Gene ID	GeneID with exon and segment	Chromosome	Strand	Exon	Section	Primer 5	Primer 3	Nucleic Acids	Amino Acids	seroreactive
PFA0110w	PFA0110we2s2	chr1	+	2	2	AACGAAGCCTACCAAGTTTT	TTCATCATATTCTTCATTGT	1557	518	yes
PFA0125c	PFA0125ce1s2	chr1	-	1	2	AACAAAGAAATGTTATCTAT	ACTTGTAAATCTTTGTTTTC	2256	752	yes
PFA0410w	PFA0410we1s3	chr1	+	1	3	ATAATGAATTTTGGAGATGT	TATCTTTTTGTCGTTGGTCT	2256	751	yes
PFA0430c	PFA0430ce1s2	chr1	-	1	2	TTGATAATCCTAATTTTGTA	CAATTTGTTCTCCACGCTTT	1626	542	yes
PFA0510w	PFA0510we1s2	chr1	+	1	2	GATATAAAAGAGAAATTAAT	TGTTGAATGTTTTTTGTCGT	2292	764	yes
PFA0510w	PFA0510we1s3	chr1	+	1	3	AAATTTAATTTAAAAGATGA	CTTTATATATATCCTTATTT	2289	763	yes
PFA0725w	PFA0725we1s1	chr1	+	1	1	ATGGCTGTTAAAATAAGTAC	ATCAAAGGTTAAACCTGGAG	795	265	yes
PFB0115w	PFB0115we1s1	chr2	+	1	1	ATGTTAAAGAAATATATTAT	TGCGTCTGTTTCTTCTACTT	1818	606	yes
PFB0150c	PFB0150ce1s1	chr2	-	1	1	ATGAAGACGACAAAAGAAAA	GAGAAAAAAATAACTGCTTTC	1518	506	yes
PFB0300c	PFB0300ce1s1	chr2	-	1	1	ATGAAGGTAATTAAAACATT	TATGAATATGGCAAAAGATA	819	272	yes
PFB0305c	PFB0305ce1s1	chr2	-	1	1	ATGAATATATTATGTATTCT	GTCAAAATGTAATCTATTTG	516	172	yes
PFB0310c	PFB0310ce1s1	chr2	-	1	1	ATGTGGATAGTTAAATTTTT	ACCTGAATTTGATGAACTTG	486	162	yes
PFB0340c	PFB0340ce2s1	chr2	-	2	1	TGTGTTATATTTAACAAAAA	ATTTTCAGTAGTATCTTTTG	834	278	yes
PFB0915w	PFB0915we2s1	chr2	+	2	1	TCTGATATAAACAAGAGTTG	ATTATCTAAAATCGAACTAA	2268	756	yes
PFB0915w	PFB0915we2s2	chr2	+	2	2	TCAGAAGAAAAGGTTGATTT	TTTTGATTTTTGCGTTCTAC	2265	754	yes
PFC0130c	PFC0130ce1s1	chr3	-	1	1	ATGTCTATAAGAAATAGAGA	GAATCTACCATTTTTTACAT	1260	419	yes
PFC0210c	PFC0210ce1s1	chr3	-	1	1	ATGATGAGAAAATTAGCTAT	ATTAAGGAACAAGAAGGATA	1194	397	yes
PFC0425w	PFC0425we1s3	chr3	+	1	3	ATTTTAAACAACTTGGGTCT	GTGATATAAATCCTTAAAAA	2775	925	yes
PFC0440c	PFC0440ce1s3	chr3	-	1	3	CTTACTCAAGAAGGACATGA	CACTTGTCGATTTGTTCTCC	2304	767	yes
PFC0805w	PFC0805we1s2	chr3	+	1	2	TATGTTGGTTTTACTGTGAG	ATTTTTTACCTTGGACTTAA	2496	832	yes
PFC0810c	PFC0810ce3s1	chr3	-	3	1	AAATTAGATAAGGAGAAGAA	ACAATTTTCATTTTTTAAAC	2844	947	yes
PFD0310w	PFD0310we1s1	chr4	+	1	1	ATGAATATTCGAAAGTTCAT	AGAATCATCTCCTTCGTCTC	474	157	yes
PFD0380c	PFD0380ce2s2	chr4	-	2	2	TATTTTTCAAATGTTATAGA	CTTTAAAAAGTGTAGGGTTA	2220	740	yes
PFD0385w	PFD0385we1s2	chr4	+	1	2	ATAAGTAATCACAAGAGTAT	TTTTGAACTTTTTTTTTTTG	2967	988	yes
PFD0430c	PFD0430ce3s1	chr4	-	3	1	AATGATAAAAAAATAAAACA	CGATTCAACTCTACTACAAG	441	147	yes
PFD0995c	PFD0995ce2s1	chr4	-	2	1	AAAAAATCCAAATCTACTAT	TATATTCCATATATCCGATA	1305	434	yes
PFE0040c	PFE0040ce2s1	chr5	-	2	1	GATATCTATACGAATTGTGA	TTCTTGTTTTTCAATTTCTT	2106	702	yes
PFE0060w	PFE0060we2s1	chr5	+	2	1	AGGTCATATCCCAAATCTGG	AGTTAGTAATAAATTATGAA	1158	385	yes
PFE0090w	PFE0090we1s2	chr5	+	1	2	GAACAAGAAGAAGAAGAGGA	TTTCTTAGTATTTTGCGATA	1641	546	yes
PFE0465c	PFE0465ce1s1	chr5	-	1	1	ATGTACGATATAAATAAGTC	AGATATCAAAGAGTTCAATG	2880	960	yes
PFE0565w	PFE0565we1s1	chr5	+	1	1	ATGAACATGATTAATATTGG	CATAAATTCCTCTTGAATTT	1146	381	yes
PFE0570w	PFE0570we1s3	chr5	+	1	3	AGTGAAAGAATAAAATATTT	TTCATTAAAATCGGTAGCTT	2796	932	yes
PFE0830c	PFE0830ce1s2	chr5	-	1	2	AGAGATGATAATGTGGTTAC	ATTTTCGTACGCTTCGATTA	2442	813	yes
PFE1085w	PFE1085we1s1	chr5	+	1	1	ATGTCGGCTTTTGAAGAGTT	TATTTGAAAGTTCAACAATT	2526	841	yes
PFE1590w	PFE1590we1s1	chr5	+	1	1	ATGAGATTCTCCAAAGTATT	TTGTTCTTTTTTGGGTTCTT	546	181	yes
PFE1600w	PFE1600we2s1	chr5	+	2	1	AATGTACTTGTTTCTAATAA	TTGATTGTTAGAGACTTCAT	1329	442	yes

MAL6P1.237	MAL6P1.237e6s2	chr6	-	6	2	AAAAATTTCTCTTTATTGTA	CTTTTCCACTAATGATAATA	1932	644	yes
MAL6P1.252	MAL6P1.252e1s3	chr6	-	1	3	GGAGACTATAGAGATATATG	CTTTAGAAAAAAGTAACTGA	2079	693	yes
MAL7P1.146	MAL7P1.146e5s1	chr7	-	5	1	AATATCTTGTATAAATTGTT	ATTATTATCTTTTTTGTATT	1566	522	yes
MAL7P1.77	MAL7P1.77e1s1	chr7	+	1	1	ATGAAGGTGTGGGGAGCTTG	CTTTAACAAATCTTTCGATA	1434	478	yes
MAL7P1.92	MAL7P1.92e5s1	chr7	-	5	1	TATAACAATCATATAATTGT	ACCATTAACAAGAATAGTAG	693	231	yes
PF07_0006	PF07_0006e2s1	chr7	+	2	1	AATTTAAAATGTAATTTTTA	ATTAATTAACATATATAAAG	1713	570	yes
PF07_0007	PF07_0007e1s1	chr7	+	1	1	ATGAGTCAACCACAAAAACA	GTAATCATATATTTGTAAGG	288	96	yes
PF07_0016	PF07_0016e1s1	chr7	+	1	1	ATGGAGAAGAATACGTACGA	GTCAATAGATATATTTTCCA	2820	940	yes
PF07_0048	PF07_0048e1s2	chr7	-	1	2	AAGGACACCACAGAAGACAC	CTTTAGAAAAAAATAAGTGA	2652	884	yes
PF07_0048	PF07_0048e2s1	chr7	-	2	1	AAAAAAACCAAAGCATCTGT	TATATTCCATATATCCGCTA	1395	464	yes
PF07_0053	PF07_0053e1s4	chr7	-	1	4	AACATGGATATGAATAATGT	AATTTGTACTATATTGTAAC	2709	902	yes
PF07_0126	PF07_0126e1s2	chr7	+	1	2	AATAATAATAAGGACAATAA	TTCCACTTTTTCGCTAGCTG	2022	673	yes
MAL8P1.156	MAL8P1.156e1s2	chr8	+	1	2	GTGGAAGAAGTATTATCCAT	TGAAGTTGCACAATATATCA	1542	513	yes
MAL8P1.23	MAL8P1.23e1s1	chr8	+	1	1	ATGAAAATACCTATACCTAA	TAATAATATTTTATATAACT	2913	971	yes
MAL8P1.23	MAL8P1.23e1s9	chr8	+	1	9	AATATATCTAATGAAAATGA	TATGAAACCGAATCCTTCTT	2904	967	yes
PF08_0034	PF08_0034e1s2	chr8	-	1	2	TTTGGTCAGCATATTCAGGG	CTGTAACTTATCGCTCTGCT	1680	560	yes
PF08_0035	PF08_0035e1s1	chr8	+	1	1	ATGGAAGTTTTACAAAACAT	TGGGACATTAAAATTCAATT	1794	598	yes
PF08_0089	PF08_0089e1s1	chr8	-	1	1	ATGCTTGATGTGTTTAGAGA	TATGTATGAAAATAAAATAC	2691	897	yes
PF08_0107	PF08_0107e1s2	chr8	-	1	2	TGTGAAATAGTACAAAAACT	CTTTAGAAAAAAATAAGTGA	2715	905	yes
PF08_0107	PF08_0107e2s1	chr8	-	2	1	AAAAAAACCAAATCATCTGT	TATATCCCACACATCTCCTA	1416	471	yes
PF08_0108	PF08_0108e1s1	chr8	+	1	1	ATGAAACGCATTAGCCCTCT	GTTTTTACTTTTTGCTCTTG	1722	573	yes
PF08_0121	PF08_0121e1s1	chr8	-	1	1	ATGAAAAATTTGAATCAGAA	TAATTCTCCGCATTCTACTA	654	217	yes
PF08_0127	PF08_0127e1s2	chr8	+	1	2	TTAAAAAAAATTATAGAAAA	CAATTTTGATTTTTGGTTTT	1893	630	yes
PF08_0137	PF08_0137e2s1	chr8	+	2	1	AATGTTGAAATATTAAAGAA	GTCATCAAAGTTTCTTCTGT	1761	587	yes
PF08_0137	PF08_0137e2s2	chr8	+	2	2	AGAAACTTTGATGAAAGAAA	TGCTCCACTATATTTTCTCA	1755	584	yes
PF08_0140	PF08_0140e2s1	chr8	-	2	1	AAAAAAACCAAATCTACTAT	TATATCCCACACATCTCCTA	1308	435	yes
