

Supp. Table 3. SNPs detected in 454 and Illumina data

VarScan SNP Prediction (Individual 454 Sequencing)								Illumina Read Counts (VarScan)		
Chrom	Position	Hs36	Var	Ref	Het	Hom	454_Freq	Ref_Reads	Var_Reads	Pool_Freq
chr1	19421930	G	C	25	15	2	0.226	3,473	1,199	0.257
chr1	19422451	T	C	29	11	2	0.179	5,052	1,676	0.249
chr1	19422576	G	A	41	1	0	0.012	12,999	138	0.011
chr1	19422624	C	T	41	1	0	0.012	11,092	99	0.009
chr1	19422687	C	T	41	1	0	0.012	5,843	67	0.011
chr1	19429868	G	C	35	7	0	0.083	2,227	293	0.116
chr1	19431662	A	G	41	1	0	0.012	2,811	2	0.001
chr1	19437237	C	G	25	15	2	0.226	8,330	3,225	0.279
chr1	19437837	G	A	41	1	0	0.012	4,478	78	0.017
chr1	19437925	C	T	32	9	1	0.131	4,733	599	0.112
chr1	19437931	C	G	16	19	7	0.393	3,175	2,222	0.412
chr1	19440079	C	T	41	1	0	0.012	13,967	135	0.010
chr1	19443013	C	G	30	12	0	0.143	3,020	318	0.095
chr1	148564816	G	A	40	2	0	0.024	2,571	78	0.029
chr1	148577451	A	C	38	4	0	0.048	11,588	2,281	0.164
chr1	148583200	A	G	37	5	0	0.060	4,444	402	0.083
chr1	148583712	G	A	41	1	0	0.012	5,979	63	0.010
chr1	148583713	C	A	41	1	0	0.012	6,215	65	0.010
chr1	148583810	C	T	41	1	0	0.012	5,215	48	0.009
chr1	148585705	T	A	27	13	2	0.202	6,280	1,930	0.235
chr1	148591855	A	G	40	2	0	0.024	2,937	96	0.032
chr1	148591950	G	A	41	1	0	0.012	1,091	36	0.032
chr1	154390044	G	A	41	1	0	0.012	11,753	159	0.013
chr1	154394961	G	A	40	2	0	0.024	4,299	51	0.012
chr1	154397249	C	G	41	1	0	0.012	7,458	103	0.014
chr1	154411595	G	A	41	1	0	0.012	3,014	43	0.014
chr1	154412193	G	A	41	1	0	0.012	4,477	41	0.009
chr1	154413264	G	A	33	9	0	0.107	3,452	424	0.109
chr1	154413950	T	C	25	15	2	0.226	2,825	1,011	0.264
chr1	195674759	C	T	41	1	0	0.012	3,072	43	0.014
chr1	195675237	G	A	0	0	42	1.000	227	13,695	0.984
chr1	195675258	G	A	41	1	0	0.012	13,715	142	0.010
chr1	195675283	C	T	25	16	1	0.214	10,822	2,870	0.210
chr1	195713660	T	C	36	6	0	0.071	3,642	278	0.071
chr1	226002144	C	G	41	1	0	0.012	3,597	57	0.016
chr1	226013448	A	T	41	1	0	0.012	4,618	65	0.014
chr1	226030114	G	T	35	5	2	0.107	2,985	405	0.119
chr1	226035419	C	T	41	1	0	0.012	5,727	103	0.018
chr11	61475963	T	C	18	18	6	0.357	6,606	3,966	0.375
chr11	61486612	G	A	25	13	4	0.250	2,687	1,485	0.356
chr11	61486759	C	T	27	13	2	0.202	4,730	1,150	0.196
chr11	61486810	T	C	17	16	9	0.405	2,070	1,664	0.446
chr11	61486990	C	A	41	1	0	0.012	2,764	21	0.008

chr11	61487003	G	T	41	1	0	0.012	2,742	22	0.008
chr11	61488553	G	A	41	1	0	0.012	3,319	91	0.027
chr11	62137308	T	C	0	3	39	0.964	149	2,183	0.936
