

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:40:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080763.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_SRR3080763 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080763.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:40:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080763.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,422,520
Mapped reads	3,869,331 / 71.36%
Unmapped reads	1,553,189 / 28.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,461 / 0.56%
Read min/max/mean length	30 / 66 / 66.19
Duplicated reads (estimated)	440,382 / 8.12%
Duplication rate	9.06%
Clipped reads	633,775 / 11.69%

2.2. ACGT Content

Number/percentage of A's	72,198,676 / 29.31%
Number/percentage of C's	50,653,378 / 20.57%
Number/percentage of T's	69,489,984 / 28.21%
Number/percentage of G's	53,871,719 / 21.87%
Number/percentage of N's	77,216 / 0.03%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0796

Standard Deviation	0.5714
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2.4. Mapping Quality

Mean Mapping Quality	44.71
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2.5. Mismatches and indels

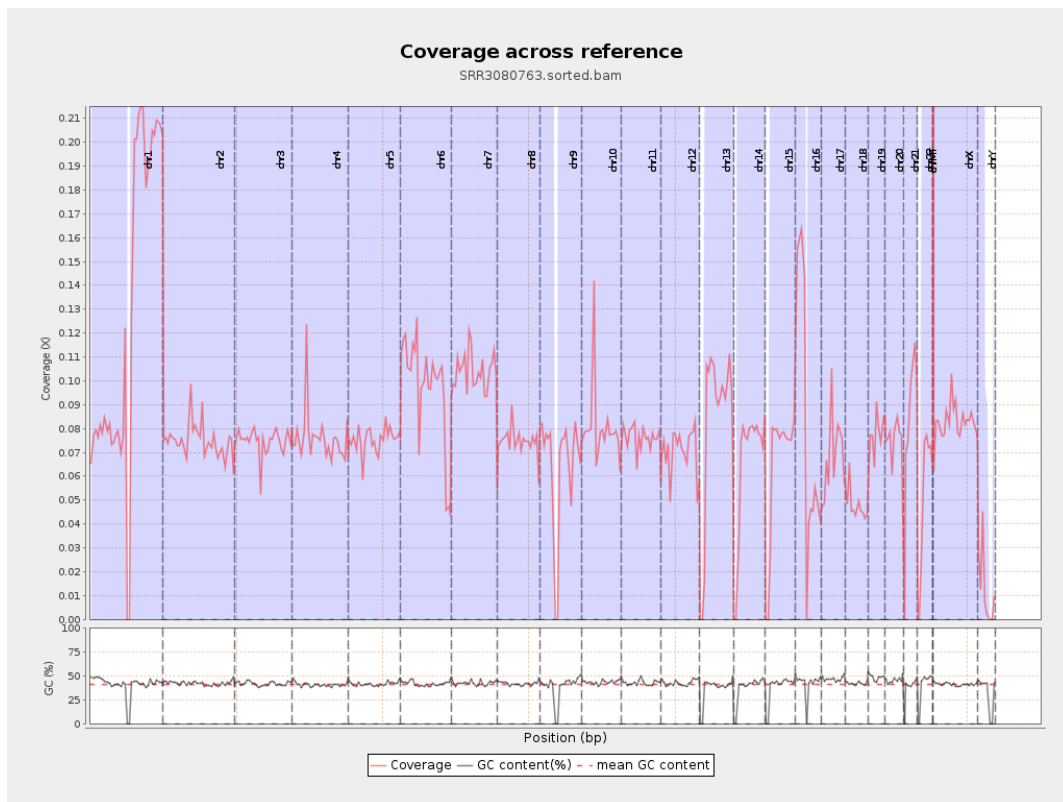
General error rate	0.88%
Mismatches	2,124,102
Insertions	18,623
Mapped reads with at least one insertion	0.48%
Deletions	46,525
Mapped reads with at least one deletion	1.19%
Homopolymer indels	43.54%

