

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:37:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063581.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_SRR6063581 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063581.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:37:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063581.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,572,806
Mapped reads	2,109,651 / 82%
Unmapped reads	463,155 / 18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,596 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	227,771 / 8.85%
Duplication rate	8.44%
Clipped reads	1,022,862 / 39.76%

2.2. ACGT Content

Number/percentage of A's	39,506,303 / 28.33%
Number/percentage of C's	26,167,033 / 18.77%
Number/percentage of T's	43,608,616 / 31.28%
Number/percentage of G's	30,067,799 / 21.56%
Number/percentage of N's	80,226 / 0.06%
GC Percentage	40.33%

2.3. Coverage

Mean	0.0451

Standard Deviation	0.4141
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2.4. Mapping Quality

Mean Mapping Quality	39.59
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2.5. Mismatches and indels

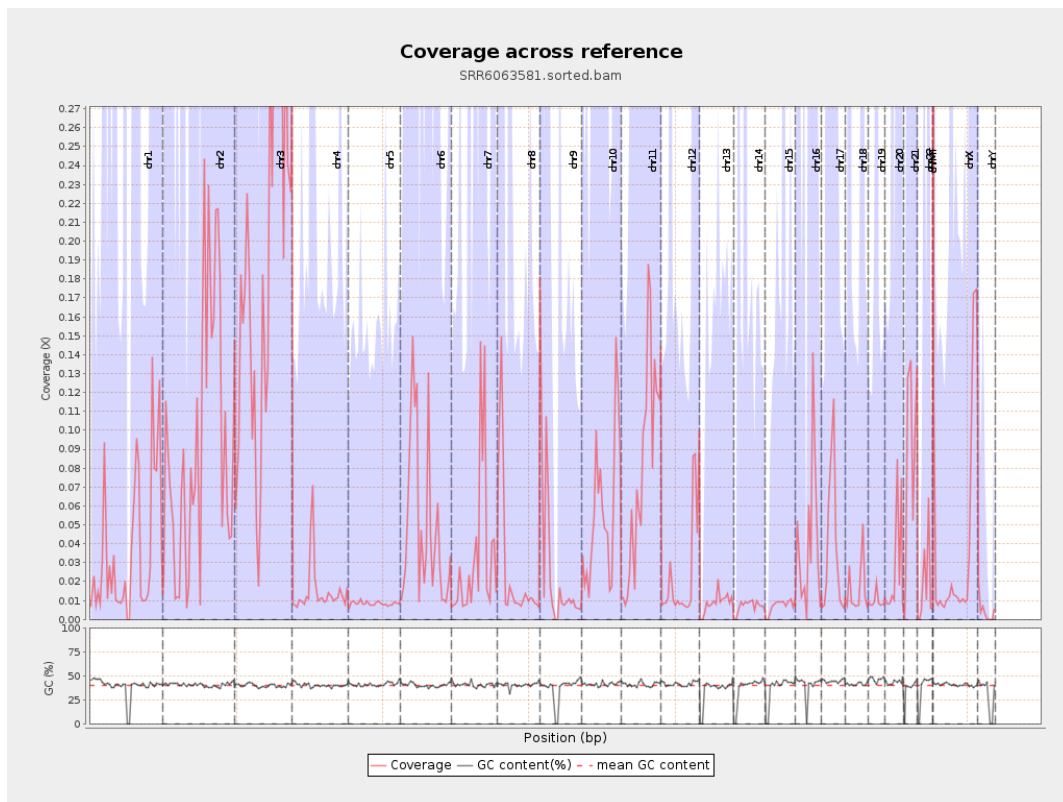
General error rate	0.86%
Mismatches	1,178,494
Insertions	9,692
Mapped reads with at least one insertion	0.46%
Deletions	33,727
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.06%

