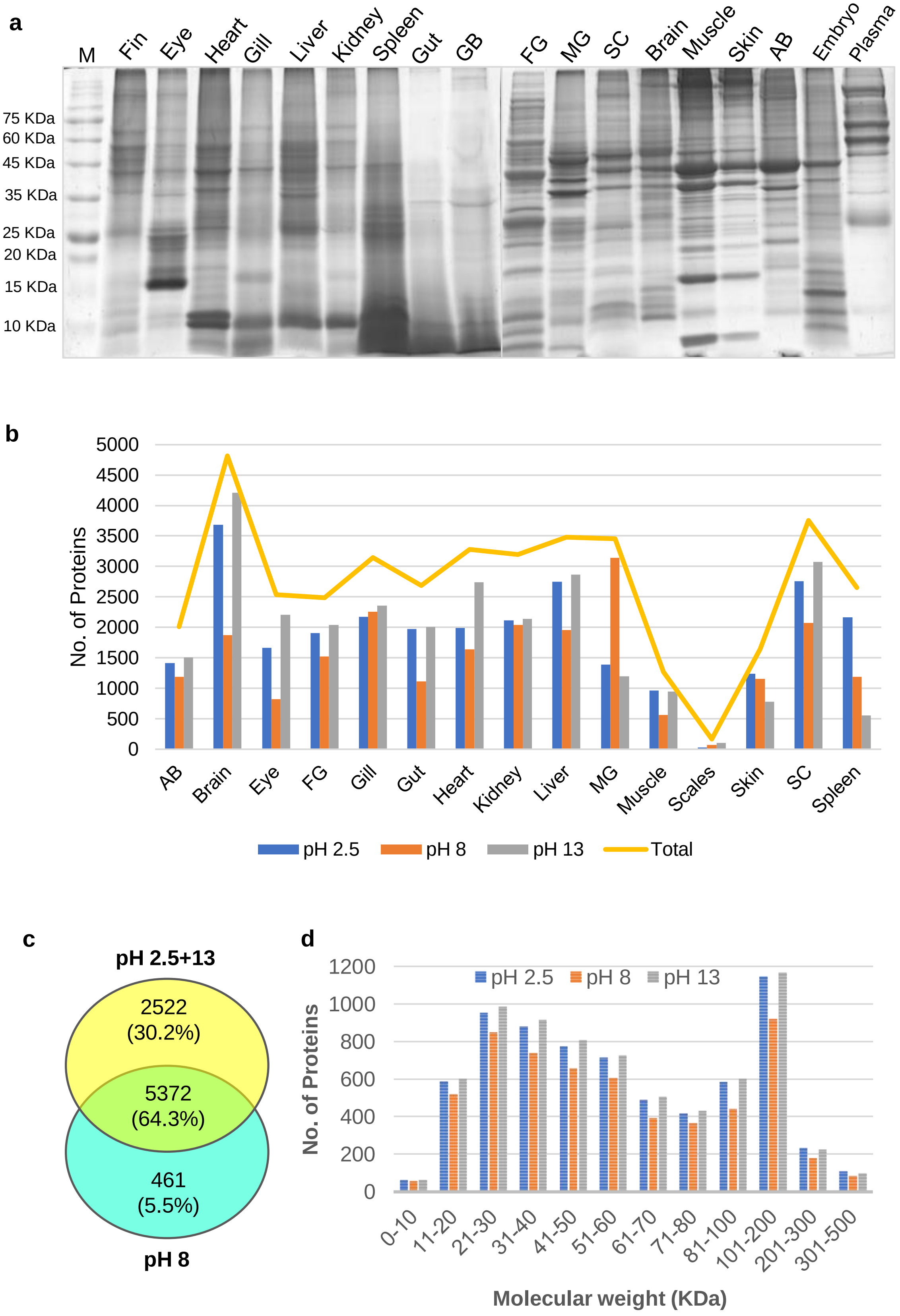
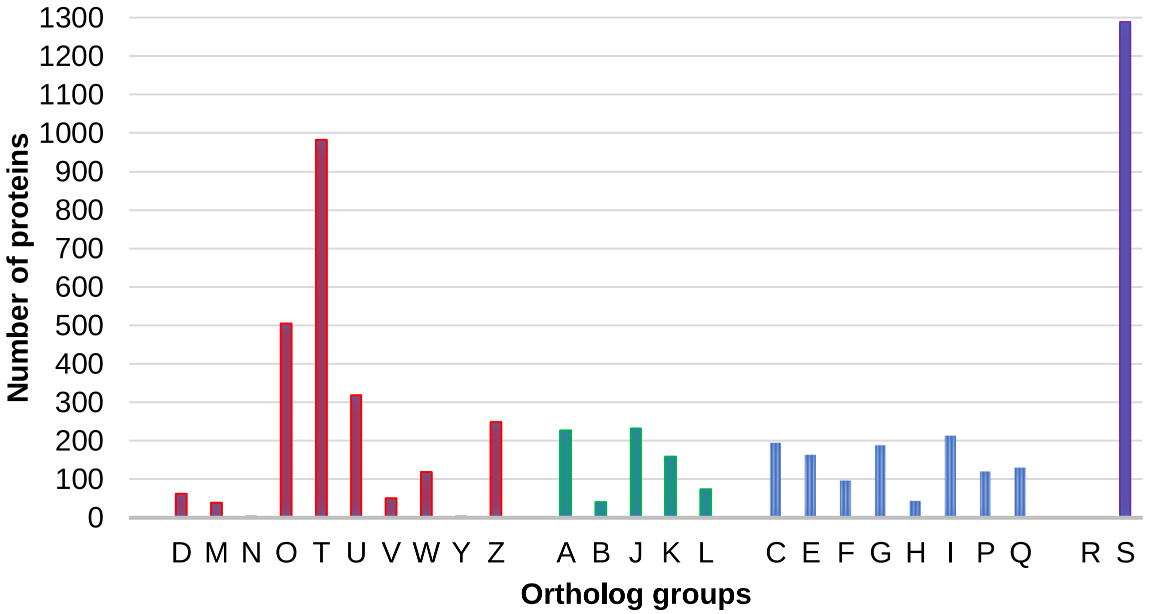
Supplementary Figure S1

