

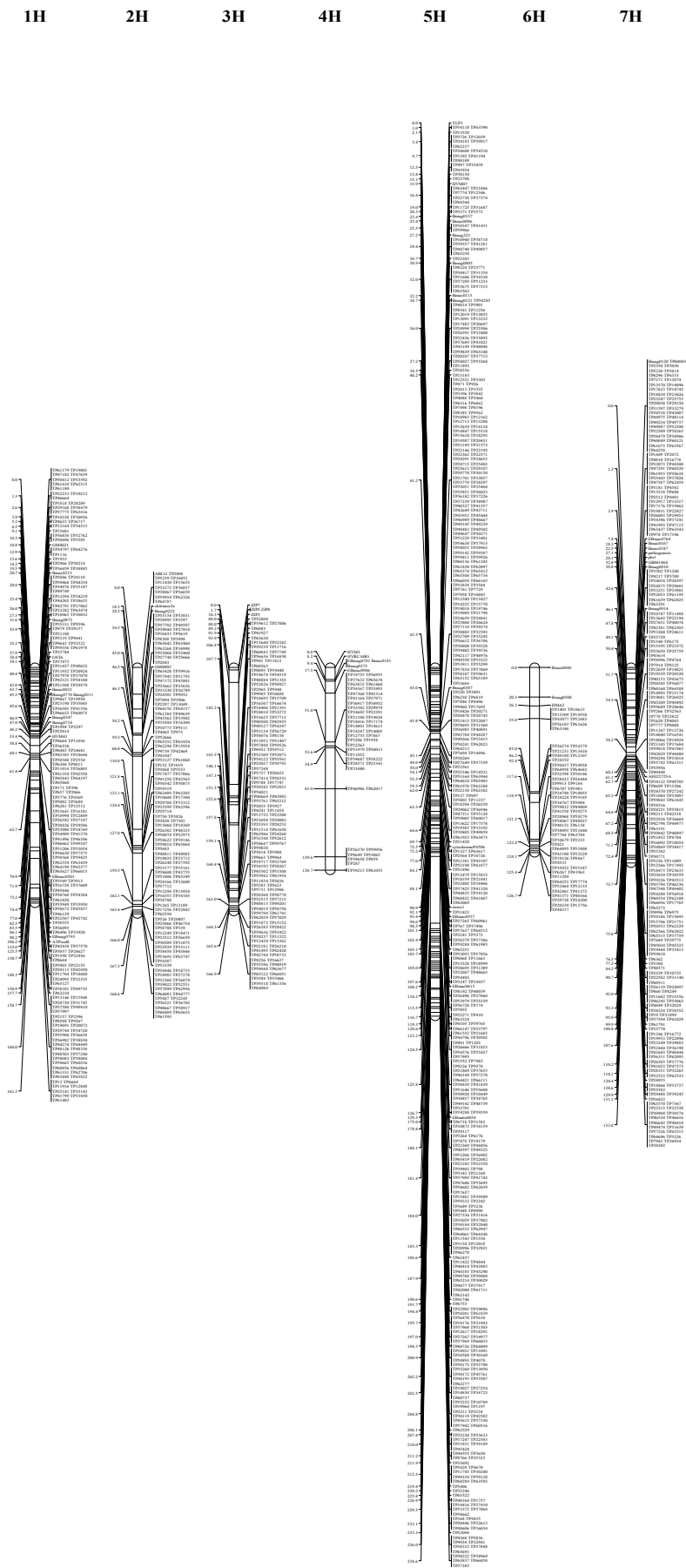


Figure S1. Genetic linkage groups of the Suyinmai 2 x Weisuobuzhi DH population. Marker distance in cM is on the left of the chromosome and marker name is on the right of the chromosome.

	10	20	30	40	50	60	70
1	ATGTCCTTGTGGGGGATGTGCAGCAAGCGTTAAACGCATTTTGGAGAATGAGCCCCAGGTGGTGTCCGCAACTGTC						
1	M S C G G C A A S V K R I L E N E P Q V V S A T V						
	85	95	105	115	125	135	145
76	AATCTTGCCACCGAGATGGCAGTTGTGTGGGCTGTGCCAGAAGATAGAGCTGTACAAGATTGGAAACTGCAGTTG						
26	N L A T E M A V V W A V P E D R A V Q D W K L Q L						
	160	170	180	190	200	210	220
151	GGTGAGAAGCTCGCTAGTCAGTTGACACATGTGGGTACAAATCCAGCCAGCGAGATTCTTCAAAGTCAGTTCA						
51	G E K L A S Q L T T C G Y K S S Q R D S S K V S S						
	235	245	255	265	275	285	295
226	CAGAATGTTTTCGAAAGAAAGATGGGCGAAAACTGCAAATCTGAAGCAAAGTGGTCGAGAACTGCTGTATCT						
76	Q N V F E R K M G E K L Q N L K Q S G R E L A V S						
	310	320	330	340	350	360	370
301	TGGGCACTATGTGCTGTTTGCCTACTGGGACATATTTCTCATCTCTTTGGAGTTAATGCACCATTGATGCACCTG						
101	W A L C A V C L L G H I S H L F G V N A P L M H L						
	385	395	405	415	425	435	445
376	TTTCATTCCACTGGATTCCATTTGTCTCTCTCAATATTTACATTTATTGGGCCTGGCCGAAGACTAATTATCGAT						
126	F H S T G F H L S L S I F T F I G P G R R L I I D						
	460	470	480	490	500	510	520
451	GGATTAAAGAGTCTATTCAAGGGTTCTCCAAACATGAATACATTGGTTGGTTTAGGTGCTCTGTCATCTTTTGCT						
151	G L K S L F K G S P N M N T L V G L G A L S S F A						
	535	545	555	565	575	585	595
526	GTCAGCTCAGTTGCAGCCTTCATTCCAAAACCTGGGATGGAAGACATTTTTTGAGGAACCAATTATGTTGATAGCT						
176	V S S V A A F I P K L G W K T F F E E P I M L I A						
	610	620	630	640	650	660	670
601	TTTGTCTTCTAGGGAAGAATCTTGAGCAGAGGGCGAAGCTAAAAGCTGCTAGTGATATGACCGGATTACTCAAT						
201	F V L L G K N L E Q R A K L K A A S D M T G L L N						
	685	695	705	715	725	735	745
676	ATACTTCCATCAAAAGCACGCCTAATGGTGGATAACGATGCTGAGCAATCATCATTACAGAGGTCCCATGTGGT						
226	I L P S K A R L M V D N D A E Q S S F T E V P C G						
	760	770	780	790	800	810	820
751	ACTCTTGCTGTTGGGGACTATATATTAGTGCTGCCTGGGGACCGCATTCCAGCCGATGGACTTGTGAAAGCTGGA						
251	T L A V G D Y I L V L P G D R I P A D G L V K A G						
	835	845	855	865	875	885	895
826	AGAAGTACAGTTGACGAGTCAAGTTTGACAGGTGAACCTATGCCGGTAACTAAGATTGCAGGGGCAGAAGTATCA						
276	R S T V D E S S L T G E P M P V T K I A G A E V S						
	910	920	930	940	950	960	970
901	GCGGGGAGCATTAAATTTAAACGGTAAACTGACAGTTGAAGTTCGACGACCTGGCGGTGAGACTGTCTGTCTGAC						
301	A G S I N L N G K L T V E V R R P G G E T V M S D						
	985	995	1005	1015	1025	1035	1045
976	ATACTTCACTTAGTGGAAGAAGCACAGACAAGGGAAGCCCTGTTCAACGATTAGCTGACAAGGTTGCTGGGAAC						
326	I L H L V E E A Q T R E A P V Q R L A D K V A G N						
	1060	1070	1080	1090	1100	1110	1120
1051	TTTACATATGGTGTTATGGCGCTTTCTTCTGCTACCTTTATGTTCTGGAGTATTTTTGGTTTCACTTGTACCT						
351	F T Y G V M A L S S A T F M F W S I F G S Q L V P						
	1135	1145	1155	1165	1175	1185	1195
1126	GCTGCTATCCAGCAGGGAAGTGCAATGTCTCTGGCTTTGCAGCTTTCTTGCAGTGTCTGGTAATTGCTTGCCCA						
376	A A I Q Q G S A M S L A L Q L S C S V L V I A C P						
	1210	1220	1230	1240	1250	1260	1270
1201	TGTGCTCTTGGTCTTGCCACACCCACTGCAGTGCTGGTTGGTACTTCGTTAGGCGCAACGAGAGGACTTCTTTTA						
401	C A L G L A T P T A V L V G T S L G A T R G L L L						

1276	1285	1295	1305	1315	1325	1335	1345
426	CGTGGTGGGGATGTTTTGGAGAAATTCGCGGAAGTTGATGCCATTGTGTTTGACAAGACCGGAACTTTAACAATT						
	R	G	G	D	V	L	E
	K	F	A	E	V	D	A
	I	V	F	D	K	T	G
	T	L	T	I			
1351	1360	1370	1380	1390	1400	1410	1420
451	GGGAAGCCTGTAGTGACAAAAGTAATAGCTTCTCACAGCGAGGGAGGTGTAAATACAAAAGATTACAGGAACAAT						
	G	K	P	V	V	T	K
	V	I	A	S	H	S	E
	G	G	V	N	T	K	D
	Y	R	N	N			
1426	1435	1445	1455	1465	1475	1485	1495
476	GAATGGACAGAAGGTGACGTTCTTAGTTTGGCTGCCGGAGTAGAATCAAATACAAACCACCCACTTGGAAAAGCC						
	E	W	T	E	G	D	V
	L	S	L	A	A	G	V
	E	S	N	T	N	H	P
	L	G	K	A			
1501	1510	1520	1530	1540	1550	1560	1570
501	ATCATGGAAGCTGCCCAGGCTGCCAACTGCATCAATATGAAGGCAAAGGATGGGTCTTTATGGAAGAACCAGGG						
	I	M	E	A	A	Q	A
	A	A	N	C	I	N	M
	K	A	K	D	G	S	F
	M	E	E	P	G		
1576	1585	1595	1605	1615	1625	1635	1645
526	TCTGGTGTGTGGCTACGATTGGTGA AAAACAGGTTTCGGTTGGGACATTAGACTGGATTAGGAGGCATGGTGT						
	S	G	A	V	A	T	I
	G	E	K	Q	V	S	V
	G	T	L	D	W	I	R
	R	H	G	V			
1651	1660	1670	1680	1690	1700	1710	1720
551	GTTTCGTGAACCATTTCTGAAGCAGAAAAATTTGGTCAGTCTGTTGCATATGTAGCAGTTGACGGTACTCTAGCT						
	V	R	E	P	F	P	E
	A	E	N	F	G	Q	S
	V	A	Y	V	A	V	D
	G	T	L	A			
1726	1735	1745	1755	1765	1775	1785	1795
576	GGTCTTATTTGTTTCGAGGATAAGATCAGAGAAGATTCTCATCAAGTTATCAATGCCCTGTCTAAGCAAGGAATT						
	G	L	I	C	F	E	D
	K	I	R	E	D	S	H
	Q	V	I	N	A	L	S
	K	Q	G	I			
1801	1810	1820	1830	1840	1850	1860	1870
601	AGTGTGTATATGTTATCTGGGGACAAGGAGAGTGCTGCTATGAATGTTGCCTCAATTGTTGGCATTTCAGTTAGAC						
	S	V	Y	M	L	S	G
	D	K	E	S	A	A	M
	N	V	A	S	I	V	G
	I	Q	L	D			
1876	1885	1895	1905	1915	1925	1935	1945
626	AAGGTGATTCTGAAGTTAAACCACACGAGAAAAAGAAGTTTCATATCTGAACCTTCAAAGGAGCACAAATTAGTT						
	K	V	I	S	E	V	K
	P	H	E	K	K	K	F
	I	S	E	L	Q	K	E
	H	K	L	V			
1951	1960	1970	1980	1990	2000	2010	2020
651	GCCATGGTTGGTGATGGCATTAAATGATGCTGCAGCCCTAGCTTTAGCTGACGTTGGAATTGCAATGGGTGGAGGT						
	A	M	V	G	D	G	I
	N	D	A	A	A	L	A
	L	A	L	A	D	V	G
	I	A	M	G	G	G	
2026	2035	2045	2055	2065	2075	2085	2095
676	GTTGGTGCAGCTAGTGACGTATCTTCAGTTGTTCTCATGGGTAATAGGTTATCTCAGCTTGTGATGCTTTAGAG						
	V	G	A	A	S	D	V
	S	S	V	V	L	M	G
	N	R	L	S	Q	L	V
	D	A	L	E			
2101	2110	2120	2130	2140	2150	2160	2170
701	TTAAGTAAAGAAACCATGAGAACAGTGAAGCAAAATCTTTGGTGGGCTTTTCTGTATAACATTGTTGGGCTACCC						
	L	S	K	E	T	M	R
	T	V	K	Q	N	L	W
	W	A	F	L	Y	N	I
	V	G	L	P			
2176	2185	2195	2205	2215	2225	2235	2245
726	GTTGCTGCTGGAGCATTGCTGCCAGTGACGGGTACGATGCTGACCCCGTCGATAGCTGGAGCACTCATGGGTTTT						
	V	A	A	G	A	L	L
	P	V	T	G	T	M	L
	T	P	S	I	A	G	A
	L	M	G	F			
2251	2260	2270	2280	2290	2300	2310	2320
751	AGTTCAGTCAGCGTGATGGCCAATTCCTTGCTTTTGAGGGCGAGGATGAGTTCAAAGCATCATGTTTCAGAGCAGA						
	S	S	V	S	V	M	A
	N	S	L	L	L	R	A
	R	M	S	S	K	H	H
	V	Q	S	R			
2326	2335	2345	2355	2365	2375	2385	2395
776	CAAAAGCCTCACAACACTATTTCTGATGTGTCAGACGGGGCTGGTGAGGTAGAGCAAAGTTATCCATCAAAATGG						
	Q	K	P	H	N	T	I
	S	D	V	S	D	G	A
	G	E	V	E	Q	S	Y
	P	S	K	W			
2401	2410						
801	AGGAGTACCTGA						
	R	S	T	*			

Figure S2. The nucleotide and amino acid sequences of *HvPAA1*

suinmai2	ATGTCCTTGTGGGGGATGTGCAGCAAGCGTTAAACGCATTTTGGAGAATGAGCCCCAGTGGTGTCCGCAACTGTCAATCTTGCCACCGAGATGGCAGTTGTGTGGGCTGTGCCAAGAAAT	120
weisuobuzhi	ATGTCCTTGTGGGGGATGTGCAGCAAGCGTTAAACGCATTTTGGAGAATGAGCCCCAGTGGTGTCCGCAACTGTCAATCTTGCCACCGAGATGGCAGTTGTGTGGGCTGTGCCAAGAAAT	120
zhenong8	ATGTCCTTGTGGGGGATGTGCAGCAAGCGTTAAACGCATTTTGGAGAATGAGCCCCAGTGGTGTCCGCAACTGTCAATCTTGCCACCGAGATGGCAGTTGTGTGGGCTGTGCCAAGAAAT	120
Consensus	atgtctcttgggggatgtgcagcaagcgttaaacgcattttggagaatgagccccagtggtgtccgcaactgtcaatcttgccaccgagatggcgagttgtgtggcgctgtgccagaagat	
suinmai2	AGAGCTGTACAAGATTGGAACCTGCAGTTGGGTGAGAAGCTCGCTAGTCAGTTGACAAACATGTGGGTACAAATCCAGCCAGCGAGATTTCTTCAAAAGTCAGTTACACAGAATGTTTTCGAA	240
weisuobuzhi	AGAGCTGTACAAGATTGGAACCTGCAGTTGGGTGAGAAGCTCGCTAGTCAGTTGACAAACATGTGGGTACAAATCCAGCCAGCGAGATTTCTTCAAAAGTCAGTTACACAGAATGTTTTCGAA	240
zhenong8	AGAGCTGTACAAGATTGGAACCTGCAGTTGGGTGAGAAGCTCGCTAGTCAGTTGACAAACATGTGGGTACAAATCCAGCCAGCGAGATTTCTTCAAAAGTCAGTTACACAGAATGTTTTCGAA	240
Consensus	agagctgtacaagattggaaactgcagttgggtgagaagctcgctagtcagttgacaacatgtgggtacaaatccagccagcgagattcttcaaaagtcagttcacagaatgttttcgaa	
suinmai2	AGAAAGATGGGCGAAAAACTGCAAAATCTGAAGCAAAGTGGTCGAGAATCTGCTGTATCTTTGGGCACTATGTGCTGTTTGCCCTACTGGGACATATTTCTCATCTCTTTGGAGTTAATGCA	360
weisuobuzhi	AGAAAGATGGGCGAAAAACTGCAAAATCTGAAGCAAAGTGGTCGAGAATCTGCTGTATCTTTGGGCACTATGTGCTGTTTGCCCTACTGGGACATATTTCTCATCTCTTTGGAGTTAATGCA	360
zhenong8	AGAAAGATGGGCGAAAAACTGCAAAATCTGAAGCAAAGTGGTCGAGAATCTGCTGTATCTTTGGGCACTATGTGCTGTTTGCCCTACTGGGACATATTTCTCATCTCTTTGGAGTTAATGCA	360
Consensus	agaaagatgggcgaaaaactgcaaaatctgaagcaaagtggctcgagaacttgcgtatcttgggcactatgtgctgtttgcccactgaggacatatttctcatctcttggaggttaatgca	
suinmai2	CCATTGATGCACCTGTTTTCATTCCACTGGATTCCATTGTCTCTCTCAATATTTACATTTATTGGGCCCTGGCCGAAGACTAATTATCGATGGATTAAAGAGTCTATTCAAGGGTTCTCCA	480
weisuobuzhi	CCATTGATGCACCTGTTTTCATTCCACTGGATTCCATTGTCTCTCTCAATATTTACATTTATTGGGCCCTGGCCGAAGACTAATTATCGATGGATTAAAGAGTCTATTCAAGGGTTCTCCA	480
zhenong8	CCATTGATGCACCTGTTTTCATTCCACTGGATTCCATTGTCTCTCTCAATATTTACATTTATTGGGCCCTGGCCGAAGACTAATTATCGATGGATTAAAGAGTCTATTCAAGGGTTCTCCA	480
Consensus	ccattgatgcacctgttttcatttccactggattccatttgcctctctcaatatttacatttattgggctcgccgaagactaattatcgatggatttaagagtcatttcaagggtttctcca	
suinmai2	AACATGAATACATTGGTTGGTTTAGGTGCTCTGTCACTTTTGTCTGCAGCTCAGTTGCAGCCTTCATTCCAAAACCTGGGATGGAAGACATTTTGTGAGGAACCAATTATGTGTATAGCT	600
weisuobuzhi	AACATGAATACATTGGTTGGTTTAGGTGCTCTGTCACTTTTGTCTGCAGCTCAGTTGCAGCCTTCATTCCAAAACCTGGGATGGAAGACATTTTGTGAGGAACCAATTATGTGTATAGCT	600
zhenong8	AACATGAATACATTGGTTGGTTTAGGTGCTCTGTCACTTTTGTCTGCAGCTCAGTTGCAGCCTTCATTCCAAAACCTGGGATGGAAGACATTTTGTGAGGAACCAATTATGTGTATAGCT	600
Consensus	aaatgaatacatttggttggttttaggtgctctgtcaatttgcctgcacagctcagttgcagccttattccaaaactgggattggaagacatttttggaggaaccaattatgttgtatagct	
suinmai2	TTTGTCTCTTAGGGAAGAACTCTGAGCAGAGGGCGAAGCTAAAAAGCTGCTAGTGATATGACCGGATTACTCAATATACTTCCATCAAAAGCAGCGCTAATGGTGGATAATGATGCTGAG	720
weisuobuzhi	TTTGTCTCTTAGGGAAGAACTCTGAGCAGAGGGCGAAGCTAAAAAGCTGCTAGTGATATGACCGGATTACTCAATATACTTCCATCAAAAGCAGCGCTAATGGTGGATAATGATGCTGAG	720
zhenong8	TTTGTCTCTTAGGGAAGAACTCTGAGCAGAGGGCGAAGCTAAAAAGCTGCTAGTGATATGACCGGATTACTCAATATACTTCCATCAAAAGCAGCGCTAATGGTGGATAATGATGCTGAG	720
Consensus	tttgtctcttagggaagaactctgagcagagggcgaaagctaaaaagctgctagtgtatgacccgattactcaatatacttccatcaaaagcagcgctaatgggtggataatgatgctgag	
suinmai2	CAATCATCATTACAGAGGTCCTCATGTGTTACTCTTGTCTTTGGGCACTATATATTAGTGCTGCCTGGGGACCGCATTCAGCCGATGGACTTGTGAAAGCTGGAAGAAGTACAGTTGAC	840
weisuobuzhi	CAATCATCATTACAGAGGTCCTCATGTGTTACTCTTGTCTTTGGGCACTATATATTAGTGCTGCCTGGGGACCGCATTCAGCCGATGGACTTGTGAAAGCTGGAAGAAGTACAGTTGAC	840
zhenong8	CAATCATCATTACAGAGGTCCTCATGTGTTACTCTTGTCTTTGGGCACTATATATTAGTGCTGCCTGGGGACCGCATTCAGCCGATGGACTTGTGAAAGCTGGAAGAAGTACAGTTGAC	840
Consensus	caatcatcattacagaggtcccatgtgttactcttgcgttggggactatatattagtgctcgttggggaccgatccagccgatggacttgtgaagctggaagaagtacagttgac	
suinmai2	GAGTCAAGTTTGACAGGTGAACCTATGCCGGTAACTAAGATTGAGGGGCGAAGATATCAGCGGGGAGCATAATTAAACGGTAAACTGACAGTTGAAGTTCGACGACCTGGCGGTGAG	960
weisuobuzhi	GAGTCAAGTTTGACAGGTGAACCTATGCCGGTAACTAAGATTGAGGGGCGAAGATATCAGCGGGGAGCATAATTAAACGGTAAACTGACAGTTGAAGTTCGACGACCTGGCGGTGAG	960
zhenong8	GAGTCAAGTTTGACAGGTGAACCTATGCCGGTAACTAAGATTGAGGGGCGAAGATATCAGCGGGGAGCATAATTAAACGGTAAACTGACAGTTGAAGTTCGACGACCTGGCGGTGAG	960
Consensus	gagtcaagtttgacaggtgaacctatgccggtaacattagattgcagggcgagaagtatcagcggggagcatlaatttaaacggttaactgcacagtttgaagttcgacgacctggcggtgag	
suinmai2	ACTGTCATGTCTGACATACTTCACTTAGTGGAAGAAGCAGACAGAGGGAAGCCCTGTTCACCGATTAGCTGACAAAGTTGCTGGGAACCTTTACATATGGTGTATTGGCGCTTTCTTCT	1080
weisuobuzhi	ACTGTCATGTCTGACATACTTCACTTAGTGGAAGAAGCAGACAGAGGGAAGCCCTGTTCACCGATTAGCTGACAAAGTTGCTGGGAACCTTTACATATGGTGTATTGGCGCTTTCTTCT	1080
zhenong8	ACTGTCATGTCTGACATACTTCACTTAGTGGAAGAAGCAGACAGAGGGAAGCCCTGTTCACCGATTAGCTGACAAAGTTGCTGGGAACCTTTACATATGGTGTATTGGCGCTTTCTTCT	1080
Consensus	actgtcatgtctgacatacttcaacttagtggagaagcagacagaaagggaagccctgttcaacgattagctgacaagttgctgtgggaactttacatatggtgttatggcgctttcttct	
suinmai2	GCTACCTTTATGTTCTGGAGTATTTTGGTTTCACAACTTGTACCTGCTGCTATCCAGCAGGGAAGTGAATGTCTCTGGCTTTGCAGCTTTCTTGCAGTGTCTTGGTAATTGCTTGCCCA	1200
weisuobuzhi	GCTACCTTTATGTTCTGGAGTATTTTGGTTTCACAACTTGTACCTGCTGCTATCCAGCAGGGAAGTGAATGTCTCTGGCTTTGCAGCTTTCTTGCAGTGTCTTGGTAATTGCTTGCCCA	1200
zhenong8	GCTACCTTTATGTTCTGGAGTATTTTGGTTTCACAACTTGTACCTGCTGCTATCCAGCAGGGAAGTGAATGTCTCTGGCTTTGCAGCTTTCTTGCAGTGTCTTGGTAATTGCTTGCCCA	1200
Consensus	gctacctttatgttctggagattttttggttcacaacttgtacctgtcgtctatccagcaggggaagtgaatgtctctggccttgacgcttcttgcagttgttctggaattgcttgccca	
suinmai2	TGTGCTCTTGGTCTTGCCACACCCACTGCAGTGCTGGTTGGTACTTCGTTAGGTGCAACGAGAGGACTTCTTTTACGTGGTGGGGATGTTTGGAGAAATTCGCGGAAGTTGATGCCATT	1320
weisuobuzhi	TGTGCTCTTGGTCTTGCCACACCCACTGCAGTGCTGGTTGGTACTTCGTTAGGTGCAACGAGAGGACTTCTTTTACGTGGTGGGGATGTTTGGAGAAATTCGCGGAAGTTGATGCCATT	1320
zhenong8	TGTGCTCTTGGTCTTGCCACACCCACTGCAGTGCTGGTTGGTACTTCGTTAGGTGCAACGAGAGGACTTCTTTTACGTGGTGGGGATGTTTGGAGAAATTCGCGGAAGTTGATGCCATT	1320
Consensus	tgtgctcttggctcttgccacacccactgcagtgctggttggtaacttcgttaggtgcaacgagaggacttctttacgtggtggggatgtttggagaaattcgcggaagttgatgccatt	
suinmai2	GTGTTTGACAAGACCGGAACCTTAAACAATTGGGAAGCCTGTAGTGACAAAAGTAATAGCTTCTCACAGCAGGGGAGGTGTAATAACAAAAGATTACAGGAACAATGAATGGACAGAAGGT	1440
weisuobuzhi	GTGTTTGACAAGACCGGAACCTTAAACAATTGGGAAGCCTGTAGTGACAAAAGTAATAGCTTCTCACAGCAGGGGAGGTGTAATAACAAAAGATTACAGGAACAATGAATGGACAGAAGGT	1440
zhenong8	GTGTTTGACAAGACCGGAACCTTAAACAATTGGGAAGCCTGTAGTGACAAAAGTAATAGCTTCTCACAGCAGGGGAGGTGTAATAACAAAAGATTACAGGAACAATGAATGGACAGAAGGT	1440
Consensus	gtgtttgacaagaccggaactttaacaattgggaagcctgtagtgcacaaagttaatagcttctcacagcgaggagggtgtaataacaaaagattacaggaacaatgaatggacagaaggt	
suinmai2	GACGTTCTTAGTTTGGCTGCCGAGTAGAATCAAAATCAAAACCACCCACTTGAAAAGGCCATCATGGAAGCTGCCAGGCTGCCAACTGCATCAATATGAAGGCAAAGGATGGGTCTCTT	1560
weisuobuzhi	GACGTTCTTAGTTTGGCTGCCGAGTAGAATCAAAATCAAAACCACCCACTTGAAAAGGCCATCATGGAAGCTGCCAGGCTGCCAACTGCATCAATATGAAGGCAAAGGATGGGTCTCTT	1560
zhenong8	GACGTTCTTAGTTTGGCTGCCGAGTAGAATCAAAATCAAAACCACCCACTTGAAAAGGCCATCATGGAAGCTGCCAGGCTGCCAACTGCATCAATATGAAGGCAAAGGATGGGTCTCTT	1560
Consensus	gacgttcttagtttggctgccggagtagaatcaaatcaaaaccaccacttggaaaagccatcatggaagctgccaggctgccaaactgcatcaatatgaaggcaaaggatgggtccttt	
suinmai2	ATGGAAGAACCAGGGTCTGGTGCTGTGGCTACGATTGGTGA AAAACAGGTTTCGGTTGGGACATTAGACTGGATTAGGAGGCATGGTGTGTTCTGTGAACCAATTTCTGAAGCAGAAAAAT	1680
weisuobuzhi	ATGGAAGAACCAGGGTCTGGTGCTGTGGCTACGATTGGTGA AAAACAGGTTTCGGTTGGGACATTAGACTGGATTAGGAGGCATGGTGTGTTCTGTGAACCAATTTCTGAAGCAGAAAAAT	1680
zhenong8	ATGGAAGAACCAGGGTCTGGTGCTGTGGCTACGATTGGTGA AAAACAGGTTTCGGTTGGGACATTAGACTGGATTAGGAGGCATGGTGTGTTCTGTGAACCAATTTCTGAAGCAGAAAAAT	1680
Consensus	atggaagaaccagggtctggtgctgtggctacgattggtgaaaaacaggttccggttgggacattagactggattaggaggcatggtgtgttctgtgaaccatttcttgaagcagaaaaat	
suinmai2	TTTGGTCAGTCTGTGCATATGTAGCAGTTGACGGTACTCTAGCTGGTCTTATTGTTTTCGAGGATAAGATCAGAGAAGATTCTCATCAAGTTATCAATGCCCTGTCTAAGCAAGGAATT	1800
weisuobuzhi	TTTGGTCAGTCTGTGCATATGTAGCAGTTGACGGTACTCTAGCTGGTCTTATTGTTTTCGAGGATAAGATCAGAGAAGATTCTCATCAAGTTATCAATGCCCTGTCTAAGCAAGGAATT	1800
zhenong8	TTTGGTCAGTCTGTGCATATGTAGCAGTTGACGGTACTCTAGCTGGTCTTATTGTTTTCGAGGATAAGATCAGAGAAGATTCTCATCAAGTTATCAATGCCCTGTCTAAGCAAGGAATT	1800
Consensus	tttggctcagctctgtgcataatgtagcagttgacggtaactctagctggtcttatttggtttcgaggataagatcagagaagattctcatcaagttatcaatgccctgtctaaagcaaggaatt	
suinmai2	AGTGTGTATATGTTATCTGGGGACAAGGAGAGTGTGCTATGAATGTTGCCTCAATTGTTGGCAATTCAGTTAGACAAAGTGATTCTGAAGTTAAACCACACGAGAAAAAGAGTTTATA	1920
weisuobuzhi	AGTGTGTATATGTTATCTGGGGACAAGGAGAGTGTGCTATGAATGTTGCCTCAATTGTTGGCAATTCAGTTAGACAAAGTGATTCTGAAGTTAAACCACACGAGAAAAAGAGTTTATA	1920
zhenong8	AGTGTGTATATGTTATCTGGGGACAAGGAGAGTGTGCTATGAATGTTGCCTCAATTGTTGGCAATTCAGTTAGACAAAGTGATTCTGAAGTTAAACCACACGAGAAAAAGAGTTTATA	1920
Consensus	agtgtgtatatgttatctggggacaaggagagtgctgctatgaatgttgcctcaattgttggcattcagtttagacaaggtgatttctgaagttaaaccacacgagaaaaagagttcata	
suinmai2	TCTGAACCTTCAAAAGGAGCACA AATTAGTTGCCATGGTTGGTGATGGCATTAAATGATGCTGCAGCCCTAGCTTTAGCTGACGTTGGAATTGCAATGGGTGGAGGTGTTGGTGCAGCTAGT	2040
weisuobuzhi	TCTGAACCTTCAAAAGGAGCACA AATTAGTTGCCATGGTTGGTGATGGCATTAAATGATGCTGCAGCCCTAGCTTTAGCTGACGTTGGAATTGCAATGGGTGGAGGTGTTGGTGCAGCTAGT	2040
zhenong8	TCTGAACCTTCAAAAGGAGCACA AATTAGTTGCCATGGTTGGTGATGGCATTAAATGATGCTGCAGCCCTAGCTTTAGCTGACGTTGGAATTGCAATGGGTGGAGGTGTTGGTGCAGCTAGT	2040
Consensus	tctgaacctcaaaaggagcacaaattagttgccatggttgggtgatggcattaatgatgctgcagccctagcttttagctgacgttggaaattgcaatgggtggaggtgttgggtgcagctagt	
suinmai2	GACGTATCTTCAGTTGTTCTCATGGGTAATAGGTTATCTCAGCTTGTGTATGCTTTAGAGTTAAGTAAAGAAACCATGAGAACAGTGAAGCAAAATCTTTGGTGGGCTTTTCTGTATAAC	2160
weisuobuzhi	GACGTATCTTCAGTTGTTCTCATGGGTAATAGGTTATCTCAGCTTGTGTATGCTTTAGAGTTAAGTAAAGAAACCATGAGAACAGTGAAGCAAAATCTTTGGTGGGCTTTTCTGTATAAC	2160
zhenong8	GACGTATCTTCAGTTGTTCTCATGGGTAATAGGTTATCTCAGCTTGTGTATGCTTTAGAGTTAAGTAAAGAAACCATGAGAACAGTGAAGCAAAATCTTTGGTGGGCTTTTCTGTATAAC	2160
Consensus	gacgtatcttcagttgttctcatgggtaataggttatctcagcttgtgtatgcttttagagtttaagtaaagaaccatgagaacagtgaaagcaaaatctttggtgggcttttctgtataac	
suinmai2	ATTGTTGGGCTACCCGTTGCTGCTGGAGCATTGCTGCCAGTGACGGGTACGATGCTGACCCCGTCGATAGCTGGAGCACTCATGGGTTTATGTTCACTCAGCGCTGATGGCCAAATTCCTTG	2280
weisuobuzhi	ATTGTTGGGCTACCCGTTGCTGCTGGAGCATTGCTGCCAGTGACGGGTACGATGCTGACCCCGTCGATAGCTGGAGCACTCATGGGTTTATGTTCACTCAGCGCTGATGGCCAAATTCCTTG	2280
zhenong8	ATTGTTGGGCTACCCGTTGCTGCTGGAGCATTGCTGCCAGTGACGGGTACGATGCTGACCCCGTCGATAGCTGGAGCACTCATGGGTTTATGTTCACTCAGCGCTGATGGCCAAATTCCTTG	2280
Consensus	attgttgggctaccggttgcctgctggagcattgctgccagtgacgggtacgatgctgaccccgctcgatagctggagcactcatgggttttagttcagtcagcgctgatggcaattccttg	
suinmai2	CTTTTGAGGGCGAGGATGAGTTCAAAAGCATCATGTTTCAGAGCAGACAAAAGCCTCACAACACTATTTCTGATGTGTGACAGCGGGCTGGTGAGGTAGAGCAAAGTTATCCATCAAAATGG	2400
weisuobuzhi	CTTTTGAGGGCGAGGATGAGTTCAAAAGCATCATGTTTCAGAGCAGACAAAAGCCTCACAACACTATTTCTGATGTGTGACAGCGGGCTGGTGAGGTAGAGCAAAGTTATCCATCAAAATGG	2400
zhenong8	CTTTTGAGGGCGAGGATGAGTTCAAAAGCATCATGTTTCAGAGCAGACAAAAGCCTCACAACACTATTTCTGATGTGTGACAGCGGGCTGGTGAGGTAGAGCAAAGTTATCCATCAAAATGG	2400
Consensus	cttttgagggcgaggatgagttcaaaagcatcatgttccagagcagacaaaagcctcacacactatttctgatgtgtcagacggygctggtgaggtagagcaagttatccatcaaaatgg	
suinmai2	AGGAGTACCTG	2411
weisuobuzhi	AGGAGTACCTG	2411
zhenong8	AGGAGTACCTG	2411
Consensus	aggagtacctg	

suyinmai2	MSCGGCAASVKRILENEPQVVSATVNLATEMAVWVAVPEDRAVDWKLQQLGEKLASQLTTCGYKSSQRDSSKVSSQNVFE	80
weisuobuzhi	MSCGGCAASVKRILENEPQVVSATVNLATEMAVWVAVPEDRAVDWKLQQLGEKLASQLTTCGYKSSQRDSSKVSSQNVFE	80
zhenong8	MSCGGCAASVKRILENEPQVVSATVNLATEMAVWVAVPEDRAVDWKLQQLGEKLASQLTTCGYKSSQRDSSKVSSQNVFE	80
Consensus	mscggcaasvkrilenepqvvsatvnlatemavwvavpedravqdwlqlgeklasqlttcgykssqrdsskvssqnvfe	
suyinmai2	RKMGEKLQNLKQSGRELAVSWALCAVCLLGHIHSHLFGVNAPLMHLFHSTGFHLSLSIFTFIGPGRRLIIDGLKSLFKGSP	160
weisuobuzhi	RKMGEKLQNLKQSGRELAVSWALCAVCLLGHIHSHLFGVNAPLMHLFHSTGFHLSLSIFTFIGPGRRLIIDGLKSLFKGSP	160
zhenong8	RKMGEKLQNLKQSGRELAVSWALCAVCLLGHIHSHLFGVNAPLMHLFHSTGFHLSLSIFTFIGPGRRLIIDGLKSLFKGSP	160
Consensus	rkmgeklqnlkqsgrelavswalcavcllgghishlfgvnaplmhlfhstgfhlslsiftfigpgrrliidglkslfkgs	
suyinmai2	NMNTLVGLGALSSFAVSSVAAFIPKLGWKTFFEEPIMLIAFVLLGKNLEQRAKKAASDMTGLLNILPSKARLMVDNDAE	240
weisuobuzhi	NMNTLVGLGALSSFAVSSVAAFIPKLGWKTFFEEPIMLIAFVLLGKNLEQRAKKAASDMTGLLNILPSKARLMVDNDAE	240
zhenong8	NMNTLVGLGALSSFAVSSVAAFIPKLGWKTFFEEPIMLIAFVLLGKNLEQRAKKAASDMTGLLNILPSKARLMVDNDAE	240
Consensus	nmntlvglgalssfavssvaafipklgwktffleepimliafvllgknleqrakkaasdmgtgllnilpskarlmvndae	
suyinmai2	QSSFTEVPCGTAVGDYILVLPGDRI PADGLVKAGRSTVDESSLTGEPMPTVKIAGAEVSAGSINLNGKLTVEVRRPGGE	320
weisuobuzhi	QSSFTEVPCGTAVGDYILVLPGDRI PADGLVKAGRSTVDESSLTGEPMPTVKIAGAEVSAGSINLNGKLTVEVRRPGGE	320
zhenong8	QSSFTEVPCGTAVGDYILVLPGDRI PADGLVKAGRSTVDESSLTGEPMPTVKIAGAEVSAGSINLNGKLTVEVRRPGGE	320
Consensus	qssftevpcgtlavgdyilvlpgdripadglvkagrstvdessltgepmpvtkiagaevsagsinlngkltvevrrpgge	
suyinmai2	TVMSDILHLVEEAQTREAPVQRLADKVAGNFTYGVMAISSATFMFWSIFGSQVLPAAIQQGSAMSLALQLSCSVLVIACP	400
weisuobuzhi	TVMSDILHLVEEAQTREAPVQRLADKVAGNFTYGVMAISSATFMFWSIFGSQVLPAAIQQGSAMSLALQLSCSVLVIACP	400
zhenong8	TVMSDILHLVEEAQTREAPVQRLADKVAGNFTYGVMAISSATFMFWSIFGSQVLPAAIQQGSAMSLALQLSCSVLVIACP	400
Consensus	tvmsdilhlveeaqtreapvqrladkvagnftygvmaissatfmfwsifgsqvlpaaiqqgsamslalqlscsvliacp	
suyinmai2	CALGLATPTAVLVGTSLGATRGLLLRGGDVLEKFAEVDIAIVFDKGTTLTGKPVVTKVIASHSEGGVNTKDYRNNEWTEG	480
weisuobuzhi	CALGLATPTAVLVGTSLGATRGLLLRGGDVLEKFAEVDIAIVFDKGTTLTGKPVVTKVIASHSEGGVNTKDYRNNEWTEG	480
zhenong8	CALGLATPTAVLVGTSLGATRGLLLRGGDVLEKFAEVDIAIVFDKGTTLTGKPVVTKVIASHSEGGVNTKDYRNNEWTEG	480
Consensus	calglatptavlvgtslgatrgrlllrggdvlekaevdaivfdktgtlttgkpvvtkviashseggvntkdyrnnewteg	
suyinmai2	DVLSLAAGVESNTNHPLGKAIMEAAQAANCINMKAKDGSFMEEPGSGAVATIGEKQVSVGTLDWIRRHGVVREPFPEAEN	560
weisuobuzhi	DVLSLAAGVESNTNHPLGKAIMEAAQAANCINMKAKDGSFMEEPGSGAVATIGEKQVSVGTLDWIRRHGVVREPFPEAEN	560
zhenong8	DVLSLAAGVESNTNHPLGKAIMEAAQAANCINMKAKDGSFMEEPGSGAVATIGEKQVSVGTLDWIRRHGVVREPFPEAEN	560
Consensus	dvlslaagvesntnhplgkaimeaaqaancinmkakdgsfmeeppsgavatiegekqvsvgtldwirrhgvvrepfpeaen	
suyinmai2	FGQSVAYVAVDGTLAGLICFEDKIREDSHQVINALSQKGISVYMLSGDKESAAMNVAIVGIQLDKVISEVKPHEKKKFI	640
weisuobuzhi	FGQSVAYVAVDGTLAGLICFEDKIREDSHQVINALSQKGISVYMLSGDKESAAMNVAIVGIQLDKVISEVKPHEKKKFI	640
zhenong8	FGQSVAYVAVDGTLAGLICFEDKIREDSHQVINALSQKGISVYMLSGDKESAAMNVAIVGIQLDKVISEVKPHEKKKFI	640
Consensus	fgqsvayvavdgtlaglicfedkiredshqvinalskqgisvymllsgdkesaamnvasivgiqldkvisevvphekkkfi	
suyinmai2	SELQKEHKLAMVGDGINDAAALALADVGIAMGGGVGAASDVSSVLMGNRLSQLVDALELSKETMRTVKQNLWWAFLYN	720
weisuobuzhi	SELQKEHKLAMVGDGINDAAALALADVGIAMGGGVGAASDVSSVLMGNRLSQLVDALELSKETMRTVKQNLWWAFLYN	720
zhenong8	SELQKEHKLAMVGDGINDAAALALADVGIAMGGGVGAASDVSSVLMGNRLSQLVDALELSKETMRTVKQNLWWAFLYN	720
Consensus	selqkehklamvgdginndaaalaladvgiamggvggaasdvssvvlmgnrlsqlvdalelsketmrtvkqnlwwaflyn	
suyinmai2	IVGLPVAAGALLPVTGTMLTPSIAGALMGFSSVSMANSLLLRARMSSKHHVQSRQKPHNTISDVSDGAGEVEQSYPSKW	800
weisuobuzhi	IVGLPVAAGALLPVTGTMLTPSIAGALMGFSSVSMANSLLLRARMSSKHHVQSRQKPHNTISDVSDGAGEVEQSYPSKW	800
zhenong8	IVGLPVAAGALLPVTGTMLTPSIAGALMGFSSVSMANSLLLRARMSSKHHVQSRQKPHNTISDVSDGAGEVEQSYPSKW	800
Consensus	ivglpvaagallpvtgtmltpsiagalmgfsssvsmanslllramsskhhvqsrqkphntisdvsdgageveqsypskw	
suyinmai2	RS	802
weisuobuzhi	RS	802
zhenong8	RS	802
Consensus	rs	

Figure S4. Alignment-based analysis of the CDS and amino acid sequences of *HvPAAI* from Suyinmai 2, Weisubuzhi and Zhenong 8. The dark blue represents 100% identity as defined by Mega7.

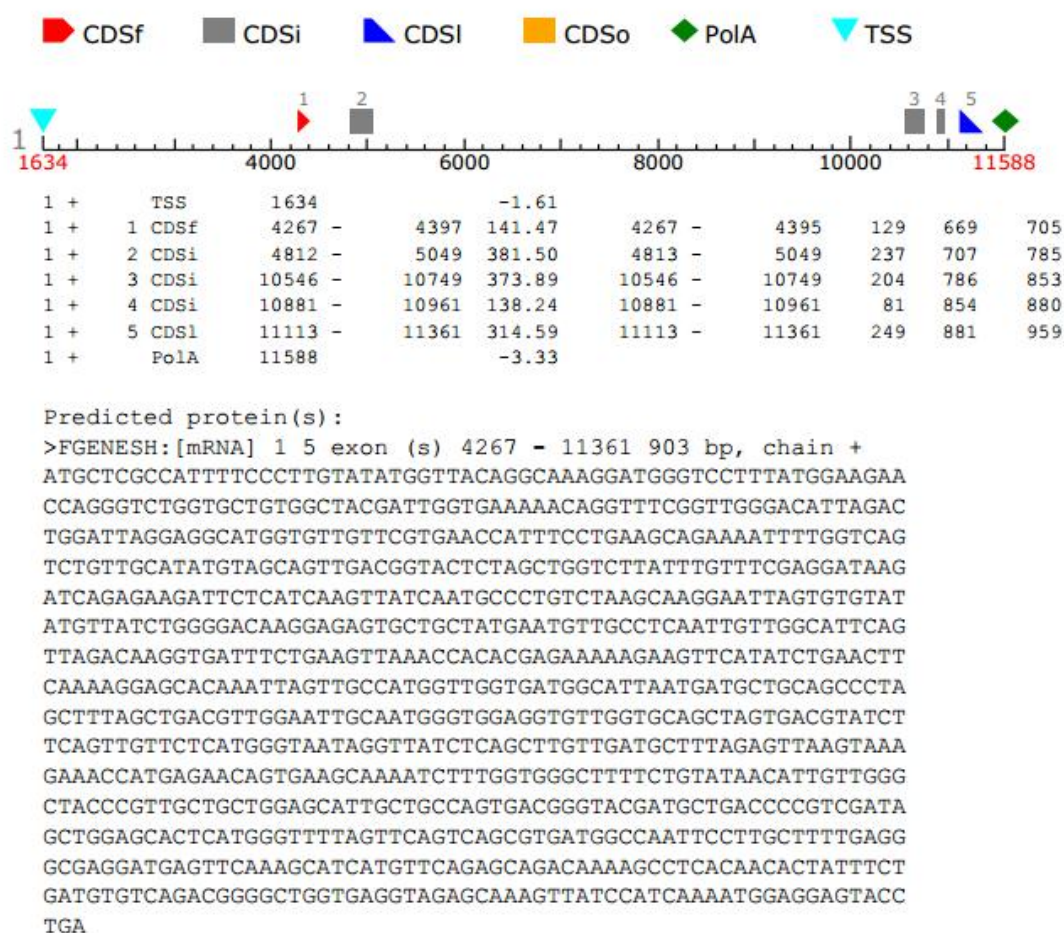


Figure S5 The predicted sequence of *HvPAAL* between the transcription start site and termination site. TSS, transcription start site. CDSf, the first CDS. CDSi, the intermediate CDS. CDSl, the last CDS. PolA, polA tag, the termination of transcription.

