

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:00:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506010.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_SRR1506010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506010.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:59:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,020,345
Mapped reads	4,428,216 / 73.55%
Unmapped reads	1,592,129 / 26.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	261 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	449,948 / 7.47%
Duplication rate	7.66%
Clipped reads	511,383 / 8.49%

2.2. ACGT Content

Number/percentage of A's	60,279,462 / 29.02%
Number/percentage of C's	43,868,453 / 21.12%
Number/percentage of T's	59,558,663 / 28.67%
Number/percentage of G's	44,019,456 / 21.19%
Number/percentage of N's	884 / 0%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0671

Standard Deviation	0.6035
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2.4. Mapping Quality

Mean Mapping Quality	44.15
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2.5. Mismatches and indels

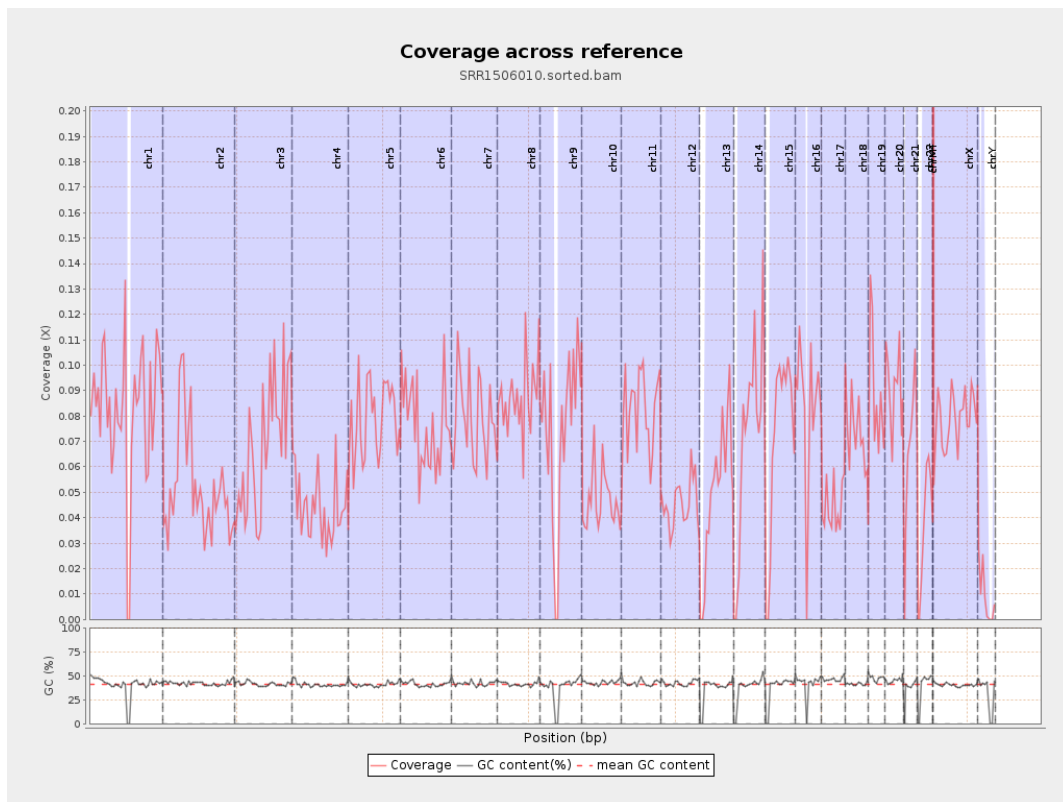
General error rate	0.49%
Mismatches	1,014,272
Insertions	8,999
Mapped reads with at least one insertion	0.2%
Deletions	31,127
Mapped reads with at least one deletion	0.7%
Homopolymer indels	45.99%

