IDENTIFICATION OF GENES THAT CAUSE MELANOMA SKIN CANCER

Enrollment no: 161508

Name of the student: Dushyant Sharma

Name of the Supervisor: Dr.Tiratha Raj Singh

Submitted in partial fulfillment of the requirement for the award of degree of

BACHELOR OF TECHNOLOGY

IN

BIOINFORMATICS

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS,

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY

WAKNAGHAT, SOLAN 173234, HIMACHAL PRADESH, INDIA

ACKNOWLEDGEMENT

Firstly, I like to extend my sincere gratitude to my final year project supervisor Dr. Tiratha Raj Singh, for providing me with an opportunity to conduct research work in my area of interest. Also, his continuous guidance, efforts, and invertible suggestions throughout the duration of the project were a blessing in disguise.

I give my greatest acknowledgement to my family and Parents in all-round support during studies.

DECLARATION BY THE STUDENT

I hereby declare that the report in the B.Tech project entitled "Identification of genes that cause Melanoma skin cancer" was submitted at the Jaypee University of Information Technology, Waknaghat, Himachal Pradesh, India, is an authentic record of my work carried out under the supervision of Dr. Tiratha Raj Singh. I have not submitted this work elsewhere for any degree or diploma.

(Signature of Student)

Dushyant Sharma

(161508)

Department of Biotechnology and Bioinformatics,

Jaypee University of Information Technology,

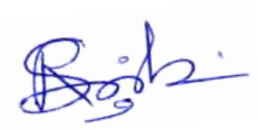
Waknaghat, Himachal Pradesh, India

Date:24/12/2021

CERTIFICATE

This is to certify that the project entitled “Identification of genes that cause Melanoma skin cancer”, submitted by Dushyant Sharma is in fulfillment for the award of the degree of Bachelors of Technology in Bioinformatics to the Jaypee University of Information Technology, Waknaghat, Solan(H.P.), India is an authentic record of candidate’s own work carried out by him under my supervision.

This work has not been submitted partially of fully to any other university or institution in order to achieve any award or other degree.



Dr. Tiratha Raj Singh

Associate Professor,

Department of Biotechnology and Bioinformatics,

Jaypee University of Information Technology,

Waknaghat, Distt, Solan(173234), Himachal Pradesh, India

TABLE OF CONTENTS

LIST OF FIGURES

Abstract

When cell duplication is continuously happens so it leads to the cancer. It is the second biggest cause of mortality worldwide, according to the World Health Organization. In 2018, 96 lakh people died worldwide due to cancer. While Lung cancer is the most dangerous type of cancer, this paper focuses on skin cancer (particularly melanoma). The most dangerous type of Carcinoma is Melanoma. Skin cancer is the abnormal development of skin cells as a result of exposure to ultraviolet (UV) rays from the sun. However, skin cancer can also affect parts of the skin that aren't exposed to the sun. Exposure to ultraviolet light can be limited or avoided to lower the risk of skin cancer. Examining the skin for abnormal changes can play a key role in the early stage diagnosis of the cancers. The best chance for a successful skin cancer treatment is to begin treatment as soon as possible.

Introduction

Life on earth began around 3.7 billion years ago. A cell divided itself into two by replication, then during the process of evolution, more complex systems life forms started forming (multicellular organisms). Multicellular oranisms are the most successful life forms on earth.

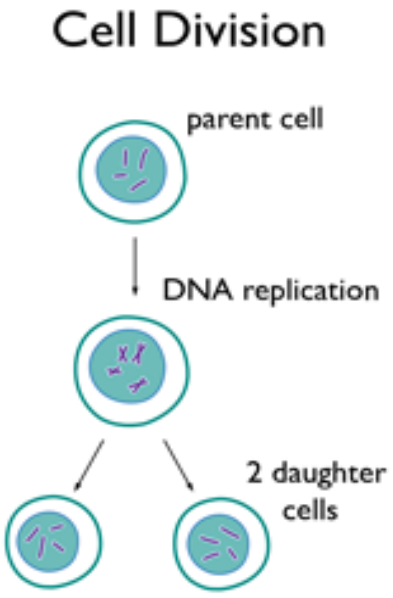


Figure 1

We humas are also multicellular, our body is made up of trillions of cells. They are the building blocks of our body. They play a crucial role in daily tasks such as absorbing nutrients from food and turning those nutrients into energy.

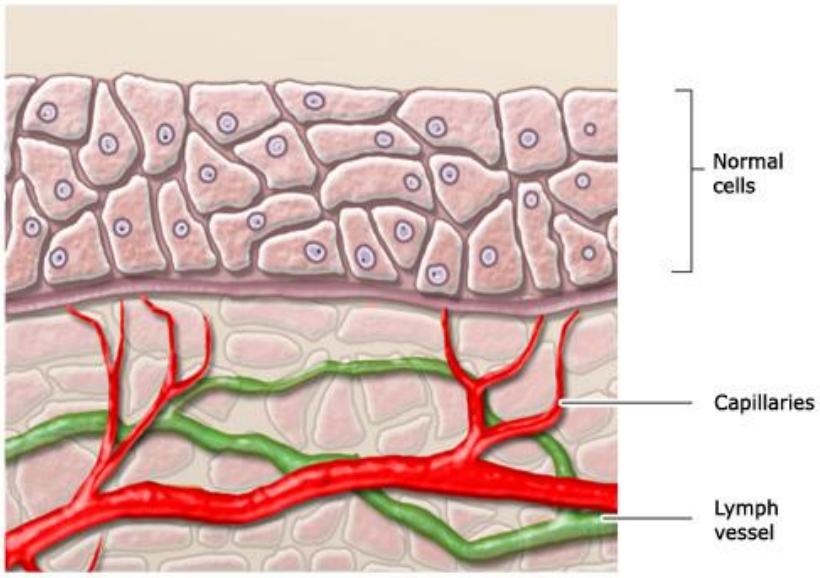


Figure 2

Each cell in our body has a pre-defined set of instructions which it has to follow which is written in their genes(DNA).

In our body, old cells are continuosly being replaced by new cells, which eventually die or become damaged due to cell division. This mechanism is extremely intricate, and when it malfunctions, aberrant or damaged cells may continue to grow and multiply instead of dying. Tumors, which are masses of tissue, form as a result of these cells. Tumors can spread or invade neighboring tissues, as well as travel to distant areas in the body to form new tumours, thanks to metastasis (when cancer cells break away from the tumour and enter the circulation or systema lymphaticum). Fluids are carried around the body by these systems. (This indicates that malignant cells can spread

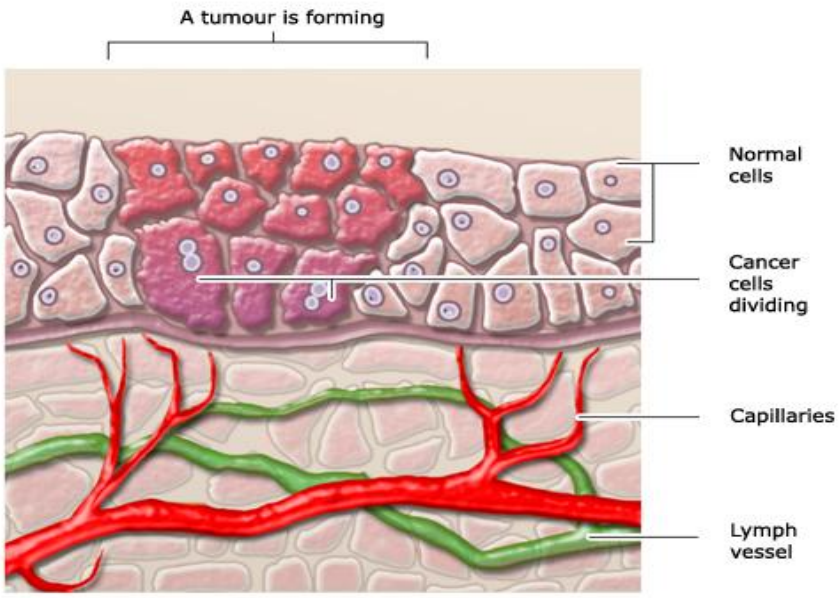


Figure 3

throughout the body and cause new tumours). Cancerous and non-cancerous tumours exist. Benign tumours are non-cancerous tumours that develop slowly and do not spread or cause harm. When benign tumours are excised, they usually do not return, whereas malignant tumours do. Malignant tumours multiply quickly, engulf and kill surrounding tissues, and spread throughout the body.

