

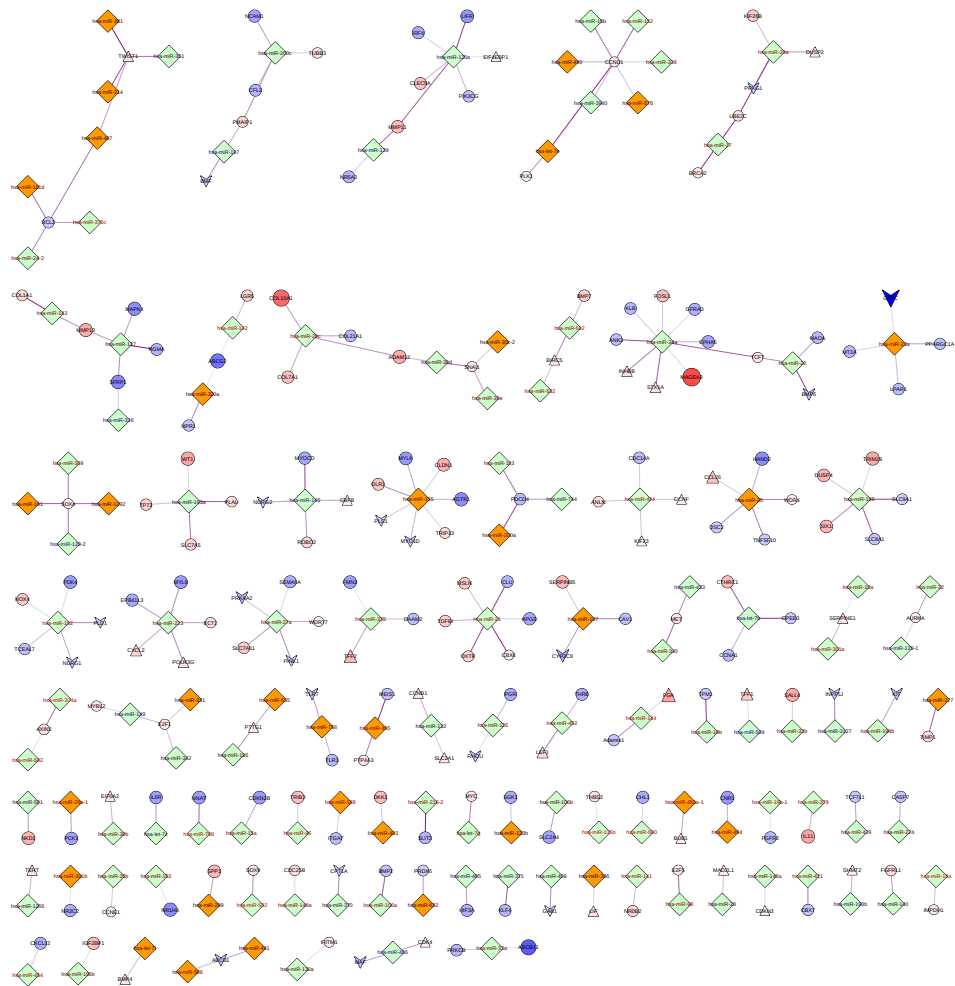


Figure 1 RSCC specific miR-mRNA interaction network clustered via MCL clustering. Validated interactions between differentially expressed genes and miRs were extracted from the miR-TAR database. The network was clustered on mRNA-miRNA co-expression strength using MCL clustering. Node color: Blue- downregulated, red- upregulated, green- commonly regulated miR and orange- uniquely regulated miR. miR label color: red- upregulated, blue- downregulated.

