TABLE 1: COMPREHENSIVE COVERAGE OF HIGH-VALUE REGIONS

	HUMANCYTOSNP-12 v1	HUMAN660W-QUAD v1	HUMAN1M-DUO v3
Overview	Efficient coverage for cost-effective GWAS and cytogenetic screening	High genomic coverage of common SNPs and CNV regions	Comprehensive genome-wide coverage and additional high-value regions
Number of Markers per Sample	299,671	657,366	1,199,187
Number of Samples per BeadChip	12	4	2
DNA Input Requirement (per sample)	200 ng	200 ng	400 ng
Genomic Coverage			
CEU (Mean / Median / $r^2 > 0.8$)	0.81 / 0.94 / 0.70	0.92 / 1.0 / 0.87	0.96 / 1.0 / 0.95
CHB+JPT	0.83 / 0.94 / 0.73	0.92 / 1.0 / 0.85	0.95 / 1.0 / 0.93
YRI	0.55 / 0.52 / 0.32	0.74 / 0.87 / 0.56	0.86 / 1.0 / 0.76
Minor Allele Frequency*			
CEU (Mean / Median)	0.22 / 0.21	0.24 / 0.23	0.20 / 0.18
CHB+JPT	0.21 / 0.20	0.21 / 0.20	0.18 / 0.16
YRI	0.21 / 0.19	0.22 / 0.21	0.20 / 0.17
Spacing (kb)			
(Mean / Median)	9.6 / 6.2	4.4 / 2.3	2.4 / 1.5
90th %ile Largest Gap	10.6	18.6	6.0
Marker Categories			
Markers Within 10kb of a RefSeq Gene	148,666	332,756	672,002
Non-Synonymous SNPs§	3,480	10,051	21,877
MHC† / ADME‡ / Indel SNPs	761 / 2,382 / 0	3,177 / 8,440 / 0	10,415 / 20,493 / 483
Sex Chromosome (X / Y / PAR Loci)	15,056 / 2,679 / 10	16,509 / 44 / 15	45,591 / 4,637 / 979
Mitochondrial SNPs	0	135	138

* Based on HapMap rel 24 for HumanCytoSNP-12 and Human660W-Quad, and rel 23 for Human1M-Duo
§ Based on RefSeq and Ensembl databases
† As defined by de Bakker, 2006
‡ Within 10kb of 333 known ADME-related gene