

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:28:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818989.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1818989 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818989.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:28:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,936,132
Mapped reads	1,875,407 / 96.86%
Unmapped reads	60,725 / 3.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,233 / 1.51%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	881,088 / 45.51%
Duplication rate	39.95%
Clipped reads	1,883,706 / 97.29%

2.2. ACGT Content

Number/percentage of A's	49,014,361 / 28.27%
Number/percentage of C's	37,241,515 / 21.48%
Number/percentage of T's	51,075,969 / 29.46%
Number/percentage of G's	36,060,032 / 20.8%
Number/percentage of N's	8,429 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.056

Standard Deviation	0.6572
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	49.23
----------------------	-------

2.5. Mismatches and indels

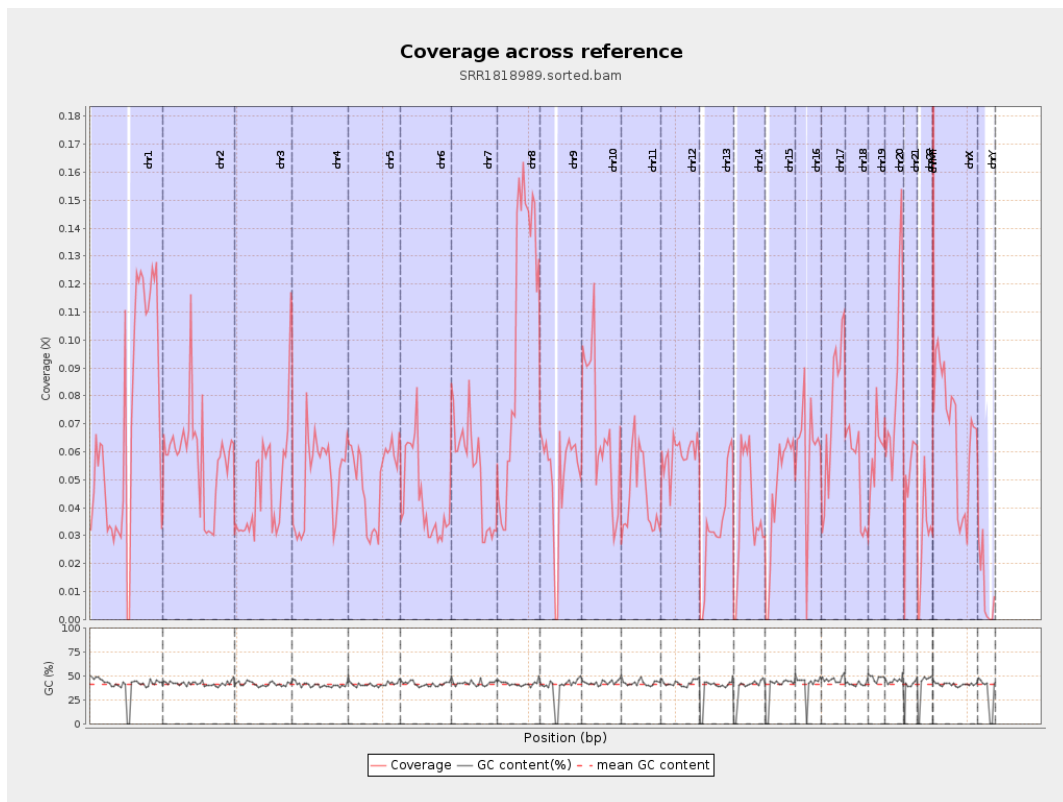
General error rate	0.67%
Mismatches	1,102,993
Insertions	28,109
Mapped reads with at least one insertion	1.46%
Deletions	56,661
Mapped reads with at least one deletion	2.96%
Homopolymer indels	42.52%

