ACCEPTANCE CRITERIA	
search engine	
name	MASCOT Server / MASCOT Daemon
version or release date	version 2.3.2
sequence database	
name	Sau_8325_BLAST_HGW
version	S.Aureus_DB_NCTC8325_NC007795_BLAST_HGW_20130327.fasta
release date	2013-03-27
number of entries	2891 database without reversed entries
spectral library	
name	20130930_StaphMascot_noProb
version	2013-09-30
source of sequences	FASTA-file, see sequence database above
source of spectra	144 raw files of this study
software used for library generation	Trans Proteomics Pipeline (TPP)
enzyme specificity	
enzyme	trypsin
missed cleavages	max. 2 allowed
non-specific cleavages	none
modifications	
fixed modifications	none
variable modifications	deamidation carbamidomethylation (C) oxidation (M) conversion of Gln to pyroGlu (N-term Q)
mass tolerance	
for precursor ions	10 ppm
for fragment ions	0.1 Da
known contaminants excluded	not excluded
threshold score used for accepting individual spectra	data from MASCOT search: ion score > 20 used for all analyzed files For each file, an ion score >20 is higher than the threshold score which indicates identity or extensive homology with $p < 0.05$. Perkins, D. N., Pappin, D. J., Creasy, D. M., Cottrell, J. S., Probability-based protein identification by searching sequence databases using mass spectrometry data. Electrophoresis 1999, 20, 3551-3567. Individual ion scores at the threshold of $p < 0.05$ for the individual files are indicated below; minimum = 13; maximum = 18; mean = 16.5; median = 17; standard deviation = 0.97 (calculated from all data sets). data from spectral library search: DOT score > 0.5 and absolute precursor tolerance < 0.01

threshold score used for accepting individual spectra (continued)	file	ion score threshold with p<0.05
	BR2_F1	17
	BR2_F2	17
	BR2_F3	18
	BR2_F4	17
	BR2_F5	17
	BR2_F6	17
	BR2_F7	16
	BR2_F8	16
	BR2_F9	17
	BR2_F10	17
	BR2_F11	17
	BR2_F12	17
	BR2_F13	16
	BR2_F14	16
	BR2_F15	16
	BR2_F16	16
	BR2_F17	16
	BR2_F18	15
	BR2_F19	15
	BR2_F20	16
	BR2_F21	16
	BR2_F22	16
	BR2_F23	16
	BR2_F24	15
	BR3_1	16
	BR3_2	17
	BR3_3	17
	BR3_4	17
	BR3_5	17
	BR3_6	16
	BR3_7	15
	BR3_8	15
	BR3_9	16
	BR3_10	16
	BR3_11	16
	BR3_12	16
	BR3_13	15
	BR3_14	15
	BR3_15	15
	BR3_16	15
	BR3_17	14
	BR3_18	13
	BR3_19	13
	BR3_20	14
	BR3_21	15
	BR3_22	15
	BR3_23	15
	BR3_24	14
	HG001_AOFS_BR1_F1	17
	HG001_AOFS_BR1_F2	17
	HG001_AOFS_BR1_F3	17
	HG001_AOFS_BR1_F4	17
	HG001_AOFS_BR1_F5	17
	HG001_AOFS_BR1_F6	17
	HG001_AOFS_BR1_F7	16
	HG001_AOFS_BR1_F8	17
	HG001_AOFS_BR1_F9	17
	HG001_AOFS_BR1_F10	17
	HG001_AOFS_BR1_F11	17
	HG001_AOFS_BR1_F12	17
	HG001_AOFS_BR1_F13	17
	HG001_AOFS_BR1_F14	17
	HG001_AOFS_BR1_F15	17
	HG001_AOFS_BR1_F16	17
	HG001_AOFS_BR1_F17	16
	HG001_AOFS_BR1_F18	16
	HG001_AOFS_BR1_F19	16
	HG001_AOFS_BR1_F20	16
	HG001_AOFS_BR1_F21	16
	HG001_AOFS_BR1_F22	15
	HG001_AOFS_BR1_F23	16
	HG001_AOFS_BR1_F24	16

threshold score used for accepting individual spectra (continued)	file	ion score threshold with p<0.05
	HG001_AOFS_BR2_F1	17
	HG001_AOFS_BR2_F2	17
	HG001_AOFS_BR2_F3	17
	HG001_AOFS_BR2_F4	17
	HG001_AOFS_BR2_F5	17
	HG001_AOFS_BR2_F6	17
	HG001_AOFS_BR2_F7	17
	HG001_AOFS_BR2_F8	17
	HG001_AOFS_BR2_F9	17
	HG001_AOFS_BR2_F10	17
	HG001_AOFS_BR2_F11	17
	HG001_AOFS_BR2_F12	17
	HG001_AOFS_BR2_F13	17
	HG001_AOFS_BR2_F14	17
	HG001_AOFS_BR2_F15	17
	HG001_AOFS_BR2_F16	17
	HG001_AOFS_BR2_F17	16
	HG001_AOFS_BR2_F18	16
	HG001_AOFS_BR2_F19	16
	HG001_AOFS_BR2_F20	16
	HG001_AOFS_BR2_F21	16
	HG001_AOFS_BR2_F22	16
	HG001_AOFS_BR2_F23	16
	HG001_AOFS_BR2_F24	16
	HG001_AOFS_BR3_F1	17
	HG001_AOFS_BR3_F2	17
	HG001_AOFS_BR3_F3	17
	HG001_AOFS_BR3_F4	17
	HG001_AOFS_BR3_F5	17
	HG001_AOFS_BR3_F6	17
	HG001_AOFS_BR3_F7	17
	HG001_AOFS_BR3_F8	17
	HG001_AOFS_BR3_F9	17
	HG001_AOFS_BR3_F10	17
	HG001_AOFS_BR3_F11	17
	HG001_AOFS_BR3_F12	17
	HG001_AOFS_BR3_F13	17
	HG001_AOFS_BR3_F14	17
	HG001_AOFS_BR3_F15	17
	HG001_AOFS_BR3_F16	17
	HG001_AOFS_BR3_F17	16
	HG001_AOFS_BR3_F18	17
	HG001_AOFS_BR3_F19	16
	HG001_AOFS_BR3_F20	16
	HG001_AOFS_BR3_F21	16
	HG001_AOFS_BR3_F22	16
	HG001_AOFS_BR3_F23	16
	HG001_AOFS_BR3_F24	16
	Salt_Steps_2mM_AOFS_BR1_1	17
	Salt_Steps_2mM_AOFS_BR2_1	17
	Salt_Steps_2mM_AOFS_BR3_1	17
	Salt_Steps_10mM_AOFS_BR1_2	17
	Salt_Steps_10mM_AOFS_BR2_2	17
	Salt_Steps_10mM_AOFS_BR3_2	17
	Salt_Steps_20mM_AOFS_BR1_3	18
	Salt_Steps_20mM_AOFS_BR2_3	18
	Salt_Steps_20mM_AOFS_BR3_3	18
	Salt_Steps_50mM_AOFS_BR1_4	18
	Salt_Steps_50mM_AOFS_BR2_4	18
	Salt_Steps_50mM_AOFS_BR3_4	18
	Salt_Steps_100mM_AOFS_BR1_5	18
	Salt_Steps_100mM_AOFS_BR2_5	18
	Salt_Steps_100mM_AOFS_BR3_5	18
	Salt_Steps_200mM_AOFS_BR1_6	18
	Salt_Steps_200mM_AOFS_BR2_6	18
	Salt_Steps_200mM_AOFS_BR3_6	18
	Salt_Steps_500mM_AOFS_BR1_7	18
	Salt_Steps_500mM_AOFS_BR2_7	18
	Salt_Steps_500mM_AOFS_BR3_7	18
	Staph_UT_BR1	17
	Staph_UT_BR2	17
	Staph_UT_BR3	17

False Discovery Rates

Percolator score FDR

(Kall, L., Canterbury, J. D., Weston, J., Noble, W. S., MacCoss, M. J., Semi-supervised learning for peptide identification from shotgun proteomics datasets. Nature methods 2007, 4, 923-925.)

FDR was calculated by a target decoy approach (TDA) in combination with the Percolator score.

minimum = 0; maximum = 2.75; mean = 0.25; median = 0.19; standard deviation = 0.32 (calculated from all data sets)

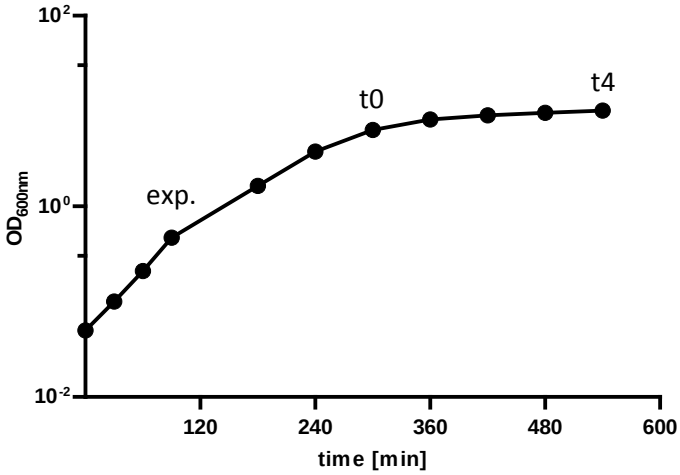
file	FDR
BR2_F1	0.31
BR2_F2	0.09
BR2_F3	0.21
BR2_F4	0.16
BR2_F5	0.3
BR2_F6	0.1
BR2_F7	0.09
BR2_F8	0.22
BR2_F9	0.22
BR2_F10	0
BR2_F11	0.24
BR2_F12	0.32
BR2_F13	0.26
BR2_F14	0.37
BR2_F15	0.65
BR2_F16	0.39
BR2_F17	0
BR2_F18	0
BR2_F19	0.32
BR2_F20	0.11
BR2_F21	0.63
BR2_F22	0.42
BR2_F23	0.42
BR2_F24	0.35
BR3_1	0.16
BR3_2	0.12
BR3_3	0.11
BR3_4	0.14
BR3_5	0.10
BR3_6	0.32
BR3_7	0.17
BR3_8	0.22
BR3_9	0.34
BR3_10	0.48
BR3_11	0.42
BR3_12	0.26
BR3_13	0.24
BR3_14	0.57
BR3_15	0.00
BR3_16	0.00
BR3_17	0.00
BR3_18	0.00
BR3_19	0.00
BR3_20	0.75
BR3_21	0.48
BR3_22	0.23
BR3_23	0.27
BR3_24	0.23
HG001_AOFS_BR1_F1	0.13
HG001_AOFS_BR1_F2	0.06
HG001_AOFS_BR1_F3	0.17
HG001_AOFS_BR1_F4	0.13
HG001_AOFS_BR1_F5	0.64
HG001_AOFS_BR1_F6	0.28
HG001_AOFS_BR1_F7	0.20
HG001_AOFS_BR1_F8	0.00
HG001_AOFS_BR1_F9	0.24
HG001_AOFS_BR1_F10	0.27
HG001_AOFS_BR1_F11	0.24
HG001_AOFS_BR1_F12	0.21
HG001_AOFS_BR1_F13	0.46
HG001_AOFS_BR1_F14	0.00
HG001_AOFS_BR1_F15	0.26
HG001_AOFS_BR1_F16	0.20
HG001_AOFS_BR1_F17	0.00
HG001_AOFS_BR1_F18	1.89
HG001_AOFS_BR1_F19	0.00
HG001_AOFS_BR1_F20	0.56
HG001_AOFS_BR1_F21	0.51

