Coordinated Tissue-Specific Regulation of Adjacent Alternative 3' Splice Sites in C. *elegans*

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SUPPLEMENTAL TABLE AND FIGURE LEGENDS

Table S1. Tissue-specific cassette exons and intron retention events. Table detailing the gene name, pattern of splicing change, genomic position, delta IR (inclusion ratio), and the minimum pvalue of alternative splicing events that change significantly between *glp-4(bn2ts)* somatic-enriched samples and dissected wildtype gonad samples as determined by SpliceTrap (Wu et al. 2011).

Table S2. Tissue-specific adjacent 3' splice sites. Table detailing the gene name, common name, method used to determine splice tissue-specificity, nucleotide difference between splice sites, alternative 3' splice site location relative to the rest of the gene, sequences preceding the proximal and distal splice sites and the existence of previous annotation of the alternative splicing event. Also shown are the number of RNA-seq reads that cross the proximal splice site (columns I, L and P), the number of reads that cross the splice junction in total (columns J, M and Q) and the proximal read percentage (PRP; columns K, N and R) for *glp-4(bn2ts)*, N2 dissected gonads and N2 whole worms, respectively. Columns O and S show the change in Proximal Read Percentage between *glp-4(bn2ts)* and N2 dissected gonads and *glp-4(bn2ts)* and N2 whole worms, respectively. Unique characteristics of some adjacent 3' splice sites are shown in column T and the amino acids gained or lost due to splicing changes are shown in column U. Note that many tissue-specific alternative 3' splice sites are found in tandem introns of the same gene and one case, *ife-3*, contains an alternative 3' splice site with two proximal splice sites that are regulated tissue-specifically.

Table S3. Adjacent alternative 3'ss detected in *smg-2* gonad RNA samples (Adjacent 3' splice sites ≤18nt apart). Table detailing introns with 3' splice sites ≤18nt apart with evidence of alternative splicing. Shown is the genetic location of the intron (column A), the gene name (column B) and the number of nucleotides between the alternative 3' splice sites (column C). Also shown is the number of RNA-seq reads that cross the proximal splice site (columns I, L and P), the number of reads that cross the splice junction in total (columns D and G) and the proximal read percentage (PRP; columns E and H) for *smg-2* and N2 dissected gonads, respectively.

Table S4. Introns With Adjacent AG Dinucleotides 6nt Apart. Table detailing 1245 annotated introns from ce6 that contain a terminal AG dinucleotide as well as an AG dinucleotide 6nt upstream from the terminal AG. These are separated by sufficiency of expression for analysis and tissue-specific splicing patterns. Shown are the terminal 14nt of the intron (column A), the Genetic Location of the intron (column B), the Gene Name (column C) and the Common Name (if known; column D). Also shown are the number of RNA-seq reads that cross the proximal splice site (columns E, H and K), the number of

reads that cross the splice junction in total (columns F, I and L) and the proximal read percentage (PRP; columns G, J and M) for *glp-4(bn2ts)*, N2 dissected gonads and N2 whole worms, respectively. Columns N and O show the change in Proximal Read Percentage between *glp-4(bn2ts)* and N2 dissected gonads and *glp-4(bn2ts)* and N2 whole worms, respectively.

Table S5. WebLogo Genetic Sequence Comparison Genes. Lists of sequences used to derive WebLogo 3' splice site motifs. Shown are the gene name (column A), DNA sequence from the distal 3' splice site to 40nt upstream for each intron (column B) and the number of introns used in each comparison (column C).

Table S6. log2 Ratios of Spliceosome Component or RNA-bnding Factor Expression Change From One Sample to Another. Using RNA-seq data from N2 dissected gonads, N2 whole worms and *glp-4(bn2ts)* whole worms, log2 ratios of expression change were determined. Shown are the gene name (column A) and the common name (if known; column B). Comparisons are made between N2 gonad and whole worm (column C), N2 whole worm and *glp-4(bn2ts)* whole worm (column D) and N2 gonad and *glp-4(bn2ts)* (column E). Empty data cells represent comparisons in expression whose p-value exceeded a maximimum threshold of 0.01.

Table S7. GO Term Analysis of 203 Tissue-specific Alternative 3' Splice Sites in *C. elegans*. Tissue-specific 3' splice site-containing gene names were entered into the Gene Enrichment Analysis tool from the Gene Ontology Consortium. Shown are the biological process term with GO annotation number, the background frequency of that term within *C. elegans* genes as a whole, the observed frequency of genes with that term in the sample set, the expected frequency of genes with that term in the sample set and the associated p-value.

Table S8. Sequences of DNA Oligonucleotide Primers Used in This Study. Sequences are 5' to 3', left to right.

Supplemental Figure 1. Expression change graph of spliceosome components and spliceosome interactors between wildtype germline and *glp-4*. $\log_2$ ratio expression change of each factor arranged from highest to lowest. Intestine-enriched *cyn-6* and germline-enriched *gld-1* are indicated for reference and the expression change for several candidate splicing factors that were tested for involvement in tissue-specific alternative 3' splice site regulation are noted. The average expression change from N2 gonad to *glp-4* among this set is shown by the solid horizontal blue line.

Supplemental Figure 2. RT-PCR of candidate splicing factor regulators of adjacent 3' splice sites in either wildtype gonad, *glp-4* mutant worms or wildtype whole worms. 6% polyacrylamide gel electrophoresis of ^{32}P RT-PCR products derived from dissected gonad or head RNA. Tissue isolation was performed on the indicated mutant worms or following RNAi of the indicated factor. Worms treated with *uaf-2* RNAi rapidly become sick and do not produce progeny. Because of this, wildtype adults were fed RNAi bacteria for 2 days before RNA was extracted from them.

Table S1 Tissue-specific cassette exons and intron retention events

Gene Name		Genomic Position	N2 Gonad to glp-4 (delta IR)	minPval
F07A11.2	Inc in glp-4/Skipping in gonad	chrII:11594345-11595322	0.952	2.26E-12
rgr-1	Inc in glp-4/Skipping in gonad	chrIII:9396425-9397919	0.767	1.28E-07
mbk-2	Inc in glp-4/Skipping in gonad	chrIV:13033197-13035915	0.707	2.18E-06
efk-1	Inc in glp-4/Skipping in gonad	chrIII:6166095-6167199	0.702	2.18E-06
hipr-1	Inc in glp-4/Skipping in gonad	chrIII:8724389-8725228	0.661	1.39E-05
Y71F9AL.10	Inc in glp-4/Skipping in gonad	chrI:2866508-2867598	0.619	8.63E-05
K10C8.3	Inc in glp-4/Skipping in gonad	chrV:12699057-12699903	0.608	1.05E-04
frm-4	Inc in glp-4/Skipping in gonad	chrI:5407130-5407627	0.607	1.05E-04
clp-1	Inc in glp-4/Skipping in gonad	chrIII:7985046-7985683	0.488	5.02E-03
Y57G11C.9	Inc in glp-4/Skipping in gonad	chrIV:14787144-14788067	0.467	9.06E-03
Y55F3AM.3	Inc in glp-4/Skipping in gonad	chrIV:1012907-1013427	0.448	1.57E-02
D1046.1	Inc in glp-4/Skipping in gonad	chrIV:8929129-8930297	0.4	4.95E-02
cas-1	Inc in glp-4/Skipping in gonad	chrX:16809381-16813570	0.382	7.60E-02
mca-3	Inc in glp-4/Skipping in gonad	chrIV:3105173-3116785	0.381	7.60E-02
T19A6.1	Inc in glp-4/Skipping in gonad	chrI:8380322-8388085	0.366	9.73E-02
ZK370.4	Inc in glp-4/Skipping in gonad	chrIII:8727790-8728761	0.364	6.24E-02
C06E7.1	Intron Inc in glp-4/Skipping in gonad	chrIV:5848641-5849740	0.366	6.03E-02
ret-1	Inc in glp-4/Skipping in gonad	chrV:14830144-14833693	0.462	7.04E-03
nuo-3	Skipping in glp-4/Inc in gonads	chrIV:14796924-14797411	0.504	2.49E-03
ZK632.10	Inc in glp-4/Skipping in gonad	chrIII:9826330-9827076	0.518	1.79E-03
nuo-3	Skipping in glp-4/Inc in gonads	chrIV:14796649-14797475	0.586	2.11E-04
gly-5	Inc in glp-4/Skipping in gonad	chrIII:13197489-13203874	0.685	5.78E-06
mes-3	Skipping in glp-4/Inc in gonad	chrI:4999572-5000352	0.724	1.82E-06
C06A6.4	Skipping in glp-4/Inc in gonads	chrIV:7827008-7827658	0.939	8.00E-11

Table S2 Tisue-specific adjacent 3' splice sites

Gene Name	Common Name	Determined By Method	Nucleotide Difference	Alternative 3' Splice Site Location	Proximal Splice Site Sequence	Distal Splice Site Sequence	Previously Annotated?	glp-4 Proximal Reads	Total glp-4 Reads Spanning Junction	glp-4 Proximal Read Percentage	N2 Gonad Proximal Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage	Delta PRP (glp-4 to N2 Gonad)	N2 Whole Proximal Reads	Total N2 Whole Reads Spanning Junction	N2 Whole Proximal Read Percentage	Delta PRP (glp-4 to N2 Whole)	Notes	Amino Acids (Gained/Lost)
B0261.2	let-363	Splicetrap	6nt	Coding	TTC AAA AAG	TTT CAG	Yes	1	28	4	17	17	100	96	79	101	78	75		IS
B0336.5	-	Splicetrap	9nt	Coding	AGT TCC CAG	AAG TTG CAG	Yes	0	39	0	22	24	92	92	150	231	65	65		KLQ
B0336.9	swp-1	Splicetrap	6nt	Coding	TCT TCA TAG	TTA CAG	Yes	0	34	0	13	26	50	50	93	190	49	49		LQ
B0348.6	ife-3	Splicetrap	3nt/9nt	Coding	GAA TCA TAG	AAG CTT CAG	Yes	0	27	0	35	70	50	50	200	362	55	55	Double Site	KLQ
C02E11.1	nra-4	Splicetrap	6nt	Coding	CGT CAA AAG	CTT CAG	Yes	1	82	1	15	22	68	67	26	69	38	36		LQ
C04A2.7	dnj-5	Splicetrap	6nt	Coding	CCA AAT CAG	TTT AAG	Yes	25	110	23	86	86	100	77	604	678	89	66		FK
C05C10.6	ufd-3	Splicetrap	6nt	Coding	TTA AAT TAG	TTC CAG	Yes	5	34	15	41	46	89	74	173	192	90	75		FQ
C07G2.2	atf-7	Splicetrap	9nt	Coding	TTT AAT TAG	GCT ATT CAG	Yes	75	150	50	21	21	100	50	247	329	75	25		AIQ
C10C5.6	daf-15	Splicetrap	18nt	Coding	TAT TAA AAG	TTG TCG AAA TGA TTC CAG	Yes	0	62	0	21	23	91	91	188	258	73	73		VVEMIP
C12C8.3	lin-41	Splicetrap	12nt	Coding	CTG TTT CAG	TTT TCT TTT CAG	Yes	0	16	0	69	100	69	69	236	369	64	64		VFFS
C24F3.1	tram-1	Splicetrap	6nt	Coding	CCC ACC TAG	TTT CAG	Yes	1	112	1	9	16	56	55	70	149	47	46		SF
C26E6.9	set-2	Splicetrap	9nt	Coding	CTG GAA AAG	CCT TCT CAG	Yes	1	13	8	13	16	81	74	104	129	81	73		PSQ
C27D6.4	crh-2	Splicetrap	10nt	Coding	GTT CGT AAG	T ATA TTT CAG	No	0	26	0	8	10	80	80	70	119	59	59		Frameshift
C28H8.9	dpff-1	Splicetrap	12nt	Coding	TTT TTG TAG	TTC GAT TTG CAG	Yes	1	55	2	21	41	51	49	95	273	35	33	Tandem Exons	VRFA
C36B1.8	gls-1	Splicetrap	9nt	Coding	GAA ATA AAG	CTA TTG CAG	Yes	6	25	24	18	18	100	76	221	250	88	64		LLQ
C37C3.2	-	Splicetrap	10nt	5' UTR	CAACATTAG	CAAATTCCAG	Yes	6	484	1	23	53	43	42	217	554	39	38		Noncoding
C39E9.14	dli-1	Splicetrap	6nt	Coding	TTG CAA AAG	TTT TAG	Yes	0	80	0	20	22	91	91	135	166	81	81		VL
C45B11.1	pak-2	Splicetrap	6nt	Coding	TAT TTT CAG	TTT CAG	Yes	1	35	3	34	62	55	52	53	106	50	47		SF
C47G2.5	saps-1	Splicetrap	6nt	Coding	TGT ATA AAG	TTT CAG	Yes	0	15	0	6	10	60	60	62	89	70	70		FQ
C48B4.4	ced-7	Splicetrap	6nt	Coding	TGT CTA AAG	TTT CAG	Yes	0	45	0	19	24	79	79	114	151	75	75		SV
F11A10.1	lex-1	Splicetrap	6nt	Coding	GAA TTT CAG	TTT CAG	Yes	11	53	21	73	90	81	60	435	597	73	52		VS
F13G3.7	-	Splicetrap	9nt	Coding	GTT CAT AAG	ATG TTA CAG	Yes	0	21	0	8	12	67	67	25	72	35	35		MLQ
F27C1.2	-	Splicetrap	12nt	Coding	CCG ACC TAG	TTT GCA CTT CAG	Yes	1	17	6	10	14	71	66	63	90	70	64		FALQ
F38A5.2	-	Splicetrap	6nt	Coding	TTT TTT TAG	TTT CAG	Yes	22	112	20	21	34	62	42	146	240	61	41		SV
F46F11.9	trpp-8	Splicetrap	6nt	Coding	TGC TAA AAG	ATT CAG	Yes	0	52	0	19	26	73	73	94	163	58	58		FR
F54E7.3	par-3	Splicetrap	9nt	Coding	ATC GAT TAG	CCC TTT CAG	Yes	1	21	5	32	51	63	58	130	225	58	53		PFS
F55B12.3	sel-10	Splicetrap	6nt	Coding	ACG TAC CAG	TTC CAG	Yes	3	64	5	64	76	84	80	256	336	76	72		SR
F56C9.10	-	Splicetrap	9nt	Coding	TTA ATT GAG	AAT GTG AAG	Yes	1	43	2	54	59	92	89	167	220	76	74	Tandem Exons	NVK
H06H21.6	ubxn-6	Splicetrap	5nt	5' UTR	CCAATTTAT	TTCAG	Yes	0	29	0	40	63	63	63	58	144	40	40	Gonad 3' Splice Site: AT	Noncoding
H14E04.2	-	Splicetrap	9nt	Coding	TTC TCC CAG	TTT TTT CAG	Yes	0	25	0	8	14	57	57	37	96	39	39		VFS
H19N07.2	math-33	Splicetrap	6nt	Coding	TTT TTA AAG	CTT CAG	Yes	10	288	3	35	57	61	58	392	803	49	45		LQ
K02A11.1	gfi-2	Splicetrap	12nt	Coding	CTG TGT AAG	TAT TAT TTC CAG	Yes	1	77	1	14	19	74	72	217	293	74	73		YYFQ
K02F2.1	dpf-3	Splicetrap	12nt	Coding	CGC GTT GAG	CAT GTC TTG CAG	Yes	0	68	0	14	27	52	52	152	322	47	47		MSCR
K03B4.3	taf-10	Splicetrap	9nt	Coding	GAT TTA AAG	TAT TTT CAG	Yes	0	37	0	15	19	79	79	367	431	85	85		YFQ
M01E5.3	-	Splicetrap	6nt	Coding	CTT CGA AAG	TTT CAG	Yes	1	93	1	16	23	70	68	172	293	59	58		VS
M03F8.3	phi-12	Splicetrap	9nt	Coding	CTT CGC TAG	TAC TTT CAG	Yes	1	53	2	34	38	89	88	181	234	77	75		YFQ
M106.4	gmps-1	Splicetrap	6nt	Coding	GTT GAA AAG	CTT CAG	Yes	1	32	3	17	29	59	55	129	177	73	70		AS
M110.5	dab-1	Splicetrap	6nt	Coding	TTA TAA AAG	TTC CAG	Yes	1	50	2	31	39	79	77	101	172	59	57	Tandem Exons	FQ
R02F2.1	-	Splicetrap	6nt	Coding	CTT CTC AAG	TTT CAG	Yes	15	236	6	36	58	62	56	485	780	62	56		NFR/K
R05D3.4	rfp-1	Splicetrap	9nt	Coding	CCG TGT GAG	AAT TTA CAG	Yes	0	13	0	21	24	88	88	111	153	73	73	Tandem Exons	NLQ
R06F6.8	-	Splicetrap	6nt	Coding	TTT AAA AAG	TTT CAG	Yes	0	18	0	12	14	86	86	53	78	68	68		FFR/L
R08C7.10	wapl-1	Splicetrap	6nt	Coding	TCC TAT TAG	CTT CAG	Yes	2	17	12	22	40	55	43	79	144	55	43		LQ
R107.5	-	Splicetrap	6nt	Coding	GAT TAT AAG	TTG CAG	Yes	3	40	8	30	42	71	64	246	339	73	65		ICR/M
R10D12.13	-	Splicetrap	6nt	Coding	TTT CAT CAG	TTT CAG	Yes	0	11	0	20	25	80	80	83	118	70	70		FQ
R13H8.1	daf-16	Splicetrap	6nt	Coding	CTT CGA AAG	TTT CAG	Yes	5	25	20	11	12	92	72	37	59	63	43		DFR/E
R144.4	wip-1	Splicetrap	6nt	Coding	TTC TGT CAG	TTT CAG	Yes	0	24	0	7	16	44	44	78	147	53	53		FQ
T01G9.2	-	Splicetrap	9nt	Coding	TTT CCA AAG	AAA TTC AAG	Yes	0	23	0	22	26	85	85	39	90	43	43		KFK
T04D1.3	unc-57	Splicetrap	6nt	Coding	TCT CTT CAG	TTT CAG	Yes	19	113	17	20	27	74	57	212	336	63	46		SF
T05F1.1	nra-2	Splicetrap	9nt	Coding	GGT TTG AAG	GGT TTT CAG	Yes	3	175	2	59	89	66	65	230	374	61	60	Tandem Exons	GFS
T10G3.5	eea-1	Splicetrap	6nt	Coding	TTT TGA TAG	TTT CAG	Yes	3	96	3	9	15	60	57	165	316	52	49		FQ
T19A6.3	spo-7	Splicetrap	6nt	Coding	ATA TTC TAG	TTA CAG	Yes	24	86	28	10	13	77	49	93	132	70	43		LQ
T24A11.1	mtm-3	Splicetrap	12nt	Coding	CAA AGT CAG	GAA TCG TTC CAG	Yes	0	13	0	24	35	69	69	126	155	81	81		ESFQ
W02B12.11	-	Splicetrap	7nt	Coding	ATT AAA TAG	T CTC CAG	No	0	27	0	8	15	53	53	75	110	68	68		Frameshift
W06A7.3	ret-1	Splicetrap	12nt	Coding	ATT AAT GAG	TTC GAT TTT CAG	Yes	1	396	0	35	52	67	67	266	687	39	38		SIFS
Y102E9.1	odr-4	Splicetrap	6nt	Coding	GTC AAA AAG	TTC TAG	Yes	0	83	0	14	19	74	74	54	102	53	53		FLD/Y
Y102E9.2	-	Splicetrap	9nt	Coding	CCG AAA TAG	TGT TCT CAG	Yes	2	52	4	27	39	69	65	186	436	43	39		CSQ
Y17G7B.2	ash-2	Splicetrap	6nt	Coding	CGC AAA AAG	TTT CAG	Yes	0	12	0	13	20	65	65	38	61	62	62		FSR/L
Y37A1B.2	lst-4	Splicetrap	6nt	Coding	GCT TGC TAG	CGT CAG	Yes	0	32	0	7	10	70	70	104	149	70	70		RQ
Y45F10A.6	tbc-9	Splicetrap	6nt	Coding	GTT TTG TAG	TTT CAG	Yes	2	19	11	21	30	70	59	49	69	71	60		FS
Y54E10A.9	vbh-1	Splicetrap	9nt	Coding	TAT TAG TAG	ACG TTA CAG	Yes	29	81	36	29	35	83	47	476	577	82	47		KRYS/N
Y65B4BR.4	wwp-1	Splicetrap	6nt	Coding	TTT TAA AAG	TTT CAG	Yes	1	255	0	21	54	39	38	236	559	42	42		FR
Y69A2AR.1	-	Splicetrap	9nt	Coding	TTT CTA AAG	CTT TTG AAG	Yes	3	166	2	75	84	89	87	892	1023	87	85		LLK
Y73B6BL.6	sqd-1	Splicetrap	9nt	Terminal Exon	TTC TAT CAG	GTT TTG CAG	Yes	12	154	8	29	32	91	83	185	295	63	55		SFAG/R
ZK546.1	zyg-12	Splicetrap	9nt	Coding	GCC GCC TAG	ACC TTT CAG	Yes	2	47	4	20	30	67	62	108	146	74	70		EPFS/D
ZK637.7	lin-9	Splicetrap	6nt	Coding	GTC TCC AAG	TTC CAG	Yes	0	43	0	7	10	70	70	304	459	66	66		FQ
B0261.2	let-363	smg-2 Gonad	9nt	Coding	GGT GTC CAG	TAA TTA TAG	Yes	0	33	0	13	13	100	100	50	82	61	61		VII
B0285.1	cdk-12	smg-2 Gonad	6nt	Coding	TGT TAA AAG	TTG CAG	No	0	22	0	22	24	92	92	96	132	73	73	Tandem Exons	FCR/L
B0334.11	ooc-3	smg-2 Gonad	6nt	Coding	ATT CAA TAG	TTT CAG	Yes	0	10	0	17	20	85	85	124	144	86	86		FQ
B0491.6	-	smg-2 Gonad	6nt	Coding	TAT TAT TAG	TTT CAG	Yes	0	77	0	6	11	55	55	73	224	33	33		LSD/H

Table S2 Tisue-specific adjacent 3' splice sites

Gene Name	Common Name	Determined By Method	Nucleotide Difference	Alternative 3' Splice Site Location	Proximal Splice Site Sequence	Distal Splice Site Sequence	Previously Annotated?	glp-4 Proximal Reads	Total glp-4 Reads Spanning Junction	glp-4 Proximal Read Percentage	N2 Gonad Proximal Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage	Delta PRP (glp-4 to N2 Gonad)	N2 Whole Proximal Reads	Total N2 Whole Reads Spanning Junction	N2 Whole Proximal Read Percentage	Delta PRP (glp-4 to N2 Whole)	Notes	Amino Acids (Gained/Lost)
C04D8.1	pac-1	smg-2 Gonad	8nt	Terminal Exon	GTT CAT AAG	TT TTC CAG	No	0	79	0	8	13	62	62	121	202	60	60		Frameshift
C09H6.1	spr-4	smg-2 Gonad	6nt	Coding	CCG CAA TAG	TTT CAG	Yes	6	157	4	23	33	70	66	268	396	68	64		FQ
C10C5.6	daf-15	smg-2 Gonad	9nt	Coding	AGC CAA AAG	GAG TTA CAG	No	0	39	0	32	59	54	54	78	192	41	41		SYR
C10C6.1	kin-4	smg-2 Gonad	9nt	Coding	TTT TCC AAG	TGT TTG CAG	Yes	0	13	0	15	27	56	56	32	77	42	42		SVC
C17G10.9	-	smg-2 Gonad	6nt	Coding	TTT TAA CAG	CTT CAG	Yes	96	294	33	72	88	82	49	462	542	85	53		SA
C18E9.10	-	smg-2 Gonad	6nt	Coding	TTA ATC AAG	TTT CAG	No	0	49	0	10	15	67	67	55	106	52	52		FR
C18F3.2	sax-7	smg-2 Gonad	9nt	Coding	CCT CAA AAG	CTG TTT CAG	Yes	1	158	1	13	23	57	56	283	470	60	60		AVS
C25A1.9	rsa-1	smg-2 Gonad	12nt	Coding	GCT TAA AAG	TCA TCA TTT CAG	Yes	1	27	4	50	54	93	89	682	765	89	85		SSFQ
C28H8.9	dpff-1	smg-2 Gonad	6nt	Coding	CCC TAA AAG	TTG CAG	No	2	108	2	24	39	62	60	339	530	64	62	Tandem Exons	RC
C29E4.3	ran-2	smg-2 Gonad	9nt	Coding	ATG AGA CAG	ACT TTA CAG	Yes	1	70	1	6	13	46	45	57	342	17	15		TLQ
C30H7.2	-	smg-2 Gonad	9nt	Coding	TTT CGT AAG	ACA TTT CAG	No	5	174	3	12	26	46	43	299	471	63	61		TFQ
C34G6.1	hpo-27	smg-2 Gonad	6nt	Coding	ACC ATC AAG	TCA CAG	No	0	15	0	13	18	72	72	24	35	69	69		SQ
C38C10.5	rgr-1	smg-2 Gonad	6nt	Coding	TTT TAA AAG	TTT CAG	No	0	15	0	12	15	80	80	68	87	78	78		FQ
C44H4.7	eor-2	smg-2 Gonad	6nt	Coding	GTG ATA AAG	TTT CAG	No	1	33	3	13	17	76	73	38	54	70	67		FQ
C46C2.1	wnk-1	smg-2 Gonad	6nt	Coding	GAT TCT TAG	TTT CAG	Yes	1	53	2	38	59	64	63	247	354	70	68		FQ
C50E10.4	sop-2	smg-2 Gonad	6nt	Coding	TTC TCA AAG	TTT CAG	Yes	1	52	2	7	12	58	56	58	95	61	59		FQ
C52E12.4	lst-6	smg-2 Gonad	6nt	Coding	TCG AAA AAG	CTT TAG	No	0	14	0	11	12	92	92	12	18	67	67		AL
C53A5.6	-	smg-2 Gonad	9nt	Coding	ATG TCA AAG	TTA TTA CAG	No	0	37	0	10	30	33	33	39	240	16	16		LLQ
C53B4.4	-	smg-2 Gonad	9nt	Coding	AAT TTT GAG	ACA TTT CAG	Yes	1	28	4	14	19	74	70	73	104	70	67		DIS
C53B4.4	-	smg-2 Gonad	7nt	Terminal Exon	TTC TAA AAG	T CTC CAG	Yes	2	73	3	12	16	75	72	218	285	76	74		Frameshift
C53B4.4	-	smg-2 Gonad	6nt	Coding	TCT GAT TAG	TTT CAG	Yes	2	25	8	29	31	94	86	99	119	83	75		FQ
E01G4.1	tbc-14	smg-2 Gonad	6nt	Coding	TTT CCA AAG	ATT CAG	No	0	58	0	14	31	45	45	33	71	46	46		DS
F10C5.2	-	smg-2 Gonad	6nt	Coding	TAT TTT AAG	TCG CAG	No	4	21	19	26	49	53	34	179	299	60	41		RR
F13G3.7	-	smg-2 Gonad	9nt	Coding	GTT CAT AAG	ATG TTA CAG	Yes	0	21	0	8	12	67	67	25	72	35	35		MLQ
F20H11.2	let-765	smg-2 Gonad	9nt	Coding	CGT TCC AAG	TCG TTT CAG	No	0	11	0	22	22	100	100	33	48	69	69		VVS
F22D3.1	ceh-38	smg-2 Gonad	6nt	Coding	TTT CCA AAG	TTT CAG	No	0	16	0	16	21	76	76	93	147	63	63		SF
F26H11.2	nurf-1	smg-2 Gonad	6nt	Coding	CAA AAA AAG	TTC CAG	Yes	0	41	0	4	11	36	36	49	110	45	45		FQ
F28F8.5	-	smg-2 Gonad	6nt	Coding	ATC TAA TAG	TTC CAG	Yes	2	21	10	9	11	82	72	37	54	69	59		VP
F31C3.2	-	smg-2 Gonad	9nt	Coding	AAA TTC AAG	ACG TTT CAG	Yes	2	16	13	16	20	80	68	116	140	83	70		DVS
F39H11.2	tlf-1	smg-2 Gonad	9nt	Coding	TTT CAA AAG	AAA TTG CAG	No	0	12	0	10	18	56	56	42	74	57	57		KLQ
F41H10.3	-	smg-2 Gonad	12nt	Coding	ATT TCC CAG	CCG AAC TTT CAG	No	0	41	0	29	38	76	76	200	425	47	47		SELSD/Y
F43G9.2	lmd-1	smg-2 Gonad	8nt	Coding	TTT CTA AAG	AT TTA CAG	Yes	1	140	1	18	40	45	44	117	449	26	25		Frameshift
F44B9.4	cit-1.1	smg-2 Gonad	6nt	Coding/5'UTR	CAA TTA AAG	TTT CAG	Yes	7	32	22	22	25	88	66	65	93	70	48		ISD/N
F46B6.3	smg-4	smg-2 Gonad	7nt	Terminal Exon	CTT TAA AAG	C TTT CAG	Yes	2	22	9	13	17	76	67	166	199	83	74		Frameshift
F53C3.13	-	smg-2 Gonad	6nt	Coding	CTG CCA AAG	TTT CAG	No	0	64	0	9	20	45	45	258	381	68	68		FQ
F53G12.5	mex-3	smg-2 Gonad	9nt	Coding	CTT GTT CAG	TTG TTC CAG	Yes	1	10	10	125	128	98	88	1220	1285	95	85		VVP
F54B3.1	-	smg-2 Gonad	6nt	Coding	TTG AAC TAG	TTA CAG	Yes	0	21	0	13	16	81	81	111	125	89	89		LQ
F54C4.3	attf-3	smg-2 Gonad	9nt	Coding	TTC CTT CAG	TTT TTC CAG	No	3	20	15	33	38	87	72	159	247	64	49		FFQ
F56C9.10	-	smg-2 Gonad	12nt	Coding	CGT GAT TAG	ATG GAA TTT CAG	No	0	84	0	28	73	38	38	133	398	33	33	Tandem Exons	MEFQ
F56D1.4	clr-1	smg-2 Gonad	6nt	Coding	ATG AAT TAG	CTT CAG	Yes	1	12	8	17	19	89	81	53	65	82	73		FFR/L
F57C2.6	spat-1	smg-2 Gonad	6nt	Coding	TCG AAA AAG	TTT CAG	Yes	0	20	0	27	36	75	75	213	316	67	67		NFR/K
F59E12.5	npl-4.2	smg-2 Gonad	6nt	Coding	TTC TCA TAG	TTT CAG	Yes	1	52	2	6	18	33	31	62	137	45	43		VS
H15N14.1	adr-1	smg-2 Gonad	6nt	Coding	ATT CTC AAG	CTC CAG	Yes	0	17	0	4	11	36	36	40	69	58	58	Tandem Exons	LQ
H37N21.1	hpo-11	smg-2 Gonad	6nt	Coding	GTT ATG AAG	TTT TAG	No	3	51	6	62	71	87	81	248	323	77	71		ILN/D
H42K12.1	pdk-1	smg-2 Gonad	6nt	Coding	CTT AGA AAG	TTT CAG	Yes	1	26	4	11	12	92	88	29	47	62	58		FR
K01G5.2	hpl-2	smg-2 Gonad	6nt	Coding	ATT CTT CAG	TTT CAG	Yes	2	34	6	7	16	44	38	95	146	65	59		FQ
K01G5.8	-	smg-2 Gonad	9nt	Coding	CGG TCC CAG	AGA TTC CAG	Yes	3	45	7	13	16	81	75	136	179	76	69		DSR
K02C4.3	-	smg-2 Gonad	6nt	Coding	TTT TTC AAG	GAA TTC CAG	No	47	169	28	117	127	92	64	778	887	88	60	Tandem Exons	NSR
K02C4.3	-	smg-2 Gonad	6nt	Coding	TCC TAA TAG	TTT CAG	No	0	10	0	18	23	78	78	112	130	86	86	Tandem Exons	FQ
K04B12.3	smg-8	smg-2 Gonad	6nt	Coding	CCT TCC AAG	CTT CAG	No	0	30	0	21	26	81	81	111	157	71	71		LQ
K04F10.3	-	smg-2 Gonad	6nt	Coding	CTT CAA AAG	TTA CAG	Yes	1	19	5	40	40	100	95	169	194	87	82		CYR/W
K07H8.2	-	smg-2 Gonad	12nt	Coding	CCG ATC CAG	TTT TCG TTT CAG	Yes	8	67	12	34	47	72	60	374	546	68	57		IFRFR/M
K12D12.2	npp-3	smg-2 Gonad	9nt	Coding	CTG TTT GAG	AGT TTA CAG	No	0	20	0	15	22	68	68	71	123	58	58		EFT
M03C11.3	-	smg-2 Gonad	8nt	Coding	CCA TAT CAG	AA TTG AAG	Yes	0	17	0	40	52	77	77	113	155	73	73		Frameshift
M110.5	dab-1	smg-2 Gonad	6nt	Coding	AAA AAC AAG	ATT CAG	Yes	14	447	3	77	96	80	77	826	1242	67	63	Tandem Exons	FR
M88.5	zbp-1	smg-2 Gonad	12nt	Coding	TTT GGG GAG	ATT ATC TTG CAG	No	2	54	4	9	27	33	30	41	245	17	13		DYLA
R05D11.9	-	smg-2 Gonad	6nt	Coding	CAT ATA AAG	TTG CAG	No	0	49	0	13	29	45	45	70	195	36	36		VA/E
R06F6.5	npp-19	smg-2 Gonad	9nt	Coding	TTA AAA AAG	ATT TTA CAG	Yes	3	116	3	60	68	88	86	875	993	88	86		ILQ
R10D12.14	sao-1	smg-2 Gonad	6nt	Coding	TCA CAC CAG	TTT CAG	Yes	12	187	6	48	62	77	71	773	1141	68	61		FQ
R11A5.2	nud-2	smg-2 Gonad	7nt	Terminal Exon	TTT ACA TAG	C TTT CAG	No	0	17	0	11	12	92	92	63	82	77	77		Frameshift
R11D1.1	-	smg-2 Gonad	9nt	Coding	TTA ATT AAG	CTG TTA CAG	Yes	6	20	30	26	26	100	70	94	106	89	59		LLQ
R13H4.4	hmp-1	smg-2 Gonad	9nt	Coding	GTT ATA AAG	AGT TTG CAG	Yes	1	95	1	17	26	65	64	163	278	59	58		VCR
T01D1.2	etr-1	smg-2 Gonad	9nt	Coding	CGA TAA AAG	TTT TTG CAG	Yes	4	30	13	7	12	58	45	55	74	74	61		VFA
T01G9.5	mei-1	smg-2 Gonad	9nt	Coding	ATC CTT AAG	ATA TTT CAG	Yes	0	22	0	24	37	65	65	192	326	59	59		RYF
T01H8.1	rskn-1	smg-2 Gonad	6nt	Terminal Exon/3' UTR	TCC ATA AAG	TTG CAG	Yes	1	27	4	28	38	74	70	178	381	47	43	Tandem Exons	CCR/Stop
T04D1.3	unc-57	smg-2 Gonad	6nt	Coding	TAT GTC CAG	TTT AAG	Yes	9	103	9	12	13	92	84	199	275	72	64		FK
T05F1.1	nra-2	smg-2 Gonad	9nt	Coding	GTT CGT AAG	ATA TTT CAG	Yes	3	383	1	30	31	97	96	370	519	71	71	Tandem Exons	KYFS/N
T05H10.5	ufd-2	smg-2 Gonad	12nt	Coding	GGC GAT TAG	TTC TTT TTT CAG	Yes	0	12	0	7	15	47	47	23	41	56	56		FFFQ
T08A11.1	-	smg-2 Gonad	6nt	Coding	TCC ATC TAG	CTT CAG	No	0	26	0	6	11	55	55	55	83	66	66	Tandem Exons	PSE/Q

Table S2 Tisue-specific adjacent 3' splice sites

Gene Name	Common Name	Determined By Method	Nucleotide Difference	Alternative 3' Splice Site Location	Proximal Splice Site Sequence	Distal Splice Site Sequence	Previously Annotated?	glp-4 Proximal Reads	Total glp-4 Reads Spanning Junction	glp-4 Proximal Read Percentage	N2 Gonad Proximal Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage	Delta PRP (glp-4 to N2 Gonad)	N2 Whole Proximal Reads	Total N2 Whole Reads Spanning Junction	N2 Whole Proximal Read Percentage	Delta PRP (glp-4 to N2 Whole)	Notes	Amino Acids (Gained/Lost)
T17E9.2	nmt-1	smg-2 Gonad	6nt	Coding	TAT AAG TAG	TTT AAG	Yes	0	23	0	20	29	69	69	49	84	58	58		FK
T24D1.1	sqv-5	smg-2 Gonad	6nt	Coding	TAT TGT CAG	TTT CAG	Yes	0	28	0	20	31	65	65	166	279	59	59		FQ
W03F11.6	afd-1	smg-2 Gonad	6nt	Coding	CCC AAC CAG	TTT CAG	No	1	46	2	14	26	54	52	34	81	42	40		SV
W04D2.6	-	smg-2 Gonad	6nt	Coding	TAT CAA AAG	TTT CAG	Yes	0	31	0	13	17	76	76	103	180	57	57		FQ
W08G11.3	-	smg-2 Gonad	6nt	Coding	TTT CAC AAG	TTC CAG	No	0	68	0	10	12	83	83	84	121	69	69		FQ
Y102A5A.1	cand-1	smg-2 Gonad	6nt	Coding	CAT TTC TAG	TTC CAG	No	1	62	2	53	82	65	63	152	224	68	66		FQ
Y105E8A.24	-	smg-2 Gonad	9nt	Coding	CCC TTA AAG	TAC TTT CAG	No	0	63	0	15	20	75	75	70	139	50	50		ILSE/K
Y113G7B.18	mdt-17	smg-2 Gonad	9nt	Coding	TCG TTC CAG	TAT TTC CAG	Yes	1	21	5	8	20	40	35	114	187	61	56		ISS
Y119C1B.8	bet-1	smg-2 Gonad	6nt	Coding	CTA ACC CAG	TTT CAG	No	1	28	4	9	10	90	86	50	77	65	61		ISG/S
Y17G7B.2	ash-2	smg-2 Gonad	9nt	Coding	ATT CTT AAG	AAC TTC CAG	No	1	27	4	8	14	57	53	122	168	73	69		TSR
Y37E3.17	-	smg-2 Gonad	9nt	Coding	CTC TGT AAG	TGA TTC CAG	No	0	560	0	20	57	35	35	50	422	12	12		DSS
Y39A1A.1	epg-6	smg-2 Gonad	6nt	Coding	AAA AAA AAG	TTC CAG	Yes	0	37	0	20	23	87	87	100	193	52	52		IPE/K
Y39A1A.5	rabx-5	smg-2 Gonad	9nt	Coding	AAA TAA AAG	TCA TTC CAG	No	0	63	0	11	27	41	41	227	470	48	48		RHS
Y39E4B.10	-	smg-2 Gonad	6nt	Coding	TCC CAT AAG	TTT CAG	No	0	12	0	10	15	67	67	62	107	58	58		LSA/P
Y44E3A.6	-	smg-2 Gonad	6nt	Coding	TTT TCC AAG	TTT CAG	Yes	10	42	24	11	13	85	61	88	116	76	52		DSV/D
Y48C3A.12	-	smg-2 Gonad	6nt	Coding	GCC GAA AAG	TTA CAG	No	0	35	0	9	21	43	43	69	170	41	41		SY
Y48G1C.7	-	smg-2 Gonad	15nt	Coding	CGC GTG TAG	GAT CCA TTT TTC CAG	No	7	19	37	16	24	67	30	149	209	71	34		DPFFQ
Y49G5B.1	-	smg-2 Gonad	6nt	Coding	CTC AAA AAG	TTT CAG	No	0	14	0	9	11	82	82	27	41	66	66		FS
Y50E8A.4	unc-61	smg-2 Gonad	12nt	Coding	GAT TCT AAG	CGT CGA TTG CAG	Yes	0	14	0	21	46	46	46	199	477	42	42		RRLQ
Y54E5B.3	let-49	smg-2 Gonad	6nt	Coding	TTT AAC AAG	ATT CAG	Yes	0	15	0	9	11	82	82	104	155	67	67		DS
Y54F10AM.4	ceh-44	smg-2 Gonad	6nt	Coding	CCC TTC AAG	TTT CAG	Yes	9	54	17	12	13	92	76	56	78	72	55		DFR/E
Y57A10A.18	pqn-87	smg-2 Gonad	9nt	Coding	GTC GAT AAG	GTC CTC CAG	Yes	7	133	5	16	27	59	54	174	284	61	56	Tandem Exons	GPP
Y57A10A.18	pqn-87	smg-2 Gonad	9nt	Coding	TTT TCC AAG	TAT CTT CAG	Yes	0	48	0	23	37	62	62	140	206	68	68	Tandem Exons	YLQ
Y59A8B.14	par-4	smg-2 Gonad	12nt	Coding	TCG TTT TTG	TCG GAA TTT CAG	Yes	2	23	9	27	26	104	95	203	218	93	84	Gonad 3' Splice Site: TG	SEFQ
Y61A9LA.8	sut-2	smg-2 Gonad	6nt	Coding	TTA TGA CAG	TTT CAG	No	0	28	0	9	14	64	64	52	110	47	47		DFS/D
Y62F5A.1	mdt-8	smg-2 Gonad	8nt	Terminal Exon	GTC CAT AAG	AA TTT CAG	Yes	0	16	0	8	12	67	67	90	163	55	55		Frameshift
Y65B4BR.5	icd-2	smg-2 Gonad	6nt	Coding	ATT GTA CGG	TTT AAG	Yes	5	2557	0	307	438	70	70	2949	4982	59	59	Gonad 3' splice site: GG	FK
Y67D8C.5	eel-1	smg-2 Gonad	9nt	Coding	TTC TTC AAG	CTT TTC CAG	No	0	56	0	10	16	63	63	116	203	57	57		FSR
Y67D8C.5	eel-1	smg-2 Gonad	6nt	Coding	GTT TCA TAG	TTT CAG	No	0	38	0	39	69	57	57	62	114	54	54		FQ
Y69H2.7	-	smg-2 Gonad	9nt	Coding	TCC CAA AAG	CTT CTC CAG	Yes	1	37	3	22	30	73	71	130	186	70	67		LLQ
Y71F9AL.12	-	smg-2 Gonad	9nt	Coding	ATT TGT CAG	ACT TTA CAG	No	1	13	8	12	25	48	40	53	114	46	39		TLQ
Y71F9AM.4	cogc-3	smg-2 Gonad	6nt	Coding	TTA AAC TAG	TTT CAG	Yes	3	61	5	17	17	100	95	105	137	77	72		FR
Y71G12B.12	atg-5	smg-2 Gonad	6nt	Coding	TTC GCC AAG	TTC CAG	Yes	7	149	5	19	24	79	74	199	277	72	67		IPD/N
Y81G3A.3	gcn-2	smg-2 Gonad	6nt	Coding	ATT AAT CAG	TTT CAG	No	0	13	0	19	24	79	79	36	43	84	84		FQ
Y97E10AR.6	-	smg-2 Gonad	6nt	Terminal Exon	TCA AAC TAG	TTA TAG	No	0	107	0	17	31	55	55	139	253	55	55		L-Stop
ZC434.6	aph-2	smg-2 Gonad	6nt	Coding	TTC CGC CAG	TTT CAG	Yes	0	109	0	12	17	71	71	133	428	31	31		FQ
ZK1290.4	nfi-1	smg-2 Gonad	9nt	Coding	CAA AAA AAG	TTT CTT CAG	No	0	16	0	6	18	33	33	42	85	49	49		FFS
ZK1307.6	fzr-1	smg-2 Gonad	6nt	Coding	ATT CTT AAG	CTT CAG	No	0	18	0	6	10	60	60	55	95	58	58		LQ
ZK328.1	cyk-3	smg-2 Gonad	9nt	Coding	TCC CAT AAG	ATT CTT CAG	Yes	1	35	3	7	11	64	61	26	104	25	22		DSS
ZK524.4	-	smg-2 Gonad	6nt	Coding	CTA AAA TAG	TTA CAG	No	2	11	18	12	25	48	30	26	78	33	15		RY/R
ZK632.7	panl-3	smg-2 Gonad	6nt	Coding	TCC AAA AAG	TTC CAG	No	1	88	1	24	28	86	85	190	274	69	68		FQ
ZK675.1	ptc-1	smg-2 Gonad	9nt	Coding	ATT TGT CAG	TCA TTT CAG	No	7	92	8	110	119	92	85	604	736	82	74		SFQ
ZK688.5	-	smg-2 Gonad	6nt	Coding	CCT CTC CAG	TTT CAG	Yes	0	38	0	13	20	65	65	73	138	53	53		VS
ZK688.8	gly-3	smg-2 Gonad	6nt	Coding	TTA AAT AAG	TTC CAG	No	3	59	5	14	11	127	122	56	92	61	56		FQ
ZK858.4	mel-26	smg-2 Gonad	12nt	Coding	TTT TTT GAG	TCG CTT TTA CAG	Yes	0	38	0	25	51	49	49	145	448	32	32		SLLQ
B0001.8	-	6nt Shift	6nt	Coding	GAA ATC AAG	TTT AAG	Yes	0	82	0	14	37	38	38	169	685	25	25		FK
C37A2.2	pqn-20	6nt Shift	6nt	Coding	ATT ATT TAG	TTG CAG	No	21	66	32	65	98	66	35	304	376	81	49		LQ
C49H3.5	ntl-4	6nt Shift	6nt	Coding	CAT TCG CAG	TTC TAG	No	4	637	1	6	17	35	35	202	604	33	33		HSR/Q
F13H10.3	-	6nt Shift	6nt	Coding	ATA TAC CAG	CTT CAG	Yes	0	68	0	8	26	31	31	15	131	11	11		LQ
F26F4.4	tag-340	6nt Shift	6nt	Coding	TTC AAA AAG	TTA CAG	No	4	174	2	18	32	56	54	279	532	52	50		YS
F26F4.7	nhl-2	6nt Shift	6nt	Coding	TCC AAA TAG	TTT CAG	No	0	10	0	11	18	61	61	104	185	56	56		SF
F36D4.3	-	6nt Shift	6nt	Coding	TTT TCA AAG	TTT CAG	Yes	0	30	0	11	26	42	42	41	157	26	26		FQ
F38A5.2	-	6nt Shift	6nt	Coding	TTT TTT TAG	TTT CAG	Yes	22	112	20	21	34	62	42	146	240	61	41		SV
F42H10.7	ess-2	6nt Shift	6nt	Coding	TTG GTA AAG	TTT CAG	Yes	2	25	8	20	40	50	42	73	221	33	25		FS
F44E2.7	-	6nt Shift	6nt	Coding	TTT ATA CAG	TTT CAG	Yes	4	18	22	10	10	100	78	165	185	89	67		SV
F52E1.13	lmd-3	6nt Shift	6nt	Coding	CTG GCA AAG	TTT CAG	No	0	76	0	11	26	42	42	49	175	28	28		FR
H05C05.1	-	6nt Shift	6nt	Coding	GTT GCC TAG	TTC CAG	No	2	42	5	10	14	71	67	114	160	71	66		FQ
H30A04.1	eat-20	6nt Shift	6nt	Coding	TTT AAA CAG	TTC CAG	Yes	4	94	4	12	22	55	50	7	32	22	18		VP
T19A6.3	spo-7	6nt Shift	6nt	Coding	TTT TCA CAG	TTT CAG	No	32	119	27	38	48	79	52	166	223	74	48		SV
W07A8.2	-	6nt Shift	6nt	Coding	GAT TTG TAG	TCT CAG	Yes	11	22	50	42	46	91	41	120	137	88	38		DLR/E
Y119C1B.8	bet-1	6nt Shift	6nt	Coding	ATA ATC TAG	CTT CAG	No	0	12	0	11	12	92	92	79	100	79	79		TSE/K
Y39E4B.10	-	6nt Shift	6nt	Coding	TCC CAT AAG	TTT CAG	No	0	12	0	10	15	67	67	62	107	58	58		LSA/P
Y44E3A.6	-	6nt Shift	6nt	Coding	GAA ATT CAG	TTC CAG	Yes	10	42	24	11	13	85	61	88	116	76	52		FPA/S
Y6B3A.1	agef-1	6nt Shift	6nt	Coding	TAA ACC AAG	TTA AAG	No	0	37	0	3	10	30	30	11	79	14	14		LK
ZK470.5	nck-1	6nt Shift	6nt	Coding	TTT TCA TAG	ATT CAG	Yes	51	118	43	10	13	77	34	95	120	79	36		IQ

