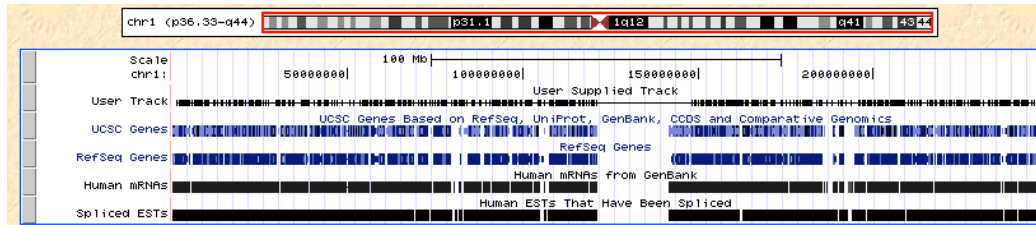
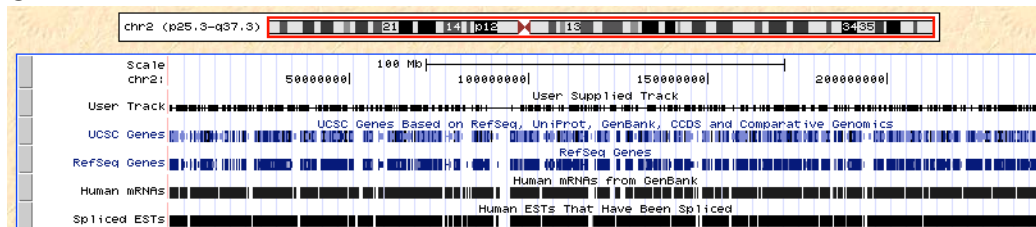


Supplementary figure 2. The coverage of the genome for the subset of immunoChIP SNPs (8,750) used for the linkage analysis. Each chromosome is presented separately. User track illustrates immunoChIP SNPs and their distribution over each chromosome. UCSC Genes, RefSeq genes, mRNAs and ESTs represent the regions that are expressed and therefore have potential function.

