

Table S1 The complete list of the 38 EGCG-related genes

#	EGCG-related genes
1	<i>MMP3</i>
2	<i>PLAU</i>
3	<i>PRKCG</i>
4	<i>MMP13</i>
5	<i>DNMT1</i>
6	<i>MMP7</i>
7	<i>PCNA</i>
8	<i>TIMP1</i>
9	<i>CXCL8</i>
10	<i>TERT</i>
11	<i>CSF2</i>
12	<i>BIRC5</i>
13	<i>CDKN2A</i>
14	<i>STAT1</i>
15	<i>CYP3A4</i>
16	<i>MMP1</i>
17	<i>CDK6</i>
18	<i>PDGFRB</i>
19	<i>KAT2B</i>
20	<i>APOB</i>
21	<i>IGFBP3</i>
22	<i>KRT18</i>
23	<i>PTGS1</i>
24	<i>IVL</i>
25	<i>MMP9</i>
26	<i>SLC2A4</i>
27	<i>UGT1A1</i>
28	<i>HDC</i>
29	<i>EGR1</i>
30	<i>ELANE</i>
31	<i>CDKN1A</i>
32	<i>MAPK10</i>
33	<i>CYP1A1</i>
34	<i>AR</i>
35	<i>MAPT</i>
36	<i>FOS</i>
37	<i>CAV1</i>
38	<i>PRKCB</i>

Table S2 The KEGG table

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
hsa05161	Hepatitis B	10/38	163/9446	5.54E-10	1.10E-07	5.19E-08	10
hsa04657	IL-17 signaling pathway	8/38	95/9446	2.96E-09	2.95E-07	1.39E-07	8
hsa05166	Human T-cell leukemia virus 1 infection	9/38	224/9446	1.81E-07	1.20E-05	5.65E-06	9
hsa05171	Coronavirus disease - COVID-19	9/38	238/9446	3.03E-07	1.51E-05	7.10E-06	9
hsa05214	Glioma	6/38	76/9446	5.00E-07	1.79E-05	8.45E-06	6
hsa05219	Bladder cancer	5/38	41/9446	5.41E-07	1.79E-05	8.45E-06	5
hsa05202	Transcriptional misregulation in cancer	8/38	201/9446	1.03E-06	2.94E-05	1.38E-05	8
hsa05417	Lipid and atherosclerosis	8/38	216/9446	1.78E-06	4.07E-05	1.92E-05	8
hsa05207	Chemical carcinogenesis - receptor activation	8/38	217/9446	1.84E-06	4.07E-05	1.92E-05	8
hsa05215	Prostate cancer	6/38	106/9446	3.57E-06	6.50E-05	3.06E-05	6
hsa05206	MicroRNAs in cancer	9/38	320/9446	3.60E-06	6.50E-05	3.06E-05	9
hsa04928	Parathyroid hormone synthesis, secretion and action	6/38	115/9446	5.74E-06	9.52E-05	4.48E-05	6
hsa04935	Growth hormone synthesis, secretion and action	6/38	122/9446	8.08E-06	0.000124	5.82E-05	6
hsa05223	Non-small cell lung cancer	5/38	73/9446	9.88E-06	0.00014	6.61E-05	5
hsa05167	Kaposi sarcoma-associated herpesvirus infection	7/38	196/9446	1.09E-05	0.000144	6.80E-05	7
hsa05212	Pancreatic cancer	5/38	77/9446	1.28E-05	0.00016	7.52E-05	5
hsa05323	Rheumatoid arthritis	5/38	95/9446	3.57E-05	0.000418	0.000197	5
hsa01522	Endocrine resistance	5/38	99/9446	4.36E-05	0.000457	0.000215	5
hsa05231	Choline metabolism in cancer	5/38	99/9446	4.36E-05	0.000457	0.000215	5
hsa04933	AGE-RAGE signaling pathway in diabetic complications	5/38	101/9446	4.80E-05	0.000478	0.000225	5