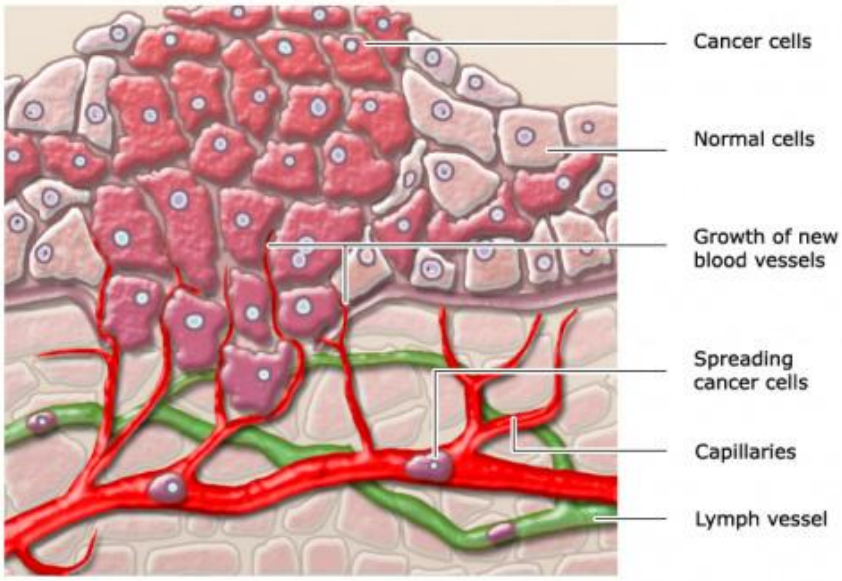


Figure 4

Skin cancer is divided into three types (rare and uncommon cancers excluded):

1. Basal cell carcinoma(BCC)- develops in the basal cells of the skin. it is most common in sun-exposed parts of the body, such as the neck and face 2. Squamous cell carcinoma (SCC) develops as a result of unrestricted growth of squamous cells. SCC most commonly affects sun-exposed regions of the body as well as internal organs such as the face, ears, hands, mouth, throat, and lungs. Squamous cell carcinoma is most common in locations that aren't frequently exposed to the sun. 3. Melanoma is the third and most lethal form of skin cancer. Melanoma usually develops on the palms of the hands or soles of the feet, or under the fingernails or toenails. Melanomas are pigmented tumors that vary in appearance depending on their clinical stage and histological subtype.

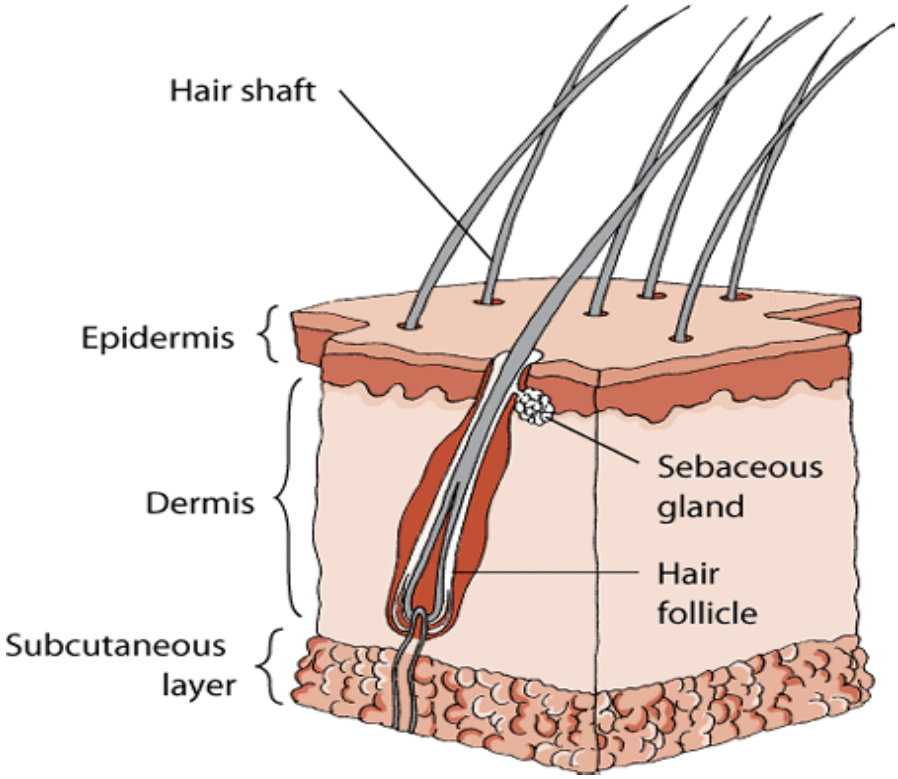


Figure 5

common moles (e.g. junctional, compound,melanocytic, and intradermal nevi), Solar lentigo, and seborrheic keratosis are all common pigmented lesions that are difficult to identify from early-stage melanoma. Visual inspection and pattern recognition can assist determine whether a pigmented lesion has melanoma-like characteristics. The ABCDE rule has been established to describe these characteristics. ABDCE stands for Asymmetry (the tumour cannot be divided in half), Border irregularity, Color variability (uneven colour distribution), Diameter (lesions are frequently larger than 6 mm in diameter), and Evolving (colour and/or size of the lesion changes with time). The ABCDE criteria aid in the diagnosis of melanomas, particularly those with a superficial spreading subtype.

Precursor lesions and Natural history

The neural crest-derived melanocytes also called normal pigment cells are responcible for the melanoma generation. These cells are present on the upper membranes of epithelial cell surfaces. Melanocytes play an important role in the production, storage, and transport of melanin pigments to surrounding epithelial cells. Melanin is produced in melanocytes by melanosomes, which are small endocytic vesicles (Vijayasaradhi et al., 1995). To generate and store pigment in

melanosomes, primary melanoma cells retain these differentiation pathways. The presence of pigment, immunological tagging of melanosome-specific proteins, and electron imaging of melanosomes distinguish melanoma from other malignancies (Chandra and Singh, 2012).

Melanomas form on the skin in the majority of cases (>90 percent), mainly in sun-exposed areas including the limbs, trunk, and face. Melanomas are more common in dark-skinned people's mucous membranes, nailbeds, palms, and soles of feet. About 3 to 5 % melanomas is formed by the non-cutaneous epithelial surfaces like esophagus, vaginal mucous membranes, rectum and mucous membranes of the oropharynx and sinuses. Approximately 5% of melanoma patients develop metastatic tumors that have no known etiology. The vast majority of these cases are almost certainly complete regressions of an initial cutaneous primary tumour (possibly via immunological or other host mechanisms), with no effect of melanoma regression at the primary site on the relatively poor prognosis of metastases, highlighting the biological differences between primary and metastatic tumours. The immune system's ability to identify melanoma cells has been proven by several lines of evidence. Melanoma research has provided us with a wealth of information regarding human cancer immunity. Immunotherapy, which includes interferons and interleukin-2, is a frequent treatment for metastatic melanoma, however, it is ineffective.

