

**Table S1. Primer sequences.**

ALDH2-F	ATGGCAAGCCCTATGTCATCT
ALDH2-R	CCGTGGTACTTATCAGCCCA
ACAT1-F	TACCAGAAGTAAAGCAGCATGG
ACAT1-R	TCATTCACTGTACTGGCATTGG
SMS-F	TAGTGGGGATGTTAATTTGGCAG
SMS-R	CCACACGTTTTTCGCATGTATTT
ASNS-F	GGAAGACAGCCCCGATTTACT
ASNS-R	AGCACGAACTGTTGTAATGTCA
GNMT-F	CTGGGGTGGACTCCATTATGC
GNMT-R	GATGACCCACTTGTCTGAAGGC
PLOD2-F	CATGGACACAGGATAATGGCTG
PLOD2-R	AGGGGTTGGTTGCTCAATAAAAA
P4HA1-F	AGTACAGCGACAAAAGATCCAG
P4HA1-R	CTCCAACCTCACTCCACTCAGTA
PAH-F	GCCTGCTCTGACAAACATCAT
PAH-R	TTATCTCGTGAAAGCTCATGGAC
KYNU-F	GGCTCTCCACCTAGATGAGGA
KYNU-R	GCTGCTATTTTGGCCCACTTAT
PDL2-F	ATTGCAGCTTCACCAGATAGC
PDL2-R	AAAGTTGCATTCCAGGGTCAC
CD155-F	TGGAGGTGACGCATGTGTC
CD155-R	GTTTGGACTCCGAATAGCTGG
FGL1-F	ATGGCAAAGGTGTTCAAGTTTCA
FGL1-R	ACAATCTGCATACTGCCTCTTG
LSECtin-F	AGTCCTTTGGGCTGTGATTCT
LSECtin-R	AGGCGTTTGTCTCAGCAG
PDL1-F	TGGCATTGCTGAACGCATTT
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GAPDH-F	GGAGCGAGATCCCTCCAAAAT
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Figure legend

