Notes	GS	FS	Representation	Up/Down	Code
For guides in the same orientation as the targets (+/+ or -/-) select guides that are	+	+	sgRNA Gene/CDS	Downstream	`Guide strand` == `Feature strand` and 0 < `Feature distance` < @before_feat'
within before_feat of the gene start	-	-	Gene/CDS sgRNA	Downstream	`Guide strand` == `Feature strand` and 0 < `Feature distance` < @before_feat'
For guides in the +/+ orientation select guides where the end is within [before_feat] of the gene start	+	+	sgRNA	Upstream	`Guide strand` == "+" and `Feature strand` == "+" and `Feature distance` == 0 and `Guide end` - `Feature start` < @after_feat'))
For guides in the -/- orientation select guides where the end is within [before_feat] of the gene start	_	-	sgRNA	Upstream	`Guide strand` == "-" and `Feature strand` == "-" and `Feature distance` == 0 and `Feature end` - `Guide start` < @after_feat'))
Select guides where target is + and guide is - and the guide is infront of the gene	-	+	sgRNA Gene/CDS	Upstream	Guide strand` == "-" and `Feature strand` == "+" and 0 < `Feature start` - `Guide end` < @before_feat'
Select guides where target is - and guide is + and the guide is infront of the gene	+	-	sgRNA	Upstream	`Guide strand` == "+" and `Feature strand` == "-" and 0 < `Guide start` - `Feature end` < @before_feat')
Select guides where target is + and guide is - and the guide is is withinbefore_feat of the gene start	_	+	sgRNA sgRNA	Upstream	Guide strand` == "-" and `Feature strand` == "+" and 0 < `Guide end` - `Feature start` < @after_feat'
Select guides where target is - and guide is + and the guide is is within before_feat of the gene start	+	_	sgRNA	Upstream	`Guide strand` == "+" and `Feature strand` == "-" and 0 < `Feature end` - `Guide start` < @after_feat'))