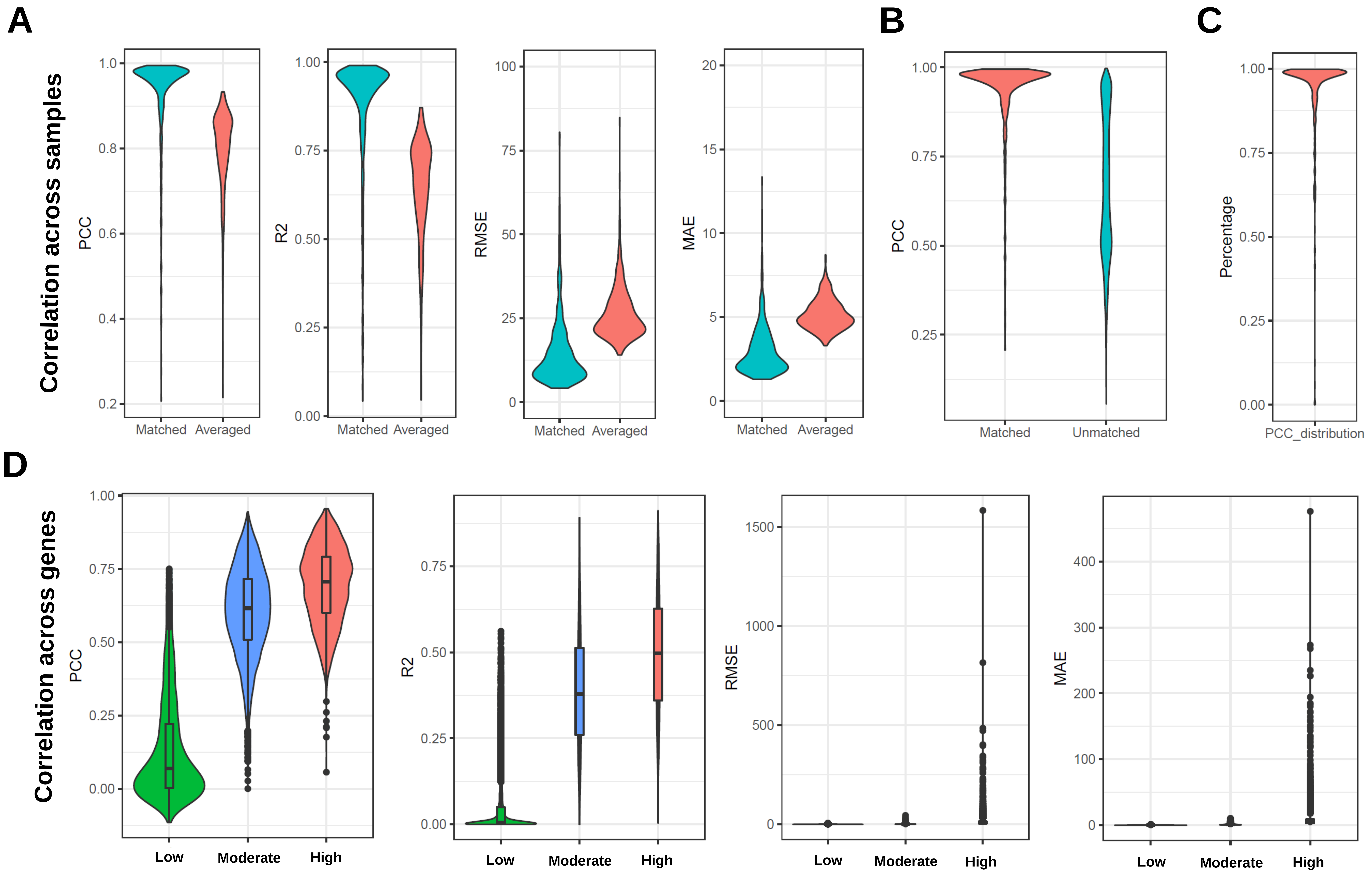

Supplemental Fig. S2. Tensor imputation performance statistics on working BrainSpan data set. **A**, PCC, R^2, RMSE and MAE comparison between imputed results with itself (matched the correct pair) against the average gene expression profiles. **B**, PCC comparison between imputed results with itself (matched the correct pair) against the correlation values with all the other samples (the incorrect pairs). **C**, the distribution of PCC for imputed results with itself (matched the correct pair) against the PCC with all samples (both correct and incorrect pairs). **D,** the comparison of PCC, R^2, RMSE and MAE values between low (FPKM $\leq$ 1), moderate (1 < FPKM $\leq$ 10) and high abundance (FPKM > 10) genes.