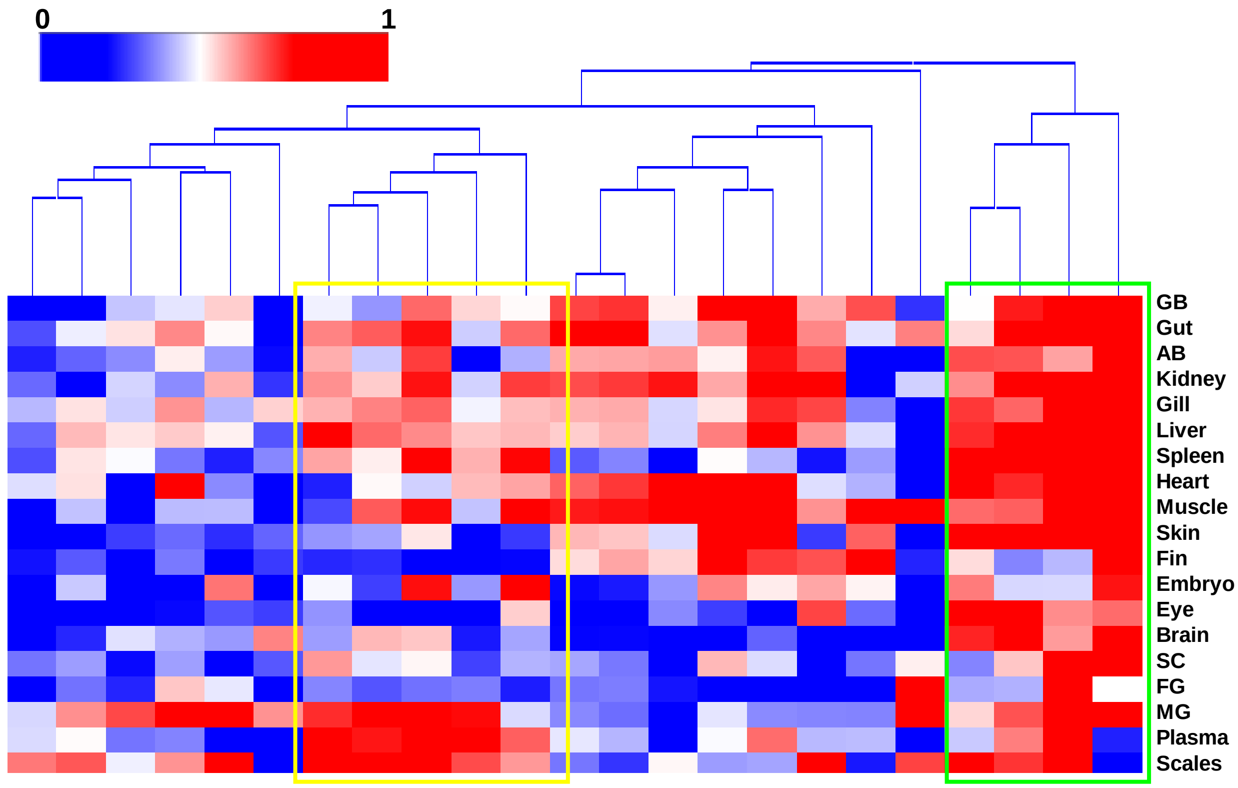


Supplementary Figure S2



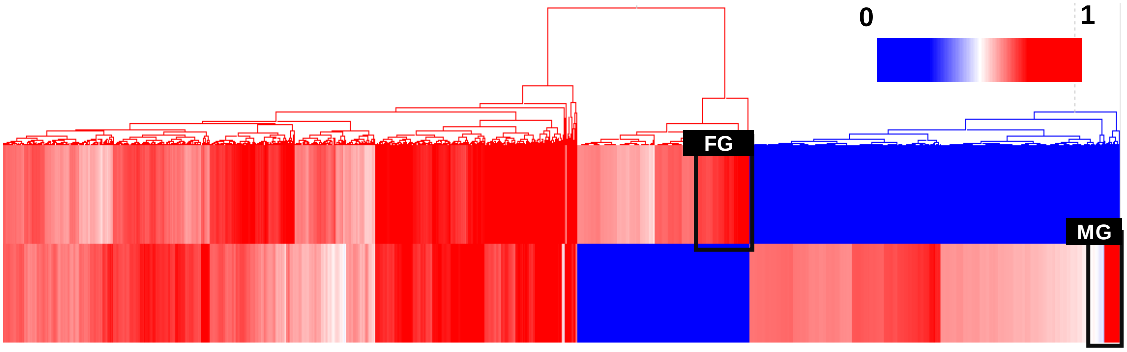
Groups	Description	No. of proteins
CELLULAR PROCESSES AND SIGNALING		
D	Cell cycle control, cell division, chromosome partitioning	62
M	Cell wall/membrane/envelope biogenesis	38
N	Cell motility	5
O	Post-translational modification, protein turnover, and chaperones	505
T	Signal transduction mechanisms	982
U	Intracellular trafficking, secretion, and vesicular transport	318
V	Defense mechanisms	50
W	Extracellular structures	119
Y	Nuclear structure	4
Z	Cytoskeleton	249
INFORMATION STORAGE AND PROCESSING		
A	RNA processing and modification	226
B	Chromatin structure and dynamics	40
J	Translation, ribosomal structure and biogenesis	232
K	Transcription	158
L	Replication, recombination and repair	74
METABOLISM		
C	Energy production and conversion	195
E	Amino acid transport and metabolism	163
F	Nucleotide transport and metabolism	96
G	Carbohydrate transport and metabolism	187
H	Coenzyme transport and metabolism	43
I	Lipid transport and metabolism	213
P	Inorganic ion transport and metabolism	120
Q	Secondary metabolites biosynthesis, transport, and catabolism	129
POORLY CHARACTERIZED		
R	General function prediction only	0
S	Function unknown	1289

Supplementary Figure S3



NCBI ID	Uniprot ID	Protein name	Category/Function
RXN10923.1	A0A498LTI4	Heat shock cognate 71 kDa	Protein folding
RXN17745.1	A0A498MKB6	L-lactate dehydrogenase (EC 1.1.1.27)	Oxidoreductase/Cell respiration
RXN31887.1	A0A498NJQ6	ATP synthase subunit beta (EC 7.1.2.2)	Nucleotide binding/ATP synthesis
RXN29259.1	A0A498N4E9	Tubulin Beta-4B Chain	Cytoskeletal element
RXN08459.1	A0A498LJB6	Beta-enolase	Metal binding/Cell respiration
RXN39545.1	A0A498LRW2	Apolipo A-I	Lipid metabolism
RXN27874.1	A0A498N853	Transferrin variant C	Metal binding glycoproteins/Iron transport
RXN16130.1	A0A498M6I9	Cytoplasmic 1	Cytoplasmic cytoskeleton
RXN22752.1	A0A498MT06	Hemoglobin Subunit Beta-Like Protein	Gaseous transport/cell respiration

