Supplementary Table 1 Some high-frequency keywords

Term	Frequency of occurrence
prostate cancer	111
metastasis	79
expression	69
cancer	68
growth	35
mouse model	32
breast cancer	30
invasion	23
cell	23
progression	22
survival	21
apoptosis	21
lung metastasis	19
in-vivo	18
angiogenesis	18
chemotherapy	17
proliferation	16
cancer cells	16
inhibition	16
protein	14
migration	14
activation	13
therapy	13
men	13
immunotherapy	13
gene-expression	13
pathway	12

radiotherapy	12
radical prostatectomy	12
lung adenocarcinoma	12
receptor	12
gene	12
prostate	11
tumor-growth	10
docetaxel	10
antigen	10
patterns	10
androgen receptor	10
e-cadherin	9
bone metastasis	9
prognosis	9
pet/ct	9
diagnosis	9
mechanism	9
in-vitro	8
identification	8
cell-lines	8
disease	8
colorectal cancer	8
bone	8
resistance	7
adhesion	7
phase-i	7
induction	7
il-12	7
differentiation	7

matrix metalloproteinases	7
lung cancer	7
mitoxantrone	6
increased survival	6
combination	6
castration-resistant prostate cancer	6
risk	6
psma	6
orthotopic implantation	6
microenvironment	6
target	5
stem-cells	5
down-regulation	5
surgery	5
promotes	5
lung	5
liver	5
impact	5
gene therapy	5
ganciclovir therapy	5
enzalutamide	5
double-blind	5
adenovirus	5
neuroendocrine differentiation	5
membrane antigen-expression	5
case report	5

mesenchymal transition	5
kinase	5
phosphorylation	4
osteosarcoma	4
epithelial-mesenchymal transition	4
allelic loss	4
visceral metastases	4
trial	4
site	4
overexpression	4
outcomes	4
mortality	4
metastasectomy	4
immunity	4
cabazitaxel	4
abiraterone acetate	4
lesions	4
immunohistochemistry	4
tumor progression	4
transformation	4
suppression	4
stat3	4
oxidative stress	4
growth-factor	4
endothelial-cells	4
efficacy	4
cathepsin-b	4
cancer metastasis	4

Supplementary Table 2 Results of GO functional annotation of DEGs with PCLM

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
BP	GO:0002181	cytoplasmic translation	124/9340	146/18800	3.68E-19	2.34E-15	1.58E-15	124
BP	GO:0070661	leukocyte proliferation	230/9340	330/18800	8.34E-14	2.65E-10	1.79E-10	230
BP	GO:0006413	translational initiation	98/9340	120/18800	3.18E-13	6.73E-10	4.56E-10	98
BP	GO:0002697	regulation of immune effector process	241/9340	353/18800	7.55E-13	1.20E-09	8.11E-10	241
BP	GO:0032943	mononuclear cell proliferation	208/9340	300/18800	2.86E-12	3.63E-09	2.45E-09	208
BP	GO:0046651	lymphocyte proliferation	205/9340	296/18800	4.83E-12	5.11E-09	3.46E-09	205
BP	GO:0030098	lymphocyte differentiation	255/9340	382/18800	7.38E-12	6.70E-09	4.53E-09	255

BP	GO:0190313	mononuclear cell differentiation	284/9340	433/18800	1.04E-11	8.28E-09	5.60E-09	284
CC	GO:0044391	ribosomal subunit	157/9761	178/19594	1.17E-27	9.09E-25	5.74E-25	157
CC	GO:0022626	cytosolic ribosome	94/9761	102/19594	2.84E-20	1.10E-17	6.95E-18	94
CC	GO:0005840	ribosome	181/9761	229/19594	4.52E-20	1.17E-17	7.37E-18	181
CC	GO:0015934	large ribosomal subunit	97/9761	112/19594	2.21E-16	4.29E-14	2.71E-14	97
CC	GO:0030055	cell-substrate junction	290/9761	428/19594	2.48E-14	3.84E-12	2.43E-12	290
CC	GO:0005925	focal adhesion	283/9761	419/19594	9.29E-14	1.20E-11	7.58E-12	283
CC	GO:0101002	ficolin-1-rich granule	141/9761	185/19594	1.31E-13	1.45E-11	9.15E-12	141
CC	GO:001593	small ribosomal subunit	63/9761	69/19594	1.67E-13	1.62E-	1.02E-	63

