

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:19:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818987.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_SRR1818987 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818987.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:19:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818987.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,728,964
Mapped reads	2,671,390 / 97.89%
Unmapped reads	57,574 / 2.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,070 / 1.58%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	1,584,824 / 58.07%
Duplication rate	48.29%
Clipped reads	2,695,531 / 98.77%

2.2. ACGT Content

Number/percentage of A's	72,733,732 / 29.45%
Number/percentage of C's	53,707,392 / 21.74%
Number/percentage of T's	70,035,299 / 28.36%
Number/percentage of G's	50,500,952 / 20.45%
Number/percentage of N's	12,489 / 0.01%
GC Percentage	42.19%

2.3. Coverage

Mean	0.0798

Standard Deviation	0.8842
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2.4. Mapping Quality

Mean Mapping Quality	49.37
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2.5. Mismatches and indels

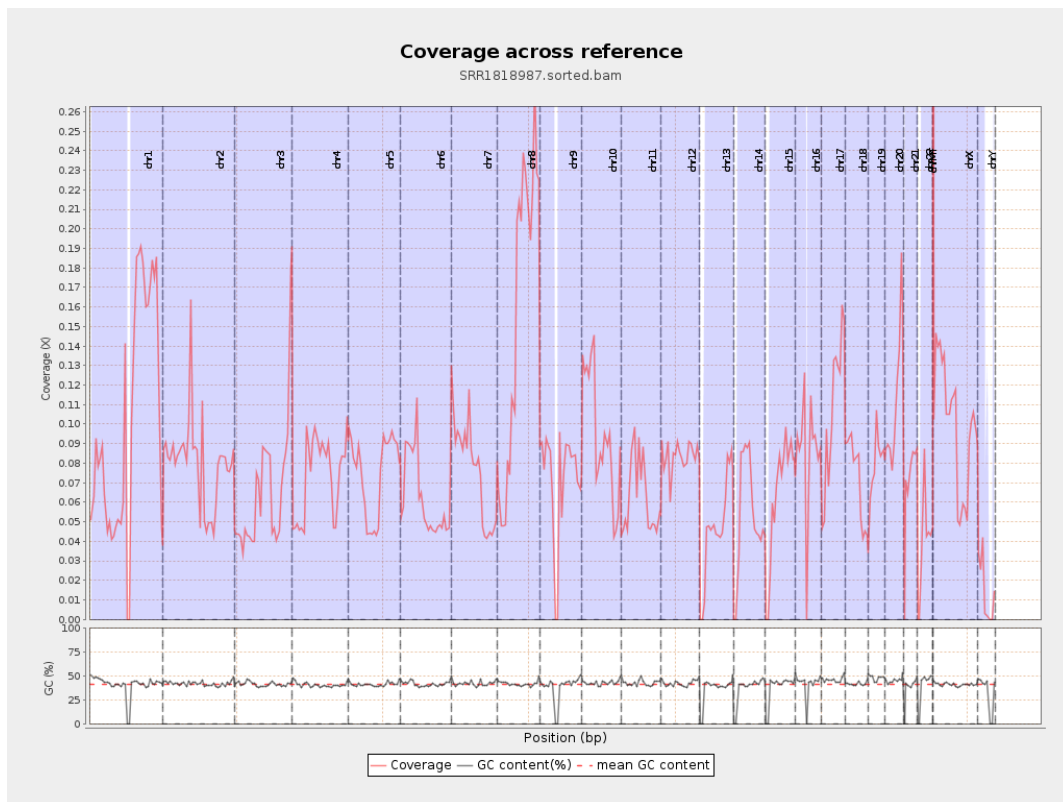
General error rate	0.66%
Mismatches	1,547,003
Insertions	36,650
Mapped reads with at least one insertion	1.34%
Deletions	81,699
Mapped reads with at least one deletion	2.99%
Homopolymer indels	43.1%

