Supplementary Tables

Supplementary Table 1. Basic information of the included external datasets. HCC, hepatocellular carcinoma; N, number; M, mean; SD, standard deviation; TP, true positive; FP, false positive; FN, false negative; TN, true negative.

Accession	Author	Year	Platform	Country	HCC			Non-cancer			TP	FP	FN	TN
					N1	M1	SD1	N2	M2	SD2				
TCGA-GTEx	/	/	/	/	371	12.50	1.19	225	12.71	0.64	105	25	266	200
GSE112790	Kaoru Mogushi, et al.	2019	GPL570	Japan	183	9.13	0.90	15	9.87	0.25	120	0	63	15
GSE117361	Yong Jiang, et al.	2019	GPL6480	China	2	9.11	1.82	2	8.78	0.94	1	0	1	2
GSE98617	Sara Torrecilla, et al.	2019	GPL14951	Spain	36	14.06	0.63	13	12.96	1.50	17	0	19	13
GSE124535	Ying Jiang, et al.	2019	GPL20795	China	35	5.32	0.81	35	5.51	0.40	20	9	15	26
GSE128274	Ge Shan, et al.	2019	GPL18573	China	4	4.74	0.61	4	4.74	0.19	2	0	2	4
GSE101685	Yun-Shien Lee, et al.	2019	GPL570	China	24	8.17	0.92	8	9.24	0.45	23	1	2	6
GSE102079	Kaoru Mogushi, et al.	2018	GPL570	Japan	152	9.02	0.94	105	9.46	0.48	77	18	75	87
GSE107170	Giacomo Diaz, et al.	2018	GPL570	Italy	124	9.51	0.86	183	9.61	0.48	26	8	98	175
GSE121248	Kam Hui, et al.	2018	GPL570	Singapore	70	9.46	0.90	37	9.80	0.34	40	9	30	28
GSE115018	Guang-Qiang Ye, et al.	2018	GPL20115	China	12	1.72	1.23	12	1.93	0.56	7	4	5	8
GSE112221	Keith D Robertson, et al.	2018	GPL16791	USA	4	4.41	0.67	6	3.62	0.60	3	1	1	5
GSE87592	Shi-Long Zhong, et al.	2018	GPL11154	China	27	5.45	0.34	26	5.53	0.35	7	2	20	24
GSE94660	Seungyeul Yoo, et al.	2018	GPL16791	USA	21	4.20	0.88	21	4.20	0.27	8	2	13	19
GSE45050	Moses Morakortoi Darpolor, et al.	2017	GPL6244	USA	6	11.00	0.54	10	10.51	0.35	5	2	1	8
GSE76297	Xin-Wei Wang, et al.	2017	GPL17586	USA	61	7.96	0.71	58	8.19	0.30	31	9	30	49
GSE84005	Jin Song, et al.	2017	GPL5175	China	38	10.26	0.96	38	10.38	0.33	24	18	14	20
GSE84402	Zhuo-An Cheng, et al.	2017	GPL570	China	14	8.10	1.09	14	8.19	0.74	7	4	7	10
GSE76427	Surya Pavan Yenamandra, et al.	2017	GPL10558	Singapore	115	12.11	0.79	52	12.08	0.57	22	2	93	50
GSE87630	Hyun Goo Woo, et al.	2017	GPL6947	South Korea	64	11.89	0.68	30	11.93	0.21	25	4	39	26
GSE89377	Jungwoo Eun, et al.	2017	GPL6947	South Korea	40	11.50	0.87	67	11.69	0.43	23	27	17	40
GSE63018	Bic Mskcc, et al.	2017	GPL16791	USA	9	11.55	0.67	9	12.98	0.61	9	3	0	6
GSE73708	Jian Chen, et al.	2017	GPL11154	USA	8	3.49	0.94	4	3.08	0.66	7	1	1	3
GSE77509	Jin Gu, et al.	2017	GPL16791	China	20	13.20	0.79	20	13.97	0.42	13	2	7	18

Accession	**Author**	**Year**	**Platform**	**Country**	**HCC**			**Non-cancer**			**TP**	**FP**	**FN**	**TN**
					N1	**M1**	**SD1**	**N2**	**M2**	**SD2**				
GSE97214	Yi Huang, et al.	2017	GPL11154	China	9	4.80	1.14	9	5.17	0.48	4	0	5	9
GSE104310	Jing-Ping Yun, et al.	2017	GPL16791	China	12	4.46	0.94	8	4.99	0.50	5	0	7	8
GSE76311-GPL17586	Xin-Wei Wang, et al.	2017	GPL17586	USA	62	7.98	0.71	59	8.19	0.30	31	31	9	50
GSE56545	Dong Shen, et al.	2016	GPL15433	USA	21	10.37	1.13	21	11.05	0.66	16	6	5	15
GSE77314	Gang Liu, et al.	2016	GPL9052	China	50	4.48	1.12	50	5.34	0.66	35	10	15	40
GSE60502	K.J. Kao, et al.	2015	GPL96	China	18	9.61	0.86	18	9.91	0.20	9	0	9	18
GSE63898	Augusto Villanueva, et al.	2015	GPL13667	USA	228	8.37	0.61	168	8.34	0.36	61	12	167	156
GSE64041	Zuzanna Makowska, et al.	2015	GPL6244	Switzerland	60	9.63	0.71	65	9.82	0.43	45	38	15	27
GSE57555	Y-H. Taguchi, et al.	2015	GPL16699	Japan	5	0.68	0.76	5	0.44	0.24	3	1	2	4
GSE67764	Bin Wu, et al.	2015	GPL17077	China	3	2.04	0.97	6	3.04	0.25	2	0	1	6
GSE74656	Hui-Yong Yin, et al.	2015	GPL16043	China	5	7.60	1.32	5	8.85	0.10	4	0	1	5
GSE57727	Manel Esteller, et al.	2015	GPL14951	Spain	57	11.28	1.01	5	11.41	0.49	39	2	18	3
GSE59259	Alberto Ferrarini, et al.	2015	GPL18451	Italy	8	12.33	0.80	8	13.09	0.30	6	1	2	7
GSE65485	Hua Dong, et al.	2015	GPL11154	China	50	4.69	1.23	5	5.09	0.26	26	0	24	5
GSE63863	Hong Zhang, et al.	2015	GPL11154	China	12	4.10	1.01	12	5.05	0.36	11	1	1	11
GSE69164	Hong Zhang, et al.	2015	GPL11154	China	11	3.90	0.76	11	5.02	0.36	11	1	0	10
GSE22405	Henry H Zhang, et al.	2014	GPL10553	USA	24	7.72	1.17	24	7.63	0.74	5	1	19	23
GSE45436	Jui-Yu Hsieh, et al.	2014	GPL570	China	93	8.04	0.98	41	8.62	0.34	44	0	49	41
GSE55092	Patrizia Farci, et al.	2014	GPL570	USA	49	9.46	1.00	91	9.78	0.43	13	0	36	91
GSE62232	Sandrine Imbeaud, et al.	2014	GPL570	France	81	8.77	0.96	10	9.36	0.21	45	0	36	10
GSE54236	Erica Villa, et al.	2014	GPL6480	Italy	81	11.57	0.91	80	12.05	0.44	31	6	50	74
GSE54238	Jie Wang, et al.	2014	GPL16955	USA	26	11.02	1.28	30	10.99	1.64	13	8	13	22
GSE39791	Sangbae Kim, et al.	2014	GPL10558	USA	72	10.26	1.16	72	10.56	0.63	21	7	51	65
GSE47595	Yujin Hoshida, et al.	2014	GPL13369	USA	88	11.15	2.54	48	10.97	2.86	43	19	45	29
GSE57957	Lee Guat Lay Caroline, et al.	2014	GPL10558	Singapore	39	12.07	0.70	39	12.32	0.40	28	12	11	27
GSE55048	Tao Cai, et al.	2014	GPL9115	China	4	5.12	0.84	4	4.77	0.42	4	3	0	1
GSE46444	Yujin Hoshida, et al.	2014	GPL15314	USA	88	11.15	2.54	48	10.97	2.86	71	35	17	13

Accession	Author	Year	Platform	Country	HCC			Non-cancer			TP	FP	FN	TN
					N1	**M1**	**SD1**	**N2**	**M2**	**SD2**				
GSE56140	Yujin Hoshida, et al.	2014	GPL13825	USA	35	11.30	0.71	34	11.40	0.25	13	2	22	32
GSE17548	Mehmet Ozturk, et al.	2013	GPL570	Turkey	17	9.07	1.07	20	9.45	0.56	8	3	9	17
GSE41804	Yuji Hodo, et al.	2013	GPL570	Japan	20	11.34	0.98	20	11.59	0.41	13	7	7	13
GSE46408	Yung-Ming Jeng, et al.	2013	GPL4133	China	6	12.06	1.14	6	13.02	0.48	5	0	1	6
GSE50579	Robert Geffers, et al.	2013	GPL14550	Germany	67	12.79	1.02	10	12.76	0.51	29	1	38	9
GSE25599	Biao-Yang Lin, et al.	2013	GPL9052	China	10	5.72	0.84	10	5.17	0.43	7	1	3	9
GSE33294	Chi-Ho Lin, et al.	2013	GPL16791	China	3	1.53	5.84	3	0.93	7.38	3	2	0	1
GSE33006	Yi Huang, et al.	2012	GPL570	China	3	11.59	0.10	3	10.13	2.21	3	1	0	2
GSE31370	Hyun Goo Woo, et al.	2012	GPL10558	South Korea	15	4.66	0.96	5	5.13	0.18	8	0	7	5
GSE36376	Cheol-Keun Park, et al.	2012	GPL10558	South Korea	240	10.75	0.83	193	10.81	0.38	53	9	187	184
GSE36411	Sang-Yeop Lee, et al.	2012	GPL10558	South Korea	42	12.37	0.92	42	12.61	0.37	19	8	23	34
GSE29721	Moshe Szyf, et al.	2011	GPL570	Canada	10	8.08	0.78	10	8.71	0.32	7	1	3	9
GSE20140-GPL18461	Yujin Hoshida, et al.	2011	GPL18461	USA	35	11.30	0.71	34	11.40	0.25	13	2	22	32
GSE25097	Chunsheng Zhang, et al	2011	GPL13369	USA	268	3.52	0.87	289	3.48	0.39	110	35	158	254
GSE20140-GPL5474	Yujin Hoshida, et al.	2011	GPL5474	USA	80	12.88	0.80	307	12.00	0.61	63	62	17	245
GSE12941	satow reiko, et al.	2010	GPL5175	Japan	10	10.35	0.59	10	10.36	0.22	4	0	6	10
GSE14520-GPL571	Xin-Wei Wang, et al.	2010	GPL571	USA	22	7.04	0.85	21	7.88	0.37	13	1	9	20
GSE14520-GPL3921	Xin-Wei Wang, et al.	2010	GPL3921	USA	225	7.57	0.95	220	8.17	0.52	114	27	111	193
GSE19665	Atsushi Kaneda, et al.	2010	GPL570	Japan	10	9.34	0.61	10	9.13	0.47	6	3	4	7
GSE22058	Julja Burchard, et al.	2010	GPL10687	USA	100	12.69	0.56	97	12.72	0.21	32	2	68	95
GSE14323	Kellie J. Archer, et al.	2009	GPL571	USA	55	8.24	0.44	60	8.47	0.60	49	40	6	20
GSE17967	Kellie J. Archer, et al.	2009	GPL571	USA	16	7.93	0.35	47	7.85	0.39	10	21	6	26
GSE6222	Ann-Ping Tsou, et al.	2008	GPL570	China	10	8.07	0.70	2	9.10	0.65	8	0	2	2
GSE9839	Luigi Terracciano, et al.	2008	GPL571	Switzerland	3	9.74	0.79	3	9.64	0.42	2	1	1	2
GSE6764	Elisa Wurmbach, et al.	2007	GPL570	USA	35	9.02	0.75	40	9.36	0.44	21	7	14	33

Supplementary Table 2. Clinical features of HCC patients based on the included datasets. HCC, hepatocellular carcinoma; N, number; M, mean; SD, standard deviation; AFP, Alpha-fetoprotein. To determine the statistical significance of difference between groups, independent-samples t-test or one-way analysis of variance (ANOVA) was used.