False Discovery Rates (continued)

Percolator score FDR

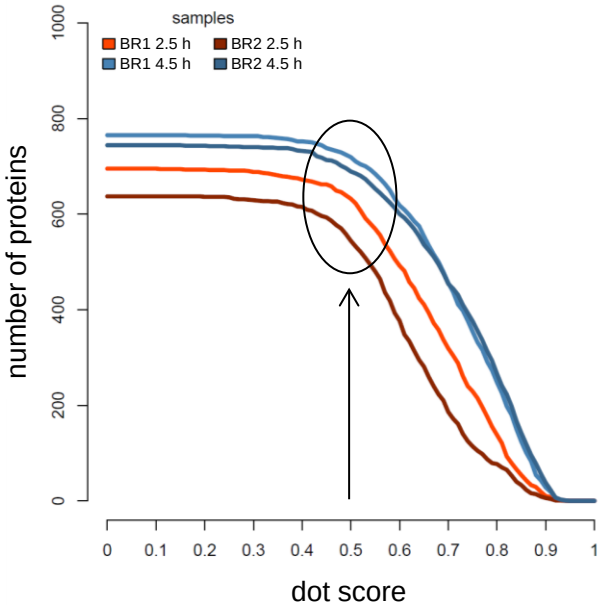
file	FDR
HG001_AOFS_BR1_F22	2.75
HG001_AOFS_BR1_F23	0.00
HG001_AOFS_BR1_F24	0.68
HG001_AOFS_BR2_F1	0.06
HG001_AOFS_BR2_F2	0.11
HG001_AOFS_BR2_F3	N/A
HG001_AOFS_BR2_F4	0.11
HG001_AOFS_BR2_F5	0.14
HG001_AOFS_BR2_F6	0.17
HG001_AOFS_BR2_F7	0.14
HG001_AOFS_BR2_F8	0.12
HG001_AOFS_BR2_F9	0.33
HG001_AOFS_BR2_F10	N/A
HG001_AOFS_BR2_F11	0.28
HG001_AOFS_BR2_F12	0.41
HG001_AOFS_BR2_F13	0.20
HG001_AOFS_BR2_F14	0.00
HG001_AOFS_BR2_F15	0.18
HG001_AOFS_BR2_F16	0.17
HG001_AOFS_BR2_F17	0.00
HG001_AOFS_BR2_F18	0.00
HG001_AOFS_BR2_F19	0.00
HG001_AOFS_BR2_F20	0.49
HG001_AOFS_BR2_F21	0.31
HG001_AOFS_BR2_F22	0.49
HG001_AOFS_BR2_F23	0.47
HG001_AOFS_BR2_F24	0.35
HG001_AOFS_BR3_F1	0.13
HG001_AOFS_BR3_F2	0.06
HG001_AOFS_BR3_F3	0.11
HG001_AOFS_BR3_F4	0.06
HG001_AOFS_BR3_F5	0.09
HG001_AOFS_BR3_F6	0.21
HG001_AOFS_BR3_F7	0.00
HG001_AOFS_BR3_F8	0.13
HG001_AOFS_BR3_F9	0.50
HG001_AOFS_BR3_F10	0.19
HG001_AOFS_BR3_F11	0.23
HG001_AOFS_BR3_F12	0.27
HG001_AOFS_BR3_F13	0.89
HG001_AOFS_BR3_F14	0.00
HG001_AOFS_BR3_F15	0.26
HG001_AOFS_BR3_F16	0.16
HG001_AOFS_BR3_F17	0.00
HG001_AOFS_BR3_F18	0.00
HG001_AOFS_BR3_F19	0.00
HG001_AOFS_BR3_F20	0.00
HG001_AOFS_BR3_F21	0.39
HG001_AOFS_BR3_F22	0.36
HG001_AOFS_BR3_F23	0.44
HG001_AOFS_BR3_F24	0.68
Salt_Steps_2mM_AOFS_BR1_1	N/A
Salt_Steps_10mM_AOFS_BR1_2	0.27
Salt_Steps_20mM_AOFS_BR1_3	0.25
Salt_Steps_50mM_AOFS_BR1_4	0.3
Salt_Steps_100mM_AOFS_BR1_5	0.08
Salt_Steps_200mM_AOFS_BR1_6	0.04
Salt_Steps_50mM_AOFS_BR1_7	0.11
Salt_Steps_2mM_AOFS_BR2_1	0.04
Salt_Steps_10mM_AOFS_BR2_2	0.16
Salt_Steps_20mM_AOFS_BR2_3	0.09
Salt_Steps_50mM_AOFS_BR2_4	0.16
Salt_Steps_100mM_AOFS_BR2_5	0.07
Salt_Steps_200mM_AOFS_BR2_6	0.00
Salt_Steps_50mM_AOFS_BR2_7	0.1
Salt_Steps_2mM_AOFS_BR3_1	0.47
Salt_Steps_10mM_AOFS_BR3_2	0.13
Salt_Steps_20mM_AOFS_BR3_3	0.17
Salt_Steps_50mM_AOFS_BR3_4	0.22
Salt_Steps_100mM_AOFS_BR3_5	0.12
Salt_Steps_200mM_AOFS_BR3_6	0.05
Salt_Steps_50mM_AOFS_BR3_7	0.17
Staph_UT_BR1	0.38
Staph_UT_BR2	0.48
Staph_UT_BR3	0

Supplemental Figure S1



Growth curve of *S. aureus* HG001 in TSB.
One representative curve of three biological replicates is depicted.
Sampling points are indicated.

Supplemental Figure S2



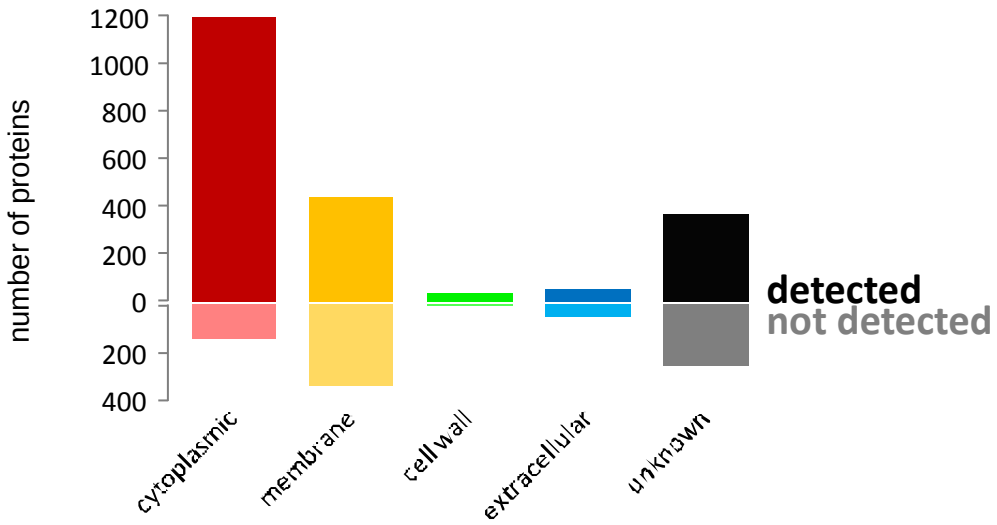
Number of identified proteins depending on score values.

The numbers of identified proteins are plotted depending on the dot score values in identification search using the spectral library generated in this study.

The arrow and circle indicate the region where the dot score starts discriminating true identifications from unspecific false identifications.

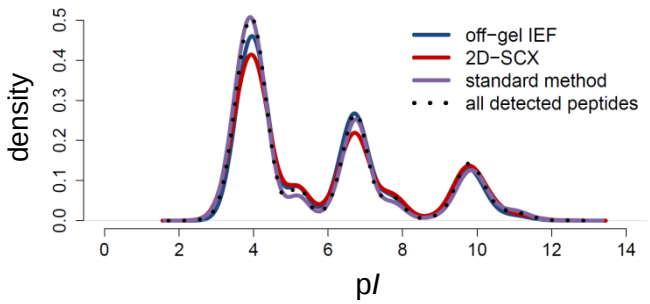
Supplemental Figure S3

	detected proteins		proteins not detected	
	number	%	number	%
total	2088	100	803	100
localization:				
cytoplasmic	1191	57.0	143	17.8
cytoplasmic membrane	437	20.9	342	42.6
cell wall	38	1.8	2	0.2
extracellular	56	2.7	53	6.6
unknown	366	17.5	263	32.8



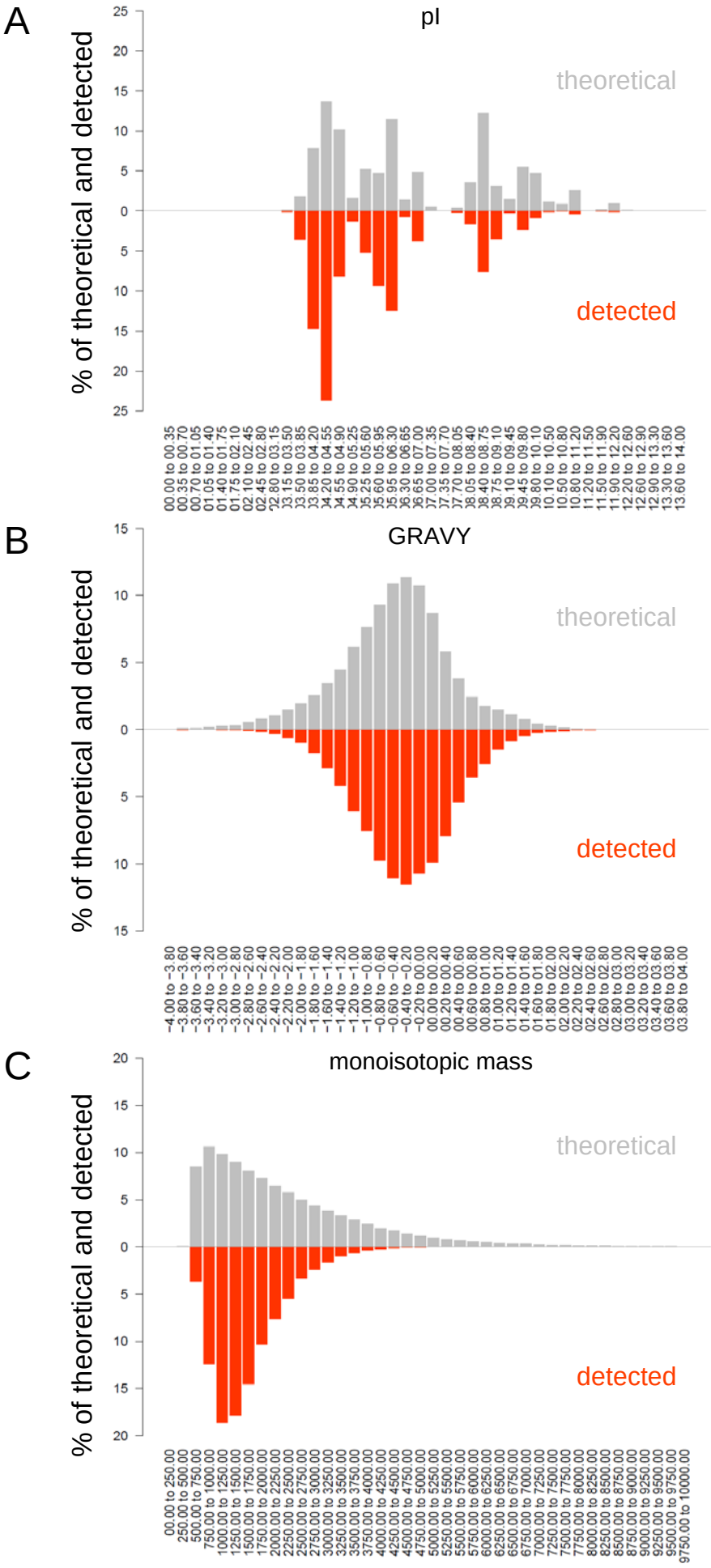
Localization of detected and non-detected proteins of *S. aureus* HG001.
Localization of proteins is depicted according to the PSort annotation. The upper part of the graph indicates numbers of detected proteins, while the lower part shows the numbers on non-detected proteins.