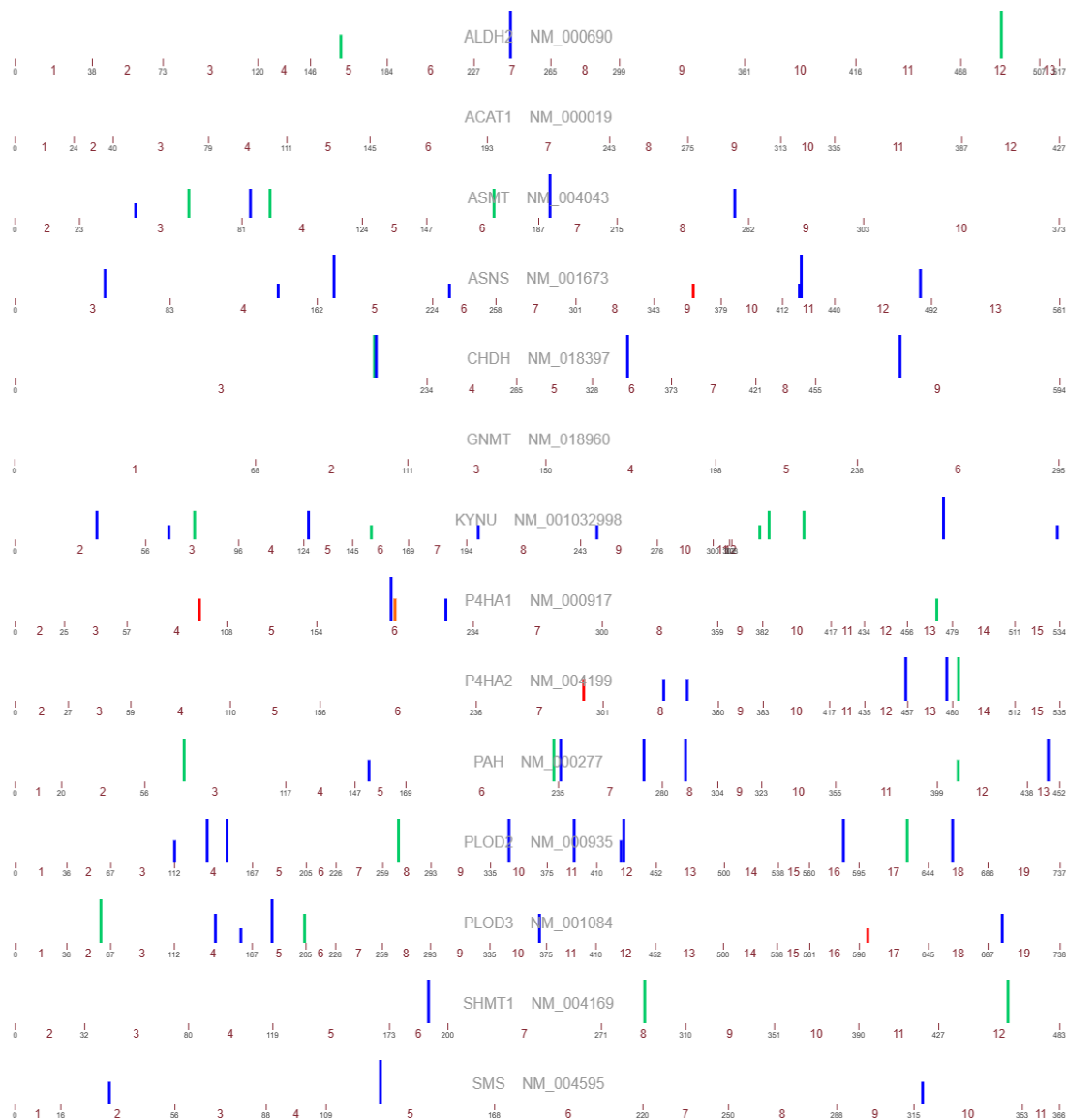


Figure S1. the mutations of AMGs in TCGA-HNC cohort. Mutation types: **silent** . **missense** . **inframe\_indel** . **frameshift** . **nonsense** .

