Genome location	Mating status	Gene name	Location	Sequence context	Micro-homology	Base repeat	Single-nucleotide micro-homology
chrV:14,897,511	Mated	H12D21.6	Exon 1/1	gtcagtcttcCGGCatgggatcaa	No	No	No
chrX:7,728,037	Mated	*vit-1*	Exon 1/5	attcaagctgTCGAtgaccgtcac	No	No	No
chrV:16,812,816	Mated	*cand-1*	Exon 11/12	acttgaccctCCAAcgtgtcgtaa	No	No	No
chrIV:4,162,865	Mated	*scrm-5*	Exon 2/4	tccaatgcatCAAAcccctcgaga	No	No	No
chrIII:5,078,650	Mated	*alh-1*	Exon 2/6	agatgtcaatATCGCTGTCAAGGTTTAAATCTAaattcgaatt	No	No	No
chrII:193,453	Mated	*abu-11*	Exon 3/4	aattcgaatt acaatcttgtTGGCactgttgctg	No	No	No
chrV:8,602,377	Mated	F41E6.15	Exon 3/4	tcagtatccaTACTactcgtatta	No	No	Yes
chrIII:12,174,671	Mated	*gly-11*	Exon 3/5	ccaattgacaCCGCCTGtgcaaacagg	No	No	No
chrV:308,725	Mated	*phf-10*	Exon 4/6	atagaggtggGATGACTCgatgacggtt	Yes	No	Yes
chrV:18,174,058	Mated	C31G12.4	Exon 5/5	gaagaagaagAAGAAGgtggtggtga	Yes	No	Yes
chrII:11,672,971	Mated	*trr-1*	Exon 6/22	atcgcacacaCCAGTGGatccatcaga	No	No	Yes
chrII:1,229,038	Mated	F53A10.2	Exon 8/11	caaccccatcGATTTTCAAGCGAGGCCAAgatttcagaa	Yes	No	No
chrI:10,715,469	Unmated	B0205.1	Exon 8/13	atatagaatgAATGgaactgatat	Yes	No	Yes
chrI:175,824	Mated	F56C11.6	Exon 9/9	cgttccgccaTTTCAAGATTgatctggacg	No	No	No
chrII:8,880,431	Mated	*rha-1*	Exon10/15	taccactcaaTCGGCTgtgatgcttc	No	No	No
chrV:16,472,301	Mated	*srw-35*	Intron 1/3	tgggaaaataATACAtttgaagcat	No	No	No
chrII:12,538,816	Unmated	F49C5.4	Intron 1/8	ttattcgtatTACGCTactactcggc	No	No	No
chrX:2,158,009	Mated	F14D1.2	Intron 2/2	attcgctatcATAATACGACTGCTATCAAAACGTACATAATCATTTAGCCTCCGCGGAAttttcaaggg	No	No	No
chrX:8,805,105	Mated	R04E5.8	Intron 3/7	tgaaggagtaGAAAGGATATAtggattttgc	No	No	No
chrII:13,586,529	Mated	Y47H9C.20	Intron 4/5	gccttgaaggCGGCCTACACCTACCtgccttaggc	No	No	No
chrII:12,838,584	Mated	*lgc-35*	Intron 5/11	tccacgtgatGTCAGCCTGACgccaggctgt	No	No	No
chrII:14,290,194	Mated	N/A		cgaaaatggaCTCGTCGGATATATTACACTATTTTctccgttcaa	No	No	No
chrIV:14,941,896	Mated	N/A		tcgcaaccccAGAAactaaaaaaa	No	No	No
chrIV:299,356	Unmated	N/A		tttttttgttTTTTTGGttttaatttg	Yes	Yes	Yes
chrV:6,231,794	Mated	N/A		gataagagttAATTTTtagcttgaat	No	No	Yes
chrX:14,534,379	Mated	N/A		tctctcttacTCTTtctttcttct	Yes	No	No
chrX:475,688	Mated	N/A		ctccttttccAAAACTTgacgatttga	No	No	No
chrX:9,780,202	Mated	N/A		gtgacgttttTGTTGATAATCTGAattgataaaa	No	No	No
chrIV:1,459,836	Mated	ZC123.10	Intron 7/8	gatcgagcgaTGTAGATCCgttgtaaaaa	No	No	No

Genome location	Mating status	Gene name	Location	Sequence context	Micro-homology	Base repeat	Single-nucleotide micro-homology
