

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:51:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004135.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_SRR6004135 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004135.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:51:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004135.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,194,417
Mapped reads	1,961,340 / 89.38%
Unmapped reads	233,077 / 10.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,265 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	85,298 / 3.89%
Duplication rate	3.18%
Clipped reads	903,412 / 41.17%

2.2. ACGT Content

Number/percentage of A's	36,957,429 / 28.27%
Number/percentage of C's	24,127,455 / 18.46%
Number/percentage of T's	41,412,816 / 31.68%
Number/percentage of G's	28,227,323 / 21.59%
Number/percentage of N's	9,165 / 0.01%
GC Percentage	40.05%

2.3. Coverage

Mean	0.0422

Standard Deviation	0.398
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2.4. Mapping Quality

Mean Mapping Quality	45.23
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2.5. Mismatches and indels

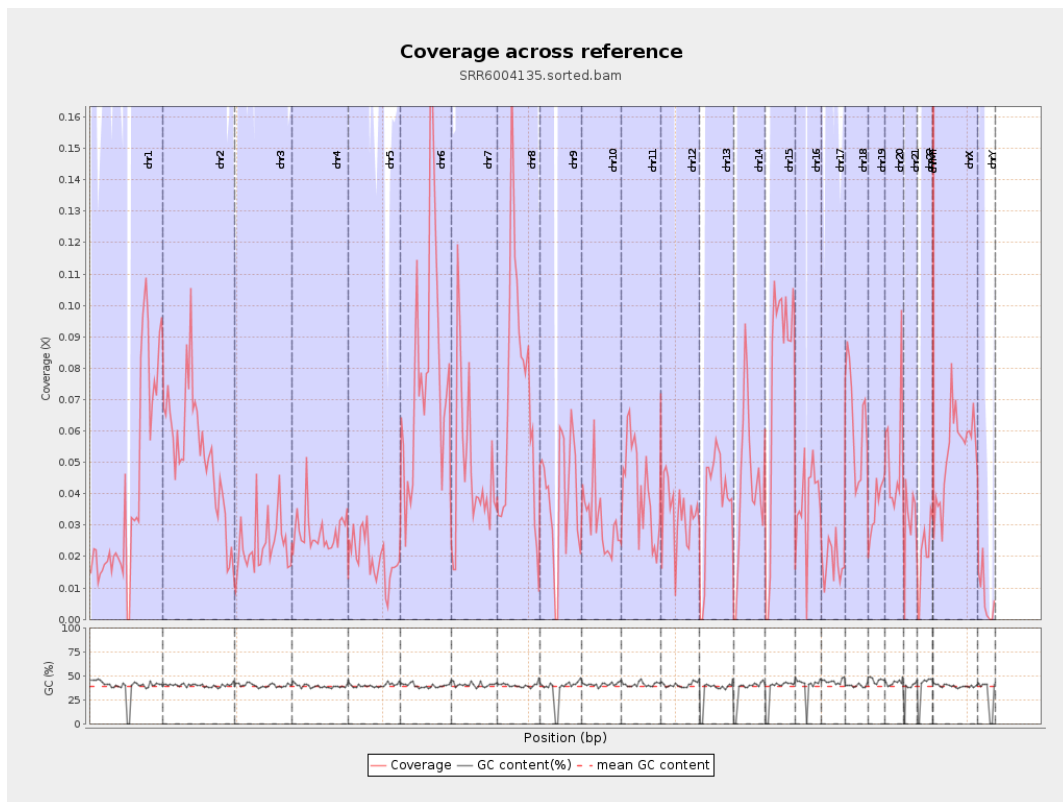
General error rate	0.94%
Mismatches	1,202,833
Insertions	10,484
Mapped reads with at least one insertion	0.53%
Deletions	32,679
Mapped reads with at least one deletion	1.65%
Homopolymer indels	45.92%