Clinical features	N	Expression level of MAOA			
		M	**SD**	**t or F**	**P-value**
Tissue					
HCC	344	12.4549	1.2029	2.2190	0.0270*
Non-cancer	33	12.9232	0.4574		
Age（years）					
<60	174	12.6178	1.0875	2.4660	0.0140*
≥60	169	12.3002	1.2869		
Sex					
Male	217	12.5002	1.2130	1.1340	0.2580
Female	94	12.3338	1.1784		
Race					
Asian	153	12.2688	1.3681	2.8830	0.0040*
Non-Asian	151	12.6664	1.0123		
Ethnicity					
Hispanic or Latino	18	12.7399	1.1187	0.9390	0.3595
Not Hispanic or Latino	340	12.4851	1.1810		
Vital status					
Alive	247	12.3685	1.2468	2.7430	0.0070*
Dead	64	12.7640	0.9631		
Pathological stage					
Stages I-II	240	12.4525	1.1501	-0.8340	0.4060
Stages III-IV	82	12.3135	1.3503		
Tumor					
T1-2	280	12.5206	1.0935	0.7615	0.4469
T3-4	94	12.4146	1.3687		
Pathologic stage					
Stage I	175	12.4424	1.0951	0.6345	0.5932
Stage II	87	12.5692	1.1467		
Stage III	86	12.3649	1.3448		
Stage IV	5	12.8406	0.3024		
Tumor					
T1	185	12.4696	1.0813	1.2426	0.2924
T2	95	12.6200	1.1160		
T3	81	12.3279	1.3935		
T4	13	12.9550	1.0982		
TX	1	12.8506	/		
Node					
Yes	4	12.4224	1.0359	-0.0321	0.9763
No	257	12.4392	1.2131		
Metastasis					

Yes	4	12.9285	0.2652	3.2193	0.0229[*]
No	270	12.4414	1.1979		
Neoplasm histologic grade					
G1	55	12.6491	0.9236	3.1157	0.0262[*]
G2	180	12.5732	1.1969		
G3	124	12.3655	1.1498		
G4	13	11.7081	1.4961		
Child pugh classification grade					
A	223	12.4861	1.1444	0.6112	0.5435
B	21	12.7682	0.7933		
C	1	12.4341	/		
Adjacent hepatic tissue inflammation status					
None	119	12.6330	0.9507	0.4732	0.6236
Mild	101	12.5451	1.3342		
Severe	19	12.3826	0.8483		
AFP (ng/mL)					
≤ 20	152	12.6351	0.9055	-2.5491	0.0113[*]
>20	132	12.2982	1.3082		
Viral hepatitis					
No	139	12.3702	1.3694	-1.1060	0.2700
Yes	189	12.5252	1.0791		
Alcohol consumption					
No	217	12.4472	1.2680	0.2680	0.7890
Yes	111	12.4834	1.0964		

Footnote: [*]A P-value < 0.05 indicates statistically significant.

Supplementary Table 3. Mutation types of MAOA in hepatocellular carcinoma patients based on the Catalogue of Somatic Mutations in Cancer.

Position	CDS Mutation	AA Mutation	Legacy Mutation ID	Count	Type
10	c.30G>T	p.A10=	COSM6251648	1	Substitution - coding silent
126	c.377A>G	p.N126S	COSM3766948	1	Substitution - Missense
129	c.385A>G	p.R129G	COSM4926748	1	Substitution - Missense
155	c.465G>T	p.M155I	COSM6333993	1	Substitution - Missense
220	c.660A>T	p.V220=	COSM5822820	1	Substitution - coding silent
232	c.695A>G	p.D232G	COSM6275505	1	Substitution - Missense
300	c.898A>G	p.M300V	COSM4950441	1	Substitution - Missense
327	c.980A>C	p.E327A	COSM131419	1	Substitution - Missense
331	c.991G>T	p.A331S	COSM6277430	1	Substitution - Missense
446	c.1338A>T	p.E446D	COSM4916798	1	Substitution - Missense

Supplementary Table 4. Disease ontology, gene ontology, and Kyoto Encyclopedia of Genes and Genomes analysis of the intersection of MAOA positively related co-expressed genes and downregulated differentially expressed genes.

ID	Description	Gene ratio	Bg ratio	P-value	Adjusted P	q-value	Gene ID	Count
Disease Ontology								
DOID:3393	coronary artery disease	34/301	348/8007	2.45E-07	0.000206	0.000181	CYP3A4, ARG1, LIPG, F11, CYP4F2, HP, CYP2C9, CYP2C8, LPA, ABCC9, APOA5, MBL2, APOC4, CYP1A2, CYP2C19, ESR1, IGF1, CD14, AGTR1, CNDP1, VKORC1, KCNMA1, CETP, HNF1A, ADAMTS13, VEGFA, ADRA2B, IGFBP3, PSMA6, TIMP3, CXCL12, CRP, NPC1L1, SELE	34
DOID:5844	myocardial infarction	27/301	279/8007	5.48E-06	0.002303	0.002029	ARG1, LIPG, F11, CYP4F2, HP, CYP2C9, CYP2C8, LPA, ABCC9, APOA5, MBL2, CYP1A2, CYP2C19, ESR1, IGF1, CD14, AGTR1, KCNMA1, CETP, ADAMTS13, VEGFA, ADRA2B, PSMA6, TIMP3, CXCL12, CRP, SELE	27
DOID:655	inherited metabolic disorder	29/301	331/8007	1.7E-05	0.004765	0.004199	BHMT, NR1I2, ABCG5, CBS, LPA, XDH, ABCC9, APOA5, BCKDHA, GCKR, CYP2E1, CYP1A2, ESR1, IGF1, ASL, LCAT, AGTR1, XBP1, PNPLA3, CETP, VEGFA, ECM1, PLIN1, HBB, CXCL12, HAMP, CRP, NPC1L1, SELE	29
DOID:13580	cholestasis	10/301	62/8007	9.19E-05	0.015759	0.013886	ABCB11, NR1I3, NR1I2, MME, SLC22A1, ESR1, CD14, SLC22A3, VEGFA, SELE	10
DOID:18	urinary system disease	35/301	478/8007	0.000102	0.015759	0.013886	CYP4A11, ACACB, HP, CYP2C9, MME, LPA, XDH, ITIH4, ADRA1A, MBL2, ESR1, IGF1, ALPL, PROZ, ADRA1B, AGTR1, CRHBP, DUSP1, CETP, MT2A, ICAM3, ADAMTS13, CCL15, PTH1R, VEGFA, NGFR, SLC34A1, TRPV1, IGFBP3, HAMP, CRP, FOS, ILK, MT1A, SELE	35
Biological Process								
GO:0016054	organic acid catabolic process	45/515	250/17913	2.95E-23	5.92E-20	5.31E-20	ACADL, MAT1A, AGXT, HPD, ALDH4A1, CYP4F3, ADHFE1, ARG1, AMACR, CBS, AGXT2, CYP4F2, TAT, CYP4A11, CYP4F12, AASS, ACACB, AKR1D1, AMDHD1, CTH, HAO2, ACADS, BCKDHA, CYP39A1, GSTZ1, TDO2, FTCD, ALDH8A1, KMO, SDS, AADAT, MTHFS, ASPA, CSAD, GLDC, HOGA1, CYP26A1,	45

							PLIN5, HAL, UROC1, IDO2, LYVE1, CEL, STAB2, PRODH	
GO:0046395	carboxylic acid catabolic process	45/515	250/17913	2.95E-23	5.92E-20	5.31E-20	ACADL, MAT1A, AGXT, HPD, ALDH4A1, CYP4F3, ADHFE1, ARG1, AMACR, CBS, AGXT2, CYP4F2, TAT, CYP4A11, CYP4F12, AASS, ACACB, AKR1D1, AMDHD1, CTH, HAO2, ACADS, BCKDHA, CYP39A1, GSTZ1, TDO2, FTCD, ALDH8A1, KMO, SDS, AADAT, MTHFS, ASPA, CSAD, GLDC, HOGA1, CYP26A1, PLIN5, HAL, UROC1, IDO2, LYVE1, CEL, STAB2, PRODH	45
GO:1901605	alpha-amino acid metabolic process	38/515	200/17913	1.17E-20	1.56E-17	1.4E-17	BHMT, CPS1, GLYAT, MAT1A, AGXT, HPD, ALDH4A1, GNMT, ADHFE1, ARG1, CBS, AGXT2, TAT, AASS, AMDHD1, CTH, NAGS, GSTZ1, TDO2, FTCD, ALDH8A1, KMO, SDS, AADAT, MTHFS, ASPA, CSAD, GLDC, HOGA1, DCT, HAL, UROC1, IDO2, MTHFD2L, ADSSL1, OAT, ACCS, PRODH	38
GO:0044282	small molecule catabolic process	52/515	404/17913	7.75E-20	7.78E-17	6.98E-17	ACADL, MAT1A, AGXT, HPD, ALDH4A1, CYP4F3, ADHFE1, ARG1, AMACR, CBS, AGXT2, CYP4F2, TAT, CYP4A11, CYP4F12, AASS, ACACB, AKR1D1, AMDHD1, CTH, HAO2, ACADS, BCKDHA, ADH4, CYP1A1, CYP39A1, GSTZ1, TDO2, FTCD, ALDH8A1, KMO, SDS, AADAT, MTHFS, SULT1B1, SULT1E1, ASPA, CSAD, CDA, GLDC, HOGA1, CYP26A1, PLIN5, HAL, UROC1, ENO3, IDO2, LYVE1, CYP46A1, CEL, STAB2, PRODH	52
GO:0006520	cellular amino acid metabolic process	47/515	347/17913	6.31E-19	5.07E-16	4.54E-16	BHMT, CPS1, GLYAT, MAT1A, AGXT, HPD, ALDH4A1, GNMT, ADHFE1, ARG1, CBS, AGXT2, TAT, AASS, PSMA2, AMDHD1, CTH, BCKDHA, NAGS, GSTZ1, TDO2, FTCD, ALDH8A1, KMO, SDS, AADAT, MTHFS, ACY1, ASPA, CSAD, GLS2, SLC7A2, GLDC, HOGA1, SCLY, DCT, HAL, UROC1, IDO2, PSMC1, ASPG, MTHFD2L, PSMA6, ADSSL1, OAT, ACCS, PRODH	47
Cellular Component								