Suyinmai_2	GGAAGGTAGGATGGGTCTTTTATGGA..ACCAGGGTCTGGTGCTGTGGC	47
Weisuobuzhi	GGATGGTAGGGATGGGTCTTTTATGGAAG..ACCAGGGTCTGGTGCTGTGGC	50
Template	ATGCTCGCCATTTTCCCTTGTATATGGTTACAGGCAAGGATGGGTCTTTTATGGAAGAACCAGGGTCTGGTGCTGTGGC	80
Consensus	ggatgggtc tttatgga accagggctcggtgctgtggc	
Suyinmai_2	TACGATTGGTGAAAAACAGGTTTCGGTTGGGACATTAGACTGGATTAGGAGGTACACTTGAATTATTTATTTCAATTGTTTG	127
Weisuobuzhi	TACGATTGGTGAAAAACAGGTTTCGGTTGGGACATTAGACTGGATTAGGAGGTACACTTGAATTATTTATTTCAATTGTTTG	130
Template	TACGATTGGTGAAAAACAGGTTTCGGTTGGGACATTAGACTGGATTAGGAGGTACACTTGAATTATTTATTTCAATTGTTTG	160
Consensus	tacgat tgggtaaaacagggttcgggtgggacattagactggattaggaggtacacttgaattatttattcaattgttg	
Suyinmai_2	TCTTAATTAAGACTTGTCTTTTCACTAAGTTGCCAAAGTTTATAGTCGTATTTCCGGTATCAGTTCTGTACTAGTGACA	207
Weisuobuzhi	TCTTAATTAAGACTTGTCTTTTCACTAAGTTGCCAAAGTTTATAGTCGTATTTCCGGTATCAGTTCTGTACTAGTGACA	210
Template	TCTTAATTAAGACTTGTCTTTTCACTAAGTTGCCAAAGTTTATAGTCGTATTTCCGGTATCAGTTCTGTACTAGTGACA	240
Consensus	tcctaaataagacttgttctttcactaagttgccaaagtttgatagtcgtatttccgggtatcagttctgtactagt gaca	
Suyinmai_2	TACTCCCTCCGTTCTTAATATAAGTCTTTTTAGAGATATCAATAGGAGACTATATACGGAGCAAAATGAGTGAATCTAC	287
Weisuobuzhi	TACTCCCTCCGTTCTTAATATAAGTCTTTTTAGAGATATCAATAGGAGACTATATACGGAGCAAAATGAGTGAATCTAC	290
Template	TACTCCCTCCGTTCTTAATATAAGTCTTTTTAGAGATATCAATAGGAGACTATATACGGAGCAAAATGAGTGAATCTAC	320
Consensus	tactccctccggttcctaaataaagtccttttagagatatcaataggagactatatacggagcaaaatgagtgaatctac	
Suyinmai_2	ACTCAAAATTAAGTCTATACATCCATATGTAGTCCCTTAATGAAACCTCTAAAAAGGCTTATATTTAGGAATGGAGGAAG	367
Weisuobuzhi	ACTCAAAATTAAGTCTATACATCCATATGTAGTCCCTTAATGAAACCTCTAAAAAGGCTTATATTTAGGAATGGAGGAAG	370
Template	ACTCAAAATTAAGTCTATACATCCATATGTAGTCCCTTAATGAAACCTCTAAAAAGGCTTATATTTAGGAATGGAGGAAG	400
Consensus	actc aaaaataagtcctatacatccat atgt agt cccctaat gaaacctct aaaaaggcttat atttaggaat ggagggaag	
Suyinmai_2	TATATGTAACTCATTTCTAGCAATACAACCTTTGTTTGGATTATTTGCATCAATTTTCTGCTCCGTTACACTAGCTCCATGT	447
Weisuobuzhi	TATATGTAACTCATTTCTAGCAATACAACCTTTGTTTGGATTATTTGCATCAATTTTCTGCTCCGTTACACTAGCTCCATGT	450
Template	TATATGTAACTCATTTCTAGCAATACAACCTTTGTTTGGATTATTTGCATCAATTTTCTGCTCCGTTACACTAGCTCCATGT	480
Consensus	tatatgttaactcattctagcaatacaactttgtttggattattgcatcaattttctgctccgttacactagctccatgt	
Suyinmai_2	GTAAATTTGTGTGTGCACCGAGGAACGTGCTCACTAGTAAACAAATGTTTTGACAATATCTCAGGCATGGTGTGTTTGG	527
Weisuobuzhi	GTAAATTTGTGTGTGCACCGAGGAACGTGCTCACTAGTAAACAAATGTTTTGACAATATCTCAGGCATGGTGTGTTTGG	530
Template	GTAAATTTGTGTGTGCACCGAGGAACGTGCTCACTAGTAAACAAATGTTTTGACAATATCTCAGGCATGGTGTGTTTGG	560
Consensus	gt aattgttgtgtgcaccgaggaactgtgctcactagt aaacaaatgttttgacaatatctcaggcatgggtgttgttcg	
Suyinmai_2	TGAACCATTTTCTGAAGCAGAAAAATTTTGGTCAGTCTGTTGCATATGTAGCAGTTGACGGTACTCTAGCTGGTCTTATTT	607
Weisuobuzhi	TGAACCATTTTCTGAAGCAGAAAAATTTTGGTCAGTCTGTTGCATATGTAGCAGTTGACGGTACTCTAGCTGGTCTTATTT	610
Template	TGAACCATTTTCTGAAGCAGAAAAATTTTGGTCAGTCTGTTGCATATGTAGCAGTTGACGGTACTCTAGCTGGTCTTATTT	640
Consensus	tgaaccatttctctgaagcagaaaaat tttggtcagtctgttgcatatgtagcagttgacggtagctctagctggctctattt	
Suyinmai_2	GTTTTGAGGATTAAGATCAGAGAAGATTCTCATCAAGTTATCAATGCCCTGTCTAAGCAAGGAATTTAGTGTGTATATGTTA	687
Weisuobuzhi	GTTTTGAGGATTAAGATCAGAGAAGATTCTCATCAAGTTATCAATGCCCTGTCTAAGCAAGGAATTTAGTGTGTATATGTTA	690
Template	GTTTTGAGGATTAAGATCAGAGAAGATTCTCATCAAGTTATCAATGCCCTGTCTAAGCAAGGAATTTAGTGTGTATATGTTA	720
Consensus	gtttcgaggataagatcagagaagattctcatcaagttatcaatgccctgtctaagcaaggaattagtggtgtat atgtta	
Suyinmai_2	TCTGGGGACAAGGAGAGTGCTGCTATGAATGTTGCCCTCAATTGTTGGCATTCAGTTAGACAAGGTAATATCAACTAAAGT	767
Weisuobuzhi	TCTGGGGACAAGGAGAGTGCTGCTATGAATGTTGCCCTCAATTGTTGGCATTCAGTTAGACAAGGTAATATCAACTAAAGT	770
Template	TCTGGGGACAAGGAGAGTGCTGCTATGAATGTTGCCCTCAATTGTTGGCATTCAGTTAGACAAGGTAATATCAACTAAAGT	800
Consensus	tctggggacaaggagagt gctgctatgaatgttgccctcaattgttggcattcagttagacaaggtaatatcaactaaagt	
Suyinmai_2	AAATTTTGTCTTTGCCGATGTGGACATTTTGTCTGGCGAATAGTCCCCTAATAAAACAACAACTTTCTGTAAATATATGA	847
Weisuobuzhi	AAATTTTGTCTTTGCCGATGTGGACATTTTGTCTGGCGAATAGTCCCCTAATAAAACAACAACTTTCTGTAAATATATGA	850
Template	AAATTTTGTCTTTGCCGATGTGGACATTTTGTCTGGCGAATAGTCCCCTAATAAAACAACAACTTTCTGTAAATATATGA	880
Consensus	aaat tttgctttgccgatgtggacattttgttctggcgaatagtcctcgt aataaaacaacaaacttctgt aatat atga	
Suyinmai_2	CATCAAAGTACGAGAATGAACATGTTGCAGGTGCTTGTGCTCCTCTTCTGCTGTTGTCTGACTTCAAGTATGCAGTTTAAA	927
Weisuobuzhi	CATCAAAGTACGAGAATGAACATGTTGCAGGTGCTTGTGCTCCTCTTCTGCTGTTGTCTGACTTCAAGTATGCAGTTTAAA	930
Template	CATCAAAGTACGAGAATGAACATGTTGCAGGTGCTTGTGCTCCTCTTCTGCTGTTGTCTGACTTCAAGTATGCAGTTTAAA	960
Consensus	catcaaagtacgagaatgaacatgttgcagggtgcttgctgcctcttctgctgttgtctgacttcaagtatgcagtttaa	
Suyinmai_2	TTTTTTTATATACATCTTGAAGGTGCACATGAAGAAAAATAAATATGAATTCATCTTTTTCATAAAGATTTTTTTTTTAAT	1007
Weisuobuzhi	TTTTTTTATATACATCTTGAAGGTGCACATGAAGAAAAATAAATATGAATTCATCTTTTTCATAAAGATTTTTTTTTTAAT	1010
Template	TTTTTTTATATACATCTTGAAGGTGCACATGAAGAAAAATAAATATGAATTCATCTTTTTCATAAAGATTTTTTTTTTAAT	1040
Consensus	ttttttat atacatcttagaagggtgcacatgaagaaaaataaatatgaattcatcttttcataaagatttttttttaat	
Suyinmai_2	TTGTGATAAAGTTATGATATTGTTATGTACAGTATCTTTGTAGGAAATACTGAAAAAGGCTTTTCGCCCCGCTTTTATAGAT	1087
Weisuobuzhi	TTGTGATAAAGTTATGATATTGTTATGTACAGTATCTTTGTAGGAAATACTGAAAAAGGCTTTTCGCCCCGCTTTTATAGAT	1090
Template	TTGTGATAAAGTTATGATATTGTTATGTACAGTATCTTTGTAGGAAATACTGAAAAAGGCTTTTCGCCCCGCTTTTATAGAT	1120
Consensus	ttgtcat aaagttatgatattgttatgtacagtatctttgtaggaaatactgaaaaaggcttttcgccccgctttatagat	
Suyinmai_2	AAAGCAAACCAACGAAGCATTAACATCCGACAACAGTCATTAACACCACACACACGCGCACTGAGGTAGCACAAACAGAGGG	1167
Weisuobuzhi	AAAGCAAACCAACGAAGCATTAACATCCGACAACAGTCATTAACACCACACACACGCGCACTGAGGTAGCACAAACAGAGGG	1170
Template	AAAGCAAACCAACGAAGCATTAACATCCGACAACAGTCATTAACACCACACACACGCGCACTGAGGTAGCACAAACAGAGGG	1200
Consensus	aaagcaaacaccgaagcat aacatccgacaacagtcataaacaccacacacgcgcgactgaggt agcacaaacagaggg	

Suyinmai_2	TACAAAGGTTACGCTGTGGGCACAACACAACAGCCCAAAGAAATAGAAACAAACACGGCGGCGTGGCCTGGAGGAGGGAA	1247
Weisuobuzhi	TACAAAGGTTACGCTGTGGGCACAACACAACAGCCCAAAGAAATAGAAACAAACACGGCGGCGTGGCCTGGAGGAGGGAA	1250
Template	TACAAAGGTTACGCTGTGGGCACAACACAACAGCCCAAAGAAATAGAAACAAACACGGCGGCGTGGCCTGGAGGAGGGAA	1280
Consensus	tacaaaggttacgctgtgggcacaacacaacagcccaaagaatagaacaaacacggcggcgtggcctggaggagggaa	
Suyinmai_2	CACTAATCCGGTTCGGAGGTGGCGGAGGTAGCGGGGGCGCAAGCGGAGAGCCATCGCACGAAGACGAGAGATGATGGA	1327
Weisuobuzhi	CACTAATCCGGTTCGGAGGTGGCGGAGGTAGCGGGGGCGCAAGCGGAGAGCCATCGCACGAAGACGAGAGATGATGGA	1330
Template	CACTAATCCGGTTCGGAGGTGGCGGAGGTAGCGGGGGCGCAAGCGGAGAGCCATCGCACGAAGACGAGAGATGATGGA	1360
Consensus	cactaatccggttcgggaggtggcggaggtagcggcggcgcaagcggagagccatcgcacgaagacgagagatgatgga	
Suyinmai_2	GTGATGGCGTCTCGGTCCCGCGAGCGGCTAAGCGGCGCGCAGAGCTGCAGATATCCACACAATTTGAACACTGCGTCAG	1407
Weisuobuzhi	GTGATGGCGTCTCGGTCCCGCGAGCGGCTAAGCGGCGCGCAGAGCTGCAGATATCCACACAATTTGAACACTGCGTCAG	1410
Template	GTGATGGCGTCTCGGTCCCGCGAGCGGCTAAGCGGCGCGCAGAGCTGCAGATATCCACACAATTTGAACACTGCGTCAG	1440
Consensus	gttgatggcgtctcggtcccgcgagcggctaaagcggcggcgagagctgcagatatccacacaatttgaacctgcgtcag	
Suyinmai_2	TAGCACGACGAAGAGGAACACGTTGAATAACAAGTTTTTCCGAACAGTCCACATCGTCCAGGCCAGAACCCTAACCGTC	1487
Weisuobuzhi	TAGCACGACGAAGAGGAACACGTTGAATAACAAGTTTTTCCGAACAGTCCACATCGTCCAGGCCAGAACCCTAACCGTC	1490
Template	TAGCACGACGAAGAGGAACACGTTGAATAACAAGTTTTTCCGAACAGTCCACATCGTCCAGGCCAGAACCCTAACCGTC	1520
Consensus	tagcacgacgaagaggaacacgttgaataacaagtttttccgaacagtcacatcgtccaggccagaaccctaacctgc	
Suyinmai_2	AGCCACCTAGTGTGGCGGACAGATGGTGGCGTAGCCTGGAGTTCCGGCGAAAAGGTGAGGGAAGTTTGTGTGGCACCAGGC	1567
Weisuobuzhi	AGCCACCTAGTGTGGCGGACAGATGGTGGCGTAGCCTGGAGTTCCGGCGAAAAGGTGAGGGAAGTTTGTGTGGCACCAGGC	1570
Template	AGCCACCTAGTGTGGCGGACAGATGGTGGCGTAGCCTGGAGTTCCGGCGAAAAGGTGAGGGAAGTTTGTGTGGCACCAGGC	1600
Consensus	agccacctagtgtggcggacagatggtggcgtagcctggagtccggcgaaaaggtcagggaagtgtgtgtggcaccaggc	
Suyinmai_2	GCCATCGACCACTTCGCGGAAACAACCTAGAGGAATTCGCGGACACGCAAGAGAAGAATATGTGATTCGAGTCTTCTC	1647
Weisuobuzhi	GCCATCGACCACTTCGCGGAAACAACCTAGAGGAATTCGCGGACACGCAAGAGAAGAATATGTGATTCGAGTCTTCTC	1650
Template	GCCATCGACCACTTCGCGGAAACAACCTAGAGGAATTCGCGGACACGCAAGAGAAGAATATGTGATTCGAGTCTTCTC	1680
Consensus	gccatcgaccacttcgcggaacaactctagaggaattcgcgggacacgcaagagaagaatatgtgattcgagtcctctc	
Suyinmai_2	CCGTGCGACAGAGCGGACATATGCCATCCCCCTGGCCCGTTCCGCTTAAGGACCTTGACACCAGAGGGGAAGGCGGCCACGA	1727
Weisuobuzhi	CCGTGCGACAGAGCGGACATATGCCATCCCCCTGGCCCGTTCCGCTTAAGGACCTTGACACCAGAGGGGAAGGCGGCCACGA	1730
Template	CCGTGCGACAGAGCGGACATATGCCATCCCCCTGGCCCGTTCCGCTTAAGGACCTTGACACCAGAGGGGAAGGCGGCCACGA	1760
Consensus	ccgtcgacagagcggacatatgccatccccctggcccgctccgcttaaggaccttgacaccagaggggaaggcgccacga	
Suyinmai_2	AGCCATTGCCAGAGGAATATTGAATCTTCAAGGGGAGTCAAATCTCCAGAGCGCGCGGAGAGGCTCGATACCCCTGGGA	1807
Weisuobuzhi	AGCCATTGCCAGAGGAATATTGAATCTTCAAGGGGAGTCAAATCTCCAGAGCGCGCGGAGAGGCTCGATACCCCTGGGA	1810
Template	AGCCATTGCCAGAGGAATATTGAATCTTCAAGGGGAGTCAAATCTCCAGAGCGCGCGGAGAGGCTCGATACCCCTGGGA	1840
Consensus	agccattgccagaggaatatcgaaatcttcaaggggagtc aaatctccagagcgccgcgagaggctcgatacctggga	
Suyinmai_2	TGGCGTTATGGCCCGGTAGAGGGACTTCGTAGAGAAACGCCCTGATGGCTCTAGCCGCCAAGAGAGACAGTCGATGGATC	1887
Weisuobuzhi	TGGCGTTATGGCCCGGTAGAGGGACTTCGTAGAGAAACGCCCTGATGGCTCTAGCCGCCAAGAGAGACAGTCGATGGATC	1890
Template	TGGCGTTATGGCCCGGTAGAGGGACTTCGTAGAGAAACGCCCTGATGGCTCTAGCCGCCAAGAGAGACAGTCGATGGATC	1920
Consensus	tggcgttatggcccgttagaggacttcgtagagaaacgccctgatggctctagccgccaaagagagacagtcgatggatc	
Suyinmai_2	GCTCCATGTCCGTTCATGAAGGGCGATGGACTCCAGGAGGTCTGCCAGGCGATCGTGTCCATAGGAGTCCCAGAAAGGCC	1967
Weisuobuzhi	GCTCCATGTCCGTTCATGAAGGGCGATGGACTCCAGGAGGTCTGCCAGGCGATCGTGTCCATAGGAGTCCCAGAAAGGCC	1970
Template	GCTCCATGTCCGTTCATGAAGGGCGATGGACTCCAGGAGGTCTGCCAGGCGATCGTGTCCATAGGAGTCCCAGAAAGGCC	2000
Consensus	gctccatgtcgttcgatgaaggcgatggactccaggaggtcctgccaggcgatcgtgtccataggagtcccgaaggcc	
Suyinmai_2	GTCTAAAAGCGAGGCGCCCGAGGTGATAGAGGCCCTCTCCATTGAGATCCGAGGCTCGACCGCGATGGAGAATAGGGCT	2047
Weisuobuzhi	GTCTAAAAGCGAGGCGCCCGAGGTGATAGAGGCCCTCTCTCCATTGAGATCCGAGGCTCGACCGCGATGGAGAATAGGGCT	2050
Template	GTCTAAAAGCGAGGCGCCCGAGGTGATAGAGGCCCTCTCTCCATTGAGATCCGAGGCTCGACCGCGATGGAGAATAGGGCT	2080
Consensus	gtctaaaagcgaggcgcccgaggtcgataagggcctcctccattgagatccgaggctcgaccgcgatggagaatagggt	
Suyinmai_2	GGGAAACGAGCAACAAGGGGGTACGCCGGGCCAGCGGTCAAACAGAACAAGGTGGATGCGCTAGAGCCAACCTCGAT	2127
Weisuobuzhi	GGGAAACGAGCAACAAGGGGGTACGCCGGGCCAGCGGTCAAACAGAACAAGGTGGATGCGCTAGAGCCAACCTCGAT	2130
Template	GGGAAACGAGCAACAAGGGGGTACGCCGGGCCAGCGGTCAAACAGAACAAGGTGGATGCGCTAGAGCCAACCTCGAT	2160
Consensus	gggaaacgagcaacaagggggtcgcggcgccagcggctcaaaccagaacaagggtggatgcgctagagccaacctcgat	
Suyinmai_2	AGAGGTCCCAATGCGAAGGACCGGGAGCAGTTGGATGAGGGACTGCCAGAACTAAGACCCCTAGACCCGCTGGCAGAAGG	2206
Weisuobuzhi	AGAGGTCCCAATGCGAAGGACCGGGAGCAGTTGGATGAGGGACTGCCAGAACTAAGACCCCTAGACCCGCTGGCAGAAGG	2209
Template	AGAGGTCCCAATGCGAAGGACCGGGAGCAGTTGGATGAGGGACTGCCAGAACTAAGACCCCTAGACCCGCTGGCAGAAGG	2240
Consensus	agagggtcccaatgcgaaggaccgggagcagctggatgagggactgccagaactaagacccccagaccgctggcagaagg	
Suyinmai_2	CTTATTCTGAATTATGCGAAGCCAGAGGCCCCCTCGCCCTTAGCAATCCCTCGGAGCCAGTGGGTGGGCAGAGCGATAT	2286
Weisuobuzhi	CTTATTCTGAATTATGCGAAGCCAGAGGCCCCCTCGCCCTTAGCAATCCCTCGGAGCCAGTGGGTGGGCAGAGCGATAT	2289
Template	CTTATTCTGAATTATGCGAAGCCAGAGGCCCCCTCGCCCTTAGCAATCCCTCGGAGCCAGTGGGTGGGCAGAGCGATAT	2320
Consensus	cttattctgaattatgcgaagccagaggccccctcgcccttagcaatcccggagccagtggtgggcagagcgatat	
Suyinmai_2	TCATACGCTTGGAGGACATGATCCCAAGTCCACCTTGCTCGCGCGGCTTGCAGATCTCGGACCATCGCACCATGTGGTAC	2366
Weisuobuzhi	TCATACGCTTGGAGGACATGATCCCAAGTCCACCTTGCTCGCGCGGCTTGCAGATCTCGGACCATCGCACCATGTGGTAC	2369
Template	TCATACGCTTGGAGGACATGATCCCAAGTCCACCTTGCTCGCGCGGCTTGCAGATCTCGGACCATCGCACCATGTGGTAC	2400
Consensus	tcatacgcttggaggacatgatcccaagtccacctgctcgcgcggttgcagatctcggaccatcgaccatgtggtac	

Suyinmai_2	TTTCTGCTTTATCTCCCTCGCCGGCCAGAGAATCGCGCCTGAACCGTGGCGATCTCATGGTGGAGGGTCTCTGGCAAGCT	2446
Weisuobuzhi	TTTCTGCTTTATCTCCCTCGCCGGCCAGAGAATCGCGCCTGAACCGTGGCGATCTCATGGTGGAGGGTCTCTGGCAAGCT	2449
Template	TTTCTGCTTTATCTCCCTCGCCGGCCAGAGAATCGCGCCTGAACCGTGGCGATCTCATGGTGGAGGGTCTCTGGCAAGCT	2480
Consensus	t t c t g c t t a t c t c c c t c g c c g g c c c a g a a g a t c g c g c c t g a a c c g t g g c g a t c t c a t g g t g g a g g g t c t c t g g c a a g c t	
Suyinmai_2	GTAGAAGCTCATCAAGAAGAGCAGCAAGCTGGACAAGGAGGAGTTGATGAGAATCGTCTGACAGCCTTGATAGCCACC	2525
Weisuobuzhi	GTAGAAGCTCATCAAGAAGAGCAGCAAGCTGGACAAGGAGGAGTTGATGAGAATCGTCTGACAGCCTTGATAGCCACC	2528
Template	GTAGAAGCTCATCAAGAAGAGCAGCAAGCTGGACAAGGAGGAGTTGATGAGAATCGTCTGACAGCCTTGATAGCCACC	2560
Consensus	g t a g a a g c t c a t c a a g a a g a g c a g c a a g c g g a c a a g g a g g a g t t g a t g a g a a t c g t c c t g a c a g c c t t g a t a g c c a c c	
Suyinmai_2	GCACCTGCCATGGTTCAATACGGTGCTGAAGCTTGGCGACCGTAGGTGCGAGCTCCGCAACCGAGGTGGGTGTCACTAAT	2605
Weisuobuzhi	GCACCTGCCATGGTTCAATACGGTGCTGAAGCTTGGCGACCGTAGGTGCGAGCTCCGCAACCGAGGTGGGTGTCACTAAT	2608
Template	GCACCTGCCATGGTTCAATACGGTGCTGAAGCTTGGCGACCGTAGGTGCGAGCTCCGCAACCGAGGTGGGTGTCACTAAT	2640
Consensus	g c a c c t g c c a t g g t t c a a t a c g g t g c t g a a g c t t g c c g a c c g t a g g t c g c a g c t c c g c a a c c g a g g t g g g t g t c a c t a a t	
Suyinmai_2	GGGGATCCCCAGGTATGAAGTGGGGAAGGAGCCCAACTGACAATTGAGGCGGTGGCAATGCTCTGGGCCGCGGGAGGAG	2685
Weisuobuzhi	GGGGATCCCCAGGTATGAAGTGGGGAAGGAGCCCAACTGACAATTGAGGCGGTGGCAATGCTCTGGGCCGCGGGAGGAG	2688
Template	GGGGATCCCCAGGTATGAAGTGGGGAAGGAGCCCAACTGACAATTGAGGCGGTGGCAATGCTCTGGGCCGCGGGAGGAG	2720
Consensus	g g g g a t c c c c a g g t a t g a a g t g g g g a a g g a g c c c a a c t g a c a a t t g a g g c g g t c g g c a a t g c t c t g g g c c g c g g c a g g a g	
Suyinmai_2	GGTAGCCCAGGACCATGACCGCACTCTTATTAAAGTTTATTTTGGAGCCGGACATATGTTGAAAGCAGAGGAGGAGGAAT	2765
Weisuobuzhi	GGTAGCCCAGGACCATGACCGCACTCTTATTAAAGTTTATTTTGGAGCCGGACATATGTTGAAAGCAGAGGAGGAGGAAT	2768
Template	GGTAGCCCAGGACCATGACCGCACTCTTATTAAAGTTTATTTTGGAGCCGGACATATGTTGAAAGCAGAGGAGGAGGAAT	2800
Consensus	g g t a g c c c a g g a c c a t g a c c g c a c t c t t a t t a a a g t t t a t t t t g a g a c c g g a c a t a t g t t g a a a g c a g a g g a g g a g g a a t	
Suyinmai_2	TTTCAGGTACGAGATGTTCATCGTCCGAGCCTTCAACCATGATGATCGTGTGTCCGCATATTGCAGGAGAGAGACGCCAAG	2845
Weisuobuzhi	TTTCAGGTACGAGATGTTCATCGTCCGAGCCTTCAACCATGATGATCGTGTGTCCGCATATTGCAGGAGAGAGACGCCAAG	2848
Template	TTTCAGGTACGAGATGTTCATCGTCCGAGCCTTCAACCATGATGATCGTGTGTCCGCATATTGCAGGAGAGAGACGCCAAG	2880
Consensus	t t c a g g t a c g a g a t g t c a t c g t c c g a g c c t t c a a c c a t g a t g a t c g t g t t g t c c g c a t a t t g c a g g a g a g a g a c g c c a a g	
Suyinmai_2	ATCTCCCACTAGGTGCGGGACGATGCCCGGGATGTGGCCGGCCTCCTTGGCCTTGTCAAGGATGGAGGCTAGCGCATCGA	2925
Weisuobuzhi	ATCTCCCACTAGGTGCGGGACGATGCCCGGGATGTGGCCGGCCTCCTTGGCCTTGTCAAGGATGGAGGCTAGCGCATCGA	2928
Template	ATCTCCCACTAGGTGCGGGACGATGCCCGGGATGTGGCCGGCCTCCTTGGCCTTGTCAAGGATGGAGGCTAGCGCATCGA	2960
Consensus	a t c t c c c a c t a g g t g c g g g a c g a t g c c g c g g a t g t g g c c g g c c t c c t t g g c c t t g t c a a g g a t g g a g g c t a g c g c a t c g a	
Suyinmai_2	CCACCATGTTAAACAAGAACGGGGAGAAAGGATCACCCTAACGAACCCACACATGGTGGGAAGTAGGGTCCGATCTCCC	3005
Weisuobuzhi	CCACCATGTTAAACAAGAACGGGGAGAAAGGATCACCCTAACGAACCCACACATGGTGGGAAGTAGGGTCCGATCTCCC	3008
Template	CCACCATGTTAAACAAGAACGGGGAGAAAGGATCACCCTAACGAACCCACACATGGTGGGAAGTAGGGTCCGATCTCCC	3040
Consensus	c c a c c a t g t t a a c a a g a a c g g g g a g a a a g g a t c a c c c t a a c g a a c c c a c a c a t g g t g g g a a g t a g g g t c c g a t c t c c c	
Suyinmai_2	CATTGATGTTTACTGCGGTACGACACAGAGGAGACTATCTGCATCACCCTAGTCACCCACCGGTGCTGGAAGCCCTTACGC	3085
Weisuobuzhi	CATTGATGTTTACTGCGGTACGACACAGAGGAGACTATCTGCATCACCCTAGTCACCCACCGGTGCTGGAAGCCCTTACGC	3088
Template	CATTGATGTTTACTGCGGTACGACACAGAGGAGACTATCTGCATCACCCTAGTCACCCACCGGTGCTGGAAGCCCTTACGC	3120
Consensus	c a t t g a t g t t t a c t g c g g t a c g a c c a g a g g a g a c t a t c t g c a t c a c c c t a g t c a c c c a c c g g t c g t c g a a g c c c t t a c g c	
Suyinmai_2	TGTAGAAGTCCCAGAGGAAATCCAGCTTAACAGTGTTCATACGCCCTTGTGAAAGTCCAGCTTCAAGAAGGGTCCCTAACA	3165
Weisuobuzhi	TGTAGAAGTCCCAGAGGAAATCCAGCTTAACAGTGTTCATACGCCCTTGTGAAAGTCCAGCTTCAAGAAGGGTCCCTAACA	3168
Template	TGTAGAAGTCCCAGAGGAAATCCAGCTTAACAGTGTTCATACGCCCTTGTGAAAGTCCAGCTTCAAGAAGGGTCCCTAACA	3200
Consensus	t g t a g a a c t t c c c g a a g g a a t c c a g c t a a c a g t g t c a t a c g c c t t g t g a a a g t c c a g c t t c a a g a a g g g t c c c t a a c a	
Suyinmai_2	GTGTCAATTTGCTTTGAGGTTTTTGGACCGGACCTCATGGATAGTCTCATGAAGGACGAGCACACCATCCAGGATGTACCG	3245
Weisuobuzhi	GTGTCAATTTGCTTTGAGGTTTTTGGACCGGACCTCATGGATAGTCTCATGAAGGACGAGCACACCATCCAGGATGTACCG	3248
Template	GTGTCAATTTGCTTTGAGGTTTTTGGACCGGACCTCATGGATAGTCTCATGAAGGACGAGCACACCATCCAGGATGTACCG	3280
Consensus	g t g t c a t t t g c c t t g a g g t t t t t g g a c c g g a c c t c a t g g a t a g t c t c a t g a a g g a c g a g c a c a c c a t c c a g g a t g t a c c g	
Suyinmai_2	GCCTCGGATGAAGGCCGATTGATCCGAATGTGTGATCTGATCAGCAAGAAGGGTACCCTATTGGCGTACCCTTGGCCA	3325
Weisuobuzhi	GCCTCGGATGAAGGCCGATTGATCCGAATGTGTGATCTGATCAGCAAGAAGGGTACCCTATTGGCGTACCCTTGGCCA	3328
Template	GCCTCGGATGAAGGCCGATTGATCCGAATGTGTGATCTGATCAGCAAGAAGGGTACCCTATTGGCGTACCCTTGGCCA	3360
Consensus	g c c t c g g a t g a a g g c c g a t t g a t c c g a a t g t g t g a t c t g a t c a g c a a g a a g g g t c a c c c t a t t g g c g t a c c c c t t g g c c a	
Suyinmai_2	GGATGCCGAAGATGACGTTGATCACCGTGATCGGCCGGAATTGGCTGATCTCAGCTGCACCCCAAACTTTTGAATTAAGC	3405
Weisuobuzhi	GGATGCCGAAGATGACGTTGATCACCGTGATCGGCCGGAATTGGCTGATCTCAGCTGCACCCCAAACTTTTGAATTAAGC	3408
Template	GGATGCCGAAGATGACGTTGATCACCGTGATCGGCCGGAATTGGCTGATCTCAGCTGCACCCCAAACTTTTGAATTAAGC	3440
Consensus	g g a t g c g g a a g a t g a c g t t g a t c a c c g t g a t c g g c c g g a a t t g g c t g a t c t c a g c t g c a c c c c a a a c t t t t g g a a t a a g c	
Suyinmai_2	GTGATAATCCCAGAGTTAAGGCGTGCGAGGTCAATTGAGCCAATGAAGAAGTCGTCAAATATGGCCATGACCTCCGGTTTT	3485
Weisuobuzhi	GTGATAATCCCAGAGTTAAGGCGTGCGAGGTCAATTGAGCCAATGAAGAAGTCGTCAAATATGGCCATGACCTCCGGTTTT	3488
Template	GTGATAATCCCAGAGTTAAGGCGTGCGAGGTCAATTGAGCCAATGAAGAAGTCGTCAAATATGGCCATGACCTCCGGTTTT	3520
Consensus	g t g a t a a t c c c g a a g t t a a g g c g t g c g a g g t c a a t t g a g c c a a t g a a g a a c t c g t c a a a t a t g g c c a t g a c c t c g g t t t	
Suyinmai_2	AATGGTGTTCAGAAATGTTTGAAGAAGCTTACCCTCAAGCCATCCGGGCCCGGGGCGGAGGTCCGGTTTCATGCCCTTGA	3565
Weisuobuzhi	AATGGTGTTCAGAAATGTTTGAAGAAGCTTACCCTCAAGCCATCCGGGCCCGGGGCGGAGGTCCGGTTTCATGCCCTTGA	3568
Template	AATGGTGTTCAGAAATGTTTGAAGAAGCTTACCCTCAAGCCATCCGGGCCCGGGGCGGAGGTCCGGTTTCATGCCCTTGA	3600
Consensus	a a t g g t g t t c a g a a t g t t t g g a a g a a c t t c a c c g t c a a g c c a t c c g g g c c g g g g c g g a g g t c g g g t t c a t g c c c t t g a	

Suyinmai 2	TGGCTGACCAAACCTCCTCCTTCGAGAAGCGGAGCCATAAGCGCCAAAGTTCCTCTCCGCAGATACGCGTCGATCGGTGGCG	3645
Weisuobuzhi	TGGCTGACCAAACCTCCTCCTTCGAGAAGCGGAGCCATAAGCGCCAAAGTTCCTCTCCGCAGATACGCGTCGATCGGTGGCG	3648
Template	TGGCTGACCAAACCTCCTCCTTCGAGAAGCGGAGCCATAAGCGCCAAAGTTCCTCTCCGCAGATACGCGTCGATCGGTGGCG	3680
Consensus	tggctgaccaaacctcctccttcgagaacggagccataagcgccaagttctcctccgcagatacgcgtcgatcggtcggc	
Suyinmai 2	CAAAATGTGAGAGGGCCAGGGACACCCCTCCCAAGGGGAAGAGGAAACAAGGCTTTACAAAAGCCATCTACGTGGGCGCG	3725
Weisuobuzhi	CAAAATGTGAGAGGGCCAGGGACACCCCTCCCAAGGGGAAGAGGAAACAAGGCTTTACAAAAGCCATCTACGTGGGCGCG	3728
Template	CAAAATGTGAGAGGGCCAGGGACACCCCTCCCAAGGGGAAGAGGAAACAAGGCTTTACAAAAGCCATCTACGTGGGCGCG	3760
Consensus	caaatgtcgagggccaggggacacccctccccaaggggaagaggaaacaaggctttacaaaagccatctacgtgggcgcg	
Suyinmai 2	GACGCTCTGCCGACCACTGCAACAGGGTATCCCCGTCGAGAGCCAGGGGATGGTGTTCGGGCCGACGCGGCCATTAGCGA	3805
Weisuobuzhi	GACGCTCTGCCGACCACTGCAACAGGGTATCCCCGTCGAGAGCCAGGGGATGGTGTTCGGGCCGACGCGGCCATTAGCGA	3808
Template	GACGCTCTGCCGACCACTGCAACAGGGTATCCCCGTCGAGAGCCAGGGGATGGTGTTCGGGCCGACGCGGCCATTAGCGA	3840
Consensus	gacgctctgccgacctgcaacagggtatccccgtccagagccaggggatggtgttcgggccgcagcggccattagcga	
Suyinmai 2	TGGCTTGAAGTAGGCCGTATTGGCGTCACCCCTTGAGGACCCACTTTTGGTGCCTCGCATCTGCCAATAATTTCTCTCG	3885
Weisuobuzhi	TGGCTTGAAGTAGGCCGTATTGGCGTCACCCCTTGAGGACCCACTTTTGGTGCCTCGCATCTGCCAATAATTTCTCTCG	3888
Template	TGGCTTGAAGTAGGCCGTATTGGCGTCACCCCTTGAGGACCCACTTTTGGTGCCTCGCATCTGCCAATAAGCTTCTCTCG	3920
Consensus	tggctt ggaagt aggcctgtattggcgtcaccccttgaggaccacttttgggtgcctcgcatctgccaataa ctctctcg	
Suyinmai 2	TTTCGAGTAGATGACGGACAGTTGGTCTCAAGATCGTATCGCAAAAAGCCATTTCGTGGGAGACAGACTCGAGGCGTCGG	3965
Weisuobuzhi	TTTCGAGTAGATGACGGACAGTTGGTCTCAAGATCGTATCGCAAAAAGCCATTTCGTGGGAGACAGACTCGAGGCGTCGG	3968
Template	TTTCGAGTAGATGACGGACAGTTGGTCTCAAGATCGTATCGCAAAAAGCCATTTCGTGGGAGACAGACTCGAGGCGTCGG	4000
Consensus	ttcgagt agatgacggacagt tggctcctcaagatcgtatcgcaaaaagccattcgtcggcagacagactcgaggcgctcgg	
Suyinmai 2	CCCTGGAGGTGAGAGAGCTGAATGGATGCTAGCAGAGCTTGCTTTTGCATCCGTAGATCCCATCCGAGGTTTCGCGCCCCA	4045
Weisuobuzhi	CCCTGGAGGTGAGAGAGCTGAATGGATGCTAGCAGAGCTTGCTTTTGCATCCGTAGATCCCATCCGAGGTTTCGCGCCCCA	4048
Template	CCCTGGAGGTGAGAGAGCTGAATGGATGCTAGCAGAGCTTGCTTTTGCATCCGTAGATCCCATCCGAGGTTTCGCGCCCCA	4080
Consensus	ccctggaggtcgagaagctgaatggatgctagcagagcttgcttttgcattcgtatcccatccgaggttcgcgcccca	
Suyinmai 2	CCCCCTCATGAATTGGCGCGAACGCTTCGCACAGAGCTTGCCATGCATCTACAGCGGAGGGTGCACGAAGGGGACGAGGTG	4125
Weisuobuzhi	CCCCCTCATGAATTGGCGCGAACGCTTCGCACAGAGCTTGCCATGCATCTACAGCGGAGGGTGCACGAAGGGGACGAGGTG	4128
Template	CCCCCTCATGAATTGGCGCGAACGCTTCGCACAGAGCTTGCCATGCATCTACAGCGGAGGGTGCACGAAGGGGACGAGGTG	4160
Consensus	ccccctcatgaattggcgcgaaacgcttcgcacagagctgccatgcattacagcggaggggtgcacgaaggggacgaggtg	
Suyinmai 2	AGCCTCCCGCCACTTATCGCACACAACCGCGCACAAACCCAGCCTGGTTAAGCCAGAATATCTTGAACCAGAACCAGGGA	4205
Weisuobuzhi	AGCCTCCCGCCACTTATCGCACACAACCGCGCACAAACCCAGCCTGGTTAAGCCAGAATATCTTGAACCAGAACCAGGGA	4207
Template	AGCCTCCCGCCACTTATCGCACACAACCGCGCACAAACCCAGCCTGGTTAAGCCAGAATATCTTGAACCAGAACCAGGGA	4239
Consensus	agcctcccgcacttatcgcacacaaccgcgacaaacccagcctggttaagccagaatatcttgaaccagaaccgagga	
Suyinmai 2	GGTTGAGGCGGACGGTCGTCAACGGAAGAGAGGGAGGGGGACATGGTCCGACCCAATCCTAGTAATCGCCTTAAGCGAAG	4285
Weisuobuzhi	GGTTGAGGCGGACGGTCGTCAACGGAAGAGAGGGAGGGGGACATGGTCCGACCCAATCCTAGTAATCGCCTTAAGCGAAG	4287
Template	GGTTGAGGCGGACGGTCGTCAACGGAAGAGAGGGAGGGGGACATGGTCCGACCCAATCCTAGTAATCGCCTTAAGCGAAG	4319
Consensus	ggttgaggcggacggtcgtcaacggaaagagagggagggggacatggtccgacccaatcctagt aatcgctt taagcgaag	
Suyinmai 2	CAAGAGGGGAGCAAAAGCTCCCACTCTGGGGAGACGAGGACCTGGTCGAGGACGGAGCGGGTCGGGTCGGCCTGGCGGTTG	4365
Weisuobuzhi	CAAGAGGGGAGCAAAAGCTCCCACTCTGGGGAGACGAGGACCTGGTCGAGGACGGAGCGGGTCGGGTCGGCCTGGCGGTTG	4367
Template	CAAGAGGGGAGCAAAAGCTCCCACTCTGGGGAGACGAGGACCTGGTCGAGGACGGAGCGGGTCGGGTCGGCCTGGCGGTTG	4399
Consensus	caagagggcagcaaaagctcccactctggggagacgaggacctggtcgaggacggagcgggtcgggtcggcctggcgggttgc	
Suyinmai 2	GTCCAGGTAAACCTGGCCCCCACTCTATCAAGTTCCCGAAGGCCAAGGTCACGATGCAATCGTTGAACATCTGCATCCT	4445
Weisuobuzhi	GTCCAGGTAAACCTGGCCCCCACTCTATCAAGTTCCCGAAGGCCAAGGTCACGATGCAATCGTTGAACATCTGCATCCT	4447
Template	GTCCAGGTAAACCTGGCCCCCACTCTATCAAGTTCCCGAAGGCCAAGGTCACGATGCAATCGTTGAACATCTGCATCCT	4479
Consensus	gtccaggt aaacctggcccccactctataagttcccgaaggccaaggtccacgatgcaatcgttgaacatctgcattct	
Suyinmai 2	TGGAAAGTTGACCAAGTTATTGCTTTTATCTGCCTCCAAGCGAATGAGATTAAAGTCGCCATCAACGACACGAGGGAGCT	4525
Weisuobuzhi	TGGAAAGTTGACCAAGTTATTGCTTTTATCTGCCTCCAAGCGAATGAGATTAAAGTCGCCATCAACGACACGAGGGAGCT	4527
Template	TGGAAAGTTGACCAAGTTATTGCTTTTATCTGCCTCCAAGCGAATGAGATTAAAGTCGCCATCAACGACACGAGGGAGCT	4559
Consensus	tggaaagt gaccaagt tattgcttttatctgcctccaagcgaatgagattaaagtcgccatcaacgaccagagggagct	
Suyinmai 2	GGGCTGCTGCTACTTTCTCTTTAATTTCTTCGAGGAAAGCGCGCGAACGGCGGTGGTCGGTCGGGCCATAGATGACGATC	4605
Weisuobuzhi	GGGCTGCTGCTACTTTCTCTTTAATTTCTTCGAGGAAAGCGCGCGAACGGCGGTGGTCGGTCGGGCCATAGATGACGATC	4607
Template	GGGCTGCTGCTACTTTCTCTTTAATTTCTTCGAGGAAAGCGCGCGAACGGCGGTGGTCGGTCGGGCCATAGATGACGATC	4639
Consensus	gggctgctgctactttcctctttaattcttcgaggaaagcgcgcgaacggcggtggtcggtcgggccatagatgacgatc	
Suyinmai 2	ACCTCCCACTTGACGTTCAAAGCCCGTTCAAAGAGTTCCATGCTAACATAGAAGCTCTCCGCCATCCATACGACCTATCTC	4685
Weisuobuzhi	ACCTCCCACTTGACGTTCAAAGCCCGTTCAAAGAGTTCCATGCTAACATAGAAGCTCTCCGCCATCCATACGACCTATCTC	4687
Template	ACCTCCCACTTGACGTTCAAAGCCCGTTCAAAGAGTTCCATGCTAACATAGAAGCTCTCCGCCATCCATACGACCTATCTC	4719
Consensus	acctcccacttgacgttcaaagcccggtcaaagagttccatgctaacatagaactctccgccatccat acgacctatctc	
Suyinmai 2	AAAGGTGGCATCCTTCACCTCTAGGAGGATGCGGCCGAGTGGCTAGTGGTCCCACTAGATGGGAGCCAGTGCCAGGCCAA	4765
Weisuobuzhi	AAAGGTGGCATCCTTCACCTCTAGGAGGATGCGGCCGAGTGGCTAGTGGTCCCACTAGATGGGAGCCAGTGCCAGGCCAA	4767
Template	AAAGGTGGCATCCTTCACCTCTAGGAGGATGCGGCCGAGTGGCTAGTGGTCCCACTAGATGGGAGCCAGTGCCAGGCCAA	4799
Consensus	aaaggtggcatccttctactccttgaaggaatgcgcgccgagtggctagt ggtcccact agatggagccagtgccaggcaa	

Suyinmai 2	ACAGATGGGAGCTCAGGGGCTTGAGCTCCGAGAGCGATAACTCAGTTTCGCAATGTCTCTCTGAATGGCATCTATGTCAATC	4845
Weisuobuzhi	ACAGATGGGAGCTCAGGGGCTTGAGCTCCGAGAGCGATAACTCAGTTTCGCAATGTCTCTCTGAATGGCATCTATGTCAATC	4847
Template	ACAGATGGGAGCTCAGGGGCTTGAGCTCCGAGAGCGATAACTCAGTTTCGCAATGTCTCTCTGAATGGCATCTATGTCAATC	4879
Consensus	acagatgggagctcaggggcttgagctccgagagcgataactcagtttcgcaatgtctctctgaatggcatctatgtcaatc	
Suyinmai 2	CGTTCCTTCAACGCATGTATTTCGATCAACTGGCGGGGGCGGCCATCCTGACTGAAACCTTCGGATGTTCCAGAAGAGCGTTTCG	4925
Weisuobuzhi	CGTTCCTTCAACGCATGTATTTCGATCAACTGGCGGGGGCGGCCATCCTGACTGAAACCTTCGGATGTTCCAGAAGAGCGTTTCG	4927
Template	CGTTCCTTCAACGCATGTATTTCGATCAACTGGCGGGGGCGGCCATCCTGACTGAAACCTTCGGATGTTCCAGAAGAGCGTTTCG	4959
Consensus	cgttcttcaacgcattgatttcgatcaactggcggcggcgcccatcctgactgaaacctcggatgttcagaaagagcgttcg	
Suyinmai 2	CATCACTGACCCATCGGGGGGGCTGCTTGACCCAGGACCCGAGAAGCGCTCTGGGCGCTAGGATAGCGGTGTGGGTGC	5005
Weisuobuzhi	CATCACTGACCCATCGGGGGGGCTGCTTGACCCAGGACCCGAGAAGCGCTCTGGGCGCTAGGATAGCGGTGTGGGTGC	5007
Template	CATCACTGACCCATCGGGGGGGCTGCTTGACCCAGGACCCGAGAAGCGCTCTGGGCGCTAGGATAGCGGTGTGGGTGC	5039
Consensus	catcactgaccatcgggggggctgcttgacccaggaccgagaagcgtctggcgcggtaggatagcgggtgtgggtgc	
Suyinmai 2	GTGTGCGGTCCAGGCCTCGACCGGCACGACCGAGTTGCGAGGGGCCCTGCTGGCATGGGGGAAGCGGAGACGTCGCT	5085
Weisuobuzhi	GTGTGCGGTCCAGGCCTCGACCGGCACGACCGAGTTGCGAGGGGCCCTGCTGGCATGGGGGAAGCGGAGACGTCGCT	5087
Template	GTGTGCGGTCCAGGCCTCGACCGGCACGACCGAGTTGCGAGGGGCCCTGCTGGCATGGGGGAAGCGGAGACGTCGCT	5119
Consensus	gtgtgcggtcccaggcctcgaccggcacgaccgagttgcgagggggccctgctggcatgggggaagcggagacgtccgct	
Suyinmai 2	CCGCCCTGGGGCTGTAAAGCGAGAGCGAGCCTCGGCAGCGAGCCATCGAGAATTTCTCGAGCACAGATCGCCTTGATTTTG	5165
Weisuobuzhi	CCGCCCTGGGGCTGTAAAGCGAGAGCGAGCCTCGGCAGCGAGCCATCGAGAATTTCTCGAGCACAGATCGCCTTGATTTTG	5167
Template	CCGCCCTGGGGCTGTAAAGCGAGAGCGAGCCTCGGCAGCGAGCCATCGAGAATTTCTCGAGCACAGATCGCCTTGATTTTG	5199
Consensus	ccgccctggggctgtaaagcgagagcgagcctcgccagccgaccatcgagaatttctcgagcacagatcgcttctgatttg	
Suyinmai 2	GACCAACGGCGGGGCGACTTCGCCCCGGAACACTATCGCAGAATCAGCCGCGATTTCGCAAGACGGCCGAGCGGAATCG	5245
Weisuobuzhi	GACCAACGGCGGGGCGACTTCGCCCCGGAACACTATCGCAGAATCAGCCGCGATTTCGCAAGACGGCCGAGCGGAATCG	5247
Template	GACCAACGGCGGGGCGACTTCGCCCCGGAACACTATCGCAGAATCAGCCGCGATTTCGCAAGACGGCCGAGCGGAATCG	5279
Consensus	gaccaacggcggggcgacttcgccccggaacactatcgagaatcagccggatttttcgcaagacggccgagcgggaatcg	
Suyinmai 2	ATTCAAGAGCCGAGATTCAAGAGCCGAGAACGAGCAGTTAGCAGTGAAGCAGGGATGGCAGGGGTACCTGGCTCCAGGT	5325
Weisuobuzhi	ATTCAAGAGCCGAGATTCAAGAGCCGAGAACGAGCAGTTAGCAGTGAAGCAGGGATGGCAGGGGTACCTGGCTCCAGGT	5327
Template	ATTCAAGAGCCGAGATTCAAGAGCCGAGAACGAGCAGTTAGCAGTGAAGCAGGGATGGCAGGGGTACCTGGCTCCAGGT	5359
Consensus	attcaagagccgagattcaagagccgagaacgagcagttagcagtgaagcagggatggcaggggtacctggctccaggt	
Suyinmai 2	TCCGCTAGCCGCCCGTAGCTCGGCCCGCTTCGGGATGGGCGGAGCAGGGCTCCCGTCGGGGTGTGCTGCCCTCGAGCCGG	5405
Weisuobuzhi	TCCGCTAGCCGCCCGTAGCTCGGCCCGCTTCGGGATGGGCGGAGCAGGGCTCCCGTCGGGGTGTGCTGCCCTCGAGCCGG	5407
Template	TCCGCTAGCCGCCCGTAGCTCGGCCCGCTTCGGGATGGGCGGAGCAGGGCTCCCGTCGGGGTGTGCTGCCCTCGAGCCGG	5439
Consensus	tccgctagccgcccgtagctggcccgcttcgggatggcggaagcagggctcccgtcggggtgtgctgcctcgagccgg	
Suyinmai 2	GCATGTGGCGAGAAGACGTGACCGGTTCGAGGATGCGCAGCCCGCCTGGAGTAGGCCCGCGTGCACGGATAGAGCGGG	5485
Weisuobuzhi	GCATGTGGCGAGAAGACGTGACCGGTTCGAGGATGCGCAGCCCGCCTGGAGTAGGCCCGCGTGCACGGATAGAGCGGG	5487
Template	GCATGTGGCGAGAAGACGTGACCGGTTCGAGGATGCGCAGCCCGCCTGGAGTAGGCCCGCGTGCACGGATAGAGCGGG	5519
Consensus	gcactgtggcgagaagacgtgaccgggtcgagga-gcgcagcccgccctggagtaggccgcggtgcacggatagagcggg	
Suyinmai 2	TGGGAAGCCACCGGAGTGGTAATCACCGCAGACGCGAGGCCCTGGCGTTCGAAGCAGAGGGCGAGGTTCGGGAGGGCCGAG	5565
Weisuobuzhi	TGGGAAGCCACCGGAGTGGTAATCACCGCAGACGCGAGGCCCTGGCGTTCGAAGCAGAGGGCGAGGTTCGGGAGGGCCGAG	5567
Template	TGGGAAGCCACCGGAGTGGTAATCACCGCAGACGCGAGGCCCTGGCGTTCGAAGCAGAGGGCGAGGTTCGGGAGGGCCGAG	5599
Consensus	tgggaagccaccggagtggtaatcacgcagacgcgaggccctggcgctcgaagcagagggcgaggtcgggagggccgag	
Suyinmai 2	CAGCACAGGGAGGCCGGGGAGACCGAACGTTCGAAGTACAGGCCGCCCGCGAAGGCCAAGCCGAGAGCGCGACCCGGGAGG	5645
Weisuobuzhi	CAGCACAGGGAGGCCGGGGAGACCGAACGTTCGAAGTACAGGCCGCCCGCGAAGGCCAAGCCGAGAGCGCGACCCGGGAGG	5647
Template	CAGCACAGGGAGGCCGGGGAGACCGAACGTTCGAAGTACAGGCCGCCCGCGAAGGCCAAGCCGAGAGCGCGACCCGGGAGG	5679
Consensus	cagcacagggaagccggggagaccgaacgtcgaagtacaggccgcccgcgaagggcgaagccgagagcgcgacccgggagg	
Suyinmai 2	GGGGGGGGGACCGCCAGCGCCACAGGTACCACTGGGGGAGGCTTGGAGACATCCGCCAGAGGTGGCTGTGGTGACCGTGT	5725
Weisuobuzhi	GGGGGGGGGACCGCCAGCGCCACAGGTACCACTGGGGGAGGCTTGGAGACATCCGCCAGAGGTGGCTGTGGTGACCGTGT	5727
Template	GGGGGGGGGACCGCCAGCGCCACAGGTACCACTGGGGGAGGCTTGGAGACATCCGCCAGAGGTGGCTGTGGTGACCGTGT	5757
Consensus	ggggggg-gaccgcagcgccacaggtaccactgggggaggttggagacatccgccagaggtggctgtggtgacgggtgt	
Suyinmai 2	CCAGAGCGCCGCCCGCGGAGGGGGCTAGGGCGACAGCGCGTCGGTGTCCAGAGCCCAAGAGTTGGGGTGGCCCGGGCC	5805
Weisuobuzhi	CCAGAGCGCCGCCCGCGGAGGGGGCTAGGGCGACAGCGCGTCGGTGTCCAGAGCCCAAGAGTTGGGGTGGCCCGGGCC	5807
Template	CCAGAGCGCCGCCCGCGGAGGGGGCTAGGGCGACAGCGCGTCGGTGTCCAGAGCCCAAGAGTTGGGGTGGCCCGGGCC	5837
Consensus	ccagagcgccgcccgcggagggggctaggcgacagcgcgctcgggtgtccagagcccgaagagtgggggtggccgcggcc	
Suyinmai 2	AGCATCACGGCAGGAGGTGGGGCGACGACGGCGGGAGCACAGCAGGCCGACGCTGGACGTGTCACTCGTCTCCGCCGA	5885
Weisuobuzhi	AGCATCACGGCAGGAGGTGGGGCGACGACGGCGGGAGCACAGCAGGCCGACGCTGGACGTGTCACTCGTCTCCGCCGA	5887
Template	AGCATCACGGCAGGAGGTGGGGCGACGACGGCGGGAGCACAGCAGGCCGACGCTGGACGTGTCACTCGTCTCCGCCGA	5917
Consensus	agcatcacggcaggaggtcggggcgacgacggcgggagcaccagcaggccgacgctggacgtgtcactcgtctccgccga	
Suyinmai 2	GCGGGTCAGGGAGGCTTGGCTGGAGAGCTCACGGGGTCCCGGCTCTGTCGCGGACGGCAGCGAGGGGAGTGAGCATCCCGG	5965
Weisuobuzhi	GCGGGTCAGGGAGGCTTGGCTGGAGAGCTCACGGGGTCCCGGCTCTGTCGCGGACGGCAGCGAGGGGAGTGAGCATCCCGG	5967
Template	GCGGGTCAGGGAGGCTTGGCTGGAGAGCTCACGGGGTCCCGGCTCTGTCGCGGACGGCAGCGAGGGGAGTGAGCATCCCGG	5997
Consensus	gcgggtcagggaggttggctggaagactcacggggtcccgctcgtcgcggaaggcagcgaagggagtgagcatcccg	

Suyinmai 2	ACCCGAGCATCCTATTATCATGCTTTTTGATTATGCATGAAAACTTTACAGCAAGCTGAAAGCCGTTAATATGTAAATTGACT	6045
Weisuobuzhi	ACCCGAGCATCCTATTATCATGCTTTTTGATTATGCATGAAAACTTTACAGCAAGCTGAAAGCCGTTAATATGTAAATTGACT	6047
Template	ACCCGAGCATCCTATTATCATGCTTTTTGATTATGCATGAAAACTTTACAGCAAGCTGAAAGCCGTTAATATGTAAATTGACT	6077
Consensus	acccgagcatcctattatcatgctttttgattatgcatgaaaactttacagcaagctgaaagccgttaatatgtaaattgact	
Suyinmai 2	TCATCTGGTATTATCAATTTTCTCATCCCCATGCACTATTGCTCGAACATAAAGATCTATATGATTGAAACCAATTTCAGCC	6125
Weisuobuzhi	TCATCTGGTATTATCAATTTTCTCATCCCCATGCACTATTGCTCGAACATAAAGATCTATATGATTGAAACCAATTTCAGCC	6127
Template	TCATCTGGTATTATCAATTTTCTCATCCCCATGCACTATTGCTCGAACATAAAGATCTATATGATTGAAACCAATTTCAGCC	6157
Consensus	tcatctggattattatcaattttctcatccccatgcactattgctcgaacataaagatctatatgattgaaaccaattcagcc	
Suyinmai 2	ACAAAAGGAAGCATGAAGAAACGGTTGTTTTCATTTATTAGGATTTCTTTTTCTTTACCATGATTTTGTGTATCCTTTTGTACC	6205
Weisuobuzhi	ACAAAAGGAAGCATGAAGAAACGGTTGTTTTCATTTATTAGGATTTCTTTTTCTTTACCATGATTTTGTGTATCCTTTTGTACC	6207
Template	ACAAAAGGAAGCATGAAGAAACGGTTGTTTTCATTTATTAGGATTTCTTTTTCTTTACCATGATTTTGTGTATCCTTTTGTACC	6237
Consensus	acaaaaggagcatgaagaaacggttgtttcattcattaggattctttttcttaccatgatttgtgtatcctttgttacc	
Suyinmai 2	TTTTTCAGTATGATTACTTTGTTTTACTTTAATTAAATGGTATCAGGTGATTTTCTGAAGTTAAACCACACGAGAAAAAGAAGTT	6285
Weisuobuzhi	TTTTTCAGTATGATTACTTTGTTTTACTTTAATTAAATGGTATCAGGTGATTTTCTGAAGTTAAACCACACGAGAAAAAGAAGTT	6287
Template	TTTTTCAGTATGATTACTTTGTTTTACTTTAATTAAATGGTATCAGGTGATTTTCTGAAGTTAAACCACACGAGAAAAAGAAGTT	6317
Consensus	ttttcagtatgattacttgtttactttaattaaatggatcaggtgatttctgaagttaaacacacgagaaaaagaagtt	
Suyinmai 2	CATATCTGAACCTTCAAAAGGAGCACAAATTAGTTGCCATGGTTGGTGATGGCATTAATGATGCTGCAGCCCTAGCTTTTAG	6365
Weisuobuzhi	CATATCTGAACCTTCAAAAGGAGCACAAATTAGTTGCCATGGTTGGTGATGGCATTAATGATGCTGCAGCCCTAGCTTTTAG	6367
Template	CATATCTGAACCTTCAAAAGGAGCACAAATTAGTTGCCATGGTTGGTGATGGCATTAATGATGCTGCAGCCCTAGCTTTTAG	6397
Consensus	catatctgaacttcaaaaggagcacaaattagttgccatggttggtgatggcattaatgatgctgcagccctagcttttag	
Suyinmai 2	CTGACGTTTGGAAATTGCAATGGGTGGAGGTGTTGGTGCAGCTAGTGACGTATCTTCAGTTGTTTCTCATGGGTAAATAGGTTTA	6445
Weisuobuzhi	CTGACGTTTGGAAATTGCAATGGGTGGAGGTGTTGGTGCAGCTAGTGACGTATCTTCAGTTGTTTCTCATGGGTAAATAGGTTTA	6447
Template	CTGACGTTTGGAAATTGCAATGGGTGGAGGTGTTGGTGCAGCTAGTGACGTATCTTCAGTTGTTTCTCATGGGTAAATAGGTTTA	6477
Consensus	ctgacgcttggaaattgcaatgggtggaggtgttgggtgcagctagtgcagctatcttcagttgttctcatgggtaataggtta	
Suyinmai 2	TCTCAGGTAAATTCATTACGACAGCTTTGGAGTTACTCGCTGATACTGTTGCCAAATTCATTTAACCTCACTCCCCTCTTTT	6525
Weisuobuzhi	TCTCAGGTAAATTCATTACGACAGCTTTGGAGTTACTCGCTGATACTGTTGCCAAATTCATTTAACCTCACTCCCCTCTTTT	6527
Template	TCTCAGGTAAATTCATTACGACAGCTTTGGAGTTACTCGCTGATACTGTTGCCAAATTCATTTAACCTCACTCCCCTCTTTT	6557
Consensus	tctcaggtaattcattacgacagcttggagttactcgctgatactgttgccaaattcatttaaccttcactcccctcttt	
Suyinmai 2	GTGCTACTATCATCTTTTCTTTTTTCTTAATAAACTGCTGTGATGGGTCTTTGATGCAGCTTGTGTATGCTTTAGAGTTAAG	6605
Weisuobuzhi	GTGCTACTATCATCTTTTCTTTTTTCTTAATAAACTGCTGTGATGGGTCTTTGATGCAGCTTGTGTATGCTTTAGAGTTAAG	6607
Template	GTGCTACTATCATCTTTTCTTTTTTCTTAATAAACTGCTGTGATGGGTCTTTGATGCAGCTTGTGTATGCTTTAGAGTTAAG	6637
Consensus	gtgctactatcatctttctttttcttaataaaactgctgtgatgggtctttgatgcagcttgttgatgcttttagagttaag	
Suyinmai 2	TAAAGAAACCATGAGAACAGTGAAGCAAAATCTTTGGTGGGCTTTTTCTGTATAACATTGTACGGTTCCCTTTTCTCGTCTC	6685
Weisuobuzhi	TAAAGAAACCATGAGAACAGTGAAGCAAAATCTTTGGTGGGCTTTTTCTGTATAACATTGTACGGTTCCCTTTTCTCGTCTC	6687
Template	TAAAGAAACCATGAGAACAGTGAAGCAAAATCTTTGGTGGGCTTTTTCTGTATAACATTGTACGGTTCCCTTTTCTCGTCTC	6717
Consensus	taaagaaaccatgagaacagtgaagcaaaacttttgggtgggcttttctgtataacattgtacggttcccttttctcgcttc	
Suyinmai 2	TTTTATGCCTTGCTCATGTGTTTTAATAAGTTATCAACTGCCAGGATAATGTTGGACCTCAATTTTTAAAGAAGTTACACTTAA	6765
Weisuobuzhi	TTTTATGCCTTGCTCATGTGTTTTAATAAGTTATCAACTGCCAGGATAATGTTGGACCTCAATTTTTAAAGAAGTTACACTTAA	6767
Template	TTTTATGCCTTGCTCATGTGTTTTAATAAGTTATCAACTGCCAGGATAATGTTGGACCTCAATTTTTAAAGAAGTTACACTTAA	6797
Consensus	tttatgccttgctcatgtgttttaataagttatacaactgccaggataatgttggacctcaattttaaagaagttacactta	
Suyinmai 2	GATTAAAAATATATGGCTGCTGGCCTCGTTATGATGTGATACTTTTCAGGTTGGGCTACCCGTTGCTGCTGGAGCATTTGC	6845
Weisuobuzhi	GATTAAAAATATATGGCTGCTGGCCTCGTTATGATGTGATACTTTTCAGGTTGGGCTACCCGTTGCTGCTGGAGCATTTGC	6847
Template	GATTAAAAATATATGGCTGCTGGCCTCGTTATGATGTGATACTTTTCAGGTTGGGCTACCCGTTGCTGCTGGAGCATTTGC	6877
Consensus	gattaaaaatataatggctgctggcctcgttatgatgtgatactttgcaggttgggctacccgttgctgctggagcattgc	
Suyinmai 2	TGCCAGTGACGGGTACGATGCTGACCCCGTCGATAGCTGGAGCACTCATGGGTTTTAGTTTCACTCAGCGTGATGGCCAAT	6925
Weisuobuzhi	TGCCAGTGACGGGTACGATGCTGACCCCGTCGATAGCTGGAGCACTCATGGGTTTTAGTTTCACTCAGCGTGATGGCCAAT	6927
Template	TGCCAGTGACGGGTACGATGCTGACCCCGTCGATAGCTGGAGCACTCATGGGTTTTAGTTTCACTCAGCGTGATGGCCAAT	6957
Consensus	tgccagtacgggtacgatgctgaccccgctcgatagctggagcactcatgggttttagttcagtcagcgtgatggccaat	
Suyinmai 2	TCCTTGCTTTTTGAGGGCGAGGATGAGTTTCAAAGCATCATGTTTCAGAGCAGACAAAAGCCTCACAACTACTATTTCTGATGT	7005
Weisuobuzhi	TCCTTGCTTTTTGAGGGCGAGGATGAGTTTCAAAGCATCATGTTTCAGAGCAGACAAAAGCCTCACAACTACTATTTCTGATGT	7007
Template	TCCTTGCTTTTTGAGGGCGAGGATGAGTTTCAAAGCATCATGTTTCAGAGCAGACAAAAGCCTCACAACTACTATTTCTGATGT	7037
Consensus	tccttgcttttgagggcgaggatgagttcaaagcatcatgttcagagcagacaaaagcctcacaaactattttctgatgt	
Suyinmai 2	GTTCAGACGGGCTGGAGTGAGCAA.....	7028
Weisuobuzhi	GTTCAGACGGGCTGGAGTGAGCAAAGGTT.....	7036
Template	GTTCAGACGGGCTGGTGAGGTAGAGCAAAGTTATCCATCAAATGGAGGAGTACCTGA	7095
Consensus	gtcagacgggctgagtgagcaa.....	

