Table S1. Antibodies used for ICC.

Antibody Specificity	Isotype	Manufacturer/ Catalogue Number	Species	Dilution
Primary antibody				
Actin	Monoclonal, IgG1	Abcam/ab3280	Mouse anti-human	1/100
Isotype control	Monoclonal, IgG1	Abcam/ab18443	Mouse anti-human	1/250
Isotype control	Monoclonal, IgG	Abcam/ab172730	Rabbit anti-human	1/250
SMAD3	Monoclonal	ThermoFisher	Rabbit anti-human	1/100
Survivin	Monoclonal	Abcam/ab76424	Rabbit anti-human	1/100
TEAD4	Monoclonal	ThermoFisher	Rabbit anti-human	1/100
Secondary antibodies				
Anti-mouse	Polyclonal, Ig	Dako/K4007	Anti-mouse	N/A
Anti-rabbit	Polyclonal, Ig	Dako/K4011	Anti-rabbit	N/A

Table S2. Characterisation of cDNA sequences confirmed by two rounds of immunoscreening.

SEREX id	# Times Found *	Gene Symbol	Gene Name	GenBank Number Sequence ID	Percent of Identity≠	Size (bp)	Chromosomal Localisation
UOH-ALL-1	1	TPM3	Tropomyosin 3, transcript variant Tpm3.1, mRNA	NM_153649.4	100	3177	1q21.3
UOH-ALL-2	1	TMCO3	Transmembrane and coiled-coil domains 3/ "C13orf11"	NM_001014283.2	99	66237	13q34
UOH-ALL-3	1	C10orf82	Chromosome 10 open reading frame 82, transcript variant 1, mRNA	NM_144661.4	100	990	10q25.3
UOH-ALL-4	1	UBE2D2	Ubiquitin conjugating enzyme E2 D2, transcript variant 1	NM_003339.3	100	2530	5q31.2
UOH-ALL-5	1	MYL12B	Myosin light chain 12B, transcript variant 1	NM_001144944.1	100	1041	18p11.31
UOH-ALL-6	1	TMA7	Translation machinery associated 7 homolog, transcript variant 1, mRNA	NM_015933.6	97.75%	561	3p21.31
UOH-ALL-7	3	PTPN1	Protein tyrosine phosphatase non-receptor type 1, transcript variant 1, mRNA,	NG_012119.2	97.12	81198	20q13.13
UOH-ALL-8	2	-	Isolate CHM13 chromosome 16	CP068262.2	97.34	963	16
UOH-ALL-9	1	Col-3	col-3 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA	AB665697.1	87.08	690	-
UOH-ALL-10	2	Wnt2b	Wnt2b mRNA for wingless-type MMTV integration site family member 2b, complete cds	AB205148.1	94.85	2427	-
UOH-ALL-11	1	V-ATPase	Vacuolar H(+)-ATPase subunit	NM_015933.6	90.79	1078	-
UOH-ALL-12	1	-	Isolate BMF2-1/1 mitochondrion	KJ801454.1	97.20	16569	-
UOH-ALL-13	1	-	Isolate H7_91_CI-9_FU_P3S2_Heavy immunoglobulin variable region mRNA, partial cds; and IGHV3-15*07, IGHJ5*01, and IGHG2 mRNAs, complete sequence.	MW176666.1	97.16	1563	-
UOH-ALL-14	1	-	Chromosome 5 clone RP11-2O17	AC026746.6	95.62	179144	5
UOH-ALL-15	2	DNMT1	DNA methyltransferase 1, RefSeqGene (LRG_362)	NG_028016.3	100	104941	19p13.2
UOH-ALL-16	1	ATXN10	Ataxin 10, mRNA (cDNA clone MGC:4152 IMAGE:3030062)	BC007508.2	99.70	1952	-
UOH-ALL-17	1	Six2	mRNA for Six2 protein	AJ316542.1	93.44	1254	-
UOH-ALL-18	1	-	Isolate 026 haplogroup N9 mitochondrion	MH553652.1	96.49	16570	-
UOH-ALL-19	1	WLS	Wnt ligand secretion mediator (WLS), transcript variant X2,	XM_003807869.4	100	2741	1
UOH-ALL-20	1	TUBA3C	Tubulin alpha 3c, mRNA Syno "bA408E5.3; TUBA2"	NM_006001.3	100	1521	13q11
UOH-ALL-21	1	SEZ6L2	Seizure related 6 homolog like 2, transcript variant 2	NM_201575.4	100	3804	16p11.2
UOH-ALL-22	1	-	DNA, chromosome 18, nearly complete genome.	AP023478.1	100	77846715	18
UOH-ALL-23	1	TCF7L2	Transcription factor 7 like 2, transcript variant X35, mRNA	XM_032177767.1	87.19	3876	10q25.2
UOH-ALL-24	2	SRRF	Stromal RNA regulating factor mRNA, alternatively spliced	AY236962.1	97.87	1931	2p22.1
UOH-ALL-25	1	MYO6	Myosin VI, transcript variant 2, mRNA "DFNA22; DFNB37"	NM_001300899.2	100	8546	6q14.1
UOH-ALL-26	1	-	Haplogroup H-T152C mitochondrion	ON688208.1	100	16570	-
UOH-ALL-27	2	FLNB	Filamin B, transcript variant 4, mRNA, ABP-278; ABP-280; AOI; FH1; FLN-B; FLN1L; LRS1; SCT; TABP; TAP	NM_001164319.2	96.91%	9369	3p14.3
UOH-ALL-28	1	-	Chromosome 16 clone RP11-89D3, complete sequence	AC022168.6	96.93%	177322	16
UOH-ALL-29	1	TIMP1	TIMP metallopeptidase inhibitor 1, mRNA	NM_003254.3	99.38%	769	Xp11.3
UOH-ALL-30	1	ATL3	Atlastin GTPase 3, RefSeqGene on chromosome 11	NG_033985.1	99.80%	54893	11q13.1
UOH-ALL-31	1	-	cDNA DKFZp686O033 (from clone DKFZp686O033)	AL833551.1	97.41%	6513	3
UOH-ALL-32	2	KIF5B	Kinesin family member 5B, mRNA	NM_004521.3	98.64		
UOH-ALL-33	2	AASDH	Aminoadipate-semialdehyde dehydrogenase-ACSF4; LYS2; NRPS1098; NRPS998"	NG_046885.1	99.12	58732	4q12
UOH-ALL-34	1	TOMM20L	Translocase of outer mitochondrial membrane 20 like, transcript variant X1, mRNA	XM_011536742.4	100	631	14
UOH-ALL-35	1	NTPCR	Nucleoside-triphosphatase, cancer-related	NM_032324.3	97.94	6324	1q42.2
UOH-ALL-36	1	KRT31	Keratin 31, mRNA	NM_002277.3	99.23	1615	17q21.2
UOH-ALL-37	2	-	Isolate E5_53_SR-6_LA_P2S23_Heavy immunoglobulin variable region mRNA, partial cds; and IGHV3-23*01, IGHJ5*02, and IGHG2 mRNAs	MW176520.1	98.33	1028	-
UOH-ALL-38	1	-	Isolate C114_Kampong_Cham_F1a1a1 mitochondrion, complete genome Sequence	KT587463.1	98.52	16567	-
UOH-ALL-39	1	TRAP1	TNF receptor associated protein 1, transcript variant 2	NM_001272049.2	100	2064	16p13.3
UOH-ALL-40	1	-	Isolate ACAD11197 haplogroup A2 mitochondrion, complete genome Sequence	KU523267.1	99.77	16568	-
UOH-ALL-41	1	-	LJ45347 fis, clone BRHIP3011082, highly similar to ubiquitin-protein isopeptide ligase (E3)	AK127280.1	98.85	5196	-
UOH-ALL-42	2	SERINC3	Serine incorporator 3, transcript variant 1, mRNA	NM_006811.4	100	4396	20q13.12
UOH-ALL-43	1	TEX43	Testis expressed 43, mRNA- C5orf48; Tseg7	NM_207408.3	100	478	5q23.2
UOH-ALL-44	1	FER	FER tyrosine kinase	NG_011445.2	99.69	456020	5q21.3

