Genome location	Mating status	Gene name	Location	Sequence context	Micro-homology	Base repeat	Single-nucleotide micro-homology
chrI:10,688,343	Random	*tag-272*	Exon 1/3	tcgctgggatTCCTAAAaatttcagag	No	No	No
chrI:11,679,992	Random	*kpc-1*	Exon 5/7	taaggtgtctTATGTGGagcacgtgca	No	No	No
chrI:5,252,722	Random	*let-363*	Exon 16/32	ttgctcaacgAGCACAAatgtcacgtg	No	No	No
chrI:6,096,169	Random	ZK484.7	Exon 3/7	agcgaactctGCGCGAAggccagctgg	No	No	No
chrI:6,189,643	Random	T05E7.3	Exon 5/14	aactgaaagaAAACAGAatattcgaac	No	No	Yes
chrI:8,927,379	Random	N/A		aaatagatggAGGGAAAgctgccaata	No	No	Yes
chrII:10,015,267	Random	*lec-2*	Exon 2/8	ttcctccttaTGTTCTTcaactggagc	No	No	No
chrII:10,500,184	Random	*myrf-1*	Exon 3/9	ttcttggcgtTTCACAGgggtgtcaag	No	No	No
chrII:11,152,211	Random	*pqm-1*	Exon 2/6	tcaggttaggGGTTCGGctgcattagg	No	No	No
chrII:11,327,511	Random	*tag-180*	Exon 3/18	ttgtgttccaCCATGTTcgacacaaaa	No	No	No
chrII:11,463,260	Random	*aars-1*	Exon 3/9	tcggtgcaagGACCACAcggaccagct	Yes	No	No
chrII:2,068,749	Random	F07E5.12	Intron 2/2	aatccattgtTTTCAGCgtctgcctgg	No	No	No
chrII:2,283,136	Random	N/A		gaattgttttCCCTTACcagccgtgga	No	No	No
chrII:6,479,205	Random	*del-10*	Exon 13/18	aatccaattgtTTTCAGCgtctgcctgga	No	No	No
chrII:705,939	Random	*thoc-1*	Intron 11/14	agaagcttaaATAAAAGtttaaattcc	No	No	No
chrII:790,467	Random	N/A		caacgattgaTATTCAAcaagaaaaa	No	No	No
chrII:9,327,522	Random	*eat-3*	Exon 6/9	aatgaaggctCTTGGCTatttcggagt	No	No	No
chrIII:1,161,582	Random	*cdh-12*	Intron 8/25	tcgatgcaccATGTCCAgaaactatgc	No	No	No
chrIII:1,346,434	Random	Y82E9BL.5	Exon 2/2	ccgagttgtGTGCATAgcaggccaca	No	No	No
chrIII:10,817,396	Random	*linc-129*	Intron 1/1	aactatagggATGTCTCgattttttgt	No	No	Yes
chrIII:11,088,227	Random	Y69H2.24	Intron 2/14	caacttatcaGTTGACAactttttgta	No	No	Yes
chrIII:13,191,389	Random	*gly-5*	Exon 4/10	acagtttggtGGAAAAGtcaagatttt	No	No	Yes
chrIII:2,530,847	Random	*ceh-44*	Intron 2/11	cggtgaaaatCGAATCAaaatatggga	No	No	No
chrIII:3,592,179	Random	*ptp-1*	Intron 3/16	gcgcgaagttTCATATGatgcatttgg	No	No	No
chrIII:5,381,437	Random	Y32H12A.6	Exon 2/3	gtcgagggtgTCGGCTGaccaccagcc	No	No	No
chrIII:6,558,464	Random	C09E7.6	Exon 1/18	acaagcatcaGAGAATGtttcgagtac	No	No	No
chrIII:7,601,357	Random	N/A		tttttggcaaAAATAATtattttccgt	No	No	No
chrIII:8,489,218	Random	*ess-2*	Exon 4/5	ttcaattttcCGGAGTCtggaaaccta	No	No	No
chrIII:8,871,622	Random	K01F9.2	Intron 4/5	ttaaattcttTAATTCTcattatagtt	No	No	No

Genome location	Mating status	Gene name	Location	Sequence context	Micro-homology	Base repeat	Single-nucleotide micro-homology
