

## **Supplementary Information**

### **ATP7B-deficient hepatocytes reveal the importance of protein misfolding induced at low copper concentration**

**Author list:** Peggy Charbonnier<sup>1</sup>, Benoît Chovelon<sup>2,3</sup>, Corinne Ravelet<sup>3</sup>, Tuan Dung Ngo<sup>1</sup>, Mireille Chevallet<sup>1</sup> and Aurélien Deniaud<sup>1,\*</sup>

### **Affiliations**

<sup>1</sup> Univ. Grenoble Alpes, CNRS, CEA, IRIG - Laboratoire de Chimie et Biologie des Métaux, F-38000 Grenoble, France

<sup>2</sup> Service de Biochimie SB2TE, Institut de Biologie et Pathologie CHU Grenoble Alpes

<sup>3</sup> Département de Pharmacochimie Moléculaire, Université Grenoble Alpes, CNRS, UMR 5063, F-38041 Grenoble, France

\* Correspondence should be addressed to Dr Aurélien Deniaud, aurelien.deniaud@cea.fr



**Figure S1.** Analysis of CrispR/Cas9 clones obtained using the sgRNA-2. (A) An acrylamide gel electrophoresis of the PCR products obtained for sg2-1 and sg2-2 clones compared with those obtained with the HepG2/C3a parental cell line. While only one band was observed with HepG2/C3a cells corresponding to the WT version of *atp7b* for the two alleles, two different products were obtained for the two clones corresponding to a deletion of 10-20 nucleotides and a deletion of 90-100 nucleotides. Sequencing results for the Sg2-1 clone confirmed the presence of a 19 nucleotide deletion for the first allele (B) and a 100 nucleotide deletion for the second allele (C).

<b>Primer designation</b>	<b>Primer sequence</b>
Sg1-short-for	CCATGTGAGTGATAAGTGGCG
Sg1-short-rev	CTCACCTGTGATGAGGGACTC
Sg1-long-for	TGCAGCAGCCAAGAGATCA
Sg1-long-rev	CCACCATATGCCAAGGCA
Sg2-short-for	CATCAAATTGGGGACATGGC
Sg2-short-rev	CTCCTTGCAGTTCCGGACC
Sg2-long-for	ACACCAGTGGCATTGTTCCA
Sg2-long-rev	TTGGTCCCAGGCTTAAGGGA
Sg3-for	CCTCCTCTCCGGGACTTA
Sg4-short-for	TGAAGGCAAGGTCCGGAAAC
Sg4-short-rev	CTCACCTGTGATGAGGGACTC
Sg4-long-for	CCAGAGAACGCTGGATGTTGT
Sg4-long-rev and Sg3-rev	TCGGCTCCATCAGGAAGAGA

**Table S1.** Sequences of the primers used to amplify the regions surrounding the different sgRNA sequences.

<b>Gene</b>	<b>Forward primer sequence</b>	<b>Reverse primer sequence</b>
HPRT	ATGGACAGGACTGGACGTCTGCT	TTGAGCACACAGAGGGCTACAATG
GAPDH	ATGGGAAAGGTGAAGGTGCG	GGGGTCATTGATGGCAACAATA
Met (MT1X)	GCTTCTCCTGCCTCGAA	TGACGTCCCTTGAGATG
GCLM	CCTCCTGCTGTGTGATGCCAC	CGTGCCTGAATGTCAGGAATGC
SOD1	TGGCCGATGTGTCTATTGAA	ACCTT GCCAAGTCATCTG
Catalase	TTGCCACAGGAAAGTACCCC	TGAGGCCAACCTTGGTGAG
HMOX1	ATGACACCAAGGACCAGAGC	GTGTAAGGACCCATCGGAGA
IL8	TGGCAGCCTTCCTGATTCT	ATTCTGTGTTGGCGCAGTG
HSPA6	AGGAGGTGGAGAGGGATGGTT	TGTCCTCTCGGAAATCTTG
DNAJ-A1	CTGCAACGGAAGGAAGATACT	GTCTCCTTCACCATGGAATGT
DNAJ-A2	CAGGGTGTGTTCGTAGTT	GTCTGGGTTGATCCAGTTGT
DNAJ-A3	AGGACAAGCCAAGCAGAAA	TCTGCACCCCTGAACGTAATG
ATG7	ACAGATGGAGTAGCAGTTCC	ACATTCACTGAGGTTACCAT
ATG13	TCCAGACAGTCGTGTTGGG	CTCAAATTGCCTGGTAGACATGA
BNIP3L	CGCCCCTGCACAACAAAC	TCATTGCCATTGCTGCTG
FUNDC1	TCAGATTGCTAGTCATAGTGGC	TGCTTGTTCGCTCGTTCT
Get3	TGAGCATGGCAAGAAGATG	GTCAAATACCACCAACGAGAAG
PINK1	TGGTCGACTACCCTGATGTG	CGCAGGGTACAGGGATAGTT
Drp1	TCACCCGGAGACCTCTCATT	TCTGCTTCCACCCATTTCCT
BSEP	ACATGCTTGCAGGGACCTTA	GGAGGTTCGTGCACCAAGGTA

**Table S2.** Sequences of the primers used for quantitative real time polymerase chain reaction.