chrI:14,226,326	Mated	*eya-1*	Intron 1/6	gctcacagagCACAcacacacac	Yes	No	No
chrI:1,874,486	Unmated	*tub-2*	Exon 1/6	ttgacgccTCGATCGTTGACGAGTTCCAC GGACCaccgatcgtc	No	No	No
chrI:5,379,904	Unmated	*pqn-44*	Intron 1/6	aatacactcgTTGTttgtttgttt	Yes	No	No
chrIII:5,039,463	Unmated	C45G9.6	Exon 7/9	taagtcacctGTCCTGATATACAATccgaatgata	No	No	No
chrIII:7,492,420	Mated	N/A		ggcaggcaggCCCTGGAACCTGACTgcccaggagc	No	No	Yes
chrIII:9,127,721	Unmated	*sec-16*	Exon 7/14	cactcaattcCGTTCGTCTCTACATccaacgacaa	No	No	Yes
chrIV:3,295,342	Unmated	W08E12.7	Exon 2/5	cgccaacattAAGGaaggagccat	Yes	No	No
chrV:19,666,563	Mated	N/A		cctcttttttTTTTcactggcagt	Yes	Yes	Yes*
chrV:4,937,761	Mated	*catp-2*	Exon 8/9	atgataccccTAAAGCAATCAAAGCTTG taaagcagct	Yes	No	No
chrV:6,631,259	Mated	N/A		gtatgtttgaAGTTCAATagttcaatag	Yes	No	Yes
chrV:9,921,378	Mated	*ceh-75*	Exon 1/4	ctgttgacaaAATTaaggccttca	No	No	Yes
chrX:10,570,041	Mated	*bet-2*	Intron 1/8	catcgacaggTTCCTGagaaaaataa	No	No	No
chrX:11,607,836	Mated	N/A		aaccttttttTTTTagtaaaacta	Yes	Yes	Yes*
chrX:17,622,725	Mated	N/A		tcccccttccCCTTCCttcccactcc	Yes	No	No
chrX:7,898,506	Mated	N/A		tattaatctttCCCTAtactgttacc	No	No	Yes
chrII:13,586,529*	Mated	Y47H9C.20	Intron 4/5	gccttgaaggCGGCCTACACCTACCtgccttaggc	No	No	No
chrV:6,231,794*	Mated	N/A		tctctcttacTCTTtctttcttct	Yes	No	No
chrX:475,688*	Mated	N/A		gtgacgttttTGTTGATAATCTGAattgataaaa	No	No	No

Supplemental Table S5. Genome context of duplex deletion disagreements longer than 3 bp. Deletion disagreements: red; microhomology (defined as a sequence repeat 5 bp or longer within 10 bp of deletion disagreement; Sharma et al. 2015): solid underline; single-nucleotide microhomology (defined as identical single base on both sides of the deletion disagreement): blue; homopolymers (defined as at least 7 consecutive identical bases that cover the deletion disagreement): dashed underline. The two segments of the table correspond to strand consensus thresholds of 0.95 (top segment) or 0.51 (bottom segment). For Supplemental Tables S5-8, an asterisk in “Genome location” column indicates that the same disagreement is found at the same location in two or more samples; an asterisk in the “Single-nucleotide microhomology” column indicates that the deletion disagreement occurs within a homopolymer stretch, and that the exact position is thus ambiguous; since all internal positions would show single-nucleotide microhomology, these disagreements are scored as positive for that microhomology.