Table S1 List of PCR primers used for *HvPAA1* cloning and functional analysis

Gene	Forward primer (5' → 3')
HvPAA1-RT-PCR-F	ATGTGCTCTTGGTCTTGCCA
HvPAA1-RT-PCR-R	TCCCTCGCTGTGAGAAGCTA
HvPAA1-CDS-F	ATGTCTTGTGGGGGATGTGCA
HvPAA1-CDS-R	TCAGGTACTCCTCCATTTTGA
35SGFP- HvPAA1-F	CTCAGGTACCATGTCTTGTGGGGGATGTGCA
35SGFP- HvPAA1-R	CTAGTCTAGAGGTACTCCTCCATTTTGATGG
HvPAA1- γ -F	GTACGCTAGCTGCAGTGCTGGTTGGTACTT
HvPAA1- γ -R	GTACGCTAGCCTCCGGCAGCCAAACTAAGA
PDS- γ -F	GTACGCTAGCCGACGAGGTTTTTATTGC
PDS- γ -R	GTACGCTAGCAGTTATTTGAGTCCCGTC
PDS- RT-PCR -F	AGTCTTTGGGTGGTGAGGTC
PDS- RT-PCR -R	CTTGAAGATATCGACTGGTG
Actin-F	TGGCTGACGGTGAGGACA
Actin-R	CGAGGGCGACCAACTATG
HvPAA-full-F	ATGCTCGCCATTTTCCCTTG
HvPAA-full-R	CAAAATGGAGGAGTACCTGA

Table S2 The sequences of SNP markers used in the genetic linkage map

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP61179	1H	0.00	bowman_contig_189321	TGCAGTCTGCACAC[A/G]TATCATTTGTCCCAGTCGG CATTTTCTTTATTTAATGGAAGTATCTAA
TP19801	1H	0.00	morex_contig_49842	TGCAGC[A/G]TGGCCCTAGGACCTGGACAGAAGGAA TTTATGAAACCGTTGTGCTTTCACGGCATCA
TP47182	1H	0.00	bowman_contig_1987022	TGCAGGCGCGCCGCGGCCAAG[A/G]CGGCGCCGAG CCCAGCGTGTGCACGCAGCTGTAGGCGGCCT
TP47659	1H	0.00	barke_contig_307038	TGCAGG[C/T]GGCAAAAGCGCGGAAGAGGGCGATGC CAGCATCTGAGGACGATCTTGTGCTGGGCATC
TP50412	1H	0.00	-	TGCAGGGCAGGCCACCT[A/T]GGCGGACTAGGCTCC AATCCGAGATCGGAAGAGCACACGTCTGAAC
TP53592	1H	0.00	-	TGCAGGTACCTGTTCTCATAATCTACGGTGC[G/A]A TCACGCCGTCGTTCTCGACCACATTCTCA
TP61410	1H	0.00	morex_contig_59652	TGCAGTGAAGC[A/G]ATTGAAGAAGCCTCCTCCTCG CCTAGGAGGAGGAGGCAGAGGATGATGCTCA
TP62315	1H	0.00	barke_contig_53331	TGCAGTGCGCCATGTTGGACTCCAGCAGCAGCCCG AGAAGGTCGTCGCTCGTGGCCTC[A/G]CCGAG
TP61180	1H	0.00	barke_contig_203110	TGCAGTCTGCACACATATCATTTGTGGGAGTCGGCA TTTTTCTTTATTTAAT[G/T]GAAGTCCCAGA
TP22233	1H	1.30	morex_contig_40797	TGCAGCCC[C/G]AGCACACCACCTCACATGGTTT GCGTCCGCTCACATCAGATTGATCAATTGCA
TP10212	1H	1.30	morex_contig_399750	TGCAGATGAGCTCTTGGCAGGAAAAGACCAGCCCA TGCAACTGGACGGGCATCATGTGCA[C/T]GGC
TP46664	1H	1.30	barke_contig_2779450	TGCAGGCGATAAGCAAAGCGGCAA[C/T]GCTGGGG AGGCAAGGAGTTGGCTTGAGCAGCGTCCAGT
TP1818	1H	2.60	barke_contig_502131	TGCAGAAGAAGGAGGCGACGATGCGCGATGAGCTC A[C/G]CAAGAGGGCCAAGGAGCTGCACGACAA
TP28289	1H	2.60	-	TGCAGCGCGACG[A/G]CAGGAGCTTTACGGCCATCT GAAGCCCCGAGATCGGAAGAGCACACGTCTG
TP29168	1H	2.60	barke_contig_1567676	TGCAGCGCTCCAATTCCACGCTTGGTTTTCTTCGAA CACGTCGTCGCGCAAATCC[A/G]TAGATGA
TP38479	1H	2.60	-	TGCAGCTTTTCTGCTTTGTTCTC[A/G]TCTTTAGTTAA ACAGCTCATTAGCTCAACTAGCTACCTGA
TP57775	1H	2.60	barke_contig_283709	TGCAGGTTTGTCACTTTCAGAGACCCA[C/G]AGCAA TCAGACATTTATTCCCTGCCCTTGTTTCTGT
TP63416	1H	2.60	barke_contig_265240	TGCAGTGTCGGGT[C/G]GCATGAATGGTTCAAGGGT ATATGAGCGGTCCGAGATCGGAAGAGCACAC
TP10338	1H	3.90	barke_contig_400447	TGCAGATGCACCCCATTCCTCCTCCTGTACACATCC ACCTTGGA[C/T]TCCGCAGCGACAACCACAT
TP30056	1H	3.90	morex_contig_267887	TGCAGCGGCCCGCG[G/T]TGATCCATCGGCGAACTG GTTGTCGTCGGTCCGAGATCGGAAGAGCACA
TP4623	1H	5.17	morex_contig_55791	TGCAGACCTTGTCGAACTCCTTGACGGCGAGAG[C/T]

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				]GCAGTCCTCCTTCTCGAGCAGCGCGCACCC
TP26717	1H	5.17	morex_contig_29228	TGCAGCGCAAAACCCGAAACGGCAAGATCGAGAAA CGTCAGTACAGCCGCGCTGCAC[G/T]CATGGG
TP12164	1H	6.50	bowman_contig_870099	TGCAGCAACACGCAGTGGTTTTGACCGTTGTCAACA AGCTGCAT[A/G]CCGCCAGCCCGCTTTCCGT
TP34315	1H	6.51	bowman_contig_65671	TGCAGCTCGAAGGTAGACACGCGGCCGCAGTGCCA GATCTGGCAGAAGAAGAG[A/C]GCGCCCTTGG
TP15481	1H	9.11	morex_contig_45711	TGCAGCAGACCGACAATCGAGAAATCAAGCGAGGA AG[A/G]AAGAAAGAAAGATCGGCGGGGGATGA
TP36838	1H	10.34	barke_contig_481914	TGCAGCTGGGCTTCAATTTCTTTGAGCTTGGCT[A/G] CCAGACGCCGCCAGGTCTTGATATGGTTGA
TP32762	1H	10.34	bowman_contig_15037	TGCAGCTACGACAACTGCGGCAAGACCTTCGTCGA[C/T]GTGGCGGCCTTGAGGAAGCACGCCACG
TP50496	1H	10.34	morex_contig_8312	TGCAGGGCATGCCAAGTTTCT[C/G]CTAGCTTCCCTT TGCTTTGCTTGCAGCCGAGATCGGAAGAGC
TP3585	1H	10.34	bowman_contig_862606	TGCAGACAATTTTTACCGCTATCAC[C/T]TCCTGTCA CTCCGAGATCGGAAGAGCACACGTCTGAAC
TP34797	1H	12.94	morex_contig_56567	TGCAGCTCGGT[C/T]GGCGAGAGCGCGAACATGTCC TCGTGGCAAGTGTGTATCGCCCGAGATCGGA
TP64276	1H	12.94	morex_contig_354257	TGCAGTTCCCCTGCA[C/T]CTAGCGTCGTCGATGGCG TAGAAAGCTCTAGCCGCATGCCCCCTCTAT
TP1116	1H	12.94	bowman_contig_143159	TGCAGAACATCATCGGTGAGGG[A/C]GGCAAGGAG ATAGCTGAGGACGATCTGGTCTGCCGAGATC
TP1933	1H	15.55	barke_contig_278762	TGCAGAAGAGGCTTTTGTGGGAAAAGGAATTTATCT CAAGAGGCTCGCTTACCA[C/T]GCCAAAGGG
TP2966	1H	18.16	barke_contig_299617	TGCAGAATCACCTTCTTGGCCTCCTCCACCGATTTC CCCAC[C/T]AACTCTGGCCACTCTGTCTTTT
TP50214	1H	18.16	morex_contig_244029	TGCAGGGCAACCTGCTCTCCCTTCGACGTTTGTGT GGGTTCAAATCTATTGTGGTGGAGC[C/G]AG
TP36459	1H	19.46	morex_contig_1562664	TGCAG[C/T]TGGAAGTAGTTGACCACAGAAGGAGGG CGACTGGATCTGGGAGGACGACGGCGCGAAC
TP38885	1H	19.46	bowman_contig_359512	TGCAGGAACAACGTCCTGAAACAATGGGATTGTT[G /T]CAGGAAAACGGTCACGGCTCGTTCACGGA
TP5886	1H	20.76	bowman_contig_69020	TGCAGAGAATGTTGGGA[A/G]AATCAGCTTCTGTAT TTTTAAACAGTTAGTCACTTTGATCTTTTAA
TP24110	1H	20.76	morex_contig_18091	TGCAGCCGCTGGACCGACGTTAGTTACGACG[C/T]G AGGCCGCTGGACCGACGTCATGTTTCGACGCG
TP59468	1H	20.76	morex_contig_48651	TGCAGTCAAAT[A/G]AATTAGTAACATCATTAGAA TATCAAGGGTTCTTCACAAGATAACTAGACT
TP44354	1H	20.76	barke_contig_62011	TGCAGGCAGGCGGTGGTATGAGAAAGATTGTGCAG CAGGCAACATTGTTT[A/G]CAGCATCAAAGGG
TP34976	1H	20.76	morex_contig_136648	TGCAGCTCTAGAACTGCTAACCCT[C/G]CAAGAATA ACAAGCATGTAAGCCTGTTTGGATCAGCTTT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP35187	1H	20.76	morex_contig_66295	TGCAGCTCTTCAATAAAA[A/G]GAGGATTTTCTCTGT GAGATGCTCCAGGAGAGCTTCATTGTTCA
TP49749	1H	20.76	barke_contig_74245	TGCAGGGAGA[A/G]GAGAGCTACATCGATGAGGAG ACGAATCTGGTGTACGTCTCGGACGCTGGCTT
TP12394	1H	23.36	morex_contig_73045	TGCAGCAACGCACGGGGTACAATTTTCTGAAAAAC AGCACTACG[A/G]TGTGAGACCTTTTCACGTT
TP34219	1H	23.36	-	TGCAGCTCCTGCCATGTGATAACCAGCGCAAGGA[C/ T]TAACCGATGAACAAGGATTTCTACATCAC
TP44205	1H	23.36	bowman_contig_221886	TGCAGGCAGCCATGGACGGTCACAACAGCCGC[G/C] CGCAGCGCCTGATTCTGGCGCTCGAGGAGTA
TP38655	1H	23.36	bowman_contig_221886	TGCAGGAAA[C/G]ATCGTGTATACGTAGTATGTATG AACCCGCGCACCCAGATATTATTACCAATAGT
TP42791	1H	25.96	morex_contig_1577249	TGCAGGATCACAAGGAC[A/G]GGGTTTCAGAGGCCT GTTCTCCGAGATCGGAAGAGCACACGTCTGA
TP27062	1H	25.96	bowman_contig_936678	TGCAGCGC[A/G]GTGGCGCGGGTCACCCGTTTCGACG GATTGCCTGAACCAAGTCGTCCCCACCGCCG
TP33282	1H	25.96	bowman_contig_179967	TGCAGCTATTTGATCAGTGGC[G/T]GCCCAAGCTTCC GCAAAGATTGAGTGTGGTGAACCAGACACG
TP63474	1H	25.96	morex_contig_1803195	TGCAGTGTGAGGTCCAGTTTTGAATTCCATGCCCGT GGTGCTTGTCTGGAGCCCGTAC[A/T]GTGCCT
TP18065	1H	27.30	morex_contig_1565287	TGCAGC[A/G]GGGAGATCTCCAACTACATGGTGTAC CTTATGTTTCGTGAACCCGAGATCGGAAGAGC
TP30032	1H	27.30	-	TGCAGCGGCCATGGACGTAG[C/G]CGCGGGCCTGGC AACACTGCATGCACCAGCTCGTCCCCCGAG
TP55331	1H	33.90	-	TGCAGGTCTGGCCACA[A/G]AAGTTCCCGAAGCATC CAGTTCTGAAAAAAAAAAAAAAAAAAAAAAAAA
TP9596	1H	33.90	barke_contig_1862685	TGCAGATCGCAAGTGACACTGCTG[A/G]CCACAACG CCGAGGTCATCCACAACCTAGCCAAGGACGT
TP479	1H	33.90	-	TGCAGAAAGAAGAAATAACCTGCTTAT[A/G]AAAAT ACTTGTGCTATTACGGGCTCAACTTCCCGAG
TP29157	1H	33.90	morex_contig_2551522	TGCAGCGCTCAACCTTAACCTACTGCCCACCGAGGA ATTAATAACGATATTAAACGCAAAAGG[A/G]
TP21188	1H	33.90	barke_contig_281740	TGCAGCCAGAGCGTGCGGTAGA[C/T]GAGGTCCGAC TTGAAGTACTCGGGGCAGACGAAGCCGACGC
TP5319	1H	35.21	bowman_contig_69116	TGCAGACGTAACCTGAATCTAAC[A/C]AGAGGAGGCC GAGCATGGGGAGAAGAAGAAGGGGACGACGA
TP9441	1H	35.21	bowman_contig_1984215	TGCAGATCCTTGTAGTGTACTTGTTCCCAAGTGTATT ACTTCTGAACCCAGAGTT[G/T]CCGAGATCG
TP9643	1H	35.21	bowman_contig_981756	TGCAGATCGCGAATGACACTGCAATATGCGCCAGA GGTCGGGGT[A/T]ATCCCCTTTTCGAAAGAAA
TP52522	1H	35.21	bowman_contig_1984215	TGCAGGGGTTTCCCTCTATATATATGCTCGAACTC[A /G]CTCTCCACTTCTTCCCGCTTCTTTATC
TP59356	1H	35.21	bowman_contig_981756	TGCAGTATGTTGTTTGCATCCCCTGGGACC[A/G]AA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				ATGTTGTGAAGTTTTGTGGACAGTCTTCCGA
TP61978	1H	35.21	barke_contig_269875	TGCAGTGCAGCATCAACGAGGAATTGAAGCAGATT GCACCTGCATTATTTACCC[C/G]AAATTGCTT
TP23784	1H	37.88	bowman_contig_75783	TGCAGCCGCCTGGTTAGATCCGACCAGCTGCCTCTC CCTGCGCTGCTTGCA[C/T]CTGTCCCAATCG
GST6	1H	38.4		GTTTTCTTGTTGGTGTGCGCAATAA[G/A]GCAATATA AGCTTGCGCGCTGG
TP37473	1H	39.12	bowman_contig_866157	TGCAGCTTCATCCAGGCCAGCTTCGCCCA[C/T]GCGC GGAACGCGTCCAGCCGAGATCGGAAGAGCA
TP31457	1H	40.41	barke_contig_139843	TGCAGCGTATACAGTCAAGCG[C/T]GGCAGGTCAGC CACGCCGACGGAGCCACTTCGACGCAGCGCG
TP49632	1H	40.41	barke_contig_2784595	TGCAGGGACGA[C/T]CCCACAGCAAACCGAAGCAGC AACCTGTCACCAACCACCGTGTGTGCTAGAT
TP11932	1H	40.41	morex_contig_1592615	TGCAGCAAAGCTGTGCC[A/T]CGTGACCGTGACCAT GGTGATGCTGCCTTAGCTGTGTCCAACATTT
TP20924	1H	40.41	morex_contig_9427	TGCAG[C/G]CACGCGCCAACCCAGCCAGACCCCGTC GCGCTGGCGGCTGCTGCCGAGATCGGAAGAG
TP27970	1H	40.41	bowman_contig_68763	TGCAGCGCCTCCATCACTCCTGGCCAGCGTGTGTCC TCCTC[A/G]GGCAGAGACTCCTCTAGGGCAC
TP37070	1H	40.41	bowman_contig_68763	TGCAGCTGTCAACGACGGGGGACTGCGTCTACCCTC TGCCAT[C/T]GTCATCGGCCATGCCCAAGGT
TP42121	1H	40.41	bowman_contig_14866	TGCAGGAGGC[A/G]TCGTGCGGCGCGGTGCGCGCCA TCTTCCGCCGCTGCTCGCCTGCACCACCAC
TP54100	1H	40.41	morex_contig_1592615	TGCAGGTCAACATGAGCCTTCTCCTTGCCCTGGAGC TGCTGCTCTTCCTGCT[C/T]GCCTTGCCATG
TP21508	1H	43.01	bowman_contig_74732	TGCAGCCAGGTGTAAGACGAGAGATGGATCATAGT CGTGGGAGGGCCGAACCTA[C/T]GATGAAGGT
TP29579	1H	43.01	barke_contig_473228	TGCAGCGGACAAGGAGACGCATCAGACGGTTCCGC GTAATCCGCTCGATTGGA[A/G]AGACCGCGC
TP9867	1H	45.61	morex_contig_62731	TGCAGATCGTGGTGATGAACATGCTCATGGGGGCCT CCACCGTCAGCAGCATCCTCTCCAC[C/T]TA
TP19950	1H	45.61	bowman_contig_125412	TGCAGCATGTGCCGCGGCGTGTGCGCTCCC[G/T]CTC ACTTTTCTCTCTCCCTCGCGAAGCGCGG
TP23190	1H	45.61	bowman_contig_125412	TGCAGCCGACCTAGCTCCTCGCCCGTGCCGTGCTCT CGATCAGCGTATAGCTACGGTACTTGT[A/T]
TP35045	1H	45.61	bowman_contig_66662	TGCAGCTCTC[C/G]GTCATCGGCTTCGTGCTCCACTT CATCTTACCCAGAGCAGCCCGCTCTGGAT
TP36585	1H	45.61	morex_contig_62731	TGCAGCTGGATGGCCTCCAGCGGCGACGCGCCGCC CATGATGAGCCCCGTCAT[G/T]GCCCCGAGA
TP41556	1H	45.61	bowman_contig_221115	TGCAGGAGCAGCAAGACAGAAGGATGCCCTCTTGT GTTTTGT[G/T]TCTGTCAAGTTATTGCACCA
TP46652	1H	45.61	barke_contig_278060	TGCAGGCGAGTAGC[A/G]GAAGTTGTGTCTTCGAAG GCCGCCGCCCAAGTCCGAGATCGGAAGAGCA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP60075	1H	45.61	morex_contig_2125372	TGCAGT[C/T]CATTCATGCGCACTGCCCCACTCGGTGG TCGGCCACCTGGTATGGTAAACACGCAGAG
TP1994	1H	48.21	morex_contig_150418	TGCAGAAGATGCGGTGCCATCTTCAAGTAATTTCTT GATTTCTTTTA[A/G]TTATGTATTGCTACCT
TP3297	1H	48.21	morex_contig_43334	TGCAGAATTAGGTAC[C/T]TGCAAAGGGACTAGAGA TTGGACTGTTGAGTGGAATTCGGGATGGAGA
TP25814	1H	48.21	barke_contig_275901	TGCAGCGACCATTCTCCTGCCTGGTGCTGAAGCCTGAA AGCAAAGGCACA[A/G]ATCTTTTGAGCAACC
TP4664	1H	58.76	barke_contig_2764424	TGCAGA[C/G]GACAACAGCAAGATTGGTCAGAGAC ATTGCTCTCCTCTCCTTGAAAACGGAACCCGC
TP11036	1H	58.76	morex_contig_109883	TGCAGATGTGGCCCC[A/G]TTGAAGCCTTCTGAAGG AACTGGGTCTCAAATTGATGCCCACTGTCCG
TP36538	1H	58.76	barke_contig_372999	TGCAGCTGGAGGTGAGCAGAGCA[C/T]CCTTGAAGC AGACATCGTTCTTGTCTCTGCTGGGAGAACC
TP6483	1H	60.06	morex_contig_162003	TGCAGAGCAGCCTTTGGCCGCTGCCAGCGCGAAG GT[C/G]TTCGGAGCCGCGCAGCCGCTGGTGAG
TP24641	1H	60.06	morex_contig_364809	TGCAGCCTCCAATGCCGTTGTGCGCG[C/T]CTGCACG ACATCCTCACCACCGTGGACCGAGATCGGA
TP43383	1H	60.06	barke_contig_372234	TGCAGGATGGTTGAGCAAGATATATGCG[G/T]CATC AACTGGCAAGCTAGGGGTGGTGGCGACATTG
TP24646	1H	60.06	-	TGCAGCCTCCACAGCCGCTGCCGCGCGTTGCACAAC ATCCTC[A/G]CCACCGTGGACCGAGATCGGA
TP38588	1H	61.35	bowman_contig_221126	TGCAGGAAAAGAGTCTGTTGAGCTTATTTTTTGTGG GAGCATCCGTCTCAATGC[A/C]GCAGACGGT
TP2554	1H	61.35	bowman_contig_1992394	TGCAGAAGGCGCCGAACCCGTGGGCTTTCTCGAGC AG[C/G]GACACCACGCAGGCCACACGGAGCAC
TP6304	1H	61.35	bowman_contig_860772	TGCAGAGATTCTACGACCCTGACGCAGGCCACATA CTTCTGGACGGGGTGGACATCCAGAA[A/G]TT
TP8811	1H	61.35	morex_contig_54738	TGCAGATATATCTCATGCATGCATGCACATCACCCCT GCCTTG[C/T]CCGAGATCGGAAGAGCACACG
TP11014	1H	61.35	morex_contig_63726	TGCAGATGTGACACTCCCATGCAGCATGCATGTAGT AGCTGGAGACGTGTTGC[A/G]TGCACGATCT
TP26803	1H	61.35	barke_contig_1855624	TGCAGCGCAATATTTTCGTTCCGCAAA[A/T]CCTCATT TTATCGAACTCTAAAACGCGTTTGCAAGTC
TP41354	1H	61.35	morex_contig_1561831	TGCAGGAGAGGGTGACACGGTGGTACATGCAGTCC CTGGCCTCGTGTGCGTCAAAGGG[A/G]GTCGG
TP42558	1H	61.35	bowman_contig_845043	TGCAGGAGTGCCGCGCGCG[C/T]GTCTAATTTTGG ACTTCCGCTTGAGCCAGCATTCACCGAGATC
TP45843	1H	61.35	barke_contig_259752	TGCAGGCCGCATCCACAGTTTCCGTGTGTTGTGGTC CGTCTCCGCCGATGCGCCATCACCC[A/G]CCA
TP64197	1H	61.35	barke_contig_128881	TGCAGTTCATTGCGCGTTAAAGGTAGACAACCTATCC TGTAGCACGTGGAGTTG[A/G]TCCAGTTGGC
TP65860	1H	61.35	morex_contig_51489	TGCAGTTTGCATGAAATCAATCGGCTCGGAACTT[C/