Table S3 The GO table

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
GO:0009416	response to light stimulus	10/38	323/18614	6.62E-10	6.60E-07	4.17E-07	10
GO:0009411	response to UV	8/38	154/18614	7.24E-10	6.60E-07	4.17E-07	8
GO:0009314	response to radiation	11/38	452/18614	1.02E-09	6.60E-07	4.17E-07	11
GO:0033002	muscle cell proliferation	9/38	249/18614	1.38E-09	6.68E-07	4.23E-07	9
GO:0048660	regulation of smooth muscle cell proliferation	8/38	176/18614	2.09E-09	7.49E-07	4.74E-07	8
GO:0048659	smooth muscle cell proliferation	8/38	180/18614	2.50E-09	7.49E-07	4.74E-07	8
GO:0022617	extracellular matrix disassembly	6/38	62/18614	2.71E-09	7.49E-07	4.74E-07	6
GO:0071492	cellular response to UV-A	4/38	11/18614	4.82E-09	1.17E-06	7.38E-07	4
GO:0070141	response to UV-A	4/38	14/18614	1.46E-08	3.13E-06	1.98E-06	4
GO:0030574	collagen catabolic process	5/38	45/18614	3.11E-08	5.65E-06	3.57E-06	5
GO:0034644	cellular response to UV	6/38	93/18614	3.21E-08	5.65E-06	3.57E-06	6
GO:0048661	positive regulation of smooth muscle cell proliferation	6/38	99/18614	4.67E-08	7.54E-06	4.77E-06	6
GO:0032963	collagen metabolic process	6/38	108/18614	7.87E-08	1.17E-05	7.42E-06	6
GO:0071478	cellular response to radiation	7/38	191/18614	1.03E-07	1.43E-05	9.05E-06	7
GO:0071482	cellular response to light stimulus	6/38	127/18614	2.07E-07	2.67E-05	1.69E-05	6
GO:0070482	response to oxygen levels	8/38	333/18614	2.96E-07	3.58E-05	2.26E-05	8
GO:0071214	cellular response to abiotic stimulus	8/38	339/18614	3.38E-07	3.64E-05	2.30E-05	8
GO:0104004	cellular response to environmental stimulus	8/38	339/18614	3.38E-07	3.64E-05	2.30E-05	8
GO:0072203	cell proliferation involved in metanephros development	3/38	10/18614	9.33E-07	9.51E-05	6.01E-05	3
GO:0001666	response to hypoxia	7/38	293/18614	1.85E-06	0.000177	0.000112	7

Table S4 The multivariate Cox regression table

Variable	HR	HR (95% CI)	P value
Age			
≥60 years	1.957	1.32–2.901	0.000825
Gender			
Male	1.269	0.89–1.809	0.189
Race			
Black or African American	1.097	0.421–2.863	0.85
Not reported	1.463	0.782–2.736	0.233
White	0.994	0.615–1.605	0.98
Grade			
G2	1.695	0.491–5.853	0.404
G3	1.866	0.559–6.233	0.311
GX	1.710	0.324–9.035	0.527
M			
M1	2.092	1.158–3.781	0.0145
N			
N1	1.430	0.872–2.343	0.156
N2	1.570	0.92–2.678	0.0978
N3	2.145	1.275–3.608	0.00406
NX	2.515	0.768–8.24	0.128
T			
T2	4.303	0.571–32.434	0.157
T3	5.805	0.778–43.31	0.0863
T4	5.621	0.745–42.427	0.0941
TX	16.863	1.69–168.223	0.0161
Riskscore	2.273	1.329–3.888	0.00271