2.6. Chromosome stats

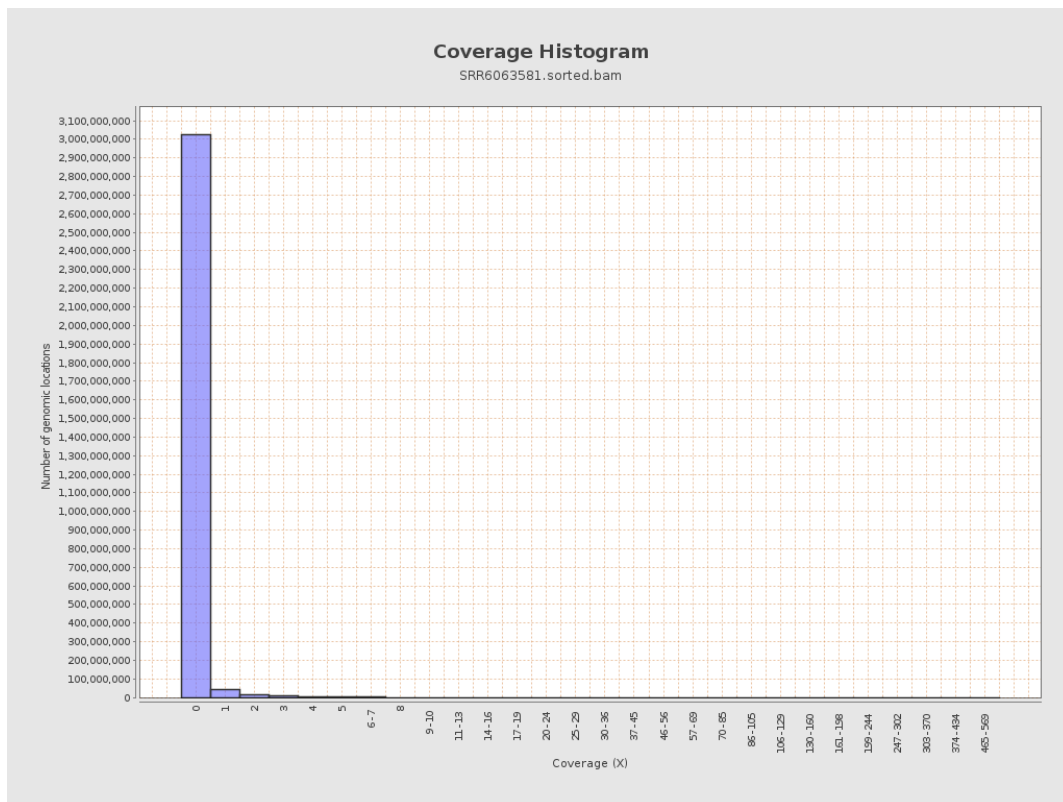
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8900336	0.0357	0.3555
chr2	243199373	22700106	0.0933	0.6201
chr3	198022430	37339419	0.1886	0.7639
chr4	191154276	2911174	0.0152	0.2169
chr5	180915260	1508967	0.0083	0.151
chr6	171115067	8569901	0.0501	0.395
chr7	159138663	5387605	0.0339	0.3416

chr8	146364022	3604658	0.0246	0.4287
chr9	141213431	3198393	0.0226	0.2667
chr10	135534747	7769170	0.0573	0.4841
chr11	135006516	10431993	0.0773	0.5323
chr12	133851895	3090892	0.0231	0.2687
chr13	115169878	1040895	0.009	0.1571
chr14	107349540	760957	0.0071	0.2588
chr15	102531392	709735	0.0069	0.2056
chr16	90354753	3630263	0.0402	0.3578
chr17	81195210	3031741	0.0373	0.3668
chr18	78077248	1305729	0.0167	0.5758
chr19	59128983	576678	0.0098	0.2635
chr20	63025520	1763845	0.028	0.3107
chr21	48129895	4040899	0.084	0.502
chr22	51304566	953395	0.0186	0.2187
chrMT	16571	82495	4.9783	4.6632
chrX	155270560	5921562	0.0381	0.3608
chrY	59373566	253367	0.0043	0.0999

