SUPPLEMENTARY INFORMATION

The Mutational Landscape of Adenoid Cystic Carcinoma

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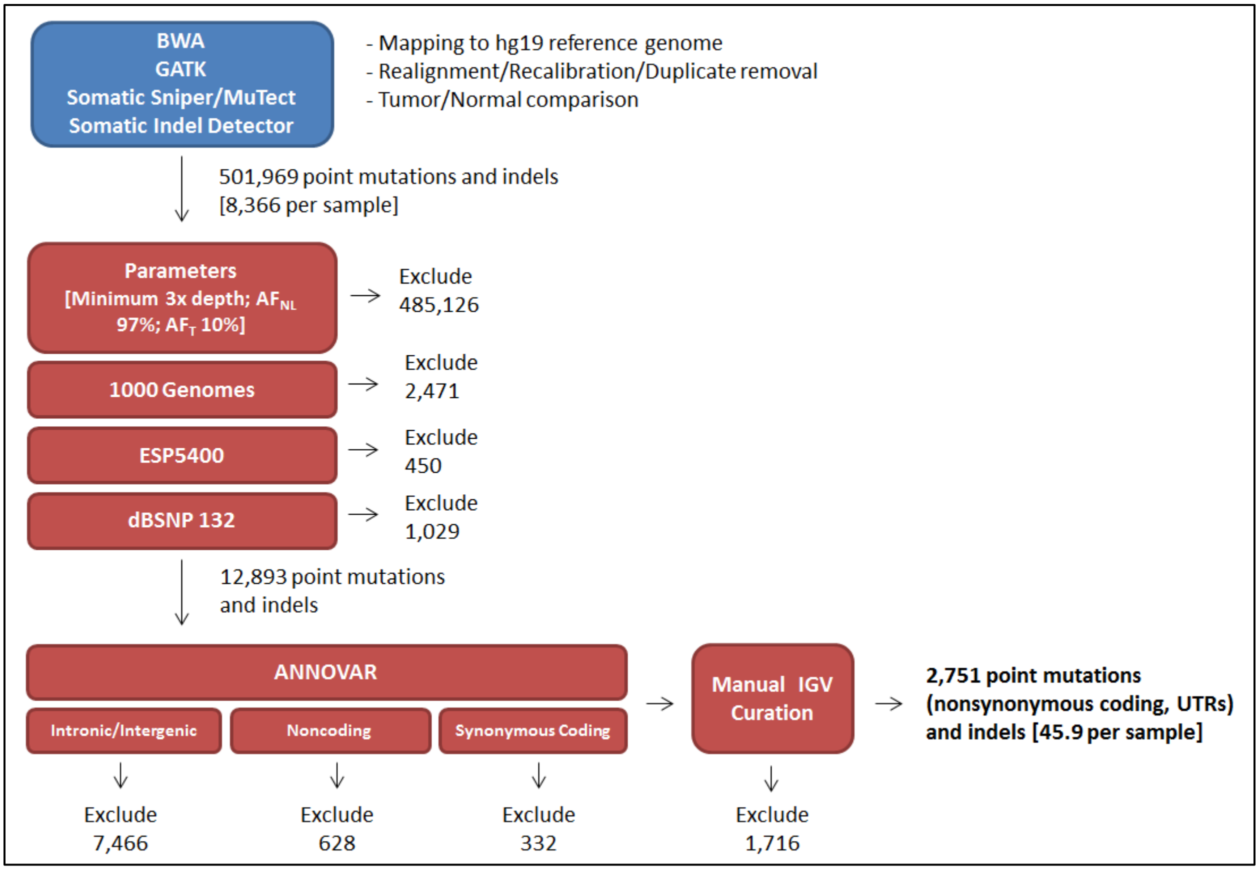
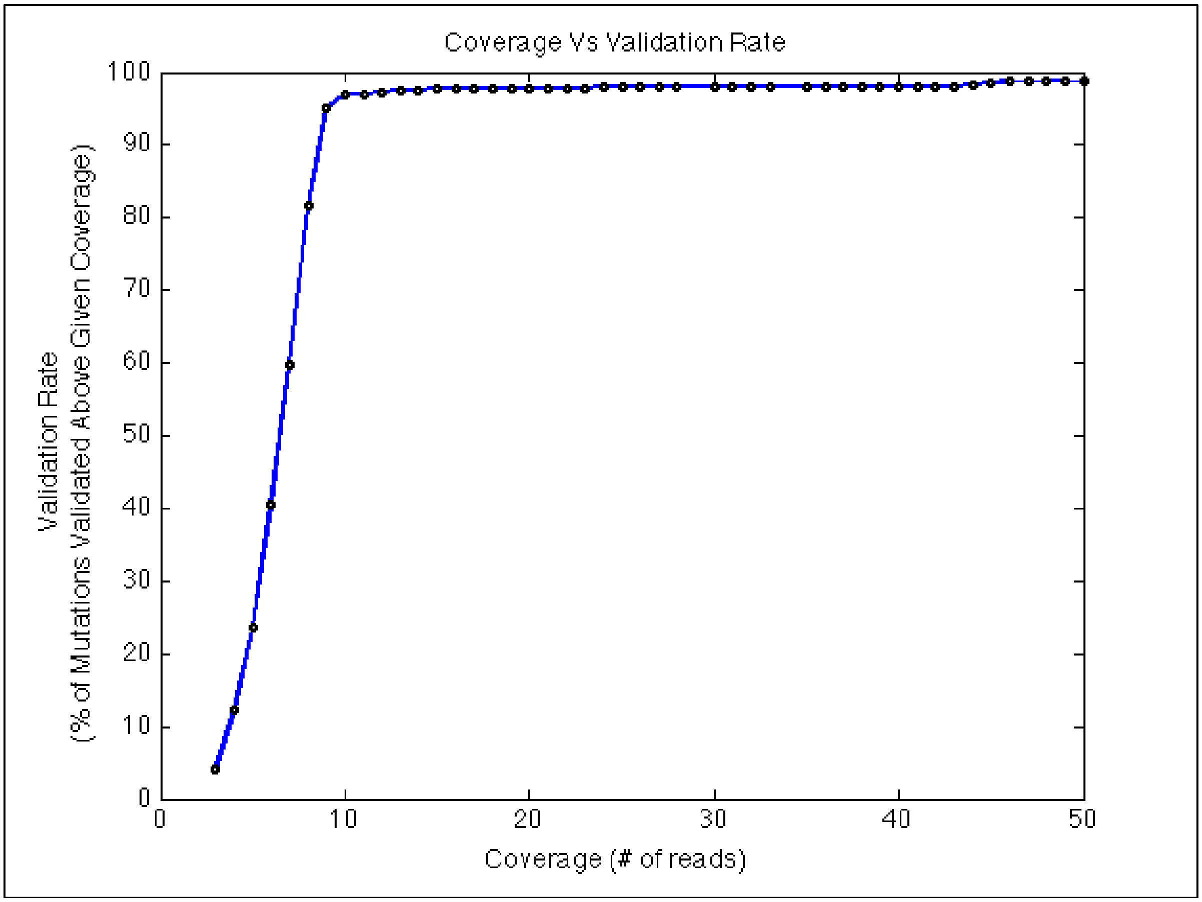
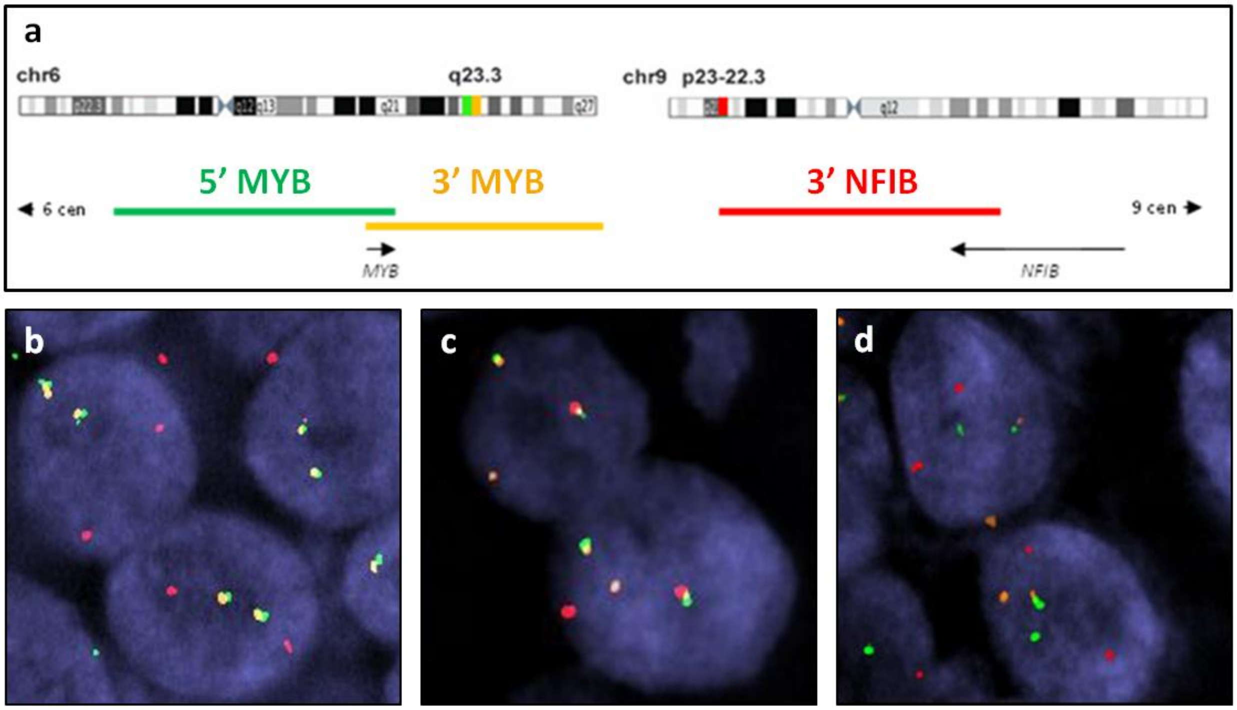


Supplementary Figure 1. Analysis pipeline. All 60 samples were evaluated by Somatic Sniper, MuTect, and Somatic Indel Detector, with SNPs (single nucleotide polymorphisms) removed by public databases. Annotation was performed by Annovar, and resulting candidates were manually reviewed using IGV to exclude calls made secondary to poor alignment or machine artifact.

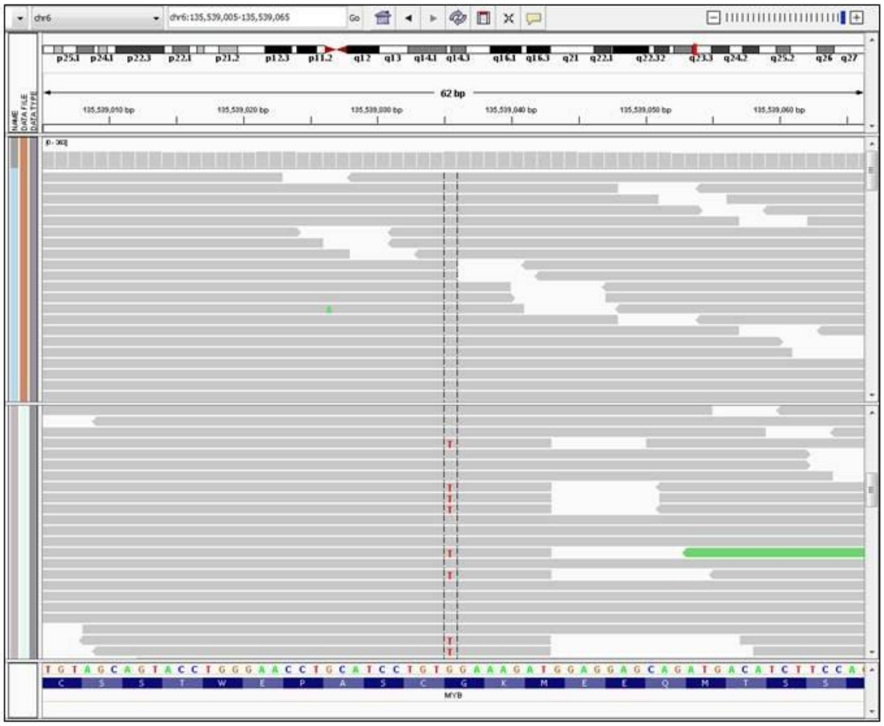


Supplementary Figure 2. Validation rate as a function of sequencing depth. Validation was performed on candidates identified with as low as 3x coverage. Deep resequencing was performed with SOLiD or MiSeq. Validation rate at minimum 10x coverage was 97%.



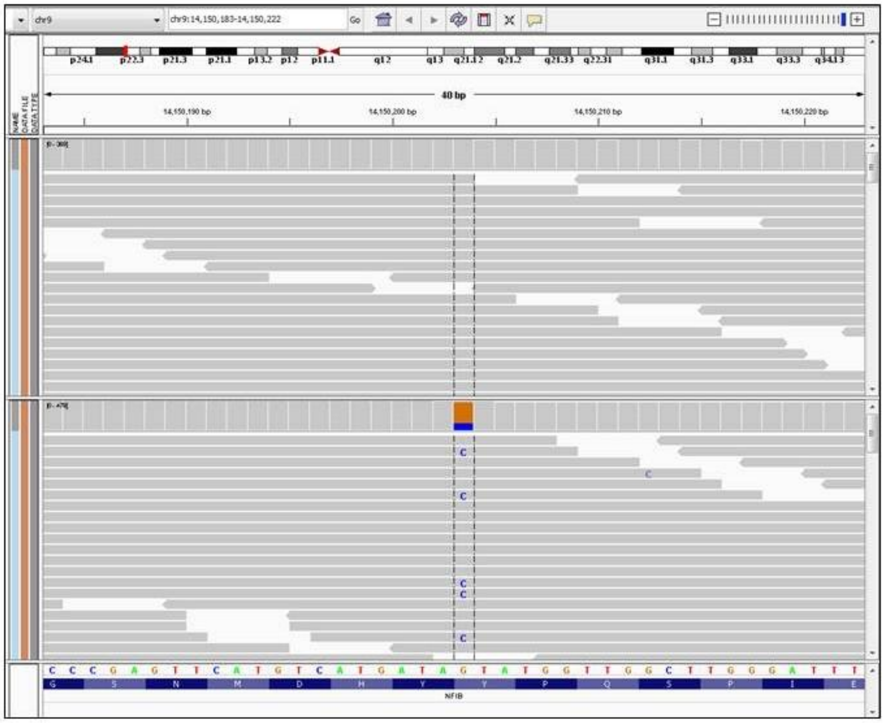
Supplementary Figure 3. ***MYB-NFIB*** **FISH.** Analysis was performed using a 3-color FISH probe mix consisting of 5’ *MYB* (green), 3’ *MYB* (orange), and 3’ *NFIB* (red). (**a**). Mapping of FISH probes to chr6 and chr9. (**b**). No *MYB-NFIB* abnormality detected (G-O, R). (**c**). Classic *MYB-NFIB* translocation (G-R). (**d**). *MYB* with unknown fusion partner (O, G).

a



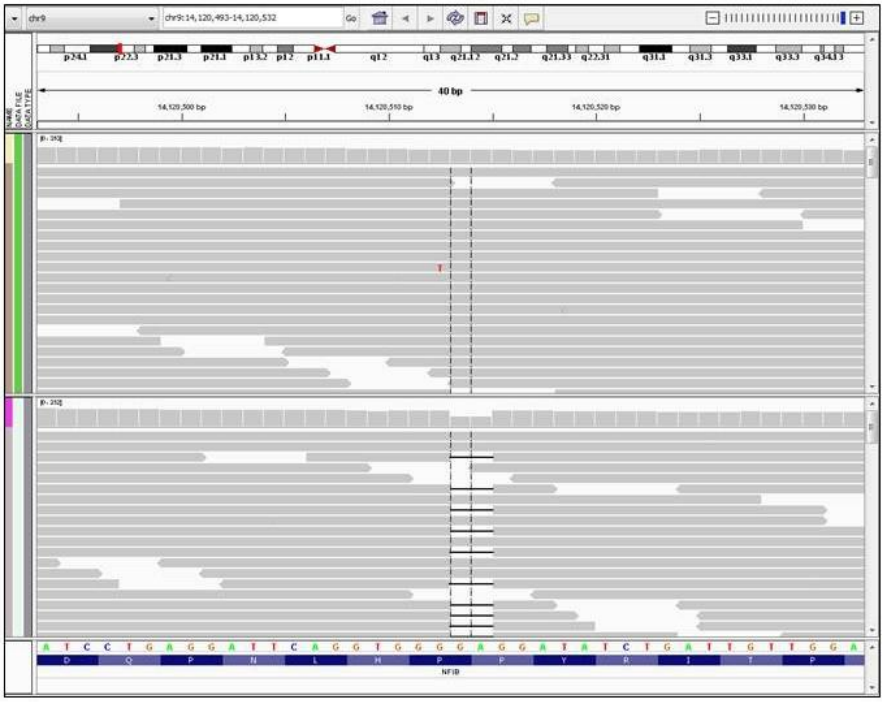
Sample 1346
Normal 183x
Tumor 105x
Tumor AF (G to T): 37%
Nonsense mutation

b



Sample 540
Normal 357x
Tumor 448x
Tumor AF (G to C): 26%
Nonsense mutation

c



NORMAL

TUMOR

Sample 2020

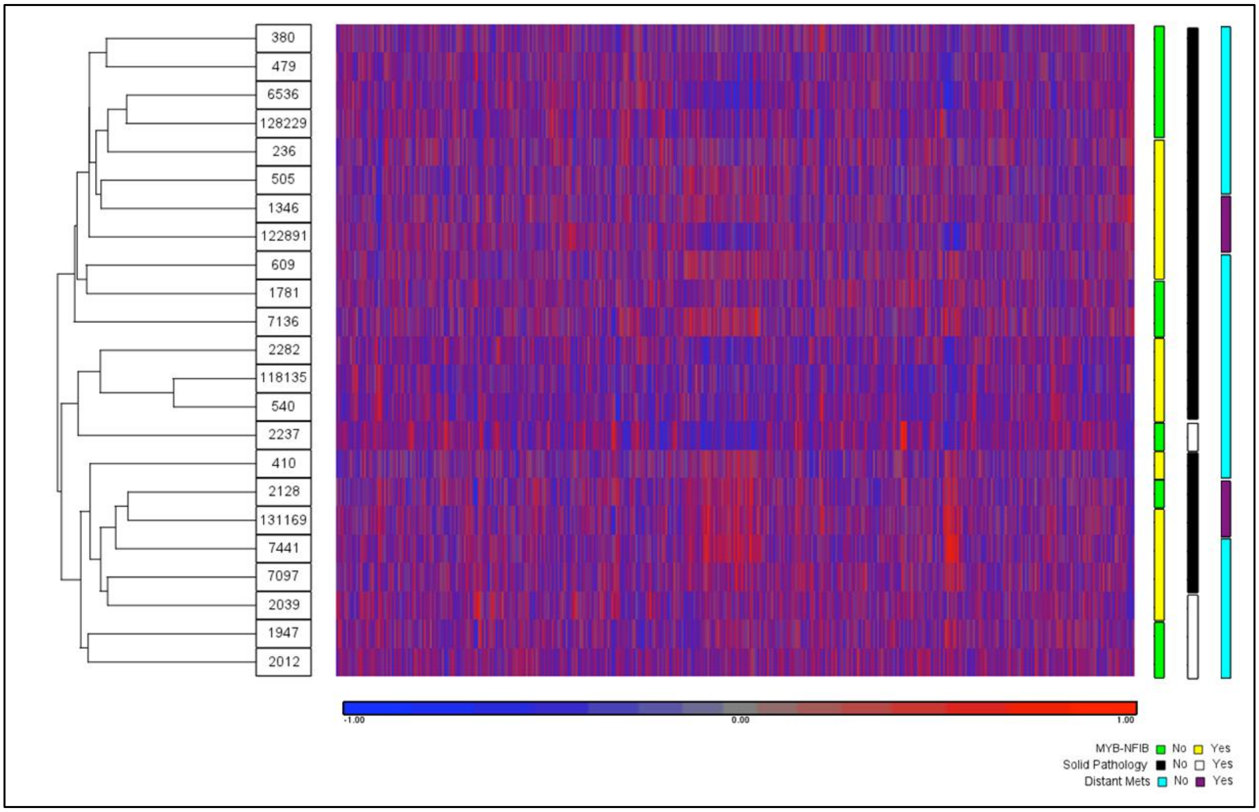
Normal coverage: 137x

Tumor coverage: 115x

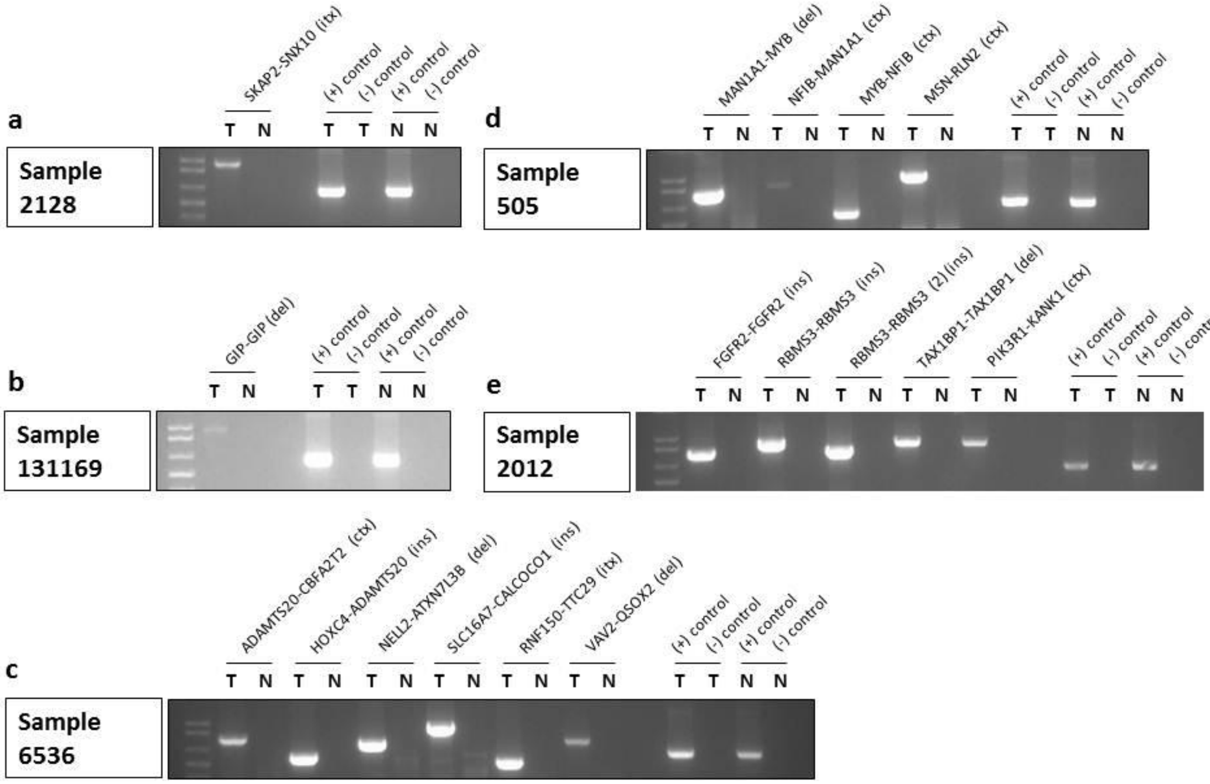
Tumor AF (GA to --): 38%

Frameshift deletion

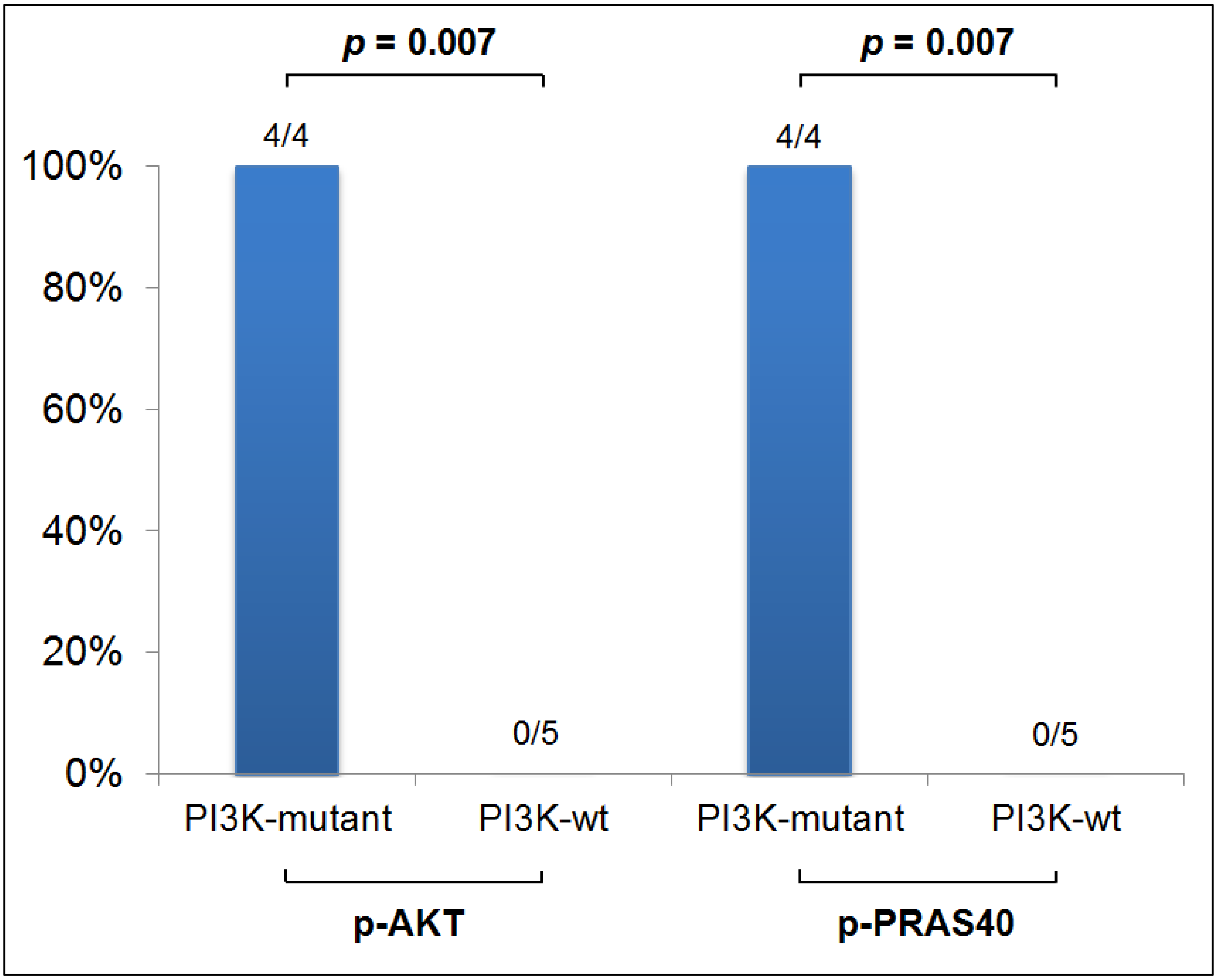
Supplementary Figure 4. IGV visualization. hg19 coordinates are listed and visualized within brackets, with reference genome and predicted codons of the gene listed at the bottom. Variant calls are listed if different from the reference genome. Representative somatic mutations are depicted. (**a**). *MYB* point mutation. (**b**). *NFIB* point mutation. (**c**). *NFIB* indel.