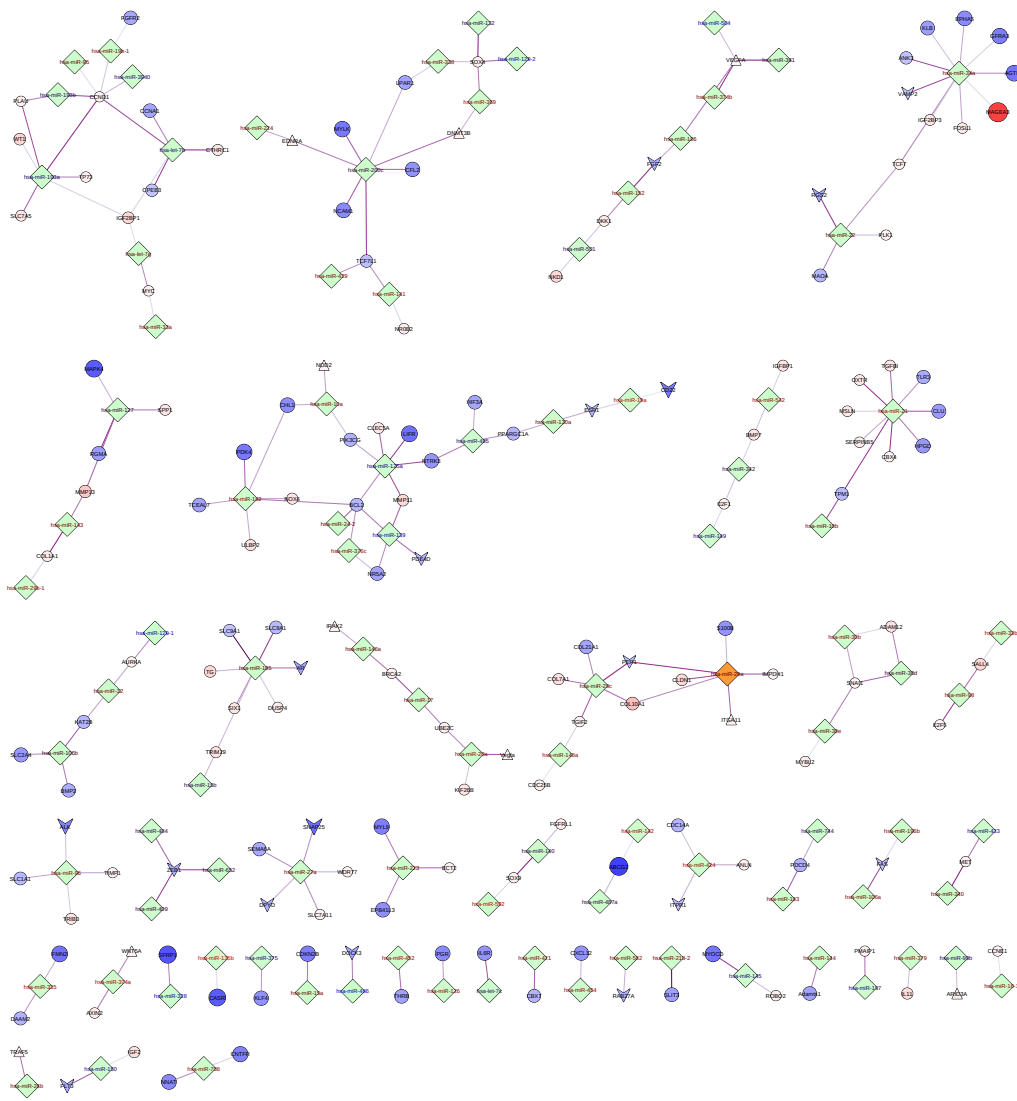


Figure 2 LSCC specific miR-mRNA interaction network clustered via MCL clustering. Validated interactions between differentially expressed genes and miRs were extracted from the miR-TAR database. The network was clustered on mRNA-miRNA co-expression strength using MCL clustering. Node color: Blue- downregulated, red- upregulated, green- commonly regulated miR and orange- uniquely regulated miR. miR label color: red- upregulated, blue- downregulated.