Supplementary Figure S4



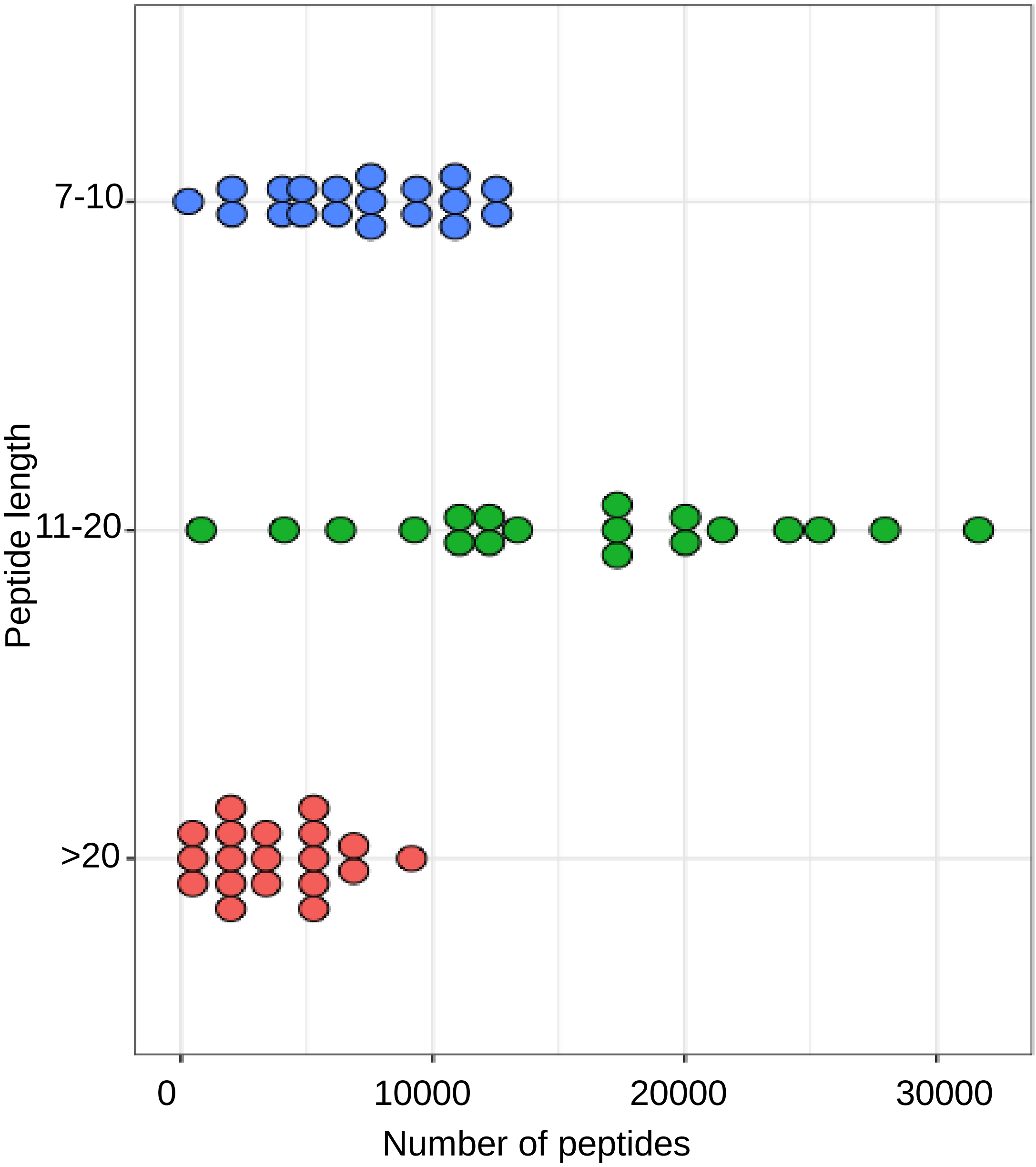
FG- Female gonad

RXN20786.1	A0A498MQD4	WFDC3-like isoform X2
RXN06915.1	A0A498LNH2	GLT8D1 isoform X1
RXN15248.1	A0A498M321	MCM3-like isoform X1
RXN26779.1	A0A498MXN1	Spindly isoform X1
RXN26748.1	A0A498MXT9	ZP2-like isoform X2
RXN06747.1	A0A498LMG9	ZP3-Like Protein

MG- Male gonad

RXN09507.1	A0A498M4Z4	ELAC2
RXN11994.1	A0A498LYP6	Box C D snoRNA1
RXN14883.1	A0A498M4T4	TOP1MT isoform X1
RXN20436.1	A0A498MP71	TDRD5-like protein
RXN22339.1	A0A498MLP7	KBTBD8
RXN17568.1	A0A498M970	RNA Helicase Tdrd9

Supplementary Figure S5

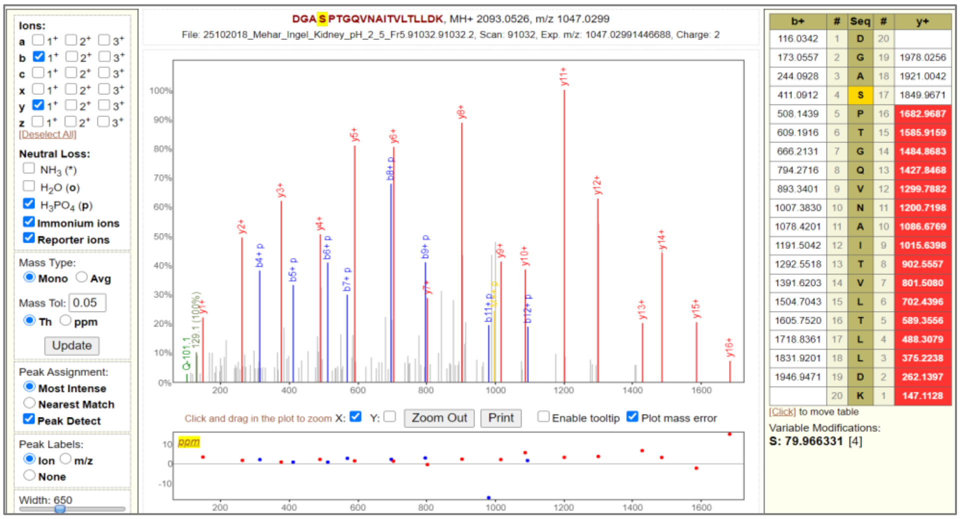


Supplementary Figure S6

DGAS[167]PTGQVNAITVLTLLDK $^{+2}$ - Protein A0A498NNQ1, S69

a

S-Phospho



Ions:
a ☐ 1^+ ☐ 2^+ ☐ 3^+
b ☑ 1^+ ☐ 2^+ ☐ 3^+
c ☐ 1^+ ☐ 2^+ ☐ 3^+
x ☐ 1^+ ☐ 2^+ ☐ 3^+
y ☑ 1^+ ☐ 2^+ ☐ 3^+
z ☐ 1^+ ☐ 2^+ ☐ 3^+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☑ H_3PO_4 (p)
☑ Immonium ions
☑ Reporter ions

Mass Type:
● Mono ○ Avg
Mass Tol: 0.05
● Th ○ ppm
Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

DGASPTGQVNAITVLTLLDK, MH+ 2093.0526, m/z 1047.0299
File: 25102018_Mehar_Ingel_Kidney_pH_2_5_Fr5.91032.91032.2, Scan: 91032, Exp. m/z: 1047.02991446688, Charge: 2

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☑ Plot mass error

b+	#	Seq	#	y+
116.0342	1	D	20	
173.0557	2	G	19	1978.0256
244.0928	3	A	18	1921.0042
411.0912	4	S	17	1849.9671
508.1439	5	P	16	1682.9687
609.1916	6	T	15	1585.9159
666.2131	7	G	14	1484.8683
794.2716	8	Q	13	1427.8468
893.3401	9	V	12	1299.7882
1007.3830	10	N	11	1200.7198
1078.4201	11	A	10	1086.6769
1191.5042	12	I	9	1015.6398
1292.5518	13	T	8	902.5557
1391.6203	14	V	7	801.5080
1504.7043	15	L	6	702.4396
1605.7520	16	T	5	589.3556
1718.8361	17	L	4	488.3079
1831.9201	18	L	3	375.2238
1946.9471	19	D	2	262.1397
	20	K	1	147.1128

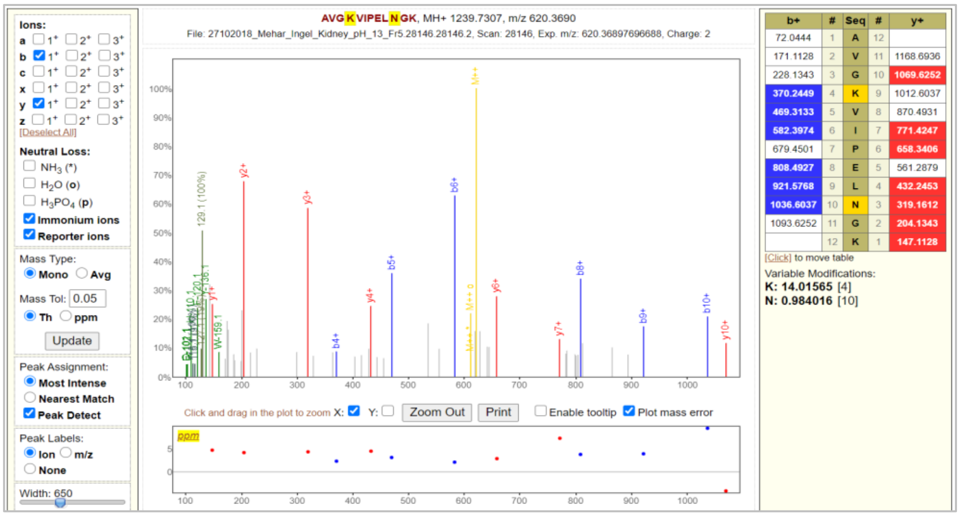
[Click] to move table

Variable Modifications:
S: 79.966331 [4]

AVGK[142]VIPELN[115]GK^{+2} - Protein A0A498L4F1, K233

b

K-Methyl



Ions:
a ☐ 1^+ ☐ 2^+ ☐ 3^+
b ☑ 1^+ ☐ 2^+ ☐ 3^+
c ☐ 1^+ ☐ 2^+ ☐ 3^+
x ☐ 1^+ ☐ 2^+ ☐ 3^+
y ☑ 1^+ ☐ 2^+ ☐ 3^+
z ☐ 1^+ ☐ 2^+ ☐ 3^+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☑ Immonium ions
☑ Reporter ions