2.6. Chromosome stats

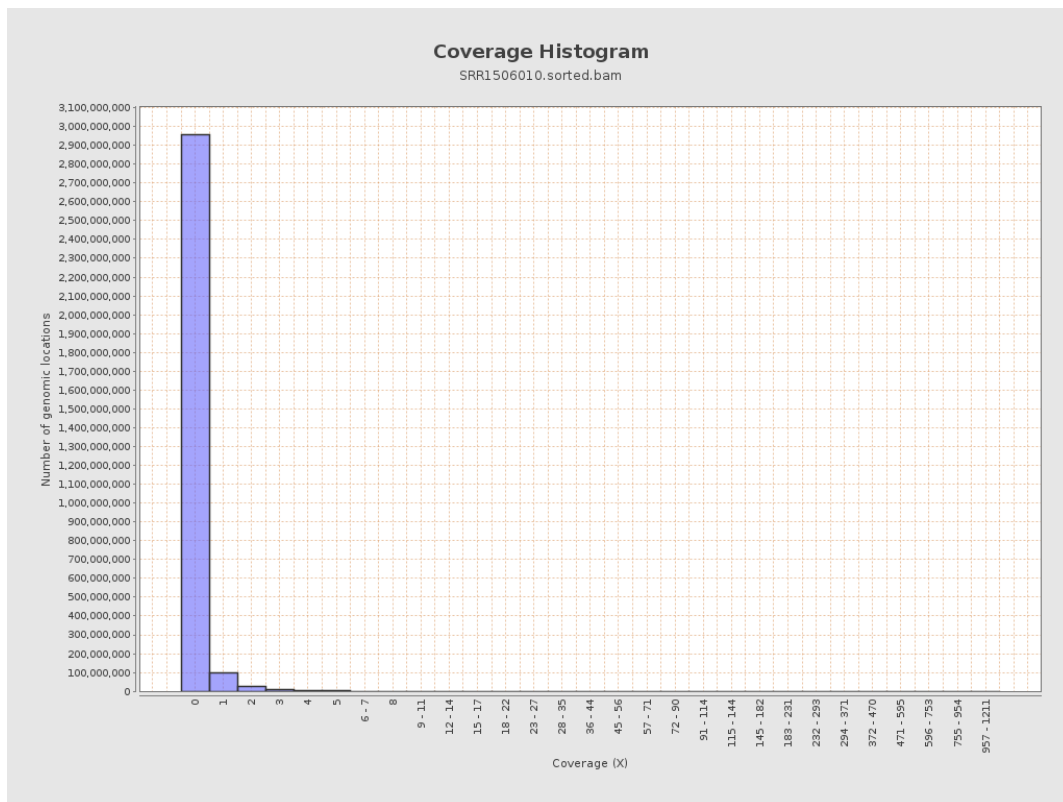
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20451121	0.0821	0.9092
chr2	243199373	12700582	0.0522	0.4527
chr3	198022430	13297986	0.0672	0.3635
chr4	191154276	8421976	0.0441	0.2981
chr5	180915260	14258767	0.0788	0.3988
chr6	171115067	13016464	0.0761	0.4527
chr7	159138663	12584654	0.0791	0.7267

chr8	146364022	12736992	0.087	0.7316
chr9	141213431	10363168	0.0734	0.4552
chr10	135534747	6320903	0.0466	0.4533
chr11	135006516	11072293	0.082	0.4865
chr12	133851895	6173396	0.0461	0.3077
chr13	115169878	5812762	0.0505	0.3141
chr14	107349540	7794065	0.0726	1.7502
chr15	102531392	7195599	0.0702	0.3741
chr16	90354753	7476495	0.0827	0.426
chr17	81195210	3587016	0.0442	0.3155
chr18	78077248	5726804	0.0733	0.6652
chr19	59128983	5181746	0.0876	0.7404
chr20	63025520	5695013	0.0904	0.4462
chr21	48129895	3168296	0.0658	0.3798
chr22	51304566	1931646	0.0377	0.2708
chrMT	16571	30509	1.8411	1.9654
chrX	155270560	12236816	0.0788	0.4332
chrY	59373566	535714	0.009	0.1444

