

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:55:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063587.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_SRR6063587 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063587.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:55:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063587.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,712,621
Mapped reads	2,219,806 / 81.83%
Unmapped reads	492,815 / 18.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,126 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	450,856 / 16.62%
Duplication rate	12.57%
Clipped reads	1,016,039 / 37.46%

2.2. ACGT Content

Number/percentage of A's	41,996,908 / 28.45%
Number/percentage of C's	27,426,511 / 18.58%
Number/percentage of T's	46,747,357 / 31.67%
Number/percentage of G's	31,427,530 / 21.29%
Number/percentage of N's	3,680 / 0%
GC Percentage	39.87%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.7846
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	43.71
----------------------	-------

2.5. Mismatches and indels

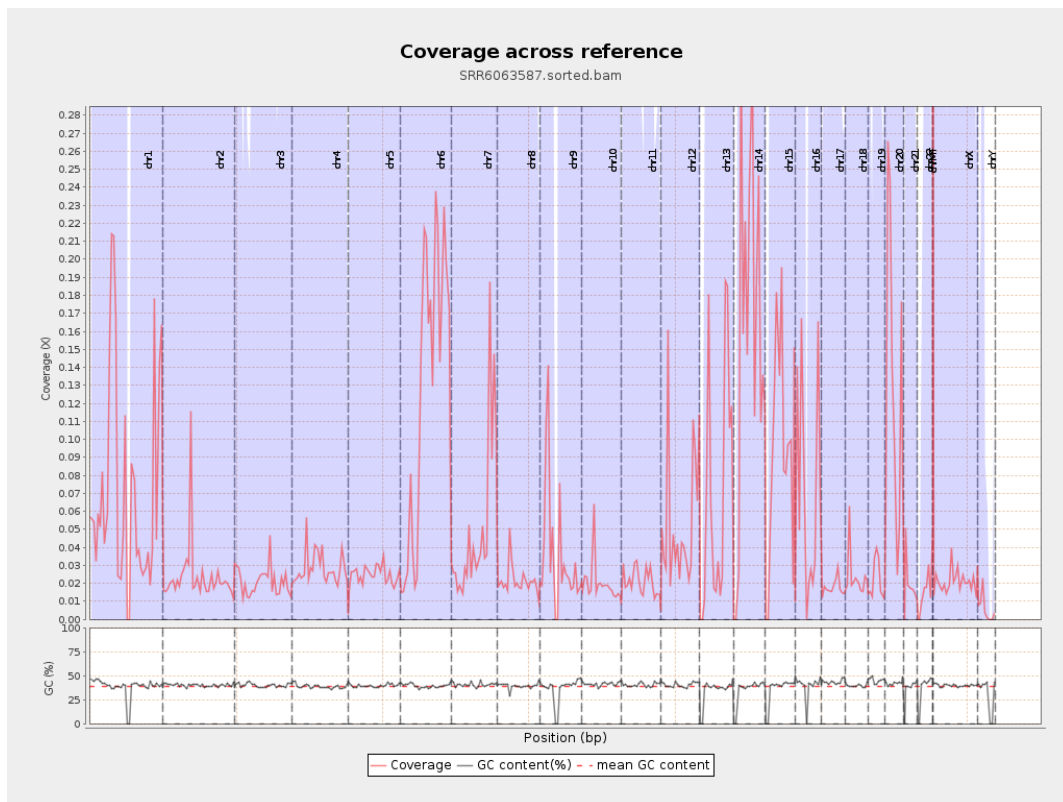
General error rate	0.83%
Mismatches	1,196,170
Insertions	12,486
Mapped reads with at least one insertion	0.56%
Deletions	35,489
Mapped reads with at least one deletion	1.58%
Homopolymer indels	46.89%