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				T]ACCAGAGGTCCTGGAGTGGAGGGTAATAA
TP171	1H	62.65	-	TGCAGAAAAGCGATAGGACTGAACTGTACCAGAAA GA[C/T]GGGGCCGCATTATTCCGAGATCGGAA
TP396	1H	62.65	bowman_contig_866236	TGCAGAAACGCGTTTCGAGCCCATGAAGCACGC[C/ T]AGGGACACGCCTATGTGCGAAAGGGAAGCA
TP657	1H	62.65	bowman_contig_175506	TGCAGAAAGTCGCACAAAACAT[A/G]GCGAAAATAT CCTAGATTTCTCCAACGAGCTGTGCGCTTGA
TP2066	1H	62.65	morex_contig_127935	TGCAGAAGCAGAAGACAGCAAAAAATA[A/G]ATTA AGAATCGCAACTCATCATACATATCTAACTGG
TP3776	1H	62.65	bowman_contig_64794	TGCAGACAGCTGCTAATTCCATAATACGGTCGACGC GAAATTGAAGCTAGAGC[A/G]JCGGGGATCTA
TP4369	1H	62.65	barke_contig_470676	TGCAGACCGCCGATCTCCTACGAGAATC[C/T]TGCCT CGAAGAATCGGCCATGGTGGACGTGTGGAC
TP5082	1H	62.65	morex_contig_42420	TGCAG[A/G]CGCTTACAAGAAAGCAGGCAATACATG CGAGTTCAAAAACACTCTATCAAGAATAATA
TP5688	1H	62.65	bowman_contig_873074	TGCAGACTTCACATGGAGA[C/T]CTAGGGCCCCATT GCAATACCATTCTTTGTCTGTCTAGCAATG
TP6281	1H	62.65	-	TGCAGAGATGGTACGTAGTAGCATGTGTTTGTTTT GTGTGTGTGACCGTTGATGTTGATGG[A/G]A
TP12512	1H	62.65	barke_contig_60431	TGCAGCAACTCCGACAACCCTC[A/T]CACCCATCAA GTTTCAGAGTCACTCCTGTTTCATGCACGGCT
TP15641	1H	62.65	-	TGCAGC[A/G]GAGCTTCACCGTCCGCTCCGAGTGCT GCAATGAAACGATCGCCGAGATCGGAAGAGC
TP16101	1H	62.65	-	TGCAGCAGCACTACACGTACACGATGACCACCGCC GAGCCTCCC[A/G]JTCCGCCGTCGCCAACCAG
TP18994	1H	62.65	barke_contig_53378	TGCAGCATATCTCAAACCTCCCC[G/T]AAATTAAGT GGATTACCCCTACAATAACACGATATCTTGG
TP22889	1H	62.65	barke_contig_66015	TGCAGCCCTAGATTGGAACGACGTCTGATAGGCTC TTCTTCCCTCTCTCTGT[C/T]TCTGTTTATG
TP26582	1H	62.65	-	TGCAG[C/T]GATGAAGAACAGCATCGCGCCGACAAC AGAAAGTGCGACAGCAAGGATCAGCCTGATG
TP27107	1H	62.65	-	TGCAGCGCATCCCACTCCCTCAAGAAGCCGCCGCA GCATGCCCG[C/T]GTGTCTCCACCGAATCTCC
TP28826	1H	62.65	morex_contig_222866	TGCAGCGCGGCTCTTTGGCGGCGCTGATGGT[C/G]TT CTAGCCAGTGTGGCGAGGATGGCCGAGATC
TP29586	1H	62.65	barke_contig_2623376	TGCAGCGG[A/C]CAGCGGGGTGCGGGCGACGTCTCT GTACGAGCGCGCTGAAGACTCACTCTCCGAG
TP33980	1H	62.65	morex_contig_40685	TGCAGCTCCGAGTTGCC[C/T]TCGGCCTCTAGGCAA AAGAGCCTACCGACCAGCCTCTTTTTGGCTT
TP34769	1H	62.65	bowman_contig_937520	TGCAGCTCGGGGCTGCGTCATTCGGACTCTCGGCAA ACCTGCATGGATTC[A/C]AGAGTGACAAATT
TP34909	1H	62.65	morex_contig_66382	TGCAGCTCGTGCGCGTTGACCGCA[C/T]GACTCGCC AATGGCCTAGCCCTATTCTCGTGCCTACGTA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP41370	1H	62.65	bowman_contig_222294	TGCAGGAGAGTTCTTCTTCTTGGTATCCATATAGTC TACTG[A/C]TGAAGCTCGTTTGTGCGCCAGGT
TP41496	1H	62.65	morex_contig_1566127	TGCAGGAGCA[A/G]GCACGGATTGTGGAGGCTGTAT AGCAGCTCCTGCTCGCAATGTTGTCTCCAGC
TP46106	1H	62.65	morex_contig_41864	TGCAGGCCGTCGACCGCTCCCTCCAGTCCTC[A/C]CA CCAGAGTACGAACCCTCTCTAGCCTTCCTC
TP46662	1H	62.65	-	TGCAGG[C/G]GAGTTGCAGTCGGCCGCACCGCCGCC GACGACGCCGCCGCAGTGCAAGAGGTTGCAC
TP49107	1H	62.65	barke_contig_57281	TGCAGGCTGGTGAGATGCGTAAGGTGAACCACGTC TACTTC[C/T]TTCTCTTTACTCTCGAGTGATT
TP51206	1H	62.65	-	TGCAGGG[C/T]GGCCGACCGAAGAGGCGTTCATGAG GTGGTGCTCGTGCTCGGCGAATCAAGGAGTT
TP53054	1H	62.65	bowman_contig_175506	TGCAGGGTGGGAAGAGGAAAT[A/G]GGAGTCTGGG ATATTTATCTCCGAGATCGGAAGAGCACACGT
TP56630	1H	62.65	morex_contig_41639	TGCAGGTGGTGGGCGCCCCCGCCGCGGCGGCC ACGG[A/T]CCGAGATCGGAAGAGCACACGTCT
TP57575	1H	62.65	-	TGCAGGTTGGTGATGAAGGACTGGCCGAAACCCCA GTTGGGCGGCACGACGTT[A/G]TGGAAGACGA
TP58568	1H	62.65	bowman_contig_64463	TGCAGTACTA[C/T]TGCGTGTTGCGGCGGTGGGCG TGGCGGTGATCGTGCTCTCGCTCACGTTTCCT
TP59425	1H	62.65	-	TGCAGTATTTTTTCT[A/G]TTGGTATGAGATACAAT GGTTTGCATAGCCCACGTGCACTTGCTAGC
TP62354	1H	62.65	-	TGCAGTGCGGATGCAATTTGAGCTTCCCTCCACTCT CTTTGACGCAAGTTTGCAAGCGTCG[A/T]GT
TP63459	1H	62.65	-	TGCAGTGTGACGCCAGAGCGCTTAGGCGTC[A/G]CA CACGCACCTATGCATTATGCAGCCCCGCGGCC
TP64199	1H	62.65	-	TGCAGTTCATTTGAG[A/C]CCTATATGTGTGCTTATC AACAAGTCATTGTACGTAGAAATCCCATTT
TP65577	1H	62.65	morex_contig_42584	TGCAGTTTACCTTTCGCAGAA[C/T]ACTGCTTGCTGG AGCAGTAGGCTCAACCCGAGATCGGAAGAG
TP65627	1H	62.65	morex_contig_46307	TGCAGTTTATTT[C/T]GAGAAGTACATTTATGTTTCC AATGATCTTGTTGCACAAGGAAATCACATC
TP66015	1H	62.65	barke_contig_1854775	TGCAGTTTTCACT[A/G]TGGAGGTCGAGAACCTCAA GGCCGAGATCGGAAGAGCACACGTCTGAACT
TP3549	1H	71.85	-	TGCAGACAAGGTTGAAGCGT[A/C]ACGAATGGCTTA ATCTTCTTTAGTTCTTTTCACTTCCAAGTGT
TP3913	1H	71.85	barke_contig_1870849	TGCAGACATGGAGAGCTGGGCGGCAGC[A/G]GAGA TGAGCCAGACGGGCAGGGGCAGTGGAACGCG
TP16728	1H	71.85	bowman_contig_64749	TGCAGCAGCGACGAGAGCTGCCGCATTCTCGCTA[A/ G]CCCAAAGAAACGGCCCGAAAGAATCGGGC
TP37609	1H	71.85	morex_contig_1564278	TGCAGCTTCGAGGCGTACCAGGACAC[A/G]CTCTAC ACGCACTCCCTCCGCCAGTTCTACCGCGGCT
TP45846	1H	71.85	morex_contig_1564278	TGCAGGCCGC[A/G]TCGGGGTCGTGGTCCGACCGTG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				GAGGCGGCCTCGCCGAGCCGATCTCCAACGG
TP30760	1H	73.15	bowman_contig_217	TGCAGCGGGAGGTTCGAGGAAAGGTGAAGCGAGTTT GGTAAAAAAAGAGGCGGG[A/G]CCGAGATGA
TP54384	1H	73.15	morex_contig_2553349	TGCAGGTCCAACCTTTTGGAAATATCACGTAGTCAG ACATGTGAGAAAGATTGACTCT[C/T]AAGTC
TP61820	1H	73.15	morex_contig_48566	TGCAGTGATTTCTCTTTTCATCAGAAGAATAAAAGA ACCAATTTAGC[A/G]CAGTGTTTGTCTTTTC
TP35949	1H	74.44	-	TGCAGCTGCGAGATTGGATCGGC[A/T]AGCACTGCG GACACCCGAAAAAAAAAAAAAAAAAAAAAAAAA
TP35950	1H	74.44	-	TGCAGCTGCGAGATTGGATCGGC[A/T]AGCACTGCG GACACCCGAGATCGGAAGAGCACACGTCTGA
TP38672	1H	74.44	bowman_contig_1025830	TGCAGGAAACCCTTTTAAAATATTTCTGAACCTATC ATTATTTGTGGAAAAAATGGTTTCAC[C/T]G
TP45857	1H	74.44	-	TGCAGGCCGCCACAGCCGCCGCGAG[A/G]CCCGTTC ACGCCGAGATCGGAAGAGCACACGTCTGAAC
TP46129	1H	74.44	bowman_contig_125597	TGCAGGCCGTTCGGCGCACGTCTGCTGGTTGGTCAGG ATCGCCGACAGCAGCGTCTGCAC[A/G]TCCT
TP22507	1H	77.04	barke_contig_316890	TGCAGCCCCTGAAGAAGGATGC[A/G]TCGCAAGTTA AGCGAAGCAAGGTCGAAATAATCAAGGAGAA
TP43742	1H	77.04	barke_contig_2782439	TGCAGGCAAGAAGAAAG[A/G]TGCAAATGTGTAATC CCTCCGAGATCGGAAGAGCACACGTCTGAAC
TP38555	1H	82.49	bowman_contig_870465	TGCAGGAAAACAACATAGTGGAGCGTGTCAAGCAC AATGTA[A/G]AAGAGTACAAGTACATAACTGA
TP26093	1H	83.50	bowman_contig_872002	TGCAGCGACTTCGTTTCGTTACATAAAT[C/T]TGATTA CCGCCGACCTGTGGGCAACTCGAGTTCTAG
TP6496	1H	86.06	bowman_contig_877463	TGCAGAGCAGCTCAGGAACGACGGTCCTGCC[C/G]C CGCGACGGCTTCTGCGACCGACTGTGCGAGT
TP33920	1H	86.06	barke_contig_126614	TGCAGTCCCGCCGTGGCACCGCCTGCAAGGAGAG GAACCTGTCTGA[C/T]GGCGTACATTGTGAGGT
ATPaseB	1H	106.2		AATATTTGGCATATGAATGTGGGAA[G/A]CACGTTC TTGTCATCTTGACAGATA
TP42438	1H	122.98	bowman_contig_859985	TGCAGGAGTACAA[A/G]GCACACGCGGACAGCTTCA TCTGCTCCATGGTGCCCGAGATCGGAAGAGC
TP57570	1H	122.98	morex_contig_1579985	TGCAGGTTGGT[C/T]GTTCTTGGGGTTGATCACACAC CATAATGTCAAGGAAGCGCTGGCCACAAAT
TP3857	1H	125.48	bowman_contig_891947	TGCAGACATATTCACAGTTGC[C/T]GATCCTCTCGAT GGGAGCACCGAGATCGGAAGAGCACACGTC
TP24627	1H	125.48	bowman_contig_22565	TGCAGCCTCATCGAGATCGACGGCGTGGT[G/T]CAC GAGTTCCAAGCCGTTCCGAGATCGGAAGAGC
TP1598	1H	130.69	morex_contig_140117	TGCAGAACTAGCCAAGTCTTGAAAGGTGTGGATG T[C/T]GTTGTCATCCCTGCCGAGATCGGAAGA
TP32456	1H	130.69	morex_contig_136849	TGCAGCGTTTAATAGGAAACGCCTATCACGCCCTTC TTCAGATCGACCGTG[G/T]TCTCTTTTAGT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP8644	1H	130.69	morex_contig_51045	TGCAGATACTGGAAGTGGCGGAACAG[C/G]TCGTCTG TCTCCCTCCTGCGAGTTGTCCATCACCGAGA
TP5903	1H	148.28	morex_contig_1580847	TGCAGAGACACAAGACAAACTATAGGAATCAGCAG GCAACACGAAGCAAGCAAACAGCAA[C/G]CGA
TP22155	1H	148.28	morex_contig_46243	TGCAGCCCATGGATCGGTGGAATCATGGATC[C/T]C TCCTCCAAC TGGAACAATCAAGATCAATGTT
TP29113	1H	148.28	morex_contig_1593140	TGCAGCGCTACCACGGTGCCGCTCTTGCCTACCTT GTTGGTCGATATC[A/G]TCTTTGTCCTGCCG
TP42450	1H	148.28	morex_contig_6024	TGCAGGAGTA[C/T]GGCCATGTGGCCGACGCCAACG TCTTCTACTGGTTCCAGAACCGCAAGTCCCG
TP11704	1H	148.28	bowman_contig_66072	TGCAGATTTTCTTGAAGCAAGTAAACCTGTTTTTTT A[A/G]TTGACAACATGGGAGCATGTAAGAGC
TP18600	1H	148.28	morex_contig_1559731	TGCAGCAGTCCCCTCCTTCATGGGGCCAAAGAGCTC CGCCATAAA[C/G]ACGGCGGAACGGGACGCG
TP24995	1H	148.28	morex_contig_1572401	TGCAGCCTGAGGCATGCACCACCATGTTC[C/T]AGC GAGAAAAACACATCTCAGGCCAATAAACCTC
TP32335	1H	148.28	morex_contig_266577	TGCAGCGTTAACAGAAAAGCAGCAGCTAGTG[C/G]T AGTGCAGTACAAGAGCCGTATACATTCCACT
TP65127	1H	148.28	bowman_contig_67492	TGCAGTTGCTAGATTGTTGGTTGTGATGGATTGGGG GCTGT[C/T]CCTTGTCCGAGATCGGAAGAGC
TP38101	1H	150.87	-	TGCAGCTTGGAGCACCTTCCGATGGCCTTGAGTCCT T[C/G]GTTGGCAACGTCACAGCATGATTCAA
TP49735	1H	150.87	bowman_contig_143462	TGCAGGGACTTTCGCGTCGTACATGGTCGTGAG[C/T]]GCGTTCACCTCGTGTTCGTCACTTTGG
TP62234	1H	157.74	barke_contig_118351	TGCAGTGCCTCGCCACGCTGGGTGTCTGCTCTTCCC TGCCGACCGACAGGTGCCATTTAAAAA[A/T]
TP13146	1H	158.73	morex_contig_66005	TGCAGCAATCTACTAC[C/T]AAAGTGCTTTTTTTTGT TTGGCCACGCAGGATGTCGGTGCCGAGATC
TP15948	1H	158.73	morex_contig_52827	TGCAGCAGCAACGTAATTAGATCAGAATGC[A/G]TT CATTCAGTCAAAATTGAATGCAAGAGGGAAG
TP28730	1H	158.73	barke_contig_8179	TGCAGCGCGGCATCGTGGCCACCAACCAGATCGCG CACAACGTGAC[G/T]TCCACGCTGCACATCAT
TP31745	1H	158.73	bowman_contig_898196	TGCAGCGTCGCCGTGGCTCCC[G/T]CGCCAAAGCTG GACCCTCCTGGCATGTGTGTAGCTCCAACAA
TP37580	1H	158.73	morex_contig_1570108	TGCAGCTTCTCCCCTGCCAGGAGAACCGAGCCCAG CTCGATGCGCTC[A/G]GGATGGAGAAGGTCG
TP49410	1H	158.73	-	TGCAGGGAACCAGTAAACAAAATTGCTACAACCAT CAATGCAAAATGCTA[C/T]GACCGAGATCGGA
TP57997	1H	158.73	-	TGCAGTAAGACACCTACAGAAAAGAAAGGGTAAAG ACATGCTCACAT[G/T]AAAACCATATACGTAT
TP2157	1H	160.03	barke_contig_54302	TGCAGAAGCCAGACTC[A/T]ACTAAAGCTTTTGACT CATTCCTTGAGAAACGTAAAGCAGCTCCATC
TP2396	1H	160.03	barke_contig_1794516	TGCAGAAGCTGGTTACAGGAGCTGCACAC[A/G]ACG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				AACGGCGCGCCGCCCTTTGCCGAAAAAAAAA
TP8588	1H	160.03	barke_contig_2804026	TGCAGATACGCGTCATGGATTGGGTTTGTGATCATC ATATAATAGTACTAG[C/T]CGTCCTTTTTTC
TP9267	1H	160.03	bowman_contig_13082	TGCAGATCCATGGTTCACTAAACACTAATCAAGTGA ATTCAAGAGCC[C/T]TTACAACCAAAGGTGG
TP19691	1H	160.03	morex_contig_44745	TGCAGCATGCCTTGGTTAGA[C/T]GACGATGCCGCT GAAGTCTCCTTCCCGAGATCGGAAGAGCACA
TP20072	1H	160.03	barke_contig_271782	TGCAGCATTGAGCAATGGAATTAGTATGTTTGATGA TTC[G/T]GTTTTGTGAAATGCATCTGAGATT
TP29744	1H	160.03	-	TGCAGCGGATGA[A/C]GCGAGGGGCAACCGTGGGG ACGGCGCCGAGATCGGAAGAGCACACGTCTGA
TP34720	1H	160.03	morex_contig_65576	TGCAGCTCGGCGTCGTCACGGCG[C/T]GTCCCTGA CCGAGACCGTCTCTTCAGCACTCGGCTCGGG
TP35906	1H	160.03	barke_contig_373008	TGCAGCTGC[C/G]GTTTCATCTATCGATCGAATCAAT CCAGGAGACGAGGCAACATTGGCCCAAAAC
TP36658	1H	160.03	bowman_contig_883131	TGCAGCTGGCCGTCGAGGAGGC[C/G]GCCAAGCTGC TGGAAGGGGAGAAGCTGGAGATCGTGGACTT
TP36982	1H	160.03	morex_contig_156695	TGCAGCTGGTTAACCAGAATAGTAGTTAGCTGGT[A/ C]AGCAATATACTACTCCATCAGGCAATTAT
TP38830	1H	160.03	morex_contig_48809	TGCAGGAAATCGTCGTCGCTGTA[C/G]CCGTCCTTG AGCCTCTCGTTGAGCACCGTCACGAACCCCG
TP44274	1H	160.03	bowman_contig_116691	TGCAGGCAGCTGATGGCGCTCGTGTTGACTTGGTG GCGCTCAAAGCTGCTCG[A/G]TTCGTACGTA
TP44449	1H	160.03	barke_contig_2779723	TGCAGGCAGTGTCGCTTTCAG[A/C]TCTGCAACCTCC CACACCGAGATCGGAAGAGCACACGTCTGA
TP48126	1H	160.03	bowman_contig_9264	TGCAGGCGT[C/G]ACCGTCACCTCCTCGATCAGCGC CTCGATCTCCGAGATCGGAAGAGCACACGTC
TP48338	1H	160.03	morex_contig_156695	TGCAGGCGTTGGGTACAACCTTAGCCATTGGCGACG GCAA[A/G]TAAAGTTGTGATAATCATGCAAGT
TP48503	1H	160.03	bowman_contig_883131	TGCAGGCTCACTGC[G/T]TTCACCACAAAAGAATC ACACCGTATATATATACCTGGGAGGGTTCTG
TP57240	1H	160.03	bowman_contig_67501	TGCAGGTTCTGGTTGTACCGCTCCTGGACG[C/T]CAT GGCGTCCGCCGAGTGCTGCTGCGCCTCCGC
TP58083	1H	160.03	barke_contig_545066	TGCAGTAATCTTA[C/T]AATTAACCATGCATGCATGC ATGAGCAGCTCGAGCCAATCGAGAACAAC
TP58084	1H	160.03	morex_contig_39104	TGCAGTAATCTTATACTTAACCATG[C/T]ATGCATGC ATGAGCAGCTGGAGCCAATCGAGAACAAC
TP59665	1H	160.03	barke_contig_271782	TGCAGTCACTCAGATGCTACTTTGGAAAATGAACT TCCAAGGAAGATGAAAA[A/G]GCTATATTAA
TP60256	1H	160.03	barke_contig_1791971	TGCAGTCCGCCGTTGATGGAGTACTCTAGTGACACT TTGTTA[A/T]TGTCGTCCGAGATCGGAAGAG
TP60856	1H	160.03	barke_contig_587847	TGCAGTCGGGAACAATTC[A/G]AGGGGGTTTTTCAA AATTTCCAATTATGTTTGACCGAGATCGGAA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP60864	1H	160.03	bowman_contig_870990	TGCAGTCGGGCACCCCAAATCCGC[C/T]TCAAACGT CCGAGCTGACGGCCCGAGATCGGAAGAGCAC
TP61331	1H	160.03	morex_contig_135979	TGCAGTCTTTGTTGCCATATGAGTCTGTACTCTTGAT GAAAT[C/G]CTCAACCCACGATGATAATAA
TP62706	1H	160.03	bowman_contig_149713	TGCAGTGGAGCGTGTCCAGGCGGTGACGATGACGG GTGCTCGATGGTTGTTTGCGAAGGACA[C/G]G
TP63448	1H	160.03	barke_contig_541871	TGCAGTGTGAAATAGTGTAaaaaaATCTACAGTCAA CAAAGC[C/T]TTTTATGCCATGACCCGAGAT
TP65822	1H	160.03	morex_contig_43798	TGCAGTTTG[A/G]CTAGCTAGCACTGTGCTACCGTTG TGATGTTGTGTAACATGGTACCATCTCCTC
TP13	1H	161.32	morex_contig_1569224	TGCAGAAAAAA[C/T]AAAAAGCGGCTTCCGCGATGC TGTCAACTGTCTGATCGAGCGGCCACTAAGC
TP6664	1H	161.32	morex_contig_2521503	TGCAGAGCCCCCTCATAGAATTGATCGAAGAAAGC CATA[A/G]TGTCTGTGCTTTCTGACGAGCTGC
TP11916	1H	161.32	barke_contig_73724	TGCAGCAA[A/G]GATGGCATGTCTTCGCAATGTGAC AGCAGAAATCCCAAGAAGAAAACCATGAGCT
TP12848	1H	161.32	barke_contig_518252	TGCAGCAAGCTTCCT[C/T]TTGCTAACCATCATCCTA GCCAGCACCACCAGCGCCACCTCCTCCTCC
TP25141	1H	161.32	morex_contig_8647	TGCAGCCTGCTCCTCCTCAC[A/G]TAACACATCGAA CAGTCTCTGCTTCTTCTGCTCTGCCTTAGAC
TP33143	1H	161.32	barke_contig_118724	TGCAGCTAGTCGTGATGTAGTA[C/T]GGAAAGAAGA TGGGAGGACCCTGCTGCTCCACGAATCTGAG
TP41799	1H	161.32	bowman_contig_21265	TGCAGGAGCGTCTTCGCCCTCGACTCCCCGCCGCTC TGGGG[C/G]CTCCAGTCCGTCTGCGGCCGCC
TP53450	1H	161.32	barke_contig_272256	TGCAGGTAAGCTCTTTCACCTCTTAGTTTTGGCG[G/T]]TGTTAGTTTCTCTTTTATCTGCTGAGGA
TP61403	1H	161.32	barke_contig_60483	TGCAGTGAAGAGGAGCGAGCCGCCACACCTGCTTC CGATT[A/C]TTCTTCATCTGGGCCTTATCCGA
ABCt2	1H	0		AGAGACTTGCATTTCTATCCACCAT[T/G]GGCTTTTA CGCTTCCTTCTTGGCTC
TP2808	2H	0.00	-	TGCAGAAGTGTCCGAC[A/G]TATAACTTTTCCAGTG AATCCGAGATCGGAAGAGCACACGTCTGAAC
TP5259	2H	0.00	barke_contig_378261	TGCAGA[C/T]GGGTGCAGCAAGAAGTCCTGCTATGT CATCTGTCAAGAGCTCACACAGTGTGGACGA
TP10453	2H	0.00	morex_contig_48487	TGCAGATGCCTTCCTTTAGTCACGAGGAC[A/G]GTG AATCAACCAATTGCTTGCCATCAACATCAAC
TP11430	2H	0.00	morex_contig_2550001	TGCAGATTGATGTCTTTGTTAATGCAAAGTTGCATG CATACAAGGATGGTGTGTTTGGCTCCCG[A/C]
TP15655	2H	0.00	bowman_contig_143370	TGCAGCAGAGGAT[C/G]TACGCGGGTGGCGGTGTCC CTGATGTTGAGCACACCGAGATCGGAAGAGC
TP33273	2H	0.00	morex_contig_48049	TGCAGCTATTGCTTCTGGTTAATTGGTCCAAGTGGA T[C/T]TCAAGTGAATCTTACCAGTTCGTGTC
TP36037	2H	0.00	bowman_contig_859994	TGCAGCTGCGGCAGGGTGTACGGCTACGCCGTCAG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				C[A/G]TCATGCCAACGCCGAGATCGGAAGAGC
TP38067	2H	0.00	morex_contig_1563469	TGCAGCTT[G/T]CTGAGGACGGCGAGGGCGCTTGCG GCGGAAAGATCCATGGACGCGGGGGGAGGCC
TP56039	2H	0.00	-	TGCAGGTGCTACACCAAAGGATGACCGCCGAATAC[G/T]CGAGTATGCCGAGATCGGAAGAGCACAC
TP59954	2H	0.00	morex_contig_267414	TGCAGTCCAATACTAAAAAGTAATCTCAGACATCTG AG[A/G]CCGAGAGGAGTGATGCTGAAAGTCT
TP62326	2H	0.00	bowman_contig_15026	TGCAGTGCGCGAC[A/G]CCGCTCCCCCTGCTGCGGC ACGTGGCGGGCCGCGCCATGGCCGCCGAGATCGG
TP64787	2H	0.00	morex_contig_41048	TGCAGTTGAA[A/G]TAGGCTCCCCTTGGCCTAGATTC GGATCTCACGTACGGCGCCATGAACGCGTA
chitinase2a	2H	18.3		AGGGCAACAAGCCGTCGAGCCACAA[C/A]GTCGCCC TACGCCGCTGGACGCCGA
TP55154	2H	34.45	-	TGCAGGTCGTC[C/T]GACGCGTTTTTTGGATGTCAGA ACATCCCGAGATCGGAAGAGCACACGTCTG
TP53831	2H	34.45	barke_contig_269593	TGCAGGTAGCTTATTGCAGATTTCAAGTGTTCGGAAT AAAAGATGACTGACAGGATCG[C/G]TATAAT
TP30995	2H	34.45	-	TGCAGCGGGTACATGTGGTGCCCATGAAA[A/G]TG TGTCGGACCGAGATCGGAAGAGCACACGTCT
TP3397	2H	34.45	bowman_contig_63848	TGCAGAAATTTGCTATTGGTCTCCTCCAAGGGCCCAA GAGGTAG[A/G]TATCTTATATACTAGTAGCA
TP57702	2H	34.45	morex_contig_67574	TGCAGGTTTCATGCAACGCACGCAATGCAAGCTGTT CGATCCAAAGCCAACTAGCTAATCACCC[A/G]
TP49597	2H	34.45	bowman_contig_1985886	TGCAGGGACCCCAAGCACTGGGA[C/T]GCCGCGGAG GAGTTCAGGCCGAGATCGGAAGAGCACACGT
TP39044	2H	34.45	bowman_contig_63848	TGCAGGAACCGAGGGGCGAG[A/G]CCGAAAGAAGT CTCGGCGGGGCAGAAAAGGAAATCTCCCGAGA
TP27814	2H	34.45	bowman_contig_10439	TGCAGCGCCG[C/T]GGGACACAGGGGGGGAGGGGG AGTGGTCGTCCTCAGCAGGAACAGCGGCGGAG
TP10433	2H	34.45	bowman_contig_125833	TGCAGATGCCGAGCTCGCGGAG[A/G]TGGGGGAAG GAGGCGCCACGCAGCGCGGCCGTGCCCGAGAT
TP9619	2H	34.45	bowman_contig_1985886	TGCAGATCGCCACGCGTTCACGAACACGGTGG[C/T]]GCCCTTGGGCACGTCGTACCCGAGGACCTT
TP8308	2H	34.45	morex_contig_44971	TGCAGAGTTTGAAATGCGATAAACCCACTGGTAAC CACCTG[A/G]GCCTCAAGTTCTGGGAAGAGTC
TP5998	2H	34.45	morex_contig_55908	TGCAGAGACGTCCAT[A/G]GCCGTGCCGTCGTCTCC AAAGCCTGCCGAGATCGGAAGAGCACACGTC
TP65042	2H	45.00	morex_contig_44492	TGCAGTTGCCCCGCTTAACCCTGTTACCCAAGGCCTC ACAGTACC[A/G]ACTTTCTTCGCCCCGAGATC
TP63460	2H	45.00	bowman_contig_149324	TGCAGTGTGACGCCGAGAGCTTAGGCGCCACACAT GCA[C/T]TTATGCTCGGCGCTCAGGCACTCTT
TP63268	2H	45.00	morex_contig_44492	TGCAGTGGTT[C/T]GCCGACAAGGGCCTCACCGCCT ACAGCATCTCCTGCGGCACCTCCCTGCTGTA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP34998	2H	45.00	-	TGCAGCTCTATC[A/G]ATCCTCCTCCCATGATCTTCT TGCTTACAGCGATGCTGATTGGGCGAGCTG
TP33068	2H	45.00	bowman_contig_69836	TGCAGCTAGCTGAACCCGTCGACGTTTCG[A/T]GCAG ATATTTTCGCCTTCTGAATCTCCATTGCTGG
TP32460	2H	45.00	morex_contig_276521	TGCAGCGTTTCCACTTTTGGGGACCTTTGAGAGT[A/ T]TCCTAGAAGTTTTTCTGGCTTTGGGCCT
TP27748	2H	45.00	-	TGCAGCGCCGCGCGCTGTACGGCGTCGGCATCGG[C/T]GCTCCGAGATCGGAAGAGCACACGTCTG
TP25666	2H	45.00	-	TGCAGCGA[A/T]TAGCAGTTTCCCCTCAAAAATGGG TCACCTCGTCACCACTTCGACTCCCCGAGAT
TP2043	2H	45.00	morex_contig_8694	TGCAGAAGCACCAGATCAGCGAGTCAGCACGCTCG AACCCCATGGCACCGCCCCCAATCG[C/T]CC
TP63428	2H	46.30	-	TGCAGTGTCT[A/C]CATACACCACATGTCCACATATG GCTGGATGCAATCGTTTTCTGCTAGGAAAC
TP59916	2H	46.30	-	TGCAGTCATTTTCGGGCAGCATGGAAGAGAGC[T/A] CAAATTCTATATCCCGTCCATGCATTTCAT
TP57945	2H	46.30	barke_contig_380722	TGCAGTAACCAGTTTGTCACTACTT[C/T]AATAGATA TAATAGAGTATACTCATCATCGTGTAAAGCA
TP51793	2H	46.30	morex_contig_37899	TGCAGGGGATCACCGACTCGTTGTAGAACGC[A/G]G AGAAGGACACGCAACAATGCGGCGGCTTGCC
TP47172	2H	46.30	bowman_contig_859491	TGCAGGCGCGCATGGAGCAGAGTGCTCGGCTTCTG ACACCAACTCTGTCAAGGCCCAAGCT[C/T]AC
TP43801	2H	46.30	morex_contig_48444	TGCAGGCAATCCTCGGCATGACTGTGCTGCTGCCTC ATTGGATAGTGCATCCCATATGCCATC[A/C]
TP35662	2H	46.30	-	TGCAGCTGCACCTGCACGGCGGCACCAGCG[A/G]CG GCGGCGGCATTGTTGGTTGTGCGCCGAGAG
TP35636	2H	46.30	-	TGCAGCTGCACATGCACGGCGGCACCAG[C/G]GGCT GCGGCATTGTTGGTTGTGCGCCGAGAGCGA
TP33330	2H	46.30	-	TGCAGCTCAACTTTGTGTTGCTATCTACGGAAGGC CAACATCCCTCA[A/G]CAAAATGATCACATT
TP26789	2H	46.30	morex_contig_54751	TGCAGCGC[A/G]AGGCAGAGGGCCGTTGCTGTGCGT GATATGAAGAGGCCGACGACCCAACTGGC
TP24501	2H	46.30	-	TGCAGCCTA[C/T]TCCTCCGATGCAGTGGCCGTCAAT ACAGAATCAGAGATACGCAAGGGATCATAG
TP9952	2H	46.30	bowman_contig_878275	TGCAGATCTCGAACCCTGATTCAATCGACTCCTAAC ACATAAGCAACCAGCTAGA[C/T]CACCAGCT
TP7094	2H	46.30	bowman_contig_871991	TGCAGAGCTCCACTTGCGGGAGCCTCTTATTTAACA CTCTTTGCGTCAATTAAGAGGTCTTT[A/T]
TP3906	2H	46.30	barke_contig_396116	TGCAGACATGCCATGCATATGGCTGACAAATGGCGA AAA[C/T]ACAACCCATGACGAGCAGGCGTCTC
TP2297	2H	46.30	morex_contig_135631	TGCAGAAGCTACAGCGTTCTCAGCAAGGCG[A/G]AC TCGACGGTGCCGAGATCGGAAGAGCACACGT
TP13049	2H	46.30	-	TGCAGCAATAAAGG[G/T]CAAAAAATCCCCGTCATC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				ACTGAGCTGTGGGGCACACGCGCCTCTCCC
TP64156	2H	58.21	-	TGCAGTTCATCCACATCGCGAAGG[C/T]ATTTTTTCT ACTTACAAAAATGGCGTCCGAAAAAAAAAA
TP64157	2H	58.21	-	TGCAGTTCATCCACATCGCGAAGG[C/T]ATTTTTTCT ACTTACAAAAATGGCGTCCGAGATCGGAAG
TP61284	2H	58.21	bowman_contig_849574	TGCAGTCTTCCCCTCCCCGTTTCACTTTT[A/C]GTGA GCGTTTTCTTATCCACACGCACTCGCGGCC
TP49639	2H	58.21	bowman_contig_1982097	TGCAGGGACGAGATGCGCAGGGTGCTCGGCGT[G/C] GCGCTGCTCTGCGCCTCCAGCCTCCCGATCA
TP43562	2H	58.21	bowman_contig_884450	TGCAGGATTGCTGCCGCGCAGA[C/T]GGGCTCAGCT CCAAGAGCCCCAAGATCAGCATGCCAGTAG
TP33902	2H	58.21	morex_contig_51248	TGCAGCTCCCGAAGGGGGAGCAGCTTATTTGGGCG CCTCTTCTCAAGCACCGCTGGATCCA[A/C]AT
TP31050	2H	58.21	bowman_contig_13395	TGCAGCGGGTGCGGTACCT[C/G]AACGTCGGCATCT ACCCGTTACCTCCATCTTCTGCTCACCTA
TP16309	2H	58.21	morex_contig_37304	TGCAGCAGCAGGAC[G/T]ATGACGACCACCGACGCC ACGAACGAGGTCGAGTTGCAGTAGAAGAAGG
TP10773	2H	58.21	morex_contig_39661	TGCAGATGGCGGTGAAAATGCATGTGTCAGCAAAT ATAGGACTGATCCATCATTTTGGAAATG[A/G]
TP9111	2H	58.21	morex_contig_164370	TGCAGATC[A/C]TAGGAGAGGTGGATTATCGAACAG GTCTGAAGTAATTAACCAACATCTACTAGGT
TP4465	2H	58.21	barke_contig_268711	TGCAGACC[G/T]TGGTCACCACTCGCCACCACAAAT TTTCTATCCCTGGATGACCGAGATCGGAAGA
TP975	2H	58.21	morex_contig_37304	TGCAGAACAAACGTGTTGCTGCTCTATGCCATGAACA CGGCGATCGTGCTGGACCTGCTCGG[C/T]CT
TP52666	2H	59.51	morex_contig_66374	TGCAGGGTCATCTGGTTCATGGCAGAGTAGAGGGC C[A/G]CCGAGATCGGAAGAGCACACGTCTGAA
TP65352	2H	60.81	-	TGCAGTTGGTCC[A/G]AACCATGCAATGCGTGCGCT GGCATGCGGCACAGCCTTGAGTACTTGGACA
TP63424	2H	60.81	-	TGCAGTGTCGTGCT[A/G]GGTCCAGGCGGGCCAGCA TAGCCATCCGCGAATACGTCCATGGAGGATC
TP62294	2H	60.81	morex_contig_1575898	TGCAGTGCGAGCCAAACCCTCT[C/G]GACTACCTGT CCTTCCCGATAGTCAGCACGGCGATCGAATA
TP15954	2H	60.81	barke_contig_54782	TGCAGCAGCAACTGCTTCGGCAAGATGAGC[A/G]AC AGTGAAATCATATTTATGGATCAAATGCAAG
TP9739	2H	60.81	morex_contig_1561391	TGCAGATCGGCGA[C/G]CCGTTCTCCTCCTCATCACC ACGACCACCACCGAGATCGGAAGAGCACAC
TP42469	2H	60.81	morex_contig_140099	TGCAGGAGTAGCAGCCAACCTCTTCTGAATCTGC CTGTAGAC[A/G]TGCAAGCAACGTACTTTTA
TP41047	2H	60.81	bowman_contig_67102	TGCAGGACT[G/T]CTATAAGCCCATGCACCTTCCCCT GCTCTTCGATGGCTCGCACGTGCCCTGCAC
TP53127	2H	110.81	morex_contig_160066	TGCAGGGTGTGGGCGGGGAGCTGCCACCCGTGACG CCGCGCCATGGCGGCGC[C/T]GCCGCGGCGGG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP61068	2H	110.81	bowman_contig_1985453	TGCAGTCTATTTCTTAACCTTCTGAGTCACTTTTCACT GAAAGCCGAATTATA[A/T]CTATCTTGGA
TP152	2H	121.78	morex_contig_1560381	TGCAGAAAAGACGAGAACACATGTGAGGCGTACTG CGTACAGT[A/T]CAGCACAGTACAGCGGTTCA
TP1019	2H	121.78	bowman_contig_851495	TGCAGAACACATGACCAATCAAGAAT[A/C]TATACA TGCTACAAGCCCCTTCACAAATAATCCTTTT
TP3868	2H	121.78	barke_contig_2783595	TGCAGACATCATTTTCCATGTAAATTATGGAGAC[A/ G]GTAGGTCCTGCACCGTCTACCAGGTTGTG
TP5553	2H	121.78	morex_contig_41384	TGCAGACTCGAGTATCGGGGCGGCAGGGTTTCGAT CG[A/G]GAGGAATCCGAGATCGGAAGAGCACA
TP17477	2H	121.78	bowman_contig_1987151	TGCAGCAGCTTTG[C/T]CAGGCCAGGTTTATTTTCTG TCATGGTTCAGGGTGTCTAACTGTATTTAA
TP27066	2H	121.78	barke_contig_4583	TGCAGCG[C/T]ATAAAAATCCCTTCGATCGATTCGTC AGCGGCAGCAACAGTGATGAGCTTGGTAGT
TP41250	2H	121.78	morex_contig_50474	TGCAGGAGACGCCCGTTATTCACCTCAGACGGAGC AGCGGGA[C/G]GGGTTGGTTGACTCGAGACCG
TP43565	2H	121.78	bowman_contig_10214	TGCAGGATTGGACATGGAAGTACACTTTTACTC[A/G]TGATGTTAGGCATGTTTTACACACATGAAA
TP50342	2H	121.78	morex_contig_2551748	TGCAGGGCACGTAAGAGGATTATTAGAGGAACGGT TAAC[C/G]AAGCAAGAAATGCATGGCGTCGTT
TP50873	2H	121.78	morex_contig_2550755	TGCAGGGCGAAGAAGATGGTGCAGCAGCAG[A/G]A TAGTAGCTGCGGCGATCGTCCTATGTTCCACG
TP59519	2H	121.78	barke_contig_271057	TGCAGTC[A/C]AGCAGTACAGAGCTGGCCGCAAGCC CGCCGAGATCGGAAGAGCACACGTCTGAACT
TP62489	2H	123.08	morex_contig_38845	TGCAGTGCTCGCTC[A/C]CGTGCTAATCTAATCAAAC CTAGTGCAATCCCCTAAAAGTGCAGGTTTG
TP63205	2H	123.08	-	TGCAGTGGTCTTTGGTGGCGGCGGCATGGGTCTCTC CTCAAGCTTCATC[A/G]GGATGTGCACGGTG
TP10600	2H	124.38	barke_contig_274041	TGCAGATGCTGGACTACAACGTGCCTGGAGGTGAG CAGCAGCTGGCCGATCA[C/T]CCCTCCTCGTT
TP17300	2H	124.38	-	TGCAGCAGCTGCACCTGGAGGAACGGCTGCTGCG[C /T]CGCACCAGCGATAACTGGTGCATCGTCAA
TP29704	2H	124.38	barke_contig_1802081	TGCAGCGGATAAGCATTATTCATGGTTGCCTTCCAA GTATAG[A/C]ATAGGCACATAGTAGAGCGGA
TP33312	2H	124.38	morex_contig_45337	TGCAGCTCAACCCTGATGAAAAAAGCGATCAACAA GTCGGCCGTCCTCGTGATCCT[C/T]CTAAATC
TP35599	2H	124.38	bowman_contig_887399	TGCAGCTGCAAGCGATAC[C/T]CTCACGTCGGGCCA GTCGCTCGCTGTGCGCGGCAGCAAGCTCGTC
TP62596	2H	124.38	-	TGCAGTGCTTGGCGTAGATGAGGAAGAGGAAGAG[A/C]CCCAGGAGGACGCCGAGATCGGAAGAGCA
TP29714	2H	124.38	barke_contig_1802081	TGCAGCGGATCACGACTGCACGAATTATTGGA[T/C] GGTTCAAATACAAGGTGAGAATGGCAAAGGC
TP750	2H	126.98	morex_contig_1569720	TGCAGAAATCGCTGTCACTTTTGGTTTCAGCAGTCA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				GGA[C/T]TATAATTTTCTTATCGACGATCCC
TP3826	2H	126.98	bowman_contig_116691	TGCAGACAGTTTCAAAAAACACAT[A/G]AATTAATT AAGCCCCCTCCAGCTCGTACGTGCTCACCGA
TP3830	2H	126.98	bowman_contig_129881	TGCAGACAGTTTGAATCGCGTGACAGATTT[A/T]G CAGGAAGCCGAGATCGGAAGAGCACACGTCT
TP7301	2H	126.98	morex_contig_55057	TGCAGAGGAAGCTGCTACTTTAATTGCTT[C/G]GTTA CTGAAATTTGTCAAATTTGCAGGTCGGTAT
TP15860	2H	126.98	barke_contig_1780560	TGCAGCAGATGTACGCATA[C/G]CCGCACTTAATTC GAGGCCTTACGATCTTGCATAGTAATTTGGC
TP18369	2H	126.98	bowman_contig_1993208	TGCAGCAGGTGC[C/G]GTCGGATGAGTAGGCGCCGC TGCCGACCTCACCTCCGAGATCGGAAGAGCA
TP26382	2H	126.98	bowman_contig_852828	TGCAGCGAGGGGACAGGGTG[C/T]GCAGCAGGGCA ATGCGGCAGCGGCAGGAGTGGGTGGGGGACTG
TP48323	2H	126.98	bowman_contig_125967	TGCAGGCGTTGAGGTCGGCAGC[A/G]GCTCCTACTC CGACGGCACCTGCACCCCAGAATCAGTACGA
TP50074	2H	126.98	barke_contig_269115	TGCAGGGATCGCGATCCCCAACACAATTACGTGA AGCAATGC[A/G]GAACCATTTTGAAGCGGCGT
TP52973	2H	126.98	bowman_contig_90361	TGCAGGGTGCGGGGAG[A/G]GAGTCAGCGAGATGA CGCATCGGCGCGAGCCGCTGGAGGTGGAGGAG
TP58622	2H	126.98	bowman_contig_1982422	TGCAGTACTGGTGGCAACCTTGTTAACTC[C/G]GTT CATAGTAGTAGTAAAGTTCTTGAGGCATAC
TP59146	2H	126.98	morex_contig_47410	TGCAGTATATGCAACCCGTTATCTCTACGGTTTGTG ATAAGTAGTGTTGAAGCTGCTG[C/T]GCGAC
TP59814	2H	126.98	barke_contig_132880	TGCAGTCAGTGTGGCTCAGTGCACGGGTCATGAAA AAA[A/C]ACACGAAAAACAGTCATGGGACGCG
TP65864	2H	126.98	bowman_contig_2020879	TGCAGTTTGCCATGTAACCTGCTCGGCGATCGTCAA CTTTATC[A/G]CTTAAATTCATAAGGTGCGA
TP5683	2H	126.98	bowman_contig_12872	TGCAGACTT[A/G]GGAATCTTCAACGTAATCCGTAA AACTTCCCGCATCCGTTCTGTTGCCAGAAAA
TP48811	2H	159.46	bowman_contig_17582	TGCAGGCTGAGAGCCGCCGCCACGTGCGCAGAGG[C/T]GGCGTTATTCGAAAGGGCCTCGGCGCCC
TP44985	2H	159.46	morex_contig_87345	TGCAGGCC[A/T]GTCTACATCAACACGCCAGGGGCA GCGGACGACAGTACGAGGTGCCCAATGAACG
TP19035	2H	159.46	barke_contig_282216	TGCAGCATCAAATAGGGATTGTCCTCTCCCGCTTGC TGGCG[C/T]ATGCTGCGCCCTCCCGTGAGCC
TP23713	2H	159.46	morex_contig_416253	TGCAGCCGCCGCGCACGTCCACGACGCCGCAGAGC ACGGTGTGCCAC[A/G]GGGGCTGACGCGGCGG
TP26248	2H	159.46	bowman_contig_847367	TGCAGCGAGCGCAAAAATATTTGGCAACGCACTGT ATCATT[C/T]GACTGTAGCCATGTGTGCCGTG
TP27592	2H	159.46	morex_contig_61005	TGCAGCG[C/G]CCGCTGAACCGATGGAATTCATGGC GTGGTACTGCGCAGGTGGCAGGAGGGGCAGCG
TP33177	2H	159.46	morex_contig_120368	TGCAGCTATAGATCTGGGTGCAC[A/C]AGCGCCGTA TCACCCTTCATACTGGGCTCTATAGATCTGG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP35161	2H	159.46	-	TGCAGCTCTGTAAAATCTCAGGATCTGC[A/G]AAGC ACCTCTTTCCCCGCTCTGTAATTTTTGACTG
TP38600	2H	159.46	bowman_contig_64529	TGCAGGAA[A/T]AGGGCGAGTAACCGCGATGTCCAC CTGTCCTTGTACTGTGCCGAAGAGAATTTTA
TP43755	2H	159.46	-	TGCAGGCAAGATTTCTCGCTTTTCCCCATTGGCCCA TAGAGCTCCGC[A/G]TCGAAGGCCGAGATCG
TP51006	2H	159.46	morex_contig_2549358	TGCAGGGCGATGGGGCGACCAGCTCGAGGGCGACGA GGG[A/G]CAGCACATGAAGTACCGAGATCGGA
TP65249	2H	159.46	morex_contig_135472	TGCAGTTGGCAAAGGCAGAGGGCTACAAGGGGTAG GCCTCGGCGTCG[A/C]CGCCGAAGTTGCGTAG
TP24166	2H	159.46	barke_contig_411457	TGCAGCCGCTTGG[A/G]TCCCATGCAGGCCACCGCT GAGGCGCCGCCACCGTACATAGCCGAGATCG
TP32600	2H	159.46	bowman_contig_142572	TGCAGCTAATCTAACCTCTAATGTTTTCCCATCAA[C /T]CAGGCGCCCATTCATGCGTTCAATAGCT
TP57712	2H	159.46	bowman_contig_852869	TGCAGGTTTCGATGCTCAGGGATTCAAGAG[C/T]AC CTTCCGAGATCGGAAGAGCACACGTCTGAAC
TP13294	2H	162.06	-	TGCAG[C/G]AATTTACAGCGGACAACCTCTACAGTACC ACGAGTGCCGATTTGCCGAGATCGGAAGAGC
TP13954	2H	162.06	-	TGCAGCACCCATCCATCCAT[C/T]ACACGCTGCTGCT GCTGCTGCTGCTGAGGCGCTCGACCACCAT
TP16553	2H	162.06	bowman_contig_200644	TGCAGCAGCCAGGCTGCTTACACGTGCATGCACACC CTTGATG[G/T]GCTCAGTTACAGCAGGCGGA
TP34103	2H	162.06	barke_contig_274248	TGCAGCTCCTCACGGGGCGCCGTGTTGCA[C/T]CAA GGGCGAGGCAAGACGAAGAGGCACAACATGC
TP38708	2H	162.06	bowman_contig_314376	TGCAGGAAACTTGAAAA[C/G]GGTCATCCTCGCGTCG CTGTGACTCCCCGAGATCGGAAGAGCACACG
TP1265	2H	163.37	-	TGCAGAACCGAAGCAGGGGAAGGAGCTCTGGGAAC TC[A/G]TCGTTGACGTGGTCGGGGCCGTCGGT
TP13189	2H	163.37	-	TGCAGCAATGCTTATTGCCCTTACGCCGCCGAGGGGA AGGAGGTTT[A/G]GGGGAAGCTTCCGTCCGA
TP17256	2H	163.37	-	TGCAGCAGCTCTTCCAGCAGCACAAGCTCCAGGCCC AGGCCGACGACTCCACTTCAGCAGGCA[C/T]
TP52842	2H	163.37	barke_contig_58240	TGCAGGGTGAAGGCGGTGACCCTCGGGCAGCAGCA ACCACCTCTGGGGTGGAAGCGCG[A/G]GTCG
TP62550	2H	163.37	morex_contig_1568924	TGCAGTGCTGGTGCCTCAACTTCCGTGGCCGCGTGA CGGTGGCCTC[A/G]GTCAAGAACTTCCAGCT
TP526	2H	165.98	barke_contig_1784968	TGCAGAAAGAGGCCTAATGAGGACTTGGGCAGACA GCAACCAGCATGAGC[C/T]TTGAAGTCTGATA
TP20807	2H	165.98	morex_contig_54095	TGCAGCCACCGTCCTACATAGATACAATGTTGCG[G/ T]TGGTACAAGGATGTTTCGTACCCCGATGA
TP25066	2H	165.98	barke_contig_369923	TGCAGCCTGCATTTTACTAGTTTTAGCCCAATTCGA TATAGTTTAGTTAAATATGCCTGAA[A/G]TA
TP46754	2H	165.98	morex_contig_6358	TGCAGGCGATGTGCCGTGCGCAGGGTCTGGCGCTG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				GACTCGACGCCTTTCGA[G/T]GAGTGCATCAA
TP58708	2H	165.98	barke_contig_447730	TGCAGTAGAGGAAAATTTAAAGGAGAATCATGTTC AAGGAGGTGCAT[C/G]GATGCATCAATGCCAC
TP539	2H	165.98	bowman_contig_10941	TGCAGAAAGCAAAATTTATAA[C/G]GGCTTCATGAA ATAGATTCAACATGAATGAATCTTATACTGT
TP12249	2H	165.98	barke_contig_1794812	TGCAGCAACATTGTGTCTATGCGCTTCAC[A/G]CCC TCCACGCCTGGGATCCTCCGAGATCGGAAG
TP18471	2H	165.98	morex_contig_1561486	TGCAGCAGTAAGGAATTCTTGAG[G/T]CGTGAGATG AAGATGTATAGGGCAGACCTATATATGAAAA
TP23512	2H	165.98	-	TGCAGCCGCGAGTAATTAGCGCAACAACACTGGAT ATATACT[A/C]CTGCTGGACTGGGCTCACTGA
TP26659	2H	165.98	bowman_contig_331123	TGCAGCGATGTCTTGTGCTCAGACAGTGGCTT[G/C] AGCTGATGACCATCTCGGTCGCAATCAGCAG
TP30509	2H	165.98	bowman_contig_859696	TGCAGCGGCTCACCGTGGACTACGCGCAGAGGGGC GTCGTCTGCCCAAGCCT[C/T]CCCCCGAGAT
TP31075	2H	165.98	morex_contig_169130	TGCAGCGGGTTGGGCCCCGCTGACGTGGCAGTGCAG GTGCAGCGTCATCTCCCCTCC[G/T]CCCGAGA
TP32939	2H	165.98	morex_contig_2549473	TGCAGCTAGACGGAGATGATGACGAGACGGCGTGT TA[C/T]CTCCAGGATAACTCGCGAATTTTCTC
TP35111	2H	165.98	bowman_contig_157425	TGCAGCTCTGCGTCGGCCGCAGCTGCCTC[A/G]TCTT CCAGCTCCTCCACGCCGACTACGTCCCCGCC
TP38458	2H	165.98	morex_contig_42752	TGCAGCTTTTCCCCCAGGCACCCTAG[A/T]AATGGC AGCTTCTCCCGAGATCGGAAGAGCACACGTC
TP43846	2H	165.98	morex_contig_1578068	TGCAGGCACACCAT[C/G]TGCGACACGATTAGCCAC GGATCCCCTCCATCGCCACATCCAACGTCT
TP53693	2H	165.98	bowman_contig_872278	TGCAGGTACTCGGACAAGATGTTGCTGTAGGTCTTA CCACCCTTGACCATTGATCGGTCAA[C/T]A
TP63747	2H	165.98	morex_contig_511440	TGCAGTTAATCTTGGTCTTGAATTCCTGACATGGTT ATGATTGTTAATCCAG[A/C]TACTGTATATG
TP54387	2H	165.98	bowman_contig_851002	TGCAGGTCCAAGTAAATAGACCGTCCCTTTCTTCT CCCCAAC[C/T]GCCAATGCAAAACCAGCCGA
TP53339	2H	167.28	bowman_contig_125273	TGCAGGGTTTTCGTTCCATGGTGAGCGCTACGACTC CGAATGCTCGCTATGG[G/T]TTCCGTGGTG
TP10446	2H	168.58	bowman_contig_9518	TGCAGATGCCGTCTCTTTTCGATCGACGTCTTAA[C/T] TTGCCTTCTCTTTCGTGTGGAGCCATGCCT
TP18733	2H	168.58	morex_contig_49284	TGCAGCAGTGGTGAAAATATCATAATGGACTGACC TTGAAACAAGCAATCT[A/T]TTACAACTAAG
TP18983	2H	168.58	bowman_contig_125417	TGCAGCATATATGCATGTTTAACTTACTTTTATCTTC GAAACCACCGCA[C/T]TGTCCGAGATCGGA
TP27278	2H	168.58	morex_contig_159638	TGCAGCGCCACCACAGGCCCTCCCTAGCGCC[A/G]C CGCCGATGACACAGGCCCTCGCTAGCACCTC
TP32360	2H	168.58	morex_contig_42598	TGCAGCGTT[C/T]AGTGACGTGAGATGATTGGTGTA GCCATCCGCCGCCACCGTGTTCCGCCGAGATC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP36074	2H	168.58	-	TGCAGCTGCG[G/T]GACGCCGTGGCGTGCCGCCCCG TGTCGCGCCTCTTCCGAGATCGGAAGAGCAC
TP39022	2H	168.58	bowman_contig_14546	TGCAGGAACCCCACCATGAGGGCCGTCCACGACAC GACGTTCCCTCTC[A/G]GGCATTCCGTCTGAACA
TP52551	2H	168.58	morex_contig_2546833	TGCAGGGTACATGGATCCTGAGTATGTGGTGACCCA GGAGCTGACGGAGAAGAG[C/T]GACATCTAC
TP57099	2H	168.58	morex_contig_54190	TGCAGGTTCCAGCAAAAAAGTCTCAAGGCCACTGG CGTCGCCGCC[C/T]AGCACCATCCGTTGGATG
TP62956	2H	168.58	-	TGCAGTGGCTCCTGAGGCGGAGGTTCTGCGAGAGCG GCGTCACGGTGTGACGC[A/G]AAGACGGGGC
TP64083	2H	168.58	bowman_contig_10364	TGCAGTTCCTGAAACCACAATGAAGAAAATTAA[G /T]TCCTTCCTTTTTTGGGGGGGTCTCCTGAT
TP64777	2H	168.58	barke_contig_1785443	TGCAGTTCCTTGTTCGATTTTTCTGCAAATGATTTACC TATTGTGGCCGC[G/T]ATAGATTTTCTAGG
TP5487	2H	168.58	bowman_contig_10364	TGCAGACTATGCTGTGATAGTT[C/G]AAGGTTTGT TTGCTATATATGTCTCCAGCCCAAATCAGA
TP32245	2H	168.58	morex_contig_135396	TGCAGCGTGGTGTGTTGGG[C/T]CCCATAGTCTGCTCCG TGCTCTGCCCTTGAGGTACACGGACGCGT
TP36221	2H	168.58	bowman_contig_142085	TGCAGCTGCTCGTGCCACCTCGGGGACTTGTTCTTG AGAACCAGCGGGCTCTCCTTGTC[C/T]CCG
TP36702	2H	168.58	bowman_contig_849131	TGCAGCTGGCGCGAGGCGGACCAGGAGCGGGACAC GCTCCAGGACAGGGACCT[A/G]AAGTGGGAGC
TP40667	2H	168.58	morex_contig_7844	TGCAGGACGAGGTGGGCCTGGTGGAAATTCATCGCG GTGG[C/T]GGTGGGGGATACCATGGTTACAGA
TP58917	2H	168.58	barke_contig_58240	TGCAGTAGGAGGATCCCGTCGACCGAGTCGAGGA[C /T]GCGATAGTCGTCAGGAAGTCGAGGGCAAA
TP60489	2H	168.58	-	TGCAGTCGAGCCACTCCTCCGAGCTCTCCTTTCTCC CATTTTTAG[A/G]TTCTCCTCTAATATATAC
TP63633	2H	168.58	morex_contig_9839	TGCAGTGTGTCGAACTAAAATGACACGTTGATATA CCTGCGGTAACAC[A/G]GTGGCTGGCCGCAG
TP61593	2H	168.58	bowman_contig_1986375	TGCAGTGAGAAAACAAAGTGTAATAACCC[C/T]GCA AAGAAGGTATAAATGTAGAGAAAGGTGTGAT
ZIP7	3H	0		AATGCCTGATTGCGCAGGGGCTCC[T/G]AGACACCC CAAGCGACAGCCCAATG
ZIP5	3H	1.7		CCCGGAGGCCTTCGAGCGGCTCGGC[T/C]CGCCGTG CCTCGTCGACGGGCCGTG
ZIP5	3H	1.7		TCGGCGCATCCCAGAGCGCCAGCAC[G/-]ATCAGAC CACTGGTGGTCGCGCTAA
TP32808	3H	80.00	-	TGCAGCTACGTGTATATATGTGCTGCTGGCAC[T/C]G TCGTAAAAAAGGAAAATGACCGATCGTCAC
TP19612	3H	87.98	morex_contig_2550528	TGCAGCATGATGTCATTGGACCTTGCCAG[C/T]ATTT CACTGAATGGCTTGCTCATCTTGGTGATT
TP27006	3H	87.98	-	TGCAGCGC[A/G]GCGGCGTCCACGGAGTCGGCCGCG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				CCGCACGTCAGGATGCTGTGGAGAACCCGCG
TP6083	3H	89.17	bowman_contig_14726	TGCAGAGAGCCAGTCCAGCCAGCAGCAGCACGCG[C/T]GCAGCTCAGCAGAAGAGGTACCCAACGGC
TP41927	3H	91.88	morex_contig_334012	TGCAGGAGCTGGGGAAAGGAGCTGATTGAGAAG[A/G]AGATAAGAAGAATTTAGCGGTGCAAGGATC
TP63630	3H	93.86	bowman_contig_1987587	TGCAGTGTGTATGGTGTGCTGAGTGTGGCCAACTAAAGGCGACATGTGCAG[C/T]AGTTAGGTGTA
TP13640	3H	106.39	morex_contig_54717	TGCAGCACATCAAGACGTCCATGCGTTGAGCAAAAGTGAATAGCACCGTTGAAATC[A/T]CCATCGT
TP32582	3H	106.39	barke_contig_2783003	TGCAGCTAAGGATGAAGCAAATCCTATGATCATATAAGTATATGC[C/G]AACCAAAGGGGAGCTGGA
TP29239	3H	106.39	morex_contig_67684	TGCAG[C/T]GCTCTGTGCACATTTTCGCGGAATGCACATGGAGGGGTATGGGGGTATGGCTACGGATG
TP11716	3H	106.39	barke_contig_370701	TGCAGATTTTGTTCCTTGCATCGTTCA[C/T]TACAGCAGTATTGTCAAGCTGTGCTCATAAACCGAGA
TP60843	3H	107.69	morex_contig_1579788	TGCAGTCGGCGTGGTCTTTGCCGCACGCTGGCCGCGGCGGC[A/G]GCATCACGCTGGCGGCCCTGAT
TP57749	3H	107.69	bowman_contig_864906	TGCAGGTTTGCAACCCAAATATCCAACCAAAACCA GTTGTC[A/C/G]CCTACAGCAAATCCTTCAATT
TP56636	3H	107.69	barke_contig_71785	TGCAGGTGGTGT[A/G]CGTTGTTGTTGAACTTTGAAAGCCTTTGTTGATCGATCGTGTGCAGATTC
TP16830	3H	107.69	morex_contig_45263	TGCAGCAGCGCCGTCGTGGGGAGCACGAAGGAGACGTTGTTACGGCCGCCGC[A/G]AACCGAGATC
TP941	3H	107.69	barke_contig_588249	TGCAGAACAAAATCGCTCAAG[C/G]CAGCATGAGGCACAGCATCCGCCGTGCTGAGCCACGGCTCGA
TP11812	3H	107.69	morex_contig_1579788	TGCAGCAAACAAAGCAGCAGAGCATCAAATCCAAC TGCCAC[C/T]GTTATATTGCAGGTAGTAGCAA
TP60565	3H	107.69	morex_contig_45263	TGCAGTCGCA[C/T]TACACGGGGATGTCCAACGGGGTGTA CTCTCCA ACTTCCCCGCCGTGCCCAA
TP8095	3H	142.15	bowman_contig_847525	TGCAGAGTGACATTTGTGCATCAAAGTTCT[A/T]TTATTATCTAGGGCCGAGATCGGAAGAGCAC
TP19440	3H	142.15	bowman_contig_142689	TGCAGCATCTCGCG[C/T]GGTCGCCTTCGGTCACCGCCGTCAGGCACAACGGCTGCCGAGATCGGAA
TP19670	3H	142.15	bowman_contig_62411	TGCAGCATGCCCCGCCATGGCCTTGTCG[C/T]GCTCCA AAGCACACGGGGATAGCCTCTCGTCCGAAC
TP34519	3H	142.15	morex_contig_244073	TGCAGCTCGCCGACGTGCTCC[A/G]CGGCCGAGGCC TCGCCATCACCATCCTCCACACCACCTTCAA
TP48884	3H	142.15	bowman_contig_916079	TGCAGGCTGCATCCTCTTTCTCGGGGTCTGGCTAC TGGTTTCGTTCTTCTAGTGATC[C/T]CTACG
TP51383	3H	142.15	barke_contig_2790737	TGCAGGGCGTGGACAGTTCACATGACTC[A/G]GGGGAGGCCCTGCAAGCCGCGAAGGCATTGGCACG
TP52826	3H	142.15	morex_contig_7979	TGCAGGGTG[A/G]AAGCAAACCTATAATAGTATTTGACACGGCAGCTGAGTCGTTCCGAGATCGGAA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP58927	3H	142.15	bowman_contig_221597	TGCAGTAGGATCCACCACAGGTGGTGTGACATTCAT [A/G]GCTCGCCCCCTCGGAGCCGAGATCGGA
TP2965	3H	142.15	barke_contig_2781116	TGCAGAATCACCGACTGAAAACAATTAAAGCTTGG CCAGAATCTTGAAAGAGCTTT[C/G]ACCAACC
TP5940	3H	142.15	morex_contig_6555	TGCAGAGACCAT[C/T]AATGCTTATACTTGGGTCTT CATCCCTTGTTATCCCTGGATGTGTAGACC
TP9985	3H	142.15	bowman_contig_846731	TGCAGATCTGCGGCGA[C/G]CATGCGGACGGCAGCA GGAGCGACACCTCTCCGTCGCAGCAGCCGTC
TP10688	3H	142.15	bowman_contig_2002163	TGCAGATGGAGCATGACGGCGACTAA[C/T]TCGTGG TGAATCCGAGATCGGAAGAGCACACGTCTGA
TP10695	3H	142.15	bowman_contig_17214	TGCAGATGGAGGAGAACCTG[G/T]TGGTGTTCGACG AGGAGAAGCAGACGATGGCCTTCACCGAGAT
TP15709	3H	142.15	bowman_contig_1184523	TGCAGCAG[A/G]TACCATGCTCGATTCGCCAGTGGA TGCACAACGGACCGCCGAGATCGGAAGAGCA
TP16507	3H	142.15	barke_contig_2789793	TGCAGCAGCCACATGTCTTCCTTGCCAAGGTGG[A/G]]AGCTTGCCCGCGATCTTATCTTCAAGATGC
TP16674	3H	142.15	bowman_contig_26047	TGCAGCAGCCTAAGAAGACGTA[A/G]CAGCCCCAGG TCCACGCCGTGCACATCCCGTGCCGCCTTGC
TP18406	3H	142.15	morex_contig_159562	TGCAGC[A/G]GGTGGCGTCGCGTCGGCCCCCGCCGT GAAGCCACGCGCCCCCTTCTCAAAGCTCCCA
TP21391	3H	142.15	bowman_contig_195149	TGCAGCCAGCTCGGAACATCAACCTCCTTCCAATCC ATCTTTTTTGGCTTT[C/T]CCTTGATGTTAT
TP24010	3H	142.15	bowman_contig_86295	TGCAGCCGCTCCTCGGCAAC[C/T]CTTGCGTCGATGA GCCCCGCGGTGGGACTGGGGTGAAAAAGGA
TP33272	3H	142.15	morex_contig_68252	TGCAGCTATTGCTCTGACCCTCGGTCGGAGTTACCG AGCGC[A/G]TGCCACGATCAACGCTTTCGTC
TP33625	3H	142.15	barke_contig_443213	TGCAGCTCATGTGGATATAGATAGCTAGGCCGTAA GCAGCAGC[A/C]CCACACTCAACTGCCCTCA
TP37712	3H	142.15	barke_contig_1808605	TGCAGCTTCTATCTTCTCTGCTG[C/T]TGCTGCCTGCT CCAAGACTGCTGCGGCCCTTCTTCGGAC
TP40500	3H	142.15	bowman_contig_83164	TGCAGGACCTCTCTGGCATTCTTCTCTAGACAAT GATTTTCTATGCACATCGCGTCCG[C/T]CAA
TP42935	3H	142.15	morex_contig_39773	TGCAGGATCGCCA[A/G]TGGACACTGCACGCGATGA GTTAGCTAGGTTGATTAGCAAGGTTGAGATT
TP49127	3H	142.15	bowman_contig_263279	TGCAGGCTGTCAAAATTCGTTGCCAATTTCAAGGGC ACAGGCAACAGGTCGCG[C/T]GCCACAGATG
TP54347	3H	142.15	barke_contig_269985	TGCAGGTCATGCCTTTTTGAGGGATACAGCCACCCA CGGTCGTGGGCTTCTGGCAAAGTC[A/G]TCT
TP55134	3H	142.15	barke_contig_2789793	TGCAGGTCGTACGGTTCTTGTCAG[C/G]CTTTCCTA ACGGACATCGCAATATATCATCTCACTCCT
TP56729	3H	142.15	morex_contig_47201	TGCAGGTGTCGTCGAAGAAGACGGCGGAGGATCTG TGGGCGAGCCTGAAGAC[A/T]CGGTTTCATCGG
TP58076	3H	142.15	bowman_contig_151644	TGCAGTAATCAGGATACGACTTCACCACGTTTTTA[C/