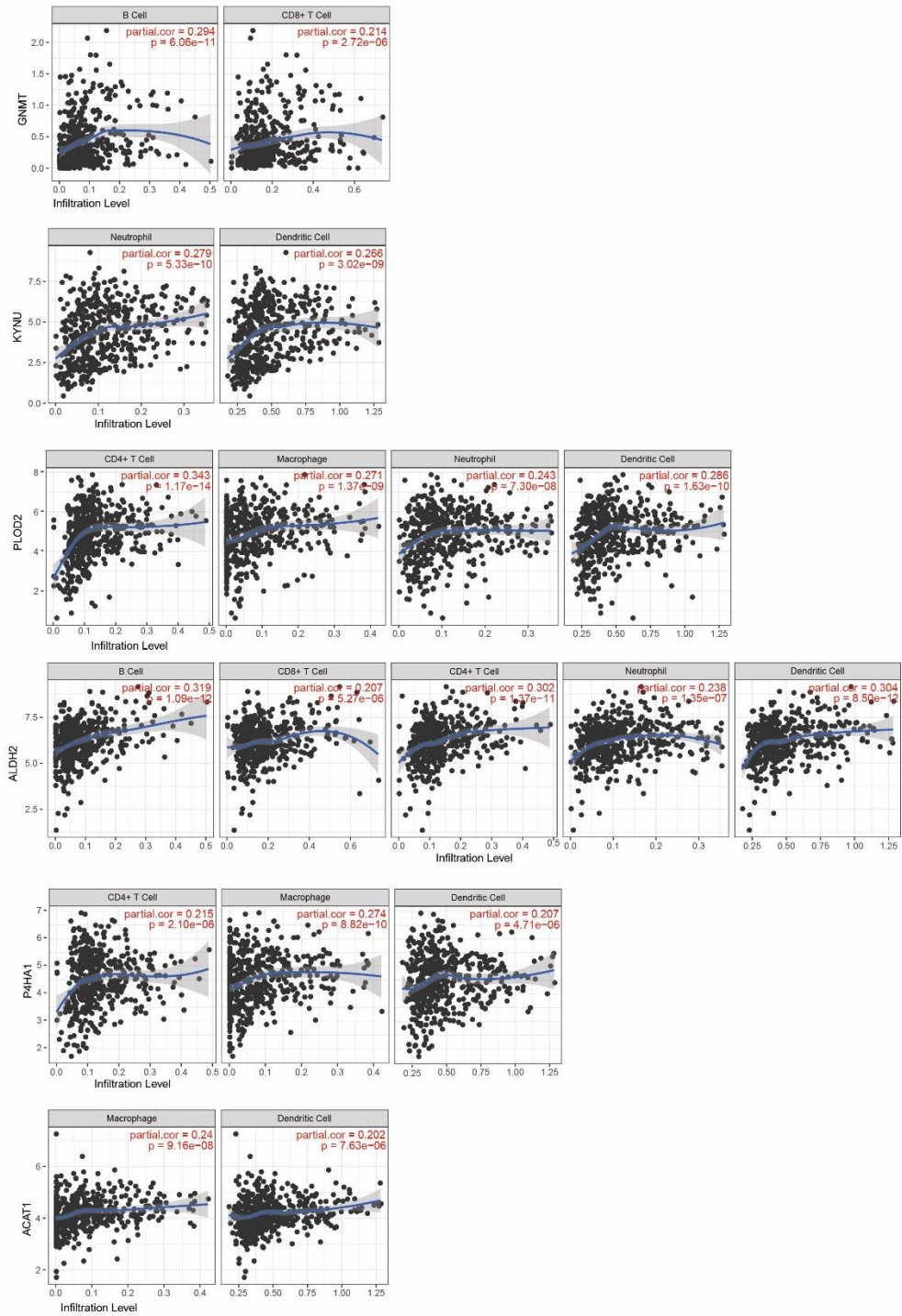


Figure S2. The correlation between these nine genes and the number of infiltration of multiple major immune cells (correlation coefficient >0.2, P value <0.05).

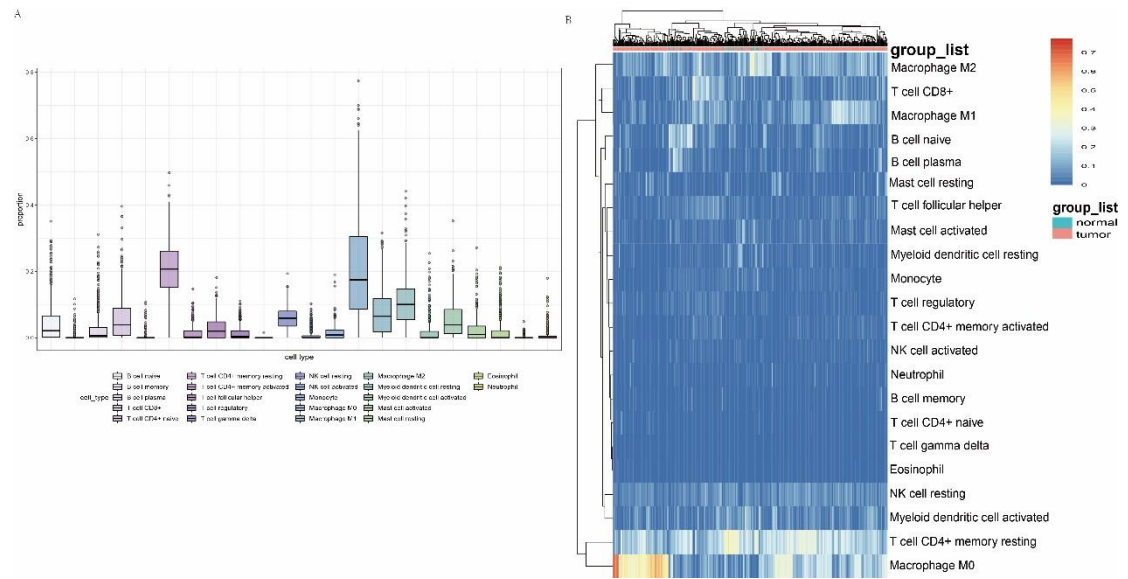


Figure S3. A, boxplot of 22 types of immune cell infiltration in HNC patients. B:heat map of immune infiltration in HNC patients.

