**Text S2**

**Evaluation of cis- and trans acting copy number alterations**

In order to identify both cis- and trans-acting CNVs, we performed an L1-constrained regression (Lasso-regression) on the important genes that was identified previously. This method assumes that the predictor variables are independent, so first we implemented a dimensionality reduction with the help of the „CGHregions” R package. This algorithm results in CNV regions, in which the clones are very much alike, with minimal information loss. The L1-constrained regression was performed with the „lol” R package using cross-validation optimizer. The resulted significant CNV regions were identified as cis-acting elements if they were on the same chromosome or were closer than 50 Mb to the investigated gene and as trans-acting elements otherwise. We assessed the score, which represents dependency of the response variable from the predictors, using the following equitations.

where

represents the variance of the prediction residuals of the model with all significant predictors included

represents the variance of the prediction residuals of the model with only the significant cis predictors included

represents the variance of the prediction residuals of the model without the significant predictors