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				T]AGACAACAATTTTCGACAAGATAGCCATTT
TP8158	3H	142.15	barke_contig_269985	TGCAGAGTGCTGAGCAGAACAGGATGAAGCCCTG ATGGAAGCCGCGATTGTTGAT[C/G]TATGCAG
TP13952	3H	142.15	bowman_contig_291958	TGCAGCACCCATATACTAACGGTGTTCTTGTCATGG TCATTGCAATAGATGCC[A/G]AGCGTGTCAT
TP51407	3H	142.15	morex_contig_52042	TGCAGGG[C/T]GTGTATTGATGGACGAGCGTAGGAT GGTGGCGTTGTCTGTCGTCGTGATGGCGTCA
TP57888	3H	142.15	barke_contig_517867	TGCAGTAAAGACAGGCA[C/T]GTAATTGTTGGATAG GCCAGCCACGTAAACCTAAGAAAACTCAAA
TP59526	3H	142.15	bowman_contig_62187	TGCAGTCAAGCTTAGAAGATTCAGTGCAGTTCAG[A/ G]AGGATATCTCGCAATACACTTCTGTAAAC
TP6952	3H	143.45	morex_contig_138554	TGCAGAGCGGCCCTTCTGCACGTAGAGCGCGACGCG AAGCTTTTCCTGTGGAG[A/G]CGCCACGAAAA
TP39512	3H	143.45	bowman_contig_221016	TGCAGGAAGCTGTCTGGGATGCTGACATTGTGGTGA ATGG[C/G]CTGCCGTCCACTGAAACAAGGGA
TP52309	3H	143.45	-	TGCAGGGGTCATTGAT[A/G]GTGCGATGTAAATTGT AATGCTAATCGGCGGTTGTCAGCGTTGCGAT
TP53073	3H	143.45	morex_contig_1558152	TGCAGGGTGGTGCGCAGATGCTGGTGTCCCAGATC GCCGTGGGAACCTCTTATTGC[G/T]GTGAGGTT
TP54122	3H	143.45	bowman_contig_69819	TGCAGGT[C/G]AAGCTCAACGGCGTCGCAACCATCA TCGGCAAGATCGGGCTCGCCTTCGCGGTGCT
TP55561	3H	143.45	bowman_contig_850485	TGCAGGTGAGGAAAAACGGCAGGTGGTACCCG[T/C] TGAACCCGCTGCCAGGCGCCCTCGTCATCAA
TP5727	3H	147.34	morex_contig_347651	TGCAGACTTGTTAAGTTCAGTAGACATCACACGACC ACCTACCCTATTACAGAAGA[C/G]GCAGTAC
TP20423	3H	147.34	bowman_contig_292580	TGCAGCCAAGGCAGGGGCGGCGGCTGGGGAGGGG AGCTAGAGCTAGAGACGACCGATGGCCGT[C/G]
TP57414	3H	147.34	bowman_contig_292580	TGCAGGTTGCCGTCCTATCTTCGTTTGCCAGCGAGT GAGCTCGT[C/T]GGTCTGGTCTCCGAGATCG
TP58331	3H	147.34	morex_contig_44373	TGCAGTACCATGAGGAGCCAACTCTTTGAAACGTG ACAAA[A/C]ATAGACCACCGAGATCGGAAGAG
TP9788	3H	151.25	bowman_contig_203765	TGCAGATCGGGGCGGAGGAGGACAGGTTAGAAA[G/ T]ATACTAGCAGTAGCAGTGATAGGAGAGTGA
TP17747	3H	151.25	barke_contig_2785736	TGCAGCAGGCAGCAGAGTCCTCCTCCTTCTCCTCTG CTGCTTCTTGATCATCTTGCGA[G/T]TCCC
TP29242	3H	151.25	bowman_contig_72607	TGCAGCGCTCTTCTTTGTCCTCCTCGCCCTGGCCACA ATGCTGCCGCAGACCGC[A/G]TCGTCCGAG
TP52851	3H	151.25	barke_contig_513111	TGCAGGGTGACAAGAAGGCCCCACGAGCAACGGTG CTGCT[C/G]CTCCTGGCCGTTCCGAGATCGGA
TP54021	3H	151.25	barke_contig_303223	TGCAGGTATCTGTCTGATATATCACCAGAAATGTCT GGTTGACTCCCA[C/G]GAATGAAGCACGGGC
TP40669	3H	152.55	bowman_contig_69031	TGCAGGA[C/T]GAGTCTGTATTGATATGGTTTTCAGG GAAAGAGGAGAAGCATCTAAGGTTGAGCCA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP43983	3H	152.55	bowman_contig_872180	TGCAGGCACGAGTTAACGTGCATTTTGTAACTTGC ACCTG[C/T]CGCGTTCTTCAATAGTCCGAGA
TP55761	3H	152.55	morex_contig_1568777	TGCAGGTGCAGCAGCAGCAGCAGAAGAAGCCCACC CATC[A/G]CACGGCCTAATGCGACTCGCTTCT
TP65212	3H	152.55	morex_contig_2547323	TGCAGTTGGAAGCCCCGAACGATGGACCAAAGGCG AAGGAATTCTG[C/T]GGCAAACGCGCAAGTTGT
TP2055	3H	157.76	morex_contig_2554032	TGCAGAAGCACGGGAATTGCGCGCACGCATCAGCA A[C/G]CCTGGACCGAGATCGGAAGAGCACACG
TP3927	3H	157.76	morex_contig_40749	TGCAG[A/C]CATGGGGTTCTGCTGCGGGCCTTCGGA TGTCCAGGTGCTCCCAAGAACACCTCCTCAT
TP4241	3H	157.76	barke_contig_269491	TGCAGACC[C/G]TACGTCCACCTATGCTATGCGTGTT CCGATCAAACATGCAAGCACGTTGTGTAG
TP11454	3H	157.76	bowman_contig_1983379	TGCAGATTGCCATTGAGCAATTCGAGCATGAGGCA GC[A/G]GAGGCGGCTCGGCTCGCCAAGCTCAA
TP13732	3H	157.76	-	TGCAGCACCAACACCGACGCGGC[A/G]GAGCCACAC CGTAGCACCGAGATCGGAAGAGCACACGTCT
TP23280	3H	157.76	bowman_contig_852007	TGCAGCCGAGGCACCAGAGG[G/T]CTGGCACGATTG GCCTATTGTCATCTATACCGAGATCGGAAGA
TP23694	3H	157.76	barke_contig_1854278	TGCAGCCGCCGCCGATGCATG[C/T]TGCACATGCAA TGATGTCCGTCGATGCGCCGCTGCTCCCCAC
TP24083	3H	157.76	bowman_contig_293952	TGCAGCCGCTGCCGCTG[C/T]ATGCTGCACATGCAA TGATGTCCGCCGATGCGCCGCTGTTCCCCAC
TP25393	3H	157.76	morex_contig_46889	TGCAGCCTTCTCATGCTCG[A/G]TTTCCTGCCGAGTT TTTCGCAACTCGGCCGAGATCGGAAGAGCA
TP28253	3H	157.76	bowman_contig_2004203	TGCAGCGCGAAGGCGTGCGTCTGGTGTGTTGGGAC AGCTCT[A/C]TCTCCCCTGACTAGACGGAGGT
TP31518	3H	157.76	barke_contig_269491	TGCAGCGTCACCACCGCGTGACGTTGCTCCAT[T/C]G CAACACTAAATGCCTCGTCGAAGTTCCATC
TP61630	3H	157.76	morex_contig_368179	TGCAGTGAGCATGAAGGCCTAATTTCTCATACACGG ATACAC[C/G]TCAGAGATAATTGCACCAGTA
TP63986	3H	159.06	barke_contig_294599	TGCAGTTATTCATGCCATCTTTTATTTCTTCAAATG AATCGTGTGCATATCATTA[A/T]TGGGGGA
TP24268	3H	159.06	-	TGCAGCCGTCGCTCTCCACGGCGAGCTTGCATGCGA ACTGCGGCGC[A/G]CCTGGCGCCTTGCCGTC
TP32348	3H	159.06	barke_contig_1783305	TGCAGCGTTATAT[C/T]GGCCAAGGGGAGCCTAGCA ACGGAAAAGCTGCTCCAAATCCGATGACGAA
TP52612	3H	159.06	morex_contig_43211	TGCAGGGTCAACGGGCG[C/T]GGCTACCACACCACT AGGGCTAGCTACTTGGAACAGAAAGTAAGCA
TP58647	3H	159.06	morex_contig_369094	TGCAGTACTTGATCTGATCTGTTC[A/C]TCTTCCATC CAACAGGGTATCCTGGATGAGAAGGCCGAG
TP59767	3H	159.06	-	TGCAGTCAGCTGTGTAGCACAAAA[G/T]TCGCATCG TCCCCTATCTTCGGTTCTTCTGGTTTCCTCT
TP59820	3H	159.06	morex_contig_302872	TGCAGTCAGTTGT[C/G]CAGCACAAAATTCGCATCG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				TCCCCTACCTTCGGTCTTCTGGTTTCCTCT
TP3814	3H	160.36	morex_contig_46051	TGCAGACAGTGGAAAGAG[A/C]AGACAGGGCCAAA TTAAAGATCGTGATCTTCCAATAAAACGTAAC
TP3980	3H	160.36	bowman_contig_981669	TGCAGACCAAGACGATGCGCGCCTGCTCGACCGTC AGTCACC[A/T]CGACACACGACAGTCGACAAC
TP9663	3H	160.36	morex_contig_139553	TGCAGATCGCGGTCTTCCGTGTATA[A/T]CTCACCAA TGCCGTAGTATATGCAGTTCCCGTCGACGG
TP9964	3H	160.36	morex_contig_46315	TGCAGATCTCGGGCACGTTACTAACCATGCTGCTGC T[C/G]TCCAAGTACCGAGATCGGAAGAGCAC
TP19717	3H	160.36	bowman_contig_201409	TGCAGCATGCGGGAGATACGAAGGTGGTCG[G/T]CT CGTTAGCGTGATTGATGGACCATCGCGGTTG
TP32769	3H	160.36	morex_contig_66533	TGCAGCTACGAGGGGCAAACAAGCTCAA[C/G]CTCG AAACGCACCCCGACGCCGCCCGAGATCGGA
TP34193	3H	160.36	-	TGCAGCTCCTCTGCCTCGACCGAACCCCGACTGCCT CCCGTC[A/G]CGTCAGCCGCGGGTGCCGCC
TP38267	3H	160.36	barke_contig_374155	TGCAGCTTGTCTAGTCCCTTTAAAAACAAGGA[G/A] ACGTTTTACGCCGAGATCGGAAGAGCACACG
TP45302	3H	160.36	barke_contig_540780	TGCAGGC[C/T]CCGTAGACGAGGCCAGTACCCCA CGACGAGCCAGAAGATATCAGGAGAGCCGAG
TP53308	3H	160.36	bowman_contig_145704	TGCAGGGTTTCATTTACCTTCACG[A/G]GCCTTCTCG CTGGATTTTCATTGAGAGATGAGGAGGATGA
TP55942	3H	160.36	barke_contig_375360	TGCAGGTGCCTTGGGGTCCATGACAGGGG[C/G]CCA ACAGGTGGCTGGCCACATGTCACTGGCCCA
TP61954	3H	160.36	-	TGCAGTGCAGAGCAG[G/T]TTTGTTGCATTATATTT CCTGTACCACTTTTCTGTACATGCCACAT
TP11854	3H	162.96	bowman_contig_129429	TGCAGCAAACCTCACCCAA[A/C]CCATCGTGCCCTC CTCTTCCTCTGTCTGCGCGAACCCCTAGCCAC
TP2656	3H	162.96	bowman_contig_1997223	TGCAGAAGGTCATGCAGTAGGCGCAGAAGGCGAGG CACTTGTTGGGGCAGGTCTTGGGGCA[G/T]GA
TP5583	3H	162.96	-	TGCAGACTCTGGACGTCAGGGGAACATCCATTGTTA CCATGCCAGAAAGCATCATCAATCTAC[A/G]
TP5623	3H	162.96	bowman_contig_63211	TGCAGACTGCGACGTCATCGGTGCTAGTGATGGCG GC[C/G]AGGATACAACCTGTTTGAAGTTGGCGG
TP5731	3H	162.96	barke_contig_276490	TGCAGA[C/T]TTTACATCATCGGTCGCCTGAAACGG AAGGTGTCACCTCAAATAAAAAGCATGTTAT
TP12906	3H	162.96	bowman_contig_898075	TGCAGCAAGGCGCATGAGGCAACTGATAGATCCCG TGGATCGTCAA[A/G]GCTAGATGTGTTCCGGTG
TP20360	3H	162.96	bowman_contig_223262	TGCAGCC[A/G]ACTCAGAGCAGATAGAGTTGAGGAT GGCCAGCTGCTCCGAGATCGGAAGAGCACAC
TP30778	3H	162.96	bowman_contig_871968	TGCAGCGGGATGACAAATTCCACGGGCAAGTGGGT GGA[A/G]ACCACAAGCTTAGGCGACCATGCCT
TP32515	3H	162.96	morex_contig_1570908	TGCAGCTAAACAAACAGTTACCACGGTTTATCAACC ATGACAACCTGTCCC[G/T]CAGGGGCACGCGG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP37215	3H	162.96	morex_contig_41573	TGCAGCTGTGGTGGC[C/G]ACTTCACCTGGGAAGAT CCCACCACCTGAGGTGGTGGGTCCCTTCCCT
TP48815	3H	162.96	bowman_contig_63211	TGCAGGCTGAGCCACCAGGAGGCT[A/G]GGTGGTCG ACAAGGAAATATTTTCAGGACCGAGATCGGA
TP49201	3H	162.96	bowman_contig_871968	TGCAGGCTTCATCGACTAGTTCAAACACCGTGAAAG AGGG[G/T]CTGCGGTCAAAATCGCTGGTCAC
TP54019	3H	162.96	bowman_contig_884775	TGCAGGTATCTCCTCTCCCTCCTCTCTTTTCTACTCC CTCCGT[A/C]CCGAAGTTAATGTCTGGACGC
TP58758	3H	162.96	morex_contig_134322	TGCAGTAGCAACAAAAGTTCAAGACATTAAGTAAC CAAAGTAGAGCTACA[A/G]ATTATGACTGTAA
TP59794	3H	162.96	bowman_contig_200541	TGCAGTCAGTC[A/C]ACGACTCCACGTACGAAAAC CAAGCAATTAATTAGTTTACACATGGAGGTG
TP61741	3H	162.96	morex_contig_172232	TGCAGTGATCTGACCCGAGGCGGCCGCGACGGCGA[C/T]GCGGAGAGGAGTGCCGCCCGCAGAGTG
TP62029	3H	162.96	morex_contig_66933	TGCAGTGCAGTGCAGTAGTACTAGGAGGTGGTGCA A[A/C]GACATTGCAGAGGAACAGCTAAATGGT
TP57029	3H	162.96	bowman_contig_944991	TGCAGGTTTCAG[A/G]AAAAGTGGAGTAGTTGGTTTC GACAGAGAGCAGATTTATCTACGCGTTGGCG
TP51873	3H	164.26	morex_contig_134629	TGCAGGGGCAGCAAGTTAAGGGTCAAGGAACAGGG CAGCATA[A/G]TTAAAAAGAAAAGATAACCAA
TP15152	3H	164.26	morex_contig_307995	TGCAGCACTGCTCTTAGCCCTCACGTCCGCCAT[G/T] AACATCACTGCCCAGAATGACGACGCTGAC
TP26385	3H	164.26	-	TGCAGCGAGGGGCACGTCAGTGATGATTTGTTGGG GTCGC[C/T]TATGCTGCATTGCAACATGACGG
TP28422	3H	164.26	morex_contig_440286	TGCAGCGCGATGGCGGGAGCTTTACGGGTGTGGAG AGCCTGGTCGGGCCT[A/G]TGGGCCACGAGC
TP39636	3H	164.26	-	TGCAGGAAGTCAAGGGAAAAGGTTTCCTGCTGGTTT CTAC[G/T]GACATAGCGAGCAGAGGGTTTGA
TP55422	3H	164.26	-	TGCAGGTGAACTAGCTAGTAACCCTAGTCAAGTCA AAAAAACTCCCTCT[A/G]TCCTGAATTACTTG
TP10237	3H	165.56	bowman_contig_1989888	TGCAGATGAGTAATTTG[C/G]TTATCCTGAATCTGTG ATGTTAGATGGAGCCCTGGACATGTACTCT
TP11522	3H	165.56	morex_contig_2555775	TGCAGATTGGTCACTG[A/G]CCTGGTTCACACTTAAT TGGCTACTAAAGTACTAGCTGCCATGGCAG
TP12420	3H	165.56	bowman_contig_200926	TGCAGCAACGCGCGGGGCATC[A/G]ACTAGTTCAAG GAGTGAAGGCTCCAGTTCCAGTGCATACGAG
TP13362	3H	165.56	bowman_contig_16057	TGCAGCACAACTTTTCTGCATTGTCCCTTCTAAGAT CGTACAATTAAGCTC[C/G]CTACTACTGCTA
TP22181	3H	165.56	-	TGCAGCCCCAAAGAGGGAATCTTCA[C/T]AGTGCAT GTTACGTCATCTCGATCAGCTAGGTTTCTA
TP26210	3H	165.56	-	TGCAGCGAGCATAACAGTGCATTTGTCGT[C/G]TGTTT TGGTCTCCACCGTCTAATCTCCGAGATCGG
TP41495	3H	165.56	morex_contig_132528	TGCAGGAGCAAGATGGCGCATTTTCATGGTGCCTAG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				GAA[A/G]GTGGTGTTCGTGATGAGCTGCCCCA
TP42420	3H	165.56	bowman_contig_894189	TGCAGGA[G/T]GTTAAAGTCCAGCTTTGCAAGCTCC AAAAGAACTGGATTATGGCCTTCTTCTTGTT
TP42744	3H	165.56	bowman_contig_62467	TGCAGGATATAGG[A/G]TCGATGCCGCTAGCTTTGC ATCAGCATTGGAATATCATGATGCTGCATTC
TP58733	3H	165.56	bowman_contig_71010	TGCAGTAGAT[A/C]CTTTGCGTGTTGTGCCTTTTTTG AAGCAAATTCCTTTTTCCTCATGGCATTCA
TP4256	3H	166.86	bowman_contig_63375	TGCAGACCCTGCTAACAAAACGGATGAACTCATCTC [C/T]GACAGATCTGTGGAATAAAGGACATAT
TP16637	3H	166.86	bowman_contig_200279	TGCAGCAGCCGCCCTCGCTGCGGCAACGGTCTCTTG GCCGCCAGCTGCTCGAGACCCG[C/T]CGAGG
TP35586	3H	166.86	morex_contig_135201	TGCAGCTGCAACCAGAGAACCATCATGAGACATTC CACCA[C/T]CTACATAAATCTTTGTGTGGCCG
TP48019	3H	166.86	bowman_contig_200279	TGCAGGCGGTGATGGAGGCGGGGCCTCT[C/G]CTGG AGAGCCTGCTGGTGGCAGGGCCTGTGCCGCA
TP59048	3H	166.86	-	TGCAGTAGTGAGGAGGC[C/T]TTTTTTTTAGAGAAG GAGGTCAAACCCCGAGATCGGAAGAGCACA
TP63677	3H	166.86	barke_contig_274949	TGCAGTTAAACAAACATGGAAGAGGGG[C/T]CGTTC GGAGGTGAGGGCGCGTGCTGACTGTCACGCG
TP65122	3H	166.86	morex_contig_1559531	TGCAGTTG[C/G]TACTGTAGTAAGTAAGCTATAGTT ATGCATATCTTTAGATGGTGCTCTACAAGCT
TP66051	3H	166.86	morex_contig_96865	TGCAGTTTTCTTGTTGGTGGGCGAGACCGAGAAGA GTGTTGATGCTGCTGCTGCTGCTGCTG[C/G]T
TP3588	3H	166.86	barke_contig_479624	TGCAGACACAACCAAATTT[C/T]TGAAAAAAAATTG CTGCCAAAAGAAACCAAGCCCGTGATGGATC
TP35466	3H	166.86	bowman_contig_1983915	TGCAGCTGA[G/T]GTGAAGTATGAAGAAAAGCTTGC TTCATCTCTCTTTTTTTCATCATGTGAGATG
TP39318	3H	166.86	bowman_contig_67331	TGCAGGAAGAGAAGATGATCCTGCCCTCACAATCT CCAAGGATCATACCAGCTCCAGCGCC[A/G]CC
TP61356	3H	166.86	-	TGCAGTGAAATGGATCGATCATGAGAGTAAGATTA ATTTTACCGATGACCGAA[C/T]TGCCCGTGTG
TP64084	3H	166.86	bowman_contig_891926	TGCAGTTCAGAAAAAGGTG[A/G]AGCGGACGAGCA GTTGGTTTCGACGGAGCAGATTCATCTGCGCG
TP19755	4H	51.00	bowman_contig_10798	TGCAGCATGGAAGGCCTGAGCTCCTCACACCGTAA AAATGTTTGCTTGACTG[C/T]TGCATCATGAT
TP36955	4H	51.00	-	TGCAGCTGGTGGAGCAC[A/G]GGATGATCGTGCACA AGTCGTGGAGGCTGCCAGCGGAGAATGAGGC
TP27632	4H	51.00	-	TGCAGCGCCGAAGGTGGTATCCACCTCTCCC[C/T]C GCCTCCCCCTTCGGCGGGAGCGGCGAGGTC
TP65670	4H	51.00	bowman_contig_190290	TGCAGTTTCAGTAGTCAGGTTTGGGTACAGTTTAGG [A/G]CATGGGCAAGAGCTGATTTCTTGATTC
TP63833	4H	51.00	barke_contig_272404	TGCAGTTACTA[C/T]GAAGCTTAGGCAGGAATGGAC ACTGTTCTTCAAGTTCAGTAGAGTTTATAGCT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP61460	4H	51.00	bowman_contig_846860	TGCAGTGAATCCAAACACACAAATTTATGCAACAG AGATCTATCGTTC[C/T]GAGTGCTGTAGAAGA
TP54367	4H	51.00	bowman_contig_223778	TGCAGGTCATGTATGGCGGTAATGCAATCCTT[A/C] AGCTCGGATGCCCTGTACCCGAGATCGGAAG
TP52493	4H	51.00	-	TGCAGGGGTTCTGAAC[A/C]CGCAACCTGCGGTGTGG AGGCACGGTGCGGCTGTCATTGCGCTAGGAA
TP47368	4H	51.00	barke_contig_269639	TGCAGGCGCTCGTTTGCAAAATTGCATTGCAACGGA TGCTTGTGACGCCAAATAG[A/G]TTTTGCCA
TP45314	4H	51.00	-	TGCAGGCCCCGACACCAC[A/G]CCATGTGGCACTACG CGGTGCCTTCGGACTCCACTCAGTCTCATCC
TP41164	4H	51.00	morex_contig_188347	TGCAGGAGAAGATGGCCAAAGCCAAGCGGGACGTG GACGCGGAAGCTGCCAGGATGAC[A/G]GCACA
TP37971	4H	51.00	morex_contig_136802	TGCAGCTTGCACGGCCGCGTCGCGTTGCAGTCAAG CCCAAACAAGCTGC[G/T]GTGATTTGACGTC
TP36917	4H	51.00	bowman_contig_235704	TGCAGCTGGTCGCGTCAGCGGGAAGC[C/T]GACGGG ATGGATGGAACCGAGATCGGAAGAGCACACG
TP34952	4H	51.00	barke_contig_1570100	TGCAGCT[C/T]GTTGCGGTGCAGATGTTGCTCTGTCC CTGGTCCGAGATCGGAAGAGCACACGTCTG
TP33382	4H	51.00	bowman_contig_125160	TGCAGCTCACAAAGGCTGCTGGTACCGTCTCAAATG TCCGTCTGTTTCGTGGCTGAACAC[A/C]TCT
TP29979	4H	51.00	bowman_contig_196689	TGCAGCGGCATGCCACGAGGAGGACGTGGCCAAGA CAACAACGGC[A/G]ATGGAGGCTCCAGAGGTG
TP24692	4H	51.00	barke_contig_1839671	TGCAGCCTCCCGATCGCACCGCCTGCCGCCCTGGC[C/T]GCCACCGCCTCCAGGGGTGCTAGCCGAC
TP22291	4H	51.00	morex_contig_345976	TGCAGCCCCCTGGTGGCAGTGCTCCTGGCGCTAGG AGCAGGGGCCGATGGGGCTGGTTTG[C/T]TG
TP21580	4H	51.00	-	TGCAGCCAGTGGTAGTACCGCTGGAGTGCCAGC[A/ G]GTAGTACCGCCGAGATCGGAAGAGCACACG
TP19038	4H	51.00	morex_contig_1559081	TGCAGCATCAACATTGCGAACGGAGTCATG[A/G]CG ATTCGAGACCCCTCGCGGTGTATGATGGCGC
TP18416	4H	51.00	morex_contig_8401	TGCAGCAGGTGGTGGGAAATAATCGTAATCACTGG CACCCTTTTGGCACACGTCGG[C/T]TGTTGGT
TP17174	4H	51.00	-	TGCAGCAGCTCACCCAGGTCAACTTGTTTTATCCCA AGGATCGAGA[C/T]CGAACTCCCGTCTCAGG
TP14801	4H	51.00	-	TGCAGCACGGCGTTC[C/G]CCGCAAGATGGTGCGGC TGTAGGCTAAAGTGTGCCAAGAAGCTGGAGA
TP14615	4H	51.00	-	TGCAGCACGCCTCATGAGATCGCGAG[A/C]AGACAC TCCTAGGCTTCGTTGGGCCCGAGATCGGAAG
TP14247	4H	51.00	bowman_contig_860704	TGCAGCACCTCCTTGCAGCAAGTCGCCGATCGTC[A/ G]CAGCACCGTCTCGCAACCCATCGTCGGTG
TP14005	4H	51.00	morex_contig_91117	TGCAGCACCCGCCGCCGTCGCCC[C/T]CGTGCTGCG ACGCCCTCGTCCCCGACACGCCTCCCGAGAT
TP12755	4H	51.00	morex_contig_1571157	TGCAGCAAGCATTTGAAACCTATCTACCT[C/G]CCTT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				AGATAATATGAATATTCTCCTATTTAAGCT
TP7867	4H	51.00	bowman_contig_290955	TGCAGAGGTGCGTATAGGAGAATCAGTCTGTAGTA TGGAAG[A/C]GGACATGCGTCGCCGAGATCGG
TP3206	4H	51.00	-	TGCAGAATGGAGGGGAGTGGCTCGGTA[C/G]ACACG GAGAACTCGCGGCCATGGTTGTGGCCACACC
TP1938	4H	51.00	morex_contig_40547	TGCAGAAGAGGTCAAATGCATCAGACTTGCTCAAT GGCTCGAGCTCAAGGTGACG[A/G]GTGGGAGA
TP22263	4H	51.00	morex_contig_1576868	TGCAGCCCCATGGTATGGAGGGACTCGCAGCGCGA GATCACCTT[C/T]GGTGTTCGTCTTTCCCGA
TP51979	4H	53.60	bowman_contig_144774	TGCAGGGGCGCGG[A/T]GGTCGGCCATGGGTGCTCG TGAGGCTGGAGCGGGGGCGGCAGGATGATCG
TP30013	4H	53.60	-	TGCAGCGGCCAGACGAGCGCGGCGGTTGCCGCAGC TGTGGCGGTTGCCAGGGCAGCCA[C/T]GACGG
TP11052	4H	53.60	bowman_contig_148663	TGCAGATGTGTTGTTGCTAGCCACCCAGCAATTGG TGCTAGCTATT[C/T]GTCGGTTTCGGCTGAT
TP59687	4H	54.86	barke_contig_370058	TGCAGTCACTGGTGCACGAACAAGAGCCACGAGAG AAGGTGGTGACGCA[C/G]CGCAAACGCCTCCG
TP38222	4H	54.86	bowman_contig_128628	TGCAGCTTGTACAGTACCATAGTA[G/T]CATTACAGT ACACTTGGTGGTACAAACATAATAGCAGCT
TP28571	4H	54.86	morex_contig_1558498	TGCAGCGCGCGCAGCCACCAAACGGGGTCTCGGA[C /G]GTGCTGCCTGCCATCTCGTCTGCCACCCC
TP23343	4H	54.86	morex_contig_41456	TGCAGCCGATGGCGAGGATGATCATTTCCGAGAAT CCCAGTGAGTGAGTTGT[C/G]ATGACATGTGT
TP21080	4H	54.94	-	TGCAGCCACTGCTCCAGGCAGGCC[C/G]AATGGAAG ATGTGCTTGCAGCGCAGCTGGATCAGCCTGT
TP46986	4H	82.98	barke_contig_272322	TGCAGGCGCC[A/G]CTTTACGAAAATGCATACGAAT GAAGGCTTGAACACTAAATAGGAAACACTG
TP62017	4H	83.00	bowman_contig_844574	TGCAGTGCAGTGAATCAGTCACATGCATGCCATAGC CTT[A/G]TCATCTTTCCGTGTAGATGATCC
TP26370	4H	129.60	-	TGCAGCGAGGCTGCGTCGTCCACGCCACCTTGAGAT CCCTCCGTAAGTGAACCTCCATCTCCA[A/T]
TP59956	4H	129.60	morex_contig_87276	TGCAGTCCAATGAAGCGCTAACTGCTAAGCATACCT GAAGCAAT[C/T]GCCTTAGCGGCAACCTTGA
TP8649	4H	129.60	morex_contig_87276	TGCAGATACTGTAGTGGGATC[C/G]TTGGATTCTCTT TGTTAGGATCCTAATTGTGAGCACAGTGAG
TP53065	4H	129.60	-	TGCAGGGTGGGGTCGGGCCTGTAACGGGGC[A/G]TC GGCATGGCCGAGATCGGAAGAGCACACGTCT
TP39658	4H	129.60	morex_contig_367754	TGCAGGAAGTCGCCGACGTTACCAACCAGCGACGC CTCCCCC[A/G]CCGCCGAGATCGGAAGAGCAC
TP859	4H	129.60	barke_contig_276869	TGCAGAAATTGGATGTACCTATCTTTTTTAGAAAAG GAGGA[C/T]GACCCCCGAGATCGGAAGAGCA
TP287	4H	129.60	-	TGCAGAAACAATAGTCAGATTGGAACCCCCCTCTCT TGGCGGTAGGCGCGCCAGGTGA[C/T]ACGTG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP59213	4H	138.70	barke_contig_269320	TGCAGT[A/T]TCGGACAGGATGTTCTTTTCGATAGTC TCTGTGGATACCGAGATCGGAAGAGCACAC
TP61055	4H	138.70	bowman_contig_11063	TGCAGTCTACTTACGTGTCGAGTACTCGAGTACAGA GGGAGGAGCTTGCCTGCTTCC[A/G]CCCAT
TLP3	5H	0		GCTTCTACCACTACGGCATCACTAC[G/A]GACAAGG GGTCAACCTGCCGCTGG
TP54118	5H	1.00	bowman_contig_1998759	TGCAGGTCAAGATGTTTTTCTTACAACCTAGTACAAA TGC[C/T]CGTGCGTTGCACCGAGATCGGAAG
TP63590	5H	1.00	bowman_contig_219311	TGCAGTGTTATTGTAAGTCAGCCCTAAGCTGAGAAG GTAT[C/G]TTTATAAGGAGACTAGATCGACG
TP13528	5H	2.07	bowman_contig_10320	TGCAGCACAGAATTTGTAGTGTGTGTAT[A/G]GAAA ACAACTACAAATGTTTCAAGGCCATTATGTT
TP3726	5H	3.37	morex_contig_141545	TGCAGACAGACAGATACTAACACATGATGAACTTC AAGTGAGCAGCATGTATC[A/G]CGATGAATGG
TP12039	5H	3.37	bowman_contig_221981	TGCAGCAAATCGCGACGGCAGTT[A/G]CAGCTAGAT GGGACACTGGTGGTAGCAATTTCAATGCCG
TP24182	5H	3.37	morex_contig_141545	TGCAGCCGTAAGCGGCCACATGTG[A/G]CCTTGCCT AGTTCTTGTTCTGCTTCTAGTTCTTGTTCTA
TP59917	5H	3.37	barke_contig_269588	TGCAGTCCAA[A/C]ACCAAAATGGACGAAAGTTGTG CCTACTACAAGATTCGTTTTTTGGATATTCC
TP62237	5H	3.37	barke_contig_2786554	TGCAGTGCCTCGGCGATGTTGTGGTAGAAGGATGC ATCGT[C/G]AGCAAGGGCTCCGTCAGAGGGAG
TP38608	5H	4.67	morex_contig_73732	TGCAGGAAAATATAGAGAAGCAAGGACACTAGTGT CTC[A/C]GCGTGGATCGCTGACTCTATCCCAA
TP54510	5H	4.67	bowman_contig_1984153	TGCAGGTCCGACAGAAGGTGTGGATAATGCT[A/C]A GCAACAATTTCGAGAAAACCTCCGCTTCTTTGA
TP1392	5H	4.67	bowman_contig_144877	TGCAGAACGACACCTGGAACGGCACCTCCCCTCAG CA[C/G]GGCACGTACGCGGCGCCGAGATCGGA
TP41194	5H	4.67	bowman_contig_67402	TGCAGGAGAAGTCCATGGGGACGTTATACCCATCG ATGACCGAGATGT[C/T]GTAGTAGTCCTGCGA
TP48109	5H	4.67	morex_contig_1582097	TGCAGGCGTAGACGGGAT[A/T]TTTAGACGAGACAC ACGAGGCCGAGATCGGAAGAGCACACGTCTG
TP497	5H	12.52	barke_contig_371009	TGCAGAAAGAC[A/C]GAGTAGCTAGGCCTTACGCAG CGCCGAGATCGGAAGAGCACACGTCTGAACT
TP33438	5H	12.52	bowman_contig_13818	TGCAGCT[C/G]ACGATACGCCAGTTGAATCCAGCAA GCGCGACGTGCTCCGATGACAGCGGCGAGGG
TP43934	5H	12.52	bowman_contig_865713	TGCAGGCACCCGTTTGCCTCTTGGCGCCAGCAGCG CTCCA[C/T]GCCGAGATCGGAAGAGCACACG
TP38150	5H	13.82	morex_contig_60728	TGCAGCTTGGCGCTGGCGCT[C/T]TGTTGGTCGCTGA AGCGGCCGAGATCGGAAGAGCACACGTCTG
TP32708	5H	15.13	morex_contig_46634	TGCAGCTACCATGT[C/G]AGTAGGAAGATAACAGGA TCTTATCCGAGATCGGAAGAGCACACGTCTG
TP63447	5H	16.42	barke_contig_282158	TGCAGTGTGAAACTTCCACAAAACCTGTCAATTTTCGC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				ACCGCGCCC[A/G]CCGCATTTCATTCCGAGAT
TP21886	5H	16.42	morex_contig_67868	TGCAGCCATTGCTCCTACGCCTCTACTGGTGAGTT TATACTTTTCACCGTCTAAAACGGGTG[A/T]
TP7774	5H	16.42	morex_contig_1581968	TGCAGAGGGGGCGGGTCGATGTATGTATATCTGGCT TTGA[C/T]GAGGAACCGAGATCGGAAGAGCA
TP12346	5H	16.42	morex_contig_72763	TGCAGCAACCTATTAAGCGTCATGGTTGTTTTGATG CCACACCTGAGTACT[A/G]TGTGTTTGGTTT
TP22738	5H	16.42	barke_contig_282309	TGCAGCC[C/T]GCCGCTTCTTTAATTGCAGTATCATG CACTGACCGAGATCGGAAGAGCACACGTCT
TP37374	5H	16.42	morex_contig_65198	TGCAGCTTATGTAATGGTTTTACTTTGGTTGGAACA T[C/G]AGGTCTCTGCTTCTAGTTCATCCCAG
TP64344	5H	16.42	-	TGCAGTTCCTCTTTAATTC[A/C]AGACCTGACCTGGT AAGGAGTACTATTAACCGAGATCGGAAGA
TP11725	5H	19.03	morex_contig_56495	TGCAGATTTTTCTTTACTCACAATGATTTCAA[C/T] TTGTTTGTCTGTAATAGGAGAGAACTTGAT
TP31687	5H	19.03	bowman_contig_861463	TGCAGCGTCCTCGGCGTAGGCTACGGCGGAGGCGG GGCGCTC[C/G]AGGCGGCAGGTGAAGCAGCGG
TP3371	5H	20.31	morex_contig_83442	TGCAGAATTGTCGTTGTACAATCTTGAGCGCTAGCA ATGTTTCCTTC[G/T]TGTCTTTTCCTTGTA
TP3372	5H	20.31	morex_contig_83442	TGCAGAATTGTCGTTGTACAATCTTGAGCGCTAGCA ATGTTTCCTCGTGT[C/T]TTTTCCTTGTA
TP10347	5H	25.54	bowman_contig_62910	TGCAGATGCACTCGATCCACGACC[C/T]GACGAATG CGGCGACGACCGACGATTAGTCACTACGGCC
TP41431	5H	25.54	bowman_contig_924366	TGCAGGAGATGATTGACGGAGGAGGAAGAGATCAA TA[C/T]GGAGATGGGCCTTGCTGCTCCACGTC
TP59966	5H	25.54	morex_contig_1592368	TGCAGTCCACAGTAGCCGCTGCCCATGTGC[A/G]AG GACAGAAGTCTACAGTAGCCAGCACACCCAT
TP16940	5H	29.44	-	TGCAGCAGCGGAGACAACACATG[C/T]CTTTACAGG GTACCCTACATGGACCGAGATCGGAAGAGCA
TP38718	5H	29.44	barke_contig_4003	TGCAGGAAAGAAAAGGCTTTTTATGCTCTGTTA[C/T] CGATACTGTTTGCTCCTGCAAATCTAAACA
TP39357	5H	29.44	morex_contig_80211	TGCAGGA[A/G]GATATATACGTATGGAGCTTTTGCT GACCCAATGGATTGAGGACATAGGTGTAT
TP41281	5H	29.44	barke_contig_1799546	TGCAGGAGAGACAGATTCAATCATTTGAGTCCTGC GGTCACCTTTTGAAAAGGG[A/G]GAAAACAC
TP44740	5H	29.44	morex_contig_37437	TGCAGGCCAAGCTATTATGTACACCCAGATTTTATT TTCTGCACCGCGAATGAGGATGCA[A/G]CAC
TP49057	5H	29.44	morex_contig_1561753	TGCAGGCTGGCG[C/G]ACCTGCATGCATGCCGTCCG TCCATGTTTTGCACGAACCCCGATGTCGACG
TP65258	5H	29.44	morex_contig_48893	TGCAGTTGGCCA[G/T]AGCCGTCAACTCTGTATTGG GGTTGCCAGCTGGAAGGTTGTACCGCGCGCT
TP22385	5H	30.74	barke_contig_1799546	TGCAGCCCCGCACCTTCTTCCCGC[C/T]ATTCGGCCA CGCCACCCCTTCCACCGCGGGACCTCAAGG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP8224	5H	32.04	morex_contig_1559060	TGCAGAGTGTGTCACAACGCAGCCCTCACGATCAA CGCAGTCCTCAGGTC[G/T]AGGCTCTTGGACC
TP23771	5H	32.04	bowman_contig_900313	TGCAGCCGCCTCGAAGGAAAAGACTGGTGCGAGAC GACACGGCATAGTTGCCCCCA[A/G]AGAGCTC
TP30417	5H	32.04	morex_contig_125350	TGCAG[C/G]GGCGGGCCCATGGTGACACGATGTTT TCTATGCACCAACAGAGTTATGGCGGATGCT
TP31354	5H	32.04	bowman_contig_900313	TGCAG[C/T]GGTTTCAACGCGTCGGCGGGCGTCGGA TGCAGCGTGCCCGTGGACGTACAGTCCAGGC
TP31606	5H	32.04	morex_contig_1592149	TGCAGCGTC[A/G]TTGAGGTTGTTGCGGTAGCAACA AGATGAACGAGCACCGAGATCGGAAGAGCAC
TP34330	5H	32.04	bowman_contig_128296	TGCAGCTCGACAGTGCTCCATTGCAACCCCAGGACG CTGCAATGA[A/G]TCCCGACGGCGCTTCAAT
TP37289	5H	32.04	barke_contig_275310	TGCAGCTGTTTTGTAACCTTGTGTGAATC[A/G]AATTC TGTATTACTCTGTACTATGAATCTACGATA
TP51233	5H	32.04	barke_contig_1884202	TGCAGGGCGGCGCGATGACTGGCGGTGGCAC[C/T]C TGGGTGGGCCTGTCGTGGGCTTTCGACGTC
TP55675	5H	32.04	bowman_contig_255014	TGCAGGTGATGTGGGCTATGGGCGGCCGCATG[G/T] CGCCGAGATCGGAAGAGCACACGTCTGAACT
TP57315	5H	32.04	barke_contig_2782335	TGCAGGTTGAG[A/G]GGCTTGGTGGCGAAGAGAAGC CGTCGGCGTCGGGATCCCTTCCTCGTCCATC
TP63562	5H	32.04	morex_contig_52357	TGCAGTGTGTGTGCCGTCGTTTCCGCCACC[A/C]CCA GCACAAGCCACACATTCGTCTGCCGAGATC
TP54285	5H	34.72	barke_contig_1824120	TGCAGGTCAGGTTTCGATCCCACACGTTTCCA[T/C]T ATTATTTCTACACAGAGTCCAGGCCCAACC
TP4814	5H	35.95	-	TGCAG[A/G]CGCACTACAAGCGGAGGCACTGTGCCA AGCCATTCCCTCTGCCGCAAGTGCGGCAAGGC
TP5901	5H	35.95	barke_contig_2781259	TGCAGAGA[C/T]AAGGACCTCACACGGCAAAAGCCA CTCACAACCGTGTAGCCCCGACCCGATACCT
TP8541	5H	35.95	-	TGCAGATACAGGTAAAATTATTTTATTCAGTGATGC CAAAAGAACGTC[C/G]AAAGAGTATGCCCCA
TP11256	5H	35.95	barke_contig_315490	TGCAGATTCCACTTGGCG[A/C]TTTCCTTGTAATTC ACTAAGGGTGTCTTTTGAGTTGGTCAAGC
TP12019	5H	35.95	barke_contig_2495902	TGCAGCAAATACCTAGCGCCACCGCTAGAAGTTTCG TC[A/G]CCGCGAGGAACAGCTTCACTACCTC
TP13055	5H	35.95	barke_contig_265532	TGCAGCAATAATGGAAGCCCGACGATGGGGGC[G/A]]GGCGGAGGCACGAGTCCGACAATGTTCTCTT
TP13091	5H	35.95	barke_contig_1860061	TGCAGCAATATTTAAAGTGAGGTCACGCCCAGAGA TCCTCCCTCGACTCC[C/G]TGCAAGGAAGCAA
TP13232	5H	35.95	-	TGCAGCAATGTCTTT[C/G]GAAGAGACAGAAGCTCC AACAAATATCTCTACGTTGGTAGCCGAGATC
TP17485	5H	35.95	bowman_contig_220994	TGCAGCAGGAAATACTTCT[A/T]CACTTGACTTTTCT TGAACCGAGATCGGAAGAGCACACGTCTGA
TP20697	5H	35.95	bowman_contig_882388	TGCAGCCACCACG[C/T]TCCGCAACCTTTCACCGAG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				CACCAGCGGGAGGAACTTCGGTGGAGCTACG
TP24994	5H	35.95	bowman_contig_143375	TGCAGCCTGAGGAGGACGCC[A/G]AGCAGGTCCTCA TCTCTCTCAGGCGCCGAGATCGGAAGAGCAC
TP25506	5H	35.95	-	TGCAGCCTTTTTAATCGCACTGGAA[G/T]AGCGCAA GATCATGTGAAATGAAACGTACCAGCCGAGA
TP26591	5H	35.95	morex_contig_1598031	TGCAGCGATG[A/G]CGTATTATAAGCTACTGTTTGGT AAAAAAGGCTGCTGCAAATTAGAATTGGAA
TP32400	5H	35.95	morex_contig_52950	TGCAGCGTTG[A/C]CCTTCCCTGCCACGGCGTCGGC GCCTATCGTCGCCCCGAGATCGGAAGAGCACA
TP32436	5H	35.95	bowman_contig_861370	TGCAGCGTTGGGGCTGGGTGCATGGTAGTAGCATA GCTAGGCTCGGTTTCCTTTCGCGTCGGG[A/G]T
TP35895	5H	35.95	barke_contig_8115	TGCAGCTGCCGTCGCTAGCAGCACAT[C/G]AATGGC AAAGGCATCCATCGTACATGATGGTTGATGT
TP37689	5H	35.95	bowman_contig_10137	TGCAGCTTCGTCTT[C/G]GGCGTCGCGGAGCTGGGC GTCCGCAGCCAGGAGTGCCGCGACCACACCA
TP41021	5H	35.95	bowman_contig_1991579	TGCAGG[A/G]CTCGAGGCTTTGGATCGGAACGACGG TGCCCGCTGGTGCACCCTGGACGTGTGCGGG
TP43149	5H	35.95	-	TGCAGGATGAGGTGGAGCTTCAAGATGGGGC[A/T]A TAGCATGATGTTACGGAGCTTGGTGAGATCC
TP48096	5H	35.95	-	TGCAGGCGTACAGCCAAGTCCACCATGAGCTCCCG CGGGAC[A/G]CCTTCTGCGCCACTGTTATATA
TP59839	5H	35.95	-	TGCAGTCATATAACTTGCCTATGCATGCAAAACG[A/ T]TCACTTCTTCCGAGATCGGAAGAGCACAC
TP65348	5H	35.95	-	TGCAGTTGGTACGCGCCATGGT[C/T]GCGTCGACGG ACACGCACGGCTGCGTCGAGCACGGCACGGT
TP20247	5H	37.24	barke_contig_270304	TGCAGCCAAATAAAATGAAACCACGAATTCAAAGG ATGTGTGCCTCAGA[A/G]TATCACGCAGTGGA
TP37715	5H	37.24	barke_contig_129454	TGCAGCTTCTC[A/G]AGATGAAGCTCGGCTAGCAAG GCACCCTGTGGGATCGCCTGGAGAACAGGGT
TP54027	5H	37.24	barke_contig_2785050	TGCAGGTATGAGCTAGGTAGGCCCCGCTGGGGTCTTC ACTCTTTTGAC[C/T]TGGGAGCATCAATCAT
TP55268	5H	37.24	morex_contig_41158	TGCAGGTCTCCACCGTATCAAACCTCC[C/T]TTCTGCC ACCGCTATCTTCCGCACCGAGATCGGAAGA
TP11893	5H	37.24	morex_contig_2547773	TGCAGCAAAGAACCTTGTCTCGCGGGTGTCAAGTC TGTAACCTTGCA[C/T]GATGATGGTAATGTG
TP24336	5H	38.53	barke_contig_1968067	TGCAGCCGTGGAGTTAACCGTG[C/A/G]TGAGACCAC AAAGGGATGCAATGGGTTACCGAGATCGGAA
TP13185	5H	40.19	morex_contig_216174	TGCAGCAATGCTAGCTCCTCCTTGGCCTCC[C/G]CCT CGCCTTGGCGGGCGACGTCGAGGGCGGGAT
TP12521	5H	41.16	-	TGCAGCAACTCGCCTTGTGGGCAGGCCGTGCCCT[C/ T]GGGTTTGTCAATTCCTTGTATTGATCTAG
TP3303	5H	41.16	bowman_contig_887289	TGCAGAATTATTTTTTCCATAACAGAAGACACGCGG GAGACTTGAGAACCAAGGCACG[G/T]GACCT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP471	5H	41.16	-	TGCAGAAAGAAATAGCAGCCTGAAC[A/G]CTCCAAA AGTCCAACCATGTGACCTCCGAGATCGGAAG
TP926	5H	41.16	morex_contig_60397	TGCAGAAATTTTGTCCAAAGAT[G/T]CTGCAACAGT TATGAACCTGGTAGCAGGGTGGTGTCTGCAAC
TP2413	5H	41.16	barke_contig_63654	TGCAGAAG[C/T]TTCTGCTGCTGCTGACAATGATAA AAGAACAGTAACAGTTGATGAACCAGTGTG
TP3335	5H	41.16	morex_contig_61229	TGCAGAATTCTGATGCTGATAGAATGATAAGACATT TATAAGTTACTAAT[G/T]TGGAGAACAACCT
TP3396	5H	41.16	barke_contig_411017	TGCAGAATTTGCTATACATATTGATTAATACTCACA GTTGTAC[C/G]ATGGAACAAGCTCGTATAAA
TP3842	5H	41.16	barke_contig_267982	TGCAG[A/G]CATACTGATGTCAACAAATGGGAAGTA TGTATATAACAATATGTCAACTGAGATTAGC
TP4088	5H	41.16	-	TGCAGAC[C/T]ATAACAATGACTTAAGCTAAATCGC TCTTCCATCAATGGCAATTTGCAGGAGTTAC
TP5468	5H	41.16	morex_contig_66584	TGCAGACTAGCAATGGTAAGGCGTGCTCGGCTCATC TGATGCC[A/G]CAAATCTGACGGCTCGCGAC
TP6316	5H	41.16	morex_contig_38131	TGCAGAGATTGTTCTTGGATGCGCCGTTTTGC[G/A]A CCGAGATCGGAAGAGCACACGTCTGAACTC
TP6862	5H	41.16	morex_contig_38131	TGCAGAGCGCCAC[A/G]AGCGCCGTGTTGACCGTGA CGGCGTCGAACGGGACGCCGCGCTTGACAT
TP7498	5H	41.16	morex_contig_51506	TGCAGAG[G/T]CAGATCAGCGTGCTGCACATGTCCC AGGCTGCTGCCGCCGCCAGAGCATCCGTCGG
TP8196	5H	41.16	bowman_contig_2010139	TGCAGAGTGGTGTCTCTTCCCAGCCAAAGTCAGCT GAGTC[A/G]AAGCAGCACTTGCGAATCACAA
TP8385	5H	41.16	bowman_contig_879642	TGCAGATAAAACATTACCCACCTGTACTGTTTTAGA TACATAAATCTACACCTTGCAACTGT[A/C]G
TP9562	5H	41.16	-	TGCAGATCGATACTGCAAATTCAAACATACTAGTT[C/G]GCGCTAGAAACATATCACCGAGATCGGA
TP10983	5H	41.16	morex_contig_38410	TGCAGATGTTCGATTGTCAGTTTCTGATC[A/G]TCTAT AACTATGAGTGTGCAGATACAATCAGTACT
TP12162	5H	41.16	bowman_contig_895903	TGCAGCAACACGAT[C/T]CATCGAACCATATGTGTA TATCCAATTAGAACAAAACCTTTAGTTTATCC
TP12713	5H	41.16	barke_contig_606900	TGCAGCAAGCAAAATAACTTCAA[C/G]TAGACTTGT AAATAAAGCTATGCTCCCCGAGATCGGAAGA
TP13208	5H	41.16	-	TGCAGCAATGGCGCCGTGCCAGTGGTCGTGGAGC[G /T]TACCGAGATCGGAAGAGCACACGTCTGAA
TP13639	5H	41.16	-	TGCAGCACATCAAAATCATCACGCAGAGACAACAC CTCCTGGAGATCCGCGTCATCA[A/G]TCGCCT
TP14124	5H	41.16	morex_contig_369170	TGCAGCACCGCCACACCTCATTTAACAGATGG[A/G]AGGCTGACGATACCCGTGCCGAGATCGGAA
TP14847	5H	41.16	bowman_contig_88897	TGCAGCACGGTCAACTATATATCAACAAGACTTACA CCGC[C/T]ATCACAGCCGAAGAGTTAAGAGC
TP15318	5H	41.16	-	TGCAG[C/T]AGAACGAGGTCGTTGAAAGGCGCAATC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				GAACCGTTGTTGACATGGCAAGGAGTTTACT
TP15610	5H	41.16	-	TGCAGCAGAGCACTGTAGCCATGTCCTGCCC[A/G]A GGCTCCCGAGATCGGAAGAGCACACGTCTGA
TP18295	5H	41.16	bowman_contig_1317130	TGCAGCAGGTCCCCCTCCGTACGTGGAGGGGAGG AAGTCGC[C/G]CTGGATCCGTCCCGCCGAGAT
TP19507	5H	41.16	barke_contig_57234	TGCAGCATCTTCACAAGCGATACCAGTT[C/T]TGCTG GGGATACCGAGATCGGAAGAGCACACGTCT
TP20451	5H	41.16	morex_contig_1797732	TGCAGCCAAGTTGAGGACA[C/T]GCGTGCGGAATAT CTCGATGTTTTTCATGATGAGAACGCCGACCG
TP21189	5H	41.16	bowman_contig_843599	TGCAGCCAGAGCTCCACATACA[A/G]CCTCATATGG CGTTTGGACGCGGACGAGGGGCTCACCGAGAT
TP21573	5H	41.16	-	TGCAGCCAGTGGCAGCCCCGTCGACCGTGGTGGGG GAGGCTGGAGTGGACGGGGA[C/T]GCCGAGAT
TP22146	5H	41.16	barke_contig_314565	TGCAGCCCATGCACACTAC[A/G]CATGCATAAGAAG CAACATCGCGAGGCTAACCTGCCGAGATCGG
TP22195	5H	41.16	bowman_contig_131167	TGCAGCCCCA[A/T]GGGTGGCCCTGGACCCCTGGGG AGGTCGCAGCTGACCACAGCTTCGGCCATGG
TP22362	5H	41.16	-	TGCAGCCCCGACGCGGGGCAACTCCTACGCGTAGG GCGACGATGACGGGGCCGA[C/T]GAAACTCCGA
TP22571	5H	41.16	morex_contig_60397	TGCAGCCCGAACTGCGGTAACATGAGAGCATGGTT AACAGCAC[A/G]TCCGAGATCGGAAGAGCACA
TP24291	5H	41.16	-	TGCAGCCGTCTCCTCCCCCTCCTCCT[A/G]GTCTCGTC CTCTCCCTTCTGGATCAAAGGGGAGCTCTG
TP24655	5H	41.16	-	TGCAGCCTCCACCCT[A/G]ACAAAGGGGCAGACGAT CAAGCTCGAGGCGCGGAAGAAGAAGGGGAAG
TP24715	5H	41.16	bowman_contig_129823	TGCAGCCTC[C/T]GCCATGACAAAGGGGCAGACTAG CAAGCTAGAGGCGGGGAAGAAGAAGGGGAAC
TP25403	5H	41.16	morex_contig_1569564	TGCAGCCTTCTGATGTGAAGTTATTTCTCTTTT[C/G] TGCTTTGACATAGTACTCTTGTTATACTT
TP25613	5H	41.16	bowman_contig_67252	TGCAGCGAAGAGAGATCGAATGACGCCGAAAGTTC TTCCTCGAGCGACATTGACG[A/G]GGTGGCAG
TP29107	5H	41.16	bowman_contig_91228	TGCAGCGCTAC[A/G]ACTTTGGCGTTTCGCTTCCGAGC TTGGATGGCCATCCTGCTATCTTCAGCAAG
TP29770	5H	41.16	bowman_contig_201679	TGCAGCGGATTCCCCACTGCCGTCTCCAATAGAAGC AGCCACTGACCATAAC[A/C]TATTGCTAGTA
TP30150	5H	41.16	bowman_contig_79643	TGCAGCGG[C/T]GACGAGCTCCTCAATGCCGTGGAG CCAATCGTTGTGGCGGTCAGGGGCGGGCCGA
TP31701	5H	41.16	bowman_contig_11695	TGCAGCGTCGAAGACGTGCGACGAAATGATAGGGA AGCG[C/T]TTGGCATTGTAGGTGTTGGTCCAG
TP33057	5H	41.16	barke_contig_199004	TGCAGCTAGCTAGGGCACACATGCACGCACG[C/T]A CGTACGTACACGTGGTGGAAGGAAGTGTGGA
TP33779	5H	41.16	barke_contig_1854775	TGCAGCTCCATAGT[C/G]GGCTGCCTCTCTCTGCGCA CCCGAGATCGGAAGAGCACACGTCTGAACT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP34297	5H	41.16	-	TGCAGCTCGAACATGGAGTACAGGGCATCCTCGAC CTCTCGCGCAGCCAT[A/G]GACGGCCTCGTCC
TP35051	5H	41.16	morex_contig_127915	TGCAGCTCTCCTCGTAATCGCAGGCCCACGTGCAGA GGTAGTAGAC[A/G]TAGTTGGTAGCAGGAGA
TP35464	5H	41.16	bowman_contig_863279	TGCAGCTGAGGTCATCGTCCGCCCCGTCCGCCAGCAC GCGTCTCTT[C/T]CAGTGCAGTCCAGTTCCG
TP35851	5H	41.16	-	TGCAGCTGCCGCACAAGCCAAGCCGCTAC[C/T]GCC GTGCACCTCATCGCCGAGATCGGAAGAGCAC
TP36023	5H	41.16	morex_contig_2659267	TGCAGCTGCGGAGG[G/T]CGGCACGAGCGCCCGTGT TGGCGGAGGGGTGTGGGGCCGCGGTCGCCGC
TP36182	5H	41.16	-	TGCAGCTGCTCCTCGGGCTAGAGGCAGGAGCCTTCG GGGGCTCG[A/G]GGCTACGAGCATGTTCGACG
TP37226	5H	41.16	morex_contig_1564422	TGCAGCTGTGTGG[C/T]TGCACCTGCTGGCCGCAGC GGTATATATGTACACACGATCGACACAAGAA
TP37239	5H	41.16	bowman_contig_2050429	TGCAGCTGTTCAATCTTCTTCCCATGTGTTTCGTTCTG CTGACTGTTCCGGTCTATTCTAT[A/T]AGGG
TP38987	5H	41.16	bowman_contig_111327	TGCAGGAACATCTGTCTGGGAT[C/T]CCACTGCGGT CCCTGCCCCTGCGGCCGCCCAAATGAGCTCG
TP40327	5H	41.16	barke_contig_64855	TGCAGGACC[A/G]ATGATGGACATTGTGCTAGAGGA GGACAGTCACCAGACAGGATTTCTGGCCTCC
TP41557	5H	41.16	bowman_contig_1984088	TGCAGGAGCAG[C/G]AGCACAAGCTGGCGGCAGCA TTGGTGGACGTGGAGCAATGGCGCCGAGATCG
TP42649	5H	41.16	-	TGCAGGAGTTGGTCCCGCCAGGCCTGCAAAAT[G/T] TAGATGTTAGTTCAAAATGTACTGCCAACAT
TP43711	5H	41.16	bowman_contig_127247	TGCAGGCAACC[A/G]TGCGCGCAAACACTGAGACAA ACGAGGCCTATTCTTGTTGGCCAATTTCGGCA
TP43953	5H	41.16	barke_contig_366989	TGCAGGCACCGTTTTCCATAACCGACGCTGAAGCGC CGAATAGGAGGTCCCCTTTTTTTA[C/T]AGG
TP45444	5H	41.16	morex_contig_159411	TGCAGGCCCTCTGCAAAGCAATGCGCGAGGCGCTG AGTCCCATCGCCATC[A/G]GGGCGAGCATGCA
TP46989	5H	41.16	bowman_contig_899379	TGCAGGCGCCAGAGGCA[A/T]GCGGAGCTCCTAGTC AGCGCTACAGGCACTGGTTAACGATCCGAGA
TP48667	5H	41.16	bowman_contig_112624	TGCAGGCTCGGAGCCCGAGCACCATGGCGAGGCGG CAGCATCCCCTGGGG[C/T]GGAGGCTGTTGAT
TP49145	5H	41.16	bowman_contig_176481	TGCAGGCTGTCTTTTTTTCACAAACAAATCTCCAGT ACATGCACGTCCA[A/G]CTCGCAACTTCCCG
TP49239	5H	41.16	morex_contig_136756	TGCAGGCTTGAATCCGTACGGTT[A/T]AAAAAGGTA ATAAAAAAAGTCTACCTTGCCCAACTAAA
TP49483	5H	41.16	-	TGCAGGGAAGGAACGT[C/T]CGCTACTCAATTCTGA ACGATTAACTTTCCATAACAGTTATAGTACT
TP49502	5H	41.16	bowman_contig_867044	TGCAGGGAAGTGTGGCCATGCATGCCCCGTGCACTGT TTTGGTCCTAGCCCAA[C/G]AATGTTCTAC
TP49647	5H	41.16	morex_contig_135879	TGCAGGGACGATAAGGCGACCCCTTACTTGGTCCCT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				TTTAGGT[C/G]GACTCGTCTTCGTGGGACGC
TP50271	5H	41.16	morex_contig_42293	TGCAGGGCA[C/T]AACCTCTTATTTACCTATCGAGG TTGACCACCAGAGTCTCTCCGAGATCGGAA
TP53229	5H	41.16	bowman_contig_854679	TGCAGGGTTCTGTGAATAGGAAAGTGTCTATGACAC ATATGAATCATG[C/G]GAGTAGTCGCTCCCA
TP53401	5H	41.16	morex_contig_6554	TGCAGGTAACCAATACTTGAATTCCTCCCCATGTT[C/T]GAGAAATCAGCCGCACCAAATGTGCGC
TP54638	5H	41.16	barke_contig_364158	TGCAGGTCCTTCAAGGATCTCACCCGAGCTATG[A/T]TCCGAGATCGGAAGAGCACACGTCTGAACT
TP57913	5H	41.16	morex_contig_1610622	TGCAGTAAATCGAGTATGTCAATTCCTGCAT[C/T]CG CCAACCACTGTCCACTTCTCAGCTGCAAAA
TP58055	5H	41.16	barke_contig_1854775	TGCAGTAATAAAAATCGCACAGGAACGA[A/G]GCCA ACCCGAGATCGGAAGAGCACACGTCTGAACTC
TP58963	5H	41.16	bowman_contig_2074103	TGCAGTAGGGCCGAACATGTCAGCGCGTACTGCTG[A/C]TGCGGTAGACTCTGATCATTCTGCTTTGT
TP59142	5H	41.16	bowman_contig_99214	TGCAGTATATATGCAGTGCAAGA[C/G]CTGTTAGAT AAAGCGAGATCAAAGGATCACAAGTTATTTA
TP59387	5H	41.16	morex_contig_59753	TGCAGTATTGCAACCGTATGAA[C/T]ACCAGACATC TTTACAGAAGTAGATTAACTCTACGCAAGAT
TP59811	5H	41.16	barke_contig_458195	TGCAGTCAGTGGGGACAAGATGCTC[C/T]CCATCCC CAGCACCCAAGAGCGGGGTGAGCATCGAAAA
TP59926	5H	41.16	morex_contig_60995	TGCAGTCCAACACTCCA[A/G]ACAACCCAAACTAGG CAGTGCAGCTCCGAGATCGGAAGAGCACACG
TP60136	5H	41.16	morex_contig_61229	TGCAGTCCCCTGGTCGAAGTGTTGGAAACG[A/G]AA GTAAGAACAAGGCAGTAGGATTTGGAACAAA
TP61245	5H	41.16	barke_contig_421793	TGCAGTCTGGTGACACCACTGCACTACACAC[C/G]G TAGGTACAGTAGCCATGCATCTGTGAATTGA
TP61830	5H	41.16	bowman_contig_853407	TGCAGTGCAAAGAACAACCATCACGGGAACGACCA ACAATGACAGATGTT[C/G]TGGCTGAGCTCAA
TP63097	5H	41.16	barke_contig_53074	TGCAGTGGGGCATC[A/C]AGCCTATCTTTTCATCTTCT TGTCAACTATAGCTAACACATCTTTGTAGC
TP65374	5H	41.16	-	TGCAGTTGGTGGAGCACGGAATGATTGCGCATAAG TCGTGGAGGTT[G/T]CCGAGATCGGAAGAGCA
TP65412	5H	41.16	bowman_contig_152375	TGCAGTTGTAGCTAACTGACTAGGATTACCAGATCG [C/G]AGATCTTCTCATGTGCACGTCGGCGAC
TP65588	5H	41.16	bowman_contig_179016	TGCAGTTT[A/G]CTTTTGCAATAATTTTCCAGAGGCT GGAAAGACACTAGGCCGAGATCGGAAGAGC
TP65734	5H	41.16	-	TGCAGTTTCGCTGTTGTTTGTGTTTTCGTATCCCGT CGCT[C/G]GTCTCTCGCCTTCTTCTCCTAC
TP66054	5H	41.16	morex_contig_1576126	TGCAGTTTTG[A/T]ATTCTTGAGAAACAAAAATCA ATTGAAATTGTAGAAAATTACATGTACGGGA
TP66165	5H	41.16	-	TGCAGTTTTTTTTTACAAC[A/T]GACGCTTTGTTGCAT CTTTTTTTATTATTTTGAACAATCATTT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP33838	5H	42.46	bowman_contig_270988	TGCAGCTCCCAT[A/C]TCCCATGGCCCGCAGTGCA CCTCACCCCGAGATCGGAAGAGCACACGTCT
TP3584	5H	42.46	-	TGCAGACAATTTGAACAATAATACGCG[A/T]ATTCC TTTTTGTGTTATCCCAAATCCTATGATTGT
TP5761	5H	42.46	-	TGCAGAGAAAC[C/T]TGCCGAGCGAGCCAAGGCAA AGCATCCAGAACCATGTCCTGGTCCAAGGCGG
TP7729	5H	42.46	morex_contig_1558640	TGCAGAGGGCGCCGCCTGTCTCCGATGCCCATGAC GCCGCAAGCATTT[C/G]CTCCATCGCGCCAT
TP7958	5H	42.46	morex_contig_49466	TGCAGAGTACCTCTTGTC[C/G]AGCTCTGCAATTTTT ACTTGCTGCTCCTCCAACCTCGAGATCGGA
TP10885	5H	42.46	-	TGCAGATGGTCTTTTATCTCTTTCAAAGTTTATTTAA CTTTGTACTAATT[A/T]ATCCCGAGATCGG
TP12380	5H	42.46	barke_contig_361544	TGCAGCAACGAGACCAGCCCCGATGTCCTCCCTGAT GTC[A/G]CCGAGATCGGAAGAGCACACGTCT
TP13427	5H	42.46	-	TGCAGCACACACACCGTGCATCC[A/G]CTCCATTCC GTGCCGAGATCGGAAGAGCACACGTCTGAAC
TP14225	5H	42.46	-	TGCAGCACCTCCATCACCGCCATCACCTCTCCCAT TT[C/T]CCCTTCTCGCAGTCGCCCGCCGCCA
TP15770	5H	42.46	-	TGCAGCAGATCCTGCTAAGAATGCCCTCTACACGGA GTCGACGGATGGCCACGACACCGACAC[A/G]
TP19018	5H	42.46	-	TGCAGCAT[A/C]TTCACCACAGCCCTCATTGGTGGG CGTTTGCTCGGGGCGGCGTTGACGCACAGCA
TP19746	5H	42.46	-	TGCAGCATGCTGGCCGCCAGAGGCATCACGACCGC AGCCACAACCACCTCGCCGCACGAC[C/T]AAG
TP19989	5H	42.46	morex_contig_47079	TGCAGCATGTTGACG[A/G]TGAAGATCTAGCAGATG TGTGTGCCGTGGGGCCGAGATCGGAAGAGCA
TP21798	5H	42.46	barke_contig_138539	TGCAGCCATGGCCAACGGTGGAGC[C/G]GCGTTACA ACACCCGATGTTAGGACGTCGGTGCTGAGCT
TP24659	5H	42.46	-	TGCAGCCTCCACTATGACGAAGGGGCAGACGAGCA AGCTCGAGGCG[G/T]AGAAGAAGAAGAAGACG
TP24841	5H	42.46	-	TGCAGCCTCGTAGGTAGGGCGCTTTCGCCTTGACCT AGCCCTCTATCCTCATACGTT[C/T]TCCTAA
TP25800	5H	42.46	bowman_contig_903304	TGCAGCGACCA[C/T]CAGGGATTCCAACATGACCG CATTCTGAAAAATACATATGCATAAGCGGTG
TP26624	5H	42.46	barke_contig_381272	TGCAGCGATGCTGGCTCAGATCCGCAAGATGAGGC ATGCACT[C/T]GTGAGTCTTTTTGTAACCTC
TP27134	5H	42.46	morex_contig_274333	TGCAGCGCATCGCCTGGGTGCGGACGACCACGAG CGCTTCCTCTCCAA[A/G]TTCAAGGACCGCGT
TP29274	5H	42.46	barke_contig_501348	TGCAGCGCTGCATAGGAGCTCCCTCAATCCGCCGCA AAGTGCGGTAGATAG[C/G]AGATCCAAACAA
TP30803	5H	42.46	morex_contig_128321	TGCAGCGGGCAGTTGTGCGCACTTCATGAACGGCAAT G[C/G]TGAGCCGAGATCGGAAGAGCACACGT
TP32593	5H	42.46	bowman_contig_925657	TGCAGCTAAGTGCATCTTCACCCGCGTCCCCAACAG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				GCTTCCAA[C/T]GCCCTTTTACCGTTGACG
TP32709	5H	42.46	bowman_contig_1984151	TGCAG[C/G]TACCATTAACGCCCAAAGTGACTTTCT GCGGGTGGCTGCGCTTCACACGCTACGCGTC
TP35245	5H	42.46	-	TGCAGCTCTTGTTGGA AAAAGAAAAGGCATACT[G/T]]TTTGTATGTGGCCGAGATCGGAAGAGCACA
TP36612	5H	42.46	morex_contig_85755	TGCAGCTGGCATGAGTCAAAGGCAGGGACACGACA [G/T]CTCGGGCGAGCGCATGCAAACGTGCGC
TP36706	5H	42.46	bowman_contig_64133	TGCAGCTGGCGCGCGCTCCCGCG[A/G]GACGAGGAT GTCGTGGTCGATTTCGATCCCTGGTGGTTTCG
TP38808	5H	42.46	bowman_contig_142662	TGCAGGAAATAGCATAA[C/T]TGATGAGACAAACGT ATATAACAGATCATCCATTAAAGCGGGTCAT
TP39328	5H	42.46	-	TGCAGGAAGAGCATGGCCAGCGGCGGTTCTGTCC[C/ G]CGCACAACTGCGAGGCCTCCGAGATCGGAA
TP39402	5H	42.46	morex_contig_274423	TGCAGGAAGCATCGTCGCGGTGTGTTTCAGAGAGAC GATGTAC[C/G]TATATCGCCGTGTGCGAGGCT
TP39536	5H	42.46	-	TGCAGGAAGGAGCTCGTC[C/T]GTAACCCGAAGCTG ACGAGGAAGTGGCTGTCTGAAGACAACGCGCT
TP42117	5H	42.46	-	TGCAGGAGGCAGGCGGCGCGGTTGCTGTGGAAGAC GGCGCGGTCTGGGATGGCC[A/T]CGCGGGGCAA
TP48976	5H	42.46	barke_contig_394590	TGCAGGCTGCTCGTCGAGCTCAGCGGCGGGGAAGG GTACTGCATTCTGCAACACGTAGGA[C/T]GAGA
TP49350	5H	42.46	-	TGCAGGGAAAACGGAAAGGCCAAGGGGCGCGTCCA CTTA[C/T]CCAAGTCAGCAGCGGCGGGGCCGA
TP53525	5H	42.46	bowman_contig_877666	TGCAGGT[A/G]CAGGGGTGGGGAGAGAAGACGTGG CTTTGGCGAACCCAAGTGTGAGCGTCACCACG
TP53911	5H	42.46	bowman_contig_867723	TGCAGGTAGGTTCCCTGAATACATTTGTCTGTAGAT GTGGTG[C/T]CCAATTTGGTTAGCTATCTCA
TP55299	5H	42.46	-	TGCAGGTCTCTGCCTTCGCA[G/T]ATGTGGAAGATGT AGCGGAGTCGGAGGGCTCCGAGCCGCCCGA
TP57834	5H	42.46	-	TGCAGGTTTTGTACTGCTACAACATTATCTTA[T/C]T GCAATATACTACTTGCTCCTATGCGTTTTT
TP57869	5H	42.46	barke_contig_63596	TGCAGTAAAATGCACTAGCCGTCATTGAACTTGTCC CGATAGCTTATTTTGATCATCGTATTT[A/T]
TP58107	5H	42.46	morex_contig_67290	TGCAGTAATT[A/G]GGTGACGCGCCGCCACCATCCG CCGCCGTCTCCACGCCTCTCTTCCCCGCCG
TP59631	5H	42.46	-	TGCAGTCACCTCGCTAATCCTGGGTGGATGCGACA C[C/G]CTCCCAGCTGGGTCCAGTTTGTCTT
TP65152	5H	42.46	barke_contig_1783299	TGCAGTTGCTCTGGTTGACTGACACCGCTTTTAGTC ACCAGCTTGCTTCCACTACATAGCCTC[C/T]
TP65189	5H	42.46	barke_contig_1823530	TGCAGTTGCTTAATTAGAGCATCTCCAACAGCCACG CTAAACTAGCGCCGCG[A/C]CGCAAATCCGA
TP33684	5H	42.46	morex_contig_131234	TGCAGCTCCACCA[C/T]CCCTTCATCCTCTATCTCAA CCGAGATCGGAAGAGCACACGTCTGAACTC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP220	5H	43.76	morex_contig_208770	TGCAGAAAATATTTGCCATTTATTTGGTCTCTTTTGT TTTTGCAATATGG[C/T]TGTTTTTGCGAAA
TP3891	5H	43.76	-	TGCAGACATGACGGATGTTTG[A/G]GACTGAAAGGC TTGTTGTTGTTGTTGTTGTTGTTGTCAGACAT
TP6238	5H	43.76	-	TGCAGAGATCGATTTCGT[A/T]TTCGAGGCGTTCGTAC GTACGAACGTGCGTACGAGTAATACATGCG
TP6819	5H	43.76	bowman_contig_16293	TGCAGAGCGACGTGTACGCGTTCGGCGTCGTCCTCC TGGAGCTGCT[C/G]ACCGAGATCGGAAGAGC
TP7886	5H	43.76	barke_contig_1785439	TGCAGAGGTGTCGTCCCTCAAGGAGTCGCTCAAGG CTACAAC[A/G]TTGGAGGAGAAATCGTCCGAG
TP8496	5H	43.76	bowman_contig_1983012	TGCAGATAATGGGCTCAG[C/T]AATCTGCACAGGAA TCATGCAGAATAGTTAGTTAACTCAACCCTT
TP9960	5H	43.76	-	TGCAGATCTCGCGTGCTGCGGCACGG[A/G]AATGGG TTCAGGGGGTCTTGGCGACTCTCCTGGTGGT
TP17695	5H	43.76	-	TGCAGCAGGATCTCGTTCCACGTGTCGAT[A/G]GGG CCAGGGAGGCACCAGTGCACGCAGTCGTTTCG
TP19426	5H	43.76	bowman_contig_11204	TGCAGCATCTCCTCATTTGCTTCAAAATTTTGAAGA GTTTGCAGACTAGTGGAATGC[C/T]ATTTGC
TP20271	5H	43.76	barke_contig_2785616	TGCAGCCAACAACACAGGCAATAGAGGCGGTGACT TGTA[A/G]CCCACCGAGATCGGAAGAGCACAC
TP20478	5H	43.76	-	TGCAGCCAATCGCCGTATTCTTGCGGTATTTTTCAG[C/T]GAGGCGTATTTTCCGTAGTTGTCTCT
TP20745	5H	43.76	-	TGCAGCCACCCGAAGGCCGTGCCGCGGTGGTCGTC GTCGGTGAGTCGGCCACCAGTGACTG[G/T]A
TP21813	5H	43.76	bowman_contig_861561	TGCAGC[C/T]ATGGCGGTTGCACAGAGTGCACCCTC TGCTGCTTAGGCCACGCCGAGATCGGAAGAG
TP22087	5H	43.76	-	TGCAGCCCAGG[A/G]CGTTCAGAACGCCTGACTGTC GCGAAGTGATGACTACTCTCTGGTTTAGTGC
TP29695	5H	43.76	morex_contig_1568669	TGCAGCGGAGGTCCAATGACCCGAGGAGGAAGAA[A/G]GCGGCAAGCGGGCGCTACGGTGCCCTCCA
TP31560	5H	43.76	bowman_contig_16293	TGCAGCGTCAGCTTCCCCGTCTGCACGCGAGATGGA GTCTCGTTAGTGCAACCAGTACCAG[G/T]A
TP36985	5H	43.76	bowman_contig_146457	TGCAGCTGTTACAACTTTATATGTCTTGGGCTGG TTCAGTGGAACTC[C/G]TGGAAATCTGATA
TP40891	5H	43.76	morex_contig_39358	TGCAGGACGGTGGCGGA[A/G]TGTGCGGCGAAGAA GAAGCTGGTGGAGCCGAGATCGGAAGAGCACA
TP43784	5H	43.76	bowman_contig_69889	TGCAGGCAAGGCATGCACGCGCCCATCCATGGCGG GACGTACG[A/T]ACGTGTTCCGTTAGCTCACG
TP44287	5H	43.76	barke_contig_586761	TGCAGGCAGG[A/G]AGCTAATCGAGCAAGTAATGA ATCATCACACAGGGGAGAAAAAGACGGATAGA
TP49266	5H	43.76	barke_contig_1810049	TGCAGGCTTGCGA[C/T]CATCCCATGAAGCACCAGT GATGCTCCGAGATCGGAAGAGCACACGTCTG
TP53415	5H	43.76	-	TGCAGGT[A/G]ACGAGGCTTGCGGATATGCGCGCGG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				ACGCTCACCCCGAGATCGGAAGAGCACACGT
TP58241	5H	43.76	bowman_contig_1990868	TGCAGTACAGGAAGGAGTATATGGCGG[C/T]GCAGACCCTGAACGGAATCGCGATGGCCGTGTACAG
TP62023	5H	43.76	-	TGCAGTGCAGTGCACAGCACACCAAGCAAAATGAA GTGAGGATTCT[C/T]ATTGTGCTGGAGCAAAT
TP64213	5H	43.76	morex_contig_56912	TGCAGTTCCACCACAAGTCGGGCGACCT[G/T]TACG TCGCCGACGCCTACCTGGGGCTGATGAGGGT
TP7694	5H	45.05	morex_contig_190738	TGCAGAGGGAGATGGGCTGGCCCAGTTGATTTTCGC CCCTGTGCGTTTGCCCAA[C/T]TATTTGACGC
TP14496	5H	45.05	-	TGCAGCACGAGCGG[C/T]CATGTACATGCATGCGAC AGTGCTAGGACTAGGAGCAAGTCGGAATTGA
TP38269	5H	45.05	morex_contig_47842	TGCAGCTTGTCTGGGTTCTTCCCGCTCATCACAAGC TCTCTATCTGCCTACACCAAGAT[A/T]ATAA
TP27649	5H	48.97	bowman_contig_1986783	TGCAGCGCCGACCGCACCTGATCTGT[C/T]AGATGA GCGGCCGAGATCGGAAGAGCACACGTCTGAA
TP57339	5H	48.97	morex_contig_140159	TGCAGGTTGAGTTGCTAGTGAAGCCTGGGCAGGAT CAGCTGGCTGGGCACTTGGTG[C/T]TGGTGCA
TP22561	5H	50.04	barke_contig_277976	TGCAGCCCGAAAGAAGTTCAGTCAGCATACAATGC GAGTTAGAAGAAGGCTTGAA[G/T]CCTTTTCT
TP25346	5H	54.11	bowman_contig_9828	TGCAGCCTTCATTCCAATATCGAACACGTCCCCCAA TGTCTCCTGCAACG[C/G]ACCACTCTGAGCA
TP14521	5H	54.11	morex_contig_47526	TGCAGCACGATCCCCTCCCACCATCCGCCGTGCATC CGCGC[A/G]TCGACGACGACACCGACGGCCA
TP53164	5H	55.47	barke_contig_364076	TGCAGGGTTAAATCTTTCGGAAAGTC[A/G]TGCCCG CGGTTATGTGGAGAACTTGGAACTTTGTAT
TP63944	5H	55.47	-	TGCAGTTATACACGACCAAGGGAGGGGGTTTGATT[A/G]TGTTTTTGTTCAGATCGAGTGGTGTG
TP64610	5H	55.47	morex_contig_39146	TGCAGTTCGTGAAGG[A/G]AAAATCTGAGCCCTGGC ACGACTTTCACACTGTCTCTGGGCCGCGAGA
TP65403	5H	55.47	bowman_contig_66286	TGCAGTTGTACTCCCTCCCGCGCAACGGCAG[T/C] GCAGGCGCGCGCCCGAGATCGGAAGAGCACA
TP61970	5H	59.47	-	TGCAGTGCAGATTGGTCGCAAAATTTTCAGAAAATCTC ATGCACATGCACATGC[A/T]ACCCATGCACG
TP63388	5H	59.47	-	TGCAGTGTCCGCGATT[A/T]AAACCTTGATGAAAAC TGTACCCGAGATCGGAAGAGCACACGTCTGA
TP22150	5H	61.98	bowman_contig_14155	TGCAG[C/T]CCATGCCCCAACCGATACAGAAGACAC GCGAGGGAATACGTACGGATTGATCGCTCGA
TP62302	5H	61.98	bowman_contig_1982336	TGCAGTGCGATAT[A/T]CTTTGCCAAATCCAATCCTC TAAACTTGTACAAAATTCATGAAATCCCAA
TP137	5H	63.27	morex_contig_137527	TGCAGAAAACCTCCAGCAGCGGTAGGAACGGTACGC [A/G]GCACTGCAAGCTGAATTCGTTTTTGAT
TP697	5H	63.27	morex_contig_1574269	TGCAGAAAT[A/T]CGACGCGGTGGTGGCGGACATGA CCATCACGGCTAAGCGATCAAACCACGTGGA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP3803	5H	63.27	bowman_contig_69638	TGCAGACAGTATAAATAATCTCTCCGATAGCGTCAC GCAGCACCATAACATCCCCCAG[C/G]AGCTCC
TP11237	5H	63.27	-	TGCAGATTTCATAGCGAAATCGAGGGGAAGATTGAG C[A/G]GACTGCCATCCACCGAGATCGGAAGAG
TP18294	5H	63.27	bowman_contig_370012	TGCAGCAGGTCCCCCTCCGTCACCGTGGAGGGGAG GAAGTCGCCCTGGATCCAT[C/T]CGCCGAGAT
TP26529	5H	63.27	-	TGCAG[C/T]GATCACACATGATGACCGATAGAGGCT CGCCGATGAGCAGTTGTGCGAGGGTTGAGTC
TP29062	5H	63.27	barke_contig_1788313	TGCAGCGCGTGGTCCAACGACGGGGCCTTCTGCTAC GGCTG[C/T]CAGTCGTGCAAGGCCGAGATCG
TP36946	5H	63.27	barke_contig_373500	TGCAGCTGGTGCTATCTAGGCAAAACTACGATTCTT AACCTTGTT[A/T]TTCTGCTGAAATTAACAT
TP47311	5H	63.27	-	TGCAGGCGCTAGTTTCCCTAGCGGG[C/T]GCCACG CACCATCGCCCCGTGGGCCGAGATCGGAAGA
TP55128	5H	63.27	morex_contig_132683	TGCAGGTCGGTGTCAGTCAG[C/G]CAAGGAGATCTC CAGGGACGAAGAACGGAAGAAGCCATCGCTG
TP59005	5H	63.27	-	TGCAGTAGTACCTGTACATGTACACGTCTTTGTCCG G[A/G]CTGAGCTCCCTCCGAGATCGGAAGAG
TP60017	5H	63.27	morex_contig_1574269	TGCAGTCCAGCTACAC[C/G]GCCAGCCTCACCTCCTT GCTCACGGTGCCGCGGATCGGGCCGAGATC
TP13622	5H	64.57	barke_contig_59565	TGCAGCACAGTTTTTTGAACAT[A/G]GCCACTATGA AACTAGTCTTGGTGTCACGAAAACCTCTACAG
TP17578	5H	64.57	bowman_contig_65258	TGCAGCAGGACGAGCAGGAGGCAGAGGAGGATCG GGAAGACGGTGATGTGGGAGGGC[A/G]ACGGGG
TP19385	5H	64.57	bowman_contig_846564	TGCAGCATCGTG[A/G]ACGTTAGTTAGCCCCGAAGA TAAGCCACACGCAGCAATGTCGCAGTCCGAA
TP33192	5H	64.57	bowman_contig_856820	TGCAGCTATATGTGTGCTGTTGGGGCTCTTGAA[A/G] CTTCTGTCTTGTCATTTTCACCTACGTGGT
TP39805	5H	64.57	morex_contig_42789	TGCAGGAATCATCACAAAAATTAACGAACCGAGAC GCTGAATA[C/G]CTGGCCTGAACTGGACTGCG
TP49859	5H	64.57	morex_contig_1559383	TGCAGGGAGCTAATTTTCATGAGAGACACATTGATGT [G/T]GTTGGTTCTAGAAATTACTATTCTTCA
TP61923	5H	64.57	-	TGCAGTGCACGTCGTGCCACGGCTC[C/T]CTCGGTCC GCCGTACCGCAGCGAGGCGTGCCTGAAGTT
TP63873	5H	64.57	bowman_contig_86300	TGCAGTTAGAACTTAGAACCCTATGACTCCTGCTA T[C/G]TAATGATTGATTAGAACTTGCAGAAG
TP21428	5H	69.69	-	TGCAGCCAGG[C/T]AAGCTGCGCCATGCATGCACGT AGAGCGACGGGCAGCGGCTGGCCCAGGCCGA
cytochrome P450b	5H	72.5		GTGCTGGCCAACCTGCTGTATCACT[T/A]TGACTGGG CGATTCCGTGGGGAA
TP1327	5H	75.18	morex_contig_46046	TGCAGAACCTCTTCTTGTCTATCTCCTTCCTTGTTGC TCTATACTCCATAAGCTAGGCG[C/T]JTTA
TP63617	5H	75.18	morex_contig_159734	TGCAGTGTTGCATAGGAGCTCCCGCTAGCGCTGGTT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				AGGAGTTCT[C/T]GATGTTAGTGAGGGAAAA
TP2564	5H	77.63	barke_contig_1854775	TGCAGAAAGGCGGCGCGCCGACGCCATTG[A/G]TTTC TGCCGAGATCGGAAGAGCACACGTCTGAACT
TP10726	5H	77.63	bowman_contig_105040	TGCAGATGGCATCCAGCATGTTACCTGCGCAAAACC ACTAGGGTTTGATTAC[A/G]GACATTGCTCT
TP21381	5H	77.63	-	TGCAGCCAGCTCATCATCTATCTCCATGACATCCAC CCACT[C/G]GGAGGATGCGAGCCCCGAAAAAA
TP43107	5H	77.63	morex_contig_158756	TGCAGGATG[A/G]AGTCAGGCATGGATAAACATAGC CGCAACCAGCTCTTCCCTTCGTCCGAGATCG
TP52198	5H	77.63	bowman_contig_844272	TGCAGGGGGCT[C/T]GCCATCATCAAGGACTTGGCA ACCACCGCGGACCAGCGGCGGGAGCTCTGCG
TP61877	5H	77.63	bowman_contig_125479	TGCAGTGCACAAATGGAGATCGATCCGCAGAAAAC AACGGAGCGG[C/T]GATGGCGTGATTGGCGAA
TP21896	5H	84.09	morex_contig_53162	TGCAGCCATTGGTCGTGCATTGCTTCCCCAGCCTGC CTCCTGAACCCCA[C/T]GGCTCGATCGCTAG
TP13479	5H	88.09	bowman_contig_71185	TGCAGCACACGAGACGCCACGGACGGAACGGATCA CCGAGCGAGGATGGAGCGGTGCATG[C/G]AGA
TP15815	5H	88.09	bowman_contig_10226	TGCAGCAGATGATGC[C/T]GCTTCAGGTGTCCCTGTC ATGGAAGAGCAGGTGTGTTACTCCCCCTCCC
TP18359	5H	88.09	morex_contig_6830	TGCAGCAGGTGCACTGTGCGCG[C/T]ACGTACGTAC GTACGTGGCCAGCTGCATGCGGCGTACTTGG
TP21841	5H	88.09	morex_contig_36884	TGCAGCCATGTTTTCCGTTTCGTCCGA[C/T]CCATTGC AGAACAGCATGTCAGCATTCCCCGAGATCG
TP32805	5H	88.09	morex_contig_41925	TGCAGCTACGTGACGGAGGGCGGCGACGTCGAGGT CGACAACGTGACGAG[C/T]CCCTCATCCTCG
TP34406	5H	88.09	morex_contig_160351	TGCAGCTCGAGCCTCCTCTCCCCTACACTCGCCGT[C /G]AGCTTGCCGCGAGGGAGGCCATGAAGTT
TP37425	5H	88.09	bowman_contig_861425	TGCAGCTTCACTTTCCAAAAGCACATATTCACGCGC TCCT[C/T]CCCCTATCTCATCTGCAATCGAG
TP41320	5H	88.09	barke_contig_272400	TGCAGGAGAGGAGATTTGTAGCGACCCAAGCGTGT GACCTGCCACAAGCG[A/G]CGACAGCGCCATG
TP44835	5H	88.09	morex_contig_41925	TGCAGGC[C/T]ACCTCCGAGGACATGGCGGCGGACG GCCTCGTTGCCCCGAGATCGGAAGAGCACACG
TP54120	5H	88.09	-	TGCAGGTCAAGCAGCTAGCTACCCACATCGGCAGG ACAAGTGGTCTGAACTGTCGAG[A/T]TGCGCG
TP60422	5H	88.09	barke_contig_396930	TGCAGTCCTTTCTTTAACTAG[C/T]ACTACTGTCCTA AAGGAATGGACTACGGAGTTCTGCATTCTT
TP61807	5H	88.09	-	TGCAGTGATTCCGCTGTAAACATGTCCTAAGTGGTT[A/T]ATATTCATGGTGCAAAATGAACACATT
TP62069	5H	88.09	-	TGCAGTGCATGCAGGATAGGG[A/G]TCGGAGATCCG CACGAGCCGAGATCGGAAGAGCACACGTCTG
stress1	5H	90.9		GCTCTGGTCACGGCGTCGGCGC[-/A]GCTGTCGCCGA CGTTCTACGACACG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP31423	5H	92.08	bowman_contig_1983607	TGCAGCGTACTGGACGACTTTTTTTGTTTTTTGAGG GAAGCGTACTGGA[C/G]TACTGGTGCTGCCG
TP27265	5H	94.60	-	TGCAGCGCCACACGCAGGTTGCAGGCAGGAGGTCG TGG[A/T]ACGTCCTGACATGTGTTTTTTATCT
TP60961	5H	94.60	bowman_contig_11370	TGCAGTCGTAGCTCGGCGGCGCGTGGAAGCACGGC TCCATGGACGTGCGCTG[C/G]ACGCAGGGCGG
TP767	5H	98.51	morex_contig_162013	TGCAGAAATGAACCCTCATGTCAGCCGTACGCGAT ACTACCAA[A/T]TGCCAATACAGAGCATTTTT
TP57496	5H	98.51	morex_contig_162013	TGCAGGTTGGCAA[C/T]CCGTACCTCGATGACTACA TGAACACAAAGGGGACGTTTCGAGTTCCTCTG
TP57637	5H	101.11	bowman_contig_67781	TGCAGGTTGTGGAAGCCGCTGAGAGCTTCTTGCAAG TGCACGACGGCGC[C/T]GCTGTAGTTGACGA
TP64512	5H	101.11	bowman_contig_67781	TGCAGTTCGGACGGCGCCTAGCATCACGGAGGCGG C[C/T]GTGGGGAGGATCGCGCAGGGGACCAAG
TP8909	5H	101.11	morex_contig_43849	TGCAGATCAA[A/G]CCATACAATGGAGAGGTAGAAC GCACCACTTCTCGTGAAGAGGACGAAGGAGA
TP3241	5H	102.41	barke_contig_559486	TGCAGAATGGTGGTATGGG[C/T]CGAGACTGCTTAA ATAGAGGGGAGATGAGGTGGTCGCGTGCATG
TP5372	5H	102.41	morex_contig_46457	TGCAGACGTGCGTGAGCGTACTCGT[C/T]AGTTTTTC TTCCTTTTTTCGGAAGATTGTATATCTTGC
TP38379	5H	102.41	bowman_contig_67912	TGCAGCTTTCTTTCCTGGGGAATGCTGCCGCCACTG TGGTAAAAGCAGTAAATTTCTTCA[C/T]TT
TP57386	5H	102.41	bowman_contig_861930	TGCAGGTTGCATGGGTGCGCGAACGA[C/T]GGCGTG GACGACTAGCGAGGGCGGCAAACGACGACGA
TP59288	5H	102.41	bowman_contig_861930	TGCAGTATGCAGCTCTTAGCGAGCTCGACTGCCTTG CTACAATCACCATGCATATATGCTA[C/T]AA
TP61985	5H	102.41	morex_contig_111665	TGCAGTGCAGCCGTAGTAGAAA[A/G]CCTATTTCATG ACGCATATGTCCAATGAACCTTTAGTCATAT
TP65251	5H	103.05	morex_contig_223455	TGCAGTTGGCAAGCTGTCC[A/T]CAAATCAACTGGC CAAGCCTGCGTGAGCATGTGAATACAAAAC
TP53055	5H	103.71	morex_contig_37227	TGCAGGGTGGGCCGAGGACCCGAAGTGAGATGCAC TGGAGCCCCAAGCTGTAGGTGTGAACCA[A/G]
TP57856	5H	103.71	-	TGCAGT[A/T]AAAATGTGCTGCGAAACTGAAGCAGC ACTTATCCGCGACTACGCGACGCCCGCGGAG
TP6068	5H	105.01	morex_contig_66092	TGCAGAGAGATTTGGTAGCTCTCTCACTGTGGCTTC GAC[C/T]GAAAGTCCCAAACCATGGCGATGC
TP11663	5H	105.01	bowman_contig_260417	TGCAGATTTGGTCACTTGAGAACGAAACGGAGCAA AGGTGGAGCCAGAAGTTCATAATTAG[C/T]A
TP15528	5H	105.01	bowman_contig_845997	TGCAGCAGA[C/T]GGAGGCTCGAGGCAGAGGTTCGA GACCACTGAATTCATCATCCAATCCGAGATC
TP18999	5H	105.01	-	TGCAGCATATGAAGATCAGGATTATTATGGTCCTCG TAA[A/G]TTCTGGATCAGAGATATAGATGGG
TP28695	5H	105.01	bowman_contig_320547	TGCAGCGCGGAGACGAAGGCGGAGGAGGGCGGCG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				ACGG[C/T]GAGCCGAGGTAGGGCGAGGCGGGGC
TP31389	5H	105.01	morex_contig_52892	TGCAGCGTACAACAAGCTAGCTAGCAAAGAT[A/G]GCCATGGCTAGGAGCTCCAGCCTAGTGCTCGT
TP32607	5H	105.01	barke_contig_274849	TGCAGCTAATGCATAAACTACGGTGA[A/G]AATAAACCTATACAATCTCTTGTGAAAATAAGTCTA
TP48663	5H	105.01	morex_contig_55755	TGCAGGCT[C/T]GCGGCGCCCCGCCGCCCCACGCCGAGCTCCTGAACGACGACCAGGCCAGGGTCGA
TP54493	5H	105.01	bowman_contig_71764	TGCAGGTCCCGAGGCCACCTAGCCATTGCAGGACACGCGGTGGCAAG[C/T]GGAGGGCGCGGCCACG
TP3247	5H	107.61	barke_contig_68684	TGCAGAATGTAA[A/G]CCATTGGATGAAAGAAGAATCCATGCTGCCCTTTCTGAATAAAGTGTAACA
TP33037	5H	107.61	morex_contig_357672	TGCAGCT[A/T]GCGCTCAAGTACAACGAGAAGAGGATGATCTGCCGCAAGTACGTGCATGATCAACC
TP8192	5H	110.21	bowman_contig_62579	TGCAGAGTGGTCACAGTTCAGTGTTCAATAATGACCACAGAATGTGAATACACAATA[A/G]TTTGAA
TP40039	5H	110.21	-	TGCAGGACA[A/G]CGGCAGCGCGAGGACTCGAAGCTGTCGGCGCAATCATTTAAGACGAAGACTTTG
TP26496	5H	110.21	barke_contig_371622	TGCAGCGATAAACATCACTCATTCACTCCCCTTCGCCTTGAGACACGCA[C/T]CATGTTTTTAGCCT
TP27060	5H	110.21	bowman_contig_69363	TGCAGCGCAGTGGAGTGCAACGCAAGTTCGCTCTCCTTGCTCGACCCGTTGACACTGACAG[A/C]A
TP53979	5H	110.21	bowman_contig_853190	TGCAGGTATAGTAGGAACTGGAAATCTCCGTTGTTC TTCAGAAACATCATATAATGGAGAA[A/G]AC
TP25339	5H	110.21	morex_contig_37259	TGCAGCCTTCAACTTGCCAACTGTCTCAGATTCTATGAGTGTATGAACTAGAGATCTCCC[A/C]TCA
TP56728	5H	113.47	barke_contig_378550	TGCAGGTGTCGGTTAATATCTAGTATTTTCGTTAGCTGACGGCTGTAGCGTCCTTAAATG[A/G]CCGA
TP174	5H	113.47	barke_contig_371809	TGCAGAAAAGCTCCCCTTATCTAACAGGAAAACATC[A/G]TCATGTTAGAATAAGGTGAAATCAAA
TP7055	5H	113.47	barke_contig_2806663	TGCAGAGCTAAGCTGGAGAGAACGCATCCACACAAACAAT[A/G]TGCAAAACTTGTTTTTTAATCCA
TP22271	5H	116.71	-	TGCAGCCCCCAACCTCTCTCTTTCTGTGTTCTTTT TTTTACCCACTTCTTGC[C/T]CTTGCACCC
TP410	5H	116.71	barke_contig_56335	TGCAGAAACGTTGAATACCGTGAAGACCATGAAAGT[C/T]GACCGAATCCAGACGGATCCACTAGAA
TP63324	5H	116.71	morex_contig_138656	TGCAGTGTAGAGTTGTTGGCTCGCAATCTCGCATGATTATATAATCTGAGCTGATTTTA[C/T]CA
TP4105	5H	119.31	morex_contig_44590	TGCAGACCATCCG[A/C]CACATGCTCCAGATTCACGTCCTCGTCGACTACTACGGCGGCAAGAAGCT
TP59765	5H	119.31	morex_contig_49500	TGCAGTC[A/G]GCTGGAGCTGCTCTCCTTGAGCCAGTGTGGCTCTAGCTCCGACTCCGTGCTACGCA
TP66147	5H	120.64	bowman_contig_1149810	TGCAGTTTTTGTGTCAAAATTTCAAAAACA[A/G]CAACTTCAATCTTGTTTTGGCCACAACCTTTT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP23797	5H	120.64	morex_contig_1562535	TGCAGCCGCGACAGAG[C/G]ACCAACGACTCCCCAT CGGCGCTCCATTGCAGTGCATGTGACGCTGC
TP61552	5H	123.21	barke_contig_373428	TGCAGTGACGGATCGAGCAAAGAACTGTGGCTCTA GTCCTT[A/G]AACCGCACAGCAGTACAAGAAC
TP21685	5H	123.21	bowman_contig_201213	TGCAGCCATCCA[C/T]GACGCTTGCCTAGAGAGGGT CAGTCCGTCGTCATGACTGTCTCCACCGCCG
TP44796	5H	123.21	bowman_contig_858672	TGCAGGCCACAGCGAGCGAGCGTACTGAAAATTGT[C/G]AGCCTTCCATACCGAGATCGGAAGAGCA
TP30502	5H	123.21	barke_contig_1854775	TGCAGCGGCTATGCCAT[C/T]TCGAGGTGTTTGAATG CCCAGATCGGAAGAGCACACGTCTGAACT
TP481	5H	124.51	barke_contig_55586	TGCAGAAAGAAGCA[A/C]ACAAAAGCATCTGATTGC GGCAGGCACACAAAGAATTACGGAGAAGCAA
TP1203	5H	124.51	morex_contig_158491	TGCAGAACCGCTACAGTATGGTACAGAGGTAATA ATAAGCAAACCGAGGAGAA[C/G]CACCGAGAT
TP26666	5H	124.51	-	TGCAGCGATGTTTCTTTGGGGATGCTTTCGAGATGT TATGGGCGGATG[C/T]TGGACCCACGATAAT
TP31853	5H	124.51	morex_contig_1573938	TGCAGCGTCTCGG[A/C]CGACTTGTGCTGCTGCGC GCGCCGAGATCGGAAGAGCACACGTCTGAAC
TP54576	5H	124.51	morex_contig_5956	TGCAGGTCCTCACGGGGCTGCTCGACCTAAACATCG TCGAGCAGGTGCAGGA[A/G]GCGATGAAGAT
TP55427	5H	124.51	barke_contig_275876	TGCAGGTGAAGAAAGACAACGCGTACCCTGAAATT GGGAGCATC[G/T]TCTGGTCAACAGGAAGGAT
TP57995	5H	124.51	barke_contig_54270	TGCAGT[A/G]AGAATTACCCCCACGATTAGGAGTCA GATAGTCCGAGATCGGAAGAGCACACGTCTG
TP1552	5H	125.81	barke_contig_1885936	TGCAGAACGTCGCCCCGTCCATTAGGCCACACGTGT[A/C]ATCCATCCGAGATCGGAAGAGCACACGT
TP7983	5H	125.81	bowman_contig_872797	TGCAGAGTATCATCATGGACGGTGTCTGTGTGT[T/C] GTCGAGGAAGAACTACGTATGGCTGTTCAT
TP9226	5H	125.81	bowman_contig_860067	TGCAGATCCAGAAATTGAAG[A/G]AGTTTGTGGAAA TTACAAAAACCTGCCACCGCTAAGTGAATA
TP9378	5H	125.81	bowman_contig_66315	TGCAGATCCTCAAAATTCCAGCATGCCTTCAAGATG GTTGATGAGATGAGAAA[A/G]AGTGGAATTG
TP21869	5H	125.81	barke_contig_2791097	TGCAGCCATTCTGGCCTCCTGGAGCAAGGGAGAGC CTTCTTTGAGT[C/T]GATGGTGTCTGTCCATG
TP37653	5H	125.81	bowman_contig_855219	TGCAGCTTCGGCAACACCGACCA[A/G]CATTGCATG CCGCCGAGATCGGAAGAGCACACGTCTGAAC
TP46144	5H	125.81	-	TGCAGGCCGTCTTCAACAAGATCCTGAACGTGGCTG TGGCGGGCGCGCTG[C/T]CCAAGGACATGAT
TP57270	5H	125.81	bowman_contig_1981664	TGCAGGTTCTTTTATGC[C/T]TCGAGTGCTTGCATCT ACCCTGAATTTAAGCAGCTGGAAACTGTAG
TP64421	5H	125.81	morex_contig_46296	TGCAGTTCGAGAGACATG[A/C]ACATGCTCATGCCA GTTGCTGCATATTACACCATAACAGCAGCAAC
TP66111	5H	125.81	bowman_contig_864459	TGCAGTTTTTAGGTGAACCCGTGAAGGGGTCAGTGA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				GAAGAGGTTAAGCTCAAATCTTG[A/G]CCTG
TP38439	5H	125.81	-	TGCAGCTTTGTGAAAGGTCCACACACAAGCGCATC GTCACGCTTCATCGTAAAT[A/C]TCTCTTAC
TP41829	5H	125.81	barke_contig_347920	TGCAGGAGCTATTGCAGGCATTTCTGCGTTAGCTA TGACGACAAGTTC[C/T]GTAAATGCCACAGC
TP51646	5H	125.81	bowman_contig_127664	TGCAGGGGAAAAGTTTTCGTACACCTGC[C/G]TAA AATGTTACGACGAACCAAAAATATGAAAAGC
TP55608	5H	125.81	morex_contig_7556	TGCAGGTGATCACT[C/G]CTACTACCACGGCTACTCC ATTTCTTTCTCCTCCGAGATCGGAAGAGCA
TP30920	5H	125.81	morex_contig_47850	TGCAGCGGGG[A/C]GAACTACTACTACTCGCCCTCG ACGTCGCCGAGATCGGAAGAGCACACGTCTG
TP10449	5H	125.81	barke_contig_54858	TGCAGATGCCTGCCCGTCTGGCAAAAGTTGGTGCCT TTTATATCCAACAGCGACAGAAT[C/G]GTTA
TP30857	5H	125.81	morex_contig_54269	TGCAGCGGGCGCGTGGCCGACGGGTCGCTCGGGGCT CGGGGTGTTTCTGCCGCCGCC[G/T]CCGCGCA
TP38765	5H	125.81	barke_contig_370074	TGCAGGAAAGGCGACATATGCATGTAGGAG[C/T]AC GTACGTAGCAAATTAGGCGGCAGATCTGAAC
TP49142	5H	125.81	morex_contig_56378	TGCAGG[C/T]TGTCTCAGTCGAAGAGCAGGCGCCGT CGCAGGGACTTGGGTATCCTTTTTGTCAAGT
TP48739	5H	125.81	morex_contig_110432	TGCAGGCTCTGGCGCGACGCCGTCGACGAGC[G/T]C ACGACGGAGATGCACAGCCGCGCCAAGGCC
TP32701	5H	125.81	barke_contig_389322	TGCAGCTACCAGCCAGGAACCAAGGCAGATTCCAG ACCAAAC[A/T]CACGTGCAACTCACAGCCAAC
TP19288	5H	126.67	bowman_contig_63697	TGCAGCATCGAGTCGGGTGAAGCATGCATTGCTGG ACTACGCCTTACCACAAGGAGCTCCGTC[A/G]
TP59559	5H	126.67	barke_contig_271560	TGCAGTCACAAAAGCATTTCGCCATAAAC[A/G]AATT ATGTCAGTACTGTACAATATACCATTAAGAT
TP6718	5H	175.03	bowman_contig_9961	TGCAGAGCCGTGTGCTCCTTTAGGCCCTTGTGGACG GAC[C/G]TCTTCTTCTTCTTCAGCCAAAGAA
TP51583	5H	175.03	barke_contig_467928	TGCAGGGCTTCCT[G/T]GTCTTCAACGCCGTCGGCGG TGGAACCGAGATCGGAAGAGCACACGTCTG
TP10873	5H	178.79	morex_contig_51415	TGCAGATGGTCCACACCTCCTGAATTTTTAGGTTGC GAGCGCACA[C/T]GTCAGAGGGTCAATGTTA
TP34159	5H	178.79	morex_contig_160060	TGCAGCTCCTCCTTGTCTCCTACTCTAGCGGCAGC CCGCAGAGCCCAAGGGGACGG[C/T]GTCGGA
TP39117	5H	178.79	morex_contig_52159	TGCAGGAACGGAAACAGAAAGGGGAAAACACTGA ACAAAATTATCTGAAATCTCAACAC[C/T]TGCA
TP3264	5H	180.09	-	TGCAGAATGTCTCAGGTTACATGTCGCCGT[A/G]TC GTCGTCTGCTCAAATGGTTTGATCTGCTGGG
TP6176	5H	180.09	barke_contig_320982	TGCAGAGAGTGGCCGCCCCATGGTAGAGAGATGTT AAGGCCATCTCCA[A/C]CGCACCATCCCATCC
TP7478	5H	180.09	bowman_contig_1982499	TGCAGAGGCAACTACTCGTA[C/T]AGGAAGGGTAAT AAGGCCAGGGATTCCGATGCCGCCAAGGAGG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP19179	5H	180.09	morex_contig_231457	TGCAGCATCCAGTT[A/G]TGGTACTGCGAGAGGCCG TTGAGCCGCCGCAGGCATCCCGTCCGAGATC
TP23369	5H	180.09	bowman_contig_66744	TGCAGCCGCAAACCATTTGG[G/T]ACAACGAGAGAGG CAGCAAGAGAAAGGGGACCTCCAGATCTGCC
TP44456	5H	180.09	barke_contig_1781958	TGCAGGCAGTTCATGTACTCGTCGCCGACCTCCGAC GACCCGAAGCTCCCCGTGTTGGAGCT[C/G]G
TP48597	5H	180.09	bowman_contig_66744	TGCAGGCTCCCGCAGCCGCTGCTCCGTTTCATCC[A/C] CCAGCAGCACCAGTACGTCACTCAGACGGG
TP49325	5H	180.09	barke_contig_2783582	TGCAGGCTTTGCTCGGACAAATAACGACAAAACAG TTAGTGCAG[A/G]CAATCCTCCAAGAACATCA
TP53206	5H	180.09	barke_contig_1794363	TGCAGGGTTCA[A/C]AGCGGAGCCCCTGAGAGCGTG TTGCGGCGGGGTGGGCGGTACAACATAAC
TP56902	5H	180.09	-	TGCAGGTAAATTAGCAGGAGAC[A/G]AGCATTTATA GGCTAAACACATGATCACTAGGCTAGGCGGT
TP65419	5H	180.09	barke_contig_58717	TGCAGTTGTATATAAT[A/C]TATATAGGTCCAGATA AGCACCTTGTGGACCATGGATGATTACAGGT
TP22082	5H	180.09	barke_contig_428513	TGCAGC[C/T]CAGCTGCAAGGTCACATGGAGGAGAC GGCAGAGTGGCGTTGTGGTCCAGCAGCCAGG
TP22103	5H	181.39	morex_contig_139963	TGCAGCCCAGTCCACGAGCAGACCAGA[C/T]CTTCG TTCTCGATTCTTCCGCTCGAGAGGAAAAAA
TP22358	5H	181.39	-	TGCAGCCCCGACCTACATGCGGCAGCTTCAGCAGCT TCAGGG[A/C]CTGGTGTAGCTGGATAGCAGA
TP39803	5H	181.39	bowman_contig_218365	TGCAGGAATCAGG[C/T]GATCGACGGCGAGCTCACC TGGCCGAGGTCCACCGCCGAGATCGGAAGAG
TP798	5H	181.39	morex_contig_47725	TGCAGAAATGGCGCAAGAGAGTTGGAAAGAGGCAG AGGATACGGGTGTCCACGCACC[C/T]GAGGCC
TP3343	5H	181.39	morex_contig_2550379	TGCAGAATTGAAAATC[G/T]TATATTCAGACAAACG AATTAGTTTGCAACTTCGATACGCTTACGGT
TP21169	5H	181.39	barke_contig_53394	TGCAGCCAGACTAATCTAACCTCCTACACAT[A/C]T GGACACGTCCGAGATCGGAAGAGCACACGTC
TP37989	5H	181.39	-	TGCAGCTTGCCAGCAGGGTTGGTCGGTTCTGGCTGG GGAGT[C/T]GGCGCGGCGGTCTCGAGGATGG
TP41742	5H	181.39	morex_contig_70254	TGCAGGAGCGCGCAAACATGCTGGTGCCGAGGAAG GCGATGCGC[A/G]GGACGCCGCGCTCCGCTGC
TP47606	5H	181.39	bowman_contig_67440	TGCAGGCGGAGAGCTGCGCGGTGG[A/G]CATCCTCG AATGGCTCGCGTCCCAGATCGGAAGAGCAC
TP55695	5H	181.39	bowman_contig_860717	TGCAGGTGCAAATCTACTTAAGTTACTACTTCAT[G/ T]CCTCAGAAGGAACTGGCAATGATTTTTTT
TP58602	5H	181.39	morex_contig_46503	TGCAGTACTCTTTTTTTGATAGGATAGTATTTAAAA TTTGCTTCTATTGAGGCAAAGC[A/T]AGTAC
TP62039	5H	181.39	morex_contig_41924	TGCAGTGCAGTTCTTGACTCTTGTAACCTCGTAAAAT ACAGTCGAACACTTACC[A/G]CCGTTGCACT
TP57657	5H	181.39	morex_contig_277371	TGCAGGTTGTTGAGTTAGATTTTCTGTATCCAAGTG