chr11	62138384	G	C	40	0	2	0.048	9,148	316	0.033
chr11	62138401	G	A	41	1	0	0.012	11,720	37	0.003
chr11	62138854	A	C	31	11	0	0.131	2,384	1	0.000
chr11	62138974	A	G	39	3	0	0.036	2,131	8	0.004
chr11	118718992	A	T	35	7	0	0.083	7,059	1,272	0.153
chr11	118719704	A	T	41	1	0	0.012	7,488	2	0.000
chr11	118720256	C	T	41	1	0	0.012	12,390	68	0.005
chr11	118720463	G	C	11	16	15	0.548	3,700	4,861	0.568
chr11	118720466	C	T	13	17	12	0.488	4,410	5,059	0.534
chr11	118720548	G	A	41	1	0	0.012	11,351	245	0.021
chr11	118721331	G	A	40	2	0	0.024	13,657	409	0.029
chr11	118721352	C	A	41	1	0	0.012	12,452	160	0.013
chr11	118721441	A	G	1	3	38	0.940	1,314	14,994	0.919
chr11	118721489	G	A	29	13	0	0.155	12,154	2,547	0.173
chr11	118722464	C	T	9	17	16	0.583	1,193	1,666	0.583
chr11	118722665	C	T	12	14	16	0.548	998	1,549	0.608
chr12	107563709	T	G	41	1	0	0.012	4,916	47	0.009
chr12	107565386	T	C	41	0	1	0.024	3,451	85	0.024
chr12	107572318	G	T	41	1	0	0.012	8,854	14	0.002
chr13	27490546	T	C	31	10	1	0.143	2,532	382	0.131
chr13	27495449	C	A	41	1	0	0.012	4,962	42	0.008
chr13	27495449	C	T	39	3	0	0.036	4,962	142	0.028
chr13	27505989	T	G	7	10	25	0.714	1,052	2,766	0.724
chr13	27507935	T	C	41	1	0	0.012	2,828	50	0.017
chr13	27507991	T	C	6	13	23	0.702	982	2,323	0.703
chr13	27507997	T	C	5	12	25	0.738	983	2,422	0.711
chr13	27521699	G	T	39	3	0	0.036	4,949	437	0.081
chr13	27521759	C	T	36	6	0	0.071	5,010	429	0.079
chr13	27542830	A	G	34	6	2	0.119	3,829	608	0.137
chr13	27545534	T	G	39	3	0	0.036	18,158	844	0.044
chr13	27545573	C	A	41	1	0	0.012	12,382	7	0.001
chr13	27545573	C	T	36	4	2	0.095	12,382	1,870	0.131
chr14	20832643	A	T	41	1	0	0.012	12,155	4	0.000
chr14	20832821	C	G	41	1	0	0.012	7,819	165	0.021
chr14	20863299	C	T	40	2	0	0.024	2,435	35	0.014
chr14	20866624	G	C	32	10	0	0.119	1,567	432	0.216
chr14	20881020	C	T	41	1	0	0.012	14,248	145	0.010
chr14	20881142	C	T	41	1	0	0.012	19,886	190	0.009
chr14	20889304	G	C	41	1	0	0.012	3,309	22	0.007
chr14	23619451	C	G	40	2	0	0.024	7,179	267	0.036
chr14	23620064	C	T	20	9	13	0.417	2,073	2,946	0.587
chr14	23653952	G	T	40	2	0	0.024	3,644	69	0.019
chr14	67261538	A	G	40	2	0	0.024	11,206	286	0.025

chr14	67263484	G	A	33	8	1	0.119	4,058	920	0.185
chr14	103056008	C	T	15	17	10	0.440	2,127	1,314	0.382
chr14	103056018	A	G	41	1	0	0.012	3,562	65	0.018
chr15	69893507	C	T	41	1	0	0.012	2,930	38	0.013
chr15	69893603	A	G	41	1	0	0.012	4,860	6	0.001
chr17	1501377	G	C	41	1	0	0.012	4,790	64	0.013
chr17	1501386	C	T	38	4	0	0.048	4,189	362	0.080
chr17	1506676	C	G	41	1	0	0.012	2,102	21	0.010
