

Table S4. TCGA LIHC – GPD1L mTRNA Low vs High Groups

Variable	Overall, N = 359 ¹	high, N = 176 ¹	low, N = 183 ¹	p-value ²
TP53				0.016
Mutant	111 (31%)	65 (37%)	46 (25%)	
WT	248 (69%)	111 (63%)	137 (75%)	
CTNNB1				<0.001
Mutant	96 (27%)	30 (17%)	66 (36%)	
WT	263 (73%)	146 (83%)	117 (64%)	
AXIN1				0.24
Mutant	23 (6.4%)	14 (8.0%)	9 (4.9%)	
WT	336 (94%)	162 (92%)	174 (95%)	
ARID1A				0.91
Mutant	30 (8.4%)	15 (8.5%)	15 (8.2%)	
WT	329 (92%)	161 (91%)	168 (92%)	
CDKN2A				0.14
Mutant	11 (3.1%)	3 (1.7%)	8 (4.4%)	
WT	348 (97%)	173 (98%)	175 (96%)	
ARID2				0.20
Mutant	20 (5.6%)	7 (4.0%)	13 (7.1%)	
WT	339 (94%)	169 (96%)	170 (93%)	
RPS6KA3				0.24
Mutant	14 (3.9%)	9 (5.1%)	5 (2.7%)	
WT	345 (96%)	167 (95%)	178 (97%)	

¹ n (%)