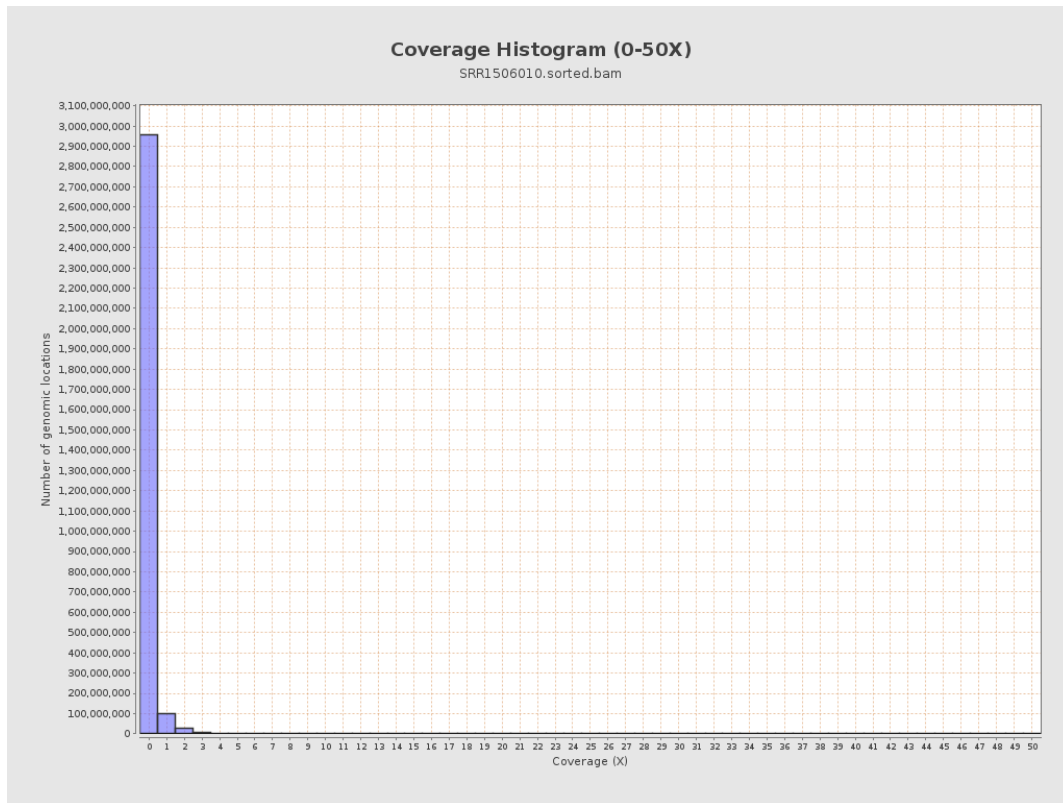
3. Results : Coverage across reference



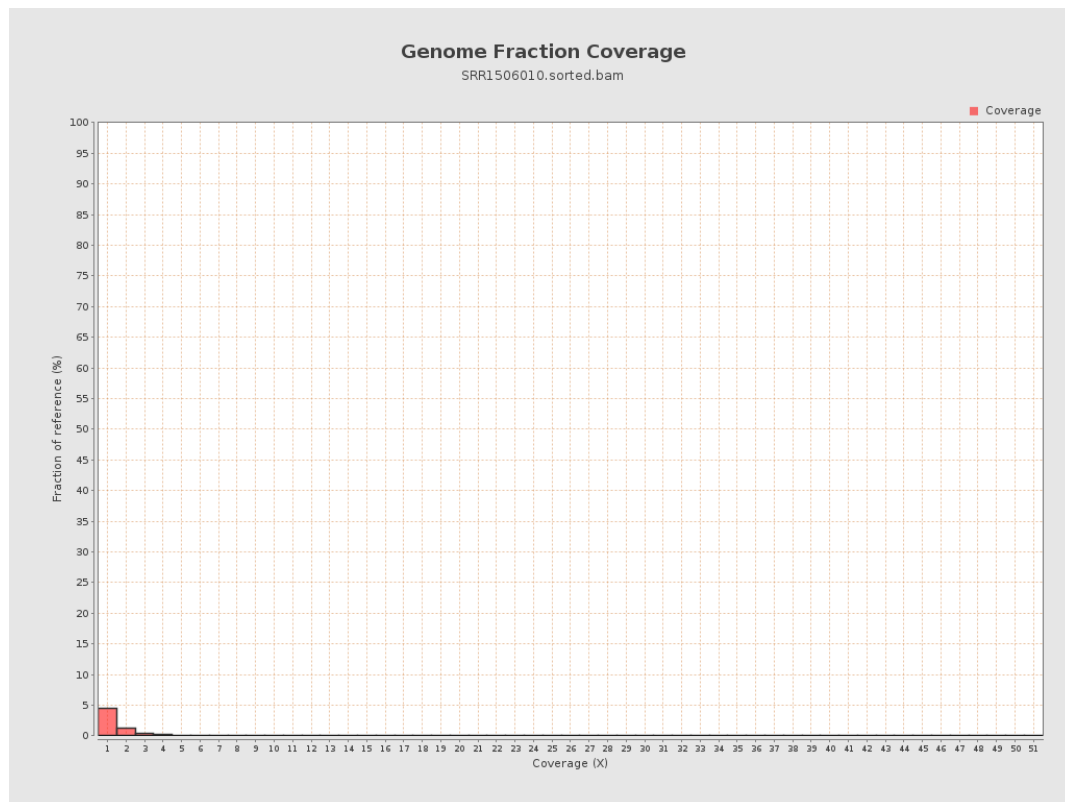