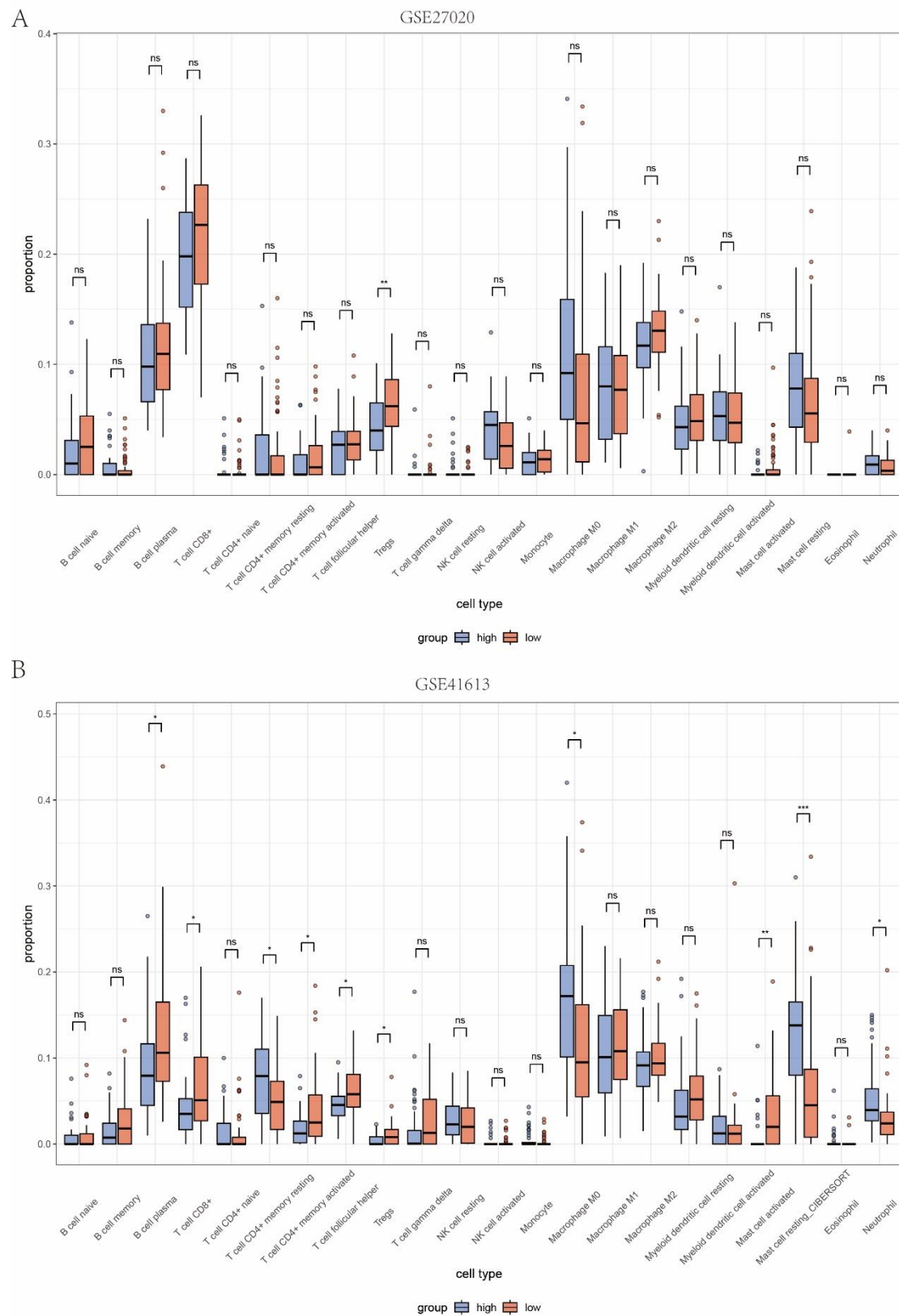
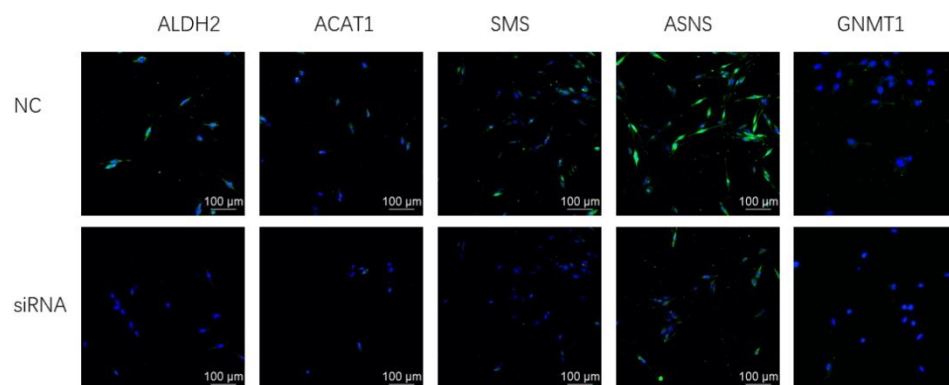
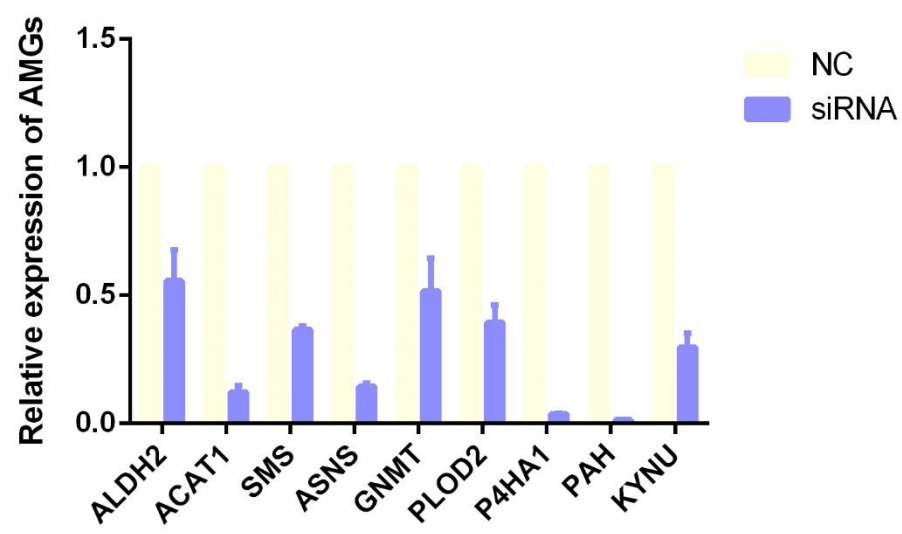


