# Brg1 promotes liver regeneration after partial hepatectomy via regulation of cell cycle

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#### **Figure legends**

## Figure S1

(A) ALT levels were measured using serum samples of 2-month-old Control and Brg1 KO mice, n=3. (B,C) Liver weight and body weight of 2-month-old Control and Brg1 KO mice, n=6. (D,F) Representative immunofluorescence images for Glutamine synthetase (GS)/Arginase-1 (Arg-1), GS/Lymphatic vessel endothelial hyaluronan receptor 1 (Lyve1)/Endomucin (Emcn) and Rh Family B Glycoprotein (Rhbg) of the liver of 2-month-old Control and Brg1 KO mice, n=3. GS und RhbG show staining pattern in pericentral hepatocytes and Arg1 in the periportal hepatocytes. Liver endothelial cells show a zonated expression pattern as well, with Endomucin (EMCN) in pericentral liver sinusoidal endothelial cells (LSECs) and central vein endothelial cells (CVECs), and LYVE1 in midzonal LSECs<sup>S1</sup>.

#### Figure S2

(A) Representative H&E staining of Control and Brg1 KO mice at 40h after PH. (B) ALT levels were measured using serum samples of post-PH Control and Brg1 KO mice, n>4.

#### Figure S3

Heatmap of significantly regulated cell cycle pathway related genes analysed in the liver of Control and Brg1 KO mice at 48h after PH. Shown is the z-scaled gene expression for genes, being significantly regulated between time points 0h and 48h, within both the Control and Brg1 KO group, and overlap with the cell cycle pathway annotation from Reactome.

#### Figure S4

Full length gels of all Western blots shown in the figures.

## **Table Legends**

## Table S1

Differences in gene expression levels between time points 4h, 24h, 40h, and 48h post-PH and time point 0hrs for both Control and Brg1 KO mice. For each gene, the baseline gene expression, the log2 fold change and the associated adjusted p-value is reported.

# Table S2

Pathway analysis results for differentially expressed genes at time points 4h, 24h, 40h and 48h post-PH compared to baseline expression pre-PH for Control and Brg1 KO mice.

### Reference

S1. Leibing, T, et al. Angiocrine Wnt signaling controls liver growth and metabolic maturation in mice. Hepatology; 10.1002/hep.29613(2017).













Areas of the gel shown in Figure 1A are marked in red.

The membrane was probed first with anti-Brg1 and subsequently with anti- $\beta$ -tubulin antibodies. Predicted molecular weights for Brg1 and  $\beta$ -tubulin are indicated.



Areas of the gel shown in Figure 2A are marked in red.

The membrane was probed with anti-Brg1 and anti- $\beta$ -tubulin antibodies. Predicted molecular weights for Brg1 and  $\beta$ -tubulin are indicated.



Areas of the gel shown in Figure 4A part1 are marked in red.

The membrane was probed with anti-PCNA and anti- $\beta$ -tubulin antibodies. Predicted molecular weights for PCNA and  $\beta$ -tubulin are indicated.



Areas of the gel shown in Figure 4A part2 are marked in red.

The membrane was probed with  $anti-\beta$ -tubulin and anti-PH3 antibodies.

Predicted molecular weights for PH3 and  $\beta$ -tubulin are indicated.



Areas of the gel shown in Figure 6B part1 are marked in red.

The membrane was probed with anti-Cyclin B1 and anti- $\beta$ -actin antibodies. Predicted molecular weights for Cyclin B1 and  $\beta$ -actin are indicated.



Areas of the gel shown in Figure 6B part2 are marked in red.

The membrane was probed first with anti-Cdk1 and subsequently with anti- $\beta$ -tubulin antibodies. Predicted molecular weights for Cdk1 and  $\beta$ -tubulin are indicated.



Areas of the gel shown in Figure 7B are marked in red.

The membrane was probed with anti-p53 and anti-GAPDH antibodies. Predicted molecular weights for p53 and GAPDH are indicated.