Table S3 *smg-2* gonad introns (Adjacent 3' splice sites 18nt apart)

Genetic Location	Gene Name	# of nt Between Sites	smg-2 Gonad Prox Reads	Total smg-2 Gonad Reads Spanning Junction	smg-2 Gonad Proximal Read Percentage	N2 Gonad Prox Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage	
INTR00002933 at chrI:5018925-5018981	F54C1.7	2	77	79	97	113	117	97	
INTR00003862 at chrI:5825078-5826082	C32F10.8	2	8	19	42	6	29	21	
INTR00029880 at chrIV:2312907-2313789	Y38F2AL.3	2	47	64	73	54	54	100	
INTR00023023 at chrIII:5854162-5854209	F01F1.8	2	103	109	94	133	132	101	
INTR00004250 at chrI:6215990-6216063	T08B2.5	3	3	12	25	3	6	50	
INTR00006130 at chrI:8290422-8290474	T01G9.6	3	59	149	40	56	210	27	
INTR00008193 at chrI:10477953-10478006	F37D6.2	3	37	41	90	26	30	87	
INTR00043605 at chrV:15395735-15395789	T06E6.2	3	59	62	95	113	122	93	
INTR00049212 at chrX:9707178-9707298	F15G9.1	3	64	67	96	51	52	98	
INTR00014040 at chrII:6857588-6857639	C04A2.7	3	10	11	91	16	22	73	
INTR00033236 at chrIV:8891955-8892030	C27B7.1	3	25	92	27	27	88	31	
INTR00033963 at chrIV:9993319-9994700	C47E12.5	3	175	191	92	177	198	89	
INTR00022831 at chrIII:5602824-5602874	C05D2.6	3	15	16	94	15	15	100	
INTR00024005 at chrIII:6925517-6927094	F57B9.7	3	22	24	92	25	25	100	
INTR00024031 at chrIII:6937411-6938844	F57B9.4	3	4	14	29	0	7	0	
INTR00028168 at chrIII:12530156-12534639	Y111B2A.25	3	6	10	60	0	0	0	
INTR00028733 at chrIII:13623623-13623740	T12D8.6	3	99	100	99	135	134	101	
INTR00038300 at chrV:4371937-4371989	F32D1.9	4	45	46	98	107	107	100	
INTR00040542 at chrV:9346753-9346812	K07B1.7	4	46	47	98	13	12	108	
INTR00041414 at chrV:11000195-11000245	F53B7.3	4	64	62	103	75	72	104	
INTR00042469 at chrV:12952674-12952720	T16G1.10	4	4	15	27	0	2	0	
INTR00042979 at chrV:13962885-13962939	R10D12.13	4	150	149	101	27	28	96	
INTR00046976 at chrX:4835427-4835653	F39C12.1	4	9	10	90	7	7	100	
INTR00015405 at chrII:8564103-8564539	F54C9.2	4	25	27	93	12	12	100	
INTR00016668 at chrII:10391922-10391973	T09F3.2	4	13	15	87	19	20	95	
INTR00018670 at chrII:14223811-14225970	Y48B6A.13	4	11	13	85	7	7	100	
INTR00031222 at chrIV:5813766-5813818	C31H1.8	4	38	38	100	30	30	100	
INTR00031651 at chrIV:6636240-6636289	C01B10.8	4	49	52	94	53	52	102	
INTR00032955 at chrIV:8512342-8512528	C09G4.5	4	12	13	92	14	14	100	
INTR00021722 at chrIII:4585782-4585835	F35G12.5	4	17	18	94	9	9	100	
INTR00024825 at chrIII:7927425-7927477	C29E4.1	4	29	30	97	33	33	100	
INTR00026179 at chrIII:9491631-9492456	B0464.2	4	23	25	92	30	30	100	
INTR00027519 at chrIII:11287059-11287250	Y47D3A.2	4	13	14	93	1	1	100	
INTR00007880 at chrI:10091516-10093666	B0379.4	5	11	12	92	20	20	100	
INTR00002643 at chrI:4649744-4650249	B0041.5	5	1	45	2	1	35	3	
INTR00003946 at chrI:5936671-5936787	B0207.6	5	59	170	35	2	103	2	
INTR00038548 at chrV:5049735-5050141	K11D12.2	5	5	31	16	4	33	12	x
INTR00043100 at chrV:14183997-14184467	ZC376.5	5	36	37	97	21	21	100	
INTR00045341 at chrX:878915-878966	ZC13.1	5	9	11	82	18	17	106	
INTR00049420 at chrX:10056015-10056127	ZC373.1	5	7	14	50	2	2	100	
INTR00050712 at chrX:12877553-12877603	K02A4.1	5	59	62	95	79	81	98	
INTR00030233 at chrIV:3215227-3215678	M4.1	5	29	30	97	22	23	96	
INTR00030913 at chrIV:4809488-4809537	H06H21.6	5	23	49	47	40	63	63	x
INTR00032075 at chrIV:7393366-7394072	C48A7.2	5	42	44	95	61	62	98	
INTR00034897 at chrIV:11314841-11314892	B0035.3	5	15	20	75	8	8	100	
INTR00021666 at chrIII:4567751-4567798	F35G12.1	5	15	54	28	3	34	9	
INTR00021894 at chrIII:4758730-4758782	B0393.3	5	87	89	98	88	88	100	
INTR00024539 at chrIII:7499719-7499780	C07H6.4	5	19	36	53	7	33	21	
INTR00000339 at chrI:536310-536358	Y65B4BR.5	6	249	360	69	307	438	70	
INTR00000345 at chrI:539731-539803	Y65B4BR.4	6	23	51	45	21	54	39	
INTR00000473 at chrI:861922-864405	Y95B8A.7	6	3	14	21	1	9	11	
INTR00000767 at chrI:1710998-1712716	Y71G12B.12	6	16	26	62	19	24	79	
INTR00000987 at chrI:2164105-2164827	W03F11.6	6	11	24	46	14	26	54	
INTR00001065 at chrI:2316391-2316446	Y39G10AR.7	6	4	11	36	17	20	85	
INTR00001106 at chrI:2406600-2407822	Y39G10AR.2	6	23	24	96	20	23	87	
INTR00001359 at chrI:2943022-2943077	Y71F9AM.4	6	26	30	87	17	17	100	
INTR00001451 at chrI:3083228-3083957	M01B12.4	6	3	23	13	6	41	15	
INTR00001605 at chrI:3340601-3340648	Y44E3A.6	6	11	12	92	11	13	85	
INTR00001608 at chrI:3343625-3344573	Y44E3A.6	6	7	15	47	13	17	76	
INTR00002487 at chrI:4500924-4502570	T01A4.1	6	40	97	41	16	42	38	
INTR00002525 at chrI:4530005-4530060	Y119C1B.8	6	14	17	82	11	12	92	
INTR00002597 at chrI:4613018-4613279	C44E4.1	6	7	10	70	2	7	29	
INTR00002614 at chrI:4630177-4631501	Y41E3.460	6	24	26	92	26	34	76	
INTR00002673 at chrI:4676648-4677676	T04D1.3	6	8	10	80	20	27	74	
INTR00003028 at chrI:5126087-5126281	Y110A7A.17	6	6	15	40	2	32	6	
INTR00003186 at chrI:5252953-5253203	B0261.2	6	12	15	80	17	17	100	
INTR00003449 at chrI:5482653-5482699	C09D4.4	6	29	37	78	29	36	81	

Table S3 *smg-2* gonad introns (Adjacent 3' splice sites 18nt apart)

Genetic Location	Gene Name	# of nt Between Sites	smg-2 Gonad Prox Reads	Total smg-2 Gonad Reads Spanning Junction	smg-2 Gonad Proximal Read Percentage	N2 Gonad Prox Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage
INTR00003622 at chrI:5614688-5614737	F46F11.9	6	11	17	65	19	26	73
INTR00003813 at chrI:5795645-5795692	B0414.7	6	5	54	9	2	27	7
INTR00003932 at chrI:5908900-5909271	C34G6.1	6	8	16	50	9	18	50
INTR00004166 at chrI:6125596-6125652	T27A3.1	6	13	21	62	5	10	50
INTR00004357 at chrI:6358751-6358799	K04F10.3	6	28	31	90	40	40	100
INTR00004594 at chrI:6567678-6567832	F57B10.4	6	5	14	36	3	24	13
INTR00004613 at chrI:6584157-6584275	F57B10.1	6	3	10	30	6	6	100
INTR00004767 at chrI:6796768-6796873	C37A2.2	6	21	39	54	59	98	60
INTR00004972 at chrI:6953925-6954133	T10B11.8	6	18	37	49	15	26	58
INTR00005142 at chrI:7143235-7143284	H37N21.1	6	32	36	89	62	71	87
INTR00005353 at chrI:7350599-7350648	F07A5.1	6	34	59	58	63	90	70
INTR00005412 at chrI:7462571-7462623	ZK524.4	6	10	17	59	12	25	48
INTR00005746 at chrI:7775147-7775195	H15N14.1	6	5	15	33	4	11	36
INTR00005831 at chrI:7850052-7850520	F30F8.8	6	16	26	62	3	12	25
INTR00006017 at chrI:8052435-8052481	K04G2.8	6	17	21	81	19	24	79
INTR00006058 at chrI:8108253-8108726	C09H6.1	6	17	29	59	23	33	70
INTR00006176 at chrI:8324804-8324928	F52B5.5	6	4	19	21	4	9	44
INTR00006242 at chrI:8399196-8399251	T19A6.3	6	22	30	73	38	48	79
INTR00006245 at chrI:8399314-8399368	T19A6.3	6	8	11	73	10	13	77
INTR00006435 at chrI:8574333-8574425	T01H8.1	6	13	23	57	28	38	74
INTR00006437 at chrI:8574569-8574805	T01H8.1	6	7	48	15	13	55	24
INTR00006465 at chrI:8593643-8594035	R05D11.9	6	4	24	17	13	29	45
INTR00006975 at chrI:9013183-9013287	F36F2.3	6	2	22	9	9	26	35
INTR00007142 at chrI:9223073-9223431	C45G3.1	6	2	23	9	3	24	13
INTR00007627 at chrI:9743100-9743382	K02A11.1	6	36	38	95	28	27	104
INTR00007772 at chrI:9948202-9949082	T24D1.1	6	24	35	69	22	33	67
INTR00007794 at chrI:9966103-9966601	T23D8.1	6	7	36	19	5	29	17
INTR00008054 at chrI:10344502-10344559	ZC434.6	6	23	32	72	14	20	70
INTR00008187 at chrI:10476721-10476769	F37D6.2	6	27	30	90	28	30	93
INTR00009351 at chrI:12975309-12975393	C47B2.6	6	3	11	27	4	14	29
INTR00009462 at chrI:13282390-13282441	M01E5.3	6	15	23	65	16	23	70
INTR00009466 at chrI:13282682-13283761	M01E5.3	6	16	17	94	22	24	92
INTR00009641 at chrI:13605945-13606383	Y6B3A.1	6	1	16	6	1	7	14
INTR00010239 at chrI:14783418-14783757	F39B2.4	6	22	25	88	20	20	100
INTR00010286 at chrI:14820502-14820629	Y54E5B.3	6	6	10	60	11	13	85
INTR00037264 at chrV:7385-7432	B0348.6	6	35	67	52	35	70	50
INTR00037492 at chrV:912074-913073	H24K24.3	6	1	15	7	1	11	9
INTR00037543 at chrV:1048409-1048462	C02E11.1	6	13	18	72	15	22	68
INTR00038013 at chrV:3219261-3220715	K08D9.3	6	11	12	92	12	13	92
INTR00038360 at chrV:4571944-4572289	Y61A9LA.3	6	18	45	40	4	13	31
INTR00038382 at chrV:4606129-4606751	Y61A9LA.11	6	2	11	18	0	5	0
INTR00039938 at chrV:8012720-8012829	Y97E10AR.6	6	48	62	77	17	31	55
INTR00040133 at chrV:8429342-8429786	F52E1.13	6	8	24	33	11	26	42
INTR00040560 at chrV:9392544-9393150	F36D4.3	6	3	22	14	9	26	35
INTR00041426 at chrV:11038958-11039004	C45B11.1	6	14	32	44	34	62	55
INTR00041456 at chrV:11117822-11117868	H19N07.2	6	41	57	72	35	57	61
INTR00041602 at chrV:11506364-11506854	C55A6.10	6	17	30	57	5	9	56
INTR00042242 at chrV:12502210-12502546	W04D2.6	6	4	15	27	13	17	76
INTR00042641 at chrV:13314502-13314591	C50B6.3	6	29	43	67	23	40	58
INTR00042714 at chrV:13497027-13497073	T10G3.5	6	7	16	44	9	15	60
INTR00042917 at chrV:13819567-13819614	F55B12.3	6	42	46	91	64	76	84
INTR00042976 at chrV:13962706-13962754	R10D12.13	6	66	102	65	20	25	80
INTR00043126 at chrV:14196265-14196316	ZC376.7	6	8	17	47	5	7	71
INTR00043650 at chrV:15575043-15575312	F28F8.5	6	22	25	88	9	11	82
INTR00043818 at chrV:16370744-16370815	W08G11.3	6	14	16	88	10	12	83
INTR00043928 at chrV:16804375-16805044	Y102A5A.1	6	36	62	58	53	82	65
INTR00044833 at chrV:20722694-20722748	W07A8.2	6	25	33	76	42	46	91
INTR00045541 at chrX:1325667-1326074	H42K12.1	6	12	14	86	11	12	92
INTR00046645 at chrX:4246807-4246863	F48D6.4	6	10	18	56	35	44	80
INTR00011956 at chrII:3507605-3508470	Y49F6B.1	6	6	13	46	4	16	25
INTR00012108 at chrII:3926073-3926909	F53C3.13	6	7	15	47	9	20	45
INTR00013156 at chrII:5621764-5622380	C17G10.9	6	74	80	93	72	88	82
INTR00013160 at chrII:5624464-5624540	F59E12.5	6	4	10	40	6	18	33
INTR00013174 at chrII:5632926-5633021	F59E12.4	6	6	10	60	8	22	36
INTR00013995 at chrII:6783761-6783811	T13C2.6	6	39	125	31	60	201	30
INTR00014028 at chrII:6854082-6854131	C04A2.7	6	62	64	97	86	86	100
INTR00014141 at chrII:6953608-6953727	F22D3.1	6	7	21	33	16	21	76

Table S3 *smg-2* gonad introns (Adjacent 3' splice sites 18nt apart)

Genetic Location	Gene Name	# of nt Between Sites	smg-2 Gonad Prox Reads	Total smg-2 Gonad Reads Spanning Junction	smg-2 Gonad Proximal Read Percentage	N2 Gonad Prox Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage
INTR00015055 at chrII:8053580-8053690	T05H10.4	6	16	48	33	13	50	26
INTR00015081 at chrII:8081970-8082027	K02C4.3	6	11	12	92	18	23	78
INTR00015196 at chrII:8227409-8227490	M110.5	6	17	23	74	31	39	79
INTR00015199 at chrII:8228126-8228176	M110.5	6	56	73	77	77	96	80
INTR00016245 at chrII:9641127-9641210	ZK1307.6	6	6	11	55	6	10	60
INTR00016281 at chrII:9670969-9671177	ZK1320.12	6	9	13	69	27	30	90
INTR00016413 at chrII:9941242-9941294	C05C10.6	6	34	40	85	41	46	89
INTR00016608 at chrII:10266108-10266573	F54B3.1	6	22	25	88	13	16	81
INTR00016963 at chrII:10866526-10866649	M106.4	6	9	18	50	17	29	59
INTR00016966 at chrII:10868359-10868564	M106.4	6	6	17	35	12	19	63
INTR00017217 at chrII:11298133-11298179	C47G2.5	6	9	11	82	6	10	60
INTR00017266 at chrII:11347634-11347681	B0491.6	6	10	19	53	6	11	55
INTR00017366 at chrII:11495005-11495056	B0334.11	6	7	10	70	17	20	85
INTR00017520 at chrII:11667804-11667852	C47D12.1	6	12	13	92	22	25	88
INTR00017764 at chrII:11980636-11980686	Y17G7B.2	6	7	10	70	13	20	65
INTR00017992 at chrII:12342184-12342550	C50E10.4	6	6	12	50	7	12	58
INTR00018251 at chrII:13085553-13085611	Y81G3A.3	6	13	13	100	19	24	79
INTR00018359 at chrII:13376423-13377356	Y48C3A.12	6	7	21	33	6	21	29
INTR00018406 at chrII:13445159-13446296	E01G4.1	6	21	28	75	14	31	45
INTR00018824 at chrII:14442114-14442825	K04B12.3	6	17	22	77	21	26	81
INTR00018874 at chrII:14530373-14531050	F57C2.6	6	25	33	76	27	36	75
INTR00019105 at chrII:15220348-15222732	Y46E12BL.4	6	7	13	54	1	2	50
INTR00028933 at chrIV:194967-196845	Y38C1AA.2	6	22	23	96	6	7	86
INTR00029057 at chrIV:363874-363975	Y66H1B.2	6	10	21	48	11	28	39
INTR00029199 at chrIV:568891-569598	F56A11.5	6	6	26	23	8	33	24
INTR00029562 at chrIV:1415903-1417702	Y77E11A.7	6	5	44	11	3	31	10
INTR00030184 at chrIV:3048955-3049279	Y67D8C.5	6	43	66	65	39	69	57
INTR00030695 at chrIV:4445412-4445456	R08C7.10	6	21	38	55	22	40	55
INTR00031036 at chrIV:5363794-5363842	F41H10.6	6	7	63	11	10	72	14
INTR00031338 at chrIV:6118946-6118993	M03D4.1	6	23	35	66	18	25	72
INTR00031591 at chrIV:6585115-6585191	F38A5.2	6	7	14	50	21	34	62
INTR00032420 at chrIV:7795095-7795187	C33H5.15	6	9	19	47	7	17	41
INTR00032939 at chrIV:8503954-8504038	C28C12.10	6	1	11	9	3	12	25
INTR00033315 at chrIV:8981339-8981680	C53B4.4	6	10	16	63	29	31	94
INTR00033440 at chrIV:9203356-9203692	C46C2.1	6	26	37	70	38	59	64
INTR00033539 at chrIV:9340981-9341330	T20D3.7	6	9	55	16	6	54	11
INTR00034142 at chrIV:10220573-10220620	C24F3.1	6	6	10	60	9	16	56
INTR00034612 at chrIV:11014793-11014840	F13H10.3	6	5	13	38	8	26	31
INTR00034662 at chrIV:11057841-11059376	F36H1.4	6	12	25	48	10	21	48
INTR00035184 at chrIV:11656961-11657015	ZK809.5	6	6	15	40	7	22	32
INTR00035409 at chrIV:12080017-12080064	F11A10.1	6	42	54	78	73	90	81
INTR00035485 at chrIV:12139118-12139176	B0001.8	6	5	28	18	14	37	38
INTR00036035 at chrIV:13097793-13097842	C39E9.14	6	16	18	89	20	22	91
INTR00036317 at chrIV:13478078-13478125	Y45F10A.6	6	16	23	70	21	30	70
INTR00019355 at chrIII:473982-474445	F10C5.2	6	19	36	53	22	49	45
INTR00020299 at chrIII:2544635-2544829	Y54F10AM.4	6	13	15	87	12	13	92
INTR00021319 at chrIII:4250977-4251342	T08A11.1	6	8	17	47	4	7	57
INTR00021325 at chrIII:4253897-4257682	T08A11.1	6	12	16	75	6	11	55
INTR00021411 at chrIII:4315573-4316032	H38K22.2	6	7	46	15	18	64	28
INTR00021431 at chrIII:4334296-4336198	B0285.1	6	24	28	86	22	24	92
INTR00021943 at chrIII:4797172-4797538	C38D4.5	6	5	10	50	0	4	0
INTR00021960 at chrIII:4807107-4807647	C38D4.6	6	23	58	40	28	55	51
INTR00022044 at chrIII:4898494-4898798	F26F4.7	6	4	18	22	11	18	61
INTR00022051 at chrIII:4901435-4902017	F26F4.4	6	19	32	59	18	32	56
INTR00022266 at chrIII:5019499-5019807	R144.4	6	8	13	62	7	16	44
INTR00022573 at chrIII:5315729-5315773	F52C9.8	6	6	14	43	6	14	43
INTR00022605 at chrIII:5347079-5347457	Y32H12A.2	6	13	13	100	22	23	96
INTR00022630 at chrIII:5383554-5383908	Y32H12A.7	6	7	14	50	5	7	71
INTR00022749 at chrIII:5505161-5505211	R02F2.1	6	13	27	48	36	58	62
INTR00022920 at chrIII:5703061-5703107	B0336.9	6	11	27	41	13	26	50
INTR00023103 at chrIII:5905858-5905983	C28H8.9	6	39	52	75	24	39	62
INTR00023264 at chrIII:6116114-6116161	T17E9.2	6	13	18	72	20	29	69
INTR00023586 at chrIII:6449671-6449753	T26A5.6	6	5	10	50	7	9	78
INTR00023833 at chrIII:6733069-6733122	Y102E9.1	6	9	12	75	14	19	74
INTR00024291 at chrIII:7208513-7208739	R151.3	6	9	195	5	1	290	0
INTR00024778 at chrIII:7886193-7886352	ZK688.5	6	8	13	62	13	20	65
INTR00024800 at chrIII:7915071-7915844	ZK688.8	6	12	20	60	14	11	127

Table S3 *smg-2* gonad introns (Adjacent 3' splice sites 18nt apart)

Genetic Location	Gene Name	# of nt Between Sites	smg-2 Gonad Prox Reads	Total smg-2 Gonad Reads Spanning Junction	smg-2 Gonad Proximal Read Percentage	N2 Gonad Prox Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage
INTR00024910 at chrIII:8007932-8007990	F44B9.4	6	16	19	84	22	25	88
INTR00024984 at chrIII:8076453-8076569	K12H4.8	6	2	14	14	0	7	0
INTR00025349 at chrIII:8406026-8406290	ZK353.1	6	19	27	70	12	19	63
INTR00025410 at chrIII:8488727-8488853	F42H10.7	6	18	62	29	19	39	49
INTR00025716 at chrIII:8847311-8848073	F44E2.7	6	18	19	95	8	8	100
INTR00025762 at chrIII:8903520-8903565	ZK637.7	6	7	8	88	7	10	70
INTR00025896 at chrIII:9052282-9052331	R107.5	6	34	45	76	30	42	71
INTR00026313 at chrIII:9573544-9573595	C48B4.4	6	14	26	54	19	24	79
INTR00026511 at chrIII:9819845-9820063	ZK632.7	6	10	13	77	24	28	86
INTR00027088 at chrIII:10597009-10597928	Y39A1A.1	6	12	21	57	20	23	87
INTR00028303 at chrIII:12872906-12873831	Y37D8A.9	6	16	39	41	23	49	47
INTR00028383 at chrIII:13147456-13150066	Y39E4B.10	6	7	13	54	10	15	67
INTR00028533 at chrIII:13352285-13352501	F53A2.8	6	18	25	72	16	20	80
INTR00028631 at chrIII:13466798-13466846	T27E9.4	6	15	43	35	8	33	24
INTR00028780 at chrIII:13690996-13691495	ZK520.4	6	13	20	65	28	41	68
INTR00028818 at chrIII:13759122-13759170	K08E3.3	6	11	41	27	10	59	17
INTR00000251 at chrI:385229-386078	R119.6	7	7	16	44	3	11	27
INTR00002478 at chrI:4482423-4483442	T01A4.2	7	4	14	29	0	9	0
INTR00002742 at chrI:4772377-4772969	M04F3.4	7	3	20	15	1	22	5
INTR00003012 at chrI:5119690-5119739	Y110A7A.9	7	6	19	32	1	20	5
INTR00003828 at chrI:5801112-5801200	B0414.7	7	7	20	35	4	22	18
INTR00004458 at chrI:6462932-6463070	K06A5.4	7	2	13	15	0	11	0
INTR00005762 at chrI:7815078-7815248	D2005.4	7	14	16	88	10	13	77
INTR00005937 at chrI:7963818-7964335	T22C1.10	7	4	55	7	0	30	0
INTR00006254 at chrI:8408490-8409126	F02E9.2	7	25	114	22	21	74	28
INTR00008263 at chrI:10570207-10570252	F25H2.12	7	12	15	80	6	6	100
INTR00009233 at chrI:12780444-12781216	B0019.2	7	1	20	5	0	7	0
INTR00038587 at chrV:5117903-5118885	C04F5.9	7	11	14	79	1	4	25
INTR00039375 at chrV:6656205-6656337	T10H9.4	7	1	26	4	0	21	0
INTR00039439 at chrV:6785579-6785750	ZC404.3	7	17	18	94	24	27	89
INTR00041510 at chrV:11227430-11228253	T19B10.4	7	5	52	10	3	40	8
INTR00042584 at chrV:13163690-13164277	T09E8.1	7	5	29	17	0	27	0
INTR00045787 at chrX:2257695-2257752	AH9.2	7	2	36	6	0	22	0
INTR00048420 at chrX:7683648-7683714	F27D9.1	7	1	17	6	1	15	7
INTR00049160 at chrX:9563250-9563298	F49E2.1	7	5	13	38	3	28	11
INTR00051834 at chrX:15494419-15494474	H13N06.3	7	13	14	93	11	12	92
INTR00011211 at chrII:1307514-1307562	F56D12.1	7	4	23	17	0	10	0
INTR00014515 at chrII:7312907-7313032	F45E12.1	7	1	12	8	0	23	0
INTR00014563 at chrII:7396219-7396282	C07D10.2	7	15	79	19	7	69	10
INTR00014972 at chrII:7944412-7944719	ZK669.1	7	4	31	13	2	24	8
INTR00015973 at chrII:9177826-9177875	T23G7.5	7	18	80	23	10	68	15
INTR00016688 at chrII:10417229-10417288	E04D5.1	7	162	184	88	249	248	100
INTR00017326 at chrII:11465147-11465208	W02B12.8	7	2	13	15	1	10	10
INTR00017342 at chrII:11474134-11474190	W02B12.11	7	34	40	85	8	15	53
INTR00017436 at chrII:11576858-11576915	F54D5.1	7	16	28	57	0	11	0
INTR00017872 at chrII:12148059-12148398	Y57A10A.2	7	27	38	71	2	7	29
INTR00029229 at chrIV:655532-655579	K11H12.8	7	9	38	24	0	29	0
INTR00029995 at chrIV:2640677-2640740	Y69A2AR.30	7	5	14	36	2	16	13
INTR00031127 at chrIV:5537436-5537484	F35D6.1	7	12	25	48	2	20	10
INTR00031406 at chrIV:6324270-6324323	Y73B6BL.6	7	80	89	90	143	153	93
INTR00031856 at chrIV:7013988-7014050	C06G3.7	7	17	25	68	2	25	8
INTR00032555 at chrIV:7949942-7950660	F20D12.2	7	2	11	18	1	19	5
INTR00033325 at chrIV:8983829-8983934	C53B4.4	7	7	12	58	12	16	75
INTR00034418 at chrIV:10695547-10695708	R102.5	7	29	109	27	35	174	20
INTR00034999 at chrIV:11405527-11405843	H02I12.8	7	2	39	5	0	48	0
INTR00036202 at chrIV:13320360-13320589	Y67H2A.9	7	10	12	83	0	0	0
INTR00036634 at chrIV:14465088-14465154	LLC1.3	7	11	12	92	59	59	100
INTR00019344 at chrIII:469693-469803	Y55B1BR.4	7	10	18	56	0	3	0
INTR00020436 at chrIII:2786418-2786480	Y71H2AM.5	7	1	66	2	2	84	2
INTR00020813 at chrIII:3502045-3502118	M01F1.8	7	11	15	73	7	10	70
INTR00021077 at chrIII:3864544-3864593	C36A4.9	7	2	23	9	0	32	0
INTR00024378 at chrIII:7288798-7289063	B0361.8	7	81	82	99	76	76	100
INTR00025374 at chrIII:8431812-8431864	ZK1236.5	7	33	36	92	49	49	100
INTR00025403 at chrIII:8479250-8479308	F42H10.6	7	10	15	67	0	1	0
INTR00025697 at chrIII:8828036-8828103	F44E2.3	7	4	34	12	1	26	4
INTR00026355 at chrIII:9627918-9628116	F58A4.8	7	4	44	9	0	30	0
INTR00026803 at chrIII:10215800-10215860	T20G5.2	7	2	67	3	1	118	1

Table S3 *smg-2* gonad introns (Adjacent 3' splice sites 18nt apart)

Genetic Location	Gene Name	# of nt Between Sites	smg-2 Gonad Prox Reads	Total smg-2 Gonad Reads Spanning Junction	smg-2 Gonad Proximal Read Percentage	N2 Gonad Prox Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage
INTR00027264 at chrIII:10844374-10844434	R17.2	7	15	16	94	17	17	100
INTR00028245 at chrIII:12702246-12704702	Y111B2A.24	7	6	21	29	8	28	29
INTR00000636 at chrI:1377361-1379232	Y92H12BL.4	8	10	28	36	2	11	18
INTR00002981 at chrI:5106625-5106883	Y110A7A.11	8	4	39	10	0	20	0
INTR00003417 at chrI:5430709-5430775	F27C1.2	8	11	16	69	10	14	71
INTR00005268 at chrI:7258417-7258474	R06C7.9	8	18	33	55	37	45	82
INTR00006513 at chrI:8610301-8610349	F43G9.2	8	14	35	40	18	40	45
INTR00008049 at chrI:10342204-10342551	ZC434.6	8	2	11	18	0	3	0
INTR00008219 at chrI:10519507-10519894	F59C6.5	8	4	12	33	0	16	0
INTR00037719 at chrV:1879844-1880797	Y32G9A.8	8	10	25	40	2	27	7
INTR00038871 at chrV:5682270-5682552	F25B4.5	8	2	13	15	0	22	0
INTR00040211 at chrV:8569795-8569854	F25G6.9	8	12	15	80	35	37	95
INTR00041057 at chrV:10339860-10339915	K07C5.2	8	20	21	95	22	22	100
INTR00041285 at chrV:10792221-10792319	D1054.10	8	1528	1564	98	1359	1388	98
INTR00041395 at chrV:10966074-10966140	F17C11.9	8	11	246	4	2	257	1
INTR00042743 at chrV:13561162-13561210	C56A3.8	8	8	15	53	3	9	33
INTR00042986 at chrV:13964577-13964915	R10D12.13	8	41	57	72	48	62	77
INTR00049097 at chrX:9440788-9441072	B0272.2	8	1	23	4	0	21	0
INTR00011582 at chrII:2509861-2510495	F59H5.1	8	17	18	94	12	12	100
INTR00015229 at chrII:8276772-8276820	K01C8.7	8	23	42	55	0	14	0
INTR00017391 at chrII:11527279-11531359	Y62F5A.1	8	10	12	83	8	12	67
INTR00019069 at chrII:15068402-15069699	Y53F4B.18	8	3	19	16	0	13	0
INTR00028900 at chrIV:122551-123700	F29C4.7	8	7	19	37	3	7	43
INTR00031462 at chrIV:6415627-6415687	Y73B6BL.3	8	4	20	20	0	26	0
INTR00031644 at chrIV:6634503-6634613	C01B10.9	8	3	15	20	1	6	17
INTR00033406 at chrIV:9105253-9105350	C01F6.4	8	11	60	18	4	45	9
INTR00020551 at chrIII:3068458-3068571	H06I04.4	8	394	642	61	528	542	97
INTR00020910 at chrIII:3663517-3663587	C46F11.4	8	1	15	7	0	16	0
INTR00022702 at chrIII:5454502-5454941	F48E8.4	8	6	12	50	0	4	0
INTR00023591 at chrIII:6451709-6451762	T26A5.7	8	16	54	30	4	40	10
INTR00024335 at chrIII:7233477-7233696	T20H4.5	8	1	38	3	0	30	0
INTR00024544 at chrIII:7500351-7500408	C07H6.4	8	57	52	110	44	45	98
INTR00025437 at chrIII:8517639-8518124	C04D8.1	8	18	24	75	8	13	62
INTR00025609 at chrIII:8748316-8748519	ZK370.7	8	1	16	6	1	10	10
INTR00026936 at chrIII:10408176-10408257	M03C11.3	8	49	58	84	40	52	77
INTR00000020 at chrI:26682-26732	Y74C9A.4	9	14	36	39	26	37	70
INTR00000097 at chrI:129125-129175	F53G12.5	9	108	109	99	125	128	98
INTR00000224 at chrI:361588-363072	R119.1	9	28	42	67	9	12	75
INTR00000981 at chrI:2143093-2144879	Y37E3.17	9	7	50	14	20	57	35
INTR00001280 at chrI:2872755-2873115	Y71F9AL.12	9	10	24	42	12	25	48
INTR00001492 at chrI:3161695-3161739	Y54E10A.9	9	23	25	92	29	35	83
INTR00002618 at chrI:4631852-4632596	C44E4.2	9	19	37	51	24	34	71
INTR00003115 at chrI:5184770-5184829	F56A3.2	9	14	21	67	6	14	43
INTR00003391 at chrI:5417210-5417941	C30H7.2	9	7	21	33	12	26	46
INTR00003975 at chrI:5988764-5988832	C06A5.3	9	5	11	45	8	10	80
INTR00003992 at chrI:5998658-5998711	C06A5.7	9	10	18	56	24	30	80
INTR00004323 at chrI:6319345-6319452	F26B1.2	9	9	39	23	4	23	17
INTR00004744 at chrI:6782071-6782122	C37A2.4	9	12	15	80	14	16	88
INTR00004865 at chrI:6856760-6856816	T21G5.3	9	15	17	88	29	29	100
INTR00005061 at chrI:7057954-7057998	W01A8.1	9	22	135	16	42	179	23
INTR00005314 at chrI:7305155-7305203	F13G3.7	9	13	23	57	8	12	67
INTR00005744 at chrI:7775036-7775086	H15N14.1	9	5	12	42	1	9	11
INTR00006127 at chrI:8287988-8288040	T01G9.2	9	13	29	45	22	26	85
INTR00006142 at chrI:8296214-8296541	T01G9.5	9	10	22	45	24	37	65
INTR00006967 at chrI:9009930-9010058	F36F2.3	9	15	16	94	6	12	50
INTR00007215 at chrI:9290657-9291099	F26H9.2	9	2	25	8	0	32	0
INTR00007511 at chrI:9621275-9621325	T05F1.1	9	61	93	66	59	89	66
INTR00007512 at chrI:9621450-9621498	T05F1.1	9	26	35	74	30	31	97
INTR00007924 at chrI:10162475-10162529	C25A1.1	9	20	21	95	12	13	92
INTR00008565 at chrI:10941297-10941575	Y95D11A.3	9	15	21	71	12	17	71
INTR00010085 at chrI:14571766-14572705	Y105E8A.24	9	4	15	27	12	19	63
INTR00010138 at chrI:14648483-14650019	Y105E8B.4	9	1	31	3	0	41	0
INTR00010441 at chrI:15037995-15038048	F31C3.2	9	11	18	61	13	18	72
INTR00037345 at chrV:197345-198926	Y108G3AL.7	9	14	28	50	14	28	50
INTR00037752 at chrV:2062509-2063330	Y40B10A.8	9	21	24	88	18	18	100
INTR00038415 at chrV:4687175-4687225	K03B4.3	9	15	18	83	15	19	79
INTR00038970 at chrV:5941233-5941577	M03F8.3	9	51	60	85	34	38	89

Table S3 *smg-2* gonad introns (Adjacent 3' splice sites 18nt apart)

Genetic Location	Gene Name	# of nt Between Sites	smg-2 Gonad Prox Reads	Total smg-2 Gonad Reads Spanning Junction	smg-2 Gonad Proximal Read Percentage	N2 Gonad Prox Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage
INTR00041789 at chrV:11850859-11851608	R13H4.4	9	16	23	70	17	26	65
INTR00043027 at chrV:14035967-14036022	T08G5.5	9	8	26	31	6	25	24
INTR00043273 at chrV:14544375-14544474	C53A5.6	9	8	40	20	10	30	33
INTR00044308 at chrV:18693507-18695494	Y69H2.7	9	16	25	64	22	30	73
INTR00044567 at chrV:19900647-19901370	Y60A3A.13	9	34	46	74	19	19	100
INTR00044705 at chrV:20250381-20251695	Y113G7B.18	9	14	27	52	8	20	40
INTR00050233 at chrX:11546302-11546353	C35C5.3	9	18	29	62	26	33	79
INTR00010724 at chrII:167079-167903	T01D1.2	9	7	11	64	12	15	80
INTR00012526 at chrII:4793287-4793735	F26G1.1	9	5	21	24	3	19	16
INTR00012640 at chrII:4951534-4951586	ZK546.1	9	11	13	85	20	30	67
INTR00013229 at chrII:5669241-5669570	C25H3.17	9	2	13	15	0	8	0
INTR00013409 at chrII:5907034-5907084	F59G1.8	9	4	13	31	5	9	56
INTR00014469 at chrII:7292332-7292381	C30G12.6	9	12	14	86	15	16	94
INTR00014718 at chrII:7682006-7682059	F18A1.3	9	17	18	94	8	9	89
INTR00014923 at chrII:7893419-7893469	ZK675.1	9	76	117	65	110	119	92
INTR00015082 at chrII:8082362-8082672	K02C4.3	9	62	78	79	117	127	92
INTR00015802 at chrII:8969147-8969197	C18E9.3	9	5	14	36	9	14	64
INTR00015873 at chrII:9047743-9047796	T24B8.7	9	18	19	95	11	11	100
INTR00015878 at chrII:9048911-9048963	T24B8.7	9	16	22	73	14	22	64
INTR00016140 at chrII:9363075-9363141	C06C3.1	9	8	15	53	5	8	63
INTR00016895 at chrII:10796888-10796939	R06F6.5	9	62	62	100	60	68	88
INTR00017521 at chrII:11667990-11668048	C47D12.1	9	50	53	94	41	50	82
INTR00017529 at chrII:11673063-11673116	C47D12.1	9	9	13	69	9	14	64
INTR00017699 at chrII:11873516-11873669	K12D12.2	9	9	16	56	15	22	68
INTR00017766 at chrII:11982170-11982924	Y17G7B.2	9	6	10	60	8	14	57
INTR00017938 at chrII:12209746-12210727	Y57A10A.18	9	14	27	52	16	27	59
INTR00017940 at chrII:12211089-12211704	Y57A10A.18	9	17	31	55	23	37	62
INTR00018220 at chrII:13025141-13025358	Y38F1A.10	9	5	16	31	1	12	8
INTR00029401 at chrIV:1039173-1039714	Y55F3AM.11	9	1	15	7	0	1	0
INTR00029483 at chrIV:1217133-1218140	W09G12.9	9	4	12	33	2	14	14
INTR00029708 at chrIV:1873692-1875649	F55A8.2	9	5	35	14	3	30	10
INTR00029919 at chrIV:2381117-2381736	Y38F2AR.13	9	1	15	7	2	14	14
INTR00030012 at chrIV:2667247-2667361	Y69A2AR.1	9	55	65	85	75	84	89
INTR00030177 at chrIV:3040089-3040494	Y67D8C.5	9	10	20	50	10	16	63
INTR00030802 at chrIV:4708579-4709312	K08F11.3	9	8	53	15	7	65	11
INTR00031409 at chrIV:6325218-6325303	Y73B6BL.6	9	10	22	45	29	32	91
INTR00032625 at chrIV:8082618-8082670	C18F3.2	9	20	28	71	13	23	57
INTR00033129 at chrIV:8746805-8747756	F20C5.1	9	20	35	57	25	34	74
INTR00033323 at chrIV:8983628-8983682	C53B4.4	9	4	11	36	14	19	74
INTR00033447 at chrIV:9207977-9208062	C46C2.1	9	9	12	75	5	8	63
INTR00033588 at chrIV:9387118-9387242	C10C5.6	9	21	41	51	32	59	54
INTR00034105 at chrIV:10178076-10178127	K04D7.2	9	54	59	92	67	74	91
INTR00036129 at chrIV:13241162-13241212	JC8.6	9	17	20	85	19	23	83
INTR00036131 at chrIV:13241360-13241419	JC8.6	9	19	20	95	13	13	100
INTR00019158 at chrIII:84771-85767	F54C4.3	9	20	25	80	33	38	87
INTR00021586 at chrIII:4492728-4492777	C07G2.2	9	25	31	81	21	21	100
INTR00021705 at chrIII:4581330-4581380	F35G12.4	9	11	13	85	12	14	86
INTR00022089 at chrIII:4916539-4916707	F26F4.1	9	1	16	6	4	35	11
INTR00022398 at chrIII:5175429-5175590	K10D2.3	9	21	30	70	20	27	74
INTR00022691 at chrIII:5448070-5448121	F48E8.7	9	25	31	81	28	38	74
INTR00022875 at chrIII:5672646-5673078	F54E7.3	9	15	32	47	32	51	63
INTR00022901 at chrIII:5693166-5693214	B0336.5	9	9	10	90	22	24	92
INTR00023745 at chrIII:6598541-6598665	F20H11.2	9	12	15	80	22	22	100
INTR00023822 at chrIII:6726385-6726432	Y102E9.2	9	22	41	54	27	39	69
INTR00023955 at chrIII:6888514-6888830	K04C2.4	9	12	17	71	9	18	50
INTR00024424 at chrIII:7333350-7333534	F56C9.1	9	33	41	80	54	59	92
INTR00024849 at chrIII:7937061-7937118	C29E4.3	9	4	13	31	6	13	46
INTR00025280 at chrIII:8360516-8360652	R05D3.4	9	25	30	83	21	24	88
INTR00025417 at chrIII:8496159-8496969	F42H10.9	9	4	13	31	4	9	44
INTR00025839 at chrIII:8981025-8981175	R08D7.6	9	17	18	94	8	11	73
INTR00026391 at chrIII:9707100-9707158	C07A9.3	9	13	46	28	15	48	31
INTR00027187 at chrIII:10740480-10740526	K01G5.8	9	10	12	83	13	16	81
INTR00027994 at chrIII:12245973-12247981	Y75B8A.22	9	54	56	96	44	45	98
INTR00027993 at chrIII:12245982-12247981	Y75B8A.22	9	5	57	9	7	52	13
INTR00028396 at chrIII:13166123-13167279	Y39E4B.2	9	4	95	4	0	99	0
INTR00028722 at chrIII:13614887-13615350	T12D8.8	9	2	30	7	2	21	10
INTR00000783 at chrI:1751861-1752614	Y71G12B.10	10	10	11	91	5	5	100

Table S3 *smg-2* gonad introns (Adjacent 3' splice sites 18nt apart)