Staging, Diagnosis and conventional therapy

Because of early discovery at the early phases of tumour progression, approximately 85% of the paitient can be cured. While Melanoma can be extremely dangerous, spreading to nearly any organ in the body. Identification of melanoma in later stages of tumour progression is related with poor prognosis. Asymmetry, irregular borders, color variability, and a breadth greater than 6 mm are all common clinical features of melanoma skin lesions (the so-called "ABCD's" of carcinoma). The melanoma identification is a very critical

task. To make a decision, a pathology examination is required. The two cardinal characteristics of malignancy, invasion, and metastases, are used to determine the pathologic verdict and staging of melanoma. A excellent paradigm for malignant changeover, invasion, and metastases is the well-defined process of malignant changeover from normal melanocytes to metastatic carcinomas. Melanoma has two stages: (1) radial growth, which is marked by horizontal outspread of converted melanocytic cells within the epidermis and small nests of invasive cells limited to the upper part of the dermis, and (2) vertical growth, which is marked by melanoma cells incursion into the deeper dermis and supporting subcutaneous tissues. Only vertical phase melanoma lesions are usually related with metastasis, while pure radial growth phase melanomas are almost never associated with metastasis. These data suggest that invasion is essential for metastasis, and that invasion depth, which is the most important prognostic predictor, affects the outcome. Clark et al. (1969) used Clark's technique (based on anatomic skin markers) or Breslow's approach to stage primary melanomas according to the depth of invasion into the dermis (a direct measure of the depth of invasion from the epidermis). To assess the stage of disease, the TNM classification system is employed (T, primary tumor; N, local lymph nodes; M, metastases). Melanomas that are still in situ (stage 0) are noninvasive and haven't broken down the epidermal basement membrane (these lesions aren't counted in melanoma statistics). Melanomas in stages I and II (typically 2.0 mm in depth) are small, localised growths that are surgically removed. Localized spread across lymphatic channels characterizes stage III melanoma, which is treated with surgery and/or interferon-2b adjuvant therapy. Hematogenous spread is used to disseminate distant metastases in stage 4 melanoma. Systemic therapy (chemotherapy and immunotherapy) is employed in combination with surgery and radiation therapy, although only a tiny percentage of cases result in complete remission (Yadav and Singh, 2021).

Melanoma genes and pathways have a role in both sporadic and hereditary melanoma.

Cell cycle regulation damage

A CDK4 mutation (R24C) was found in three melanoma families, however such mutations are uncommon in melanoma families (Zuo et al., 1996). The activity of cyclin-dependent kinases 4 and 6 (CDK4 and CDK6), which regulate early phosphorylation of the Rb protein, is reduced by p16Ink4a, which prevents the G1-S transition. The R24C mutation prevents p16INK4A from binding to CDK4, and knock-in mice with a mutant CDK4 R24C allele generate melanomas, proving that the Rb pathway is active (Sotillo et al., 2001). In spontaneous (nonfamilial) melanomas, somatic mutations in p16Ink4a are infrequent (varying from 0 percent to 28 percent). Epigenetic inactivation of p16Ink4a has been discovered in a small number of cases due to methylation of the promoter region. Upregulation of Id-1, a transcriptional repressor of p16INK4A, was detected in early melanomas in a preliminary investigation, revealing another way to quiet p16Ink4a (Polsky et al., 2001c). Amplification of cyclin D1 has been found in melanomas that form on sun-protected acral (hands and feet) surfaces, but only in sun-protected acral (hands and feet) surfaces (Sauter et al., 2002). The p53 tumour suppressor pathway is still a mystery to scientists. P53 mutations are uncommon in melanomas, in contrast to many other kinds of cancer. The p53 inhibitor HDM2, on the other hand, is upregulated in early melanomas, showing that the p53 pathway is similarly dysregulated (Polsky et al., 2001a). Mice with mutant ras alleles produce melanomas in a p53-deficient environment, suggesting that the p53 pathway may be involved (Bardeesy et al., 2001). Apaf-1 inactivation, an apoptotic effector downstream of p53, is common in metastatic melanomas and may explain melanoma resistance to cytotoxic drugs (Shukla et al., 2019; Soengas et al., 2001).

Ras pathway involvement in melanoma

Despite the fact that RAS family gene mutations are infrequent in melanoma specimens (less than 10%), animal studies suggest that this essential pathway is important in carcinogenesis (Chin et al., 1999, Bardeesy et al., 2000). Overexpression of the mutant Ha-Ras oncoprotein causes malignant transformation of normal human melanocytes, according to this study (Albino et al., 1992). Furthermore, invasive melanomas developed when transgenic mice were pushed to express mutant Ha-Ras in cutaneous melanocytes and placed on a CDKN2-deficient background, despite the fact that mutant Ha-Ras alone was unable to cause complete transformation (Chin et al., 1999).

Surprisingly, mutant Ha-Ras expression was essential to keep tumours growing. In experimental models, the bFGF receptor, which is upstream of ras, has been demonstrated to contribute to melanoma carcinogenesis. Activating mutations in BRAF are widespread in melanomas, according to a recent study based on human data, with activating mutations discovered in 59 percent of melanoma cell lines and 6 out of 9 melanoma specimens. Davies et al. (Davies et al., 2002). BRAF is a cytoplasmic serine/threonine kinase whose activity is regulated by RAS (RAS-RAF-MEK-ERK-MAP kinase). BRAF would become a legitimate target for experimental melanoma therapy if confirmed in a larger panel of melanoma tissues (including primary tumours). Overexpression of RhoC, a member of the Rho family of GTP-hydrolyzing proteins, has been associated to the progression of localised melanoma to metastatic illness, according to another study (Clark et al., 2000). Changes in the Ras pathway are crucial in human melanoma, according to these human-based articles.

UV mutations Missing fingerprints

UV-B causes cyclobutane pyrimidine dimers, primarily thymidine dinucleotides. Lesions that are not repaired by nucleotide excision repair might cause GCAT transitions, which leave a mutagenic fingerprint. In nonmelanoma skin cancers, UV-B signature mutations in the tumour suppressor gene p53 are

prevalent (Sehgal and Singh, 2014). UV signature mutations in Ink4a or BRAF have not been discovered in melanoma specimens at all. Based on these data, there is little evidence for UV radiation's mutagenic impact on the development of melanoma. Epidemiologic evidence suggesting a relationship between solar exposure and health in Caucasian populations, on the other hand, is compelling. Sunburn UV-B exposure resulted in a significant increase in melanocytic lesions in newborn mice expressing hepatocyte growth factor from a transgene (including those typical of in situ melanomas). Irradiated older mice were compared to unirradiated older mice with a possible precursor lesion of invasive melanoma (Noonan et al., 2001; Sehgal and Singh, 2015). Other types of UV exposure during childhood and adolescence may be important, and target genes are still being discovered, but nonmutagenic mechanisms like immune suppression, UV induction of melanocyte growth factors by inflammatory cells or damaged keratinocytes, and UV production of mutagenic oxidative radicals during inflammation or melanogenesis should be taken more seriously.

Methods for data collection

The genes involved in the cancer were collected from various databases such as OMIM, HGNC, Ensembl, GeneCard, and Gene. A database is collection of data in such a way that makes it easy to access and maintain. The purpose of making a database is to keep information easily accessible and organized. It reduces the time you spend managing the data. Its features include minimum duplicity and redundancy, saves storage cost, anyone can work on it. The NCBI gene database was extensively used to collect gene-related data, along with other databases to correlate the information. OMIM (online mendelian inheritance in man), HGNC (HUGO gene nomenclature committee), Ensembl genome browser, and GeneCards-human gene database were among the other databases used. Collection of information was from various sources and is shown in the excel sheet.

Results

Genes and environmental factors were collected from the papers, and are mentioned in (Table 1). Columns were created named gene, protein, aliases and location. A total of 229 genes and their information is collected.

