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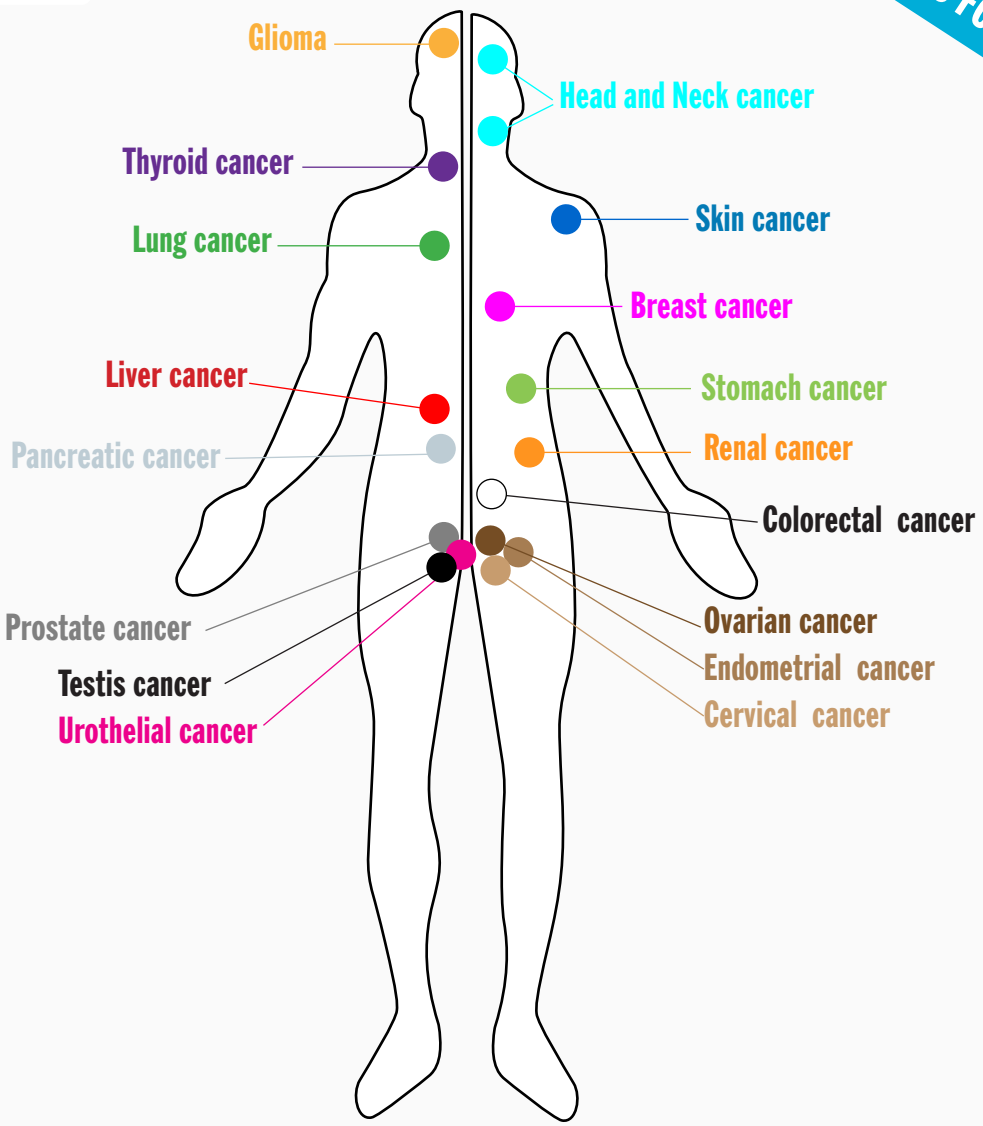
FULL CATALOG - MARKERS FOR 17 CANCER TYPES



TRIPLE A POLYCLONALS ANTIBODIES FOR

CANCER RESEARCH

ATLAS ANTIBODIES

INDEX

PRIMARY ANTIBODIES

Precise. Accurate.Targeted.
PrecisA Monoclonals™ are mouse monoclonal primary antibodies developed against a number of carefully selected targets. Clones are selected to recognize only unique non-overlapping epitopes and isotypes. Available as **25 µL** and **100 µL** unit size.

Atlas Antibodies Advanced Polyclonals.
Triple A Polyclonals™ are rabbit polyclonal primary antibodies developed within the Human Protein Atlas project. IHC characterization data from 44 normal and 20 cancer tissues is available on the Human Protein Atlas portal. Available as **25 µL** and **100 µL** unit size.

CONTROL ANTIGENS

PrEST Antigens

PrEST Antigens™ are the immunogens used for the generation of Triple A Polyclonals and PrecisA Monoclonals, for use as blocking agents and positive assay controls together with the corresponding antibody. The protein-specific PrEST sequences are designed to have a sequence identity as low as possible to other human proteins. The product numbers of PrEST control antigens start with **”APrEST”** and they are specified on the product pages for all antibodies under “related products”.

ENHANCED VALIDATION

Enhanced Validation

At Atlas Antibodies, we extensively validate our antibodies in IHC, WB, and ICC-IF. Enhanced Validation is performed as an additional layer of security in an application and context-specific manner.

Enhanced validation offers increased security of antibody specificity in a defined context.

This is ensured by using the ideal validation method for each combination of protein, sample, and application. Enhanced Validation follows the guidelines proposed by the International Working Group for Antibody Validation (IWGAV).

RECOMBINANT EXPRESSION VALIDATION

The antibody binding is verified using and over-expressed or tagged version of the target protein.

ORTHOGONAL VALIDATION

The antibody is validated by comparing the results with a non-antibody based method across multiple samples.

VALIDATION BY INDEPENDENT ANTIBODIES

The antibody specificity is demonstrated by comparing two antibodies targeting different regions of the same protein.

GENETIC VALIDATION

Antibody specificity is confirmed by downregulating the target protein at a genetic level using siRNA.

MIGRATION CAPTURE MS VALIDATION

The staining pattern and the protein size detected by the antibody is compared with results obtained by a capture Mass Spectrometry (MS) method.

LEARN MORE ABOUT ENHANCED VALIDATION

THE HUMAN PROTEIN ATLAS

The Human Protein Atlas is a Swedish-based program initiated in 2003 with the aim to map all the human proteins in cells, tissues and organs using an integration of various omics technologies, including antibody-based imaging, mass spectrometry-based proteomics, transcriptomics and systems biology. All the data in the knowledge resource is open access to allow scientists both in academia and industry to freely access the data for exploration of the human proteome.

The Human Protein Atlas consists of six separate parts, each focusing on a particular aspect of the genome-wide analysis of human proteins:

The Tissue Atlas shows the distribution of proteins across all major tissues and organs in the human body.

The Cell Atlas shows the subcellular localization of proteins in single cells.

The Pathology Atlas shows the impact of protein levels for survival of patients with cancer.

The Brain Atlas explores the protein expression in the mammalian brain by integration of data from three mammalian species: human, pig and mouse.

The Blood Atlas shows the cell types and proteome of human blood.

The Single Cell Type Atlas contains single cell RNA sequencing data and immunohistochemically stained sections from 13 different human tissues.

LEARN MORE ABOUT
THE HUMAN PROTEIN ATLAS

Unfavorable and favorable genes

Created by the Human Protein Atlas

The Human Protein Atlas project, is an integration of antibody-based imaging, proteomics, and transcriptomics with the aim of mapping all the human proteins in cells, tissues and organs.

Our Triple A Polyclonals are developed within the Human Protein Atlas project (*proteinatlas.org)*, and are affinity-purified, reproducible, selective, and specific for their target proteins through an enhanced validation process.

The Pathology Atlas

The Pathology Atlas contains mRNA and protein expression data from 17 different forms of human cancer. Correlation analyses based on mRNA expression levels of human genes in cancer tissue and the clinical outcome for almost 8000 cancer patients is presented in a gene-centric manner, including more than 18000 Kaplan-Meier plots with high significance ($p<0.001$).

Analysis of each protein and its corresponding cancer type in patients, using immunohistochemistry (IHC) analysis based on tissue microarrays (TMAs), is presented for a majority of the protein-coding genes.

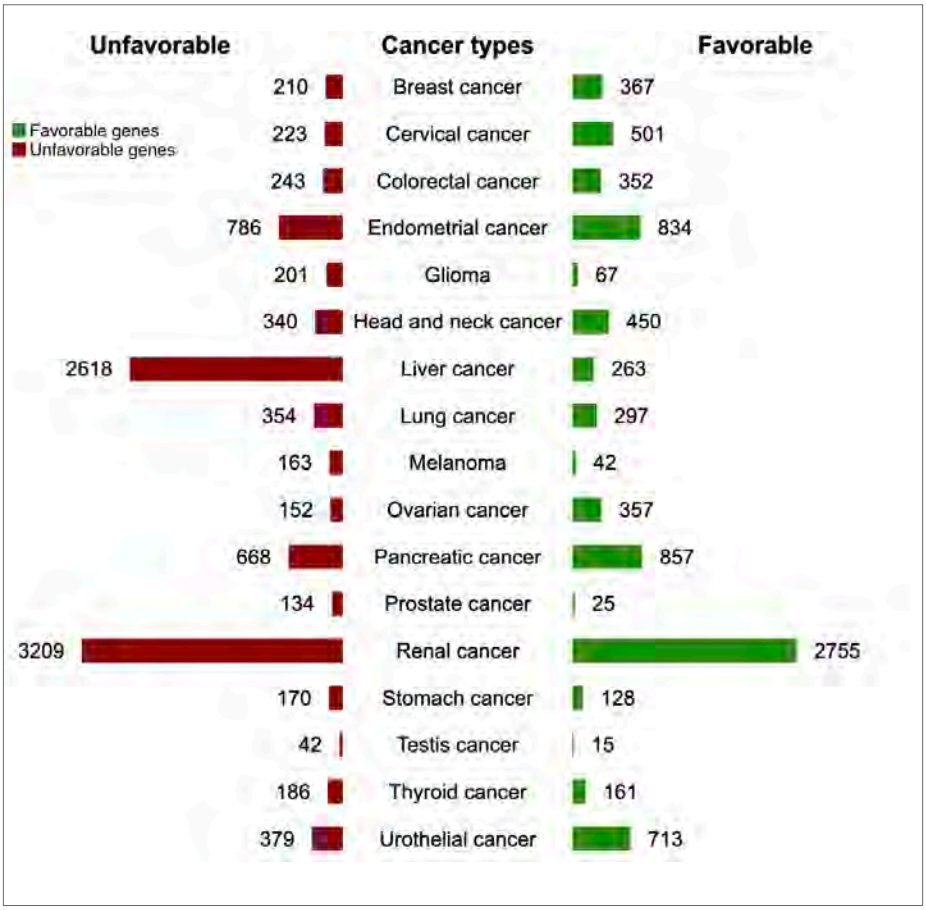
Correlation analysis and prognostic genes

Correlation analysis resulted in more than 10,000 prognostic genes. The number of prognostic genes with regard to cancer type and association with the favorable or unfavorable clinical outcome are summarized in the schematic below.

All transcriptomics data has been retrieved from the Cancer Genome Atlas and all proteomics data has been generated in-house using the same antibodies as in protein expression profiling in normal human tissues.

A gene is considered prognostic if correlation analysis of gene expression and clinical outcome resulted in Kaplan-Meier plots with high significance ($p<0.001$). A gene may be prognostic in more than one cancer type.

This catalog, based on the Pathology Atlas, contains a selection of our Triple A Polyclonals antibodies that are suitable markers for 17 human cancer types.



For **unfavorable genes**, higher relative expression levels at diagnosis give significantly **lower** overall survival for patients.

For **favorable genes**, higher relative expression levels at diagnosis give significantly **higher** overall survival for patients.

The schematic on the left, from The Pathology Atlas, shows the number of unfavorable and favorable genes for 17 human cancer types.

To explore the full atlas visit The Human Protein Atlas webpage at *proteinatlas.org.*

Breast cancer

Breast cancer is the most common invasive cancer form in women worldwide and the leading cause of cancer-related mortality in women. The global age-adjusted incidence rate for breast cancer is 124 per 100,000 women per year.

Male breast cancer is exceedingly rare and accounts for around 1% of cases. Although the rate of breast cancer diagnosis increased during the 1990's, it has decreased since the year 2000 and the overall breast cancer death rate has dropped steadily in the western world.

The majority of breast cancers develop sporadically, but for 5-10% of patients there is a hereditary component. The most well known genes associated with increased breast cancer risk are BRCA1 and BRCA2. Women with abnormal BRCA1 or BRCA2 experience up to 60% risk to develop breast cancer by the age of 90.

Other risk factors include early menarche and late menopause. Pregnancy has been reported to decrease risk, probably due to the changes in breast tissue.

Breast cancer forms in tissues of the breast, usually the ducts (tubes that carry milk to the nipple) and lobules (glands where the milk is produced). Based on the presumed site of origin and morphology, breast cancer is broadly classified as ductal or lobular cancers.

The transcriptome analysis shows that 72% (n=14227) of all human genes (n=19670) are expressed in breast cancer.

158 genes show some level of elevated expression in breast cancer compared to other cancers .

There are 210 genes associated with unfavorable prognosis in breast cancer.

There are 367 genes associated with favorable prognosis in breast cancer.

Data collected from 1075 patients (1063 females and 12 males).

The most significant genes related to unfavorable and favorable prognosis are listed in Tables 1 and 2.

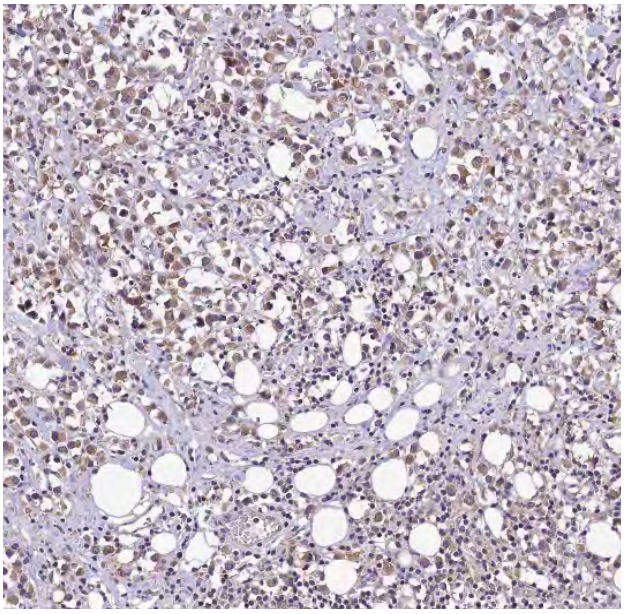


Figure 1. Immunohistochemistry using the anti-PGK1 (HPA045385) antibody on breast duct carcinoma (female, age 61) shows a moderate cytoplasmic/nuclear staining of tumor cells, in brown.

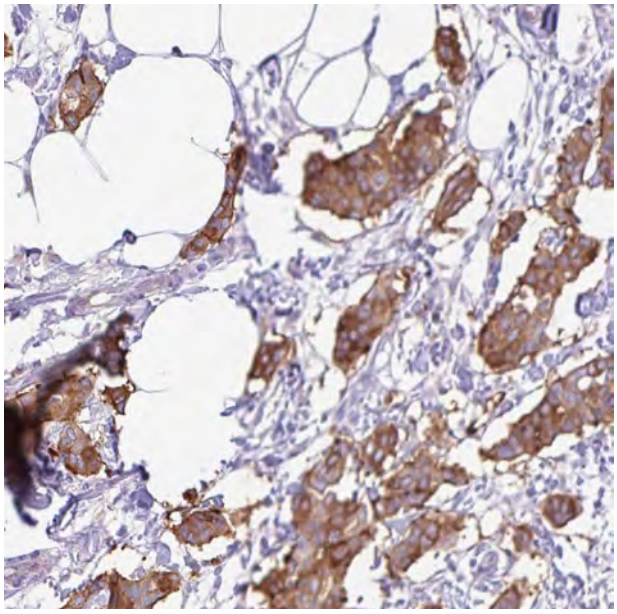


Figure 2. Immunohistochemistry using the anti-TPD52 (HPA062167) antibody on breast duct carcinoma (female, age 62) shows a moderate cytoplasmic/membranous staining of tumor cells, in brown.

Table 1. Top genes with highest significance associated with unfavorable prognosis in breast cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ATG4A	APG4A, AUTL2	HPA064759	WB, ICC-IF	91% / 88%
Anti-ATP5B	ATPSB	HPA001520	IHC*, WB*, ICC-IF	95% / 95%
Anti-CD24	CD24A	HPA045879	ICC-IF	49% / 45%
Anti-DCTPP1	CDA03, MGC5627, RS21C6	HPA002832	IHC, WB*, ICC-IF	80% / 78%
Anti-FAM173B	-	HPA074513	ICC-IF	87% / 84%
Anti-LIMCH1	LIMCH1A, LMO7B	HPA063840	IHC, WB*, ICC-IF	95% / 95%
Anti-LRP11	bA350J20.3, MANSC3	HPA064002	ICC-IF	81% / 79%
Anti-MORC4	FLJ11565, ZCW4, ZCWCC2	HPA000395	IHC*, WB, ICC-IF	66% / 67%
Anti-PCMT1	-	HPA003239	IHC, WB*, ICC-IF	94% / 94%
Anti-PDSS2	bA59I9.3, C6orf210	HPA029685	IHC, WB, ICC-IF	90% / 91%
Anti-PGK1	-	HPA045385	IHC	97% / 97%
Anti-PTGES3	cPGES, p23, TEBP	HPA038672	IHC*, WB*, ICC-IF	97% / 97%
Anti-RAB5B	-	HPA068337	WB, ICC-IF	100% / 93%
Anti-RTN4IP1	NIMP	HPA036357	IHC, WB	91% / 91%
Anti-SPDYC	Ringo2	HPA039891	IHC	28% / 28%
Anti-TAGLN2	HA1756, KIAA0120	HPA001925	IHC, WB, ICC-IF	95% / 95%
Anti-TIMM17A	TIM17, TIM17A	HPA010083	IHC, WB, ICC-IF	92% / 95%
Anti-TPD52	D52, hD52, N8L	HPA062167	IHC*, WB, ICC-IF	80% / 84%
Anti-TRMT2B	CXorf34, FLJ12687	HPA035120	IHC, WB	78% / 32%
Anti-XRCC4	-	HPA006801	IHC*, WB*, ICC-IF	67% / 63%

Table 2. Top genes with highest significance associated with favorable prognosis in breast cancer

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-APOBEC3D	APOBEC3E, ARP6	HPA055116	IHC	37% / 33%
Anti-ARID5A	MRF-1, RP11-363D14	HPA023879	IHC, WB, ICC-IF	72% / 71%
Anti-C6orf141	MGC46457	HPA036199	IHC, ICC-IF	34% / 36%
Anti-CA3	CAIII, Car3	HPA021775	IHC*, WB*	89% / 89%
Anti-CCL19	CKb11, ELC, MIP-3b, SCYA19	HPA067758	IHC*	76% / 76%
Anti-DEF6	IBP, SLAT, SWAP70L	HPA038976	IHC*, WB*	91% / 90%
Anti-GSTK1	GST13	HPA006311	IHC*	75% / 77%
Anti-JCHAIN	IGCJ, IGJ, JCH	HPA044132	IHC*	79% / 80%
Anti-MAP2K6	MEK6, MKK6, SAPKK3	HPA031134	IHC*, WB, ICC-IF	98% / 97%
Anti-NEFH	-	HPA061615	IHC*	88% / 94%
Anti-NFKBIA	IKBA, MAD-3, NFKBI	HPA029207	IHC, WB, ICC-IF	89% / 88%
Anti-NFKBIE	IKBE	HPA005941	IHC, WB, ICC-IF	74% / 71%
Anti-PEX10	RNF69	HPA049458	ICC-IF	36% / 38%
Anti-PIGR	-	HPA012012	IHC*, WB	65% / 67%
Anti-SERPINA1	A1A, A1AT, PI, PI1	HPA000927	IHC*, WB*, ICC-IF	62% / 67%
Anti-SGK3	SGK2, SGKL	HPA027146	IHC	96% / 96%
Anti-SNX22	FLJ13952	HPA038470	IHC, ICC-IF	96% / 96%
Anti-TFPI2	PP5, REF1, TFPI-2	HPA049158	IHC*	47% / 47%
Anti-ZMYM6	MYM, ZBED7, ZNF198L4	HPA071865	ICC-IF	80% / 82%
Anti-ZNF385B	FLJ25270, ZNF533	HPA046086	WB, ICC-IF	88% / 87%

* Products with enhanced validation for indicated application

Cervical cancer

Cervical cancer is the third most common type of cancer in women worldwide. The survival rate varies greatly depending on the cancer stage.

