

Figure S1

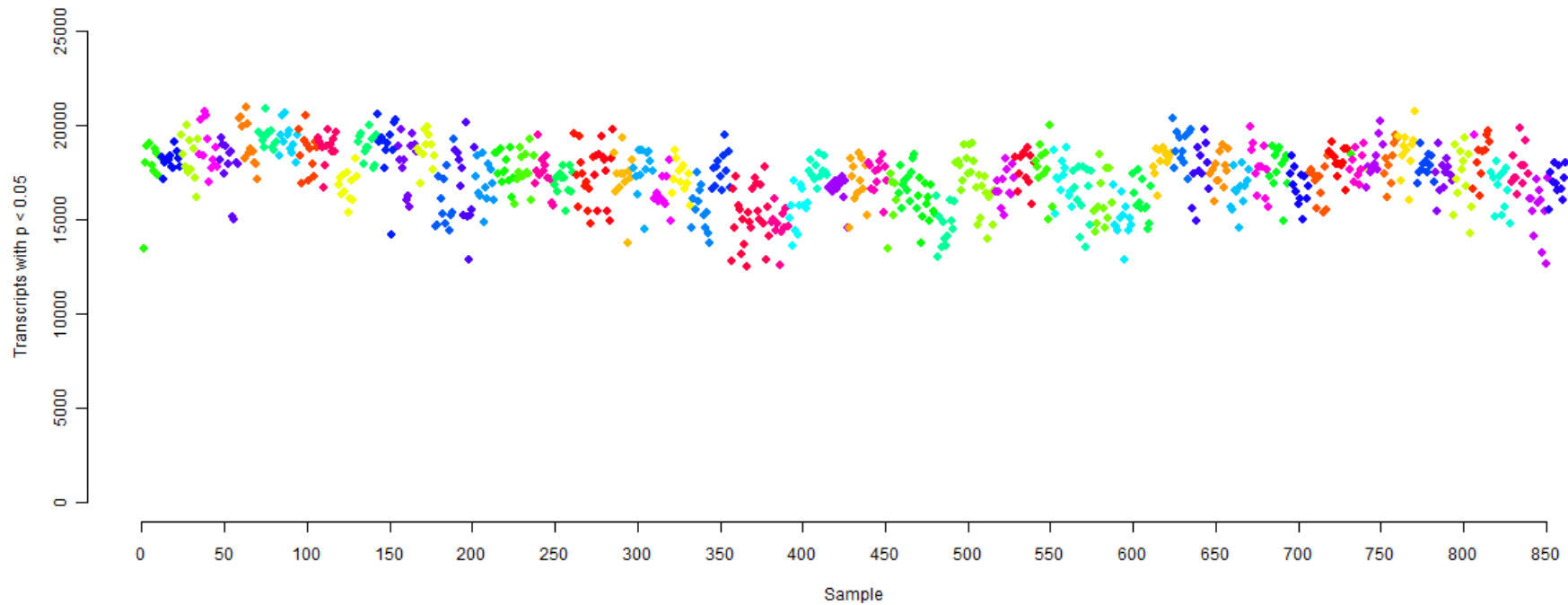


Figure S1 | GenomeStudio provides a p -value for each transcript in each sample. For a given sample the number of transcripts with p -values below a given threshold provides an indication of its quality. Figure S1 shows the number of transcripts with $p < 0.05$ for each sample with each colour representing a single chip.

Figure S2

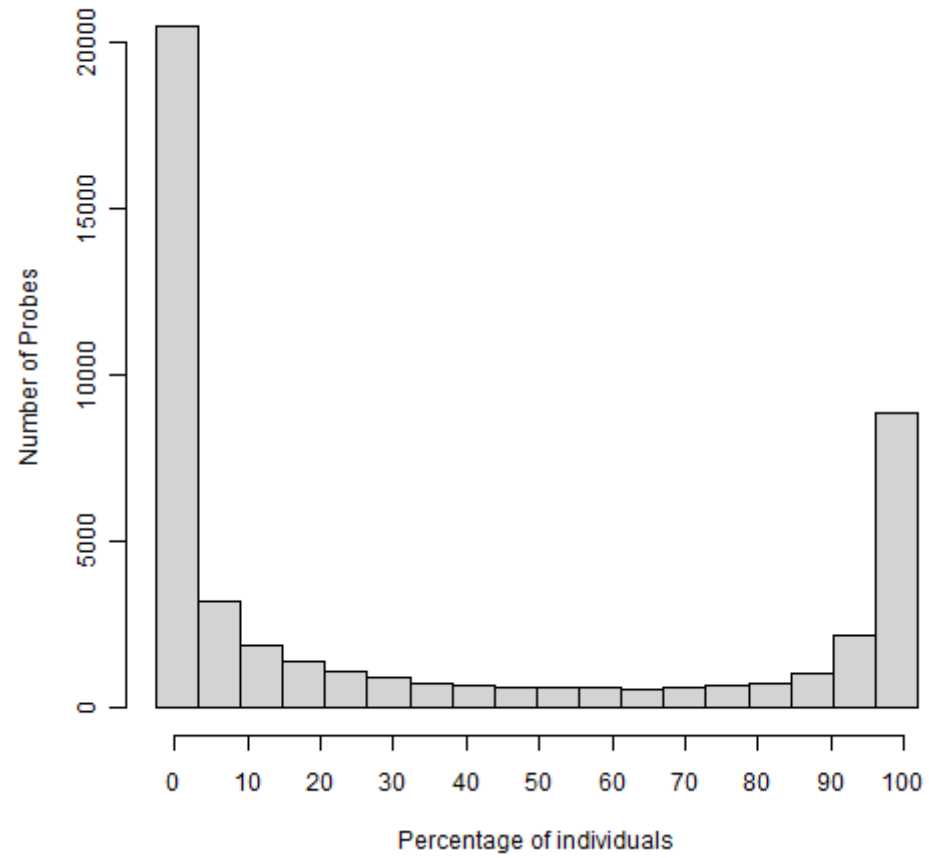


Figure S2 | The distribution of the number of probes detected as expressed in stage II. A total of 47,323 are measured on the Illumina HT-12 v4.0 chip, of these 5,364 (11.3%) are not detected as expressed in any of the individuals, whilst 6,281 (13.3%) are detected as expressed in all individuals.

