



Porcine salivary proteome analysis identifies potential early pregnancy-specific protein biomarkers

MONTI DAS¹, ANKAN DE², PARTHASARATHI BEHERA¹, MOHAMMAD AYUB ALI¹, PRASANT KUMAR SUBUDHI¹, GIRIN KALITA¹, ASHULI KHOZHIIO KAYINA¹ and JAGAN MOHANARAO GALI¹✉

Central Agricultural University, Selesih, Aizawl, Mizoram 796 014 India

Received: 21 December 2021; Accepted: 12 January 2023

Supplementary Table 1. List of proteins significantly differentially expressed in all the groups

Protein Ids (Uniprot)	Name of the protein (Uniprot)	Gene name	Name of the Protein (NCBI/ Uniprot)	Sum PEP score	Coverage (%)	No. of peptides	MW (in kDa)	pI	Normalized abundance Non-preg 1	Normalized abundance Non-preg 2	Normalized abundance Non-preg 3	Normalized abundance Preg 1	Normalized abundance Preg 2	Normalized abundance Preg 3	Mean	Std. dev.	Student's T-test q-value PRG_NPR	Abundance Ratio: (PRG) / (NPR)	Abundance Ratio (log2) : (PRG) / (NPR)
Q863D3	Pheromaxin A subunit OS=Sus scrofa GN=PHEROA PE=4 SV=1	PHEROA		158.71	63	17	12.3	8.56	0.787182391	0.815740466	0.839036703	-0.787182391	-1.31449163	-0.814484179	26.63759899	3.982259577	0	0.01	-6.64
F1SQ51	Uncharacterized protein OS=Sus scrofa GN=TP23 PE=4 SV=3	TP23	Basic proline-rich protein precursor	14.86	5	1	46	11.31	0.824843764	0.754269242	0.747278035	-0.798995256	-1.412610412	-0.747278035	21.64188957	5.084026056	0.0144	0.01	-6.64
F1RII5	Uncharacterized protein OS=Sus scrofa GN=LOC100515788 PE=1 SV=2	LOC100515788	GLOBIN domain-containing protein	46.928	48	7	15.6	8.19	0.384214282	0.469230026	0.452087879	-0.384214282	-1.958307981	-0.667254329	23.79660892	3.69104644	0.032346939	0.048	-4.38
P34930	Heat shock 70 kDa protein 1A OS=Sus scrofa GN=HSPA1A PE=1 SV=2	HSPA1A		21.454	9	4	70	5.48	0.787139058	0.793050289	0.791543663	-0.787139058	-1.347221971	-0.830871224	20.37217903	3.924591167	0	0.066	-3.93
A0A287ALY4	Alpha-crystallin B chain OS=Sus scrofa GN=CRYAB PE=1 SV=1	CRYAB		3.273	4	1	25.8	9.86	0.70092088	0.406614929	0.561483026	-0.681580901	-1.843426943	-0.406614929	20.34671402	3.051462837	0.027503448	0.066	-3.93
K7GNR8	Hemoglobin subunit theta 1 OS=Sus scrofa GN=HBQ1 PE=3 SV=2	HBQ1		3.912	6	1	15.6	9.45	0.668121457	0.769802451	0.771980762	-0.668121457	-1.501129627	-0.815651357	20.82741928	2.772192778	0.010285714	0.077	-3.7
F1RGX4	Uncharacterized protein OS=Sus scrofa GN=LOC100737768 PE=1 SV=1	LOC100737768	Hemoglobin subunit alpha	134.158	99	16	15.2	8.7	0.592425287	0.924590707	0.965404749	-0.592425287	-1.443989277	-0.652752042	24.89384365	2.877048633	0.011571429	0.087	-3.52
F1RII7	Hemoglobin subunit beta OS=Sus scrofa GN=HBB PE=3 SV=1	HBB		149.111	96	15	16.2	7.25	0.694442332	0.762525141	0.629848123	-0.629848123	-1.126076818	-1.369247556	26.01972294	1.81025436	0.013935484	0.089	-3.49
A7J150	Long palate lung and nasal epithelium protein 2 OS=Sus scrofa PE=2 SV=1	BPIFB2		7.522	4	2	49.8	7.18	0.810419559	0.640432298	0.787483215	-0.640432298	-1.532298923	-0.744878054	19.32250023	2.982890375	0.012226415	0.089	-3.48
A8U4R4	Transketolase OS=Sus scrofa GN=tkf PE=1 SV=1	tkf		78.255	29	18	67.8	7.49	0.490341812	0.494639307	0.505471289	-0.490341812	-1.932515383	-0.53324008	24.37378883	3.803604924	0.029146067	0.09	-3.47
I3LGY1	Uncharacterized protein OS=Sus scrofa GN=BPIFB2 PE=4 SV=1	BPIFB2	BPI fold-containing family B member 2 precursor	11.344	9	3	49.8	7.18	0.82292366	0.685380518	0.83046937	-0.685380518	-1.440062642	-0.7873016	19.50721645	3.056777266	0.011368421	0.091	-3.45

Supplementary Table 1 (Contd..)

Supplementary Table 1. (Contd..)																			
