



Figure S3. Overlap with previous studies. 26 genomic regions were chosen randomly and their overlap with previous studies was calculated, this was repeated 1000 times. (a) overlap between 1Mb regions and the results from Attanasio *et al* 2014. (b) overlap between 500 Kb regions and Attanasio *et al* 2014. (c) overlap of 1Mb regions and Maga *et al* 2015.