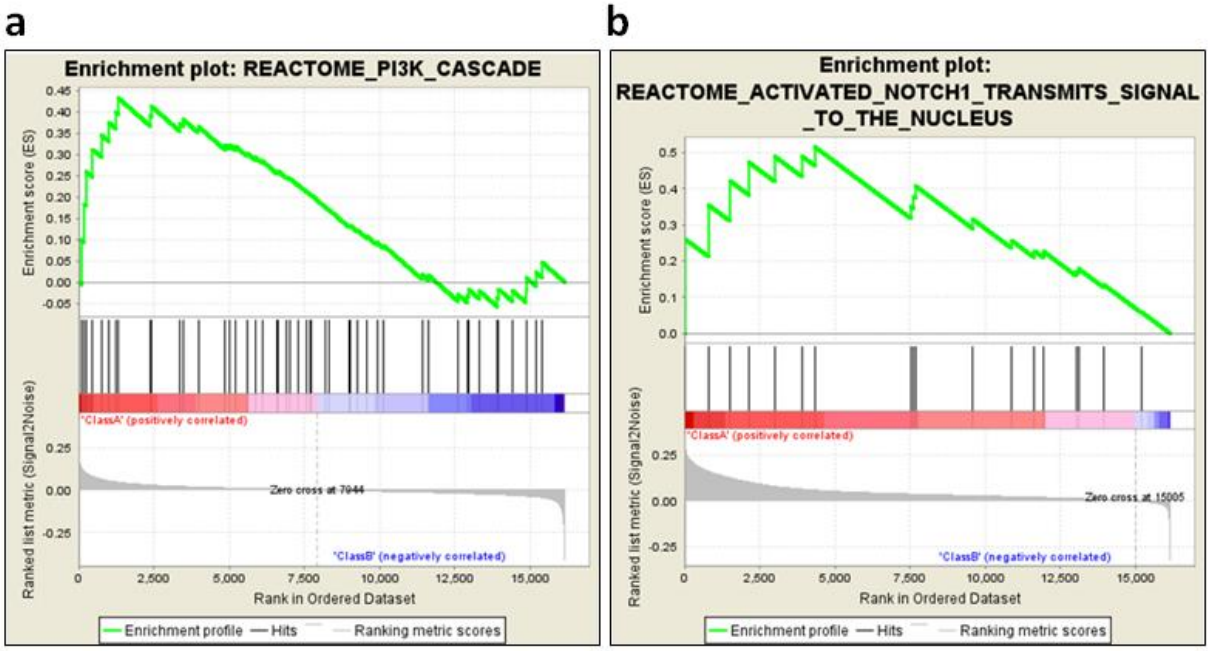
Supplementary Figure 5. Expression analysis of ACC samples. Unsupervised hierarchical clustering of 23 ACC samples with Pearson dissimilarity metric after quantile normalization. Data was clustered via average agglomeration method. Tumor IDs and annotations are listed on the left and right sides, respectively.



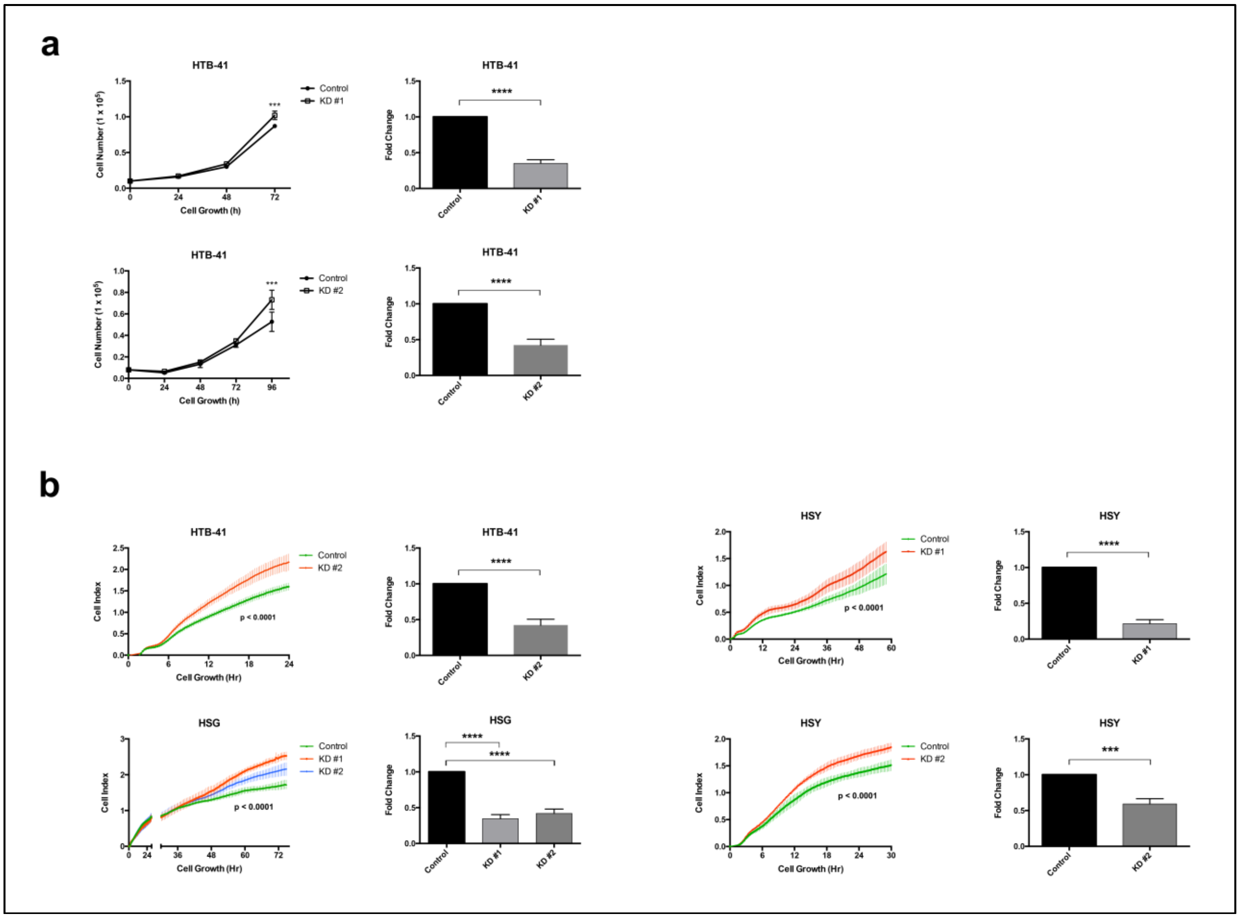
Supplementary Figure 6. Validated ACC structural variations predicted by CREST. Primers tested on tumor (T) and normal (N) whole-genome-amplified (WGA) DNA. Positive controls were performed using T and N DNA with standard primers for *PIK3CA* amplifying a 569bp region. Negative controls were performed using primers without DNA. ctx, inter-chromosomal translocation; itx, intra-chromosomal translocation; ins, insertion; del, deletion. (**a**). Sample 2128. (**b**). Sample 131169. (**c**). Sample 6536. (**d**). Sample 505. (**e**). Sample 2012.



Supplementary Figure 7. Comparative incidence of PI3K immunohistochemistry staining. All 4 PI3K-mutant ACC samples demonstrated positive staining for both p-AKT and p-PRAS40, while none of the 5 PI3K-wt ACC samples stained positive (p = 0.007). wt, wildtype.



Supplementary Figure 8. Enrichment plots of ACC expression data. Analysis was performed for 23 ACC samples with expression data using GSEA. (**a**). PI3K-altered samples demonstrated significant enrichment of the Reactome PI3K Cascade pathway ($p < 0.001$). (**b**). Notch pathway-mutated samples demonstrated enrichment of the Reactome Notch nuclear signaling pathway with borderline significance ($p = 0.10$).



Supplementary Figure 9. ***FAT4* knockdown.** RNAi knockdown in HSG (human immortalized salivary), HTB-41 (human salivary epidermoid carcinoma), and HSY (human salivary adenocarcinoma) cells demonstrated increased growth via (**a**). standard growth curves using Vi-Cell XR Cell Viability Analyzer or (**b**). the xCELLigence System in triplicate or quadruplicate, respectively. ***p < 0.001, ****p < 0.0001 (ANOVA) for knockdown compared to RNAi control. Error bars, ± 1 S.E.M. Relative knockdown fold change normalized to respective controls. KD, knockdown.

Supplementary Table 1. ACC exome sequencing data by patient

Normal Statistics	236	380	410	479	540	609	705	1346	1739	1781
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	13,885,265,850	9,544,761,387	12,932,070,736	10,928,308,862	8,107,276,801	13,169,065,240	13,357,339,297	11,974,972,927	9,307,967,458	12,876,936,401
Bases Mapped to Genome	8,161,626,110	5,486,153,397	7,647,695,074	6,522,182,112	4,889,976,689	7,842,220,038	7,926,021,446	7,246,713,051	5,338,730,644	7,698,974,374
Bases Mapped to Targeted Region	3,637,693,889	2,233,045,476	3,532,133,856	3,126,584,094	2,309,526,210	3,176,530,437	3,687,914,371	3,098,245,204	2,428,604,586	3,381,882,279
Mean Target Coverage	161.15	108.45	151.11	128.95	96.80	154.94	156.67	143.27	105.43	151.95
Targeted bases with at least 10 reads (%)	94.62	93.34	94.45	93.98	93.01	94.69	94.57	94.44	93.12	94.75

Normal Statistics	1947	2020	2039	2237	2238	2282	7097	7136	7441	65103
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	15,468,580,143	13,550,105,978	13,168,967,575	2,170,771,349	15,656,513,542	7,812,359,583	6,240,432,708	6,840,280,174	14,656,750,005	6,807,918,488
Bases Mapped to Genome	9,269,585,520	8,065,119,738	7,830,086,743	1,270,607,588	9,370,809,031	4,521,617,727	3,701,984,663	4,024,792,622	9,085,643,975	4,073,105,997
Bases Mapped to Targeted Region	4,151,170,675	3,751,183,972	3,586,751,325	592,371,234	4,454,610,860	2,018,314,505	1,718,246,565	1,616,976,535	3,844,581,162	1,989,101,314
Mean Target Coverage	183.18	159.13	154.58	25.35	185.08	89.32	73.34	79.69	179.15	80.68
Targeted bases with at least 10 reads (%)	95.04	94.93	94.64	78.28	94.96	93.21	91.68	92.23	95.19	91.61

Normal Statistics	65115	111097	118135	122891	128229	142990	11_17815	148632	3492	671204
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	9,502,417,923	13,531,646,643	11,640,983,958	14,110,188,629	12,480,669,926	12,365,748,984	9,693,613,611	3,708,779,988	10,683,915,736	11,550,643,232
Bases Mapped to Genome	5,606,206,430	8,148,979,981	6,734,984,342	8,432,492,276	7,451,729,915	7,288,068,948	5,499,226,097	2,282,164,045	6,190,999,641	6,625,482,522
Bases Mapped to Targeted Region	2,583,132,493	3,566,588,515	2,981,934,522	3,770,580,489	3,457,274,804	3,302,151,160	3,119,573,484	1,404,238,359	3,587,331,405	3,800,211,138
Mean Target Coverage	110.77	161.14	133.12	166.67	147.32	143.88	108.88	45.46	122.43	130.97
Targeted bases with at least 10 reads (%)	93.21	94.16	93.95	94.53	94.05	94.18	91.96	86.08	93.91	93.98

Normal Statistics	05_6986	07_16582	09_12352	11_3089	11_3318	2000120	2000136	2000756	2453	352
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	8,711,481,920	8,900,511,298	7,175,692,061	6,919,563,871	6,983,249,972	6,520,977,291	7,658,756,901	9,403,179,548	11,586,345,972	5,243,776,051
Bases Mapped to Genome	5,425,390,032	5,494,324,065	4,498,449,739	4,391,023,025	4,521,870,919	4,143,315,757	4,838,618,132	5,922,214,171	6,563,316,135	3,209,265,790
Bases Mapped to Targeted Region	3,378,726,747	3,391,536,359	2,819,974,677	2,786,354,398	2,927,943,073	2,632,463,953	3,056,777,650	3,729,715,729	3,717,770,735	1,964,032,152
Mean Target Coverage	107.45	108.89	89.30	87.17	89.78	82.14	95.94	117.24	130.05	63.66
Targeted bases with at least 10 reads (%)	92.30	92.28	90.90	91.31	91.17	90.98	91.97	93.31	93.16	89.60

Normal Statistics	36773720	4133	4332	6112	6277	80872	9534	980452	990149	505
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	8,614,178,781	7,689,277,585	7,114,654,397	8,681,212,156	6,244,238,933	8,016,626,583	6,265,105,092	8,560,604,929	8,451,240,222	3,041,092,154
Bases Mapped to Genome	5,393,443,722	4,910,982,523	4,366,207,359	5,381,820,371	3,997,590,874	5,096,708,838	4,061,579,525	5,354,652,860	5,339,025,123	2,230,493,557
Bases Mapped to Targeted Region	3,376,765,000	3,136,418,632	2,679,406,104	3,336,265,793	2,559,173,728	3,240,191,870	2,632,959,543	3,349,164,015	3,372,742,256	1,618,439,433
Mean Target Coverage	106.72	97.42	86.66	106.72	79.27	101.12	80.59	105.97	105.86	44.11
Targeted bases with at least 10 reads (%)	92.41	92.02	91.31	92.89	90.91	92.08	91.37	92.61	92.42	96.10

Normal Statistics	2012	2128	6536	131169	06_2532	09_4178	09_4615	10_5283	10_5342	11_6165
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	3,061,924,282	2,781,227,711	3,192,634,779	2,957,697,435	5,735,671,124	7,360,874,536	5,626,929,694	6,175,124,594	6,436,463,092	7,394,943,739
Bases Mapped to Genome	2,250,134,459	2,037,134,931	2,340,080,960	2,169,958,625	3,649,521,459	4,408,208,539	3,558,143,068	3,928,253,799	4,037,460,368	4,547,903,894
Bases Mapped to Targeted Region	1,638,520,911	1,478,224,554	1,694,646,850	1,576,728,826	2,322,048,173	2,639,842,459	2,249,874,350	2,498,829,022	2,532,517,203	2,796,865,389
Mean Target Coverage	44.42	40.23	46.27	42.87	72.57	87.30	70.68	77.99	80.23	90.22
Targeted bases with at least 10 reads (%)	96.23	95.94	96.21	96.14	88.71	91.32	89.20	89.70	90.04	91.32

Tumor Statistics	236	380	410	479	540	609	705	1346	1739	1781
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	9,322,764,865	9,684,882,834	13,320,125,241	9,582,902,437	9,539,781,882	10,242,047,276	11,456,158,233	8,899,941,751	7,598,541,111	8,865,593,160
Bases Mapped to Genome	5,530,237,371	5,609,881,990	7,945,766,835	5,712,587,504	5,671,683,358	6,155,361,401	6,926,897,598	5,414,508,825	4,312,619,875	5,317,431,940
Bases Mapped to Targeted Region	2,431,501,586	2,438,783,998	3,783,964,865	2,712,622,176	2,583,843,116	2,929,274,937	3,074,261,057	2,679,792,024	1,914,889,477	2,609,726,470
Mean Target Coverage	109.30	110.90	157.01	112.96	112.19	121.70	136.94	107.20	85.16	105.20
Targeted bases with at least 10 reads (%)	93.18	93.48	94.72	93.50	93.72	93.66	94.25	93.12	92.65	93.12

Tumor Statistics	1947	2020	2039	2237	2238	2282	7097	7136	7441	65103
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	9,277,328,540	10,447,491,388	10,830,032,846	2,064,510,597	10,066,684,535	6,297,736,527	5,021,219,537	7,639,912,893	12,947,280,921	6,277,860,581
Bases Mapped to Genome	5,615,020,665	6,229,389,485	6,470,217,275	1,174,222,815	6,077,984,821	3,631,143,992	3,003,742,001	4,479,996,072	8,040,849,510	3,742,078,006
Bases Mapped to Targeted Region	2,276,407,988	2,842,869,103	2,293,355,573	538,108,741	2,901,958,165	1,640,946,650	1,520,875,676	1,869,771,161	3,683,931,285	1,851,838,401
Mean Target Coverage	110.93	122.95	127.70	23.44	120.18	71.75	59.64	88.68	158.59	74.21
Targeted bases with at least 10 reads (%)	93.04	94.17	94.61	76.03	93.82	92.05	89.76	92.47	94.67	91.40

Tumor Statistics	65115	111097	118135	122891	128229	142990	11_17815	148632	3492	671204
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	9,858,130,744	11,027,006,763	9,842,210,232	13,944,245,771	14,074,835,158	14,043,365,017	7,550,309,404	11,075,612,898	9,169,485,635	6,937,609,575
Bases Mapped to Genome	5,833,736,193	6,590,267,317	5,862,342,241	8,389,961,519	8,438,594,552	8,394,354,906	4,569,024,414	6,663,287,704	5,576,597,799	3,974,107,117
Bases Mapped to Targeted Region	2,469,484,702	3,046,733,303	2,672,090,768	3,921,761,663	4,012,762,674	3,944,859,933	2,764,789,777	4,008,573,913	3,391,368,915	2,276,396,375
Mean Target Coverage	115.21	130.31	116.03	165.81	166.81	165.70	90.53	132.02	110.37	78.71
Targeted bases with at least 10 reads (%)	93.52	94.07	92.97	94.54	94.85	94.54	91.29	93.52	93.21	91.44

Tumor Statistics	05_6986	07_16582	09_12352	11_3089	11_3318	2000120	2000136	2000756	2453	352
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	9,186,499,861	8,019,094,988	6,358,204,803	5,630,916,061	5,445,291,020	6,578,900,123	8,041,844,538	7,104,490,256	7,164,723,012	4,696,256,008
Bases Mapped to Genome	5,707,249,125	5,058,073,456	4,025,007,934	3,591,942,200	3,561,834,385	3,860,399,679	4,855,712,132	4,544,390,717	4,519,426,823	3,156,830,439
Bases Mapped to Targeted Region	3,545,571,446	3,190,273,613	2,547,902,472	2,291,199,355	2,329,756,691	2,265,112,674	2,931,767,304	2,906,705,912	2,850,691,741	2,121,948,814
Mean Target Coverage	112.97	100.27	79.93	71.34	70.75	76.44	96.23	90.06	89.70	62.70
Targeted bases with at least 10 reads (%)	92.80	91.99	90.72	90.12	90.10	90.99	92.03	91.47	91.10	89.17

Tumor Statistics	36773720	4133	4332	6112	6277	80872	9534	980452	990149	505
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	8,529,504,281	5,082,562,113	6,242,232,638	6,667,294,649	5,579,933,659	7,790,325,628	5,627,592,584	7,532,878,476	8,201,910,362	3,180,130,113
Bases Mapped to Genome	5,234,776,109	3,161,729,655	3,993,089,362	4,067,110,836	3,565,039,069	4,841,206,986	3,473,133,115	4,625,033,314	5,188,965,414	2,340,265,515
Bases Mapped to Targeted Region	3,212,582,098	1,966,750,770	2,554,231,521	2,480,876,603	2,277,628,595	3,008,388,957	2,143,395,478	2,839,539,203	3,282,664,056	1,709,535,876
Mean Target Coverage	103.62	62.86	79.26	80.72	70.73	96.08	68.95	91.58	102.82	46.23
Targeted bases with at least 10 reads (%)	91.93	88.89	91.18	90.90	90.38	91.28	89.83	92.03	92.45	96.37

Tumor Statistics	2012	2128	6536	131169	06_2532	09_4178	09_4615	10_5283	10_5342	11_6165
Target Regions	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378	334,378
Bases in Target Region	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122	51,756,122
Bases Sequenced (after quality filtering)	2,950,772,729	2,944,373,356	3,206,207,587	3,813,250,029	10,866,465,657	5,961,109,553	6,187,310,783	5,230,043,835	5,284,886,865	6,454,110,813
Bases Mapped to Genome	2,171,093,976	2,165,711,923	2,359,455,467	2,800,878,110	6,572,767,610	3,780,733,702	3,914,787,077	3,160,062,218	3,356,037,625	3,973,233,599
Bases Mapped to Targeted Region	1,584,679,322	1,580,122,910	1,717,827,507	2,028,521,967	3,975,505,625	2,397,775,340	2,476,838,806	1,909,277,991	2,131,087,248	2,445,882,871
Mean Target Coverage	42.85	42.71	46.65	55.32	130.07	74.99	77.73	62.82	66.78	78.90
Targeted bases with at least 10 reads (%)	96.05	96.17	96.13	96.31	93.53	90.15	89.55	87.94	88.47	90.15

