

GRanges object with 6 ranges and 1 metadata column:

	seqnames	ranges	strand	gene_id
	<Rle>	<IRanges>	<Rle>	<character>
[1]	chrX	100627109-100639991	-	ENSG00000000003.14
[2]	chrX	100584802-100599885	+	ENSG00000000005.5
[3]	chr20	50934867-50958555	-	ENSG000000000419.12
[4]	chr1	169849631-169894267	-	ENSG000000000457.13
[5]	chr1	169662007-169854080	+	ENSG000000000460.16
[6]	chr1	27612064-27635277	-	ENSG000000000938.12

seqinfo: 25 sequences (1 circular) from hg38 genome

**Transcripts/
Gene / Peaks**

rowData
rowRanges

Samples

assays

colData

DataFrame with 6 rows and 4 columns

	names	id	line	condition
	<character>	<character>	<factor>	<factor>
1	SAMEA103885102	diku_A	diku_1	naive
2	SAMEA103885347	diku_B	diku_1	IFNg
3	SAMEA103885043	diku_C	diku_1	SL1344
4	SAMEA103885392	diku_D	diku_1	IFNg_SL1344
5	SAMEA103885182	eiwy_A	eiwy_1	naive
6	SAMEA103885136	eiwy_B	eiwy_1	IFNg