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

NGS: Next-generation sequencing
QTL: Quantitative Trait Loci