Figure S4. landscape of tumor immune microenvironment between high and low AMI groups.  
 \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ , ns, no statistical significance.



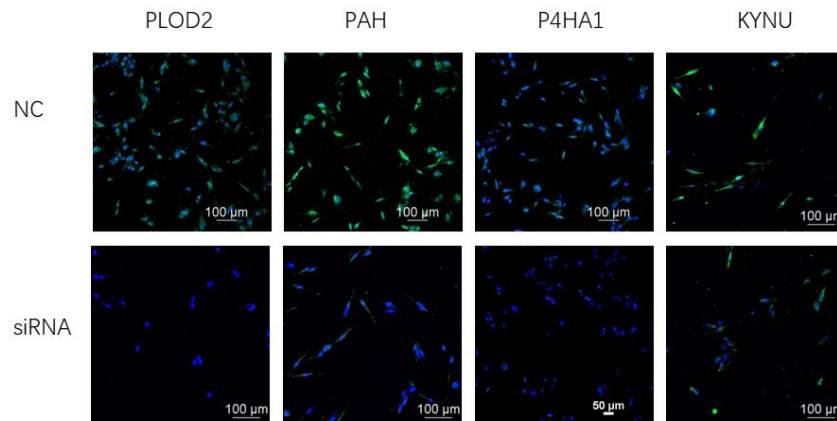


Figure S5. Verification of siRNAs suppresses AMGs expression by RT-qPCR before the invasion assay.

#### gene set names

KEGG\_AMINOACYL\_TRNA\_BIOSYNTHESIS  
 KEGG\_ALANINE\_ASPARTATE\_AND\_GLUTAMATE\_METABOLISM  
 KEGG\_GLYCINE\_SERINE\_AND\_THREONINE\_METABOLISM  
 KEGG\_CYSTEINE\_AND\_METHIONINE\_METABOLISM  
 KEGG\_VALINE\_LEUCINE\_AND\_ISOLEUCINE\_DEGRADATION  
 KEGG\_VALINE\_LEUCINE\_AND\_ISOLEUCINE\_BIOSYNTHESIS  
 KEGG\_LYSINE\_DEGRADATION  
 KEGG\_ARGININE\_AND\_PROLINE\_METABOLISM  
 KEGG\_HISTIDINE\_METABOLISM  
 KEGG\_TYROSINE\_METABOLISM  
 KEGG\_PHENYLALANINE\_METABOLISM  
 KEGG\_TRYPTOPHAN\_METABOLISM  
 KEGG\_BETA\_ALANINE\_METABOLISM  
 KEGG\_TAURINE\_AND\_HYPOTHAURINE\_METABOLISM  
 KEGG\_SELENOAMINO\_ACID\_METABOLISM  
 KEGG\_GLUTATHIONE\_METABOLISM  
 KEGG\_BUTANOATE\_METABOLISM  
  