2.6. Chromosome stats

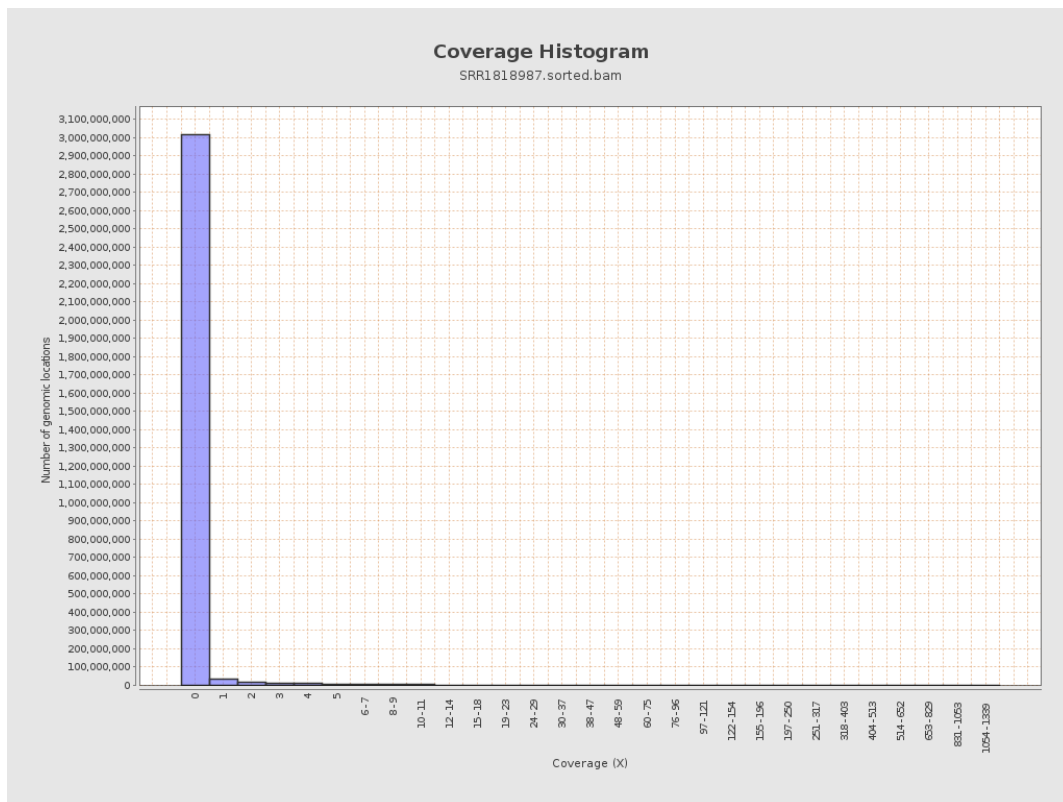
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25069570	0.1006	1.3947
chr2	243199373	19500563	0.0802	1.2641
chr3	198022430	12850767	0.0649	0.5836
chr4	191154276	14080592	0.0737	0.6818
chr5	180915260	13536641	0.0748	0.6441
chr6	171115067	10716435	0.0626	0.6578
chr7	159138663	12147369	0.0763	0.9047

chr8	146364022	23273488	0.159	1.0088
chr9	141213431	10138447	0.0718	0.8173
chr10	135534747	12713570	0.0938	0.9995
chr11	135006516	8407466	0.0623	0.6547
chr12	133851895	11221355	0.0838	0.6777
chr13	115169878	5445860	0.0473	0.4986
chr14	107349540	5850961	0.0545	0.5496
chr15	102531392	6400202	0.0624	0.581
chr16	90354753	7643127	0.0846	1.0095
chr17	81195210	8699187	0.1071	0.8299
chr18	78077248	5671532	0.0726	0.9021
chr19	59128983	4706146	0.0796	1.213
chr20	63025520	7145868	0.1134	0.8433
chr21	48129895	3418985	0.071	0.6824
chr22	51304566	1999693	0.039	0.4876
chrMT	16571	37853	2.2843	3.9072
chrX	155270560	15607719	0.1005	0.7912
chrY	59373566	849448	0.0143	0.8199

