Outlier Comparison Inside Inversion 0.3 -0.2 0.1 0.0 Outside Inversion 0.3 whichTests 0.2 none FST crit_OutFLANK 0.1 crit_OutFLANK_PCAdapt OutFLANK 0.0 neut 0.3 -0.2 0.1 0.0 500000 1000000 1500000 Ó 2000000 Genome Position