 REACTOME\_METABOLISM\_OF\_AMINO\_ACIDS\_AND\_DERIVATIVES

#### Sample list

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### **561 AM genes**

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PDHA2  
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BDH1  
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ACSM1  
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ECHS1  
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GAD1  
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ACSM3  
GAD2  
ACSM4  
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EHHADH  
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ALDH5A1  
BDH2  
OXCT2  
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ACSM5  
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TDO2  
HAAO  
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GSTP1

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GSTT1  
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PRODH2  
OAT  
CKM  
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FARS2  
MAR2  
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GFPT2

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GLYCTK  
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AGXT2

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SDS  
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OXCT1

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IL4I1  
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DBT  
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DLD  
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PCCA  
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HIBADH  
ACAA1  
OXCT2  
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MCCC2  
BCAT1  
AUH  
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MCCC1  
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PDHA2  
LARS1  
LARS2  
VARS1  
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IARS1

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EHMT2

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AASS  
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DOT1L  
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EHHADH  
OGDHL  
SETD1A  
GCDH  
KMT5C  
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MAOA  
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IDO1  
CAT  
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ACAT1  
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OGDHL  
CNDP1  
SRM  
ECHS1  
ALDH9A1  
ALDH3A2  
GAD1  
GAD2  
AOC2  
ALDH1B1  
HIBCH  
ABAT  
EHHADH  
ALDH2  
ACADM  
UPB1  
ALDH7A1  
AOC3  
DPYS  
DPYD  
MLYCD  
HADHA

SMS  
 GPX2  
 GPX3  
 IDH2  
 GPX4  
 IDH1  
 OPLAH  
 GCLM  
 GGT6  
 METTL6  
 AHCY  
 BUD23  
 SEPHS1  
 GGT1  
 SEPHS2  
 METTL2B  
 HEMK1  
 GGT6  
 LCMT2  
 PAPSS1  
 PAPSS2  
 TRMT11  
 MARS2  
 SCLY  
 AHCYL1  
 GGT7  
 GGT5  
 MAT2B  
 MAT1A  
 LCMT1  
 CBS  
 AHCYL2  
 CTH  
 MAT2A  
 MARS1  
 GCDH  
 ALDH7A1  
 AOC1  
 INMT

Multiple hypothesis testing of K-M analysis

ALDH2	Chi-square	df	significance
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Log Rank (Mantel-Cox)	6.372	1	.012
Breslow (Generalized Wilcoxon)	3.745	1	.053
Tarone-Ware	4.779	1	.029

	Chi-square	df	significance
<b>ACAT1</b>			
Log Rank (Mantel-Cox)	3.609	1	.057
Breslow (Generalized Wilcoxon)	5.719	1	.017
Tarone-Ware	5.035	1	.025

	Chi-square	df	significance
<b>SMS</b>			
Log Rank (Mantel-Cox)	11.716	1	.001
Breslow (Generalized Wilcoxon)	15.689	1	.000
Tarone-Ware	15.217	1	.000

	Chi-square	df	significance
<b>ASNS</b>			
Log Rank (Mantel-Cox)	17.728	1	.000
Breslow (Generalized Wilcoxon)	8.466	1	.004
Tarone-Ware	11.635	1	.001

	Chi-square	df	significance
<b>GNMT</b>			
Log Rank (Mantel-Cox)	10.751	1	.001
Breslow (Generalized Wilcoxon)	11.821	1	.001
Tarone-Ware	11.724	1	.001

<b>PAH</b>	Chi-square	df	significance
Log Rank (Mantel-Cox)	4.557	1	.033
Breslow (Generalized Wilcoxon)	.617	1	.432
Tarone-Ware	1.611	1	.204

<b>KYNU</b>	Chi-square	df	significance
Log Rank (Mantel-Cox)	1.305	1	.253
Breslow (Generalized Wilcoxon)	1.391	1	.238
Tarone-Ware	1.647	1	.199

<b>P4HA1</b>	Chi-square	df	significance
Log Rank (Mantel-Cox)	19.556	1	.000
Breslow (Generalized Wilcoxon)	24.656	1	.000
Tarone-Ware	24.234	1	.000
<b>PL0D2</b>	Chi-square	df	significance
Log Rank (Mantel-Cox)	9.953	1	.002
Breslow (Generalized Wilcoxon)	7.103	1	.008
Tarone-Ware	8.244	1	.004