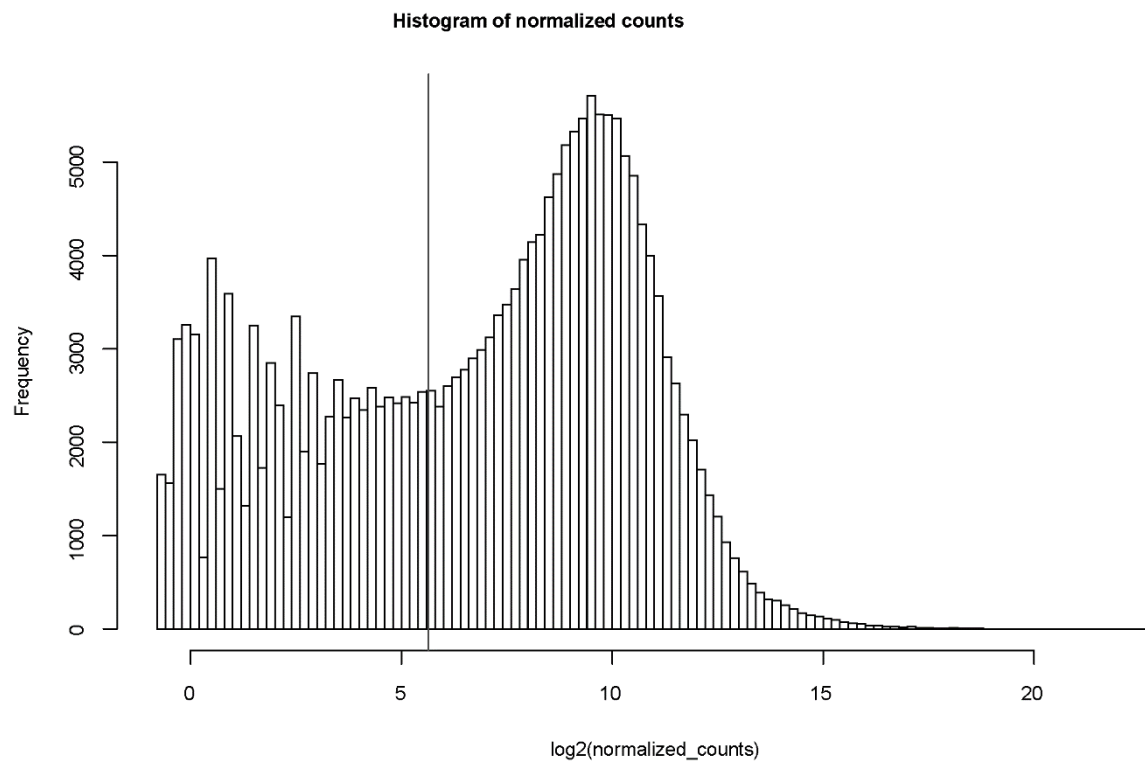


Generation and characterization of rat liver stem cell lines and their engraftment in a rat model of liver failure

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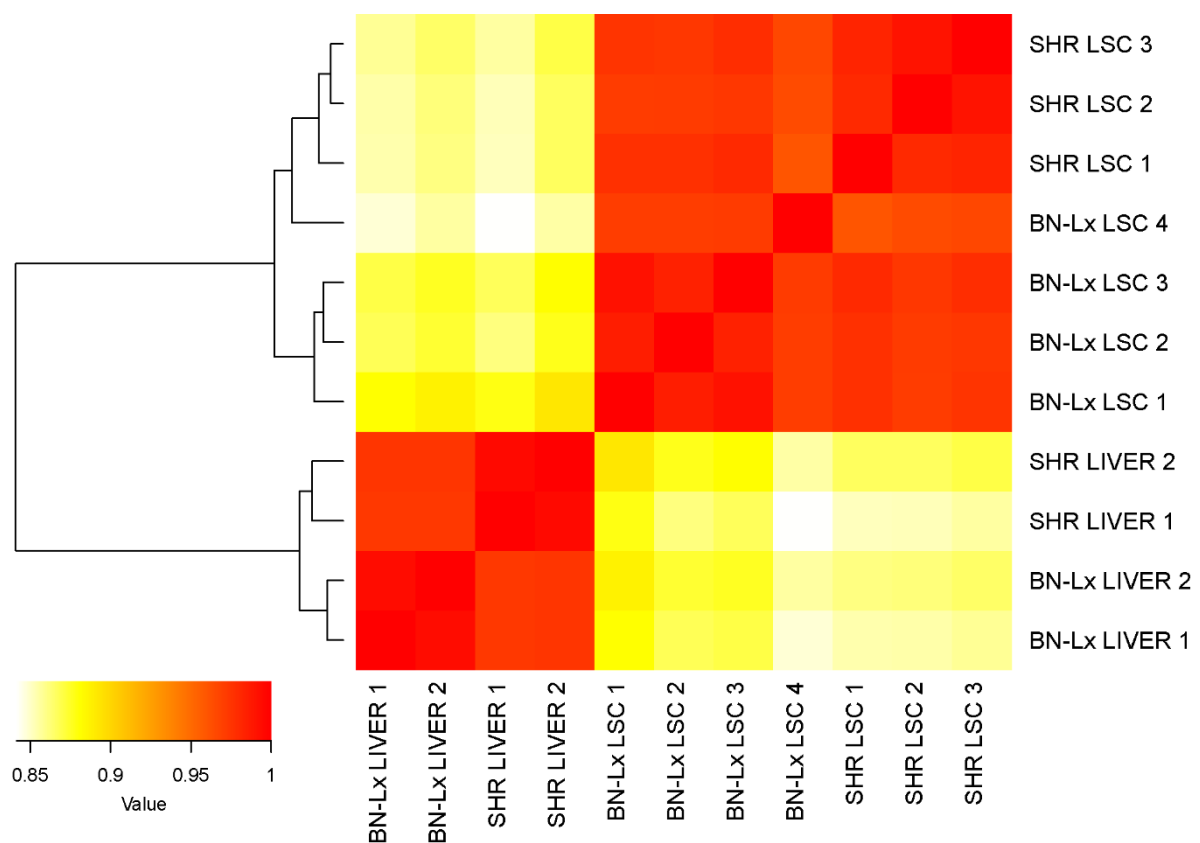
Supplemental figures



Supplemental figure S1: Histogram of normalized counts

Histogram of the non-zero normalized gene counts shows a bimodal distribution.

Vertical line indicates threshold (50) of expression, which was used to select genes for Spearman's rank correlation.



Supplementary figure S2: Hierarchical clustering of samples used for RNA-seq

Hierarchical clustering of samples used for RNA-seq based on the Spearman's rank correlation between the samples using the normalized counts of expressed genes. Color indicates Spearman's rank correlation between the samples, and hierarchical clustering divides liver and liver stem cell (LSC) samples into two groups.