Genetic Location	Gene Name	# of nt Between Sites	smg-2 Gonad Prox Reads	Total smg-2 Gonad Reads Spanning Junction	smg-2 Gonad Proximal Read Percentage	N2 Gonad Prox Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage
INTR00001880 at chrI:3703782-3703997	F21A9.3	10	8	43	19	1	1	100
INTR00005676 at chrI:7685158-7691215	T23G11.5	10	7	49	14	8	42	19
INTR00039869 at chrV:7855880-7855934	C37C3.2	10	54	125	43	23	53	43
INTR00042097 at chrV:12271158-12271238	F55C5.5	10	31	83	37	1	67	1
INTR00048323 at chrX:7494391-7494486	F48E3.4	10	473	477	99	396	394	101
INTR00048443 at chrX:7769270-7769486	?	10	5	32	16	1	2	50
INTR00010909 at chrII:463380-464019	W10D9.4	10	5	20	25	0	29	0
INTR00017394 at chrII:11534147-11534206	Y62F5A.12	10	6	19	32	0	15	0
INTR00017595 at chrII:11729466-11729522	F13D12.4	10	2	17	12	0	54	0
INTR00019115 at chrII:15233467-15234511	Y46E12BL.2	10	1	10	10	0	7	0
INTR00031987 at chrIV:7143830-7143898	C34D4.14	10	1	32	3	1	50	2
INTR00033300 at chrIV:8960503-8960719	D1046.5	10	7	35	20	3	6	50
INTR00034223 at chrIV:10359172-10359469	R11A8.2	10	2	60	3	0	50	0
INTR00034362 at chrIV:10560334-10560413	T07G12.11	10	1	18	6	0	12	0
INTR00035963 at chrIV:12855649-12855711	ZK896.9	10	14	15	93	13	12	108
INTR00036125 at chrIV:13240357-13240491	JC8.3	10	485	479	101	341	340	100
INTR00003240 at chrI:5283628-5283707	C01G8.4	11	1	18	6	0	9	0
INTR00006959 at chrI:9006295-9006383	F36F2.6	11	3	27	11	0	43	0
INTR00038237 at chrV:4168028-4168794	Y45G5AM.7	11	24	28	86	26	26	100
INTR00041003 at chrV:10249031-10249825	C12D8.1	11	2	31	6	0	27	0
INTR00042381 at chrV:12765609-12765843	F18E2.3	11	4	46	9	2	66	3
INTR00043657 at chrV:15578132-15578193	F28F8.9	11	9	18	50	1	7	14
INTR00043857 at chrV:16539016-16539075	Y32B12B.2	11	23	23	100	29	31	94
INTR00012801 at chrII:5187379-5187451	C27D6.4	11	5	27	19	4	33	12
INTR00020188 at chrIII:2376412-2376502	H14E04.2	11	9	18	50	8	14	57
INTR00020974 at chrIII:3726314-3726365	C14B1.9	11	36	58	62	43	51	84
INTR00023804 at chrIII:6721724-6721789	F37A4.9	11	1	16	6	0	14	0
INTR00028621 at chrIII:13463608-13463671	T27E9.1	11	475	472	101	631	623	101
INTR00002276 at chrI:4214821-4214873	C18E3.9	12	1	11	9	2	32	6
INTR00004820 at chrI:6838960-6839014	K02F2.1	12	15	33	45	14	27	52
INTR00006288 at chrI:8427414-8427470	F02E9.10	12	23	26	88	35	39	90
INTR00006793 at chrI:8807363-8807413	F36A2.1	12	10	16	63	13	19	68
INTR00007075 at chrI:9134431-9134978	ZK858.4	12	11	53	21	24	51	47
INTR00007259 at chrI:9338796-9338846	C12C8.3	12	53	83	64	69	100	69
INTR00007625 at chrI:9742915-9742969	K02A11.1	12	12	16	75	14	19	74
INTR00007860 at chrI:10080557-10080609	B0379.3	12	5	30	17	7	35	20
INTR00007962 at chrI:10187207-10187260	C25A1.9	12	32	34	94	52	55	95
INTR00039399 at chrV:6706424-6706483	W02F12.4	12	1	16	6	2	27	7
INTR00039934 at chrV:8010795-8010902	Y97E10AR.7	12	8	51	16	5	35	14
INTR00042709 at chrV:13493686-13494705	T10G3.5	12	2	33	6	0	48	0
INTR00043376 at chrV:14731697-14731752	Y50E8A.4	12	19	46	41	21	46	46
INTR00043420 at chrV:14830089-14830144	W06A7.3	12	17	29	59	35	52	67
INTR00044167 at chrV:18101610-18101674	Y59A8B.14	12	40	41	98	27	26	104
INTR00014120 at chrII:6942715-6944674	F22D3.2	12	8	15	53	3	13	23
INTR00015062 at chrII:8062739-8062792	T05H10.5	12	3	13	23	2	15	13
INTR00031058 at chrIV:5372557-5372674	F41H10.3	12	28	41	68	29	38	76
INTR00032194 at chrIV:7547637-7547732	F49E8.3	12	2	17	12	6	32	19
INTR00032769 at chrIV:8291818-8292758	K07H8.2	12	27	54	50	34	47	72
INTR00036309 at chrIV:13455695-13455763	Y38H8A.7	12	1	21	5	1	12	8
INTR00036664 at chrIV:14657155-14657221	Y57G11C.33	12	11	12	92	8	10	80
INTR00021009 at chrIII:3799843-3799896	T24A11.1	12	21	31	68	24	35	69
INTR00021639 at chrIII:4554325-4554544	M88.5	12	11	30	37	9	27	33
INTR00023100 at chrIII:5905554-5905603	C28H8.9	12	15	49	31	21	41	51
INTR00024422 at chrIII:7332751-7332866	F56C9.1	12	9	35	26	28	73	38
INTR00024605 at chrIII:7585654-7586031	R13A5.1	12	9	18	50	15	20	75
INTR00025888 at chrIII:9047642-9047752	R107.4	12	1	19	5	5	34	15
INTR00000950 at chrI:2080903-2081114	Y37E3.11	13	1	28	4	1	34	3
INTR00004206 at chrI:6185688-6185747	T09B4.1	13	112	114	98	97	96	101
INTR00007310 at chrI:9392601-9392840	F16A11.2	13	13	15	87	14	14	100
INTR00008095 at chrI:10381176-10381718	F45H11.5	13	1	19	5	0	24	0
INTR00010638 at chrII:52139-52214	C23H3.4	13	1	39	3	0	39	0
INTR00014048 at chrII:6872069-6872349	C44B7.5	13	3	915	0	0	792	0
INTR00035954 at chrIV:12839145-12839901	M02B1.3	13	6	30	20	16	60	27
INTR00023407 at chrIII:6247523-6247585	T12A2.8	13	9	10	90	32	33	97
INTR00023923 at chrIII:6867446-6867511	R13F6.10	13	35	36	97	64	64	100
INTR00028046 at chrIII:12351705-12351785	Y75B8A.31	13	29	42	69	29	29	100
INTR00001750 at chrI:3548868-3549601	Y47G6A.4	14	3	12	25	0	18	0

Table S3 *smg-2* gonad introns (Adjacent 3' splice sites 18nt apart)

