Supplementary Table S1: List of primers used for RT-PCR MYB-NFIB transcript detection and for the validation of mutations using amplicon resequencing (MiSeq), and Nanostring Codesets.

Primer sets used for *MYB-NFIB* transcript detection (Fehr *et al*., 2011)

Set	*MYB* primer (exon)/sequence	*NFIB* primer (exon)/sequence	Exons tested
1	1910 F (14): AGCTCCGTTTTAATGGCACC	1096R (8c): GGGTATAAATGCCTGCCGTT	14-8c
2	1925 F (14): GCACCAGCATCAGAAGATGA	1197R (9): CCGGTAAGATGGGTGTCCTA	14-9
3	1925 F (14): GCACCAGCATCAGAAGATGA	862R (8a) GCCAGGCACTTTCCCTACTAC	14-8a
4	1693 F (12): GCAGGATGTGATCAAACAGG	1197R (9): CCGGTAAGATGGGTGTCCTA	12-9
5	1432 F (10): CTCAGACTTGGAAATGCCTTC	1197R (9): CCGGTAAGATGGGTGTCCTA	10-9
6	1334 F (9): CAGGGCACCATTCTGGATAA	1952R (9): GTGCTGCAATTGCTGGTCTA	9-9
7	1334 F (9): CAGGGCACCATTCTGGATAA	1197R (9): CCGGTAAGATGGGTGTCCTA	9-9

NanoString Codeset design

Definition	Identifier	Target Sequence	Comments
Endogenous	MYB_5prime	CCGCGCCCGCCGCGCCATGGCCCGAAGACCCCGGCACAGCATATATAGCAGTGACGAGGATGATGAGGACTTTGAGATGTGTGACCATGACTATGATGGG	targets ex1-2 junction
Endogenous	MYB_3prime	AACTGTTGCATGGATCCTGTGTTTGCAACTGGGGAGACAGAAACTGTGGTTGATAGCCAGTCACTGCCTTAAGAACATTTGATGCAAGATGGCCAGCACT	targets 3'UTR
Endogenous	NFIB_5prime	GGTCAATCTTCAGAGGTCTCTGTCTTCTCCACCAAGCAGCAAAAGACCCAAAACTATATCCATAGATGAAAATATGGAACCAAGTCCTACAGGAGACTTT	targets ex5-6 junction
Endogenous	NFIB_3prime	GGCTGCAAAGCGACTGTTCTGCCTACTGTGACAAACTTCAACTTACACAGGTTCCCCTCTCTAACTTCCCACCTGGGTTGCAAGCTGAACTCATTACTGG	targets 3'UTR
Control (Housekeeping)	POLR1B	GGAGAACTCGGCCTTAGAATACTTTGGTGAGATGTTAAAGGCTGCTGGCTACAATTTCTATGGCACCGAGAGGTTATATAGTGGCATCAGTGGGCTAGAA	
Control (Housekeeping)	TUBB	TGGTGGATCTAGAACCTGGGACCATGGACTCTGTTCGCTCAGGTCCTTTTGGCCAGATCTTTAGACCAGACAACTTTGTATTTGGTCAGTCTGGGGCAGG	
Control (Housekeeping)	NAGA	AAAGGAGACCTTGGCTCCCTCAGGTCACCAATAAACCTGTTCTTTAATCAAGTAGTTGTAATATGGACCTGGGGTACCTTTAGTTAGGGACTCTGGTGGC	
Control (Housekeeping)	NPAS1	AGCGCTCCTTCTTTGTCCGCATGAAATCCACGCTCACCAAGAGGGGGCTGCACGTCAAGGCCTCAGGGTACAAGGTCATCCACGTGACTGGGCGCCTTCG	
Control (Housekeeping)	B2M	CGGGCATTCCTGAAGCTGACAGCATTCGGGCCGAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAGGCTATCCA	
Control (Housekeeping)	WAS	GGCCGAGGAGCACCAGCGGTTCAGCAGAACATACCCTCCACCCTCCTCCAGGACCACGAGAACCAGCGACTCTTTGAGATGCTTGGACGAAAATGCTTGA	
Control (Housekeeping)	CD40	CCCAGGAAGCCATATACACAGATGCCCATTGCAGCATTGTTTGTGATAGTGAACAACTGGAAGCTGCTTAACTGTCCATCAGCAGGAGACTGGCTAAATA	

Primer sets used for validation of mutations using targeted amplicon resequencing (MiSeq)

Primer name	Sequence
F_(BRAF_D594G)	AGCCTCAATTCTTACCATCCAC
R_(BRAF_D594G)	TCTTCATAATGCTTGCTCTGATAGG
F_(FGFR2_P253R)	GGCTGGGCATCACTGTAAA
R_(FGFR2_P253R)	CAGCCCTCTGGACAACAC
F_(MTOR_R1749G)	AGATGTCAGCAATCAGCCA
R_(MTOR_R1749G)	TCCAGACCATGCAGCAAC
F_(MYB_I181V)	AGGGAAAGGTCTCTGTTAGAAA
R_(MYB_I181V)	GTTCTTCTGGAAGCTTGTGG
F_(MYB_P687L)	TCAGGAAACTTCTTCTGCTCAC
R_(MYB_P687L)	AAAGAGGGAGTGCTGAAACC
F_(NFKB2_Y294C)	GGGCTAAATTAGGCTAAGGACTC
R_(NFKB2_Y294C)	TTCCACCAGAGGGTAATAGGT
F_(PTPN11_A72V)	CCTCCCTTTCCAATGGACTATTT
R_(PTPN11_A72V)	GCACAGTTCAGAGGATATTTAAGC
F_(SF3B1_R625H)	CTCGCTTGCCAGGACTTC
R_(SF3B1_R625H)	CTCATGACTGTCCTTTCTTTGTTTAC
F_(TSC2_L823M)	GAGATGGTCTACTGCCTGGA
R_(TSC2_L823M)	GGACTCACTGGACAGGAACT
F_(USP6_R133K)	TGGGCTGACTGCCATTT
R_(USP6_R133K)	AGGCTTACTTGGCTCCATATC
F_(VRK3_N451H)	TTAAGCCTCACAAGCTCTTCC
R_(VRK3_N451H)	GGGTTGTCTTGACCACAGAG
F_(ALOX15_G135S)	CATCCTGCGCCCTCTTC
R_(ALOX15_G135S)	GGTTCTGCAACTGGATCTCT
F_(ASB4_C307Y)	CGCCGAAGCCAATCTCAT
R_(ASB4_C307Y)	CTGCCATTTGAATCTTCCTCAAC
F_(ATP1B2_G162S)	CGCTATTACGAACAGCCAGATAA
R_(ATP1B2_G162S)	ATCCTTCCTCCATTCACCCT
F_(C1QTNF9B_C243S)	GCATCTCTGGTGTGCAGTATT
R_(C1QTNF9B_C243S)	CCTTCTTCAGATGTGCCCATTA
F_(CAPZB_E247K)	CTGAGAGAAAGCAGCAGAGAAG
R_(CAPZB_E247K)	TCTCTGACTTGGAATGTTTCTGT
F_(CASQ1_E378G)	GGACTTAGCTTCCGTCCCT
R_(CASQ1_E378G)	GGCTGAAAGATGGTTGCCATA
F_(CHAC1_T125M)	GGGTCAGCGGGATTGATAAAG
R_(CHAC1_T125M)	AAGAGCCTATGAGCTCTCTCTG
F_(CRY1_I481S)	AACAGCTGCCAAAGAAACAAAG
R_(CRY1_I481S)	CTGGAATGCACCAGAAGGTATC
F_(GFM2_I281T)	GATAAGTGGTGCACACATTGG
R_(GFM2_I281T)	AGTGGTGGATGTAGTAATGAAAGA
F_(GPR142_G290D)	GGTTGACCGCTACACTGC
R_(GPR142_G290D)	GGGATGAAATAGACAGTGAGACAG
F_(ILDR2_C222Y)	TGTCAGGTAGAGAGGTAGACATT
R_(ILDR2_C222Y)	TTTGTTGGCCTGGTGCT
F_(LRCH4_G250R)	GACTTACCAGGGACTGAAACT
R_(LRCH4_G250R)	CTTGGATAGCTGAGCAGGAT
F_(OR2B11_L212S)	TTGTGTCGTCCCTTGGAG
R_(OR2B11_L212S)	GCAGGTGCTGAACAACTTT
F_(PGF_V59G)	GCACACAGTGCAGATTCTCAT
R_(PGF_V59G)	TCTCTGCTGGCCTGACC
F_(PLXNB2_G70V)	CAGCAGCTGGTTGACATTG
R_(PLXNB2_G70V)	CACCTGGCTGTGGATGAG
F_(PTPN7_R339W)	ACCCTTGGCTCCTAGTGAA
R_(PTPN7_R339W)	CTCCCTCCCTCCTAGAAATGT
F_(SLCO2A1_C450S)	GAGGTTGCAGAGCTCATGTT
R_(SLCO2A1_C450S)	GGTCTTGCTTTGTTTGATTCCC
F_(TLN2_R93Q)	CAGTGTGAAATTTGTATGTGGTTTG
R_(TLN2_R93Q)	GACATAATGAAGGTGTATGAATGCT
F_(TRIM55_I324T)	ATCTCGGAAGCATCAAAGGC

Primer name	Sequence
R_(TRIM55_I324T)	TTTCCTCCCACCCAACTCT
F_(WDR87_Y417N)	GTGAGGTGCCTAAGAGATACTTG
R_(WDR87_Y417N)	CCACTGAGGATGGCTTGTT
F_(ABCB7_E731D)	TGACTTAGCACGAACAGTTTCC
R_(ABCB7_E731D)	GGTTTGCTTGCTAACCCTCATA
F_(ANKRD29_T105N)	GAAACATAAATTCGTACCATAGATGAGG
R_(ANKRD29_T105N)	GTCAGGTACAACTGCCCTATTC
F_(CAPZB_V246I)	CTGAGAGAAAGCAGCAGAGAAG
R_(CAPZB_V246I)	TCTCTGACTTGGAATGTTTCTGT
F_(CDH3_W591*)	TGCTGAACATCACGGACAA
R_(CDH3_W591*)	TAGGAACGTGTGCAGAATCC
F_(CDK11A_SpliceSite)	TCTGATCGATTTCCGAATTCCC
R_(CDK11A_SpliceSite)	CTTGGTGCCAAGGTGAGT
F_(COPA_SpliceSite)	AAAGAAGCAAGCCCAGAATAATG
R_(COPA_SpliceSite)	CTTATCTCCAGAAGAAGGGCTATC
F_(DLG4_K722R)	GAGCTCTTTCTAATCCGAGCAA
R_(DLG4_K722R)	TCAGGTGGGTCCAGTCTC
F_(DND1_P76L)	GAGCTGTAGCGGGCATAG
R_(DND1_P76L)	GGCCTTGCATACCCTCTT
F_(ENO3_K427E)	GAGGCTGTTAGGTTGGAAGTT
R_(ENO3_K427E)	GGTTGGCACCAGTGTTTATTTC
F_(GRIN2A_I836T)	GTGTACTGACCCTGCTGATG
R_(GRIN2A_I836T)	AACGAGAAGAACGAGGTGATG
F_(GRIN2B_H1187Q)	AGCTGCGGCAGAAGTTG
R_(GRIN2B_H1187Q)	TCTACAAGGAGCGGAGTGAT
F_(HMX2_N269H)	GGGACAGTTCGCTGCTG
R_(HMX2_N269H)	GGAGCCCTGCTTACAGTACA
F_(HSDL1_M184L)	CAGCTGAGGAGTGGGTTTG
R_(HSDL1_M184L)	TGGTAAATAACGTGGGTGTGT
F_(LRRC36_A583V)	CCCGAGATTTGCTTCTGTCTT
R_(LRRC36_A583V)	GTTGTAGTTCTGCTGCTCTGT
F_(MAML3_P727S)	TGGGCCCGCTGATCAAT
R_(MAML3_P727S)	GCATCTCCCTCTCTCTTGTCTT
F_(MAP1B_R64*)	CTCCCTGAAAGCCTGAGAAATA
R_(MAP1B_R64*)	GGGACTTCAGGAGAGAATCTTG
F_(MAP4K4_SpliceSite)	ACTGTCCCATTTATCTTGTCCTT
R_(MAP4K4_SpliceSite)	TTTGTACCACACAGGAGTCTTC
F_(MEX3C_A383P)	GCCACCTTCAAAGCTTACATC
R_(MEX3C_A383P)	CAGACCCACACCTACATAGTAAC
F_(MTTP_Y341*)	CCTAGGAGAACACCCTTTGTAAAT
R_(MTTP_Y341*)	ATCTCTTCTTTCTTCGCAGTCC
F_(MYO5A_R1226H)	CATCAAGCTCCTCGCTCAC
R_(MYO5A_R1226H)	AGTTGAGGATGACAGCAATGAA
F_(NHSL2_Y715*)	CACTACACCTTCCCAACTCTC
R_(NHSL2_Y715*)	TCAGGTACCACTGGACGTA
F_(PGC_V5G)	GCTTTAGGCTCCCATCCAG
R_(PGC_V5G)	GAAAGAGTGCCCAGGTCTTC
F_(QRICH2_Q521*)	AGGTTGAGCCAAATCACTCTG
R_(QRICH2_Q521*)	TGGTACAGCCTGGTGTAGAT
F_(RNF4_G138*)	CACTCACGTGACAGGGTATAAT
R_(RNF4_G138*)	GGAAGATCCTGTCTCATCCAAT
F_(SETD1B_SpliceSite)	GTTCTGCAAGAGCCACATTC
R_(SETD1B_SpliceSite)	GCATGTCTGCGATCACCT
F_(SH3RF3_V314M)	GGAACTGCAGGACGAGATTC
R_(SH3RF3_V314M)	GGGCTTGAAGGTCAGGTG
F_(SHQ1_Y284*)	GTTTACTCAGCACAGTCATCTA
R_(SHQ1_Y284*)	GAAGAGAAGTATCAGCTACGAAA
F_(SKAP2_D293A)	GTAAATCACATCACCACGCTTAAA
R_(SKAP2_D293A)	GATCTAGGGCATCATTTAATTTCTACTG
F_(SLC16A14_N313D)	ACAAATTGACGATTTCTGGGA
R_(SLC16A14_N313D)	CTCCGGATTCTGAAGACTGT