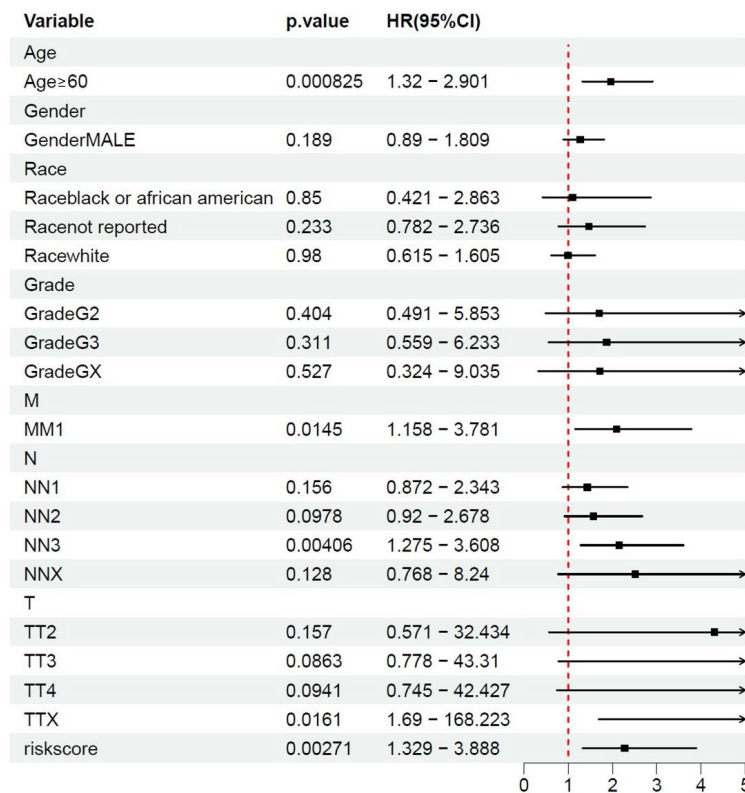


Figure S1 Forest plot showing the results of multivariate Cox regression analysis of clinicopathological variables and risk score for overall survival in gastric cancer patients. The hazard ratios (HRs) and corresponding 95% confidence intervals (CIs) are shown in the forest plot. Age greater than 60 years ($P < 0.001$, 95% CI: 1.32–2.90), M1 ($P = 0.015$, 95% CI: 1.16–3.78), TX ($P = 0.016$, 95% CI: 1.69–168.2), and risk score ($P = 0.003$, 95% CI: 1.33–3.89). No significant associations were observed for the remaining clinicopathological variables ($P > 0.05$).

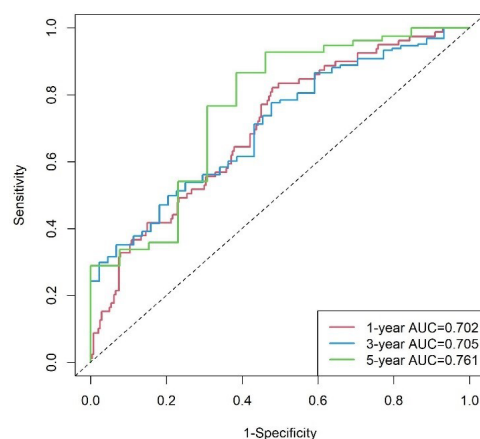


Figure S2 Time-dependent ROC analysis yielded AUC values of 0.702, 0.705, and 0.761 for predicting 1-, 3-, and 5-year overall survival of the integrated prognostic model.

