

Supplementary Table 2. Gene ontology (GO) analysis of the edited genes identified in all 3 non-tumor liver specimens

| GO Term | No. of Genes | % | P-value | Benjamin | FDR* |
|---|--------------|-----|----------|----------|----------|
| acute inflammatory response | 63 | 3.2 | 7.70E-21 | 2.80E-17 | 1.40E-17 |
| response to wounding | 161 | 8.2 | 7.70E-21 | 1.40E-17 | 1.40E-17 |
| oxidation reduction | 176 | 9 | 3.20E-19 | 3.80E-16 | 5.80E-16 |
| cofactor metabolic process | 78 | 4 | 2.60E-15 | 2.30E-12 | 4.70E-12 |
| response to organic substance | 170 | 8.7 | 1.90E-13 | 1.40E-10 | 3.60E-10 |
| complement activation | 33 | 1.7 | 3.50E-13 | 2.10E-10 | 6.50E-10 |
| inflammatory response | 99 | 5.1 | 4.60E-13 | 2.40E-10 | 8.40E-10 |
| coenzyme metabolic process | 63 | 3.2 | 6.10E-13 | 2.80E-10 | 1.10E-09 |
| activation of plasma proteins involved in acute inflammatory response | 33 | 1.7 | 6.40E-13 | 2.60E-10 | 1.20E-09 |
| wound healing | 71 | 3.6 | 1.60E-12 | 5.60E-10 | 2.90E-09 |
| complement activation, classical pathway | 27 | 1.4 | 2.10E-12 | 6.80E-10 | 3.80E-09 |
| organic acid catabolic process | 51 | 2.6 | 5.00E-12 | 1.50E-09 | 9.20E-09 |
| carboxylic acid catabolic process | 51 | 2.6 | 5.00E-12 | 1.50E-09 | 9.20E-09 |
| humoral immune response mediated by circulating immunoglobulin | 27 | 1.4 | 9.10E-12 | 2.50E-09 | 1.70E-08 |
| immunoglobulin mediated immune response | 35 | 1.8 | 1.70E-11 | 4.40E-09 | 3.10E-08 |
| protein maturation | 53 | 2.7 | 1.80E-11 | 4.30E-09 | 3.20E-08 |
| protein processing | 50 | 2.5 | 3.40E-11 | 7.70E-09 | 6.20E-08 |
| B cell mediated immunity | 35 | 1.8 | 4.00E-11 | 8.50E-09 | 7.30E-08 |
| translational elongation | 47 | 2.4 | 4.80E-11 | 9.60E-09 | 8.80E-08 |
| protein maturation by peptide bond cleavage | 42 | 2.2 | 1.10E-10 | 2.10E-08 | 2.00E-07 |
| lymphocyte mediated immunity | 38 | 1.9 | 1.50E-10 | 2.70E-08 | 2.80E-07 |
| immune effector process | 53 | 2.7 | 2.90E-10 | 5.00E-08 | 5.30E-07 |
| coagulation | 45 | 2.3 | 3.20E-10 | 5.30E-08 | 5.90E-07 |
| blood coagulation | 45 | 2.3 | 3.20E-10 | 5.30E-08 | 5.90E-07 |
| innate immune response | 53 | 2.7 | 6.70E-10 | 1.10E-07 | 1.20E-06 |
| hemostasis | 45 | 2.3 | 1.40E-09 | 2.10E-07 | 2.60E-06 |
| translation | 89 | 4.5 | 1.90E-09 | 2.80E-07 | 3.50E-06 |
| cellular amino acid catabolic process | 35 | 1.8 | 3.10E-09 | 4.30E-07 | 5.60E-06 |
| leukocyte mediated immunity | 39 | 2 | 3.20E-09 | 4.30E-07 | 5.90E-06 |
| negative regulation of apoptosis | 92 | 4.7 | 3.70E-09 | 4.80E-07 | 6.80E-06 |
| negative regulation of programmed cell death | 92 | 4.7 | 6.40E-09 | 8.10E-07 | 1.20E-05 |
| sulfur metabolic process | 45 | 2.3 | 6.80E-09 | 8.30E-07 | 1.30E-05 |
| negative regulation of cell death | 92 | 4.7 | 7.20E-09 | 8.40E-07 | 1.30E-05 |
| adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 36 | 1.9 | 7.70E-09 | 8.70E-07 | 1.40E-05 |
| adaptive immune response | 36 | 1.9 | 7.70E-09 | 8.70E-07 | 1.40E-05 |