2.6. Chromosome stats

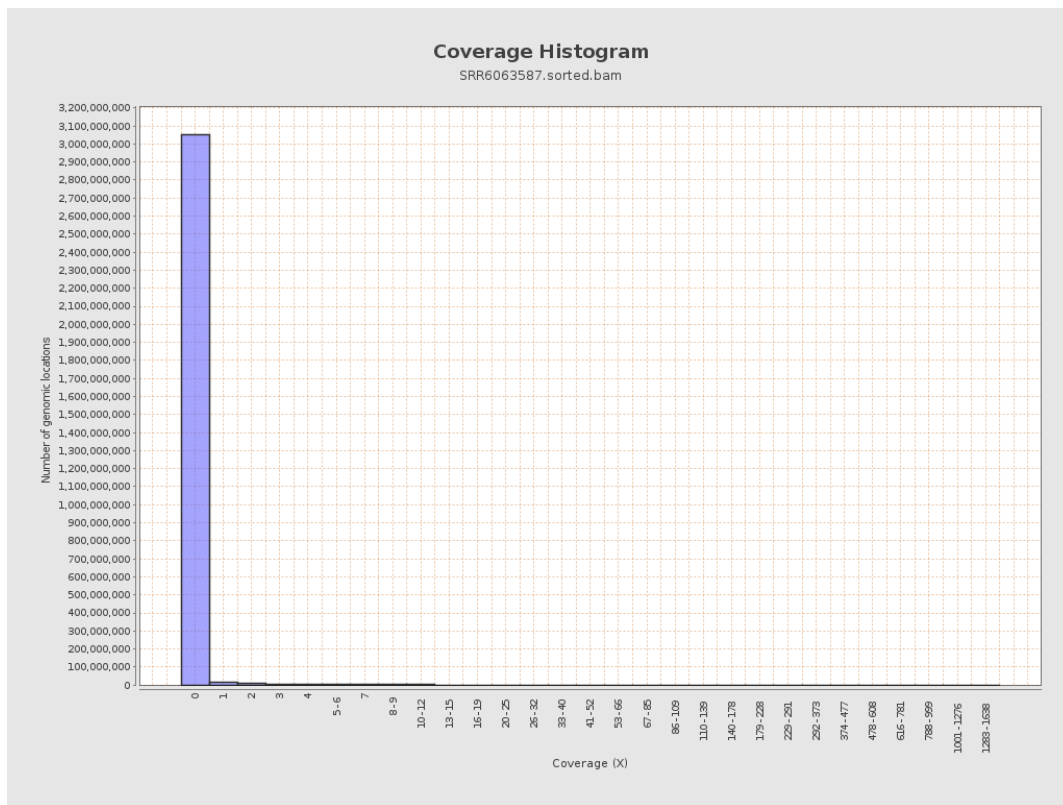
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18168035	0.0729	1.466
chr2	243199373	5729956	0.0236	0.8218
chr3	198022430	4159238	0.021	0.3588
chr4	191154276	5396442	0.0282	0.4915
chr5	180915260	4465726	0.0247	0.3824
chr6	171115067	21559866	0.126	0.9235
chr7	159138663	7976032	0.0501	0.632

chr8	146364022	3160381	0.0216	1.084
chr9	141213431	5185858	0.0367	0.6501
chr10	135534747	2704150	0.02	0.4749
chr11	135006516	2844630	0.0211	0.5527
chr12	133851895	7059363	0.0527	0.5812
chr13	115169878	8133042	0.0706	0.6815
chr14	107349540	17377102	0.1619	1.0704
chr15	102531392	9396475	0.0916	0.8264
chr16	90354753	5883969	0.0651	0.6689
chr17	81195210	1452004	0.0179	0.3114
chr18	78077248	1863847	0.0239	1.2609
chr19	59128983	1352034	0.0229	0.7756
chr20	63025520	8411859	0.1335	0.9283
chr21	48129895	967518	0.0201	0.3591
chr22	51304566	772610	0.0151	0.2912
chrMT	16571	9507	0.5737	1.4265
chrX	155270560	3279823	0.0211	0.3825
chrY	59373566	350410	0.0059	0.2181

