Table S1 Primer sequences of GAPDH and other signatures involved in this study

Gene	Primer Sequence
GAPDH	F: 5'-TCGGAGTCAACGGATTTGGT-3'
	R: 5'-TTCCCGTTCTCAGCCTTGAC-3'
HILPDA	F: 5'-GGAGTCCCTAGAGGGCTTACT-3'
	R: 5'-GGGCTCTGTGTTGGCTAGTT-3'
PPARD	F: 5'-TGGAAGCAGTTGGTGAATGG-3'
	R: 5'-TAACCTGGTCGTTGAGGAAGA-3'
ETNK1	F: 5'-GTCGTCGTGGTGGTAGTCTC-3'
	R: 5'-TCCTCCTGATCCTGAACGGT-3'
ST3GAL2	F: 5'-TCCTGCAGCAAGTCTATGCC-3'
	R: 5'-TCAGCAGCACAAACAGTTGC-3'
NCOA2	F: 5'-TTCTCAGTGGCCACCAGTTC-3'
	R: 5'-TTCTGGGCCAACATCTGCTT-3'
MBTPS2	F: 5'-CCTCTCAGGAGCTCTGGCTA-3'
	R: 5'-GCAGCCAAAAGTACACTGCC-3'
SPHK2	F: 5'-AACCACGTGCTTCCCATGAT-3'
	R: 5'-GATCTAGGAGCCCGTTCAGC-3'
AKR1C4	F: 5'-AGGGTGTTGCACGACATCTA-3'
	R: 5'-TAGCTGAAGTTGCCAAGCAG-3'
ACHE	F: 5'-CTGCCTGTACCTCAACGTGT-3'
	R: 5'-TCATGGACACCAGCACAGTC-3'
HACD1	F: 5'-ACTGGGGTCCAAGTGAGTTC-3'
	R: 5'-ATCTCTGTCACAGTCCACGC-3'
UGT8	F: 5'-CACGAGAGAGGCCACCATAC-3'
	R: 5'-TAGCGCTGGAGGCTGTAATG-3'
LPIN2	F: 5'-CGTTTCTTCTCTGGTCGCCT-3'
	R: 5'-AGGATGCTCTGTGGGGATCT-3'
FASN	F: 5'- CCTGGATAGCCTCTTCAACG-3'
	R: 5'-TGCCTGGAGTAGGACACCAT-3'
SCD1	F: 5'-CTGCGTCTCTACCACGAGAA-3'
	R: 5'-CAGCTCTACACCAACGACCC-3'

Relative expression levels of 12 genes (HILPDA, ACHE, PPARD, ETNK1, ST3GAL2, NCOA2, HACD1, MBTPS2, UGT8, LPIN2, SPHK2 and AKR1C4) involved in prognostic signature in normal lung tissues and LUAD tissues in GEPIA online database.

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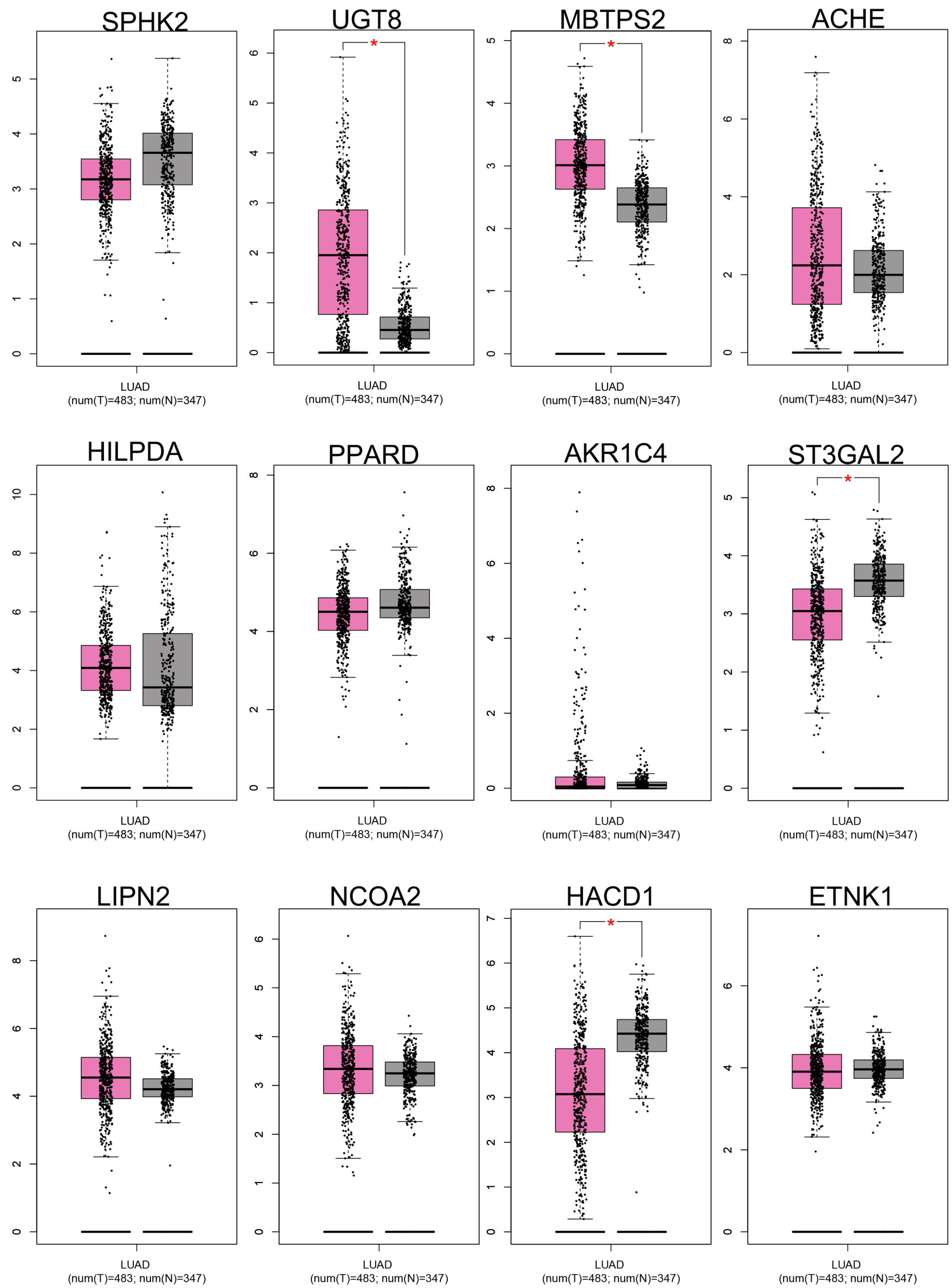

Figure S1 Relative expression levels of 12 genes (*HILPDA*, *ACHE*, *PPARD*, *ETNK1*, *ST3GAL2*, *NCOA2*, *HACD1*, *MBTPS2*, *UGT8*, *LPIN2*, *SPHK2 and AKR1C4*) involved in prognostic signature in normal lung tissues and lung adenocarcinoma (LUAD) tissues in Gene Expression Profiling Interactive Analysis (GEPIA) online database. Note: T represents tumor (pink box); N represents normal (grey box). *, P<0.05.

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