

Gene Name	Description	Studies	Studies with FC	Total Sample Sizes	Total Sample Sizes with FC	Mean Fold Change	Range
4 Studies - Greatest sample size							
PCNA	Proliferating cell nuclear antigen	4 [21,22,51,54]	4	249	249	3.34	1.20 to 4.80
GTF3A	General transcription factor IIIA	4 [17,21,22,54]	4	235	235	3.03	1.50 to 3.35
SOX4	SRY (sex determining region Y)-box 4	4 [21,22,48,54]	3	244	199	2.41	2.02 to 2.72
SOX9	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	4 [21,22,48,54]	3	280	235	2.36	1.89 to 2.25
VEGFA	Vascular endothelial growth factor A	4 [21,55,56,59]	2	270	224	2.07	1.81 to 2.33
4 Studies – Moderate sample size							
ETV4	Ets variant gene 4 (E1A enhancer binding protein, E1AF)	4 [22,48,51,54]	3	234	189	32.64	2.08 to 92.00
MMP1	Matrix metalloproteinase 1 (interstitial collagenase)	4 [17,20,21,22]	4	162	162	8.26	3.47 to 21.00
CXCL3	Chemokine (C-X-C motif) ligand 3	4 [17,20,21,22]	4	162	162	7.28	2.48 to 13.00
NPM1	Nucleophosmin (nucleolar phosphoprotein B23, numatrin)	4 [8,19,48,54]	3	174	129	7.10	4.27 to 12.00
HMGA1	High mobility group AT-hook 1	4 [22,51,54,58]	3	229	189	5.50	2.90 to 7.09
RPS2	Ribosomal protein S2	4 [8,19,54,57]	3	169	129	5.16	2.39 to 8.13
RPL8	Ribosomal protein L8	4 [19,22,54,57]	3	183	143	3.50	2.16 to 5.35
EIF3S9	Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa	4 [22,51,54,57]	3	229	189	3.29	2.53 to 4.30
PRKDC	Protein kinase, DNA-activated, catalytic polypeptide	4 [21,22,54,56]	3	221	199	2.49	1.33 to 3.23
4 Studies - Lowest sample size							
MMP7	Matrix metalloproteinase 7 (matrilysin, uterine)	4 [20,21,22,49]	4	158	158	9.39	3.32 to 21.00
HSPD1	Heat shock 60kDa protein 1 (chaperonin)	4 [8,47,50,59]	3	82	58	4.90	4.12 to 5.99
RAN	RAN, member RAS oncogene	4 [8,48,51,57]	2	157	72	4.60	3.30 to 5.90

	family						
PABPC1	Poly(A) binding protein, cytoplasmic 1	4 [8,19,22,53]	3	80	62	3.99	3.00 to 5.75
HSP90AB1	Heat shock protein 90kDa alpha (cytosolic), class B member 1	4 [8,22,47,59]	3	106	82	3.72	2.87 to 5.34
	3 Studies – Greatest sample size						
RPL29	Ribosomal protein L29	3 [48,54,57]	1	188	103	5.35	5.35 to 5.35
RRM2	Ribonucleotide reductase M2 polypeptide	3 [22,51,54]	3	189	189	4.85	2.06 to 6.80
RPS7	Ribosomal protein S7	3 [22,48,54]	2	184	139	3.96	2.21 to 5.71
MIF	Macrophage migration inhibitory factor (glycosylation-inhibiting factor)	3 [22,54,57]	2	179	139	3.68	2.62 to 4.74
FPRL1	Formyl peptide receptor-like 1	3 [21,49,54]	3	195	195	3.67	2.92 to 5.15
ENC1	Ectodermal-neural cortex (with BTB-like domain)	3 [22,49,55]	3	232	232	3.34	2.62 to 3.92
BMP4	Bone morphogenetic protein 4	3 [22,54,58]	2	179	139	3.24	2.92 to 3.55
CPNE1	Copine I	3 [21,47,54]	3	187	187	3.04	1.48 to 4.41
POLR1D	Polymerase (RNA) I polypeptide D, 16kDa	3 [22,54,58]	2	179	139	2.51	2.10 to 2.91
TGIF1	TGFB-induced factor (TALE family homeobox)	3 [21,22,54]	3	199	199	2.40	1.38 to 3.60
TRAP1	TNF receptor-associated protein 1	3 [22,54,58]	2	179	139	2.28	2.17 to 2.38
MCM3	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	3 [21,22,54]	3	199	199	2.22	1.30 to 2.98
SNRPB	Small nuclear ribonucleoprotein polypeptides B and B1	3 [21,22,54]	3	199	199	2.18	1.01 to 3.03
ITGA2	Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	3 [48,55,56]	1	231	164	2.06	2.06 to 2.06
TOMM40	Translocase of outer mitochondrial membrane 40 homolog (yeast)	3 [21,22,54]	3	199	199	1.94	1.66 to 2.13
	3 Studies – Moderate sample size						
FN1	Fibronectin 1	3 [19,21,51]	3	114	114	9.94	1.11 to 15.00
SPP1	Secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early	3 [20,21,22]	3	126	126	6.23	2.23 to 12.00