² Pearson's Chi-squared test

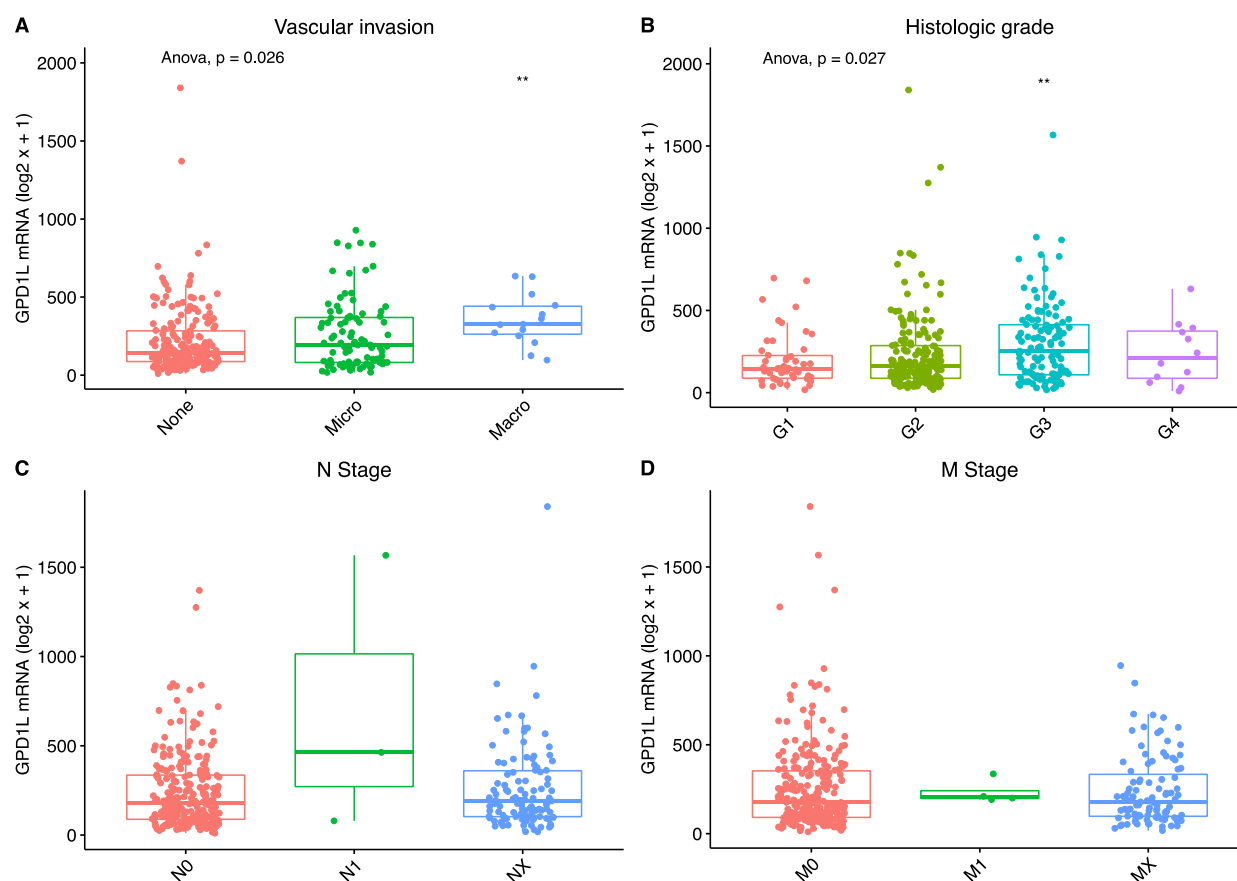


Figure S1. Association of GPD1L mRNA levels with clinicopathological factors (Dataset: TCGA-LIHC). A, Vascular Invasion; B, Histologic Grade; C, N Stage; D, M Stage. Statistical comparisons: Multi-group one-way Anova and 2-sided T-tests, with first category as the reference level (* $P < 0.05$; ** $P < 0.005$) (only significant results shown).

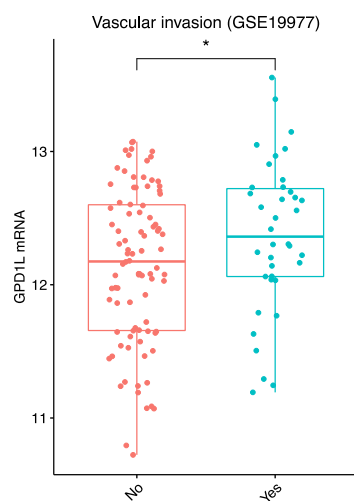


Figure S2. Association of GPD1L mRNA levels with presence or absence of vascular invasion (Dataset: GSE19977). (* $P < 0.05$)