UOH-ALL-45	2	-	cDNA DKFZp686C15213 (from clone DKFZp686C15213) Sequence	BX640874.1	97.88	1732	-
UOH-ALL-46	1	MCL1	MCL1 apoptosis regulator, BCL2 family member, transcript variant 1, mRNA	NM_021960.5	99.37	3950	1q21.2
UOH-ALL-47	1	ANKRD17	Ankyrin repeat domain 17, transcript variant 3, mRNA	NM_001286771.3	95.99	10358	4q13.3
UOH-ALL-48	1	-	cDNA fis, A-COL04217, highly similar to Homo sapiens mitochondrion, NADH dehydrogenase subunit 2 Sequence	AK026903.2	99.49	1054	-
UOH-ALL-49	1	CCDC89	Coiled-coil domain containing 89	NM_152723.3	95.8	2348	11q14.1
UOH-ALL-50	1	HMG20	Ubiquitin C, mRNA (cDNA clone MGC:14624 IMAGE:4076286)	BC039193.1	97.73	2222	-
UOH-ALL-51	1	-	FLJ21112 fis (full insert sequence), clone CAS05418, highly similar to AF116692 Homo sapiens PRO2207 mRNA	AK024765.1	100	1405	-
UOH-ALL-52	3	TMPO	Thymopoietin, transcript variant 2	NM_001032283.3	93.96	4136	12q23.1
UOH-ALL-53	1	HOXD8	Homeobox D8, transcript variant 3 (HOX4; HOX4E; HOX5.4)	NM_001199747.2	100	1597	2q31.1
UOH-ALL-54	1	-	Isolate PG0247 mitochondrion	MN687198.1	86.07	1656	-
UOH-ALL-55	2	-	Isolate CHM13 chromosome 15	CP068263.2	99.70	9975	15
UOH-ALL-56	1	TPT1	Tumour protein, translationally-controlled 1, transcript variant 2	NM_003295.4	96.99	4548	13q14.13
UOH-ALL-57	1	MIP	mRNA for major intrinsic protein	NM_012064.4	100	2614	12q13.3
UOH-ALL-58	1	LINC00661	Long intergenic non-protein coding RNA 661	NR_026828.1	86.07	3350	19p13.12
UOH-ALL-59	1	PCAT6	Prostate cancer associated transcript 6, transcript variant 1	NR_046325.1	99.11	764	1q32.1
UOH-ALL-60	1	HDLBP	High density lipoprotein binding protein, transcript variant X14	XM_047444076.1	100	8546	2
UOH-ALL-61	1	SUN1	Isolate 9_T haplogroup U2e1 mitochondrion	KY670862.1	99.25	16579	-
UOH-ALL-62	1	-	Sad1 and UNC84 domain containing 1, transcript variant 71	NM_001367708.1	99.10	3841	7p22.3
UOH-ALL-63	1	MYH11	Myosin heavy chain 11, transcript variant SM2B	NM_001040113.2	94.27	6940	16p13.11
UOH-ALL-64	1		Clone VMRC53-239I22 from chromosome 1	AC275668.1	95.63	1677	1
UOH-ALL-65	1	ROCK1	Rho-associated coiled-coil containing protein kinase 1,mRNA	NM_005406.3	91.01	9446	18q11.1
UOH-ALL-66	1	B9D1	B9 domain containing 1, transcript variant 2, mRNA	NM_015681.6	99.86	913	17p11.2
UOH-ALL-67	1	RAB5C	RAB5C, member RAS oncogene family, transcript variant 1, mRNA	NM_201434.3	99.83	1757	17q21.2
UOH-ALL-68	1	RAB34	RAB34, member RAS oncogene family, transcript variant 6, mRNA	NM_001256277.2	97	1344	17q11.2
UOH-ALL-69	2	APPL1	Adaptor protein, phosphotyrosine interacting with PH domain and leucine zipper 1, mRNA	NM_012096.3	99.42	6069	3p14.3
UOH-ALL-70	1	-	mRNA for hypothetical protein, complete cds	AB353305.1	100	1431	-
UOH-ALL-71	1	CLIC4	Chloride intracellular channel 4, mRNA	NM_013943.3	99.48	4253	1p36.11
UOH-ALL-72	1	TRAP1	TNF receptor associated protein 1, transcript variant 2, mRNA	NM_001272049.2	96.34	2064	16p13.3
UOH-ALL-73	1	IDI1	Isopentenyl-diphosphate delta isomerase 1, transcript variant 1, mRNA	NM_004508.4	97.76	2739	10p15.3
UOH-ALL-74	1	-	Isolate 167 mitochondrion, complete genome	MF437201.1	98	585	-
UOH-ALL-75	1	-	Isolate HGDP00779 mitochondrion, complete genome	KF451299.1	80.45	1050	-
UOH-ALL-76	1	TIMP	metallopeptidase inhibitor 1, mRNA	BC007097.1	91.67	841	-
UOH-ALL-77	1	UBE3C	Ubiquitin protein ligase E3C, mRNA	NM_014671.3	83.69	5214	7q36.3
UOH-ALL-78	1	ZNF676	Zinc finger protein 676, transcript variant X1	XM_047438352.1	92.45	2859	19p12
UOH-ALL-79	1	PTPN23	transcript variant 2, mRNA	NM_001304482.2	97.84	5109	3p21.31
UOH-ALL-80	1	SURF2	Surfeit 2, transcript variant 1, mRNA	NM_017503.5	90.69	833	9q34.2
UOH-ALL-81	1	KIF1B	mRNA for kinesin family member 1Bbeta isoform IV, (KIF1B)	AB088213.1	96.09	8572	1p36.22
UOH-ALL-82	1	TEX38	Testis expressed 38, transcript variant 3, mRNA	NM_001300864.2	90.58	689	1p33
UOH-ALL-83	2	TPPP2	Tubulin polymerization-promoting protein family member 2, mRNA (cDNA clone MGC:47825 IMAGE:5169309), complete cds	BC038970.2	90.86	791	14q11.2
UOH-ALL-84	2	BCLAF1	BCL2-associated transcription factor 1, mRNA (cDNA clone IMAGE:6501081), partial cds	BC063846.1	95.58	2277	6q23.3
UOH-ALL-85	1	LOC338963	Epididymal protein pseudogene, non-coding RNA	NR_034139.1	94.36	1381	15q25.2
UOH-ALL-86	2	FBXO22	F-box protein 22, mRNA (cDNA clone IMAGE:3349806)	BC008762.1	94.56	3768	15q24.2
UOH-ALL-87	1	UVRAG-DT	UVRAG divergent transcript, long non-coding RNA	NR_144531.1	92.79	689	11q13.5
UOH-ALL-88	1	AKAP1	A-kinase anchoring protein 1, transcript variant X8, mRNA	XM_047436869.1	88.74	2081	17q22
UOH-ALL-89	2	EIF3A	Eukaryotic translation initiation factor 3, subunit A, mRNA (cDNA clone IMAGE:4519449)	BC020285	99.79	1721	-
UOH-ALL-90	1	MYH10	variant protein, clone: hf00991	AB210026.1	100	7693	-
UOH-ALL-91	1	-	Clone FLB8503 PRO2286 mRNA, complete cds	AF130085.2	94.77	443	-

UOH-ALL-92	1	-	Ribosomal protein L28, mRNA (cDNA clone MGC:20081 IMAGE:4054251), complete cds (RPL28)	BC010173.2	99.40	511	-
UOH-ALL-93	1	MRFAP1	Morf4 family associated protein 1, transcript variant 2	NM_001272053.2	97.46	1455	4p16.1
UOH-ALL-94	1	-	Isolate PNG53 haplogroup P2 mitochondrion, complete genome	MN849846.1	100	16568	-
UOH-ALL-95	1	-	Protein tyrosine phosphatase, non-receptor type 23, mRNA (cDNA clone IMAGE:4111514), partial cds	BC027711.2	99.79	4234	-
UOH-ALL-96	1	-	FLJ21112 fis, clone CAS05418, highly similar to AF116692 Homo sapiens PRO2207 mRNA (PARL)	AK024765.1	100	1405	-
UOH-ALL-97	1	CUL1	Cullin 1, transcript variant 3, mRNA	NM_001370661.1	98.86	3198	7q36.1
UOH-ALL-98	1	LINC00251	Long intergenic non-protein coding RNA 251, long non-coding RNA (C8orf25)	NR_038901.1	100	1058	8q13.1
UOH-ALL-99	1	C18orf32	Chromosome 18 open reading frame 32, transcript variant 2, mRNA (GPIBD25)	NM_001035005.4	100	5548	18q21.1
UOH-ALL-100	1	RIG, DKK3	Ribosomal protein S15, mRNA (cDNA clone MGC:70657 IMAGE:6053159), complete cds	BC064908.1	100	539	11p15.3
UOH-ALL-101	2	PRM1	Testis specific protamine 1 (P1) mRNA, complete cds	AY651260.1	100	385	16p13.2
UOH-ALL-102	1	-	cDNA clone IMAGE:5802820	BC042915.1	100	1934	-
UOH-ALL-103	1	-	Clone FLB8503 PRO2286 mRNA, complete cds	AF130085.2	100	2359	-
UOH-ALL-104	1	-	Unknown			917	
UOH-ALL-105	1	-	Unknown			700	
UOH-ALL-106	1	-	Unknown			600	

*: found when immunoscreening the testes cDNA library; ≠: with genes from NCBI Blast.

