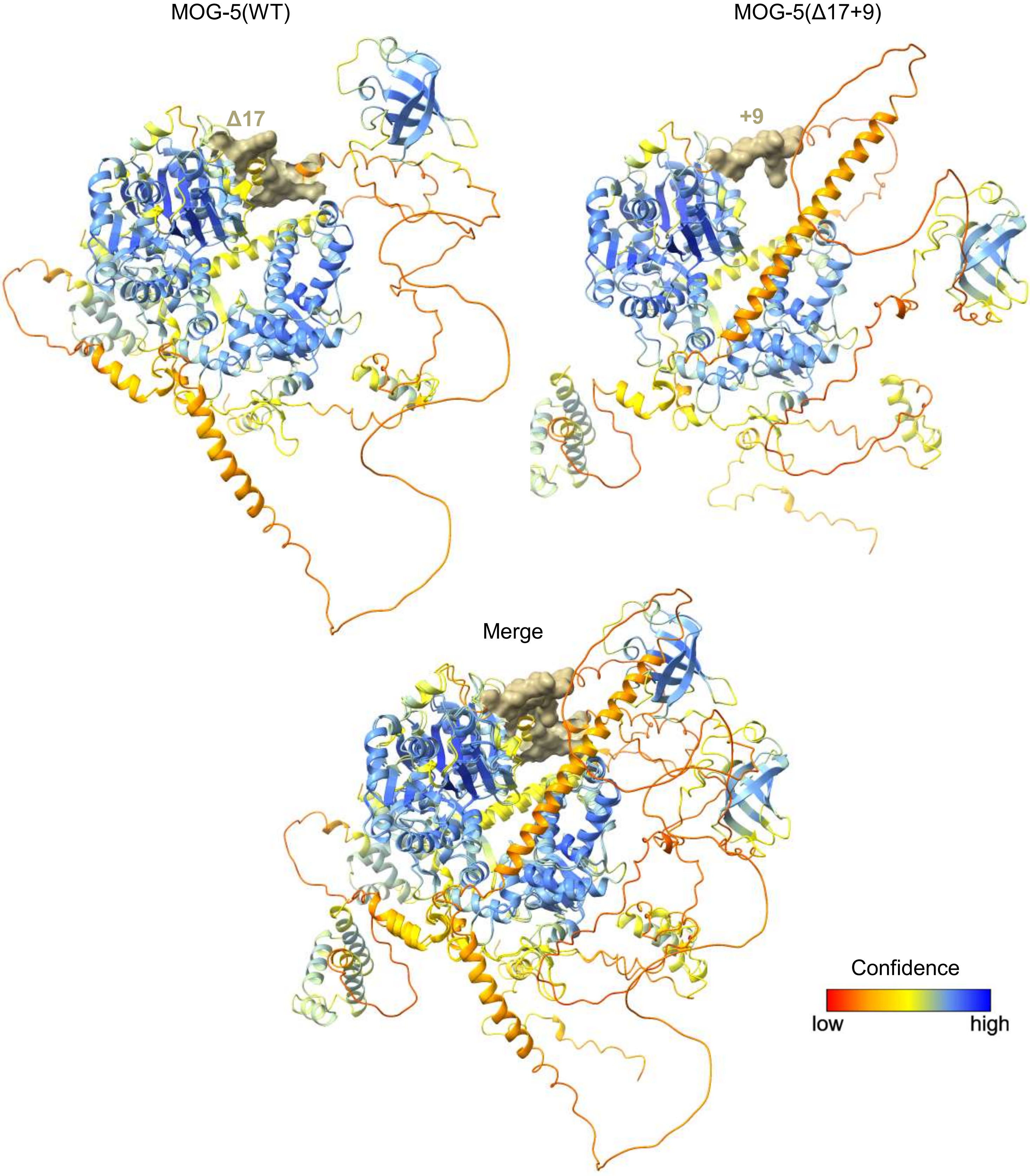
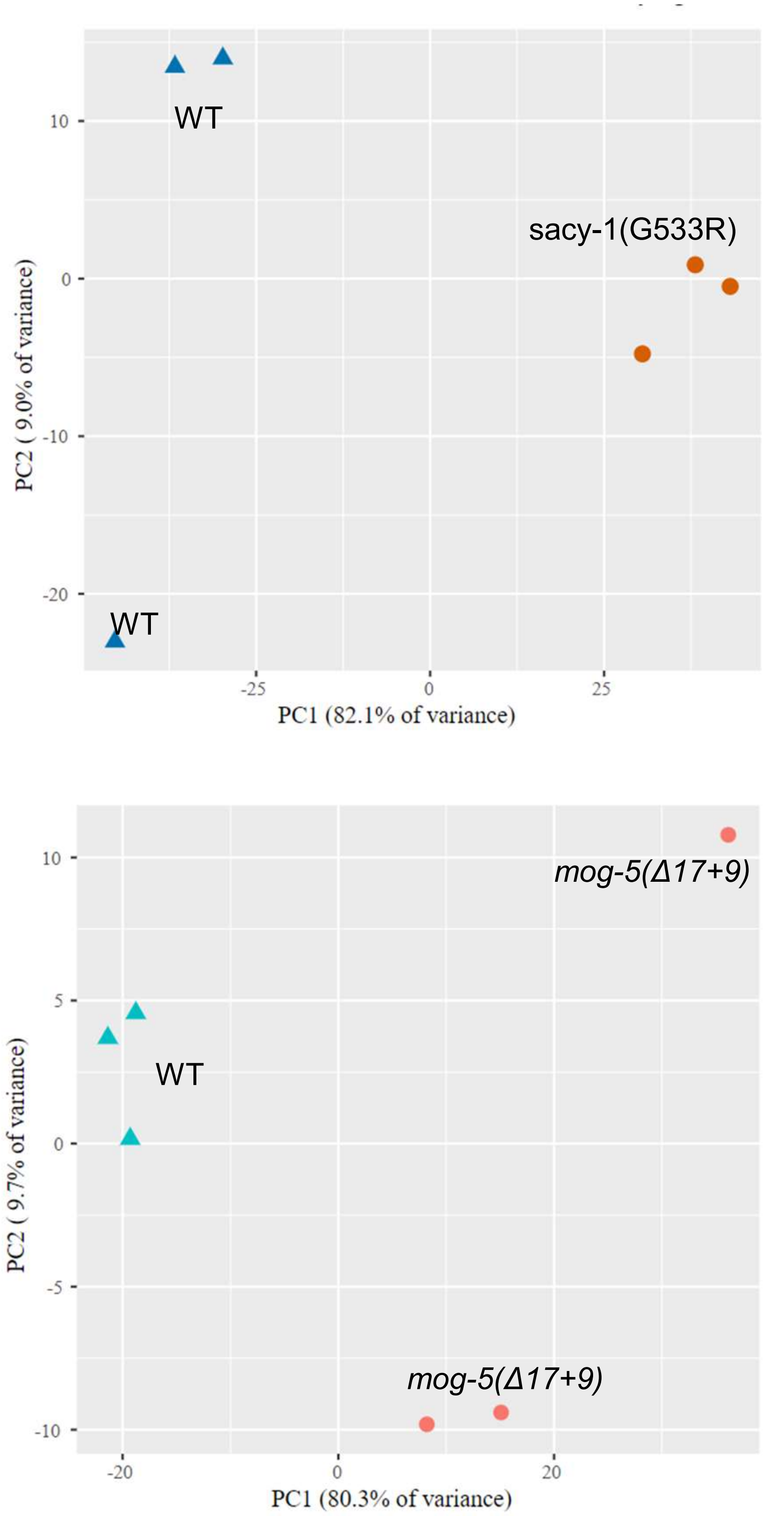
Supplemental Figure 1