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				AAGGAATCCATCAGCGATATGG[A/C]GCCGA
TP13481	5H	183.99	morex_contig_86226	TGCAGCACACGATCGATGAAGCAATAGTGCA[A/G]T ACAGACACGAGTCTAGCTAGCTCACTTGCAT
TP39509	5H	183.99	bowman_contig_65023	TGCAGGAAGCTGTATGATTACGTGAGGTATGATCTA AAAGAGATCGCCTTCCCGTC[C/T]TCTCTGC
TP59332	5H	183.99	barke_contig_274072	TGCAGTATGGTAAAAAAGTTTCAAAT[A/G]TATTTA TTTGGGGCAACCCTAGGAGCAGGCTACAACA
TP2242	5H	183.99	morex_contig_45652	TGCAGAAGCGATGTTATTGACGACA[A/G]CATTGGT GAAGACCGAGATCGGAAGAGCACACGTCTGA
TP3689	5H	183.99	barke_contig_1787638	TGCAG[A/G]CACTCTCGGACATGTCAAGCTAGCAAA CAAAAATATTAGCCATTAACAGCTCTGCCGA
TP5236	5H	183.99	morex_contig_123972	TGCAGACGGGCTGACGTGACCTCACCTC[A/G]CCA CTAAACTATGATAATTCCCATAGTTTCGTTA
TP5448	5H	183.99	barke_contig_277063	TGCAGACTACAAAATGGAAAGGAGAACGG[C/T]TCC CCTTACCACGATGCGCCCATTGTCGAGTAT
TP8990	5H	183.99	barke_contig_53425	TGCAGATCACAGACGCCGTGAGAAGACATTACT[A/ G]GTAGCATAAGCGAAGCACGATGACCGATCT
TP27336	5H	183.99	morex_contig_123972	TGCAGCGCCACGTA[C/G]GCCTTCTCCAGCCTCGAG TTGTTGGTCGCCGAGATCGGAAGAGCACACG
TP31416	5H	183.99	bowman_contig_2014329	TGCAGCGTACGTCGTCGT[C/G]TTCCTCCAGTCCTCC AGTAGCATTGGGCCATTGGCTCTCCTGAAT
TP35059	5H	183.99	barke_contig_272783	TGCAGCTCTCGCAACTGCTTA[C/G]CCGCTCGCGGG ACCGAGACGCCATCAACTCCATCATCTCTCG
TP37982	5H	183.99	barke_contig_544572	TGCAGCTTGCATTTTCCAAGAAAAATATGCAGCTTC GCACGCAACGCAACTCGT[C/T]ATCTCGTGT
TP39184	5H	183.99	morex_contig_54112	TGCAGGAACTCTCCTGCATGGCGTCGAAGAGCTCCG CCTTGAAGACG[A/G]ATGACCGAGCAGCAAG
TP52840	5H	183.99	barke_contig_271043	TGCAGGGTGAAGCTGATACATCAAGATGTTGCAGG CCACGCTTATCC[C/T]AATCAGGCTGTAGCGT
TP60335	5H	183.99	bowman_contig_853471	TGCAGTCCTCCGCCACCACCACCAGCAGCTCGTG [C/G]TCCGCCGCCGCCGAGATCGGAAGAGCA
TP62947	5H	183.99	morex_contig_42326	TGCAGTGGCTAGTTACCTTTGTCTGGCA[A/G]AGCA CAATCGCGAGCTCTAATCCTAGTTGACGCTC
TP64061	5H	183.99	barke_contig_270250	TGCAGTTCACATTTGCCCTGTTTCTTTTAAATAAGCC GTT[G/T]CCATGGCCAGAACATGCACCGTT
TP64348	5H	183.99	morex_contig_8885	TGCAGTTCCTGATCCCAATCCGAGCTGCCCCGATGCC CGTCCCAGTTCG[A/G]TATCCCAATCCGAG
TP11543	5H	185.28	-	TGCAGATTGTGATACATCTATTTGAATGCTTAAGAT CAAGATGAAACGAGTTCTTGAGTTT[C/G]CA
TP1550	5H	185.28	bowman_contig_1985505	TGCAGAACGTCTTGGTGCTGGGCGTCGGCC[C/T]TC GGGTAGAACCACAGGATGTTGTTCTGCACCA
TP3154	5H	185.28	-	TGCAGAAATGATGCAGATTCAATTGTTGCACT[G/T]TAG GGCTCAAGTTTCATGTTTCTTCTTTCTAAA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP12018	5H	185.28	bowman_contig_112649	TGCAGCAAATACAGAGTATGCTTCCTTAT[C/T]GCG AAAATGCCTTTTGGAGCTCGGCCTCCTTATC
TP20996	5H	185.28	barke_contig_269667	TGCAGCCACTAGCAAAAGTTGGACCATGTCAGTGTC CTTATGTCCCTCAAGATCC[A/G]TGTCTCTA
TP32921	5H	185.28	-	TGCAGCTAGAAATATTGGTCACGGGCACGG[G/T]GC GTCGCTGGGGAGCCTCACGGACATACTCAGA
TP46278	5H	185.28	barke_contig_57390	TGCAGGCCTCGACCCAGTTACATAT[A/G]TTGATGTT GATCAGCAAGAGAACACTGGAAGTTTGGGA
TP62437	5H	186.58	barke_contig_268803	TGCAGTGCTAAATGGGAAAGCGGGGCAGCAGGACC CACCCTGGAAATC[A/T]CGGGGGAGAAGGATT
TP11822	5H	187.88	barke_contig_2791648	TGCAGCAAACACACC[A/G]AGTTGCAAACATCATGA TAAGACACCTAGTATCATGACATGGTCAGGA
TP4844	5H	187.88	morex_contig_53026	TGCAGACGCAGGTATAAACTGGAGTT[C/G]ATCCAG GAACATACATCAATAGTGATCTCGCGATCTA
TP40414	5H	187.88	morex_contig_2548295	TGCAGGACCCGAGAAGAAATCAAAATGAAGGCCGC C[A/C]CCGAGATCGGAAGAGCACACGTCTGAA
TP43885	5H	187.88	bowman_contig_859458	TGCAGGCACATCGTGGCCACTTGTCTCCACAGGAAT GTCCTC[A/G]TAGGCATCAAAATTGATACCT
TP44185	5H	187.88	bowman_contig_66544	TGCAGGCAGCAGAACCATGTTGCATGTTTCATGGGTG TGGGAGGCATC[A/G]GGTACATGCTAGGCGT
TP45290	5H	187.88	bowman_contig_229848	TGCAGGCCCCCTGCTTCTGGGGAGATCGAGATCTGC CACT[C/T]GCTGCTGTCCGAGATCGGAAGAG
TP49768	5H	187.88	barke_contig_606190	TGCAGGGAGACGAACCTCAACGCCC[A/T]CGGGCAA TATCCAGATCGAGCCCAAGCCCACCTACCTG
TP50488	5H	187.88	morex_contig_244290	TGCAGGGCATGAGTCCTTGAGGCCAACGGTGTGTC ACACTCTATCACATG[A/G]TCGTGGAACCTGGC
TP65214	5H	187.88	morex_contig_58034	TGCAGTTGGAAGTCCAAATATTAGTTAGAGAGTTAA ATGTAAAA[A/G]GCAAGTTCTTATTTCTGTC
TP30029	5H	187.88	barke_contig_1790225	TGCAGCGGCCATGCCTAGGTGAAGCTCACACGTGTT CATGCACTGTGTTGTGGA[G/T]GCATGGTCG
TP4477	5H	187.88	morex_contig_89703	TGCAGACCTAATCGGTGCGTCTACGGATCGATGGG[C/T]TTTGTGCGGGAGCAAGCCCAGTTAACCA
TP37917	5H	187.88	bowman_contig_1984825	TGCAGCTTGAGCACCTTGAACCCGTCGTGCAC[G/A] GCGATGAAGTGCGGTTCTGGGGCTGTACATGA
TP42000	5H	187.88	barke_contig_2787691	TGCAGGAGGAATGGACGCAGCGG[A/G]TGAGTAGA ACCTGTTCTGTGGGCGTGGGAAGCATCGGGGAC
TP61711	5H	187.88	morex_contig_442138	TGCAGTGATCAATCCGCTGCCGTATTGCGGCTATTG C[C/T]TTTGCATGCGTGAGCTGAGGCAGGTA
TP62143	5H	187.88	morex_contig_1566620	TGCAGTGCCAC[A/G]CCGCGGCGAGCCACAGCGCC GCCAGAGGAGAGCGCCGAGATCGGAAGAGCA
TP41746	5H	190.56	morex_contig_242440	TGCAGGAGCGCGCGGCGGGC[C/T]TCGTTCGGTGGGC AGCTTGCGGGCCGACTCCTCGAGGTCAGCGA
TP6753	5H	191.72	morex_contig_85302	TGCAGAGCCTCTACAACCTCGGAGCGCGCAAGGTG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				TTGTTTCCTTGGCACGGG[A/G]CCGAGATCGGA
TP32903	5H	194.39	barke_contig_512818	TGCAGCTACTGTTGGTCGTAG[C/T]AGCGTCAATCTA CCGCAAGCCCAACCACATACAGGGATAACA
TP39096	5H	194.39	barke_contig_13080	TGCAGGAACGCCATCCTCCCCGAGACCCCTGCGAAA CAC[A/G]GCGCGGATTTTAGATTGGATGATTG
TP54281	5H	194.39	barke_contig_1799706	TGCAGGTCAGGTAGCTTGACTTGAGTTCTGATCTGA ACCGTTAAGGGTCGTTGTCACTCGCCT[C/G]
TP61839	5H	194.39	barke_contig_271923	TGCAGTGCAACACGTGGTGCT[A/G]CCAACGGACCT CGCCGAGATCGGAAGAGCACACGTCTGAACT
TP36470	5H	195.69	morex_contig_1559810	TGCAGCTGGACCAGACGGCGACAAGCGGGCCAAGA AAACGAGCCTGG[A/G]AGGAGGAGGGTTCGGT
TP5610	5H	195.69	barke_contig_402615	TGCAGACTGATCTGAAGTCCCAGCAATGTGCT[C/G]]CCAGCTCTAGTATGCATCCGCGCTGCACGC
TP10176	5H	195.69	bowman_contig_62424	TGCAGATGACGGGCGATGTGTTCATCCGTTTCATGTGT AGCCTC[A/G]TGGCTCCGTAACGGCGCCATC
TP21943	5H	195.69	morex_contig_316065	TGCAGCCCAACACTCATACTA[C/G]GCAGCGTAGCT CCGATTCCGACGGTGAACCTACGATGGAAAAC
TP37968	5H	195.69	bowman_contig_223211	TGCAGCTTGCACGCGTCCATTGGGCGACTCGTACGG GCGG[A/G]CCCCGAAAAAAAAAAAAAAAAAAAA
TP51503	5H	195.69	bowman_contig_127042	TGCAGGGCTGACGGAGATTGCAGC[C/T]AGGGGCGG CATTGCCAGGACTTCGGAGCCGCTTGCAGCA
TP12617	5H	196.99	barke_contig_64286	TGCAGCAACTTGTTTCAGGTATCTCTTCGGCCG[T/C]G ACTCCCGAGATCGGAAGAGCACACGTCTGA
TP18291	5H	196.99	-	TGCAGCAGGTCCAGCAGCTTGGCGTC[G/T]TGCTGC CTCGTCCACGCGTCCACGTGCAGCCTCGAGA
TP27267	5H	196.99	-	TGCAGCGCC[A/G]CACGGCGGGACGAGGCGGCGGC GTGGGCGAGCTGACCGAGATCGGAAGAGCACA
TP34977	5H	196.99	bowman_contig_1276882	TGCAGCTCTAGAAGTTGTGGCATGATCCGAGCGGG ATCCCCTTGCC[A/G]CCCTGGCAGCCGACGGA
TP37969	5H	196.99	bowman_contig_223211	TGCAGCTTGCACGCGTCCATTGGGCGACTCGTACGG GCGG[A/G]CCCGAGATCGGAAGAGCACACGT
TP66033	5H	196.99	barke_contig_66480	TGCAGTTTT[C/T]GATGAAGGGGCGGAGGATGCCTA TATCCAGAATACAAGTGCAGAGTAGTTTGTG
TP60726	5H	198.29	morex_contig_142158	TGCAGTCGCTGGTGCCG[A/C]AGCTGCCGACGTGCT GCCGAGATCGGAAGAGCACACGTCTGAACTC
TP64809	5H	198.29	morex_contig_13130	TGCAGTTGA[A/G]TGAAGAGAGCACACCACATCAGA TCAGAGCAGATAGATACACAAACACATCA
TP10921	5H	200.89	bowman_contig_201794	TGCAG[A/G]TGGTGTCTACATCTGGAGCAACGAAGT TTCCTTCTAACATTCCCCGTTCCACGCATGT
TP11091	5H	200.89	bowman_contig_11993	TGCAGATGTTTCTTCATCAAACCTCAATGCAAGTGCA CTGCTG[C/T]ACAAAAATCCAGTGATGGTCT
TP34588	5H	200.89	morex_contig_2551295	TGCAGCTCGCGGAAGTCCCGCTCCAAGCCCTC[G/C] ACCCTCCTCTCGCCGCGCCGCTGCGGCGCCG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP30169	5H	200.89	morex_contig_1567717	TGCAGCGGCGAGACCAGGCCCGAGTGCTTCAGGTA CAGGGTGCTGGGCCTTCCGCGGGGG[A/C]GGC
TP59893	5H	200.89	morex_contig_137174	TGCAGTCATGGGGTGCTCCCTCGTGGTGTACCTC[G/ T]CGGGGTGGAGGACGTACCGAGATCGGAAG
TP4070	5H	200.89	morex_contig_1563308	TGCAGACCAGCCCGAAATATCTGTTTGC GTAC[G/C] TGGATGCGATGGCTCAGTATCAGATCTGAGA
TP50175	5H	200.89	bowman_contig_128539	TGCAGGGATTTTATGTGCTCGAATTTTTTGC GGGTT CAG[A/G]ATTTTCTGTGATGTGGAGAATCTG
TP55790	5H	200.89	morex_contig_2547596	TGCAGGTGCAGGACGAGC[C/T]CAACTGAACTCTCG GCCGTCTTCCAACGGCTTCAGTCCGACGTAC
TP55260	5H	202.19	barke_contig_395496	TGCAGGTCTCACCATAGGTTGTTGACCTCTACGTCC CACCCAAC[C/G]CTGCCGCTGGAGCCAAAAC
TP13050	5H	202.19	morex_contig_319918	TGCAGCAATAACATGTA ACTCA[A/T]CGGCGGCAGG GCGGCGCCGACGGAGGGCCTCGGGTTCGGCCG
TP30172	5H	202.19	bowman_contig_846417	TGCAGCGGCGAGAGAGAAAGATTCG[A/G]GGCGAG GGGGAGGGGACAAGAACTAAACGAGAGCAAGA
TP45761	5H	202.19	barke_contig_1789262	TGCAGGCCGAGTCCA[A/G]GAAGTCGACGAGGGCGT GGGCCGTAGTCACGGTGCGCATCAGCGTACG
TP48193	5H	202.19	-	TGCAGGCGTTCG[G/T]TTAAATGCATTTTGCTTAAGT AATAGGCCGAGATCGGAAGAGCACACGTCT
TP53507	5H	202.19	morex_contig_91427	TGCAGGTACACGCCGATGGCCGTGAACTTGATGAA GT[G/T]GCCGCCGATCTCCATCCCGCGCACGC
TP62277	5H	202.19	barke_contig_62361	TGCAGTGCGAAGGTCGCTGTTTTGAAGGTGACGAG AG[A/G]GGCTTTTGTTCACGAATAATTCATT
TP19027	5H	203.49	morex_contig_60807	TGCAGCATATTGCATTGACTGAACA ACTTCACCCGT GCATGCAAGCTGTACT[A/G]CCCTATTTGAT
TP27254	5H	203.49	bowman_contig_62237	TGCAGCGCCAAGCTCCGTCCTTCCGTGCAG[A/G]CC TGCAACATCGTCGTCAGGGCTCTGGGCAGGA
TP14830	5H	203.49	-	TGCAGCACGGGGATTGGCT[C/G]GCTGTAGTCTGT CTGTGCGACCATCCATCCCTCCATGGCGCCG
TP34723	5H	203.49	bowman_contig_1988567	TGCAGCTCGGCTCAGCTCCTACCTCTG[C/G]GACGA AACGTAGGTTTAGGTGGTGCCTGCCTACCTG
TP60737	5H	203.49	morex_contig_134518	TGCAGTCGCTTCC[A/G]CCGCACGGGGAGAAAGACG GCGCGTGTTCGCTGCCGATGGGGAAGGTGCG
TP55232	5H	204.79	barke_contig_503370	TGCAGGTCTAACTTATCAAAGAACTCATCCAAGTCA TCATCTTT[C/T]CCTTGGGATCCACGATTTG
TP10789	5H	204.79	barke_contig_272710	TGCAGATGGCTTCTCATGGCGTATTATCGCCTCCA[C/ T]CGCCAGCACCCAGGGTTAATTGCTTGCT
TP19964	5H	204.79	barke_contig_276429	TGCAGCATGTGGATTCGAGCGGCCTGAC[C/T]CACC TGATCCCACAAAATAATCCCATAGGTTCTTT
TP1197	5H	204.79	bowman_contig_14487	TGCAGAACCAGAGCTGGAGCGGCCTCGCCTTCGTC ATCCTCCCTTTCTGGCTAAACACT[A/G]CCGC
TP2211	5H	204.79	barke_contig_148484	TGCAGA[A/G]GCCGACAAGTTTGGCGTTTCGACGCC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				G TTCCTTGGCTCGGTGCGTGCGGCCTTGAAC
TP2234	5H	204.79	barke_contig_272710	TGCAGAAGCGAACGATCGAACAAATGGTCTCTCCT CCGCCGATGAGC[A/G]CTCTCGCCCGTTAAAT
TP30119	5H	204.79	morex_contig_145048	TGCAGCGGCCTGCACATTCCAGCGTGGAGTGCCAC[A/G]ATGCCGAGATCGGAAGAGCACACGTCTG
TP42582	5H	204.79	bowman_contig_1983327	TGCAGGAGTGGGAAAAACTACGGTTGC[C/G]AGAAC CATATATCATCGGTATGGACGGGAGTTCCAG
TP45615	5H	204.79	bowman_contig_240	TGCAGGCCGAAGATTCAGAACAGCAGAATCAAAAC GCACAAGTAA[C/G]TGGGTGTGTGGGGGTGGA
TP57330	5H	204.79	-	TGCAGGTTGAGGAGTTGGCGGCGGCGGAGAGGGCG GCGG[C/T]GGGCGGGGTGAGGATGATGCTGAT
TP57942	5H	204.79	bowman_contig_65586	TGCAGTAACCACTAGTTTGTACC[A/G]TACTTGAA AATTTTGTGTGTTTATTTCTATTTATTCT
TP60516	5H	204.79	barke_contig_479626	TGCAGTCGATCGACCTCCACACCTCTTTCAGACAAA ACATCAAGCGCATG[A/G]GCTGCATTAGTCA
TP62529	5H	206.09	morex_contig_67914	TGCAGTGCTGCTCAT[C/T]GCCTACGTTCCCAAGGCG TACAGACGCTGGTCGAGGGACGCAGGCAGC
TP35230	5H	207.39	barke_contig_358023	TGCAGCTCTTGCCACAGCA[C/T]AGCTAACATTCTGT CCATCACTTGCCTGCGAGACCACCCTCTTA
TP53633	5H	207.39	-	TGCAGGTACGCTTCCAAACTAAAGCACCCGATCT[C/ T]CTCTCCGAGATCGGAAGAGCACACGTCTG
TP17247	5H	209.99	morex_contig_156786	TGCAGCAGCTCGTCGCCCCGCGAGACCAACCCGCTCC AAGGCGC[A/G]GTGGTGTGCGGTGACCACCAT
TP22583	5H	209.99	morex_contig_156786	TGCAGCCCGAATTCCGAACACTTCTTCTACCTCTCA ACAACAGAAACAGAGGCGAA[A/T]GCAGAGC
TP31831	5H	209.99	bowman_contig_11564	TGCAGCGTCTACAAAAGAATGCTTTGAAGTACCGCC AAGAGCAATCGGGTT[A/G]ATCTCTGAGAGA
TP39189	5H	209.99	barke_contig_582834	TGCAGGAACTCTTGACTTGTAATCTCCAAACATTC CACATCTGAGACCAA[A/G]CCCCTCTTGCAT
TP45424	5H	209.99	bowman_contig_864780	TGCAGGCCCTCAGAAATCCCTTTAATTATTTTGTAG CACGTTTCGCCACTCA[C/T]GATCTGCATCTA
TP44555	5H	211.23	barke_contig_518669	TGCAGGCATGGCGTGGAGCAACCACGAAACCCCTG GCA[C/T]GACGGCCCAGAGTTCATAACGCAGC
TP3650	5H	211.23	-	TGCAGACACCTA[A/C]CTCCGCCTCTGTTGTGCCCCG TCAAGCCGCCGTCCGCCTCGCCGAGATCGG
TP8766	5H	211.23	barke_contig_408575	TGCAGATAGGTGTGGCACTGTTGATTAGTGTTTGTG GATTTTTTGAGCGCA[G/T]GTAGAGGAAGT
TP25323	5H	211.23	bowman_contig_200307	TGCAGCCTTACTGCATGCCTTAGCTCAACCTCTTTC ATCTTATTAGGTCTCTGTCCTCCT[A/C]TAG
TP33692	5H	211.85	-	TGCAGCTCCACCCCTTGACATGTACCTCGGGGACC CTCAACGTGAGCTCG[C/T]CACCACCAAGGC
TP5429	5H	212.47	morex_contig_2546879	TGCAGACGTTGTCGTTCCCCTTCACCTACA[C/T]GTC GCCTCCTCGGGGCCTTTCACCTTGACCATG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP4670	5H	212.47	bowman_contig_66345	TGCAGACGACCAATACAAAGGTTGCATAATAATAT TTTTAGA[G/T]GATATGAATCATGAATAATAC
TP11745	5H	212.47	barke_contig_272767	TGCAGC[A/G]AAAACCGTACCCAAAAATCGATTTTT TAAAACAGAATTTTGCATTTCGATAAATTTA
TP30240	5H	212.47	bowman_contig_865289	TGCAGCGGCGCCAAGGACGGTGGCGCTGTAGCGG[C /T]GGCTCCGTGGCCTGCCGAGATCGGAAGAG
TP49334	5H	212.47	bowman_contig_222682	TGCAGGCTTTT[A/T]AATTGTGTGAATTGTAGGACGC CACTTGTGTAGCGGCGACCAGTATGCGTGT
TP59128	5H	212.47	bowman_contig_126736	TGCAGTATACTCGTTTATTATGAATGGATGGAGGGT TGTA[G/T]ATCTAACCTTGCTTGCTGGCCTT
TP60289	5H	212.47	bowman_contig_1982916	TGCAGT[C/G]CGTGCAGTGGAGTGCTTTCGTGGCTTT GCTCTGCTTCGTTAGTCTTCTGGGCTGGAG
TP63592	5H	212.47	barke_contig_272767	TGCAGTGTTCAGTACAACGTAATGGCGCACGACA TGGTGACAATGAGCTCAG[C/T]GGGGTACAAA
TP5406	5H	219.43	morex_contig_43922	TGCAGACGTTTCATGTTGACTCACACTCCTGAGACCT AGCCGAAATCTTTTTTTTTT[A/T]AAAGGAGG
TP35246	5H	220.20	bowman_contig_848115	TGCAGCTCTTTAAACCATAAACCAGTACATAAACCA GTACTCCTGGCAGT[A/C]AAAAATCTCTGCA
TP63322	5H	225.82	morex_contig_1563668	TGCAGTGTACTTTATCCAGACGACT[A/G]TAAAAGG GGATTGTTGGTCTAGTTTGATGAATTTACTA
TP48164	5H	226.86	bowman_contig_69746	TGCAGGCGTCGATTAAAGTGCATTTTTCTTAATCGG TGCCCGCAGC[A/G]CCGAGATCGGAAGAGCA
TP1757	5H	226.86	bowman_contig_15108	TGCAGAAGAAATAAGCCTTCCCTTTCCTTCGCCGA GGTCCATGC[A/C]CAGACCATGGTCGCGTGT
TP14416	5H	229.49	morex_contig_42299	TGCAGCACGAAGATGGTCTTCGTCGGCTACGA[T/A] GCGGGCTCAAAGGCGTATAGGTTGTATGATC
TP27410	5H	229.49	barke_contig_1805875	TGCAGCGCCAGCGTGAACGGGGGTGTGGCGCTGAC GACTTAGGCGCCACATAGT[A/G]TAGTGTGGC
TP53372	5H	229.49	morex_contig_1647134	TGCAGGTAAACACGCCTC[A/G]TGCGGGGAGGGCCT CGCGTAGAACTTCGCGATGTTATCCCCGAGA
TP57064	5H	229.49	bowman_contig_64048	TGCAGGTTTCATCCACTACCCTCCTTCTCAAGGCAAC C[G/T]TCATCGCCGCCATGCTCGCAGTCCTA
TP58662	5H	229.49	barke_contig_423851	TGCAGT[A/G]GAAATCAGTAAGGCATACAAATCACC ATTCACATTTACATCTGTAACGCGGTGGA
TP168	5H	232.09	morex_contig_2553377	TGCAGAAAAGCC[C/T]GACTTCGAATTAACAAAGCC ATCAACCGAGATCGGAAGAGCACACGTCTGA
TP9435	5H	232.09	barke_contig_505944	TGCAG[A/G]TCCTTGCAGCTCATTCCTACGGCCTGAG CCCACTCCGAGATCGGAAGAGCACACGTCT
TP20446	5H	232.09	barke_contig_360216	TGCAGCCAAGTGAAGTTTGTGATGGACCACCTTGT CTGTGTGAGT[C/G]TGGCTAGATCCGAGATC
TP22613	5H	232.09	barke_contig_554943	TGCAGCCCGAGATGTAGTTCCCCCGCAA[A/G]TGAA AGGTAAATAGAAAAGATGGTACGTGCCAAAA
TP48606	5H	232.09	-	TGCAGGCTCCGCCTCCTCCTCCTCCT[C/G]TTCCTCC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				TCCGAGATCGGAAGAGCACACGTCTGAACT
TP16034	5H	232.09	bowman_contig_12310	TGCAGCAGCACCGCCAG[A/C]CGAGCAAGACAAAC CCAAAGAGGAACCACCACCGCCGCGGAGATCG
TP52094	5H	233.32	bowman_contig_849388	TGCAGGGGCTTCGTCGACCGATGACGCATCGGAAT CCATTGTTGAAGTATGGCTCTTCTTCCC[A/G]
TP4268	5H	236.00	morex_contig_38449	TGCAGACCCTGGTAGACCACAGCAC[C/G]AACCCCA TGCCCATCCCGAACATGAGCCCCGCCGCCCG
TP5836	5H	236.00	bowman_contig_13213	TGCAGAGAAGCCA[G/T]ATCTATTGGGCCAATCCGA AATGAACCTTGCAGGCCACCCACCCAGGCC
TP9934	5H	236.00	morex_contig_44270	TGCAGATCTCATCAACAGAATATCTTTCCAGGTAAA TCCTTTTACAGTTTCAC[C/T]ATGGTTTTTC
TP32941	5H	236.00	morex_contig_158733	TGCAGCTAGAG[A/G]AACTACAACCACGGGAATCAC CCACAACATGCTCCTGCGTTTGTGTTGAGA
TP38332	5H	236.00	barke_contig_425270	TGCAGCTTTCCTCCAGCATCTCTCC[C/T]GTCTGCC TCTGTTTTTAAACCAAACAGAGCAAACATG
TP57848	5H	236.00	-	TGCAGTAAAAACGGATCGTACGTACATATATACGT ACATTAGATTTGGT[C/T]TACCGTGGAGTAAT
TP65691	5H	236.00	morex_contig_1577539	TGCAGTTTCCATGACCAGTGGC[A/G]ACAGGTTCTC GTCCTCGGAGATATTGGCCGAGATCGGAAGA
TP50222	5H	238.59	bowman_contig_88215	TGCAGGGCAAC[G/T]TTGACGTCTCGCTCCGCAGC AGCATCTCAGACACCTCCGCCGAGATCGGAA
TP58969	5H	238.59	morex_contig_140269	TGCAGTAGGGGAGCACGTTGCCGTCCACCACGTCGT CCTCCTGCTGCTGCACCTG[A/C]CCTTGCTG
TP63837	5H	238.59	barke_contig_282096	TGCAGTTACTATGGTGCATGTTCTC[A/G]TCGGGAT GGCTAGGCTAATACGAGCCATCTCGTGGAC
TP66058	5H	238.59	barke_contig_305794	TGCAGTTTTGAGATAACAATTAATAAATCTGATATG AAAAAG[C/T]CACATCCGACGTAACATAACAG
TP37385	5H	238.59	bowman_contig_117472	TGCAGCTTC[A/G]ACACCATGACCAGGGAAGACAAA CCCCCAAGGTATACACCGACACCGACTCAG
HMA2	6H	26.3		GTGAGGGGATTTAACGGTGAAATTGG[T/C]GGAGAG GGCGTATATGTTGGGAACA
TP1401	6H	35.00	bowman_contig_222947	TGCAGAACGACGGCGT[G/T]GTGAACCCCGAGGCCA TCATGATGCAGGCCATCGCCGAGATCGGAAG
TP10615	6H	35.00	morex_contig_37357	TGCAGATGCTGGTGATGATATCC[A/T]CCCAGCACC TGGTGGTGCAGCTGGTAGTGGTCCCCGAGAT
TP15309	6H	35.00	morex_contig_37357	TGCAGCAGAACCCCGTCATCTCCAAGAACCTGCCAT GGATCATCATCAATTCATCATCATC[A/C]AG
TP19558	6H	35.00	bowman_contig_62186	TGCAGCATGACACCCT[C/T]GTAATGACTCGGGACG CCATCAACAGAATCGTTGAGCGGATGCACAC
TP43077	6H	35.00	morex_contig_37912	TGCAGG[A/G]TCTTCCACAACCACTGCAAGGACAAC GGCATCGCCCTGGAGGACAAGAACTTCACCC
TP52483	6H	35.00	morex_contig_37357	TGCAGGGGTGTTGGATCATGAGCAAAGCATAGGGC CA[G/T]TTTGGGGTGCACTTCAGAAACGCAG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP56183	6H	35.00	morex_contig_37357	TGCAGGTGCTGTGCTCCACAAAGTC[G/T]GGGCGCT TCGTCCGCATCATGGACGAGATCGCCGCCCT
TP61626	6H	35.00	bowman_contig_846256	TGCAGTGAGCAGGCCG[A/T]CGTCCCTCTTTGCTTGG CCGAGGTAGTTGATTGCCGAATGCACTAGC
TP63346	6H	35.00	morex_contig_114452	TGCAGTGTATTATCTCCTAATAATCTTCAGACAATG CAACGAAGGAGGATGTGT[C/T]TGTTCTTTC
TP26274	6H	85.00	barke_contig_58737	TGCAGCGAGCGGTTACTGACGCCTGCTCATGTTTGC AACG[A/G]CAGCAACCTCTCAGGGTTCAATC
TP24379	6H	85.00	bowman_contig_845032	TGCAGC[C/G]GTGTGTAGGTTTAAACGGAAGCAAGT GCGTACGTACGTACAGCGCCGAGATCGGAAG
TP21231	6H	85.00	barke_contig_58737	TGCAGCCAG[C/T]AAATGGAGCAATAAGATTTTCGCA AGCAACGGAGAGCTGCTTACAGAGCTGCAAC
TP13410	6H	85.00	bowman_contig_151876	TGCAGCACAATCTAATTCTTTTATAATTATTCCTTCA TTGGTG[A/T]GTATAGACCGAGATCGGAAG
TP49189	6H	86.24	morex_contig_1564053	TGCAGGCTTAGGTGTGTGTGTGCATGTGAGTTTACT GTGT[C/T]GGACAGGATTGTTTAACTCATAT
TP12107	6H	86.24	morex_contig_2547976	TGCAG[C/T]AACAAATAGCGCCCTGTTACTCATCCTC CTTCCGTAGAAAATCGCGAATTATACAAAA
TP24352	6H	92.39	morex_contig_162970	TGCAGCCGTGGGGATAACCGTGCGTGAGACCG[T/C] GAAGAGATGCGATGTGTTACAAGCCGAGATC
TP50437	6H	117.60	-	TGCAGGGCATAACGAAGATC[A/G]GTAAGTAAGTTCA GTTACCCGAGATCGGAAGAGCACACGTCTGA
TP34958	6H	117.60	morex_contig_50809	TGCAGCTCGTTTTGTTTATGG[A/G]GTGATACAGCGA GCCAGCGACTGAATATTCAGCGGCGCGACC
TP64958	6H	117.60	bowman_contig_63088	TGCAGTTGCACGTCCGTGTACACGCGCACAAGTACTAGT TACATGTTGCTTGGGTTTGTAC[C/G]AGATC
TP64683	6H	117.60	morex_contig_2549403	TGCAGTTCTGACTGATCCTTTGTTGTTGTCCTT[A/C]T TGTTGCGCAGACGAAGGGAACGGGCAGCT
TP32398	6H	117.60	morex_contig_45229	TGCAGCGTTGAACGCCCCGCCAAAAAATATATCGGC GTGTTTGGTG[C/G]CCTGCATGCAGCCGAGAT
TP30146	6H	117.60	bowman_contig_13308	TGCAGCGGCG[A/C]CCGCTCACAGACGCATCATTAT CCACCTCCAGCCACGCCGAGATCGGAAGAGC
TP28433	6H	117.60	bowman_contig_860499	TGCAGCGCGCAAGCTGTGGAAAGCACGGCGCAATT AGCAAGGCCACATGTCGTC[A/G]GTCAGTACT
TP26484	6H	117.60	bowman_contig_861033	TGCAGCGAGTTATGGGCCAAACGCACACAAGGTAG CGAGGCGAAGGATTTT[A/G]ATGAGCTGGCCC
TP9913	6H	117.60	barke_contig_7267	TGCAG[A/G]TCTAGATGGATCGGGTCGAGCTTGCAG ATAACAGTTTATAAAGCAGCAAGAGCTCACT
TP9184	6H	117.60	barke_contig_1786619	TGCAGATCATTCTGCACCCGAACCAGGGACGTGTTT TGAC[C/T]GTCCGCGAGAACGCTAGGCTGCA
TP6707	6H	117.60	bowman_contig_22879	TGCAGAGCCGCGTGAAGAGCTCCTTCTTGGAAGTGG AGCAGTCGC[A/G]GCGGTCATCGTCGTCGTC
TP3983	6H	117.60	-	TGCAGACCAAGATACAC[A/G]TACGTAGTCTACAAT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				CATTACCAAATGATTACGTACCTCTCACTGG
TP34790	6H	118.90	-	TGCAGCTCGGTCATGGCCGCAGGGGA[C/T]AGAATG TCGGGCCGAGATCGGAAGAGCACACGTCTGA
TP10055	6H	118.90	-	TGCAG[A/G]TGAAACGAAGGTGGGAATAGCGAATT AAGTTGGTGGGTAGACGGGTCGGATCAAAGC
TP24224	6H	118.91	morex_contig_157599	TGCAGCCGTC[A/T]ACCAGCAGCACCGTGTCTGTTGTT GCTCCGCCGCATCGTCGGACGCTGCTGCTG
TP59185	6H	118.91	morex_contig_136042	TGCAGTATCCA[A/C]AGAATCGGCATCGGTTACTTT GAGCAAGGGTATATCATTAAGTGGTAAACTT
TP34767	6H	121.50	bowman_contig_954043	TGCAGCTCGGGGAGATAAGAGAGTGAGAGTGAGTG CACTAGTGGAACCGGG[C/T]CTTTGGCCTGG
TP3084	6H	121.50	barke_contig_321152	TGCAGAATCTCTACAAA[A/G]CTCGGACAGTCTAGT CAAGCACAGGATCGAACCGAGATCGGAAGAG
TP59832	6H	121.50	bowman_contig_64727	TGCAGTCATAGAAAATGTGGGGCAAAGAAGGGAAA T[A/G]TGGAGCAGCTTCTGTTGTGACCTGGAG
TP49009	6H	121.50	-	TGCAGG[C/T]TGGACATGCACATCATTGTGGTCGGC AAGTGGCCGATCGATGGTGAGGTTGGTATGG
TP41558	6H	121.50	morex_contig_38713	TGCAGGAGCAGCAGCAGCAGC[A/G]GCGGCGGCGG CTGGTTGATTTGATCTGATTAGTTGAGAATCA
TP39275	6H	121.50	morex_contig_41348	TGCAGGAAGAAGCTGCGCGCCGCCGTGAGGGGCCCT CAGGCAGGCCGC[G/T]GGCGTGCAAGCGGTGC
TP20968	6H	121.50	-	TGCAGCCA[C/G]GTACGTGCTCTCGTCCGTCCGTCC ATTTGTTCCACTACTTGTGCTATATATATC
TP59279	6H	121.50	-	TGCAGTATGATGAACTTCATT[A/T]AGACACAATTC AAATGAAGCGAAATTTTCCGAATGTAAACAA
TP58067	6H	121.50	morex_contig_1582761	TGCAGTAATATAGTCAAAAAGAATTCCAGTGCT[G/T] GCTTCCTTCCGAGATCGGAAGAGCACACGTC
TP48037	6H	121.50	bowman_contig_1985801	TGCAGGCGGTGCTCATGGACCAGAACCACGGCGGC GGC[A/G]CCTCCGCCGAGGAGCTCAGCATGTA
TP40151	6H	121.50	barke_contig_63367	TGCAGGACACTTTTC[A/G]TAGTTCATTTACACATGG CACTTCAAAAATAATCCAAGCAACTAGGAA
TP6138	6H	121.50	bowman_contig_845528	TGCAGAGAGGCGTCAAGTTGATGAACGTGTCCAGA AGATCATTGAATT[A/G]AAAAATAAGGTATTT
TP38093	6H	121.50	morex_contig_1567204	TGCAGCTTGGACCGCAGGCAGCCTGTTTCGACGAAA TGT[C/G]CAGGAGGCTGAAGGAGGAGGGAAGC
TP21840	6H	121.50	bowman_contig_62231	TGCAGCCATGTGTTGCTCCCATG[A/G]AAGTGATTG GTTGAAAGTTGAAATTAACATCTATAACAGA
TP7744	6H	121.50	bowman_contig_845528	TGCAGAGGGCTGTGATTGAA[C/T]TGAATTAACGG AAACAAAATGATGTTAGTACAGTTGTTAGTA
TP62784	6H	121.50	morex_contig_46762	TGCAGTGGCAAGGAAGAAGAAATGTAGTTTCAGTT T[A/C]TGTTTCCCATGCTGTAAAAGCAACACT
TP10679	6H	122.80	bowman_contig_849014	TGCAGATGGAGAGAGCAGGGATGAGATGAATAAGC CATCCACACACAAAGATCAAAGGA[A/C]GAGA

