

Table S4: Results from the gene ontology enrichment analysis for larval anoxia tolerance. Only clusters with enrichment scores > 2 were shown.

Annotation Cluster 1	Enrichment Score: 2.5063184924448074										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni corrected	
UP_KEYWORDS	Alternative splicing	7	24.1379	0.0003	PDE11, LASP, FS(1)H, CHIF, DRE4, PRM, CG31145	22	631	13921	7.0197	0.0115	
UP_KEYWORDS	Coiled coil	10	34.4828	0.0003	PDE11, CG42231, LASP, CG8910, FS(1)H, CHIF, DRE4, PRM, CG2258, X11LBETA	22	1594	13921	3.9697	0.0120	
UP_SEQ_FEATURE	splice variant	5	17.2414	0.0309	PDE11, LASP, FS(1)H, CHIF, DRE4	8	610	3113	3.1895	0.7641	
UP_KEYWORDS	Phosphoprotein	5	17.2414	0.0444	LASP, FS(1)H, CHIF, DRE4, PRM	22	909	13921	3.4806	0.8703	
Annotation Cluster 2	Enrichment Score: 2.3720705430248015										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni corrected	
UP_KEYWORDS	SH3 domain	3	10.3448	0.0024	LASP, CG2258, CG32082	22	49	13921	38.7412	0.1042	
INTERPRO	IPR001452:Src homology-3 domain	3	10.3448	0.0045	LASP, CG2258, CG32082	17	70	10984	27.6908	0.1813	
SMART	SM00326:SH3	3	10.3448	0.0069	LASP, CG2258, CG32082	12	61	5218	21.3852	0.1173	
Annotation Cluster 3	Enrichment Score: 0.3333377086874277										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni corrected	
GOTERM_CC_DIRECT	GO:0016021~integral component of mem	6	20.6897	0.3530	CG43795, FS(1)H, CG33144, CG9747, CG31145, CG43954	15	2814	10026	1.4252	1.0000	
UP_KEYWORDS	Transmembrane helix	6	20.6897	0.4799	CG43795, FS(1)H, CG33144, CG9747, CG31145, CG43954	22	2985	13921	1.2719	1.0000	
UP_KEYWORDS	Transmembrane	6	20.6897	0.4815	CG43795, FS(1)H, CG33144, CG9747, CG31145, CG43954	22	2990	13921	1.2698	1.0000	
UP_KEYWORDS	Membrane	6	20.6897	0.5690	CG43795, FS(1)H, CG33144, CG9747, CG31145, CG43954	22	3266	13921	1.1625	1.0000	