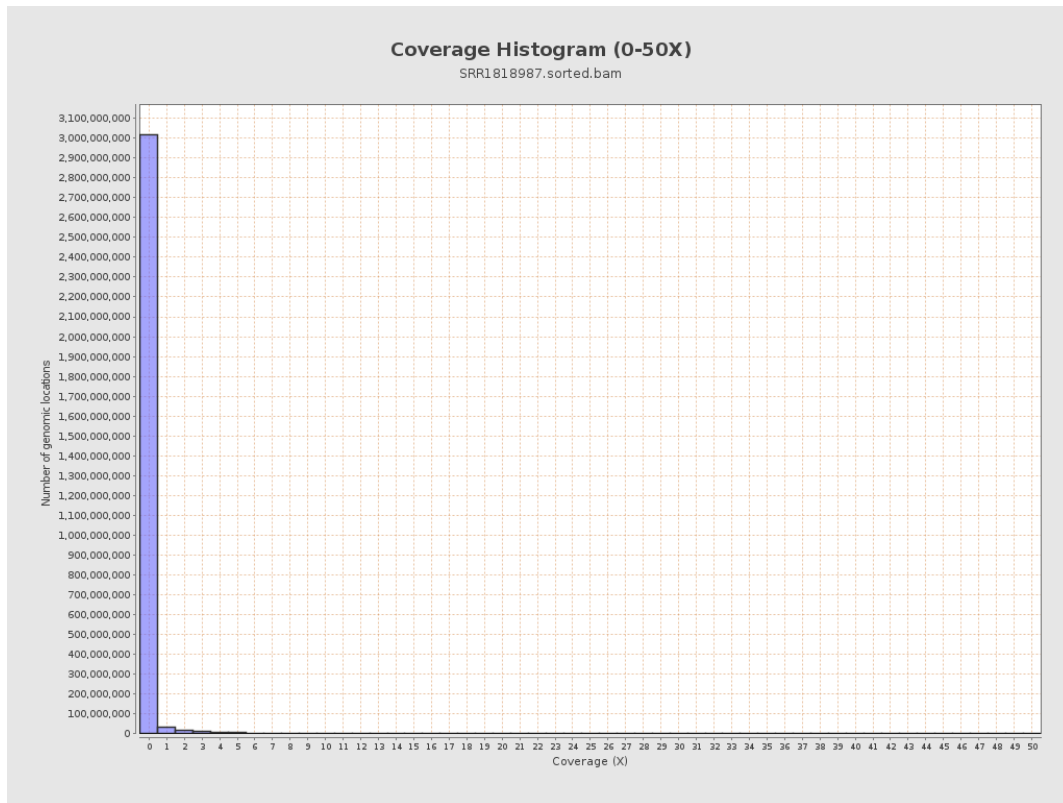
3. Results : Coverage across reference



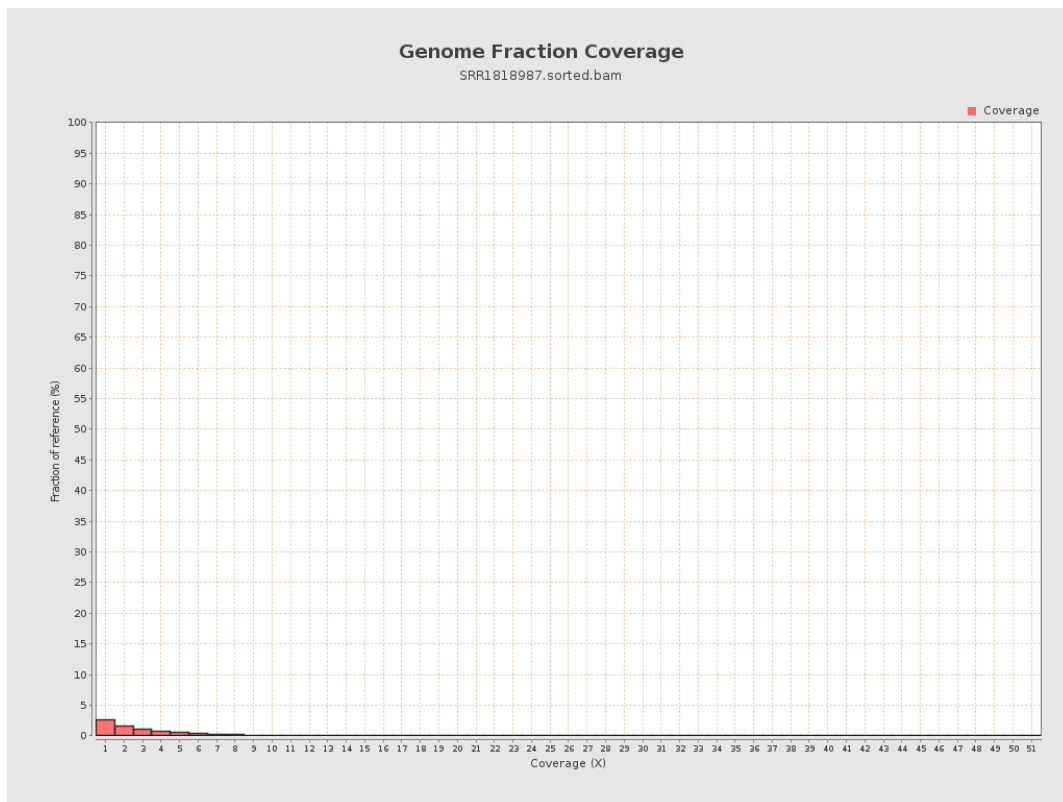