4. Results : Coverage Histogram



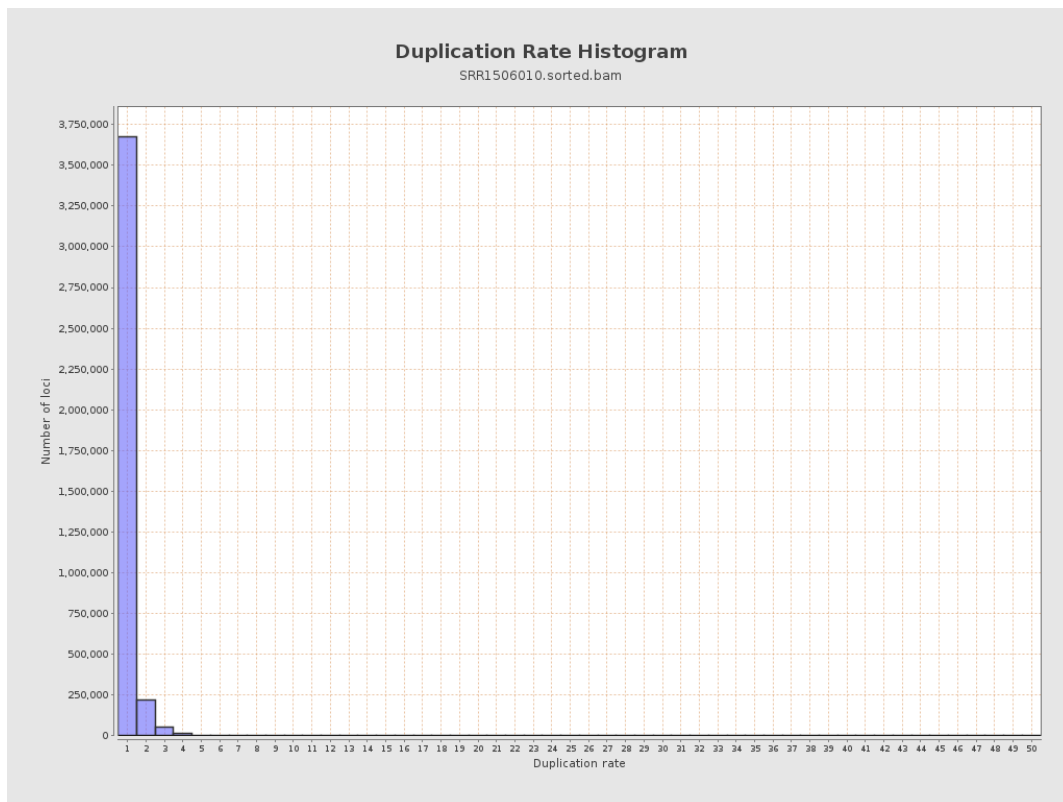
5. Results : Coverage Histogram (0-50X)