Supplementary Table 2. ACC clinical data and *MYB-NFIB* FISH status

Patient ID	Set	Source	Age (yrs)	M/F	Stage	Early vs Advanced	Site	Perineural invasion	Angiolymphatic invasion	Adjuvant treatment	Pathology	*MYB-NFIB* status	Recurrence	F/U period (mo)	Status
2237	A	MSK HN Bank	46	M	T4bN0	Advanced	maxilla	Yes	Yes	RT	solid/high-grade	Negative		1.4	NED
1781	A	MSK HN Bank	72	M	T4bN0	Advanced	maxilla	Yes	No	RT	cribiform/tubular	Negative		37.3	NED
236	A	MSK HN Bank	55	F	T4bN0	Advanced	maxilla	Yes	Yes	RT	cribiform/tubular	Positive		50.3	NED
2012	A	MSK HN Bank	50	M	T4bN0	Advanced	maxilla	No	No	RT	solid/dedifferentiated	Negative		25.1	NED
410	A	MSK HN Bank	43	F	T1N0	Early	BOT	Yes	No	RT	cribiform	Positive		49.1	NED
705	A	MSK HN Bank	88	F	T4aN0M1	Advanced	tongue	Yes	No	None	cribiform	Positive	locoregional	65.0	Dead
2128	A	MSK HN Bank	51	M	T3N2C	Advanced	BOT	Yes	Yes	RT	cribiform	Negative	lung mets	20.8	Alive w/dz
380	A	MSK HN Bank	38	F	T2N0	Early	BOT	Yes	No	RT	cribiform/tubular	Negative		87.8	NED
609	A	MSK HN Bank	49	F	T3N2b	Advanced	BOT	Yes	No	RT	cribiform/tubular	Positive		33.7	NED
1739	A	MSK HN Bank	67	M	T2N0	Early	BOT	Yes	Yes	RT	cribiform/tubular	Negative	lung mets	41.0	Alive w/dz
2020	A	MSK HN Bank	48	M	T3N0	Advanced	soft palate	Yes	No	RT	cribiform/tubular	Positive		26.5	NED
505	A	MSK HN Bank	63	F	T3N0	Advanced	trachea	No	No	RT	cribiform	Positive		76.4	NED
479	A	MSK HN Bank	67	F	T1N0	Early	chin	Yes	No	None	tubular	MYB+		3.8	NED
1947	A	MSK HN Bank	51	M	T2N0	Early	parotid	Yes	No	RT	>30% solid	MYB+		18.7	NED
2238	A	MSK HN Bank	29	F	T2N0	Early	SMG	Yes	No	RT	cribiform	Positive		13.3	NED
2039	A	MSK HN Bank	64	M	T4aN0	Advanced	SMG	Yes	No	chemoRT	>50% solid	Positive		11.2	NED
1346	A	MSK HN Bank	52	F	T4aN0	Advanced	parotid	Yes	No	RT	cribiform	Positive	lung mets	58.3	Alive w/dz
540	A	MSK OR	74	F	T1N0	Early	SMG	Yes	No	None	cribiform	Positive		12.3	NED
6536	A	MSK OR	70	F	T2N0	Early	BOT	Yes	No	RT	cribiform/tubular	Negative		11.4	NED
2282	A	MSK OR	49	M	T2N0	Early	hard palate	Yes	No	None	cribiform/tubular	Positive		8.6	NED
7097	A	MSK OR	56	F	T2N2B	Advanced	BOT	Yes	No	RT	cribiform/tubular	Positive		10.3	NED
7136	A	MSK OR	58	F	T2N0	Early	sublingual	Yes	No	RT	cribiform/tubular	Negative		10.7	NED
7441	A	MSK OR	53	M	T4aN0	Advanced	hard palate	Yes	No	chemoRT	cribiform/tubular	Positive		10.8	NED
111097	A	MSK TPS	37	F	T1N0	Early	sublingual	No	No	None	cribiform	Positive		71.3	NED
118135	A	MSK TPS	39	F	T3N0	Advanced	SMG	Yes	No	RT	cribiform	Positive		73.5	NED
122891	A	MSK TPS	73	F	T3N0	Advanced	parotid	Yes	No	None	cribiform	Positive	lung mets	14.2	Alive w/dz
128229	A	MSK TPS	80	F	T1N0	Early	SMG	Yes	No	None	cribiform and tubular	Negative		3.8	NED
131169	A	MSK TPS	64	M	T1N0	Early	SMG	Yes	No	RT	cribiform	Negative	lung mets	45.9	Alive w/dz
142990	A	MSK TPS	78	M	T2N0	Early	maxilla	Yes	Yes	chemoRT	solid/high-grade	Positive		16.7	NED
65115	A	Proteogenex	34	F	T3N0	Advanced	parotid	N/A	N/A	N/A	cribiform	Negative		N/A	Lost to f/u
65103	A	Proteogenex	27	F	T3N0	Advanced	buccal mucosa	N/A	N/A	N/A	tubular	Positive		N/A	Lost to f/u
352	B	MSK HN Bank	48	M	T4bN0	Advanced	maxilla	Yes	Yes	RT	solid	Negative	locoregional	43.6	Dead
9534	B	MSK OR	53	F	T4aN0M1	Advanced	FOM	Yes	No	chemoRT	cribiform	Negative	lung mets at dx	6.6	Alive w/dz
6277	B	MSK OR	60	M	T4aN1	Advanced	hard palate	Yes	Yes	RT	cribiform/tubular	Positive		8.1	NED
4332	B	MSK OR	52	F	T4aN0	Advanced	buccal muc	Yes	No	RT	cribiform	Positive		5.9	NED
2453	B	MSK OR	21	F	T4aN0	Advanced	palate	Yes	No	RT	cribiform/tubular	Positive		5.4	NED
6112	B	MSK OR	43	F	T2N0	Early	SMG	Yes	No	RT	cribiform	Positive		3.7	NED
4133	B	MSK OR	85	F	T2N0M1	Advanced	FOM	Yes	No	chemoRT	cribiform/tubular	Negative		4.6	NED
80872	B	MSK OR	50	F	T3N0	Advanced	thyroid	No	Yes	RT	cribiform	Negative		2.7	NED
3492	B	MSK OR	48	M	T2N2BM1	Advanced	SMG	Yes	No	RT	solid	Positive		2.5	Alive w/dz
148632	B	MSK TPS	74	F	T4N0	Advanced	lacrimal gland	Yes	No	RT	solid	Negative		2.8	NED
980452	B	Singapore	51	M	T4N0	Advanced	FOM	Yes	Yes	RT	cribiform	Negative	locoregional	85.2	Alive w/dz
990149	B	Singapore	39	F	T2NO	Early	FOM	Yes	No	None	cribiform	Positive	lung mets	86.3	Alive w/dz
2000120	B	Singapore	75	M	T2N0	Early	sublingual	Yes	No	None	cribiform/tubular	Negative	lung mets	109.6	Alive w/dz
2000136	B	Singapore	40	F	T4N0	Advanced	hard palate	Yes	No	None	cribiform	Positive		N/A	lost to f/u
2000756	B	Singapore	75	M	T4N0	Advanced	hard palate	Yes	No	Yes	cribiform	Negative	lung mets	140.0	Alive w/dz
36773720	B	Singapore	83	M	T4N0	Advanced	buccal mucosa	Yes	No	None	cribiform/tubular	Positive		2.1	Dead-MI
671204	B	Singapore	65	M	T4N0	Advanced	hard palate	Yes	No	Yes	cribiform	Positive	spine mets at dx	7.1	Alive w/dz
05_6986	B	Amsterdam	75	M	T2N0	Early	parotid	no	N/A	N/A	cribiform/tubular	Positive	lung mets	52.3	Dead
07_16582	B	Amsterdam	67	F	T1N0	Early	parotid	yes	N/A	N/A	cribiform	Negative		46.5	NED
09_12352	B	Amsterdam	72	F	T1N0M1	Advanced	SMG	yes	N/A	N/A	cribiform/tubular	Negative	bone mets	6.0	Dead
11_3089	B	Amsterdam	42	F	T2N0	Early	trachea	yes	N/A	N/A	cribiform/tubular	Negative		11.2	NED
11_3318	B	Amsterdam	58	F	T2N0	Early	palate	yes	N/A	N/A	cribiform/tubular	Positive		11.0	NED
11_17815	B	Amsterdam	69	M	T3N0	Advanced	sinonasal	no	N/A	N/A	cribiform/tubular	Negative		1.1	NED
06_2532	B	Pittsburgh	83	F	T4BN0	Advanced	RMT	Yes	N/A	RT	tubular	Positive	lung mets	62.0	Dead-Other
09_4615	B	Pittsburgh	53	M	T4AN0	Advanced	parotid	Yes	N/A	RT	cribiform/tubular	Positive		35.8	NED
10_5283	B	Pittsburgh	80	M	T2N0	Early	SMG	Yes	N/A	RT	cribiform	Negative		22.4	NED
10_5342	B	Pittsburgh	31	F	T3N2B	Advanced	parotid	Yes	N/A	RT	cribiform	Positive	lung mets	24.7	Alive w/dz
11_6165	B	Pittsburgh	48	F	T4BN0	Advanced	parotid	No	N/A	RT	tubular	Negative		11.0	NED
09_4178	B	Pittsburgh	62	M	T2N2B	Advanced	BOT	Yes	N/A	chemoRT	cribiform/tubular	Negative		38.1	NED
Median			**54**											**16.7**	

Supplementary Table 3. Validated ACC nonsynonymous mutations

Gene	Sample	Entrez Gene ID	Type	Nucleotide (genomic)	Nucleotide (cDNA)	Amino acid (protein)	Refseq mRNA ID	Polyphen 2 Class	MutationAssessor Class
ABCA7	671204	10347	Splice Site	g.chr19:1046406G>A	c.1622_splice	p.V541_splice	NM_019112		
ABCA9	6536	10350	Missense	g.chr17:67016724A>G	c.2405T>C	p.I802T	NM_080283	neutral	neutral
ACADL	3492	33	Missense	g.chr2:211085501G>A	c.103C>T	p.R35C	NM_001608	deleterious	low
ACD	142990	65057	Missense	g.chr16:67691738G>A	c.1483C>T	p.R495C	NM_001082486	deleterious	low
ACOX2	1781	8309	Splice Site	g.chr3:58510332C>T	c.1347G>A	p.R449R	NM_003500		
ACTB	671204	60	Missense	g.chr7:5567474T>C	c.1033A>G	p.I345V	NM_001101	neutral	medium
ACTB	10_5283	60	Missense	g.chr7:5568871C>T	c.284G>A	p.R95H	NM_001101	deleterious	medium
ACTG2	2000756	72	Indel	g.chr2:74141809_74141810delGA	c.616_617delGA	p.E206fs	NM_001615		
ACVR1B	2237	91	Missense	g.chr12:52380724G>A	c.1259G>A	p.G420E	NM_004302	deleterious	medium
ADAM2	671204	2515	Missense	g.chr8:39624426A>G	c.1448T>C	p.I483T	NM_001464	neutral	low
ADAM2	7097	2515	Missense	g.chr8:39645667G>A	c.746C>T	p.T249I	NM_001464	neutral	neutral
ADAM32	6112	203102	Missense	g.chr8:39103660G>T	c.1877G>T	p.C626F	NM_145004	deleterious	low
ADAMTS16	705	170690	Missense	g.chr5:5146307G>A	c.240G>A	p.M80I	NM_139056	deleterious	neutral
ADAMTSL2	11_6165	9719	Missense	g.chr9:136420739C>T	c.1336C>T	p.H446Y	NM_001145320	neutral	neutral
ADCY10	2039	55811	Missense	g.chr1:167847744A>G	c.1346T>C	p.V449A	NM_018417	neutral	low
ADNP2	131169	22850	Missense	g.chr18:77894928G>T	c.1632G>T	p.Q544H	NM_014913	deleterious	medium
ADSS	09_4178	159	Missense	g.chr1:244582154T>C	c.853A>G	p.M285V	NM_001126	neutral	neutral
AEBP1	09_4615	165	Missense	g.chr7:44148519C>T	c.962C>T	p.P321L	NM_001129	deleterious	low
AFF2	410	2334	Missense	g.chrX:148037237G>T	c.1662G>T	p.E554D	NM_002025	deleterious	low
AFF2	11_6165	2334	Missense	g.chrX:147743437A>T	c.189A>T	p.K63N	NM_002025	deleterious	low
AGBL4	11_6165	84871	Missense	g.chr1:49056576C>T	c.1033G>A	p.D345N	NM_032785	neutral	low
AGPAT4	540	56895	Missense	g.chr6:161574393T>G	c.649A>C	p.S217R	NM_020133	neutral	low
AHNAK	148632	79026	Missense	g.chr11:62293274T>G	c.8615A>C	p.K2872T	NM_001620	deleterious	medium
AICDA	7097	57379	Missense	g.chr12:8758078C>T	c.160G>A	p.G54S	NM_020661	deleterious	medium
AIFM3	10_5283	150209	Missense	g.chr22:21333921G>C	c.1582G>C	p.G528R	NM_144704	deleterious	low
ALG10B	2000756	144245	Missense	g.chr12:38714144T>A	c.551T>A	p.M184K	NM_001013620	deleterious	medium
ALOXE3	705	59344	Missense	g.chr17:8015480G>A	c.715C>T	p.R239C	NM_021628	neutral	low
ALS2CR11	1947	151254	Splice Site	chr2:202430450insA	c.977+2T>-		NM_001168221		
ALS2CR12	65115	130540	Splice Site	g.chr2:202207155C>A	c.463_splice	p.L155_splice	NM_139163		
ANGPT1	09_4615	284	Missense	g.chr8:108296914A>G	c.1201T>C	p.Y401H	NM_001146	deleterious	high
ANGPT2	2012	285	Nonsense	g.chr8:6389855G>A	c.442C>T	p.Q148*	NM_001147		
ANK1	2237	286	Missense	g.chr8:41577348G>C	c.938C>G	p.A313G	NM_020476	neutral	medium
ANKRD12	2000120	23253	Missense	g.chr18:9254521C>G	c.1256C>G	p.S419C	NM_015208	deleterious	medium
ANKRD17	2000756	26057	Missense	g.chr4:73944488T>C	c.7279A>G	p.I2427V	NM_032217	neutral	low
ANKS4B	609	257629	Missense	g.chr16:21261927C>T	c.1040C>T	p.P347L	NM_145865	deleterious	medium
APC	3492	324	Nonsense	g.chr5:112176863C>T	c.5572C>T	p.R1858*	NM_001127511		
APOBEC3D	2237	140564	Missense	g.chr22:39425492G>T	c.730G>T	p.V244F	NM_152426	deleterious	low
APPBP2	09_4615	10513	Missense	g.chr17:58571881C>T	c.325G>A	p.A109T	NM_006380	neutral	low
ARAP2	2237	116984	Missense	g.chr4:36230225G>A	c.884C>T	p.S295L	NM_015230	neutral	low
ARHGAP10	11_17815	79658	Missense	g.chr4:148778744A>G	c.425A>G	p.Y142C	NM_024605	deleterious	low
ARHGAP44	05_6986	9912	Nonsense	g.chr17:12852538G>T	c.943G>T	p.E315*	NM_014859		
ARHGEF15	671204	22899	Indel	g.chr17:8216328delC	c.690delC	p.G230fs	NM_173728		
ARHGEF40	3492	55701	Missense	g.chr14:21555235G>A	c.4214G>A	p.R1405Q	NM_018071	deleterious	neutral
ARHGEF5	10_5283	7984	Missense	g.chr7:144077106G>A	c.4751G>A	p.R1584Q	NM_005435	deleterious	low
ARID1A	07_16582	8289	Indel	g.chr1:27105930_27105931insG	c.5541_5542insG	p.G1847fs	NM_006015		
ARID4B	1739	51742	Indel	g.chr1:235424022insACT	c.52_53insAGT	p.A18delinsSA	NM_001206794		
ARID5B	148632	84159	Nonsense	g.chr10:63850714G>T	c.1492G>T	p.E498*	NM_032199		
ARNT2	9534	9915	Splice Site	g.chr15:80866561G>A	c.1389G>A	p.Q463Q	NM_014862		
ARRDC3	479	57561	Missense	g.chr5:90669514G>C	c.1175C>G	p.P392R	NM_020801	deleterious	medium
ASAP2	7441	8853	Missense	g.chr2:9496405A>G	c.1258A>G	p.T420A	NM_003887	neutral	medium
ASF1B	9534	55723	Missense	g.chr19:14231281T>C	c.599A>G	p.D200G	NM_018154	deleterious	low
ASTN1	9534	460	Missense	g.chr1:176833574C>T	c.3731G>A	p.R1244Q	NM_004319	neutral	low
ASXL3	7441	80816	Missense	g.chr18:31319128G>T	c.1760G>T	p.G587V	NM_030632	deleterious	low
ATCAY	6536	85300	Splice Site	g.chr19:3907733C>T	c.360C>T	p.D120D	NM_033064		
ATF7IP	36773720	55729	Missense	g.chr12:14577937G>A	c.1088G>A	p.R363Q	NM_018179	neutral	neutral
ATM	65115	472	Missense	g.chr11:108188116G>A	c.6215G>A	p.G2072E	NM_000051	deleterious	high
ATM	65115	472	Missense	g.chr11:108196143C>T	c.6679C>T	p.R2227C	NM_000051	deleterious	medium
ATRX	11_6165	546	Missense	g.chrX:76937140G>A	c.3608C>T	p.S1203L	NM_000489	deleterious	neutral
ATXN2	410	6311	Missense	g.chr12:111951163C>T	c.2036G>A	p.G679E	NM_002973	deleterious	low
ATXN3L	07_16582	92552	Missense	g.chrX:13337924C>T	c.130G>A	p.E44K	NM_001135995	deleterious	medium
AXDND1	148632	126859	Missense	g.chr1:179437776C>T	c.1997C>T	p.S666L	NM_144696	neutral	neutral
AXIN1	148632	8312	Nonsense	g.chr16:396299C>A	c.727G>T	p.E243*	NM_003502		
B3GNT2	05_6986	10678	Missense	g.chr2:62449369G>T	c.14G>T	p.R5L	NM_006577	deleterious	medium
BAI1	122891	575	Missense	g.chr8:143602248G>A	c.2986G>A	p.A996T	NM_001702	neutral	low
BAIAP3	07_16582	8938	Missense	g.chr16:1391848C>A	c.862C>A	p.Q288K	NM_003933	deleterious	low
BAP1	1346	8314	Missense	g.chr3:52439805C>G	c.907G>C	p.A303P	NM_004656	neutral	low
BBS1	128229	582	Missense	g.chr11:66283195T>G	c.511T>G	p.S171A	NM_024649	deleterious	medium
BCOR	705	54880	Nonsense	g.chrX:39932914G>T	c.1685C>A	p.S562*	NM_001123385		
BCORL1	980452	63035	Missense	g.chrX:129149009T>C	c.2261T>C	p.I754T	NM_021946	deleterious	medium
BEST3	06_2532	144453	Missense	g.chr12:70049136G>A	c.1558C>T	p.H520Y	NM_032735	neutral	neutral
BICD1	4133	636	Missense	g.chr12:32480497C>T	c.1108C>T	p.R370W	NM_001714	deleterious	medium
BOLL	11_6165	66037	Missense	g.chr2:198641827C>T	c.232G>A	p.V78I	NM_033030	neutral	low
BRCA1	2237	672	Missense	g.chr17:41242984G>C	c.4162C>G	p.Q1388E	NM_007294	deleterious	medium
BRCA1	2237	672	Missense	g.chr17:41243523G>A	c.4025C>T	p.S1342L	NM_007294	neutral	medium
BRD1	671204	23774	Missense	g.chr22:50216803T>C	c.1163A>G	p.H388R	NM_014577	deleterious	high
BRD3	09_4615	8019	Missense	g.chr9:136915621C>T	c.589G>A	p.A197T	NM_007371	neutral	low

BRI3	2237	25798	Missense	g.chr7:97920462C>G	c.285C>G	p.I95M	NM_015379	deleterious	medium
BTAF1	2238	9044	Missense	g.chr10:93768668T>C	c.3896T>C	p.L1299S	NM_003972	deleterious	high
BTN3A2	11_17815	11118	Splice Site	g.chr6:26370832G>T	c.715_splice	p.D239_splice	NM_007047		
BUB1B	671204	701	Missense	g.chr15:40462300G>T	c.217G>T	p.D73Y	NM_001211	deleterious	high
BUB1B	11_17815	701	Missense	g.chr15:40510712T>C	c.2906T>C	p.L969P	NM_001211	deleterious	medium
BZRAP1	6277	9256	Missense	g.chr17:56384224C>T	c.5089G>A	p.A1697T	NM_004758	neutral	low
C10orf129	148632	142827	Missense	g.chr10:96954367T>A	c.125T>A	p.V42D	NM_207321	neutral	neutral
C14orf43	2039	91748	Splice Site	g.chr14:74193532C>T	c.2305_splice	p.V769_splice	NM_194278		
C16orf11	148632	146325	Indel	g.chr16:613726delG	c.432delG	p.V144fs	NM_145270		
C18orf63	11_17815	644041	Missense	g.chr18:72021317T>A	c.990T>A	p.D330E			low
C19orf24	131169	55009	Missense	g.chr19:1275594G>C	c.46G>C	p.A16P	NM_017914	none	neutral
C19orf24	131169	55009	Missense	g.chr19:1275595C>T	c.47C>T	p.A16V	NM_017914	none	neutral
C19orf29	2237	58509	Missense	g.chr19:3612326C>G	c.1872G>C	p.E624D	NM_001080543		medium
C19orf44	3492	84167	Missense	g.chr19:16623863G>A	c.1678G>A	p.A560T	NM_032207	neutral	medium
C1orf141	540	400757	Splice Site	g.chr1:67592939T>A			NM_001013674		
C1orf173	2000120	127254	Missense	g.chr1:75038462C>T	c.2932G>A	p.E978K	NM_001002912	deleterious	neutral
C1orf50	10_5283	79078	Missense	g.chr1:43241004T>G	c.539T>G	p.L180R	NM_024097	deleterious	medium
C20orf11	7097	54994	Missense	g.chr20:61574929G>A	c.398G>A	p.G133D	NM_017896	deleterious	medium
C6orf170	36773720	221322	Missense	g.chr6:121638817A>G	c.319T>C	p.Y107H	NM_152730	deleterious	medium
C6orf222	142990	389384	Missense	g.chr6:36291252C>G	c.1289G>C	p.R430T	NM_001010903	neutral	neutral
C6orf222	142990	389384	Missense	g.chr6:36291177C>G	c.1364G>C	p.R455T	NM_001010903	deleterious	low
C6orf62	7441	81688	Missense	g.chr6:24714569C>A	c.406G>T	p.D136Y	NM_030939	neutral	neutral
C8orf33	10_5342	65265	Missense	g.chr8:146278780G>T	c.501G>T	p.R167S	NM_023080	deleterious	medium
CA1	07_16582	759	Indel	g.chr8:86245760_86245761insA	c.443_444insT	p.L148fs	NM_001738		
CA14	2000756	23632	Missense	g.chr1:150235756T>C	c.779T>C	p.V260A	NM_012113	neutral	medium
CACNA1C	122891	775	Missense	g.chr12:2622126A>G	c.1366A>G	p.M456V	NM_199460	neutral	neutral
CADM2	2000756	253559	Missense	g.chr3:86114775C>G	c.1084C>G	p.Q362E	NM_153184	neutral	low
CALCOCO1	6536	57658	Missense	g.chr12:54115820C>G	c.598G>C	p.E200Q	NM_020898	neutral	low
CALCOCO1	6536	57658	Missense	g.chr12:54115261C>G	c.748G>C	p.E250Q	NM_020898	deleterious	medium
CALM2	2020	805	Missense	g.chr2:47389754T>C	c.82A>G	p.I28V	NM_001743	deleterious	
CAMK4	06_2532	814	Missense	g.chr5:110818621C>T	c.967C>T	p.R323W	NM_001744	deleterious	medium
CAPN6	07_16582	827	Missense	g.chrX:110489945C>T	c.1786G>A	p.V596I	NM_014289	neutral	medium
CASZ1	2000756	54897	Missense	g.chr1:10714034G>A	c.2080C>T	p.R694C	NM_001079843	deleterious	medium
CBLN1	1947	869	Missense	g.chr16:49314872A>T	c.346T>A	p.F116I	NM_004352	deleterious	medium
CCDC111	671204	201973	Missense	g.chr4:185615719A>G	c.1469A>G	p.N490S	NM_152683	neutral	neutral
CCDC14	980452	64770	Missense	g.chr3:123633973C>T	c.2515G>A	p.E839K	NM_022757	deleterious	low
CCDC141	11_6165	285025	Missense	g.chr2:179736246G>A	c.388C>T	p.L130F	NM_173648	deleterious	neutral
CCDC7	07_16582	221016	Missense	g.chr10:32833205A>G	c.1110A>G	p.I370M	NM_145023	neutral	low
CD1D	2453	912	Missense	g.chr1:158152715C>T	c.655C>T	p.R219C	NM_001766	neutral	medium
CD22	1781	933	Missense	g.chr19:35829077C>T	c.992C>T	p.P331L	NM_001771	deleterious	medium
CD226	6112	10666	Missense	g.chr18:67562961C>T	c.703G>A	p.V235M	NM_006566	deleterious	medium
CDC25B	06_2532	994	Missense	g.chr20:3783581G>A	c.1219G>A	p.G407R	NM_021873	deleterious	medium
CDON	671204	50937	Missense	g.chr11:125848220C>T	c.3335G>A	p.R1112Q	NM_016952	deleterious	neutral
CECR2	11_6165	27443	Missense	g.chr22:18028762T>G	c.3719T>G	p.M1240R	NM_031413	deleterious	low
CELSR3	142990	1951	Missense	g.chr3:48682531C>T	c.7909G>A	p.V2637M	NM_001407	deleterious	medium
CEP120	540	153241	Missense	g.chr5:122720708G>C	c.1700C>G	p.S567C	NM_153223	neutral	low
CEP135	1781	9662	Indel	g.chr4:56831978delAAA	c.997_999del	p.333_333del,	NM_025009		
CEP97	05_6986	79598	Indel	g.chr3:101451414_101451415insA	c.644_645insA	p.P215fs	NM_024548		
CHD9	2000120	80205	Missense	g.chr16:53281369A>G	c.3619A>G	p.M1207V	NM_025134	deleterious	high
CHI3L1	148632	1116	Missense	g.chr1:203154370C>G	c.199G>C	p.D67H	NM_001276		low
CHPF2	2000120	54480	Missense	g.chr7:150931315T>G	c.218T>G	p.V73G	NM_019015	deleterious	medium
CHRM1	3492	1128	Missense	g.chr11:62677267G>C	c.1306C>G	p.R436G	NM_000738	deleterious	low
CHRNA4	6112	1137	Missense	g.chr20:61981129G>C	c.1634C>G	p.T545R	NM_000744	deleterious	low
CHRNB1	1947	1140	Splice Site	g.chr17:7350821delG	c.462-1G>-		NM_000747		
CHRND	2000120	1144	Missense	g.chr2:233393633C>A	c.571C>A	p.R191S	NM_000751	deleterious	medium
CHST5	142990	23563	Missense	g.chr16:75563606G>A	c.677C>T	p.P226L	NM_024533	deleterious	high
CHST5	6536	23563	Nonsense	g.chr16:75563521C>T	c.762G>A	p.W254*	NM_024533		
CLCA2	148632	9635	Missense	g.chr1:86896578G>A	c.509G>A	p.R170H	NM_006536	deleterious	medium
CNDP2	65115	55748	Missense	g.chr18:72179722G>A	c.697G>A	p.G233R	NM_018235	deleterious	high
CNTN6	65115	27255	Missense	g.chr3:1415377A>T	c.1876A>T	p.S626C	NM_014461	deleterious	high
CNTNAP5	1781	129684	Splice Site	g.chr2:124999971G>T	c.381_splice	p.W127_splice	NM_130773		
COL15A1	2237	1306	Missense	g.chr9:101802807C>T	c.2480C>T	p.P827L	NM_001855	deleterious	low
COL6A6	05_6986	131873	Nonsense	g.chr3:130285860C>T	c.1597C>T	p.R533*	NM_001102608		
COL7A1	36773720	1294	Missense	g.chr3:48611724G>T	c.6472C>A	p.R2158S	NM_000094	neutral	medium
CORO6	7441	84940	Missense	g.chr17:27944012C>T	c.802G>A	p.G268R	NM_032854	deleterious	high
CPT1B	122891	1375	Missense	g.chr22:51015399C>T	c.346G>A	p.V116I	NM_001145137	neutral	low
CREBBP	3492	1387	Missense	g.chr16:3788596A>T	c.4358T>A	p.I1453N	NM_004380	none	high
CREBBP	1781	1387	Missense	g.chr16:3788618G>A	c.4336C>T	p.R1446C	NM_004380	none	high
CREBBP	671204	1387	Missense	g.chr16:3843416G>C	c.1187C>G	p.T396R	NM_004380	deleterious	medium
CREBBP	2000756	1387	Missense	g.chr16:3786796C>G	c.4415G>C	p.W1472S	NM_004380	none	high
CRHR1	6536	1394	Missense	g.chr17:43911172G>T	c.1109G>T	p.R370L	NM_001145146	neutral	low
CRHR2	06_2532	1395	Missense	g.chr7:30704795C>T	c.434G>A	p.R145H	NM_001883	deleterious	low
CSMD1	671204	64478	Missense	g.chr8:4494868C>T	c.298G>A	p.V100M	NM_033225	neutral	neutral
CSMD3	1947	114788	Missense	g.chr8:113988270A>G	c.1138T>C	p.S380P	NM_198123	neutral	low
CTAG2	65103	30848	Missense	g.chrX:153881555C>T	c.235G>A	p.G79R	NM_020994	deleterious	neutral
CTCF	2000756	10664	Missense	g.chr16:67670734A>G	c.1979A>G	p.N660S	NM_006565	neutral	low
CTNNB1	1947	1499	Missense	g.chr3:41278106G>T	c.1982G>T	p.R661L	NM_001904		medium
CTNND2	06_2532	1501	Missense	g.chr5:11732346C>T	c.76G>A	p.E26K	NM_001332	neutral	neutral
CTSL1	11_3089	1514	Missense	g.chr9:90344547C>A	c.681C>A	p.D227E	NM_001912	neutral	low
CUL3	6536	8452	Missense	g.chr2:225376290G>T	c.664C>A	p.Q222K	NM_003590	neutral	low
CUX1	05_6986	1523	Missense	g.chr7:101833099G>A	c.1024G>A	p.E342K	NM_181552	deleterious	low