GENE	PROTEIN	ALIASES	LOCATION
BRAF	Serine/threonine protein kinase	NS7, BRAF1, RAFB1, B-RAF1, B-raf	7q34
NRAS	NRas and GTPase	NRAS1, NS6, NCMS, N-ras, ALPS4, and CMNS	1p13.2
CDKN2A	"cyclin-dependent kinase inhibitor 2A"	INK4A, MTS1, CDK4I, MTS-1, P16INK4, P16INK4A, P14ARF, ARF, CDKN2, P14, CMM2, TP16, P19, MLM, P16, INK4, P19ARF, P16-INK4A	9p21.3
KIT	Growth factor receptor kit for mast or stem cell	CD117, MASTC C-Kit, SCFR, PBT	4q12
CTNNB1	catenin beta-1	EVR7, CTNNB, MRD19, NEDSDV, armadillo	3p22.1
MITF	"Microphthalmia-associated transcription factor"	WS2, bHLHe32 COMMAD, MI, WS2A, CMM8,	3p13
AR	"Androgen receptor"	KD, DHTR, SMAX1, SBMA, NR3C4, AR8, TFM, AIS, HYSP1, HUMARA	Xq12
CDK4	"Cyclin-dependent kinase 4"	PSK-J3, CMM3	12q14.1

MC1R	"Melanocyte-stimulating hormone receptor"	MSH-R, CMM5 and SHEP2	16q24.3
FGF2	"Fibroblast growth factor 2"	HBGF-2 FGFB, FGF-2, BFGF,	4q28.1
TP53	Tumour protein antigen p53	BFGF, FGFB, HBGF-2 FGF-2,	17p13.1
MCAM	cell surface glycoprotein MUC18	CD146, MUC18, HEMCAM, METCAM, MelCAM	11q23.3
MLANA	"Melanoma antigen recognized by T-cells 1"	MART-1 and MART1	9p24.1
GNAQ	"Guanine nucleotide-binding protein G(q) subunit alpha"	CMC1, SWS, GAQ, G-ALPHA-q	9q21.2
GNA11	"Guanine nucleotide-binding protein subunit alpha-11"	FBH, FBH2, FHH2, HHC2, GNA-11, HYPOC2	19p13.3
CDKN1A	"Cyclin-dependent kinase inhibitor 1"	MDA-6, CAP20, CIP1, p21CIP1 WAF1, P21, SDI1, CDKN1,	6p21.2
BAP1	"Ubiquitin carboxyl-terminal hydrolase BAP1"	UCHL2, HUCEP-13, hucep-6	3p21.1
TERT	"Telomerase reverse transcriptase"	EST2, DKCB4, hTRT, hEST2, CMM9, DKCA2, TCS1, TP2, PFBMFT1 TRT,	5p15.33
CXCL1	"Growth-regulated alpha protein"	GRO1, NAP-3, MGSA, GROa, SCYB1, FSP, MGSA-a	4q13.3
MMP2	72 kDa type IV collagenase	CLG4A, MMP-II MONA, TBE-1, MMP-2, CLG4	16q12.2

HLA-B	“Major histocompatibility complex, class I, B”	HLAB, B-4901, AS	6p21.33
SOX10	“Transcription factor SOX-10”	WS4C, PCWH, DOM,WS2E, WS4	22q13.1
CAMP	“Cathelicidin antimicrobial peptide”	CAP18, CRAMP, CAP-18, HSD26, FALL39, FALL-39 LL37,	3p21.31
BRKA2	“Breast cancer type 2 susceptibility protein”	PNCA2, BROVCA2 FACD, BRCC2, GLM3, FAD1, XRCC11, FAD, FANCD1, FANCD	13q13.1
HRAS	GTPase HRas	C-H-RAS, C-HA-RAS1 RASH1, KRAS, RASK2, HRAS1, c-Ki-ras, C-BAS/HAS, p21ras, CTLO, H-RASIDX, Ki-Ras, c-K-ras, HAMSV, KRAS2,	11p15.5
PMEL	“Melanocyte protein PMEL”dv	P100, ME20M, D12S53E SI, ME20-M, gp100, SIL, ME20, SILV, P1, PMEL17,	12q13.2
IL24	“Interleukin-24”	IL10B MOB5, C49A, FISP, MDA7, ST16,	1q32.1
IL4	“Interleukin-4”	BCGF-1 IL-4, BCGF1, BSF1, BSF-1	5q31.1
TYRP1	“5,6-dihydroxyindole-2-carboxylic acid oxidase”	TRP1, CAS2, TRP, GP75, TYRP, b-PROTEIN OCA3, CATB	9p23

CTLA4	cytotoxic T-lymphocyte protein 4	GSE, CTLA-4, CD, ALPS5, GRD4, CD152, CELIAC3 IDDM12	2q33.2
MYB	“Transcriptional activator Myb”	Cmyb, Efg, c-myb_CDS c-myb	6q23.3
RAF1	“RAF proto-oncogene serine/threonine-protein kinase”	CRAF, CMD1NN c-Raf, Raf-1, NS5	3p25.2
MAGEA3	“Melanoma-associated antigen-3”	MAGE3, HYPD, MAGEA6 CT1.3, HIP8	Xq28
MAGEA1	“Melanoma-associated antigen-1”	MAGE1 and CT1.1	Xq28
FOXP3	“Forkhead box protein P3”	AIID, JM2, IPEX, PIDX, XPID, DIETER	Xp11.23
CDKN2C	“Cyclin-dependent kinase 4 inhibitor C”	INK4C, p18, p18-INK4C	1p32.3
RAC1	“Ras-related C3 botulinum toxin substrate 1”	p21-Rac1 MIG5, TC-25, Rac-1, MRD48	7p22.1
PAX3	“Paired box protein Pax-3”	HUP2 CDHS, WS1, WS3	2q36.1
CDK6	“Cyclin-dependent kinase 6”	PLSTIRE and MCPH12	7q21.2
ICAM1	“Intercellular adhesion molecule 1”	CD54, BB2, P3.58	19p13.2
BAD	“Bcl2-associated agonist of cell death”	BCL2L8 and BBC2	11q13.1
MAP2K1	“Dual specificity mitogen-activated protein kinase kinase 1”	PRKMK1 MEK1, MKK1, MAPKK1, CFC3	15q22.31
TFAP2C	“Transcription factor AP-2-alpha”	hAP-2g, TFAP2G, ERF1, AP2-GAMMA	20q13.31
RREB1	“Ras-responsive element-binding protein 1”	HNT, FINB, RREB-1 LZ321, Zep-1	6p24.3

CD63	CD63 antigen	LAMP-3, OMA81H, ME491, TSPAN30 MLA1,	12q13.2
PARP1	“Poly [ADP-ribose] polymerase 1"	ADPRT1, ADPRT, ADPRT PPOL, pADPRT-1 ARTD1, 1, PARP, PARP-1	1q42.12
WNT5A	“Protein Wnt-5a”	hWNT5A	3p14.3
CD80	“T-lymphocyte activation antigen CD80”	CD28LG, LAB7, CD28LG1 BB1, B7.1, B7-1, B7	3q13.33
ATF1	“Cyclic AMP-dependent transcription factor ATF-1”	FUS/ATF-1, TREB36, EWS-ATF1	12q13.12
STAT1	“Signal transducer and activator of transcription 1-alpha/beta”	IMD31A, CANDF7, ISGF-3, IMD31B, STAT91, IMD31C	2q32.2
TIMP1	“Metalloproteinase inhibitor 1”	EPO, TIMP-1 EPA, CLGI, HCI, TIMP	Xp11.3
ASIP	“Agouti-signalling protein”	ASP, AGTI, SHEP9 AGTIL, AGSW,	20q11.22
SPARC	SPARC	BM-40, ON, OI17,	5q33.1
MMP1	interstitial collagenase	CLGN, CLG	11q22.2
PRAME	“Melanoma antigen preferentially expressed in tumours”	OIP-4 MAPE, OIP4, CT130,	22q11.22
MAP2K2	“Dual specificity mitogen-activated protein kinase kinase 2”	MAPKK2, MEK2, PRKMK2 CFC4, MKK2	19p13.3
PIGS	“GPI transamidase component PIG-S”	GPIBD18	17q11.2
RHOC	“Rho-related GTP-binding protein RhoC”	EYCL2, EYCL3, BEY2, ARHC, SHEP1, ARH9, PED,	1p13.2