chrIV:13,141,912	Random	F09E8.1	Exon 3/6	aagatcacacCAGCCACtgtatctctc	No	No	No
chrIV:13,674,942	Random	*oac-48*	Exon 4/12	tgtcatttacTGTCACAttgattcttc	No	No	No
chrIV:14,620,437	Random	*dmd-6*	Intron 2/4	catccctcgaATCTACGaatcttgttt	Yes	No	Yes
chrIII:2,317,481	Random	*iffb-1*	Intron 4/9	ggattttccaGGGAAAAacgtgatttt	No	No	Yes
chrIV:15,822,650	Random	*daf-38*	Intron 1/6	cttaaatgttTTCAGCTaagcgaacga	No	No	No
chrIV:17,242,307	Random	N/A		ttatttggaaCTGCCCGatactgaaat	No	No	Yes
chrIV:2,085,223	Random	*mca-2*	Exon 4/11	ccgtactgctCTCCGGCactcacgcta	No	No	No
chrIV:3,941,695	Random	*clec-174*	Intron 2/3	tgaaaatcaaCTATTATttttttaaag	No	No	No
chrIV:4,373,899	Random	F55F10.1	Exon 1/10	tggtctatcgACAATCGgcaacccagt	No	No	Yes
chrIV:4,499,173	Random	*gbb-2*	Exon 10/19	ggtggtgaccATCCTTTtgtggtacta	No	No	No
chrIV:4,884,473	Random	*str-166*	Intron 1/7	accggtaagtTCATTAAactcagtttg	No	No	No
chrIV:8,427,395	Random	T26A8.2	Exon 2/7	accgttcatcAGAATGTagttggtccg	No	No	No
chrIV:9,998,901	Random	N/A		ccatcaagaaACGACCAtcactgaaag	No	No	No
chrV:10,245,171	Random	N/A		gaaggtcttgAAATCCTagtcatcaag	No	No	No
chrV:12,820,904	Random	*ugt-18*	Intron 2/7	aacctaaacgTGTTTGAatttgaaaag	No	No	No
chrV:14,223,519	Random	N/A		aaaagagcttTTCTTGTcaaatgatta	No	No	No
chrV:14,500,230	Random	*N/A*		tgtagataaaGTTCTCAcaaaagagat	No	No	No
chrV:14,865,224	Random	*gcy-14*	Exon 9/14	agtcgtgtttCATCGCCgcaagaatat	No	No	No
chrV:15,159,261	Random	*str-45*	Exon 1/4	tagtttttatCTGGTTAatattggcat	No	No	No
chrV:5,291,294	Random	Y69H.21	Intron 1/4	actggttgctGCTGTTGtcctagaatt	No	No	Yes
chrV:556,150	Random	N/A		acatggttacCTATAAAaacttcatgt	No	No	No
chrV:7,621,906	Random	C50E3.12	Intron 1/4	atttgtcttcTAAAACAttcatgttaa	No	No	No
chrX:10,671,379	Random	F13E6.2	Exon 8/19	cgctccatgtGTTCTCGgagggttctt	No	No	No
chrX:13,143,587	Random	N/A		attcattacgATGACTActacgggaac	Yes	No	No
chrX:14,333,955	Random	*sel-7*	Intron 5/6	ttattgaaaaAAATAAGtttcgaagtg	No	No	No
chrX:17,421,426	Random	N/A		gcgtgaactcCGCCCCAcaataccgcc	No	No	Yes
chrX:3,183,429	Random	F56E3.10	Exon 1/1	agcatgccttTCTCCTCctcattcccc	No	No	No
chrX:5,422,338	Random	C41A3.1	Intron 14/29	aattcgaccgTCCAACGtccacttctt	No	No	No
chrX:5,517,094	Random	N/A		gagagccataGTTGCAAtagttgagag	No	No	No
chrX:5,964,282	Random	R07E4.1	Intron 6/21	ggggttgaagGGAATTTtttgaaatat	No	No	No
chrX:8,185,992	Random	C17H11.6	Intron 16/16	ttttacttatTTTCACCtttgctcttg	No	No	Yes

Supplemental Table S8. Genome context of randomly selected regions.
Similar to Supplemental Table S5 but for randomly selected regions with simulated 7 bp deletion disagreement.