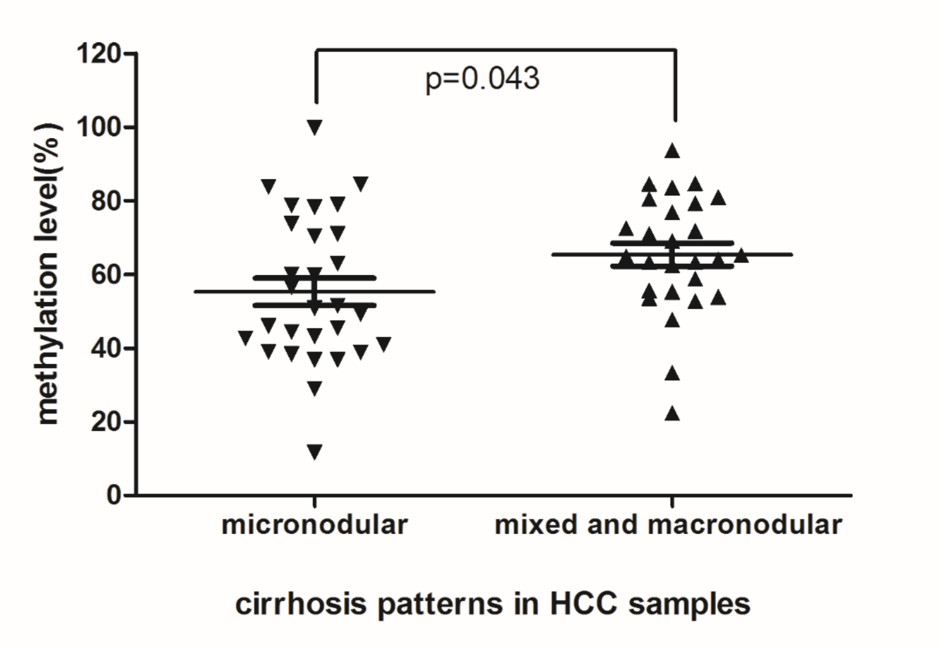

Supplementary Figure1: The methylation levels of RASA3 in HCC between mircronodular and mixed and macronodular patients.

Supplemental Table 1. The primers of amplicons for methylation genotyping

Amplicon	Primers	Sequence
Amplicon1	Forward	5’aggaagagagGGTATTTTTGGTGAAGGTAATTGAA3’
	Reverse	5’cagtaatacgactcactatagggagaaggctAAAAACAAAATACAAACCCATTTCC3’
Amplicon2	Forward	5’aggaagagagGGGTTTTAGTAGTTTTTGAAGTGGG3’
	Reverse	5’cagtaatacgactcactatagggagaaggctACTACAAACCCTAAAAACCTCTCCA3’

Supplementary Table 2. The summary positions of the 12 CpG sites in the amplicon 1.

Gene	ID	Position
RASA3	cg06698414	Chr13: 114843024
	CpG1	Chr13: 114843725
	CpG2	Chr13: 114843684
	CpG3	Chr13: 114843679
	CpG4	Chr13: 114843649
	CpG5	Chr13: 114843625
	CpG6	Chr13: 114843622
	CpG7	Chr13: 114843614
	CpG8	Chr13: 114843609
	CpG9	Chr13: 114843606
	CpG10	Chr13: 114843595
	CpG11	Chr13: 114843541
	CpG12	Chr13: 114843513
	cg17596359	Chr13: 114844124

Supplementary Table 3. The summary positions of the 6 CpG sites in amplicon2

Gene	ID	Position
RASA3	cg11570367	Chr13: 114896683
	CpG1	Chr13: 114897018
	CpG2	Chr13: 114897012
	CpG3	Chr13: 114897006
	CpG4	Chr13: 114896893
	CpG5	Chr13: 114896840
	CpG6	Chr13: 114896838
	cg00098553	Chr13:114897502

Supplementary Table 4. The comparison between methylation levels of the 6 CpG sites

CpGs	Group	mean	⊿mean	P Value	P Value (Bonferroni correction)
CpG1	Tumor	29.0%	0.19%	0.787	1
	Normal	28.8%			
CpG2.3	Tumor	40.6%	1.21%	0.070	0.280
	Normal	39.4%			
CpG4	Tumor	20.8%	-0.05%	0.951	1
	Normal	20.8%			
CpG5.6	Tumor	33.1%	2.01%	0.012	0.048
	Normal	31.1%			

Supplementary Table 5. The correlation of the methylation among the 11 genotyped CpG sites

Correlations		R^2							
		CpG1	**CpG2.3**	**CpG4**	**CpG5.6**	**CpG7.8**	**CpG9**	**CpG10**	**CpG11**
P VALUE	**CpG1**	**1.00**	**0.64**	**0.60**	**0.45**	**0.62**	**0.45**	**0.41**	**0.48**
	CpG2.3	**1.46E-33**	**1.00**	**0.75**	**0.48**	**0.72**	**0.61**	**0.40**	**0.50**
	CpG4	**3.41E-29**	**4.72E-53**	**1.00**	**0.49**	**0.77**	**0.59**	**0.59**	**0.65**
	CpG5.6	**1.44E-14**	**5.02E-17**	**2.41E-17**	**1.00**	**0.58**	**0.43**	**0.29**	**0.43**
	CpG7.8	**5.97E-32**	**1.16E-46**	**7.90E-58**	**2.01E-26**	**1.00**	**0.68**	**0.47**	**0.60**
	CpG9	**1.59E-15**	**1.14E-30**	**1.11E-27**	**1.90E-13**	**2.40E-40**	**1.00**	**0.40**	**0.50**
	CpG10	**2.22E-13**	**2.89E-13**	**5.02E-30**	**4.89E-7**	**8.53E-19**	**6.11E-13**	**1.00**	**0.64**
	CpG11	**2.14E-18**	**4.57E-20**	**1.26E-36**	**2.07E-13**	**1.32E-30**	**6.26E-20**	**1.54E-37**	**1.00**

Supplementary Table 6, the methylation difference and the correlation analysis

Probe ID	Position	Methylation Changes (n=50)				Methylation-Expression correlation (n=231)	
		Mean-T	Mean-N	Diff	P value	r	P value
cg06698414	Chr13:114843024	0.068	0.308	-0.241	5.53E-08	0.669	2.57E-31
cg17596359	Chr13:114844124	0.123	0.323	-0.199	6.69E-08	0.472	3.29E-14
cg11570367	Chr13:114896683	0.098	0.098	0.000	0.990	-0.126	0.057
cg00098553	Chr13:114897502	-0.291	-0.363	0.071	0.018	-0.422	2.18E-11

Mean-T, the mean methylation levels in tumor tissues, Mean-N, the mean methylation levels in normal tissues

Diff, the mean different between tumor and normal tissues