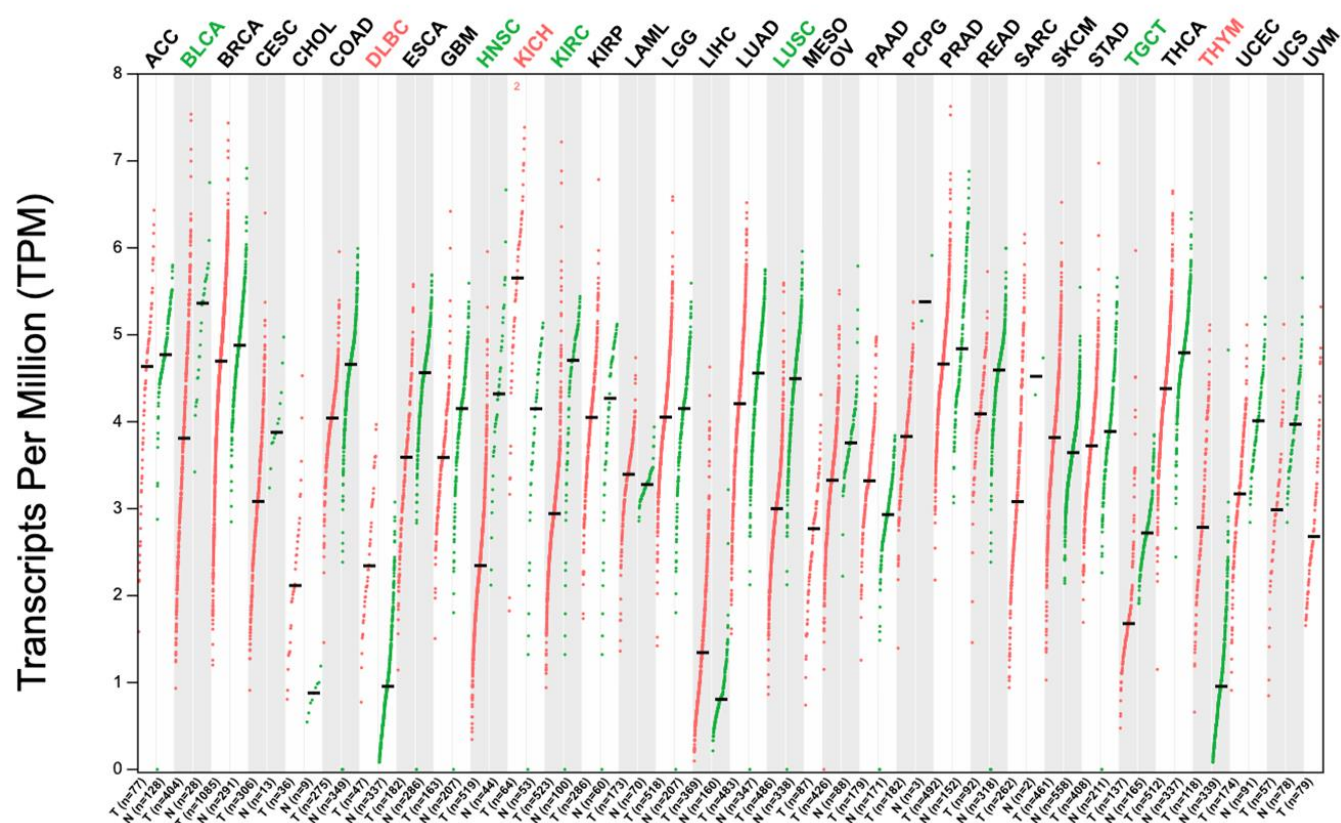


Figure S3. GPD1L mRNA levels in tumour and normal tissue in TCGA

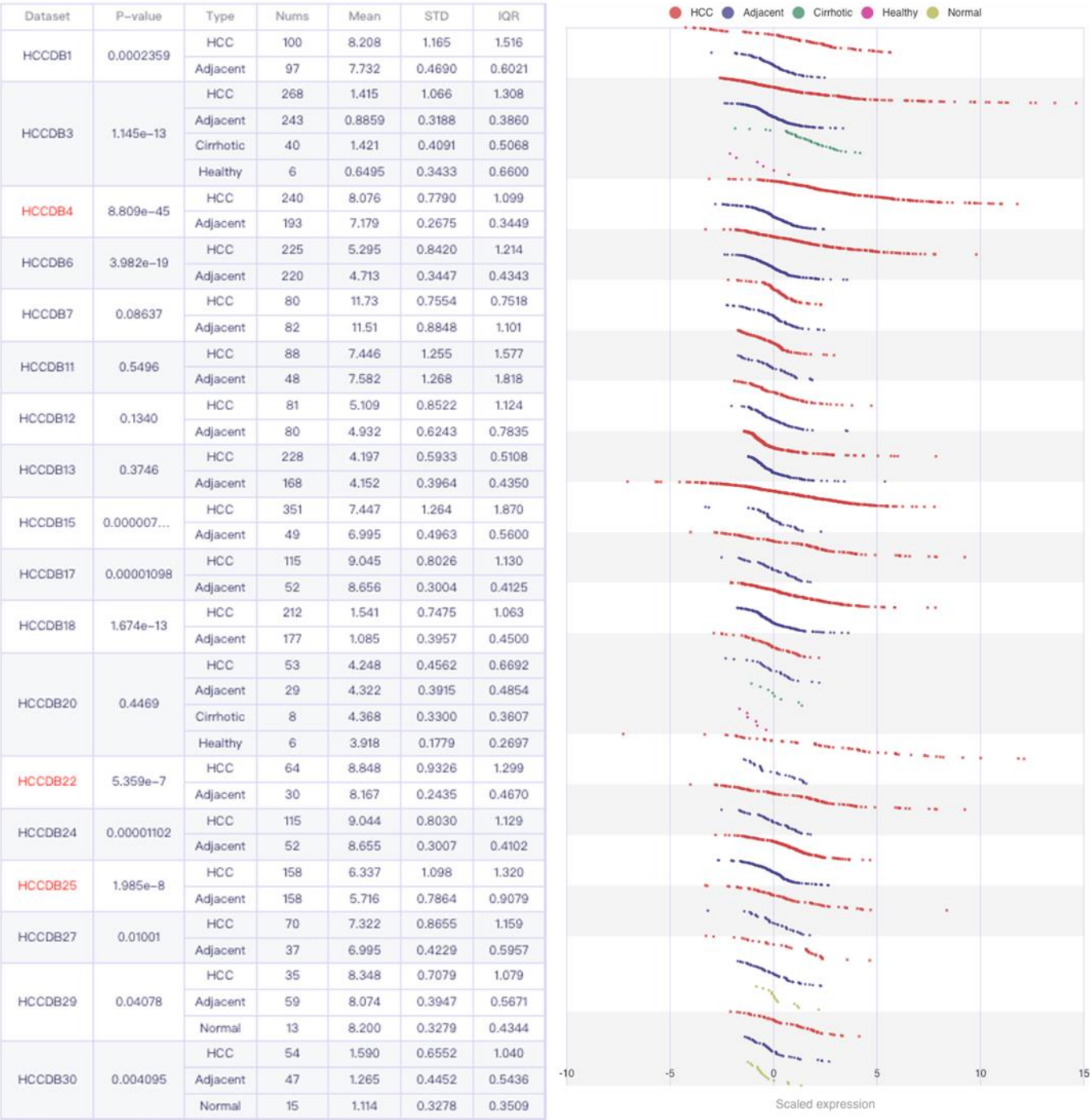


Figure S4. GPD1L mRNA levels in tumour and