Table S3. Expression of SEREX-identified genes and their function in health and cancer tissues.

Gene	Function and Expression in Normal Tissue	Expression in Cancer
AASDH/ UOH-ALL-33	It is encoded a non-ribosome peptide synthetase enzyme. It involves in lipid metabolism and modified gene and protein following transcription and translational. It is found in all tissues such as breast, retina, thymus, tonsil, and pancreas [67].	It is upregulated in HCC and associated with shorter survival and poor outcome [68]. It has been reported that circ-AASDH is upregulated in lung adenocarcinoma and promotes tumour progression via sponging to miR140-3p and inhibits its action on E2F7 transcription [69].
APPL1/ UOH-ALL-69	It is encoded an adapter protein that has a regulatory role in cell proliferation, immune response and cell trafficking via binding to membrane receptors, signalling proteins. APPL1 interacts with RAB5A and regulates signalling pathway of cell proliferation. It also inhibits Fc-gamma receptor-mediated phagocytosis via PI3K/Akt signalling interaction [70]. It involves in TGFBR1 signalling. It has wide distribution in ribosomes, pancreas, thyroid, and bone marrow [71].	APPL1 expression is correlated to TNM stage of gastric cancer and poor prognosis [72]. It activates Akt pathway via acting as a scafflod protein and phosphorylates Akt that leads to activation of Cdc42-associated kinase 1 that promote tumour growth. APPL1 induces angiogenesis via activating of nuclear factor κB [73].
ANKRD17 (FLJ22206, GTAR, KIAA0697, MASK2)/UOH-ALL-47	It belongs to ankyrin repeat-containing protein. It involves in DNA replication control and innate immune pathways against virus and bacteria. It also regulates blood vessel formation and circular system. It is expressed in all tissues such as neurons and bone marrow [74].	It is overexpressed in urinary bladder cancer and its knockdown results in inhibit cancer proliferation. Ankyrin 17 is a mask protein that is required for YAP transport to the nucleus as overexpression of YAP upregulates gene transcription and leads to tumour progression [75].
APPL1/UOH-ALL-69	It is encoded an adapter protein that has a regulatory role in cell proliferation, immune response and cell trafficking via binding to membrane receptors, signalling proteins. APPL1 interacts with RAB5A and regulates signalling pathway of cell proliferation. It also inhibits Fc-gamma receptor-mediated phagocytosis via PI3K/Akt signalling interaction [70]. It involves in TGFBR1 signalling. It has wide distribution in ribosomes, pancreas, thyroid, and bone marrow [71].	APPL1 expression is correlated to TNM stage of gastric cancer and poor prognosis [72]. It activates Akt pathway via acting as a scaffold protein and phosphorylates Akt that leads to activation of Cdc42-associated kinase 1 that promote tumour growth. APPL1 induces angiogenesis via activating of nuclear factor κB [73].
ATL3/ UOH-ALL-30	It encodes a GTPase integral membrane protein and involves in biogenesis of endoplasmic reticulum network. They are various variants produced by the alternative splicing. It is highly enriched in testis and is expressed in different levels in many tissues such as skin, thymus, adipose tissues, and colon [76].	Loss of ATL3 leads to reduction of axonal lysosomes and autophagy. This results in axon deformity and neuropathy [77].
ATXN10/ UOH-ALL-16	It encodes an ataxin 10 protein which involves in neuron differentiation and survival via	It is overexpressed in cancer cachexia which a multifactorial process that leads to loss of

	activating Ras-MAP kinase pathway. It also has a role in maintaining homeostasis and intracellular glycosylation and is found in all tissues [78].	adipose tissues and skeletal muscles and associated with 30% of cancer morbidity. Ataxin 10 along with a panel of cytokines including Adamts like 4, chemokine ligand 2, syntaxin 7, multiple inositol polyphosphate phosphatase1, bridging integrator1, and glucosidase alpha acid are used as a signature of cachexia in colorectal cancer. Measuring serum level of ataxin 10 may be used a predictive biomarker for cardiomyopathy in cachexic patients [79].
B9D1/ UOH-ALL-66	It encodes a B9 domain-containing protein that a component of the tectonic-like complex. It involves in ciliogenesis and hedgehog signalling. It is found in ciliated cells, endometrium, spermatids, respiratory tract, and renal cells [80].	B9D1 deletion is found in Meckel syndrome [81]. It acts as tumour suppressor gene and is inactivated in liver cancer. Its inhibition associated RAS/MAPK signalling activation promoting liver tumour in mice [82].
BCLAF1/ UOH-ALL-84	It is encoded a transcriptional repressor interacting with BCL2 proteins and inducing apoptosis. It is expressed ubiquitously in most tissues [83].	BCLAF1 is upregulated in AML and associated shorter survival as well as low miR-194-5p. Its knockdown induces blast differentiation [84].
C10orf82/UOH-ALL-3	It is uncharacterised protein and recently suggested as CTA. It is highly enriched in the testis and small expression found in the ovary [85].	Its expression correlated to the overall survival to ovarian cancer [85].
C18orf32/UOH-ALL-99	It is involved in the activation of NF-kappa-B pathway. It is found ubiquitinated in all tissues [86].	C18orf32 loss is associated with the autosomal recessive neurodevelopmental disorder with hypotonia and contractures [87].
CCDC89/UOH-ALL-49	CCDC89 involves in cilium organisation and sperm motility.	Not found.
CLIC4/UOH-ALL-71	It encodes CLIC4 protein that belongs to the p64 family. It regulates cellular processes such as cell volume regulation, intracellular pH maintenance, and cell membrane stabilisation and transport. It expresses in many cells including pancreas, skeletal muscle, heart, B-cell, endothelial cells, and kidney [88].	It is highly expressed in AML and associated with adverse prognosis. CLIC4 is regulated by TGF-β and c-Myc. It also induces the NF-κB-dependent activation of hypoxia-inducible factor (HIF) that promotes tumour proliferation and microenvironment [89].
CUL1/UOH-ALL-97	It belongs to E3 ubiquitin ligase that involved in ubiquitination of cell cycle components and related proteins involved in signal transduction. It is broadly found in most tissues and highly enriched in the testis [90].	It is upregulated in osteosarcoma and associated with poor prognosis via inducing EMT and Wnt pathway activation as well as miR-377-3p inhibition [91].
DKK3/UOH-ALL-100	It belongs to the dickkopf family that inhibits wnt activation. It is mainly expressed in many tissues with high expression in heart and brain [92].	It is downregulated in head and neck cancer and correlated to shorter survival [93].
DNMT1/ UOH-ALL-15	This gene is encoded for the enzyme that transfer methyl group to cytosine in DNA. DNA methylation is important for epigenetic regulation. It is widely expressed in highly proliferate cells such as spermatocytes,	It is highly expressed in liver cancer and associated with poor prognosis (p=0.001) [95]. High expression was found in cB-ALL and increased the disease burden [96].

