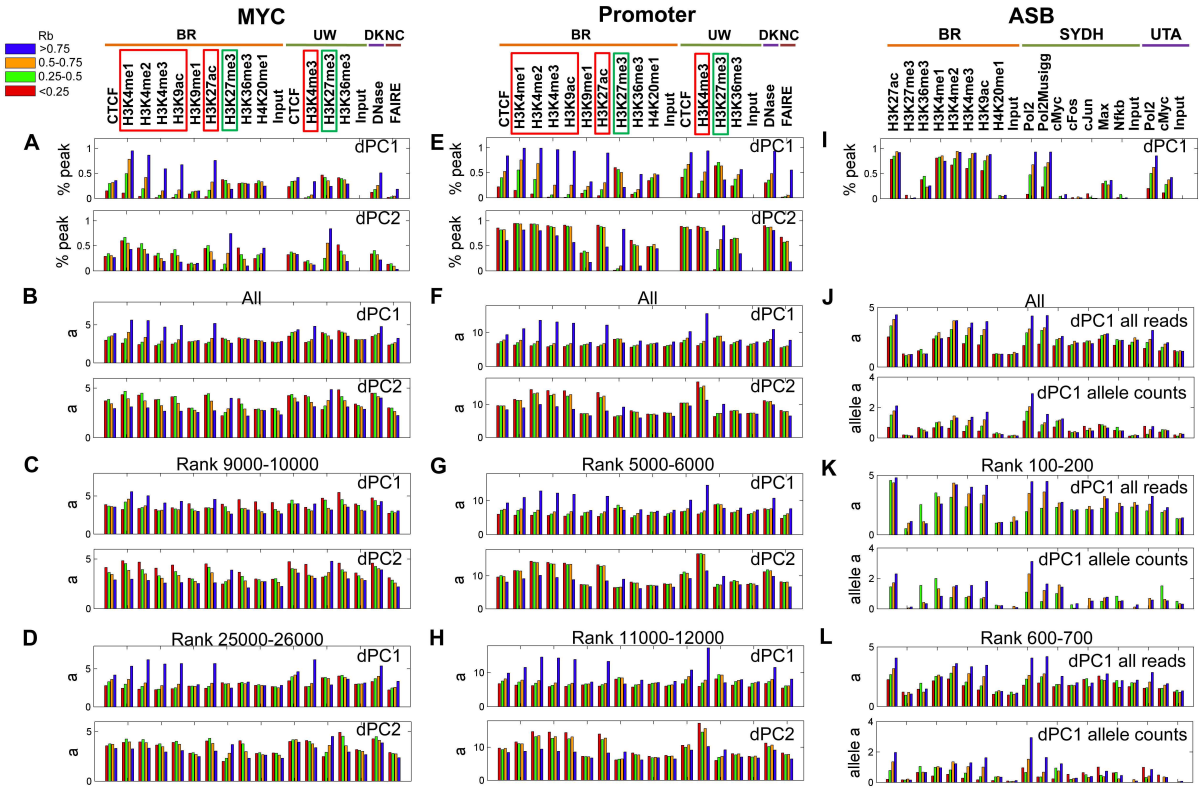

Fig. S9. Exploration of the R^B statistic. **(A)-(D)**: Exploration in the MYC analysis. **(A)** For each dPC, differential loci (5% FDR) are grouped into four bins: $R^B \in$ [0,0.25],(0.25,0.5],(0.5,0.75],(0.75,1]. For each bin, the percentage of loci that are associated with binding peak calls in at least one cell type in each dataset is shown. **(B)** For each dPC and each of the four R^B bins, the mean $a_{gm} = \bar{x}_{g1m} + \bar{x}_{g2m}$ is computed across all differential loci in the bin for each dataset m. The plot shows the mean a_{gm} for each dataset and each R^B bin. **(C)-(D)** For each dPC, differential loci are stratified based on their ranks in dPCA. Each stratum contains 1000 loci which are grouped into four R^B bins as above. We repeated the analysis in (B) for each stratum. In other words, for each R^B bin, the mean of a_{gm} is computed for each dataset m using all differential loci in that bin. (C) and (D) show results from two representative strata. Loci in (C) have rank $\in$ (9000,10000]. Loci in (D) have rank $\in$ (25000,26000]. **(E)-(H)**: Exploration in the Promoter analysis, similar to (A)-(D). **(I)-(L)**: Exploration in the ASB analysis. **(I)** Similar to (A), differential loci for dPC1 are grouped into four R^B bins. For each bin, the percentage of loci that have peak calls is shown. **(J)** For dPC1 and each of the four R^B bins, the plot shows the mean $a_{gm} = \bar{x}_{g1m} + \bar{x}_{g2m}$ computed using all differential loci in the bin for each dataset m. In the top panel, a_{gm} is based on counting all reads in the 300bp flanking window centered at each heterozygote SNP. These include reads not mapped to heterozygote SNPs, reflecting the fact that all reads in the ChIP-seq samples are used for peak calling. In the bottom panel, $\bar{x}_{gim}$ is based on only counting the reads mapped to the heterozygote SNP. These are the reads used to compute d_{gm} in dPCA for studying differences and inferring allele-specificity. **(K)-(L)** Differential loci from dPC1 are stratified based on their ranks in dPCA. Each stratum contains 100 loci which are grouped into four R^B bins as above. We repeated the analysis in (J) for each stratum. (K) and (L) show results from two representative strata. Loci in (K) have rank $\in$ (100,200]. Loci in (L) have rank $\in$ (600,700].