4. Results : Coverage Histogram



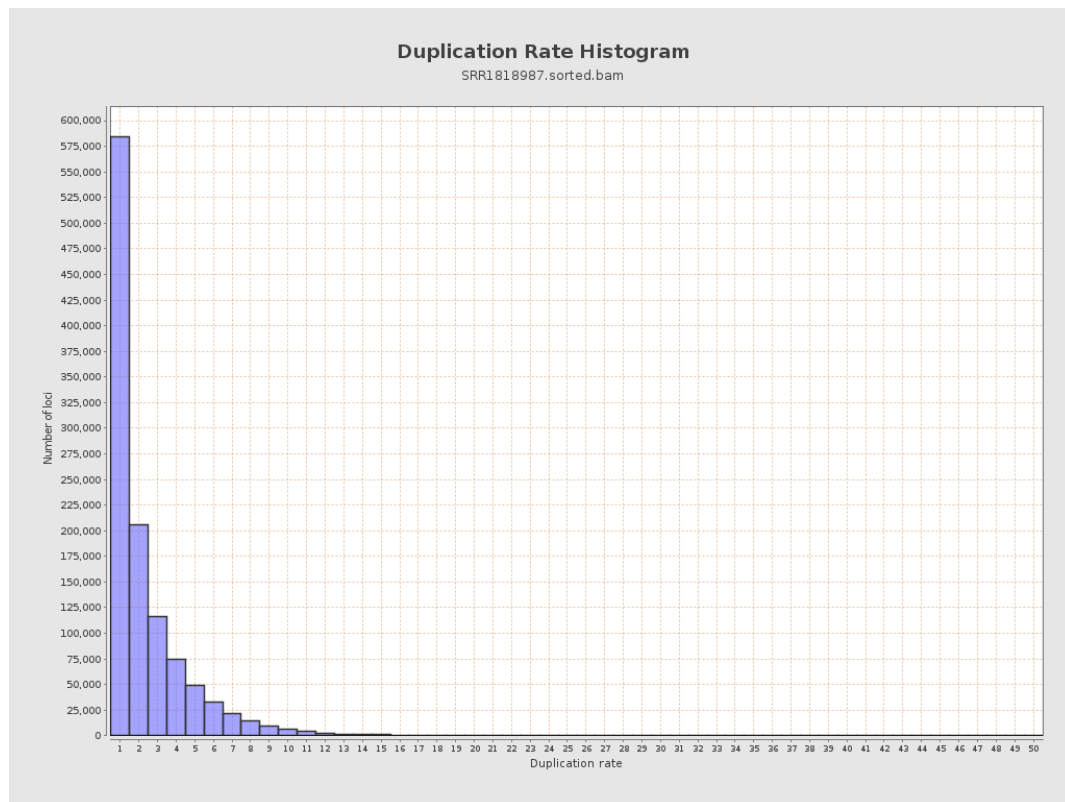
5. Results : Coverage Histogram (0-50X)