2.6. Chromosome stats

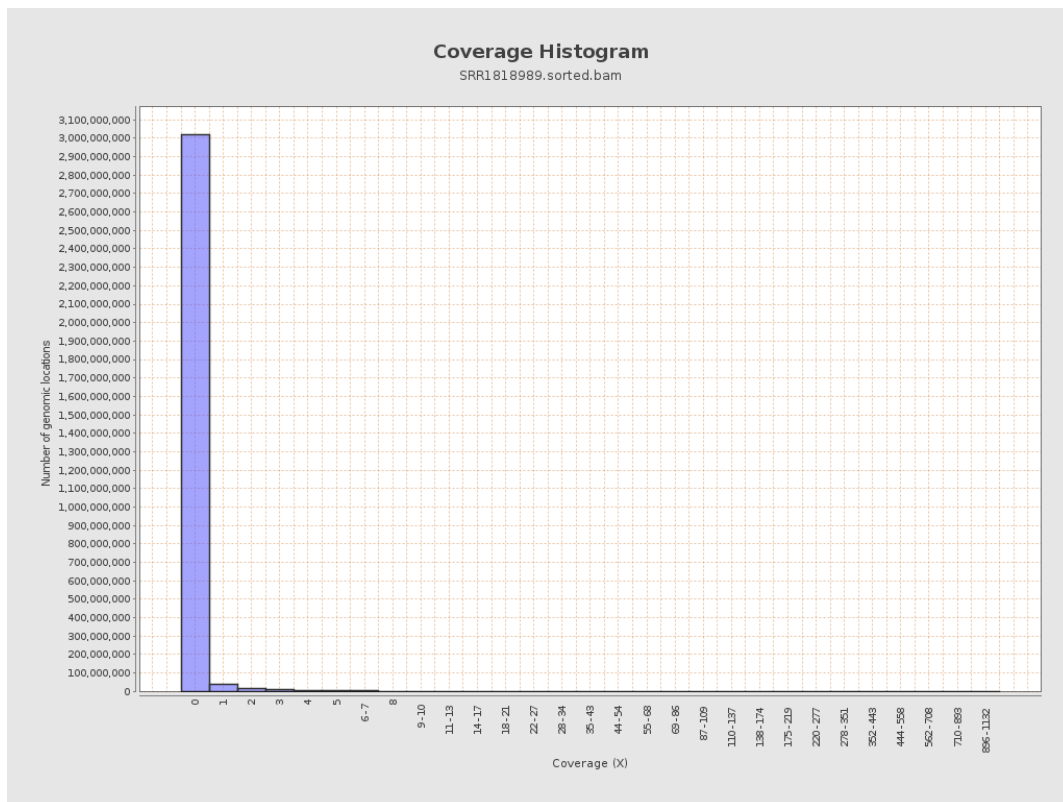
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17295938	0.0694	1.1468
chr2	243199373	14106022	0.058	0.915
chr3	198022430	9365190	0.0473	0.402
chr4	191154276	9657451	0.0505	0.4721
chr5	180915260	9155457	0.0506	0.4298
chr6	171115067	7405371	0.0433	0.4576
chr7	159138663	8479458	0.0533	0.6904

chr8	146364022	15341423	0.1048	0.6769
chr9	141213431	7288431	0.0516	0.6047
chr10	135534747	9142306	0.0675	0.7669
chr11	135006516	5974279	0.0443	0.4576
chr12	133851895	7962387	0.0595	0.4626
chr13	115169878	3861466	0.0335	0.3475
chr14	107349540	4137377	0.0385	0.38
chr15	102531392	4609461	0.045	0.3995
chr16	90354753	5445350	0.0603	0.7069
chr17	81195210	6062369	0.0747	0.5711
chr18	78077248	4092529	0.0524	0.7009
chr19	59128983	3525503	0.0596	1.0483
chr20	63025520	5528595	0.0877	0.6059
chr21	48129895	2467681	0.0513	0.4654
chr22	51304566	1434409	0.028	0.3436
chrMT	16571	25988	1.5683	2.6723
chrX	155270560	10507983	0.0677	0.5566
chrY	59373566	632172	0.0106	0.596