chr17	1508221	G	A	41	1	0	0.012	4,919	78	0.016
chr17	1508257	A	C	41	1	0	0.012	3,593	57	0.016
chr17	1509985	G	A	41	1	0	0.012	4,069	5	0.001
chr17	1510422	A	G	32	10	0	0.119	745	15	0.020
chr17	1510635	C	T	41	1	0	0.012	10,391	125	0.012
chr17	1510639	A	C	40	2	0	0.024	10,703	274	0.025
chr17	1511042	A	G	41	1	0	0.012	3,144	18	0.006
chr17	1511961	T	C	40	2	0	0.024	5,722	172	0.029
chr17	1512033	C	T	41	1	0	0.012	7,006	91	0.013
chr17	1512211	A	G	37	5	0	0.060	6,691	796	0.106
chr17	1525689	C	T	27	13	2	0.202	9,679	2,452	0.202
chr17	1527524	T	C	41	1	0	0.012	3,544	28	0.008
chr17	1527679	G	C	29	11	2	0.179	3,774	855	0.185
chr17	1527840	G	A	41	1	0	0.012	3,939	56	0.014
chr17	1528955	G	A	29	11	2	0.179	2,682	820	0.234
chr17	1530882	T	C	41	1	0	0.012	6,305	100	0.016
chr17	1531074	A	G	27	13	2	0.202	2,403	746	0.237
chr17	1531880	A	G	33	8	1	0.119	2,562	689	0.212
chr17	1532155	T	G	38	4	0	0.048	3,194	95	0.029
chr17	1532372	T	C	41	1	0	0.012	2,607	11	0.004
chr17	1533785	C	G	41	1	0	0.012	2,359	42	0.017
chr17	6268113	G	A	35	7	0	0.083	3,894	486	0.111
chr17	6268215	C	T	33	9	0	0.107	2,553	349	0.120
chr17	6268265	G	A	41	1	0	0.012	3,796	35	0.009
chr17	6268267	G	A	40	2	0	0.024	3,636	92	0.025
chr17	6268275	G	A	27	11	4	0.226	2,587	754	0.226
chr17	6268302	G	A	41	0	1	0.024	2,059	130	0.059
chr17	6268326	G	A	41	1	0	0.012	1,469	38	0.025
chr17	6269688	C	A	40	2	0	0.024	7,450	198	0.026
chr17	6270678	A	G	41	1	0	0.012	8,569	275	0.031
chr17	6270792	T	C	6	10	26	0.738	537	6,204	0.920
chr17	6270833	G	A	23	15	4	0.274	2,396	3,705	0.607
chr17	6271127	A	G	37	3	2	0.083	12,999	1,472	0.102
chr17	6279008	A	G	41	1	0	0.012	12,060	129	0.011
chr17	6279254	G	T	37	5	0	0.060	9,322	1,175	0.112
chr17	6305477	A	G	0	10	32	0.881	1,717	13,247	0.885
chr17	6305605	T	C	35	7	0	0.083	11,159	1,082	0.088
chr17	6308857	G	C	41	1	0	0.012			

chr17	6314285	G	A	40	2	0	0.024	9,014	180	0.020
chr17	6314461	C	T	10	19	13	0.536	5,124	6,962	0.576
chr17	6314504	C	T	41	1	0	0.012	12,584	166	0.013
chr17	6318389	C	T	41	1	0	0.012	10,764	134	0.012
chr17	6318392	C	A	15	20	7	0.405	5,732	4,707	0.451
chr17	6318555	A	G	41	1	0	0.012	12,394	249	0.020
chr17	6322663	G	A	8	13	21	0.655	1,041	1,976	0.655
chr17	6327671	G	A	41	1	0	0.012	3,070	67	0.021
chr17	6328206	G	C	7	14	21	0.667	1,095	2,520	0.697
chr17	6347455	T	C	15	22	5	0.381	2,436	1,208	0.332
chr17	6347607	C	T	21	15	6	0.321	2,778	2,198	0.442
chr17	6381931	C	T	25	15	2	0.226	15,527	5,651	0.267
chr17	6382100	G	A	33	8	1	0.119	17,051	2,585	0.132
