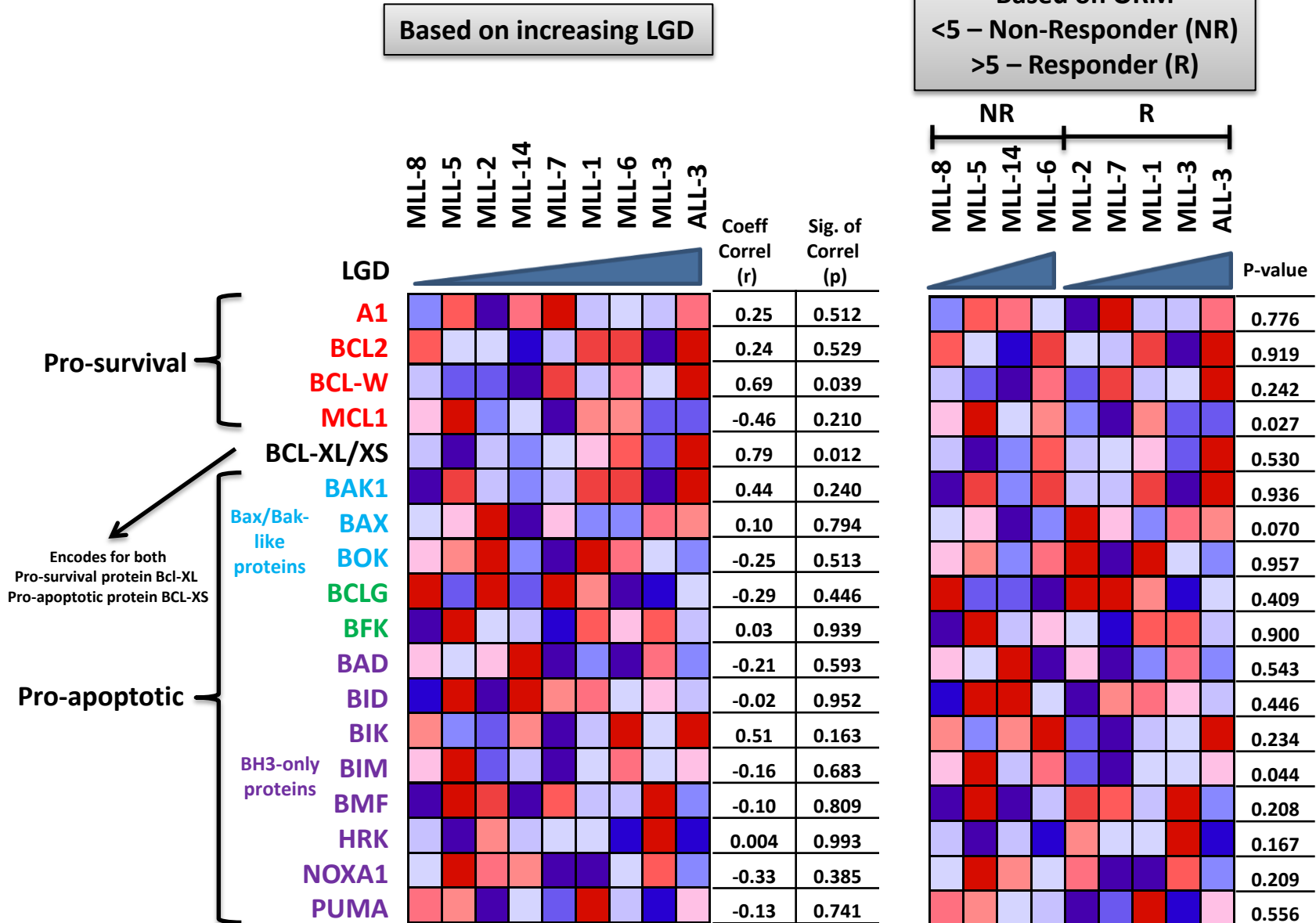
