

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	TCAACTTCTTGTAAAATAAAAGGAAATAA	23	32	143	198	32
ATM	chr11	108098462	108098632	GTGTGATAGTAAACCCATTAATTTCTT	AAATTTGAAATAGAAATACCTAAAACAGCATCC	30	32	109	171	30
ATM	chr11	108098508	108098694	AGTTGAGAAATTTAAGCGCTGT	ACACACAAAAGTAATACACACAGAA	24	27	136	187	29
ATM	chr11	108099820	108100000	CTTTGTGATGGCATGAACAGCT	ATCTTTTTCGCTGGAGGCTTG	23	23	135	181	31
ATM	chr11	108099927	108100103	AAAGAAAACAGAAATGTCTGAGAAATAGC	CACCGGCAGATAATCTGTTAAGC	26	23	128	177	36
ATM	chr11	108106328	108106504	AGTTGCCATTCGAATGCTAT	TGAGTAGATGTGTCTACAATCAGC	23	23	129	177	31
ATM	chr11	108106395	108106590	AGGAGCACCTAGGCTAAATGTC	ATTCACAAAACACACCTTCAAAC	23	25	148	196	35
ATM	chr11	108114576	108114764	TCCTTTTCTGTATGGGATATGGA	ACAGATGAATTAATCTAGCCACT	25	24	140	189	26
ATM	chr11	108114683	108114870	TGTTCTCTGTGTACTTACGGCTG	ACAAAAGAAAAAGAGATAGATACCTCG	23	29	136	188	37
ATM	chr11	108114719	108114918	CACAAGATGTTCATAGAGTTTAGTGG	CTGAGTCTAAAACATGGTCTCG	27	23	150	200	35
ATM	chr11	108114741	108114919	AGTGGCTAGAATAATCTATGCTGT	ACTAGTCTAAAACATGGTCTCG	24	24	131	179	35
ATM	chr11	108115460	108115633	TGTACAGTTTGTCCCCCTGTT	TGGGAAGAATTTCACTCTCAATTCACA	23	28	128	174	40
ATM	chr11	108115551	108115750	AGCAGCTCTTACTATCTCCCTCA	TTTCTTGGGTTTTGGCTCTCTC	23	23	154	200	35
ATM	chr11	108115614	108115808	AGGAGATGAATTTCTCCCACTTT	ACTTCTATGTTTGAAGAAGAAACGAA	24	26	145	195	31
ATM	chr11	108117623	108117815	TTTGTGGAGCTAGCAGTGTAAA	TTTGACCGCAATATACGAAATCC	23	24	146	193	31
ATM	chr11	108117236	108117932	ATGATCTGGTAGTGAATAGATAAGT	TTTAAAGCCCAAAATGCCAGT	26	23	148	197	33
ATM	chr11	108117791	108117986	AGGATCTCTAATATGGCTCAAAG	AGGAATAGTGTATGACAGAGTCA	26	25	145	196	34
ATM	chr11	108119559	108119753	GATACAGGATCTGCTGTCC	TCCTTTTCAAGGACACTGTATAT	21	24	150	195	36
ATM	chr11	108119688	108119880	AGATTTCAATCTACACTACTACA	AAATACACAGAGATAAATGACACTGAA	28	29	136	193	35
ATM	chr11	108121365	108121538	TTTCCCTTAGTTTGTAAATGATGGA	CCATGCTGCTGGGGTAG	28	20	126	174	34
ATM	chr11	108121468	108121666	AGTTTACCTAACCTGAGCTGTT	AGGTAATAACACAAATTTATCCAGAT	24	29	146	199	40
ATM	chr11	108121552	108121722	TATGTGTACGATGCTTACGGGA	GGCTCCAGTAAGCCAAAGTTTC	23	24	124	171	37
ATM	chr11	108121652	108121851	TTGGTGTATTAACCTTCTGGTT	TGTGTCTGGTGTGTGTATCTGTAAGT	27	27	150	200	37
ATM	chr11	108122503	108122698	AGATAAAGCTTTGCCCTCCAA	AAGAGCAATTCATATTTGATTCCTTT	23	27	146	196	37