chr17	7850498	G	A	38	4	0	0.048	8,850	676	0.071
chr17	7851573	T	A	41	1	0	0.012	12,160	7	0.001
chr17	7858844	G	T	33	9	0	0.107	2,663	307	0.103
chr17	7858848	G	C	41	1	0	0.012	2,923	34	0.011
chr17	7858871	C	T	34	8	0	0.095	2,868	315	0.099
chr17	23898022	G	T	33	8	1	0.119	2,556	3	0.001
chr17	23898370	G	A	41	1	0	0.012	5,392	64	0.012
chr17	55589622	C	T	41	1	0	0.012	11,495	93	0.008
chr17	77110200	C	T	41	1	0	0.012	1,688	32	0.019
chr17	77110461	G	A	41	1	0	0.012	1,292	18	0.014
chr17	77111406	T	C	41	1	0	0.012	4,571	209	0.044
chr17	77111540	C	T	41	1	0	0.012			
chr17	77111631	C	A	29	13	0	0.155			
chr17	77111632	T	C	41	1	0	0.012			
chr17	77111711	G	A	41	1	0	0.012	1,343	6	0.004
chr17	77113830	G	A	41	1	0	0.012	4,383	111	0.025
chr17	77113877	G	A	40	2	0	0.024	5,601	194	0.033
chr19	12798227	G	C	39	3	0	0.036	6,412	4	0.001
chr19	12800792	T	C	10	14	18	0.595	9,325	13,969	0.600
chr19	53016999	T	C	36	4	2	0.095	13,228	1,447	0.099
chr19	53029624	C	T	31	10	1	0.143	3,012	686	0.186
chr19	53029709	G	A	32	9	1	0.131	2,595	521	0.167
chr19	53034608	G	A	39	2	1	0.048	1,716	106	0.058
chr19	53035436	A	T	29	8	5	0.214	7,431	3,670	0.331
chr19	53035437	A	C	28	9	5	0.226	7,408	3,611	0.328
chr19	53036325	G	A	35	6	1	0.095	13,710	2,802	0.170
chr19	53036382	G	A	19	18	5	0.333	9,129	4,494	0.330
chr19	53036491	T	A	11	15	16	0.560	3,677	6,921	0.653
chr19	53036828	C	T	40	2	0	0.024	5,112	188	0.035
chr19	53037142	C	T	18	19	5	0.345	3,693	2,074	0.360
chr19	53037207	C	T	34	7	1	0.107	3,310	562	0.145
chr19	53037219	T	C	11	14	17	0.571	1,456	2,040	0.584
chr19	53038206	G	A	41	1	0	0.012	6,639	55	0.008

chr19	59317779	G	A	41	1	0	0.012	4,596	47	0.010
chr19	59317819	C	T	38	4	0	0.048	3,524	140	0.038
chr19	59317866	T	C	34	7	1	0.107	2,508	389	0.134
chr19	59317867	C	G	24	15	3	0.250	1,948	921	0.321
chr19	59318585	A	G	41	1	0	0.012	14,568	43	0.003
chr3	50207957	G	A	32	10	0	0.119	794	2	0.003
chr3	50208219	T	G	18	14	10	0.405	1,924	1,346	0.412
chr3	50208321	C	T	25	14	3	0.238	1,661	1,046	0.386
chr3	130735294	C	A	35	7	0	0.083	8,680	1,566	0.153
chr3	130735483	A	G	37	3	2	0.083	26,721	2,686	0.091
chr3	130735564	C	T	39	3	0	0.036	19,984	723	0.035
chr3	130735739	T	C	41	1	0	0.012	2,235	21	0.009
chr3	130735995	G	T	41	1	0	0.012	5,768	286	0.047
chr3	130736163	A	G	29	9	4	0.202	1,820	635	0.259
chr3	130736176	T	C	41	1	0	0.012	2,100	107	0.048
chr4	619829	G	C	41	1	0	0.012	10,609	307	0.028
chr4	639680	G	C	41	1	0	0.012	5,409	17	0.003
chr4	639692	C	T	41	1	0	0.012	5,445	71	0.013
chr4	639876	C	T	30	10	2	0.167	4,883	1,086	0.182
