

Supplementary Table 6. The 32 marker genes of the diagnostic model for early HCC.

Gene	Gene Body		H3K4me1 ^c		H3K27ac ^c		Enhancer ^c	
	Position ^a	Coefficient ^b	r	p-value	r	p-value	r	p-value
RAPGEF5	chr7:22157856-22396763	1.868	0.703	<0.001	0.651	<0.001	0.255	<0.001
FGD6	chr12:95470525-95611258	1.359	0.376	<0.001	0.314	<0.001	0.140	<0.001
PRKAA1	chr5:40759481-40798476	1.201	0.715	<0.001	0.737	<0.001	-	-
EVC	chr4:5712924-5816032	1.130	0.774	<0.001	0.624	<0.001	0.262	<0.001
GNRH1	chr8:25276774-25282556	1.094						
CHST9	chr18:24486445-24765281	0.991	0.891	<0.001	0.799	<0.001		
NPBWR1	chr8:53850991-53853677	0.987	0.830	<0.001				
UBE2G2	chr21:46188495-46221934	0.936	0.676	<0.001	0.399	<0.001	0.201	<0.001
MEIS2	chr15:37181405-37393500	0.913	0.888	<0.001	0.880	<0.001	0.520	<0.001
CAP2	chr6:17393447-17558023	0.911	0.450	<0.001	0.660	<0.001		
CCNI2	chr5:132083137-132090095	0.898	0.447	<0.001			0.120	<0.001
LRRRC61	chr7:150019728-150035239	0.765	0.231	<0.001	0.268	<0.001	0.174	<0.001
A2M	chr12:9220260-9268825	0.677	0.300	<0.001	0.602	<0.001		
CHI3L1	chr1:203148059-203155877	0.629	0.678	<0.001	0.630	<0.001		
FREM2	chr13:39261266-39461268	0.610	0.712	<0.001	0.259	<0.001		
DUSP23	chr1:159750722-159752333	0.525	0.596	<0.001	0.603	<0.001	0.028	NS
MYT1	chr20:62783144-62873606	0.490	0.786	<0.001	0.768	<0.001		
PARD6G	chr18:77915115-78005429	0.437	0.448	<0.001	0.571	<0.001		
NDUFA3	chr19:54606036-54612564	0.406	0.854	<0.001	0.120	<0.001		
FGF19	chr11:69513000-69519410	0.307	0.834	<0.001	0.741	<0.001		
PDX1	chr13:28494157-28500368	0.257	0.771	<0.001				
SOX9	chr17:70117161-70122561	0.208	0.694	<0.001	0.462	<0.001	0.324	<0.001
F11	chr4:187187099-187209960	-0.192	0.882	<0.001	0.862	<0.001		
PRTG	chr15:55903744-56035288	-0.261	0.242	<0.001	0.024	NS		
NR2F2	chr15:96869167-96883492	-0.503	0.667	<0.001	0.666	<0.001		
ABAT	chr16:8768422-8878432	-0.673	0.752	<0.001	0.868	<0.001	0.320	<0.001
ARHGAP19-SLIT1	chr10:98912802-99052394	-0.757	0.341	<0.001	0.212	<0.001		
PTPRS	chr19:5158506-5340814	-0.863	0.794	<0.001	0.730	<0.001		
OTUD7A	chr15:31767601-32162992	-1.223	0.163	<0.001	0.075	0.012		
LGR4	chr11:27387508-27494322	-1.978	0.783	<0.001	0.838	<0.001		
STEAP1B	chr7:22459063-22672544	-2.289	0.530	<0.001	0.514	<0.001		
RORA	chr15:60780483-61521518	-2.900	0.908	<0.001	0.915	<0.001	0.734	<0.001

Notes: ^a Based on the human genome reference (hg19) ^b Coefficient was based on the final multivariable logistic model to distinguish early HCC from non-HCC. ^c Pearson's correlation coefficients and p-values were calculated for the normalized 5hmC counts for each gene body and the combined normalized 5hmC counts for each feature associated with a marker gene. The liver-derived H3K4me1/H3K27ac peak regions were obtained from the Roadmap Epigenomics Project. The predicted enhancers were obtained from the EnhancerAtlas database based on the ENCODE Project (GM12878). NS: not significant at p<0.001.