

SUPPLEMENTAL TABLE 1

pairSum=9 for $\Delta\text{PSI} \geq 0.15$ Average $\Delta\text{PSI} > 0.20$

Alternative 5'ss Events - A5

Negative value in "Distance Between 5'ss" indicates that mutant promotes upstream 5'ss usage

Positive value in "Distance Between 5'ss" indicates that mutant promotes downstream 5'ss usage

A5 SZ211 snrp-27(M141T) vs. N2

event_name	Gene	Upstream 5'ss	Downstream 5'ss	Distance Between 5'ss	Avg ΔPSI	Genome Position
A5.00377	rskn-2	GTAATGT	GTGAGAA	-5	70.53%	ce10::chrI:8019510-8019846
A5.02960	gon-14	GTCAAGT	GTGAGCT	-34	70.20%	ce10::chrV:6606743-6607634
A5.00077	W03F11.5	GCAGTGA	GTGAGAT	-3	60.92%	ce10::chrI:2217078-2217391
A5.02596	ltah-1.1	GTTGTGA	GTGATTT	-3	59.37%	ce10::chrIV:12279926-12280270
A5.01208	Y17G7B.8	GGATGGG	GTTATTT	-7	55.96%	ce10::chrIII:12025816-12026217
A5.02595	C42C1.13	GCAAGAA	GTGAATT	-8	55.91%	ce10::chrIV:12278835-12279171
A5.00248	gpa-14	GTGAGTT	GTTGTAA	11	-54.08%	ce10::chrI:5942827-5943857
A5.00387	kcnl-2	GTAGCGT	GTTTCGTT	-20	50.82%	ce10::chrI:8207887-8208594
A5.01451	Y71H2AM.2	GTAAGGA	GTTGAGT	-7	48.24%	ce10::chrIII:2824523-2825830
A5.01029	pch-2	GTTGTGA	GTGAGCG	-3	45.12%	ce10::chrIII:8158285-8158545
A5.02919	ncx-2	GTAACGG	GTTTGTG	-6	42.47%	ce10::chrV:5308471-5308917
A5.00046	Y34D9A.8	GTTTGTG	GTAGAGT	18	-41.57%	ce10::chrI:1051917-1052238
A5.01447	Y71H2AM.20	GTTAATT	GTAAAAA	21	-40.89%	ce10::chrIII:2782797-2784072
A5.03493	T01D3.6	GTCAGTA	GTACCGC	36	-40.61%	ce10::chrV:13718434-13718767
A5.03669	nhr-65	GTGAGTT	GTAAAAA	12	-40.24%	ce10::chrV:18841168-18841720
A5.01963	ssl-1	GTAAAAA	GTATGGA	9	-38.54%	ce10::chrIII:12738149-12740028
A5.03422	F45D3.2	GTACACA	GTTAGTA	-8	37.97%	ce10::chrV:12541820-12542403
A5.04294	K04C1.2	GTACAGG	GTCAGTT	-27	37.63%	ce10::chrX:14238681-14239042
A5.02362	T14A8.2	GTGAGTT	GTAATGT	15	-37.39%	ce10::chrIV:7822017-7822620
A5.00193	M04F3.4	GTCCTTT	GTGATTT	-17	36.99%	ce10::chrI:4771344-4771687
A5.01464	Y53G8AR.8	GTTTCAG	GCGATTT	-27	36.72%	ce10::chrIII:3293673-3294054
A5.04108	ubc-22	GTCATGT	GTTAGTT	-12	35.94%	ce10::chrX:8867948-8868632
A5.00968	nhr-21	GTCCGAG	GTACCTA	-6	35.63%	ce10::chrIII:7347333-7347680
A5.02177	Y67D8C.25	GCAAGTT	GTTTTCA	25	-35.25%	ce10::chrIV:3137034-3137773
A5.00102	itx-1	GTATGGT	GTGAGTT	-13	34.85%	ce10::chrI:2814210-2815614
A5.02245	Y4C6B.7	GTAAGAA	GTTTCGTG	-8	34.78%	ce10::chrIV:5351431-5351901
A5.02223	hoe-1	GTAAGGG	GTTTGTG	-6	34.38%	ce10::chrIV:4743295-4744271
A5.02850	T20D4.3	GTTAGTA	GTATGAA	21	-33.21%	ce10::chrV:3419174-3419444
A5.04159	mig-15	GTGAGTC	GTTTTGT	15	-32.99%	ce10::chrX:10425190-10425705
A5.03532	F14D7.6	GTTTCGTT	GTAATTT	37	-32.76%	ce10::chrV:14302154-14305416
A5.03883	lst-2	GTGGTGA	GTGAGAA	-3	32.38%	ce10::chrX:4379331-4379658
A5.03784	dgk-1	GTAAGGG	GTCAGAT	-6	32.12%	ce10::chrX:988928-9889630
A5.03318	K10D6.2	GTTGGTA	GTAGTTT	4	-31.93%	ce10::chrV:11193895-11194330
A5.00154	unc-73	GTGAGTG	GTAGGAA	45	-31.38%	ce10::chrI:4002365-4002746
A5.04365	ZK54.3	GTGAATC	GTAAGGC	12	-31.38%	ce10::chrX:17465584-17466072
A5.02793	nhr-56	GTAATGT	GTGAGTT	-5	30.11%	ce10::chrV:2220142-2220479
A5.01378	Y82E9BR.5	GTAAGTG	GTGAGTA	-4	29.28%	ce10::chrIII:1385081-1387559
A5.03552	hil-1	GTTAGTG	GTACTGT	12	-29.07%	ce10::chrV:14951846-14952475

