## List of supplementary tables

**Supplementary Table 1: Anatomy Classification.** The table gives the anatomy classification of the samples as provided by (Roadmap Epigenomics Consortium et al, 2015)[10].

**Supplementary Table 2: GWAS Results.** The table provides combinations of specific GWAS and specific datasets that had an uncorrected p-value <0.001 based on a Mann-Whitney U test (**see Methods**). The first column indicates whether the dataset is of observed or imputed data. The second column indicates which of the tier 1 marks was being analyzed. The third column displays the trait being considered and fourth column the Pubmed ID associated with the study. The fifth column displays the Reference Epigenome of the sample ID and the sixth column the corresponding name. The seventh column indicates whether the significant association with the signal is a positive enrichment based on the average rank of the signal for study SNPs being above average compared to the GWAS catalog background or a negative enrichment otherwise. The eight column gives the uncorrected p-value. The ninth column displays an estimated FDR for each mark and observed/imputed combination separately, but considering testing all available samples and study combinations. The tenth column gives the number of study SNPs used in the test.

**Supplementary Table 3: Individual Dataset Imputation Agreement Scores.** Each row in the table corresponds to an imputed dataset for which there is also an observed dataset. For datasets other than DNA methylation the entries from left to right are: (1) mark, (2) reference epigenome ID for each sample, (3) sample name, (4) % of top 1% imputed locations in top 1% observed locations (5) correlation of the imputed data with the observed data. For DNA-methylation columns 5 is empty and instead in the sixth column is the % agreement based on the concordance 0.25 measure. The samples for each mark are sorted based on column 4, except for DNA-methylation where it is sorted based on the sixth column.