Effects of MOG-5(Δ17+9) on AlphaFold structural predictions. MOG-5(WT) Prediction was retrieved from https://alphafold.ebi.ac.uk/. MOG-5(Δ17+9) was generated by Alphafold using ColabFold. "Δ17" highlighted in beige are the 17 amino acids which are removed, and "+9" are the 9 remplacing amino acids, of MOG-5(Δ17+9). Images and Merge of the two structures was generated on ChimeraX. Amino acids colors correspond to confidence as shown in key.

Supplemental Figure 2



PCA analysis of all libraries sequenced for this work. Generated using the built-in R function “prcomp”.

Supplemental Table 1

Table of A3 Events

Auxin Treatment, CA1200 vs. DG4703, FASTQ from (Tsukamoto *et al.* 2020)

Gene	Location (ce10)	Average ΔPSI	Splice Site Interval	Proximal Splice Site	Distal Splice Site
R10E9.1	chrIII:3965790-3966413	67.49	9	CTCAAG	TTTCAG
F33D4.2	chrIV:7692168-7692353	59.48	9	ATTAAG	TTTCAG
R07H5.8	chrIV:11210189-11210384	59.11	12	GTGTTG	TTTCAG
T01D1.2	chrII:167981-168615	57.61	6	ATAAAG	TTCCAG
F59A6.12	chrII:5011874-5012058	55.43	6	TATTAG	TTCCAG
R02F2.1	chrIII:5504748-5505362	54.7	6	CTCAAG	TTTCAG
E01G4.1	chrII:13445113-13446386	51.95	6	CCAAAG	ATTCAG
F56C9.10	chrIII:7332876-7333726	51.12	9	ATTGAG	GTGAAG
Y57A10A.18	chrII:12211043-12211793	50.8	9	TCCAAG	CTTCAG
C28D4.2	chrIV:9732806-9732994	49.6	9	TCAAAG	TTCCAG
H37N21.1	chrI:7141939-7142121	48.29	9	TTATAG	TTTCAG
F59A6.12	chrII:5011650-5011833	48.25	10	TTCGAG	AAAAAG
C06C3.1	chrII:9362909-9363296	47.33	9	TGCTAG	TTTAAG
C34D10.2	chrX:8024394-8024584	47.26	12	TTTCAG	CTTCAG
D2045.1	chrIII:10467088-10467281	47	8	ATGAAG	TTGAAG
F38A6.3	chrV:20783707-20784361	46.25	6	TATCAG	TTGCAG
ZK418.6	chrIII:7077444-7077627	45.33	8	AAATAG	TTCTAG
F46H5.7	chrX:7240636-7240823	45.14	9	AATTAG	TTTCAG
Y41C4A.4	chrIII:11685110-11688236	44.23	6	TCTCAG	TTTCAG
C26C6.5	chrI:7539171-7539497	44.09	9	TAAAAG	TTACAG
Y119C1B.8	chrI:4529938-4530128	42.42	6	ATCTAG	CTTCAG
B0001.6	chrIV:12162327-12162858	41.71	6	ATTAAG	TTTCAG
B0041.2	chrI:4656536-4657488	41.35	6	CAAAAG	ATTCAG
K01G5.8	chrIII:10740426-10740673	40.39	9	TCCCAG	TTCCAG
C05E11.1	chrX:4589830-4590013	40.05	12	TTGTAG	TTTCAG
T24A11.1	chrIII:3799783-3800036	40	12	AGTCAG	TTCCAG
C30H7.2	chrI:5417143-5418008	39.92	9	CGTAAG	TTTCAG
M01F1.4	chrIII:3507125-3507314	39.73	6	AAAAAG	TTCCAG
Y48C3A.5	chrII:13281371-13282568	39.58	6	TTCCAG	CTACAG
Y104H12BR.1	chrIV:1289951-1291507	39.58	9	TCGGAG	TTTCAG
Y57A19A.18	chrII:12209700-12210815	39.34	9	GATAAG	CTCCAG
Y41C4A.4	chrIII:11688032-11691408	39.09	9	CTTTAG	TTCCAG
M106.4	chrII:10866031-10866728	39.07	6	GAAAAG	CTTCAG
Y57G11C.45	chrIV:14783929-14784126	38.82	9	TTTTAG	TTTCAG
C27C12.4	chrX:14854947-14855570	38.72	6	TTTCAG	TTTCAG
C05E4.3	chrV:753972-754316	38.49	6	TAACAG	TTTTAG
F21D12.1	chrII:7348085-7348387	38.38	6	TTAAAG	TTATAG
Y71G12B.12	chrI:1710931-1712784	37.53	6	GCCAAG	TTCCAG
ZC376.7	chrV:14196200-14196404	37.35	6	AAATAG	TTTCAG
Y97E10AR.6	chrV:8012653-8012896	37.23	6	AACTAG	TTATAG
R11A5.2	chrI:7858215-7858616	37.03	7	ACATAG	TTTCAG
B0379.4	chrI:10093700-10100719	37.02	6	TATCAG	TTTCAG