A5.03311	math-33	GTGAGTT	GTAAGTT	9	-29.04%	ce10::chrV:11117403-11117727
A5.00985	npp-21	GTCAGTG	GTTAGTA	-6	29.02%	ce10::chrII:7606342-7606684
A5.01360	fbxa-11	GTGAATT	GTGGGTT	13	-28.20%	ce10::chrIII:950846-951330
A5.03854	sax-3	GTGAGCT	GTATTTT	15	-26.57%	ce10::chrX:3452959-3453373
A5.01859	rnf-113	GTGAGAT	GTACTTT	11	-26.53%	ce10::chrIII:10757191-10757547
A5.01139	stip-1	GTGGGGT	GTGAGAT	-5	25.97%	ce10::chrII:10349659-10349972
A5.00049	grh-1	GTAAGGG	GTTAGTC	-6	25.24%	ce10::chrI:1264768-1265570
A5.03734	B0250.12	GTTTGTA	GTAATTT	4	-25.08%	ce10::chrV:20466725-20467638
A5.00978	F35D2.3	GTCAGTC	GTGGTGT	12	-24.98%	ce10::chrII:7571591-7571933
A5.04332	nhr-48	GTATTCT	GTCAGTA	-18	24.69%	ce10::chrX:15711273-15711635
A5.00528	cdc-26	GTGGTCA	GTCAATG	-3	24.55%	ce10::chrI:10639298-10639636
A5.00899	C30B5.2	GTACGGG	GTTAGTT	-6	24.39%	ce10::chrII:6197332-6197654
A5.01501	hse-5	GTTAGTA	GTAAGAA	4	-23.70%	ce10::chrIII:4348821-4349854
A5.01417	W04B5.3	GTGATTC	GTAAAAT	30	-23.27%	ce10::chrIII:2419147-2419738
A5.02643	pik-1	GTAGAGT	GTTTCGTT	-5	23.22%	ce10::chrIV:13419370-13421032
A5.03472	Y2H9A.4	GTATATA	GTGAGAT	-9	23.02%	ce10::chrV:13446560-13447229
A5.00740	btb-9	GTGAGTT	GTTAGGC	15	-22.63%	ce10::chrII:1728528-1728893
A5.03959	acs-17	GTGAGTA	GTATGTT	9	-21.98%	ce10::chrX:5939673-5940216
A5.03202	swt-5	GTATTGA	GTTTGTT	-23	21.75%	ce10::chrV:9503623-9504446