Primer name	Sequence
F_(SLC19A1_L448*)	CTGTGCTGCCTTCTCCTC
R_(SLC19A1_L448*)	GTAGGGTGCCAGTGTCC
F_(SLC25A1_SpliceSite)	GATACTGAAGTGAGAGGCACAG
R_(SLC25A1_SpliceSite)	CCTGCCTGCTGATGTCC
F_(SLITRK2_R646H)	CTGAAGTTCCACTGTCTGTCTT
R_(SLITRK2_R646H)	ATCGTGAGTCTCAGTGTTGTAAG
F_(SMARCA5_R186*)	GTAGGCTTAGATGAAGAGATTGCC
R_(SMARCA5_R186*)	AACTACCAACACATACCATTTCATC
F_(SPOCD1_S594*)	GGGAGAGAAGAATCATAGCAG
R_(SPOCD1_S594*)	AGCACAGCCTCAATTCC
F_(STAG3_A646V)	CCACAGCACACCATCTTCT
R_(STAG3_A646V)	GCGGTCAGTCAGCAAATCTA
F_(THSD4_E723Q)	GAGTGCAGCAAGACCTGTG
R_(THSD4_E723Q)	CTGCGTACCGAGGTCCA
F_(TLN1_L1481S)	TGCCTCACCTCCCTCTAC
R_(TLN1_L1481S)	CCAATAGCCAAGCTGGACA
F_(VCAN_R155M)	CTAAGTTGATACATTGCTCCAATGAG
R_(VCAN_R155M)	CTGCTCTGGAGTTGCTATGAC
F_(WDR81_T1726R)	CCGCAAGAGCGTCTTCTTC
R_(WDR81_T1726R)	CCCAAACTCCGCAGCATTA
F_(ZBTB8A_S326I)	TGTGGTGAAGCGGAAGGCAGAC
R_(ZBTB8A_S326I)	CCAGCCTGGCAACAAGAGTGAAAC
F_(ZNF667_D624Y)	TTGCATGTATATGGCTTCTCTC
R_(ZNF667_D624Y)	GAACATCAAAGAATTCATACTGGAG
F_(MLL2_InDel)	GGCAGACGGGTGGAAAT
R_(MLL2_InDel)	CTATCAGCGAGCACCCTATC
F_(CDH1_InDel)	AACAAAGACAAAGAAGGCAAGG
R_(CDH1_InDel)	AAATCCTGGGTGGATGTTACC
F_(LHX5_InDel)	TGAGGCCGGTCTCCTG
R_(LHX5_InDel)	CCCAAAGAGACGGACAACTC
F_(SLAIN2_InDel)	GCGCAGTTCTGGTTCATCTT
R_(SLAIN2_InDel)	GAGGTGAATTTCTGGGTGACTG
F_(ZMYM3_InDel)	TTTGCACCTACCAGTGAGC
R_(ZMYM3_InDel)	GGGACAAATCCAGCCTCAG
F_(OR6Y1_V129L)	GCAGTCATGAGTCCACAGAA
R_(OR6Y1_V129L)	GACAAGAGTATTTCCTTCAATGGC
F_(XPNPEP2_E209D)	CTCCAAGGCTCTAACAGACAG
R_(XPNPEP2_E209D)	AGTTTGCCACCTACGGAATAG
F_(ZNF3_N184S)	TCTCTGATGTTGAATAAGGTCTGAA
R_(ZNF3_N184S)	AAGTGACAGTTGAGGAGAAGC
F_(ARAP1_S207C)	AGGCCATCCACCCAGAG
R_(ARAP1_S207C)	CCACTAAGGAGGAGGAGTCATT
F_(MKI67_S1447N)	GGGCTTGTCAGTGCATACT
R_(MKI67_S1447N)	CACAGATAAAGTACCAGGAGGTG
F_(CES1_I50V)	CGAGGTGGCATTCTTCACAAAG
R_(CES1_I50V)	ATGTCCAGCAGGGCATCC
F_(COA6_R23G)	CCCTCTATGGAAAGTAAATGGTAGC
R_(COA6_R23G)	TCGACGGGAGGAAACTGT
F_(PMCH_A54V)	GTCACATTGCCACTTACCTTTG
R_(PMCH_A54V)	TTCAGCATCCAAGTCCATAAGA
F_(SMYD2_K231R)	TTCTCTTCTGACTGACAGTGTTG
R_(SMYD2_K231R)	AGATCTGTCCACATTGCCTTT
F_(TNFAIP_ V442G)	TCTGGCTCCCTGGGTATG
R_(TNFAIP_ V442G)	TCAGGTCCTCATGCAGGTT
F_(ZNF132_ H22N)	CATCAAGGAGCTCCCACTC
R_(ZNF132_ H22N)	AGAGATATTAGTGGTAGATGTATCAGG
F_(C10orf54_R74H)	CATGGTGCAGGTGAAGGT
R_(C10orf54_R74H)	CCGTATTCCCTGTATGTCTGTC
F_(OR8K1_ N235Y)	TCTCAGGCTGTAATTTGCTCTT
R_(OR8K1_ N235Y)	CTGGACTTGGGTTGCAAGTA
F_(ERVV-1_SpliceSite)	GGAGAGCTTCCAATTCCTCTTC

Primer name	Sequence
R_(ERVV-1_SpliceSite)	TGGTTCGATGGAGTGTTTAGTG
F_(OR2T2_R132W)	GCAGTTCAGATCTTCCTCTACC
R_(OR2T2_R132W)	GTGACAGGAGTCAGCATGAA
F_(GOLGA8R-W275R)	TCTGATGCCAGTCCTGCT
R_(GOLGA8R-W275R)	GAAGGAGAGGGCAGCCT
F_(MUC16_S13577N)	GGAAGAGACTCCAACCACATC
R_(MUC16_S13577N)	GCAGCCACCAAAGTGGA
F_(CPA2_R394S)	GGAAGCATTGACTGGTCCTAT
R_(CPA2_R394S)	TTTAATGGCTCTTGTTTCTTCCC
F_(PCDHGB6_H290Y)	CCCTGTGTTGCAAGTGACA
R_(PCDHGB6_H290Y)	CGTCCTTCGCTTCCACTTC
F_(INPP5D_T848M)	GCAGCTGCCCATCTACAC
R_(INPP5D_T848M)	TATTCGACAGCTTTGCTGAGAG
F_(TMEM26_G327C)	TCGTCGGAGGTGACTGG
R_(TMEM26_G327C)	TTGCAACTCTACCGCTTGG
F_(RALY_G231S)	TAAGGTGCTGCCCTAGACA
R_(RALY_G231S)	TGCCTCAGAAGTTGTGTTCTC
F_(GPRASP2_S56F)	GCCTGAGAGAGAGAATGATGT
R_(GPRASP2_S56F)	TTCCTTGAGCCTCCGTTT
F_(TMEM155_T110P)	AAGGCAGTTATATATCCAGCTACAA
R_(TMEM155_T110P)	CCCACAAGAAGAAGGAGGAAG
F_(RBMX_G115R)	AGCTTGCAGTCCCTAACTTATAC
R_(RBMX_G115R)	GAACAAGCCACCAAACCATC
F_(MRS2_Q161H)	AAATGAAGCAGTCTTCTCCCA
R_(MRS2_Q161H)	TTGAAAGATTGCAGTGAACACC
F_(TFR2_S383G)	CAGCCGAAGATGTTGTTGATG
R_(TFR2_S383G)	GATTTGGACTCTTCTGGGTCTC
F_(AKAP2_E840EAE)	AATGCCATTCAACAAGCCATAG
R_(AKAP2_E840EAE)	GGCAGAATCTTTGGTAATACATCC
F_(NFAT5_InDel)	TGCAAGCAGGGAGTTTCA
R_(NFAT5_InDel)	GGCTTACACCACTCTGAATTTG
F_(USP9X_Y1477*)	AGCATTGCTAATATGTAATCCCTTT
R_(USP9X_Y1477*)	TCACACAGCCAACAGCTAAT
F_(ATP10D_R606Q)	AAATCCACCAATGGAAACTTTGT
R_(ATP10D_R606Q)	TTATCCATATATCAAGCTCAGTACAGATA
F_(MAGT1_N164K)	GATCCACCGGGCAATCT
R_(MAGT1_N164K)	ATGCCTAAATTTCAAGATGTTAACTG
F_(PCMTD1_P342S)	TTTAACTCCTAACAAATGCTACA
R_(PCMTD1_P342S)	AGATCACAATGAAGCAATGAA
F_(PDE3A_SpliceSite)	AGATTGGAACAACCTGATTATTCTTT
R_(PDE3A_SpliceSite)	CCCGTGGCTGAAAGTGTTA
F_(STAG2_InDel)	TTGTGAATTCATTGGCGTGTTAG
R_(STAG2_InDel)	CATCTCAAATCTAAGACAATATGCAGAA
F_(FGF20_G50C)	GCAGGATCTGCAGGTGGAAG
R_(FGF20_G50C)	GGCCAGCAGGTGGGTTC
F_(TMPRSS11F_S80P)	CACCCACATTCAAAGTGATGC
R_(TMPRSS11F_S80P)	CCTTTCAGATGATAAGTCTTTCTATTACC
F_(ZNF479_C67R)	CTTCATTCGCTCTCACCTAC
R_(ZNF479_C67R)	ATCCTCTAAGCATAATACTAATTTGG
F_(CCDC22_SpliceSite)	CCCAGGCCTCACATCCG
R_(CCDC22_SpliceSite)	GATTCGGTCCGCCTCCTC
F_(TENM4_T216M)	GCGCACCTGGTCTCCA
R_(TENM4_T216M)	CTCTCGCACGCCCACA
F_(SEMA5B_Q79*)	AGTCTGGTACCTGCTG
R_(SEMA5B_Q79*)	CCTGGCCTGTGTCTCT
F_(FBXW7_D642G)	TTGAGGCTCTGATCCGCCAC
R_(FBXW7_D642G)	TTGGTTTTTGTCTAGGTCCCAAC
F_(PARD3B_R444*)	AAACTATCTAGTGTAGAAGGAGATAACAAG
R_(PARD3B_R444*)	CATTACCAACTCTCGGGGC
F_(USP9X_Y1757*)	TCGTTTTTAGGTACGAATGTGAAGAATCTTTTACG
R_(USP9X_Y1757*)	CATTAAATGTAATCAAAATTAAACAAAACTGGA

Primer name	Sequence
F_(OSBPL1A_W251*)	TCGTATTTCAAAATTTATACAGTGAAATTTGATAAGTG
R_(OSBPL1A_W251*)	TATGACTGTCCTCACTTAATTACTTTTTATCAGTCAAGC
F_(CPS1_D1402Y)	TGTTCCATAAAAATAAGAAATCACTGTGATACGG
R_(CPS1_D1402Y)	ATCCTCTAAATTATTTCAGAAAACAGTATGCCTAGTTC
F_(RASA1_L481P)	GGATCAAGAACAAGTACTCAATG
R_(RASA1_L481P)	CTCATGTCAAAACTTATTAAATATATATCAC
F_(HCRTR2_R248H)	GACTTTCATCCTAGGTGAAATTTATCCC
R_(HCRTR2_R248H)	TTGGAAGGAATAACAAATAACAAATTATGTG
F_(VPS26A_M261L)	GTTATGTGACTATATTTAATCATCTTTAGAATTAAGTAG
R_(VPS26A_M261L)	CCAGCCCAAGTGGCACCATAC
F_(IQSEC2_A1269S)	GAGCCCAGCTGGGGCAAG
R_(IQSEC2_A1269S)	CTTCATCTGCTTCTTCCACGC
F_(LARP1_R1002P)	AGCAGGAGGTGGCGGC
R_(LARP1_R1002P)	GACTCTTACCCACCCTACCCC
F_(WDR37_L72P)	TCTTCTTCTGCAGGATTCTAAACTGC
R_(WDR37_L72P)	GTGATGAATGTCTATTCATAAATTTGACTATGGA
F_(SOS1_M269K)	GTAAATGTAGGCTTTTATGCAGACTTTTCG
R_(SOS1_M269K)	TGTGTTTTCCCCCAAACAGGATGTAG
F_(ARAF_A379V)	TCCCCACCTCTGACACTGC
R_(ARAF_A379V)	GGGCAGTCTGCCGGGCC
F_(CACNA1G_T1404M)	CAGGGTCAAGGGACAAGGG
R_(CACNA1G_T1404M)	AGCTGGCCCCCAGAACC
F_(SLIT2_R332*)	CATTGCAGACGTTTGGAACAGAACAC
R_(SLIT2_R332*)	TTTAAGCTGTCAAACACTTATATACTCATACTTAAG
F_(CDH23_InDel)	CTCCCCACCCTTTTCCCTC
R_(CDH23_InDel)	GCAAAGACCCAGCCCCTC
F_(DOPEY1_InDel)	CCTTGTATTTCAGGAACCACACACAC
R_(DOPEY1_InDel)	TAGGTTTTGCTCCTGGTTGTTTACC
F_(BRD1_InDel)	GGGACACTCAGGTCACCGAG
R_(BRD1_InDel)	GATGCCCCGTGTGCCTG
F_(USP9X_InDel)	TGGAGAGCTTCCAGCTGAACAG
R_(USP9X_InDel)	TGAAACATTGAAATGATCAATTATCACATTC
F_(ADAMTS14_P548L)	GCTCAGCAGCAGCAGCC
R_(ADAMTS14_P548L)	GTTGTTGCAGCTCCGGCT
F_(GPR116_H603P)	AGACTCCACATATGTGAAATAATATACCC
R_(GPR116_H603P)	TCTAAAGCTGAACATCATGGTTGATC
F_(TLN2_V16A)	GACATTCTAAGTGAGACTGTCCACATCA
R_(TLN2_V16A)	AAGAAGCCAGTAAATAACCCATGACCTAC
F_(MAP1LC3B_Y113C)	CCTTCTTCCTGTTGGTGAACG
R_(MAP1LC3B_Y113C)	CATGATCTGTGATTGGATGAACT
F_(BMS1_M976L)	TAGGGTGGAGGAGGTTTCAG
R_(BMS1_M976L)	AATCTTGGCAACAGGCAAGT
F_(PANK3_I301F)	AGGACTCCAATTCACATTTTTGA
R_(PANK3_I301F)	TTTTTATCAGCAGATTTGACTTTATTT
F_(FUT2_Y150*)	CCTGCCGGTGCTGCACAG
R_(FUT2_Y150*)	GCTCCCGTTCACCTGCAG
F_(TAF1D_Q125*)	TTTTTCTCCAAGGTGCGTTT
R_(TAF1D_Q125*)	TACCAGCCAACAGGAAGACC
F_(PRKD1_G598C)	TCGCTTTTTAAAATATAACTAGCAAAA
R_(PRKD1_G598C	TTTTCATTGGGCTTGTACCTC

Supplementary Table S2: Clinico-pathologic characteristics of breast AdCCs included in this study.

Sample ID	Grade	ER	PR	HER2	Growth pattern	Age at diagnosis (years)	Tumor size (mm)	Sentinel lymph nodes	Axillary lymph nodes	Neoadjuvant chemotherapy	Surgery	Adjuvant chemotherapy	Radio-therapy	Follow-up (years)	Status	Loco-regional recurrence	Distant metastasis
AdCC1T	1	-	-	-	Tubular-cribriform	57	15	-	0/7	-	Breast conservation, mastectomy	-	-	11	Alive	-	-
AdCC2T	1	-	-	-	Tubular-cribriform	52	25	0/3	-	-	Breast conservation	-	+	12	Alive	-	Lung; 10 yrs after diagnosis
AdCC3T	1	-	-	-	Cribriform	62	23	-	0/15	-	Breast conservation	-	+	7	Alive	-	-
AdCC4T	1	-	-	-	Tubular-cribriform	67	35	-	0/7	Adriamycine, Endoxan, Taxotere	Mastectomy	-	+	8	Alive	-	-
AdCC5T	2	-	-	-	Tubular-cribriform	66	40	-	0/13	-	Breast conservation, mastectomy	-	-	8	Alive	+	-
AdCC6T	2	-	-	-	Solid-trabecular	77	22	0/1	-	-	Breast conservation	-	+	3	Dead (unrelated cause)	-	-
AdCC8T	1	-	-	-	Tubular-cribriform	53	17	0/3	0/1	-	Breast conservation, mastectomy	-	-	3	Alive	-	-
AdCC9T	2	-	-	-	Cribriform	69	45	-	0/5	-	Breast conservation, mastectomy	-	-	4	Alive	-	-
AdCC10T	1	-	-	-	Tubular-cribriform	52	25	-	-	-	Breast conservation	-	+	10	Alive	-	-
AdCC11T	2	-	-	-	Tubular-cribriform	53	24	-	-	-	Breast conservation	-	-	10	Alive	-	-
AdCC12T	2	-	-	-	Solid-cribriform	63	20	0/1	-	-	Breast conservation	FEC 100 + taxanes	+	3	Alive	-	-
AdCC32T	1	-	-	-	Tubular-cribriform	78	35	0/1	-	-	Mastectomy	-	-	3	Alive	-	-

FEC, 5-fluorouracil, epirubicin, cyclophosphamide; -, negative/not performed; +, positive/performed.

Supplementary Table S3: Whole exome massively parallel sequencing statistics.