Genetic Location	Gene Name	# of nt Between Sites	smg-2 Gonad Prox Reads	Total smg-2 Gonad Reads Spanning Junction	smg-2 Gonad Proximal Read Percentage	N2 Gonad Prox Reads	Total N2 Gonad Reads Spanning Junction	N2 Gonad Proximal Read Percentage
INTR00046646 at chrX:4246813-4246863	F48D6.4	14	10	18	56	35	44	80
INTR00036728 at chrIV:14825997-14826151	Y57G11C.16	14	1	277	0	0	389	0
INTR00000073 at chrI:100324-100394	Y48G1C.7	15	16	23	70	16	24	67
INTR00000095 at chrI:128897-128958	F53G12.5	15	88	90	98	99	100	99
INTR00004764 at chrI:6795908-6796023	C37A2.2	15	12	16	75	16	20	80
INTR00044286 at chrV:18660931-18661052	Y69H2.19	15	62	75	83	101	120	84
INTR00019298 at chrIII:346868-347037	W07B3.2	15	1	17	6	1	15	7
INTR00005293 at chrI:7282575-7282633	F21C3.4	16	20	21	95	26	26	100
INTR00044515 at chrV:19676199-19677182	Y43F8C.12	16	25	26	96	24	24	100
INTR00022929 at chrIII:5705277-5705361	B0336.9	16	2	12	17	1	7	14
INTR00027799 at chrIII:11843433-11844748	Y56A3A.1	16	1	17	6	0	19	0
INTR00027938 at chrIII:12057098-12057877	Y79H2A.6	16	1	14	7	0	20	0
INTR00027385 at chrIII:11071979-11072047	W09D6.1	17	11	18	61	3	4	75
INTR00048521 at chrX:7911886-7911974	C39D10.7	18	546	541	101	500	500	100
INTR00033599 at chrIV:9391204-9391263	C10C5.6	18	12	16	75	21	23	91
INTR00006490 at chrI:8602828-8602893	R05D11.8	19	41	43	95	61	63	97
INTR00034058 at chrIV:10142663-10142727	K08F4.7	19	31	33	94	19	19	100
INTR00020727 at chrIII:3411076-3416786	F59A2.6	19	1	12	8	0	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
No Expression In Any Tissue														
attgttagttacag	chrX:17714641-17714744	6R55.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
aaactgagtttcag	chrV:10313242-10313389	B0024.6	gcy-6	0	0	0%	0	0	0%	0	0	0%	0	0
aaaaatagttacag	chrII:5968098-5968157	B0034.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
aagttcagttacag	chrV:3975615-3975704	B0213.8	str-82	0	0	0%	0	0	0%	0	0	0%	0	0
ctcctgagtttcag	chrV:3975737-3976064	B0213.8	str-82	0	0	0%	0	0	0%	0	0	0%	0	0
tatgtaagtttcag	chrV:9135631-9135695	B0222.2	pitr-2	0	0	0%	0	0	0%	0	0	0%	0	0
gctaaaagtttcag	chrIII:4372543-4372791	B0285.10	ckb-3	0	0	0%	0	0	0%	0	0	0%	0	0
ggaacaagtttcag	chrII:4542747-4542958	B0304.7	sra-34	0	0	0%	0	0	0%	0	0	0%	0	0
ctcataagttacag	chrV:15603459-15604155	B0391.6	fbxa-154	0	0	0%	0	0	0%	0	0	0%	0	0
tcggcaagctccag	chrII:3052099-3052228	B0454.2	sri-31	0	0	0%	0	0	0%	0	0	0%	0	0
aattggaggtttag	chrII:3048873-3049016	B0454.3	sri-28	0	0	0%	0	0	0%	0	0	0%	0	0
tacttgagcttcag	chrIV:7448845-7449153	B0496.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
tgaaaaagtttcag	chrV:5976688-5976868	C10F3.3	acy-2	0	0	0%	0	0	0%	0	0	0%	0	0
aaactaagtttcag	chrI:6306060-6306204	C10G11.10	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttctgagtttcag	chrIV:6161145-6161316	C11D2.6	unc-77	0	0	0%	0	0	0%	0	0	0%	0	0
ttccaaagctttag	chrV:7272290-7272752	C13A2.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttttgagttttag	chrV:4978756-4978975	C13D9.4	srsx-11	0	0	0%	0	0	0%	0	0	0%	0	0
aaaatcagttacag	chrV:564500-564939	C14C6.10	-	0	0	0%	0	0	0%	0	0	0%	0	0
tgtataaggttcag	chrV:545247-545360	C14C6.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
aacaaaagcttcag	chrX:10249335-10249424	C14H10.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
agtagtagtttaag	chrX:6502851-6502991	C15B12.7	cdf-1	0	0	0%	0	0	0%	0	0	0%	0	0
atatggagatcaag	chrII:4224654-4224892	C16A11.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
tattcaagttttag	chrII:3841018-3841265	C17A2.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttccgtagttttag	chrI:11617821-11618083	C17D12.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttcttaagattcag	chrII:5602430-5602525	C17G10.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
tctgcgagtttcag	chrI:13121228-13121390	C17H1.9	-	0	0	0%	0	0	0%	0	0	0%	0	0
atatacagtttcag	chrV:7491856-7491999	C18B10.2	srbc-10	0	0	0%	0	0	0%	0	0	0%	0	0
aatcaaagatttag	chrV:7489299-7489418	C18B10.3	srbc-9	0	0	0%	0	0	0%	0	0	0%	0	0
gaaacaagtttcag	chrV:2738757-2738891	C24B9.11	-	0	0	0%	0	0	0%	0	0	0%	0	0
aatgcaagtttcag	chrIV:10210221-10210412	C24F3.5	abt-1	0	0	0%	0	0	0%	0	0	0%	0	0
aaattaaggttcag	chrV:19423586-19424358	C25F9.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
gttcacagcttcag	chrIII:4451716-4451779	C28A5.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
aaaaaaagattcag	chrIV:17359410-17359545	C30H6.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
gctaatagttttag	chrV:16315790-16316166	C31A11.9	str-214	0	0	0%	0	0	0%	0	0	0%	0	0
aaaactagattcag	chrII:13658952-13659068	C31C9.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttttaagtttaag	chrV:10646495-10646822	C32C4.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
aatttcagtgccag	chrX:3056595-3056674	C33D12.6	tag-312	0	0	0%	0	0	0%	0	0	0%	0	0
actccaagttcaag	chrIV:7799344-7799570	C33H5.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
gcattaagtttcag	chrII:8709001-8709133	C34C6.1	srg-15	0	0	0%	0	0	0%	0	0	0%	0	0
ctcaaaagtttcag	chrIV:4077664-4077831	C35B1.8	-	0	0	0%	0	0	0%	0	0	0%	0	0
aatgagagtttcag	chrIII:4810276-4810345	C38D4.7	-	0	0	0%	0	0	0%	0	0	0%	0	0
taacatagtttcag	chrV:17555821-17556027	C38D9.7	fbxa-174	0	0	0%	0	0	0%	0	0	0%	0	0
aaagtgagtttcag	chrV:17549792-17549884	C38D9.9	fbxa-176	0	0	0%	0	0	0%	0	0	0%	0	0
cataatagttacag	chrIII:2244153-2244355	C39B5.11	srd-67	0	0	0%	0	0	0%	0	0	0%	0	0
attacaagtttcag	chrV:1261801-1262310	C39F7.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttatcagtttcag	chrII:8109005-8109108	C41C4.3	lron-4	0	0	0%	0	0	0%	0	0	0%	0	0
gtgaagagtttcag	chrV:15212356-15212550	C41G6.11	sri-24	0	0	0%	0	0	0%	0	0	0%	0	0
cgtaccagtttcag	chrIV:12260723-12260890	C42C1.1	sre-14	0	0	0%	0	0	0%	0	0	0%	0	0
ttccaaagttttag	chrIV:12266801-12266857	C42C1.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
gtattcagtttcag	chrIV:12270104-12270283	C42C1.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
tatcaaagctttag	chrX:11697279-11697355	C44C10.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
tagtgaagtttcag	chrV:2977359-2977594	C44C3.1	srw-124	0	0	0%	0	0	0%	0	0	0%	0	0
atttcaagtttcag	chrV:2962322-2962928	C44C3.3	srw-138	0	0	0%	0	0	0%	0	0	0%	0	0
tatacaagtttcag	chrIV:894451-894586	C44C8.10	fbxc-9	0	0	0%	0	0	0%	0	0	0%	0	0
tttaaaagttgtag	chrV:2147357-2147594	C45H4.11	srbc-20	0	0	0%	0	0	0%	0	0	0%	0	0
ccgatgagtttcag	chrV:2180600-2180900	C45H4.2	cyp-33C1	0	0	0%	0	0	0%	0	0	0%	0	0
ctgggtagtttcag	chrV:2170222-2170329	C45H4.6	srbc-18	0	0	0%	0	0	0%	0	0	0%	0	0
aaaataagttgcag	chrI:12315343-12315447	C47F8.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
actttaagctttag	chrI:12320367-12320508	C47F8.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
attaaaagttaaag	chrIII:9597647-9598179	C48B4.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
gttcgcagttttag	chrX:13362345-13362412	C49F8.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
ccaaaaagttccag	chrV:4048803-4049121	C49G7.2	srh-169	0	0	0%	0	0	0%	0	0	0%	0	0
ataatcagtttcag	chrV:13341885-13341953	C50B6.11	lgc-48	0	0	0%	0	0	0%	0	0	0%	0	0
aagaaaagttgaag	chrV:7616921-7616977	C50E3.15	-	0	0	0%	0	0	0%	0	0	0%	0	0
catataagcttcag	chrV:3061132-3061572	C50H11.10	srt-15	0	0	0%	0	0	0%	0	0	0%	0	0
ctaatcagtttcag	chrV:3057698-3057774	C50H11.9	str-244	0	0	0%	0	0	0%	0	0	0%	0	0
atctgaagtttcag	chrV:9906866-9907043	C50H2.2	egl-47	0	0	0%	0	0	0%	0	0	0%	0	0
cgtatcagtttcag	chrV:10159097-10159235	C51E3.5	srsx-30	0	0	0%	0	0	0%	0	0	0%	0	0
cagaaaagttttag	chrIV:8970240-8970347	C53B4.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
gttatgagtttcag	chrX:13048569-13048677	C53C7.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttcaaagtctcag	chrI:12447874-12448306	C54C8.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
tagataagcttcag	chrV:18815096-18815256	C54E10.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
aaaaggagcttcag	chrI:1006014-1006324	C54G6.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
tagctaagatttag	chrV:15622040-15622268	C55A1.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
cccttaagttctag	chrV:15635863-15636039	C55A1.14	srz-43	0	0	0%	0	0	0%	0	0	0%	0	0
catggaagttttag	chrV:15628099-15628217	C55A1.3	str-248	0	0	0%	0	0	0%	0	0	0%	0	0
gcttcgagtttcag	chrV:13562320-13562966	C56A3.1	grl-17	0	0	0%	0	0	0%	0	0	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
catttgagctccag	chrV:7516878-7517079	C5F6.7	srb-18	0	0	0%	0	0	0%	0	0	0%	0	0
cctccaagtttgag	chrIII:4841615-4841969	clec-156	F26A1.11	0	0	0%	0	0	0%	0	0	0%	0	0
tgccaaagtttcag	chrX:1463504-1463567	D1005.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
cattatagttttag	chrIII:5508541-5508620	D1044.7	-	0	0	0%	0	0	0%	1	0	0%	0	0
gataggagttttag	chrI:8465851-8465989	D1081.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
aattcaagttgtag	chrIII:2438505-2438586	E02H9.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
cttcagagttacag	chrI:12434570-12434674	E03H4.11	-	0	0	0%	0	0	0%	0	0	0%	0	0
gaaaaaagtttcag	chrI:12409489-12409801	E03H4.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
tgtttgagttttag	chrI:12410738-12410924	E03H4.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
actgaaagtttcag	chrI:12410955-12411089	E03H4.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
gactggagttccag	chrI:12414757-12415119	E03H4.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttccatagcttcag	chrI:12421894-12421995	E03H4.7	oac-13	0	0	0%	0	0	0%	0	0	0%	0	0
aatatcagttatag	chrII:7202670-7202822	E04F6.14	srd-56	0	0	0%	0	0	0%	0	0	0%	0	0
ttaaaaagttgtag	chrX:6967563-6967721	F01E11.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttatatagttttag	chrV:3133861-3133969	F02C9.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
gtttgaagttccag	chrX:13459314-13459385	F02D10.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
atggttagtttcag	chrII:3272345-3272487	F02E11.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
tatgtcagtttcag	chrV:9231936-9232069	F07C3.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
atgcacagtttcag	chrX:1723496-1723742	F07G6.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
tgaactagtttcag	chrII:2778887-2779014	F08D12.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
gagtgaagttttag	chrV:13860593-13860673	F09F3.11	srx-135	0	0	0%	0	0	0%	0	0	0%	0	0
aataaaagttacag	chrV:13850871-13851082	F09F3.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
tcggaaagtttcag	chrV:16166571-16167382	F10A3.13	str-108	0	0	0%	0	0	0%	0	0	0%	0	0
tcggacagtttcag	chrV:16152468-16152630	F10A3.9	str-254	0	0	0%	0	0	0%	0	0	0%	0	0
attttaagtttcag	chrV:7149167-7149267	F10D2.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttataaagttttag	chrV:7148669-7148858	F10D2.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
tattcaagttctag	chrV:7145637-7145826	F10D2.7	ugt-38	0	0	0%	0	0	0%	0	0	0%	0	0
atcatcagtttcag	chrIII:4639517-4639594	F10F2.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
tataatagttttag	chrV:16191178-16191647	F11A5.1	srh-281	0	0	0%	0	0	0%	0	0	0%	0	0
aaataaagcttcag	chrX:17409579-17409723	F11C7.4	crb-1	0	0	0%	0	0	0%	0	0	0%	0	0
tcttcaagttacag	chrX:11180388-11180475	F13D2.2	gnrr-6	0	0	0%	0	0	0%	0	0	0%	0	0
tttcatagttttag	chrII:3331020-3331374	F14D2.6	irld-5	0	0	0%	0	0	0%	0	0	0%	0	0
tttaccagtttcag	chrV:14310473-14310632	F14D7.11	-	0	0	0%	0	0	0%	0	0	0%	0	0
cttcagagcttcag	chrV:16696281-16696494	F14F8.12	srz-101	0	0	0%	0	0	0%	0	0	0%	0	0
cgaaacagtttcag	chrX:13478988-13479196	F15A2.4	srd-50	0	0	0%	0	0	0%	0	0	0%	0	0
cgctgaagttccag	chrII:12459200-12459425	F15A4.1	sre-38	0	0	0%	0	0	0%	0	0	0%	0	0
ttaactagctatag	chrX:14085661-14085803	F16B12.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
atttcaagttgtag	chrII:2377200-2377409	F16G10.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
ctttctagttacag	chrV:18199423-18199694	F16H6.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
atcggcagttttag	chrX:12330126-12330219	F17A2.7	srd-45	0	0	0%	0	0	0%	0	0	0%	0	0
tatacaagttccag	chrII:3411420-3412353	F18A12.7	-	0	0	0%	0	0	0%	0	0	0%	0	0
cgtccaagtttcag	chrI:8078509-8078603	F18C12.1	che-3	0	0	0%	0	0	0%	0	0	0%	0	0
tttataagttatag	chrI:8074098-8074324	F18C12.1	che-3	0	0	0%	0	0	0%	0	0	0%	0	0
attcatagtttcag	chrII:6574327-6574530	F18C5.8	-	0	0	0%	0	0	0%	0	0	0%	0	0
agttaaagtttcag	chrV:7425240-7425308	F18E3.4	srw-68	0	0	0%	0	0	0%	0	0	0%	0	0
tagaaaagtttcag	chrV:16232668-16232896	F21H7.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
agtataagttctag	chrV:20571181-20571396	F26F2.6	clec-263	0	0	0%	0	0	0%	0	0	0%	0	0
atcccaagttacag	chrI:12689463-12689623	F28C12.1	sra-17	0	0	0%	0	0	0%	0	0	0%	0	0
tggagaagttttag	chrI:12689972-12690182	F28C12.1	sra-17	0	0	0%	0	0	0%	0	0	0%	0	0
tgacaaagtttcag	chrI:12693252-12693468	F28C12.2	sra-18	0	0	0%	0	0	0%	0	0	0%	0	0
tcttgaagcttcag	chrX:17554100-17554363	F31A3.1	abu-3	0	0	0%	0	0	0%	0	0	0%	0	0
ccaaatagtgtcag	chrX:1787699-1787908	F31A9.3	arg-1	0	0	0%	0	0	0%	0	0	0%	0	0
atcattagtttcag	chrIII:6977269-6977532	F31E3.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttcccaagttccag	chrI:11505668-11505961	F32B4.8	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttttcaagtttcag	chrV:4376687-4376759	F32D1.8	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttttcaagttttag	chrV:10554052-10554183	F32G8.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
aaaaacagttacag	chrI:8990993-8991220	F32H2.8	-	0	0	0%	0	0	0%	0	0	0%	0	0
atatttagtttcag	chrII:11044500-11044709	F33A8.9	col-83	0	0	0%	0	0	0%	0	0	0%	0	0
ccaacaagtgccag	chrI:5845224-5845477	F33D11.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
catcacagtttcag	chrI:12578363-12578848	F33E2.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
gcacctagtttcag	chrII:2581546-2581779	F33H12.4	sri-74	0	0	0%	0	0	0%	0	0	0%	0	0
acatttagtttcag	chrI:11742238-11742390	F35E2.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
agatcaagtttcag	chrV:3308924-3309148	F35F10.2	srbc-3	0	0	0%	0	0	0%	0	0	0%	0	0
ctttcaagtttcag	chrV:9414093-9414215	F36D4.7	-	0	0	0%	0	0	0%	0	0	0%	0	0
acaacaagttatag	chrV:2094033-2094163	F36F12.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
agcaaaagtttcag	chrV:15952320-15952484	F36G9.16	srw-56	0	0	0%	0	0	0%	0	0	0%	0	0
gttgccagtttcag	chrV:15966462-15966558	F36G9.8	sri-1	0	0	0%	0	0	0%	0	0	0%	0	0
aatatgagatttag	chrV:2858659-2858830	F37B4.11	srj-54	0	0	0%	0	0	0%	0	0	0%	0	0
ttggaaagttatag	chrV:4105765-4105949	F38H12.1	srj-39	0	0	0%	0	0	0%	0	0	0%	0	0
tttgaaagttttag	chrV:4103058-4103242	F38H12.2	srj-40	0	0	0%	0	0	0%	0	0	0%	0	0
ttcaatagttgcag	chrX:15427907-15428192	F39D8.4	nas-13	0	0	0%	0	0	0%	0	0	0%	0	0
ctgtaaagtttcag	chrV:17179766-17179971	F40D4.1	srh-174	0	0	0%	0	0	0%	0	0	0%	0	0
gtgaaaagtttcag	chrV:17174156-17174396	F40D4.6	srbc-25	0	0	0%	0	0	0%	0	0	0%	0	0
atcaatagtttcag	chrV:14281098-14281214	F40G12.15	srt-74	0	0	0%	0	0	0%	0	0	0%	0	0
ttgtatagattcag	chrII:3689621-3689835	F40H7.4	srx-101	0	0	0%	0	0	0%	0	0	0%	0	0
tttcataggtccag	chrII:3693549-3693763	F40H7.5	srx-102	0	0	0%	0	0	0%	0	0	0%	0	0
acttcgagcttcag	chrV:835323-835465	F41H8.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
aagccgagttacag	chrIV:3341438-3341543	F42A6.2	-	0	0	0%	0	0	0%	0	0	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
aaacctagttgtag	chrII:2365732-2365937	F43C11.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
ctcagaagtttcag	chrII:2345576-2345625	F43C11.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
aggcacagtttcag	chrII:11772109-11772395	F44E5.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
attcttagtttcag	chrIV:7639305-7639480	F45E4.7	nep-16	0	0	0%	0	0	0%	0	0	0%	0	0
tctttgagttgcag	chrV:20595750-20597442	F46B3.17	col-163	0	0	0%	0	0	0%	0	0	0%	0	0
agaaatagttacag	chrII:823941-824169	F46F5.10	-	0	0	0%	0	0	0%	0	0	0%	0	0
tccatgagtttcag	chrX:3769716-3769906	F47B7.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttgccagatcaag	chrII:1260035-1260310	F47F6.9	-	0	0	0%	0	0	0%	0	0	0%	0	0
ccgagaagtttcag	chrIV:1939060-1939187	F52C12.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
caaattagtttaag	chrII:1923003-1923082	F52C6.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
tcaaatagttccag	chrII:3891615-3891704	F53C3.8	-	0	0	0%	0	0	0%	0	0	0%	0	0
gcctaaaggtctag	chrI:138002-138143	F53G12.3	duox-2	0	0	0%	0	0	0%	0	0	0%	0	0
ataagaagtttcag	chrI:141885-142023	F53G12.3	duox-2	0	0	0%	0	0	0%	0	0	0%	0	0
cataaaagtttaag	chrII:2490396-2490659	F53G2.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
cattcaagtttcag	chrV:20384834-20385081	F53H2.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
ccccgaagtttcag	chrII:1381993-1382336	F54D12.7	-	0	0	0%	0	0	0%	0	0	0%	0	0
aaatatagttacag	chrX:1363324-1363408	F56C3.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttcttagttgcag	chrIV:3905413-3905462	F56D6.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttcatagttgcag	chrV:84366-84553	F56E10.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
acttgaagcttcag	chrI:12300339-12300473	F56H6.7	-	0	0	0%	0	0	0%	0	0	0%	0	0
gcgcacagttgcag	chrX:10587003-10587147	F57C7.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
atattcagttttag	chrIV:7973520-7973596	F57H12.4	frpr-10	0	0	0%	0	0	0%	0	0	0%	0	0
gttttaagttccag	chrII:5153101-5153512	F58A6.10	srb-12	0	0	0%	0	0	0%	0	0	0%	0	0
aacgtaagtttcag	chrII:6387823-6387900	F58F12.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
atctacagtttcag	chrV:17665378-17665553	F59A1.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
atcataagatttag	chrV:2001291-2001430	F59A7.1	clec-206	0	0	0%	0	0	0%	0	0	0%	0	0
attgaaagttccag	chrV:3620144-3620391	F59B1.3	srx-93	0	0	0%	0	0	0%	0	0	0%	0	0
tccctcagttttag	chrV:8984500-8984606	F59E11.15	str-85	0	0	0%	0	0	0%	0	0	0%	0	0
cttttaagttttag	chrII:2012310-2012392	F59H6.6	ceh-85	0	0	0%	0	0	0%	0	0	0%	0	0
aacgttagtctcag	chrX:2584927-2585001	H01M10.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
gctttgagtttcag	chrIV:5872262-5872388	H04M03.6	srv-19	0	0	0%	0	0	0%	0	0	0%	0	0
aatcaaagtttcag	chrI:7982616-7982771	H05F14.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
gatctaagtttcag	chrIV:4815337-4815478	H06H21.1	srw-94	0	0	0%	0	0	0%	0	0	0%	0	0
ataataagttttag	chrV:3839219-3839350	H10D18.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
atcaagagtttcag	chrV:14916092-14916346	H12D21.11	-	0	0	0%	0	0	0%	0	0	0%	0	0
aaccaaagtttcag	chrIV:14139074-14139380	H12I19.2	srz-31	0	0	0%	0	0	0%	0	0	0%	0	0
tactgtagtttcag	chrIII:2390324-2390520	H14E04.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
attataagttacag	chrV:15947928-15948082	H24D24.2	srw-58	0	0	0%	0	0	0%	0	0	0%	0	0
tcagagagtttcag	chrV:2943226-2943832	H27D07.4	srw-137	0	0	0%	0	0	0%	0	0	0%	0	0
ttttgtagatttag	chrV:2942570-2942653	H27D07.4	srw-137	0	0	0%	0	0	0%	0	0	0%	0	0
atatgaagttgcag	chrII:6159468-6159547	H35N03.1	exp-1	0	0	0%	0	0	0%	0	0	0%	0	0
tttggcagtttcag	chrV:11396148-11396333	K03B8.3	nas-18	0	0	0%	0	0	0%	0	0	0%	0	0
cgtcatagtttcag	chrIII:6514424-6514554	K03F8.2	acr-5	0	0	0%	0	0	0%	0	0	0%	0	0
tttgctagttacag	chrI:8059596-8060472	K04G2.10	-	0	0	0%	0	0	0%	0	0	0%	0	0
taataaagcttcag	chrI:14252256-14252349	K04H8.1	clec-116	0	0	0%	0	0	0%	0	0	0%	0	0
ttttaaagttgtag	chrI:14254419-14254494	K04H8.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
tgagacagtttcag	chrV:16181044-16181724	K05D4.2	str-105	0	0	0%	0	0	0%	0	0	0%	0	0
ttttataggttcag	chrII:1572520-1573306	K05F6.1	fbxb-49	0	0	0%	0	0	0%	0	0	0%	0	0
aatattagttccag	chrV:584678-584809	K06H6.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
agaattagacctag	chrV:3235604-3235763	K08D9.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttttgagtttcag	chrX:3275215-3275265	K09C4.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttctctagttttag	chrV:3999714-4000140	K09D9.11	-	0	0	0%	0	0	0%	0	0	0%	0	0
actgatagttcaag	chrIV:12305954-12306078	K09E10.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
acatagagatttag	chrI:7119651-7119782	K10D3.1	glr-3	0	0	0%	0	0	0%	0	0	0%	0	0
acttctagttttag	chrV:3020733-3020945	K12D9.12	irld-12	0	0	0%	0	0	0%	0	0	0%	0	0
gctgagagtttcag	chrII:2828462-2828566	K12H6.8	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttcaaagttatag	chrV:15255108-15255276	M01B2.9	srsx-39	0	0	0%	0	0	0%	0	0	0%	0	0
ctacccagtttcag	chrIV:15106157-15106444	M199.1	srt-44	0	0	0%	0	0	0%	0	0	0%	0	0
aatgaaagttttag	chrX:13549921-13550034	R01E6.1	odr-1	0	0	0%	0	0	0%	0	0	0%	0	0
gtgtatagttttag	chrV:249868-249976	R02C2.3	oac-39	0	0	0%	0	0	0%	0	0	0%	0	0
aggtcaagttgcag	chrX:4108877-4109002	R02E4.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
atattcagtctcag	chrX:7803502-7803652	R03G5.3	irld-13	0	0	0%	0	0	0%	0	0	0%	0	0
tttgtgagtttcag	chrX:13083829-13084021	R03G8.5	str-10	0	0	0%	0	0	0%	0	0	0%	0	0
ggttagagtttcag	chrV:9014951-9015391	R03H4.4	srt-18	0	0	0%	0	0	0%	0	0	0%	0	0
aaaacaagtttaag	chrV:12309902-12310024	R04F11.1	hpo-30	0	0	0%	0	0	0%	0	0	0%	0	0
tttcccagttttag	chrIV:14182672-14182896	R05A10.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
taattcagtttcag	chrV:2775408-2775592	R05D8.2	srj-18	0	0	0%	0	0	0%	0	0	0%	0	0
aattaaagttgcag	chrIV:7532386-7532454	R05G6.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
attcgaagtttcag	chrII:6513353-6513492	R05G9R.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
aacactagtttcag	chrIII:974036-974220	R06B10.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
agacttagtttcag	chrX:9869757-9869901	R07B1.7	-	0	0	0%	0	0	0%	0	0	0%	0	0
taaactagttttag	chrV:9838285-9838483	R07B5.5	srsx-21	0	0	0%	0	0	0%	0	0	0%	0	0
caaacaagtttcag	chrII:944912-945019	R07C3.1	clec-43	0	0	0%	0	0	0%	0	0	0%	0	0
caggcaaggaaaag	chrIV:4454766-4454945	R08C7.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttagtaagtttcag	chrV:15382638-15382830	R08H2.2	str-88	0	0	0%	0	0	0%	0	0	0%	0	0
tgaccaagtttcag	chrIV:10710755-10711015	R102.9	glb-21	0	0	0%	0	0	0%	0	0	0%	0	0
ttttacagtttcag	chrV:13969296-13969597	R10D12.15	-	0	0	0%	0	0	0%	0	0	0%	0	0
aatttaagttgcag	chrII:9504042-9504357	R134.1	gcy-3	0	0	0%	0	0	0%	0	0	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
acccaaagtttcag	chrV:7408121-7408558	R13D7.10	srt-6	0	0	0%	0	0	0%	0	0	0%	0	0
atcagaagtttcag	chrV:7403541-7403891	R13D7.3	srj-13	0	0	0%	0	0	0%	0	0	0%	0	0
caaaacagttttag	chrV:7394222-7394443	R13D7.6	srx-9	0	0	0%	0	0	0%	0	0	0%	0	0
ttgtgaagttttag	chrV:15828629-15828856	R54B8.10	-	0	0	0%	0	0	0%	0	0	0%	0	0
ctttaaagtttcag	chrV:9869859-9869963	T11A5.3	srab-18	0	0	0%	0	0	0%	0	0	0%	0	0
aaattaagtttcag	chrI:12397830-12398009	T15D6.11	-	0	0	0%	0	0	0%	0	0	0%	0	0
gacctgagttccag	chrI:12399919-12400281	T15D6.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
ccacaaagttttag	chrI:12380378-12380524	T15D6.2	gly-16	0	0	0%	0	0	0%	0	0	0%	0	0
agtgaaagtttcag	chrI:12378202-12378325	T15D6.3	gly-17	0	0	0%	0	0	0%	0	0	0%	0	0
tcgcaaagtttcag	chrI:12377802-12377948	T15D6.3	gly-17	0	0	0%	0	0	0%	0	0	0%	0	0
atgcaaagtttcag	chrI:12374985-12375116	T15D6.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
atatcgagtttcag	chrX:12438128-12438218	T18D3.8	-	0	0	0%	0	0	0%	0	0	0%	0	0
aattttagttatag	chrV:6872360-6872405	T19F4.1	frpr-18	0	0	0%	0	0	0%	0	0	0%	0	0
atctatagattcag	chrV:16828206-16828487	T20B3.4	srh-214	0	0	0%	0	0	0%	0	0	0%	0	0
atcgacagtttcag	chrV:3407217-3407345	T20D4.8	-	0	0	0%	0	0	0%	0	0	0%	0	0
cttactagtttcag	chrIII:10202121-10202254	T20G5.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
atttatagtttcag	chrII:12497316-12497487	T21B4.4	ador-1	0	0	0%	0	0	0%	0	0	0%	0	0
ccttcaagtttcag	chrX:10917281-10917400	T21B6.5	nstp-9	0	0	0%	0	0	0%	0	0	0%	0	0
atgttcagtttcag	chrV:1159544-1159890	T21H3.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
gctctgagtttcag	chrI:11695836-11695971	T22H2.3	sri-1	0	0	0%	0	0	0%	0	0	0%	0	0
agaattagttacag	chrX:12790601-12790700	T22H6.4	str-123	0	0	0%	0	0	0%	0	0	0%	0	0
ttgtttagttttag	chrIII:4673028-4673186	T23F11.5	srg-13	0	0	0%	0	0	0%	0	0	0%	0	0
caaataagttttag	chrII:6406048-6406113	T25D10.3	spp-11	0	0	0%	0	0	0%	0	0	0%	0	0
attccaagtttcag	chrV:6761513-6761605	T25F10.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
attcttagttccag	chrV:6761328-6761480	T25F10.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
taaattagttccag	chrII:9243208-9243276	T26C5.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttttgaagttacag	chrI:12686853-12687013	T26E3.9	sra-25	0	0	0%	0	0	0%	0	0	0%	0	0
atttcgagattcag	chrV:15302506-15302720	T26H8.2	srx-48	0	0	0%	0	0	0%	0	0	0%	0	0
agtcgaagtttcag	chrV:3726199-3726405	T27C4.3	str-30	0	0	0%	0	0	0%	0	0	0%	0	0
cctcaaagttccag	chrV:3260529-3260763	T28A11.7	srbc-5	0	0	0%	0	0	0%	0	0	0%	0	0
gatttcagcttcag	chrIII:13494961-13495101	T28A8.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttttcgagttacag	chrX:6582608-6582759	T28B4.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
tgcattagttcaag	chrII:6476869-6476985	T28D9.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttaggcagtttcag	chrV:4514487-4514567	T28F12.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
tgcaatagtttcag	chrI:7480444-7480590	T28F4.2	asic-2	0	0	0%	0	0	0%	0	0	0%	0	0
ccttaaagtttcag	chrI:7482773-7482889	T28F4.2	asic-2	0	0	0%	0	0	0%	0	0	0%	0	0
aatgagaggttcag	chrIII:5440403-5440446	W03A5.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
actttcagttcaag	chrIV:5189092-5189181	W03F8.9	gpa-18	0	0	0%	0	0	0%	0	0	0%	0	0
aaaatgagtttcag	chrI:11631232-11631334	W04G5.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
tattttagttgcag	chrI:11653260-11653403	W04G5.7	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttcaatagttccag	chrV:12672302-12672516	W05B10.5	srsx-116	0	0	0%	0	0	0%	0	0	0%	0	0
ttctgtagcttcag	chrV:16652434-16652508	W06G6.21	-	0	0	0%	0	0	0%	0	0	0%	0	0
gaaataagtttcag	chrV:13035844-13036019	W07G4.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
gttttctagttccag	chrII:13176636-13176759	W09H1.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
caaggtagtttcag	chrII:3583064-3583157	W10G11.10	srh-59	0	0	0%	0	0	0%	0	0	0%	0	0
tttggtagttacag	chrII:3578959-3579025	W10G11.12	clec-133	0	0	0%	0	0	0%	0	0	0%	0	0
cgaggtagtttcag	chrII:3585653-3585746	W10G11.9	srh-60	0	0	0%	0	0	0%	0	0	0%	0	0
agttaaagctttag	chrV:17008039-17008182	Y102A5C.32	sri-69	0	0	0%	0	0	0%	0	0	0%	0	0
atattcagtttcag	chrIV:15798408-15798611	Y105C5A.22	-	0	0	0%	0	0	0%	0	0	0%	0	0
aaactcagtttcag	chrIV:16058702-16058972	Y105C5B.23	-	0	0	0%	0	0	0%	0	0	0%	0	0
agatggagtttcag	chrIV:4399171-4399298	Y24D9A.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
tctactagttctag	chrIV:4399872-4400007	Y24D9A.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
cttgcaagtttcag	chrII:3092752-3092910	Y25C1A.10	srg-22	0	0	0%	0	0	0%	0	0	0%	0	0
agttagagtttcag	chrII:3099937-3100095	Y25C1A.12	srg-24	0	0	0%	0	0	0%	0	0	0%	0	0
attcagagtttcag	chrII:3102420-3102869	Y25C1A.4	clec-121	0	0	0%	0	0	0%	0	0	0%	0	0
aataaaagatttag	chrI:13093908-13094425	Y26D4A.13	-	0	0	0%	0	0	0%	0	0	0%	0	0
tcagacagtttcag	chrV:16611659-16611817	Y32B12C.2	srw-54	0	0	0%	0	0	0%	0	0	0%	0	0
atttttagttaaag	chrIV:3756038-3756312	Y37E11AR.1	best-20	0	0	0%	0	0	0%	0	0	0%	0	0
aatactagttttag	chrV:18277362-18277475	Y37H2C.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
gtattgagtttcag	chrV:20520316-20520634	Y38H6C.12	srh-166	0	0	0%	0	0	0%	0	0	0%	0	0
ctattgagattcag	chrIV:12234109-12234300	Y39C12A.5	sre-16	0	0	0%	0	0	0%	0	0	0%	0	0
tctaagagtttcag	chrV:365347-365558	Y39D8B.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
atcaaaagtttcag	chrV:378966-379144	Y39D8B.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
gtcaagagttacag	chrII:779386-779699	Y39F10A.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
atgttgagtttcag	chrIV:1636807-1636929	Y41D4B.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttagaaagcttcag	chrV:19710436-19710672	Y43F8C.16	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttatgaagcttcag	chrV:19628946-19629066	Y43F8C.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
tccaaaagttccag	chrV:20635437-20635556	Y44A6B.1	srxa-14	0	0	0%	0	0	0%	0	0	0%	0	0
aatgtgagtttcag	chrV:2857184-2857300	Y45G12A.1	srj-55	0	0	0%	0	0	0%	0	0	0%	0	0
taaaatagtttcag	chrV:4140298-4140358	Y45G5AL.2	lgc-29	0	0	0%	0	0	0%	0	0	0%	0	0
attaagagtttcag	chrV:1808684-1808850	Y46H3A.1	srt-42	0	0	0%	0	0	0%	0	0	0%	0	0
acctagagattcag	chrV:1711686-1711844	Y46H3C.1	srw-100	0	0	0%	0	0	0%	0	0	0%	0	0
gcaaaaaggttcag	chrV:1637428-1637752	Y46H3D.3	str-222	0	0	0%	0	0	0%	0	0	0%	0	0
tatggtagttccag	chrV:1634214-1634527	Y46H3D.4	irld-17	0	0	0%	0	0	0%	0	0	0%	0	0
cgttagagttttag	chrII:2702532-2702672	Y47G7B.3	sri-60	0	0	0%	0	0	0%	0	0	0%	0	0
cataaaagttgcag	chrI:62774-62989	Y48G1C.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttttcgagtttcag	chrV:693961-694077	Y49C4A.6	srj-53	0	0	0%	0	0	0%	0	0	0%	0	0
ctcggtagtttcag	chrII:3589333-3589426	Y49F6A.2	srh-57	0	0	0%	0	0	0%	0	0	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
tggagtagcgctag	chrV:18304417-18304537	Y51A2A.7	-	0	0	0%	0	0	0%	0	0	0%	0	0
ctaacaagttacag	chrIV:16723705-16723851	Y51H4A.23	-	0	0	0%	0	0	0%	0	0	0%	0	0
aatttgagtttcag	chrI:11301590-11301654	Y53H1B.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
aaatacagtttcag	chrI:14697148-14697334	Y54E5A.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
atgataagttttag	chrIV:2898499-2898602	Y54G2A.20	-	0	0	0%	0	0	0%	0	0	0%	0	0
aagtggagttgcag	chrIII:442409-442576	Y55B1BR.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
tataaaagttccag	chrV:7058254-7058489	Y57E12AL.2	-	0	0	0%	0	0	0%	0	0	0%	0	0
cgaaagagacgcag	chrV:19958702-19959369	Y60A3A.27	-	0	0	0%	0	0	0%	0	0	0%	0	0
aaaaaaaggttcag	chrV:19970255-19970451	Y60A3A.4	srh-173	0	0	0%	0	0	0%	0	0	0%	0	0
atcacgagttcaag	chrI:13717102-13718421	Y6B3B.3	-	0	0	0%	0	0	0%	0	0	0%	0	0
aacttgagttacag	chrV:16706237-16706393	Y70C5C.2	clec-9	0	0	0%	0	0	0%	0	0	0%	0	0
taaaaaagtttcag	chrI:13939930-13940035	Y71A12B.8	-	0	0	0%	0	0	0%	0	0	0%	0	0
ttgtgcagttttag	chrIV:15339588-15339730	Y73F8A.18	irld-59	0	0	0%	0	0	0%	0	0	0%	0	0
catggaagtttcag	chrIV:15517757-15517908	Y73F8A.33	-	0	0	0%	0	0	0%	0	0	0%	0	0
aattcgagatttag	chrV:1356912-1357037	Y75B7AL.3	snt-3	0	0	0%	0	0	0%	0	0	0%	0	0
acaggtagtttcag	chrIV:2037903-2038105	Y76B12C.1	cng-2	0	0	0%	0	0	0%	0	0	0%	0	0
ttctatagtttcag	chrX:15801232-15801503	Y7A5A.7	-	0	0	0%	0	0	0%	0	0	0%	0	0
tgaaagagttgcag	chrI:914004-914127	Y95B8A.12	-	0	0	0%	0	0	0%	0	0	0%	0	0
catttgaggtttag	chrV:7926326-7926603	Y97E10B.4	srsx-7	0	0	0%	0	0	0%	0	0	0%	0	0
tcgaaaagtttcag	chrIV:4916348-4916441	Y9C9A.10	str-155	0	0	0%	0	0	0%	0	0	0%	0	0
agttgaagtttcag	chrIV:4942321-4942414	Y9C9A.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
cttataagtgacag	chrX:899709-899896	ZC13.10	-	0	0	0%	0	0	0%	0	0	0%	0	0
attaaaagtctcag	chrV:20293671-20293783	ZC15.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
tttgttagtttcag	chrV:8728224-8728337	ZC196.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
caagcaagtttcag	chrII:1644252-1644469	ZC204.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
agttctagtttcag	chrII:3196565-3196685	ZC239.7	gcy-15	0	0	0%	0	0	0%	0	0	0%	0	0
tttagcagtttcag	chrV:4699954-4700053	ZC266.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
taaaacagtttcag	chrV:6799287-6799502	ZC404.13	dmsr-9	0	0	0%	0	0	0%	0	0	0%	0	0
gtgccgagtttcag	chrIII:12750231-12750313	ZC482.2	irld-60	0	0	0%	0	0	0%	0	0	0%	0	0
cgaatcagttttag	chrIII:12756106-12756237	ZC482.6	srw-10	0	0	0%	0	0	0%	0	0	0%	0	0
aatgaaagctcaag	chrV:8064873-8064988	ZC513.10	fbxa-223	0	0	0%	0	0	0%	0	0	0%	0	0
acgaaaagttccag	chrV:15307937-15308101	ZK1037.11	srz-10	0	0	0%	0	0	0%	0	0	0%	0	0
agtttcagtttcag	chrV:15317056-15317204	ZK1037.4	nhr-246	0	0	0%	0	0	0%	0	0	0%	0	0
tactgtagttacag	chrV:15318291-15318401	ZK1037.4	nhr-246	0	0	0%	0	0	0%	0	0	0%	0	0
gaactaagtttcag	chrV:7715398-7715736	ZK105.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
atttccagtttcag	chrI:13237680-13237828	ZK1053.7	-	0	0	0%	0	0	0%	0	0	0%	0	0
attttaaggttcag	chrII:5842919-5843211	ZK1248.1	nep-25	0	0	0%	0	0	0%	0	0	0%	0	0
ttattgagtggcag	chrII:11640887-11641149	ZK20.2	kin-6	0	0	0%	0	0	0%	0	0	0%	0	0
ctaaccagtttcag	chrV:17103421-17103680	ZK218.6	nhr-248	0	0	0%	0	0	0%	0	0	0%	0	0
ataagcagttttag	chrII:1967455-1967747	ZK250.9	-	0	0	0%	0	0	0%	0	0	0%	0	0
ccagttagtttcag	chrV:18427361-18427421	ZK262.6	srw-83	0	0	0%	0	0	0%	0	0	0%	0	0
atgtcaagtttcag	chrV:18732177-18732302	ZK384.1	scl-19	0	0	0%	0	0	0%	0	0	0%	0	0
aagtagagtttaag	chrX:11329696-11330021	ZK455.3	npr-9	0	0	0%	0	0	0%	0	0	0%	0	0
gacttcagttttag	chrV:600714-600794	ZK488.4	nhr-251	0	0	0%	0	0	0%	0	0	0%	0	0
atcaggagtttcag	chrV:601885-602101	ZK488.4	nhr-251	0	0	0%	0	0	0%	0	0	0%	0	0
ttccgaagtttcag	chrV:593476-593638	ZK488.5	-	0	0	0%	0	0	0%	0	0	0%	0	0
gtgaccagtgtcag	chrIII:7907419-7907539	ZK688.6	-	0	0	0%	0	0	0%	0	0	0%	0	0
attcgcagttttag	chrIV:11666237-11666674	ZK809.9	-	0	0	0%	0	0	0%	0	0	0%	0	0
cataggagtttcag	chrIV:11949364-11949462	ZK829.2	hdl-1	0	0	0%	0	0	0%	0	0	0%	0	0
aacttaagttttag	chrII:10006849-10007059	ZK892.4	-	0	0	0%	0	0	0%	0	0	0%	0	0
aaaatcagttccag	chrV:8510584-8510671	ZK994.1	-	0	0	0%	0	0	0%	0	0	0%	0	0
Not Enough Expression In N2 Gonad														
ttataaagtttcag	chrV:10397514-10397706	AC3.7	ugt-1	0	13	0%	0	0	0%	0	8	0%	0	0
gtattaagtttcag	chrIV:12162769-12162843	B0001.6	-	4	111	4%	0	2	0%	9	69	13%	-4	9
atttaaagttctag	chrV:10322996-10323201	B0024.14	crm-1	0	5	0%	0	0	0%	0	4	0%	0	0
atcaaaagttacag	chrV:10324228-10324333	B0024.14	crm-1	0	15	0%	0	0	0%	0	21	0%	0	0
ttcaaaagattcag	chrI:4657198-4657488	B0041.2	ain-2	2	33	6%	5	5	100%	61	102	60%	94	54
ttgaatagttacag	chrX:12044963-12045213	B0198.3	-	0	1	0%	0	2	0%	0	0	0%	0	0
aaaaatagtttcag	chrI:10741748-10741826	B0205.4	-	1	67	1%	0	0	0%	0	1	0%	0	-1
ttccatagtttcag	chrI:5923360-5923620	B0207.5	-	0	0	0%	0	1	0%	0	0	0%	0	0
tacggtagtttcag	chrII:6911159-6911300	B0252.2	asm-1	0	10	0%	0	5	0%	0	15	0%	0	0
atctatagtttcag	chrII:2297939-2298099	B0281.4	-	0	0	0%	0	3	0%	0	26	0%	0	0
tgagctagtttcag	chrIII:4334083-4334295	B0285.1	cdk-12	1	17	6%	7	8	88%	45	73	62%	82	56
attcatagttacag	chrIII:8703352-8703508	B0303.11	-	0	70	0%	0	0	0%	0	51	0%	0	0
aaaatcagtttcag	chrI:10083177-10083252	B0379.3	mut-16	1	19	5%	3	4	75%	12	34	35%	70	30
tgtatcagtttcag	chrI:10093667-10093780	B0379.4	-	0	39	0%	4	8	50%	42	118	36%	50	36
acgttgagtttcag	chrIII:4777358-4777477	B0393.7	-	0	1	0%	0	0	0%	0	0	0%	0	0
aaaccaagctttag	chrX:9296237-9296410	B0416.6	gly-13	0	34	0%	0	8	0%	0	27	0%	0	0
aagcaaagtttcag	chrII:3047710-3047803	B0454.10	-	0	1	0%	0	0	0%	0	0	0%	0	0
ttaaaaagatttag	chrII:11349227-11349601	B0491.1	-	0	6	0%	1	5	20%	1	9	11%	20	11
aggatcagtttcag	chrIV:13122269-13122360	B0564.10	unc-30	0	2	0%	0	0	0%	0	1	0%	0	0
aatgttagtttcag	chrX:7421798-7421886	C10A4.9	-	0	3	0%	0	0	0%	0	1	0%	0	0
tacaaaagctacag	chrIV:9363848-9363960	C10C5.1	-	1	87	1%	0	3	0%	1	59	2%	-1	1
atttttagtttcag	chrV:5989928-5990069	C10F3.6	fut-8	0	18	0%	1	2	50%	0	5	0%	50	0
tcaacaagtttcag	chrX:9615466-9615724	C11E4.6	-	0	20	0%	0	0	0%	0	3	0%	0	0
catgaaagcttcag	chrX:16335181-16335858	C11G6.1	-	0	0	0%	0	0	0%	0	3	0%	0	0
gaataaagtttcag	chrV:7681890-7682069	C12D5.11	sre-11	0	1	0%	0	0	0%	0	0	0%	0	0
attaaaagttctag	chrV:7290305-7290398	C13A2.1	-	0	3	0%	0	0	0%	0	0	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
tctataagtttcag	chrV:4992650-4992942	C13D9.8	ncx-9	0	1	0%	0	0	0%	0	3	0%	0	0
aattgtagtttcag	chrX:8895526-8895705	C13E3.1	-	0	1	0%	0	0	0%	0	1	0%	0	0
atataaagtttcag	chrX:2798681-2798764	C14A11.3	cgef-1	1	143	1%	1	6	17%	56	214	26%	16	25
ataacaagttccag	chrV:19339339-19339558	C14B4.2	-	0	11	0%	0	0	0%	0	13	0%	0	0
ttccacagttccag	chrV:5645818-5646026	C14C11.5	srx-117	1	1	100%	0	0	0%	0	0	0%	0	0
caaattagttttag	chrX:6238345-6238567	C14F11.6	-	0	490	0%	0	0	0%	0	2	0%	0	0
tcccaaagtttcag	chrX:6483351-6483477	C15B12.5	gar-1	0	2	0%	0	0	0%	0	0	0%	0	0
aactaaagtttcag	chrII:6980611-6980774	C15F1.2	-	0	165	0%	0	3	0%	0	0	0%	0	0
agaagaagtttcag	chrX:3965219-3965338	C16B8.2	-	0	3	0%	0	0	0%	0	1	0%	0	0
tcgattagtttaag	chrII:1890336-1890465	C16C4.14	math-9	0	0	0%	0	0	0%	0	1	0%	0	0
attgtcaggtgaag	chrX:6941080-6941249	C16E9.1	-	0	8	0%	0	0	0%	0	2	0%	0	0
tgctctagtttcag	chrII:3853328-3853408	C17A2.1	nhr-257	0	0	0%	0	0	0%	0	2	0%	0	0
caaaacagtttcag	chrII:5591417-5591473	C17G10.4	cdc-14	4	60	7%	0	3	0%	14	53	26%	-7	20
atcaaaagttccag	chrX:3602301-3602422	C18B2.3	-	1	42	2%	0	1	0%	0	19	0%	-2	-2
gtttgaagtttcag	chrII:8963803-8963916	C18E9.10	-	0	8	0%	0	5	0%	0	20	0%	0	0
ccatgcagttccag	chrX:12219795-12219907	C23H4.2	-	0	4	0%	0	0	0%	0	0	0%	0	0
ttgaacagtttcag	chrX:4305994-4306062	C24A8.3	pqn-15	0	2	0%	0	2	0%	0	4	0%	0	0
cgatatagttccag	chrX:4333168-4333337	C24A8.4	cst-2	0	73	0%	0	4	0%	0	34	0%	0	0
cctaaaagtttcag	chrV:5526768-5526877	C24G6.2	-	0	8	0%	0	0	0%	0	1	0%	0	0
atcgaaagtttcag	chrI:4110132-4110378	C24G7.1	-	0	11	0%	0	0	0%	0	0	0%	0	0
ttcagaagtttcag	chrIII:11799081-11799214	C24H11.8	twk-39	0	2	0%	0	0	0%	0	1	0%	0	0
tcctccagtttcag	chrX:5445427-5445564	C25F6.7	-	0	85	0%	0	0	0%	0	1	0%	0	0
tttatgagttttag	chrIV:12462572-12463024	C25G4.8	-	0	0	0%	0	0	0%	0	1	0%	0	0
ctgcgaagtttcag	chrX:5341223-5341321	C26B9.2	-	0	3	0%	0	0	0%	0	0	0%	0	0
actcatagtttcag	chrX:5332109-5332236	C26B9.5	-	2	477	0%	0	4	0%	0	237	0%	0	0
aatacgagtttcag	chrI:7511123-7511302	C26C6.7	glb-8	0	0	0%	0	0	0%	0	1	0%	0	0
tttcaaagctttag	chrIII:4931116-4931302	C26E6.12	-	0	41	0%	0	6	0%	0	157	0%	0	0
caaattagttccag	chrIV:12666448-12667398	C26H9A.2	-	0	51	0%	0	0	0%	3	52	6%	0	6
tatcatagtttcag	chrIV:12655836-12656052	C26H9A.2	-	0	4	0%	0	1	0%	0	2	0%	0	0
actctaagttccag	chrIV:12658007-12658078	C26H9A.2	-	0	10	0%	0	2	0%	0	7	0%	0	0
taaagtagttacag	chrIV:12664413-12664816	C26H9A.2	-	0	7	0%	0	2	0%	0	14	0%	0	0
tctaaaagtttaag	chrV:12143381-12143548	C27A7.3	-	0	4	0%	0	0	0%	0	1	0%	0	0
tttctgagtttttag	chrV:12141999-12142157	C27A7.3	-	0	8	0%	0	0	0%	0	1	0%	0	0
aatttaagtttcag	chrV:12160275-12160429	C27A7.5	-	12	18	67%	0	1	0%	12	17	71%	-67	4
catttcagtttcag	chrX:14855479-14855685	C27C12.4	-	15	31	48%	3	6	50%	13	23	57%	2	8
atagacagttttag	chrX:14850278-14850389	C27C12.5	acd-3	0	59	0%	0	0	0%	0	29	0%	0	0
aaataaagttttag	chrX:14836278-14836362	C27C12.7	dpf-2	0	16	0%	0	0	0%	0	25	0%	0	0
atcaaaagttgcag	chrIII:4987602-4987739	C27F2.1	-	0	1	0%	0	0	0%	0	0	0%	0	0
caccaaagtttcag	chrIV:13956244-13956364	C27H2.2	-	0	199	0%	0	6	0%	28	123	23%	0	23
tgtaaaagtttcag	chrIV:8503656-8503968	C28C12.10	tag-77	0	24	0%	1	9	11%	32	104	31%	11	31
atctcaagtttcag	chrIV:8482283-8482618	C28C12.5	spp-8	0	330	0%	0	1	0%	0	186	0%	0	0
tttgaaagcttcag	chrX:8833574-8833710	C28G1.3	sec-15	0	22	0%	0	1	0%	1	19	5%	0	5
tatgaaagttgcag	chrIII:7931316-7931483	C29E4.4	npp-15	0	5	0%	0	0	0%	19	29	66%	0	66
gttataagtttcag	chrV:15359722-15360477	C29F3.1	ech-1	0	5	0%	0	0	0%	0	0	0%	0	0
attcaaagttgtag	chrII:6293330-6293451	C29F5.4	mps-1	0	4	0%	0	0	0%	0	0	0%	0	0
tttgccagtttcag	chrIII:132729-132967	C29F9.1	-	0	5	0%	0	0	0%	0	6	0%	0	0
tttacaagtttcag	chrII:6112438-6112830	C29H12.5	cec-9	0	0	0%	0	4	0%	0	21	0%	0	0
taattgagtttcag	chrX:17052808-17052964	C30G4.3	gcy-11	0	0	0%	0	0	0%	0	1	0%	0	0
atttgaagcttcag	chrV:14937775-14937999	C30G7.2	-	0	1	0%	0	0	0%	0	0	0%	0	0
tcttggagctttag	chrV:16305919-16306084	C31A11.5	oac-6	1	100	1%	0	2	0%	0	19	0%	-1	-1
ttaacaagtttcag	chrV:16310008-16310209	C31A11.7	oac-7	0	19	0%	0	0	0%	0	2	0%	0	0
tggggaagttatag	chrV:2909362-2909462	C31B8.8	-	0	4	0%	0	0	0%	0	0	0%	0	0
gaagcaagttccag	chrX:13989769-13989916	C31E10.4	-	0	1	0%	0	0	0%	0	2	0%	0	0
cattatagttccag	chrX:14004288-14004357	C31E10.8	tbc-19	0	3	0%	0	0	0%	0	2	0%	0	0
cggcatagtttcag	chrX:14003767-14003856	C31E10.8	tbc-19	0	9	0%	0	1	0%	0	6	0%	0	0
tactgaagtttcag	chrII:965850-966857	C32B5.14	fbxc-18	0	0	0%	0	0	0%	0	4	0%	0	0
ctcatgagtttcag	chrI:5205312-5205554	C32E12.5	sem-2	1	20	5%	0	0	0%	2	10	20%	0	15
tatcttagttacag	chrI:3799883-3800043	C32E8.10	unc-11	0	10	0%	0	1	0%	29	44	66%	0	66
gcaatgagttgtag	chrX:3056979-3057235	C33D12.6	tag-312	0	1	0%	0	3	0%	0	2	0%	0	0
tatgaaagtttcag	chrV:6995926-6996122	C33G8.11	nhr-107	0	15	0%	0	0	0%	0	3	0%	0	0
aataaaagttttag	chrIV:7814378-7814569	C33H5.18	-	0	11	0%	0	3	0%	10	32	31%	0	31
aacacgagttacag	chrI:8332214-8332306	C34B7.1	-	0	0	0%	0	0	0%	0	2	0%	0	0
ccacggagttacag	chrII:8692542-8692772	C34C6.3	-	0	6	0%	0	0	0%	0	0	0%	0	0
gtttttagctgcag	chrII:8704897-8705090	C34C6.6	prx-5	13	16	81%	0	0	0%	13	16	81%	0	0
aaacttagttatag	chrII:8707514-8707790	C34C6.7	-	0	3	0%	0	1	0%	0	6	0%	0	0
tgaattagttgcag	chrX:8022704-8022854	C34D10.2	-	29	71	41%	1	2	50%	16	30	53%	9	12
taaaaaagttacag	chrIII:5251901-5252160	C34E10.8	-	0	4	0%	1	5	20%	11	63	17%	20	17
ttgaatagtttcag	chrI:4256416-4256881	C34E11.3	met-1	0	5	0%	1	4	25%	2	27	7%	25	7
acttcaagtttcag	chrX:11202966-11203085	C34F6.11	-	0	7	0%	0	0	0%	0	4	0%	0	0
aaaacaagttttag	chrX:11220160-11220381	C34F6.9	-	0	15	0%	0	2	0%	0	11	0%	0	0
ctatttagttttag	chrX:6159605-6160073	C34H3.2	odd-2	2	26	8%	0	1	0%	0	25	0%	-8	-8
aatataagttgcag	chrV:10511392-10511585	C35A5.7	dmsr-8	0	8	0%	0	0	0%	0	1	0%	0	0
ttctcaagtttcag	chrI:10844242-10844369	C35E7.2	-	0	9	0%	0	0	0%	0	4	0%	0	0
aagtagagttacag	chrIII:3833119-3833320	C36A4.1	cyp-25A1	0	13	0%	0	0	0%	0	20	0%	0	0
acgtgtagttttag	chrIII:3989558-3989681	C36E8.2	glp-11	1	10	10%	1	1	100%	1	3	33%	90	23
attaaaagtttcag	chrI:14155652-14155765	C37A5.2	fipr-22	0	26	0%	0	1	0%	0	18	0%	0	0
ctccgaagtttcag	chrI:14153772-14153885	C37A5.4	fipr-23	0	0	0%	0	0	0%	0	2	0%	0	0
cctcagagtttcag	chrI:14153290-14153440	C37A5.4	fipr-23	0	2	0%	0	0	0%	0	1	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
tttctaagtttcag	chrV:1497098-1497437	C38C3.3	-	0	0	0%	0	0	0%	0	3	0%	0	0
actactagtttcag	chrII:14642113-14642371	C38C6.2	-	0	41	0%	0	5	0%	0	10	0%	0	0
tttaaaagcttcag	chrIII:4797524-4797707	C38D4.5	tag-325	0	22	0%	0	4	0%	45	100	45%	0	45
atattgagtttcag	chrIII:4804522-4804650	C38D4.9	-	0	3	0%	0	0	0%	0	9	0%	0	0
acagttagtttaag	chrIV:13066915-13067098	C39E9.3	col-131	0	27	0%	0	0	0%	0	0	0%	0	0
tttgttagttccag	chrIV:13082443-13082530	C39E9.8	-	135	369	37%	0	2	0%	147	355	41%	-37	5
ttgtaaagctatag	chrII:1995258-1995657	C40D2.3	math-21	2	8	25%	0	0	0%	0	0	0%	0	0
tattgaagttttag	chrII:8100879-8101081	C41C4.2	sre-2	0	0	0%	0	0	0%	0	1	0%	0	0
agatgaagcttcag	chrII:3004850-3005042	C41H7.4	-	0	20	0%	0	1	0%	0	20	0%	0	0
gcctgaagttttag	chrIV:12299676-12299726	C42C1.7	-	0	2	0%	0	0	0%	0	0	0%	0	0
tctgaaagtttcag	chrX:5089723-5089894	C42D8.3	pnk-4	0	4	0%	0	2	0%	1	3	33%	0	33
tattgaagtttcag	chrX:2396056-2396161	C43H6.6	-	0	1	0%	0	0	0%	0	1	0%	0	0
ttttctagttccag	chrI:4612027-4613032	C44E4.1	-	4	30	13%	2	7	29%	65	99	66%	15	52
ttcaaaagttccag	chrI:4626466-4627216	C44E4.7	-	0	8	0%	3	4	75%	18	23	78%	75	78
actacaagtttcag	chrX:6077241-6077482	C45B2.4	ggr-2	0	4	0%	0	0	0%	0	0	0%	0	0
ctaaacagtttcag	chrIII:5070392-5070501	C45G9.12	-	17	89	19%	0	2	0%	2	17	12%	-19	-7
ttggaaagttccag	chrX:15471460-15471596	C46E1.3	-	0	2	0%	0	0	0%	0	2	0%	0	0
taaaatagatttag	chrIV:9973339-9973532	C47E12.10	-	0	0	0%	0	0	0%	0	2	0%	0	0
aaattgagttccag	chrI:6908838-6909055	C48B6.6	smg-1	0	12	0%	0	3	0%	1	37	3%	0	3
agttttagtttaag	chrI:6265744-6266066	C48E7.8	oac-9	0	0	0%	0	0	0%	0	1	0%	0	0
aatcctagttttag	chrIV:6215964-6216128	C49A9.5	-	0	28	0%	0	0	0%	0	14	0%	0	0
aatacgagttttag	chrIV:17312716-17312865	C49C3.1	snf-9	0	1	0%	0	1	0%	0	13	0%	0	0
tcttctagctttag	chrIV:17314446-17314560	C49C3.1	snf-9	0	0	0%	0	1	0%	0	3	0%	0	0
tattcaagtttcag	chrX:13364024-13364122	C49F8.1	-	0	48	0%	0	0	0%	0	41	0%	0	0
gcggtgagtttcag	chrV:4031825-4031984	C49G7.8	cyp-35A4	0	5	0%	0	0	0%	0	3	0%	0	0
gatctgagtttcag	chrV:7589187-7589292	C50E3.6	-	0	42	0%	0	0	0%	0	4	0%	0	0
tattctagttttag	chrV:3089225-3089338	C50H11.1	acs-21	0	6	0%	0	0	0%	0	3	0%	0	0
aagaaaagtttcag	chrV:9892888-9893083	C50H2.1	fshr-1	0	87	0%	0	0	0%	0	45	0%	0	0
aataaaagtttcag	chrV:12304612-12305354	C51F7.1	frm-7	0	5	0%	0	4	0%	0	14	0%	0	0
tgtttcagttgcag	chrX:1297554-1297754	C52B11.3	dop-4	0	0	0%	0	0	0%	0	5	0%	0	0
tttctcagttccag	chrIV:17189397-17189603	C52D10.1	-	8	235	3%	1	2	50%	1	25	4%	47	1
ctttcaagttttag	chrII:1852267-1852485	C52E2.3	-	0	0	0%	0	0	0%	0	1	0%	0	0
tgaaacagttgcag	chrII:1842003-1842242	C52E2.5	-	0	2	0%	0	0	0%	0	1	0%	0	0
acaaaaagtttcag	chrI:12445712-12445843	C54C8.2	-	0	2	0%	0	0	0%	0	0	0%	0	0
tttactagttgcag	chrV:12439361-12439587	C54D10.7	anr-30	0	4	0%	0	0	0%	0	1	0%	0	0
cagaaaagtttcag	chrV:12440098-12440206	C54D10.7	anr-30	0	29	0%	0	2	0%	0	0	0%	0	0
ttcaatagtttcag	chrX:7829910-7830102	C54D2.4	sul-3	0	1	0%	0	0	0%	0	1	0%	0	0
tcttcgagttttag	chrI:8015851-8016172	C54G4.1	-	0	82	0%	1	5	20%	0	57	0%	20	0
agtattagtttcag	chrI:7996468-7996578	C54G4.5	-	0	2	0%	0	1	0%	0	3	0%	0	0
ttcaaaagctatag	chrV:11506840-11507129	C55A6.10	-	0	22	0%	7	9	78%	37	73	51%	78	51
tcataaagttacag	chrV:13555822-13556154	C56A3.6	-	0	21	0%	0	2	0%	0	49	0%	0	0
tttcaaagttacag	chrX:7386785-7386950	C56G3.1	npr-8	0	2	0%	0	0	0%	0	1	0%	0	0
aaatttagatttag	chrV:5600514-5600642	CD4.8	-	0	2	0%	1	7	14%	0	34	0%	14	0
ataataagtttcag	chrX:1484915-1485060	D1005.4	-	0	6	0%	0	0	0%	0	4	0%	0	0
aaacaaagttacag	chrI:4598536-4598645	D1007.7	nrd-1	0	12	0%	0	8	0%	7	109	6%	0	6
ttttctagtttcag	chrX:8908651-8908753	D1009.3	-	1	3	33%	0	0	0%	1	1	100%	0	67
aactcaagttctag	chrIII:5544654-5544752	D1044.1	-	1	53	2%	0	0	0%	2	27	7%	0	6
ccaaatagttctag	chrIV:8927891-8928008	D1046.1	cfim-2	0	17	0%	0	3	0%	3	31	10%	0	10
aaaaacagtttcag	chrV:4074244-4074578	D1065.1	otpl-2	0	0	0%	0	0	0%	0	2	0%	0	0
ctctttagtttcag	chrI:6598714-6598854	D2092.6	-	1	1	100%	0	0	0%	0	0	0%	0	0
tataaaagcttcag	chrI:4145965-4146189	E01A2.10	poml-3	0	300	0%	0	2	0%	0	132	0%	0	0
aagttgagtttcag	chrII:14951075-14951447	E01F3.1	pde-3	0	32	0%	0	4	0%	0	30	0%	0	0
gacatgagtttcag	chrV:9358150-9358294	E02C12.5	gpa-3	0	1	0%	0	0	0%	0	0	0%	0	0
ttcttcagtttcag	chrIII:2449690-2449862	E02H9.8	nhr-121	18	27	67%	0	0	0%	7	14	50%	0	-17
ggaacgagtttcag	chrI:12430877-12431023	E03H4.10	clec-17	0	1	0%	0	0	0%	0	1	0%	0	0
gtgtaaagtttcag	chrI:12431051-12431210	E03H4.10	clec-17	0	11	0%	0	0	0%	0	3	0%	0	0
tcatccagtttcag	chrII:7218352-7218433	E04F6.11	clh-3	0	32	0%	0	4	0%	7	53	13%	0	13
ttaaaaagttttag	chrII:5413487-5413870	EEED8.14	-	0	0	0%	0	6	0%	0	37	0%	0	0
atcggtagtttcag	chrV:6579079-6579209	EGAP9.3	-	0	9	0%	0	0	0%	0	2	0%	0	0
aattagagattcag	chrII:14019040-14019192	F01D5.10	-	0	17	0%	0	0	0%	0	1	0%	0	0
aatatgagtttcag	chrIV:10258286-10258504	F01G10.9	-	0	113	0%	0	0	0%	0	3	0%	0	0
ttgtgcagcttcag	chrX:13402710-13402932	F02C12.1	-	0	12	0%	0	0	0%	0	9	0%	0	0
tcgcccagtttcag	chrII:11632933-11633022	F07A11.6	-	0	16	0%	0	0	0%	0	21	0%	0	0
caatcaagttgaag	chrV:8856573-8857388	F07B7.12	-	0	1	0%	0	0	0%	0	0	0%	0	0
aatattagtttcag	chrV:9253769-9254013	F07C3.1	ptd-2	0	4	0%	0	0	0%	0	1	0%	0	0
attaatagtttcag	chrV:7317044-7317190	F07G11.9	-	0	2	0%	0	0	0%	0	0	0%	0	0
aaggaaagtttcag	chrI:12952658-12953005	F08A8.4	-	0	222	0%	0	1	0%	0	54	0%	0	0
actttgagtttcag	chrX:11391043-11391254	F08B12.1	prmn-1	1	55	2%	0	0	0%	0	11	0%	0	-2
cttgaaagtttaag	chrX:7588716-7588804	F08C6.1	-	0	0	0%	0	0	0%	0	3	0%	0	0
cctgaaagttgcag	chrII:2781908-2782033	F08D12.2	-	0	10	0%	0	1	0%	0	12	0%	0	0
tttactagtttcag	chrIII:7344639-7344753	F08F8.6	-	0	0	0%	0	0	0%	0	1	0%	0	0
aaagatagtttcag	chrIV:12429944-12430049	F08G5.5	ugt-65	0	39	0%	0	0	0%	1	15	7%	0	7
atgtcgagtttcag	chrX:10161142-10161201	F09B9.4	-	0	40	0%	0	0	0%	0	15	0%	0	0
ttgagaagtttcag	chrX:1490267-1490342	F09D10.5	-	0	3	0%	0	0	0%	0	1	0%	0	0
tgcacgagttttag	chrII:5367915-5368382	F09E5.12	-	1	7	14%	0	2	0%	0	4	0%	-14	-14
aaacttagttttag	chrV:12023078-12023326	F10C2.3	-	0	9	0%	0	0	0%	0	4	0%	0	0
cacggaagttttag	chrI:8440262-8440366	F10D11.3	-	0	0	0%	0	0	0%	0	2	0%	0	0
aatccaagttttag	chrV:7161450-7161697	F10D2.11	ugt-41	0	29	0%	0	0	0%	0	27	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
cctaatagttccag	chrII:7104691-7104878	F10E7.8	farl-11	0	0	0%	0	1	0%	0	4	0%	0	0
tttacaagttccag	chrIII:4597358-4597627	F10F2.1	sel-2	0	34	0%	0	5	0%	0	40	0%	0	0
gttgaaagtttcag	chrIII:4642310-4642404	F10F2.2	-	0	110	0%	0	2	0%	0	64	0%	0	0
catattagttttag	chrV:7328625-7328781	F10G2.3	clec-7	0	15	0%	0	2	0%	0	17	0%	0	0
aaaccgagtttcag	chrX:12979152-12979274	F11C1.4	-	0	3	0%	0	0	0%	0	0	0%	0	0
agctttagttccag	chrX:12989627-12989713	F11C1.7	-	0	2	0%	0	0	0%	4	9	44%	0	44
cagaacagttacag	chrI:14872352-14872507	F11C3.2	unc-122	0	5	0%	0	0	0%	0	1	0%	0	0
gctcaaagttgcag	chrX:3322567-3322808	F11D5.3	ddr-2	0	7	0%	0	0	0%	0	5	0%	0	0
ttttaaagtttcag	chrX:3323020-3323112	F11D5.3	ddr-2	0	8	0%	0	0	0%	0	1	0%	0	0
gacaacagtttcag	chrX:3322843-3322987	F11D5.3	ddr-2	0	6	0%	0	2	0%	0	1	0%	0	0
taaaatagttccag	chrIII:7027975-7028051	F11H8.4	cyk-1	0	7	0%	0	0	0%	21	51	41%	0	41
attcgaagttgcag	chrX:8275292-8275377	F13B9.5	ksr-1	0	1	0%	0	3	0%	0	3	0%	0	0
ctataaagttgcag	chrX:597103-597239	F13C5.3	-	0	1	0%	0	0	0%	0	0	0%	0	0
aatacaagtttcag	chrX:5831600-5831696	F13D11.1	acp-5	0	105	0%	0	0	0%	0	70	0%	0	0
attccaagttacag	chrIV:10871428-10871603	F13E9.1	-	0	7	0%	0	9	0%	4	75	5%	0	5
atttgaagtttcag	chrI:7295483-7295685	F13G3.2	srd-53	0	2	0%	0	0	0%	0	3	0%	0	0
tccaacagttacag	chrIV:10992658-10992928	F13H10.5	-	0	3	0%	0	0	0%	0	1	0%	0	0
tttcgaagtttaag	chrX:6924096-6924237	F14B8.7	otpl-3	0	12	0%	0	0	0%	0	14	0%	0	0
acaactagattaag	chrX:10517339-10517631	F14F3.1	vab-3	0	3	0%	0	1	0%	0	1	0%	0	0
gagcacagtttcag	chrV:10404551-10404842	F15H10.7	-	0	0	0%	0	0	0%	0	1	0%	0	0
tcttaaagattcag	chrI:12148485-12148696	F15H9.4	sri-16	0	1	0%	0	0	0%	0	0	0%	0	0
tccattagtttcag	chrX:14106494-14107188	F16B12.6	-	0	23	0%	2	8	25%	17	73	23%	25	23
caattgagtttcag	chrV:1619909-1620018	F16B4.12	-	0	9	0%	0	0	0%	0	4	0%	0	0
aaatttagtttcag	chrX:8454457-8455449	F16F9.2	dpy-6	0	32	0%	0	0	0%	0	1	0%	0	0
ttgaaaagcttcag	chrX:4671168-4671294	F16H11.1	-	0	8	0%	0	1	0%	0	4	0%	0	0
tgaataagttatag	chrI:13186634-13186851	F17B5.1	-	0	15	0%	0	0	0%	0	0	0%	0	0
aattttagttccag	chrX:13114070-13114173	F17H10.2	-	4	16	25%	1	3	33%	9	30	30%	8	5
attattagttacag	chrX:13117235-13117390	F17H10.3	snx-17	0	8	0%	0	2	0%	0	7	0%	0	0
agagagagtttcag	chrII:3400230-3400477	F18A12.6	nep-10	0	0	0%	0	0	0%	0	3	0%	0	0
gtttacagtttcag	chrI:8078005-8078147	F18C12.1	che-3	0	0	0%	0	0	0%	0	1	0%	0	0
aaaaaaagttacag	chrV:12753197-12753341	F18E2.5	gpa-13	0	1	0%	0	0	0%	0	0	0%	0	0
agtttaagtttaag	chrX:8587462-8587573	F18E9.3	-	0	10	0%	0	0	0%	0	21	0%	0	0
actataagttccag	chrIV:331367-331640	F18F11.4	-	0	19	0%	0	0	0%	0	0	0%	0	0
cgtcacagttttag	chrII:3660571-3660786	F19B10.4	-	0	1	0%	0	0	0%	0	1	0%	0	0
aaagacagttgcag	chrX:10017350-10017481	F19C6.4	-	0	1	0%	0	1	0%	0	5	0%	0	0
aataatagtttcag	chrII:14624797-14624913	F19H8.5	mltn-10	0	2	0%	0	0	0%	0	0	0%	0	0
ttgagaaggttcag	chrIV:12172142-12172462	F20B10.1	nlr-1	0	18	0%	0	2	0%	0	12	0%	0	0
ctaaatagttttag	chrX:17698604-17698942	F20B4.6	cgt-2	0	8	0%	0	1	0%	0	12	0%	0	0
ccatctagtttcag	chrX:14974044-14974324	F20D1.2	tbc-1	0	6	0%	0	2	0%	28	49	57%	0	57
atttaaagttatag	chrII:7348247-7348368	F21D12.1	nhr-21	1	10	10%	2	2	100%	2	4	50%	90	40
cccaaaagttgcag	chrX:9895826-9896038	F21G4.3	-	0	8	0%	0	0	0%	0	0	0%	0	0
tgagttaggttcag	chrX:9911559-9911955	F21G4.6	-	0	6	0%	0	0	0%	0	5	0%	0	0
tttactagctacag	chrX:9916506-9916634	F21G4.6	-	0	4	0%	0	5	0%	0	4	0%	0	0
tataaaagctgcag	chrIII:5118383-5118524	F21H11.2	-	0	4	0%	0	5	0%	3	21	14%	0	14
cgaaaaagttccag	chrX:6520389-6520550	F22A3.1	ets-4	2	22	9%	0	0	0%	0	4	0%	0	-9
tttcttagttccag	chrV:10460210-10460315	F22E12.3	-	3	22	14%	0	0	0%	0	0	0%	0	0
agttcgagtttcag	chrII:2660269-2660389	F22E5.3	gcy-21	0	2	0%	0	0	0%	0	0	0%	0	0
acaaatagtttcag	chrX:6004713-6004901	F22F4.1	-	0	143	0%	0	1	0%	0	0	0%	0	0
ttgaaaagttacag	chrX:5990140-5990292	F22F4.3	klp-13	0	1	0%	0	0	0%	0	0	0%	0	0
ttcaaaagtttaag	chrII:35301-35540	F23F1.6	-	0	9	0%	0	0	0%	0	66	0%	0	0
atctgaagttttag	chrIII:6496851-6497184	F23F12.13	-	0	7	0%	0	0	0%	0	2	0%	0	0
ttaactagtctcag	chrV:12372674-12372847	F23H12.7	-	0	1	0%	0	0	0%	0	1	0%	0	0
ctcctaagtttcag	chrI:4887298-4887456	F25F8.1	glc-2	0	11	0%	0	0	0%	0	10	0%	0	0
tttataagtttcag	chrI:9205579-9205739	F25H5.1	-	0	24	0%	0	2	0%	0	21	0%	0	0
gttctaagtttcag	chrIV:9945234-9945498	F25H8.3	gon-1	0	12	0%	0	2	0%	0	10	0%	0	0
aaataaagtttcag	chrV:13456971-13457095	F25H9.3	lurp-3	0	2	0%	0	0	0%	0	2	0%	0	0
aaaacaagtttcag	chrI:9778594-9778690	F26E4.7	-	1	5	20%	0	0	0%	0	3	0%	0	-20
caaaaaagttgcag	chrV:20577453-20577564	F26F2.7	-	0	2	0%	0	0	0%	32	52	62%	0	62
atctgcagttccag	chrII:14396978-14397124	F26H11.2	-	0	6	0%	0	1	0%	25	47	53%	0	53
tcttccagtttcag	chrI:7705207-7705470	F27D4.2	lsy-22	2	20	10%	4	6	67%	65	92	71%	57	61
aagattagatttag	chrX:7664200-7664330	F27D9.6	dhs-29	0	34	0%	0	0	0%	0	0	0%	0	0
taaactagtttcag	chrI:4943856-4944396	F28B3.1	-	0	8	0%	1	3	33%	26	48	54%	33	54
attgatagcttcag	chrI:4946635-4946961	F28B3.1	-	0	38	0%	0	8	0%	18	91	20%	0	20
taaactagttgcag	chrI:4921404-4921460	F28B3.8	imb-1	0	5	0%	1	4	25%	26	46	57%	25	57
ctgataagtttcag	chrIII:6811210-6811292	F28F5.3	lim-8	0	35	0%	0	0	0%	0	18	0%	0	0
ataatcagttacag	chrIII:6811634-6811820	F28F5.3	lim-8	0	14	0%	0	1	0%	0	18	0%	0	0
atgaaaagtttaag	chrV:10747986-10748428	F28F7.2	-	0	1	0%	0	0	0%	0	0	0%	0	0
attttgagctacag	chrX:14143413-14143565	F28H6.2	ceh-89	0	14	0%	0	1	0%	0	8	0%	0	0
gtatttaggttcag	chrII:13108322-13109413	F29C12.3	rict-1	55	87	63%	0	0	0%	0	0	0%	0	0
tttcaaagtttaag	chrII:13113775-13114080	F29C12.3	rict-1	0	13	0%	0	2	0%	32	42	76%	0	76
gcaatgagttacag	chrIV:139551-139610	F29C4.8	col-99	0	1	0%	0	0	0%	0	1	0%	0	0
tttcccagtttcag	chrV:10674310-10674414	F29F11.5	-	0	2	0%	0	0	0%	1	3	33%	0	33
gatcagagtttcag	chrX:11507707-11508062	F29G6.1	-	0	21	0%	0	0	0%	0	1	0%	0	0
atcataagtttcag	chrI:14831511-14831805	F32A7.3	eva-1	0	6	0%	0	0	0%	0	0	0%	0	0
aattcgagtttcag	chrI:2673246-2673406	F32B5.7	-	0	20	0%	0	0	0%	0	5	0%	0	0
catctgagtttcag	chrV:10895029-10895183	F32D8.5	-	0	22	0%	2	8	25%	12	91	13%	25	13
cttttcagtttcag	chrV:10899595-10899707	F32D8.7	-	4	7	57%	0	0	0%	1	1	100%	0	43
tgatcaagattcag	chrIV:7572749-7573633	F32E10.3	clec-180	0	110	0%	0	0	0%	0	0	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
aacccaagtttcag	chrV:13361974-13362290	F32H5.4	-	0	3	0%	0	0	0%	0	1	0%	0	0
caaaaaagtttcag	chrI:12582816-12582906	F33E2.4	-	0	19	0%	0	0	0%	0	2	0%	0	0
tataaaagtttcag	chrII:2685637-2685732	F34D6.3	sup-9	0	5	0%	0	0	0%	0	2	0%	0	0
aaatccagtttcag	chrII:2691591-2691669	F34D6.4	set-11	0	2	0%	0	0	0%	0	0	0%	0	0
ttttgaagtttcag	chrX:3798905-3799006	F35A5.3	abu-10	0	3	0%	0	0	0%	0	0	0%	0	0
aatcagagtttcag	chrX:3790246-3790345	F35A5.4	-	0	9	0%	0	0	0%	0	0	0%	0	0
gtaatgagtttcag	chrV:11617472-11617561	F35B12.8	glb-15	0	8	0%	0	0	0%	0	7	0%	0	0
ttaattagttttag	chrX:17026299-17026399	F35B3.5	ptrn-1	0	45	0%	0	5	0%	0	35	0%	0	0
gggaaaagttgcag	chrX:17036950-17037063	F35B3.7	-	0	4	0%	0	1	0%	0	2	0%	0	0
caataaagttttag	chrII:8243489-8243622	F35C11.1	nlp-5	0	2	0%	0	0	0%	0	6	0%	0	0
tgtatcagttccag	chrII:12893061-12893255	F35C5.5	clec-62	340	384	89%	1	1	100%	146	161	91%	11	2
tcaattagttccag	chrX:5358576-5358744	F35C8.7	chtl-1	0	8	0%	0	8	0%	0	42	0%	0	0
ttacaaagttccag	chrV:13722326-13722453	F35E12.2	-	0	1	0%	0	0	0%	0	1	0%	0	0
tattaaagtttcag	chrV:13749218-13749606	F35E12.8	-	0	58	0%	0	0	0%	0	16	0%	0	0
tatttaagtttcag	chrV:3292155-3292295	F35F10.4	-	0	3	0%	0	0	0%	0	1	0%	0	0
tcaacaagttacag	chrIV:8299155-8299614	F35H10.7	nprl-3	0	12	0%	1	2	50%	3	34	9%	50	9
cgtgaaagattcag	chrX:929138-929355	F35H12.2	tbc-11	0	15	0%	0	7	0%	0	8	0%	0	0
ccaatgagtttcag	chrIV:4268102-4268192	F36A4.4	-	0	0	0%	0	0	0%	0	4	0%	0	0
gaaccaagtttcag	chrIV:4266450-4266555	F36A4.5	-	0	3	0%	0	5	0%	0	25	0%	0	0
aattctagtctcag	chrV:9403118-9403455	F36D4.4	-	0	0	0%	0	0	0%	0	1	0%	0	0
aaatatagttttag	chrV:15981996-15982656	F36G9.14	fbxa-99	0	5	0%	0	0	0%	0	3	0%	0	0
tcaaatagttacag	chrII:1774320-1774446	F36H5.1	math-26	0	16	0%	0	0	0%	0	6	0%	0	0
aattcaagtttcag	chrV:1790881-1791041	F36H9.2	-	0	2	0%	0	0	0%	0	1	0%	0	0
aaatatagtttcag	chrI:6431064-6431160	F37E3.3	-	0	0	0%	0	0	0%	0	2	0%	0	0
gcttaaagttatag	chrIV:6592970-6593094	F38A5.11	irld-7	0	0	0%	0	0	0%	0	1	0%	0	0
ataaaaagttatag	chrV:20761746-20762024	F38A6.2	elp-1	0	38	0%	0	1	0%	0	38	0%	0	0
atttcaagttgcag	chrIV:9464900-9465009	F38E11.6	-	1	1	100%	0	0	0%	0	0	0%	0	0
aaagtcagttgcag	chrX:482899-483182	F38G1.1	che-2	0	1	0%	0	0	0%	0	0	0%	0	0
tctgaaagtttaag	chrX:15241583-15241716	F39B1.1	piki-1	0	15	0%	0	1	0%	1	14	7%	0	7
aaaaaaagttccag	chrI:14763511-14763620	F39B2.8	-	0	2	0%	0	1	0%	0	2	0%	0	0
cttaaaagtttcag	chrX:16892193-16892392	F39F10.3	-	0	0	0%	0	2	0%	0	21	0%	0	0
gtgtaaagttccag	chrX:838919-839022	F39H12.3	-	0	32	0%	0	6	0%	0	35	0%	0	0
ttcaaaagttttag	chrX:846462-846574	F39H12.4	igcm-1	0	48	0%	0	1	0%	0	3	0%	0	0
gtagagagtttcag	chrX:14678665-14678776	F40E10.4	slt-1	0	6	0%	0	0	0%	0	1	0%	0	0
ctgttcagttacag	chrII:11134148-11134228	F40F8.5	-	0	123	0%	0	9	0%	0	65	0%	0	0
gaattgagttccag	chrIII:182839-182980	F40G9.15	-	0	1	0%	0	0	0%	0	2	0%	0	0
tctagtagtttcag	chrI:12272971-12273091	F41D3.9	-	0	1	0%	0	0	0%	0	0	0%	0	0
cactcaagtttcag	chrX:8391146-8391288	F41D9.3	-	0	19	0%	0	7	0%	0	30	0%	0	0
agaaacagattcag	chrX:10283084-10283193	F41E7.3	npr-6	0	1	0%	0	0	0%	0	0	0%	0	0
ccaaaaagtttcag	chrV:4646652-4646870	F41F3.2	soc-1	1	30	3%	0	6	0%	5	33	15%	-3	12
atcgagagttttag	chrII:6770046-6770219	F41G3.12	agr-1	0	2	0%	0	0	0%	0	0	0%	0	0
taatttagttgcag	chrIV:3357390-3357529	F42A6.1	-	0	0	0%	0	0	0%	0	2	0%	0	0
cctctgagtttcag	chrIV:8609745-8609903	F42A9.6	-	0	1	0%	0	5	0%	0	46	0%	0	0
ccattgagttgcag	chrIII:776856-777015	F42G9.5	alh-11	0	47	0%	0	1	0%	0	42	0%	0	0
attattagttttag	chrIII:768538-768853	F42G9.9	-	0	33	0%	0	0	0%	0	22	0%	0	0
tcgcagagtttcag	chrIII:8489513-8489701	F42H10.7	ess-2	0	1	0%	0	6	0%	0	22	0%	0	0
aaaaatagtttaag	chrX:16666726-16666921	F43B10.2	tag-343	0	8	0%	0	0	0%	0	1	0%	0	0
agtagaagtttcag	chrIII:10490840-10491064	F43D9.1	-	1	19	5%	0	1	0%	0	0	0%	-5	0
tgttcaagttacag	chrII:7362976-7363112	F43E2.3	insc-1	0	6	0%	0	0	0%	0	5	0%	0	0
ttcctcagttgcag	chrIII:8013040-8013214	F44B9.3	cit-1.2	0	10	0%	1	1	100%	14	32	44%	100	44
tagcagagtttcag	chrV:2237048-2237573	F44C8.1	cyp-33C4	0	11	0%	0	0	0%	0	2	0%	0	0
gttcaaagttccag	chrII:8828918-8829034	F44E2.3	-	0	14	0%	0	7	0%	1	24	4%	0	4
ttttccagttgcag	chrII:10893663-10893864	F44F4.5	sra-10	1	1	100%	0	0	0%	0	0	0%	0	0
tctctgagttttag	chrX:7989884-7990028	F45E1.7	sdpn-1	0	15	0%	0	0	0%	0	7	0%	0	0
cttctaagtttcag	chrII:11060121-11060156	F45E10.1	unc-53	0	1	0%	0	0	0%	0	0	0%	0	0
tatgcaagtttcag	chrIV:7639873-7640119	F45E4.7	nep-16	0	3	0%	0	0	0%	0	0	0%	0	0
catttaagttttcag	chrV:9773902-9774403	F46B6.2	-	0	1	0%	0	0	0%	0	0	0%	0	0
aatagtagcttcag	chrV:9780177-9780403	F46B6.5	-	1	9	11%	3	8	38%	61	97	63%	26	52
atgtttagtttaag	chrX:7538257-7538397	F46C8.7	glb-16	0	1	0%	0	0	0%	0	0	0%	0	0
ttgaatagttccag	chrX:10374503-10374684	F46F6.1	rme-4	0	6	0%	0	3	0%	0	9	0%	0	0
aactcaagttatag	chrX:13345618-13345720	F46G10.5	ptr-24	0	140	0%	0	0	0%	0	88	0%	0	0
aactatagttttag	chrX:7259870-7260028	F46H5.8	lact-1	0	8	0%	0	0	0%	0	6	0%	0	0
taactaagtttcag	chrX:9811284-9812288	F47A4.2	dpy-22	0	44	0%	0	3	0%	0	29	0%	0	0
ctgaaaagtttcag	chrX:10894901-10895155	F47B10.2	haly-1	0	231	0%	0	0	0%	0	186	0%	0	0
aatttcagttccag	chrV:14326459-14326545	F47B8.5	-	21	23	91%	0	0	0%	0	0	0%	0	0
ttcccaagtttcag	chrV:14332048-14332364	F47B8.8	-	0	49	0%	0	4	0%	0	44	0%	0	0
atcatcagttgcag	chrV:3850112-3850404	F47C10.2	btb-21	0	11	0%	0	0	0%	0	11	0%	0	0
taacaaagttttag	chrV:3843374-3843725	F47C10.6	ugt-32	0	15	0%	0	0	0%	0	1	0%	0	0
aatccgagtttcag	chrX:3894454-3894559	F47F2.3	-	0	10	0%	0	0	0%	0	2	0%	0	0
cataaaagtttcag	chrX:2389460-2389565	F47G3.1	-	0	12	0%	0	0	0%	0	5	0%	0	0
aagaatagttgcag	chrX:2387470-2387595	F47G3.1	-	0	23	0%	0	0	0%	0	10	0%	0	0
ttgaatagttgcag	chrV:11315378-11315975	F47G9.3	cutl-18	0	5	0%	0	0	0%	0	3	0%	0	0
acatacagttttag	chrV:11315061-11315171	F47G9.3	cutl-18	0	318	0%	0	0	0%	0	53	0%	0	0
ttcggaagtttcag	chrV:17359064-17359772	F47H4.2	-	0	2	0%	0	0	0%	0	0	0%	0	0
attatcagtttcag	chrV:17354159-17354437	F47H4.2	-	1	49	2%	0	2	0%	0	0	0%	-2	0
tgttaaagtttcag	chrI:6594552-6594907	F48A9.1	-	1	57	2%	0	3	0%	0	94	0%	-2	-2
cgaacaagttctag	chrX:2147861-2147962	F48B9.5	npax-2	0	7	0%	0	0	0%	0	0	0%	0	0
attcatagatttag	chrX:7504631-7504768	F48E3.7	lgc-11	0	3	0%	0	0	0%	0	3	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
aaattgagtttcag	chrV:641667-641903	F48G7.11	nhr-190	0	1	0%	0	1	0%	0	6	0%	0	0
caaatcagtttcag	chrV:16862869-16863028	F49A5.4	clec-24	0	1	0%	0	0	0%	0	1	0%	0	0
tttgttaggtatag	chrV:16865945-16866130	F49A5.5	clec-28	4	4	100%	0	0	0%	2	2	100%	0	0
agctagagttttag	chrX:1100601-1100907	F49E7.1	rme-6	0	18	0%	0	3	0%	0	33	0%	0	0
tatataagtttcag	chrX:1096067-1096148	F49E7.2	-	0	118	0%	0	1	0%	0	74	0%	0	0
actaaaagtttcag	chrX:2086479-2086725	F49H12.2	-	0	3	0%	0	0	0%	0	1	0%	0	0
atccaaagcttcag	chrI:8324914-8325021	F52B5.5	-	0	2	0%	4	9	44%	41	93	44%	44	44
aaaatcagttgtag	chrX:11587250-11587378	F52D10.1	abts-2	0	7	0%	0	0	0%	0	1	0%	0	0
tccccaagctccag	chrX:16276869-16277173	F52E10.1	sdc-1	0	8	0%	0	1	0%	0	11	0%	0	0
caataaagtttcag	chrIV:13547339-13547659	F52G2.3	-	0	23	0%	0	2	0%	1	17	6%	0	6
tctctcaggttcag	chrX:2861761-2862165	F53B3.2	comt-1	0	1	0%	0	0	0%	0	0	0%	0	0
ctaccaagtttcag	chrX:2866066-2866178	F53B3.3	-	0	2	0%	0	0	0%	0	2	0%	0	0
aattcaagtttaag	chrV:13408430-13408566	F53F1.3	-	0	28	0%	0	7	0%	0	51	0%	0	0
ttaactagcttcag	chrII:10262788-10262945	F54B3.1	-	1	13	8%	4	5	80%	33	42	79%	72	71
aaaactagtttcag	chrI:4991701-4991844	F54C1.5	dyf-1	0	1	0%	0	0	0%	0	2	0%	0	0
caaactagtttcag	chrII:3827603-3827757	F54D10.8	-	0	2	0%	0	0	0%	0	0	0%	0	0
ccgaatagttacag	chrX:14614402-14614734	F54E4.1	rbc-1	0	19	0%	0	2	0%	2	22	9%	0	9
atgtctagtttcag	chrV:13815353-13815561	F55B12.2	-	0	1	0%	0	0	0%	0	0	0%	0	0
tattaaagcttcag	chrIV:7467918-7468220	F55G1.7	-	0	0	0%	0	0	0%	0	5	0%	0	0
attcggagtttcag	chrI:588632-588775	F56A6.2	hum-7	0	17	0%	0	1	0%	0	11	0%	0	0
atctctagttgcag	chrX:3546470-3546604	F56B6.2	-	0	3	0%	4	6	67%	17	27	63%	67	63
gaattgagattcag	chrX:865606-865727	F56F10.4	lgl-1	0	56	0%	0	2	0%	0	34	0%	0	0
cctatgagtttcag	chrIII:4466637-4466756	F56F3.2	ndg-4	0	15	0%	0	4	0%	0	25	0%	0	0
tggtcaagattcag	chrI:6144175-6144321	F56F4.3	-	0	0	0%	0	0	0%	0	1	0%	0	0
attatgagtttcag	chrI:6135555-6135690	F56F4.5	pept-3	0	7	0%	0	0	0%	0	6	0%	0	0
agtcaaagttccag	chrI:6135128-6135524	F56F4.5	pept-3	0	9	0%	0	0	0%	0	6	0%	0	0
ggttcgagtttcag	chrI:11340587-11340759	F56G4.1	-	0	89	0%	0	1	0%	0	38	0%	0	0
tatctaagttacag	chrX:565285-565554	F57C12.4	mrp-2	0	33	0%	0	5	0%	0	3	0%	0	0
agaaaaagttgcag	chrX:578960-579107	F57C12.5	mrp-1	0	45	0%	0	3	0%	0	29	0%	0	0
ccaaatagtttaag	chrV:16481680-16481972	F57E7.1	-	0	1	0%	0	0	0%	0	0	0%	0	0
gtacacagttttag	chrX:11016602-11016778	F58A3.2	egl-15	0	9	0%	0	0	0%	0	2	0%	0	0
tatttaagcttcag	chrIII:9614642-9614827	F58A4.6	-	0	10	0%	0	6	0%	4	50	8%	0	8
tagtatagatccag	chrIII:9623722-9623954	F58A4.7	hlh-11	26	37	70%	0	0	0%	22	31	71%	0	1
aatcagagcttcag	chrII:5140033-5140121	F58A6.4	nas-29	0	8	0%	0	0	0%	0	0	0%	0	0
atgtgaagtttcag	chrV:10921229-10921365	F58B4.1	nas-31	0	4	0%	0	0	0%	0	2	0%	0	0
catcagagcttcag	chrII:1673707-1673907	F58E1.6	nhx-6	0	1	0%	0	0	0%	0	1	0%	0	0
cggaaaagttgtag	chrII:12943244-12943363	F58G1.6	arrd-10	0	21	0%	0	0	0%	0	10	0%	0	0
taataaagttatag	chrV:8093778-8093921	F58G4.6	str-146	0	1	0%	0	0	0%	0	0	0%	0	0
aatcccagttccag	chrV:11964242-11964382	F58H1.7	-	3	6	50%	0	0	0%	3	4	75%	0	25
tctattagttccag	chrII:5011759-5011949	F59A6.12	-	0	0	0%	0	4	0%	0	52	0%	0	0
aatcttagtttcag	chrX:16607186-16607298	F59C12.3	-	0	76	0%	0	5	0%	0	39	0%	0	0
aaaaaaagttgcag	chrX:16603620-16603746	F59C12.3	-	0	79	0%	0	5	0%	0	64	0%	0	0
ttgatgagtttcag	chrI:10507694-10507906	F59C6.7	che-13	0	6	0%	0	0	0%	0	2	0%	0	0
tggaagagttttag	chrV:3024972-3025458	F59D6.3	asp-8	0	20	0%	0	0	0%	0	9	0%	0	0
ctatcaagtttcag	chrV:3027505-3027885	F59D6.3	asp-8	0	181	0%	0	0	0%	0	37	0%	0	0
attctaagttttag	chrX:11005984-11006154	F59F3.4	del-5	0	8	0%	0	0	0%	0	15	0%	0	0
agggaaagttacag	chrX:10560234-10560361	F59F5.7	-	0	1	0%	0	0	0%	0	0	0%	0	0
tttttgagttgcag	chrII:5896240-5896327	F59G1.4	-	0	4	0%	0	0	0%	0	2	0%	0	0
tttataagttttag	chrI:7974278-7974454	H05F14.1	-	0	0	0%	0	0	0%	0	3	0%	0	0
ttaccaagttacag	chrIII:17421-17576	H10E21.4	-	0	42	0%	0	0	0%	0	1	0%	0	0
tttaagagtttcag	chrV:14900055-14900170	H12D21.10	-	0	16	0%	0	0	0%	0	9	0%	0	0
tgaacgagtttcag	chrV:8925398-8925436	H12N18.4	-	0	13	0%	0	0	0%	0	3	0%	0	0
aaaagaagtttcag	chrV:8926479-8926743	H12N18.4	-	0	42	0%	0	0	0%	0	15	0%	0	0
tttcatagttccag	chrX:17625180-17625535	H18N23.2	-	0	49	0%	0	6	0%	3	26	12%	0	12
acttgcagttacag	chrX:17624269-17624429	H18N23.2	-	3	303	1%	0	9	0%	2	204	1%	-1	0
attgaaagcttcag	chrIV:16232635-16232898	H25K10.5	hpa-1	0	0	0%	0	0	0%	0	1	0%	0	0
ttgaaaagtttcag	chrX:5239255-5239370	H28G03.6	mtm-5	0	3	0%	2	2	100%	3	6	50%	100	50
cagataagatttag	chrIV:5934695-5934897	H32C10.1	-	0	1	0%	0	0	0%	0	4	0%	0	0
tgtgttagttgcag	chrX:12650120-12650265	H36L18.1	-	0	1	0%	0	0	0%	0	0	0%	0	0
aatagtagtttcag	chrV:13652307-13652531	H37A05.1	lpin-1	0	26	0%	4	9	44%	23	78	29%	44	29
tttgccagttccag	chrX:1325056-1325158	H42K12.1	pdk-1	1	18	6%	3	7	43%	5	6	83%	37	78
tcctcaagttacag	chrV:12398542-12398684	K01D12.5	-	0	6	0%	0	0	0%	0	0	0%	0	0
cttgatagtttcag	chrIII:10757968-10758081	K01G5.10	-	0	16	0%	0	0	0%	0	18	0%	0	0
tattctagttgcag	chrI:8530334-8530414	K02B12.8	zhp-3	0	0	0%	0	6	0%	0	30	0%	0	0
ttttccagctcaag	chrX:13939236-13939353	K02B9.4	-	17	96	18%	1	4	25%	20	78	26%	7	8
gaatagagtttcag	chrIV:318189-318308	K02D7.4	dsc-4	0	240	0%	0	0	0%	0	69	0%	0	0
tcttaaagtttcag	chrI:6820762-6820926	K02F2.6	ser-3	0	4	0%	0	0	0%	0	7	0%	0	0
acgacaagttttag	chrX:6452056-6452224	K04E7.3	nas-33	0	10	0%	0	0	0%	0	3	0%	0	0
aaacaaagttttag	chrX:6454576-6454684	K04E7.3	nas-33	0	15	0%	0	0	0%	0	5	0%	0	0
atatcaagtttcag	chrI:8042937-8043114	K04G2.6	vacl-14	0	37	0%	0	8	0%	1	87	1%	0	1
gattgaagtttcag	chrV:9498831-9499139	K06A4.3	gsnl-1	0	105	0%	0	2	0%	0	40	0%	0	0
tccaaaagtttcag	chrV:9503104-9503242	K06A4.4	swt-5	0	5	0%	0	0	0%	0	0	0%	0	0
ttttaaagaagtag	chrIII:7482684-7482997	K07D8.1	mup-4	0	52	0%	0	2	0%	1	73	1%	0	1
tcattgagttccag	chrIV:6101482-6101570	K08B4.1	lag-1	0	4	0%	3	4	75%	30	58	52%	75	52
tgctgaagctttag	chrIV:1707494-1707617	K08D12.4	-	0	9	0%	0	0	0%	0	5	0%	0	0
aaacgaagtttcag	chrIV:12588038-12588392	K08E7.7	cul-6	0	50	0%	0	3	0%	0	18	0%	0	0
ctaaaaagttatag	chrX:15592397-15592512	K09A9.4	usp-33	0	7	0%	0	3	0%	0	15	0%	0	0
ttttggagttttag	chrX:15582793-15582947	K09A9.6	-	0	14	0%	0	0	0%	0	8	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
gtttcgagttttag	chrX:3300058-3300167	K09C4.1	-	0	5	0%	0	1	0%	0	7	0%	0	0
agtttgagttttag	chrX:10969018-10969187	K09C8.4	lge-1	0	5	0%	0	0	0%	0	1	0%	0	0
aacgaaagtttcag	chrV:5714744-5714993	K09H11.9	-	0	1	0%	0	0	0%	0	1	0%	0	0
ttgacaagtttcag	chrII:6373747-6373863	K10B2.1	lin-23	0	31	0%	1	8	13%	0	91	0%	13	0
agatatagtttcag	chrX:3109061-3109220	K10B3.6	-	0	46	0%	0	0	0%	0	36	0%	0	0
atttccagttttag	chrIV:12991362-12991489	K10D11.5	-	0	62	0%	0	1	0%	0	23	0%	0	0
agtaagagttacag	chrI:7123874-7124040	K10D3.2	unc-14	0	55	0%	0	7	0%	0	48	0%	0	0
tttttcagaaacag	chrIII:10279577-10279730	K10G9.3	pad-2	2	4	50%	1	1	100%	10	16	63%	50	13
ttgataagtttcag	chrV:5054015-5054109	K11D1.1	cwp-4	0	1	0%	0	0	0%	0	0	0%	0	0
aaaaaaagttctag	chrV:5054146-5054251	K11D1.1	cwp-4	0	1	0%	0	0	0%	0	0	0%	0	0
cctataagtttcag	chrIV:669233-669470	K11H12.11	-	0	29	0%	0	0	0%	0	0	0%	0	0
tacacaagtttcag	chrV:12214236-12214464	K12F2.2	-	0	20	0%	0	0	0%	0	8	0%	0	0
ttgaaaagttccag	chrI:5559756-5560078	M01A10.2	-	0	47	0%	0	1	0%	0	18	0%	0	0
aatcttagcttcag	chrIII:9259755-9259921	M01A8.1	-	0	16	0%	0	0	0%	0	12	0%	0	0
aaaaaaagctttag	chrI:5568128-5568214	M01E11.4	-	0	416	0%	0	1	0%	0	313	0%	0	0
ttaaaaagttgcag	chrI:5568245-5568301	M01E11.4	-	3	803	0%	0	2	0%	3	660	0%	0	0
ttttaaagttttag	chrX:708726-708876	M02A10.2	irk-2	0	0	0%	0	0	0%	0	1	0%	0	0
cttctaagcttcag	chrX:703845-704003	M02A10.2	irk-2	0	4	0%	0	0	0%	0	8	0%	0	0
gcagtaagtttcag	chrIV:3797184-3797302	M02B7.3	osm-3	0	1	0%	0	0	0%	0	0	0%	0	0
cgatagagtttcag	chrV:5611922-5612056	M03E7.4	-	0	3	0%	0	0	0%	0	0	0%	0	0
gaattcagtttcag	chrIV:11531897-11532015	M04B2.7	-	0	1	0%	0	0	0%	0	3	0%	0	0
cttgcgagtttcag	chrII:8486418-8486604	M05D6.7	gbh-2	0	23	0%	0	0	0%	0	9	0%	0	0
ccgtccagttccag	chrII:8361180-8361344	M195.2	-	0	1	0%	0	0	0%	0	0	0%	0	0
ctgtctagtttcag	chrII:10646647-10646868	M28.4	-	0	1	0%	0	0	0%	0	6	0%	0	0
aaactgagttccag	chrX:8259911-8260012	M60.7	-	0	2	0%	0	0	0%	0	1	0%	0	0
ttcaaaagttgaag	chrIV:11086430-11086587	M7.3	bcc-1	1	107	1%	0	1	0%	0	22	0%	-1	-1
ttatccagtttcag	chrIII:4556805-4556975	M88.5	-	0	5	0%	0	6	0%	16	37	43%	0	43
gatcaaagttccag	chrIII:4557536-4557719	M88.5	-	0	78	0%	0	9	0%	13	169	8%	0	8
tctaaaagtttgag	chrX:4109798-4109959	R02E4.2	-	0	1	0%	0	0	0%	0	0	0%	0	0
agaaaaagtttcag	chrX:15435605-15435709	R03A10.3	mocs-1	0	9	0%	0	0	0%	0	1	0%	0	0
tctaatagttacag	chrX:6767201-6767353	R03E9.4	irk-1	0	2	0%	0	0	0%	0	1	0%	0	0
aaaaagagattcag	chrX:13091510-13091671	R03G8.3	-	0	1	0%	0	0	0%	0	1	0%	0	0
tttgatagttttag	chrX:375828-376194	R04A9.2	nrde-3	0	7	0%	0	5	0%	0	15	0%	0	0
actatgagtttaag	chrV:10086188-10086317	R04B5.6	-	0	2	0%	0	0	0%	0	0	0%	0	0
tttgttagttacag	chrX:8816561-8816710	R04E5.2	-	1	109	1%	0	0	0%	0	77	0%	0	-1
atgccgagttccag	chrIII:8357518-8357828	R05D3.8	-	0	9	0%	0	2	0%	0	56	0%	0	0
aaatagaggtttag	chrV:2766993-2767435	R05D8.9	-	0	1	0%	0	0	0%	0	0	0%	0	0
atattaagtttcag	chrII:4910718-4910960	R05F9.1	-	0	26	0%	0	5	0%	1	80	1%	0	1
atgaatagtttcag	chrIV:7515666-7515941	R05G6.9	-	0	12	0%	0	0	0%	0	0	0%	0	0
agttagagttgtag	chrI:7255737-7255841	R06C7.9	ztf-15	0	0	0%	1	9	11%	0	52	0%	0	0
gttttgagtttcag	chrX:10742454-10743060	R07A4.1	egl-36	0	6	0%	0	0	0%	0	8	0%	0	0
atatagagtttcag	chrV:12099725-12100005	R07B7.16	nhr-209	0	3	0%	0	0	0%	0	0	0%	0	0
ggtatgagttacag	chrII:944753-944874	R07C3.1	clec-43	0	3	0%	0	0	0%	0	2	0%	0	0
tttctaagttacag	chrX:10331337-10331499	R07E3.4	-	0	324	0%	0	8	0%	0	240	0%	0	0
tttcatagtttcag	chrX:10342203-10342366	R07E3.7	-	0	56	0%	1	2	50%	0	11	0%	50	0
taagtaagttccag	chrIV:11208909-11209113	R07H5.9	-	0	2	0%	0	0	0%	0	2	0%	0	0
attatcagttttag	chrX:4827555-4827672	R08E3.1	-	0	383	0%	0	2	0%	0	185	0%	0	0
atcagcagttttag	chrV:15381539-15381742	R08H2.1	dhs-23	0	2	0%	0	1	0%	0	2	0%	0	0
tctgcgagttccag	chrIII:4292726-4292818	R10E4.5	-	0	0	0%	0	1	0%	1	33	3%	0	0
ttcgaaagttccag	chrX:3661624-3662121	R11G1.1	-	0	1	0%	0	0	0%	0	0	0%	0	0
aatgttagttgcag	chrX:3639754-3639839	R11G1.6	-	0	10	0%	0	0	0%	0	1	0%	0	0
attcctagttgcag	chrV:13513231-13513398	R11G10.2	-	0	1	0%	0	0	0%	0	0	0%	0	0
caacccagtttcag	chrV:518268-518476	R11G11.12	nhr-210	0	12	0%	0	0	0%	0	2	0%	0	0
aatcaaagttttag	chrX:13220326-13220464	R12H7.2	asp-4	0	536	0%	0	8	0%	0	409	0%	0	0
aattttagttttag	chrIV:7201144-7201296	R13A1.4	unc-8	0	0	0%	0	0	0%	0	1	0%	0	0
cttccgagtttcag	chrIII:7557502-7557654	R13A5.5	ceh-13	0	31	0%	0	0	0%	1	27	4%	0	4
aattggagtttcag	chrIII:6862302-6862375	R13F6.9	sma-3	0	23	0%	0	3	0%	0	18	0%	0	0
taattgagttacag	chrIII:5005654-5005772	R144.12	-	0	8	0%	0	0	0%	0	19	0%	0	0
aatcatagtttcag	chrIII:5016794-5017137	R144.7	-	0	7	0%	2	9	22%	4	97	4%	22	4
ttcactagtttcag	chrX:4389652-4389832	R160.1	dpy-23	0	33	0%	1	5	20%	2	15	13%	20	13
tttttgagtttaag	chrV:12975958-12976033	R186.5	shw-3	0	1	0%	0	0	0%	0	0	0%	0	0
tggaatagtttcag	chrV:11924647-11924936	R31.3	osm-6	0	2	0%	0	0	0%	0	0	0%	0	0
tgagttagttttag	chrX:15179850-15180132	T10B10.3	-	0	2	0%	0	4	0%	2	18	11%	0	11
ttttgcagtttcag	chrI:6532203-6532333	T10E9.7	-	1	5	20%	0	6	0%	0	32	0%	-20	-20
tctagaagtttcag	chrV:13474314-13474369	T10G3.8	-	0	4	0%	0	1	0%	0	4	0%	0	0
agtcccagtttcag	chrX:2296668-2296869	T10H10.2	-	0	322	0%	0	9	0%	0	58	0%	0	0
atatctagttccag	chrIV:11757437-11757547	T12A7.2	-	13	32	41%	0	2	0%	4	17	24%	-41	-17
attacaagttacag	chrIV:12049903-12050226	T12G3.8	bre-5	0	12	0%	0	0	0%	0	26	0%	0	0
ccgaaaagtttcag	chrIV:6273082-6273196	T13A10.10	aat-4	0	15	0%	0	2	0%	0	9	0%	0	0
ttacacagttacag	chrX:6185587-6185699	T13C5.2	-	0	1	0%	0	0	0%	0	0	0%	0	0
tttggaagttgcag	chrX:6207270-6207390	T13C5.6	-	0	5	0%	0	6	0%	0	9	0%	0	0
cctgtcagattcag	chrIV:9796121-9796234	T13F2.3	pis-1	5	12	42%	5	5	100%	104	110	95%	58	53
tcaacaagttctag	chrX:1175152-1175284	T13G4.3	tmc-1	0	22	0%	0	0	0%	0	8	0%	0	0
tagtaaagttctag	chrX:1176572-1176743	T13G4.3	tmc-1	0	26	0%	0	0	0%	0	5	0%	0	0
gaaagaagtttcag	chrX:1172353-1172779	T13G4.3	tmc-1	0	12	0%	0	1	0%	0	2	0%	0	0
attcgtagtttcag	chrX:1190679-1190765	T13G4.4	-	0	3	0%	0	0	0%	0	0	0%	0	0
tttttcagtttcag	chrX:4615389-4615499	T13H2.4	pqn-65	0	2	0%	2	3	67%	9	12	75%	67	75
gtaataagtttgag	chrII:8495427-8495582	T13H5.1	-	0	8	0%	0	0	0%	0	2	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
aactagagtttcag	chrII:6733016-6733137	T14B4.9	-	0	2	0%	0	0	0%	0	0	0%	0	0
gatttaagttacag	chrX:6566265-6566444	T14E8.3	dop-3	0	0	0%	0	0	0%	1	1	100%	0	0
attaaaagttgcag	chrIV:10153080-10153202	T14G10.5	-	0	70	0%	0	7	0%	3	63	5%	0	5
ttatcgagtttcag	chrIV:10150315-10150426	T14G10.6	tsp-12	0	12	0%	0	6	0%	0	104	0%	0	0
acaaaaagatttag	chrX:12863350-12863445	T14G8.3	-	0	2	0%	0	0	0%	0	1	0%	0	0
ttgttcagtttcag	chrIII:5294829-5294909	T15B12.1	-	0	26	0%	0	4	0%	0	68	0%	0	0
gtattaagtttaag	chrV:6833199-6833281	T15B7.14	-	0	0	0%	0	0	0%	0	2	0%	0	0
gaacatagttctag	chrV:12929554-12929704	T16G1.2	-	0	21	0%	0	0	0%	0	0	0%	0	0
tgttctagttttag	chrV:12940364-12940453	T16G1.4	-	0	28	0%	0	0	0%	0	4	0%	0	0
gataacagttttag	chrV:12950224-12950389	T16G1.9	-	0	29	0%	0	3	0%	0	15	0%	0	0
caatcaagtttcag	chrIII:10077373-10077554	T16G12.9	-	0	0	0%	0	1	0%	0	0	0%	0	0
ttctgaagttttag	chrI:2454659-2454910	T16H5.1	inx-19	0	0	0%	0	1	0%	0	0	0%	0	0
ctagataggtttag	chrIII:731526-731627	T17H7.4	-	0	90	0%	0	6	0%	0	70	0%	0	0
tttccaagttacag	chrV:11223791-11223965	T19B10.3	-	0	28	0%	0	0	0%	0	28	0%	0	0
actaaaagttacag	chrIII:608027-608272	T19C3.1	best-17	0	17	0%	0	0	0%	0	9	0%	0	0
attccaagttttag	chrX:3936148-3936225	T19D2.1	-	0	7	0%	0	0	0%	0	1	0%	0	0
tgaaacagtttcag	chrV:16840571-16840731	T20B3.13	clec-40	0	2	0%	0	0	0%	0	1	0%	0	0
acatcaagtttcag	chrV:3409083-3409234	T20D4.7	-	0	3	0%	0	4	0%	0	0	0%	0	0
cattgaagtttcag	chrI:10301751-10301961	T20F10.5	-	0	3	0%	0	0	0%	0	3	0%	0	0
taaatgagtttcag	chrI:10301258-10301357	T20F10.5	-	0	8	0%	0	0	0%	0	2	0%	0	0
aattatagtttcag	chrIII:7247385-7247487	T21D11.1	-	0	3	0%	0	0	0%	0	0	0%	0	0
atttaaagttttag	chrV:1143009-1143156	T21H3.4	cutl-22	0	3	0%	0	0	0%	0	0	0%	0	0
ttttaaagctttag	chrII:8621331-8621690	T22C8.3	-	0	3	0%	0	1	0%	1	2	50%	0	50
ttcataagtttcag	chrIV:6926798-6926898	T22D1.11	-	0	18	0%	0	2	0%	0	4	0%	0	0
attaatagttacag	chrX:12783304-12783469	T22H6.2	alh-13	97	607	16%	0	0	0%	14	100	14%	0	-2
acaaggagttgcag	chrX:12782434-12782555	T22H6.2	alh-13	2	1183	0%	0	4	0%	1	213	0%	0	0
agttaaagttacag	chrX:12802561-12802867	T22H6.6	-	0	7	0%	0	0	0%	0	8	0%	0	0
gttaagagttccag	chrIV:3154534-3154775	T23E1.1	-	0	1	0%	0	0	0%	0	0	0%	0	0
atgtcgagcttcag	chrX:17671104-17671204	T23E7.2	-	0	167	0%	0	3	0%	0	86	0%	0	0
ctaaatagtttcag	chrX:5498522-5498697	T23F2.2	-	0	15	0%	0	0	0%	0	1	0%	0	0
tcaactagttacag	chrIII:3792038-3792810	T24A11.1	mtm-3	0	6	0%	0	0	0%	18	34	53%	0	53
aaagttagttacag	chrX:6170645-6170764	T25B2.2	-	0	1	0%	0	2	0%	0	24	0%	0	0
taaaccagctttag	chrIV:10762316-10762405	T25B9.7	ugt-54	0	2	0%	0	0	0%	0	1	0%	0	0
gaagtcagttttag	chrX:11498256-11498403	T25C12.3	-	0	188	0%	0	3	0%	0	125	0%	0	0
cgaataagtttcag	chrV:16766086-16766226	T25E12.4	dkf-2	0	20	0%	0	7	0%	0	65	0%	0	0
tgattaagtttcag	chrX:17227204-17227312	T25G12.6	-	0	27	0%	0	0	0%	0	11	0%	0	0
tcactaagttacag	chrIII:6470903-6471075	T26A5.2	-	0	2	0%	0	2	0%	3	31	10%	0	10
gatatcagtttcag	chrIII:6449521-6449685	T26A5.6	-	0	31	0%	7	9	78%	85	134	63%	78	63
tctgtcagtttcag	chrII:9232101-9232196	T26C5.1	gst-13	0	178	0%	0	6	0%	0	74	0%	0	0
agacgaagtttcag	chrV:15791874-15792052	T26E4.4	-	0	2	0%	0	0	0%	0	0	0%	0	0
attgaaagttgcag	chrI:6108876-6109062	T27A3.7	-	0	2	0%	0	5	0%	1	51	2%	0	2
tatcttagtttcag	chrX:16537904-16538041	T27B1.2	pat-9	17	38	45%	0	0	0%	0	3	0%	0	-45
tgaaatagattcag	chrV:11632298-11632454	T27F2.2	sipa-1	2	13	15%	0	1	0%	5	14	36%	-15	20
aaaacgagattcag	chrIII:11337803-11338084	T28D6.5	-	0	10	0%	0	2	0%	0	3	0%	0	0
tgttcaagtttcag	chrV:4503934-4504216	T28F12.2	-	0	12	0%	0	0	0%	0	14	0%	0	0
aatctaagattcag	chrII:11470981-11471694	W02B12.9	mfn-1	0	15	0%	0	0	0%	1	30	3%	0	3
caacaaagtttcag	chrIII:676422-676538	W02B3.2	grk-2	0	8	0%	0	1	0%	0	4	0%	0	0
tcacctagttccag	chrIII:682136-682284	W02B3.4	-	0	3	0%	0	0	0%	0	8	0%	0	0
ggtaaaagtttcag	chrIII:5440071-5440182	W03A5.6	-	0	3	0%	0	1	0%	3	27	11%	0	11
tactatagtttcag	chrIV:4057293-4057430	W03D2.6	-	0	6	0%	0	0	0%	0	3	0%	0	0
tttgtgagcttcag	chrI:2794281-2794382	W03D8.8	-	0	31	0%	0	0	0%	1	8	13%	0	13
ggtttcagtttcag	chrI:2219209-2219418	W03F11.5	-	1	34	3%	0	1	0%	1	6	17%	-3	14
taatcaagtttcag	chrX:12108214-12108363	W03G11.2	-	0	0	0%	0	0	0%	0	1	0%	0	0
gacttgagttttag	chrX:11083906-11084027	W04G3.6	-	0	48	0%	0	0	0%	0	25	0%	0	0
tgtaaaagttttag	chrV:11694198-11694355	W05E10.5	-	0	1	0%	0	0	0%	0	1	0%	0	0
aactgaagttttag	chrIII:13735589-13735671	W06F12.3	-	0	1	0%	0	0	0%	0	0	0%	0	0
ctagctagtttcag	chrV:6130898-6131047	W06H8.8	ttn-1	0	17	0%	0	2	0%	0	10	0%	0	0
cccaacagttccag	chrII:1133797-1134072	W09B6.4	-	0	32	0%	0	6	0%	0	61	0%	0	0
attagaagtttcag	chrI:13657821-13658126	W09C5.7	-	0	23	0%	0	9	0%	4	106	4%	0	4
attcaaagtttcag	chrI:9101167-9101240	W10D5.3	gei-17	0	12	0%	1	2	50%	0	9	0%	50	0
aatataagttctag	chrX:2021115-2023365	Y102A11A.3	-	0	110	0%	0	2	0%	0	80	0%	0	0
aattccagttacag	chrIII:6732092-6732297	Y102E9.1	odr-4	3	5	60%	0	0	0%	2	2	100%	0	40
cccccaagtttcag	chrIV:15999110-15999283	Y105C5B.21	jac-1	5	34	15%	1	1	100%	19	26	73%	85	58
taaatcagttccag	chrI:14476323-14476472	Y105E8A.17	ekl-4	0	6	0%	2	3	67%	20	26	77%	67	77
tgagaaagttagag	chrI:10113045-10113350	Y106G6D.3	-	0	0	0%	0	0	0%	6	6	100%	0	0
attagcagcttcag	chrI:5125350-5125500	Y110A7A.17	mat-1	0	72	0%	1	6	17%	9	197	5%	17	5
ttccaaagtttcag	chrV:19877044-19877154	Y116F11B.12	-	0	96	0%	0	6	0%	11	105	10%	0	10
cctcatagttccag	chrI:4514791-4514971	Y119C1B.5	-	2	13	15%	0	1	0%	0	11	0%	-15	-15
gcgaaaagtttcag	chrIII:2915611-2915750	Y119D3B.26	cdh-1	0	1	0%	0	0	0%	0	2	0%	0	0
tttgaaagttacag	chrV:16612764-16613036	Y32B12C.3	-	0	2	0%	0	0	0%	0	0	0%	0	0
tcaatcagtttcag	chrIII:5383353-5383568	Y32H12A.7	-	0	45	0%	5	7	71%	63	209	30%	71	30
ttggagagttccag	chrV:20510272-20510405	Y38H6C.8	-	0	1	0%	0	0	0%	0	0	0%	0	0
agtccgagtttcag	chrIII:10785928-10786046	Y39A1B.2	ptr-19	0	12	0%	0	0	0%	0	0	0%	0	0
tgcaaaagttccag	chrV:19121767-19121907	Y39B6A.12	bed-1	3	22	14%	3	7	43%	62	80	78%	29	64
cgaaaaagtttcag	chrV:19189728-19189824	Y39B6A.3	-	0	14	0%	5	8	63%	43	64	67%	63	67
cttcaaagtttcag	chrV:18980685-18980906	Y39B6A.40	-	0	3	0%	0	7	0%	0	277	0%	0	0
ccaactagttccag	chrV:3762736-3762878	Y39H10A.2	oac-55	0	1	0%	0	0	0%	0	0	0%	0	0
gttcaaagtttcag	chrI:13352980-13353237	Y40B1A.3	-	0	16	0%	4	7	57%	16	26	62%	57	62

