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Integrative molecular characterization of head and neck cancer cell model genomes

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Abstract

Background—Cell lines are invaluable model systems for the investigation of cancer. Knowledge of the molecular alterations that exist within cell models is required to define the mechanisms governing cellular phenotypes.

Methods—Five tongue squamous cell carcinomas cell lines and one submaxillary salivary gland epidermoid carcinoma cell line were analyzed for copy number and mRNA expression by tiling-path DNA microarrays and Agilent Whole Human Genome Oligoarrays, respectively.

Results—Integrative analysis of genetic and expression alterations revealed the molecular landscape of each cell line. Molecular results for individual cell lines and across all samples have been summarized and made available for easy reference.

Conclusion—Our integrative genomic analyses have defined the DNA and RNA alterations for each individual line. These data will be useful to anyone modelling oral cancer behaviour, providing a molecular context that will be useful for deciphering cell phenotypes.

Keywords

oral cancer; head and neck cancer; cell models; copy number alteration; RNA expression alteration

INTRODUCTION

Head and neck squamous cell carcinoma (HNSCC) is the eighth most common cancer in the world.(1) It is a heterogeneous disease primarily affecting the oral cavity, salivary glands, oropharynx, hypopharynx, and larynx. Model systems, such as cell lines are often used as research tools to study many cancer types, including HNSCC.(2,3) They allow for manipulation of tumour cells in a laboratory setting. However, tumourigenic cell lines in such studies have often not been fully characterized at the molecular level. Like tumours themselves, cancer cell lines can vary greatly with respect to their genetic background. Analysis of cell phenotypes without concurrent analysis of underlying molecular changes represents a lost opportunity to understand the mechanistic basis for disease.

One characteristic of most solid tumours is genomic instability. This is demonstrated by the numerous DNA gains and deletions present in tumour genomes.(4) DNA alterations can lead to aberrant expression of oncogenes and tumour suppressor genes that drive tumourigenesis. For HNSCC development, gene alterations such as loss of chromosomes 3p and 9p, mutation of *p53*, loss of 13q, and high-level amplification of *CCND1* have been associated with premalignant disease stages.(5–8) Loss of chromosomes 4q and 8p, on the other hand, are believed to occur as later events in tumourigenesis.(9) Such DNA alterations, including high-level amplification of *CCND1*,(10) often leads to overexpression, while homozygous deletion of *CDKN2A* leads to silencing of *p16^{INK4A}* in oral tumours.(11)

Established HNSCC cell lines — particularly SCC-4, SCC-9, SCC-15, SCC-25, A253, and Cal27 — are widely used as models of head and neck cancer. A preliminary search in PubMed reveals 407 publications that use at least one of these lines, demonstrating their importance as tools for modeling biochemical, immunological, and pharmacological behaviours. These various behaviours could be influenced by the molecular alterations that exist in each line, yet few efforts have been made to characterize such changes. Previously, genetic alterations of four of the OSCC cell lines (SCC-4, SCC-9, SCC-15, and SCC-25) have been characterized by cDNA microarrays with low resolution and with no data on intragenic regions.(12) Thus, comprehensive characterization of genomic alterations in the most commonly used cell models are needed. In addition, *a priori* knowledge of both genomic and gene expression changes for a given cell line would facilitate selection of the most appropriate model system for a given *in vitro* analysis. In this report we provide full characterization of genome and transcriptome alterations in six commonly used HNSCC cell lines. These data will serve as an excellent resource when designing future experiments that attempt to model HNSCC behaviour.

MATERIALS AND METHODS

Cell lines

Five tongue squamous cell carcinomas cell lines (SCC-4,(13) SCC-9,(13) SCC-25,(13) SCC-15,(13) and Cal27(14)) and one submaxillary salivary gland epidermoid carcinoma cell line (A-253)(15) were purchased from the American Type Culture Collection (ATCC). All cell lines were cultured according to ATCC recommendations. Cells were harvested for DNA and RNA extractions when they reached ~ 80% confluency. Genomic DNA was extracted by the standard phenol-chloroform extraction protocol, and total RNA was extracted using the TRIzol (Invitrogen, Carlsbad, CA) protocol followed by DNase I treatment.

Tiling-path DNA microarray

Extracted DNA from each cell line was analyzed by whole genome tiling-path microarrays (SMRT v.2) developed at the British Columbia Cancer Research Centre Array Laboratory. (16) For this array, the whole genome is represented as more than 26,000 overlapping bacterial artificial chromosome (BAC) clones spotted in duplicate with tiling coverage of the human genome. Pooled normal male DNA was used as reference for all microarray experiments. Labelling, hybridization, scanning, and washing of the slides were performed as previously described.(8)

Imaging and analysis of genomic data

Array images were analyzed with GenePix Pro 6.1. A three-step normalization procedure, including locally weighted linear regression (LOWESS) fitting, spatial, and median normalization was used to remove systematic biases.(17) *SeeGH* software was used to combine duplicate spot data and display log₂ signal intensity ratios in relation to genomic

locations in the hg18 assembly (NCBI Build 36.1).(18) Data points with standard deviation >0.075 and signal to noise ratio <3 in either channel were removed from each sample.

Two separate algorithms, *aCGH-Smooth* and *DNAcopy*, were used to detect copy number gains and losses.(19,20) An alteration was only called when detected concurrently by both algorithms. *aCGH-Smooth* employs a local search algorithm that uses a maximum likelihood estimation to smooth the observed array CGH values between consecutive breakpoints to a common value.(19) The Lambda and the maximum number of breakpoints in initial pool were set to 6.75 and 100 respectively.(8) *DNAcopy* employs a circular binary segmentation algorithm that uses a random permutation test to determine the statistical significance of change points.(20) Default settings in *DNAcopy* were used for our data.

A third algorithm based on moving-average was used for the identification of high-level DNA amplification and presumptive homozygous deletions.(21) The threshold was set at $\log_2$ signal intensity ratio >0.8 for high-level amplification or ≤ -0.8 for homozygous deletions. Only regions containing ≥ 3 overlapping clones with such calls were identified in order to avoid false-positives due to hybridization artefacts.

Gene expression profiling

Total RNA collected from each cell line was analyzed by Agilent Whole Human Genome Microarray 4 $\times$ 44K. This array represents more than 41,000 unique human transcripts. Labelling and hybridizations were performed according to manufacturer's instructions (Agilent Technologies). Hybridized arrays were scanned using Axon GenePix 4000B and 4200A scanner.

Data analysis of expression profiles

Array images were analyzed using GenePix Pro 6.1. For normalization processing, each background-subtracted intensity value was divided by the median array intensity of each microarray. The median array intensity was calculated based on the background-subtracted intensity value for all spots excluding control type spots on the array. Genes within regions of high-level copy number change were extracted for each cell line. Oral cell lines with no high-level copy number change serve as the baseline for the genes in each alteration region and the mean of each median-normalized intensity value of each probe was compared with those of the cell lines with high-level change.