Sample ID	Total reads	On-target bases (Gb)	Mean target coverage (x)	% target bases at 2x	% target bases at 10x	% target bases at 20x	% target bases at 30x	% target bases at 40x	% target bases at 50x	% target bases at 100x
AdCC1T	71357407	2.86	57.3	94.83%	87.04%	78.02%	67.51%	56.35%	45.70%	13.96%
AdCC1N	68323351	2.75	55.2	94.51%	85.98%	76.27%	65.39%	54.28%	43.86%	13.21%
AdCC2T	70368184	2.83	56.8	94.37%	85.93%	76.43%	65.85%	54.99%	44.75%	14.16%
AdCC2N	68962255	2.73	54.7	94.74%	86.31%	76.48%	65.33%	53.87%	43.21%	12.80%
AdCC3T	101224987	3.90	79.4	93.20%	89.06%	83.89%	78.07%	71.68%	64.84%	30.39%
AdCC3N	103408560	3.76	76.5	93.17%	88.94%	83.81%	78.18%	72.03%	65.31%	28.71%
AdCC4T	117732392	4.17	84.7	93.36%	89.37%	84.87%	79.94%	74.61%	68.82%	35.72%
AdCC4N	209558130	6.42	129.2	94.62%	91.26%	88.61%	85.68%	82.51%	79.12%	59.06%
AdCC5T	92941978	3.53	72.2	92.86%	89.18%	84.11%	77.92%	70.84%	63.04%	24.32%
AdCC5N	106278761	3.80	77.5	92.96%	88.90%	83.75%	77.92%	71.61%	64.86%	29.86%
AdCC6T	182766162	5.69	116.5	89.48%	79.78%	75.26%	71.93%	68.86%	65.87%	50.40%
AdCC6N	131788006	5.02	102.2	93.23%	89.91%	86.21%	82.14%	77.81%	73.16%	46.15%
AdCC8T	87761728	3.61	74.1	92.47%	88.05%	82.46%	76.44%	69.86%	62.72%	26.34%
AdCC8N	80435347	3.16	64.9	91.08%	85.32%	78.78%	71.82%	64.32%	56.35%	19.75%
AdCC9T	119634083	4.16	83.3	95.16%	92.61%	88.86%	83.51%	76.93%	69.62%	33.26%
AdCC9N	124827340	4.03	80.6	95.32%	92.63%	88.52%	82.67%	75.66%	68.10%	31.23%
AdCC10T	52590857	2.17	43.8	93.48%	82.99%	69.79%	55.56%	42.42%	31.64%	7.51%
AdCC10N	51937323	2.12	42.7	93.80%	83.48%	70.09%	55.38%	41.74%	30.68%	6.71%
AdCC11T	104867454	3.83	78.9	89.87%	82.44%	77.25%	72.23%	67.05%	61.56%	32.42%
AdCC11N	100845413	3.90	79.7	93.02%	89.27%	84.50%	79.01%	72.90%	66.22%	30.56%
AdCC12T	112634947	4.20	85.9	92.61%	88.95%	84.37%	79.06%	73.27%	67.13%	35.71%
AdCC12N	143970171	5.00	101.5	93.66%	90.41%	87.05%	83.13%	78.80%	74.11%	46.46%
AdCC32T	120950308	3.96	79.2	95.27%	92.60%	88.50%	82.48%	75.10%	66.92%	29.23%
AdCC32N	100224178	3.19	63.9	95.13%	92.02%	86.36%	78.01%	68.00%	57.55%	16.86%

Supplementary Table S4: Non-silent and silent mutations identified in breast AdCC by whole exome massively parallel sequencing.

Non-silent mutations								
Sample ID	**Gene**	**Amino acid change**	**Effect**	**Chromo-some**	**Position**	**Reference allele**	**Alternate allele**	**Mutant allele fraction**
AdCC1T	BMS1	M93L	NON_SYNONYMOUS_CODING	10	43316112	A	T	44.70%
AdCC1T	CASQ1	E378G	NON_SYNONYMOUS_CODING	1	160171108	A	G	20.70%
AdCC1T	CES1	I49V	NON_SYNONYMOUS_CODING	16	55862791	T	C	20%
AdCC1T	COA6	R23G	NON_SYNONYMOUS_CODING	1	234509279	A	G	36.40%
AdCC1T	COPA	.	SPLICE_SITE_DONOR	1	160268634	C	T	37.70%
AdCC1T	ENO3	K427E	NON_SYNONYMOUS_CODING	17	4860316	A	G	10.40%
AdCC1T	FUT2	Y150*	STOP_GAINED	19	49206663	C	A	20%
AdCC1T	LRCH4	G250R	NON_SYNONYMOUS_CODING	7	100176122	C	T	59.30%
AdCC1T	LRRC36	A583V	NON_SYNONYMOUS_CODING	16	67410717	C	T	6.20%
AdCC1T	MAP4K4	.	SPLICE_SITE_DONOR	2	102459144	G	T	14.70%
AdCC1T	MUC2	T1728S	NON_SYNONYMOUS_CODING	11	1093364	C	G	20%
AdCC1T	MYB	P566L	NON_SYNONYMOUS_CODING	6	135522886	C	T	44.40%
AdCC1T	NFAT5	S809_V811del	CODON_DELETION	16	69726206	ATCTTCAGTT	A	44.07%
AdCC1T	PGC	V5G	NON_SYNONYMOUS_CODING	6	41715059	A	C	17.30%
AdCC1T	PMCH	A54V	NON_SYNONYMOUS_CODING	12	102591388	G	A	44.70%
AdCC1T	PTPN7	R234W	NON_SYNONYMOUS_CODING	1	202122870	G	A	22.60%
AdCC1T	SHQ1	Y284*	STOP_GAINED	3	72866411	A	T	6.40%
AdCC1T	SLC16A14	N313D	NON_SYNONYMOUS_CODING	2	230910905	T	C	38.60%
AdCC1T	SMYD2	K231R	NON_SYNONYMOUS_CODING	1	214501054	A	G	39.50%
AdCC1T	STAG3	A646V	NON_SYNONYMOUS_CODING	7	99798468	C	T	29.20%
AdCC1T	TNFAIP2	V442G	NON_SYNONYMOUS_CODING	14	103598002	T	G	66.70%
AdCC1T	ZNF132	H22N	NON_SYNONYMOUS_CODING	19	58948582	G	T	6%
AdCC2T	ATP1B2	G162S	NON_SYNONYMOUS_CODING	17	7557507	G	A	46.10%
AdCC2T	BX284668.1	A21T	NON_SYNONYMOUS_CODING	1	17198583	C	T	9.70%
AdCC2T	BX284668.1	R6P	NON_SYNONYMOUS_CODING	1	17198627	C	G	10.60%
AdCC2T	C10orf54	R74H	NON_SYNONYMOUS_CODING	10	73521645	C	T	43.50%
AdCC2T	CPS1	D1396Y	NON_SYNONYMOUS_CODING	2	211540476	G	T	12.50%
AdCC2T	DSCAM	V589I	NON_SYNONYMOUS_CODING	21	41710046	C	T	56.20%
AdCC2T	EPHB2	S339T	NON_SYNONYMOUS_CODING	1	23191417	T	A	7.50%
AdCC2T	FAM153B	L222F	NON_SYNONYMOUS_CODING	5	175528584	C	T	4.50%
AdCC2T	GPR116	H603P	NON_SYNONYMOUS_CODING	6	46834688	T	G	46.60%
AdCC2T	GPR142	G290D	NON_SYNONYMOUS_CODING	17	72368219	G	A	25%
AdCC2T	GRIN2A	I836T	NON_SYNONYMOUS_CODING	16	9862796	A	G	24.50%
AdCC2T	HSDL1	M184L	NON_SYNONYMOUS_CODING	16	84163707	T	A	38.10%
AdCC2T	ILDR2	C222Y	NON_SYNONYMOUS_CODING	1	166905866	C	T	50%
AdCC2T	MAP1B	R64*	STOP_GAINED	5	71411530	C	T	19%
AdCC2T	AKAP2	E608_E609insAE	CODON_INSERTION	9	112900341	G	GGAAGCT	33.33%
AdCC2T	PRKD1	G590C	NON_SYNONYMOUS_CODING	14	30095720	C	A	14.60%
AdCC2T	PTPN11	A72V	NON_SYNONYMOUS_CODING	12	112888199	C	T	45.20%
AdCC2T	SKAP2	D293A	NON_SYNONYMOUS_CODING	7	26724464	T	G	6.50%
AdCC2T	SLAIN2	V335fs	FRAME_SHIFT	4	48384724	AG	A	10.98%
AdCC2T	TLN2	R93Q	NON_SYNONYMOUS_CODING	15	62944247	G	A	15%
AdCC2T	USP9X	M1526fs	FRAME_SHIFT	X	41057975	A	AT	22.22%
AdCC2T	USP9X	Y1477*	STOP_GAINED	X	41057831	T	G	5.60%
AdCC2T	USP9X	Y1757*	STOP_GAINED	X	41073902	T	G	9.30%
AdCC2T	ZMYM3	K493fs	FRAME_SHIFT	X	70469018	TTC	T	30.77%
AdCC3T	GOLGA8R	W116R	NON_SYNONYMOUS_CODING	15	30700159	A	G	20%
AdCC3T	LRRC26	T228K	NON_SYNONYMOUS_CODING	9	140063628	G	T	12.50%
AdCC3T	MAGT1	N132K	NON_SYNONYMOUS_CODING	X	77112989	G	T	14.60%
AdCC3T	MUC16	N13579N	NON_SYNONYMOUS_CODING	19	8999445	C	T	8.50%
AdCC3T	OR2T2	R132W	NON_SYNONYMOUS_CODING	1	248616492	C	T	29.80%
AdCC3T	SAA2	V75A	NON_SYNONYMOUS_CODING	11	18267463	A	G	36.40%
AdCC3T	TLN1	L1481S	NON_SYNONYMOUS_CODING	9	35708366	A	G	40.90%
AdCC4T	ANKRD29	T105N	NON_SYNONYMOUS_CODING	18	21218829	G	T	8.30%
AdCC4T	C12orf40	P85S	NON_SYNONYMOUS_CODING	12	40040181	C	T	7.60%
AdCC4T	C1QTNF9B	C243S	NON_SYNONYMOUS_CODING	13	24465703	A	T	40%

Non-silent mutations

Sample ID	Gene	Amino acid change	Effect	Chromo-some	Position	Reference allele	Alternate allele	Mutant allele fraction
AdCC4T	CDH3	W591*	STOP_GAINED	16	68721617	G	A	19.50%
AdCC4T	CDK11A	.	SPLICE_SITE_ACCEPTOR	1	1635380	C	G	6.40%
AdCC4T	CPA2	R394S	NON_SYNONYMOUS_CODING	7	129929507	C	A	6.90%
AdCC4T	DISP2	G3R	NON_SYNONYMOUS_CODING	15	40650529	G	C	25%
AdCC4T	DOPEY1	T1276fs	FRAME_SHIFT	6	83847586	A	AT	17.14%
AdCC4T	FGF20	G50C	NON_SYNONYMOUS_CODING	8	16859394	C	A	33.30%
AdCC4T	FGFR2	P253R	NON_SYNONYMOUS_CODING	10	123279674	G	C	18.20%
AdCC4T	IQSEC2	A1259S	NON_SYNONYMOUS_CODING	X	53264063	C	A	8.10%
AdCC4T	LARP1	R1079P	NON_SYNONYMOUS_CODING	5	154193601	G	C	6.80%
AdCC4T	MAML3	P723S	NON_SYNONYMOUS_CODING	4	140651722	G	A	12.70%
AdCC4T	PCDHGB6	H290Y	NON_SYNONYMOUS_CODING	5	140788637	C	T	7.20%
AdCC4T	SLITRK2	R646H	NON_SYNONYMOUS_CODING	X	144905880	G	A	29.60%
AdCC4T	SPTBN2	A635S	NON_SYNONYMOUS_CODING	11	66472844	C	A	5.10%
AdCC4T	STAG2	D210fs	FRAME_SHIFT	X	123179178	CTCACAAG	C	16.98%
AdCC4T	TAF1D	Q125*	STOP_GAINED	11	93471361	G	A	44.70%
AdCC4T	THSD4	E723Q	NON_SYNONYMOUS_CODING	15	72039307	G	C	20.80%
AdCC4T	TMPRSS11F	S80P	NON_SYNONYMOUS_CODING	4	68956285	A	G	10.50%
AdCC4T	TRIM55	I324T	NON_SYNONYMOUS_CODING	8	67062687	T	C	4.70%
AdCC4T	TSC2	L823M	NON_SYNONYMOUS_CODING	16	2124312	C	A	9.40%
AdCC4T	ZNF667	D496Y	NON_SYNONYMOUS_CODING	19	56952878	C	A	24.30%
AdCC5T	CAPZB	E218K	NON_SYNONYMOUS_CODING	1	19671683	C	T	19.20%
AdCC5T	CAPZB	V217I	NON_SYNONYMOUS_CODING	1	19671686	C	T	19.60%
AdCC5T	INPP5D	T848M	NON_SYNONYMOUS_CODING	2	234102590	C	T	39.30%
AdCC5T	MEX3C	A383P	NON_SYNONYMOUS_CODING	18	48703554	C	G	4.70%
AdCC5T	MUC6	P1465T	NON_SYNONYMOUS_CODING	11	1018408	G	T	11.40%
AdCC5T	SEMA5B	Q25*	STOP_GAINED	3	122680038	G	A	44.20%
AdCC5T	SLCO2A1	C450S	NON_SYNONYMOUS_CODING	3	133664051	C	G	40.80%
AdCC5T	SOS1	M269K	NON_SYNONYMOUS_CODING	2	39278343	A	T	37.50%
AdCC5T	SPOCD1	S594*	STOP_GAINED	1	32265412	G	T	57.10%
AdCC5T	TMEM26	G327C	NON_SYNONYMOUS_CODING	10	63170208	C	A	48.60%
AdCC5T	WDR37	L72P	NON_SYNONYMOUS_CODING	10	1123923	T	C	54.90%
AdCC6T	ADAMTS14	P545L	NON_SYNONYMOUS_CODING	10	72498632	C	T	27.80%
AdCC6T	ARAF	A379V	NON_SYNONYMOUS_CODING	X	47428176	C	T	5.70%
AdCC6T	CCDC22	.	START_GAINED	X	49092016	C	T	36.80%
AdCC6T	CDH23	E3157fs	FRAME_SHIFT	10	73572317	AG	A	29.41%
AdCC6T	CRY1	I481S	NON_SYNONYMOUS_CODING	12	107391316	A	C	25.80%
AdCC6T	GFM2	I281T	NON_SYNONYMOUS_CODING	5	74041510	A	G	45.30%
AdCC6T	GPRASP2	S56F	NON_SYNONYMOUS_CODING	X	101969964	C	T	28.60%
AdCC6T	IGFN1	G2007R	NON_SYNONYMOUS_CODING	1	201180040	G	A	5.80%
AdCC6T	MAP1LC3B	Y113C	NON_SYNONYMOUS_CODING	16	87436663	A	G	19.40%
AdCC6T	MS4A3	L141I	NON_SYNONYMOUS_CODING	11	59834493	C	A	36.80%
AdCC6T	MUC4	P1952S	NON_SYNONYMOUS_CODING	3	195512597	G	A	17.60%
AdCC6T	PCMTD1	P342S	NON_SYNONYMOUS_CODING	8	52732961	G	A	12%
AdCC6T	RALY	G231S	NON_SYNONYMOUS_CODING	20	32664866	G	A	31.30%
AdCC6T	RNF4	G138*	STOP_GAINED	4	2514847	G	T	4.80%
AdCC6T	SLC25A1	.	SPLICE_SITE_DONOR	22	19163933	C	A	48.30%
AdCC6T	TMEM155	T110P	NON_SYNONYMOUS_CODING	4	122681514	T	G	34.50%
AdCC6T	USP6	R133K	NON_SYNONYMOUS_CODING	17	5037195	G	A	5.70%
AdCC6T	VRK3	N451H	NON_SYNONYMOUS_CODING	19	50482425	T	G	27%
AdCC6T	ZNF479	C67R	NON_SYNONYMOUS_CODING	7	57193788	A	G	28.60%
AdCC8T	ALOX15	G113S	NON_SYNONYMOUS_CODING	17	4542725	C	T	20%
AdCC8T	CACNA1G	T1404M	NON_SYNONYMOUS_CODING	17	48681557	C	T	35.90%
AdCC8T	DND1	P76L	NON_SYNONYMOUS_CODING	5	140052407	G	A	11.50%
AdCC8T	KRTAP4-6	S123P	NON_SYNONYMOUS_CODING	17	39296361	A	G	38.50%
AdCC8T	KRTAP9-9	S161Y	NON_SYNONYMOUS_CODING	17	39412119	C	A	14.30%
AdCC8T	MRS2	Q161H	NON_SYNONYMOUS_CODING	6	24411023	G	T	31.50%
AdCC8T	MTTP	Y314*	STOP_GAINED	4	100518256	C	G	37.50%
AdCC8T	PDE3A	.	SPLICE_SITE_ACCEPTOR	12	20709592	A	G	26.90%
AdCC8T	PGF	V59G	NON_SYNONYMOUS_CODING	14	75416199	A	C	33.30%