A5 SZ370 snu-66(H765G) vs. N2

event_name	Gene	Upstream 5'ss	Downstream 5'ss	Distance Between 5'ss	AvgΔPSI	Genome Position
A5.02960	gon-14	GTCAAGT	GTGAGCT	-34	82.10%	ce10::chrV:6606743-6607634
A5.03011	ddo-2	GTGAGGT	GTTCTTT	5	-76.38%	ce10::chrV:7434437-7434972
A5.01914	Y41C4A.12	GCAAGTC	GTCGAAT	4	-75.55%	ce10::chrIII:11723948-11724259
A5.00652	Y105E8B.7	GTGAGGT	GTTACAC	5	-70.88%	ce10::chrI:14645995-14646546
A5.04108	ubc-22	GTCATGT	GTTAGTT	-12	63.39%	ce10::chrX:8867948-8868632
A5.01647	C09E7.7	GTGTTCA	GTGAGAA	-9	59.72%	ce10::chrIII:6550487-6550821
A5.00118	zip-4	GTGAGGT	GTGCCAG	5	-58.63%	ce10::chrI:3264333-3264677
A5.03552	hil-1	GTTAGTG	GTTACTGT	12	-57.75%	ce10::chrV:14951846-14952475
A5.00827	hlh-1	GTGAGCT	GTTAGTA	22	-56.41%	ce10::chrII:4521586-4522110
A5.00377	rskn-2	GTAATGT	GTGAGAA	-5	54.98%	ce10::chrI:8019510-8019846
A5.02115	Y41D4A.6	GTGGGGG	GTTCTTC	6	-54.55%	ce10::chrIV:1741285-1741629
A5.00046	Y34D9A.8	GTTTGTTG	GTAGAGT	18	-54.29%	ce10::chrI:1051917-1052238
A5.00248	gpa-14	GTGAGTT	GTTGTAA	11	-53.68%	ce10::chrI:5942827-5943857
A5.02366	ntl-4	GTCGGTG	GTTTCGTA	-6	52.43%	ce10::chrIV:7911487-7911824
A5.00193	M04F3.4	GTCTTTT	GTGATTT	-17	50.16%	ce10::chrI:4771344-4771687
A5.03883	lst-2	GTGGTGA	GTGAGAA	-3	47.61%	ce10::chrX:4379331-4379658
A5.00077	W03F11.5	GCAGTGA	GTGAGAT	-3	47.41%	ce10::chrI:2217078-2217391
A5.02596	ltah-1.1	GTTGTGA	GTGATTT	-3	47.06%	ce10::chrIV:12279926-12280270
A5.00899	C30B5.2	GTACGGG	GTTAGTT	-6	47.05%	ce10::chrII:6197332-6197654
A5.01701	cup-5	GTCGGTG	GTGCGTG	-4	46.00%	ce10::chrIII:7590471-7591017
A5.01339	cox-17	GTGAGGT	GTTTTGA	5	-44.96%	ce10::chrIII:190973-191910
A5.01663	T07E3.4	GTAGGTT	GTTAAGC	4	-44.53%	ce10::chrIII:6897950-6898258
A5.00387	kcnl-2	GTAGCGT	GTTTCGTT	-20	44.49%	ce10::chrI:8207887-8208594
A5.00595	W05B5.1	GTGAGGA	GTTTATG	13	-43.34%	ce10::chrI:13035248-13035646
A5.01996	pdr-1	GTAGGTC	GTCAAGT	4	-41.58%	ce10::chrIII:13771543-13771926