RESULTS AND DISCUSSION

Cancer cell lines are important model systems for investigating the biology of head and neck cancers. They allow for characterization of a variety of disease phenotypes and also serve as a tool for functional screens. When using such models, it is imperative to determine how closely the model resembles clinical disease. However, genome-wide characterization of most cell lines has not previously been attempted. Characterizing DNA alterations in these cells and determining the contribution of these changes to mRNA expression would provide a very valuable reference point for interpreting experimental results generated using these cell lines. The set of six genomic and six expression profiles has been deposited to Gene Expression Omnibus (GEO) database at NCBI, series accession number GSE16872.

High-level DNA amplification is a common mechanism for driving overexpression of oncogenes, while homozygous deletion is known to inactivate tumour suppressor genes and also contribute to cancer processes.(21–23) High resolution genomic analysis delineates the precise boundaries of amplified or deleted regions, thus defining genes that warrant further investigation. Parallel analysis of gene expression data from the same cells helps to differentiate between "driver" and "passenger" genes in a given segmental DNA change, the

former being genes that contribute to the cancer phenotype, the latter being altered simply due to its proximity to a "driver" gene.(21,24) For example, any candidate gene in an amplicon that is not overexpressed is unlikely to represent a "driver" gene. Figure 1 displays a summary of altered regions detected in each oral cell line, while the specific base pair positions are listed in Supplemental tables S1 to S6. Furthermore, as this paper serves as a reference, the copy number status of well known cancer genes obtained from the Cancer Gene Census is catalogued in Table 1.(25) Whole genome copy number karyogram of each cell line and description of each cell line is represented in Supplemental figure S1.

It is known that head and neck cancers, like many solid tumours, are a molecularly heterogeneous group where several regions of alteration and genes have been reported at high frequencies but may occur in various combinations in a given tumour. Genetic alterations frequently occurring in tumours indicate an importance for carcinogenesis. Loss of chromosome 3p and 9p are genetic events frequently documented in head and neck tumours, and both have been implicated as one of the earliest changes in oral premalignant lesions and associated with progression risks.(6,9) All six cell lines revealed segmental losses of chromosome 3p and 9p (detailed regions of genetic alterations are listed in Supplemental Tables S1 to S6). Cal27 revealed only one region of segmental loss of 9p24.1-p23, while the remaining five cell lines exhibited copy number loss at 9p21.3, which contain the tumour suppressor *CDKN2A*. Genetic loss of chromosome 8p is also an expected change that has been frequently described in clinical specimens.(26,27) Whole arm 8p loss was found in SCC-15, SCC-9, Cal27, while A253 exhibited a region of homozygous deletion on 8p23.2-p23.2 and a region of high-level DNA amplification on 8p22. Gain of chromosome 8q is also a frequent genetic alteration in head and neck tumours, harbouring the known oncogene *MYC*.(26) Cell lines A253, SCC-15, SCC-4, SCC-25, and SCC-9 all showed low level gain of 8q24 (*MYC*). Regions of high-level amplification, including 3q26, 7p11 and 11q13, occur frequently in head and neck tumours.(26–30) These regions have been associated with *PIK3CA*, *EGFR*, and *CCND1* respectively. SCC-4 and SCC-9 did not reveal genetic gain of 3q26.32 whereas the lines A253, SCC-15, and SCC-25 showed low level gains. Cell lines SCC-15 and Cal27 exhibited region of high-level amplification at the *EGFR* locus, and cell lines SCC-4, SCC-9, and A-253 exhibited low-level copy number gain. Cell lines SCC-9 and Cal27 showed genetic gain of the *CCND1* locus, whereas four cell lines A253, SCC-15, SCC-4, and SCC-25 displayed high-level amplification of this locus. Complex alterations on chromosome arm 11q were revealed SCC-15, SCC-4, SCC-25, and A253 (Fig. 2).

One common characteristic of the cell lines is the presence of high-level amplifications, where many of the lines contained multiple regions of high-level DNA amplification. This is similar to tumour genomes where it has been reported that high-level amplification is observed in ~65% of cases, although usually only one or two regions per tumour.(26) High-level amplifications indicating multiple copy numbers and regions of homozygous deletion, where both copies are lost, often result in gene overexpression and underexpression.(21,22,31) These types of alteration often arise under selective pressure of genes important for the growth of cancer cells. Therefore we focused our analysis on the expression of genes within these regions. The expression levels of genes within all the regions of high-level DNA amplification and homozygous deletion detected in the six cell lines are presented in Supplemental figure S2. In general regions of homozygous deletion often resulted in lower expression levels for many of the genes within the region, while higher level of expression was often observed in at least one gene within an amplicon compared to cell lines without such amplicon. For example, a common region of high-level amplification of 4.15 Mbp in size on 11p13-p12 was detected in Cal27 and A-253, which contains 20 RefSeq genes (Fig. 3). The expression of 17 of these genes were analyzed, and the gene *CD44* has a two-fold increase in expression compared to the other four cell lines without such high-level

amplification. Other genes inside this amplicon, *PDHX* and *CAT*, also have a 5-fold increase in expression. The expression of *CD44* is also among the top five-percentile of all expressed genes in the six cell lines, suggesting that while high-level DNA amplification causes higher expression of the gene, other mechanisms might also cause its high expression in cell lines without such amplicon. However, as there are many ways to regulate gene expression, some of the amplified regions do not show the expected changes in gene expression. Further molecular examinations of epigenetic alterations and sequence analyses would be essential to fully characterize the different molecular aspects of each cell line.

CONCLUSIONS

Head and neck cancer cell lines are important model systems for investigating head and neck cancer biology. Comprehensive characterization of their genetic alterations is useful for the selection and interpretation of studies using cell lines. Our data presents the first comprehensive catalogue of copy number and expression alterations in six commonly used and easily obtainable oral cancer cell lines, thus providing a good resource for researchers to select and use these cell lines in experiments.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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REFERENCES

