

Additional file 6. Sequence alignments for the annotated Nematode-Specific Peptide family, group F (NSPF) orthologs in 11 *Caenorhabditis* species. Gene identifiers are comprised of the species code, scaffold or chromosome and the first three digits of the sequence position. If the gene was previously annotated, the species code and gene ID number are given. The transcript number is given for *C. sp.* 33. The predicted signal cleavage site is between residues 20 and 21.

NSPF-1

	1	20	40	60	80	89
CBG_05952	MRF-FTIAL-FFCILSNVFAWYHGDRAALADDEYDPEAIENRQ	HI	AK	EYMA	REKLRRRVREEIAKEEIRH-MYQREKIRKAMES-FNE-	
CNG_IV_9_344	I-.....	V.....	Q.....			
CSN_7_0_121	...-F...-.....	HT...V.....	V...Q.....	F.....	R...D-.SD-	
CRE_3_5_858	...-I...-...FI.....	HY...V.....	VA...Q.....	LI...F.T...Q.....	L-.....R...D-.DN	
CLA_103_0_109	...-I...-...F.....	HY...V.....	VA...Q.....	LI...F.T...Q.....	L-.....R...D-.DN	
sp33_DN22189g1	...-I...-...I.....	NY...V...E.....	A...Q.....	LI...F.T...Q.....	L-.....R...D-.DN	
CTP_g7984	...LI...-...FV.....	NY...V.....	S...VA...Q.....	LI...F.T.....	L-.....R...DE-.DN	
CWL_4_4_472	.K.-.I...-...V.....	NY..SVG.....	N...VA..RQ..M..LA...	F.T...Q..R..L...T..R..K..DQ-.DN		
CE_nspf-1	...-L.ITLAV....PTI..SHR.ERIEF.N.....	Y..HQLAR..IET.QA.SNI..DV....V..I.RL...KKNVEMY.GDR				
CKA_174_0_13	.N.L.FV...-..VL....VA.NM..AIN.V.E....QAVM..RQLAR..K....F.A.....	-QHV.AD.....D-.GDY				

NSPF-3

	1	20	40	60	80	88
CBG_05951	MRFFT-IALFFCILSNV-FAWYHGDRVALADDEYDPEAIENRQ	Q	IAKE	YMA	REKFRRRIREEIAKEEIEHKYRREKIRAMEA-FNE-	
CNG_IV_9_343		-.....			S-....	
CSN_7_0_123	F-.....	-...HT.....	V.....	V.....	R...Q.....-SD-	
CRE_3_5_857	I-.....FI...-...HY..QI..D...S...VA.....	LI.....	T...A....L...Q....K...E-.DM			
CLA_103_0_108	..L.L-.....FI...-...HY..QI..D...S...VA..R.....	LI.....	T...A....L...Q....K...D-.DM			
sp33_DN3463g1	I-.....FF..I-...HY.N.I..D...S...VS..R.....	LI.....	T...A....L...Q....K...E-.DM			
CTP_g7983	...LV-F....FFVA.A-...NY...V..M...S...VA..R...M..L.....	T.....	L...Q....K...E-...M			
CWL_4_4_473	.K..V-L.....IA...-...SY...V..Y..SN...VA..R...M..L.....	TS...L..Q..L...Q....KE..E-...M				
CDG_455_30_9	.K..I-.....V...NY..SI.L...N...VA..E.....	T.....	R...R...K....K..QT-...M			
CE_nspf-3	.R.LFIT.V.....PTI-..RHR.ERIEF.T.....LY..H.L.R..IET.QA.SN...DV.....	R.IM.LRE.KKNV.MY.GDR				
CKA_174_0_12	.KLLILV.....L....-VSWNM..AI.LV.E.A..Q.VL..R.L.R..K...Q.RA.V.....	R.Q.A.D...Q.INE-...DY				