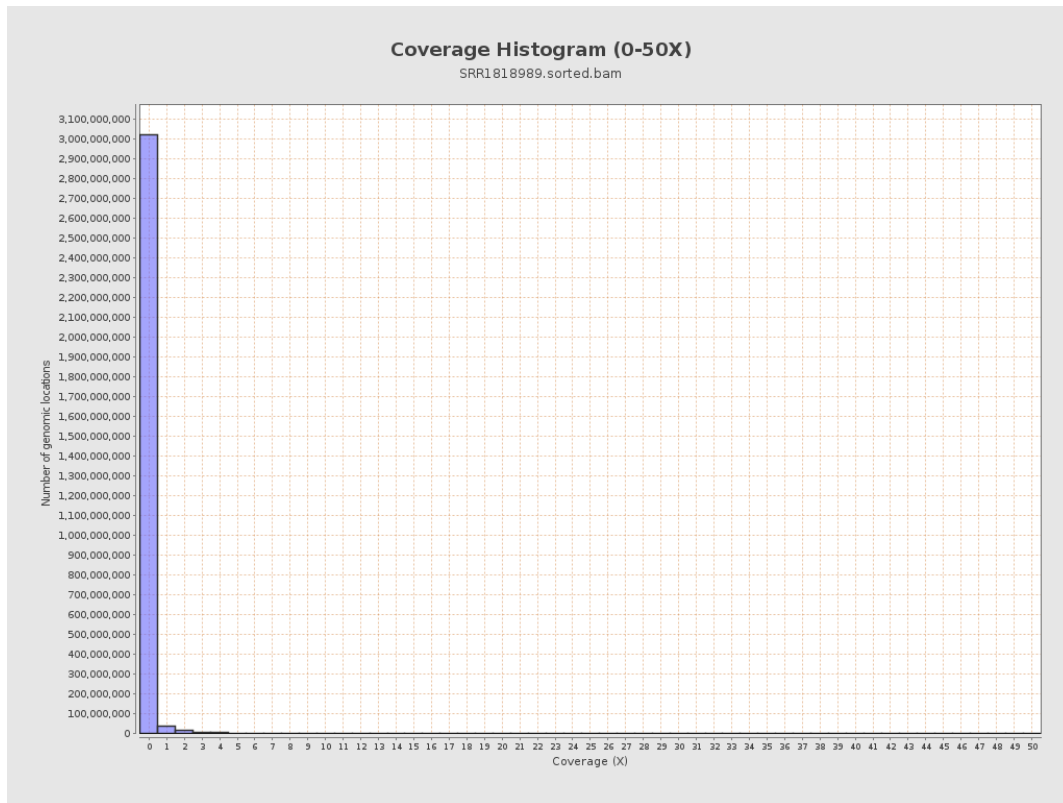
3. Results : Coverage across reference



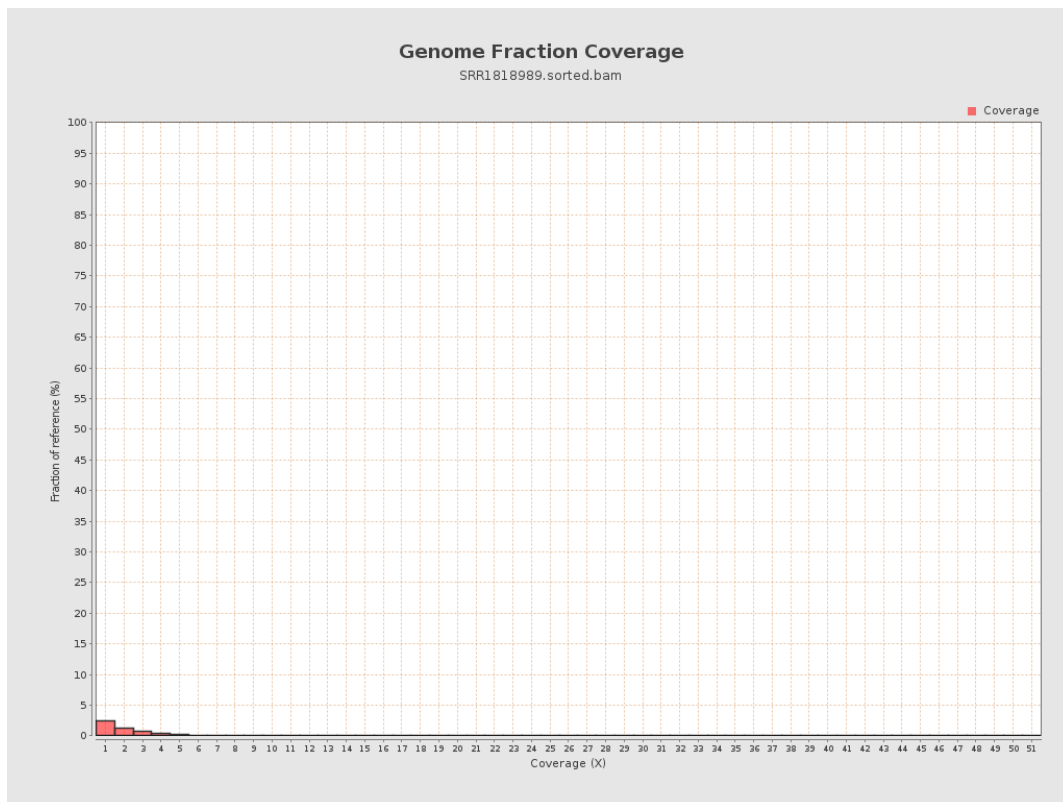