Non-silent mutations								
Sample ID	**Gene**	**Amino acid change**	**Effect**	**Chromo-some**	**Position**	**Reference allele**	**Alternate allele**	**Mutant allele fraction**
AdCC8T	RBMX	G115R	NON_SYNONYMOUS_CODING	X	135960119	C	T	30%
AdCC8T	SLIT2	R328*	STOP_GAINED	4	20512185	C	T	5.60%
AdCC8T	ZNF814	D404E	NON_SYNONYMOUS_CODING	19	58385546	G	T	11.50%
AdCC9T	ABCB7	E730D	NON_SYNONYMOUS_CODING	X	74273274	C	A	27.60%
AdCC9T	ASB4	C307Y	NON_SYNONYMOUS_CODING	7	95157557	G	A	44.20%
AdCC9T	BRAF	D594G	NON_SYNONYMOUS_CODING	7	140453154	T	C	46.80%
AdCC9T	CRIPAK	M215I	NON_SYNONYMOUS_CODING	4	1388944	G	A	30.80%
AdCC9T	DLG4	K679R	NON_SYNONYMOUS_CODING	17	7094618	T	C	61.50%
AdCC9T	MLL2	A2832fs	FRAME_SHIFT	12	49432644	G	GCAAAT	.
AdCC9T	MUC5B	R2628S	NON_SYNONYMOUS_CODING	11	1265992	C	A	15.40%
AdCC9T	NBPF10	D1168E	NON_SYNONYMOUS_CODING	1	145323667	C	G	13.20%
AdCC9T	SLC19A1	L448*	STOP_GAINED	21	46936005	A	T	23.30%
AdCC9T	TFR2	S383G	NON_SYNONYMOUS_CODING	7	100228635	T	C	16.70%
AdCC9T	VCAN	R155M	NON_SYNONYMOUS_CODING	5	82789383	G	T	52.60%
AdCC10T	AP1B1	.	SPLICE_SITE_DONOR	22	29758989	C	G	36.70%
AdCC10T	HERC2	R1211C	NON_SYNONYMOUS_CODING	15	28483865	G	A	6.70%
AdCC10T	LRRC37B	L570I	NON_SYNONYMOUS_CODING	17	30351758	C	A	8.60%
AdCC10T	MTOR	R1749G	NON_SYNONYMOUS_CODING	1	11194409	G	C	15.40%
AdCC10T	MYO5A	R1226H	NON_SYNONYMOUS_CODING	15	52643623	C	T	35.50%
AdCC10T	NHSL2	Y349*	STOP_GAINED	X	71359543	C	A	33.30%
AdCC10T	OR5H14	R143W	NON_SYNONYMOUS_CODING	3	97868656	C	T	9%
AdCC10T	OR6Y1	V129L	NON_SYNONYMOUS_CODING	1	158517511	C	A	13.60%
AdCC10T	PANK3	I301F	NON_SYNONYMOUS_CODING	5	167988433	T	A	12.50%
AdCC10T	PARD3B	R444*	STOP_GAINED	2	205990357	C	T	26.90%
AdCC10T	SF3B1	R625H	NON_SYNONYMOUS_CODING	2	198267483	C	T	36.40%
AdCC10T	ZBTB8A	S326I	NON_SYNONYMOUS_CODING	1	33060808	G	T	12%
AdCC11T	ARMCX4	A1821V	NON_SYNONYMOUS_CODING	X	100749038	C	T	100%
AdCC11T	MUC12	E4106K	NON_SYNONYMOUS_CODING	7	100645731	G	A	12.90%
AdCC11T	SH3RF3	V314M	NON_SYNONYMOUS_CODING	2	109988132	G	A	7.30%
AdCC11T	SIMC1	H325Y	NON_SYNONYMOUS_CODING	5	175717557	C	T	16.70%
AdCC11T	WDR87	Y378N	NON_SYNONYMOUS_CODING	19	38385094	A	T	15.70%
AdCC11T	XPNPEP2	E209D	NON_SYNONYMOUS_CODING	X	128881719	G	T	21.20%
AdCC11T	ZNF3	N184S	NON_SYNONYMOUS_CODING	7	99669556	T	C	28%
AdCC12T	ARAP1	S207C	NON_SYNONYMOUS_CODING	11	72425256	G	C	50%
AdCC12T	CHAC1	T125M	NON_SYNONYMOUS_CODING	15	41246442	C	T	39.40%
AdCC12T	CNN2	Q5E	NON_SYNONYMOUS_CODING	19	1026673	C	G	47.60%
AdCC12T	DLG3	A49V	NON_SYNONYMOUS_CODING	X	69665197	C	T	23.90%
AdCC12T	FBXW7	D642G	NON_SYNONYMOUS_CODING	4	153244232	T	C	52.90%
AdCC12T	GRIN2B	H1187Q	NON_SYNONYMOUS_CODING	12	13716611	G	C	45.50%
AdCC12T	HMX2	N269H	NON_SYNONYMOUS_CODING	10	124909622	A	C	37.60%
AdCC12T	KIF13B	F1752L	NON_SYNONYMOUS_CODING	8	28928248	A	G	45.50%
AdCC12T	KRTAP4-7	Y40C	NON_SYNONYMOUS_CODING	17	39240577	A	G	50%
AdCC12T	MKI67	S1447N	NON_SYNONYMOUS_CODING	10	129905764	C	T	50.70%
AdCC12T	MUC4	A2542T	NON_SYNONYMOUS_CODING	3	195510827	C	T	100%
AdCC12T	NFKB2	Y294C	NON_SYNONYMOUS_CODING	10	104158170	A	G	13.40%
AdCC12T	OSBPL1A	W251*	STOP_GAINED	18	21897344	C	T	33.30%
AdCC12T	PLXNB2	G70V	NON_SYNONYMOUS_CODING	22	50728805	C	A	50%
AdCC12T	QRICH2	Q521*	STOP_GAINED	17	74288749	G	A	43.50%
AdCC12T	SETD1B	.	SPLICE_SITE_DONOR	12	122265762	T	G	48.60%
AdCC12T	SMARCA5	R186*	STOP_GAINED	4	144446639	C	T	44.40%
AdCC12T	TLN2	V16A	NON_SYNONYMOUS_CODING	15	62939556	T	C	42.70%
AdCC32T	ATP10D	R606Q	NON_SYNONYMOUS_CODING	4	47556924	G	A	9.30%
AdCC32T	BRD1	F987fs	FRAME_SHIFT	22	50169273	AC	A	35.42%
AdCC32T	CDH1	T217fs	FRAME_SHIFT	16	68842714	CAG	C	28.92%
AdCC32T	CKAP2	H141R	NON_SYNONYMOUS_CODING	13	53035380	A	G	44.60%
AdCC32T	ERVV-1	.	START_GAINED	19	53517185	C	T	31.30%
AdCC32T	HCRTR2	R248H	NON_SYNONYMOUS_CODING	6	55128601	G	A	40.90%
AdCC32T	LHX5	R184fs	FRAME_SHIFT	12	113906056	CG	C	29%

Non-silent mutations

Sample ID	Gene	Amino acid change	Effect	Chromo-some	Position	Reference allele	Alternate allele	Mutant allele fraction
AdCC32T	MYB	I181V	NON_SYNONYMOUS_CODING	6	135513475	A	G	42.90%
AdCC32T	OR2B11	L212S	NON_SYNONYMOUS_CODING	1	247614650	A	G	11.60%
AdCC32T	OR8K1	N235Y	NON_SYNONYMOUS_CODING	11	56114217	A	T	3.80%
AdCC32T	RASA1	L481P	NON_SYNONYMOUS_CODING	5	86658477	T	C	40.40%
AdCC32T	TENM4	T216M	NON_SYNONYMOUS_CODING	11	78614415	G	A	56.80%
AdCC32T	VPS26A	M261L	NON_SYNONYMOUS_CODING	10	70928298	A	T	24.40%
AdCC32T	WDR81	T675R	NON_SYNONYMOUS_CODING	17	1637508	C	G	31.90%
AdCC32T	ZDHHC11B	C194S	NON_SYNONYMOUS_CODING	5	751328	C	G	43.30%

Silent mutations

Sample ID	Gene	Amino acid change	Effect	Chromo-some	Position	Reference allele	Alternate allele	Mutant allele fraction
AdCC9T	AARS	Y547	SYNONYMOUS_CODING	16	70296279	G	A	16.50%
AdCC9T	HPR	L146	SYNONYMOUS_CODING	16	72110371	C	T	12.30%
AdCC9T	SREBF1	R625	SYNONYMOUS_CODING	17	17720272	C	T	41.80%
AdCC9T	LAMA5	A863	SYNONYMOUS_CODING	20	60909392	C	A	9.40%
AdCC9T	PIP	D93	SYNONYMOUS_CODING	7	142836245	C	T	34.80%
AdCC9T	PNPLA7	F1059	SYNONYMOUS_CODING	9	140358627	G	A	38.50%
AdCC9T	SLC25A5	R106	SYNONYMOUS_CODING	X	118603830	A	G	13.50%
AdCC9T	SPANXN5	P30	SYNONYMOUS_CODING	X	52825657	T	C	45.50%
AdCC8T	KRTAP5-7	C24	SYNONYMOUS_CODING	11	71238418	T	C	12.00%
AdCC8T	KRTAP9-9	T152	SYNONYMOUS_CODING	17	39412093	C	A	13.00%
AdCC8T	SEMA6B	F352	SYNONYMOUS_CODING	19	4550876	G	A	30.40%
AdCC8T	ATRAID	T167	SYNONYMOUS_CODING	2	27438384	C	T	4.40%
AdCC8T	KMT2C	P335	SYNONYMOUS_CODING	7	151970797	A	T	20.00%
AdCC8T	NOTCH1	F1259	SYNONYMOUS_CODING	9	139401292	G	A	15.70%
AdCC6T	C1orf68	Y109	SYNONYMOUS_CODING	1	152692324	C	T	30.00%
AdCC6T	ITIH2	A547	SYNONYMOUS_CODING	10	7773953	G	A	30.40%
AdCC6T	MRGPRD	L256	SYNONYMOUS_CODING	11	68747688	C	T	43.30%
AdCC6T	ATP2A2	V347	SYNONYMOUS_CODING	12	110765768	T	C	21.20%
AdCC6T	ATP2C2	T567	SYNONYMOUS_CODING	16	84485567	G	A	37.50%
AdCC6T	PRDM1	P467	SYNONYMOUS_CODING	6	106553436	G	A	15.80%
AdCC5T	PCGF5	G219	SYNONYMOUS_CODING	10	93024271	C	T	36.20%
AdCC5T	LDLRAD3	P321	SYNONYMOUS_CODING	11	36250872	G	A	49.50%
AdCC5T	ASXL3	K770	SYNONYMOUS_CODING	18	31319678	G	A	47.20%
AdCC5T	ARF4	N95	SYNONYMOUS_CODING	3	57563088	G	A	44.00%
AdCC4T	PLA2G5	T60	SYNONYMOUS_CODING	1	20412715	C	T	34.90%
AdCC4T	RNF17	S270	SYNONYMOUS_CODING	13	25363512	A	C	19.40%
AdCC4T	COG6	A630	SYNONYMOUS_CODING	13	40325146	C	T	25.20%
AdCC4T	DDX52	T216	SYNONYMOUS_CODING	17	35990159	T	G	39.70%
AdCC4T	USP34	G1551	SYNONYMOUS_CODING	2	61515908	A	G	19.80%
AdCC4T	ISM1	T334	SYNONYMOUS_CODING	20	13279713	G	A	4.90%
AdCC4T	FGL2	G260	SYNONYMOUS_CODING	7	76826136	C	G	22.00%
AdCC4T	PABPC5	T78	SYNONYMOUS_CODING	X	90690810	C	T	8.80%
AdCC3T	CDC27	S102	SYNONYMOUS_CODING	17	45247354	G	A	16.70%
AdCC3T	HLA-B	R258	SYNONYMOUS_CODING	6	31323215	T	C	18.50%
AdCC32T	MST1L	I342	SYNONYMOUS_CODING	1	17085795	G	T	10.70%
AdCC32T	AMPD3	K44	SYNONYMOUS_CODING	11	10483171	A	G	39.60%
AdCC32T	SLC25A47	T43	SYNONYMOUS_CODING	14	100792550	G	T	49.30%
AdCC32T	ADPRH	D47	SYNONYMOUS_CODING	3	119301157	C	T	36.20%
AdCC32T	GALNT15	A71	SYNONYMOUS_CODING	3	16216871	T	A	31.50%
AdCC2T	OR8H1	G203	SYNONYMOUS_CODING	11	56057930	A	G	10.30%
AdCC2T	SLC4A8	A683	SYNONYMOUS_CODING	12	51868867	G	A	82.80%
AdCC2T	PDE4C	T626	SYNONYMOUS_CODING	19	18322000	C	T	43.50%
AdCC2T	SCN2A	A215	SYNONYMOUS_CODING	2	166165901	G	C	12.50%
AdCC2T	OSBPL10	T640	SYNONYMOUS_CODING	3	31710310	G	A	49.40%
AdCC2T	PSD2	S290	SYNONYMOUS_CODING	5	139193803	C	T	22.40%
AdCC2T	GPR98	A4741	SYNONYMOUS_CODING	5	90086869	C	T	9.20%
AdCC2T	HSP90AB1	T537	SYNONYMOUS_CODING	6	44219884	C	A	43.30%

Silent mutations								
Sample ID	**Gene**	**Amino acid change**	**Effect**	**Chromo-some**	**Position**	**Reference allele**	**Alternate allele**	**Mutant allele fraction**
AdCC2T	PRSS35	T298	SYNONYMOUS_CODING	6	84234054	G	A	7.30%
AdCC1T	KANK4	G212	SYNONYMOUS_CODING	1	62740140	A	C	20.00%
AdCC1T	ALKBH2	R193	SYNONYMOUS_CODING	12	109526218	T	C	40.00%
AdCC1T	NEO1	K1143	SYNONYMOUS_CODING	15	73580672	A	G	42.60%
AdCC1T	PLEKHM1	K978	SYNONYMOUS_CODING	17	43516968	C	T	33.30%
AdCC1T	SHANK1	G2111	SYNONYMOUS_CODING	19	51165375	A	C	15.00%
AdCC1T	TSPEAR	S423	SYNONYMOUS_CODING	21	45945603	G	A	47.50%
AdCC1T	TPRN	T693	SYNONYMOUS_CODING	9	140086621	T	G	26.70%
AdCC12T	OR4K17	L34	SYNONYMOUS_CODING	14	20585665	C	T	48.90%
AdCC12T	ADAMTS18	T867	SYNONYMOUS_CODING	16	77334233	A	G	20.80%
AdCC12T	SPOPL	R99	SYNONYMOUS_CODING	2	139308567	C	A	8.10%
AdCC12T	ATP6V1B1	A512	SYNONYMOUS_CODING	2	71192245	G	A	11.60%
AdCC12T	OGFRL1	S352	SYNONYMOUS_CODING	6	72011452	C	T	40.20%
AdCC12T	SUPT20HL2	T813	SYNONYMOUS_CODING	X	24328994	G	A	54.40%
AdCC12T	WNK3	E992	SYNONYMOUS_CODING	X	54275805	C	T	40.10%
AdCC11T	IL18	N191	SYNONYMOUS_CODING	11	112014328	G	A	18.30%
AdCC11T	MAPK7	D695	SYNONYMOUS_CODING	17	19285701	C	T	31.00%
AdCC11T	CYP4F12	P13	SYNONYMOUS_CODING	19	15784378	G	T	20.00%
AdCC11T	PNLDC1	L126	SYNONYMOUS_CODING	6	160225586	C	T	17.90%
AdCC11T	C6orf163	I180	SYNONYMOUS_CODING	6	88066207	C	T	11.50%
AdCC11T	FAM3C	C64	SYNONYMOUS_CODING	7	121011434	G	A	7.50%
AdCC11T	GPR101	C182	SYNONYMOUS_CODING	X	136113288	G	A	9.90%
AdCC10T	SUCO	H876	SYNONYMOUS_CODING	1	172558416	T	C	31.70%
AdCC10T	DDX11	A380	SYNONYMOUS_CODING	12	31244703	C	T	26.30%
AdCC10T	TUBA3D	L259	SYNONYMOUS_CODING	2	132238043	A	C	7.30%
AdCC10T	HCLS1	P368	SYNONYMOUS_CODING	3	121351315	G	A	40.90%

Supplementary Table S5: Targeted amplicon resequencing validation of somatic mutations identified by massively parallel sequencing in breast AdCCs, clonal frequencies, and mutation function prediction.