2.6. Chromosome stats

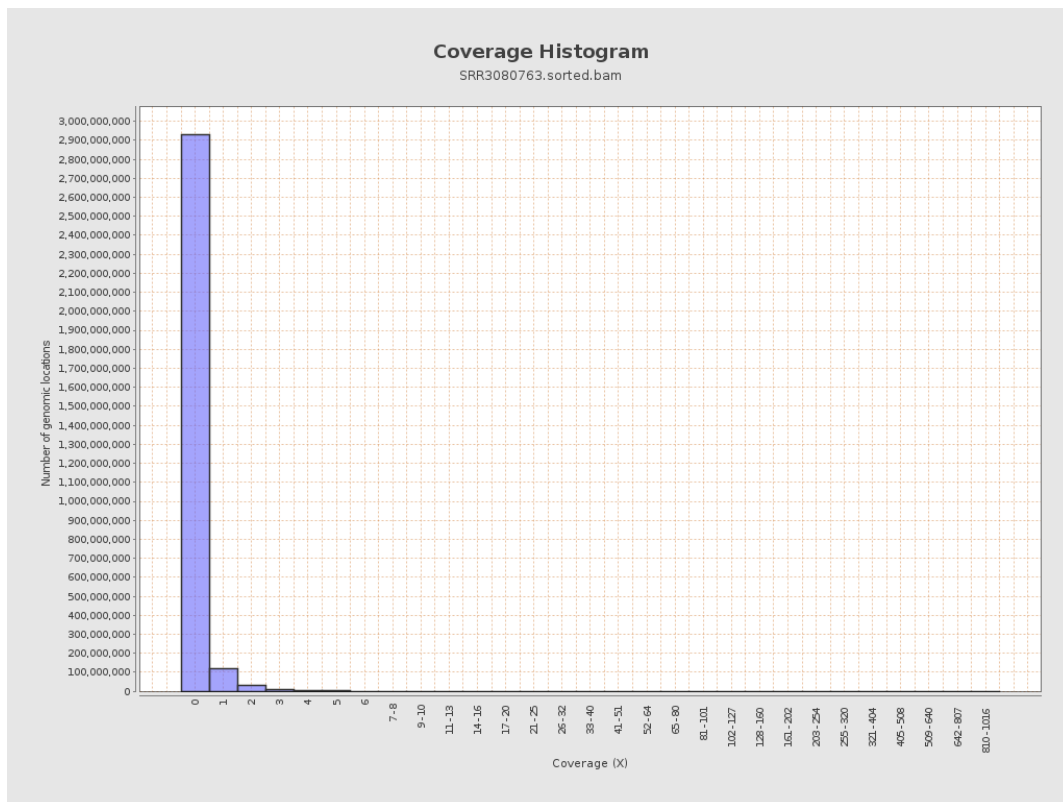
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	31606950	0.1268	0.9633
chr2	243199373	18277636	0.0752	0.5007
chr3	198022430	14779308	0.0746	0.3796
chr4	191154276	14583565	0.0763	0.4461
chr5	180915260	13623167	0.0753	0.3804
chr6	171115067	16815537	0.0983	0.644
chr7	159138663	16569897	0.1041	0.7825

chr8	146364022	10926046	0.0746	0.6565
chr9	141213431	9019820	0.0639	0.4616
chr10	135534747	10860063	0.0801	0.6871
chr11	135006516	10279394	0.0761	0.5269
chr12	133851895	9506753	0.071	0.383
chr13	115169878	9574101	0.0831	0.4045
chr14	107349540	6964825	0.0649	0.4161
chr15	102531392	6484893	0.0632	0.3505
chr16	90354753	7493692	0.0829	0.4404
chr17	81195210	5581278	0.0687	0.3838
chr18	78077248	3755902	0.0481	0.8322
chr19	59128983	4588436	0.0776	0.8427
chr20	63025520	4719440	0.0749	0.4054
chr21	48129895	4089799	0.085	0.4852
chr22	51304566	2609171	0.0509	0.3251
chrMT	16571	67969	4.1017	3.7091
chrX	155270560	12858697	0.0828	0.4431
chrY	59373566	740232	0.0125	0.3707

