Table S1 Genetic markers used in this study, their coordinates, and primer sequences.

Marker	Scaffold[1]	Scaffold coords.	Chr.	Chr. coords.[2]	Forward	Reverse
SSR72	12822	1724188-1724354	2	1724188-1724354	TGCAGTCAAAACTGGGTCAA	GCAAGACCAAAAGTGCGAGT
SSR33	13047	16959223-16959455	2	6359965-6360197	CATTTCCTGCTGGCTAGCTT	GTCAGACACAGCGACGACAT
SSR74	13047	14987288-14987501	2	8331938-8332112	CCTTGGCATGTTTTAGAGCAA	AAGCGACGCGCAAAATATAC
va	12855	N/A	2	N/A	N/A	N/A
SSR81	12855	9909979-9910129	2	33229398-33229548	TGCACGTAAGTGTGAATCTGC	GTGCCAATCACATCGCAGT
SSR66	12823	997910-998114	5	997910-998118	CTCGCTGTCGCAATGTTTAC	GCCGCAAATAAAATGGTGAT
SSR104	12823	1689490-1689676	5	1689490-1689676	CGTCACGTACCGAGAAGACA	AGTACGTGTGGCATCAGCAA
SSR121	10324	594567-594746	5	3069112-3069291	TGCGCACTAAATGAGATGCT	CAAAGGCGTCATGGTAACCT
SSR123	12875[3]	912756-912964	5	4530387-4530596	AAGGTTTCCAGCGAATAGGC	CGTTGCTTACGTCAATCGAG
SSR119	12875	20444191-20444368	5	5610567-5610743	GAGAAGCGAGAGGCACACTT	CCAGGTAGGCTCTGTCCAAC
SSR58	12875	19509634-19509842	5	6545087-6545300	TGCCTAGCATTTGGCACTTA	AAAAGAGCGTGGCAAAGAAA
SSR192	12875	18634421-18634630	5	7420304-7420513	ATCAAGACCCAAGCCGGAAACCAG	CTGGTTTCCGGCTTGGGTCTTGAT
SSR190	12875	17808454-17808680	5	8246254-8246480	TGCCTGCTGATGAATCACGTGAC	TGTCACGTGATTCATCAGCAGGCA
SSR95	12875	16718920-16719133	5	9335798-9336014	TGTGCCTGCTGACAAAACAT	ACACTGCCTGCTTGCATTTA
SSR138	12875	16037240-16037447	5	10017486-10017694	TCGTACCAATGTTGTCAATGC	ACAGGAAGTGGGTGGAAGTG
SSR155	12875	15450044-15450076	5	10604771-10604976	TGGGACAAATGTGCCAAATA	ATATGCTCGGTCGGAGATTC
SSR169	12875	14987033-14987196	5	11067738-11067901	CATCAAGGAGCTGGCCTATC	ACTTCTCCGCCGTACAACTG
pup	12875	14961086-14964626	5	11084412-11091072	N/A	N/A
SSR181	12875	14501333-14501602	5	11553332-11553601	CAAGGGCATTGACTTCTACG	GGTTTTGGCTCAAAATCCAG
SSR23	12875	14309322-14309540	5	11745404-11745612	AAACTGGCAGATGGGCATAG	CCACGATTTCAGAAGCACAA
SSR179	12875	13607115-13607443	5	12447491-12447819	TGACGCAGTTGGCAATTAAC	ACTTGCCGATGAAGTTTTCG
SSR178	12875	13299025-13299315	5	12755619-12755909	AGTGCCACAAAACCGAAAAC	GAATGCCGCATAGATTCCTC
SSR93	12875	12612982-12613197	5	13441731-13441952	TCGAACTCGATCTTCTAGCTTCT	TTGAACTCTTCACGCGACTTT
B	12875	12492243-12542471	5	13512463-13562691	N/A	N/A
SSR188	12875	11790642-11790879	5	14264055-14264292	CGACGCACACAAACGCAATACTTTG	CAAAGTATTGCGTTTGTGTGCGTCG
SSR60	12875	10970098-10970252	5	15084664-15084836	CAAAAGTGTTGCCTTGATGG	GGGTTCTAGCCCCCAAATAA
SSR90	12875	9976996-9977241	5	16077689-16077938	ACTTTGCCAAGCTGTGAAGG	GCGTCTCGTATGCTCTGCTA
SSR176	12875	9364934-9365179	5	16689755-16690000	TGCCATTTGCGTATTTTGTG	CTGCAATAGGGGGTCAAATAG
SSR116	12875	8785474-8785673	5	17269263-17269460	CCCCATTGAAAGTTCATCCA	GTCAGGAGGCCACATTGTTT
SSR118	12875	8359663-8359861	5	17695072-17695271	GCCCAAAATTCTTAGCCAAA	TGGCTTGGGTACTGGTTTCT
SSR88	12875	8014665-8014816	5	18040111-18040269	CCAAAAGGCAGGACCATAAA	TTGCGTAGACACCACAAGGT
SSR124	12875	7542114-7542326	5	18512607-18512820	CGCTTAAACGATCCAACGAT	GTTCATAACCGGTGCTCGAT
SSR125	12875	7024865-7025043	5	19029891-19030069	AGCGCTGATGCTTAAACTGC	TTACTTGCTGACCCACTTACG
SSR87	12875	7014393-7014574	5	19040357-19040541	CAGCGCGTGCTGATTAGTTA	TACAGCTGGCTGCGTTTATG
SSR126	12875	6381246-6381454	5	19673479-19673688	AATTGCCAAAGAAACCACCA	AGCGGCTCGTCGTCTGTA
SSR129	12875	6028577-6028753	5	20026180-20026357	ACCATGAGCAGGCATCAGA	CCGGCAATCGTTCTTTAACT
SSR133	12875	5581289-5581484	5	20473430-20473645	CTCGCAACTTGGCAGACATA	TGCCCCAATGTAACTGCTATC
SSR62	12875	4985233-4985531	5	21069407-21069701	TGTTAGTTGGCAGCGCAAT	GATTATGCGTGTTGCAGTCG
SSR183	12875	4001657-4001814	5	22053120-22053277	CGTATTTGAGTGCAACGCGTTTG	CCAAACGCGTTGCACTCAAATACG
SSR13	12875	3052296-3052513	5	23002420-23002638	CTTTATCCCGATGTGCGAGT	GCCGCAATAAACTGGAAAAG
SSR11	12875	2002257-2002505	5	24052429-24052677	TTGGCAGAGCTTTCTCACCT	CTAAACGGGCCTCCACATT

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[1] FlyBase genome release dvir1.2.

[2] Chromosome coordinates based on arrangement of genome scaffolds on Muller elements (Schaeffer *et al.* 2008; Ahmed-Braimah and Sweigart 2015).

[3] Misplaced scaffold portion in original genome assembly (Schaeffer *et al.* 2008).