

Additional File 1. Most abundantly represented novel transcripts in a dataset of an unstressed culture of the fast desiccation strategist nematode *Panagrolaimus* sp.

<i>Cluster ID</i>	<i>Number of ESTs</i>	<i>Predicted AA Sequence</i>	<i>Predicted pI</i>	<i>Predicted Signal Peptide</i>	<i>Composition (%)</i>	<i>Charged Amino Acids</i>	
1	PSC00006	71	GDTNIFVISS	7.96	Yes	13.5	12
2	PSC00009	70	MKTFHIILLA	9.99	Yes	24.6	0
3	PSC00076	54	MLSRTGQAA	9.51	No	4.1	23
4	PSC00137	49	MSKTAQERGI	6.49	No	8.3	10
5	PSC00051	35	MNFLTTLFFF	9.25	Yes	18.1	6
6	PSC00163	29	LLTTTANPKT	5.97	No	7.1	16
7	PSC00182	29	GKSESFTLRK	8.56	Yes	9.3	8
8	PSC00025	28	RGRGSIGAVA	9.36	Yes	6.9	7
9	PSC00883	27	GVQKKRKVII	6.24	No	4.9	31
10	PSC00633	27	MLEYFEPPI	6.81	No	6.1	13
11	PSC00203	25	GINSDFLIVL	9.55	Yes	18.7	2
12	PSC00316	24	FIIYHLLALFI	7.02	Yes	2.9	2
13	PSC00610	24	MFAKLFALM	9.29	Yes	8.3	11
14	PSC00241	22	MYLFCAVSFL	8.99	No	8.2	23
15	PSC00429	22	MKLTVAVFLC	9.13	Yes	11.8	13
16	PSC00004	21	GQKRFTSFSS	9.81	Yes	26.9	1
17	PSC00010	21	GDFQKKCVPI	9.6	No	1.9	11
18	PSC00122	17	SSIPTLVSRN	11.14	No	6.7	3
19	PSC00097	16	HFFFAGFVFL	8.44	Yes	11.1	2
20	PSC00127	15	GESVLSNNFY	8.85	Yes	6	10
21	PSC00725	15	GVNSDFLIVL	9.87	Yes	25.3	1
				641	Yes 13 = 61.9%		
				Total = 641	No 8 = 38.1%		

Set of 7,606 ESTs prepared from a mixed stage

<i>Positively</i>	<i>Charged Amino Acids</i>	<i>GrAv</i>	<i>Predicted Protein Length</i>	<i>Predicted Disordered Amino Acids</i>	<i>Predicted Percent Disordered</i>
	13	0.257	163	2	1%
	6	0.109	65	0	0%
	34	-0.669	195	55	28%
	9	0.065	121	1	1%
	12	-0.038	149	0	0%
	8	-1.973	70	70	100%
	10	0.137	86	18	21%
	10	-0.697	58	53	91%
	30	-0.867	162	130	80%
	13	-0.543	115	1	1%
	8	0.155	107	0	0%
	2	1.059	34	0	0%
	20	0.486	206	0	0%
	29	-0.787	184	80	43%
	20	-0.583	152	44	29%
	8	0.08	93	0	0%
	27	-0.121	216	7	3%
	13	-0.692	60	19	32%
	4	0.346	54	2	4%
	14	0.13	166	3	2%
	8	0.392	99	0	0%
