

Supplementary Material to “Molecular Insights into ANPEP in Gastric Adenocarcinoma”

Table S1 - Genes co-expressed with ANPEP in GAC.

Gene	ρ Spearman	log2FC	FC Management	Correlation with ANPEP	Functional Annotation
ALPL	0.635	3.602	UP	Positive	
VSIR	0.664	3.473	UP	Positive	Negative immune checkpoint (VISTA)
NCF4	0.635	3.370	UP	Positive	NADPH oxidase complex / ROS
ITGB2	0.667	3.311	UP	Positive	Leukocyte adhesion
SLC16A3	0.640	3.223	UP	Positive	Lactate exporter / Warburg
ZYX	0.671	3.213	UP	Positive	Organisation of the actin cytoskeleton
TNFRSF1B	0.695	3.018	UP	Positive	TNF signalling / inflammation
IL17RA	0.695	2.975	UP	Positive	IL-17 receptor / immune response
LSP1	0.672	2.963	UP	Positive	Leukocyte motility
CNN2	0.645	2.925	UP	Positive	Cell contraction and motility
SLC11A1	0.719	2.897	UP	Positive	Mitochondrial iron transport
SPI1	0.668	2.896	UP	Positive	Transcription factor / IL-6-JAK-2-

Gene	ρ Spearman	log2FC	FC Management	Correlation with ANPEP	Functional Annotation
					STAT3
SIRPA	0.662	2.772	UP	Positive	Inhibitory receptor / immune evasion
PXN	0.724	2.437	UP	Positive	Focal adhesion / tumour invasion
ARAP1	0.672	2.405	UP	Positive	ARF/Rho cytoskeletal remodelling
DEDD2	0.697	2.376	UP	Positive	Cell death pathway / apoptosis
SLC25A37	0.644	1.933	UP	Positive	Mitochondrial iron transport
RARA	0.741	1.833	UP	Positive	Retinoic acid receptor / transcriptional regulation
MBP	0.637	-7.008	DOWN	Positive	Highest FC magnitude in the set — downregulated
NLRP6	0.674	3.369	UP	Positive	Inflammasome / pyroptosis
NLRP12	0.633	3.115	UP	Positive	Downregulation of NF- κ B
STAT6	0.641	2.888	UP	Positive	IL-4/IL-13 signalling / M2 polarisation
ATG16L2	0.664	2.648	UP	Positive	Autophagy
TGFB1	0.655	2.542	UP	Positive	Immunosuppression / TME / EMT
MYH9	0.694	2.087	UP	Positive	Myosin / tumour migration and invasion

Gene	ρ Spearman	log2FC	FC Management	Correlation with ANPEP	Functional Annotation
HELLS	-0.639	2.060	UP	Negative	Chromatin remodelling / epigenetics
KDM6B	0.673	1.981	UP	Positive	H3K27 demethylase / epigenetic regulation
ATG2A	0.675	1.879	UP	Positive	Autophagy
MCL1	0.651	1.824	UP	Positive	Anti-apoptotic / treatment resistance
NFKB2	0.632	1.784	UP	Positive	Nf- κ B pathway / tumour survival
G6PD	0.635	1.771	UP	Positive	Pentose pathway / oxidative stress
TOM1	0.712	1.637	UP	Positive	Endosomal trafficking / ubiquitination
FTH1	0.658	1.480	UP	Positive	Ferritin / iron metabolism / ferroptosis
NUMB	0.652	1.438	UP	Positive	Tumour suppressor / Notch pathway
MAST3	0.703	1.236	UP	Positive	Kinase / cell signaling
PSD4	0.635	3.872	UP	Positive	
SH3BGRL3	0.633	3.858	UP	Positive	
CCDC113	-0.639	3.746	UP	Negative	
PCDH7	-0.649	-3.711	DOWN	Negative	

