DATA MINING METHODS APPLIED TO CHROMOSOME ABERRATIONS IN SQUAMOUS CELL CARCINOMA KARYOTYPES

THESIS

Presented to the Graduate Council
of Texas State University –San Marcos
in Partial Fulfillment of
the Requirements

for the Degree

Master of SCIENCE

by

Jeremy Slatton, B.S.

San Marcos, Texas
December 2005

ACKNOWLEDGEMENTS

I would like to thank my mother, Donna Slatton, for providing the foundation that has shaped my character and taught me to work hard to achieve my goals. Additionally, I would like to thank my father, Dennis Slatton, for fueling my educational quest and my siblings, Andrew, Felicia, and Jason for reinforcing the importance of my journey.

I wish to thank my co-workers, friends, and extended family for their support and kind words of encouragement throughout this and all endeavors in my life.

I would also like to acknowledge the Seton Healthcare Network for providing me with the resources, tools, and incentives to conquer my educational aspirations. I am particularly thankful to the Seton Medical Center Auxillary Committee and Mrs. George Montz for their gracious donation to my education.

A very special thanks goes to Dr. Ram Shanmugam for the bioinformatics and biostatistics skills without which this thesis would not be possible. His cooperation, lengthy dedication, and insight offered throughout this endeavor will not be forgotten. I thank him for enhancing and guiding my educational experience.

Most importantly, I wish to thank the skilled faculty members of the Health Services Research Department at Texas State University-San Marcos, Dr. Jean Brender, Dr. Charles Johnson, and Dr. Ram Shanmugam, for their guidance. Thank you for the knowledge and opportunities I have been afforded throughout this entire process.

This manuscript was submitted on August 3, 2005.

TABLE OF CONTENTS

LIST OF TABLES

Table

LIST OF FIGURES

Figure

ABSTRACT

DATA MINING METHODS APPLIED TO CHROMOSOME ABERRATIONS IN SQUAMOUS CELL CARCINOMA KARYOTYPES

by

Jeremy Slatton, B.S.

Texas State University-San Marcos

December 2005

SUPERVISING PROFESSOR: RAM SHANMUGAM

This analysis used three types of karyotype parsing systems, Karyo Reader, Progenetix ISCN2matrix, and CyDAS to convert published squamous cell carcinoma karyotypes from the Mitelman Database of recurrent chromosome aberrations in cancer into statistical data for mining procedures. The goal of this study was to examine the input requirements and output options available in each system to determine the system's usability and accuracy for potential mining experiments. Each karyotype parsing system was utilized to pinpoint high frequency recurrent chromosome aberrations that potentially influence the development of squamous cell carcinoma.

Output results from CyDAS were deemed best suited for database storage of karyotype data and production of graphical representations of chromosome aberrations while Progenetix proved useful only for examining a summary of the structural chromosome gains and losses in the data. Karyo Reader output provided data for binary statistical analyses as well as analysis of structural and numerical chromosome gains and losses in the data.

From the Mitelman Database of Chromosome Aberrations in cancer, 574 cases were extracted representing 92 literature references from 25 journals. Karyo Reader was able to parse 85.44% of structural aberrations, similar to the 85.71% of cases parsed by CyDAS, but much lower than the 94.95% parsed by Progenetix. However, Karyo Reader identified more than three times as many aberrations than Progenetix or CyDAS. High frequency recurrent chromosome aberrations identified by Karyo Reader and CyDAS were consistent with literature, though results from Progenetix ISCN2matrix were not. As a result, Karyo Reader provided the only accurate, suitably formatted output to use for statistical analysis.

Karyo Reader binary aberration data was used to perform a principal component analysis (PCA) on the binary chromosome aberration data extracted from Karyo Reader. For early evolutionary mutagenic pathways, aberrations were eliminated from PCA if they were not present in at least 30% of cases.

The top 19 chromosome aberrations occurring in the squamous cell carcinoma Karyo Reader binary data were deletions of chromosomes and chromosome regions: Y, 8p22, 8p23, 10, 13, 14, 15, 18, 21, 22, 4, 8p22, 8p23, 3p13, 3p14, 3p21, 3p22, 3p23, 3p24, 3p25, and 3p26. The NIPT distributions for each of these chromosome bands

indicated that aberrations dY, d8p22, d8p23, and d3p13 are early aberrations, that chromosome aberrations d10, d14, d18, d13, d22, d3p14, d3p24, d3p25, d3p23, and d3p26 are moderate stage aberrations, and that aberrations d21, d15, d3p22, d3p21 appear as later stage aberrations in squamous cell carcinoma development.

Principal component analysis (PCA) of the statistical output yielded a concise set of nine potential evolutionary mutagenic pathways for squamous cell carcinoma development. Two principal components were extracted from the data, representing two separate early mutagenic pathways occurring in squamous cell carcinoma cases.

The analysis identified deletions of chromosome Y, 8p22, 8p23, and 3p13 as early chromosome aberrations involved in squamous cell carcinoma development. PCA showed a very divergent path of mutagenesis for later stage aberrations resulting in entire chromosome deletions or further deletions of bands within the chromosome segment 3p.

Armed with the knowledge that these aberrations potentially play a predominate role in development of squamous cell carcinoma, chromosome regions can be pinpointed for further research into the biological pathways impacted by squamous cell carcinoma as well as target chromosome regions for gene therapy or interventional treatments.

CHAPTER 1

INTRODUCTION

Cancer is a group of diseases characterized by uncontrolled spreading and growth of abnormal cells that if uncontrolled can result in death. Some cancers, like squamous cell carcinoma, a nonmelanoma skin cancer, are highly curable. These cancers often do not receive the public or governmental attention needed to fund extensive research projects.

In the past few years, a wealth of genomic data has become accessible in the form of online repositories, providing data for statistical research. After decades of work, a standardized nomenclature for human cytogenetics was established, the International System for Human Cytogenetic Nomenclature, and is now widely accepted as an important element in improving and maintaining international collaboration on cellular mutations (Mitelman, 1995).

The adoption of ISCN nomenclature has facilitated the growth of genomic data repositories. However, in order to utilize the data contained in these repositories for statistical analysis, a conversion is needed to transform the complex nomenclature into a form suitable for statistical analysis. In ISCN nomenclature, each case is supplemented with a karyotype, or symbolic description, of the specific mutation. ISCN nomenclature offers a variety of complexities that limit the ability of algorithms to parse the data into statistical form. Several parsing systems have been developed, along with many custom

made scripts, to transform karyotype data into a statistically usable form, though all are still considered experimental.

Without a solid approach available to understand the methods and limitations in transforming and utilizing karyotype data, very little research has taken place to exploit the abundant genetic data available. Potential outcomes of statistical analysis on karyotype data include identification of the evolutionary pathways involved in the development of the disease, targeting of potential genetic indicators of the disease, and mapping regions of chromosomes specific to the disease.

Why Focus on Squamous Cell Carcinoma?

Squamous cell carcinoma is the second most common skin cancer after basal cell carcinoma, afflicting more than 200,000 Americans every year (Skin Cancer Foundation, 2004). Since squamous cell carcinoma is considered a curable form of cancer, it is often excluded from many analyses or grouped in an "other" category as if unworthy of specification.

The National Institutes of Health estimate overall costs for cancer in 2004 at $189.8 billion: $69.4 billion for direct medical costs; $16.9 billion for indirect morbidity costs (lost productivity due to illness); and $103.5 billion for indirect mortality costs (cost of lost productivity due to premature death) (ACS, Facts & Figures, 2005). Considering the number of yearly afflictions of squamous cell carcinoma in conjunction with the physician offices visits and pathology tests needed for diagnosis and treatment of the disease, an enormous amount of money is spent on this curable form of cancer.

Cancer research is a money-driven industry and requires funding from governmental and private sectors in order to operate. Most curable forms of cancer do

not receive the public and governmental support for research funding despite their costly burden on our healthcare delivery system. With 17% of Americans under age 65 uninsured and 33% of Americans over 65 only covered by Medicare (ACS, Facts and Figures, 2005), squamous cell carcinoma presents a large financial burden on the healthcare industry.

Potentially the development of targeted genetic treatments could lead to less expensive and self-administered means of dealing with squamous cell carcinomas. The eventual development of an over the counter topical treatment or removal tool would reduce the costs associated with early stage squamous cell carcinoma treatment. For later stage cases, medical treatment costs could be reduced through more targeted therapeutic treatments and drugs. Based on the knowledge of the evolutionary pathways of the disease, quick interventional gene therapy drugs could be developed to stop the spread of mutated cells and prevent them from mutating into more complex forms of the disease.

Rightly, most cancer research is targeted towards deadly forms of cancer, where high costs are associated with disease treatment. However, a short-term investment in reducing the costs of a curable squamous cell carcinoma could lead to a more long-term financial savings for the healthcare industry that can be used to target more research on deadlier forms of disease.

Squamous Cell Carcinoma

What is it?

Squamous cell carcinoma accounts for the majority of non-small cell lung cancer, other bronchial tree cancers, and cancers arising throughout the upper aerodigestive tract including the oral cavity, paranasal sinuses, pharynx, larynx, trachea, and esophagus. In

addition, squamous cell carcinoma arises at many other sites such as salivary glands, esophagus, bladder, penis, and the female genital tract (Van Dyke 2001). Squamous cell carcinoma accounts for 20 percent of skin cancers in the United States (Memorial Sloan-Kettering Cancer Center, 2001).

Squamous cell carcinoma of the skin arises from the epidermis as a malignant tumor, resembling the squamous cells that comprise the upper layers of skin. This carcinoma can occur on all areas of the body, including mucous membranes, but typically appears in areas exposed to sunlight (Skin Cancer Foundation, 2004). Squamous cell carcinomas typically remain confined to the epidermis for some time before penetrating the underlying tissues, if untreated. In some cases, squamous cell carcinomas metastasize to distant tissues and organs, resulting in fatality (Skin Cancer Foundation, 2004).

Warning signs of squamous cell carcinoma include a wart-like growth that crusts or bleeds, a scaly red patch with irregular borders that crusts or bleeds, or a persistent open sore that occasionally crusts or bleeds (Skin Cancer Foundation, 2004).

Risk Factors

Chronic sunlight exposure causes most cases of squamous cell carcinoma, as evidenced by tumors occurring more frequently on parts of the body exposed to the sun. Though most unprotected ultraviolet (UV) radiation exposure comes from sunlight, some may come from artificial sources such as tanning booths (ACS, 2004).

There are three classes of UV light: A, B, and C. UV type B is more likely to cause burning and perhaps nonmelanoma skin cancer, especially squamous cell carcinoma. UVA may cause less burning and less skin cancer, but this is uncertain. Tanning lamps claim to have more UVA and less UVB, but it isn't clear if this is well

regulated since there is no governmental oversight for the health effects of tanning lamps. UVC doesn't penetrate our atmosphere and is not normally a risk factor for skin cancer (ACS, 2004).

Most squamous cells metastasize on sites of chronic inflammatory skin conditions, particularly those due to chronic sunlight exposure, mucous membranes, or lips. Squamous cell carcinoma may occur where skin has suffered an injury such as burns, scars, long-standing sores, x-ray exposed sites, and on chemically exposed sites such as the lung. Sometimes squamous cell carcinoma appears on healthy, undamaged tissue. Children and young adults often receive a lot of intense sun exposure that may not result in actual cancer for many years or decades (ACS, 2004).

The risk of skin cancer is at least twenty times higher for whites than for dark-skinned African-Americans. This is due to the protective effect of melanin (skin pigment). Whites with fair (light-colored) skin that freckles or burns easily are at especially high risk for squamous cell carcinoma. Individuals with albinism, a congenital absence of pigment, also have a high risk of getting skin cancers. Males are three times as likely as women to have squamous cell carcinomas of the skin. This risk factor is thought to be due to higher sun exposure in males, but remains unproven (ACS, 2004).

Chemical exposure to large amounts of arsenic, a heavy metal used in insecticides, increases the risk of developing squamous cell carcinoma. Workers exposed to industrial tar, coal, paraffin, and certain types of oil may also have an increased risk for squamous cell carcinoma. People who have had radiation treatment also have a higher risk of developing this cancer in the area that received the treatment (ACS, 2004).

Squamous cell carcinomas are one of the more common primary malignancies of the lung, most often seen in smokers. Other environmental exposures such as alcohol, chronic mucosal irritation, and low dose radiation can increase the risk of developing squamous cell carcinomas (Van Dyke, 2001).

There is strong evidence that squamous cell carcinoma has a genetic basis. For families with smoking-related malignancies, genetic segregation analysis showed strong evidence favoring an autosomal dominant pattern of inheritance to predisposition for malignancy. Some individuals with squamous cell carcinoma appear to have a heritable sensitivity to chromosome breakage (Van Dyke, 2001).

Precancerous conditions or lesions such as keratosis (actinic or solar), actinic cheilitis, leukoplakia, and Bowen's disease are also risk factors for squamous cell carcinoma. UV light treatments such as psoralen plus ultraviolet light A (PUVA), used in patients with psoriasis (a long-lasting inflammatory skin disease), show a significant increase in incidence of squamous cell carcinomas (ACS, 2004).

Patients with xeroderma pigmentosum, a very rare inherited condition, lack the normal DNA repair mechanisms, reducing the skin's ability to repair damaged DNA caused by sun exposure. Patients with this condition are prone to squamous cell carcinomas as well as patients undergoing ionizing radiation for Hodgkin disease or thyroid cancer (ACS, 2004).

Human papillomavirus (HPV) is believed to play a predominate role in the development of squamous cell carcinomas of the penis, vulva, and periungual region. Many nonmelanoma skin cancers, such as squamous cell carcinoma, contain a type of HPV. HPVs are a group of more than 100 viruses that can cause papillomas, or warts.

The types of warts that people commonly get on their hands and feet appear to be unrelated to any form of cancer (ACS, 2004). The DNA of HPV types 16, 18, and 31 have been found in human genital cancers and HPV 16 and 18 have been recognized in verrucous carcinomas of the larynx and squamous cell carcinoma of the tongue and tonsil (Van Dyke, 2001). Epstein Barr virus is a risk factor for nasopharyngeal squamous cell carcinoma in southern China and the Aleutians (Van Dyke, 2001).

Diagnosis and Treatment

Skin cancers rarely cause symptoms until they become quite large, at which point they may bleed or even hurt (ACS, 2004). Squamous cell carcinomas may appear as growing lumps, often with a rough surface, or as flat reddish patches in the skin that grow slowly. Squamous cell carcinoma may develop showing only slight changes from normal skin (ACS, 2004).

Typically a physician recognizes squamous cell carcinoma during a medical history examination, due to a patient concern or complaint, or during a physical examination. The physician typically questions the patient on potential exposures, family history, and changes in size and appearance of the infected site. The physician will note the size, shape, color, and texture of the area and note any bleeding or scaling. The rest of the body may be checked for spots or moles related to skin cancer as well as the lymph nodes to determine if the cancer has spread (ACS, 2004).

Diagnosis of squamous cell carcinoma is performed through a biopsy of the infected site. All biopsy samples obtained to diagnose squamous cell carcinoma must reach at the depth of the mid-dermis to allow for determination of the presence or absence of an invasive disease.

Different methods can be used for a skin biopsy depending on the type of skin cancer, location on the body, and size of the affected area. A shave biopsy involves a local anesthetic where the doctor "shaves" off the top layers of the skin using a surgical blade. A punch biopsy involves a tool that resembles a tiny round cookie cutter. The skin is numbed with local anesthetic in this procedure and the tool is rotated on the surface of the skin until it cuts through all the layers of the skin, including the dermis and upper layers of the subcutaneous layer (ACS, 2004).

Incision and excisional biopsies occur when there is a need to examine a tumor in the deeper layers of the skin. Incisional biopsy involves removing only a portion of the tumor while excisional biopsy involves removal of the entire tumor. A surgical knife is used to cut through the full thickness of the skin, a wedge of skin is removed for examination, and the wound is sewn together. These procedures also occur under local anesthetic (ACS, 2004).

A lymph node biopsy can be performed if the lymph nodes are too large or firm. This biopsy determines whether the cancer has spread from the skin to one or more of the lymph nodes. A fine need aspiration (FNA) biopsy can also be employed, using a thin needle to remove very small tissue fragments from a tumor. This test may be performed under a local anesthetic, but is only used to biopsy large lymph nodes near a skin cancer to determine if the cancer has metastasized (spread). If the result of an FNA is negative or unclear, a surgical lymph node biopsy can be performed where the lymph node is surgically extracted using local anesthesia, resulting in a small scar (ACS, 2004).

The tissues surrounding a squamous cell carcinoma often exhibit genetic damage and premalignant lesions, and this entire "cancerization field" appears to be at risk for

second primary cancers, which may also require diagnosis and treatment (Van Dyke, 2001).

Early-stage squamous cell carcinomas can also be removed by electrodessication and curettage where the tissue is destroyed by an electrical current and removed by scraping with a curette. Cryosurgery can also be used on early stage skin cancers where the tissue is destroyed through a freezing technique (Memorial Sloan-Kettering Cancer Center, 2001).

Mohs' Surgery is a high specialized technique in which a trained Mohs' surgeon removes tumor tissue surgically layer by layer, mapping each layer and examining the tissue layer for tumor cells under a microscope before proceeding to the next layer. This procedure is extremely precise, complex, and time consuming. Mohs' surgery ensures that the entire tumor is removed and it minimizes scarring by preserving as much normal skin as possible. Mohs' surgery has the highest cure rate of all therapies for squamous cell carcinomas and is particularly effective for large tumors, recurring tumors, and tumors in areas where skin preservation is particularly important such as the face (Memorial Sloan-Kettering Cancer Center, 2001).

Photodynamic therapy (PDT) uses Porfimer sodium (Photofrin) combined with light from a laser to treat patients with certain types of cancer. Aminolevulinic acid (Levulan Kerastick) is a drug applied directly to the skin and is used to treat actinic keratosis, a skin condition that can develop into cancer. This treatment is only approved for the face or scalp and utilizes a special blue light rather than the laser light used in PDT (ACS, 2004). Studies are now in progress to test the use of PDT for squamous cell carcinoma.

Stages of Nonmelanoma Skin Cancers

Histologic grading and evaluation of tumor thickness have been used to predict survival and to develop algorithms for further treatment of squamous cell carcinoma. The most common system used to describe the stages of nonmelanoma skin cancers is the TNM system. The letter T stands for tumor, indicating the size and how far it has spread within the skin and neighboring tissues. The letter N stands for spread to lymph nodes and the letter M stands for metastasis or spread to distant organs (ACS, 2004).

To assign a stage, information about the tumor and whether it has spread to lymph nodes and other organs in the body is combined, according to a process called stage grouping. The stages are described using the number 0 and Roman numerals from I to IV (ACS, 2004). The possible values for T are:

TX: Primary tumor cannot be assessed
T0: No evidence of primary tumor
Tis: Carcinoma in situ
T1: The tumor is 2.0cm or smaller
T2: The tumor is larger than 2.0cm but smaller than 5.0cm
T3: The tumor is larger than 5.0cm
T4: Tumor of any size that invades deeply into muscle, cartilage, or bone

The possible values for N are:

NX: Regional lymph nodes cannot be assessed
N0: No regional lymph node metastasis
N1: Metastasis to nearby lymph nodes

The possible values of M are:

MX: Presence of distant metastasis cannot be assessed
M0: No distant metastasis
M1: Distant metastasis is present

Tis, N0, M0 characterize stage 0 of squamous cell carcinoma in the TMN system. This squamous cell carcinoma in situ, also called Bowen's disease, is the earliest stage of

the disease. The cancer only involves the epidermis and has not spread to the dermis at this stage in squamous cell carcinoma of the skin (ACS, 2004).

Stage I of squamous cell carcinoma is characterized in the TMN system by T1, N0, M0. This cancer is no larger than 2cm and has not spread to the lymph nodes or other organs (ACS, 2004).

T2 or 3, N0, M0, characterize stage II in the TMN system. At this stage, the cancer is larger than 2cm but has not spread to the lymph nodes or other organs (ACS, 2004).

T4, N0, M0 or any T, N1, M0 characterize stage III of squamous cell carcinoma in the TMN system. At this stage, the cancer has spread to the tissues beneath the skin, and/or it has spread to the nearby lymph nodes. However, the cancer has not spread to other organs such as the lungs or brain (ACS, 2004).

Any T, any N, M1 characterize stage IV of squamous cell carcinoma in the TMN system. The cancer can be any size and may or may not have spread to the local lymph nodes, but it has spread to other organs such as the lungs or brain (ACS, 2004).

Prognosis

DNA content and ploidy are correlated with tumor aggressiveness and responsiveness to some treatments. In addition to adverse biological and clinical behavior, abnormal DNA content has been thought to reflect an altered proliferation capacity of tumor cells. Prognosis of squamous cell carcinomas largely depends on the pathological site at diagnosis, which in turn depends to a great extent on the anatomic site. For example, skin and larynx squamous cell carcinomas have a relatively favorable prognosis due to their frequent identification at early stages. Squamous cell carcinoma of

the nasopharyngeal area is rarely detected early and the rich blood supply and nearby lymph nodes encourage metastasis of the disease, resulting in a less favorable prognosis (Van Dyke, 2001).

Prevention and Early Detection

The best way to prevent skin cancer is through protection from excessive exposure to sunlight. Skin cancer prevention needs to be practiced daily by wearing protective clothing, avoiding the midday sun, and using sunscreen (Memorial Sloan-Kettering Cancer Center, 2001). For other types of squamous cell carcinomas, limitation of exposure to environmental risk factors provides the only method of disease prevention.

Squamous cell carcinomas have an excellent cure rate when found early. It is particularly important to identify these cancers early because some can metastasize to other organs. Periodic skin self-examinations should be performed in conjunction with regular visits to a dermatologist or other physician for early detection of squamous cell carcinoma of the skin (Memorial Sloan-Kettering Cancer Center, 2001). However, detection of other morphologies of squamous cell carcinoma typically are not recognized through examination and may go unnoticed until disease progression prompts attention.

Regular head-to-toe skin examinations are the key to diagnosing skin cancer at its earliest stage. The American Cancer Society recommends a cancer-related checkup, including skin examination, every three years for people between 20 and 40 years old and every year for people age 40 or older (Memorial Sloan-Kettering Cancer Center, 2001). The American Cancer Society has made no recommendations on guidelines for prevention of other morphologies of squamous cell carcinoma.

Obstacles to Cancer Screening

Health insurance coverage is an important determinant of access to health care, and studies document that people who lack health care insurance have reduced access to preventative care and are less likely to get timely cancer screening examinations (ACS, Facts & Figures, 2005). During 1994-2001, among those under age 65, 16-17% had no health insurance, 9-11% had Medicaid coverage, and 70-73% had private insurance. The uninsured population is more likely to be at or below the poverty level. The number of uninsured is steadily on the rise, reaching 45 million in 2003, up 3.8 million from 2001 (ACS, Facts & Figures, 2005). Millions more Americans face erosion of coverage, higher deductibles, and periods without insurance due to unemployment. Low-wage workers are much more likely to forgo preventive health care, including cancer screening due to lack of health insurance and health-related benefits such as paid sick leave.

Clinicians and the healthcare system play a major role in enabling patient participation in cancer screening and ensuring quality services. Research on barriers related to cancer screening shows that multiple factors, such as public policy, organizational systems, practice settings, clinicians, and patients influence cancer screening and that a diverse set of intervention strategies targeting each of these factors can improve cancer screening rates. Studies have also shown that people who received a clinician's recommendation for cancer screening are more likely to be screened than those who did not receive a recommendation (ACS, Facts & Figures, 2005).

Genetic testing is another method of cancer screening that is typically used in higher risk categories for cancers whose evolutionary mutagenic pathways are known. The ultimate goal of genetic testing research is the development of clinical applications

for risk assessment, early detection, and appropriate interventions for individual risk reduction and disease prevention. However, the potential of such research raises questions about who will have access to genetic information and how this information might be used to compromise individual privacy (ACS, Prevention & Early Detection, 2005).

Genetic testing involves a complexity of fears for patients involving privacy and discrimination considerations. As knowledge about the genetic basis of common disorders grows, so does the potential for discrimination in insurance and employment. For example, a genetic test for inherited breast cancer would allow thousands of women to find out whether they carry the altered gene and potentially provide them with useful medical options. However, many women chose not to be tested for fear the information may affect their employment or will be used to deny them and their families access to the health insurance coverage they need. Many patients question the influence of genetic information on other forms of insurance, such as life insurance and disability insurance (ACS, Prevention & Early Detection, 2005).

Emerging Trends in Cancer Research

Gene Therapy

Gene therapy involves inserting a specific gene into cells to restore a missing function or to give the cells a new function. Because missing or damaged genes cause certain diseases, such as cancer, it is only logical that adding or fixing the damaged gene will treat the disease. The biggest obstacle in gene therapy is how to do this.

Most current gene therapy clinical trials are now cancer related particularly because cancer is much more common than inherited genetic disorders (ACS, Gene Therapy, 2005). Some ways that scientists are trying to use gene therapy include:

- Adding functional genes to cells that have abnormal or missing genes. For example, cells typically have tumor suppressor genes that prevent cancer from developing. It may be possible to replace a faulty copy of this gene with a new copy to bring the cancer cells under control (ACS, Gene Therapy, 2005).
- Stopping oncogenes or other necessary cancer genes from working. Oncogenes are mutated versions of normal genes that cause cells to divide uncontrollably, causing cancer. Other genes allow cancer cells to metastasize. Stopping these genes or their protein production may prevent cancer from growing (ACS, Gene Therapy, 2005).
- Adding genes to cancer cells to make them more vulnerable to chemotherapy or radiation. This may include blocking genes that develop cancer cell resistance to chemotherapy drugs (ACS, Gene Therapy, 2005).
- Adding genes to tumor cells to make them more easily detected and destroyed by the body's immune system. A variation on this idea includes adding genes to the immune system cells to make them better able to detect cancer cells (ACS, Gene Therapy, 2005).
- Stopping the genes that facilitate angiogenesis, or new blood vessel formation. Tumors need a constant supply of blood to grow. If the supply

is cut off, tumors may stop growing or even shrink (ACS, Gene Therapy, 2005).

In order to treat someone with gene therapy, the physician must know which gene is altered or missing. Lab tests are currently being developed to look for genetic mutations. So far, the biggest obstacle to gene therapy has been the ability to get the genes into the cells. There are two main ideas on how to do accomplish this task (ACS, Gene Therapy, 2005).

In Vivo techniques are one approach to gene therapy in which the gene is somehow put directly into the body, where the targeted cells will take it up. Usually a plasmid or a virus is used (ACS, Gene Therapy, 2005).

Viruses reproduce by injecting their genes into the cells they infect. Many viruses attack only certain kinds of cells; therefore it is possible to direct them at specific types of tumors. The virus that causes the common cold, the adenovirus, is most often used in clinical trials. The needed gene is put into the virus, the harmful viral gene extracted, and the virus is given to the patient to infect the cancer cells, passing the gene on. Unfortunately researchers can't always control exactly where the viral gene will be inserted into the cell's DNA. Incorrect insertion could potentially lead to an unwanted mutation or unwanted immune reaction (ACS, Gene Therapy, 2005).

Plasmids are used in another In Vivo technique to insert a raw copy of the gene directly into the cells. Plasmids are small, circular pieces of DNA. This method may cut down on the chances of an improper insertion, but is less likely for the DNA to end up inside the cells. The DNA must be injected into the tumor itself, limiting this method to skin cancers and other easily reached tumors (ACS, Gene Therapy, 2005).

Another approach to gene therapy are Ex Vivo techniques in which some of the targeted cells are taken out of the body, the needed gene is added in a lab, and then the cells are placed back into the body. This method is used to ignite the body's immune system into attacking the remaining cancer cells. This procedure may involve altering the tumor or immune systems cells (ACS, Gene Therapy, 2005).

Comparative Genomic Hybridization (CGH)

The CGH technique is a florescence in situ hybridization (FISH) technique that allows the detection and mapping of chromosome imbalances in a tumor genome relative to a normal genome, using total genomic DNA as a probe. CGH is an analytic method based on FISH and digital fluorescence ratio measurement that enables one to compare cytogenetically the entire genome of malignant cells and normal cells, as well as to map gains and losses of DNA in tumor cells. Thereby, CGH makes analysis of whole genomes possible. CGH has been used to analyze the genomic alterations in several malignant tumors. Amplifications and deletions detected by CGH analysis might reveal any oncogenes or tumor suppressor genes playing an important role in the tumorigenesis of the cancer (Keser, 1999).

The CGH hybridization is analyzed using a digital image analysis system. Ten metaphases are analyzed for chromosomal locations of DNA sequence gains and losses. These regions are determined by using green-to-red fluorescence intensity ratio profiles (Keser, 1999).

The CGH technique has implications in the detection of chromosomal gains and losses in tumors, determinations of specific genes and regions of the genome involved in cancer progression, the analysis of evolutionary pathways, the dissection of genetic

changes in experimental models of tumor progression, and prenatal diagnosis of disease (Keser, 1999).

Chromosome Aberrations and the Clonal Evolution Theory of Tumorigenesis

It is widely recognized that cancer is caused by deregulation of growth-controlling molecular signal-transduction pathways, due to mutations in genes coding for the protein components of the pathways. The mutations result in the inactivation or aberrant expression of these proteins, disrupting the normal flow of signals. Often, these mutations are the result of chromosome aberrations (Cornelisse, 2003).

The clonal evolution hypothesis for tumorigenesis states that tumor development starts with the clonal outgrowth of one mutant, genetically unstable cell. Additional mutations accumulate in successive generations of daughter cells, starting a Darwinian evolutionary process, driven by natural selection, towards cells with a natural growth advantage. Thus, carcinoma progression is explained by the emergence of malignant daughter cells, or subclones, resulting from additional mutations. Different stages in the evolution of cancer are marked by a stepwise accumulation of specific molecular genetic changes (Cornelisse, 2003). When measured, these steps can indicate a time-series component for the duration of the cancer.

Neoplastic transformation and progression is the result of genetic defects arising in normal cells and giving rise to a malignant clone. During oncogenesis, some of the usually multiple steps required for acquisition of the full neoplastic phenotype may represent themselves as numerical or structural abnormalities in the chromosomes of the transformed cells. Regardless of type, the abnormality can be responsible for the

interruption of the signal-transduction pathways that lead to the creation of malignant daughter cells (Baudis et al., 2001).

The identification of frequently imbalanced chromosome regions in tumors may point toward tumor suppressor genes or proto-oncogenes mapped to the respective chromosome band. Typically information regarding imbalanced chromosome regions is presented in a text format consisting of symbols and numbers based on the International System for Human Cytogenetic Nomenclature (ISCN) (Baudis et al., 2001).

Chromosome Banding

In ISCN nomenclature, the construction of a karyotype consists of the autosomes numbered from 1 to 22 in decreasing order of length. Sex chromosomes are referred to as X and Y. Each chromosome in the human somatic cell complement is considered to consist of a continuous series of bands, with no unbanded areas. A band is a part of a chromosome clearly distinguishable from adjacent parts by its lighter or darker staining intensity. Bands are allocated to various regions along the chromosome arms, and landmarks delimit these regions. Landmarks are defined as consistent and distinct morphologic features important in identifying chromosomes. Landmarks include the ends of the chromosome arms, the centromere, and certain bands. Bands and regions are numbered from the centromere outward. Regions are areas of the chromosome lying between two adjacent landmarks (Mitelman, 1995).

Numerous techniques have been reported that produce banding patterns on chromosomes. Bands that stain darkly with one method may stain lightly with other methods. Chromosomes are visualized as consisting of a continuous series of light and dark bands, so that no intermediary bands exist. One method of banding involves using

quinacrine mustard or quinacrine dihydrochloride to produce a fluorescent banding pattern, termed Q-banding. The numbers assigned to each chromosome 1 to 22 were determined by their respective Q-banding pattern. Techniques that utilize Giemsa dye mixture as the staining agent are referred to as G-bands and produce an almost identical pattern of light and dark bands along the chromosomes as Q-banding. Some banding techniques give patterns that are opposite in staining intensity to those obtained by the G-staining methods and are termed R-bands due to the reverse staining methods of the procedures (Mitelman, 1995).

Banding techniques are classified into two distinct groups: those resulting in bands distributed along the whole length of the chromosome such as G-, Q- and R-bands, and those that stain specific chromosome structures resulting in a limited number of bands. Methods that stain specific portions of the chromosome may reveal constitutive heterochromatin (C-bands), telomeric bands (T-bands), and nucleolus organizing regions (NORs). Banding techniques are labeled by up to a three-letter code, with the first letter denoting the type of the banding (C-, Q-, R-, etc.), the second letter denoting the general technique (fluorescence, barium hydroxide, etc.), and the third letter depicting the stain (Giemsa, quinacrine, etc.) (Mitelman, 1995).

Banding patterns observed in different cells stained with either the Q-, G-, or R-banding techniques agree sufficiently to allow the construction of a single diagram representative of all three techniques. In this representation, the chromosome bands were designated on the basis of their midpoints and not by their margins. Intensity was taken into account in determining which bands should serve as landmarks on each chromosome

in order to divide the chromosome into natural, easily recognizable morphologic regions (Mitelman, 1995).

Regions and bands are numbered consecutively from the centromere outward along each chromosome arm. The symbols p and q are used to designate the short and long arms of each chromosome respectively. The centromere itself is designated 10, the part of the chromosome facing the short arm is labeled p10, and the part of the chromosome facing the long arm is designated q10. The two regions adjacent to the centromere are labeled as 1 in each arm with the more distal regions labeled 2 and so forth. A band used as a landmark is considered as belonging entirely to the region distal to the landmark and is given the band number of 1 in that region (Mitelman, 1995).

In band designation, there are four required items: the chromosome number, the arm symbol, the region number, and the band number within that region. These items are given in order in ISCN nomenclature without spacing or punctuation. Since bands can be subdivided into further regions or sub-bands, a decimal point is placed after the original band designation and is followed by the number assigned to each sub-band. Sub-bands are numbered sequentially from the centromere outward just like with bands. Sub-bands and bands are numbered sequentially but do not necessarily represent equal divisions within a chromosome or band. If a sub-band is further subdivided, additional digits, without further punctuation are used. Although a band can be subdivided into any number of new bands at any one stage, they are typically subdivided into only three sub-bands with any number of further subdivisions in the sub-bands (Mitelman, 1995).

Bands and sub-bands determine locations within a chromosome to pinpoint specific chromosomal locations of interest. Chromosome aberrations occur at specific

locations within the chromosome that can include an entire chromosome arm, band, sub-band, or further division of a sub-band. Karyotypes exemplify the particular chromosomal aberrations associated with particular morphologies of cancer in a symbolic form (Mitelman, 1995).

Types of Chromosome Aberrations

Chromosome aberrations occur in two types: structural aberrations and numerical aberrations. Structural aberrations result from chromosome breakage. When chromosomes break, two unstable ends are produced. Typically repair mechanisms immediately rejoin these ends. However, if multiple breaks occur, repair mechanisms may be unable to distinguish one end from another and may rejoin the wrong ends (Malcolm, 2001).

Numerical chromosomal aberrations result from non-disjunction, the failure of a pair of homologous chromosomes or pair of sister chromatids to separate during cell division. Human somatic cells normally contain 46 chromosomes, termed a diploid. Ploidy levels are expressed in relation to the haploid number of chromosomes, 23 in humans as found in gametes. Hence triploid humans have 69 chromosomes and so forth. All ploidy levels above two (diploid) are referred to as polyploidy (Malcolm, 2001). In ISCN nomenclature, all numerical changes are expressed in relation to the appropriate ploidy level (Mitelman, 1995). Near-haploid cells with chromosome numbers up to 34 are expressed in relation to 23 chromosomes, near-diploid cells with chromosome numbers 35-57 in relation to 46 chromosomes, near-triploid cells with chromosome numbers 58-80 in relation to 69 chromosomes, and so on (Mitelman, 1995).

Aneuploidy usually arises from non-disjunction, the failure of pair chromosomes to separate at anaphase or from anaphase lag, the delayed movement of a chromosome at anaphase producing two cells: one with trisomy, an extra copy of a chromosome and one with monosomy, a missing copy of a chromosome (Malcolm, 2001). Non-disjunction can be either meiotic or mitotic and though the cause of each is unknown, the results are the gain or loss of a chromosome.

Interpretation of ISCN Nomenclature

In ISCN nomenclature, the first item to be recorded in the description of a karyotype is the total number of chromosomes, including the sex chromosomes, followed by the sex chromosome constitution separated by a comma. In the description of chromosome abnormalities, sex chromosome aberrations are presented first, followed by abnormalities of the autosomes listed in numerical order irrespective of the aberration type (Mitelman, 1995). Common symbols and abbreviated terms for ISCN nomenclature are shown Table 1.

Letter designations are used to specify structurally altered chromosomes as shown in Table 1. In single chromosome rearrangements, the chromosome involved in the change is specified within the parentheses immediately following the symbol identifying the type of rearrangement, e.g., inv(2). If two or more chromosomes have been altered, a semicolon is used to separate their designations. If one of the rearranged chromosomes is a sex chromosome, it is listed first. Otherwise, the chromosome having the lowest number is always specified first, e.g., t(1;12) (Mitelman, 1995). The exception to this rule is in three-break rearrangements where a part of one chromosome is inserted at a

Table 1: Common Symbols and abbreviated terms for ISCN nomenclature

Symbol	Meaning
add	additional material of unknown origin
arrow (-->)	From - to
approximate sign (~)	
cen	centromere
colon, single ( )	break
colon, double (‥)	break and reunion
comma (,)	separates chromosome number, sex chromosomes, and chromosome abnormalities
decimal point (.)	denotes sub-bands
del	deletion
de novo	designates a chromosome which has not been inherited
der	derivative chromosome
dic	dicentric
dup	duplication
fra	fragile site
h	heterochromatin, constitutive
hsr	homogeneously staining region
i	isochromosome
idic	isodicentric chromosome
ins	insertion
inv	inversion
ish	in situ hybridization
mar	marker chromosome
mat	maternal origin
minus sign (-)	loss
or	alternative interpretation
p	short arm of chromosome
parentheses	surround structurally altered chromosomes and breakpoints
pat	paternal origin
plus sign (+)	gain
q	long arm of chromosome
question mark (?)	questionable identification of a chromosome or chromosome structure
r	ring chromosome
rec	recombinant chromosome
s	satellite
sce	sister chromatid exchange
semicolon (;)	separates altered chromosomes and breakpoints in structural rearrangements involving more than one chromosome
slant line	separates clones
t	translocation
ter	terminal (end of chromosome)
upd	uniparental disomy

(Table Courtesy of Coriell Institute for Medical Research, 2005)

point of breakage in another chromosome. In this case, the receptor chromosome is specified first regardless of whether it is a sex chromosome (Mitelman, 1995).

For balanced translocations involving three separate chromosomes, with one breakpoint in each chromosome, the rule remains that the sex chromosome or lowest numbered autosome is specified first. The chromosome listed next is the one that receives the segment from the first chromosome and the chromosome specified last is the one that donates a segment to the first chromosome (Mitelman, 1995).

A plus or minus sign is placed before a chromosome to indicate additional or missing normal or abnormal chromosomes. The multiplication sign can be used to describe copies of a rearranged chromosome but is not used to denote multiple copies of normal chromosomes. A question mark or an approximate sign may indicate uncertainty in chromosome or band designation. The term 'or' is used to indicate alternative interpretations of an aberration (Mitelman, 1995).

The band in which the break occurred specifies the location of any breakpoint. A break suspected at an interface between two bands is assigned arbitrarily to the higher of the two band numbers, as it is more distal to the centromere (Mitelman, 1995). A break may sometimes appear to be located in either of two consecutive bands in which case the break can be specified by both band numbers separated by the term 'or'. If a break can be localized to a region, but not a band, only the region number is specified or the uncertainty may be indicated with a question mark (Mitelman, 1995).

Two systems for designating structural abnormalities exist. One is a short karyotype system in which the bands or regions in which the breaks occur can readily identify the rearrangements and breakpoints of chromosomes. The other is the detailed system, which identifies the type of rearrangement and defines each abnormal chromosome in terms of its band composition. Most publicized cases are notated in short

karyotype nomenclature or are rewritten into short karyotype form for database submissions. In the short karyotype system, structurally altered chromosomes are defined only by their breakpoints. The breakpoints are specified within parentheses immediately following the designation of the type of rearrangement and the chromosome(s) involved. Band designations are used to identify breakpoints and are listed in the same order as the chromosomes involved (Mitelman, 1995).

When both arms of a chromosome are involved in a two-break rearrangement, the breakpoint in the short arm is always specified before the breakpoint in the long arm, e.g., 46,XX,inv(8)(p1q21). If two chromosomes are involved in a rearrangement, also called a translocation, the chromosome with the lowest number is always listed first, e.g., 46, XY,t(9;18)(p3,q11), unless it is a sex chromosome which is always listed first, e.g. 46,XY,t(Y;18)(p3,q11) (Mitelman, 1995).

Three-break rearrangements provide an exception to the rule that sex chromosomes and chromosomes with the lowest number are specified first (Mitelman, 1995). In a three-break rearrangement (translocation), the donor chromosome is always listed last. When an insertion within a single chromosome occurs, the breakpoint at which the chromosome segment is inserted into is always specified first. The remaining breakpoints are specified as in the two-break rearrangement; the closer breakpoint of the inserted segment is specified first and the more distal one last if the inversion is direct and vice versa if it is inverted (Mitelman, 1995). Direct insertion of a short arm segment between bands 2p11 and 2p21 into the long arm at band 2q13 would be designated 46, XX, ins(2)(q13p11p21). Inverted insertion of the short-arm segment between bands 2p11

and 2p21 into the long arm at band 2q13 would be designated 46,XX, ins(2)(q13p21p11) since band 2p23 is not closer to the centromere due to the inverted insertion .

In translocations involving three chromosomes with one breakpoint in each, the rule is still followed that the sex chromosome or lowest numbered autosome is listed first. The second chromosome listed is the one that receives a segment from the first chromosome and the chromosome listed last is the one that donates a segment to the first chromosome (Mitelman, 1995). For example, if the segment of chromosome 11 distal to 11q34 has been translocated onto chromosome 18 at band 18q11, the segment of chromosome distal to 18q11 has been translocated onto chromosome 17 at 17q22, and the segment of chromosome 17 distal to 17q22 has been translocated onto chromosome 11 at 11q34, the short karyotype designation would be: 46, XY, t(11;22;17)(q34;q11;q22).

A single colon (:) is used in short karyotype designation to indicate a chromosome break and a double colon (::) is used to indicate a break and reunion. In short karyotype designation, an arrow (->), meaning from – to, is employed to locate the break and reunion (Mitelman, 1995). The end of a chromosome may be designated either by band location or by the symbol ter (terminal), preceded by the arm designation: pter indicates the end of the short arm and qter indicates the end of the long arm. To indicate the centromere in short karyotype designation, the abbreviation cen is used (Mitelman, 1995).

Derivative chromosomes are indicated in a short karyotype by the term der. This term always refers to the chromosome(s) that has an intact centromere (Mitelman, 1995). Derivative chromosomes are structurally rearranged chromosomes generated either by more than one rearrangement in a single chromosome, or due to unbalanced products in a

two or more break translocation (Mitelman, 1995). The derivative chromosome is specified in parentheses followed by all aberrations involved in the generation of the derivative chromosome. The aberrations are listed according to the breakpoints of the derivative chromosome from pter to qter and are not separated by a comma (Mitelman, 1995). For example, to specify a derivative chromosome 2 generated by two translocations, one involving the short arm with a breakpoint in 1p32 and the other involving the long arm with breakpoint in 2q25 would have a designation of der(2)t(1;7)(p32;q21)t(2;11)(q25;q13).

In karyotype designation, sex chromosome aberrations are specified first, with X abnormalities presented before those involving Y, and followed by abnormalities of the autosomes listed in numerical order irrespective of aberration type (Mitelman, 1995). For each chromosome, numerical abnormalities are specified before structural changes. Multiple structural changes of the same chromosome are presented in alphabetical order according to the abbreviated term of the abnormality (Mitelman, 1995). For example, 47,X,t(X;13)(q21;q11),inv(9)(p11q21), +21 specifies the sex chromosome abnormality followed by the autosomal abnormalities in order of chromosome number irrespective of whether the aberrations are numerical or structural. Numerical aberrations only take precedence to structural aberrations if they occur in the same chromosome number.

Unidentified ring chromosomes (r), marker chromosomes (mar), and double minute chromosomes (dmin) are listed last, in that order, while derivative chromosomes whose centromere is unknown should be placed after all identified abnormalities but prior to the unidentified ring, marker, and double minute chromosomes (Mitelman, 1995). A marker chromosome is a structurally abnormal chromosome in which no part can be

identified. Marker chromosomes are always preceded by a plus sign in ISCN nomenclature. Double minute chromosomes are a special kind of acentric structures that are recorded in the karyotype when found in more than one metaphase cell (Mitelman, 1995). Double minute chromosomes are not included in the chromosome count or associated ploidy level. The symbol dmin is used to designate double minute chromosomes, but unlike with the symbol mar, the dmin designation is not preceded with a plus sign. However, the number of double minutes per cell is listed and the dmin is recorded after any centric marker as in: 49, XX, … , +3mar, 1dmin. Double minute cell counts can also exist as a range, mean, or in absolute numbers (Mitelman, 1995).

Constitutional sex chromosome abnormalities are due to the acquisition or loss of sex chromosomes prior to development, while acquired sex chromosomes are due to chromosome mutations (Mitelman, 1995). Constitutional sex chromosome abnormalities are given without the use of a plus/minus sign. For example, an individual with Turner syndrome will have a karyotype designation 45, X. Acquired sex chromosome abnormalities are expressed with a plus or minus sign as in 45,X,-Y. Acquired chromosome abnormalities in individuals with constitutional sex abnormalities are distinguished with the use of letter c after the constitutional abnormality, which is designated first in ISCN nomenclature (Mitelman, 1995). For example, tumor cells with an acquired X chromosome in a patient with Turner syndrome would appear as 46,Xc,+X.

The symbol add is used in karyotype designation to indicate additional material of unknown origin attached to a chromosome or band. The symbol dic is used to specify dicentric chromosomes in which the dicentric chromosome replaces one or two normal

chromosomes. There is no need to indicate the missing normal chromosomes as they can be implied from the overall karyotype. Dicentric chromosomes are formed when two chromosomal fragments from a breakage, each containing a centromere, rejoin together to form a new chromosome with two centromeres (Walden et al., 1989). Isodicentric chromosomes are designated idic and are formed when two copies of the same segment of a chromosome, each containing a centromere, are joined through chromosome breakage (Contact a Family, 2004).

In ISCN nomenclature, the symbol dup indicates duplication and the symbol ins indicates insertion. Each can be preceded by the abbreviations dir or inv to indicate direct or inverted duplications and insertions. However, this information is rarely specified, as the order of the bands with respect to the centromere will also differentiate direct and inverted duplications or insertions (Mitelman, 1995).

Whole arm translocations are described by assigning the breakpoints to the centromeric bands p10 and q10. In balanced whole-arm exchanges, the breakpoint in the chromosome, which has the lowest number, or is the sex chromosome, is assigned to p10 (Mitelman, 1995).

Squamous Cell Carcinoma Cytogenetics

A common sequence of squamous cell carcinoma karyotype evolution appears to be the initial loss of chromosomes or segments, followed by tetraploidization, and ultimately loss of previously uninvolved chromosomes from the tetraploid population. The hypotetraploid cell population can have a near triploid or even lower DNA index and number of chromosomes. Many tumors exhibit both diploid and tetraploid cell

subclones. Polyploidy is associated with a more aggressive growth pattern, high histopathologic grade, and poor survival (Van Dyke, 2001).

Earlier stage squamous cell carcinomas tend to have more simple karyotypes. However, within every pathological stage of the disease, some tumors have more complex karyotypes. As a result, it has been difficult to assemble evolutionary genetic pathways that have broad applicability in squamous cell carcinoma, because most of the recurrent abnormalities have been observed at every histopathologic stage (Van Dyke, 2001).

Molecular level studies have clarified some of the cytogenetic observations of recurrent gain and loss of specific segments. The most frequent autosomal abnormality is loss of 3p. Other deletions on chromosome arm 3p reveal three independent regions of loss at 3p14, 3p21, and 3p24-25. Deletions at 3p14 are typically associated with the FHIT/FRA3B gene. Losses at 3p21 have not been clearly associated with any gene, but DCL1 is a candidate. The von Hipple Lindau (VHL) locus may be the target of the 3p24-25 deletion (Van Dyke, 2001).

Duplication in chromosome arm 3q is often associated with isochromsome formation resulting in squamous cell carcinoma and there is almost always 3p loss in the same tumor. CGH studies suggest one or more regions of amplification within 3q and gene TP63 as a possible target of gain at 3q27-3q29 (Van Dyke, 2001).

In chromosome arm 5q, 5q12-q31 deletion is very common, and appears to be associated with an unfavorable prognosis in squamous cell carcinomas. Target candidate genes include MCC and APC at 5q21, and the a-catenin locus at 5q31. In esophageal

squamous cell carcinomas, reduced expression of -catenin has been associated with tumor dedifferentiation, infiltration, and lymph node metastasis (Van Dyke, 2001).

Frequent gains of chromosome arm 7p may permit increased activity of EGFR, which is amplified in some cases of squamous cell carcinoma. In esophageal squamous cell carcinoma, amplification of this gene is associated with lymph node involvement (Van Dyke, 2001).

Distal 8p loss is a recurrent abnormality in squamous cell carcinomas and may target different genes in 8p21, 8p22-p23, and 8p23. FEZ1 is a transcription factor located at 8p22 and may be one genetic target for deletion. 8p deletion is an intermediate event in squamous cell carcinomas of the lung, following after 3p and 9p deletion (Van Dyke, 2001).

Loss of chromosome arm 9p is a common, early event in the development of squamous cell carcinomas. The tumor suppressor gene CDKN2/MTS1 at 9p22 is the most likely primary target of deletions. In cervical squamous cell carcinoma, 9p deletion is associated with lymph node metastasis. Loss of chromosome arm 10p has also been observed in many cases of squamous cell carcinoma (Van Dyke, 2001).

Commonly duplicated or amplified region 11q13-23, includes several probable target genes: HST1, INT2, PRAD1/CCND1, and EMS1. PRAD1/CCND1 and EMS1 are often amplified and over expressed in cases of squamous cell carcinoma. PRAD1/CCND1 over-expression may be associated with radiosensitivity. 11q duplication is associated with lower survival in esophageal squamous cell carcinoma as well as disease progression in squamous cell carcinomas of the head and neck (Van Dyke, 2001).

