Supplementary Figures

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	PPAR signaling pathway	4.636e-10	1.405e-7	6.16	132.32
2	Focal adhesion	1.054e-9	1.597e-7	3.41	70.58
3	Human papillomavirus infection	5.677e-8	0.000005734	2.51	41.84
4	PI3K-Akt signaling pathway	8.236e-8	0.000006239	2.42	39.55
5	Proteoglycans in cancer	2.011e-7	0.00001218	2.92	44.99
6	Pathways in cancer	2.913e-7	0.00001471	2.06	31.05
7	ECM-receptor interaction	0.000001791	0.00007752	4.00	52.97
8	Regulation of lipolysis in adipocytes	0.000003127	0.0001185	5.09	64.55
9	Adherens junction	0.000004954	0.0001668	4.28	52.26
10	AMPK signaling pathway	0.00002270	0.0006879	3.05	32.66
11	Prostate cancer	0.00003111	0.0008568	3.31	34.36
12	MAPK signaling pathway	0.00006869	0.001734	2.09	20.03
13	Tight junction	0.00009985	0.002327	2.48	22.80
14	Malaria	0.0001178	0.002468	4.28	38.71
15	Rap1 signaling pathway	0.0001222	0.002468	2.27	20.46
16	Axon guidance	0.0001387	0.002572	2.37	21.07
17	Ras signaling pathway	0.0001443	0.002572	2.18	19.29
18	Notch signaling pathway	0.0001579	0.002658	3.83	33.53
19	cAMP signaling pathway	0.0002028	0.003234	2.20	18.68
20	Melanoma	0.0003604	0.005460	3.27	25.94
21	Breast cancer	0.0004899	0.007069	2.39	18.22
22	Fatty acid degradation	0.0005650	0.007782	4.10	30.67
23	Phenylalanine metabolism	0.0006890	0.009077	7.37	53.66
24	Transcriptional misregulation in cancer	0.0007688	0.009706	2.13	15.27
25	Glucagon signaling pathway	0.001047	0.01269	2.56	17.58
26	Insulin resistance	0.001164	0.01331	2.53	17.12
27	Pyruvate metabolism	0.001186	0.01331	3.66	24.64
28	Protein digestion and absorption	0.001846	0.01998	2.49	15.69
29	TGF-beta signaling pathway	0.001926	0.02013	2.57	16.09
30	Adipocytokine signaling pathway	0.002537	0.02562	2.85	17.03

Figure S1. Pathway enrichment analysis of DEGs in grade I tumors. The most significantly enriched biological pathways are associated with the PPAR signaling pathway, Focal adhesion, and human papillomavirus infection.

ndex	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	Focal adhesion	2.819e-12	8.597e-10	3.51	93.29
2	Pathways in cancer	1.447e-9	1.848e-7	2.12	43.16
3	Rap1 signaling pathway	1.818e-9	1.848e-7	2.97	59.83
4	Tight junction	3.534e-9	2.695e-7	3.22	62.74
5	Proteoglycans in cancer	7.056e-9	4.304e-7	2.90	54.48
6	ECM-receptor interaction	1.928e-8	9.802e-7	4.30	76.31
7	PI3K-Akt signaling pathway	5.504e-8	0.000002398	2.24	37.50
8	Adherens junction	6.975e-8	0.000002659	4.64	76.52
9	AGE-RAGE signaling pathway in diabetic complications	9.498e-8	0.000003219	3.77	61.02
10	Human papillomavirus infection	2.647e-7	0.000008074	2.21	33.43
11	Leukocyte transendothelial migration	5.316e-7	0.00001474	3.31	47.83
12	MAPK signaling pathway	6.175e-7	0.00001570	2.25	32.10
13	Complement and coagulation cascades	0.000002486	0.00005833	3.59	46.36
14	PPAR signaling pathway	0.000002934	0.00006391	3.83	48.85
15	Regulation of lipolysis in adipocytes	0.000007207	0.0001465	4.32	51.20
16	Axon guidance	0.00003560	0.0006787	2.31	23.66
17	Relaxin signaling pathway	0.00006001	0.001056	2.56	24.92
18	Ras signaling pathway	0.00006231	0.001056	2.08	20.18
19	Regulation of actin cytoskeleton	0.00007077	0.001101	2.11	20.21
20	Pyruvate metabolism	0.00007222	0.001101	4.10	39.05
21	Fluid shear stress and atherosclerosis	0.00008995	0.001306	2.44	22.76
22	Endocytosis	0.00009660	0.001339	2.00	18.47
23	Fatty acid degradation	0.0001098	0.001388	4.18	38.12
24	Transcriptional misregulation in cancer	0.0001105	0.001388	2.16	19.69
25	Cell adhesion molecules	0.0001138	0.001388	2.36	21.43
26	Malaria	0.0001513	0.001775	3.75	33.01
27	Apelin signaling pathway	0.0001745	0.001971	2.38	20.56
28	cGMP-PKG signaling pathway	0.0001897	0.002066	2.21	18.92
29	Prostate cancer	0.0002331	0.002452	2.67	22.34
30	cAMP signaling pathway	0.0002646	0.002573	2.00	16.51