2.6. Chromosome stats

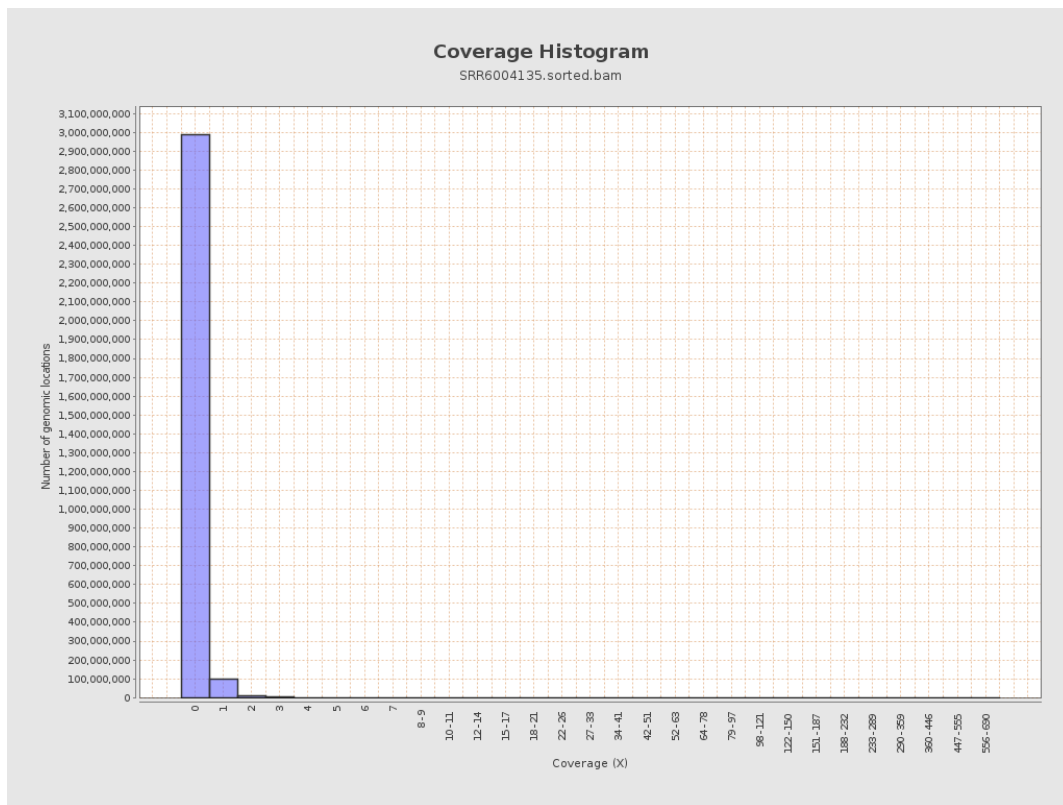
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10106498	0.0405	0.5619
chr2	243199373	12814186	0.0527	0.5139
chr3	198022430	4667632	0.0236	0.1744
chr4	191154276	5362533	0.0281	0.2178
chr5	180915260	3526361	0.0195	0.1641
chr6	171115067	13359897	0.0781	0.5124
chr7	159138663	7488357	0.0471	0.5567

chr8	146364022	10095296	0.069	0.5781
chr9	141213431	5665002	0.0401	0.4213
chr10	135534747	4240225	0.0313	0.2998
chr11	135006516	5590868	0.0414	0.349
chr12	133851895	4454111	0.0333	0.2154
chr13	115169878	4387640	0.0381	0.2223
chr14	107349540	4683990	0.0436	0.2553
chr15	102531392	7906588	0.0771	0.3176
chr16	90354753	3355921	0.0371	0.2748
chr17	81195210	1452441	0.0179	0.1756
chr18	78077248	4955219	0.0635	0.8412
chr19	59128983	2138506	0.0362	0.4356
chr20	63025520	3277651	0.052	0.2688
chr21	48129895	1507245	0.0313	0.2342
chr22	51304566	1038108	0.0202	0.1588
chrMT	16571	66429	4.0088	3.0349
chrX	155270560	8229042	0.053	0.3016
chrY	59373566	418253	0.007	0.1639

