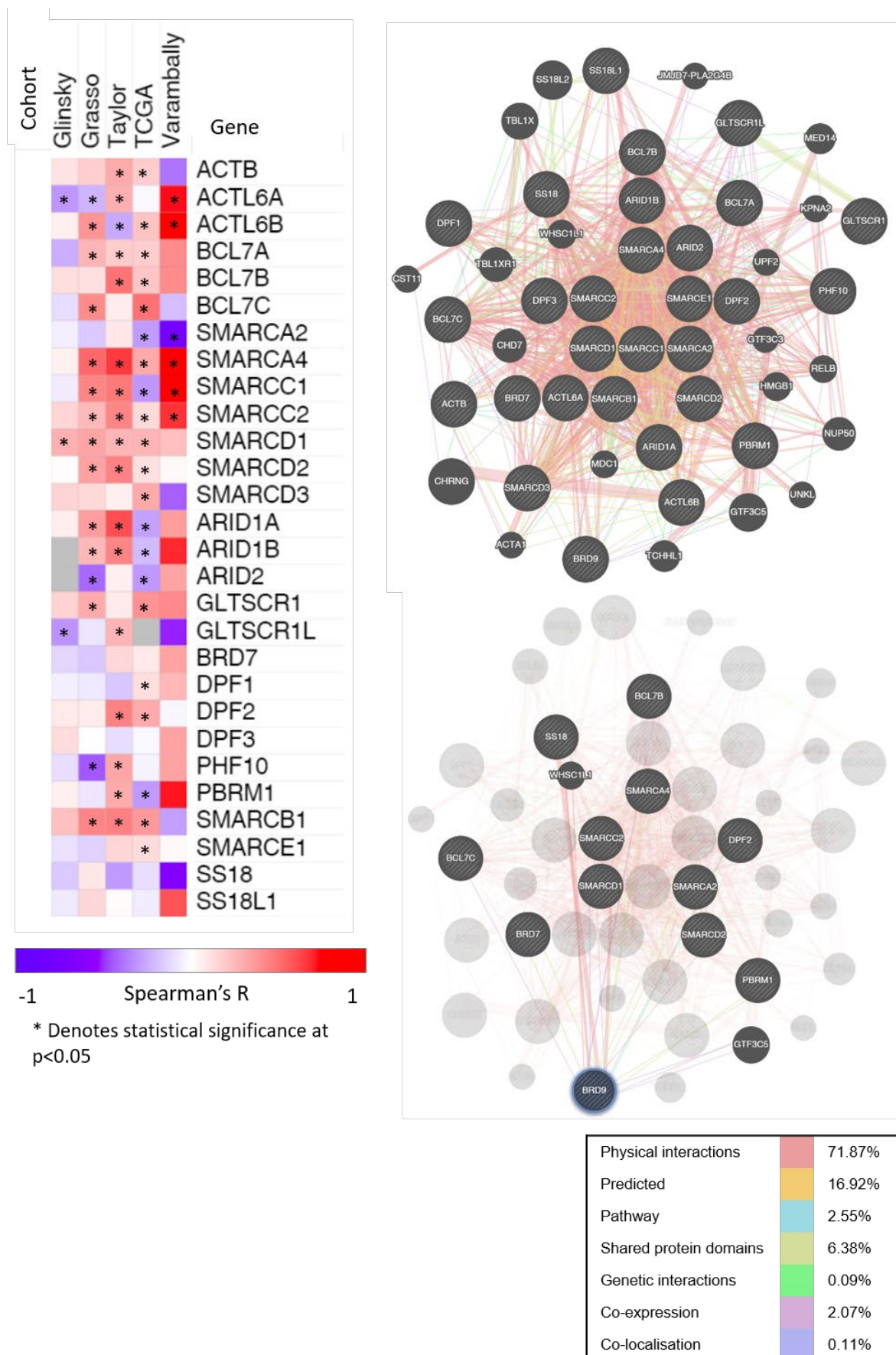
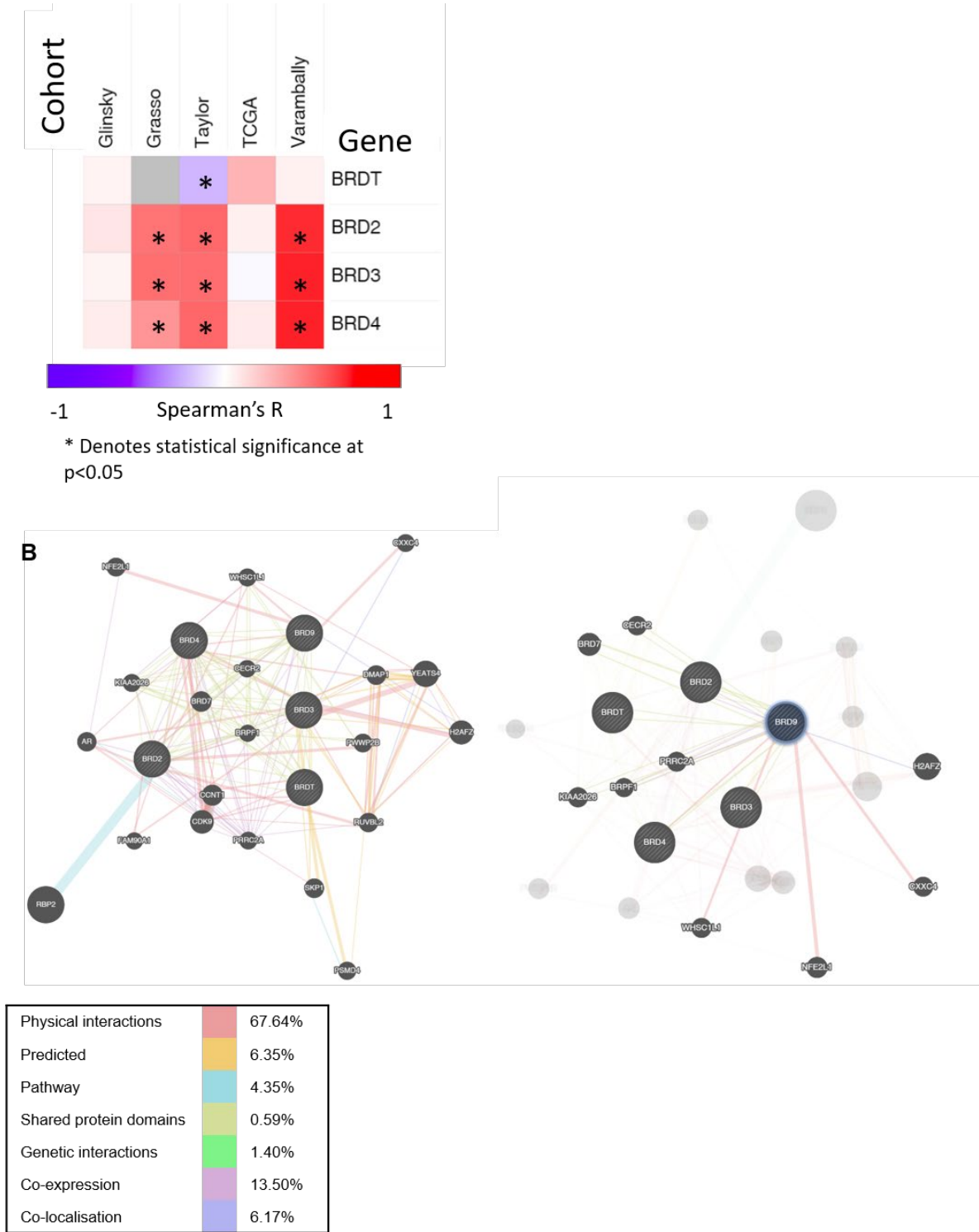