Figure S2. Pathway enrichment analysis of DEGs in grade II tumors. Enriched pathways are predominantly involved in focal adhesion, pathways in cancer, Rap1 signaling pathway.

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	Focal adhesion	3.295e-14	1.015e-11	3.80	118.02
2	PI3K-Akt signaling pathway	7.148e-13	1.101e-10	2.77	77.51
3	Pathways in cancer	1.191e-12	1.223e-10	2.36	64.85
4	Proteoglycans in cancer	1.353e-11	1.042e-9	3.34	83.60
5	Rap1 signaling pathway	3.733e-10	2.299e-8	3.07	66.61
6	Regulation of lipolysis in adipocytes	1.335e-8	6.259e-7	5.86	106.17
7	Ras signaling pathway	1.422e-8	6.259e-7	2.69	48.64
8	Prostate cancer	7.009e-8	0.000002699	3.85	63.49
9	MAPK signaling pathway	9.041e-8	0.000003094	2.35	38.11
10	Phospholipase D signaling pathway	1.328e-7	0.000003997	3.06	48.43
11	AGE-RAGE signaling pathway in diabetic complications	1.427e-7	0.000003997	3.69	58.21
12	ECM-receptor interaction	4.854e-7	0.00001076	3.76	54.72
13	Human papillomavirus infection	5.145e-7	0.00001076	2.16	31.27
14	Signaling pathways regulating pluripotency of stem cells	5.209e-7	0.00001076	2.97	42.90
15	Tight junction	5.241e-7	0.00001076	2.76	39.91
16	FoxO signaling pathway	5.859e-7	0.00001128	3.07	44.07
17	Fatty acid degradation	0.000001073	0.00001944	5.61	77.05
18	Regulation of actin cytoskeleton	0.000001653	0.00002828	2.41	32.06
19	Adherens junction	0.000001915	0.00003104	3.98	52.38
20	Complement and coagulation cascades	0.000003458	0.00005325	3.52	44.20
21	Relaxin signaling pathway	0.000003868	0.00005674	2.88	35.85
22	Transcriptional misregulation in cancer	0.000005369	0.00007516	2.42	29.41
23	Leukocyte transendothelial migration	0.000008076	0.0001062	2.94	34.51
24	Breast cancer	0.000008273	0.0001062	2.64	30.91
25	Insulin resistance	0.000008619	0.0001062	3.01	35.05
26	Axon guidance	0.000009064	0.0001074	2.42	28.15
27	Calcium signaling pathway	0.000009730	0.0001110	2.20	25.34
28	Fluid shear stress and atherosclerosis	0.00001866	0.0002052	2.61	28.43
29	Tryptophan metabolism	0.00002187	0.0002323	4.72	50.70
30	Prolactin signaling pathway	0.00002283	0.0002344	3.53	37.67

Figure S3. Pathway enrichment analysis of DEGs in grade III tumors. The analysis reveals significant enrichment in pathways related to focal adhesion, the PI3K-Akt signaling pathway, and pathways in cancer.

Supplementary Table 1. Top-scoring modules identified by Molecular Complex Detection (MCODE) analysis in the Grade II and Grade III PPI networks.
The highest-scoring module in the Grade III network showed a slightly greater number of nodes and edges, as well as a higher MCODE score, compared with the corresponding module in the Grade II network, indicating a denser local interaction pattern.

Grade	Module	Nodes	Edges	MCODE score
Grade II	Highest-scoring module	27	321	24.692
Grade III	Highest-scoring module	29	379	27.071