Supplemental Figure S4



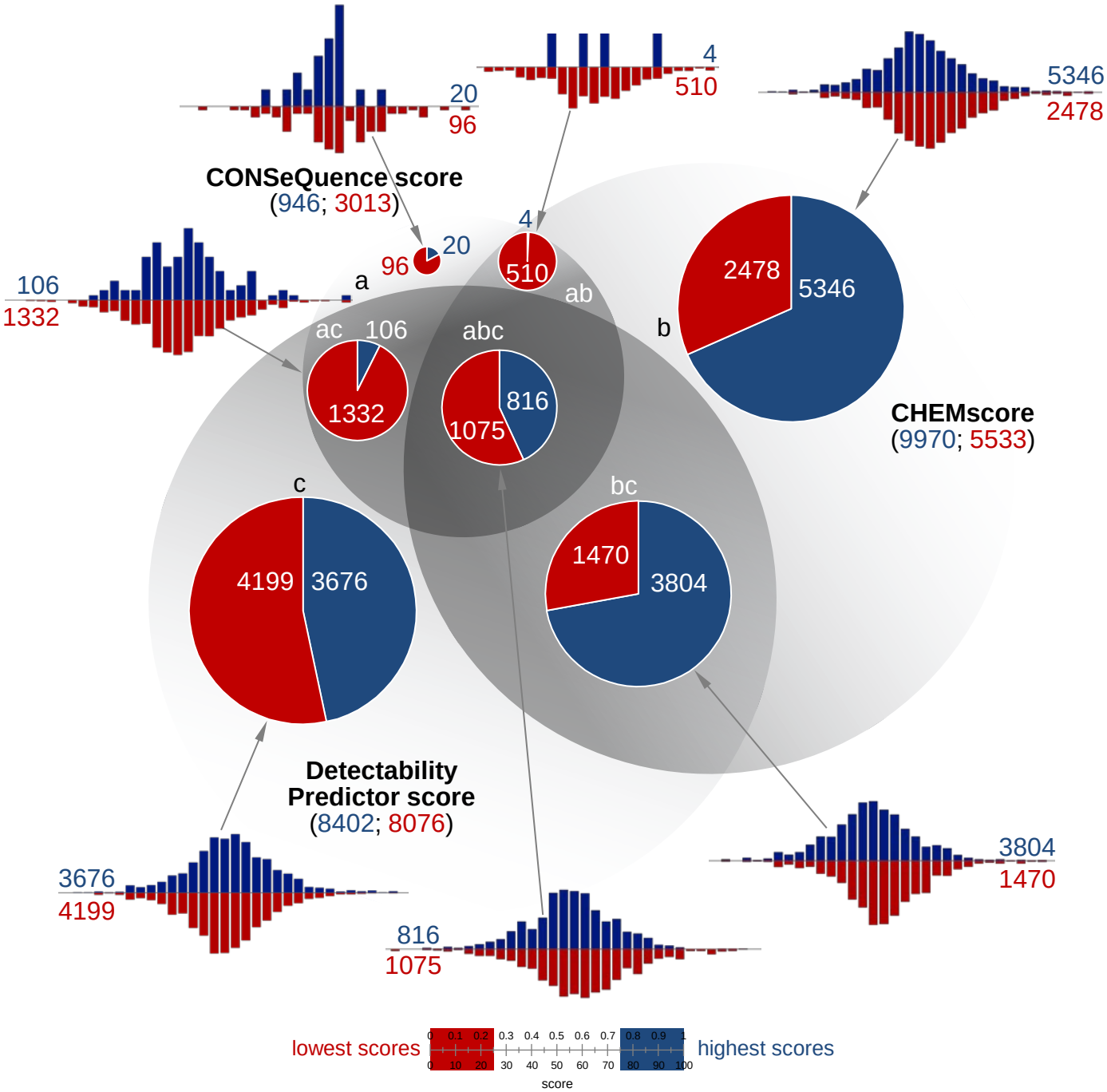
Comparison of the distribution of peptide identifications along the p*I* range for the three methods under investigation.
p*I* values of detected peptides were exported from the ProteomeCenter tool. The density function and plots were generated using R scripts.

Supplemental Figure S5

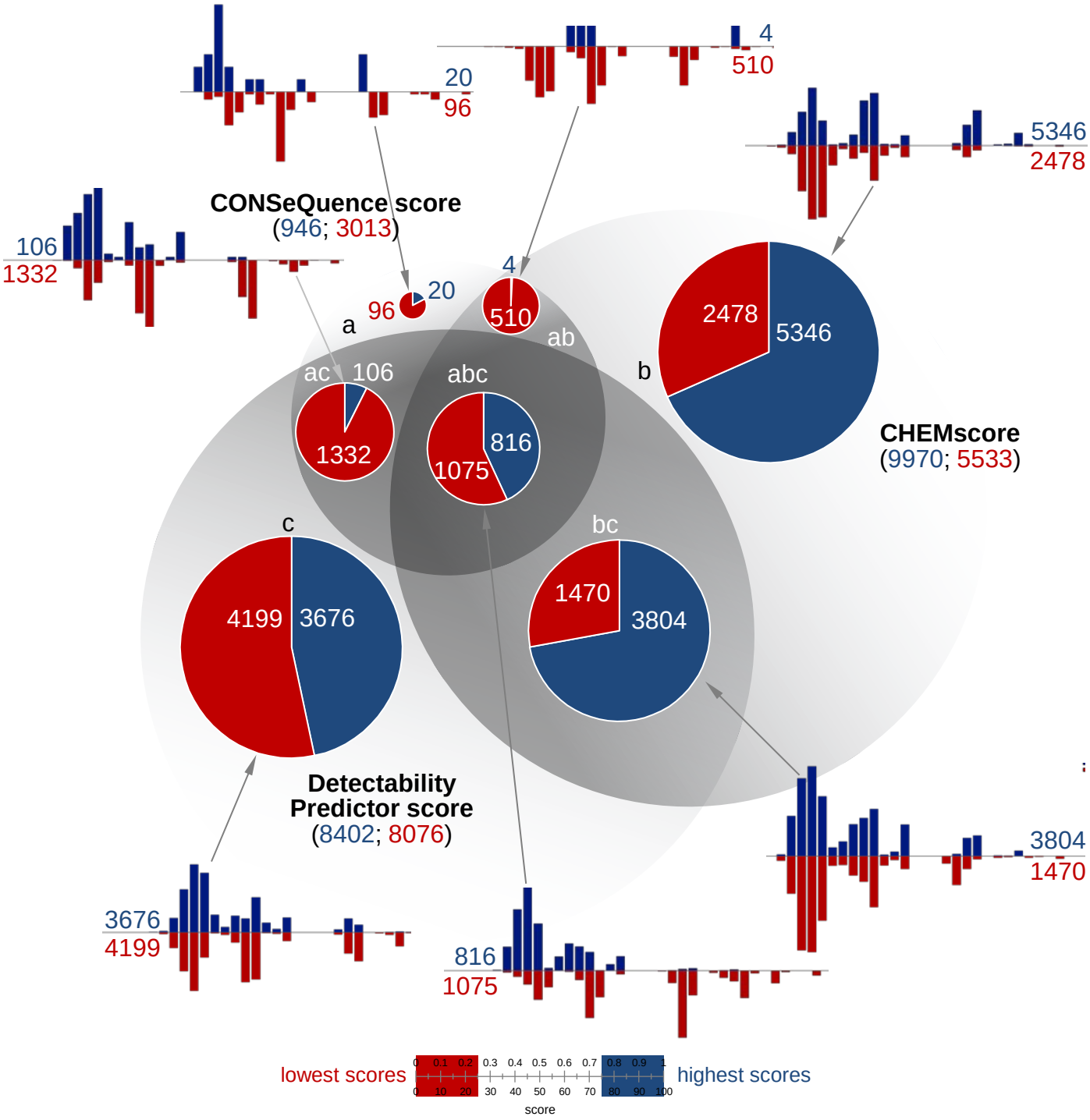


Characterization of the detected peptides and peptides retrieved from an *in silico* digestion by physicochemical properties.
The frequency of peptides is depicted in classes of p*I* values (A), GRAVY score (B), and monoisotopic mass (C). The upper part of the histograms refers to the set of theoretical peptides from the *in silico* digestion (gray), and the lower part of the histograms displays the data set of detected peptides (orange).