ATM	chr11	108122626	108122820	TGGGAATAGAGCAAAATATGTTGAA	AGTGGAGAGAGCTGTATAAAACA	26	23	146	195	34
ATM	chr11	108123492	108123662	TCCTTACATGGCTTTGGCTTCT	AAGAGCATATAGATAACATCACTCG	24	30	117	171	33
ATM	chr11	108123547	108123725	TTTTCCCTACTTGTACTGGGAAA	GATCGACAGACTCCCAAGTAAA	25	23	131	177	33
ATM	chr11	108124488	108124684	AGGCAAAAGCATAGGCTACTGGT	GAGAAGCCAATCTGGACTGGT	23	23	151	197	35
ATM	chr11	108124529	108124727	ACTTCTTGAAGTGAACACCACA	CAGAGACACAGCTCACTGAT	24	23	152	199	39
ATM	chr11	108124643	108124842	AGAATGTGGATGAAAAGCACCA	CCCTATTTCTCTTCTAACAG	24	23	153	200	38
ATM	chr11	108126837	108127036	GAACCTTTGTTTTTAAATGATGATGTT	GCTTCTCTTCAGCTATACACC	36	24	140	200	31
ATM	chr11	108126940	108127114	AGATTACAATTCGAAACTTTGTC	ATTTCAATCAAATTCGAAACTTTATGAT	27	33	115	175	37
ATM	chr11	108128126	108128315	CCAAGATACAAAGTCACTGAAAAGCA	GCAACCTGTACATAGCTCAICA	28	23	139	190	33
ATM	chr11	108128198	108128373	TTCAACAATGCTCTAATGCAATGTG	TCCTATCTCAAAAACAAAACAGAA	26	28	122	176	35
ATM	chr11	108129666	108129837	TGTTTTTATTTCTTGTGTTGTT	teaaantagATGACAAAACAGGAAGC	28	27	117	172	31
ATM	chr11	108137849	108138043	TGCTCTGCAAGAAGCCAT	TCGTTGTACTCACTACTATCA	19	27	149	195	40
ATM	chr11	108137915	108138110	GCCATTGACCCGTGGAGAATG	AAAGAAGTAAAGAATCCAAAGTAGTAAA	22	30	144	196	37
ATM	chr11	108139084	108139260	TATATGGCTGTTGTCCTTCT	GCTGCCCTAAAGGACACAGTATT	23	23	131	177	37
ATM	chr11	108139135	108139327	AGGTGCCATTAATCCTTTAGCTG	GTTGGAGGATTTGGTAGGTTCT	23	24	148	193	40
ATM	chr11	108139255	108139439	GGCAGCTGATATCGGAGGAAT	TCAAATCTCAAAAGACCAATGTGA	23	25	137	185	38
ATM	chr11	108141739	108141891	AAAAGTAAATGATTTGGGATAAACCTGA	AAGGTTTTTAATTTTACAGTATGGTT	28	28	97	153	36
ATM	chr11	108141813	108142007	TTCTGGGAGAAGAGTACCCTTG	TGGTCACAGCAATCAAAAGACA	23	23	149	195	33
ATM	chr11	108141856	108142052	ACTTCTGAACCCTACTCTAAAGAA	TCTCACAGTAAAGGACATGGTT	25	23	149	197	29
ATM	chr11	108141993	108142192	GTATCGTGTGACCAAGATGTT	TGCATCTGTATCCACAGATAGCA	23	23	154	200	38
ATM	chr11	108143152	108143347	AGCACAGAAGAACAATTTGGAAT	TGCAAAAACCTCACTCAAGCAAA	24	23	149	196	33
ATM	chr11	108143256	108143454	CAGGCATCAACAAAGGAGAGGA	ATCACCTACGGGAAAAGAACTG	23	23	153	199	32
ATM	chr11	108143380	108143553	AAGCAGCTCTTGTGTGAATGAT	GCGCAACTGGTGTGATGTCAG	25	23	126	174	34
ATM	chr11	108143427	108143626	AACCACAGTCTTCTCCCGTAGG	TGCCATCTGCAGCATCCAAATA	23	23	154	200	39
ATM	chr11	108150143	108150331	ATGCTTTGGAAAGTAGGGTTGA	TCTCTACTTCTTCTGAGCTTT	23	23	143	189	37