Protein Ids (Uniprot)	Name of the protein (Uniprot)	Gene name	Name of the Protein (NCBI/ Uniprot)	Sum PEP score	Coverage (%)	No. of peptides	MW (in kDa)	pI	Normalized abundace Non-preg 1	Normalized abundace Non-preg 2	Normalized abundace Non-preg 3	Normalized abundace Preg 1	Normalized abundace Preg 2	Normalized abundace Preg 3	Mean	Std. dev.	Student's T-test q-value PRG_NPR	Abundance Ratio: (PRG) / (NPR)	Abundance Ratio (log2) : (PRG) / (NPR)
F1RS36	78 kDa glucose-regulated protein OS=Sus scrofa GN=HSPA5 PE=1 SV=3	HSPA5		19.898	10	5	68.7	5.17	0.604374766	0.989227414	0.886485517	-1.179871678	-0.604374766	-1.054958582	20.34300423	3.211356203	0.014896552	0.095	-3.4
M3V836	Glutathione S-transferase pi 1 OS=Sus scrofa GN=GSTP1 PE=1 SV=1	GSTP1		25.193	49	5	23.6	7.8	0.766435027	0.67996943	0.83032012	-0.67996943	-1.519812346	-0.698998749	21.08370495	2.930389927	0.01296	0.109	-3.2
A0A287AZ91	Uncharacterized protein OS=Sus scrofa GN=LOC100739163 PE=1 SV=1	LOC100739508	Glutathione S-transferase P-like isoform X3	25.193	47	5	24.6	7.36	0.693457186	0.6152246	0.751259267	-0.6152246	-1.672644973	-0.632441998	21.08370495	3.238777591	0.0081	0.109	-3.2
A0A287AV07	Acetyl-CoA acetyltransferase 2 OS=Sus scrofa GN=ACAT2 PE=1 SV=1	ACAT2		13.058	6	2	46.3	7.66	0.460493267	0.401440948	0.610379279	-0.401440948	-1.968039274	-0.46892941	21.58611012	2.759232437	0.041502439	0.111	-3.18
I3LDF4	Adenosine deaminase OS=Sus scrofa GN=ADA PE=1 SV=2	ADA		240.874	56	27	44	5.48	0.769944012	0.766670287	0.794486284	-0.766670287	-1.394907236	-0.809101164	26.71129704	2.316505835	0.018	0.112	-3.15
F1RYY6	Transaldolase OS=Sus scrofa GN=TALDO1 PE=1 SV=3	TALDO1		10.755	14	4	37.4	6.71	0.481325954	0.630170107	0.498097748	-0.481325954	-1.19251585	-1.571413636	20.65008068	2.961023802	0.008526316	0.112	-3.15
A0A287AFC1	L-lactate dehydrogenase OS=Sus scrofa GN=LDHA PE=1 SV=1	LDHA		6.976	10	3	37.9	8.28	0.405519545	0.65331465	0.490209311	-0.405519545	-1.919898033	-0.563891888	20.66439438	1.624865183	0.029775401	0.115	-3.11
B0F9U1	Alpha 1 S haptoglobin OS=Sus scrofa PE=2 SV=1	HP		11.315	29	4	21	5.87	0.394492328	1.385990024	1.182123899	-0.394492328	-0.80215472	-0.852592528	20.2752943	2.538841686	0.008307692	0.117	-3.1
A0A287ARJ8	Uncharacterized protein OS=Sus scrofa GN=LOC396685 PE=1 SV=1	LOC100156325	SERPIN domain-containing protein	2.959	4	1	46.9	6.54	1.221996069	1.516819835	0.169709146	-0.341453016	-1.015770912	-0.169709146	17.80725098	2.167292038	0.030097297	0.116	-3.1
A0A286ZW70	Peptidyl-prolyl cis-trans isomerase OS=Sus scrofa GN=PPIB PE=1 SV=1	PPIB		4.037	13	2	23.8	9.41	0.928884089	0.90278852	0.796370625	-0.837066829	-1.163208485	-0.796370625	18.46431923	2.687547204	0	0.118	-3.08
F1SDR7	Tyrosine 3-monooxygenase/ tryptophan 5-monooxygenase activation protein beta OS=Sus scrofa GN=YWHAB PE=1 SV=1	YWHAB		45.793	26	9	28.1	4.83	0.818500817	0.690427959	0.849990606	-0.820633054	-1.407392025	-0.690427959	20.55750561	2.807077152	0.0135	0.12	-3.05
F1RYW2	Calmodulin like 5 OS=Sus scrofa GN=CALML5 PE=4 SV=1	CALML5		7.973	17	2	16.6	4.73	0.703668594	0.706689715	0.435112894	-0.435112894	-1.787995815	-0.655640543	20.79200077	2.667418845	0.023541985	0.122	-3.04
F1S8Y5	Phosphoglycerate mutase OS=Sus scrofa GN=PGAM1 PE=1 SV=3	PGAM1		17.415	17	4	29.9	6.89	0.692036808	0.919407189	0.875299335	-0.921922445	-1.257287025	-0.692036808	19.36705875	3.192490599	0	0.123	-3.02
Supplementary Table 1 (Contd..)																			

Supplementary Table 1. (Contd..)																			
