

Genome location	Mating status	Gene name	Location	Sequence context	Micro-homology	Base repeat	Single-nucleotide micro-homology
chrI:10,616,075	Mated	<i>lam-3</i>	Exon 8/13	aatgaaattgAaaaaattacga	Yes	No	Yes*
chrI:12,266,789	Mated	N/A		cttttggtcTttttttt - - - - -	Yes	Yes	Yes*
chrI:12,267,819	Mated	F41D3.6	Intron 2/3	atcatctgcAaaaaaaaaagg - - - - -	No	Yes	Yes*
chrI:12,511,790	Mated	<i>unc-101</i>	Intron 5/6	actgaaaaatAaaaaaaaaag - - - - -	Yes	Yes	Yes*
chrI:14,182,757	Unmated	Y41C4A.23	Intron 3/3	tttgcaaccAaaaaaaaaa - - - - -	Yes	Yes	Yes*
chrI:9,719,815	Mated	<i>ocr1-1</i>	Intron 5/13	cgttgcagaTtttttttg - - - - -	Yes	Yes	Yes*
chrII:2,347,582	Mated	F43C11.4	Intron 1/2	gcacattgctAaaaaaaaaacc - - - - -	No	Yes	Yes*
chrII:4,782,199	Mated	N/A		gttggtgtaTttttttt - - - - -	Yes	Yes	Yes*
chrII:5,222,007	Mated	<i>dsh-1</i>	Intron 5/13	gtgagcggacAaaaaaaaaact - - - - -	No	Yes	Yes*
chrII:6,777,517	Mated	<i>ssup-72</i>	Intron 3/3	ggctgttgaTtaaaaaaat	No	No	No
chrII:943,121	Mated	N/A		ttaatggtgTtttttttc - - - - -	Yes	Yes	Yes*
chrIII:11,513,017	Mated	<i>such-1</i>	Exon 12/12	ccgatgattGgggcttgca	No	No	No
chrIII:12,170,944	Mated	N/A		aaaaatcaacAaaaaaaaaaca - - - - -	No	Yes	Yes*
chrIII:3,047,979	Mated	N/A		ctaacgagatAaaaaaaaaagag - - - - -	No	Yes	Yes*
chrIII:8,940,621	Mated	N/A		aattttttgTttttttt - - - - -	Yes	Yes	Yes*
chrIII:9,454,454	Mated	AU219096	Exon 4/5	tcatttttAtatctgtct	No	No	Yes
chrIII:9,486,868	Mated	N/A		tcttcttgTtttttttc - - - - -	Yes	Yes	Yes*
chrIV:1,179,194	Mated	F56E10.6	Intron 1/4	aaaaataaccAaaaaaaaaaaa - - - - -	Yes	Yes	Yes*
chrIV:13,182,798	Mated	N/A		cttttctcTtttaaatca	Yes	No	No
chrIV:13,647,059	Mated	C08F11.11	Intron 1/2	tgtactgaaaTttttttt - - - - -	Yes	Yes	Yes*
chrIV:14,981,947	Mated	<i>atln-2</i>	Intron 1/7	atttttaacTtttttttg - - - - -	Yes	Yes	Yes*
chrIV:1,657,780	Mated	ZC123.10	Intron 7/8	tgtgtgcatcTtttttatg - - - - -	No	Yes	Yes*
chrIV:7,852,857	Mated	C06A6.2	Intron 8/10	tattccatcTtttcagcca	No	No	Yes*
chrIV:8,543,411	Mated	<i>hyl-1</i>	Intron 6/7	tatgggaattAaaaaaaaaaaa - - - - -	Yes	Yes	Yes*
chrIV:9,928,732	Mated	N/A		atcgttcaatCctttttttt	No	No	No
chrV:20,774,044	Mated	F38A6.4	Exon 2/3	gcagcgagacTttgaaactc	No	No	No
chrV:20,837,028	Mated	<i>num-1</i>	Intron 9/9	tggaatttgAaaaaaaaaaca - - - - -	No	Yes	Yes*
chrV:3,356,130	Unmated	<i>scrm-3</i>	Intron 3/4	cctcaactgTttttttt - - - - -	Yes	Yes	Yes*
chrX:12,961,578	Mated	N/A		tgtttggtgTttttttt - - - - -	Yes	Yes	Yes*
chrX:17,155,820	Mated	<i>npr-21</i>	Intron 7/9	tgaatgaccTtttttttc - - - - -	Yes	Yes	Yes*

Supplemental Table S7. Genome context of duplex insertion disagreements shorter than 3 bp.
Similar to Supplemental Table S5, with a randomly-selected subset (n = 30 / 399).