ATM	chr11	108150215	108150412	AAAGTGTTCAGGACACGAAGG	CCAACTTTGGTGAAGTATTTATGGA	23	27	148	198	37
ATM	chr11	108151619	108151817	TGTGTATAGCTTGTCAAAAATCTGG	AGGGCTACAGGATAAAACCCACAG	26	23	150	199	29
ATM	chr11	108151640	108151837	TCTGGAGTTCAAGTTGGATTTAT	AAAGCTGTTTTTCGACATAGG	24	23	151	198	30
ATM	chr11	108151724	108151896	CCATAGTGTGAGAACCTGCGAAA	CCTTTTTCACAAAGGAGGTTCTA	23	26	126	173	39
ATM	chr11	108151805	108151985	ATCCTGTAGCCCTATTCGCGAAA	AAGTGGCCACTCAGAAAATCTAGC	23	23	135	181	36
ATM	chr11	108153336	108153531	tgatGTTGTTTCTAGGCTCACTC	AGATTTAGCCATTTCAAAAACAGA	25	24	147	196	29
ATM	chr11	108153425	108153622	TGGTTCGTCAGGTTTAGAGAA	TCATGTATAAATCTACTATAAATCTCAAT	23	23	142	193	30
ATM	chr11	108153489	108153681	TGGCATCTCATTAGATTAICTGG	GGTGGGGGGACTGCTAAGTATT	25	23	145	198	28
ATM	chr11	108154946	108155121	ATTTTAGATCTTTTAAAGGTTTGTATCC	TCTGCTGACCTCATAGGCAAA	32	23	121	176	35
ATM	chr11	108154966	108155165	GGTTTGAATCCACATCTGGTGA	CATAGACCTTGGTAGCAGTCTCTC	23	24	153	200	41
ATM	chr11	108155026	108155211	TCAGATTCAAGAGGACTGGAAAAGT	TGAAGCATTACTCTGTTTCCCAA	25	23	138	186	40
ATM	chr11	108155137	108155333	GCAAAAGAGAGCTGCTACCAGG	TGCTAGATAATGATTACCAAGCTAAGT	23	29	145	197	30
ATM	chr11	108158251	108158445	AAATATAGCTTTTGAAGCTGCTTG	TACCCTGAAAGGCTCAGAGGCTC	25	23	147	195	35
ATM	chr11	108158316	108158499	TGCCCTGACAGATGATCACTTA	ACTTCTTTAAAACCTTGTGAAGTTAGAGC	23	29	132	184	38
ATM	chr11	108159628	108159799	TCATTTTGAAGATTCAGCTGGTCA	TTAACTTGGTTTTATGCAATGCTG	24	27	121	172	34
ATM	chr11	108159697	108159875	CTGTAGGGAATTTGATCTGCTG	AAAAAGGAAGGATGTTCTATTTAACTCAICA	34	24	122	177	33
ATM	chr11	108160276	108160447	TGTAGCCAGTATCAATAAACAAGT	TCTTTCAGTAAATAAACAACAGGAT	27	29	116	172	28
ATM	chr11	108160360	108160539	GTGAGCAAGCAGCTGAAACAAT	ATGTTATTTACTTGTGTGTATAGTGAAT	23	26	180	232	29
ATM	chr11	108160418	108160588	TCACCTGTTGTTAGTTTATTAAGTAAAG	aaAAACAGGAAGAACAGGATAGAAAAGA	29	27	115	171	33
ATM	chr11	108163250	108163437	AGAGATGCTGCAAAAAGGACTTC	TACAGTAAAGTCAACCTGCTCTGG	24	27	141	188	37
ATM	chr11	108163372	108163553	TACGTAGCTTCCCTTTGTTGT	AAATACCATTTTGAAGATGAGTCAGAAA	23	28	131	182	40
ATM	chr11	108163979	108164165	TGTTGGTCTACTTAAAAATTTCTCTCT	TGTGCTGAGTAAATGCGAAAATCT	30	23	134	187	28
ATM	chr11	108164114	108164284	AGATCCCTTTCTGACCATTTGTT	ACTGTAGGACTATACAGATTTTGA	25	26	120	171	32
ATM	chr11	108165598	108165782	TTATTTCAAGCTTAAACAATAGC	AGAAGCTCTCAATAATGCTCCACA	25	23	137	185	35
