



Figure S5. Manhattan plot analysis for Ancestry Informative Marker (AIM) identification. A total of 70,733 LD-pruned Illumina Omni-quad 1M array markers were used to identify 2687 AIMS distinguishing the Ju/'hoan from our study (n=19) to the Illumina iControl database Yoruba (n=90), defined as a significant allele frequency difference between these population identifiers at $-\log_{10} P > 5$.