Sample ID	**Chromo -some**	**Genomic position**	**Gene**	**Amino acid change**	**Effect**	**Reference allele**	**Alternate allele**	**Validat-ion**	**Sequence depth (x)**	**Mutant allele fraction**	**CHASM Breast**	**Mutation Taster**	**5000S - Lawrence *et al*. (Nature, 2014)**	**127 genes; Kandoth *et al*. (Nature, 2013)**	**Cancer Gene Census**	**Consensus impact**	**Cancer cell fraction (ABSO-LUTE)**	**Mutated in salivary gland AdCCs; Ho *et al* (Nat Genet 2013)**	**Mutated in salivary gland AdCCs; Stephens *et al* (JCI 2013)**
AdCC1T	10	43316112	BMS1	M976L	NON_SYNONYMOUS_CODING	A	T	validated	7763	44.45%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC1T	1	160171108	CASQ1	E378G	NON_SYNONYMOUS_CODING	A	G	validated	6454	0.48%	passenger	D	no	no	no	non-passenger	49.00%		
AdCC1T	16	55862791	CES1	I49V	NON_SYNONYMOUS_CODING	T	C	validated	7058	26.48%	passenger	N	no	no	no	passenger	47.00%		
AdCC1T	1	234509279	COA6	R23G	NON_SYNONYMOUS_CODING	A	G	validated	6805	0.22%	passenger	N	no	no	no	passenger	86.00%		
AdCC1T	1	160268634	COPA	.	SPLICE_SITE_DONOR	C	T	validated	7720	47.02%		D	no	no	no	non-passenger	89.00%		
AdCC1T	17	4860316	ENO3	K427E	NON_SYNONYMOUS_CODING	A	G	validated	7389	2.69%	passenger	D	no	no	no	non-passenger	25.00%		
AdCC1T	19	49206663	FUT2	Y150*	STOP_GAINED	C	A	validated	7236	0.11%		A	no	no	no	non-passenger	47.00%		
AdCC1T	7	100176122	LRCH4	G250R	NON_SYNONYMOUS_CODING	C	T	validated	7579	48.19%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC1T	16	67410717	LRRC36	A583V	NON_SYNONYMOUS_CODING	C	T	validated	7454	4.67%	passenger	D	no	no	no	non-passenger	15.00%		
AdCC1T	11	1093364	MUC2	T1728S	NON_SYNONYMOUS_CODING	C	G	not tested	not tested	not tested	passenger	N	no	no	no	passenger	47.00%		
AdCC1T	6	135522886	MYB	P687L	NON_SYNONYMOUS_CODING	C	T	validated	7568	44.12%	passenger	D	no	no	yes	non-passenger	100.00%	yes	
AdCC1T	16	69726206	NFAT5	S809_V811del	CODON_DELETION	ATCTTCAGTT	A	validated	7144	0.21%	.	P	no	no	no	passenger	100.00%		
AdCC1T	12	102591388	PMCH	A54V	NON_SYNONYMOUS_CODING	G	A	validated	7757	44.59%	passenger	N	no	no	no	passenger	100.00%		
AdCC1T	1	202122870	PTPN7	R339W	NON_SYNONYMOUS_CODING	G	A	validated	5942	50.89%	passenger	D	no	no	no	non-passenger	53.00%		
AdCC1T	3	72866411	SHQ1	Y284*	STOP_GAINED	A	T	validated	7880	0.18%		A	no	no	no	non-passenger	15.00%		
AdCC1T	2	230910905	SLC16A14	N313D	NON_SYNONYMOUS_CODING	T	C	validated	7524	42.46%	passenger	D	no	no	no	non-passenger	91.00%		
AdCC1T	1	214501054	SMYD2	K231R	NON_SYNONYMOUS_CODING	A	G	validated	7334	46.20%	passenger	N	no	no	no	passenger	93.00%		
AdCC1T	7	99798468	STAG3	A646V	NON_SYNONYMOUS_CODING	C	T	validated	6797	38.59%	passenger	D	no	no	no	non-passenger	69.00%		
AdCC1T	14	103598002	TNFAIP2	V442G	NON_SYNONYMOUS_CODING	T	G	validated	7683	0.20%	passenger	N	no	no	no	passenger	100.00%		
AdCC2T	17	7557507	ATP1B2	G162S	NON_SYNONYMOUS_CODING	G	A	validated	7397	48.32%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC2T	1	17198583	BX284668.1	A21T	NON_SYNONYMOUS_CODING	C	T	not tested	not tested	not tested	passenger		no	no	no	passenger	21.00%		
AdCC2T	1	17198627	BX284668.1	R6P	NON_SYNONYMOUS_CODING	C	G	not tested	not tested	not tested	passenger		no	no	no	passenger	23.00%		
AdCC2T	10	73521645	C10orf54	R74H	NON_SYNONYMOUS_CODING	C	T	validated	7416	48.75%	passenger	N	no	no	no	passenger	95.00%		
AdCC2T	2	211540476	CPS1	D1402Y	NON_SYNONYMOUS_CODING	G	T	validated	7855	13.43%	passenger	D	no	no	no	non-passenger	27.00%		
AdCC2T	21	41710046	DSCAM	V589I	NON_SYNONYMOUS_CODING	C	T	not tested	not tested	not tested	passenger	D	no	no	no	non-passenger	100.00%		
AdCC2T	1	23191417	EPHB2	S339T	NON_SYNONYMOUS_CODING	T	A	not tested	not tested	not tested	passenger	D	no	no	no	non-passenger	16.00%		
AdCC2T	5	175528584	FAM153B	L222F	NON_SYNONYMOUS_CODING	C	T	not tested	not tested	not tested	passenger	N	no	no	no	passenger	10.00%		
AdCC2T	6	46834688	GPR116	H603P	NON_SYNONYMOUS_CODING	T	G	validated	7880	45.33%	passenger	N	no	no	no	passenger	100.00%		
AdCC2T	16	9862796	GRIN2A	I836T	NON_SYNONYMOUS_CODING	A	G	validated	7379	15.88%	passenger	D	no	no	no	non-passenger	53.00%		
AdCC2T	16	84163707	HSDL1	M184L	NON_SYNONYMOUS_CODING	T	A	validated	7630	47.44%	passenger	D	no	no	no	non-passenger	83.00%		
AdCC2T	1	166905866	ILDR2	C222Y	NON_SYNONYMOUS_CODING	C	T	validated	7343	52.19%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC2T	5	71411530	MAP1B	R64*	STOP_GAINED	C	T	validated	7517	17.93%		A	no	no	no	non-passenger	41.00%		

Sample ID	**Chromosome**	**Genomic position**	**Gene**	**Amino acid change**	**Effect**	**Reference allele**	**Alternate allele**	**Validation**	**Sequence depth (x)**	**MAF**	**CHASM Breast**	**Mutation Taster**	**5000S - Lawrence *et al*. (Nature, 2014)**	**127 genes; Kandoth *et al*. (Nature, 2013)**	**Cancer Gene Census**	**Consensus impact**	**Cancer cell fraction (ABSOLUTE)**	**Mutated in salivary gland AdCCs; Ho *et al* (Nat Genet 2013)**	**Mutated in salivary gland AdCCs; Stephens *et al* (JCI 2013)**
AdCC2T	9	112900341	AKAP2	E608_E609insAE	CODON_INSERTION	G	GGAAGCT	validated	7471	40.14%	.	P	no	no	no	passenger	73.00%		
AdCC2T	14	30095720	PRKD1	G598C	NON_SYNONYMOUS_CODING	C	A	validated	7511	17.89%	driver	D	no	no	no	non-passenger	32.00%	yes	
AdCC2T	12	112888199	PTPN11	A72V	NON_SYNONYMOUS_CODING	C	T	validated	7399	46.40%	passenger	D	yes	yes	yes	non-passenger	98.00%		
AdCC2T	7	26724464	SKAP2	D293A	NON_SYNONYMOUS_CODING	T	G	validated	7940	0.20%	passenger	D	no	no	no	non-passenger	14.00%		
AdCC2T	4	48384724	SLAIN2	V335fs	FRAME_SHIFT	AG	A	validated	7800	12.78%	.	A	no	no	no	non-passenger	24.00%		
AdCC2T	15	62944247	TLN2	R93Q	NON_SYNONYMOUS_CODING	G	A	validated	7877	12.09%	passenger	D	no	no	no	non-passenger	33.00%		
AdCC2T	X	41057975	USP9X	M1526fs	FRAME_SHIFT	A	AT	validated	6326	2.97%	.	A	no	yes	no	non-passenger	48.00%		
AdCC2T	X	41057831	USP9X	Y1477*	STOP_GAINED	T	G	validated	7834	2.73%		A	no	yes	no	non-passenger	20.00%		
AdCC2T	X	41073902	USP9X	Y1757*	STOP_GAINED	T	G	validated	7800	4.71%		A	no	yes	no	non-passenger	12.00%		
AdCC2T	X	70469018	ZMYM3	K493fs	FRAME_SHIFT	TTC	T	validated	787	32.53%	.	A	no	no	no	non-passenger	67.00%		
AdCC3T	15	30700159	GOLGA8R	W275R	NON_SYNONYMOUS_CODING	A	G	validated	7284	2.88%	passenger		no	no	no	passenger	43.00%		
AdCC3T	9	140063628	LRRC26	T228K	NON_SYNONYMOUS_CODING	G	T	not tested	not tested	not tested	passenger	N	no	no	no	passenger	40.00%		
AdCC3T	19	8999445	MUC16	S13577N	NON_SYNONYMOUS_CODING	C	T	validated	7175	0.14%	passenger		no	no	no	passenger	27.00%	yes	
AdCC3T	1	248616492	OR2T2	R132W	NON_SYNONYMOUS_CODING	C	T	validated	7760	24.92%	passenger	N	no	no	no	passenger	94.00%		
AdCC3T	11	18267463	SAA2	V75A	NON_SYNONYMOUS_CODING	A	G	not tested	not tested	not tested	passenger	N	no	no	no	passenger	100.00%		
AdCC3T	9	35708366	TLN1	L1481S	NON_SYNONYMOUS_CODING	A	G	validated	7318	48.51%	passenger	D	no	no	no	non-passenger	100.00%	yes	
AdCC4T	18	21218829	ANKRD29	T105N	NON_SYNONYMOUS_CODING	G	T	validated	7468	1.57%	passenger	D	no	no	no	non-passenger	38.00%		
AdCC4T	12	40040181	C12orf40	P85S	NON_SYNONYMOUS_CODING	C	T	not tested	not tested	not tested	passenger	N	no	no	no	passenger	50.00%		
AdCC4T	13	24465703	C1QTNF9B	C243S	NON_SYNONYMOUS_CODING	A	T	validated	7266	4.38%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC4T	16	68721617	CDH3	W591*	STOP_GAINED	G	A	validated	7674	30.11%		A	no	no	no	non-passenger	88.00%		
AdCC4T	1	1635380	CDK11A	.	SPLICE_SITE_ACCEPTOR	C	G	validated	6866	3.42%		D	no	no	no	non-passenger	29.00%		
AdCC4T	7	129929507	CPA2	R394S	NON_SYNONYMOUS_CODING	C	A	validated	7416	5.47%	passenger	N	no	no	no	passenger	31.00%		
AdCC4T	15	40650529	DISP2	G3R	NON_SYNONYMOUS_CODING	G	C	not tested	not tested	not tested	passenger	N	no	no	no	passenger	100.00%		
AdCC4T	6	83847586	DOPEY1	L1276Ffs	FRAME_SHIFT	A	AT	validated	7412	16.62%	.	A	no	no	no	non-passenger	95.00%		
AdCC4T	8	16859394	FGF20	G50C	NON_SYNONYMOUS_CODING	C	A	validated	6682	0.16%	passenger	N	no	no	no	passenger	100.00%		
AdCC4T	10	123279674	FGFR2	P253R	NON_SYNONYMOUS_CODING	G	C	validated	7556	18.90%	passenger	A	yes	yes	yes	non-passenger	82.00%		yes
AdCC4T	X	53264063	IQSEC2	A1269S	NON_SYNONYMOUS_CODING	C	A	validated	5752	0.12%	passenger	D	no	no	no	non-passenger	37.00%		
AdCC4T	5	154193601	LARP1	R1002P	NON_SYNONYMOUS_CODING	G	C	validated	4100	9.51%	passenger	D	no	no	no	non-passenger	31.00%		
AdCC4T	4	140651722	MAML3	P727S	NON_SYNONYMOUS_CODING	G	A	validated	7520	22.62%	passenger	D	no	no	no	non-passenger	58.00%	yes	
AdCC4T	5	140788637	PCDHGB6	H290Y	NON_SYNONYMOUS_CODING	C	T	validated	7414	5.95%	passenger	N	no	no	no	passenger	33.00%		
AdCC4T	X	144905880	SLITRK2	R646H	NON_SYNONYMOUS_CODING	G	A	validated	7872	22.29%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC4T	11	66472844	SPTBN2	A635S	NON_SYNONYMOUS_CODING	C	A	not tested	not tested	not tested	passenger	N	no	no	no	passenger	23.00%		
AdCC4T	X	123179178	STAG2	D210fs	FRAME_SHIFT	CTCACAAG	C	validated	7194	0.53%	.	A	yes	yes	yes	non-passenger	77.00%		
AdCC4T	11	93471361	TAF1D	Q125*	STOP_GAINED	G	A	validated	7762	27.72%		A	no	no	no	non-passenger	100.00%		

Sample ID	Chromo -some	Genomic position	Gene	Amino acid change	Effect	Reference allele	Alternate allele	Validat- ion	Sequence depth (x)	MAF	CHASM Breast	Mutation Taster	5000S - Lawrence *et al.* (Nature, 2014)	127 genes; Kandoth *et al.* (Nature, 2013)	Cancer Gene Census	Consensus impact	Cancer cell fraction (ABSO- LUTE)	Mutated in salivary gland AdCCs; Ho *et al* (Nat Genet 2013)	Mutated in salivary gland AdCCs; Stephens *et al* (JCI 2013)
AdCC4T	15	72039307	THSD4	E723Q	NON_SYNONYMOUS_CODING	G	C	validated	7745	20.83%	passenger	D	no	no	no	non-passenger	94.00%		
AdCC4T	4	68956285	TMPRSS11F	S80P	NON_SYNONYMOUS_CODING	A	G	validated	7095	3.85%	passenger	N	no	no	no	passenger	48.00%		
AdCC4T	8	67062687	TRIM55	I324T	NON_SYNONYMOUS_CODING	T	C	validated	2607	9.09%	passenger	D	no	no	no	non-passenger	21.00%		
AdCC4T	19	56952878	ZNF667	D624Y	NON_SYNONYMOUS_CODING	C	A	validated	7439	31.13%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC5T	1	19671683	CAPZB	E247K	NON_SYNONYMOUS_CODING	C	T	validated	7515	22.86%	passenger	D	no	no	no	non-passenger	46.00%		
AdCC5T	1	19671686	CAPZB	V246I	NON_SYNONYMOUS_CODING	C	T	validated	7217	21.96%	passenger	D	no	no	no	non-passenger	45.00%		
AdCC5T	2	234102590	INPP5D	T848M	NON_SYNONYMOUS_CODING	C	T	validated	7574	46.96%	passenger	N	no	no	no	passenger	91.00%		
AdCC5T	18	48703554	MEX3C	A383P	NON_SYNONYMOUS_CODING	C	G	validated	7204	6.75%	passenger	D	no	no	no	non-passenger	11.00%		
AdCC5T	11	1018408	MUC6	P1465T	NON_SYNONYMOUS_CODING	G	T	not tested	not tested	not tested	passenger	N	no	no	no	passenger	27.00%		
AdCC5T	3	122680038	SEMA5B	Q79*	STOP_GAINED	G	A	validated	7518	44.72%		A	no	no	no	non-passenger	100.00%		
AdCC5T	3	133664051	SLCO2A1	C450S	NON_SYNONYMOUS_CODING	C	G	validated	7521	46.90%	passenger	D	no	no	no	non-passenger	95.00%		
AdCC5T	2	39278343	SOS1	M269K	NON_SYNONYMOUS_CODING	A	T	validated	6276	54.46%	passenger	D	no	no	no	non-passenger	87.00%		
AdCC5T	1	32265412	SPOCD1	S594*	STOP_GAINED	G	T	validated	7808	45.61%		A	no	no	no	non-passenger	100.00%		
AdCC5T	10	63170208	TMEM26	G327C	NON_SYNONYMOUS_CODING	C	A	validated	7377	44.84%	passenger	N	no	no	no	passenger	100.00%		
AdCC5T	10	1123923	WDR37	L72P	NON_SYNONYMOUS_CODING	T	C	validated	7787	43.87%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC6T	10	72498632	ADAMTS14	P548L	NON_SYNONYMOUS_CODING	C	T	validated	7621	34.47%	passenger	N	no	no	no	passenger	45.00%		
AdCC6T	X	47428176	ARAF	A379V	NON_SYNONYMOUS_CODING	C	T	validated	7233	0.19%	driver	D	no	no	no	non-passenger	15.00%		
AdCC6T	X	49092016	CCDC22	.	START_GAINED	C	T	validated	7769	41.68%			no	no	no	passenger	97.00%		
AdCC6T	10	73572317	CDH23	E3157fs	FRAME_SHIFT	AG	A	validated	5941	35.28%	.	A	no	no	no	non-passenger	77.00%		
AdCC6T	12	107391316	CRY1	I481S	NON_SYNONYMOUS_CODING	A	C	validated	7378	33.86%	passenger	D	no	no	no	non-passenger	68.00%		
AdCC6T	5	74041510	GFM2	I281T	NON_SYNONYMOUS_CODING	A	G	validated	7850	32.84%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC6T	X	101969964	GPRASP2	S56F	NON_SYNONYMOUS_CODING	C	T	validated	7233	27.75%	passenger	N	no	no	no	passenger	75.00%		
AdCC6T	1	201180040	IGFN1	G2007R	NON_SYNONYMOUS_CODING	G	A	not tested	not tested	not tested	passenger	N	no	no	no	passenger	21.00%		
AdCC6T	16	87436663	MAP1LC3B	Y113C	NON_SYNONYMOUS_CODING	A	G	validated	7531	19.51%	passenger	D	no	no	no	non-passenger	51.00%		
AdCC6T	11	59834493	MS4A3	L141I	NON_SYNONYMOUS_CODING	C	A	not tested	not tested	not tested	passenger	N	no	no	no	passenger	97.00%		
AdCC6T	3	195512597	MUC4	P1952S	NON_SYNONYMOUS_CODING	G	A	not tested	not tested	not tested	passenger	N	no	no	no	passenger	46.00%	yes	
AdCC6T	20	32664866	RALY	G231S	NON_SYNONYMOUS_CODING	G	A	validated	5294	1.38%	passenger	N	no	no	no	passenger	82.00%		
AdCC6T	4	2514847	RNF4	G138*	STOP_GAINED	G	T	validated	6105	8.89%		D	no	no	no	non-passenger	13.00%		
AdCC6T	22	19163933	SLC25A1	.	SPLICE_SITE_DONOR	C	A	validated	7103	33.93%		D	no	no	no	non-passenger	100.00%		
AdCC6T	4	122681514	TMEM155	T110P	NON_SYNONYMOUS_CODING	T	G	validated	7732	33.79%	passenger	N	no	no	no	passenger	91.00%		
AdCC6T	17	5037195	USP6	R133K	NON_SYNONYMOUS_CODING	G	A	validated	7777	2.58%	passenger	D	no	no	yes	non-passenger	15.00%		
AdCC6T	19	50482425	VRK3	N451H	NON_SYNONYMOUS_CODING	T	G	validated	7862	33.55%	passenger	D	no	no	no	non-passenger	71.00%		
AdCC6T	7	57193788	ZNF479	C67R	NON_SYNONYMOUS_CODING	A	G	validated	7545	20.38%	passenger	N	no	no	no	passenger	75.00%		
AdCC8T	17	4542725	ALOX15	G135S	NON_SYNONYMOUS_CODING	C	T	validated	7347	0.12%	passenger	D	no	no	no	non-passenger	57.00%		yes