Loss on chromosome arm 13q is associated with lymph node metastasis in esophageal squamous cell carcinoma where genes RB1 or BRCA2 may or may not be the target. 16q deletion is less common but a recurrent finding in squamous cell carcinomas of several anatomic sites (Van Dyke, 2001).

TP53 gene mutations are typically early or initiating events in squamous cell carcinoma regardless of anatomic site, already evident in premalignant lesions. These mutations are usually not correlated with tumor aggressiveness or survival. Deletion of 17p, where this gene resides, is very common and may frequently serve to inactivate the remaining normal homolog in a tumor with a TP53 mutation. 17p loss appears to be a late event correlated with tumor invasion for cervical squamous cell carcinoma. The mutagen involved, e.g, smoking and alchol in the larynx, betel nut in buccal mucosa, and HPV in vulvar squamous cell carcinoma direct the specific mutations in 17p (Van Dyke, 2001).

A very poor prognostic indicator in squamous cell carcinoma at many sites, including head and neck and the female genital tract, is loss of 18q, specifically 18q21-q22. The primary gene target of loss in squamous cell carcinoma is unknown for chromosome arm 18q, but may possibly include Smad2, Smad4, and DCC (Van Dyke, 2001).

Loss of chromosome Y is observed in about 50% of cases of squamous cell carcinoma in males, and loss of the short arm of the inactivated X is common in squamous cell carcinoma of females (Van Dyke, 2001).

Karyotype Statistical Considerations and Outcomes

The karyotype of squamous cell carcinomas is very complex, but features common in squamous cell carcinoma at one anatomic site are often similar to features at other anatomic sites. This is irrespective of the events such as tobacco, alcohol, HPV, etc., that might have initiated the disease. These common changes suggest that the initiation, development, and progression of squamous cell carcinomas involve some of the same genetic pathways, irrespective of anatomic site (Van Dyke, 2001).

Statistically, mismatch repair gene mutations play a negligible role in the etiology and evolution of squamous cell carcinomas. Microsatellite instability has been reported, but does not appear to be a major factor in most cases of squamous cell carcinoma (Van Dyke, 2001). These two factors can drastically skew the results of statistical analyses performed on karyotypes since the parsed aberrations might not be cancer-related.

Statistical analysis of karyotype data requires an interpretation from ISCN nomenclature to binary data indicating the presence or absence of each type of aberration. This binary data can be used for several applications such as calculating hidden chromosomal abnormalities to uncover novel recurrent aberrations, characterizing cytogenetic patterns for individual types of cancers, guiding array comparative genomic hybridization (aCGH) design for diagnostic purposes, and exploring the cancer's evolutionary pathways by comparing different evolutionary stages of individual cancer types (Deeb et al., 2004).

Objective

The objective of this study is to evaluate three automated systems of karyotype parsing: Karyo Reader, Progenetix ISCN2matrix, and CYDAS and to use the output

from one karyotype parsing system to examine early stage evolutionary pathways of chromosome aberrations leading to squamous cell carcinoma. Squamous cell carcinoma is examined as an example of the use of data extracted from karyotypes and its applicability to cancer research in the identification of key aberrations responsible for squamous cell carcinoma development.

Research Questions

1. What systems are available to translate karyotype data into statistical data and what types of analyses are the outputs suitable for?
2. What are the most frequent chromosome aberrations observed in squamous cell carcinoma according to each karyotype parsing system and which results correlate closely to published literature?
3. Is squamous cell carcinoma sex related in terms of chromosome aberrations responsible for the disease?
4. What are the primary evolutionary mutagenic pathways involved in squamous cell carcinoma development and progression?
5. Are the evolutionary mutagenic pathways and chromosome aberrations truly consistent across different sites of squamous cell carcinoma?

Significance of the Study

The literature regarding the use of automated karyotype parsing systems is non-existent with most karyotype parsing systems having been developed in the past few years and still considered in the experimental phase. Though studies evaluating chromosome aberrations for specific loci or across specific sites exist, studies evaluating

chromosome aberrations across all sites of a cancer, like squamous cell carcinoma, do not.

Since most studies agree that squamous cell carcinomas are relatively the same across all sites of tumorigenesis, perhaps chromosome aberration analysis of the disease across all sites will uncover some novel or recurrent aberrations eliminated by insufficient data involved in site-specific analysis. With the identification of potential, uninvestigated chromosome aberrations comes an inherit potential for the identification of additional evolutionary pathways involved in the progression of the disease.

Clinical observation and testing have classified squamous cell carcinomas regardless of site, indicating that a potential common link exists in the underlying aberrations or evolutionary pathways associated with the disease. Understanding of these aberrations and pathways can lead to more targeted treatments, preventative measures, and improved screening methods, thereby reducing the financial burden this curable cancer puts on the healthcare delivery system.

CHAPTER 2

REVIEW OF THE RELATED LITERATURE

Chromosome Aberrations Identified in Squamous Cell Carcinoma

Viegas-Pequignot et al. (1990) examined chromosomal aberrations in lung squamous cell carcinomas. The study set out by first examining the ploidy levels of the cases, with chromosome numbers varying from 38 to 538 and most cases consisting of hypotriploid karyotypes with complex rearrangements. Chromosome losses were observed in regions 3p, 5q, 8p, Y, 5p, 10p, 13, 8q, 9, 10q, 11pter, 14, 15, and 21. Chromosome gains were observed in the regions 1q, 3q, and 1q.

Since most chromosome rearrangements were found to have occurred after a breakage in the constitutive heterochromatin and no recurrent breakpoints were found in euchromatin except 11p15, the study concluded with the postulation that perhaps the squamous cell carcinomas of the lung were the consequence of chromosomal imbalances related to the ploidy level changes rather than to alterations of the genes (Viegas-Pequignot et al., 1990).

Bradford et al. (1991) postulated that low E7 antigen expression in a subset of squamous cell carcinoma cell lines might be associated with chromosomal rearrangement or deletion involving the E7 locus on 11p. The locus, MICI, controlling the expression of E7 and related cell surface antigens is mapped to chromosome band 11p13, which has been identified as a region of cancer-associated aberrations and the probable locus for a

tumor suppressor gene. E7 and related surface antigens exhibit strong expression in normal cell lines, but variable expression in squamous cell carcinoma cell lines.

Karyotypes were prepared from 19 squamous cell carcinoma cell lines, including 11 with weak and eight with strong E7 expression. Eight of the 11 lines with weak E7 expression had 11p abnormalities, four of which were 11p deletions, and four of which were 11p breakpoints. In the four tumors with 11p deletions, the smallest region of overlap corresponded to the 11p13-p14 region. Statistical analysis indicated that 11p deletions or breakpoints contained 100 times lower E7 expression levels when compared to lines with no 11p abnormality. The study boasts over a 98% significance level and the results indicate that the E7 antibody identifies tumors with 11p13-14 deletions and other 11p rearrangements. In addition, this study identifies the 11p region as a site of nonrandom chromosome rearrangements in some human squamous cell carcinomas, (Bradford et al., 1991).

Jin et al. (1993) studied the effects of two different culturing mediums on resulting karyotypic pattern in short-term cultures of squamous cell carcinomas of the head and neck. The study used 115 cases, 80 of which were cultured by one method, and 35 of which were cultured in another medium that stimulates epithelial growth while inhibiting fibroblasts. A total of 83 tumors with karyotypic abnormalities were detected in the two groups. The tumors in the second group contained a higher proportion of tumors with polyploid complex karyotypic changes and a lower proportion of tumors with near-diploid simple rearrangements. The study indicates that the different culture conditions favored growth and further mutation of cell populations.

Rearrangements of 1p22 were mainly found in the first group of cultures, whereas the distribution of other structural aberrations was similar in the two groups and clustered to several regions: 11q13, 1p22, 1p11-12, 3p11-q11, 5q13, 1q25, 15q10, and 8q10. Unbalanced aberrations were more common in the second group with losses in chromosome regions: 11q, 13p, 14p, and 15p. Gains in unbalanced aberrations common to the second group included: 1q, 3q, 8q, and 15q (Jin et al., 1993).

In a 1994 study, Van Dyke et al., characterized the breakpoints, gains, and losses of chromosome material in squamous cell carcinomas of the head and neck region. Using 29 patients, cell lines were karyotyped using GTG-banding, C-banding, RGB-staining and AgNOR-staining (Van Dyke et al., 1994).

The tumors consisted of a mixed population of near-diploid, diploid, near-triploid, triploid, and near-tetraploid karyotypes, but many had subclones representing essentially the same karyotypic pattern. The most frequently observed changes were deletions with losses affecting regions: 3p13-24, 5q12-q23, 8p22-p23, 9p21-24, and 18q22-q23. Frequencies of these losses ranged from 40-60% of the tumors. Losses on the short arm of the inactive X occurred in 70% of tumors from female patients and loss or rearrangement of Y occurred in 74% of tumors from male patients. Chromosome gains were found in 3q12-qter, 5p, 7p, 8q, and 11q13-q23 in 28-38% of the tumors (Van Dyke et al., 1994).

The study found that loss of 18q appeared to be associated with short survival, as did the presence of multiple deletions in a single tumor. A translocation between proximal 1p and proximal 8p or 9p was observed in squamous cell carcinomas of the head and neck region, but not in female genital tract tumors. No other abnormalities

found appeared to be site specific, suggesting that the pattern of genetic evolution in squamous cell carcinoma is independent of anatomic site (Van Dyke et al., 1994).

Analysis of Karyotypes

Tai et al. (2004) used recurrent chromosomal imbalances to investigate the association between genetic changes and clinical features. Using two sets of patients, one with adenocarcinoma (AC) and the other with squamous cell carcinoma (SCC), a comparative genomic hybridization analysis was performed to compare the genetic changes in patients with AC and SCC and the association of these changes with clinical features. By quantifying the gains and losses of chromosomes as the respective lung carcinomas progressed, researchers were able to isolate specific aberrations that were significantly more prevalent for each type of lung carcinoma (Tai et al., 2004).

Frigyesi et al. (2003) demonstrated that the distribution of the number of aberrations per tumor (NAPT) follow a power law distribution with an exponent close to unity for breast, colorectal, and renal cell carcinomas. In this research, the NAPT score was estimated by scoring the number of entries in each karyotype. Unfortunately this type of scoring considers every aberration as one event when in fact some cases have entries that represent more than one event, like in the case of three-way translocations. Since these situations were considered rare, the NAPT measure was considered a good estimate of the number of changes present in each tumor. The results of this study indicated that a tumor, progressing from one generation to the next (t_0 to t_1) acquires an additional aberration with a probability directly proportional to the number of aberrations present at generation t_0. To obtain a value for the time of appearance of a chromosomal change, all of the tumors with the given change were selected and the distribution of the

number of changes per tumor plotted. The philosophy with this approach is that an aberration that frequently occurs in low complex karyotypes, and hence early in the karyotypic evolution, will produce distributions with peak frequencies at low values of the number of changes per tumor. Changes occurring late in the evolution of the karyotype would produce peak frequencies at higher values. In this type of consideration, the mean is not a good estimate of the time of occurrence (TO) because the frequency distributions are often skewed, so the modes of the distributions are used as the TO (Frigyesi et al. 2003).

Another approach to multivariate analysis of tumor karyotypes involves identifying frequent chromosome aberrations and imbalances. Each tumor is assessed for the presence (1) or absence (0) of selected aberrations and the results are tabulated in a binary form. This data matrix is subsequently used for statistical evaluation. Hoglund et al. (2002) assessed the number of cytogenetic imbalances per tumor (NIPT) as a score used to indicate the biological age of the tumor. The NIPT distributions in the population of the tumor samples was used to give clues to the mode of karyotypic evolution as a stable tumor type would have a different distribution than an unstable tumor type. Three different types of distributions were observed in the data, one monotonically decreasing (breast, colon, bladder, kidney, and neuroglial tumors), one unimodal (hyperdiploid multiple myelomas and hyperdiploid acute lymphoblastic leukemias), and one bimodal (ovary, lung, pancreatic, head and neck cancers) indicating different modes of karyotypic evolution at work in each type of distribution (Hoglund et al., 2002).

In their temporal analysis, Hoglund et al. (2002) plotted the NIPT distribution for tumor containing a given imbalance to determine if the imbalance occurs early or late.

The modal values of the distributions were used to indicate where when a given imbalance typically occurs since the distributions were too skewed to use median or mean values. The modal value was used as the time of occurrence for the abnormality. The temporal analysis was applied to seven tumor types and results indicated that relative TO values for a set of frequent imbalances were surprisingly consistent across tumor types, suggesting a general temporal order of imbalances. To investigate whether a given imbalance adheres to the one produced by random assortment of imbalances in a population with the observed NIPT distribution and aberration frequencies, Monte Carlo simulation was used (Hoglund et al., 2002). Simulations may reveal if the imbalance is seen significantly earlier or later than was expected.

To identify karyotypic pathways, Hoglund et al. (2002) employed principal component analysis (PCA) to condense the data. In the analysis, abnormalities belonging to the same pathway are placed close to together, whereas those from different pathways are placed far apart. Thus, late changes in tumor progression are placed apart from those occurring in the early stages. By clustering tumors with PCA, researchers discerned chromosomal changes that characterized cytogenetic subgroups within the tumor type (Hoglund et al., 2002).

CHAPTER 3

METHODS

Data Extraction

This study used existing data from the Mitelman Database of Chromosome Aberrations in cancer. The Mitelman Database is an initiative of the Cancer Genome Anatomy Project (CGAP), a program of the National Cancer Institute (NCI) whose purpose is to determine the gene expression profiles of normal, precancer, and cancer cells to improve detection, diagnosis, and treatment for patients. Extracted data from the Mitelman database was coded according to the International System for Cytogenetic Nomenclature (ISCN), a symbolic nomenclature depicting the chromosomal differences between normal cell DNA and DNA extracted from the cancerous cell. The following variables were obtained from the Mitelman database: band designation, chromosome abnormality, morphology, and topography.

Data from the Mitelman database was extracted based on the criteria that the case morphology was squamous cell carcinoma, including any other combination of malignancies, across all topographies. The study population extracted is representative of all cases of squamous cell carcinoma for which DNA extraction and sequencing has been performed to determine the cancer karyotype and which have been cited and extracted from literature for inclusion in the Mitelman database through CGAP initiatives, or which have been submitted by researchers for inclusion in the Mitelman database.

Cases were limited to those containing structural aberrations since those containing only numerical aberrations potentially stem from maternal or paternal genetic abnormalities. Cases with structural aberrations did not have their component numerical aberrations excluded as these more likely arose as part of the progression of squamous cell carcinoma rather than from heredity. A total of 574 cases were extracted from the Mitelman database, detailed in ISCN nomenclature. Data extracted in ISCN form was converted to binary statistical data using Karyo-Reader, Progenetix ISCN2matrix, and CYDAS karyotype parsing systems. Available outputs for data mining from each system were investigated as well as input and file formatting requirements to determine the applicability of each system to different data mining procedures utilizing karyotypes.

Karyo-Reader

Karyo-Reader is a web-based program designed to decode karyotypic data into binary form with band designations used as variables. Karyo-Reader boasts the ability to calculate all implied chromosomal aberrations from Mitelman database extracts or custom input files. Karyo-Reader includes a band validation algorithm to check for non-existent bands or aberrant formats in the original data. The system calculates a list of gains, losses, and structural aberrations per chromosome band and can display binary data for each case across all aberrations. Data from the Mitelman database was input directly into Karyo-Reader and the output contained binary data for each case across all potential aberrations housed in the Karyo-Reader system. The output from Karyo-Reader was limited to include only those aberrations that occurred in at least 30% of cases. The resulting recurrent chromosome aberrations identified by Karyo-Reader was compared to significant aberrations listed in literature.

Progenetix ISCN2matrix

Progenetix ISCN2matrix is another web-based program designed to decode chromosomal aberration information from an ISCN format, though not through direct Mitelman database extracts, into a band specific matrix suitable for data mining experiments. Progenetix also includes a band validation algorithm to check for non-existent bands or aberrant formats in the original input data. Progenetix has two banding resolutions for input files, 393 bands and 862 bands. First, the data extracted from the Mitelman database was reformatted to the input specifications required by Progenetix, including the 100 case limitation for each query. Then, using an 862 band resolution, binary data was extracted from Progenetix representing the gains, losses, and breakpoints of structural aberrations across all 862 potential aberrations (Baudis et al., 2001). One hundred cases were processed at a time, as allowed by the system, and the resulting output files were merged. The top scoring aberrations were compared to those found in literature.

CyDAS

CyDAS (Cytogenetic Data Analysis System) exists as a PC-based and a web-based system that can take direct input of Mitelman database extractions and decode the ISCN karyotype data into summarizations of gains, losses, and break aberrations per chromosome band, displaying only the totals for each aberrant band. CyDAS offers band resolutions of 400 bands and 550 bands and boasts integration to Microsoft Access and a graphical visualization (chromosome ideograms) of the gains, losses, and breaks per structural chromosomal aberration. CyDAS also produces a commented listing of errors encountered in parsing the karyotypes (Hiller et al., 2004). The data extracted from the

Mitelman database was directly input into the CyDAS system and the output, with banding resolution of 550 bands, was evaluated. The CyDAS output was examined for the most frequent chromosome aberrations and these were compared to those listed in literature.

Evaluation of Karyotype Parsers

The results of each karyotyping procedure and any error files were examined graphically and with frequencies to gain insight into the ability of the parser to read the ISCN data. Karyotype parsers were evaluated on their ability to accommodate user input, take Mitelman database extracts, parse particularly difficult karyotypes including "idem" or subclones, and on the applicability of the output to data mining procedures. Many cases exploiting these traits were eliminated by the systems as "unprocessable" and occured in the error file, which was analyzed where available.

Examination of Evolutionary Pathways

To examine early stage evolutionary pathways, the output from Karyo-Reader was used in assigning NIPT values, producing NIPT distributions, and in factor analysis to identify early stage chromosome aberrations responsible for squamous cell carcinoma. For the factor analysis, only aberrations occurring in at least 30% of cases were considered as early stage evolutionary aberrations. Principal component analysis was used as the extraction method for factor analysis and a Varimax rotation was employed to fully resolve the factors into two principal components.

Plausibly, aberrations that act in complementary fashion in the carcinogenic process should frequently be seen in the same tumor cases, whereas biologically incompatible aberrations would rarely be seen in the same case. Thus, when calculating

the correlation between the presence of different imbalances in a given tumor type, a positive correlation was used to indicate membership of the same karyotypic pathway, whereas a negative correlation was used to indicate different pathways. The scree plot, correlation matrix, and component plots were examined under these guidelines to make conclusions on the possible karyotypic evolutionary pathways in the extracted squamous cell carcinoma cases.

CHAPTER 4

RESULTS

From the Mitelman Database of Chromosome Aberrations in cancer, 574 cases were extracted representing 92 literature references from 25 journals as shown in Appendix A. Some cases contain uncertainty data as indicated by a "?" in ISCN nomenclature. Exclusions of uncertainty data were handled after the data was extracted from the Mitelman Database. The selected cases contain 18 different topographies, or locations of squamous cell carcinoma. A breakdown of cases by topography is shown in Table 2.

In reading karyotypes, particular emphasis is placed on the ploidy level of the cases. In ISCN nomenclature, the number of chromosomes in the cancerous cell, or ploidy level, should be specified first. Ploidy levels can be grouped based on the number of chromosomes and its closeness to a particular level. In cases of no ploidy level, the cancerous cell has no chromosomes but some cases have a near no ploidy level, in that they have zero to eleven chromosomes. In this manner, the relative ploidy level can be determined for each case as: no ploidy/near no ploidy level (0-11 chromosomes), haploid/near haploid (12-34 chromosomes), diploid/near diploid (35-57 chromosomes), triploid/near triploid (58-80 chromosomes), tetraploid/near tetraploid (81-103 chromosomes). The number and percentage of cases, grouped by ploidy level is shown

in Table 3. In the process of determining ploidy level, three cases contained an indeterminate ploidy level due to uncertainty in the specification of the number of chromosomes.

The results in Table 3 indicate that the majority of the cases included in the analysis have a diploid or near diploid amount of chromosomes. These results are favorable for investigating early stage chromosome aberrations as this indicates that the cells of most cases have not mutated far from normal, or diploid, chromosome numbers that most cells contain prior to development of cancerous mutations.

TABLE 2. Percentage of squamous cell carcinoma cases by topography

Topography	Percent of Cases
Anus	1.2%
Bladder	0.52%
Larynx	16 72%
Lip	0 17%
Lung	25 61%
Nasal Cavity/Paranasal sinuses	1 39%
Nasopharynx	4 36%
Oesophagus	2.26%
Oral Cavity	11.50%
Oro- and hypopharynx	5.92%
Penis	0.52%
Salivary gland	0.52%
Skin	4.88%
Soft tissue	0.35%
Thymus	0.52%
Tongue	8.89%
Urethra	0.17%
Uterus, cervix	7 67%
Vagina	6 79%
Total	**100.0%**

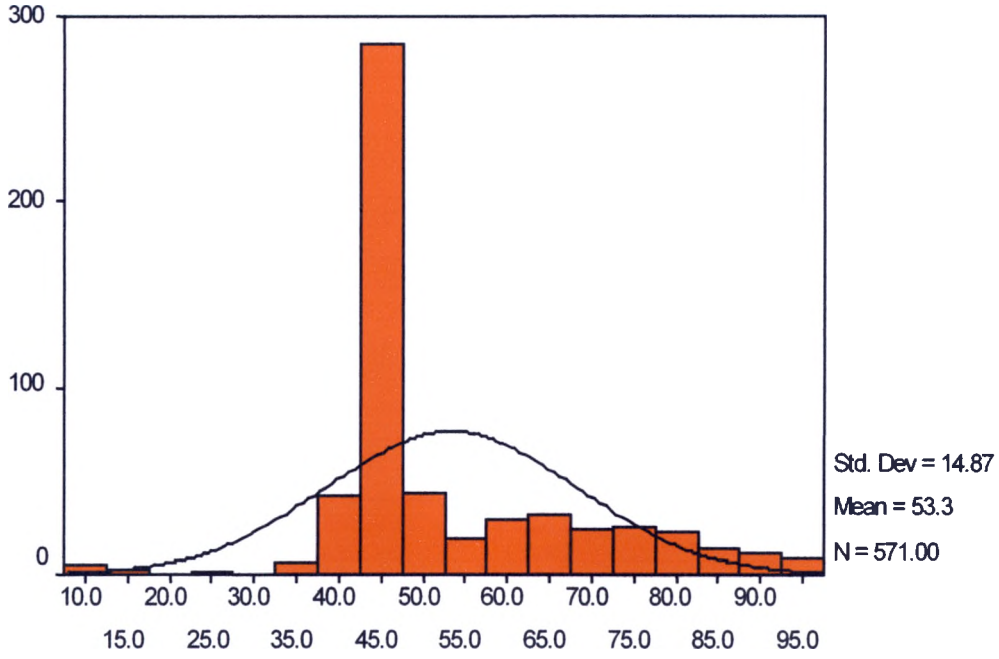
TABLE 3. Percentage and number of cases by relative ploidy level

Ploidy Level	Number of Cases	Percentage of Cases
No Ploidy Level (0-11)	4	0.70%
Haploid/Near Haploid (12-34)	5	0 88%
Diploid/ Near Diploid (35-57)	395	69.18%
Triploid/Near Triploid (58-80)	125	21 89%
Tetraploid/Near Tetraploid (81-103)	42	7 36%
Total Number of Cases	**571**	**100.00%**

A histogram plot of the number of chromosomes is shown in Figure 2. Notice that the distribution of the number of chromosomes in the squamous cell carcinoma cell follows a normal distribution. Ploidy levels are particularly important because individuals with more available chromosomes can experience more aberrations and vice versa for individuals with less available chromosomes. As expected, the mean number of chromosomes, 53.3, is relatively close to the diploid level of 46 chromosomes. Since the mean is greater than the normal diploid level, it can be assumed from the data that there are more aberrations resulting in chromosomal gains than aberrations resulting in chromosomal losses. The distribution of the histogram in Figure 2 is skewed to the right, which is expected as very low ploidy levels typically result in loss of the cell. The standard deviation of 14.87 indicates that all diploid and near diploid cells are included within one standard deviation of the mean.

The data queried from the Mitelman database can be saved as a tab-delimited text file. This format allows the data to be easily importable to a variety of Windows and Unix systems applications for analysis. To further analyze the data, the karyotype for each case must be parsed. Three extraction systems were used for karyotype parsing: Karyo Reader, Progenetix ISCN2matrix, and CyDAS.

FIGURE 1: Histogram Plot of the Number of Chromosomes per Case



Karyo Reader

Input and File Formatting

To parse the data in Karyo Reader, the extracted data from the Mitelman database of chromosome aberrations, was fed directly into the program in its raw tab delimited text file format as queried and saved from the database. When importing a file directly saved from a Mitelman database query to Karyo Reader, all input columns not used in parsing the karyotype, like topography, are still retained in the output file.

For data extractions in other file formats, queries from other databases, or custom created karyotype files; Karyo Reader also allows the user to specify their own unique input file format. For this method, the user is allotted nine columns of data to import; two columns that are used for unique identifiers, one column for the karyotype, and seven additional columns for input data to be retained with the output.

Custom input files for Karyo Reader are required to have at least one unique identifier present in the input file. For Mitelman database extracts, Karyo Reader utilizes the reference number, case number, and investigation number to compile a Karyo Reader identifier. The Karyo Reader identifier simply reads as reference number – case number – investigation number and is easily linked back to the original input data.

Data Exclusions

Using Karyo Reader, karyotypes with breakpoint uncertainty data can automatically be excluded, as in this analysis, since only proven breakpoints are of interest in this study. Uncertainty data includes any particular chromosome aberrations specified in ISCN nomenclature with a ? used in the position of the chromosome or band designation involved in an aberration. Using this option excludes the particular aberration associated with the ?, not all aberrations represented in the case.

Karyo Reader allows for the exclusion of polyploid karyotypes, which includes all karyotypes with chromosome numbers above 60, a moderate near-triploid ploidy level. This exclusion method does not exclude aberrations that represent frequent chromosome losses, as evidenced in very low chromosome numbers or almost no ploidy level.

With Karyo Reader, the aberrations identified can be limited to breakpoints only. This feature limits the identification of the chromosome aberrations to structural aberrations only, in which chromosomes break at specific points. Using this option excludes numerical chromosome aberrations in which whole chromosomes are gained or lost. As in this study, when data mining for unknown aberrations associated with a disease or evolutionary pathways of chromosome aberrations, entire chromosome gains

and losses can account for disruption of a biological pathway, resulting in cancer just as specific breakpoints can.

Another data exclusion feature of Karyo Reader is the ability of the program to or not to parse idem concatenates. Idem concatenates are related clones or subclones present in a tumor. Idem concatenates are notated in ISCN nomenclature first by the specification of the clone cell or stemline and then by specification of the idem concatenate, notated by the symbol idem. With idem concatenates, only the additional changes in relation to the stemline are reported for each concatenate. Karyo Reader gives the researcher the option of parsing the idem concatenates or not. However, since the stemline cell reported first typically contains the most basic anomaly, as specified in ISCN nomenclature, elimination of idem concatenates may eliminate novel chromosome aberrations. Novel aberrations could hold evolutionary linkages important for understanding the evolutionary mutagenic pathways of the disease and thus idem concatenates were parsed in this analysis.

Output

Karyo Reader offers four types of output including aberration frequency data, aberrations in binary format, and one aberration or one case per line. Aberration frequency data output represents the various chromosome aberrations, parsed from the input file, as rows and the number of occurrences of gains, deletions, and flags are summed for each individual aberration. This type of output is suitable for an initial analysis of the possible chromosome aberrations involved in the development and progression of disease or to determine the frequency of a given aberration in a sample

population, but this type of output fails to reveal any insight into the evolutionary pathways of disease.

The one aberration per line output contains one aberration per case per line of the output. The resultant file contains a column with each aberration listed for each case, a column identifying the type (loss, gain, flag), and the identification, morphology, and topography information originally supplied in the input file. This type of output also displays the subtype of any structural aberration. The available subtypes identified by Karyo Reader are shown in Table 4. This type of output is suitable for analysis by

TABLE 4: Karyo Reader Subtype Symbols and Meanings

Subtype Symbol	Meaning
add	addition of unknown origin chromosomal material
del	deletion
der	derivative chromosome
dera	derivative chromosome formed by gaining of additional chromosomal material of unknown origin
derd	derivative chromosome formed by deletion of some regions
dert	derivative chromosome formed by translocation events
dic	dicentric chromosomes
dup	duplications
dupr	inverted duplications
hsr	homogeneously staining region
i	isochromosomes
idic	isodicentric chromosomes
ins	insertions
inv	inversions
qdp	quadruplications
r	ring chromosomes
t	translocations
tas	telomeric associations
trp	triplications
t	translocations
tas	telomeric associations
trp	triplications

aberration subtype, studies with separate treatments of numerical and structural aberrations, or studies involving analysis of individual patient cases.

The one case per line Karyo Reader output produces a file that contains one row for each case in the input file with columns for the identification, morphology, and topography fields from the original input file. The parsed karyotype for each case is presented as a column in the output file with a colon (:) separating each parsed element of the karyotype. Each parsed aberration is followed by the aberration type (loss, gain, flag) and the structural aberration subtype shown in Table 4 for structural chromosome aberrations. Each of these three elements is separated by the underscore (_) symbol for easy parsing by most office programs. This type of output is most suitable for analyzing chromosomal gains, losses, and breakpoints (flag) for selected groups of cases or similarity scoring between difference cases.

The aberrations in binary format output from Karyo Reader retains the identification, morphology, and topography information supplied in the original input file as columns. Each case from the input file is represented as a row in this output file along with a binary presence (1) or absence (0) value for each chromosome aberration, listed in columns. A list of the 957 chromosome aberrations parsed by Karyo Reader is shown in Appendix B.

For comparison purposes, the aberrations in binary format demonstrates the ability of the program to effectively interpret expressed and implied aberrations only. However, the aberration frequency output can be used to identify potential recurrent chromosome aberrations in the data and was utilized for this purpose. For determination

of evolutionary mutagenic pathways involved in the development of squamous cell carcinoma, the aberrations in binary format output was utilized.

In the aberrations in binary format and aberration frequency outputs, Karyo Reader allows the user to specify a minimum aberration frequency that must be satisfied in order for the aberration to appear as a column in the output file. Limiting the output aberration columns by these means helps to exclude chromosome aberrations unimportant to the development or mutagenic evolution of the disease.

Karyo Reader Parsing Results

Table 5 shows that out of the 574 cases, Karyo Reader was able to parse 540 cases. This indicates that 34 cases contained incomplete or uncertain information in the karyotype and were subsequently removed from further analysis. All excluded cases contained either one identified aberration that contained an uncertainty in chromosome or band designation or no identified aberrations at all, leaving no data for Karyo Reader to parse out of the karyotype. This determination was made based on identification of missing cases in the output file and visual inspection of the respective cases in the input file.

The percentage of fields parsed by Karyo-Reader is 87.16%, and the percentage of structural aberrations parsed is 85.44%. Given that there is a level of uncertainty in the ability of Karyo Reader to parse all aberrations as well as a margin of error in the recording and entering of the data into the Mitelman database, these percentages indicate that Karyo-Reader is powerful in interpreting implied and expressed aberrations.

TABLE 5: Karyo Reader Processing Statistics

Total number of input cases	574
Total number of parsed cases	540
Percent of cases parsed	94.08
Total number of input fields	7866
Total number of fields parsed	6856
Percent of fields parsed	87.16
Total number of numeric aberrations	3975
Total number of structural aberrations	3372
Total number of parsed structural aberrations	2881
Percent of structural aberrations parsed	85.44

In examining the aberration frequency output data from Karyo Reader, a sample of which is shown in Tables 6-8, aberrations with the highest frequency are more important. Higher frequency aberrations indicate that the aberration is closely associated with squamous cell carcinoma and may take part in the early stages of the evolutionary pathway of the disease.

TABLE 6: Karyo Reader 10 Highest Frequency Gain Aberrations

band	gain	del	flag
7	146	49	0
20	128	73	0
8q23	94	13	1
8q24	93	15	18
1q32	91	90	13
1q44	89	104	20
1q43	88	103	3
1q31	87	87	7
1q41	86	100	0
1q42	86	101	5

Table 6 shows the ten highest frequency aberrations where an extra copy of a chromosome was gained (gain). Table 7 shows the ten highest frequency aberrations

where a loss of a chromosome region occurred (loss). Table 8 shows the ten highest frequency breakpoints for structural aberrations (flag).

TABLE 7: Karyo Reader 10 Highest Frequency Loss Aberrations

band	gain	del	flag
Y	27	297	0
21	18	275	0
3p23	40	222	7
3p22	40	221	0
3p24	44	220	2
3p26	44	219	7
18	25	218	0
3p25	44	214	10
22	55	213	0
13	27	213	0

TABLE 8: Karyo Reader 10 Highest Frequency Flag Aberrations

band	gain	del	flag
14p11	8	96	69
13p11	9	58	64
15p11	2	62	63
19q13	21	9	59
3p11	17	96	49
1q21	61	55	48
1p11	33	45	48
11q21	50	38	48
1p13	62	100	47
8p11	18	99	45

The common bands with high frequency aberrations across all aberration types (gain, loss, and flag) are 3p and 1q, indicating that these bands probably play a major role in the initial development of squamous cell carcinoma. Primarily, bands 7, 20, 8q23, 8q24, 1q32, 1q44, 1q43, 1q31, 1q41, 1q42, Y, 21, 3p23, 3p22, 3p24, 3p26, 18, 3p25, 22, 13,

14p11, 13p11, 15p11, 19q13, 3p11, 1q21, 1p11, 11q21, 1p13, and 8p11 were identified by Karyo Reader as the potential key aberrations involved in squamous cell carcinoma development and progression.

The bands identified in tables 6-8 are potential recurrent chromosome aberrations associated with squamous cell carcinoma solely based on their frequency within the data. Since each of the aberrations occurred over an unspecified period of time, it is incorrect to assume that aberration frequency alone identifies the recurrent chromosome aberrations associated with a disease. Possibly the population of cases selected may represent simply one stage in the evolution of the disease, resulting in identification of insignificant aberrations unrelated to the evolutionary progression of the disease, but simply representative of the diseases at one point in their progression.

For the aberrations in binary format output from Karyo Reader, it is important to establish a threshold or minimal frequency of aberrations required to be included in the parsed data. This eliminates later stage aberrations and allows the data to be more representative of aberrations that occur at the onset of disease. The threshold requirement for this analysis is 30%, indicating that the aberration must occur in at least 30% of cases to be included in the parsed data set. The threshold requirement reduced the output variables or aberration band designations from 940 variables to 19 variables including: d10, d13, d14, d15, d18, d21, d22, d3p13, d3p14, d3p21, d3p22, d3p23, d3p24, d3p25, d3p26, d4, d8p22, d8p23, and dY where the d indicates a deletion. Due to their inclusion, these deletions must exist in at least 30% of cases. Note that no numerical or structural chromosomal gains were present in at least 30% of the cases. Table 9 shows a sample of the Karyo Reader binary aberration output.

TABLE 9. Karyo Reader Sample Binary Aberration Output

ID	morphology	topography	d18	d21	d3p22	d3p26	dY
5912-5-1	Squamous Cell Carcinoma	Lung	0	0	0	0	1
6026-42-1	Squamous Cell Carcinoma	Larynx	1	0	0	0	1
6026-34-1	Squamous Cell Carcinoma	Oro- and hypo pharynx	1	1	1	1	1
5080-8-1	Squamous Cell Carcinoma	Lung	0	1	1	1	0
4895-3-1	Squamous Cell Carcinoma	Larynx	0	0	0	0	1
6026-26-1	Squamous Cell Carcinoma	Oro- and hypo pharynx	0	0	0	0	1
10308-123-1	Squamous Cell Carcinoma	Tongue	0	0	0	0	1
5245-13-1	Squamous Cell Carcinoma	Oro- and hypo pharynx	1	1	0	0	1
6026-18-1	Squamous Cell Carcinoma	Tongue	0	1	0	0	1
10308-115-1	Squamous Cell Carcinoma	Oral Cavity	0	0	0	0	0
6180-147-1	Squamous Cell Carcinoma	Oral Cavity	1	1	1	1	1
8463-5-1	Squamous Cell Carcinoma	Larynx	0	0	0	0	1
2338-29-1	Squamous Cell Carcinoma	Lung	0	0	0	0	0
2066-5-1	Squamous Cell Carcinoma	Anus	0	1	0	0	0

TABLE 10. Karyo Reader Aberration Frequency and Percentage of Cases

Aberration	Number of Cases	Percentage of Cases
d10	110	4 83%
d13	118	5 18%
d14	99	4 35%
d15	116	5.10%
d18	122	5.36%
d21	139	6.11%
d22	110	4 83%
d3p13	88	3 87%
d3p14	112	4.92%
d3p21	121	5 32%
d3p22	128	5.62%
d3p23	124	5 45%
d3p24	124	5 45%
d3p25	125	5 49%
d3p26	130	5.71%
d4	104	4.57%
d8p22	92	4.04%
d8p23	95	4.17%
dY	219	9.62%
Total	**2276**	**100.00%**

Table 10 shows the number and percentage of cases that contained each aberration. This table also demonstrates that 2276 total aberrations were counted for the 540 cases included in the analysis. This indicates that many cases contained more than one of the identified aberrations. Table 11 shows a breakdown of the number of aberrations per case as found in the Karyo Reader binary output for the 19 included aberrations.

The results in Table 11 indicate that the majority of cases (74.81%) contained at least one of the 19 aberrations with the highest frequencies from the squamous cell

TABLE 11. Karyo Reader Case Breakdown by Aberration Count

Aberration Count	Number of Cases	Percentage of Cases
19	2	0.37%
18	1	0.19%
17	4	0 74%
16	10	1.85%
15	11	2.04%
14	15	2 78%
13	14	2.59%
12	13	2.41%
11	14	2 59%
10	9	1.67%
9	7	1 30%
8	21	3.89%
7	29	5.37%
6	17	3.15%
5	25	4.63%
4	30	5.56%
3	18	3.33%
2	36	6.67%
1	128	23.70%
0	136	25 19%
Total	**540**	**100.00%**

carcinoma data. Also important to note in the parsed Karyo Reader data is the percentage of cases with only one identified aberration. Since this 23% of cases have one identified

aberration, the aberration is likely to be one of the primary evolutionary events related to the development of squamous cell carcinoma.

Progenetix ISCN2matrix

Input and File Formatting

Progenetix ISCN2matrix accommodates three input file formats: tab delimited text files, Progenetix XML files, and precluster files. Tab-delimited text files work best for data extracted from the Mitelman database due to the content of data available in extract form. Progenetix XML files are produced through a direct query of karyotype data available in the Progenetix data repository, much in the same fashion as with the Mitelman database. A list of the chromosome aberrations utilized by and produced in the output of Progenetix ISCN2matrix is shown in Appendix C. The XML file produced from the Progenetix query can be directly fed into ISCN2matrix without alteration. Precluster files can be used in Progenetix to create a visual representation of chromosomal losses and gains, but precluster files exist only after karyotype parsing.

To parse the data in Progenetix, the extracted tab delimited text data from the Mitelman database of chromosome aberrations must first be reformatted to accommodate the required data structure. The Mitelman database reports a reference number, case number, investigation number, publication author, year of publication, journal name, volume, page number, and karyotype in case output while Progenetix ISCN2matrix only accommodates a case number, ICD-O code, PubMed ID, diagnosis, and experiment type (CGH or banding) in addition to the karyotype.

Unlike with Karyo Reader, Progenetix ISCN2matrix requires a one column case number and will not combine multiple identifiers to create a unique identifier for each

karyotype to be parsed. For this reason, the user cannot simply leave the reference number, case number, or investigation number from the Mitelman extract file to suffice as the unique identifier because these identifiers alone are not unique to each case. Either the user can combine these three fields to create a unique identifier or manually create one, complicating the ability of the user to link back to the original data.

The International Classification of Disease for Oncology (ICD-O) codes are numerical codes used to indicate the morphology and topography of a cancer. The Mitelman database of chromosome aberrations in cancer does not report ICD-O codes, but rather reports a standardized, textual description of the topography and morphology of the disease per case. To this event, direct Mitelman extracts require recoding to ICD-O in order to utilize this column in the input file.

Though available when looking at individual cases, the Mitelman database does not include the PubMed ID in queried file extractions. As a result, this field in Progenetix ISCN2matrix input cannot be utilized unless the PubMed ID is manually extracted or scripted from the Mitelman database.

To ease the transition of data from the Mitelman database to Progenetix, all variables except karyotype were stripped from the Mitelman output and a unique case number was created to satisfy the requirements of Progenetix ISCN2matrix.

Once the data is reformatted and fed into Progenetix, the file type must be specified. The ISCN2matrix program accommodates three varieties of cytogenetic input data: CGH (comparative genomic hybridization), banding (karyotypes), and array CGH. CGH data comes directly from experimental results while banding data typically comes from queries and literature extractions, as in the case of data extracted from the Mitelman

database. Since all the extracted data represents banding data, an additional column variable for the experiment type was not necessary. Rather, an overall data type of banding was selected through Progenetix ISCN2matrix. The file was then saved as a tab delimited text file for importation into Progenetix ISCN2matrix.

Unfortunately Progenetix ISCN2matrix can only accommodate 100 cases per web submission. Depending on the number of karyotype cases, the input file for Progenetix has to be split into several input files, each separately analyzed. Afterwards, the data files have to be merged back together to retrieve all the necessary binary data.

Data Exclusions

Using Progenetix ISCN2matrix, karyotypes with breakpoint uncertainty data are automatically handled by elimination of any uncertainty breakpoints, including complete elimination of cases with only uncertainty breakpoints. No user specification options are available to adjust how data is excluded.

ISCN2matrix only parses structural chromosome aberrations found in karyotypes, classifying each as a gain, loss, or breakpoint. No numerical aberrations are recorded or parsed by Progenetix, resulting in exclusion of numerical aberrations from the analysis.

Progenetix ISCN2matrix does produce very detailed error files citing specific reasons for why the application was unable to parse a particular aberration or read a particular karyotype. Fortunately these error files can be imported into office applications for analysis.

Output

Progenetix has the ability to parse karyotypes in a low or high band resolution mode. Low band resolution parsing includes only 393 bands, and hence 393 columns of

potential chromosome aberrations, a number adequately accommodated by most statistical and spreadsheet applications. High band resolution parsing includes 862 bands or potential chromosome aberrations, a number of variables not easily handled by some spreadsheet applications. Since ISCN2matrix does not contain any features to limit the amount of output such as an occurrence threshold, using high resolution band parsing can present a challenge to data analysis.

For the purposes of data mining in this study, high band resolution output is necessary to ensure that as many chromosome aberrations as possible are considered in the analysis. Including fewer aberrations could potentially eliminate key aberrations associated with squamous cell carcinoma and other cancers. Unfortunately, Progenetix ISCN2matrix can only parse structural chromosome aberrations, omitting any potential numerical chromosome aberrations involved in mutagenic pathways. Appendix C shows the chromosome aberrations included in Progenetix ISCN2matrix. Aberrations found in this list, all structural, are the only aberrations Progenetix ISCN2matrix can identify. This limitation puts Progenetix at a disadvantage for researchers who need to include numerical chromosome aberrations in an analysis.

Unfortunately the options available for selecting output from Progenetix ISCN2matrix are virtually non-existent. Outside of setting the band resolution, Progenetix ISCN2matrix is very rigid in it's output settings. Progenetix produces produces an output file consisting of each aberration band as variables with the values –1 to indicate a loss aberration, 1 to indicate a gain aberration, and 0 to indicate no aberration. This format is suitable for binary statistical analysis, but complicates statistical output unless it is recoded.

Additionally, Progenetix ISCN2matrix can further process the binary output file by performing a cluster analysis. Unfortunately the output results of the cluster analysis function are only available in visual form. When dealing with large amounts of chromosome aberrations, as in this dataset, it is impossible to visually decipher different evolutionary pathways emerging from the cluster analysis, particularly without any of the cluster analysis statistics.

Progenetix ISCN2matrix Parsing Results

Progenetix ISCN2matrix was capable of reading and interpreting data from the majority of cases. Of the 574 case input, 545 were parsed by Progenetix as shown in Table 12.

TABLE 12: Progenetix Case Processing Summary

Total number of input cases	574
Total number of parsed cases	545
Percent of cases parsed	94.95

Progenetix ISCN2matrix handles uncertainty data in a manner similar to Karyo Reader in that uncertainty aberration data is excluded from the output dataset. However, unlike with Karyo Reader, ISCN2matrix produces an output log file of errors associated with parsing the karyotype data. These errors may have resulted in exclusion of unidentified aberrations in certain karyotypes or entire elimination of the case if no portion of the karyotype could be parsed.

A summary of the errors associated with parsing the squamous cell carcinoma data extracted from the Mitelman database are shown in Table 13. The highest percentage of the total uncertainty aberrations was associated with "incomplete

karyotypes". Typically these errors are associated with uncertainty data, represented by a "?" in the karyotype, as determined by inspection of the errored aberrations.

TABLE 13: Progenetix Uncertainty Aberration by Type

Type of Uncertainty	Number	% of Total Uncertainty
Strangeness in losses	9	1.16%
Strangeness in breaks	9	1.16%
Something unresolved	216	27 73%
Several abnormal clones ("idem" concatenates)	180	23 11%
Incomplete karyotype	365	46 85%
Total uncertainty aberrations	779	100.00%

The second largest percentage of uncertainties in the data was due to something unresolved. This error indicates that there was an error in the ISCN data conventions. Many of these cases represent extra commas or other hanging qualifiers without any subsequent information.

The third largest percentage of uncertainties in the data concern the "idem" concatenates or subclones that indicate additional changes in the stemline, the first listed clone. ISCN2matrix parser simply eliminates subclones as an error in the data, though unique aberrations might exist in a single subclone that might not necessarily be present in all subclones or listed in the stem cell. Fortunately for the purposes of data mining, subclones do not present a challenge as they typically exist in small subset of affected cells and represent novel aberrations with almost no impact on the early mutagenic pathways related to the karyotype.

The lowest category of errors, strangeness in losses and breaks, are the result of data indicating a chromosomal translocation without specifying the donor or receiver

chromosome location. Many of these cases have multi-way translocations that are simply too complex for the ISCN2matrix converter to analyze.

Table 14 shows the ten highest frequency structural (flag) chromosome aberrations in the Progenetix output. Note that Progenetix ISCN2matrix does not include numerical aberrations (gains and losses).

TABLE 14: Progenetix 10 Highest Frequency Structural Aberrations

Band	Flag
Yq11.1	208
Yq11.21	208
Yq11.221	208
Yq11.222	208
Yq11.223	208
Yq11.23	208
Yp11.32	207
Yp11.31	207
Yp11 2	207
Yp11.1	207

Of the 574 total cases parsed by ISCN2matrix parser, 443 cases presented errors that were unresolved. With 77.2% of cases presenting a challenge for this parser, the validity of the results of any analysis using this parsed data is suspect.

In addition, the highest frequency structural aberrations observed in the parsed Progenetix data are all linked to the Y chromosome, a very unlikely possibility for a disease that is not completely gender bias. The top recurrent chromosome aberrations identified by Progenetix include Yq11.1, Yq11.21, Yq11.221, Yq11.222, Yq11.223, Yq11.23, Yp11.32, Yp11.21, Yp11.2, Yp11.1.

CyDAS

Input and File Formatting

Using CyDAS (Cytogenetic Data Analysis System), data extracted from the Mitelman database can be input to the web-based or PC-based program for karyotype parsing without any reformatting.

The web-based CyDAS application is limited to 500 cases and thus does not suffice for a large data set as in the case of the Mitelman database squamous cell carcinoma extract. For these larger datasets, the PC-based CyDAS system must be employed.

The PC-based CyDAS application requires a moderately extensive computer background to install and configure. Though instructions are available, they miss a number of steps and do not aid the user in configuration of additional Microsoft components (such as MDAC 2.7, Microsoft .NET framework 1.1, Microsoft ODBC .NET Data Provider) required for the application. In addition, the CyDAS installation documentation does not address issues of integration with backend database platforms (SQL server, MySQL, Microsoft Access).

The web-based CyDAS application accommodates a variety of input file formats including direct Mitelman extracts. Custom ISCN format input files, such as those produced from banding analysis, can be easily imported into CyDAS with two columns, one specifying an identifier and the second containing the karyotype. Custom ISCN input files cannot contain any blank identifiers or karyotypes in the file and the elements in the file must be separated by a tab, pipe, or single blank.

The web-based CyDAS system allows for a custom CGH input file format that follows the requirements of the custom ISCN format except that the karyotype is written in CGH format. Typically, data from CGH analysis is utilized for this format.

Each of the input formats available in the web-based CyDAS application is offered in the PC-based CyDAS application. In total, the PC-based CyDAS application includes four predefined custom input file formats and two predefined custom CGH file formats. Additional user-specified file formats could be added or removed from the PC-based CyDAS application as needed. Both the PC and web based CyDAS applications easily import Mitelman database extracts through specification of the file. The only input specification available for either system is the specification of the filter used for the file format.

Upon importing data in the PC-based application, database tables are populated with information about each case and it's respective karyotype(s). During the import, CyDAS calculates and records a multitude of information about each karyotype. Of particular importance is the cytoband table, which records the gains, losses, and breaks for each chromosome aberration.

Once data is imported into the PC-based CyDAS application, a group can be specified to label or differentiate the imported data. For analyses of disease that vary across different morphologies, CyDAS also offers the ability to specify subgroups of data. Squamous cell carcinoma does not vary across different morphologies according to literature, so specification of subgroups was not needed for this Mitelman data.

In order for data to be selected for analysis in the PC-based CyDAS application, the active group that houses the data (group, subgroup, or new data group) must be

selected. Without the selection of an active group, CyDAS will only allow ISCN analysis of single karyotypes, analysis of single derivative chromosomes, and development of karyograms, visual representations of karyotypes, for individual cases.

Data Exclusions

Like Progenetix ISCN2matrix, CyDAS only provides chromosome aberration data on structural aberrations. However, CyDAS does record a total aberration count inclusive of the numerical aberrations contained in the data. This aberration count provides valuable information about the evolutionary age of the malignancy, but does not provide detail information on the numerical aberrations represented in the data.

The CyDAS web-based application, much like Progenetix ISCN2matrix, has a high band and a low band resolution mode. High band resolution mode includes 550 bands, while low resolution mode contains 400 bands. The 550 bands utilized by and produced in the output from CyDAS are shown in Appendix D. Additionally, CyDAS includes a two-digit resolution mode that only displays the chromosome, arm, and primary band designation in reporting gain, loss, and break structural aberrations. Upon importing data into the PC-based CyDAS application, all 550 bands are used in parsing the karyotype, but viewer and report outputs can be limited to a resolution of 400 bands or 2 digits.

