

Output of TSD

- The output includes three part:
 - result.txt
 - report.txt
 - seq_pic/*.pdf

Result.txt

- It report the fragment composition of PacBio reads

The diagram illustrates the structure of a PacBio read with a gap. The read is represented as a table with two rows of data. The first row corresponds to the first fragment, and the second row corresponds to the second fragment. The fields in the table are: Read ID, Strand, Genome Name, Gap ID, Start Position, End Position, Gap ID, Strand, and Positions. The first fragment starts at position 298 and ends at position 5. The second fragment starts at position 3193 and ends at position 488. The gap between the two fragments is 2941 bases long. The read is from the positive strand of the genome.

Read ID	Strand	Genome Name	Gap ID	Start Position	End Position	Gap ID	Strand	Positions
m54079_171127_175044/56033499/16924_21783	insert	-1	4	298	0	5	insert	-1 2942 3220 0 0 insert -1 1416 2454 1000 -4 3 1 131453121 131456375
m54079_171127_175044/28639574/26058_27813	insert	-1	2941	3193	488	0	insert	-1 1416 2454 1000 -4 3 1 131453121 131453572

report.txt

- It reports the SVs and their information

SV ID	Fragment number	Chromosome name of first fragment	Start position of first fragment	The gap with next fragment																
seq26	m54079_171127_175044/55968255/117_5923	3	12	5	1	12,12,5	3	1	131448333	131451703	-4	insert	-1	432	1407	121	15	1	20299915	20301123
seq27	m54079_171127_175044/38142632/38625_45242	3	415	3	1	3,415,415	3	1	131446286	131449231	193	3	1	131449230	131451463	0	insert	-1	512	1621

seed ID

The number of PacBio reads in this SV/fragment

Strand name of first fragment

end position of first fragment

Chromosome name of next fragment

seq_pic/*.pdf

- They are the plots for SV structure
- Each *.pdf is one SV
- It is plot like:

