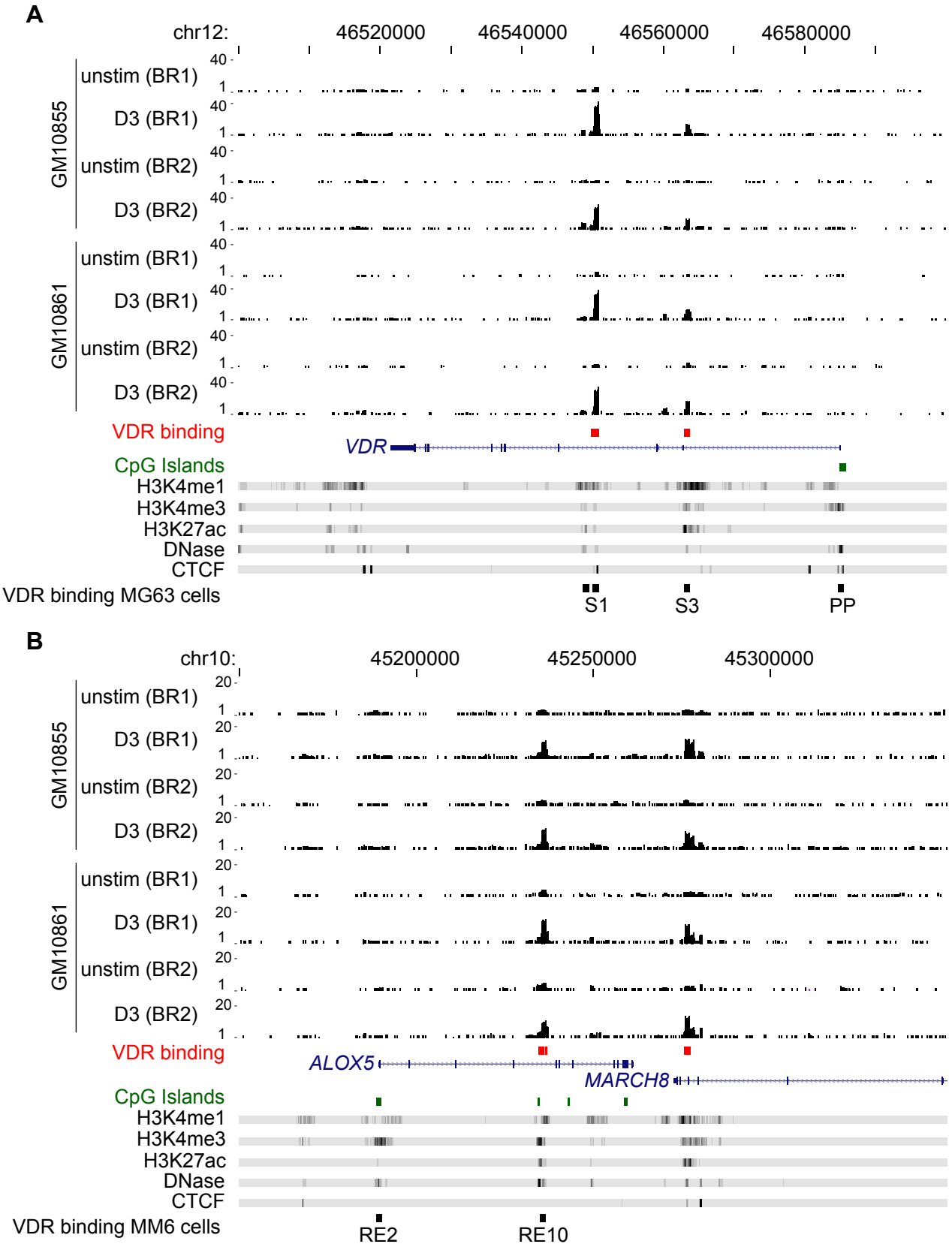
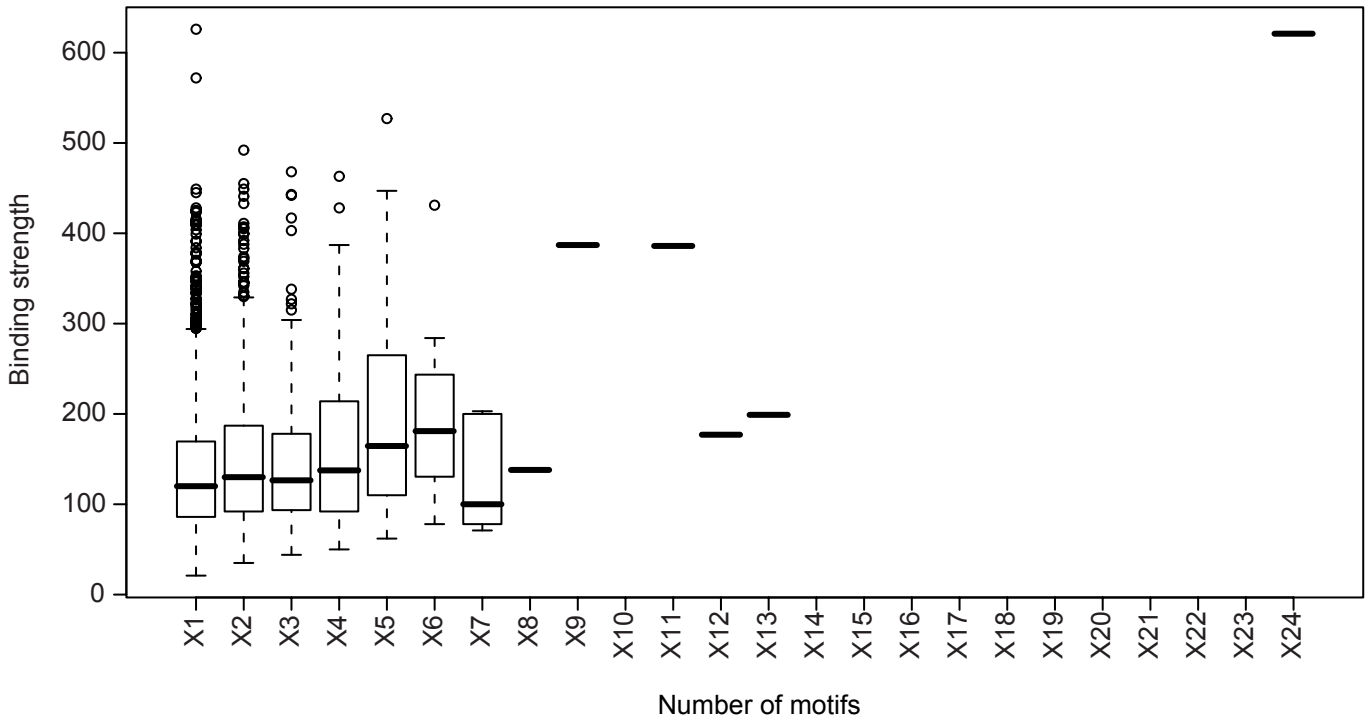
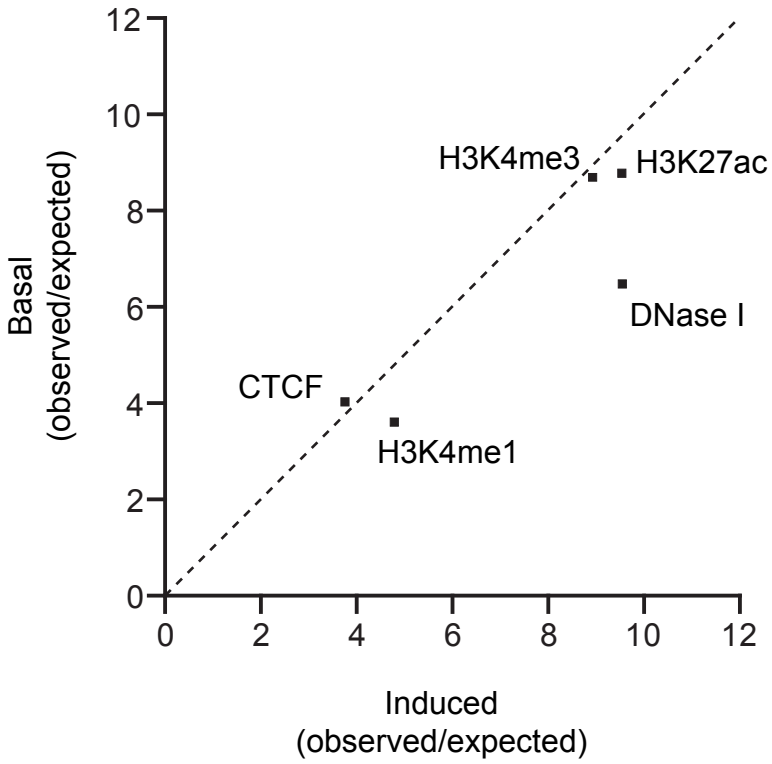


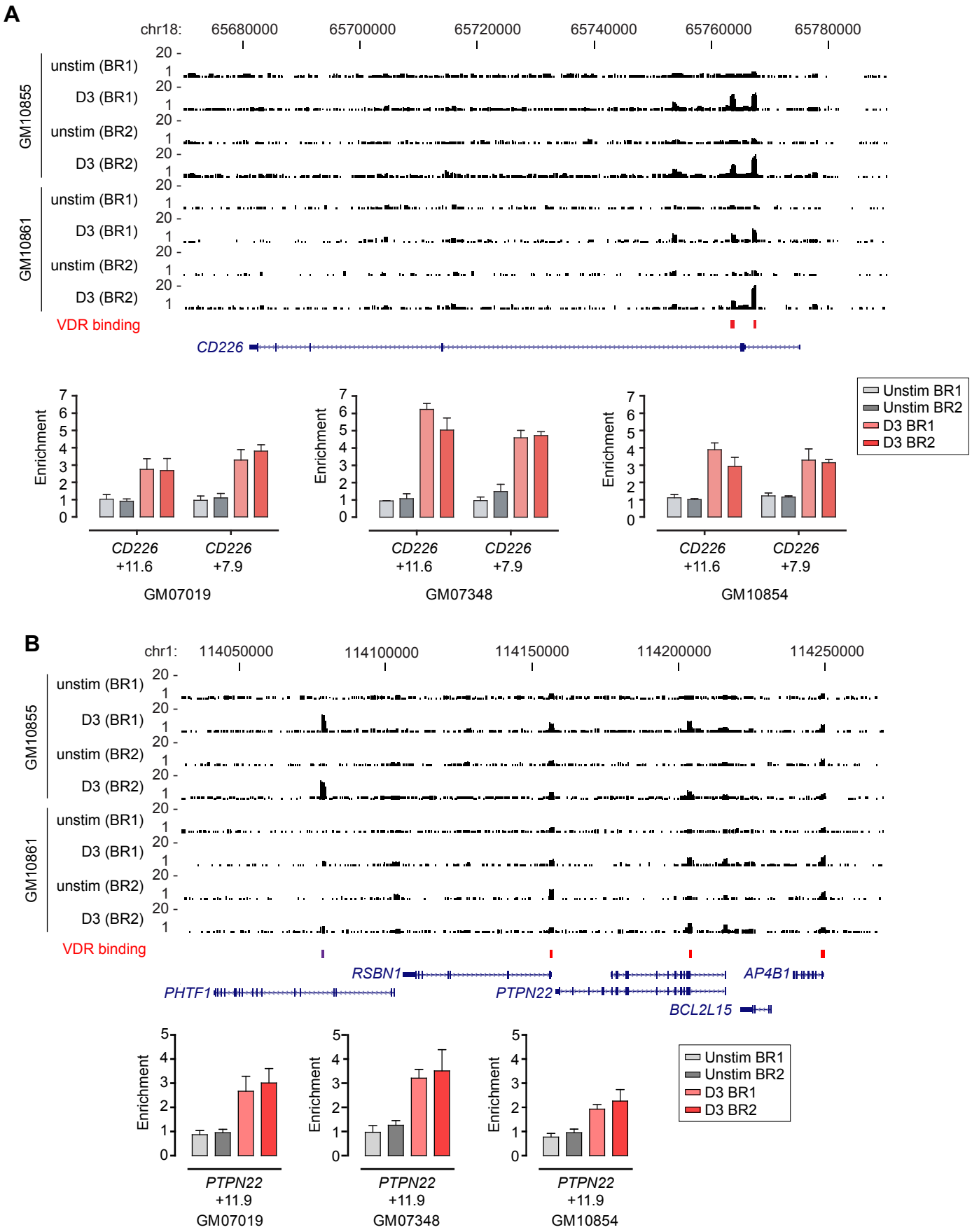

**Supplementary Fig 1. VDR ChIP-Seq analysis for *VDR* and *ALOX5*.** VDR ChIP-Seq data shown for two biological replicates of two LCLs, GM10855 and GM10861, either resting or after induction with calcitriol for 36 h (a) *VDR* and flanking sequences (chr12:46,500,000-46,600,000) with two inducible intronic sites of VDR occupancy noted corresponding to the previously reported VDR binding sites S1 and S3 in MG63 cells while no occupancy was seen for the primary promoter at exon 1a (Zella et al. 2010) (b) *ALOX5* and flanking