

Supporting Information

The following supporting information is available free of charge at ACS website <http://pubs.acs.org>

Title: Quantitative proteomic analysis of the slime and ventral mantle glands of the striped pyjama squid (*Sepioloidea lineolata*)

Authors: Nikeisha J. Caruana^{1*}, Jan M. Strugnell^{1,2}, Julian Finn³, Pierre Faou⁴, Kim M. Plummer⁵, Ira R. Cooke^{4,6}

¹ Department of Ecology, Environment and Evolution, La Trobe University, Melbourne, VIC 3086, Australia

² Centre for Sustainable Tropical Fisheries and Aquaculture, James Cook University, Townsville, QLD 4811, Australia

³ Sciences, Museums Victoria, Carlton, VIC 3053, Australia

⁴ Department of Biochemistry and Genetics, La Trobe Institute for Molecular Science, La Trobe University, Melbourne, VIC 3086, Australia

⁵ Department of Animal, Plant and Soil Sciences, AgriBio, La Trobe University, Melbourne, VIC 3086, Australia

⁶ Department of Molecular and Cell Biology, James Cook University, Townsville, QLD 4811, Australia

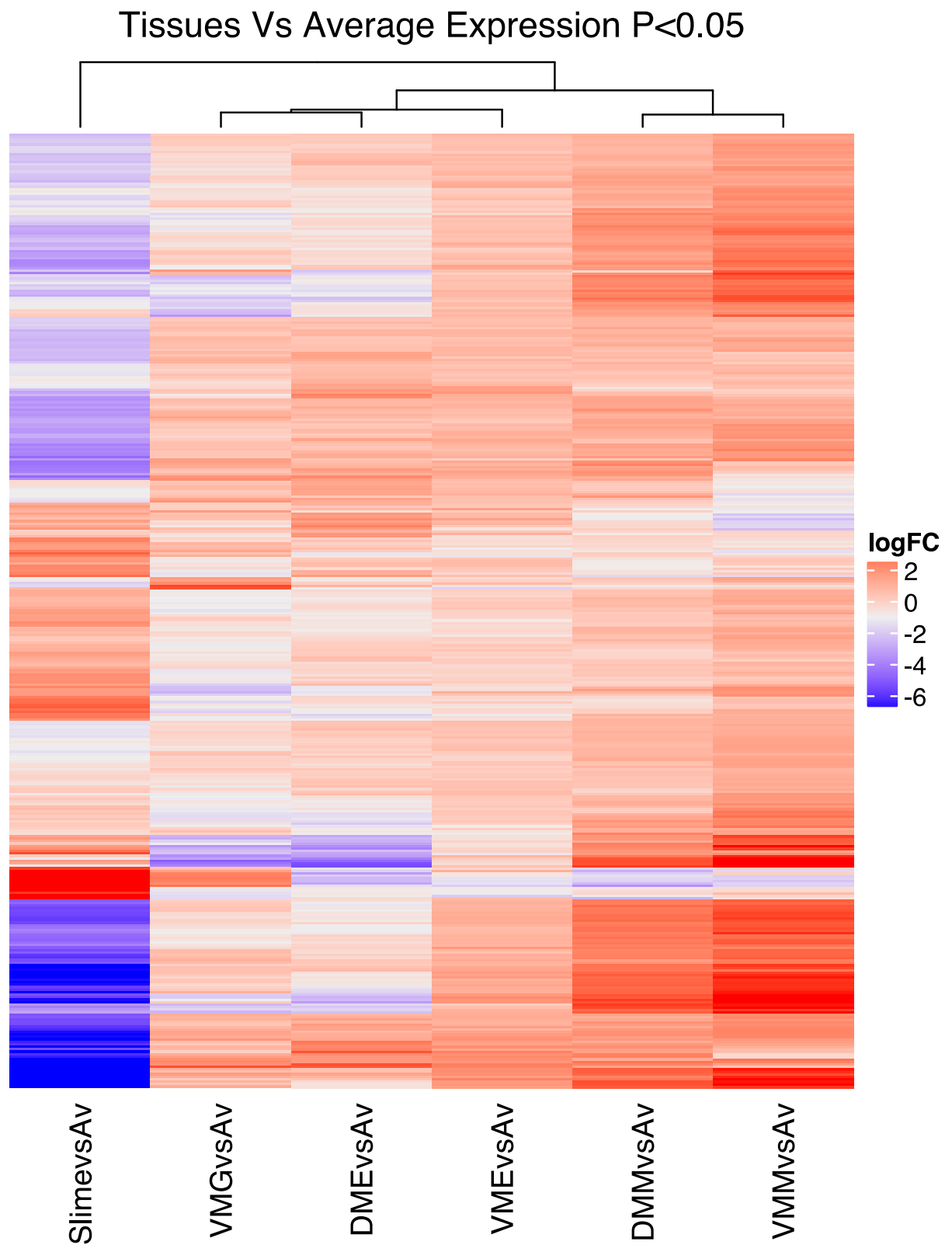
Corresponding author: njcaruana@students.latrobe.edu.au