W08G11.3	chrV:16370683-16370889	36.5	6	CACAAG	TTCCAG
C44E4.1	chrI:4612027-4613674	36.27	6	TTCTAG	TTCCAG
Y61A9LA.3	chrV:4571715-4572374	36.17	6	AAATAG	TTTCAG
F58H1.7	chrV:11964246-11964789	35.99	6	TCCCAG	TTCCAG
Y119C1B.8	chrI:4529070-4529939	35.6	6	ACCCAG	TTTCAG
C24F3.1	chrIV:10219964-10220758	35.45	6	ACCTAG	TTTCAG
F40F12.7	chrIII:9914570-9914756	35.24	9	CACCAG	TTTCAG
Y105E8A.24	chrI:14571700-14572773	35.23	9	TTAAAG	TTTCAG
C34D10.2	chrX:8021268-8022793	35.08	6	AATTAG	TTGCAG
Y54F10AM.4	chrIII:2544353-2544886	34.9	6	TTCAAG	TTTCAG
F27C1.2	chrI:5430642-5430842	34.6	12	ACCTAG	CTTCAG
K11E8.1	chrIV:10329075-10331121	34.49	6	TTAAAG	ATTTAG
C43H6.7	chrX:2401798-2401989	34.41	6	ATACAG	TTTCAG
K07B1.5	chrV:9332737-9333038	34.33	6	AAATAG	TTTCAG
F54B3.1	chrII:10265676-10266779	34.17	6	AACTAG	TTACAG
T27A3.1	chrI:6125515-6125719	34.16	6	TGTTAG	TTTCAG
M110.5	chrII:8227361-8227566	34.08	6	TAAAAG	TTCCAG
T04C10.2	chrX:14817170-14817763	33.65	6	TTATAG	CTTCAG
T12A2.15	chrIII:6225726-6226194	33.48	6	AACTAG	TTTCAG
T04D1.3	chrI:4677660-4678641	33.23	6	GTCCAG	TTTAAG
W04D2.6	chrV:12502145-12502617	32.85	6	CAAAAAG	TTTCAG
C18E9.10	chrII:8962583-8963887	32.8	6	ATCAAG	TTTCAG
ZK688.8	chrIII:7915009-7915917	31.61	6	AATAAG	TTCCAG
H12C20.6	chrV:11572037-11572220	31.33	8	CTAAAG	TTACAG
H12C20.6	chrV:11571870-11572055	30.79	7	TGATAG	TTCCAG
C36B1.8	chrI:8740955-8741362	30.32	9	ATAAAG	TTGCAG
T13C2.6	chrII:6783666-6783974	30.3	6	TGATAG	TTTCAG
F39H11.2	chrI:8701349-8701587	30.29	9	CAAAAG	TTGCAG
W06A7.3	chrV:14829724-14830302	29.8	12	AATGAG	TTTCAG
H14E04.2	chrIII:2376319-2376681	29.78	9	TCCCAG	TTTCAG
T12A2.8	chrIII:6247182-6247371	29.46	9	AAAAAG	TTTCAG
R13H8.1	chrI:10763579-10764485	29.12	6	CGAAAG	TTTCAG
Y45G5AM.1	chrV:4188450-4188666	28.98	5	TTATAG	GGCCAG
F21D12.1	chrII:7347418-7347600	28.95	6	TTTCAG	TTTCAG
Y113G7B.18	chrV:20254893-20256343	28.91	9	TTCCAG	TTCCAG
T19A6.3	chrI:8399130-8399316	28.31	6	TCACAG	TTTCAG
Y17G7B.2	chrII:11980564-11981032	28.22	6	AAAAAG	TTCCAG
F59E12.4	chrII:5632869-5633098	28.18	6	TCATAG	TTTCAG
C53B4.4	chrIV:8983455-8983833	28	9	TTTGAG	TTTCAG
T01G9.2	chrI:8287857-8288117	28	9	CCAAAG	TTCAAG
M110.5	chrII:8227509-8228336	27.99	6	AACAAG	ATTCAG
C01G8.5	chrI:5286384-5286603	27.82	9	GTTTTG	GTACAG
ZK520.4	chrIII:13690949-13691576	27.71	6	TATTAG	TTCCAG
ZK675.1	chrII:7893374-7893537	27.64	9	TGTCAG	TTTCAG
T28B4.1	chrX:6595645-6595833	27.48	9	GCTAAG	TTCCAG
C29F9.3	chrIII:124817-124998	27.03	5	CTGAAG	GTTCAG
M88.5	chrIII:4559481-4559672	26.39	7	TAACAG	TTTCAG

F53C3.13	chrII:3926014-3926987	26.16	6	CCAAAG	TTTCAG
F26H11.2	chrII:14400607-14400786	25.92	6	AAAAAG	TTCCAG
Y39A1A.5	chrIII:10606134-10609976	25.27	9	TAAAAG	TTCCAG
R01B10.4	chrV:6047201-6047384	24.97	8	TAAAAG	TTACAG
C37C3.2	chrV:7855732-7856115	24.83	10	CATTAG	TTCCAG
F16A11.3	chrI:9365077-9365259	24.78	12	ACCTAG	TTGCAG
R13A5.1	chrIII:7585595-7586108	24.62	12	AGTTAG	TTTCAG
F32D1.9	chrV:4372813-4372979	24.47	15	AAATAG	TTTCAG
Y73B6BL.6	chrIV:6325156-6325375	24.37	9	TATCAG	TTGCAG
C06G3.3	chrIV:7036111-7036299	24.3	10	AAAAAG	TTTCAG
C16H3.2	chrX:17600403-17600595	23.96	9	AAAAAG	TTTCAG
C35C5.3	chrX:11546220-11546429	23.89	9	AAGTAG	TTTCAG
Y69H2.3	chrV:18660883-18661115	23.82	15	TTAAAG	CGCCAG
F13G3.7	chrI:7305002-7305512	23.48	9	CATAAG	TTACAG
Y42H9AR.3	chrIV:8104590-8105216	23.36	6	TTTGAG	TTCCAG
Y53C12B.3	chrII:9748203-9748437	22.95	9	CCTCAG	TTTCAG
F28E10.2	chrIV:4564239-4564596	22.75	9	TTTGAG	TTTCAG
C08B6.1	chrV:10102957-10103141	22.59	12	TTATAG	TTCAAG
C17G10.9	chrII:5621647-5622465	22.23	6	TAACAG	CTTCAG
Y102E9.1	chrIII:6732724-6733288	21.83	6	AAAAAG	TTCTAG
K02A11.1	chrI:9742857-9743010	21.18	12	TGTAAG	TTCCAG
C07G2.2	chrIII:4492621-4493070	21.15	9	ATTTAG	ATTCAG
K10B3.9	chrX:3115501-3116215	21.11	11	AGTTAG	TTCCAG
Y39B6A.3	chrV:19189750-19189936	21.09	6	AAAAAG	TTTCAG
C56G2.6	chrIII:6338976-6339169	20.49	12	AAAAAG	ACTCAG
C47B2.6	chrI:12975174-12975624	20.03	6	CTTCAG	TTACAG
D1009.1	chrX:8938432-8938620	19.28	7	TCAAAG	TTTCAG
C08F1.4	chrII:1777898-1778082	18.8	6	TCGTAG	TTGCAG
M02B1.3	chrIV:12839082-12839976	18.51	13	ATTAAG	TTTCAG
T14G10.1	chrIV:10162583-10162764	18.23	6	AAAAAG	CTTCAG
F37C12.2	chrIII:7183493-7183669	18.14	6	TGATAG	TTTCAG
F07H5.3	chrII:8784828-8785261	17.62	7	ATCTAG	TTGCAG
F35C5.5	chrII:12893195-12893381	17.52	6	TATCAG	TTCCAG