Similar to Progenetix ISCN2matrix, the web-based CyDAS application produces output error files associated with parsing the karyotype data. The error file in CyDAS gives a very detailed explanation of the error that occurred in parsing the karytoype. The PC-based CyDAS application does not produce an output error file, as this feature is still in development, but the error information is stored in the karyotype table of the database.

The backend database used for the PC-based CyDAS application was queried to retrieve information on the errors encountered in parsing the Mitelman extract squamous cell carcinoma karyotypes.

Output

CyDAS output primarily displays a graphical visualization of the chromosome aberrations in a given dataset. Many analysis features of CyDAS are available as options in the system but result in a response that they are "not yet available" including cluster analysis, statistics, and error list. Other output features of the CyDAS application simply do not function in its current version including evolution trees and dependence networks. Still other features of the PC-based CyDAS application result in calculations that overflow the processor such as drawing the breakpoints of all structural aberrations represented in the dataset or graphical representation of all the gains and losses represented in a large dataset.

Fortunately the PC-based CyDAS system utilizes a backend database platform that contains much of the raw information utilized to compile the graphical representations and output reports CyDAS cannot currently produce. However, this backend database does not perform data mining procedures such as those associated with the generation of evolution trees and dependence networks. For the purposes of this analysis, output was directly queried from the database to determine gains, losses, and breakpoints of structural chromosome aberrations.

CyDAS has the ability to produce a graphical representation of the gains and losses or breakpoints for structural aberrations available in a dataset. This representation can be limited to banding resolutions of 400 bands, 550 bands or 2 digits. The program

also allows the user to select a cutoff value in which aberrations are included in the output only if they are present in a percentage of cases above the cutoff value. The cutoff value can be specified manually or automatically assigned by CyDAS in output generation. With the CyDAS graphical output, either Ensemble or NCBI map viewers can be utilized to view the aberrations graphically as well as link to the Ensemble or NCBI website information on the chromosome, the known chromosome bands, and homo sapiens clones.

A graphical representation of the structural chromosome aberrations in the database was produced using CyDAS with a band resolution of 2 digits and a 30% cutoff value in which an aberration has to be present in at least 30% of cases to be included in the graphical representation. This representation was the least complex arrangement available and the only arrangement allowable for a PC processor. For the graphical viewer, Ensemble was selected. The same selections were utilized for both the structural gains and losses output and the structural breakpoints output.

Output options involving analysis of a single karyotype all function in both the PC-based and web-based CyDAS applications. Features such as drawing a single karyogram, drawing a derivative chromosome, and ISCN analysis of a single karyotype all function and were performed using an example karyotype from the dataset to examine the quality of the output information.

CyDAS Parsing Results

Table 15 below shows the number and percentage of parsed cases and karyotypes by CyDAS.

TABLE 15: CyDAS Case Processing Summary

Total number of input cases	574
Total number of parsed cases	492
Percent of cases parsed	85.71
Total number of aberrations	945
Total number of parsed aberrations	844
Percent of aberrations parsed	89.31

Unlike the 94-95% with Karyo Reader and Progenetix, CyDAS was only able to process karyotypes in 85.71% of cases. In addition, a total of 101 potential aberrations were unable to be parsed by CyDAS representing 10.69% of the total aberrations parsed. CyDAS parsed a total of 89.31% of the total aberrations. Though this percentage is slightly higher than the percentage of structural aberrations parsed by Karyo Reader, CyDAS parsing only resulted in a total of 945 structural aberrations compared to the 3372 structural aberrations encountered by Karyo Reader.

Though a custom query is necessary to extract error data from the PC-based CyDAS, the information stored in the database is very specific to the actual error encountered by the program in reading the karyotype. Each of these individual errors was classified into four distinct categories as shown in Table 16.

TABLE 16: CyDAS Uncertainty Aberrations by Type

Type of Uncertainty	Number	% of Total Uncertainty
Missing/uncertain band designations	54	53.47%
Something unresolved	19	18.81%
(Iso)derivative chromosome errors	19	18.81%
Several abnormal clones ("idem" concatenates)	9	8.91%
Total uncertainty aberrations	101	100.00%

In examining the aberration frequency data from CyDAS, a sample of which is shown in Tables 17-19, aberrations with the highest frequency are more important.

Higher frequency aberrations indicate that the aberration is closely associated with squamous cell carcinoma and may take part in the early stages of the evolutionary pathway of the disease. Table 17 shows the ten highest frequency aberrations where an extra copy of a chromosome region was gained (gain) from a structural aberration. Table 18 shows the ten highest frequency aberrations where a loss of a chromosome region occurred (loss) from a structural aberration. Table 19 shows the ten highest frequency chromosome breakpoints (flag) for structural aberrations.

TABLE 17: CyDAS 10 Highest Frequency Gain Aberrations

Band	Gains
8q22	253
8q24	252
8q23	251
7p21	233
7p22	232
7p15	232
7p13	228
8q21	227
7p11	226
7p12	226

TABLE 18: CyDAS 10 Highest Frequency Loss Aberrations

Band	Losses
3p23	293
3p21	290
3p22	289
3p24	288
3p26	287
3p25	285
8p23	281
14p13	281
3p14	279
8p22	279

TABLE 19: CyDAS 10 Highest Frequency Flag Aberrations

Band	Flag
8q10	108
11q13	106
14q10	102
3q10	94
13q10	85
5p10	83
1q10	81
15q10	77
22q10	71
1p13	67

The common bands with high frequency aberrations of all three types are 8q, 3p, and 11q, indicating that these bands probably play a major role in the initial development of squamous cell carcinoma. For the purposes of clinical research, these bands should be evaluated for possible genetic markers of squamous cell carcinoma.

The common bands with high frequency aberrations of all three types are 8q, 3p, and 11q, indicating that these bands probably play a major role in the initial development of squamous cell carcinoma. For the purposes of clinical research, these bands should also be evaluated for possible genetic markers of squamous cell carcinoma.

Figure 2 shows the graphical output karyogram produced by CyDAS for the structural breakpoints identified in the data. Each separately indicated region of the chromosome represents a different band of the chromosome in which an aberration occurred. When viewing this output within CyDAS, clicking on a particular band links to the Ensemble data available for that particular band. Additionally, a mouse roll-over feature is used on each band segment in this output to display the band designation.

Figure 3 shows the graphical output karyogram produced by CyDAS for the structural gains and losses identified in the data. Each separately indicated region of the

chromosome represents a separate region of gain or loss of a chromosome segment through a structural aberration. When viewing this output within CyDAS, rolling the mouse over a particular band will identify the band with a pop-up window. As with breakpoint karyograms, a mouse roll-over feature is used on each band segment in this output to display the band designation.

For any one karyotype, both the PC-based and web-based CyDAS applications can produce a karyogram visual representation of the aberration and it's resultant chromosome structure. An example of an individual karyogram produced by CyDAS is shown in Figure 4. The karyotype used to generate this karyogram is 46, XY, t(1;5)(q21;p12) indicating that a switch occurred between the long arm portion of chromosome 1 after band 21 and the short arm portion of chromosome 5 after band 12. In the karyogram, chromosomes are colored differently to distinctly show when parts of one interchange with another. Also, changes in the chromosomes are notated by a # sign to easily spot changes that are recorded in the karyotype.

FIGURE 2: CyDAS Breakpoints Karyogram

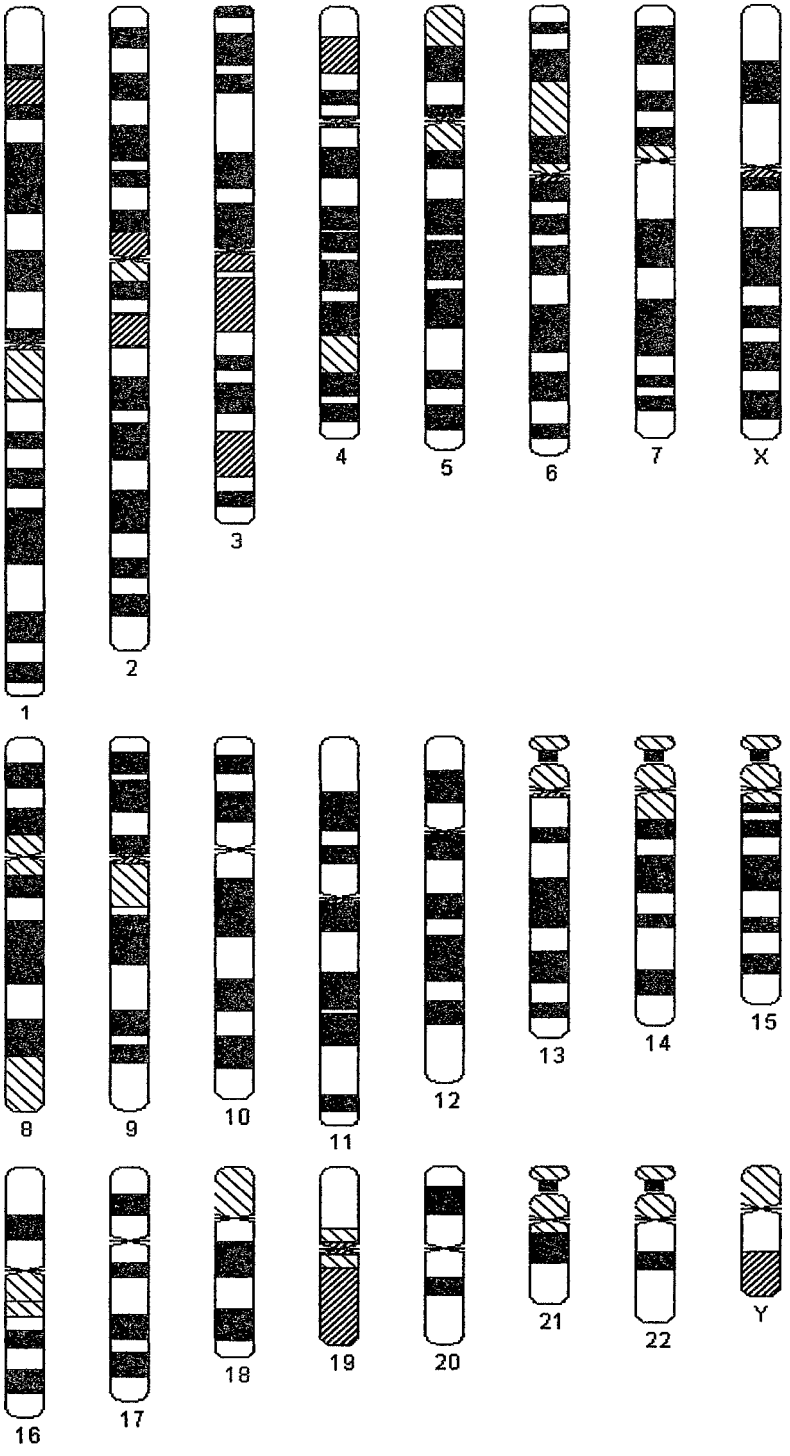


FIGURE 3: CyDAS Gains & Losses Karyogram

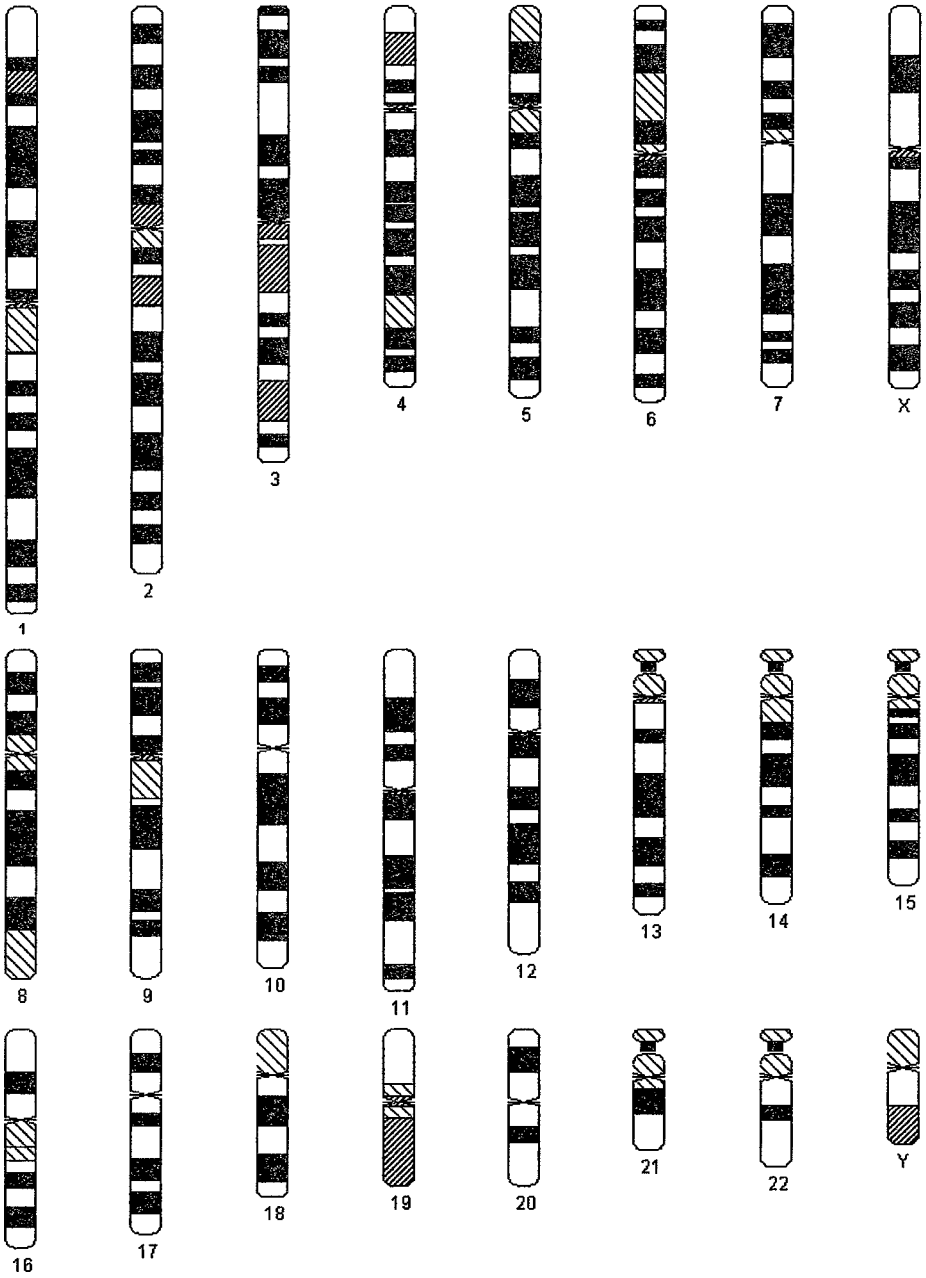
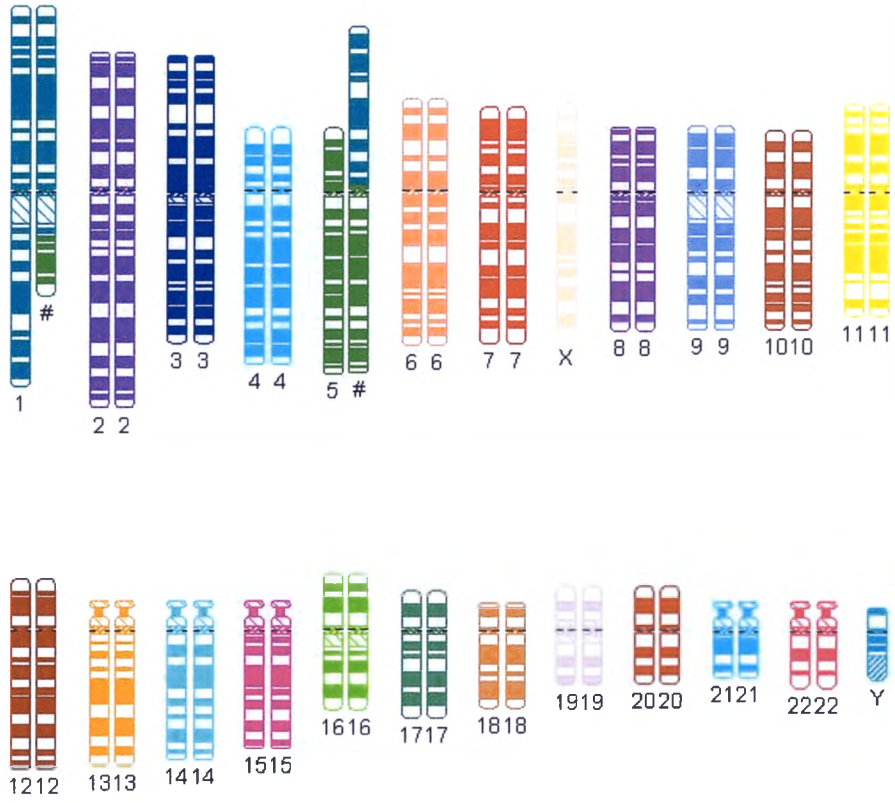


FIGURE 4: Example CyDAS Karyogram



NIPT Score Analysis Using Karyo Reader Binary Data

For many cancer types, the number of chromosome rearrangements is roughly proportional to the extent of malignancy since chromosome aberrations accumulate over time. Thus, a number of cytogenetic imbalances per tumor (NIPT) score can be created to estimate the biological age of the malignancy. A distribution of the NIPT score in population of cancer samples may give rise to information about the karyotypic evolutionary pathways for that particular cancer type.

For each parsed case from Karyo Reader, a NIPT score was assigned equal to the total number of parsed aberrations, both numerical and structural, for the tumor. Out of 540 parsed cases, 8 cases contained a NIPT score of 0. Upon investigation, it was found that the aberrations in these cases contained material of unknown origin, which was not

parsed by Karyo Reader. The distribution for the squamous cell carcinoma NIPT scores is shown in Figure 5.

This monotonically decreasing distribution of the NIPT scores indicates that squamous cell carcinoma is characterized by a successive decrease in frequency with increasing NIPT values, resulting in a geometrical distribution. The biological explanation for such a distribution is that imbalances occur at low frequencies and are independent of prior aberrations. However, typical monotonically decreasing distributions for karyotypes terminate at moderate NIPT values. The ongoing frequency in higher NIPT scores indicates that a second component exists in the distribution. This second component also resembles a monotonically decreasing distribution as shown in the rescaled Figure 6.

A possible third, fourth, and fifth monotonically decreasing portion to the distribution could potentially be identified for later stage evolutionary pathways as indicated in the rescaled NIPT distribution in Figure 6. For the purposes of early stage evolutionary pathways, NIPT scores from 1-20 were used to indicate the early stage aberrations involved in squamous cell carcinoma. The bimodality of this early portion of the distribution, best illustrated in Figure 5, indicates that possibly two different modes of karyotypic evolution are represented in the primary evolutionary stages of squamous cell carcinoma development. The second mode in the distribution might be indicative of a second mode of karyotypic or may possibly be due to an increased level of chromosomal instability. However, given the remarkably low NIPT value of the second mode, 11, it is unlikely that chromosome instability primarily accounts for these aberrations.

FIGURE 5: Distribution of Squamous Cell NIPT Scores

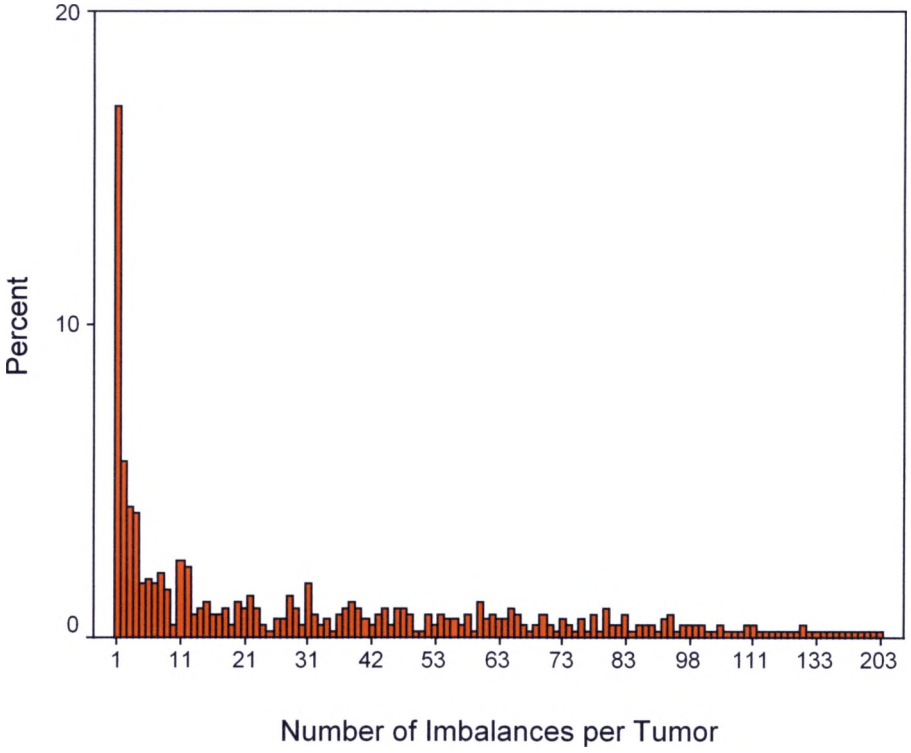
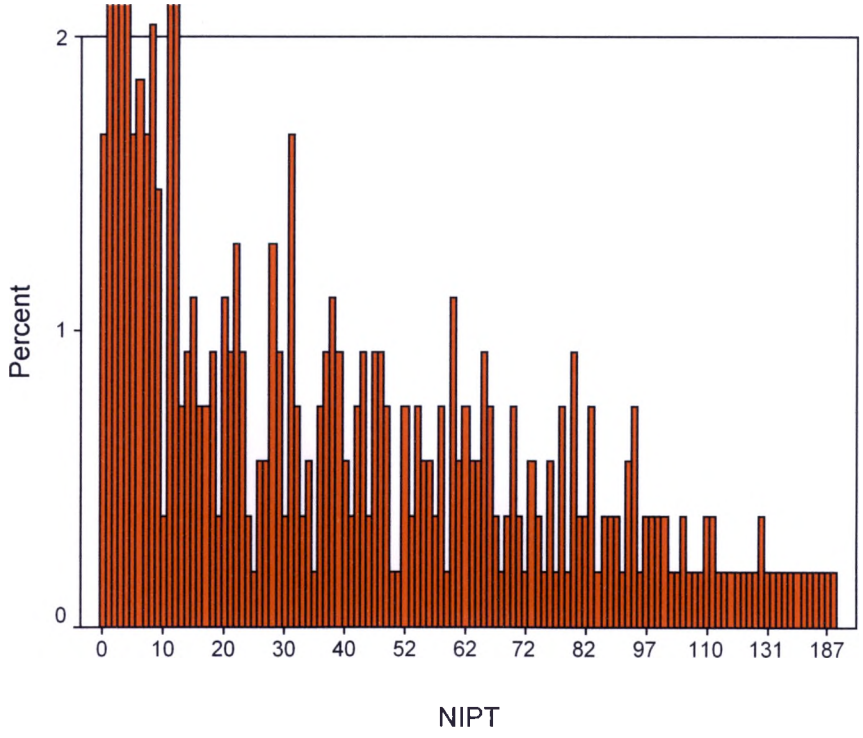


FIGURE 6: Rescaled Distribution of Squamous Cell NIPT Scores



Imbalances appearing early in tumor progression should appear in both simple and complex karyotypes whereas imbalances that appear late in tumor progression should predominately be seen in complex tumors. Hence, by plotting a NIPT frequency distribution for tumors containing a given imbalance, it would be possible to determine if the aberration occurs early or late.

Using the binary output from Karyo Reader, aberrations occurring in at least 30% of cases can be investigated. Karyo Reader identified 19 of these aberrations as shown in table 10. For each aberration identified in at least 30% of cases by Karyo Reader, the NIPT frequency distribution can be drawn as shown in Figures 7 - 25.

FIGURE 7: NIPT Frequency Graph for Cases with Aberration d10

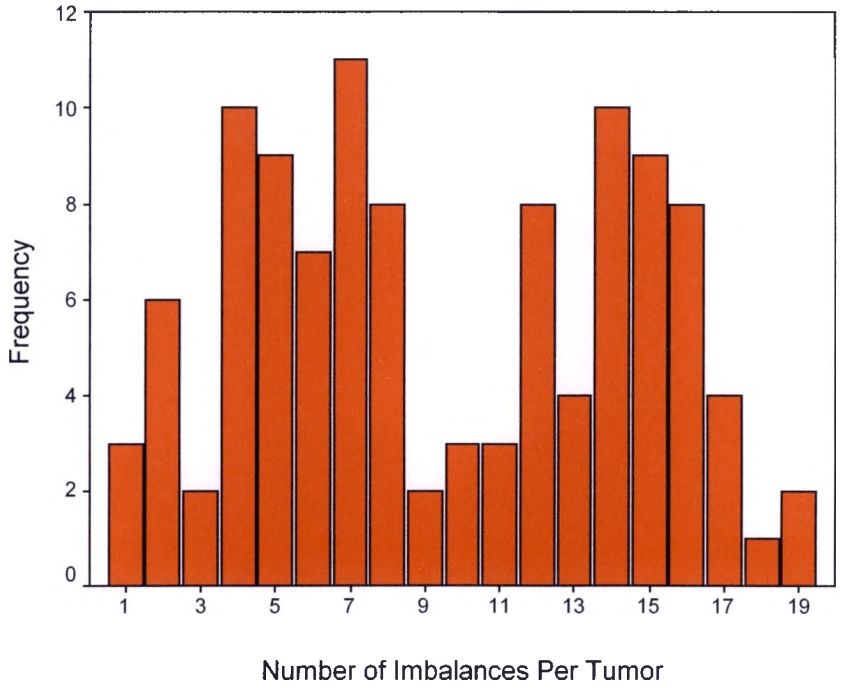
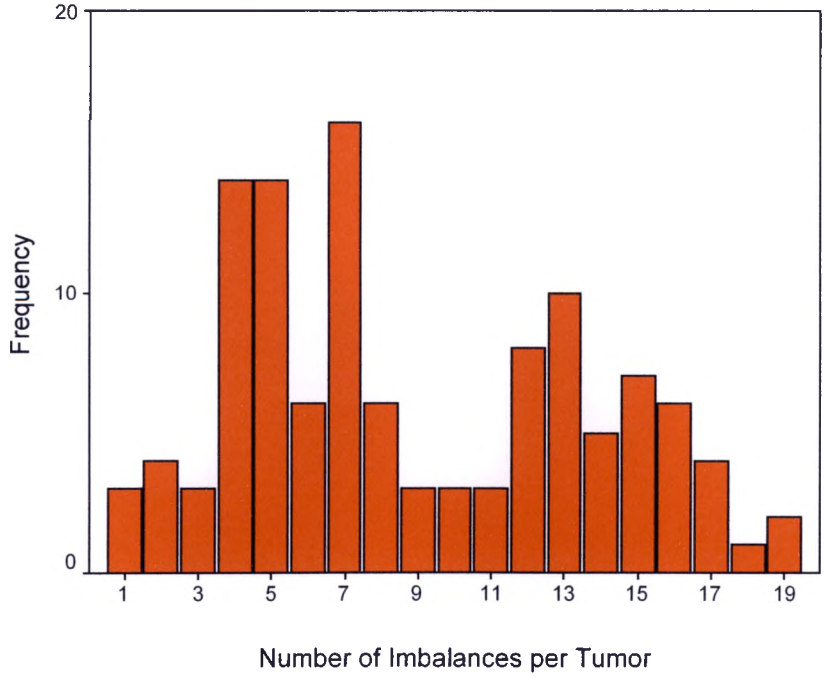


Figure 7 shows the NIPT frequency graph for cases with a numerical chromosome loss of chromosome 10. Since the NIPT score is an estimation of the age of a tumor, the almost bimodality of this distribution indicates that the chromosome aberration occurs in

both simple (early) and complex (late) karyotypes. By definition, early aberrations should appear in both complex and simple karyotypes, indicating that the aberration d10 is likely an early chromosome aberration in the development of squamous cell carcinoma.

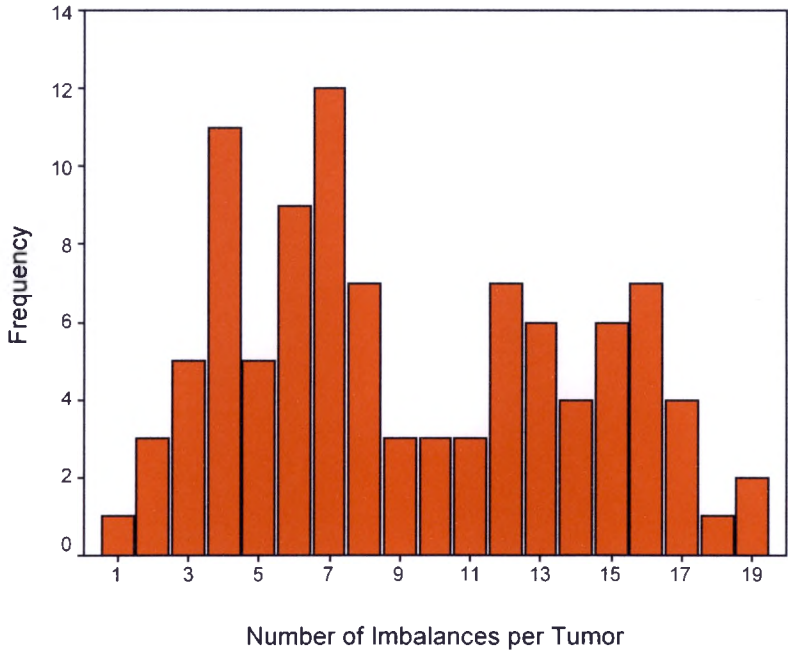
Figure 8 displays the NIPT frequency graph for cases with a numerical chromosome loss of chromosome 13. From the graph it is apparent that this aberration occurs in both early and late karyotypes. However, the frequency of occurrence is higher for simpler karyotypes than for complex karyotypes. This might indicate that a loss of chromosome 13 is an early chromosome aberration in the development of squamous cell carcinoma but that the aberration is not critical to the progression of the disease. Additionally, the low frequency of NIPT values at 1 and 2 indicate that potentially this aberration is dependent on the presence of other aberrations.

FIGURE 8: NIPT Frequency Graph for Cases with Aberration d13



The frequency graph for the loss of chromosome 14 and 15, shown in Figure 9 and 10 respectively, demonstrate that each aberration is present in both early and late karyotypes. The low frequencies observed at low NIPT values in these graphs indicate that the aberrations are likely dependent on the presence of another aberration since neither is common as the sole aberration in individual cases.

FIGURE 9: NIPT Frequency Graph for Cases with Aberration d14



The NIPT frequency graph for cases with a loss of chromosome 18 and 21 are shown in Figures 11 and 12 respectively. Though each aberration is present in both early and late karyotypes, neither aberration contains even a moderate frequency of very low NIPT values. This indicates that the loss of chromosome 18 or 21 may occur as an early stage aberration in squamous cell carcinoma, but possibly these aberrations are dependent on the presence of another aberration.

FIGURE 10: NIPT Frequency Graph for Cases with Aberration d15

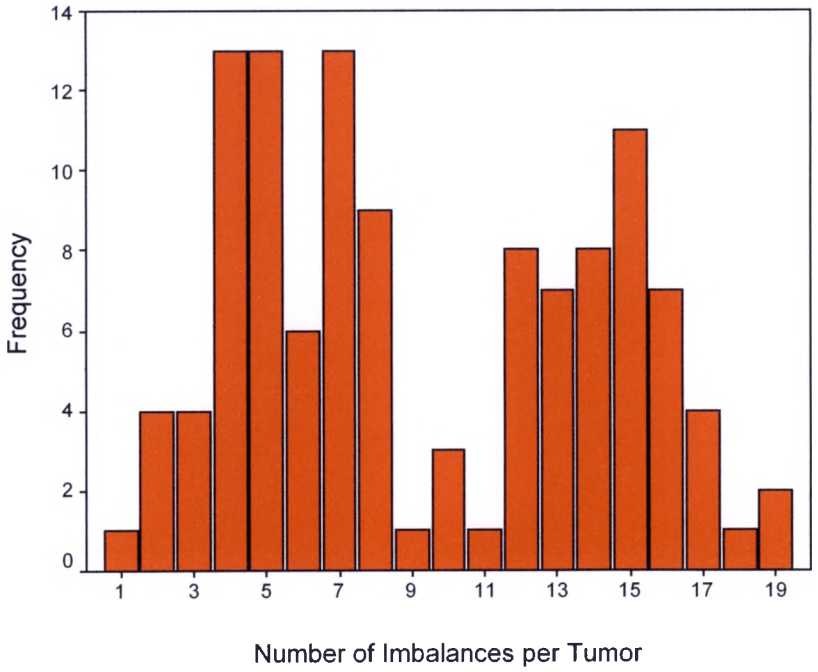


FIGURE 11: NIPT Frequency Graph for Cases with Aberration d18

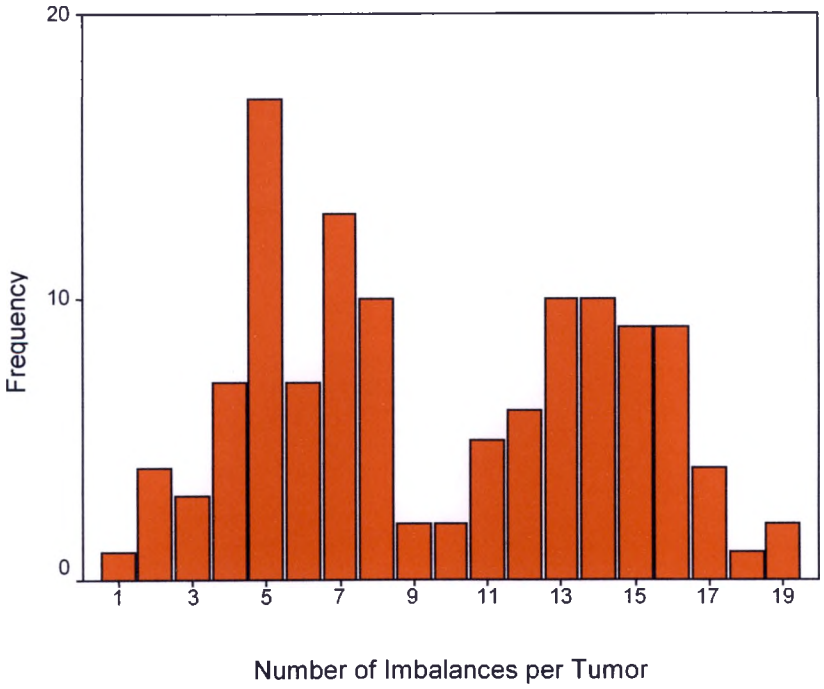


FIGURE 12: NIPT Frequency Graph for Cases with Aberration d21

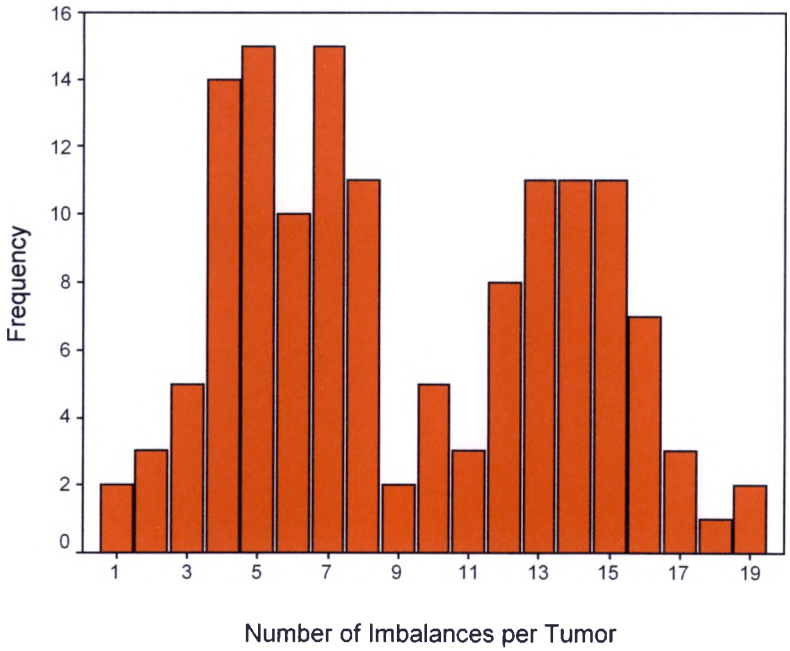
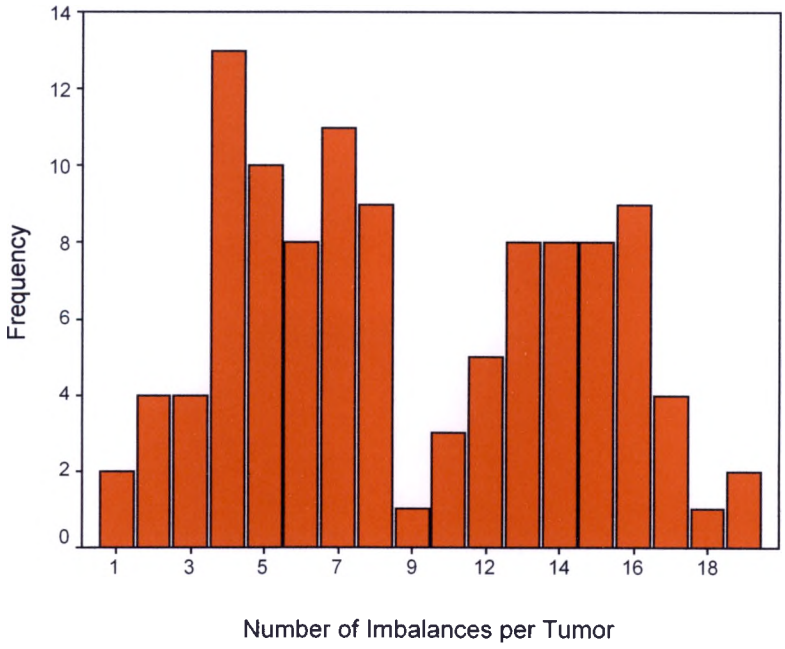


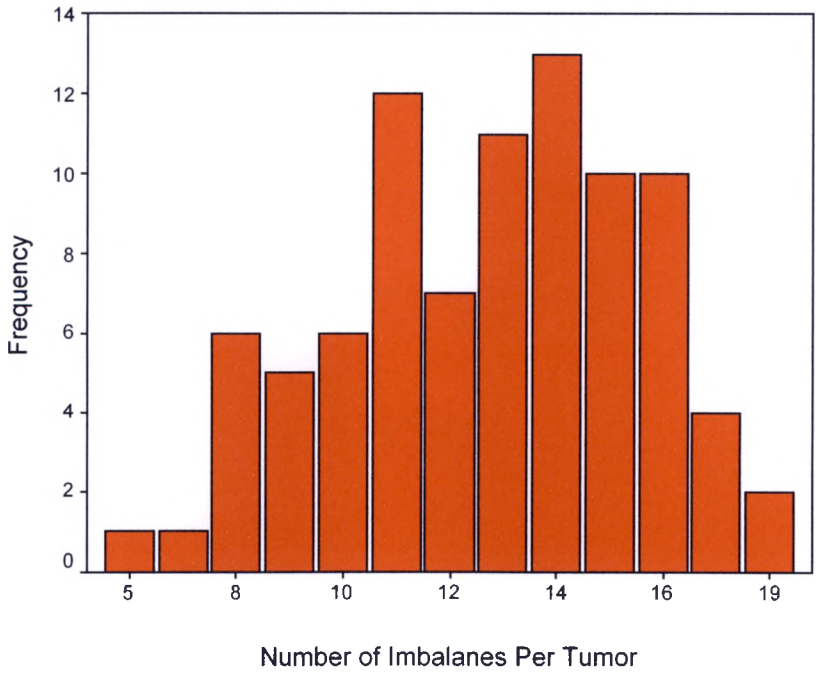
FIGURE 13: NIPT Frequency Graph for Cases with Aberration d22



Similarly, the NIPT frequency for the loss of chromosome 22, shown in Figure 13, demonstrates a potential early stage aberration in the development of squamous cell carcinoma. However, as with many of the other identified chromosome losses, the low frequency of very low NIPT scores indicates that potentially this chromosome loss is dependent on the presence of another aberration.

Figures 14 and 15 represent the NIPT frequency graphs for cases with structural chromosome loss aberrations on breakpoints 3p13 and 3p14 respectively. Both graphs indicate that the aberrations occur more frequently in moderate to high complexity karyotypes. The right-sided skewedness of the NIPT distribution graphs indicates that these aberrations are more common in moderate and highly complex karyotypes. Since the aberrations are relatively non-existent at NIPT values below 7, these two aberrations

FIGURE 14: NIPT Frequency Graph for Cases with Aberration d3p13



are likely moderate stage aberrations, dependent on the occurrence of one or two additional aberrations in order to occur.

FIGURE 15: NIPT Frequency Graph for Cases with Aberration d3p14

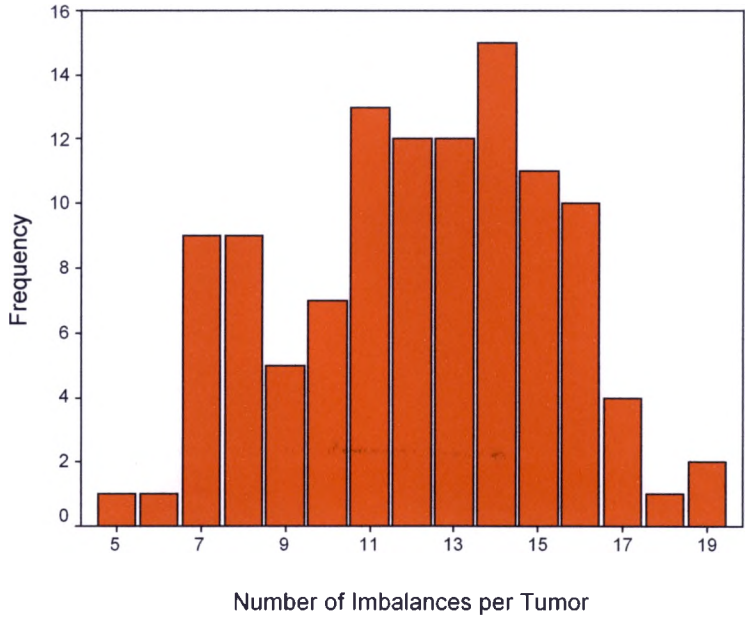
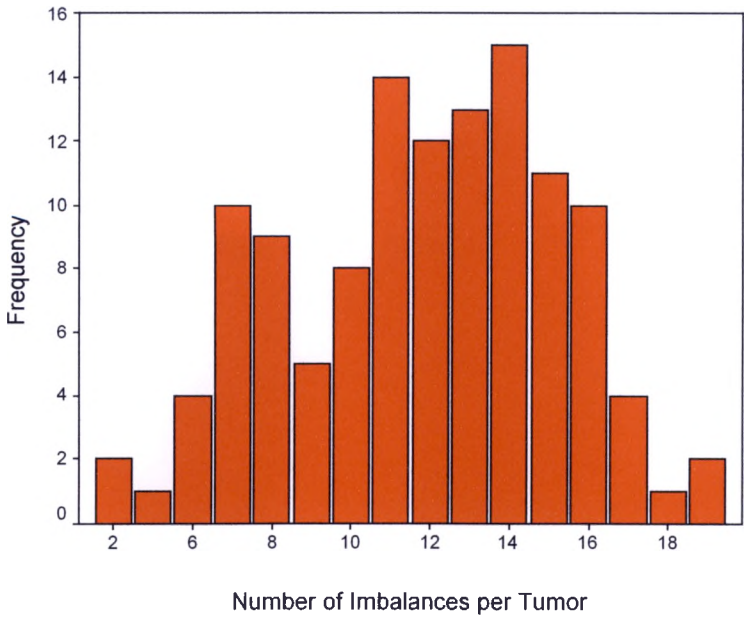


FIGURE 16: NIPT Frequency Graph for Cases with Aberration d3p21



The structural chromosome loss aberration 3p21, shown in Figure 16, is similar to the structural aberrations at 3p14 and 3p15. The NIPT distribution indicates that the aberration is a moderate aberration, likely dependent on one or more early stage chromosome aberrations in order to arise.

Structural chromosome loss aberrations 3p22 and 3p23, shown in Figures 17 and 18 respectively, demonstrate moderate stage occurrence aberrations as evidenced by the low frequency in early NIPT values. The high frequency values for moderate NIPT scores indicates that potentially these aberrations arise as the result of a predecessor aberration.

FIGURE 17: NIPT Frequency Graph for Cases with Aberration d3p22

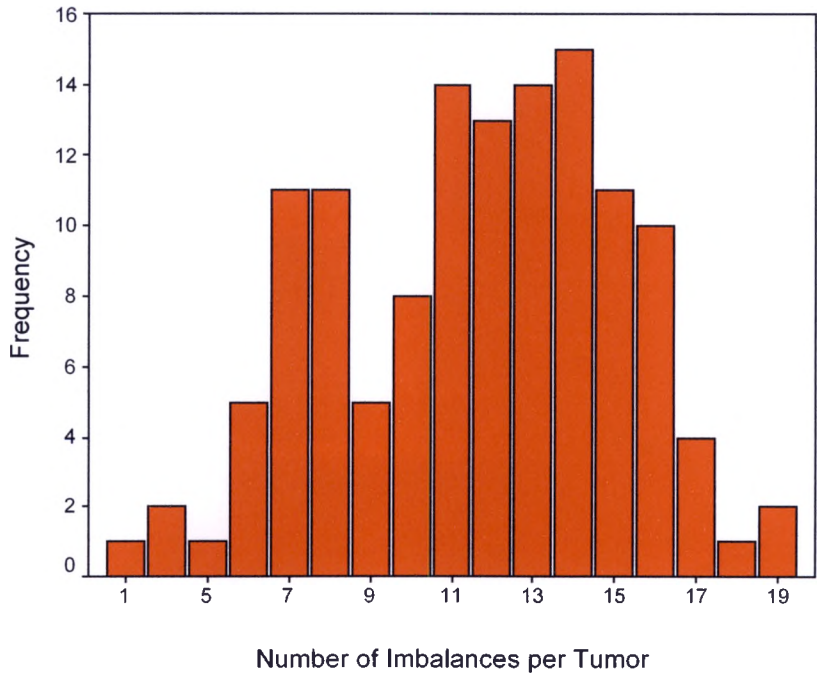


Figure 19 shows the NIPT frequency distribution for the structural chromosome loss aberration 3p24. Since the earliest NIPT score available in the cases that contain this aberration is six, this particular aberration cannot be an early stage aberration. Cases

typically have at least five aberrations prior to acquisition of this aberration, and thus this may be considered a moderate stage chromosome aberration at best.

FIGURE 18: NIPT Frequency Graph for Cases with Aberration d3p23

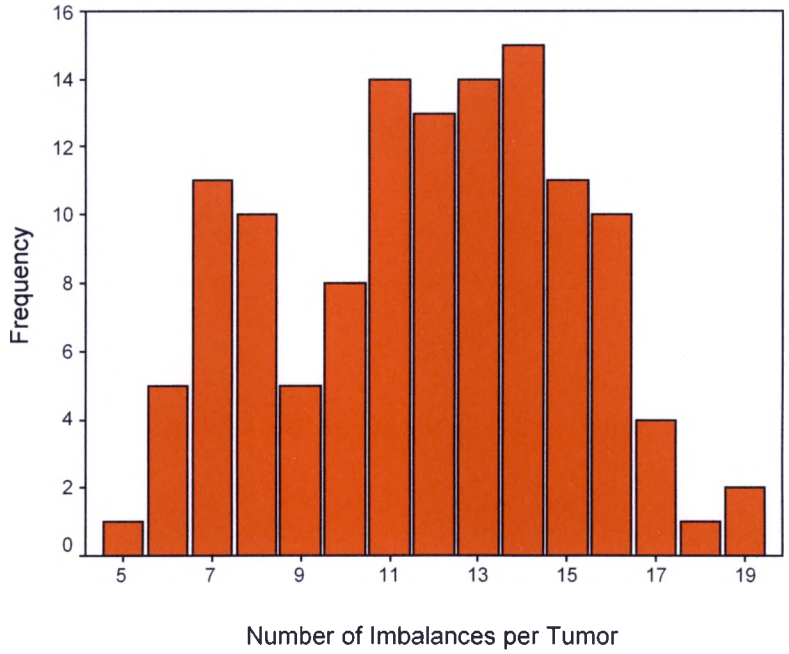
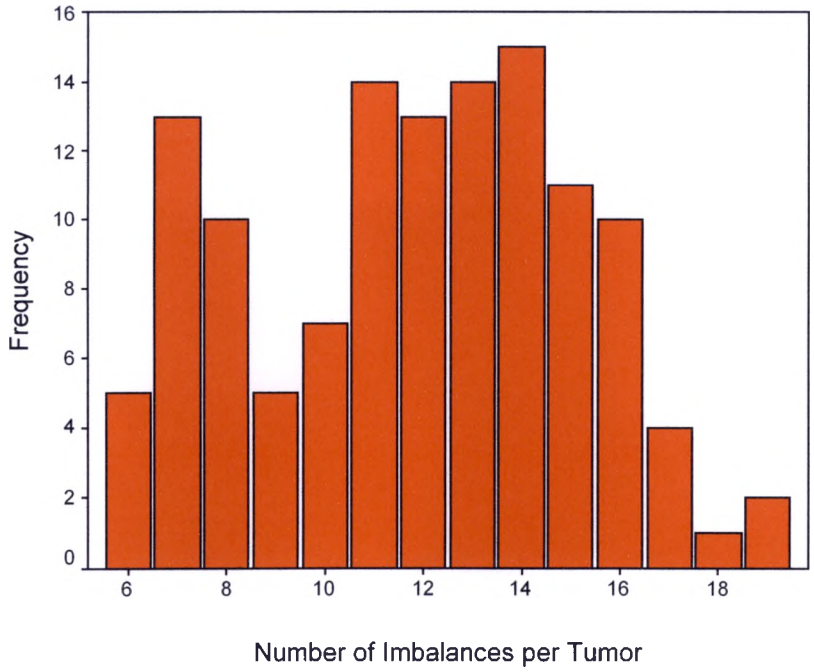
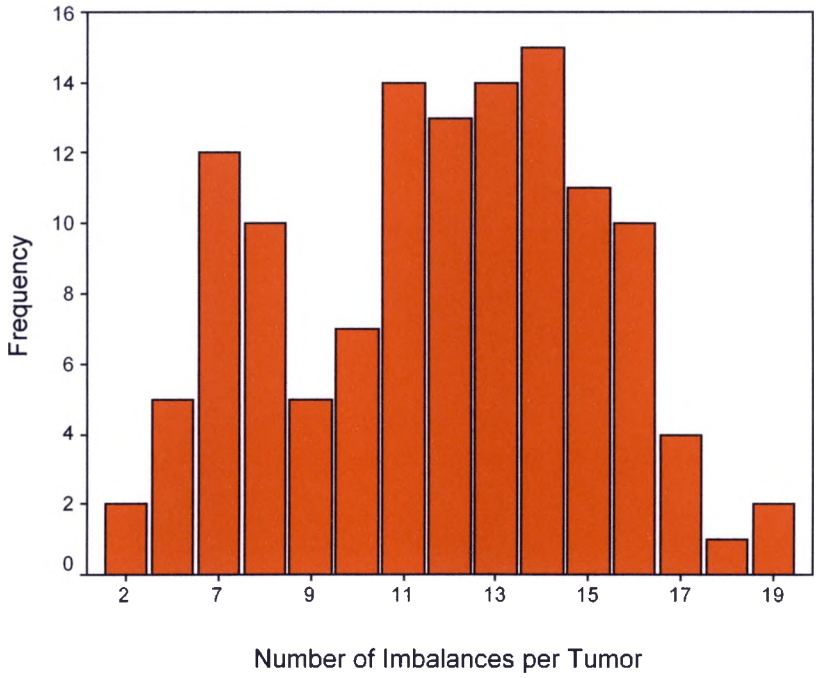


FIGURE 19: NIPT Frequency Graph for Cases with Aberration d3p24



Figures 20 and 21 show the NIPT frequency distribution for structural chromosome loss aberrations on 3p25 and 3p26 respectively. The NIPT distribution for each aberration is slightly skewed to the right, indicating that the aberrations are moderate stage. Neither aberration demonstrates high frequencies of very low NIPT values, further reinforcing that these aberrations are moderate stage and possibly dependent on the presence of a preceding aberration.