adjacent normal tissue in HCCDB v2.0 datasets.

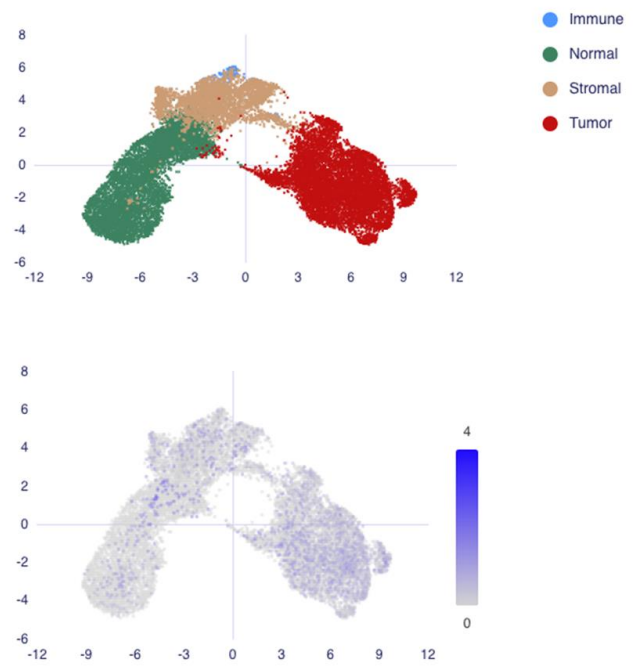
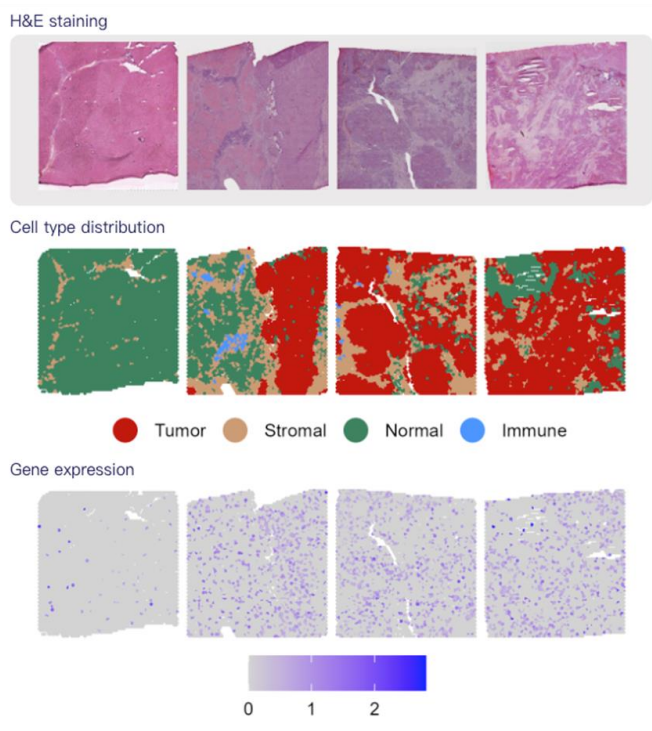


Figure S5. Spatial Transcriptomic HCC-2 dataset from HCCDB v2.0.