With treatment at the earlier stages, survival rates are much higher:
- 80 to 90% of women with stage I
- 50 to 65% of women with stage II

are alive 5 years after diagnosis.

However, survival rates falls significantly at late stages:
- 25 to 35% of women with stage III
- 15% or lower of women with stage IV

are alive after 5 years after diagnosis.

Two strains of Human Papilloma Virus (HPV), that can spread through sexual intercourse, are the cause of nearly all cervical cancers.

Risk factors include having sex at an early age, multiple sexual partners, smoking and poor socio-economic status. There is an approved vaccine for the prevention of HPV infection.

Most cervical cancers are squamous cell carcinomas originating from the squamous epithelium of the distal portion of the cervix.

Cancers arising from the columnar cells in the endocervical channel (defined as adenocarcinomas) are more rare.

The transcriptome analysis shows that 71% (n=14005) of all human genes (n=19670) are expressed in cervical cancer.

108 genes show some level of elevated expression in cervical cancer compared to other cancers

There are 223 genes associated with unfavorable prognosis in cervical cancer.

There are 501 genes associated with favorable prognosis in cervical cancer.

Data collected from 291 patients with squamous cell carcinoma or adenocarcinoma.

The most significant genes related to unfavorable and favorable prognosis are listed in Tables 3 and 4.

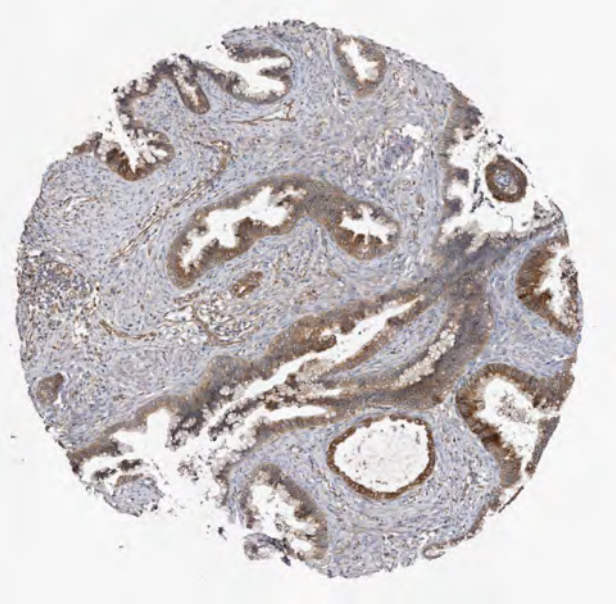


Figure 3. Immunohistochemistry using the anti-PON2 antibody (HPA029193) on cervix adenocarcinoma (female, age 44) shows a moderate cytoplasmic/nuclear staining of tumor cells, in brown.

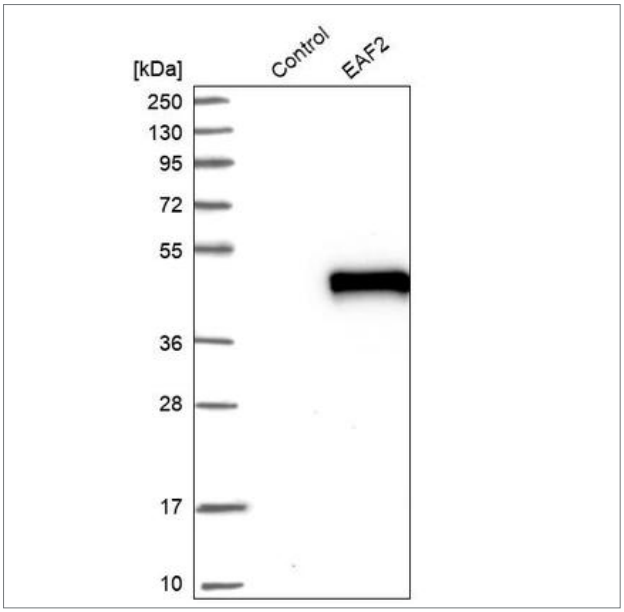


Figure 4. Western blot analysis using the anti-EAF2 antibody (HPA008411) in control (vector only transfected HEK293T lysate) and EAF2 over-expression lysate (Co-expressed with a C-terminal myc-DDK tag (~3.1 kDa) in mammalian HEK293T cells, LY413036).

Table 3. Top genes with highest significance associated with unfavorable prognosis in cervical cancer

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-AIG1	AIG-1, dJ95L4.1, FLJ10485	HPA060766	IHC, ICC-IF	100% / 100%
Anti-ASL	-	HPA016646	IHC*, WB*	92% / 86%
Anti-C1orf74	FLJ25078	HPA028496	IHC, WB, ICC-IF	79% / 76%
Anti-CXCL8	3-10C, GCP1, IL-8, NAP1	HPA057179	IHC, WB, ICC-IF	51% / 49%
Anti-EGLN1	C1orf12, HIFPH2, SM-20	HPA022129	IHC, ICC-IF	94% / 96%
Anti-ERG	erg-3, p55	HPA046598	IHC	96% / 97%
Anti-ESD	-	HPA039700	IHC, WB, ICC-IF	90% / 88%
Anti-FASN	FAS, SDR27X1	HPA006461	IHC*, WB*, ICC-IF	64% / 68%
Anti-FUT11	MGC33202	HPA014033	IHC, ICC-IF	87% / 89%
Anti-GALNT2	GalNAc-T2	HPA011222	IHC, WB*, ICC-IF	96% / 96%
Anti-ITGA5	CD49e, FNRA	HPA002642	IHC*, WB*	85% / 82%
Anti-LOXL2	WS9-14	HPA036257	ICC-IF	87% / 86%
Anti-MOCS1	MOCOD	HPA045783	IHC, WB, ICC-IF	98% / 98%
Anti-P4HA2	C-P4Halpha(II)	HPA016997	IHC*, WB*, ICC-IF	90% / 91%
Anti-PRKCDBP	CAVIN3, HSRBC, MGC20400	HPA073327	ICC-IF	53% / 57%
Anti-PON2	-	HPA029193	IHC*, WB*	91% / 89%
Anti-SPRYD7	C13orf1, CLLD6	HPA043934	IHC, ICC-IF	100% / 100%
Anti-SUMF2	DKFZp566I1024	HPA024040	IHC*	76% / 77%
Anti-TAF1A	SL1, TAFI48	HPA054334	IHC, ICC-IF	87% / 84%
Anti-TGFBI	BIGH3, CDB1, LCD1	HPA017019	IHC*, WB	88% / 87%

Table 4. Top genes with highest significance associated with favorable prognosis in cervical cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-AKR1A1	ALR, DD3	HPA019649	IHC, WB*, ICC-IF	94% / 94%
Anti-CETN1	CEN1, CETN	HPA028956	IHC	96% / 97%
Anti-DDX49	FLJ10432	HPA041870	IHC, WB	99% / 91%
Anti-EAF2	BM040, TRAITS, U19	HPA008411	IHC*, WB*	93% / 89%
Anti-F8A1	DXS522E, F8A	HPA046960	IHC, WB	92% / 95%
Anti-ISCU	hnifU, IscU, ISU2, NIFUN	HPA038602	IHC, ICC-IF	99% / 99%
Anti-KIF22	Kid, KNSL4, OBP-1, OBP-2	HPA041076	IHC, WB*	90% / 89%
Anti-MEI1	MGC40042, SPATA38	HPA049240	IHC	86% / 81%
Anti-NCAPH2	384D8-2, CAP-H2, hCAP-H2	HPA069056	IHC*, WB*, ICC-IF	81% / 82%
Anti-NMRAL1	FLJ25918, HSCARG, SDR48A1	HPA041353	IHC, WB*, ICC-IF	80% / 85%
Anti-PLA1A	ps-PLA1	HPA059740	ICC-IF	71% / 68%
Anti-PRSS36	FLJ90661	HPA036079	IHC	79% / 78%
Anti-PCNA	-	HPA030522	IHC*, WB, ICC-IF	99% /100%
Anti-RIBC2	C22orf11, FLJ25720	HPA003210	IHC	72% / 76%
Anti-SH3GLB2	KIAA1848	HPA021438	IHC, WB, ICC-IF	100% / 98%
Anti-SLC2A8	GLUT8, GLUTX1	HPA011935	IHC	83% / 77%
Anti-TEX30	C13orf27	HPA053545	IHC*, WB	95% / 94%
Anti-TARDBP	ALS10, TDP-43	HPA017284	IHC, WB, ICC-IF	96% / 32%
Anti-TNFRSF13C	BAFFR, CD268	HPA003246	IHC*, WB*	57% / 49%
Anti-ZER1	C9orf60, Hzyg, ZYG, ZYG11BL	HPA048464	WB*, ICC-IF	98% / 98%

* Products with enhanced validation for indicated application

Colorectal cancer

Colorectal cancer is the third most common cancer in the world and the fifth leading cause of cancer-related mortality.

Environmental factors, including meat consumption, are contributing risk factors. The overall mortality is approximately 50%.

The surgical stage at diagnosis is the most important factor for predicting prognosis and the survival rate varies greatly depending on the stage. The 5-year survival rate is more than 90% for stage I and less than 10% for stage IV. Most colorectal cancer cases are detected at an advanced stage. Bleeding and hematochezia are two of the most common symptoms associated with rectal lesions.

Colorectal cancer is considered to originate from normal colon epithelium that develops into precursor lesions termed adenomas that subsequently may progress to invasive colorectal adenocarcinomas with metastatic potential.

Depending on the origin site, colorectal cancer is divided into two subtypes:
- COAD: colon adenocarcinomas
- READ: rectum adenocarcinomas.

The transcriptome analysis shows that 69% (n=13488) of all human genes (n=19670) are expressed in colorectal cancer.

170 genes show some level of elevated expression in colorectal cancer compared to other cancers

There are 243 genes associated with unfavorable prognosis in colorectal cancer.

There are 352 genes associated with favorable prognosis in colorectal cancer.

Data collected from 597 patients in total:
438 COAD (204 females and 234 males) and
159 READ (71 females and 88 males).

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 5 and 6.

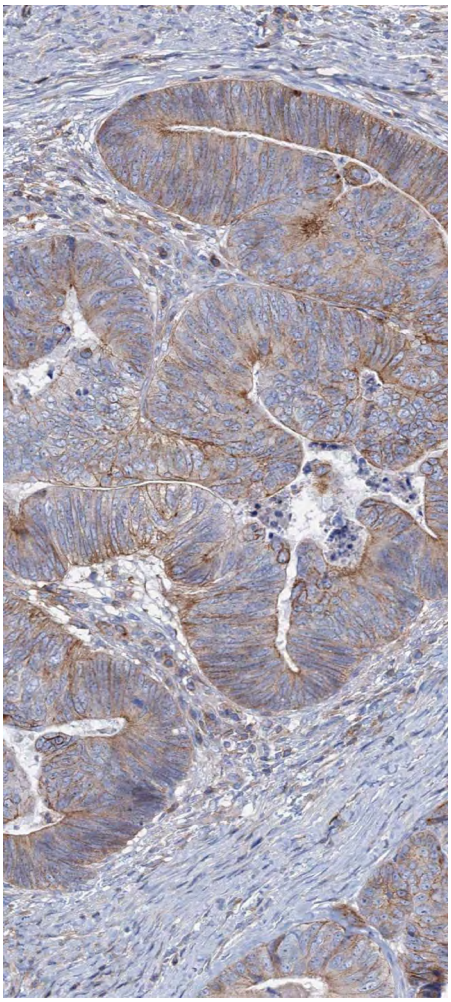


Figure 5. Immunohistochemistry using the anti-LRCH4 antibody (HPA037668) on colon adenocarcinoma (female, age 67) shows a moderate cytoplasmic/ membranous staining of tumor cells, in brown.

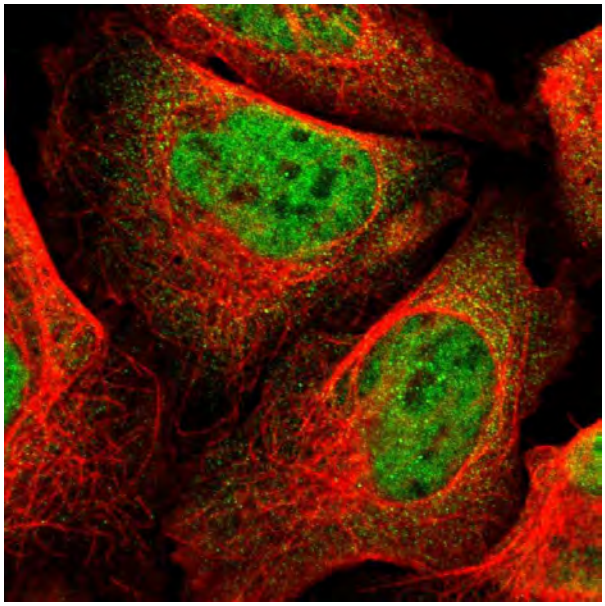


Figure 6 Immunofluorescent staining of human cell line U-2 OS using the anti-RBM3 antibody (HPA003624) shows localization to nucleoplasm, in green. Microtubules are shown in red.

Table 5. Top genes with highest significance associated with unfavorable prognosis in colorectal cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ARHGAP4	p115, RhoGAP4, SrGAP4	HPA001012	IHC*, WB	70% / 72%
Anti-ARL8A	ARL10B, FLJ45195, Gie2	HPA038759	IHC, WB	97% / 97%
Anti-ASB6	-	HPA004341	IHC, WB	88% / 43%
Anti-CLK3	clk3	HPA046817	IHC, WB, ICC-IF	98% / 100%
Anti-CNPY3	CAG4A, TNRC5	HPA016560	IHC, WB*	89% / 88%
Anti-CRACR2B	EFCAB4A, MGC45840	HPA046217	IHC, WB*	77% / 77%
Anti-DAPK1	DAPK	HPA040472	IHC	96% / 96%
Anti-DPP7	DPPII	HPA021282	IHC, WB, ICC-IF	87% / 83%
Anti-EGFL7	ZNEU1	HPA050716	IHC	75% / 75%
Anti-EXOC3L4	C14orf73	HPA043661	IHC, WB	66% / 67%
Anti-FAM69B	C9orf136, MGC20262	HPA046812	IHC	94% / 93%
Anti-HSPA1A	HSP70-1, HSPA1	HPA052504	IHC, WB, ICC-IF	100% / 100%
Anti-INAFM1	PRR24	HPA064015	IHC	45% / 45%
Anti-LRCH4	LRN, LRRN1	HPA037667	IHC*, ICC-IF	80% / 79%
Anti-NPDC1	CAB-, CAB1, DKFZp586J0523	HPA008189	IHC, ICC-IF	87% / 85%
Anti-PAQR6	FLJ22672, PRdelta	HPA073505	WB, ICC-IF	26% / 26%
Anti-POFUT2	C21orf80, FUT13, KIAA0958	HPA044297	IHC	97% / 97%
Anti-RHBDD2	NPD007, RHBDL7	HPA051960	IHC, WB*, ICC-IF	86% / 84%
Anti-SEMA4C	Semacl1, Semaf, SEMAI	HPA011090	IHC	89% / 89%
Anti-SPAG4	CT127, SUN4	HPA048393	IHC	89% / 89%

Table 6. Top genes with highest significance associated with favorable prognosis in colorectal cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ABCD3	PMP70, PXMP1, ZWS2	HPA032027	IHC*, ICC-IF	96% / 96%
Anti-AP3B1	ADTB3A, HPS2	HPA038737	IHC, ICC-IF	82% / 80%
Anti-CASP6	MCH2	HPA011337	IHC*, WB*, ICC-IF	91% / 91%
Anti-CLCC1	MCLC	HPA013210	IHC*, ICC-IF	79% / 81%
Anti-DDX46	KIAA0801, Prp5, PRPF5	HPA036554	IHC, WB*	95% / 96%
Anti-DLAT	DLTA, PDC-E2	HPA040786	IHC*, WB*, ICC-IF	91% / 93%
Anti-EIF4A3	DDX48, EIF4AIII, KIAA0111	HPA021878	IHC*, W, ICC-IF	97% / 99%
Anti-FBXO7	Fbx, FBX7, PARK15	HPA032113	WB, ICC-IF	79% / 79%
Anti-GRSF1	-	HPA036985	IHC*, WB*, ICC-IF	83% / 80%
Anti-HOOK1	HK1	HPA018537	IHC*, WB	94% / 94%
Anti-NGLY1	FLJ11005, PNG1	HPA036825	IHC	87% / 87%
Anti-NOL11	DKFZP586L0724	HPA022010	IHC, WB, ICC-IF	86% / 87%
Anti-PARS2	DKFZp727A071	HPA028314	IHC, WB*	78% / 78%
Anti-PRPSAP1	PAP39	HPA062396	ICC-IF	100% / 100%
Anti-PSMA5	ZETA	HPA028398	IHC, WB, ICC-IF	100% / 100%
Anti-RBM3	IS1-RNPL	HPA003624	IHC, WB*, ICC-IF	94% / 96%
Anti-SORT1	Gp95, NT3	HPA006889	IHC*, WB*	89% / 89%
Anti-TEX2	HT008, KIAA1738, TMEM96	HPA057116	ICC-IF	100% / 100%
Anti-USP53	KIAA1350	HPA035844	IHC, ICC-IF	67% / 66%
Anti-ZYG11B	FLJ13456, ZYG11	HPA028156	IHC, ICC-IF	100% / 100%

* Products with enhanced validation for indicated application

Endometrial cancer

Endometrial cancer is the fifth most common cancer in women, and one of the most common forms of gynecological cancer in developed countries.

The incidence of endometrial cancer is rising due to the increased life expectancy and the epidemic of obesity. The 5-year survival rate in patients without metastatic disease varies from 74% to 91%.

Around 80% of endometrial cancers represent endometrioid histology. These are considered hormone dependent and the prognosis of endometrioid cancers is generally favorable. The majority of endometrial cancers are detected at an early stage with the disease restricted to the uterus.

Endometrial cancer originates from the endometrium - the mucosal lining of the uterus.

The common form of endometrial cancer, referred to as
- type 1 (or estrogen-related endometrial cancer), which usually occurs in younger, premenopausal women and tends to be of lower histological grade.
- type 2 (or non-estrogen-related endometrial cancer) which occurs in postmenopausal women, and is the more aggressive form of endometrial cancer.

The transcriptome analysis shows that 73% (n=14315) of all human genes (n=19670) are expressed in endometrial cancer.

192 genes show some level of elevated expression in endometrial cancer compared to other cancers.

There are 786 genes associated with unfavorable prognosis in endometrial cancer.

There are 834 genes associated with favorable prognosis in endometrial cancer.

Data collected from 541 female patients.

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 7 and 8.