4. Results : Coverage Histogram



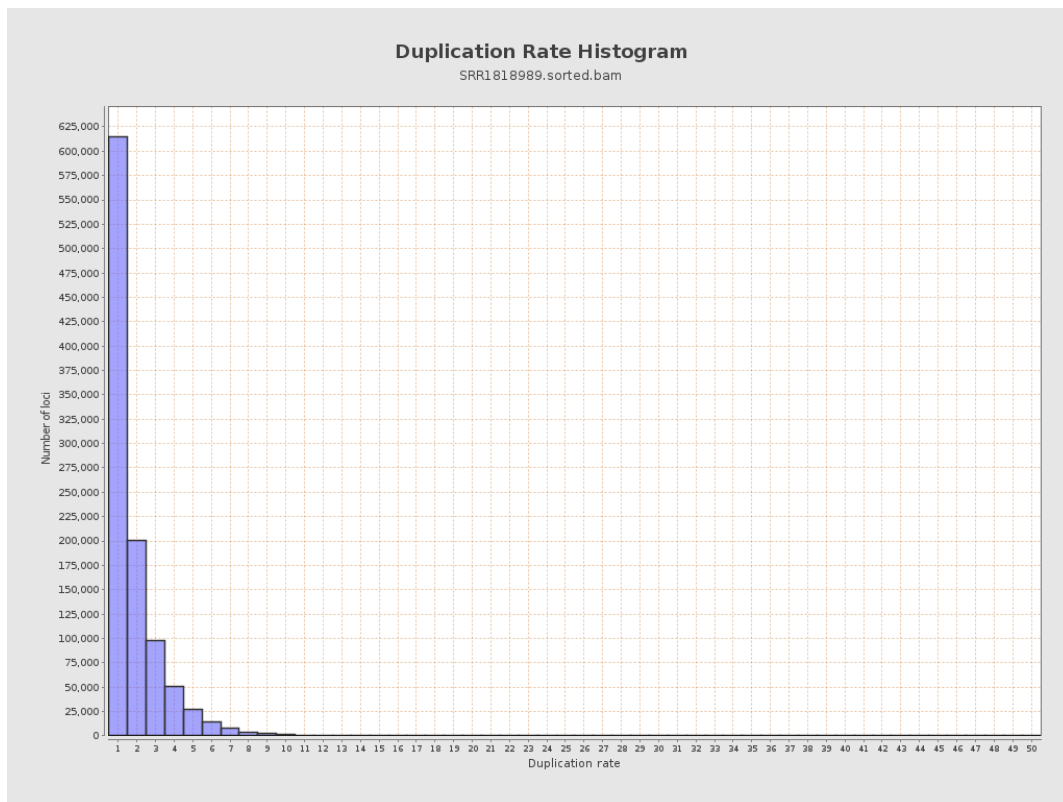
5. Results : Coverage Histogram (0-50X)