A5.01151	mpz-1	GTTGGTA	GTAAGCA	12	-41.38%	ce10::chrII:10740233-10741190
A5.01029	pch-2	GTTGTGA	GTGAGCG	-3	41.33%	ce10::chrII:8158285-8158545
A5.02948	cest-33	GCAAGTT	GTTCCACC	4	-40.85%	ce10::chrV:6364973-6365289
A5.00469	irx-1	GTGAGGT	GTGAATA	13	-39.82%	ce10::chrI:9537044-9538343
A5.01576	molo-1	GTCAGTT	GTTTGAT	13	-38.09%	ce10::chrIII:5576459-5577124
A5.00897	exp-1	GTTAGAT	GTTATCT	45	-37.77%	ce10::chrII:6159885-6160183
A5.03834	tra-4	GTAGGTT	GTTCCAGC	4	-37.58%	ce10::chrX:2855268-2855613
A5.00174	eri-7	GTTAGTT	GTGCAGC	30	-37.05%	ce10::chrI:4454892-4455451
A5.00985	npp-21	GTCAGTG	GTTAGTA	-6	36.90%	ce10::chrII:7606342-7606684
A5.02362	T14A8.2	GTGAGTT	GTAATGT	15	-36.31%	ce10::chrIV:7822017-7822620
A5.03318	K10D6.2	GTTGGTA	GTAGTTT	4	-36.16%	ce10::chrV:11193895-11194330
A5.01689	kap-1	GCATGCA	GTTTCTA	9	-36.14%	ce10::chrIII:7340385-7340724
A5.01378	Y82E9BR.5	GTAAGTG	GTGAGTA	-4	36.13%	ce10::chrIII:1385081-1387559
A5.01644	acr-5	GTATGGG	GTAAGCA	-18	36.06%	ce10::chrIII:6514429-6514756
A5.01809	ZK632.5	GTAGGTT	GTTTGAC	4	-35.90%	ce10::chrIII:9808446-9808735
A5.03902	dnj-14	GTATGGG	GTCTGTT	-6	35.63%	ce10::chrX:4710087-4710434
A5.04156	pkn-1	GTCAGTA	GTGAGTA	-18	35.31%	ce10::chrX:10400056-10400563
A5.00760	math-41	GCAAGTA	GTACAGT	4	-34.44%	ce10::chrII:1827136-1829057
A5.03311	math-33	GTGAGTT	GTAAGTT	9	-34.44%	ce10::chrV:11117403-11117727
A5.00154	unc-73	GTGAGTG	GTAGGAA	45	-34.02%	ce10::chrI:4002365-4002746
A5.03578	C06B8.12	GTTGGTC	GTCAAAT	4	-33.75%	ce10::chrV:15482232-15482542
A5.02919	ncx-2	GTAACGG	GTTTGTG	-6	33.38%	ce10::chrV:5308471-5308917
A5.03196	K07B1.7	GTGTTAG	GTTAGTT	-2	33.17%	ce10::chrV:9346621-9346958
A5.04134	nra-3	GTAGGTT	GTTAAAA	4	-32.66%	ce10::chrX:9931081-9931413
A5.03784	dgk-1	GTAAGGG	GTCAGAT	6	-32.46%	ce10::chrX:988928-989630
A5.03475	T10G3.1	GTTCCGAG	GTCCATA	15	-32.21%	ce10::chrV:13470645-13473513
A5.01464	Y53GAR.8	GTTTCAG	GCGATTT	-27	32.13%	ce10::chrIII:3293673-3294054
A5.01411	polh-1	GTGGGTA	GTAAGCT	-4	32.02%	ce10::chrIII:1949924-1950266
A5.01859	rnf-113	GTGAGAT	GTACTTT	11	-31.83%	ce10::chrIII:10757191-10757547
A5.00009	Y48G1C.8	GTGAGCA	GTTTTGA	10	-31.63%	ce10::chrI:97815-98441
A5.03442	F15B9.10	GTGGTGG	GTGAGAT	-6	31.55%	ce10::chrV:13007126-13007463
A5.00287	T10E9.3	GCAAGTT	GTTGATT	4	-31.33%	ce10::chrI:6536502-6536804
A5.03893	lnp-1	GCAAGTT	GTTTTTG	4	-30.73%	ce10::chrX:4588730-4589036
A5.03669	nhr-65	GTGAGTT	GTAAAAA	12	-30.64%	ce10::chrV:18841168-18841720
A5.01963	ssl-1	GTAAAAA	GTATGGA	9	-30.31%	ce10::chrIII:12738149-12740028
A5.04159	mig-15	GTGAGTC	GTTTTGT	15	-30.20%	ce10::chrX:10425190-10425705
A5.01041	skpo-1	GTAGAAG	GTAAGTT	-6	29.59%	ce10::chrII:8425418-8426118
A5.01616	C23G10.7	GTGAGCA	ATTAGTC	27	-29.50%	ce10::chrIII:6196154-6196545
A5.03532	F14D7.6	GTTTCGTT	GTAATTT	37	-29.15%	ce10::chrV:14302154-14305416
A5.00210	apm-1	GTTAAAG	GTGATTA	-6	28.76%	ce10::chrI:5342994-5343337
A5.01646	C09E7.7	GTGTTCA	GTGAGAA	-9	28.53%	ce10::chrIII:6550487-6550824
A5.00716	ptr-3	GTCAGAA	GCAAGAA	-9	27.85%	ce10::chrII:367320-367564
A5.01451	Y71H2AM.2	GTAAGGA	GTTGAGT	-7	27.75%	ce10::chrIII:2824523-2825830
A5.00721	T07D3.4	GTTTTAA	GTTTGAA	-9	27.72%	ce10::chrII:888718-889043
A5.03242	C51E3.10	GTGAGGT	GTGAATA	5	-27.14%	ce10::chrV:10160479-10161003
A5.02718	T02D1.8	GTAGGTC	GTCTACA	4	-27.03%	ce10::chrIV:17387198-17387529
A5.00819	H20J04.9	GTTAAAG	GTGCTTA	-6	26.29%	ce10::chrII:4352129-4353042
A5.01591	mdt-15	GTAAGTT	GTAGAGT	9	-26.06%	ce10::chrIII:5829544-5830287
A5.02476	Y11D7A.10	GTAAGCG	GTTGTTT	10	-25.92%	ce10::chrIV:9259533-9259765

A5.02514	F01G10.10	GTGAGGT	GTATGTC	5	-25.78%	ce10::chrIV:10247573-10248290
A5.01310	hhat-1	GTGAGGT	GTTCAGG	5	-25.61%	ce10::chrII:14679188-14679589
A5.00091	ptr-12	GTGAGGT	GTCATTT	5	-23.62%	ce10::chrI:2591001-2592034
A5.01245	Y48C3A.20	GTCACTG	GTAATAG	-32	23.44%	ce10::chrII:13370532-13372010
A5.03051	F52E1.5	GTTAGTT	GTTATCA	13	-23.18%	ce10::chrV:8379561-8380216
A5.02222	yars-2	GTACGTG	GTGAGTC	-14	23.16%	ce10::chrIV:4712278-4712593
A5.01708	egl-5	GTGAGTT	GTCAGTT	12	-22.97%	ce10::chrIII:7815119-7816078
A5.03854	sax-3	GTGAGCT	GTATTTT	15	-21.70%	ce10::chrX:3452959-3453373
A5.03517	D1086.12	GTGGGTT	GTATTTG	9	-20.36%	ce10::chrV:14101693-14101992

A5 SZ371 snu-66(H765L) vs. N2

event_name	Gene	Upstream 5'ss	Downstream 5'ss	Distance Between 5'ss	AvgΔPSI	Genome Position
A5.02960	gon-14	GTCAAGT	GTGAGCT	-34	83.05%	ce10::chrV:6606743-6607634
A5.00377	rskn-2	GTAATGT	GTGAGAA	-5	76.20%	ce10::chrI:8019510-8019846
A5.03011	ddo-2	GTGAGGT	GTTCTTT	5	-73.08%	ce10::chrV:7434437-7434972
A5.01059	T01B7.13	GTGGGTA	GTATCAT	4	-68.37%	ce10::chrII:8715381-8715705
A5.00248	gpa-14	GTGAGTT	GTTGTAA	11	-63.76%	ce10::chrI:5942827-5943857
A5.01914	Y41C4A.12	GCAAGTC	GTCGAAT	4	-62.51%	ce10::chrIII:11723948-11724259
A5.02115	Y41D4A.6	GTGGGGG	GTTCTTC	6	-59.04%	ce10::chrIV:1741285-1741629
A5.00979	syd-1	GTTAGTG	GTGAGTT	-4	48.60%	ce10::chrII:7585968-7586802
A5.01610	mapk-15	GTGGGTA	GTAATTA	4	-48.09%	ce10::chrIII:6070614-6071060
A5.00193	M04F3.4	GTCTTTT	GTGATTT	-17	47.14%	ce10::chrI:4771344-4771687
A5.01996	pdr-1	GTAGGTC	GTCAAGT	4	-45.72%	ce10::chrIII:13771543-13771926
A5.01464	Y53G8AR.8	GTTTCAG	GCGATTT	-27	45.50%	ce10::chrIII:3293673-3294054
A5.02366	ntl-4	GTCGGTG	GTTTCGTA	-6	44.47%	ce10::chrIV:7911487-7911824
A5.01647	C09E7.7	GTGTTCA	GTGAGAA	-9	43.45%	ce10::chrIII:6550487-6550821
A5.00138	smp-2	GTGAGCA	GTTTTGA	33	-42.76%	ce10::chrI:3667189-3667866
A5.03552	hil-1	GTTAGTG	GTACTGT	12	-42.35%	ce10::chrV:14951846-14952475
A5.02362	T14A8.2	GTGAGTT	GTAATGT	15	-42.02%	ce10::chrIV:7822017-7822620
A5.00387	kcnl-2	GTAGCGT	GTTTCGTT	-20	40.80%	ce10::chrI:8207887-8208594
A5.03311	math-33	GTGAGTT	GTAAGTT	9	-40.27%	ce10::chrV:11117403-11117727
A5.02596	ltah-1.1	GTTGTGA	GTGATTT	-3	39.29%	ce10::chrIV:12279926-12280270
A5.03883	lst-2	GTGGTGA	GTGAGAA	-3	39.24%	ce10::chrX:4379331-4379658
A5.03318	K10D6.2	GTTGGTA	GTAGTTT	4	-38.95%	ce10::chrV:11193895-11194330
A5.01616	C23G10.7	GTGAGCA	ATTAGTC	27	-38.84%	ce10::chrIII:6196154-6196545
A5.02919	ncx-2	GTAACGG	GTTTGTG	-6	38.81%	ce10::chrV:5308471-5308917
A5.00154	unc-73	GTGAGTG	GTAGGAA	45	-38.07%	ce10::chrI:4002365-4002746
A5.01378	Y82E9BR.5	GTAAGTG	GTGAGTA	-4	37.90%	ce10::chrIII:1385081-1387559
A5.04294	K04C1.2	GTACAGG	GTCAGTT	-27	37.49%	ce10::chrX:14238681-14239042
A5.01029	pch-2	GTTGTGA	GTGAGCG	-3	37.22%	ce10::chrII:8158285-8158545
A5.03532	F14D7.6	GTTTCGTT	GTAATTT	37	-36.91%	ce10::chrV:14302154-14305416
A5.00652	Y105E8B.7	GTGAGGT	GTTACAC	5	-36.51%	ce10::chrI:14645995-14646546
A5.03475	T10G3.1	GTTTCGAG	GTCCATA	15	-36.41%	ce10::chrV:13470645-13473513
A5.00046	Y34D9A.8	GTTTGTG	GTAGAGT	18	-36.03%	ce10::chrI:1051917-1052238
A5.01456	daf-2	GTGGGTC	GTCTAGT	4	-35.57%	ce10::chrIII:3010401-3012324
A5.00827	hlh-1	GTGAGCT	GTTAGTA	22	-35.51%	ce10::chrII:4521586-4522110
A5.00118	zip-4	GTGAGGT	GTGCCAG	5	-35.46%	ce10::chrI:3264333-3264677