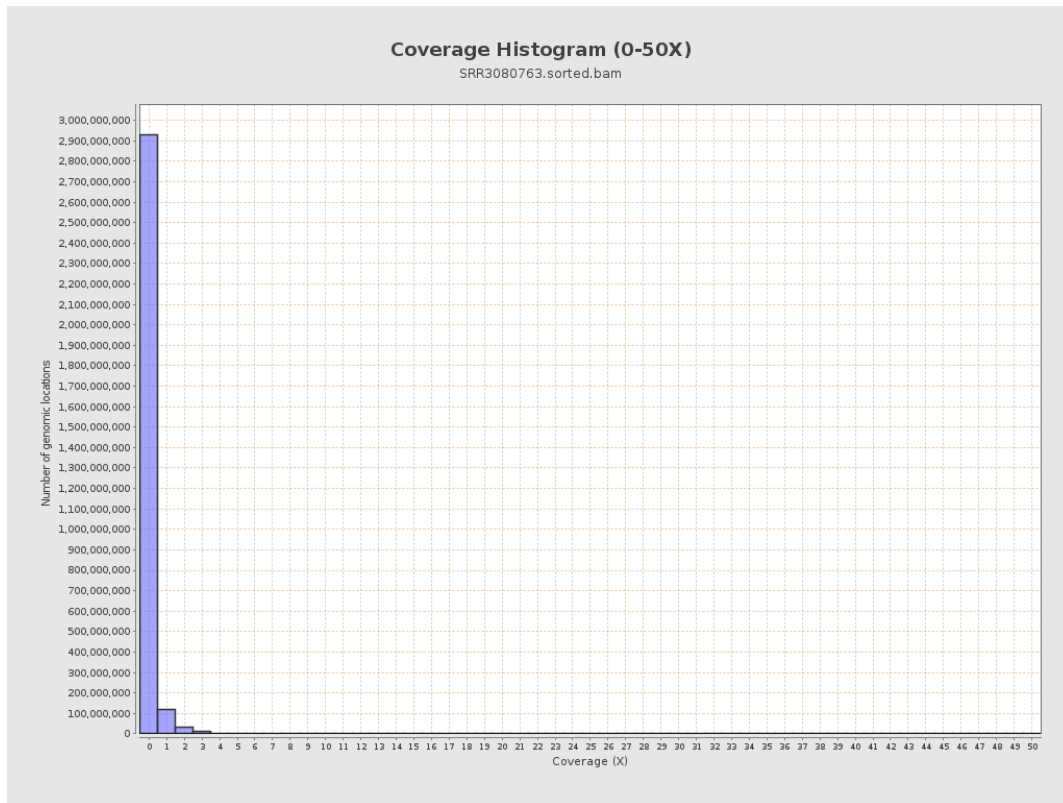
3. Results : Coverage across reference



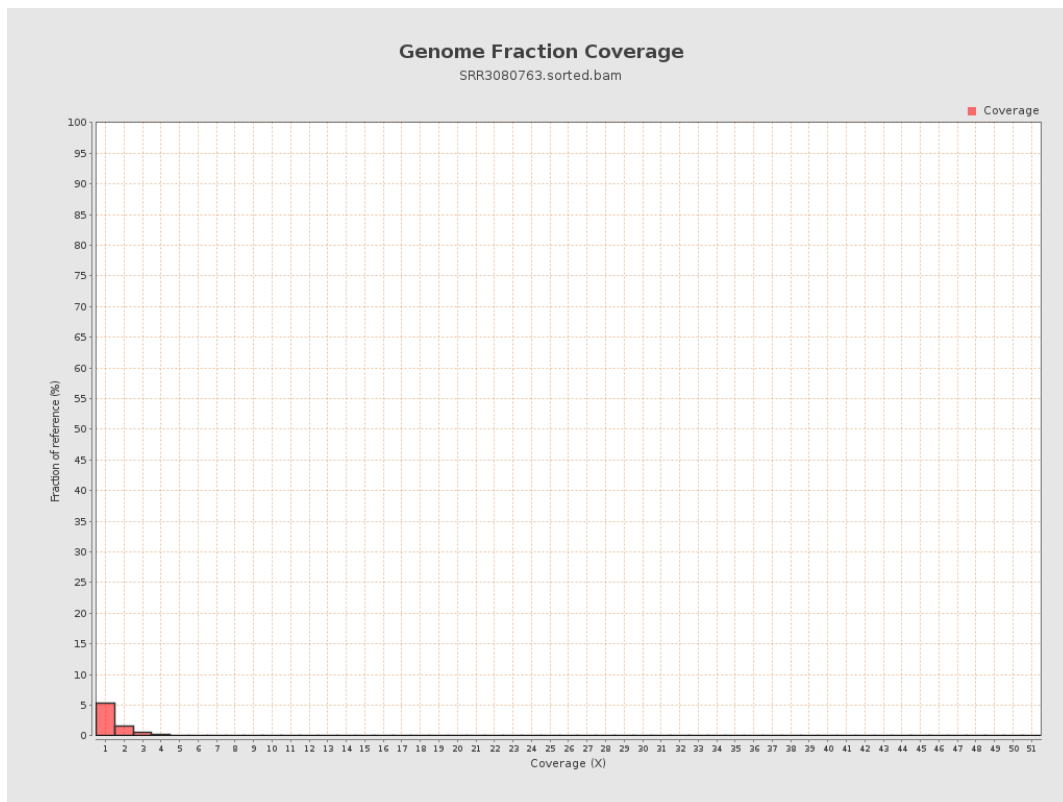