PF08_0141	PF08_0141e1s2	chr8	+	1	2	GACGTATGTGGTATAACGGA	CTCTTTTCTTATATCATATG	2505	835	yes
PF08_0141	PF08_0141e2s1	chr8	+	2	1	AAAAAACCGAAATCACCTGT	TATATTCCATACATCCGATA	1179	392	yes
PFI0170w	PFI0170we1s1	chr9	+	1	1	ATGTTTTTTAACGATGGGGA	TTTGGAAACACTTTCATCCT	2106	702	yes
PFI0265c	PFI0265ce7s1	chr9	-	7	1	GTTTTCACCGCCTTATACAA	CAATTCATTTTCAGAAGTAA	669	222	yes
PFI0315c	PFI0315ce1s1	chr9	-	1	1	ATGAAGAAAGATAATAAGAA	TGAATTTATATTTCTTTTTT	2514	837	yes
PFI0345w	PFI0345we1s1	chr9	+	1	1	ATGAGTGAATTGAAACCATT	TATAAATTTATATTGACTAT	1731	577	yes
PFI0355c	PFI0355ce1s1	chr9	-	1	1	ATGAAAAACCTTGACGCAAA	TATGATATATTTTTTTAAGT	2769	922	yes
PFI0370c	PFI0370ce1s1	chr9	-	1	1	ATGGAAGCTTATTTAAATAA	AAATGTCATTCTATGATGTG	840	279	yes
PFI0410c	PFI0410ce17s1	chr9	-	17	1	TGGTATAATAAGGGTTCAAA	CTCTTCCGCCTCCATAGCAT	654	218	yes
PFI0460w	PFI0460we1s1	chr9	+	1	1	ATGGAAGTTATAACAGAAAA	GTACCACTTTTTTGTTTCTC	1470	489	yes
PFI0510c	PFI0510ce1s2	chr9	-	1	2	ATTTTTATAAAGAAGTATAT	GGTGGTCATATGATTTATAT	2571	856	yes
PFI0630w	PFI0630we2s1	chr9	+	2	1	GGAGCTTTTGAGGCTGAAGA	ATTTTTCTTGTCCTTTTTTG	498	165	yes
PFI1475w	PFI1475we1s1	chr9	+	1	1	ATGAAGATCATATTCTTTTT	ATTGTTCATACTATCATATA	2610	870	yes

PFI1475w	PFI1475we1s2	chr9	+	1	2	AATATTCAAAATAACATACC	AATGAAACTGTATAATATTA	2607	868	yes
PFI1500w	PFI1500we2s2	chr9	+	2	2	ATGTATGGTAAGACAATATG	ATTTATGAAGATATCTCTAT	2745	915	yes
PFI1520w	PFI1520we1s1	chr9	+	1	1	ATGCTTTCCATAGCAAGTAC	TTCATTTTTGTTTATTTCCT	918	305	yes
PFI1735c	PFI1735ce2s1	chr9	-	2	1	TTATTAAATTCTATAAAGGA	ATTAAATACAGAACTTTCTA	1953	650	yes
PF10_0075	PF10_0075e1s2	chr10	-	1	2	ATTGGAAAAAATTTCCAGAT	TAAATGTTCTGTTTGAATTT	2421	806	yes
PF10_0079	PF10_0079e1s1	chr10	+	1	1	ATGATGGAAAGAGGAAGATC	ATTCATCATTGCTCTTTTTA	2934	978	yes
PF10_0115	PF10_0115e1s2	chr10	+	1	2	GATATGTTATATTATTGTGG	ATTTTCATTTGATTGTTTTT	1734	577	yes
PF10_0138	PF10_0138e1s1	chr10	+	1	1	ATGAATCGAATATTTTATTT	AAGGTGTTCATAAAAATTGT	2214	738	yes
PF10_0138	PF10_0138e1s2	chr10	+	1	2	TATTTCCCAACCAAAGATAT	TGGATTTCTAAAATCTAGTG	2208	735	yes
PF10_0143	PF10_0143e1s3	chr10	-	1	3	GCCGAATTGTTATTAGCAGA	TAATTTTAAGGATTTTTTGG	2613	870	yes
PF10_0177	PF10_0177e1s1	chr10	-	1	1	ATGGATGTACAAAAAAAAAA	TGATTGTATGTCCAGTATTA	2997	999	yes
PF10_0214	PF10_0214e3s1	chr10	+	3	1	GGCGCAAATTTATTTTTATA	CATATATTTATTGACATTAT	2742	913	yes
PF10_0224	PF10_0224e1s3	chr10	-	1	3	GAGGAAAGTAAAATGTTTTT	CATAATTGATGATAAAGCAC	2892	964	yes
PF10_0242	PF10_0242e2s2	chr10	+	2	2	TTATATTCAAATGGAAAACA	AGAACTTAACCATGGAGCTG	2334	777	yes
PF10_0251	PF10_0251e2s3	chr10	-	2	3	TTGGATGTTAGTCTTATTAA	GTGTTTTTTTAGATACAGAT	2070	690	yes
PF10_0323	PF10_0323e1s1	chr10	+	1	1	ATGAAAGTTGGTAAAATATT	TTCTTTTCTGACTCTTGGTG	1068	355	yes
PF10_0343	PF10_0343e1s1	chr10	+	1	1	ATGAATAGAATCTTGTCTGT	CATTCCAATTAACATATTAA	1758	585	yes
PF10_0348	PF10_0348e1s1	chr10	+	1	1	ATGAAGAAAATATATAGTAT	TTTTTGAAATAAATCTGTCA	2094	697	yes
PF10_0356	PF10_0356e2s1	chr10	+	2	1	AAAGACTTGCTGAGACTTGC	GCTTTGTTGCCCCTGTAACT	1578	526	yes
PF10_0356	PF10_0356e2s2	chr10	+	2	2	AGCGATCTAGAACAAGAGAA	TAGTTTCATAAAATATTTAG	1572	523	yes
PF10_0374	PF10_0374e6s2	chr10	+	6	2	CCTGAAGAACTAGTAGAAGA	CTTAGTTCTTCTGGTACCAC	2343	781	yes
PF11_0008	PF11_0008e1s1	chr11	-	1	1	ATGGGGTCACAAACATCAAA	TTTAAAGTGTTTTTCAACTA	2610	870	yes
PF11_0008	PF11_0008e1s2	chr11	-	1	2	GCAACAACACCCGGGGTGAA	ACCTGTAGTTTTGTTGGGTG	2610	870	yes
PF11_0008	PF11_0008e2s1	chr11	-	2	1	AAAAAATCCAAATCTTCTGT	TATATTCCATACATCCGATA	1269	422	yes
PF11_0037	PF11_0037e2s1	chr11	-	2	1	AATGTACCTAGTATTGAAGA	ACCTATATAAGGAGCTTCTG	1713	570	yes
PF11_0226	PF11_0226e1s1	chr11	-	1	1	ATGAAACATACAAAAATAAC	TAATTCATTACTTTTCA ATT	2064	688	yes
PF11_0232	PF11_0232e1s1	chr11	+	1	1	ATGGAGAATAATAAAGATAA	GACTCGAGTAAATACTTTTG	2043	681	yes
PF11_0240	PF11_0240e2s3	chr11	+	2	3	AAAATATTAAATACAAAACT	TTCATTAGCTTCTTCTAAAC	2619	873	yes
PF11_0294	PF11_0294e1s1	chr11	-	1	1	ATGGATATCGAGAATTCA AA	GTGAAATTGTTGGGAACATA	1881	627	yes
PF11_0344	PF11_0344e1s1	chr11	+	1	1	ATGAGAAAATTATACTGCGT	ATAGTATGGTTTTTCCATCA	1869	622	yes
PF11_0351	PF11_0351e1s1	chr11	+	1	1	ATGGCATCACTCAATAAAAA	TGCATTATCTTTATTTTCTT	1992	663	yes
PF11_0404	PF11_0404e2s3	chr11	-	2	3	AAAAGTAATGAGAAACTTGA	CTGTTTATTTTCATGTCCTA	2187	729	yes
PF11_0418	PF11_0418e1s2	chr11	-	1	2	TTACAGAATGGTAATGACCA	ACTTAAAATATTACGAGATT	2313	771	yes
PF11_0479	PF11_0479e3s1	chr11	-	3	1	GGTATTCACAGTGGCATGAC	ATTATTTGAGTTGGTAATCT	2814	938	yes
PF11_0507	PF11_0507e1s1	chr11	+	1	1	ATGAAAGAACTAGAAAGTGA	TTTAACTGAATCTTCTTCAT	2802	934	yes
PF11_0507	PF11_0507e1s4	chr11	+	1	4	GTTACTGAAGAAATAGTAGA	TTCAGGAACTAATTGTTCTT	2802	934	yes
PF11_0507	PF11_0507e1s6	chr11	+	1	6	TCTACTGAAGGTTTAGAAGA	GTTCTCATTTACACTAAATT	2784	927	yes
PF11_0509	PF11_0509e2s1	chr11	+	2	1	GGAAATTTTGGATATAATGG	CTTCATATCTGCATTAACTC	1569	523	yes
PFL0275w	PFL0275we1s2	chr12	+	1	2	ACATTTCTTAAGATAAAACC	ATTATTCATTTTGATGGACT	2703	900	yes

PFL0440c	PFL0440ce1s1	chr12	-	1	1	ATGATAAAGAAAAGAAAAAA	AAAATTACCTTTTCCTATTT	1800	600	yes
PFL0470w	PFL0470we1s1	chr12	+	1	1	ATGGTACTTGAATTAGTTGT	TCCCTTTGTATATTTCCATA	2379	792	yes
PFL0590c	PFL0590ce1s1	chr12	-	1	1	ATGAGTTCTCAAAATAATAA	TTGTTCAGATTTCTCTTCTA	2394	798	yes
PFL0795c	PFL0795ce1s1	chr12	-	1	1	ATGAAGTATCCCAACTTTTT	ATCACTATCACTGTGTGTTT	666	221	yes
PFL1070c	PFL1070ce1s1	chr12	-	1	1	ATGAAATTAAATAACATATA	TAATTCGTCACTTTTATCAT	2466	821	yes
PFL1085w	PFL1085we1s2	chr12	+	1	2	GCAAATAAATTTAAAAATTT	ACATTTGTTTTCATCATCAT	2472	824	yes
PFL1385c	PFL1385ce1s1	chr12	-	1	1	ATGATGAACATGAAAATTGT	TTTTGATTCTTCAGTTGTCA	2232	743	yes
PFL1745c	PFL1745ce2s1	chr12	-	2	1	ATGAATAACGAAATCGTAAA	CGAATTTGTATTTTCCACAG	1338	445	yes
PFL1925w	PFL1925we1s1	chr12	+	1	1	ATGAGTTCGAAGTATGACAA	GTCGCTTTTAAATATGTCAA	2643	880	yes
PFL1930w	PFL1930we1s5	chr12	+	1	5	ACTCTTGAATATTTAGAAGA	TATATCCTTTTCTGCACATT	2931	977	yes