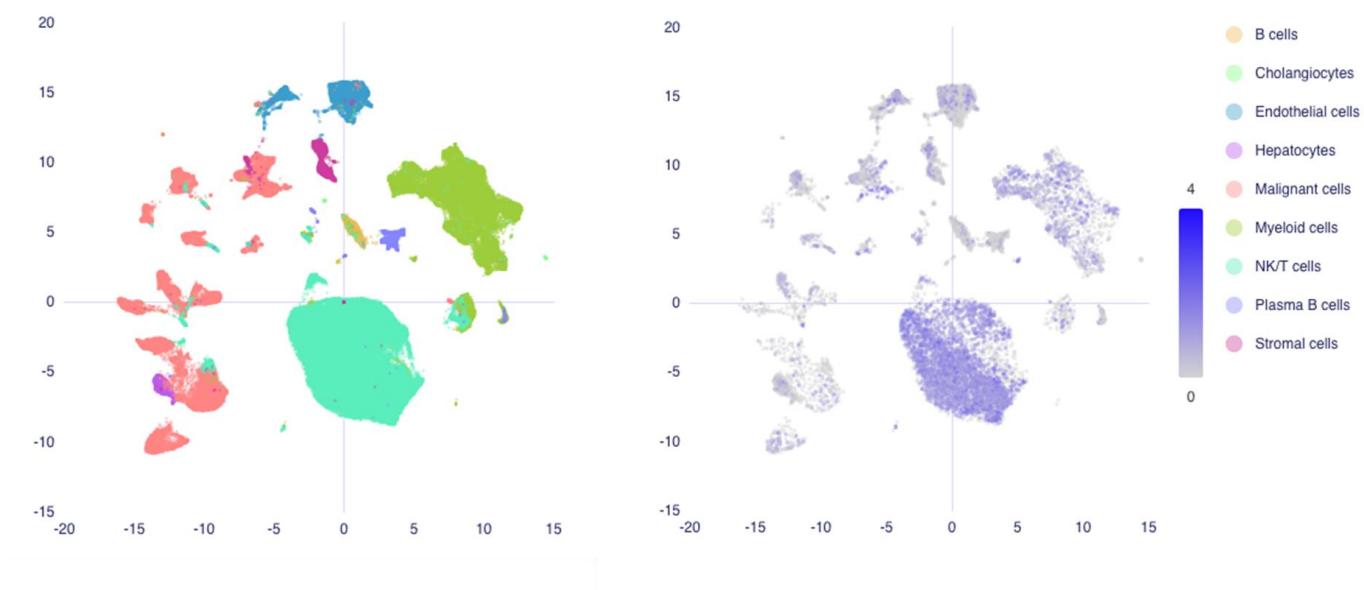


Figure S6. Single Cell RNA-Seq from HCCDB. tSNE plots showing cell population (left) and GPD1L expression in single cells marked in blue (right).