GO:0072562	blood microparticle	18/539	147/18678	2.51E-07	0.00011	0.000106	C8A, AFM, HP, ITIH4, CFB, C1R, CFHR3, A1BG, ORM1, SERPINA3, FCN2, C9, CD5L, ORM2, FCN3, HBB, PZP, HBD	18
GO:0034358	plasma lipoprotein particle	7/539	37/18678	7.78E-05	0.008693	0.00836	LPA, APOA5, APOC4, APOF, LCAT, SAA4, CETP	7
GO:1990777	lipoprotein particle	7/539	37/18678	7.78E-05	0.008693	0.00836	LPA, APOA5, APOC4, APOF, LCAT, SAA4, CETP	7
GO:0034364	high-density lipoprotein particle	6/539	26/18678	7.9E-05	0.008693	0.00836	APOA5, APOC4, APOF, LCAT, SAA4, CETP	6
GO:0032994	protein-lipid complex	7/539	39/18678	0.000111	0.009727	0.009355	LPA, APOA5, APOC4, APOF, LCAT, SAA4, CETP	7
Molecular Function								
GO:0004497	monooxygenase activity	23/511	86/16969	5.11E-16	3.25E-13	2.79E-13	CYP3A4, CYP4F3, CYP4F2, CYP4A11, CYP4F12, CYP2C9, CYP2C8, CYP3A43, CYP1A1, CYP39A1, CYP2E1, CYP1A2, CYP2C19, CYP2A6, CYP2B6, KMO, CYP2A7, CYP26A1, CYP4A22, DBH, CYP46A1, CYP11B1, MICAL3	23
GO:0048037	cofactor binding	49/511	438/16969	1.86E-15	5.91E-13	5.08E-13	ACADL, CYP3A4, AGXT, CYP4F3, CBS, AGXT2, CYP4F2, OGDHL, TAT, CYP4A11, CYP4F12, ACACB, CTH, XDH, ACADS, CYP3A43, ADH4, CYP1A1, CYP39A1, CYP2E1, CYP1A2, CYP2C19, CYP2A6, CYP2B6, NDUFV2, TDO2, GPD1, KMO, SDS, AADAT, GCH1, CSAD, DHODH, VKORC1, GLDC, CYP26A1, HPGD, PNPLA3, IDO2, CYP4A22, DBH, CYP46A1, AOC2, CYP11B1, STEAP4, ACCS, GSTM2, MICAL3, PRODH	49
GO:0020037	heme binding	21/511	106/16969	5.58E-12	1.18E-09	1.01E-09	CYP3A4, CYP4F3, CBS, CYP4F2, CYP4A11, CYP4F12, CYP3A43, CYP1A1, CYP39A1, CYP2E1, CYP1A2, CYP2C19, CYP2A6, CYP2B6, TDO2, CYP26A1, IDO2, CYP4A22, CYP46A1, CYP11B1, STEAP4	21
GO:0046906	tetrapyrrole binding	21/511	116/16969	3.41E-11	5.41E-09	4.65E-09	CYP3A4, CYP4F3, CBS, CYP4F2, CYP4A11, CYP4F12, CYP3A43, CYP1A1, CYP39A1, CYP2E1, CYP1A2,	21

							CYP2C19, CYP2A6, CYP2B6, TDO2, CYP26A1, IDO2, CYP4A22, CYP46A1, CYP11B1, STEAP4	
GO:0005506	iron ion binding	23/511	144/16969	5.66E-11	7.19E-09	6.17E-09	CYP3A4, CYP8B1, CYP4F3, CYP4F2, CYP4A11, CYP4F12, CYP2C9, CYP2C8, XDH, CYP3A43, CYP1A1, CYP39A1, BBOX1, CYP2E1, CYP1A2, CYP2C19, CYP2A6, CYP2B6, CYP2A7, CYP26A1, CYP4A22, CYP46A1, CYP11B1	23
KEGG pathway								
hsa00830	Retinol metabolism	15/325	67/8011	4.9E-08	1.34E-05	1.21E-05	CYP3A4,ADH1A,CYP4A11,RDH16,CYP2C9,CYP2C8,ADH4,CYP1A1,CYP1A2,CYP2A6,CYP2B6,RDH5,CYP26A1,CYP4A22,UGT2B17	15
hsa05204	Chemical carcinogenesis	16/325	82/8011	1.36E-07	1.87E-05	1.68E-05	CYP3A4,ADH1A,CYP2C9,CYP2C8,CYP3A43,ADH4,CYP1A1,NAT2,CYP2E1,CYP1A2,CYP2C19,CYP2A6,GSTA5,UGT2B17,GSTT2,GSTM2	16
hsa00982	Drug metabolism - cytochrome P450	14/325	72/8011	8.76E-07	8E-05	7.19E-05	CYP3A4,ADH1A,CYP2C9,CYP2C8,ADH4,CYP2E1,CYP1A2,CYP2C19,CYP2A6,CYP2B6,GSTA5,UGT2B17,GSTT2,GSTM2	14
hsa00980	Metabolism of xenobiotics by cytochrome P450	13/325	76/8011	9.61E-06	0.000658	0.000592	CYP3A4,ADH1A,CYP2C9,ADH4,CYP1A1,CYP2E1,CYP1A2,CYP2A6,CYP2B6,GSTA5,UGT2B17,GSTT2,GSTM2	13
hsa00140	Steroid hormone biosynthesis	11/325	60/8011	2.38E-05	0.001093	0.000982	CYP3A4,AKR1D1,CYP1A1,CYP2E1,SRD5A2,CYP1A2,SULT1E1,HSD3B2,HSD17B3,UGT2B17,CYP11B1	11

Supplementary Table 5. Disease ontology, gene ontology, and Kyoto Encyclopedia of Genes and Genomes analysis of the intersection of MAOA negatively related co-expressed genes and upregulated differentially expressed genes.

ID	Description	Gene ratio	Bg ratio	P-value	Adjusted P	q-value	Gene ID	Count
Disease Ontology								
DOID:12155	lymphocytic choriomeningitis	3/93	8/8007	8.14E-05	0.031742	0.026821	CCR5,CD86,CXCR3	3
DOID:2377	multiple sclerosis	9/93	169/8007	0.000141	0.031742	0.026821	BDKRB1,CCL5,CCR5,CD1A,CHIT1,CXCR3,HLA-DPB1,HLA-DRA,SLC1A3	9
DOID:3213	demyelinating disease	9/93	175/8007	0.000184	0.031742	0.026821	BDKRB1,CCL5,CCR5,CD1A,CHIT1,CXCR3,HLA-DPB1,HLA-DRA,SLC1A3	9
DOID:6367	acral lentiginous melanoma	2/93	3/8007	0.000397	0.051276	0.043326	CDKN2A,CSPG4	2
DOID:14268	sclerosing cholangitis	3/93	15/8007	0.000624	0.051276	0.043326	CCL5,CCR5,CDKN2A	3
Biological Process								
GO:0042110	T cell activation	18/158	443/17913	7.60E-08	0.000192	0.000173	AIF1,CCL5,CD2,CD3D,CD3G,CD74,CD83,CD86,FOXJ1,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,PLA2G2D,RELB,SIT1,TNFRSF4,ZNF683	18
GO:0051249	regulation of lymphocyte activation	16/158	401/17913	5.35E-07	0.000676	0.00061	AIF1,CCL5,CD2,CD74,CD83,CD86,FOXJ1,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,IL27RA,SIT1,SOX11,TNFRSF4,ZNF683	16
GO:0002694	regulation of leukocyte activation	17/158	492/17913	1.70E-06	0.001429	0.001288	AIF1,C1QA,CCL5,CD2,CD74,CD83,CD86,FOXJ1,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,IL27RA,SIT1,SOX11,TNFRSF4,ZNF683	17
GO:0050863	regulation of T cell activation	13/158	307/17913	3.42E-06	0.002162	0.001949	AIF1,CCL5,CD2,CD74,CD83,CD86,FOXJ1,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,SIT1,ZNF683	13
GO:0070098	chemokine-mediated	6/158	51/17913	5.56E-06	0.002808	0.002531	CCL26,CCL5,CCR5,CCR8,CXCR3,ROBO1	6

	signaling pathway							
Cellular Component								
GO:0042613	MHC class II protein complex	7/163	16/18678	3.63E-11	8.78E-09	7.79E-09	CD74,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,HLA-DQB2,HLA-DRA	7
GO:0042611	MHC protein complex	7/163	25/18678	1.43E-09	1.73E-07	1.53E-07	CD74,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,HLA-DQB2,HLA-DRA	7
GO:0030669	clathrin-coated endocytic vesicle membrane	6/163	40/18678	1.21E-06	9.76E-05	8.66E-05	CD74,FZD2,HLA-DPA1,HLA-DPB1,HLA-DQB2,HLA-DRA	6
GO:0071556	integral component of lumenal side of endoplasmic reticulum membrane	5/163	29/18678	4.77E-06	0.00022	0.000195	CD74,HLA-DPA1,HLA-DPB1,HLA-DQB2,HLA-DRA	5
GO:0098553	lumenal side of endoplasmic reticulum membrane	5/163	29/18678	4.77E-06	0.00022	0.000195	CD74,HLA-DPA1,HLA-DPB1,HLA-DQB2,HLA-DRA	5
Molecular Function								
GO:0032395	MHC class II receptor activity	4/154	10/16969	1.31E-06	0.000376	0.000334	HLA-DOA,HLA-DPA1,HLA-DQB2,HLA-DRA	4
GO:0023026	MHC class II protein complex binding	4/154	16/16969	1.09E-05	0.00156	0.001389	CD74,HLA-DMB,HLA-DOA,HLA-DRA	4
GO:0015026	coreceptor activity	5/154	40/16969	2.94E-05	0.0028	0.002494	CCR5,CCR8,CD86,IGSF1,RAMP2	5