PFL2120w	PFL2120we1s2	chr12	+	1	2	AATATTATACTTTTCTTACT	ACCTTTCCTCTTTTCTATTT	1716	572	yes
PFL2390c	PFL2390ce1s3	chr12	-	1	3	AAATTTTTATGTAAACATCC	TCTGTTTTTCTCCATCATTG	2751	917	yes
PFL2505c	PFL2505ce8s2	chr12	-	8	2	AATTTCAATAAAAAAAAAAA	TGGTATGTAAATTTCCCTCT	2124	707	yes
PFL2610w	PFL2610we2s1	chr12	+	2	1	GAGAATTATCTAAATAACCA	CTTACATAAATGTTTCTTGC	819	272	yes
MAL13P1.176	MAL13P1.176e1s1	chr13	-	1	1	ATGGAAATTAAAACAATAGT	TCTTTCTTTCTCTTGTTTTT	1704	568	yes
MAL13P1.176	MAL13P1.176e1s2	chr13	-	1	2	GAAGAAAGAAAAGAGAGAGA	AAAATATTTTTCTTCATTTT	1698	565	yes
MAL13P1.234	MAL13P1.234e1s3	chr13	+	1	3	GATAAGAGGAATTATAATAT	GTTGTTATTTTTATTGTTAT	3039	1013	yes
MAL13P1.323	MAL13P1.323e1s1	chr13	+	1	1	ATGGATTTTGCATACAAACA	ATTATAACTATTTGTAACAT	2493	831	yes
PF13_0003	PF13_0003e1s1	chr13	-	1	1	ATGGGGAATACACAATCATC	TGAACGATTGGCTTCCCACC	2985	995	yes
PF13_0003	PF13_0003e2s1	chr13	-	2	1	AAAAAACCGAAATCACCTGT	TATATTCCATACATCCGATA	1197	398	yes
PF13_0153	PF13_0153e1s2	chr13	+	1	2	GAAGGATCAAGAAATCAGCG	ATGAAATATATTATTCAACC	1533	510	yes
PF13_0190	PF13_0190e1s1	chr13	+	1	1	ATGGTCGACGATAAGAATAA	CATTTTATTATACTCTTGCG	1575	524	yes
PF13_0197	PF13_0197e1s1	chr13	-	1	1	ATGAAGAGTAATATCATATT	CATTGTGTTTAGTAAATTAA	1056	351	yes
PF13_0210	PF13_0210e1s1	chr13	-	1	1	ATGAAACCAAATGATAATTT	TATGTTATTATTTTTATTTA	2484	828	yes
PF13_0210	PF13_0210e1s3	chr13	-	1	3	ATGGTTAATTATAAAAATGA	ATCTTTTTCTTTACATTTTT	2484	828	yes
PF13_0262	PF13_0262e2s1	chr13	-	2	1	AAAGATAAGAAAAAAGAGGA	ATTTGCTGGTCGCATAGTGG	1551	516	yes
PF13_0275	PF13_0275e2s1	chr13	-	2	1	GGAAACGTTAGTACTAATGT	AGCTTCAACTACTTCTTCCT	660	219	yes
PF13_0278	PF13_0278e1s2	chr13	+	1	2	AATGATTATAATAATAATAA	ATTACTTAATACAGGATCTG	1773	590	yes
PF14_0096	PF14_0096e1s1	chr14	+	1	1	ATGAGTTATTTGAGCAACAT	TGCGTTTGTTGTATTTTCCA	1545	514	yes
PF14_0102	PF14_0102e1s1	chr14	+	1	1	ATGAGTTTCTATTTGGGTAG	ATCTAATCTCTTGAAGGCAA	2349	782	yes
PF14_0170	PF14_0170e1s5	chr14	+	1	5	ACAAATGTCGAAATGGATAA	TTTTGTATTTTTTATAAGTT	2700	900	yes
PF14_0198	PF14_0198e1s1	chr14	+	1	1	ATGTTTTTTTTTGAGAATAA	GGAATCCAAAACCTGCTGTG	2640	879	yes
PF14_0315	PF14_0315e2s5	chr14	-	2	5	GAGGATAAGGATATAATTAT	AATATCACCATCATTGTCAT	3003	1000	yes
PF14_0326	PF14_0326e2s4	chr14	-	2	4	ATATATATACTTAAGCATTT	AAAATTATAACTATCGTCAT	2787	929	yes
PF14_0327	PF14_0327e1s1	chr14	+	1	1	ATGAATAAGAACAACAATAA	AAAGTCGGGACCACGAGATA	1887	628	yes
PF14_0344	PF14_0344e1s1	chr14	+	1	1	ATGAGAATAATAATATTAGC	ATTGTCGTCCTCTTCTTCGT	2982	993	yes
PF14_0377	PF14_0377e1s1	chr14	+	1	1	ATGAAACTTTTAAGAGTAAC	ACCATCTGCTAAATTTGGGT	501	167	yes
PF14_0419	PF14_0419e9s2	chr14	-	9	2	GAAATGTTTATACTAAATAA	AGTAGATAATATATCATCCA	2340	780	yes
PF14_0463	PF14_0463e1s3	chr14	-	1	3	ATGAATAATTATACTCCTGC	ACTTTCCTCATCATCTATAT	2763	921	yes

PF14_0495	PF14_0495e1s1	chr14	+	1	1	ATGTTAAAATTTTTCATATT	ATCATAGTCACTATCACTAT	2229	743	yes
PF14_0588	PF14_0588e1s1	chr14	+	1	1	ATGTATTCCTCTCCAAAAAA	TACCTTTTTATTCACATTCT	2772	924	yes
PF14_0593	PF14_0593e1s1	chr14	-	1	1	ATGAATAAACTATTTTTTTT	ATGATCATTAAATAATGAAT	2067	689	yes
PF14_0626	PF14_0626e4s2	chr14	+	4	2	AGTACAACAAAAGAATCATT	TATTCTTTTATATTTATAAG	2913	971	yes
PF14_0631	PF14_0631e1s2	chr14	-	1	2	TCTGAAAGTCAAAAATTCCG	CAGAACATTCGTCTTATTCA	2352	784	yes
PF14_0631	PF14_0631e1s3	chr14	-	1	3	AATAAGGTAAATTCTGTCAA	GTTCATTGAACTATATAAAT	2352	784	yes
PF14_0736	PF14_0736e2s1	chr14	+	2	1	TATATATGTCGAATTATAAG	AGAATCTTTAATTGTATCAA	2793	930	yes
PFA0170c	PFA0170ce1s1	chr1	-	1	1	ATGCTTTTTAAAAATGAAGA	TATAGCATTACTACTTATAT	2460	820	no
PFA0410w	PFA0410we1s1	chr1	+	1	1	ATGGAATCCTATATAAGGGA	ATTACTAATTTTAAAAATAT	2259	753	no
PFA0410w	PFA0410we1s2	chr1	+	1	2	CAGATGATACAATTTTCTAT	ATTTTTATTCATTGCACAAG	2259	753	no
PFA0430c	PFA0430ce1s1	chr1	-	1	1	ATGAAATTTTATAGTCCTTT	ATACATCATTTTTTTAAACA	1629	543	no
PFA0555c	PFA0555ce4s1	chr1	-	4	1	GGTAAAATCGTGCCGGTGGA	TCCACAAGTTAATCCTCTAT	447	149	no
PFB0115w	PFB0115we1s2	chr2	+	1	2	GATACAGATGATTCAGACAA	TAATGCTTTGTTTGCATTTG	1815	604	no
PFB0150c	PFB0150ce2s2	chr2	-	2	2	CTTTATAATAATTTATCTTC	ATTCTTTTCATTATTCTTTT	2520	840	no
PFB0150c	PFB0150ce2s3	chr2	-	2	3	AAGAATAATGAAAAGAATAA	TTTCTGGGATTGTTCAGTCC	2517	838	no
PFB0260w	PFB0260we2s1	chr2	+	2	1	GCCGTATCTATACAAGTTCC	CTGTCCAACACGAACAGACA	2685	895	no
PFB0265c	PFB0265ce1s2	chr2	-	1	2	AATGATATTATAAGAGATAC	TTTTTTTTTCTTGCTTGATT	2301	766	no
PFB0315w	PFB0315we1s1	chr2	+	1	1	ATGGATAGTGATAAATATAA	ACCACACATTTTCTTTTCTT	2598	866	no
PFB0335c	PFB0335ce1s1	chr2	-	1	1	ATGTCTACAGAACAGCATAG	ACTCTTTGATTCTTCGTTAG	393	131	no
PFB0405w	PFB0405we1s1	chr2	+	1	1	ATGAAGAAAATTATAACGCT	ATTCTTAGGAAATAGAATAC	2394	798	no
PFB0465c	PFB0465ce2s1	chr2	-	2	1	ATTAGCGGTATCATATTCAT	AAATGCTAGTGCTAACATGA	942	313	no
PFB0540w	PFB0540we1s2	chr2	+	1	2	GATGAACTGTCTTATAACCC	GTGCAGGTAATTTTTTTCTT	2793	930	no
PFB0635w	PFB0635we1s1	chr2	+	1	1	ATGAAAAATAATGAGGACAC	GAAGGCTTCGTCATAGTCAG	1575	524	no
PFB0640c	PFB0640ce1s2	chr2	-	1	2	ACAGAAAATGAAAAGATAAA	ACTTGATGGAGGGGGGGAAC	1995	665	no
PFB0645c	PFB0645ce2s1	chr2	-	2	1	TGGCAGAGTTATCCATTTTT	CAAAATGGTAAAGGTCTTTA	552	183	no
PFB0895c	PFB0895ce1s1	chr2	-	1	1	ATGAGTTCGAAGGACAAAAA	TTTTGCTTTTTTCATAGATT	2715	904	no
PFC0085c	PFC0085ce2s1	chr3	-	2	1	AAATCATATTATGTATATAA	ATTTTTTTTTGATTTTTTAT	771	256	no
PFC0120w	PFC0120we1s1	chr3	+	1	1	ATGGTTTCATTTTTTAAAAC	GGCTATTAAATGAGGACCTA	858	286	no
PFC0150w	PFC0150we2s2	chr3	+	2	2	ATGATAGAAAAAGTACGAGA	ACTTTCGGTATTTCCAAAAG	1641	547	no
PFC0170c	PFC0170ce1s1	chr3	-	1	1	ATGTTTGTGAAGAATGTACT	TTCCAATAGTGGTCCTAGGG	1347	448	no
PFC0180c	PFC0180ce4s1	chr3	-	4	1	AAGTATATTCCCAAGGATGC	TTTATCACAAAAATAGTTAC	2124	707	no
PFC0425w	PFC0425we1s4	chr3	+	1	4	AAAACAAAGAAGGATTATAA	TTTATATTGATTATCAAATA	2775	925	no
PFC0430w	PFC0430we1s1	chr3	+	1	1	ATGCAAAATAATAAAAGAAT	ATCCAAATCTAAATAATCTA	1749	583	no