FIGURE 20: NIPT Frequency Graph for Cases with Aberration d3p25



The NIPT distribution for the numerical chromosome loss aberration of chromosome 4, shown in Figure 22, shows low frequencies of NIPT values around 1 and 2. However, the higher frequencies beyond NIPT values of 3 indicate that this aberration is likely an early stage aberration with a dependency on the occurrence of a single aberration.

FIGURE 21: NIPT Frequency Graph for Cases with Aberration d3p26

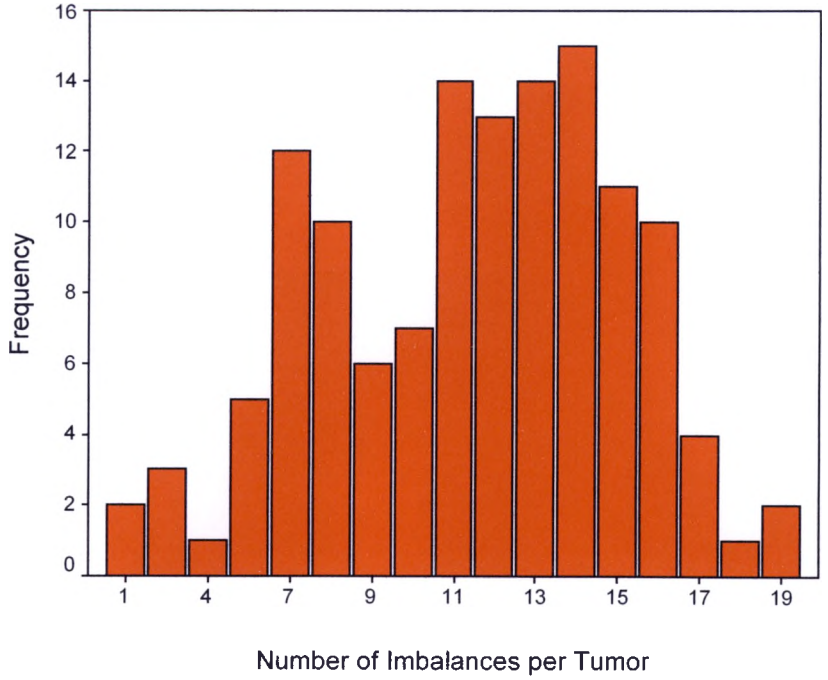
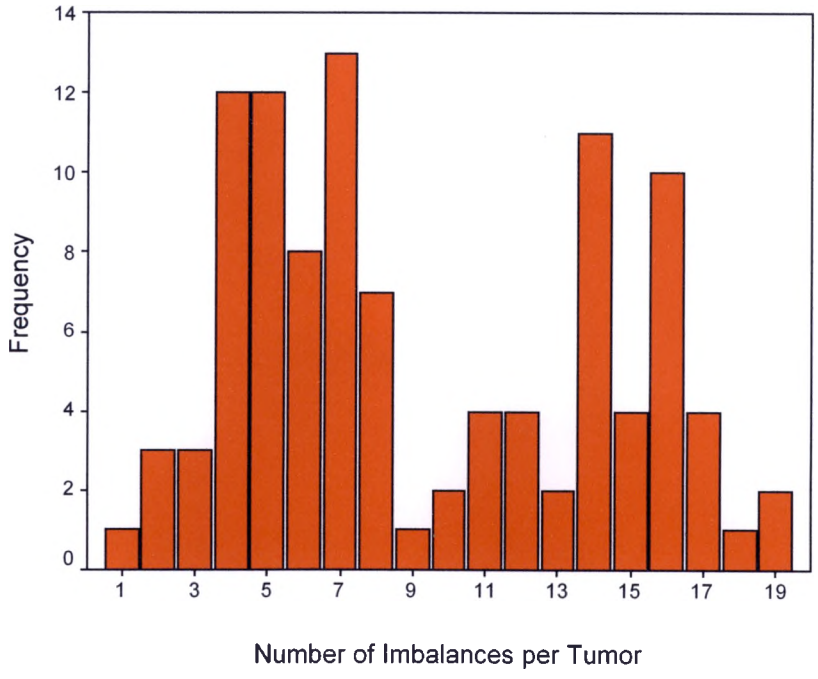


FIGURE 22: NIPT Frequency Graph for Cases with Aberration d4



Figures 23 and 24 show the NIPT frequency distributions for structural chromosome loss aberrations on chromosome 8 at bands p22 and p23 respectively. Both distributions show a mode at a NIPT value of 2, indicating that many cases contained these aberrations as one of the only two aberrations in the karyotype. Since neither aberration occurs as the sole aberration in a single case karyotype, each must be directly preceded and dependent on a sole aberration in order to occur. Since these aberrations, 8p22 and 8p23 are so closely related on the chromosome and occur very early in the karyotype evolution, potentially this chromosome location may map to a tumor suppressor gene or other gene whose disruption is responsible for the mutagenesis.

FIGURE 23: NIPT Frequency Graph for Cases with Aberration d8p22

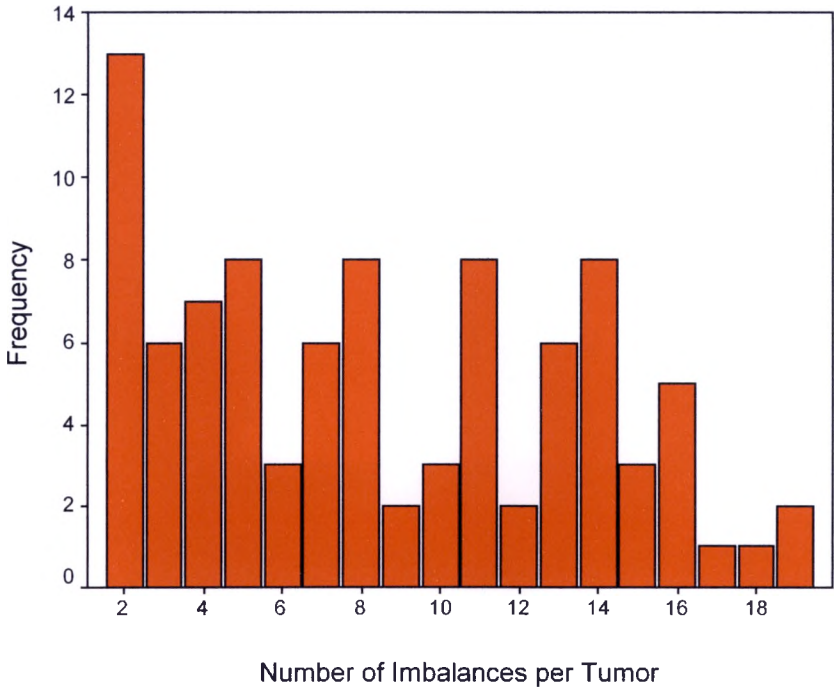


FIGURE 24: NIPT Frequency Graph for Cases with Aberration d8p23

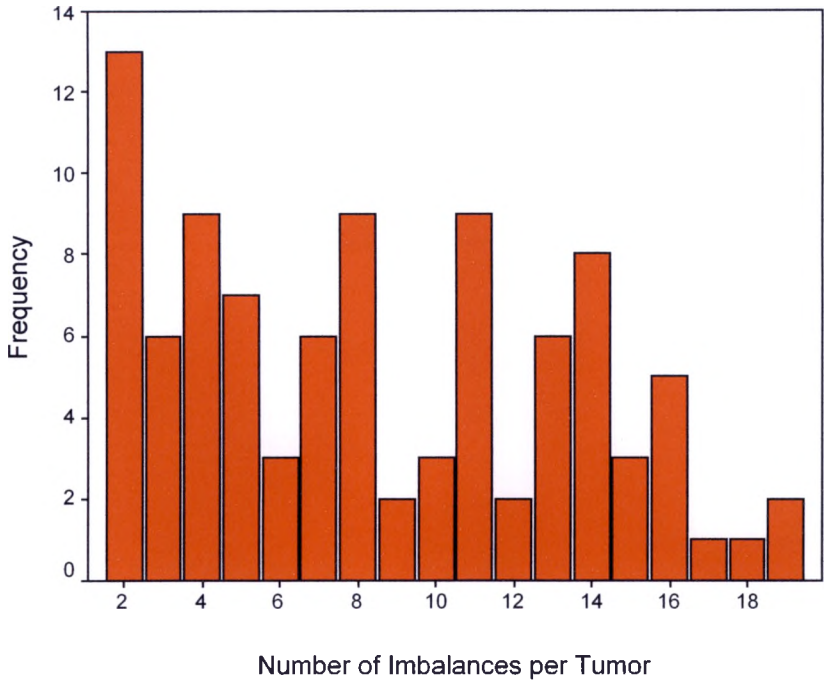
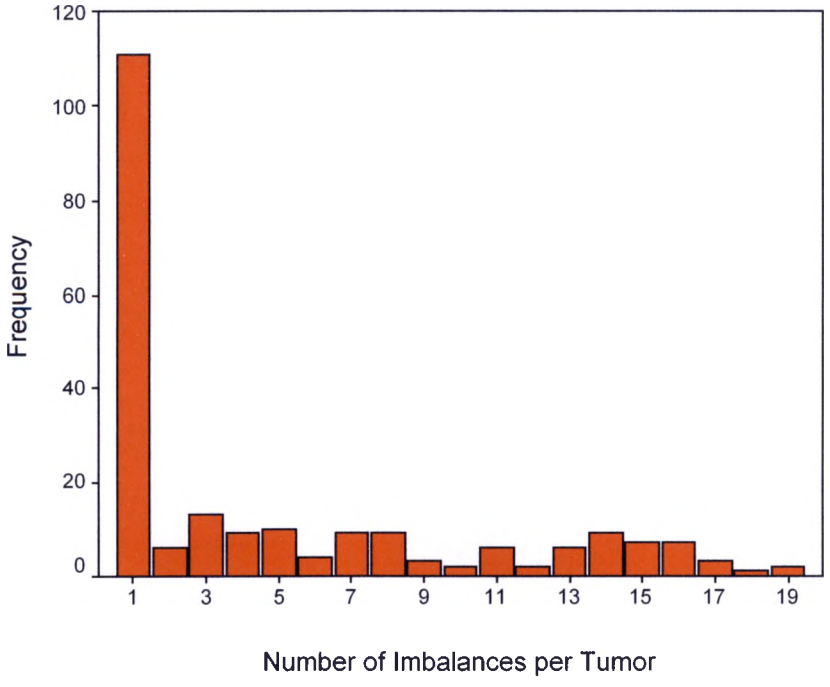


FIGURE 25: NIPT Frequency Graph for Cases with Aberration dY



The NIPT frequency distribution for the numerical chromosome loss of Y is shown in Figure 25. As indicated in the Progenetix analysis, the Y chromosome appears to have a significant importance on the development of squamous cell carcinoma. The modal NIPT value of 1 indicates that the loss of chromosome Y is a primary stage evolutionary start on the mutagenesis of a cell into squamous cell carcinoma. The frequency of this chromosome loss far exceeds that of any other potential aberration identified in the analysis.

Since 69% of the cases used in this analysis are males, it is no surprise that chromosome Y might appear with such high frequency. Though 31% of the cases extracted from the Mitelman database contain a sex designation of female, over 3% of these cases contain an uncertainty in the ISCN sex designation.

Examination of Evolutionary Mutagenic Pathways

To identify possible karyotypic pathways, aberrations that act in a synergistic or complementary fashion in the carcinogenic process should frequently be seen in the same tumor cases, whereas incompatible chromosome aberrations typically will not be present in the same case. This indicates that when calculating the correlation between the presence of different imbalances in a given tumor type, positive correlation would indicate membership of the same karyotypic pathway, whereas negative correlation would indicate different pathways.

Principal component analysis was used to condense the information in the Karyo Reader binary dataset limited to aberrations present in at least 30% of cases as well as produce a correlation matrix between the chromosome aberrations to develop information about the karyotypic evolutionary pathways.

The principal component correlation matrix, shown in Appendix E, demonstrates a significant ($p < .05$) correlation between almost every chromosome aberration identified in the Karyo Reader data. Loss of chromosome Y (dY) was the only aberration not significantly correlated with all other aberrations in the data. This aberration only showed significant correlations with aberrations d22 and d14.

Since principal component results rely on the assumption that some degree of collinearity exists among the variables but not so extreme that the variables are singular. If no collinearity exists, a factor analysis will produce as many components as variables, yielding no results. To determine if the Karyo Reader data meets this requirement, two tests are available; Kaiser-Meyer-Olkin measure of sampling adequacy and Bartlett's test of sphericity, whose results are displayed in Table 20.

TABLE 20: Kaiser-Meyer-Olkin Measure and Bartlett's Test

Kaiser-Meyer-Olkin Measure of Sampling Adequacy.		.902
Bartlett's Test of Sphericity	Approx. Chi-Square	13328.818
	df	171
	Sig.	.000

The Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy is a measure of the common variance between variables (aberrations) to determine how extensive the collinearity is between variables. KMO values range from 0 to 1, with values closer to 1 indicating larger amounts of collinearity. In the case of this principal component analysis, the KMO measure is .902, which is extremely high and indicates that the degree of common variance or collinearity among the aberrations is high. With such a high

collinearity, the components extracted by principal component analysis will account for a large portion of the variance.

Bartlett's test of sphericity is a chi-squared statistic computed under the null hypothesis that the correlation matrix comes from a population in which the variables are noncollinear. The indication of this hypothesis is that all non-zero correlations in the correlation matrix are due to sampling error. As shown in Table 20, the Karyo Reader data had a very high chi-squared value, indicating significance at $p < .001$. The indication of this test is that the null hypothesis is rejected, meaning that the non-zero correlations in the correlation matrix are not due to sampling error, but rather due to collinearity. Thus, the extracted principal components will account for a large portion of the common variance.

Table 21 shows the communalities for the aberration variables. Communality extractions display the percentage of variance within a variable (aberration) that is common variance. Strong communalities are associated with all d3p aberrations as expected by the perceived dependence of these aberrations on preceding aberrations. A very weak communality is associated with the dY numerical chromosome loss aberration as expected based on the NIPT distribution indication that dY is a primary evolutionary aberration in the development of squamous cell carcinoma. Aberrations d8p22 and d8p23 show very low communalities as expected from the NIPT distribution indication that these aberrations rely on one preceding aberration and typically occur as the second aberration in the mutagenesis of squamous cell carcinoma.

Moderate communalities are demonstrated by the other aberrations in the analysis as was expected from their early to moderate stage evolutionary appearance dependent on

the presence of other chromosome aberrations as determined by the NIPT distribution analysis.

TABLE 21: Principal Component Communalities

	Initial	Extraction
D10	1.000	.436
D13	1.000	.463
D14	1.000	.401
D15	1.000	.547
D18	1.000	.574
D21	1.000	.606
D22	1.000	.475
D3P13	1.000	.731
D3P14	1.000	.909
D3P21	1.000	.940
D3P22	1.000	.953
D3P23	1.000	.971
D3P24	1.000	.950
D3P25	1.000	.948
D3P26	1.000	.912
D4	1.000	.461
D8P22	1.000	.141
D8P23	1.000	.144
DY	1.000	3.516E-03

Principal component analysis was performed using a Varimax rotation to more fully resolve aberrations to individual principal components. Additionally, output was limited to two principal components for ease of interpretation. Table 22 shows the variance explained by the two principal components. About 60.9% of the variance in the data is explained through the first two principal components. Even after Varimax rotation is applied, the explanation of variance by the principal components remains unchanged in the rotation sums of squared.

FIGURE 26: Scree Plot for Principal Component Analysis

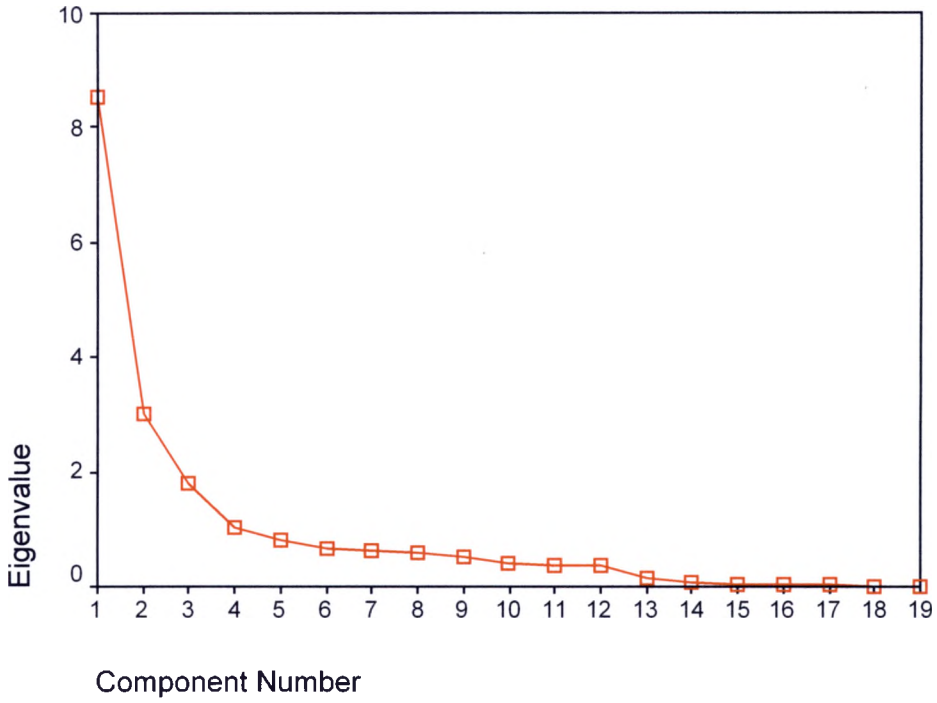


Figure 26 shows the scree plot produced in the principal component analysis. Typically eigenvalues over 1.0 are extracted for analysis of principal components. However, the Johnson-Need technique, when applied to the cumulative percent explanation of variance for each identified component in Table 22 indicates that two principal components are sufficient for the analysis as the second largest change is cumulative variance is between the second and third components.

TABLE 22: Total Variance Explained by Principal Components

	Initial			Extraction Sums of Squared			Rotation Sums of Squared		
Compone	Total	% of	Cumulative	Total	% of	Cumulative	Total	% of	Cumulative
1	8 537	44 93	44 93	8 537	44 93	44 93	7 342	38 64	38 64
2	3 028	15 93	60 86	3 028	15 93	60 86	4 224	22 22	60 86
3	1 792	9 431	70 30						
4	1 016	5 347	75 64						
5	793	4 176	79 82						
6	665	3 498	83 32						
7	613	3 227	86 54						
8	589	3 100	89 64						
9	499	2 625	92 27						
10	411	2 164	94 43						
11	370	1 946	96 38						
12	353	1 861	98 24						
13	142	749	98 99						
14	6 808E-	358	99 35						
15	3 883E-	204	99 55						
16	3 109E-	.164	99 71						
17	2 724E-	143	99 86						
18	1 387E-	7 300E-	99 93						
19	1 229E-	6 468E-	100 00						

Extraction Method Principal Component

As demonstrated by the scree plot in Figure 26, the first two principal components account for most eigenvalues over 1.0. However, the third identified principal component does contain an eigenvalue that is relatively close to 1.0. Exclusion of this component should not have a large impact on the variance in the data explained.

TABLE 23: Varimax Rotated Component Matrix

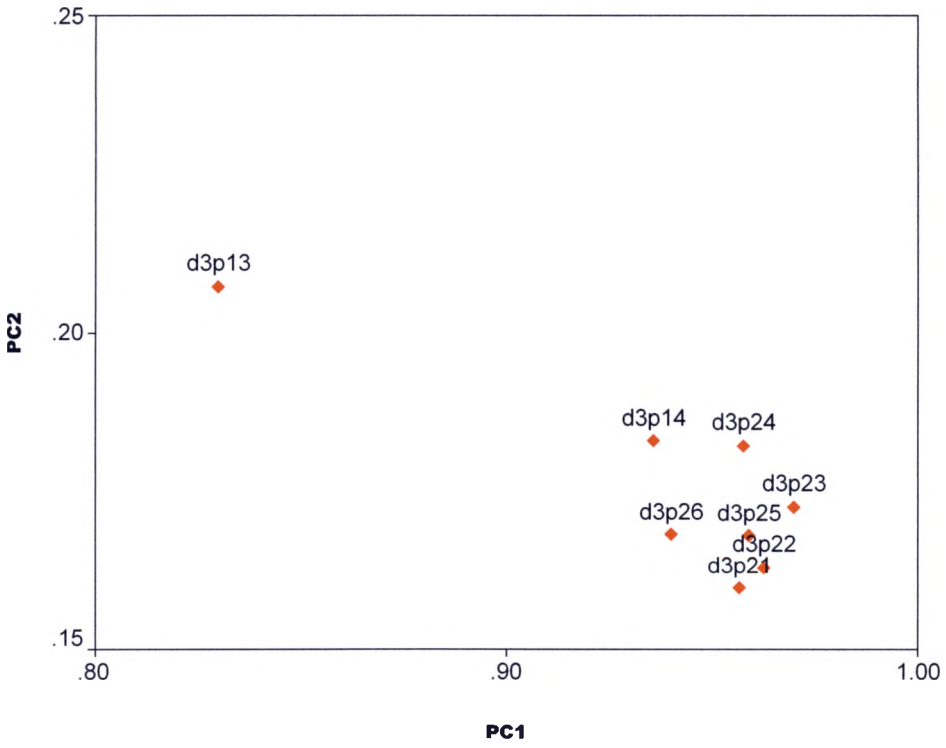
	Component	
	1	2
D10	.202	.628
D13	.117	.670
D14	.130	.619
D15	.139	.726
D18	.190	.733
D21	.177	.758
D22	.131	.676
D3P13	.830	.207
D3P14	.936	.183
D3P21	.957	.160
D3P22	.962	.163
D3P23	.970	.173
D3P24	.958	.182
D3P25	.959	.168
D3P26	.940	.168
D4	.116	.669
D8P22	.208	.313
D8P23	.208	.318
DY	-1.65E-02	5.695E-02

The Varimax rotated component matrix is shown in Table 23. Varimax rotation was used to fully resolve the aberrations into the two principal components. The first principal component (PC1) is characterized by high loadings on d3p13, d3p14, d3p21, d3p22, d3p23, d3p24, d3p25, and d3p26. The second principal components (PC2) is characterized by moderate to high loadings on d10, d13, d14, d15, d18, d21, d22, and d4.

Other aberrations contain extremely low loadings on both components such as d8p22, d8p23, and dY.

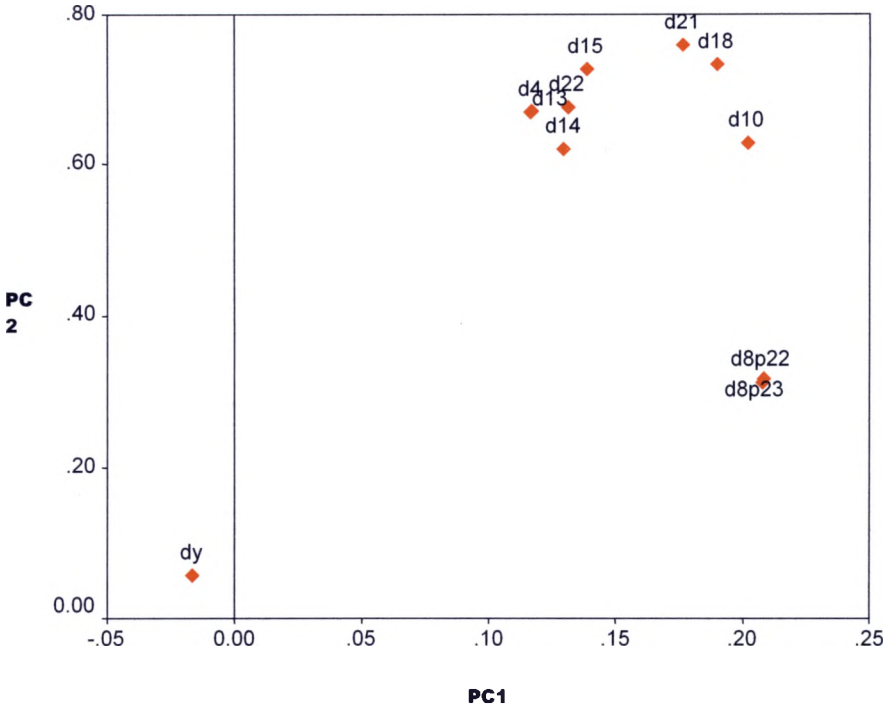
For graphical representation of the evolutionary relatedness of the Karyo Reader chromosome aberrations, a component plot of PC1 and PC2 was produced as shown in Figure 27 and 28. For display purposes, Figure 27 shows the portion of the component plot associated with high loadings on PC1. Figure 28 shows the portion of the component plot associated with low loadings on PC1.

FIGURE 27: Component Plot of PC1 and PC2 (High PC1 loadings)



Based on the component loading plots it appears that aberrations dY, d8p22, d8p23, d3p13 are likely important aberrations development of squamous cell carcinoma. Based on the NIPT distribution analysis, dY is likely a sole chromosome aberration that alone can result in development of mutations leading to squamous cell carcinoma.

FIGURE 28: Component Plot of PC1 and PC2 (Low PC1 Loadings)



Aberrations d8p22 and d8p23 appear to be related aberrations that based on the NIPT distribution analysis are the second aberrations that occur in the development of squamous cell carcinoma. Based on the proximity of these aberrations to the nearby d10, d13, d14, d15, d18, d21, d22, and d4 along with their positive correlations to d8p22 and d8p23, it can be inferred that d8p22 and/or d8p23 are likely needed precursors to development of these numerical chromosome aberrations.

Also based on proximity, it is likely that aberration d10 is a precursor to aberration d18, which is a precursor to the d21 aberration. Additionally, it is likely that aberration d14 is a precursor to aberrations d13, d4, and d22, which are precursors to aberration d15.

Aberration d3p13 is likely dependent on precursors d8p22 and/or d8p23 based on proximity and positive correlation. Aberrations d3p14, d3p21, d3p22, d3p23, d3p24, d3p25, d3p26 appear dependent on the d3p13 aberration to arise. Aberration d3p14 is

likely a needed precursor to aberration d3p24, which is a likely precursor to d3p23 or d3p25. Additionally, aberration d3p14 is a likely precursor to d3p26, which is a likely precursor to d3p25. Aberration d3p23 likely precedes aberration d3p25 if it even occurs. Since the same mutagenic pathway can exist without aberration d3p23, this aberration cannot be critical to the development of squamous cell carcinoma. Aberration d3p25 is potentially a precursor to d3p22, which is a likely precursor to d3p21.

Table 24 shows a summarization of the potential chromosome aberration evolutionary pathways identified in the squamous cell carcinoma data. These pathways do not represent all potential mutagenic pathways involved in the development of squamous cell carcinoma, but does highlight the major pathways presented in the dataset.

TABLE 24: Identified Chromosome Aberration Evolutionary Pathways

Chromosome Aberration Evolutionary Pathways
dY
d8p22/d8p23 --> d10 --> d18 --> d21
d8p22/d8p23 --> d14 --> d4 --> d15
d8p22/d8p23 --> d14 --> d13 --> d15
d8p22/d8p23 --> d14 --> d22 --> d15
d8p22/d8p23 --> d3p13 --> d3p14 --> d3p24 --> d3p25 --> d3p22 --> d3p21
d8p22/d8p23 --> d3p13 --> d3p14 --> d3p24 --> d3p23 -->d3p25 --> d3p22 --> d3p21
d8p22/d8p23 --> d3p13 --> d3p14 --> d3p24 --> d3p25 --> d3p22 --> d3p21
d8p22/d8p23 --> d3p13 --> d3p14 --> d3p26 --> d3p25 --> d3p22 --> d3p21

CHAPTER 5

CONCLUSION

The most commonly reported chromosome aberrations associated with squamous cell carcinoma in published literature are chromosome losses of 3p14, 3p21, 3p24, 3p25, 8p21, 8p22, 8q23, 13q, 18q, 10p, 5q12-31 and 9p22. Chromosome gains of 11q13-23, 9p22, and 17p are also reported as frequent chromosome aberrations in some locations of squamous cell carcinoma.

Progenetix ISCN2matrix only managed to capture aberrations associated with chromosome Y. Though consistent with reported aberrations for squamous cell carcinomas, Progenetix failed to adequately detect other aberrations associated with the disease. CyDAS appropriately encountered most structural aberrations reported in literature for squamous cell carcinoma, but failed to recognize or tabulate any of the numerical chromosome aberrations associated with the disease. Karyo Reader identified chromosome aberrations that were most consistent with literature. Additionally, Karyo Reader parsed numerical and structural aberrations, unlike the other karyotype parsing systems.

Not only did Karyo Reader identify aberrations most consistently with published literature, it also reported more aberrations than either Progenetix or CyDAS. This indicates that Karyo Reader has a much more powerful algorithm in place for reading karyotypes and identifying implied chromosome aberrations. For a visual representation

of the chromosome gains and losses occurring in sets of karyotype data however, Karyo Reader does not offer any graphical representations. CyDAS however, can produce a chromosome map with the chromosome aberrations identified and quantified. This tool proves useful for presentations. Progenetix provides very little resources and output to the user for examining chromosome aberrations. This system exists solely to read karyotypes and produce limited, unusable statistical output with a poor algorithm.

Another important difference between the three systems is the ability of the system to accommodate user input and output selections as well as produce output that is easily manipulated. Karyo Reader offers a very extensive array of input and output options for analyses, including four separate output formats and custom input specifications. Additionally, Karyo Reader can receive direct extracts of Mitelman data and produce output that is easily imported into statistical and spreadsheet computer programs for manipulation.

CyDAS also offered extensive input and output options, but many of these features are still not available in the current version, whether utilized in the PC-based or web-based system. CyDAS is the only system that can take direct extracts of Mitelman data and provides integration into several popular databases for user manipulation. However, until CyDAS undergoes a few more releases, this tool proves useful only for populating karyotype data into a database or producing graphical representations of karyotype data.

Unfortunately, Progenetix does not offer many input or output specifications. With this system, the user is forced into using a specified input that requires alteration of extracts from the Mitelman database and given an output file in only one form. Input file

formats are not an issue with extracts from the Progenetix database of aberrations, but even utilizing this data does not provide flexible output options to the user.

Banding resolution is important in selecting a karyotype parsing system as the number of bands available in a system indicates the number of potential aberrations the system can recognize. Karyo Reader and Progenetix have a maximum band resolution of 862 and 957 bands, respectively, while CyDAS has a maximum band resolution of 550 bands. Another indication of the power of a karyotype parsing system is the number of chromosome aberrations the program is unable to parse. CyDAS and Karyo Reader each parsed about 84% of the total recognized aberrations by each system, though Karyo Reader recognized 3372 structural and numerical aberrations compared to 945 by CyDAS. Progenetix does not offer the user information on processing statistics such as the total number of identified aberrations. Instead, Progenetix only allows the user to view error files from the processing and the binary statistical output indicating the parsed aberrations. Since errors range from aberration to case exclusions, it is impossible to tell how many aberrations were recognized and how many were parsed.

Overall, Karyo Reader provides the most powerful analysis for the most accurate chromosome aberrations of all three systems, and does so with an ease of use. For these reasons, Karyo Reader output data was selected for use in analyzing the potential evolutionary mutagenic pathways responsible for squamous cell carcinoma development.

The NIPT distribution of the chromosome aberrations occurring in at least 30% of cases indicates an aberrational age for each chromosome aberration. The top 19 chromosome aberrations occurring in the squamous cell carcinoma karyotype data were deletions of chromosomes and chromosome regions: Y, 8p22, 8p23, 10, 13, 14, 15, 18,

21, 22, 4, 8p22, 8p23, 3p13, 3p14, 3p21, 3p22, 3p23, 3p24, 3p25, and 3p26. The NIPT distributions for each of these chromosome bands indicated that aberrations dY, d8p22, d8p23, and d3p13 are early chromosome aberrations in the development of squamous cell carcinoma. The NIPT distribution indicated that chromosome aberrations d10, d14, d18, d13, d22, d3p14, d3p24, d3p25, d3p23, and d3p26 are moderate stage chromosome aberrations involved in squamous cell carcinoma development. Additionally, the NIPT distribution placed chromosome aberrations d21, d15, d3p22, d3p21 as later stage chromosome aberrations in squamous cell carcinoma development.

Principal component analysis (PCA) of the statistical output from the Karyo Reader yielded a concise set of nine potential evolutionary mutagenic pathways for squamous cell carcinoma development, shown in Table 24. Two principal components were extracted from the data, representing two separate mutagenic pathways occurring in squamous cell carcinoma cases. These mutagenic pathways do not represent every step of mutagenesis undergone in the development of squamous cell carcinoma. Since many of these individual aberrations are specific to the topography of the disease, only those aberrations that were consistently found across different locations of squamous cell carcinoma were evaluated. The data is consistent in that deletions of chromosome Y are considered initial chromosome aberrations that can start the development of squamous cell carcinoma. As a second, but unrelated, step in the evolutionary mutagenic pathway of the disease is the acquisition of a chromosome deletion on 8p22 and/or 8p23. In some cases this aberration shortly followed by a deletion on chromosome 3p13, though there are likely other aberrations occurring in between these two events. Beyond these early stage chromosome aberrations identified, the PCA showed a very divergent path of

mutagenesis resulting in entire chromosome deletions or further deletions of bands within the chromosome segment 3p which is consistent with literature on squamous cell carcinoma of the head and neck.

Though squamous cell carcinoma is thought to occur more predominantly in males due to higher sun exposure, this analysis provided a much different result. The PCA indicates that deletion of the Y chromosome is often the first step in a mutagenic pathway that results in squamous cell carcinoma development. The data thus indicates that there is very likely a genetic linkage between sex and development of squamous cell carcinoma. Aberrations on chromosome Y is consistent with literature in that more than three times as many cases of squamous cell carcinoma occur in males than females.

Though several applications have become available to analyze the wealth of genomic karyotype data presented in ISCN format, the limitations of each program drive its applicability to particular types of analyses. For binary statistical analyses of karyotype data using numerical and structural chromosome aberrations, Karyo Reader far surpasses other available systems. For the four early stage mutagenic chromosome aberrations found associated with squamous cell carcinoma in this study; d8p22, d8p23, dY, and d3p13, further analysis is necessary to determine the biological implications these mutations may have on cellular function. Other important chromosome aberrations identified in this study may also prove to be key aberrations in the development of squamous cell carcinoma. Evaluation of these potential aberrations may unlock keys to gene therapy for prevention of squamous cell carcinoma, reducing the burden this disease places on the healthcare industry.

APPENDIX A

Extracted Karyotypes from the Mitelman Database

Aledo et al 1989, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Skin**

44-46,Y,dic(X;12)(q28;q24),dic(1;12)(p36;q24),dic(2;18)(q37;p11),dic(3,4)(q29;q35),dic(3;7)(q29;q36),dic(3;12)(q29,q24),dic(4;12)(q35;q24),dic(4,22)(q35,p13),dic(9;22)(q34;p13),dic(11,12)(q25,q24),dic(12,20)(q24;p13),dic(13,22)(p13;p13),dic(14,22)(p13;p13),inc

Aledo et al 1989, Int J Cancer

Case No. 16 **Squamous cell carcinoma** **Skin**

46,XY,t(1,2,9,10)(p33;q35,q22,q21)/46,XY,inv(1)(p35q31)/46,XY,inv(1)(p21q31)/46,XX,t(1;5)(p21,q23)/46,XY,t(1,6)(p22;p12)/46,XY,t(2,6)(p12;q2?)/46,XY,t(3;20)(q13,q11)/46,XY,t(12;14)(q13;q32)/46,XY,add(18)(q22)

Case No. 3 **Squamous cell carcinoma** **Skin**

46,XY,?t(4,10,8)(q32;q23;q24),t(8,15)(q23,q26),del(20)(p12)/46,XY,t(2;10)(q32;q25)/46,XY,t(16;21)(p13,q21)

Case No. 8 **Squamous cell carcinoma** **Skin**

84,XXX,-X,i(1)(p10),i(1)(q10),der(3)t(3,14)(q?;q?),+6,-8,-11,-13,-14,-14,del(19)(p23),der(19)t(8,19)(q21;q11),-21,-22,-22

Atkin & Baker 1979, Cancer

Case No. 1 **Squamous cell carcinoma** **Uterus, cervix**

40,XX,add(1)(q?),inc

Case No. 14 **Squamous cell carcinoma** **Uterus, cervix**

51,XX,+1,inc

Case No. 16 **Squamous cell carcinoma** **Uterus, cervix**

62-68,XX?,i(1)(q10),inc

Case No. 17 **Squamous cell carcinoma** **Uterus, cervix**

64-70,XX?,del(1)(p?),der(1)add(1)(p?)del(1)(q?),inc

Case No. 2 **Squamous cell carcinoma** **Uterus, cervix**

41,XX,add(1)(p?),inc

Case No. 21 **Squamous cell carcinoma** **Uterus, cervix**

72-82,XX?,der(1)add(1)(p?)del(1)(q?),inc

Case No. 22 **Squamous cell carcinoma** **Uterus, cervix**

77-84,XX?,del(1)(p?),inc

Case No. 23 **Squamous cell carcinoma** **Uterus, cervix**

80-88,XX?,der(1)del(1)(p?)add(1)(q?),i(1)(q10),inc

Case No. 3 **Squamous cell carcinoma** **Uterus, cervix**

43,XX,del(1)(p?),inc

Case No. 4 **Squamous cell carcinoma** **Uterus, cervix**

44,XX,+1,inc

Case No. 7 **Squamous cell carcinoma** **Uterus, cervix**

46,XX,der(1)(p?),inc

Case No. 8 **Squamous cell carcinoma** **Uterus, cervix**

47,XX,der(1)(p?),inc

Case No. 9 **Squamous cell carcinoma** **Uterus, cervix**

47,XX,i(1)(q10),inc

Atkin & Baker 1984, Cancer Genet Cytogenet

Case No. 12 **Squamous cell carcinoma** **Uterus, cervix**

65,XXX,-1,der(3)t(1,3)(q21;q21),-4,-5,der(6)t(5,6)(q13;q15),-7,-8,-9,-13, +16,+19, +20,-21,-22,+2mar

Case No. 13 **Squamous cell carcinoma** **Uterus, cervix**

65,XX,-X,+1,+i(1)(q10),-2,-4,-5,der(11)t(1,11)(q21,p13),-12,-13,-15,-16, der (19)t(1;19)(q21,q13),-21,+3mar

Case No. 16 **Squamous cell carcinoma** **Uterus, cervix**

80,XX,-X,+3,-4,+5,+i(5)(p10),+7,+8,+10,-12,+14,+14,+15,der(17)t(1;17) (q25,p11),+19,+19,+20,+20,+21,dmin

Case No. 19 **Squamous cell carcinoma** **Uterus, cervix**

82,XXXX,del(1)(p11)x2,-2,hsr(2)(q?),-4,-4,-5,del(6)(q21),-7,-8,-9,-10,-10, -11,-12,-13,-14,?der(14,15)(q10,q10),add(15)(q?),+16,+16,-17,-17,-18,-18, -19,-20,-21,-21,-22,-22,inc

---

Atkin & Baker 1987, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Uterus, cervix**

69,XX?,dmin,inc

Atkin & Baker 1989, Cancer Genet Cytogenet

Case No. 12 **Squamous cell carcinoma** **Uterus, cervix**

46,XX,add(17)(p?)

Case No. 13 **Squamous cell carcinoma** **Uterus, cervix**

76,XX?,add(17)(p?),inc

Case No. 5 **Squamous cell carcinoma** **Uterus, cervix**

76,XX?,del(1)(p22),i(2)(q10),del(6)(q?),add(17)(p?),i(17)(q10),inc

Case No. 7 **Squamous cell carcinoma** **Uterus, cervix**

80,XX?,add(1)(q31),del(5)(q12q32),add(11)(q?),add(13)(q?),add(17)(p?),+hsr (?),inc

---

Atkin & Fox 1991, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Vagina**

85,XX,-X,-X,del(3)(p?),del(5)(q?) or i(5)(p10),i(8)(q10),del(11)(?q13q23), add(15)(p?),?del(18)(q21),add(22)(p?),inc

---

Atkin & Fox 1992, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Skin**

82-89,XX,-Y,-Y,add(1)(p?),?i(5)(p10)x2,der(16)t(?13,16)(?q13-14,q22)x2,i (17)(q10),inc

Case No. 2 **Squamous cell carcinoma** **Larynx**

41-87,X,-Y,add(1)(p?),der(16)t(?13;16)(?q13-14,q22),?i(18)(p10),inc

---

Atkin et al 1983, Acta Cytol

Case No. 2 **Squamous cell carcinoma** **Uterus, cervix**

65-82,XX?,del(1)(q31),del(6)(q21),i(17)(q10),inc

Atkin et al 1988, Cytobios

Case No. 1 **Squamous cell carcinoma** **Skin**

42,XX,+der(1)i(1)(q10)add(1)(q24-32),der(2)t(2,4)(q25,q12),-4,+i(4) (p10) or i(5)(p10),-9,-11,-13,-14,-15,add(18)(q21),-21,-21,-22,+mar

---

Atkin et al 1990, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Uterus, cervix**

45,XX,add(1)(q25),+2,-4,+i(?5)(p10)x2,-11,der(11)t(11,14)(p11,q13),-14, der (15)t(9;15)(q13,q26),-17

Case No. 10 **Squamous cell carcinoma** **Uterus, cervix**

47,XX,+i(2)(q10),-5,+?add(9)(q?),-10,-11,-14,add(17)(p?),+2mar

Case No. 12 **Squamous cell carcinoma** **Uterus, cervix**

52,XX,+X,+1,+3,+i(?5)(p10),+i(6)(q10),+mar

Case No. 13 **Squamous cell carcinoma** **Uterus, cervix**

61,XX,-X,+i(1)(q10),+2,-4,i(?5)(p10),+6,i(6)(q10)x2,-7,-8,-9, -10,-11,-13, -14,-16,-17,+19,+20,-21,-22

Case No. 14 **Squamous cell carcinoma** **Uterus, cervix**

66,XXX,-2,-4,i(?5)(p10),-11,-14,-16,+i(17)(q10),-18,+19,+19,+19,-22

Case No. 15 **Squamous cell carcinoma** **Uterus, cervix**

69,XXX,+1,-2,-3,-4,+i(?5)(p10)x2,-7,+9,-14,-15,add(16)(q?),+18,-19,-22, +3mar

Case No. 17 **Squamous cell carcinoma** **Uterus, cervix**

84,XXX,-X,-1,add(1)(p?),i(1)(q10),+2,-3,-4,-5,-6,-10,-12,-13,
der(13,15) (q10,q10),-15,+add(16)(p?)x2,+17,-18,-18,-19,-21,-21,-22,+4mar

Case No. 18 **Squamous cell carcinoma** **Uterus, cervix**

85,XXX,-X,+1,del(1)(q11)x2,+2,+3,+del(3)(p?),-4,-5,-6,-6,add(6)(q?),-7,-7,
-10,-11,der(11)t(5,11)(q11,p15),-13,-15,-15,-16,+17,-19,+21,
+der(21)t(1,21) (q11,p11)x2,-22

Case No. 19 **Squamous cell carcinoma** **Uterus, cervix**

85,XXXX,+X,-1,-2,-3,add(3)(q?),-4,-4,i(?5)(p10)x2,-7,-9,-10,-10,+12,-13,-13,
+der(14,14)(q10,q10),-17,-19,+20,+20,+20,-21,-22

Case No. 2 **Squamous cell carcinoma** **Uterus, cervix**

48,XX,+i(1)(q10),+i(?5)(q10),+add(9)(p?),+10,add(11)(p?),-15,-18

Case No. 21 **Squamous cell carcinoma** **Uterus, cervix**

76,XX?,add(17)(p?),inc

Case No. 22 **Squamous cell carcinoma** **Uterus, cervix**

48-50,X?,i(?5)(p10),i(17)(q10),inc

Case No. 23 **Squamous cell carcinoma** **Uterus, cervix**

78-80,XX?,der(1)add(1)(p?)add(1)(q?),i(?5)(p10)x2,del(3)(q?)x2,inc

Case No. 24 **Squamous cell carcinoma** **Uterus, cervix**

80,XX?,i(?5)(p10),add(11)(p?)x2,inc

Case No. 3 **Squamous cell carcinoma** **Uterus, cervix**

51,X?,i(1)(p10),i(?5)(p10),inc

Case No. 4 **Squamous cell carcinoma** **Uterus, cervix**

70,XX?,del(1)(p?),i(?5)(p10),add(9)(p?),add(11)(p?),dmin,inc

Case No. 7 **Squamous cell carcinoma** **Uterus, cervix**

87-91,XX?,del(1)(q?),ı(?5)(p10),i(17)(q10),ınc

Case No. 8 **Squamous cell carcinoma** **Uterus, cervix**

96,XXXX,+X,-1,-2,-4,-4,-7,-8,+10,-11,-11,+12,+12,-15,-16,-16,-17, -19,-20, -21,-22,+16mar

Case No. 9 **Squamous cell carcinoma** **Uterus, cervix**

46,XX,+del(1)(p?),del(4)(q?),+ı(?5)(p10),+del(7)(q?),-9,-11, -14,-14,-15,+16, +16,-18,dmın

---

Ayraud 1975, Biomedicine

Case No. 5 **Squamous cell carcinoma** **Lung**

100,XY?,del(1)(p?),del(1)(q?),inv(3)(q?),t(12,16),ınc

Barbich et al 1985, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Uterus, cervix**

46,XX,t(1,5)(q25,q32)/45,idem,-2/85-92,idemx2,dmın,ınc

Berker-Karaüzüm et al 1998, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Lung**

48,XY,+X,+20

Case No. 10 **Squamous cell carcinoma** **Lung**

45,XY,del(7)(q32),-18/88,XXY,+del(X)(q13),-Y,+1,+1,+2,-3,-4,-4,-5,-7,del(7), -8,+9,+9,-10,-12,-14,-14,+15,+17,+17,-20,-20,-22

Case No. 12 **Squamous cell carcinoma** **Lung**

47,XX,+X

Case No. 16 **Squamous cell carcinoma** **Lung**

65,XXY,+del(X)(q22),+1,+del(1)(p31),+2,+4,+4,+5,der(5)t(5,16)(q12,q24)x2,+7,
+i(7)(p10),tas(7,16)(q36,q24),-8,-8,-8,-9,-14,-15,-15,+16,-17,-18,-20,-21,
i (21)(q10),-22,-22

Case No. 18 **Squamous cell carcinoma** **Lung**

87-93,XXYY,-5,-8,-11,-12,+13,-14,-17,-18,+19,-20,+21/93,XXY,+X,+X,-Y,
+del (1)(q12),+4,+6,+del(6)(q12),-8,-9,+10,+10,-11,-11,-12,-12,-12,-13,-14,
+18, -19,-20,+21,-22,-22

Case No. 20 **Squamous cell carcinoma** **Lung**

45,X,-Y/46,XY,del(1)(q11),del(2)(p14)

Case No. 21 **Squamous cell carcinoma** **Lung**

46,XY,+del(2)(p16),+3,+del(8)(q22),+del(9)(q22),-10,+13,-15,-16,-16,-20,+21,
-22/76,XY,del(X)(q24),+1,+del(1)(p35),+del(2),+3,+6,+del(8)(q12)x2,+11,-13,
-14,+15,+17,-18,+20,+20,-21,-22

Case No. 22 **Squamous cell carcinoma** **Lung**

153,XXX,-X,-X,-Y,del(1)(p22),t(1,22)(q25,q13),del(3)(p14),dup(4)(q13q15),-5,
-5,-5,-5,-6,del(7)(q11),der(7)t(7,14)(q11,q11),der(7)t(7,15)(p11,q11),der
(8)t(8,11)(q11,q11),del(10)(q24),der(11)t(11,12)(q11,q11),der(13)t(13,13)
(q11,p11),inv(13)(q13q22)/94,XXYY,+X,+X,+3,-4,+5,der(7)t(7,10)(p11,q11),
+der(7)t(7,20)(q36,p13),+9,-10,-10,-10,-11,-11,+13,-14,+15,+16,-17,-17,+18,
+18,-19,-20,-20

