

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:38:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818745.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_SRR1818745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818745.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:38:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,258,692
Mapped reads	2,206,765 / 97.7%
Unmapped reads	51,927 / 2.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,585 / 0.78%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,082,269 / 47.92%
Duplication rate	42.46%
Clipped reads	2,202,701 / 97.52%

2.2. ACGT Content

Number/percentage of A's	42,545,012 / 28.39%
Number/percentage of C's	31,385,846 / 20.94%
Number/percentage of T's	43,567,062 / 29.07%
Number/percentage of G's	32,367,124 / 21.6%
Number/percentage of N's	9,317 / 0.01%
GC Percentage	42.54%

2.3. Coverage

Mean	0.0484

Standard Deviation	0.5811
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2.4. Mapping Quality

Mean Mapping Quality	47.8
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2.5. Mismatches and indels

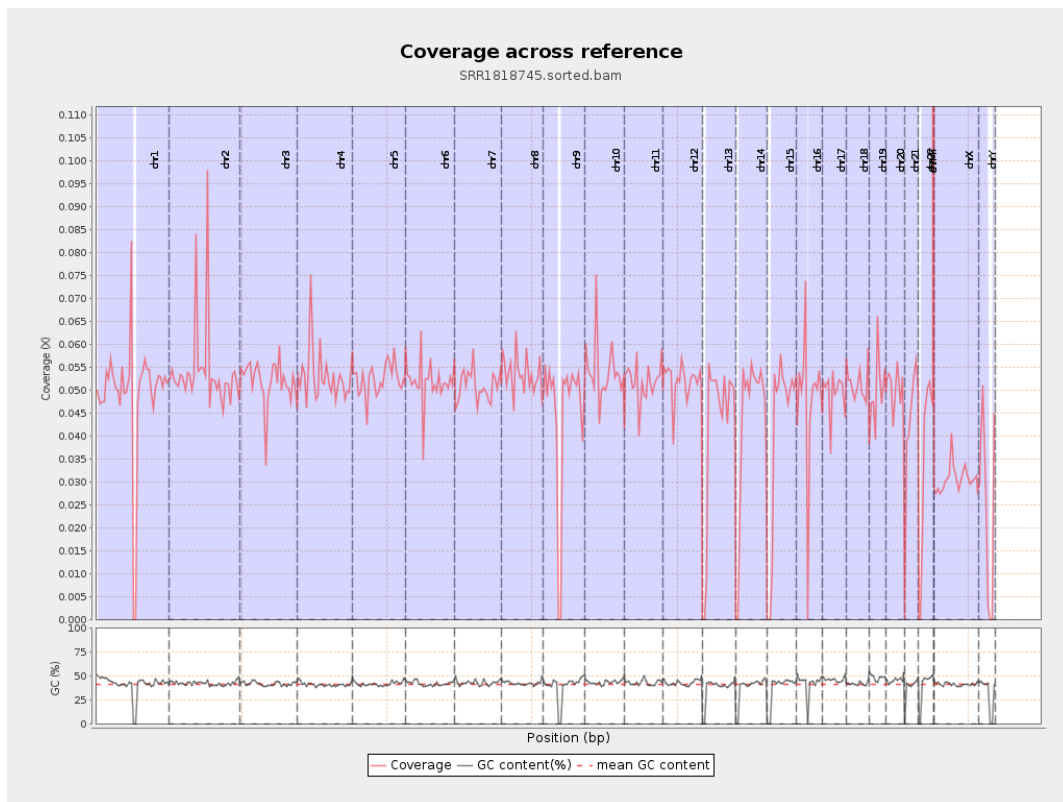
General error rate	0.52%
Mismatches	750,457
Insertions	17,187
Mapped reads with at least one insertion	0.77%
Deletions	38,840
Mapped reads with at least one deletion	1.74%
Homopolymer indels	41.71%