PFC0590c	PFC0590ce2s1	chr3	-	2	1	AGGAAAAATGGACCCCTCCC	TTTTTTTTTTTTTAATTGTA	2082	694	no
PFC0635c	PFC0635ce1s1	chr3	-	1	1	ATGAAGTATTTAACATTTAA	TCTATGTATGTGACTAAGAC	684	227	no
PFC0720w	PFC0720we1s1	chr3	+	1	1	ATGAATAAGATGGCTAGCAC	CATGTTTGCGCTGATATCCT	1386	461	no
PFC0760c	PFC0760ce1s3	chr3	-	1	3	AGAAATGAAATTGACAAATT	TTCATCTGTTAAAAAATCTT	2589	863	no
PFC0875w	PFC0875we1s1	chr3	+	1	1	ATGAAAGACTTTTTATCATA	ATATTTATCTACATTTTTAT	3033	1011	no
PFC1065w	PFC1065we2s1	chr3	+	2	1	GAAGTGGATTATGTGATTAA	AACAAGTTGTCTTTCTGCTT	2658	885	no

PFC0710w	PFC0710we3s1	chr3	+	3	1	AAAGAAGATAAACATTATGA	AGGTGTCCATATGTTGAGAT	417	138	no
PFD0225w	PFD0225we1s3	chr4	+	1	3	GAAATGGACGCCGCAGAAAA	AGTATGTATATTATTTCGAT	2529	843	no
PFD0225w	PFD0225we1s5	chr4	+	1	5	GACATACTAAATCTTGGAAG	TTTTTTATTTATTATCCCTT	2517	838	no
PFD0265w	PFD0265we2s1	chr4	+	2	1	GGGAGTGACGTTTTAACAAA	ACCAGAATTATAGTCCTCTT	2382	794	no
PFD0295c	PFD0295ce4s1	chr4	-	4	1	GGTTACTTAAATATCCAAGT	TGCGCAGAAAAAAAGATTAA	1536	511	no
PFD0445c	PFD0445ce1s1	chr4	-	1	1	ATGGTCATCATATATATTTA	TATTATATATATTTTGGAAA	2607	869	no
PFD0995c	PFD0995ce1s2	chr4	-	1	2	GAAGGTGAAGATGGTGAAGA	CTTTAGTAGAAAGTAACTCA	2601	867	no
PFD1060w	PFD1060we1s3	chr4	+	1	3	TCTTTTTATATATTTGATCA	CTCCTCCACGTTAATCTTAA	2907	968	no
PFD0105c	PFD0105ce1s1	chr4	-	1	1	ATGCATTTTGTAGTTGAATT	TTTGTTAAATAATATAAAAA	2370	790	no
PFE0055c	PFE0055ce3s1	chr5	-	3	1	GATTACTATGCTGTATTAGG	ATTTGATCTGCTTGATCTAG	402	134	no
PFE0055c	PFE0055ce4s1	chr5	-	4	1	AATATTTTTTCTCGATCATT	CGTATTTTCCAAGGTTTCCT	567	189	no
PFE0090w	PFE0090we1s1	chr5	+	1	1	ATGCCAAATGTATATTTACC	ACTTGAAAAAAGGCTTCTTT	1644	548	no
PFE0270c	PFE0270ce1s1	chr5	-	1	1	ATGGCATCATCTAACAAAAA	ATTATTAACATTTGTCATAT	1647	549	no
PFE0335w	PFE0335we1s1	chr5	+	1	1	ATGTCTAGCAGACTACTGAA	TACCTTTTTGTCTTTGTACA	2451	817	no
PFE0380c	PFE0380ce1s1	chr5	-	1	1	ATGAGTACGATAATTATAAG	TATCTTTACTGATGTTAACA	1596	531	no
PFE0465c	PFE0465ce1s3	chr5	-	1	3	ATGTCGGGAAGAGAAGGTTT	ACCTGTATGGGTCATGAAAT	2874	958	no
PFE0655w	PFE0655we2s3	chr5	+	2	3	ACATCCACTATAATAAATGA	TCTTAACAAGTCATCAAATA	2367	789	no
PFE0780w	PFE0780we6s1	chr5	+	6	1	CAACATACAAAAAAGAATTT	ATTTGAGTTCAATATTTGAT	1521	507	no
PFE0935c	PFE0935ce1s1	chr5	-	1	1	ATGTATATTTGTTTGTATAA	CCCGTGGTAGTAATACAACT	2331	777	no
PFE1010w	PFE1010we1s1	chr5	+	1	1	ATGAGTTTATTAACCAATTA	CAAAGTGTTACTTATATTAA	1536	512	no
PFE1025c	PFE1025ce1s1	chr5	-	1	1	ATGAAGGAAAATTATATGAT	ATATTGTTTTGCCCATCCTA	906	301	no
PFE1120w	PFE1120we3s1	chr5	+	3	1	TACGAAATGTTTCTCACAGC	TAATTGTTCAATACATACTT	2802	934	no
PFE1120w	PFE1120we3s2	chr5	+	3	2	TTAAGTATGGGTAGTGCCAG	CTTTTTCATATTGCATTTCG	2802	934	no
PFE1120w	PFE1120we3s3	chr5	+	3	3	TTAACCGATACAGTTAGTAA	TATTCCTATAAAATGTATTA	2802	934	no
PFE1120w	PFE1120we3s5	chr5	+	3	5	TCAATAAAAATGTCATCAAC	AATACTATTTGTTTCTATTT	2802	934	no
PFE1120w	PFE1120we3s6	chr5	+	3	6	AATCATTTTGTTGATTTTAA	TTTATTCCTATTCACGTATT	2802	934	no
PFE1120w	PFE1120we3s7	chr5	+	3	7	ATTATTAGTAGCAACCAAAA	ATAGTGCCTCAATATTCTTA	2793	931	no
PFE1120w	PFE1120we4s2	chr5	+	4	2	CATGCTAATTCTTCTAAATA	ATAAATCATTTTTACTGAGT	2667	889	no
PFE1120w	PFE1120we4s3	chr5	+	4	3	ACATACTTAAATAGATATAA	AACCTTTTTTTTTCCTACTT	2661	886	no
PFE1320w	PFE1320we1s1	chr5	+	1	1	ATGTTTAAAAGTAACAAGAT	ATCATTGTCTCCACATTTAT	2106	702	no
PFE1355c	PFE1355ce2s1	chr5	-	2	1	TGGCAACTGACGAATGTCCC	TTCCTTAATATCCATATTCA	1719	572	no
MAL6P1.131	MAL6P1.131e1s1	chr6	+	1	1	ATGAGTGAGAATAGTGATGA	TGAATTCTTTTCATCCATTT	2853	951	no
MAL6P1.131	MAL6P1.131e1s3	chr6	+	1	3	AAAAAAATATGGGAAAAAAA	ATGACAACTATTTTTGGTAT	2853	951	no
MAL6P1.131	MAL6P1.131e1s4	chr6	+	1	4	AAAAACATTTCGAATGAAGA	ATTATTATTATTATTATTAT	2853	951	no
MAL6P1.131	MAL6P1.131e1s5	chr6	+	1	5	AATATTTTAAACTTTAATGG	TCCTGTGTATTTTTCATCAT	2853	951	no
MAL6P1.146	MAL6P1.146e1s2	chr6	+	1	2	TCGATTATAAATTCTATTAA	ATTATGTACAACACGATACA	2346	782	no
MAL6P1.146	MAL6P1.146e1s3	chr6	+	1	3	GTTAGTGATGGAGATTCTTT	ATTATTCTTTCTAAGAACCT	2346	782	no
MAL6P1.201	MAL6P1.201e1s1	chr6	+	1	1	ATGGCGAGACGTATGAACTT	ATTATATGTTTGGAAATTAT	2202	734	no
MAL6P1.201	MAL6P1.201e1s2	chr6	+	1	2	TTTAAAAAAGATGTTCTAAT	TCCTTCAGTGTTGTATATAT	2196	731	no

MAL6P1.237	MAL6P1.237e6s1	chr6	-	6	1	ATTGATGATGAAGGTATAGA	AAATAAAGAAAGGTTCGTAT	1938	646	no
MAL6P1.252	MAL6P1.252e1s1	chr6	-	1	1	ATGGGTCCCGCGCCTAGGAC	ATCTTCTAATTCATGTTCTA	2085	695	no
MAL6P1.252	MAL6P1.252e1s2	chr6	-	1	2	ACAGAACATTCACAGGATGC	TTTTAACGTCTTAATCACGT	2085	695	no
MAL6P1.252	MAL6P1.252e2s1	chr6	-	2	1	AAAAAAACCAAATCTACTAT	AATAGGTTTAGAATTCATAT	1044	347	no
MAL7P1.102	MAL7P1.102e1s1	chr7	-	1	1	ATGAGTGTATTAAAATATAT	TACACCACTCATATGATCTA	2628	876	no
MAL7P1.102	MAL7P1.102e1s2	chr7	-	1	2	GATAATTTGAGTGGTGTAGA	TTTTTTTTTATCTTCTGAAT	2622	873	no
MAL7P1.126	MAL7P1.126e1s2	chr7	-	1	2	TATAATATAAATGAATTTAT	TATTTTAAGTTTTGGATCTC	1716	572	no
MAL7P1.134	MAL7P1.134e2s2	chr7	-	2	2	CGAAATAATAACTATGATCA	GAGAGAGATGACAATTTTTG	2400	800	no
MAL7P1.134	MAL7P1.134e2s3	chr7	-	2	3	CTATCACTTTTAAGAAATAA	CTGGTTATAGTGAGGCTTGT	2397	798	no
MAL7P1.138	MAL7P1.138e1s1	chr7	+	1	1	ATGGGTGTTTTAAAATTAAA	ACAATCCACCAGAGATAAAA	2283	761	no
MAL7P1.14	MAL7P1.14e1s1	chr7	-	1	1	ATGTTGGATAATTTTATTCA	TGTACATGGATCGGGTAAAG	750	249	no
MAL7P1.146	MAL7P1.146e5s2	chr7	-	5	2	AATTTTATGAATAACAAGAA	ATTATTCTTTATATCTGTAA	1563	521	no
MAL7P1.23	MAL7P1.23e1s2	chr7	+	1	2	GATCATAATGCTACTAATAA	CCTCTTTTTTAAAATTGTCT	1734	578	no
MAL7P1.29	MAL7P1.29e1s2	chr7	-	1	2	AATCATGTATTCCAGAAAAA	ACCTATCTCCAAGTCGTTGA	1632	544	no
MAL7P1.29	MAL7P1.29e2s1	chr7	-	2	1	GGTCTGGCAGACACCGAATG	GCCATTATTTCGTAGTGTAT	2652	884	no
MAL7P1.32	MAL7P1.32e1s1	chr7	+	1	1	ATGACCACACCATTTTCTTT	AAATTGCATATATTCAACAC	1191	396	no
PF07_0004	PF07_0004e2s1	chr7	-	2	1	TATGGAATAAAATATAATGA	TCTTAATGGTTGTGCTACAT	2781	926	no
PF07_0020	PF07_0020e1s1	chr7	-	1	1	ATGAACGCTGAGAATTTGAA	ATTATTATGGCCATAAATAT	1575	525	no
PF07_0020	PF07_0020e1s2	chr7	-	1	2	AATGGACAAGAACATATTTT	ATCTCCATTCATTTCAATAT	1572	524	no