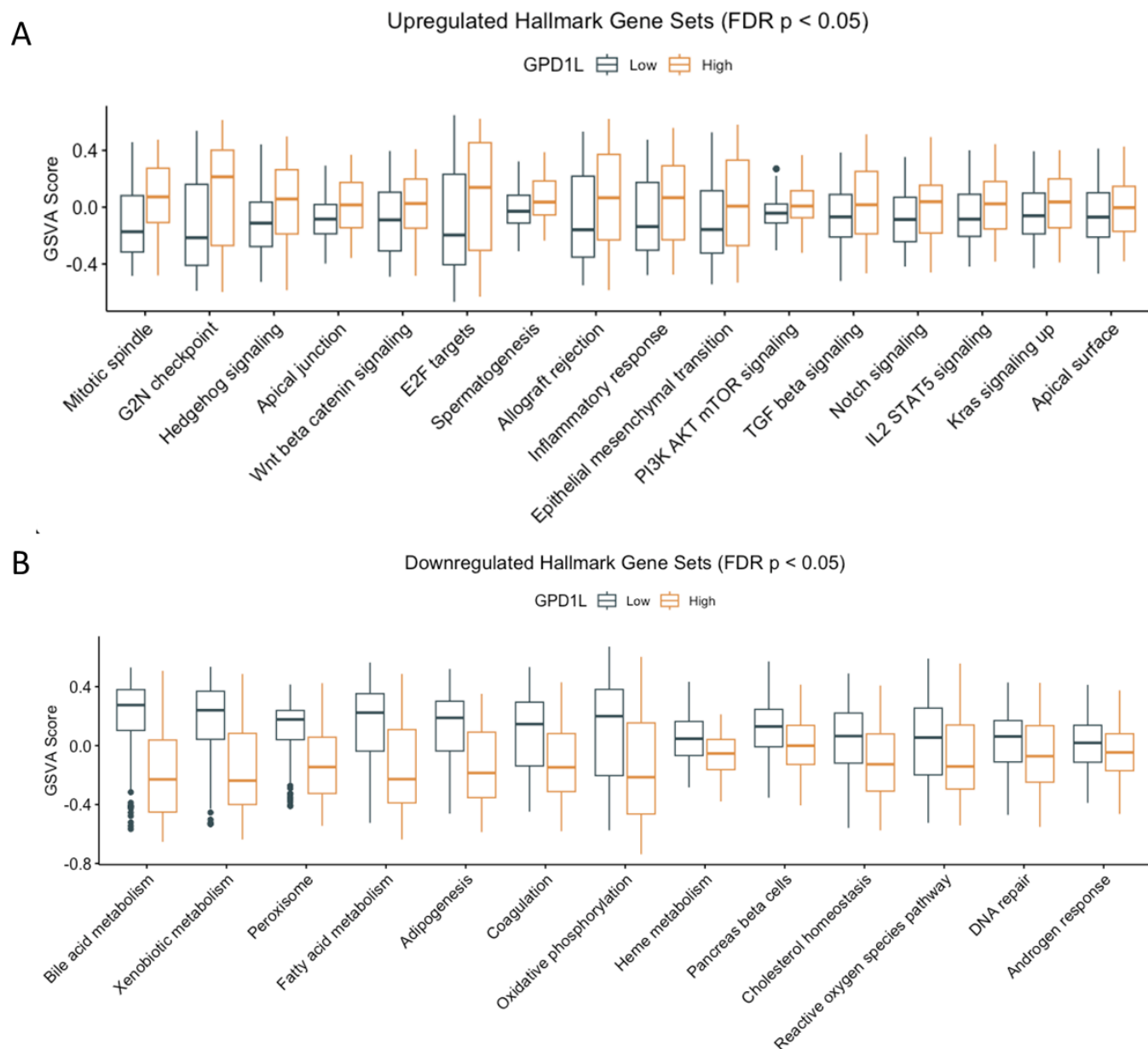


Figure S7. GSVA analysis of HALLMARK gene sets in TCGA-LIHC stratified by GPD1L mRNA levels.

TF		stats	
Term name	Term ID	p _{adj}	-log ₁₀ (p _{adj})
Factor: E2F-3; motif: GGCGGGN; match class: 1	TF:M02089_1	7.577×10 ⁻¹⁸	16.12
Factor: E2F-1; motif: NNNNGGCGGGAARN; match class...	TF:M09892_1	8.742×10 ⁻¹⁰	9.94
Factor: E2F-4; motif: NNTTCCCGCCNN; match class: 1	TF:M04823_1	3.629×10 ⁻⁷	6.74
Factor: E2F-6; motif: NGGCGGGGARRNN	TF:M09895	1.350×10 ⁻⁶	6.17
Factor: E2F-4; motif: NGGCGGGAARN; match class: 1	TF:M07084_1	1.706×10 ⁻⁴	3.52
Factor: E2F-1; motif: NKTSSCGC	TF:M00428	8.327×10 ⁻⁴	3.19
Factor: E2F-4; motif: NTTTCSGCC; match class: 1	TF:M07380_1	1.251×10 ⁻³	2.89
Factor: E2F-4; motif: GCGGGAAANA; match class: 1	TF:M02090_1	2.594×10 ⁻³	2.60

Figure S8. gProfiler functional enrichment analysis of genes with positive correlation with GPD1L in TCGA-LIHC.