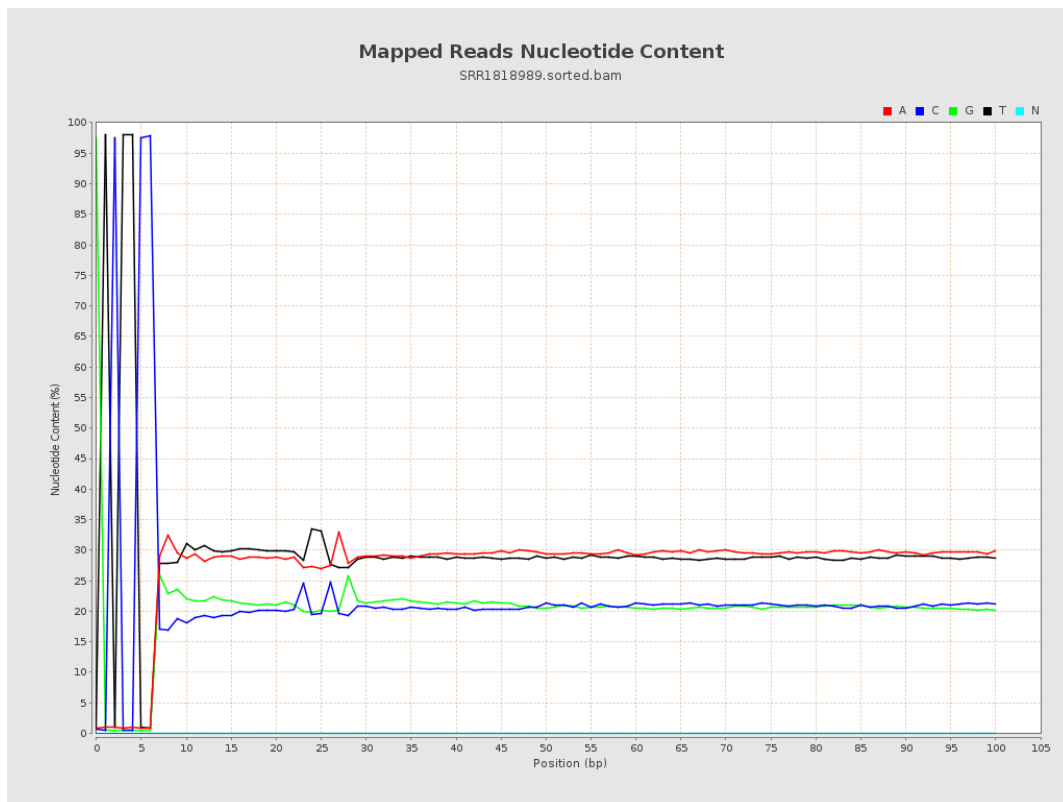
6. Results : Genome Fraction Coverage



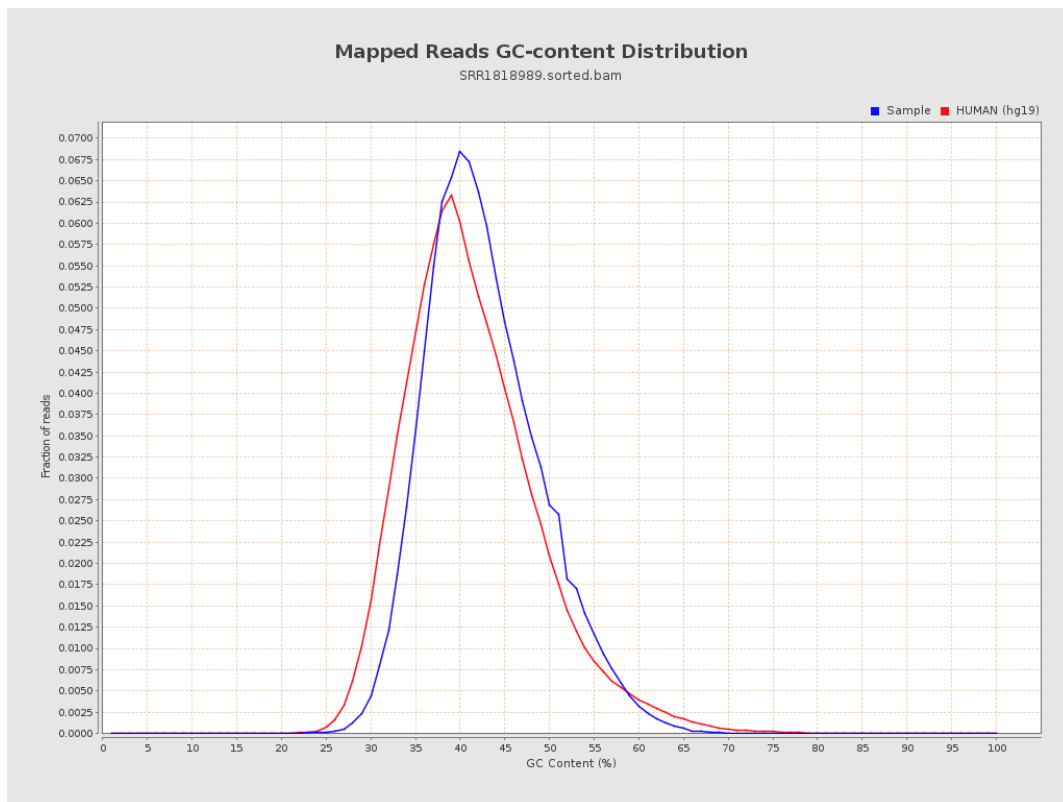