CXorf30	7136	645090	Missense	g.chrX:36368172G>A	c.961G>A	p.E321K	NM_001098843	neutral	neutral
CXorf36	2128	79742	Missense	g.chrX:45059992C>T	c.80G>A	p.S27N	NM_176819	deleterious	low
CYP2C19	705	1557	Missense	g.chr10:96602752G>A	c.1120G>A	p.V374I	NM_000769	neutral	neutral
CYP3A43	09_4615	64816	Missense	g.chr7:99457591T>C	c.1004T>C	p.I335T	NM_057095	deleterious	high
DAGLB	2000756	221955	Missense	g.chr7:6449596T>C	c.1891A>G	p.I631V	NM_139179	neutral	low
DCAF12L2	2000120	340578	Missense	g.chrX:125298898C>T	c.1010G>A	p.R337H	NM_001013628	deleterious	low
DCLRE1A	2237	9937	Missense	g.chr10:115609522C>G	c.1342G>C	p.E448Q	NM_014881	neutral	neutral
DCLRE1A	2237	9937	Missense	g.chr10:115609519C>T	c.1345G>A	p.E449K	NM_014881	deleterious	low
DDX12	65115	440081	Missense	g.chr12:9578105G>A	c.1724C>T	p.T575M	NM_004400		
DDX42	705	11325	Missense	g.chr17:61885144A>G	c.907A>G	p.K303E	NM_007372	deleterious	high
DDX60L	2237	91351	Missense	g.chr4:169348371C>T	c.1780G>A	p.E594K	NM_001012967	deleterious	low
DEPDC5	05_6986	9681	Missense	g.chr22:32270318C>T	c.3530C>T	p.A1177V	NM_014662	deleterious	medium
DERL1	148632	79139	Missense	g.chr8:124042917C>A	c.193G>T	p.G65C	NM_024295	deleterious	high
DHODH	236	1723	Missense	g.chr16:72056354A>C	c.799A>C	p.I267L	NM_001361	deleterious	medium
DHX37	11_3318	57647	Missense	g.chr12:125437084C>T	c.2728G>A	p.V910M	NM_032656	neutral	low
DHX9	09_4178	1660	Nonsense	g.chr1:182827275T>A	c.710T>A	p.L237*	NM_001357		
DIEXF	4133	27042	Missense	g.chr1:210004331G>A	c.331G>A	p.G111S	NM_014388	neutral	low
DIS3	2000756	22894	Missense	g.chr13:73346338C>T	c.1462G>A	p.D488N	NM_014953	deleterious	high
DKK4	2039	27121	Missense	g.chr8:42232330C>G	c.364G>C	p.E122Q	NM_014420	deleterious	low
DNAH11	111097	8701	Missense	g.chr7:21882352T>C	c.10903T>C	p.L3635L	NM_003777		
DNAH11	2020	8701	Missense	g.chr7:21779253C>T	c.7897C>T	p.P2633S	NM_003777	deleterious	
DNAH5	7136	1767	Missense	g.chr5:13719002C>A	c.12488G>T	p.R4163I	NM_001369	deleterious	high
DNAH9	6536	1770	Missense	g.chr17:11725366G>A	c.8837G>A	p.R2946Q	NM_001372	neutral	medium
DNAJC12	10_5283	56521	Missense	g.chr10:69565535C>A	c.308G>T	p.W103L	NM_021800	deleterious	medium
DOCK11	07_16582	139818	Missense	g.chrX:117739268G>A	c.2630G>A	p.R877Q	NM_144658	neutral	low
DOCK8	128229	81704	Missense	g.chr9:439318G>C	c.5153G>C	p.C1718S	NM_203447	deleterious	medium
DTX4	2238	23220	Missense	g.chr11:58940272A>T	c.204A>T	p.Q68H	NM_015177	deleterious	medium
DUOX1	11_3089	53905	Missense	g.chr15:45434251T>C	c.1763T>C	p.F588S	NM_017434	deleterious	medium
DYNC1LI1	09_4615	51143	Missense	g.chr3:32568386A>C	c.1477T>G	p.L493V	NM_016141	deleterious	medium
DYSF	2237	8291	Missense	g.chr2:71681189G>T	c.61G>T	p.D21Y	NM_003494	deleterious	medium
DYSF	11_6165	8291	Missense	g.chr2:71740999G>T	c.611G>T	p.R204L	NM_003494	neutral	medium
ECEL1	410	9427	Splice Site	g.chr2:233349690C>T	c.966_splice	p.N322_splice	NM_004826		
EDC4	2000120	23644	Missense	g.chr16:67912962A>G	c.1390A>G	p.I464V	NM_014329	neutral	low
EGF	11_17815	1950	Missense	g.chr4:110914451G>C	c.2783G>C	p.S928T	NM_001963	neutral	neutral
EHF	3492	26298	Missense	g.chr11:34680407C>T	c.832C>T	p.R278C	NM_012153	deleterious	medium
EIF3B	4133	8662	Indel	g.chr7:2412384_2412385delTG	c.1764_1765delTG	p.S588fs	NM_003751		
EIF4G1	118135	1981	Missense	g.chr3:184039487C>T	c.1115C>T	p.P372L	NM_198241	deleterious	low
ELOVL3	09_4178	83401	Missense	g.chr10:103987439A>G	c.158A>G	p.N53S	NM_152310	neutral	low
ENC1	36773720	8507	Missense	g.chr5:73932240T>A	c.71A>T	p.H24L	NM_003633	deleterious	medium
ENC1	2000756	8507	Indel	g.chr5:73931844_73931845insAC	c.466_467insGT	p.S156fs	NM_003633		
ENOX1	80872	55068	Missense	g.chr13:43930154G>A	c.724C>T	p.R242W	NM_001127615	deleterious	medium
ENPEP	148632	2028	Missense	g.chr4:111441166G>A	c.1512G>A	p.M504I	NM_001977	neutral	neutral
EP300	7441	2033	Splice Site	g.chr22:41565621G>T	c.4286_splice	p.G1429_splice	NM_001429		
EPPK1	36773720	83481	Missense	g.chr8:144942098T>C	c.5324A>G	p.H1775R	NM_031308		neutral
EPS8L1	2012	54869	Missense	g.chr19:55591149G>A	c.209G>A	p.R70Q	NM_133180	deleterious	medium
ERAP2	2000136	64167	Nonsense	g.chr5:96230974G>T	c.1150G>T	p.E384*	NM_022350		
ERBB2IP	2000120	55914	Splice Site	g.chr5:65321806G>T	c.1020_splice	p.E340_splice	NM_018695		
ERCC2	09_4178	2068	Missense	g.chr19:45872365G>A	c.146C>T	p.T49I	NM_000400	deleterious	high
ERGIC3	131169	51614	Missense	g.chr20:34130630C>G	c.307C>G	p.L103V	NM_015966	neutral	neutral
ESRP1	36773720	54845	Splice Site	g.chr8:95654183G>A	c.133_splice	p.V45_splice	NM_017697		
ESYT3	2000136	83850	Missense	g.chr3:138189851A>C	c.1723A>C	p.M575L	NM_031913	deleterious	medium
EXOC6	505	54536	Nonsense	g.chr10:94659373A>T	c.430A>T	p.K144*	NM_019053		
FAM134A	07_16582	79137	Missense	g.chr2:220044915T>A	c.503T>A	p.F168Y	NM_024293	neutral	low
FAM135A	05_6986	57579	Missense	g.chr6:71235512G>A	c.2725G>A	p.A909T	NM_001162529	neutral	low
FAM177A1	3492	283635	Missense	g.chr14:35548216C>T	c.421C>T	p.R141W	NM_001079519	deleterious	medium
FAM194B	09_4178	220081	Nonsense	g.chr13:46149035C>T	c.992G>A	p.W331*	NM_182542		
FAM196A	671204	642938	Missense	g.chr10:128974617C>T	c.43G>A	p.E15K	NM_001039762	neutral	medium
FAM207A	07_16582	85395	Splice Site	g.chr21:46380085T>G	c.352_splice	p.K118_splice	NM_058190		
FAM65C	06_2532	140876	Missense	g.chr20:49206268G>C	c.2604C>G	p.D868E	NM_080829	deleterious	low
FAT3	4332	120114	Nonsense	g.chr11:92539627C>T	c.9193C>T	p.R3065*	NM_001008781		
FAT4	2128	79633	Missense	g.chr4:126371875C>T	c.9704C>T	p.S3235L	NM_024582	deleterious	low
FAT4	7136	79633	Nonsense	g.chr4:126372080C>G	c.9909C>G	p.Y3303*	NM_024582		
FBN1	1739	2200	Missense	g.chr15:48797267A>G	c.1915T>C	p.C639R	NM_000138	deleterious	medium
FBN2	11_3089	2201	Missense	g.chr5:127685092T>C	c.2936A>G	p.H979R	NM_001999	neutral	neutral
FBXO43	36773720	286151	Missense	g.chr8:101146449C>G	c.1818G>C	p.L606F	NM_001029860	deleterious	low
FBXW7	609	55294	Missense	g.chr4:153249384C>T	c.1394G>A	p.R465H	NM_033632	deleterious	high
FCHO1	148632	23149	Missense	g.chr19:17887449G>A	c.1213G>A	p.A405T	NM_001161358	neutral	neutral
FCRL5	11_3318	83416	Missense	g.chr1:157509139G>A	c.1139C>T	p.P380L	NM_031281	deleterious	medium
FGD6	410	55785	Missense	g.chr12:95483365T>C	c.3958A>G	p.I1320V	NM_018351	neutral	low
FGF16	6536	8823	Missense	g.chrX:76709693G>A	c.47G>A	p.R16Q	NM_003868	deleterious	
FGFR4	505	2264	Missense	g.chr5:176518079G>A	c.577G>A	p.G193R	NM_002011	deleterious	medium
FGGY	36773720	55277	Missense	g.chr1:60091693C>A	c.1045C>A	p.P349T	NM_018291	neutral	low
FIGF	148632	2277	Missense	g.chrX:15364323C>A	c.997G>T	p.A333S	NM_004469	neutral	low
FILIP1	9534	27145	Nonsense	g.chr6:76022271G>A	c.3277C>T	p.R1093*	NM_015687		
FILIP1L	09_4615	11259	Missense	g.chr3:99567698G>C	c.2822C>G	p.T941R	NM_182909	deleterious	medium
FKBP9	9534	11328	Indel	g.chr7:33014299_33014300insTT	c.292_293insTT	p.L98fs	NM_007270		
FLG	671204	2312	Missense	g.chr1:152282080C>T	c.5282G>A	p.R1761H	NM_002016	none	low
FLJ44082	1781	389762	Missense	g.chr9:84562507A>G	c.2339A>G	p.N780S	NM_207416	neutral	neutral
FMNL1	05_6986	752	Missense	g.chr17:43321321C>T	c.2377C>T	p.R793C	NM_005892	none	medium
FNIP1	980452	96459	Missense	g.chr5:131042228T>C	c.790A>G	p.S264G	NM_133372	deleterious	medium
FOXK1	148632	221937	Missense	g.chr7:4796626A>G	c.1052A>G	p.N351S	NM_001037165	deleterious	high

FOXO3	7097	2309	Missense	g.chr6:108985403C>A	c.1367C>A	p.P456Q	NM_201559	neutral	neutral
FOXP2	2237	93986	Missense	g.chr7:114284748A>T	c.998A>T	p.H333L	NM_014491	none	low
FOXP2	1781	93986	Missense	g.chr7:114298130G>C	c.1276G>C	p.V426L	NM_014491	none	medium
FRAS1	11_17815	80144	Missense	g.chr4:79461758T>G	c.11519T>G	p.V3840G	NM_025074	deleterious	medium
FREM2	142990	341640	Missense	g.chr13:39424333C>T	c.6538C>T	p.R2180C	NM_207361	deleterious	medium
FSD1	131169	79187	Missense	g.chr19:4311959G>A	c.611G>A	p.R204Q	NM_024333	neutral	medium
FSIP2	9534	401024	Missense	g.chr2:186653523G>T	c.1033G>T	p.D345Y			low
FTSJD1	11_6165	55783	Missense	g.chr16:71319399T>C	c.425A>G	p.H142R	NM_001099642	deleterious	medium
FTSJD1	07_16582	55783	Nonsense	g.chr16:71319480C>T	c.344G>A	p.W115*	NM_001099642		
FUT6	705	2528	Missense	g.chr19:5832521G>C	c.58C>G	p.L20V	NM_001040701	neutral	medium
GABRA1	06_2532	2554	Missense	g.chr5:161302603G>T	c.514G>T	p.D172Y	NM_000806	deleterious	low
GABRA3	09_4178	2556	Missense	g.chrX:151532936T>A	c.107A>T	p.E36V	NM_000808	neutral	low
GABRB1	7441	2560	Nonsense	g.chr4:47163485C>T	c.460C>T	p.R154*	NM_000812		
GBP5	990149	115362	Missense	g.chr1:89729441C>T	c.1340G>A	p.R447Q	NM_052942	neutral	neutral
GCK	65115	2645	Missense	g.chr7:44186189T>C	c.892A>G	p.M298V	NM_000162	deleterious	medium
GCN1L1	122891	10985	Missense	g.chr12:120599377C>G	c.2353G>C	p.D785H	NM_006836	neutral	medium
GEMIN5	2237	25929	Missense	g.chr5:154271225A>T	c.3838T>A	p.F1280I	NM_015465	neutral	low
GLB1L	11_6165	79411	Missense	g.chr2:220107983G>C	c.126C>G	p.D42E	NM_024506	deleterious	medium
GNAI2	05_6986	2771	Missense	g.chr3:50284505G>C	c.5G>C	p.R2T	NM_001166425		neutral
GNB4	111097	59345	Missense	g.chr3:179137211G>C	c.179C>G	p.A60G	NM_021629	neutral	high
GPATCH4	1781	54865	Missense	g.chr1:156568027T>G	c.253A>C	p.T85P	NM_015590	deleterious	low
GPATCH8	06_2532	23131	Missense	g.chr17:42478169T>C	c.1276A>G	p.T426A	NM_001002909	none	neutral
GPR113	11_17815	165082	Missense	g.chr2:26540943C>T	c.227G>A	p.R76Q	NM_001145168	neutral	neutral
GPR119	4133	139760	Missense	g.chrX:129518908C>T	c.514G>A	p.V172I	NM_178471	neutral	low
GPR20	9534	2843	Missense	g.chr8:142367102C>T	c.922G>A	p.V308I	NM_005293	neutral	low
GPR64	05_6986	10149	Missense	g.chrX:19027744C>A	c.1422G>T	p.Q474H	NM_001079858	deleterious	medium
GRIA2	11_17815	2891	Missense	g.chr4:158233974C>T	c.613C>T	p.R205W	NM_001083619	deleterious	high
GRIN2B	7136	2904	Missense	g.chr12:13764773C>T	c.1666G>A	p.A556T	NM_000834	deleterious	low
GRM4	2237	2914	Nonsense	g.chr6:34101247C>T	c.27G>A	p.W9*	NM_000841		
GSTM4	65115	2948	Nonsense	g.chr1:110199381C>A	c.84C>A	p.Y28*	NM_000850		
GTF3C1	122891	2975	Splice Site	g.chr16:27506083C>T	c.2778_splice	p.K926_splice	NM_001520		
GUCY1A2	2000120	2977	Missense	g.chr11:106680807G>A	c.1604C>T	p.A535V	NM_000855	deleterious	high
HARS	2128	3035	Nonsense	g.chr5:140054646C>A	c.1267G>T	p.E423*	NM_002109		
HAUS7	7441	55559	Missense	g.chrX:152721101C>G	c.859G>C	p.D287H	NM_017518	deleterious	low
HEATR7B2	122891	133558	Missense	g.chr5:41008757G>A	c.3559C>T	p.R1187W	NM_173489	deleterious	low
HELT	671204	391723	Missense	g.chr4:185941590G>T	c.648G>T	p.E216D	NM_001029887	neutral	low
HEPH	148632	9843	Missense	g.chrX:65418848C>G	c.1851C>G	p.F617L	NM_138737	deleterious	medium
HERC1	1346	8925	Missense	g.chr15:63901348T>C	c.14518A>G	p.I4840V	NM_003922	deleterious	medium
HERC1	1346	8925	Missense	g.chr15:63901348T>C	c.14518A>G	p.I4840V	NM_003922	deleterious	medium
HIST1H1E	9534	3008	Missense	g.chr6:26156843G>C	c.225G>C	p.K75N	NM_005321	deleterious	medium
HIST1H2AL	7441	8332	Missense	g.chr6:27833185G>T	c.53G>T	p.R18L	NM_003511	none	
HOGA1	10_5283	112817	Nonsense	g.chr10:99358863G>T	c.358G>T	p.E120*	NM_138413		
HOXB3	4133	3213	Indel	g.chr17:46629590delG	c.247delC	p.L83fs	NM_002146		
HRAS	2000120	3265	Missense	g.chr11:534289C>A	c.34G>T	p.G12C	NM_005343	neutral	medium
HRC	11_6165	3270	Missense	g.chr19:49657777G>T	c.718C>A	p.H240N	NM_002152	deleterious	low
HSD17B13	10_5283	345275	Missense	g.chr4:88238359C>T	c.335G>A	p.G112D	NM_178135	deleterious	high
HSD3B2	1947	3284	Missense	g.chr1:119964452G>A	c.328G>A	p.A110T	NM_000198	neutral	medium
HSPG2	131169	3339	Missense	g.chr1:22155512G>A	c.12053C>T	p.A4018V	NM_005529	deleterious	low
HSPG2	7441	3339	Missense	g.chr1:22202816G>A	c.2909C>T	p.S970F	NM_005529	neutral	low
HTR6	10_5342	3362	Missense	g.chr1:20005568C>T	c.1030C>T	p.R344C	NM_000871	deleterious	low
ICAM4	980452	3386	Missense	g.chr19:10398349G>A	c.532G>A	p.E178K	NM_001544	deleterious	low
IDH1	7097	3417	Missense	g.chr2:209113112C>T	c.395G>A	p.R132H	NM_005896	deleterious	high
IGFBP2	118135	3485	Missense	g.chr2:217498311T>C	c.44T>C	p.L15P	NM_000597	none	neutral
IGSF9B	4133	22997	Nonsense	g.chr11:133790388G>A	c.3232C>T	p.R1078*	NM_014987		
IKBKAP	4133	8518	Missense	g.chr9:111674666G>A	c.1067C>T	p.P356L	NM_003640	neutral	medium
IL17A	148632	3605	Missense	g.chr6:52054071T>C	c.449T>C	p.I150T	NM_002190	deleterious	medium
IL17F	11_17815	112744	Missense	g.chr6:52101944A>G	c.277T>C	p.Y93H	NM_052872	deleterious	medium
IL17RD	122891	54756	Indel	g.chr3:57136550delTG	c.935_936del	p.312_312del	NM_017563		
INO80D	609	54891	Missense	g.chr2:206869733G>T	c.2443C>A	p.Q815K	NM_017759	deleterious	neutral
INSRR	07_16582	3645	Missense	g.chr1:156821785C>A	c.836G>T	p.R279L	NM_014215	neutral	neutral
INSRR	2039	3645	Missense	g.chr1:156823915T>G	c.266A>C	p.Y89S	NM_014215	neutral	low
INTS2	540	57508	Missense	g.chr17:59996779G>C	c.655C>G	p.P219A	NM_020748	deleterious	medium
INTS4	2238	92105	Missense	g.chr11:77635919C>T	c.1391G>A	p.R464Q	NM_033547	deleterious	medium
IQGAP2	07_16582	10788	Missense	g.chr5:75885446A>G	c.533A>G	p.E178G	NM_006633	deleterious	medium
IRAK1	2000136	3654	Nonsense	g.chrX:153278656C>A	c.1768G>T	p.E590*	NM_001569		
IRAK1	4133	3654	Missense	g.chrX:153278880T>C	c.1544A>G	p.Y515C	NM_001569	deleterious	medium
IRF7	2237	3665	Missense	g.chr11:612770C>G	c.1387G>C	p.E463Q	NM_001572	deleterious	medium
ITGA8	2238	8516	Missense	g.chr10:15561383G>C	c.3011C>G	p.P1004R	NM_003638	deleterious	medium
ITGB8	980452	3696	Missense	g.chr7:20438538T>G	c.1202T>G	p.F401C	NM_002214	deleterious	medium
ITIH3	2000756	3699	Missense	g.chr3:52841807G>C	c.2306G>C	p.G769A	NM_002217	neutral	medium
ITM2B	1739	9445	Nonsense	g.chr13:48833055C>A	c.687C>A	p.Y229*	NM_021999		
ITPRIPL2	148632	162073	Missense	g.chr16:19126738G>A	c.955G>A	p.V319I	NM_001034841	neutral	low
JMJD1C	1781	221037	Missense	g.chr10:64927857A>G	c.7571T>C	p.V2524A	NM_032776	deleterious	medium
KCNH6	2000136	81033	Missense	g.chr17:61621622C>G	c.2354C>G	p.P785R	NM_030779	neutral	neutral
KCNJ10	2238	3766	Missense	g.chr1:160011714C>G	c.609G>C	p.M203I	NM_002241	deleterious	medium
KDM6A	11_3318	7403	Splice Site	g.chrX:44966782G>T	c.4005_splice	p.E1335_splice	NM_021140		
KDM6A	148632	7403	Missense	g.chrX:44942839G>A	c.3419G>A	p.G1140E	NM_021140	deleterious	high
KDM6A	11_3318	7403	Missense	g.chrX:44950030A>G	c.3799A>G	p.I1267V	NM_021140	neutral	low
KDM6A	3492	7403	Missense	g.chrX:44969442T>C	c.4124T>C	p.L1375P	NM_021140	deleterious	medium
KDM6A	671204	7403	Missense	g.chrX:44938456A>G	c.3004A>G	p.T1002A	NM_021140	deleterious	medium
KDM6B	2000756	23135	Missense	g.chr17:7751023T>C	c.1417T>C	p.C473R	NM_001080424		low

