



Figure S7. Clustered heat map of characteristics distribution of studied lincRNAs of human chromosome 18.

Principal component analysis (PCA) was performed using ClustVis (<https://biit.cs.ut.ee/clustvis/>) with following settings: pre-processing options – ‘no transformation’, ‘row centering’, ‘no scaling’ was applied to rows; SVD with imputation is used to calculate principal components. X- and Y-axis show PC-1 and PC-2 that explain 26.6% and 17.2% of the total variance, respectively.

Heat map options – columns are centered, no scaling is applied to columns, imputation is used for missing value estimation, rows are clustered using Manhattan distance and single linkage, and columns are clustered using Manhattan distance and average linkage.

Right color scale denotes cluster distances.

Figure legend

Hallmark symbol	Description of hallmark	Conditions
A	Somatic gene mutations	Cancer
B	Gene fusions	Cancer/Normal
C	Gene knockouts effects	Cancer/Normal
D	Copy number variations (amplifications or deletions)	Cancer
E	Differential promoter methylation	Cancer
F	Tissue-specific expression	Normal
G	Type-specific differential expression	Cancer
H	Subtype-specific differential expression	Cancer
J	Interactions with microRNAs	Cancer
K	Interactions with cellular proteins	Cancer
M	Predicted involvement in cancer-associated pathways	Cancer
N	smORF-proteins	Cancer
O	Potential prognostic value	Cancer
P	Potential predictive value	Cancer
Q	Gene expression signatures for drug predictions	Cancer
R	Literature data	Cancer