Sample ID	**Chromo -some**	**Genomic position**	**Gene**	**Amino acid change**	**Effect**	**Reference allele**	**Alternate allele**	**Validat- ion**	**Sequence depth (x)**	**MAF**	**CHASM Breast**	**Mutation Taster**	**5000S - Lawrence *et al.* (Nature, 2014)**	**127 genes; Kandoth *et al.* (Nature, 2013)**	**Cancer Gene Census**	**Consensus impact**	**Cancer cell fraction (ABSO- LUTE)**	**Mutated in salivary gland AdCCs; Ho *et al* (Nat Genet 2013)**	**Mutated in salivary gland AdCCs; Stephens *et al* (JCI 2013)**
AdCC8T	17	48681557	CACNA1G	T1404M	NON_SYNONYMOUS_CODING	C	T	validated	5570	11.65%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC8T	17	39296361	KRTAP4-6	S127P	NON_SYNONYMOUS_CODING	A	G	not tested	not tested	not tested	passenger	P	no	no	no	passenger	100.00%	yes	
AdCC8T	17	39412119	KRTAP9-9	S161Y	NON_SYNONYMOUS_CODING	C	A	not tested	not tested	not tested	passenger	N	no	no	no	passenger	41.00%		
AdCC8T	6	24411023	MRS2	Q161H	NON_SYNONYMOUS_CODING	G	T	validated	7956	29.30%	passenger	N	no	no	no	passenger	90.00%		
AdCC8T	4	100518256	MTTP	Y341*	STOP_GAINED	C	G	validated	7460	30.43%		A	no	no	no	non-passenger	100.00%	yes	
AdCC8T	12	20709592	PDE3A	.	SPLICE_SITE_ACCEPTOR	A	G	validated	7810	28.48%		D	no	no	no	non-passenger	77.00%		
AdCC8T	4	20512185	SLIT2	R332*	STOP_GAINED	C	T	validated	7606	2.41%		A	no	no	no	non-passenger	16.00%		
AdCC8T	19	58385546	ZNF814	D404E	NON_SYNONYMOUS_CODING	G	T	not tested	not tested	not tested	passenger	N	no	no	no	passenger	33.00%		
AdCC9T	X	74273274	ABCB7	E731D	NON_SYNONYMOUS_CODING	C	A	validated	7611	26.95%	passenger	D	no	no	no	non-passenger	62.00%		
AdCC9T	7	95157557	ASB4	C307Y	NON_SYNONYMOUS_CODING	G	A	validated	7588	43.45%	passenger	D	no	no	no	non-passenger	99.00%		
AdCC9T	7	140453154	BRAF	D594G	NON_SYNONYMOUS_CODING	T	C	validated	7632	42.18%	driver	D	yes	yes	yes	non-passenger	100.00%		
AdCC9T	4	1388944	CRIPAK	M215I	NON_SYNONYMOUS_CODING	G	A	not tested	not tested	not tested	passenger	N	no	yes	no	non-passenger	70.00%		
AdCC9T	12	49432644	MLL2	A2832fs	FRAME_SHIFT	G	GCAAAT	validated	7449	41.71%	.	A	yes	yes	yes	non-passenger	42.00%		
AdCC9T	11	1265992	MUC5B	R2631S	NON_SYNONYMOUS_CODING	C	A	not tested	not tested	not tested	passenger	N	no	no	no	passenger	35.00%		
AdCC9T	1	145323667	NBPF10	D1168E	NON_SYNONYMOUS_CODING	C	G	not tested	not tested	not tested	passenger	N	no	no	no	passenger	30.00%		
AdCC9T	21	46936005	SLC19A1	L448*	STOP_GAINED	A	T	validated	NA	NA		D	no	no	no	non-passenger	52.00%		
AdCC9T	7	100228635	TFR2	S383G	NON_SYNONYMOUS_CODING	T	C	validated	NA	NA	passenger	N	no	no	no	passenger	37.00%		
AdCC9T	5	82789383	VCAN	R155M	NON_SYNONYMOUS_CODING	G	T	validated	7785	47.32%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC10T	22	29758989	AP1B1	.	SPLICE_SITE_DONOR	C	G	not tested	not tested	not tested		D	no	no	no	non-passenger	100.00%		
AdCC10T	15	28483865	HERC2	R1211C	NON_SYNONYMOUS_CODING	G	A	not tested	not tested	not tested	passenger	D	no	no	no	non-passenger	19.00%		
AdCC10T	17	30351758	LRRC37B	L597I	NON_SYNONYMOUS_CODING	C	A	not tested	not tested	not tested	passenger	N	no	no	no	passenger	33.00%		
AdCC10T	1	11194409	MTOR	R1749G	NON_SYNONYMOUS_CODING	G	C	validated	3828	76.91%	driver	D	yes	yes	no	non-passenger	44.00%		
AdCC10T	15	52643623	MYO5A	R1226H	NON_SYNONYMOUS_CODING	C	T	validated	7299	43.57%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC10T	X	71359543	NHSL2	Y715*	STOP_GAINED	C	A	validated	7280	0.18%		D	no	no	no	non-passenger	96.00%		
AdCC10T	3	97868656	OR5H14	R143W	NON_SYNONYMOUS_CODING	C	T	not tested	not tested	not tested	passenger	N	no	no	no	passenger	35.00%		
AdCC10T	1	158517511	OR6Y1	V129L	NON_SYNONYMOUS_CODING	C	A	validated	7454	0.15%	passenger	N	no	no	no	passenger	39.00%		
AdCC10T	2	205990357	PARD3B	R444*	STOP_GAINED	C	T	validated	7330	45.93%		A	no	no	no	non-passenger	77.00%		
AdCC10T	2	198267483	SF3B1	R625H	NON_SYNONYMOUS_CODING	C	T	validated	7378	40.09%	passenger	D	yes	yes	yes	non-passenger	100.00%	yes	yes
AdCC11T	X	100749038	ARMCX4	A1821V	NON_SYNONYMOUS_CODING	C	T	not tested	not tested	not tested	passenger	N	no	no	no	passenger	100.00%		
AdCC11T	7	100645731	MUC12	E4106K	NON_SYNONYMOUS_CODING	G	A	not tested	not tested	not tested	passenger	N	no	no	no	passenger	48.00%		
AdCC11T	2	109988132	SH3RF3	V314M	NON_SYNONYMOUS_CODING	G	A	validated	3696	8.58%	passenger	D	no	no	no	non-passenger	27.00%		
AdCC11T	5	175717557	SIMC1	H325Y	NON_SYNONYMOUS_CODING	C	T	not tested	not tested	not tested	passenger	N	no	no	no	passenger	62.00%		
AdCC11T	19	38385094	WDR87	Y417N	NON_SYNONYMOUS_CODING	A	T	validated	7429	23%	passenger	D	no	no	no	non-passenger	58.00%	yes	
AdCC11T	X	128881719	XPNPEP2	E209D	NON_SYNONYMOUS_CODING	G	T	validated	6715	8.13%	passenger	N	no	no	no	passenger	79.00%		

Sample ID	Chromo-some	Genomic position	Gene	Amino acid change	Effect	Reference allele	Alternate allele	Validat-ion	Sequence depth (x)	MAF	CHASM Breast	Mutation Taster	5000S - Lawrence *et al*. (Nature, 2014)	127 genes; Kandoth *et al*. (Nature, 2013)	Cancer Gene Census	Consensus impact	Cancer cell fraction (ABSO-LUTE)	Mutated in salivary gland AdCCs; Ho *et al* (Nat Genet 2013)	Mutated in salivary gland AdCCs; Stephens *et al* (JCI 2013)
AdCC11T	7	99669556	ZNF3	N184S	NON_SYNONYMOUS_CODING	T	C	validated	3642	46.46%	passenger	N	no	no	no	passenger	100.00%		
AdCC12T	11	72425256	ARAP1	S207C	NON_SYNONYMOUS_CODING	G	C	validated	7302	41.93%	passenger	N	no	no	no	passenger	100.00%		
AdCC12T	15	41246442	CHAC1	T125M	NON_SYNONYMOUS_CODING	C	T	validated	7633	48.66%	passenger	D	no	no	no	non-passenger	85.00%		
AdCC12T	19	1026673	CNN2	Q5E	NON_SYNONYMOUS_CODING	C	G	not tested	not tested	not tested	passenger	N	no	no	no	passenger	100.00%		
AdCC12T	X	69665197	DLG3	A49V	NON_SYNONYMOUS_CODING	C	T	not tested	not tested	not tested	passenger	D	no	no	no	non-passenger	51.00%		
AdCC12T	4	153244232	FBXW7	D642G	NON_SYNONYMOUS_CODING	T	C	validated	4475	67.71%	driver	D	yes	yes	yes	non-passenger	61.00%	yes	
AdCC12T	12	13716611	GRIN2B	H1187Q	NON_SYNONYMOUS_CODING	G	C	validated	4999	64.31%	passenger	D	no	no	no	non-passenger	98.00%	yes	
AdCC12T	10	124909622	HMX2	N269H	NON_SYNONYMOUS_CODING	A	C	validated	7336	46.32%	passenger	D	no	no	no	non-passenger	81.00%		
AdCC12T	8	28928248	KIF13B	F1752L	NON_SYNONYMOUS_CODING	A	G	not tested	not tested	not tested	passenger	D	no	no	no	non-passenger	98.00%		
AdCC12T	17	39240577	KRTAP4-7	Y40C	NON_SYNONYMOUS_CODING	A	G	not tested	not tested	not tested	passenger	N	no	no	no	passenger	100.00%		
AdCC12T	10	129905764	MKI67	S1447N	NON_SYNONYMOUS_CODING	C	T	validated	5134	23.33%	passenger	N	no	no	no	passenger	100.00%		
AdCC12T	3	195510827	MUC4	A2542T	NON_SYNONYMOUS_CODING	C	T	not tested	not tested	not tested	passenger	P	no	no	no	passenger	100.00%		
AdCC12T	10	104158170	NFKB2	Y294C	NON_SYNONYMOUS_CODING	A	G	validated	6929	18.14%	passenger	D	no	no	yes	non-passenger	29.00%		
AdCC12T	18	21897344	OSBPL1A	W251*	STOP_GAINED	C	T	validated	7670	49.75%		D	no	no	no	non-passenger	72.00%		
AdCC12T	22	50728805	PLXNB2	G70V	NON_SYNONYMOUS_CODING	C	A	validated	6432	44.96%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC12T	17	74288749	QRICH2	Q521*	STOP_GAINED	G	A	validated	4415	32.23%		A	no	no	no	non-passenger	94.00%		
AdCC12T	12	122265762	SETD1B	.	SPLICE_SITE_DONOR	T	G	validated	7587	45.89%		D	no	no	no	non-passenger	100.00%		
AdCC12T	4	144446639	SMARCA5	R186*	STOP_GAINED	C	T	validated	7570	50.61%		A	no	no	no	non-passenger	96.00%		
AdCC12T	15	62939556	TLN2	V16A	NON_SYNONYMOUS_CODING	T	C	validated	7580	46.48%	passenger	D	no	no	no	non-passenger	92.00%		
AdCC32T	4	47556924	ATP10D	R606Q	NON_SYNONYMOUS_CODING	G	A	validated	7800	9.69%	passenger	D	no	no	no	non-passenger	22.00%		
AdCC32T	22	50169273	BRD1	F987fs	FRAME_SHIFT	AC	A	validated	7329	41.89%	.	D	no	no	no	non-passenger	83.00%		
AdCC32T	16	68842714	CDH1	T217fs	FRAME_SHIFT	CAG	C	validated	7415	42.16%	.	A	yes	yes	yes	non-passenger	68.00%		
AdCC32T	13	53035380	CKAP2	H141R	NON_SYNONYMOUS_CODING	A	G	not tested	not tested	not tested	passenger	N	no	no	no	passenger	100.00%		
AdCC32T	6	55128601	HCRTR2	R248H	NON_SYNONYMOUS_CODING	G	A	validated	2659	85.37%	passenger	D	no	no	no	non-passenger	96.00%		yes
AdCC32T	12	113906056	LHX5	R184fs	FRAME_SHIFT	CG	C	validated	5971	40.13%	.	A	no	no	no	non-passenger	68.00%		
AdCC32T	6	135513475	MYB	I181V	NON_SYNONYMOUS_CODING	A	G	validated	4424	74.93%	passenger	D	no	no	yes	non-passenger	100.00%	yes	
AdCC32T	1	247614650	OR2B11	L212S	NON_SYNONYMOUS_CODING	A	G	validated	7580	14.46%	passenger	D	no	no	no	non-passenger	27.00%		
AdCC32T	11	56114217	OR8K1	N235Y	NON_SYNONYMOUS_CODING	A	T	validated	7099	2.21%	passenger	N	no	no	no	passenger	9.00%		
AdCC32T	5	86658477	RASA1	L481P	NON_SYNONYMOUS_CODING	T	C	validated	7671	40.79%	passenger	D	yes	no	no	non-passenger	95.00%		
AdCC32T	11	78614415	TENM4	T216M	NON_SYNONYMOUS_CODING	G	A	validated	6678	37.87%	passenger	D	no	no	no	non-passenger	100.00%		
AdCC32T	10	70928298	VPS26A	M261L	NON_SYNONYMOUS_CODING	A	T	validated	4765	13.03%	passenger	D	no	no	no	non-passenger	58.00%		
AdCC32T	17	1637508	WDR81	T1726R	NON_SYNONYMOUS_CODING	C	G	validated	7476	42.19%	passenger	D	no	no	no	non-passenger	75.00%		
AdCC32T	5	751328	ZDHHC11B	C194S	NON_SYNONYMOUS_CODING	C	G	not tested	not tested	not tested		N	no	no	no	passenger	100.00%		

Supplementary Table S6: Recurrent copy number gains and losses identified in AdCCs of the breast.