Mass Type:
● Mono ○ Avg
Mass Tol: 0.05
● Th ○ ppm
Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

AVGKVIPELNGK, MH+ 1239.7307, m/z 620.3690
File: 27102018_Mehar_Ingel_Kidney_pH_13_Fr5.28146.28146.2, Scan: 28146, Exp. m/z: 620.36897696688, Charge: 2

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☑ Plot mass error

b+	#	Seq	#	y+
72.0444	1	A	12	
171.1128	2	V	11	1168.6936
228.1343	3	G	10	1069.6252
370.2449	4	K	9	1012.6037
469.3133	5	V	8	870.4931
582.3974	6	I	7	771.4247
679.4501	7	P	6	658.3406
808.4927	8	E	5	561.2879
921.5768	9	L	4	432.2453
1036.6037	10	N	3	319.1612
1093.6252	11	G	2	204.1343
	12	K	1	147.1128

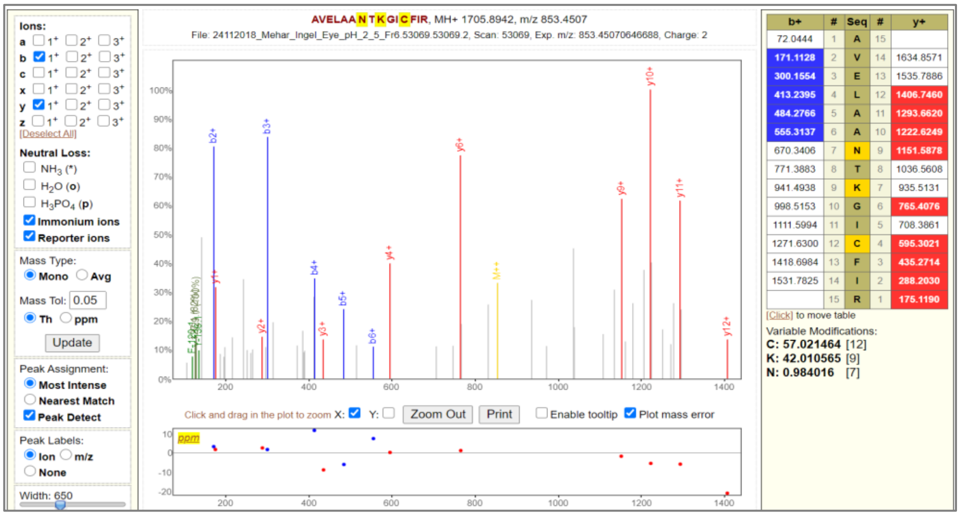
[Click] to move table

Variable Modifications:
K: 14.01565 [4]
N: 0.984016 [10]

AVELAAN[115]TK[170]GIC[160]FIR $^{+2}$ – Protein A0A498L5H4, K468

c

K-Acetyl



Ions:
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b ☑ 1^+ ☐ 2^+ ☐ 3^+
c ☐ 1^+ ☐ 2^+ ☐ 3^+
x ☐ 1^+ ☐ 2^+ ☐ 3^+
y ☑ 1^+ ☐ 2^+ ☐ 3^+
z ☐ 1^+ ☐ 2^+ ☐ 3^+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☑ Immonium ions
☑ Reporter ions

Mass Type:
● Mono ○ Avg
Mass Tol: 0.05
● Th ○ ppm
Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

AVELAANTKGICFIR, MH+ 1705.8942, m/z 853.4507
File: 24112018_Mehar_Ingel_Eye_pH_2_5_Fr6.53069.53069.2, Scan: 53069, Exp. m/z: 853.45070646688, Charge: 2

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☑ Plot mass error

b+	#	Seq	#	y+
72.0444	1	A	15	
171.1128	2	V	14	1634.8571
300.1554	3	E	13	1535.7886
413.2395	4	L	12	1406.7460
484.2766	5	A	11	1293.6620
555.3137	6	A	10	1222.6249
670.3406	7	N	9	1151.5878
771.3883	8	T	8	1036.5608
941.4938	9	K	7	935.5131
998.5153	10	G	6	765.4076
1111.5994	11	I	5	708.3861
1271.6300	12	C	4	595.3021
1418.6984	13	F	3	435.2714
1531.7825	14	I	2	288.2030
	15	R	1	175.1190

[Click] to move table

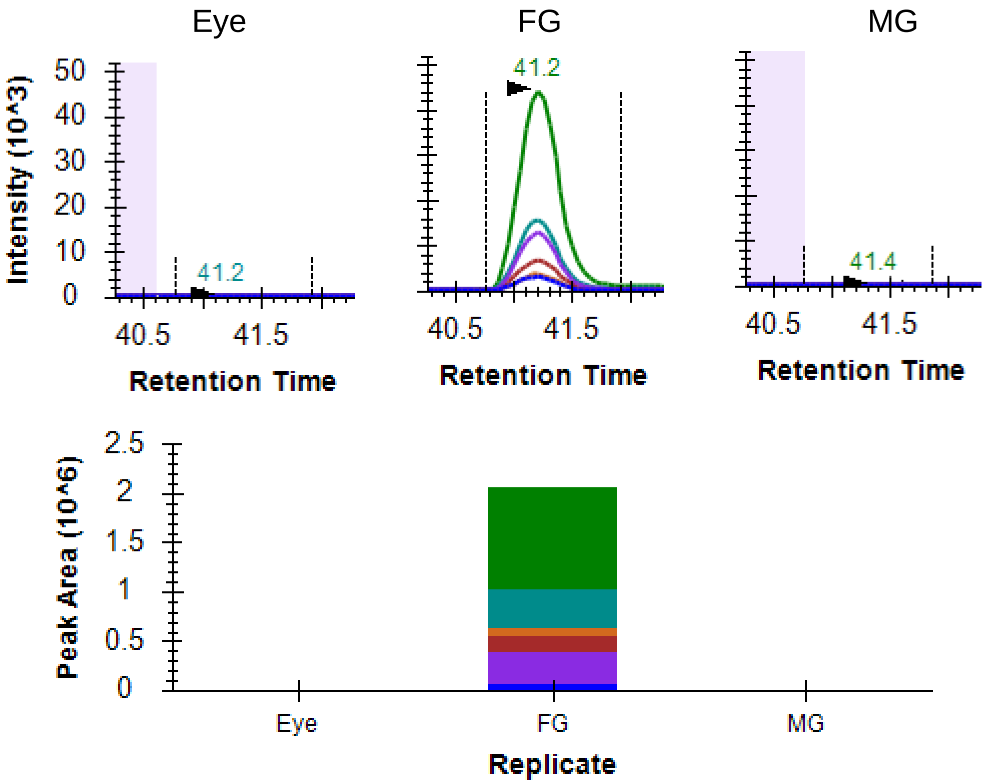
Variable Modifications:
C: 57.021464 [12]
K: 42.010565 [9]
N: 0.984016 [7]

