

Supplementary Table 7. Histone marks and predicted enhancers associated with the 32 marker genes of the diagnostic model for early HCC.

Gene	H3K4me1		H3K27ac		Enhancer	
	Position ^a	Coefficient ^b	Position ^a	Coefficient ^b	Position ^a	Coefficient ^b
RAPGEF5	chr7:22187689-22188293 chr7:22232431-22235063 chr7:22240647-22246172 chr7:22254078-22257440 chr7:22269198-22271161 chr7:22273686-22275119 chr7:22276158-22279263 chr7:22280394-22281920 chr7:22369227-22370851 chr7:22371548-22374510 chr7:22375647-22388202 chr7:22389375-22392022 chr7:22394426-22400094	0.117 -0.027 0.018 -0.059 0.084 -0.115 -0.006 0.042 0.185 0.369* 0.367* 0.116 0.123	chr7:22160620-22170577 chr7:22186512-22188746 chr7:22214271-22215497 chr7:22238518-22264595 chr7:22269210-22271645 chr7:22276653-22279279 chr7:22280376-22282051 chr7:22369338-22375261 chr7:22376546-22399978	-0.161 -0.043 -0.032 -0.179 0.058 0.023 0.066 0.444* 0.405*	chr7:22122130-22123740 chr7:22384560-22387260 chr7:22390090-22392400 chr7:22423890-22427020	-0.168 0.198* 0.117 -0.009
FGD6	chr12:95477194-95480229 chr12:95489836-95492660 chr12:95510121-95513044 chr12:95530196-95531311 chr12:95535687-95537833 chr12:95562237-95563640 chr12:95567074-95568018 chr12:95584214-95585837 chr12:95590903-95595093 chr12:95595993-95600407 chr12:95606347-95610996	-0.186 -0.030 0.068 0.134 -0.113 -0.284* -0.253* 0.120 0.165 -0.202 -0.075	chr12:95477748-95480932 chr12:95510836-95513645 chr12:95525363-95527655 chr12:95557492-95558616 chr12:95561955-95564184 chr12:95584953-95585364 chr12:95595939-95600020 chr12:95609180-95613171	-0.210 0.085 0.062 -0.058 -0.286* 0.051 -0.175 -0.212* - - -	chr12:95510560-95511370 chr12:95576600-95577480	0.138 0.070
PRKAA1	chr5:40774795-40777131 chr5:40778443-40797540 chr5:40798468-40799705	-0.035 -0.164 0.071	chr5:40775579-40777263 chr5:40778330-40799675	-0.030 -0.142		
EVC	chr4:5708488-5714814 chr4:5717887-5725615	0.322* 0.412*	chr4:5709457-5714034 chr4:5718658-5720047 chr4:5722993-5724220	0.284* 0.273* 0.085	chr4:5705550-5706400 chr4:5823890-5826800 chr4:5997460-5998840	0.106 0.159 -0.017
GNRH1						
CHST9	chr18:24499622-24501795 chr18:24504686-24507357 chr18:24540808-24545927 chr18:24598592-24599609 chr18:24620314-24623243 chr18:24636755-24639701 chr18:24698622-24700890 chr18:24709657-24711137 chr18:24714295-24718718 chr18:24722140-24724849 chr18:24764061-24767874	0.181 0.211* 0.407* 0.293* 0.145 0.298* 0.287* 0.320* 0.183* 0.051 0.170*	chr18:24500234-24501398 chr18:24620703-24623304 chr18:24636673-24639719 chr18:24699089-24700022 chr18:24722826-24724374 chr18:24764115-24767398	0.164 0.190* 0.297* 0.029 -0.053 0.158		
NPBWR1	chr8:53850746-53855409	0.413*				