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
ttcaacagtttcag	chrIV:15219647-15219835	Y40H7A.11	-	0	1	0%	0	0	0%	0	6	0%	0	0
catcccagtttcag	chrIII:11651386-11651608	Y41C4A.2	faah-6	0	1	0%	0	0	0%	0	1	0%	0	0
tttgagagttccag	chrIII:11655806-11655984	Y41C4A.2	faah-6	0	9	0%	0	0	0%	0	17	0%	0	0
gttctcagtttcag	chrIII:11687998-11688217	Y41C4A.4	-	2	28	7%	3	7	43%	32	63	51%	36	44
aagcaaagttacag	chrIV:1620304-1620404	Y41D4B.8	nhr-92	0	7	0%	0	0	0%	0	1	0%	0	0
caagcgagttatag	chrX:2989744-2989970	Y41G9A.1	osm-5	0	3	0%	0	0	0%	0	0	0%	0	0
cttttgagttccag	chrIV:8104462-8104666	Y42H9AR.3	rabs-5	0	0	0%	1	1	100%	0	2	0%	0	0
atttctagtttcag	chrIII:13226397-13226480	Y43F4A.1	-	0	39	0%	0	0	0%	0	3	0%	0	0
cgttgaagttccag	chrIV:13769247-13769495	Y45F10D.13	sorb-1	0	11	0%	0	0	0%	0	2	0%	0	0
tgagaaagttacag	chrV:4144738-4144915	Y45G5AL.1	-	0	19	0%	6	6	100%	47	71	66%	100	66
actggaagtttcag	chrIV:3961310-3961508	Y46C8AL.9	clec-75	0	1	0%	0	0	0%	0	0	0%	0	0
gttgaaagatttag	chrIV:3967771-3968022	Y46C8AR.1	clec-76	0	1	0%	0	0	0%	0	0	0%	0	0
ctaaaaagctacag	chrII:15222718-15223093	Y46E12BL.4	spsb-1	0	22	0%	1	2	50%	48	90	53%	50	53
atattcagttccag	chrII:12764834-12765052	Y46G5A.10	cnp-2	4	129	3%	0	1	0%	0	32	0%	-3	-3
ttcactagttttag	chrII:12836796-12836911	Y46G5A.26	lgc-35	0	1	0%	0	0	0%	1	3	33%	0	33
ttgttgagtttcag	chrV:1809367-1809468	Y46H3A.1	srt-42	0	1	0%	0	0	0%	0	1	0%	0	0
tcggcaagtttcag	chrV:1759793-1759931	Y46H3B.2	clec-204	0	5	0%	0	0	0%	0	4	0%	0	0
ttccccagttccag	chrI:3580343-3580776	Y47G6A.29	-	0	15	0%	3	3	100%	51	61	84%	100	84
tgctcgagtttcag	chrIII:11021908-11022035	Y48A6B.6	kvs-4	0	11	0%	0	0	0%	0	9	0%	0	0
ttaataagtttcag	chrII:14168326-14168583	Y48B6A.4	eat-2	0	3	0%	0	0	0%	0	0	0%	0	0
aaagaaagtttcag	chrII:13594969-13595071	Y48E1B.15	fbxc-23	0	6	0%	0	0	0%	0	2	0%	0	0
cattgcagtttcag	chrII:3609121-3609207	Y49F6A.5	-	0	0	0%	0	0	0%	0	9	0%	0	0
tcattaagcttcag	chrIII:234903-235032	Y50D7A.5	hpo-38	0	4	0%	0	0	0%	0	10	0%	0	0
taaaatagttttag	chrI:10968552-10968728	Y52B11A.2	-	0	1	0%	0	3	0%	8	10	80%	0	80
acttcgagatttag	chrI:11981051-11981174	Y53C10A.4	rga-2	0	1	0%	0	0	0%	0	2	0%	0	0
ttcctcagtttcag	chrI:11402825-11403026	Y53H1C.2	ego-2	0	38	0%	1	6	17%	17	65	26%	17	26
gctaatagtttcag	chrI:3159924-3160123	Y54E10A.9	vbh-1	0	41	0%	1	8	13%	21	169	12%	13	12
ccttttagtttcag	chrIII:2541713-2542666	Y54F10AM.4	ceh-44	1	1	100%	1	4	25%	0	13	0%	-75	-100
acggaaagcttcag	chrII:14464056-14464227	Y54G11B.1	dmsr-6	0	6	0%	0	0	0%	0	0	0%	0	0
tattccagattcag	chrIV:3013961-3014275	Y54G2A.3	-	47	50	94%	6	7	86%	145	156	93%	-8	-1
ttagcaagtttcag	chrII:13709614-13710183	Y54G9A.3	kqt-3	1	7	14%	0	1	0%	0	4	0%	-14	-14
tctaaaagttccag	chrIV:12613360-12613608	Y55D9A.1	-	0	7	0%	6	8	75%	20	74	27%	75	27
tctaaaagtttcag	chrV:5082029-5082708	Y58A7A.4	-	0	2	0%	0	0	0%	0	0	0%	0	0
gaaaagagtttcag	chrIV:5209340-5209435	Y59E9AL.4	-	0	1	0%	0	0	0%	0	1	0%	0	0
tccataagtttcag	chrIV:11066672-11066817	Y5F2A.2	ttr-17	0	762	0%	0	4	0%	0	1435	0%	0	0
gtataaagttacag	chrV:19976752-19977000	Y60A3A.24	-	0	1	0%	0	1	0%	0	1	0%	0	0
atgtgaagatttag	chrIV:430513-430623	Y66H1A.6	hum-8	0	82	0%	0	0	0%	0	59	0%	0	0
ccctaaagtttcag	chrIV:373962-374539	Y66H1B.3	-	0	11	0%	0	4	0%	0	36	0%	0	0
catcaaagtttcag	chrIV:14380097-14380317	Y67A10.8	paqr-3	0	11	0%	0	0	0%	0	2	0%	0	0
atcacaagtttcag	chrI:13605809-13605959	Y6B3A.1	agef-1	0	38	0%	1	7	14%	4	49	8%	14	8
attctgagtttcag	chrI:14047139-14047315	Y71A12C.2	-	0	1	0%	0	0	0%	0	4	0%	0	0
aaaacgagttgcag	chrI:2765093-2765693	Y71F9B.10	sop-3	0	5	0%	1	1	100%	3	11	27%	100	27
atctaaagcttcag	chrIV:6738751-6738906	Y73B6A.3	-	0	15	0%	0	0	0%	0	6	0%	0	0
atctgtagtttcag	chrI:13506738-13506959	Y87G2A.14	ndx-8	0	2	0%	0	0	0%	0	2	0%	0	0
gtttatagtttcag	chrI:13492971-13493101	Y87G2A.17	-	0	23	0%	0	1	0%	0	32	0%	0	0
aaaccgagttgcag	chrIV:2745920-2746069	Y94H6A.1	nhr-277	0	2	0%	0	0	0%	0	2	0%	0	0
tcgctcagtttcag	chrV:12615759-12616049	ZC116.3	-	0	8	0%	0	1	0%	0	3	0%	0	0
caatctagtttcag	chrX:877955-878094	ZC13.1	-	0	11	0%	0	3	0%	0	22	0%	0	0
attaccagtttcag	chrV:20302710-20302862	ZC15.1	-	0	0	0%	0	0	0%	0	1	0%	0	0
aatcatagttttag	chrV:8741461-8741589	ZC196.2	-	0	2	0%	0	0	0%	0	3	0%	0	0
tgagtaagtttcag	chrV:8736906-8737082	ZC196.3	-	0	1	0%	0	0	0%	0	0	0%	0	0
gtgggaagtttcag	chrV:5797854-5798009	ZC250.3	nstp-3	0	4	0%	0	0	0%	0	0	0%	0	0
aaaactagttttag	chrI:6414415-6414591	ZC328.3	-	0	10	0%	0	0	0%	0	7	0%	0	0
atcttgagtttcag	chrX:10063974-10064176	ZC373.4	-	0	40	0%	0	3	0%	0	52	0%	0	0
tcttccagttccag	chrV:14174697-14174909	ZC376.2	-	3	19	16%	0	0	0%	1	11	9%	0	-7
tgaagaagttttag	chrV:14171838-14172154	ZC376.2	-	0	427	0%	0	0	0%	0	418	0%	0	0
tgaaatagtttcag	chrV:14196302-14196397	ZC376.7	-	0	22	0%	5	7	71%	26	39	67%	71	67
tgaaaaagttctag	chrV:12782483-12782681	ZC455.1	-	0	4	0%	0	0	0%	0	1	0%	0	0
atattgagatttag	chrV:6729064-6729187	ZC487.1	-	0	2	0%	0	0	0%	3	4	75%	0	75
cactgaagattcag	chrX:10412846-10413015	ZC504.2	acr-8	0	11	0%	0	0	0%	0	2	0%	0	0
gttattagtttcag	chrV:8057211-8057364	ZC513.1	-	0	83	0%	0	0	0%	0	4	0%	0	0
atttccagaaacag	chrX:3845371-3845547	ZC64.3	ceh-18	8	10	80%	2	2	100%	7	7	100%	20	20
actaaaagttttag	chrI:11451795-11451865	ZK1025.2	-	0	158	0%	0	0	0%	0	0	0%	0	0
acaataagttacag	chrII:2321158-2321218	ZK1240.3	-	0	26	0%	0	0	0%	0	29	0%	0	0
aaaacaagttacag	chrIV:4502089-4502245	ZK180.2	gbb-2	0	7	0%	0	0	0%	0	3	0%	0	0
attggaagtttcag	chrIV:4543801-4543912	ZK185.5	-	0	10	0%	0	0	0%	0	8	0%	0	0
aggcaaagtttcag	chrV:9678820-9678973	ZK287.3	-	0	13	0%	0	0	0%	0	36	0%	0	0
agtatgagattcag	chrIII:8742412-8742579	ZK370.6	-	0	2	0%	0	0	0%	0	0	0%	0	0
ctttctagtcgcag	chrX:3482460-3482732	ZK377.1	wrt-6	144	197	73%	0	0	0%	0	0	0%	0	0
tttaaaagctttag	chrIV:6966263-6966393	ZK381.2	-	0	5	0%	0	0	0%	0	0	0%	0	0
atcataagttttag	chrIV:6968193-6968655	ZK381.8	-	0	3	0%	0	0	0%	0	0	0%	0	0
cgagaaagtttcag	chrI:7456505-7456666	ZK524.1	spe-4	0	6	0%	0	0	0%	0	6	0%	0	0
aaaacaaggttcag	chrIV:5403812-5403967	ZK616.1	-	0	3	0%	0	0	0%	0	0	0%	0	0
acgttgagttccag	chrIII:8882981-8883109	ZK637.1	svop-1	0	22	0%	0	0	0%	0	14	0%	0	0
ttaaacagtttcag	chrV:9280959-9281094	ZK682.4	hlh-10	0	4	0%	0	0	0%	0	1	0%	0	0
ccaacaagtttcag	chrIII:7910327-7910542	ZK688.1	-	0	1	0%	0	0	0%	0	1	0%	0	0
cgataaagttgcag	chrX:8793208-8793285	ZK721.1	chup-1	0	9	0%	0	1	0%	0	15	0%	0	0
ctcataagtttcag	chrIII:7628285-7628914	ZK783.1	fbn-1	0	47	0%	0	0	0%	0	0	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
ctaataagtttcag	chrX:3449456-3449647	ZK813.5	-	0	1	0%	0	0	0%	0	0	0%	0	0
gtatccaggttgag	chrI:14188007-14188126	ZK849.2	gopc-1	1	4	25%	0	0	0%	3	3	100%	0	75
ttccgaagctttag	chrV:12177103-12177207	ZK863.9	clec-224	0	6	0%	0	0	0%	0	2	0%	0	0
gaacatagtttcag	chrX:9513340-9513698	ZK899.8	gap-2	0	17	0%	0	2	0%	6	22	27%	0	27
actgaaagattaag	chrII:10103035-10103306	ZK945.4	-	0	2	0%	0	4	0%	0	9	0%	0	27
attttcagcttcag	chrII:10106033-10106385	ZK945.6	-	1	1	100%	0	0	0%	2	3	67%	0	-33
Not Enough Expression In glp-4														
aactatagagacag	chrV:11029155-11029274	C13G3.3	pptr-2	0	8	0%	11	16	69%	36	64	56%	69	56
ataatgagttttag	chrIV:7007145-7007250	C25A8.4	-	0	1	0%	0	57	0%	0	111	0%	0	0
tctcaaagattcag	chrIV:7794972-7795109	C33H5.15	sgo-1	1	8	13%	7	17	41%	335	620	54%	29	42
ttccctagtttcag	chrI:8737246-8737411	C36B1.8	gls-1	0	9	0%	2	18	11%	5	62	8%	11	8
ttcgccagttgcag	chrII:11667625-11667818	C47D12.1	trr-1	1	6	17%	22	25	88%	68	78	87%	71	71
cttaatagtttcag	chrV:13314577-13315356	C50B6.3	-	0	7	0%	23	40	58%	91	133	68%	58	68
gaaaatagttacag	chrI:8422838-8422939	F02E9.4	sin-3	1	7	14%	11	12	92%	72	83	87%	77	72
cccactagttgcag	chrI:7350553-7350613	F07A5.1	inx-14	0	2	0%	63	90	70%	275	682	40%	70	40
tcgaccagttccag	chrI:13168301-13168695	F22G12.5	-	2	6	33%	11	13	85%	141	158	89%	51	56
atgtatagtttcag	chrIII:5960462-5960981	F25B5.2	nop-1	0	1	0%	5	27	19%	9	83	11%	19	11
agttatagtttcag	chrV:4975855-4976910	F26G5.1	-	0	0	0%	4	12	33%	10	57	18%	0	0
ttttggagtttcag	chrI:9288738-9288923	F26H9.1	prom-1	0	0	0%	0	10	0%	0	54	0%	0	0
aaaataaggtttag	chrV:6025476-6025776	F29G9.2	-	1	9	11%	5	32	16%	24	145	17%	5	5
ttttttagttgcag	chrI:7834227-7834556	F30F8.1	-	0	0	0%	0	15	0%	0	64	0%	0	0
ttcaaaagtttcag	chrI:8807751-8807880	F36A2.1	cids-2	0	1	0%	4	11	36%	25	54	46%	36	46
tttgaaagtttcag	chrIV:11063051-11063143	F36H1.4	lin-3	0	5	0%	2	12	17%	9	172	5%	17	5
caaaaaagttctag	chrI:14783050-14783432	F39B2.4	sur-2	0	4	0%	20	20	100%	64	76	84%	100	84
atgaaaagttgtag	chrI:5703304-5703545	F46F11.9	-	0	0	0%	0	11	0%	0	9	0%	0	0
aaaataagtttcag	chrIII:5587716-5587883	F56D2.2	-	0	5	0%	0	16	0%	0	84	0%	0	0
atttatagttttag	chrI:6567818-6568189	F57B10.4	-	0	1	0%	3	24	13%	15	128	12%	13	12
tctcttagtttcag	chrI:8052467-8054029	K04G2.8	apr-1	0	6	0%	19	24	79%	22	37	59%	79	59
aatgaaagttgcag	chrIII:13759156-13759228	K08E3.3	toca-2	1	7	14%	14	59	24%	103	518	20%	9	6
tccgctagttccag	chrIV:6118979-6119293	M03D4.1	zen-4	0	3	0%	18	25	72%	133	193	69%	72	69
ttaaaaagttccag	chrIV:3214494-3214677	M4.1	-	0	2	0%	13	13	100%	96	109	88%	100	88
tgaaatagttgcag	chrIII:8359880-8360515	R05D3.4	rfp-1	0	4	0%	10	12	83%	41	50	82%	83	82
tataacagtaacag	chrV:12057277-12057471	R07B7.2	-	0	2	0%	0	13	0%	42	117	36%	0	36
aagcccagtttcag	chrIV:10381616-10381779	R11A8.7	-	0	5	0%	8	11	73%	42	67	63%	73	63
attcaaagtgaaag	chrII:9047522-9047766	T24B8.7	-	0	5	0%	11	11	100%	40	48	83%	100	83
aatgtcagatgcag	chrI:9105852-9106061	W10D5.3	gei-17	5	5	100%	12	12	100%	30	34	88%	0	-12
ccatcaagttacag	chrIII:5346716-5347093	Y32H12A.2	-	0	8	0%	22	23	96%	60	68	88%	96	88
taacctagttccag	chrI:2316432-2316588	Y39G10AR.7	-	0	1	0%	17	20	85%	77	148	52%	85	52
tgcactagtttcag	chrII:3508456-3508591	Y49F6B.1	cyh-1	0	7	0%	4	16	25%	68	121	56%	25	56
aattaaagttacag	chrV:14733584-14733766	Y50E8A.4	unc-61	0	2	0%	5	12	42%	16	30	53%	42	53
cccattagtttcag	chrIV:2686519-2686725	Y94H6A.11	egrh-3	7	7	100%	14	14	100%	60	70	86%	0	-14
taatgtagtttcag	chrIV:11657001-11657273	ZK809.5	-	1	5	20%	7	22	32%	35	109	32%	12	12
Significant Hits From Previous Methods Detected In This Analysis														
gttaaaagttgcag	chrIII:4336184-4336325	B0285.1	cdk-12	0	22	0%	22	24	92%	96	132	73%	92	73
cccagaagttgcag	chrIII:5693200-5693530	B0336.5	-	0	39	0%	22	24	92%	150	231	65%	92	65
cttcatagttacag	chrIII:5702527-5703075	B0336.9	swp-1	0	34	0%	13	26	50%	93	190	49%	50	49
tttaacagcttcag	chrII:5621637-5621778	C17G10.9	-	96	294	33%	72	88	82%	462	542	85%	49	53
ccacctagtttcag	chrIV:10219957-10220587	C24F3.1	tram-1	1	112	1%	9	16	56%	70	149	47%	55	46
cctaaaagttgcag	chrIII:5905604-5905872	C28H8.9	dpff-1	2	108	2%	24	39	62%	339	530	64%	60	62
ccatcaagtcacag	chrI:5909257-5909647	C34G6.1	hpo-27	0	15	0%	13	18	72%	24	35	69%	72	69
tgcaaaagttttag	chrIV:13097548-13097807	C39E9.14	dli-1	0	80	0%	20	22	91%	135	166	81%	91	81
tgataaagtttcag	chrX:14603926-14604363	C44H4.7	eor-2	1	33	3%	13	17	76%	38	54	70%	73	67
attttcagtttcag	chrV:11038576-11038972	C45B11.1	pak-2	1	35	3%	34	62	55%	53	106	50%	52	47
gtataaagtttcag	chrII:11298165-11298314	C47G2.5	saps-1	0	15	0%	6	10	60%	62	89	70%	60	70
gtctaaagtttcag	chrIII:9573365-9573558	C48B4.4	ced-7	0	45	0%	19	24	79%	114	151	75%	79	75
tctcaaagtttcag	chrII:12342536-12343420	C50E10.4	sop-2	1	52	2%	7	12	58%	58	95	61%	56	59
cgaaaaagctttag	chrII:7018554-7018762	C52E12.4	lst-6	0	14	0%	11	12	92%	12	18	67%	92	67
ctgattagtttcag	chrIV:8981666-8982063	C53B4.4	-	2	25	8%	29	31	94%	99	119	83%	86	75
ttccaaagattcag	chrII:13444932-13445173	E01G4.1	tbc-14	0	58	0%	14	31	45%	33	71	46%	45	46
attttaagtcgcag	chrIII:474431-474664	F10C5.2	-	4	21	19%	26	49	53%	179	299	60%	34	41
tctaatagttccag	chrV:15574720-15575057	F28F8.5	-	2	21	10%	9	11	82%	37	54	69%	72	59
aattaaagtttcag	chrIII:8007882-8007946	F44B9.4	cit-1.1	7	32	22%	22	25	88%	65	93	70%	66	48
gctaaaagattcag	chrI:5614440-5614702	F46F11.9	-	0	52	0%	19	26	73%	94	163	58%	73	58
tgaactagttacag	chrII:10266559-10266760	F54B3.1	-	0	21	0%	13	16	81%	111	125	89%	81	89
cgtaccagttccag	chrV:13819600-13819705	F55B12.3	sel-10	3	64	5%	64	76	84%	256	336	76%	80	72
tctcatagtttcag	chrII:5624526-5624689	F59E12.5	npl-4.2	1	52	2%	6	18	33%	62	137	45%	31	43
ttctcaagctccag	chrI:7775181-7775727	H15N14.1	adr-1	0	17	0%	4	11	36%	40	69	58%	36	58
ttttaaagcttcag	chrV:11117854-11117941	H19N07.2	math-33	10	288	3%	35	57	61%	392	803	49%	58	45
ttagaaagtttcag	chrX:1326060-1326125	H42K12.1	pdk-1	1	26	4%	11	12	92%	29	47	62%	88	58
ttcaaaagttacag	chrI:6358785-6358887	K04F10.3	-	1	19	5%	40	40	100%	169	194	87%	95	82
aaaacaagattcag	chrII:8228162-8228318	M110.5	dab-1	14	447	3%	77	96	80%	826	1242	67%	77	63
tataaaagttccag	chrII:8,228,162-8,228,186	M110.5	dab-1	1	50	2%	31	39	79%	101	172	59%	77	57
atataaagttgcag	chrI:8594021-8594168	R05D11.9	-	0	49	0%	13	29	45%	70	195	36%	45	36
cctattagcttcag	chrIV:4445219-4445426	R08C7.10	wapl-1	2	17	12%	22	40	55%	79	144	55%	43	43
attataagttgcag	chrII:9052087-9052296	R107.5	-	3	40	8%	30	42	71%	246	339	73%	64	65
ttcatcagtttcag	chrV:13962740-13962884	R10D12.13	-	0	11	0%	20	25	80%	83	118	70%	80	70
cacaccagtttcag	chrV:13964901-13965047	R10D12.14	sao-1	12	187	6%	48	62	77%	773	1141	68%	71	61
ttcgaaagtttcag	chrI:10764331-10764485	R13H8.1	-	5	25	20%	11	12	92%	37	59	63%	72	43