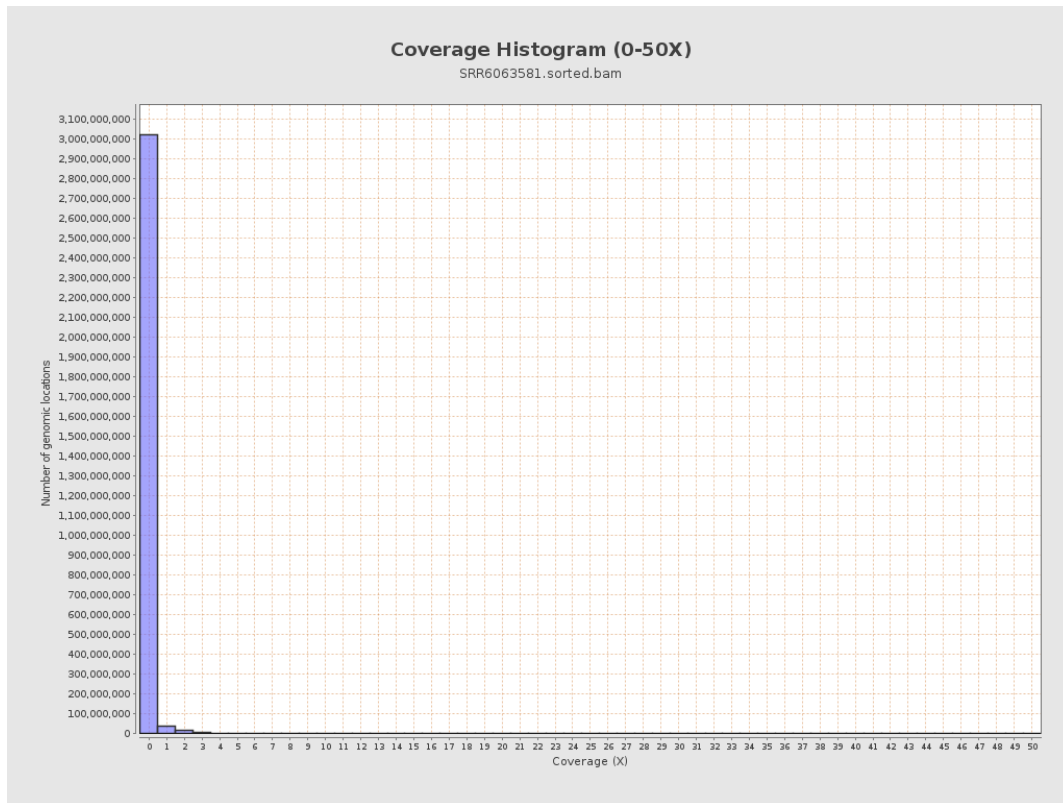
3. Results : Coverage across reference



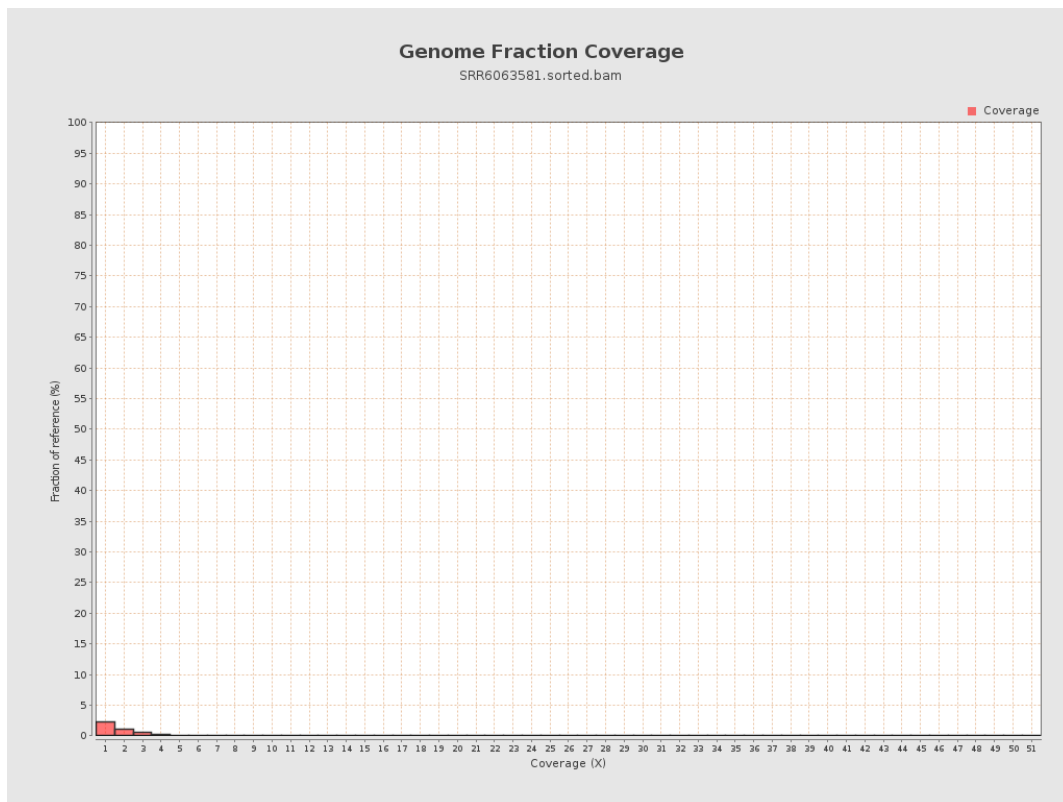