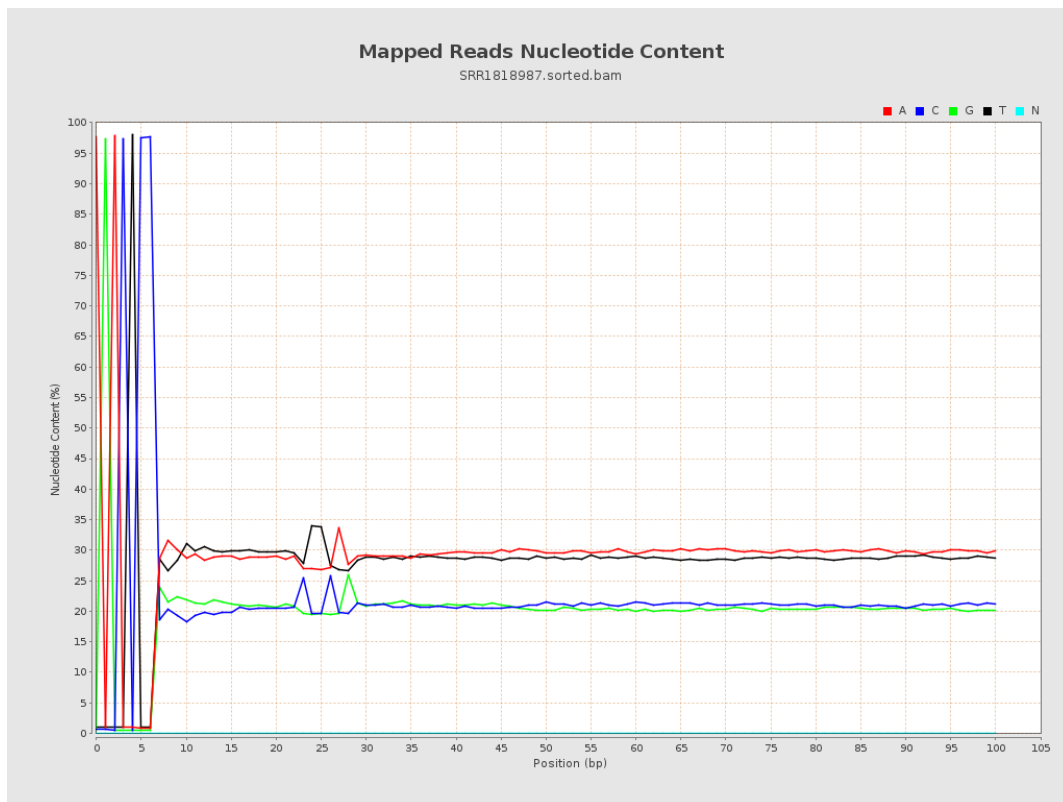
6. Results : Genome Fraction Coverage



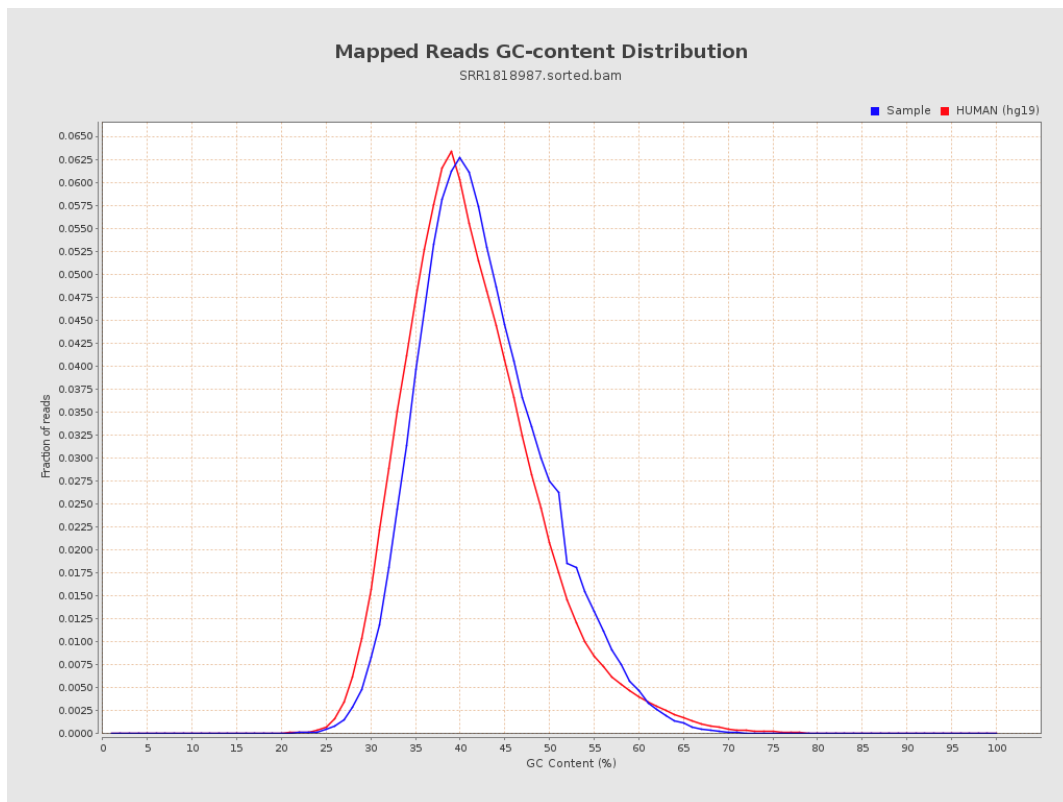