Protein Ids (Uniprot)	Name of the protein (Uniprot)	Gene name	Name of the Protein (NCBI/ Uniprot)	Sum PEP score	Coverage (%)	No. of peptides	MW (in kDa)	pI	Normalized abundace Non-preg 1	Normalized abundace Non-preg 2	Normalized abundace Non-preg 3	Normalized abundace Preg 1	Normalized abundace Preg 2	Normalized abundace Preg 3	Mean	Std. dev.	Student's T-test q-value PRG_NPR	Abundance Ratio: (PRG) / (NPR)	Abundance Ratio (log2) : (PRG) / (NPR)
I3L8W7	Uncharacterized protein OS=Sus scrofa GN=ZNF180 PE=4 SV=2	ZNF180	Zinc finger protein 180	1.691	1	1	69.9	7.31	0.84483552	0.79545182	0.648091853	-0.648091853	-1.46578896	-0.815429866	18.94294643	2.208271636	0.010536585	0.124	-3.01
I3LRS5	Aldehyde dehydrogenase 1 family member A1 OS=Sus scrofa GN=ALDH1A1 PE=1 SV=2	ALDH1A1		36.252	19	9	54.8	7.59	0.624035358	0.506654024	0.669463038	-0.546548009	-1.830379128	-0.506654024	22.61598587	3.340275069	0.025392593	0.127	-2.98
I3LLY3	Actinin alpha 1 OS=Sus scrofa GN=ACTN1 PE=1 SV=1	ACTN1		6.161	3	2	102.3	5.63	0.195264608	0.298514992	0.296149045	-1.197568536	-1.820098162	-0.195264608	21.6304369	3.237566368	0.04191133	0.128	-2.97
F1SBS4	Complement C3 OS=Sus scrofa GN=C3 PE=1 SV=3	C3		4.114	1	1	186.9	6.54	0.858450055	0.96650815	0.824260354	-0.824260354	-1.025228143	-0.958656669	19.22637177	1.92956926	0	0.128	-2.96
F1S505	BPI fold-containing family A member 1 OS=Sus scrofa GN=BPIFA1 PE=4 SV=2	BPIFA1		9.86	29	3	24.9	4.75	0.680449069	0.569924653	0.983797967	-0.569924653	-1.601000786	-0.596907735	21.24507523	1.982341863	0.008	0.132	-2.93
A0A287AX20	Cholinesterase OS=Sus scrofa GN=BCHE PE=1 SV=1	BCHE		2.127	2	1	51.7	9.61	0.694936454	0.613295078	0.714841902	-0.993075073	-1.505856752	-0.613295078	17.97227669	2.706830151	0.0096	0.134	-2.9
F1RPH0	Phosphoglycerate kinase OS=Sus scrofa GN=PGK1 PE=1 SV=3	PGK1		13.632	7	2	44.5	7.9	0.573801517	0.670003653	0.68417269	-0.573801517	-1.730795503	-0.65486908	19.95798874	2.627264448	0.019058824	0.137	-2.87
A0A287B8F3	Fructose-bisphosphate aldolase OS=Sus scrofa GN=ALDOA PE=1 SV=1	ALDOA		11.466	13	3	45	8.09	0.195034519	0.945173085	0.974356532	-0.195034519	-1.743354917	-0.204728648	20.02375031	2.510174115	0.049235521	0.14	-2.83
Q27HS3	Vascular smooth muscle alpha-actin OS=Sus scrofa PE=2 SV=1	ACTA2		9.126	29	2	7.9	8.19	0.792091727	0.881581604	0.636415124	-0.636415124	-1.517960548	-0.69365114	24.1398325	2.134787567	0.012	0.148	-2.75
A0A286ZRV2	Triosephosphate isomerase OS=Sus scrofa GN=TPI1 PE=1 SV=1	TPI1		32.394	21	8	34.3	6.99	0.516932309	0.899082601	0.892846763	-0.527264953	-1.606869221	-0.516932309	21.26140022	3.529448263	0.018202247	0.151	-2.73
I3LDM6	Keratin 3 OS=Sus scrofa GN=KRT3 PE=1 SV=2	KRT3		3.105	2	1	64.8	7.94	0.427765131	0.984579444	0.906216621	-0.427765131	-1.335681796	-1.029253602	17.76175308	1.760388173	0.009126761	0.153	-2.71
F1S501	Uncharacterized protein OS=Sus scrofa PE=1 SV=2	LOC102162701	vomeromodulin-like isoform X1	42.299	21	7	49.6	6.33	0.486174136	0.498084337	0.488971531	-0.486174136	-1.940051317	-0.525632024	23.55327988	3.017117588	0.03026087	0.164	-2.61
A0A287AJE3	Uncharacterized protein OS=Sus scrofa GN=LOC106504547 PE=1 SV=1	LOC106504547	SERPIN domain-containing protein	5.072	2	2	43.6	7.96	0.597189963	0.722024143	0.583927214	-0.583927214	-1.753681064	-0.603909075	23.24183655	2.522466202	0.027574468	0.166	-2.59
F1RFY1	Profilin OS=Sus scrofa GN=PFN1 PE=1 SV=1	PFN1		6.13	14	2	15	8.28	0.876227319	0.767481446	1.127189875	-0.819900751	-1.054218173	-0.767481446	19.8747797	2.121508779	0	0.17	-2.55
F1RN76	Uncharacterized protein OS=Sus scrofa GN=CD5L PE=1 SV=3	CD5L	CD5 antigen-like precursor	3.642	6	2	59.5	5.25	0.487992108	0.52830565	0.518350303	-0.487992108	-1.828825355	-0.794563711	19.93964291	2.430128559	0.022666667	0.178	-2.49

Supplementary Table 1. (Contd..)																			