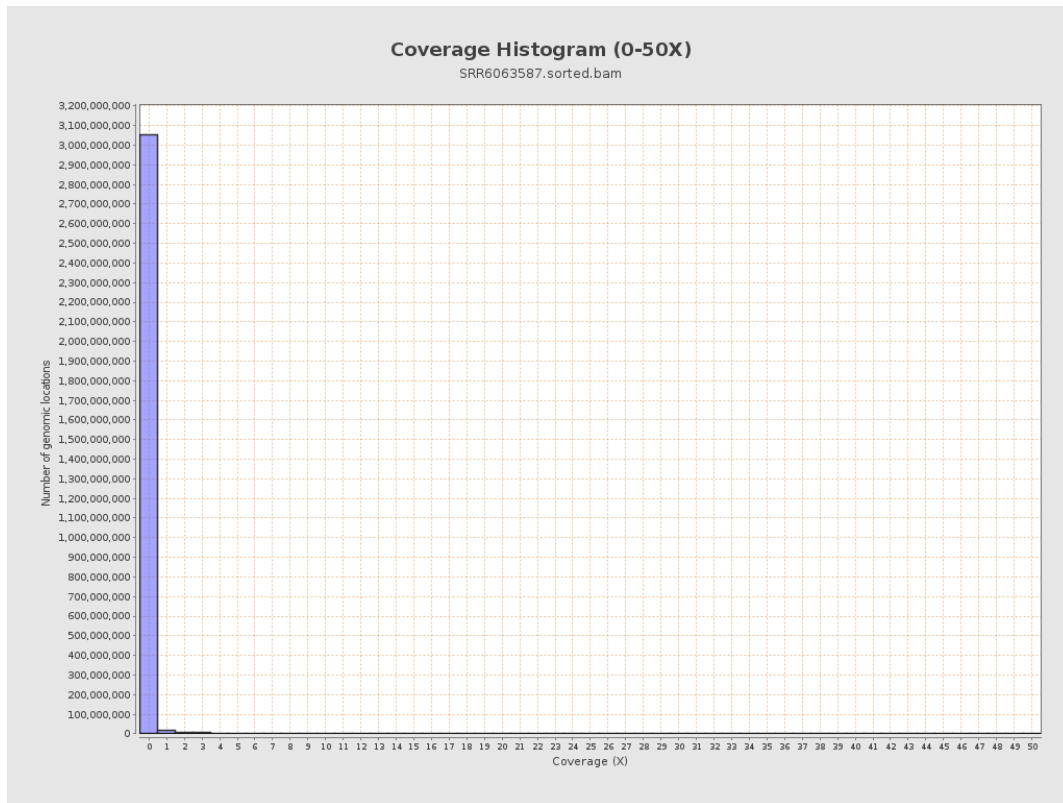
3. Results : Coverage across reference



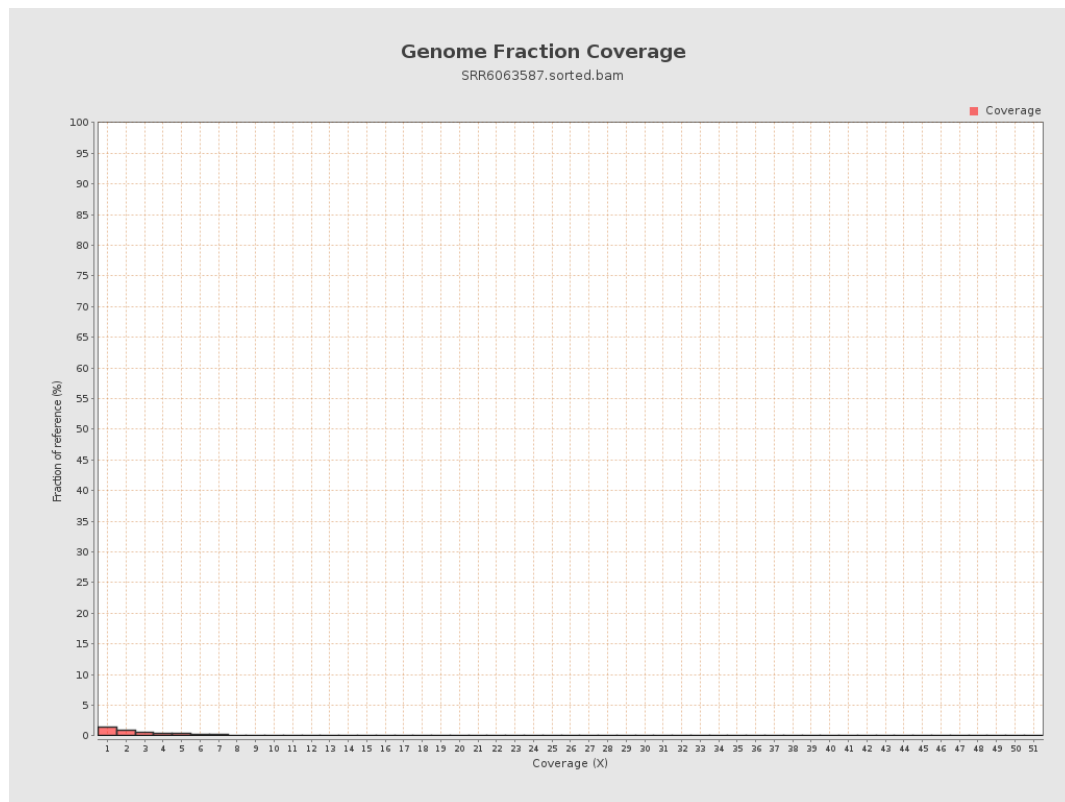