	trophoblast cells, and acts a transcription factor [94].	
EIF3A/UOH-ALL-89	It enables RNA binding activity regulating translation initiation factor activity mainly DNA synthesis [97].	Upregulation of eIF3a mediates chemo-resistance of SCLC via inducing of cellular senescence. EIF3A Knockdown inhibits tumour progression and chemotherapy resistance via reversing TGF-β1 [98].
FBXO22/ UOH-ALL-86	It is encoded a member of the F-box protein that functions in ubiquitination of transcriptional target catalysing their degradation. It is found in the most tissues [90].	It promotes AML progression especially with MLL subtype sustaining leukaemia stem cell (LSC). Targeting FBXO22 increases BACH1 and eradicate LSC [99].
FER/UOH-ALL-44	It is encoded a non-transmembrane receptor tyrosine kinase protein that belongs to FPS/FES family. It functions in regulating cell adhesion and growth factor receptors which mediates signalling between the cell surface and cytoskeleton. It also acts a downstream of EGFR and enhances NF-KB activation. They are multiple variants which are produced by alternative splicing and the related pseudogene is in chromosome X. it is found in many tissues such as parathyroid, testis, smooth muscle, ovary, and skin [100].	It is highly increased in renal cancer and associated with poor prognosis. It knockdowns resulting in cell cycle arrest in G0/G1 phase [101].
FLNB/UOH-ALL-27	It belongs to the filamin family, and the encoded protein connects cell membrane components to the actin cytoskeleton. It involves in cell migration, morphology, and integrin activity. It is found in many tissues such as thyroid, pancreatic cell, enterocytes, and adrenal cells [102].	It is overexpressed in liver cancer and associated with poor prognosis. FLNB promotes metastasis and angiogenesis via inducing endothelial cell motility and interacting with Rac-1 and Vav2. This complex interaction leads VEGF activation and thus increases the angiogenesis processes [103].
HDLBP/UOH-ALL-60	It involves in regulating excess cholesterol levels and sterol metabolism in cells and encodes for the protein binding to HDL. It also induces formation of heterochromatin via binding RNA. It expresses in most tissues in various levels and is enriched in pancreas and placenta [104].	It is overexpressed in hepatocellular carcinoma and is involved in tumour growth and proliferation. Knockdown of vigilin leads to inhibit carcinogenesis and sensitized to cisplatin [105]. However, it acts a tumour suppressor in breast cancer as it binds to the 3′ untranslated mRNA region of the c-fms proto-oncogene. The c-fms proto-oncogene is encoded for the receptor of macrophage colony stimulating factor (CSF1) which is function as a surface tyrosine kinase. This interaction inhibits translation of CSF1 and destabilises it [106].
HNRNPLL (SRRF)/ UOH-ALL-24	It encodes an RNA-binding protein that a key regulator of alternative splicing including CD45/PTPRC, and STAT5A. it is widely expressed in many tissues including bone marrow, retina, adrenal gland, stomach in ubiquitous form [107].	HNRNPLL overexpression is found in colorectal cancer, and it acts a protein stabiliser for mRNA that are encoded for the regulators DNA replication. Whereas it acts a metastasis inhibitor via modulating the alternative splicing of CD44 during EMT [108].

HOXD8/UOH-ALL-53	It belongs to the homeobox family which is a highly conserved transcription factor and plays a role in morphogenesis and cellular processes. It is expressed in the kidney, ovary, testis, and adrenal [109].	It acts a tumour suppressor inducing apoptosis. It is downregulated in TNBC and increased its expression results in decreased cancer proliferation via inhibiting AKT/mTOR pathway [110].
IDI1 /UOH-ALL-73	It is encoded a peroxisomally-localised enzyme that involves in cholesterol synthesis. It catalyses farnesyl diphosphate synthesis by converting isopentenyl diphosphate (IPP) to dimethylallyl diphosphate (DMAPP). It expresses in many cells such as breast, adrenal gland, skeletal muscle, liver, and bone marrow [111].	IDI1 is downregulated in clear cell renal carcinoma and associated with the adverse outcome [112].
KIF1B/UOH-ALL-81	It is similar KIF5B [113].	KIF1B polymorphism increases the risk of HCC [114].
KIF5B/UOH-ALL-32	It belongs the motor protein involved in mitochondria transport and movement of synaptic vesicle. It is found in all most tissues [113].	It downregulated with increased expression of miR125b), miR-99a and miR-100 in cB-ALL resistant to vincristine [115].
KRT 31/UOH-ALL-36	It belongs to keratin gene family. It expresses skin, hair, squamous epithelial cell, endometrial ciliated cells. It involves in cell homeostasis [116].	KRT 31 is downregulated in head and neck squamous carcinoma [117].
LINC00251/UOH-ALL-98	It belongs to long non-coding RNA and strictly expressed in the testis. It has synonym C8orf25; NCRNA00251 [118].	LINC00251 polymorphism with other genes (PMP7, DOK5) increase the risk of osteonecrosis in children with B-ALL [119].
LINC00661/UOH-ALL-58	It belongs to long non-coding RNA (lncRNAs) that lacks protein translation with function of regulating gene transcription. It is restricted expressed in testis [120].	It is overexpressed in Cholangiocarcinoma (CCA) and associated with lower overall survival along with other lncRNAs including CHRM3.AS2 and MIR205HG. LINC00661 overexpression is involved in autophagy dysfunction [121].
LOC338963/UOH-ALL-85	It belongs to long non-coding RNA and strictly expressed in the testis [118].	It is highly expressed in Lambert-Eaton myasthenic syndrome (LEMS) which is an autoimmune neuromuscular junction disorder [122].
MCL1/UOH-ALL-46	It encodes an antiapoptotic protein that belongs to the Bcl2 family. It has three isoforms: isoform 1 inhibits apoptosis and enhances cell survival whereas variant 2 and 3 induce apoptosis and cell death. It is mainly enriched in bone marrow and expressed in many tissues such as liver, urinary bladder, and appendix [123].	It is upregulated in AML and associated with poor prognosis and treatment resistance. Direct inhibitors of MCL1 are challenging as it inhibits it function in normal tissues may interfere with safety profiles [124].
MIP/UOH-ALL-57	It has a crucial role in maintaining lens homeostasis and transparency [125] as well as intracellular communication. It is found in eye and other tissues such as testis, liver, brain and adrenal.	MIP [126] is involved in promoting cancer growth and proliferation via activating the PI3K/Akt signalling in breast cancer.
MRFAP1/UOH-ALL-93	It is a nuclear protein that involved in cellular growth and maintained normal histone modification [127].	MRFAP1 is downregulated in gastric cancer and its overexpression decreases cancer proliferation. As it is highly expressed in

		response to inhibition of neddylation activation enzyme (NAE) which plays a crucial role in protein turnover [128].
MYH10/UOH-ALL-90	It belongs a member of the myosin superfamily. It involved in regulating in cell motility and cytokinesis. It found in many tissues lung [129].	MYH10 loss is associated with HCC metastasis and poor prognosis via the activation of EGFR pathway [130].
MYH11/UOH-ALL-63	It encodes a smooth muscle myosin protein. It utilises the ATP hydrolysis for conversion chemical energy into mechanical energy that mainly acts as a contractile protein. It is highly expressed in intestine, smooth muscle, Sertoli cells, and peritubular cells [131].	It is downregulated in colon cancer and associated with poor survival [132]. Furthermore, DNA methyltransferase 3b (DNMT3B) inhibits the expression of MYH11 via DNA methylation. Loss of MYH11 reduces its inhibitory effect on TNFRSF14 transcription and thus promoting tumour progression in gastric cancer [133].
MYL12B/UOH-ALL-5	It encoded of a non-muscle myosin II regulating myosin assembly. It is found in all tissues lung, colon [129].	MYL12B upregulation is associated with melanoma resistant. Inhibition of MYL12B results inducing ROS and pro-survival pathways leading to cell arrest and apoptosis.
MYO6/UOH-ALL-25	It is encoded a reverse-direction motor protein and belongs to actin motor family with ATPase activity. It involves in many intracellular processes including structural integrity, vesicular membrane trafficking, regulates actin cytoskeleton via control the association of septins with actin. It is widely found in transport membrane, skeletal muscle, kidney, retina, and intestine [134].	MYO6 is overexpressed in gastric cancer and associated with the poor survival. MYO6 knockdown decrease colony formation and proliferation of cancer cells via inducing G0/G1 cell cycle arrest. Further analysis, it reveals increased in cell-cycle inhibitor p21, and apoptosis related proteins Bax and caspase3 as well as decreased cyclin A, Bcl-2 expression, and cyclin D1 that are significantly induced apoptosis and cell migration inhibition [135].
NTPCR/UOH-ALL-35	It encodes a non-specific nucleoside triphosphatase. It involves in basic cellular processes that hydrolyses ATP and energy production and expresses in all tissues such as skeletal muscle and pancreas [136].	NTPCR is significantly decreased in ovarian cancer. Increasing expression of NTPCR inhibits G2/M phase and consequently cell invasion and migration. It has a target STAT3, and GATAS2 and binds to them acting as tumour suppressor [137].
PARL/UOH-ALL-96	It is a key regulator of mitochondrial homeostasis regulating apoptosis and remodelling. It is found in the most tissues [138].	It is downregulated in pancreatic cancer and associated with chemo-resistance [139].
PCAT6/ UOH-ALL-59	PCAT6 is belongs to lncRNAs and expresses in salivary, skin, ovary and highly expressed in testis [140].	PCAT6 increases the metastasis of lung cancer. In addition, overexpression of PCAT6 involves EMT transition via regulating miR-326/KLF pathway. PCAT6 Knockdown significantly inhibits tumour proliferation and M2 polarization [141].
PRM1/UOH-ALL-101	It is involved in DNA packaging and spermatid development. It is restricted found in the testis [142].	PRM1 is highly upregulated in colon cancer and correlated to the stage and prognosis. Inhibition of PRM1 results in the decrease cancer proliferation [143].