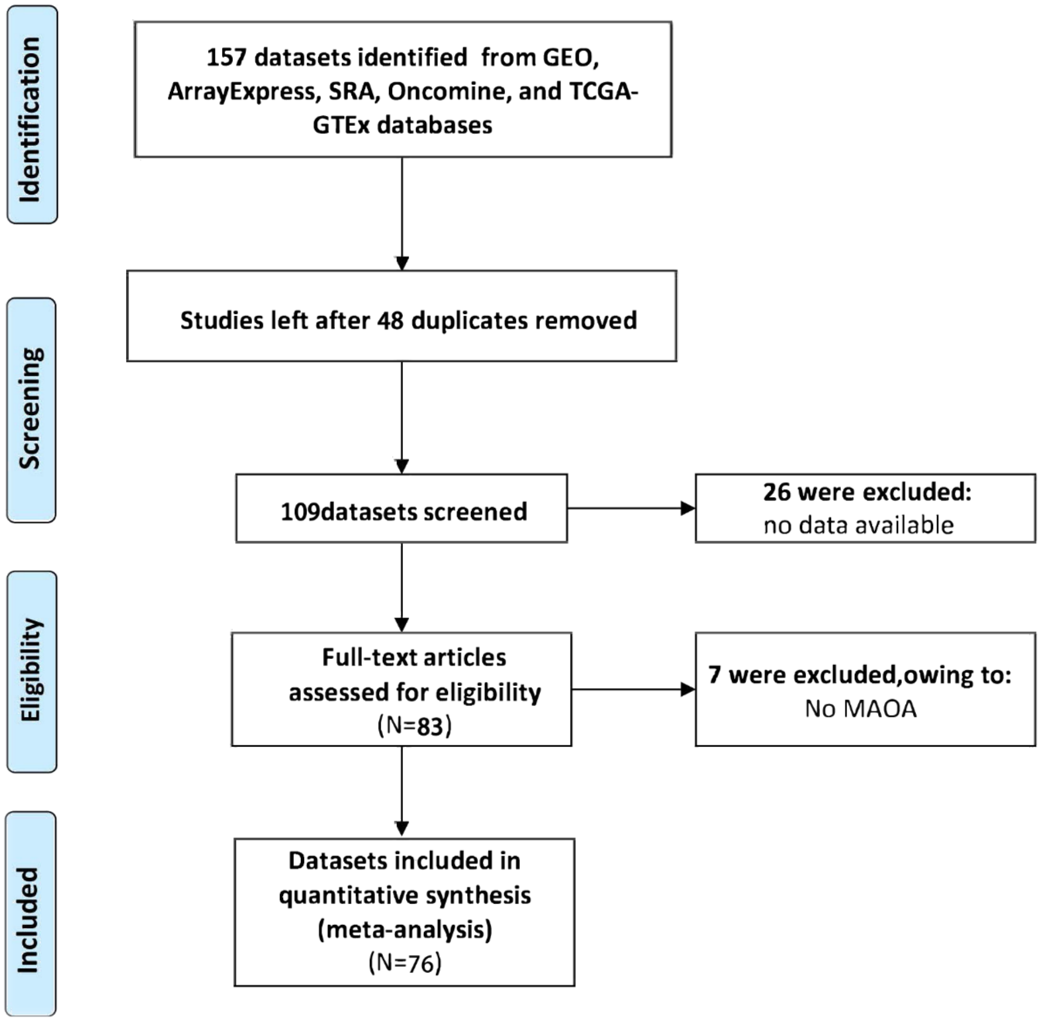
GO:0023023	MHC protein complex binding	4/154	25/16969	7.11E-05	0.005086	0.00453	CD74,HLA-DMB,HLA-DOA,HLA-DRA	4
GO:0042277	peptide binding	8/154	215/16969	0.000782	0.041215	0.03671	BDKRB1,C1QA,CD74,HLA-DPA1,HLA-DPB1,HLA-DRA,MSR1,RAMP2	8
KEGG pathway								
hsa05323	Rheumatoid arthritis	11/79	93/7946	1.45E-09	2.25E-07	1.76E-07	ACP5,ATP6V0D2,CCL20,CCL5,CD86,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,HLA-DRA,LTB	11
hsa04640	Hematopoietic cell lineage	10/79	99/7946	4.02E-08	3.12E-06	2.43E-06	CD1A,CD2,CD3D,CD3G,CD5,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,HLA-DRA	10
hsa05166	Human T-cell leukemia virus 1 infection	13/79	219/7946	1.96E-07	1.01E-05	7.92E-06	BUB1B,CD3D,CD3G,CDKN2A,E2F1,E2F2,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,HLA-DRA,MSX1,RELB	13
hsa05150	Staphylococcus aureus infection	9/79	96/7946	3.85E-07	1.49E-05	1.16E-05	C1QA,C1QC,C3AR1,FPR3,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,HLA-DRA	9
hsa05330	Allograft rejection	6/79	38/7946	1.71E-06	5.29E-05	4.13E-05	CD86,HLA-DMB,HLA-DOA,HLA-DPA1,HLA-DPB1,HLA-DRA	6

Supplementary Table 6. Clinical significance of MAOA protein expression level based on in-house tissue microarray.

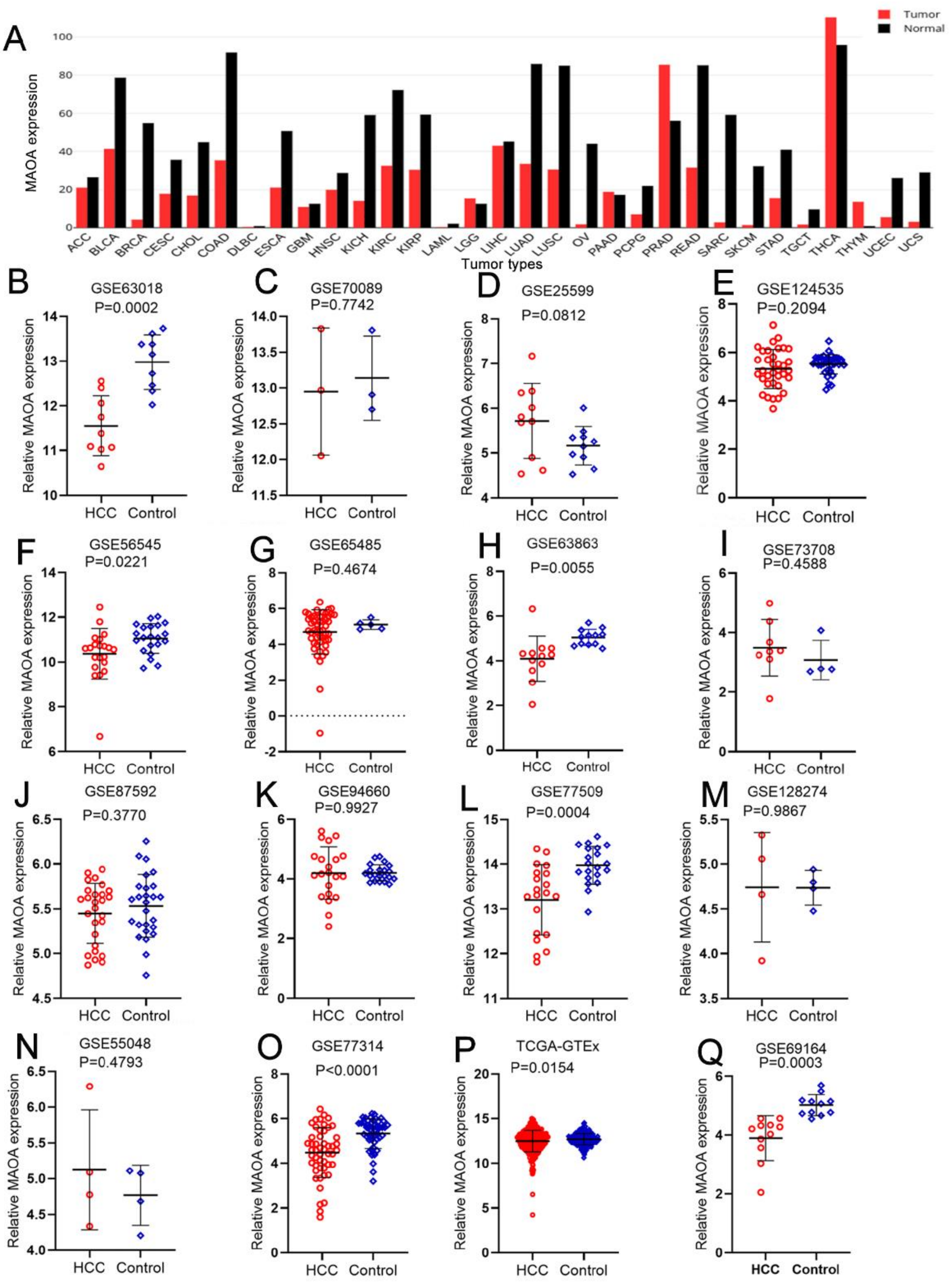
Clinical features	**MAOA protein expression level**			**t**	**df**	**P-value**
	N	**M**	**SD**			
Tissue						
HCC	315	8.4190	2.4886	18.3753	495.1975	<0.0001*
non-HCC	192	11.5208	1.3023			
Age						
<60	231	8.5714	2.4782	1.8087	313.0000	0.0715
>=60	84	8.0000	2.4837			
Gender						
Male	274	8.4672	2.5651	1.1064	64.2379	0.2727
Female	41	8.0976	1.8948			
Pathological stage						
I	17	8.7059	2.1144	0.1547	312.0000	0.9608
I-II	25	8.1600	2.4440			
II	204	8.4314	2.4735			
II-III	27	8.5926	2.6495			
III	40	8.4000	2.6871			
TNM						
T1-T2	235	9.0894	2.0351	8.0882	109.9644	<0.0001*
T3-T4	79	6.4304	2.6732			
TNM_T						
T1	3	12.0000	0.0000	30.5695	313.0000	<0.0001*
T2	232	9.0517	2.0209			
T3	72	6.4444	2.7316			
T4	7	6.2857	2.1381			
TNM_N						
N0	307	8.4300	2.4992	0.4507	312.0000	0.6525
N1	7	8.0000	2.3094			
TNM_M						
M0	313	8.4345	2.4839	1.7825	312.0000	0.0756
M1	1	4.0000	/			
Smoking						
No	91	8.2198	2.6907	0.3919	159.0000	0.6956
Yes	70	8.0571	2.5015			
Alcohol consumption						
No	82	8.3415	2.6815	0.9551	159.0000	0.3410
Yes	79	7.9494	2.5212			
Hepatitis history						
No	60	8.4000	2.7259	0.7184	147.0000	0.4736
Yes	89	8.0899	2.4847			
Family liver cancer history						
No	132	8.3939	2.5615	-0.0574	139.0000	0.9543

Yes	9	8.4444	2.4037			
Tumor size (cm)						
<3	10	9.6000	2.7968	1.7131	133.0000	0.0890
>=3	125	8.0960	2.6622			

Footnote: [*]A P-value < 0.05 indicates statistical significance.

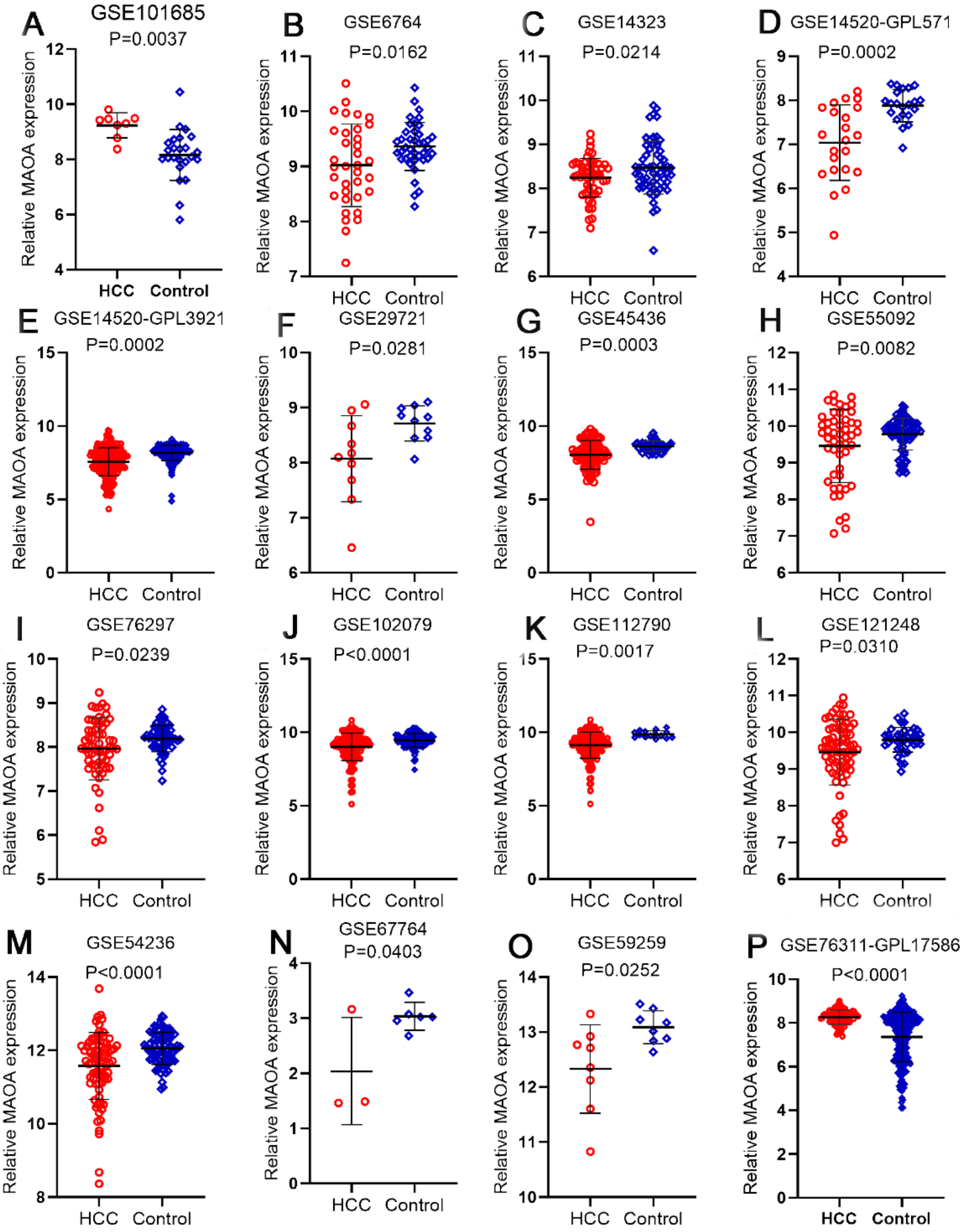


Supplementary Figure 1. The flow chart of the included datasets for differentially expressed gene analysis.