PF07_0029	PF07_0029e2s1	chr7	+	2	1	ATCACCGAATTACTCCGATT	GTCAACTTCTTCCATTTTAG	807	268	no
PF07_0035	PF07_0035e1s1	chr7	+	1	1	ATGTTTACTTTTCTTGTTAT	TAAAGAAAATTCCTCTAAAG	1902	634	no
PF07_0047	PF07_0047e1s1	chr7	-	1	1	ATGAAAGTAAGAAAAATGCA	AAAAATAATACATGGTGTTT	1875	625	no
PF07_0087	PF07_0087e1s1	chr7	+	1	1	ATGTCGAGACTTTTCTCTTT	TTCAGTCACATAACATACTG	735	244	no
PF07_0118	PF07_0118e1s6	chr7	-	1	6	ATATTAAGAAATAAGCTCAT	TAAATTTCCTATGAAAAAAC	2811	936	no
PF07_0128	PF07_0128e1s1	chr7	+	1	1	ATGAAATGTAATATTAGTAT	TAGGTTAGAACATTTTTCCG	2163	721	no
PF07_0128	PF07_0128e1s2	chr7	+	1	2	TCTATAAAACCAGAAGTTTA	ACTTGAAAAAGCCTCCTTTC	2157	719	no
PF07_0129	PF07_0129e1s1	chr7	+	1	1	ATGAATATTTCATTTACGGT	TTTATTTAATTCTAATTCTT	2436	811	no
MAL8P1.11	MAL8P1.11e2s1	chr8	-	2	1	ATGAATAATGTCGCCTATGA	ATCATCACTATAAGAATTAT	1806	602	no
MAL8P1.132	MAL8P1.132e3s1	chr8	+	3	1	CGATCAAGTAGGTCTCATGC	CTGCATTTTCCTCAACATTT	237	79	no
MAL8P1.139	MAL8P1.139e1s1	chr8	-	1	1	ATGGATCGTTCCTGTAAGGA	CATATGTTTGTATTTGAACA	2748	916	no
MAL8P1.139	MAL8P1.139e2s2	chr8	-	2	2	AATAATAATAATGATGATGA	TTTTGTTTCTTTCGATGCAT	2124	708	no
MAL8P1.139	MAL8P1.139e2s3	chr8	-	2	3	TTATACAAAAAGAACCTGAC	CCTGTCCTCTGCCAATATCA	2121	707	no
MAL8P1.142	MAL8P1.142e2s1	chr8	+	2	1	GCTAGCTATGGTAGTTATGC	CCACATACATCCAGCAGGTG	714	237	no
MAL8P1.23	MAL8P1.23e1s3	chr8	+	1	3	TGCAAAAAATACAATGATTA	ATTATTTATGGTCTCTTGGG	2913	971	no
MAL8P1.23	MAL8P1.23e1s4	chr8	+	1	4	CGTGAATATAATAATAACTT	AACCACATTATTATATGTAG	2913	971	no
MAL8P1.23	MAL8P1.23e1s8	chr8	+	1	8	AATGTAAACAGTGTAAATAA	ATTCGGCACATTGTTCATTA	2913	971	no
MAL8P1.60	MAL8P1.60e15s1	chr8	+	15	1	GAAAATATTGAGAGCCTCTT	ATCTTTTATTGAGAAAAATA	1110	370	no
MAL8P1.60	MAL8P1.60e4s1	chr8	+	4	1	GAAATTTTCGTAAAGACCAA	ATTTATGTCGATATCCTTTT	306	102	no
MAL8P1.69	MAL8P1.69e3s1	chr8	-	3	1	TCCGTTGCTTATAAGAATGC	TTTGTTACCTTCGGTCTGAT	600	199	no

PF08_0012	PF08_0012e1s2	chr8	-	1	2	ATATTAATATTATTAAATTT	ATTATTGTTGTTATTATTAT	2439	813	no
PF08_0012	PF08_0012e1s3	chr8	-	1	3	AATAATGATAATAATATTGA	ACCTATGTAACCTTTACACT	2430	809	no
PF08_0018	PF08_0018e1s1	chr8	-	1	1	ATGAACAAGATAAAAATAAG	CTTTACATTTTTATTTTCTT	2127	709	no
PF08_0018	PF08_0018e1s2	chr8	-	1	2	GCATTTGAAGTAGTATGTAG	TGAAAGGTCAAATGATTTTA	2121	706	no
PF08_0020	PF08_0020e1s1	chr8	-	1	1	ATGGTGGATAAAATTAAAGA	ATTATTATAATATTTCTCGT	2019	673	no
PF08_0020	PF08_0020e1s2	chr8	-	1	2	GTACATTTGGTTTTAAAGTG	CATATTTGAAGTTTCATTTT	2016	671	no
PF08_0054	PF08_0054e1s1	chr8	-	1	1	ATGGCTAGTGCAAAAGGTTC	ATCAACTTCTTCAACTGTTG	2034	677	no
PF08_0089	PF08_0089e1s2	chr8	-	1	2	GTCTATAAAAGTTTTACAAT	ACTTACTATTATTCCATTAA	2691	897	no
PF08_0102	PF08_0102e1s2	chr8	+	1	2	AAAGAAATGTTAAATTTATA	AAAAAAATAAGCATACAAAT	2001	666	no
PF08_0135	PF08_0135e1s1	chr8	+	1	1	ATGATAAAATCTTTTATAAA	TTCATCCAGGTGCACCGTTT	1650	549	no
PF08_0140	PF08_0140e1s1	chr8	-	1	1	ATGGTTCCCCCTGTCCGTTC	ATTCAGGTTCAAATTCTCCA	2583	861	no
PFI0010c	PFI0010ce2s1	chr9	-	2	1	ATATATAATCAAAGGAACCA	TTCTTTCAATAATTTTATAT	1077	358	no
PFI0235w	PFI0235we2s1	chr9	+	2	1	GACTTATTATTTCGTATTAG	TAGTTTTTGTTTTTTGGAGT	1443	480	no
PFI0240c	PFI0240ce1s1	chr9	-	1	1	ATGGCTAAATTGTCATTAAC	ATTATCACCTTTTTTATTAT	2487	829	no
PFI0240c	PFI0240ce1s2	chr9	-	1	2	TTCAGAAAAAGCGATATATC	TCCTTCCTCGTCTTGATAAT	2487	829	no
PFI0260c	PFI0260ce1s5	chr9	-	1	5	CCCAAAGGTGATTATAATGA	CAAACCAATATCCACACTTT	2670	890	no
PFI0260c	PFI0260ce1s5	chr9	-	1	5	CCCAAAGGTGATTATAATGA	CAAACCAATATCCACACTTT	2670	890	no
PFI0345w	PFI0345we1s2	chr9	+	1	2	TTCGAAAATATTGAAAATCA	AAATGTGTGAGCATCGTCTA	1725	574	no
PFI0410c	PFI0410ce18s1	chr9	-	18	1	GTGTTGAAGCACCATTGTGG	CTTCCTTATTTTGAGGTAAA	1425	474	no
PFI0550w	PFI0550we1s2	chr9	+	1	2	ATGCATTCATTCATATTTCC	TCCCGGACAATAAAAATGTA	2400	800	no
PFI0580c	PFI0580ce2s1	chr9	-	2	1	GATAATAACAGCTACTCATT	TTGCACGTTTAACTCTACAA	1176	391	no
PFI0855w	PFI0855we1s1	chr9	+	1	1	ATGGCAATTAATAATGAAGA	AACCGTTTGTGCCCATAACT	2046	681	no
PFI0925w	PFI0925we1s2	chr9	+	1	2	ATGAGTATGTGTTGTCAACA	TGCACTCAGTTCGTACATTT	1620	539	no
PFI1000w	PFI1000we1s2	chr9	+	1	2	TTTGTATCCTTCAATATATC	AAGATTTAGAAGAAAATATT	2805	934	no
PFI1265w	PFI1265we1s1	chr9	+	1	1	ATGAAGAATAATGAAGATAT	ATCATTAGAATATGTTATGT	2661	887	no
PFI1425w	PFI1425we2s1	chr9	+	2	1	CTGAATCTTATTGAAAACAT	CTTCTTTTGTAAATAATATG	1053	350	no
PFI1620c	PFI1620ce1s1	chr9	-	1	1	ATGAATAATATAAATTTTAG	TTCTTCTGAATTCACTATCT	2298	766	no
PFI1730w	PFI1730we2s1	chr9	+	2	1	GCTGTTGGGCATTTTATTAC	ATTTAAAACTCCAACGAAAT	606	202	no
PF10_0013	PF10_0013e2s1	chr10	+	2	1	AAATATATTCAAAATTTTGT	AGTTATATATCTATCTTCGT	624	207	no
PF10_0041	PF10_0041e1s2	chr10	-	1	2	AAAAATTATCATCGTCCAGA	AAAATATTCTGAAAATTCAT	1878	625	no
PF10_0078	PF10_0078e1s2	chr10	+	1	2	AACGAATCATATAATGAAGA	AATTTTAATTTTTCTTTCTG	2418	806	no
PF10_0079	PF10_0079e1s3	chr10	+	1	3	AACAACCATAATAATAACAG	GAGGGTCATTTGACTATTGG	2934	978	no
PF10_0085	PF10_0085e1s1	chr10	-	1	1	ATGCTCATTTTAGTTGAAAC	CTTCCTTTTTTGCTTCTTTA	1410	469	no
PF10_0092	PF10_0092e3s1	chr10	-	3	1	ATACGACTACGTAAAACCAA	TATATAATTACCATCATTTT	831	276	no
PF10_0124	PF10_0124e1s1	chr10	+	1	1	ATGGATATGAAAAATATATA	AATATCTTCAAAAAAGTTAA	2040	680	no
PF10_0124	PF10_0124e1s2	chr10	+	1	2	ATAAAAGTACATGGATATAA	ACCCTTTAAAACTTGTTTTC	2037	679	no
PF10_0132	PF10_0132e1s2	chr10	+	1	2	CAAATATTTAGTACAAGTAA	ACAATAATTAATGTCATAAA	1989	663	no
PF10_0133	PF10_0133e1s1	chr10	+	1	1	ATGAATACTTTGAAAGGTAA	TTCTAGAGTAGCTTCAACTT	2277	759	no
PF10_0133	PF10_0133e1s2	chr10	+	1	2	AATTTACTTAAATTGAAGGA	CTCTTTTTGTGTTATAATAT	2277	759	no

PF10_0140	PF10_0140e2s1	chr10	+	2	1	AATATATGTTTAAACGTTCC	TTGAAATATAGATAATCTTT	276	91	no
PF10_0143	PF10_0143e1s1	chr10	-	1	1	ATGAATATAAATAAATATGA	TGAACCTCCACCTGATCCTG	2616	872	no
PF10_0143	PF10_0143e1s2	chr10	-	1	2	AATTATATGAATAATACAAA	CTGTTGTGGTAAATCGGATT	2616	872	no
PF10_0153	PF10_0153e2s1	chr10	-	2	1	GGTTGCAATAAGTTGGCCGA	ATACATTCCCCCCATATCAC	1602	533	no