PTPN1/UOH-ALL-7	It encodes non-receptor type PTPN that regulates pre-mRNA splicing and assembly of small ribonucleo-protein. It is found in most all tissues [144].	It is a negative regulator for JAK/STAT signalling pathway that have been found reduced or truncated or inactive in classical Hodgkin lymphoma and associated TKI [145]
PTPN23/UOH-ALL-79	It is similar to PTPN1 [144].	It is a tumour suppressor gene and its loss in BC associated with poor survival. Induction of PTPN23 inhibits FYN kinase and B-catenin [146]
RAB34/UOH-ALL-68	It encodes Rab protein that belongs to Golgi-bound member of the secretory pathway. It functions in micropinocytosis activation and lysosomes repositioning. It has many different variants which are produced by the alternative splicing of the transcript. It has low tissue specificity and expresses in many cells such as theca cell, peritubular cells, bone marrow, thyroid, and renal cells [147].	It is overexpressed in HCC and correlated with poor prognosis. RAB34 knockdown results in a significant reduced proliferation and metastasis rate via arrest of G1 phase and mesenchymal-epithelial transition [148].
RAB5C/UOH-ALL-67	It encodes a Rab protein and belongs to a small GTPase of the Ras superfamily. It involves in docking, endocytosis, and vesicular transport. It is found many cells such as bone marrow, kidney, skin, urinary bladder, colon, rectum, and pancreas [149].	It is overexpressed in B-ALL and its knockdown inhibit the growth. Its expression is regulated by miR509 that is a tumour suppressor and decreased in B-ALL [150].
ROCK1/UOH-ALL-65	It encodes a serine/threonine kinase protein that binds to GTP-bound form of Rho upon activation. It functions in regulating cell polarity and cytoskeletal organization, adhesion, and motility. It expresses in bone marrow, lung, urinary bladder, and adipose tissues [151].	ROCK1 is overexpressed in AML and associated with poor survival. ROCK1 knockdown enhances tumour cell apoptosis and significantly inhibits the blast proliferation. It has been suggested that miR340-5p downregulation is the main cause of ROCK1 upregulation. This confirms that ROCK1 may be a therapeutic target in AML [45].
RPL28/UOH-ALL-92	It encodes the 60S large subunit components of ribosomal protein L28E family. It catalysed protein synthesis and found in many tissues in spleen, ovary [152].	RPL28 overexpression found colorectal cancer and associated with shorter survival via high expression of extracellular matrix [153].
SERINC3/UOH-ALL-42	It encodes a transmembrane protein that is required for inhibiting lentiviruses infectivity as it impairs viral penetration to the cytoplasm. It is also involved in cell cycle regulation. It is found in many tissues such as liver, placenta, thymus, and parathyroid and it's enriched in testis [154].	It acts a tumour suppressor, and it is downregulated in ovarian cancer. Methylation of SERINC3 enhances tumour escape from apoptosis and increases the survival [155].
SEZ6L2/UOH-ALL-21	It is found on the cell surface and encodes a seizure related protein. It is normally expressed in lung, adrenal, brain, testis [156].	Overexpression of SEZ6L2 has been found in breast cancer and associated with TNM stage. SEZ6L2 expression is regulated by upstream transcription factor 1 (USF1). SEZ6L2 knockdown result in significant decreased of BC growth and metastasis [157].
SIX2/ UOH-ALL-17	It belongs to homeobox genes and encodes proteins that firstly identified to be involved in limbs and eye development. High expression	It is upregulated in HCC and associated with poor prognosis. It enhances metastasises and

	is normally found in salivary tissue, prostate and stomach. It also plays transcriptional regulator role [158].	EMT via activation of TGF-β/Smad signalling [159].
SUN1 /UOH-ALL-62	SUN1 encodes a nuclear envelope protein with SUN domain and belongs to the unc-84 homolog family. It plays a role in migration and nuclear anchorage. There are different variants that produced by the alternative splicing. It expresses ubiquitously in many cells such as skin, endometrium, fat, and testis [160].	It acts a tumour suppressor and decrease its expression in colon cancer. High expression of SUN1 is associated with good prognosis. It reduces the expression of brain derived neurotrophic factor (BDNF) and therefore inhibiting BDNF/tropomyosin-related kinase B (TrkB) signalling. It also increases the acetylation of methyl-CpG binding protein 2 (MeCP2) and associates with SIRT1 for interfering with the BDNF promoter [161].
SURF2/UOH-ALL-80	This gene has a bidirectional promoter with surfeit 1 (SURF1). It is expressed in many tissues and acts as a cargo receptor [162].	It is down-stream regulator of the oncogene, superoxide dismutase 2 (SOD2), which is highly expressed in head and neck cancer and associated radiotherapy resistance [163].
TCF7L2/UOH-ALL-23	It encodes for high motility (HMG) box-containing transcription factor and it is enriched in many tissues such as fat, ovarian, stomach. It plays an important in glucose homeostasis and acts as transcriptional factor in Wnt pathways [164].	It is overexpressed in CML and associated with increased transcription of Wnt related genes such as cyclin D. It also cooperates with MYC and promotes tumour progression [165].
TEX43/UOH-ALL-43	TEX43 involves in sperm motility. It is highly enriched in testis and small amount in colon.	Not found.
TIMP1/UOH-ALL-29	It encodes a natural inhibitor of the matrix metalloproteinase and belongs to TIMP family. It functions in degradation and regulation of the extracellular matrix, and it also promotes cell proliferation via increasing cytokines, hormone, and antiapoptotic protein. It involves in signalling pathways via CD63 and ITGB1 activation. It is expressed in GI tract, salivary, testis, cervix, adipose tissue [166].	It is highly expressed in cB-ALL and associated poor over survival. TIMP1 and CD34+CD38− CSC could be useful biomarkers for B-ALL diagnosis and correlated to MRD [167].
TMA7/UOH-ALL-6	It is involved in the epithelial-mesenchymal interactions have an important role in folliculomorphogenesis and mature hair follicle cycling [168].	HSPC016 expression is associated with aggressive dermal papilla cells (DPC)[169].
TMCO3/UOH-ALL-2	It is encoded of the monovalent cation: proton antiporter 2 (CPA2) regulating proton (Na, K) transport across cellular membranes [170]	It acts as an oncogene, its upregulation found in HCC and associated with poor prognosis. Knockdown of TMCO3 results in the increase of p53/p21 inducing cell apoptosis as well as reduction of EMT [171].
TMPO/UOH-ALL-52	This gene encodes multiple distinct LEM domain-containing protein isoforms that are produced by the alternative splicing. It is involved in several cellular functions such as chromatin organization, regulation of gene expression, and cell cycle control. There are three isoforms: alpha, beta, and gamma isoform. It is widely expressed ubiquitously in	It is overexpressed in glioblastoma. TMPO knockdown results in enhanced apoptosis and inhibited cell proliferation via increasing the cleavage of caspase3 and PARP protein [173]

