

Column A: Title ;	Column B: Mean ;	Column C: Example ;
Title	Mean	Example
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ProbeName	Probe name	hsa_circ_0000026
ControlType	quality control site (pos:Quality Control Point, FALSE: Non-Quality Control Point)	Pos/FALSE
Sample_NS	Normalized signal values of probes in samples	7.023509
Sample_flag	Detection and determination of samples: A: There is no significant difference between the signal of the probe and background; P: There is significant difference between the signal of the probe and background; M: The difference between the signal of the probe and background is between A and P.	P/M/A
Fold_change(1_vs_2)	(formula : foldchange=average(power(2,signal(CASE)))/ average(power(2,signal(CONTROL)))) Multiple differences of two groups (Biologically repetitive samples) or two (No biologically duplicated samples)	3.4
foldchange (abs)	Absolute value of multiple differences of two groups (Biologically repetitive samples) or two (No biologically duplicated samples)	3.4
Regulation(1_vs_2)	Up-down trend of two groups (Biologically repetitive samples) or two (No biologically duplicated samples)	up/down
Type	RNAtype: circRNA/lncRNA / mRNA	circRNA/lncRNA/mRNA
ProbeSeq	Probe sequence	AAGGTATCTTAAGGAAAGTTC AAGGTAAAAAGACAGAGGTGT TTATGGTTACATGTGTGT
circRNA_ID	Gene ID in circbase database	hsa_circ_0082053
chrom	circRNA derived chromosome	Chr7
Hsa_hg19_circRNA_start	Sequence starting position	91787463
Hsa_hg19_circRNA_end	Sequence termination position	91810001
Hsa_hg19_circRNA_strand	Sources of positive and negative chain of circRNA sequence	+/-
genomic_length	Sequence length on genome	53243
spliced_seq_length	Sequence length after splicing	2700
best_transcript	Best transcript	NM_024913
gene_symbol	Source parent gene name	CCDC88C