Table of Contents

S-1 – Supplementary Figure 1: Heatmap of all differentially expressed proteins.

S-2 – Supplementary Table 1: Top 28 most positively differentially expressed proteins within the slime and ventral mantle glands and also negatively differentially expressed proteins in mantle muscle of *So. lineolata*

S-3 – Supplementary Figure 2: TopGO analysis of significant proteins differentially expressed proteins.



Supplementary Figure 1 - Heatmap of all differentially expressed proteins in all tissues vs average expression (normalized LogFC $P < 0.05$). Tissues are SLIME – slime, VMG - ventral mantle gland, DME – dorsal mantle epithelium, DMM – dorsal mantle muscle, VME – ventral mantle epithelium, VMM – ventral mantle muscle.

Supplementary Table 1 – Top 28 most positively differentially expressed proteins within the slime and ventral mantle glands and negatively differentially expressed proteins in the mantle muscle of *S. lineolata*. ID's are given according to protein groups found in the proteingroups.txt file from *MaxQuant*. Log2 expression values from left to right – SlimevsAv – Slime compared to the average expression of all tissues and slime, VMEvsAv – ventral mantle epithelium compared to the average expression of all tissues and slime, VMGvsAv – ventral mantle gland compared to the average expression of all tissues and slime, DMMvsAv – Dorsal mantle muscle compared to the average expression of all tissues and slime, DMEvsAv - dorsal mantle epithelium compared to the average expression of all tissues and slime, ventral mantle muscle compared to the average expression of all tissues and slime.