4. Results : Coverage Histogram



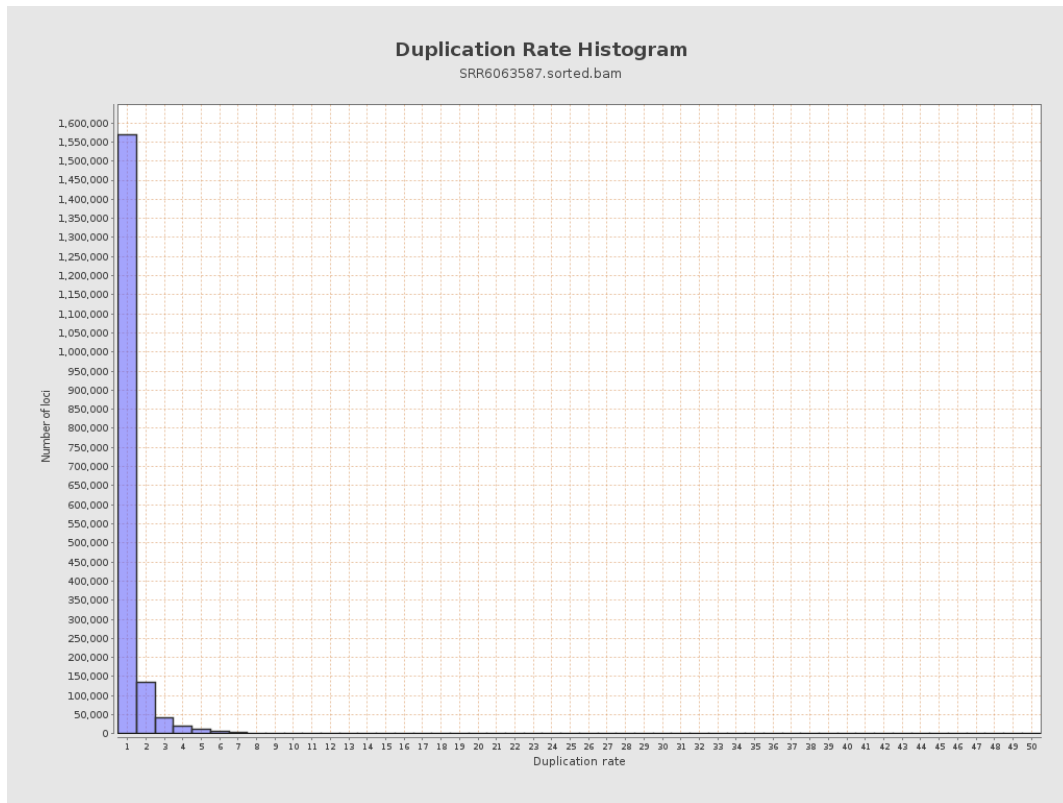
5. Results : Coverage Histogram (0-50X)



