

**Table S1:** Normalized expression of angiogenesis-associated genes in endometrial cancer tissues and adjacent control tissues. Endometrial cancer tissue, n= up to 548; adjacent control tissue, n= up to 35; paired samples, n= up to 23. Data are from the GDC TCGA Endometrioid Cancer (UCEC) study, downloaded from UCSC Xena server [1]. FC, fold change; FR, fold-regulation.

GENE	tissue	AVERAGE (log2 value)	EXPRESSION (antilog value)	FC (tumor/normal)	FR (tumor/normal)	p-value <sup>†</sup>		Adjusted p-value <sup>‡</sup>
<b>ADAMTS1</b>	normal	19.884	967565.632	0.2	<b>-4.2</b>	<0.0001	****	0.0092
	tumor	17.808	229433.889					
<b>AMOT</b>	normal	16.761	111094.554	0.8	<b>-1.2</b>	0.6811	ns	1.0000
	tumor	16.494	92322.701					
<b>ANG</b>	normal	17.497	184923.805	0.4	<b>-2.5</b>	0.0024	*	0.1983
	tumor	16.193	74896.438					
<b>ANGPT1</b>	normal	13.808	14339.571	0.2	<b>-5.0</b>	<0.0001	****	0.0092
	tumor	11.491	2878.010					
<b>ANGPT2</b>	normal	15.133	35928.900	1.4	<b>1.4</b>	0.1818	ns	1.0000
	tumor	15.590	49315.816					
<b>ANGPT4</b>	normal	12.618	6285.075	0.0	<b>-20.0</b>	0.0001	***	0.0092
	tumor	8.293	313.577					
<b>ANGPTL1</b>	normal	17.757	221530.046	0.0	<b>-42.0</b>	<0.0001	****	0.0092
	tumor	12.366	5279.936					
<b>ANGPTL2</b>	normal	18.737	437046.897	0.4	<b>-2.5</b>	0.0053	*	0.3867
	tumor	17.416	174899.651					
<b>ANGPTL3</b>	normal	8.191	292.284	0.6	<b>-1.7</b>	0.8462	ns	1.0000
	tumor	7.439	173.486					
<b>ANGPTL4</b>	normal	16.188	74672.309	2.2	<b>2.2</b>	0.0010	**	0.0879
	tumor	17.294	160743.159					
<b>CD44</b>	normal	19.461	721465.773	0.5	<b>-2.0</b>	0.0018	*	0.1527
	tumor	18.482	366248.545					
<b>CDH5</b>	normal	17.758	221661.702	0.5	<b>-2.1</b>	0.0059	*	0.4198
	tumor	16.692	105871.339					
<b>CEACAM1</b>	normal	15.650	51408.321	2.1	<b>2.1</b>	0.0013	*	0.1128
	tumor	16.753	110452.435					
<b>CHGA</b>	normal	13.658	12929.945	4.9	<b>4.9</b>	0.0903	ns	0.9998
	tumor	15.954	63468.443					
<b>COL15A1</b>	normal	18.769	446583.811	0.3	<b>-3.6</b>	0.0003	**	0.0272
	tumor	16.926	124553.420					
<b>COL18A1</b>	normal	19.830	932019.103	1.4	<b>1.4</b>	0.1445	ns	1.0000
	tumor	20.346	1332877.847					
<b>COL4A1</b>	normal	19.460	721037.259	1.3	<b>1.3</b>	0.1375	ns	1.0000
	tumor	19.829	931052.923					
<b>COL4A2</b>	normal	20.637	1630470.765	0.9	<b>-1.1</b>	0.5824	ns	1.0000
	tumor	20.482	1464920.062					
<b>COL4A3</b>	normal	11.909	3846.304	0.3	<b>-3.5</b>	0.0021	*	0.1759
	tumor	10.088	1088.272					
<b>CSF3</b>	normal	13.165	9183.501	0.4	<b>-2.2</b>	0.5399	ns	1.0000
	tumor	12.010	4123.395					
<b>CXCL10</b>	normal	15.957	63605.202	3.6	<b>3.6</b>	0.0301	*	0.9399
	tumor	17.801	228368.422					
<b>CXCL12</b>	normal	19.761	888756.433	0.1	<b>-16.8</b>	<0.0001	****	0.0092
	tumor	15.690	52854.045					
<b>CXCL2</b>	normal	16.282	79668.086	0.6	<b>-1.7</b>	0.0360	*	0.9657
	tumor	15.543	47742.343					
<b>CXCL8</b>	normal	14.040	16840.281	4.4	<b>4.4</b>	0.0163	*	0.7795
	tumor	16.172	73816.282					
<b>EDIL3</b>	normal	16.950	126607.207	0.2	<b>-4.8</b>	0.0006	***	0.0537
	tumor	14.675	26155.267					
<b>ENPP2</b>	normal	19.099	561584.214	0.2	<b>-5.9</b>	<0.0001	****	0.0092
	tumor	16.534	94865.434					
<b>EPHB2</b>	normal	14.342	20766.925	1.8	<b>1.8</b>	0.0475	*	0.9886
	tumor	15.188	37333.766					
<b>F2</b>	normal	7.274	154.803	3.8	<b>3.8</b>	0.0462	*	0.9871
	tumor	9.184	581.475					
<b>FBLN5</b>	normal	19.774	896712.333	0.2	<b>-4.7</b>	<0.0001	****	0.0092
	tumor	17.533	189668.482					
<b>FGA</b>	normal	5.820	56.506	1.2	<b>1.2</b>	0.4038	ns	1.0000
	tumor	6.110	69.082					
<b>FGF1</b>	normal	14.245	19410.793	0.6	<b>-1.6</b>	0.1404	ns	1.0000
	tumor	13.560	12078.374					
<b>FGF2</b>	normal	17.137	144114.617	0.1	<b>-17.5</b>	<0.0001	****	0.0092