	many tissues such as bone marrow, lymph nodes, appendix, and ovaries [172].	
TOMM20/UOH-ALL-34	It encodes a translocase of outer mitochondrial membrane 20L receptor which belongs TOM complex. It plays an important in mitochondrial protein transport. It is enriched in testis and small amount is found GI, endocrine tissues [174].	TOMM20 is overexpressed in colon cancer and associated with high metastatic rate. Its knockdown results in a significant reduction of tumour proliferation and metastasis [175].
TPM3/UOH-ALL-1	It belongs to actin-binding protein regulating other binding proteins via copolymerisation. It is enriched in bone marrow, appendix, and found ubiquitous in other tissues [176]	It is overexpressed in ovarian cancer [177]. Targeting of TPM3 uses ATM-3507 synergistically with anti-microtubules such as vinorelbine inducing cell death.
TPPP2/UOH-ALL-83	It is involved in tubulin binding activity and regulating the sperm motility. It is mainly found in testis and salivary gland [178]. (P18; CT152; C14orf8; p25beta)	TPPP2 deficiency is related to male infertility [178]. It is associated with poor prognosis in hepatocellular cancer [179].
TPT1/UOH-ALL-56	It encodes a regulatory protein that involves in the control of cell growth and proliferation including protein synthesis, cell division, and apoptosis. It also plays an important role in mitotic and meiotic cell divisions through phosphorylation and binding to microtubules. It is found in many tissues such as the urinary bladder, thyroid, bone marrow, lung, ovary, and lymph node [180].	It is upregulated in diffuse large B-cell lymphoma (DLBCL) and the knockdown of TCPT leads to a reduction of cell-mediated adhesion via regulating the p-CREB/BCL-2 signalling pathway [181].
TRAP1/UOH-ALL-72	It encodes a mitochondrial chaperone protein which belongs to the HSP90 family. It involves in regulating cellular stress response as it has ATPase activity interacting with TNF1. It has various transcript variants that are produced by the alternative splicing. It is found in many cells such as heart, skeletal muscle, liver, tongue, bone marrow, and adrenal glands [182].	It is overexpressed in ulcerative colitis and proceeded to colon cancer. It was found that oxidative stress induces the production of TRAP1 which promotes neoplastic change and progression [183]. Upregulation of TRAP1 in T-ALL leads to apoptosis resistance and chemotherapy resistance [184].
TUBA3C/ UOH-ALL-20	It encodes for microtubules assembly, and it is strictly expressed in the testis [185].	TUBA3C is upregulated in breast cancer and it is a good biomarker for taxane sensitivity as its level decreased in chemo-resistance cases [186]. TUBA3C is highly increased in NSCLC with poor survival with p-value=0.007 [187]
UBC/UOH-ALL-50	UBC is encoded for a polyubiquitin protein that is conjugated to monomers or polymers. Ubiquitination has an important role in regulation of signalling pathways, DNA repair, protein degradation, and kinase modification. It is found in many cells such as skeletal muscle, tongue, gall bladder, and bone marrow [188]. UBC reduction plays a pivotal role in replicative senescence of bone marrow mesenchymal stromal cells.	As UBC involves in cell cycle control, downregulation of UBC is associated with decrease in cell cycle components such as CDK1. Increased expression of UBC enhances the proliferation of MSC and accompanied with proliferative genes in cell cycle [189]. It is overexpressed in renal cancer and associated with poor prognosis [190].
UBE2D2/UOH-ALL-4	It belongs E3 ubiquitin ligases and their substrates p53, and peroxisomal biogenesis	Circ_UBE2D2 upregulation found in breast cancer and poor prognosis. It targets miR-

	factor 5 (PEX5). It is expressed in many tissues such as bone marrow, thyroid [191].	200a-3p and its downregulation increases tamoxifen sensitivity [192].
UBE3C/UOH-ALL-77	It is similar to UBE2D2 [191].	It is upregulated in renal carcinoma via activating wnt pathway and associated with metastasis [193].
UBE3D/ UOH-ALL-41	It encodes an E3 ubiquitin-protein ligase that transfers ubiquitin to the target gene. Gene ubiquitination mainly promotes their degradation by proteasome. It also enables cyclin binding activity. It is widely expressed in tissues such as neuron, and oligodendrocytes [194].	It is highly expressed in breast cancer. UBE3D stabilizes CPSF73 and protects it from degradation. CPSF73 plays an important role in maintaining cancer proliferation and recurrence especially self-renewal cells. Knockdown of UBE3D depletes CPSF73 that resulting in the inhibition of tumour growth [195].
UVRAG-DT/UOH-ALL-87	It is a ncRNA and highly expressed in testis and fat. It is involved in regulating smooth muscle veins [196].	circUVRAG [197] is upregulated in bladder cancer and associated with poor survival. Its silencing inhibits cancer progression and metastasis via targeting miR-223/fibroblast growth factor receptor 2 (FGFR2).
WLS /UOH-ALL-19	It enables Wnt protein activation and involves in protein transport and positive regulation of cell communication. It is expressed in many tissues such as kidney, Golgi apparatus, endothelial tissues, gall bladder [198].	It is highly expressed in gastric cancer and associated with advanced metastasis [199]. It overexpressed in cB-ALL and associated with poor prognosis and relapse. It involves in proliferation and anti-apoptotic activity via regulating GSK3β activation [200].
WNT2B/UOH-ALL-10	It has low tissue specificity and finds in ECM, fibroblast, peritubular and Leydig cells. It involves in cell regulation and developmental processes [198].	Wnt2b is decreased in B-ALL (p=0.033) [201].
ZNF676/ UOH-ALL-78	It is involved in transcription regulation enabling DNA-binding transcription factor, RNA polymerase II specific DNA binding activity as well as telomerase haemostasis. It has a broad expression in many tissues [202].	ZNF676 overexpression is found in pituitary neuroendocrine tumour and correlated to invasive tumour [203].

Table S4. Gene expression and association with above and below median expression using MILE data.

Method of identification	Antigen	Probe set	Expression B-ALL compared to healthy BM (p-value)	Survival (p-value)
SEREX	CUL1	238509-at	ALL with t(1;19) and ALL hyperdiploid (p<0.01)	0.0422
		207614-s-at	ALL with t(1;19) and ALL hyperdiploid (p<0.01)	0.0161
	DKK3	202196-s-at	ALL t(8;14) and pre-B-ALL except t(9;22) (NS)	0.0233
	HMG20	211296-x-at	Pre-B-ALL t(9;22) and pre-B-ALL except t(9;22) (NS)	0.0002
	IDI1	208881-x-at	All types of B-ALL p<0.01, except ALL t(8;14) (NS)	0.0007
		204615-x-at	All types of B-ALL p<0.01, except ALL t(8;14) (NS)	p<0.0001
	KIF5B	201992-s-at	ALL t(12;21), Pre-B-ALL no t(9;22) and hyperdiploid (p<0.001)	0.0066
	PARL	218271-s-at	Downregulated in B-ALL (p<0.01)	0.0017
	PTPN23	223149-s-at	All types of B-ALL (p<0.001)	0.0378
	ROCK1	213044-at	All types of B-ALL (p<0.05) except ALL t(8;14), ALL t(1;19) and Pre-B-ALL t(9;22) (NS)	0.0014
		214578-s-at	All types of B-ALL (p<0.05) except ALL t(8;14), ALL t(1;19) and Pre-B-ALL t(9;22) (NS)	0.0057

	SERINC3	221472-at	Pro-B-ALL t(11q23), MLL and Pre-B-ALL t(9;22) (p<0.05)	0.0246
	WLS	228949-at	Downregulated in all types of B-ALL (p<0.01)	0.0045
CTA database (26)	MAGEA4	214254-at	Mature B-ALL, ALL with t(8;14) (p<0.05)	0.00404
	TEX101	223906-s-at	B-ALL with t(8;14) (NS)	0.00539
	GPATCH	243704-at	ALL t(1;19) (p<0.001)	0.009
	CTAGE5	**204055-s-at**	**ALL hyperdiploid (p<0.001)**	**0.0129**
	RQCD1	213179-at	ALL t(1;19) (p<0.001)	0.0137
	DNAJB2	202500-at	c- and pre-B-ALL t(9;22) (p<0.01)	0.0183
	DNAJB4	203810-at	ALL t(12;21) (NS)	0.0185
	MORC3	213000-at	ALL t(12;21) (p<0.01)	0.0232
	SYCP2L	236337-at	ALL with t(1;19) (p<0.001)	0.0246
	CTCFL	1552368-at	Downregulated in B-ALL, except Pro-B-ALL t(11q23), MLL and B-ALL with t(8;14) (NS)	0.028
	NR6A1	211402-x-at	Downregulated in B-ALL (p<0.01)	0.0345
	MAGEA6	214612-x-at	c- and pre-B-ALL t(9;22) (NS)	0.0468
	MORC4	219038-at	Downregulated in B-ALL, except ALL hyperdiploid (NS)	0.0473
Protoarray (8)	BMX	206464-at	Downregulated in B-ALL (p<0.001)	0.0461
	SEPT9	1559025-at	ALL subtypes of B-ALL (p<0.001)	0.0205
LAAs (25)	HOMER1	226651-at	ALL subtypes of B-ALL (p<0.05)	0.000581
	HOMER3	215489-x-at	Downregulated in B-ALL (p<0.001)	0.0311
	CDKN2B	207530-s-at	Downregulated in B-ALL, except t(8;14) (NS)	0.0193
	IKZF1	1565817-at	ALL t(12;21) and t(8;14) p<0.001 and t(1;19) (p<0.05)	0.0304
GSE38403 (23)	FLT4	210316-at	ALL subtypes, except B-ALL with t(8;14) and t(1;19) (p<0.001)	0.0353
		229902-at		0.0107
	MRC1	204438-at	ALL subtypes p<0.001 except B-ALL with t(8;14) (p<0.05)	0.00117
	EMP1	201324-at	ALL subtypes p<0.001; t(12;21) p<0.01 however c- and pre-B-ALL and t(9;22) (NS)	0.0343
		201325-s-at		0.0115
	DPPA4	219651-at	(NS)	0.0194
	CYTL1(C17)	219837-s-at	ALL subtypes of B-ALL (p<0.001)	0.00945
	PLVAP(FELS)	221529-s-at	ALL subtypes except B-ALL with t(8;14), t(12;21) and t(1;19) (p<0.001)	0.0445
GSE13204 (24)	LIN7A	240027-at	Downregulated in B-ALL (p<0.001)	0.0179
	LILRA3	206881-s-at	Downregulated in B-ALL p<0.001 except B-ALL with t(8;14) (NS)	0.0118
	VSTM1	23581-at	Downregulated in B-ALL (p<0.001)	0.00196
	P2RY2	206277-at		0.00144
	PTGS2	1554997-a-at		0.013
	CYP4F2	210452-x-at		0.00313
Hippo pathway	**TEAD4**	41037-at	B-ALL with t(8;14), t(1;19) or c- and Pre-B-ALL t(9;22) (p<0.001)	0.0223
	MOB1b	225997-at	Downregulated in B-ALL (p<0.001)	0.0145
	TAOK1	216310-at	ALL subtypes except B-ALL with t(8;14) - p<0.001 and ALL t(1;19) (p<0.05)	0.0328
	FRMD6	225464-at	Downregulated in B-ALL (p<0.001)	0.00172
Wnt pathway	**DKK3**	202196-s-at	B-ALL with t(8;14) (NS)	0.0233
	TCF4	212382-at	ALL all subtypes (p<0.001)	0.00214
		203753-at	ALL hyperdiploid and ALL t(1;19) (p<0.001)	0.0215
		212385-at		0.00603
		213891-s-at	ALL hyperdiploid and ALL t(1;19) (p<0.001)	0.0292
		212386-at	ALL hyperdiploid and ALL t(1;19) (p<0.001)	0.0172
		212387-at	ALL hyperdiploid and ALL t(1;19) (p<0.001)	0.012
	TCF3	215260-s-at	ALL all subtypes (p<0.001)	0.0297

