## Phenotype information

The data is deposited into the Short Read Archive as BioProject PRJNA245228 (<http://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA245228>) . This project has 48 different samples, where a sample is a different person and library extraction method. The authors studied 3 different populations of RNA: “total”, “cytosol”, and “nucleus”. These populations refers to RNA present in different parts of the cell, “total” indicates that the RNA comes from both the cytosol and the nucleus. The authors did polyA+ selection to removed ribosomal RNA; this is the standard assay for RNA sequencing.

For “total” RNA samples, the authors studied 6 different age groups: fetal (<0 years), infant (0-1 years), child (1-10 years), adolescent (10-20 years), adult (20-50 years) and old, (50+ years), and each age group had 6 individuals.

The individual samples has names such as “Br5341C1\_DLPFC\_polyA\_RNAseq\_cytosol” (<http://www.ncbi.nlm.nih.gov/biosample/2999562>), which indicates individual “Br5341C1” from the “DLPFC” project (the authors studied the human dorsolateral prefrontal cortex) isolated using “polyA” from the “cytosol”. In the link you can see some additional phenotype information such as age (-0.4 years), sex (male), RIN number (10; this is a measure of RNA quality). The age is measured as weeks after conception converted to years before term (which is why the age is negative for this sample; it indicates a fetal sample).