	tumor	13.011	8256.851					
<b>FGF4</b>	normal	1.657	3.153	17.6	<b>17.6</b>	0.0002	**	0.0182
	tumor	5.797	55.601					
<b>FLT1</b>	normal	16.605	99668.994	0.6	<b>-1.5</b>	0.2861	ns	1.0000
	tumor	15.981	64680.363					
<b>FLT4</b>	normal	16.689	105665.351	0.2	<b>-4.4</b>	<0.0001	****	0.0092
	tumor	14.542	23857.166					
<b>FN1</b>	normal	19.485	734004.087	0.5	<b>-1.9</b>	0.0005	**	0.0450
	tumor	18.585	393101.896					
<b>FOXC2</b>	normal	12.487	5740.770	0.1	<b>-7.4</b>	0.0004	***	0.0361
	tumor	9.591	771.094					
<b>FST</b>	normal	14.996	32677.274	0.3	<b>-3.1</b>	0.0027	*	0.2202
	tumor	13.341	10378.578					
<b>GAPDH</b>	normal	23.141	9248943.477	3.3	<b>3.3</b>	<0.0001	****	0.0092
	tumor	24.852	30278073.390					
<b>GRN</b>	normal	20.833	1868103.370	2.2	<b>2.2</b>	<0.0001	****	0.0092
	tumor	21.985	4150920.873					
<b>GUSB</b>	normal	18.738	437133.460	1.3	<b>1.3</b>	0.0026	*	0.2130
	tumor	19.099	561562.702					
<b>HEY1</b>	normal	15.225	38302.285	1.9	<b>1.9</b>	0.0135	*	0.7136
	tumor	16.124	71419.620					
<b>HGF</b>	normal	14.429	22055.596	0.1	<b>-7.2</b>	0.0049	**	0.3636
	tumor	11.571	3042.247					
<b>HPRT1</b>	normal	18.324	328215.925	1.6	<b>1.6</b>	<0.0001	****	0.0092
	tumor	18.972	514135.221					
<b>HSPG2</b>	normal	18.820	462790.589	0.6	<b>-1.8</b>	<0.0001	****	0.0092
	tumor	17.982	258976.830					
<b>IFNB1</b>	normal	2.488	5.611	3.0	<b>3.0</b>	0.8040	ns	1.0000
	tumor	4.072	16.824					
<b>IFNG</b>	normal	8.361	328.765	3.7	<b>3.7</b>	0.8117	ns	1.0000
	tumor	10.258	1224.777					
<b>IL12A</b>	normal	13.049	8472.497	0.5	<b>-2.1</b>	0.0059	**	0.4198
	tumor	11.978	4032.885					
<b>ITGA4</b>	normal	13.497	11562.317	1.0	<b>1.0</b>	0.6705	ns	1.0000
	tumor	13.553	12019.608					
<b>ITGAV</b>	normal	18.555	385171.880	0.5	<b>-2.0</b>	<0.0001	****	0.0092
	tumor	17.559	193137.673					
<b>ITGB3</b>	normal	14.869	29926.643	0.3	<b>-3.8</b>	<0.0001	****	0.0092
	tumor	12.935	7830.747					
<b>KDR</b>	normal	17.923	248544.191	0.2	<b>-4.5</b>	<0.0001	****	0.0092
	tumor	15.749	55062.305					
<b>KIT</b>	normal	15.574	48770.268	0.3	<b>-3.1</b>	0.0027	**	0.2202
	tumor	13.920	15500.503					
<b>LEP</b>	normal	7.345	162.618	0.5	<b>-1.8</b>	0.4977	ns	1.0000
	tumor	6.459	87.976					
<b>LYVE1</b>	normal	15.873	60031.353	0.1	<b>-8.1</b>	<0.0001	****	0.0092
	tumor	12.852	7395.362					
<b>MDK</b>	normal	21.547	3063728.752	2.8	<b>2.8</b>	<0.0001	****	0.0092
	tumor	23.034	8587542.294					
<b>MMP2</b>	normal	20.978	2065005.632	0.5	<b>-2.1</b>	0.1601	ns	1.0000
	tumor	19.933	1000658.484					
<b>NRP1</b>	normal	18.221	305630.410	0.4	<b>-2.7</b>	<0.0001	****	0.0092
	tumor	16.798	113950.478					
<b>NRP2</b>	normal	17.681	210203.705	0.4	<b>-2.7</b>	<0.0001	****	0.0092
	tumor	16.244	77609.283					
<b>PDGFB</b>	normal	17.273	158392.320	0.8	<b>-1.3</b>	0.0709	ns	0.9988
	tumor	16.946	126233.030					
<b>PDGFRA</b>	normal	17.943	251963.834	0.1	<b>-7.8</b>	<0.0001	****	0.0092
	tumor	14.981	32335.355					
<b>PDGFRB</b>	normal	19.571	778934.697	0.3	<b>-3.5</b>	<0.0001	****	0.0092
	tumor	17.759	221870.958					
<b>PECAM1</b>	normal	18.770	447026.242	0.5	<b>-2.2</b>	0.0060	**	0.4252
	tumor	17.655	206348.908					
<b>PF4</b>	normal	8.441	347.573	1.3	<b>1.3</b>	0.9240	ns	1.0000
	tumor	8.780	439.655					
<b>PLG</b>	normal	9.464	706.443	0.4	<b>-2.4</b>	0.0006	***	0.0537
	tumor	8.179	289.783					
<b>PRL</b>	normal	9.380	666.353	0.8	<b>-1.2</b>	0.9854	ns	1.0000
	tumor	9.123	557.511					
<b>PROK1</b>	normal	10.540	1488.603	0.4	<b>-2.5</b>	0.7928	ns	1.0000
	tumor	9.198	587.189					