L3 worms, N2 vs DG3430[*sacy-1(G533R)*]

Gene	Location (ce10)	Average ΔPSI	Splice Site Interval	Proximal Splice Site	Distal Splice Site
F32A6.3	chrX:5286790-5287117	81.47	12	AAAAAG	TTCCAG
C26C6.5	chrI:7539111-7539445	75.17	9	TAAAAG	TTACAG
Y105C5B.21	chrIV:15999136-15999878	74.08	6	CCCAAG	TTTCAG
F21H11.2a	chrIII:5118386-5118704	72.8	9	CTGGAG	TTTTAG
Y57A10A.18	chrII:12209620-12210895	71.95	9	GATAAG	CTCCAG
Y39B6A.12	chrV:19121774-19122072	70.96	6	CAAAAG	TTCCAG
F46F6.1	chrX:10374533-10374856	69.52	6	GAATAG	TTCCAG
B0261.2	chrI:5260285-5260585	69.31	12	ACTCAG	CTACAG
C53B4.4	chrIV:8983488-8983834	69.08	9	TTTGAG	TTTCAG
C25A1.12	chrI:10191980-10192307	67.77	15	AATCAG	CTTCAG
Y92H12A.5	chrI:1491337-1492534	66.49	9	CGTAAG	TTTCAG
Y39B6A.43	chrV:18966682-18967592	66.22	9	CACCAG	TTCCAG
Y17G7B.2	chrII:11982044-11983061	66.21	9	CTTAAG	TTCCAG
ZC376.6	chrV:14189961-14190282	64.68	12	CAAAAG	TTCCAG
Y71F9B.10	chrI:2765533-2765886	63.19	18	AAAAAG	TTGCAG
Y67D8C.5	chrIV:3039943-3040642	62.54	9	TTCAAG	TTCCAG
T27A3.1	chrI:6125449-6125774	62.43	6	TGTTAG	TTTCAG
Y73B6BL.6	chrIV:6325076-6325455	61.79	9	TATCAG	TTGCAG
T19A6.3	chrI:8399119-8399319	59.53	6	TCACAG	TTTCAG
Y41C4A.4	chrIII:11689572-11691340	59.53	9	CTTTAG	TTCCAG
F44G4.4	chrII:8998686-8999026	59.21	9	GAGCAG	TTGCAG
Y69H2.7	chrV:18693367-18695647	57.73	9	CAAAAG	CTCCAG
C28D4.2	chrIV:9732751-9732996	57.09	9	TCAAAG	TTCCAG
Y38E10A.6	chrII:12602074-12603510	56.87	6	AAAAAG	TTCCAG
Y67H2A.10	chrIV:13285937-13286287	56.45	9	TTCAAG	ATTAAG
Y67H2A.6	chrIV:13302729-13303073	55.77	15	CTTTAG	TTCCAG
T01D1.2	chrII:166955-168048	55.72	9	TAAAAG	TTGCAG
F44B9.7	chrIII:8027305-8027937	55.26	9	CTGAAG	ATTCAG
ZK546.1	chrII:4951468-4951741	55.23	9	GCCTAG	TTTCAG
T24D11.1	chrX:16407727-16408071	54.92	9	GATTAG	TTTCAG
F54C4.3	chrIII:85018-85912	53.76	9	CTTCAG	TTCCAG
C03B8.4	chrIII:7709137-7709462	53.55	6	AGAAAG	TTTCAG
R107.6	chrIII:9057997-9058320	53.51	9	TGTCAG	TTGCAG
R06F6.5	chrII:10796765-10797026	53.44	9	AAAAAG	TTACAG
K11E4.5	chrX:13747785-13748630	52.61	9	TCAAAG	TTTCAG
H37N21.1	chrI:7141858-7142205	51.98	9	TTATAG	TTTCAG
C29E4.4	chrIII:7931147-7931482	51.71	6	TGAAAG	TTGCAG
T04D1.4	chrI:4697044-4697649	51.41	9	TCAAAG	TTTCAG
K07H8.2	chrIV:8291700-8292878	50.28	12	ATCCAG	TTTCAG
F12B6.1	chrI:2267329-2267754	49.6	7	GAAAAG	TTCCAG
F31C3.2	chrI:15037851-15038197	49.26	9	TTCAAG	TTTCAG
F52G3.1	chrX:16966482-16968024	48.76	9	CCCAAG	TTCCAG
F36H2.3	chrI:9254307-9255153	48.6	9	TTATAG	TTCCAG
Y111B2A.14	chrIII:12635506-12635763	48.08	9	CTAAAG	TTCCAG