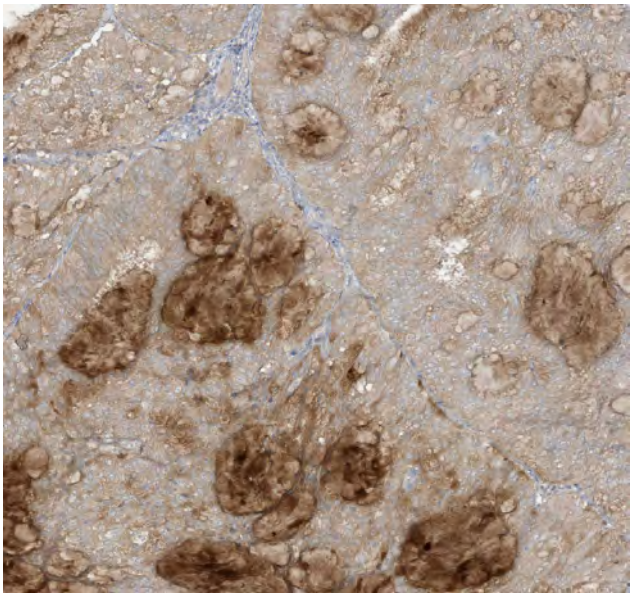


Figure 7. Immunohistochemistry using the anti-LRRN2 antibody (HPA029124) on endometrium adenocarcinoma (female, age 81) shows a medium cytoplasmic/membranous staining of tumor cells, in brown.

Enhanced Validation

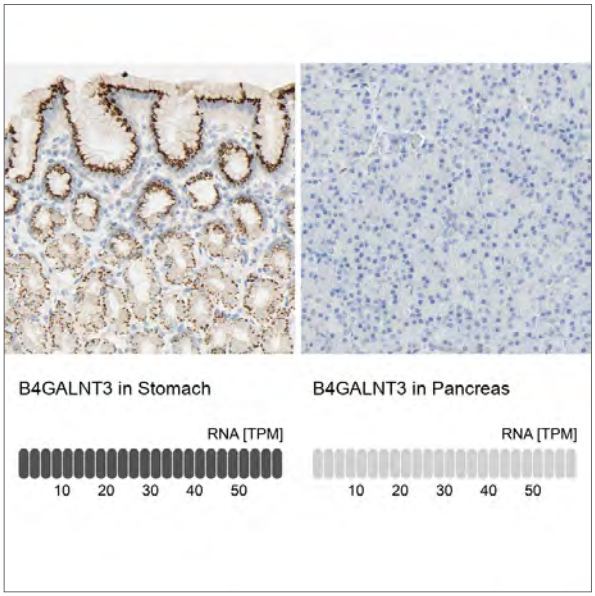


Figure 8. Immunohistochemistry analysis in human stomach and pancreas tissues using the anti-B4GALNT3 (HPA011404) antibody. Corresponding B4GALNT3 RNA-seq data are presented for the same tissues. Orthogonal validation of protein expression using IHC by comparison to RNA-seq data of corresponding target in high and low expression tissues.

Table 7. Top genes with highest significance associated with unfavorable prognosis in endometrial cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ADA	-	HPA001399	IHC*, WB, ICC-IF	85% / 83%
Anti-ASS1	ASS, CTLN1	HPA020934	IHC*, WB*, ICC-IF	95% / 97%
Anti-CDKN2A	ARF, MTS1, p14, p14ARF	HPA047838	ICC-IF	44% / 43%
Anti-DAGLA	C11orf11, DAGLALPHA, KIAA0659	HPA062497	IHC	100% / 100%
Anti-ERBB2	CD340, HER2, NEU, NGL	HPA001383	IHC, WB, ICC-IF	82% / 81%
Anti-FAM110B	C8orf72, MGC39325	HPA008318	IHC, WB, ICC-IF	96% / 95%
Anti-GGH	-	HPA025226	IHC, WB	77% / 73%
Anti-GPRIN2	KIAA0514, MGC15171	HPA038129	IHC, ICC-IF	73% / 68%
Anti-HIF3A	bHLHe17, IPAS, MOP7	HPA041141	IHC	72% / 70%
Anti-IGSF1	IGDC1, INHBP, KIAA0364	HPA035582	IHC*	99% / 97%
Anti-KHK	-	HPA007040	IHC*, WB	91% / 88%
Anti-L1CAM	CD171, HSAS, MIC5, S10	HPA005830	IHC*	75% / 75%
Anti-LRRN2	GAC1, LRANK1, LRRN5	HPA029124	IHC, WB*	85% / 85%
Anti-MAP1LC3C	ATG8J	HPA072670	ICC-IF	50% / 50%
Anti-MARK4	FLJ90097, KIAA1860, PAR-1D	HPA039186	IHC, ICC-IF	90% / 92%
Anti-MBOAT2	FLJ14415, FLJ90298, OACT2	HPA014836	IHC, WB*	70% / 70%
Anti-MGAT4A	GnT-4a, GnT-Iva	HPA007608	IHC*, WB, ICC-IF	93% / 95%
Anti-PTX3	TNFAIP5, TSG-14	HPA069320	IHC	85% / 90%
Anti-RNF44	KIAA1100	HPA038981	IHC, WB, ICC-IF	75% / 38%
Anti-TRIM46	FLJ23229, TRIFIC	HPA030389	ICC-IF	97% / 97%

Table 8. Top genes with highest significance associated with favorable prognosis in endometrial cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-B4GALNT3	B4GalNacT3, FLJ16224, FLJ40362	HPA011404	IHC*	60% / 57%
Anti-CCDC159	-	HPA047126	IHC	70% / 73%
Anti-CRELD2	MGC11256	HPA000603	IHC	78% / 79%
Anti-DHRS7B	CGI-93, MGC8916, SDR32C1	HPA012132	IHC, WB*	81% / 81%
Anti-GPR108	LUSTR2	HPA041924	IHC, ICC-IF	70% / 72%
Anti-HEXA	-	HPA054583	IHC, WB*	81% / 82%
Anti-HMG20B	BRAF25, SMARCE1r, SOXL	HPA050220	ICC-IF	93% / 93%
Anti-MSX1	HOX7, HYD1, OFC5	HPA073604	IHC*	93% / 93%
Anti-NXNL2	C9orf121	HPA045526	IHC	88% / 86%
Anti-P2RX4	P2X4	HPA039494	IHC*, WB, ICC-IF	83% / 77%
Anti-PGR	NR3C3, PR	HPA004751	IHC*	88% / 88%
Anti-PLPP2	LPP2, PAP-2c, PPAP2C	HPA055540	IHC, ICC-IF	47% / 50%
Anti-SAMM50	CGI-51, OMP85, TOB55, TRG-3	HPA034537	IHC*, WB, ICC-IF	96% / 95%
Anti-SCGB2A1	LPHC, MGB2, UGB3	HPA034584	IHC*, WB*	35% / 32%
Anti-SERINC2	FKSG84, PRO0899, TDE2	HPA005974	IHC*, WB	77% / 74%
Anti-SLC47A1	FLJ10847, MATE1	HPA021987	IHC*	49% / 51%
Anti-SPAG4	CT127, SUN4	HPA048393	IHC	89% / 89%
Anti-SPDEF	bA375E1.3, PDEF	HPA055707	ICC-IF	79% / 79%
Anti-STX18	Ufe1	HPA003019	IHC, ICC-IF	88% / 87%
Anti-ZAP70	SRK, STD, ZAP-70	HPA003134	IHC*, WB	88% / 87%

* Products with enhanced validation for indicated application

Glioma

Intracranial tumors comprise approximately 2% of all adult cancers, but form a larger fraction within the group of childhood tumors.

Gliomas are tumors with an estimated origin from glial cells, accounting for approximately 80% of all malignant intracranial tumors. Gliomas are classified according to cell type of origin, differentiation and malignancy grade.

According to cell type of origin, differentiation and malignancy grade, gliomas are classified as:
-astrocytoma,
-oligodendrocytoma
-ependymoma.

Survival time after diagnosis with glioma varies significantly depending on grade. The prognosis for high-grade gliomas is poor due to limited possibilities of curative treatment.

The most common form of glioma is astrocytoma, representing approximately 50% of all gliomas.

Grade IV astrocytoma, also known as glioblastoma or glioblastoma multiforme (GBM) is the most common and aggressive glioma with a very poor 5-year survival (less than 5%).

There is currently no cure for GBM but it is normally treated with surgery followed by chemotherapy and radiotherapy to increase the length of survival.

The transcriptome analysis shows that 72% (n=14217) of all human genes (n=19670) are expressed in glioma.

682 genes show some level of elevated expression in glioma compared to other cancers.

There are 201 genes associated with unfavorable prognosis in GBM.

There are 67 genes associated with favorable prognosis in GBM.

Data collected from 153 patients (54 females and 99 males).

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 9 and 10.

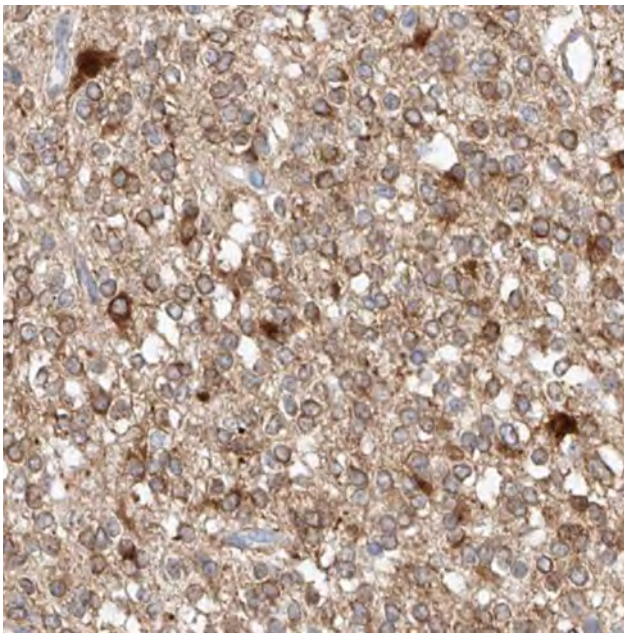


Figure 9. Immunohistochemistry using the anti-REEP2 antibody (HPA031813) on high grade glioma (male, age 34) shows a strong cytoplasmic/membranous staining of tumor cells, in brown.

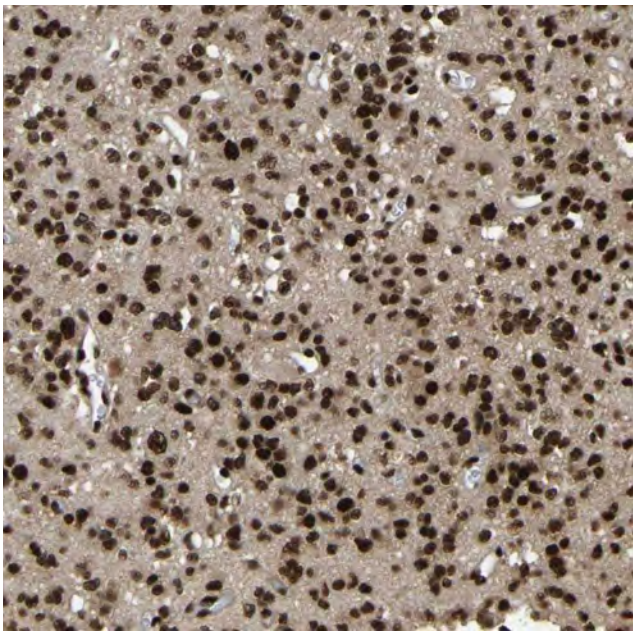


Figure 10. Immunohistochemistry using the anti-TBL1XR1 antibody (HPA019182) on high grade glioma (male, age 38) shows a strong nuclear staining of tumor cells, in brown.

Table 9. Top genes with highest significance associated with unfavorable prognosis in glioma.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ADAM15	MDC15	HPA011633	IHC, WB	82% / 84%
Anti-ARMC10	MGC3195, SVH	HPA011036	IHC*, WB*, ICC-IF	89% / 83%
Anti-CEND1	BM88, FLJ90066	HPA042527	IHC*, WB*	75% / 74%
Anti-DBNL	HIP-55, SH3P7	HPA020265	IHC*, WB*	95% / 95%
Anti-EN2	-	HPA045646	ICC-IF	87% / 87%
Anti-FAM174A	TMEM157, UNQ1912	HPA019539	IHC, WB*, ICC-IF	100% / 100%
Anti-HPCA	-	HPA043245	IHC	100% / 100%
Anti-KDELR2	ELP-1, ERD2.2	HPA016459	IHC	29% / 28%
Anti-LRRC61	FLJ31392, HSPC295, MGC3036	HPA019355	IHC, WB*, ICC-IF	89% / 90%
Anti-MED10	L6, MGC5309, NUT2, TRG20	HPA042795	WB*, ICC-IF	100% / 100%
Anti-PGBD5	DKFZp761A0620, FLJ11413	HPA065010	ICC-IF	92% / 93%
Anti-PODNL1	FLJ23447, SLRR5B	HPA042807	IHC	81% / 81%
Anti-PTPRN	IA-2	HPA007179	IHC*	77% / 81%
Anti-RPL39L	RPL39L1	HPA047105	IHC	95% / 95%
Anti-RPP25	FLJ20374	HPA046900	IHC, WB, ICC-IF	84% / 85%
Anti-SLC6A6	TAUT	HPA016488	IHC*	78% / 78%
Anti-STC1	STC	HPA023918	IHC	100% / 100%
Anti-TSPAN13	NET-6, TM4SF13	HPA007426	IHC, ICC-IF	89% / 87%
Anti-WFDC2	EDDM4, HE4, WAP5	HPA042302	IHC*, WB, ICC-IF	63% / 41%
Anti-ZBED6CL	C7orf29	HPA019724	IHC, WB*	29% / 30%

Table 10. Top genes with highest significance associated with favorable prognosis in glioma.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ETNPPL	AGXT2L1	HPA044546	IHC*, WB*	64% / 65%
Anti-EFCAB7	KIAA1799, RP4-534K7.1	HPA029611	IHC, ICC-IF	90% / 87%
Anti-MARS2	mtMetRS, SPAX3	HPA035589	IHC, ICC-IF	92% / 93%
Anti-MIER1	hMI-ER1, KIAA1610, MI-ER1	HPA019589	IHC*, ICC-IF	97% / 96%
Anti-MTHFD2	-	HPA049657	IHC	88% / 85%
Anti-NEUROD1	BETA2, BHF-1, MODY6	HPA003278	IHC, WB*	98% / 97%
Anti-PATZ1	MAZR, ZNF278, ZSG	HPA047893	IHC, ICC-IF	100% / 100%
Anti-RCOR3	FLJ10876	HPA007413	IHC*, ICC-IF	96% / 97%
Anti-RRAGA	FIP-1, RAGA	HPA003734	IHC, WB, ICC-IF	99% / 99%
Anti-SAMD13	-	HPA058929	IHC*, ICC-IF	100% / 50%
Anti-SLC39A10	FLJ90515, KIAA1265	HPA036512	IHC, ICC-IF	93% / 93%
Anti-SOX21	SOX25	HPA048337	IHC	96% / 37%
Anti-STARD7	GTT1	HPA064958	ICC-IF	97% / 95%
Anti-TBL1XR1	C21, DC42, IRA1	HPA019182	IHC*, WB, ICC-IF	96% / 97%
Anti-ZBTB6	ZID, ZNF482	HPA076894	ICC-IF	88% / 86%
Anti-ZFP1	FLJ34243, ZNF475	HPA044916	ICC-IF	70% / 76%
Anti-ZNF322	HCG12, ZNF388, ZNF489	HPA046692	IHC, ICC-IF	58% / 62%
Anti-ZNF420	FLJ32191	HPA059675	IHC, ICC-IF	31% / 31%
Anti-ZNF639	ANC-2H01, ZASC1	HPA049023	IHC, ICC-IF	87% / 86%
Anti-ZNF821	-	HPA036372	IHC*, ICC-IF	74% / 77%

* Products with enhanced validation for indicated application

Head and neck cancer

Head and neck cancer arises in the nasal cavity, sinuses, lips, mouth, salivary glands, throat, or larynx (voice box). Head and neck cancers are common in several regions of the world where tobacco usage and alcohol consumption is high.

Head and neck cancers comprise approximately 10% of all newly diagnosed cancers in the western world, but one-third in India. The variation in incidence between regions is mostly related to the relative distribution of major risk factors such as tobacco and alcohol consumption. Head and neck cancer has a 5-year survival rate of approximately 60%, depending on locations on primary tumor and grade.

There is increasing evidence that viruses might contribute to the cause of head and neck cancer. DNA from human papillomavirus (HPV) has been detected in cancerous tissue from the head and neck and infection with Epstein-Barr virus is associated with nasopharyngeal cancer.

Surprisingly, patients with advanced forms of cancer in the upper portion of the throat have a better outcome if the tumor is positive for HPV. The occurrence of head and neck cancer in young adults and that falls to non-users of tobacco and alcohol suggests that genetic predisposition may be a possible etiological factor.

Most head and neck cancers arise from squamous epithelium and are squamous cell carcinomas of different histologic grades. The tumor cells in well-differentiated cancers closely resemble normal squamous epithelium, whereas poorly differentiated cancers are difficult to classify as being of squamous epithelial origin.

Salivary gland tumors (mainly adenocarcinomas) comprise a minority of head and neck tumors.

The transcriptome analysis shows that 69% (n=13629) of all human genes (n=19670) are expressed in head and neck cancer.

269 genes show some level of elevated expression in head and neck cancer compared to other cancers.

There are 340 genes associated with unfavorable prognosis in head and neck cancer.

There are 450 genes associated with favorable prognosis in head and neck cancer.

Data collected from 499 patients with head and neck cancer.

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 11 and 12.

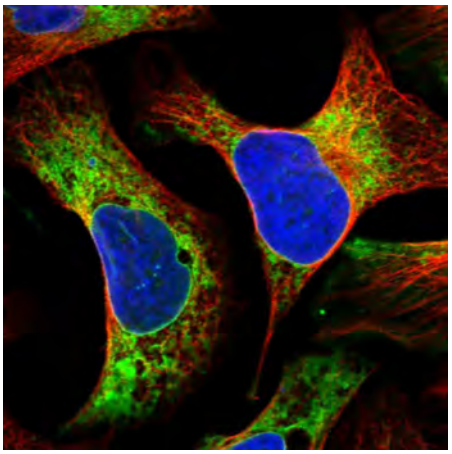


Figure 11. Immunofluorescent staining of human cell line U-2 OS with the anti-LRRC59 (HPA030827) antibody showing localization to endoplasmic reticulum, in green.

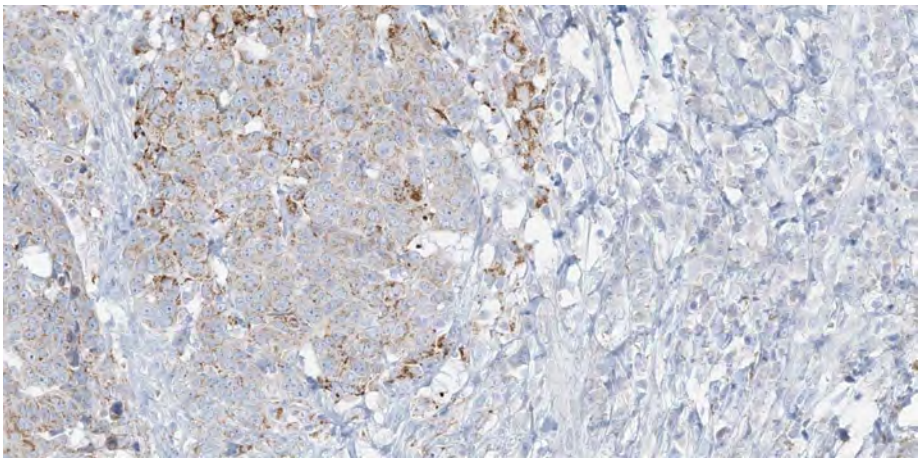


Figure 12. Immunohistochemical staining using the anti-ZDHHC4 antibody (HPA032124) on squamous cell carcinoma (head-neck cancer tissue from male age 66) showing a medium cytoplasmic/membranous staining in tumor cells, in brown.