KHDRBS1	131169	10657	Missense	g.chr1:32497129A>G	c.512A>G	p.N171S	NM_006559	deleterious	medium
KIAA0556	80872	23247	Missense	g.chr16:27720036G>A	c.1400G>A	p.R467K	NM_015202	neutral	neutral
KIAA1267	2039	284058	Nonsense	g.chr17:44117170T>A	c.2101A>T	p.K701*	NM_015443		
KIAA1324L	36773720	222223	Missense	g.chr7:86541434C>A	c.2123G>T	p.G708V	NM_001142749	deleterious	medium
KIF18A	148632	81930	Missense	g.chr11:28104775G>C	c.1090C>G	p.L364V	NM_031217	neutral	neutral
KIF20B	671204	9585	Missense	g.chr10:91518568A>G	c.4609A>G	p.I1537V	NM_016195	neutral	low
KIF4B	705	285643	Missense	g.chr5:154393993G>A	c.574G>A	p.E192K	NM_001099293	deleterious	medium
KIR2DL4	2237	3805	Missense	g.chr19:55316353C>T	c.182C>T	p.T61M	NM_002255	neutral	low
KLF5	148632	688	Missense	g.chr13:73638016A>C	c.1190A>C	p.H397P	NM_001730	deleterious	high
KLF8	1947	11279	Missense	g.chrX:56291748G>A	c.217G>A	p.E73K	NM_007250	deleterious	low
KLHL12	3492	59349	Missense	g.chr1:202863872T>A	c.1141A>T	p.I381F	NM_021633	deleterious	medium
KLHL26	990149	55295	Missense	g.chr19:18779963G>A	c.1756G>A	p.D586N	NM_018316	neutral	low
KLHL31	2237	401265	Missense	g.chr6:53519331C>G	c.740G>C	p.R247T	NM_001003760	deleterious	high
KLHL4	36773720	56062	Nonsense	g.chrX:86888841C>T	c.1642C>T	p.R548*	NM_019117		
KNTC1	36773720	9735	Nonsense	g.chr12:123052911C>T	c.1708C>T	p.R570*	NM_014708		
KPNA5	3492	3841	Missense	g.chr6:117047658G>T	c.1126G>T	p.A376S	NM_002269	neutral	medium
KPNA5	3492	3841	Missense	g.chr6:117047659C>T	c.1127C>T	p.A376V	NM_002269	neutral	medium
KRT25	80872	147183	Missense	g.chr17:38906791G>A	c.1016C>T	p.A339V	NM_181534	neutral	medium
KRT35	4133	3886	Missense	g.chr17:39633882G>A	c.1108C>T	p.R370W	NM_002280	deleterious	high
KRT36	9534	8689	Missense	g.chr17:39643859C>T	c.830G>A	p.R277H	NM_003771	neutral	medium
KRT4	36773720	3851	Missense	g.chr12:53202107G>A	c.1318C>T	p.R440W	NM_002272		medium
KRTAP13-4	05_6986	284827	Nonsense	g.chr21:31802760G>A	c.167G>A	p.W56*	NM_181600		
KRTAP21-1	236	337977	Missense	g.chr21:32127473C>T	c.224G>A	p.C75Y	NM_181619	none	
KRTAP4-6	09_4178	81871	Missense	g.chr17:39296412T>A	c.292A>T				neutral
KRTAP5-1	2453	387264	Missense	g.chr11:1606133T>C	c.347A>G	p.K116R	NM_001005922	none	neutral
L1CAM	3492	3897	Missense	g.chrX:153132320G>A	c.2215C>T	p.R739W	NM_000425	deleterious	medium
LAMA3	505	3909	Missense	g.chr18:21441610T>A	c.4423T>A	p.F1475I	NM_198129	deleterious	low
LAMA3	118135	3909	Missense	g.chr18:21364000T>A	c.1482T>A	p.N494K	NM_198129	deleterious	medium
LAP3	142990	51056	Missense	g.chr4:17586654G>A	c.599G>A	p.R200H	NM_015907	deleterious	high
LARP4B	6536	23185	Missense	g.chr10:875513T>C	c.937A>G	p.I313V	NM_015155	deleterious	medium
LHFPL4	148632	375323	Missense	g.chr3:9594227C>A	c.137G>T	p.W46L	NM_198560	deleterious	high
LHX6	2000120	26468	Missense	g.chr9:124979490G>A	c.452C>T	p.A151V	NM_014368	neutral	neutral
LILRA4	2238	23547	Missense	g.chr19:54848198G>A	c.1169C>T	p.A390V	NM_012276	neutral	medium
LIPJ	9534	142910	Missense	g.chr10:90366552A>G	c.989A>G	p.H330R	NM_001010939	neutral	low
LIX1	2000756	167410	Missense	g.chr5:96460232G>A	c.184C>T	p.P62S	NM_153234	deleterious	neutral
LMLN	36773720	89782	Nonsense	g.chr3:197717491C>T	c.991C>T	p.R331*	NM_033029		
LMNB2	7441	84823	Missense	g.chr19:2444438C>T	c.305G>A	p.G102E	NM_032737	deleterious	low
LOXHD1	10_5283	125336	Missense	g.chr18:44087564C>T	c.5443G>A	p.D1815N	NM_144612	deleterious	low
LPAR4	3492	2846	Missense	g.chrX:78010565C>T	c.199C>T	p.R67C	NM_005296	deleterious	low
LPAR4	11_3318	2846	Missense	g.chrX:78010998T>C	c.632T>C	p.V211A	NM_005296	deleterious	medium
LRP11	2238	84918	Missense	g.chr6:150185135T>C	c.22A>G	p.S8G	NM_032832	none	neutral
LRP1B	65115	53353	Missense	g.chr2:141143548T>A	c.10445A>T	p.Q3482L	NM_018557	deleterious	low
LRP2	980452	4036	Missense	g.chr2:170147426T>C	c.851A>G	p.K284R	NM_004525	neutral	low
LRRC23	6277	10233	Missense	g.chr12:7014864G>A	c.67G>A	p.E23K	NM_001135217	none	low
LRRC3C	2453	1.01E+08	Missense	g.chr17:38100551G>A					medium
LRRC69	1781	1.00E+08	Missense	g.chr8:92213001G>A	c.914G>A	p.R305Q	NM_001129890	neutral	neutral
LRRC7	11_6165	57554	Missense	g.chr1:70488846G>A	c.1469G>A	p.R490H	NM_020794	neutral	neutral
LRRTM1	9534	347730	Missense	g.chr2:80530334G>C	c.611C>G	p.S204C	NM_178839	deleterious	medium
LRWD1	148632	222229	Missense	g.chr7:102110239T>C	c.1352T>C	p.V451A	NM_152892	deleterious	medium
LYPD4	7136	147719	Missense	g.chr19:42341380C>T	c.578G>A	p.R193H	NM_173506	deleterious	low
MAGEC3	6536	139081	Missense	g.chrX:140984506A>C			NM_138702		neutral
MAGI1	3492	9223	Indel	g.chr3:65415431_65415432delAC	c.1930_1931delGT	p.V644fs	NM_001033057		
MAGI2	2237	9863	Missense	g.chr7:77764508A>T	c.2861T>A	p.I954N	NM_012301	deleterious	medium
MAGT1	148632	84061	Nonsense	g.chrX:77131056C>T	c.237G>A	p.W79*	NM_032121		
MAML3	2000136	55534	Missense	g.chr4:140812120A>T	c.470T>A	p.L157Q	NM_018717	neutral	medium
MAN2C1	7441	4123	Missense	g.chr15:75660528G>A	c.113C>T	p.A38V	NM_006715	neutral	medium
MAP2K2	980452	5605	Missense	g.chr19:4110556T>C	c.401A>G	p.Y134C	NM_030662	deleterious	high
MASTL	3492	84930	Missense	g.chr10:27458958C>T	c.1070C>T	p.T357M	NM_032844	deleterious	low
MBD5	2039	55777	Missense	g.chr2:149240820G>A	c.2660G>A	p.S887N	NM_018328	neutral	low
MCM4	7441	4173	Missense	g.chr8:48883928C>T	c.1828C>T	p.R610C	NM_182746	deleterious	high
MED12	36773720	9968	Missense	g.chrX:70349948G>A	c.3931G>A	p.V1311M	NM_005120	neutral	neutral
MEIS1	09_4178	4211	Missense	g.chr2:66794591T>G	c.972T>G	p.I324M	NM_002398	deleterious	high
MGA	505	23269	Splice Site	g.chr15:42021360A>T	c.3658_splice	p.I1220_splice	NM_001164273		
MGA	11_3318	23269	Nonsense	g.chr15:42003509C>T	c.3046C>T	p.R1016*	NM_001080541		
MGAT4A	122891	11320	Missense	g.chr2:99260483A>G	c.923T>C	p.I308T	NM_012214	neutral	medium
MGAT4C	2237	25834	Missense	g.chr12:86374058C>T	c.446G>A	p.R149H	NM_013244	deleterious	medium
MGEA5	118135	10724	Missense	g.chr10:103563588G>C	c.940C>G	p.P314A	NM_012215	deleterious	medium
MLL3	6112	58508	Missense	g.chr7:152027760A>C	c.315T>G	p.I105M	NM_170606	neutral	neutral
MORF4L1	1346	10933	Missense	g.chr15:79186470C>G	c.817C>G	p.L273V	NM_206839	deleterious	high
MOV10L1	11_6165	54456	Missense	g.chr22:50552163C>A	c.830C>A	p.T277K	NM_018995	deleterious	medium
MPG	609	156565	Indel	g.chr16:129298insC	c.7_8insC	p.T3fs,	NM_002434		
MPHOSPH9	3492	10198	Nonsense	g.chr12:123694652A>T	c.689T>A	p.L230*	NM_022782		
MRPL45	7136	84311	Missense	g.chr17:36478044G>A	c.696G>A	p.M232I	NM_032351	deleterious	low
MT1M	4133	4499	Missense	g.chr16:56667294G>A	c.71G>A	p.C24Y	NM_176870	deleterious	
MTTP	2000120	4547	Missense	g.chr4:100521781T>G	c.1127T>G	p.L376W	NM_000253	deleterious	medium
MUC16	05_6986	94025	Splice Site	g.chr19:8974101G>A	c.42570C>T	p.G14190G	NM_024690		
MUC16	65115	94025	Missense	g.chr19:9076729G>A	c.10717C>T	p.R3573C	NM_024690	none	neutral
MUC16	1781	94025	Missense	g.chr19:9069032G>T	c.18414C>A	p.S6138R	NM_024690	none	neutral
MUC4	4332	4585	Missense	g.chr3:195508174G>T	c.9893C>A	p.P3298H	NM_018406		neutral
MUC4	131169	4585	Nonsense	g.chr3:195492248C>T	c.13307G>A	p.W4436*	NM_018406		
MYB	7441	4602	Splice Site	g.chr6:135518098G>T			NM_005375		

MYB	7441	4602	Splice Site	g.chr6:135518099G>T			NM_005375		
MYBL1	2128	4603	Missense	g.chr8:67511341T>C	c.235A>G	p.K79E	NM_001080416	neutral	medium
MYCBP2	1947	23077	Nonsense	g.chr13:77663083G>A	c.10495C>T	p.R3499*	NM_015057		
MYCN	11_6165	4613	Missense	g.chr2:16085866A>G	c.1042A>G	p.K348E	NM_005378	deleterious	medium
MYH1	2039	4619	Missense	g.chr17:10398310C>A	c.5404G>T	p.D1802Y	NM_005963	deleterious	high
MYOM2	990149	9172	Missense	g.chr8:2057234G>A	c.3092G>A	p.R1031Q	NM_003970	neutral	neutral
MYST3	1781	7994	Missense	g.chr8:41790003T>C	c.5735A>G	p.N1912S	NM_001099412	deleterious	low
N4BP1	11_6165	9683	Nonsense	g.chr16:48595187G>T	c.1367C>A	p.S456*	NM_153029		
NAA16	236	79612	Missense	g.chr13:41894863G>A	c.305G>A	p.C102Y	NM_024561	deleterious	high
NAB2	505	4665	Indel	g.chr12:57484990delTCC	c.166_168del	p.56_56del,	NM_005967		
NAP1L3	9534	4675	Missense	g.chrX:92927507G>C	c.797C>G	p.P266R	NM_004538	none	neutral
NAPSA	6536	9476	Missense	g.chr19:50864201T>C	c.665A>G	p.N222S	NM_004851	deleterious	neutral
NAT8B	671204	51471	Missense	g.chr2:73928065C>T	c.368G>A	p.G123E	NM_016347	deleterious	medium
NCAM2	36773720	4685	Nonsense	g.chr21:22790859A>T	c.1450A>T	p.R484*	NM_004540		
NCAPG	148632	64151	Missense	g.chr4:17819667G>T	c.1074G>T	p.E358D	NM_022346	neutral	low
NDUFS3	3492	4722	Missense	g.chr11:47603931A>G	c.538A>G	p.N180D	NM_004551	deleterious	medium
NFIB	2020	4781	Indel	chr9:14120513delGA	c.1170_1171del	p.390_391del,NFIB	NM_005596		
NFIB	540	4781	Nonsense	g.chr9:14150203G>C	c.747C>G	p.Y249*	NM_005596		
NFIX	2012	4784	Indel	chr19:13184245insTT	c.632_633insTT	p.S211fs,	NM_002501		
NLGN2	11_3318	57555	Missense	g.chr17:7319074C>T	c.1282C>T	p.R428W	NM_020795	deleterious	medium
NLRC3	2000756	197358	Missense	g.chr16:3614583C>T	c.355G>A	p.A119T	NM_178844	neutral	
NLRP12	540	91662	Missense	g.chr19:54314225C>T	c.688G>A	p.V230M	NM_144687	deleterious	low
NOTCH1	7097	4851	Missense	g.chr9:139412240C>A	c.1405G>T	p.D469Y	NM_017617	deleterious	high
NOTCH1	3492	4851	Missense	g.chr9:139390907G>C	c.7284C>G	p.H2428Q	NM_017617	neutral	low
NOTCH1	3492	4851	Missense	g.chr9:139390906G>C	c.7285C>G	p.L2429V	NM_017617	neutral	neutral
NOTCH1	2012	4851	Nonsense	g.chr9:139405607G>A	c.2584C>T	p.Q862*	NM_017617		
NOTUM	2237	147111	Missense	g.chr17:79915743C>A	c.634G>T	p.V212L	NM_178493	neutral	low
NPC1	2039	4864	Missense	g.chr18:21112227T>C	c.3776A>G	p.K1259R	NM_000271	neutral	low
NR1H3	11_6165	10062	Missense	g.chr11:47290233G>A	c.1330G>A	p.D444N	NM_005693	deleterious	medium
NR1H3	4133	10062	Missense	g.chr11:47282193C>T	c.466C>T	p.R156C	NM_005693	deleterious	medium
NRCAM	05_6986	4897	Missense	g.chr7:107864227T>C	c.832A>G	p.S278G	NM_001037132	deleterious	medium
NSD1	1346	64324	Missense	g.chr5:176666853G>C	c.4289G>C	p.G1430A	NM_022455	deleterious	medium
NT5C3	505	51251	Missense	g.chr7:33060887T>G	c.452A>C	p.E151A	NM_001002010	deleterious	medium
NT5C3	1739	51251	Missense	g.chr7:33055293G>T	c.898C>A	p.L300I	NM_001002010	deleterious	medium
NTNG1	671204	22854	Missense	g.chr1:107691402G>A	c.187G>A	p.V63M	NM_001113226	deleterious	medium
NUP50	148632	10762	Missense	g.chr22:45579374C>T	c.1177C>T	p.L393F	NM_007172	deleterious	medium
NUP50	148632	10762	Missense	g.chr22:45579373G>C	c.1176G>C	p.Q392H	NM_007172	deleterious	medium
NXPH4	148632	11247	Missense	g.chr12:57618927G>C	c.324G>C	p.W108C	NM_007224	deleterious	medium
OBSCN	3492	84033	Missense	g.chr1:228564967G>A	c.23254G>A	p.E7752K	NM_001098623	neutral	high
ODZ2	2000756	57451	Missense	g.chr5:167689316T>G	c.7799T>G	p.M2600R	NM_001122679		low
ODZ3	4133	55714	Missense	g.chr4:183696121A>G	c.5119A>G	p.I1707V	NM_001080477	neutral	neutral
ODZ4	7097	26011	Missense	g.chr11:78381509C>T	c.5881G>A	p.V1961M	NM_001098816		low
OPN3	236	23596	Missense	g.chr1:241761094G>A	c.899C>T	p.S300L	NM_014322	deleterious	medium
OPRK1	80872	4986	Missense	g.chr8:54163351C>A	c.247G>T	p.V83L	NM_000912	neutral	medium
OPRM1	990149	4988	Missense	g.chr6:154412237G>A	c.794G>A	p.R265H	NM_000914	deleterious	medium
OR10A2	2237	341276	Missense	g.chr11:6891762G>T	c.777G>T	p.K259N	NM_001004460	deleterious	high
OR10H5	2282	284433	Missense	g.chr19:15905193C>A	c.335C>A	p.S112Y	NM_001004466	deleterious	high
OR10J1	11_6165	26476	Missense	g.chr1:159409708A>T	c.160A>T	p.I54F	NM_012351	neutral	low
OR11H1	3492	81061	Missense	g.chr22:16449539A>G	c.266T>C	p.V89A	NM_001005239	neutral	medium
OR13C4	671204	138804	Missense	g.chr9:107288811C>T	c.680G>A	p.R227Q	NM_001001919	neutral	medium
OR13D1	07_16582	286365	Missense	g.chr9:107457728T>A	c.1026T>A	p.H342Q	NM_001004484	deleterious	low
OR2W3	05_6986	343171	Missense	g.chr1:248059607C>T	c.719C>T	p.T240I	NM_001001957	deleterious	high
OR5D16	122891	390144	Missense	g.chr11:55606759C>G	c.532C>G	p.H178D	NM_001005496	deleterious	high
OR5L2	11_6165	26338	Missense	g.chr11:55594894C>T	c.200C>T	p.S67F	NM_001004739	deleterious	high
OR6K3	7136	391114	Missense	g.chr1:158687115G>T	c.839C>A	p.T280N	NM_001005327	deleterious	low
OR8B8	10_5283	26493	Missense	g.chr11:124310419G>A	c.563C>T	p.A188V	NM_012378	neutral	low
OSR1	10_5283	130497	Indel	g.chr2:19552135_19552136delTT	c.701_702delAA	p.Q234fs	NM_145260		
OTP	09_4178	23440	Missense	g.chr5:76926516A>G	c.551T>C	p.F184S	NM_032109	deleterious	medium
OVOL1	2000756	5017	Missense	g.chr11:65561564C>T	c.163C>T	p.P55S	NM_004561	neutral	neutral
PABPC3	36773720	5042	Missense	g.chr13:25671348G>C	c.1012G>C	p.V338L	NM_030979	deleterious	high
PAPPA2	2237	60676	Missense	g.chr1:176563998C>T	c.1258C>T	p.R420C	NM_020318	deleterious	medium
PAX2	2000120	5076	Missense	g.chr10:102566259C>G	c.758C>G	p.A253G	NM_003990	neutral	neutral
PC	6277	5091	Missense	g.chr11:66618600C>T	c.2134G>A	p.D712N	NM_022172	neutral	low
PCDH18	990149	54510	Missense	g.chr4:138449961A>G	c.2501T>C	p.L834P	NM_019035	deleterious	medium
PCDHA2	07_16582	56146	Missense	g.chr5:140176744G>A	c.2195G>A	p.R732H	NM_018905	neutral	low
PCDHB10	2237	56126	Missense	g.chr5:140572612G>A	c.487G>A	p.G163R	NM_018930	deleterious	high
PCDHB11	1346	56125	Missense	g.chr5:140580699T>C	c.1352T>C	p.F451S	NM_018931	deleterious	high
PCDHGB4	505	8641	Missense	g.chr5:140769277C>T	c.1826C>T	p.A609V	NM_003736	deleterious	medium
PCDHGC3	6536	5098	Missense	g.chr5:140856401A>G	c.718A>G	p.N240D	NM_002588	deleterious	high
PCF11	479	51585	Missense	g.chr11:82875435G>A	c.694G>A	p.A232T	NM_015885	deleterious	medium
PDE3B	609	5140	Missense	g.chr11:14880694C>A	c.2626C>A	p.H876N	NM_000922	neutral	low
PDE8A	05_6986	5151	Missense	g.chr15:85657110A>C	c.1192A>C	p.N398H	NM_002605	deleterious	medium
PDZD2	9534	23037	Missense	g.chr5:32059371G>A	c.2227G>A	p.A743T	NM_178140	deleterious	low
PGR	609	5241	Missense	g.chr11:100998812G>T	c.990C>A	p.D330E	NM_000926	deleterious	medium
PHC2	06_2532	1912	Missense	g.chr1:33820083G>A	c.1474C>T	p.H492Y	NM_198040	deleterious	low
PHF2	148632	5253	Missense	g.chr9:96408054A>G	c.443A>G	p.D148G	NM_005392	deleterious	medium
PHF20	3492	51230	Nonsense	g.chr20:34430571_34430572insA	c.160_161insA	p.Y54fs	NM_016436		
PHOX2B	07_16582	8929	Missense	g.chr4:41750440C>A	c.188G>T	p.G63V	NM_003924	neutral	neutral
PIGO	07_16582	84720	Missense	g.chr9:35093044G>A	c.1102C>T	p.H368Y	NM_032634	neutral	low
PIK3CA	2237	5290	Missense	g.chr3:178927980T>C	c.1258T>C	p.C420R	NM_006218	deleterious	medium
PIK3CA	2012	5290	Missense	g.chr3:178952072A>G	c.3127A>G	p.M1043V	NM_006218	deleterious	neutral