1. Parkin DM, Bray F, Ferlay J, Pisani P. Global cancer statistics, 2002. *CA Cancer J Clin.* 2005; 55(2):74–108. [PubMed: 15761078]
2. Lin CJ, Grandis JR, Carey TE, et al. Head and neck squamous cell carcinoma cell lines: established models and rationale for selection. *Head Neck.* 2007; 29(2):163–188. [PubMed: 17312569]
3. Martin CL, Reshmi SC, Ried T, et al. Chromosomal imbalances in oral squamous cell carcinoma: examination of 31 cell lines and review of the literature. *Oral Oncol.* 2008; 44(4):369–382. [PubMed: 17681875]
4. Singh B. Molecular pathogenesis of head and neck cancers. *J Surg Oncol.* 2008; 97(8):634–639. [PubMed: 18493941]
5. Califano J, van der Riet P, Westra W, et al. Genetic progression model for head and neck cancer: implications for field cancerization. *Cancer Res.* 1996; 56(11):2488–2492. [PubMed: 8653682]
6. Mao L, Lee JS, Fan YH, et al. Frequent microsatellite alterations at chromosomes 9p21 and 3p14 in oral premalignant lesions and their value in cancer risk assessment. *Nat Med.* 1996; 2(6):682–685. [PubMed: 8640560]
7. Rosin MP, Cheng X, Poh C, et al. Use of allelic loss to predict malignant risk for low-grade oral epithelial dysplasia. *Clin Cancer Res.* 2000; 6(2):357–362. [PubMed: 10690511]
8. Tsui IF, Rosin MP, Zhang L, Ng RT, Lam WL. Multiple aberrations of chromosome 3p detected in oral premalignant lesions. *Cancer Prev Res (Phila Pa).* 2008; 1(6):424–429. [PubMed: 19138989]
9. Mao L, Hong WK, Papadimitrakopoulou VA. Focus on head and neck cancer. *Cancer Cell.* 2004; 5(4):311–316. [PubMed: 15093538]

10. Akervall JA, Michalides RJ, Mineta H, et al. Amplification of cyclin D1 in squamous cell carcinoma of the head and neck and the prognostic value of chromosomal abnormalities and cyclin D1 overexpression. *Cancer*. 1997; 79(2):380–389. [PubMed: 9010112]
11. Nakahara Y, Shintani S, Mihara M, Ueyama Y, Matsumura T. High frequency of homozygous deletion and methylation of p16(INK4A) gene in oral squamous cell carcinomas. *Cancer Lett*. 2001; 163(2):221–228. [PubMed: 11165758]
12. Jarvinen AK, Autio R, Kilpinen S, et al. High-resolution copy number and gene expression microarray analyses of head and neck squamous cell carcinoma cell lines of tongue and larynx. *Genes Chromosomes Cancer*. 2008; 47(6):500–509. [PubMed: 18314910]
13. Rheinwald JG, Beckett MA. Tumorigenic keratinocyte lines requiring anchorage and fibroblast support cultures from human squamous cell carcinomas. *Cancer Res*. 1981; 41(5):1657–1663. [PubMed: 7214336]
14. Gioanni J, Fischel JL, Lambert JC, et al. Two new human tumor cell lines derived from squamous cell carcinomas of the tongue: establishment, characterization and response to cytotoxic treatment. *Eur J Cancer Clin Oncol*. 1988; 24(9):1445–1455. [PubMed: 3181269]
15. Giard DJ, Aaronson SA, Todaro GJ, et al. In vitro cultivation of human tumors: establishment of cell lines derived from a series of solid tumors. *J Natl Cancer Inst*. 1973; 51(5):1417–1423. [PubMed: 4357758]
16. Ishkanian AS, Malloff CA, Watson SK, et al. A tiling resolution DNA microarray with complete coverage of the human genome. *Nat Genet*. 2004; 36(3):299–303. [PubMed: 14981516]
17. Khojasteh M, Lam WL, Ward RK, MacAulay C. A stepwise framework for the normalization of array CGH data. *BMC Bioinformatics*. 2005; 6:274. [PubMed: 16297240]
18. Chi B, deLeeuw RJ, Coe BP, Ng RT, MacAulay C, Lam WL. MD-SeeGH: a platform for integrative analysis of multi-dimensional genomic data. *BMC Bioinformatics*. 2008; 9:243. [PubMed: 18492270]
19. Jong K, Marchiori E, Meijer G, Vaart AV, Ylstra B. Breakpoint identification and smoothing of array comparative genomic hybridization data. *Bioinformatics*. 2004; 20(18):3636–3637. [PubMed: 15201182]
20. Olshen AB, Venkatraman ES, Lucito R, Wigler M. Circular binary segmentation for the analysis of array-based DNA copy number data. *Biostatistics*. 2004; 5(4):557–572. [PubMed: 15475419]
21. Lockwood WW, Chari R, Coe BP, et al. DNA amplification is a ubiquitous mechanism of oncogene activation in lung and other cancers. *Oncogene*. 2008; 27(33):4615–4624. [PubMed: 18391978]
22. Hahn SA, Schutte M, Hoque AT, et al. DPC4, a candidate tumor suppressor gene at human chromosome 18q21.1. *Science*. 1996; 271(5247):350–353. [PubMed: 8553070]
23. Snijders AM, Schmidt BL, Fridlyand J, et al. Rare amplicons implicate frequent deregulation of cell fate specification pathways in oral squamous cell carcinoma. *Oncogene*. 2005; 24(26):4232–4242. [PubMed: 15824737]
24. Haber DA, Settleman J. Cancer: drivers and passengers. *Nature*. 2007; 446(7132):145–146. [PubMed: 17344839]
25. Futreal PA, Coin L, Marshall M, et al. A census of human cancer genes. *Nat Rev Cancer*. 2004; 4(3):177–183. [PubMed: 14993899]
26. Baldwin C, Garnis C, Zhang L, Rosin MP, Lam WL. Multiple microalterations detected at high frequency in oral cancer. *Cancer Res*. 2005; 65(17):7561–7567. [PubMed: 16140918]
27. Smeets SJ, Braakhuis BJ, Abbas S, et al. Genome-wide DNA copy number alterations in head and neck squamous cell carcinomas with or without oncogene-expressing human papillomavirus. *Oncogene*. 2006; 25(17):2558–2564. [PubMed: 16314836]
28. Redon R, Muller D, Caulee K, Wanherdrick K, Abecassis J, du Manoir S. A simple specific pattern of chromosomal aberrations at early stages of head and neck squamous cell carcinomas: PIK3CA but not p63 gene as a likely target of 3q26-qter gains. *Cancer Res*. 2001; 61(10):4122–4129. [PubMed: 11358835]
29. Huang X, Godfrey TE, Gooding WE, McCarty KS Jr, Gollin SM. Comprehensive genome and transcriptome analysis of the 11q13 amplicon in human oral cancer and synteny to the 7F5

- amplicon in murine oral carcinoma. *Genes Chromosomes Cancer*. 2006; 45(11):1058–1069. [PubMed: 16906560]
30. Huang X, Gollin SM, Raja S, Godfrey TE. High-resolution mapping of the 11q13 amplicon and identification of a gene, TAOS1, that is amplified and overexpressed in oral cancer cells. *Proc Natl Acad Sci U S A*. 2002; 99(17):11369–11374. [PubMed: 12172009]
31. Albertson DG. Gene amplification in cancer. *Trends Genet*. 2006; 22(8):447–455. [PubMed: 16787682]

Figure 1.

Summary of copy number alteration in each cell line. Copy number gain is presented as vertical lines on the right side of the chromosome, and vertical lines on the left side indicate copy number loss. High-level copy number change is represented by a star on the right (DNA amplification) or left (homozygous deletion) of the chromosome. Genetic alteration of each cell line is labelled with different colours, SCC-15 (blue), SCC-4 (red), SCC-25 (green), SCC-9 (purple), A-253 (orange), and Cal27 (pink).

