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Supplemental Material

"The CCT3-*LINC00326* axis regulates hepatocarcinogenic lipid metabolism"

Søndergaard *et al.*

SUPPLEMENTARY FIGURES

Figure S1. Molecular characteristics of RBPs in HCC
Figure S2. Survival analysis of the TCGA-LIHC cohort
Figure S3. Estimation of hazard ratio and HCC patient survival based on RBP gene expression
Figure S4. siRNA transfection efficiency and RBP-KD perturbation effects in human HCC cells
Figure S5. Gene Ontology (GO) and KEGG analyses of deregulated genes upon RBP-KD
Figure S6. Cellular and molecular phenotype assessment upon lincRNA-OE
Figure S7. GO and KEGG analyses of deregulated genes upon OE
Figure S8. CCT3 works in a chaperoning-independent manner to interact with *LINC00326*
Figure S9. GO and KEGG analyses of deregulated genes shared upon RBP-KD and lincRNA OE
Figure S10. *LINC00326* is highly expressed in healthy testis and diminished upon cancer progression
Figure S11. Molecular model for *LINC00326* regulating lipid metabolism-associated gene expression

SUPPLEMENTARY TABLES

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Table S5. RBP KD RNAseq raw counts
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Supplementary tables and microscopic imaging files are accessible via Figshare:
https://figshare.com/s/2c05765158269b3b4ff2
https://figshare.com/s/a83dbee52555e922ca8d
https://figshare.com/s/08b0f84f2ea241b03c8d

SUPPLEMENTARY MATERIALS & METHODS

Cell-based and molecular assays as well as xenograft experiments are described in the supplementary materials and methods.

ARRAYEXPRESS ACCESSION

Australian HCC patient cohort RNA-seq: E-MTAB-8915
RBP-KD RNA-seq: E-MTAB-9587
lncRNA-OE RNA-seq: E-MTAB-9586

CODE ACCESSIBILITY

github.com/jonasns/LiveRNome