#	Field	Description
1	Sample ID	Unique identification code of the DNA
2	Sample Name	Unique identification code of the DNA
3	Sample Index	Row index indicating the position of the Sample Name in BeadStudio project
4	SNP Name	Unique identification code of the SNP
5	SNP Index	Row index indicating the position of the SNP Name ID in BeadStudio project
6	SNP	Nucleotide change of a SNP
7	Chr	Chromosome number of the SNP
8	Position	SNP position on chromosome
9	Allele1 - AB	Allele definition at the locus in a A vs B format (indicating homozygosity or heterozygosity)
10	Allele2 - AB	
11	Allele1 - Forward	Allele definition expected based on the comparison with reference sequence. This nomenclature is genome build-dependent
12	Allele2 - Forward	
13	Allele1 - Top	Illumina's allele definition that let you code the allele without ambiguity and changes due to the genome build you're referring to: 1. NOT-ambiguous SNPs, like A/C,G or T/C,G, Allele1 is always A or T, but A is Allele1-TOP and T is Allele1-BOT (Bottom). 2. In the case of ambiguous SNPs, like A/T and C/G Illumina's method goes reading -n-bases upstream and +n-bases downstream the SNP position up to an unambiguous situation. When such a condition is found, the nomenclature is referred to the NOT-ambiguous SNP calling (for more details see Annex 1)
14	Allele2 - Top	
15	X	Normalized intensity of the A allele, referred to the A vs B format
16	Y	Normalized intensity of the B allele, referred to the A vs B format
17	X Raw	Raw intensity of the A allele, referred to the A vs B format
18	Y Raw	Raw intensity of the B allele, referred to the A vs B format
19	R	Normalized R-value (also named NormR) of a SNP for the sample. R-value is the intensity of the fluorescence signal
20	Theta	Normalized Theta-value (also named NormTheta) of a SNP for the sample, where Theta represents the angle deviation from pure allele A signal. Theta = 0 means pure

		A signal (AA homozygous); Theta = 1 means pure B signal (BB homozygous); Theta = 0.5 means AB heterozygous. This parameter is used together with R parameter in order to generate a polar coordinates SNP graphical view
21	GC Score	GenCall score per single SNP is primarily designed to rank and filter out failed genotypes. The sensitive region of the GenCall Score is between the values of 0.2 and 0.7. Scores below 0.2 generally indicate failed genotypes, while scores above 0.7 usually report well-behaving genotypes
22	Log R Ratio	Base-2 log ratio of observed R for a SNP divided by the expected R
23	B Allele Freq	Theta-value for a SNP corrected for cluster positions. Cluster positions are generated from a large set of normal individuals. B allele frequency indicates the SNP allele composition and is linearly interpolated between 0 and 1. When SNPs are well clustered, B allele frequency values are grouped around 0, 0.5 or 1, meaning AA, AB or BB respectively
24	GT Score	GenTrain score is a number between 0 and 1 indicating how well the samples clustered for this locus: 0 means that SNP is not well clustered; 1 means the best SNP clustering
25	Cluster Sep	Cluster separation score: value 1 means that SNP is not polymorphic