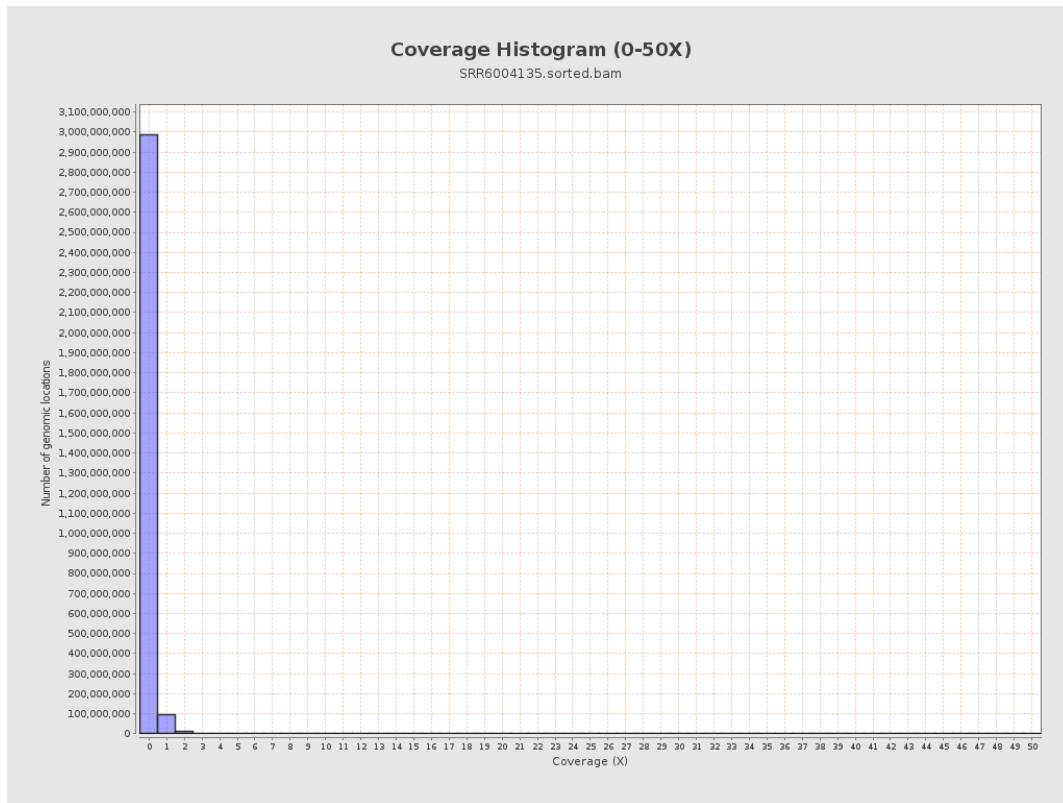
3. Results : Coverage across reference



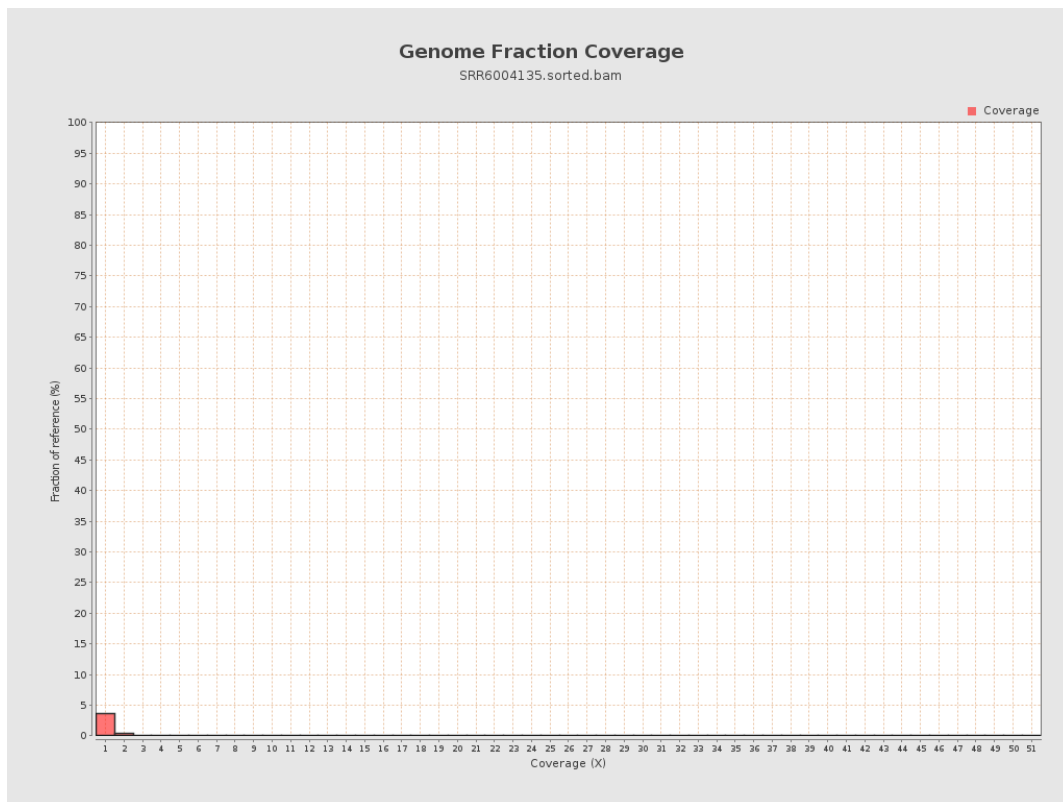
4. Results : Coverage Histogram