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
tttgatagtttcag	chrV:13496091-13497041	T10G3.5	eea-1	3	96	3%	9	15	60%	165	316	52%	57	49
ataagtagtttaag	chrIII:6115981-6116128	T17E9.2	nmt-1	0	23	0%	20	29	69%	49	84	58%	69	58
tattctagttacag	chrI:8399354-8399502	T19A6.3	spo-7	24	86	28%	10	13	77%	93	132	70%	49	43
ccaaccagtttcag	chrI:2164813-2164986	W03F11.6	afd-1	1	46	2%	14	26	54%	34	81	42%	52	40
ttcacaagttccag	chrV:16370801-16371197	W08G11.3	-	0	68	0%	10	12	83%	84	121	69%	83	69
atttctagttccag	chrV:16805030-16805558	Y102A5A.1	cand-1	1	62	2%	53	82	65%	152	224	68%	63	66
tcaaaaagttctag	chrIII:6733108-6733281	Y102E9.1	odr-4	0	83	0%	14	19	74%	54	102	53%	74	53
taacccagtttcag	chrI:4528954-4529151	Y119C1B.8	bet-1	1	28	4%	9	10	90%	50	77	65%	86	61
gcaaaaagttccag	chrII:11980672-11981011	Y17G7B.2	ash-2	0	12	0%	13	20	65%	38	61	62%	65	62
cttgctagcgtcag	chrIV:14062658-14063007	Y37A1B.2	lst-4	0	32	0%	7	10	70%	104	149	70%	70	70
tttccaagtttcag	chrI:3343335-3343639	Y44E3A.6	-	10	42	24%	11	13	85%	88	116	76%	61	52
ttttgtagtttcag	chrIV:13477961-13478092	Y45F10A.6	tbc-9	2	19	11%	21	30	70%	49	69	71%	59	60
ccgaaaagttacag	chrII:13377342-13377452	Y48C3A.12	-	0	35	0%	9	21	43%	69	170	41%	43	41
tcaaaaagtttcag	chrV:5228120-5228308	Y49G5B.1	-	0	14	0%	9	11	82%	27	41	66%	82	66
ttaacaagattcag	chrI:14820615-14820711	Y54E5B.3	let-49	0	15	0%	9	11	82%	104	155	67%	82	67
tatgacagtttcag	chrV:4562841-4562937	Y61A9LA.8	sut-2	0	28	0%	9	14	64%	52	110	47%	64	47
tttaaaagtttcag	chrI:539789-540011	Y65B4Br.4	wwp-1	1	255	0%	21	54	39%	236	559	42%	38	42
tcgccaagttccag	chrI:1712702-1712829	Y71G12B.12	atg-5	7	149	5%	19	24	79%	199	277	72%	74	67
ttaatcagtttcag	chrII:13085597-13085753	Y81G3A.3	gcn-2	0	13	0%	19	24	79%	36	43	84%	79	84
caaactagttatag	chrV:8012621-8012734	Y97E10AR.6	-	0	107	0%	17	31	55%	139	253	55%	55	55
tccgccagtttcag	chrI:10344545-10344821	ZC434.6	aph-2	0	109	0%	12	17	71%	133	428	31%	71	31
ttcttaagcttcag	chrII:9640917-9641141	ZK1307.6	fzr-1	0	18	0%	6	10	60%	55	95	58%	60	58
tctccaagttccag	chrIII:8902923-8903534	ZK637.7	lin-9	0	43	0%	7	10	70%	304	459	66%	70	66
ctctccagtttcag	chrIII:7885959-7886207	ZK688.5	-	0	38	0%	13	20	65%	73	138	53%	65	53
taaataagttccag	chrIII:7914921-7915085	ZK688.8	gly-3	3	59	5%	14	11	127%	56	92	61%	122	56
Novel Significant Splice Changes Between glp-4 and N2 Gonad														
aaatcaagtttaag	chrIV:12138992-12139132	B0001.8	-	0	82	0%	14	37	38%	169	685	25%	38	25
ttatttagttgcag	chrI:6796859-6797329	C37A2.2	pqn-20	21	66	32%	65	98	66%	304	376	81%	35	49
attcgcagttctag	chrIV:7912843-7913140	C49H3.5	ntl-4	4	637	1%	6	17	35%	202	604	33%	35	33
tataccagcttcag	chrIV:11014695-11014807	F13H10.3	-	0	68	0%	8	26	31%	15	131	11%	31	11
tcaaaaagttacag	chrIII:4902003-4902420	F26F4.4	tag-340	4	174	2%	18	32	56%	279	532	52%	54	50
ccaaatagtttcag	chrIII:4898148-4898508	F26F4.7	nhl-2	0	10	0%	11	18	61%	104	185	56%	61	56
tttcaaagtttcag	chrV:9393136-9393400	F36D4.3	-	0	30	0%	11	26	42%	41	157	26%	42	26
ttttttagtttcag	chrIV:6584893-6585129	F38A5.2	-	22	112	20%	21	34	62%	146	240	61%	42	41
tggtaaagtttcag	chrIII:8488369-8488741	F42H10.7	ess-2	2	25	8%	20	40	50%	73	221	33%	42	25
ttatacagtttcag	chrII:8846735-8847325	F44E2.7	-	4	18	22%	10	10	100%	165	185	89%	78	67
tggcaaagtttcag	chrV:8429178-8429356	F52E1.13	lmd-3	0	76	0%	11	26	42%	49	175	28%	42	28
ttgcctagttccag	chrIII:2958208-2958852	H05C05.1	-	2	42	5%	10	14	71%	114	160	71%	67	66
ttaaacagttccag	chrX:15522839-15522985	H30A04.1	eat-20	4	94	4%	12	22	55%	7	32	22%	50	18
tttcacagtttcag	chrI:8399237-8399313	T19A6.3	spo-7	32	119	27%	38	48	79%	166	223	74%	52	48
atttgtagtctcag	chrV:20722585-20722708	W07A8.2	-	11	22	50%	42	46	91%	120	137	88%	41	38
taatctagcttcag	chrI:4529873-4530019	Y119C1B.8	bet-1	0	12	0%	11	12	92%	79	100	79%	92	79
cccataagtttcag	chrIII:13147178-13147470	Y39E4B.10	-	0	12	0%	10	15	67%	62	107	58%	67	58
aaattcagttccag	chrI:3340560-3340615	Y44E3A.6	-	10	42	24%	11	13	85%	88	116	76%	61	52
aaaccaagttaaag	chrI:13623584-13623739	Y6B3A.1	agef-1	0	37	0%	3	10	30%	11	79	14%	30	14
tttcatagattcag	chrX:4150072-4150251	ZK470.5	nck-1	51	118	43%	10	13	77%	95	120	79%	34	36
Less Than 10% Proximal Site Usage In Every Sample														
taacccagttttag	chrIV:12162249-12162389	B0001.6	-	2	352	1%	0	13	0%	3	302	1%	-1	0
tttgcaagtttcag	chrI:5795567-5795659	B0414.7	mtk-1	0	71	0%	2	27	7%	9	291	3%	7	3
cagcaaaggttcag	chrV:537201-537376	C14C6.5	-	0	1624	0%	0	15	0%	0	902	0%	0	0
tttatgagtttcag	chrI:9436457-9436970	C17E4.10	-	0	49	0%	0	40	0%	0	192	0%	0	0
atgatcagtttcag	chrX:9105115-9105243	C25A11.4	-	4	335	1%	0	14	0%	2	162	1%	-1	0
atctggagtttcag	chrIV:8495316-8495485	C28C12.12	-	0	10	0%	0	41	0%	0	195	0%	0	0
atgacaagatttag	chrII:6125632-6125753	C29H12.1	rars-2	0	14	0%	0	30	0%	0	105	0%	0	0
attataagtttcag	chrI:5081627-5081820	C30F8.2	vha-16	0	1244	0%	2	120	2%	0	1064	0%	2	0
tgaaaaagttccag	chrIII:4000689-4000802	C36E8.1	-	0	114	0%	0	24	0%	12	241	5%	0	5
aataacagattcag	chrIV:10001314-10001408	C47E12.3	-	0	86	0%	0	16	0%	0	104	0%	0	0
acaaccagttacag	chrX:4262164-4262282	C52B9.4	-	0	65	0%	0	10	0%	0	60	0%	0	0
aacaatagtttgag	chrV:14522012-14522182	C53A5.2	-	0	19	0%	0	14	0%	0	98	0%	0	0
aatttcagtttcag	chrI:7569767-7570130	D2030.1	mans-1	0	30	0%	1	18	6%	0	79	0%	6	0
caaataagtttcag	chrI:7580269-7580698	D2030.3	-	0	12	0%	0	31	0%	0	127	0%	0	0
tcaataagtttcag	chrII:8663078-8663181	D2085.3	-	0	39	0%	1	17	6%	4	71	6%	6	6
aaacaaagtttcag	chrX:9262486-9262566	F18G5.6	-	0	50	0%	0	18	0%	0	67	0%	0	0
ctttcgagttgcag	chrIV:12332627-12333024	F19B6.1	-	0	25	0%	0	27	0%	5	164	3%	0	3
aaatctagtttcag	chrX:14985717-14986183	F20D1.6	rbg-1	1	97	1%	0	12	0%	2	134	1%	-1	0
ataaaaagattcag	chrIII:5946328-5946657	F25B5.6	-	1	124	1%	1	12	8%	12	240	5%	8	4
atcctaagttacag	chrI:15024414-15024585	F33H2.2	-	0	93	0%	0	60	0%	0	411	0%	0	0
ttcacaagtttcag	chrX:3801503-3801607	F35A5.8	erp-1	0	16	0%	1	14	7%	2	47	4%	7	4
atgaaaagctttag	chrIII:4569586-4569705	F35G12.2	idhg-1	0	78	0%	0	50	0%	0	305	0%	0	0
attttcagttttag	chrI:8806085-8806201	F36A2.1	cids-2	0	43	0%	0	30	0%	5	525	1%	0	1
gaattaagtttcag	chrI:14785458-14785645	F39B2.4	sur-2	0	12	0%	0	11	0%	2	23	9%	0	9
atttcaagttttag	chrII:4741142-4741198	F41C3.4	-	0	704	0%	0	22	0%	0	1354	0%	0	0
ggttgtagtttaag	chrX:8390890-8391055	F41D9.3	-	2	33	6%	1	15	7%	2	34	6%	1	0
tctgaaagttgtag	chrII:8560019-8560186	F54C9.1	iff-2	3	2471	0%	0	99	0%	3	1167	0%	0	0
aagctaagtttcag	chrII:8582083-8582280	F54C9.10	arl-1	0	38	0%	0	12	0%	0	60	0%	0	0
cattttagtttcag	chrV:4616404-4616729	F54D11.4	-	2	123	2%	0	57	0%	10	874	1%	-2	0
tccttgagttttcag	chrIII:9521122-9521204	F55H2.6	clu-1	0	65	0%	0	58	0%	0	271	0%	0	0
ttgatgagttttag	chrIII:5593386-5593512	F56D2.1	ucr-1	0	129	0%	0	12	0%	0	148	0%	0	0

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
atgaaaagtttcag	chrI:6561546-6561692	F57B10.6	xpg-1	0	15	0%	0	13	0%	0	90	0%	0	0
tacttgagtttcag	chrII:5906875-5907033	F59G1.8	-	0	10	0%	0	28	0%	0	253	0%	0	0
ttcgaaagttacag	chrV:8923465-8923634	H14N18.3	ttr-47	0	147	0%	0	51	0%	0	216	0%	0	0
ttctctagtttcag	chrI:6839787-6840047	K02F2.1	dpf-3	1	263	0%	1	44	2%	41	835	5%	2	5
agcgtgagatttag	chrI:9611160-9611288	K07A1.8	ile-1	0	116	0%	0	15	0%	4	146	3%	0	3
ttctagagtttcag	chrV:9337433-9337552	K07B1.2	coq-6	0	47	0%	0	14	0%	0	72	0%	0	0
ctaagaagtttcag	chrIII:13760761-13760985	K08E3.4	-	0	63	0%	3	35	9%	8	191	4%	9	4
aatgatagcttcag	chrI:9873686-9873811	K10C3.6	nhr-49	1	238	0%	0	12	0%	11	388	3%	0	2
tttttaagtttcag	chrII:6787321-6787634	T13C2.6	-	0	102	0%	1	41	2%	11	253	4%	2	4
atttaaagtttcag	chrX:2238684-2239193	T14F9.1	vha-15	0	559	0%	0	28	0%	0	416	0%	0	0
tgaaaaagcttcag	chrIV:10162676-10163768	T14G10.1	pps-1	0	642	0%	0	42	0%	57	601	9%	0	9
gtttaaagttacag	chrX:2686213-2686475	T14G11.3	inmt-1	0	56	0%	0	12	0%	0	36	0%	0	0
taaataagtttaag	chrX:3732864-3732966	T14G12.3	tag-18	0	321	0%	0	33	0%	1	250	0%	0	0
cgaacaagttttag	chrX:12868999-12869193	T14G8.3	-	0	295	0%	0	20	0%	0	110	0%	0	0
tggaaaagttccag	chrX:16868264-16868373	T20F7.6	aakg-2	1	118	1%	0	23	0%	1	84	1%	-1	0
aaaattagtttcag	chrI:7693548-7693698	T23G11.5	ribp-1	0	11	0%	0	50	0%	1	44	2%	0	2
taacctagcttcag	chrII:9049635-9049746	T24B8.7	-	0	12	0%	1	19	5%	2	69	3%	5	3
cagcaaagtttcag	chrI:13682871-13683094	W04A4.2	-	0	10	0%	3	48	6%	1	37	3%	6	3
attttgagtttcag	chrV:20731628-20731734	W07A8.3	dnj-25	0	53	0%	0	15	0%	0	98	0%	0	0
aatcggagtttcag	chrIII:346767-346882	W07B3.2	-	0	27	0%	0	15	0%	0	132	0%	0	0
ctatgaagttctag	chrV:1132688-1133037	W07B8.5	cpr-5	6	5113	0%	0	25	0%	3	1724	0%	0	0
ttgtaaagtttcag	chrIV:15942496-15942676	Y105C5B.12	-	0	86	0%	0	59	0%	0	340	0%	0	0
caaaaaagttccag	chrIV:17121774-17122419	Y116A8C.36	itsn-1	0	66	0%	0	42	0%	0	266	0%	0	0
tcagagagttttag	chrV:2352466-2352932	Y19D10A.9	clec-209	0	1165	0%	0	17	0%	0	995	0%	0	0
aggacgagcttcag	chrX:13915272-13915652	Y26E6A.1	ekl-5	0	25	0%	0	37	0%	0	140	0%	0	0
tacaatagttgtag	chrII:13017178-13017343	Y38F1A.10	max-2	0	111	0%	0	37	0%	0	425	0%	0	0
aaaccaagtttcag	chrIII:10625246-10625468	Y39A1A.23	hpr-9	0	24	0%	0	14	0%	6	310	2%	0	2
agtttaagtttcag	chrIII:1777076-1777229	Y39A3CL.4	-	0	24	0%	0	12	0%	0	67	0%	0	0
ttattaagtttcag	chrIII:6142068-6142255	Y42G9A.6	wht-7	0	26	0%	1	31	3%	5	154	3%	3	3
atcagaagttacag	chrII:3506746-3506859	Y49F6B.1	cyh-1	0	53	0%	3	35	9%	8	225	4%	9	4
actccgagttccag	chrIII:11926619-11926943	Y56A3A.13	nft-1	0	66	0%	0	16	0%	0	97	0%	0	0
ataaaaagtttcag	chrIV:8593303-8593731	Y59H11AR.2	catp-7	0	351	0%	0	15	0%	0	146	0%	0	0
tcacatagtttcag	chrIV:6368114-6368207	Y73B6BL.18	smg-3	0	31	0%	2	29	7%	3	160	2%	7	2
attatgagattcag	chrIII:5271430-5271519	ZC395.8	ztf-8	0	36	0%	0	48	0%	0	459	0%	0	0
tttgcaagttttag	chrX:9967147-9967383	ZC506.3	pssy-1	0	178	0%	0	10	0%	0	169	0%	0	0
cacaaaagttccag	chrII:5835655-5835887	ZK1248.14	fzo-1	0	60	0%	1	44	2%	6	167	4%	2	4
aaaatcagttgcag	chrII:5837877-5838039	ZK1248.15	-	0	15	0%	0	31	0%	13	161	8%	0	8
ttaaaaagtttcag	chrII:9659892-9659995	ZK1320.3	-	0	1745	0%	0	27	0%	0	1183	0%	0	0
acgaatagtttaag	chrI:14880597-14880848	ZK270.2	frm-1	0	22	0%	0	10	0%	0	20	0%	0	0
tatcaaagtttcag	chrIV:11974171-11974438	ZK617.1	unc-22	0	234	0%	0	25	0%	0	60	0%	0	0
tttcgaagtttcag	chrII:7944912-7945002	ZK669.4	-	0	54	0%	0	13	0%	0	87	0%	0	0
No Significant Change Detected														
tcatacagttgcag	chrIII:5712550-5713651	B0336.3	-	1	80	1%	3	10	30%	126	542	23%	29	22
ctagtaagtttcag	chrIII:4918627-4919211	C26E6.8	ula-1	0	61	0%	1	14	7%	27	143	19%	7	19
aagtctagattcag	chrIV:7140784-7141059	C34D4.14	hecd-1	8	188	4%	7	36	19%	28	253	11%	15	7
aaattaaggtgcag	chrX:7880047-7880175	C39D10.8	-	139	341	41%	4	10	40%	116	260	45%	-1	4
actttcagatcaag	chrX:5113438-5113575	C42D8.8	apl-1	179	179	100%	16	19	84%	59	59	100%	-16	0
gttaaaagtttcag	chrI:9222702-9223087	C45G3.1	aspm-1	0	17	0%	3	24	13%	37	221	17%	13	17
gtcttcagttacag	chrI:12975379-12975623	C47B2.6	gale-1	73	186	39%	10	20	50%	68	170	40%	11	1
aactgaagattcag	chrIII:9575761-9576761	C48B4.4	ced-7	14	130	11%	0	73	0%	29	347	8%	-11	-2
ttttttcagctgaag	chrIII:7349335-7349438	F08F8.9	-	57	61	93%	33	33	100%	168	171	98%	7	5
gaattcagcttcag	chrIV:12104878-12105044	F11A10.4	mon-2	33	43	77%	12	15	80%	37	51	73%	3	-4
tttattagtttcag	chrI:9509445-9510116	F30A10.10	usp-48	0	29	0%	2	11	18%	17	129	13%	18	13
accaaaagtttcag	chrI:7850506-7850900	F30F8.8	taf-5	0	19	0%	3	12	25%	37	98	38%	25	38
tcaaccagtttcag	chrI:9013080-9013197	F36F2.3	tag-214	2	30	7%	9	26	35%	57	201	28%	28	22
tgtatcagttgcag	chrV:20779515-20779780	F38A6.3	hif-1	87	443	20%	6	19	32%	128	384	33%	12	14
gatttcagtttcag	chrIII:13352487-13353442	F53A2.8	mtm-6	27	41	66%	16	20	80%	118	150	79%	14	13
aaatcaagtttcag	chrV:913059-913494	H24K24.3	-	0	132	0%	1	11	9%	26	186	14%	9	14
cttatcagttacag	chrIII:4316018-4316449	H38K22.2	dcn-1	0	99	0%	18	64	28%	36	321	11%	28	11
accttcagattcag	chrX:7295266-7295374	K03A1.2	lron-7	171	207	83%	11	12	92%	192	209	92%	9	9
ctcaacagtttcag	chrIII:5175106-5175428	K10D2.3	cid-1	5	25	20%	3	11	27%	36	76	47%	7	27
ttttaaagatttag	chrIV:10329068-10329181	K11E8.7	-	104	164	63%	7	10	70%	41	61	67%	7	4
atagtcagtttcag	chrI:3082945-3083242	M01B12.4	-	1	25	4%	6	41	15%	15	83	18%	11	14
ttttccagatgcag	chrI:13282563-13282696	M01E5.3	-	47	49	96%	22	24	92%	196	206	95%	-4	-1
agccaaagtttcag	chrIII:10931248-10931340	M142.5	-	0	44	0%	3	12	25%	21	57	37%	25	37
aatgatagtttcag	chrII:6783797-6783955	T13C2.6	-	17	284	6%	60	201	30%	285	681	42%	24	36
tgtttcagtttcag	chrIV:9340824-9340995	T20D3.7	vps-26	10	32	31%	6	54	11%	25	178	14%	-20	-17
atttcaagttacag	chrI:9966587-9966966	T23D8.1	mom-5	3	95	3%	5	29	17%	97	414	23%	14	20
tatgttagtttcag	chrI:6125638-6125721	T27A3.1	-	129	313	41%	5	10	50%	187	295	63%	9	22
caaaaaaggttaag	chrI:6112538-6112645	T27A3.2	usp-5	0	100	0%	2	24	8%	26	114	23%	8	23
taaaccagattcag	chrIII:13466832-13466915	T27E9.4	kel-3	2	50	4%	10	33	30%	59	127	46%	26	42
tttttcagataaag	chrV:16366560-16366851	W08G11.4	-	69	75	92%	17	19	89%	120	120	100%	-3	8
attaaaagttacag	chrI:5125879-5126101	Y110A7A.17	mat-1	0	105	0%	2	32	6%	106	713	15%	6	15
attagaagttttag	chrI:5137728-5137841	Y110A7A.5	mtm-1	0	132	0%	2	17	12%	12	260	5%	12	5
ttgtttagttccag	chrIII:12872692-12872920	Y37D8A.9	mrg-1	44	83	53%	30	55	55%	450	698	64%	2	11
cccccaagttacag	chrI:14814787-14814969	Y54E5B.1	-	1	34	3%	3	13	23%	7	64	11%	20	8
ttaaatagtttcag	chrV:4572275-4572374	Y61A9LA.3	-	2	32	6%	4	13	31%	46	106	43%	25	37
taatccagttccag	chrIV:363771-363888	Y66H1B.2	fln-1	47	215	22%	11	28	39%	156	310	50%	17	28

Table S4 Introns With Adjacent AG Dinucleotides 6nt Apart

Intronic Terminal 14nt	Genetic Location	Gene Name	Common Name	glp-4 Prox	glp-4 Total	glp-4 Prox %	Gonad Prox	Gonad Total	Gonad Prox %	Whole Prox	Whole Total	Whole Prox %	delta PSI (glp-4 to gonad)	delta PSI (glp-4 to whole)
tatcacagcttcag	chrIV:1415669-1415917	Y77E11A.7	-	0	12	0%	3	31	10%	18	124	15%	10	15
atccacagtttcag	chrI:864391-864821	Y95B8A.7	-	0	17	0%	1	19	5%	47	142	33%	5	33
tttttcaggtcaag	chrIV:9091811-9092005	ZC410.5	-	35	40	88%	20	25	80%	35	41	85%	-8	-2
aaaaaaagtttcag	chrI:11756593-11757071	ZK1151.1	vab-10	0	155	0%	2	12	17%	18	159	11%	17	11

Table S5 WebLogo Genetic Sequence Comparison Genes

	6nt Randomly-Selected Typical 3' Splice Sites	n=25
aak-1	TCTGAAAGGAATGTTGCAAAAGTAGTCGGAAAGTTTTCAG	
baf-1	TTTCTCAAATTTTCGATCAATGTTAAAATTTGAATTTCAG	
cab-1	GAAAACTTTGCAATATATTCCCATTTTCTCAACATTTCAG	
daf-1	TCTTTTTTGACATCCGGATTTTGAATTTTCAAATTTTCAG	
eaf-1	AAATTTAAAAATATAAAATCGAAATAGCTAAAATTTACAG	
fat-1	AATGTTCAAATTAAATTTTAAAAAACCCCCAAATTTGCAG	
gab-1	AACTTGCTCGGCGGGGAAACATTAAAACAAAAAATTTCAG	
haf-1	TTAGCTTCACATCTTCAGATGAATTCGAACTTTTTTATAG	
iars-1	CAATTTCAATATTTTAATTTAAATCAAAAATGTTTTCCAG	
jac-1	AACAAAAATTGGATTTGAATTTAAACAATCACTGTTTCAG	
kap-1	TGCAATTGTACATATTACATTGAAAATGGTTCAATTCCAG	
lab-1	AACTTGTTTAGAATATATGTCAAGTCTGGAATTTTTCCAG	
mat-1	TATATATGTATATTTATTCATTATTTTAATTTTTCTTTAG	
nap-1	GCATTTCATTGTTTTCGAAAGTTAATGTTTTGAACTTCAG	
oac-1	TTTCTGCGAATTTTCAACAATTTTCCCCAACTAATTCCAG	
paa-1	GAAAAGAATAACTAAAGCAATCTAAATTAATTATTTTCAG	
qui-1	AGCTGAAGTCCTTTTTTTTAACAAAATATAGTAATTTTAG	
rab-1	TAAAAAGCTTATAACAATAAATATTATGAGCATTTTTCAG	
sac-1	TGACTTTTGGTCTGATCTAAATATAAATTTATAATTACAG	
tac-1	AAATTTAATTTGCAACATGTAAGAATATATTTCAATTCAG	
uev-1	CGGAATTAATCATTTTTTATTATTAGTTTTTTGCTTTCAG	
vab-1	ATGCCTTTTAATACCCCATTTTAATTCCATTTATTTTCAG	
wago-1	GTGAATTTCGAAAATTATTAAAAGCATCGCTTCATTTTAG	
xnd-1	CCATGAAAATTTGATTTTTTAAAGCTCATTTTCTCTTCAG	
yop-1	AAAAATTTGAAACCCATTTTTTAAATGATTTTTTTTTCAG	

	Tissue-specific adjacent 3' splice sites (6nt Separation)	n=25
B0336.9	ATTCTTGCAAAATTTATGTATCATCTCTTCATAGTTACAG	
C02E11.1	AAATTATAATTCCACATATAACCCCCGTCAAAAGCTTCAG	
C04A2.7	GATGATTCCCCACGATATTCTTATGCCAAATCAGTTTAAG	
C05C10.6	AATCGTTTTTTACTGGATTTTAAAGTTAAATTAGTTCCAG	
C24F3.1	AAAATCCAAATAGTTTTAAACTTTTCCCACCTAGTTTCAG	
C39E9.14	TAAAGAAAAATAAAATAAATGATGTTTGCAAAAGTTTTAG	
C45B11.1	TTGTTTCTGACAATTTTTTGTAATTTATTTTCAGTTTCAG	
C47G2.5	GAATACGAACACTCCAAAGACCCTCTGTATAAAGTTTCAG	
C48B4.4	TGCATAAATGTGTTTCCTTCAATTCTGTCTAAAGTTTCAG	
F11A10.1	ATCGCATAATTTCAAAAATATAAGCGAATTTCAGTTTCAG	
F46F11.9	TTCTCTGATATTGAATATTTACAATTGCTAAAAGATTCAG	
F55B12.3	TTTTGTAGTGAATATTTATAGCAAAACGTACCAGTTCCAG	
H19N07.2	TGTTTAATTTCCACACCTTTCATATTTTTTAAAGCTTCAG	
M01E5.3	ATTTTTGAAACAAAATTAAATAATTCTTCGAAAGTTTCAG	
M110.5	ATTATAAAAGTCCATTGTTATGACTTTATAAAAGTTCCAG	
R02F2.1	TCGTTAAATCTTTGAAATTGTAATTCTTCTCAAGTTTCAG	
R06F6.8	TAATAACTTTGCAATTGTTTTAATTTTTAAAAAGTTTCAG	
R107.5	GCCTTGTTTTTGACAAATAATGTTCGATTATAAGTTGCAG	
R10D12.13	GAGTGGTTCAACAAGATTATAATTGTTTCATCAGTTTCAG	
R13H8.1	AAATGCAAAAATGTTTTTCTAACTTCTTCGAAAGTTTCAG	
T10G3.5	GATTAATCTCTGATTCAATAGAATTTTTTGATAGTTTCAG	

Table S5 WebLogo Genetic Sequence Comparison Genes

Y102E9.1	GTTTTATTTGACTATGAGACCAATCGTCAAAAAGTTCTAG
Y37A1B.2	TTGTAGATTTCGACGCTTACTAACCGCTTGCTAGCGTCAG
Y45F10A.6	ATTGTTTAATCGATAATCGATGAACGTTTTGTAGTTTCAG
ZK637.7	TTTAAAACAATTGTATTGTTGTCATGTCTCCAAGTTCCAG
	Tissue-specific adjacent 3' splice sites (9nt Separation) n=25
B0261.2	ACAGCCCATAAACCTGTAATCCGGTGTCAAGTAATTATAG
B0336.5	TGAATAAAGAAAATTTTAACAAAGTTCCCAGAAGTTGCAG
C10C5.6	ATTAACAAAAATGCAATCTTAAAGCCAAAAGGAGTTACAG
C26E6.9	TTTTAAATAAGCATTATTAATCCTGGAAAAGCCTTCTCAG
C36B1.8	TTGAAAAGAACGAATCTATTCCGAAATAAAGCTATTGCAG
F13G3.7	ATCCGATATTAAAAGTTCTAATGTTCATAAGATGTTACAG
F13G3.7	ATCCGATATTAAAAGTTCTAATGTTCATAAGATGTTACAG
F54E7.3	AAATTTTGAATTCACTAACCCAATCGATTAGCCCTTTCAG
F56C9.10	CTCGATAACCCGTCATAATTTTTTAATTGAGAATGTGAAG
H14E04.2	AACTTGATTAAAAATTCCCAATTTCTCCCAGTTTTTTCAG
K03B4.3	ATTTAATTGATTAAAATTAACCGATTTAAAGTATTTTCAG
M03F8.3	GATTTAAAGAGCTCACTAATCGCTTCGCTAGTACTTTCAG
R05D3.4	GTCTGTTCATATCTCTACAATCCCGTGTGAGAATTTACAG
T01G9.2	TCAAAAAATCAATAATAAATATTTTCCAAAGAAATTCAAG
T05F1.1	AAAGGAGAGTGTCGTTTTACCGGTTTTGAAGGGTTTTCAG
T05F1.1	TAAAAGTTTATTGATTTTAATCGTTCGTAAGATATTTCAG
Y102E9.2	ACTTTTAAAAACCATTATTCACCCGAAATAGTGTTCTCAG
Y113G7B.18	AATAATTTCCGTCCCACTAACGTCGTTCCAGTATTTCCAG
Y17G7B.2	TTTTGATTTTTCCCCTCTAACCATTCTTAAGAACTTCCAG
Y54E10A.9	TTTAAATCTGAATTACAATTTTTATTAGTAGACGTTACAG
Y69A2AR.1	TTTTTTTTTTTTCATTTCTAATTTTCTAAAGCTTTTGAAG
Y71F9AL.12	TAACCTTCTAAATTCTCAACAAATTTGTCAGACTTTACAG
Y73B6BL.6	AAGGAATGCATCAGTATACTTATTCTATCAGGTTTTGCAG
ZK1290.4	TAAAATCAATGTCTTGTCTAACCAAAAAAAGTTTCTTCAG
ZK546.1	GAACTTTCCACCGATTCTATATGCCGCCTAGACCTTTCAG
	Tissue-specific adjacent 3' splice sites (12nt Separation) n=16
C12C8.3	TATTCTACAGTAATTCAAACTGTTTCAGTTTTCTTTTCAG
C25A1.9	CCAAGAACACTTTCTCATCGCTTAAAAGTCATCATTTCAG
C28H8.9	TCAGAACGATTCAACCTAATTTTTGTAGTTCGATTTGCAG
F27C1.2	TCATTAAAAAATATCTTATCCGACCTAGTTTGCACTTCAG
F41H10.3	AAAGGTATTTTCTAAAATAATTTCCCAGCCGAACTTTCAG
F56C9.10	GATAAACATAAATTCCTACCGTGATTAGATGGAATTTCAG
K02A11.1	AAAAAAGAGATTGCATCATCTGTGTAAGTATTATTTCCAG
K02F2.1	TTGACTATTCTTGTTAATCCGCGTTGAGCATGTCTTGCAG
K07H8.2	TTCCAAACAGTATATTAATCCGATCCAGTTTTCGTTTCAG
M88.5	TTCGTTGTTTTCAACCGTTTTTGGGGAGATTATCTTGCAG
T05H10.5	GACATTTTATATACTCATAGGCGATTAGTTCTTTTTTCAG
T24A11.1	AGCTTCTTATAATGCTAACCAAAGTCAGGAATCGTTCCAG
W06A7.3	GCACTTCTAGGCTACAACCATTAATGAGTTCGATTTTCAG
Y50E8A.4	AATATTGTTTCGTTTCACTGATTCTAAGCGTCGATTGCAG
Y59A8B.14	AAGTTTCTCAAACTTTTTCTCGTTTTTGTCGGAATTTCAG
ZK858.4	CCAACTTGATTGCATCTTTTTTTTTGAGTCGCTTTTACAG

