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**Supplementary figure 1** Twenty lncRNA heat maps (red: up-regulated; green: down-regulated) with the most significant differential expression in 50 pairs of liver cancer and paracancerous paired specimens in the TCGA database, where the red arrow indicates the location of RP11-422N16.3.

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**Supplementary figure 2** RP11-422N16.3 was mapped to Human (GRCh38.p10) chr8(q23.2)(A) with 2 exons and a transcript length of 3,075 bps (B). Sequence analysis revealed that the RP11-422N16.3 local sequence and the DMGDH promoter region local sequence can be reverse-complementary paired binding, which may have targeted regulation (C).



**Supplementary figure 3** Multiple algorithms in the online database lncipedia predicted that RP11-422N16.3 did not have protein coding capability (lncipedia.org/db/transcript/lnc-RP11-422N16.3.1-9:1).

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**Supplementary figure 4**

**A:** Wound healing assay showed that over-expression of pcDNA3.1-RP11-422N16.3 or down-regulation of miR-23b-3p could significantly reduce cell migrated distance;

**B**: Transwell chamber assay showed that over-expression of pcDNA3.1-RP11-422N16.3 or down-regulation of miR-23b-3p could significantly reduce invasion cell number. \* indicated that P < 0.05 compared to blank group.