

Table S3: Results from the gene ontology enrichment analysis for adult anoxia tolerance.

Annotation Cluster 1	Enrichment Score: 2.4975622754832516	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Category	Term									
INTERPRO	IPR007110:Immunoglobulin-like domain	8	6.722689076	1.08E-04	CG13506, FAS3, BABOS, VN, DIP-GAMMA, KEK5, CG15630, DPR3	90	135	10984	7.232263374	0.021587771
INTERPRO	IPR013783:Immunoglobulin-like fold	8	6.722689076	5.68E-04	CG13506, FAS3, BABOS, VN, DIP-GAMMA, KEK5, CG15630, DPR3	90	177	10984	5.516133082	0.108476635
INTERPRO	IPR003598:Immunoglobulin subtype 2	6	5.042016807	0.001880545	CG13506, VN, DIP-GAMMA, KEK5, CG15630, DPR3	90	109	10984	6.718042813	0.316294365
INTERPRO	IPR003599:Immunoglobulin subtype	6	5.042016807	0.002037133	CG13506, BABOS, DIP-GAMMA, KEK5, CG15630, DPR3	90	111	10984	6.596996997	0.337623162
SMART	SM00408:IGc2	6	5.042016807	0.006899341	CG13506, VN, DIP-GAMMA, KEK5, CG15630, DPR3	59	109	5218	4.8682942	0.35348885
SMART	SM00409:IG	6	5.042016807	0.0074426	CG13506, BABOS, DIP-GAMMA, KEK5, CG15630, DPR3	59	111	5218	4.780577187	0.375395947
INTERPRO	IPR013098:Immunoglobulin I-set	4	3.361344538	0.016300742	CG13506, VN, KEK5, CG15630	90	66	10984	7.396632997	0.963842915
UP_KEYWORDS	Immunoglobulin domain	3	2.521008403	0.053129894	FAS3, BABOS, VN	111	47	13921	8.005175388	0.995504788

Annotation Cluster 2	Enrichment Score: 2.4641388084339306	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Category	Term									
UP_KEYWORDS	Transmembrane helix	38	31.93277311	2.03E-03	OATP58DA, OATP58DB, PPK30, SDC, SHAWL, FZ, SLO2, OR46A, CG43201, LERP, APP, CG12902, WUN2, CG7557, SEMA-1A, IR93A, OATP58DC, PPK19, PMCA, PDFR, NCKX30C, BABOS, AXO, FUCTA, AC13E, MELTRIN, FZ2, CG18031, FAS3, CG3036, CG12917, CG13723, KEK5, MCT1, PGRP-LA, SLOB, CG3822, CG17600	111	2985	13921	1.59656541	0.181909333
UP_KEYWORDS	Transmembrane	38	31.93277311	2.09E-03	OATP58DA, OATP58DB, PPK30, SDC, SHAWL, FZ, SLO2, OR46A, CG43201, LERP, APP, CG12902, WUN2, CG7557, SEMA-1A, IR93A, OATP58DC, PPK19, PMCA, PDFR, NCKX30C, BABOS, AXO, FUCTA, AC13E, MELTRIN, FZ2, CG18031, FAS3, CG3036, CG12917, CG13723, KEK5, MCT1, PGRP-LA, SLOB, CG3822, CG17600	111	2990	13921	1.593895568	0.18704542
UP_KEYWORDS	Membrane	39	32.77310924	0.005430775	OATP58DA, OATP58DB, PPK30, SDC, SHAWL, FZ, SLO2, OR46A, CG43201, LERP, APP, CG12902, WUN2, CG7557, SEMA-1A, DALLY, IR93A, OATP58DC, PPK19, PMCA, PDFR, NCKX30C, BABOS, AXO, FUCTA, AC13E, MELTRIN, FZ2, CG18031, FAS3, CG3036, CG12917, CG13723, KEK5, MCT1, PGRP-LA, SLOB, CG3822, CG17600	111	3266	13921	1.497600172	0.416734024
GOTERM_CC_DIRECT	GO:0016021~integral component of membrane	35	29.41176471	0.0060518	PPK30, SDC, FZ, SHAWL, SLO2, OR46A, CG43201, LERP, APP, CG12902, WUN2, CG7557, SEMA-1A, IR93A, OATP58DC, PPK19, PMCA, PDFR, NCKX30C, BABOS, AXO, FUCTA, AC13E, MELTRIN, FZ2, CG18031, FAS3, CG3036, CG12917, CG13723, MCT1, PGRP-LA, SLOB, CG3822, CG17600	83	2814	10026	1.502427621	0.403076192