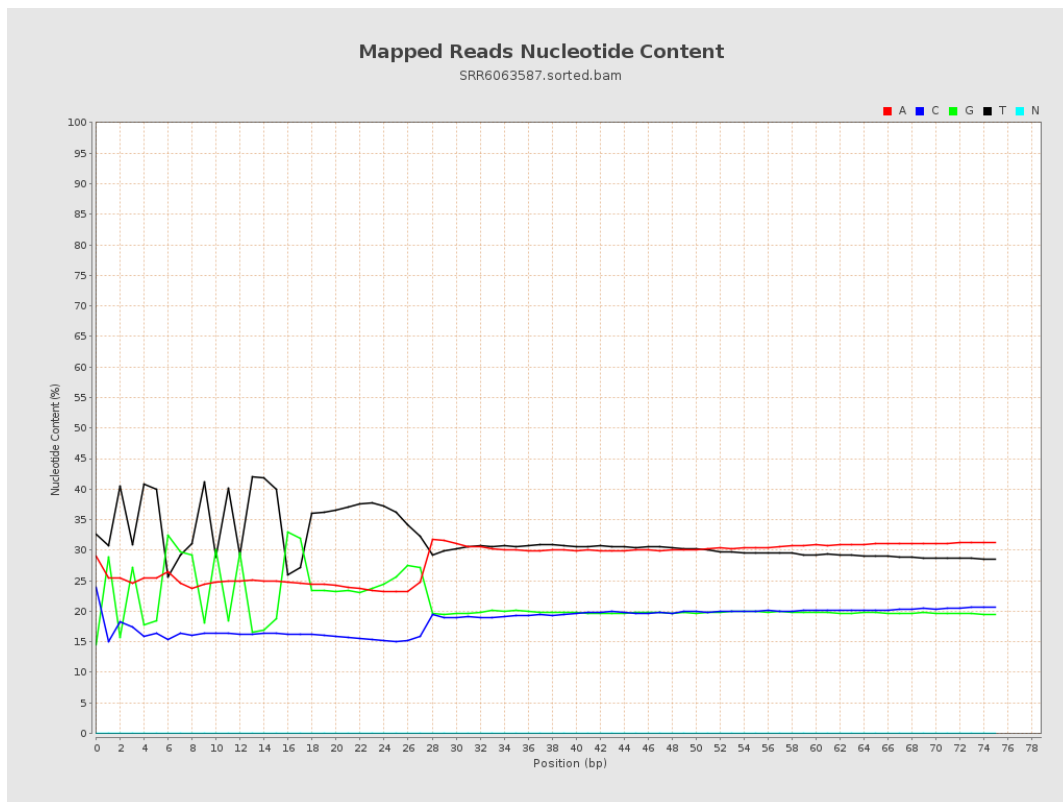
6. Results : Genome Fraction Coverage



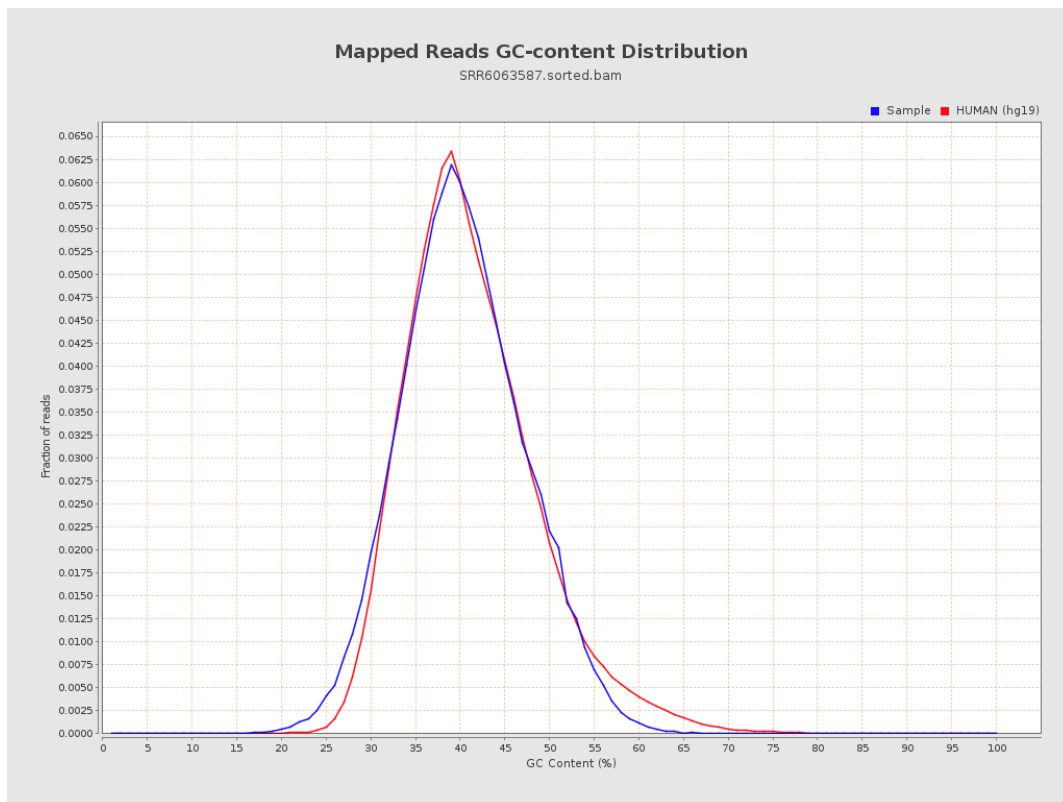