<i>PROX1</i>	normal	14.241	19368.553	0.2	<b>-4.2</b>	0.0007	***	0.0624
	tumor	12.187	4663.570					
<i>PTN</i>	normal	19.439	710688.162	0.2	<b>-4.8</b>	0.0112	*	0.6452
	tumor	17.176	148033.656					
<i>S1PR1</i>	normal	18.052	271818.800	0.2	<b>-4.1</b>	<0.0001	****	0.0092
	tumor	16.031	66968.087					
<i>SEMA3F</i>	normal	17.583	196282.419	2.0	<b>2.0</b>	0.0109	*	0.6352
	tumor	18.550	383743.030					
<i>SERPINB5</i>	normal	10.203	1178.412	7.1	<b>7.1</b>	0.0384	*	0.9727
	tumor	13.021	8310.591					
<i>SERPINC1</i>	normal	9.437	693.139	1.2	<b>1.2</b>	0.0228	*	0.8802
	tumor	9.700	831.528					
<i>SERPINF1</i>	normal	21.185	2384786.316	0.2	<b>-6.1</b>	<0.0001	****	0.0092
	tumor	18.574	390110.120					
<i>TEK</i>	normal	17.063	136936.058	0.2	<b>-5.1</b>	0.0003	***	0.0272
	tumor	14.715	26886.578					
<i>TGFA</i>	normal	14.359	21006.838	3.8	<b>3.8</b>	0.0003	***	0.0272
	tumor	16.301	80712.861					
<i>TGFB1</i>	normal	18.861	476084.173	0.7	<b>-1.5</b>	0.0035	**	0.2757
	tumor	18.276	317385.328					
<i>THBS1</i>	normal	20.091	1117178.723	0.2	<b>-5.2</b>	<0.0001	****	0.0092
	tumor	17.707	213909.694					
<i>THBS2</i>	normal	18.506	372272.623	0.2	<b>-4.5</b>	<0.0001	****	0.0092
	tumor	16.343	83126.981					
<i>TIE1</i>	normal	17.787	226140.073	0.3	<b>-3.4</b>	0.0002	***	0.0182
	tumor	16.035	67163.194					
<i>TIMP2</i>	normal	21.578	3131203.221	0.2	<b>-5.0</b>	<0.0001	****	0.0092
	tumor	19.246	621943.223					
<i>TIMP3</i>	normal	15.705	53421.870	0.1	<b>-13.6</b>	<0.0001	****	0.0092
	tumor	11.940	3927.894					
<i>TNF</i>	normal	12.937	7844.608	4.1	<b>4.1</b>	0.2861	ns	1.0000
	tumor	14.957	31798.550					
<i>TNFSF15</i>	normal	12.790	7080.887	2.5	<b>2.5</b>	0.0980	ns	0.9999
	tumor	14.106	17628.212					
<i>TNMD</i>	normal	10.790	1770.783	0.1	<b>-12.7</b>	0.0163	*	0.7795
	tumor	7.127	139.797					
<i>TNNI1</i>	normal	12.152	4552.183	2.7	<b>2.7</b>	0.0060	**	0.4252
	tumor	13.595	12370.755					
<i>TYMP</i>	normal	16.785	112958.129	3.4	<b>3.4</b>	0.0484	*	0.9896
	tumor	18.556	385435.889					
<i>VASH1</i>	normal	16.613	100243.062	0.5	<b>-1.9</b>	<0.0001	****	0.0092
	tumor	15.658	51721.819					
<i>VEGFA</i>	normal	17.265	157547.635	1.5	<b>1.5</b>	0.0049	**	0.3636
	tumor	17.896	243967.951					
<i>VEGFB</i>	normal	20.491	1473542.400	0.9	<b>-1.1</b>	0.7202	ns	1.0000
	tumor	20.405	1388565.916					
<i>VEGFC</i>	normal	17.635	203486.200	0.4	<b>-2.6</b>	0.0001	***	0.0092
	tumor	16.248	77807.831					

†Wilcoxon matched-pairs signed rank test; ‡ Bonferroni-Šidák corrections for multiple comparisons

**Table S2:** Normalized levels of angiogenesis-associated proteins in endometrial cancer tissues and adjacent control tissues (n= up to 527). Data are from the CPTAC UCEC Discovery Study – Proteome, PDC ID: PDC000125 [2]. FC, fold change; FR, fold-regulation.