RIGHT

LEFT

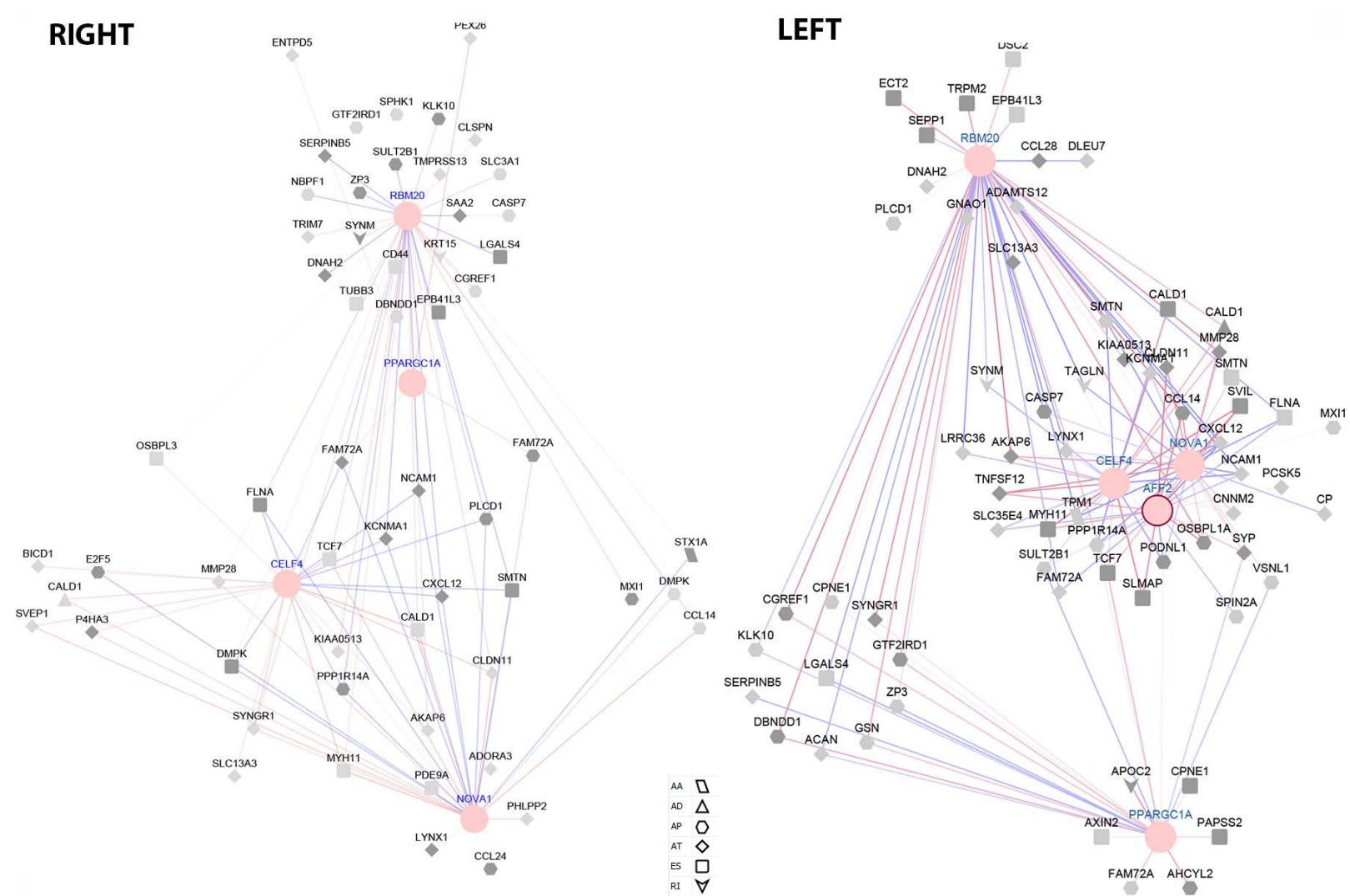


Figure 3 - Correlation network of splicing factors and AS events- the correlation network for left and right tumors captures the correlation between splicing factors (differentially regulated RBPs) and sigAS events occurring in each side. Blue edges indicated anti-correlation, red- correlation. Pink nodes are the splicing factors, grey nodes indicate sigAS events. The shapes correspond to each of the six events identified and presented in legend within figure.