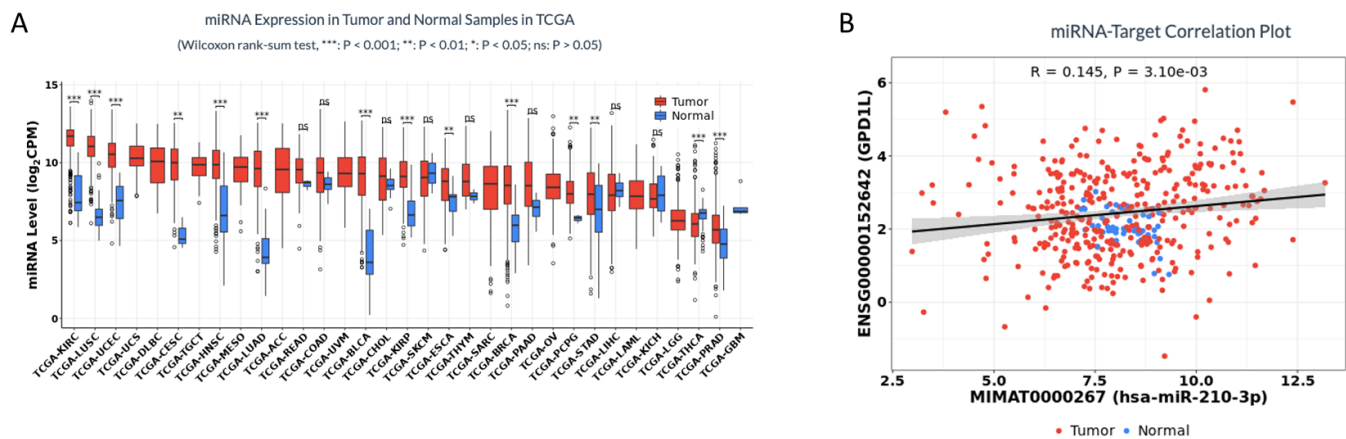


Figure S9. (A) miRNA expression in tumour and normal samples in the TCGA dataset. (B) Correlation plot for miR-210 and GPD1L expression in TCGA-LIHC.

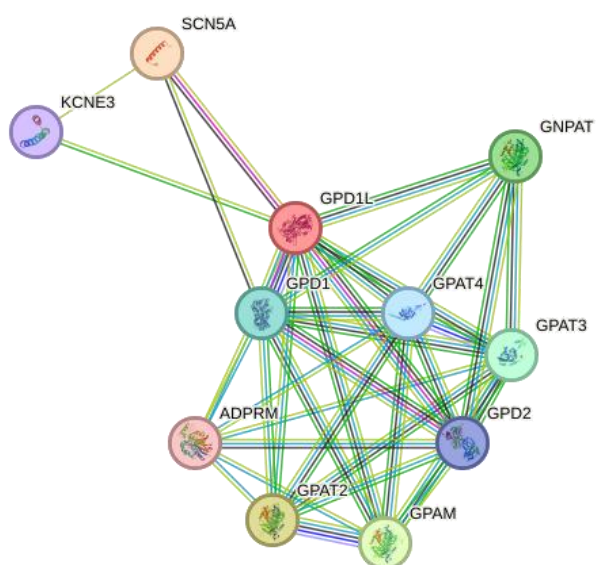


Figure S10. Protein-protein interaction network for GPD1L downloaded from STRING-DB


REAC				stats							
<input type="checkbox"/>	Term name	Term ID		Padj	-log ₁₀ (Padj)						
					0	≤16					
<input type="checkbox"/>	Phospholipid metabolism	REAC:R-HSA-1...		5.084×10 ⁻⁷	<div></div>						
<input type="checkbox"/>	Glycerophospholipid biosynthesis	REAC:R-HSA-1...		1.787×10 ⁻⁵	<div></div>						
<input type="checkbox"/>	Synthesis of PA	REAC:R-HSA-1...		8.291×10 ⁻⁵	<div></div>						
<input type="checkbox"/>	Metabolism of lipids	REAC:R-HSA-5...		2.708×10 ⁻⁴	<div></div>						
<input type="checkbox"/>	Metabolism	REAC:R-HSA-1...		4.964×10 ⁻²	<div></div>						

