

**Supplementary Table 3.** Gene ontology (GO) analysis of the edited genes identified in all 3 HCC specimens

GO Term	No. of Genes	%	P-value	Benjamin	FDR*
translation	135	4.6	5.80E-15	2.30E-11	1.10E-11
acute inflammatory response	63	2.1	1.90E-14	3.80E-11	3.60E-11
translational elongation	60	2	1.80E-12	2.40E-09	3.30E-09
cellular macromolecule catabolic process	212	7.2	2.50E-10	2.50E-07	4.60E-07
macromolecular complex assembly	197	6.7	5.00E-10	4.00E-07	9.20E-07
macromolecule catabolic process	222	7.5	5.50E-10	3.70E-07	1.00E-06
macromolecular complex subunit organization	206	7	7.90E-10	4.50E-07	1.50E-06
protein localization	243	8.3	8.40E-10	4.20E-07	1.60E-06
protein folding	77	2.6	8.70E-10	3.90E-07	1.60E-06
mRNA metabolic process	126	4.3	1.20E-09	4.70E-07	2.20E-06
protein transport	215	7.3	2.30E-09	8.30E-07	4.30E-06
establishment of protein localization	215	7.3	4.20E-09	1.40E-06	7.80E-06
intracellular transport	189	6.4	6.10E-09	1.90E-06	1.10E-05
proteolysis involved in cellular protein catabolic process	176	6	8.70E-09	2.50E-06	1.60E-05
protein catabolic process	180	6.1	1.00E-08	2.80E-06	1.90E-05
cellular protein catabolic process	176	6	1.20E-08	2.90E-06	2.20E-05
modification-dependent protein catabolic process	168	5.7	1.80E-08	4.30E-06	3.40E-05
modification-dependent macromolecule catabolic process	168	5.7	1.80E-08	4.30E-06	3.40E-05
ubiquitin-dependent protein catabolic process	89	3	3.30E-08	7.40E-06	6.20E-05
complement activation	30	1	4.30E-08	9.10E-06	8.10E-05
response to wounding	156	5.3	4.70E-08	9.40E-06	8.70E-05
regulation of cellular protein metabolic process	143	4.8	6.80E-08	1.30E-05	1.30E-04
activation of plasma proteins involved in acute inflammatory response	30	1	6.90E-08	1.30E-05	1.30E-04
RNA splicing	98	3.3	8.00E-08	1.40E-05	1.50E-04
complement activation, classical pathway	24	0.8	1.30E-07	2.10E-05	2.30E-04
proteolysis	264	9	1.90E-07	3.10E-05	3.60E-04
protein complex assembly	147	5	2.10E-07	3.20E-05	3.90E-04
protein complex biogenesis	147	5	2.10E-07	3.20E-05	3.90E-04
proteasomal ubiquitin-dependent protein catabolic process	48	1.6	2.30E-07	3.40E-05	4.30E-04
proteasomal protein catabolic process	48	1.6	2.30E-07	3.40E-05	4.30E-04
humoral immune response mediated by circulating immunoglobulin	24	0.8	3.90E-07	5.60E-05	7.30E-04

nuclear mRNA splicing, via spliceosome	62	2.1	4.10E-07	5.60E-05	7.50E-04
RNA splicing, via transesterification reactions	62	2.1	4.10E-07	5.60E-05	7.50E-04
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	62	2.1	4.10E-07	5.60E-05	7.50E-04
RNA processing	155	5.3	4.40E-07	5.90E-05	8.20E-04
lymphocyte mediated immunity	38	1.3	4.50E-07	5.80E-05	8.40E-04
acute-phase response	27	0.9	6.70E-07	8.40E-05	1.20E-03
mRNA processing	102	3.5	8.10E-07	9.90E-05	1.50E-03
sulfur metabolic process	50	1.7	1.30E-06	1.60E-04	2.50E-03
generation of precursor metabolites and energy	99	3.4	1.40E-06	1.60E-04	2.60E-03
regulation of catabolic process	44	1.5	2.20E-06	2.40E-04	4.00E-03
protein maturation by peptide bond cleavage	41	1.4	2.40E-06	2.60E-04	4.40E-03
inflammatory response	101	3.4	2.70E-06	2.80E-04	5.00E-03
immunoglobulin mediated immune response	30	1	4.60E-06	4.70E-04	8.50E-03
negative regulation of cellular protein metabolic process	65	2.2	5.30E-06	5.30E-04	9.80E-03
protein maturation	50	1.7	5.30E-06	5.20E-04	9.80E-03
posttranscriptional regulation of gene expression	72	2.4	5.80E-06	5.50E-04	1.10E-02
immune effector process	53	1.8	6.00E-06	5.60E-04	1.10E-02
regulation of lipid metabolic process	47	1.6	6.50E-06	6.00E-04	1.20E-02
protein processing	47	1.6	6.50E-06	6.00E-04	1.20E-02
leukocyte mediated immunity	39	1.3	8.00E-06	7.10E-04	1.50E-02
B cell mediated immunity	30	1	8.40E-06	7.30E-04	1.60E-02
response to hydrogen peroxide	30	1	8.40E-06	7.30E-04	1.60E-02
regulation of cellular catabolic process	32	1.1	8.80E-06	7.50E-04	1.60E-02
response to organic substance	183	6.2	1.00E-05	8.40E-04	1.90E-02
cellular macromolecule localization	117	4	1.30E-05	1.00E-03	2.40E-02
response to inorganic substance	69	2.3	1.30E-05	1.10E-03	2.50E-02
oxidation reduction	165	5.6	1.40E-05	1.10E-03	2.50E-02
negative regulation of protein metabolic process	65	2.2	1.40E-05	1.10E-03	2.70E-02
positive regulation of catabolic process	27	0.9	1.80E-05	1.30E-03	3.30E-02
cellular protein localization	116	3.9	1.80E-05	1.30E-03	3.30E-02
cofactor metabolic process	66	2.2	1.80E-05	1.30E-03	3.40E-02
positive regulation of cellular catabolic process	23	0.8	2.20E-05	1.60E-03	4.10E-02
response to reactive oxygen species	35	1.2	2.40E-05	1.70E-03	4.40E-02

\*FDR: false discovery rate