

**Table S1.** Primer sequences and amplicon details. Partially overlapping amplicons were tiled across the target regions with a maximum amplicon length (forward and reverse primer length plus intervening unique sequence) of 200-bp. Primers were designed with melting temperature range 59.0°-61.0° C. Each primer included an orientation-specific tail sequence for subsequent ligation of adapter and barcode sequences.

Gene	Chr	Start	End	F-Primer	R-Primer	F-Primer Length	R-Primer Length	Unique Sequence Length	Total Amplicon Length	GC %
ATM	chr11	108098316	108098513	TTACAGACAGTGATGTGTCT	TCAACTTCTTTGAAATAAAAAGGAAATAA	23	32	143	198	32
ATM	chr11	108098462	108098632	GTGTGATAGTAAACCCATTAATTTCTT	AAATTTGAAATAGAAATACCTAAAACAGCATCC	30	32	109	171	30
ATM	chr11	108098508	108098694	AGTTGAGAAATTTAAGCGCTGAT	ACACACAAAAGTAATACACACAGAA	24	27	136	187	29
ATM	chr11	108099820	108100000	CTTTGTGATGGCATGAACAGCT	ATCTTTTCTGGCTGGAGGCTTG	23	23	135	181	31
ATM	chr11	108099927	108100103	AAAGAAAACAGAATGCTGAGAAATAGC	CACGGCAGAGTAATCTGTTAAGC	26	23	128	177	36
ATM	chr11	108106328	108106504	AGTTGCCATTCGAAGTCTTAT	TGAGTAGATGTGCTACAATCAGC	23	23	129	177	31
ATM	chr11	108106395	108106590	AGGAGCACCTAGGCTAAAATGTC	ATTCACAAAACACACCTTCAAAC	23	25	148	196	35
ATM	chr11	108114576	108114764	TCCTTTTCTGTATGGGATATGGA	ACAGATGAATTAATCTAGCCACT	25	24	140	189	26
ATM	chr11	108114683	108114870	TGTTCTCTGTGACTTACGGCTG	ACAAAAGAAAAAGAGATAGATACCTCG	23	29	136	188	37
ATM	chr11	108114719	108114918	CACAAGATGTTCAATAGAGTTTATGGG	CTGAGTCTAAAACATGGTCTCG	27	23	150	200	35
ATM	chr11	108114741	108114919	AGTGGCTAGATAAATCATGCTGT	ACTGAGTCTAAAACATGGTCTCG	24	24	131	179	35
ATM	chr11	108115460	108115633	TGTACAGTTTGTCCCTGGTT	TGGGAAGAATTTCACTCTCAATTCACA	23	28	123	174	40
ATM	chr11	108115551	108115750	AGCAGCTTCTACTTCTCCCTCA	TTTCTGGGTTTGGCTCTCTC	23	23	154	200	35
ATM	chr11	108115614	108115808	AGGAGATGAATTTCTCCCACTTT	ACTTCTATGTTTGAAGAAGAAACAA	24	26	145	195	31
ATM	chr11	108117623	108117815	TTTGTGGAGCTAGCAGTGTAAA	TTTGACCGCAATATACGAAATCC	23	24	146	193	33
ATM	chr11	108117236	108117932	ATGATCTGCTAGTGAATGAGATAAGT	TTTAAAGGCCAAAATGCCAGT	26	23	148	197	33
ATM	chr11	108117791	108117986	AGGATTTCTAAATTTGCCGTCAAAG	AGGAATAGTGTGATGACAGAGTCA	26	25	145	196	34
ATM	chr11	108119559	108119753	GATACGAGATCTGCTGTCC	TCCTTTTCAAGGGACACTGTAAT	21	24	150	195	36
ATM	chr11	108119688	108119880	AGATTTCAACTTACACTACTACACA	AACATACAGAGATTAATAATGACACTGAA	28	29	136	193	35
ATM	chr11	108121365	108121538	TTTCTTTAGTTTGTAAATGATGGA	CCATGCTGCTGGGGTAG	28	20	126	174	34