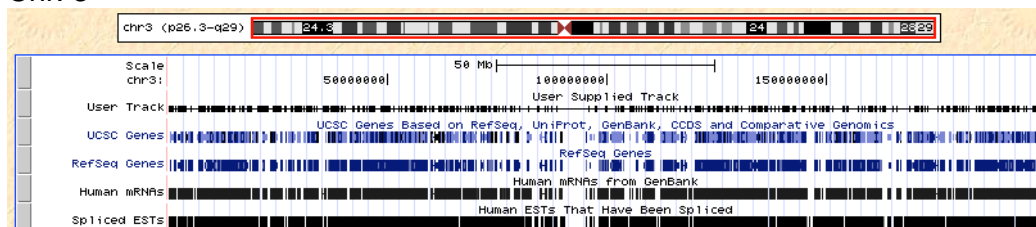
### Chr. 1



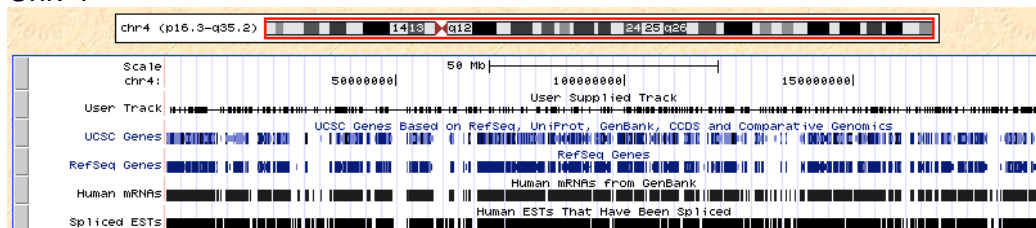
### Chr. 2



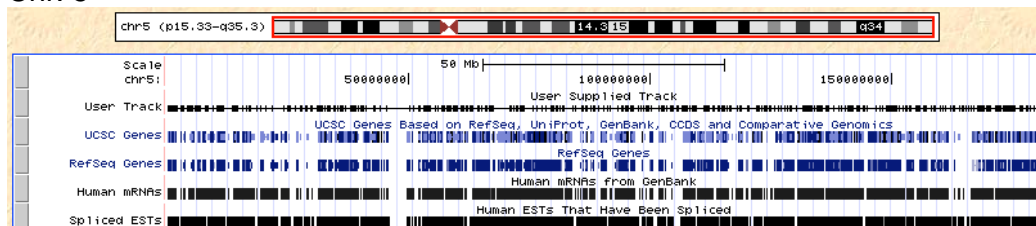
### Chr. 3



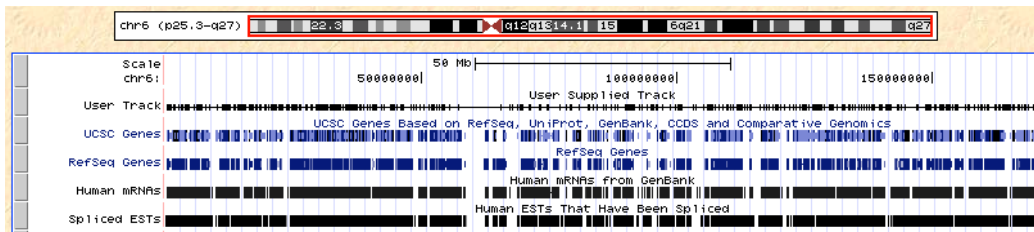
### Chr. 4



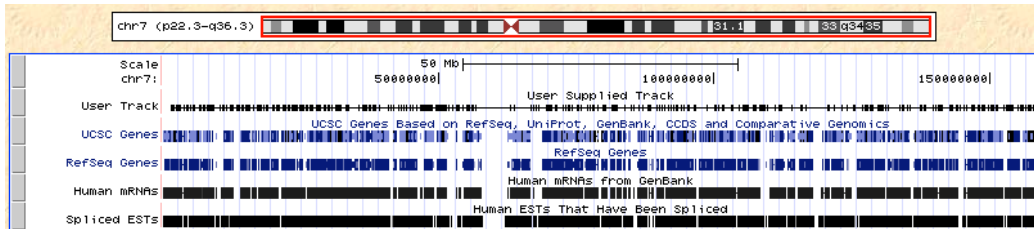
### Chr. 5



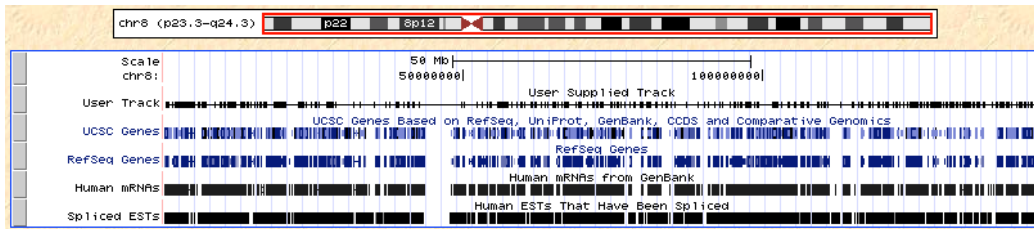
### Chr. 6



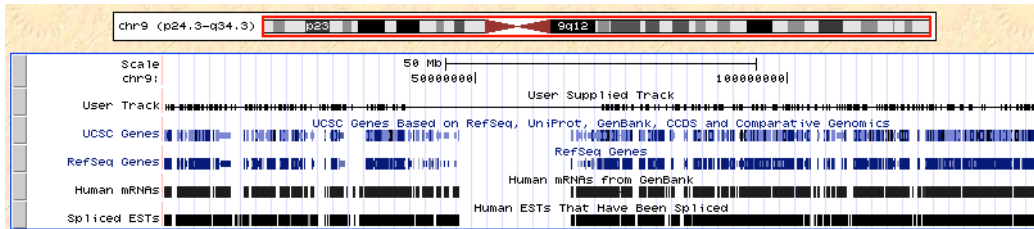