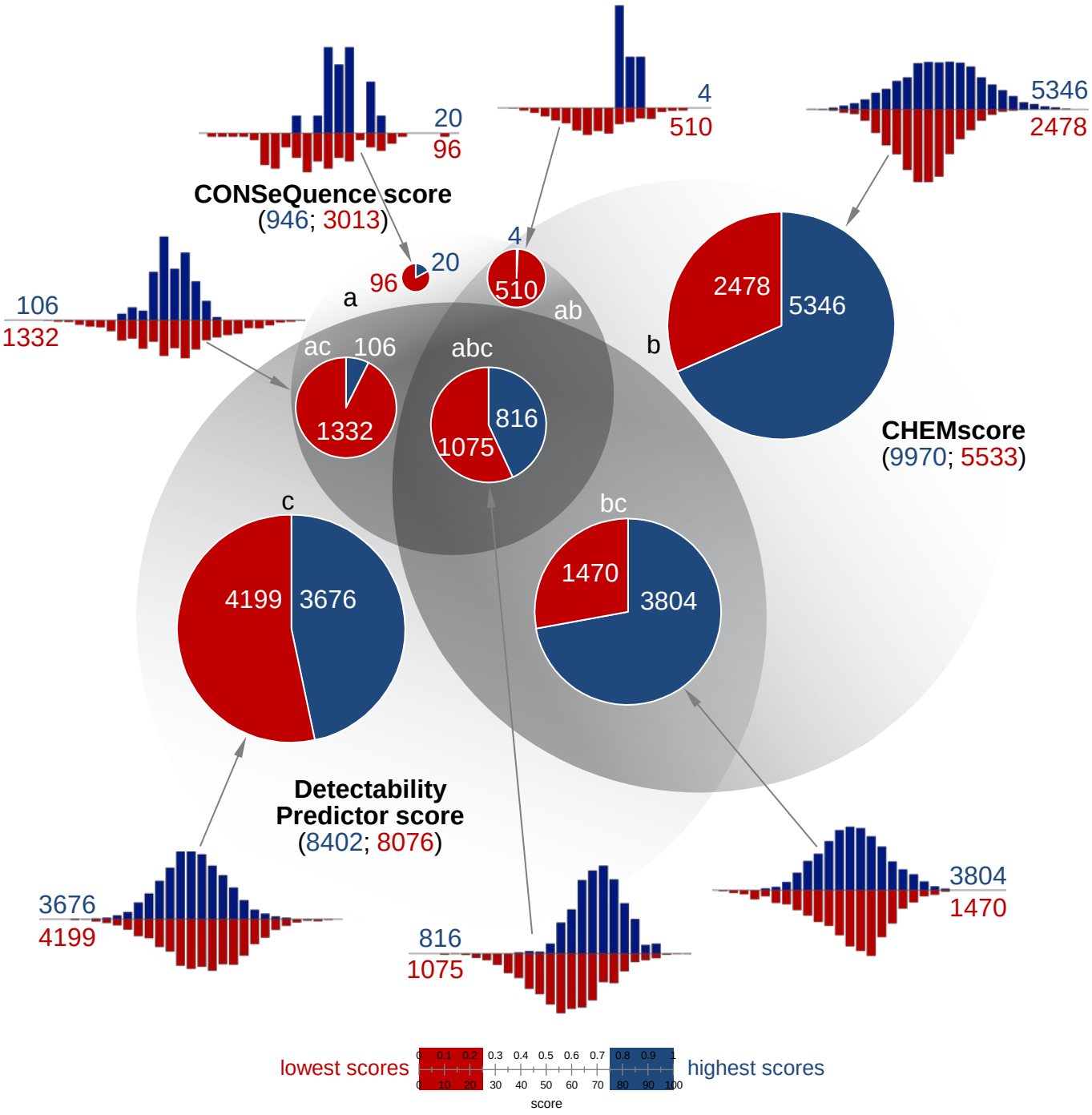
Supplemental Figure S6 A – emPAI –



Supplemental Figure S6 B – p*I* –



Supplemental Figure S6 C – GRAVY –

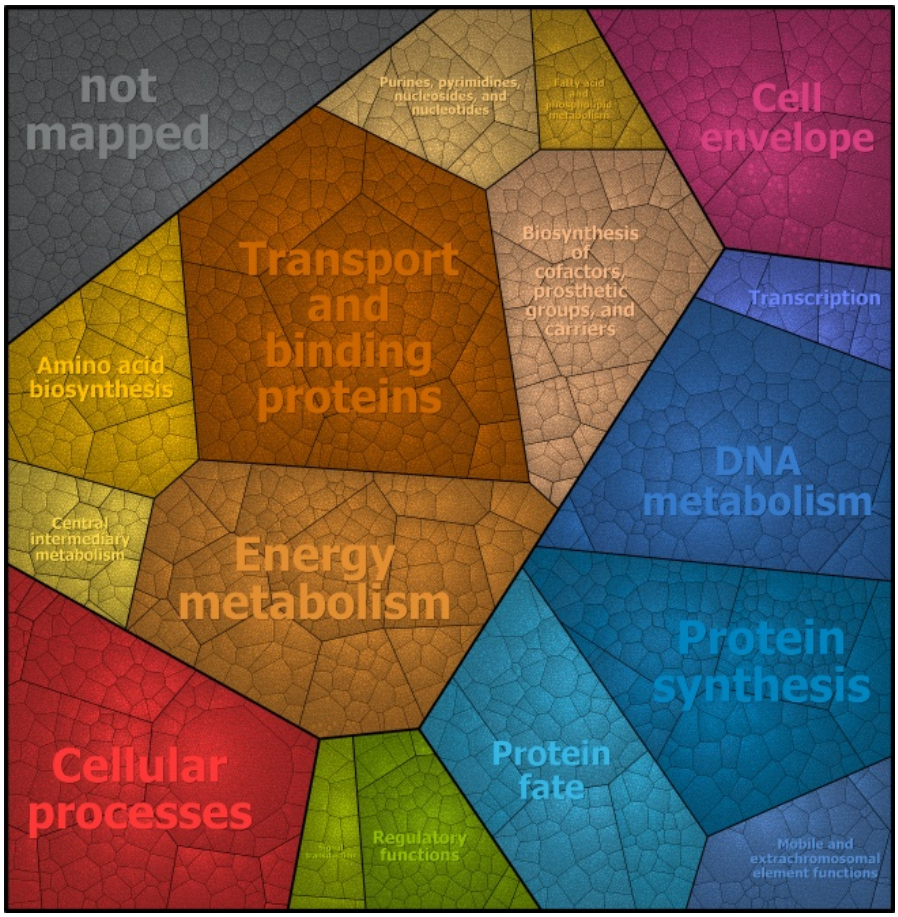


(Supplemental Figure S6)

Comparison of detected peptides with the lowest and the highest score values.
Venn diagrams depict the comparison of peptides with CONSeQuence score > 0.75, CHEMscore > 75, and DetectabilityPredictor score > 0.75, which constitute groups of high score values (colored blue), and of peptides with CONSeQuence score < 0.25, CHEMscore < 25, and DetectabilityPredictor score < 0.25, which were selected as groups of low score values (colored red). Superimposed on the Venn diagram subsets, pie charts correlated by area show the number of peptides with highest and lowest score values. The pie charts are furthermore labeled with the small type characters a (CONSeQuence score), b (CHEMscore), and c (DetectabilityPredictor score) or combinations of them in order to indicate the corresponding Venn diagram intersections. Associated histograms show the distribution and frequency of emPAI (A), p*I* (B), and GRAVY score (C) values for the subsets of the Venn diagrams. Again, blue indicates the group with highest score values, red marks the group with lowest score values. The x-axis shows categories of values. The y-axis indicates the percentage of values in the corresponding category.