Figure 2.

Multiple levels of segmental copy number alterations are detected in six cell lines on chromosome 11q. Each BAC clone is displayed as vertical line representing its genomic coverage. Data points to the left and right of the centre line (purple) represent DNA copy number losses and gains, respectively. Regions of gain are highlighted in red and loss is shaded in green.

Figure 3.

Integrative analysis of genetic and expression levels of genes within 11p13-p12 amplicon. *A*, Alignment of chromosome region 11p for six cell lines. Each BAC clone is displayed as vertical line representing its genomic coverage. Minimal region of DNA amplification of A-253 and Cal27 is marked by two black lines and is 4.15 Mbp in size. *B*, The expression level of 17 genes within this amplicon is analyzed by expression arrays. For each cell line, median-normalized expression values are represented on the y-axis and the corresponding gene is listed on the x-axis.

Table 1

Copy number status of cancer genes in the six head and neck cancer cell lines.

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
ABL1	abl-interactor 1	10006	10p12.1	-	-	-	-	-	-
ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	25	9q34.12	+	+	+	+	+	+
ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2	27	1q24-q25	-	-	+	-	-	-
ACSL6	acyl-CoA synthetase long-chain family member 6	23305	5q23.3	-	-	-	-	-	-
AF15Q14	AF15q14 protein	57082	15q15.1	-	-	-	-	-	-
AF1Q	ALL1-fused gene from chromosome 1q	10962	1q21.2	-	-	+	-	-	-
AF5q31	ALL1 fused gene from 5q31	27125	5q31.1	-	-	-	-	-	-
AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	10142	7q21.2	+	+	-	-	+	-
AKT1	v-akt murine thymoma viral oncogene homolog 1	207	14q32.33	-	+	+	-	-	-
AKT2	v-akt murine thymoma viral oncogene homolog 2	208	19q13.2	+	-	-	-	-	-
ALK	anaplastic lymphoma kinase (Ki-1)	238	2p23.2	-	-	-	-	-	-
ALO17	KIAA1618 protein	57714	17q25.3	+	-	-	+	-	-
APC	adenomatous polyposis of the colon gene	324	5q22.2	-	-	-	-	-	-
ARHGAP26	GTPase regulator associated with focal adhesion kinase pp125(FAK)	23092	5q31.3	+	-	-	-	-	-
ARHGEF12	RHO guanine nucleotide exchange factor (GEF) 12 (LARG)	23365	11q23.3	-	-	+	+	-	-

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
ARNT	aryl hydrocarbon receptor nuclear translocator	405	1q21						
ASPSR1	alveolar soft part sarcoma chromosome region, candidate 1	79058	17q25.3	+	-		+		
ATF1	activating transcription factor 1	466	12q13.12			+	-		
ATIC	5-aminimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	471	2q35		-				
ATM	ataxia telangiectasia mutated	472	11q22.3	-	-		+	-	-
BCL10	B-cell CLL/lymphoma 10	8915	1p22.3			-			
BCL11A	B-cell CLL/lymphoma 11A	53335	2p16.1						
BCL11B	B-cell CLL/lymphoma 11B (CTIP2)	64919	14q32.2		++	+			
BCL2	B-cell CLL/lymphoma 2	596	18q21.33	-	-			-	-
BCL3	B-cell CLL/lymphoma 3	602	19q13.31	+					
BCL5	B-cell CLL/lymphoma 5	603	17q23.2						
BCL6	B-cell CLL/lymphoma 6	604	3q27.3	+	+	+	+	+	+
BCL7A	B-cell CLL/lymphoma 7A	605	12q24.31		-	+	+		
BCL9	B-cell CLL/lymphoma 9	607	1q21		-				
BCR	breakpoint cluster region	613	22q11.23		-	+		+	
BIRC3	baculoviral IAP repeat-containing 3	330	11q22.2	+	-		+	-	+
BLM	Bloom Syndrome	641	15q26.1						
BMP1A	bone morphogenetic protein receptor, type IA	657	10q23.2					-	

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
BRAF	v-raf murine sarcoma viral oncogene homolog B1	673	7q34	-	-	-	-	-	-
BRCA1	familial breast/ovarian cancer gene 1	672	17q21.31	-	-	-	+	-	-
BRCA2	familial breast/ovarian cancer gene 2	675	13q13.1	-	+	-	-	-	-
BRD4	bromodomain containing 4	23476	19p13.12	-	-	-	-	-	-
BRIP1	BRCA1 interacting protein C-terminal helicase 1	83990	17q23.2	-	-	-	-	-	-
BTG1	B-cell translocation gene 1, anti-proliferative	694	12q22	-	-	-	-	-	-
BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	701	15q15.1	-	-	-	-	-	-
C12orf9	chromosome 12 open reading frame 9	93669	12q14.3	-	-	-	-	-	-
C15orf21	chromosome 15 open reading frame 21	283651	15q21.1	-	-	-	-	-	-
CARD11	caspase recruitment domain family, member 11	84433	7p22.2	+	+	+	+	+	+
CARS	cysteinyl-tRNA synthetase	833	11p15.4	-	-	-	-	-	-
CBFA2T1	core-binding factor, runt domain, alpha subunit 2;translocated to, 1 (ETO)	862	8q21.3	+	+	+	+	-	-
CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3 (MTG-16)	863	16q24.3	-	-	-	-	-	-
CBFB	core-binding factor, beta subunit	865	16q22.1	-	-	+	-	-	-
CBL	Cas-Br-M (murine) ecotropic retroviral transforming	867	11q23.3	-	-	+	+	-	-

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
CCDC6	coiled-coil domain containing 6	8030	10q21.2					-	
CCNB1IP1	enhancer of invasion 10 - fused to HMG A2	57820	14q11.2	+		+			++
CCND1	cyclin D1	595	11q13.3	++	++	++	+	++	+
CCND2	cyclin D2	894	12p13.32			+	-	-	
CCND3	cyclin D3	896	6p21.1	+		+	+	-	
CDH1	cadherin 1, type 1, E-cadherin (epithelial) (ECAD)	999	16q22.1			+			
CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	1009	16q21						
CDK4	cyclin-dependent kinase 4	1019	12q14.1			+			
CDK6	cyclin-dependent kinase 6	1021	7q12		++			+	
CDKN2A-p14ARF	cyclin-dependent kinase inhibitor 2A--p14ARF protein	1029	9p21.3	-	-	-	-	-	
CDKN2A-p16(INK4a)	cyclin-dependent kinase inhibitor 2A (p16(INK4a)) gene	1029	9p21.3	-	-	-	-	-	
CDX2	caudal type homeo box transcription factor 2	1045	13q12.2	-	+		-		
CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	1050	19q13.11	+					
CEP1	centrosomal protein 1	11064	9q33.2	+		+		+	+
CHEK2	CHK2 checkpoint homolog (S. pombe)	11200	22q12.1			+			
CHIC2	cysteine-rich hydrophobic domain 2	26511	4q12					-	-
CHN1	chimerin (chimaerin) 1	1123	2q31.1						
CIC	capicua homolog (Drosophila)	23152	19q13.2	+					
CLTC	clathrin, heavy polypeptide (Hc)	1213	17q23.2						