chr4	642826	C	T	38	4	0	0.048	4,901	237	0.046
chr4	645881	C	G	30	11	1	0.155	10,543	2,051	0.163
chr4	648089	G	A	30	11	1	0.155	9,846	2,380	0.195
chr4	654310	C	T	41	1	0	0.012	568	7	0.012
chr4	15579299	G	C	3	7	32	0.845	858	4,229	0.831
chr4	15595140	G	A	0	1	41	0.988	67	4,633	0.986
chr4	15596610	T	A	4	19	19	0.679	464	437	0.485
chr4	15598289	C	A	36	0	6	0.143	156	170	0.521
chr4	15598289	C	T	3	1	38	0.917	156	2,032	0.929
chr4	15604616	C	T	41	1	0	0.012	2,593	30	0.011
chr4	15604681	G	A	41	1	0	0.012	3,340	21	0.006
chr4	15619667	C	T	41	1	0	0.012	4,462	58	0.013
chr4	15623834	C	A	39	2	1	0.048	2,588	153	0.056
chr4	15626996	T	G	38	4	0	0.048	14,927	771	0.049
chr4	15629260	C	T	31	9	2	0.155	3,764	752	0.167
chr4	15633983	A	G	2	12	28	0.810	866	3,788	0.814
chr4	15634951	A	G	32	8	2	0.143	14,752	3,068	0.172
chr4	15635093	A	G	41	1	0	0.012	15,272	127	0.008
chr4	15635794	C	T	41	1	0	0.012	5,391	76	0.014
chr4	15635833	T	C	41	1	0	0.012	4,561	35	0.008
chr4	15635867	A	C	38	4	0	0.048	4,356	5	0.001
chr4	15635874	A	T	41	1	0	0.012	4,760	1	0.000
chr4	15635875	T	A	40	2	0	0.024			
chr4	15636081	T	C	37	5	0	0.060	4,438	464	0.095
chr4	15646450	C	T	16	17	9	0.417	4,781	4,411	0.480
chr4	15649715	C	T	41	1	0	0.012	3,687	24	0.006
chr4	15686499	G	A	38	4	0	0.048	3,263	172	0.050

chr4	15686613	G	A	40	2	0	0.024	2,286	81	0.034
chr4	15686906	G	A	8	9	25	0.702	1,083	3,676	0.772
chr5	43281679	C	T	21	18	3	0.286	1,555	790	0.337
chr5	43281716	G	A	41	1	0	0.012			
chr5	43312832	A	G	40	2	0	0.024	3,248	4	0.001
chr6	42231231	T	C	41	1	0	0.012	16,302	224	0.014
chr6	42231295	A	C	4	14	24	0.738	3,596	8,893	0.712
chr6	42231372	T	C	39	3	0	0.036	12,940	34	0.003
chr6	42249304	A	G	39	2	1	0.048	2,914	204	0.065
chr6	42254276	G	C	32	10	0	0.119	3,595	437	0.108
chr6	42259213	C	T	23	14	5	0.286	5,258	1,964	0.272
chr6	42260028	C	T	34	8	0	0.095	14	3	0.176
chr6	42260080	T	C	41	1	0	0.012			
chr6	42260102	C	T	41	1	0	0.012	8,741	97	0.011
chr6	42260311	T	C	35	7	0	0.083	16,737	2,230	0.118
chr6	42260688	T	C	39	3	0	0.036	13,247	721	0.052
chr6	42261388	C	T	41	1	0	0.012	6,214	137	0.022
chr6	42270553	A	G	3	6	33	0.857	811	4,512	0.848
chr6	42773010	G	T	29	10	3	0.190	3,473	971	0.218
chr6	42773249	G	A	4	20	18	0.667	1,391	2,852	0.672
chr6	42773468	C	T	5	17	20	0.679	2,021	3,858	0.656
chr6	42797733	A	G	10	19	13	0.536	1,000	944	0.486
chr6	72946121	A	G	40	2	0	0.024	5,809	174	0.029
chr6	73008877	C	T	40	2	0	0.024	3,986	6	0.002
chr6	73008879	T	A	40	2	0	0.024	3,973	1	0.000
chr6	73027854	A	G	41	1	0	0.012	5,427	38	0.007