PROTEIN	tissue	AVERAGE (log2 value)	PROTEIN LEVEL (antilog value)	FC (tumor/n ormal)	FR (tumor/norm al)	P-VALUE†		Adjusted p value‡
ADAMTS1	normal	0.099	1.071	1.0	1.0	0.1974	ns	1.0000
	tumor	0.122	1.088					
AMOT	normal	0.314	1.243	0.8	-1.3	0.0150	*	0.6141
	tumor	-0.068	0.954					
ANGPT2	normal	0.077	1.055	1.0	-1.0	0.9530	ns	1.0000
	tumor	0.038	1.027					
ANGPT4	normal	/	/	/	/	/		
	tumor	-0.457	0.729					
ANGPTL1	normal	0.606	1.522	0.6	-1.8	0.1094	ns	0.9993
	tumor	-0.247	0.843					
ANGPTL2	normal	1.273	2.417	0.3	-3.0	<0.0001	****	0.0063
	tumor	-0.309	0.807					
ANGPTL4	normal	0.045	1.032	1.0	1.0	0.0210	*	0.7374
	tumor	0.073	1.052					
CD44	normal	0.053	1.037	0.9	-1.1	0.6231	ns	1.0000
	tumor	-0.078	0.947					
CDH5	normal	0.575	1.489	0.5	-1.9	<0.0001	****	0.0063
	tumor	-0.366	0.776					
CEACAM1	normal	-0.366	0.776	1.4	1.4	<0.0001	****	0.0063
	tumor	0.122	1.088					
CHGA	normal	-0.031	0.979	1.6	1.6	0.1074	ns	0.9992
	tumor	0.618	1.534					
COL15A1	normal	2.227	4.681	0.2	-6.2	<0.0001	****	0.0063
	tumor	-0.404	0.756					
COL18A1	normal	1.528	2.884	0.3	-3.5	<0.0001	****	0.0063
	tumor	-0.265	0.832					
COL4A1	normal	0.808	1.751	0.4	-2.3	<0.0001	****	0.0063
	tumor	-0.364	0.777					
COL4A2	normal	0.484	1.399	0.6	-1.8	<0.0001	****	0.0063
	tumor	-0.324	0.799					
CTGF	normal	0.447	1.363	0.7	-1.5	0.0031	**	0.1777
	tumor	-0.100	0.933					
CXCL10	normal	-0.106	0.929	1.3	1.3	0.0391	*	0.9190
	tumor	0.226	1.170					
CXCL12	normal	2.612	6.112	0.1	-8.2	<0.0001	****	0.0063
	tumor	-0.427	0.744					
CXCL8	normal	-0.274	0.827	1.6	1.6	0.0457	*	0.9475
	tumor	0.406	1.325					
EDIL3	normal	0.590	1.505	0.6	-1.6	0.0034	**	0.1931
	tumor	-0.088	0.941					
ENPP2	normal	0.826	1.773	0.4	-2.3	<0.0001	****	0.0063
	tumor	-0.397	0.760					
EPHB2	normal	-0.229	0.853	1.2	1.2	0.0395	*	0.9211
	tumor	-0.022	0.985					
FBLN5	normal	1.463	2.757	0.2	-4.0	<0.0001	****	0.0063
	tumor	-0.553	0.682					
FGA	normal	0.377	1.298	0.6	-1.6	0.0035	**	0.1982
	tumor	-0.289	0.819					
FGF1	normal	0.505	1.419	0.6	-1.6	<0.0001	****	0.0063
	tumor	-0.187	0.879					
FGF2	normal	2.263	4.800	0.1	-7.4	<0.0001	****	0.0063
	tumor	-0.617	0.652					
FGF4	normal	-0.292	0.817	1.8	1.8	0.2500	ns	1.0000
	tumor	0.564	1.478					
FLT1	normal	0.533	1.447	0.6	-1.6	<0.0001	****	0.0063
	tumor	-0.113	0.925					
FN1	normal	0.464	1.379	0.6	-1.6	0.0211	*	0.7391
	tumor	-0.222	0.857					

