Predicted Transcription Factor Binding Sites in the mouse syntenic region of a second minimal region identified in cases of human DSD

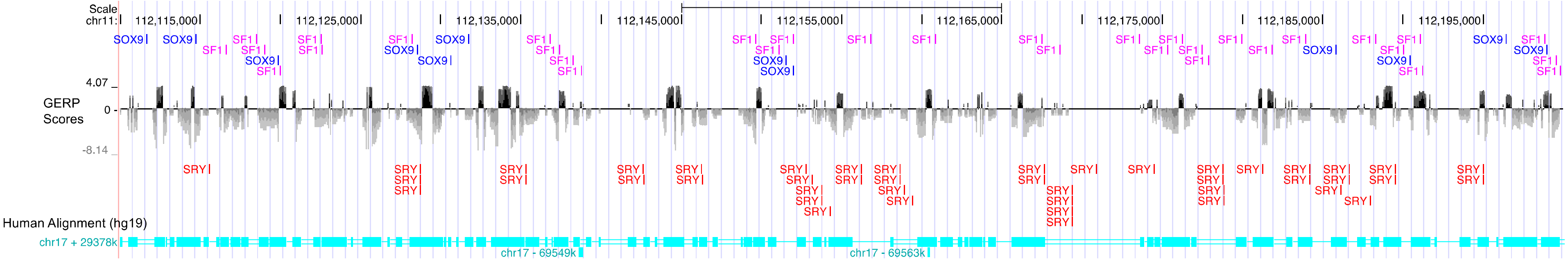

Figure S4 Sry, Sox9 and Sf1 binding sites in mouse region syntenic to the human minimal 90kb protective region identified from human cases of 46,XX and 46,XY DSD. Using MatInspector, we identified predicted transcription factor binding sites for Sry(red), Sox9(blue), and Sf1(pink) in the mouse genomie region spanning 112,110,000 to 112,200,000bp on chromosome 11. Here, 25bp regions representing predicted transcription factor binding sites regions are indicated by the vertical lines and colored to represent one of three factors, as stated above. Additionally, GERP scores were used to identify regions that are undergoing positive selection (GERP score > 0) or neutral selection (GERP score < 0). We show that the majority of predicted binding sites did not fall into highly conserved regions, based on GERP scores. At the bottom in turquoise, we show the alignment to the human genome hg19. The solid boxes indicate regions where there alignment between mouse and human reference sequence. Single lines represent gaps between the mouse and human alignment due to either deletion in the human reference or insertion in the mouse assembly. Double lines represent more complex regions that have gaps in either mouse, humans, or both. Scale bar (at top) = 20kb