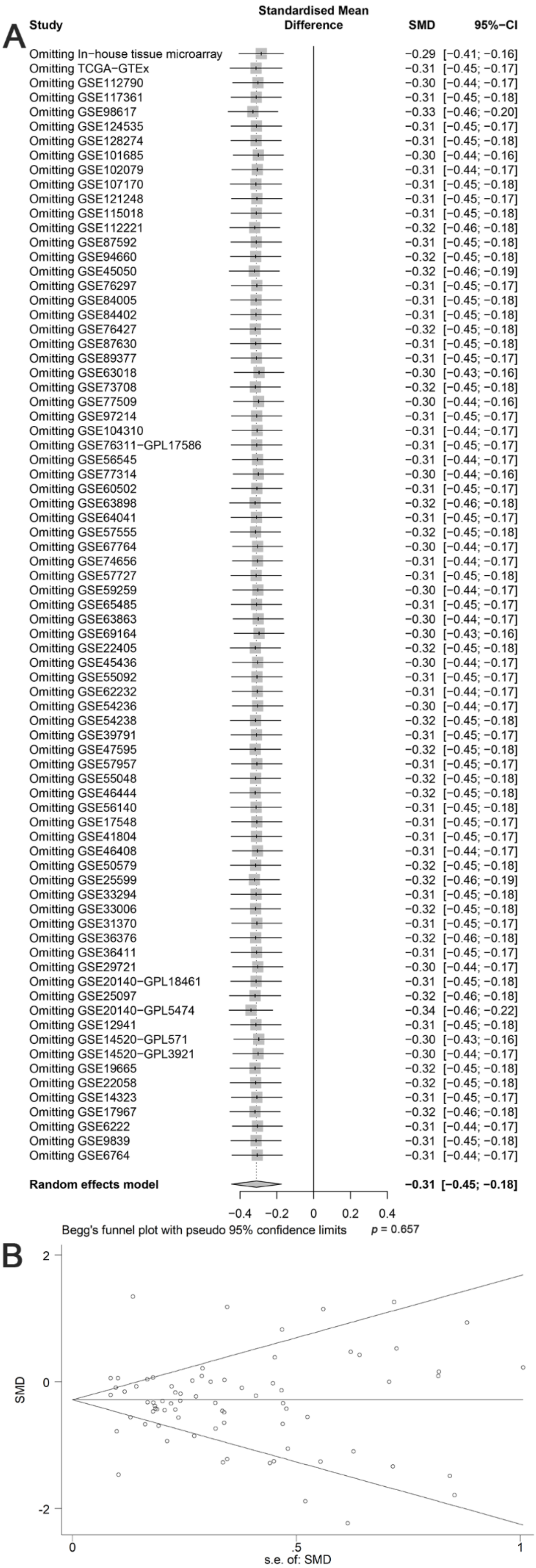
Supplementary Figure 2. The expression status of *MAOA* in various tumors and scatter plot of the *MAOA* expression levels. Decreased *MAOA* expression levels were found in hepatocellular carcinoma patients compared to non-cancer groups based on the included RNA sequencing datasets. TCGA, the Cancer Genome Atlas; GTEx, the Genotype-Tissue Expression; LIHC, liver hepatocellular carcinoma. The error bars in the scatter dot plot line at mean with standard deviation.

(A) The expression statuses in 31 kinds of tumors from Gene Expression Profiling Interactive Analysis (GEPIA). **(B)** GSE63018, **(C)** GSE70089, **(D)** GSE25599, **(E)** GSE124535, **(F)** GSE56545, **(G)** GSE65485, **(H)** GSE63863, **(I)** GSE73708, **(J)** GSE87592, **(K)** GSE94660, **(L)** GSE77509, **(M)** GSE128274, **(N)**GSE55048, **(O)** GSE77314, **(P)** TCGA-GTEx, and **(Q)** GSE69164.

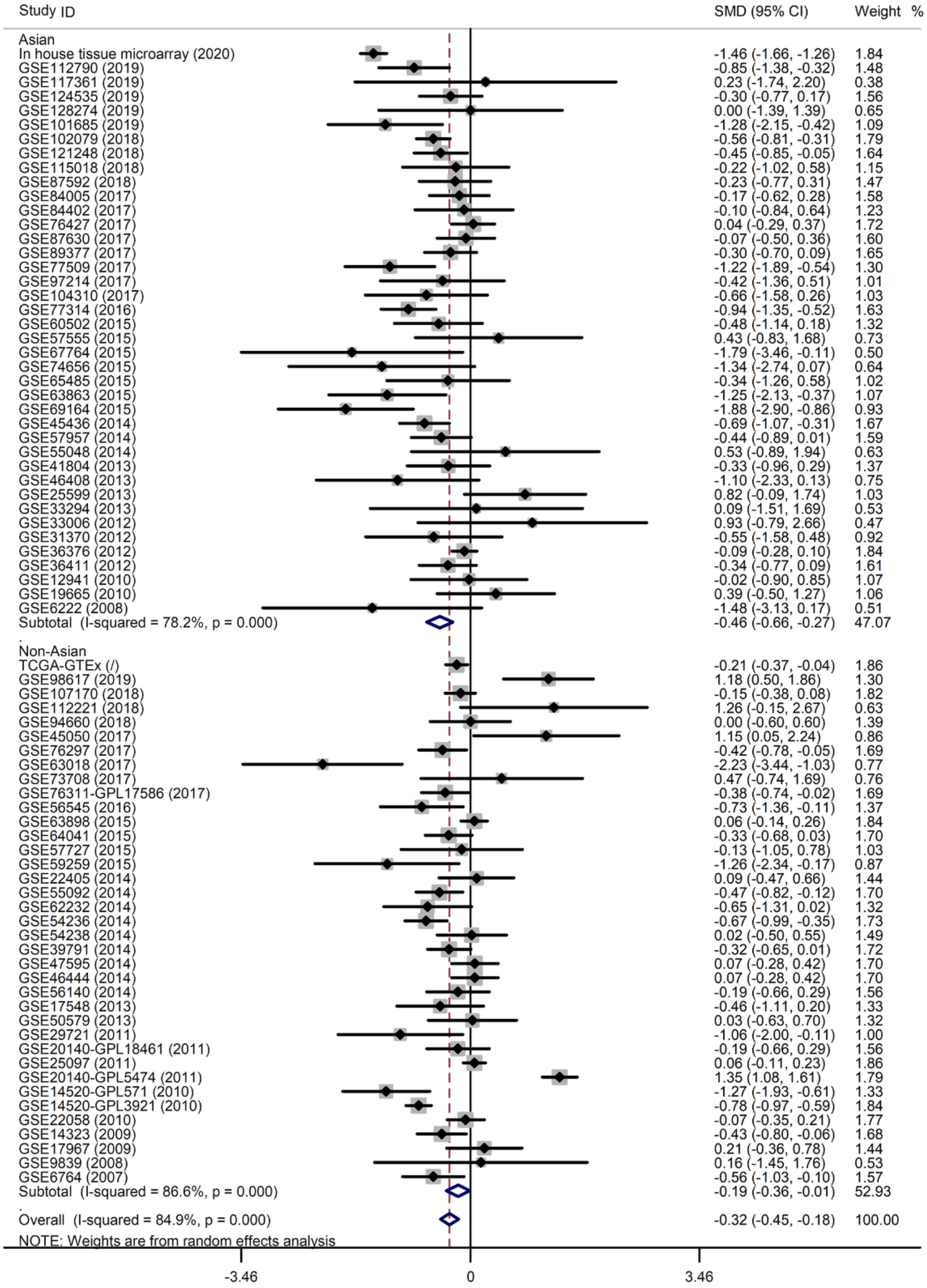


Supplementary Figure 3. Scatter plot of the MAOA expression between hepatocellular carcinoma patients and non-cancer groups based on the included genechip datasets. The error bars in the scatter dot plot line at mean with standard deviation.

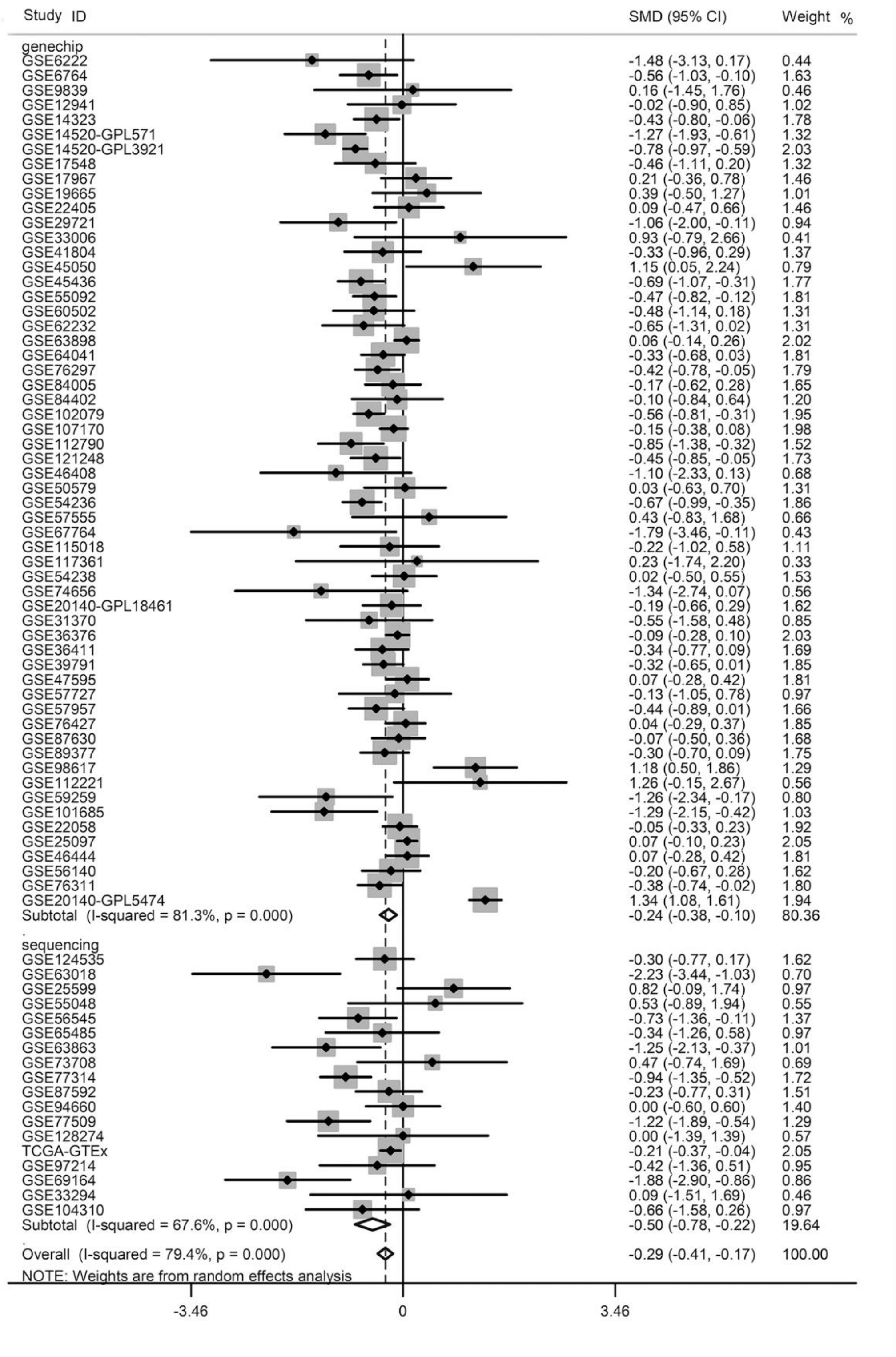
(A) GSE101685, **(B)** GSE6764, **(C)** GSE14323, **(D)** GSE14520-GPL571, **(E)** GSE14520-GPL3921, **(F)** GSE29721, **(G)** GSE45436, **(H)** GSE55092, **(I)** GSE76297, **(J)** GSE102079, **(K)** GSE112790, **(L)** GSE121248, **(M)** GSE54236, **(N)** GSE67764, **(O)** GSE59259, and **(P)** GSE76311-GPL17586.



