BeadChip Contents

BeadChip	Sample	Markers per Sample	Custom Marker Add-On Capability	Data Set Used for Content Selection	Content Description
HumanOmni 5-Quad	4	4.3 million	500,000	1000 Genomes Dec 2012 release (MAF ≥ 1%)	Access the highest value content, plus 500K of your own.
HumanOmni 5Exome	4	~ 4.5 million	200,000	1000 Genomes Dec 2012 release (MAF ≥ 1%), plus exome content selected from 12,000 individual exome sequences taken from various large sequence projects	The most powerful microarray. 4.3 million whole-genome variants down to 1% MAF, combined with novel functional exonic variants taken from over 12,000 sequenced exomes.
HumanOmni 2.5-8	8	~2.5 million	200,000	1000 Genomes Project Pilot (MAF ≥ 2.5%)	Common and rare variants targeting down to 2.5% MAF selected from the 1000 Genomes Project
HumanOmni 2.5Exome	8	~ 2.7 million	N/A	1000 Genomes Project Pilot (MAF 〉 2.5%), plus exome content selected from 12,000 individual exome sequences taken from various large sequence projects	Common and rare variants targeting down to 2.5% MAF selected from the 1000 Genomes Project, combined with novel functional exonic variants taken from over 12,000 sequenced exomes.
HumanOmni Express	12	> 700,000	200,000	HapMap MAF ≥ 5%	The most economical way to scan thousands of samples per week using optimized common tag SNPs.
HumanOmni ExpressExome	8	> 900,000	30,000	HapMap MAF ≥ 5%, plus exome content selected from 12,000 individual exome sequences taken from various large sequence projects	The most economical way to scan thousands of samples per week using optimized common tag SNPs and novel functional exonic variants taken from over 12,000 sequenced exomes.
HumanOmni 2.5S	8	~2.5 million	500,000	1000 Genomes Dec 2012 release (MAF ≥ 1%)	Add novel data from the 1,000 Genomes Project to your Omni2.5 or OmniExpress study, covering MAF down to 1%.
HumanOmni 1S	8	~1.1 million	N/A	1000 Genomes Project Pilot (MAF ≥2.5%)	Add novel data from the first releases of the 1,000 Genomes Project to your OmniExpress study, covering low MAF to ~2.5%.

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HumanCytoSNP FFPE-12 v2.1	24	> 262,000	200,000	HapMap Project contents MAF>5%	Mix of tag SNPs for genotyping and markers for CNV analysis, with a particular focus on regions that are highly associated with cancer studies.
HumanCytoSNP -12 v2.1	12	> 262,000		HapMap Project contents MAF>5%	Many types and sizes of structural variation in the human genome that affect phenotypes can be detected with the HumanCytoSNP-12 BeadChip, including duplications, deletions, amplifications, copy-neutral LOH, and mosaicism.
Human Exome v1.1	48	> 240,000		1KGP pilot.	The exonic contents concerning a range of common conditions, such as type 2 diabets, cancer, metabolic, psychiatric disorders.
HumanOmniExpress FFPE-12 v1.0	24	> 693,000		HapMap Project contents MAF>5%	Mix of tag SNPs for genotyping and markers for CNV analysis, with a particular focus on regions that are highly associated with cancer studies.
Infinium HumanCore v1	48	> 250,000	50,000	1000 Genomes Project contents	A variety of downstream applications, including common variant, mtDNA, ancestry, sex confirmation, loss-of-variant, indel, and CNV detection studies.
Infinium HumanCoreExome v1	48	> 550,000			Common varant genome-wide association studies large-scale CNV detection mtDNA studies and ancestry tracking sex confirmation and general sample QC Loss of function and indel variant analysis.
Mouse Mapping 5K SNP kit	-	> 5K	-	-	Approximately 5,500 SNPs were selected from an initial set of 565,062 SNPs present in dbSNP build 121 and mapped in mouse genome build 32.
Mouse Diversity Genotyping array	-	> 62K	-	-	The Mouse Diversity Genotyping Array, designed by The Jackson Laboratory and the University of North Carolina, contains more than 623,000 SNPs and more than 916,000 non-polymorphic copy number probes that are targeted to functional elements and regions known to harbor segmental duplications.

CytoSNP-12 BeadChip은 모든 알려진 cytogenetic region에 대한 common SNP들로 구성되어 있어 cytogenetic screening (Gain, Loss, copy-neutral LOH, polyploidy, aneuploidy, mosaicism 등)에 효율적으로 사용할 수 있습니다. Pericentromere, subtelomere, sex chromosome, syndrome과 관련된 region, disease-associated region에 대부분의 marker가 집중되어 있습니다.