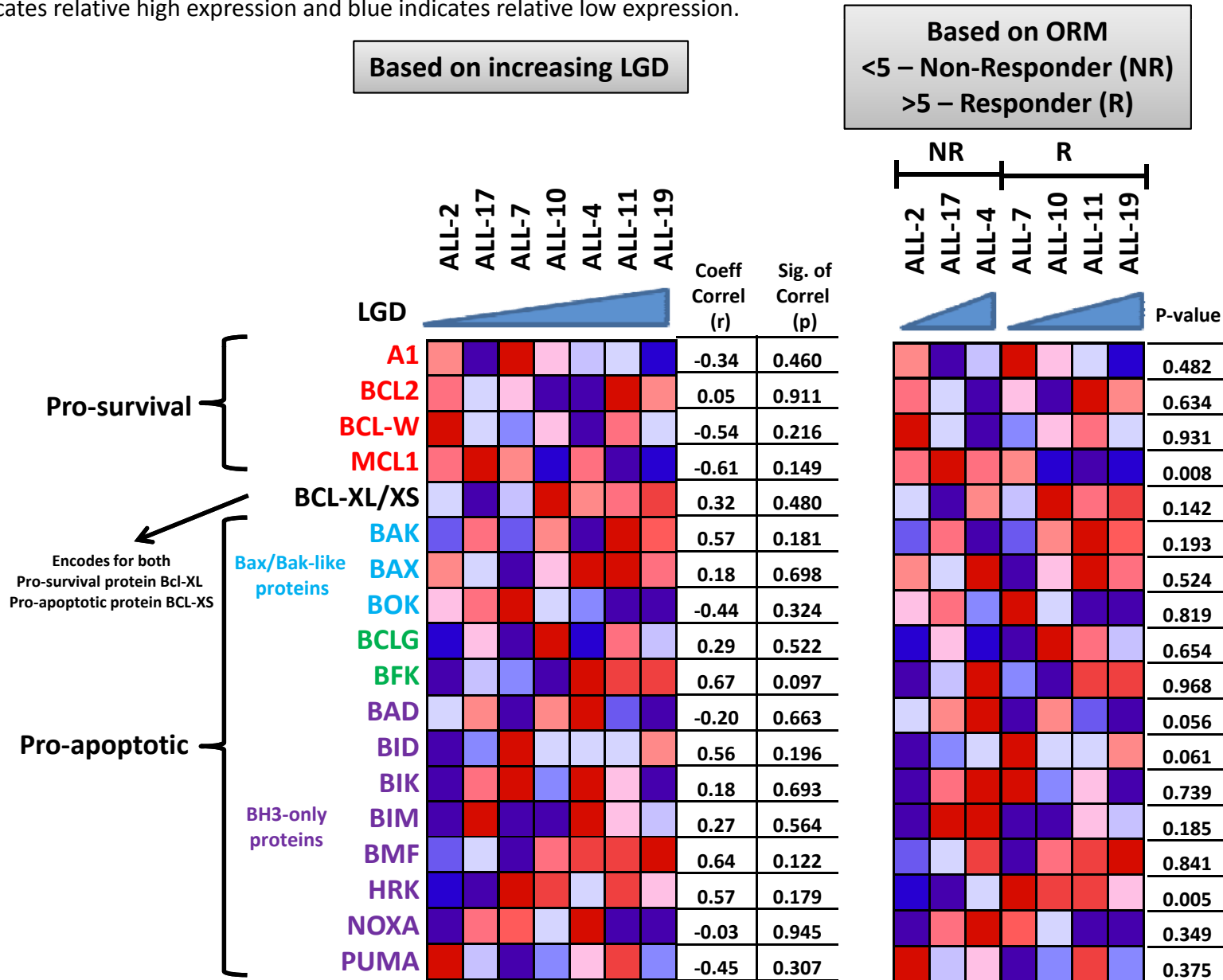