PIK3CA	3492	5290	Missense	g.chr3:178921553T>A	c.1035T>A	p.N345K	NM_006218	deleterious	medium
PIK3CG	2039	5294	Missense	g.chr7:106508152G>A	c.146G>A	p.R49H	NM_002649	neutral	medium
PKD1L1	6536	168507	Missense	g.chr7:47945520T>A	c.1442A>T	p.Y481F	NM_138295	deleterious	neutral
PKD2	505	5311	Missense	g.chr4:88977258T>G	c.1737T>G	p.F579L	NM_000297	neutral	medium
PKHD1	09_4178	5314	Missense	g.chr6:51503691G>C	c.11462C>G	p.S3821C	NM_138694	deleterious	medium
PLA2G2C	07_16582	391013	Missense	g.chr1:20490579C>T	c.358G>A	p.V120M	NM_001105572		medium
PLA2G6	2000756	8398	Missense	g.chr22:38516860G>A	c.1648C>T	p.R550W	NM_003560	deleterious	medium
PLCD1	2237	5333	Missense	g.chr3:38058148C>T	c.262G>A	p.A88T	NM_006225	neutral	low
PLCL1	6536	5334	Missense	g.chr2:198949880G>A	c.1639G>A	p.D547N	NM_001114661	neutral	low
PLCZ1	1947	89869	Missense	g.chr12:18854436T>C	c.1016A>G	p.K339R	NM_033123	neutral	neutral
PLCZ1	1781	89869	Missense	g.chr12:18876362G>A	c.250C>T	p.R84W	NM_033123	deleterious	medium
PLXNB1	10_5283	5364	Missense	g.chr3:48453983C>G	c.4901G>C	p.R1634P	NM_002673	deleterious	high
POGK	2012	57645	Missense	g.chr1:166819104G>A	c.1288G>A	p.G430R	NM_017542	deleterious	medium
POMGNT1	990149	55624	Missense	g.chr1:46654554G>C			NM_017739		
POU2F3	9534	25833	Nonsense	g.chr11:120175748C>T	c.454C>T	p.H152Y	NM_014352		neutral
PPM1A	980452	5494	Missense	g.chr14:60749782G>A	c.361G>A	p.G121S	NM_021003	neutral	low
PRDM16	1346	63976	Missense	g.chr1:3328395C>T	c.1634C>T	p.A545V	NM_022114	neutral	low
PRKCI	148632	5584	Missense	g.chr3:170002369C>G	c.1188C>G	p.D396E	NM_002740	deleterious	high
PRKD1	6277	5587	Missense	g.chr14:30100004G>A	c.1616C>T	p.A539V	NM_002742	deleterious	medium
PRKD2	7097	25865	Missense	g.chr19:47184936A>C	c.2041T>G	p.L681V	NM_001079881	deleterious	high
PRKDC	705	5591	Missense	g.chr8:48691321T>C	c.11525A>G	p.N3842S	NM_001081640		
PRKG1	1781	5592	Missense	g.chr10:52913011T>G	c.354T>G	p.C118W	NM_001098512	deleterious	medium
PSMB9	2039	5698	Missense	g.chr6:32826231G>C	c.445G>C	p.A149P	NM_148954	neutral	medium
PTEN	609	5728	Missense	g.chr10:89692946A>C	c.430A>C	p.K144Q	NM_000314	neutral	low
PTEN	609	5728	Indel	g.chr10:89692905delG	c.389delG	p.R130fs	NM_000314		
PTPDC1	2000756	138639	Missense	g.chr9:96847560A>G	c.110A>G	p.Y37C	NM_177995	deleterious	medium
PTPRG	380	5793	Nonsense	g.chr3:62204575G>T	c.2206G>T	p.E736*	NM_002841		
PTPRH	111097	5794	Nonsense	g.chr19:55708669C>T	c.1806G>A	p.W602*	NM_002842		
PTPRJ	142990	5795	Missense	g.chr11:48188825C>T	c.3925C>T	p.L1309F	NM_002843	deleterious	low
PTPRK	09_4178	5796	Indel	g.chr6:128410928_128410929insC	c.1371_1372insG	p.L457fs	NM_002844		
PXDN	06_2532	7837	Missense	g.chr2:1643087G>A	c.4060C>T	p.R1354W	NM_012293	deleterious	low
PXK	7136	54899	Missense	g.chr3:58382830T>C	c.887T>C	p.L296P	NM_017771	deleterious	medium
RAB3GAP2	131169	25782	Missense	g.chr1:220364615C>T	c.1282G>A	p.A428T	NM_012414	deleterious	medium
RAB40B	09_4178	10966	Missense	g.chr17:80615812C>G	c.764G>C	p.R255P	NM_006822	neutral	low
RABGAP1	2012	23637	Missense	g.chr9:125748532G>A	c.424G>A	p.E142K	NM_012197	deleterious	medium
RABGAP1	2012	23637	Nonsense	g.chr9:125748604G>T	c.496G>T	p.E166*	NM_012197		
RALA	609	5898	Missense	g.chr7:39726340T>A	c.74T>A	p.V25E	NM_005402	deleterious	high
RANBP17	11_17815	64901	Missense	g.chr5:170626749A>G	c.2114A>G	p.N705S	NM_022897	neutral	neutral
RAP1B	142990	5908	Missense	g.chr12:69042538G>A	c.34G>A	p.G12R	NM_001089704	deleterious	
RASL11A	07_16582	387496	Missense	g.chr13:27847330T>C	c.428T>C	p.I143T	NM_206827	neutral	low
RB1	131169	5925	Missense	g.chr13:49030342A>G	c.1817A>G	p.Y606C	NM_000321	deleterious	medium
REC8	36773720	9985	Missense	g.chr14:24641808C>T	c.47C>T	p.A16V	NM_005132	none	medium
REC8	7097	9985	Missense	g.chr14:24647379C>T	c.947C>T	p.P316L	NM_005132	neutral	neutral
RGNEF	7097	64283	Missense	g.chr5:73179619C>T	c.2965C>T	p.R989C	NM_001080479	deleterious	medium
RGSL1	11_3318	353299	Missense	g.chr1:182509456A>C	c.2569A>C	p.N857H	NM_001137669	deleterious	medium
RIMBP2	2000120	23504	Missense	g.chr12:130926642T>A	c.1204A>T	p.I402F	NM_015347	deleterious	medium
RIMBP2	540	23504	Missense	g.chr12:130907016C>T	c.2452G>A	p.V818M	NM_015347	neutral	neutral
RIN2	2237	54453	Missense	g.chr20:19937318G>A	c.218G>A	p.R73Q	NM_018993	deleterious	low
RIPPLY2	6277	134701	Missense	g.chr6:84567055T>A	c.334T>A	p.Y112N	NM_001009994	deleterious	medium
RIT1	142990	6016	Missense	g.chr1:155874272C>T	c.259G>A	p.D87N	NM_006912	deleterious	high
RIT1	505	6016	Missense	g.chr1:155880486T>C	c.67A>G	p.K23E	NM_006912	deleterious	high
RLF	2237	6018	Nonsense	g.chr1:40705233C>G	c.4859C>G	p.S1620*	NM_012421		
RLIM	2000756	51132	Missense	g.chrX:73812846G>A	c.304C>T	p.L102F	NM_183353	deleterious	medium
RNF111	1739	54778	Missense	g.chr15:59383319T>C	c.2705T>C	p.I902T	NM_017610	deleterious	low
RNF148	2000756	378925	Missense	g.chr7:122342759A>G	c.46T>C	p.S16P	NM_198085	neutral	low
RNF219	07_16582	79596	Nonsense	g.chr13:79212993C>A	c.514G>T	p.E172*	NM_024546		
RNF32	2000120	140545	Missense	g.chr7:156447287A>T	c.292A>T	p.I98F	NM_030936	neutral	neutral
RNF40	36773720	9810	Missense	g.chr16:30775607C>G	c.550C>G	p.R184G	NM_014771	deleterious	medium
RNPEP	4133	6051	Missense	g.chr1:201973602T>G	c.1772T>G	p.V591G	NM_020216	deleterious	medium
RORA	2000756	6095	Missense	g.chr15:60803461C>T	c.883G>A	p.G295S	NM_134260	neutral	low
RP1L1	09_4615	94137	Missense	g.chr8:10480624C>T	c.88G>A	p.V30I	NM_178857	neutral	neutral
RSBN1	148632	54665	Missense	g.chr1:114308720G>A	c.2291C>T	p.S764L	NM_018364	neutral	low
RSPH3	2000120	83861	Missense	g.chr6:159420665T>C	c.344A>G	p.H115R	NM_031924	deleterious	low
RUNX1	980452	861	Nonsense	g.chr21:36171600G>C	c.884C>G	p.S295*	NM_001001890		
RYR2	705	6262	Splice Site	g.chr1:237868513G>A	c.9450G>A	p.R3150R	NM_001035		
RYR3	2012	6263	Nonsense	g.chr15:34078011C>A	c.9417C>A	p.C3139*	NM_001036		
RYR3	1346	6263	Missense	g.chr15:33872202A>G	c.1294A>G	p.I432V	NM_001036	neutral	neutral
RYR3	671204	6263	Missense	g.chr15:33954455G>A	c.4724G>A	p.R1575H	NM_001036	deleterious	medium
RYR3	09_4615	6263	Missense	g.chr15:34157408A>G	c.14594A>G	p.Y4865C	NM_001036	deleterious	medium
SAMHD1	7136	25939	Missense	g.chr20:35540873A>G	c.1145T>C	p.I382T	NM_015474	neutral	medium
SBNO1	2000756	55206	Missense	g.chr12:123780460C>A	c.4177G>T	p.A1393S	NM_018183	neutral	neutral
SCEL	118135	8796	Missense	g.chr13:78138015T>A	c.271T>A	p.S91T	NM_144777	deleterious	low
SCUBE3	111097	222663	Splice Site	g.chr6:35209689T>A	c.1417_splice	p.E473_splice	NM_152753		
SDSL	3492	113675	Missense	g.chr12:113866997G>T	c.247G>T	p.A83S	NM_138432	neutral	medium
SEC24A	671204	10802	Missense	g.chr5:134029429T>A	c.1792T>A	p.L598I	NM_021982	deleterious	medium
SELP	2237	6403	Nonsense	g.chr1:169586615A>T	c.132T>A	p.Y44*	NM_003005		
SEMA3G	09_4615	56920	Missense	g.chr3:52473743A>G	c.1420T>C	p.S474P	NM_020163	neutral	low
SEMA4D	2012	10507	Missense	g.chr9:92002518G>C	c.1113C>G	p.I371M	NM_006378	deleterious	medium
SEMA4G	142990	57715	Missense	g.chr10:102738764C>T	c.802C>T	p.R268C	NM_017893	deleterious	high
SEMA5A	6277	9037	Missense	g.chr5:9190558T>G	c.1094A>C	p.Y365S	NM_003966	deleterious	neutral
SERTAD4	479	56256	Missense	g.chr1:210412892T>C	c.230T>C	p.F77S	NM_019605	deleterious	low

SETD2	1781	29072	Missense	g.chr3:47164831C>T	c.1295G>A	p.R432H	NM_014159	deleterious	low
SEZ6L	1947	23544	Missense	g.chr22:26706742C>T	c.1621C>T	p.R541C	NM_021115	deleterious	medium
SF3A3	148632	10946	Nonsense	g.chr1:38453346G>A	c.202C>T	p.R68*	NM_006802		
SF3B1	7136	23451	Missense	g.chr2:198267484G>A	c.1873C>T	p.R625C	NM_012433	deleterious	high
SF3B1	10_5283	23451	Missense	g.chr2:198267483C>A	c.1874G>T	p.R625L	NM_012433	deleterious	high
SIPA1L2	410	57568	Missense	g.chr1:232539886G>A	c.4801C>T	p.H1601Y	NM_020808	deleterious	medium
SIRT6	9534	51548	Missense	g.chr19:4180893G>C	c.80C>G	p.P27R	NM_016539	deleterious	medium
SLC16A4	671204	9122	Missense	g.chr1:110906527G>T			NM_004696		
SLC22A12	1781	116085	Splice Site	g.chr11:64361031C>T	c.661C>T	p.L221L	NM_144585		
SLC22A5	118135	6584	Missense	g.chr5:131705729T>A	c.65T>A	p.F22Y	NM_003060	deleterious	low
SLC25A2	11_17815	83884	Missense	g.chr5:140682943C>T	c.490G>A	p.D164N	NM_031947	neutral	low
SLC25A2	11_17815	83884	Missense	g.chr5:140682944C>A	c.489G>T	p.K163N	NM_031947	neutral	low
SLC25A24	148632	29957	Missense	g.chr1:108686203T>C	c.1060A>G	p.I354V	NM_013386	neutral	low
SLC37A3	6277	84255	Splice Site	g.chr7:140055468C>T	c.618G>A	p.E206E	NM_207113		
SLC4A10	4133	57282	Missense	g.chr2:162762373A>G	c.1973A>G	p.D658G	NM_022058	neutral	low
SLC9A4	705	389015	Missense	g.chr2:103124727C>T	c.1388C>T	p.T463I	NM_001011552	deleterious	high
SLC9A7	705	84679	Missense	g.chrX:46529111G>C	c.724C>G	p.Q242E	NM_032591	deleterious	low
SLIT3	80872	6586	Missense	g.chr5:168098402G>A	c.3928C>T	p.R1310C	NM_003062	deleterious	medium
SMARCA2	2039	6595	Missense	g.chr9:2110356G>T	c.3395G>T	p.G1132V	NM_003070	deleterious	high
SMARCA2	7441	6595	Missense	g.chr9:2115855G>T	c.3490G>T	p.G1164W	NM_003070	deleterious	high
SMARCA2	705	6595	Missense	g.chr9:2110338C>T	c.3377C>T	p.T1126I	NM_003070	deleterious	medium
SMARCE1	1346	6605	Missense	g.chr17:38793763T>C	c.218A>G	p.Y73C	NM_003079	deleterious	high
SMC1A	2000756	8243	Missense	g.chrX:53426627G>C	c.2446C>G	p.R816G	NM_006306	deleterious	medium
SMR3B	07_16582	10879	Indel	g.chr4:71255545delC	c.220delC	p.P74fs	NM_006685		
SNUPN	10_5342	10073	Missense	g.chr15:75913259C>G	c.134G>C	p.R45P	NM_005701	deleterious	medium
SNX14	479	57231	Missense	g.chr6:86252955T>C	c.1334A>G	p.H445R	NM_153816	deleterious	medium
SORCS1	131169	114815	Missense	g.chr10:108923870C>G	c.415G>C	p.E139Q	NM_052918	neutral	neutral
SP100	2039	6672	Missense	g.chr2:231327186T>C	c.1010T>C	p.V337A	NM_003113	neutral	neutral
SPATA13	352	221178	Missense	g.chr13:24797159G>T	c.92G>T	p.C31F	NM_001166271		neutral
SPATA7	36773720	55812	Missense	g.chr14:88904395G>C	c.1429G>C	p.A477P	NM_018418	neutral	low
SPEF2	11_3089	79925	Missense	g.chr5:35712980A>G	c.2906A>G	p.K969R	NM_024867	deleterious	low
SPTBN1	1947	6711	Missense	g.chr2:54873496C>T	c.4750C>T	p.R1584C	NM_003128	deleterious	high
SRCAP	09_4615	10847	Missense	g.chr16:30748617A>G	c.7256A>G	p.Q2419R	NM_006662	none	neutral
SRCRB4D	11_17815	136853	Missense	g.chr7:76023182A>C	c.986T>G	p.L329R	NM_080744	neutral	neutral
SSFA2	705	6744	Missense	g.chr2:182785370C>T	c.3191C>T	p.P1064L	NM_001130445	deleterious	medium
STAM	6536	8027	Missense	g.chr10:17726706G>A	c.158G>A	p.R53K	NM_003473	deleterious	low
STOX2	05_6986	56977	Missense	g.chr4:184931421G>A	c.1430G>A	p.R477Q	NM_020225	deleterious	medium
STX12	11_3318	23673	Missense	g.chr1:28128213C>T	c.313C>T	p.R105C	NM_177424	deleterious	medium
SYNDIG1L	05_6986	646658	Missense	g.chr14:74876153C>T	c.295G>A	p.E99K	NM_001105579	neutral	neutral
SYNE1	36773720	23345	Missense	g.chr6:152786517C>T	c.1808G>A	p.S603N	NM_182961	deleterious	low
SYTL5	11_3089	94122	Missense	g.chrX:37969646C>G	c.1507C>G	p.R503G	NM_001163335	deleterious	medium
SZT2	07_16582	23334	Missense	g.chr1:43897471G>A	c.2476G>A	p.A826T	NM_015284		medium
TANC1	2000120	85461	Missense	g.chr2:160074130G>T	c.3367G>T	p.G1123W	NM_033394	deleterious	high
TANC2	09_4178	26115	Missense	g.chr17:61391974G>C	c.1163G>C	p.C388S	NM_025185	deleterious	low
TATDN2	2020	9797	Missense	g.chr3:10291236C>G	c.352C>G	p.R118G	NM_014760	neutral	neutral
TBC1D4	05_6986	9882	Missense	g.chr13:75923344G>T	c.1370C>A	p.P457Q	NM_014832	deleterious	medium
TBC1D5	11_3318	9779	Missense	g.chr3:17550043T>G	c.20A>C	p.E7A	NM_014744	deleterious	medium
TBC1D5	2039	9779	Missense	g.chr3:17333416G>T	c.1216C>A	p.L406I	NM_014744	neutral	medium
TCN1	2000136	6947	Missense	g.chr11:59631402G>C	c.237C>G	p.I79M	NM_001062	neutral	low
TEKT1	6277	83659	Missense	g.chr17:6719267C>G	c.371G>C	p.G124A	NM_053285	deleterious	medium
TEX15	07_16582	56154	Nonsense	g.chr8:30694753C>T	c.7898G>A	p.W2633*	NM_031271		
TFAP2A	09_12352	7020	Missense	g.chr6:10410466T>G	c.148A>C	p.N50H	NM_003220	deleterious	medium
THAP3	705	90326	Missense	g.chr1:6688576C>T	c.92C>T	p.P31L		deleterious	medium
THSD7A	10_5342	221981	Missense	g.chr7:11630233C>T	c.1307G>A	p.R436H	NM_015204	neutral	low
THSD7A	1781	221981	Missense	g.chr7:11468693A>G	c.3124T>C	p.S1042P	NM_015204	deleterious	medium
TIGD6	1947	81789	Indel	g.chr5:149375303insC	c.609_610insG	p.G203fs,	NM_030953		
TIMD4	36773720	91937	Missense	g.chr5:156381740G>A	c.86C>T	p.T29M	NM_138379	deleterious	low
TLK1	122891	9874	Missense	g.chr2:171913024C>T	c.506G>A	p.R169H	NM_012290	neutral	medium
TLN1	352	7094	Missense	g.chr9:35719765T>C	c.1550A>G	p.D517G	NM_006289	neutral	low
TLN1	7441	7094	Missense	g.chr9:35713028C>G	c.3365G>C	p.R1122P	NM_006289	deleterious	medium
TMC6	142990	11322	Missense	g.chr17:76115069C>T	c.1870G>A	p.V624I	NM_007267	neutral	neutral
TMEM206	131169	55248	Missense	g.chr1:212558758A>C	c.353T>G	p.L118W	NM_018252	neutral	medium
TMEM237	980452	65062	Missense	g.chr2:202498103C>T	c.326G>A	p.R109Q	NM_001044385	neutral	neutral
TNIP1	540	10318	Missense	g.chr5:150425486G>A	c.872C>T	p.P291L	NM_006058	deleterious	medium
TNKS2	65115	80351	Missense	g.chr10:93621830C>T	c.3356C>T	p.P1119L	NM_025235	deleterious	medium
TNN	540	63923	Splice Site	g.chr1:175105958A>G	c.3429A>G	p.G1143G	NM_022093		
TNPO2	06_2532	30000	Missense	g.chr19:12816371G>A	c.1798C>T	p.P600S	NM_001136196	deleterious	high
TNPO3	36773720	23534	Missense	g.chr7:128630032C>T	c.1481G>A	p.R494Q	NM_012470	deleterious	low
TNRC18	505	84629	Indel	g.chr7:5401258insG	c.4628_4629insC	p.R1543fs,	NM_001080495		
TNRC6B	609	23112	Missense	g.chr22:40657967G>T	c.247G>T	p.A83S	NM_001162501	neutral	medium
TNRC6C	990149	57690	Missense	g.chr17:76069128C>T	c.2870C>T	p.A957V	NM_018996	deleterious	low
TOB1	142990	10140	Indel	g.chr17:48940492insGG	c.887_888insCC	p.I296fs,	NM_005749		
TOMM40L	1781	84134	Missense	g.chr1:161198068G>C	c.577G>C	p.A193P	NM_032174	neutral	low
TP53	2237	7157	Missense	g.chr17:7578479G>A	c.451C>T	p.P151S	NM_001126112	deleterious	medium
TP53	142990	7157	Nonsense	g.chr17:7578212G>A	c.637C>T	p.R213*	NM_001126112		
TP53	36773720	7157	Nonsense	g.chr17:7574003G>A	c.1024C>T	p.R342*	NM_001126112		
TPP1	2237	1200	Missense	g.chr11:6638547G>C	c.493C>G	p.P165A	NM_000391	neutral	low
TRAPPC12	3492	51112	Missense	g.chr2:3464058G>A	c.1628G>A	p.R543H	NM_016030	deleterious	medium
TRIM36	2237	55521	Missense	g.chr5:114469712T>C	c.1379A>G	p.E460G	NM_018700	deleterious	neutral
TRIM39	148632	56658	Missense	g.chr6:30297210C>G	c.116C>G	p.P39R	NM_021253	deleterious	high
TRIP10	118135	9322	Missense	g.chr19:6744586C>G	c.664C>G	p.R222G	NM_004240	deleterious	medium

TRIP13	6536	9319	Missense	g.chr5:895042C>T	c.233C>T	p.T78I	NM_004237	neutral	medium
TRPC4	05_6986	7223	Missense	g.chr13:38320391G>A	c.580C>T	p.R194C	NM_016179	deleterious	medium
TRRAP	11_17815	8295	Missense	g.chr7:98563369G>T	c.7006G>T	p.A2336S	NM_003496	neutral	neutral
TRRAP	11_17815	8295	Missense	g.chr7:98563370C>T	c.7007C>T	p.A2336V	NM_003496	neutral	low
TSPAN17	2012	26262	Missense	g.chr5:176081974C>T	c.535C>T	p.R179W	NM_012171	deleterious	high
TTC21A	7441	199223	Missense	g.chr3:39178524C>T	c.3251C>T	p.A1084V	NM_145755	neutral	neutral
TTC40	07_16582	54777	Missense	g.chr10:134672672T>C	c.4456A>G	p.M1486V	NM_017609		neutral
TTL	142990	150465	Missense	g.chr2:113260508C>T	c.625C>T	p.H209Y	NM_153712	deleterious	medium
TTLL10	09_4178	254173	Missense	g.chr1:1119350C>G	c.1139C>G	p.S380C	NM_001130045	neutral	low
TTN	2000120	7273	Missense	g.chr2:179494077A>T	c.36671T>A	p.I12224N	NM_133378	neutral	medium
TXNIP	2012	10628	Indel	g.chr1:145439839insT	c.385_386insT	p.L129fs,	NM_006472		
TYMP	09_4178	1890	Missense	g.chr22:50967961C>T	c.178G>A	p.A60T	NM_001113756	neutral	medium
UBE3B	122891	89910	Missense	g.chr12:109936085A>G	c.867A>G	p.I289M	NM_130466	neutral	neutral
UBL7	111097	84993	Missense	g.chr15:74741661T>C	c.748A>G	p.S250G	NM_032907	neutral	neutral
UCP2	7441	7351	Missense	g.chr11:73687916C>G	c.484G>C	p.A162P	NM_003355	deleterious	high
UGT3A2	1947	167127	Missense	g.chr5:36039728T>C	c.926A>G	p.N309S	NM_174914	neutral	neutral
UHRF1	11_17815	29128	Missense	g.chr19:4930857G>A	c.538G>A	p.E180K	NM_001048201	deleterious	low
UHRF1	1739	29128	Missense	g.chr19:4930785G>A	c.466G>A	p.V156M	NM_001048201	neutral	medium
UNC79	3492	57578	Missense	g.chr14:93963525A>G	c.260A>G	p.Y87C	NM_020818	deleterious	medium
USP1	2128	7398	Missense	g.chr1:62916300T>C	c.2006T>C	p.L669P	NM_001017415	deleterious	medium
USP22	142990	23326	Missense	g.chr17:20919166T>C	c.737A>G	p.H246R	NM_015276	deleterious	low
USP29	2039	57663	Missense	g.chr19:57640135A>C	c.92A>C	p.Q31P	NM_020903	neutral	neutral
USP29	10_5283	57663	Missense	g.chr19:57642522A>G	c.2479A>G	p.S827G	NM_020903	neutral	low
USP31	1346	57478	Missense	g.chr16:23083513T>C	c.2341A>G	p.T781A	NM_020718	deleterious	medium
USP35	671204	57558	Nonsense	g.chr11:77910662G>A	c.828G>A	p.W276*	NM_020798		
USP38	09_4178	84640	Missense	g.chr4:144106607G>C	c.4G>C	p.D2H	NM_032557	deleterious	medium
USP50	4133	373509	Missense	g.chr15:50822032A>C	c.913T>G	p.F305V	NM_203494		low
WAPAL	7136	23063	Missense	g.chr10:88203049G>C	c.3394C>G	p.L1132V	NM_015045	neutral	low
WARS2	236	10352	Missense	g.chr1:119575617C>T	c.1000G>A	p.V334I	NM_015836	neutral	low
WDFY2	07_16582	115825	Missense	g.chr13:52313214G>T	c.628G>T	p.V210F	NM_052950	neutral	low
WDFY4	36773720	57705	Missense	g.chr10:49917965T>C	c.188T>C	p.I63T	NM_020945	neutral	neutral
WDR53	6536	348793	Missense	g.chr3:196281678C>T	c.481G>A	p.V161M	NM_182627	deleterious	low
WDR87	2000756	83889	Missense	g.chr19:38383983A>G	c.2243T>C	p.V748A	NM_031951	neutral	low
WFDC10B	671204	280664	Missense	g.chr20:44314624G>A	c.8C>T	p.P3L	NM_172006	deleterious	
WTAP	4332	9589	Missense	g.chr6:160176393C>G	c.941C>G	p.S314C	NM_004906	neutral	medium
WWC3	2237	55841	Missense	g.chrX:10062190G>A	c.526G>A	p.D176N	NM_015691	deleterious	low
XKR7	609	343702	Missense	g.chr20:30584917C>T	c.1397C>T	p.A466V	NM_001011718	neutral	low
ZBTB16	142990	7704	Missense	g.chr11:113934722C>T	c.700C>T	p.R234W	NM_006006	deleterious	low
ZBTB45	131169	84878	Missense	g.chr19:59025545T>C	c.1412A>G	p.K471R	NM_032792	deleterious	low
ZCCHC16	122891	340595	Nonsense	g.chrX:111698767C>T	c.811C>T	p.R271*	NM_001004308		
ZFC3H1	1947	196441	Missense	g.chr12:72017206C>A	c.4678G>T	p.V1560L	NM_144982	neutral	low
ZFHX3	10_5283	463	Missense	g.chr16:72821559C>T	c.10616G>A	p.C3539Y	NM_006885	none	neutral
ZFP36L1	148632	677	Missense	g.chr14:69256668T>C	c.599A>G	p.H200R	NM_004926	deleterious	medium
ZHX2	2000120	22882	Missense	g.chr8:123965309G>A	c.1559G>A	p.R520H	NM_014943	deleterious	low
ZMIZ1	2020	57178	Missense	g.chr10:81058173C>T	c.1502C>T	p.P501L	NM_020338	deleterious	low
ZMYM2	2000120	7750	Missense	g.chr13:20568053A>G	c.841A>G	p.N281D	NM_003453	deleterious	low
ZNF143	9534	7702	Missense	g.chr11:9530210T>C	c.1192T>C	p.F398L	NM_003442	deleterious	high
ZNF16	2237	7564	Missense	g.chr8:146157387C>A	c.786G>T	p.E262D	NM_001029976	neutral	medium
ZNF213	6277	7760	Missense	g.chr16:3191241G>A	c.1273G>A	p.G425S	NM_004220	deleterious	medium
ZNF217	7136	7764	Missense	g.chr20:52198608G>C	c.758C>G	p.S253C	NM_006526	neutral	neutral
ZNF311	65115	282890	Missense	g.chr6:28967269G>A	c.305C>T	p.S102L	NM_001010877	deleterious	medium
ZNF35	09_4178	7584	Indel	g.chr3:44700517_44700518insT	c.662_663insT	p.P221fs	NM_003420		
ZNF395	148632	55893	Missense	g.chr8:28206676C>T	c.1396G>A	p.V466I	NM_018660	neutral	medium
ZNF445	11_17815	353274	Missense	g.chr3:44489097G>C	c.2066C>G	p.T689S	NM_181489	deleterious	neutral
ZNF462	2039	58499	Missense	g.chr9:109773267G>T	c.7477G>T	p.A2493S	NM_021224	neutral	low
ZNF462	2237	58499	Missense	g.chr9:109687875A>C	c.1682A>C	p.Q561P	NM_021224	none	neutral
ZNF507	2000120	22847	Nonsense	g.chr19:32844617C>G	c.881C>G	p.S294*	NM_001136156		
ZNF513	2012	130557	Missense	g.chr2:27600573G>A	c.1465C>T	p.R489C	NM_144631	deleterious	medium
ZNF524	7441	147807	Missense	g.chr19:56114128C>T	c.650C>T	p.A217V	NM_153219	neutral	neutral
ZNF572	09_4615	137209	Missense	g.chr8:125989681A>G	c.1171A>G	p.K391E	NM_152412	deleterious	medium
ZNF630	1947	57232	Missense	g.chrX:47919148A>G	c.683T>C	p.I228T	NM_001037735	deleterious	low
ZNF75A	11_17815	7627	Missense	g.chr16:3367445C>A	c.467C>A	p.A156E	NM_153028	neutral	low
ZNF783	1781	1.00E+08	Missense	g.chr7:148963758G>T					medium
ZNF792	705	126375	Missense	g.chr19:35449135T>C	c.1624A>G	p.T542A	NM_175872	deleterious	neutral
ZNF804A	07_16582	91752	Missense	g.chr2:185802558G>A	c.2435G>A	p.R812Q	NM_194250	deleterious	neutral
ZNF844	671204	284391	Missense	g.chr19:12186146G>C	c.211G>C	p.V71L	NM_001136501	neutral	neutral
ZZEF1	65103	23140	Missense	g.chr17:3959588C>G	c.5217G>C	p.W1739C	NM_015113	deleterious	medium