Table 11. Top genes with highest significance associated with unfavorable prognosis in head and neck cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-AIG1	AIG-1, dJ95L4.1, FLJ10485	HPA060766	IHC, ICC-IF	100% / 100%
Anti-CAMK2N	CaMKIINalpha	HPA050835	ICC-IF	96% / 96%
Anti-CTTN	EMS1	HPA057242	IHC, WB, ICC-IF	96% / 97%
Anti-DDX19A	DDX19L, FLJ11126	HPA045252	IHC, WB	88% / 88%
Anti-EFNB2	EPLG5, Htk-L, HTKL, LERK5	HPA008999	IHC, WB, ICC-IF	97% / 97%
Anti-HK1	-	HPA007044	IHC, WB*	97% / 94%
Anti-KARS	DFNB89, KARS1, KARS2	HPA041345	IHC*, WB*,ICC-IF	94% / 90%
Anti-LIMA1	EPLIN	HPA023871	IHC*, WB*, ICC-IF	74% / 74%
Anti-LRRC59	FLJ21675, PRO1855	HPA030827	IHC*, WB, ICC-IF	93% / 93%
Anti-MANF	ARMET, ARP	HPA011175	IHC, WB, ICC-IF	97% / 97%
Anti-NDFIP1	MGC10924, N4WBP5	HPA009682	IHC, WB	92% / 90%
Anti-PCTP	STARD2	HPA022979	IHC, ICC-IF	79% / 78%
Anti-PGK1	-	HPA045385	IHC	97% / 97%
Anti-SEC14L2	C22orf6, KIAA1186, SPF, TAP	HPA064466	IHC, ICC-IF	81% / 81%
Anti-SGCE	DYT11	HPA074790	WB, ICC-IF	94% / 96%
Anti-STC2	STC-2	HPA045372	IHC, WB*, ICC-IF	72% / 68%
Anti-TCEAL8	MGC45400, WEX3	HPA059115	IHC, ICC-IF	71% / 71%
Anti-TMCO1	HP10122, TMCC4	HPA054768	ICC-IF	100% / 100%
Anti-TMED2	P24A, RNP24	HPA014060	IHC, WB, ICC-IF	100% / 100%
Anti-ZDHHC4	FLJ10479, ZNF374	HPA032124	IHC, WB	74% / 74%

Table 12. Top genes with highest significance associated with favorable prognosis in head and neck cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-CCR7	BLR2, CD197, CMKBR7, EBI1	HPA031383	ICC-IF	83% / 85%
Anti-CD6	CD301, CLECSF13, HML, HML2	HPA021937	IHC, WB*	71% / 71%
Anti-CD27	S152, TNFRSF7, Tp55	HPA038936	IHC*, WB	68% / 66%
Anti-CLEC14A	C14orf27	HPA039468	IHC, WB*, ICC-IF	64% / 64%
Anti-FGD3	FLJ00004, ZFYVE5	HPA021018	IHC, ICC-IF	73% / 72%
Anti-GZMM	LMET1, MET1	HPA015624	IHC*	81% / 78%
Anti-IRF4	LSIRF, MUM1	HPA002038	IHC*, WB	90% / 90%
Anti-JCHAIN	IGCJ, IGJ, JCH	HPA044132	IHC*	79% / 80%
Anti-PITPNM3	ACKR6, CORD5, NIR1, RDGBA3	HPA022432	IHC*, ICC-IF	90% / 91%
Anti-PPFIA3	KIAA0654, LPNA3, MGC126567	HPA043567	IHC*	92% / 94%
Anti-S1PR4	EDG6	HPA060601	ICC-IF	83% / 83%
Anti-SMIM14	C4orf34, FLJ13289	HPA051299	IHC	100% / 97%
Anti-SZT2	C1orf84, FLJ10387, SZT2A	HPA029012	IHC	72% / 71%
Anti-TPSB2	-	HPA049153	IHC, WB	70% / 73%
Anti-TYK2	JTK1	HPA005157	IHC, WB, ICC-IF	64% / 63%
Anti-ZAP70	SRK, STD, ZAP-70	HPA003134	IHC*, WB	88% / 87%
Anti-ZNF266	HZF1	HPA054110	IHC, ICC-IF	50% / 44%
Anti-ZNF414	MGC15716, Zfp414	HPA053769	IHC, ICC-IF	49% / 53%
Anti-ZNF557	MGC4054	HPA029291	IHC, ICC-IF	59% / 46%
Anti-ZNF846	-	HPA034617	IHC, WB	42% / 42%

* Products with enhanced validation for indicated application

Liver Cancer

Liver cancer is the 6th most common cancer and the third leading in cancer death worldwide. It is associated with a poor prognosis due to the lack of early detection.

Hepatocellular carcinoma is the most common type of primary liver cancer. The overall median survival is 4 months and the overall 5-year survival rate is 3%.

The tumor predominantly affects males who are over 50 years of age. Risk factors include infection with hepatotropic viruses such as hepatitis B and C viruses, liver cirrhosis, liver cell dysplasia, exposure to aflatoxins and inborn errors of metabolism.

Serum elevation of α-fetoprotein occurs in a large proportion of patients (up to 75%) with hepatocellular carcinoma. Most tumors are detected at an advanced stage are not suitable for liver transplantation.

Cholangiocarcinomas, also known as intrahepatic bile duct cancers, are relatively rare and account for 10-20% of all cases.

Cholangiocarcinomas occur in older individuals, usually after the age of 60, and have an overall mean survival time of less than 2 years.

This type of tumor has been associated with parasitic infestation of the liver (clonorchis sinensis), multiple bile duct hamartomas, intrahepatic lithiasis and congenital hepatic fibrosis.

In general, most patients with cholangiocarcinoma show no symptoms until the disease has progressed to a late stage with local spread or metastasis.

The transcriptome analysis shows that 66% (n=12948) of all human genes (n=19670) are expressed in liver cancer.

487 genes show some level of elevated expression in liver cancer compared to other cancers

There are 2618 genes associated with unfavorable prognosis in liver cancer.

There are 263 genes associated with favorable prognosis in liver cancer.

Data collected from 365 patients in total (119 females and 246 males).

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 13 and 14.

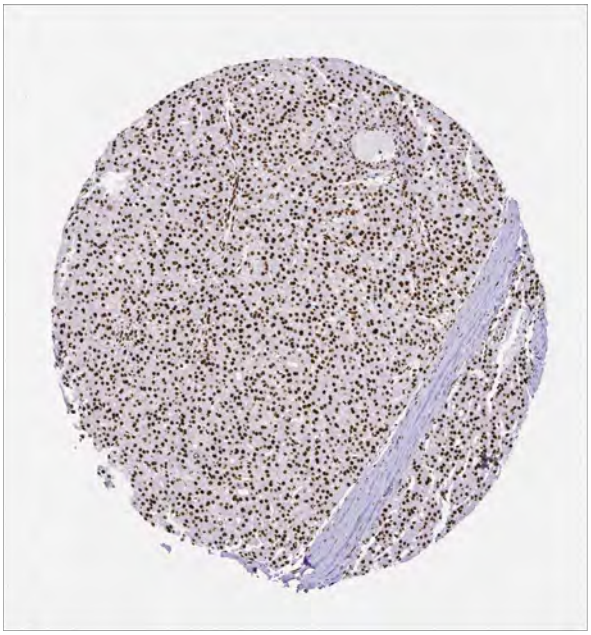


Figure 13. Immunohistochemistry using the anti-SFPQ antibody (HPA054689) on hepatocellular carcinoma (male, age 67) shows a strong nuclear staining of tumor cells, in brown.

Enhanced Validation

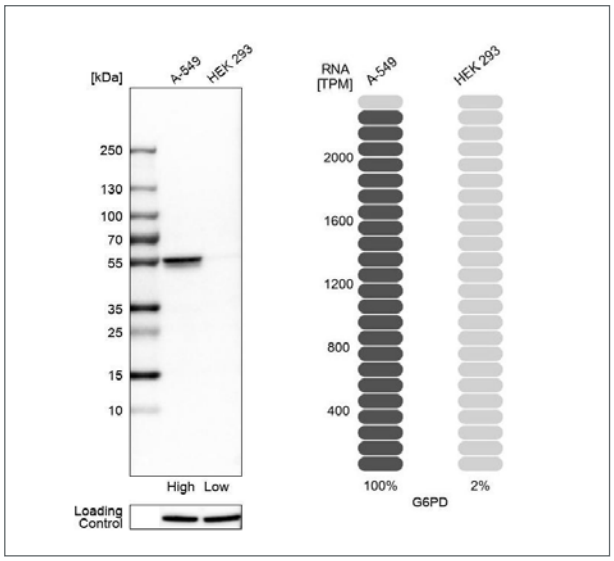


Figure 14. Western blot analysis in human cell lines A-549 and HEK293 using anti-G6PD antibody. Corresponding G6PD RNA-seq data are presented for the same cell lines. Loading control: anti-HSP90B1. Orthogonal validation of protein expression using WB by comparison to RNA-seq data of corresponding target in high and low expression cell lines.

Table 13. Top genes with highest significance associated with unfavorable prognosis in liver cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-CAD	-	HPA057266	WB*, ICC-IF	-
Anti-CCT4	Cctd	HPA029349	IHC*, WB, ICC-IF	99% / 99%
Anti-CCT5	KIAA0098	HPA005958	IHC*, WB*, ICC-IF	97% / 97%
Anti-CDCA8	BOR, DasraB, FLJ12042	HPA028120	IHC*, WB*, ICC-IF	64% / 66%
Anti-EIF5B	FLJ10524, IF2, KIAA0741	HPA040095	ICC-IF	81% / 81%
Anti-G6PD	G6PD1	HPA000247	IHC*, WB*, ICC-IF	96% / 96%
Anti-GTPBP4	FLJ10690, NGB, NOG1	HPA039618	IHC, WB*, ICC-IF	93% / 93%
Anti-GTSE1	B99, GTSE-1	HPA060544	IHC	56% / 57%
Anti-HDAC2	RPD3, YAF1	HPA011727	IHC, WB*, ICC-IF	97% / 95%
Anti-HILPDA	C7orf68, FLJ21076, HIG-2, HIG2	HPA010515	IHC, ICC-IF	76% / 68%
Anti-INTS13	ASUN, C12orf11, NET48	HPA039543	IHC	99% / 99%
Anti-KDM1A	AOF2, BHC110, LSD1	HPA053660	ICC-IF	100% / 100%
Anti-KIF20A	RAB6KIFL	HPA036910	IHC, WB*	78% / 77%
Anti-KPNA2	IPOA1, QIP2, RCH1, SRP1alpha	HPA041270	IHC*, WB, ICC-IF	92% / 94%
Anti-PSMD1	P112, Rpn2, S1	HPA036736	IHC*, WB, ICC-IF	100% / 100%
Anti-RBM28	FLJ10377	HPA026672	IHC*, WB, ICC-IF	94% / 94%
Anti-SFPQ	PPP1R140, PSF	HPA047513	IHC*, WB*, ICC-IF	100% / 100%
Anti-SNX5	-	HPA051187	IHC, WB	99% / 99%
Anti-TRMT6	CGI-09, GCD10, MGC5029	HPA047032	IHC, WB, ICC-IF	91% / 89%
Anti-YARS	tyrRS, YRS, YTS	HPA018954	IHC*, WB*, ICC-IF	95% / 93%

Table 14. Top genes with highest significance associated with favorable prognosis in liver cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ALDH2	-	HPA051065	IHC, WB	92% / 96%
Anti-ANXA10	ANX14	HPA005469	IHC*, WB	95% / 97%
Anti-APOC1	-	HPA051518	IHC	65% / 65%
Anti-APOH	B2G1, BG	HPA001654	IHC*, WB*, ICC-IF	76% / 85%
Anti-BDH1	BDH, SDR9C1	HPA030947	IHC*, WB, ICC-IF	90% / 91%
Anti-CLEC3B	TN, TNA	HPA034794	IHC, WB	82% / 83%
Anti-CHP1	CHP, p22, p24, Sid470p	HPA006616	IHC, ICC-IF	98% / 98%
Anti-CYP2C9	CYP2C10, P450IIC9	HPA015066	IHC, WB	79% / 75%
Anti-GHR	GHBP	HPA057705	ICC-IF	68% / 74%
Anti-HAGH	GLO2, GLXII, HAGH1	HPA061143	IHC, WB	93% / 89%
Anti-HMGCS2	-	HPA027442	IHC*, WB*, ICC-IF	81% / 79%
Anti-KNG1	BDK, BK, KNG	HPA001645	IHC*, WB*	59% / 58%
Anti-LCAT	-	HPA044767	WB*, ICC-IF	88% / 89%
Anti-LIMS2	-	HPA058340	IHC*, WB, ICC-IF	75% / 71%
Anti-MARC2	FLJ20605, MOSC2	HPA015085	IHC*, WB	74% / 74%
Anti-MTHFS	HsT19268	HPA054177	IHC, WB, ICC-IF	79% / 79%
Anti-PDE2A	-	HPA031192	IHC*	99% / 97%
Anti-PON1	ESA, PON	HPA001610	IHC, WB	78% / 76%
Anti-RBP4	-	HPA001641	IHC	90% / 90%
Anti-UPB1	BUP1	HPA000728	IHC*, WB*	86% / 85%

* Products with enhanced validation for indicated application

Lung Cancer

Lung cancer is the most prevalent cancer in the world and the leading cause of cancer-related deaths. Smoking is accepted as the major risk factor, responsible for 70-90% of all lung cancer cases, although the etiology of lung cancer appears multifactorial with both environmental and genetic factors playing a role.

Lung cancer patients have a poor outcome with a 5-year survival rate of 13.6% among men and 19.4% among women across all stages. The poor prognosis is partly explained by late diagnosis, but also by lack of effective treatments.

Based on histology, lung cancer is primarily divided into:
- SCLC: small cell lung cancer
- NSCLC: non-small cell lung cancer.

SCLC originates from neuroendocrine cells and accounts for approximately 15% of all primary lung cancers.

This extremely rapidly proliferating cancer is generally treated with chemotherapy with an initial good response which unfortunately in most cases is followed by resistance to treatment and poor survival outcome.

NSCLC is suggested to originate from bronchogenic or alveolar cells. It is the most common form of primary lung cancer and represents approximately 80-85% of all lung cancer cases.

Based on histology, NSCLC can further be divided into different subtypes, with adenocarcinoma and squamous cell carcinoma being most common.

Treatment for NSCLC is mainly based on the tumor extent. In principle, limited stage tumors are surgically treated, sometimes with the addition of chemotherapy and radiotherapy whereas tumors with advanced stages are palliatively treated with a combination of cytotoxic drugs and recently developed targeted drugs.

Unfortunately, the treatment effect is limited and the majority of patients experience only modest survival prolongation.

The transcriptome analysis shows that 74% (n=14627) of all human genes (n=19670) are expressed in lung cancer.

97 genes show some level of elevated expression in lung cancer compared to other cancers.

There are 354 genes associated with unfavorable prognosis in lung cancer.

There are 297 genes associated with favorable prognosis in lung cancer.

Data collected from 994 patients in total: 494 patients with squamous cell carcinoma (LUSC) and 500 patients with adenocarcinoma (LUAD). The total dataset included 398 females and 596 males.

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 15 and 16.

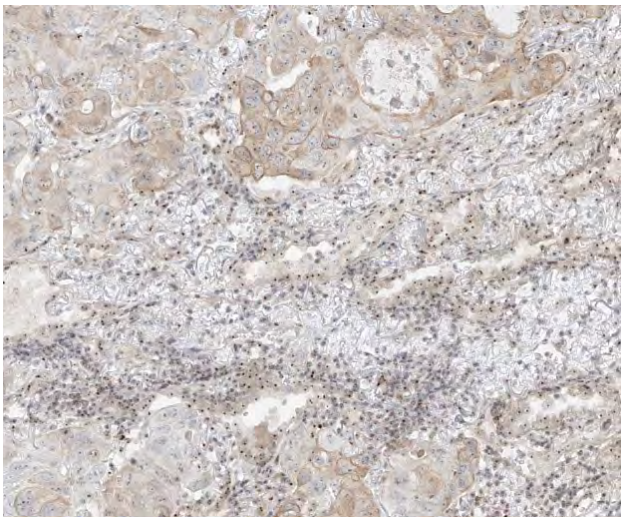


Figure 15. Immunohistochemistry using the anti-ZNF512 antibody (HPA031430) on lung cancer (Squamous cell carcinoma) (female, age 73) shows a moderate cytoplasmic/membranous staining of tumor cells, in brown.

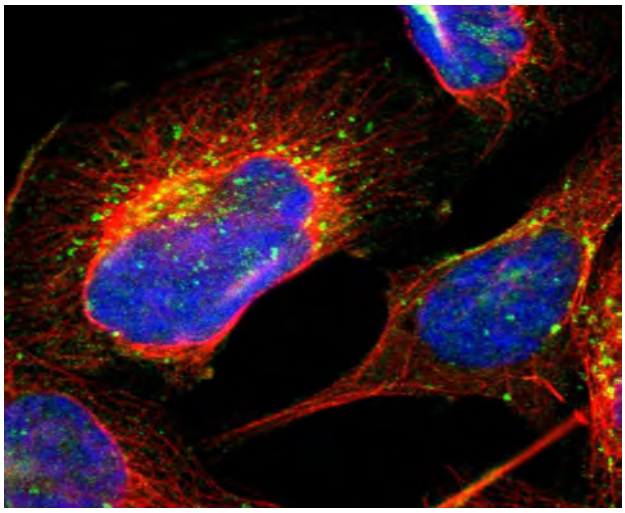


Figure 16. Immunofluorescent staining of human cell line U-2 OS using the anti-RAAGA antibody (HPA003734) shows localization to the Golgi apparatus & vesicles, in green. Microtubules in red and nuclei in blue.

Table 15. Top genes with highest significance associated with unfavorable prognosis in lung cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-BCAR3	NSP2, SH2D3B	HPA014858	IHC, WB*, ICC-IF	79% / 81%
Anti-CMIP	-	HPA054424	WB*, ICC-IF	100% / 100%
Anti-COL22A1	-	HPA024830	IHC, ICC-IF	99% / 99%
Anti-FLNC	ABP-280, ABPL, FLN2	HPA006135	IHC*, ICC-IF	99% / 99%
Anti-FSTL3	FLRG, FSRP	HPA045378	IHC, ICC-IF	84% / 85%
Anti-GALNT2	GalNAc-T2	HPA011222	IHC, WB*, ICC-IF	96% / 96%
Anti-GPRIN1	GRIN1, KIAA1893	HPA070892	IHC*, ICC-IF	75% / 33%
Anti-IER5L	bA247A12.2	HPA021327	ICC-IF	97% / 96%
Anti-ITGB1	CD29, FNRB, GPIIA, MSK12	HPA059297	IHC*, WB	91% / 91%
Anti-L1CAM	CD171, HSAS, HSAS1, MASA	HPA005830	IHC*	75% / 75%
Anti-LDHAL6B	LDH6B, LDHAL6, LDHL	HPA053962	IHC*	48% / 30%
Anti-LOXL2	WS9-14	HPA036257	ICC-IF	87% / 86%
Anti-MYO1E	HuncM-IC, MGC104638, MYO1C	HPA023886	IHC, WB	94% / 92%
Anti-PLCD3	-	HPA053665	IHC, WB	96% / 95%
Anti-PLIN3	M6PRBP1, PP17, TIP47	HPA006427	IHC, WB*, ICC-IF	71% / 71%
Anti-PTX3	TNFAIP5, TSG-14	HPA069320	IHC	85% / 90%
Anti-RCN1	FLJ37041, PIG20, Rcal, RCN	HPA038474	IHC, WB*, ICC-IF	92% / 92%
Anti-SERPINE1	PAI, PAI1, PLANH1	HPA050039	IHC, ICC-IF	84% / 83%
Anti-SP6	Epfn, KLF14	HPA024516	WB, ICC-IF	95% / 96%
Anti-STK24	MST-3, MST3, STE20, STK3	HPA026502	IHC*, WB*, ICC-IF	93% / 92%

Table 16. Top genes with highest significance associated with favorable prognosis in lung cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ANKRD65	-	HPA065720	IHC*, WB, ICC-IF	57% / 51%
Anti-CLIC6	CLIC1L, CLIC5	HPA065285	IHC	35% / 35%
Anti-FAM117A	-	HPA022531	IHC, ICC-IF	85% / 86%
Anti-GKN1	AMP18, BRICD1, CA11	HPA047684	IHC*	74% / 77%
Anti-GC	DBP, hDBP, VDBP	HPA001526	IHC*, WB	69% / 64%
Anti-GNG7	FLJ00058	HPA057790	IHC	100% / 100%
Anti-HLF	MGC33822	HPA068156	ICC-IF	94% / 94%
Anti-LRIG1	DKFZP586O1624, LIG-1, LIG1	HPA011846	IHC, WB*, ICC-IF	74% / 74%
Anti-NSMCE4A	C10orf86, FLJ20003, NSE4A	HPA037459	IHC, WB, ICC-IF	87% / 87%
Anti-PPFIBP2	Cclp1	HPA001935	IHC*, ICC-IF	76% / 80%
Anti-RFXAP	-	HPA032035	ICC-IF	96% / 96%
Anti-SLC11A2	DCT1, DMT1, NRAMP2	HPA032140	IHC, ICC-IF	85% / 88%
Anti-SLC47A1	FLJ10847, MATE1	HPA021987	IHC*	49% / 51%
Anti-SMIM4	C3orf78	HPA047771	IHC, ICC-IF	97% / 37%
Anti-THYN1	THY28	HPA038732	IHC, WB, ICC-IF	93% / 93%
Anti-TMEM168	DKFZp564C012, FLJ13576	HPA020389	IHC	92% / 93%
Anti-TTC39B	C9orf52, FLJ33868	HPA054804	IHC	94% / 94%
Anti-USP4	UNP, Unph	HPA018499	IHC, WB, ICC-IF	88% / 83%
Anti-ZNF77	pT1	HPA023397	IHC, ICC-IF	39% / 41%
Anti-ZNF512	KIAA1805	HPA031430	IHC, ICC-IF	91% / 91%

* Products with enhanced validation for indicated application

Melanoma

Malignant melanoma is the leading cause of skin-related death in Caucasians, but rare in populations with darker pigmented skin color. The incidence has increased dramatically during the last decades, with an almost four-fold increase in the Nordic countries in the time period 1964-2003.