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP2233	6H	122.80	bowman_contig_251246	TGCAGAAGCCTTTGCTGCCATGACGACCCG[A/C]CA CCCTGTCCGAGATCGGAAGAGCACACGTCTG
TP421	6H	122.80	morex_contig_59606	TGCAGAAACTCAATAGAAGACGTTGACCAAAA[G/A] AAAGGAAAATGAATCGCTTGGACAAAGACAC
TP64895	6H	124.10	barke_contig_512992	TGCAGTTGATAATCTCAAGTTGGCTGAGTTGAGGGT GTTCCACTTGTAGAGAAGACGAGAT[C/G]TC
TP55808	6H	124.10	barke_contig_199432	TGCAGGTGCAGGTCAAACTAACTAAAATCCGTCC GT[C/G]GAGAAGGAAATCGAGAATGCATGCAT
TP43100	6H	124.10	-	TGCAGGATGAAGCAAAGGCTCAATATGGCGCGTCC TC[A/G]TCTGGATCCCGTGAGAACCTTTATCC
TP32229	6H	124.10	morex_contig_136822	TGCAG[C/T]GTGGTCAAAAGCAACAGGGATTAGGGA TAACACTCATGCTACAGCCTTCAGTAACAGG
TP19126	6H	124.10	morex_contig_40556	TGCAGCATCAGGTTGCACGA[A/G]CAACAGAGGCGC AGGAGCCACCTGCACCTGCTCCGAGATCGGA
TP8867	6H	124.10	bowman_contig_855242	TGCAGATATTATGGCGAGTCCGACCTCCTCGGCTTC GACGACGACGGCGG[C/T]GACAAACACGGCG
TP4533	6H	124.10	-	TGCAGACCTGAACGTC[A/G]ATGTCAGGTCAGACAT GGAGGTGCTCCGAGATCGGAAGAGCACACGT
TP35032	6H	125.40	bowman_contig_63959	TGCAGCTCTCCCTCCTCACCCCATACATCCAGGTAA CTCCCC[A/G]CCTCGCCGAGATCGGAAGAGC
TP25247	6H	125.40	barke_contig_303061	TGCAGCCTGTAGCCGTCGAGCTCGTCGATCACATCG TCG[A/G]CATCGTAGAGCAGCTCCTTGACGG
TP6267	6H	125.40	bowman_contig_85559	TGCAGAGATGGACGGCGTGGAGAGCCAGATACCCG ATCCCGATGG[A/G]CATCAAGAGATGAATAAT
TP41963	6H	125.40	barke_contig_64472	TGCAGGAGCTTGTTCATGGAGGAC[A/G]TGTGTAATT TCCGAGATCGGAAGAGCACACGTCTGAACTC
TP11284	6H	125.40	barke_contig_465957	TGCAGATTCGATAATGT[A/G]GAGTGCTATCTAAAA TCGGTGTTGTCGTCAATCCATCCACATAACG
TP64253	6H	126.70	barke_contig_67682	TGCAGTTCCATATAGCCCAAAGAAGTGCACAAACT CCTATA[C/T]GGATTTGTCTTGCAATCGTCAT
TP57774	6H	126.70	bowman_contig_1986938	TGCAGGTTTGTATCAAATAAGTGGTTTGGAGCTTTG GTGTCCAGTGGAATTTT[G/T]CTCGGGCGAC
TP53464	6H	126.70	morex_contig_55855	TGCAGGTA[A/G]TCGAACAGCTCCCTCTTCTTGCCGT CGCGCTCCGAGATCGGAAGAGCACACGTCT
TP52135	6H	126.70	morex_contig_55855	TGCAGGGGGAGGCCAACTCGTCGCTGGAGCT[C/G]C TGCACAAGTGCGCCGAGGTGGACAGGAAGGA
TP42401	6H	126.70	bowman_contig_87490	TGCAGGAGGTGGCCAGTGTGCGCCCTCGTTGT[C/G]A AATCCCATAGCCGAGATCGGAAGAGCACACG
TP41372	6H	126.70	morex_contig_269568	TGCAGGAGATAAAAACCAAGCCTGTGGGAGGAAG[A/G]CCGAGATCGGAAGAGCACACGTCTGAACT
TP41371	6H	126.70	bowman_contig_78535	TGCAGGAGATAAAAACCAAGCCTGAGGATGGAAGG CCGAC[A/G]CGAGGAAGGCTGGTGGTTTGTGG
TP40166	6H	126.70	barke_contig_56433	TGCAGGACAG[C/G]AAGGCAAAGCAAAGTCAGGGG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				CACGAATGAATCCAACCTGAACCGAACCTGAAA
TP29738	6H	126.70	barke_contig_55198	TGCAGCGGATCTCACTCCACTCATCGGTGACTGTGA GGTCAAAGCACGGAGCCCAC[A/G]CTGACGT
TP24200	6H	126.70	barke_contig_134907	TGCAGCCGTACGCGCGGCAGCGGGTATCTCCGCGG CCGCCGCGTCGCCGTCGACCTCTCGT[C/T]GT
TP20339	6H	126.70	bowman_contig_13674	TGCAGCCAACGCCTCCCTCTCCTACTCCGCTCCAGC GCCA[C/G]TGCCGCCGAGATCGGAAGAGCAC
TP13756	6H	126.70	morex_contig_46523	TGCAGCACCAAAACACCAAGTCAGCGACATCATA TACATGCTTCTC[G/T]CTCAGCAACTGAAACT
TP44317	6H	126.70	morex_contig_57887	TGCAGGCAGGCAGGAACAGGGCAACACCAAAAGTT TCAGTCAGGTACAAAATTGAACATGG[C/T]CA
TP60043	7H	0.00	bowman_contig_142790	TGCAGTCCATCCATGGCATTGGACGGGCACGCGCCC GCCAGATCCTTTTCAGAG[C/T]TCAATTTAGA
TP2350	7H	0.00	barke_contig_275930	TGCAGAAGCTGAAAGATTGGAGTAGCACCGTGGTG TACGTCGCTGGCACGCTCTGACCAA[A/G]CC
TP3030	7H	0.00	barke_contig_52828	TGCAGAATCGAAGGGCTGAGTATGTCTCAG[A/C]AA TTCTAGAGAAGCTTGTGTCGTGGGAAATGGT
TP5230	7H	0.00	-	TGCAGACGGGCAGGACCATGACCTAC[A/G]ACCTCC AACTCCAAGACGGTGCCGAGATCGGAAGAGC
TP5814	7H	0.00	bowman_contig_222246	TGCAGAGAACTACAAGTGACATGGG[C/T]TGGATTG TGGATGCCACCAGTAATTCGTCCAGTTTTTT
TP6296	7H	0.00	bowman_contig_9428	TGCAGAGATTATT[A/T]TTTTGTACTCACTCTGCTTT GCTCTGTTTCTGTTTTTCCCCTTCATATCT
TP6333	7H	0.00	morex_contig_40276	TGCAGAGCAAAGTACCTCAATTGTTGAAGATGTTAA CCATTGCTTGGGC[A/G]AGTGTCTGGTCAGA
TP7271	7H	0.00	bowman_contig_164394	TGCAGAGGAACGAAGACCGATTGATGAGCATTGCT GCTGGTGTACAG[C/G]GCATGAGATAAGGGGG
TP12874	7H	0.00	morex_contig_300315	TGCAGCAAGGAGTCGATTGGCCTAAT[A/G]CCACCA ACATAATAGGATTCTTACTTTGTTCTTGCAG
TP13570	7H	0.00	morex_contig_41777	TGCAGCACAGCGGCGAGGTGAGCGCT[C/G]GTCCCG CCGATGAGCCAGAACTGCTCATTCTCCACC
TP14096	7H	0.00	morex_contig_43514	TGCAGCACCGCACGCACGA[C/T]AGCTTAAATGCAT CACCTGTGGCGTCCAATGACGCTCCATTGCA
TP17633	7H	0.00	-	TGCAGCAGGAGCGATAGTAGCAAGTACTTAACCGA GCCACCTTGAATAATTAAG[C/T]GTGGCCGCC
TP18745	7H	0.00	bowman_contig_61715	TGCAGCAGTGTGCG[A/G]CGGACGGACGAGGCGAGG AAGCAATCCGAGATCGGAAGAGCACACGTCTG
TP18839	7H	0.00	bowman_contig_11475	TGCAGCAGTTGGAACCTGGCGGCGTCGACATGGAG CTTGAGCGCGCTCATGT[A/C]CCAGCCCCCG
TP23026	7H	0.00	bowman_contig_883846	TGCAG[C/T]CCTGTGACGTTGTCCCTGTAGAAGTAGT GCACCGTGGTGAGCTCCAACGTAGCCCCAT
TP23247	7H	0.00	bowman_contig_883846	TGCAGCCGAGCAAC[A/G]ACGCGCTGGCCATCATGG TGCTGGTGGCCCCCACGCCACGGTGAGCGT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP25755	7H	0.00	bowman_contig_1992273	TGCAG[C/T]GACAGCGACACGGTGCTGAACGACCTC GACTCCCGCGCCTCCGAGATCGGAAGAGCAC
TP29038	7H	0.00	morex_contig_39067	TGCAGCGCGTGCTGGACGAGCGGCGGGCCAGGGGA GGGAAGAC[A/G]GCGGCGGGTGCGGCGGCGCC
TP29150	7H	0.00	barke_contig_300067	TGCAGCGCTATCTCTTGCTCTTCCGTGAAGCTTTCCG TCCCCA[A/G]TGAGACCAGACTTCAAGTG
TP31597	7H	0.00	bowman_contig_222575	TGCAGCGTCATCGTTGT[C/T]GTCGGCGGCGCCGCCC CAGCTCCAGCTGACGAAGCTCTTGGCGCCG
TP33279	7H	0.00	bowman_contig_864293	TGCAGCTATTGTTGCAAAAGGCGGGGATGCCTTCAC TTCTCCATCGACTCCTCATGCAG[A/G]ATAT
TP38518	7H	0.00	morex_contig_37137	TGCAGCTTTTTCTCCGA[C/T]CTCTTCAGCAGGTCTG TTATCTCATGCGTGAGAACCTCAATTGCC
TP43007	7H	0.00	barke_contig_266341	TGCAGGATCTCGCTGTTGATGGTGAGCTTGAAGCCG ACCGCGATGG[A/C]GTTGAGGTTGACCATCA
TP44975	7H	0.00	barke_contig_2823051	TGCAGGCCAGGTTTGTGGCCGACGTGGCTCCCCTGG C[C/G]CTGGGCGTTGTGCAGCAGGCCTTGCG
TP48114	7H	0.00	barke_contig_1788463	TGCAGGCGTAGTTTTCAGCTGGCCAAGTAT[A/T]GAC CAGGCACCAAGGGAAAATTACGCCGCTTATG
TP49234	7H	0.00	morex_contig_46236	TGCAGGCTTCTTTCTTTTGACCGCCATTGTGAAGAG TGGACCTTCA[C/T]GGATCCTCTCCTGTAT
TP49737	7H	0.00	morex_contig_46236	TGCAGGGACTTTTTTGACGTCCTGGTTTCTCTTGA[C/ G]GATGCAAACGGACAACCGTTGCTCTCCG
TP49887	7H	0.00	morex_contig_12243	TGCAGGGAGGAGATGAGGCTAGTTGATCCAT[C/G]G AGTAAAGCCGAGATCGGAAGAGCACACGTCT
TP52500	7H	0.00	-	TGCAGGGGTTGAAGCAGCGTTACGAAG[A/G]CCACC ATGGACTGAAAATTCACGACGACGCTCTTTC
TP52509	7H	0.00	bowman_contig_103664	TGCAGGGGTTGGAATCACCTGTTGAAATCCGCAA GCCGAACACC[A/G]TCCTTGGTGTGCTTTTCC
TP58365	7H	0.00	morex_contig_1577866	TGCAGTACCGCGGACGACACGATA[G/T]ATCAGATC TGATAAACACATAACCGCATAATTTAAACTAA
TP58479	7H	0.00	morex_contig_57798	TGCAGTACGCGGACGACA[C/T]GCTTATCATCTTCCT TGTTGATCCGAGATCGGAAGAGCACACGTC
TP58906	7H	0.00	bowman_contig_9428	TGCAGTAGGAAGGAACCAACCAAAAAATCAAGATC AATTCAGCAACAGCTGCGTGCC[G/T]TCCTCC
TP60049	7H	0.00	-	TGCAGTCCATCCTTTCGCCGC[A/G]CCGCGCCGTTGG GTTGGGTTGGCATTTCCCAGATGGTCTCAG
TP60121	7H	0.00	morex_contig_80182	TGCAGTCCCCACCGCCATCGTCAGGGTACTACGCGT CCTCGGAGGGTTC[A/G]GACGGGTACCTGAC
TP61675	7H	0.00	bowman_contig_25598	TGCAGTGAGGTTGCTCGTGCGACCTCACTCTCCTCC[A/G]TCGGCGCTTCATCTCCTTTGCCTACCG
TP63567	7H	0.00	morex_contig_1563311	TGCAGTGTGTTCAATTT[A/G]ACGGAATGAGTTGATTG CTGATTGAGTGTGACTCATTTACAGGGAA
TP64258	7H	0.00	morex_contig_140449	TGCAGTTCCATGCAGCCCACAAAAGTGCACAAGTT[