chr6	73027939	A	T	9	13	20	0.631	2,217	3,434	0.608
chr6	73028029	A	G	41	1	0	0.012	5,896	36	0.006
chr6	73028054	A	G	41	1	0	0.012	6,069	211	0.034
chr6	73028752	A	G	40	2	0	0.024	786	334	0.298
chr6	73040844	C	T	39	3	0	0.036	19,971	1,398	0.065
chr6	73040935	A	T	41	1	0	0.012	17,031	84	0.005
chr6	73079896	A	T	41	1	0	0.012	2,470	13	0.005
chr6	73156885	C	T	39	3	0	0.036	3,247	105	0.031
chr6	73159245	T	A	41	1	0	0.012	7,507	20	0.003
chr6	73165326	A	T	41	1	0	0.012			
chr6	73167420	A	G	41	1	0	0.012	2,398	29	0.012
chr6	73168175	A	G	17	19	6	0.369	1,640	1,440	0.468
chr6	73168213	A	G	38	4	0	0.048	5,005	178	0.034
chr6	80251270	G	A	19	15	8	0.369	792	434	0.354
chr6	80251336	G	T	41	1	0	0.012			
chr6	80251337	T	A	41	1	0	0.012	1,340	1	0.001
chr6	80252396	T	G	39	3	0	0.036	4,032	206	0.049
chr6	80253217	T	C	20	21	1	0.274	2,160	1,893	0.467
chr6	80253567	C	T	19	15	8	0.369	2,211	1,619	0.423
chr6	80258948	G	C	41	1	0	0.012	10,937	103	0.009

chr6	80259054	A	T	41	1	0	0.012	15,786	8	0.001
chr6	80259055	T	A	41	1	0	0.012	15,916	17	0.001
chr6	80260142	T	G	36	6	0	0.071	7,754	2,237	0.224
chr6	80285254	T	G	31	11	0	0.131	3,591	1,033	0.223
chr6	80285260	A	G	2	15	25	0.774	1,003	3,718	0.788
chr6	80285392	T	C	3	14	25	0.762	1,990	5,982	0.750
chr6	80438306	T	C	34	7	1	0.107	2,668	456	0.146
chr6	80438328	T	C	37	4	1	0.071	2,841	262	0.084
chr6	80565391	G	T	27	12	3	0.214	6,541	2,774	0.298
chr7	23112362	G	C	20	16	6	0.333	7,537	5,648	0.428
chr7	23130000	A	T	41	1	0	0.012	4,719	1	0.000
chr7	33100951	G	C	40	1	1	0.036	3,672	165	0.043
chr7	33105400	A	T	13	17	12	0.488	1,516	1,439	0.487
chr7	127821632	C	G	41	1	0	0.012	4,268	14	0.003
chr7	127822124	G	A	32	4	6	0.190	191	6,108	0.970
chr7	127824076	C	A	37	5	0	0.060	11,279	17	0.002
chr7	127825791	C	G	33	8	1	0.119	6,162	1,873	0.233
chr7	127828215	G	T	41	1	0	0.012	21,637	678	0.030
chr7	138469985	C	T	41	1	0	0.012	2,728	25	0.009
chr7	138475414	A	G	41	1	0	0.012	5,348	74	0.014
chr7	138483476	T	C	40	2	0	0.024	1,995	57	0.028
chr7	138483756	T	A	41	1	0	0.012			
chr7	138500514	C	T	41	1	0	0.012	4,741	61	0.013
chr7	138524583	T	C	39	3	0	0.036	2,423	115	0.045
chr8	1716146	C	A	36	6	0	0.071	3,392	6	0.002
chr8	1716624	C	T	5	9	28	0.774	3,374	11,738	0.777
chr8	1716627	C	T	39	3	0	0.036	13,885	579	0.040
chr8	1716826	G	A	41	1	0	0.012			
chr8	1716921	A	G	14	11	17	0.536			
chr8	1718411	T	G	40	2	0	0.024	2,483	34	0.014
chr8	1718909	A	T	41	1	0	0.012	2,917	333	0.102
chr8	1718932	A	G	41	1	0	0.012	4,888	77	0.016
chr8	1718936	C	T	41	1	0	0.012	5,070	47	0.009