FST	normal	1.556	2.940	0.2	-4.8	<0.0001	****	0.0063
	tumor	-0.707	0.613					
GRN	normal	-0.307	0.808	1.4	1.4	<0.0001	****	0.0063
	tumor	0.167	1.122					
HGF	normal	1.377	2.597	0.3	-3.7	<0.0001	****	0.0063
	tumor	-0.494	0.710					
HSPG2	normal	1.611	3.055	0.3	-3.7	<0.0001	****	0.0063
	tumor	-0.265	0.832					
ITGA4	normal	-0.023	0.984	1.1	1.1	0.0965	ns	0.9983
	tumor	0.070	1.050					
ITGAV	normal	-0.277	0.825	1.1	1.1	0.0087	**	0.4233
	tumor	-0.079	0.946					
ITGB3	normal	0.156	1.115	0.8	-1.2	0.3165	ns	1.0000
	tumor	-0.155	0.898					
LEP	normal	0.485	1.399	0.6	-1.6	0.0938	ns	0.9980
	tumor	-0.191	0.876					
LYVE1	normal	1.286	2.439	0.3	-3.2	<0.0001	****	0.0063
	tumor	-0.371	0.773					
MDK	normal	-0.081	0.946	1.2	1.2	0.0048	**	0.2615
	tumor	0.190	1.141					
MMP2	normal	0.741	1.672	0.5	-2.2	0.0001	***	0.0063
	tumor	-0.382	0.767					
NRP1	normal	0.245	1.185	0.7	-1.5	<0.0001	****	0.0063
	tumor	-0.373	0.772					
NRP2	normal	0.260	1.198	0.8	-1.3	0.0604	ns	0.9803
	tumor	-0.090	0.940					
PDGFRA	normal	0.826	1.773	0.4	-2.6	0.0313	*	0.8651
	tumor	-0.557	0.680					
PDGFRB	normal	0.831	1.779	0.4	-2.3	<0.0001	****	0.0063
	tumor	-0.361	0.779					
PECAM1	normal	0.551	1.465	0.5	-1.8	0.0001	***	0.0063
	tumor	-0.312	0.806					
PF4	normal	0.311	1.241	0.8	-1.3	0.3449	ns	1.0000
	tumor	-0.093	0.938					
PLG	normal	1.096	2.137	0.3	-3.1	<0.0001	****	0.0063
	tumor	-0.517	0.699					
PROX1	normal	-0.265	0.832	1.3	1.3	0.4037	ns	1.0000
	tumor	0.062	1.044					
PTN	normal	2.035	4.097	0.2	-6.4	<0.0001	****	0.0063
	tumor	-0.646	0.639					
RNASE4	normal	1.610	3.053	0.3	-3.5	<0.0001	****	0.0063
	tumor	-0.199	0.871					
SEMA3F	normal	-0.193	0.875	1.2	1.2	0.0313	*	0.8651
	tumor	0.121	1.087					
SERPINB5	normal	-0.183	0.881	1.7	1.7	0.0691	ns	0.9890
	tumor	0.571	1.486					
SERPINC1	normal	1.913	3.766	0.2	-5.3	<0.0001	****	0.0063
	tumor	-0.487	0.713					
SERPINF1	normal	1.399	2.637	0.3	-3.3	<0.0001	****	0.0063
	tumor	-0.329	0.796					
TGFA	normal	0.394	1.314	0.6	-1.5	0.9999	ns	1.0000
	tumor	-0.236	0.849					
TGFB1	normal	0.162	1.119	0.8	-1.3	0.0025	**	0.1459
	tumor	-0.184	0.880					
THBS1	normal	0.428	1.345	0.7	-1.4	0.2799	ns	1.0000
	tumor	-0.014	0.991					
THBS2	normal	0.489	1.404	0.7	-1.4	0.0025	**	0.1459
	tumor	-0.043	0.970					
TIMP2	normal	1.088	2.126	0.4	-2.7	<0.0001	****	0.0063
	tumor	-0.367	0.775					
TIMP3	normal	2.170	4.499	0.2	-5.6	<0.0001	****	0.0063
	tumor	-0.325	0.798					
TYMP	normal	-0.807	0.572	2.3	2.3	<0.0001	****	0.0063
	tumor	0.412	1.331					
VASH1	normal	-0.011	0.993	1.0	1.0	0.9515	ns	1.0000
	tumor	0.058	1.041					

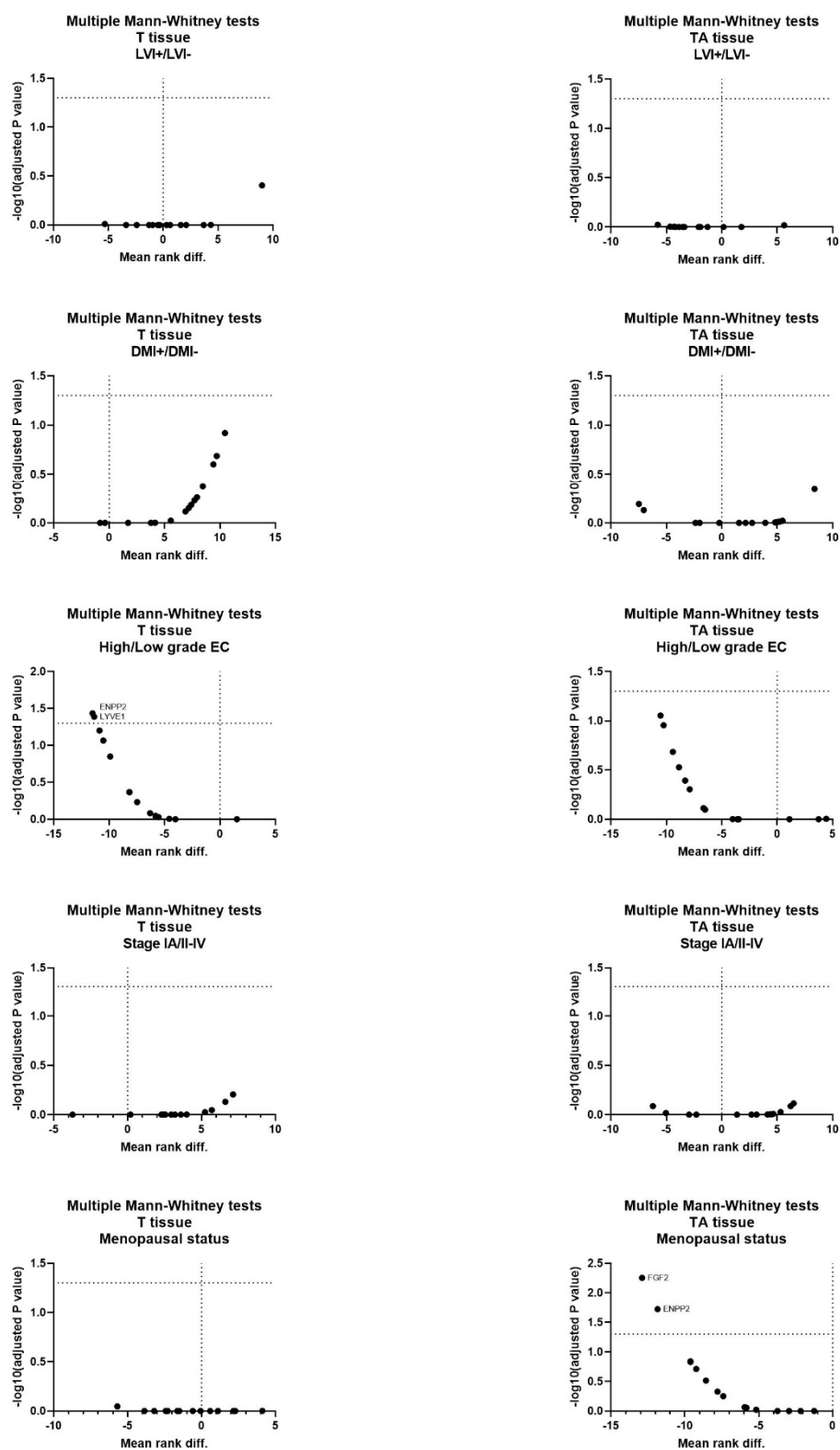
VEGFA	normal	-0.271	<b>0.829</b>	1.2	<b>1.2</b>	<b>0.1424</b>	ns	0.9999
	tumor	0.004	<b>1.003</b>					
VEGFB	normal	0.513	<b>1.427</b>	0.7	<b>-1.4</b>	<b>0.0313</b>	*	0.8651
	tumor	-0.012	<b>0.992</b>					