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
CLTCL1	clathrin, heavy polypeptide-like 1	8218	22q11.21			+		+	
CMKOR1	chemokine orphan receptor 1	57007	2q37.3						
COL1A1	collagen, type I, alpha 1	1277	17q21.33						
COPEB	core promoter element binding protein (KLF6)	1316	10p15.1		-			-	-
COX6C	cytochrome c oxidase subunit VIc	1345	8q22.2	+	+	+	+		
CREB1	cAMP responsive element binding protein 1	1385	2q33.3		-				
CREB3L2	cAMP responsive element binding protein 3-like 2	64764	7q32-q34		-			-	
CREBBP	CREB binding protein (CBP)	1387	16p13.3		+	+		+	
CTNNB1	catenin (cadherin-associated protein), beta 1	1499	3p22.1	-	-	-		-	-
CXXC6	Leukemia-associated protein with a CXXC domain	80312	10q21.3			+		-	
CYLD	familial cylindromatosis gene	1540	16q12.1			+			
DDB2	damage-specific DNA binding protein 2	1643	11p11.2			+	+		
DDIT3	DNA-damage-inducible transcript 3	1649	12q13.3		+	+			
DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	1662	11q22.3	-	-		+	-	-
DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	1656	11q23.3	-	-	+	+	-	-
DEK	DEK oncogene (DNA binding)	7913	6p22.3	+			+	-	
DUX4	double homeobox, 4	22947	4q35.2	-	-	-	-	-	-
EGFR	epidermal growth factor receptor (erythroblastic	1956	7p12.3-p12.1	++	+	+	+	+	++

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
	leukemia viral (v-erb-b) oncogene homolog, avian)								
EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	1974	3q27.3	+	+	+	+	+	+
ELKS	ELKS protein	23085	12p13.33			+		-	
ELL	ELL gene (11-19 lysine-rich leukemia gene)	8178	19p13.11						
ELN	elastin	2006	7q11.23		+				
	echinoderm microtubule associated protein like 4	27436	2p21						
EML4	300 kd E1A-Binding protein gene	2033	22q13.2						
EP300	epidermal growth factor receptor pathway substrate 15 (AF1p)	2060	1p32						
EPS15	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	2064	17q12						
ERBB2	excision repair cross-complementing rodent repair deficiency, complementation group 2 (xeroderma pigmentosum D)	2068	19q13.32	+					
ERCC2	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	2071	2q14.3						
ERCC3	excision repair cross-complementing rodent repair deficiency, complementation group 4	2072	16p13.12			+	-	+	
ERCC4	excision repair cross-complementing rodent repair deficiency, complementation group 4	2073	13q33.1	+	+				
ERCC5	excision repair cross-complementing rodent repair deficiency, complementation group 4								

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
	complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))								
ERG	v-ets erythroblastosis virus E26 oncogene like (avian)	2078	21q22.2	-	-	-	-	-	
ETV1	ets variant gene 1	2115	7p21.2	+	+			+	+
ETV4	ets variant gene 4 (E1A enhancer binding protein, E1AF)	2118	17q21.31						
ETV5	ets variant gene 5	2119	3q37.2	+	+	+	+	+	+
ETV6	ets variant gene 6 (TEL oncogene)	2120	12p13.2	+	+	+	-	-	
EV11	ecotropic viral integration site 1	2122	3q26.2	+		+		+	+
EWSR1	Ewing sarcoma breakpoint region 1 (EWS)	2130	22q12.2			+			
EXT1	multiple exostoses type 1 gene	2131	8q24.11	+	+	+	+	+	
EXT2	multiple exostoses type 2 gene	2132	11p11.2			+	+		
FANCA	Fanconi anemia, complementation group A	2175	16q24.3						
FANCC	Fanconi anemia, complementation group C	2176	9q22.32	+		+		+	+
FANCD2	Fanconi anemia, complementation group D2	2177	3p25.3	-	-	-			-
FANCE	Fanconi anemia, complementation group E	2178	6p21.31	+		+	+		
FANCF	Fanconi anemia, complementation group F	2188	11p14.3					-	

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
FANCG	Fanconi anemia, complementation group G	2189	9p13.3	-	-	-	++	+	
FBXW7	F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila)	55294	4q31.3	-				-	-
FCGR2B	Fc fragment of IgG, low affinity IIb, receptor for (CD32)	2213	1q23		-	+			
FEV	FEV protein - (HSRNAFEV)	54738	2q35						
FGFR1	fibroblast growth factor receptor 1	2260	8p12	-			-	-	-
FGFR1OP	FGFR1 oncogene partner (FOP)	11116	6q27	+		+	+		
FGFR2	fibroblast growth factor receptor 2	2263	10q26.12-q26.13						
FGFR3	fibroblast growth factor receptor 3	2261	4p16.3						
FH	fumarate hydratase	2271	1q42.1		+			-	
FIP1L1	FIP1 like 1 (S. cerevisiae)	81608	4q12					-	-
FLCN	folliculin, Birt-Hogg-Dube syndrome	201163	17p11.2	+	+	+	+	+	
FLI1	Friend leukemia virus integration 1	2313	11q24.3	-	-	+	+	-	-
FLT3	fms-related tyrosine kinase 3	2322	13q12.2	-	+		-		
FNBP1	formin binding protein 1 (FBP17)	23048	9q34.11	+		+		+	+
FOXO1A	forkhead box O1A (FKHR)	2308	13q14.11	-			-		
FOXO3A	forkhead box O3A	2309	6q21						
FOXPI	forkhead box P1	27086	3p13	-	-	-	-	-	-
FSTL3	follostatin-like 3 (secreted glycoprotein)	10272	19p13.3						
FUS	fusion, derived from t(12;16) malignant	2521	16p11.2			+			