ATM	chr11	108121468	108121666	AGTTTACCTAAGTGTGAGCTGGT	AGGTAATACACAAATTTATCCAGATG	24	29	146	199	40
ATM	chr11	108121552	108121722	TATGTTTACGATGCTTACGGGA	GGCTCCAGTAAGCCAAAGTTTTC	23	24	124	171	37
ATM	chr11	108121652	108121851	TTTGGTATATACCTTCTGGTT	TGTGTTCTGGTGTGTTTATCTGTAAGT	27	27	150	200	37
ATM	chr11	108122503	108122698	AGATAAAGCTTTGCCCTCCAA	AAGAGCAATTCATTTATGATCTCTTT	23	27	146	196	37
ATM	chr11	108122626	108122820	TGGGAATAGAGCAAAAATGTGTGAA	AGTGGAGAGAGCTGTATAAACA	26	23	146	195	34
ATM	chr11	108123492	108123662	TCCTTACATGGCTTTGGCTTCT	AAGAGCATATAGATAACATCACTCTG	24	30	117	171	33
ATM	chr11	108123547	108123725	TTTTCTCACTTGTACTGGGAAA	GATCGACAGACTCCACGCTAAA	25	23	131	177	33
ATM	chr11	108124488	108124684	AGGCAAAGCATAGTACTTGGT	GAGAAGCCAATCTGGACTGGT	23	23	151	197	35
ATM	chr11	108124529	108124727	ACTTCTTGAAGTGAACACACCA	CAGAGACACAGCTCAGTGAAT	24	23	152	199	39
ATM	chr11	108124643	108124842	AGAAATGGTATGAAAAGCACCA	CCCTTATCTCTCTTAACAG	24	23	153	200	38
ATM	chr11	108126837	108127036	GAACCTTTTGTTTTAAATGATGATGATGTT	GCTTCTCTTCAGCTATACACCC	36	24	140	200	31
ATM	chr11	108126940	108127114	AGATTACAATTCGAAACTTGTGCC	ATTTCAATCAAATTCGAAACTTGTAGT	27	33	115	175	37
ATM	chr11	108128126	108128315	CCAAGATAAAGTCACTGAAAAGCA	GCAACTGTGATCACTGATCA	28	23	139	193	33
ATM	chr11	108128198	108128373	TTCAACAATGCTCTAATGCAATGTG	TCCTATCTCAAAAAAACAAGAA	26	28	122	176	35
ATM	chr11	108129666	108129837	TGTTTTTATTCTTTGTTGGTTGTT	teaaantagATGACAAAACAGGAAGC	28	27	117	172	31
ATM	chr11	108137849	108138043	TGCTCTGCAAGAAGCCAT	TCGTTTGTACTCACTACTATCA	19	27	149	195	40
ATM	chr11	108137915	108138110	GCCATTTGACCCGTGGAGAATG	AAAGAAGTAAAGAAATCCCAAGTAGTAAA	22	30	144	196	37
ATM	chr11	108139084	108139260	TATATGGCTGTTGTCCTTCTC	GCTGCCTAAAGGACACAGTAT	23	23	131	177	37
ATM	chr11	108139135	108139327	AGGTGCCATTAATCTTTAGCTG	GTTGAGGGATTTGGTAGGTTCT	23	22	148	193	40
ATM	chr11	108139255	108139439	GGCAGCTGATATCGGAGGAAAT	TCAAATTTCAAAGACACCATGTGA	23	25	137	185	38
ATM	chr11	108141739	108141891	AAAGTAAATGATTTGGGATAAACCTGA	AAGGTTTTAATTTTACAGTAAGTGGT	28	28	97	153	36
ATM	chr11	108141813	108142007	TTCTGGGAGAGAGTACCCTTG	TGGTCAAGCAGTAAAGAAACA	23	23	149	195	33
ATM	chr11	108141856	108142052	ACTTCTGAACCACTACTGTAAGAA	TCTCACAGTAAAGGACATGGTT	25	23	149	197	29
ATM	chr11	108141993	108142192	GTATCGTGTGACCAAGATGTT	TGCATCTGATCCACAGATAGCA	23	23	154	200	38
ATM	chr11	108143152	108143347	AGCACAGAAAAGACATATGGAAGT	TGCAAAAACCTCACTCAAGCAAA	24	23	149	196	33
ATM	chr11	108143256	108143454	CAGGCATCTAACAAAGGAGAGGA	ATCAGCTACGGGAAAAGAACTG	23	23	153	199	32