†Wilcoxon matched-pairs signed rank test; ‡ Bonferroni-Šidák corrections for multiple comparisons

**Table S3:** Expression of angiogenesis-associated genes in endometrial cancer tissue (n= up to 527). Data are from the TCGA Pan-Cancer study [3].

Gene	mRNA expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2)	SD	Gene	mRNA expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2)	SD
<i>MDK</i>	18267.75	14206.90	<i>TIE1</i>	395.18	351.54
<i>COL18A1</i>	16148.50	11747.65	<i>KDR</i>	390.16	342.72
<i>COL4A2</i>	12913.68	8832.25	<i>ANGPT2</i>	386.21	350.38
<i>GRN</i>	12674.28	7719.52	<i>S1PR1</i>	250.72	221.36
<i>FN1</i>	10472.11	19006.95	<i>ITGA4</i>	237.83	296.47
<i>HSPG2</i>	9320.44	6691.21	<i>ANG</i>	235.19	258.93
<i>COL4A1</i>	8674.58	7144.93	<i>FLT4</i>	198.86	165.24
<i>MMP2</i>	7478.64	8846.14	<i>ITGB3</i>	189.88	546.20
<i>CD44</i>	4761.79	7723.18	<i>VEGFC</i>	181.54	154.98
<i>TIMP2</i>	4469.03	3400.49	<i>CXCL2</i>	179.02	351.07
<i>VEGFA</i>	3642.50	2980.86	<i>KIT</i>	157.84	284.90
<i>CHGA</i>	3347.87	13011.92	<i>TEK</i>	143.39	159.57
<i>CCN2</i>	3099.48	3530.17	<i>SERPINB5</i>	136.73	307.67
<i>ITGAV</i>	2241.80	1577.89	<i>FGF2</i>	127.44	175.78
<i>THBS1</i>	2221.83	2725.16	<i>TNF</i>	127.01	254.38
<i>ADAMTS1</i>	1933.68	2453.26	<i>CSF3</i>	120.73	606.01
<i>PDGFRB</i>	1865.27	1670.35	<i>TNNI1</i>	94.68	144.80
<i>SEMA3F</i>	1814.86	1550.70	<i>ANGPTL1</i>	78.98	188.42
<i>TIMP3</i>	1811.47	2514.89	<i>FGF1</i>	77.94	89.96
<i>NRP1</i>	1686.45	1357.42	<i>EDIL3</i>	57.34	82.69
<i>VEGFB</i>	1618.82	949.99	<i>ANGPT1</i>	46.48	181.63
<i>SERPINF1</i>	1611.30	1804.28	<i>FST</i>	42.82	132.45
<i>TYMP</i>	1293.09	1450.48	<i>ADGRB1</i>	42.79	119.20
<i>NRP2</i>	1089.81	1191.26	<i>COL4A3</i>	36.83	153.65
<i>FBLN5</i>	1080.58	1195.57	<i>PROX1</i>	36.57	132.80
<i>COL15A1</i>	1077.84	1153.32	<i>LYVE1</i>	29.87	26.20
<i>AMOT</i>	1054.77	1195.04	<i>FGA</i>	22.54	132.17
<i>CEACAM1</i>	967.82	1031.49	<i>TNFSF15</i>	20.68	25.90
<i>FLT1</i>	918.18	723.83	<i>IL12A</i>	19.09	43.44
<i>ENPP2</i>	820.21	1093.42	<i>HGF</i>	17.60	45.26
<i>TGFB1</i>	810.16	646.44	<i>TNMD</i>	15.53	234.67
<i>THBS2</i>	754.77	1132.91	<i>PLG</i>	13.60	84.03
<i>PECAM1</i>	730.22	562.79	<i>F2</i>	11.62	87.36
<i>ANGPTL2</i>	718.82	582.33	<i>IFNG</i>	10.78	34.88
<i>ANGPTL4</i>	715.81	1180.25	<i>CNMD</i>	9.33	59.13
<i>PDGFRA</i>	674.74	1096.33	<i>PROK1</i>	6.59	21.46
<i>TGFA</i>	655.51	797.61	<i>VEGFD</i>	6.31	13.08
<i>EPHB2</i>	645.82	729.06	<i>PRL</i>	5.63	35.03
<i>CDH5</i>	602.33	481.09	<i>FOXC2</i>	5.45	13.20
<i>CXCL10</i>	545.38	903.37	<i>PF4</i>	3.93	11.92
<i>CXCL12</i>	540.60	743.52	<i>ANGPT4</i>	3.35	11.83
<i>PTN</i>	529.22	1027.89	<i>SERPINC1</i>	2.57	9.40
<i>PDGFB</i>	503.11	372.73	<i>FGF4</i>	2.25	15.45
<i>VASH1</i>	479.33	298.00	<i>IFNB1</i>	1.52	5.15
<i>CXCL8</i>	424.51	693.92	<i>ANGPTL3</i>	1.10	2.94
<i>RNASE4</i>	421.10	457.71	<i>LEP</i>	0.91	2.55
<i>HEY1</i>	408.30	640.72			

