

## Supplemental Information file

### Co-Expression Network Analysis Unveiled lncRNA-mRNA Links Correlated to Epidermal Growth Factor Receptor-Tyrosine Kinase Inhibitor Resistance and/or Intermediate Epithelial-to-Mesenchymal Transition Phenotypes in a Human Non-Small Cell Lung Cancer Cellular Model System

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The document contains the following files:

**Figure S1.** Correlation between WGCNA parameters. Scatterplots of gene significance for ERL-resistance and EMT intermediate phenotypes versus module membership and connectivity of selected modules. The absolute values of both module membership and gene significance are shown. In *brown4*, *magenta4*, and *plum4*, gene significance for ERL-resistance and/or EMT intermediate phenotype exhibit good significant correlations ( $\rho_s > 0.3$ , p-value  $< 0.05$ ) implying that hub genes of the module also tend to be correlated with the biological phenotypes of interest. Conversely, the module membership and connectivity parameters of the *deeppink* module members don't show any significant correlation with either ERL-resistance or EMT intermediate phenotypes. ERL = erlotinib; EMT = epithelial-mesenchymal transition.

**Figure S2. Network of the brown4 module.** lncRNAs (diamonds) and mRNAs (ellipses) at probe-level are shown in an organic layout. Nodes are connected by edges whose sizes are proportional to their WGCNA weights: the higher, the thicker. Node size is proportional to the intramodular connectivity measure (kWithinScaled) and node border color and width indicate the fold-change between Erl-sensitive/epithelial and -resistant/hybrid\_intermediate NSCLC cell lines: red = up-regulation ( $|\text{fold-change}| > 1.5$ ); blue = down-regulation ( $|\text{fold-change}| < 0.5$ ); white = no expression variation; thickness= the higher, the thicker. Nodes of selected lncRNAs are filled in green.

**Figure S3. Network of the magenta4 module.** lncRNAs (diamonds) and mRNAs (ellipses) at probe-level are shown in an organic layout. Nodes are connected by edges whose sizes are proportional to their WGCNA weights: the higher, the thicker. Node size is proportional to the intramodular connectivity measure (kWithinScaled) and node border color and width indicate the fold-change between Erl-sensitive/epithelial and -resistant/hybrid\_intermediate EMT NSCLC cell lines: red = up-regulation ( $|\text{fold-change}| > 1.5$ ); blue = down-regulation ( $|\text{fold-change}| < 0.5$ ); white = no expression variation; thickness= the higher, the thicker. Nodes of selected lncRNAs are filled in green.

**Table S1.xls** Gene expression data and WGCNA results of whole NSCLC cell line dataset.

**Table S2.xls** Phenotypical traits of cell lines.

**Table S3.xls** Gene expression data and WGCNA results of whole NSCLC cell line dataset of the *brown4* module.

**Table S4.xls** Gene expression data and WGCNA results of whole NSCLC cell line dataset of the *deeppink* module.

**Table S5.xls** Gene expression data and WGCNA results of whole NSCLC cell line dataset of the *magenta4* module.

**Table S6.xls** Gene expression data and WGCNA results of whole NSCLC cell line dataset of the *plum4* module.

**Table S7.xls** Results of DAVID functional enrichment analysis of *brown4* module. The last column indicates the protein coding genes connected to selected lncRNAs in the WGCNA network.

**Table S8.xls** Results of DAVID functional enrichment analysis of *magenta4 module*. The last column indicates the protein coding genes connected to selected lncRNAs in the WGCNA network.

**Table S9.xls** Results of DAVID functional enrichment analysis of *plum4* module. The last column indicates the protein coding genes connected to selected lncRNAs in the WGCNA network.

**Table S10.xls** Details of the top lncRNAs correlated to intermediate epithelial to mesenchymal transition (int-EMT) and/or erlotinib resistance (ERL-res).

**Table S11.xls** Sequences of oligonucleotide primers used in qPCR in Figure 4.