		RHOH9P, D15S12 EYCL, BEY1, BOCA, H9, HCL3, BEY	
OCA2	P protein		15q12-q13.1
PRKN	E3 ubiquitin-protein ligase parkin	AR-JP, LPRS2, PARK2, PDJ	6q26
CD274	“Programmed cell death 1 ligand 1”	PDCD1LG1, B7-H, PDL1, B7H1, PDCD1L1, hPDL1, PD-L1	9p24.1
ABCB5	“ATP-binding cassette sub-family B member 5”	ABCB5beta, ABCB5alpha EST422562,	7p21.1
CTAG1B	“Cancer/testis antigen 1”	CT6.1, CTAG, LAGE-2, NY-ESO-1 ESO1, LAGE2B, CTAG1,	Xq28
HLA-C	“HLA class I histocompatibility antigen, Cw-1 alpha chain”	PSORS1, D6S204, MHC, HLA-JY3, HLAC, HLC-C	6p21.33
HLA-DRB1	“Major histocompatibility complex, class II, DR beta 1”	DRB1, HLA-DR1B, HLA-DRB, SS1	6p21.32
MAGEA2	“Melanoma-associated antigen 2”	MAGE2, CT1.2, MAGEA2A	Xq28
AKT3	“RAC-gamma serine/threonine-protein kinase”	STK-2, RAC-gamma, PKBG, RAC-PK-gamma MPPH, PKB-GAMMA, MPPH2, PRKBG,	1q43-q44
XPC	“DNA repair protein complementing XP-C cells"	XP3, p125, RAD4, XPCC	3p25.1
MIA	“Melanoma-derived growth regulatory protein”	CD-RAP	19q13.2
CD68	“Macrosialin”	LAMP4, GP110, SCARD1	17p13.1
S100A6	“protein S100-A6”	CABP, PRA, CACY, 2A9, 5B10, S10A6	1q21.3

MTAP	“S-methyl-5'-thioadenosine phosphorylase”	HEL-249 c86fus, BDMF, LGMBF, DMSMFH, DMSFH, MSAP	9p21.3
S100B	protein S100-B	S100beta, NEF, S100-B, S100	21q22.3
FAS	“Tumor necrosis factor receptor superfamily member 6”	ALPS1A, TNFRSF6, APT1, APO-1, FAS1, FASTM, CD95	10q23.31
IL2	“Interleukin-2”	IL-2, lymphokine, TCGF	4q27
APAF1	“Apoptotic protease-activating factor 1”	APAF-1, CED4	12q23.1
SF3B1	“Splicing factor 3B subunit 1”	Hsh155, PRP10, SAP155, SF3b155, PRPF10, MDS	2q33.1
CIITA	“MHC class II transactivator”	CIITAIV, C2TA, NLRA, MHC2TA,	16p13.13
KISS1	“Metastasis-suppressor Kiss-1”	KiSS-1, HH13	1q32.1
SKI	“Ski oncogene”	SKV, SGS	1p36.33-p36.32
GAST	“Gastrin”	GAS	17q21.2
CXCL10	“C-X-C motif chemokine 10”	IFI10, IP-10, C7, INP10, crg-2, gIP-10, mob-1, SCYB10	4q21.1
CLPTM1L	“Cleft lip and palate transmembrane protein 1-like protein”	CRR9	5p15.33
ERBB4	“Receptor tyrosine-protein kinase erbB-4”	ALS19, HER4, p180erbB4	2q34
MIRLET7B	“MicroRNA let-7b”	hsa-let-7b, MIRNLET7B, LET7B, let-7b	22q13.31
TAP1	“Antigen peptide transporter 1”	PSF1, ABCB2, D6S114E, ABC17, APT1, TAP1*0102N,	6p21.32

		TAP1N, PSF-1, RING4	
CD86	“T-lymphocyte activation antigen CD86”	CD28LG2, B7.2, B70, B7-2, LAB72	3q13.33
GSTT1	“Glutathione S-transferase theta-1"		22q11.23
GRM1	“Metabotropic glutamate receptor 1”	MGLUR1, GPRC1A, SCAR13, PPP1R85, SCA44, MGLU1	6q24.3
L1CAM	“Neural cell adhesion molecule L1”	HSAS1, N-CAML1, SPG1, CD171, CAML1, MIC5, NCAM-L1, HSAS, S10, N-CAM-L1, MASA	Xq28
ITCH	“E3 ubiquitin-protein ligase Itchy homolog”	ADMFD, AIP4, NAPP1, AIF4	20q11.22
POT1	“Protection of telomeres protein 1”	CMM10, GLM9, HPOT1	7q31.33
MAGEB2	“Melanoma-associated antigen B2”	DAM6, MAGE-XP-2, CT3.2	Xp21.2
ATF2	“Cyclic AMP-dependent transcription factor ATF-2”	TREB7, CREB-2, CRE-BP1, CREB2, HB16	2q31.1
IRF4	“Interferon regulatory factor-4”	LSIRF, NF-EM5, MUM1, SHEP8	6p25.3
KDM5B	“Lysine-specific demethylase 5B”	PUT1, PLU-1, CT31, RBP2-H1, RBBP2H1A, PLU1, JARID1B, PPP1R98, MRT65	1q32.1
BCL2A1	“Bcl-2-related protein A1”	ACC-1, ACC2, BCL2L5, ACC-2, BFL1, HBPA1, ACC1, GRS	15q25.1

CCR7	"C-C chemokine receptor type 7"	CCR-7, CD197, CDw197, EBI1, CC-CKR-7, CMKBR7, BLR2	17q21.2
TLR3	"Toll-like receptor 3"	IIAE2, CD283	4q35.1
GDF15	"Growth/differentiation factor 15"	GDF-15, PDF, PLAB, NAG-1, MIC-1, PTGFB, MIC1	19p13.11
EDNRB	"Endothelin receptor type B"	ET-BR, ETBR, ETB1, WS4A, HSCR, ET-B, ETB, ABCDS, HSCR2 ETRB	13q22.3
CITED1	"cbp/p300-interacting transactivator 1"	MSG1	Xq13.1
TRB		TRB, TCRB	7q34
CD27	"CD27 antigen"	Tp55, TNFRSF7, S152, T14, S152. LPFS2	12p13.31
YES1	"Tyrosine-protein kinase Yes"	HsT441, P61-YES, c-yes, Yes	18p11.32
NEDD9	"Enhancer of filamentation 1"	CAS-L, CASL, HEF1, CAS2, CASS2	6p24.2
TRG		TRG, TCRG	7p14.1
TERC		PFBMFT2, hTR, DKCA1, TR, TRC3, SCARNA19	3q26.2
BIRC7	"Baculoviral IAP repeat-containing protein 7"	KIAP, ML-IAP MLIAP, LIVIN, RNF50,	20q13.33
MAGEA4	"Melanoma-associated antigen 4"	MAGE-41, MAGE4A, CT1.4, MAGE4, MAGE4B, MAGE-X2	Xq28
CEACAM1	"Carcinoembryonic antigen-related cell adhesion molecule 1"	BGPI, BGP, BGP1	19q13.2

