

Table S1 Primers used in this study to bridge gaps between scaffolds

Chr	Primer 1	sequence	Primer 2	sequence 2	scaffold
2/4	6479	GGCGACAGCACGACCAGTACCCC	6485	GGAAGCAGGAGTGACTGAGGC	1
4	6591	GTTGCGTGTGCACAGTAGAGGG	6611	cagtgtactccggaggagcattcac	3+42
4	6964	GTGTAATAGACGACCCATG	6965	GAAGGCTTATGCTGGAGC	42+1p
4/2	6480	GGTATGTAAGTAAAACCAG	6486	CATAAGGAAAAGTAAGCAATG	4
7	6482	CTCTTAATAAAGAAAGGTGCAAAGAA	6488	TAGTCCACCTGTACTTGGGCCG	6
7	6593	CTGATTCATAGCCTCGTAtAG	6613	GCTCAGAGTTTACCAAGAGAG	6+32
7	6481	CTTAATAAAGAAAGATGTAATAAGT	6487	GTTGTTCCAGGCATACTCGCA	2
7	6594	CCAGTAGGTCCTCTGTAAGAC	6614	CCAATGTCGACCCAGACGAG	32+77
7	6595	CAACCACCAGATTTGATGTTT	6615	GAGATTCGCCAAGCAGACGTC	77+59
8	6596	CATAAATTTGATCTTAGCATC	6616	GGACAACGTGGATAGCAAGGAC	50+22
8/15	6520	GTTATTTTCGTTCCGGTCTCAAGG	6528	CTGTAAGGATTATTTGGTCAAACCTC	27+15
8/15	6551	CTGTGATCCAAAGGCTGACTTG	6552	GTATACTACCTTATTATATGTATTAC	27+15
10	6598	GGAGAATATTGACAGTTACAC	6618	GTGAAAGTTCTTTGCAAGATG	24+23
10	6599	GGATTGCAGACCATTTTCATC	6619	GAATTTTCGTTATTCCTACCTTC	25+37
10	6600	CAGATTTCCAAATTAATG	6620	GAAGAAGCTGCCATTTCCG	37+28
11	6601	CTCGAAGACAGTTCATCGTATG	6621	CTGTGTGTTCCGTAGTTCACC	53+10
12	6602	GATGACCGTAAATGCTGCTTG	6622	CGAACGACTTGTGACGACGC	5+40
13	6517	GGTGATACGGATGGTAATGGGCATCG	6526	CATTGCTACCTCTACTAAGGTT	39+51
13	6604	CTGGTGGGGCTGTGTGGATGC	6624	CTACCCGTAATCAAGTTGCC	11+41
13	6515	GCAAGTAATTCGAATTAATGG	6523	CTATTGGGTGTACCGAGTATCCTG	41+47
13	6517	GGTGATACGGATGGTAATGGGCATCG	6525	CATTGCCACCTCCACCAACGTC	39+30
13	6548	CCGTTCTACCTGAACTACGAG	6549	TCACGACTTATAGCTGCAATTAATCAC	39+30
13	6605	CCATTGTTGACCTGATTCTG	6625	GATGAAGGCCTTCGACCGTC	30+16
13	6515	GCAAGTAATTCGAATTAATGG	6524	CTTTATACGTCGCTCCCTCAG	16+47
14	6606	CAGCGAAGTGGAAGATGACC	6626	GAACATCAAGGCTTTGGACC	46+14
14	6607	GACATTGTCTTGTGGAGCC	6627	GCAATGATAAGGTGTTCTTC	14+36
15	6608	GACGAAGACAGTTAGCTTTAC	6628	GAGCGGACCATTGCAAGTGG	44+17
15	6519	gtcgctgtcgaagtcaagaacgc	6527	GTTGGGGACGAGTCGCCTTGAG	17+15
15	6550	CAGAATCCAAGGTCCAAACTACG	6528	CTGTAAGGATTATTTGGTCAAACCTC	17+15
15/8	6609	GCCATCTCATTTAGCACCAGC	6629	GTCACCATCTCTCATTCCAAG	9+43
16	6521	GCACCAGCAGAAGAGTTAGTC	6529	TGAGTCAGAATCATCAGCGGCAGAAG	18+20
16	6521	GCACCAGCAGAAGAGTTAGTC	6530	GGAGTCGAGTCGTTAGCAGCAGGCA	18+26
16	6522	GAAAGTGTGTGGCAGGATTG	6531	CTCTTTCTCGTTATTCAGATTG	20+52