ATM	chr11	108143380	108143553	AAGCAGTCTTTGTTGTAATGAT	GCGCAACTTGGTGTGATGTCAG	25	23	126	174	34
ATM	chr11	108143427	108143626	AACCACAGTCTTTCCCGTAGG	TGCCATCTGCAGCATCCAAATA	23	23	154	200	39
ATM	chr11	108150143	108150331	ATGCTTTGGAAAGTAGGGTTGA	TCTCTACTTCTTCTGAGCTTT	23	23	143	189	37
ATM	chr11	108150215	108150412	AAAGTTGTTCCAGGACACGAAGG	CCAACTTGGTGAAGTATTTATGGGA	23	27	148	198	37
ATM	chr11	108151619	108151817	TGTGTATAGCTTGTCAAAAATCTGG	AGGGCTACAGGATAAAACCCACAG	26	23	150	199	29
ATM	chr11	108151640	108151837	TCTGGAGTTCAGTTGGGATTTAT	AAAGCTCTTTTCCGACATAGG	24	23	151	198	30
ATM	chr11	108151724	108151896	CCATATGCTGAGAACCTGCGAAA	CCTTTTACAAAGGTTGAGGTTCTA	23	23	126	173	39
ATM	chr11	108151805	108151985	ATCCTGTAGCCCTATTCGCGAAA	AGATGCCACTCAGAAAATCTAGC	23	23	135	181	36
ATM	chr11	108153336	108153531	tgatGTTGTTTCTAGGCTCACTC	AGATTTAGCCATTTCAAACCCAGA	25	24	147	196	29
ATM	chr11	108153425	108153622	TGGTTCGTGCAAGTTTATAGAAA	TCATGTATAAATCTCAATAAATCTCAAT	23	23	142	193	30
ATM	chr11	108153489	108153681	TGGCATCTCATTTAGATTAICTGG	GGTGAAGGGGACTGCTAAGTATT	25	23	145	198	28
ATM	chr11	108154946	108155121	ATTTTATAGTCTTTAATAAGGTTTGTATCC	TCTGCTGACCTCATAGGCAAA	32	23	121	176	35
ATM	chr11	108154966	108155165	GGTTTTGATCCACATCTGGTGA	CATAGACCTTGGTAGCAGTCTCTC	23	24	153	200	41
ATM	chr11	108155026	108155211	TCAGATTCAAGAGGACTGAAAAGT	TGAAGCATTACTCTGTTTCCCAA	25	23	138	186	40
ATM	chr11	108155137	108155333	GCAAAGAGAGACTGCTACCAAGG	TGCTAGATAATGATTACCAAGCTAAGT	23	29	145	197	30
ATM	chr11	108158251	108158445	AAATATAGCTTTTGGAGTCTCTTG	TACCTGAAAAGTCCACAGAGGTC	25	23	147	195	35
ATM	chr11	108158316	108158499	TGCCCTTGCAGATGATCACTTA	ACTTCTTTAAAACCTTGTGAAGTTAGAGC	23	29	132	184	38
ATM	chr11	108159628	108159799	TCATTTTGAAGATTCACCTGGTCA	TTTAACTTGGTTTATGACAAATGCTG	24	27	121	172	34
ATM	chr11	108159697	108159875	CTGTAGGGATTTGGATCTGCT	AAAAAGGAAGGATGTTCTATTAATAACTCA	24	34	122	179	33
ATM	chr11	108160276	108160447	TGTAGCCAGTATCAATTAACAAGT	TCCTTCAGTAAATAACAACAAGGAT	27	29	116	172	28
ATM	chr11	108160360	108160539	GTGAGCAAGCAGCTGAAACAAAT	ATGTTATTTACTTGGTTGATATAGTGAAT	23	32	126	180	32
ATM	chr11	108160418	108160588	TCACCTGTTGTTAGTTTATTAAGTAAAG	aaAAACAGGAAGAACAGGATAGAAAAG	29	27	115	171	33
ATM	chr11	108163250	108163437	AGAGATGCTGACAAAAGGACTTTC	TACAGTAAAGTCCAGCTGCTGG	24	27	141	188	37
ATM	chr11	108163372	108163553	TACGTAGTCTTCCCTTTGTGTT	AAATACCATTTTGAAGATGAGTCAGAAA	23	28	131	182	40
ATM	chr11	108163979	108164165	TGTTGGTCTACTTAAAAATTTCTCTCT	TGTCTGAGTAAATGCGAAAATCT	30	23	134	187	28