**Figure S1:** Volcano plots identifying significant changes in gene expression within the tumour and tumour-adjacent tissue separately, in EC patients stratified according to the presence of LVI or DMI, EC grade, FIGO stage, and menopausal status.





**Table S4:** The calculated distribution fit correlation with the original data, including the p-values and estimated upper and lower bounds for the 95% confidence intervals for the TCGA dataset. All results are significant at  $p < 0.001$ .

DATA POINT	A	B	CORRELATION COEFFICIENT	P-VALUE	LOWER BOUND	UPPER BOUND
T_IL8	0.865526	0.002878	0.905640	0.0000	0.821542	0.951169
T_CXCL12	0.794219	0.000954	0.789788	0.0000	0.622871	0.887929
T_FGF2	1.071074	0.000068	0.675944	0.0000	0.446581	0.821948
T_LEP	2.084855	0.000000	0.819681	0.0000	0.672152	0.904610
T_LYVE1	0.630536	0.000004	0.605505	0.0001	0.345750	0.779062
T_NRP1	1.581737	0.000020	0.830570	0.0000	0.690435	0.910623
T_TIMP2	1.476134	0.000019	0.847401	0.0000	0.719050	0.919850
T_TIMP3	0.666441	0.000051	0.778116	0.0000	0.603981	0.881345
T_CSF3	0.718792	0.000000	0.858897	0.0000	0.738849	0.926106
T_ENPP2	0.884903	0.000169	0.879080	0.0000	0.774116	0.937001
T_FBLN5	1.199094	0.000026	0.917302	0.0000	0.842739	0.957330
T_FST	0.642057	0.000000	0.768969	0.0000	0.589314	0.876158
T_PDGFRB	1.519883	0.000012	0.815921	0.0000	0.665881	0.902526
T_TEK	1.075751	0.000006	0.774892	0.0000	0.598798	0.879520
T_SERPINF1	1.082361	0.000075	0.912356	0.0000	0.833721	0.954722
TA_IL8	0.714176	0.001788	0.821890	0.0000	0.675846	0.905833
TA_CXCL12	2.376653	0.001271	0.955058	0.0000	0.912992	0.977030
TA_FGF2	2.363325	0.000102	0.927692	0.0000	0.861822	0.962789
TA_LEP	2.999550	0.000000	0.731613	0.0000	0.530617	0.854710
TA_LYVE1	1.505071	0.000004	0.920799	0.0000	0.849141	0.959171
TA_NRP1	4.049333	0.000015	0.871276	0.0000	0.760402	0.932802
TA_TIMP2	3.801149	0.000026	0.923189	0.0000	0.853529	0.960427
TA_TIMP3	2.644840	0.000046	0.987744	0.0000	0.975896	0.993787

<b>TA_CSF3</b>	0.53529 9	0.000001	0.646848	0.0000	0.404212	0.804432
<b>TA_ENPP2</b>	2.01939 4	0.000241	0.957371	0.0000	0.917379	0.978225
<b>TA_FBLN5</b>	3.35754 3	0.000027	0.974838	0.0000	0.950822	0.987203
<b>TA_FST</b>	1.93315 2	0.000000	0.933093	0.0000	0.871816	0.965615
<b>TA_PDGFRB</b>	7.52730 4	0.000006	0.945569	0.0000	0.895098	0.972114
<b>TA_TEK</b>	3.54141 3	0.000004	0.956357	0.0000	0.915455	0.977702
<b>TA_SERPINF 1</b>	5.22976 9	0.000047	0.945371	0.0000	0.894726	0.972011

**Table S5:** The calculated distribution fit correlation with the original data, including the p-values and estimated upper and lower bounds for the 95% confidence intervals for the study dataset. All results are significant at  $p < 0.001$ .

