**Figure S4.** *in silico* Independent Validation Analysis. (A) The dataset from Miller et al [1] was composed of 251 human tumor samples, of which 31 were derived from young women, which we used in our re-analysis. Our progression signature gene list was sufficient to separate patients in Miller *et. al*.'s study into two clusters which differed significantly with the p53 mutation status. The cluster which had high expression of these genes comprised nearly of all the p53 mutant tumors. (B) GSE7390 [2] and GSE12093 [3]datasets were used for independent validation analyses. Genes, including *RRM2, BIRC5, TOP2A, NUSAP1, TPX2, and CCNB2* were of significant clinical relevance for identifying patients at high risk patients groups (result for *RRM2* has been shown)

**(A)**



**(B)**



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