Supplementary Table 4. Significantly mutated CHASM genes

Includes genes with point mutations deemed significant by CHASM (BHFDR<0.35), indels, splice site, and nonsense mutations.
Additional mutations identified within these genes also are included.

Hugo_Symbol	Sample ID	Chr:Pos	Reference_Allele	Tumor_Allele	AA Change	Type	Refseq_mRNA_Id	CHASM	PValue	BHFDR
IDH1	7097	chr2:209113112	C	T	R132H	Missense	NM_005896	0.04	0	0.05
PIK3CA	2237	chr3:178927980	T	C	C420R	Missense	NM_006218	0.05	0	0.05
PIK3CA	2012	chr3:178952072	A	G	M1043V	Missense	NM_006218	0.022	0	0.05
PIK3CA	3492	chr3:178921553	T	A	N345K	Missense	NM_006218	0.052	0	0.05
TP53	2237	chr17:7578479	G	A	P151S	Missense	NM_001126112	0.004	0	0.05
TP53	142990	chr17:7578212	G	A	p.R213*	Nonsense	NM_001126112			N/A
TP53	36773720	chr17:7574003	G	A	p.R342*	Nonsense	NM_001126112			N/A
KLHL12	3492	chr1:202863872	T	A	I381F	Missense	NM_021633	0.034	0	0.05
SLC9A4	705	chr2:103124727	C	T	T463I	Missense	NM_001011552	0.108	0.002	0.1
FBXW7	609	chr4:153249384	C	T	R465H	Missense	NM_033632	0.076	0.001	0.1
PRKG1	1781	chr10:52913011	T	G	C118W	Missense	NM_001098512	0.082	0.001	0.1
PTEN	609	chr10:89692946	A	C	K144Q	Missense	NM_000314	0.076	0.001	0.1
PTEN	609	g.chr10:89692905	G	--	p.R130fs	Indel	NM_000314			N/A
MGEA5	118135	chr10:103563588	G	C	P314A	Missense	NM_012215	0.104	0.002	0.1
PAX2	2000120	chr10:102566259	C	G	A230G	Missense	NM_000278	0.078	0.001	0.1
KIAA1324L	36773720	chr7:86541434	C	A	G541V	Missense	NM_152748	0.12	0.003	0.15
CTNNB1	1947	chr3:41278106	G	T	R661L	Missense	NM_001904	0.14	0.004	0.2
GNB4	111097	chr3:179137211	G	C	A60G	Missense	NM_021629	0.154	0.006	0.2
FGFR4	505	chr5:176518079	G	A	G193R	Missense	NM_002011	0.148	0.005	0.2
TANC1	2000120	chr2:160074130	G	T	G1115W	Missense	NM_001145909	0.156	0.006	0.2
CALM2	2020	chr2:47389754	T	C	I28V	Missense	NM_001743	0.218	0.011	0.25
WDR53	6536	chr3:196281678	C	T	V161M	Missense	NM_182627	0.178	0.008	0.25
NT5C3	1739	chr7:33055293	G	T	L300I	Missense	NM_001002010	0.256	0.014	0.25
NT5C3	505	chr7:33060887	T	G	E151A	Missense	NM_001002010	0.456	0.05	0.4
RALA	609	chr7:39726340	T	A	V25E	Missense	NM_005402	0.25	0.013	0.25
MCM4	7441	chr8:48883928	C	T	R610C	Missense	NM_182746	0.182	0.008	0.25
SMARCA2	7441	chr9:2115855	G	T	G1164W	Missense	NM_003070	0.254	0.014	0.25
SMARCA2	2039	chr9:2110356	G	T	G1132V	Missense	NM_003070	0.5	0.065	0.45
SMARCA2	705	chr9:2110338	C	T	T1126I	Missense	NM_003070	0.538	0.084	0.5
TLN1	7441	chr9:35713028	C	G	R1122P	Missense	NM_006289	0.19	0.01	0.25
TLN1	352	g.chr9:35719765	T	C	p.D517G	Missense	NM_006289			N/A
UCP2	7441	chr11:73687916	C	G	A162P	Missense	NM_003355	0.24	0.012	0.25
ATM	65115	chr11:108188116	G	A	G2072E	Missense	NM_000051	0.164	0.007	0.25
ATM	65115	chr11:108196143	C	T	R2227C	Missense	NM_000051	0.404	0.037	0.35
GRIN2B	7136	chr12:13764773	C	T	A556T	Missense	NM_000834	0.234	0.012	0.25
DHODH	236	chr16:72056354	A	C	I267L	Missense	NM_001361	0.24	0.012	0.25
CNDP2	65115	chr18:72179722	G	A	G233R	Missense	NM_018235	0.194	0.01	0.25
ACTB	10_5283	chr7:5568871	C	T	R95H	Missense	NM_001101	0.206	0.011	0.25
ACTB	671204	chr7:5567474	T	C	I345V	Missense	NM_001101	0.244	0.013	0.25
BRD1	671204	chr22:50216803	T	C	H388R	Missense	NM_014577	0.236	0.012	0.25
C6orf170	36773720	chr6:121638817	A	G	Y107H	Missense	NM_152730	0.174	0.008	0.25
HRAS	2000120	chr11:534289	C	A	G12C	Missense	NM_176795	0.222	0.011	0.25
NDUFS3	3492	chr11:47603931	A	G	N180D	Missense	NM_004551	0.274	0.015	0.25
RAB3GAP2	131169	chr1:220364615	C	T	A428T	Missense	NM_012414	0.334	0.026	0.35
ASAP2	7441	chr2:9496405	A	G	T420A	Missense	NM_003887	0.394	0.036	0.35
SPTBN1	1947	chr2:54873496	C	T	R1584C	Missense	NM_003128	0.344	0.027	0.35
DNAH5	7136	chr5:13719002	C	A	R4163I	Missense	NM_001369	0.324	0.024	0.35
MAGI2	2237	chr7:77764508	A	T	I954N	Missense	NM_012301	0.392	0.036	0.35
LARP4B	6536	chr10:875513	T	C	I313V	Missense	NM_015155	0.388	0.035	0.35
STAM	6536	chr10:17726706	G	A	R53K	Missense	NM_003473	0.414	0.041	0.35
CYP2C19	705	chr10:96602752	G	A	V374I	Missense	NM_000769	0.368	0.033	0.35
INTS4	2238	chr11:77635919	C	T	R464Q	Missense	NM_033547	0.44	0.045	0.35
FBN1	1739	chr15:48797267	A	G	C639R	Missense	NM_000138	0.396	0.036	0.35
CREBBP	1781	chr16:3788618	G	A	R1446C	Missense	NM_004380	0.306	0.022	0.35
CREBBP	2000756	chr16:3786796	C	G	W1434S	Missense	NM_001079846	0.368	0.033	0.35
CREBBP	671204	chr16:3843416	G	C	T396R	Missense	NM_001079846	0.344	0.027	0.35
CREBBP	3492	chr16:3788596	A	T	I1415N	Missense	NM_001079846	0.328	0.025	0.35
SMARCE1	1346	chr17:38793763	T	C	Y73C	Missense	NM_003079	0.32	0.023	0.35
BRCA1	2237	chr17:41242984	G	C	Q1388E	Missense	NM_007294	0.39	0.035	0.35
BRCA1	2237	chr17:41243523	G	A	S1342L	Missense	NM_007294	0.368	0.033	0.35
BUB1B	671204	chr15:40462300	G	T	D73Y	Missense	NM_001211	0.452	0.048	0.35
BUB1B	11_17815	chr15:40510712	T	C	L969P	Missense	NM_001211	0.514	0.072	N/A
CAPN6	07_16582	chrX:110489945	C	T	V596I	Missense	NM_014289	0.416	0.041	0.35
DIS3	2000756	chr13:73346338	C	T	D458N	Missense	NM_001128226	0.402	0.037	0.35
ERCC2	09_4178	chr19:45872365	G	A	T25I	Missense	NM_001130867	0.316	0.023	0.35
FOXK1	148632	chr7:4796626	A	G	N351S	Missense	NM_001037165	0.296	0.02	0.35
FTSJD1	11_6165	chr16:71319399	T	C	H142R	Missense	NM_001099642	0.424	0.041	0.35
FTSJD1	07_16582	g.chr16:71319480C>T	C	T	p.W115*	Nonsense	NM_001099642			N/A
GABRA3	09_4178	chrX:151532936	T	A	E36V	Missense	NM_000808	0.428	0.042	0.35
GLB1L	11_6165	chr2:220107983	G	C	D42E	Missense	NM_024506	0.418	0.041	0.35
GNAI2	05_6986	chr3:50284505	G	C	R2T	Missense	NM_001166425	0.434	0.043	0.35
GRIA2	11_17815	chr4:158233974	C	T	R158W	Missense	NM_001083620	0.394	0.036	0.35
LHFPL4	148632	chr3:9594227	C	A	W46L	Missense	NM_198560	0.4	0.037	0.35
MASTL	3492	chr10:27458958	C	T	T357M	Missense	NM_001172304	0.358	0.031	0.35
NR1H3	11_6165	chr11:47290233	G	A	D384N	Missense	NM_001130101	0.342	0.027	0.35
NR1H3	4133	chr11:47282193	C	T	R111C	Missense	NM_001130102	0.398	0.037	0.35
NUP50	148632	chr22:45579373	G	C	Q364H	Missense	NM_153645	0.354	0.03	0.35
NUP50	148632	chr22:45579374	C	T	L365F	Missense	NM_153645	0.598	0.115	0.55
OR11H1	3492	chr22:16449539	A	G	V89A	Missense	NM_001005239	0.438	0.045	0.35
PHC2	06_2532	chr1:33820083	G	A	H492Y	Missense	NM_198040	0.394	0.036	0.35

RLIM	2000756	chrX:73812846	G	A	L102F	Missense	NM_016120	0.376	0.033	0.35
RORA	2000756	chr15:60803461	C	T	G207S	Missense	NM_134262	0.324	0.024	0.35
TRIM39	148632	chr6:30297210	C	G	P39R	Missense	NM_172016	0.438	0.045	0.35
TRPC4	05_6986	chr13:38320391	G	A	R194C	Missense	NM_001135956	0.42	0.041	0.35
ZNF143	9534	chr11:9530210	T	C	F398L	Missense	NM_003442	0.354	0.03	0.35
ABCA7	671204	g.chr19:1046406	G	A	p.V541_splice	Splice Site	NM_019112			N/A
ACOX2	1781	g.chr3:58510332	C	T	p.R449R	Splice Site	NM_003500			N/A
ACTG2	2000756	g.chr2:74141809_74141810	GA	--	p.E206fs	Indel	NM_001615			N/A
ALS2CR11	1947	chr2:202430450	--	A		Splice Site	NM_001168221			N/A
ALS2CR12	65115	g.chr2:202207155	C	A	p.L155_splice	Splice Site	NM_139163			N/A
ANGPT2	2012	g.chr8:6389855	G	A	p.Q148*	Nonsense	NM_001147			N/A
APC	3492	g.chr5:112176863	C	T	p.R1858*	Nonsense	NM_001127511			N/A
ARHGAP44	05_6986	g.chr17:12852538	G	T	p.E315*	Nonsense	NM_014859			N/A
ARHGEF15	671204	g.chr17:8216328	C	--	p.G230fs	Indel	NM_173728			N/A
ARID1A	07_16582	g.chr1:27105930_27105931	--	G	p.G1847fs	Indel	NM_006015			N/A
ARID4B	1739	g.chr1:235424022	--	ACT	p.A18delinsSA	Indel	NM_001206794			N/A
ARID5B	148632	g.chr10:63850714	G	T	p.E498*	Nonsense	NM_032199			N/A
ARNT2	9534	g.chr15:80866561	G	A	p.Q463Q	Splice Site	NM_014862			N/A
ATCAY	6536	g.chr19:3907733	C	T	p.D120D	Splice Site	NM_033064			N/A
AXIN1	148632	g.chr16:396299	C	A	p.E243*	Nonsense	NM_003502			N/A
BCOR	705	g.chrX:39932914	G	T	p.S562*	Nonsense	NM_001123385			N/A
BTN3A2	11_17815	g.chr6:26370832	G	T	p.D239_splice	Splice Site	NM_007047			N/A
C14orf43	2039	g.chr14:74193532	C	T	p.V769_splice	Splice Site	NM_194278			N/A
C16orf11	148632	g.chr16:613726	G	--	p.V144fs	Indel	NM_145270			N/A
C1orf141	540	g.chr1:67592939	T	A		Splice Site	NM_001013674			N/A
CA1	07_16582	g.chr8:86245760_86245761	--	A	p.L148fs	Indel	NM_001738			N/A
CEP135	1781	g.chr4:56831978	AAA	--	p.333_333del,	Indel	NM_025009			N/A
CEP97	05_6986	g.chr3:101451414_101451415	--	A	p.P215fs	Indel	NM_024548			N/A
CHRNB1	1947	g.chr17:7350821	G	--		Splice Site	NM_000747			N/A
CHST5	142990	g.chr16:75563606	G	A	p.P226L	Missense	NM_024533			N/A
CHST5	6536	g.chr16:75563521	C	T	p.W254*	Nonsense	NM_024533			N/A
CNTNAP5	1781	g.chr2:124999971	G	T	p.W127_splice	Splice Site	NM_130773			N/A
COL6A6	05_6986	g.chr3:130285860	C	T	p.R533*	Nonsense	NM_001102608			N/A
DHX9	09_4178	g.chr1:182827275	T	A	p.L237*	Nonsense	NM_001357			N/A
ECEL1	410	g.chr2:233349690	C	T	p.N322_splice	Splice Site	NM_004826			N/A
EIF3B	4133	g.chr7:2412384_2412385	TG	--	p.S588fs	Indel	NM_003751			N/A
ENC1	2000756	g.chr5:73931844_73931845	--	ACT	p.S156fs	Indel	NM_003633			N/A
ENC1	36773720	g.chr5:73932240	T	A	p.H24L	Missense	NM_003633			N/A
EP300	7441	g.chr22:41565621	G	T	p.G1429_splice	Splice Site	NM_001429			N/A
ERAP2	2000136	g.chr5:96230974	G	T	p.E384*	Nonsense	NM_022350			N/A
ERBB2IP	2000120	g.chr5:65321806	G	T	p.E340_splice	Splice Site	NM_018695			N/A
ESRP1	36773720	g.chr8:95654183	G	A	p.V45_splice	Splice Site	NM_017697			N/A
EXOC6	505	g.chr10:94659373	A	T	p.K144*	Nonsense	NM_019053			N/A
FAM194B	09_4178	g.chr13:46149035	C	T	p.W331*	Nonsense	NM_182542			N/A
FAM207A	07_16582	g.chr21:46380085	T	G	p.K118_splice	Splice Site	NM_058190			N/A
FAT3	4332	g.chr11:92539627	C	T	p.R3065*	Nonsense	NM_001008781			N/A
FAT4	2128	g.chr4:126371875	C	T	p.S3235L	Missense	NM_024582			N/A
FAT4	7136	g.chr4:126372080	C	G	p.Y3303*	Nonsense	NM_024582			N/A
FILIP1	9534	g.chr6:76022271	G	A	p.R1093*	Nonsense	NM_015687			N/A
FKBP9	9534	g.chr7:33014299_33014300	--	TT	p.L98fs	Indel	NM_007270			N/A
GABRB1	7441	g.chr4:47163485	C	T	p.R154*	Nonsense	NM_000812			N/A
GRM4	2237	g.chr6:34101247	C	T	p.W9*	Nonsense	NM_000841			N/A
GSTM4	65115	g.chr1:110199381	C	A	p.Y28*	Nonsense	NM_000850			N/A
GTF3C1	122891	g.chr16:27506083	C	T	p.K926_splice	Splice Site	NM_001520			N/A
HARS	2128	g.chr5:140054646	C	A	p.E423*	Nonsense	NM_002109			N/A
HOGA1	10_5283	g.chr10:99358863	G	T	p.E120*	Nonsense	NM_138413			N/A
HOXB3	4133	g.chr17:46629590	G	--	p.L83fs	Indel	NM_002146			N/A
IGSF9B	4133	g.chr11:133790388	G	A	p.R1078*	Nonsense	NM_014987			N/A
IL17RD	122891	g.chr3:57136550	TG	--	p.312_312del	Indel	NM_017563			N/A
IRAK1	2000136	g.chrX:153278656	C	A	p.E590*	Nonsense	NM_001569			N/A
IRAK1	4133	g.chrX:153278880	T	C	p.Y515C	Missense	NM_001569			N/A
ITM2B	1739	g.chr13:48833055	C	A	p.Y229*	Nonsense	NM_021999			N/A
KDM6A	11_3318	g.chrX:44966782	G	T	p.E1335_splice	Splice Site	NM_021140			N/A
KDM6A	148632	g.chrX:44942839	G	A	p.G1140E	Missense	NM_021140			N/A
KDM6A	11_3318	g.chrX:44950030	A	G	p.I1267V	Missense	NM_021140			N/A
KDM6A	3492	g.chrX:44969442	T	C	p.L1375P	Missense	NM_021140			N/A
KDM6A	671204	g.chrX:44938456	A	G	p.T1002A	Missense	NM_021140			N/A
KIAA1267	2039	g.chr17:44117170	T	A	p.K701*	Nonsense	NM_015443			N/A
KLHL4	36773720	g.chrX:86888841	C	T	p.R548*	Nonsense	NM_019117			N/A
KNTC1	36773720	g.chr12:123052911	C	T	p.R570*	Nonsense	NM_014708			N/A
KRTAP13-4	05_6986	g.chr21:31802760	G	A	p.W56*	Nonsense	NM_181600			N/A
LMLN	36773720	g.chr3:197717491	C	T	p.R331*	Nonsense	NM_033029			N/A
MAGI1	3492	g.chr3:65415431_65415432	AC	--	p.V644fs	Indel	NM_001033057			N/A
MAGT1	148632	g.chrX:77131056	C	T	p.W79*	Nonsense	NM_032121			N/A
MGA	505	g.chr15:42021360	A	T	p.I1220_splice	Splice Site	NM_001164273			N/A
MGA	11_3318	g.chr15:42003509	C	T	p.R1016*	Nonsense	NM_001080541			N/A
MPG	609	g.chr16:129298	--	C	p.T3fs,	Indel	NM_002434			N/A
MPHOSPH9	3492	g.chr12:123694652	A	T	p.L230*	Nonsense	NM_022782			N/A
MUC16	05_6986	g.chr19:8974101	G	A	p.G14190G	Splice Site	NM_024690			N/A
MUC16	05_6986	g.chr19:8974101	G	A	p.G14190G	Splice Site	NM_024690			N/A
MUC16	65115	g.chr19:9076729	G	A	p.R3573C	Missense	NM_024690			N/A
MUC16	1781	g.chr19:9069032	G	T	p.S6138R	Missense	NM_024690			N/A
MUC4	4332	g.chr3:195508174	G	T	p.P3298H	Missense	NM_018406			N/A
MUC4	131169	g.chr3:195492248	C	T	p.W4436*	Nonsense	NM_018406			N/A
MYB	7441	g.chr6:135518098	G	T		Splice Site	NM_005375			N/A
MYB	7441	g.chr6:135518099	G	T		Splice Site	NM_005375			N/A