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| cellular amino acid derivative metabolic process | 56 | 2.9 | 8.70E-09 | 9.60E-07 | 1.60E-05 |
| amine catabolic process | 36 | 1.9 | 1.00E-08 | 1.10E-06 | 1.90E-05 |
| defense response | 132 | 6.8 | 1.30E-08 | 1.30E-06 | 2.40E-05 |
| organic acid biosynthetic process | 53 | 2.7 | 1.70E-08 | 1.70E-06 | 3.10E-05 |
| carboxylic acid biosynthetic process | 53 | 2.7 | 1.70E-08 | 1.70E-06 | 3.10E-05 |
| lipid localization | 53 | 2.7 | 2.30E-08 | 2.30E-06 | 4.30E-05 |
| proteasomal ubiquitin-dependent protein catabolic process | 41 | 2.1 | 3.20E-08 | 3.10E-06 | 5.90E-05 |
| proteasomal protein catabolic process | 41 | 2.1 | 3.20E-08 | 3.10E-06 | 5.90E-05 |
| regulation of body fluid levels | 48 | 2.5 | 6.70E-08 | 6.20E-06 | 1.20E-04 |
| acute-phase response | 24 | 1.2 | 1.10E-07 | 9.90E-06 | 2.00E-04 |
| cellular amino acid biosynthetic process | 27 | 1.4 | 1.20E-07 | 1.00E-05 | 2.10E-04 |
| lipid transport | 48 | 2.5 | 1.30E-07 | 1.10E-05 | 2.40E-04 |
| regulation of apoptosis | 155 | 7.9 | 2.00E-07 | 1.70E-05 | 3.70E-04 |
| generation of precursor metabolites and energy | 78 | 4 | 2.00E-07 | 1.70E-05 | 3.70E-04 |
| negative regulation of protein metabolic process | 56 | 2.9 | 2.20E-07 | 1.70E-05 | 4.00E-04 |
| negative regulation of cellular protein metabolic process | 54 | 2.8 | 2.50E-07 | 2.00E-05 | 4.50E-04 |
| complement activation, alternative pathway | 15 | 0.8 | 2.90E-07 | 2.20E-05 | 5.30E-04 |
| humoral immune response | 33 | 1.7 | 3.10E-07 | 2.40E-05 | 5.80E-04 |
| regulation of cellular protein metabolic process | 104 | 5.3 | 3.20E-07 | 2.30E-05 | 5.80E-04 |
| regulation of programmed cell death | 155 | 7.9 | 3.30E-07 | 2.40E-05 | 6.00E-04 |
| regulation of response to external stimulus | 50 | 2.5 | 3.60E-07 | 2.50E-05 | 6.60E-04 |
| regulation of cell death | 155 | 7.9 | 3.90E-07 | 2.70E-05 | 7.10E-04 |
| response to drug | 60 | 3.1 | 3.90E-07 | 2.70E-05 | 7.20E-04 |
| activation of immune response | 36 | 1.9 | 4.40E-07 | 3.00E-05 | 8.10E-04 |
| lipoprotein particle clearance | 15 | 0.8 | 6.20E-07 | 4.10E-05 | 1.10E-03 |
| response to inorganic substance | 57 | 2.9 | 7.80E-07 | 5.10E-05 | 1.40E-03 |
| hydrogen peroxide metabolic process | 18 | 0.9 | 8.30E-07 | 5.30E-05 | 1.50E-03 |
| homeostatic process | 143 | 7.3 | 1.10E-06 | 7.10E-05 | 2.10E-03 |
| peptide metabolic process | 26 | 1.3 | 1.30E-06 | 7.70E-05 | 2.30E-03 |
| organic ether metabolic process | 26 | 1.3 | 1.30E-06 | 7.70E-05 | 2.30E-03 |
| serine family amino acid metabolic process | 18 | 0.9 | 1.30E-06 | 8.20E-05 | 2.50E-03 |
| amine biosynthetic process | 32 | 1.6 | 2.10E-06 | 1.30E-04 | 3.90E-03 |
| anti-apoptosis | 56 | 2.9 | 2.40E-06 | 1.40E-04 | 4.40E-03 |
| response to hormone stimulus | 83 | 4.2 | 2.40E-06 | 1.40E-04 | 4.50E-03 |
| response to endogenous stimulus | 89 | 4.5 | 2.50E-06 | 1.40E-04 | 4.60E-03 |
| cellular lipid catabolic process | 30 | 1.5 | 3.10E-06 | 1.70E-04 | 5.70E-03 |
| glutathione metabolic process | 18 | 0.9 | 3.20E-06 | 1.80E-04 | 6.00E-03 |

