



Rare Genetic Variants in Health and Disease: 10,000 Genomes - The UK10K Project

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4,000 whole genome
samples sequenced

Average 6x depth

2,000 ALSPAC

2,000 TwinsUK

SNP, indel and larger structural
variants associated with
phenotypic traits to determine
which were linked to disease and
which were not

Candidate variants identified in
subjects with extreme disease
phenotypes

Low frequency variants (down to
0.1% allele frequency) imputed into
studies of non-sequenced individuals
with GWAS data to increase study
power

>5,500 whole exome
samples sequenced

Average 72x depth

3,000 Neuro disorders

2,113 Schizophrenia
887 Autism

>1,500 Obesity

1,000 SCOOP study
430 Generation Scotland
68 TwinsUK

1,000 Rare disorders

125 Ciliopathies
125 Coloboma
125 Severe insulin resistance
125 Congenital heart disease
125 Familial hypercholesterolaemia
125 Neuromuscular disease
125 Learning disability (FIND study)
125 Thyroid disorders

BAM and VCF files deposited
in the European Genome-
phenome Archive to create a
managed-access data resource

The data generated by UK10K is a valuable resource for research into human genetics, and it is hoped the discovery of rare and low frequency disease-causing variants will lead to further insight into the diagnosis and treatment of disease