Protein Ids (Uniprot)	Name of the protein (Uniprot)	Gene name	Name of the Protein (NCBI/ Uniprot)	Sum PEP score	Coverage (%)	No. of peptides	MW (in kDa)	pI	Normalized abundace Non-preg 1	Normalized abundace Non-preg 2	Normalized abundace Non-preg 3	Normalized abundace Preg 1	Normalized abundace Preg 2	Normalized abundace Preg 3	Mean	Std. dev.	Student's T-test q-value PRG_NPR	Abundance Ratio: (PRG) / (NPR)	Abundance Ratio (log2) : (PRG) / (NPR)
Q9GMA6	Alpha-1-antichymotrypsin 2 OS=Sus scrofa GN=SERPINA3-2 PE=3 SV=1	SERPINA3-2		10.007	6	3	46.6	6.76	0.608649731	0.822433531	0.879000485	-0.646921575	-1.546462059	-0.608649731	18.58631039	2.132118472	0.009391304	0.18	-2.47
Q19KE2	Fatty acid binding protein 5 OS=Sus scrofa GN=FABP5 PE=2 SV=1	FABP5		58.561	56	8	13.9	6.14	0.459216684	0.497524023	0.765167117	-0.841183662	-1.74288249	-0.459216684	23.73931313	1.294657257	0.026181818	0.184	-2.45
F1S395	Uncharacterized protein OS=Sus scrofa GN=NQO1 PE=1 SV=1	NQO1	NAD(P)H dehydrogenase quinone 1	10.724	8	3	30.9	8.9	0.411788762	0.536980391	0.5797351	-0.430066168	-1.962514281	-0.411788762	21.44727802	3.113345167	0.041705882	0.183	-2.45
F1SKB1	Uncharacterized protein OS=Sus scrofa GN=CP PE=1 SV=4	CP	Ceruloplasmin isoform X1	7.564	3	2	123.8	6.3	0.547582388	0.516149044	0.588526666	-0.582854629	-1.86581099	-0.516149044	19.68940353	2.122554319	0.02656338	0.183	-2.45
I3VKE6	Ceruloplasmin OS=Sus scrofa PE=2 SV=1			7.564	3	2	125.5	6.07	0.589366496	0.555534542	0.633435071	-0.627330244	-1.800174117	-0.555534542	19.68940353	1.97207242	0.02445283	0.183	-2.45
A0A287AAT5	Uncharacterized protein OS=Sus scrofa PE=3 SV=1	LOC110261637	SERPIN domain-containing protein	11.323	12	3	33.1	6.38	0.790518701	0.373589009	0.941652298	-0.648743629	-1.669839859	-0.373589009	20.45533276	2.064186102	0.021922481	0.19	-2.4
F1RWT2	Plastin 3 OS=Sus scrofa GN=PLS3 PE=1 SV=3	PLS3		7.13	5	2	63.8	6.05	0.278681219	0.349451959	0.375731021	-0.66687566	-2.033878088	-0.278681219	20.98136902	3.206101583	0.049120623	0.193	-2.38
F1SMW3	Serpin family B member 5 OS=Sus scrofa GN=SERPINB5 PE=3 SV=1	SERPINB5		4.403	7	2	42.1	6.32	0.59811306	0.547700226	0.729902864	-0.987919092	-1.591718316	-0.547700226	19.63586235	2.412939522	0.009671642	0.197	-2.35
F1ST01	Selenium binding protein 1 OS=Sus scrofa GN=SELENBP1 PE=1 SV=2	SELENBP1		5.338	6	2	56	7.01	0.613876998	0.592398763	0.775272012	-1.143491149	-1.418683767	-0.592398763	19.03683186	2.486862366	0.011076923	0.198	-2.34
F1SCF0	Alpha-1-antitrypsin OS=Sus scrofa GN=SERPINA1 PE=3 SV=2	SERPINA1		13.119	14	4	46.9	5.85	0.411125273	0.369517863	0.424127072	-0.369517863	-2.002728939	-0.605873346	20.62952614	2.450460557	0.046433962	0.2	-2.32
A0A2C9F366	Heat shock protein beta-1 OS=Sus scrofa GN=HSPB1 PE=1 SV=1	HSPB1		31.574	25	5	25.5	9.07	0.702213287	0.820696771	1.170158863	-0.759531081	-1.180716157	-0.702213287	22.31030655	1.962926726	0.01728	0.21	-2.25
F1RII6	Hemoglobin subunit epsilon OS=Sus scrofa GN=HBE1 PE=3 SV=1	HBE1		3.612	7	1	16.1	8.19	0.341093659	0.389766812	0.270457566	-0.270457566	-2.044351339	-0.637236238	23.19966316	3.248396373	0.049819549	0.21	-2.25
A0A286ZIB9	Uncharacterized protein OS=Sus scrofa PE=4 SV=1	IgC_CH1	Immunoglobulin gamma chain 5a	1.626	6	1	12.3	5.25	0.620375156	0.523505092	0.601410687	-0.523505092	-1.802685738	-0.675017774	21.56620216	2.20661154	0.02253913	0.212	-2.24
F1SLW8	Uncharacterized protein OS=Sus scrofa GN=A2ML1 PE=4 SV=3	A2ML1	Alpha-2-macroglobulin-like protein 1	58.357	20	16	100.4	6.09	0.610680938	0.600387335	0.615252495	-0.600387335	-1.74595046	-0.692286253	25.25236034	1.714351441	0.007714286	0.222	-2.17
F1SGG3	Keratin 1 OS=Sus scrofa GN=KRT1 PE=1 SV=2	KRT1		6.639	3	2	64.8	8.15	0.32369256	0.454160392	0.374949843	-0.532082736	-2.039726734	-0.32369256	21.07324505	2.76133791	0.048930233	0.225	-2.15

Supplementary Table 1. (Contd..)																			