	5					11	11	
MF	GO:0003735	structural constituent of ribosome	151/9575	181/18410	5.18E-19	6.33E-16	5.10E-16	151
MF	GO:0030546	signaling receptor activator activity	323/9575	496/18410	1.50E-09	9.14E-07	7.36E-07	323
MF	GO:0005125	cytokine activity	166/9575	235/18410	3.70E-09	1.51E-06	1.22E-06	166
MF	GO:0048018	receptor ligand activity	316/9575	489/18410	7.62E-09	2.33E-06	1.87E-06	316
MF	GO:0045296	cadherin binding	223/9575	333/18410	1.70E-08	4.17E-06	3.36E-06	223
MF	GO:0003743	translation initiation factor activity	44/9575	51/18410	2.53E-07	5.15E-05	4.15E-05	44
MF	GO:0009055	electron transfer activity	92/9575	125/18410	5.87E-07	0.000103	8.26E-05	92
MF	GO:0046873	metal ion transmembrane transporter activity	272/9575	428/18410	7.14E-07	0.000109	8.78E-05	272

Supplementary Table 3 Results of KEGG functional annotation of DEGs with PCLM

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
hsa05022	Pathways of neurodegeneration - multiple diseases	343/4719	476/8390	1.86E-13	6.20E-11	4.22E-11	343
hsa05171	Coronavirus disease - COVID-19	173/4719	232/8390	3.48E-09	5.81E-07	3.96E-07	173
hsa05012	Parkinson disease	193/4719	266/8390	1.81E-08	1.98E-06	1.35E-06	193
hsa03010	Ribosome	128/4719	167/8390	2.38E-08	1.98E-06	1.35E-06	128
hsa05014	Amyotrophic lateral sclerosis	253/4719	364/8390	7.82E-08	5.23E-06	3.56E-06	253
hsa05020	Prion disease	195/4719	273/8390	1.10E-07	6.12E-06	4.17E-06	195
hsa03050	Proteasome	42/4719	46/8390	2.03E-07	9.20E-06	6.26E-06	42
hsa04514	Cell adhesion molecules	119/4719	157/8390	2.20E-07	9.20E-06	6.26E-06	119
hsa03030	DNA replication	34/4719	36/8390	3.95E-07	1.47E-05	9.98E-06	34
hsa05010	Alzheimer disease	259/4719	384/8390	2.89E-06	9.64E-05	6.57E-05	259
hsa05016	Huntington disease	208/4719	306/8390	1.27E-05	0.000386	0.000263	208
hsa04727	GABAergic synapse	69/4719	89/8390	2.12E-05	0.000591	0.000402	69
hsa04080	Neuroactive ligand-receptor interaction	244/4719	367/8390	2.74E-05	0.000704	0.000479	244
hsa04723	Retrograde endocannabinoid signaling	107/4719	148/8390	3.58E-05	0.000854	0.000581	107

hsa05323	Rheumatoid arthritis	71/4719	93/8390	4.09E-05	0.00091	0.00062	71
hsa05132	Salmonella infection	170/4719	249/8390	5.39E-05	0.001125	0.000766	170
hsa01230	Biosynthesis of amino acids	58/4719	75/8390	0.00011	0.002151	0.001465	58
hsa01200	Carbon metabolism	84/4719	115/8390	0.000135	0.002512	0.00171	84
hsa04060	Cytokine-cytokine receptor interaction	196/4719	295/8390	0.000177	0.003109	0.002116	196
hsa04024	cAMP signaling pathway	152/4719	225/8390	0.00029	0.004595	0.003128	152

Supplementary Table 4 Top 20 key proteins in cell adhesion molecules ranked by MCC method

Rank	Name	Score
1	ITGAM	1.34E+14
2	PTPRC	1.34E+14
3	CD8A	1.34E+14
4	CD86	1.34E+14
5	CD80	1.34E+14
6	ICAM1	1.34E+14
7	CTLA4	1.34E+14
8	CD28	1.34E+14
9	SELL	1.33E+14
10	ITGA4	1.32E+14
11	CD2	1.32E+14
12	NCAM1	1.32E+14
13	PECAM1	1.28E+14
14	SPN	1.26E+14
15	ITGAL	9.06E+13
16	CD34	8.87E+13
17	CD40LG	6.77E+13
18	ITGB1	6.63E+13
19	ITGB2	4.54E+13
20	SDC1	4.34E+13

Supplementary Table 5 Top 20 key proteins in cadherin binding ranked by MCC method

Rank	Name	Score
1	CTNNB1	1.22E+17
2	CDH1	1.22E+17

3	CTNNA1	1.22E+17
4	CDH17	1.22E+17
5	CDH5	1.22E+17
6	CDH2	1.22E+17
7	CDH4	1.22E+17
8	CDH20	1.22E+17
9	CDH10	1.22E+17
9	CDH18	1.22E+17
11	CDH11	1.22E+17
12	CDH13	1.22E+17
13	CDH22	1.22E+17
14	CDH7	1.22E+17
14	CDH6	1.22E+17
16	CDH3	1.22E+17
17	CDH8	1.22E+17
18	CDH19	1.22E+17
18	DCHS1	1.22E+17
18	CDH23	1.22E+17