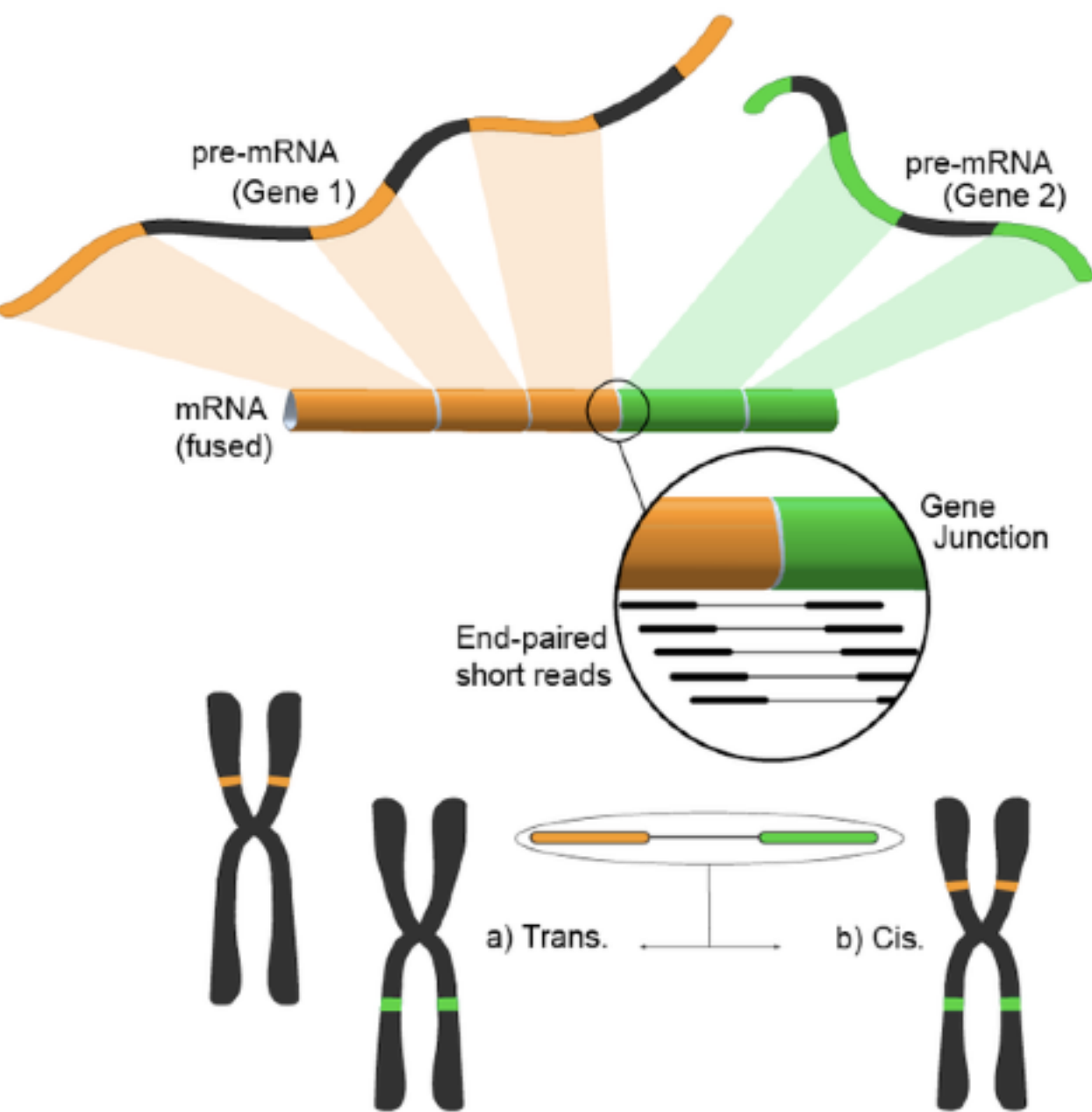
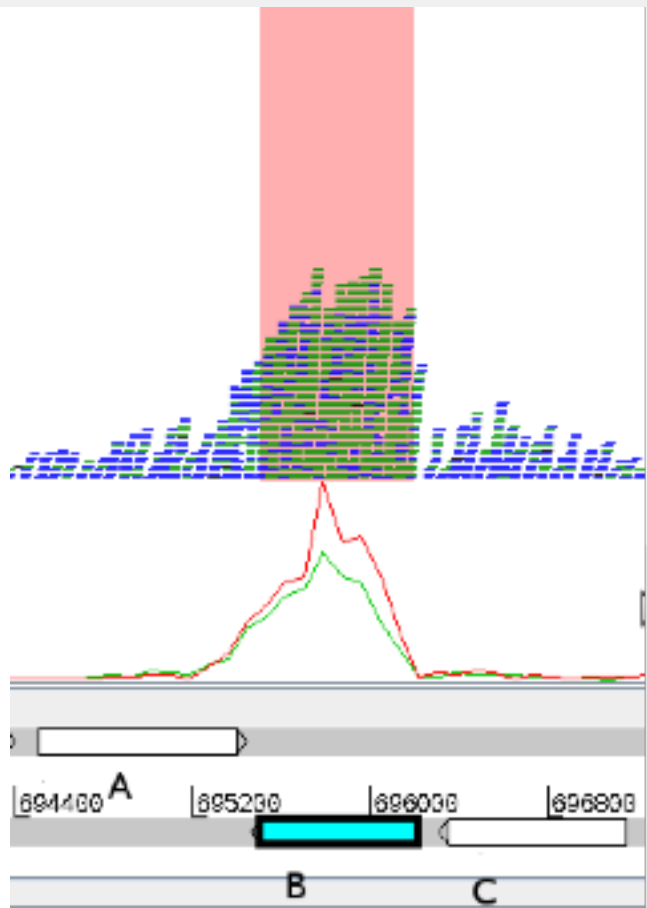


# Contar o que?

- A medida base é o número de reads.
- Contam-se o número de reads mapeadas a uma feature.
- Reads curtos
- Single read (quantificação) - paired-end (splice)



##gff-version 3						
ctg123	.	mRNA	1300	9000	.	ID=mrna0001;Name=sonichedgehog
ctg123	.	exon	1300	1500	.	ID=exon00001;Parent=mrna0001
ctg123	.	exon	1050	1500	.	ID=exon00002;Parent=mrna0001
ctg123	.	exon	3000	3902	.	ID=exon00003;Parent=mrna0001
ctg123	.	exon	5000	5500	.	ID=exon00004;Parent=mrna0001
ctg123	.	exon	7000	9000	.	ID=exon00005;Parent=mrna0001



# Quem expressa mais?

	Exp1	Exp2	Exp3	Ctrl1	Ctrl2	Ctrl3
Gene A	0,010%	0,015%	0,012%	0,02%	0,030%	0,029%
Gene B	0,0072%	0,0062%	0,0095%	0,0031%	0,0040%	0,0015%
Gene C	1%	1,5%	1,2%	2%	3%	2,9%
Gene D	72%	62%	95%	31%	40%	15%