A5.03669	nhr-65	GTGAGTT	GTAAAAA	12	-35.10%	ce10::chrV:18841168-18841720
A5.04156	pkn-1	GTCAGTA	GTGAGTA	-18	34.82%	ce10::chrX:10400056-10400563
A5.01830	T16H12.3	GTTAATT	GTAAACT	12	-34.06%	ce10::chrIII:10081668-10082004
A5.03517	D1086.12	GTGGGTT	GTATTTG	9	-33.78%	ce10::chrV:14101693-14101992
A5.00899	C30B5.2	GTACGGG	GTTAGTT	-6	33.60%	ce10::chrIII:6197332-6197654
A5.01859	rnf-113	GTGAGAT	GTACTTT	11	-33.49%	ce10::chrIII:10757191-10757547
A5.01644	acr-5	GTATGGG	GTAAGCA	-18	33.44%	ce10::chrIII:6514429-6514756
A5.01701	cup-5	GTCGGTG	GTGCGTG	-4	32.95%	ce10::chrIII:7590471-7591017
A5.01451	Y71H2AM.2	GTAAGGA	GTTGAGT	-7	31.66%	ce10::chrIII:2824523-2825830
A5.04159	mig-15	GTGAGTC	GTTTTGT	15	-31.65%	ce10::chrX:10425190-10425705
A5.01151	mpz-1	GTTGGTA	GTAAGCA	12	-31.48%	ce10::chrIII:10740233-10741190
A5.00760	math-41	GCAAGTA	GTACAGT	4	-30.01%	ce10::chrII:1827136-1829057
A5.04030	sgca-1	GTAGTAA	GTAAGAA	-3	29.92%	ce10::chrX:6788323-6788615
A5.04365	ZK54.3	GTGAATC	GTAAGGC	12	-28.68%	ce10::chrX:17465584-17466072
A5.01653	rbf-1	GTGGTTA	GTTAGTG	-3	28.53%	ce10::chrIII:6697930-6698675
A5.02121	C23H5.8	GTACTCC	GTTGGGC	-9	28.14%	ce10::chrIV:2111941-2112500
A5.01447	Y71H2AM.20	GTTAATT	GTAAAAAT	21	-27.87%	ce10::chrIII:2782797-2784072
A5.00469	irx-1	GTGAGGT	GTGAATA	13	-27.79%	ce10::chrI:9537044-9538343
A5.01591	mdt-15	GTAAGTT	GTAGAGT	9	-27.06%	ce10::chrIII:5829544-5830287
A5.03788	lmp-2	GTGGGTT	GTATTTT	10	-26.36%	ce10::chrX:1125565-1125869
A5.03934	T23F2.2	GTTTGT	GTTCTCA	12	-26.09%	ce10::chrX:5497170-5497833
A5.03365	mpst-1	GTCATGT	GTAAAAG	-5	25.83%	ce10::chrV:11826022-11826361
A5.04065	twk-17	GTTGGTC	GTAAAAC	15	-23.81%	ce10::chrX:7600273-7601045
A5.04332	nhr-48	GTATTCT	GTCAGTA	-18	22.76%	ce10::chrX:15711273-15711635
A5.01636	C05D11.8	GTACTCG	GTAAGTT	-6	22.75%	ce10::chrIII:6427092-6427393
A5.00462	twk-29	GTGGGTT	GTAAATT	20	-22.68%	ce10::chrI:9468019-9468401
A5.03493	T01D3.6	GTCAGTA	GTACCGC	36	-20.53%	ce10::chrV:13718434-13718767