UBE2G2	chr21:46198026-46201499 chr21:46205068-46207327 chr21:46210565-46214471 chr21:46218626-46221471	-0.277* -0.141 -0.272* -0.247*	chr21:46211462-46214359 chr21:46220959-46222522	-0.226* -0.018	chr21:46209360-46210990 chr21:46237230-46237860 chr21:46285360-46287300 chr21:46291600-46293410 chr21:46331220-46332560 chr21:46367880-46370240	-0.163 0.091 -0.116 -0.025 0.047 0.119
MEIS2	chr15:37189153-37190180 chr15:37195895-37199600 chr15:37203564-37205107 chr15:37205803-37208260 chr15:37209047-37211322 chr15:37231169-37234568 chr15:37252171-37254749 chr15:37256912-37259666 chr15:37299387-37303626 chr15:37306357-37309772 chr15:37319726-37321589 chr15:37332162-37333823 chr15:37372246-37372990 chr15:37388673-37396931	0.242* 0.206 0.244* 0.154 0.284* 0.234* 0.079 0.024 0.120 0.263* 0.004 0.108 0.260* 0.315*	chr15:37205684-37208117 chr15:37209714-37210960 chr15:37213258-37214697 chr15:37232641-37233612 chr15:37257050-37258416 chr15:37281554-37282104 chr15:37288387-37291292 chr15:37299811-37303123 chr15:37305226-37313750 chr15:37371911-37372202 chr15:37377068-37380382 chr15:37383110-37395125	0.150 0.334* -0.001 0.096 -0.094 -0.058 0.300* 0.130 0.288* 0.115 0.229* 0.408*	chr15:37306680-37308070 chr15:38084070-38084650	0.219* 0.043
CAP2	chr6:17393009-17395859 chr6:17405137-17407255 chr6:17490883-17493544 chr6:17501740-17503281	0.066 0.208* -0.008 0.188	chr6:17393244-17395176 chr6:17404433-17407233 chr6:17417878-17419371 chr6:17469506-17471477 chr6:17491812-17494115	0.047 0.205* 0.052 0.001 0.050		
CCNI2	chr5:132082480-132083717	0.094			chr5:131170020-131171880 chr5:131208790-131214090 chr5:131223580-131225770 chr5:132085370-132086500 chr5:132962080-132964240	-0.089 -0.023 -0.103 -0.007 0.031
LRRC61	chr7:150010162-150023386 chr7:150029290-150044022	-0.294* 0.066	chr7:150007814-150024091 chr7:150026439-150042264	-0.322* 0.074	chr7:150053190-150054030 chr7:150102990-150104670	0.105 0.003
A2M	chr12:9215777-9235207 chr12:9236057-9246832 chr12:9261105-9280403	0.039 0.302* -0.190	chr12:9215697-9223237 chr12:9224213-9250169 chr12:9253298-9291066	-0.131 0.482* 0.063		
CHI3L1	chr1:203143342-203151357 chr1:203153879-203156965	-0.121 -0.032	chr1:203154019-203156840	-0.002		
FREM2	chr13:39259114-39262628 chr13:39337607-39338867 chr13:39348443-39350751 chr13:39358992-39359775 chr13:39421209-39424322 chr13:39439712-39444648 chr13:39445428-39446219 chr13:39452881-39454383	0.075 0.074 0.135 -0.109 0.197* 0.011 0.086 -0.033	chr13:39338015-39339442	0.050		
DUSP23	chr1:159749253-159753901	-0.110	chr1:159749054-159754098	-0.082	chr1:158829940-158832510	-0.008