Y69A2AR.1	chrIV:2667126-2667502	47.96	9	CTAAAG	TTGAAG
R07G3.3	chrII:7606034-7606378	47.86	9	TAATAG	TTCCAG
Y113G7A.8	chrV:20082132-20083212	47.64	9	TCAAAG	TTTCAG
F39D8.1	chrX:15409385-15409604	47.62	9	TACCAG	TTAAAG
T04C10.2	chrX:14817407-14817752	47.01	6	TTATAG	CTTCAG
C25A1.9	chrI:10187119-10187401	46.93	12	TAAAAG	TTTCAG
C34D10.2	chrX:8024314-8024651	46.92	12	TTTCAG	CTTCAG
F39H11.3	chrI:8704385-8704685	46.63	12	CCCAAG	TTACAG
K06C4.17	chrV:8900584-8901079	46.58	8	TTTAAG	TTTCAG
F32D1.9	chrV:4372733-4373084	46.51	15	AAATAG	TTTCAG
M88.5	chrIII:4559404-4559752	46.13	10	GAACAG	TTTCAG
Y54F10AM.4	chrIII:2544490-2544895	46.12	6	TTCAAG	TTTCAG
Y53C12B.3	chrII:9748121-9748521	45.94	9	CCTCAG	TTTCAG
Y17G7B.18	chrII:12107320-12107696	45.43	9	TCTCAG	TTGCAG
T25D3.4	chrII:147191-147477	45.23	7	AAAAAG	TTTCAG
F36A2.1	chrI:8807282-8807520	45.1	12	CCATAG	ATGCAG
T16G1.9	chrV:12949014-12949358	45.04	12	TTCTAG	TTACAG
T08G5.5	chrV:14036741-14037087	44.97	9	TTTGAG	TTTCAG
T24B8.7	chrII:9047615-9047962	44.94	9	TGAAAG	TTTCAG
C18E9.3	chrII:8969097-8969358	44.93	9	GCAAAG	CTCTAG
R10E8.7	chrV:18232805-18233141	44.83	13	TTGCAG	TTTAAG
K10D2.3	chrIII:5174926-5175266	44.03	6	CAACAG	TTTCAG
F54B3.1	chrII:10262819-10263165	43.81	15	CGCCAG	TTTCAG
C16H3.2	chrX:17600325-17600621	43.76	9	AAAAAG	TTTCAG
C36B1.8	chrI:8740972-8741338	43.71	9	ATAAAG	TTGCAG
Y59A8B.21	chrV:17988652-17990597	43.68	9	TTGTAA	TTCCAG
C44E4.2	chrI:4631705-4632741	43.34	9	CCAAAG	TTCCAG
B0379.3	chrI:10082997-10083284	43.29	6	AATCAG	TTTCAG
M03C11.3	chrIII:10408120-10408420	43.28	8	TATCAG	TTGAAG
C26E6.9	chrIII:4925647-4926606	43.02	9	GAAAAG	TCTCAG
T12A2.8	chrIII:6247104-6247451	42.77	9	AAAAAG	TTTCAG
R07H5.8	chrIV:11210138-11210464	42.27	12	GTGTTG	TTTCAG
C47D12.1	chrII:11667450-11667791	41.91	12	CCTTAG	TTCCAG
T28C6.7	chrIV:8832537-8832988	41.9	12	AAAAAG	TTTCAG
F27C1.2	chrI:5430574-5430922	41.85	12	ACCTAG	CTTCAG
F53G12.5	chrI:128978-129322	41.84	9	GTTCAG	TTCCAG
T24A11.1	chrIII:3799704-3800041	41.71	12	AGTCAG	TTCCAG
T08A11.1	chrIII:4257834-4258158	41.4	6	CAATAG	TTCCAG
D2085.5	chrII:8673555-8673869	41.4	9	TTTCAT	TTACAG
F02E9.4	chrI:8422655-8423000	41.07	6	AAATAG	TTACAG
T05H10.5	chrII:8062672-8062956	40.79	12	GATTAG	TTTCAG
T23B12.4	chrV:8464298-8464682	40.58	15	TTTCTG	TTCCAG
Y48G1C.7	chrI:100184-100538	40.53	15	GTGTAG	TTCCAG
M110.4	chrII:8217140-8217397	40.41	12	TTCAAG	ATTCAG
Y59A8B.14	chrV:18101504-18101823	40.06	12	TTTTTG	TTTCAG
F56C9.10	chrIII:7333212-7333690	40.03	9	ATTGAG	GTGAAG
Y111B2A.22	chrIII:12741802-12743551	39.82	9	TCCAAG	TTCCAG

