Supplemental Table 3

Expression of the components of adrenergic mechanism

			Developmental Stages				
	Genes	*M.fr*	EC	LC		LB	EG
		S.pur	EC	LC	EB	LB	EG
		L.var	EC	LC	EB	LB	EG
		P.liv	EC		EB	LB	EG
Enzyme	*DBH*	*M.fr*	NS	0,003		0,005	NS
		S.pur	NS	NS	NS	NS	NS
		L.var	0,005	0,006	NS	0,008	0,023
		P.liv	0,019		0,02	0,017	0,007
α-Adrenoreceptors	*α1A-adrR*	*M.fr*	0,264	0,049		0,08	0,092
		S.pur	0,535	0,015	0,01	0,02	0,017
		L.var	1,013	0,994	1,009	1,02	1
		P.liv	NS		NS	NS	NS
	α1B-adrR	*M.fr*	NS	NS		0,004	NS
		L.var	0,016	0,043	0,006	0,353	NS
	α1D-adrR	*M.fr*	0,012	0,028		0,189	0,026
		L.var	0,742	0,662	1,84	0	18
	α2A-adrR	*L.var*	0,01	0,02	0,015	0,255	0
	α2B-adrR	*M.fr*	0,011	NS		NS	0,12
		L.var	0,016	0,007	0,006	5,138	0,333
	α2C-adrR	*M.fr*	0,026	0,023	0,02	0,027	0,004
β-Adrenoreceptors	*β1-adrR*	*M.fr*	0,053	0,014		0,043	0,133
		S.pur	0,016	0,07	0,054	NS	0,005
		L.var	0,073	0,069	0,0345	0,667	0,583
	β2-adrR	*M.fr*	0,036	0,04		0,23	0,052
		S.pur	4,969	0,511	0,095	0,082	0,079
		L.var	0,3027	0,225	0,2487	0,2	1,382
		P.liv	1,089		0,064	0,045	0,014
	β3-adrR	*M.fr*	0,024	0,01		0,009	NS
		S.pur	0,004	0,53	0,636	0,5	0,244
		L.var	0,067	0,03	0,029	1,553	0,972
		P.liv	0,899		0,597	0,394	0,495
Octopamine receptor	*OctR*	*M.fr*	0,067	0,007		0,012	NS
Tyramine receptor	*TyrR1*	*M.fr*	0,124	0,029		NS	NS
		L.var	0,028	0,026	0,031	0,128	0,079
Transporter	*NET*	*M.fr*	NS	NS		0,004	0,005
		S.pur	0,035	0,012	NS	NS	NS
		L.var	1,205	1,126	0,89	1,785	1,5
		P.liv	0,053		NS	NS	0,008

NRPM (GHG)

Color bar:

≥ 5
4,0
3,0
2,0
1,0
0,5
0,4
0,3
0,2
0,1
0,01
0,003
0

Developmental Stages: EC - early cleavage; LC - late cleavage; EB - early blastula; LB - late blastula; EG - early gastrula. **Species names**: *M.fr - Mesocentrotus franciscanus; S.pur - Strongylocentrotus purpuratus; L.var - Lytechinus variegatus; P.liv - Paracentrotus lividus* . **Gene names**: *DBH* - Dopamine-β-hydroxylase; *AdrR* – adrenoreceptor; *OctR* - octopamine receptor; *TyrR* - tyramine receptor; *NET* - noadrenaline ransporter. **Data definitions:** NRPM - RPM normalized to the geometric mean of the three housekeeping genes (GHG); NS - NS - not significant value.

Transcriptomic data for this analysis were obtained from publicly available datasets:

1) Wong, J.M.; Gaitán-Espitia, J.D.; Hofmann, G.E. Transcriptional Profiles of Early Stage Red Sea Urchins (Mesocentrotus Franciscanus) Reveal Differential Regulation of Gene Expression across Development. Mar Genomics 2019, 48, 100692, doi:10.1016/j.margen.2019.05.007.

2) Hogan, J.D.; Keenan, J.L.; Luo, L.; Ibn-Salem, J.; Lamba, A.; Schatzberg, D.; Piacentino, M.L.; Zuch, D.T.; Core, A.B.; Blumberg, C.; et al. The Developmental Transcriptome for Lytechinus Variegatus Exhibits Temporally Punctuated Gene Expression Changes. Dev Biol 2020, 460, 139–154, doi:10.1016/j.ydbio.2019.12.002.

3) Gildor, T.; Malik, A.; Sher, N.; Avraham, L.; Ben-Tabou de-Leon, S. Quantitative Developmental Transcrip-tomes of the Mediterranean Sea Urchin Paracentrotus Lividus. Mar Genomics 2016, 25, 89–94, doi:10.1016/j.margen.2015.11.013.

4) Tu, Q.; Cameron, R.A.; Davidson, E.H. Quantitative Developmental Transcriptomes of the Sea Urchin Strongylocentrotus Purpuratus. Dev Biol 2014, 385, 160–167, doi:10.1016/j.ydbio.2013.11.019.