**Supplementary material**

* Figure S1
* Figure S2
* Figure S3
* Figure S4
* Supplementary method

**日历

描述已自动生成**

**Figure S1.** Distribution of nine key stemness predictor genes between two stemness clusters. \*\*\*\**P* <0.0001.

**图表, 地图, 折线图

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**Figure S2.** Kaplan-Meier curves of OS according to the nine key stemness predictor genes.

**图片包含 图示

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**Figure S3.** **Distinct microenvironment patterns between two stemness clusters. A**. Distributions of 12 immune and stromal cells between two clusters. **B**. Distributions of 27 immune checkpoint molecules between two clusters. ns*P* >0.05, \**P* <0.05, \*\**P* <0.01, \*\*\**P* <0.001, \*\*\*\**P* <0.0001.

**图表, 日程表, 树状图

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**Figure S4**. Using the stemness cluster predictor, CRC patients from GSE35640 were categorized into C1 or C2.

**Supplementary method**

**Quantitative Real-Time PCR (qRT-PCR)**

Total RNA was isolated from CRC tissues using RNAiso Plus reagent RNA quality was evaluated using a NanoDrop One C (Waltham, MA, USA), and RNA integrity was assessed using agarose gel electrophoresis. An aliquot of 1 μg of total RNA was reverse transcribed into complementary DNA (cDNA) according to the manufacturer's protocol using a High-Capacity cDNA Reverse Transcription kit (TaKaRa BIO, Japan). qRT-PCR was performed using SYBR Assay I Low ROX (Eurogentec, USA) and SYBR® Green PCR Master Mix (Yeason, Shanghai, China) to detect the expression of 16 lncRNAs expression. The expression value was normalized to *GAPDH*, and then log2 transformed for subsequent analysis. The primer sequences of the included nine genes and *GAPDH* were shown in Table S2.