4. Results : Coverage Histogram



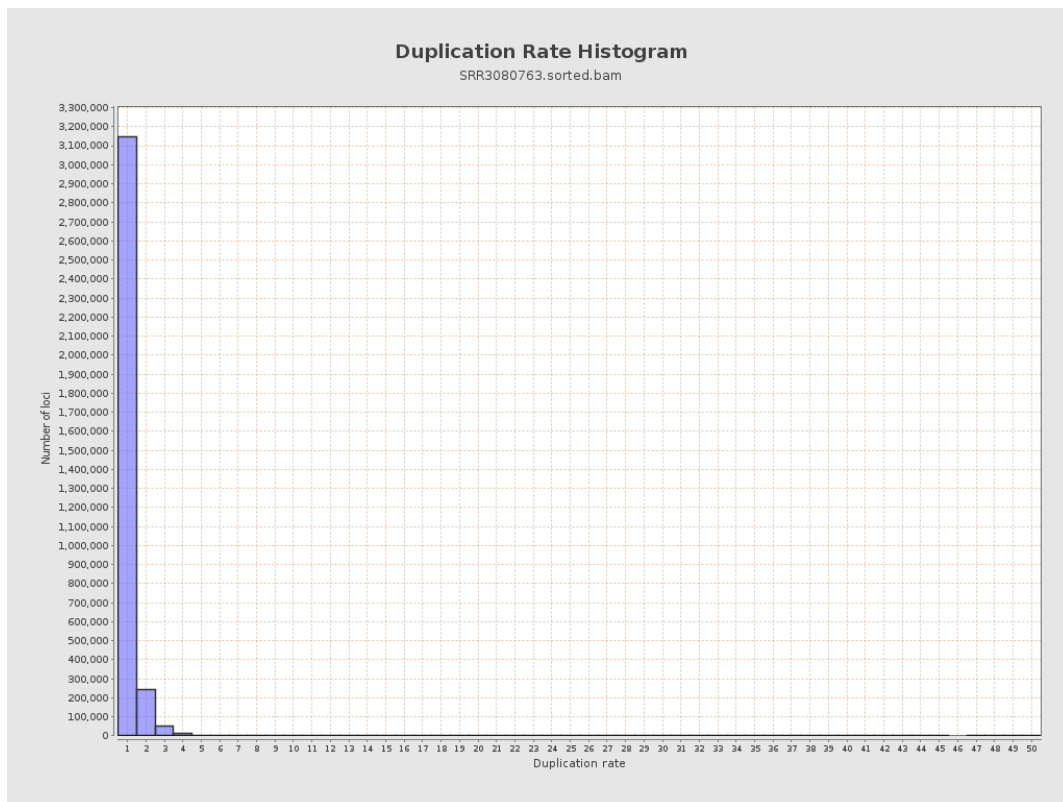
5. Results : Coverage Histogram (0-50X)