2.6. Chromosome stats

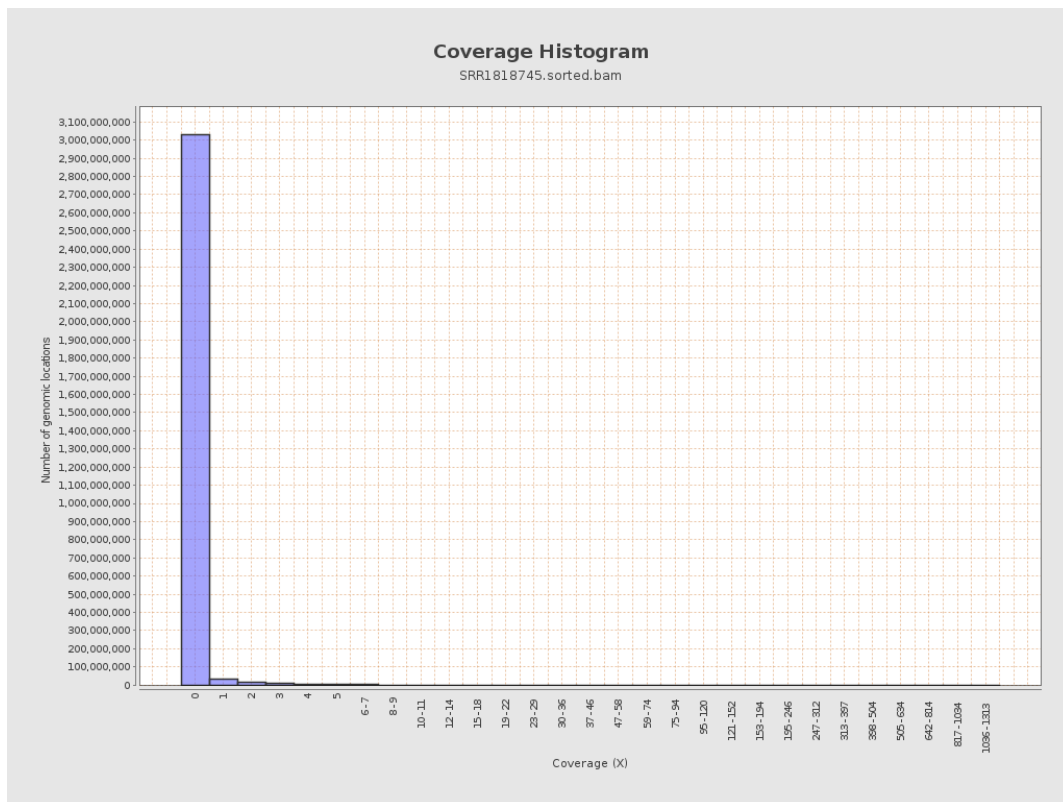
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12257641	0.0492	0.8481
chr2	243199373	13179970	0.0542	0.9089
chr3	198022430	10295726	0.052	0.4386
chr4	191154276	10097902	0.0528	0.5115
chr5	180915260	9478834	0.0524	0.4551
chr6	171115067	8874412	0.0519	0.4798
chr7	159138663	8108070	0.0509	0.5146

chr8	146364022	7842971	0.0536	0.503
chr9	141213431	6330727	0.0448	0.4813
chr10	135534747	7309325	0.0539	0.6003
chr11	135006516	6990013	0.0518	0.4907
chr12	133851895	6944177	0.0519	0.4952
chr13	115169878	4814952	0.0418	0.3909
chr14	107349540	4655060	0.0434	0.444
chr15	102531392	4227723	0.0412	0.3912
chr16	90354753	4333938	0.048	0.6043
chr17	81195210	3993611	0.0492	0.4483
chr18	78077248	4000649	0.0512	0.6536
chr19	59128983	2967085	0.0502	0.7099
chr20	63025520	3159752	0.0501	0.4499
chr21	48129895	2062763	0.0429	0.4164
chr22	51304566	1737139	0.0339	0.376
chrMT	16571	68598	4.1396	4.4211
chrX	155270560	4774365	0.0307	0.3809
chrY	59373566	1430191	0.0241	0.9661