ATM	chr11	108165662	108165833	CCATTTTCTCAGAGTATGTTATGATGC	TCAA AAAAGAAACAGTGAATATAGCC	30	26	116	172	38
ATM	chr11	108167958	108168157	AAACAAGGTTGTTCTTCATGCT	TGATCGCAGTGTACTGAAA	23	20	157	200	36
ATM	chr11	108170538	108170737	TGAAGTACAGAAAACAGCAATAGT	TAAAGGCCCTGGTAAAGATGC	23	23	149	200	34
ATM	chr11	108170456	108170645	GCTTGGGAGAAGTGGTCTACT	GAGATTACATAAAGTATAAATACTACCA	22	35	133	190	37
ATM	chr11	108170556	108170731	ACTTCAGTGGACTCATAATGCT	AGACACTGAGATTTAAA AAAAGGACAAA	24	27	125	176	34
ATM	chr11	108172289	108172487	AGTTTGAATTTTTCAGTGGAGT	GATAGCCAGCTAGTGGATCTGTT	26	23	150	199	35
ATM	chr11	108172386	108172571	GATCAGCAGCTGTACTTGGTTG	ACAGAATCTTTTGAATGCTGGTT	26	23	177	186	35
ATM	chr11	108173515	108173710	TGTGTAGGAAAAGTCAATGATTTCCA	CCACTGTCAAAAAGGACAAAGT	27	23	146	196	35
ATM	chr11	108173609	108173802	AAACCTTTTGAAGGCTGGATG	ACAGGTCAAAAACAGGATATATACAGC	33	30	141	194	34
ATM	chr11	108175309	108175508	ATATGCAACGGGGCATGAAAT	CCCTGAACATGTGTAGAAAAGCAG	23	23	154	200	31
ATM	chr11	108175408	108175579	ACTGACTTTTGTACAGACTTCTC	CTGATCTTCTGTCAGGCTG	25	23	124	172	41
ATM	chr11	108175504	108175674	CAGGATTTTTCACAGCTGTCT	ATCTCTGTAAGGCTTTTATGGGGA	23	26	122	171	39
ATM	chr11	108178569	108178745	GAAAGTGTGAAGCAAGAAATGCC	TCCTAAAACCTGAAGGCAAACTCA	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	TCAGGAGCTCCAAATAGATTTCT	ATGAGATAAATCTGTATAAATAAGAGCC	26	32	130	188	32
ATM	chr11	108186449	108186630	AGTTGGGAGTTACATATTGTAATGA	GGGTTGAACTACTTCCCTCCAC	23	23	133	182	35
ATM	chr11	108186584	108186775	AGCCAGATAGTTGTATGGCTGT	CTTTGCCCCACATGCTCTG	23	20	149	192	37
ATM	chr11	108186693	108186863	TGTGTGTGTA AAAACCAAGCTA	ACCAAATCTGGGAAA AAAATGTACCTG	23	26			

ATM	chr11	108196144	108196316	GCACAGTCAITTTGGAGATCCTG	AGGAAAGTCAAGAGGTAAGATGAC	23	24	126	173
ATM	chr11	108196740	108196939	ATCAGTAGTAAAAGTAAITATCCCAATGTG	GCATCCAACCTTTTGATCAITTTGCT	22	25	143	200
ATM	chr11	108196815	108196990	CAGTACAATTCAGTACGTGTGGAG	ACAGTAAAACACTAAATCCAGCCAA	25	24	127	176
ATM	chr11	108198316	108198507	GTTGGGTACAGTCATGATGATGC	AGGGTGTCCAAAATCTTAAC	23	24	145	192
ATM	chr11	108198368	108198557	ACAGAACAAATCCAGCTAAACAT	ATTGATCTTGATGAAAAGATGAAGCA	24	26	140	190
ATM	chr11	108199673	108199848	ACCTTAATTTGAGTGATTTTGAATGAT	TGAGTATCTGAAAACCCGGCTAA	31	23	122	176
ATM	chr11	108199730	108199910	GGTTGTGTTTTCTTGAAGGCAAGTAG	TCAGGAGAGCTGCTGTTTTTCA	25	23	133	181