The increased incidence reflects in part different UV exposure behavior in the population, but hereditary risk factors including skin type are also important.

Short intermittent exposure with sunburns appears to be the main risk factor. Other important risk factors include the number of melanocytic nevi and the number of dysplastic melanocytic nevi.

Primary cutaneous malignant melanoma is thought to develop in a multi-step process. Precursor lesions, such as dysplastic melanocytic nevi develop into a melanoma in situ stage and further into invasive melanoma and eventually metastatic melanoma.

Invasive malignant melanoma is traditionally divided into four principal histopathological subgroups based on the microscopical appearance: superficial spreading melanoma (SSM), nodular malignant melanoma (NMM), lentigo maligna melanoma (LMM) and acral lentiginous melanoma (ALM).

The transcriptome analysis shows that 69% (n=13491) of all human genes (n=19670) are expressed in melanoma.

260 genes show some level of elevated expression in melanoma compared to other cancers.

There are 163 genes associated with unfavorable prognosis in melanoma.

There are 42 genes associated with favorable prognosis in melanoma.

Data collected from 102 patients with skin cutaneous melanoma in total. The total dataset included 42 females and 60 males.

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 17 and 18.

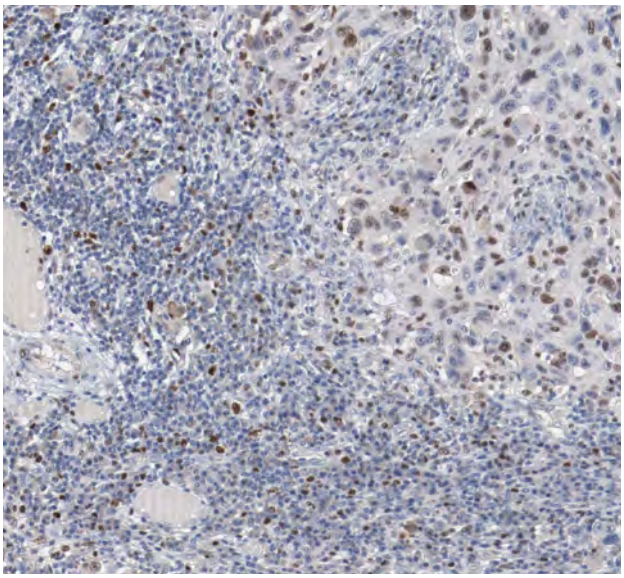


Figure 17. Immunohistochemistry using the anti-MCM6 antibody (HPA004818) on melanoma (male, age 53) shows a moderate nuclear staining of tumor cells, in brown.

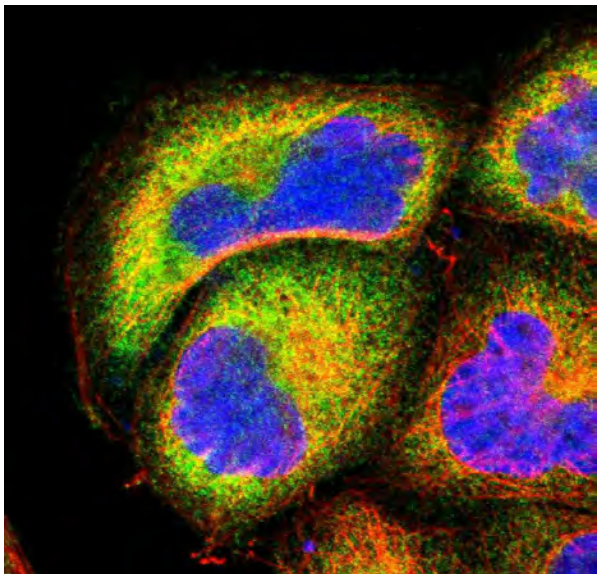


Figure 18. Immunofluorescent staining of human cell line A-431 using the anti-NFKB2 antibody (HPA008422) shows localization to cytosol, in green. Microtubules in red and nuclei in blue.

Table 17. Top genes with highest significance associated with unfavorable prognosis in skin cancer (melanoma).

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-CCNB2	HsT17299	HPA008873	IHC*, WB, ICC-IF	81% / 27%
Anti-CDC5L	CDC5, hCDC5, PCDC5RP	HPA011361	IHC, WB, ICC-IF	99% / 98%
Anti-KCTD14	MGC2376	HPA041118	IHC*, WB*	67% / 70%
Anti-MARK3	CTAK1, KP78, PAR-1A	HPA024652	IHC, WB	93% / 91%
Anti-MAT2A	MATA2, MATII, SAMS2	HPA043028	IHC, WB, ICC-IF	100% / 100%
Anti-MCM3	-	HPA004790	IHC, WB, ICC-IF	99% / 99%
Anti-MCM6	Mis5	HPA004818	IHC*, WB*, ICC-IF	97% / 97%
Anti-MED20	PRO0213, TRFP	HPA040717	IHC, ICC-IF	99% / 99%
Anti-NUDT15	FLJ10956, MTH2	HPA038969	IHC	90% / 90%
Anti-PAPSS2	ATPSK2	HPA071224	ICC-IF	85% / 81%
Anti-PUS7	FLJ20485	HPA024116	IHC, WB, ICC-IF	95% / 95%
Anti-RCC2	TD-60	HPA072281	IHC	93% / 92%
Anti-SFSWAP	SFRS8, SWAP	HPA039362	IHC, ICC-IF	90% / 90%
Anti-SKP2	FBL1, FBXL1, p45	HPA051196	WB*, ICC-IF	88% / 88%
Anti-STK38	KIAA0965, NDR2	HPA051324	ICC-IF	100% / 100%
Anti-TDG	-	HPA052263	IHC, ICC-IF	100% / 100%
Anti-TICRR	C15orf42, SLD3, Treslin	HPA046746	ICC-IF	44% / 43%
Anti-TIMELESS	hTIM, TIM, TIM1	HPA060655	IHC*, WB, ICC-IF	85% / 84%
Anti-ZNF544	AF020591	HPA002732	IHC, ICC-IF	73% / 72%
Anti-ZNF551	DKFZp686H1038	HPA038187	ICC-IF	42% / 40%

Table 18. Top genes with highest significance associated with favorable prognosis in skin cancer (melanoma)

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-CD2	SRBC	HPA003883	IHC*, WB*	63% / 67%
Anti-CD3E	-	HPA040957	IHC*, WB	43% / 50%
Anti-CD5	LEU1, T1	HPA060839	IHC*	61% / 64%
Anti-CD7	GP40, LEU-9, Tp40, TP41	HPA039079	IHC*	33% / 32%
Anti-CXCR3	CD183, CKR-L2, GPR9, IP10-R	HPA045942	IHC*	67% / 67%
Anti-DLGAP4	DAP4, KIAA0964, SAPAP4	HPA054105	IHC, WB	96% / 98%
Anti-DOK2	Dok-2, p56dok-2	HPA066571	IHC*	66% / 66%
Anti-EGR3	PILOT	HPA006206	IHC	100% / 100%
Anti-GNLY	D2S69E, LAG-2, LAG2, NKG5	HPA058021	IHC*	28% / 28%
Anti-IDO1	IDO, INDO	HPA023072	IHC*, WB*	58% / 57%
Anti-IKZF3	Aiolos, ZNFN1A3	HPA024377	IHC*, ICC-IF	77% / 77%
Anti-LCK	-	HPA003494	IHC*, WB, ICC-IF	95% / 95%
Anti-NFKB2	LYT-10, NF-kB2, p105, p52	HPA008422	IHC*, WB*, ICC-IF	93% / 92%
Anti-NR1D1	ear-1, THRA1, THRAL	HPA007935	IHC, ICC-IF	96% / 96%
Anti-OTUD7B	CEZANNE, ZA20D1	HPA027045	IHC, WB, ICC-IF	86% / 87%
Anti-SDC3	N-syndecan, SYND3	HPA048085	WB, ICC-IF	76% / 78%
Anti-SIT1	SIT	HPA018506	IHC*	77% / 78%
Anti-SLAMF6	CD352, KALI, NTBA, SF2000	HPA051903	IHC, WB	45% / 52%
Anti-SPOCK2	KIAA0275, testican-2	HPA044605	IHC, WB*	86% / 85%
Anti-SPN	CD43, GPL115, LSN	HPA055244	IHC*	65% / 65%

* Products with enhanced validation for indicated application

Ovarian cancer

Epithelial carcinoma of the ovary is one of the most common gynecologic malignancies and the fifth most frequent cause of cancer death in women. 50% of all ovarian cancers are diagnosed in women older than 65 years of age.

Approximately 5 to 10% of ovarian cancers are familial and women with mutations in the genes BRCA1 or BRCA2 have about a 50% higher risk of developing ovarian cancer.

Ovarian cancer is typically denoted as a silent cancer since symptoms occur late in the course of the disease. A majority of ovarian epithelial cancers are diagnosed during or after abdominal exploration to investigate a pelvic or abdominal mass detected on physical examination.

By the time of discovery, approximately 70% of the tumors have spread beyond the ovary and are in such cases rarely curable by surgical resection or surgery combined with postoperative chemotherapy and/or radiation therapy. The dismal prognosis has stimulated research efforts for early detection of ovarian cancer.

Ovarian epithelial cancer is bilateral (involving both ovaries) in one-third to one-half of the cases.

The FIGO (International Federation of Gynaecology and Obstetrics) staging system recognizes four stages for ovarian cancer. Patients with Stage I tumors have a 5-year survival of 80%, while the 5-year survival of Stage IV patients is merely 8%.

The transcriptome analysis shows that 72% (n=14227) of all human genes (n=19670) are expressed in ovarian cancer.

151 genes show some level of elevated expression in ovarian cancer compared to other cancers

There are 152 genes associated with unfavorable prognosis in ovarian cancer.

There are 357 genes associated with favorable prognosis in ovarian cancer.

Data collected from 373 females with ovarian serous cystadenocarcinoma.

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 19 and 20.

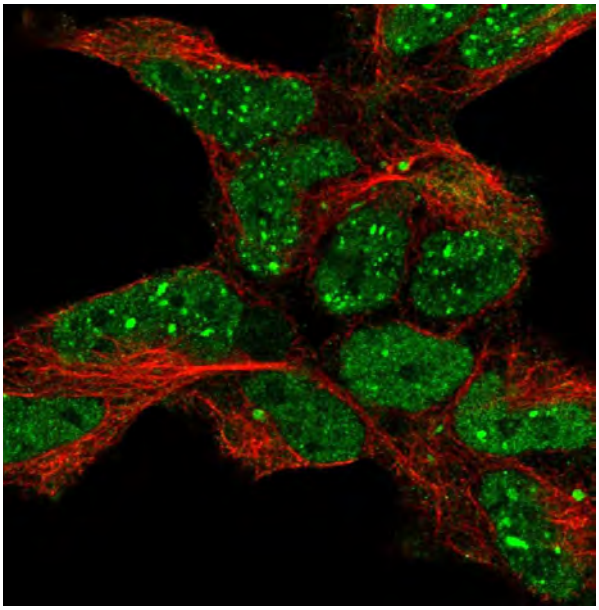


Figure 19. Immunofluorescent staining of human cell line HEK 293 using the anti-TDP2 antibody (HPA008422) shows localization to nucleoplasm, nuclear bodies & aggresome, in green. Microtubules in red.

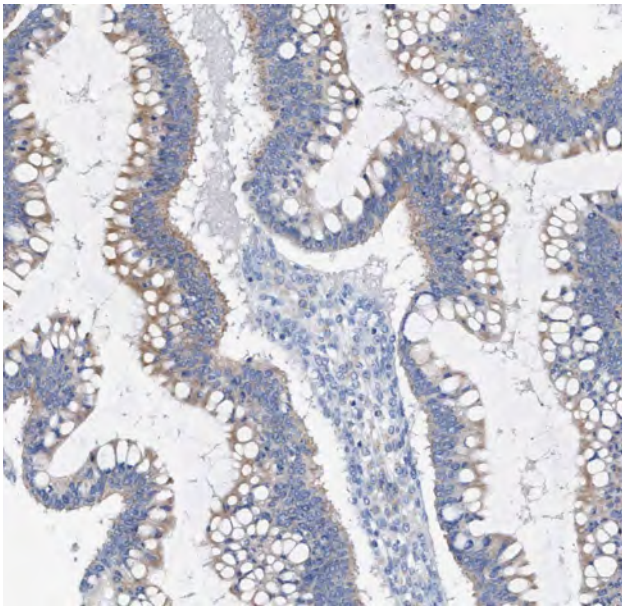


Figure 20. Immunohistochemistry using the anti-MCM6 antibody (HPA004818) on ovary cystadenocarcinoma, mucinous (female, age 73) shows a moderate cytoplasmic/ membranous staining of tumor cells, in brown.

Table 19. Top genes with highest significance associated with unfavorable prognosis in ovarian cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-AGFG1	HRB, RAB, RIP	HPA008741	IHC, WB, ICC-IF	97% / 94%
Anti-CST4	-	HPA044763	IHC	58% / 58%
Anti-DAGLB	DAGLBETA, KCCR13L	HPA069377	WB, ICC-IF	78% / 80%
Anti-FAM20C	DMP4, IMAGE:4942737	HPA019823	ICC-IF	87% / 87%
Anti-FAM98C	FLJ44669	HPA040930	IHC, WB, ICC-IF	70% / 70%
Anti-FANCD2	FA-D2, FACD, FAD, FANCD	HPA063742	ICC-IF	72% / 76%
Anti-FCGBP	FC(GAMMA)BP	HPA003517	IHC*	82% / 80%
Anti-JMY	FLJ37870	HPA043308	IHC, WB	91% / 87%
Anti-KRT7	CK7, K2C7, K7, SCL	HPA007272	IHC*, WB*	90% / 90%
Anti-LYVE1	LYVE-1, XLKD1	HPA042953	IHC, WB	63% / 61%
Anti-PC	PCB	HPA043922	IHC*, WB*, ICC-IF	97% / 97%
Anti-PI3	ELAFIN, SKALP, WAP3	HPA017737	IHC*	31% / 31%
Anti-PPTC7	TA-PP2C	HPA039335	IHC, WB*, ICC-IF	99% / 99%
Anti-RCBTB1	CLLD7, CLLL7, FLJ10716	HPA056783	ICC-IF	100% / 100%
Anti-RIPK4	ANKK2, ANKRD3, DIK, PKK	HPA030942	IHC*	90% / 91%
Anti-RPL7A	L7A, SURF3, TRUP	HPA046794	ICC-IF	100% / 100%
Anti-RPS6KA2	HU-2, RSK, RSK3	HPA045061	IHC, ICC-IF	90% / 88%
Anti-SLC39A13	FLJ25785	HPA043971	IHC	92% / 88%
Anti-SOGA1	C20orf117, FLJ44670, KIAA0889	HPA043992	IHC, ICC-IF	89% / 89%
Anti-TGFBI	BIGH3, CDB1, LCD1	HPA017019	IHC*, WB	88% / 87%

Table 20. Top genes with highest significance associated with favorable prognosis in ovarian cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-AADAC	CES5A1, DAC	HPA002911	IHC	73% / 69%
Anti-ACOT13	HT012, THEM2	HPA019881	IHC, WB, ICC-IF	92% / 90%
Anti-AP1S2	MRXS5, PGS, SIGMA1B	HPA049894	IHC*	96% / 44%
Anti-C18orf21	HsT3108, PNAS-124	HPA065505	IHC, WB, ICC-IF	65% / 63%
Anti-CCDC160	-	HPA044684	IHC	46% / 46%
Anti-CACYBP	S100A6BP, SIP	HPA057038	ICC-IF	94% / 94%
Anti-FAM166B	-	HPA045540	IHC	66% / 25%
Anti-FMC1	C7orf55, HSPC268	HPA050553	IHC, WB*, ICC-IF	93% / 96%
Anti-GPR27	SREB1	HPA029395	WB, ICC-IF	91% / 91%
Anti-KLHDC9	KARCA1	HPA032058	IHC, WB*	81% / 80%
Anti-MAGOH	MAGOH1, MAGOHA	HPA043036	IHC, WB	100% / 100%
Anti-MED19	LCMR1	HPA040860	IHC, WB*, ICC-IF	96% / 96%
Anti-MRS2	MRS2L	HPA017642	IHC, WB	90% / 93%
Anti-PRR3	CAT56, Em:AB023052.2	HPA064061	ICC-IF	86% / 83%
Anti-SNRPD1	HsT2456, Sm-D1, SNRPD	HPA040516	IHC, WB	100% / 100%
Anti-TDP2	TTRAP	HPA074011	ICC-IF	77% / 76%
Anti-UBE2L3	UBCH7	HPA062415	IHC, WB, ICC-IF	100% / 51%
Anti-UTP4	CIRH1A, KIAA1988, TEX292	HPA043542	ICC-IF	98% / 96%
Anti-ZNF85	HPF4, HTF1	HPA044760	IHC, ICC-IF	35% / 35%
Anti-ZNF429	-	HPA004139	ICC-IF	31% / 31%

* Products with enhanced validation for indicated application

Pancreatic cancer

Pancreatic cancer is the 11th most common cancer globally and is associated with poor prognosis. Estimated 5-year survival rate is less than 5% and pancreatic cancer accounts for 4% of all deaths that occur worldwide each year.

The risk of pancreatic cancer increases with age and the tumor is slightly more common in women than in men. Most patients suffering from pancreatic cancer are above 50 years of age and pain, jaundice and weight loss are the most common symptoms.

The cause of pancreatic cancer is unknown. However, pancreatic cancer is more common in people with diabetes and chronic pancreatitis (persistent inflammation in the pancreas) as well as in tobacco smokers.

Pancreatic exocrine tumors are the most common form of pancreatic cancer, accounting for 95% of cases, with ductal adenocarcinoma being the most prevalent exocrine cancer.

Pancreatic endocrine tumors constitute the remaining 5% of reported cases. Due to diffuse symptoms, pancreatic cancer is often detected at such a late stage of the disease that curative surgery is not possible.