F13H10.4	chrIV:11018455-11018782	39.58	9	TGTGTAG	TTTCAG
F54B3.1	chrII:10261983-10262966	39.15	6	AACTAG	CTTCAG
Y48C3A.12	chrII:13387349-13388555	39.12	11	GTGAAG	TTCCAG
F11A10.4	chrIV:12103477-12104719	39.05	9	TTTTCG	TTCTAG
C04D8.1	chrIII:8496022-8497126	38.92	9	TAATAG	TTTCAG
Y48A6B.11	chrIII:11064311-11065115	38.86	9	CCAAAG	TTACAG
K07C5.8	chrV:10363007-10363276	38.56	9	TCTAAG	TTACAG
F39H11.2	chrI:8701327-8701633	38.45	9	CAAAAG	TTGCAG
W06A7.3	chrV:14829949-14830298	38.43	12	AATGAG	TTTCAG
F56B6.2	chrX:3547601-3547906	38.33	9	CATAAG	CTTCAG
R10E9.1	chrIII:3965711-3966490	37.99	9	CTCAAG	TTTCAG
Y73F8A.24	chrIV:15449062-15449379	37.69	12	CCCTAG	TTGCAG
C44H4.7	chrX:14603789-14604095	37.25	6	ATAAAG	TTTCAG
F39B3.2	chrX:17568941-17569212	37.07	9	TATCAG	TTCCAG
T05F1.1	chrI:9621316-9621646	36.51	9	CGTAAG	TTTCAG
Y34B4A.8	chrX:5272498-5273061	36.49	9	CATAAG	TTTCAG
F58A4.7	chrIII:9619672-9622175	36.37	9	GTAAAG	TTTCAG
F39H11.2	chrI:8701709-8702026	36.06	9	CGAAAG	TTACAG
D2089.4	chrII:10678697-10679007	35.91	9	TCATAG	TTGAAG
F38A6.3	chrV:20783888-20784257	35.85	6	TATCAG	TTGCAG
Y105E8A.24	chrI:14571620-14572853	35.77	9	TTAAAG	TTTCAG
F54E7.3	chrIII:5672505-5673229	35.76	9	GATTAG	TTTCAG
K02F2.1	chrI:6838813-6839150	35.69	12	GTTGAG	TTGCAG
B0285.1	chrIII:4333416-4334245	35.56	6	AGCTAG	TTTCAG
F10C2.5	chrV:12045699-12046045	35.42	11	CATAAG	TTCCAG
ZK675.1	chrII:7893340-7893629	35.23	9	TGTCAG	TTTCAG
Y40B1A.3	chrI:13353088-13354204	35.15	9	TGAAAG	TTACAG
B0513.1	chrIV:13890372-13890795	34.74	9	CTTCAG	TTTCAG
H14E04.2	chrIII:2376317-2376645	34.18	9	TCCCAG	TTTCAG
K10D2.3	chrIII:5175284-5175739	34.07	9	GTCAAG	TTTCAG
Y32H12A.8	chrIII:5404652-5404998	33.51	12	CGCCAG	TTCAAG
H20J04.3	chrII:4336134-4337163	33.47	9	TCTTAG	CTTCAG
B0261.2	chrI:5258608-5259454	33.46	9	GTCAAG	TTATAG
T05C12.6	chrII:8182430-8182883	33.16	13	AATTAG	TTCCAG
B0336.5	chrIII:5693026-5693363	32.94	9	TCCCAG	TTGCAG
D1046.1	chrIV:8926311-8926536	32.57	6	TTTTTG	ATCCAG
R13A5.1	chrIII:7585517-7586186	32.42	12	AGTTAG	TTTCAG
F58A4.7	chrIII:9623548-9623897	32.2	6	GTATAG	ATCCAG
C24A8.3	chrX:4304457-4304735	32.14	9	AAATAG	TTCCAG
Y119C1B.8	chrI:4528990-4530018	32.13	6	ACCCAG	TTTCAG
Y92H12A.1	chrI:1567550-1570497	31.98	12	AAAAAG	ACGCAG
C34D4.14	chrIV:7140904-7141215	31.94	6	GTCTAG	ATTCAG
C53A5.6	chrV:14545310-14545652	31.34	9	AAAAAG	TTGCAG
Y113G7A.6	chrV:20059612-20061476	31.31	9	ATACAG	TTTCAG
F15A8.5	chrX:4411561-4411903	31.2	9	ATTTAG	GTCAAG
R13H8.1	chrI:10763550-10764490	30.72	6	CGAAAG	TTTCAG
T22H6.2	chrX:12782452-12783474	30.3	6	TAATAG	TTACAG

F23H11.2	chrIII:897066-897531	30.29	40	TTCCAG	CTTCAG
F20H11.2	chrIII:6597793-6598234	30.18	12	TGGTAG	TTTCAG
R02F2.1	chrIII:5505017-5505361	30.08	6	CTCAAG	TTTCAG
C09H10.10	chrII:11095299-11095639	30.05	9	CTCCAG	TTTCAG
T13F2.3	chrIV:9796116-9796369	29.92	6	TGTCAG	ATTCAG
C05D10.4	chrIII:6089150-6089469	29.83	9	AAAAAG	CTTCAG
K05B2.2	chrX:4911160-4911462	29.76	9	TTGAAG	TTTCAG
C53B4.4	chrIV:8981197-8981832	29.47	6	GATTAG	TTTCAG
ZK858.4	chrI:9134281-9135105	29.42	12	TTTGAG	TTACAG
C05E11.1	chrX:4589773-4590093	29.26	12	TTGTAG	TTTCAG
W05F2.7	chrI:3355095-3355410	29.14	11	CCCCAG	TTTTAG
Y113G7B.18	chrV:20254839-20256422	29.12	9	TTCCAG	TTCCAG
H05C05.1	chrIII:2957333-2958371	28.72	6	GCCTAG	TTCCAG
C34D10.2	chrX:8021188-8022864	28.68	6	AATTAG	TTGCAG
C10C5.6	chrIV:9391064-9391414	28.67	18	TAAAAG	TTCCAG
Y57G11C.33	chrIV:14657042-14657309	28.61	12	GGTTAG	GGTCAG
F28E10.2	chrIV:4564243-4564673	28.61	9	TTTGAG	TTTCAG
F26H9.2	chrI:9293414-9293794	28.01	9	CGATAG	TTTCAG
F45F2.10	chrV:8514701-8515004	27.95	9	TTTTAG	ATTTAG
C05C10.2	chrII:9930126-9930535	27.94	6	TAATAG	TTTCAG
F41H10.3	chrIV:5372413-5372824	27.8	12	TCCCAG	TTTCAG
T27B1.2	chrX:16537721-16538066	27.74	6	TCTTAG	TTTCAG
C53B4.4	chrIV:8983687-8984086	27.61	7	TAAAAG	CTCCAG
C39E9.14	chrIV:13097654-13097996	27.53	6	CAAAAG	TTTTAG
Y66H1B.2	chrIV:363769-364318	27.09	6	ATCCAG	TTCCAG
F58H1.7	chrV:11964241-11964826	26.83	6	TCCCAG	TTCCAG
F33D4.2	chrIV:7692118-7692434	26.69	9	ATTAAG	TTTCAG
Y61A9LA.8	chrV:4562830-4564498	26.37	6	TGACAG	TTTCAG
Y106G6E.6	chrI:10230269-10230620	26.36	15	CATCAG	TTACAG
T08A11.1	chrIII:4250831-4251441	26.22	6	AATAAG	GTTCAG
F40A3.2	chrV:7880979-7881340	25.78	27	TTTTAG	ATCCAG
E01G4.4	chrII:13454791-13455084	25.51	9	TCGAAG	TTTCAG
C09H6.1	chrI:8108107-8108874	25.45	6	CAATAG	TTTCAG
M03F8.3	chrV:5941086-5941724	25.37	9	CGCTAG	TTTCAG
ZK1127.3	chrII:7055697-7056031	25.34	7	TCATAG	TTTCAG
R119.5	chrI:391667-392196	25.31	3	TCCCAG	CAGCAG
C50C3.7	chrIII:8160297-8160594	24.86	7	TCACAG	TTCCAG
ZK1193.5	chrX:427854-428687	24.81	9	TTTTAG	TTTCAG
F55A12.5	chrI:5347139-5347468	24.6	9	CCGAAG	TTCCAG
Y45F10D.13	chrIV:13769005-13769416	24.46	6	TTGAAG	TTCCAG
C46C2.1	chrIV:9210514-9211381	23.84	7	CATCAG	TTCCAG
Y113G7B.23	chrV:20239830-20241375	23.71	9	AAAAAG	TTTCAG
H15N14.1	chrI:7774890-7775224	23.7	9	TATTAG	CTTCAG
C17G10.9	chrII:5621638-5622498	23.67	6	TAACAG	CTTCAG
Y110A2AL.8	chrII:2848163-2848502	23.65	9	ATATAG	ACGCAG
K02C4.3	chrII:8082239-8082837	23.63	9	TTCAAG	TTCCAG
M88.5	chrIII:4554179-4554681	23.47	12	GGGGAG	TTGCAG