ATM	chr11	108199828	108200004	AGCCCGTTTTTCAGATCACTCAAT	TGGTGAACATAAAATGTCACTGTAGAAA	23	30	124	37
ATM	chr11	108200875	108201072	TGTTGTGATTTGTAGTCTGTAAAGTTC	TGTTCTTCCACTTAATAAAGCAAT	29	26	143	193
ATM	chr11	108200990	108201182	CGTGCACTGAAAAGAGGATGTAA	CACAGGATGAGAATAITGGGCTGA	23	23	147	36
ATM	chr11	108202126	108202312	TGAAAATCCTGTGTTCTTAATTTGTGTC	TTTTCATTTGCTAAGGCCAGT	29	25	133	187
ATM	chr11	108202479	108202677	CAGGCATACACGCTCACCC	ACTGAAATACACACTTAAAGGGTACG	20	22	157	35
ATM	chr11	108202628	108202810	ATCACCCCAATCACACTTTGTTT	TAAGCATCACAAAAGGCTCAC	23	28	132	183
ATM	chr11	108203392	108203580	TGTGCAATAAATCTGTTTTTCTTTGTTT	TAAGCATCACAAAAGGCTCAC	30	23	136	189
ATM	chr11	108203491	108203679	TCGAACAGAGGCTGCAAAATGAA	ACAGAGATTAACACAGCAAGAAAGT	23	25	141	189
ATM	chr11	108204495	108204691	GAGCCTGAAACACAGATGACAA	ATTTCCATAGTAGGGAACAACA	23	24	150	197
ATM	chr11	108204623	108204802	TATTCAGACAGACCAGCAATA	TGCCAAATTAACAATTTTGACCT	23	26	131	180
ATM	chr11	108205618	108205812	TGCCAATTAATAATGTTTTCTTAAAGTGC	GCCATCGGAACCTACACAATCA	31	23	195	23
ATM	chr11	108205689	108205874	TTAATAGGTGGACACACAGGAG	AAAACCTTAAGGGTAAAGCCAGA	23	23	146	186
ATM	chr11	108206475	108206666	CAGATTTGGTTTGAAGTGCCTTTT	TTCTCTTCTGATTTCCGTGTT	23	23	140	192
ATM	chr11	108206559	108206750	AATTAATCTGAAGGGCCGTGATG	caaccacacAAAAGGCATCTTTA	23	24	145	192
ATM	chr11	108213864	108214058	TTGCATGACTCTGATAGCTGAA	GGCTGTGATCTTTATGAGCACCA	23	41	148	195
ATM	chr11	108213975	108214162	TGTTCTTGAATGGTGCACAGGA	CGCTGACAGTTTAATAAGCCATT	23	23	145	188
ATM	chr11	108216364	108216557	TCATCTTATTTGCCCTATCTGTG	TGCAGTAAGCAACGGGAAACTGGT	22	23	143	26
ATM	chr11	108216503	108216680	GAAGTCTTCATGGATGTGTGGC	CCAAACAACAAGGGTCTCAATCT	22	23	133	178
ATM	chr11	108217970	108218167	CAGTGATTTTCAGATFTGTFTCTTTT	CAAGTGTGTTGTTGATCACTTCA	29	23	146	198
ATM	chr11	108224395	108224580	AACATGTTGTTCTTGCCCTTTG	ATGGCCATGCCATCCACAATCA	23	23	140	186
ATM	chr11	108224489	108224668	TTAAGTGTGGTTTTGAACAGGG	gcccagcCAGTGTAAITTTGAC	23	22	135	180
ATM	chr11	108225438	108225608	GCATAGGCTACGATACACCA	ACTTTACCTCAATGGTTAACAAGA	23	26	122	171
ATM	chr11	108225539	108225720	TCTGTGAGCAAAAACAGTGAAGT	CCAGCCACATCCCCTATGTGTA	23	22	137	182
ATM	chr11	108225716	108225915	ACTGGCTTATTTGATGATACCTGTG	GCATTCAGAGTGGGTAAGCTC	27	23	150	207
ATM	chr11	108235828	108236007	TCTTGACTGGACCAATGATCCCT	AGGCCTTGGATAAGAAAATCTG	24	24	132	180
ATM	chr11	108235968	108236167	CCGTTTGTCAGTTTTTTCAGATTTCT	GCAAAITGGTATGCCCAACA	27	23	150	201
