



**Figure S1.** (A) The cell lines of the Human Protein Atlas have been analyzed by RNAseq to estimate the transcript abundance of each protein-encoding gene. We have reproduced the abundance as transcript per million (TPM) for all genes highlighted in this study. (B) Fluorescence microscopy of GFP-SKL in control and *PEX13* KO HEK-293 cells. (C) HSD17B4 immunoblot of 4 KO clones and 2 control HEK-293 samples. The HSD17B4 antibody recognizes the full length (79kD) and a proteolytically processed fragment (45kD; enoyl-CoA hydratase component). KO clones with fully deficient HSD17B4 (KO1 and KO2) were used for our studies. (D) ABCD3 immunoblot of one ABCD3 KO clone, one CPT2/ABCD3 double KO clone and 2 control clones. Each sample was analyzed in duplicate. The position of the molecular weight markers is indicated in kDa. Alpha Tubulin ( $\alpha$  Tub) was used as a loading control. (E) Production of C6-, C8-, C10- and C12-carnitine in the extracellular medium of WT and *PEX13* KO clonal cell lines after loading with C12:0 in the presence of increasing concentrations of the CPT2 inhibitor L-AC. Data are means  $\pm$  SD of 2 or 4 independent observations. (F) Production of C6-, C8-, C10- and C12-carnitine in the extracellular medium of WT, *CPT2* KO and *CPT2/PEX13* double KO clonal cell lines after loading with C12:0. (G) Production of C6-, C8-, C10-, C12-, C14- and C16-carnitine in the extracellular medium of WT, *CPT2* KO and *CPT2/PEX13* double KO clonal cell lines after loading with C16:0.