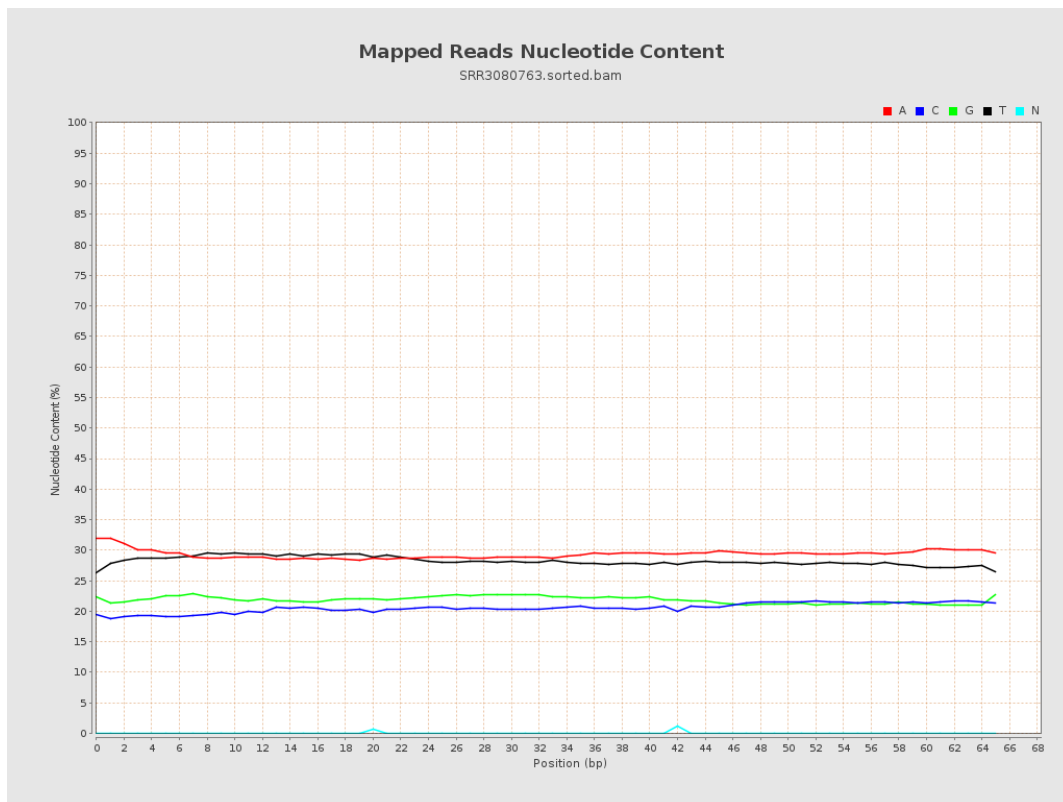
6. Results : Genome Fraction Coverage



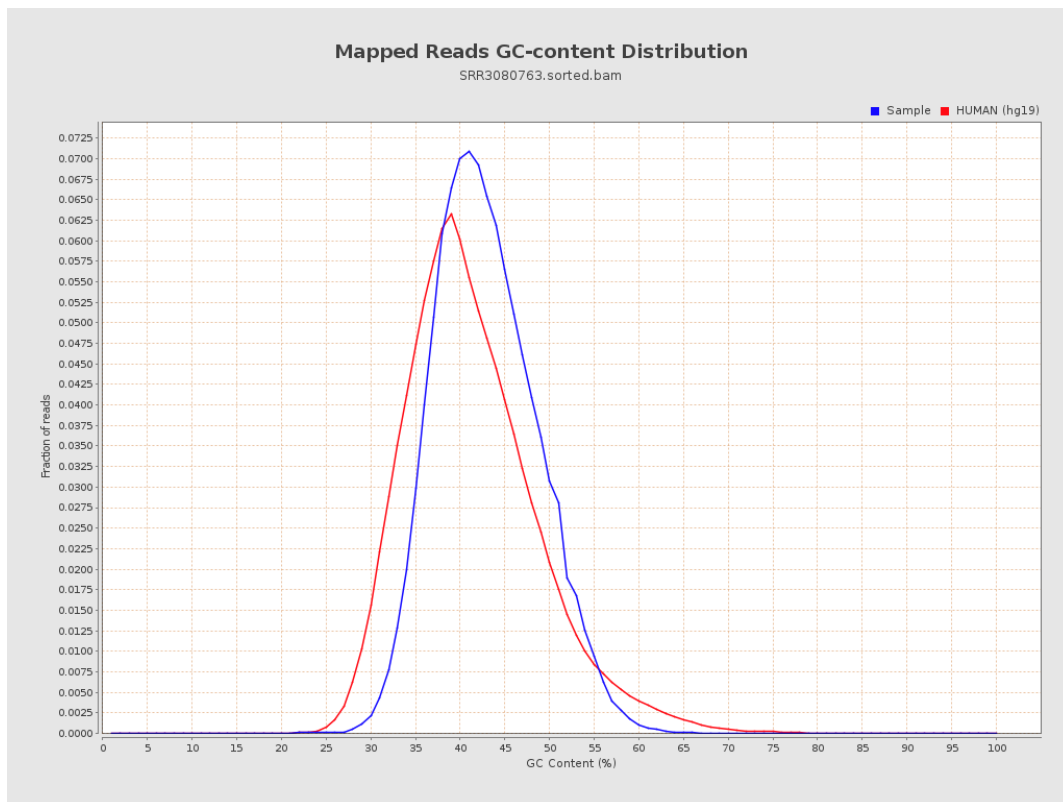