Figure S3

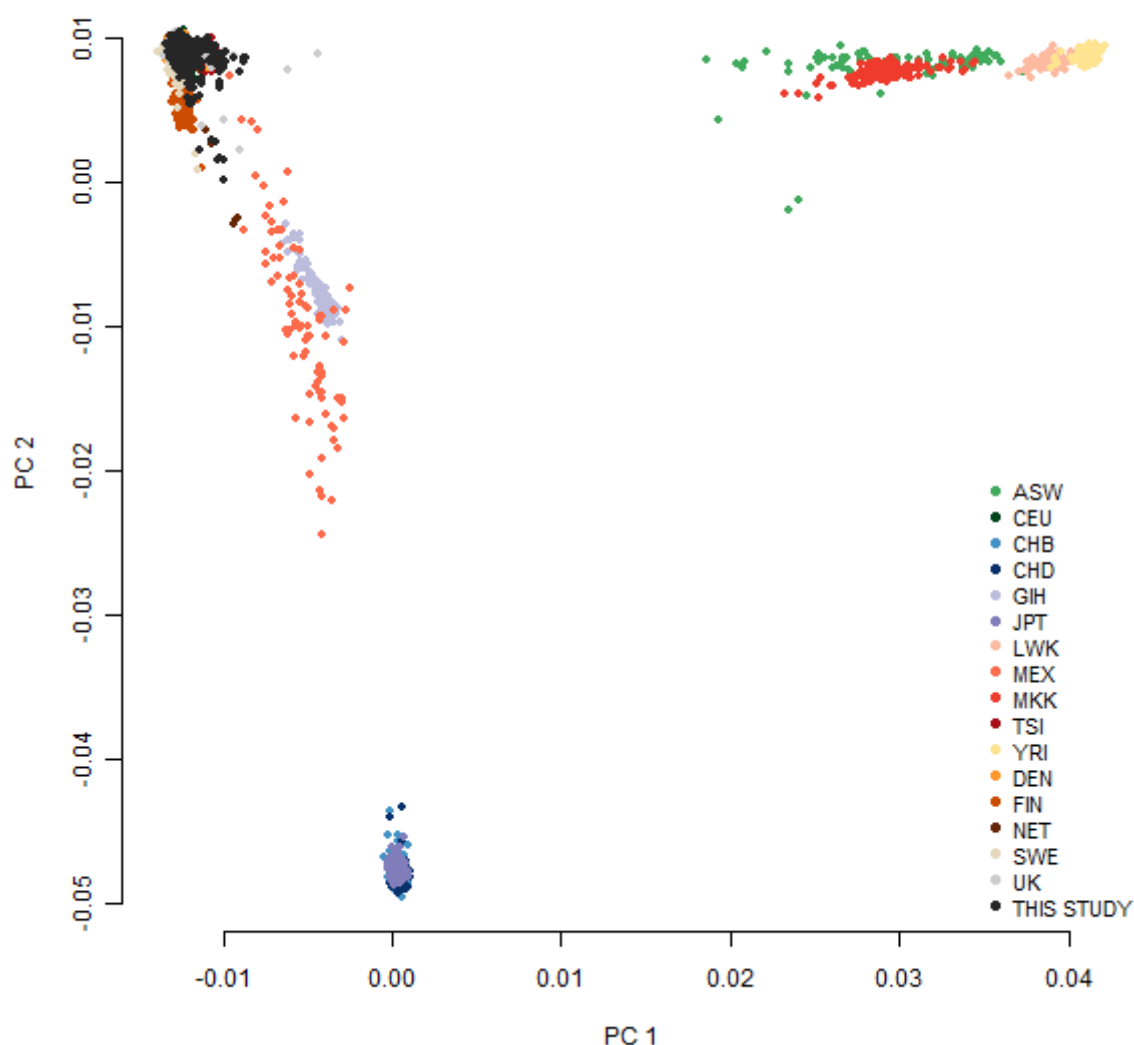


Figure S3 | A Principle Component Analysis (PCA) of 16 global populations and the individuals collected in this study. Principal Component one (PC1) and two (PC2) values were derived from approximately 280,000 autosomal markers. Populations samples marked with *1 were collected as part of the HapMap3 project [1] and *2 as part of the GenomEUtwin project [2]. **ASW**^{*1} African Americans, **CEU**^{*1} European Americans, **CHB**^{*1} Han Chinese, **CHD**^{*1} Chinese, **GIH**^{*1} Gujarati-Indians, **JPT**^{*1} Japanese, **LWK**^{*1} Luhya Kenyans, **MEX**^{*1} Mexicans, **MKK**^{*1} Maasai Kenyans, **TSI**^{*1} Italians, **TRI**^{*1} Yorubans Nigeria, **DEN**^{*2} Danish, **FIN**^{*2} Finish, **NET**^{*2} Dutch, **SWE**^{*2} Swedish, **UK**^{*2} British.

References

1. International HapMap 3 Consortium. 2010. Integrating common and rare genetic variation in diverse human populations. *Nature* **467**(7311): 52-58.
2. Peltonen L. 2003. GenomEUtwin: a strategy to identify genetic influences on health and disease. *Twin Res* **6**(5): 354-360.