



## Abstract

**Background:** Despite recent advances in the treatment of both early and advanced colorectal cancer, it remains the second leading cause of cancer deaths in the western world. G9a-dependent H3K9 methylations (G9a) have been shown to mediate epigenetic silencing of several tumours suppressor genes including DSC3, MASPIN, and

**Keywords:** Colorectal cancer; H3K9 Methylations; G9a; Silencing; Epigenetics

**Introduction**  
Colorectal cancer (CRC) is the second leading cause of cancer death in the United States. Although the incidence of CRC has declined in the United States, it remains a leading cause of cancer death. The pathogenesis of CRC is complex and involves a combination of genetic and epigenetic factors. Epigenetic changes, such as DNA methylation and histone modifications, play a critical role in the regulation of gene expression and are often altered in cancer. H3K9 methylations (G9a) are a type of histone modification that is associated with gene silencing. G9a is a histone methyltransferase that catalyzes the methylation of H3K9. G9a-dependent H3K9 methylations have been shown to mediate epigenetic silencing of several tumour suppressor genes, including DSC3, MASPIN, and

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H3K9 G9a EM  
H3K9 G9a EM  
H3K9 G9a EM  
H3K9 G9a EM

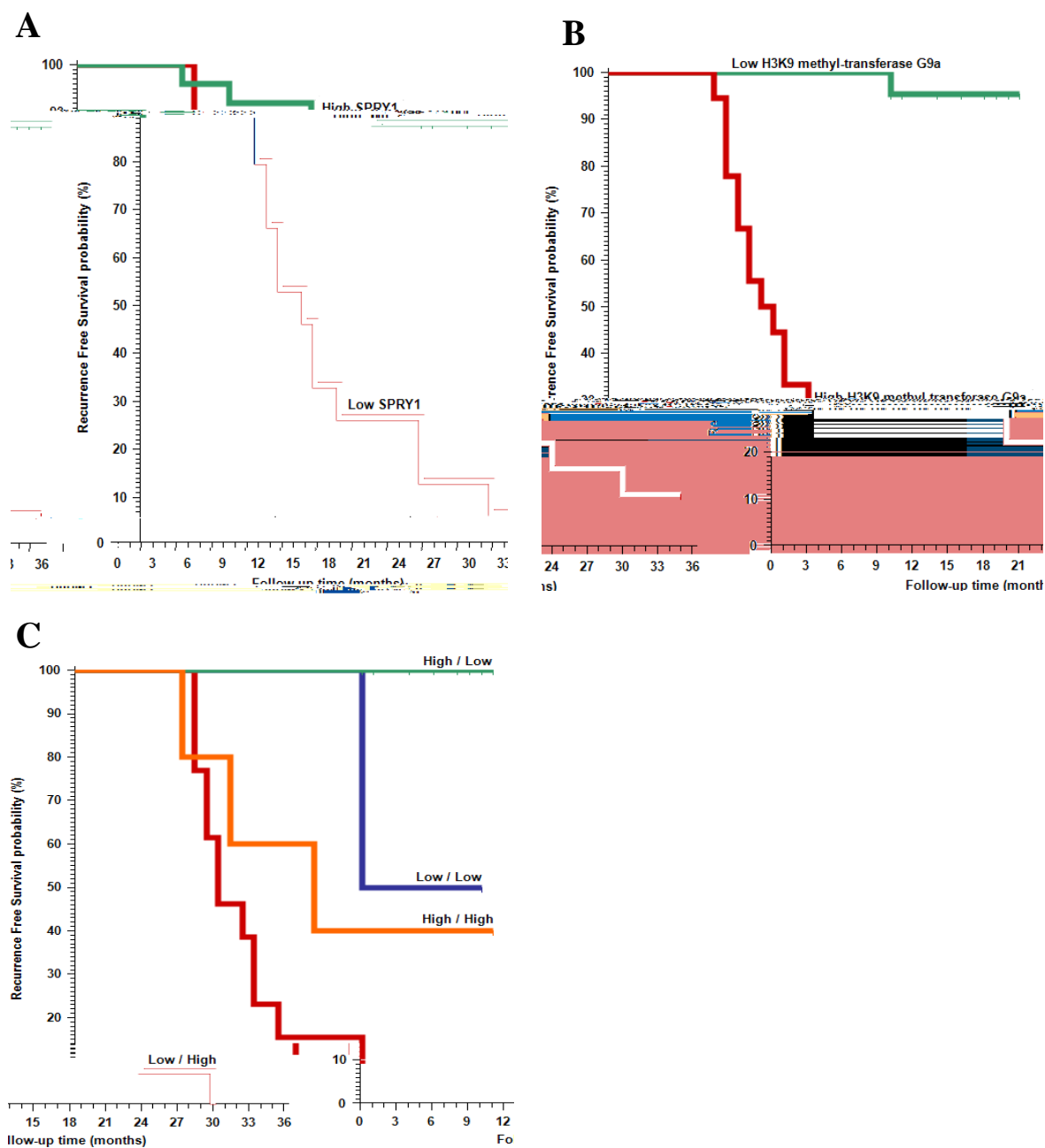
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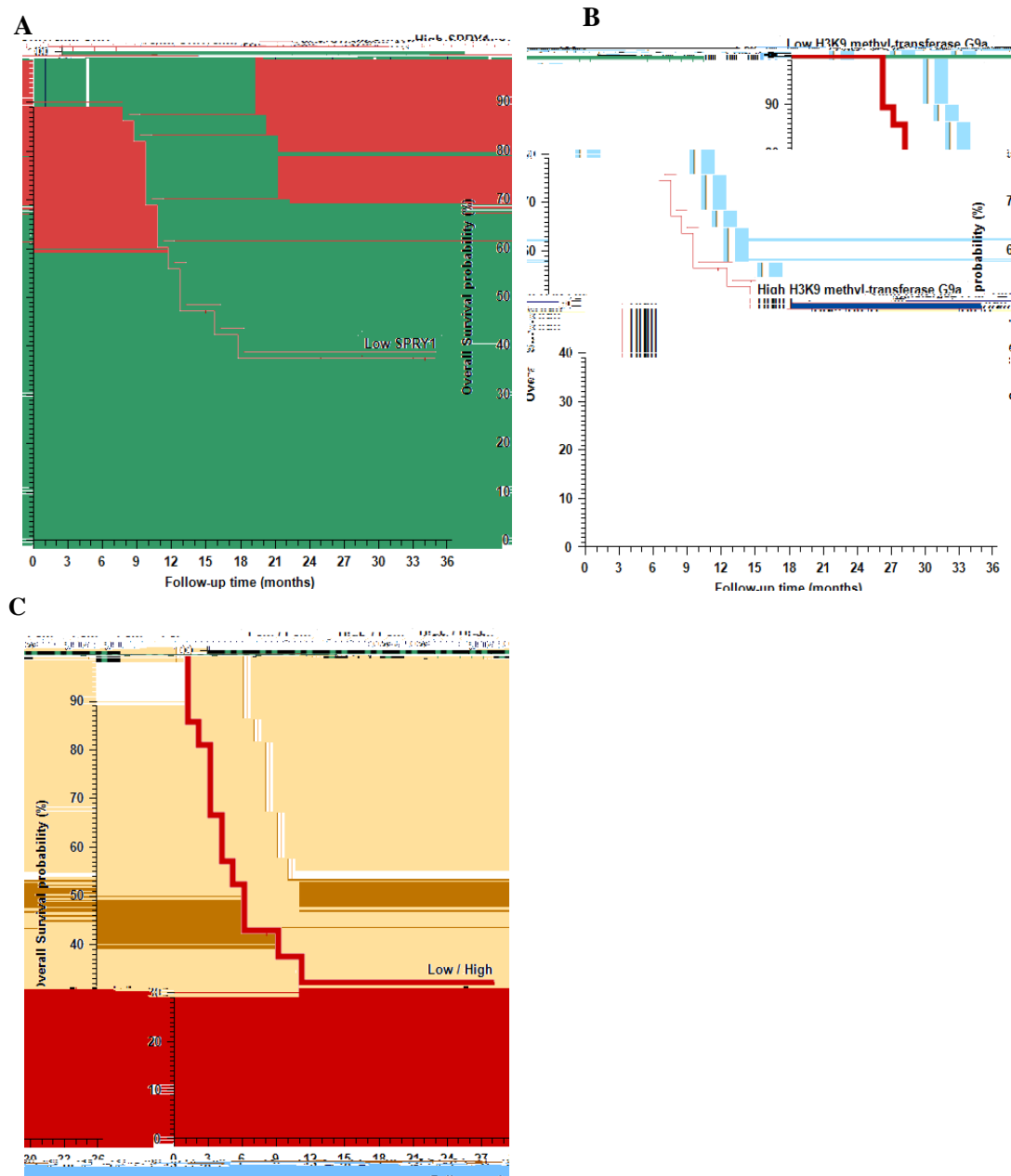




**Figure 3:** Kaplan-Meier plot of recurrence free survival: (A) stratified according to SPRY1, (B) stratified according to H3K9 methyl-transferase G9a, (C) stratified according to SPRY1 and H3K9 methyl-transferase G9a.

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 ...  
 ... EM ...  
 S ... C ...  
 ...  
 S ... S ...  
 S ...

... CRC ...  
 ... S ... (HCC),  
 ... S ... 1 RNA ...  
 ... HCC ...  
 ... S ...



**Figure 4:** Kaplan-Meier plot of overall survival: (A) stratified according to SPRY1, (B) stratified according to H3K9 methyl-transferase G9a, (C) stratified according to SPRY1 and H3K9 methyl-transferase G9a.

H3K9 G9  
H3K9 G9  
CRC  
CRC

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