	DVL3	201908-at	ALL all subtypes except B-ALL with t(8;14), t(9;22) (p<0.001)	0.0279
TGFβ pathway	TGF 1	203085-s-at	Downregulated in B-ALL (p<0.001)	0.000832
	SMURF2	227489-at	ALL subtypes of B-ALL (p<0.001) except B-ALL with t(8;14) (NS)	0.0208
		232020-at	ALL subtypes of B-ALL (p<0.001) except B-ALL with t(8;14) (NS)	0.0305
	SMAD3	218284-at	ALL subtypes of B-ALL (p<0.05)	0.0317
		205398-s-at	ALL subtypes of B-ALL (p<0.05)	0.005
		205396-at	ALL subtypes of B-ALL (p<0.05)	<0.0001

NS: not significant.

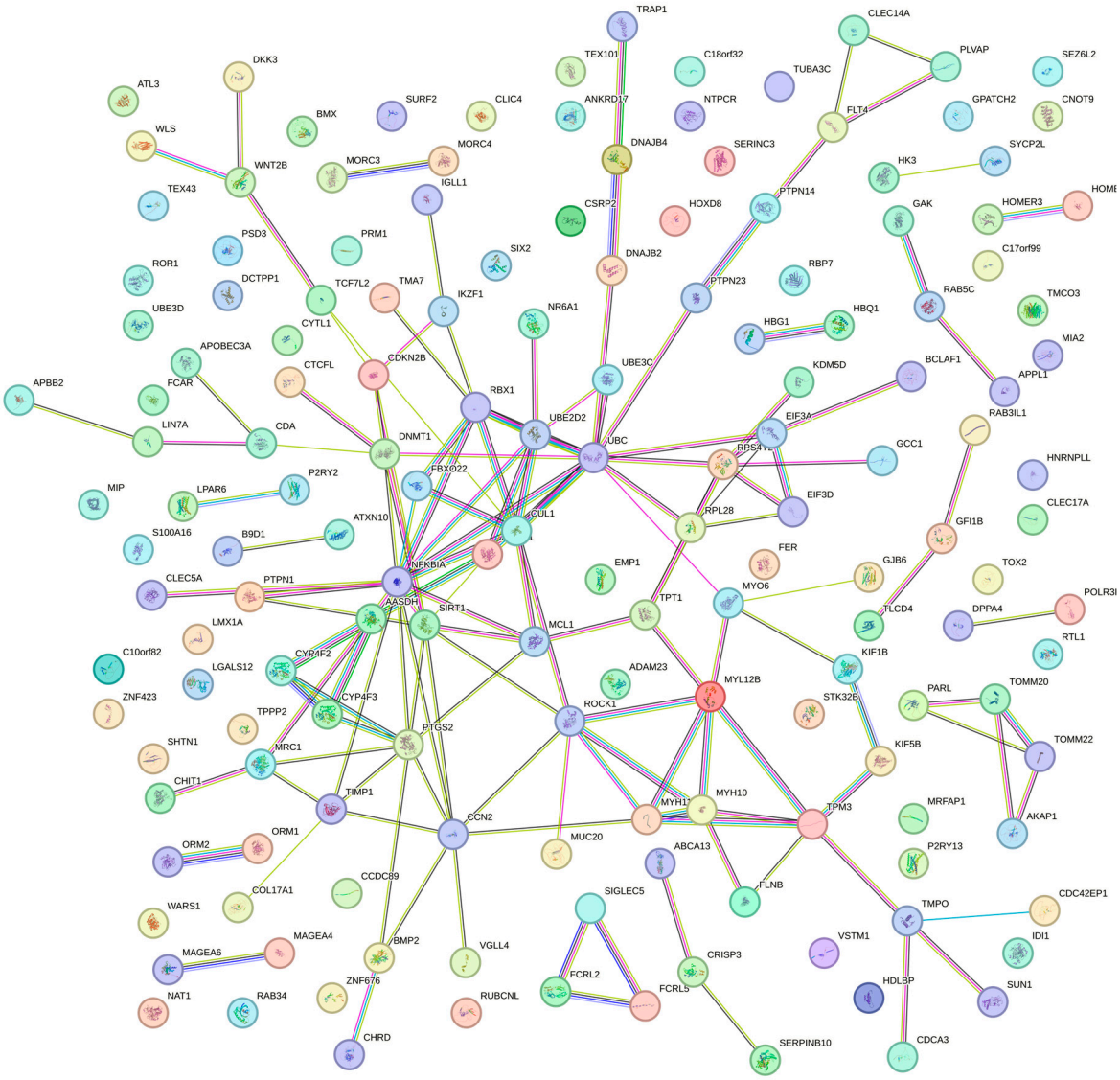


Figure S1. Protein-protein interaction of LAAs using STRING. Most of the LAAs were involved in binding followed by transcription regulator activity. PMP2, PMP4, CDKN2B, RBX, CUL1 involved in TGFβ enrichment. Wnt2B, CDKN2B, RBX, PMP2, PTGS2 were involved in cancer pathways. The lack of interactions among other genes in this signature is likely explained by a variety of other biological pathways utilised within B-ALL. SEREX identified genes that were involved in ubiquitination included UBC, UBE2C, UBE2D2, CUL1, RBX1, and SKP2. Genes involved in regulating the intrinsic apoptosis process were BCLAF2, PARL, SERINC3, TRAP1, TPT1, MCL1, and PTPN1.

(A)