### Chr. 7



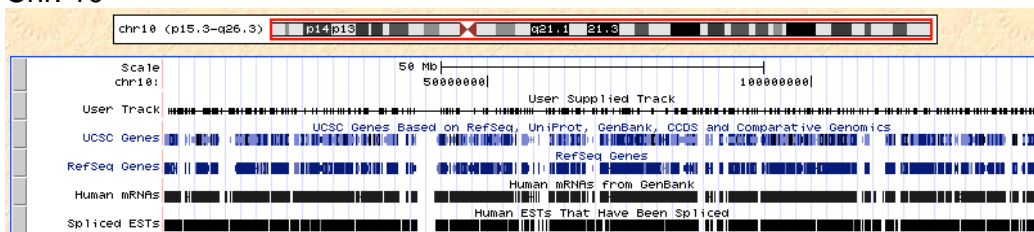
### Chr. 8



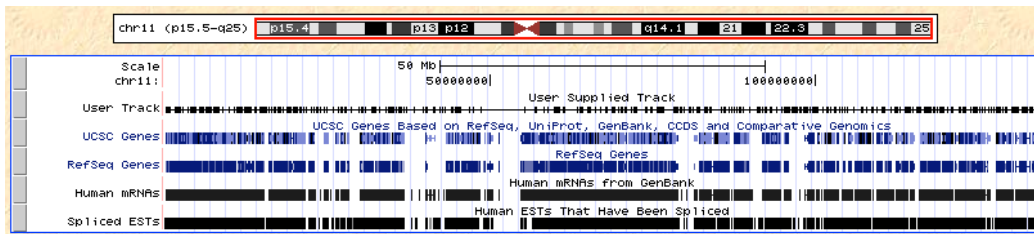
### Chr. 9



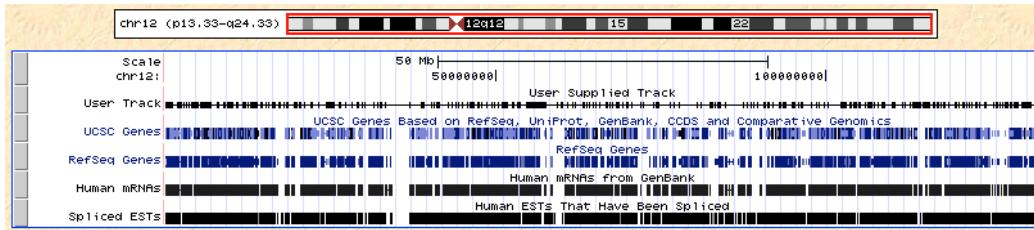
### Chr. 10



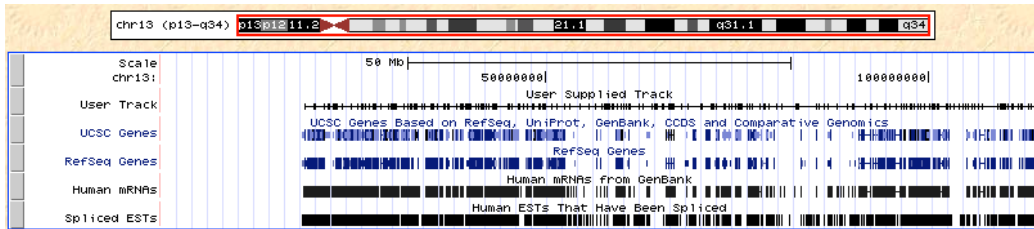
### Chr. 11



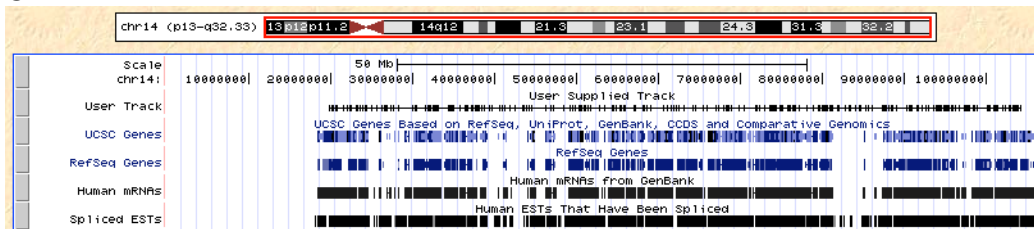
Chr. 12



Chr. 13



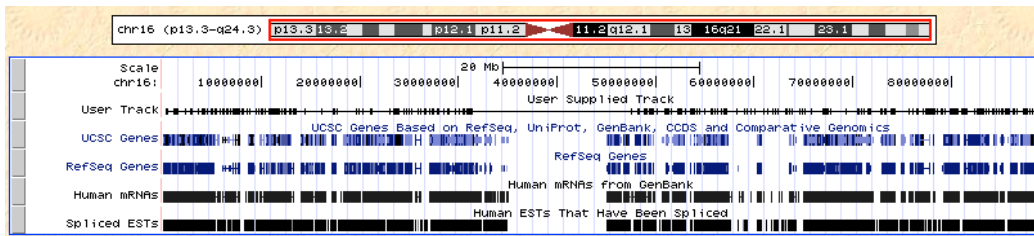
