Supplementary Material

1 Supplementary Figures and Tables

1.1 Supplementary Figures
**Supplementary Figure 1.** Distribution of spontaneous and PhIP-induced mutations in the coding region of the gpt gene in hepatic organoids.

**Hot Spot Mapping**

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1   ATGAGCGAAA AATACATCGT CACCTGGGAC ATGTTCAGA TCCATGCACG TAAACTCGCA AGCCGACTGA 70
71  TGCCTTCTGA ACAATGGAAA GGCATTATTG CCGTAAGCCC TGGCCTCTCG GTCCTGGGTG CGTTACTGCC 140
141 GCGTGAAGCTG GGTATTGAGTCA ATGTTCAGATAC CGTTGTATTT TCCAGCTACG ATCAGCGACA CCAGCGCGAG 210
211 CTTAAAGTGC TGAAACGCGC AGAAGGCAGT GGCAGAGGCT TCATCGTTAT TGGGACCTGC GTGGATAACC 280
281 GTGGGAAGTGC GGGTGCCATT CTGAAATATGT ATCCAAAGGC GCACTTTCGTC ACCATTCCTG CAAAACCGGC 350
351 TGGTCTCTCGG CTTGTATGATG ACTATGGTTG TGGATATTCCG CAAGATACCT GGTGGAACCA CGGCGGCTGA 420
421 ATGGGCGTCG TATTCGCTCG GCCCAATCTCC GGTGCTAA

▲ Control   ○ PhIP   ● deletion
▲ X 1 ▲ X 5   ○ X 1 ○ X 5   ● A ● T ● C ● G   ♦ Control ♦ PhIP
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**Supplementary Figure 2.** Relative expression levels of *CYP2E1* in the lung-derived organoids in the absence of the S9 mix. Real-time PCR analysis is used to determine the mRNA expression levels of *CYP2E1*. In untreated controls, values are set at 1.0, and relative levels are expressed as mean ± SE (n = 6). *GAPDH* mRNA levels are used to normalize data. Data significantly different from the AA(-)/S9(+) group is indicated as *p < 0.05*, **p < 0.01.**