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				C/T]CAACCCGAGATCGGAAGAGCACACGTCT
TP1449	7H	1.30	morex_contig_718103	TGCAGAACGCCGCGTCGCCCTGTACATGTAGGCGT GGCGGTCCGAG[A/G]CGATGCGGCGCTTGCA
TP2072	7H	1.30	morex_contig_2528380	TGCAGAAAGCAGAGAAG[A/G]AAGCGGTCCATGGTG TGGCAACGGTCGGTGGAGCTTACGGAGCGGGG
TP4810	7H	1.30	bowman_contig_78045	TGCAGA[C/T]GCACGGCCAACGGTGAGGGGCGAGC AGTAGTACACGGCTGGCACGTCGGTCTTGTTG
TP16778	7H	1.30	barke_contig_1792629	TGCAGC[A/T]GCGCAGGTGGAGCATGGAAGCACATG TCGTCGATGCCGAGATCGGAAGAGCACACGT
TP33073	7H	1.30	bowman_contig_65032	TGCAGCTAGCTGGCTTAGATCGTTTCCAACCTAACT ATTGACAAC[C/T]GAAGCACATGACCAGCTT
TP44300	7H	1.30	bowman_contig_877413	TGCAGGCAGGAGCAGATGGACATGGACGCCGC[G/A]]CTGGCCGCCGTCGCGCGCCGAGATCGGAAGA
TP47291	7H	1.30	-	TGCAGGCGCGTGACTGCTAGGCATCCAACGAGGAG C[C/G]GAGCGGCAGCGTGGTGGCAGTGTGCTT
TP60520	7H	1.30	barke_contig_2780678	TGCAGTCGATCGGCAGGCTATGTGGAGCGCGACGT CTTCCTTCTGGGAAGATG[A/G]TACGTTATAA
TP61955	7H	1.30	bowman_contig_877413	TGCAGTG[C/T]AGAGCGCTGGAGTAGTGATCGGTGCG GCCATGGAGTCGAGGCACGGGAAGGCGGCAT
TP58638	7H	1.30	-	TGCAGTACTTCGAAGCGGCCA[C/T]GGGAACGGAGT TCAAGGTGCCGAGATCGGAAGAGCACACGTC
TP35443	7H	1.30	morex_contig_136340	TGCAGCTGAGGAAAAGAGAGGTCCCGCCGCTGCC[A/ G]ATGCCGACCGAGATCGGAAGAGCACACGT
TP37026	7H	1.30	morex_contig_1572075	TGCAGCTGTACAGCCCGAGCCACGGGACGGCGGCG TCGCTGAAGACGGA[C/G]GTCCACCAGGCCAT
TP47587	7H	1.30	morex_contig_49664	TGCAGGCGGACGAGGTAGAGCGAGGGGGCCATCTT GCTCTTGAGCAT[C/G]GGCGTGAGCAGGTATC
TP62459	7H	1.30	morex_contig_1574023	TGCAGTGCTCACCGTTTGTATGACAAGCC[A/C]GCGG CTGTTGGTCCGCTCCACGAACCTCTCCGAGA
TP3181	7H	3.90	bowman_contig_144193	TGCAGAAATGCCAGGCAGCTCTGTAACCAAGGTGGT[A/G]GGTGACGGAAGGTGAATAGATGATCTTC
TP4582	7H	3.90	morex_contig_122840	TGCAGACCTGTAAAGTGATGCAA[C/G]AAGGTTGAA AAACTCAGCAATTTCTATCTTATTGAACTT
TP13518	7H	3.90	bowman_contig_850798	TGCAGC[A/T]CACTGGCTTCGCACCCACGAGCGGG CAACCGAGATCGGAAGAGCACACGTCTGAAC
TP688	7H	3.90	bowman_contig_10020	TGCAGAAATAATTCTGCAACAAGGTTTGTATTTCAA TGATGAATGCGTGCTT[C/G]GCTGCTTGACA
TP2512	7H	3.90	bowman_contig_95121	TGCAGAAAGGCACGGGA[A/G]CTGGCAGCGTCTGTGC CAGCAGAGGCGGTTCCCGTGCTCCTTCCAGC
TP4491	7H	3.90	bowman_contig_11044	TGCAGACCTAGGAACAATAGC[A/G]ATAGCCTTATC TGCTGTGCCGAGATCGGAAGAGCACACGTCT
TP12917	7H	3.90	morex_contig_1607885	TGCAGCAAGGCTCCATC[A/C]CCTCTTCTGCTCCGTC TCTGTTCAACCCCTGTCCTCCAACCGCCCC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP13517	7H	3.90	bowman_contig_850798	TGCAGC[A/T]CACTGGCTTCGCACCCACGAGCGGG CAACCGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
TP17176	7H	3.90	bowman_contig_276908	TGCAGCAGCTCACCGCCGCATG[C/T]TTCCTCGGCCC CATCGCCTTCTTCCGAGATCGGAAGAGCAC
TP19462	7H	3.90	morex_contig_2548032	TGCAGCATCTCGTTGCTCCACGGGAACCCGTCGGCA TCGG[A/C]GCCGAGATCGGAAGAGCACACGT
TP19831	7H	3.90	bowman_contig_10020	TGCAGCATGGCGTTGCTCCACGGGAAGCCGCCGTTG GCGGAGTAGGCCCCCGA[C/T]GTCTTCTCCG
TP22827	7H	3.90	bowman_contig_10112	TGCAGCCCGTGCACGATCCCCGTGGC[A/G]AACGTC GCGAAGCTGATCTCCTTCTTCTTGCCGCCAG
TP26003	7H	3.90	bowman_contig_62956	TGCAGCGACGGGTGAACATGGACTTG[C/T]TGCGGT ATGGCAGCGGATTGGGAGCACGACAAAGTCT
TP29953	7H	3.90	bowman_contig_276908	TGCAGCGGCATACAGTGGTGCAAGAGATAGAGGGA GCTG[C/T]GCGGTGTAGTGCTGTGCTGTAGGT
TP34396	7H	3.90	-	TGCAGCTCGAGACCATG[A/G]CCGACATGAAGCGCG AGTCGGTGGCGCTGCATGAGATGGTCATCTC
TP37241	7H	3.90	barke_contig_271919	TGCAGCTGTTTCAT[C/G]GGTTGGCTTCGATGATGGG GCTCTACGGTGAAATCGGAGTCATCCGTTCA
TP41993	7H	3.90	morex_contig_39172	TGCAGGAGGAAGGCGGCCGCGCGCGGGGTTCTC GGGGGTCTACGGGGC[G/T]CGGGGCCACGCCC
TP47115	7H	3.90	bowman_contig_120362	TGCAGGCGCCGTTGTTTCGTGGAGACCAA[C/T]ATGA CGTTGGGGGTGGCTGCTTCTCGCAAGCGACG
TP63437	7H	3.90	bowman_contig_9981	TGCAGTGTCTGGGCCATCCATACCCTGTTAATAACA ATTCAAAAATAAA[A/C]TCGTTATATTCCAC
TP63543	7H	3.90	bowman_contig_856044	TGCAGTGTGTAAGTGGCTAATTAGCCACCAAACCCA TACAGGCTTGA[A/T]ATTTCCACATAGGGT
TP978	7H	3.90	barke_contig_366025	TGCAGAACAACTTATTGATCAATGCGTCGACAACA GACCTTCTCTTTGATAT[A/G]AACACTACAAA
TP17196	7H	3.90	bowman_contig_202627	TGCAGCAGCTCCCAGCCGTCGAGGAA[C/T]TACATT TGACAAACTGCCCAAGTTGTGTGGAGCCTT
pathogenesis	7H	27.1		CCGAGAATGCAGACGCCCAAGCTAG[C/T]CATCTTG CTCGCCCTAGCCATGGCA
pbr1	7H	28.1		GACGCCCAAGCTAGCCATCTTGCTC[C/G]CCCTAGC CATGC3CAGCCGCCATGGT
TP3502	7H	42.61	morex_contig_134884	TGCAGACAA[C/T]GTACAAGGAAGGCTGTTTATCTG AGGCGGCGGAGGCATCCATAGTTTCCTTCAT
TP1240	7H	42.61	morex_contig_274279	TGCAGAACC[C/T]CTTCCTCTACGTCCTCCTCAGCCA GGGGATCTCCAGGCGGCAGATCGTGTTCTG
TP4217	7H	42.61	bowman_contig_1983791	TGCAGAC[C/T]CGCCTCCCCGATGACCTCTCCGTGAC CGTGTTCCGTCGCCAGCCGAGATCGGAAGA
TP5709	7H	42.61	barke_contig_403715	TGCAGACTTGCAGCAGACCGCC[A/G]CACGGTGCCT GAACAACATACCACATGTCCCGAGATCGGAA
TP10034	7H	42.61	barke_contig_119107	TGCAGATCTTGGCCATGGACATCAACCGCGAGAAC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				TACGAGCTGGGG[C/T]TGCCGTGCATCGAGAA
TP20397	7H	42.61	morex_contig_2600128	TGCAGCCAAGCCCCA[C/T]CTATAAAAAATCTCCGA CGCATCTCCAGCCCGTCCGAGATCGGAAGAG
TP24875	7H	42.61	morex_contig_140545	TGCAGC[C/T]TCTCCACTAGTCCCCAAACACAAAGC AGCAGGTTCAAGAAACCACAGCAGCAACCACT
TP29601	7H	42.61	-	TGCAG[C/G]GGACCGCTCCGCAACAGCCTTTGACAT CCCGAACATCTGAGCAACACAAACCAAGTGG
TP33251	7H	42.61	morex_contig_244362	TGCAGCTATGGGCTGTGGCTAGTTGGTTATAATTAG GGGGGGAATCATTTCGTAATTAACAT[A/T]
TP33901	7H	42.61	morex_contig_137884	TGCAGCTC[C/G]CGAAAATTTGTGTTTGCTGTTGCTG GTCGAAGGCCAGTGCCCCAACCATAAAATA
TP52053	7H	42.61	morex_contig_56149	TGCAGGGGCTCGGCCTCGTGACCCGCAGGCCGTG CACCGCTTCTACGACGAGCT[C/T]CACGCGTA
TP61195	7H	42.61	morex_contig_49594	TGCAGTCTGCATCCCCTTGACCCAATGTCCGCATGA G[C/T]CTAAGAACTCGGATGTGCAAGAATGG
TP61659	7H	42.61	bowman_contig_16630	TGCAGTGAGGCGACCGATCGAATAACACACAGTGC CATGATTG[A/G]CGAACACAGAGCAGACACCT
TP62025	7H	42.61	bowman_contig_876452	TGCAGTGCAGTGCAGACAGTGCGGCCAATTAAGTC GTGGTTATCCATGAAGATCTAG[A/C]GTTATA
TP63291	7H	42.61	barke_contig_1783906	TGCAGTGTAATAAAAA[C/T]AGTGTATTTTCATCAT GGACAGGGAGAAGATGTATTTGAGGCATTC
TP10787	7H	47.82	morex_contig_2547471	TGCAGATGGCTGCAACCA[C/T]GCCGCCTGCAACTT GGGCCCATTTCGTTGGTTTAATCGGCCTT
TP11488	7H	47.82	bowman_contig_64572	TGCAGATTGGAAG[G/T]GTTGCAAGGAAACCTGAAG GAGCAGAGAGGTTACCGCCGAGATCGGAAGA
TP15643	7H	47.82	barke_contig_67211	TGCAGCAGAGCTTCACGTCGTTGTGCTCCTGGAG[A/ G]CGCCGCCGAGATCGGAAGAGCACACGTCT
TP22194	7H	47.82	barke_contig_132498	TGCAGCCCCAAGGGGTGGGGATCA[C/G]AGGGGATT TGATGACCCGCTCCACCCATTTTCCGAGATC
TP27651	7H	47.82	bowman_contig_1988792	TGCAGCGCCGACCGCAGCTTGCGGGCTTCCTCTGCA TCATTGGATGCAGACAGCAGGCC[C/G]AGGT
TP40078	7H	47.82	morex_contig_2547568	TGCAGGACAAGGTGGTGTACGGCACGGCGGACCAT GG[A/G]GGGCCGTGCGCGCCCTTCGCCAAGAG
TP42381	7H	47.82	morex_contig_41188	TGCAGGAGGTGCAGGGAGAGGC[G/T]TCGGAGGCG GCGCATCGCCGAGATCGGAAGAGCACACGTCT
TP62503	7H	47.82	barke_contig_66494	TGCAGTGCTCTGCT[A/G]TGGCATCGCCTGATGGGA ACCAAGGTCCTGGAAGCGAGGTTACCCGAGA
TP53304	7H	47.82	barke_contig_372067	TGCAGGGTTTCAAACCCAACTCTCTCTCTCTC[A/ G]TCTGAACATATATACATATGCAGCACT
TP24611	7H	47.82	barke_contig_67211	TGCAGCCTCAG[C/T]GAAAAGCTGCGCGTAGAGTCT CTCGGTGGCTACGTGGACGACGGCTACCTGA
TP35729	7H	49.12	bowman_contig_238685	TGCAGCTGCATCGCAACTCACAAG[C/G]AACGTAA CACGGTGTACGTCCGTGCGCCGAGATCGGAAG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP1540	7H	50.42	barke_contig_756104	TGCAGAACGGTTTCGGTGGGCAAGAAAGAACCAGC GCCATACTACTCGCGTCGCGTG[C/G]CCCCCT
TP6175	7H	50.42	morex_contig_45950	TGCAGAGAGTGC GCGACGACGGCGGCCGAGCGGTT GGC[G/T]TCGATGAGAGGCTGCACGCCGAGAT
TP15395	7H	50.42	barke_contig_2002164	TGCAGCAGAAGTACACATGGCCAACTCCC[C/T]GTC AAGCTGGCCGAGATCGGAAGAGCACACGTCT
TP23372	7H	50.42	morex_contig_2547134	TGCAGCCGCAACATCTCAAACCTCTAGGTGGGACC AAATCCTACGACTGCCCAAGAACC[C/G]AAGA
TP25650	7H	50.42	bowman_contig_75801	TGCAGCGAAGGGATTCTGGGCCTTAATTAGACGGGG ATTACGTGCGTGGCAGCGTAGTA[C/G]GAATG
TP25759	7H	50.42	bowman_contig_1996090	TGCAGCGACAG[C/T]GATGTCCGTGGTCTGTCACCCT CCTCCTTCCGCGGATCTCCCATCCGCCTCGA
TP43614	7H	50.42	bowman_contig_1991407	TGCAGGATTTGAGTTTATTTGATGGGTGCTTCTCCT[C/T]GACCGAGATCGGAAGAGCACACGTCTG
TP58996	7H	51.72	morex_contig_1560116	TGCAGTAGGTTTGGCACAATTA[A/G]CAAAAAACTG AAGTCCATGCAAGGCAACTAGCTATTCACT
TP4764	7H	51.72	bowman_contig_270926	TGCAGACGATGATGGCACTCTTGTGCCT[G/T]CCACC TCGCCTTCTTTCTCCTCCGACTCGTACGCG
TP7914	7H	51.72	morex_contig_135845	TGCAGAGGTTGTCCAA[C/T]CGCAGATTGATGGGTG TTACGACAACGAATCGGGGACAGGAGCAGCC
TP8125	7H	51.72	barke_contig_1782197	TGCAGAGTGC[A/G]TCCCTGACGAAGCTGGGCGCCG AGATGGCTGCACGGACAACGTGCTCGCGCCG
TP12659	7H	51.72	morex_contig_52505	TGCAGCAAGACGGTCAGTGCCACCTCCT[C/T]CTCC ATCCACCAAAGCTTTCTCCACGGCGACATGC
TP14821	7H	51.72	morex_contig_135128	TGCAGCACGGGCGGGAGCCAGCGAGTTAGTTACG[A /G]CCGCGAGGGTTTGCGGGGCGCGGGGACTG
TP19529	7H	51.72	bowman_contig_900075	TGCAGC[A/T]TCTTGGCTTACCTCTCCGTGCCCAAGC TCGTGGAGCTTGCGGAGGTTCCCATCCCGA
TP20520	7H	51.72	morex_contig_1560212	TGCAGCCAATTTGTCAT[C/T]GTACTTAATAACAAGT ATGGGAATTTGAACGCTTACGATGCCTTAG
TP40153	7H	51.72	barke_contig_349487	TGCAGGA[C/G]AGAAGTACGATGACATGTGAATCAA TCCAAGAGGGAGCGGTTTCCTCAATCTACAA
TP43675	7H	51.72	barke_contig_370060	TGCAGG[C/T]AAAGAGCTGAAACAGATAGTCTGGCC AGGCGAAACGGCCACCGTGCCGATTGGGTGG
TP50545	7H	51.72	bowman_contig_900075	TGCAGGGCCACATCAACTCGATGCTTCATTTTCGC[C/ T]GCGGGTCTCCTCGACGCCGAGATCGGAAG
TP56077	7H	51.72	bowman_contig_847047	TGCAGGTGCTCGCGGGCATCCTCAACGTGTGCGCGC TCGTGGG[C/G]TCGCTCACC GCCGAGATCGG
TP60160	7H	51.72	barke_contig_1796573	TGCAGTCCCT[C/G]ATAAGTTTCATCGACGAGATTG ACAGGCAGGAATCCACGTACGTTCTCTCTAG
TP64388	7H	51.72	bowman_contig_902616	TGCAGTTCG[A/G]AATCAAGCTAGTCAAACCAGATC GATCGAAGGATCGAGTACGTTAATTCATCAT
TP14993	7H	54.32	morex_contig_136277	TGCAGCA[C/T]GTTGATCCACTGTTAAGCAACGTGC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				ATACAGGACACATGAGCCGAGATCGGAAGAG
TP15174	7H	54.32	bowman_contig_846025	TGCAGCACTGTAAGCGACATCTTTGTTTC[A/C]TTGT AGTCGCGGCGTCGTCCCATATCCTTCCGTC
TP19081	7H	54.32	morex_contig_2549457	TGCAGCATCACGCCGCAACTGTTGTTGGCTTCGCAC CAACTCTCCATGA[A/T]GATGATGGCATCGC
TP26925	7H	54.32	barke_contig_715696	TGCAGCGCACTATTTC[A/G]CCCTACAAAATCCTGTT TTATTGCACTGTAAACGATTTTTGCGGGTC
TP45209	7H	54.32	-	TGCAGGCCCAGCGCGCGCCGCAGCCCGCGCCCTAC CTCTCCACGAA[C/T]CCCAGATCGGAAGAG
TP49492	7H	54.32	bowman_contig_855106	TGCAGGGAAGGCGGCGCCAACATGATTTGCTCGGC TTCGTTTCTCCCACCAAC[A/G]GGCATATTG
TP59689	7H	54.32	-	TGCAGTCACTGTCACTTCAGCTTCAATACAACGATA ACATGCAATTA[C/T]TTGGCTCCTCTATAGG
TP28646	7H	54.32	-	TGCAGCGCGCTCGAGAAATCAATCAACGCCAAGAT GAGTCAAATCAA[G/T]AAACAGAATAAAATCG
TP5266	7H	58.22	-	TGCAGACGGTAGATCAGAATTTGAGGCAAAGTAAC ACCAAAAAAGA[C/T]TACTACGTGCTAGCAT
TP32563	7H	58.22	bowman_contig_849072	TGCAGCTAACTCCATGGCCTTTAACTGTGCTGGACG TCCACTCACATGTT[A/G]TGCTAGATGTGCG
TP778	7H	58.22	morex_contig_135454	TGCAGAAATGCACAGTTGCTGA[A/G]AAATTACCAA CAACTAGCTCAGCAATCCGAACGCGTGGTAA
TP23822	7H	58.22	bowman_contig_861345	TGCAGCCGCGATAGACGGACCGATCCATTCTGTTTT TAGAGAAAC[C/T]TCAAAAAGGTGGGTCAAC
TP1620	7H	58.22	-	TGCAGAA[C/T]TCCAGCCGCTGTAAATTCAGCATGA ACATGGCGTTGGATATCCCTCACTAAACCGT
TP4043	7H	58.22	-	TGCAGACCACTAGAATGACGACCATGCCGCGTGGA TCTC[A/G]GGCACTTTCGTTCGATGTGGGGTAG
TP7777	7H	58.22	bowman_contig_852829	TGCAGAGGGGGGCCATCCTGGAGCACGCA[C/G]TGG AGAAGGAGGCCAAGGGCGCCGCCGAGATCGG
TP8088	7H	58.22	morex_contig_37191	TGCAGAGTGAAGCAGTGACTGCATGTACTGGAGGT TGGCA[G/T]CCTGGGCTGTCTGCTCTTGCAGC
TP11347	7H	58.22	barke_contig_349158	TGCAGATTCTGCCGATCCGTCAAA[A/G]GAATCGTA TGCCGCGGCAGAGGATTTTTTCTGCCATCA
TP13726	7H	58.22	-	TGCAGCA[C/T]CAAATAGGATTTGCCCCGAAAGAGC GTCATATAGGTGCTCCCTTCCAAAAGATCCC
TP14040	7H	58.22	morex_contig_54207	TGCAGCACCGAACTGGATGCGTCGTTGGTTGCATGA GGAAGTTGCAGAAATGGTGCCT[C/G]TCATC
TP16541	7H	58.22	barke_contig_15520	TGCAGCAGCCAGCCAGCCAGCCAGACAGCAAAAAA T[C/T]AGTTCAGGACTAGTCGATCAAGAATTG
TP18066	7H	58.22	-	TGCAGCAGGGAGCAA[C/T]GGCAATGGCGTCGCGGT GAAGCAGCAGCAGCAGCAGCAGCTTGGAGGC
TP18924	7H	58.22	-	TGCAGCATACGCGCCTCCGCC[A/G]CCGTGGCTCGC CTCACTGGCCCCGCTCCACAGCAGCGGCCCC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP21345	7H	58.22	bowman_contig_1223400	TGCAGCCAG[C/T]GGTACTACCGCCAGGACCACAGC GGTACTACCGCCGAGATCGGAAGAGCACACG
TP37684	7H	58.22	barke_contig_681542	TGCAGCTTCGTCCTCCACTGTGAGGACAA[A/G]TTA CAATGATGATATCGTGCCACCGAGATCGGAA
TP39018	7H	58.22	morex_contig_54207	TGCAGGA[A/G]CCATTCGTCGAGATACCCGATGAGA AAATCCGAGATCGGAAGAGCACACGTCTGAA
TP41965	7H	58.22	barke_contig_328005	TGCAGGAGCTTGTCTGCCACGCCCCAGCAGCCGCGC AGGTC[C/G]AGGAACTTGAGGTCGTGGCACC
TP42029	7H	58.22	bowman_contig_1322559	TGCAGGAGGAGATGGCCAAAACCTGCGGGGCGTG GAAGCGGAAGCCGCCAGGATGG[C/T]GGCACA
TP44480	7H	58.22	morex_contig_1574953	TGCAGGCATAGATAGGGGCTATGG[C/T]GGATGCCT CATCTGAAGAAGCAGCGCCGTGGCCGCGCAC
TP50294	7H	58.22	-	TGCAGGGCA[C/T]CGAACCTTTAGCAGCAAAATAGC AGGTGTCAGTCATATGCATTTCGGAGGCAAGG
TP53014	7H	58.22	-	TGCAGGGTGGATCCGCGTCCA[G/T]CTCCAGCTCCA ATCCACGGTGAGCGGGTCGGCCGAGCCGAGA
TP55742	7H	58.22	barke_contig_68005	TGCAGGTGCAGAAAAAAGCATCATCTTTCTACCCAA AAAAA[A/C]CCCCGAGATCGGAAGAGCACAC
TP61211	7H	58.22	morex_contig_48455	TGCAGTCTGCGGTCTGCACCC[A/G]TCACCGTCAGTC ATCGCACAAACGATCGGATCGACAGTGAGCT
TP35956	7H	58.22	barke_contig_2289641	TGCAGCTGCGATGAGAGGAAAGGAATGACCC[A/G] CGAGATTCTGTTGACCACATCGAACGAGCGAC
TP49448	7H	60.07	morex_contig_137938	TGCAGGGAAGAAGCGGTGTATATGGA[A/C]CCAAGC AGCATGGTTCGATGGATGGCAGACGTCGTGC
TP34122	7H	62.72	barke_contig_395800	TGCAGCTCCTCCAGCATCTGCTGGCCTACATGGAAT G[A/G]CTTGAAATGTTTCAGCAAACCTCTAGGA
TP49703	7H	62.72	-	TGCAGGGACTAATGGAAGCGA[C/T]GTTTTTGTATG CAGACCACGCAAACGGCCAAAGGGAAGGGGA
TP8699	7H	63.29	barke_contig_265380	TGCAGATAGCAAAAAAGTTGC[C/T]ACTCCCAGAGA TAGCCGAGATCGGAAGAGCACACGTCTGAAC
TP15206	7H	63.29	-	TGCAGCACTT[C/T]GAGCGGGAGCACACGACAAGG TGCGCGGGTGGGTGGGGTTCTCCGTGCGCCT
TP24370	7H	63.29	morex_contig_2045184	TGCAGCCGTGTCAAGTTGCAGGCGTTTGCCACCTC TATGGCG[C/T]AGCGCAGCGCAGGAGCAACA
TP27242	7H	63.29	barke_contig_484159	TGCAGCGCCAAATCGGATTTGCCTTTCCCCAGTCGA AGGATATCCTTA[C/G]GTCCTGGCCCAGCT
TP51084	7H	63.29	-	TGCAGGGCGCGAGCGGGCGGCCGAGAGGCACTTG TTGGGCGCGAAGTGC[C/T]TGGGGCCGAACCT
TP53007	7H	63.29	barke_contig_1781877	TGCAGGGTGGACTGGCATGGCACGGACATGCATGT GGCGT[C/G]CGTTATTAACTGATTGATCCAC
TP59843	7H	63.29	barke_contig_281461	TGCAGTCATATTGG[C/G]TTTCCTCGATCGCACGTCA GCACCTCATCGTTAGTTCAACTCCATGTAA
TP61845	7H	63.29	barke_contig_1785894	TGCAGTGCAACCCACTTGATTG[C/T]CAGCAACTGG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				TCGCTGGAGCTATCACCAATCACGAGCCACC
TP58516	7H	63.29	-	TGCAGTACGTAGA[C/G]CAGCCGAACAAGGAGAGC AACACGTGAGCGGCCACAATAGGCTGGAGGAG
TP28221	7H	64.59	-	TGCAGCGCGAAATAAGATTTCCCA[G/T]TTGGAGCC AGTACCGAGATCGGAAGAGCACACGTCTGAA
TP55815	7H	64.59	barke_contig_1810563	TGCAGGTGCATACACACCGCGAGTGGGAC[C/G]TGA TAAGCATACGAAGGACAAGAAGTGGACAACC
TP8213	7H	64.59	morex_contig_50040	TGCAGAGTGTGAA[C/T]CTTGCAGAGAGCATTTTAC AATATTACTGGGTCTGAACTAGACGGTACCC
TP42518	7H	64.59	barke_contig_269315	TGCAGGAGTCGGAAGTTACAGGAGCAGAGACGGA TGGGGTAGGTGATTGGCCGAGTGGCT[C/G]AG
TP22938	7H	67.19	bowman_contig_1305932	TGCAGC[C/T]CTCCTTAGTCTTTTCTCGATTGCGCGG TATTGTTGGATTGAAGTGGTCTGGACCAAC
TP36669	7H	67.19	morex_contig_160365	TGCAG[C/T]TGGCCTTGTTTCAGACATAATAACGTAAT GAGCAGGTGTATCTGAGGTTACACAGTTGG
TP42798	7H	67.19	bowman_contig_865093	TGCAGGATCACCTTCTCGTGATCGGACGT[C/T]GAA GACGATGAGGAACTCGAAGGCTGGAGCTGCT
TP44977	7H	67.19	bowman_contig_862842	TGCAGGCCAGTACGATCAAAA[A/T]CCTATTGCCAT GAATTACATTTCACTTATTAGCTGTACGACT
TP63191	7H	67.19	morex_contig_48256	TGCAGTGGTCGACCCATGAGGTATGCTATTCGGTAC CAACACTTCATTCTCAACATAAGGTT[G/T]T
TP39842	7H	68.49	-	TGCAGGAATCTCGTAGACGGGTTGTTTGCT[G/T]CCT AGAATCTCGGCAATGAACCGAGATCGGAAG
TP40897	7H	68.49	morex_contig_2553047	TGCAGGA[C/T]GTAAGAGGACCGTTCAGTTCATGCT GAGTAGCAGTTTTTACCACCTTTTAATTTA
TP53452	7H	71.09	morex_contig_1567895	TGCAGGTA[A/C]GGAAAATCACATTATCAGTTCGTG TTTTGCAGCTGTGGATGCTTGTGGCCTTTTC
TP8704	7H	71.09	bowman_contig_866777	TGCAGATAGCACTAGTGCACCTGATCCTCTTTTCTT[C/T]CCCCCTACTGCTGCCGTTCTGTTCTGA
TP16092	7H	71.09	bowman_contig_270877	TGCAGCAGCACGTCCACCAT[A/G]TCCCTCGCCGCG AAGCTCTCCCCTTCCATTGCGCCGAGATCGGA
TP18054	7H	71.09	morex_contig_42803	TGCAGCAGGGACAGCGTACACACTGCGCGCAC[T/C] ACGCGCAGGACAGAGGAGGGGGCGCTTGCTT
TP34869	7H	71.09	morex_contig_157691	TGCAGCTCGTCGATCACCGCACGGCCGCCGCGTGG ATGCAGAAGTGCTCGAACGCCATGCG[A/G]A
TP38417	7H	71.09	bowman_contig_1981570	TGCAGCTTTGGATGGTG[A/G]CGCGACGGCGCCACG ATGGTGGCGGTGCACCGACGTGGAAGGATCT
TP55342	7H	71.09	barke_contig_1854775	TGCAGGTCTGTAACGCATGCATGGTCCGAGCA[A/C] CCGAGATCGGAAGAGCACACGTCTGAACTCC
TP30771	7H	72.39	-	TGCAGCGGGATCCCGCGAGGCGGCTA[A/G]GGTACG CAGGCGGCGCCGACGAGATCCGAGATCGGAA
TP3256	7H	73.69	morex_contig_50681	TGCAGAAATGTCAATGGTACGGGCGTA[C/G]GGCATA CCTGCACGGTATGAACGAATGTCAATGGTGC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP11089	7H	73.69	barke_contig_1781940	TGCAGATGTTTATGGAGAACGATGGAAGTTGTGAG GA[C/T]ATGGGTCCTCGTGCTTTCCCAGATC
TP12266	7H	73.69	barke_contig_1854775	TGCAGCAACCACA[C/T]GTGTCTTTCGTAAATCATGC ACCGAGATCGGAAGAGCACACGTCTGAACT
TP17492	7H	73.69	morex_contig_101827	TGCAGCAGGAACACCTCCTCCTCCATTGCACGTGT[C/T]GACTCGATGACCTTGTGGCTGCTGCGCG
TP18473	7H	73.69	morex_contig_1559127	TGCAGCAGTAATCGGTGTCAATG[C/T]CACTATAAC CAACAATGTCTATAACACTAAGCTCCCTAGC
TP23633	7H	73.69	morex_contig_343347	TGCAGCCGCCCCGCACCACCCATGAGCC[C/T]AACT CCCTCCTCAATGCAGCCGACGGGAGTGGA
TP32654	7H	73.69	morex_contig_62319	TGCAGCTACACTGCACCACACTCCACCCTCCTCACC AACTACACAACCA[G/T]GCAGTTGCACGCTC
TP38559	7H	73.69	barke_contig_318169	TGCAGGAAAACAGGCACATGTTTGATCTTGTTATCA GTGATGT[A/G]CACATGACAGACATGGATGG
TP39236	7H	73.69	bowman_contig_849108	TGCAGGAACTTCCAAGCCCAGCATCAAGAATCTAA TGGTCCCTGCTTCCACTCCACC[G/T]CCACCT
TP43513	7H	73.69	barke_contig_1781940	TGCAGGATTCCATTCTCATCTTCCT[C/T]GCTGTGCC TGGTGCGCCACCAATGCCGATGAGTGTGCT
TP43794	7H	73.69	bowman_contig_855915	TGCAGGCAATCAAC[C/T]CATAGAGCGACAGTGTGA ACCAACGCGGTTTCCTCAGTAATCACACGGC
TP46236	7H	73.69	morex_contig_158676	TGCAGGCCTAGCAAGCTAGCTAGCTAGTGGCCTACT ACAGAAAACATA[A/G]GTCTACCTAGTAGAG
TP47548	7H	73.69	-	TGCAGGCGCTTGTGCAG[A/G]GTCTCGAAGCCGCGC AAGTCCTCCTTCAAAGCCTCCACGTCCGAGA
TP49402	7H	73.69	bowman_contig_1487581	TGCAGGGAACAGGAACCGTGAGCCGCGGCTGACTC GGACGGAGAATCTATCCGTTCCGA[A/G]CGGG
TP54288	7H	73.69	bowman_contig_862842	TGCAGGTCAGTACGATCAAGAACCTATGAATTGTGT TTTATGAGTATGTG[C/T]TCTGTCTGCCGAG
TP56918	7H	73.69	morex_contig_40019	TGCAGGTTACCATTAGGGACGTAGTTGTAGAGCAA GAGCTT[G/T]ACAGACTTGTTGAGCAGTAAC
TP60554	7H	73.69	morex_contig_70903	TGCAGTCGCACACCACCGTGACACCGACTGCACC GACGA[C/G]TCCGAGATCGGAAGAGCACACGT
TP62108	7H	73.69	barke_contig_317578	TGCAGTGCCAC[C/T]AGGTAGCGTGTGTCATACCAT ATGACGTGCCTGAGGACTGAATCCCACCGAG
TP66056	7H	73.69	bowman_contig_859124	TGCAGTTTTG[A/T]CAATTCTTTTTGGGATTTCGTAGT ACGGAATCCCTGGATAGGGGTTTGCTTGCT
TP17765	7H	73.69	morex_contig_138415	TGCAGCAGGCCAAACTTGAGTTGCAGTTCTTTTTTG A[A/G]GGATTGCTCACTTTTTTTAGTTCTTT
TP65273	7H	73.69	bowman_contig_896268	TGCAGTTGGCCGCCTACGTCACCCTCTGCGAGG[A/G]]CTTCCAAGGGATCGAGCCGCGCCTGGACCT
TP4996	7H	74.99	bowman_contig_142178	TGCAGACGCTCCGTTTCG[A/T]TGTTAGGAAAACAC TCATCTGGCAGTTTAGCACCAGGTACCAAAT
TP6975	7H	74.99	bowman_contig_127825	TGCAGAGCGGGCAGCTGGAGTGGGAGGCAAGCCAC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				ATGTTCGACGCACTCGGTGTGGAA[A/G]CCGTG
TP10186	7H	74.99	barke_contig_338946	TGCAGATGAGA[A/G]GAGCAGCAGCAGCAGAAGAA GAGTTAAAAAAAAGTCAACACCACGATTACAA
TP15693	7H	74.99	-	TGCAGCAGAGTTACATAGTAGC[A/G]TCCCGTCAGA CGTCGGCAAGATGCGGGGGTTTGACAACCA
TP15706	7H	74.99	bowman_contig_1179618	TGCAGCAGATAATGGGCTCCGTGCACAGTGCGAAA AGCAATACACA[C/G]AATATGCACTAGTAGAA
TP21751	7H	74.99	morex_contig_43876	TGCAGCCATGAGGGTAAAGAGTTGATATGA[C/T]CA AGTTTGGTGACTCTGCATATCGGGTGAACCC
TP50553	7H	74.99	bowman_contig_127825	TGCAGGGCCACCGTCGGCAAG[C/G]CCGACGCGTCG CAGGCGCTTACATCGACGAGTCTCCCTTCCC
TP62329	7H	74.99	bowman_contig_15910	TGCAGTGCGCGCACACCACGCCAGGC[G/T]CCACAC GCGGGAATGCGTCCCGCATTTTCAGCTTTGTT
TP62566	7H	74.99	morex_contig_2547915	TGCAGTGCTTCACCATCAGCAGCACCACCACCA[C/G]]CAGCAGCAGCATCACGTCGTGGACGAGCAC
TP63022	7H	74.99	barke_contig_1837716	TGCAGTGGGACACTTAGCGGATAA[C/G]TGTGCGTC TCGTTTCTGCACAACTTTAACCATTTTGAC
TP65515	7H	74.99	bowman_contig_291120	TGCAGTTGTTGACCAGTCCCATGACCTCTCCGAAGT C[A/G]GCCAGGATGGCACTAGTAGAAAAGAG
TP37759	7H	74.99	-	TGCAGCTTCTCGCTGGCCAGCACCTCCTGGCGCCCG CAAGCTGTGCTTGC[C/G]TGAGCTTGCACTC
TP7689	7H	74.99	morex_contig_61296	TGCAGAGGGAGATAGGCAGGTCCAGTTTATCG[T/C] GCCCCTGTGCGTTTGCCCAACAATTTGATAC
TP29775	7H	74.99	-	TGCAGCGGATTTGCTATCATTACCCGATAGATTGA TAGATGCTAGT[C/T]CCGAGATCGGAAGAGC
TP45010	7H	74.99	barke_contig_71884	TGCAGGCCATCAACAAACAAAAACAGGGTAA[C/G]T AAGCAGTATTGGACTCTGATTCTTCTCTCG
TP45323	7H	74.99	bowman_contig_291243	TGCAGGCCCCGA[C/T]GCGGTCTCGAATATGCCTAGG ATGCCCTTACAGCGAGCACCTCATCCATCT
TP19444	7H	74.99	barke_contig_2793114	TGCAGCATCTCGCGTGGTCACCCTCGATCACCGC[C/ T]GTCAGGCGCAGCGGCTGCCAGTGGAGAAG
TP33415	7H	74.99	bowman_contig_145211	TGCAGCTCACCGAAGAGGACGCAGAGGCTGCCAAC ATCAGTGGTAAGATCA[C/T]CGATGGGATTGG
TP59818	7H	74.99	barke_contig_2781556	TGCAGTCAGTTCTCAAATGTTAT[A/G]TACTGCCTTA AAATATATTTTAGAATCACATGAAGAGAGG
TP6362	7H	76.28	bowman_contig_879126	TGCAGAGCAAGCAGCAGCGAACGAGGCGGGCATCC ATGGACGT[A/G]CGGCGCGTTCTCTCGATACG
TP3304	7H	77.26	morex_contig_56831	TGCAGAATTCAA[C/T]ATGAAGATACATTAGGACCA ATATCTGGAAATGTTGCTTCAGTCTGCTGCA
TP48571	7H	84.19	bowman_contig_1983479	TGCAGGCTCCAACTTTGCCCCGATGTCGTGTA[C/T] CTTGGTGGCATGTAACAACTCTATTCTCC
TP2529	7H	90.73	barke_contig_2787307	TGCAGAAGGCCCTTTATATGCCTGCAAAAATAATC[G/ T]CCAGTTTATGGTTTTGTGTGAAAAAAGTG

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP10725	7H	90.73	-	TGCAGAT[G/T]GCAGGTGCCATTGACGTTGAAATCA AACAGTTCGTAAGCAGAGCGGCGACATACGT
TP22582	7H	90.73	bowman_contig_857366	TGCAGCCCGAATAAGGTTTGTGCCCCAAATTATAAA ATTTAACTCTAAGGTAATGCTTCCGA[G/T]
TP31140	7H	90.73	-	TGCAGCGGTACTACCG[C/T]TGATCCCATGGTAGTG CAAGGACACAACCGAGATCGGAAGAGCACAC
TP60511	7H	90.73	bowman_contig_11574	TGCAGTCGATAGGCCAGCTCTAGCTTTAGATCAAC TCGGGCCCAACTC[C/T]AGCTTCCGATCGAC
TP26119	7H	92.02	morex_contig_39091	TGCAGCGAG[A/G]ATCAAGAGGAGAGGAAGAGCCT GGCGATGCCTGGTTGCGTGCTGCGTGCGTCTG
TP24997	7H	92.02	bowman_contig_869648	TGCAGCCTGAGGGAGCGGCGTTTCGGGAACCTACCTC ATACAGTACGCCTTAGC[C/T]CTGGTGCTGAA
TP860	7H	92.02	morex_contig_83111	TGCAGAAATTGGGTAGTAGGC[C/G]GTGTGCTCATA CTTTTGCACACTTGCAAAGAAACTCGACAA
TP8249	7H	92.02	bowman_contig_63887	TGCAGAGTTATGCCAAGGGCACCGTGGAGGACTCT GCTCGCTGACTGT[A/C]TCTGCTGGCAGCTGA
TP11682	7H	92.02	bowman_contig_946769	TGCAGATTTTAGTTTCAATA[A/C]TTCGCAAACCAGA TCAGTAACATTGAGATGGCTCAGATAGGAA
TP15356	7H	92.02	-	TGCAGCAGAAGCACGCTCTGCTGCTTCGTCGATGTT CAGAGTGCAGACTACTCTCCACTGTTA[A/T]
TP46245	7H	92.02	morex_contig_57291	TGCAGGCCTCAAGTTTTGTTTTTGGCATGTGATAAC TAGGGTTGCTG[C/T]TAGACAAGGAAGATCG
TP55063	7H	92.02	bowman_contig_70129	TGCAGGTCGG[C/T]GGCGGAGACTGGCAGCCATCAC ATCCGAGATCGGAAGAGCACACGTCTGAACT
TP4849	7H	93.29	barke_contig_1806244	TGCAGACGCAGTGCCGCGCGAA[A/C]ACAGCAAAC ATTTCTTCTAGTTAATCACCAGAAACACGAA
TP32029	7H	93.29	-	TGCAGCGTGCCAGCAGCGGCGGCGACATG[A/G]CGA CGGAGCCGAGATCGGAAGAGCACACGTCTGA
TP38324	7H	93.29	barke_contig_1800968	TGCAGCTTTAGTA[C/T]TATTCATCACCATGTGGTAA GTTCCGCTCACTCAAGTTATTGTTGGCAGG
TP38352	7H	93.29	bowman_contig_75231	TGCAGCTTTCCTGCTAGCCGAGGTACGAGGGCTTGG GGCAGGTCGATCTAGGGTGTGCGGCGG[C/T]
TP19	7H	95.86	morex_contig_302433	TGCAG[A/G]AAAAACGAAAGCGACTTCGACGAACA CGGGACGCTGTCGACTGTCTGATCAACACATG
TP31899	7H	95.86	bowman_contig_62443	TGCAGCGTCTTCATCTGCCCGACCTCTCG[C/T]GGGA TCGCGCCGAGATCGGAAGAGCACACGTCTG
TP37594	7H	95.86	morex_contig_1572438	TGCAGCTTC[C/T]TGGCGAACCTGCACAGGCACCGC CTCACC GCGTGCCCCTTGGGCGCGGCCGCGT
TP41029	7H	95.86	barke_contig_2786562	TGCAGGACTGAATCCTAAACAAAAAATAGTTGG[G/ T]CCACGCTGGAAAAATTGCAAGCAGTGCGCC
TP61791	7H	99.93	bowman_contig_12253	TGCAGTGATGTGATAA[C/T]AACAATATCAGCAGAA TTAGAACAGTTACACAAAAACACTGAAGTCG
TP35770	7H	100.78	bowman_contig_2078905	TGCAGCTGCCAAATTGTACCACCA[C/G]ACCCTAGC

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				TGTGCCTCTAATCCTCTACAACCTCCGTCGAT
TP1246	7H	107.64	morex_contig_58412	TGCAGAACCCGACGCTAG[A/G]CTCGTACTGTATGT GGTACACCGTGTGGCGGGCCGAGATCGGAAG
TP16772	7H	107.64	bowman_contig_958852	TGCAGCAGCGCACTGCTCTCCTGGCCACGGCGAGG CCCCGCGGAGGCGGCGGAGCT[C/T]GGACGAT
TP19933	7H	107.64	morex_contig_38701	TGCAGC[A/G]TGTCGGCGGCCACGAGGCGGCCGTTT ATGGCGTAGGGGTCGTTGGTGGAGACCAGGT
TP22896	7H	107.64	bowman_contig_66971	TGCAGCCCTAGCTAGAGGCCCATC[A/C]CCATCCG TCATAGCTGCTTGCGACAAAGCCGTCGGAAC
TP23249	7H	107.64	-	TGCAGCCGAGCAAGCAAAGCGAGGGGAAATCCTAT TTAGCGTCACAGG[C/T]GCCGAGATCGGAAGA
TP29882	7H	107.64	morex_contig_76302	TGCAGCGGCAGCAACCTCGTCGAGGACGCGCGCAT AAGCATCACTCCTCCGAGCGGACCTC[A/G]GC
TP32444	7H	107.64	bowman_contig_147432	TGCAGCGTTGGTGCTACCCTATTGCAGCTTCACCT[A /G]TTGCCGAGATCGGAAGAGCACACGTCTG
TP36198	7H	107.64	morex_contig_60065	TGCAGCTGCTCGCACCCCCGTGCTCGACCGAGGCTG TCGCTGTTGCTCGCGCCCCCGTGC[A/C]TGG
TP41643	7H	107.64	bowman_contig_10186	TGCAGGAGCCATCGTGTTTGCAAAGAAA[C/G]TGCG GAGAAAGCCGTGCACATTAGATGCCGACAAA
TP48444	7H	107.64	-	TGCAGGCTAGTATTTTCATTTTTTGTATTGTTGGCCT GGTAGGA[A/G]ATAACCGAGATCGGAAGAG
TP56311	7H	107.64	bowman_contig_1982368	TGCAGGTGGCAAGCCAGGTGATAAACTGGCTTCAC GAGGAGACACAGGTCCTGGGGATGAGCG[C/T]
TP62093	7H	107.64	morex_contig_83798	TGCAGTGCATTATAA[C/G]ACGATTACTACAAAACG AGAAGAACTGAAATATTACGCCTCGAGCGC
TP26585	7H	110.23	-	TGCAGCGATGAAGAGCGGCACGGCGGCGCTCCATT GCAGCGT[C/G]GACGCAACCGAGATCGGAAGA
TP37776	7H	110.23	barke_contig_119580	TGCAGCTTCTG[A/G]TCTTCACTTTCTCGTGAATTTG TATGTGGTGAAGAAGTTGTATACAGCTCGC
TP41023	7H	110.23	-	TGCAGGACTCGGCAGCCAACACGACGGAGATCCTG AT[C/T]CATACACGAATCCGAGATCGGAAGAG
TP47373	7H	110.23	morex_contig_83798	TGCAGGCGCTCTCGAGGGAGCAAGAAGGATAGGGA CAAG[A/C]AGAAGATAGCCGAGATCGGAAGAG
TP28351	7H	118.07	-	TGCAGCGCGAGCTTCCTGTAGTTCCAC[C/G]CCGTGT AGGCCTCCGAGATCGGAAGAGCACACGTCT
TP32265	7H	118.07	morex_contig_158332	TGCAGCGTGTCCGCGTCACGATTCAAAGCGGTGGTG CCCGTCAGTCAGGCTCCACGATGGG[C/T]GG
TP52533	7H	118.07	morex_contig_43850	TGCAGGGTAAATTGAGCAGGAAATTACAGCGGTTA TG[C/G]GAACCTCCGAGATCGGAAGAGCACAC
TP62533	7H	118.07	morex_contig_158332	TGCAGTGCTGCTGCGGAGGCAGGGGAAGGAAGGAA GGT[A/G]GGCAGGGGGAGTCCGAGATCGGAAG
TP24955	7H	120.35	-	TGCAGCCTGAAGCTCCTTCGTCCGCCGCTTTGGGTG ACAGCTC[G/T]TGCAGTGCTTCCGTCCCGAT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
TP14866	7H	128.55	morex_contig_212778	TGCAGCACGGTGGTGAGCCTGGGTTTTCTGTATCTT CTCAACAGGAGCGA[A/G]GAGCACACCACGC
TP53737	7H	128.55	bowman_contig_201101	TGCAGGTAGACACCAACACACACCACCGTTA[A/G]A TGAATGATCCAGCTCACGCGCCGCCGTTGAA
TP55582	7H	128.55	barke_contig_2782945	TGCAGGTGAGGTGATGGAGGGGCACGTTAATATAT TCA[G/T]GTGGTTCAGCTGGCCGCGTGATCCA
TP29488	7H	129.85	barke_contig_57841	TGCAGCGCTTTAATCCATATAATAGTTTT[C/T]GGTA TTTTGATAGCCTCTCCGAGATCGGAAGAGC
TP39245	7H	129.85	morex_contig_62194	TGCAGG[A/G]ACTTGCCCGTGGGGAAGCTGACGGCG AAGGAGAGGGGGCCGAGATCGGAAGAGCACA
TP56832	7H	131.08	barke_contig_410719	TGCAGGTGTTGCCGCACCGCATGATCGATGTGGACG TACGCTGAGTGAATGAACGC[C/T]GTCATTC
TP63570	7H	133.75	-	TGCAGTGTGTTGTGCGCTACTAACA[A/G]CAGGAGC AGCACGGGTCGGCCACGAGCGGGAGCGGCAG
TP7367	7H	133.75	morex_contig_1560296	TGCAGAGGAGCAAATCAATGGACGGATCGGAGCGG TGGCA[A/T]TGGCACGTACCCCTGGCCGTCT
TP22215	7H	133.75	morex_contig_132551	TGCAGCCCCACCGTCTGCTCGCGTCGCA[G/T]CCCCT CTGCCTGCTCGCGCTGCCCCGCCACCAGCT
TP22538	7H	133.75	morex_contig_38058	TGCAGCCCCTGTCCCA[A/G]TCGTCCAGCAGCACGT AGAGATGCTGCTGCTGCCGCCGCTCGAACGG
TP30904	7H	133.75	morex_contig_38226	TGCAG[C/T]GGGCTGGCAACTACACCGCCAGCACCC AGCCGCTCGTCGCCGCTCCCCTGACTCCCGA
TP38574	7H	133.75	morex_contig_53679	TGCAGG[A/G]AAACGGGGAGTAGGTGCTGGACGAG CTAGGGTCGAAGAGCGGGTCCGCCTGCGGGTG
TP46524	7H	133.75	barke_contig_274885	TGCAGGCGACACCAGACAAAACGCACGCAAGACCA TTGCTACATACAGGGGCTGTTGCCGATT[G/T]
TP46616	7H	133.75	bowman_contig_860394	TGCAGGCGAGCTTGAATGCCT[C/T]CCGACGTGGCT ACGTACGTACGTACCTACGTACACGACCAGC
TP46642	7H	133.75	barke_contig_274885	TGCAGGCGAGGTAATGGAATTCCTAAGCTCATTGC GTCAAGATGTC[A/G]CTGTTTCACAACCTAGC
TP48418	7H	133.75	-	TGCAGGCTACGTG[C/T]CTGGCCAGCTACACGCACG GATGGCGTGTGACCGAGATCGGAAGAGCACA
TP49474	7H	133.75	morex_contig_38941	TGCAGGGAAGC[G/T]ATTCTTTGAGGAATTGGATAG AGATGGTGATGGCGAAGTTACCCTAGGTCTC
TP51639	7H	133.75	barke_contig_2152046	TGCAGGGCTTTTGGATCGCCAGAGCAATGCCATCCG AGATTCCCAC[A/G]GGGGAACCTGTGTGTACA
TP57226	7H	133.75	barke_contig_57104	TGCAGGTTCTGCTTCAGGTCTCCCAGGCACTCTATC AGGAAGTGCGCCCTCAATGCTGCCACA[A/G]
TP63213	7H	133.75	-	TGCAGTGGTGAGCATG[C/G]GCGTTGCCCTGTTATC ACGCCGAGATCGGAAGAGCACACGTCTGAAC
TP64696	7H	133.75	bowman_contig_9692	TGCAGTTCTGCCTGACA[C/T]GACACCATCATTTAGA AGTAGATGACGTCTCATCAACTGTATCCTC
TP5326	7H	133.75	morex_contig_54769	TGCAGACGT[A/T]GTACTCTAGTATTGAACTATTGAT

Marker_ID	Chr.	cM	Barley_Contig	Sequence
				CATGCGTCTTGGAGCATCTCCAACCTCAAC
TP7943	7H	133.75	morex_contig_63520	TGCAGAGT[A/G]ATCTTCAAACCTTACTTGTGCCACA ACCACAACGGTCGTCGTCGTTGCCTGCCTCT
TP36934	7H	133.75	barke_contig_662270	TGCAGCTGGTGATGAAGAGCGGCAAGTACAC[C/G]C TCGGCTACAAGACCGTCCTCAAGACGCTCCG
TP38302	7H	133.75	barke_contig_662270	TGCAGCTTGTTGTTGATGTTCTCCGTGCTCTTCTTCT GCACA[C/G]AGTCGGAATCGAGGTCCGTCA

SNP is shown in square brackets

Table S3 The primer sequences used to amplify SSR markers used in the genetic linkage map

Marker ID	Chr.	cM	Forward primer	Reverse primer
GMS021	1H	10.8	CTATCACACGACGCAACATG	CCTGAGAAAGAAAGCGCAAC
Bmac0213	1H	20.7	ATGGATGCAAGACCAAAC	CTATGAGAGGTAGAGCAGCC
Bmag0872	1H	31.6	ATGTACCATTACGCATCCA	GAAATGTAGAGATGGCACTTG
Bmac0032	1H	43.7	CCATCAA AGTCCGGCTAG	GTCGGGCCTCATACTGAC
Bmag0770	1H	45.5	AAGCTCTTTCTTGTATTCGTG	GTCCATACTCTTTAACATCCG
Bmag0211	1H	45.5	ATTCATCGATCTTGTATTAGTCC	ACATCATGTGCGATCAAAGC
Bmag0347	1H	46.9	CTGGGATTGGATCACTCTAA	AA AACAAGTACTGAAAATAGGAGA
Bmag0718	1H	47	ATCGTGACATCTCAAGAACA	CCTGATACTGCCTAGCATTAG
HVM43	1H	53.4	GGATTTTCTCAAGAACACTT	GCGTGAGTGCATAACATT
EBmac0501	1H	70.9	ACTTAAGTGCCATGCA A AG	AGGGACAAAAATGGCTAAG
EBmag0793	1H	98.2	ATATATCAGCTCGGTCTCTCA	AACATAGTAGAGGCGTAGGTG
Bmag0222	2H	28.5	ATGCTACTCTGGAGTGGAGTA	GACCTTCAACTTTGCCTTATA
GMS002	2H	46.2	CCGACAACATGCTATGAAGC	CTGCAGCAAATACCCATGTG
HVM3	4H	0	ACACCTTCCCAGGACAATCCATTG	AGCACGCAGAGCACCGAAAAAGTC
HVRCABG	4H	8.2	ACACCTTCCCAGGACAATCC	CAGAGCACCGAAAAAGTCTGTA
EBmag0781	4H	9.4	CTATTTTCTAATGCTTGGACC	TGTCTAGTTCATCATCATTGC
Bmac0181	4H	9.4	ATAGATCACCAAGTGAACCAC	GGTTATCACTGAGGCAAATAC
Bmag0375	4H	9.4	CCCTAGCCTTCCTTGAAG	TTACTCAGCAATGGCACTAG
EBmac0906	4H	17.5	CAAATCAATCAAGAGGCC	TTTGAAGTGAGACATTTCCA
HVM07	5H	15.9	ATGTAGCGGAAAAAATACCATCAT	CCTAGCTAGTTCGTGAGCTACCTC
Bmag0337	5H	23.4	ACAAAGAGGGAGTAGTACGC	GACCCATGATATATGAAGATCA
Bmac0096	5H	25.4	GCTATGGCGTACTATGTATGGTTG	TCACGATGAGGTATGATCAAAGA
Bmag323	5H	27.2	TTTGTGACATCTCAAGAACAC	TGACAAACAAATAATCACAGG
Bmag0005	5H	30.9	TCCATGATGATGTGTGCATAGA	CGGATCCCAACA A ACACAC
Bmac0113	5H	32.2	TCAAAAGCCGGTCTAATGCT	GTGCAAAGAAAATGCACAGATAG
Bmag0121	5H	34.7	ATAAGATAGGTCACCGCAATA	AGTAGTTC AATACAGACCTACAGG
Bmag0387	5H	43	CGATGACCATTGTATTGAAG	CTCATGTTGATGTGTGGTTAG
EBmac0557	5H	93.4	ATGCATGTGTAGATGTAGATGTG	AACAAGGATA A ACTAACATGGG
EBmac0615	5H	108.8	AATTGGTTCGAGTCATAGCT	CTAGTGGGTGTATGCAAGTG
EBmatc0054	5H	129.3	TGACCACCATTGTGAGACAG	AGTGGTAGTGGGAGGAGGAG
Bmac0040	6H	0	AGCCCGATCAGATTTACG	TTCTCCCTTTGGTCCTTG
Bmag0500	6H	20.3	GGGAAGTTGCTAATGAAGAG	AATGTAAGGGAGTGTCCATAG
Bmag0120	7H	0	ATTTTCATCCCAAAGGAGAC	GTCACATAGACAGTTGTCTTCC
EBmac0764	7H	7.8	AGAATCAAGATCGACCAAAC	AAA AACATGAACCGATGAA
Bmac0167	7H	18.3	CATTTCCACTTCAAAATATCC	CCAAAGTTTGAGTGCAGAC
Bmac0187	7H	22.5	GCTCTCTCTCAGAAAAATGAA	GAATTATTCTAGGGCTGTGAA
GBM1464	7H	32.8	ATAGCCGTGCTCTTGCTCAT	CAAGACCACCATTTCGATTG
Bmag0010	7H	38.8	AGTAGTTCACCTTGGGGCT	AGCACGTGATACATCAAGAACG
Bmag0914	7H	46.1	GGGCAATATACAGTTCAACTC	ATGAACTGGAGGCAGTAAATA
AF022725A	7H	61.1	AGTATGGGGAATTTATTG	GCTGCAAAGTATGACAATATG

Primer sequence were either obtained from the following databases

<http://www.genetics.org/cgi/content/full/156/4/1997/DC1>, http://germinate.scri.ac.uk/ssr/barley_s.html,

http://bioinf.scri.ac.uk/ssr/ssr_table.html

and <http://wheat.pw.usda.gov/cgi-bin/graingenes/browse.cgi?class=marker>

Table S4 The annotated genes within the QTL marker interval between TP18054 and TP11089

Gene	cM	Description
MLOC_22078.1	68.06	Heat shock protein DnaJ, N-terminal
MLOC_5322.3	68.06	Cellular retinaldehyde-binding/triple function, N-terminal;Cellular retinaldehyde-binding/triple function, C-terminal
MLOC_63870.4	68.06	Zinc finger, CCCH-type;Zinc finger, C3HC4 RING-type
MLOC_37511.2	68.41	Helix-loop-helix DNA-binding domain
MLOC_74450.1	68.41	Serine-threonine/tyrosine-protein kinase
MLOC_43588.1	68.84	Glycosyltransferase AER61, uncharacterised
MLOC_69030.3	68.84	Aminotransferase, class V/Cysteine desulfurase
AK360719	69.11	Multi antimicrobial extrusion protein
AK371088	69.11	Ethylene insensitive 3
MLOC_14372.1	69.11	Peptidase C48, SUMO/Sentrin/Ubl1
MLOC_48422.3	69.11	C2 calcium-dependent membrane targeting;GRAM
MLOC_65913.1	69.11	Serine/threonine-protein kinase, active site;Serine/threonine-protein kinase-like domain;Protein kinase, catalytic domain;Serine/threonine-protein kinase domain;Protein kinase, ATP binding site
AK253105.1	69.26	Mov34/MPN/PAD-1
AK355136	69.26	ATPase-like, ATP-binding domain;Heat shock protein Hsp90;Heat shock protein Hsp90, conserved site;Heat shock protein Hsp90, N-terminal
AK369877	69.26	BTB/POZ
MLOC_3499.1	69.26	Pentatricopeptide repeat
MLOC_6357.1	69.26	Glycosyltransferase AER61, uncharacterised
MLOC_6476.1	69.26	Glycerophosphoryl diester phosphodiesterase
MLOC_65139.1	69.26	Ribosomal protein L31e
AK356978	69.33	Fatty acid desaturase, type 2
AK359310	69.56	Zinc finger, A20-type;Zinc finger, AN1-type
AK373386	69.56	Phosphofructokinase;Phosphofructokinase domain
AK373844	69.56	Pentatricopeptide repeat
AK374613	69.56	Aux/IAA-ARF-dimerisation;Transcriptional factor B3;Auxin response factor;AUX/IAA protein
AK375094	69.56	Short-chain dehydrogenase/reductase SDR;Glucose/ribitol dehydrogenase
MLOC_14286.1	69.56	Alpha/beta hydrolase fold-1;AB-hydrolase-associated lipase region
MLOC_18369.1	69.56	Pathogenic type III effector avirulence factor Avr cleavage site
MLOC_39328.2	69.56	FAS1 domain
MLOC_55370.1	69.56	Haem peroxidase, plant/fungal/bacterial
MLOC_55371.1	69.56	Glycoside hydrolase, family 19, catalytic
MLOC_60995.3	69.56	Ion transport
MLOC_64612.1	69.56	Zinc finger, Dof-type

Gene	cM	Description
MLOC_6490.2	69.56	Pentatricopeptide repeat
MLOC_6492.5	69.56	EXS, C-terminal;SPX, N-terminal
MLOC_6766.2	69.56	Protein kinase, catalytic domain;Serine/threonine-protein kinase, active site;Serine/threonine-protein kinase-like domain
MLOC_67834.1	69.56	Helix-loop-helix DNA-binding domain
MLOC_70730.1	69.56	O-methyltransferase, family 3
MLOC_75288.1	69.56	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding;D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
MLOC_80269.1	69.56	BURP
MLOC_80270.1	69.56	Nonaspanin (TM9SF)
AK355848	69.82	Heavy metal-associated domain, HMA;ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter;ATPase, P type, cation/copper-transporter;Haloacid dehalogenase-like hydrolase;ATPase, P-type phosphorylation site;ATPase, P-type, ATPase-associated domain
AK248860.1	70.13	Methyl-CpG DNA binding;Zinc finger, CW-type
AK249904.1	70.13	Transcription factor, MADS-box;Transcription factor, K-box
AK353608	70.13	DNA topoisomerase I, C-terminal, eukaryotic-type;DNA topoisomerase I, active site;DNA topoisomerase I, DNA binding, eukaryotic-type;DNA topoisomerase I, C-terminal;DNA topoisomerase I, catalytic core, eukaryotic-type
AK354984	70.13	NAD-dependent epimerase/dehydratase
AK358287	70.13	RNA recognition motif domain
AK361661	70.13	Uridine kinase;Phosphoribulokinase/uridine kinase;Phosphoribosyltransferase
AK362747	70.13	Zinc finger, CW-type;Methyl-CpG DNA binding
AK365423	70.13	Serine/threonine-protein kinase, active site;Legume lectin, beta chain;Serine/threonine-protein kinase-like domain;Protein kinase, catalytic domain;Protein kinase, ATP binding site
AK365615	70.13	Protein of unknown function DUF3546;Zinc finger, C2H2-like;Arsenite-resistance protein 2;Zinc finger, C2H2
AK366556	70.13	Twin-arginine translocation pathway, signal sequence
AK369089	70.13	Bromodomain;SANT domain, DNA binding;Myb, DNA-binding
AK372126	70.13	Rab-GAP/TBC domain
AK372300	70.13	DNA mismatch repair protein;DNA mismatch repair protein Mlh1
AK373688	70.13	Endonuclease/exonuclease/phosphatase;Inositol polyphosphate-related phosphatase;WD40 repeat
AK377123	70.13	Serine/threonine-protein kinase-like domain;Leucine-rich repeat-containing N-terminal, type 2;Protein kinase, catalytic domain
MLOC_13746.2	70.13	Ribosomal protein L32e
MLOC_13859.1	70.13	Mitochondrial transcription termination factor-related
MLOC_13932.1	70.13	No apical meristem (NAM) protein
MLOC_15839.1	70.13	DSBA-like thioredoxin domain