**Figure S1.** *BRD9* expression by cancer stage in cancer omics cohorts. (A) Violin plot showing how *BRD9* expression varies with cancer stage in the TCGA cohort. P-values were obtained using Dunn's post-hoc test. (B) Stacked bar chart showing *BRD9* mutation distribution at different cancer stages and the number of patients at each stage in the TCGA cohort. P-value was obtained using Fisher's exact test. (C) Violin plot showing how *BRD9* expression varies with cancer stage in the Ren cohort. P-values were obtained using Dunnett's T3 post-hoc test. (D) Stacked bar chart showing *BRD9* mutation distribution at different cancer stages and the number of patients at each stage in the Ren cohort. P-value was obtained using Fisher's exact test. (E) Violin plot showing how *BRD9* expression varies with cancer stage in the Gerhauser cohort. P-values were obtained using Dunn's post-hoc test. (F) Violin plot showing how *BRD9* expression varies with cancer stage in the Barbieri cohort. P-values were obtained using Dunnett's T3 post-hoc test. (G) Violin plot showing how *BRD9* expression varies with cancer stage in the Taylor cohort. P-values were obtained using Dunn's T3 post-hoc test. Stages were combined into three stage groups due to small sample sizes (n) at individual stages (e.g. T2a). Y axis scales on violin plots vary due to experimental variation.