Chr. 14



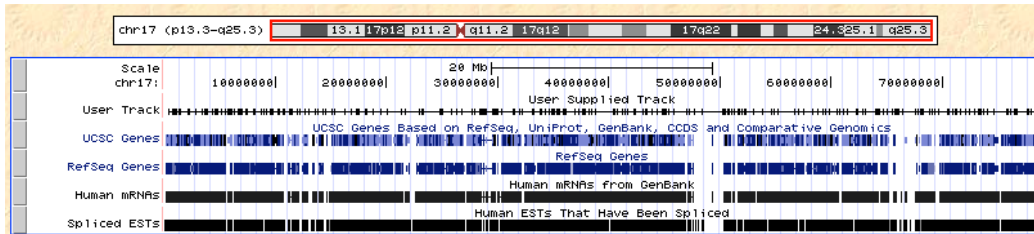
Chr. 15



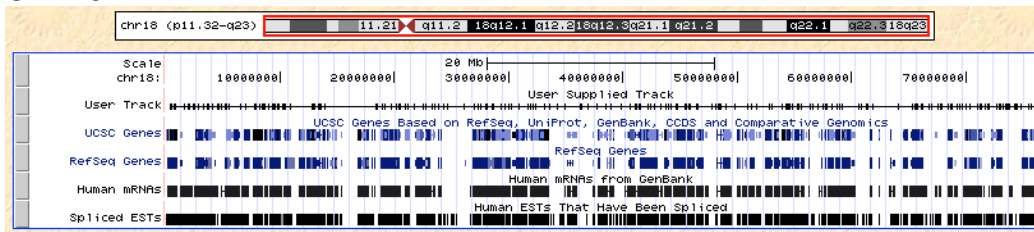
Chr. 16



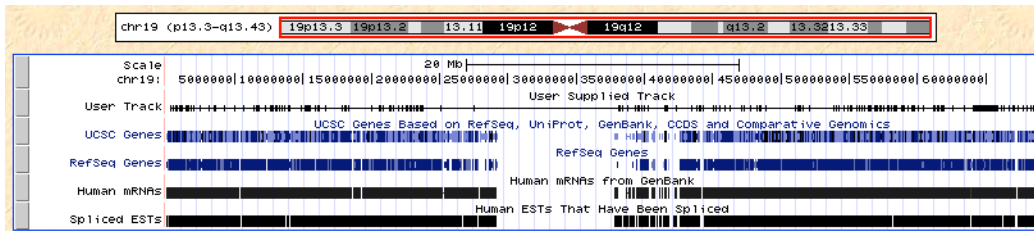
### Chr. 17



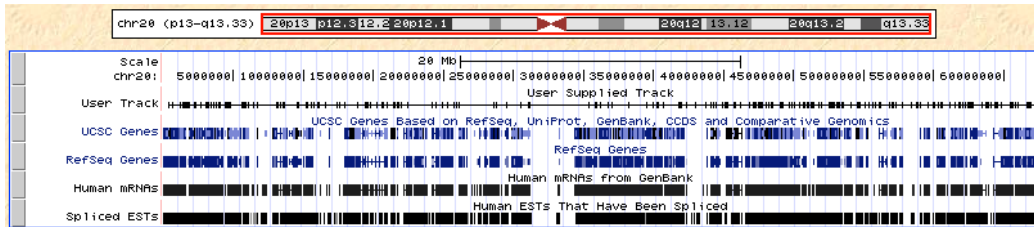
### Chr. 18



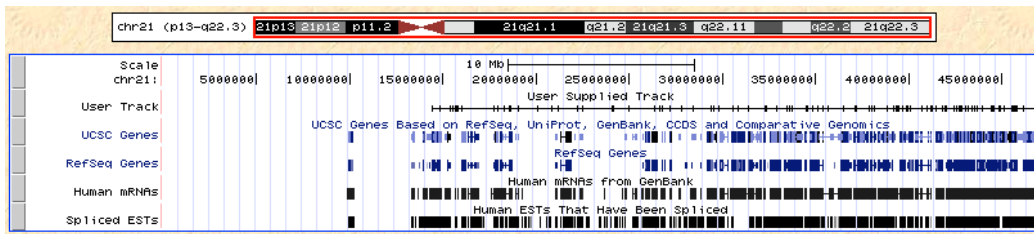
### Chr. 19



### Chr. 20



### Chr. 21



## Chr. 22