Table S5 WebLogo Genetic Sequence Comparison Genes

	Minimally Used Proximal 3'SS (From 1245 introns with 6nt separated AG dinucleotides)	n=25
C14C6.5	AGCTTTTTAAGACACAAAGTAGTCACCAGCAAAGGTTCAG	
C17E4.10	AATTCTTCTTTTTTTCTCTTGAATATTTTATGAGTTTCAG	
C28C12.12	TTGAATATTTCTATAAAATAACTATAATCTGGAGTTTCAG	
C29H12.1	TGTATCAAAATTTAAATTTAAAAACAATGACAAGATTTAG	
C47E12.3	AGTGAGCAGGAAAAGAGAGAGGTTTCAATAACAGATTCAG	
C52B9.4	TTTTTTTTCATGATCTCGGGAGTATTACAACCAGTTACAG	
C53A5.2	CCAAAATTATTGAAAGCTCAATATAAAACAATAGTTTGAG	
D2030.3	ACATATTCTGTCATGGATCCATTCATCAAATAAGTTTCAG	
F18G5.6	GAAAACTACGTAATCATTCAGTTGAAAAACAAAGTTTCAG	
F33H2.2	GGGAGAAATGTTTGAAAAATTCTTAAATCCTAAGTTACAG	
F35G12.2	TTTAAATCGATTTGTACAAATTTCAAATGAAAAGCTTTAG	
F41C3.4	CTAACGAATCAGGATTTTTATCAATTATTTCAAGTTTTAG	
F54C9.10	ATTTCTGGCTGAAAACAAAACCATATAAGCTAAGTTTCAG	
F55H2.6	AAAAATCTAAAATTAGTTTTTTTTTATCCTTGAGTTTCAG	
F56D2.1	TGAATTTTTCAATTCAAACCGTAATTTTGATGAGTTTTAG	
F57B10.6	TAATTACACATGTGATGGAGTCCCTTATGAAAAGTTTCAG	
F59G1.8	TTTTCATTACCAATATGACAACTATATACTTGAGTTTCAG	
H14N18.3	AAAAAAAAACACAACCCACTCTTTTATTCGAAAGTTACAG	
K07B1.2	TATCAATTTCTTAAAGAATTATTTATTTCTAGAGTTTCAG	
T14F9.1	TTAAGTTTGCAATTTTAATTTTATGAATTTAAAGTTTCAG	
T14G11.3	ATTTTTTAAGCGTAATTTTCATAACAGTTTAAAGTTACAG	
T14G8.3	GTGAAGATATGTAGTGCCTTACTAATCGAACAAGTTTTAG	
W07A8.3	AGATTTAAATTTTATATGTATATTCAATTTTGAGTTTCAG	
Y105C5B.12	CAGCCATAAACTAATATTTTTGTTAATTGTAAAGTTTCAG	
Y116A8C.36	CGCGTTTAATCTATATGCAAATTACCCAAAAAAGTTCCAG	

	Highly Used Proximal 3'SS in glp-4 (From 1245 introns with 6nt separated AG dinucleotides)	n=25
T13F2.3	ATTTTAAAAGTAAAAATGTCTAATTTCCTGTCAGATTCAG	
ZK470.5	TTACCCCAATGCAATTTAATAATCATTTTCATAGATTCAG	
T27B1.2	ATAACAGCGTTATCAAAACTTATATATATCTTAGTTTCAG	
C27C12.4	TTCATCAAGAAGCTTATACCTAATCTCATTTCAGTTTCAG	
W07A8.2	TTTTTTTTTAAACGAATTTTTGCATGATTTGTAGTCTCAG	
Y37D8A.9	TGAAACAGTTACGATGTAAGGATGAATTGTTTAGTTCCAG	
F29C12.3	GAATTGAAAAAAAAATTTATTAAAAAGTATTTAGGTTCAG	
K11E8.7	CTCTGTACGTCTATGTCTATTGATATTTTTAAAGATTTAG	
F53A2.8	CTGTGCTTCATTCACTAATGTCGACTGATTTCAGTTTCAG	
C27A7.5	ATTTTACGATTTCAAAAACATAAATGAATTTAAGTTTCAG	
E02H9.8	ACAAAATTCCCCCCTAAAATCCAAATTTCTTCAGTTTCAG	
F58A4.7	AAGGTGGTGAGTACTGTAACTTTATATAGTATAGATCCAG	
ZK377.1	ATGTCAACTAATTCTACTAGTACTAACTTTCTAGTCGCAG	
F11A10.4	TTTCGGTGTACTCGGTAACAACCCTCGAATTCAGCTTCAG	
ZC64.3	TGATCACGATAAAGTGTTAATATTTTATTTCCAGAAACAG	
C34C6.6	TCAAGTAAAAATTAACAAAAAAAAAAGTTTTTAGCTGCAG	
K03A1.2	TACTAATCCTATTACAACTTAAAATCACCTTCAGATTCAG	
ZC410.5	AACTTGAGCATCAACTAAAATATACTTTTTTCAGGTCAAG	

Table S5 WebLogo Genetic Sequence Comparison Genes

F35C5.5	CCATAATCTGCCAAAGTTCTTATCCCTGTATCAGTTCCAG
F47B8.5	GCGTGTCAAGACAAAACAATAACACTAATTTCAGTTCCAG
W08G11.4	GCTTCAAGACCCAAAAAAATCTATATTTTTTCAGATAAAG
F08F8.9	AATGGCAAAGTGGTAATACACATATTTTTTTCAGCTGAAG
Y54G2A.3	ACACGAGACGTTCCTGTCAAAATTGATATTCCAGATTCAG
M01E5.3	ATTTTTCTAATTAAAAATTTATTATATTTTCCAGATGCAG
C42D8.8	CTGAAAGTTTATCTGTAATTTATGGAACTTTCAGATCAAG

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
B0035.1		-0.44	-0.81	-1.26
B0035.12		-0.80	-1.68	-2.48
B0041.7	xnp-1		-0.84	-1.05
B0205.7	kin-3	-0.27	-0.21	-0.48
B0252.4	cyn-10	-0.40	-2.55	-2.95
B0272.1	tbb-4		2.62	2.60
B0285.1		-0.83	-1.17	-2.00
B0286.3		1.87	1.32	3.19
B0336.3			-1.68	-1.70
B0336.9	swp-1		-1.65	-1.66
B0361.2		-0.74	-1.53	-2.27
B0365.1		-0.94	-1.03	-1.98
B0393.1	rps-0		0.58	0.60
B0414.8		-1.04	-1.12	-2.15
B0432.7		-1.11	-0.69	-1.80
B0464.5	spk-1	-0.24	-0.71	-0.95
B0495.2			-1.43	-1.46
B0495.6			-0.69	
B0495.8		-0.73	-1.32	-2.05
B0511.10	eif-3.e	-0.60		-0.47
B0511.6		-0.39	-0.73	-1.12
B0564.1	exos-4.1	0.46	-1.14	-0.68
C01G8.9	let-526	-0.24	-0.75	-1.00
C02F5.9			-0.38	-0.57
C03D6.4	npp-14	-0.66	-2.12	-2.78
C04G2.6	dis-3	-0.42	-1.39	-1.81
C04H5.6	mog-4		-1.15	-1.42
C06A1.1	cdc-48.1	-0.99	-0.82	-1.81
C07A9.2		-0.34	-1.26	-1.64
C07E3.1	stip-1		-2.13	-2.21
C07G2.3	cct-5	-0.20	-0.60	-0.80
C07H6.4			-1.37	-1.26
C07H6.5	cgh-1		-3.95	-4.11
C07H6.8	cux-7	-0.99	-1.53	-2.52
C08B11.5				
C12D8.1			-1.53	-1.67
C13B9.3		-0.24	0.69	0.46
C14A4.4	crn-3	-0.77	-2.15	-2.92
C14B1.4	tag-125	0.44	-1.69	-1.25
C14B9.2		1.03	2.44	3.47
C14C10.1		Inf	Inf-	
C15H11.3	nxf-1	-0.65	-1.02	-1.67
C15H11.6	nxf-2		-3.86	-3.69
C15H11.7	pas-1	-0.57	-0.67	-1.24

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
C15H9.6	hsp-3	-0.49	1.84	1.35
C16A3.8	thoc-2	0.26	-2.12	-1.86
C16A3.9		-0.45	0.28	
C16C10.6	ccdc-55		-1.78	-1.94
C17E4.5	pabp-2		-0.61	-0.44
C17G10.9		-0.34	-0.26	-0.60
C17H12.1	dyci-1	-0.67	-0.43	-1.09
C18A3.5		-0.26	-0.85	-1.11
C18D11.4	rsp-8	1.29	-1.20	
C18E3.2			-1.56	-1.41
C18E3.5			-4.05	-4.46
C25A1.1		0.65	-2.58	-2.44
C25A1.10	dao-5		-1.15	-1.29
C25D7.6	mcm-3	-1.27	-3.41	-4.68
C26C6.1	pbrm-1	-0.88	-1.93	-2.81
C26D10.2	hel-1	-0.46	-1.05	-1.51
C26E6.3			-1.23	-1.37
C27D11.1	egl-45	-0.25	-0.64	-0.89
C27H5.3		1.94	-0.21	1.73
C27H6.2	ruvb-1		-2.05	-2.04
C28G1.3	sec-15	-1.60	1.03	-0.57
C28H8.9			-1.51	-1.57
C30B5.4			-1.70	-1.82
C30C11.2	rpn-3	-0.56	-0.51	-1.07
C32E8.5		-0.34	-2.12	-2.46
C32F10.5	hmg-3	-0.77	-6.05	-6.82
C33F10.12			-5.61	-4.03
C33H5.10	tag-322	-0.82	-1.10	-1.92
C33H5.12	rsp-6	0.60	-1.24	-0.64
C33H5.9	sec-10	-1.26		-1.43
C34D4.12	cyn-12		-1.97	-1.96
C35D10.16	arx-6	0.55		0.41
C36B1.3	rpb-3	-0.42	-1.95	-2.37
C36B1.5		-0.64	-1.74	-2.38
C36E6.1		-0.46	0.78	
C36E8.5		-0.87	0.28	-0.59
C39E9.13	rfc-3	-0.93	-3.09	-4.02
C41C4.8	cdc-48.2	-0.75	-0.24	-0.99
C41D11.2	eif-3.h			
C42D4.8	rpc-1	-0.54	-1.70	-2.24
C43E11.1	acin-1			
C44B7.2		-0.88	-1.21	-2.09
C44E4.4			-1.06	-1.18
C46A5.9	hcf-1		-2.50	-2.32

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
C46F11.4		0.73	-1.21	-0.48
C47B2.3	tba-2	-0.58		-0.49
C47D12.1	trr-1	-1.38	-2.20	-3.58
C47E12.5	uba-1	-0.58	-0.61	-1.19
C47E8.4			-2.37	-2.56
C47E8.5	daf-21	-0.94		-2.08
C47F8.9				
C48E7.2			-2.09	-2.37
C50C3.6	prp-8	-0.81	-1.04	-1.85
C50D2.5		-0.94	-0.85	-1.79
C50D2.8		-0.70	-2.24	-2.94
C50F2.3		-0.41	-1.18	-1.59
C52E4.3	snr-4		-1.02	-1.02
C54C6.2	ben-1	-1.22	0.39	-0.83
C54C6.6		-0.95	-1.39	-2.34
C55B7.8	dbr-1	-0.50	-1.70	-2.20
CC4.3	smu-1		-1.61	-1.35
D1005.1		-0.48	0.82	0.34
D1007.7	nrd-1	-0.74	-1.74	-2.48
D1009.2	cyn-8	-1.44	0.44	-1.00
D1046.1		-0.87	-1.40	-2.27
D1054.14		-0.78	-2.00	-2.78
D1054.15		-0.91	-0.74	-1.65
D1081.8		-0.33	-1.54	-1.87
D2085.1	pyr-1	-1.57	1.91	0.34
D2089.1	rsp-7		-1.50	-1.66
D2089.4	ptb-1		1.91	1.88
DY3.2	lmn-1	-0.47	-0.95	-1.43
E01A2.2			-1.61	-1.74
E01A2.4			-1.90	-1.99
E04D5.1			-1.52	-1.65
EEED8.5	mog-5	-0.70	-1.48	-2.18
F01F1.12		-0.52	0.80	0.27
F01F1.7	ddx-23	-0.67	-1.59	-2.26
F01F1.8		-0.26	-0.61	-0.87
F01G4.1	psa-4	-0.76	-1.20	-1.95
F01G4.6			0.57	0.50
F08B4.7		-0.73	-0.38	-1.12
F08D12.1		-0.52		-0.60
F08G12.2		-0.89	-0.64	-1.53
F09D1.1			-1.51	-1.78
F09F7.3		-0.40	-1.02	-1.42
F09G2.4	cpsf-2	-0.95	-1.75	-2.70
F10B5.2			-1.76	-1.71

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
F10G7.2	tsn-1	-0.50	0.45	
F10G7.8	rpn-5	-0.50	-0.39	-0.88
F10G8.3	npp-17		-2.00	-2.24
F11A10.2		-0.84	-0.94	-1.78
F11A10.8	cpsf-4		-2.89	-2.81
F11A3.2		-0.59	-1.24	-1.83
F13D12.2	ldh-1		0.46	0.29
F16A11.2			-1.22	-1.62
F17A9.2		-0.54	-2.19	-2.72
F17C11.10		-0.50	-3.12	-3.62
F17C11.9		-0.49		-0.45
F18C12.2	rme-8	-0.46	-0.19	-0.65
F18C5.3	tag-184	-0.53	-1.50	-2.03
F18E2.3	scc-3	-0.70	-2.12	-2.81
F18H3.3	pab-2	-0.34	1.49	1.16
F19F10.9		-0.47	-1.16	-1.63
F21H12.1			-2.38	-2.54
F22B5.7	zyg-9	-0.42	-1.65	-2.07
F22D6.5	prpf-4	-0.39	-2.03	-2.42
F23B12.8	bmk-1	-0.88	-3.16	-4.05
F23F12.6	rpt-3	-1.03	-0.48	-1.51
F25B4.5		-0.59	-1.05	-1.64
F25G6.2		-0.65		-1.73
F26A3.2	ncbp-2	-1.04	-1.53	-2.58
F26B1.2			-2.06	-1.88
F26D10.3		-0.95	-0.43	-1.38
F26E4.8		-0.80	-0.14	-0.95
F26F12.7	let-418		-0.51	-0.69
F26F4.10		-0.68	-0.55	-1.12
F28B3.7		-0.67	-2.55	-3.22
F28B3.8	imb-1	-0.92	-1.28	-2.20
F28C6.3	cpf-1	-0.98	-2.11	-3.10
F28C6.6	suf-1		-1.64	-1.73
F28D9.1	rsr-1	1.10	-1.01	
F28F8.3	lsm-5		-0.97	-0.64
F29C4.7			-1.14	-1.01
F29G9.5	rpt-2	-0.57	-0.50	-1.08
F31C3.1	cyn-5		1.38	1.60
F31D4.1	exos-7		-1.52	-1.15
F31E3.5	eft-3	-0.93	0.15	-0.77
F31E8.2	snt-1		2.24	4.11
F32A5.7	lsm-4		-1.26	-1.15
F32B6.3		-0.93	-1.96	-2.89
F32D1.10	mcm-7	-0.69	-3.92	-4.61

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
F32H2.5	fasn-1	-2.87	1.62	-1.25
F33A8.1	let-858	-0.52	-0.99	-1.51
F33D11.10		-1.08	-1.31	-2.39
F33G12.2		-0.95	-1.81	-2.76
F33H1.2	gpd-4	-1.21	-5.52	-6.73
F35F11.1			-1.13	-1.50
F35H12.3	sel-12	-0.86		-0.98
F35H8.5	exc-7		2.69	2.33
F36F2.3	tag-214	-0.39	-1.66	-2.05
F37A4.2				
F37A4.8	isw-1	-0.80	-2.62	-3.41
F37C12.13	exos-9	-0.69	-1.18	-1.87
F37E3.1	ncbp-1	-0.76	-1.12	-1.88
F37F2.2		-1.15		
F38E11.11				
F38E11.5			0.49	
F39B2.10	dnj-12		-0.94	-0.82
F39B2.4	sur-2	-0.88	-1.62	-2.50
F39H2.2	sig-7	-0.85	-1.20	-2.05
F40F8.10	rps-9		0.26	0.43
F40F8.9	lsm-1		-1.33	-1.52
F40G12.14				
F41E6.4	smk-1	-0.69	-1.12	-1.81
F42A6.7	hrp-1		-1.14	-1.04
F42C5.8		0.34	0.50	0.84
F42G9.1		-0.61	-1.63	-2.24
F42G9.2	cyn-6		4.72	5.38
F42G9.9	ptl-1	1.37	1.87	3.23
F42H10.7			-2.82	-2.70
F43E2.8		-0.54	-0.20	-0.74
F43G9.10			-1.38	-1.60
F43G9.12		-0.56	-1.56	-2.13
F43G9.5			-1.62	-2.01
F44F4.11	tba-4	1.59	1.96	3.55
F47A4.2	dpy-22	-0.97	0.54	-0.42
F49D11.1	prp-17	-0.71	-1.47	-2.18
F52C9.7			-2.12	-2.33
F53A3.3		0.66	0.45	1.12
F53B7.3		-0.93	-1.63	-2.56
F53F4.14		-1.45	-1.57	-3.02
F53H1.1		0.40	-1.30	-0.90
F54A3.3	cct-3	-0.48	-0.50	-0.98
F54B3.3		-0.72	-0.77	-1.49
F54D5.8	dnj-13		-0.81	-0.47

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
F55C5.8		-0.56	-0.32	-0.88
F55F8.4			-1.59	-1.77
F56C9.1	gsp-2			
F56D12.5	vig-1	0.66	-0.82	
F56D2.6			-1.02	-1.21
F56F11.4		-0.78	-6.65	-7.43
F56H1.4		-0.29	-0.48	-0.77
F57B9.10	rpn-6	-1.02	-0.57	-1.59
F57B9.6			-0.37	-0.33
F58B3.5	mrs-1		-0.56	-0.66
F58B3.7			-1.79	-1.94
F58D5.1	hrp-2		-0.93	-0.99
F58E10.3		-0.44	-1.33	-1.77
F58G11.5	tag-65		-1.99	-1.69
F59A2.3			-0.30	-0.49
F59C6.4	exos-3	-0.65	-2.10	-2.76
F59E10.2	cyn-4	-1.14	-1.08	-2.22
H06O01.1	pdi-3	-0.71	1.36	0.66
H12C20.2	pms-2		-2.27	-2.46
H14N18.1	unc-23	1.03	1.96	2.99
H19N07.1			-0.53	-0.44
H19N07.2	math-33		-0.49	-0.66
H20J04.2			-2.59	-2.44
H20J04.8	sap-1/mog-2	0.51	-1.37	-0.85
H27M09.1	sacy-1	-0.53	-1.30	-1.83
H43I07.2		-0.87		-1.64
K01C8.10	cct-4	-0.63	-0.75	-1.39
K01C8.9	nst-1	-0.67	-1.28	-1.95
K01G5.1	tag-331		-1.65	-1.88
K01G5.4	ran-1	-0.86	-1.01	-1.87
K01G5.5		0.22	-1.78	-1.56
K01G5.7		-0.97	-0.13	-1.10
K02F2.3	tag-203		-1.42	-1.60
K02F3.11			-1.30	-1.35
K03H1.2	mog-1	-0.58	-1.33	-1.91
K04D7.1	rack-2			
K04G7.10	rnp-7	-0.44	-0.87	-1.31
K04G7.11				
K04G7.3	ogt-1	-0.44		-0.59
K05C4.6	hmp-2	-0.44	-1.37	-1.81
K07A1.12	lin-53	-0.82	-1.99	-2.81
K07B1.7		0.68	-1.72	-1.04
K07C5.4		0.41	-1.34	-0.94
K07C5.6			-2.40	-2.36

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
K07D4.3	rpn-11	-0.25	-0.38	-0.63
K07F5.13	npp-1	-0.78	-2.03	-2.81
K08A8.3	coh-1	-1.12		-1.34
K08D10.3	rnp-3		-1.37	-1.20
K08D10.4	rnp-2	0.36	-0.97	-0.60
K08E3.6		-0.27	-3.40	-3.66
K08F4.1			-1.47	-2.11
K09B11.9		-1.05	0.48	-0.57
K09E4.3			-0.69	-0.93
K10B3.10	spc-1	-0.86	1.41	0.54
K10B3.7	gpd-3	0.40	1.39	1.79
K10B3.8	gpd-2	0.66	1.52	2.18
K11C4.3	unc-70	-0.26	1.30	1.04
K12D12.1	top-2	-0.73	-2.38	-3.11
K12D12.2	npp-3	-0.83	-1.46	-2.29
M01A10.1		-0.76	-6.21	-6.97
M01E11.2			-1.26	-1.50
M02B7.3	osm-3			
M03C11.7			-1.26	-1.24
M03C11.8			-1.53	-1.55
M03D4.1	zen-4	-0.72	-4.01	-4.74
M03F8.3		-0.78	-1.29	-2.07
M04F3.4			0.84	
M28.5		0.49	-2.04	-1.55
R03A10.3		2.19	1.38	3.57
R03G5.1	eft-4		2.48	2.55
R05D11.7		-0.76	-1.63	-2.40
R05D3.4	rfp-1	-0.36	-1.94	-2.30
R05G6.4			-1.11	-1.57
R06A10.4			1.59	
R06A4.9			-0.84	-0.86
R06C1.1			-2.16	-2.25
R07E5.1		-0.53	-1.75	-2.28
R07E5.14	rnp-4	-0.77	-0.86	-1.63
R07E5.16				
R07E5.3		-0.71	-1.34	-2.05
R07G3.5			-0.74	-0.71
R08C7.10	wapl-1	-1.53	-1.59	-3.12
R08D7.1			-1.98	-1.75
R09B3.5	mag-1	-0.74	-0.22	-0.96
R10E11.1	cbp-1	-0.73	-0.99	-1.71
R10E9.1	msi-1		1.08	0.95
R11A8.2			-2.52	-2.68
R11A8.6	iars-1			

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
R11H6.5			-1.89	-1.86
R12E2.3	rpn-8	-0.69	-0.66	-1.36
R186.7		-0.97	-1.18	-2.15
T01B7.4	cyn-11	-0.45	-1.30	-1.75
T01C3.6	rps-16		0.39	0.56
T01C3.7		0.47	-1.60	-1.13
T01D1.2	etr-1	-1.19	0.30	-0.88
T01G9.6			-0.29	-0.33
T02C12.3			-2.35	-2.66
T02G5.9	kars-1			
T02H6.2	thoc-1		-1.44	-1.66
T04H1.5		-1.52	-1.98	-3.49
T05C12.7		-0.31	-0.72	-1.03
T05E11.3		-0.20	1.18	0.98
T05F1.8		Inf	-3.50	
T05G5.3		-0.90	-3.26	-4.16
T05H4.14	gad-1	-0.53	-1.92	-2.45
T07A9.1			-2.03	-1.93
T07D4.3	rha-1		-1.67	-1.83
T07D4.4	ddx-19		-1.93	-1.87
T08A11.2		-0.28	-1.39	-1.67
T08B2.5			-1.39	-1.19
T08B2.9	frs-1			
T08D10.2	lsd-1	-0.93	-1.97	-2.89
T09F3.3	gpd-1	-0.98	-4.89	-5.87
T10B5.5	cct-7	-0.40	-0.44	-0.85
T10C6.5		-0.83	-1.52	-2.35
T10F2.4		-0.37	-1.15	-1.52
T10G3.6	gut-2	-1.10	-1.49	-2.58
T11F9.15				
T11G6.8		-0.79	-0.85	-1.65
T12A2.7				
T13H5.4			-1.05	-1.23
T14G8.1	chd-3	-0.78	1.33	0.55
T20B12.8	hmg-4	-0.84	-1.72	-2.56
T20F5.2	pbs-4	-0.59		-0.67
T20G5.1	chc-1	-0.70	0.16	-0.54
T20H4.4		-0.52	-1.79	-2.32
T21B10.7	cct-2	-0.58	-0.65	-1.23
T21D12.3			-1.54	-1.73
T21E12.4	dhc-1	-0.80	-0.63	-1.43
T22C1.6			-0.68	-0.80
T22D1.10	ruvb-2	-0.59	-2.43	-3.02
T22D1.3			-0.71	-0.90

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
T22D1.9	rpn-1	-0.78	-0.65	-1.43
T23B12.7	dnj-22		-2.90	-2.76
T23D8.4		-0.54	-0.12	-0.67
T23G11.3	gld-1	0.60	-7.02	-6.42
T23G7.4	sec-5	-0.94	-0.54	-1.48
T23G7.5	pir-1	-1.21	-1.85	-3.06
T23H2.1	npp-12	-0.72	-1.26	-1.98
T24H7.1	phb-2	-0.60	-0.38	-0.98
T25C8.2		0.86	1.88	2.74
T27E9.7	abcf-2		-0.23	
T27F2.1	skp-1	-0.60	-1.35	-1.95
T28D9.10	snr-3	-0.35	-1.35	-1.70
W01B11.3	nol-5		-1.39	-1.41
W02B12.2	rsp-2		-0.51	-0.80
W02B12.3	rsp-1	-0.39	-1.13	-1.52
W02D3.11	hrpf-1	-0.35	-1.31	-1.66
W02D9.1		4.29	-2.33	-2.55
W03F9.10		-0.35	-0.65	-1.01
W03H9.4	cacn-1	-0.62	-1.65	-2.26
W04A4.5		-0.47	-1.93	-2.40
W04A8.7	taf-1	-0.56	-1.51	-2.07
W04D2.6			-1.66	-1.75
W07E6.4	prp-21		-0.75	-0.93
W08D2.7	mtr-4	-0.77	-1.24	-2.01
W08E3.1	snr-2		-1.47	-1.65
W09B6.2	taf-6.1		-2.15	-2.63
W09G10.4	apd-3		-0.61	-0.81
Y102A5A.1	cand-1	-0.70	-0.38	-1.08
Y105E8A.26	tag-301	-0.77	1.46	0.68
Y105E8A.9	apg-1		0.24	0.39
Y106G6E.5	ced-12			
Y106G6H.2	pab-1	0.86	0.51	1.37
Y106G6H.7	sec-8	-0.32	-0.68	-1.01
Y108G3AL.2			-1.46	-1.69
Y110A7A.8		-0.70	-1.12	-1.83
Y111B2A.18		-0.32	-1.16	-1.48
Y113G7B.17		0.29	-1.96	-1.68
Y113G7B.23	psa-1	-0.56	-0.75	-1.31
Y116A8C.32	sfa-1		-1.20	-1.23
Y116A8C.34	cyn-13		-1.09	-0.73
Y116A8C.35	uaf-2			
Y116A8C.42	snr-1		-1.13	-1.07
Y17G7B.2	ash-2		-1.07	-1.07
Y17G7B.5	mcm-2	-0.39	-3.69	-4.08

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
Y17G7B.9	cyn-16	-0.50	-1.00	-1.50
Y18H1A.2		0.93	-1.21	
Y22D7AL.5		-0.39	-0.49	-0.87
Y25C1A.5			0.60	0.80
Y37A1B.1			1.28	
Y37E11AM.1	smgl-2		-2.28	-2.20
Y37E3.15	npp-13	-0.84	-0.98	-1.83
Y39A1B.3	dpy-28	-1.00	-2.29	-3.29
Y39G10AR.14		-0.78	-3.43	-4.21
Y39G8C.1	xrn-1	-0.39	-0.22	-0.60
Y40B1B.6			-1.66	-1.54
Y41E3.10	eef-1B.2	-0.59		
Y41E3.11		0.28	-1.76	-1.47
Y41E3.4	ers-1		-0.33	-0.41
Y43F4B.6	klp-19	-0.31	-2.89	-3.20
Y46E12BL.2		-1.40	-0.66	-2.06
Y46G5A.13			-0.73	-0.74
Y46G5A.4			-1.32	-1.33
Y47D3A.26	smc-3			
Y47D3A.27	teg-1	-1.38	-0.74	-2.12
Y47D3A.4	cku-70	-0.33	-1.06	-1.39
Y47G6A.11	msh-6	-0.74	-3.47	-4.21
Y47G6A.20	rnp-6	-0.89	-1.12	-2.01
Y48B6A.3	xrn-2	0.64	-1.30	-0.66
Y48G8AL.5			-0.94	-0.99
Y48G8AL.6	smg-2		-0.90	-0.89
Y48G9A.3		-1.22	-0.84	-2.07
Y49E10.1	rpt-6	-0.67		-0.75
Y49E10.15	snr-6	0.59	-1.06	-0.47
Y49F6B.4	smu-2	-0.91	-1.85	-2.77
Y50D4C.3			-1.19	-1.10
Y52B11A.9			-2.13	-2.23
Y53F4B.13		-0.41	-1.35	-1.76
Y54E10A.9	vbh-1	0.32	-1.42	-1.09
Y54E2A.11	eif-3.b	-0.41		-0.55
Y54F10AM.4	ceh-44		-0.84	-1.01
Y54F10BM.14	phf-5		-0.75	
Y55D9A.2		-0.55	-2.83	-3.37
Y55F3AM.3		0.76	-1.90	-1.14
Y55F3AR.3	cct-8		-0.75	-0.87
Y55F3BR.1			-1.04	-0.88
Y57A10A.25	parn-2			
Y57G11C.16			0.31	0.29
Y59A8B.6			-0.32	

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
Y62E10A.12	lsm-3			
Y62F5A.1	mdt-8	-0.44	-2.17	-2.60
Y65B4A.1		0.84	-1.61	-0.77
Y65B4A.6			-0.50	-0.78
Y66D12A.8			-1.35	-1.77
Y66D12A.9			-0.97	-0.58
Y66H1B.2	fln-1			
Y67D2.6			-1.16	-1.04
Y67H2A.1	cpsf-3	0.49	-1.06	-0.56
Y71D11A.2	smr-1		-1.01	-0.98
Y71F9AL.17		-0.22	0.66	0.44
Y71F9AL.18			-2.68	-2.65
Y71F9B.16	dnj-30	-0.52	-0.95	-1.47
Y71F9B.4	snr-7		-0.84	-1.24
Y71G12B.14	lsm-6		-1.05	-1.35
Y71G12B.8			-1.31	-1.42
Y71H2AM.17			-1.44	-1.43
Y71H2AM.19			-0.69	-0.89
Y73B6BL.3	exos-2	-1.24	-1.70	-2.94
Y73B6BL.32			-1.51	-1.40
Y73B6BL.33			-2.36	-2.24
Y73B6BL.6	sqd-1	0.38	0.23	0.61
Y76B12C.7	cpsf-1		-0.92	-0.91
Y77E11A.13	npp-20			
Y80D3A.2	emb-4	-0.44	-1.03	-1.47
Y81G3A.3		-1.71	-0.83	-2.54
Y87G2A.5	vrs-2	0.24	0.33	0.57
Y87G2A.6	cyn-15	-0.82	-0.75	-1.57
Y92C3B.2	uaf-1		-0.63	-0.69
Y92H12A.4		-1.07	-0.85	-1.92
Y95B8A.7			-2.13	-2.19
ZC302.1	mre-11	-0.83	-3.69	-4.52
ZC504.3			-1.05	-1.43
ZK1010.1		-0.22	0.45	0.24
ZK1010.3		-1.13	-0.87	-2.00
ZK1058.4	ccdc-47		-0.43	
ZK1067.6	sym-2		5.20	4.41
ZK1098.1			-1.38	-1.59
ZK1127.6		-0.48	-1.75	-2.23
ZK1127.9		-0.75	-1.79	-2.54
ZK1128.5	tag-246	0.45	-1.41	-0.96
ZK1307.9		-0.89	-2.82	-3.71
ZK328.2	eft-1	-0.57	-0.79	-1.36
ZK418.9			-0.32	-0.55

Table S6 log2 Ratios of Spliceosome Component or RNA-binding Factor Expression Change From One Sample to Another

Empty spaces (Columns C-E) represent comparisons in expression for which the p-value exceeded 0.01

Gene Name	Common Name	Gonad to Whole Worm	Whole Worm to glp4	Gonad to glp4
ZK593.7	lsm-7		-1.69	-2.33
ZK617.1	unc-22	-0.45	1.86	1.42
ZK632.1	mcm-6	-1.37	-2.70	-4.07
ZK652.1	snr-5	-0.76	-1.04	-1.16
ZK686.4		-1.06	-1.14	-2.20
ZK742.1			-1.46	-1.51
ZK856.13	tag-315	-1.04	-2.15	-3.19
ZK945.2	pas-7	-0.75	-0.29	-1.04
ZK973.6	anc-1	-2.70	1.06	-1.64
Average Change		-0.49	-1.10	-1.47

Table S7

GO Term Enrichment Analysis of Tissue-specific alternative 3' splice site genes (Table S2)

Term (Biological Process)	Background frequency	Sample frequency	Expected	P-value
single-organism developmental process (GO:0044767)	4569	124	3.47E+01	1.00E-48
developmental process (GO:0032502)	4583	124	3.48E+01	1.43E-48
anatomical structure development (GO:0048856)	3846	116	2.92E+01	3.99E-48
multicellular organismal development (GO:0007275)	4329	121	3.29E+01	5.03E-48
multicellular organismal process (GO:0032501)	4740	124	3.60E+01	6.80E-47
single-multicellular organism process (GO:0044707)	4624	122	3.51E+01	6.44E-46
embryo development (GO:0009790)	3042	104	2.31E+01	1.78E-45
embryo development ending in birth or egg hatching (GO:0009792)	2991	103	2.27E+01	4.10E-45
nematode larval development (GO:0002119)	2012	87	1.53E+01	4.22E-43
larval development (GO:0002164)	2014	87	1.53E+01	4.57E-43
post-embryonic development (GO:0009791)	2031	87	1.54E+01	8.92E-43
single-organism process (GO:0044699)	7511	139	5.70E+01	2.59E-39
organic substance metabolic process (GO:0071704)	3834	106	2.91E+01	5.80E-38
primary metabolic process (GO:0044238)	3726	104	2.83E+01	3.32E-37
cellular process (GO:0009987)	5899	125	4.48E+01	3.79E-37
reproduction (GO:0000003)	2545	89	1.93E+01	5.23E-37
regulation of biological process (GO:0050789)	3086	96	2.34E+01	7.53E-37
cellular metabolic process (GO:0044237)	3326	98	2.53E+01	6.07E-36
localization (GO:0051179)	2787	91	2.12E+01	9.16E-36
reproductive process (GO:0022414)	1493	71	1.13E+01	1.14E-35
metabolic process (GO:0008152)	5090	116	3.86E+01	2.46E-35
biological regulation (GO:0065007)	3599	100	2.73E+01	8.28E-35
establishment of localization (GO:0051234)	2147	79	1.63E+01	6.04E-33
single-organism cellular process (GO:0044763)	4675	109	3.55E+01	1.44E-32
regulation of cellular process (GO:0050794)	2481	83	1.88E+01	3.55E-32
cellular macromolecule metabolic process (GO:0044260)	2337	79	1.77E+01	2.23E-30
locomotion (GO:0040011)	1575	67	1.20E+01	3.00E-30
biological_process (GO:0008150)	10122	146	7.69E+01	3.85E-30
macromolecule metabolic process (GO:0043170)	2838	85	2.16E+01	1.11E-29
transport (GO:0006810)	2073	74	1.57E+01	2.42E-29
single organism reproductive process (GO:0044702)	1207	59	9.16E+00	5.83E-29
system development (GO:0048731)	1227	59	9.32E+00	1.39E-28
developmental process involved in reproduction (GO:0003006)	1178	58	8.94E+00	1.59E-28
anatomical structure morphogenesis (GO:0009653)	1060	55	8.05E+00	7.25E-28
multi-organism process (GO:0051704)	932	52	7.08E+00	1.58E-27
positive regulation of biological process (GO:0048518)	865	50	6.57E+00	5.74E-27
multicellular organism reproduction (GO:0032504)	784	48	5.95E+00	8.72E-27
multicellular organismal reproductive process (GO:0048609)	780	47	5.92E+00	7.80E-26
multi-organism reproductive process (GO:0044703)	832	48	6.32E+00	1.17E-25
protein metabolic process (GO:0019538)	1763	65	1.34E+01	1.48E-25
vesicle-mediated transport (GO:0016192)	932	50	7.08E+00	1.68E-25
biosynthetic process (GO:0009058)	1409	59	1.07E+01	1.98E-25
sex differentiation (GO:0007548)	923	49	7.01E+00	1.08E-24
cellular protein metabolic process (GO:0044267)	1285	56	9.76E+00	1.09E-24
cellular biosynthetic process (GO:0044249)	1341	57	1.02E+01	1.09E-24
gene expression (GO:0010467)	1035	51	7.86E+00	2.02E-24
organic substance biosynthetic process (GO:1901576)	1363	57	1.04E+01	2.47E-24
cellular component organization or biogenesis (GO:0071840)	1364	57	1.04E+01	2.57E-24
cell differentiation (GO:0030154)	877	47	6.66E+00	1.14E-23
single-organism metabolic process (GO:0044710)	1839	64	1.40E+01	1.16E-23
cellular developmental process (GO:0048869)	927	48	7.04E+00	1.26E-23
nitrogen compound metabolic process (GO:0006807)	1858	64	1.41E+01	2.04E-23
organic cyclic compound metabolic process (GO:1901360)	1671	61	1.27E+01	2.48E-23
cellular nitrogen compound metabolic process (GO:0034641)	1676	61	1.27E+01	2.90E-23
cellular aromatic compound metabolic process (GO:0006725)	1624	60	1.23E+01	4.07E-23
heterocycle metabolic process (GO:0046483)	1633	60	1.24E+01	5.43E-23
cellular macromolecule biosynthetic process (GO:0034645)	1014	49	7.70E+00	6.67E-23
endocytosis (GO:0006897)	822	45	6.24E+00	7.51E-23
nucleobase-containing compound metabolic process (GO:0006139)	1584	59	1.20E+01	8.28E-23
organ development (GO:0048513)	969	48	7.36E+00	8.44E-23
macromolecule biosynthetic process (GO:0009059)	1021	49	7.75E+00	9.00E-23
cellular component organization (GO:0016043)	1300	54	9.87E+00	1.28E-22
regulation of metabolic process (GO:0019222)	1369	55	1.04E+01	1.93E-22
development of primary sexual characteristics (GO:0045137)	847	45	6.43E+00	2.52E-22
gonad development (GO:0008406)	847	45	6.43E+00	2.52E-22
reproductive system development (GO:0061458)	856	45	6.50E+00	3.86E-22
reproductive structure development (GO:0048608)	856	45	6.50E+00	3.86E-22
organelle organization (GO:0006996)	870	45	6.61E+00	7.42E-22
body morphogenesis (GO:0010171)	618	39	4.69E+00	1.82E-21
cell cycle (GO:0007049)	502	36	3.81E+00	2.21E-21
receptor-mediated endocytosis (GO:0006898)	719	41	5.46E+00	4.03E-21

Table S7

GO Term Enrichment Analysis of Tissue-specific alternative 3' splice site genes (Table S2)

regulation of response to stimulus (GO:0048583)	325	30	2.47E+00	2.29E-20
cell cycle process (GO:0022402)	432	33	3.28E+00	3.58E-20
sexual reproduction (GO:0019953)	547	36	4.15E+00	3.75E-20
cell development (GO:0048468)	697	38	5.29E+00	1.19E-18
protein localization (GO:0008104)	375	30	2.85E+00	1.24E-18
regulation of primary metabolic process (GO:0080090)	1066	44	8.09E+00	1.73E-17
small molecule metabolic process (GO:0044281)	858	40	6.51E+00	2.10E-17
regulation of cellular metabolic process (GO:0031323)	1078	44	8.18E+00	2.65E-17
regulation of multicellular organismal process (GO:0051239)	729	37	5.54E+00	4.75E-17
cellular localization (GO:0051641)	467	31	3.55E+00	4.83E-17
gamete generation (GO:0007276)	468	31	3.55E+00	5.13E-17
single-organism organelle organization (GO:1902589)	609	34	4.62E+00	1.15E-16
nucleic acid metabolic process (GO:0090304)	1128	44	8.56E+00	1.47E-16
programmed cell death (GO:0012501)	492	31	3.74E+00	2.09E-16
regulation of macromolecule metabolic process (GO:0060255)	1198	45	9.10E+00	2.16E-16
catabolic process (GO:0009056)	827	38	6.28E+00	3.73E-16
behavior (GO:0007610)	465	30	3.53E+00	4.56E-16
regulation of developmental process (GO:0050793)	686	35	5.21E+00	5.00E-16
germ cell development (GO:0007281)	357	27	2.71E+00	6.70E-16
cellular process involved in reproduction in multicellular organism (GO:002	357	27	2.71E+00	6.70E-16
RNA metabolic process (GO:0016070)	907	39	6.89E+00	1.09E-15
apoptotic process (GO:0006915)	482	30	3.66E+00	1.21E-15
death (GO:0016265)	532	31	4.04E+00	1.86E-15
cell death (GO:0008219)	532	31	4.04E+00	1.86E-15
hermaphrodite genitalia development (GO:0040035)	733	35	5.57E+00	3.85E-15
genitalia development (GO:0048806)	739	35	5.61E+00	4.94E-15
organic substance catabolic process (GO:1901575)	794	36	6.03E+00	5.92E-15
macromolecule localization (GO:0033036)	957	39	7.27E+00	6.61E-15
negative regulation of biological process (GO:0048519)	698	34	5.30E+00	7.00E-15
regulation of gene expression (GO:0010468)	1030	39	7.82E+00	7.60E-14
regulation of signal transduction (GO:0009966)	223	21	1.69E+00	1.06E-13
regulation of cellular component organization (GO:0051128)	258	22	1.96E+00	1.41E-13
translation (GO:0006412)	230	21	1.75E+00	1.94E-13
negative regulation of cellular process (GO:0048523)	370	25	2.81E+00	2.01E-13
regulation of cell communication (GO:0010646)	268	22	2.04E+00	3.06E-13
regulation of signaling (GO:0023051)	268	22	2.04E+00	3.06E-13
single-organism localization (GO:1902578)	1324	43	1.01E+01	3.20E-13
organic substance transport (GO:0071702)	382	25	2.90E+00	4.14E-13
multi-organism behavior (GO:0051705)	348	24	2.64E+00	5.49E-13
nuclear division (GO:0000280)	314	23	2.38E+00	6.73E-13
organelle fission (GO:0048285)	318	23	2.41E+00	8.78E-13
macromolecule modification (GO:0043412)	950	36	7.21E+00	1.50E-12
regulation of cell cycle (GO:0051726)	226	20	1.72E+00	1.92E-12
single-organism catabolic process (GO:0044712)	459	26	3.49E+00	2.89E-12
mitotic cell cycle process (GO:1903047)	232	20	1.76E+00	3.13E-12
establishment of localization in cell (GO:0051649)	418	25	3.17E+00	3.14E-12
mitotic cell cycle (GO:0000278)	233	20	1.77E+00	3.39E-12
multicellular organismal aging (GO:0010259)	812	33	6.17E+00	4.11E-12
determination of adult lifespan (GO:0008340)	812	33	6.17E+00	4.11E-12
aging (GO:0007568)	813	33	6.17E+00	4.26E-12
multicellular organismal reproductive behavior (GO:0033057)	343	23	2.60E+00	4.28E-12
movement of cell or subcellular component (GO:0006928)	383	24	2.91E+00	4.40E-12
multi-organism reproductive behavior (GO:0044705)	346	23	2.63E+00	5.13E-12
reproductive behavior (GO:0019098)	346	23	2.63E+00	5.13E-12
multi-multicellular organism process (GO:0044706)	349	23	2.65E+00	6.14E-12
localization of cell (GO:0051674)	279	21	2.12E+00	8.23E-12
cell motility (GO:0048870)	279	21	2.12E+00	8.23E-12
oviposition (GO:0018991)	329	22	2.50E+00	1.90E-11
positive regulation of metabolic process (GO:0009893)	298	21	2.26E+00	2.91E-11
female gamete generation (GO:0007292)	262	20	1.99E+00	2.94E-11
organonitrogen compound metabolic process (GO:1901564)	771	31	5.85E+00	4.32E-11
regulation of cellular biosynthetic process (GO:0031326)	888	33	6.74E+00	4.98E-11
regulation of biosynthetic process (GO:0009889)	889	33	6.75E+00	5.14E-11
cell migration (GO:0016477)	271	20	2.06E+00	5.46E-11
oogenesis (GO:0048477)	238	19	1.81E+00	6.28E-11
phosphorus metabolic process (GO:0006793)	1269	39	9.63E+00	6.44E-11
regulation of cell cycle process (GO:0010564)	150	16	1.14E+00	9.39E-11
chromosome segregation (GO:0007059)	182	17	1.38E+00	1.23E-10
single-organism transport (GO:0044765)	1249	38	9.48E+00	2.01E-10
regulation of cellular macromolecule biosynthetic process (GO:2000112)	878	32	6.67E+00	2.19E-10
phosphate-containing compound metabolic process (GO:0006796)	1253	38	9.51E+00	2.21E-10
regulation of macromolecule biosynthetic process (GO:0010556)	884	32	6.71E+00	2.62E-10
cellular catabolic process (GO:0044248)	615	27	4.67E+00	3.25E-10