Protein Ids (Uniprot)	Name of the protein (Uniprot)	Gene name	Name of the Protein (NCBI/ Uniprot)	Sum PEP score	Coverage (%)	No. of peptides	MW (in kDa)	pI	Normalized abundace Non-preg 1	Normalized abundace Non-preg 2	Normalized abundace Non-preg 3	Normalized abundace Preg 1	Normalized abundace Preg 2	Normalized abundace Preg 3	Mean	Std. dev.	Student's T-test q-value PRG_NPR	Abundance Ratio: (PRG) / (NPR)	Abundance Ratio (log2) : (PRG) / (NPR)
F1S145	Calmodulin 2 OS=Sus scrofa GN=CALM2 PE=4 SV=2	CALM2	Cytosolic non-specific dipeptidase isoform X1	16.543	21	4	22.4	4.74	0.309940606	0.268909991	0.319073737	-1.668028474	-1.369373918	-0.268909991	21.86620712	1.002005326	0.0275	0.239	-2.06
F1SNL7	Uncharacterized protein OS=Sus scrofa GN=CNDP2 PE=1 SV=1	CNDP2		2.152	2	1	52.7	5.48	0.279059172	1.150002837	1.083782434	-0.334659308	-1.495046616	-0.279059172	18.5917244	1.964220864	0.028700565	0.254	-1.98
F1SN92	Salivary lipocalin OS=Sus scrofa GN=SAL1 PE=3 SV=1	SAL1		266.309	91	31	21.6	5.3	0.705488205	0.766848385	0.69653827	-0.744309604	-1.545930743	-0.69653827	30.19456673	1.192368341	0.013787234	0.256	-1.97
A0A287AS29	Nucleoside diphosphate kinase OS=Sus scrofa GN=NME1 PE=1 SV=1	NME1		6.286	16	3	17.1	6.19	0.622000575	0.715360701	0.370750397	-0.370750397	-1.905421019	-0.442530572	20.95623207	2.434746608	0.035658291	0.266	-1.91
F1SLX2	Alpha-2-macroglobulin OS=Sus scrofa GN=A2M PE=1 SV=3	A2M		109.711	20	27	166.9	6.29	0.482357115	0.529631793	0.676449001	-0.482357115	-1.882659435	-0.502158999	25.55788708	1.560022851	0.027905325	0.278	-1.85
A0A287B0H6	Uncharacterized protein OS=Sus scrofa GN=ACTG2 PE=1 SV=1	ACTG2		54.76	27	10	36	6.23	0.655623078	0.728139102	0.514335513	-0.514335513	-1.735527277	-0.706282437	24.96240425	2.083917339	0.023478261	0.281	-1.83
I3LBA6	Transglutaminase 3 OS=Sus scrofa GN=TGM3 PE=4 SV=2	TGM3		8.225	5	2	84.1	8.29	0.816331685	0.792733252	0.842795849	-0.792733252	-1.17919898	-0.987894475	19.44262886	1.366429173	0	0.287	-1.8
F1SJB5	Annexin OS=Sus scrofa GN=ANXA1 PE=1 SV=3	ANXA1		33.616	31	8	38.7	6.81	0.70595485	0.636055589	0.390582353	-0.578962028	-1.859235048	-0.390582353	22.46151829	1.414536739	0.028327485	0.289	-1.79
A0A287AAR4	Actin, cytoplasmic 1 OS=Sus scrofa GN=ACTB PE=1 SV=1	ACTB		79.842	38	15	40	5.48	0.590269327	0.60295701	0.522895515	-0.544067562	-1.85611856	-0.522895515	25.49294949	2.234361955	0.026751773	0.299	-1.74
A0A287BF33	Actin, alpha skeletal muscle OS=Sus scrofa GN=ACTA1 PE=1 SV=1	ACTA1		60.525	30	11	38	5.19	0.628137171	0.724523544	0.497235358	-0.497235358	-1.774438143	-0.661356688	25.09088993	2.11062927	0.023142857	0.299	-1.74
C3S7K5	Protein S100 OS=Sus scrofa GN=S100A8 PE=1 SV=1	S100A8		43.253	66	9	10.4	5.11	0.323846519	0.743695199	0.971102774	-0.323846519	-1.760510683	-0.441277355	25.34241581	1.475906712	0.029935484	0.303	-1.72
Q9GLW8	Peroxiredoxin 5 OS=Sus scrofa GN=PRDX5 PE=2 SV=1	PRDX5		7.707	18	1	17.3	6	0.695584595	0.678803384	0.427455097	-1.440081358	-1.271266341	-0.427455097	19.64879227	1.917325457	0.008756757	0.303	-1.72
D0G784	Phosphoglycerate kinase OS=Sus scrofa GN=PGK1 PE=2 SV=1	PGK1		4.84	5	1	35.4	8.82	0.50396508	0.859227657	0.502794623	-0.502794623	-1.779748797	-0.578477561	18.96353245	1.996237365	0.024333333	0.303	-1.72
F2Z5E2	Uncharacterized protein OS=Sus scrofa GN=SERPINC1 PE=1 SV=1	SERPINC1		4.622	3	1	52.4	6.58	0.74147588	0.470387161	0.176717862	-0.735992193	-1.903892517	-0.176717862	19.33136082	1.349552912	0.046978355	0.306	-1.71
Q9GMA7	Alpha-1- antichymotrypsin 1 OS=Sus scrofa GN=SERPINA3-1 PE=2 SV=1	SERPINA3-1		13.681	11	4	24.7	5.34	0.279014051	0.744297981	0.723819375	-0.311198592	-1.915610552	-0.279014051	24.16640759	2.44637273	0.05092562	0.307	-1.7

Supplementary Table 1. (Contd..)																			
