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Supplemental information

CLN7/MFSD8 may be an important factor for SARS-CoV-2 cell entry

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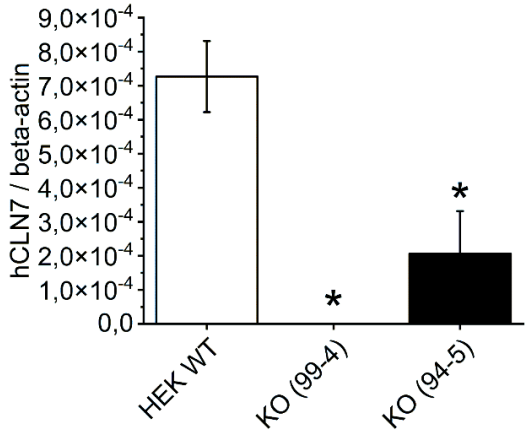
Figure S1: Genotyping of HEK293T CLN7 knockout cells, Related to STAR Methods

a)



b)

Line 94-5: Exon 11 (CLN7 genomic DNA NG_008657.1)

WT:

408 423

L Y T P V I H L A Q F L T S A V

CTCTACACCCC**GGTG**ATTCATCTGGCCCAGTTCCTTACATCAGCTGTG

94-5: **GGTG** deleted and frameshift from P411

408 423

L Y T P F I W P S S L H Q L C *

CTCTACACCCC**ATTCATCTGGCCCAGTTCCTTACATCAGCTGTGTTAA**

>> Frameshift leads to a premature stop codon in exon 11

Line 99-4: Exon 2 (CLN7 genomic DNA NG_008657.1)

WT:

.....exon.....v..intron..

12 20

L L G D T P G S R

CTCTTAGGCGACACACCTGGA**AGCAGGTGA**

99-4: **AGCAGG** deleted

.....exon.....

12 19

L L G D T P G *

CTCTTAGGCGACACACCTGGA**TGA**

>> Deletion leads to a shift of a **stop codon** from intron to previous exon 2 or splicing is affected

a) Measurement of CLN7 mRNA expression in our CLN7-deficient HEK293T cell lines using quantitative PCR. In line 99-4 (middle bar) CLN7 mRNA could no longer be detected. In line 94-5 (right bar), approximately 30% CLN7 mRNA could still be detected compared to wild-type cells (left bar). b) Genomic DNA from both HEK293T knockout cell lines was isolated, amplified and sequenced. For line 94-5, we observed a deletion of 4 bases in exon 11, causing a frameshift and thus a premature stop codon at amino acid position 423. In line 99-4, a deletion of 6 bases occurs directly at the boundary between exon 2 and the following intron. Most likely, this causes a stop codon from the intron to enter exon 2, resulting in premature termination of the CLN7 protein. Alternatively, splicing could be affected.