Table S7

GO Term Enrichment Analysis of Tissue-specific alternative 3' splice site genes (Table S2)

cellular protein modification process (GO:0006464)	897	32	6.81E+00	3.87E-10
protein modification process (GO:0036211)	897	32	6.81E+00	3.87E-10
cell division (GO:0051301)	197	17	1.50E+00	4.31E-10
regulation of nucleobase-containing compound metabolic process (GO:001	850	31	6.45E+00	5.49E-10
regulation of cell division (GO:0051302)	140	15	1.06E+00	5.51E-10
regulation of nitrogen compound metabolic process (GO:0051171)	853	31	6.48E+00	6.02E-10
regulation of intracellular signal transduction (GO:1902531)	143	15	1.09E+00	7.43E-10
cytoskeleton organization (GO:0007010)	354	21	2.69E+00	7.59E-10
nucleobase-containing compound biosynthetic process (GO:0034654)	752	29	5.71E+00	9.14E-10
regulation of organelle organization (GO:0033043)	176	16	1.34E+00	1.03E-09
regulation of growth (GO:0040008)	413	22	3.14E+00	1.66E-09
aromatic compound biosynthetic process (GO:0019438)	774	29	5.88E+00	1.84E-09
positive regulation of cellular process (GO:0048522)	332	20	2.52E+00	2.15E-09
heterocycle biosynthetic process (GO:0018130)	785	29	5.96E+00	2.59E-09
cellular nitrogen compound biosynthetic process (GO:0044271)	790	29	6.00E+00	3.02E-09
organic cyclic compound biosynthetic process (GO:1901362)	804	29	6.10E+00	4.61E-09
regulation of developmental growth (GO:0048638)	392	21	2.98E+00	5.08E-09
regulation of RNA metabolic process (GO:0051252)	824	29	6.26E+00	8.32E-09
carbohydrate derivative metabolic process (GO:1901135)	660	26	5.01E+00	1.05E-08
protein transport (GO:0015031)	243	17	1.85E+00	1.14E-08
positive regulation of developmental process (GO:0051094)	414	21	3.14E+00	1.39E-08
positive regulation of GTPase activity (GO:0043547)	118	13	8.96E-01	1.53E-08
positive regulation of growth (GO:0045927)	373	20	2.83E+00	1.70E-08
regulation of GTPase activity (GO:0043087)	120	13	9.11E-01	1.88E-08
positive regulation of multicellular organismal process (GO:0051240)	421	21	3.20E+00	1.89E-08
regulation of multicellular organism growth (GO:0040014)	376	20	2.86E+00	1.95E-08
establishment of protein localization (GO:0045184)	252	17	1.91E+00	1.99E-08
regulation of Ras protein signal transduction (GO:0046578)	95	12	7.21E-01	2.07E-08
regulation of catalytic activity (GO:0050790)	296	18	2.25E+00	2.59E-08
regulation of transcription, DNA-templated (GO:0006355)	807	28	6.13E+00	2.82E-08
regulation of nucleic acid-templated transcription (GO:1903506)	807	28	6.13E+00	2.82E-08
regulation of RNA biosynthetic process (GO:2001141)	813	28	6.17E+00	3.35E-08
positive regulation of hydrolase activity (GO:0051345)	130	13	9.87E-01	4.98E-08
regulation of small GTPase mediated signal transduction (GO:0051056)	103	12	7.82E-01	5.18E-08
regulation of molecular function (GO:0065009)	311	18	2.36E+00	5.73E-08
positive regulation of multicellular organism growth (GO:0040018)	355	19	2.70E+00	5.92E-08
positive regulation of developmental growth (GO:0048639)	357	19	2.71E+00	6.51E-08
macromolecular complex subunit organization (GO:0043933)	505	22	3.83E+00	7.74E-08
nucleobase-containing small molecule metabolic process (GO:0055086)	505	22	3.83E+00	7.74E-08
regulation of nuclear division (GO:0051783)	114	12	8.66E-01	1.63E-07
cellular macromolecule localization (GO:0070727)	176	14	1.34E+00	1.66E-07
cellular protein localization (GO:0034613)	176	14	1.34E+00	1.66E-07
lipid metabolic process (GO:0006629)	333	18	2.53E+00	1.70E-07
oxoacid metabolic process (GO:0043436)	291	17	2.21E+00	1.79E-07
organic acid metabolic process (GO:0006082)	291	17	2.21E+00	1.79E-07
RNA processing (GO:0006396)	213	15	1.62E+00	1.86E-07
nucleoside metabolic process (GO:0009116)	389	19	2.95E+00	2.71E-07
glycosyl compound metabolic process (GO:1901657)	390	19	2.96E+00	2.83E-07
mitotic nuclear division (GO:0007067)	124	12	9.41E-01	4.19E-07
positive regulation of catalytic activity (GO:0043085)	156	13	1.18E+00	4.51E-07
regulation of biological quality (GO:0065008)	856	27	6.50E+00	5.47E-07
positive regulation of molecular function (GO:0044093)	159	13	1.21E+00	5.66E-07
response to stimulus (GO:0050896)	1969	42	1.50E+01	7.09E-07
carboxylic acid metabolic process (GO:0019752)	276	16	2.10E+00	7.20E-07
regulation of protein metabolic process (GO:0051246)	237	15	1.80E+00	7.92E-07
nervous system development (GO:0007399)	278	16	2.11E+00	7.97E-07
purine ribonucleoside metabolic process (GO:0046128)	372	18	2.82E+00	9.73E-07
purine nucleoside metabolic process (GO:0042278)	372	18	2.82E+00	9.73E-07
nucleotide metabolic process (GO:0009117)	474	20	3.60E+00	1.07E-06
regulation of hydrolase activity (GO:0051336)	204	14	1.55E+00	1.10E-06
nucleoside phosphate metabolic process (GO:0006753)	480	20	3.64E+00	1.33E-06
organophosphate metabolic process (GO:0019637)	590	22	4.48E+00	1.38E-06
neurogenesis (GO:0022008)	250	15	1.90E+00	1.62E-06
ribonucleoside metabolic process (GO:0009119)	386	18	2.93E+00	1.73E-06
transcription, DNA-templated (GO:0006351)	601	22	4.56E+00	1.94E-06
purine nucleoside triphosphate metabolic process (GO:0009144)	342	17	2.60E+00	2.00E-06
purine ribonucleoside triphosphate metabolic process (GO:0009205)	342	17	2.60E+00	2.00E-06
molting cycle, collagen and cuticulin-based cuticle (GO:0018996)	297	16	2.26E+00	2.03E-06
molting cycle (GO:0042303)	297	16	2.26E+00	2.03E-06
meiotic chromosome segregation (GO:0045132)	144	12	1.09E+00	2.21E-06
nucleic acid-templated transcription (GO:0097659)	606	22	4.60E+00	2.25E-06
ribonucleoside triphosphate metabolic process (GO:0009199)	345	17	2.62E+00	2.28E-06
cellular component biogenesis (GO:0044085)	498	20	3.78E+00	2.47E-06

Table S7

GO Term Enrichment Analysis of Tissue-specific alternative 3' splice site genes (Table S2)

nucleoside triphosphate metabolic process (GO:0009141)	348	17	2.64E+00	2.59E-06
RNA biosynthetic process (GO:0032774)	611	22	4.64E+00	2.61E-06
negative regulation of response to stimulus (GO:0048585)	90	10	6.83E-01	3.63E-06
regulation of cellular protein metabolic process (GO:0032268)	227	14	1.72E+00	4.22E-06
regulation of multicellular organismal development (GO:2000026)	315	16	2.39E+00	4.64E-06
chromosome organization (GO:0051276)	191	13	1.45E+00	4.99E-06
purine-containing compound metabolic process (GO:0072521)	415	18	3.15E+00	5.29E-06
regulation of locomotion (GO:0040012)	157	12	1.19E+00	5.74E-06
meiotic nuclear division (GO:0007126)	233	14	1.77E+00	5.85E-06
protein catabolic process (GO:0030163)	276	15	2.10E+00	6.05E-06
proteolysis (GO:0006508)	473	19	3.59E+00	6.49E-06
regulation of Ras GTPase activity (GO:0032318)	70	9	5.31E-01	6.70E-06
meiotic cell cycle (GO:0051321)	239	14	1.81E+00	8.03E-06
macromolecule catabolic process (GO:0009057)	377	17	2.86E+00	8.38E-06
regulation of transcription from RNA polymerase II promoter (GO:0006357)	204	13	1.55E+00	1.08E-05
generation of neurons (GO:0048699)	247	14	1.88E+00	1.21E-05
single-organism biosynthetic process (GO:0044711)	387	17	2.94E+00	1.23E-05
negative regulation of signal transduction (GO:0009968)	77	9	5.85E-01	1.51E-05
regulation of localization (GO:0032879)	211	13	1.60E+00	1.60E-05
meiotic cell cycle process (GO:1903046)	173	12	1.31E+00	1.66E-05
purine ribonucleotide metabolic process (GO:0009150)	397	17	3.01E+00	1.77E-05
negative regulation of cell communication (GO:0010648)	79	9	6.00E-01	1.88E-05
negative regulation of signaling (GO:0023057)	79	9	6.00E-01	1.88E-05
purine nucleotide metabolic process (GO:0006163)	399	17	3.03E+00	1.91E-05
ion transport (GO:0006811)	565	20	4.29E+00	2.01E-05
ribonucleotide metabolic process (GO:0009259)	406	17	3.08E+00	2.45E-05
ribose phosphate metabolic process (GO:0019693)	406	17	3.08E+00	2.45E-05
regulation of mitotic cell cycle (GO:0007346)	83	9	6.30E-01	2.85E-05
small molecule catabolic process (GO:0044282)	58	8	4.40E-01	2.87E-05
microtubule cytoskeleton organization (GO:0000226)	148	11	1.12E+00	3.45E-05
aromatic compound catabolic process (GO:0019439)	365	16	2.77E+00	3.55E-05
cellular nitrogen compound catabolic process (GO:0044270)	365	16	2.77E+00	3.55E-05
heterocycle catabolic process (GO:0046700)	366	16	2.78E+00	3.68E-05
organic cyclic compound catabolic process (GO:1901361)	369	16	2.80E+00	4.11E-05
cellular component assembly (GO:0022607)	428	17	3.25E+00	5.22E-05
positive regulation of Ras GTPase activity (GO:0032320)	63	8	4.78E-01	5.40E-05
regulation of behavior (GO:0050795)	92	9	6.99E-01	6.80E-05
actin filament-based process (GO:0030029)	198	12	1.50E+00	7.13E-05
regulation of vulval development (GO:0040028)	250	13	1.90E+00	1.13E-04
establishment of organelle localization (GO:0051656)	131	10	9.95E-01	1.19E-04
intracellular transport (GO:0046907)	209	12	1.59E+00	1.27E-04
posttranscriptional regulation of gene expression (GO:0010608)	209	12	1.59E+00	1.27E-04
nucleobase-containing compound catabolic process (GO:0034655)	353	15	2.68E+00	1.47E-04
transmembrane transport (GO:0055085)	769	22	5.84E+00	1.50E-04
microtubule-based process (GO:0007017)	213	12	1.62E+00	1.55E-04
organophosphate catabolic process (GO:0046434)	305	14	2.32E+00	1.59E-04
organelle localization (GO:0051640)	136	10	1.03E+00	1.68E-04
intracellular signal transduction (GO:0035556)	260	13	1.97E+00	1.76E-04
regulation of post-embryonic development (GO:0048580)	261	13	1.98E+00	1.84E-04
regulation of nematode larval development (GO:0061062)	261	13	1.98E+00	1.84E-04
chromatin organization (GO:0006325)	105	9	7.97E-01	2.06E-04
cell communication (GO:0007154)	1373	30	1.04E+01	2.18E-04
inductive cell migration (GO:0040039)	144	10	1.09E+00	2.82E-04
negative regulation of developmental process (GO:0051093)	228	12	1.73E+00	3.19E-04
organonitrogen compound catabolic process (GO:1901565)	378	15	2.87E+00	3.50E-04
organelle assembly (GO:0070925)	230	12	1.75E+00	3.50E-04
protein complex subunit organization (GO:0071822)	380	15	2.89E+00	3.74E-04
ATP metabolic process (GO:0046034)	232	12	1.76E+00	3.83E-04
single organism signaling (GO:0044700)	1338	29	1.02E+01	4.31E-04
signaling (GO:0023052)	1338	29	1.02E+01	4.31E-04
actin cytoskeleton organization (GO:0030036)	192	11	1.46E+00	4.54E-04
ion transmembrane transport (GO:0034220)	448	16	3.40E+00	5.50E-04
purine ribonucleoside catabolic process (GO:0046130)	289	13	2.19E+00	5.77E-04
purine nucleoside catabolic process (GO:0006152)	289	13	2.19E+00	5.77E-04
cellular protein complex assembly (GO:0043623)	197	11	1.50E+00	5.84E-04
purine-containing compound catabolic process (GO:0072523)	290	13	2.20E+00	5.99E-04
cellular macromolecular complex assembly (GO:0034622)	243	12	1.85E+00	6.22E-04
ribonucleoside catabolic process (GO:0042454)	292	13	2.22E+00	6.47E-04
carbohydrate metabolic process (GO:0005975)	292	13	2.22E+00	6.47E-04
nucleoside catabolic process (GO:0009164)	293	13	2.22E+00	6.72E-04
purine ribonucleoside monophosphate metabolic process (GO:0009167)	245	12	1.86E+00	6.78E-04
purine nucleoside monophosphate metabolic process (GO:0009126)	245	12	1.86E+00	6.78E-04
glycosyl compound catabolic process (GO:1901658)	294	13	2.23E+00	6.98E-04

Table S7

GO Term Enrichment Analysis of Tissue-specific alternative 3' splice site genes (Table S2)

ribonucleoside monophosphate metabolic process (GO:0009161)	252	12	1.91E+00	9.08E-04
nucleoside monophosphate metabolic process (GO:0009123)	254	12	1.93E+00	9.86E-04
chromatin modification (GO:0016568)	93	8	7.06E-01	1.01E-03
single fertilization (GO:0007338)	65	7	4.94E-01	1.17E-03
positive regulation of endocytosis (GO:0045807)	9	4	6.83E-02	1.18E-03
cellular component morphogenesis (GO:0032989)	314	13	2.38E+00	1.44E-03
negative regulation of cell cycle (GO:0045786)	68	7	5.16E-01	1.57E-03
fertilization (GO:0009566)	68	7	5.16E-01	1.57E-03
regulation of endocytosis (GO:0030100)	23	5	1.75E-01	1.57E-03
carbohydrate derivative catabolic process (GO:1901136)	372	14	2.82E+00	1.66E-03
regulation of meiotic cell cycle (GO:0051445)	136	9	1.03E+00	1.73E-03
phosphorylation (GO:0016310)	553	17	4.20E+00	1.81E-03
cellular response to stimulus (GO:0051716)	1447	29	1.10E+01	2.10E-03
protein complex assembly (GO:0006461)	275	12	2.09E+00	2.23E-03
protein complex biogenesis (GO:0070271)	276	12	2.10E+00	2.32E-03
purine nucleoside triphosphate catabolic process (GO:0009146)	283	12	2.15E+00	2.99E-03
purine ribonucleoside triphosphate catabolic process (GO:0009207)	283	12	2.15E+00	2.99E-03
ribonucleoside triphosphate catabolic process (GO:0009203)	283	12	2.15E+00	2.99E-03
nucleoside triphosphate catabolic process (GO:0009143)	284	12	2.16E+00	3.10E-03
regulation of cell proliferation (GO:0042127)	109	8	8.28E-01	3.23E-03
regulation of cell differentiation (GO:0045595)	76	7	5.77E-01	3.25E-03
regulation of vesicle-mediated transport (GO:0060627)	27	5	2.05E-01	3.42E-03
negative regulation of metabolic process (GO:0009892)	340	13	2.58E+00	3.43E-03
negative regulation of multicellular organismal process (GO:0051241)	237	11	1.80E+00	3.44E-03
purine ribonucleotide catabolic process (GO:0009154)	287	12	2.18E+00	3.45E-03
purine nucleotide catabolic process (GO:0006195)	287	12	2.18E+00	3.45E-03
ribonucleotide catabolic process (GO:0009261)	287	12	2.18E+00	3.45E-03
digestive system development (GO:0055123)	110	8	8.35E-01	3.45E-03
digestive tract development (GO:0048565)	110	8	8.35E-01	3.45E-03
oxidation-reduction process (GO:0055114)	581	17	4.41E+00	3.50E-03
ubiquitin-dependent protein catabolic process (GO:0006511)	111	8	8.43E-01	3.69E-03
single-organism carbohydrate metabolic process (GO:0044723)	193	10	1.47E+00	3.85E-03
negative regulation of cellular metabolic process (GO:0031324)	193	10	1.47E+00	3.85E-03
muscle structure development (GO:0061061)	193	10	1.47E+00	3.85E-03
lipid localization (GO:0010876)	589	17	4.47E+00	4.20E-03
tube development (GO:0035295)	113	8	8.58E-01	4.20E-03
nucleotide catabolic process (GO:0009166)	293	12	2.22E+00	4.25E-03
response to external stimulus (GO:0009605)	294	12	2.23E+00	4.40E-03
nucleoside phosphate catabolic process (GO:1901292)	294	12	2.23E+00	4.40E-03
modification-dependent protein catabolic process (GO:0019941)	115	8	8.73E-01	4.77E-03
positive regulation of transport (GO:0051050)	29	5	2.20E-01	4.83E-03
protein localization to synapse (GO:0035418)	13	4	9.87E-02	5.02E-03
modification-dependent macromolecule catabolic process (GO:0043632)	116	8	8.81E-01	5.08E-03
mRNA metabolic process (GO:0016071)	116	8	8.81E-01	5.08E-03
striated muscle cell development (GO:0055002)	157	9	1.19E+00	5.50E-03
striated muscle cell differentiation (GO:0051146)	158	9	1.20E+00	5.79E-03
muscle cell development (GO:0055001)	158	9	1.20E+00	5.79E-03
cellular macromolecule catabolic process (GO:0044265)	203	10	1.54E+00	5.97E-03
cation transport (GO:0006812)	359	13	2.73E+00	6.14E-03
negative regulation of vulval development (GO:0040027)	206	10	1.56E+00	6.79E-03
male sex differentiation (GO:0046661)	86	7	6.53E-01	7.25E-03
macromolecular complex assembly (GO:0065003)	309	12	2.35E+00	7.26E-03
positive regulation of cellular biosynthetic process (GO:0031328)	122	8	9.26E-01	7.32E-03
positive regulation of biosynthetic process (GO:0009891)	122	8	9.26E-01	7.32E-03
negative regulation of post-embryonic development (GO:0048581)	208	10	1.58E+00	7.38E-03
negative regulation of nematode larval development (GO:0061064)	208	10	1.58E+00	7.38E-03
cellular homeostasis (GO:0019725)	88	7	6.68E-01	8.40E-03
proteolysis involved in cellular protein catabolic process (GO:0051603)	125	8	9.49E-01	8.73E-03
negative regulation of intracellular signal transduction (GO:1902532)	33	5	2.51E-01	8.99E-03
nucleotide biosynthetic process (GO:0009165)	126	8	9.57E-01	9.24E-03
protein modification by small protein conjugation or removal (GO:0070647)	90	7	6.83E-01	9.71E-03
cellular protein catabolic process (GO:0044257)	127	8	9.64E-01	9.78E-03
nucleoside phosphate biosynthetic process (GO:1901293)	127	8	9.64E-01	9.78E-03
cell fate commitment (GO:0045165)	128	8	9.72E-01	1.04E-02
muscle cell differentiation (GO:0042692)	170	9	1.29E+00	1.04E-02
regulation of phosphorus metabolic process (GO:0051174)	91	7	6.91E-01	1.04E-02
regulation of phosphate metabolic process (GO:0019220)	91	7	6.91E-01	1.04E-02
positive regulation of cellular component organization (GO:0051130)	35	5	2.66E-01	1.19E-02
carbohydrate derivative biosynthetic process (GO:1901137)	220	10	1.67E+00	1.20E-02
negative regulation of macromolecule metabolic process (GO:0010605)	325	12	2.47E+00	1.20E-02
regulation of meiosis (GO:0040020)	94	7	7.14E-01	1.28E-02
DNA conformation change (GO:0071103)	62	6	4.71E-01	1.33E-02
positive regulation of cell death (GO:0010942)	36	5	2.73E-01	1.36E-02

Table S7

GO Term Enrichment Analysis of Tissue-specific alternative 3' splice site genes (Table S2)

spindle organization (GO:0007051)	95	7	7.21E-01	1.37E-02
maintenance of location (GO:0051235)	579	16	4.40E+00	1.43E-02
regulation of mitosis (GO:0007088)	17	4	1.29E-01	1.43E-02
feeding behavior (GO:0007631)	37	5	2.81E-01	1.55E-02
ncRNA metabolic process (GO:0034660)	136	8	1.03E+00	1.60E-02
negative regulation of gene expression (GO:0010629)	229	10	1.74E+00	1.69E-02
regulation of reproductive process (GO:2000241)	65	6	4.94E-01	1.73E-02
purine ribonucleoside monophosphate biosynthetic process (GO:0009168)	38	5	2.89E-01	1.77E-02
purine nucleoside monophosphate biosynthetic process (GO:0009127)	38	5	2.89E-01	1.77E-02
regulation of feeding behavior (GO:0060259)	38	5	2.89E-01	1.77E-02
myosin filament assembly (GO:0031034)	138	8	1.05E+00	1.77E-02
myosin filament organization (GO:0031033)	138	8	1.05E+00	1.77E-02
striated muscle myosin thick filament assembly (GO:0071688)	138	8	1.05E+00	1.77E-02
pattern specification process (GO:0007389)	66	6	5.01E-01	1.88E-02
positive regulation of transcription from RNA polymerase II promoter (GO:0	100	7	7.59E-01	1.91E-02
DNA metabolic process (GO:0006259)	233	10	1.77E+00	1.95E-02
embryonic morphogenesis (GO:0048598)	140	8	1.06E+00	1.96E-02
negative regulation of cellular component organization (GO:0051129)	39	5	2.96E-01	2.00E-02
regulation of multi-organism process (GO:0043900)	68	6	5.16E-01	2.23E-02
histone modification (GO:0016570)	68	6	5.16E-01	2.23E-02
covalent chromatin modification (GO:0016569)	68	6	5.16E-01	2.23E-02
response to temperature stimulus (GO:0009266)	68	6	5.16E-01	2.23E-02
cation transmembrane transport (GO:0098655)	292	11	2.22E+00	2.40E-02
monocarboxylic acid metabolic process (GO:0032787)	104	7	7.90E-01	2.45E-02
response to stress (GO:0006950)	679	17	5.16E+00	2.63E-02
anatomical structure formation involved in morphogenesis (GO:0048646)	242	10	1.84E+00	2.69E-02
regulation of protein catabolic process (GO:0042176)	20	4	1.52E-01	2.70E-02
organic acid catabolic process (GO:0016054)	42	5	3.19E-01	2.84E-02
regulation of oviposition (GO:0046662)	42	5	3.19E-01	2.84E-02
positive regulation of locomotion (GO:0040017)	42	5	3.19E-01	2.84E-02
carboxylic acid catabolic process (GO:0046395)	42	5	3.19E-01	2.84E-02
cellular lipid metabolic process (GO:0044255)	194	9	1.47E+00	2.92E-02
positive regulation of transcription, DNA-templated (GO:0045893)	107	7	8.12E-01	2.93E-02
positive regulation of RNA biosynthetic process (GO:1902680)	107	7	8.12E-01	2.93E-02
positive regulation of nucleic acid-templated transcription (GO:1903508)	107	7	8.12E-01	2.93E-02
regulation of transport (GO:0051049)	108	7	8.20E-01	3.11E-02
tissue development (GO:0009888)	108	7	8.20E-01	3.11E-02
sister chromatid segregation (GO:0000819)	43	5	3.27E-01	3.18E-02
positive regulation of growth rate (GO:0040010)	21	4	1.59E-01	3.26E-02
positive regulation of RNA metabolic process (GO:0051254)	109	7	8.28E-01	3.29E-02
membrane organization (GO:0061024)	152	8	1.15E+00	3.51E-02
DNA replication (GO:0006260)	74	6	5.62E-01	3.56E-02
actomyosin structure organization (GO:0031032)	154	8	1.17E+00	3.85E-02
myofibril assembly (GO:0030239)	154	8	1.17E+00	3.85E-02
ribonucleoside monophosphate biosynthetic process (GO:0009156)	45	5	3.42E-01	3.94E-02
cellular amino acid metabolic process (GO:0006520)	155	8	1.18E+00	4.03E-02
nematode male tail tip morphogenesis (GO:0045138)	77	6	5.85E-01	4.44E-02
signal transduction (GO:0007165)	1262	24	9.58E+00	4.47E-02
positive regulation of nucleobase-containing compound metabolic process (	115	7	8.73E-01	4.61E-02
male anatomical structure morphogenesis (GO:0090598)	78	6	5.92E-01	4.77E-02
nucleoside monophosphate biosynthetic process (GO:0009124)	47	5	3.57E-01	4.84E-02
organic anion transport (GO:0015711)	48	5	3.64E-01	5.34E-02
nucleobase-containing compound transport (GO:0015931)	48	5	3.64E-01	5.34E-02
positive regulation of nitrogen compound metabolic process (GO:0051173)	118	7	8.96E-01	5.42E-02
ATP biosynthetic process (GO:0006754)	24	4	1.82E-01	5.47E-02
positive regulation of macromolecule metabolic process (GO:0010604)	162	8	1.23E+00	5.49E-02
positive regulation of macromolecule biosynthetic process (GO:0010557)	119	7	9.03E-01	5.72E-02
response to abiotic stimulus (GO:0009628)	165	8	1.25E+00	6.24E-02
regulation of phosphorylation (GO:0042325)	82	6	6.23E-01	6.27E-02
chemotaxis (GO:0006935)	121	7	9.19E-01	6.34E-02
positive regulation of gene expression (GO:0010628)	121	7	9.19E-01	6.34E-02
methylation (GO:0032259)	121	7	9.19E-01	6.34E-02
purine nucleoside biosynthetic process (GO:0042451)	50	5	3.80E-01	6.47E-02
purine ribonucleoside biosynthetic process (GO:0046129)	50	5	3.80E-01	6.47E-02
negative regulation of mitotic cell cycle (GO:0045930)	50	5	3.80E-01	6.47E-02
protein modification by small protein conjugation (GO:0032446)	83	6	6.30E-01	6.71E-02
synaptic transmission (GO:0007268)	83	6	6.30E-01	6.71E-02
mitotic spindle organization (GO:0007052)	84	6	6.38E-01	7.16E-02
regulation of growth rate (GO:0040009)	26	4	1.97E-01	7.44E-02
positive regulation of cellular metabolic process (GO:0031325)	170	8	1.29E+00	7.67E-02
pronuclear migration (GO:0035046)	52	5	3.95E-01	7.78E-02
organonitrogen compound biosynthetic process (GO:1901566)	222	9	1.69E+00	8.20E-02
negative regulation of organelle organization (GO:0010639)	27	4	2.05E-01	8.61E-02

Table S7

GO Term Enrichment Analysis of Tissue-specific alternative 3' splice site genes (Table S2)

mRNA processing (GO:0006397)	88	6	6.68E-01	9.23E-02
cell redox homeostasis (GO:0045454)	54	5	4.10E-01	9.28E-02
taxis (GO:0042330)	129	7	9.79E-01	9.44E-02
regulation of cellular protein catabolic process (GO:1903362)	10	3	7.59E-02	9.65E-02
cellular response to organonitrogen compound (GO:0071417)	10	3	7.59E-02	9.65E-02
cell projection organization (GO:0030030)	227	9	1.72E+00	9.70E-02
purine nucleoside triphosphate biosynthetic process (GO:0009145)	28	4	2.13E-01	9.89E-02
purine ribonucleoside triphosphate biosynthetic process (GO:0009206)	28	4	2.13E-01	9.89E-02
nuclear migration (GO:0007097)	55	5	4.18E-01	1.01E-01
cell fate specification (GO:0001708)	90	6	6.83E-01	1.04E-01
nucleus localization (GO:0051647)	56	5	4.25E-01	1.10E-01
establishment of nucleus localization (GO:0040023)	56	5	4.25E-01	1.10E-01
positive regulation of response to stimulus (GO:0048584)	56	5	4.25E-01	1.10E-01
neuron projection development (GO:0031175)	181	8	1.37E+00	1.18E-01
microtubule cytoskeleton organization involved in mitosis (GO:1902850)	11	3	8.35E-02	1.28E-01
response to organonitrogen compound (GO:0010243)	11	3	8.35E-02	1.28E-01
regulation of lipid metabolic process (GO:0019216)	11	3	8.35E-02	1.28E-01
homeostatic process (GO:0042592)	137	7	1.04E+00	1.37E-01
lipid storage (GO:0019915)	558	14	4.24E+00	1.45E-01
endosomal transport (GO:0016197)	31	4	2.35E-01	1.46E-01
ribonucleoside triphosphate biosynthetic process (GO:0009201)	31	4	2.35E-01	1.46E-01
cellular component assembly involved in morphogenesis (GO:0010927)	189	8	1.44E+00	1.59E-01
3'-phosphoadenosine 5'-phosphosulfate transport (GO:0046963)	2	2	1.52E-02	1.62E-01
purine ribonucleotide transport (GO:0015868)	2	2	1.52E-02	1.62E-01
purine nucleotide transport (GO:0015865)	2	2	1.52E-02	1.62E-01
purine nucleoside transmembrane transport (GO:0015860)	2	2	1.52E-02	1.62E-01
purine-containing compound transmembrane transport (GO:0072530)	2	2	1.52E-02	1.62E-01
N-terminal protein amino acid modification (GO:0031365)	2	2	1.52E-02	1.62E-01
3'-phospho-5'-adenylyl sulfate transmembrane transport (GO:1902559)	2	2	1.52E-02	1.62E-01
adenine nucleotide transport (GO:0051503)	2	2	1.52E-02	1.62E-01
nucleoside biosynthetic process (GO:0009163)	61	5	4.63E-01	1.64E-01
ribonucleoside biosynthetic process (GO:0042455)	61	5	4.63E-01	1.64E-01
glycosyl compound biosynthetic process (GO:1901659)	61	5	4.63E-01	1.64E-01
regulation of ARF protein signal transduction (GO:0032012)	12	3	9.11E-02	1.65E-01
nitrogen compound transport (GO:0071705)	99	6	7.52E-01	1.75E-01
fatty acid metabolic process (GO:0006631)	62	5	4.71E-01	1.76E-01
nucleoside triphosphate biosynthetic process (GO:0009142)	33	4	2.51E-01	1.85E-01
organophosphate biosynthetic process (GO:0090407)	194	8	1.47E+00	1.89E-01
neuron development (GO:0048666)	196	8	1.49E+00	2.03E-01
ribonucleoprotein complex biogenesis (GO:0022613)	102	6	7.74E-01	2.05E-01
small GTPase mediated signal transduction (GO:0007264)	102	6	7.74E-01	2.05E-01
mitotic sister chromatid segregation (GO:0000070)	34	4	2.58E-01	2.08E-01
regulation of engulfment of apoptotic cell (GO:1901074)	13	3	9.87E-02	2.09E-01
mRNA transport (GO:0051028)	13	3	9.87E-02	2.09E-01
regulation of apoptotic cell clearance (GO:2000425)	13	3	9.87E-02	2.09E-01
regulation of translation (GO:0006417)	65	5	4.94E-01	2.19E-01
epithelium development (GO:0060429)	65	5	4.94E-01	2.19E-01
macromolecule methylation (GO:0043414)	65	5	4.94E-01	2.19E-01
apoptotic cell clearance (GO:0043277)	104	6	7.90E-01	2.28E-01
tRNA aminoacylation for protein translation (GO:0006418)	35	4	2.66E-01	2.32E-01
translational initiation (GO:0006413)	35	4	2.66E-01	2.32E-01
regulation of pharyngeal pumping (GO:0043051)	35	4	2.66E-01	2.32E-01
collagen and cuticulin-based cuticle development (GO:0040002)	105	6	7.97E-01	2.40E-01
cell-cell signaling (GO:0007267)	105	6	7.97E-01	2.40E-01
cuticle development (GO:0042335)	106	6	8.05E-01	2.52E-01
phagocytosis (GO:0006909)	106	6	8.05E-01	2.52E-01
establishment of mitotic spindle localization (GO:0040001)	36	4	2.73E-01	2.58E-01
regulation of catabolic process (GO:0009894)	36	4	2.73E-01	2.58E-01
polyol metabolic process (GO:0019751)	14	3	1.06E-01	2.59E-01
vulval development (GO:0040025)	107	6	8.12E-01	2.65E-01
cytoplasmic transport (GO:0016482)	69	5	5.24E-01	2.89E-01
post-embryonic organ development (GO:0048569)	110	6	8.35E-01	3.07E-01
protein ubiquitination (GO:0016567)	70	5	5.31E-01	3.08E-01
lipid modification (GO:0030258)	38	4	2.89E-01	3.17E-01
tRNA aminoacylation (GO:0043039)	38	4	2.89E-01	3.17E-01
amino acid activation (GO:0043038)	38	4	2.89E-01	3.17E-01
organic hydroxy compound metabolic process (GO:1901615)	71	5	5.39E-01	3.29E-01
neuron differentiation (GO:0030182)	212	8	1.61E+00	3.44E-01
nucleus organization (GO:0006997)	39	4	2.96E-01	3.49E-01
inositol phosphate metabolic process (GO:0043647)	3	2	2.28E-02	3.62E-01
inositol phosphate dephosphorylation (GO:0046855)	3	2	2.28E-02	3.62E-01
phosphorylated carbohydrate dephosphorylation (GO:0046838)	3	2	2.28E-02	3.62E-01
regulation of receptor-mediated endocytosis (GO:0048259)	3	2	2.28E-02	3.62E-01

Table S7

GO Term Enrichment Analysis of Tissue-specific alternative 3' splice site genes (Table S2)

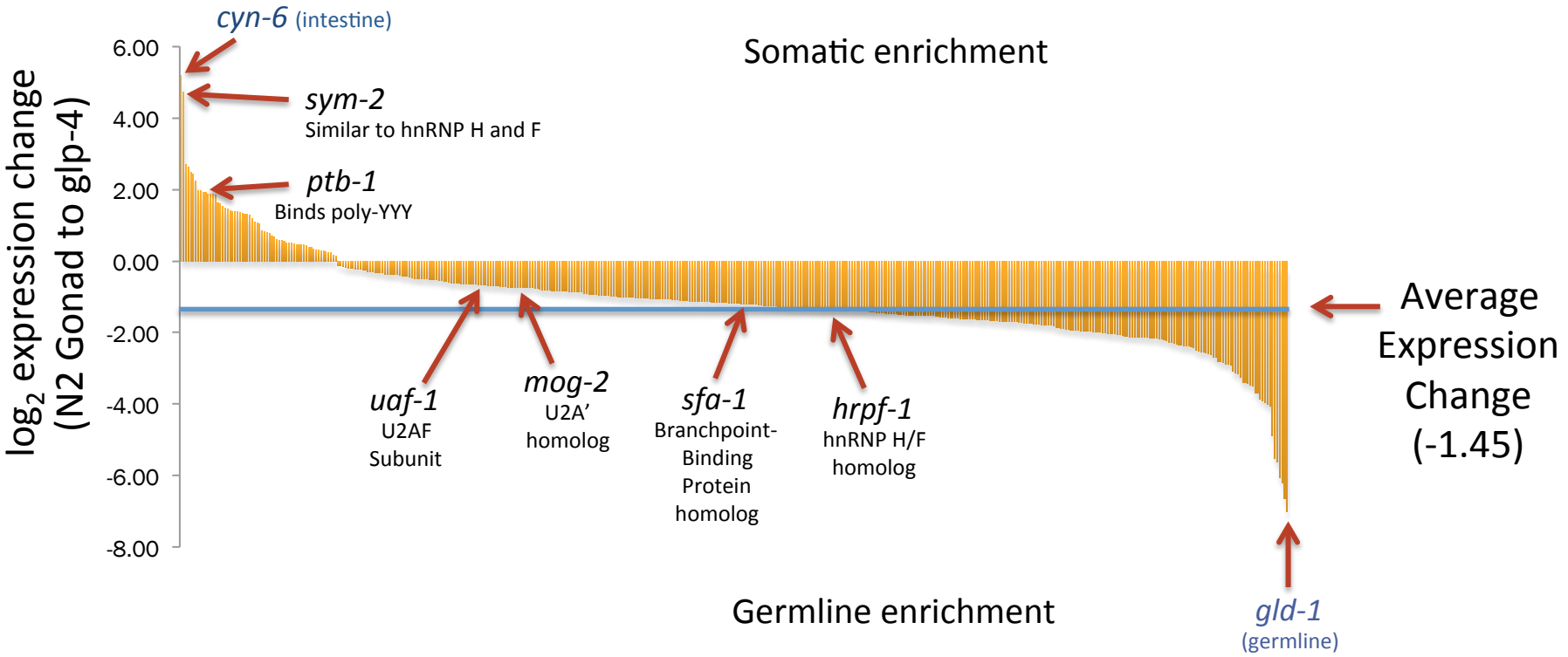
inositol phosphate catabolic process (GO:0071545)	3	2	2.28E-02	3.62E-01
regulation of phagocytosis, engulfment (GO:0060099)	16	3	1.22E-01	3.82E-01
response to oxygen-containing compound (GO:1901700)	40	4	3.04E-01	3.84E-01
intracellular protein transport (GO:0006886)	115	6	8.73E-01	3.89E-01
anion transport (GO:0006820)	116	6	8.81E-01	4.07E-01
ribosome biogenesis (GO:0042254)	75	5	5.69E-01	4.22E-01
regulation of phagocytosis (GO:0050764)	17	3	1.29E-01	4.56E-01
cellular response to oxygen-containing compound (GO:1901701)	17	3	1.29E-01	4.56E-01
negative regulation of cytoskeleton organization (GO:0051494)	17	3	1.29E-01	4.56E-01
regulation of chemotaxis (GO:0050920)	17	3	1.29E-01	4.56E-01
regulation of cell death (GO:0010941)	77	5	5.85E-01	4.76E-01
dendrite development (GO:0016358)	43	4	3.27E-01	5.04E-01
purine ribonucleotide biosynthetic process (GO:0009152)	78	5	5.92E-01	5.04E-01
sulfur compound metabolic process (GO:0006790)	78	5	5.92E-01	5.04E-01
negative regulation of nitrogen compound metabolic process (GO:0051172)	79	5	6.00E-01	5.34E-01
cytokinesis (GO:0000910)	79	5	6.00E-01	5.34E-01
purine nucleotide biosynthetic process (GO:0006164)	79	5	6.00E-01	5.34E-01
negative regulation of nucleobase-containing compound metabolic process	79	5	6.00E-01	5.34E-01
organophosphate ester transport (GO:0015748)	18	3	1.37E-01	5.38E-01
maintenance of location in cell (GO:0051651)	18	3	1.37E-01	5.38E-01
maintenance of protein location in cell (GO:0032507)	18	3	1.37E-01	5.38E-01
monovalent inorganic cation transport (GO:0015672)	228	8	1.73E+00	5.56E-01
establishment of spindle localization (GO:0051293)	45	4	3.42E-01	5.97E-01
spindle localization (GO:0051653)	45	4	3.42E-01	5.97E-01
tRNA metabolic process (GO:0006399)	81	5	6.15E-01	5.98E-01
cellular response to nitrogen compound (GO:1901699)	19	3	1.44E-01	6.30E-01
ATP synthesis coupled proton transport (GO:0015986)	19	3	1.44E-01	6.30E-01
energy coupled proton transport, down electrochemical gradient (GO:0015	19	3	1.44E-01	6.30E-01
regulation of protein modification process (GO:0031399)	82	5	6.23E-01	6.32E-01
ATP catabolic process (GO:0006200)	177	7	1.34E+00	6.39E-01
regulation of lipid biosynthetic process (GO:0046890)	4	2	3.04E-02	6.40E-01
mitotic cell cycle arrest (GO:0071850)	4	2	3.04E-02	6.40E-01
RNA (guanine-N7)-methylation (GO:0036265)	4	2	3.04E-02	6.40E-01
inositol metabolic process (GO:0006020)	4	2	3.04E-02	6.40E-01
purine ribonucleoside monophosphate catabolic process (GO:0009169)	178	7	1.35E+00	6.61E-01
ribonucleoside monophosphate catabolic process (GO:0009158)	178	7	1.35E+00	6.61E-01
purine nucleoside monophosphate catabolic process (GO:0009128)	178	7	1.35E+00	6.61E-01
nucleoside monophosphate catabolic process (GO:0009125)	178	7	1.35E+00	6.61E-01
protein phosphorylation (GO:0006468)	429	11	3.26E+00	6.82E-01
response to nitrogen compound (GO:1901698)	20	3	1.52E-01	7.30E-01
RNA methylation (GO:0001510)	20	3	1.52E-01	7.30E-01
dauer larval development (GO:0040024)	85	5	6.45E-01	7.43E-01
hermaphrodite germ-line sex determination (GO:0040021)	48	4	3.64E-01	7.60E-01
negative regulation of cellular macromolecule biosynthetic process (GO:200	86	5	6.53E-01	7.83E-01
engulfment of apoptotic cell (GO:0043652)	86	5	6.53E-01	7.83E-01
phagocytosis, engulfment (GO:0006911)	86	5	6.53E-01	7.83E-01
negative regulation of macromolecule biosynthetic process (GO:0010558)	86	5	6.53E-01	7.83E-01
rRNA processing (GO:0006364)	49	4	3.72E-01	8.20E-01
purine-containing compound biosynthetic process (GO:0072522)	87	5	6.61E-01	8.25E-01
negative regulation of cellular biosynthetic process (GO:0031327)	87	5	6.61E-01	8.25E-01
ribonucleotide biosynthetic process (GO:0009260)	87	5	6.61E-01	8.25E-01
ribose phosphate biosynthetic process (GO:0046390)	87	5	6.61E-01	8.25E-01
maintenance of protein location (GO:0045185)	21	3	1.59E-01	8.41E-01
protein acylation (GO:0043543)	21	3	1.59E-01	8.41E-01
membrane invagination (GO:0010324)	88	5	6.68E-01	8.68E-01
negative regulation of biosynthetic process (GO:0009890)	88	5	6.68E-01	8.68E-01
rRNA metabolic process (GO:0016072)	50	4	3.80E-01	8.84E-01
pharynx development (GO:0060465)	51	4	3.87E-01	9.52E-01
mitotic cytokinesis (GO:0000281)	22	3	1.67E-01	9.61E-01
growth (GO:0040007)	190	7	1.44E+00	9.68E-01
histone H4 deacetylation (GO:0070933)	5	2	3.80E-02	9.96E-01
negative regulation of Notch signaling pathway (GO:0045746)	5	2	3.80E-02	9.96E-01
regulation of spindle organization (GO:0090224)	5	2	3.80E-02	9.96E-01

Table S8 PCR and RT-PCR Primer Sequences

top-1 Forward	TCGAATCATCACTCGAACGG
top-1 Reverse	CTTCCGTTTCAAGAGTCAGC
efk-1 Forward	ATCCGTTCTTCGATTCGGTC
efk-1 Reverse	CTCACGATATCATGAGCTCG
F07A11.2 Forward	GAGTACAACATTCACTGCGG
F07A11.2 Reverse	TGTTTGGAGTCTCGACGAAC
hipr-1 Forward	ACTGAAATTGTCGCAGCTGG
hipr-1 Reverse	TCCTGAGCTTCTTCTCCTTC
K10C8.3 Forward	CAATCAGCAATCGGATCTGG
K10C8.3 Reverse	AGAGCTGGATATGCTTGTGC
frm-4 Forward	TGGAAACGTCGGCAGTTATG
frm-4 Reverse	CTTCATGTCGCCTAAGGATG
rgr-1 Forward	TGCCTTCGTCTCGATAATCG
rgr-1 Reverse	ATCTTCAGAGGATCCAGGAG
taf-10 Forward	CCAGAGCAATATGAGCCTTC
taf-10 Reverse	TACAGAATCGGGAATCGTCG
ufd-3 Forward	ATTGCAGTTTTTGGCCCGAG
ufd-3 Reverse	TAAGTGTTGGGAAGATCCGG
Y69A2AR.1 Forward	CCGAAGAGGAGAAACCAAAG
Y69A2AR.1 Reverse	ACGTGAACGTCATTGTCAGC
cdk-12 A1	AAACACCATCAGTTCAGCGC
cdk-12 A2	AATGTATGGCAATCCTGGCG
cdk-12 B1	CTCCGCGACACTCAAATTTC
cdk-12 B2	GTTACCGTCGCGACAATTTC
Ce-daf-15 Forward	CCATAGAGATCGGATTGAGC
Ce-daf-15 Reverse	GACATTGGAAGCCATTGACC
Cb-daf-15 Forward	GTCAGCAATCTAGCGGATAG
Cb-daf-15 Reverse	TTGACTTTCGACTCGTCCTG
Ce-atx-2 Forward	CTATCCGATGATAATGCCCC
Ce-atx-2 Reverse	CCAGATTGTTGACCAGATGG
Cb-atx-2 Forward	ACATGCAGCAACCTCAGATG
Cb-atx-2 Reverse	TTGGGAGGAGGGATTTACAC
par-4 Forward	GGAAGAGCATCCAATACCAG
par-4 Reverse	CATAATTTTGACGGCCCGTC
ubxn-6 Forward	TTGGCACTATCATTGCGTGG
ubxn-6 Reverse	GGACTCGCTTTTTGTTGAGG
icd-2 Fprward	AAGCAAGTGACTGGTGTCTC
icd-2 Reverse	ACAAGCTCGATGTCCTTCTC

Ragle_SuppFig1

Spliceosome (and associated) Factor Expression



Ragle_SuppFig2