4. Results : Coverage Histogram



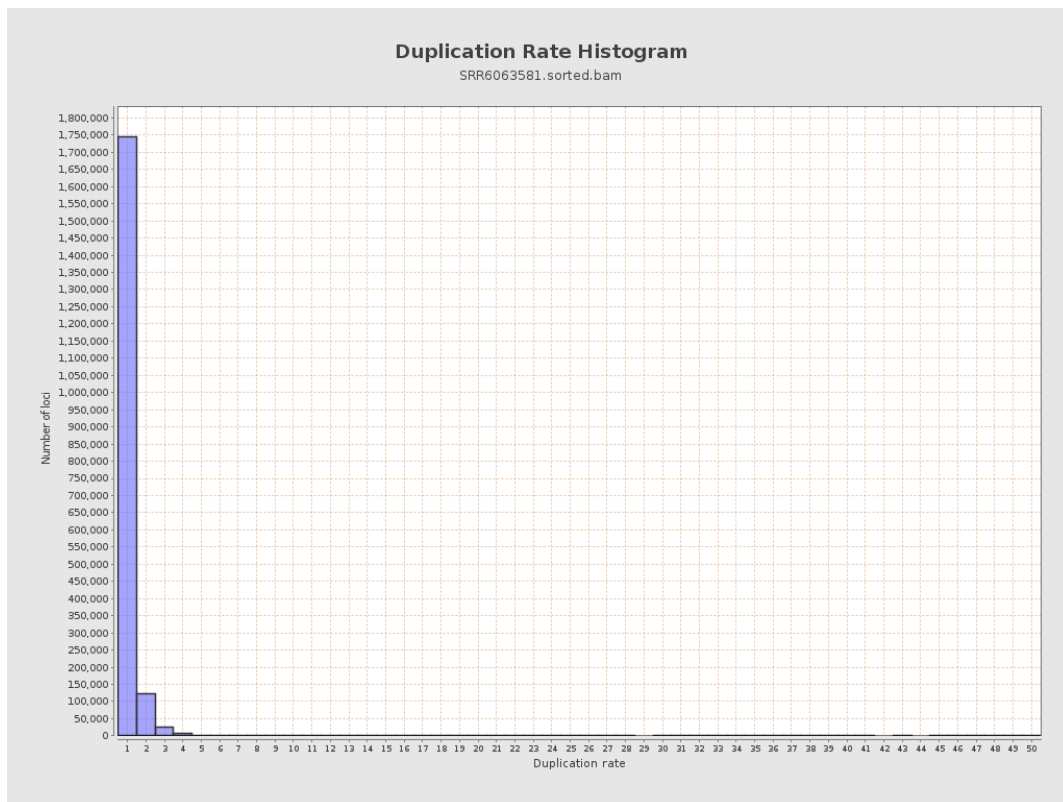
5. Results : Coverage Histogram (0-50X)