Tissue / Cell
vagina / squamous epithelial cells
urinary bladder / urothelial cells
tonsil / squamous epithelial cells
tonsil / non-germinal center cells
tonsil / germinal center cells
thyroid gland / glandular cells
testis / spermatogonia cells
testis / sertoli cells
testis / round or early spermatids
testis / preleptotene spermatocytes
testis / peritubular cells
testis / pachytene spermatocytes
testis / Leydig cells
testis / elongated or late spermatids
testis / cells in seminiferous ducts
stomach 2 / glandular cells
stomach 1 / glandular cells
spleen / cells in white pulp
spleen / cells in red pulp
soft tissue 2 / peripheral nerve
soft tissue 2 / fibroblasts
soft tissue 2 / chondrocytes
soft tissue 1 / peripheral nerve
soft tissue 1 / fibroblasts
soft tissue 1 / chondrocytes
smooth muscle / smooth muscle cells
small intestine / paneth cells
small intestine / goblet cells
small intestine / glandular cells
small intestine / enterocytes - Microvilli
small intestine / enterocytes
small intestine / endocrine cells
skin 2 / vascular mural cells
skin 2 / melanocytes
skin 2 / lymphocytes
skin 2 / langerhans cells
skin 2 / fibrohistiocytic cells
skin 2 / extracellular matrix
skin 2 / epidermal cells
skin 2 / endothelial cells
skin 2 / cells in spinous layer
skin 2 / cells in granular layer
skin 2 / cells in corneal layer
skin 2 / cells in basal layer
skin 1 / vascular mural cells
skin 1 / melanocytes
skin 1 / lymphocytes
skin 1 / langerhans cells
skin 1 / Langerhans
skin 1 / keratinocytes
skin 1 / fibrohistiocytic cells
skin 1 / fibroblasts
skin 1 / extracellular matrix
skin 1 / endothelial cells
skin 1 / cells in spinous layer
skin 1 / cells in granular layer
skin 1 / cells in corneal layer
skin 1 / cells in basal layer
skeletal muscle / myocytes
seminal vesicle / glandular cells
salivary gland / glandular cells
rectum / peripheral nerve/ganglion
rectum / mucosal lymphoid cells
rectum / goblet cells
rectum / glandular cells
rectum / fibroblasts
rectum / enterocytes - Microvilli
rectum / enterocytes
rectum / endothelial cells
rectum / endocrine cells
prostate / glandular cells
placenta / trophoblastic cells
placenta / syncytiotrophoblasts - microvilli
placenta / syncytiotrophoblasts - cell body
placenta / hofbauer cells
placenta / endothelial cells
placenta / decidual cells
placenta / cytotrophoblasts
parathyroid gland / glandular cells
pancreas / pancreatic endocrine cells
pancreas / exocrine glandular cells
ovary / ovarian stroma cells
ovary / follicle cells
oral mucosa / squamous epithelial cells
nasopharynx / respiratory epithelial cells
nasopharynx / goblet cells
nasopharynx / ciliated cells (tip of cilia)
nasopharynx / ciliated cells (ciliary rootlets)
nasopharynx / ciliated cells (cilia axoneme)
nasopharynx / ciliated cells (cell body)
nasopharynx / basal cells
lymph node / non-germinal center cells
lymph node / germinal center cells
lung / macrophages
lung / endothelial cells
lung / alveolar cells type II
lung / alveolar cells type I
lung / alveolar cells
liver / hepatocytes
liver / cholangiocytes
kidney / proximal tubules (microvilli)
kidney / proximal tubules (cell body)
kidney / distal tubules
kidney / collecting ducts
kidney / cells in tubules
kidney / cells in glomeruli
kidney / bowman's capsule
hippocampus / neuronal cells
hippocampus / glial cells
heart muscle / cardiomyocytes
gallbladder / glandular cells
fallopian tube / non-ciliated cells
fallopian tube / glandular cells
fallopian tube / ciliated cells (tip of cilia)
fallopian tube / ciliated cells (ciliary rootlets)
fallopian tube / ciliated cells (cilia axoneme)
fallopian tube / ciliated cells (cell body)
esophagus / squamous epithelial cells
epididymis / glandular cells
endometrium 2 / glandular cells
endometrium 2 / cells in endometrial stroma
endometrium 1 / glandular cells
endometrium 1 / cells in endometrial stroma
duodenum / paneth cells
duodenum / goblet cells
duodenum / glandular cells
duodenum / enterocytes - Microvilli
duodenum / enterocytes
duodenum / endocrine cells
colon / peripheral nerve/ganglion
colon / mucosal lymphoid cells
colon / goblet cells
colon / glandular cells
colon / fibroblasts
colon / enterocytes - Microvilli
colon / enterocytes
colon / endothelial cells
colon / endocrine cells
cervix / squamous epithelial cells
cervix / glandular cells
cerebral cortex / neuropil
cerebral cortex / neuronal cells
cerebral cortex / glial cells
cerebral cortex / endothelial cells
cerebellum / white matter cells - nucleus
cerebellum / white matter cells - cytoplasm/membrane
cerebellum / synaptic glomeruli - core
cerebellum / synaptic glomeruli - capsule
cerebellum / Purkinje cells - nucleus
cerebellum / Purkinje cells - dendrites
cerebellum / Purkinje cells - cytoplasm/membrane
cerebellum / Purkinje cells
cerebellum / processes in white matter
cerebellum / processes in molecular layer
cerebellum / processes in granular layer
cerebellum / molecular layer cells - nucleus
cerebellum / molecular layer cells - cytoplasm/membrane
cerebellum / molecular layer - neuropil
cerebellum / granular cells - nucleus
cerebellum / granular cells - cytoplasm/membrane
cerebellum / GLUC cells - nucleus
cerebellum / GLUC cells - cytoplasm/membrane
cerebellum / cells in molecular layer
cerebellum / cells in granular layer
cerebellum / Bergmann glia - nucleus
cerebellum / Bergmann glia - cytoplasm/membrane
caudate / neuronal cells
caudate / glial cells
bronchus / respiratory epithelial cells
bronchus / goblet cells
bronchus / ciliated cells (tip of cilia)
bronchus / ciliated cells (ciliary rootlets)
bronchus / ciliated cells (cilia axoneme)
bronchus / ciliated cells (cell body)
bronchus / basal cells
breast / myoepithelial cells
breast / glandular cells
breast / adipocytes
bone marrow / hematopoietic cells
appendix / non-germinal center cells
appendix / lymphoid tissue
appendix / goblet cells
appendix / glandular cells
appendix / enterocytes - Microvilli
appendix / enterocytes
appendix / endocrine cells
adrenal gland / glandular cells
adipose tissue / adipocytes
SOX4
TCF21
ROCK1
YAP1
SMAD3
TEAD4
TCF4
PTPN13
KLF6
WIS
FBXO6
HMG20
SEPT9
KIF5B
IDI1
HOMER3
ARHGAP1
MO81b
SMURF1
SMURF2
HOMER1
CUL1
DDX3
SERINC3
TAOK1
Genes
level
High
Medium
Low
Not detected

(B)

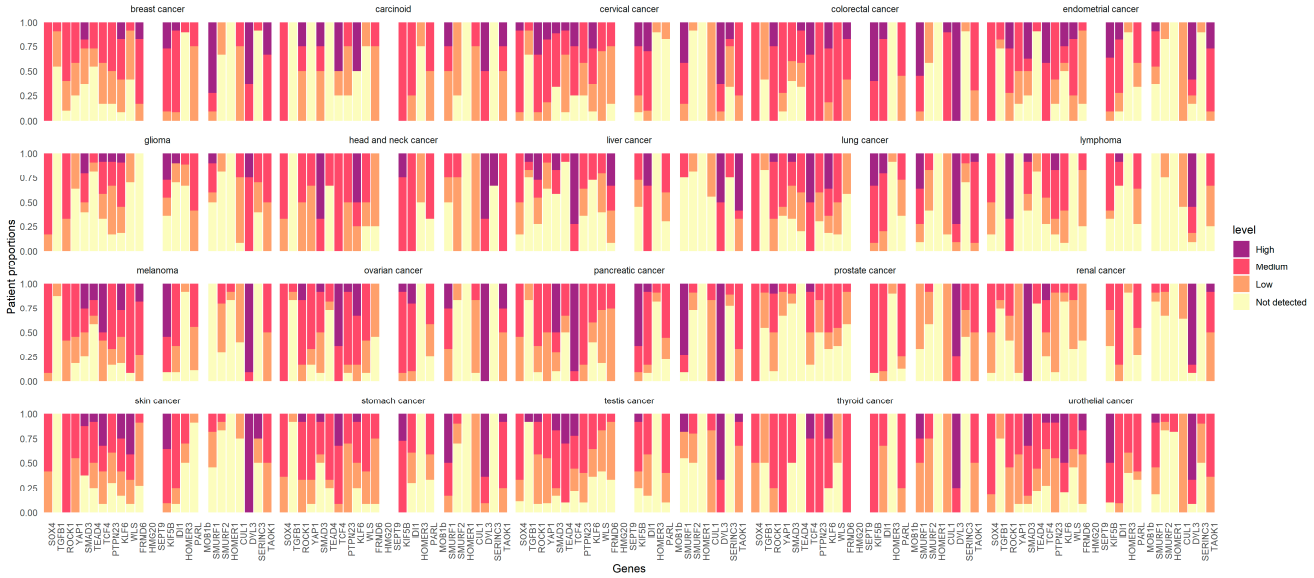


Figure S2. In silico analysis of the antigens revealed the levels of expression of each shortlisted antigen in healthy and cancerous tissues. Heatmap showing the expression levels of each protein in (A) healthy cells and (B) different tumour types, with the y-axes representing the proportion of patients expressing each tumour antigen. The purple, red, and orange colours indicate very high to low levels of expression, pale yellow represents no expression detected, and white represents no data available in the corresponding histology in the Human Protein Atlas.

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