sequences (chr10:45,150,000-45,350,000) with VDR occupancy noted in intron 4, a known strong VDR binding site (denoted RE10) corresponding to a CpG island, site of DNase hypersensitivity and histone modifications (Seuter et al. 2007). No significant enrichment was seen at the *ALOX5* promoter contrasting with previous reports for MM6 cells (Seuter et al. 2007) however a novel VDR binding site was seen at the 3' end of *MARCH8* co-localising to a CTCF binding site. Also shown is ChIP-seq and DNase-seq data for GM12878 generated by the ENCODE Project (Broad Institute and Duke/UNC/UT-Austin/EBI) and downloaded from UCSC browser.




**Supplementary Fig 2. Box plot showing the relationship between the number of motifs in a VDR binding interval and binding strength as assessed by peak height.**




**Supplementary Fig 3. Enrichment in VDR binding in relation to chromatin accessibility, histone modifications and CTCF binding.** Observed vs expected number of VDR intervals in basal state and following calcitriol induction are shown for DNase I, histone H3 K4me1 and me3, histone H3K27ac and CTCF for GM12878 using data from the ENCODE project.




**Supplementary Fig 4. VDR ChIP-Seq analysis for *CD226* and *PTPN22*.** VDR ChIP-Seq data shown for two biological replicates of two LCLs, GM10855 and GM10861, either resting or after induction with calcitriol for 36 h. Validation of VDR binding by ChIP for GM07019, GM07348 and GM10854 analysed by quantitative real time PCR is shown below ChIP-Seq tracks. Mean fold difference (+/- SD) in enrichment of each of the PCR amplicons is expressed relative to input DNA. (**A**) Data shown for *CD226* (chr18:65,670,000-65,790,000) with VDR occupancy noted at +7.9kb and +11.6kb relative to the transcriptional start site (TSS) of *CD226.* (**B**) Data shown for *PTPN22* and flanking genes (chr1:114,030,000-114,270,000) with VDR occupancy noted in the third intron of *PHTF1* (for GM10855 but not GM10861), at the 3' end of *PTPN22* and in the first intron of *PTPN22* (+11.9kb relative to the TSS), and promoter region of *AP4B1*.