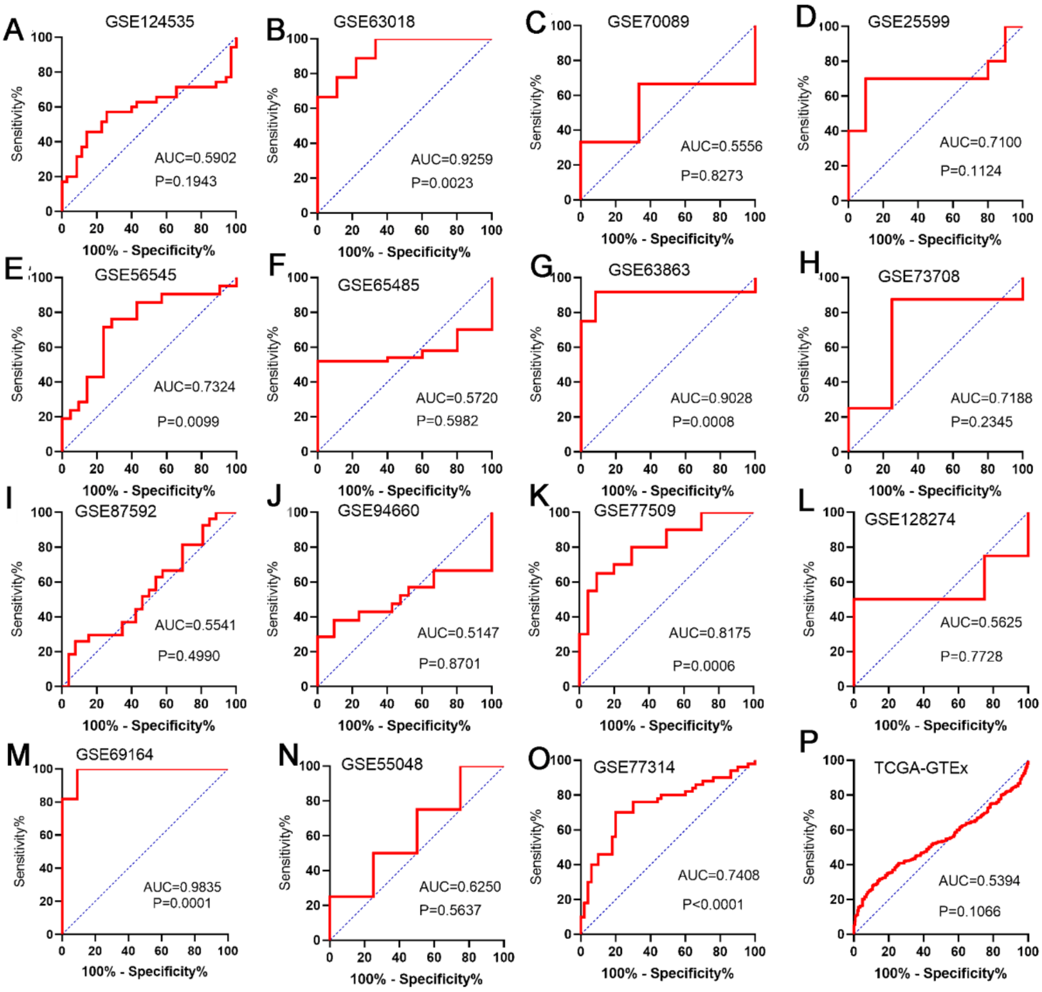
Supplementary Figure 4. Assessment of the heterogeneity source. **(A)** Sensitive analysis indicated that no significant difference existed among the enrolled studies. **(B)** Begg's funnel plot showed that there was no significant publication bias.



Supplementary Figure 5. Subgroup analysis based on the ethnicities of hepatocellular carcinoma patients. No significant difference between subgroups was found.

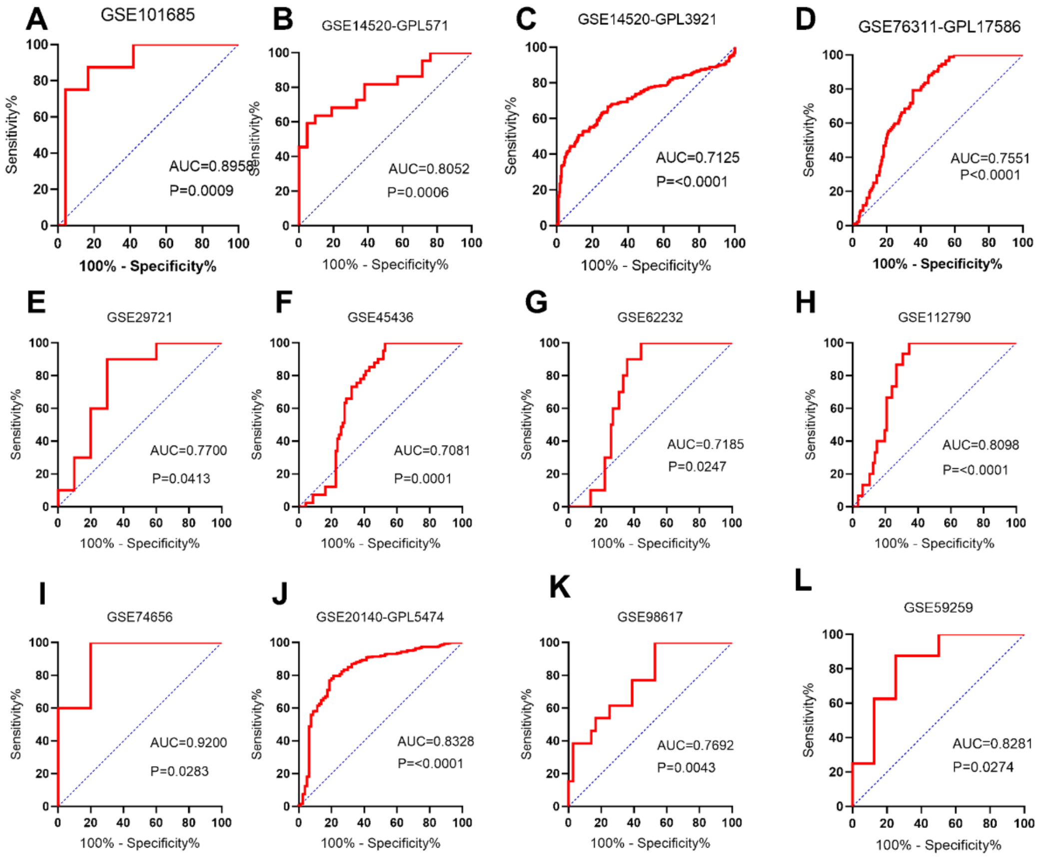


Supplementary Figure 6. Subgroup analysis based on the included datasets in terms of the methods used to determine the expression levels of *MAOA* in hepatocellular carcinoma patients (i.e., genechip and RNA-sequencing). No significant difference between subgroups was found.

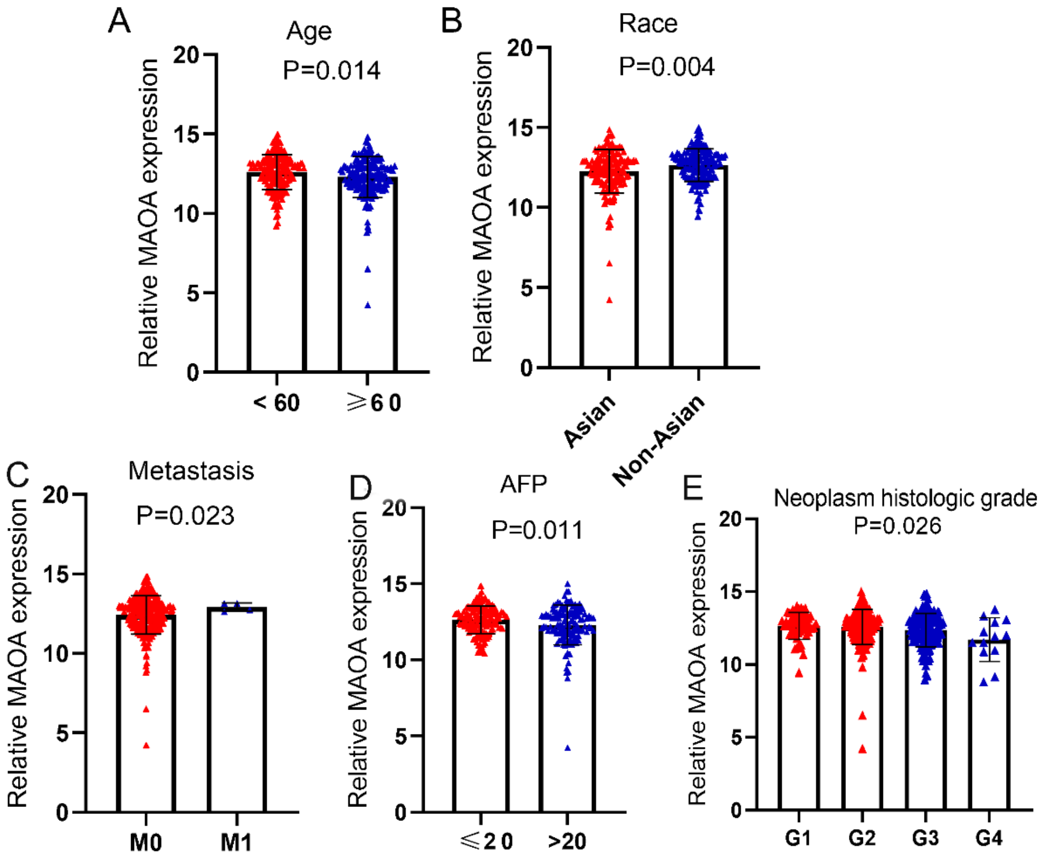


Supplementary Figure 7. The Receiver Operating Characteristic (ROC) curve of *MAOA* expression based on the included RNA sequencing datasets. TCGA, the Cancer Genome Atlas; GTEx, the Genotype-Tissue Expression.