	T-lymphocyte activation 1)						
TACSTD2	Tumor-associated calcium signal transducer 2	3 [21,22,49]	3	128	128	6.04	4.53 to 7.84
BGN	Biglycan	3 [20,54,58]	2	173	133	5.23	4.46 to 6.00
WEE1	WEE1 homolog (S. pombe)	3 [21,47,51]	3	134	134	4.70	1.16 to 6.75
RPS19	Ribosomal protein S19	3 [19,54,57]	2	147	107	4.59	4.05 to 5.13
SERPINE1	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	3 [20,21,56]	2	112	90	4.32	1.64 to 7.00
CXCL2	Chemokine (C-X-C motif) ligand 2	3 [20,21,22]	3	126	126	4.23	2.21 to 8.00
FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	3 [21,51,52]	2	131	110	4.22	2.73 to 5.70
RPL31	Ribosomal protein L31	3 [48,53,54]	1	166	103	4.08	4.08 to 4.08
RPS5	Ribosomal protein S5	3 [19,54,57]	2	147	107	3.79	2.67 to 4.90
HSPE1	Heat shock 10kDa protein 1 (chaperonin 10)	3 [17,22,54]	3	175	175	3.74	2.54 to 4.80
EIF3S6	Eukaryotic translation initiation factor 3, subunit 6 48kDa	3 [8,48,54]	2	170	125	3.73	3.26 to 4.20
HOMER1	Homer homolog 1 (Drosophila)	3 [20,49,54]	3	165	165	3.65	2.55 to 5.00
ODC1	Ornithine decarboxylase 1	3 [8,54,57]	2	165	125	3.59	3.27 to 3.90
HMGB2	High-mobility group box 2	3 [8,48,54]	2	170	125	3.42	2.30 to 4.54
PYCR1	Pyrroline-5-carboxylate reductase 1	3 [17,21,57]	2	136	96	3.27	1.23 to 5.30
RPS18	Ribosomal protein S18	3 [19,47,54]	3	131	131	3.25	2.02 to 4.80
TRIM28	Tripartite motif-containing 28	3 [19,22,54]	3	143	143	2.90	2.02 to 4.57
SORD	Sorbitol dehydrogenase	3 [17,21,22]	3	132	132	2.86	1.19 to 4.70
HNRPH1	Heterogeneous nuclear ribonucleoprotein H1 (H)	3 [18,52,54]	1	142	103	2.81	2.81 to 2.81
PPIB	Peptidylprolyl isomerase B (cyclophilin B)	3 [22,46,54]	2	149	139	2.63	2.50 to 2.75
IMPDH2	IMP (inosine monophosphate) dehydrogenase 2	3 [8,54,57]	2	165	125	2.57	2.32 to 2.81
GSTP1	Glutathione S-transferase pi	3 [22,53,54]	2	157	139	2.43	2.38 to 2.48
C2	Complement component 2	3 [20,21,57]	2	130	90	2.21	1.42 to 3.00
GGH	Gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	3 [21,22,58]	2	136	96	1.87	1.47 to 2.27

CDKN3	Cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	3 [21,22,52]	2	117	96	1.80	1.11 to 2.48
MYBL2	V-myb myeloblastosis viral oncogene homolog (avian)-like 2	3 [21,52,58]	1	121	60	1.69	1.69 to 1.69
3 Studies – Lowest sample size							
GNB2L1	Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	3 [19,46,48]	1	59	4	8.30	8.30 to 8.30
COL1A1	Collagen, type I, alpha 1	3 [19,21,59]	2	88	64	8.20	2.39 to 14.00
CLDN2	Claudin 2	3 [19,22,59]	2	64	40	7.44	3.88 to 11.00
BST2	Bone marrow stromal cell antigen 2	3 [19,21,22]	3	100	100	6.82	1.19 to 3.28
AHCY	S-adenosylhomocysteine hydrolase	3 [17,19,20]	3	70	70	5.78	4.00 to 7.33
LDHB	Lactate dehydrogenase B	3 [8,22,57]	2	98	58	4.26	2.05 to 6.47
RPL30	Ribosomal protein L30	3 [8,53,57]	1	80	22	4.10	4.10 to 4.10
CFB	Complement factor B	3 [6,18,58]	1	94	36	3.70	3.70 to 3.70
RPL6	Ribosomal protein L6	3 [8,48,57]	1	107	22	3.46	3.46 to 3.46
BMP7	Bone morphogenetic protein 7 (osteogenic protein 1)	3 [49,52,58]	1	93	32	3.42	3.42 to 3.42
NME1	Non-metastatic cells 1, protein (NM23A) expressed in	3 [19,22,48]	2	85	40	3.37	2.57 to 4.17
EEF1A1	Eukaryotic translation elongation factor 1 alpha 1	3 [8,46,48]	1	77	22	3.12	3.12 to 3.12
CCT7	Chaperonin containing TCP1, subunit 7 (eta)	3 [8,22,57]	2	98	58	2.94	2.40 to 3.47
RPSA	Ribosomal protein SA	3 [19,46,48]	1	59	4	2.74	2.74 to 2.74
RPL3	Ribosomal protein L3	3 [8,19,57]	2	66	26	2.33	2.30 to 2.36