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
	liposarcoma								
FVT1	follicular lymphoma variant translocation 1	2531	18q21.33	-	-	-	-	-	-
GAS7	growth arrest-specific 7	8522	17p13.1	+		+	+	+	
GATA2	GATA binding protein 2	2624	3q21.3					-	
GMPS	guanine monophosphate synthetase	8833	3q25.31	+	+	+	+	+	++
GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	2776	9q21.2	+	-	+			+
GNAS	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1	2778	20q13.32	+	+	+	+	+	+
GOLGA5	golgi autoantigen, golgin subfamily a, 5 (PTC5)	9950	14q32.12		++	+			
GOPC	golgi associated PDZ and coiled-coil motif containing	57120	6q22.1	+					
GPHN	gephyrin (GPH)	10243	14q23.3		+	+	+	+	
HCMOGT-1	sperm antigen HCMOGT-1	92521	17p11.2	+		+	+	+	
HEAB	ATP-GTP binding protein	10978	11q12.1	-		+	+		+
HIP1	huntingtin interacting protein 1	3092	7q11.23		+				
HIST1H4I	histone 1, H4i (H4FM)	8294	6p22.1	+			+	-	
HLF	hepatic leukemia factor	3131	17q22						
HLXB9	homeo box HB9	3110	7q36		-		-	-	
HMGA1	high mobility group AT-hook 1	3159	6p21.31	+		+	+		
HMGA2	high mobility group AT-hook 2 (HMGIC)	8091	12q14.3						

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
HNRNP A2B1	heterogeneous nuclear ribonucleoprotein A2/B1	3181	7p15.2	+	+		+	+	+
HOXA11	homeo box A11	3207	7p15.2	+	+		+	+	+
HOXA13	homeo box A13	3209	7p15.2	+	+		+	+	+
HOXA9	homeo box A9	3205	7p15.2	+	+		+	+	+
HOXC11	homeo box C11	3227	12q13.13			+	+		
HOXC13	homeo box C13	3229	12q13.13			+	+		
HOXD11	homeo box D11	3237	2q31.1						
HOXD13	homeo box D13	3239	2q31.1						
HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	3265	11p15.5						
HRPT2	hyperparathyroidism 2	3279	1q21-q31						-
HSPCA	heat shock 90kDa protein 1, alpha	3320	14q32.31						
HSPCB	heat shock 90kDa protein 1, beta	3326	6p21.1	+		+	+		-
IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	3417	2q33.3		-				
IGH@	immunoglobulin heavy locus	3492	14q32.33		+				
IGKC	immunoglobulin kappa locus	50802	2p11.2						
IGL@	immunoglobulin lambda locus	3535	22q11.1-q11.2		-	+		+	
IKZF1	IKAROS family zinc finger 1	10320	7p12.2	+	+		+	+	+
IL2	interleukin 2	3558	4q27	-				-	-
IL21R	interleukin 21 receptor	50615	16p12.1			+		+	
IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	3572	5q11.2	+	-				
IRF4	interferon regulatory factor 4	3662	6p25.3	-		+	+	-	

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
IRTA1	immunoglobulin superfamily receptor translocation associated 1	83417	1q23.1	-	-	+			
ITK	IL2-inducible T-cell kinase	3702	5q33.3						
JAK2	Janus kinase 2	3717	9p24.1	-	-	-	-	+	
JAK3	Janus kinase 3	3718	19p13.11						
JAZF1	juxtaposed with another zinc finger gene 1	221895	7p15.2-p15.1	+	+	+	+	+	+
KIAA1549	KIAA1549	57670	7q34		-			-	
KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	3815	4q12					-	-
KRAS2	v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog	3845	12p12.1		+		-	-	
KTNI	kinectin 1 (kinesin receptor)	3895	14q22.3		+	+	++	+	
LAF4	lymphoid nuclear protein related to AF4	3899	2q11.2		+				
LASP1	LIM and SH3 protein 1	3927	17q12				+		
LCK	lymphocyte-specific protein tyrosine kinase	3932	1p35-p34.3			+			
LCPI	lymphocyte cytosolic protein 1 (L-plastin)	3936	13q14.13	-			-		
LHFP	lipoma HMGIC fusion partner	10186	13q13.3	-			-		
LIFR	leukemia inhibitory factor receptor	3977	5p13.1		+	+	+	+	+
LMO1	LIM domain only 1 (rhombotin 1) (RBTN1)	4004	11p15.4						
LMO2	LIM domain only 2 (rhombotin-like 1) (RBTN2)	4005	11p13				+	++	++
LPP	LIM domain containing preferred translocation partner in lipoma	4026	3q27.3-q28	+	+	+	+	+	+

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
LYL1	lymphoblastic leukemia derived sequence 1	4066	19p13.13			+			
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog	4094	16q23.1						
MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	9935	20q12	+	+	+	+	+	+
MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	10892	18q21.31	-	-	-	-	-	-
MAML2	mastermind-like 2 (Drosophila)	84441	11q21	-	-	-	+	-	+
MAP2K4	mitogen-activated protein kinase kinase 4	6416	17p11.2	+	-		+	+	
MDM2	Mdm2 p53 binding protein homolog	4193	12q15						
MDS1	myelodysplasia syndrome 1	4197	3q26.2	+		+			+
MDS2	myelodysplastic syndrome 2	259283	1p36.12-p36.11					-	
MECT1	mucopidermoid translocated 1	94159	19p13.11					+	
MEN1	multiple endocrine neoplasia type 1 gene	4221	11q13.1	+	+	+	+	+	+
MET	met proto-oncogene (hepatocyte growth factor receptor)	4233	7q31.2		-				
MHC2TA	MHC class II transactivator	4261	16p13.13		+	+	-	+	
MITF	microphthalmia-associated transcription factor	4286	3p13	-	-	-	-	-	-
MKL1	megakaryoblastic leukemia (translocation) 1	57591	22q13.1-q13.2						

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
MLF1	myeloid leukemia factor 1	4291	3q25.32	+		+	+	+	+
MLH1	E.coli MutL homolog gene	4292	3p22.3	-	-	-		-	-
MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	4297	11q23.3	-	-	+	+	-	-
MLLT1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1 (ENL)	4298	19p13.3						+
MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10 (AF10)	8028	10p12.31					-	-
MLLT2	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2 (AF4)	4299	4q21.3	-		-		-	-
MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (AF9)	4300	9p21.3	-	-	-	-	-	
MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (AF6)	4301	6q27	+		+	+		
MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6 (AF17)	4302	17q21				+		
MNI	meningioma (disrupted in balanced translocation) 1	4330	22q12.1			+			

Gene	Gene Name	Gene ID	Locus	SCC- 15	SCC- 4	SCC- 25	SCC- 9	A- 253	Cal27
	myeloproliferative leukemia virus oncogene, thrombopoietin receptor	4352	1p35.1			+			
MPL									
MSF	MLL septin-like fusion	10801	17q25	+			+		
MSH2	mutS homolog 2 (E. coli)	4436	2p21		-				
MSH6	mutS homolog 6 (E. coli)	2956	2p16.3		-				
MSI2	musashi homolog 2 (Drosophila)	124540	17q23.2						
MUC1	mucin 1, transmembrane	4582	1q22	-		+			
MUTYH	mutY homolog (E. coli)	4595	1p34.1			+			
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	4609	8q24.21	+	+	+	+	+	
MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	4610	1p34.2			+			
MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	4613	2p24.3						
MYH11	myosin, heavy polypeptide 11, smooth muscle	4629	16p13.11			+	-	+	
MYH9	myosin, heavy polypeptide 9, non-muscle	4627	22q12.3						
MYST4	MYST histone acetyltransferase (monocytic leukemia) 4 (MORF)	23522	10q22.2			+		-	
NACA	nascent-polypeptide-associated complex alpha polypeptide	4666	12q13.3			+	+		
NBS1	Nijmegen breakage	4683	8q21.3	+	+		+	-	