Annotation Cluster 3	Enrichment Score: 2.3636463213015095	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Category	Term									
GOTERM_BP_DIRECT	GO:0071702~organic substance transport	3	2.521008403	1.68E-03	OATP58DA, OATP58DB, OATP58DC	88	8	10996	46.85795455	0.495566789
GOTERM_BP_DIRECT	GO:0043252~sodium-independent organic anion transport	3	2.521008403	1.68E-03	OATP58DA, OATP58DB, OATP58DC	88	8	10996	46.85795455	0.495566789
INTERPRO	IPR004156:Organic anion transporter polypeptide OATP	3	2.521008403	0.001761049	OATP58DA, OATP58DB, OATP58DC	90	8	10984	45.76666667	0.2995592
GOTERM_MF_DIRECT	GO:0022804~active transmembrane transporter activity	3	2.521008403	0.001793674	OATP58DA, OATP58DB, OATP58DC	77	8	9284	45.21428571	0.196698109
GOTERM_MF_DIRECT	GO:0015347~sodium-independent organic anion transmembrane transporter activity	3	2.521008403	0.001793674	OATP58DA, OATP58DB, OATP58DC	77	8	9284	45.21428571	0.196698109
GOTERM_MF_DIRECT	GO:0022857~transmembrane transporter activity	4	3.361344538	0.033242277	OATP58DA, OATP58DB, CG3036, OATP58DC	77	86	9284	5.607973422	0.983828388
INTERPRO	IPR020846:Major facilitator superfamily domain	5	4.201680672	0.053570711	OATP58DA, OATP58DB, CG3036, MCT1, OATP58DC	90	175	10984	3.486984127	0.999985215

Annotation Cluster 4	Enrichment Score: 2.0575085413985867	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Category	Term									
UP_KEYWORDS	Ion transport	9	7.56302521	2.41E-04	OATP58DA, OATP58DB, PPK30, NCKX30C, SHAWL, OATP58DC, PMCA, PPK19, CG3822	111	208	13921	5.426585239	0.02362354
UP_KEYWORDS	Transport	10	8.403361345	3.44E-02	OATP58DA, OATP58DB, PPK30, NCKX30C, OBP99A, SHAWL, OATP58DC, PMCA, PPK19, CG3822	111	564	13921	2.22365983	0.968877516
UP_KEYWORDS	Ion channel	4	3.361344538	0.080826204	PPK30, SHAWL, PPK19, CG3822	111	128	13921	3.91920045	0.999762116

Annotation Cluster 5	Enrichment Score: 1.842111602621688	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Category	Term									
UP_KEYWORDS	Alternative splicing	20	16.80672269	4.55E-07	CPO, LAB, NCKX30C, SPT5, EIP75B, MOB2, VN, UBX, SDC, RDX, SICK, OR46A, FAS3, HOW, ARGK, PROS, TET, PGRP-LA, SLOB, SHROOM	111	631	13921	3.975100298	5.04E-04
UP_SEQ_FEATURE	compositionally biased region:Gln-rich	10	8.403361345	4.45E-05	CPO, H15, LAB, HOW, EIP75B, VN, CDK8, SICK, RDX, PROS	36	160	3113	5.404513889	0.05316126
UP_SEQ_FEATURE	splice variant	18	15.12605042	9.81E-05	CPO, LAB, NCKX30C, SPT5, EIP75B, MOB2, VN, UBX, SDC, FZ, RDX, SICK, FAS3, HOW, ARGK, PROS, PGRP-LA, SHROOM	36	610	3113	2.551639344	0.117093332
UP_KEYWORDS	Developmental protein	14	11.76470588	7.96E-04	CPO, LAB, EIP75B, SNA, SDC, UBX, VN, FZ, RDX, FZ2, FAS3, HOW, SEMA-1A, PROS	111	593	13921	2.960879936	0.878738306
UP_KEYWORDS	Transcription	10	8.403361345	0.008304846	MED6, H15, LAB, EIP75B, SPT5, MED16, FOXF, UBX, CDK8, PROS	111	442	13921	2.83743019	8.824873132
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	7	5.882352941	0.009309158	BTEB2, H15, LAB, SPT5, SNA, PROS, TET	88	228	10996	3.836323764	12.25910997
UP_KEYWORDS	Transcription regulation	9	7.56302521	0.01725534	MED6, H15, LAB, EIP75B, SPT5, MED16, UBX, CDK8, PROS	111	416	13921	2.71329262	17.53769963
UP_SEQ_FEATURE	compositionally biased region:Poly-Ala	5	4.201680672	0.029545846	CPO, H15, EIP75B, UBX, RASGAP1	36	106	3113	4.078878407	30.10273847
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	5	4.201680672	0.030326748	EIP75B, SPT5, SNA, UBX, PROS	88	149	10996	4.193105552	34.99008614

