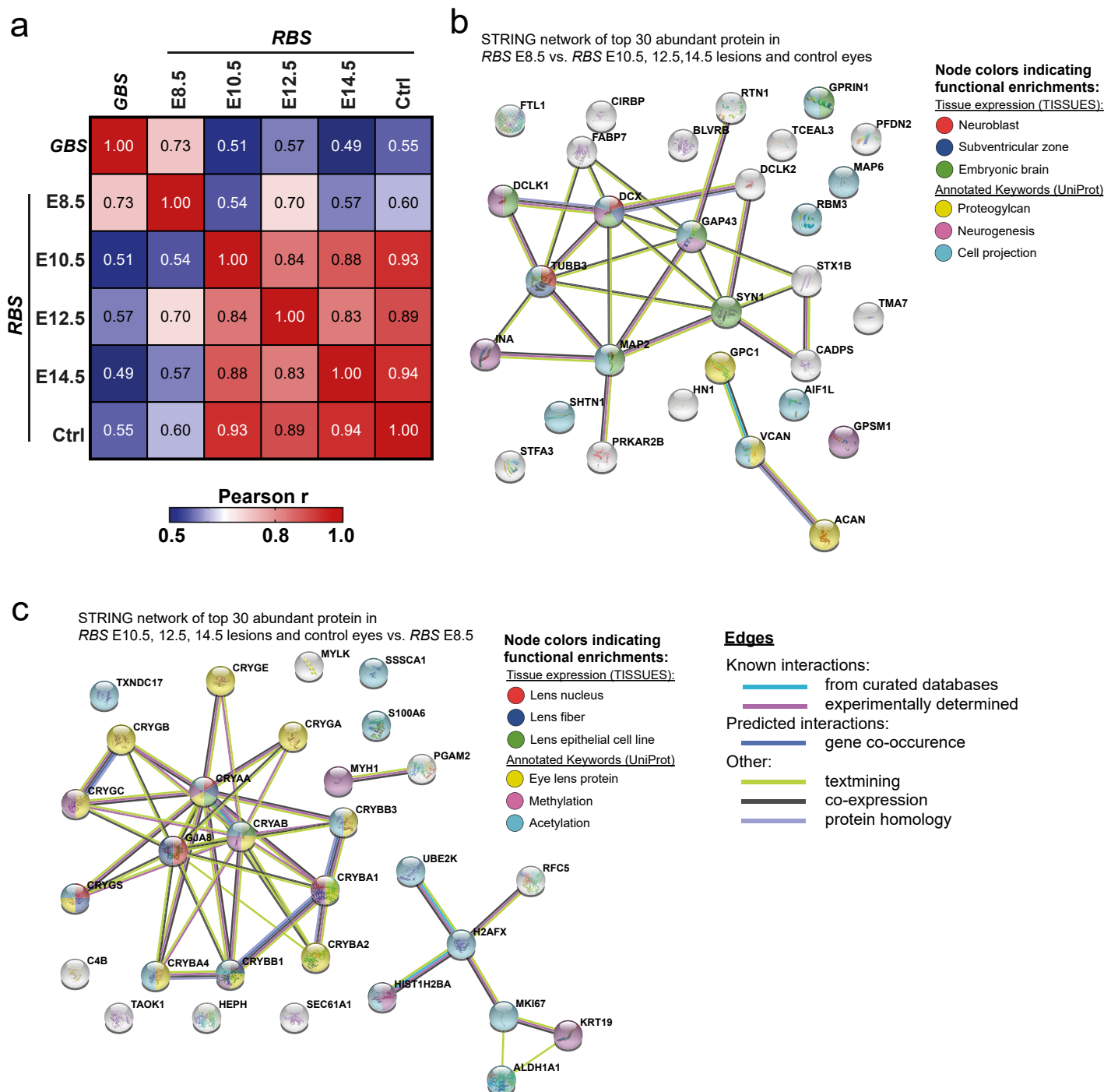




Supplementary Figure 3: RBS E8.5 lesions show distinct proteomic profiles and demonstrate similarity with ETMR-like murine embryonal brain tumors of E18.5 *hGFAP-cre::Ctnnb1(ex3)^{fl/+} SmoM2^{fl/+}* (GBS) mice

a) Correlation matrix of previously published murine ETMR-like GBS tumors (8) and RBS eyes after different tamoxifen injection time points. RBS E8.5 lesions showed stronger correlation with GBS tumors compared to RBS eyes after later injection time points and control eyes. Matrix is based on Pearson correlation of the top 100 variant proteins.

b - c) STRING connectivity network of the top 30 differentially abundant proteins of RBS E8.5 lesions vs. RBS 10.5, 12.5, 14.5 and control eyes (b) and vice versa (c). Network nodes represent proteins. Edges represent protein-protein associations. Colored nodes represent proteins affiliated with the top 3 strongest functional enrichments of the tissue expression database (TISSUES) (58) and annotated keywords of the Universal Protein Resource (UniProt) (59). Networks were generated via default parameters (full string network; medium confidence score 0.4; medium FDR stringency 5%) of STRING (Version 11.5) (ref. 60).