7. Results : Duplication Rate Histogram



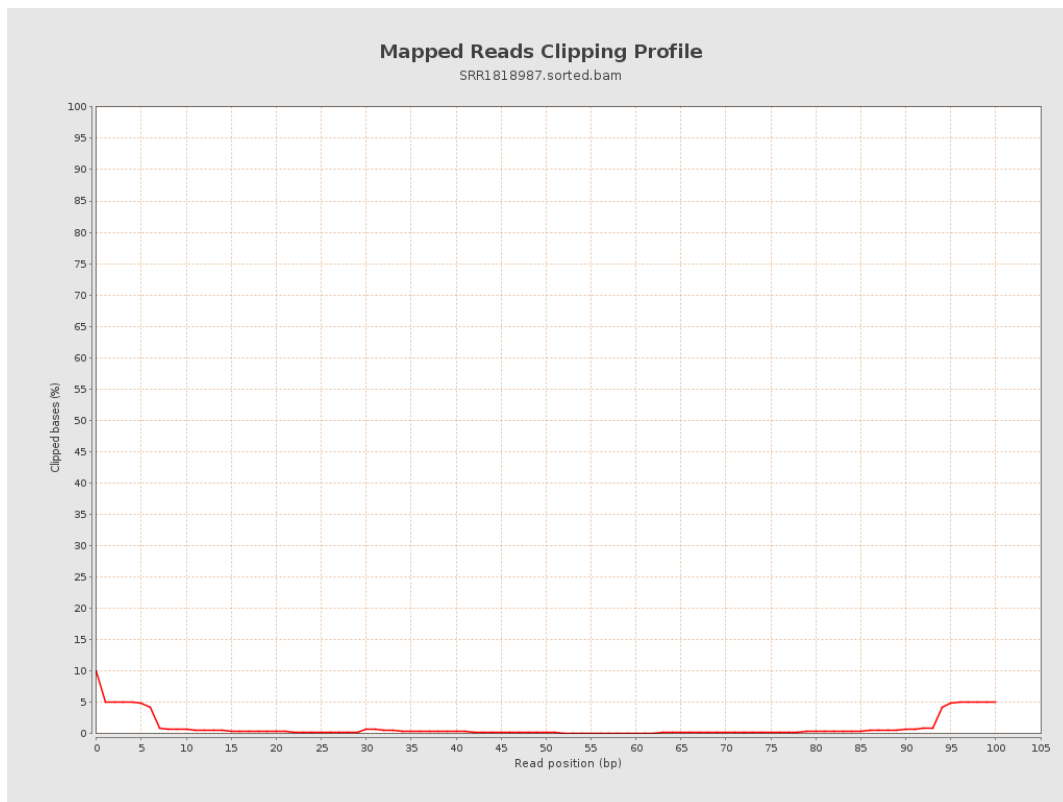
8. Results : Mapped Reads Nucleotide Content