S-2

Protein ID	blastx	blastx Evalue	Pfam	Pfam Evalue	Signal Peptide	Start Codon	Stop Codon	SlimevsAv	VMEvsAv	VMGvsAv	DMMvsAv	DMEvsAv	VMMvsAv
SL_1911	NA	NA	NA	NA	*	N	Y	6.63826455	-1.3979665	1.71972085	-2.3673047	-2.8852292	-1.7074851
SL_160	Fatty acid-binding protein, heart	E:9e-24	Lipocalin_7	E:3.2e-10		N	Y	6.33336136	-1.9657544	-1.5867874	-1.2252047	-1.190557	-0.3650579
SL_493	Carboxypeptidase E	E:5e-136	Peptidase_M14	E:1.7e-80	*	Y	Y	6.08499841	-1.8932907	2.37687191	-3.3434766	-1.4311573	-1.7939457
SL_923	Neuroendocrine convertase 1	E:0	PeptidaseS8 pro-domain	E:6.2e-20		Y	Y	5.81215663	-1.5026746	2.01090697	-1.7740836	-2.404494	-2.1418114
SL_414	NA	NA	HSP20	E:0.00015	*	Y	Y	5.10578407	-1.4093451	2.17746834	-1.7087931	-2.3822714	-1.7828428
SL_1292	NA	NA	NA	NA		N	Y	4.74840269	0.40262369	-1.5710456	-2.5168473	-0.4377225	-0.625411
SL_1553	NA	NA	ETX_MTX2^Clostridium epsilon toxin ETX/Bacillus mosquitocidal toxin MTX2	E:1.6e-05		Y	Y	4.45286527	-0.9655027	-1.2456214	-0.8696777	-0.8344995	-0.5375639
SL_2089	NA	NA	NA	NA		N	N	4.17356979	0.9470107	-1.2882731	0.4795999	-0.9717695	0.4869167
SL_1927	SUMO-activating enzyme subunit 2	E:1e-58	ThiF family	E:2.3e-07		N	Y	4.15433318	0.7370802	1.15612374	-2.5995135	-1.8133093	-1.6347143
SL_800	WSC domain-containing protein 2	E:7e-10	WSC domain	E:3.3e-09	*	N	Y	4.10691703	-0.8303382	2.01301768	-1.5024367	-1.8829891	-1.9041706
SL_1815	Angiotensin-converting enzyme	E:2e-165	Angiotensin-converting enzyme	E:3.3e-206		N	Y	4.00296016	-0.8224672	1.98219245	-1.8558635	-3.0885459	-0.218276
SL_1377	NA	NA	NA	NA	*	Y	N	3.4956952	-0.3688516	0.22012101	-1.735118	-1.3778019	0.2340447
SL_229	Profilin-1B	E:1e-10	Profilin	E:4.1e-19		Y	Y	2.77957831	-0.6837999	0.13834463	-0.0653487	-1.3403157	-0.8284586
SL_1908	C3 and P2P-like alpha 2-macroglobulin domain-containing protein 8	E:5e-08	Farnesic acid O-methyl transferase	E:7.7e-16		Y	Y	2.51863674	0.28205	-0.8692736	-1.634967	1.31072012	-1.6071663
SL_804	CD63 antigen	E:4e-29	Tetraspanin family	E:2.2e-49		Y	Y	2.06071846	-1.3774173	0.78583225	-0.2915525	-0.8866001	-0.2909808
SL_1814	Synaptic vesicle membrane protein VAMP-1 homolog-like	E:5e-146	Alcohol dehydrogenase GroES-like domain	E:2.2e-12	*	N	Y	2.0419749	-0.6588568	1.02551277	0.8284292	-0.1052436	-1.4749581
SL_312	NA	E:9e-111	SPFH domain / Band 7 family	E:1.9e-32		Y	Y	2.01505506	-0.6399294	-0.3129034	-0.3076079	-0.2596822	-0.4949322
SL_1986	Universal stress protein in OAH/OAS sulphydrylase 3'region	E:5e-09	Universal stress protein family	E:1.7e-29		Y	Y	2.00839405	-0.4761407	-0.5643122	-0.3614787	0.23992042	-0.8463828
SL_958	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	E:6e-75	Short chain dehydrogenase	E:1.2e-40		Y	Y	1.8638006	0.35743361	-0.7622823	-1.010149	0.31059586	-0.7593988
SL_1885	von Willebrand factor A domain-containing protein 5A	E:9e-105	Vault protein inter-alpha-trypsin domain	E:2e-07		Y	Y	1.69984097	0.00626999	-1.2483245	-0.6477244	0.81325625	-0.6233183
SL_640	Annexin A7	E:4e-112	Annexin	E:3.5e-25		Y	Y	1.59465761	-0.2928906	-0.9488367	-0.2587616	-0.0540772	-0.0400915
SL_504	Calmodulin-2	E:2e-12	EF-hand_7	E:4.4e-11		Y	Y	1.45246272	-0.6933099	0.55646347	-0.495039	-0.2381123	-0.582465
SL_2116	Protocadherin Fat 4	E:7e-171	Cadherin	E:4.9e-11		Y	Y	1.40390751	-0.7721791	0.37259794	-0.105102	1.4308388	-2.3300631
SL_1095	Ras-related protein Rab-1A	E:3e-86	Ras family	E:1.6e-37		N	Y	1.27719867	0.05886675	-0.2185485	-0.4267997	0.03179483	-0.7225121
SL_1362	Caspase-7	E:5e-67	Peptidase_C14	E:6.3e-47		Y	Y	1.23372436	-0.2749376	0.33995907	-0.3978749	-0.022267	-0.8786039
SL_480	Glutaredoxin-1	E:2e-10	Glutaredoxin	E:1.1e-13	*	Y	Y	1.23112679	0.47523734	-0.6491431	-0.4220695	1.14896342	-1.7841149
SL_557	Annexin A4	E:3e-86	Annexin	E:2e-191		Y	Y	1.19311619	-1.1557651	0.53871876	-0.5720473	0.3133798	-0.3174023
SL_1664	Major vault protein	E:0	Major Vault Protein repeat	E:3.3e-13		Y	Y	1.11787584	0.43568111	0.22508153	-1.0601572	1.42213828	-2.1406196