Case No. 23 **Squamous cell carcinoma** **Lung**

93-101,XXYY

Case No. 26 **Squamous cell carcinoma** **Lung**

46,XY,t(2,11)(q11;q25)/70,XY,del(X)(q24),+der(X)t(X,12)(q24,q11),del(1)
(q11),+del(1)(q22),+der(1)t(1,3)(q11,p11),+der(1)t(1,8)(q23,q24),
+der(3)t (3,10)(q11;q11),+4,-5,der(6)t(6,15)(p21,p11),del(7)(q22),
der(7)t(3,7) (p21;p21),-11,der(11)t(11;12)(q11,q11),+12,-13,-14,
-14,+16,+17,-18,-18,der (19)t(19,21)(p13,q11)x3,-20,-21,-21,i(21)(q10),+2mar

Case No. 27 **Squamous cell carcinoma** **Lung**

119,XXYY,-X,+1,+1,+1,+del(1)(p11),i(2)(p10),ı(2)(q10),-3,-3,-3,-4,
der(5)t (5;12)(q31;q24),-6,-6,-6,del(7)(q22),+der(7)t(3,7)(q11,q36)x2,del(8)(q22),
del(9)(q22),ı(9)(q10),+10,+10,+10,+10,+11,+11,+11,-12,-12,-13,-13,-13,
der (13)t(13,14)(q11,q11),der(14)t(14,15)(q11,q11),ı(14)(q10),-15,ı(15)(q10), +16,
+16,-17,-17,-18,-18,-18,+19,-20,+22,+22,+22,+22/66,XY,del(X)(q23),-1,-1,
del(1)(p32),-t(2,10)(p11,q11),der(3)t(3,7)(q11,q11),-5,del(5)(p15q13),
der (5)t(5,12)x2,del(6)(q16),+7,+7,der(8)t(8,13)(q11,q11),+9,ı(10)(p10)x2,-13, -13,
ı(15)(q10),-16,-17,-17,-18,+19,+19,+19,+20,-21,+22,+mar

Case No. 28 **Squamous cell carcinoma** **Lung**

46,XY,ınv(9)(p11q13)/47,ıdem,del(1)(p12),+4,+der(7)t(?4,7)(q21,q36),-11/73,
XXY,+1,+del(1),ı(2)(p10),+3,+4,+7,+7,del(7)(q11)x3,+der(7)t(?4,7),+8,
+del (8)(q12),inv(9)x2,-10,-10,der(10)t(10,11)(q21;q14),+13,+13,-14,-15,-16,
-16, +20,-22

Case No. 29 **Squamous cell carcinoma** **Lung**

46,XY,ınv(9)(p11q13)

Case No. 6 **Squamous cell carcinoma** **Lung**

46,X,-Y,t(4,7)(q24,q32),+del(6)(q13),+15,-17/84,XXY,-Y,+X,+1,+1,+1,
del(3) (q11)x2,-5,i(6)(p10),-7,ı(7)(p10),del(9)(q22),+del(10)(q23),-11,-13,
-14,-14, -15,-15,-16,-17,-19,-19,-21,-22,+4mar

Case No. 7 **Squamous cell carcinoma** **Lung**

45,X,-Y/46,XY,del(6)(q22)

Berrieman et al 2004, Br J Cancer

Case No. 1 **Squamous cell carcinoma** **Lung**

48-57,der(X)t(X,11),+der(X)t(X,12,7;1),-Y,+der(1)t(X,6,1),+der(2)t(2,11,10),
+der(3)t(3,10),-4,+del(5)(?q),?ı(5)(p10),+der(6)t(1;6),+der(7)t(7,12),-8,
der(8)t(Y,8),-10,der(10)t(5,10),-11,der(?11)t(11,16,11),
+der(14)t(5,14),-21, ?ı(21)(q10),-22,+der(?)t(?,4,13)x2,+der(?)t(?,5,22),
+der(?)t(?,7,12)

Case No. 2 **Squamous cell carcinoma** **Lung**

37-48,XY,?del(2)(p?),der(2)t(2,9),?del(3)(p?)x2,der(4)t(4;5),?i(5)(p10),-6, der(8)t(8,11),der(9)t(5,9),der(10)t(3,8,10),der(?11)t(5,12,7,11),+der(?11)t (5,14,11),+der(11)t(11,18),der(12),i(13)(q10),der(14)t(14,18),der(16)t (16,19),?del(17)(p?)x2,der(?18)t(6,18,11;8),+der(?18)t(6,18)x2, der(19)t (8,19),der(22)t(1;5,22)

Casalone et al 1990, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Oesophagus**

47,XY,+Y

Casalone et al 2000, Cancer Genet Cytogenet

Case No. 74 **Squamous cell carcinoma** **Skin**

50,XX,+1,der(1)t(1,17)(q36,q21)x2,dup(7)(q12q36),+8,+9,i(14)(q10),+16,+21

Case No. 75 **Squamous cell carcinoma** **Skin**

49,XX,+6,+8,+11

Case No. 76 **Squamous cell carcinoma** **Skin**

67-82,XY,-X,inc

Chen et al 1994, Cancer Genet Cytogenet

Case No. 9 **Squamous cell carcinoma** **Lung**

63,Y,-X,der(X),+Y,del(1)(p?),+der(1),der(3)(q?),-5,+del(7)(p?)x2,-9,+10, del (11)(p?),+12,+add(12)(p?),-15,-17,+add(19)(q?),+20,add(21)(p?), add(22)(p?), i(22)(q10),+12mar

Clerici et al 1989, Tumori

Case No.		
17	**Squamous cell carcinoma**	**Lung**

45,XY,-3

Case No.		
8	**Squamous cell carcinoma**	**Lung**

47-50,XX,+13,+14,+15

Dave et al 1995, Int J Oncol

Case No.		
1	**Squamous cell carcinoma**	**Lung**

46-52,X,-Y,+1,-2,+der(3)t(3,11)(p14,q13)x2,der(4)t(X,4)(q11,q11),+5,del(5)(q11)x2,+add(6)(q27),+7,+8,del(9)(q22),der(9)t(9,14)(p11,q11),+10,+add(10)(q24),-11,-12,-14,-14,-15,add(15)(p13),-16,-17,-20,+2mar

Case No.		
3	**Squamous cell carcinoma**	**Lung**

55-66,XX,-X,-1,+2,-2,-2,-3,add(3)(q21),-4,-5,add(5)(q11),-6,+7,+7,-8,
add(9) (p24),-10,-10,-11,+12,+12,+12,+12,-13,-13,+14,+14,-14,-15,
-16,-16,add(16) (p13),+17,-18,+19,-19,-20,-21,-21,-22/79-86,X,-X,-X,
+dic(2;16)(q37,p13),+3, +3,del(5)(q11),+del(5)x2,+7,+7,+7,+7,
dic(8,18)(q24,q23),+9,+9,+i(9)(q10), -11,+12,+12,+12,+12,+12,-14,
+15,+15,+16,-18,-19,+1-5mar

Case No.		
5	**Squamous cell carcinoma**	**Lung**

42-55,XY,+X,+X,+del(1)(p34)x2,+der(1)t(1,3)(p32-34,p21),+2,+der(3)t(1,3)(p34,p21),+dic(3,4)(p21,q34),+add(4)(p12),+add(4)(p16),+add(6)(p21),del(7) (q11),-8,+del(9)(q32),inv(9)(p23q32),del(10)(q22),+12,+12,+12,+der(12)t (3;12)(p21;q24),-14,-15,add(16)(p13),+17,-19,-19,-20,+der(21)t(9,21) (q11;p13),-22,+1-3mar

Drouin et al 1993, Genes Chromosomes Cancer

Case No.	Squamous cell carcinoma	Lung
1		

27,X,+X,+5,+7,+22

Fadl-Elmula et al 1998, Cancer Genet Cytogenet

Case No.	Squamous cell carcinoma	Bladder
1		

76-87,XX,-X,+1,der(1)add(1)(p22)t(1,9)(q42,q22)x2,+2,del(2)(q13)x2,+3,del
(3)(q27)x2,+4,+5,+der(6)t(6,10)(p21,q11),del(6)(q21q23)x2,+7,
+del(7)(q11)x2, add(8)(p11)x2,der(8)t(X,8)(q13,q24),
+der(8)t(X,8),-9,-9,-9,+10,add(10) (q26)x2,del(11)(p11),
der(11)t(3;11)(q11,p11)del(3)(q27),
der(11)del(11)t (3,11)(q21,q23),+12,-13,der(13)t(1,13)(p12,p32),
der(15)t(15,17)(p11,q11), -17,-17,-17,add(18)(q21)x2,add(18)(q22),+19,
der(19)t(2,19)(q13,p13)x2,+20, -21,+add(22)(p11),
+der(?)t(?,9)(?,q13),+8mar

Case No.	Squamous cell carcinoma	Bladder
2		

94-109,XX,-X,-X,-1,-1,-1,-1,-2,add(2)(q35)x2,der(2)add(2)(q35)t(2,13)
(p11;q13),add(3)(p11),der(3)t(3,5)(p12,q13)x2,+4,der(4)t(1,4)(q25;q31)x2,
add(5)(q11)x2,der(5)t(5,17)(q11;q21)ins(5,?)(p11,?),+i(5)(p10)x2,+7,+add(7)
(q11),+der(7)t(1,7)(p22;q21),+8,del(8)(p12)x2,der(8)t(1,8)(q21,p11)add(1)
(q32)x2,+der(8)t(2,8)(q11,q11)x2,-9,add(9)(p11),der(9,17)(q10,q10),
i(9) (q10),+der(10)t(3,10)(p21,q22)x2,-12,-12,-13,-13,-15,der(16)t(8,16)
(q13,p12)x2,+der(16)t(3,16)(q11,q11-12),+add(17)(p11),der(17)t(13,17)
(q14,p11)x2,+19,add(19)(q13)x2,+add(19)(p11-12)x2,
der(19)t(1,19)(q12,p12)x2, -20,-20,der(21)t(21,22)(p13,q11)x2,
der(21)t(21;22)t(7,22)(q11,q13)t(1;7)
(p22;q21),der(21)t(21,22)t(7,22)t(7;12)(q21;q13),+der(21)t(3,21)(q11;p13),
-22,-22,der(22)t(1,22)(p13,p11),+der(?)t(?,2)(?,p11),+der(?)t(?,3)(?;p14),
+2-4r,+6mar/190-220,idemx2

Fadl-Elmula et al 1998, Genes Chromosomes Cancer

Case No.	Squamous cell carcinoma	Urethra
1		

45-47,X,-Y,add(2)(p21),del(2)(q31q33),+I(3)(q10),der(4)t(4,8)(p11,q11),del
(6)(q16),del(7)(q32),add(11)(q14),+20,+mar/90-96,idemx2

Feder et al 1998, Cancer Genet Cytogenet

Case No.		
	Squamous cell carcinoma	**Lung**
65		

59-68,XY,-X,add(3)(p14),del(3)(p13p21),+5,-6,i(8)(q10)x2,-9,-9,-9,-10,-10,
add(11)(p11),+13,add(14)(p12),-15,-16,-16,-17,add(17)(p11),-18,
+add(19) (q13),-21,-21,-22,-22,+der(?)t(?,7)(?,p11),+7-9mar

Fitchett et al 1984, J Med Genet

Case No.		
	Squamous cell carcinoma	**Skin**
1		

46,XY,del(13)(q14q14)

Fu & Li 1997, Cancer Genet Cytogenet

Case No.		
	Squamous cell carcinoma	**Lung**
1		

62-76,XX,-Y,-1,add(1)(p22),del(1)(p31),del(1)(p12)x2,del(1)(q12)x2,der(1)t
(1,22)(p11,q12),+2,ins(3,?)(p21-22,?)x2,-4,-5,-5,+der(6)t(6,11)(p24,p13),
+add(7)(p12),-8,-8,add(8)(p?)x2,i(8)(q10)x2,+9,-10,-11,add(11)(p?),-12,
add (14)(p?),-15,-15,-16,-17,-18,-18,-18,+19,-20,-21,+22,+2mar

Case No.		
	Squamous cell carcinoma	**Lung**
19		

44-49,XX,-6,del(7)(q11q22),-9,-10,der(11)del(11)(p12)del(11)(q23),
-18,-19, -20,+4mar

Case No.		
	Squamous cell carcinoma	**Lung**
21		

42-51,XY,del(6)(q23),-7,-13,-21,+2mar

Case No. 3 **Squamous cell carcinoma** **Lung**

47-54,X,-Y,del(1)(q22),del(1)(p22),der(1,7)(p10,q10),+2,del(3)(q12),
-4,-4,ı (5)(p10),del(6)(q21)x2,ı(6)(p10),-8,+9,+9,add(10)(p11),-11,
del(11)(p11),del (12)(q22),-13,-13,-14,-15,-15,-16,+19,-21,-21,-22,
-22,+4mar

Case No. 49 **Squamous cell carcinoma** **Lung**

45-47,X,-Y,der(1,11)(q10,p10),ins(3,?)(p14-21,?),-5,del(6)(q12),
del(6)(q21), i(8)(q10),-11,-12,-14,-15,-17,-18,-21,-22,+3mar

Case No. 53 **Squamous cell carcinoma** **Lung**

47-56,X,-Y,add(1)(p?),del(1)(p12),del(1)(q31),+3,-4,-4,+6,
del(7)(q11q22),-8, hsr(9)(q11),ı(9)(q10),del(11)(p11),-12,+14,-15,
add(15)(p?),-16,-16,+17,+20, -22,+3mar

Case No. 6 **Squamous cell carcinoma** **Lung**

54-81,-X,-Y,+1,+del(1)(p22),-2,del(3)(p11)x3,ı(3)(p10),-4,-5,-5,-5,-6,del
(6)(q23),add(7)(q23),del(7)(p15),der(8,9)(q10,q10),+9,der(9,11)(q10,q10),
-10,-10,add(11)(q23),del(11)(p11),-12,-13,-13,-13,-14,-15,-15,-16,-17,-18,
-18,+19,-20,-21,-22,-22,+12mar

85-96,XY,-Y,del(1),+ınv(1)(p13p35),-2,der(2,3)(p10,q10),del(3)(q11)x2,
del (4)(q22),-5,ı(5)(p10),-6,del(6)(q16),+7,+add(7)(q12),-8,-8,-9,-10,-10,
add (10)(q?),+11,-12,-12,-13,-13,-13,-14,-15,-15,-16,add(16)(q?),-17,-18,
-19, -20,-20,-21,-21,-21,-21,+18mar

Füzesi et al 1994, Int J Oral Maxillofac Surg

Case No. 1 **Squamous cell carcinoma** **Oral cavity**

46,XY,del(5)(q13),der(18)t(5,18)(q13,p11)/49,XY,+5,+7,+10

Heim et al 1989, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Skin**

45,XY,ı(9)(q10),-13/46,ıdem,+21/46,XY,t(3,17)(p21;q21)

Case No. 2 **Squamous cell carcinoma** **Skin**

47,XY,+7/46,XY,t(7,14)(p11;p13)/47,XY,der(1)t(1;6)(q21,p23),
der(6)t(1,6)t (6,11)(q25;p15),+7,der(11)t(6,11)/46,XY,del(2)(p21),
del(4)(p13)/46,XY,inv (11)(q13q21)

Case No. 3 **Squamous cell carcinoma** **Skin**

46,XY,t(4,10)(p16,q11)/46,idem,t(10,15)(q26;q14)

Hermsen et al 1996, Genes Chromosomes Cancer

Case No. 120 **Squamous cell carcinoma** **Tongue**

44-50,X,der(X,14)(p10,q10),der(1;10)(q10,q10),der(1)t(1,11)(p36,q13)
hsr(11)(q13),add(3)(p11),der(5;14)(q10,q10),+i(5)(p10),+9,-10,
der(14)t(1,14) (p13,q11),add(15)(p11),-19,+2-4mar/80-99,idemx2

Case No. 147 **Squamous cell carcinoma** **Oral cavity**

54-75,X,-X,-Y,-2,der(2;4)(q10,q10),der(3,4)(q10,q10),der(3)t(3,15)(p24,q21),
-4,-4,-4,i(5)(p10),+6,der(6,14)(p10,q10)x2,-7,add(7)(q36),-8,-9,-10,add(11)
(q11),+der(11)del(11)(q13)hsr(11)(q13)x2,+add(12)(q24),-13,add(13)(q32),
-14, -15,-15,-17,-18,-19,-20,-21,-22,+0-3mar

Case No. 40 **Squamous cell carcinoma** **Tongue**

46,X,-X,add(3)(q27),+9,add(18)(q22)/46,idem,add(12)(q24)

Hermsen et al 1996, Genes Chromosomes Cancer

Case No. 41 **Squamous cell carcinoma** **Oral cavity**

37-44,X,-Y,der(3,11)(q10,q10),der(3,11)(q10,q10)add(3)(q29),+der(3;15)
(p10;q10),der(4,14)(q10,q10),i(5)(p10),-9,der(9)t(9,14)(p13;q13),-11,-13,
i (13)(q10),-14,-14,-15,-18,+2-4mar/77-83,idemx2

Case No. 59 **Squamous cell carcinoma** **Oro- and hypopharynx**

58-76,add(X)(p11),add(X)(q11),der(X)t(X,13)(q13;q1?),
+der(1)t(1,5)(p13,q13), del(2)(p13)x2,+i(2)(p10),add(3)(p10-
11)x2,+der(3)t(3,5)(q21,q13),i(5)(p10), +add(7)(q32),+i(8)(q10),
hsr(11)(q13),+14,+20,-21,-21,-21,-22,-22,-22, +2-6mar

Case No. 78 **Squamous cell carcinoma** **Tongue**

55-84,X,der(X,11)(q10,q10)x2,+i(X)(q10),add(1)(q11),
del(1)(p13),der(3)add (3)(q11)hsr(3)(q11),i(3)(q10),
add(8)(p11),+i(8)(q10)x2,-10,der(10)t(10;15) (q24,q21),-11,
der(11)t(1,11)(p32;q21-22),+del(12)(q13),+der(13,14)(q10,q10),
-14,add(14)(p11),-15,-15,+17,+20,+20,-21,-21,+1
-4mar/98-139,idemx2

Case No. 80 **Squamous cell carcinoma** **Tongue**

53-73,X,-X,add(Y)(p11),+der(Y,1)(q10;q10),add(1)(q11),
der(1;7)(p10,p10), +der(1,15)(p10;q10),-2,i(3)(q10),-4,add(4)(q31),-
5,der(5,7)(q10,p10),-6,del (7)(q22q32),add(8)(p11),del(9)(p13),
-10,i(10)(q10),-11,add(12)(q13),der (12)t(2,12)(q21,q13),-13,-
14,der(14)t(12,14)(q21,p11),-15,-15,add(15)(p11), -16,-17,-18,-
18,add(19)(p13),+der(19)t(11,19)(q11,q13),i(21)(q10),-22,+der
(?)t(?,5)(?,q14)hsr(5)(q14),+1-3mar/106-143,idemx2

Case No. 94 **Squamous cell carcinoma** **Tongue**

71-85,add(X)(p22)x2,i(X)(q10),der(1,14)(p10,q10),i(1)(q10),+2,+3,
add(3) (p13-14)x2,+5,+5,+6,+7,i(8)(q10),+i(8)(q10)x2,del(9)(p12p23),
+del(9) (p12p23)x3,+12,-13,-13,i(13)(q10),-14,-15,+15,+16,
+add(16)(q22),+17,+del (17)(p12-13),+19,-21,
der(21,22)(q10,q10),i(21)(q10),-22,-22,+der(?)t(?;13) (?;q12)x2,
+2-3mar

Case No. 96 **Squamous cell carcinoma** **Oro- and hypopharynx**

49-62,X,-X,-Y,der(1)t(1,1)(q11,p31)der(1,9)(q10,q10)x2,der(3)
add(3)(p25)add (3)(q27),der(3,21)(p10,q10),i(3)(q10),-
4,der(4,21)(q10,q10),add(5)(q22),del (6)(p21),+del(7)(q21q34),
-9,-9,-9,del(10)(p13-14),der(10)t(3;10)(p12;p12),
add(11)(p14),der(11)t(9,11)(q13,q13)hsr(11)(q13),add(13)(p11),
der(13)t (3,13)(p13;p11),-14,add(14)(p11),
+der(14)t(14,?)(p11;?)t(?,3)(?,q13)x2,add (15)(p11),add(16)(p11),
+add(16)(p11),+17,-18,-18,-18,-19,add(19)(p11)x2,+20, -21,-21,
-21,-22,-22,+der(?)t(?,10)(?,q11),+2-5mar

54-64,X,-X,-Y,add(1)(p21),der(1,9),-2,-2,-4,add(4)(q31),
add(7)(p11),der (7,10)(q10,q10),add(8)(p21-22),-9,-9,-
10,der(11)t(1,11)(p13,p11)add(11) (q23),der(11)t(9,11)hsr(11),-
12,add(12)(q15),add(13)(p10-11)x2,-14,add(14) (p10-11),
der(14),-15,add(15),i(16)(q10),-18,der(18)t(12,18)(q21,q12),-19,
add(19),+der(19,21)(q10,q10),-20,add(20)(q11),-21,-21,i(21)(q10),
+3-5mar

Jin et al 1988, Cancer Genet Cytogenet

Case No. 1	Squamous cell carcinoma	Larynx

46,XY,inv(2)(p22q24),t(9,13)(q34,q12),t(11,18)(q23,q21)

Jin et al 1988, Cancer Genet Cytogenet

Case No. 1	Squamous cell carcinoma	Tongue

46,X,der(X)t(X,1)(q26,p32),der(1)t(X,1)(q26,p32)del(1)(p32)
del(1)(q42),del(13)(q11q21),add(15)(q26)/46,XX,add(1)(p34),
inv(2)(p21q11)/46,XX,t(1;10)(p32;q24)/46,XX,+der(1)t(1,12)
(p11,p11)ins(1;11)(q32,q13q22)del(1)(q42),del (11)(q13q22),-
12,der(17)t(1,17)(q42;p13)/46,XX,inv(1)(p22q44)/47,XX,del(1)
(q32),der(1)inv(1)(q25q44)t(1;17)(p22q25),+14,ins(14,7)
(q11,q22q36),der(17)t(1,17)/46,XX,t(1,4)(q23,q35)/
46,XX,t(1,21)(q25,q22),t(2,10)(q31,q26),add(22)(q12)/
46,XX,del(1)(q32)/46,XX,t(1,8)(q44;q21)/
46,XX,t(2,21) (q11,p11)/46,XX,t(9;11)(q34,q13)

Jin et al 1988, Cancer Genet Cytogenet

Case No. 1	Squamous cell carcinoma	Larynx

46,XY,t(6,7)(q23,p22)

Jin et al 1988, Cancer Genet Cytogenet

Case No. 1	Squamous cell carcinoma	Nasopharynx

46,XY,inv(4)(p15q26)

Jin et al 1990, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Larynx**

45,X,-Y,t(2,5,9)(p11,q13,p24)/46,XY,t(1,1,15)(q21,p12,p13),
t(14,16) (q24,p13)

Case No. 2 **Squamous cell carcinoma** **Larynx**

45,X,-Y,t(1,4)(p22,q28),del(8)(q13),del(13)(q22),inv(16)(p11q24),-19,
+mar/44,X,-Y,t(1,18)(p31;q23)/45,X,-Y,-1,add(5)(q35),add(6)(p25),
add(6) (p24),del(8)(p21),t(11,20)(q13,q13),der(13)t(1,13)(p11,p11),
-14,del(15) (q22),add(19)(p11),+2mar

Case No. 3 **Squamous cell carcinoma** **Larynx**

46,XY,t(1,3)(q44,p12)/46,idem,t(7,15)(q22;q24)/46,XY,t(1,5)(q25,p15)/
46,XY, der(1)del(1)(p22)t(1;12)(q43;q22),t(2,5)(q21,q33),der(6)t(1,6)
(p22;q25),del(7)(q32),add(9)(p?),der(10)t(1,10)(q43,q22),
der(12)t(10,12)(q22,q22)/46,XY,t(3,6,14)(q12,q23,p11),
t(5,8,12)(q12,q11;p11),del(10)(q23q25)/46,XY,add(7)
(q?)/46,XY,t(9,10)(q22;q26)/46,XY,t(9;11)(q34;q21)/
46,XY,t(11,19)(p11,q13), t(13,20)(q14,q13)/46,XY,t(13,17)(q32;q21)

Case No. 4 **Squamous cell carcinoma** **Larynx**

46,XY,add(16)(q24)

Case No. 5 **Squamous cell carcinoma** **Larynx**

47,XY,+i(5)(p10)

Jin et al 1990, Genes Chromosomes Cancer

Case No. 1 **Squamous cell carcinoma** **Oral cavity**

46,XY,t(3,4)(q29,q21)/46,XY,t(2,2)(q37,q23)/45,X,+X,-Y,
add(3)(p11),add(5) (q35),+der(11)t(11,13)(q13,q12),-13,
add(13)(p13),-14,i(15)(q10),der(21)t (9;21)(q13,p13),
der(21)t(18,21)(q11;p13)

Case No. 2 **Squamous cell carcinoma** **Oral cavity**

45,-Y,t(X;17)(q22;q21),del(1)(q42),t(2,11)(q33,p15),t(3,5)(p26,q11),t(4;15)
(p16,q22)/46,XY,t(8,12,22)(q22,q13;q13),t(10,15)(q24,p13),t(14,20)(q24,q11)

Case No. 3 **Squamous cell carcinoma** **Oral cavity**

46,XY,t(1,6)(p11;p12)/46,XY,t(3;10)(p13;p13)

Case No. 4 **Squamous cell carcinoma** **Nasopharynx**

92,XXYY,t(1,8)(q21,q22)x2/92,XXYY,t(1;1)(p22,q44)x2

Case No. 5 **Squamous cell carcinoma** **Oro- and hypopharynx**

46,XY,t(6,10)(q12,p15)/46,XY,t(7;7)(p14,p22)/46,XY,
t(4,8)(q21,q24)

Case No. 6 **Squamous cell carcinoma** **Tongue**

66-76,XX,-Y,+1,+3,-4,del(4)(q31),+ı(5)(p10)x2,-6,del(7)(q31),
+add(10)(q26), add(11)(q13),-13,-13,-13,+del(16)(q22),-18,
+20,-22,+2-6mar

Case No. 7 **Squamous cell carcinoma** **Tongue**

47,XY,+7/46,ıdem,-Y

Case No. 8 **Squamous cell carcinoma** **Oro- and hypopharynx**

45,X,-Y

Case No. 9 **Squamous cell carcinoma** **Tongue**

45,X,-Y

Jin et al 1990, Genes Chromosomes Cancer

Case No. 1 **Squamous cell carcinoma** **Nasopharynx**

38-41,X,-Y,der(1)t(1,10)(p12,q11),add(2)(p11-13),i(3)(q10),
der(4)t(4,13) (p12,q11),ı(8)(q10),-9,-10,-10,der(11)
t(1,11)(p12,q13)hsr(1,11)(p12,q13), -13,-
13,add(14)(q32),der(15,21)(q10,q10),der(16)t(9;16)(q13,p13),
inv(18) (p11q22),-21,+2-3mar

Case No. 10 **Squamous cell carcinoma** **Tongue**

46,XX,t(3,19)(q22,p13)/46,XX,t(3,17)(q22,p13),t(6,14)(p21;q32)

Case No. 11 **Squamous cell carcinoma** **Larynx**

45,X,-Y/47,XY,+Y/47,XY,+7/46,XY,t(1,2)(p22,p13),t(6,13)
(q21,p13)/46,XY,t (1,2)(p22,q21),del(10)(p?)/
46,XY,t(1;14)(p36,p13)/46,XY,der(1)t(1,8)
(p21;q12),der(4)t(1,4)(p21,p13)t(4,10)(q21,q11),
der(8)t(4,8)(p13;q12),der (10)t(4,10),t(12,20)(p11,p13)/45,X,-
Y,t(3,14)(q22;p12)/46,XY,t(4,10)(q21,p11)/
46,XY,t(6;13)(q21,p13)/46,XY,t(6,21)(p21,q22)

Case No. 12 **Squamous cell carcinoma** **Nasopharynx**

45,X,-Y/47,XY,+Y/46,XY,t(1;4)(p22,q25),t(3,5)(q13,p15),
t(3;10)(p25,p11)

Case No. 13 **Squamous cell carcinoma** **Larynx**

45,X,-Y/46,idem,+7/47,XY,+7/46,XY,t(1,2)(p22,q21)

Case No. 14 **Squamous cell carcinoma** **Larynx**

47,XY,t(1,2)(q21,q23),+7/47,idem,t(1,18)(p36,q21)

Case No. 15 **Squamous cell carcinoma** **Oral cavity**

46,XY,inv(3)(p21q29)

Case No. 2 **Squamous cell carcinoma** **Nasopharynx**

39,XY,add(1)(p12),der(2)t(2,4)(p13,q21),-3,-4,i(5)(q10),
add(7)(q21),-8,-9, -9,-10,-10,add(11)(q25),der(11)add(11)(p14)
ins(11;?)(q13,?),der(12)t(1,12)(p12,q24),der(13)add(13)(p?)
inv(13)(q12q21),der(14)t(3,14)(p11,p11),add(15) (p?),
+der(15,21)(q10,q10),-18,-19,-22,-22,+3mar/71-78,XXY,
der(1)t(1,10) (p12;q11)x2,+2,der(2)x2,-3,-4,der(4),+5,
i(5)(q10)x2,+6,+7,add(7)x2,+8,add (8)(p11)x2,-9,-9,-9,-
10,add(11)(q21),+add(11)(q25),der(11)x2,+12,der(12)x2,
+13,der(13)x2,+14,der(14)x2,add(15),+der(15,21),+16,+17,
-18,-20,-22,i(22) (q10),+2-6mar

Case No. 3 **Squamous cell carcinoma** **Oro- and hypopharynx**

59-60,-X,-X,-Y,-1,-2,del(2)(q13),der(2)t(2;8)(q33,q13),der(3)t(3,4)
(p25;q11),der(4)t(4;12)(q11,q15),i(4)(q10),-5,add(7)(q11),
+del(7)(q11),-8, der(8)t(8,8)(p11,q13),-
9,add(11)(q13),der(12)t(12,12)(p11,q13)add(12)(q13),
+der(12)t(3;12)(q11;q24),i(12)(p10),-13,der(13)t(5,13)(p11,p13),
der(13)t (3;13)(p11,q14),-14,der(15)t(1,15)(q11,p13),
der(15)t(15,17)(p11,q11),+der (15,21)(q10,q10),-
17,der(17)t(7,17)(q11;p13)ins(17,?)(p13,?),-18,-18,-18,
add(19)(p13),+20,-21,-21,-21,-22,der(22)t(11,22)(p11,p11),
+2-7mar,dmin

Case No. 5 **Squamous cell carcinoma** **Nasal cavity/Paranasal sinuses**

46,Y,t(X,22)(q22,q13),ins(1,3)(p36,p21p25),t(2,5)(q37;q12),
t(3,6)(q13,q23), t(6,16)(q21,q22),ins(8,16)(p21,q22q24)/45,X,-Y,
t(1,4)(p34,q33),-22, +mar/67-69,XY,hsr(5)(q13),der(11)
add(11)(p11)ins(11,?)(q13,?),inc

Case No. 6 **Squamous cell carcinoma** **Larynx**

46,XY,t(1,16)(p22,q24),t(6,18)(q27,q21)/46,XY,
t(1,15)(q11,q15),inv(5) (q22q33)/46,Y,t(X,1)(p11,q25)/46,XY,
t(1,11)(p12;q23)/45,-Y,t(X,2,5) (p11,q21,q13p15)/
46,XY,t(6,15)(q11,p11)/
46,XY,t(6,10)(p12;p15)/47,XY,+7/
50, XY,t(1;14,16)(p22,q22,p13),+7,+8,+15,+22

Case No. 7 **Squamous cell carcinoma** **Oral cavity**

46,XY,t(1,7)(p13,p22)/46,idem,add(11)(q23)/46,XY,
ins(5,14)(p13;q11q32)/92, XXYY,ins(5,14)x2/46,XY,
t(5,14)(q15,q32)

Case No. 8 **Squamous cell carcinoma** **Larynx**

45,X,-Y/46,XY,del(2)(p23p23),t(4,14)(q12,p11),inv(12)(p13q22)/
46,XY,t(2,12) (q35,q13),t(8,20,22)(q22,p11,q13)/
46,XY,t(3,12)(q25,q22)/46,XY,t(12;14) (q13,p13)

Case No. 9 **Squamous cell carcinoma** **Larynx**

47,XY,+7/46,idem,-Y/46,XY,t(2,8,17)(p23,q22,q23),
t(7,9)(p13,p13)/46,XY,t (3,5)(q25,q13)/46,XY,
t(3,5,13)(p13,q33,q32)

Jin et al 1993, Cancer Res

Case No. 1 **Squamous cell carcinoma** **Nasopharynx**

45,X,-Y

Case No. 10 **Squamous cell carcinoma** **Oral cavity**

45,X,-Y

Case No. 11 **Squamous cell carcinoma** **Oral cavity**

45,X,-Y/47,XY,+Y

Case No. 12 **Squamous cell carcinoma** **Nasopharynx**

45,X,-Y/47,XY,+Y

Case No. 13 **Squamous cell carcinoma** **Skin**

45,X,-Y/46,idem,+7

Case No. 14 **Squamous cell carcinoma** **Nasopharynx**

45,X,-Y/47,XY,+7

Case No. 15 **Squamous cell carcinoma** **Oral cavity**

47,XX,+7

Case No. 16 **Squamous cell carcinoma** **Nasopharynx**

47,XX,+18

Case No. 17 **Squamous cell carcinoma** **Oral cavity**

47,XX,+X

Case No. 18 **Squamous cell carcinoma** **Nasopharynx**

47,XX,+X

Case No. 19 **Squamous cell carcinoma** **Larynx**

47,XY,+8,t(9,20)(q22,q11)

Case No. 2 **Squamous cell carcinoma** **Larynx**

45,X,-Y

Case No. 20 **Squamous cell carcinoma** **Nasopharynx**

45,X,-Y/46,idem,+7/46,XY,del(1)(p32)

Case No. 21 **Squamous cell carcinoma** **Oral cavity**

45,X,-Y/47,XY,+Y/46,XY,t(1,6)(q21;p21)/46,XY,inv(2)(p25q14)

Case No. 22 **Squamous cell carcinoma** **Oral cavity**

45,X,-Y/47,XY,+7/46,XY,t(1,14)(q25,p11)/46,XY,inv(5)(p13q21)

Case No. 23 **Squamous cell carcinoma** **Nasopharynx**

45,X,-Y/47,XY,+Y/46,XY,t(1,16)(p22;p13)

Case No. 24 **Squamous cell carcinoma** **Nasopharynx**

46,XY,t(3,14)(q21;p13)

Case No. 25 **Squamous cell carcinoma** **Nasopharynx**

46,XY,t(1,8;16)(p31;q21;p11)/46,XY,t(1;15)(p32,q22),
t(5,11)(q15;q21)/46,XY, t(15,19)(q15,q13)

Case No. 26 **Squamous cell carcinoma** **Larynx**

46,XY,del(1)(q11)/46,XY,t(1;2;6)(p34,q37,p21)/46,XY,-1,
der(2)t(2,3) (q37;p23),der(4)t(1;4)(q25,q27),add(4)(p16),der(8)
t(1,8)(p22,q22)ins(8;?)(q22,?),ins(15,5)(p?;q13q31),dup(17)(q12q12),
+mar/46,XY,t(3;9)(q21,q34)/46, XY,t(3,9,12)(p11q21,q34;p11)/
46,XY,t(3,15)(q21,p11)

Case No. 27 **Squamous cell carcinoma** **Nasopharynx**

46,XY,der(1)t(1;11)(q44,q13)

Case No. 28	**Squamous cell carcinoma**	**Tongue**

45,X,-Y

Case No. 29	**Squamous cell carcinoma**	**Oral cavity**

45,X,-Y

Case No. 3	**Squamous cell carcinoma**	**Larynx**

45,X,-Y

Case No. 30	**Squamous cell carcinoma**	**Nasopharynx**

45,X,-Y/47,XY,+Y/47,XY,+7

Case No. 31	**Squamous cell carcinoma**	**Nasopharynx**

45,X,-Y

Case No. 32	**Squamous cell carcinoma**	**Tongue**

47,XX,+X

Case No. 33	**Squamous cell carcinoma**	**Tongue**

45,X,-Y/47,XY,+Y

Case No. 35	**Squamous cell carcinoma**	**Oral cavity**

38-40,X,-Y,-3,-4,-5,der(5)t(1,5)(p22,p14),+add(6)(q15),der(7)
t(4;7) (q11,q22),i(7)(q10),-8,-9,der(11)t(4,11)(q21,p15)inv(11)(p13q25),
+der (11)add(11)(q13)hsr(11,?)(q13,?),-12,-14,der(14)
t(12;14)(q15,p11),der(15)t (3,15)(p11,p11)inv(3)(p13p21),
add(16)(p13),-17,-18,-22,+2-4mar

Case No. 36	**Squamous cell carcinoma**	**Oral cavity**

46,X,der(X)del(X)(p11)t(X;17)(q22,q21),t(1,15;15)(p34q21,q22,q22),del(5)
(q13),der(17)t(5,17)(q13,q21)/46,X,t(X,5)(p22,q13),t(1,12)(q25,q13),t(6,16)
(q15,p13),inv(7)(p15q36),del(15)(q22)/46,X,t(X,15)(p11;q24),-2,add(5)(q35),
der(19)t(2,19)(p11;p13),+mar/46,XX,t(1,14)(p34,q22),t(4,16)(p15,q24)/46,XX,
t(1,17)(p36p36,q21q25),t(1,3)(q42,q21),del(2)(q33),del(7)(p21)

Case No. 37	**Squamous cell carcinoma**	**Oro- and hypopharynx**

74-79,XXY,+Y,der(1)t(1,15)(p11,q14)x2,+2,add(3)(p13),+der(3)t(3;15)
(p11;q15),+4,+6,+7,+8,-11,add(11)(p15)x2,-13,der(13)t(1,13)(p11,p13)x2,-15, -
15,der(20)t(13;20)(q11-14;q11-13),-21,der(21)t(17;21)(q11,p11),+22,der
(22)t(10,22)(q11;p11)x2,+der(?)t(?,1)(?,q11)hsr(?;1)(?;q11),+4-9mar

Case No. 38 **Squamous cell carcinoma** **Tongue**

78-88,XXX,del(X)(p21),der(1)t(1,21)(p11,q11)x2,-2,der(3)t(3,11)(p11,p11),
der(3)t(3,?18)(p11,q11),+4,der(?4)t(4,16)(q11;q11)x2,-5,del(6)(q14),+der
(7)t(7,13)(q21,q12)ins(7,?)(q21,?),i(8)(q10)x2,-10,der(10)t(8,10)(q11,p11),
-12,-14,der(14,15)(q10,q10),-15,-15,-15,-16,der(16)t(14,16)(q13,q13),-17,
-17,-18,-18,-18,-18,der(19)t(1,19)(p31,p13)x2,+20,-21,+2-6mar

Case No. 39 **Squamous cell carcinoma** **Larynx**

66-69,X?,inc

Case No. 4 **Squamous cell carcinoma** **Oro- and hypopharynx**

45,X,-Y

Case No. 40 **Squamous cell carcinoma** **Larynx**

46,XY,t(2,7)(p21;q22)

Case No. 41 **Squamous cell carcinoma** **Oral cavity**

46,XY,add(1)(q21),-2,add(4)(q31),der(4)t(4;5)(p13,q15),add(5)(q31),add(5)
(q13),t(8,13)(q24,q11),add(12)(q24),inv(14)(q11q32),der(15)t(1;15)(q25,q22),
der(18)t(2,18)(q21,p11),der(22)t(1,22)(q23,p13),+mar

Case No. 42 **Squamous cell carcinoma** **Nasopharynx**

63-66,XY,inc

Case No. 43 **Squamous cell carcinoma** **Oral cavity**

77-83,XY,-X,add(5)(p15),del(6)(q21),i(8)(q10),add(12)(q24),der(14,15)
(q10,q10),add(19)(p13),inc

Case No. 44 **Squamous cell carcinoma** **Larynx**

82,XX,-Y,-Y,?add(6)(q11),+der(?)t(?,7)(?,q11),inc

Case No. 45 **Squamous cell carcinoma** **Nasopharynx**

69-72,XX,-Y,der(2)add(2)(p11)hsr(2)(p11),+3,-4,-5,i(5)(q10),-8,-9,-9,-10, -
10,hsr(11)(q13),-12,i(12)(q10),-13,-13,i(14)(q10),+add(15)(p11),+16,+20,
+20,+add(22)(p11),+7-10mar

Case No. 46 **Squamous cell carcinoma** **Tongue**

66-69,X?,add(1)(p11),add(3)(p25),add(6)(p24),add(12)(p11),add(17)(p?),inc

Case No. 47 **Squamous cell carcinoma** **Larynx**

46,XY,der(5)t(5,10)(q13,q11),i(7)(q10),der(10)t(7,10)(p11;q11),der(15)
t (5;15)(q13,p13)

Case No. 48 **Squamous cell carcinoma** **Nasopharynx**

68-72,X,-X,-Y,der(1)t(1,8)(q11,q21),+2,der(2)t(1;2)(q25;q33)x2,-3,del(4)(p14)x3,der(5)t(3,5)(q11,q11),+6,+7,add(7)(q32)x2,+8,i(8)(q10)x2,+10,+11,add(11)(q23)x2,-13,der(13)t(5,13)(q13,p11)x2,-14,+15,der(15,21)(q10,q10)x2,-17,add(17)(p11),-18,+20,-21,-21,-21,-22,+3-5mar

Case No. 49 **Squamous cell carcinoma** **Tongue**

47,XY,t(1,22)(q21,p13),i(3)(q10),del(4)(q28),+i(7)(p10),i(8)(q10)

Case No. 5 **Squamous cell carcinoma** **Oro- and hypopharynx**

45,X,-Y

Case No. 50 **Squamous cell carcinoma** **Oral cavity**

72-79,XX,-Y,+add(1)(p11),+2,+3,i(3)(q10)x2,+4,der(4)t(4,7)(p15;p13)x2,+5,+6,add(6)(p23)x2,+7,der(8)t(8,?9)(p11,q13),+i(8)(q10),-9,-9,-9,+11,der(11)trp(11)(q14q22)add(11)(q23)x2,-13,-13,i(13)(q10),+14,der(14;17)(q10;q10)x2,der(15,22)(q10;q10)x4,-16,-17,+18,der(18)dup(18)(q11q12)dup(18)(q22q23)x2,+19,add(19)(p13)x2,+20,-21,-21,-21,+3-5mar

Case No. 6 **Squamous cell carcinoma** **Tongue**

45,X,-Y

Case No. 7 **Squamous cell carcinoma** **Larynx**

45,X,-Y

Case No. 8 **Squamous cell carcinoma** **Nasopharynx**

45,X,-Y

Case No. 9 **Squamous cell carcinoma** **Oral cavity**

45,X,-Y

Jin et al 1995, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Salivary gland**

91,XXYY,add(6)(q21),-11,t(11,22)(q13,q11),ins(15,?)(q22;?)/91,XXYY,add(6),-11,add(11)(p11),ins(15;?),der(22)t(11,22)(p11,q11)/91,XXYY,add(6)(q11),-11,add(11),ins(15;?),der(22)/45,X,-Y

Jin et al 1995, Int J Cancer

Case No. 4 **Squamous cell carcinoma** **Nasal cavity/Paranasal sinuses**

46,Y,t(X,11)(p22;q14),add(1)(q21),+der(1)del(1)(p34)add(1)(q32),der(2)add (2)(p13)add(2)(q35),der(3)t(3,8)(q29,q13),add(4)(p16),-6,del(6)(q13),der (8)t(1,8)(p34,q13),der(8)t(2,8)(p13,q21),-12,add(12)(q13),-13,+19,der(20)t (1,20)(p13,q13)add(1)(p36),add(21)(q22),+mar/46,XY,t(1,11)(p13,q13),t(2,5) (q11,q13),t(6,7)(q13,q36),t(6,21)(q31,q22)/47,XY,t(1,16)(q32,p13),del(2) (q13),ins(3,?)(p21,?),t(6,19)(p21,p13),-7,del(7)(q11q22),add(8)(p11),der (9)t(9,13)(q34,q12),inv(10)(p11q22),-13,der(18)t(7;18)(p11,q23),+der(21)t (7,21)(q11,q22),+2mar/45,X,-Y,t(1,7)(p22,p13),del(2)(q31),der(2)t(2,10) (p23;q11),-3,der(3)t(1,3)(q12,q29)del(3)(p12),der(4)t(3,4)(p12,p16),-5,add (8)(q24),-10,del(10)(q24),del(11)(q22),del(12)(p12),del(16)(q22),-20, +5mar/47,XY,t(1,22)(p32,q11),del(4)(p14),del(4)(q25),+r/46,XY,t(2;4) (p13,p16),del(3)(q25),add(5)(p15),del(9)(p21),t(9,20)(q13,q13),t(11,19) (q12,p13),inv(12)(p13q24)

Case No. 5 **Squamous cell carcinoma** **Nasal cavity/Paranasal sinuses**

49,XY,der(6)hsr(6)(p21)add(6)(q23),+7,add(8)(p21),add(8)(q24),+add(13)(p11), der(13)t(11,13)(q13,q34)ins(13;?)(q34,?),i(14)(q10),add(15)(p11),dup(16) (q13q14),-19,+add(20)(q13),add(21)(q22),del(21)(q22),add(22)(q11),+del(22) (q11),+mar/97-102,idemx2

Case No. 6 **Squamous cell carcinoma** **Nasal cavity/Paranasal sinuses**

45,X,-X,del(6)(q15),der(7)t(3,7)(q21,p22)/46,idem,del(5)(q11),+i(5)(q10)

Jin et al 1995, Cancer Res

Case No. 1 **Squamous cell carcinoma** **Oral cavity**

45,X,-Y

Case No. 10 **Squamous cell carcinoma** **Oral cavity**

46-49,X,-Y,-3,der(4)t(4,6)(p11,p11),del(5)(p11),+i(5)(p10),i(8)(q10),add (21)(q22),+2-4mar

Case No. 11 **Squamous cell carcinoma** **Tongue**

72-82,XXX,+X,+i(1)(q10),del(3)(p13p23),del(6)(q23),+7,add(8)(p11),i(8)(q10), del(9)(q22),add(10)(q24),del(11)(p13),+dup(11)(q13q23),+der(12)t(12,13) (q15,q11),-13,add(13)(p11),-14,add(14)(p11),der(14,15)(q10,q10),add(16) (q24),der(16)add(16)(p13)hsr(16)(p13),add(17)(p13),add(20)(q13),-21,+1-2r, +3-14mar,dmin/150,idemx2

Case No. 12 **Squamous cell carcinoma** **Tongue**

46,XX,t(1,3)(p34;q11),add(2)(p11),add(4)(q26),der(16)t(2,16)(p11,p11)ins (16,?)(p11,?)