ATM	chr11	108236070	108236269	CAACAAGTAGCTGAACGTGCTAT	AGGCTGAATGAAAAGGTAATTCAT	24	25	151	200
CHEK2	chr22	29083764	29083961	TGACTGTGAAAAGAACAATTAATGTCAT	GAAGAGGGCCCCGGAAG	28	18	152	198
CHEK2	chr22	29083884	29084080	TTACACACAGCAGCAGCACCT	ACATCAAAAGCCCCACTTACT	22	23	152	197
CHEK2	chr22	29085056	29085244	TCATCACTTGTGTATCACCTCT	CTCTCAGACACAGTCTATG	25	23	141	189
CHEK2	chr22	29089944	29090135	TGTCCTTGTCTCAATGCTCTCA	TTCACTTGATTTGCCAATGTG	23	23	146	192
CHEK2	chr22	29091010	29091198	ACAGAATTGACAGGAGAAAACCA	GGACTAAAGTCTGATGAAGGAT	25	23	141	189
CHEK2	chr22	29091109	29091283	TCATACCTTTCTGAGACTCTGCT	CCACTGAGAAAGCCACTTGAAT	25	23	127	175
CHEK2	chr22	29091641	29091818	TGTGACTTCACTAATCACTCTCT	TCATGAGAACCTTAATGTGAAACC	24	23	131	178
CHEK2	chr22	29091714	29091901	CTCCAAAACCTCAGCAGTCCAC	TGGCAAGTCAACATTAATCCCT	22	23	143	188
CHEK2	chr22	29092834	29093019	AGTTTCTGAAACAATCAACAGGA	ATCTACGATCAATCTGAGGCT	25	23	138	186
CHEK2	chr22	29095758	29095954	TGCCTAATTCAGGGAGTAACTCAAC	GAACCCCTTGCCCTGCCCC	25	20	152	197
CHEK2	chr22	29099400	29099584	CAGGATGAGAAAAGCAGCCAC	ACTTCCCTTTTTTCTCCCCCTC	23	23	139	185
CHEK2	chr22	29105921	29106700	ACTGAAAGGCTTTAATCTTCTCAAT	CTCTGTTTGTCTTATCAAAAGGCC	29	28	93	150
CHEK2	chr22	29105986	29106135	ATACTTACATGATTTAGCTTTTTCAAAATTTCT	CTTGAGTCAACTGAGTTTAACTGAAATGTTTTT	36	24	80	150
CHEK2	chr22	29107772	29107951	ACTCAAAAATTCATCACTTAAGCA	AGCCATAAAGATCATCAGCAAAAAGG	25	25	130	180
CHEK2	chr22	29107872	29108071	TGATCAGCTTTTATTTGGTACTACTG	CCCGGAGTGGTAGGCTCATA	22	21	151	200
CHEK2	chr22	29115310	29115504	CAGAAAATGAGAAAACCACCAATG	TGAAACCCATTTTACTCTTTTCTC	25	26	144	195
CHEK2	chr22	29120878	29121073	ACCATATCTGTAAAGGACAGCAAAA	GATCACAGTGGCAATGGAACTCT	26	34	147	36
CHEK2	chr22	29120969	29121145	ATTTCTGTTAGTGACAGTGCAAA	TCAAAAGTCTGAAAACAAATGTTCT	23	28	126	177
CHEK2	chr22	29121130	29121325	TTGTTTCAGACTTTGAAATAGCAGAG	GGGCAAAAAGCTGTGAAATATGCT	25	24	147	196
CHEK2	chr22	29121185	29121384	GACCAAAATACCACTCTCCCT	GGCCTGTGATGATGCTTTTAT	21	22	157	200
CHEK2	chr22	29130301	29130491	AACTCCAATCAGAACCTTCCACC	TATTCCTGGAGGACCAAGAACCTG	23	22	145	191
CHEK2	chr22	29130405	29130587	CCATCTGAAAGGCCCAATAAT	CTTCCACAGCAGATGCCAAA	22	21	140	183
CHEK2	chr22	29130478	29130650	ggctccaggAATAGAAATGAGTTC	GCCCATGCGAGCGTTA	15	17	131	173
CHEK2	chr22	29130506	29130690	AGTGGACACTGTCTAAGGAGC	TTGAGGCTCAGCAGTCTCATG	23	22	140	185
