**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.

$$score\_{i}=-ln\left(\frac{σ\_{with all}^{2}}{σ\_{without all}^{2}}\right)$$

$$score\_{i}^{cis}=-ln\left(\frac{σ\_{with cis}^{2}}{σ\_{without all}^{2}}\right)$$

$$score\_{i}^{trans}=-ln\left(\frac{σ\_{with cis}^{2}-σ\_{with all}^{2}}{σ\_{without all}^{2}}\right)$$

where

$σ\_{with all}^{2}$ represents the variance of the prediction residuals of the model with all significant predictors included

$σ\_{with cis}^{2}$ represents the variance of the prediction residuals of the model with only the significant cis predictors included

$σ\_{without all}^{2}$ represents the variance of the prediction residuals of the model without the significant predictors