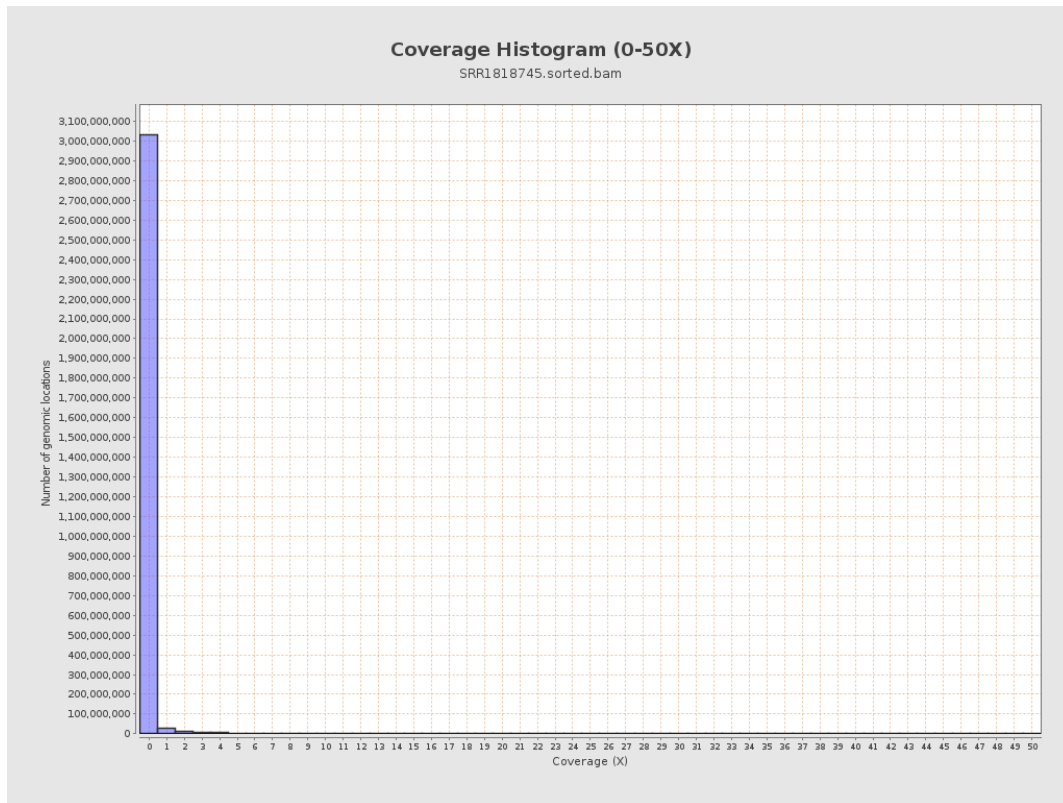
3. Results : Coverage across reference



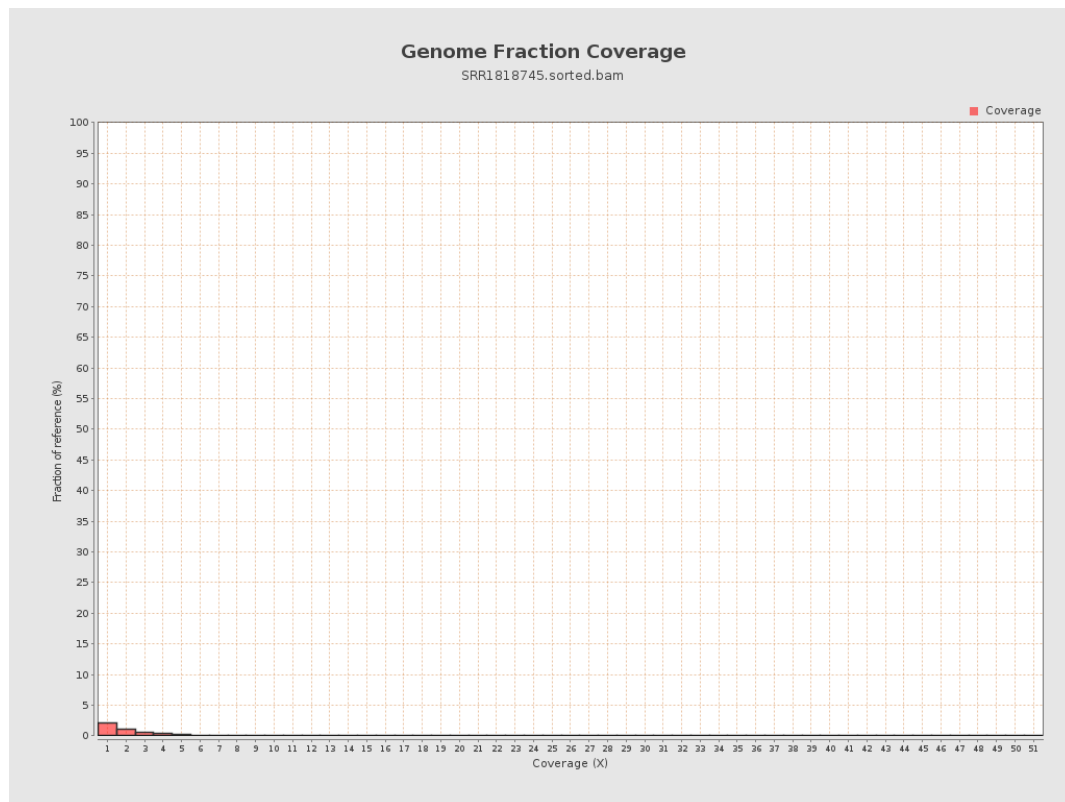
