TABLE S12: Genes set enrichment analysis revealed a significant overrepresentation of the DANG_MYC_TARGETS_UP set in high Combo score patients compared to low Combo score patients (*P*< 0.002).

PROBE	GENE SYMBOL	GENE_TITLE	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
NBN	NBN	nibrin	-0.053661507	-0.65107596	Yes
HSPD1	HSPD1	heat shock 60kDa protein 1 (chaperonin)	-0.069516964	-0.6412293	Yes
CCND2	CCND2	cyclin D2	-0.071466759	-0.5963849	Yes
TOP1	TOP1	topoisomerase (DNA) I	-0.077072568	-0.55628675	Yes
BCAT1	BCAT1	branched chain aminotransferase 1, cytosolic	-0.084116891	-0.5140258	Yes
TP53	TP53	tumor protein p53 (Li-Fraumeni syndrome)	-0.092572831	-0.46930388	Yes
MGST1	MGST1	microsomal glutathione S-transferase 1	-0.097474456	-0.41094923	Yes
EMP1	EMP1	epithelial membrane protein 1	-0.149763241	-0.37062183	Yes
CCNB1	CCNB1	cyclin B1	-0.170906231	-0.2681044	Yes
UCHL1	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	-0.200972006	-0.14425816	Yes
TYMS	TYMS	thymidylate synthetase	-0.23626557	0.007501727	Yes