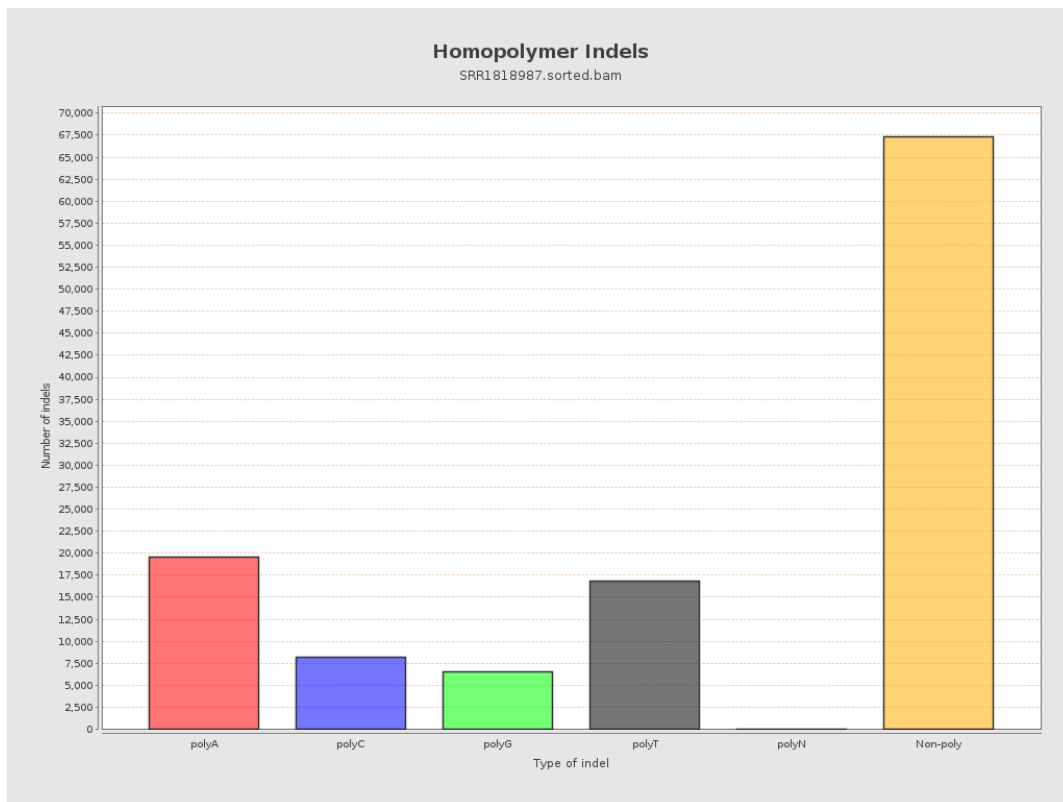
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