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| response to glucocorticoid stimulus | 30 | 1.5 | 4.70E-06 | 2.60E-04 | 8.60E-03 |
| chemical homeostasis | 104 | 5.3 | 5.10E-06 | 2.70E-04 | 9.40E-03 |
| secondary metabolic process | 30 | 1.5 | 5.70E-06 | 3.00E-04 | 1.10E-02 |
| sterol metabolic process | 35 | 1.8 | 6.20E-06 | 3.20E-04 | 1.10E-02 |
| response to oxidative stress | 47 | 2.4 | 6.40E-06 | 3.30E-04 | 1.20E-02 |
| cellular homeostasis | 96 | 4.9 | 6.50E-06 | 3.30E-04 | 1.20E-02 |
| fatty acid metabolic process | 53 | 2.7 | 6.80E-06 | 3.40E-04 | 1.30E-02 |
| regulation of lipid metabolic process | 36 | 1.9 | 1.10E-05 | 5.40E-04 | 2.00E-02 |
| acylglycerol metabolic process | 23 | 1.2 | 1.20E-05 | 5.70E-04 | 2.20E-02 |
| cholesterol transport | 20 | 1 | 1.20E-05 | 5.70E-04 | 2.20E-02 |
| sterol transport | 20 | 1 | 1.20E-05 | 5.70E-04 | 2.20E-02 |
| triglyceride metabolic process | 21 | 1.1 | 1.20E-05 | 5.80E-04 | 2.20E-02 |
| regulation of inflammatory response | 29 | 1.5 | 1.30E-05 | 5.90E-04 | 2.30E-02 |
| positive regulation of immune response | 42 | 2.2 | 1.30E-05 | 6.10E-04 | 2.40E-02 |
| regulation of fibrinolysis | 11 | 0.5 | 1.40E-05 | 6.30E-04 | 2.50E-02 |
| regulation of protein processing | 9 | 0.5 | 1.50E-05 | 6.60E-04 | 2.70E-02 |
| regulation of protein maturation by peptide bond cleavage | 9 | 0.5 | 1.50E-05 | 6.60E-04 | 2.70E-02 |
| neutral lipid metabolic process | 23 | 1.2 | 1.50E-05 | 6.70E-04 | 2.80E-02 |
| response to nutrient levels | 51 | 2.6 | 1.60E-05 | 6.90E-04 | 2.90E-02 |
| negative regulation of molecular function | 74 | 3.8 | 1.70E-05 | 7.20E-04 | 3.10E-02 |
| cholesterol metabolic process | 32 | 1.6 | 1.70E-05 | 7.20E-04 | 3.10E-02 |
| response to corticosteroid stimulus | 30 | 1.5 | 1.80E-05 | 7.50E-04 | 3.30E-02 |
| negative regulation of response to stimulus | 33 | 1.7 | 1.80E-05 | 7.60E-04 | 3.30E-02 |
| lipid homeostasis | 23 | 1.2 | 1.90E-05 | 8.10E-04 | 3.60E-02 |
| glycerol ether metabolic process | 23 | 1.2 | 1.90E-05 | 8.10E-04 | 3.60E-02 |
| protein oligomerization | 47 | 2.4 | 2.10E-05 | 8.80E-04 | 3.90E-02 |
| positive regulation of molecular function | 111 | 5.7 | 2.20E-05 | 9.00E-04 | 4.10E-02 |
| anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process | 26 | 1.3 | 2.30E-05 | 9.10E-04 | 4.20E-02 |
| negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle | 26 | 1.3 | 2.30E-05 | 9.10E-04 | 4.20E-02 |
| positive regulation of response to stimulus | 57 | 2.9 | 2.30E-05 | 9.00E-04 | 4.20E-02 |
| antigen processing and presentation of peptide antigen | 17 | 0.8 | 2.50E-05 | 9.60E-04 | 4.50E-02 |
| oxidoreduction coenzyme metabolic process | 23 | 1.2 | 2.50E-05 | 9.60E-04 | 4.60E-02 |
| steroid metabolic process | 51 | 2.6 | 2.70E-05 | 1.00E-03 | 4.90E-02 |

*FDR: false discovery rate