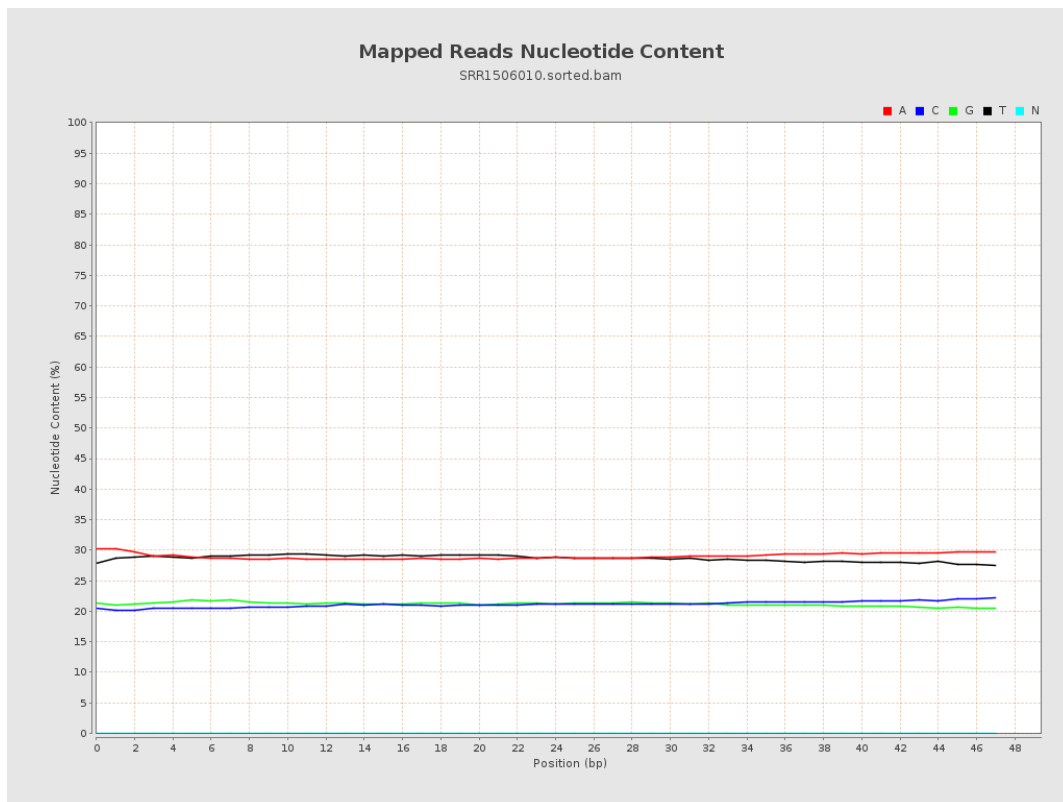
6. Results : Genome Fraction Coverage



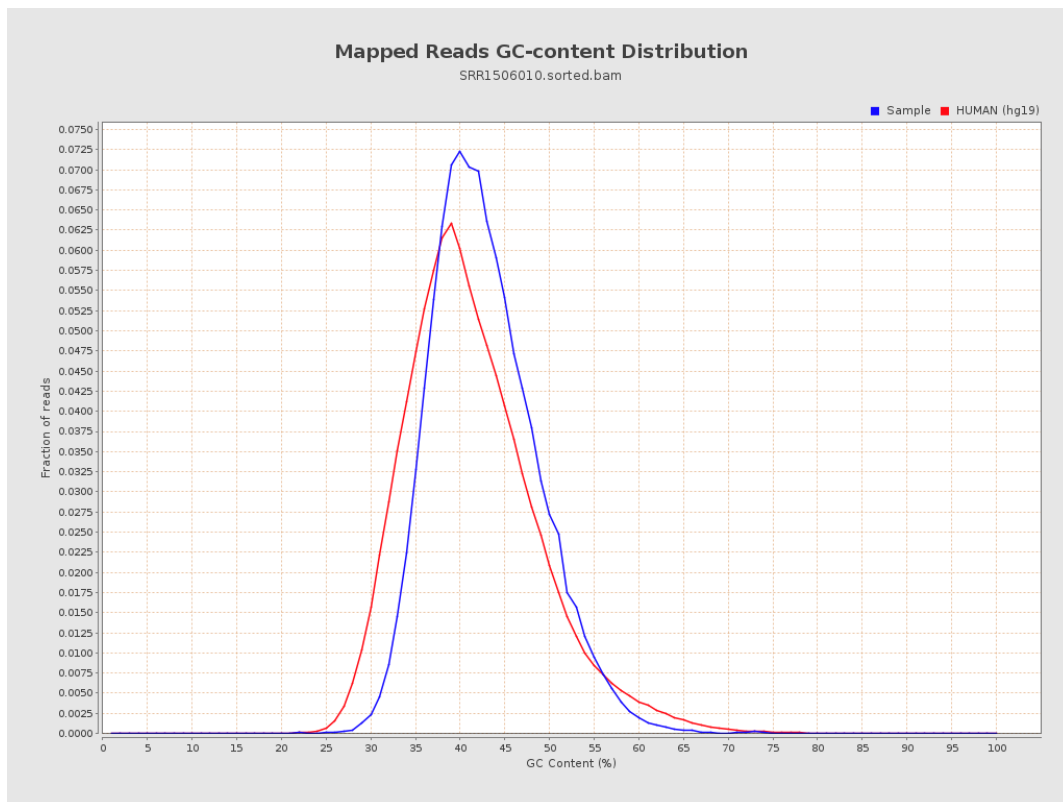