Case No. 13 **Squamous cell carcinoma** **Tongue**

71-76,XX,-Y,add(1)(q11)x2,add(1)(p1?),+add(1)(p1?),der(2)t(2,3)(p14,p21), +add(3)(p11),i(5)(p10),-8,-8,i(8)(q10),-11,add(11)(q21)x2,add(12)(p13)x2, add(12)(q24),-14,add(14)(p11),+17,add(18)(q23),+der(?)t(?,1)(?,p13)x2, inc/45,X,-Y/47,XY,+Y

Case No. 14 **Squamous cell carcinoma** **Oral cavity**

38-44,XY,i(1)(q10),inc

Case No. 15 **Squamous cell carcinoma** **Oral cavity**

80-91,XXYY,add(1)(q21),del(1)(p13),del(1)(q11),+der(1)t(1,1)(p13-22,q23-25), -2,-2,add(3)(p21-23),-4,add(4)(p?),+del(5)(p11),i(5)(p10)x2,i(8)(q10)x2,add (15)(q22),-22,inc

Case No. 16 **Squamous cell carcinoma** **Tongue**

46,XY,add(1)(p36)/46,XY,der(3)t(3,7)(p13,q11),add(7)(q11),der(9)t(3,9) (p21,p13),add(10)(p15)/46,XY,del(7)(q22q32)

Jin et al 1995, Cancer Res

Case No. 18 **Squamous cell carcinoma** **Tongue**

69-76,XX,-Y,-1,add(2)(q13),-3,-3,der(4;13)(q10,q10),+der(4)t(1,4) (p13;p14)dup(1)(p13p32),-5,der(6)t(5,6)(q15,q15),t(6;?,9)(q11,?;q11),t (6,?13)(q11-14,q12-14),inv(7)(q11q36),add(8)(p11),del(8)(p21),der(8)t(1,8) (q21;p23),-9,-10,add(10)(q22),+add(11)(q13-14),-13,add(13)(p11),-14,add(14) (p11)x2,add(15)(p11),der(15)t(10,15)(q11,p13),del(16)(q23),-17,der(18)t (1,18)(p13;q23)dup(1)(p13p32),-19,+20,-21,?add(21)(q21),der(22)t(6,22) (q15;p12)ins(22,?)(p12,?)x2,inc

Case No. 19 **Squamous cell carcinoma** **Oral cavity**

40-43,X,-X,der(3)t(3,4)(p13,q21),+der(3)t(3,9)(q11,q12),i(3)(q10),-4,der (8;13)(q10;q10),-9,hsr(?11)(q13),-13,-18,+add(19)(p13),-20,-22, +3-5mar/79-85,XX,-X,-X,der(3)t(3,4)x2,der(3)t(3,9)x2,-4,-4,der(8;13)x2,der (9;22)(q10,q10)x2,hsr(?11)(q13)x2,-13,-13,-16,-18,-18,-18,-22,-22,inc/40-42, X,-X,der(3)t(3,4),-4,add(5)(p15),-6,der(9;22)(q10,q10),-13,-13,-18,-18,-19, add(19)(p13),+4mar

Case No. 2 **Squamous cell carcinoma** **Oral cavity**

45,X,-Y

Case No. 20 **Squamous cell carcinoma** **Tongue**

45-48,XX,add(1)(p11),+del(1)(q11),del(3)(p11),-4,add(8)(p11),+i(8)(q10), +del(9)(p13),-11,+mar

Case No. 22	**Squamous cell carcinoma**	**Oral cavity**

40-45,X,-Y,del(1)(p22),der(1)ı(1)(p10)del(1)(p13p22),add(2)(q12),-3,add(3)(q29),add(4)(q12),add(8)(p11),der(15,22)(q10,q10),-21,-22,inc/87-104,ıdemx2

Case No. 23	**Squamous cell carcinoma**	**Oral cavity**

43-159,X,-Y,add(2)(q34),del(7)(q22),i(8)(q10),der(9)t(9,13)(p11,q11),hsr (11)(p12-14),-13,add(19)(q13),add(21)(p?),ınc

Case No. 25	**Squamous cell carcinoma**	**Oro- and hypopharynx**

45,X,-Y

Case No. 26	**Squamous cell carcinoma**	**Oro- and hypopharynx**

45,X,-Y

Case No. 27	**Squamous cell carcinoma**	**Oro- and hypopharynx**

45,X,-Y/47,XY,+Y

Case No. 28	**Squamous cell carcinoma**	**Oro- and hypopharynx**

67-71,X,-X,-Y,add(1)(p11),del(2)(p13),der(2)t(1,2)(p13,q33),-3,der(3)t(X;3)(p11,p13),ı(5)(p10),+i(7)(p10),-8,ı(8)(q10),der(9)t(1,9)(p13-22;p13-22),add(13)(p11),ı(13)(q10),-18,add(19)(p13),+der(?)t(?;1)(?;q11),+der(?)t(?,3) (?,p21),ınc

Case No. 29	**Squamous cell carcinoma**	**Oro- and hypopharynx**

43,X,-X,add(7)(q11),-10,del(11)(q23),-14,add(16)(q13)

Case No. 3	**Squamous cell carcinoma**	**Oral cavity**

47,XY,+Y

Case No. 30	**Squamous cell carcinoma**	**Oro- and hypopharynx**

70,XXY,+Y,der(1)t(1;3)(q23,p23)x2,t(1,14)(q23,q32)x2,add(3)(p11)x2,-6,+8,+9,del(10)(q24),dıc(11,20)(q13,q13)x2,-14,-16,+20

Case No. 31	**Squamous cell carcinoma**	**Oro- and hypopharynx**

70,XY?,del(3)(p12)x2,del(7)(q32),add(13)(p11),?add(17)(p?),add(19)(q13),inc/45,X,-Y

Case No. 32	**Squamous cell carcinoma**	**Oro- and hypopharynx**

46,XY,del(1)(p36)/46,XY,t(2,15)(q21,q15)

Case No. 33	**Squamous cell carcinoma**	**Oro- and hypopharynx**

45,X,-Y

Case No. 34	**Squamous cell carcinoma**	**Oro- and hypopharynx**

63-65,XX,-Y,add(1)(q42),der(1,16)(q10,p10),i(1)(q10),+del(2)(q33),+3,add(3)(p11)x2,-4,-4,i(4)(q10),-5,-6,add(6)(q23),+add(7)(q36),-8,del(9)(q22),der(9)t(1,9)(p13,q11),dic(9,?)ins(9,?)(q11,?),add(10)(p11),der(11)add(11)(q25)trp(11)(q13),del(12)(p11),+13,add(13)(p11)x2,-14,add(14)(p11),-15,add(16)(q22),+add(17)(p11),-18,-19,-19,add(19)(p13),-20,-21,-21,add(21)(p11), -22,inc

Case No. 35	**Squamous cell carcinoma**	**Oro- and hypopharynx**

46,XX,t(2,7)(p25,q32),t(11,19)(q13,q13)

Case No. 36	**Squamous cell carcinoma**	**Larynx**

45,X,-Y

Case No. 37	**Squamous cell carcinoma**	**Larynx**

45,X,-Y

Case No. 38	**Squamous cell carcinoma**	**Larynx**

45,X,-Y

Case No. 39	**Squamous cell carcinoma**	**Larynx**

46,XY,del(1)(q11)/46,XY,t(3,20)(p25,p13),der(6)t(6,?11)(q21,q21),der(16)t(6,16)(q21,p13)

Case No. 4	**Squamous cell carcinoma**	**Oral cavity**

45,X,-Y/47,XY,+Y

Case No. 40	**Squamous cell carcinoma**	**Larynx**

84-90,XXYY,del(2)(p13),der(2)t(X,2)(p11,p14),del(3)(p21),der(3,7)(q10,q10)x2,der(7,12)(p10,q10),del(10)(p11),der(14)t(11,14)(q13;p11),der(14;15)(q10,q10),i(14)(q10),+der(?)t(?,16)(?,q11),+der(?)t(?;18)(?,q11),inc

Case No. 41	**Squamous cell carcinoma**	**Larynx**

46,XX,t(13,17)(q32;p11)

Case No. 42	**Squamous cell carcinoma**	**Larynx**

73,XX,+X,-Y,+1,+add(1)(p35),?der(1,19)(q10;q10)x2,+del(5)(p14),-6,+8,+9,+12, -13,add(14)(p11),-15,+17,-18,-18,+19,?der(20)hsr(20)(q11)add(20)(q11), +2mar/45,X,-Y

Case No. 43	**Squamous cell carcinoma**	**Larynx**

46,XY,t(7,10,15)(q11,p11q26;p11)

Case No. 5 **Squamous cell carcinoma** **Oral cavity**

46,X,-X,+der(1,15)(p10,q10),-2,add(6)(q21),der(7)t(7,21)(p11,q11),der(9)t(2,9)(p15,p22),-10,add(11)(q21),-12,-13,der(14)t(7,14)(p13,q32),-15,-16,+18, +20,-21,der(22)t(11,22)(q13,p1?),+r,+4mar

Case No. 6 **Squamous cell carcinoma** **Oral cavity**

42-45,XY,del(1)(q22q24),der(1)t(1,4)(p36,q11),add(2)(p16),+add(2)(q11),add(3)(p25),-4,ins(6,?)(q1?,?),t(7,9)(p10,q10),-8,-16,+der(?)t(?,11)(?;q14), +1-2mar/45-46,XY,del(1)(q12),del(1)(q23),+2,add(3)(p26),-4,add(5)(p15),del(6)(q15),der(7)t(1,7)(q31,q31),del(12)(q13),add(13)(q22),-17,+1-2mar

Case No. 7 **Squamous cell carcinoma** **Oral cavity**

50-54,XY,i(8)(q10),inc

Case No. 8 **Squamous cell carcinoma** **Tongue**

76-87,XXXX,-1,-3,-3,+i(5)(p10),del(8)(p11),i(8)(q10),-17,del(18)(q21),-19, -19,-19,-20,inc

Case No. 9 **Squamous cell carcinoma** **Tongue**

73-77,XXY,+6,i(8)(q10),inc/88-101,XXYY,+Y,del(3)(p11),i(8)(q10),+9,der(11)t(1,11)(p11,p11),i(11)(q10),inc/115-142,XY?,i(8)(q10),inc

---

Jin et al 1995, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Oesophagus**

73-74,XXY,+1,der(1,5)(q10;q10),del(4)(p14),+del(4)(q23),-5,der(5)t(1,5)(q25,p15),der(6)t(6;22)(p23,q11)ins(6,?)(p23,?),+der(6)add(6)(p21)del(6)(q23),+add(7)(p15),-8,-8,-8,+11,der(11)hsr(11)(q13)dup(11)(q14q23)x2,-13,idic(13)(p13),-14,der(15)t(?9,15)(p13,p13),+16,-17,-21,-22,inc/133-144,idemx2,add(3)(q11),add(3)(p11),der(13)t(1,13)(q23,p11)ins(13;?)(p11,?),inc

---

Jin et al 1998, Genes Chromosomes Cancer

Case No. 1 **Squamous cell carcinoma** **Oral cavity**

54-58,X,+der(X)t(X,9)(p11,q13)ins(X,?)(p11;?),-Y,der(1)t(1,1)(p13,q25),der(2)t(2,3)(p16,q11)ins(2,?)(p16,?),+der(2)t(2,7)(q11,p11)ins(2,?)(q11,?),+der(4)inv(4)(p13q21)t(4,7)(q21,p13),der(5,22)(q10,q10),+i(5)(p10),+del(6)(q13),+ins(7,?)(q22;?),der(8)t(8;8)(p23,q22),+der(8,21)(q10,q10)x2,-9,-10,add(11)(q24),der(11)t(10,11)(q11,p11),+der(11)t(11,16)(q13,q11)hsr(11)(q13),der(13)t(1;13)(p13,p13)x2,del(14)(q24),i(15)(q10),+i(19)(q10),+20,+add(22)(p11),+2mar

Case No. 11 **Squamous cell carcinoma** **Oral cavity**

45,XY,der(3,17)(q10,q10)/45,idem,der(13)t(3,13)(p21,p11)/62-69,XX,-Y,-1,-2, add(2)(p11),-3,der(4)t(4,11)(p11,q13)hsr(11)(q13)add(11)(q13)x2,-5,-6,der (7)add(7)(p15)add(7)(q32),-8,+9,add(9)(q11)x2,add(10)(p11),-11,-11,-11,add (12)(q24),-13,add(14)(p11),+der(14)t(11,14)(q13,p11)hsr(11)(q13)add(11) (q13),add(15)(q15),-16,+17,+der(17,21)(q10,q10),-18,-19,add(19)(p11),-21, -22,-22,-22,+der(?)t(?,3)(?,p11),+der(?)t(?;13)(?,q13)x2,+6mar

Case No. 12 **Squamous cell carcinoma** **Oral cavity**

42-43,X,-Y,del(2)(q33),del(3)(p12),-4,+add(5)(q11),der(8)t(8,8)(p11;q13), der(9)t(9,10)(p24,q11),-10,-14,der(17)t(?16,17)(q13,q23)/85-86,idemx2,-der (9),+9,+9

Case No. 13 **Squamous cell carcinoma** **Oral cavity**

91-106,XX,+der(X)t(X,11)(p11,q13)hsr(11)(q13)add(11)(q13),+der(X,1) (q10;q10)x2,-Y,-Y,add(1)(q11),der(1,7)(p10;p10),-2,del(3)(p11),+der(3,5) (q10;p10)x3,-4,del(4)(q27)x2,der(4)t(4,13)(q13,q11),add(7)(q11)x2,+add(7), +der(7,14)(p10,q10)x2,ins(7,?)(q11,?)x2,+8,+8,+der(8)t(6,8)(q11,q24),+9,+9, +der(9,12)(q10,q10),der(10;22)(q10,q10)x2,-11,del(11)(p13),add(12)(q13), +ins(12,?)(q13,?),add(14)(q32),der(14)t(11,14)(q13,p11)hsr(11)(q13)add(11) (q13),-15,der(15,19)(q10,p10),+17,+19,+20,+20,+der(20)t(11,20)(q13,p13)dup (11)(q21q13)add(11)(q13),+21,+22

Case No. 15 **Squamous cell carcinoma** **Oral cavity**

58-61,XXX,-1,-2,-3,add(3)(p11),i(3)(p10),-4,-5,-6,-7,-7,-8,der(8)t(5,8) (q11,q22),add(9)(p24),+der(9)?t(9,12)(p13;q21),-10,-10,-11,-12,der(12)t (?3,12)(q13,q15),-13,-14,-15,der(15,21)(q10,q10),der(16)t(8,16)(q11,p11), der(16)t(?15,16)(p13,q12),add(17)(p11),-18,-19,-21,-22,+der(?)t(?,1) (?,q12)add(1)(q34),+6-8mar

Case No. 2 **Squamous cell carcinoma** **Oral cavity**

68-70,XX,-Y,+der(1)t(1,1)(p13,q25),dup(3)(q29q11),i(3)(q10),-4,del(5)(p11), +der(5;17)(p10,q10)x2,+i(5)(p10)x2,+7,+der(7,22)(p10,q10)x2,+8,i(8)(q10),-9, -10,add(11)(q1?),-12,-13,add(13)(p11)x2,-14,+15,add(15)(p11)x2,-16,-17,+18, der(18)t(9;18)(q13-22,q21-23)x2,-19,add(19)(p12)x2,+20,-22,+mar

Case No. 3 **Squamous cell carcinoma** **Larynx**

40-44,X,-Y,add(1)(p11),+der(1)t(1;8)(q11,q13)hsr(1;8)(q11,q13),add(2)(p21), der(3)del(3)(p11p23)ins(3,11)(p11,q13q13)hsr(11)(q13),der(5)t(5,22) (p11,q11),der(8;21)(q10,q10),der(9)t(9,15)(p13,q15),der(11;17)(p10,q10),-13, -15,-15,-18,-19,-21,-22,-22,inc/40-44,idem,-der(3),+der(3)del(3)ins (3,11)hsr(11)t(3,4)(p26,q21)ins(3,?)(p26,?),-16,add(16)(p13)

Case No. 4 **Squamous cell carcinoma** **Tongue**

37-48,X,-Y,del(3)(p11),add(4)(p11),-6,add(7)(q22),-10,-11,-13,der(13,16) (q10,p10),der(14)t(11;14)(q13,p11)hsr(11)(q13)add(11)(q13),add(16)(p11),-18, -19,add(19)(q13),-21,-22,inc/37-48,idem,-del(3),+der(3,15)(q10,q10),-15

Case No. 6	Squamous cell carcinoma	Tongue

68-71,XXY,del(1)(p13)x2,der(1)hsr(1)(p32)add(1)(p32),-2,-3,-4,-5,-7,-8,-10, der(11)del(11)(q13)hsr(11)(q13),+der(11)hsr(11)(q13)add(11)(q13),-13,-13, add(14)(q24),add(15)(p11),der(15)t(3,15)(q12,p11),add(18)(p11),der(18)t (1,18)(p22,p11),-19,-21,+3mar,inc

Case No. 9	Squamous cell carcinoma	Oro- and hypopharynx

39-42,X,-Y,der(1;21)(q10,q10),add(3)(p11),del(3)(p11),+der(3,4)(q10,q10)del (3)(q26),del(8)(p22),-9,-10,der(11)add(11)(q13)hsr(11)(q13),der(13,14) (q10,q10),der(14,22)(q10,q10),add(15)(p11),+20/82-83,idemx2

Jin et al 1999, Genes Chromosomes Cancer

Case No. 1	Squamous cell carcinoma	Skin

45,X,-Y/47,XY,+7/70-78,XX,-Y,t(1,4)(p32,p16),i(8)(q10),inc

Case No. 10	Squamous cell carcinoma	Skin

44-45,X,-Y

Case No. 11	Squamous cell carcinoma	Skin

47,XY,+18

Case No. 12	Squamous cell carcinoma	Skin

42-47,XX,add(1)(p36),der(8,21)(q10,q10),+2mar

Case No. 13	Squamous cell carcinoma	Skin

45,X,-X

Case No. 2	Squamous cell carcinoma	Skin

75-78,XXY,der(1;19)(p10,p10),i(1)(q10),i(1)(p10),+3,der(3)t(3,3)(p13,q22)x2, +i(5)(p10)x2,+add(7)(q11)x2,+8,i(8)(q10)x2,der(9,?14)(q10,q10),-10,+11,+12, -13,-16,-18,+20,-21,-21,add(21)(p?),+3-15mar

Case No. 3	Squamous cell carcinoma	Lip

59-69,XX,-X,+i(1)(q10),der(2)t(1,2)(p31,q12),add(4)(p11),der(4)hsr(4) (p11)add(4),-5,add(7)(q11),-8,-9,add(9)(p22),-10,add(11)(p15)x2,del(11) (q21),+del(11),-13,-13,-14,-15,-16,-18,-21,-21,-21,-22,-22,+3-6mar,inc

Case No. 4	Squamous cell carcinoma	Skin

46,XY,t(2,10)(p24,q23),?ins(4,4)(q25,q?q?)/47,XY,+18/46,XY,t(1;1) (p36,q25)/46,XY,t(2,12)(p13,q24)/45,X,-Y,t(7;18)(q36,q11)/46,XY,inv(11) (p15q13)/47,XY,+7/46,XY,inv(11)(q14q25)/46,XY,t(1,18)(q21,p11),t(5,16) (q13,p13)

Case No. 6 **Squamous cell carcinoma** **Skin**

44-48,Y,-X,del(1)(q12),inc/46,XY,t(1,2)(q32,q37)/46,XY,i(8)(q10)/45-46,XY, inv(11)(q21q25),add(14)(q24),add(18)(q21),+mar

Case No. 7 **Squamous cell carcinoma** **Skin**

88-98,XXYY,+1,der(1,3)(q10,q10)x1-2,add(1)(q10)x1-2,add(3)(p13),-4,i(5) (q10),+6,+6,-7,+8,i(8)(q10)x2-3,+9,+10,+10,-11,-13,-15,+16,-17,der(17,21) (q10,q10)x3,-18,-18,-19,-19,+20,-21,-22,inc

Case No. 8 **Squamous cell carcinoma** **Skin**

45-46,XY,t(2,3)(q31;q28)/92,XXYY,t(1,15)(p32,q22)

Case No. 9 **Squamous cell carcinoma** **Skin**

45,X,-Y,hsr(12)(p13)/45,X,-Y,der(12)hsr(12)add(12)(p13)/44,X,-Y,der(12)hsr (12)add(12),-22/37-46,X?,add(2)(p23),der(9)hsr(9)(p22)add(9)(p22),hsr(12)

Jin et al 2000, Genes Chromosomes Cancer

Case No. 10 **Squamous cell carcinoma** **Larynx**

45,X,-Y/46,idem,+3/46,XY,t(6,8)(q27,q13),t(7,11,15)(p11;q11,q15)/46,XY,t (2,6)(q33,q21)

Case No. 11 **Squamous cell carcinoma** **Larynx**

46,XY,der(2)t(2,6)(q33,p11),t(3;7)(p13,q11),der(6)inv(6)(p11q15)t(2,6)/46, XY,t(2,15)(q37,q22)/46,XY,add(1)(p34),+der(?)t(?,1)(?,p34)

Case No. 12 **Squamous cell carcinoma** **Larynx**

45,X,-Y

Case No. 13 **Squamous cell carcinoma** **Larynx**

43-45,X,-Y,+3,-13

Case No. 14 **Squamous cell carcinoma** **Larynx**

57-78,XXY,del(1)(p11p32),+del(1),t(1,9)(q25;p13)x2,del(2)(q33),add(4) (p11)x2,add(4)(p15),+add(4)(p15),-5,-5,-5,t(6,11)(p21;q13)x2,add(8)(p11),+9, -11,del(12)(q22)x2,der(13)t(?3,13)(q12,p11),+14,i(14)(q10)x2,+16,-17,der (17,19)(q10,p10)x2,+19,+19,+add(19)(p13)x2,-20,-21,-22,+hsr(?)x2,inc

Case No. 15 **Squamous cell carcinoma** **Larynx**

44,XX,add(1)(p33),add(2)(q23)

Case No. 16 **Squamous cell carcinoma** **Larynx**

46,XX,t(2,3)(p25,q21)

Case No. 17 **Squamous cell carcinoma** **Larynx**

40-43,X,-Y,del(1)(p32),del(2)(q3?1),add(3)(p13),+i(3)(q10),del(4)(p14),-5, add(11)(q13),-13,add(13)(q34),-14,-14,-15,i(15)(q10),-16,-17,-19,-21,-21, +4mar,inc

Case No. 18 **Squamous cell carcinoma** **Larynx**

60-65,XX,-X,add(1)(p12),der(1)add(1)(p35)hsr(?),-2,-3,add(4)(p11),-5,-5,+7, -10,der(10,22)(q10,q10),+der(11)t(5,11)(q11,p12),der(15;21)(q10;q10)x2,+16, -17,-21,inc

Case No. 19 **Squamous cell carcinoma** **Larynx**

75-83,XXX,+X,+2,+3,i(3)(q10)x2,-5,add(7)(q11),+8,+8,+9,+9,+10,der(11)add (11)(q13)hsr(11)(q13),der(12)t(7,12)(q11,p13)ins(12,?)(p13,?)x2,+13,add(13) (q14)x2,-14,-14,-15,-17,-18,+19,+20,-21,+2-3mar

Case No. 2 **Squamous cell carcinoma** **Larynx**

45,X,-Y,t(4,16)(p13,p11),inv(12)(p11q22),add(14)(q22)

Case No. 20 **Squamous cell carcinoma** **Larynx**

43-46,X,-X,del(2)(q33),del(3)(p11),i(3)(q10),-4,add(7)(p22),der(8,21) (q10,q10),del(11)(q23),add(22)(p11),+3mar

Case No. 22 **Squamous cell carcinoma** **Larynx**

47,XY,+20

Case No. 23 **Squamous cell carcinoma** **Larynx**

46,XY,add(1)(p22),+del(1)(q11),-2,del(3)(p21)x2,-5,dup(5)(q21q35),del(6) (q15),+7,+8,add(11)(p15),+del(11)(q14),add(12)(q24),der(12)t(3,12)(q12,p13), add(13)(p11),+add(13)(q34),der(13,22)(q10;q10),der(14,22)(q10,q10),+i(14) (q10),-19,+20,-21,+add(22)(p11)

Case No. 24 **Squamous cell carcinoma** **Larynx**

45,X,-Y/46,XY,t(1,4)(q11,p15)

Case No. 25 **Squamous cell carcinoma** **Larynx**

45,X,-Y/92,XXYY,del(3)(q21)

Case No. 26 **Squamous cell carcinoma** **Larynx**

47,XY,+20

Case No. 27 **Squamous cell carcinoma** **Larynx**

46,XY,t(2,3)(p23,p21),t(3,7,6)(q21,q36,q22)/81-86,XX,-Y,-Y,-1,inv(1)(p11p36),del(2)(p21)x2,del(3)(q26),der(3)t(3,?5)(p21,q13),-4,del(4)(p1?),+5,?i(5)(p10)x2,del(7)(q31)x2,i(8)(q10)x2,add(9)(q34)x2,-10,-10,add(11)(q21)x2,+der(11)add(11)(q13)hsr(11)(q13),-12,-12,i(12)(q10),-13,-13,der(13,14)(q10,q10)x2,-14,add(15)(p11),-18,-18,-21,-21,?add(21)(p11)x2,-22,inc

Case No. 28 **Squamous cell carcinoma** **Larynx**

50,XX,i(1)(q10),der(3;10)(p10,q10),i(8)(q10),add(10)(p11),add(11)(p11)x2,der(15)t(15,15)(p11,q11),der(16)t(?11;16)(q13;p11)hsr(?11)(q13)del(11)(q21),i(17)(q10),inc

Case No. 3 **Squamous cell carcinoma** **Larynx**

46,XY,t(2,7)(q23,p13),add(3)(q29),der(4)t(4,8)(p11;p21),t(6;19)(p25,p12),del(8)(p21),add(16)(q11)

Case No. 30 **Squamous cell carcinoma** **Larynx**

45,X,-Y

Case No. 31 **Squamous cell carcinoma** **Larynx**

47,X,-Y,+7,+mar/48,idem,+mar/49,idem,+r,+mar/47,XY,t(1;6)(p21,q25),+9

Case No. 34 **Squamous cell carcinoma** **Larynx**

78-81,XX,+X,-Y,+1,+2+i(3)(q10),+5,?i(5)(p10)x2,der(6,9)(p10,q10)x1-2,+7,+i(9)(q10),+10,+11,add(11)(q23)x2,+12,-13,der(13)t(13;13)(p13,q12)x2,+14,+16,+17,del(17)(p11)x2,+19,+20,-21,+22/76-80,idem,der(X)t(X,2)(q28;q13)/75-81,idem,der(X)t(X;2),add(7)(q32)/77-79,idem,der(X)t(X,2),add(13)(p13)

Case No. 35 **Squamous cell carcinoma** **Larynx**

41-44,X,-Y,der(1,11)(p10,q10),+i(1)(q10),add(2)(q37),del(2)(q33),der(3)t(3;7)(p11;p12),i(3)(q10),add(6)(q1?),der(7)t(?2,7)(q14,p22),-8,-9,der(9,13)(q10,q10),add(11)(q24),-14,-18,-21,-22,?add(22)(p11),+2mar,inc

Case No. 37 **Squamous cell carcinoma** **Larynx**

46-50,X,-Y,add(1)(q44),del(2)(p11),+der(2)t(2;3)(q11,q11)ins(2,?)(q11,?),del(3)(q11),der(3;21)(q10,q10),der(4)t(4,5)(q21;q13-15),add(5)(q13),add(6)(p11),+del(7)(q31)x2,i(8)(q10),del(9)(p22)x2,+del(9),i(11)(q10),der(13,14)(q10,q10),?del(14)(q22),+15,+15,-18,?add(18)(p11),+20,-21,+add(22) (p11)/85-89,idemx2,-add(1),der(1,15)(p10,q10),+ider(1)(q10)add(1),-del(7)x2, -del(9),-10,i(10)(q10),-15,-15,+?add(18),-19,-20

Case No. 38 **Squamous cell carcinoma** **Larynx**

45,X,-Y

Case No. 39 **Squamous cell carcinoma** **Larynx**

45,X,-Y/90,idemx2

Case No. 4 **Squamous cell carcinoma** **Larynx**

46,XY,t(2,18)(q23,p11),t(4,13)(p11,p11),add(6)(q21),add(17)(q21)/45,idem, -Y/46,XY,-1,t(4,17)(q21,p13),t(5,14)(q31,q32),der(6)t(1,6)(q11;q27),inv(6)(p21q21),-7,t(9,11)(q22,p15),t(12,17)(p11;p11),t(16;16)(p11,p13),der(19)t(7,19)(q11,q13),+der(?)t(?,1)(?,p22),+r

Case No. 40 **Squamous cell carcinoma** **Larynx**

42-46,XY,t(1,4)(p36,q21),-3,del(3)(p12),ider(3)(q10)t(3;8)(q25,q22),-4,der(4)t(4,17)(q35,q12),add(5)(p13),del(6)(q23),i(8)(q10),+9,der(9,15)(q10;q10),del(10)(p11),der(11)add(11)(q13)?hsr(11)(q13),del(13)(q22),+der(16)del(16)(p11)t(3,16)(p23,q22),-17,-19,-21,-22,+r,+mar

Case No. 41 **Squamous cell carcinoma** **Larynx**

70-72,XXY,add(1)(p11),+del(1)(p22),der(2,3)(q10,p10),+add(3)(p11),+add(3)(p12),der(3,15)(q10;q10),?i(5)(p10),+del(7)(q22),+11,add(19)(q13),+20,inc

Case No. 42 **Squamous cell carcinoma** **Larynx**

39-40,XY,del(3)(p13),-4,-5,i(6)(p10),add(7)(q11),-8,-9,-10,-11,der(12;14)(q10,q10),add(14)(p11),del(16)(q13),-18,-21,-22,+4mar/59-61,XXY,add(1)(p11),del(3)(p13),+?i(3)(q10),?i(5)(p10),i(6)(p10),der(12,14),add(15)(p11),del (16),inc

Case No. 43 **Squamous cell carcinoma** **Larynx**

94-96,XXXX,+der(?)t(?,1)(?,p13),inc

Case No. 5 **Squamous cell carcinoma** **Larynx**

45,X,-Y,t(1,7)(q44,p15),add(2)(p11),der(6)t(2,6)(p14,p11),der(10)t(6,10)(p11,p13),der(19)t(Y,19)(q11,q12)

Case No. 6 **Squamous cell carcinoma** **Larynx**

96-98,XYY,-X,-2,add(3)(p11)x2,-6,-7,-8,-9,del(9)(p11),-10,-11,del(11)(q21),+13,+13,-14,?i(16)(q10)x2,+20,-21,+5mar,inc

Case No. 7 **Squamous cell carcinoma** **Larynx**

47,XY,+18/45,X,-Y/47,XY,+Y

Case No. 8 **Squamous cell carcinoma** **Larynx**

40-45,XY,-2,-2,-8,der(8)t(3,8)(p11;q24),-9,-10,-10,-11,der(11)t(6,11)(p12,p15),add(12)(p?),-13,ins(14,?)(q11,?),-15,-17,-18,-18,+r,+6mar,inc/46, X,-Y,t(1,2)(p32;p11),t(2;5)(q21,q22),+7,del(10)(p11)

Case No. 9 **Squamous cell carcinoma** **Larynx**

87,XXYY,-1,del(3)(p11)x2,+del(3)x2,t(3,18)(q12,q23)x2,-4,+5,der(5,22)(q10,q10),?i(5)(p10)x2,der(8,14)(q10,q10)x2,del(9)(p22)x2,-10,-10,-13,-15,i(15)(q10),-19,+del(20)(q11),-21,-21,-21,+der(?)t(?;12)(?;q22)/87,idem,add(21)(p11)/89,XXYY,-1,del(3)x4,+der(3)t(3,18)x2,-4,+5,der(5,22)x2,?i(5)(p10)x2,+8,der(8,14)x2,del(9)x2,-10,-10,-11,-15,i(15)(q10),-18,der(18)t(3,18)(q12,q23),-19,del(20)x2,-21,-21,-21,+22

Jin et al 2000, Chromosoma

Case No. 2 **Squamous cell carcinoma** **Oral cavity**

54-56,X,+add(X)(p11),-Y,+del(3)(p12),del(5)(p11),+ı(5)(p10),+7,+9,+10,der(10,22)(q10,q10),+der(11)t(8,11)(q22,q21)x2,+12,del(13)(q22),ı(14)(q10),+mar/54-56,ıdem,add(7)(q11),+8/54-56,ıdem,+i(8)(q10)/54-56,ıdem,del(8)(p10)/54-56,idem,add(8)(p10)

Jin et al 2002, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Oral cavity**

45,XX,der(3,13)(q10,q10),?del(13)(q21)/47,XX,der(3,13),+5,ı(7)(p10),+9,add(10)(q26),der(14)t(7,14)(q11;p13)/47,X,t(X,13)(q11,p11),der(3,13),+5,ı(7)(p10),+9,add(10),der(14)t(7,14)/48,XX,der(3;13),+5,del(6)(q16),ı(7)(p10),+9,add(10),der(14)t(7,14),+?der(18)t(5;18)(q11-12;q11-12)/47,XX,der(3,13),+5,ı(7)(p10),+9,t(11,12)(q25,q12),der(14)t(7;14)/48,XX,der(3;13),+5,ı(7)(p10),+9,der(11)t(11;12),der(12)t(12,18)(q11-12,q11),der(14)t(7,14),+del(18)(q11)/88,XXXX,add(1)(q21),-2,der(3;13)x2,+5,+ı(5)(p10),+6,ı(7)(p10),-8,+9, +9,-10,-10,-12,-16,-18,+20,-22,+3mar/96,XX,-X,add(X)(p11),der(1;7)(q10,p10)x2,+der(1,14)(p10,q10),+ı(1)(p10),-2,-3,ı(3)(q10),-4,+der(5)t(5,15)(q33,q21),+der(6)t(6,13)(q11,q14)x2,+7,+7,+8,+8,+8,+9,+9,der(10)t(10,11)(q22,q12),-11,+12,-13,i(14)(q10)x2,-15,add(16)(q12),+17,-18,der(18)t(9,18)(q12,p11)ıns(18,?)(p11,?),+20,+20,+20,-21,-22

Case No. 10 **Squamous cell carcinoma** **Larynx**

63-66,Y,-X,der(X)t(X;11)(p22,q13),add(1)(p11),der(1,8)(q10,q10),-2,der(3,4)(q10,q10)add(4)(q35),+der(3)t(1,3)(p22;p11)ıns(3;?)(p11;?),-5,-6,add(6)(q13),der(6)t(1,6)(p13,q23),+der(7)add(7)(p11)add(7)(q36),del(8)(p21),-9, -10,der(10;14)(q10,q10),der(11)t(1,11)(p13,q22),+?ıns(11)(p15q25q22),add(13)(q22),+der(13)t(5;13)(q32,q31),add(16)(p13),-17,-18,-18,-19,-19,del(20)(q11),-21,add(21)(p13),-22,-22,inc/63-66,Y,der(X)t(X;11),?ı(X)(q10),add(1),der(1,8),-2,der(3)t(1,3)ıns(3,?),-4,-5,-5,-6,add(6),der(6)t(1,6),del(8),-9, -10,der(10;14),+der(11)t(1;11),?dup(12)(q23q24),der(13)t(5,13),der(13)i(13)(q10)t(13,13)(p11,q34),-15,add(16),-17,-17,-18,-18,-19,-19,del(20)(q11),-21,add(21),-22,-22,+2mar,inc

Case No. 11 **Squamous cell carcinoma** **Larynx**

39,XX,-3,del(4)(p11),der(5,15)(p10,q10),del(6)(q15),der(8)t(8,11)(p21,q13)trp(11)(q13q23)t(11,11)(q23,q13),-9,der(11,?21)(p10,q10),der(12)t(12,?19)(p11,q11)add(12)(q24),der(13)t(13,14)(p11,q24),-14,der(16)del(16)(q21)t(16,17)(p13,q21),+der(16)t(13,16)(q14,p11)add(16)(q13),+der(16)t(3,16)(q12,q13),-17,del(17)(q21),-18,-19,-21,-22,ı(22)(q10),+mar/79-80,idemx2/39-41,idem,-der(5,15),add(21)(p11)/81-82,idemx2,-der(5;15)x2,add (21)x2

Case No. 12 **Squamous cell carcinoma** **Larynx**

39-43,X,-Y,add(1)(q44),-3,der(5)t(3,5)(q12,p1?5)ins(5,?)(p1?5,?),add(6)(q11),der(7;?)dic(7,?)(p22;?)hsr(7)(p22),-8,-9,add(9)(q34),-10,-11,-12,-14,+15,add(15)(p11)x2,del(16)(q22)x2,add(18)(q12),+3mar/85-87,XX,-Y,-Y,add(1),-3,der(5)t(3,5)ins(5,?),add(6),der(7;?)dic(7,?)hsr(7),-8,add(9),-11,-12,add(15),del(16)x2,-17,add(18),inc/46,XY,t(1,9)(q25,p22)/46,XY,t(9,12)(q22,q13)/46,XY,i(17)(q10)/86-89,XX,-Y,-Y,der(1;?8)(q10,q10)x2,inc/46,XY,t(1;8)(p12,p21)/46,XY,t(1,9)(q22,q22)/45,XY,add(3)(p23),+mar/46,XY,t(9,15)(q32,q15)/46,XY,t(12,15)(p10,p10)

Case No. 13 **Squamous cell carcinoma** **Larynx**

60-66,X,i(X)(q10),-Y,der(1)t(1,7)(q21;p13),+?2,-3,add(3)(p11),del(3)(p11),del(3)(p21),-4,-4,add(4)(p14),-5,add(5)(p13),der(5)t(?1,5)(p34,p15),+6,+7,der(7)t(3;7)(p21;q36)x2,+der(7)t(3,7)add(7)(p22),der(8)t(8,8)(p23,q22),-9,-9,der(10,14)(q10,q10),?del(11)(q13),der(11)t(1,11)(q21,q13)hsr(11)(q13),-12,add(12)(p11),-13,add(13)(p11),der(13)t(3,13)(q21,q34),add(14)(q32),+?hsr(14)(p11),-15,add(15)(p11),-16,+16,add(16)(q24),-17,-17,-18,-19,-20,-20,-22,?add(22)(p11),+der(?)t(?,8)(?,q13),+hsr(?),+mar,2-3dmin,inc

Case No. 14 **Squamous cell carcinoma** **Oral cavity**

47-52,XY,add(1)(q22),del(2)(p11),i(3)(q10),add(5)(q11),+add(8)(p11),-9,der(10,22)(q10,q10),+del(11)(p11),+der(11)t(9,11)(q13,p11),+der(16)t(1,16)(q12;q11)del(1)(q41),der(18)t(1,18)(p11,p11),+der(20)t(5,20)(q13,q13),-22,+mar/100-101,idemx2,add(6)(q11)x2,+7,der(7)add(7)(p11)inv(7)(q22q36)x2,+der(?)t(?,4)(?,q11)/44-53,XY,der(1)t(1,11)(p11,q25),del(2),i(5)(p10),add(6),-7,+add(8),-9,-10,del(11),der(11)t(9,11),+der(18)t(1;18),-19,+der(20)t(5,20)

Case No. 15 **Squamous cell carcinoma** **Oro- and hypopharynx**

42-62,XY,-X,del(1)(q12),i(1)(q10),-2,i(3)(q10),-4,?i(5)(p10),-6,der(6)add(6)(p12)?hsr(?),der(11)add(11)(q13)?hsr(?),der(11)del(11)(p13)del(11) (q11q13),-12,-13,der(13)t(13;13)(p13,q12),-14,-14,-15,add(15)(p11),-18,-21,-22,inc/46,XY,t(1,1;15)(p13,p35,q12)/46,XY,t(5,9)(q33,q12)/46,XY,t(1;3)(q11,q22)/61-63,-X,add(X)(p11),-Y,-1,der(1)t(1,?7)(q42,p15),i(3)(q10),-4,-5,i(5)(q10),-6,+add(7)(q11),+add(8)(p21),+der(9,21)(q10,q10)x2,-10,der(11)add(11)?hsr(?),del(11)(q11q13),-13,der(13)t(13,13),der(13;15)(q10,q10),-14,der(14,22)(q10,q10),i(14)(q10),-15,add(15),del(16)(q22)x2,idic(16)(p11),+idic(16),add(17)(p11),-18,der(19)add(19)(p13)?hsr(?),der(22)add(22)(q13)hsr(22)(q13),+der(?)t(?,11)(?,q13)t(?,15)(?,q11),+r/69-74,-X,-X,-Y,del(3)(q11),i(3)(q10),+4,-6,add(7),+del(7)(q32),add(8)x2,+add(8)(q24),+i(8)(q10),+der(9,13),+der(9,21),der(11)add(11)?hsr(?)x2,+der(11)t(11;13)(q25,q11-12),der(13)t(13,13),-14,-14,-14,+15,add(15)x2,+16,+16,+17,+18,+20,-21,-22,-22/58-59,-X,del(X)(p22),-Y,del(1)(q12),i(1)(q10),-2,i(3)(q10),der(4,22) (q10,q10),i(5)(p10),-6,-7,add(8),+9,der(9,21),der(11)add(11)?hsr(?),der (11)del(11)del(11),-12,-13,der(13)t(13,13),i(14)(q10),+del(16),-18,-21,add (21)(p11),-22,-22,+5mar/45,X,-Y/55-58,add(X),-Y,der(1)t(1,?7),+i(1)(q10),+2,+7,+der(7;22)(p10,q10),+add(8),+9,der(9,21),del(10)(p11),del(11)(q11q13),+der(11)add(11)?hsr(?),+12,der(13)t(13,13),der(13,15),der(14;22),i(14)(q10),+add(15)x2,del(16),+idic(16),+der(19)add(19)?hsr(?),+20,+22,+22

Jin et al 2002, Cancer Genet Cytogenet

Case No. 16	**Squamous cell carcinoma**	**Oro- and hypopharynx**

35-39,X,-Y,der(1)del(1)(p11p13)t(1,?22)(p13,q11),add(2)(q33),der(3,13)(q10,q10),der(4)t(4,15)(q31,q14),+der(4)t(4,8)(q31,q13),-7,-8,-9,-9,der(11)add(11)(q13)hsr(11)(q13),del(12)(p12),-13,add(14)(p11),-15,del(16)(q22),-19,-21,-22,+der(?)t(?,1)(?,p21),inc/75-76,XX,-Y,add(1)(p10),add(1)(q11),der(1)del(1)t(1,22),+i(1)(p10),+2,add(2)x2,+3,der(3,13)x2,der(4)t(4,15),+der(4)t(4,8)x2,+5,+add(6)(q21),-7,-8,-9,-9,-9,-10,+10,+del(11)(q23),der(11)add(11)hsr(11)x2,+del(12),-13,-14,add(14),-15,add(15)(p11),+16,del(16)x3,+17,-19,+19,+20,-21,+der(?)t(?,1)x2,+2mar,inc

Case No. 17	**Squamous cell carcinoma**	**Oral cavity**

84-90,XXXX,-1,dup(1)(q32q42) or dup(1)(q42q44),-2,+i(5)(p10)x2,del(8)(p21)x1-2,+i(8)(q10),i(9)(q10),+del(12)(q1?3q2?2),-13,-15,-16,-17,-18,-18,-19,-21,-22,+r,+mar/84-90,idem,+9,-i(9)(q10)/83-92,idem,+2,-3,-4,-12,-del(12),+17,add(19)(q13)x2,+22,-r,-mar,inc

Case No. 18	**Squamous cell carcinoma**	**Oral cavity**

75-76,X,-X,-Y,add(1)(p11),+add(2)(q35),add(3)(p11),-4,-4,-5,+del(7)(p13),del(8)(p11),+i(8)(q10),der(11)t(?4;11)(q13,q23),-13,-13,add(14)(q32),+16,-17,-17,-18,-19,der(20)t(3;20)(q11,q13)ins(20,?)(q13;?),-22,inc/70-79,X,-X,-Y,add(1),+add(2),add(3),-4,-4,add(4)(p?),-5,+6,+7,del(8),+i(8)(q10),+add(9)(p11),-11,-13,-13,-14,add(14),+15,+16,-17,-17,-18,-19,der(20)t(3,20)ins(20,?),-22,inc

Case No. 19	**Squamous cell carcinoma**	**Oral cavity**

77-79,der(X)t(X,15)(p22,q12)x2,-Y,+1,add(2)(q35),+3,del(3)(p11)x2,der(4)t(4,12)(q13,q11),ins(4,?)(q31,?),+5,i(5)(p10)x2,der(8;15)(q10,q10)x2,der(8)t(?1,8)(p34,q24),+der(8)t(?1,8),+add(9)(p11),+add(9)(q22)x1-2,-10,-10,-10,+11,+11,add(11)(q21)x3,-12,+13,+14,-15,+16,add(18)(q21),+20,add(20)(q13)x2,-21,+22,+2mar

Case No. 3	**Squamous cell carcinoma**	**Oral cavity**

42-43,X,-X,der(2)t(2,?17)(q35,q21),del(3)(p14),del(5)(q15),-6,i(7)(p10),i(8)(q10),-17,add(17)(q21),-18,der(20)t(7,20)(q11,q12)ins(20,?)(q12,?),-21,+2mar/44-45,XX,der(1)inv(1)(q25q42)t(1;15)(p12,q11),der(1,13)(q10,q10),del(3),i(8)(q10),der(15)t(1;15)(p21,q11),-18,-19,+der(?)t(?,1)(?,p11)/46,XX,t(5,11)(q13,q25),?del(13)(q22)/42-43,X,-X,der(2)t(2,?17),del(3),del(5),i(7)(p10),i(8)(q10),add(17),-18,der(20)t(7,20)ins(20,?),-21/44-45,XX,der(1)inv(1)t(1,15),der(1;13),del(3),-6,i(8)(q10),add(9)(p22),add(14)(p11),der(15)t (1,15),-18,-19,+der(?)t(?;1)/44,XX,der(1)inv(1)t(1,15),del(3),del(6)(p12)i(8)(q10),add(9),der(10)t(?9,10)(q21,p11),-13,der(15)t(1,15),-18,-19,+2mar

Case No. 4	**Squamous cell carcinoma**	**Tongue**

51,X,+add(X)(p11),-Y,+del(3)(p12),+9,+10,der(10,22)(q10,q10),+der(11)t(8,11)(q22,q21)x2,+12,ı(14)(q10),-22,+mar/52-53,ıdem,+add(7)(q11),del(13)(q22),+22,+mar/54-55,ıdem,+ı(7)(p10),+14,+22/53-55,ıdem,+ı(7)(p10),+i(8)(q10),+22/52-54,ıdem,+?ı(5)(p10),+7,der(11)t(5;11)(q11,p11),-14,+der(14,22)(q10,q10),+mar/53-55,ıdem,+?ı(5)(p10),+add(7)(p11),der(11)del(11)(p11)ıns(11,?),der(12)add(12)(q15)add(12)(p11)ıns(12,?)(q15,?),+22/94-107,ıdemx2,+?i(5)(p10),+7,+7,der(12)add(12)add(12)ıns(12,?)x2,+22,+22/54-56,X,+add(X),-Y,+del(3),+?ı(5)(p10),+7,+del(8)(p12),+9,+10,der(10,22),+add(11)(q21)x2,+12,del(13),i(14)(q10),+mar

Case No. 5	**Squamous cell carcinoma**	**Tongue**

42-44,XY,add(3)(p21)x2,ı(5)(p10),der(10)t(8,10)(q22;q24),ı(11)(q10),?ıns(12,?)(q13,?),add(14)(p11),der(19)t(17;19)(p13,q21),add(21)(p13)/82-87,ıdemx2,-Y,+1,+?add(1)(p?32),der(1,9)(p10,q10)x2,-6,add(7)(q21),t(8;8)(p2?3,q?11),add(10)(p11),ı(13)(q10)x2,dıc(15;15)(p11;p11),-17,-17,-18,-18, -22,-22,ınc/42-82,XXY,?add(1),add(3)x2,ı(5)(q10),ins(12;?),ı(13)(q10),add(15)(p13),der(19)t(17,19),ınc/46,XY,t(1,3)(p35;p21)

Case No. 6	**Squamous cell carcinoma**	**Tongue**

64-69,X,-X,-Y,+1,dıc(1,12)(p34,q24),+add(2)(p23),ı(3)(q10),-4,add(5)(q11),ı(5)(p10),+del(7)(q22),-8,i(8)(q10),-9,-11,+13,der(13)t(13,13)(p11,q14)ıns(13,?)(p11,?)x1-2,der(14)t(14;?17)(p13,q11),-15,+add(16)(p13),-17,-17,-18, -19,-19,+20,-21,der(21)t(?11,21)(p12,p11)x2,-22,+hsr(?),+3mar/64-65,ıdem, -dic(1,12),+add(1)(p13),-6,-12,-der(14)t(14;?17),+3mar/66-71,X,-X,-Y,+ıdıc(1)(p11),+2,ı(3)(q10),+5,add(5)(q11)x2,del(7),ı(8)(q10),-9,-11,-12,+13,der(13)t(13,13)ıns(13,?),-15,-16,-17,-17,-18,-19,-19,+20,-21,der(21)t(?11,21),+6mar

Case No. 7	**Squamous cell carcinoma**	**Tongue**

66-68,X,-X,-X,add(1)(q21)x2,+der(1)dup(1)(p13p34)t(1,?8)(q25,q12),-2,ı(3)(q10),+ı(5)(p10),+6,der(8,14)(q10,q10)x2,+ı(8)(q10),+?add(9)(q13),i(9) (q10)x2,-10,der(10,13)(q10,q10),der(11,15)(q10,q10),der(12)t(4,12)(q12,p11)ıns(12;?)(p11,?)hsr(?),add(13)(p11),+add(14)(p11),-17,-18,-19,?add(20)(q11),-21,-21,+5mar/66-68,idem,+X,-6,-6,+mar,inc/134-149,idemx2,+2mar,inc

Case No. 8	**Squamous cell carcinoma**	**Larynx**

45,X,-Y/47,XY,+7

Case No. 9	**Squamous cell carcinoma**	**Larynx**

45,X,-Y/46,XY,add(21)(p13)

Jin et al 2002, Cancer Genet Cytogenet

Case No. 3A **Squamous cell carcinoma** **Skin**

46,XX,t(4,19)(q33,q11)/92,ıdemx2

Jin et al 2004, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Oesophagus**

53-62,XX,-Y,+del(1)(p22),-2,+der(3,9)(q10,q10),der(4)t(4,11)(p13,q13)hsr (11)(q13),del(5)(q14),+der(7,19)(q10,q10),der(8)t(8,12)(p22,?),-9,-9,-10, der(10,18)(q10,q10),-11,del(11)(p13),-12,add(14)(p11),der(15)t(11,15) (q13,p11)hsr(2,11)(?,q13)t(2,12)(?;q15),+der(16)t(14,16)(q14,q12),-17,-18, add(18)(p11),+der(20)t(8,20)(q13,q13),-21,ı(21)(q10),der(21,22)(q10,q10), -22,+r/45,X,-Y

Case No. 2 **Squamous cell carcinoma** **Oesophagus**

47,X,der(Y)t(Y,17)(q12,q11),+2,ı(3)(q10),dup(6)(q22q27),+7,der(8)t(8,19) (q24,q11),+der(8,13)(q10,q10)x3,der(9,21)(p10,q10),der(11)dup(11) (q14q23)hsr(11)(q13),+ı(14)(q10),ıder(14)(q10)t(9,14)(q12,q24)x2,-17,add (22)(q?)