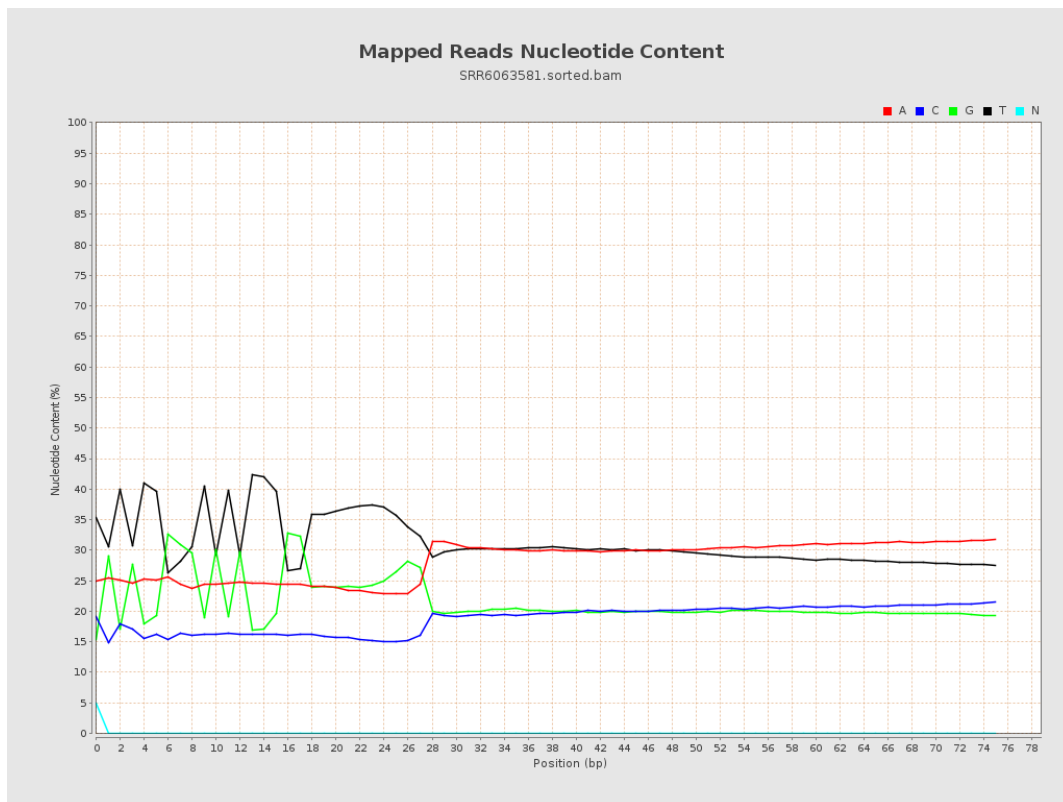
6. Results : Genome Fraction Coverage



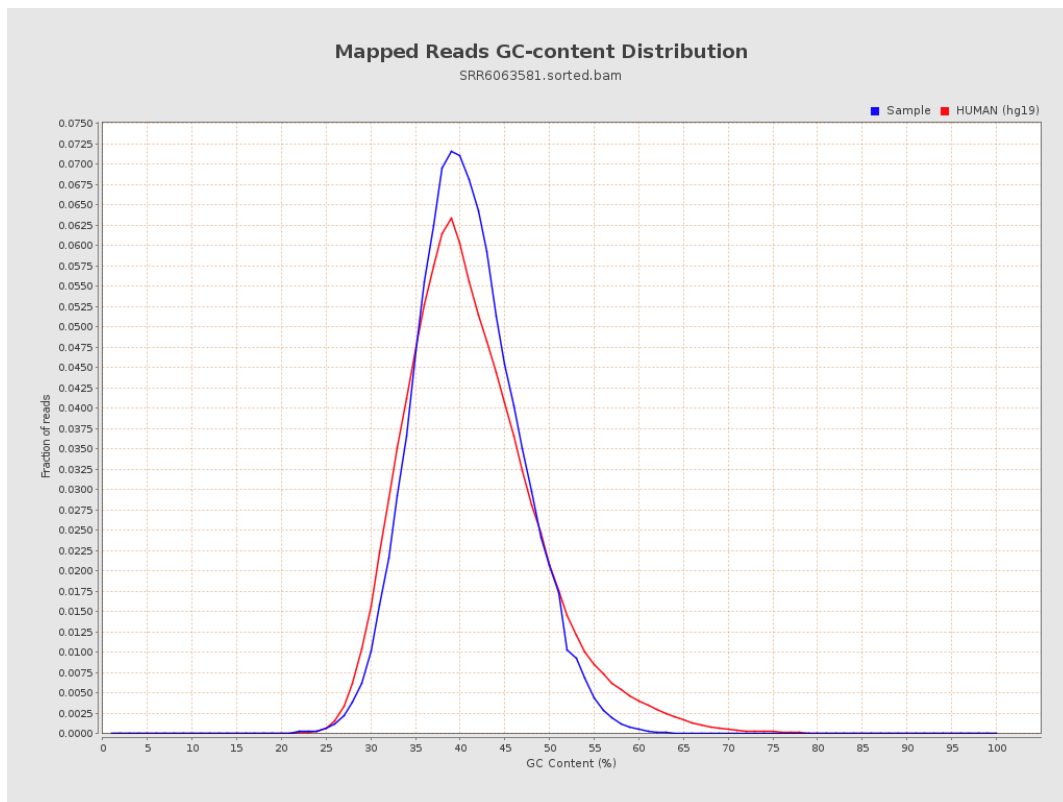