4. Results : Coverage Histogram



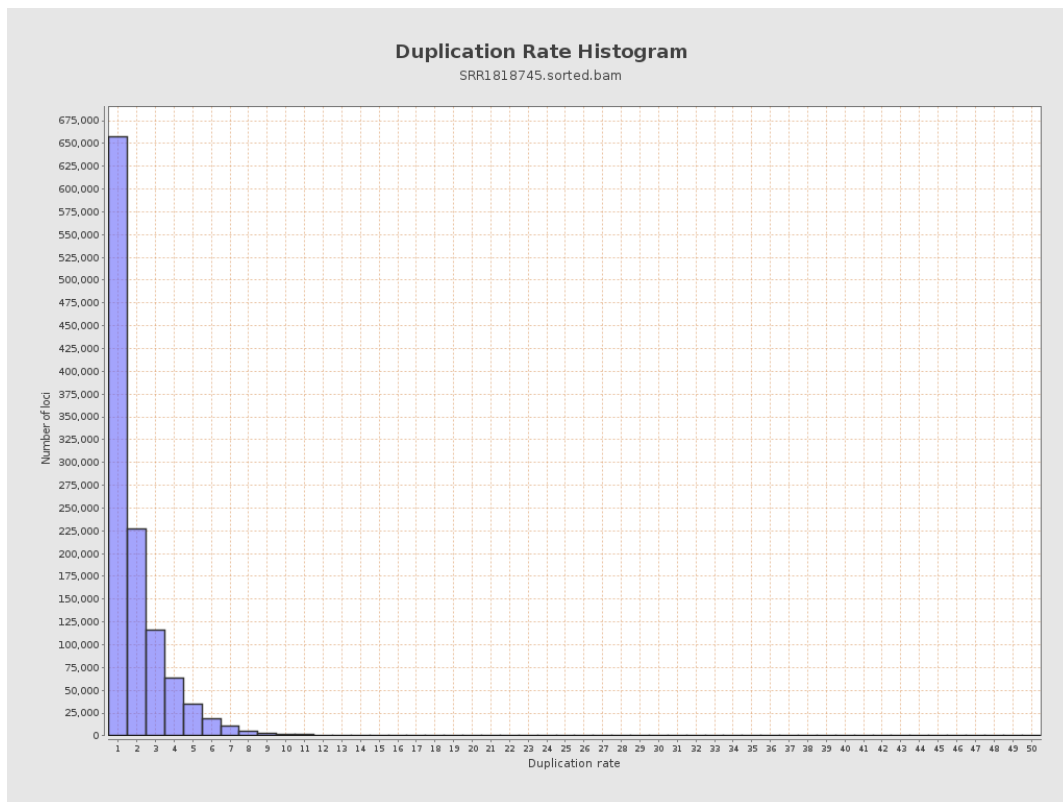
5. Results : Coverage Histogram (0-50X)