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
	syndrome 1 (nibrin)								
NCKIPSD	SH3 protein interacting with Nck, 90 kDa (ALL1 fused gene from 3p21)	51517	3p21.31	-					
NCOA1	nuclear receptor coactivator 1	8648	2p23.3						
NCOA2	nuclear receptor coactivator 2 (TIF2)	10499	8q13.3	+			+	-	
NCOA4	nuclear receptor coactivator 4 - PTC3 (ELE1)	8031	10q11.23					-	
NF1	neurofibromatosis type 1 gene	4763	17q11.2		-				
NF2	neurofibromatosis type 2 gene	4771	22q12.2			+			
	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	4791	10q24.32			+			
NFKB2									
NIN	ninein (GSK3B interacting protein)	51199	14q22.1		+	+	+		
	Notch homolog 1, translocation-associated (Drosophila) (TAN1)	4851	9q34.3	+		+		+	+
NOTCH1									
	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	4869	5q35.1	+				+	
NPM1									
NR4A3	nuclear receptor subfamily 4, group A, member 3 (NOR1)	8013	9q31.1	+				+	+
NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	4893	1p13.2			+			
	nuclear receptor binding SET domain protein 1	64324	5q35.2-q35.3	+				+	
NSD1									
	neurotrophic tyrosine kinase, receptor, type 1	4914	1q23.1	-	-	+	-	-	
NTRK1									
NTRK3	neurotrophic tyrosine	4916	15q25.3						

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
	kinase, receptor, type 3								
NUMA1	nuclear mitotic apparatus protein 1	4926	11q13.4	+	++	++	+	-	+
NUP214	nucleoporin 214kDa (CAN)	8021	9q34.13	+		+		+	+
NUP98	nucleoporin 98kDa	4928	11p15.4						
NUT	nuclear protein in testis	256646	15q14				-	-	
	oligodendrocyte lineage transcription factor 2 (BHLHB1)	10215	21q22.11	-			+		
OMD	osteomodulin	4958	9q22.31	+		+		+	+
	platelet-activating factor acetylhydrolase, isoform 1b, beta subunit 30kDa	5049	11q23.3	-	-	+	+	-	-
PAFAH1B2	partner and localizer of BRCA2	79728	16p12.1			+		+	
PALB2	paired box gene 3	5077	2q36.1						
PAX3	paired box gene 5 (B-cell lineage specific activator protein)	5079	9p13.2	-	-	-	-	+	
PAX5	paired box gene 7	5081	1p36.13			+		-	
PAX7	paired box gene 8	7849	2q13						
PAX8	pre-B-cell leukemia transcription factor 1	5087	1q23.3	-	-	+		-	
PBX1	pericentriolar material 1 (PTC4)	5108	8p22-p21.3	-		-	-	++	-
PCM1	proprotein convertase subtilisin/kexin type 7	9159	11q23.3	-	-	+	+	-	-
PCSK7	phosphodiesterase 4D interacting protein (myomegalin)	9659	1q21.1	-	-	+			
PDE4DIP	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	5155	22q13.1						
PDGFB									

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
PDGFRA	platelet-derived growth factor, alpha-receptor	5156	4q12					-	-
PDGFRB	platelet-derived growth factor receptor, beta polypeptide	5159	5q32	+	-				
PER1	period homolog 1 (Drosophila)	5187	17p13.1	+			+	+	
PHOX2B	paired-like homeobox 2b	8929	4p13			-		-	+
PICALM	phosphatidylinositol binding clathrin assembly protein (CALM)	8301	11q14.2	-	-		+	-	+
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	5290	3q26.32	+		+		+	+
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	5295	5q13.1						
PIM1	pim-1 oncogene	5292	6p21.2	+		+	+	-	
PLAG1	pleiomorphic adenoma gene 1	5324	8q12.1	+	+				
PML	promyelocytic leukemia	5371	15q24.1			+	-	-	
PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	5378	2q32.2		-				
PMS2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	5395	7p22.1	+	+	+	+	+	+
PNUTL1	peanut-like 1 (Drosophila)	5413	22q11.21			+		+	
POU2AF1	POU domain, class 2, associating factor 1 (OBF1)	5450	11q23.1	-	-		+	-	-
POU5F1	POU domain, class 5, transcription factor 1	5460	6p21.33	+			+		
PPARG	peroxisome proliferative activated receptor, gamma	5468	3p25.2	-	-	-			-
PRCC	papillary renal cell	5546	1q23.1	-	-	+			

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
	carcinoma (translocation-associated)								
PRDM16	PR domain containing 16 protein kinase, cAMP-dependent, regulatory, type 1, alpha (tissue specific extinguisher 1)	63976	1p36.32			+			
PRKAR1A		5573	17q24.2				+		
PRO1073	PRO1073 protein (ALPHA)	29005	11q13.1	+	+	+	+	+	+
PRRX1	paired mesoderm homeo box 1	5396	1q24.2		+	+		-	
PSIP1	PC4 and SFRS1 interacting protein 1 (LEDGF)	11168	9p22.3	-	-	-	-	-	
PTCH	Homolog of Drosophila Patched gene	5727	9q22.32	+		+		+	+
PTEN	phosphatase and tensin homolog gene	5728	10q23.31					-	
PTPN11	protein tyrosine phosphatase, non-receptor type 11	5781	12q24.13			+	+	-	
RABEP1	rabaptin, RAB GTPase binding effector protein 1 (RABPT5)	9135	17p13.2	+			+	+	
RAD51L1	RAD51-like 1 (S. cerevisiae) (RAD51B)	5890	14q24.1	+	+	+	+	+	
RANBP17	RAN binding protein 17	64901	5q35.1	+				+	
RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	5910	4q23	-				-	-
RARA	retinoic acid receptor, alpha	5914	17q21.2				+		
RB1	retinoblastoma gene	5925	13q14.2	-			-		
RBM15	RNA binding motif protein 15	64783	1p13.3			++			
RECQL4	RecQ protein-like 4	9401	8q24.3	+	+	+	+	+	+