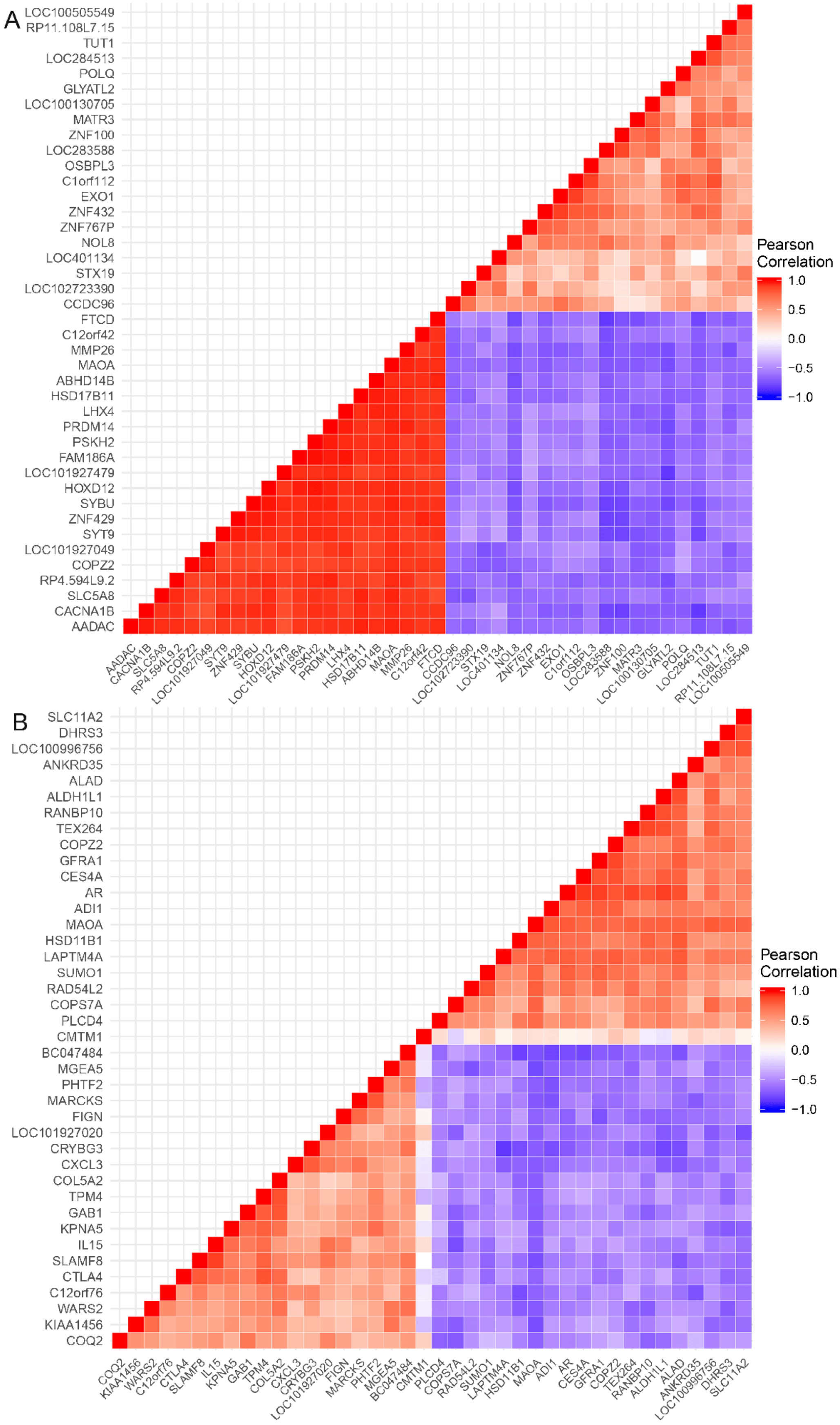
(A) GSE124535, **(B)** GSE63018, **(C)** GSE70089, **(D)** GSE25599, **(E)** GSE56545, **(F)** GSE65485, **(G)** GSE63863, **H**）GSE73708,**(I)** GSE87592, **(J)** GSE94660,(K) GSE77509, **(L)** GSE128274, **(M)** GSE69164, **(N)** GSE55048, **(O)** GSE77314, and **(P)** TCGA-GTEx.



Supplementary Figure 8. The Receiver Operating Characteristic (ROC) curve of MAOA expression based on the included genechip datasets.
(A) GSE101685, **(B)** GSE14520-GPL571, **(C)** GSE14520-GPL3921, **(D)** GSE76311-GPL17586, **(E)** GSE29721, **(F)** GSE45436, **(G)** GSE62232, **(H)** GSE112790, **(I)** GSE74656, **(J)** GSE20140-GPL5474, **(K)** GSE98617, and **(L)** GSE59259.

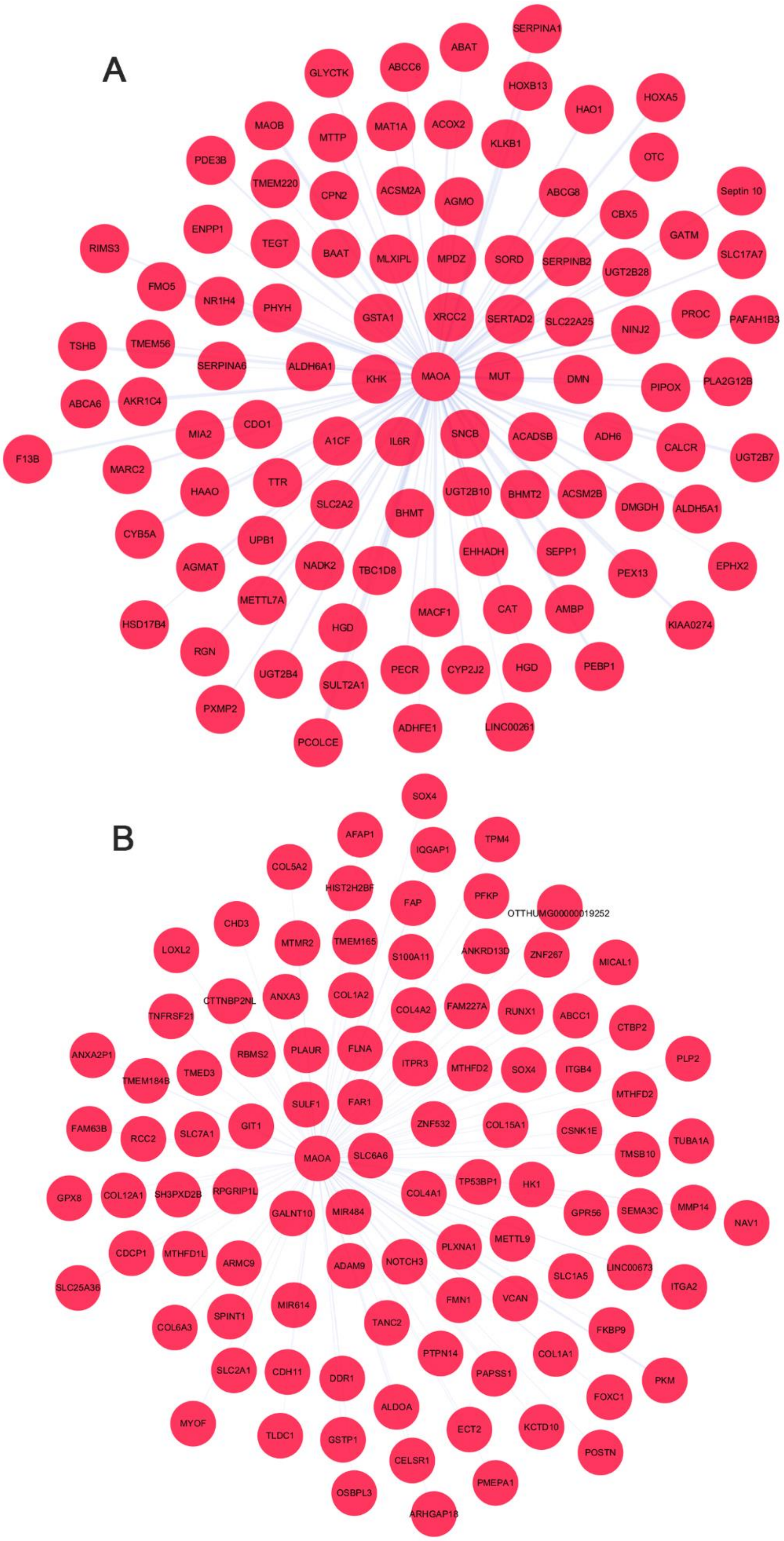


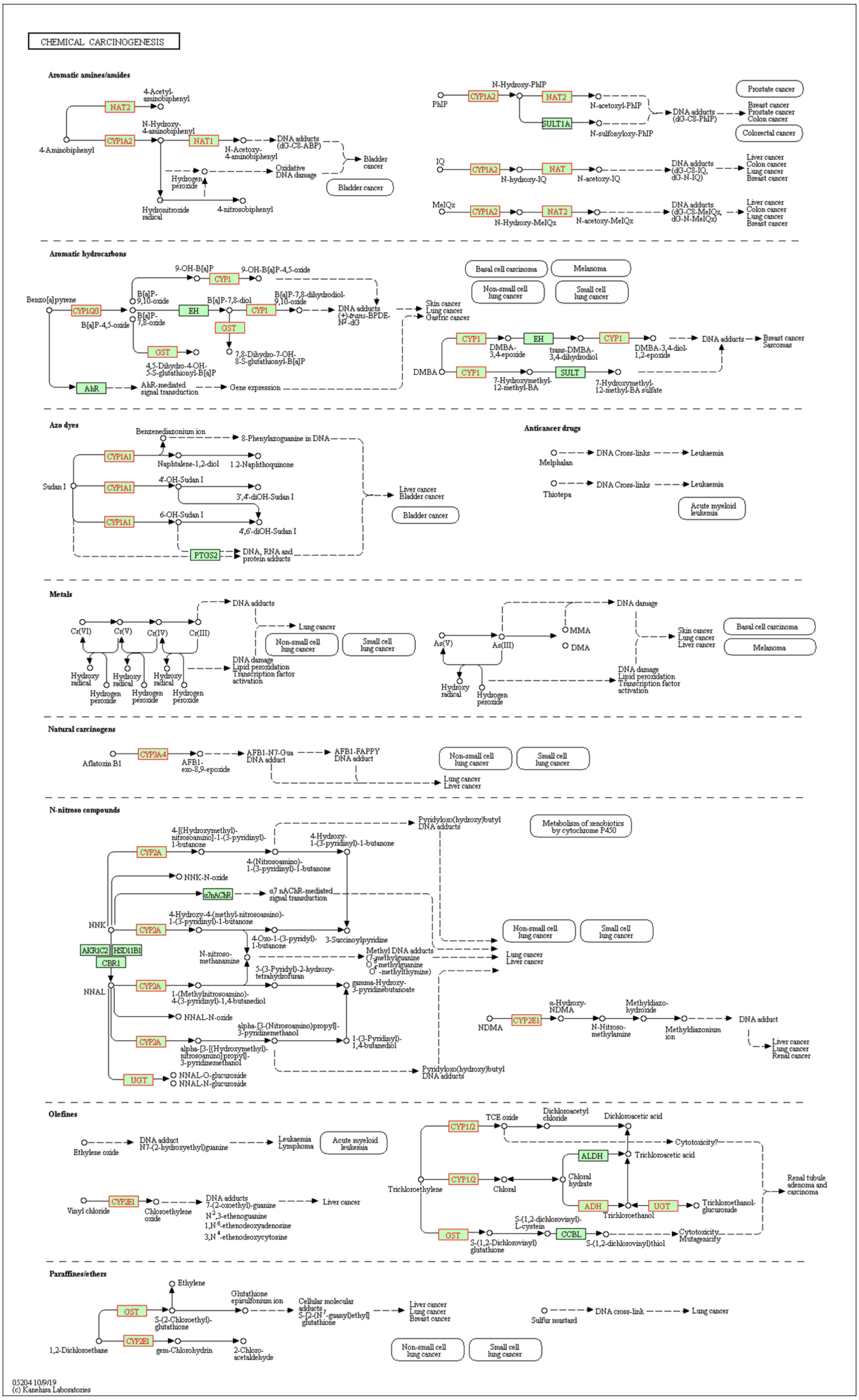
Supplementary Figure 9. The relationships between the clinical features of HCC patients and *MAOA* mRNA expression level. The down-regulated expression level of *MAOA* was relevant to age, race, tumor metastasis status, neoplasm histologic grade, and AFP concentration (> 20 ng/mL) (all with P-values < 0.05).