DATA POINT	A	B	CORRELATION COEFFICIENT	P-VALUE	LOWER BOUND	UPPER BOUND
T_IL8	0.689577	615.611904	0.733600	0.0000	0.691516	0.770720
T_CXCL12	0.982751	550.091291	0.746537	0.0000	0.706152	0.782082
T_FGF2	1.001729	127.220793	0.749339	0.0000	0.709326	0.784539
T_LEP	0.139387	9.920558	0.486866	0.0000	0.418872	0.549431
T_LYVE1	1.703864	17.531297	0.829551	0.0000	0.800884	0.854424
T_NRP1	1.862639	905.409032	0.874982	0.0000	0.853343	0.893611
T_TIMP2	2.115066	2112.948146	0.892638	0.0000	0.873850	0.908764
T_TIMP3	1.201862	1507.220707	0.728567	0.0000	0.685833	0.766295
T_CSF3	0.180336	669.781675	0.310728	0.0000	0.231458	0.385899
T_ENPP2	1.076607	761.844598	0.753251	0.0000	0.713760	0.787968
T_FBLN5	1.323874	816.222788	0.792192	0.0000	0.758073	0.821987
T_FST	0.314102	137.296118	0.493572	0.0000	0.426123	0.555563
T_PDGFBRB	1.851507	1007.434155	0.823138	0.0000	0.793515	0.848870
T_TEK	1.454318	98.592971	0.749232	0.0000	0.709204	0.784445
T_SERPINF1	1.210736	1330.840563	0.809321	0.0000	0.777665	0.836883
TA_IL8	0.489189	352.721598	0.701191	0.0003	0.396924	0.866606
TA_CXCL12	0.831011	9572.143563	0.941913	0.0000	0.863030	0.975953
TA_FGF2	6.445643	202.961500	0.985955	0.0000	0.965830	0.994262
TA_LEP	0.279601	11.188484	0.794556	0.0000	0.560817	0.910991
TA_LYVE1	1.050753	534.399004	0.825833	0.0000	0.620146	0.925279
TA_NRP1	3.446996	1012.546962	0.964297	0.0000	0.914473	0.985319
TA_TIMP2	1.590801	13860.605010	0.964402	0.0000	0.914719	0.985362
TA_TIMP3	1.238316	15977.840950	0.973597	0.0000	0.936330	0.989173
TA_CSF3	0.202173	1278.145710	0.730288	0.0001	0.446001	0.880725
TA_ENPP2	1.024887	4131.928738	0.943870	0.0000	0.867463	0.976776
TA_FBLN5	1.608749	2777.478876	0.977029	0.0000	0.944471	0.990590
TA_FST	0.999620	62.177321	0.899825	0.0000	0.770538	0.957995
TA_PDGFBRB	2.085009	2551.811220	0.973161	0.0000	0.935300	0.988993
TA_TEK	0.843587	999.543226	0.959695	0.0000	0.903764	0.983403
TA_SERPINF 1	1.832375	4023.756396	0.950340	0.0000	0.882207	0.979493

**Table S6:** Comparison between the training and test datasets using the Wilcoxon Rank Sum Test. None of the variables is significantly different between the datasets.

VARIABLE	WILCOXON RANK SUM P-VALUE	
AGE	0.7711	ns
WEIGHT	0.7443	ns
GRADESUMMARY	0.1671	ns
R_IL8	0.5794	ns
R_CXCL12	0.9348	ns
R_FGF2	0.0735	ns
R_LEP	0.0920	ns
R_LYVE1	0.4293	ns
R_NRP1	0.5307	ns
R_TIMP2	0.4729	ns
R_TIMP3	0.7095	ns
R_CSF3	0.8345	ns
R_ENPP2	0.3881	ns
R_FBLN5	0.4729	ns
R_FST	0.4618	ns
R_PDGFRB	0.4729	ns
R_TEK	0.5072	ns
R_SERPINF1	0.3881	ns
T_IL8_NORM	0.9348	ns
T_CXCL12_NORM	0.7368	ns
T_FGF2_NORM	0.5671	ns
T_LEP_NORM	0.0855	ns
T_LYVE1_NORM	0.5671	ns
T_NRP1_NORM	0.7643	ns
T_TIMP2_NORM	0.4084	ns
T_TIMP3_NORM	0.2716	ns
T_CSF3_NORM	0.4508	ns
T_ENPP2_NORM	0.3684	ns
T_FBLN5_NORM	0.2878	ns
T_FST_NORM	0.1160	ns
T_PDGFRB_NORM	0.3132	ns
T_TEK_NORM	0.1817	ns
T_SERPINF1_NORM	0.1877	ns
TA_IL8_NORM	0.5427	ns
TA_CXCL12_NORM	0.6562	ns
TA_FGF2_NORM	0.3132	ns
TA_LEP_NORM	0.0574	ns
TA_LYVE1_NORM	0.6173	ns
TA_NRP1_NORM	0.0827	ns
TA_TIMP2_NORM	0.1758	ns
TA_TIMP3_NORM	0.3588	ns
TA_CSF3_NORM	0.5919	ns
TA_ENPP2_NORM	0.6694	ns
TA_FBLN5_NORM	0.9204	ns
TA_FST_NORM	0.8062	ns

TA_PDGFRB_NORM	0.6562	ns
TA_TEK_NORM	0.8203	ns
TA_SERPINF1_NORM	0.3684	ns
R_IL8_NORM	0.9204	ns
R_CXCL12_NORM	0.6046	ns
R_FGF2_NORM	0.8203	ns
R_LEP_NORM	0.9204	ns
R_LYVE1_NORM	0.9493	ns
R_NRP1_NORM	0.1001	ns
R_TIMP2_NORM	0.5189	ns
R_TIMP3_NORM	0.6694	ns
R_CSF3_NORM	0.9638	ns
R_ENPP2_NORM	0.2796	ns
R_FBLN5_NORM	0.5548	ns
R_FST_NORM	0.1486	ns
R_PDGFRB_NORM	0.7922	ns
R_TEK_NORM	0.1877	ns

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