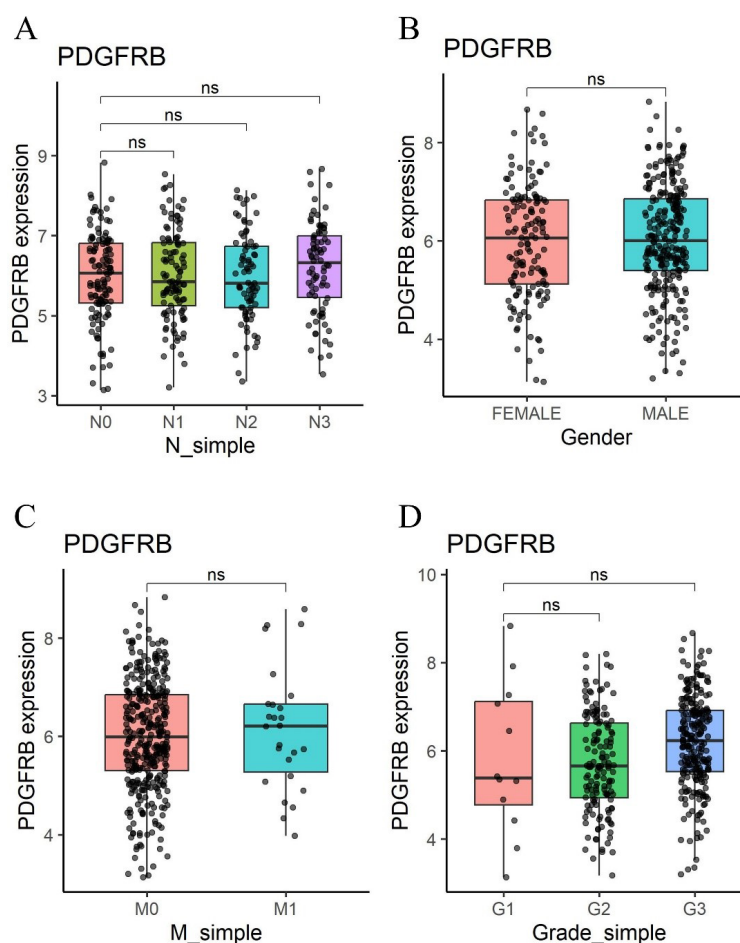


Figure S3 Association between PDGFRB expression and clinicopathological characteristics in gastric cancer patients. Boxplots showing the association between PDGFRB expression and clinicopathological variables in gastric cancer patients. (A) Comparison of PDGFRB expression among lymph node metastasis stages. No significant differences were observed between N1–N3 stages and N0 stage ($P>0.05$). (B) Comparison of PDGFRB expression between female and male patients, showing no significant difference ($P>0.05$). (C) Comparison of PDGFRB expression between M1 and M0 stages, which did not reveal a statistically significant difference ($P>0.05$). (D) Comparison of PDGFRB expression across tumor grades. No significant differences were observed between G2–G3 and G1 ($P>0.05$).

Table S5 Dunn's post hoc multiple comparisons of PDGFRB expression among TCGA gastric cancer molecular subtypes

Comparison	Z	P.adj
CIN-EBV	-0.086	0.93
CIN-GS	-3.64	0.002
EBV-GS	-2.39	0.034
CIN-MSI	0.42	1.000
EBV-MSI	0.36	0.86
GS-MSI	3.41	0.002

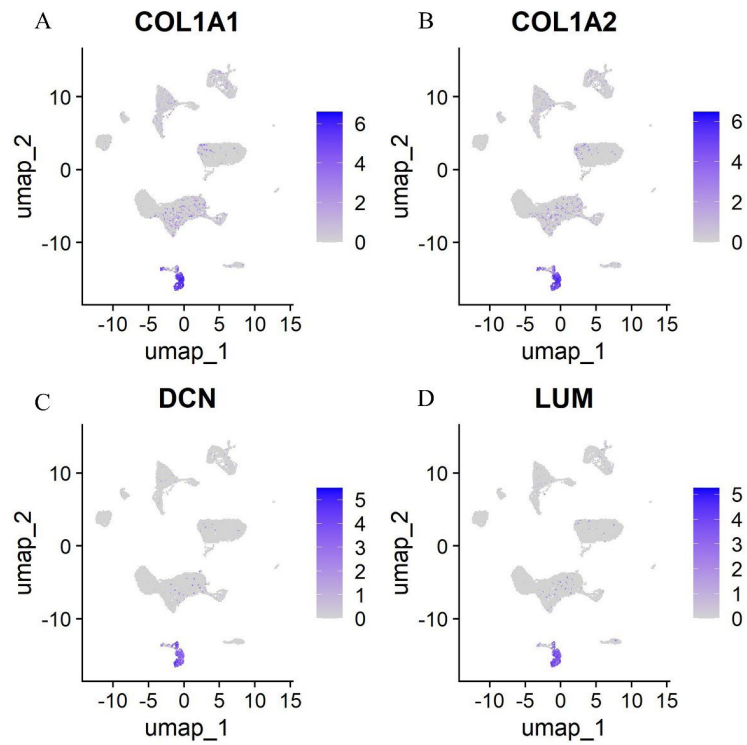


Figure S4 Validation of cancer-associated fibroblast (CAF) annotation using canonical marker genes (*COL1A1*, *COL1A2*, *DCN*, and *LUM*) (A-D).