CHEK2	chr22	29130550	29130749	GAGAGGACTGGCTGGAGTTTG	ACTCACCTTTGTGTTGGACAT	21	23	156	200
PALB2	chr16	23614718	23614903	ACTCCAAAATAACTAAGAGGCCAAA	GTGTACTGCCCTCCCTCCA	26	19	141	186
PALB2	chr16	23614813	23614984	TTTTTGTCCAGCCAGCAAAATGAG	GGAAAGGTGACGTAAGAATCACT	23	23	126	177
PALB2	chr16	23614918	23615095	GTCCCAAATGGCAATTTGTTCCAG	TTTTTCTCTTGTGGGTTTTG	23	23	132	178
PALB2	chr16	23619121	23619297	TTTTTGTGTTGACAGCTGCCCTT	AAAGAGATGAGTCTGTGGGAAG	23	23	131	177
PALB2	chr16	23619192	23619382	CCTGCCCTGGAGGAAGACA	ACATACTTTGACAGTCTAATGGGA	19	26	146	191
PALB2	chr16	23625270	23625462	CACTTAATGAGACCAACAGTAACAC	ACTGTTTGTGGGAAGAATGTGA	25	23	145	193
PALB2	chr16	23625298	23625497	TTAATCTCACAACAACCTGTAATAAT	GCAAAGAAAACCAATTTTGATGCC	23	25	148	200
PALB2	chr16	23626256	23626447	AACTGAGGACTAGAGGGAAAGC	ACTAGGAACTGTTTGTAGTCAA	27	23	153	199
PALB2	chr16	23634201	23634397	ACGAGATCTCAATTAACCAACTT	TGGAATAATAAAGCTGTGCTTGGC	24	25	148	197
PALB2	chr16	23634333	23634503	AAAGGTTCCACTGCTACTAATC	TATTAAGAAGTTTACTCTCACATACC	23	28	120	171
PALB2	chr16	23635275	23635447	AGCTGACAGAGCAAAAGATGAAGG	AGCAATTTTGGCTGCTGTTGTT	25	25	124	173
PALB2	chr16	23637478	23637667	CCAATTTGGTAAAGCTGCCCTT	CGGGTTGTAAAGAGCCATGTAT	23	23	144	190
PALB2	chr16	23637543	23637741	AGATTTCCACTTACTCTGCGAA	CAGAACTGTGCCATTTGTGTCAG	23	23	153	199
PALB2	chr16	23637669	23637839	CTTCCCAAACAATGGCACTCAC	AAGACTTAAATTTTACTACTGTTTCA	23	31	117	171
PALB2	chr16	23640434	23640632	AGAACAAGAAGCTAATGACTGAATCTT	AAGTGTAGACTAATGATGACTTTTG	29	27	143	199
PALB2	chr16	23640891	23641085	TCATGCTGTTTACATCTACTAAGGC	CAACTACCTGTGACTGTGACTCT	25	23	147	195
PALB2	chr16	23640986	23641180	TGCTGGCATGTGTTTCTACAGAG	CTCAGTCTTCTGCCAGTGATA	23	23	149	195
PALB2	chr16	23641064	23641260	GAGTCACAGTCAAGTATAGGTTG	CTCAAGGCTCTATGAAAAAGC	23	23	151	197
PALB2	chr16	23641189	23641388	ATGAGCAAGTGGGTTGTGC	CGGGCTTTCTTCCATCATTAAT	20	25	155	200
PALB2	chr16	23641246	23641444	ATAGGAGCTTGAAGGCCAAA	TTACCCAGGAAAATACACATCCA	21	23	155	199
PALB2	chr16	23641297	23641488	AGGTGAACACATGTCTGTGGTAG	CGCATGATACAGAAATGGAGGA	23	23	146	192
PALB2	chr16	23641355	23641541	GGAGTATAAAGTAAATGGGATGAAGAAGC	AGAGACATCTTAAAGAGGGAAGCTG	31	25	131	187
PALB2	chr16	23641463	23641633	AAGTCTCCATTTCTGTATCAATGC	ACTTGAAGAAGACTTTGGACCTC	25	23	123	171
PALB2	chr16	23641559	23641731	TCAAAGGGCTCCACTGGTTTTC	CTCTTGGATGATGAGGTTTTCAC	23	23	127	173
PALB2	chr16	23641644	23641843	CTGTGATACTGAGAAAAGACAGTAGT	TGTCCTGTTTTGTGGGTTTTGTT	26	23	151	200
