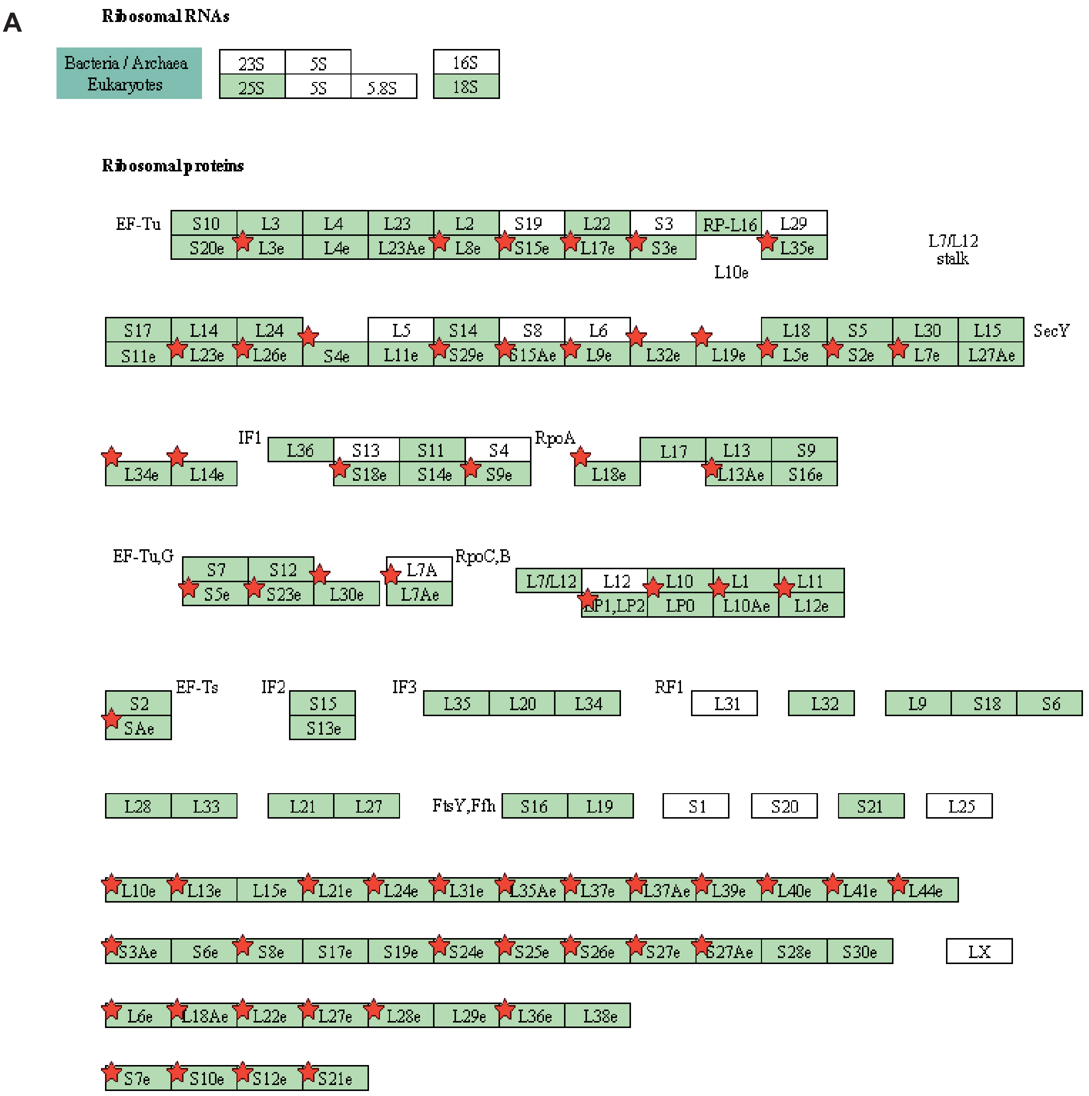
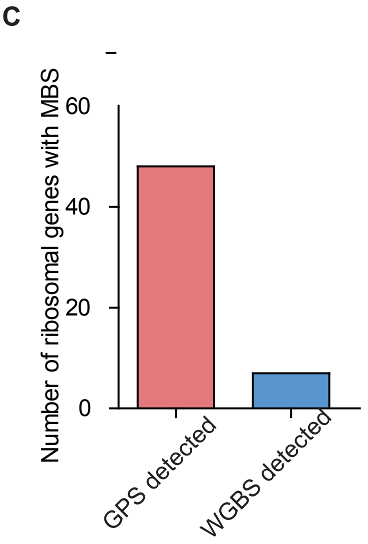


B

GPS	
KEGG pathway	*P*-value
Ribosome	$4.5x10^{-24}$
Cell cycle	$2.7x10^{-14}$
Focal adhesion	$1.6x10^{-5}$
Oocyte meiosis	$8.9x10^{-4}$
Neurotrophin signaling pathway	$1.0x10^{-3}$

WGBS	
KEGG pathway	*P*-value
Cell cycle	$1.1x10^{-6}$



Supplementary Figure S12. Biological significance of MBS determined by GPS and WGBS.

(A) Ribosomal genes with MBS identified by GPS. Among 60 up-regulated ribosomal genes, 50 ribosomal genes were identified with MBS extension to the downstream of TSS in 97L compared with Liver, which are marked with red stars in KEGG ribosome pathway. **(B)** KEGG analysis of genes related to MBS. 4119 genes were identified as up-regulated in hepatoma cell line 97L as compared to normal liver cells. On the promoter of these 4119 genes, 2089 MBS were determined by GPS whereas only 1069 MBS determined by WGBS with same amount of raw sequencing data (375M paired reads). KEGG analysis showed 2089 genes detected by GPS were significantly enriched in ribosome, cell cycle, focal adhesion, oocyte meiosis and neurotrophin signaling pathway. However, 1069 genes detected by WGBS were only enriched in cell cycle (*P*-value threshold $1.0x10^{-3}$). **(C)** Ribosomal genes detected with MBS. Among 60 up-regulated ribosomal genes, 48 ribosomal genes with MBS were identified by GPS, but only 7 by WGBS.