7. Results : Duplication Rate Histogram



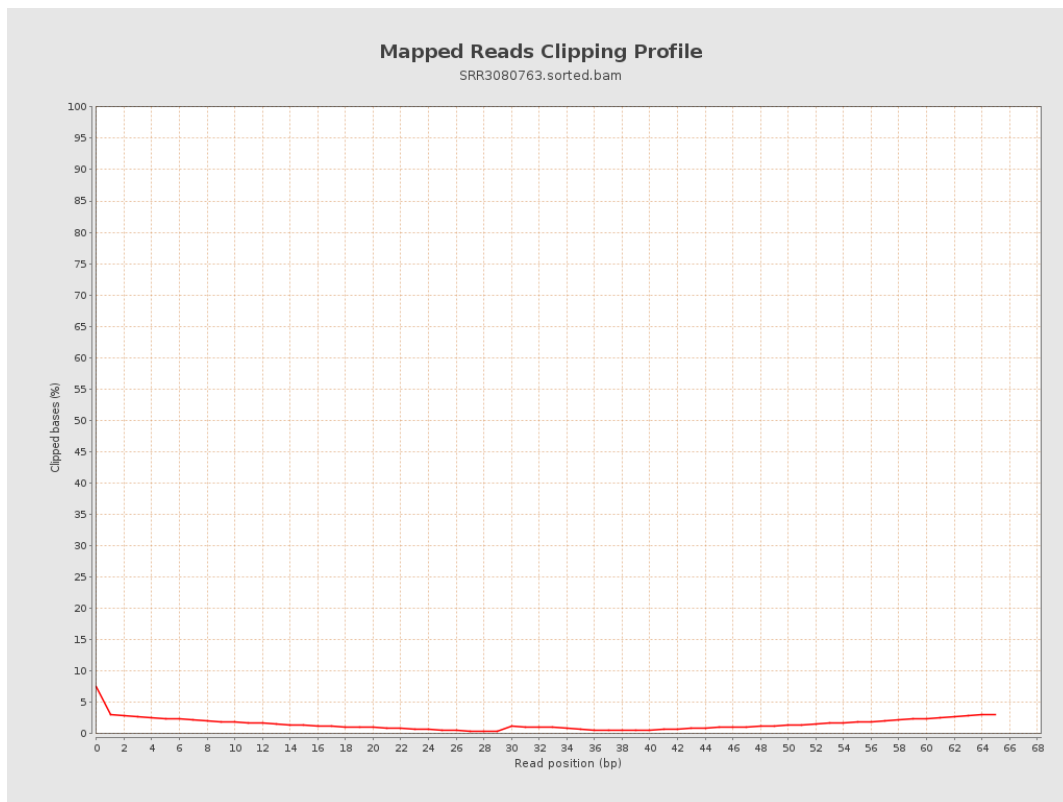
8. Results : Mapped Reads Nucleotide Content