7. Results : Duplication Rate Histogram



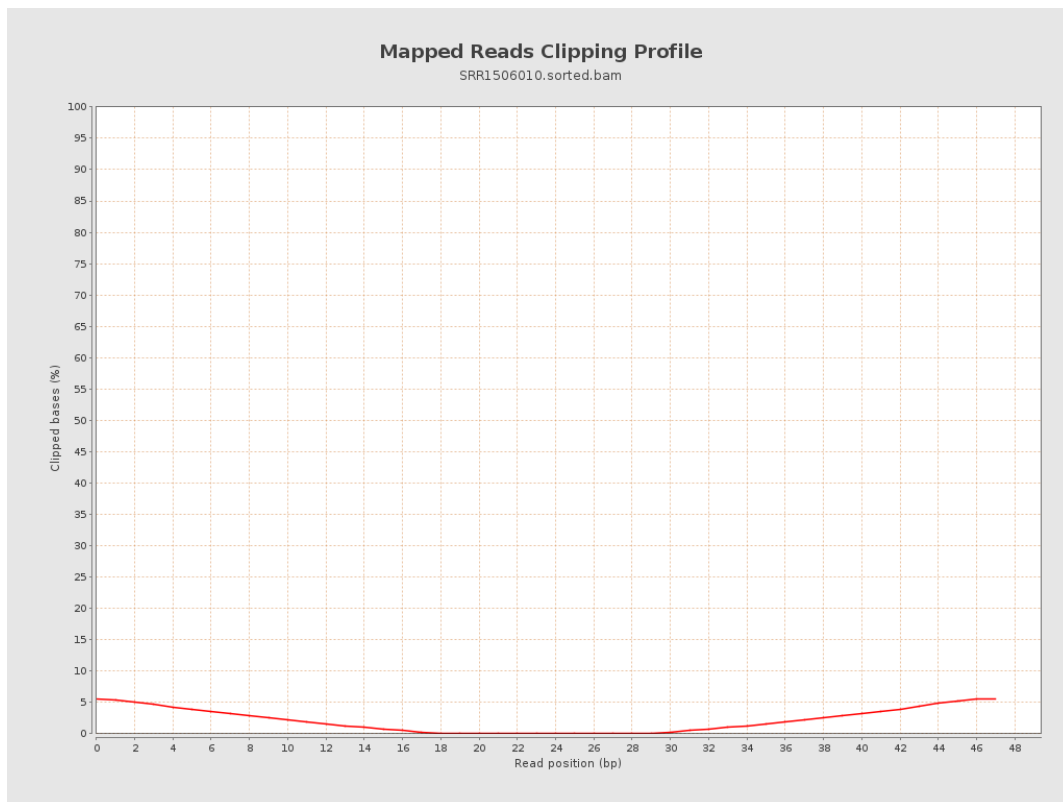
8. Results : Mapped Reads Nucleotide Content