PF10_0161	PF10_0161e1s1	chr10	-	1	1	ATGAAAAAATCGAGAATATT	ATATGGGTGGTTCTTAAATG	687	229	no
PF10_0211	PF10_0211e1s2	chr10	-	1	2	ATATCTAAGCAGAATGAAGC	AGGTACTTCTTTACATAATT	2121	707	no
PF10_0211	PF10_0211e1s3	chr10	-	1	3	AAATATAAATATCTAGAATC	ATCATTCTGTTGATAATTAT	2112	704	no
PF10_0214	PF10_0214e2s1	chr10	+	2	1	ATGAACAAAAAACATAATAA	GCCTGGTGGTCCATCTTTTA	1542	514	no
PF10_0215	PF10_0215e2s1	chr10	-	2	1	CAGTCGTCCAAATTAATTGG	CTTTAAACTATCAATTATCA	720	240	no
PF10_0224	PF10_0224e1s4	chr10	-	1	4	GGATATTTAACAAAAAACAA	TAATTCTACATGTGTAGTAT	2892	964	no
PF10_0264	PF10_0264e2s1	chr10	+	2	1	GTGCATATAGGTACAAAAAA	CCACTCTTCAGCGGCTATTG	729	242	no
PF10_0320	PF10_0320e1s1	chr10	-	1	1	ATGGATGACTCTTTAAACAA	ATATTTATTGGTGTGTGTAT	2601	867	no
PF10_0322	PF10_0322e1s2	chr10	-	1	2	GCGACGAATAATAATGATAA	CCAATGTTTGTTTGGTTGCC	2178	725	no
PF10_0356	PF10_0356e1s1	chr10	+	1	1	ATGAAACATATTTTGTACAT	TTTTTCTTTAGCAAGTCTCT	1698	566	no
PF10_0369	PF10_0369e2s1	chr10	+	2	1	TTAAAAGATAGCACAAATGG	TCCTAACTGTGTTGTATCCA	774	258	no
PF10_0379	PF10_0379e1s1	chr10	+	1	1	ATGAATAATTTAACTTTAGG	TTGCACGTATAAATTTGAAA	1080	359	no
PF10_0401	PF10_0401e2s1	chr10	+	2	1	GCACATAATAAAAATA AATC	TTTTTTTTTTCTTCGATAAC	834	277	no
PF11_0008	PF11_0008e1s3	chr11	-	1	3	TCATGTGGTTATTTCTGTGG	CTTGAGTAAAAAGTAAGTCA	2604	868	no
PF11_0048	PF11_0048e1s1	chr11	+	1	1	ATGGAAAATAGTGATTCGAA	CGTTTCAGAAATTTGTAGTT	738	245	no
PF11_0049	PF11_0049e1s1	chr11	+	1	1	ATGAATAATAATTTTAATAT	ATTTTTTGACATAACAAAAT	2571	857	no
PF11_0053	PF11_0053e1s2	chr11	-	1	2	TCTGGGAAAATGTCTTTATT	CCCCTTGATTTGGTCGTATT	1923	641	no
PF11_0067	PF11_0067e1s1	chr11	-	1	1	ATGTATAAAATAAAACAGTC	ACTTAAGTAATAACTAAACT	2277	758	no
PF11_0069	PF11_0069e1s1	chr11	+	1	1	ATGATCCTTAATATATATAT	CGAATCTCCTTTTATAATTC	207	69	no
PF11_0129	PF11_0129e1s1	chr11	-	1	1	ATGAATTTGTTTAAAGGGTT	TCTCTTTGCTTTTTTTGACT	2397	799	no
PF11_0156	PF11_0156e1s1	chr11	+	1	1	ATGTCCAAAGATAAGAGAAA	ATTTTGGTCGATATATGATG	690	230	no
PF11_0158	PF11_0158e1s1	chr11	+	1	1	ATGACGACGCTTAGAAGAAA	ACATGTATCATTTATATTTA	2520	840	no
PF11_0158	PF11_0158e1s2	chr11	+	1	2	TATCATTCCAATAATAAAAT	TCTATCCATCTCATCCATAT	2520	840	no
PF11_0161	PF11_0161e1s1	chr11	-	1	1	ATGGATTACCACATGGATTA	TTCAATTAATGGAATGAATG	1449	482	no
PF11_0162	PF11_0162e1s1	chr11	-	1	1	ATGGAATATCATATGGAATA	TTCAAGTAATGGTACATAAG	1479	492	no
PF11_0165	PF11_0165e1s1	chr11	-	1	1	ATGGATTACAACATGGATTA	TTCAATTAATGGAATGAATG	1455	484	no
PF11_0175	PF11_0175e4s1	chr11	-	4	1	CCATTGGATAATAAAAGCAA	GGTCTTAGATAAGTTTATAA	2409	802	no
PF11_0225	PF11_0225e1s1	chr11	+	1	1	ATGATGGAAGAACTTTTTAA	TATTTTATTGTTAAGTAATA	2448	815	no
PF11_0226	PF11_0226e1s3	chr11	-	1	3	TTTCTTTCTGATTACACTAC	TATCTCTATTTTTGTTCTTA	2055	684	no
PF11_0240	PF11_0240e2s2	chr11	+	2	2	AATAAAAATTTAGATAATGA	AAAATTGCCTCTATTATAAT	2619	873	no
PF11_0240	PF11_0240e2s5	chr11	+	2	5	ATAAGCGAAGAAGAGGAAGA	ATTTAGATCTATTGAACAAA	2610	870	no
PF11_0245	PF11_0245e1s1	chr11	+	1	1	ATGAATGAACCTTTTAGTTT	ACCCAATGTTCTTGCCAACA	768	256	no
PF11_0270	PF11_0270e1s1	chr11	-	1	1	ATGAAAAAAATAATTATGGT	TACTAATTCACTCTTTTTTT	1551	517	no
PF11_0270	PF11_0270e1s2	chr11	-	1	2	GATAGTTTACAAAGAGTATA	AATGGTTTGGTTTGAGTTAA	1545	514	no
PF11_0302	PF11_0302e1s1	chr11	+	1	1	ATGATTAAAATAATATTAGC	GCTCGATATTGGTGTGTTTT	1359	452	no

PF11_0307	PF11_0307e1s2	chr11	+	1	2	GTATTACCGTTCCAAGATAT	GTGCGTATTTTTTTTTTTAT	2034	677	no
PF11_0341	PF11_0341e1s2	chr11	+	1	2	ATTGTATTTTCGAAAATTCA	CTCGTTATAATCAAACTTTC	1536	512	no
PF11_0356	PF11_0356e1s2	chr11	+	1	2	TATGCAAATTGTTTAACATC	TATATTTAAAAGATCATATG	2571	856	no
PF11_0358	PF11_0358e2s1	chr11	-	2	1	GATAATAACGATTATAAGAA	CACTACGGCATTCGTACCAC	1563	521	no
PF11_0358	PF11_0358e2s2	chr11	-	2	2	GATTATGAATTTTATGGAGT	CTTCATGTCAAAAACATTTT	1557	518	no
PF11_0374	PF11_0374e2s1	chr11	+	2	1	GGCGGAGTATCACAGGAAAG	ATTTTTTTTCTTTGAGATGT	1641	547	no
PF11_0395	PF11_0395e1s2	chr11	-	1	2	ACAGAATTAATTTCTGACGA	TTTACTTTTTAATTCATTAT	2580	860	no
PF11_0395	PF11_0395e1s3	chr11	-	1	3	AATATACAGAAATATAAACA	CCTGTTGTTGTCGTTCCTAA	2580	860	no
PF11_0395	PF11_0395e1s4	chr11	-	1	4	GTTGAAAATAATTTGATTAA	TGTATTAAATGTATTCATAT	2580	860	no
PF11_0395	PF11_0395e1s5	chr11	-	1	5	GATTCTAATATAAATGAAGG	CAAATTCGACTGGCGATCGT	2577	858	no
PF11_0407	PF11_0407e1s1	chr11	-	1	1	ATGCCTTTTTATGATAATTT	TTCATTTCTTTTGTCGCTCA	1518	505	no
PF11_0422	PF11_0422e1s2	chr11	+	1	2	ATGAAGAACGATGAAAGAAA	AGATTGACTTGGAAAATAAT	2601	867	no
PF11_0512	PF11_0512e2s1	chr11	-	2	1	TATAATTTTACATATAGTGG	ATGTTCCCTTTTCTCCATTT	798	266	no
PFL0015c	PFL0015ce2s1	chr12	-	2	1	GTGTATAGTAAAAACAAACC	TTGATTTAATAATTTTGTGT	969	322	no
PFL0085c	PFL0085ce2s1	chr12	-	2	1	TTTATTTCTGATAAGCCTTT	TACTATATTTTTATCTCCAT	567	188	no
PFL0130c	PFL0130ce1s1	chr12	-	1	1	ATGGCAAAACAAAGATTAAC	AGCAAACGTTTTAGGTTTCA	1875	625	no
PFL0185c	PFL0185ce3s1	chr12	-	3	1	TACGATGATAAAATGACCGA	AGAAGTAAGAGGATCCTCAT	963	320	no
PFL0305c	PFL0305ce2s1	chr12	-	2	1	GTTATGAATTCAGATATGAA	TCCAACATCATCTATCAAAT	240	80	no
PFL0405w	PFL0405we3s1	chr12	+	3	1	GGAGATATTAATTATGATAA	ATATTCCTTAGTATATATTT	1803	601	no
PFL0445w	PFL0445we1s1	chr12	+	1	1	ATGGAATTCCTGAGCAATAT	TCTTACAATTACATTCTCGT	2193	731	no
PFL0545w	PFL0545we3s1	chr12	+	3	1	GTTGGAAATGATGAGGTTTA	TATGTTTCGTCCTGGAGGAA	2631	877	no
PFL0555c	PFL0555ce1s1	chr12	-	1	1	ATGAAATGTTTTTATGAACA	TTGAACTATTCCATTTCGTT	2778	926	no
PFL0625c	PFL0625ce1s1	chr12	-	1	1	ATGCAAACGTTTCAGAAACC	CTTTAATAGTTTTTCATTTT	2097	699	no
PFL0635c	PFL0635ce1s2	chr12	-	1	2	TTTAATGTTATAAAAAATCC	TATTTTAGCGTCATAACCTT	1659	552	no
PFL0730w	PFL0730we1s1	chr12	+	1	1	ATGAACATAAGCAACAGTAG	CCTTTTCATTGGGAAACATG	2766	922	no
PFL1010c	PFL1010ce1s2	chr12	-	1	2	AGAATGAAACAAATAAAGAA	ATCATCAAGTTTAACAGATT	2367	789	no
PFL1010c	PFL1010ce1s3	chr12	-	1	3	ATGAATATGTTTGAAAATAA	ACTTGTAGACATAGTTCTTT	2364	787	no