Protein Ids (Uniprot)	Name of the protein (Uniprot)	Gene name	Name of the Protein (NCBI/ Uniprot)	Sum PEP score	Coverage (%)	No. of peptides	MW (in kDa)	pI	Normalized abundace Non-preg 1	Normalized abundace Non-preg 2	Normalized abundace Non-preg 3	Normalized abundace Preg 1	Normalized abundace Preg 2	Normalized abundace Preg 3	Mean	Std. dev.	Student's T-test q-value PRG_NPR	Abundance Ratio: (PRG)/ (NPR)	Abundance Ratio (log2) : (PRG)/ (NPR)
G9F6X8	Protein disulfide- isomerase OS=Sus scrofa GN=P4HB PE=2 SV=1	P4HB		84.585	28	17	56.4	4.89	0.57428056	0.54290849	0.724346459	-0.594891548	-1.789449334	-0.54290849	24.46286201	1.701726124	0.023448276	0.315	-1.66
F1SIH8	Transitional endoplasmic reticulum ATPase OS=Sus scrofa GN=VCP PE=1 SV=3	VCP		3.15	2	1	90.9	5.62	0.345280141	0.494687974	1.095412135	-1.676885486	-0.710615396	-0.345280141	18.57238579	0.95095613	0.028675676	0.322	-1.64
A0A286ZX29	Serpin family B member 12 OS=Sus scrofa GN=SERPINB12 PE=3 SV=1	SERPINB12		40.016	21	8	46.2	5.3	0.678968012	0.618110657	0.569952488	-0.569952488	-1.583442688	-0.999979615	22.52350235	1.631407638	0.011172414	0.332	-1.59
G9F6X7	Tyrosine 3-monooxygenase tryptophan 5-monooxygenase activation protein OS=Sus scrofa PE=2 SV=1	YWHAZ		146.327	64	28	27.7	4.79	0.482211083	0.48313117	0.634752631	-0.482211083	-1.88535285	-0.586568594	26.6369381	1.446976673	0.027496855	0.357	-1.49
F1SH33	Serpin family I member 1 OS=Sus scrofa GN=SERPINI1 PE=3 SV=1	SERPINI1		1.969	2	1	46.4	4.91	0.55022186	0.49996385	0.669882774	-0.5979563	-1.841475964	-0.49996385	18.32462788	1.579679229	0.02558209	0.385	-1.38
I3LQ17	Uncharacterized protein OS=Sus scrofa PE=1 SV=2	PZP		7.561	1	1	150.4	7.8	0.548908174	0.796439886	1.310877085	-0.548908174	-1.246447325	-0.700752079	20.1568737	1.506081004	0.010451613	0.388	-1.37
F1RXC2	Carbonic anhydrase 2 OS=Sus scrofa GN=CA2 PE=1 SV=2	CA2		3.359	4	1	29.2	7.01	0.401209891	0.76001519	0.785217106	-0.401209891	-1.799764872	-0.494690657	19.31221771	1.613785407	0.026987654	0.388	-1.37
I3LL32	Uncharacterized protein OS=Sus scrofa GN=CHIA PE=3 SV=2	CHIA	Chitinase	40.09	15	7	52.1	5.08	0.517093718	0.502871573	0.492610931	-0.514212787	-1.931317806	-0.492610931	24.38816261	2.247036059	0.029675978	0.393	-1.35
A0A2C9F356	Haptoglobin OS=Sus scrofa GN=HP PE=1 SV=1	HP		28.021	24	8	38.4	6.79	0.314668894	0.721414983	0.652918398	-0.314668894	-1.919447184	-0.413457841	24.01771069	1.432698685	0.046288372	0.401	-1.32
A0A287A134	Aspartic peptidase retroviral like 1 OS=Sus scrofa GN=ASPRV1 PE=4 SV=1	ASPRV1		4.778	6	1	28.8	5.66	1.201883316	0.464225262	1.207377553	-1.042562723	-0.761425376	-0.464225262	16.84657192	1.167127418	0.011368421	0.42	-1.25
A0A288CFV5	Serotransferrin OS=Sus scrofa GN=TF PE=3 SV=1	TF		193.372	46	33	78.8	7.36	0.301676273	0.438498676	0.478425354	-0.301676273	-2.021509647	-0.55705452	26.71899509	1.121861456	0.049512605	0.445	-1.17
Q06DE7	Squamous epithelial induced stress protein 53 OS=Sus scrofa PE=4 SV=1	CRNN		47.026	19	8	64.3	5.47	0.494954646	0.323150486	0.58820045	-0.526700795	-1.980599403	-0.323150486	24.04948235	1.057731362	0.045557522	0.448	-1.16
C6YXH2	Cellular retinoic acid binding protein 2 OS=Sus scrofa PE=2 SV=1	CRABP2		16.513	36	6	15.7	5.22	0.503631651	1.173634887	1.212533236	-1.05304265	-0.503631651	-0.732226491	21.23284626	0.849173147	0.0135	0.488	-1.04
A0A287B0P6	Calreticulin OS=Sus scrofa GN=CALR PE=1 SV=1	CALR		4.366	2	1	42.6	4.48	0.859645009	0.49323529	0.472026259	-0.472026259	-1.761109829	-0.686005771	19.78586769	1.3264831	0.021935484	0.508	-0.98

Supplementary Table 1. (Contd..)																			