PALB2	chr16	23646073	23646272	accttggccCTGTCACTTTT	CAACTCTAGCCCTGCGAATGTT	22	23	155	200
PALB2	chr16	23646250	23646438	AACAATCGACAGCTAGAAAGTTG	ACCTCTCAGAACTCTGATTAAT	23	26	140	189
PALB2	chr16	23646305	23646480	GTGCAGGCTGATTTCTTTTC	ATTAGAGTGTGCGCAATGATC	23	23	130	176
PALB2	chr16	23646420	23646592	AGAGAAGTTCAGAGGTTCTTGA	GGAGGCTGTAATCAGAGTCAAT	25	23	125	173
PALB2	chr16	23646508	23646698	AAGGTTAAATTTTACTGCAATCTTAT	CTCGAAGAAAACATCTTGACA	31	23	137	191
PALB2	chr16	23646599	23646791	ACTTTCCTTGGCAATGGACAT	GTGACACTTGTATGGCAGGAAAT	23	23	147	193
PALB2	chr16	23646723	23646929	AGGTTGACTTGAATCTCACTTCTG	GCCAACTGCCCAAGTTCTAAT	27	23	147	197
PALB2	chr16	23646919	23647101	GGGCAATTTGGCACTTTACTTCA	AGGCGTATGATGACAGCACTT	23	21	139	183
PALB2	chr16	23646992	23647191	TGTGCTTCAAATTAACAGGT	ACTGCCCAACAGAAAAGGT	21	21	158	200
PALB2	chr16	23647117	23647307	TAAAGGAACCTGATGCGCCCT	CTGTAGACTCACAGTAACCTGAA	22	24	145	191
PALB2	chr16	23647173	23647351	CTTTTCTGTTGGGCAAGTTGG	TGGAAAAGCACTAAAGGAACAGGA	22	24	133	179
PALB2	chr16	23647303	23647497	AGCAGGATTTTGTACTGATTTCT	AAAAGAACAATTTTCCACAG	25	23	147	195
PALB2	chr16	23647438	23647630	CAGCTCTGCTTTTGTCCACC	TGCAGAGTACACATCAAAACCCA	21	24	148	193
PALB2	chr16	23647607	23647786	TGGGTTTGTAGTGTAACTGTGAT	TGAATGAATGACTACTTCTTAAAT	31	21	124	180
PALB2	chr16	23649110	23649300	AGCCAAAATTAACCTGGGAAATGA	TTCTGGGGCTGTTTTGTCTCC	24	22	145	191
PALB2	chr16	23649324	23649504	AGAGTCAAGAACCTGTTTTAAATTTGTTG	CTCTGACTCCACTTTCCACTGT	23	29	129	181
PALB2	chr16	23652326	23652511	AGATGATAGTCTGCCCTCG	GAGCGTCTCTTCTTGTCTG	20	22	144	186
XRCC2	chr7	152345680	152345871	TTAAGGCTTGGCTGATGACCTG	actTGTGAAGCACAGGATGTTT	23	23	146	192
XRCC2	chr7	152345730	152345916	ACAAAATTAACCCCACTTTCC	TGTGGACAAGACTACAGACCTT	24	23	140	187
XRCC2	chr7	152345847	152346021	GAAAAACATCTGTGCTTACCA	TGTAATAAGACTACTGCTGGTTCT	24	24	128	175
XRCC2	chr7	152345919	152346111	ACACAGTCTGAGAGGCAAT	TTTTTACTGGATGACCGCGTCA	20	23	150	193
XRCC2	chr7	152346023	152346203	GCTTCTCTAAGCACTGAGAACAT	AGCAACCCTACTTCTTACAT	23	23	135	181
XRCC2	chr7	152346086	152346283	CATTGACCGGTTCTATCCAGTAA	TTGAGCAGACACTTCCAAAGC	23	23	152	198
XRCC2	chr7	152346180	152346364	AAGTGAAGAAGTAAAGTGCTG	AATCAGAAGGTGGCCTGGGAATG	24	23	138	185
XRCC2	chr7	152346259	152346438	GAGCTTTGGGATAGTCTGTGCTC	TGAATTTCAATGGCCAGAAAGAA	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		