PFL1135c	PFL1135ce1s1	chr12	-	1	1	ATGGAAGAAATTGAAAATGC	CACTTCTATATGTTCAGCCT	537	179	no
PFL1135c	PFL1135ce2s1	chr12	-	2	1	GTGTTTACCAAAGTTCAGAT	ATGTTGAAAATTATATACAA	2103	701	no
PFL1255c	PFL1255ce1s1	chr12	-	1	1	ATGAAAGTTCTTAATTTCCC	CTTGCAGAAATTAAAGTGAG	2439	813	no
PFL1300c	PFL1300ce1s1	chr12	-	1	1	ATGTTTATAATAAAATGCAT	ATTTTCCGTAATATAATTTT	1488	495	no
PFL1395c	PFL1395ce1s1	chr12	-	1	1	ATGTATATTGAGAAGTTAAA	CTTATGAGATACCTCGTACT	2451	817	no
PFL1395c	PFL1395ce1s4	chr12	-	1	4	TTAAGACCATCATGTTGTAA	TAAACATAACTCGTGGAAAT	2439	812	no
PFL1410c	PFL1410ce1s1	chr12	-	1	1	ATGATGAGACGGAGAAGCGT	TTTTTTTTTACAATCGCTTT	2148	716	no
PFL1410c	PFL1410ce1s3	chr12	-	1	3	AAAATTGGAAGACCTCTAAT	ATTTAATTGTTTTTCTTGAA	2139	712	no
PFL1545c	PFL1545ce1s1	chr12	-	1	1	ATGAGAATGAAAAGAATTCA	ATGTACCACTTTTATTGCGC	1023	341	no
PFL1605w	PFL1605we1s2	chr12	+	1	2	GAGGATAAGCATTATGAATC	GTCGTCAAATGCTAAAGGTC	2145	714	no
PFL1620w	PFL1620we1s3	chr12	+	1	3	GATGAAAATAATAATAGAAA	ATAAGGATAATTGTTATCAT	2733	911	no
PFL1620w	PFL1620we1s4	chr12	+	1	4	TGCAACAAAGCAGATAATTT	TCTCCAGTATTTTATGTTTA	2733	911	no

PFL1680w	PFL1680we1s2	chr12	+	1	2	GCATCATCTAATAGTTCACA	CCTCAAAATAAAGACAGAAT	1779	593	no
PFL1880w	PFL1880we1s1	chr12	+	1	1	ATGAAAATGGATATTATTAA	CTTATTTCTTGATTTATAAA	2379	792	no
PFL2190c	PFL2190ce1s2	chr12	-	1	2	AATATGAAATTAAATATGGA	TGTGTTATATTGAGAAGTGT	2433	810	no
PFL2335w	PFL2335we1s2	chr12	+	1	2	ATGTTAGGTGATGAAAAATT	TTCAGGAAGCTTATCCTGTA	3009	1002	no
PFL2430c	PFL2430ce1s1	chr12	-	1	1	ATGGATTTACATGTAAAAAA	GTCAAAACTCAAGTCCATAT	2040	679	no
PFL2440w	PFL2440we2s2	chr12	+	2	2	AAAACGGTGGATGTTATAAG	TGAGTGGAATAAGAATGCCA	2403	800	no
MAL13P1.107	MAL13P1.107e1s1	chr13	-	1	1	ATGAATATTCCTCTTATCAT	ATTTGTTTTTATATTTTCCT	2259	753	no
MAL13P1.107	MAL13P1.107e1s2	chr13	-	1	2	GAAGAAAATATTAACACAAA	TTCGTTTATGTAAAATACAT	2256	751	no
MAL13P1.114	MAL13P1.114e3s1	chr13	-	3	1	CCCAAAAGATTGGAAAATCG	CATATAATTTTCTGATTTAT	2919	973	no
MAL13P1.123	MAL13P1.123e1s1	chr13	+	1	1	ATGGAAAATCGCAAAGTTTT	ATTAGGGATATTAGAAGATC	2529	843	no
MAL13P1.133	MAL13P1.133e3s1	chr13	-	3	1	CTATACAACTACATAATCCT	ATTGGGTGTATTAAATAATT	591	196	no
MAL13P1.140	MAL13P1.140e1s3	chr13	-	1	3	ACAAACCCTTATGCTATTAA	CTCATCGGAGAGTTTTCCTA	2778	926	no
MAL13P1.148	MAL13P1.148e3s2	chr13	+	3	2	GTAAGTCGTGCAGGTTACCC	ACATTTATGTGTTATAATAT	2109	703	no
MAL13P1.178	MAL13P1.178e2s1	chr13	+	2	1	GGATCTCTTACAGGGAAAGT	AACATTTTCTTCAATGGAAT	1053	350	no
MAL13P1.19	MAL13P1.19e1s1	chr13	-	1	1	ATGAATGAAAATAATAGCAA	ATGAATAGAATGATTTTGTT	2832	944	no
MAL13P1.201	MAL13P1.201e1s1	chr13	+	1	1	ATGCATTTCTGTAGCAAGAG	AGCATATTTGCACCTATATA	1728	576	no
MAL13P1.218	MAL13P1.218e2s1	chr13	-	2	1	ATGATGCAAAAAGTTTTTGA	TGAATTAATATTCCTTTGCA	1785	594	no
MAL13P1.22	MAL13P1.22e2s1	chr13	-	2	1	TTAAAATGTTTCTCTTTTCC	TTCACTTTCAGTATCATCAT	2544	847	no
MAL13P1.230	MAL13P1.230e1s1	chr13	-	1	1	ATGAAGGACGAAATAGAAGA	ATCGTTAATTCTGGAAGAAA	1938	646	no
MAL13P1.234	MAL13P1.234e1s1	chr13	+	1	1	ATGTTCGAATCACTAGTTGA	TTCCTCATCATCATCGTTAT	3039	1013	no
MAL13P1.234	MAL13P1.234e1s4	chr13	+	1	4	AACAATAAAAGCAACCATAA	ATTGACATCCTCATTAGCAT	3039	1013	no
MAL13P1.234	MAL13P1.234e1s6	chr13	+	1	6	TCGTCTGTTATATATCCTAG	AAGGGCAGAATTATTGGCGC	3027	1009	no
MAL13P1.278	MAL13P1.278e1s5	chr13	+	1	5	AGAAATAATGAAAAAATATC	TGTTGTCTTATTTAAAATTG	2463	820	no
MAL13P1.285	MAL13P1.285e2s1	chr13	-	2	1	GGGCTTGATTTATTCTTTAC	ATTTTGATCTGATTTTGTGT	2943	981	no
MAL13P1.323	MAL13P1.323e1s2	chr13	+	1	2	AAGGATTTATCAAATGTTAG	ATTTTTATCATCTCCTTTAT	2493	831	no
MAL13P1.323	MAL13P1.323e1s3	chr13	+	1	3	TTTATACCTAAAGAATATTA	ATAACATATTATGAGGAAGT	2493	831	no
MAL13P1.346	MAL13P1.346e1s2	chr13	-	1	2	AATAATAATGTCAACATGTC	TGATATATTTTCATTTAAAA	2577	858	no
MAL13P1.39	MAL13P1.39e4s1	chr13	-	4	1	ATACATACAGATTTGTTATT	CTTCGTACTACTAAACCTAC	2142	714	no
MAL13P1.56	MAL13P1.56e1s1	chr13	+	1	1	ATGAAATTAACAAAAGGCTG	TAAAAATTGAACACTTCTTA	1659	553	no
MAL13P1.78	MAL13P1.78e1s2	chr13	-	1	2	CAAAATATTAATGCATCTGA	TAGTTGTGAATATATCAAAT	1647	548	no
PF13_0012	PF13_0012e1s1	chr13	-	1	1	ATGAAGGTCTCTAAATTAGT	GTTCTCTTCTTGAGATAAAT	690	229	no
PF13_0014	PF13_0014e1s1	chr13	-	1	1	ATGGATGCTGTTCAAAAGAG	TCTCTTTCCAATAATTTCAC	420	140	no
PF13_0021	PF13_0021e1s1	chr13	-	1	1	ATGAGCGAAAATAATTTAAG	ATCTATTTCTATTTTTTTTT	636	211	no
PF13_0040	PF13_0040e2s1	chr13	-	2	1	AAGAACCCTGAGAGACATAA	TATTCCTTCATCGTATATTT	1752	583	no
PF13_0044	PF13_0044e2s1	chr13	-	2	1	GATTTTAAAACAGTTGGGAG	TCTTTCATTAATTTCTTTTA	2406	802	no
PF13_0044	PF13_0044e2s2	chr13	-	2	2	ATAACAGAAAATAGAACATT	ATTATAATTAGAACAATTCA	2406	802	no
PF13_0062	PF13_0062e1s1	chr13	+	1	1	ATGGCATGTATAAGCGCTAT	GGACATTCTGACCTGATAGT	1314	437	no
PF13_0080	PF13_0080e1s3	chr13	+	1	3	TACATTTTTGCCGATTCATA	ATTTTTTATTTTGAACATGT	2553	850	no
PF13_0121	PF13_0121e3s1	chr13	+	3	1	GAAACCATTAAAGTACCTAG	ACAATCAATTAACATTAGAT	1131	376	no

PF13_0153	PF13_0153e1s1	chr13	+	1	1	ATGGCTTCGGGAAAAGGTAA	TGATATAAAATGTTCAAAAT	1536	512	no
PF13_0157	PF13_0157e1s1	chr13	-	1	1	ATGATTTACAAATTTTACAA	TACTTTCATTTCTATTTGTC	1683	560	no
PF13_0161	PF13_0161e1s2	chr13	-	1	2	ATAAAAAAAGATGATAATAC	AATGCAATTACAATAATTCG	2718	905	no
PF13_0173	PF13_0173e1s1	chr13	+	1	1	ATGAAAAAGAAAAAAAAGAG	CCCTGACGATTCCAATTTTA	1674	558	no
PF13_0179	PF13_0179e1s1	chr13	-	1	1	ATGTTAAGATTTGTCAATGA	TATAGGTGTACCCCAATATC	1938	646	no
PF13_0182	PF13_0182e1s1	chr13	+	1	1	ATGAATATTTTGTGCATCCA	TGGATACACAACTTGACTAC	2787	929	no
PF13_0201	PF13_0201e1s1	chr13	-	1	1	ATGAATCATCTTGGGAATGT	ATTCCACTCGTTTTCTTCAG	1725	574	no
PF13_0214	PF13_0214e2s1	chr13	+	2	1	AAATTACTTGCTCCCAAAAA	TTTCCATACCTTTCTGTCGA	1227	408	no
PF13_0248	PF13_0248e1s1	chr13	-	1	1	ATGTGTATGGGAAGAATGAT	TATGCTAACATACATGTAAA	1320	439	no
PF13_0285	PF13_0285e1s1	chr13	-	1	1	ATGACGAATTACTCTAAAAT	AGAATTGGCGTCCAATTTAG	2412	803	no
PF13_0327	PF13_0327e1s1	chr13	+	1	1	ATGTTTAAGTTTAATTCTAA	CCATTGTCTTCCAATAACCT	633	211	no