7. Results : Duplication Rate Histogram



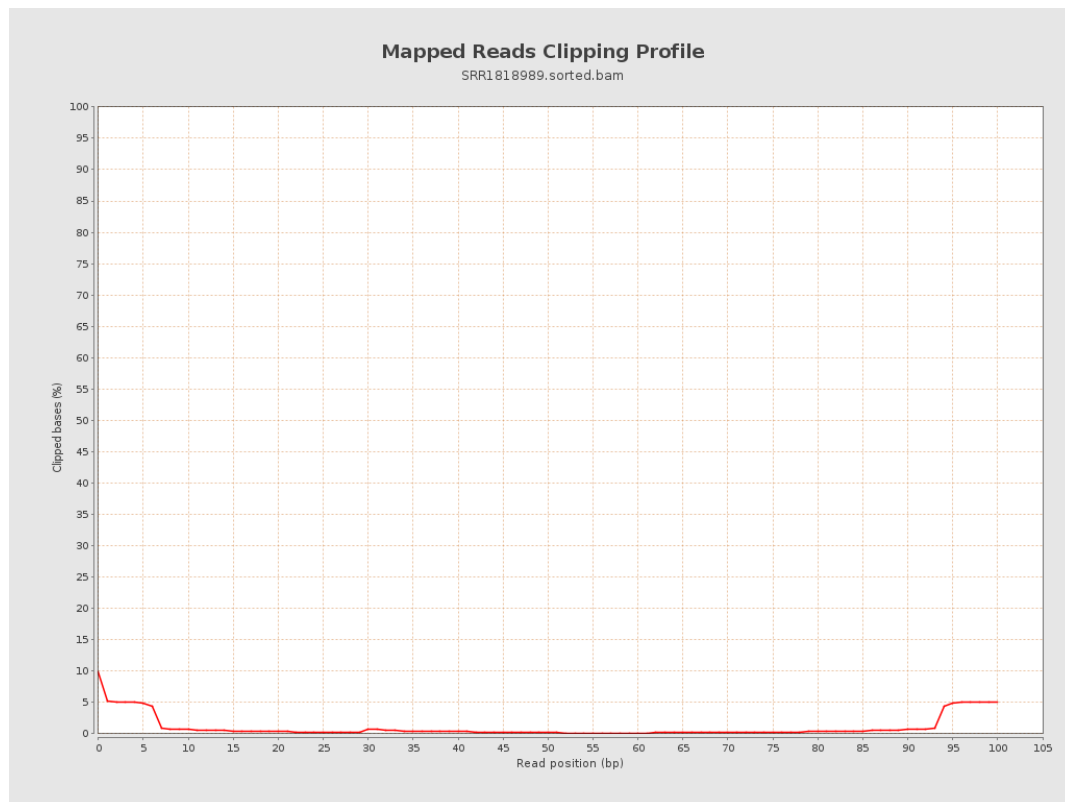
8. Results : Mapped Reads Nucleotide Content