Case No. 3 **Squamous cell carcinoma** **Oesophagus**

67,XY,-X,+Y,+2,i(3)(q10),-4,-5,der(6,17)(p10,q10)add(17)(q25),del(6)(q13), +7,+7,+ı(8)(q10),+9,del(9)(p22)x2,-10,add(12)(p13)x1-2,-15,-17,-18,-19,-21, -22

Case No. 4 **Squamous cell carcinoma** **Oesophagus**

65-69,XY,i(X)(p10)x1-2,del(1)(q11q25),der(1;16)(q10,p10),dıc(1;7)(p12,p22), -3,-4,der(5;9)(q10,q10),add(7)(q36)x2-4,-9,-10,-10,-11,ı(11)(q10),-12,-13, -13,-14,-15,-18,-18,+add(19)(q13),+20,-21,-22,ınc/100-110,XYY,ı(X)(p10)x2, del(1)(q11q25)x2,add(1)(p11)x2,add(3)(p11)x1-2,der(4)add(4)(q31)hsr(4)(q31), -5,+7,add(7)(q36)x3-4,-8,-8,-8,-9,-10,-10,-10,-11,-11,i(11)(q10),-12,-12, -13,-13,-14,-14,-15,-15,-16,-17,-18,-18,-18,add(19)(q13),-21,-21,-22,-22, ınc/107-117,XXY,+der(X,15)(p10,q10),+ı(X)(p10)x2,add(1)(p11)x4,+del(1)x2, dıc(1;7),der(2;8)(q10,q10)x2,add(3)(p11)x2,del(3)(q21),-4,der(4)add(4) (q31)hsr(4)(q31)x2,add(5)(p11),i(5)(p10),+dıc(5,13)(q13,p13)x2,+7,add(7)x4, -8,-9,-9,-10,-10,-10,-11,-11,ı(11)(q10),-12,-12,-13,add(14)(p11)x3,-15,+16, -17,-18,-18,-18,+add(19)x2,+20,-21,?i(21)(q10),-22,-22,+r,ınc

---

Jin et al 2005, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Tongue**

80-83,X,t(X;2)(q28;q33),-Y,-Y,-1,+2,der(3)t(3,7)(p25,q11),i(3)(q10)x2,-4,ı (8)(q10)x2,-14,-14,-16,-18,-18,-19,-21,+2mar

80-81,XXY,der(1)t(1,2)(q21,p13)add(1)(p36)x2,der(2)t(1,2)x2,der(2)t(2,11) (p11,p11)t(2,15)(q37,q22)x2,ı(3)(q10)x2,der(3)t(3;7)x2,ı(8)(q10)x2/74-80,XX, -Y,der(1)t(1;1)(q44,q13),der(1)t(1,2)(q21,p13)t(1,3)(p36,q21),der(2)t (1;2)x2,der(2)t(2,11)t(2,15)x2,add(3)(p11),+der(3)t(3,7)x2,ı(3)(q10)x2,+5, +add(7)(q11),+8,i(8)(q10)x1-2,+9,+10,+der(11)t(2,11),+12,t(13;19)(q14;q13), der(15)t(2,15),-18,+19,+add(20)(p13)

Case No. 10 **Squamous cell carcinoma** **Oro- and hypopharynx**

65-70,XX,-X,+add(1)(p36),+del(1)(q11),der(1;?12)(q10,p10),ınv(1)(p36q25), der(2)t(2,14)(p21,q13),+add(3)(q12)x2,der(3)t(3,9)(p11,q13)x2-3,der(4)t (4,?10)(p16,q22)add(4)(q35)x3,-5,+7,-8,der(8)t(8;13)(p23;q14)x2,der(8,9) (q10,q10),+9,+9,-10,-10,+der(11)t(3,11)(q21,q13)hsr(3,11)(q21,q13),+ı(13) (q10),-14,der(14)t(7,14)(p11,p11)ıns(14,?)(p11,?),i(14)(q10),-15,-15,ı(15) (q10),-16,add(16)(p13),-18,-18,-20,-21,add(21)(p11),ıdic(22)(p1?2),+2mar

65-67,XX,-X,der(1;?12),+ınv(1),der(2)t(2,14),add(3)+add(3),der(3)t(3,9)x2, der(4)t(4;?10)add(4)x3,-5,+7,der(8)t(8,13)x2,der(8,9),+9,-10,+der(11)t (3,11)hsr(3;11)x2,-14,der(14)t(7,14)ıns(14,?),ı(14)(q10),-15,-15,ı(15)(q10), -16,-18,-18,-21,add(21)x2,idıc(22),+mar

Case No. 11 **Squamous cell carcinoma** **Oral cavity**

86-93,XXY,-Y,-2,del(3)(p12)x2,-4,-5,-5,i(6)(p10),-8,ı(8)(q10),+del(9) (p11)x1-2,-10,del(10)(p11)x1-2,i(10)(q10),+11,+11,+del(11)(q13),-12,der (13)t(?3,13)(q12,q22)ıns(13;?)(q22,?),+add(15)(q22),-17,-18,-18,-19,+20,-21, -22,-22,+der(?)t(?,2)(?,q21),+4mar/87-91,XXY,-Y,-2,del(3)x2,-4,-5,-5,del(5) (q13q22),ı(6)(p10),-8,ı(8)(q10),del(9),-10,del(10)x1-2,+11,+11,der(13)t (?3,13)ıns(13,?),+14,+add(15),-17,-18,-18,+19,+20,+20,-21,-22,-22,+der(?)t (?,2),+4mar

86-92,XXY,-Y,del(3)x2,-4,-5,-5,ı(6)(p10),ı(7)(p10),-8,-8,ı(8)(q10),+9,-10, del(10)x1-2,ı(10)(q10),+11,+del(11)(p11),-13,der(13)t(3,13)ins(13,?),-18, -18,-19,+20,-21,-22,+5mar

Case No. 12 **Squamous cell carcinoma** **Oral cavity**

57-60,X,der(X)t(X;15)(p11,q13),-Y,add(1)(q11),der(1,3)(q10,p10),+der(1)t (1,?6)(p22,q21),add(2)(p21),-3,del(3)(q21),ı(3)(q10),-4,-4,der(4,14) (q10,q10),-5,-6,del(6)(q21),add(7)(q32),del(7)(q22),+der(7)t(5,7)(q11,p22), add(8)(p11),-9,-10,der(11)add(11)(q13)hsr(11)(q13),add(12)(q13),-13,-14,-14, add(14)(p11),-15,-15,add(16)(q2?),del(16)(q22),-18,add(18)(q21),-19,-21,-21, -21,-22,-22,inc

55-62,X,der(X)t(X;15),-Y,add(1),der(1,3),+der(1)t(1,?6),+add(2),-3,del(3),ı (3)(q10),-4,der(4,14),-5,-6,del(6),add(7),+der(7)t(5,7),add(8),-9,-10,add (12),-13,-14,-14,-15,-15,add(16),del(16),-18,add(18),ınc

Case No. 2 **Squamous cell carcinoma** **Larynx**

46,XY,del(1)(q42),add(4)(p16),del(9)(q32),t(9,11)(q22,q13),add(10)(q26),add (17)(q25)/46,XY,del(1)(q42),t(1;14)(q25,q22),der(6)t(6,16)(p21,q22),add(12) (p12),der(16)add(16)(p12)t(6,16),add(17)(q11),der(17)t(16,17) (q12-13,q11-21)add(17)(p11),add(19)(q13)

41-43,X,+i(X)(p10),-Y,add(1)(p11),add(3)(p11),der(3)t(3,?10)(q27,q22),-4, der(4)t(4;8)(q35,q22),-5,-7,der(7)t(7,7)(p11,q31),-8,der(8)t(2,8)(p14;p23), -9,-9,-10,add(10)(p11),-11,add(13)(q32),-14,-15,der(16)t(11;16)(q13,q13)der (11)t(11,11)(q25,q13)ins(11,?)(q13,?),+der(16)del(16)(p12)t(11,16)t (11,11)ins(11,?),-18,-18,-19,add(20)(p11),-21,-22,+der(?)t(?;1)(?,q21),+der (?)t(?,3)(?,p11)t(3,5)(p26,q11),+der(?)t(?,7)(?,q11),+5-7mar

Case No. 3 **Squamous cell carcinoma** **Tongue**

43-44,XY,dic(1;11)(q10,p11),der(3,19)(q10,q10),ins(4,?)(p14,?),del(6)(q15), i(6)(p10),+i(6)(q10),i(8)(q10),-11,-12,der(13,14)(q10,q10),-14,del(16)(q13), -17,-18,-19,-21,+der(?)t(?,1)(?,p22),+1-2mar/45,Y,add(X)(q13),del(1)(p13), der(1)t(1;7)(q44;p15),t(2,9)(p11,q34),der(7)t(1;7)(p13,p13),der(13)t(13;14) (p11;q13),-14/45,XY,t(11,18)(q23,q21),t(12;16)(q11,p11),der(13)t(13,14) (p11,q13),-14

40-44,XY,dic(1;11),der(3,19),ins(4,?),del(6),i(6)(p10),+i(6)(q10),i(8)(q10), -11,-12,der(13,14),-14,del(16),-17,-18,-19,-21,+der(?)t(?,1),+1-2mar/46,X,t (Y;6)(q12;q21),t(1;7)(p36,p15),add(5)(p13),inv(7)(p13q36),t(8,9)(q22,q34), del(10)(p13),add(11)(p15),t(12,19)(q15,q13)

Case No. 5 **Squamous cell carcinoma** **Oro- and hypopharynx**

58-65,X,-X,-Y,add(1)(p11),add(1)(q11),+i(1)(q10),-2,add(2)(p11),-3,der(3)t (3,3)(p13,q22),-4,+add(5)(q11)x2,der(5,17)(p10,q10),der(5)t(3;5)(p21;p15), del(7)(p15),der(7)t(3,7)(q11,q22)ins(7,?)(q22,?),-8,-9,-10,add(10)(p11),-11, -12,-13,add(13)(p11),-14,add(14)(p11),-15,add(16)(q22),del(16)(q22),del(18) (q12),+der(18)t(11,18)(q13,p11)hsr(11,18)(q13,p11)add(11)(q13),-19,-20,-21, -21,-22,+der(?)t(?,X)(?,q11),+der(?)t(?,11)hsr(11)(q13)add(11)(q13),+r, +3mar

58-65,X,-X,-Y,add(1)(p11),add(1)(q11),+i(1)(q10),-2,add(2),-3,der(3)t(3,3), -4,+add(5)x2,der(5,17),der(5)t(3;5),del(7),der(7)t(3;7)ins(7;?),-8,-9,-10, add(10),-11,-12,-13,add(13),-14,add(14),-15,der(15,18)(q10,p10),-16,add(16), del(16),del(18),+der(18)t(11;18)hsr(11;18)add(11),-19,-20,-21,-21,-22,+der (?)t(?,X),+der(?)t(?,11)hsr(11)add(11),+r,+3mar

Case No. 6 **Squamous cell carcinoma** **Larynx**

65-73,X,add(X)(p11),der(X)t(X,14)(q22,q24),+der(1)t(1,8)(p21,q21),t(1,5) (p21,q35),del(3)(p23p25),add(4)(q34),-6,i(8)(q10),-9,add(11)(p11),der (11)add(11)(q13)hsr(11)(q13),+der(11)t(9,11)(q13,q13)hsr(9;11)(q13,q13),-12, -13,der(13,22)(q10;q10),-14,add(14)(q22),-15,add(15)(p?),-16,add(17)(p13), dic(18,?)(q23,?),-19,-20,-21,+1-5mar

66-68,X,-X,add(X),+der(1)t(1,8),t(1,5),del(3),del(4)(p11),-6,-7,-8,i(8) (q10),-9,-9,-10,add(11),der(11)add(11)hsr(11),+der(11)t(9;11)hsr(9,11),-13, -13,-13,-14,add(14)(p11),-15,-15,add(17)(p11),+20,-21,-21,-21,+8-15mar

Case No. 7	Squamous cell carcinoma	Tongue

31-53,X,-Y,-5,+7,+del(8)(p11)x2,-9,+11,+add(11)(q23)x2,add(13)(p11),i(14)(q10),add(17)(q25),-18,-19,+20,inc

---

Johansson et al 1995, Cancer Genet Cytogenet

Case No. 1	Squamous cell carcinoma	Lung

128,XY,add(1)(p32-34),del(3)(p12p24)x4,del(3)(q13q26-28),i(5)(q10),add(6)(q15-16),del(6)(p22),add(9)(q34),der(10)t(4,10)(q11,p15),add(14)(p11),+22,add(22)(p?)x2,dmin,inc

Case No. 10	Squamous cell carcinoma	Lung

45,X,-Y

Case No. 11	Squamous cell carcinoma	Lung

45,X,-Y

Case No. 12	Squamous cell carcinoma	Lung

45,X,-Y

Case No. 13	Squamous cell carcinoma	Lung

45,X,-Y

Case No. 14	Squamous cell carcinoma	Lung

45,X,-Y

Case No. 15	Squamous cell carcinoma	Lung

45,X,-Y

Case No. 16	Squamous cell carcinoma	Lung

45,X,-Y

Case No. 17	Squamous cell carcinoma	Lung

47,XY,+Y/45,X,-Y

Case No. 18	Squamous cell carcinoma	Lung

45,X,-Y/47,XY,+7

Case No. 19	Squamous cell carcinoma	Lung

47,XY,+r

Case No. 2 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 20 **Squamous cell carcinoma** **Lung**

45-48,X,add(X)(q21),+der(1,18)(q10;q10),+2,der(2)t(2,3)(q37,q21)x2,add(3)(p25),-4,del(11)(p11),+12,add(15)(q2?),del(15)(q22),-18,add(20)(p13),-22

Case No. 21 **Squamous cell carcinoma** **Lung**

53-64,XY,-X,del(1)(q21),der(7)t(7,7)(p21,q11),der(11)t(4,11)(q25;p15),add(13)(p?),add(20)(p13),inc

Case No. 22 **Squamous cell carcinoma** **Lung**

60-67,XY,-X,+Y,der(1)hsr(1)(p13)add(1)(p13),der(1,2)(q10,q10),+i(1)(q10),-3,-4,i(5)(p10),i(6)(p10),+add(7)(p13),-8,der(9,15)(q10,q10),-10,hsr(10)(q26),der(11)t(8;11)(q21;p15),-12,-13,-14,-15,-15,-16,hsr(16)(p13),add(17)(q25),+add(17),der(17)del(17)(q23)t(1,17)(p13,p11)del(1)(p32p35)x2,-19,-20,-21,add(21)(p13),+1-8mar/130-134,idemx2

Case No. 23 **Squamous cell carcinoma** **Lung**

65-70,XX,-Y,-1,del(1)(p13p32),+der(2)t(2;11)(p25;q13),-4,del(6)(q15),del(7)(q32),-9,-10,der(13,15)(q10,q10),add(14)(p?),der(?)t(?,1)(?,q12)x2, +1-5mar/45,X,-Y

Case No. 24 **Squamous cell carcinoma** **Lung**

70-75,XX,inc

Case No. 25 **Squamous cell carcinoma** **Lung**

80-87,XY,inc

Case No. 26 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 27 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 28 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 29 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 3 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 30	Squamous cell carcinoma	Lung
	45,X,-Y	
Case No. 31	Squamous cell carcinoma	Lung
	45,X,-Y	
Case No. 32	Squamous cell carcinoma	Lung
	45,X,-Y	
Case No. 33	Squamous cell carcinoma	Lung
	45,X,-Y	
Case No. 34	Squamous cell carcinoma	Lung
	45,X,-Y	
Case No. 35	Squamous cell carcinoma	Lung
	45,X,-Y	
Case No. 36	Squamous cell carcinoma	Lung
	45,X,-Y	
Case No. 37	Squamous cell carcinoma	Lung
	45,X,-Y	
Case No. 38	Squamous cell carcinoma	Lung
	47,XY,+7/45,X,-Y	
Case No. 39	Squamous cell carcinoma	Lung
	45,X,-Y/47,XY,+20	
Case No. 4	Squamous cell carcinoma	Lung
	45,X,-Y	
Case No. 40	Squamous cell carcinoma	Lung
	47,XY,+r	
Case No. 41	Squamous cell carcinoma	Lung
	43-64,XY,del(1)(p13),der(1)t(1,8)(p13,q11),i(5)(p10),add(12)(p13),add(16)(q24),inc/45,X,-Y	
Case No. 42	Squamous cell carcinoma	Lung
	56-60,X,add(X)(p22),-Y,add(1)(p36),add(3)(q29),del(3)(p21),-4,del(5)(q13q33),del(5)(p12p14),add(6)(p23),+der(7)hsr(7)(p15)add(7)(q22),-9,add(11)(p15),add(12)(q24),inc	

Case No. 43 **Squamous cell carcinoma** **Lung**

59-62,add(X)(q22),der(X)t(X,8)(q21-22,q13),-Y,add(1)(p13),add(2)(p21),add (3)(q11),der(3)dup(3)(p23p25)add(3)(q21),+der(3)dup(3)(p23p25)del(3)(q21), -4,-5,add(6)(q11),-7,der(7)t(7,9)(p11,q13)ins(7,?)(p11;?),-8,-9,-10,add(11) (p11),-12,add(12)(p13),-13,add(13)(p?),-14,add(14)(p?),-15,-16,-17,-18, +2-5mar/45,X,-Y

Case No. 44 **Squamous cell carcinoma** **Lung**

66-68,XX,-Y,-4,-4,del(5)(q13),del(6)(p21),+7,+8,del(8)(p21)x2,add(9)(p11), der(9,15)(q10,q10)x2,dup(10)(q24q26),+11,-13,i(13)(q10),add(16)(q13)x2,+17, del(17)(p11)x2,add(18)(q23),-19,-21,-22,+1-2mar

Case No. 45 **Squamous cell carcinoma** **Lung**

62-64,XXY,-1,der(2)t(1,2)(q21,q24),-3,-6,i(6)(p10),+7,dic(8,19)(p11,p11),-9, der(11)t(7;11)(q11,p11),add(12)(p12),-13,-14,-15,-16,add(17)(p11),-18, +1-3mar/44-46,X,-Y,-1,der(2)t(1,2),-6,i(6)(p10),dic(8,19),add(17),+1-3mar

Case No. 46 **Squamous cell carcinoma** **Lung**

63-70,X,-X,i(X)(q10),del(1)(p22),+del(1)(q41),+add(2)(p11),-3,-6,+7,+7,-8, +9,+10,der(12)t(3,12)(q11,p13)ins(12)(p13),-13,der(14,15)(q10,q10),-15,add (16)(p13),+17,der(17)t(9,17)(q11,p11)x2,inc

Case No. 47 **Squamous cell carcinoma** **Lung**

67-73,XXY,+Y,i(3)(q10),+i(5)(p10),-6,+7,+8,+9,der(9)t(6;9)(p21,p12)x2,-10, +11,add(11)(q13)x2,+12,-13,+14,add(15)(q24),-17,+19,+20,add(20)(p13)x2,-21, -22,+2-5mar

Case No. 48 **Squamous cell carcinoma** **Lung**

65-74,XX,-Y,add(1)(p11),?del(1)(q42),der(3;7)(q10;q10)x2,inc

Case No. 49 **Squamous cell carcinoma** **Lung**

62-82,XY,inc

Case No. 5 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 50 **Squamous cell carcinoma** **Lung**

70-85,XXY,del(3)(p13),der(3)del(3)(p13)add(3)(q29),i(5)(p10),del(6)(q25), inc

Case No. 51 **Squamous cell carcinoma** **Lung**

78-91,XXY,-Y,add(1)(p34),der(1)t(1,12)(p34,q13)ins(1;?)(p34;?),+i(5)(p10), der(11)qdp(11)(q13q25)add(11)(q25),inc

Case No. 52 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 53 **Squamous cell carcinoma** **Lung**

51-58,XY,del(2)(p21),del(7)(p13),del(7)(q22),der(8)t(2,8)(q21;q24)ins(8,?)(q24,?),add(12)(q24),der(12)t(1,12)(q21,p13),der(13,14)(q10,q10),add(14)(p11),add(16)(q24),inc/45,X,-Y

Case No. 54 **Squamous cell carcinoma** **Lung**

57-65,XX,-Y,add(1)(q44),der(1)del(1)(p11)add(1)(q44),+dic(1,17)(q24,p12),+del(3)(q13q26),+dic(5,12)(p15,q22),+del(7)(q11),add(8)(p21),t(9,9)(p24,q13),+der(10)t(10;21)(p11,q11),add(14)(q32),add(15)(q26),add(16)(p13)x2,+20,inc/114-130,idemx2

Case No. 55 **Squamous cell carcinoma** **Lung**

74-80,-X,hsr(X)(q28),Y,+Y,+del(1)(p34)x2,+dic(2,22)(p23,p11),-3,add(3)(q12)x2,-6,add(7)(p15),+dic(7,7)(p22,p22),hsr(7)(p22),der(8)t(8,11)(p22,q12),+i(8)(q10),-10,+del(11)(p11-13),add(13)(p13)x3,+der(13,15)(q10;q10),add(14)(p?),-15,i(15)(q10),-18,inc

Case No. 56 **Squamous cell carcinoma** **Lung**

63-83,XY,inc

Case No. 6 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 7 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 8 **Squamous cell carcinoma** **Lung**

45,X,-Y

Case No. 9 **Squamous cell carcinoma** **Lung**

45,X,-Y

Kumari et al 1995, Indian J Cancer

Case No. 1 **Squamous cell carcinoma** **Nasopharynx**

45-47,XY,add(2)(p12),add(3)(q27),t(4,11)(p?,q23),-9,+11

Case No. 2 **Squamous cell carcinoma** **Nasopharynx**

46,XX,del(3)(p24)/47,idem,-9,-9,+10,-12,+15,+2mar

Lee et al 1987, Cancer Res

Case No. 8	**Squamous cell carcinoma**	**Lung**
	47,XX,+7/47,XX,+9	
Case No. 9	**Squamous cell carcinoma**	**Lung**
	47,XY,+7	

Lese et al 1995, Genes Chromosomes Cancer

Case No. 13	**Squamous cell carcinoma**	**Oral cavity**
	44-45,XX,-21	
Case No. 16	**Squamous cell carcinoma**	**Tongue**
	58-75,XX,-X,add(1)(p21),+del(1)(p22),+del(1)(q21),-2,-4,-5,-7,-7,-8,-9,i(9)(q11),der(10)t(7,10)(p11,p11),+hsr(11)(q13),-12,-13,-14,-14,-18,-18,-20,+3mar/41-55,X,-X,+add(1),+del(1)(p22),+del(1)(q21),-2,+3,+i(3)(q10),+4,-7, -8,-8,i(9)(q11),-10,der(10)t(7,10),+11,+hsr(11),-12,-13,-14,+16,+19,-20,-21,+22,+2mar	
Case No. 2	**Squamous cell carcinoma**	**Tongue**
	81-84,XXX,-X,del(1)(p33),der(1)t(1;12)(p11,p11)t(1,11)(q25;q13),der(1)t(1,19)(q44,q11)ins(1;?)(q44,?),-2,-3,-3,-4,der(4)t(4,14)(q11,q11),-5,del(5) (p11),-6,-6,der(6)t(6,10)(q11,q11)x2,-7,-8,del(8)(p21),del(9)(q21q31),-10, -10,-13,-14,der(14)t(6,14)(?q15,p12),-15,-16,-17,-18,-18,+19,+20,+20,-21, +22,+5mar	
Case No. 29	**Squamous cell carcinoma**	**Oral cavity**
	75-80,XY,-X,del(1)(p22),+2,der(3)t(3,15)(p11;q11)x2,+i(3)(p10),+5,-6,+7,der(7)t(7;14)(q11,q11)x2,+der(7)t(3;7)(q11;q11),+der(7)t(6,7)(p11;q11),+8,-9,+11,der(11)del(11)(q13q23)hsr(11)(q13)x2,+12,+13,-14,-14,-14,-15,del(15)(q24),+16,i(16)(q10)x2,+17,-18,add(18)(q21),+19,+20,+i(20)(p10),-21,der(21)t(14;21)(q11,p11),-22/81-84,XXY,-Y,del(1),-3,der(3)t(3;15)x2,-5,-5,-6,der(7)t(6,7)x2,+der(7)t(7;14),+der(7)t(3,7),-8,-8,-9,-9,-10,-10,hsr(11)x2, -12,-14,-14,-14,-15,del(15)x2,i(16)(q10)x2,+17,-18,add(18)x2,+i(20)(p10), -21,-21,der(21)t(14,21),-22	

Case No. 3	**Squamous cell carcinoma**	**Oral cavity**

38-42,X,-X,+2,-3,-4,-4,i(5)(p11),-8,-9,-10,-10,der(11)hsr(11)(q23)add(11) (q25),-12,-13,i(13)(q10),-14,-15,add(15)(p11),+16,-18,-20,-21,der(21)t(14,21)(q11;p11),-22,+4mar/76-79,XX,-X,+1,+2,-3,-4,+i(5)(p11),+7,-9,+der(11)x2,+i(13)(q10)x2,add(15),+18,+19,der(21)x2,+3mar/83,XX,-X,-X,-2,-3,-3, -4,-4,-4,-4,+i(5)(p11),-6,-8,-9,-9,-10,der(11)x2,-12,-12,-13,-13,i(13) (q10)x2,-14,-14,-14,-15,-15,-15,add(15),-17,-20,-21,-21,-21,der(21),-22,-22, +7mar

Case No. 30	**Squamous cell carcinoma**	**Tongue**

60-72,X,-X,-Y,+del(1)(p22),-2,-3,+der(3)t(3;4)(q11,q12),-5,der(6)t(3;6)(q11,q11),+7,-8,+9,+10,+11,del(11)(q21)x2,-12,-13,-14,-14,-15,add(15)(p11), -16,der(16)t(5,16)(q14,p13),-17,-17,-18,-18,-19,-21,-22,+2mar

Case No. 44	**Squamous cell carcinoma**	**Tongue**

71-80,XX,-X,+2,del(3)(p21),-4,+5,-7,-8,+9,i(9)(q11)x2,del(10)(p11),+11,+der(11)del(11)(q14)hsr(11)(q13)x2,+12,-13,-13,-13,der(14)t(14,21)(p11,q11),-15,der(15)t(15,22)(p11,q11),-16,-17,-18,+19,-20,-21,add(21)(p11)x2,-22,-22,+6mar/81-84,X,-X,-X,-X,del(1)(p21),+del(1)(q11),+3,del(3)x3,-4,-6,-7,-7,-8, -8,-9,i(9)(q11),-10,-10,del(10)(p11),der(11)del(11)hsr(11)x2,+12,-13,-13, -13,-13,der(14)t(14,21)x2,-15,-15,-15,der(15)t(15,22),-17,-18,-18,-19,-20, -21,-21,-21,add(21),-22,-22,-22,+8mar

---

Sozzi et al 1991, Cancer Res

Case No. 1	**Squamous cell carcinoma**	**Lung**

46,XY,del(3)(p21p23)/46,idem,t(12,14)(q13,q32)/91,XXYY,del(3),t(12,14),t(11,14)(p15;q12),t(11,15)(p15,q15)

Case No. 10	**Squamous cell carcinoma**	**Lung**

49,XY,add(3)(p25),+del(3)(p14),+add(7)(p?),+mar

Case No. 12	**Squamous cell carcinoma**	**Lung**

45,XY,inv(2)(p22p24),add(3)(q?),-8

Case No. 15	**Squamous cell carcinoma**	**Lung**

46,XY,del(3)(p14p23)

Case No. 2	**Squamous cell carcinoma**	**Lung**

46,XY,t(3;15)(q13;q26)/46,XY,t(3,20)(q13,q13)

Case No. 9	**Squamous cell carcinoma**	**Lung**

85,XXYY,del(3)(p14p23),inc

Teixeira et al 1999, Cancer Genet Cytogenet

Case No. 10	**Squamous cell carcinoma**	**Vagina**

42-44,X,-X,add(1)(q23),add(3)(p11),del(4)(q31),del(6)(q15),add(9)(q34),del(10)(q24),del(11)(q23),del(16)(q22),del(18)(q21),inc/84,idemx2

Case No. 3	**Squamous cell carcinoma**	**Vagina**

47,XX,+18

Case No. 5	**Squamous cell carcinoma**	**Vagina**

43-47,X,-X,ins(3;?)(p11,?),add(4)(q12),der(11)t(4,11)(q13,q22),+r

Case No. 7	**Squamous cell carcinoma**	**Vagina**

84-87,XXXX,+der(1)del(1)(p22)del(1)(q32)x2,-3,-3,del(4)(q21),i(5)(p10),-7,add(8)(p21),del(8)(p21),-10,add(11)(q25)x2,-14,-14,-15,-17,-17,-17,-18,add(19)(q13),+1-4mar

Case No. 9	**Squamous cell carcinoma**	**Vagina**

47,XX,+7

Testa et al 1994, Genes Chromosomes Cancer

Case No. 41	**Squamous cell carcinoma**	**Lung**

51-64,X,-X,add(1)(q21-22),del(3)(p21),+i(3)(q10),der(8,14)(q10,q10),der(8,21)(q10,q10),-9,add(9)(p2?4),-10,del(11)(p13),+12,add(12)(q24)x2,der(14)t(8;14)(q11,p11-12)ins(14,?)(p11-12,?),+der(14)t(3,14)(p23,p11-12)ins(14,?)(p11-12,?),+i(14)(q10),der(15)t(15,16)(p12-13,q11),-16,-19,-20,+der(?)t(?,11)(?,q11),+11-16mar

Case No. 42	**Squamous cell carcinoma**	**Lung**

50-56,XY,+add(X)(p11),del(1)(q12),+der(1,9)(p10,q10),der(2)t(2,5)(q13;p11-12),+der(2)t(1;2)(q?12,q21)ins(2,?)(q21;?),-3,add(3)(p12),-4,add(4)(p15-16),+der(5,22)(p10,q10),+der(7)t(1,7)(q?12,q11)ins(7,?)(q11;?),+der(7)t(7,7)(q11;p11)ins(7,?)(q11,?),+der(7,10)(q10,q10),i(7)(p10),-8,-10,+der(12)t(3,12)(q2?1,q24),-13,add(15)(p11),del(15)(q22q24),+del(17)(p11)x2,-18,+der(19)t(8,19)(q11,q13)x2,der(20)t(3,20)(q13-21,q13),add(22)(p11),+add(22)(p12),+6-9mar

Case No. 43	**Squamous cell carcinoma**	**Lung**

50-68,XXY,der(1)t(1,5)(p32,q13),der(1)del(1)(p13)del(1)(q42),-2,-3,add(3)(p12),add(4)(p12),-5,add(5)(p13),-7,der(7)t(7,7)(p15-21,q11)ins(7,?)(p15-21,?),-8,-8,-8,-9,-9,-10,-11,-11,del(11)(q14),add(12)(p13),add(12)(q24)x2,-13,-13,add(13)(q22),-14,-14,-15,add(15)(p1?2),-16,-16,-17,-17,-17,-18,add(19)(q13),+der(19)t(17,19)(q21-22,q13)x2,-20,-21,-21,-22,add(22)(p12),+der(?)t(?;11)(?,q13),+10-16mar

Case No. 44 **Squamous cell carcinoma** **Lung**

52-81,XY,add(X)(p11),add(1)(p13),add(1)(q11),+add(1)(q12),add(3)(p21),i(3)(q10),-4,-5,-7,-8,-8,add(8)(p21),-9,-11,del(11)(p11),der(11)t(11,11) (p15,q12),-12,-13,der(14;15)(q10,q10),der(14,22)(q10,q10),-15,-15,-16,-17, add(17)(p11),-18,add(19)(q13)x2,add(21)(p11),add(22)(p11),add(22)(p13),+der(?)t(?,7)(p?,q11)t(?,7)(q?,q11),+20-22mar

Case No. 46 **Squamous cell carcinoma** **Lung**

58-67,XXX,+add(X)(q22),der(1,13)(q10,q10),add(3)(p25-26),der(3)add(3)(q27)ins(3,?)(p13,?),i(3)(p10),-4,der(4)t(3,4)(p25,p16),-6,i(6)(p10)x2,-7, del(9)(p13),-11,-14,-14,-14,-15,add(15)(p12),der(16)t(16,17)(p11,q11),-17, -18,-19,add(19)(q13)x2,+20,-21,-21,-21,+der(?)t(?,21)(?;q21)x2,-22,+3-7mar

Case No. 47 **Squamous cell carcinoma** **Lung**

50-68,XY,-X,+add(1)(p13)x2,add(1)(p1?1),-3,-4,+add(5)(q11),-6,-6,+7,add(9)(p13)x2,der(9)t(9,13)(p13,q12)x2,-10,-13,-13,-13,-14,-16,-17,-19,-20,i(20)(q10)x2,+4-6mar

Case No. 48 **Squamous cell carcinoma** **Lung**

49-74,X,-X,add(X)(q2?8),add(1)(p13)x2,add(3)(p12)x2,-5,-6,i(6)(p10),+7,+add(7)(q22),-8,-9,add(10)(q22),i(10)(q10)x2,-11,-13,-13,-14,-14,i(14)(q10),-15, -15,add(16)(q12-13),-17,-18,-19,+20,+20,-21,-21,add(22)(q11),+7-13mar

Case No. 49 **Squamous cell carcinoma** **Lung**

86-90,XY,-X,-Y,add(1)(p11),+add(1)(q21),-2,-2,-2,-2,-3,add(3)(p23),add(3)(p12)x2,-4,-4,add(4)(q2?5)x2,-7,-8,-9,-9,add(9)(p22),-10,-10,-10,-11,add(11)(p1?3),-12,-14,-14,-15,add(15)(p11),-16,-17,-18,-18,-21,-22,-22, +20-27mar

Case No. 50 **Squamous cell carcinoma** **Lung**

58-68,XX,-X,-1,+del(2)(q11),-3,-4,-6,der(6)t(1,6)(q11,q27),+8,del(11) (q21q23-24),-13,-15,+17,-18,-19,-21,+4mar

Case No. 51 **Squamous cell carcinoma** **Lung**

67-83,XX,-Y,+1,der(1)t(1,9)(p13,q12)x2,+2,add(2)(p21)x2,+3,add(3)(p11)x2,+dic(3,?)(p12;?)x2,-4,add(5)(q13),add(6)(q13),+7,+7,+add(7)(q11),del(9)(p21)x4,-10,+11,+12,-13,-13,-14,add(15)(p12)x2,der(15,21)(q10,q10),-16,i(16)(q10),-17,-17,-17,+18,+add(19)(p12),-20,add(20)(p13),add(20)(p12-13), -21,+22,+7-13mar

Case No. 52	**Squamous cell carcinoma**	**Lung**

52-61,X,-X,-Y,-1,der(1)t(1;15)(p13,q11),-2,der(2)t(1,2)(q12,q23),add(3)(p12),der(3,11)(p10,q10),der(3,19)(p10,p10),-4,add(5)(q11),-6,add(6)(q11),+add(7)(q11),add(8)(p11),-9,-9,add(9)(q11),-10,-11,der(11)t(2,11)(p11,q23),-13,-13,add(13)(p11),-14,add(14)(p12),der(14)t(9,14)(q12,q32),-15,-15,-16,add(16)(p11),der(17)t(1,17)(p11,p13)ins(17;?)(p13,?),dic(17,22)(p11,p11),-18,add(18)(p11),der(19)t(11,19)(q11,p12),-20,-21,-21,-22,add(22)(q11),+der(?)t(?;13)(?,q12),+7-8mar/90-120,XX,-X,-Y,-Y,-1,-1,der(1)t(1,7)(p13;p11),-2,der(2)t(1,2)x2,add(3),der(3,11),der(3,19)x2,i(3)(q10),-4,-4,+5,add(5)x2,-6,add(6)x2,+add(7)(q?21),+8,add(8)x2,-9,-9,-9,-9,add(9),-10,-11,-11,-11,der(11)t(2,11)x2,+der(12)t(12,19)(p11,p11)add(12)(q24),-13,-13,-13,-13,add(13),add(14)(p12)x2,der(14)t(9;14),der(14)add(14)(p11)t(9,14)(q12,q32)x2,-15,-16,add(16),der(17)t(1,17)ins(17,?)x2,dic(17,22),-18,-18,add(18)x2,+der(19)t(11,19)x2,-21,-21,-21,-22,add(22)x2,+der(?)t(?,13)x2,+10-16mar

Case No. 53	**Squamous cell carcinoma**	**Lung**

48-68,XXY,add(1)(p22),i(2)(p10),-3,-4,+5,add(5)(q11)x2,der(6)t(6,13)(q12-13;q12),-9,der(9)t(3,9)(q23-24;p13),add(10)(q11),-11,der(11)t(2,11)(q11;p11),-12,-13,-13,add(13)(q34),der(14)t(8,14)(q11,p13),-15,-16,-17,-18,-19,der(20)t(10,20)(q22,q13)x2,-21,-22,der(22)t(12,22)(q13,p13),+der(?)t(?,7)(?,q11),+1-3mar

Teyssier 1987, J Natl Cancer Inst

Case No. 29	**Squamous cell carcinoma**	**Lung**

44-95,X?,der(1)del(1)(p21)del(1)(q25),der(7)t(7,8)(p14,q13),inc

Case No. 34	**Squamous cell carcinoma**	**Larynx**

43-96,X?,del(3)(p14),add(11)(p14),der(11)del(11)(p12)del(11)(q21),inc

Tharapel & Lester 1990, Cancer Genet Cytogenet

Case No. 1	**Squamous cell carcinoma**	**Tongue**

46,XY,t(2,6)(p23;q21),t(18,19)(q21;q13)

Toretsky et al 2003, Am J Clin Oncol

Case No. 1	**Squamous cell carcinoma**	**Thymus**
	46,XY,t(11,15,19)(p15,q12,p13) 92,XXYY,t(11,15,19)x2/92,ıdem,add(1)(q44)	

Van Dyke et al 1994, Genes Chromosomes Cancer

Case No. 12	**Squamous cell carcinoma**	**Larynx**
	49,XY,der(4)t(4,18)(p16;q21),+5,+7,+i(8)(q10)/50,ıdem,+9,ı(17)(q10)/98, ıdemx2	
Case No. 13	**Squamous cell carcinoma**	**Oro- and hypopharynx**
	46,XY,t(1;5)(p11,q12),t(11;12)(p15,q13)/63,XX,-Y,der(1)t(1,1)(p21,q12),der (1)t(1,1)add(1)(q42),inv(2)(p13q21),-3,der(5)t(1,5)(p13,p11),+ı(5)(q10),der (6)t(3,6)(p21,p25)x3,+der(6),-7,der(8)t(1,8)(p13,p11),del(9)(p12p24)x3,+i (9)(p10),+10,-11,add(12)(q22),der(13)t(1,13)(q31;p11),der(15)t(12,15) (p12;p11)x2,der(15)t(9,15)(p13,p11),+der(16)t(6,16)(p21;q24),-18,-19,der (19)inv(19)(p13q13)t(7,19)(q11,p13)x2,-21,-22,-22,ı(22)(q10),+1-3mar	
Case No. 15	**Squamous cell carcinoma**	**Oral cavity**
	67-69,XX,der(X)t(X,1)(p11;q11),der(1)t(1,19)(q11,p12),dıc(1,21)(p11,p11),+ı (1)(q10),add(2)(p21),t(2,17)(q11,q23),+hsr(4)(q21),t(4,5)(p13,p15),+ı(5) (p10),+6,+der(7)t(7,15)(q22,q22),der(8)t(8,8)(p22;q11)x2,dıc(8,9)(q11,q11), dıc(10,19)(p11,p12),der(11)t(7,11)(q22,p15),der(11)dıc(11,15)(q13,p11)hsr (11)(q13),t(11,22)(p11,p11),der(13)t(8,13)(p22,p11)x2,der(13)t(10,13) (p11,p11),ı(14)(q10),-15,-16,t(18,19)(q11,q13),der(18)t(8,18)(q21,q11),+20, -21,-22,ı(22)(q10)	
Case No. 16	**Squamous cell carcinoma**	**Oro- and hypopharynx**
	42,XY,del(3)(p11),der(4)t(4;9)(p11,p11),i(5)(p10),-9,ı(9)(q10),del(10)(q22), del(13)(q14),-15,-16,-21/84,idemx2	
Case No. 19	**Squamous cell carcinoma**	**Soft tissue**
	45,XY,?del(17)(p13),-22	
Case No. 20	**Squamous cell carcinoma**	**Oro- and hypopharynx**
	46,XY,del(3)(p11p24),+ı(5)(p10),del(11)(q14q25),del(13)(q13),del(14)(q21), del(16)(q13),-21/92,ıdemx2	
Case No. 28	**Squamous cell carcinoma**	**Larynx**
	38-48,XY,t(4,9)(q21;p22),ınc/46,XY,del(2)(p15p23),t(10;17)(p11,q11)	

Case No. 29	**Squamous cell carcinoma**	**Skin**

49,XX,der(4)t(4;9)(q33,q11),add(8)(p11),+der(9)t(9,9)(p12,q21),i(9)(p10)x2, der(10)t(8,10)(q11,p11),+20,+r/83-90,XXX,der(X)t(X;9)(p22,q21),-2,-4,der(4), +8,add(8),der(9)x2,+i(9)(p10)x4,-10,-10,+11,-12,der(15)t(2,15)(p11,p11),-16, -18,+20,+1-2mar/180,idemx4/48,XX,+5,+8,t(11,14)/45,X,-X,add(9)/47,X,-X,+7, +mar

Case No. 3	**Squamous cell carcinoma**	**Oro- and hypopharynx**

46,XY,der(1)t(1,9)(q43,q13),?del(8)(p23),dup(11)(p11p15)/71,X,dic(X,6) (p11,q12),der(Y,13)t(Y,13)(q12,p13)ins(Y,17)(q12,q24q25)add(13)(q34),+der (Y)t(Y,21)(p11,q11),+dic(1,12)(p13,q24),-2,i(3)(q10),i(4)(p10),dic(6,12) (q11,q11),add(7)(q32),+dup(7)(q11q21)x2,i(7)(p10),+inv(7)(p22q11),-8,del(8) (p21p22),der(8)t(2;8)(p11;p23),+der(8)t(8,8)(p12;q11)x3,-9,der(9)t(9,11) (p22,q14)x2,add(11)(q21),+der(11)t(?9;11)(q32,q21)x2,-12,-13,dic(13,15) (p13,p13),-14,dic(14,18)(p11,p11),-15,-15,der(15)t(1,4,15)(q25,q11q35,p13), i(16)(q10),der(17)t(Y,17)(q12,q24),der(17)t(3,17)(q13;p13)x2,+i(17)(p10), -18,der(19)t(2,19)(q13,p13),+20,-21,der(21)t(7,21)(q11,p13),+1-4mar

Case No. 33	**Squamous cell carcinoma**	**Oral cavity**

88-92,XX,dic(Y,15)(p13,p11)x2,+dic(Y,15)x2,der(1)t(1,17)(q21,q11)x3,+der (1)i(1)(q10)add(1)(q12),+der(2)t(2,?9)(p11,p11),-3,add(3)(p26)x3,+dic(3,18) (p11,q11)x2,-4,der(5)t(5;21)(q11;q11),der(7)t(7,11)(p22,q13)x2,inv(7) (q11q21)x2,-9,-10,der(10)t(1,10)(q25,p13),-11,-11,+12,-13,der(13)t(13,22) (p11,q11)x3,der(14)t(11,14)(q23;p11)dup(11)(q13q23)x2,+16,-18,-18,-18,add (18)(p11),add(19)(q13)x2,+20,+20,add(20)(q13)x4,-21,-21,add(21)(p11)x2, +2-6mar

Case No. 4	**Squamous cell carcinoma**	**Oral cavity**

45,X,-Y,dic(1,14)(p11,p11),der(4)t(4;5)(q35,q22),i(5)(p10),del(8)(p11p23),i (8)(q10),der(10)t(9,10)(q13,p11),+der(13)t(2,13)(q11,p11),dic(14,22) (p11,p11),der(18)t(1,18)(p11,q11),der(21)t(10,21)(p11,q22),-22,+1-3mar/90, idemx2

Case No. 42	**Squamous cell carcinoma**	**Soft tissue**

42-43,XY,+add(2)(q11),+i(5)(p10),del(9)(p11p24),add(11)(p11-13),add(11) (q11),add(13)(p12),i(14)(q10),?add(15)(p12)

Case No. 6	**Squamous cell carcinoma**	**Oro- and hypopharynx**

41,X,-Y,dic(1,14)(p13,p11),del(2)(p16p24),+der(2)t(2,15)(q13;q21),der(3)t (3,17)(p12,q12),der(4)t(4;17)(q12,q12),r(4)(p16q35),der(8)t(8,18)(p11,q11)t (13,18)(q14;q22),-9,der(11)t(9,11)(q12;q13)hsr(11)(q13),-13,der(13)t(1;13) (p22;p11),der(14)t(4,14)(q12,p11),dic(14,21)(p11,p11),-15,-17,-18,der(19)t (18,19)(p11,p13),-21,der(22)t(5;22)(q31,p11),+1-2mar/82,idemx2/77,XX,-Y,+1, dic(1,14)(q11;p13)x2,add(2)(p25),del(2),+der(2)x2,der(3),der(4)x2,trc (4,7;15)(p16q35,q36,p11),-5,-9,-9,-11,der(11),-12,-13,der(13),+14,-15,der (15)t(3,15)(q12;p11),-16,-17,i(19)(q10),-21,-21,der(22)x2

Case No. 69	**Squamous cell carcinoma**	**Oral cavity**

141,XXY,i(X)(q10),-Y,-Y,+1,del(1)(p12p36)x3,der(1)t(1,8)(p32,q11)t(Y,1)(q11,q44)x2,-2,der(2)t(2,3)(q33,p14)x2,+3,i(3)(q10)x3,-4,-4,del(4)(q12q35), -5,del(5)(q11q32),i(5)(q10),+6,+6,+del(6)(q11q23),+del(7)(p21p22)x3,+der(7)t(7,22)(q11,q11)x3,i(7)(p10)x2,-8,-8,+9,der(9)t(2,9)(q33,p23)x2,+i(9)(p10)x3,-10,i(10)(q10),+add(11)(p15)x2,+del(11)(q11q25)x2,+13,der(14)t(5,14)(q11,p11),i(14)(q10),+15,der(17)t(1,17)(p22,q25)x3,-18,-18,del(18)(q11q22),-19,+20,+20,+20,+20,-21,-21,-21,-22,-22,+1-4mar

Case No. 80	**Squamous cell carcinoma**	**Oro- and hypopharynx**

61,X,inv(Y)(p11q11),der(1)t(1,14)(p11,q11),der(3)t(1,3)(q31,q29)x2,i(3) (q10),-4,add(5)(p16),der(5)t(5,10)(q11,p11),-6,dic(7,10)(q11,p11),der(8)t(8;19)(q24,q11),dic(8,19)(p11,q11),+i(8)(q10),+9,dic(9;15)(p12,q26)x2,-10, -10,der(11)t(11,18)(p15,q12),+i(12)(p10),+15,-16,+i(17)(p10),-18,der(18)t(Y,18)(q11,q12),idic(18)(q22),-19,-19,-20,-21,-21,der(21)idic(21)(p11)ins(21,?)(p11,?),idic(22)(q13)x2,+1-2mar

Case No. 82	**Squamous cell carcinoma**	**Tongue**

94,der(X)t(X,19)(q11,q12)x2,der(X)t(X,21)(p21,q11)x2,+X,der(1)t(1,13)(p13,q12)x2,-2,-3,-4,+6,+del(7)(q21q36),del(8)(p21p22)x2,-9,+t(9,21)(p22,q21)x3,+11,der(11)dup(11)(p13p14)t(1,11)(p13,q14)x2,-13,-15,-16,-16, -17,+18,der(18)t(?11,18)(q14,p11)ins(18,?)(p11,?)x2,-19,-19,+20,-21,+22, +1-7mar/94,der(X)t(X,19)x2,+der(X)t(X;21)x2,t(X,9)(p11,p11)x2,+X,+1,der (1)x3,-4,+5,+7,-8,del(8),t(9,21)x2,+11,der(11)x3,-13,-13,i(14)(q10),add(15) (p11)x3,-18,der(18)x2,+1-7mar

---

Vang Nielsen et al 1982, Hereditas

Case No. 1	**Squamous cell carcinoma**	**Uterus, cervix**

46,X,-X,+mar/61,XXX,-2,ins(2,?)(q23,?),-3,-4,-5,-8,-13,-14,+?t(14;15),-15, -16

Vanni et al 1988, Cancer Genet Cytogenet

Case No. 30	**Squamous cell carcinoma**	**Bladder**

47,XX,+7,der(22)t(3,22)(p21,q13)

Viegas-Péquignot et al 1990, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Lung**

38,XY,del(3)(p11p24),-5,-8,-9,add(11)(p15),-13,-14,-15,-16,-18,-19,-21,add (22)(p12),inc

Case No. 2 **Squamous cell carcinoma** **Lung**

45,X,-Y,del(1)(q?),i(3)(q10),-5,-10,add(11)(p15),add(12)(p11),-13,-14,add (22)(p12),inc

Case No. 3 **Squamous cell carcinoma** **Lung**

78,XX,-Y,+der(1)(q?),+i(3)(q10),-5,-5,-6,+7,+7,+i(7)(q10)x2,add(8)(p12),i (8)(q10),+9,i(10)(q10),add(11)(q22),+12,add(12)(q24)x2,-13,-15,der(15,15) (q10,q10),-18,-19,-21,-21,der(21)(q?),+22,inc

Case No. 4 **Squamous cell carcinoma** **Lung**

50-70,X?,del(1)(p?),del(1)(q12),del(3)(p13),i(4)(q10),add(6),dic(9,14) (p21,q32),der(15)(q?),?hsr(17),inc

Case No. 5 **Squamous cell carcinoma** **Lung**

58,X,-X,-Y,-1,der(1,7)(p10,q10),der(3,?22)(q10,q10),i(3)(q10),-4,-6,del(7) (q31),-8,der(8),-9,-9,del(9)(q31),-10,-10,-11,hsr(11),-12,-13,der(14,21) (q10,q10),-15,add(15)(p11),-16,-17,add(17)(p11),hsr(18),-19,+20,-21,-21,-22, -22,inc

Case No. 6 **Squamous cell carcinoma** **Lung**

53-58,X?,add(1),hsr(2)(p?),der(3),del(5)(q?),add(6),hsr(7)(q1?),i(13)(q10), der(14,21)(q10,q10),?hsr(17)(q?),der(18),der(21,22)(q10,q10),inc

---

Waghray et al 1992, Genes Chromosomes Cancer

Case No. 1 **Squamous cell carcinoma** **Nasop harynx**

74,XX,i(X)(p10),+1,+der(1)t(1;7)(q21,p15),-3,dup(3)(q25q2?7) or add(3)(q27), -4,der(4)t(4,8)(p12,q13),-5,-6,del(6)(p22) or inv(6)(p23q26),+del(7)(q2?2), i(8)(q10),+9,+9,-10,-11,+der(12)t(12,22)(p13,q11),i(13)(q10),+14,-15,add (15)(p13)x2,+17,-18,-21,-21,-22,-22,-22,+10mar/76,idem,+3,+mar/77,idem,-X, -1,+3,+6,+11,-der(12),-20,+21,+3mar/78,idem,-1,+3,+del(3)(p11),+del(5)(p12), +6,-7,+11,-der(12),-17,+21,+21,+21/79,idem,+2,+del(3)(p11),+11,+15,+21/75, idem,-9,+11,+21

Case No. 2 **Squamous cell carcinoma** **Nasop harynx**

51,XX,dup(3)(q25q2?7) or add(3)(q27),del(6)(q22),+7,+17,+18,+22,del(22) (q11)x2,+mar/52,idem,del(1)(p32),del(3)(q2?7),+mar/53,idem,del(1),del(3), +2mar/54,idem,+3,+2mar

---

Worsham et al 1991, Genes Chromosomes Cancer

Case No. 1 **Squamous cell carcinoma** **Vagina**

82,XXXX,inv(1)(p36q32),-2,del(4)(q12),dic(4;11)(q12,p11),i(5)(p10)x2,der(6)t(3,6)(q25,p21),add(8)(p11)x3,del(8)(q13q22),-10,-11,-11,-11,-13,-13,idic(13)(p11),+add(14)(p11),der(14)t(8,14)(q11,p11)x2,-15,-16,-17,i(18)(p10)x2,-19,der(19,19)t(11,19)(p11,p13)t(11,11)(p15;p15)t(11,19)(p11,p13),+1-4mar

Case No. 2A **Squamous cell carcinoma** **Vagina**

73,X,i(X)(q10),-X,-3,+del(4)(q12q35),+5,del(5)(q12q33)x2,+der(6)t(6,15)(q13,q13),+der(7,15)t(7;15)(p21;q13)t(15,18)(p13,q12),i(8)(q10),del(9)(p13p24),+del(10)(q11q25),+del(11)(p12p15),trp(11)(q13q23)x2,+der(12)t(7;12)(p21,p13),+dic(14,21)(p11,p11),-15,+17,-18,-19,-20,-21,-21,+2-3mar

