

Supplementary

Histone Methyltransferase G9a-Promoted Progression of Hepatocellular Carcinoma is Targeted by Liver-Specific Hsa-miR-122

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Fig. 2A

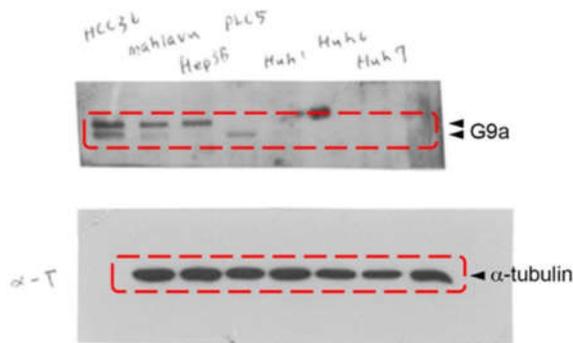


Fig. 2B

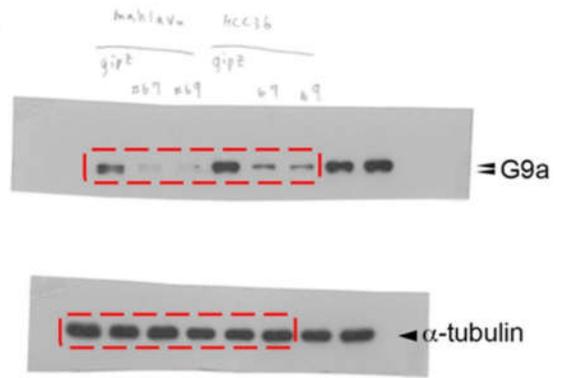


Fig. 5C

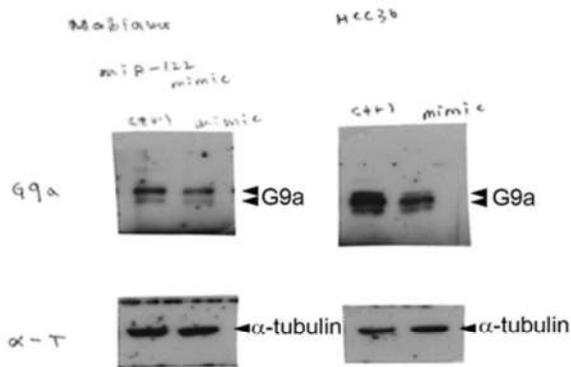


Fig. 5D

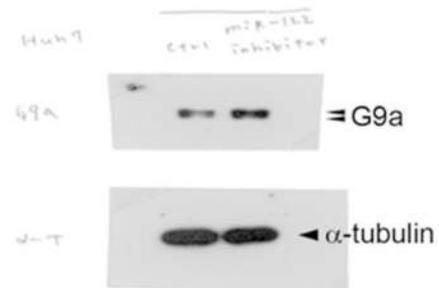


Fig. 5F

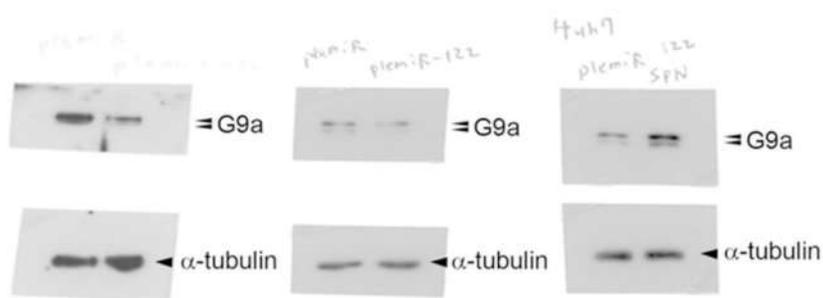


Figure S1. Uncropped blots used in main figures.

Table 1. Primer and probe sequences used for quantitative PCR.

Gene	Primer sequences (5'-3')
<i>G9a/EHMT2</i>	(F) GGAGCCACGAGGGGTGTCCA (R) CGGCATTGCAGCCTGACAGC
<i>ACTIN</i>	(F) GCGGGCACCACCATGTACCCT (R) AGGGGCCGGACTCGTCATACT
Gene	Probe sequences (5'-3')
<i>has-miR-122</i>	UGGAGUGUGACAAUGGUGUUUG (AB Assay ID 002245)
<i>RUN6B</i>	CGCAAGGATGACACGCAAATTCGTG AAGCGTTCATATTTTT (AB Assay ID 001093)

Table S2. The correlation between CpG methylation and G9a gene expression.

CpG sites*	Spearman's coefficient of rank correlation (rho) (95%CI)	Significance
cg07829740	-0.356 (-0.442 to -0.264)	$p < 0.0001$
cg07498938	-0.297 (-0.387 to -0.201)	$p < 0.0001$
cg21190306	-0.29 (-0.380 to -0.194)	$p < 0.0001$
cg02758274	-0.282 (-0.373 to -0.185)	$p < 0.0001$
cg08848598	-0.28 (-0.371 to -0.183)	$p < 0.0001$
cg21087321	-0.276 (-0.367 to -0.179)	$p < 0.0001$
cg07898120	-0.273 (-0.364 to -0.176)	$p < 0.0001$
cg17756143	-0.271 (-0.362 to -0.174)	$p < 0.0001$
cg03146965	-0.262 (-0.355 to -0.165)	$p < 0.0001$
cg27363691	-0.261 (-0.353 to -0.163)	$p < 0.0001$
cg22240884	-0.259 (-0.352 to -0.162)	$p < 0.0001$
cg04637007	-0.258 (-0.351 to -0.160)	$p < 0.0001$
cg21831287	-0.255 (-0.347 to -0.157)	$p < 0.0001$
cg03164052	-0.254 (-0.346 to -0.156)	$p < 0.0001$
cg03945301	-0.253 (-0.346 to -0.155)	$p < 0.0001$
cg19770715	-0.252 (-0.345 to -0.154)	$p < 0.0001$
cg21356750	-0.251 (-0.344 to -0.153)	$p < 0.0001$

* The CpG sites within G9a promoter region and gene locus with $\rho < -0.25$ and $p < 0.0001$ are shown.