chr8	1720675	C	T	41	1	0	0.012	15,018	486	0.031
chr8	1720752	C	T	41	1	0	0.012	8,855	166	0.018
chr8	1720776	C	T	41	1	0	0.012	6,579	82	0.012
chr8	10501354	A	C	6	11	25	0.726	2,423	7,556	0.757
chr8	10501371	A	T	41	1	0	0.012	9,546	152	0.016
chr8	10501571	G	A	36	5	1	0.083	6,738	758	0.101
chr8	10501589	C	G	36	5	1	0.083	5,714	604	0.096
chr8	10502014	T	C	38	4	0	0.048	6,604	295	0.043
chr8	10502102	A	T	41	1	0	0.012	2,607	36	0.014
chr8	10502165	C	T	25	13	4	0.250	2,421	949	0.282
chr8	10502206	G	C	41	1	0	0.012	3,112	22	0.007
chr8	10502295	T	C	12	20	10	0.476	4,746	4,758	0.501
chr8	10503892	G	A	26	13	3	0.226	4,616	3,282	0.416

chr8	10504534	G	C	26	11	5	0.250	2,893	1,085	0.273
chr8	10505057	G	C	40	2	0	0.024	2,719	314	0.104
chr8	10506643	A	G	17	8	17	0.500	649	836	0.563
chr8	10507478	C	T	15	15	12	0.464	522	826	0.613
chr8	10508325	A	G	9	7	26	0.702	657	1,598	0.709
chr8	10508351	C	T	0	0	42	1.000	5	1,755	0.997
chr8	10516155	C	T	29	11	2	0.179	7,245	1,511	0.173
chr8	10516227	A	G	41	1	0	0.012	3,637	87	0.023
chr8	10516296	C	G	41	1	0	0.012			
chr8	10516307	A	G	2	3	37	0.917	50	122	0.709
chr8	10516394	C	T	9	22	11	0.524			
chr8	10517956	G	A	41	1	0	0.012	3,748	94	0.024
chr8	10549921	G	C	7	12	23	0.690	907	1,715	0.654
chr8	10549963	C	T	41	1	0	0.012	2,740	33	0.012
chr8	55701444	A	G	41	1	0	0.012	7,541	85	0.011
chr8	55702597	A	G	41	1	0	0.012	3,875	26	0.007
chr8	55703504	T	C	41	1	0	0.012	4,524	51	0.011
chr8	55703507	A	G	41	1	0	0.012	4,402	47	0.011
chr8	55704170	A	G	20	17	5	0.321	2,738	1,517	0.357
chr9	32531880	G	C	41	1	0	0.012	1,919	4	0.002
chrX	38029009	A	G	31	7	4	0.179	8,299	1,948	0.190
chrX	38029665	T	C	41	1	0	0.012	24,922	1,004	0.039
chrX	38029766	C	T	34	6	2	0.119	24,557	2,729	0.100
chrX	38029800	G	T	41	1	0	0.012	25,066	18	0.001
chrX	38029800	G	A	39	2	1	0.048	25,066	2,861	0.102
chrX	38029965	A	T	41	1	0	0.012	8,466	347	0.039
chrX	38031545	G	A	40	2	0	0.024	15,223	1,006	0.062
chrX	38035450	T	C	41	1	0	0.012	10,645	118	0.011
chrX	38041354	T	C	41	0	1	0.024	12,355	101	0.008
chrX	38041415	A	G	41	1	0	0.012	13,469	136	0.010
chrX	38041621	C	T	40	2	0	0.024	24,421	2,015	0.076
chrX	38048740	C	G	41	1	0	0.012	14,380	546	0.037
chrX	38067013	T	G	41	0	1	0.024	16,605	81	0.005
chrX	38067074	T	C	41	1	0	0.012	15,517	411	0.026
chrX	38067103	C	T	40	1	1	0.036	14,594	506	0.034
chrX	38067736	C	T	32	6	4	0.167	6,716	1,485	0.181
chrX	46604442	C	G	41	0	1	0.024			
chrX	46604442	C	T	41	0	1	0.024	22,105	216	0.010
chrX	46624652	T	A	41	0	1	0.024	17,604	332	0.019
chrX	46625052	A	G	41	0	1	0.024	31,951	734	0.022