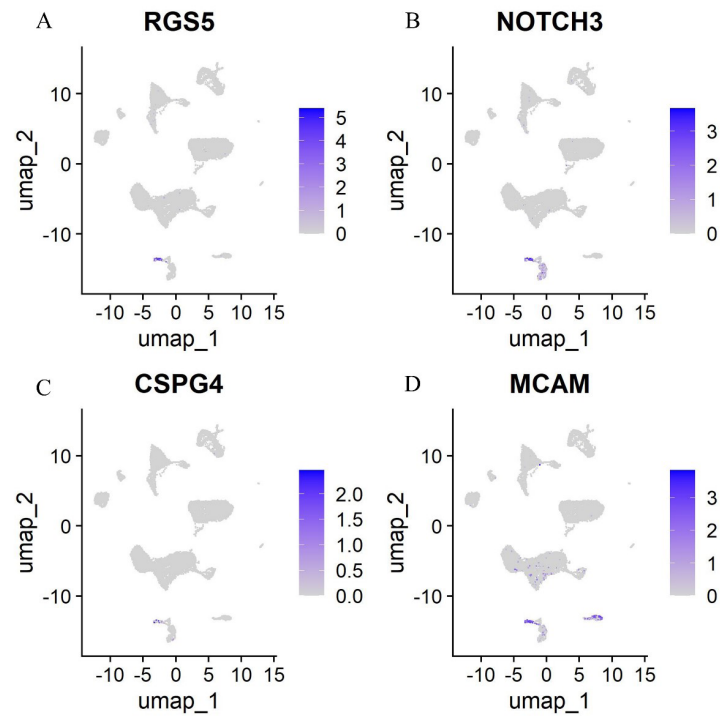


Figure S5 Validation of pericyte annotation using canonical marker genes (*RGS5*, *NOTCH3*, *CSPG4*, and *MCAM*) (A-D).

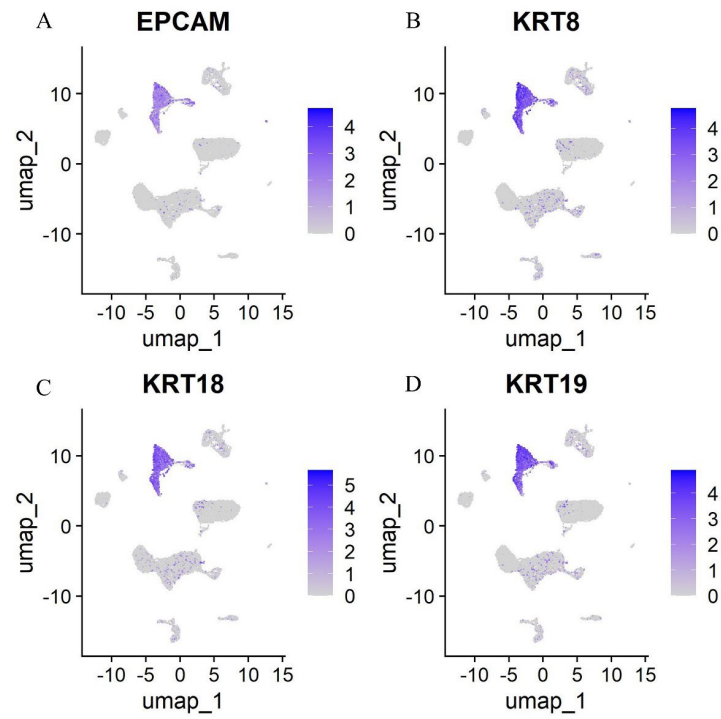


Figure S6 Validation of epithelial cell annotation using canonical marker genes (*EPCAM*, *KRT8*, *KRT18*, and *KRT19*) (A-D).

Table S6 The expression of HGC27 and AGS in depmap cell line

Depmap ID	Cell Line Name	Lineage	Expression Public 26Q1
ACH-000847	HGC27	Esophagus/Stomach	2.243742
ACH-000880	AGS	Esophagus/Stomach	0.26704

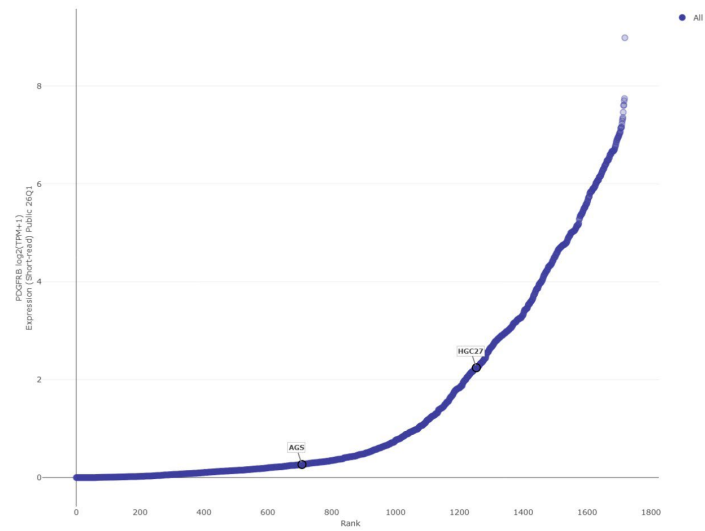


Figure S7 The ranked expression of HGC-27 and AGS in DepMap. HGC-27 cells exhibited substantially higher PDGFRB expression than AGS cells [$\log_2(\text{TPM}+1)$; 2.24 vs. 0.27].