ValueType	ColumnName	Required for processed CRISPR screen analysis (CRISPR guide_quantifications BED3+14 format)	Required for cCRE-gene analysis (CRISPR element_quantifications BED3+22 format)	example	Definition
string	chrom	TRUE	TRUE	chrX	Chromosome of the target of the perturbation (e.g., guideRNA, guideRNA pair). For guideRNA, use PAM. For element, use the element's chromosomal coordinates
uint	chromStart	TRUE	TRUE	48397949	Zero-based starting position of the target of the perturbation (e.g., guideRNA, guideRNA pair). As with BED format, the start position in each BEDPE feature is therefore interpreted to be 1 greater than the start position listed in the feature. For guideRNA, use PAM. For guideRNA, use PAM. For element, use the element's chromosomal coordinates
uint	chromEnd	TRUE	TRUE	48397952	One-based ending position of the target of the tested perturbation (e.g., guideRNA, guideRNA pair). For guideRNA, use PAM. For guideRNA, use PAM. For element, use the element's chromosomal coordinates
string	name	TRUE	TRUE	GATA1|chrX:48397930-48397949:+	gene|PerturbationTargetID. For non-expression screens, gene is 'NA'. For guide files, PerturbationTargetID is the guide's PAM in standard bed format. For negative controls (safes or non-targeting), gene is 'NA'. For safe-targeting controls, PerturbationTargetID is its PAM. For non-targeting controls, PerturbationTargetID is NT_n, where n is the unique identifying number for that sgRNA. For the element-level file format, the PerturbationTargetID is the element's chromosomal coordinates. Names must be unique
float	EffectSize	FALSE	TRUE	-0.25	Effect size can be determined according to the data depositor's preference. The effect sizes can be across replicates or within replicate. Enhancers (positive regulators) of the measured gene's expression should have a positive effect size. Repressors (negative regulators) of the measured gene's expression should have a negative effect size. This may require additional formatting of the EffectSize column
uint	SeqCounts	TRUE	FALSE	200	Sequencing counts associated with the guide for a collected population

char[1]	strandPerturbationTarget	TRUE	TRUE	+	Strand of perturbation target [+,-,.]; For guideRNA, this is the strand of the guideRNA. For element, use the element's strand. if strandedness is unclear or unnecessary, use '.' for the strand
string	PerturbationTargetID	TRUE	TRUE	chrX:48397930-48397949:+	See name column for details on defining PerturbationTargetID
string	chrTSS	TRUE	TRUE	chrX	Chromosome of the TSS of the tested/measured gene TSS. 'NA' for screens that measure phenotypes other than gene expression
string	startTSS	TRUE	TRUE	48786590	Zero-based starting position of the tested/measured TSS. As with BED format, the start position in each BEDPE feature is therefore interpreted to be 1 greater than the start position listed in the feature. 'NA' for screens that measure phenotypes other than gene expression
string	endTSS	TRUE	TRUE	48786591	One-based ending position of the tested/measured gene TSS. 'NA' for screens that measure phenotypes other than gene expression
string	strandGene	TRUE	TRUE	+	Strand of gene TSS [+,-,.]. 'NA' for screens that measure phenotypes other than gene expression; if strandedness is unclear or unnecessary, use '.' for the strand
string	EffectSize95ConfidenceIntervalLow	FALSE	TRUE	-0.26	Lower bound of 95% confidence interval of effect size. 'NA' for screens that measure phenotypes other than gene expression
string	EffectSize95ConfidenceIntervalHigh	FALSE	TRUE	-0.24	Upper bound of 95% confidence interval of effect size. 'NA' for screens that measure phenotypes other than gene expression
string	measuredGeneSymbol	TRUE	TRUE	GATA1	HGNC Gene Symbol of target measured gene. 'NA' for screens that measure phenotypes other than gene expression
string	measuredEnsemblID	TRUE	TRUE	ENSG00000102145	Ensembl Gene ID. 'NA' for screens that measure phenotypes other than gene expression
string	guideSpacerSeq	TRUE	TRUE	CCTGGCCTCTGGTACCACTT	For element-level files, this is a semicolon separated list of gRNA protospacer sequences assigned to this connection, as applicable. 'NA' if not provided in element-level files. For single guides, there is only one protospacer sequence
string	guideSeq	TRUE	TRUE	GCCTGGCCTCTGGTACCACTT	The gRNA sequence targeting the protospacer, as synthesized -- i.e. with the 'default' 5' G appended ONLY if it was included in the synthesis design. If no 5' G was appended to each guide, the value here is identical to the guideSpacerSeq column. For element-level files, this is a semicolon separated list of such gRNA sequences targeting the element. 'NA' if not provided in element-level files
string	guideType	TRUE	FALSE	targeting	A qualitative classifier for the type of guide. Must be either 'negative_control' or 'targeting'

Type	Field	Col3	Col4	Example	Description
enum('TRUE','FALSE')	Significant	FALSE	TRUE	TRUE	'TRUE' or 'FALSE', depending on whether the connection was called significant in the original publication, or by the analysis method used
string	pValue	FALSE	TRUE	0.00001	Nominal p-value from the test
string	pValueAdjusted	FALSE	TRUE	0.01	The multiple hypothesis adjusted p-value used to determine significance
string	PowerAtEffectSize10	FALSE	TRUE	0.5	Power to detect 10% decrease in gene expression. 'NA' if not provided
string	PowerAtEffectSize25	FALSE	TRUE	0.8	Power to detect 25% decrease in gene expression. 'NA' if not provided
string	PowerAtEffectSize50	FALSE	TRUE	0.99	Power to detect 50% decrease in gene expression. 'NA' if not provided
enum('TRUE','FALSE')	ValidConnection	FALSE	TRUE	TRUE	'TRUE' for valid E-P connections. If not true, directly provide an invalidating reason for connections that should be removed -- for instance because they are in the promoter of the tested gene, or are an element in the gene body of the tested gene (in a KRAB-dCas9 experiment). 'NA' can also be provided, in which case no interpretation should be made using this column
string	Notes	TRUE	TRUE	NA	Free text; 'NA' if no notes