Copy number gains				
Chromosome	**Cyto-band**	**Cases altered (n)**	**Sample IDs**	**Genes**
17	q21.32	3	AdCC4, AdCC11, AdCC10	ITGB3, C17orf57, CBX1, CDK5RAP3, COPZ2, KPNB1, LRRC46, MIR1203, MIR152, MRPL10, MRPL45P2, NFE2L1, NPEPPS, OSBPL7, PNPO, PRR15L, SCRN2, SKAP1, SNX11, SP2, SP6, TBKBP1, TBX21, hsa-mir-1203, hsa-mir-52, HOXB1, HOXB13, HOXB13AS1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXB9, LOC404266, MIR10A, MIR196A1, MIR3185, PRAC, TTLL6, hsa-mir-10a, hsa-mir-196a-1, hsa-mir-3185, CALCOCO2, ATP5G1, B4GALNT2, GIP, IGF2BP1, SNF8, UBE2Z, GNGT2, ABI3, FLJ40194, PHOSPHO1, ZNF652
17	q21.33	3	AdCC4, AdCC11, AdCC10	NGFR, NXPH3, PHB, SPOP, SLC35B1, FAM117A, KAT7, TAC4, ABCC3, ACSF2, ANKRD40, CACNA1G, CHAD, COL1A1, DLX3, DLX4, EME1, EPN3, FLJ45513, HILS1, ITGA3, LINC00483, LOC253962, LOC284080, LRRC59, LUC7L3, MRPL27, MYCBPAP, PDK2, PPP1R9B, RSAD1, SAMD14, SGCA, SPATA20, TMEM92, WFIKKN2, XYLT2
17	q22	3	AdCC4, AdCC11, AdCC10	C17orf67, DGKE, MIR3614, MTVR2, NOG, TRIM25, COIL, SCPEP1, AKAP1, RNF126P1, MSI2, MRPS23, CUEDC1, DYNLL2, SRSF1, VEZF1, MSX2P1, OR4D1, BZRAP1, C17orf47, EPX, HSF5, LOC100506779, LPO, MIR142, MIR4736, MKS1, MPO, MTMR4, OR4D2, RNF43, 4-Sep, SUPT4H1, TEX14, hsa-mir-142, PPM1E, RAD51C, GDPD1, MIR301A, MIR454, MIR4729, PRR11, SKA2, SMG8, TRIM37, YPEL2, hsa-mir-301a, hsa-mir-454
17	q23.1	3	AdCC4, AdCC11, AdCC10	DHX40, CLTC, PTRH2, VMP1, MIR21, TUBD1, hsa-mir-21, RPS6KB1, CA4, HEATR6, LOC645638, LOC653653, MIR4737, RNFT1, TBC1D3P1-DHX40P1, USP32
17	q23.2	3	AdCC4, AdCC11, AdCC10	C17orf64, SCARNA20, APPBP2, PPM1D, BCAS3, C17orf82, NACA2, TBX2, TBX4, BRIP1, INTS2, MED13, EFCAB3, METTL2A, TBC1D3P2, TLK2, 10-Mar, MIR548W, MRC2, TANC2, hsa-mir-633
17	q23.3	3	AdCC4, AdCC11, AdCC10	ACE, CYB561, DCAF7, KCNH6, TACO1, MAP3K3, LIMD2, LOC729683, STRADA, CCDC47, C17orf72, CD79B, CSH1, CSH2, CSHL1, DDX42, ERN1, FTSJ3, GH1, GH2, ICAM2, PSMC5, SCN4A, SMARCD2, SNORA76, SNORD104, TCAM1P, TEX2, PECAM1, MILR1, POLG2, DDX5, MIR3064, MIR5047, CEP95, SMURF2
17	q24.1	3	AdCC4, AdCC11, AdCC10	AMZ2P1, GNA13, LOC146880, LRRC37A3, PLEKHM1P, hsa-mir-4315-2, RGS9, AXIN2, CEP112
17	q24.2	3	AdCC4, AdCC11, AdCC10	APOH, PRKCA, MIR634, hsa-mir-634, CACNG1, CACNG4, CACNG5, HELZ, PSMD12, PITPNC1, BPTF, NOL11, SNORA38B, hsa-mir-548d2, C17orf58, KPNA2, LOC100499466, LOC440461, AMZ2, ARSG, SLC16A6, MIR635, PRKAR1A, WIPI1, hsa-mir-635, ABCA6, ABCA8, ABCA9, FAM20A, MIR4524A
17	q24.3	3	AdCC4, AdCC11, AdCC10	ABCA10, ABCA5, MAP2K6, KCNJ16, KCNJ2, KCNJ2-AS1, LINC00511, LOC100499467, SLC39A11, SOX9
17	q25.1	3	AdCC4, AdCC11, AdCC10	C17orf80, CDC42EP4, COG1, CPSF4L, FAM104A, SDK2, SSTR2, LINC00469, BTBD17, CD300A, CD300C, CD300LB, DNAI2, GPR142, GPRC5C, KIF19, LOC400620, MGC16275, RPL38, TTYH2, CD300LD, C17orf77, CD300E, CD300LF, RAB37, ACOX1, ARMC7, ATP5H, C17orf109, C17orf110, C17orf28, CASKIN2, CDR2L, FADS6, FBF1, FDXR, GALK1, GGA3, GRB2, GRIN2C, H3F3B, HN1, ICT1, ITGB4, KCTD2, KIAA0195, LLGL2, LOC100287042, MIF4GD, MIR3615, MIR3678, MIR4738, MRPL38, MRPS7, MYO15B, NAT9, NT5C, NUP85, OTOP2, OTOP3, RECQL5, SAP30BP, SLC16A5, SLC25A19, SLC9A3R1, SUMO2, TMEM104, TRIM47, TRIM65, TSEN54, UNC13D, UNK, USH1G, WBP2
12	p11.1	2	AdCC4, AdCC10	ALG10, SYT10
12	q12	2	AdCC4, AdCC10	ALG10B
12	p11.22	2	AdCC4, AdCC10	CCDC91, FAR2, ERGIC2, OVCH1, TMTC1
12	p11.21	2	AdCC4, AdCC10	IPO8, AMN1, C12orf35, CAPRIN2, DDX11, DENND5B, FAM60A, FLJ13224, H3F3C, LOC100287314, LOC100506660, METTL20, TSPAN11, BICD1, FGD4, DNM1L, YARS2, PKP2
17	q11.1	2	AdCC4, AdCC10	TBC1D3P5, KSR1
17	q11.2	2	AdCC4, AdCC10	C17orf108, LGALS9, NOS2, NLK, PYY2, KRT18P55, PPY2, IFT20, MIR4723, POLDIP2, SARM1, SEBOX, TMEM199, TMEM97, TNFAIP1, VTN, SLC46A1, SLC13A2, FOXN1, UNC119, PIGS, ALDOC, SPAG5, KIAA0100, SGK494, SPAG5-AS1, SDF2, SUPT6H, PROCA1, C17orf63, NEK8, RAB34, RPL23A, SNORD42A, SNORD42B, SNORD4A, SNORD4B, TLCD1, TRAF4, ERAL1, MIR451A, MIR451B, hsa-mir-451, CRYBA1, DHRS13, FLOT2, MIR144, MIR4523, MIR4732, MYO18A, NUFIP2, PHF12, PIPOX, SEZ6, TAOK1, TIAF1, hsa-mir-144, ABHD15, ANKRD13B, CORO6, EFCAB5, GIT1, SSH2, TP53I13, MIR3184, MIR423, NSRP1, hsa-mir-3184, hsa-mir-423, SLC6A4, BLMH, TMIGD1, ADAP2, ATAD5, CPD, CRLF3, DPRXP4, GOSR1, LRRC37BP1, RNF135, SH3GL1P2, SUZ12P, TBC1D29, TEFM, MIR4733, NF1, EVI2A, EVI2B, OMG, RAB11FIP4, MIR4724, MIR193A, hsa-mir-193a, MIR4725, C17orf79, MIR365B, hsa-mir-365-2, UTP6, ARGFXP2, LRRC37B, RHOT1, SH3GL1P1, SUZ12, C17orf75, MIR632, PSMD11, RHBDL3, ZNF207, hsa-mir-632, ACCN1, CDK5R1, MYO1D, SPACA3, TMEM98

Copy number gains				
Chromo-some	**Cyto-band**	**Cases altered (n)**	**Sample IDs**	**Genes**
17	q12	2	AdCC4, AdCC10	AA06, CCL2, CCL7, CCL11, CCL8, CCL13, CCL1, C17orf102, TMEM132E, CCT6B, ZNF830, LIG3, RAD51D, RAD51L3-RFFL, RFFL, FNDC8, NLE1, UNC45B, SLC35G3, SLFN11, SLFN12, SLFN13, SLFN5, SLFN12L, AP2B1, GAS2L2, PEX12, RASL10B, SLFN14, SNORD7, C17orf50, MMP28, TAF15, C17orf66, CCL5, AATF, CCL14, CCL14-CCL15, CCL15, CCL16, CCL18, CCL23, CCL3, CCL3L1, CCL3L3, CCL4, CCL4L1, CCL4L2, DHRS11, GGNBP2, LHX1, LYZL6, MRM1, MYO19, PIGW, RDM1, TBC1D3B, TBC1D3C, TBC1D3G, TBC1D3H, ZNHIT3, MIR2909, hsa-mir-2909, ACACA, C17orf78, TADA2A, DUSP14, SYNRG, DDX52, HNF1B, LOC284100, LOC440434, MRPL45, TBC1D3, TBC1D3F, ARHGAP23, C17orf96, C17orf98, CISD3, CWC25, FBXO47, GPR179, LASP1, LOC100505576, MIR4726, MIR4727, MIR4734, MLLT6, PCGF2, PIP4K2B, PSMB3, RPL23, SNORA21, SOCS7, SRCIN1, ARL5C, CACNB1, FBXL20, FLJ43826, LOC100131347, PLXDC1, RPL19, STAC2, MED1, CDK12, ERBB2, GRB7, IKZF3, MIEN1, MIR4728, NEUROD2, PGAP3, PNMT, PPP1R1B, STARD3, TCAP, ZPBP2, GSDMB, ORMDL3, LRRC3C
17	q21.1	2	AdCC4, AdCC10	GSDMA, PSMD3, CSF3, MED24, SNORD124, CASC3, MSL1, NR1D1, RAPGEFL1, THRA, WIPF2
17	q21.2	2	AdCC4, AdCC10	CDC6, GJD3, IGFBP4, RARA, TNS4, TOP2A, CCR7, KRT10, KRT12, KRT222, KRT24, KRT25, KRT26, KRT27, KRT28, SMARCE1, TMEM99, KRT20, KRT23, KRT39, KRT40, KRTAP1-1, KRTAP1-3, KRTAP1-5, KRTAP2-1, KRTAP2-2, KRTAP2-4, KRTAP3-1, KRTAP3-2, KRTAP3-3, KRTAP4-1, KRTAP4-11, KRTAP4-12, KRTAP4-2, KRTAP4-3, KRTAP4-4, KRTAP4-5, KRTAP4-6, KRTAP4-7, KRTAP4-8, KRTAP4-9, KRTAP9-1, KRTAP9-2, KRTAP9-3, KRTAP9-4, KRTAP9-8, KRTAP9-9, LOC730755, KRTAP16-1, KRTAP17-1, KRT13, KRT14, KRT15, KRT16, KRT17, KRT19, KRT31, KRT32, KRT33A, KRT33B, KRT34, KRT35, KRT36, KRT37, KRT38, KRT42P, KRT9, LOC100505782, LOC147093, EIF1, GAST, HAP1, ACLY, CNP, DNAJC7, FKBP10, JUP, KLHL10, KLHL11, LEPREL4, NT5C3L, TTC25, NKIRAS2, ATP6V0A1, CCR10, CNTNAP1, COASY, DHX58, EZH1, FAM134C, GHDC, HCRT, HSD17B1, HSPB9, KAT2A, KCNH4, MLX, NAGLU, PLEKHH3, PSMC3IP, PTRF, RAB5C, STAT3, STAT5A, STAT5B, TUBG1, TUBG2, ZNF385C
17	q21.31	2	AdCC4, AdCC10	AARSD1, AOC2, AOC3, AOC4, ARL4D, BECN1, BRCA1, C17orf105, CCDC56, CNTD1, DHX8, DUSP3, ETV4, G6PC, IFI35, LOC100130581, LOC100190938, LOC388387, MEOX1, MIR2117, MPP3, NBR1, NBR2, PSME3, RAMP2, RND2, RPL27, RUNDC1, SOST, TMEM106A, VAT1, VPS25, WNK4, hsa-mir 2117, CD300LG, MPP2, ADAM11, ASB16, ATXN7L3, C17orf104, C17orf53, C17orf65, CCDC43, DBF4B, FAM171A2, FAM215A, FZD2, G6PC3, GJC1, GPATCH8, GRN, HDAC5, HIGD1B, ITGA2B, LSM12, NAGS, PPY, PYY, RUNDC3A, SLC25A39, SLC4A1, TMEM101, TMUB2, UBTF, EFTUD2, C1QL1, CCDC103, DCAKD, GFAP, KIF18B, NMT1, ACBD4, ARHGAP27, ARL17A, ARL17B, C17orf46, C17orf69, CRHR1, FMNL1, HEXIM1, HEXIM2, IMP5, KIAA1267, LOC100128977, LOC100130148, LOC100133991, LOC644172, LOC644246, LRRC37A, LRRC37A2, LRRC37A4, MAP3K14, MAPT, MGC57346, MIR4315-1, MIR4315-2, NSF, NSFP1, PLCD3, PLEKHM1, STH, WNT3, hsa-mir-4315-1
17	q21.32	2	AdCC4, AdCC10	CDC27, GOSR2, MYL4, RPRML, WNT9B
17	q21.33	2	AdCC4, AdCC10	TOB1, LOC400604, NME1, NME1-NME2, SPAG9, NME2, MBTD1, UTP18, CA10
17	q22	2	AdCC4, AdCC10	KIF2B, LOC100506650, TOM1L1, COX11, HLF, STXBP4, MMD, TMEM100, PCTP, ANKFN1
17	q25.1	2	AdCC4, AdCC10	AANAT, CDK3, CYGB, EVPL, EXOC7, FAM100B, FOXJ1, GALR2, LOC100507218, LOC100507246, PRCD, PRPSAP1, QRICH2, RHBDF2, RNF157, SNORD1A, SNORD1B, SNORD1C, SPHK1, SRP68, ST6GALNAC2, TEN1, TEN1-CDK3, UBE2O, ZACN, MXRA7, ST6GALNAC1, JMJD6, METTL23, MFSD11, MIR636, SRSF2, hsa-mir-636
17	q25.2	2	AdCC4, AdCC10	LINC00338, MGAT5B, SEC14L1, SCARNA16, SEPT9
17	q25.3	2	AdCC4, AdCC10	AFMID, BIRC5, C17orf99, CYTH1, DNAH17, FLJ45079, LOC100131096, LOC100507351, MIR4316, PGS1, SOCS3, SYNGR2, TK1, TMC6, TMC8, TMEM235, TNRC6C, USP36, hsa-mir-4316, C1QTNF1, CANT1, CARD14, CBX2, CBX4, CBX8, CCDC40, EIF4A3, ENGASE, ENPP7, GAA, LGALS3BP, LOC100507410, LOC100653515, MIR4739, RBFOX3, RNF213, SGSH, SLC26A11, TBC1D16, TIMP2, LOC100294362, AATK, AATKAS1, ACTG1, ALYREF, ANAPC11, ARHGDIA, ARL16, ASPSCR1, AZI1, BAHCC1, BAIAP2, C17orf56, C17orf70, C17orf89, C17orf90, CCDC137, CCDC57, CHMP6, DCXR, DUS1L, ENDOV, FAM195B, FASN, FLJ90757, FSCN2, GCGR, GPS1, HGS, LINC00482, LRRC45, MAFG, MAFGAS1, MIR1250, MIR3065, MIR3186, MIR338, MIR4730, MIR4740, MIR657, MRPL12, MYADML2, NOTUM, NPB, NPLOC4, NPTX1, P4HB, PCYT2, PDE6G, PPP1R27, PYCR1, RAC3, RFNG, RPTOR, SIRT7, SLC25A10, SLC38A10, STRA13, TMEM105, TSPAN10, hsa-mir-1250, hsa-mir-3065, hsa-mir-3186, hsa-mir-338, hsa-mir657, B3GNTL1, C17orf101, C17orf62, CD7, CSNK1D, FLJ43681, FN3K, FN3KRP, FOXK2, HEXDC, METRNL, NARF, RAB40B, SECTM1, SLC16A3, TBCD, TEX19, UTS2R, WDR45L, ZNF750