In addition to local spread in the pancreas and surrounding tissues, pancreatic cancer often spreads to regional lymph nodes and to the liver. Over 80% of all patients have metastasis at the time of diagnosis.

The transcriptome analysis shows that 74% (n=14468) of all human genes (n=19670) are expressed in pancreatic cancer.

192 genes show some level of elevated expression in pancreatic cancer compared to other cancers.

There are 668 genes associated with unfavorable prognosis in pancreatic cancer.

There are 857 genes associated with favorable prognosis in pancreatic cancer.

(data collected from 176 patients in total, with 80 female and 96 male patients).

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 21 and 22.

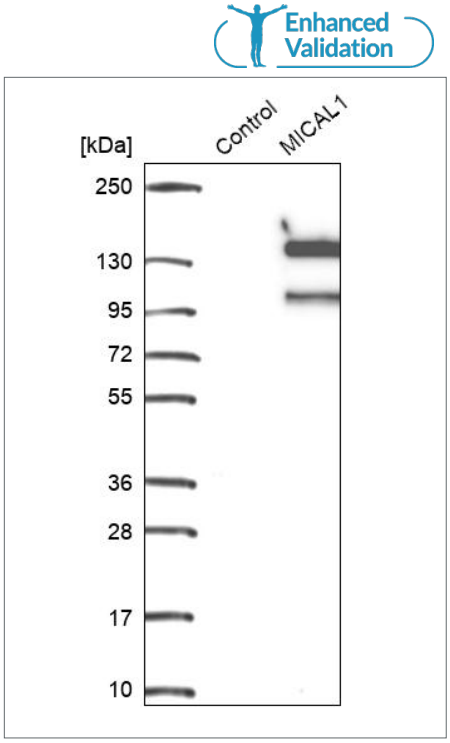


Figure 21. Recombinant expression validation in WB using target protein overexpression. Western blot analysis using the anti-MICAL1 (HPA030178) in control (vector only transfected HEK293T lysate) and MICAL1 over-expression lysate (Co-expressed with a C-terminal myc-DDK tag (~3.1 kDa) in mammalian HEK293T cells, LY402940).

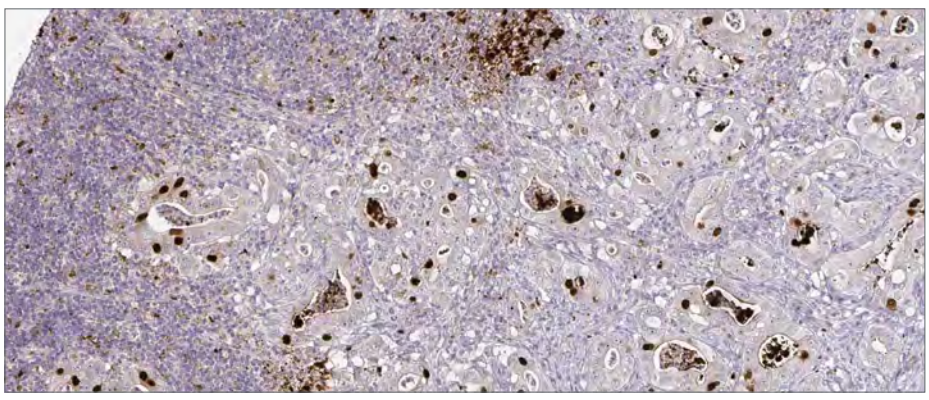


Figure 22. Immunohistochemistry using the anti-ANLN antibody (HPA005680) on pancreatic cancer (male, age 71) shows a strong nuclear staining of tumor cells, in brown.

Table 21. Top genes with highest significance associated with unfavorable prognosis in pancreatic cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-AHNAK2	C14orf78	HPA002940	IHC*, ICC-IF	66% / 63%
Anti-ANLN	ANILLIN, scra, Scraps	HPA050556	IHC*,WB*, ICC-IF	86% / 85%
Anti-ARMC10	MGC3195, SVH	HPA011036	IHC*,WB*, ICC-IF	89% / 83%
Anti-CA12	HsT18816	HPA008773	IHC, ICC-IF	88% / 88%
Anti-CDK6	PLSTIRE	HPA002637	IHC*,WB*, ICC-IF	92% / 92%
Anti-CHEK1	CHK1	HPA044364	ICC-IF	92% / 93%
Anti-COMMD2	HSPC042	HPA044190	IHC, WB	92% / 90%
Anti-EPS8	-	HPA003897	IHC, ICC-IF	80% / 80%
Anti-FZD6	Hfz6	HPA017991	IHC,WB*, ICC-IF	55% / 62%
Anti-ITGB6	-	HPA023626	IHC, ICC-IF	90% / 88%
Anti-JAG1	AGS, AHD, CD339, HJ1, JAGL1	HPA021555	IHC*	94% / 93%
Anti-KPNA4	IPOA3, MGC26703, QIP1, SRP3	HPA045500	IHC,WB*, ICC-IF	97% / 97%
Anti-LAMA3	epiligrin, kalinin-165kDa, LAMNA	HPA009309	IHC, ICC-IF	74% / 71%
Anti-LY6D	E48	HPA024755	IHC*,WB*	61% / 53%
Anti-MET	DFNB97, HGFR, RCCP2	HPA055607	ICC-IF	97% / 97%
Anti-MRPL3	MRL3, RPML3	HPA043665	IHC, WB	86% / 87%
Anti-MYEOV	OCIM	HPA012949	IHC, ICC-IF	19% / 21%
Anti-WNT7A	-	HPA015719	IHC	100% / 100%
Anti-ZFP91	PZF, ZNF757	HPA024037	IHC	99% / 97%
Anti-ZNF488	FLJ32104	HPA035957	IHC,WB*, ICC-IF	33% / 39%

Table 22. Top genes with highest significance associated with favorable prognosis in pancreatic cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ANAPC2	APC2, KIAA1406	HPA066539	ICC-IF	95% / 95%
Anti-ARNT2	bHLHe1, KIAA0307	HPA001056	ICC-IF	98% / 97%
Anti-CAMTA2	KIAA0909	HPA051147	ICC-IF	90% / 90%
Anti-DEF8	FLJ20186	HPA041745	IHC	97% / 97%
Anti-INPP5K	SKIP	HPA031044	IHC, WB	83% / 80%
Anti-LRSAM1	FLJ31641	HPA021844	IHC, WB, ICC-IF	89% / 88%
Anti-MAMDC4	AEGP, DKFZp434M1411	HPA059977	IHC, ICC-IF	77% / 79%
Anti-MICAL1	FLJ21739, MICAL, NICAL	HPA030178	IHC, WB*	74% / 72%
Anti-MUM1	MUM-1	HPA048063	IHC, ICC-IF	37% / 42%
Anti-PHLDB3	FLJ40193	HPA043425	IHC, ICC-IF	84% / 82%
Anti-PPP1R3F	Hb2E	HPA000244	ICC-IF	88% / 28%
Anti-SGSM2	KIAA0397, RUTBC1	HPA021641	IHC, ICC-IF	80% / 80%
Anti-TBKBP1	KIAA0775, ProSAPiP2	HPA062347	IHC, ICC-IF	95% / 98%
Anti-TSPOAP1	BZRAP1, PRAX-1, RIM-BP1	HPA024662	IHC*	60% / 59%
Anti-TSPYL2	CDA1, DENTT, HRIHFB2216	HPA044133	IHC	55% / 54%
Anti-USP20	KIAA1003	HPA006287	IHC, WB*	90% / 88%
Anti-WDR37	KIAA0982	HPA037376	IHC*, WB	100% / 100%
Anti-ZNF48	FLJ31751, MGC43952, ZNF553	HPA023806	IHC, WB, ICC-IF	61% / 68%
Anti-ZNF222	-	HPA004086	IHC, WB, ICC-IF	38% / 31%
Anti-ZNF383	FLJ35863	HPA063945	IHC, ICC-IF	51% / 60%

* Products with enhanced validation for indicated application

Prostate cancer

Prostate cancer is one of the most common malignancies in men. The vast majority of primary prostate cancer cases are adenocarcinomas, and the cancers often show characteristics such as multifocality and differentiation pattern heterogeneity.

The rate of prostate tumor growth varies and is often low. Since the median age at diagnosis is high (65-70 years), most patients, especially those with localized tumors, often die of other complications without ever having suffered significant disability from the cancer.

Approximately 15% of patients with prostate cancer are in high-risk of disease-related symptoms and death. However, certain patients may have prolonged survival even after the cancer has metastasized to distant sites.

Prostate cancer is often stimulated by hormones (androgens) and anti-hormonal therapies can be effective to limit and slow down tumor growth, while radical prostatectomy is an option for treating localized prostate cancer.

Both normal prostatic glands and prostate cancer cells express the protein PSA (encoded by the gene KLK3) and the detection of elevated levels of PSA in the blood is today heavily used as a screening tool to detect the growth of prostate cancer.

Prostate cancer can be diagnosed using rectal examination (palpation), and histological examinations of tissue biopsies using the Gleason Grade scoring system, where dominant histological characteristics of the cancer cells are used to determine the cancer stage. Immunostaining of relevant molecular markers is also important.

The transcriptome analysis shows that 70% (n=13686) of all human genes (n=19670) are expressed in prostate cancer.

248 genes show some level of elevated expression in prostate cancer compared to other cancers

There are 134 genes associated with unfavorable prognosis in prostate cancer.

There are 25 genes associated with favorable prognosis in prostate cancer.

Data collected from 494 male patients with prostate adenocarcinoma.

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 23 and 24.

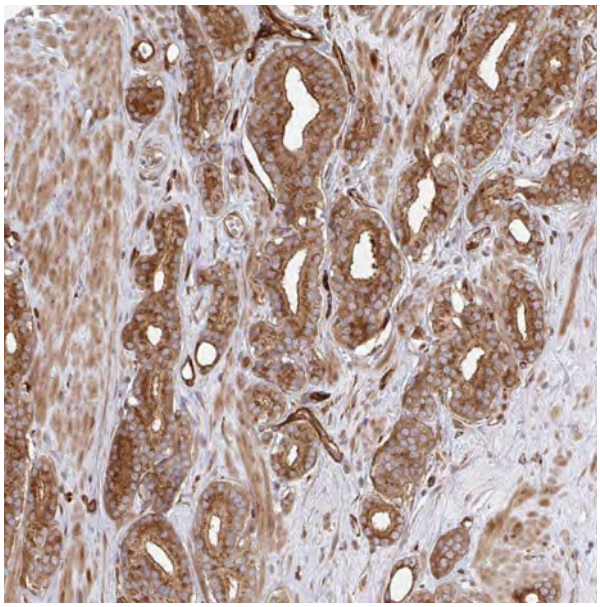


Figure 23. Immunohistochemistry using the anti-DVL3 antibody (HPA058265) on prostate adenocarcinoma, high grade (male, age 66) shows a moderate cytoplasmic/ membranous staining of tumor cells, in brown.

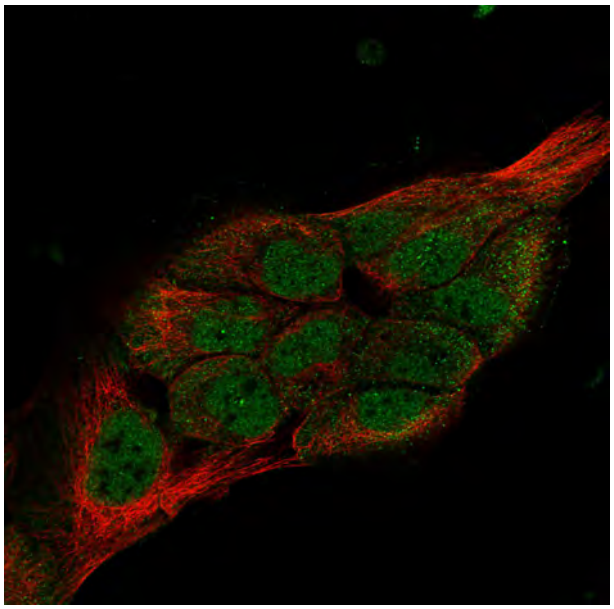


Figure 24. Immunofluorescent staining of human cell line A-431 using the anti-MBD2 antibody (HPA067582) shows localization to nucleoplasm and cytosol, in green. Microtubules in red.

Table 23. Top genes with highest significance associated with unfavorable prognosis in prostate cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ARRB2	ARR2, BARR2, DKFZp686L0365	HPA065681	ICC-IF	94% / 94%
Anti-CEP70	BITE, FLJ13036	HPA036942	IHC*, WB, ICC-IF	78% / 74%
Anti-COPS3	CSN3, SGN3	HPA021997	IHC, WB, ICC-IF	100% / 100%
Anti-DNAJC9	JDD1, SB73	HPA035215	IHC, WB*, ICC-IF	93% / 93%
Anti-DVL3	KIAA0208	HPA058265	IHC, WB, ICC-IF	95% / 95%
Anti-FBXO45	Fbx45	HPA040730	IHC, ICC-IF	99% / 99%
Anti-HKR1	ZNF875	HPA036126	IHC, ICC-IF	29% / 34%
Anti-HOOK2	HK2	HPA050351	IHC, WB	85% / 84%
Anti-LMNB2	LMN2	HPA047863	IHC*, WB	89% / 87%
Anti-MBD1	CXXC3, PCM1	HPA068850	WB, ICC-IF	68% / 66%
Anti-MTF2	M96, PCL2, TDRD19A	HPA069066	WB, ICC-IF	100% / 99%
Anti-RANBP1	HTF9A	HPA065931	IHC*, ICC-IF	93% / 90%
Anti-RBM8A	BOV-1C, RBM8, RBM8B, ZNRP	HPA018403	IHC, WB*, ICC-IF	100% / 100%
Anti-RNF8	KIAA0646	HPA064925	ICC-IF	77% / 78%
Anti-RPAIN	hRIP, MGC4189, RIP	HPA031526	IHC, WB*, ICC-IF	71% / 73%
Anti-SRC	ASV, c-src, SRC1	HPA030875	IHC, WB*, ICC-IF	95% / 98%
Anti-TEX30	C13orf27	HPA053545	IHC*, WB	95% / 94%
Anti-USP53	KIAA1350	HPA035844	IHC, ICC-IF	67% / 66%
Anti-ZNF330	HSA6591, NOA36	HPA015705	IHC, WB*	97% / 97%
Anti-ZNF654	FLJ10997, FLJ21142	HPA036173	IHC, WB*, ICC-IF	67% / 64%

Table 24. Top genes with highest significance associated with favorable prognosis in prostate cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-AK5	-	HPA019128	IHC*, WB*, ICC-IF	84% / 83%
Anti-AOC1	ABP1, DAO	HPA031032	IHC, WB	78% / 81%
Anti-ARL2	ARFL2	HPA044610	IHC, ICC-IF	89% / 89%
Anti-ATP6V1E1	ATP6E2, ATP6V1E, P31, Vma4	HPA029196	IHC*, WB, ICC-IF	98% / 99%
Anti-COMT	-	HPA001169	IHC*, WB*	82% / 82%
Anti-CRACR2A	EFCAB4B, MGC4266	HPA038686	IHC*	60% / 59%
Anti-CSRP2	CRP2, LMO5, SmLIM	HPA045617	IHC	100% / 100%
Anti-EPHX1	EPHX	HPA020593	IHC*, WB*	83% / 83%
Anti-FOS	AP-1, c-fos	HPA018531	IHC, ICC-IF	94% / 94%
Anti-FOXQ1	HFH1	HPA059700	ICC-IF	100% / 59%
Anti-GPAT4	AGPAT6, LPAAT-zeta, TSARG7	HPA016471	IHC	98% / 98%
Anti-HBEGF	DTR, DTS, HEGFL	HPA053243	IHC	76% / 80%
Anti-NTNG2	KIAA1857, Lmnt2, NTNG1	HPA065089	ICC-IF	100% / 100%
Anti-RFPL2	RNF79	HPA048320	ICC-IF	50% / 43%
Anti-RNF122	FLJ12526	HPA003888	IHC	94% / 94%
Anti-SESN1	PA26, SEST1	HPA073659	ICC-IF	95% / 93%
Anti-SLC35B2	UGTrel4	HPA029638	IHC	89% / 91%
Anti-TMEM158	p40BBp, RIS1	HPA074974	IHC	96% / 96%
Anti-TSKU	E2IG4, LRRC54, TSK	HPA008164	IHC, WB*, ICC-IF	92% / 93%
Anti-TXN2	MT-TRX	HPA000994	IHC, ICC-IF	91% / 89%

* Products with enhanced validation for indicated application

Renal cancer

Most renal cancers are renal cell carcinoma, which is almost exclusively cancer of adults and it is two to three times more common in males than in females.

It is the ninth most common cancer in men and 14th most common in women worldwide. The clinical course is highly unpredictable and recurrence more than ten years after the initial resection of a primary tumor is not uncommon.

Several cases present as metastatic carcinomas of unknown primary origin. Although smoking, industrial chemicals and obesity have been implicated as risk factors, in most cases the underlying carcinogenic source is unknown.

Renal cell carcinoma consists of a family of carcinomas which are derived from the epithelium of renal tubules.

The most frequent forms are:
-clear cell renal cell carcinoma,
-papillary renal cell carcinoma,
-chromophobe renal cell carcinoma
-collecting duct carcinoma.

Approximately two thirds of all renal cell carcinomas are clear cell renal cell carcinomas and are signified by the appearance of tumor cells with abundant clear cytoplasm.

Tumors can arise anywhere in the renal cortex and are typically surrounded by a fibrous pseudocapsule.

The transcriptome analysis shows that 72% (n=14124) of all human genes (n=19670) are expressed in renal cancer.

283 genes show some level of elevated expression in renal cancer compared to other cancers There are 3209 genes associated with unfavorable prognosis in renal cancer.

There are 2755 genes associated with favorable prognosis in renal cancer.

Data collected from 877 patients in total (286 females and 591 males): 64 patients with chromophobe renal cell carcinoma (KICH), 528 clear cell kidney carcinoma (KIRC), and 285 papillary kidney carcinoma (KIRP).

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 25 and 26.
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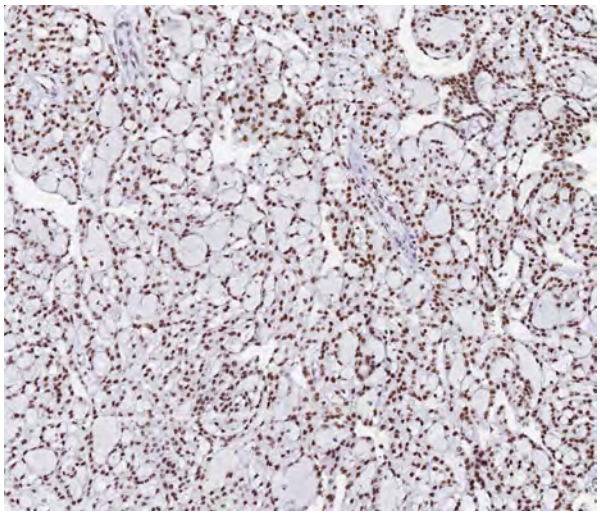

Figure 25. Immunohistochemistry using the anti-SNRPA1 antibody (HPA045622) on kidney adenocarcinoma (male, age 63) shows a strong nuclear staining of tumor cells, in brown.

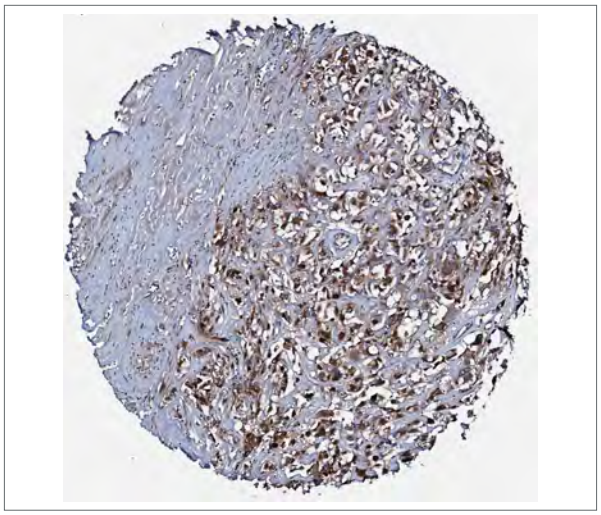

Figure 26. Immunohistochemistry using the anti-ACSS3 antibody (HPA047956) on kidney adenocarcinoma (female, age 52) shows a strong cytoplasmic/membranous staining of tumor cells, in brown.