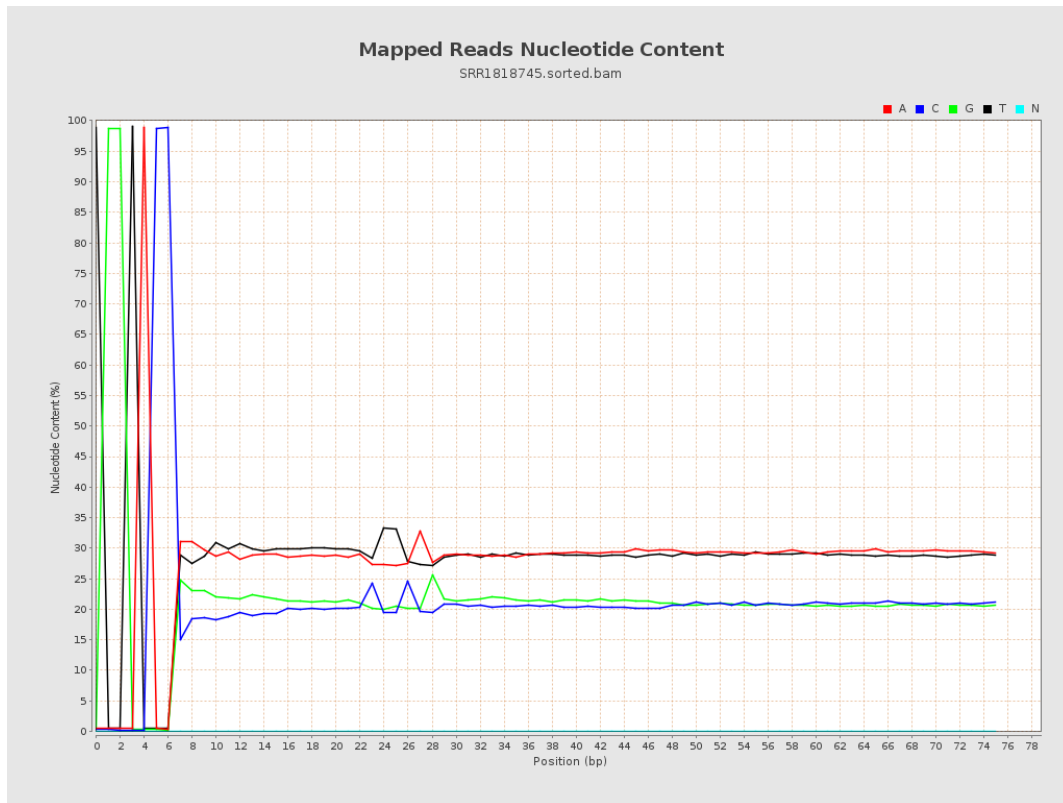
6. Results : Genome Fraction Coverage



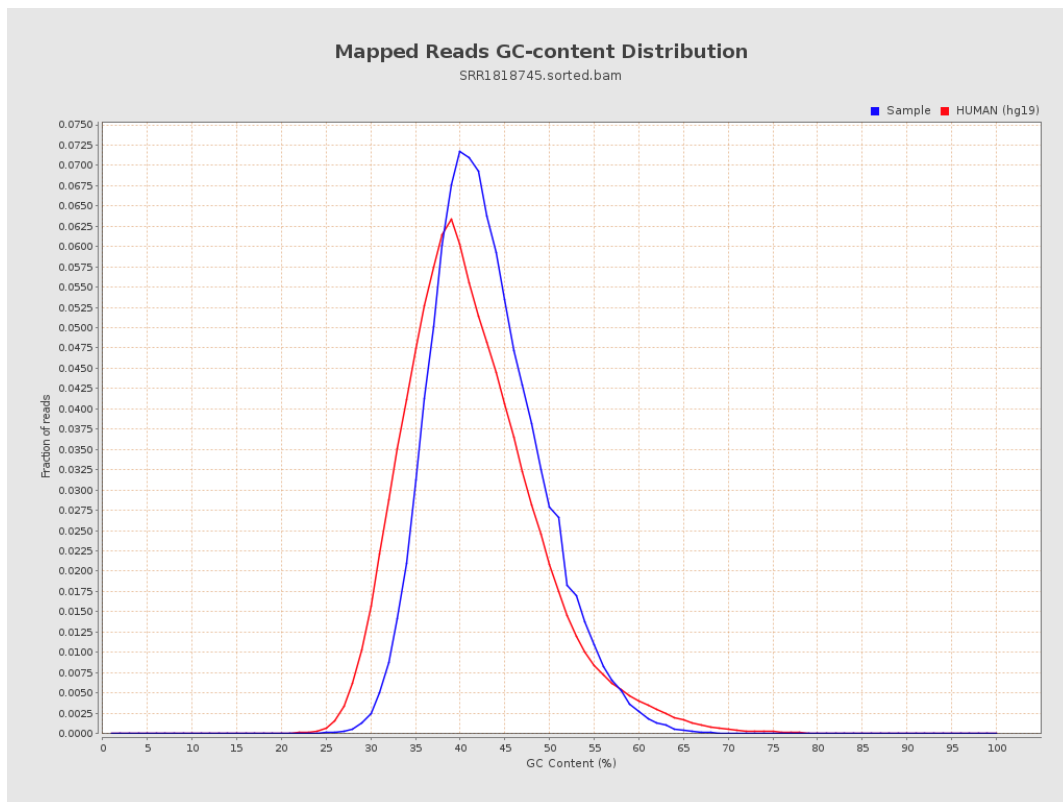