7. Results : Duplication Rate Histogram



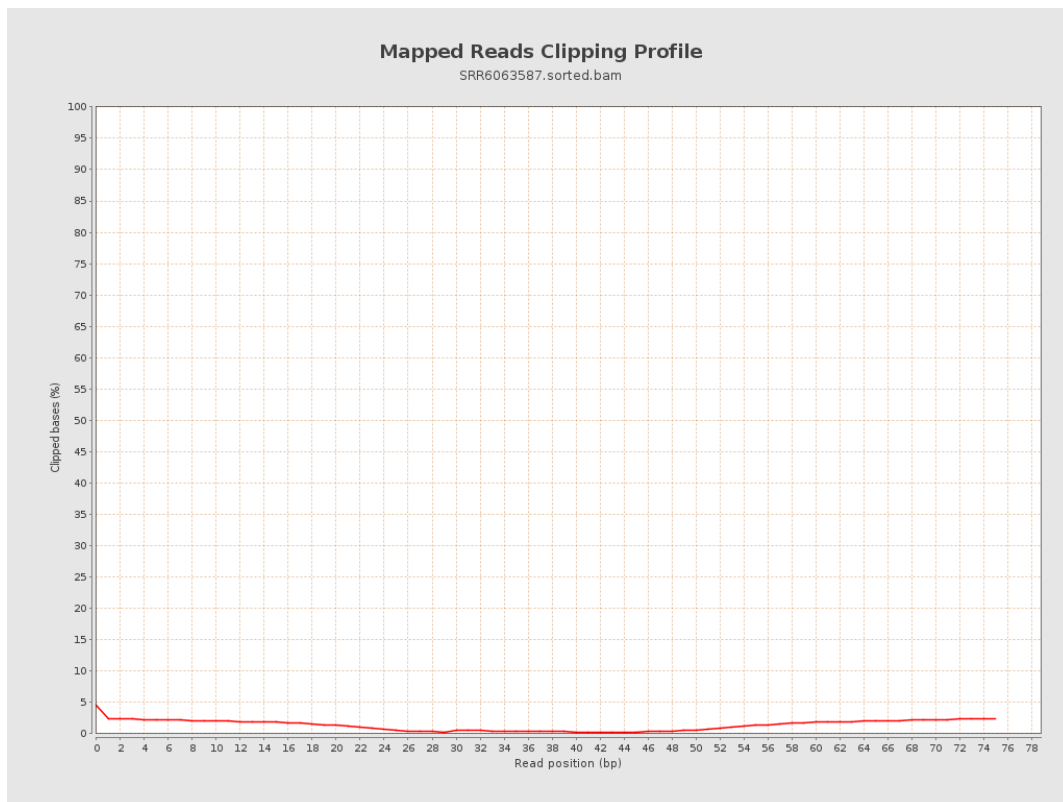
8. Results : Mapped Reads Nucleotide Content