R11A8.7	chrIV:10378445-10378794	23.16	12	AATTAG	TTACAG
F39B1.1	chrX:15241591-15241910	23.12	6	TGAAAG	TTTAAG
B0261.2	chrI:5252806-5253343	23.02	6	AAAAAG	TTTCAG
T05F1.1	chrI:9621129-9621457	22.93	9	TTGAAG	TTTCAG
C07G2.2	chrIII:4492619-4492925	22.9	9	AATTAG	ATTCAG
T27F2.2	chrV:11632303-11632835	22.84	6	AAATAG	ATTCAG
C18H9.3	chrII:6684193-6684789	22.72	9	TTAAAG	TTTCAG
F26B1.2	chrI:6319198-6319599	21.85	9	ATGAAG	TTTCAG
F40F12.7	chrIII:9914491-9914827	21.77	9	CACCAG	TTTCAG
C17G10.9	chrII:5620914-5621257	21.54	9	CTACAG	TTCCAG
C05G5.2	chrX:14749746-14750091	21.21	7	TACTAG	TTTCAG
Y119C1B.8	chrI:4529867-4530207	21.16	6	ATCTAG	CTTCAG
F07H5.3	chrII:8784847-8785235	20.89	7	ATCTAG	TTGCAG
C12C8.3	chrI:9338650-9338970	20.86	12	TTTCAG	TTTCAG
F22G12.5	chrI:13167409-13168463	20.79	6	GACCAG	TTCCAG
F59F4.3	chrX:15843961-15844302	20.78	12	TCATAG	TTGCAG
T01B10.4	chrX:8474109-8474455	20.25	8	ATTTAG	TAACAG
C02E11.1	chrV:1048263-1048592	19.74	6	CAAAAG	CTTCAG
T05A10.1	chrX:10780890-10781236	19.54	3	CGTTAG	TAGCAG
C24F3.1	chrIV:10220433-10220764	19.13	6	ACCTAG	TTTCAG
F26C11.1	chrII:9896147-9896431	18.8	9	TTTTTG	ATCCAG
C01G8.9	chrI:5302504-5302814	17.79	10	GTCAAG	TTCCAG
F44A6.1	chrX:10199397-10199788	17.6	6	CAACAAG	CTTCAG
Y41C4A.4	chrIII:11685059-11688178	16.77	6	TCTCAG	TTTCAG
F29C12.1	chrII:13108176-13108511	16.65	6	ATTTAG	GTTCAG

L3 worms, N2 vs SZ454[*mog-5(Δ17 + 9)*]

Gene	Location (ce10)	Average ΔPSI	Splice Site Interval	Proximal Splice Site	Distal Splice Site
F32A6.3	chrX:5286790-5287117	56.79	12	AAAAAG	TTCCAG
C26C6.5	chrI:7539111-7539445	46.26	9	TAAAAG	TTACAG
C15A11.3	chrI:7390516-7391998	44.47	15	CAACAG	CTACAG
Y71F9B.10	chrI:2765533-2765886	43.86	18	AAAAAG	TTGCAG
Y41C4A.4	chrIII:11688090-11691347	43.54	9	CTTTAG	TTCCAG
Y105C5B.21	chrIV:15999136-15999878	43.53	6	CCCAAG	TTTCAG
T27A3.1	chrI:6125449-6125774	42.37	6	TGTTAG	TTTCAG
H37N21.1	chrI:7141858-7142205	41.42	9	TTATAG	TTTCAG
VF11C1L.1	chrX:12975319-12975641	39.35	9	TGATAG	CTTCAG
C34D10.2	chrX:8024314-8024651	38.25	12	TTTCAG	CTTCAG
T02C5.1	chrX:2697846-2698126	38.19	16	CATAAG	CTTCAG
Y57A10A.18	chrII:12209620-12210895	37.79	9	GATAAG	CTCCAG
M110.4	chrII:8217140-8217397	37.48	12	TTCAAG	ATTCAG
M04B2.5	chrIV:11505031-11505631	36.44	8	CAACAG	TTCCAG
T04C10.2	chrX:14817407-14817752	35.57	6	TTATAG	CTTCAG
C29E4.4	chrIII:7928972-7929227	33.25	15	ATTTAG	CTTCAG
F46F6.1	chrX:10374533-10374856	32.92	6	GAATAG	TTCCAG
ZC376.6	chrV:14189961-14190282	32.78	12	CAAAAG	TTCCAG
C31H1.8	chrIV:5813470-5813775	31.16	6	CCAAG	TTTCAG
D1009.3	chrX:8908103-8908760	31.11	6	TTCTAG	TTTCAG
Y54F10AM.4	chrIII:2544490-2544895	31.1	6	TTCAAG	TTTCAG
Y113G7A.8	chrV:20082132-20083212	30.63	9	TCAAAG	TTTCAG
T24D11.1	chrX:16407727-16408071	30.56	9	GATTAG	TTTCAG
F44G4.4	chrII:8998686-8999026	29.46	9	GAGCAG	TTGCAG
T04D1.4	chrI:4697044-4697649	29.19	9	TCAAAG	TTTCAG
T19E10.1	chrII:10778888-10779553	29.14	9	TGTTAG	TTTCAG
T19A6.3	chrI:8399119-8399319	28.88	6	TCACAG	TTTCAG
Y57G11C.33	chrIV:14657042-14657309	28.77	12	GGTTAG	GGTCAG
C28D4.2	chrIV:9732751-9732996	28.54	9	TCAAAG	TTCCAG
Y73B6BL.6	chrIV:6325076-6325455	28.27	9	TATCAG	TTGCAG
Y37A1C.1	chrIV:14115393-14115669	28.2	6	TCCAAG	TTTCAG
F58H1.7	chrV:11964241-11964826	28.13	6	TCCCAG	TTCCAG
Y92H12A.5	chrI:1491337-1492534	28.09	9	CGTAAG	TTTCAG
C34D10.2	chrX:8021188-8022864	28.05	6	AATTAG	TTGCAG
Y69A2AR.1	chrIV:2667126-2667502	27.97	9	CTAAAG	TTGAAG
F21D12.1	chrII:7348084-7348404	27.86	6	TTAAAG	TTATAG
F32D1.9	chrV:4372733-4373084	27.83	15	AAATAG	TTTCAG
C03B8.4	chrIII:7709137-7709462	27.77	6	AGAAAG	TTTCAG
C06A6.2	chrIV:7852863-7853211	26.76	9	CTCTAG	ATTCAG
C36B1.8	chrI:8740972-8741338	26.49	9	ATAAAG	TTGCAG
Y48C3A.12	chrII:13387349-13388555	26.34	11	GAAGAG	TTCCAG
C25A1.12	chrI:10191980-10192307	26	15	AATCAG	CTTCAG
T08G5.5	chrV:14036741-14037087	25.76	9	TTTGAG	TTTCAG
Y39B6A.12	chrV:19121774-19122072	25.64	6	CAAAAG	TTCCAG