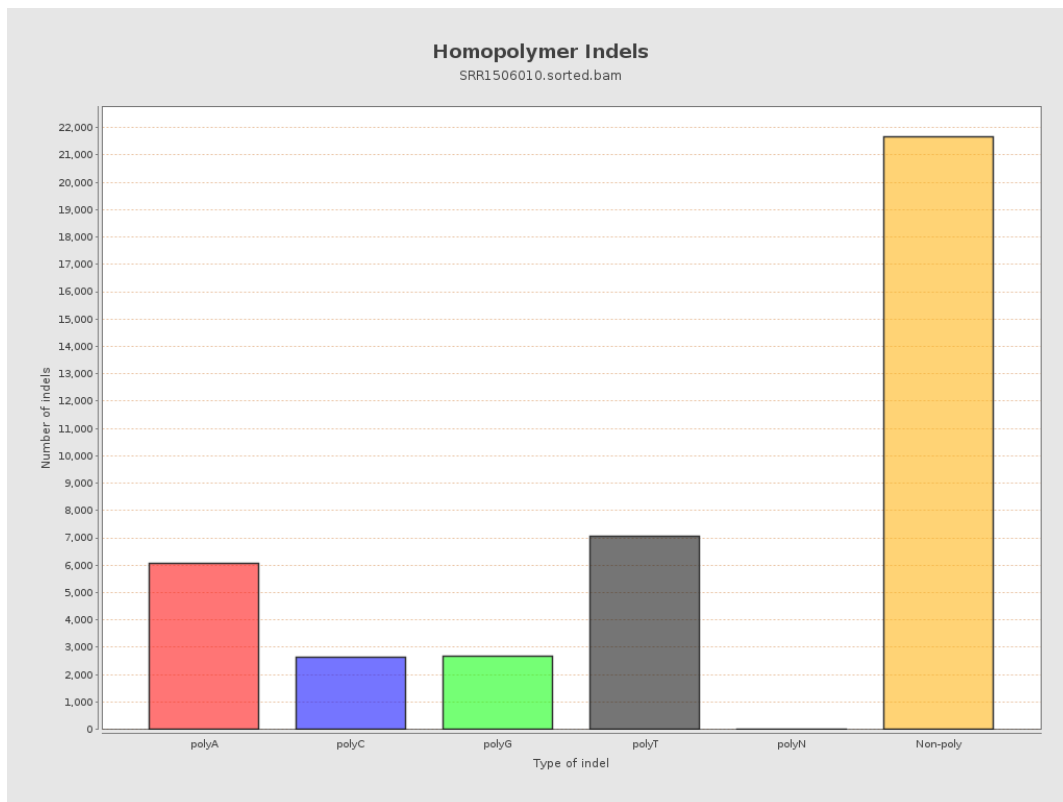
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