PF13_0339	PF13_0339e1s1	chr13	-	1	1	ATGAATGTAGAAGATAATTC	GCCCTTAATATACATATCAT	2751	917	no
PF13_0350	PF13_0350e1s1	chr13	-	1	1	ATGATTGATGTCATTAACAT	ACTTAAGGCCTTAACAACCA	1731	576	no
PF13_0320	PF13_0320e13s2	chr13	+	13	2	TCTAAAGATGGTGTTTCTTA	CGCCTGTGGCTCGTTTTGTA	2925	974	no
PF13_0320	PF13_0320e9s1	chr13	+	9	1	CAAATTTGTGAGGATGATGA	CATTGATTCTACATTTGTCA	1077	359	no
PF14_0013	PF14_0013e2s1	chr14	-	2	1	AATAACGGAGATCGAAATTC	TTCATTAGAACTTTCTAACA	1341	446	no
PF14_0031	PF14_0031e4s2	chr14	-	4	2	AAGTGTGATATTATTGCAGG	CTTCCTCTCTTCATTTTTAC	2955	984	no
PF14_0144	PF14_0144e1s1	chr14	+	1	1	ATGATCACGAGTACATATCA	CTTTGCTTTTCTATTTCTGG	1563	520	no
PF14_0145	PF14_0145e1s2	chr14	-	1	2	GAGGAGATATCAGAATATAT	ATAACACAAAGATTTATTTA	2103	700	no
PF14_0170	PF14_0170e1s1	chr14	+	1	1	ATGAGGATGGATTACCATGA	GCAAACACTTTTTTTATTTT	2706	902	no
PF14_0170	PF14_0170e1s3	chr14	+	1	3	AATAATCTCATATGTAATTC	GATGTTGCTGATATTTTTGA	2706	902	no
PF14_0170	PF14_0170e1s4	chr14	+	1	4	AGTATTGAAAACAGCAATGG	ATTTATATCTTCTTCTTTAT	2706	902	no
PF14_0188	PF14_0188e1s2	chr14	-	1	2	ATAAGTTTATTAAATAAATA	ATCTTTTAAAATATGAGCAT	2118	706	no
PF14_0196	PF14_0196e1s1	chr14	-	1	1	ATGCAGGAATTTGTTATGAA	ATTCAATAAAAGTAATAAGA	1899	633	no
PF14_0228	PF14_0228e1s1	chr14	-	1	1	ATGAATAAACAATCGGATTC	AACTTCAATTGAAATAATAT	2367	789	no
PF14_0249	PF14_0249e1s1	chr14	+	1	1	ATGGTTTTAGGTTTTAAATT	TAAATTAACAGGTATATATA	1785	595	no
PF14_0315	PF14_0315e2s3	chr14	-	2	3	AGAAATAAAAATACATGTGA	ATTTTTTTTATCTTCCAAAT	3006	1002	no
PF14_0316	PF14_0316e1s1	chr14	-	1	1	ATGGCGAAAAATAAAACTAT	GGAACCTAATATAAAATTTT	2124	708	no
PF14_0334	PF14_0334e1s1	chr14	-	1	1	ATGGGGAAAGAAAATATAGA	TATAATATGTGGAAAATCAG	2373	791	no
PF14_0338	PF14_0338e1s1	chr14	-	1	1	ATGAATAAAATGAAGAAAAC	ACTATAATTATTACTTGGAT	891	297	no
PF14_0338	PF14_0338e9s1	chr14	-	9	1	AGAAAAGAAGAGGCTAATCC	TGTGGGGCTCATACCATGAG	966	321	no
PF14_0370	PF14_0370e1s1	chr14	+	1	1	ATGAAGGAAAGAATAAATGA	TTTATTTGTCTCATTTCTAG	2124	708	no
PF14_0370	PF14_0370e2s1	chr14	+	2	1	GGTAGTGGAAAAACAGTTAT	ATTTTTACGTTTTTCTTGAA	1545	515	no
PF14_0370	PF14_0370e2s2	chr14	+	2	2	CAATTTGATGATAAAGCTTT	CCATTGTACATTCTGAGATG	1542	514	no
PF14_0384	PF14_0384e1s1	chr14	+	1	1	ATGAAAGAATCAAGTTCTAA	TAATAATGTAGATAAAACAG	1662	553	no
PF14_0392	PF14_0392e5s1	chr14	+	5	1	AAACTCTATTTGGACGAAGT	AAGCTCACTATTATTAGTCC	2076	692	no
PF14_0401	PF14_0401e2s1	chr14	-	2	1	AAAATAACACTGCAATATAA	TGATATTGTTCCTTGATTTA	1080	359	no
PF14_0407	PF14_0407e1s2	chr14	+	1	2	TTGAAAAAAAAAAAACATTA	ATTTCCTTTCTTAGACTTTC	2580	860	no
PF14_0412	PF14_0412e2s1	chr14	-	2	1	GCCGATATAAATAACATAAG	AAAAGCCACAAACGCCCAGA	2337	778	no

PF14_0419	PF14_0419e6s1	chr14	-	6	1	GATAATGATTCTGAAGATAT	CTGAGCCCTTATTGGTATAT	1779	593	no
PF14_0433	PF14_0433e4s1	chr14	+	4	1	CAAATGAACAAGAGACCTAG	ATCTCCTTGGTTATAATTGT	939	313	no
PF14_0456	PF14_0456e2s2	chr14	-	2	2	ATATGGAATATGAATAATTT	TTGACCCTTTGCATGCCCCT	1887	628	no
PF14_0461	PF14_0461e1s1	chr14	-	1	1	ATGGCTACTATCGAAAAAAA	TTCTTTGTCCTCTTGATATT	2493	831	no
PF14_0463	PF14_0463e1s4	chr14	-	1	4	TATAATTGTAATGATTTAGA	TTTTTTGGATGGTATAATGT	2757	919	no
PF14_0470	PF14_0470e2s1	chr14	-	2	1	TCTTACATTTTGGTGATAAG	GGAACTAACTCCTGAATCAT	1920	640	no
PF14_0494	PF14_0494e1s2	chr14	-	1	2	GATTTTATTTGCTCATATGA	TAACATGAGGGCA TGTCTTT	1569	522	no
PF14_0495	PF14_0495e1s2	chr14	+	1	2	AATACGAATGACAGTATGCT	ATTATTTATATTTTCTATAT	2229	743	no
PF14_0515	PF14_0515e1s1	chr14	-	1	1	ATGGAAGAAGGAAGGAATGA	ATTTGAATTATCCCATGTAT	2136	712	no
PF14_0515	PF14_0515e1s2	chr14	-	1	2	AAAATAACCAACATTGATGA	TTCATTCAAATTAAAAGTAA	2133	710	no
PF14_0546	PF14_0546e1s1	chr14	-	1	1	ATGGTGGGTATGAATAAAAA	TACGGTTGTCATAACTCCTT	1920	639	no
PF14_0589	PF14_0589e1s2	chr14	+	1	2	CTTGTAGGTGATAATAAGCC	TGCATTCTTTAAACACTCAT	1662	553	no
PF14_0597	PF14_0597e2s1	chr14	-	2	1	TTTCGATTGTATTTGATTAA	TAAATATTTGATTTTTCCAA	1110	369	no
PF14_0620	PF14_0620e1s1	chr14	+	1	1	ATGGAGGTATTTCTTCAATT	TCTGAATGATTTAATAATGC	1899	633	no
PF14_0626	PF14_0626e5s2	chr14	+	5	2	AAACATATTTTTAAAATAAT	TTCTATTTCTTTTAATAGTC	2493	831	no
PF14_0632	PF14_0632e1s1	chr14	+	1	1	ATGAGATTTGAAAATCAGTT	AGATAAAACCATAAAAGATT	1674	558	no
PF14_0632	PF14_0632e1s2	chr14	+	1	2	TCTTTAGGTGTTGTATATAA	CGTGTTATTATTAGAATTTT	1671	557	no
PF14_0633	PF14_0633e1s1	chr14	-	1	1	ATGGAAGATAACAATATGAA	AGATTCAGAATTATCATATG	2442	813	no
PF14_0647	PF14_0647e3s2	chr14	+	3	2	AATAATGATAATAATGATAA	TTTCAAATTCCATATTTCAA	2388	795	no
PF14_0649	PF14_0649e2s1	chr14	-	2	1	GCAAGTAAAAACTTCAGCCT	AAATAAGAATACAGATAAAC	2565	855	no
PF14_0649	PF14_0649e2s2	chr14	-	2	2	GGACATACTACACATTTAGT	TGCATCTTTATCACTACCTT	2565	855	no
PF14_0664	PF14_0664e1s1	chr14	+	1	1	ATGCCTAACAATGCTCATAA	TTGTAATTGGATAGATATTA	2427	809	no
PF14_0664	PF14_0664e1s3	chr14	+	1	3	TCATCCTATCAAAATAATAA	ACAATTATATTTGTTATCAT	2427	809	no
PF14_0664	PF14_0664e1s4	chr14	+	1	4	TATAATGTGGAAGATGATAA	TTCACATCTAGCCATTTTTT	2421	807	no
PF14_0668	PF14_0668e1s3	chr14	+	1	3	TATGAAAATGATATAGGAGA	CCTATGTACTAATAACTGAA	2412	803	no
PF14_0678	PF14_0678e3s1	chr14	-	3	1	GCCTTGAGAGAAATATGGGA	TTCTTTATTTTCATCTTTTT	552	183	no
PF14_0681	PF14_0681e2s1	chr14	-	2	1	TTTGGAGTAAATGAGATAAT	CAAAATATTTTTCAAGACAT	1434	477	no
PF14_0690	PF14_0690e1s2	chr14	+	1	2	TTTAATTCAAGCGAAAAACA	ATTATAAAGAATACTATTAT	2277	759	no
PF14_0690	PF14_0690e1s3	chr14	+	1	3	GGTTTAACCGAAGCGGCTAA	TCTTTTACAATTCTCAAGAT	2268	756	no
PF14_0699	PF14_0699e2s1	chr14	-	2	1	GATTCCTATCTTAAAAATTG	ACCCAAATATATGGAGGGTA	747	248	no
PF14_0722	PF14_0722e3s3	chr14	-	3	3	ATACTTGGATATTTTAAATG	TTCATTTTCCTTAATATTTT	3042	1014	no
PF14_0751	PF14_0751e1s1	chr14	+	1	1	ATGCGTATTGTATACATTAT	AGCATATACGGTATGCCTTT	879	293	no
PF14_0345	PF14_0345e1s1	chr14	+	1	1	ATGATTCTCAAAAACATTTT	CAAAATAAGAAAGAAATTGT	1899	633	no
PF14_0345	PF14_0345e2s1	chr14	+	2	1	AGTGTCATGGATTCATCGCG	TAATAAACCTCTGAATGGTG	1302	433	no