IL18	“Interleukin-18”	IGIF, IL-1g, IL1F4, IL-18	11q23.1
SPRY4	“Protein sprouty homolog 4”	HH17	5q31.3
YBX1	“Nuclease-sensitive element-binding protein 1”	YB1, CSDA2, NSEP-1, CBF-A, MDR-NF1 EFI-A, YB-1, CSDB, BP-8, NSEP1, DBPB	1p34.2
BAGE	“B melanoma antigen 1”	CT2.1, BAGE1,	21p11.1
MSN	“Moesin”	IMD50, HEL70	Xq12
PEBP1	“Phosphatidylethanolamine-binding protein 1”	HEL-S-96, HEL-S-34, PBP, PEBP-1, HEL-210, RKIP, HCNPpp, HCNP, PEBP	12q24.23
ATF3	“Cyclic AMP-dependent transcription factor ATF-3”		1q32.3
DDB2	“DNA damage-binding protein 2”	UV-DDB2, XPE, DDBB,	11p11.2
PDCD1	“Programmed cell death protein 1”	CD279, PD1, hPD-l, hSLE1, SLEB2, hPD-1, PD-1	2q37.3
RARB	“Retinoic acid receptor beta”	MCOPS12, HAP, RARbeta1 NR1B2, RRB2,	3p24.2
TBX2	T-box transcription factor TBX2	VETD	17q23.2
PTPRD	“Receptor-type tyrosine-protein phosphatase delta”	PTPD, HPTP, HPTPDELTA, HPTPD, RPTPDELTA	9p24.1-p23
GAGE1	“G antigen 1”	GAGE-4, GAGE4, GAGE-1, CT4.1, CT4.4	Xp11.23
AIM1	“beta/gamma crystallin domain-containing protein 1”	AIM1, ST4	6q21

CXCL9	“C-X-C motif chemokine 9”	SCYB9, Humig, crg-10, CMK, MIG	4q21.1
MXI1	“max-interacting protein 1”	bHLHc11 MXI, MXD2, MAD2,	10q25.2
CD70	“CD70 antigen”	LPFS3, TNFSF7, TNLG8A CD27-L, CD27LG, CD27L	19p13.3
ULBP2	“UL16-binding protein 2”	RAET1L, RAET1H, NKG2DL2, ALCAN-alpha, N2DL2	6q25.1
“VCAN”	“versican core protein”	WGN1, ERVR, PG-M, WGN, CSPG2, GHAP	5q14.2-q14.3
“TFEB”	“Transcription factor EB”	BHLHE35, TCFEB, ALPHATFEB	6p21.1
“HSPB1”	“Heat shock protein beta-1”	HEL-S-102 SRP27, HMN2B, HSP28, CMT2F, HSP27, HS.76067, Hsp25	7q11.23
“SMARCA2”	“Probable global transcription activator SNF2L2”	hBRM, SNF2LA, SWI2, hSNF2a BAF190, Sth1p, BRM, SNF2, SNF2L2, NCBRS	9p24.3
BMP7	“Bone morphogenetic protein 7”	OP-1	20q13.31
SFPQ	“Splicing factor, proline-and glutamine-rich”	POMP100, PPP1R140 PSF,	1p34.3
NGFR	“Tumor necrosis factor receptor superfamily member 16”	p75(NTR), TNFRSF16, p75NTR, CD271, Gp80-LNGFR	17q21.33
NFATC2	“Nuclear factor of activated T-cells, cytoplasmic 2”	NFATP , NFAT1	20q13.2

OSCAR	"Osteoclast-associated immunoglobulin-like receptor"	PIgR-3, PIGR3	19q13.42
RBX1	"E3 ubiquitin-protein ligase RBX1"	RNF75, ROC1, BA554C12.1	22q13.2
CAST	"Calpastatin"	PLACK, BS-17	5q15
HSF-1	"Heat shock factor protein 1"	HSTF1	8q24.3
EFNB2	"Ephrin-B2"	Htk-L, LERK5 EPLG5, HTKL	13q33.3
STAT2	"Signal transducer and activator of transcription 2"	IMD44, P113, ISGF-3, STAT113	12q13.3
YY1AP1	"YY1-associated protein 1"	HCCA1, YY1AP, HCCA2, GRNG	1q22
ETV1	"ETS translocation variant 1"	ER81	7p21.2
FABP7	"Fatty acid-binding protein 7"	BLBP, FABPB, MRG, B-FABP	6q22.31
IRF9	"Interferon regulatory factor 9"	IRF-9, ISGF3, p48, ISGF3G	14q12
EIF3E	"Eukaryotic translation initiation factor 3 subunit E"	EIF3S6, EIF3-P48, INT6, eIF3-p46	8q23.1
ADRB2	"Beta-2 adrenergic receptor"	B2AR, BAR, ADRB2R, BETA2AR ADRBR,	5q32
CHUK	"Inhibitor of nuclear factor kappa-B kinase subunit alpha"	IKK-alpha, NFKBIKA, IKKA, IKK1, IKBKA, TCF16	10q24.31
POSTN	"Periostin"	PN, OSF2, PDLPOSTN OSF-2,	13q13.3
TBX3	"T-box transcription factor TBX3"	UMS, TBX3-ISO, XHL	12q24.21
MAP2	"Microtubule-associated protein 2"	MAP2B, MAP-2, MAP2C, MAP2A	2q34

HLA-DRA	"HLA class II histocompatibility antigen, DR alpha chain"	HLA-DRA1	6p21.32
TIMP2	"Metalloproteinase inhibitor 2"	CSC-21K, DDC8	17q25.3
PERP	"p53 apoptosis effector related to PMP-22"	KCP1, KRTCAP1, PIGPC1, dJ496H19.1 THW,	6q23.3
MAP3K5	"Mitogen-activated protein kinase 5"	ASK1, MEKK5, MAPKKK5	6q23.3
SLC9A1	"Sodium/hydrogen exchanger 1"	LIKNS, APNH, NHE-1, NHE1, PPP1R143	1p36.11
TRPM8	"Transient receptor potential cation channel subfamily M member 8"	trp-p8, TRPP8, LTrpC-6 LTRPC6,	2q37.1
NONO	"non-POU domain-containing octamer-binding protein"	MRXS34, NMT55, PPP1R114 NRB54, P54NRB, P54	Xq13.1
DUSP6	"Dual specificity protein phosphatase 6"	PYST1, MKP3, HH19	12q21.33
IGFBP7	"Insulin-like growth factor-binding protein 7"	IGFBP-7, IGFBPRP1, IGFBP-7v, FSTL2, IBP-7, PSF, AGM, RAMSVPS, TAF, MAC25	4q12
BRMS1	"Breast cancer metastasis-suppressor 1"		11q13.2
ING4	"Inhibitor of growth protein 4"	p29ING4, my036	12p13.31
ITGA4	"Integrin alpha-4"	IA4, CD49D	2q31.3
RAP1GAP	"Rap1 GTPase-activating protein 1"	RAP1GAPII RAPGAP, RAP1GA1, RAP1GAP1,	1p36.12
CD59	"CD59 glycoprotein"	MEM43, EL32, HRF20, p18-20 MIRL, MSK21, 16.3A5,	11p13

		MACIF, HRF-20, EJ16, G344, MIN2, MIN3, MAC-IP, 1F5, MIC11, EJ30, MIN1	
MCM5	"DNA replication licensing factor MCM5"	P1-CDC46, CDC46, MGORS8	22q12.3
IL12B	"Interleukin-12 subunit beta"	CLMF, NKSF2, IMD28, IL-12B IMD29, NKSF, CLMF2	5q33.3
HOXB7	"Homeobox protein Hox-B7"	HHO.C1, HOX2, Hox-2.3 HOX2C	17q21.32
MMP3	"Stromelysin-1"	CHDS6, MMP-3, STMY, SL-1, STR1, STMY1	11q22.2
ICOS	"Inducible T-cell co stimulatory"	CD278, CVID1 AILIM	2q33.2
PPP1R15A	"Protein phosphatase 1 regulatory subunit 15A"	GADD34	19q13.33
PTPRK	"Receptor-type tyrosine-protein phosphatase kappa"	R-PTP-kappa	6q22.33
HSPA8	"Heat shock cognate 71 kDa protein"	NIP71, LAP1, HEL-33, HSPA10, HSC71, HSP71, LAP-1, HSC70, HSC54, HSP73, HEL-S-72p	11q24.1
ANGPTL4	"Angiopoietin-related protein 4"	HARP, pp1158 FIAF, UNQ171, PGAR, ARP4, NL2, TGQTL, HFARP	19p13.2
HPSE	"Heparanase"	HPSE1 HPA, HPA1, HPR1, HSE1	4q21.23
MMP8	"Neutrophil collagenase"	PMNL-CL HNC, CLG1, MMP-8,	11q22.2
ARID2	"AT-rich interactive domain-containing protein 2"	BAF200, CSS6, p200	12q12
S100A2	"Protein S100-A2"	S100L , CAN19	1q21.3