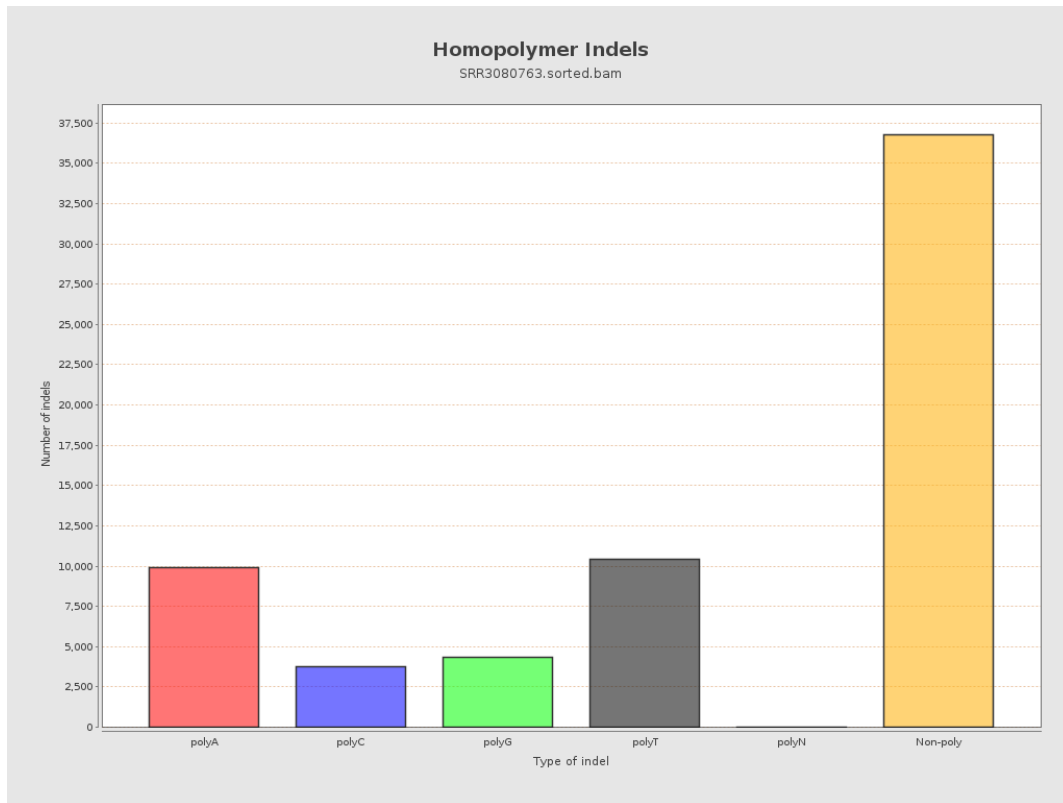
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

