

# Meta-analysis of DNA methylation biomarkers in hepatocellular carcinoma

## Supplementary Materials

### Supplementary Document S1: 144 eligible studies in the meta-analysis

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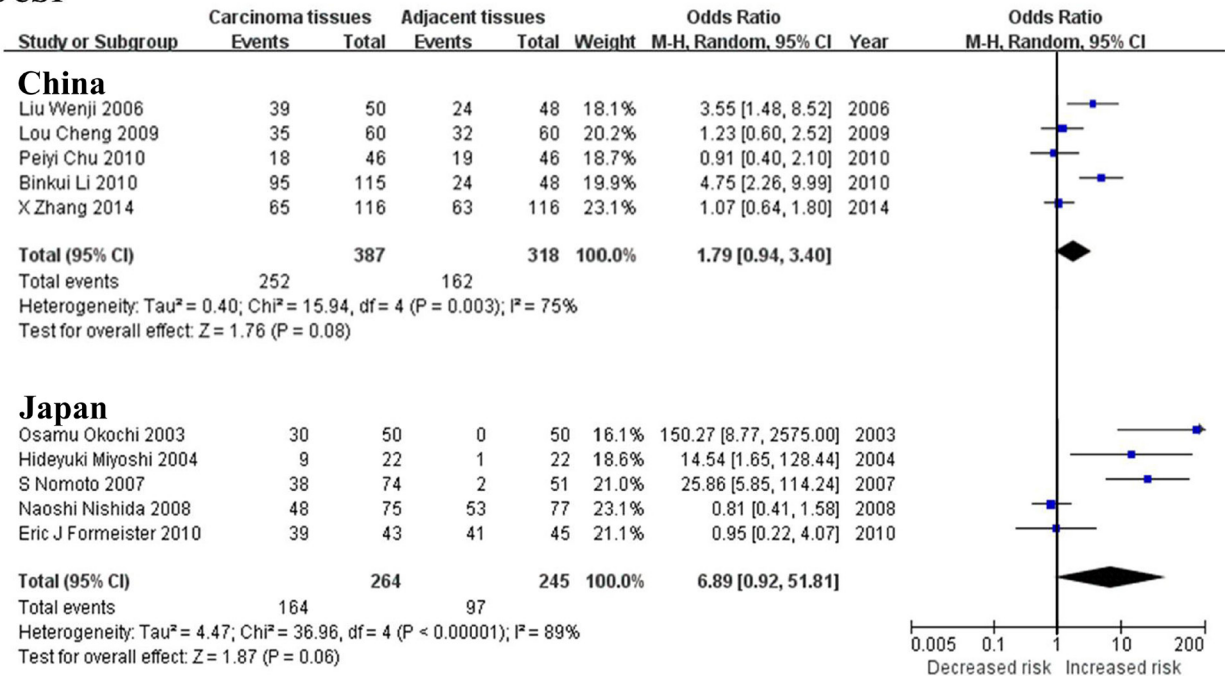
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## SOCS1



**Supplementary Figure S1: Forest plots of *SOCS1* methylation between HCC tumor tissues and adjacent tissues in the meta-analysis.**

**Supplementary Table S1: Analysis of heterogeneity sources of 24 aberrant methylated genes between HCC tumor tissues and adjacent tissues in geographical populations.** See Supplementary\_Table\_S1

**Supplementary Table S2: Analysis of heterogeneity sources of 17 aberrant methylated genes between HCC tumor tissues and normal tissues in geographical populations.** See Supplementary\_Table\_S2

**Supplementary Table S3: Analysis of heterogeneity sources of six aberrant methylated genes between HCC tumor serums and normal serums in geographical populations**

Gene	Geographical population	Studies (n)	Coefficient	95% CI	P value
<i>RASSF1A</i>	China	14	0.5639	[-3.3362, 4.464]	0.756
	Egypt	1	1.29449	[-2.76, 5.349]	0.497
	Singapore	1	—	—	—
<i>p16</i>	China	8	-2.6813	[-8.585, 3.222]	0.296
	Singapore	1	—	—	—
<i>CDH1</i>	China	2	—	—	—
	Singapore	1	—	—	—
<i>RUNX3</i>	China	2	—	—	—
	Singapore	1	—	—	—
<i>GSTP1</i>	China	3	—	—	—
<i>WIF1</i>	China	3	—	—	—

Analysis of heterogeneity sources of *RASSF1A* in Singapore, *p16* in Singapore, *CDH1* in China and Singapore, *RUNX3* in China and Singapore, *GSTP1* in China and *WIF1* in China was not applicable, because the data of these genes were insufficient.