FLNA	“Filamin-A”	FLN-A, MNS, ABPX, FMD, CVD1, OPD1, XLVD, FLN, FLN1, ABP-280 XMVD, OPD, CSBS, OPD2, NHBP, FGS2,	Xq28
ISG15	“Ubiquitin-like protein ISG15”	UCRP, IP17, hUCRP G1P2, IFI15, IMD38	1p36.33
TFPI2	“Tissue factor pathway inhibitor 2”	TFPI-2, PP5, REF1	7q21.3
CXCL11	“C-X-C motif chemokine 11”	I-TAC, SCYB9B IP9, b-R1, H174, SCYB11, IP-9	4q21.1
CD163	“Scavenger receptor cysteine-rich type 1 protein M130”	M130, SCARI1, MM130	12p13.31
NOX4	“NADPH oxidase 4”	RENOX KOX-1, KOX,	11q14.3
AR11	“ADP-ribosylation factor-like protein 11”	ARLTS1	13q14.2
ASAH1	“Acid ceramidase”	PHP32, PHP, SMAPME AC, ASAH, ACDase,	8p22
CTSL	“Cathepsin L1”	CATL, MEP, CTSL1	9q21.33
LARS	“Leucine--tRNA ligase, cytoplasmic”	HSPC192, RNTLS, LRS, LFIS, LARS, hr025Cl PIG44, ILFS1, LEURS, LEUS	5q32
TYRO3	“Tyrosine-protein kinase receptor TYRO3”	Etk-2 Rek, Tif, Sky, Dtk, BYK, RSE	15q15.1
HTRA2	“Serine protease HTRA2, mitochondrial”	PRSS25 MGCA8, OMI, PARK13	2p13.1
GRASP	“General receptor for phosphoinositides 1-associated scaffold protein”	TAMALIN	12q13.13
PPP2R1A	“Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha	PP2AAALPHA, PP2AA, PR65A, MRD36, PP2A-	19q13.41

	isoform"	Aalpha	
MCM4	"DNA replication licensing factor MCM4"	CDC54, P1-CDC21 NKCD, hCdc21, NKGCD, CDC21, IMD54	8q11.21
ING3	"Inhibitor of growth protein 3"	ING2, p47ING3 Eaf4, MEAF4	7q31.31
AQP3	"Aquaporin-3"	AQP-3, GIL	9p13.3
RIN1	"Ras and Rab interactor 1"		11q13.2
PAEP	Glycodelin"	GdF, PEP, PAEG, GD, ZIF-1 GdS, PP14, GdA	9q34.3
PDCD6	"Programmed cell death protein 6"	ALG2, ALG-2, PEF1B	5p15.33
RTEL1	"Regulator of telomere elongation helicase 1"	NHL, RTEL, DKCB5, C20orf41 PFBMFT3, DKCA4	20q13.33
ELK4	"ETS domain-containing protein Elk-4"	SAP1	1q32.1
MAP3K8	"Mitogen-activated protein kinase 8"	COT, MEKK8, c-COT Tpl-2, ESTF, EST, TPL2, AURA2	10p11.23
TGFBI	"Transforming growth factor-beta-induced protein ig-h3"	CDB1, CSD1, CSD2, EBMD, CDGG1 CSD, BIGH3, CSD3, CDG2, LCD1	5q31.1
PPP2CA	"Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform"	PP2Ac, PP2CA, NEDLBA, PP2Calpha RP-C	5q31.1
TRIM24	"Transcription intermediary factor 1-alpha"	TIF1, PTC6, TIF1A, TIF1ALPHA TF1A, hTIF1, RNF82	7q33-q34
ITGAM	"Integrin alpha-M"	SLEB6 MAC-1, MO1A, MAC1A, CD11B, CR3A	16p11.2

MAFG	“Transcription factor MafG”	hMAF	17q25.3
HAVCR2	“Hepatitis A virus cellular receptor 2”	TIM3, CD366, KIM-3, Tim-3, TIMD3, TIMD-3, HAVcr-2 SPTCL	5q33.3
ARNTL	“Aryl hydrocarbon receptor nuclear translocator-like protein 1”	TIC, BMAL1, BMAL1c, MOP3, PASD3, JAP3, bHLHe5	11p15.3
PTPRT	“Receptor-type tyrosine-protein phosphatase T”	RPTPrho	20q12-q13.11
CANT1	“Soluble calcium-activated nucleotidase 1”	SCAN-1 EDM7, DBQD1, DBQD, SCAN1, SHAPY,	17q25.3
ITGAX	Integrin alpha-X	SLEB6, CD11C,	16p11.2
TNFRSF9	“Tumor necrosis factor receptor superfamily member 9”	4-1BB, CD137, CDw137, ILA	1p36.23
PTPRF	“Receptor-type tyrosine-protein phosphatase F”	LAR, BNAH2	1p34.2
PPP1R3A	“Protein phosphatase 1 regulatory subunit 3A”	PPP1R3 GM, PP1G	7q31.1
PNN	“Pinin”	DRS, SDK3, memA, DRSP	14q21.1
FLNC	“Filamin-C”	MPD4, ABP-280, CMH26, ABPL, RCM5, ABPA, MFM5, FLN2, ABP280A	7q32.1
ADAM7	“Disintegrin and metalloproteinase domain-containing protein 7”	GP83, GP-83, 7, ADAM-7 ADAM, EAPI	8p21.2
KDM5A	“Lysine-specific demethylase 5A”	RBBP-2 RBBP2, RBP2,	12p13.33
MAS1	“Proto-oncogene Mas”	MGRA, MAS	6q25.3

HOXD11	"Homeobox protein Hox-D11"	HOX4F,HOX4	2q31.1
BIN1	"Myc box-dependent-interacting protein 1"	SH3P9, AMPHL, CNM2, AMPH2	2q14.3
TNFRSF8	"Tumor necrosis factor receptor superfamily member 8"	CD30, D1S166E Ki-1	1p36.22
FBXO11	"F-box only protein 11"	VIT1, FBX11, UBR6, UG063H01 IDDFBA, PRMT9	2p16.3
KNL1	"Kinetochore scaffold 1"	hKNL-1, AF15Q14, D40, PPP1R55, hSpc105 Spc7, MCPH4, CASC5, CT29,	15q15.1
BLM	"Bloom syndrome protein"	BS, MGRISCE1 RECQL3, RECQ2, RECQL2	15q26.1
TFAP2B	"Transcription factor AP-2-beta"	AP-2B, AP2-B PDA2,	6p12.3

Table 1. The detailed information of genes involved in cancer.

Conclusion

There's still a lot to learn about melanoma's pathogenesis. What receptors and signaling pathways are involved in the uncontrolled proliferation, invasion, and metastasis of cancer cells? What role does UV exposure have in the progression of melanoma? As genetics and cell biology reveals pathways and essential molecules, new targets for prevention and therapy will emerge. Using mouse models that mimic human melanoma and the underlying mechanisms, better preclinical models for screening and developing novel classes of therapeutic medicines should be possible. The information compiled in the form of genes names and identifiers will provide a supplement to the academicians and researchers working in this domain. It is believed that this information will be of utmost use to the scientific community.

