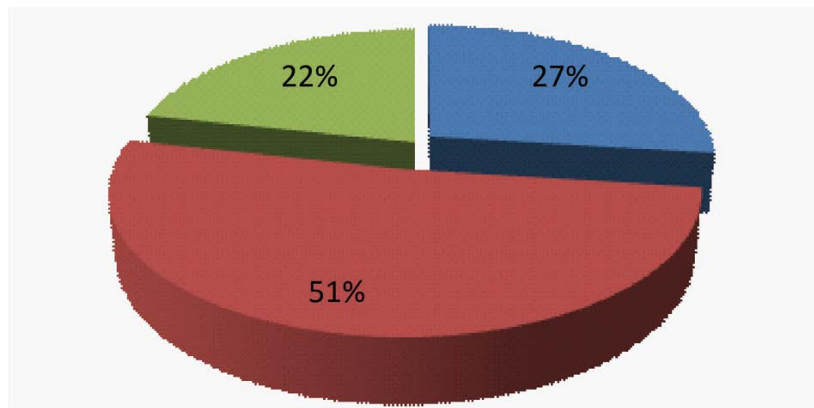


■ Hypermethylation ■ Hypomethylation ■ No methylation



**Supplementary information, Figure S8** The Detection and quantitation of *MPZLI* methylation in 37 paired HCC and adjacent paracancer tissues by real-time methylation-specific PCR. We examined the methylation status of CpG islands within *MPZLI* promoter using quantitative real-time methylation-specific PCR on 37 cases of paired HCC and non-tumor tissues. Totally, 35 out of 37 HCC tissues were methylation-positive. Furthermore, among the 35 methylation-positive HCC cases, the methylation of *MPZLI* promoter was also observed in 33 corresponding non-tumor tissues. However, the methylation levels in 17 HCC tissues were lower than those in the corresponding non-tumor tissues. In summary, the frequency of hypomethylation was approximately 51.4% (19/37) in HCCs, which accounted for the upregulation of *MPZLI* mRNA level in HCC tissues in addition to that caused by genomic gain of 1q24.1-24.2 loci.