Protein Ids (Uniprot)	Name of the protein (Uniprot)	Gene name	Name of the Protein (NCBI/ Uniprot)	Sum PEP score	Coverage (%)	No. of peptides	MW (in kDa)	pI	Normalized abundace Non-preg 1	Normalized abundace Non-preg 2	Normalized abundace Non-preg 3	Normalized abundace Preg 1	Normalized abundace Preg 2	Normalized abundace Preg 3	Mean	Std. dev.	Student's T-test q-value PRG_NPR	Abundance Ratio: (PRG) / (NPR)	Abundance Ratio (log2) : (PRG) / (NPR)
F1RUN2	Serum albumin OS=Sus scrofa GN=ALB PE=1 SV=1	ALB		693.958	81	84	69.6	6.38	0.387970746	0.601484776	0.728562355	-0.387970746	-1.880045533	-0.521343529	30.70944309	1.29404432	0.030593407	0.555	-0.85
F1S574	Alpha-amylase OS=Sus scrofa GN=AMY2 PE=3 SV=3	AMY2		28.38	18	7	57.1	6.77	0.344483823	0.376579732	0.70744741	-0.558038414	-1.951655865	-0.344483823	23.71911049	1.11335697	0.042666667	0.627	-0.67
F1RK90	Periplakin OS=Sus scrofa GN=PPL PE=1 SV=3	PPL		1.846	1	1	203.6	5.55	0.28543213	0.124067634	0.140988007	-0.124067634	-1.329020977	-1.761127114	21.09364128	1.843277723	0.047830508	0.631	-0.66
F6Q109	Glutamine synthetase OS=Sus scrofa GN=GLUL PE=3 SV=1	GLUL		2.783	3	1	42.9	6.74	0.318518698	0.664147615	0.57101512	-0.318518698	-1.833138347	-0.818257272	20.412817	1.057441448	0.026179641	0.648	-0.63
F1RSB4	Eosinophil peroxidase OS=Sus scrofa GN=EPX PE=1 SV=3	EPX		1.956	3	1	80	10.05	0.797058165	0.538880348	0.596133411	-1.661362171	-0.817566395	-0.538880348	19.5478735	1.167668009	0.008202532	0.648	-0.63
A0A287BBZ0	Carboxylic ester hydrolase OS=Sus scrofa GN=CES1 PE=1 SV=1	CES1		3.609	6	1	61.8	6.15	0.237738967	0.109442018	0.369620293	-1.489982009	-1.600893378	-0.109442018	19.07789803	1.533065977	0.046074074	0.656	-0.61
Q866S8	von Ebner gland protein OS=Sus scrofa PE=2 SV=1	OBP2B		116.684	63	12	19.4	5.1	0.275686622	0.487937897	0.567624807	-0.275686622	-2.015735388	-0.473838419	29.21498489	0.997943908	0.049876923	0.686	-0.54
A0A287B057	Lipocalin-1 OS=Sus scrofa GN=LCN1 PE=3 SV=1	LCN1		116.684	63	12	19.2	4.78	0.275686622	0.487937897	0.567624807	-0.275686622	-2.015735388	-0.473838419	29.21498489	0.997943908	0.049685824	0.686	-0.54
Q95KQ9	Cystatin B OS=Sus scrofa GN=cstb PE=4 SV=1	cstb		10.824	48	1	2.9	4.72	0.420649081	0.473251373	0.648526788	-0.420649081	-1.845492244	-0.771824539	24.25735378	0.94054282	0.027333333	0.705	-0.5
A5H1Q0	Desmoglein 1 OS=Sus scrofa PE=2 SV=1	DSG1		11.776	5	3	91.5	4.65	0.35368818	0.593801856	0.714678586	-0.35368818	-1.858977437	-0.656236112	22.56869984	1.087508152	0.029364162	0.799	-0.32
Q8WMH1	Odorant binding protein OS=Sus scrofa GN=OBP PE=2 SV=1	OBP		115.144	69	15	19.4	4.39	0.364538699	0.426882982	0.579162478	-0.364538699	-1.980904579	-0.540908158	29.850667	0.739268943	0.042369668	0.861	-0.22
A0A287B6S5	Uncharacterized protein OS=Sus scrofa GN=ENO1 PE=1 SV=1	ENO1	2-phospho-D- glycerate hydro- lyase	111.521	44	17	47.4	6.57	0.265760303	0.329509616	0.440137029	-0.265760303	-2.020345926	-0.68894738	26.10251427	1.139125693	0.050302041	0.9	-0.15
A0A286ZK96	Histone H2B OS=Sus scrofa PE=3 SV=1	LOC100512420		13.624	23	4	12.6	10.48	0.13883093	0.822896481	1.172118425	-0.13883093	-1.659892917	-0.393938094	24.43494129	1.626868247	0.047574468	1.017	0.02
Q6H319	Glandular kallikrein OS=Sus scrofa GN=KLK1 PE=2 SV=1	KLK1		12.887	10	2	28.9	5.17	0.525099397	0.374487609	0.749932528	-0.374487609	-1.867684364	-0.627012908	23.27528572	1.394687249	0.029195402	1.436	0.52
A0A287AHM5	Uncharacterized protein OS=Sus scrofa GN=LOC100737030 PE=1 SV=1	LOC100737030	IF rod domain- containing protein	6.175	4	3	50	5.16	-1.626119137	-0.690564871	-0.439542502	1.114512086	0.50032407	0.439542502	18.41472054	1.08409811	0.022479339	1.547	0.63
A0A287BN15	Keratin 14 OS=Sus scrofa GN=KRT14 PE=1 SV=1	KRT14		6.175	4	3	47	5	-0.786812901	-0.941724896	-0.59940511	1.519862771	0.682293057	0.59940511	18.41472054	0.794966841	0.009818182	1.547	0.63