Figure S11. g:Profiler functional annotation of GPD1L co-expressed lipid metabolism genes

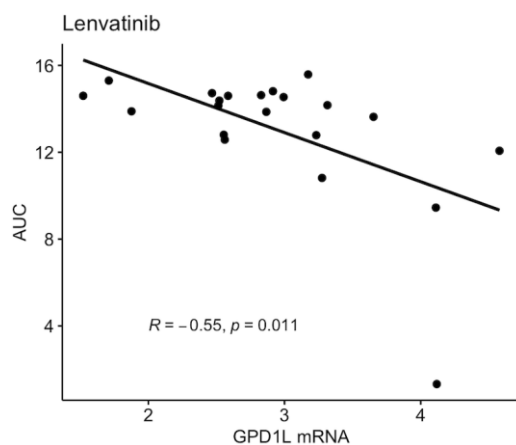


Figure S12. Correlation between hepatocellular cancer cell line mRNA and lenvatinib drug response (area under the curve, AUC). Data source: Rees et al (PMID: 26656090)

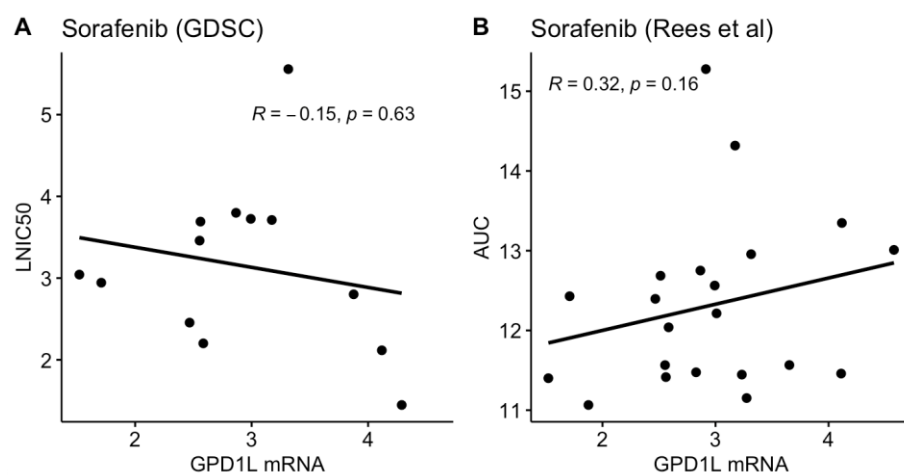


Figure S13. Correlation between hepatocellular cancer cell line mRNA and sorafenib drug response (area under the curve, AUC). Data sources: GDSC and Rees et al (PMID: 26656090)

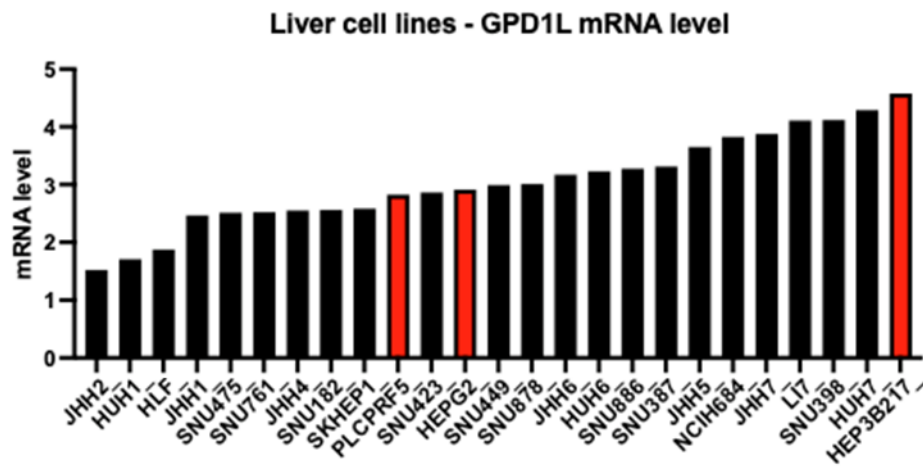


Figure S14. GPD1L mRNA levels in liver cell lines