				chr1:159808080-159810500	-0.260*
				chr1:159858990-159860260	-0.183
				chr1:159909920-159912140	-0.115
				chr1:160030690-160032830	-0.099
				chr1:160138780-160140360	-0.152
MYT1	chr20:62819503-62821653	-0.053	chr20:62820064-62821752	-0.014	
	chr20:62826980-62828542	0.245*	chr20:62843912-62845017	-0.066	
	chr20:62843701-62845389	-0.071	chr20:62853146-62856811	0.114	
	chr20:62850946-62856387	0.131	chr20:62864044-62870751	0.019	
	chr20:62863968-62866488	-0.030	chr20:62872051-62875161	0.083	
	chr20:62867242-62877576	0.108			
PARD6G	chr18:77914597-77916428	-0.091	chr18:77938914-77941761	0.102	
	chr18:77928257-77929902	0.014	chr18:77949577-77960042	-0.012	
	chr18:77939154-77941171	0.131	chr18:78001243-78005818	-0.110	
	chr18:77954096-77960645	-0.004			
	chr18:77966268-77966863	0.242*			
	chr18:77987526-77987936	0.112			
	chr18:78003394-78006080	-0.093			
NDUFA3	chr19:54605524-54610441	0.056	chr19:54603531-54606785	-0.164	
FGF19	chr11:69515173-69520990	0.197*	chr11:69514277-69516812	-0.084	
PDX1	chr13:28490995-28496997	0.365*			
	chr13:28498061-28504327	0.374*			
SOX9	chr17:70112015-70119591	0.284*	chr17:70115417-70119022	0.091	chr17:69846280-69847380
	chr17:70121229-70122119	0.261*			0.184*
F11	chr4:187175943-187190339	0.146	chr4:187175260-187191447	0.146*	
	chr4:187191264-187194484	0.151*			
PRTG	chr15:56032746-56036315	-0.026	chr15:56034364-56035433	0.048	
NR2F2	chr15:96860194-96875966	0.093	chr15:96860239-96905794	0.193*	
	chr15:96876687-96904968	0.213*			
ABAT	chr16:8766999-8782048	-0.128	chr16:8767281-8805379	-0.038	chr16:8748900-8749840
	chr16:8784405-8799004	0.015	chr16:8807487-8809852	-0.015	chr16:8796180-8799130
	chr16:8807645-8808204	-0.016	chr16:8814984-8818259	0.019	chr16:8944050-8946500
	chr16:8811849-8816007	-0.088	chr16:8820894-8826038	-0.004	chr16:9102260-9103140
	chr16:8819299-8825891	-0.019	chr16:8827517-8840495	-0.103	
	chr16:8830334-8837158	-0.201	chr16:8841561-8847589	-0.144	
ARHGAP19-SLIT1	chr10:98944505-98946466	0.075	chr10:98987330-98989886	-0.166	
	chr10:98955692-98956622	0.085	chr10:99015377-99016729	-0.127	
	chr10:98970282-98970545	0.101	chr10:99037423-99040503	-0.173	
	chr10:98984209-98985004	-0.235*	chr10:99051366-99054479	-0.285*	
	chr10:98987003-98990341	-0.250*			
	chr10:99026542-99027649	-0.291*			
	chr10:99034674-99034959	0.122			
	chr10:99037384-99039754	-0.183			
	chr10:99050404-99054960	-0.244*			
PTPRS	chr19:5259036-5260082	-0.284*	chr19:5280747-5282933	-0.381*	
	chr19:5287215-5294809	-0.317*	chr19:5290548-5294676	-0.316*	