Table 25. Top genes with highest significance associated with unfavorable prognosis in renal cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ANLN	ANILLIN, scra, Scraps	HPA050556	IHC*, WB*, ICC-IF	86% / 85%
Anti-CCNA2	CCN1, CCNA	HPA020626	WB*, ICC-IF	75% / 75%
Anti-CCNB2	HsT17299	HPA008873	IHC*, WB, ICC-IF	81% / 27%
Anti-CDCA5	-	HPA023691	IHC, WB, ICC-IF	66% / 64%
Anti-CDK1	CDC2, CDC28A	HPA003387	IHC*, WB, ICC-IF	98% / 98%
Anti-CEP55	C10orf3, CT111, FLJ10540	HPA023430	IHC, WB, ICC-IF	71% / 77%
Anti-COLGALT1	FLJ22329, GLT25D1	HPA047821	IHC, WB	90% / 88%
Anti-FKBP10	FKBP6, FLJ23833, hFKBP65	HPA057021	IHC*, WB	87% / 88%
Anti-FOXM1	FKHL16, HFH-11, HNF-3, INS-1	HPA029974	IHC	73% / 75%
Anti-KIF11	Eg5, HKSP, KNSL1, TRIP5	HPA010568	IHC*, WB	88% / 83%
Anti-KIF20A	RAB6KIFL	HPA036910	IHC, WB*	78% / 77%
Anti-MELK	KIAA0175	HPA017214	IHC, WB*	58% / 22%
Anti-PLK1	PLK	HPA051638	IHC	88% / 90%
Anti-PRR11	FLJ11029	HPA023923	IHC, WB*	76% / 74%
Anti-RIPK2	CARD3, CARDIAK, RICK, RIP2	HPA015273	IHC, WB, ICC-IF	73% / 73%
Anti-SPC24	FLJ90806, SPBC24	HPA051234	IHC, WB, ICC-IF	85% / 91%
Anti-TNNT1	ANM, NEM5, STNT, TNT	HPA058448	IHC*	97% / 95%
Anti-TOP2A	TOP2	HPA006458	IHC*, WB	63% / 60%
Anti-TPX2	C20orf2, DIL-2, p100	HPA005487	IHC*, WB, ICC-IF	84% / 86%
Anti-TRIP13	16E1BP	HPA005727	IHC*, WB*, ICC-IF	88% / 89%

Table 26. Top genes with highest significance associated with favorable prognosis in renal cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ACAT1	ACAT, THIL	HPA004428	IHC*, WB*, ICC-IF	92% / 92%
Anti-ACO2	ACONM	HPA001097	IHC*, WB, ICC-IF	97% / 97%
Anti-ACSS3	FLJ21963	HPA047956	IHC, WB*	85% / 88%
Anti-AUH	-	HPA004171	IHC*	70% / 67%
Anti-C1orf210	MGC52423	HPA013788	IHC, WB*	79% / 77%
Anti-CDS1	-	HPA036187	IHC, ICC-IF	91% / 91%
Anti-CRAT	CAT1	HPA022815	WB*, ICC-IF	91% / 91%
Anti-CRB3	MGC17303	HPA013835	IHC*, ICC-IF	91% / 91%
Anti-GNG7	FLJ00058	HPA057790	IHC	100% / 100%
Anti-HADH	HADH1, HADHSC, SCHAD	HPA043888	WB*, ICC-IF	95% / 95%
Anti-IMPA2	-	HPA029561	IHC, WB*, ICC-IF	92% / 91%
Anti-IRF6	LPS, OFC6, VWS, VWS1	HPA063121	IHC*, WB*, ICC-IF	95% / 96%
Anti-KIF13B	GAKIN, KIAA0639	HPA025023	IHC*, WB	86% / 81%
Anti-LRBA	BGL, CDC4L, LAB300, LBA	HPA019366	IHC, ICC-IF	72% / 73%
Anti-PAFAH1B1	LIS1, MDCR, MDS, PAFAH	HPA020036	IHC*, ICC-IF	99% / 99%
Anti-PCCA	-	HPA047792	IHC*, WB	93% / 84%
Anti-PINK1	PARK6	HPA001931	IHC	85% / 87%
Anti-TMEM25	FLJ14399	HPA012163	IHC, ICC-IF	86% / 86%
Anti-TOLLIP	IL-1RAcPIP	HPA038621	IHC*, WB*, ICC-IF	88% / 88%
Anti-ZNF844	FLJ14959	HPA046982	IHC	37% / 27%

* Products with enhanced validation for indicated application

Stomach cancer

Stomach cancer, or gastric cancer or gastric carcinoma, is the fifth most common cancer in the world and the fourth leading cause of cancer-related mortality. The global 5-year survival rate is 20%.

Stomach cancer occurs most often in men over the age of 40 and is common in Japan, Chile, and Iceland. The main risk factor for developing this type of cancer is Helicobacter pylori infection.

Other risk factors include a history of adenomatous gastric polyps, chronic atrophic gastritis or pernicious anemia as well as smoking and consumption of salted, cured or smoked foods. A genetic component is present in approximately 10% of all cases.

Stomach cancer originates from the mucosa of the stomach and consist of adenocarcinoma of varying architecture, grade of differentiation and mucin content. Clinical classification into different stages is necessary for determining the most suitable therapy.

Tumors restricted to the stomach and with no metastasis are treated with a combination of surgery, chemotherapy, radiotherapy and/or target therapy. Metastasized tumors are not curable and associated with more dismal prognosis.

The transcriptome analysis shows that 73% (n=14401) of all human genes (n=19670) are expressed in stomach cancer.

143 genes show some level of elevated expression in stomach cancer compared to other cancers

There are 170 genes associated with unfavorable prognosis in stomach cancer.

There are 128 genes associated with favorable prognosis in stomach cancer.

Data collected from 354 patients in total (125 females and 229 males).

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 27 and 28.

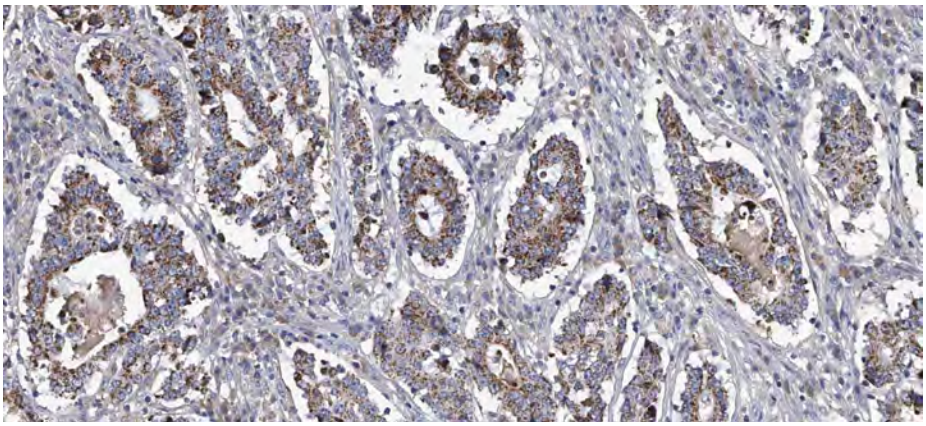

Figure 27. Immunohistochemistry using the anti-NRP1 antibody (HPA030278) on stomach adenocarcinoma (male, age 59) shows a medium cytoplasmic/membranous staining of tumor cells, in brown.

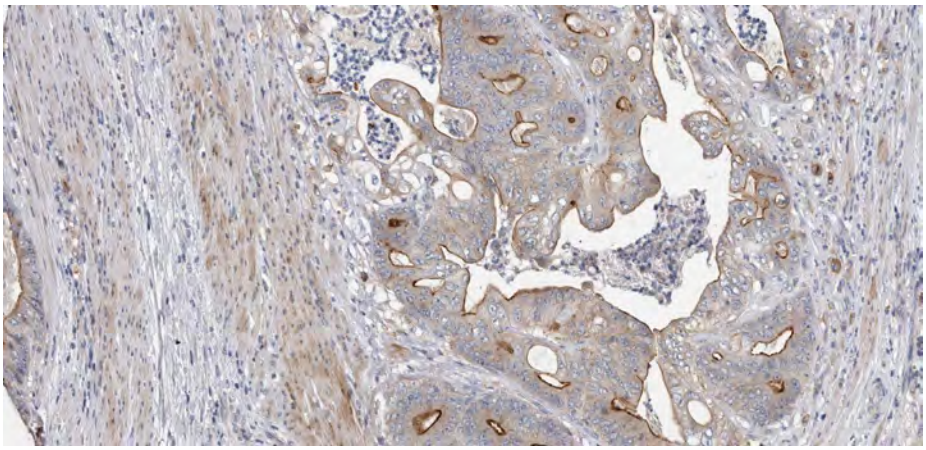

Figure 28. Immunohistochemistry using the anti-FAM83G antibody (HPA023369) on stomach adenocarcinoma (female, age 73) shows a moderate cytoplasmic/membranous staining of tumor cells, in brown.

Table 27. Top genes with highest significance associated with unfavorable prognosis in stomach cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-AKR1B1	ALDR1, AR	HPA026425	IHC*, ICC-IF	80% / 80%
Anti-CAST	-	HPA036881	IHC, ICC-IF	67% / 69%
Anti-CCPG1	CPR8, KIAA1254	HPA026861	IHC	76% / 73%
Anti-CD109	CPAMD7, FLJ38569	HPA015723	IHC*	65% / 61%
Anti-CYTL1	C17, C4orf4	HPA067201	ICC-IF	78% / 78%
Anti-DUSP1	CL100, HVH1, MKP-1, PTPN10	HPA069577	WB, ICC-IF	94% / 96%
Anti-ELL2	-	HPA013569	WB, ICC-IF	84% / 83%
Anti-FN1	CIG, FINC, GFND2, LETS, MSF	HPA027066	IHC, WB	95% / 95%
Anti-GJA1	CX43, GJAL, ODD, SDTY3	HPA035097	IHC*	96% / 97%
Anti-GPR176	Gm1012	HPA039943	IHC, WB*	84% / 78%
Anti-ITGAV	CD51, MSK8, VNRA, VTNR	HPA004856	IHC, ICC-IF	88% / 90%
Anti-MATN3	EDM5, HOA	HPA051250	ICC-IF	81% / 74%
Anti-NRP1	CD304, NRP, VEGF165R	HPA030278	IHC	97% / 92%
Anti-NT5E	CALJA, CD73, eN, eNT, NT5	HPA017357	IHC,WB, ICC-IF	90% / 92%
Anti-OPN1SW	BCP, BOP, CBT	HPA013562	IHC*	88% / 88%
Anti-PPP1R3B	FLJ14005, GL, PPP1R4	HPA028731	IHC	83% / 88%
Anti-RNF144A	KIAA0161, RNF144, UBCE7IP4	HPA049939	IHC, ICC-IF	100% / 100%
Anti-SERPINE1	PAI, PAI1, PLANH1	HPA050039	IHC, ICC-IF	83% / 84%
Anti-SLC2A3	GLUT3	HPA006539	IHC, ICC-IF	65% / 64%
Anti-SPRED1	FLJ33903, PPP1R147	HPA061805	WB, ICC-IF	98% / 92%

Table 28. Top genes with highest significance associated with favorable prognosis in stomach cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-BICDL1	BICDR-1, CCDC64, FLJ26450	HPA061116	IHC*, WB, ICC-IF	97% / 97%
Anti-C3orf62	FLJ43654	HPA043328	WB*, ICC-IF	74% / 79%
Anti-CSK	-	HPA028425	IHC, WB*, ICC-IF	98% / 95%
Anti-DPP9	-	HPA036059	IHC, ICC-IF	81% / 75%
Anti-FAAH	FAAH-1	HPA007425	IHC	87% / 84%
Anti-FAM83G	FLJ41564, PAWS1	HPA023369	IHC*, WB, ICC-IF	78% / 78%
Anti-MAP2K2	MEK2, PRKMK2	HPA051993	IHC, WB, ICC-IF	100% / 98%
Anti-MEN1	-	HPA030342	IHC, ICC-IF	99% / 99%
Anti-MISP3	-	HPA042225	IHC	35% / 29%
Anti-NCLN	NET59, NICALIN	HPA006625	IHC	94% / 94%
Anti-PICK1	MGC15204, PRKCABP	HPA067384	ICC-IF	100% / 100%
Anti-PRR15L	ATAD4, MGC11242	HPA022918	IHC, ICC-IF	91% / 88%
Anti-SLC52A3	C20orf54, hRFT2, RFVT3	HPA049391	IHC	50% / 50%
Anti-TAF5	TAF2D, TAFII100	HPA006474	IHC, WB, ICC-IF	100% / 100%
Anti-TIMM29	C19orf52	HPA041858	IHC, WB, ICC-IF	85% / 88%
Anti-TMEM259	C19orf6, MBRL, MGC4022	HPA042669	IHC, WB	92% / 90%
Anti-TNFAIP2	B94, EXOC3L3	HPA030624	ICC-IF	-
Anti-TSEN54	SEN54, SEN54L	HPA053097	IHC, WB	89% / 93%
Anti-TTC9C	MGC29649	HPA055169	IHC, ICC-IF	93% / 97%
Anti-ZNF101	DKFZp570I0164, HZF12	HPA023449	IHC, WB	43% / 43%

* Products with enhanced validation for indicated application

Testis cancer

Testis cancer constitutes approximately 1% of cancer in males. Tumors of germ cell origin account for approximately 95% of all testis cancers.

Pathology plays a key role in the management of patients with testicular tumors by allowing for accurate classification of tumors to provide the prognostic parameters needed for optimizing decisions regarding treatment and follow-up.

Testis cancer is divided into two major categories:
-seminoma
-non-seminomatous germ cell tumors.

Seminomas account for approximately 45% of all germ cell tumors and are characterized histologically by evenly spaced and relatively large uniform tumor cells with distinct cell borders.

Tumor cell nuclei are often centrally localized and show distinct nuclear membranes and one or two distinct nucleoli. The characteristic tumor stroma in seminoma is built up by a delicate fibrovascular network with thin collagenous septa containing variable amounts of small lymphocytes.

Of the non-seminomatous tumors, embryonal carcinoma accounts for 15-30% and represents the second most frequent pure type of testicular cancer.

Embryonal cancer displays an acinar, tubular, papillary or solid growth pattern with areas of necrosis, hemorrhage and fibrosis. Tumor cells are highly pleomorphic with large, irregular nuclei and indistinct cell borders.

The transcriptome analysis shows that 75% (n=14746) of all human genes (n=19670) are expressed in testis cancer.

479 genes show some level of elevated expression in testis cancer compared to other cancers

There are 42 genes associated with unfavorable prognosis in testis cancer.

There are 15 genes associated with favorable prognosis in testis cancer.

Data collected from 134 males with seminoma or non-seminomatous germ cell tumors.

The top most significant genes related to unfavorable and favorable prognosis are listed in Tables 29 and 30.

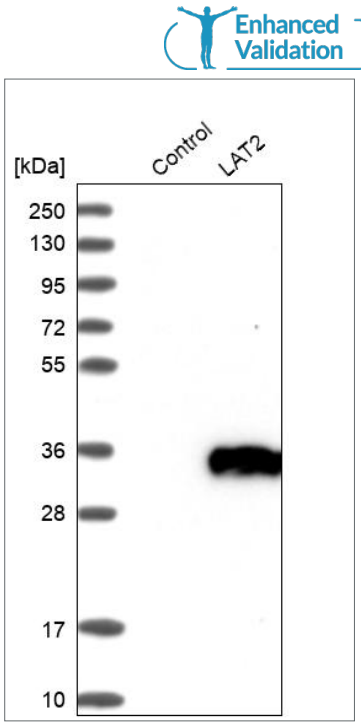

Figure 29. Recombinant expression validation in WB using target protein overexpression. Western blot analysis using the anti-LAT2 antibody (HPA003462) in control (vector only transfected HEK293T lysate) and LAT2 over-expression lysate (Co-expressed with a C-terminal myc-DDK tag (~3.1 kDa) in mammalian HEK293T cells, LY410097).

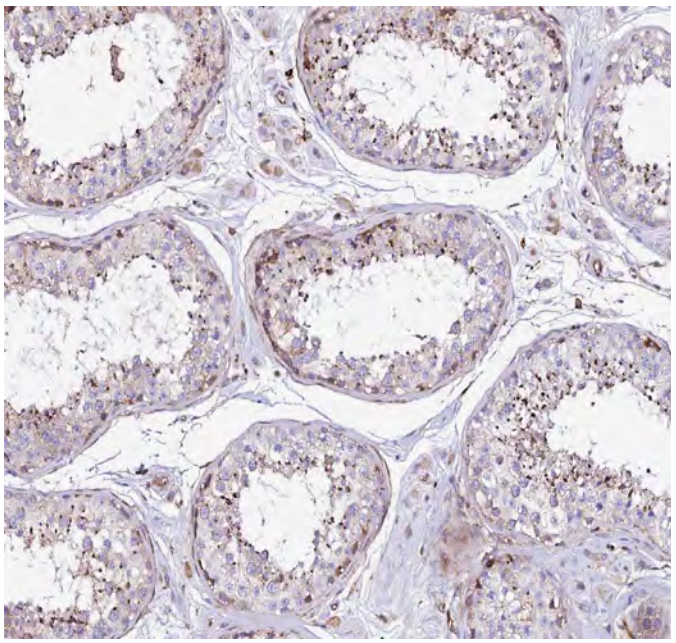

Figure 30. Immunohistochemistry using the anti-TRPV2 antibody (HPA044993) on testis, normal tissue, (male, age 25) shows a high cytoplasmic/membranous staining in seminiferous ducts cells, and a medium cytoplasmic/membranous staining in Leydig cells, in brown.