Gene	ρ Spearman	log2FC	FC Management	Correlation with ANPEP	Functional Annotation
B3GNT8	0.722	3.536	UP	Positive	
PEAK3	0.634	3.495	UP	Positive	
MYADM	0.638	3.472	UP	Positive	
MOB3A	0.673	3.393	UP	Positive	
C5AR2	0.644	3.336	UP	Positive	
FRAT2	0.636	3.293	UP	Positive	
XKR8	0.633	3.283	UP	Positive	
GMIP	0.651	3.249	UP	Positive	
ABTB1	0.685	3.244	UP	Positive	
PGGHG	0.679	3.236	UP	Positive	
COBLL1	-0.645	3.210	UP	Negative	
IFITM2	0.631	3.197	UP	Positive	
FOLR3	0.655	3.188	UP	Positive	
LRRC25	0.644	3.180	UP	Positive	
ARHGAP27	0.668	3.159	UP	Positive	
TYK2	0.632	3.111	UP	Positive	
ARHGAP4	0.652	3.055	UP	Positive	

Gene	ρ Spearman	log2FC	FC Management	Correlation with ANPEP	Functional Annotation
UNC13D	0.643	3.046	UP	Positive	
NADK	0.652	2.993	UP	Positive	
PRAM1	0.639	2.950	UP	Positive	
AP5B1	0.716	2.844	UP	Positive	
RAB3D	0.650	2.840	UP	Positive	
PPCDC	0.631	2.839	UP	Positive	
LITAF	0.641	2.817	UP	Positive	
ZNF467	0.647	2.771	UP	Positive	
MBOAT7	0.695	2.770	UP	Positive	
DHX34	0.647	2.761	UP	Positive	
RIN3	0.674	2.721	UP	Positive	
LARP1B	-0.630	2.715	UP	Negative	
ZNF516	0.658	2.714	UP	Positive	
NBEAL2	0.668	2.676	UP	Positive	
CSRNP1	0.636	2.664	UP	Positive	
SH3BP2	0.666	2.629	UP	Positive	
TNC	-0.634	2.625	UP	Negative	

Gene	ρ Spearman	log2FC	FC Management	Correlation with ANPEP	Functional Annotation
FRAT1	0.667	2.622	UP	Positive	
CYP4F3	0.651	2.596	UP	Positive	
ELL	0.631	2.575	UP	Positive	
METTL15	-0.632	2.525	UP	Negative	
SHKBP1	0.685	2.506	UP	Positive	
ATXN7L3	0.639	-2.448	DOWN	Positive	
CAMK2G	0.631	-2.407	DOWN	Positive	
NUAK2	0.637	2.393	UP	Positive	
BCCIP	-0.652	2.391	UP	Negative	
SUSD6	0.669	2.359	UP	Positive	
PLCB2	0.647	2.339	UP	Positive	
TLN1	0.632	2.339	UP	Positive	
IGF2R	0.662	2.327	UP	Positive	
SLC15A3	0.687	2.313	UP	Positive	
PIK3R5	0.641	2.261	UP	Positive	
ZBTB7B	0.633	2.254	UP	Positive	
ITPRIP	0.642	2.211	UP	Positive	

Gene	ρ Spearman	log2FC	FC Management	Correlation with ANPEP	Functional Annotation
AADAT	-0.643	2.195	UP	Negative	
NATD1	0.641	2.181	UP	Positive	
LRCH4	0.631	2.169	UP	Positive	
ARRB2	0.666	2.158	UP	Positive	
RNF166	0.644	2.148	UP	Positive	
ZNF746	0.666	2.121	UP	Positive	
FMNL1	0.650	2.054	UP	Positive	
RRP12	0.636	2.029	UP	Positive	
RPGRIP1L	-0.653	-2.023	DOWN	Negative	
MKNK2	0.676	2.002	UP	Positive	
PISD	0.635	1.798	UP	Positive	
PTPRE	0.651	1.786	UP	Positive	
LIMK2	0.662	1.698	UP	Positive	
PLEKHG3	0.678	1.676	UP	Positive	
RHOG	0.652	1.623	UP	Positive	
DUSP1	0.645	1.589	UP	Positive	
AMPD2	0.671	1.353	UP	Positive	

Gene	ρ Spearman	log2FC	FC Management	Correlation with ANPEP	Functional Annotation
GPR180	-0.631	1.311	UP	Negative	
GRK6	0.658	1.309	UP	Positive	
CSK	0.667	1.218	UP	Positive	
KLF13	0.671	-1.177	DOWN	Positive	
ITPK1	0.635	1.165	UP	Positive	
SLC43A2	0.664	1.041	UP	Positive	
PGS1	0.684	1.007	UP	Positive	