	chr19:5338849-5341638	-0.072				
OTUD7A	chr15:31779606-31782787	-0.200	chr15:31780512-31782479	-0.186		
	chr15:31790817-31794050	-0.209*	chr15:31792426-31794816	-0.208*		
	chr15:31808213-31811394	-0.236*	chr15:32162696-32163490	-0.076		
	chr15:31832476-31834393	0.030				
	chr15:32159102-32163851	-0.211				
LGR4	chr11:27382721-27389596	-0.182	chr11:27388461-27408588	-0.117		
	chr11:27391290-27408315	-0.148	chr11:27409898-27452544	0.027		
	chr11:27410133-27429055	-0.166	chr11:27465744-27467446	-0.013		
	chr11:27429866-27440584	0.042	chr11:27471377-27495488	-0.169		
	chr11:27441778-27449992	0.111				
	chr11:27450926-27454306	0.036				
	chr11:27458583-27461071	0.153				
	chr11:27461830-27467552	0.041				
	chr11:27468781-27493276	-0.216				
	chr11:27494230-27496074	-0.223*				
STEAP1B	chr7:22491764-22493464	0.035	chr7:22483483-22485701	0.052		
	chr7:22539286-22540224	0.019	chr7:22614631-22618329	-0.105		
	chr7:22588901-22590219	0.014	chr7:22626105-22630180	-0.052		
	chr7:22599878-22606711	-0.081				
	chr7:22614729-22618433	-0.113				
RORA	chr15:60780378-60783655	-0.043	chr15:60800285-60803131	-0.231*	chr15:60839770-60840860	0.189*
	chr15:60785000-60788594	0.016	chr15:60810750-60833668	-0.202	chr15:60849130-60850070	0.025
	chr15:60799766-60805286	-0.377*	chr15:60836151-60839283	-0.004	chr15:60851400-60852150	0.239*
	chr15:60812213-60814776	-0.126	chr15:60840491-60852034	0.037	chr15:60854910-60858400	0.131
	chr15:60816682-60839382	-0.201	chr15:60859452-60869124	0.048	chr15:60859820-60864430	0.057
	chr15:60840163-60842167	0.080	chr15:60870244-60886748	0.271*	chr15:60864490-60869140	0.256*
	chr15:60842911-60852177	-0.067	chr15:60897678-60898670	-0.078	chr15:60871300-60879220	0.206*
	chr15:60853121-60858035	0.124	chr15:60900004-60900555	-0.049	chr15:62344920-62345560	-0.031
	chr15:60860023-60883646	0.151	chr15:60948329-60949674	-0.067		
	chr15:60884932-60890261	0.257*	chr15:60952247-60954310	0.156		
	chr15:60898034-60901568	-0.107	chr15:60972138-60978595	0.269*		
	chr15:60906336-60909235	0.018	chr15:60980843-60989613	0.261*		
	chr15:60941890-60942977	-0.119	chr15:60991580-60994638	0.058		
	chr15:60947666-60950229	-0.135	chr15:61010434-61011953	-0.001		
	chr15:60951932-60953966	0.141	chr15:61021402-61034230	0.265*		
	chr15:60971639-60979853	0.255*	chr15:61035692-61038882	0.030		
	chr15:60980730-60990155	0.241*	chr15:61042500-61046693	0.214*		
	chr15:61000119-61001794	0.187	chr15:61047864-61051459	0.219*		
	chr15:61009772-61015982	0.116	chr15:61056018-61058322	0.087		
	chr15:61021661-61034274	0.273*	chr15:61091148-61094924	0.196		
	chr15:61042546-61046986	0.207*	chr15:61132857-61134878	-0.003		
	chr15:61047836-61051885	0.223*	chr15:61163275-61165408	0.187*		
	chr15:61089381-61095604	0.215*	chr15:61205240-61213125	-0.111		
	chr15:61098612-61102991	0.037	chr15:61237398-61238014	0.008		
	chr15:61103978-61105700	0.076	chr15:61325113-61329803	-0.180		

chr15:61132670-61135413	-0.070	chr15:61340921-61345178	-0.022
chr15:61161881-61165159	0.195*	chr15:61354993-61357050	0.212*
chr15:61181761-61183324	-0.224	chr15:61360672-61365427	0.141
chr15:61188270-61189703	0.100	chr15:61374663-61379290	0.181
chr15:61191198-61192735	0.044	chr15:61382814-61385334	-0.179
chr15:61198167-61201439	0.181	chr15:61388293-61390647	0.037
chr15:61204574-61212371	-0.133	chr15:61496892-61497930	0.052
chr15:61236917-61238570	-0.047	chr15:61518040-61522504	0.010
chr15:61285933-61288072	0.067		
chr15:61323678-61328522	-0.330*		
chr15:61333857-61335886	0.140		
chr15:61342122-61344417	-0.038		
chr15:61347297-61348630	0.181		
chr15:61354247-61366979	0.191		
chr15:61371808-61372906	-0.007		
chr15:61374758-61381502	0.144		
chr15:61387241-61393038	0.023		
chr15:61404144-61405797	0.116		
chr15:61419284-61419905	0.033		
chr15:61424942-61427223	0.152		
chr15:61428750-61430301	0.061		
chr15:61432703-61435009	0.129		
chr15:61460875-61462344	0.023		
chr15:61463382-61465588	0.072		
chr15:61478356-61480279	-0.090		
chr15:61487352-61490297	-0.093		
chr15:61508744-61510044	0.071		
chr15:61516711-61524575	-0.080		

Notes: ^a Based on the human genome reference (hg19) ^b Coefficient was based on the logistic regression adjusted for age and gender for each feature to distinguish early HCC from non-HCC in the training set. * Coefficient with p<0.05. 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).