Case No. 2D **Squamous cell carcinoma** **Vagina**

77,X,i(X)(q10),-X,der(1)t(1,8)(q21;q11),+der(2)t(2,19)(q11,q11),-3,+del(4),+del(5)(q12q33)x2,i(5)(q10),+der(6)t(6,15),+der(7,15)t(7;15)t(15,18),add(8)(q11),del(8)(p21p23),+i(8)(q10),+9,+del(10),+del(11),trp(11)x2,+der(12)t(7,12),+dic(14,21),-15,+17,-18,-19,-19,-20,-21,-21,-22,+2-7mar

Case No. 3 **Squamous cell carcinoma** **Vagina**

49,X,-X,+der(1)i(1)(q10)inv(1)(q12q44),+der(1)t(1,19)(p21;q13)ins(19,7)(q13;p22p21),dic(1;18)(p11;q11),i(1)(p10),der(2)t(2;18)(q24;q11),i(3)(q10),+del(5)(q11q33),+der(7)t(7,19)(p22,q13),+8,i(8)(q10)x2,+11,del(11)(p11p14)x2,-18,-19,der(19)t(2,19)(q24;q13),der(21)t(3,21)(p14;p11),i(22) (p10)

Case No. 4 **Squamous cell carcinoma** **Vagina**

103,XXX,-X,i(3)(q10),+4,+4,inv(4)(p12q31)x3,+5,i(5)(p10)x2,+7,+7,+7,-8,der(8)t(4,8)(p12,p11),+10,+11,+13,+13,+13,+13,-14,-15,-19,add(19)(p13),+20,+20, +20,+22,+22

Case No. 5 **Squamous cell carcinoma** **Vagina**

45,X,-X,der(2)t(2,12)(p12,q12),i(3)(q10),der(6)t(4;6)(p13;p22),del(9)(p22p24),der(9)t(4,9)(q21,p24)t(4,11)(q33;q21),del(10)(p11p15),der(10)t(3,10)(p21,q23),der(11)t(11,15)(p15;q22)t(4;11)(q33,q21)hsr(4,11)(q33;q21),add(12)(q12),add(13)(p13),dup(14)(q11q32),add(15)(q22),+der(16)t(16,17)(q13,q21),-17,der(17)t(6,17)(p22;q21),del(18)(q12q23),der(22)add(22)(p13)del(22)(q13)

Case No. 6 **Squamous cell carcinoma** **Vagina**

45,X,-X,der(1)t(1,10)(p11,q22),der(2)t(1,2)(p11,q11),der(3)i(3)(q10)ins(3,?)(q11,?),i(5)(p10),del(7)(q21q36),i(8)(q10),add(10)(q22),der(10)t(10,20)(p14,q11),dup(11)(q12q23),der(13)idic(13)(p11)del(13)(q12q14),add(18)(q22),-20,-22,+2mar

---

Worsham et al 1992, Genes Chromosomes Cancer

Case No. 1 **Squamous cell carcinoma** **Larynx**

45,X,-Y,add(9)(p22)

Worsham et al 1993, Genes Chromosomes Cancer

Case No. 1 **Squamous cell carcinoma** **Skin**

45,XY,-4,t(5;7)(q11,p22),i(9)(p10),ı(9)(q10)/90,idemx2/44,XY,-4,i(9)(p10),ı(9)(q10),der(11)t(10,11)(q21,p14),-21/88,XXYY,-4,-4,ı(9)(p10)x2,ı(9)(q10)x2,der(11)x2,-21,-21/44,XY,-4,i(9)(p10),ı(9)(q10),der(14)t(13,14)(q21,q32),-21/88,XXYY,-4,-4,ı(9)(p10)x2,i(9)(q10)x2,der(14)x2,-21,-21/45-46,XY,der(3)t(3,14)(q24;q24)add(3)(p26),del(4)(q21q35),del(7)(p13p22),+der(7)t(7,?8)(q11,q11),-8,del(10)(p11p15),add(11)(p15),t(16,19)(q24,p13),add(17)(q23),+mar/45,t(X;9)(p11,p11),-Y,del(1)(p13),+del(1)(q31q42),del(2)(q11),+del(2)(p13p23),t(3,17)(p11,p13),-4,dic(5,12)(p11,p11),dıc(6,11)(q23,p15),der(15)t(6,15)(q23,q21),der(16)t(12,16)(p11,q13),der(19)t(16,19)(q13,q13),-20, +1-2mar

Worsham et al 1995, Hum Pathol

Case No. 1 **Squamous cell carcinoma** **Oral cavity**

80-86,XX,dic(Y,14)(q11,p11)x2,del(1)(p22p36)x2,add(2)(q37),+del(2)(q11),dıc(3,11)(p11,q12)x2,add(4)(p12)x2,del(4)(p12p16)x2,del(5)(q11q22)x2,-6,del(6)(p11p25),der(8)t(2;8)(q24,q24)x2,der(8)t(8,9)(p11;q12)x2,-9,-9,del(10)(p12p15)x2,-11,-11,-12,-13,-13,add(13)(p11),ı(13)(q10)x2,add(15)(p11)x2,der(15)t(9,15)(q12,p11)x2,-16,-16,add(16)(q11)x2,del(17)(p11p13)x2,-19,-19,-21,add(21)(p11),-22,+3-9mar

68-72,XX,dıc(Y,14),+dic(Y,14),del(1)(p22p36),del(1)(p11),+dıc(1,16)(p11;q11),-2,del(2),-3,add(3)(q11),dıc(3,11),-4,-4,add(4),del(4),del(5)x2,der(5)t(3;5)(q21,p14),-6,-6,del(6),der(8)t(2,8),der(8)t(8,9)x2,+der(8)t(2,8)add(2)(q24),-9,-9,add(9)(p23),-10,-10,del(10),-11,-11,-12,add(13),del(13)(q11q14),der(13)t(2,13)(q11,p11),add(15),der(15)t(9,15)x2,add(16)x2,add(16)(p13),-17,del(17)x2,-19,-19,add(19)(q13),-21,ı(21)(q10),-22,-22, +8-12mar

Xiao et al 1992, Cancer Genet Cytogenet

Case No. 1 **Squamous cell carcinoma** **Penis**

46,XY,del(2)(q33q36),add(4)(p16),der(5,15)(q10,q10),der(8)t(8;?13)(q21,?), -13,-13,-15,+3mar

Zaslav et al 1991, Cancer Genet Cytogenet

Case No. 1	**Squamous cell carcinoma**	**Nasal cavity/Para nasal sinuses**
	60-100,XX?,+X,-3,del(4)(p14),+5,-7,del(8)(q24),add(12)(p13),+11,+der(11)(p13q21),+12,+13,+14,+15,+19,dmin,inc	
Case No. 10	**Squamous cell carcinoma**	**Larynx**
	46,XX,inv(14)(q13q23)	
Case No. 2	**Squamous cell carcinoma**	**Oro- and hypopharynx**
	50-70,XY?,+1,+1,del(4)(p11),add(5)(q35),+del(8)(q22),add(13)(p13)x2,+add(14)(p13),+16,add(16)(q24)x2,+17,+17,+17,+20,dmin,inc	
Case No. 4	**Squamous cell carcinoma**	**Larynx**
	40-50,XY,del(3)(p11),del(6)(q12),add(7)(p22),add(11)(p15),add(12),add(14)(q24),der(15)t(15,15)(p11;p11),del(16)(q22),der(21)t(21,21)(p11;p11)x2,add(22)(q13),dmin,inc	
Case No. 5	**Squamous cell carcinoma**	**Larynx**
	75-100,XX?,add(5)(p15),del(5)(p13),add(6)(q23),add(11)(q23),add(11)(q25),i(11)(q10),der(14)t(14,14)(p11,p11),dmin,inc	
Case No. 6	**Squamous cell carcinoma**	**Larynx**
	50-100,XY?,del(8)(q21),del(8)(q24),t(9,11)(p22,p13),t(13,14)(p11;p11),dmin,inc	
Case No. 9	**Squamous cell carcinoma**	**Larynx**
	100,XY?,del(X)(p11),del(5)(p31),der(11)t(1;11)(p32,p15)x2,der(13)t(13,14)(p11,p11),+20,dmin,inc	

da Silva Veiga et al 2003, Cancer Genet Cytogenet

Case No. 115	**Squamous cell carcinoma**	**Oral cavity**
	42-50,X,-X,-2,-10,del(12)(p12),+15,-19,-20,+22,+mar	
Case No. 122	**Squamous cell carcinoma**	**Tongue**
	43-48,XY,-9,+10,-17,+22	
Case No. 123	**Squamous cell carcinoma**	**Tongue**
	44-48,X,-Y,+10,+20,+22	
Case No. 124	**Squamous cell carcinoma**	**Oro- and hypopharynx**
	41-48,X,-Y,+add(9)(p24),+13,-18,-19,+22	

Case No. 129	**Squamous cell carcinoma**	**Larynx**
	44-48,X,-Y,+7,-10,-21,+22,+del(22)(q13)	
Case No. 133	**Squamous cell carcinoma**	**Oral cavity**
	42-48,X,-Y,-3,-9,-14,-16,-18,-19,+22,+mar	
Case No. 135	**Squamous cell carcinoma**	**Larynx**
	41-48,X,-Y,-4,+6,+del(6)(q22),-11,-12,-15,-16,-19,?del(22)(q13),+mar	
Case No. 137	**Squamous cell carcinoma**	**Oro- and hypopharynx**
	44-47,X,-Y,+7,-19,-20,+22,+mar	
Case No. 166	**Squamous cell carcinoma**	**Nasal cavity/Paranasal sinuses**
	43-47,-X,-Y,del(6)(q21q23),+10,+22	
Case No. 172	**Squamous cell carcinoma**	**Tongue**
	43-47,X,-X,-21,+del(22)(q13)	
Case No. 27	**Squamous cell carcinoma**	**Tongue**
	40-46,X,-Y,-22	
Case No. 28	**Squamous cell carcinoma**	**Oral cavity**
	44-49,X,-Y,del(5)(q15q23),+8,-9,-13,-19,-21,+22,+mar	
Case No. 47	**Squamous cell carcinoma**	**Nasal cavity/Paranasal sinuses**
	43-49,XX,+5,+8,+17,-19,-20,del(22)(q13),+mar	
Case No. 48	**Squamous cell carcinoma**	**Tongue**
	42-48,XY,-10,del(10)(p13),+11,+18,+20,+del(22)(q13)	
Case No. 97	**Squamous cell carcinoma**	**Oral cavity**
	43-47,XY,-13,+22,+mar	

APPENDIX B

Karyo Reader Aberrations List

d1	d13p11	d16p12	d1p35	d2p24	d4p13	d3	d4q33
d10	d13p12	d16p13	d1p36	d2p25	d4p14	d3p11	d4q34
d10p11	d13p13	d16q11	d1q11	d2q11	d4p15	d3p12	d4q35
d10p12	d13q12	d16q12	d1q12	d2q12	d4p16	d3p13	d5
d10p13	d13q13	d16q13	d1q21	d2q13	d4q11	d3p14	d5p11
d10p14	d13q14	d16q21	d1q22	d2q14	d4q12	d3p21	d5p12
d10p15	d13q21	d16q22	d1q23	d2q21	d4q13	d3p22	d5p13
d10q11	d13q22	d16q23	d1q24	d2q22	d4q21	d3p23	d5p14
d10q21	d13q31	d16q24	d1q25	d2q23	d4q22	d3p24	d5p15
d10q22	d13q32	d17	d1q31	d2q24	d4q23	d3p25	d5q11
d10q23	d13q33	d17p11	d1q32	d2q31	d4q24	d3p26	d5q12
d10q24	d13q34	d17p12	d1q41	d2q32	d4q25	d3q11	d5q13
d10q25	d14	d17p13	d1q42	d2q33	d4q26	d3q12	d5q14
d10q26	d14p11	d17q11	d1q43	d2q34	d4q27	d3q13	d5q15
d11	d14p12	d17q12	d1q44	d2q35	d4q28	d3q21	d5q21
d11p11	d14p13	d17q21	d2	d2q36	d4q31	d3q22	d5q22
d11p12	d14q12	d17q22	d20	d2q37	d4q32	d3q23	d5q23
d11p13	d14q13	d17q23	d20p11	d3	d4q33	d3q24	d5q31
d11p14	d14q21	d17q24	d20p12	d3p11	d4q34	d3q25	d5q32
d11p15	d14q22	d17q25	d20p13	d3p12	d4q35	d3q26	d5q33
d11q11	d14q23	d18	d20q12	d3p13	d5	d3q27	d5q34
d11q12	d14q24	d18p11	d20q13	d3p14	d5p11	d3q28	d5q35
d11q13	d14q31	d18q11	d21	d3p21	d5p12	d3q29	d6
d11q14	d14q32	d18q12	d21p11	d3p22	d5p13	d4	d6p11
d11q21	d15	d18q21	d21p12	d3p23	d5p14	d4p11	d6p12
d11q22	d15p11	d18q22	d21p13	d3p24	d5p15	d4p12	d6p21
d11q23	d15p12	d18q23	d21q22	d3p25	d5q11	d4p13	d6p22
d11q24	d15p13	d19	d22	d3p26	d5q12	d4p14	d6p23
d11q25	d15q12	d19p11	d22p11	d3q11	d5q13	d4p15	d6p24
d12	d15q13	d19p12	d22p12	d3q12	d5q14	d4p16	d6p25
d12p11	d15q14	d19p13	d22p13	d3q13	d5q15	d4q11	d6q11
d12p12	d15q15	d19q11	d22q11	d3q21	d5q21	d4q12	d6q12
d12p13	d15q21	d19q12	d22q12	d3q22	d2q21	d4q13	d6q13
d12q11	d15q22	d19q13	d22q13	d3q23	d2q22	d4q21	d6q14
d12q12	d15q23	d1p11	d2p11	d3q24	d2q23	d4q22	d6q15
d12q13	d15q24	d1p12	d2p12	d3q25	d2q24	d4q23	d6q16
d12q14	d15q25	d1p13	d2p13	d3q26	d2q31	d4q24	d6q21
d12q15	d15q26	d1p21	d2p14	d3q27	d2q32	d4q25	d6q22
d12q21	d16	d1p22	d2p15	d3q28	d2q33	d4q26	d6q23
d12q22	d16p11	d1p31	d2p16	d3q29	d2q34	d4q27	d6q24
d12q23	d16p12	d1p32	d2p21	d4	d2q35	d4q28	d6q25
d12q24	d16p13	d1p33	d2p22	d4p11	d2q36	d4q31	d6q26
d13	d16q11	d1p34	d2p23	d4p12	d2q37	d4q32	d6q27

d7	d9q32	g11q14	g14q24	g18q21	g21p11	g3p14	g5p11
d7p11	d9q33	g11q21	g14q31	g18q22	g21p12	g3p21	g5p12
d7p12	d9q34	g11q22	g14q32	g18q23	g21p13	g3p22	g5p13
d7p13	dX	g11q23	g15	g19	g21q11	g3p23	g5p14
d7p14	dXp11	g11q24	g15p11	g19p11	g21q21	g3p24	g5p15
d7p15	dXp21	g11q25	g15p12	g19p12	g21q22	g3p25	g5q11
d7p21	dXp22	g12	g15p13	g19p13	g22	g3p26	g5q12
d7p22	dXq11	g12p11	g15q11	g19q11	g22p11	g3q11	g5q13
d7q11	dXq12	g12p12	g15q12	g19q12	g22p12	g3q12	g5q14
d7q21	dXq13	g12p13	g15q13	g19q13	g22p13	g3q13	g5q15
d7q22	dXq21	g12q11	g15q14	g1p11	g22q11	g3q21	g5q21
d7q31	dXq22	g12q12	g15q15	g1p12	g22q12	g3q22	g5q22
d7q32	dXq23	g12q13	g15q21	g1p13	g22q13	g3q23	g5q23
d7q33	dXq24	g12q14	g15q22	g1p21	g2p11	g3q24	g5q31
d7q34	dXq25	g12q15	g15q23	g1p22	g2p12	g3q25	g5q32
d7q35	dXq26	g12q21	g15q24	g1p31	g2p13	g3q26	g5q33
d7q36	dXq27	g12q22	g15q25	g1p32	g2p14	g3q27	g5q34
d8	dXq28	g12q23	g15q26	g1p33	g2p15	g3q28	g5q35
d8p11	dY	g12q24	g16	g1p34	g2p16	g3q29	g6
d8p12	dYq12	g13	g16p11	g1p35	g2p21	g4	g6p11
d8p21	g1	g13p11	g16p12	g1p36	g2p22	g4p11	g6p12
d8p22	g10	g13p12	g16p13	g1q11	g2p23	g4p12	g6p21
d8p23	g10p11	g13p13	g16q11	g1q12	g2p24	g4p13	g6p22
d8q12	g10p12	g13q11	g16q12	g1q21	g2p25	g4p14	g6p23
d8q13	g10p13	g13q12	g16q13	g1q22	g2q11	g4p15	g6p24
d8q21	g10p14	g13q13	g16q21	g1q23	g2q12	g4p16	g6p25
d8q22	g10p15	g13q14	g16q22	g1q24	g2q13	g4q11	g6q11
d8q23	g10q11	g13q21	g16q23	g1q25	g2q14	g4q12	g6q12
d8q24	g10q21	g13q22	g16q24	g1q31	g2q21	g4q13	g6q13
d9	g10q22	g13q31	g17	g1q32	g2q22	g4q21	g6q14
d9p11	g10q23	g13q32	g17p11	g1q41	g2q23	g4q22	g6q15
d9p12	g10q24	g13q33	g17p12	g1q42	g2q24	g4q23	g6q16
d9p13	g10q25	g13q34	g17q11	g1q43	g2q31	g4q24	g6q21
d9p21	g10q26	g14	g17q12	g1q44	g2q32	g4q25	g6q22
d9p22	g11	g14p11	g17q21	g2	g2q33	g4q26	g6q23
d9p23	g11p11	g14p12	g17q22	g20	g2q34	g4q27	g6q24
d9p24	g11p12	g14p13	g17q23	g20p11	g2q35	g4q28	g6q25
d9q11	g11p13	g14q11	g17q24	g20p12	g2q36	g4q31	g6q26
d9q12	g11p14	g14q12	g17q25	g20p13	g2q37	g4q32	g6q27
d9q13	g11p15	g14q13	g18	g20q11	g3	g4q33	g7
d9q21	g11q11	g14q21	g18p11	g20q12	g3p11	g4q34	g7p11
d9q22	g11q12	g14q22	g18q11	g20q13	g3p12	g4q35	g7p12
d9q31	g11q13	g14q23	g18q12	g21	g3p13	g5	g7p13

g7p14	gX	t12q13	t19p12	t2q23	t5q32	t9q32
g7p15	gXp11	t12q22	t19p13	t2q31	t5q33	t9q34
g7p21	gXp21	t12q24	t19q11	t2q32	t5q35	tXp11
g7p22	gXp22	t13p11	t19q13	t2q33	t6p12	tXp22
g7q11	gXq11	t13p13	t1p11	t2q35	t6p21	tXq11
g7q21	gXq12	t13q11	t1p12	t2q37	t6p22	tXq13
g7q22	gXq13	t13q12	t1p13	t3p11	t6p25	tXq22
g7q31	gXq21	t13q14	t1p21	t3p12	t6q11	tXq24
g7q32	gXq22	t13q31	t1p22	t3p13	t6q12	tXq26
g7q33	gXq23	t13q32	t1p31	t3p21	t6q13	tYq11
g7q34	gXq24	t14p11	t1p32	t3p25	t6q15	tYq12
g7q35	gXq25	t14p12	t1p34	t3p26	t6q21	
g7q36	gXq26	t14p13	t1p35	t3q11	t6q22	
g8	gXq27	t14q11	t1p36	t3q12	t6q23	
g8p11	gXq28	t14q12	t1q11	t3q13	t6q25	
g8p12	gY	t14q22	t1q12	t3q21	t6q27	
g8p21	gYp11	t14q24	t1q21	t3q22	t6q31	
g8p22	gYq11	t14q32	t1q22	t3q25	t7p11	
g8p23	gYq12	t15p11	t1q23	t3q28	t7p13	
g8q11	t10p11	t15p13	t1q24	t3q29	t7p14	
g8q12	t10p13	t15q12	t1q25	t4p11	t7p15	
g8q13	t10p15	t15q13	t1q32	t4p13	t7p22	
g8q21	t10q11	t15q14	t1q42	t4p15	t7q11	
g8q22	t10q21	t15q15	t1q44	t4p16	t7q22	
g8q23	t10q22	t15q22	t20p11	t4q11	t7q32	
g8q24	t10q23	t15q24	t20p13	t4q12	t7q33	
g9	t10q24	t15q25	t20q11	t4q13	t7q36	
g9p11	t10q25	t15q26	t20q13	t4q21	t8p21	
g9p12	t10q26	t16p11	t21p11	t4q22	t8q11	
g9p13	t11p11	t16p13	t21q21	t4q24	t8q13	
g9p21	t11p13	t16q11	t21q22	t4q25	t8q21	
g9p22	t11p14	t16q22	t22p11	t4q28	t8q22	
g9p23	t11p15	t16q23	t22p13	t4q33	t8q23	
g9p24	t11q11	t16q24	t22q11	t4q34	t8q24	
g9q11	t11q12	t17p11	t22q13	t4q35	t9p11	
g9q12	t11q13	t17p13	t2p11	t5p15	t9p13	
g9q13	t11q14	t17q11	t2p13	t5q11	t9p22	
g9q21	t11q21	t17q21	t2p21	t5q12	t9p23	
g9q22	t11q23	t17q23	t2p23	t5q13	t9p24	
g9q31	t11q25	t18p11	t2p24	t5q15	t9q11	
g9q32	t12p11	t18q11	t2p25	t5q22	t9q12	
g9q33	t12p12	t18q21	t2q11	t5q23	t9q13	
g9q34	t12q12	t18q23	t2q21	t5q31	t9q22	

APPENDIX C

Progenetix ISCN2matrix Aberrations List

1p36.33	1q24 1	2p11 1	3p25.2	3q25.1	4q26	5q15	6q12
1p36.32	1q24.2	2q11 1	3p25.1	3q25 2	4q27	5q21.1	6q13
1p36 31	1q24.3	2q11.2	3p24 3	3q25 31	4q28.1	5q21.2	6q14 1
1p36.23	1q25 1	2q12.1	3p24.2	3q25 32	4q28.2	5q21.3	6q14 2
1p36.22	1q25 2	2q12 2	3p24 1	3q25 33	4q28.3	5q22.1	6q14.3
1p36.21	1q25 3	2q12 3	3p23	3q26.1	4q31 1	5q22.2	6q15
1p36 13	1q31.1	2q13	3p22 3	3q26 2	4q31 21	5q22 3	6q16.1
1p36.12	1q31 2	2q14 1	3p22 2	3q26 31	4q31.22	5q23 1	6q16 2
1p36 11	1q31 3	2q14.2	3p22 1	3q26 32	4q31.23	5q23 2	6q16.3
1p35.3	1q32.1	2q14.3	3p21 33	3q26 33	4q31 3	5q23.3	6q21
1p35.2	1q32.2	2q21.1	3p21 32	3q27.1	4q32.1	5q31 1	6q22.1
1p35.1	1q32 3	2q21 2	3p21.31	3q27.2	4q32.2	5q31.2	6q22 2
1p34.3	1q41	2q21 3	3p21.2	3q27.3	4q32 3	5q31.3	6q22 31
1p34.2	1q42.11	2q22 1	3p21 1	3q28	4q33	5q32	6q22.32
1p34.1	1q42 12	2q22.2	3p14 3	3q29	4q34 1	5q33 1	6q22 33
1p33	1q42 13	2q22 3	3p14 2	4p16.3	4q34 2	5q33.2	6q23.1
1p32.3	1q42.2	2q23 1	3p14 1	4p16 2	4q34 3	5q33.3	6q23 2
1p32.2	1q42.3	2q23 2	3p13	4p16.1	4q35 1	5q34	6q23 3
1p32.1	1q43	2q23 3	3p12.3	4p15.33	4q35 2	5q35 1	6q24 1
1p31.3	1q44	2q24 1	3p12 2	4p15.32	5p15.33	5q35.2	6q24 2
1p31.2	2p25.3	2q24 2	3p12 1	4p15.31	5p15.32	5q35 3	6q24 3
1p31.1	2p25.2	2q24 3	3p11.2	4p15 2	5p15.31	6p25 3	6q25.1
1p22.3	2p25.1	2q31 1	3p11.1	4p15 1	5p15.2	6p25.2	6q25.2
1p22.2	2p24.3	2q31 2	3q11 1	4p14	5p15.1	6p25 1	6q25 3
1p22.1	2p24 2	2q31 3	3q11 2	4p13	5p14.3	6p24 3	6q26
1p21.3	2p24 1	2q32 1	3q12.1	4p12	5p14.2	6p24 2	6q27
1p21.2	2p23 3	2q32.2	3q12 2	4p11	5p14 1	6p24.1	7p22.3
1p21.1	2p23.2	2q32.3	3q12.3	4q11	5p13 3	6p23	7p22.2
1p13 3	2p23 1	2q33 1	3q13.11	4q12	5p13.2	6p22.3	7p22 1
1p13.2	2p22.3	2q33.2	3q13.12	4q13.1	5p13.1	6p22.2	7p21.3
1p13.1	2p22.2	2q33.3	3q13 13	4q13.2	5p12	6p22.1	7p21 2
1p12	2p22.1	2q34	3q13.2	4q13.3	5p11	6p21.33	7p21.1
1p11.2	2p21	2q35	3q13 31	4q21 1	5q11 1	6p21.32	7p15 3
1p11.1	2p16 3	2q36 1	3q13 32	4q21 21	5q11.2	6p21.31	7p15 2
1q11	2p16 2	2q36.2	3q13 33	4q21.22	5q12.1	6p21 2	7p15 1
1q12	2p16.1	2q36.3	3q21 1	4q21.23	5q12 2	6p21 1	7p14.3
1q21 1	2p15	2q37.1	3q21 2	4q21.3	5q12 3	6p12 3	7p14 2
1q21.2	2p14	2q37.2	3q21.3	4q22 1	5q13.1	6p12 2	7p14.1
1q21.3	2p13.3	2q37 3	3q22 1	4q22.2	5q13.2	6p12.1	7p13
1q22	2p13.2	3p26.3	3q22 2	4q22 3	5q13.3	6p11 2	7p12.3
1q23.1	2p13.1	3p26.2	3q22.3	4q23	5q14 1	6p11.1	7p12 2
1q23.2	2p12	3p26.1	3q23	4q24	5q14 2	6q11.1	7p12 1
1q23.3	2p11.2	3p25 3	3q24	4q25	5q14.3	6q11 2	7p11 2

7p11 1	8q12.1	9q21 11	10q21 2	11q13 4	12q21.33	13q32 1	15q11 1
7q11 1	8q12.2	9q21 12	10q21 3	11q13.5	12q22	13q32 2	15q11 2
7q11 21	8q12.3	9q21 13	10q22.1	11q14 1	12q23 1	13q32.3	15q12
7q11.22	8q13 1	9q21 2	10q22 2	11q14 2	12q23 2	13q33.1	15q13 1
7q11 23	8q13 2	9q21 31	10q22 3	11q14 3	12q23 3	13q33 2	15q13.2
7q21.11	8q13 3	9q21 32	10q23 1	11q21	12q24 11	13q33.3	15q13.3
7q21 12	8q21.11	9q21 33	10q23 2	11q22 1	12q24 12	13q34	15q14
7q21 13	8q21.12	9q22 1	10q23.31	11q22.2	12q24.13	14p13	15q15 1
7q21.2	8q21 13	9q22.2	10q23.32	11q22 3	12q24.21	14p12	15q15.2
7q21.3	8q21 2	9q22 31	10q23.33	11q23.1	12q24 22	14p11.2	15q15 3
7q22 1	8q21.3	9q22.32	10q24 1	11q23.2	12q24 23	14p11.1	15q21 1
7q22 2	8q22 1	9q22 33	10q24 2	11q23.3	12q24.31	14q11.1	15q21.2
7q22.3	8q22.2	9q31 1	10q24.31	11q24.1	12q24 32	14q11.2	15q21 3
7q31.1	8q22 3	9q31 2	10q24.32	11q24 2	12q24.33	14q12	15q22 1
7q31.2	8q23.1	9q31.3	10q24.33	11q24 3	13p13	14q13 1	15q22.2
7q31 31	8q23.2	9q32	10q25.1	11q25	13p12	14q13.2	15q22 31
7q31 32	8q23.3	9q33.1	10q25.2	12p13 33	13p11 2	14q13 3	15q22 32
7q31.33	8q24.11	9q33 2	10q25.3	12p13 32	13p11.1	14q21.1	15q22.33
7q32 1	8q24.12	9q33 3	10q26 11	12p13.31	13q11	14q21.2	15q23
7q32 2	8q24 13	9q34.11	10q26.12	12p13 2	13q12.11	14q21 3	15q24.1
7q32.3	8q24.21	9q34 12	10q26.13	12p13.1	13q12 12	14q22.1	15q24.2
7q33	8q24 22	9q34 13	10q26.2	12p12 3	13q12 13	14q22 2	15q24 3
7q34	8q24.23	9q34.2	10q26.3	12p12.2	13q12 2	14q22 3	15q25.1
7q35	8q24 3	9q34 3	11p15.5	12p12 1	13q12 3	14q23.1	15q25.2
7q36 1	9p24 3	10p15.3	11p15.4	12p11.23	13q13 1	14q23 2	15q25.3
7q36.2	9p24.2	10p15.2	11p15 3	12p11 22	13q13.2	14q23.3	15q26.1
7q36 3	9p24 1	10p15.1	11p15.2	12p11 21	13q13 3	14q24.1	15q26.2
8p23.3	9p23	10p14	11p15.1	12p11 1	13q14 11	14q24 2	15q26.3
8p23 2	9p22 3	10p13	11p14.3	12q11	13q14 12	14q24 3	16p13.3
8p23.1	9p22 2	10p12.33	11p14 2	12q12	13q14 13	14q31.1	16p13 2
8p22	9p22 1	10p12.32	11p14 1	12q13 11	13q14.2	14q31.2	16p13 13
8p21.3	9p21 3	10p12.31	11p13	12q13 12	13q14 3	14q31.3	16p13.12
8p21.2	9p21.2	10p12.2	11p12	12q13.13	13q21.1	14q32 11	16p13.11
8p21.1	9p21.1	10p12.1	11p11.2	12q13.2	13q21 2	14q32 12	16p12.3
8p12	9p13.3	10p11.23	11p11.12	12q13 3	13q21 31	14q32.13	16p12 2
8p11 23	9p13 2	10p11.22	11p11.11	12q14.1	13q21 32	14q32 2	16p12 1
8p11.22	9p13 1	10p11.21	11q11	12q14.2	13q21 33	14q32 31	16p11 2
8p11 21	9p12	10p11.1	11q12 1	12q14.3	13q22.1	14q32.32	16p11.1
8p11.1	9p11.2	10q11.1	11q12.2	12q15	13q22 2	14q32.33	16q11 1
8q11.1	9p11 1	10q11.21	11q12 3	12q21 1	13q22.3	15p13	16q11 2
8q11.21	9q11	10q11.22	11q13.1	12q21.2	13q31 1	15p12	16q12.1
8q11 22	9q12	10q11.23	11q13.2	12q21 31	13q31.2	15p11.2	16q12 2
8q11.23	9q13	10q21.1	11q13 3	12q21.32	13q31.3	15p11.1	16q13

16q21	18q12.2	20q13 11	Xp22 11	Yq11.23
16q22 1	18q12 3	20q13.12	Xp21 3	Yq12
16q22 2	18q21 1	20q13.13	Xp21.2	
16q22 3	18q21 2	20q13.2	Xp21.1	
16q23.1	18q21 31	20q13 31	Xp11.4	
16q23 2	18q21 32	20q13 32	Xp11 3	
16q23 3	18q21 33	20q13 33	Xp11 23	
16q24 1	18q22 1	21p13	Xp11 22	
16q24.2	18q22.2	21p12	Xp11.21	
16q24 3	18q22.3	21p11 2	Xp11 1	
17p13 3	18q23	21p11 1	Xq11.1	
17p13 2	19p13 3	21q11.1	Xq11.2	
17p13.1	19p13 2	21q11 2	Xq12	
17p12	19p13 13	21q21 1	Xq13.1	
17p11 2	19p13 12	21q21 2	Xq13.2	
17p11 1	19p13 11	21q21.3	Xq13.3	
17q11 1	19p12	21q22 11	Xq21.1	
17q11.2	19p11	21q22 12	Xq21.2	
17q12	19q11	21q22.13	Xq21.31	
17q21 1	19q12	21q22 2	Xq21 32	
17q21 2	19q13 11	21q22 3	Xq21 33	
17q21.31	19q13 12	22p13	Xq22 1	
17q21.32	19q13.13	22p12	Xq22 2	
17q21 33	19q13.2	22p11 2	Xq22.3	
17q22	19q13 31	22p11 1	Xq23	
17q23 1	19q13 32	22q11.1	Xq24	
17q23 2	19q13.33	22q11 21	Xq25	
17q23 3	19q13.41	22q11.22	Xq26.1	
17q24 1	19q13.42	22q11.23	Xq26 2	
17q24.2	19q13.43	22q12.1	Xq26.3	
17q24 3	20p13	22q12.2	Xq27 1	
17q25.1	20p12.3	22q12 3	Xq27.2	
17q25 2	20p12.2	22q13.1	Xq27 3	
17q25.3	20p12 1	22q13.2	Xq28	
18p11.32	20p11.23	22q13.31	Yp11 32	
18p11.31	20p11 22	22q13.32	Yp11 31	
18p11.23	20p11.21	22q13.33	Yp11 2	
18p11.22	20p11.1	Xp22.33	Yp11.1	
18p11 21	20q11.1	Xp22.32	Yq11.1	
18p11.1	20q11.21	Xp22 31	Yq11.21	
18q11.1	20q11.22	Xp22 22	Yq11.221	
18q11.2	20q11 23	Xp22 13	Yq11.222	
18q12 1	20q12	Xp22 12	Yq11.223	

APPENDIX D

CyDAS Aberrations List

1p10	1q43	2q372	4p12	5q112	6q161	7q35	9q211
1p11	1q44	2q373	4p13	5q12	6q162	7q36	9q212
1p12	2p10	3p10	4p14	5q131	6q163	8p10	9q213
1p131	2p111	3p111	4p151	5q132	6q21	8p111	9q221
1p132	2p112	3p112	4p152	5q133	6q221	8p112	9q222
1p133	2p12	3p12	4p153	5q14	6q222	8p12	9q223
1p21	2p13	3p13	4p16	5q15	6q223	8p211	9q31
1p221	2p14	3p141	4q10	5q21	6q231	8p212	9q32
1p222	2p15	3p142	4q11	5q22	6q232	8p213	9q33
1p223	2p16	3p143	4q12	5q231	6q233	8p22	9q341
1p311	2p21	3p211	4q131	5q232	6q24	8p231	9q342
1p312	2p22	3p212	4q132	5q233	6q251	8p232	9q343
1p313	2p23	3p213	4q133	5q311	6q252	8p233	10p10
1p321	2p24	3p22	4q211	5q312	6q253	8q10	10p111
1p322	2p251	3p23	4q212	5q313	6q26	8q111	10p112
1p323	2p252	3p241	4q213	5q32	6q27	8q1121	10p121
1p33	2p253	3p242	4q22	5q331	7p10	8q1122	10p122
1p341	2q10	3p243	4q23	5q332	7p111	8q1123	10p123
1p342	2q111	3p25	4q24	5q333	7p112	8q12	10p13
1p343	2q112	3p26	4q25	5q34	7p12	8q13	10p14
1p35	2q12	3q10	4q26	5q351	7p13	8q211	10p15
1p361	2q13	3q111	4q27	5q352	7p14	8q212	10q10
1p362	2q141	3q112	4q28	5q353	7p151	8q213	10q111
1p363	2q142	3q12	4q311	6p10	7p152	8q221	10q112
1q10	2q143	3q131	4q312	6p111	7p153	8q222	10q211
1q11	2q211	3q132	4q313	6p112	7p21	8q223	10q212
1q12	2q212	3q133	4q32	6p12	7p22	8q23	10q213
1q211	2q213	3q21	4q33	6p211	7q10	8q241	10q221
1q212	2q22	3q22	4q34	6p212	7q111	8q242	10q222
1q213	2q23	3q23	4q35	6p213	7q1121	8q243	10q223
1q22	2q241	3q24	5p10	6p221	7q1122	9p10	10q231
1q23	2q242	3q251	5p11	6p222	7q1123	9p11	10q232
1q24	2q243	3q252	5p12	6p223	7q211	9p12	10q233
1q25	2q31	3q253	5p131	6p23	7q212	9p13	10q241
1q31	2q321	3q261	5p132	6p24	7q213	9p21	10q242
1q321	2q322	3q262	5p133	6p25	7q22	9p22	10q243
1q322	2q323	3q263	5p14	6q10	7q311	9p23	10q251
1q323	2q33	3q27	5p151	6q11	7q312	9p24	10q252
1q41	2q34	3q28	5p152	6q12	7q313	9q10	10q253
1q421	2q35	3q29	5p153	6q13	7q32	9q11	10q261
1q422	2q36	4p10	5q10	6q14	7q33	9q12	10q262
1q423	2q371	4p11	5q111	6q15	7q34	9q13	10q263

11p10	12q11	14p12	16p111	18q123	21q223	Xq26
11p1111	12q12	14p13	16p112	18q211	22p10	Xq27
11p1112	12q131	14q10	16p12	18q212	22p111	Xq28
11p112	12q132	14q111	16p131	18q213	22p112	Yp10
11p12	12q133	14q112	16p132	18q22	22p12	Yp111
11p13	12q14	14q12	16p133	18q23	22p13	Yp112
11p14	12q15	14q13	16q10	19p10	22q10	Yp113
11p151	12q211	14q21	16q111	19p11	22q111	Yq10
11p152	12q212	14q22	16q112	19p12	22q112	Yq111
11p153	12q213	14q23	16q121	19p131	22q121	Yq1121
11p154	12q22	14q241	16q122	19p132	22q122	Yq11221
11p155	12q23	14q242	16q13	19p133	22q123	Yq11222
11q10	12q241	14q243	16q21	19q10	22q131	Yq11223
11q11	12q242	14q31	16q22	19q11	22q132	Yq1123
11q12	12q2431	14q321	16q23	19q12	22q133	Yq12
11q131	12q2432	14q322	16q24	19q131	Xp10	
11q132	12q2433	14q323	17p10	19q132	Xp111	
11q133	13p10	15p10	17p111	19q133	Xp1121	
11q134	13p111	15p111	17p112	19q134	Xp1122	
11q135	13p112	15p112	17p12	20p10	Xp1123	
11q141	13p12	15p12	17p13	20p111	Xp113	
11q142	13p13	15p13	17q10	20p112	Xp114	
11q143	13q10	15q10	17q111	20p12	Xp211	
11q21	13q11	15q111	17q112	20p13	Xp212	
11q221	13q121	15q112	17q12	20q10	Xp213	
11q222	13q122	15q12	17q211	20q111	Xp221	
11q223	13q123	15q13	17q212	20q112	Xp222	
11q231	13q13	15q14	17q213	20q12	Xp223	
11q232	13q141	15q15	17q22	20q131	Xq10	
11q233	13q142	15q211	17q23	20q132	Xq111	
11q24	13q143	15q212	17q24	20q133	Xq112	
11q25	13q211	15q213	17q25	21p10	Xq12	
12p10	13q212	15q221	18p10	21p111	Xq13	
12p111	13q213	15q222	18p111	21p112	Xq211	
12p112	13q22	15q223	18p112	21p12	Xq212	
12p121	13q31	15q23	18p1131	21p13	Xq213	
12p122	13q32	15q24	18p1132	21q10	Xq221	
12p123	13q33	15q25	18q10	21q111	Xq222	
12p131	13q34	15q261	18q111	21q112	Xq223	
12p132	14p10	15q262	18q112	21q21	Xq23	
12p133	14p111	15q263	18q121	21q221	Xq24	
12q10	14p112	16p10	18q122	21q222	Xq25	

APPENDIX E

Principal Component Analysis Correlation Matrix

Correlation Matrix

	D10	D13	D14	D15	D18	D21	D22	D3P13	D3P14	D3P21	D3P22	D3P23	D3P24	D3P25	D3P26	D4	D8P22	D8P23	DY
Correlatic D10	1 000	.367	366	396	419	449	349	287	297	280	.291	.303	314	311	296	476	150	177	013
D13	367	1 000	410	465	.411	519	345	240	249	242	232	233	233	220	216	378	154	144	020
D14	.366	410	1 000	440	419	411	378	257	242	239	231	231	242	228	226	303	.078	083	096
D15	396	465	440	1 000	569	538	.396	258	277	260	260	272	272	258	243	396	147	161	- 019
D18	419	411	.419	569	1 000	512	463	313	313	294	.303	316	.305	.302	307	444	238	239	050
D21	449	519	411	538	512	1.000	523	291	.315	303	309	313	303	289	283	.432	206	206	005
D22	349	345	378	396	463	523	1 000	250	240	.224	237	249	260	257	264	488	150	141	079
D3P1	287	240	257	258	313	291	250	1 000	863	821	792	808	772	768	748	230	213	218	044
D3P1	297	249	242	277	.313	315	240	863	1 000	.952	918	.926	894	.889	866	213	218	219	005
D3P2	280	242	239	260	.294	303	224	.821	.952	1.000	964	953	921	916	.892	211	217	218	- 019
D3P2	291	232	231	260	303	309	237	792	918	964	1 000	980	948	943	919	225	211	211	- 017
D3P2	303	.233	231	272	316	313	249	808	926	953	980	1 000	969	.963	939	236	209	210	- 003
D3P2	314	233	242	272	305	303	260	772	894	921	948	969	1 000	984	959	247	233	233	006
D3P2	311	220	.228	258	302	.289	257	768	889	916	943	963	984	1 000	975	244	218	219	003
D3P2	296	.216	226	.243	307	283	.264	748	866	892	919	939	959	975	1 000	252	217	218	- 006
D4	476	378	303	396	.444	432	488	230	213	211	225	236	247	.244	252	1 000	128	132	017
D8P2	150	.154	078	147	238	206	150	213	218	217	211	209	233	218	217	128	1 000	968	- 053
D8P2	177	144	083	161	239	206	141	218	.219	218	.211	210	233	219	218	132	968	1 000	- 045
DY	013	020	096	- 019	050	005	079	044	005	- 019	- 017	- 003	006	003	- 006	017	- 053	- 045	1 000

REFERENCES

American Cancer Society (2005). Cancer Facts and Figures 2005. Atlanta: American Cancer Society. Retrieved from http://www.cancer.org/

American Cancer Society (2005). Cancer Prevention and Early Detection Facts and Figures. Atlanta: American Cancer Society. Retrieved from http://www.cancer.org/

American Cancer Society (2004, April). Detailed Guide: Skin Cancer – Nonmelanoma. Retrieved from http://www.cancer.org/docroot/CRI/content

American Cancer Society (2005, February 8). The Future of Photodynamic Therapy. Retrieved from http://www.cancer.org/docroot/ETO/content/ETO_1_4X_The_Future_of_Photodynamic_Therapy.html

American Cancer Society (2005, February 8). How Does Gene Therapy Work?. Retrieved from http://www.cancer.org/docroot/ETO/content/ETO_1_4X_How_Does_Gene_Therapy_Work.html

Baudis M., Cleary M. (2001, December). Progenetix.net: An Online Repository for Molecular Cytogenetic Aberration Data, Bioinformatics; Vol. 17, No. 12, 1228-1229. Available Online at http://www.bioinformatics.oupjournals.org

Bradford C. R., Kimmel K. A., Van Dyke D. L., Worsham M. J., Tilley B. J., Burk D., del Rosario F., Lutz S., Tooley R., Hayashida D. J., et al. (1991). 11p Deletions and Breakpoints in Squamous Cell Carcinoma: Association with Altered Reactivity with the UM-E7 Antibody, Genes Chromosomes Cancer; Vol. 3, No. 4, 427-282.

Contact a Family (2004, December). Chromosome Disorders. Retrieved from http://www.cafamily.org.uk/Direct/c30.html

Coriell Institute for Medical Research (2005). ISCN Symbols and Abbreviated Terms. Retrieved from http://locus.umdng.edu/ccr/help/iscn.html

Cornelisse C. J. (2003, April), Genes and Cancer, MedicaMundi; Vol. 47, No. 1, 28-33. Retrieved from http://www.medical.philips.com/main/news/assets/docs/medicamundi/mm_vol47_no1/07_cornelisse.pdf

Deeb George, Wang Jianxin, Block AnneMarie W., Liang Ping (2004). Karyo-Reader, a Tool for Computational Analysis of Cytogenetic Data. Retrieved from http://falcon.roswellpark.org/KR/

Frigyesi A., Gisselsson D., Mitelman F., Hoglund M. (2003, November 1). Power Law Distribution of Chromosome Aberrations in Cancer, Cancer Research; Vol. 63, 7094-7097.

Gray J. W., Collins C. (2000, March). Genome Changes and Gene Expression in Human Solid Tumors, Carcinogenesis; Vol. 21, No. 3, 443-452.

Heng H., Stevens J. B., Liu G., Bremer S. W., Ye C. J. (2004). Imaging Genome Abnormalities in Cancer Research, Cell & Chromosome; Vol. 3, No. 1.

Hiller B., Bradtke J., Balz H., & Rieder H. (2005). CyDAS: A Cytogenetic Data Analysis System, Bioinformatics; Vol. 21, No. 7, 1282-1283.

Hiller B., Bradtke J., Balz H., & Rieder H. (2004). CyDAS Online Analysis Site. Retrieved from http://www.cydas.org/OnlineAnalysis/

Hoglund M., Gisselsson D., Hansen G. B., White V. A., Sall, T., Mitelman F., Horsman D. (2004). Dissecting Karyotype Patterns in Malignant Melanomas: Temporal Clustering of Losses and Gains in Melanoma Karyotypic Evolution, International Journal of Cancer; Vol. 108, 57-65.

Hoglund M., Gisselsson D., Sall T., Mitelman F. (2002). Coping with Complexity: Multivariate Analysis of Tumor Karyotypes, Cancer Genetics and Cytogenetics; Vol. 135 103-109.

Hoglund M., Jin C., Gisselsson D., Hansen G. B., Mitelman F., Mertens F. (2004). Statistical Analyses of Karyotypic Complexity in Head and Neck Squamous Cell Carcinoma, Cancer Genetics and Cytogenetics; Vol. 150, 1-8.

Jin Y., Mertens F., Mandahl N., Heim S., Olegard C., Wennerberg J., Biorklund A., Mitelman F (1993, May 1). Chromosome Abnormalities in Eighty-three Head and Neck Squamous Cell Carcinomas: Influence of Culture Conditions on Karyotypic Pattern, Cancer Research; Vol. 53, No. 9, 2140-2146.

Keser, Ibrahim (1999). Comparative Genomic Hybridization (CGH) in Cancer Research, Turkish Journal of Medical Sciences; Vol. 29, 85-88.

Malcolm, Sue (2001, August 8). Chromosome Abnormalities. Clinical Molecular Genetics Society. Retrieved from http://www.ich.ucl.ac.uk/cmgs/chromabs.htm

Memorial Sloan-Kettering Cancer Center (2001, May 24). Squamous Cell Carcinoma. Retrieved from http://www.mskcc.org/mskcc/html/5501.cfm

Mitelman Felix (1995). ISCN 1995: An International System for Human Cytogenetic Nomenclature. Basel, Switerzland: S. Karger Publishers, Inc.

Mitelman F., Johansson B., Mertens F. (2004, April). Fusion Genes and Rearranged Genes as a Linear Function of Chromosome Aberrations in Cancer, Nature Genetics; Vol. 36, No. 4, 331-334.

Mitelman F., Johansson B., Mertens, F. (2005). Mitelman Database of Chromosome Aberrations in Cancer. Retrieved from http://cgap.nci.nih.gov/Chromosomes/Mitelman

Skin Cancer Foundation (2004). About Squamous Cell. Retrieved from http://www.skincancer.org/squamous/index.php

Tai A. L., Yan W. S., Fang Y., Xie D., Sham J. S., Guan X. Y. (2004, May 1). Recurrent Chromosomal Imbalances in Nonsmall Cell Lung Carcinoma: The Association Between 1q Amplification and Tumor Recurrence, Cancer; Vol. 100, No. 9, 1918-1927.

Van Dyke D. L. (2001, September). Atlas of Genetics and Cytogenetics in Oncology and Haematology. Retrieved from http://www.infobiogen.fr/services/chromcancer/Tumors/SquamousCellID5130.html

Van Dyke D. L., Worsham M. J., Benninger M. S., Krause C. J., Baker S. R., Wolf G. T., Drumheller T., Tilley B. C., Carey T.E (1994, March). Recurrent Cytogenetic Abnormalities in Squamous Cell Carcinomas of the Head and Neck Region, Genes Chromosomes Cancer; Vol. 9, No. 3, 192-206.

Viegas-Pequignot E., Flury-Herard A., De Cremoux H., Chlecq C., Bignon J., Dutrillaux B. (1990, October 1). Recurrent Chromosome Aberrations in Human Lung Squamous Cell Carcinomas, Cancer Genetics and Cytogenetics; Vol. 49, No. 1, 37-49.

Walden, T. L. Jr., Farzaneh, N. K. (1989, April). Chapter 6: Radiological Assessment of Radiation Damage. Armed Forces Radiobiology Research Institute. Retrieved from http://www.afrri.usuhs.mil/www/outreach/pdf/tmm/chapter6/figure6-5.pdf

VITA

Jeremy C. Slatton was born in Franklin, Pennsylvania, on April 28, 1980. He was raised in Zebulon, North Carolina by his parents Donna M. Slatton and Dennis P. Slatton. After graduating from the prestigious North Carolina School of Science and Mathematics in Durham, North Carolina, he enrolled in college at North Carolina State University in Raleigh in 1998. Jeremy worked his way through college and received his Bachelor of Science in Chemistry from North Carolina State University in 2001. In 2002, he entered the Graduate College of Texas State University in San Marcos, Texas to work towards a Master of Science degree in Health Services Research. His professional career began in the healthcare industry in 2000 while completing his final year of undergraduate work. Since 2000, Jeremy has worked for the Seton Healthcare Network in Austin, Texas.

Permanent Address: 2000 Cedar Bend Drive Apartment 524
Austin, Texas 78758
100 Pineview Drive
Zebulon, North Carolina 27597

This thesis was typed by Jeremy Slatton.