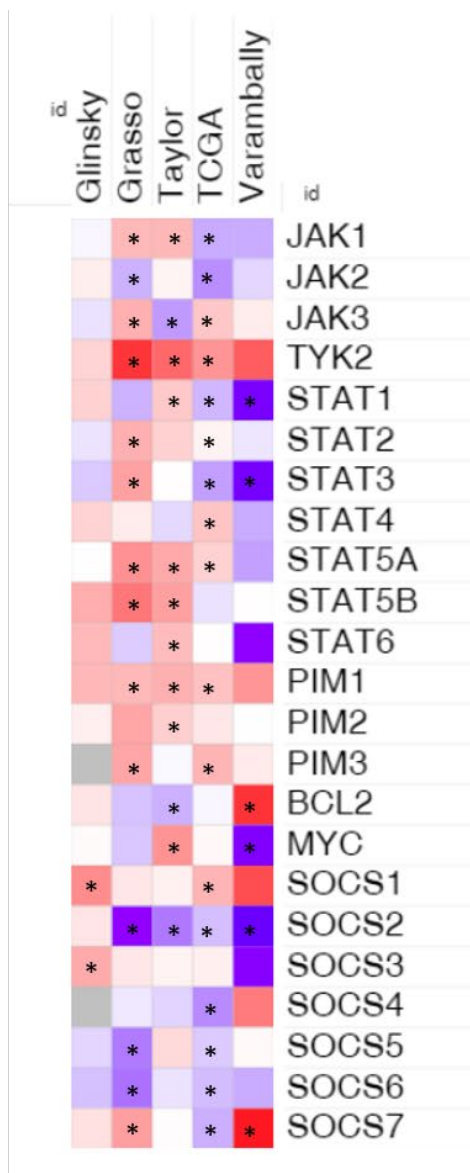
**Figure S2.** Correlation and association of *BRD9* with genes composing the SWI/SNF complex. **(A)** Heatmap showing the correlation (Spearman's R coefficient) between *BRD9* and genes that make up the SWI/SNF complex. Statistically significant correlations ( $p < 0.05$ ) are indicated by '\*'. **(B)** Gene

network map showing the associations between *BRD9* and known genes that make up the SWI/SNF complex. Heatmap made using <https://software.broadinstitute.org/morpheus/> with statistically significant correlation denotation added in Microsoft PowerPoint. Gene network map created using <https://genemania.org/>.