Supplementary Figure S7

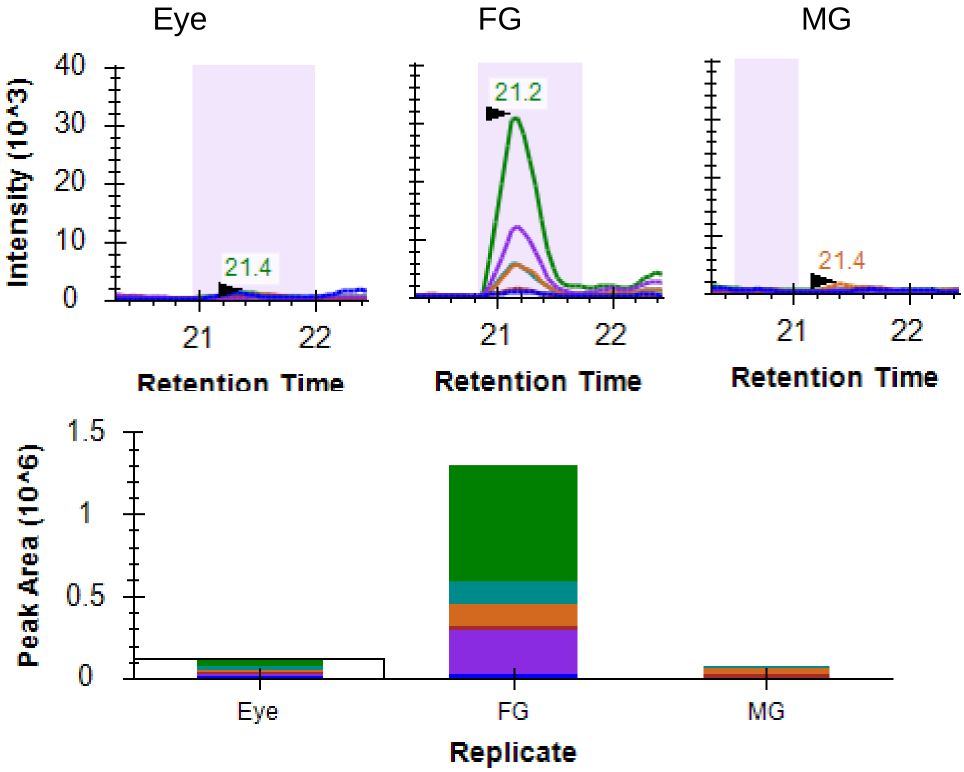
Protein 1 –ZP2-like isoform X2- High in Female gonad

RXN26748.1 A0A498MXT9

Peptide 1: R.HYAMTFTESHIVVK.I [251, 264]



Peptide 2: K.YGSTPSSQLK.I [454, 463]

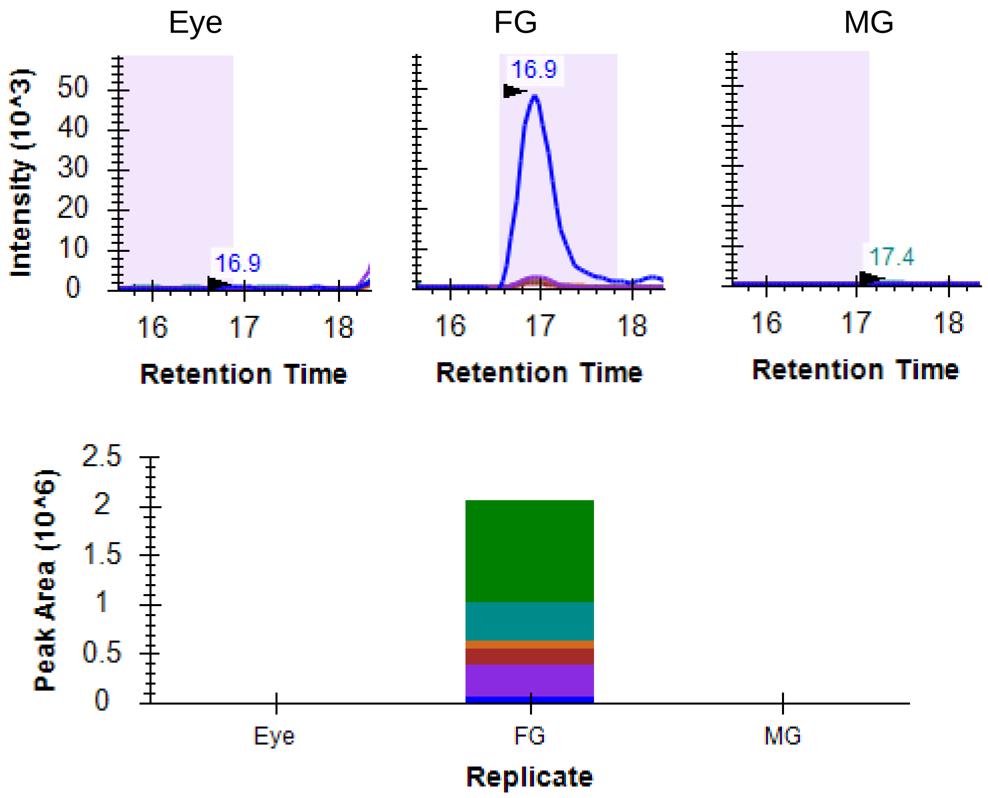


Supplementary Figure S8

Protein 1 –ZP2-like isoform X2- High in Female gonad

RXN26748.1 A0A498MXT9

Peptide 3: K.LGHMELNDK.I [466, 474]