**Supplementary Figure S6. Correlations between *BCL2* family gene expression and *in vivo* ABT-263 sensitivity in the MLL-ALL xenograft panel.** Left figure: MLL-ALL xenografts were ordered by increasing LGD from left to right with each row representing a *BCL2* family member. Right figure: Xenografts were stratified into Non-Responders (NR) and Responders (R) then ordered by increasing LGD from left to right within each category. The colours in the heatmaps represent the relative expression per gene across all samples. Red indicates relative high expression and blue indicates relative low expression.

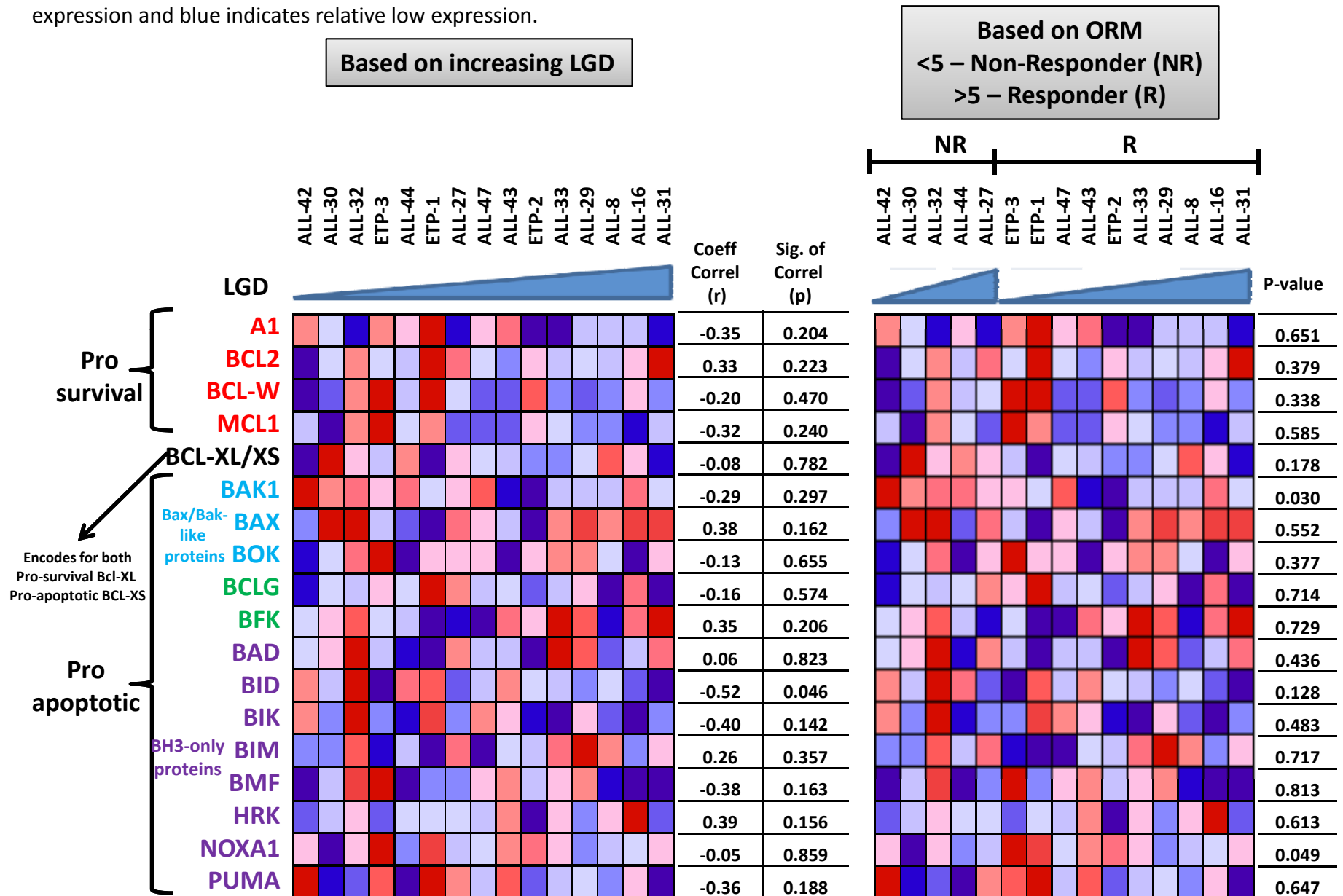


**Supplementary Figure S7. Correlations between *BCL2* family gene expression and *in vivo* ABT-263 sensitivity in the BCP-ALL xenograft panel.**

Left figure: BCP-ALL xenografts were ordered by increasing LGD from left to right with each row representing a *BCL2* family member. Right figure: Xenografts were stratified into Non-Responders (NR) and Responders (R) then ordered by increasing LGD from left to right within each category. The colours in the heatmaps represent the relative expression per gene across all samples. Red indicates relative high expression and blue indicates relative low expression.



**Supplementary Figure S8. Correlations between *BCL2* family gene expression and *in vivo* ABT-263 sensitivity in the T-ALL xenograft panel.**  
 Left figure: T-ALL xenografts were ordered by increasing LGD from left to right with each row representing a *BCL2* family member. Right figure: Xenografts were stratified into Non-Responders (NR) and Responders (R) then ordered by increasing LGD from left to right within each category. The colours in the heatmaps represent the relative expression per gene across all samples. Red indicates relative high expression and blue indicates relative low expression.



**Supplementary Figure S9. Representative immunoblot of MCL1 protein expression in ALL xenografts.** Six ABT-263 *in vivo* Non-Responders and 6 Responders were selected at random. Proteins were extracted as described in the Materials and Methods section. HL-60 and Raji cells were utilized as controls.