MYCBP2	1947	g.chr13:77663083	G	A	c.10495C>T	Nonsense	NM_015057			N/A
N4BP1	11_6165	g.chr16:48595187	G	T	c.1367C>A	Nonsense	NM_153029			N/A
NAB2	505	g.chr12:57484990	TCC	--	c.166_168del	Indel	NM_005967			N/A
NCAM2	36773720	g.chr21:22790859	A	T	c.1450A>T	Nonsense	NM_004540			N/A
NFIB	2020	chr9:14120513	GA	--	c.1170_1171del	Indel	NM_005596			N/A
NFIB	540	g.chr9:14150203	G	C	c.747C>G	Nonsense	NM_005596			N/A
NFIX	2012	chr19:13184245	--	TT	c.632_633insTT	Indel	NM_002501			N/A
NOTCH1	7097	g.chr9:139412240	C	A	c.1405G>T	Missense	NM_017617			N/A
NOTCH1	3492	g.chr9:139390907	G	C	c.7284C>G	Missense	NM_017617			N/A
NOTCH1	3492	g.chr9:139390906	G	C	c.7285C>G	Missense	NM_017617			N/A
NOTCH1	2012	g.chr9:139405607	G	A	c.2584C>T	Nonsense	NM_017617			N/A
OSR1	10_5283	g.chr2:19552135_19552136	TT	--	c.701_702delAA	Indel	NM_145260			N/A
OTP	09_4178	g.chr5:76926516	A	G	c.551T>C	Missense	NM_032109			N/A
PHF20	3492	g.chr20:34430571_34430572	--	A	c.160_161insA	Nonsense	NM_016436			N/A
POU2F3	9534	g.chr11:120175748	C	T	c.454C>T	Nonsense	NM_014352			N/A
PTPRG	380	g.chr3:62204575	G	T	c.2206G>T	Nonsense	NM_002841			N/A
PTPRH	111097	g.chr19:55708669	C	T	c.1806G>A	Nonsense	NM_002842			N/A
PTPRK	09_4178	g.chr6:128410928_128410929	--	C	c.1371_1372insG	Indel	NM_002844			N/A
RABGAP1	2012	g.chr9:125748532	G	A	c.424G>A	Missense	NM_012197			N/A
RABGAP1	2012	g.chr9:125748604	G	T	c.496G>T	Nonsense	NM_012197			N/A
RLF	2237	g.chr1:40705233	C	G	c.4859C>G	Nonsense	NM_012421			N/A
RNF219	07_16582	g.chr13:79212993	C	A	c.514G>T	Nonsense	NM_024546			N/A
RUNX1	980452	g.chr21:36171600	G	C	c.884C>G	Nonsense	NM_001001890			N/A
RYR2	705	g.chr1:237868513	G	A	c.9450G>A	Splice Site	NM_001035			N/A
RYR3	2012	g.chr15:34078011	C	A	c.9417C>A	Nonsense	NM_001036			N/A
RYR3	1346	g.chr15:33872202	A	G	c.1294A>G	Missense	NM_001036			N/A
RYR3	671204	g.chr15:33954455	G	A	c.4724G>A	Missense	NM_001036			N/A
RYR3	09_4615	g.chr15:34157408	A	G	c.14594A>G	Missense	NM_001036			N/A
SCUBE3	111097	g.chr6:35209689	T	A	c.1417_splice	Splice Site	NM_152753			N/A
SELP	2237	g.chr1:169586615	A	T	c.132T>A	Nonsense	NM_003005			N/A
SF3A3	148632	g.chr1:38453346	G	A	c.202C>T	Nonsense	NM_006802			N/A
SLC22A12	1781	g.chr11:64361031	C	T	c.661C>T	Splice Site	NM_144585			N/A
SLC37A3	6277	g.chr7:140055468	C	T	c.618G>A	Splice Site	NM_207113			N/A
SMR3B	07_16582	g.chr4:71255545	C	--	c.220delC	Indel	NM_006685			N/A
TEX15	07_16582	g.chr8:30694753	C	T	c.7898G>A	Nonsense	NM_031271			N/A
TIGD6	1947	g.chr5:149375303	--	C	c.609_610insG	Indel	NM_030953			N/A
TNN	540	g.chr1:175105958	A	G	c.3429A>G	Splice Site	NM_022093			N/A
TNRC18	505	g.chr7:5401258	--	G	c.4628_4629insC	Indel	NM_001080495			N/A
TOB1	142990	g.chr17:48940492	--	GG	c.887_888insCC	Indel	NM_005749			N/A
TXNIP	2012	g.chr1:145439839	--	T	c.385_386insT	Indel	NM_006472			N/A
USP35	671204	g.chr11:77910662	G	A	c.828G>A	Nonsense	NM_020798			N/A
ZCCHC16	122891	g.chrX:111698767	C	T	c.811C>T	Nonsense	NM_001004308			N/A
ZNF35	09_4178	g.chr3:44700517_44700518	--	T	c.662_663insT	Indel	NM_003420			N/A
ZNF507	2000120	g.chr19:32844617	C	G	c.881C>G	Nonsense	NM_001136156			N/A

Supplementary Table 5. CHASM context table

CHASM v1.0.5

Base/To	C*pG	CpG*	TpC*	G*pA	A	C	G	T
A	9	62	13	18		13	47	20
C		9		13	14		21	64
G	10		19		54	14		18
T	84	12	16	14	13	42	18	

Ratio

Base/To	C*pG	CpG*	TpC*	G*pA	A	C	G	T
A	0.015	0.100	0.021	0.029	0.000	0.021	0.076	0.032
T	0.136	0.019	0.026	0.023	0.021	0.068	0.029	0.000
C	0.000	0.015	0.000	0.021	0.023	0.000	0.034	0.104
G	0.016	0.000	0.031	0.000	0.088	0.023	0.000	0.029

Supplementary Table 6. GISTIC2.0 output of significantly altered peaks with associated genes

Cytoband	Gain/Loss	q value	Residual q value	Wide peak boundaries	Genes in wide peak
4q12	Gain	8.35E-02	8.35E-02	chr4:54439741-57173662	KIAA1211
10q11.22	Gain	8.35E-02	8.35E-02	chr10:46584418-46740464	BMS1P1
5q13.2	Loss	1.25E-06	1.67E-05	chr5:69784490-69804965	SMA5
6q23.3	Loss	2.16E-05	2.16E-05	chr6:135606716-135709084	AHI1
17q12	Loss	6.36E-05	6.36E-05	chr17:34581301-34625321	CCL3L1
4p16.1	Loss	9.52E-05	9.52E-05	chr4:9213282-9241393	USP17
1q21.1	Loss	1.72E-04	1.72E-04	chr1:144168171-144188821	[SRGAP2P2]
10p12.33	Loss	6.81E-04	6.81E-04	chr10:18064970-18168639	hsa-mir-511-2, MIR511-2
17q21.31	Loss	2.00E-03	2.00E-03	chr17:44416824-44594703	ARL17A
12q12	Loss	2.16E-05	3.99E-03	chr12:44917052-50453489	ACA2b, ACCN2
7p11.2	Loss	6.01E-03	6.01E-03	chr7:56888731-56929688	[MIR4283-1]
10q11.22	Loss	8.20E-03	8.20E-03	chr10:49267840-49371362	FRMPD2
8q13.1	Loss	9.29E-03	9.29E-03	chr8:67361064-67405829	C8orf46
14q11.2	Loss	9.29E-03	9.29E-03	chr14:19685100-19806384	[POTEG]
16p13.11	Loss	1.27E-02	1.27E-02	chr16:16415188-16423199	PKD1P1
9p22.3	Loss	2.08E-03	1.45E-02	chr9:15920225-17166895	CNTLN
15q15.3	Loss	1.65E-02	1.65E-02	chr15:43940967-43987876	CKMT1A
12q12	Loss	9.52E-05	1.81E-02	chr12:42555313-42706784	ZCRB1
15q11.2	Loss	2.92E-02	2.92E-02	chr15:20747013-20776594	GOLGA8C
1p36.21	Loss	3.34E-02	3.34E-02	chr1:13183193-13328819	PRAMEF3
7q22.1	Loss	3.34E-02	3.34E-02	chr7:102136868-102194714	SPDYE2
15q13.1	Loss	3.73E-02	3.73E-02	chr15:28775191-28835310	GOLGA8F
5q13.2	Loss	2.78E-04	4.48E-02	chr5:70400536-70671617	PMCHL2
12q13.3	Loss	7.22E-04	5.82E-02	chr12:57125450-58088470	hsa-mir-616, has-mir-1228, OS9
9p23	Loss	6.01E-03	6.68E-02	chr9:14088168-14117958	NFIB
12q24.33	Loss	7.97E-02	7.97E-02	chr12:132636768-133149100	FBRSL1
15q26.3	Loss	7.97E-02	7.97E-02	chr15:102297620-102302961	[TARSL2]
8p23.1	Loss	9.09E-02	9.09E-02	chr8:7596507-7679478	DEFB107A
9q13	Loss	3.73E-02	9.09E-02	chr9:67945162-68315950	ANKRD20A1
9q34.3	Loss	9.09E-02	9.09E-02	chr9:133553883-141213431	hsa-mir-602, has-mir-4292, ACA17, hsa-mir-126, U36C, U62B, FAM157B
9p12	Loss	4.29E-02	9.11E-02	chr9:41325222-41954730	MGC21881
8q24.3	Loss	9.41E-02	9.41E-02	chr8:145317721-145491107	SCXB
14q32.33	Loss	1.04E-01	1.04E-01	chr14:106370311-106379028	[KIAA0125]
9q21.11	Loss	6.35E-02	1.16E-01	chr9:70176686-70489871	CBWD5
12p13.31	Loss	1.30E-01	1.30E-01	chr12:7883332-7945496	NANOG
9p24.3	Loss	1.95E-01	1.95E-01	chr9:1-24561	WASH1
4q31.3	Loss	2.20E-01	2.20E-01	chr4:152679880-153560923	hsa-mir-3140, TMEM154
13q14.3	Loss	2.20E-01	2.20E-01	chr13:35782795-115169878	hsa-mir-1267, has-mir-4306, hsa-mir-623, hsa-mir-3170, hsa-mir-92a-1, hsa-mir-622, hsa-mir-3169, hsa-mir-1297, hsa-mir-759, hsa-mir-15a, ACA31, hsa-mir-3168, hsa-mir-621, hsa-mir-4305, ZNF828
7p22.3	Loss	2.47E-01	2.47E-01	chr7:550442-590032	PRKAR1B

Supplementary Table 7. Mean CHASM gene expression

Normalized to mean expression of 5.0960 with respect to Illumina HT-12 control probes

Illumna Probe ID	Gene	Mean Expression
1710193	ABCA7	6.41864
2570100	ABCA7	6.69078
5810091	ABCA7	6.43061
1010114	ACOX2	6.53886
4610390	ACTB	11.9414
5270730	ACTB	10.2536
5570132	ACTB	11.6937
4610431	ACTG2	10.2471
1450431	ALS2CR11	6.34432
2100626	ALS2CR12	6.48405
3180689	ANGPT2	6.58412
3360398	ANGPT2	6.46898
3450066	ANGPT2	6.57173
5720722	APC	6.46905
3610601	ARHGEF15	6.30132
2030471	ARID1A	6.28684
6280411	ARID1A	7.45068
2470603	ARID4B	7.96643
2940722	ARID4B	6.7175
6590722	ARID4B	7.5288
1410408	ARID5B	8.19648
4180307	ARNT2	6.9004
2750674	ASAP2	6.62593
5340646	ASAP2	7.00366
7050577	ATCAY	6.304
580537	ATM	6.28938
4250008	ATM	7.17261
6840605	ATM	7.03161
7330592	ATM	6.49995
3460754	AXIN1	6.88441
5550398	AXIN1	6.48102
510576	BCOR	7.15039
1770435	BCOR	6.58323
6760273	BCOR	6.52156
540411	BRCA1	6.36148
2810465	BRCA1	6.63313
3120672	BRCA1	6.49771
5820703	BRCA1	6.46249
1440450	BRD1	6.85148
2570253	BTN3A2	6.5883
4610674	BTN3A2	6.60382
1090047	BUB1B	6.47398
6660544	C10orf65	6.59107
5560154	C14orf43	6.41611
5890468	C14orf43	6.46055
6370201	C14orf43	7.00858
1030170	C16orf11	6.44277
6020437	C16orf11	6.41933
3400286	C1orf141	6.27277
6650253	C1orf141	6.68719
620440	C21orf70	6.67855
2600519	C21orf70	6.68704
3170746	C21orf70	6.46604
110037	C6orf170	6.61991
3930671	C6orf170	7.22948
2190139	CA1	6.29509
7100711	CALM2	10.5844
2120379	CAPN6	6.7934
270022	CEP135	6.53797
7400575	CEP97	6.50661
7650639	CHRNB1	6.72915
2630114	CHST5	6.30131
3940725	CHST5	6.48897
3390017	CNDP2	8.90573
1580243	CNTNAP5	6.33225
6660079	CNTNAP5	6.28003
780520	COL6A6	6.45451

6560438	CREBBP	6.67332
6840148	CREBBP	7.4646
3360253	CTNNB1	6.59003
3800671	CTNNB1	7.48288
4230376	CTNNB1	6.45225
4260379	CTNNB1	7.52588
5130681	CTNNB1	6.51957
5810184	CTNNB1	6.66339
7210095	CTNNB1	6.47108
5220717	CYP2C19	6.46303
630475	DHODH	6.57291
7380427	DHODH	6.47309
2900379	DHX9	6.51653
3930689	DHX9	6.84736
6900725	DHX9	6.82191
7210008	DHX9	6.43846
4640719	DIS3	6.68548
2350554	DNAH5	6.31266
6660747	ECEL1	6.33332
4390136	EIF3B	9.25813
5390280	EIF3B	6.69108
6290603	EIF3B	7.92255
7150563	ENC1	7.52845
7570068	EP300	6.72496
2260731	ERAP2	6.72397
1450441	ERBB2IP	6.49776
4480037	ERBB2IP	6.43102
4260435	ERCC2	6.82322
2850014	EXOC6	6.53012
7330196	EXOC6	6.68605
7570278	EXOC6	6.33052
2340253	FAT3	6.58899
1190338	FAT4	6.53176
6200095	FAT4	6.47306
4480593	FBN1	6.3859
1850504	FBXW7	7.27674
3930184	FBXW7	6.60274
5560661	FBXW7	7.18559
6450309	FBXW7	6.43277
70520	FGFR4	6.36485
4120433	FGFR4	6.2827
6660240	FGFR4	6.34323
6200600	FILIP1	6.47257
4260114	FKBP9	6.3848
5290086	FKBP9	6.51746
460192	FLJ32682	6.45708
6380168	FOXK1	6.5135
6860544	FOXK1	7.17025
5570615	FTSJD1	6.69214
2340093	GABRA3	6.44828
6130692	GABRB1	6.53772
2490360	GLB1L	6.47836
1300730	GNAI2	7.64595
1660246	GNB4	6.67904
2940484	GNB4	6.62279
6220750	GRIA2	6.60288
130091	GRIN2B	6.36967
1660494	GRIN2B	6.28
6840255	GRM4	6.49204
4060707	GSTM4	6.55129
6900592	GSTM4	6.42155
2750296	GTF3C1	6.82225
3940551	HARS	7.77877
2350575	HOXB3	6.48609
1770753	HRAS	6.69321
7160093	HRAS	6.41346
3180048	IDH1	6.84564
6270670	IDH1	7.50331
1240180	IGSF9B	6.58877
3450091	IL17RD	6.55565
4060017	IL17RD	8.63645
4890193	IL17RD	6.48933

990037	INTS4	6.58391
1660441	INTS4	6.5151
2810121	INTS4	7.27047
4040564	IRAK1	7.70589
540347	ITM2B	6.50376
6380315	ITM2B	9.68494
1580338	KIAA1267	7.61999
1850079	KIAA1267	7.5746
2650753	KIAA1324L	6.56477
6660152	KLHL12	7.08515
6840500	KLHL12	6.80441
1050072	KLHL4	6.32581
1510767	KLHL4	6.27374
3190524	KNTC1	6.98275
5130390	KRTAP13-4	6.57257
6100619	LARP4B	7.54022
4120093	LHFPL4	6.41936
4540047	LMLN	6.39357
870402	MAGI1	6.65257
1070296	MAGI1	6.42785
7210091	MAGI1	6.31298
2260754	MAGI2	6.35689
3190626	MAGT1	9.22476
20521	MASTL	6.6382
580470	MASTL	6.36352
2630711	MCM4	6.89527
6020170	MCM4	6.9828
3190364	MGA	6.97449
4780605	MGA	6.56299
6840356	MGEA5	8.2441
1850128	MPG	6.4619
2600189	MPG	6.60663
5720403	MPG	6.30717
6590707	MPHOSPH9	6.72824
2490070	MUC16	6.65653
110471	MUC4	6.35982
2450072	MUC4	6.5567
4260450	MUC4	6.62504
4900014	MUC4	6.6459
5260746	MUC4	6.34376
7380670	MYB	7.52676
6650451	MYCBP2	7.26145
70743	N4BP1	6.54058
2680561	N4BP1	6.92053
6250440	NAB2	6.9002
5080292	NCAM2	6.35942
1710168	NDUFS3	8.36375
5960133	NFIB	10.7585
5720129	NFIX	9.17124
5080167	NOTCH1	8.03905
3710450	NR1H3	6.90927
3940520	NT5C3	7.63872
7000398	NT5C3	7.0866
1990674	NUP50	6.5316
3990356	NUP50	6.28937
5890291	NUP50	6.32132
5690673	OR11H1	6.44695
6980414	OR11H1	6.83878
3940500	OSR1	8.5101
1940500	OTP	6.46938
2030477	OTP	6.55887
3360338	PAX2	6.34521
4830136	PAX2	6.29702
6450767	PAX2	6.5111
830142	PHC2	6.59459
1500524	PHC2	6.5853
6020452	PHC2	6.31558
4210241	PHF20	6.87943
1240520	PIK3CA	6.25603
4880367	PIK3CA	6.72328
2070661	POU2F3	6.29587
2640093	POU2F3	6.67684

6290082	PRKG1	6.54854
6860288	PRKG1	6.36815
6840072	PTEN	7.08986
450369	PTPRG	6.66824
7400768	PTPRH	6.50396
6280201	PTPRK	7.55192
5700273	RAB3GAP2	7.50377
2850538	RABGAP1	8.38912
2810382	RALA	8.06641
110754	RBM35A	6.71827
840010	RICH2	6.8414
520309	RLF	6.78895
1430333	RNF12	6.47884
1470402	RNF12	6.46334
7040368	RNF12	6.54287
2510292	RNF219	7.23447
1110180	RORA	6.65296
3940703	RORA	6.56412
4390553	RORA	6.31989
4760072	RORA	6.40746
6110500	RORA	6.28688
6770240	RORA	6.47536
4390438	RUNX1	6.30011
7050278	RUNX1	6.37665
7400368	RUNX1	7.73119
1660241	RYR2	6.5425
430253	RYR3	6.42735
240070	SCUBE3	6.35505
4810468	SELP	6.34337
1230747	SF3A3	7.80757
1450500	SLC22A12	6.50205
4640324	SLC22A12	6.47542
5690575	SLC22A12	6.30119
3420332	SLC37A3	7.34276
3800397	SLC37A3	6.92143
7560377	SLC37A3	6.64469
3130360	SLC9A4	6.46489
7320619	SLC9A4	6.50906
1770086	SMARCA2	6.52815
5290474	SMARCA2	8.3582
2650064	SMARCE1	7.46816
620326	SMR3B	7.60332
1770037	SPTBN1	6.76924
2750609	SPTBN1	6.35707
5390487	SPTBN1	8.14686
770619	STAM	6.65039
3990324	TANC1	7.3938
6620553	TEX15	6.56392
1050133	TIGD6	6.62346
6650433	TLN1	6.843
2750242	TNN	6.6276
2190367	TNRC18	6.60398
2630162	TNRC18	6.4807
4390300	TOB1	8.3704
4180500	TP53	6.97037
160240	TRIM39	6.29509
6040703	TRIM39	6.76473
7510273	TRIM39	6.43063
10367	TRPC4	6.5029
1240440	TXNIP	9.95036
6580059	UCP2	6.68936
6510468	USP35	6.64416
2710731	UTX	7.02903
430731	WDR53	6.40324
240438	ZCCHC16	6.30308
5700162	ZCCHC16	6.43173
3830403	ZNF143	6.93108
5090010	ZNF35	6.50586
7380131	ZNF507	6.5777

Supplementary Table 8. Whole genome coverage data

Genotyping performed using HumanOmni 2.5-8v1

Whole Genome Coverage Data	2012-TU	2012-NL	2128-TU	2128-NL	505-TU
Sequenced fragment length	341 +/- 28 bp	321 +/- 22 bp	359 +/- 23 bp	333 +/2 24 bp	339 +/- 23bp
Passing Filter Data Volume (Gigabases)	116.7	121	119.3	112.9	128.3
Passing Filter and Aligned Data (Gigabases)	103.4	106.7	106	100.1	114
% Passing Filter and Aligned Bases >= Q30	87.4%	87.3%	83.6%	90.9%	83.1%
Non-N Reference Mean Coverage	34.1x	35.1x	34.8x	32.8x	37.9x
Percentage of Non-N Reference Covered	97.9%	97.9%	97.9%	97.9%	98.2%
Genotyping Array % Concordance	98.7%	99.3%	99.3%	99.3%	99.3%

Whole Genome Coverage Data	505-NL	6536-TU	6536-NL	131169-TU	131169-NL	Mean
Sequenced fragment length	342 +/- 21 bp	338 +/- 16 bp	333 +/- 15 bp	343 +/- 16 bp	323 +/- 17 bp	337.2
Passing Filter Data Volume (Gigabases)	122.1	126.5	127.9	155	119.7	124.9
Passing Filter and Aligned Data (Gigabases)	108.3	113.3	113.6	139.1	107.9	111.2
% Passing Filter and Aligned Bases >= Q30	89.4%	86.9%	87.4%	85.7%	88.9%	87.1%
Non-N Reference Mean Coverage	35.8x	37.4x	37.4x	45.3x	35.6x	36.6x
Percentage of Non-N Reference Covered	98.1%	98.1%	98.1%	97.9%	97.8%	98.0%
Genotyping Array % Concordance	99.3%	99.3%	99.3%	99.3%	99.3%	99.2%

Supplementary Table 9. Validated ACC structural variants

SampleID	SV Type	Gene 1	Distance To Gene 2 (bp)	Breakpoint 1 (hg19)	Gene 2	Distance To Gene 2 (bp)	Breakpoint 2 (hg19)	Fwd Primer	Rev Primer
000505	DEL	MAN1A1	163162	chr6:119834088	MYB	0	chr6:135534745	CAAACTCGTCACTTAAAGCCATCTT	GCCTCCTGTTAAAAGTCAAGTTCTG
000505	CTX	NFIB	0	chr9:14113737	MAN1A1	163839	chr6:119834765	CAATTTCTGCCTCTCCCTAAAACAA	GAAGATACCTCAGTCCTTTCCTTGT
000505	CTX	MYB	0	chr6:135534691	NFIB	0	chr9:14113422	CTTCTCTTTTGTCTGAGTGAACACC	GAGCTTCAGGGGATATATGACTCAG
000505	CTX	MSN	0	chrX:64961204	RLN2	15822	chr9:5284046	GTGCCCTGATCCAAGTTTACTCAA	GAGCCTCTTCACACTTTCCCAG
002012	INS	FGFR2	0	chr10:123276317	FGFR2	240036	chr10:122997808	AGCAAATATTCACAGAGCAGATTCG	GGTTCTGGGTCCTCATTCTGATATT
002012	INS	RBMS3	0	chr3:29657439	RBMS3	0	chr3:29619344	GAATTCCATTTCCTAAGTGACCCA	GCTCTTCAGTCACACATTTATAGGC
002012	INS	RBMS3	0	chr3:29753932	RBMS3	0	chr3:29687489	CATTTTCCCCTCGAATAAAGCCTAC	AGAGTCTCAGCCACTTTTATTGACT
002012	DEL	TAX1BP1	0	chr7:27783375	TAX1BP1	0	chr7:27783724	TGGGTCATATGTGGAGTGTTACTAA	GGGCACTCAGTTATGTATACAGCTA
002012	CTX	PIK3R1	185096	chr5:67782745	KANK1	45812	chr9:791918	TGGAGTTCAAATCTACCAAGCTTCA	ACAATGCAGTGACTATTGTGGAATG
002128	ITX	SKAP2	34220	chr7:26938561	SNX10	74036	chr7:26487985	CTTACTGCATCATTTAGCTGTGACC	TATCGTAGTTGTAATGCTTGGAGGG
006536	CTX	ADAMTS20	131085	chr12:43616927	CBFA2T2	0	chr20:32211711	GAGAGAATTTGATTGCTGTGGTTGT	ATAGGGTTAATGCATGGACACAGTA
006536	INS	HOXC4	0	chr12:54439321	ADAMTS20	33661	chr12:43714351	TCCATAGTGAACATAACAGTCCTCG	AGTAGAGAGTAGGCTTTGCATTGAA
006536	DEL	NELL2	0	chr12:44948178	ATXN7L3B	487313	chr12:74444238	CCCAAATATGATGTAGTAAAGCGCA	AAGGGAGTAGTGTGTAAAGAGGATC
006536	INS	SLC16A7	497644	chr12:60673052	CALCOCO1	0	chr12:54114812	GGCAGAGAATTACAGTGTTGCTTAG	GAGCTCTCTACCATCTTTCCAAATG
006536	ITX	RNF150	0	chr4:141988848	TTC29	18525	chr4:147609654	CAATCAGCCCAATATGAAAGAACCA	ATCCAGCTGTCTATACTTTGCAACT
006536	DEL	VAV2	0	chr9:136804823	QSOX2	0	chr9:139127613	AAATTTATCGTGGCAGACTTTCAGG	TGCGAAGTTCCATACATCATCCTTA
131169	DEL	GIP	0	chr17:47037095	GIP	0	chr17:47037656	AATATTTAGTGCCTCGATTCTGGGA	AAATAGTTAGCCAGAGACTGTTCCC

Legend: INS: insertion; DEL: deletion; CTX: interchromosomal translocation; ITX: intrachromosomal translocation; SV: structural variant

Supplementary Note.

Tumor samples with matched normal tissue or blood were obtained at the time of surgery from Memorial Sloan-Kettering Cancer Center (New York, NY, USA), University of Pittsburgh Medical Center (Pittsburgh, PA, USA), VU University Medical Center (Amsterdam, Netherlands), and National Cancer Centre Singapore (Singapore). All patients provided informed consent as part of institutional review board-approved protocols at their respective institutions. Collected phenotypic data elements were deidentified and included age, gender, stage, disease site, histologic features, adjuvant treatment, and disease status (**Supplementary Table 2**).