A0A287A7G8	Histone H2B OS=Sus scrofa GN=HIST1H2BJ PE=3 SV=1	HIST1H2BJ		19.941	38	6	16.7	10.39	0.136813164	0.844837666	1.203763843	-0.136813164	-1.640672088	-0.328574866	24.47705269	1.556291411	0.050508197	1.625	0.7
F2Z5G3	Uncharacterized protein OS=Sus scrofa GN=CALM3 PE=1 SV=1	CALM3	Calmodulin	18.533	42	5	16.8	4.22	0.181777835	0.134607002	0.239494532	-1.43955934	-1.673627734	-0.134607002	22.0183363	0.871574682	0.047806167	1.647	0.72

Supplementary Table 1. (Concluded)																			
Protein Ids (Uniprot)	Name of the protein (Uniprot)	Gene name	Name of the Protein (NCBI/ Uniprot)	Sum PEP score	Coverage (%)	No. of peptides	MW (in kDa)	pI	Normalized abundace Non-preg 1	Normalized abundace Non-preg 2	Normalized abundace Non-preg 3	Normalized abundace Preg 1	Normalized abundace Preg 2	Normalized abundace Preg 3	Mean	Std. dev.	Student's T-test q-value PRG_NPR	Abundance Ratio: (PRG) / (NPR)	Abundance Ratio (log2) : (PRG) / (NPR)
D9D839	Superoxide dismutase [Cu-Zn] OS=Sus scrofa GN=SOD1 PE=2 SV=1	SOD1	Immunoglobulin heavy chain variable region	15.668	42	2	15.9	6.52	-0.717498899	-0.702569544	-0.882116437	1.418441176	0.841357648	0.702569544	21.85857868	0.743682365	0.013090909	1.69	0.76
A0A286ZV80	Uncharacterized protein OS=Sus scrofa PE=4 SV=1	VHB		14.149	27	2	12.6	5.38	0.798255563	0.182669953	0.674806714	-0.182669953	-1.897052407	-0.491812706	26.45914936	0.815246376	0.049894737	2.838	1.5
F1RFS9	Coiled-coil domain containing 113 OS=Sus scrofa GN=CCDC113 PE=4 SV=3	CCDC113		2.173	6	1	39.4	9.58	-0.264109075	-0.438434333	-0.265889108	1.60679388	0.264109075	1.419783235	26.18738842	0.507907093	0.028575163	2.941	1.56
Q8WMM2	Involucrin OS=Sus scrofa GN=IVL PE=4 SV=1	IVL		9.302	7	2	40.4	4.53	-0.223598495	-0.96198976	-0.63477242	1.538052917	0.223598495	1.098198771	21.22043133	0.935379108	0.026147059	4.796	2.26
A0A286ZTC4	Uncharacterized protein OS=Sus scrofa PE=4 SV=1			18.227	35	2	10.9	5.94	-0.276167393	-0.908836603	-0.043370131	1.499374747	0.043370131	1.358624697	24.20113277	1.136819393	0.047982833	4.942	2.3
A0A287AP10	Uncharacterized protein OS=Sus scrofa PE=4 SV=1	LOC100125542		19.242	29	3	15.5	8.29	0.798174024	0.169148669	0.675409317	-0.169148669	-1.908259988	-0.456137657	26.48158836	0.791699699	0.049469697	6.529	2.71
Q0Z8R0	Cystatin OS=Sus scrofa GN=CST3 PE=1 SV=1	CST3		168.699	75	14	15.7	8.73	-0.611332059	-0.62026608	-0.484341681	1.475655079	0.484341681	1.26285851	26.80117512	0.869982097	0.009529412	7.052	2.82
F1SVB0	Capping actin protein, gelsolin like OS=Sus scrofa GN=CAPG PE=1 SV=1	CAPG		16.105	11	4	38.9	6.27	-0.673369408	-0.546217263	-0.835912287	1.330772519	0.546217263	1.216619253	19.94290829	2.307799779	0.010046512	9.423	3.24
F2Z5J1	Uncharacterized protein OS=Sus scrofa GN=PSMC1 PE=1 SV=1	PSMC1	26S protease regulatory subunit 4	1.433	3	1	49.2	6.21	-0.64331001	-1.258756638	-0.557511032	0.83579725	0.557511032	1.296722651	20.97354317	1.40823176	0.010125	9.925	3.31
A5J2A8	Thioredoxin OS=Sus scrofa GN=TRX PE=4 SV=1	TRX		13.416	47	2	4.9	8	-1.599668503	-0.201452106	-0.453674555	1.042965531	0.201452106	1.032616615	20.93954086	1.6051006	0.032730964	16.097	4.01
I3L728	Uncharacterized protein OS=Sus scrofa PE=4 SV=2	IgV_L_kappa	immunoglobulin kappa variable region	28.255	39	6	15	6.01	-0.711031318	-0.639718294	-0.792140305	1.24034667	0.639718294	1.228824258	22.08922863	2.6448999	0.016615385	19.049	4.25
A0A2C9F3B6	Beta- microseminoprotein OS=Sus scrofa GN=MSMB PE=3 SV=1	MSMB		5.888	11	2	13.5	7.2	-0.429329634	-0.351588666	-0.351769775	1.478491902	0.351588666	1.502919316	19.2446413	2.138048874	0.022736842	21.258	4.41
F1RR02	Uncharacterized protein OS=Sus scrofa GN=GFAP PE=1 SV=3	GFAP	Glial fibrillary acidic protein	14.563	8	3	53.6	5.85	-0.496652216	-0.887467027	-0.33545965	1.776880383	0.76378566	0.33545965	18.5241251	4.303470488	0.027847134	100	6.64
C6L245	Putative trypsinogen OS=Sus scrofa GN=try PE=1 SV=1	try		5.949	17	1	26.2	4.83	-1.945767403	-0.90188992	-0.299485207	0.299485207	0.312088817	0.351854384	26.29301357	4.410316657	0.04028	100	6.64