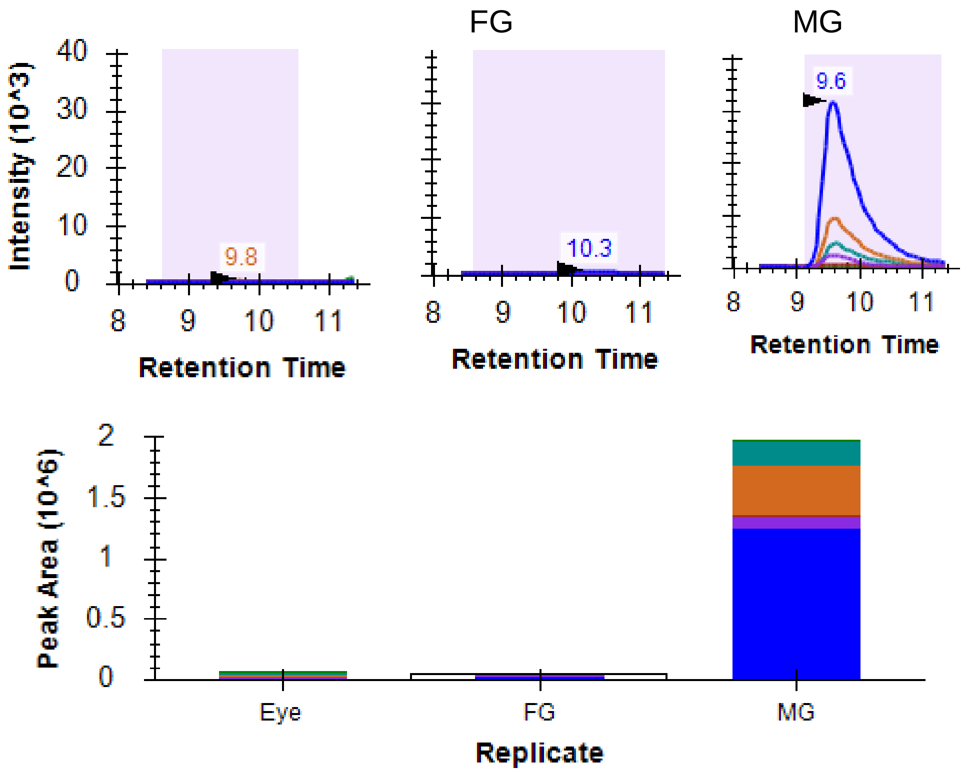


Supplementary Figure S9

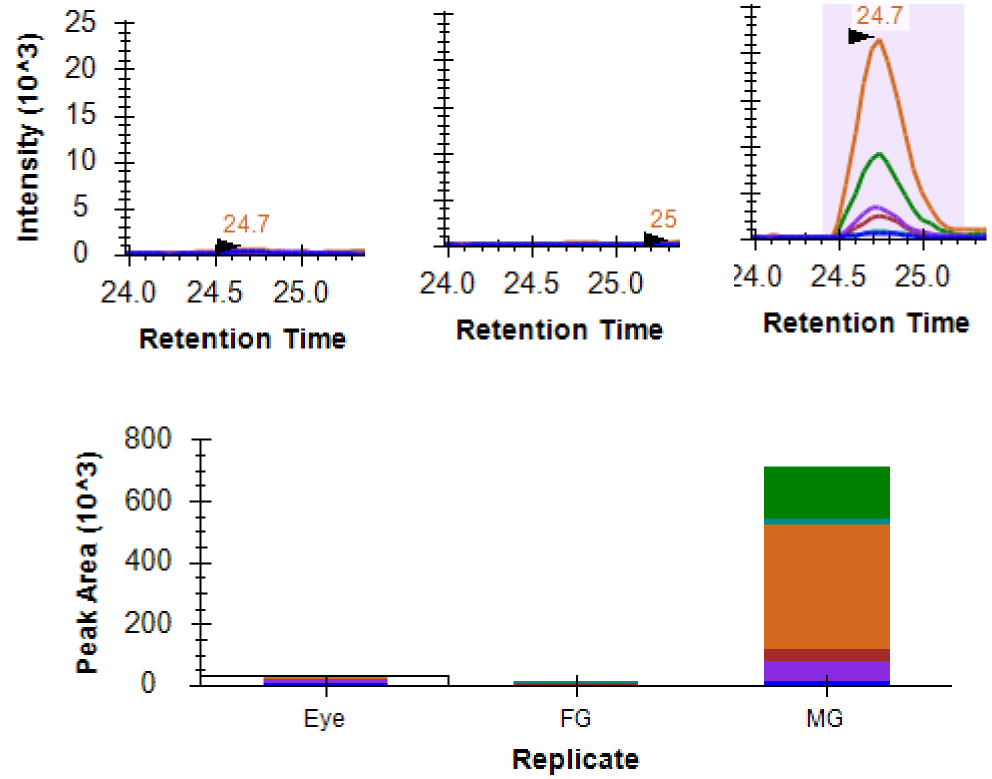
Protein 2 –TDRD5-like protein- High in Male gonad

RXN20436.1 A0A498MP71

Peptide 1: K.VASPLAAK.Q [76, 83]



Peptide 2: K.AEPSFEETIFK.L [116, 126]

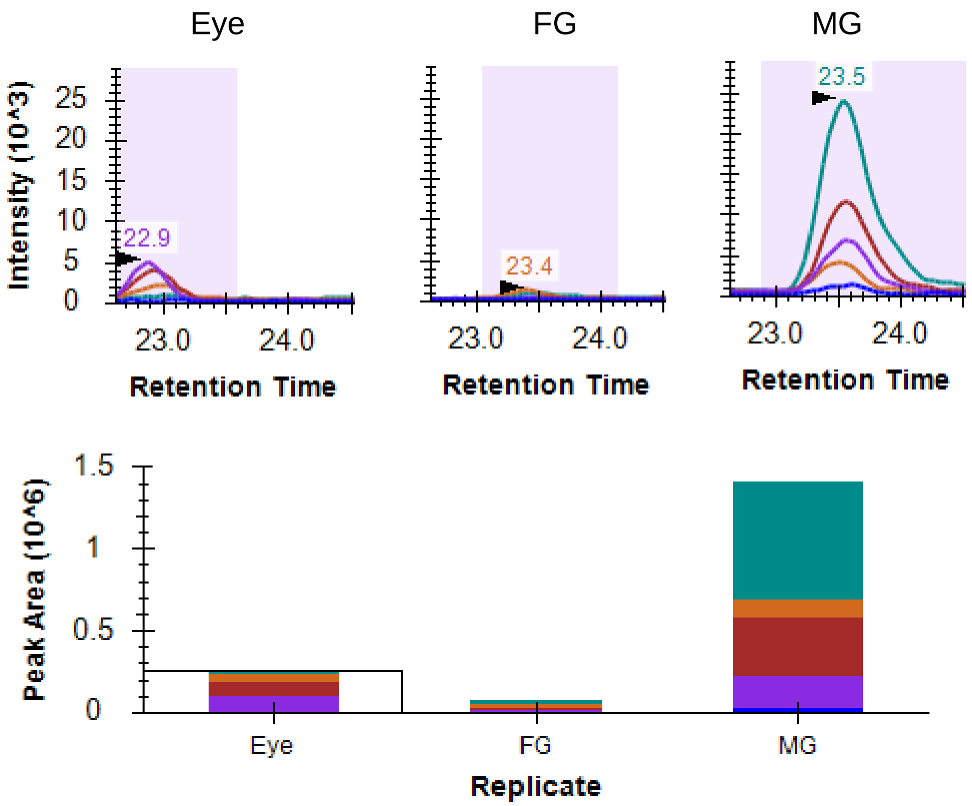


Supplementary Figure S10

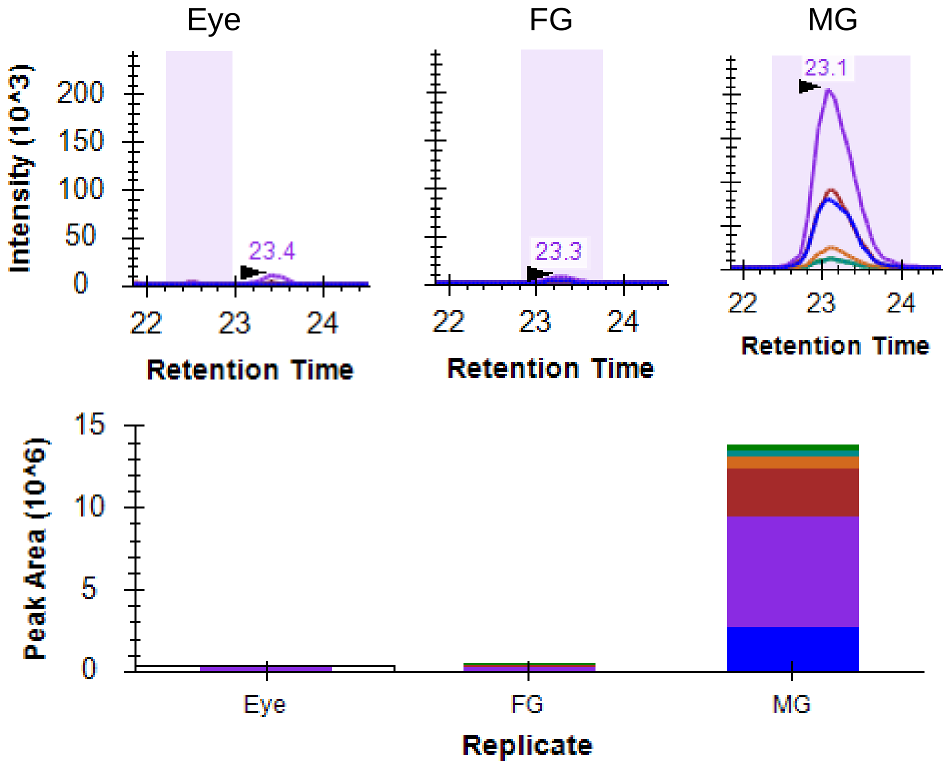
Protein 2 –TDRD5-like protein- High in Male gonad

RXN20436.1 A0A498MP71

Peptide 3: R.VSAVPPDAVR.C [300, 309]



Peptide 4: K.TQLGPDIK.T [637, 644]