Copy number losses				
Chromo-some	**Cyto-bands**	**Cases altered (n)**	**Sample IDs**	**Genes**
12	q12	5	AdCC3, AdCC8, AdCC32, AdCC2, AdCC1	ARID2, LOC400027, SCAF11
12	q13.11	5	AdCC3, AdCC8, AdCC32, AdCC2, AdCC1	SLC38A1, SLC38A2, SLC38A4, AMIGO2, FAM113B, LOC100233209, MIR4698, ENDOU, HDAC7, RAPGEF3, RPAP3, SLC48A1, VDR, COL2A1, SENP1, TMEM106C, ASB8, C12orf68, H1FNT, OR10AD1, PFKM, ZNF641, ANP32D, C12orf54, OR8S1, LALBA, KANSL2, MIR1291, SNORA34, hsa-mir-1291, SNORA2A, CCNT1, SNORA2B
12	q13.12	5	AdCC3, AdCC8, AdCC32, AdCC2, AdCC1	ADCY6, LOC255411, MIR4701, CACNB3, DDX23, RND1, ARF3, CCDC65, DDN, FKBP11, MLL2, PRKAG1, RHEBL1, WNT1, WNT10B, DHH, LMBR1L, TUBA1B, TUBA1A, TUBA1C, PRPH, C1QL4, DNAJC22, FAM186B, FMNL3, KCNH3, LOC100335030, MCRS1, PRPF40B, SPATS2, TROAP, TMBIM6, NCKAP5L, ACCN2, AQP2, AQP5, AQP6, BCDIN3D, FAIM2, LOC100286844, LOC283332, RACGAP1, SMARCD1, GPD1, C12orf62, CERS5, LIMA1, DIP2B, FAM186A, LARP4, MIR1293, hsa-mir-1293, ATF1, METTL7A, TMPRSS12, HIGD1C, SLC11A2, LETMD1, CSRNP2, TFCP2
12	q13.13	5	AdCC3, AdCC8, AdCC32, AdCC2, AdCC1	POU6F1, DAZAP2, SMAGP, BIN2, CELA1, GALNT6, SLC4A8, SCN8A, ANKRD33, FIGNL2, ACVR1B, ACVRL1, C12orf44, EIF4B, GRASP, KRT1, KRT18, KRT2, KRT3, KRT4, KRT5, KRT6A, KRT6B, KRT6C, KRT7, KRT71, KRT72, KRT73, KRT74, KRT75, KRT76, KRT77, KRT78, KRT79, KRT8, KRT80, KRT81, KRT82, KRT83, KRT84, KRT85, KRT86, LOC283403, LOC283404, NR4A1, CSAD, ESPL1, IGFBP6, ITGB7, LOC283335, MFSD5, RARG, SOAT2, SPRYD3, TENC1, ZNF740, PFDN5, C12orf10, AAAS, SP7, SP1, AMHR2, PRR13, PCBP2, MAP3K12, TARBP2, NPFF, ATF7, LOC100652999, ATP5G2, CALCOCO1, CBX5, FLJ12825, HNRNPA1, HNRNPA1P10, HOTAIR, HOXC10, HOXC11, HOXC12, HOXC13, HOXC4, HOXC5, HOXC6, HOXC8, HOXC9, LOC100240734, LOC100240735, LOC400043, MIR196A2, MIR3198-2, MIR615, NFE2, SMUG1, hsa-mir-196a-2, hsa-mir-615, COPZ1, MIR148B, hsa-mir-148b, GPR84, ZNF385A, ITGA5, GTSF1, NCKAP1L
12	q13.2	5	AdCC3, AdCC8, AdCC32, AdCC2, AdCC1	DCD, GLYCAM1, LACRT, MUCL1, PDE1B, PPP1R1A, KIAA0748, NEUROD4, OR10A7, OR6C1, OR6C3, OR6C6, OR6C74, OR9K2, OR6C65, OR6C75, OR6C2, OR6C4, OR6C68, OR6C70, OR6C76, METTL7B, OR10P1, BLOC1S1, BLOC1S1-RDH5, CD63, CDK2, DGKA, DNAJC14, ERBB3, GDF11, IKZF4, ITGA7, MMP19, ORMDL2, PA2G4, PMEL, RAB5B, RDH5, RPL41, RPS26, SARNP, SUOX, TMEM198B, WIBG, ZC3H10, ESYT1, MYL6B, MYL6, SMARCC2, RNF41
12	q13.3	5	AdCC3, AdCC8, AdCC32, AdCC2, AdCC1	OBFC2B, SLC39A5, ANKRD52, COQ10A, CS, CNPY2, PAN2, IL23A, STAT2, APOF, TIMELESS, MIP, SPRYD4, GLS2, BAZ2A, RBMS2, ATP5B, SNORD59B, SNORD59A, PTGES3, NACA, PRIM1, HSD17B6, SDR9C7, GPR182, LRP1, MIR1228, MYO1A, NAB2, NDUFA4L2, NXPH4, RDH16, SHMT2, STAC3, STAT6, TAC3, TMEM194A, ZBTB39, hsa-mir-1228, R3HDM2, ARHGAP9, DCTN2, DDIT3, DTX3, GLI1, INHBC, INHBE, KIF5A, MARS, MBD6, PIP4K2C, hsa-mir-616, ARHGEF25, SLC26A10, B4GALNT1, OS9
12	q14.1	5	AdCC3, AdCC8, AdCC32, AdCC2, AdCC1	AGAP2, AVIL, CDK4, CYP27B1, LOC100130776, 9-Mar, METTL1, METTL21B, TSFM, TSPAN31, CTDSP2, LOC100506844, MIR26A2, hsa-mir-26a-2, XRCC6BP1
12	q12	4	AdCC3, AdCC8, AdCC32, AdCC2	NELL2, TMEM117, DBX2, PLEKHA8P1, RACGAP1P, ANO6, RNY5
12	q12	3	AdCC3, AdCC8, AdCC32	ADAMTS20, PUS7L, IRAK4, TWF1
12	q14.1	3	AdCC3, AdCC2, AdCC1	LRIG3, SLC16A7
12	p11.1	2	AdCC3, AdCC32	ALG10, SYT10
12	q12	2	AdCC3, AdCC32	ALG10B, CPNE8, KIF21A, ABCD2, C12orf40, SLC2A13, LRRK2, CNTN1, PDZRN4, GXYLT1, YAF2, ZCRB1, PPHLN1, PRICKLE1
X	q21.1	2	AdCC3, AdCC1	RPS6KA6, hsa-mir-548i-4, HDX, UBE2DNL, APOOL, SATL1
9	q32	2	AdCC5, AdCC8	ZNF618, AMBP, COL27A1, KIF12, MIR455, hsa-mir-455, AKNA, ATP6V1G1, C9orf91, DFNB31, LOC100505478, ORM1, ORM2, TNFSF15, TNFSF8
9	q33.1	2	AdCC5, AdCC8	1-Dec, TNC, LINC00474, PAPPA, ASTN2, LOC100128505, TRIM32, DBC1, SNORA70C, TLR4
9	q33.2	2	AdCC5, AdCC8	CDK5RAP2, MIR147A, hsa-mir-147, C5, CNTRL, FBXW2, LOC100288842, LOC253039, MEGF9, PHF19, PSMD5, TRAF1, RAB14, GSN, GGTA1P, STOM, DAB2IP, TTLL11, LHX6, MIR4478, MORN5, NDUFA8, RBM18, MRRF, OR1B1, OR1J1, OR1J2, OR1J4, OR1L8, OR1N1, OR1N2, OR1Q1, PTGS1, OR1L1, OR1L3, OR1L4, OR1L6, OR5C1, OR1K1, PDCL, RC3H2, SNORD90, ZBTB6, ZBTB26, RABGAP1, GPR21
9	q33.3	2	AdCC5, AdCC8	MIR600, MIR600HG, STRBP, hsa-mir-600, CRB2, DENND1A, MIR601, hsa-mir-601, GPR144, LHX2, LOC100129034, MIR181A2, MIR181A2HG, MIR181B2, NEK6, NR5A1, NR6A1, OLFML2A, PSMB7, RPL35, WDR38, hsa-mir-181a-2, hsa-mir-181b-2, ARPC5L, GOLGA1, SCAI, PPP6C, RABEPK, HSPA5, GAPVD1, MAPKAP1, FAM125B, PBX3, NRON, LMX1B, RALGPS1, ZBTB34, ZBTB43, ANGPTL2, GARNL3, SLC2A8, ZNF79, RPL12, SNORA65, LRSAM1, FAM129B

Copy number losses				
Chromosome	**Cyto-bands**	**Cases altered (n)**	**Sample IDs**	**Genes**
9	q34.11	2	AdCC5, AdCC8	STXBP1, AK1, C9orf117, C9orf16, CDK9, CERCAM, CIZ1, COQ4, DNM1, DPM2, ENG, FAM102A, FPGS, GOLGA2, LCN2, LOC100289019, LOC389791, MIR199B, MIR219-2, MIR2861, MIR2964A, MIR3154, MIR3911, MIR3960, MIR4672, NAIF1, PIP5KL1, PTGES2, PTRH1, SH2D3C, SLC25A25, SLC27A4, ST6GALNAC4, ST6GALNAC6, SWI5, TOR2A, TRUB2, TTC16, URM1, hsa-mir-199b, hsa-mir-219-2, hsa-mir-2861, hsa-mir-3154
12	q14.1	2	AdCC2, AdCC1	FAM19A2, USP15, C12orf61, MIRLET7I, MON2, PPM1H, hsa-let-7i
12	q14.2	2	AdCC2, AdCC1	AVPR1A, DPY19L2, TMEM5
12	q21.31	2	AdCC1, AdCC12	C12orf26, CCDC59, TMTC2, SLC6A15, TSPAN19, ALX1, LRRIQ1, RASSF9, NTS, MGAT4C
12	q21.32	2	AdCC1, AdCC12	C12orf50, MIR548AL, MKRN9P, C12orf29
17	p13.3	2	AdCC4, AdCC10	ABR, BHLHA9, C17orf97, CRK, DBIL5P, DOC2B, DPH1, FAM101B, FAM57A, GEMIN4, GLOD4, HIC1, INPP5K, LOC100306951, LOC100506388, MIR132, MIR212, MIR22, MIR22HG, MIR3183, MYO1C, NXN, OVCA2, PITPNA, PRPF8, RILP, RNMTL1, RPA1, RPH3AL, RTN4RL1, SCARF1, SERPINF1, SERPINF2, SLC43A2, SMG6, SMYD4, TIMM22, TLCD2, TUSC5, VPS53, WDR81, YWHAE, hsa-mir-132, hsa-mir-212, hsa-mir-22, hsa-mir-3183, KIAA0664, LOC284009, METTL16, MIR1253, MNT, PAFAH1B1, RAP1GAP2, SGSM2, SNORD91A, SNORD91B, SRR, TSR1, hsa-mir-1253, OR1A1, OR1A2, OR1D2, OR1D4, OR1D5, OR1G1, OR3A1, OR3A2, OR3A4P
17	p13.2	2	AdCC4, AdCC10	ASPA, OR1E1, OR1E2, OR3A3, SPATA22, TRPV3, ANKFY1, ATP2A3, C17orf85, CAMKK1, CTNS, CYB5D2, GGT6, GSG2, ITGAE, MYBBP1A, P2RX1, P2RX5, P2RX5-TAX1BP3, SHPK, SMTNL2, SPNS2, SPNS3, TAX1BP3, TMEM93, TRPV1, UBE2G1, ZZEF1, ALOX15, ARRB2, C17orf107, CAMTA2, CHRNE, CXCL16, ENO3, GLTPD2, GP1BA, GPR172B, INCA1, KIF1C, MED11, MINK1, PELP1, PFN1, PLD2, PSMB6, RNF167, SLC25A11, SPAG7, TM4SF5, USP6, VMO1, ZFP3, ZMYND15, ZNF232, ZNF594, LOC100130950, SCIMP, RABEP1, NUP88, RPAIN, C1QBP, DHX33, DERL2, LOC728392, MIS12, NLRP1, LOC339166, WSCD1, AIPL1, FAM64A, PITPNM3, KIAA0753
17	p13.1	2	AdCC4, AdCC10	TXNDC17, MED31, C17orf100, ALOX15P1, MIR4520A, MIR4520B, ALOX12, ALOX12P2, FBXO39, LOC100506713, SLC13A5, TEKT1, XAF1, ACADVL, ACAP1, ASGR1, ASGR2, BCL6B, C17orf49, C17orf61, C17orf61-PLSCR3, C17orf74, C17orf81, CD68, CHRNB1, CLDN7, CLEC10A, CTDNEP1, DLG4, DVL2, EIF4A1, EIF5A, FGF11, FXR2, GABARAP, GPS2, KCTD11, MIR195, MIR324, MIR497, MIR497HG, MPDU1, NEURL4, NLGN2, PHF23, PLSCR3, POLR2A, RNASEK, RNASEK-C17ORF49, SAT2, SENP3, SENP3-EIF4A1, SHBG, SLC16A11, SLC16A13, SLC2A4, SLC35G6, SNORA48, SNORA67, SNORD10, SOX15, SPEM1, TMEM102, TMEM95, TNFSF12, TNFSF12-TNFSF13, TNFSF13, TNK1, YBX2, ZBTB4, hsa-mir-195, hsa-mir-324, hsa-mir-497, ATP1B2, TP53, WRAP53, EFNB3, DNAH2, CHD3, CNTROB, CYB5D1, GUCY2D, KCNAB3, KDM6B, LOC284023, LSMD1, RPL29P2, SCARNA21, TMEM88, TRAPPC1, ALOX12B, ALOX15B, ALOXE3, ARHGEF15, AURKB, C17orf59, CTC1, HES7, KRBA2, LINC00324, LOC100128288, MIR3676, MIR4314, MIR4521, ODF4, PER1, PFAS, RANGRF, SLC25A35, TMEM107, VAMP2, hsa-mir-4314, NDEL1, RNF222, RPL26, MYH10, CCDC42, MFSD6L, PIK3R6, SPDYE4, NTN1, PIK3R5, STX8, DHRS7C, GAS7, GLP2R, MYH1, MYH13, MYH2, MYH4, MYH8, RCVRN, USP43, WDR16, MYH3, SCO1, C17orf48, LOC100289255, TMEM220
17	p12	2	AdCC4, AdCC10	PIRT, SHISA6, DNAH9, ZNF18, MAP2K4, FLJ34690, MIR744, hsa-mir-744, MYOCD, ARHGAP44, ELAC2, CDRT15P1, COX10, HS3ST3A1, hsa-mir-548h-3, CDRT15, HS3ST3B1, MGC12916, CDRT7, MIR4731, PMP22, CDRT4, FAM18B2, FAM18B2-CDRT4, TEKT3, ADORA2B, CDRT1, CDRT15P2, MEIS3P1, NCOR1, TBC1D26, TRIM16, TTC19, ZNF286A, ZSWIM7
17	p11.2	2	AdCC4, AdCC10	CENPV, MIR1288, PIGL, hsa-mir-1288, UBB, TRPV2, C17orf76-AS1, SNORD49B, SNORD49A, FAM211A, SNORD65, ZNF287, ZNF624, CCDC144A, FAM106CP, KRT16P2, TNFRSF13B, USP32P1, MPRIP, ATPAF2, C17orf39, COPS3, FLCN, LRRC48, MED9, MIR33B, NT5M, PEMT, PLD6, RAI1, RASD1, SMCR5, SMCR9, SREBF1, TOM1L2, hsa-mir-33b, DRG2, ALKBH5, CCDC144B, EVPLL, FAM106A, FLII, LGALS9C, LLGL1, LOC339240, MYO15A, SHMT1, SMCR7, SMCR8, TOP3A, USP32P2
X	p21.1	2	AdCC3, AdCC1	hsa-mir-548f-5