ATM	chr11	108164114	108164284	AGATCTCTTCTGACCATGTTGTT	ACTGTAGAGCATACAGATTTTGA	25	26	120	171	32
ATM	chr11	108165598	108165782	TATTTCAAGCTGTAACCAATAGC	AGAAGCTCTCAATATGCTCCACA	25	23	137	185	35
ATM	chr11	108165662	108165833	CCATTTTCTCAGAGTATGTTATGATGC	TCAA AAAAGAAACAGTGAATAAGCC	30	26	116	172	38
ATM	chr11	108167958	108168157	AAACAAGGTTGTCTTCAATGCT	TGATCGCAGTGTACTGAAA	23	20	157	200	36
ATM	chr11	108170338	108170537	TGAAGTACAGAAAACAGCATTAAGT	TAAAGGCCCTGGTAAAGATGC	23	23	149	200	34
ATM	chr11	108170456	108170645	GCTTGGGAGAAGTGGGTCTAT	GAGATTACATAAAGTATCAATAATACTACA	22	35	133	190	37
ATM	chr11	108170556	108170731	ACTTCAGTGGACTCAATATGCT	AGACACTGAGATTTAAA AAAAGGACAAA	24	27	125	176	34
ATM	chr11	108172289	108172487	AGTTTGAATTTTTCAGTGGAGT	GATAGCCAGCATGGAATCTGTT	26	23	150	199	35
ATM	chr11	108172386	108172571	GATCAGCAGCTGTACTTGGTTG	ACAGAACTTTTATGATGCTGGT	26	23	137	186	35
ATM	chr11	108173515	108173710	TGTGTAGGAAAGGTACAATGATTTCCA	CCACTGCCAAA AAAAGCACAAAT	27	23	146	196	35
ATM	chr11	108173609	108173802	AAACCTTTTGAAGGCTGGATG	ACAGGTCAATAAACAAGGATTAATACAGC	33	30	141	194	34
ATM	chr11	108175309	108175508	ATATGCAACGGGGCATGAAAT	CCCTGAACATGTGTAGAAAAGCAG	23	23	154	200	31
ATM	chr11	108175408	108175579	ACTGACTTTTGTACAGACTTCTC	CTGATCTTGTGCTGAGGCTG	25	23	124	172	41
ATM	chr11	108175504	108175674	CAGGATTTTTCACAGCTGTCT	AATCTGTAAAGTCTTTTATGGGA	23	26	122	171	39
ATM	chr11	108178569	108178745	GAAAGTGTGTAAGCAAGAAATGCC	TCCTAAAACCTGAAAGCAACTCA	23	25	129	177	40
ATM	chr11	108180792	108180991	AAGCAGTCACTACATGATTTCTA	AGTAAAGCTGTAAGGTGAGCAGCA	25	24	151	200	32
ATM	chr11	108180910	108181102	ATGATGCTTTCTGGCTGGATTA	ACCTTATGAGCAAAATGCCAC	23	24	147	193	34
ATM	chr11	108183082	108183269	TCAGGAGCTCCAAAATGATGTTCT	ATGAGATAAATCTGTATAAATAAGAGCC	26	32	130	188	32
ATM	chr11	108186449	108186630	AGTTGGGAGTACATATGGTAATGA	GGGTTGATCACTTCCCTCCAC	26	23	133	182	35
ATM	chr11	108186584	108186775	AGCCAGATAGTTGTATGGCTGT	CTTTGCCCCACATGCTCTCG	23	20	149	192	37
ATM	chr11	108186693	108186863	TGTGTGTGTA AAAACCCAAAGCTA						

ATM	chr11	108196144	108196316	GCACAGTCAITTTGGAGATCTGT	AGGAAAGTCAAGAGGTAAGATGAC	23	24	126	173
ATM	chr11	108196740	108196939	ATCAGTAGTAAAGTATTATCCCATATGTC	GCATCCAACCTTGTGATCAITTTGCT	22	25	143	200
ATM	chr11	108196815	108196990	CAGTACAATTCAGTACGTGTGGAG	ACAGTAAAACACTAATCCAGCCAA	25	24	127	176
ATM	chr11	108198316	108198507	GTTGGGTACAGTCATGATGATGC	AGGGTGTCCAAAATCTTACCT	23	24	145	192
ATM	chr11	108198368	108198557	ACAGAACATCCACAGCTAAATCT	ATTGATCTTGATGAAAAGATGAAGCA	24	26	140	190