7. Results : Duplication Rate Histogram



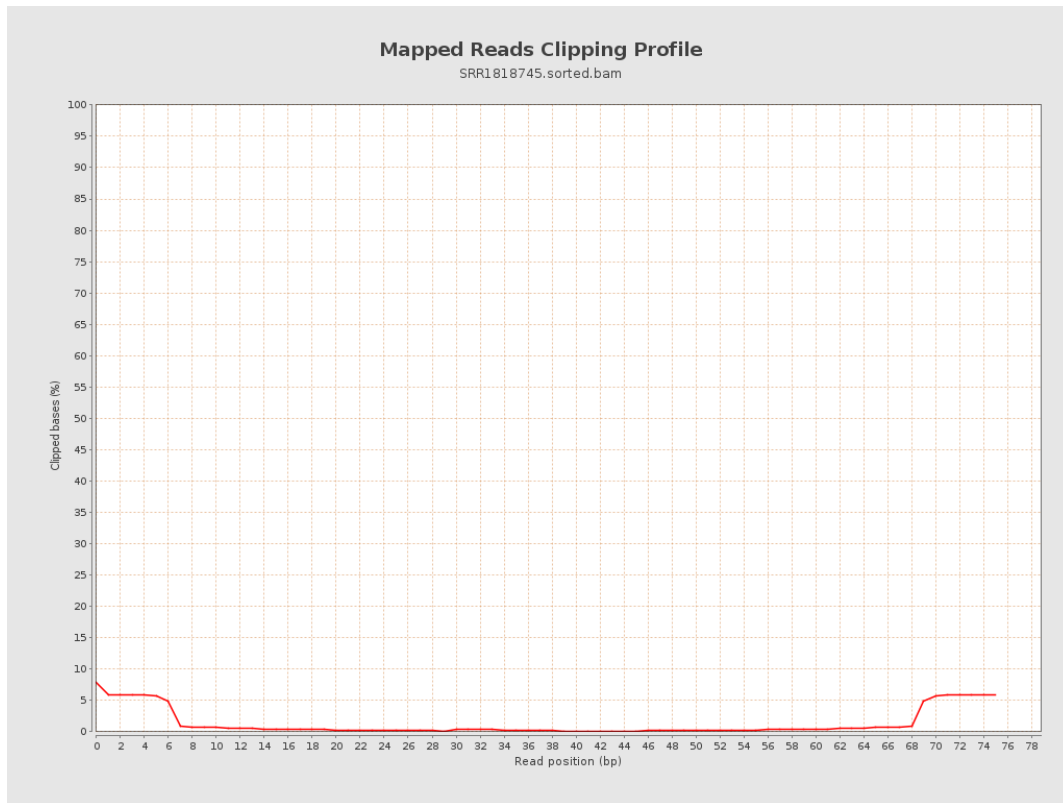
8. Results : Mapped Reads Nucleotide Content



