**Fig. 1. Top 25 most significant genetic correlations between BD subtypes and external traits.** Traits sorted top to bottom by ascending $χ^{2}$difference *p-*values. Error bars depict 95% confidence intervals. Dashed bars represent traits not surpassing a Bonferroni corrected significance threshold of 5.10E-4 (.05/98 traits).

**Fig. 2. Major Depression and Schizophrenia as Correlated Predictors of the Bipolar Subtypes. (A)** Standardized results using Genomic SEM to construct a model with MDD and SCZ as correlated predictors of BD I & II. Solid and dashed single headed arrows represent regression paths. Curved double headed arrows represent correlations among the (residual) genetic variance components for each trait. Each U represents residual variances for BD type I and II. **(B, C)** Percent variance within BD I and II accounted for by signal unique to MDD, unique to SCZ, shared by MDD and SCZ, unique to each subtype (unique residuals) and shared between the subtypes (shared residuals). Numbers in parentheses in both panels reflect the corresponding standard error.

**Fig. 3. Miami Plot of Gene Expression Hits on the Bipolar Factor.** The top and bottom orange

bar represents *Z*-statistics surpassing a Bonferroni corrected significance threshold of 7.50E-7

(.05/66,571 imputed gene expression estimates). Positive and negative values depict upward and

downward patterns of gene expression associated with the BD factor, respectively. The most

significant genes are labeled as dots colored to reflect their tissue expression.