Table 29. Top genes with highest significance associated with unfavorable prognosis in testis cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-BST2	CD317, tetherin	HPA017060	IHC, ICC-IF	29% / 29%
Anti-CD300C	CMRF35, CMRF35A, IGSF16	HPA014523	IHC, WB*	35% / 36%
Anti-CCR7	BLR2, CD197, CDw197	HPA031383	ICC-IF	83% / 85%
Anti-CLCN7	CLC7, OPTA2, PPP1R63	HPA043019	IHC, WB*, ICC-IF	96% / 96%
Anti-CLEC10A	CD301, HML, HML2	HPA021937	IHC, WB*	71% / 71%
Anti-CSF1R	C-FMS, CD115, CSFR, FMS	HPA012323	IHC, WB, ICC-IF	58% / 61%
Anti-CSF3R	CD114, GCSFR	HPA048086	IHC	58% / 60%
Anti-FCHSD1	FLJ00007	HPA043795	IHC, ICC-IF	83% / 81%
Anti-FKBP15	KIAA0674, PPP1R76, WAFL	HPA007979	IHC, WB	95% / 94%
Anti-GGA2	KIAA1080, VEAR	HPA043313	WB, ICC-IF	60% / 64%
Anti-GIMAP1	HIMAP1, IAN2, IMAP1, IMAP38	HPA053441	WB, ICC-IF	63% / 63%
Anti-LAT2	HSPC046, NTAL, WBSCR15	HPA003462	IHC*, WB*	46% / 46%
Anti-LITAF	PIG7, SIMPLE, TP53I7	HPA006960	IHC, WB, ICC-IF	87% / 89%
Anti-LY86	dJ80N2.1, MD-1	HPA044895	IHC	75% / 75%
Anti-PAG1	CBP, PAG	HPA066527	WB, ICC-IF	76% / 78%
Anti-SGSH	HSS, MPS3A, SFMD	HPA023451	IHC*, WB	81% / 79%
Anti-SIGLEC1	CD169, SIGLEC-1, SN	HPA053457	IHC	72% / 68%
Anti-TBC1D2	Armus, PARIS1, TBC1D2A	HPA030871	IHC, WB	74% / 74%
Anti-TLR4	ARMD10, CD284, hToll, TLR-4	HPA049174	IHC	64% / 62%
Anti-TRPV2	VRL, VRL-1, VRL1	HPA044993	IHC, ICC-IF	71% / 59%

Table 30. Top genes with highest significance associated with favorable prognosis in testis cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ARHGEF4	ASEF, KIAA1112, STM6	HPA018267	IHC	89% / 89%
Anti-CA9	CAIX, MN	HPA055207	IHC*	80% / 80%
Anti-CITED1	MSG1	HPA049051	IHC*, ICC-IF	77% / 76%
Anti-FUNDC1	MGC51029	HPA038773	IHC, WB*	95% / 95%
Anti-GALNT6	GalNAc-T6L, GALNT17	HPA031019	IHC, WB	93% / 37%
Anti-HRASLS	H-REV107, HRASLS1	HPA051179	IHC, ICC-IF	89% / 89%
Anti-IFT52	CGI-53, NGD2, NGD5	HPA067423	IHC*	95% / 27%
Anti-IQCC	FLJ10547	HPA028686	IHC, WB, ICC-IF	70% / 65%
Anti-PIN4	EPVH, PAR14, PAR17	HPA064504	WB*, ICC-IF	97% / 97%
Anti-PRKRA	DYT16, HSD14, PACT, RAX	HPA034996	IHC, WB*, ICC-IF	96% / 96%
Anti-PRR36		HPA062741	IHC, ICC-IF	64% / 64%
Anti-SNX31	MGC39715	HPA024284	IHC, WB	82% / 78%
Anti-TPGS2	C18orf10, HsT3006	HPA040596	IHC, WB*	91% / 89%

* Products with enhanced validation for indicated application

Thyroid cancer

The thyroid cancer is fairly common. The annual incidence is between 0,5-10 per 100,000 in various populations and 2-4 times more frequent in women compared to men.

The most common forms of thyroid cancer are:
- papillary carcinoma (70-80%),
- follicular carcinoma (10-20%),
- medullary carcinoma (5-10%)
- anaplastic carcinoma (2-10%).

The classification of thyroid cancer is dependent on histological features according to WHO. Thyroid tumors can also be classified according to aggressiveness into low-grade malignant, intermediate-grade malignant and high-grade malignant.

The prognosis for thyroid cancer is good, with a 10-year relative survival rate of approximately 98% for papillary carcinomas. Apart from age, where young patients have a considerably better prognosis, the size of the primary tumor and the tumor stage are the most significant prognostic factors.

For most thyroid tumors, diagnosis can be established by microscopic examination alone, although immunohistochemistry plays an important role in tumors exhibiting unusual morphological features.

The transcriptome analysis shows that 69% (n=13485) of all human genes (n=19670) are expressed in thyroid cancer.

190 genes show some level of elevated expression in thyroid cancer compared to other cancers

There are 186 genes associated with unfavorable prognosis in thyroid cancer.

There are 161 genes associated with favorable prognosis in thyroid cancer.

Data collected from 501 patients with thyroid carcinoma (366 females and 135 males).

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 31 and 32.

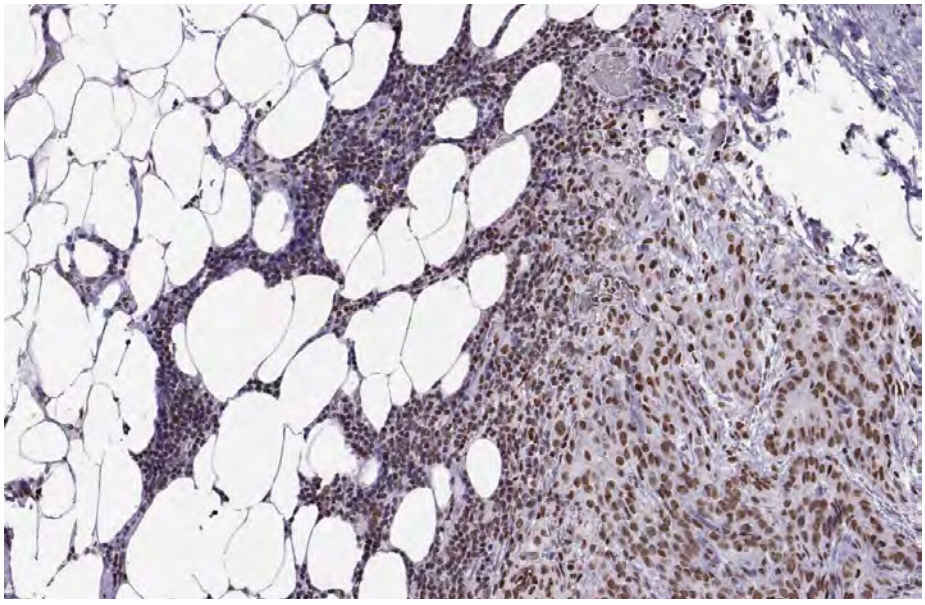

Figure 31. Immunohistochemistry using the anti-SNAI1 antibody (HPA069985) on thyroid cancer (papillary adenocarcinoma, male, age 61) shows a high nuclear staining in tumor cells, in brown.

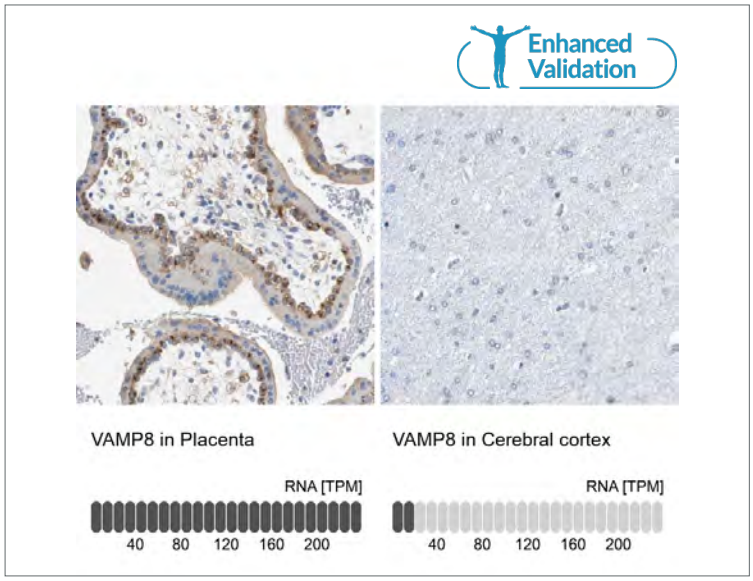

Figure 32. Orthogonal validation of protein expression using IHC by comparison to RNA-seq data of corresponding target in high and low expression tissues. Immunohistochemistry analysis in human placenta and cerebral cortex tissues using anti-VAMP8 antibody (HPA006882). Corresponding VAMP8 RNA-seq data are presented for the same tissues.

Table 31. Top genes with highest significance associated with unfavorable prognosis in thyroid cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ALDH1B1	ALDH5, ALDHX	HPA021037	IHC*, WB, ICC-IF	79% / 82%
Anti-BCKDHA	MSU, OVD1A	HPA036640	IHC	94% / 94%
Anti-CILP	HsT18872	HPA003195	IHC	91% / 89%
Anti-COPZ2	MGC23008	HPA055999	IHC	92% / 92%
Anti-FAM171A1	C10orf38, FLJ12884	HPA051345	IHC, ICC-IF	84% / 79%
Anti-FIBIN	MGC24932	HPA040120	IHC, WB*	95% / 95%
Anti-FKBP10	FKBP6, FLJ20683, FLJ22041	HPA051171	IHC* ICC-IF	93% / 91%
Anti-GAS1	-	HPA066902	IHC	89% / 89%
Anti-GUF1	FLJ13220	HPA024222	WB, ICC-IF	89% / 89%
Anti-MAP1A	MAP1L	HPA039063	IHC*	70% / 73%
Anti-PAPSS2	ATPSK2	HPA071224	ICC-IF	85% / 81%
Anti-PDLIM3	ALP	HPA004749	IHC*	95% / 94%
Anti-PRDM16	MEL1, MGC166915, PFM13	HPA050343	ICC-IF	86% / 87%
Anti-PRKAB2	-	HPA044342	IHC*, WB, ICC-IF	93% / 94%
Anti-RINT1	FLJ11785, RINT-1	HPA019875	IHC, WB	71% / 68%
Anti-SENP6	KIAA0797, SUSP1	HPA024376	IHC, ICC-IF	69% / 71%
Anti-SNAI1	SLUGH2, SNAH, SNAIL, SNAIL1	HPA069985	IHC	82% / 82%
Anti-SYNDIG1	C20orf39, FLJ14220, IFITMD5	HPA044271	ICC-IF	90% / 87%
Anti-TSHZ1	NY-CO-33, SDCCAG33, TSH1	HPA006982	IHC, WB, ICC-IF	86% / 86%
Anti-WDR37	KIAA0982	HPA037376	IHC*, WB	100% / 100%

Table 32. Top genes with highest significance associated with favorable prognosis in thyroid cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-ADRA1B	-	HPA074416	ICC-IF	96% / 94%
Anti-ANXA1	ANX1, LPC1	HPA011271	IHC*, WB*, ICC-IF	83% / 86%
Anti-C14orf119	FLJ20671	HPA003638	IHC*, WB	84% / 83%
Anti-DERA	CGI-26, DEOC	HPA055897	WB, ICC-IF	92% / 91%
Anti-DOLK	DK1, KIAA1094, TMEM15	HPA066767	ICC-IF	96% / 96%
Anti-DRAP1	NC2-alpha	HPA006790	IHC, WB*, ICC-IF	96% / 96%
Anti-GLTP	-	HPA056461	IHC, WB*, ICC-IF	96% / 96%
Anti-HECTD3	FLJ21156	HPA027467	IHC	99% / 98%
Anti-INPP1	-	HPA036699	IHC, ICC-IF	86% / 85%
Anti-KIAA1211L	C2orf55, MGC42367	HPA051082	IHC	78% / 74%
Anti-LPAR5	GPR92, GPR93, KPG010, LPA5	HPA013170	IHC	48% / 49%
Anti-MCM3	-	HPA004789	IHC, WB	95% / 93%
Anti-MYL12B	MRLC2	HPA045244	IHC, WB, ICC-IF	100% / 100%
Anti-RAB34	RAB39, RAH	HPA021366	IHC	93% / 93%
Anti-SLC37A1	-	HPA030418	IHC	60% / 55%
Anti-TPT1	fortilin, TCTP	HPA039437	IHC, WB, ICC-IF	97% / 97%
Anti-TRIM21	RNF81, Ro/SSA, RO52, SSA1	HPA005673	IHC, WB*, ICC-IF	75% / 70%
Anti-UBE2Q1	NICE-5, PRO3094, UBE2Q	HPA063368	IHC, ICC-IF	100% / 100%
Anti-VAMP8	EDB	HPA006882	IHC*, WB	95% / 92%
Anti-ZCCHC12	FLJ16123, PNMA7A, SIZN1	HPA031016	IHC, WB*, ICC-IF	76% / 74%

* Products with enhanced validation for indicated application

Urothelial cancer

Urothelial carcinoma, also termed transitional cell carcinoma or urinary bladder cancer, is a major cause of morbidity and mortality throughout the world. The highest frequency of cancer in the urinary bladder is found among urban Caucasians in Western Europe and in the USA.

Urothelial cancer typically presents in patients over the age of 50 years and is approximately three times as common in males as in females. Smoking is considered an important risk factor.

Urothelial cancer can be divided into papillary and non-papillary tumors depending on the morphological appearance. Approximately 25% of all urothelial tumors are non-invasive papillary tumors. However, 10-15% of these patients will subsequently develop an invasive tumor.

The transcriptome analysis shows that 71% (n=14059) of all human genes (n=19670) are expressed in urothelial cancer.

127 genes show some level of elevated expression in urothelial cancer compared to other cancers

There are 379 genes associated with unfavorable prognosis in urothelial cancer.

There are 713 genes associated with favorable prognosis in urothelial cancer.

Data collected from 406 patients in total. The dataset included 107 females and 299 males.

The top 20 most significant genes related to unfavorable and favorable prognosis are listed in Tables 33 and 34.

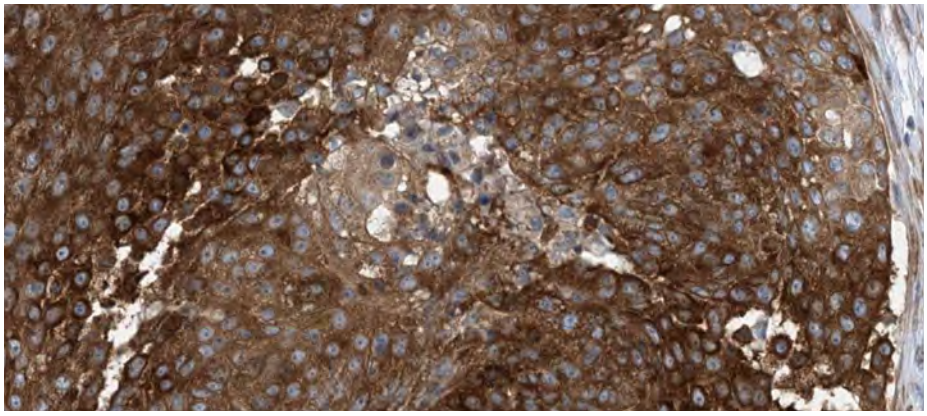

Figure 33. Immunohistochemistry using the anti-EHBP1 antibody (HPA035468) on urothelial carcinoma (female, age 63) shows a high cytoplasmic/membranous staining in tumor cells, in brown.

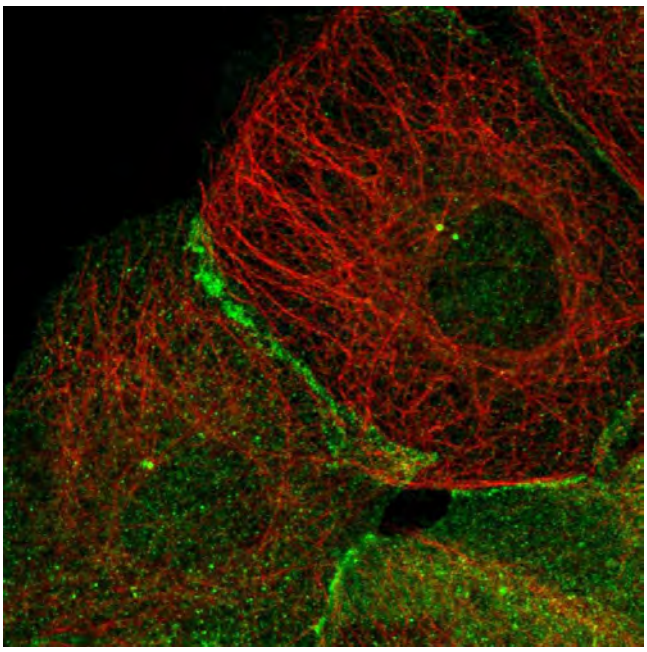

Figure 34. Immunofluorescent staining of human cell line A-431 using the anti-TRIM38 antibody (HPA031685) shows localization to plasma membrane, centrosome & cell junctions, in green. Microtubules in red.

Table 33. Top genes with highest significance associated with unfavorable prognosis in urothelial cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-AHNAK	MGC5395	HPA019010	IHC, ICC-IF	87% / 84%
Anti-ANXA1	ANX1, LPC1	HPA011271	IHC*, WB*, ICC-IF	83% / 86%
Anti-BAIAP2	BAP2	HPA023310	IHC*, WB, ICC-IF	92% / 92%
Anti-BOC	CDON2	HPA060778	ICC-IF	74% / 74%
Anti-BRMS1L	BRMS1, FLJ39177, MGC11296	HPA046623	ICC-IF	99% / 100%
Anti-CRYAB	CRYA2, HSPB5	HPA057100	IHC*	98% / 98%
Anti-DSC3	CDHF3, DSC, DSC1, DSC2	HPA049265	IHC*	79% / 76%
Anti-DTD2	C14orf126, MGC9912	HPA001117	IHC, ICC-IF	84% / 85%
Anti-EHBP1	KIAA0903, NACSIN	HPA035468	IHC*, WB, ICC-IF	69% / 76%
Anti-ECM1	-	HPA027241	IHC*, WB*	76% / 79%
Anti-FKBP9	FKBP60, FKBP63	HPA012595	IHC, WB, ICC-IF	90% / 92%
Anti-GALK1	GALK	HPA007094	IHC, WB*, ICC-IF	89% / 89%
Anti-GAS6	AXLLG, AXSF, FLJ34709	HPA008275	IHC	76% / 79%
Anti-HSPB6	FLJ32389, Hsp20, PPP1R91	HPA044153	IHC*, WB	85% / 88%
Anti-HTRA1	ARMD7, HtrA, PRSS11	HPA036655	IHC, ICC-IF	91% / 91%
Anti-KLK5	KLK-L2, SCTE	HPA014343	IHC*	72% / 72%
Anti-PLD1	-	HPA042396	IHC*, ICC-IF	90% / 85%
Anti-SHTN1	KIAA1598, shootin-1, shootin1	HPA037942	IHC*, WB*	95% / 95%
Anti-SLC1A6	EAAT4	HPA041505	IHC*, ICC-IF	85% / 82%
Anti-TM4SF1	L6, M3S1	HPA002823	IHC	75% / 77%

Table 34. Top genes with highest significance associated with favorable prognosis in urothelial cancer.

Product Name	Alternative Gene Names	Product ID	Validated Applications	Antigen seq. identity mouse / rat
Anti-APOBEC3H	ARP10	HPA021492	IHC	48% / 51%
Anti-CCNL1	ania-6a	HPA057911	ICC-IF	96% / 98%
Anti-CCNL2	ania-6b, CCNM, PCEE, SB138	HPA053137	IHC, ICC-IF	96% / 96%
Anti-CLEC2D	CLAX, LLT1, OCIL	HPA017649	IHC	47% / 47%
Anti-CXorf38	MGC39350	HPA050120	IHC, WB*, ICC-IF	69% / 66%
Anti-GRIPAP1	GRASP1, KIAA1167	HPA000615	IHC*, WB*, ICC-IF	99% / 99%
Anti-GSDMB	GSDML, PRO2521	HPA052407	IHC*	30% / 28%
Anti-IKBKB	IKK-beta, IKK2, IKKB, NFKBIKB	HPA001249	IHC, WB*, ICC-IF	89% / 87%
Anti-IL9R	CD129	HPA063240	IHC	67% / 61%
Anti-LIPT1	MGC12290, MGC13378	HPA034802	IHC, WB	75% / 77%
Anti-MITD1	LOC129531	HPA036162	IHC, WB, ICC-IF	81% / 80%
Anti-OFD1	71-7A, CXorf5, JBTS10, RP23	HPA031104	IHC	76% / 74%
Anti-OGT	FLJ23071, HRNT1, MGC22921	HPA030751	IHC, WB*	100% / 100%
Anti-PBX4	-	HPA049859	IHC, ICC-IF	57% / 63%
Anti-PTPN6	HCPH, PTP-1C, SHP-1	HPA001466	IHC*, WB, ICC-IF	92% / 91%
Anti-TRIM38	RNF15, RORET	HPA031685	IHC, WB, ICC-IF	50% / 44%
Anti-ZNF182	HHZ150, KOX14, Zfp182, ZNF21	HPA059574	IHC, ICC-IF	62% / 51%
Anti-ZNF195	-	HPA030605	IHC, ICC-IF	47% / 46%
Anti-ZNF524	MGC23143	HPA050981	IHC, WB*, ICC-IF	64% / 62%
Anti-ZNF613	FLJ13590	HPA026833	IHC, ICC-IF	36% / 38%

* Products with enhanced validation for indicated application

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