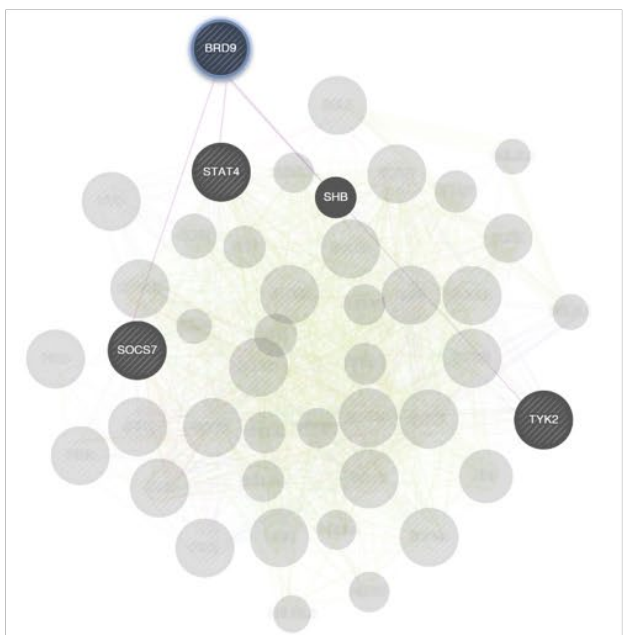
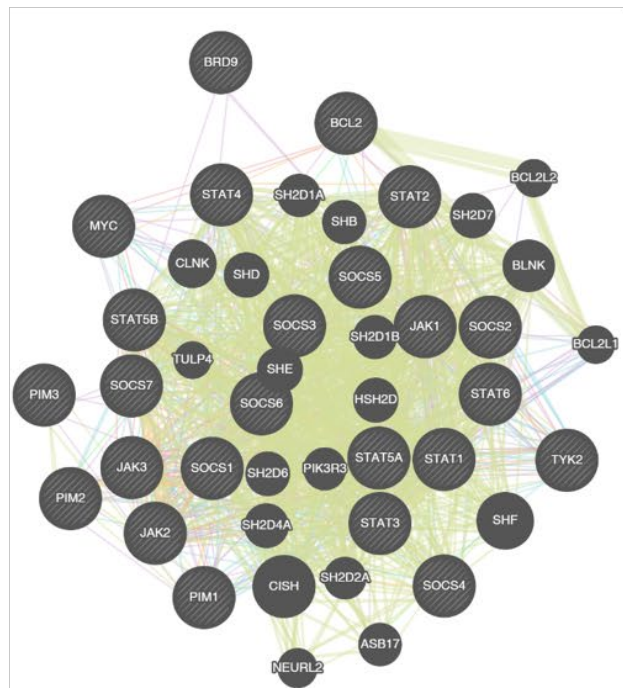
**Figure S3.** Correlation and association of *BRD9* with genes composing the BET complex. **(A)** Heatmap showing the correlation (Spearman's R coefficient) between *BRD9* and genes that make up the BET complex. Statistically significant correlations ( $p < 0.05$ ) are indicated by '\*'. **(B)** Gene network map showing the associations between *BRD9* and known genes that make up the BET complex. Heatmap made using <https://software.broadinstitute.org/morpheus/> with statistically significant

correlation denotation added in Microsoft PowerPoint. Gene network map created using <https://genemania.org/>.