T10B11.8	chrI:6953779-6954226	25.29	6	CTAAAG	TTTCAG
C18E9.3	chrII:8969097-8969358	25.27	9	GCAAAG	CTCTAG
C27C12.4	chrX:14854908-14855643	25.07	6	TTTCAG	TTTCAG
T26A5.2	chrIII:6469907-6470192	24.9	9	GGAAAG	TTTCAG
Y67D8C.5	chrIV:3039943-3040642	24.42	9	TTCAAG	TTCCAG
F39B3.2	chrX:17568941-17569212	24.31	9	TATCAG	TTCCAG
Y54G2A.28	chrIV:3006026-3006229	24.14	7	AAAAAG	TTCCAG
F02E9.4	chrI:8422655-8423000	24.08	6	AAATAG	TTACAG
B0261.2	chrI:5260285-5260585	23.7	12	ACTCAG	CTACAG
T13C2.2	chrII:6792808-6793095	23.61	12	TCCCAG	ATTCAG
R10E8.7	chrV:18232805-18233141	23.51	13	TTGCAG	TTTAAG
C27H5.3	chrII:7152863-7153236	23.3	3	TTTCAG	CAGCAG
F31C3.2	chrI:15037851-15038197	22.84	9	TTCAAG	TTTCAG
C04D8.1	chrIII:8496022-8497126	22.78	9	TAATAG	TTTCAG
R107.5	chrIII:9052153-9052488	22.71	6	TATAAG	TTGCAG
R10E9.1	chrIII:3965711-3966490	22.18	9	CTCAAG	TTTCAG
ZK1193.5	chrX:427854-428687	22.02	9	TTTTAG	TTTCAG
C08C3.2	chrIII:7775648-7775969	21.99	6	CTTTAG	TTTCAG
F45F2.10	chrV:8514701-8515004	21.89	9	TTTTAG	ATTTAG
C09B8.7	chrX:6047191-6047540	21.84	9	CTACAG	TTATAG
F21H11.2a	chrIII:5118386-5118704	21.56	9	CTGGAG	TTTTAG
ZK858.4	chrI:9134281-9135105	21.4	12	TTTGAG	TTACAG
M03C11.3	chrIII:10408120-10408420	21.22	8	TATCAG	TTGAAG
F01D4.5	chrIV:10482633-10482975	21.16	10	TATCAG	TTACAG
C24A8.3	chrX:4304457-4304735	20.55	9	AAATAG	TTCCAG
K10D2.3	chrIII:5174926-5175266	20.53	6	CAACAG	TTTCAG
F15A8.5	chrX:4411561-4411903	19.77	9	ATTTAG	GTCAAG
R11A8.7	chrIV:10378445-10378794	19.21	12	AATTAG	TTACAG
F32A5.2	chrII:7246384-7247440	18.47	6	ATCCAG	TTCCAG
C01B7.1	chrV:8787889-8788324	17.88	6	TGTTAG	TTGCAG
F39B1.1	chrX:15241591-15241910	17.81	6	TGAAAG	TTTAAG
T22H6.2	chrX:12782452-12783474	17.04	6	TAATAG	TTACAG

Supplemental Table 2

crRNA guide name	**crRNA guide sequence** (entered as DNA into IDTdna.com crRNA order form)
mog5-inter-crRNA	GCTGGTGGAAAAGCGACTTA

CRISPR repair name and description	**CRISPR repair oligonucleotides sequence** (lower case differs from wt)
mog5-522G544repair Removes PVUII cute site, creates K522G and T524G amino acid substitutions	ATGAAAGAAATGCCAGAATGGTTGAAACATGTGACAGCaGGTGGAgggGCGggaTATGGAAGAAGAACCAATTTGAGTATGGTTGAGCAGAGAGAAAG

Supplemental Table 3

icd-2SSFor = AGAAGCCAAGATCGAGGATC
icd-2SSRev = TTGTCAGCTTCCTTAAGCGC
Genomic DNA Product = 271 nt
Upstream AG usage = 228 nt
Downstream AG usage = 222 nt

lmd-1SSFor = AGGTAGCCGAAATAAAACGAG
lmd-1SSRev = ATATCCTCGACACTGGGATC
Genomic DNA Product = 266 nt
Upstream AG usage = 225 nt
Downstream AG usage = 217 nt

sax-2For = GGAAGCAATCGAAATGCGTC
sax-2Rev = TTCTCACTCTGCAACTGCTC
Genomic DNA Product = 277 nt
Upstream AG usage = 231 nt
Downstream AG usage = 222 nt

dcp-66For = ATTCAGACCATATGCCGGAC
dcp-66Rev = TTTGCTTCTGCGTACTGCTC
Genomic DNA Product = 310 nt
Upstream AG usage = 267 nt
Downstream AG usage = 258 nt

jac-1For = GGTTACCCGAGGACTTTGTC
jac-1Rev = CCGCTGAGCTTCTAACAATC
Genomic DNA Product = 668 nt
Upstream AG usage = 219 nt
Downstream AG usage = 213 nt