
晶能生物（上海）技术有限责任公司

IlluminaBeadChip数据结果光盘说明

一、服务记录

客户姓名：何东仪

单位名称：上海市光中西医结合医院

合同号：GA0123MC03-1-CH

芯片类型及样本数量：HumanMetylation450K, V1.0, 共12 个样品

二、光盘中文件列表及说明

➤ BeadChip芯片实验方法存放于“Manual”文件夹下，其中包括《QIAmap DNA mini Kit.PDF》、《BeadChip实验流程.PDF》、《EZ DNA methylation Kit.PDF》等的中英文版，以方便客户使用。

《GenomeStudio_Methylation_v1.8_User_Guide_11319130_B.pdf》是illumina分析软件GenomeStudio用户说明；

➤ “Product File“中”HumanMethylation450_15017482_v[1].1.1.bpm.txt”是芯片上的探针信息等。

➤ 实验结果数据存放于“Data Results”目录下，分别为

“IsScan Raw Data”文件夹下为扫描的原始数据：包括信号值IDAT文件和扫描图JPEG文件；idat文件需要illumina的genomestudio软件才能读取。

“Genmoestudio Export Report”是genomestudio导出txt格式的原始数据，包含每个样本平均信号值 avg-signal，平均beta值 avg beta，检测信号P值 detection pval 值，Signal A 和 B 值等（见 TableControl.txt）；和 SampleTable。其中，

TableControl_controlnorm_bg 是 control 均一化处理，减去背景后每个样本的平均信号值 avg-signal，平均beta值 avg beta，检测信号P值 detection pval 值，Signal A 和 B 值；

TableControl_nonenorm_bg 是未经均一化处理，减去背景后每个样本的平均信号值 avg-signal，平均beta值 avg beta，检测信号P值 detection pval 值，Signal A 和 B 值；

“Analysis Report”是甲基化数据GO和Pathway分析报告，说明见甲基化分析结果。

三、数据结果

1、实验说明表：

芯片条形码编号	杂交位置编号	样本编号	芯片类型
3999547166	3999547166_R01C01	jiankangJ1	HumanMetylation450K, v1
	3999547166_R01C02	panlingB4	
	3999547166_R02C01	wangqiruB1	
	3999547166_R02C02	guomengruJ5	
	3999547166_R03C01	jiankangJ2	
	3999547166_R03C02	jiangyinhuaB5	
	3999547166_R04C01	songjinfangB2	
	3999547166_R04C02	zhuliminJ3	
	3999547166_R05C01	zhufaqinB3	
	3999547166_R05C02	lizhuolingJ6	
	3999547166_R06C01	tongpingJ4	
	3999547166_R06C02	zoumeixinB6	

2、筛选标准简要说明及结果

1) 根据原始数据的表现选择归一化方法，可选择的归一化方法有如下2种：

a) *None*

b) *Control*

本实验选择的归一化方法为：*control*

2) 通过芯片图像分析软件对芯片灰度扫描图进行分析,可以得到芯片上每个基因点的原始信号值,即所有有效重复点的前景信号值减去背景信号值的平均信号值 (Avg_Beta) , Detection Pval,等。我们根据这些参数值进行后续的数值分析。

3、Excel文件中的数据字段含义说明

1) Tabel Control 注释如下：

Column	Description	Type	Visible by Default?
Columns			
Target_ID	Identifies the probe name. Also used as a key column for data import	string	Y
ProbeID_A	Illumina identifier for the probe sequence of Probe A	integer	Y
ProbeID_B	Illumina identifier for the probe sequence of Probe B	integer	Y

Column	Description	Type	Visible by Default?
ILMNID	Unique CpG locus identifier from the Illumina CG database	string	N
NAME	Unique CpG locus identifier from the Illumina CG database	string	N
ILMNSTRAND	Illumina strand (TOP or BOT)	string	N
ADDRESSA_ID	Address of probe A	integer	N
ALLELEA_PROBESEQ	Sequence for probe A	string	N
ADDRESSB_ID	Address of probe B	integer	N
ALLELEB_PROBESEQ	Sequence for probe B	string	N
GENOMBUILD	Genome build	integer	N
CHR	Chromosome on which the target locus is located	integer	N
MAPINFO	Genomic position of C in CG dinucleotide	integer	N
PLOIDY	Ploidy type	string	N
SPECIES	Species	string	N
SOURCE	Genomic position source	string	N
SOURCEVERSION	Source version	float	N
SOURCESTRAND	Illumina strand orientation for source sequence	string	N
SOURCESEQ	Original sequence of the region covered by assay probes	string	N
TOPGENOMICSEQ	Top sequence (reported regardless of whether TOP or BOT sequence is used for design)	string	N

Column	Description	Type	Visible by Default?
NEXT_BASE	The next base being incorporated	string	N
COLOR_CHANNEL	Color channel	string	N
TSS_COORDINATE	Transcription start site genomic coordinate	integer	N
GENE_STRAND	Gene strand	string	N
GENE_ID	RefSeq identifier (GeneID)	string	N
SYMBOL	RefSeq gene symbol	string	N
SYNONYM	Gene synonyms	string	N
ACCESSION	Gene accession (of the longest transcript)	string	N
GID	RefSeq entry identifier (GI number)	string	N
ANNOTATION	Gene annotation from the NCBI database	string	N
PRODUCT	Gene product description from the NCBI database	string	N
DISTANCE_TO_TSS	Distance of CG dinucleotide to transcription start site	integer	N
CPG_ISLAND	Boolean variable denoting whether or not the probe is located in a CpG island (by relaxed definition)	string	N
CPG_ISLAND_LOCATION	CpG island coordinates from the NCBI database	string	N
MIR_CPG_ISLAND	Chromosome start-end of upstream CPG island from a microRNA	string	N