-1 Spearman's R

\* Denotes statistical significance at  $p < 0.05$

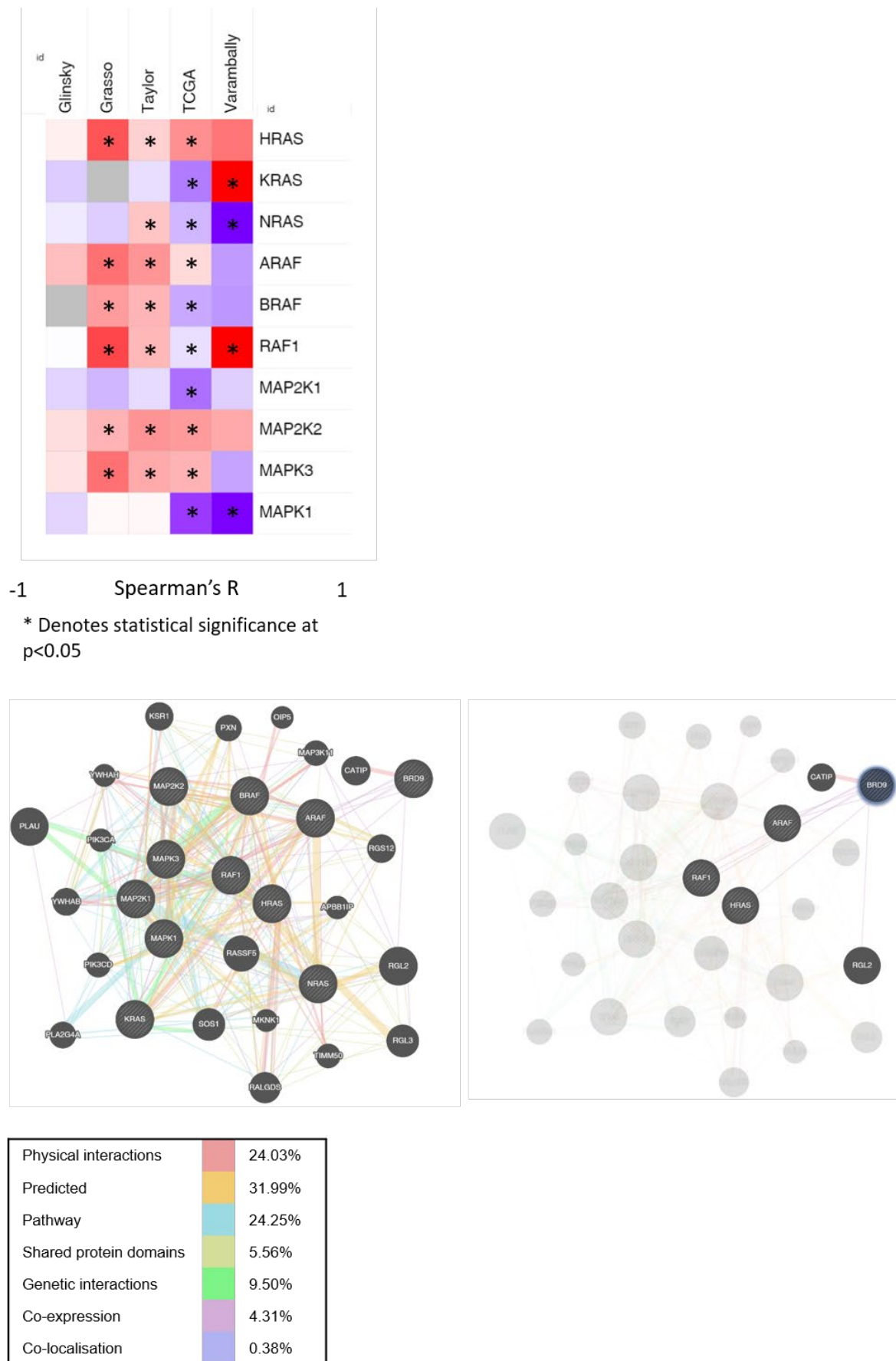


Physical interactions	4.28%
Predicted	20.28%
Pathway	16.31%
Shared protein domains	43.86%
Genetic interactions	0.06%
Co-expression	12.78%
Co-localisation	2.43%

**Figure S4.** The correlation and association of *BRD9* with genes expressed in the JAK-STAT pathway. (A) Heatmap showing the correlation (Spearman's R coefficient) between *BRD9* and genes involved in the JAK-STAT pathway. Statistically significant correlations ( $p < 0.05$ ) are indicated by '\*'. (B) Gene network map showing the associations between *BRD9* and known genes expressed in the JAK-STAT

pathway. Heatmap made using <https://software.broadinstitute.org/morpheus/> with statistically significant correlation denotation added in Microsoft PowerPoint. Gene network map created using <https://genemania.org/>.





**Figure S5.** The correlation and association of *BRD9* with genes expressed in the MAPK pathway. (A) Heatmap showing the correlation (Spearman's R coefficient) between *BRD9* and genes involved in the MAPK pathway. Statistically significant correlations ( $p < 0.05$ ) are indicated by '\*'. (B) Gene





<https://software.broadinstitute.org/morpheus/> with statistically significant correlation denotation added in Microsoft PowerPoint. Gene network map created using <https://genemania.org/>.