ATM	chr11	108199673	108199848	ACCTTAATTTGAGTATTCTTGAATGAT	TGATATCTGAAAACCCGGGCTAA	31	23	122	176
ATM	chr11	108199730	108199910	GGTTGTGTTTTCTTGAAGGCAGTAG	TCAGGAGAGCTGCTGTGTTTCA	25	23	133	181
ATM	chr11	108199828	108200004	AGCCCGTTTTTCAGATATCAAT	TGGTGAACATAAAATGTCACTGTGAGAA	23	30	124	37
ATM	chr11	108200875	108201072	TGTTGTGATTTGTAGTCTGTAAAGTTC	TGTTCTTCCACTTAATAAAGCAAT	29	26	143	193
ATM	chr11	108200990	108201182	CGTGCACTGAAAAGGAGGTGATA	CACAGGATGAGATAATTTGGGCTGA	23	23	147	36
ATM	chr11	108202126	108202312	TGAAAATCCTTGTCTTAAATTTGTGTC	ttGGTGTGATTTTCAGGTTTACT	29	25	133	187
ATM	chr11	108202479	108202677	CAGGCATACCGCTCACCC	GTTTGCATTTGCTAAGGCCAGT	20	22	157	35
ATM	chr11	108202628	108202810	ATCACCCCAATCACACTTGT	ACTGAATACACACTTAAAAGGTAAG	23	28	132	183
ATM	chr11	108203392	108203580	TGTGCAATAAATCTGTTTTCTTTGTT	TAAGCATCAAAAAGGCTCAAC	30	23	136	189
ATM	chr11	108203491	108203679	TCGAACAGAGGCTGCAAAATGAA	ACAGAGATTAACACAGCAAGAAAGT	23	25	141	189
ATM	chr11	108204495	108204691	GAGCCTGAAACACAGATGACAA	ATTTCCATAGTAGGAGCAACAA	23	24	150	197
ATM	chr11	108204623	108204802	TATTCAGACAGACCACCAATTA	TGCCAAATTTAAACCAATTTGACCT	23	26	131	180
ATM	chr11	108205618	108205812	TGCCAATTAATAATTTTCTTAAAGTGC	GCCATCGGAACTACACAACTA	31	23	195	23
ATM	chr11	108205689	108205874	TTAATAGGTGGACACACAGGAG	AAAACCTTAAGGGCTAAGCCAGA	23	23	146	186
ATM	chr11	108206475	108206666	CAGATTGGTTTGGAGTGCCTTTG	TTCTCTTCTAGTTTCCGTGTT	23	23	140	192
ATM	chr11	108206559	108206750	AATTAATCGAAGGGCCGTGATG	caaccacacAAATGGCATCTTTA	23	24	145	192
ATM	chr11	108213864	108214058	TTGCACTGACTGTGATGCTGAA	GGCTGTGATCTTTTATGAGCACCA	23	41	148	38
ATM	chr11	108213975	108214162	TGTTCTTGAATGGTGCACAGGA	GCTGTACAGTCTTAATAAGCCAT	23	23	145	188
ATM	chr11	108216364	108216557	TCATCTTATTTGCCCTATATCTGTC	TGCAGAAGTAACCGGAAAACCTGGT	26	23	143	26
ATM	chr11	108216503	108216680	GAAGTCTTCATGGATGTTGGCC	CCAAAACAACAAAGTGTCTAATCT	22	23	133	178
ATM	chr11	108217970	108218167	CAGTGATTTTCAGATGTTGTTCTTTT	CAATGATGTTGTTGTTGTTCTTTT	29	23	146	198
ATM	chr11	108224395	108224580	AACATGTTGTTCTTGCCTTTG	ATGGCCATGCCATCCACAATCA	23	23	140	186
ATM	chr11	108224489	108224668	TTAAGTGTGTTTGAACAGGG	ATGGCCATGCCATCCACAATCA	23	22	135	180
ATM	chr11	108225438	108225608	GCATAGGCTCAGCATACACCA	gcccagcCAGTGAATTTGAC	23	26	122	171
ATM	chr11	108225539	108225720	TCTGTGAGCAAAAACAGTGAAGT	ACTTTACTCTCAATGGTTAAACA	23	22	132	182
ATM	chr11	108225716	108225915	ACTGGCTTATTTGATGATACGTGTC	CCAGCCACATCCCTCATGTA	23	22	137	182
ATM	chr11	108235828	108236007	TCTTGACTGGACCAATGATCTT	GCATTCAGAGTGGTGAAGCTC	27	23	150	200