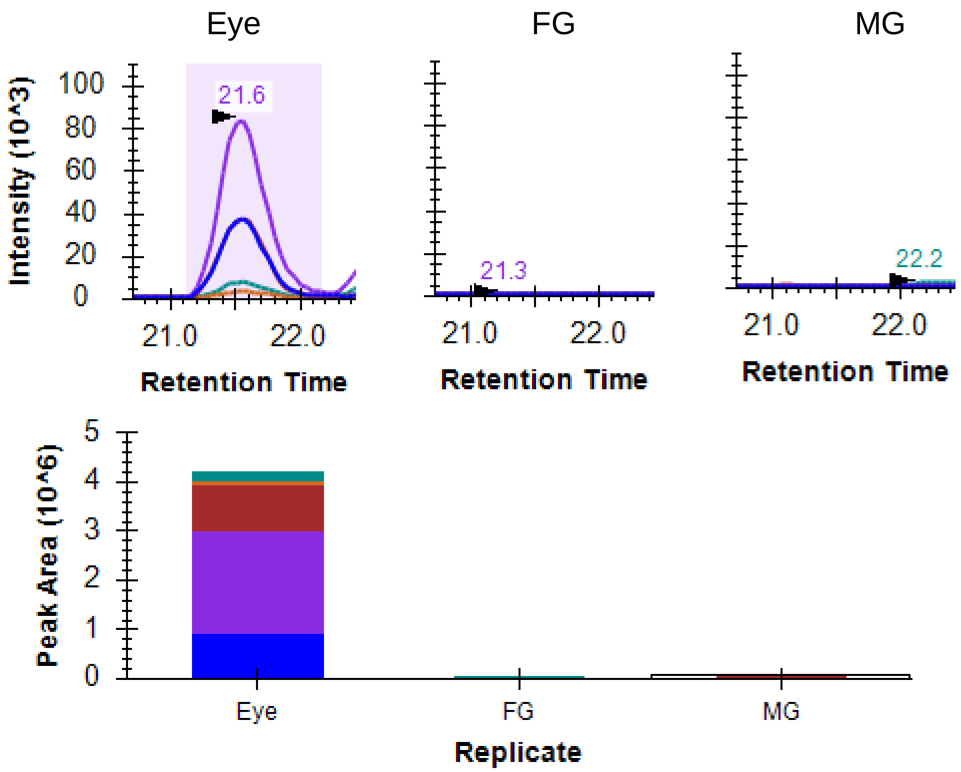


Supplementary Figure S11

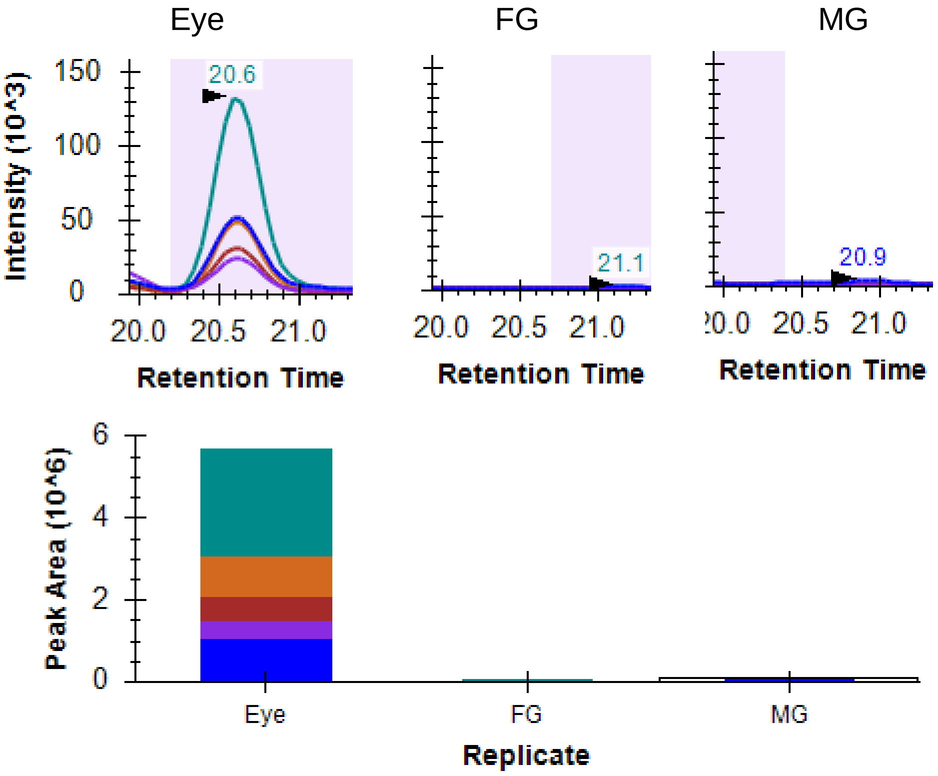
Protein 3 –Cone GNAT2 - High in Eye

RXN12081.1 A0A498LV54

Peptide 1: K.TVNVPDVK.Q [147, 154]



Peptide 2: K.NMLAAPLMNGK.D [173, 183]