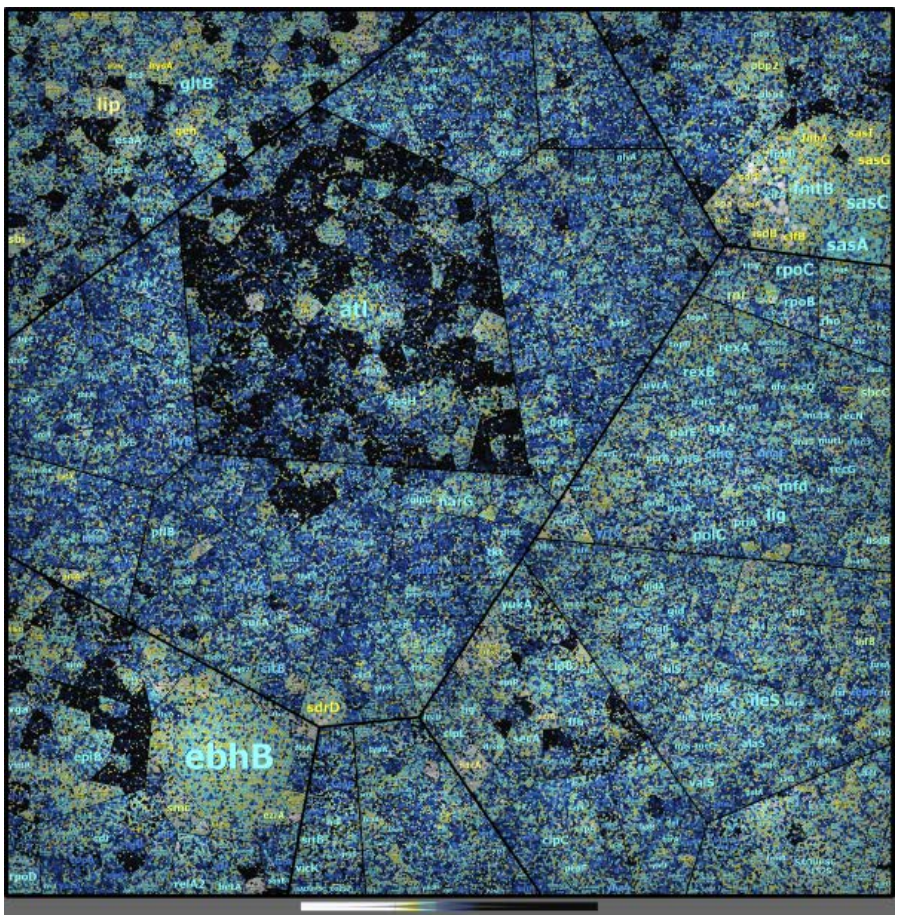
Supplemental Figure S7

A



overview

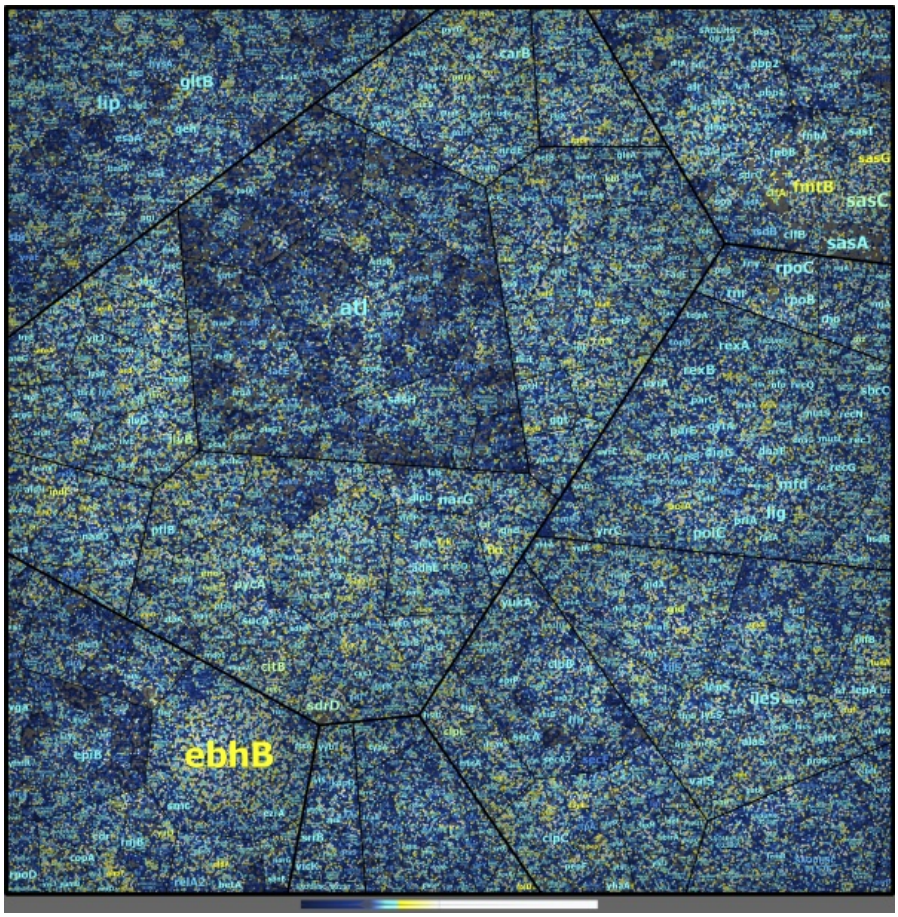
B



GRAVY

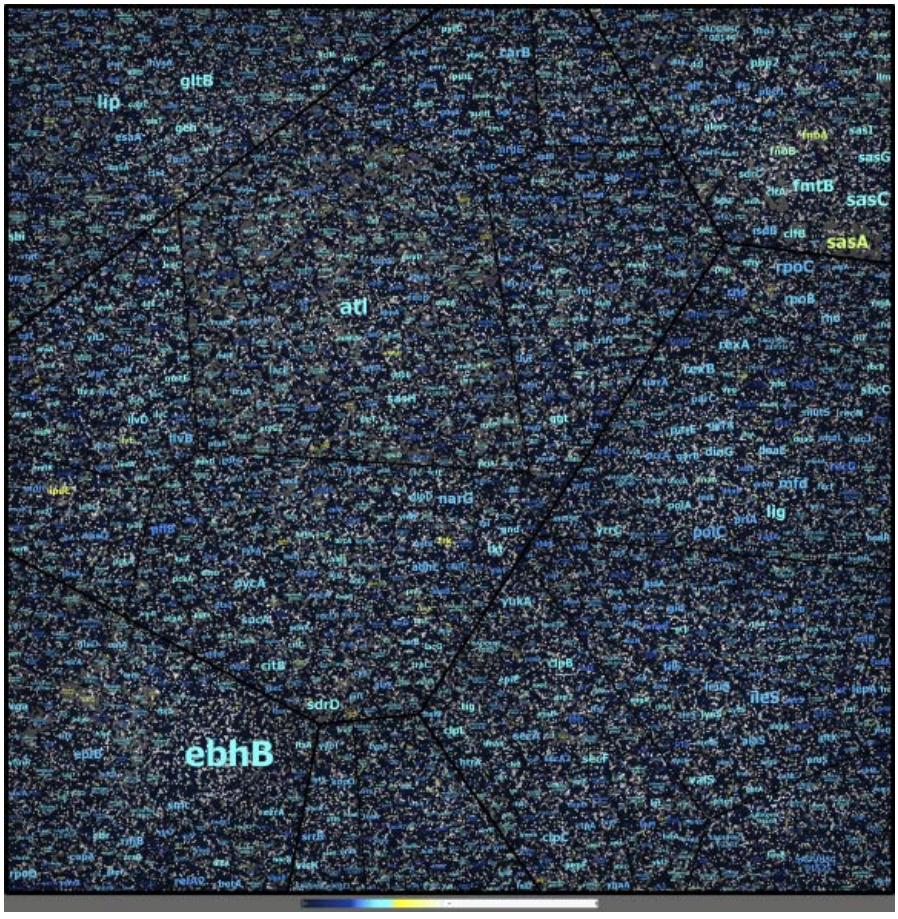
Supplemental Figure S7

C



CONSeQuence score

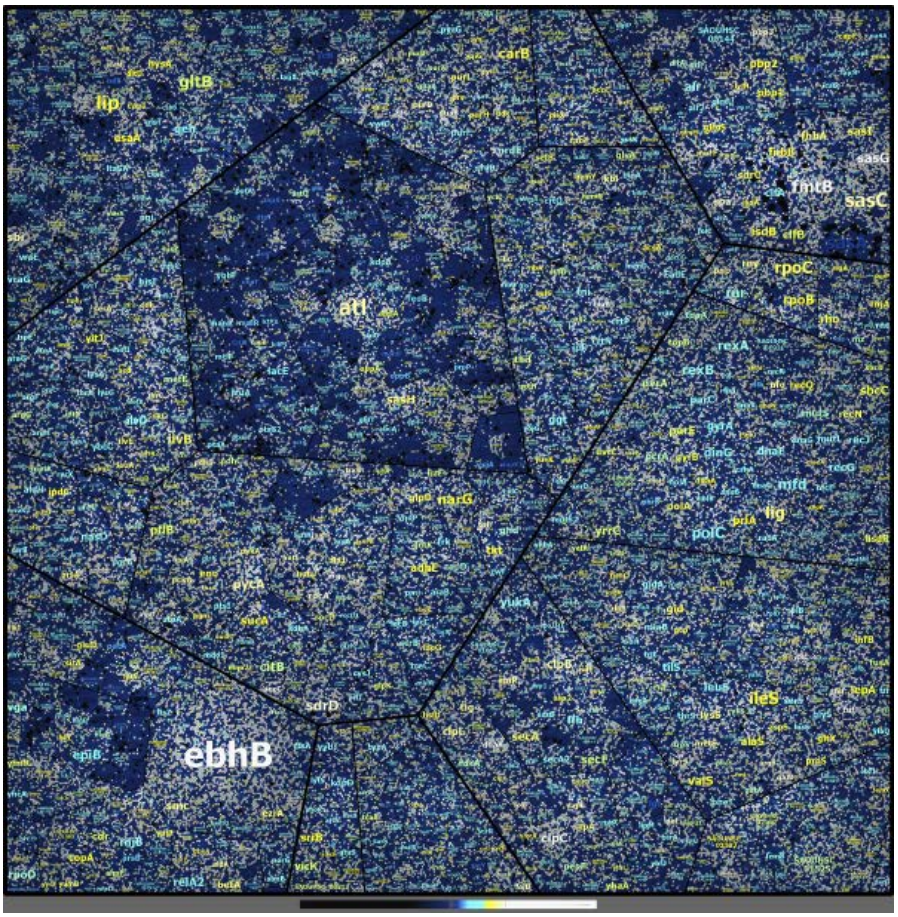
D



CHEMscore

Supplemental Figure S7

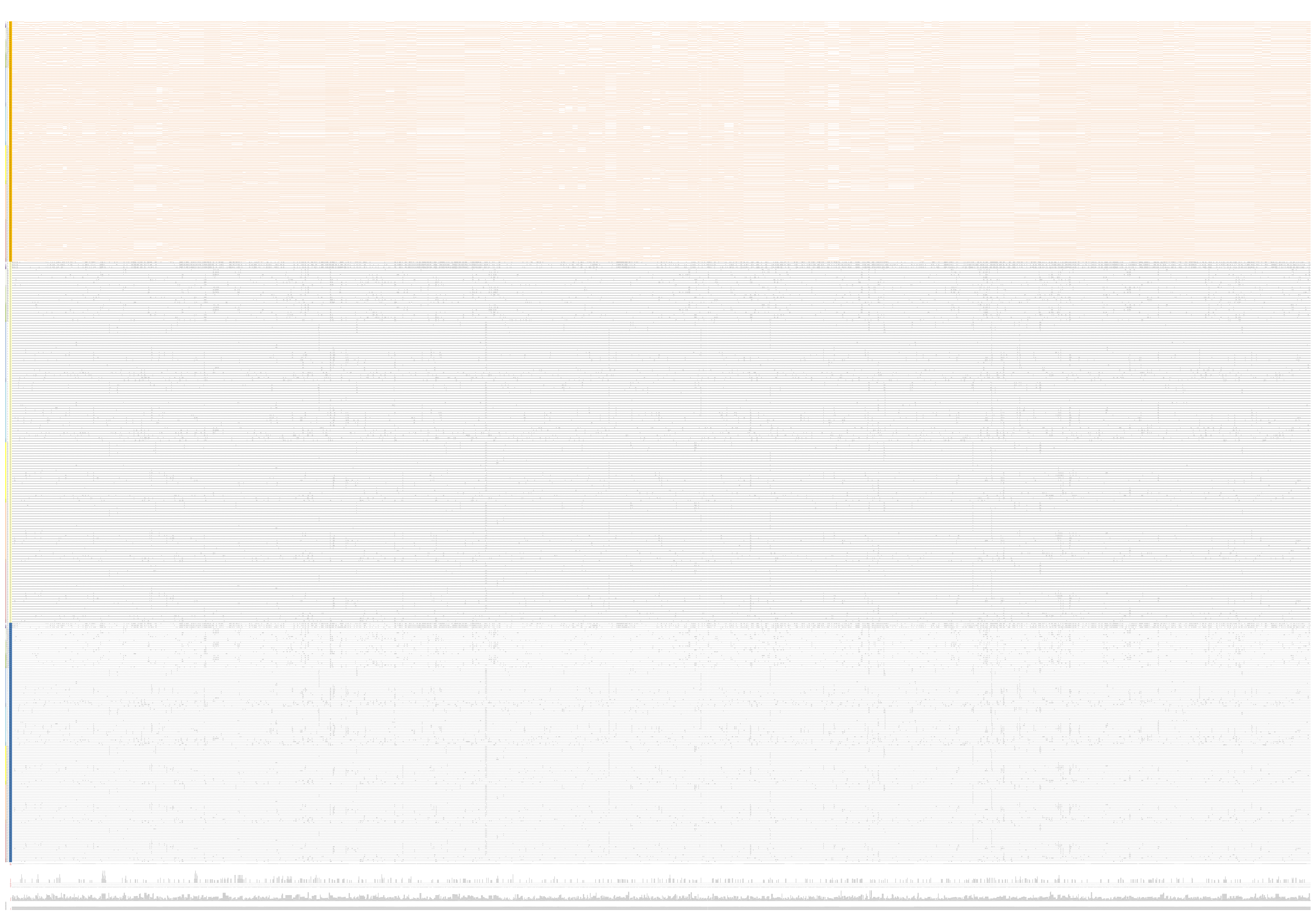
E

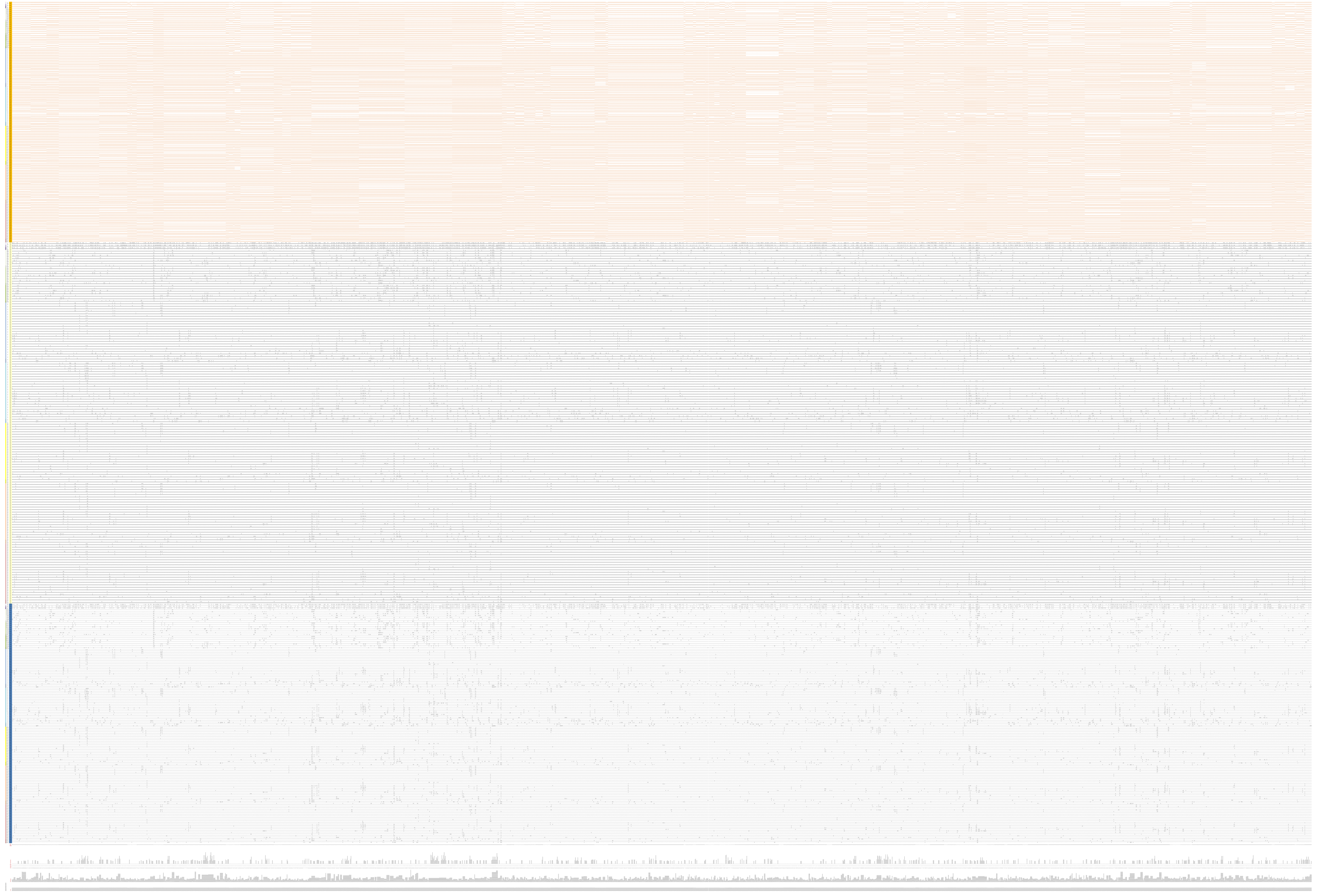


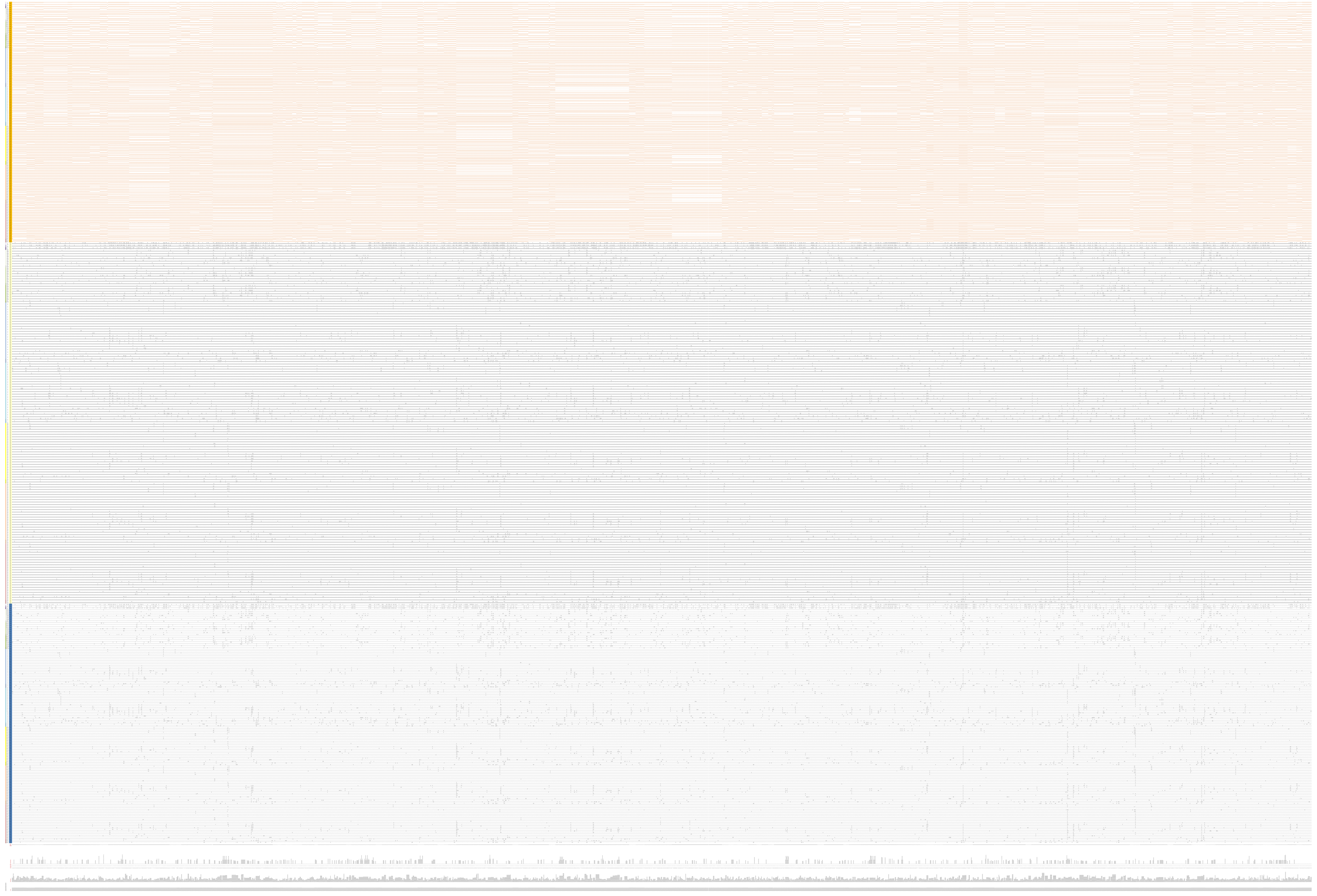
Detectability Predictor score

Representation of physicochemical parameters and score values of peptides from an *in silico* digest.

The Voronoi treemap was created on the basis the TIGRFAM protein family classification scheme [Haft et al. (2001) Nucleic acids research 29, 41-43] by using HMMER/HMMScan [Finn et al. (2011) Nucleic acids research 39, W29-37]. Peptides form the lowest level of area subdivision. The area per peptide represents the peptide length (number of amino acids). Therefore, the area per protein correlates with the protein size. Additionally, the protein label size correlates with the protein size. The overview of the included functional annotations (A) is valid for all parameter-colored Voronoi treemaps. The Voronoi treemap contains about 220,245 theoretically expected peptides from an *in silico* digestion.
Coloring indicates different GRAVY score values (B), CONSeQuence score values (C), CHEMscore values (D), and DetectabilityPredictor score values (E).
Small GRAVY score values, which indicate less hydrophobic peptides, are colored white, high GRAVY score values, which indicate very hydrophobic peptides, are indicated in dark blue, intermediate GRAVY score values are colored yellow or light blue (B). Missing values are indicated in gray (B).
High CONSeQuence score values (C), CHEMscore values (D), and DetectabilityPredictor score values (E) are indicated in white, low score values in dark blue. Intermediate values are colored light blue and yellow (C, D, E). Missing values are indicated in black (C, D, E).







Supplemental Material Table S2

Locus Tag	Peptide Sequence	# aa	missed cleavage	Peptide Charge	Peptide Modification	number of peptides per protein	HG001_AOFS_BR1 ion score	HG001_AOFS_BR2 ion score