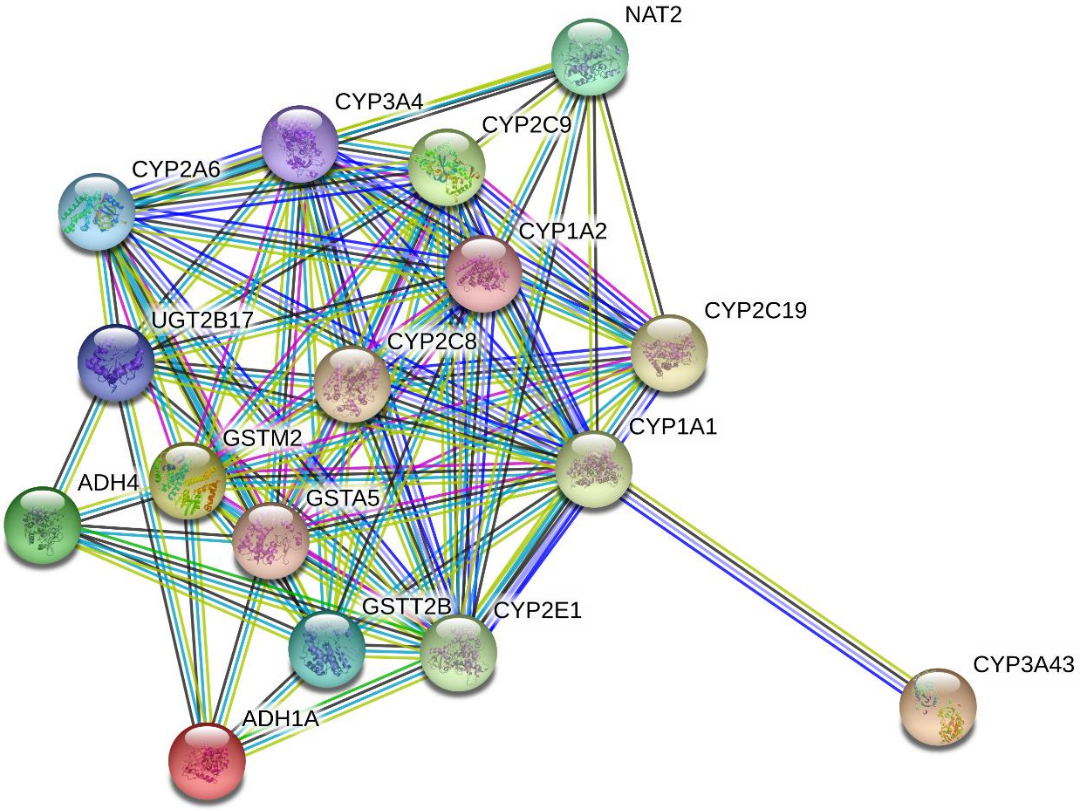
Supplementary Figure 10. Heatmaps based on the calculated Pearson's correlation coefficient of **(A)** GSE6222 and **(B)** GSE19665.

Supplementary Figure 11. Relationship network diagram based on **(A)** the positively related genes; **(B)** the negatively related genes. *PCOLCE* and *TBC1D8* were the most significant co-expressed genes positively related to *MAOA* and *PKM* were the most significant co-expressed genes negatively related to *MAOA*. The thickness of the edges was proportional to the statistical significance.

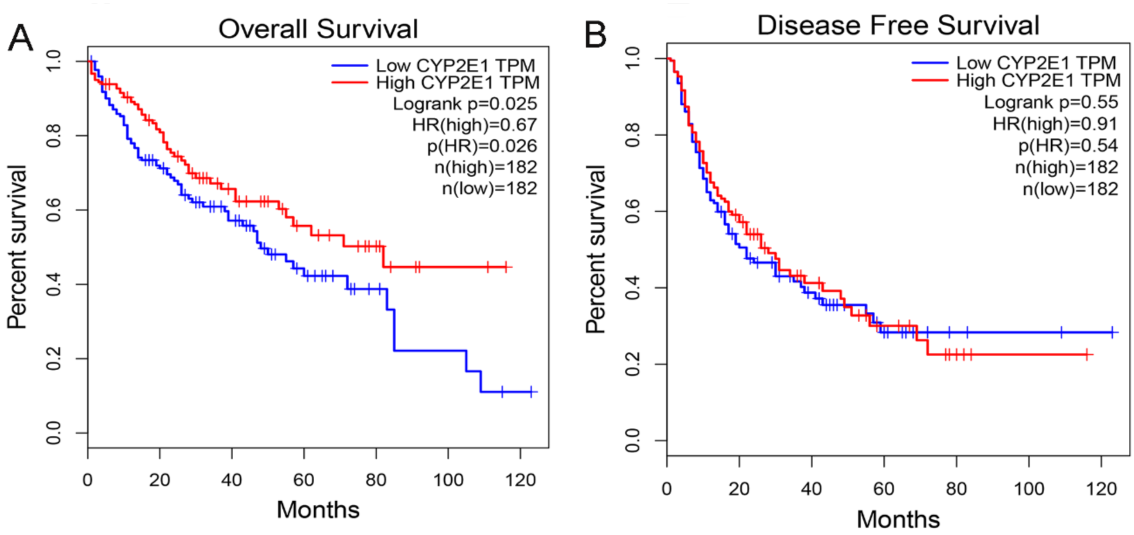




Supplementary Figure 12. The significantly clustered KEGG pathway (hsa05204) based on the intersection genes of *MAOA* positively related co-expressed genes (CEGs) and downregulated differentially expressed genes (DEGs). KEGG, the Kyoto Encyclopedia of Genes and Genomes.

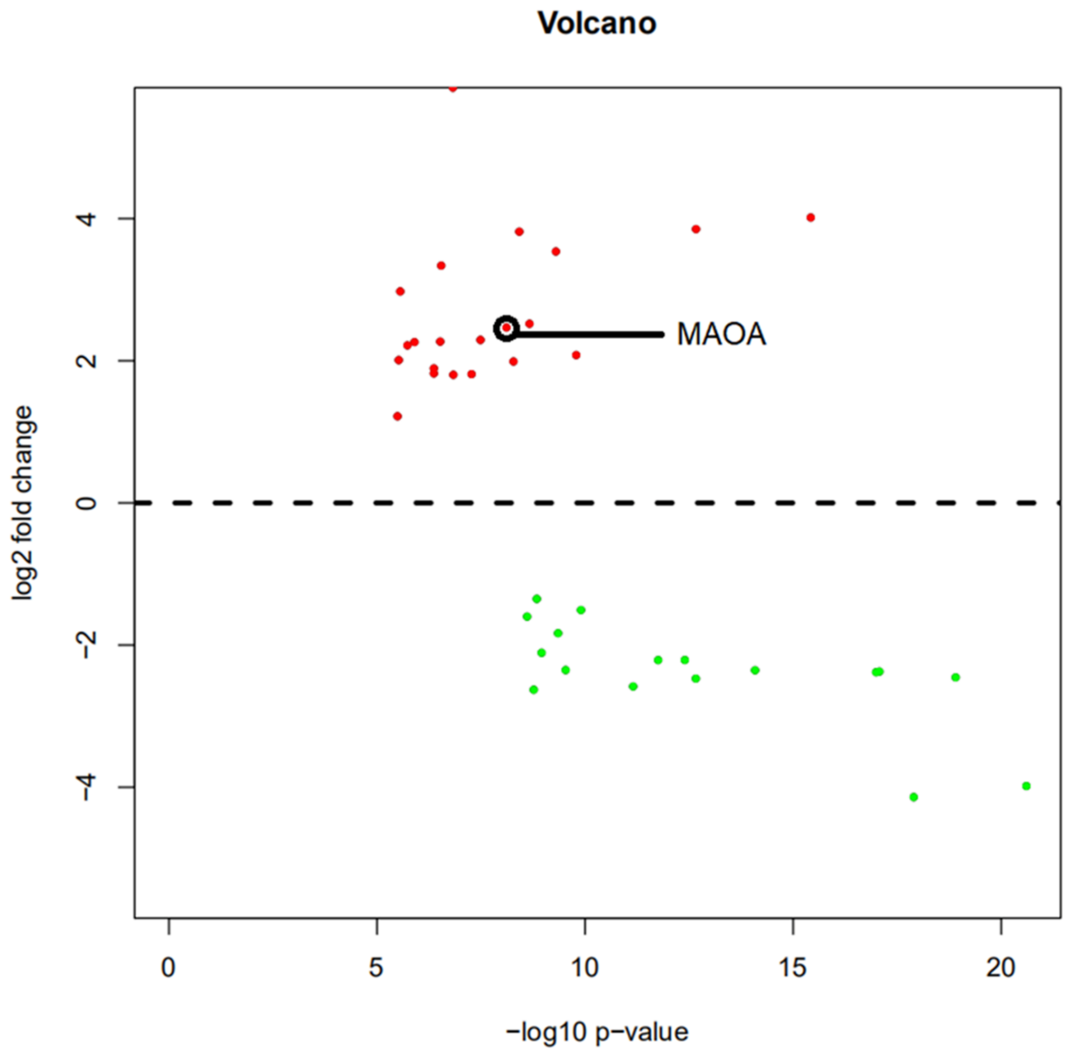


Supplementary Figure 13. Protein-to-protein interaction network based on the genes clustered in the Chemical carcinogenesis pathway.



Supplementary Figure 14. Kaplan-Meier curves of the hepatocellular carcinoma patients based on the hub gene.

(A) Low CYP2E1 correlated with reduced overall survival in HCC patients. **(B)** The disease-free survival condition of low and high CYP2E1 group in HCC patients signified no significant difference.



Supplementary Figure 15 A volcano plot based on differentially expressed genes of NC-treated HCC mouse model. *MAOA* expression level was significantly elevated in NC-treated group compared to control group. NC, nitidine chloride.