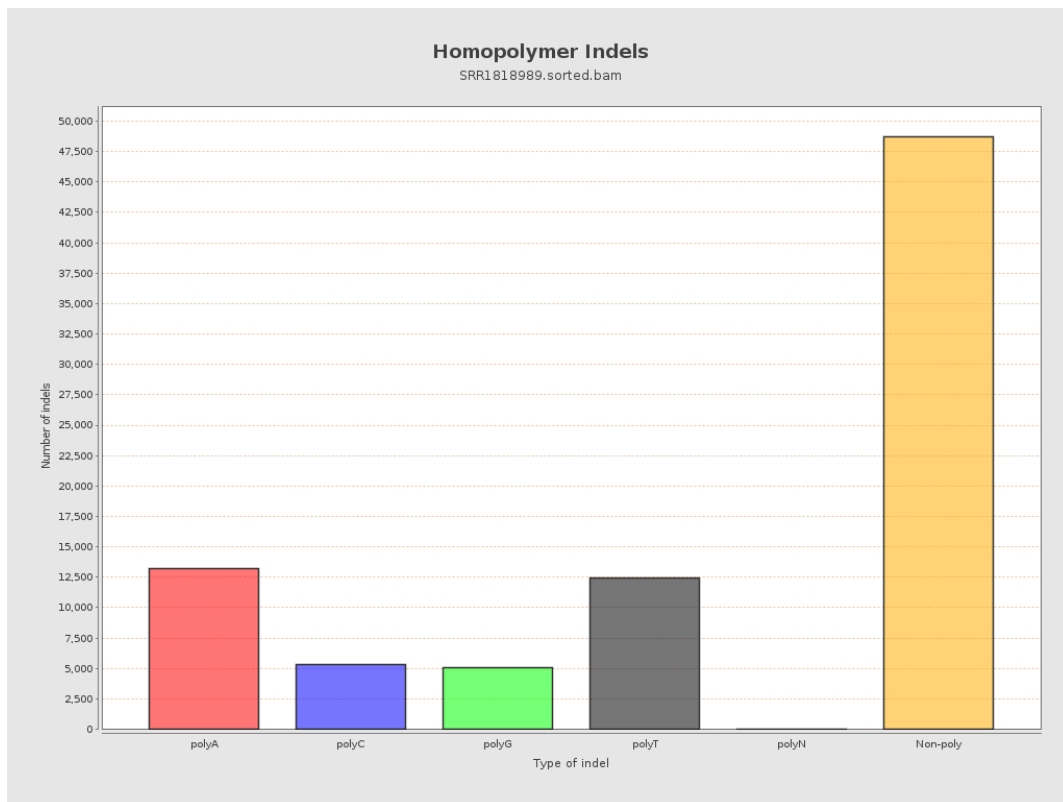
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

