Table 1: The subject count aggregated from studies deposited in dbGaP, consented for General Research Use (GRU)

| | **CVD** | **All** |
|---|---|---|
| 16s rRNA (NGS) | 0 | 92 |
| CNV Genotypes | 0 | 48972 |
| Chromatin (NGS) | 0 | 139 |
| Genomic Sequence Amplicon (NGS) | 0 | 8 |
| Methylation (CpG) | 0 | 657 |
| Methylome sequencing | 0 | 152 |
| QTL Results | 0 | 281 |
| RNA Seq (NGS) | 333 | 1498 |
| SNP Genotypes (Array) | 6658 | 113597 |
| SNP Genotypes (NGS) | 4277 | 11786 |
| SNP Genotypes (PCR) | 0 | 10 |
| SNP Genotypes (imputed) | 0 | 29693 |
| SNP/CNV Genotypes (NGS) | 0 | 936 |
| SNP/CNV Genotypes (imputed) | 0 | 9291 |
| SNV (.MAF) | 0 | 2 |
| SNV Aggregate (.MAF) | 0 | 570 |
| Targeted Genome (NGS) | 0 | 9918 |
| Whole Exome (NGS) | 5518 | 12771 |
| Whole Genome (NGS) | 0 | 1245 |
| mRNA Expression (Array) | 0 | 798 |
| miRNA (NGS) | 0 | 228 |
| Total subject count in data consented for GRU | 16786 | 242644 |
| All consent groups | 584884 | Unknown |

CNV: Copy-number variation
NGS: Next-generation sequencing
MAF: Minor Allele Frequency
QTL: Quantitative Trait Loci
SNP: Single-nucleotide polymorphism
SNV: Single-nucleotide variant