ATM	chr11	108235968	108236167	CCGTTGTGACGTTTTCAGATTTCT	AGCCCTGGGATAAGAAAATCT	24	24	132	180
ATM	chr11	108236070	108236269	CAACAAGTAGCTGAACTGTCAT	GCAAAATGTGTCACCAACA	27	23	150	200
CHEK2	chr22	29083764	29083961	TGACTGTGAAAAGAACAATTTGCCATA	AGGCTGAAATGAAAGGTAATTCATA	24	25	151	200
CHEK2	chr22	29083884	29084080	TTCAACAACAGCAGCACACT	GAAGAGGCCCCCTGAAG	28	18	152	198
CHEK2	chr22	29085056	29085244	TCATCACTTGTCTATCACCTCT	ACATCAACATGCCCCCTTACT	22	23	152	197
CHEK2	chr22	29089944	29090135	TCATCACTTGTCTATCACCTCT	TCATCAGACACAGTCTATG	25	23	141	189
CHEK2	chr22	29091010	29091198	ACAGAATTGACAGGAGAAAACCA	TCATCTGATTTGCCAATTTG	23	23	146	192
CHEK2	chr22	29091109	29091283	TCATCACTTGTCTATCACCTCT	GGACTCAAGTCTGATGAAGGAT	25	23	141	189
CHEK2	chr22	29091641	29091818	TGFGACTTCACTAATCACCTCT	CCACTGAGAATGCCACTTGAT	25	23	127	175
CHEK2	chr22	29091714	29091901	CTTCAAACTCCAGCAGTCCAC	TCATGAGAACCTTATGTGGAACC	24	23	131	178
CHEK2	chr22	29092834	29093019	AGTTTCTGAAACAATCAACAGGA	TGGCAGTCAACATTAATCCCT	22	23	143	188
CHEK2	chr22	29095758	29095954	TGCCTAATTCAGGGAGTAACTCAAC	ATCTCACTGATCAATCTGAGGCT	25	23	138	186
CHEK2	chr22	29099400	29099584	CAGGATGAGAAAAGCAGCTAC	GAACCCCTGGCTTGCCTT	25	20	152	197
CHEK2	chr22	29105921	29106700	ACTGAAAGGCTTATACTTCTCAAT	ACTTCCCTTTTTTCCCTCC	23	23	139	185
CHEK2	chr22	29105986	29106135	ATACTACATGATTAGCTTTTTCAAAATTT	CTCTGTTATCTTGTATCAAAAGGCC	29	28	93	150
CHEK2	chr22	29107772	29107951	ACTCAAAAATTCATCACTTAAGCA	CTTGAGTCAACTGAGTTTAAATGTTTT	36	24	80	150
CHEK2	chr22	29107872	29108071	TGATCAGCTTTTATTTGGTACTACT	AGCCATAAAGATCATCAGCAAAAAG	25	25	130	180
CHEK2	chr22	29115310	29115504	CAGAAATGAGAAAACCACTACACA	CCAGGAGTGGTAGGCTCATATA	22	21	151	200
CHEK2	chr22	29120878	29121073	ACCATATCTGTAAGGACAGACAAA	TGAAACCCATTTTACTCTTTCTCT	25	26	144	195
CHEK2	chr22	29120969	29121145	ATTTCTGTTAGTGCACAGTCAAA	GATCAGACTGGCAATGGAACTT	26	34	147	36
CHEK2	chr22	29121130	29121325	TTGTTTCAGACTTTGAAATAGCAGAG	TCAAAAGTCTGAAAACAAATGTTCT	23	28	126	177
CHEK2	chr22	29121185	29121384	GACCAAAATACCAGCTTCCCT	GGGCAAAAAGCTGTGAAATGCT	25	24	147	196
CHEK2	chr22	29130301	29130491	AACTCCAATCAGAACCTTCCACC	GGCCCTGTGATGATGTTT	21	22	157	200
CHEK2	chr22	29130405	29130587	CCATCTGAAGGGCCCAATACT	TATTCCTGGAGGACCAAGAACCTG	23	22	145	191
CHEK2	chr22	29130478	29130650	ggctccaggAATAGAAATGAGTTC	CTTCAACAGCAGATGCCAAA	22	21	140	183
CHEK2	chr22	29130506	29130690	AGTGGCACTGTCTAAGGAGC	GCCCATGGCAGCGTTA	25	17	131	173
CHEK2	chr22	29130550	29130749	GAGAGGACTGGCTGGAGTTTG	TTGAGGCTCAGCAGTCTCATGG	23	23	140	185
