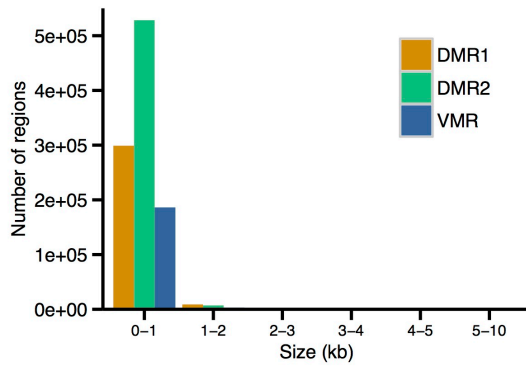
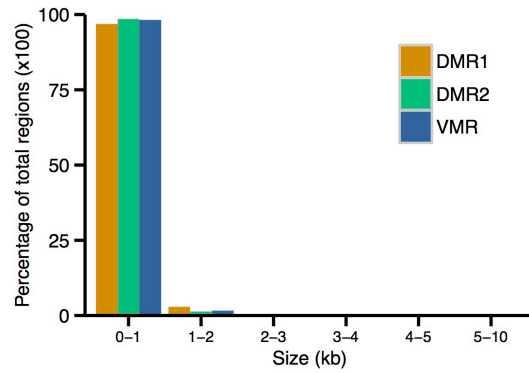


FigS15

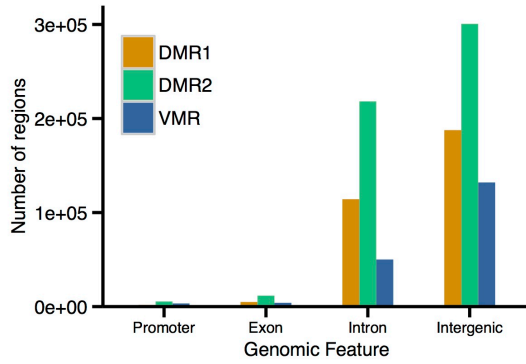
A



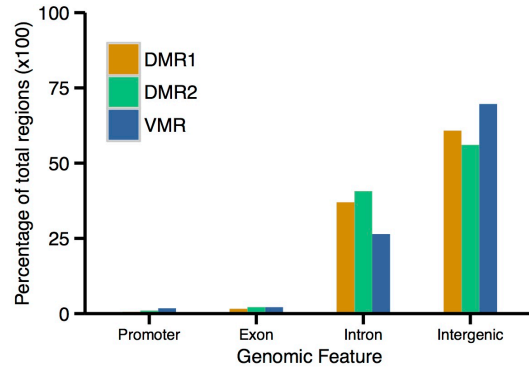
B



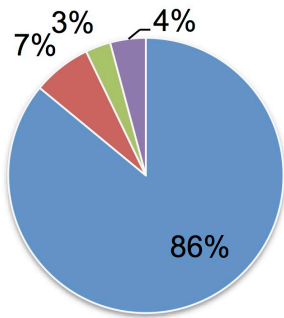
C



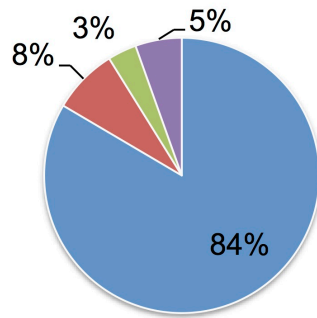
D



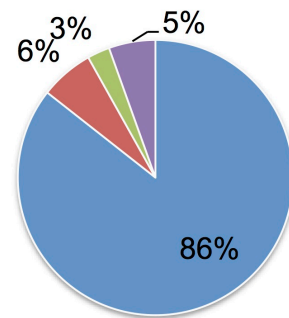
E



F



G



■ 0 ■ 1 ■ 2 ■ 3&above

Figure S15. Characterization of regions identified specifically in each study.

A. Distribution of region lengths at each range. B. Percentage of regions at each length range. C. Distribution of regions in different genomic features. D. Percentage of regions in genomic features. E-G. Co-localization between regions and transcription factor binding sites. The percentage of regions with 0, 1, 2, or 3 and more transcription factor binding peaks were plotted. E for DMR1 (Ziller et al. study); F for DMR2 (Schultz et al. study); G for VMR (this study).