References:

Albino, A.P., Sozzi, G., Nanus, D.M., Jhanwar, S.C., and Houghton, A.N. (1992). Malignant transformation of human melanocytes: induction of a complete melanoma phenotype and genotype. Oncogene 7, 2315–2321.

Balch, C., Houghton, A., Sober, A., and Soong, S.-j. (2002). Cutaneous Melanoma, Fourth Edition (St. Louis, MO: Quality Medical Publishing).

Bardeesy, N., Wong, K.K., DePinho, R.A., and Chin, L. (2000). Animal models of melanoma: recent advances and future prospects. Adv. Cancer Res. 79, 123–156.

Bardeesy, N., Bastian, B.C., Hezel, A., Pinkel, D., DePinho, R.A., and Chin, L. (2001). Dual inactivation of RB and p53 pathways in RAS-induced melanomas. Mol. Cell. Biol. 21, 2144–2153.

Berwick, M., and Halpern, A. (1997). Melanoma epidemiology. Curr. Opin. Oncol. 9, 178–182.

Bishop, D.T., Demenais, F., Goldstein, A.M., Bergman, W., Bishop, J.N., Bressac-de Paillerets, B., Chompret, A., Ghiorzo, P., Gruis, N., Hansson, J., et al. (2002). Geographical variation in the penetrance of CDKN2A mutations for melanoma. J. Natl. Cancer Inst. 94, 894–903.

Cannon-Albright, L.A., Goldgar, D.E., Meyer, L.J., Lewis, C.M., Anderson, D.E., Fountain, J.W., Hegi, M.E., Wiseman, R.W., Petty, E.M., Bale, A.E., et al. (1992). Assignment of a locus for familial melanoma, MLM, to chromosome 9p13-p22. Science 258, 1148–1152.

Chandra S., and Singh T.R., Linear B-cell epitopes prediction for epitope vaccine design against meningococcal disease and their computational validations through physicochemical properties, 2012, NetMAHIB 1(4):153-59.

Chin, L., Tam, A., Pomerantz, J., Wong, M., Holash, J., Bardeesy, N., Shen, Q., O'Hagan, R., Pantginis, J., Zhou, H., et al. (1999). Essential role for oncogenic Ras in tumor maintenance. Nature 400, 468–472.

Clark, E.A., Golub, T.R., Lander, E.S., and Hynes, R.O. (2000). Genomic analysis of metastasis reveals an essential role for RhoC. Nature 406, 532–535.

Clark, W.H., Jr., From, L., Bernardino, E.A., and Mihm, M.C. (1969). The histogenesis and biologic behavior of primary human malignant melanomas of the skin. Cancer Res. 29, 705–727.

Davies, H., Bignell, G.R., Cox, C., Stephens, P., Edkins, S., Clegg, S., Teague, J., Woffendin, H., Garnett, M.J., Bottomley, W., et al. (2002). Mutations of the BRAF gene in human cancer. Nature 417, 949–954. Fountain, J.W., Karayiorgou, M., Ernstoff, M.S., Kirkwood, J.M., Vlock, D.R., Titus-Ernstoff, L., Bouchard, B., Vijayasaradhi, S., Houghton, A.N., Lahti, J., et al. (1992). Homozygous deletions within human chromosome band 9p21 in melanoma. Proc. Natl. Acad. Sci. USA 89, 10557–10561.

Houghton, A.N., and Viola, M.V. (1981). Solar radiation and malignant melanoma of the skin. J. Am. Acad. Dermatol. 5, 477–483.

Houghton, A.N., Gold, J.S., and Blachere, N.E. (2001). Immunity against cancer: lessons learned from melanoma. Curr. Opin. Immunol. 13, 134–140.

Kripke, M.L. (1991). Immunological effects of ultraviolet radiation. J. Dermatol. 18, 429–433.

Lynch, H.T., Anderson, D.E., Smith, J.L., Jr., Howell, J.B., and Krush, A.J. (1967). Xeroderma pigmentosum, malignant melanoma, and congenital ichthyosis. A family study. Arch. Dermatol. 96, 625–635.

Noonan, F.P., Recio, J.A., Takayama, H., Duray, P., Anver, M.R., Rush, W.L., De Fabo, E.C., and Merlino, G. (2001). Neonatal sunburn and melanoma in mice. Nature 413, 271–272.

Oliveria, S., Dusza, S., and Berwick, M. (2001). Issues in the epidemiology of melanoma. Expert Rev. Anticancer Ther. 1, 453–459.

Polsky, D., Bastian, B.C., Hazan, C., Melzer, K., Pack, J., Houghton, A., Busam, K., Cordon-Cardo, C., and Osman, I. (2001a). HDM2 protein overexpression, but not gene amplification, is related to tumorigenesis of cutaneous melanoma. Cancer Res. 61, 7642–7646.

Polsky, D., Cordon-Cardo, C., and Houghton, A. (2001b). Molecular biology of melanoma, In The Molecular Basis of Cancer, Mendelson, J., Howley, P.M., Israel, M.A., and Liotta, L.A., eds (Philadelphia: W.B. Saunders Company).

Polsky, D., Young, A.Z., Busam, K.J., and Alani, R.M. (2001c). The transcriptional repressor of p16/Ink4a, Id1, is up-regulated in early melanomas. Cancer Res. 61, 6008–6011.

Sauter, E.R., Yeo, U.C., von Stemm, A., Zhu, W., Litwin, S., Tichansky, D.S., Pistritto, G., Nesbit, M., Pinkel, D., Herlyn, M., and Bastian, B.C. (2002). Cyclin D1 is a candidate oncogene in cutaneous melanoma. Cancer Res. 62, 3200–3206.

Sehgal M., and Singh T.R., DR-GAS: A database of functional genetic variants and their phosphorylation states in human DNA repair systems, 2014, DNA Repair 16, 97-103.

Sehgal M., Gupta R., Moussa A., Singh T.R., An integrative approach for mapping differentially expressed genes and network components using novel parameters to elucidate key regulatory genes in colorectal cancer, 2015, Plos one 10 (7), e0133901.

Shukla R., Munjal N.S., Singh T.R., Identification of novel small molecules against GSK3β for Alzheimer's disease using chemoinformatics approach, 2019, Journal of Molecular Graphics and Modelling 91, 91-104.

Soengas, M.S., Capodieci, P., Polsky, D., Mora, J., Esteller, M., Opitz-Araya, X., McCombie, R., Herman, J.G., Gerald, W.L., Lazebnik, Y.A., et al. (2001).

Inactivation of the apoptosis effector Apaf-1 in malignant melanoma. Nature 409, 207–211.

Sotillo, R., Garcia, J.F., Ortega, S., Martin, J., Dubus, P., Barbacid, M., and Malumbres, M. (2001). Invasive melanoma in Cdk4-targeted mice. Proc. Natl. Acad. Sci. USA 98, 13312–13317.

Vijayasaradhi, S., Xu, Y., Bouchard, B., and Houghton, A.N. (1995). Intracellular sorting and targeting of melanosomal membrane proteins: identification of signals for sorting of the human brown locus protein, gp75. J. Cell Biol. 130, 807–820.

Wang, S.Q., Setlow, R., Berwick, M., Polsky, D., Marghoob, A.A., Kopf, A.W., and Bart, R.S. (2001). Ultraviolet A and melanoma: a review. J. Am. Acad. Dermatol. 44, 837–846.

Yadav A.K., Singh T.R, Novel inhibitors design through structural investigations and simulation studies for human PKMTs (SMYD2) involved in cancer, 2021, Molecular Simulation 47 (14), 1149-1158.

Zuo, L., Weger, J., Yang, Q., Goldstein, A.M., Tucker, M.A., Walker, G.J., Hayward, N., and Dracopoli, N.C. (1996). Germline mutations in the p16INK4a binding domain of CDK4 in familial melanoma. Nat. Genet. 12, 97–99.