Supplemental Material Table S2

Supplemental Material Table S2

Locus Tag	Peptide Sequence	# aa	missed cleavage	Peptide Charge	Peptide Modification	number of peptides per protein
SAOUHSC_02254	NVVLDKEFTAPLITNDGVTIAK	22	1	4		34
SAOUHSC_02254	NVVLDKEFTAPLITNDGVTIAK	22	1	3	Deamidated (NQ)	34
SAOUHSC_02254	QAMLRGVDQLANAVK	15	1	3	Oxidation (M)	34
SAOUHSC_02254	QIAENAGLEGSVIVER	16	0	2		34
SAOUHSC_02254	QIAENAGLEGSVIVER	16	0	3		34
SAOUHSC_02254	QIAENAGLEGSVIVER	16	0	2	Deamidated (NQ)	34
SAOUHSC_02254	SALQHAASVAAMFLTTEAVVASIPEK	26	0	3	Oxidation (M)	34
SAOUHSC_02254	SQEETESDFDR	12	0	2		34
SAOUHSC_02254	SQEETESDFDR	12	0	3		34
SAOUHSC_02254	SQEETESDFDREK	14	1	2		34
SAOUHSC_02254	SQEETESDFDREK	14	1	3		34
SAOUHSC_02254	TNEIAGDGTTTATVLAQAMIQEGLK	25	0	2		34
SAOUHSC_02254	TNEIAGDGTTTATVLAQAMIQEGLK	25	0	3		34
SAOUHSC_02254	TNEIAGDGTTTATVLAQAMIQEGLK	25	0	4		34
SAOUHSC_02254	TNEIAGDGTTTATVLAQAMIQEGLK	25	0	3	Oxidation (M)	34
SAOUHSC_02254	VAVEALHENSQK	12	0	2		34
SAOUHSC_02254	VAVEALHENSQK	12	0	3		34
SAOUHSC_02254	VAVEALHENSQK	12	0	3	Deamidated (NQ)	34
SAOUHSC_02254	VAVEALHENSQKVENK	16	1	4	Deamidated (NQ)	34
SAOUHSC_02254	VENKNEIAQVGAISAADEEIGR	22	1	2		34
SAOUHSC_02254	VENKNEIAQVGAISAADEEIGR	22	1	3		34
SAOUHSC_02254	VENKNEIAQVGAISAADEEIGR	22	1	4		34
SAOUHSC_02254	VENKNEIAQVGAISAADEEIGR	22	1	3	Deamidated (NQ)	34
SAOUHSC_02254	VEVTKDNTTVVDGDGDENSIDAR	23	1	3		34
SAOUHSC_02254	VEVTKDNTTVVDGDGDENSIDAR	23	1	3	Deamidated (NQ)	34
SAOUHSC_02254	VGAASETELKER	12	1	3		34
SAOUHSC_02254	VGNDGVITIEESNGLNTELEVVEGMQFDR	29	0	3		34
SAOUHSC_02254	YISEAMEK	8	0	2		34
SAOUHSC_02254	YISEAMEK	8	0	2	Oxidation (M)	34
SAOUHSC_02255	DNETYLVLNEEDILAVIE	18	0	2		10
SAOUHSC_02255	EGDRVVFQQYAGTEVK	16	1	3		10
SAOUHSC_02255	EKSNEGVIVAVGTGR	15	1	2		10
SAOUHSC_02255	EKSNEGVIVAVGTGR	15	1	3		10
SAOUHSC_02255	EKSNEGVIVAVGTGR	15	1	3	Deamidated (NQ)	10
SAOUHSC_02255	MLKPIGNR	8	0	3		10
SAOUHSC_02255	SGIVLTDSAK	10	0	2		10
SAOUHSC_02255	SGIVLTDSAKEK	12	1	2		10
SAOUHSC_02255	SGIVLTDSAKEK	12	1	3		10
SAOUHSC_02255	SNEGVIVAVGTGR	13	0	2		10
SAOUHSC_02255	SNEGVIVAVGTGR	13	0	3		10
SAOUHSC_02255	VIIEK	5	0	2		10
SAOUHSC_02255	VVFQQYAGTEVK	12	0	2		10
SAOUHSC_02255	VVFQQYAGTEVK	12	0	3		10
SAOUHSC_02255	VVFQQYAGTEVKR	13	1	2		10
SAOUHSC_02255	VVFQQYAGTEVKR	13	1	3		10
SAOUHSC_02256	LELEVK	6	0	2		2
SAOUHSC_02256	LIIIAR	6	0	2		2
SAOUHSC_02258	AMTFDNAMEER	11	0	2		6
SAOUHSC_02258	DSISISDDELESMIAHAVK	19	0	2		6
SAOUHSC_02258	DSISISDDELESMIAHAVK	19	0	3		6
SAOUHSC_02258	GIGASLQHYNPLVDEMTSNEFNIPK	25	0	3		6
SAOUHSC_02258	GIGASLQHYNPLVDEMTSNEFNIPK	25	0	3	Oxidation (M)	6
SAOUHSC_02258	IVLLLNDNNNK	11	0	2		6
SAOUHSC_02258	IVLLLNDNNNKFWDNTK	17	1	3		6
SAOUHSC_02258	KAMTFDNAMEER	12	1	2		6
SAOUHSC_02258	KAMTFDNAMEER	12	1	3		6
SAOUHSC_02259	ADNNLGQSFSFIK	13	0	2		9
SAOUHSC_02259	ENIPVFK	7	0	2		9
SAOUHSC_02259	FPELLR	6	0	2		9
SAOUHSC_02259	IAFYVAQWPMSR	12	0	2		9
SAOUHSC_02259	NETQITQWFEK	11	0	2		9
SAOUHSC_02259	NNQIFNTAFSVNK	13	0	2		9
SAOUHSC_02259	SGQLINEYDK	10	0	2		9
SAOUHSC_02259	SIKLDLYK	8	1	3		9
SAOUHSC_02259	VQIYQLPIVFGDSSK	15	0	2		9
SAOUHSC_02260	WIIDTVNK	8	0	2		3
SAOUHSC_02260	WIIDTVNK	8	0	2	Deamidated (NQ)	3
SAOUHSC_02260	WIIDTVNKFTK	11	1	2		3
SAOUHSC_02260	WIIDTVNKFTK	11	1	3		3
SAOUHSC_02260	WIIDTVNKFTK	11	1	2	Deamidated (NQ)	3
SAOUHSC_02260	WIIDTVNKFTK	11	1	3	Deamidated (NQ)	3
SAOUHSC_02260	WIIDTVNKFTKK	12	2	2		3
SAOUHSC_02260	WIIDTVNKFTKK	12	2	3		3
SAOUHSC_02260	WIIDTVNKFTKK	12	2	4		3
SAOUHSC_02261	NNLDHIQFLQVR	12	0	2		1
SAOUHSC_02261	NNLDHIQFLQVR	12	0	3		1
SAOUHSC_02264	AQEMNIPISIEIPDEVSSINLNMIDLSR	28	0	3		8
SAOUHSC_02264	EDDMPGLR	8	0	2		8
SAOUHSC_02264	EIADNADNVLLDTIIENGFFIQK	23	0	2		8
SAOUHSC_02264	EIADNADNVLLDTIIENGFFIQK	23	0	3		8
SAOUHSC_02264	EIADNADNVLLDTIIENGFFIQK	23	0	3	Deamidated (NQ)	8
SAOUHSC_02264	GLGLSTLK	8	0	2		8
SAOUHSC_02264	IEAINNEMRK	10	1	3		8
SAOUHSC_02264	LNGIENLK	8	0	2		8
SAOUHSC_02264	NIVPMKDNLQMNAIK	15	1	3		8
SAOUHSC_02264	NQEEIETYYEYTLK	14	0	2		8
SAOUHSC_02265	DNSVETIELK	10	0	2		8
SAOUHSC_02265	DNSVETIELKR	11	1	2		8
SAOUHSC_02265	DNSVETIELKR	11	1	3		8
SAOUHSC_02265	DNSVETIELKR	11	1	2	Deamidated (NQ)	8
SAOUHSC_02265	ELSQLDDR	8	0	2		8
SAOUHSC_02265	HNIESIDSK	9	0	2		8
SAOUHSC_02265	IIDCLETAHTR	11	0	2	Carbamidomethyl (C)	8
SAOUHSC_02265	IIDCLETAHTR	11	0	3	Carbamidomethyl (C)	8
SAOUHSC_02265	LIAHLDNR	8	0	3		8
SAOUHSC_02265	QIEFYGNLK	9	0	2		8
SAOUHSC_02265	VAAMDFIFKDDPAELR	16	1	3		8
SAOUHSC_02267	DAHYQLITK	9	0	2		8
SAOUHSC_02267	DAHYQLITK	9	0	3		8
SAOUHSC_02267	ILATDVLNLTQLFENEGEEILAFSNR	26	0	3		8
SAOUHSC_02267	LFSIGEALIDFIPNVTNANLK	21	0	3		8
SAOUHSC_02267	LPLWDNAEDLR	11	0	2		8
SAOUHSC_02267	QIGGAPCNVACTVQK	15	0	2	2 Carbamidomethyl (C)	8
SAOUHSC_02267	QIGGAPCNVACTVQK	15	0	2	2 Carbamidomethyl (C); Gln->pyro-Glu (N-term Q)	8
SAOUHSC_02267	QIGGAPCNVACTVQK	15	0	3	2 Carbamidomethyl (C)	8
SAOUHSC_02267	QIGGAPCNVACTVQK	15	0	3	2 Carbamidomethyl (C); Gln->pyro-Glu (N-term Q)	8
SAOUHSC_02267	TLNANGTVVFDPNVR	15	0	2		8
SAOUHSC_02267	TLNANGTVVFDPNVR	15	0	2	Deamidated (NQ)	8
SAOUHSC_02267	TNEANTALAFVSLTEAGER	19	0	2		8
SAOUHSC_02267	TNEANTALAFVSLTEAGER	19	0	3		8
SAOUHSC_02267	VKPVDTTGAGDAFIGAVISR	20	0	3		8
SAOUHSC_02267	VKPVDTTGAGDAFIGAVISR	20	0	2		8
SAOUHSC_02268	AEGPLNPDTK	11	0	2		17
SAOUHSC_02268	ETALGYANK	9	0	2		17
SAOUHSC_02268	FPKPVISQQPEGYTSHFR	18	0	2		17
SAOUHSC_02268	FPKPVISQQPEGYTSHFR	18	0	3		17
SAOUHSC_02268	FPKPVISQQPEGYTSHFR	18	0	4		17
SAOUHSC_02268	IFPTEDALGIK	11	0	2		17
SAOUHSC_02268	LTYEHENFVELDNGFDFYAPQTFLDEK	27	0	3		17
SAOUHSC_02268	NIYQSGYILGK	11	0	2		17
SAOUHSC_02268	QQFHIQPETGLLNDPNGLIFYK	22	0	3		17
SAOUHSC_02268	QQFHIQPETGLLNDPNGLIFYK	22	0	3	Gln->pyro-Glu (N-term Q)	17
SAOUHSC_02268	QQFHIQPETGLLNDPNGLIFYK	22	0	3	2 Deamidated (NQ)	17
SAOUHSC_02268	QQFHIQPETGLLNDPNGLIFYK	22	0	3	Deamidated (NQ)	17
SAOUHSC_02268	QQFHIQPETGLLNDPNGLIFYK	22	0	3	Deamidated (NQ); Gln->pyro-Glu (N-term Q)	17
SAOUHSC_02268	QQFHIQPETGLLNDPNGLIFYK	22	0	3	Gln->pyro-Glu (N-term Q)	17
SAOUHSC_02268	QRPYPALEK	9	0	2	Gln->pyro-Glu (N-term Q)	17
SAOUHSC_02268	SDSGLLPTNVEGTTR	15	0	2		17
SAOUHSC_02268	STILDTPLK	9	0	2		17
SAOUHSC_02268	TSSTLIAYNK	10	0	2		17
SAOUHSC_02268	TSSTLIAYNKR	11	1	2		17
SAOUHSC_02268	TSSTLIAYNKR	11	1	3		17
SAOUHSC_02268	TSTESGQVYLQFTK	14	0	2		17
SAOUHSC_02268	VLIGWMGLPEIEYPTDNEGWAHCLTIPR	28	0	3	Carbamidomethyl (C)	17
SAOUHSC_02268	VLIGWMGLPEIEYPTDNEGWAHCLTIPR	28	0	4	Carbamidomethyl (C)	17
SAOUHSC_02268	VLNVENGQLK	10	0	2		17
SAOUHSC_02268	VLNVENGQLK	10	0	2	Deamidated (NQ)	17
SAOUHSC_02268	YWYNYTSDDLINFK	14	0	2		17
SAOUHSC_02268	YYAIIGAQNNDQQGR	15	0	2		17
SAOUHSC_02268	YYAIIGAQNNDQQGR	15	0	3		17
SAOUHSC_02269	GLLDQLAK	8	0	2		4
SAOUHSC_02269	MKNISDIAK	9	1	3		4
SAOUHSC_02269	MNSYAVDETIK	11	0	2		4
SAOUHSC_02269	QTHLIGAIIPR	11	0	2		4
SAOUHSC_02269	QTHLIGAIIPR	11	0	3		4
SAOUHSC_02269	QTHLIGAIIPR	11	0	2	Gln->pyro-Glu (N-term Q)	4
SAOUHSC_02271	KMATLQSGDELK	12	1	2		3
SAOUHSC_02271	KMATLQSGDELK	12	1	3		3
SAOUHSC_02271	MATLQSGDELK	11	0	2		3
SAOUHSC_02271	MIHELGTVGMVCPFPLIEAQK	21	0	3	Carbamidomethyl (C)	3
SAOUHSC_02273	AISDALQIQSATIR	14	0	2		16