EnsArch65 Events

pairSum=9 for $\Delta\text{PSI} \geq 0.15$ Average $\Delta\text{PSI} > 0.20$

SZ211 snrp-27(M141T) vs. N2

AF - Alternative First Exon

event_name	Gene	Avg ΔPSI	Genomic Position
AF.0000351	R102.4	-32.23%	ce10::chrIV:10694015-10695193

RI - Retained Intron

event_name	Gene	Avg ΔPSI	Genomic Position
RI.0000291	swp-1	-34.34%	ce10::chrIII:5704433-5704682
RI.0000497	cyp-34A9	-28.73%	ce10::chrV:3968219-3968629

SZ370 snu-66(H765G) vs. N2

AF - Alternative First Exon

event_name	Gene	Avg ΔPSI	Genomic Position
AF.0000375	ent-7	-61.48%	ce10::chrIV:10017404-10019559
AF.0000598	Y62E10A.13	38.64%	ce10::chrIV:13392323-13398775
AF.0000537	fkf-5	-37.58%	ce10::chrI:3899124-3899909
AF.0000351	R102.4	-40.60%	ce10::chrIV:10694015-10695193

AF.0000168	gck-1	30.12%	ce10::chrV:8949142-8952060
AF.0000151	bre-1	27.92%	ce10::chrIV:8987253-8988865
AF.0000419	yars-2	23.16%	ce10::chrIV:4712284-4712506

RI - Retained Intron

event_name	Gene	Avg Δ PSI	Genomic Position
RI.0000196	npp-8	-68.66%	ce10::chrIV:1595414-1595823
RI.0000291	swp-1	-48.70%	ce10::chrIII:5704433-5704682
RI.0000766	nmtn-1	-55.51%	ce10::chrI:6477212-6477528
RI.0000751	ltah1.1	-52.25%	ce10::chrIV:12279736-12280313
RI.0000286	T2D1.3	-50.03%	ce10::chrIV:6915593-6916164
RI.0000834	add-1	-34.18%	ce10::chrX:4854800-4855025
RI.0000109	ddo-2	-52.75%	ce10::chrV:7433610-7433889
RI.0000691	unc-49	-43.78%	ce10::chrIII:10529637-10529859
RI.0000816	C17C3.1	-36.75%	ce10::chrII:5570868-5571028
RI.0000664	T19D12.2	-39.14%	ce10::chrII:6664341-6664601
RI.0000468	rsp-5	-40.22%	ce10::chrII:6490769-6491030
RI.0000112	nhr-109	-36.67%	ce10::chrII:4433535-4434220
RI.0000638	chat-1	-36.67%	ce10::chrIV:4448321-4448828
RI.0000563	Y48G1C.10	-33.68%	ce10::chrI:84614-84959
RI.0000375	rbm-5	-34.47%	ce10::chrI:6215921-6216170
RI.0000153	acdh-2	-35.40%	ce10::chrII:5546556-5547280
RI.0000652	F46H5.2	-32.45%	ce10::chrX:7266688-7266996
RI.0000736	F41E6.5	-34.15%	ce10::chrV:8604534-8604875
RI.0000485	nhr-50	-32.65%	ce10::chrV:15998737-15999090
RI.0000548	F45F2.9	-33.07%	ce10::chrV:8512922-8513187
RI.0000794	Y47G6A.7	-34.44%	ce10::chrI:3502741-3503010
RI.0000120	mapk-15	-29.78%	ce10::chrIII:6068396-6068866
RI.0000760	cbp-3	-30.69%	ce10::chrIII:9915280-9915725
RI.0000678	shc-1	-26.61%	ce10::chrI:972651-972940
RI.0000359	Y50D7A.3	-23.70%	ce10::chrIII:256096-257585
RI.0000322	vps-34	-24.19%	ce10::chrI:6029161-6030657
RI.0000263	tos-1	-28.50%	ce10::chrV:9343652-9344105
RI.0000095	nac-3	-26.00%	ce10::chrIII:10152704-10153035
RI.0000787	ugt-50	-21.87%	ce10::chrX:12692594-12692824
RI.0000574	Iron-8	-24.84%	ce10::chrI:5772739-5773607
RI.0000587	ZK470.2	-23.57%	ce10::chrX:4146424-4146994

