S3 Fig: Across-study and tissue-specific gene expression variance and mean correlations with non-overlapping chromatin states through ChromHMM[1]. The across-study variance (A) and mean (B) rank metrics ("across-study" on y-axis) were associated with universal chromatin states[2] (x-axis). The tissue-level variance (A) and mean (B) rank metrics (see Methods; Supplementary Table 1; named tissues on y-axis) were associated with their respective tissue-specific chromatin states[3] (x-axis, see Supplementary Table 1). Boxes marked with an "X" are not significantly correlated; all other comparisons are significant (Benjamini-Hochberg adjusted $p < 0.05$). Het indicates heterochromatin; TSS, transcription start sites; znf, zinc finger genes.

References

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