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
	v-rel reticuloendotheliosis viral oncogene homolog (avian)	5966	2p16.1						
REL									
RET	ret proto-oncogene	5979	10q11.21					-	
	RAS homolog gene family, member H (TTF)	399	4p14			-		-	+
RHOH									
	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	6098	6q22.1						
ROS1									
RPL22	ribosomal protein L22 (EAP)	6146	1p36.31	+					
RPN1	ribophorin 1	6184	3q21.3					-	
	runt-related transcription factor 1 (AML1)	861	21q22.12		-		+	-	
RUNX1									
	runt-related transcription factor binding protein 2 (MOZZNF220)	7994	8p11.21	-	-	+	-		-
RUNXBP2									
SBDS	Shwachman-Bodian- Diamond syndrome protein	51119	7q11.21	+	+				
	succinate dehydrogenase complex, subunit B, iron sulfur (lp)	6390	1p36.13			+		-	
SDHB									
	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	6391	1q23.3		-	+			
SDHC									
	succinate dehydrogenase complex, subunit D, integral membrane protein	6392	11q23.1	-	-		+	-	-
SDHD									
SET	SET translocation	6418	9q33.2	+		+		+	+
	splicing factor proline/glutamine rich(polypyrimidine tract binding protein associated)								
SFPQ		6421	1p34.3			+			

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
SFRS3	splicing factor, arginine/serine-rich 3	6428	6p21.31	+		+	+		
SH3GL1	SH3-domain GRB2-like 1 (EEN)	6455	19p13.3						
SIL	TAL1 (SCL) interrupting locus	6491	1p33			+			
SLC45A3	solute carrier family 45, member 3	85414	1q32.1	+	+	+		-	
SMAD4	Homolog of Drosophila Mothers Against Decapentaplegic 4 gene	4089	18q21.1	-	-	-		-	-
SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	6598	22q11.23		-	+		+	
SMO	smoothened homolog (Drosophila)	6608	7q32.1		-				
SOC1	suppressor of cytokine signaling 1	8651	16p13.13		+	+	-	+	
SS18	synovial sarcoma translocation, chromosome 18	6760	18q11.2		-	+			-
SS18L1	synovial sarcoma translocation gene on chromosome 18-like 1	26039	20q13.33	+	+	+	+	+	+
STK11	serine/threonine kinase 11 gene (LKB1)	6794	19p13.3						
STL	Six-twelve leukemia gene	7955	6q22.31	+					
SUFU	suppressor of fused homolog (Drosophila)	51684	10q24.32			+			
SUZ12	suppressor of zeste 12 homolog (Drosophila)	23512	17q11.2		-			-	
SYK	spleen tyrosine kinase	6850	9q22.2	+	-	+		+	+
TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	8148	17q12		-				
TAL1	T-cell acute	6886	1p33			+			

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
	lymphocytic leukemia 1 (SCL)								
TAL2	T-cell acute lymphocytic leukemia 2	6887	9q31.2	+		+		+	+
TCEA1	transcription elongation factor A (SII), 1	6917	8q11.23	+	+		+		
TCF1	transcription factor 1, hepatic (HNF1)	6927	12q24.31		-	+	+		
TCF12	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	6938	15q21.3				-	-	
TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	6929	19p13.3						
TCL1A	T-cell leukemia/lymphoma 1A	8115	14q32.13		++	+		-	
TCL6	T-cell leukemia/lymphoma 6	27004	14q32.13		++	+		-	
TFEB	transcription factor EB	7942	6p21.1	+		+	+	-	
TFG	TRK-fused gene	10342	3q12.2						+
TFPT	TCF3 (E2A) fusion partner (in childhood Leukemia)	29844	19q13.42	+	+			+	
TFRC	transferrin receptor (p90, CD71)	7037	3q29	+	+	+	+	+	+
THRAP3	thyroid hormone receptor associated protein 3 (TRAP150)	9967	1p34.3			+			
TIF1	transcriptional intermediary factor 1 (PTC6, TIF1A)	8805	7q34		-				
TLX1	T-cell leukemia, homeobox 1 (HOX11)	3195	10q24.31			+			
TLX3	T-cell leukemia, homeobox 3 (HOX11L2)	30012	5q35.1	+				+	
TMPRSS2	transmembrane protease, serine 2	7113	21q22.3		-	-	-	-	

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
TNFRSF17	tumor necrosis factor receptor superfamily, member 17	608	16p13.13	+	+	+	-	+	
TNFRSF6	tumor necrosis factor receptor superfamily, member 6 (FAS)	355	10q23.31					-	
TOP1	topoisomerase (DNA) I	7150	20q12	+	+	+	+	+	+
TP53	tumor protein p53	7157	17p13.1	+			+	+	
TPM3	tropomyosin 3	7170	1q21.3	-		+			
TPM4	tropomyosin 4	7171	19p13.12						
TPR	translocated promoter region	7175	1q31.1					-	
TRA@	T cell receptor alpha locus	6955	14q11.2	+		+			
TRBC1	T cell receptor beta locus	6957	7q34		-		-	-	
TRD@	T cell receptor delta locus	6964	14q11.2	+		+			
TRIM33	tripartite motif-containing 33 (PTC7,TIF1G)	51592	1p13.2			+			
TRIP11	thyroid hormone receptor interactor 11	9321	14q32.12		+	+			
TSC1	tuberous sclerosis 1 gene	7248	9q34.13	+		+		+	+
TSC2	tuberous sclerosis 2 gene	7249	16p13.3		+	+		+	
TSHR	thyroid stimulating hormone receptor	7253	14q31.1		+	+		+	
TTL	tubulin tyrosine ligase	150465	2q13						
USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene)	9098	17p13.2	+			+	+	
VHL	von Hippel-Lindau syndrome gene	7428	3p25.3	-	-	-			-
WHSC1	Wolf-Hirschhorn syndrome candidate 1(MMSET)	7468	4p16.3						
WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-	54904	8p12	-			-	-	-

Gene	Gene Name	Gene ID	Locus	SCC-15	SCC-4	SCC-25	SCC-9	A-253	Cal27
	like 1 (NSD3)								
WRN	Werner syndrome (RECQL2)	7486	8p12	-		-	-	-	-
WT1	Wilms tumour 1 gene	7490	11p13				+	++	+
	xeroderma pigmentosum, complementation group A								
XPA	xeroderma pigmentosum, complementation group A	7507	9q22.33	+		+		+	+
	xeroderma pigmentosum, complementation group C								
XPC	xeroderma pigmentosum, complementation group C	7508	3p25.1	-	-	-			-
ZNF145	zinc finger protein 145 (PLZF)	7704	11q23.2	-	-		+	-	-
ZNF198	zinc finger protein 198	7750	13q12.11	-	+				
	zinc finger protein 278 (ZSG)								
ZNF278	zinc finger protein 278 (ZSG)	23598	22q12.2			+			
ZNF331	zinc finger protein 331	55422	19q13.42	+	+				
ZNF384	zinc finger protein 384 (CIZ/NMP4)	171017	12p13.31			+	-	-	
ZNF521	zinc finger protein 521	25925	18q11.2		-	+			-
	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)								
ZNF9	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	7555	3q21.3					-	
	zinc finger protein, subfamily 1A, 1 (Ikaros)								
ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)	10320	7p12.2	+	+		+	+	+

Symbols: +, low-level copy number gain; ++, high-level copy number gain; -, low-level copy number loss; --, high-level copy number loss.