7. Results : Duplication Rate Histogram



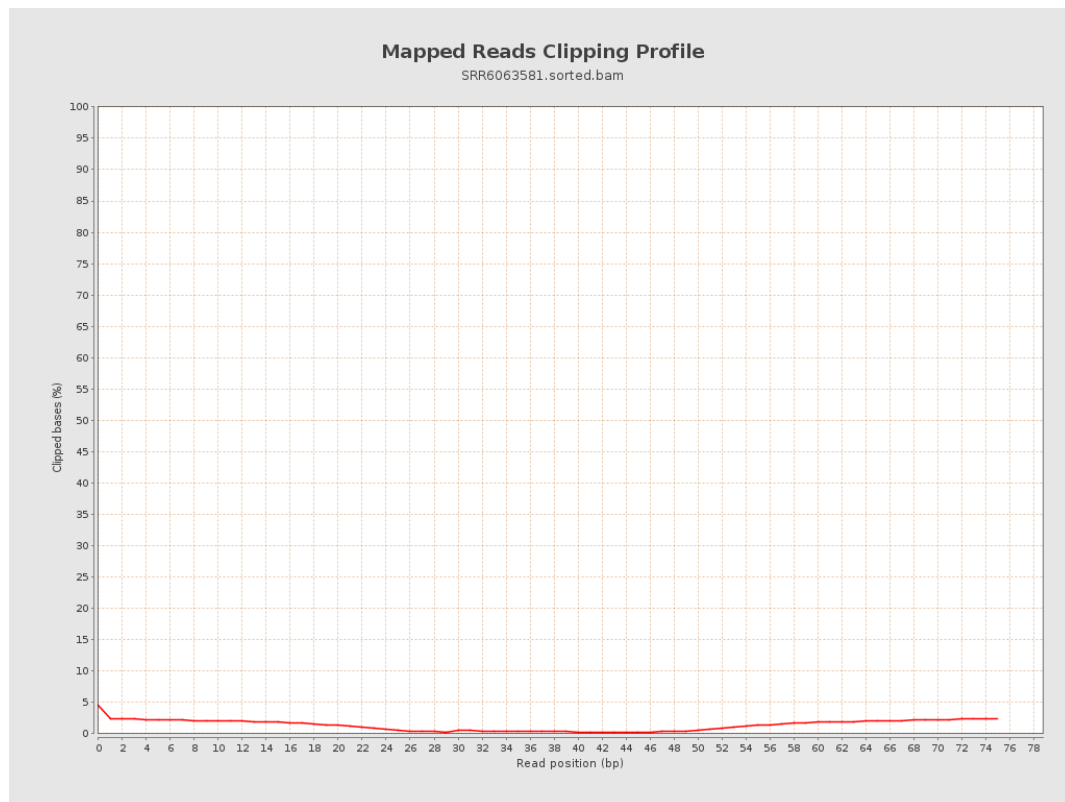
8. Results : Mapped Reads Nucleotide Content