UP_KEYWORDS	Nucleus	15	12.60504202	0.062716138	CPO, LAB, SPT5, EIP75B, MOB2, FOXF, SNA, UBX, CDK8, RDX, MED6, H15, HOW, MED16, PROS	111	1134	13921	1.658920826	51.2045871
GOTERM_MF_DIRECT	GO:0003700~transcription factor activity, sequence-specific DNA binding	6	5.042016807	0.074363637	H15, LAB, EIP75B, FOXF, UBX, PROS	77	275	9284	2.630649351	58.92231132
GOTERM_BP_DIRECT	GO:0006351~transcription, DNA-templated	7	5.882352941	0.077109357	MED6, H15, LAB, EIP75B, FOXF, UBX, PROS	88	376	10996	2.326281431	67.43984571
UP_KEYWORDS	Homeobox	3	2.521008403	0.19854376	LAB, UBX, PROS	111	104	13921	3.617723493	91.38712459
UP_KEYWORDS	DNA-binding	7	5.882352941	0.248278512	H15, LAB, EIP75B, FOXF, SNA, UBX, PROS	111	535	13921	1.640936263	95.76437749
GOTERM_CC_DIRECT	GO:0005634~nucleus	18	15.12605042	0.323097966	CPO, LAB, EIP75B, MOB2, FOXF, SNA, UBX, EIP63F-1, CDK8, RDX, FZ2, MED6, BTEB2, H15, MAMO, HOW, PROS, TET	83	1832	10026	1.186852212	98.49798877
INTERPRO	IPR009057:Homeodomain-like	3	2.521008403	0.340803719	LAB, UBX, PROS	90	149	10984	2.457270694	99.46563073
GOTERM_BP_DIRECT	GO:0006355~regulation of transcription, DNA-templated	5	4.201680672	0.392217434	LAB, FOXF, UBX, EXP, PROS	88	401	10996	1.558036726	99.90535594
GOTERM_MF_DIRECT	GO:0003677~DNA binding	6	5.042016807	0.479636502	H15, EIP75B, SNA, UBX, PROS, TET	77	555	9284	1.303474903	99.94584345
Annotation Cluster 6	Enrichment Score: 1.6094587917754268									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
UP_KEYWORDS	Glycoprotein	13	10.92436975	6.13E-04	FZ2, PDFR, CG25C, NCKX30C, FAS3, VN, SDC, FUCTA, FZ, OR46A, DALLY, SEMA-1A, PGRP-LA	111	503	13921	3.241326814	6.77E-01
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	13	10.92436975	1.47E-03	FZ2, PDFR, CG25C, NCKX30C, FAS3, VN, SDC, FUCTA, FZ, OR46A, DALLY, SEMA-1A, PGRP-LA	36	423	3113	2.657538744	1.738713222
UP_KEYWORDS	Disulfide bond	12	10.08403361	1.68E-02	MELTRIN, FZ2, CG25C, FAS3, OBP99A, AXO, VN, CG9134, FZ, KEK5, SEMA-1A, PGRP-LA	111	670	13921	2.246228318	17.08509488
UP_SEQ_FEATURE	topological domain:Extracellular	9	7.56302521	1.96E-02	FZ2, NCKX30C, PDFR, FAS3, SDC, FZ, OR46A, SEMA-1A, PGRP-LA	36	312	3113	2.494391026	21.0530594
UP_SEQ_FEATURE	disulfide bond	8	6.722689076	0.025313939	FZ2, CG25C, FAS3, OBP99A, VN, FZ, SEMA-1A, PGRP-LA	36	265	3113	2.61048218	26.37476387
UP_SEQ_FEATURE	topological domain:Cytoplasmic	10	8.403361345	0.027477992	FZ2, NCKX30C, PDFR, FAS3, SDC, FUCTA, FZ, OR46A, SEMA-1A, PGRP-LA	36	397	3113	2.178141618	28.30329301
UP_KEYWORDS	Cell membrane	7	5.882352941	0.089487136	FZ2, PDFR, FZ, OR46A, DALLY, PGRP-LA, CG3822	111	391	13921	2.245270846	64.60372757
UP_SEQ_FEATURE	signal peptide	9	7.56302521	0.096348946	FZ2, CG25C, FAS3, OBP99A, SDC, VN, FZ, SEMA-1A, DALLY	36	427	3113	1.822599532	70.17530212
UP_SEQ_FEATURE	transmembrane region	10	8.403361345	0.171307045	FZ2, NCKX30C, PDFR, FAS3, SDC, FUCTA, FZ, OR46A, SEMA-1A, PGRP-LA	36	566	3113	1.527777778	89.39563378
UP_KEYWORDS	Transducer	4	3.361344538	0.264851709	FZ2, PDFR, FZ, OR46A	111	226	13921	2.219724149	96.69130569
Annotation Cluster 7	Enrichment Score: 1.5106741430411734									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