Column	Description	Type	Visible by Default?
MIR_NAMES	Name of microRNA near locus	string	N
Subcolumns			
AVG_Beta	Methylation level (beta) of the CpG locus in the group of samples	float	Y
Intensity	Signal intensity of the locus, calculated as Signal A + Signal B	integer	Y
MIN_Beta	Minimum methylation level (beta) of the CpG locus in the group of samples	float	N
MAX_Beta	Maximum methylation level (beta) of the CpG locus in the group of samples	float	N
NARRAYS	Number of samples in the group	integer	N
ARRAY_STDEV	Standard deviation associated with sample-to-sample variability within the group (undefined when the group contains a single sample)	float	N
Avg_NBEADS_A	Average number of beads per bead type representing probes for the gene	integer	N
Avg_NBEADS_B	Average number of beads per bead type representing probes for the gene	integer	N
BEAD_STERR_A	Average standard error associated with bead-to-bead variability for the samples in group A	integer	N
BEAD_STERR_B	Average standard error associated with bead-to-bead variability for the samples in group B	integer	N

Column	Description	Type	Visible by Default?
Signal_A	Signal intensity of the unmethylated (A) probe	integer	N
Signal_B	Signal intensity of the methylated (B) probe	integer	N
Detection Pval	1-p-value computed from the background model characterizing the chance that the target sequence signal was distinguishable from the negative controls	float	N

2) Samples Table 注释如下

Column	Description	Type	Visible by Default?
Columns			
TARGETID	Identifies the probe name. Also used as a key column for data import	string	Y
PROBEID_A	Illumina identifier for probe sequence A	integer	Y
PROBEID_B	Illumina identifier for probe sequence B	integer	Y
SYMBOL	Gene symbol	string	Y
ILMNID	Unique CpG locus identifier from the Illumina CG database	string	N
NAME	Unique CpG locus identifier from the Illumina CG database	string	N
ILMNSTRAND	Illumina strand (TOP or BOT)	string	N
ADDRESSA_ID	Address of probe A	integer	N
ALLELEA_PROBESEQ	Sequence for probe A	string	N

Column	Description	Type	Visible by Default?
ADDRESSB_ID	Address of probe B	integer	N
ALLELEB_PROBESEQ	Sequence for probe B	string	N
GENOME BUILD	Genome build	integer	N
CHR	Chromosome on which the target locus is located	integer	N
MAPINFO	Genomic position of C in CG dinucleotide	integer	N
PLOIDY	Ploidy type	string	N
SPECIES	Species	string	N
SOURCE	Genomic position source	string	N
SOURCEVERSION	Source version	float	N
SOURCESTRAND	Illumina strand orientation for source sequence	string	N
SOURCESEQ	Original sequence of the region covered by assay probes	string	N
TOPGENOMICSEQ	Top sequence (reported regardless of whether TOP or BOT sequence is used for design)	string	N
NEXT_BASE	The next base being incorporated	string	N
COLOR_CHANNEL	Color channel	string	N
TSS_COORDINATE	Transcription start site genomic coordinate	integer	N
GENE_STRAND	Gene strand	string	N
GENE_ID	RefSeq identifier (GeneID)	string	N
SYNONYM	Gene synonyms	string	N

Column	Description	Type	Visible by Default?
ACCESSION	Gene accession (of the longest transcript)	string	N
GID	RefSeq entry identifier (GI number)	string	N
ANNOTATION	Gene annotation from the NCBI database	string	N
PRODUCT	Gene product description from the NCBI database	string	N
DISTANCE_TO_TSS	Distance of CG dinucleotide to transcription start site	integer	N
CPG_ISLAND	Boolean variable denoting whether or not the probe is located in a CpG island (by relaxed definition)	string	N
CPG_ISLAND_LOCATION	CpG island coordinates from the NCBI database	string	N
MIR_CPG_ISLAND	Chromosome start-end of upstream CPG island from a microRNA	string	N
MIR_NAMES	Name of microRNA near locus	string	N

Subcolumns

AVG_BETA	Methylation level (beta) of the CpG locus in the group of samples	float	Y
Intensity	Signal intensity of the locus, calculated as Signal A + Signal B	integer	Y
Avg_NBEADS_A	Average number of beads per bead type representing probes for the gene	integer	N

Column	Description	Type	Visible by Default?
Avg_NBEADS_B	Average number of beads per bead type representing probes for the gene	integer	N
BEAD_STERR_A	Average standard error associated with bead-to-bead variability for the samples in group A	integer	N
BEAD_STERR_B	Average standard error associated with bead-to-bead variability for the samples in group B	integer	N
Red	Intensity of the unmethylated (A) probe	integer	N
Green	Intensity of the methylated (B) probe	integer	N
Detection Pval	1-p-value computed from the background model characterizing the chance that the target sequence signal was distinguishable from the negative controls	float	N