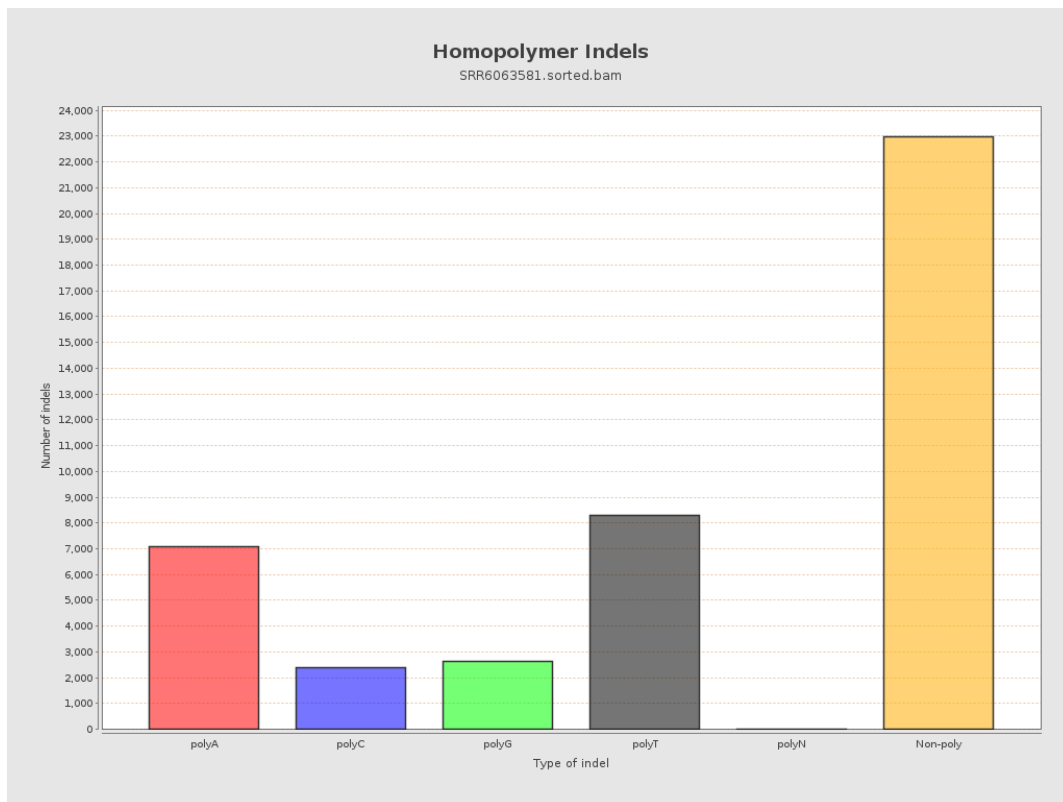
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