Supplemental Material Table S2

Locus Tag	Peptide Sequence	# aa	missed cleavage	Peptide Charge	Peptide Modification	number of peptides per protein
SAOUHSC_02649	EQPLESISQLILSK	14	0	3		12
SAOUHSC_02649	HNPMTACYFVTDDR	14	0	2	Carbamidomethyl (C); Oxidation (M)	12
SAOUHSC_02649	HNPMTACYFVTDDR	14	0	3	Carbamidomethyl (C)	12
SAOUHSC_02649	HNPMTACYFVTDDR	14	0	3	Carbamidomethyl (C); Oxidation (M)	12
SAOUHSC_02649	INDQKPVLLYAPIGLVSAQQLPLSDALFK	29	0	4		12
SAOUHSC_02649	INDQKPVLLYAPIGLVSAQQLPLSDALFK	29	0	3	Deamidated (NQ)	12
SAOUHSC_02649	NLFIEDSEQLNSPDNWLYSTK	21	0	2		12
SAOUHSC_02649	NLFIEDSEQLNSPDNWLYSTK	21	0	3		12
SAOUHSC_02649	QINVSNMQK	9	0	2	Gln->pyro-Glu (N-term Q)	12
SAOUHSC_02649	QLLINNLISQAIPVIK	16	0	2		12
SAOUHSC_02649	QLLINNLISQAIPVIK	16	0	3		12
SAOUHSC_02649	QLLINNLISQAIPVIK	16	0	2	Gln->pyro-Glu (N-term Q)	12
SAOUHSC_02649	SEKADELINSAR	12	1	3		12
SAOUHSC_02649	TVALYTPNHSQYIESQGVNEDIWR	24	0	3		12
SAOUHSC_02650	NQALQQLPNFQTALNAANNEANK	23	0	2		6
SAOUHSC_02650	NQALQQLPNFQTALNAANNEANK	23	0	3		6
SAOUHSC_02650	NQALQQLPNFQTALNAANNEANKFGSNNK	29	1	3		6
SAOUHSC_02650	QIYPFNGNK	9	0	2		6
SAOUHSC_02650	QIYPFNGNK	9	0	2	Deamidated (NQ)	6
SAOUHSC_02650	QIYPFNGNK	9	0	2	Gln->pyro-Glu (N-term Q)	6
SAOUHSC_02650	SSYVAPYYGQNAAPVAR	17	0	2		6
SAOUHSC_02650	SSYVAPYYGQNAAPVAR	17	0	3		6
SAOUHSC_02650	VYNDYSIEEHNGNYK	15	0	3		6
SAOUHSC_02650	VYNDYSIEEHNGNYK	15	0	2	Deamidated (NQ)	6
SAOUHSC_02650	VYNDYSIEEHNGNYK	15	0	3	Deamidated (NQ)	6
SAOUHSC_02650	YVFSFKDPNANGK	13	1	2		6
SAOUHSC_02650	YVFSFKDPNANGK	13	1	3		6
SAOUHSC_02650	YVFSFKDPNANGK	13	1	3	Deamidated (NQ)	6
SAOUHSC_02651	EISEQNASELVELATR	16	0	2		2
SAOUHSC_02651	EISEQNASELVELATR	16	0	3		2
SAOUHSC_02651	GSQLIELAEK	10	0	2		2
SAOUHSC_02652	DALATQDHNAVVK	13	0	2		12
SAOUHSC_02652	DLMPENLHEIK	11	0	2		12
SAOUHSC_02652	DLMPENLHEIK	11	0	3		12
SAOUHSC_02652	GASGGVGTLAVLMLNELGYK	20	0	2		12
SAOUHSC_02652	GASGGVGTLAVLMLNELGYK	20	0	3		12
SAOUHSC_02652	GFQVIVTSYDLGVSHYGGFSEYAR	24	0	3		12
SAOUHSC_02652	GVNILGIDSVFTAMK	15	0	2		12
SAOUHSC_02652	KPLASSTWQACVDPVGGEGINYVTK	25	0	3	Carbamidomethyl (C)	12
SAOUHSC_02652	LPDTLTLEESMIYGTAGYTAGLAIER	26	0	3		12
SAOUHSC_02652	QDVSDQLLELGAK	13	0	2		12
SAOUHSC_02652	QVITFDELPEQLNK	14	0	2		12
SAOUHSC_02652	QVITFDELPEQLNK	14	0	3		12
SAOUHSC_02652	SEWIIK	6	0	2		12
SAOUHSC_02652	SYPMIPGIDLAGTIVESEAPGFEK	24	0	2		12
SAOUHSC_02652	SYPMIPGIDLAGTIVESEAPGFEK	24	0	3		12
SAOUHSC_02652	VGMNIEDGPVLVR	13	0	2		12
SAOUHSC_02652	VGMNIEDGPVLVR	13	0	2	Oxidation (M)	12
SAOUHSC_02653	FGFIPTEPDSGGMYIKY	17	1	2		1
SAOUHSC_02654	CNTLLSETSSK	11	0	2	Carbamidomethyl (C)	5
SAOUHSC_02654	DKDVLSGGGNTALDWAHDIAK	22	1	4		5
SAOUHSC_02654	SHLIASAFSDGANAANLAK	19	0	2		5
SAOUHSC_02654	SHLIASAFSDGANAANLAK	19	0	3		5
SAOUHSC_02654	TLVTDLNVK	9	0	2		5
SAOUHSC_02654	TYIQPDANAEGYVSSHHEVFK	21	0	4		5
SAOUHSC_02658	DLPIGILNIEDKGTTIQDK	18	1	3		5
SAOUHSC_02658	QMLPESYQK	9	0	2		5
SAOUHSC_02658	QSLETLTSQNVK	12	0	2		5
SAOUHSC_02658	VDNEKLNK	8	1	2		5
SAOUHSC_02658	VNAADINGLTNPVKVDNEK	19	1	3		5
SAOUHSC_02659	QPISVDELAK	10	0	2		1
SAOUHSC_02660	NLRLLNK	7	1	2	Deamidated (NQ)	3
SAOUHSC_02660	NNITNKQLFK	10	1	2	2 Deamidated (NQ)	3
SAOUHSC_02660	SLVYFLAALK	10	0	2		3
SAOUHSC_02661	DLFFSGK	7	0	2		1
SAOUHSC_02662	LVLNDESLVNEEALNNMDVVK	21	0	2		2
SAOUHSC_02662	LVLNDESLVNEEALNNMDVVK	21	0	3		2
SAOUHSC_02662	QSAEEILNAIGGEENLDAMAHCATR	25	0	3	Carbamidomethyl (C)	2
SAOUHSC_02662	QSAEEILNAIGGEENLDAMAHCATR	25	0	3	Carbamidomethyl (C); Gln->pyro-Glu (N-term Q)	2
SAOUHSC_02663	ERGYIEQLWR	10	1	2		1
SAOUHSC_02663	ERGYIEQLWR	10	1	3		1
SAOUHSC_02664	EILDELDK	8	0	2		10
SAOUHSC_02664	EILDELDKTNYPK	13	1	3		10
SAOUHSC_02664	HLLQSSNYIK	10	0	2		10
SAOUHSC_02664	NIGLAIAIK	9	0	2		10
SAOUHSC_02664	NIGQSIIDTLLK	12	0	2		10
SAOUHSC_02664	NIGQSIIDTLLK	12	0	3		10
SAOUHSC_02664	NYLHFSPK	8	0	3		10
SAOUHSC_02664	QDFIFHNELPQDSLMIK	18	0	3		10
SAOUHSC_02664	QLILTFLQGNQDYK	14	0	2		10
SAOUHSC_02664	SLIADLISTPTSSSLMGK	18	0	2		10
SAOUHSC_02664	TELAVQEETGR	11	0	2		10
SAOUHSC_02665	DNPAAYVLLGYNDTTNR	17	0	2		8
SAOUHSC_02665	DNPAAYVLLGYNDTTNR	17	0	3		8
SAOUHSC_02665	EDPELCVLR	9	0	2	Carbamidomethyl (C)	8
SAOUHSC_02665	EIKDNPAAYVLLGYNDTTNR	20	1	3		8
SAOUHSC_02665	MSNSQAIQAIENVLVTSK	18	0	2		8
SAOUHSC_02665	SLDTPIKIDL	10	1	2		8
SAOUHSC_02665	SNSQAIQAIENVLVTSK	17	0	2		8
SAOUHSC_02665	SNSQAIQAIENVLVTSK	17	0	3		8
SAOUHSC_02665	SNSQAIQAIENVLVTSK	17	0	3	Deamidated (NQ)	8
SAOUHSC_02665	VGVLSTAYNNKPNSR	15	0	3		8
SAOUHSC_02665	VGVLSTAYNNKPNSR	15	0	3	Deamidated (NQ)	8
SAOUHSC_02665	YMVFYNDGLTLYTK	14	0	2		8
SAOUHSC_02666	GDFVIVYK	8	0	2		10
SAOUHSC_02666	KDTYYGIMK	9	1	2		10
SAOUHSC_02666	KGDFVIVYK	9	1	2		10
SAOUHSC_02666	KGDFVIVYK	9	1	3		10
SAOUHSC_02666	KVDHDDVPHGLMMK	14	1	3		10
SAOUHSC_02666	KVDHDDVPHGLMMK	14	1	4	Oxidation (M)	10
SAOUHSC_02666	LPSDSDVKVK	10	1	2		10
SAOUHSC_02666	MISEKDESIEK	11	1	2		10
SAOUHSC_02666	MISEKDESIEK	11	1	3		10
SAOUHSC_02666	MISEKDESIEK	11	1	3	Oxidation (M)	10
SAOUHSC_02666	MISEKDESIEKNVK	14	2	3		10
SAOUHSC_02666	NVKLPSDSDVK	11	1	2		10
SAOUHSC_02666	NVKLPSDSDVK	11	1	3		10
SAOUHSC_02666	NVKLPSDSDVKVK	13	2	4		10
SAOUHSC_02666	VDHDDVPHGLMMK	13	0	3		10
SAOUHSC_02667	TCVNVIGNALSTIVIAK	17	0	2	Carbamidomethyl (C)	2
SAOUHSC_02667	TCVNVIGNALSTIVIAK	17	0	3	Carbamidomethyl (C)	2
SAOUHSC_02667	WENVYDK	7	0	2		2
SAOUHSC_02668	DEPGVTYVVQPISTNK	16	0	2		4
SAOUHSC_02668	DEPGVTYVVQPISTNK	16	0	3		4
SAOUHSC_02668	EVTFKDEPGVTYVVQPISTNK	21	1	2		4
SAOUHSC_02668	EVTFKDEPGVTYVVQPISTNK	21	1	3		4
SAOUHSC_02668	EVTFKDEPGVTYVVQPISTNK	21	1	4		4
SAOUHSC_02668	GLFVEGFDTETKK	13	1	2		4
SAOUHSC_02668	GLFVEGFDTETKK	13	1	3		4
SAOUHSC_02668	NIQLIDSYLEEK	12	0	2		4
SAOUHSC_02669	EASDINNLR	10	0	2		7
SAOUHSC_02669	MYVENSYLSK	10	0	2		7
SAOUHSC_02669	NLQISLTEQGK	11	0	2		7
SAOUHSC_02669	SPLAEISVK	9	0	2		7
SAOUHSC_02669	VFLDSGTLTPLLK	13	0	2		7
SAOUHSC_02669	VFNEFNISER	10	0	2		7
SAOUHSC_02669	YVENSYLSK	9	0	2		7
SAOUHSC_02670	IKPSNETTSSTSIPIS	16	0	2		4
SAOUHSC_02670	QFDFEAVDK	9	0	2		4
SAOUHSC_02670	SEQLILDER	9	0	2		4
SAOUHSC_02670	YKSEQLILDER	11	1	2		4
SAOUHSC_02670	YKSEQLILDER	11	1	3		4
SAOUHSC_02672	INIIR	5	0	2	Deamidated (NQ)	1
SAOUHSC_02674	GLSLIDTSILNK	12	0	2		2
SAOUHSC_02674	ISDLQLIR	8	0	3	Deamidated (NQ)	2
SAOUHSC_02675	ELEILPLIAK	10	0	2		6
SAOUHSC_02675	LTTSLVNEFVSNSNQDTANTTDPFK	25	0	2		6
SAOUHSC_02675	LTTSLVNEFVSNSNQDTANTTDPFK	25	0	3		6
SAOUHSC_02675	NAPDEQLLLAIR	12	0	2		6
SAOUHSC_02675	RELEILPLIAK	11	1	3		6
SAOUHSC_02675	SKPELVEYALK	11	1	3		6
SAOUHSC_02675	VMEYKPDVLLMDLSMPPGESGLIATSK	27	1	3		6
SAOUHSC_02676	AELVSGSVNIETK	13	0	2		7
SAOUHSC_02676	DILSEEDNYSAVANAICHR	19	0	3	Carbamidomethyl (C)	7
SAOUHSC_02676	GIHAFTLQNVSSQIEQQEK	19	0	3		7
SAOUHSC_02676	IIAMNDAAK	9	0	2	Deamidated (NQ)	7
SAOUHSC_02676	LIDDIR	6	0	2		7
SAOUHSC_02676	LLEDAENIEYIVAK	14	0	2		7
SAOUHSC_02676	YADVNEINVGIR	12	0	2		7
SAOUHSC_02677	NQVYGVLLFGQR	12	0	2		1
SAOUHSC_02679	TFEETISK	8	0	2		1
SAOUHSC_02680	LAFPLHPEFR	10	0	3		4
SAOUHSC_02680	LPIEYLANIFTAGDTEPVK	19	0	3		4
SAOUHSC_02680	NTTQNPDAFPAIEEMR	17	0	2		4
SAOUHSC_02680	SQVTQQPFDTSR	12	0	2		4
SAOUHSC_02681	EVIPTAVFPGSNK	13	0	2		7
SAOUHSC_02681	GGPTVWISNEDAEK	14	0	2		7
SAOUHSC_02681	HIQTPGSEITDTR	13	0	2		7
SAOUHSC_02681	HIQTPGSEITDTR	13	0	3		7
SAOUHSC_02681	IKYPYIR	7	1	3		7
SAOUHSC_02681	NVADAILSISSATNGK	16	0	2		7
SAOUHSC_02681	NVADAILSISSATNGK	16	0	3		7
SAOUHSC_02681	QSVVIQVAK	9	0	2		7
SAOUHSC_02681	QTQFAIEDPQLKK	13	1	2		7
SAOUHSC_02683	QGPLSEGTVSGEYVFCPLHDQK	22	0	3	Carbamidomethyl (C)	3
SAOUHSC_02683	VTTIDELTPLIGK	13	0	2		3
SAOUHSC_02683	VTTIDELTPLIGKK	14	1	3		3
SAOUHSC_02684	AFVIPVPGSTLPSVIGWR	18	0	3		11
SAOUHSC_02684	ANQSVTTANGIEVSYDK	17	0	2		11
SAOUHSC_02684	DQIVTQIR	8	0	2		11