INTERPRO	IPR000210:BTB/POZ-like	4	3.361344538	2.21E-02	CG11275, MAMO, SHAWL, RDX	90	74	10984	6.596996997	2.44E+01
INTERPRO	IPR011333:BTB/POZ fold	4	3.361344538	3.15E-02	CG11275, MAMO, SHAWL, RDX	90	85	10984	5.743267974	33.130197
SMART	SM00225:BTB	4	3.361344538	4.22E-02	CG11275, MAMO, SHAWL, RDX	59	70	5218	5.053753027	35.39291287
Annotation Cluster 8	Enrichment Score: 1.4768770120012642									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
UP_KEYWORDS	Activator	5	4.201680672	1.46E-02	MED6, SPT5, MED16, UBX, CDK8	111	119	13921	5.269513211	1.51E+01
GOTERM_CC_DIRECT	GO:0016592~mediator complex	3	2.521008403	2.96E-02	MED6, MED16, CDK8	83	33	10026	10.98138007	27.63601562
GOTERM_MF_DIRECT	GO:0001104~RNA polymerase II transcription cofactor activity	3	2.521008403	3.13E-02	MED6, MED16, CDK8	77	34	9284	10.63865546	30.68876267
GOTERM_BP_DIRECT	GO:0006367~transcription initiation from RNA polymerase II promoter	3	2.521008403	9.11E-02	MED6, MED16, CDK8	88	64	10996	5.857244318	73.69818428
Annotation Cluster 9	Enrichment Score: 1.3591453957574986									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
INTERPRO	IPR016187:C-type lectin fold	4	3.361344538	6.45E-03	CG15358, CG25C, CG9134, RGN	90	47	10984	10.38676123	7.80E+00
INTERPRO	IPR001304:C-type lectin	3	2.521008403	4.53E-02	CG15358, CG9134, RGN	90	42	10984	8.717460317	44.15239643
INTERPRO	IPR016186:C-type lectin-like	3	2.521008403	4.93E-02	CG15358, CG9134, RGN	90	44	10984	8.321212121	46.99514068
SMART	SM00034:CLECT	3	2.521008403	7.24E-02	CG15358, CG9134, RGN	59	40	5218	6.63050847	53.2711787
GOTERM_MF_DIRECT	GO:0030246~carbohydrate binding	3	2.521008403	0.153412136	CG15358, CG9134, RGN	77	85	9284	4.255462185	85.30262144
Annotation Cluster 10	Enrichment Score: 1.2456397566889965									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
UP_KEYWORDS	Sodium transport	3	2.521008403	4.92E-02	PPK30, NCKX30C, PPK19	111	45	13921	8.360960961	4.28E+01
UP_KEYWORDS	Sodium	3	2.521008403	5.31E-02	PPK30, NCKX30C, PPK19	111	47	13921	8.005175388	45.38183388
GOTERM_BP_DIRECT	GO:0006814~sodium ion transport	3	2.521008403	7.02E-02	PPK30, NCKX30C, PPK19	88	55	10996	6.815702479	63.84923541
Annotation Cluster 11	Enrichment Score: 1.2268476011602796									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
GOTERM_BP_DIRECT	GO:0007411~axon guidance	7	5.882352941	3.42E-03	FZ2, FAS3, SDC, CDK8, SEMA-1A, SM, PROS	88	185	10996	4.728009828	4.68E+00
UP_KEYWORDS	Neurogenesis	3	2.521008403	1.45E-01	FAS3, SDC, SEMA-1A	111	85	13921	4.426391097	82.4149932
UP_KEYWORDS	Differentiation	3	2.521008403	4.20E-01	FAS3, SDC, SEMA-1A	111	181	13921	2.078691952	99.76095986
Annotation Cluster 12	Enrichment Score: 1.0608530571366437									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
KEGG_PATHWAY	dme04310:Wnt signaling pathway	3	2.521008403	6.46E-02	FZ2, FZ, DALLY	14	89	2737	6.58988764	3.78E+01
UP_KEYWORDS	Cell membrane	7	5.882352941	8.95E-02	FZ2, PDFR, FZ, OR46A, DALLY, PGRP-LA, CG3822	111	391	13921	2.245270846	64.60372757
GOTERM_BP_DIRECT	GO:0016055~Wnt signaling pathway	3	2.521008403	1.14E-01	FZ2, FZ, DALLY	88	73	10996	5.135118306	81.46559309