

Genome location	Mating status	Gene name	Location	Sequence context	Micro-homology	Base repeat	Single-nucleotide micro-homology
chrI:258,384	Unmated	Y48G1BR.1	Intron 2/9	cccaggccacCaccaaaaaaa	Yes	No	No
chrI:3,880,108	Unmated	C50F2.3	Exon 7/7	tatcctctggCaattcgaaa	No	No	No
chrI:4,015,245	Unmated	<i>unc-73</i>	Intron 3/15	ttgtttcaaAttatttct	No	No	No
chrI:4,689,790	Mated	<i>chd-7</i>	Exon6/9	ttgaaatcttCaccaaaagcc	No	No	No
chrI:7,656,926	Mated	N/A		tcgtaaaataAtcattagaaa	No	No	No
chrI:7,914,017	Mated	F20G4.2	Exon 5/5	tattgtcggcTtaatccaga	No	No	No
chrII:10,098,439	Mated	<i>lact-2</i>	Exon 5/5	ttggttacggtGgcagcacagt	No	No	No
chrII:10,432,721	Mated	N/A		ggaaattcaaTgtcctctct	No	No	No
chrII:11,017,468	Mated	K03E5.7	Intron 2/3	cacacatcgcTtaatatttg	No	No	No
chrII:12,326,455	Mated	<i>sre-56</i>	Intron 1/2	aaaaaaacgcTAAtaaacccaag	No	No	No
chrII:12,733,049	Mated	<i>snrp-200</i>	Exon 5/12	ctgggagattTgattaagatg	No	No	No
chrII:13,497,310	Unmated	N/A		taTTTTTTTAcggccacat	Yes	Yes	Yes*
chrII:6,588,333	Mated	<i>icd-1</i>	Intron 2/4	tgttgacctgAaaagtacag	No	No	No
chrII:6,939,194	Unmated	<i>flcn-1</i>	Intron 10/15	actcagataaAtcgaaccacg	No	No	No
chrII:8,002,154	Mated	<i>pgp-11</i>	Intron 1/16	gtagggatatCagagtgaat	No	No	No
chrII:8,870,100	Mated	T07D4.2	Exon 6/7	tatacaaagtTcattaactgc	No	No	No
chrIII:239,087	Unmated	<i>hpo-29</i>	Intron 3/11	ctgaaaaaaaAtgcgaatttt	No	Yes	Yes*
chrIII:5,561,802	Unmated	<i>rpc-2</i>	Exon 7/9	gatgagaattTatctccaagt	No	No	No
chrIII:5,682,482	Unmated	N/A		tccaattttTcatttttc	Yes	No	Yes*
chrIV:10,194,788	Unmated	N/A		aaaaactcagTTTTTTTct	No	Yes	Yes*
chrIV:12,887,646	Mated	K08D8.6	Intron 5/3	ttcaggtggcTTTTTTTca	No	Yes	Yes*
chrIV:1,352,815	Unmated	<i>rhc-2</i>	Exon 7/7	acttcgaaacTcaactctcc	No	No	No
chrIV:14,774,496	Mated	N/A		atatagcaggAaaaatcaagg	No	No	Yes*
chrIV:1,7396,393	Mated	<i>srp-15</i>	Exon 1/5	ccgttacttgTGagagcacaat	No	No	No
chrIV:17,411,008	Mated	<i>npr-26</i>	Intron 1/5	gccttacttgTTTTTTTct	No	Yes	Yes*
chrIV:2,340,221	Mated	<i>ppgn-1</i>	Intron 6/9	aaaattttaAGagaaaaatag	No	No	Yes
chrIV:5,314,565	Unmated	ZK354.2	Intron 4/5	tgaaaaaaaAgttattttaa	No	Yes	Yes*
chrIV:5,565,001	Unmated	N/A		aaaaaacttCAatgagagac	No	No	Yes
chrIV:648,757	Unmated	N/A		agagagagagAGccttctctg	Yes	No	No
chrIV:7,888,863	Unmated	<i>atic-1</i>	Intron 5/17	gagagagagaGAtaaaacaaaa	Yes	No	No

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chrIV:8,494,932	Mated	C28C12.12	Exon 6/6	tgggtttgttCagggtgtagt	No	No	No
chrV:12,404,951	Unmated	N/A		ataatagaaaActactgcaaa	No	No	No
chrV:13,025,934	Mated	<i>fmi-1</i>	Intron 7/20	gatctttccaTtttttgcg _-_-_-	No	Yes	Yes*
chrV:13,934,181	Unmated	R10D12.1	Exon 2/4	aagaactgtcTttcctgtcg	No	No	No
chrV:2,218,228	Mated	Y22D7AR.17	Intron 2/7	gcttctggtAGgatagacacg	No	No	No
chrV:4,991,589	Mated	<i>ncx-9</i>	Exon 10/10	gtcggacagtAaagcgtgaa	No	No	No
chrV:6,440,459	Unmated	T05H4.15	Intron 4/4	ttttttttTcagatctggt _-_-_-	Yes	Yes	Yes*
chrX:10,095,647	Unmated	W07E11.1	Intron 5/17	agtaaaagacAaaaaaaaaa _-_-_-	Yes	Yes	Yes*
chrX:12,595,237	Mated	N/A		gccgtggtgcAaaaaatggca	No	No	Yes*
chrX:15,255,230	Mated	N/A		gacaaatcacCaagcgcggt	No	No	No
chrX:15,258,414	Unmated	F46F2.4	Exon 4/4	ctaccctcttGgatccccgtt	No	No	No
chrX:15,549,609	Mated	<i>Iron-3</i>	Intron 1/4	gtaattttccTttttttta _-_-_-	Yes	Yes	Yes*
chrX:15,687,778	Mated	N/A		tgaaaaaaaAgtcggaaaaa _-_-_-	No	Yes	Yes*
chrX:16,014,591	Mated	VB0395L.1	Intron 4/7	caattttttCAcctgatggt	No	No	No
chrX:16,692,682	Mated	N/A		tttatgataTtttttctgt _-_-	No	Yes	Yes*
chrIV:7,610,484	Unmated	<i>tag-80</i>	Intron 14/31	ccataaatacTtttttctgt _-_-	No	Yes	Yes*
chrX:4,756,203	Mated	N/A		atttgtcacAaaatactgt	No	No	No
chrX:6,581,777	Mated	N/A		cgagcattttTccgtagtca	No	No	Yes*
chrX:6,763,397	Unmated	N/A		accaggactgAaaaacaggcc	No	No	Yes*
chrX:7,275,608	Mated	<i>unc-10</i>	Exon 17/25	acttcacgcaAtcgtcgaca	No	No	No

Supplemental Table S6. Genome context of duplex deletion disagreements shorter than 3 bp.

Similar to Supplemental Table S5, except for the following difference: because of the large number of disagreements, a random subset was selected from disagreements meeting a strand consensus threshold of 0.95 (n = 60 / 969).