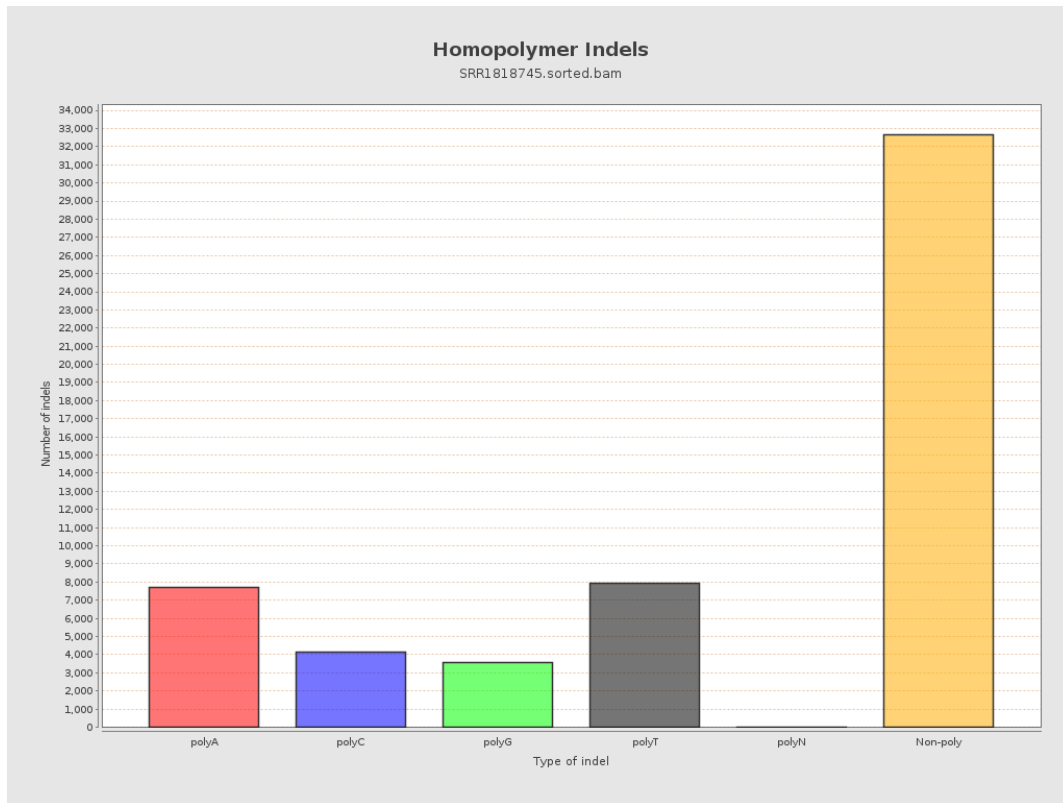
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