PALB2	chr16	23614718	23614903	ACTCCAAAAATCAAGAGGCCAAA	ACTCACCTTTGTTGGACACT	21	23	156	200
PALB2	chr16	23614813	23614984	TTTTTTGTCAGCCAGCAAAATGAG	GTGACTGCCCTCCCTCCA	26	19	141	186
PALB2	chr16	23614918	23615095	GTCCCAAATGGCAATTTGTCAG	GGAAAGGTGACGAAAGATCACT	23	23	126	177
PALB2	chr16	23619121	23619297	TTTTTTGTTTGCACAGTCCCTTT	TTTGTCTCTGTTGGGTTTTG	23	23	132	178
PALB2	chr16	23619192	23619382	CCTGCCCTGGAGGAGACAC	AAAGAGACTGAGCTGTGCGAAG	23	23	131	177
PALB2	chr16	23625270	23625462	CACTTAATGAGACCAACAGTAACAC	ACATACTTTGACAGTCTAATGGGA	19	26	146	191
PALB2	chr16	23625298	23625497	TTAATCTCACAACAACCTGTAATAAT	ACTGTTTGTGGAAGAAATGTA	25	23	145	193
PALB2	chr16	23626256	23626447	AACTGAGGACCTAGAGGGAAGC	GCAAAGAAAACCAATTTTATGATCC	23	25	148	200
PALB2	chr16	23634201	23634397	ACGAGATCTCAATTAACCAACTT	ACTAGAGACTGTTTATGTCAA	27	23	153	199
PALB2	chr16	23634333	23634503	AAAGGTTCCACTGCTACTAAT	TGAAAATATAAAGCTGTGCTGGC	24	28	148	197
PALB2	chr16	23635275	23635447	AGCTGACAGAGCAAAAGATGAAGG	TATTAAGAAGTTACTCTCATCACCC	23	28	120	171
PALB2	chr16	23637478	23637667	CCAATTTGGTAAAGCTGCCCTT	AGCAATTTTGGCTGCTTTGTT	25	25	124	173
PALB2	chr16	23637543	23637741	AGATCCCACTTACCTCTGCGAA	CGGTTGTGAAAAGGCCAATGAT	23	23	144	190
PALB2	chr16	23637669	23637839	CTTCCCAAACATGGCACTCAC	CAGAACTGTGCCATTTGTTCAG	23	23	153	199
PALB2	chr16	23640434	23640632	AGAACAAGAAGCTAATGACTGAATCTT	AAGACTTAAATTTTACACTACTGTTCA	23	31	117	171
PALB2	chr16	23640891	23641085	TCATGCTGTTTACATCTACTAAGGC	AAGTGTAGACTAATGATGTACTTTG	29	27	143	199
PALB2	chr16	23640986	23641180	TCTGGCATGTGTTTCTACAGAG	ACACTACCTGTGACTGTGACTCT	25	23	147	195
PALB2	chr16	23641064	23641260	GAGTCAACAGTCAAGTATGAGTTG	CTCAGTCTTCTGCCAGTGAATA	23	23	149	195
PALB2	chr16	23641189	23641388	ATGAGCAAGTGGGGTGTGC	CTCAAGGCTCTATGAAAAAGC	23	23	151	197
PALB2	chr16	23641246	23641444	ATAGGAGCCTTGAAGGCCAAA	CGGGCTTTCTTCCATATTAAT	25	25	155	200
PALB2	chr16	23641297	23641488	AGGTGAACACATGTCTGTGGTAG	TTACCAGGAAAATACACATCCA	21	23	155	199
PALB2	chr16	23641355	23641541	GGAGTATAAAGTAAATGGATGAAAGAGC	CGCATGGATACAGAAATGGAGGA	23	23	146	192
PALB2	chr16	23641463	23641633	AAGTCTCCATTTCTGATCAATGC	AGAGACATCTTAAAGAGGGAAGCTG	31	25	131	187
PALB2	chr16	23641559	23641731	TCAAAGGGCTCCACTGGTTTTC	ACTTGAAGAAGACTTTGGACCTC	25	23	123	171
PALB2	chr16	23641644	23641843	CTGTGATCTGAGAAAAGACAGTAGT	CTTGTGATGATGAGGCTTTCAC	23	23	127	173
PALB2	chr16	23646073	23646272	acactggcCTGTCACTTTT	TGCTGTTTGTGGGTTTTGTT	26	23	151	200
PALB2	chr16	23646250	23646438	AACAATCGACAGCTAGAAAGTTG	CAACTCTAGCCTGTGCAATTT	22	23	155	200