SE - Skipped Exon

event_name	Gene	Avg Δ PSI	Genomic Position
SE.0000168	ced-1	28.23%	ce10::chrI:11851944-11855810
SE.0000454	F49E2.5	30.01%	ce10::chrX:9553880-9556660

SZ371 snu-66(H765L) vs. N2

A3 - de novo alternative 3'ss discovery

event_name	Gene	Avg Δ PSI	Genomic Position
A3.03927	dop-1	-25.19%	ce10::chrX:4411558-4411902

AF - Alternative First Exon

event_name	Gene	Avg Δ PSI	Genomic Position
AF.0000598	Y62E10A.13	48.08%	ce10::chrIV:13392323-13398775
AF.0000168	gck-1	40.79%	ce10::chrV:8949142-8952060
AF.0000537	fkf-5	-38.48%	ce10::chrI:3899124-3899909
AF.0000351	R102.4	-36.00%	ce10::chrIV:10694015-10695193
AF.0000559	lmp-2	26.36%	ce10::chrX:1125167-1125858
AF.0000116	nadk-2	-22.21%	ce10::chrII:12049519-12054767

MX - Mutually Exclusive Exons

event_name	Gene	Avg Δ PSI	Genomic Position
MX.0000009	lev-11	-21.92%	ce10::chrI:14621164-14622886

RI - Retained Intron

event_name	Gene	Avg Δ PSI	Genomic Position
RI.0000497	cyp-34A9	-41.67%	ce10::chrV:3968219-3968629
RI.0000291	swp-1	-44.82%	ce10::chrIII:5704433-5704682
RI.0000766	nmtn-1	-47.19%	ce10::chrI:6477212-6477528
RI.0000691	unc-49	-34.10%	ce10::chrIII:10529637-10529859
RI.0000109	ddo-2	-38.61%	ce10::chrV:7433610-7433889
RI.0000003	gar-2	-29.95%	ce10::chrIII:6319279-6319554
RI.0000468	rsp-5	-34.31%	ce10::chrII:6490769-6491030
RI.0000664	T19D12.2	-27.83%	ce10::chrII:6664341-6664601
RI.0000112	nhr-109	-34.41%	ce10::chrII:4433535-4434220
RI.0000546	aat-5	-27.66%	ce10::chrI:2573743-2574269
RI.0000638	chat-1	-28.41%	ce10::chrIV:4448321-4448828
RI.0000222	F27D4.6	-24.05%	ce10::chrI:7736997-7737203
RI.0000787	ugt-50	-22.89%	ce10::chrX:12692594-12692824
RI.0000263	tos-1	-27.76%	ce10::chrV:9343652-9344105
RI.0000760	cbp-3	-25.78%	ce10::chrIII:9915280-9915725
RI.0000751	ltah1.1	-22.66%	ce10::chrIV:12279736-12280313

SE - Skipped Exon

event_name	Gene	Avg Δ PSI	Genomic Position
SE.0000597	C53B7.3	35.69%	ce10::chrX:6845296-6845860