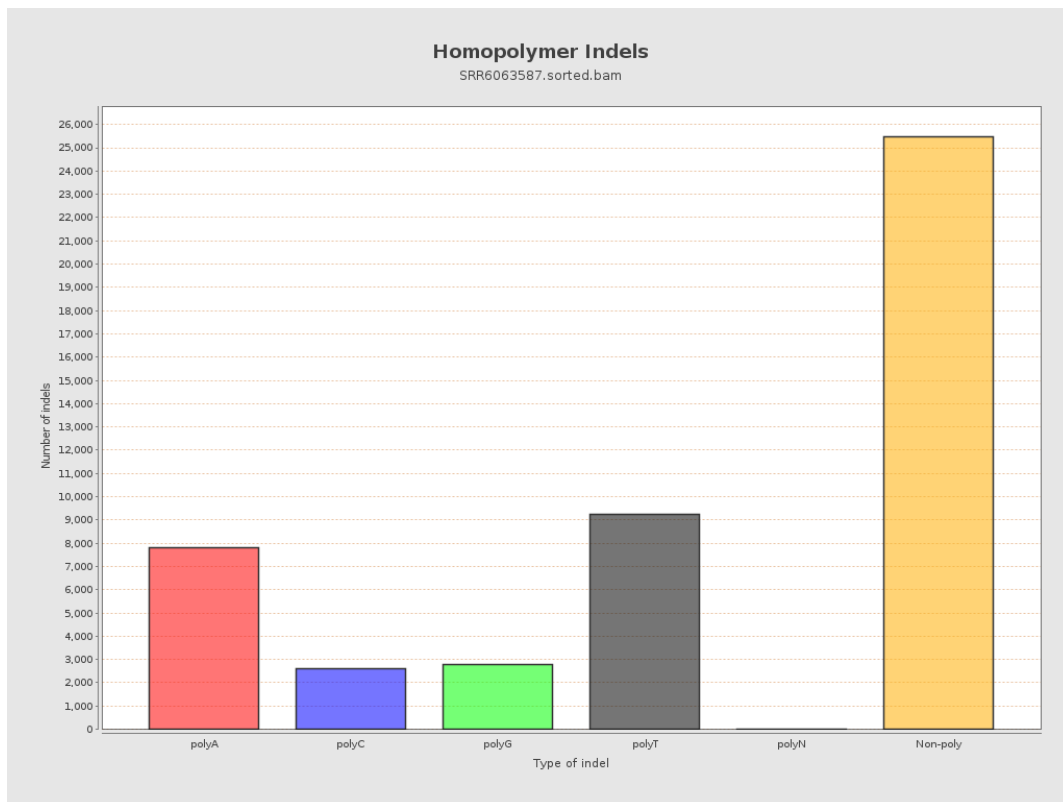
9. Results : Mapped Reads GC-content Distribution



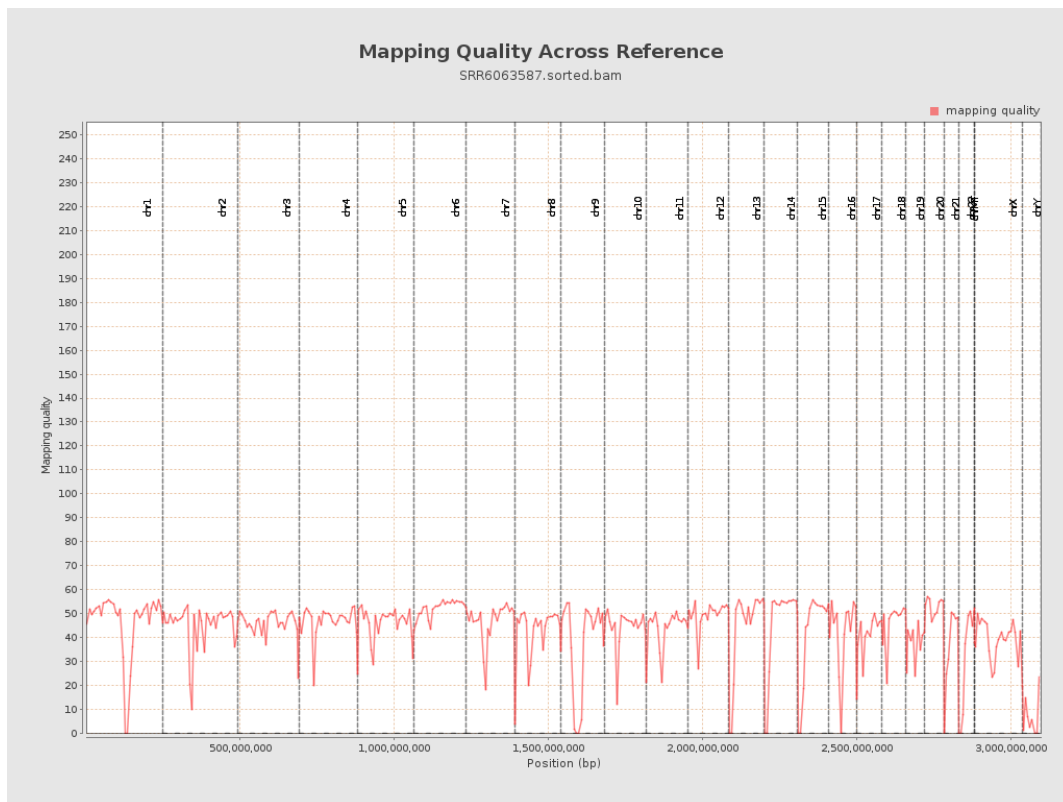
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