PALB2	chr16	23646305	23646480	GTGCAGCTGATTTCTTTTCC	ACCTCTCAGAACTCTCTAATGAT	23	26	140	189
PALB2	chr16	23646420	23646592	AGAGAAGTTTCTGAGAGTTCTGGA	ATTAGAGTGTCTGGCAATGAC	23	23	130	176
PALB2	chr16	23646508	23646698	AAGGTTAAATTTTACTGCACTTAT	GGAGGCTGTCAATCAGATCAT	25	23	125	173
PALB2	chr16	23646599	23646791	ACTTTCCTTGGCAATGGACAT	CTGCAGAAAACATCTTGACA	31	23	137	191
PALB2	chr16	23646733	23646929	AGTTTGAATGAAATCTTCTTCTG	GTGACACTTGTATGGCAGGAT	23	23	147	193
PALB2	chr16	23646919	23647101	GGGAGTGTGCCACTTTACTTATA	GCCAACTGCCCAAGTTCTAAT	27	23	147	197
PALB2	chr16	23646992	23647191	TGTGCTTCAAATCTACAGT	AGGAGTATGATGACACACTT	23	21	139	183
PALB2	chr16	23647117	23647307	TAAAGGAACCTGATGCGCCCT	ACTGCCCAACAGAAAAGGT	21	21	158	200
PALB2	chr16	23647173	23647351	CTTTTCTGTTGGGCAAGTTGG	CTGTAGACTCACAGTAACCTGAA	22	24	145	191
PALB2	chr16	23647303	23647497	AGCAGGATTTTGTACTGATTTCT	TGGAAAAGCACTAAAGGAACAGGA	22	24	133	179
PALB2	chr16	23647438	23647630	CAGCTTCTGCTTTTGTCCACC	AAAAGAACAATTTTCCACAG	25	23	147	195
PALB2	chr16	23647607	23647786	TGGGTTTTGATGTGAACTGTGATC	TGACAAGTTACACATCAAAACCCA	21	24	148	193
PALB2	chr16	23649110	23649300	AGCCAAAATTAACCTGGGAAATGA	TGAATGAATGCTACTTCTTAAAT	31	24	124	180
PALB2	chr16	23649324	23649504	AGAGTCAAGAACCTGTTTTAAATTTGTTG	TTCTGGGGCTGTTTTGTCTCC	24	22	145	191
PALB2	chr16	23652326	23652511	AGATGATAGCTGCTGCCCTCG	CTCTGACTCCACTTCCACTGT	23	29	129	181
XRCC2	chr7	152345680	152345871	TTAAGGTTGGCTGATGACCTGT	GAGCGTCTCTTCTTGTCTG	20	22	144	186
XRCC2	chr7	152345730	152345916	ACAAAATTAACCCCACTTCTCC	actTGTGAAGCACAGGATTTTT	23	23	146	192
XRCC2	chr7	152345847	152346021	GAAAAACATCTGTGCTTACCA	TGTGGACAAGACTACAGACCTT	24	23	140	187
XRCC2	chr7	152345919	152346111	ACACAGTCTGAGAGGACAT	TGAAAATGACTACTGCTGGTCT	24	24	128	175
XRCC2	chr7	152346023	152346203	GCTTCTCAAGCACTGAGAACAT	TTTTTACTGGATAGACCCGGTCA	20	23	150	193
XRCC2	chr7	152346086	152346283	CATTGACCGGTTCTATCCAGTAA	AGCAACCACTACTTCTTACAT	23	23	135	181
XRCC2	chr7	152346180	152346364	AAGTGAAGAAGTAAGTGGGTGCT	TTGACAGACACTTCCAAAAGC	24	23	152	198
XRCC2	chr7	152346259	152346438	GAGCTTGGGATGATCTGTGCTC	AATCAGAAGGTGGCTGGAAGT	24	23	138	185
					TGAATTCATGGCCAGAAAGAA	23	23	134	180

XRCC2	chr7	152346296	152346494	GCCGGAGCAATCAAAGTGGTAA	CCCTTGAGTACTGCATTTGAC	23	23	153	199	39
XRCC2	chr7	152357715	152357901	ACATGTGAGTTATGTGAAAAATCCT	AAATAAGATTTTCCTTCTCTGTTTT	26	29	132	187	32
XRCC2	chr7	152373031	152373227	CCCCAAGCCTCCAATCC	CAGTTGGTGAATGGGTGGT	18	21	158	197	66
								138.5258216		