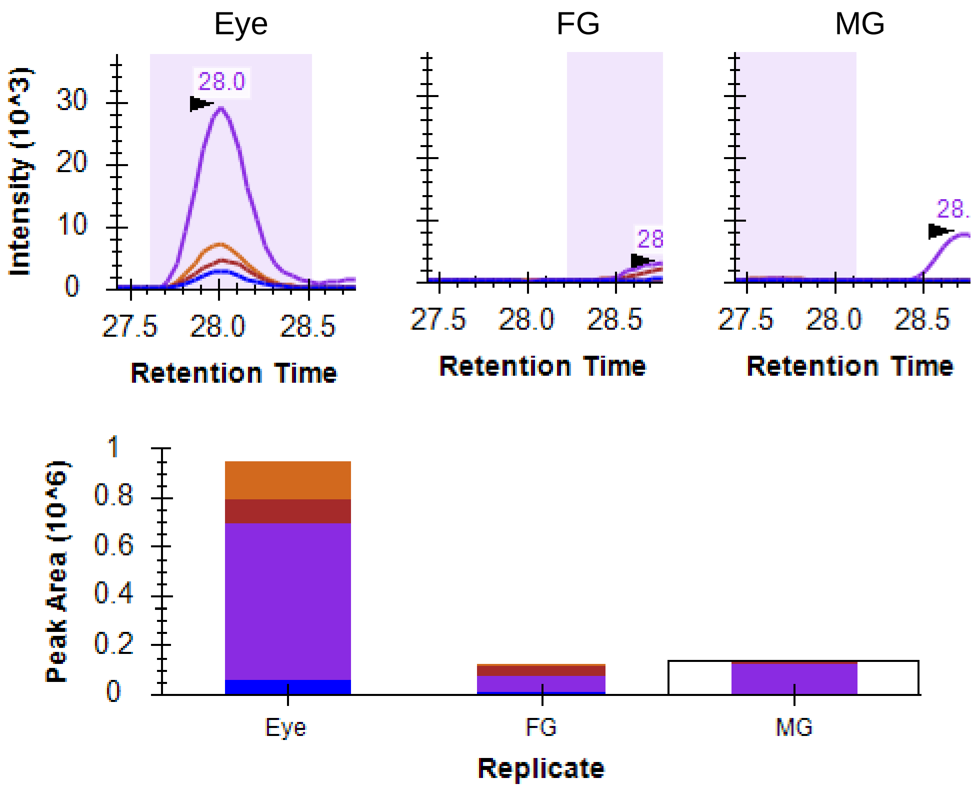


Supplementary Figure S12

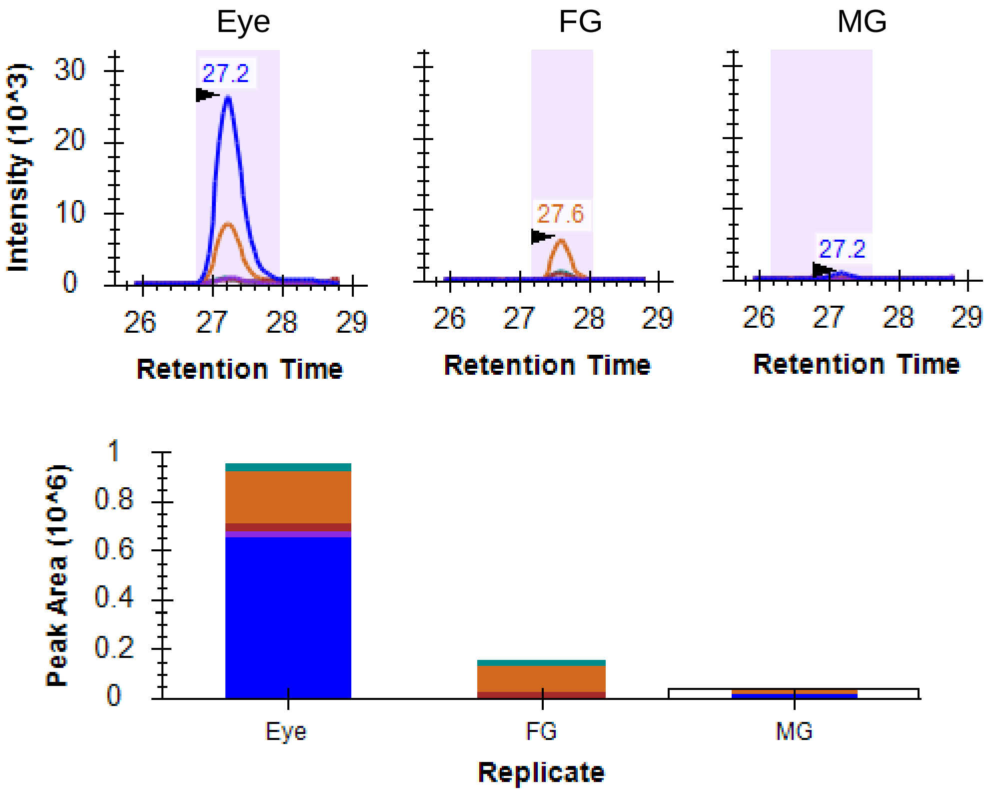
Protein 3 –Cone GNAT2 - High in Eye

RXN12081.1 A0A498LV54

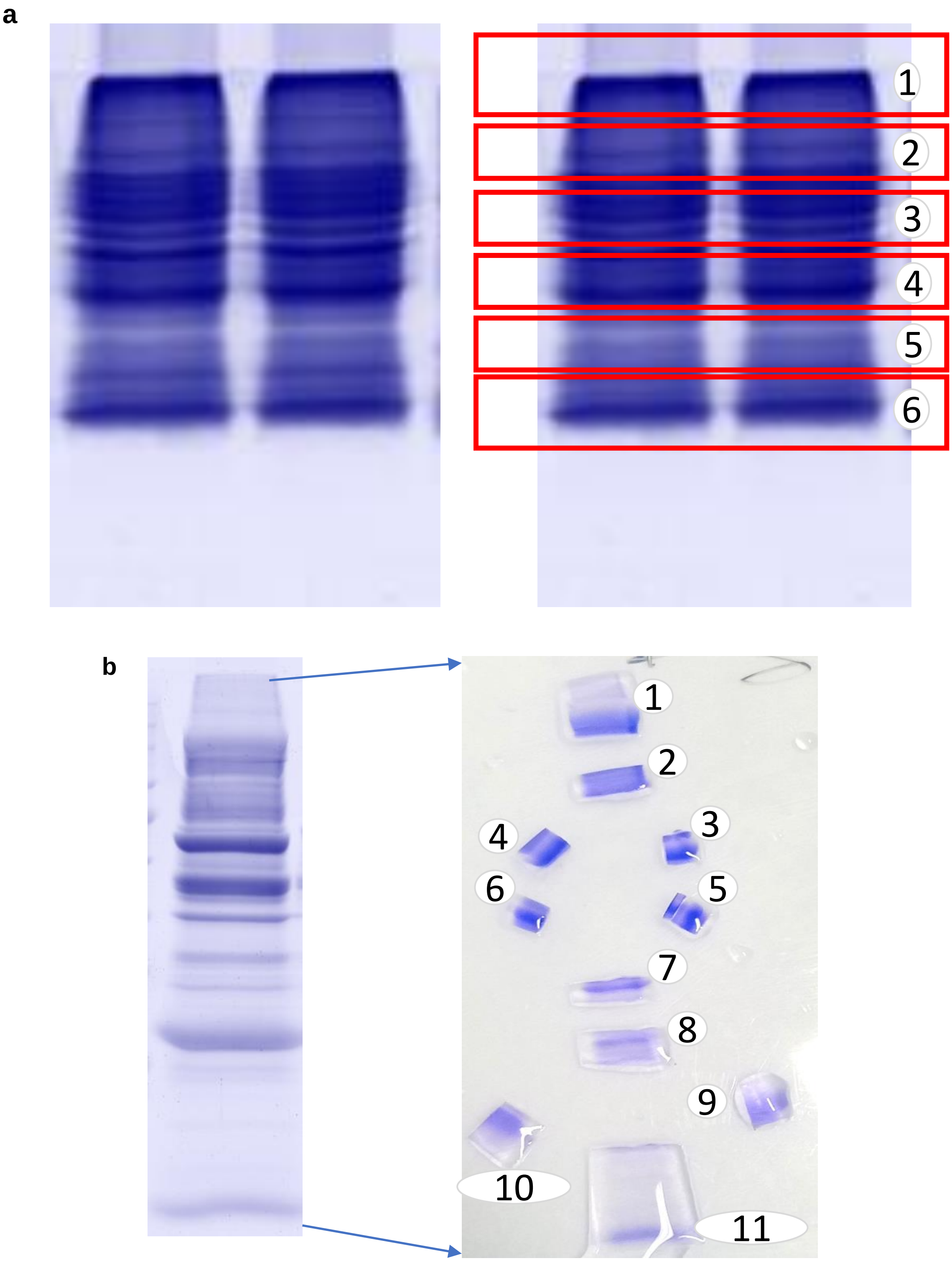
Peptide 3: K.LGDVEPYK.G [293, 300]



Peptide 4: K.EITPMFDGLNNNR.V [791, 803]



Supplementary Figure S13



Supplementary figures legends:

Figure S1| Overall protein profile and protein frequency based on molecular weights **a.** SDS-PAGE profile of all organs showing different band pattern across (GB- gall bladder, FG- female gonad, MG- male gonad, SC- spinal cord, **b.**
Number of proteins identified in fifteen organs where proteins were extracted with pH shift method with respective buffers, **c-d.** Venn diagram showing the fraction of proteome identified using three pHs and frequency distribution of total number of identified proteins based on molecular weights.

Figure S2| An overview of phylogenetically annotated orthologs for the identified proteins, showing distribution of identified proteins mapped against each ortholog group

Figure S3| Heatmap for shared proteome expression across all studied organs; highlighting few proteins with similar expression along with their description and functional details

Figure S4| Heatmap for proteome expression for gonads highlighting few important proteins for male and female gonad

Figure S5| Frequency distribution of identified peptides based on peptide length, where each node represents the experiment (sample).

Figure S6| Representative spectra for phosphorylation, methylation and acetylation

Figure S7-S8| Comparative intensity of individual peptides for ZP2 (Zona-pellucida sperm binding protein 2 like-isoform X2): Upper panel shows peak view for each transition of a peptide and lower bar graph shows the comparative peak area across three organs. Each color represents one transition.

Figure S9-S10| Comparative intensity of individual peptides for TDRD5 (TUDOR domain containing-5 protein): Upper panel shows peak view for each transition of a peptide and lower bar graph shows the comparative peak area across three organs. Each color represents one transition.

Figure S11-S12| Comparative intensity of individual peptides for GNAT2 (cone cGMP-specific 2'-5' cyclic phosphodiesterase subunit alpha): Upper panel shows peak view for each transition of a peptide and lower bar graph shows the comparative peak area across three organs. Each color represents one transition.

Figure S13| **Fractionation of samples for in gel digestion; a. Liver tissue sample, b. Plasma sample**