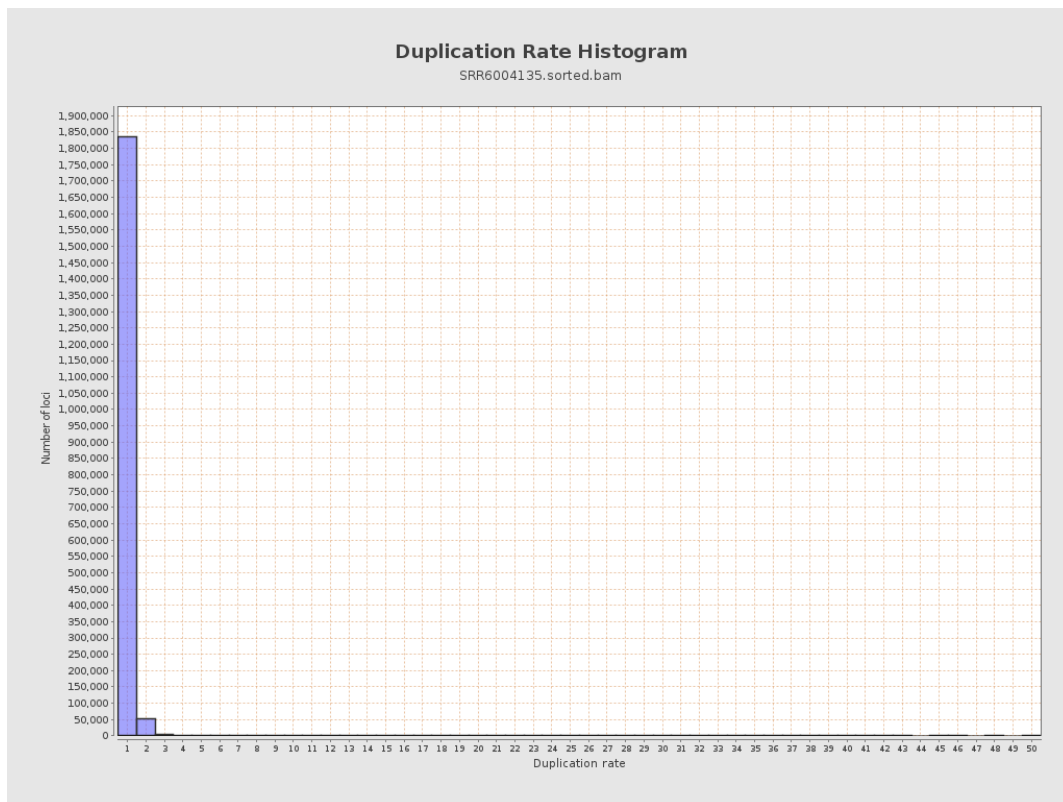
5. Results : Coverage Histogram (0-50X)



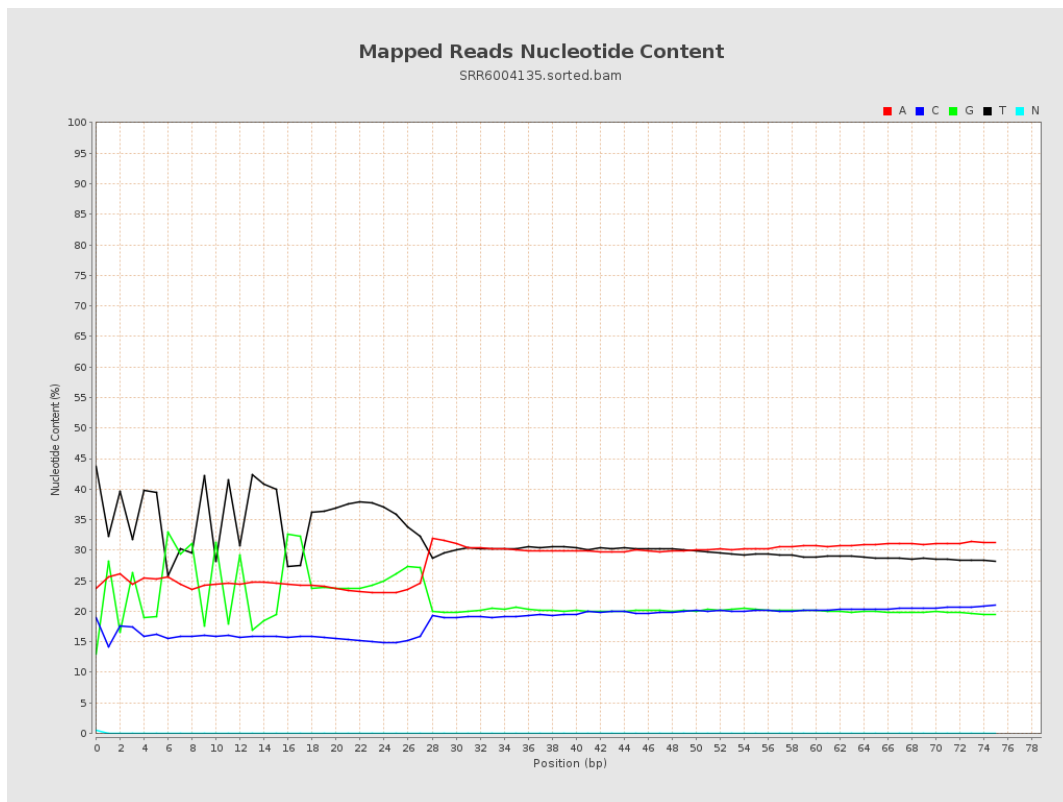
6. Results : Genome Fraction Coverage



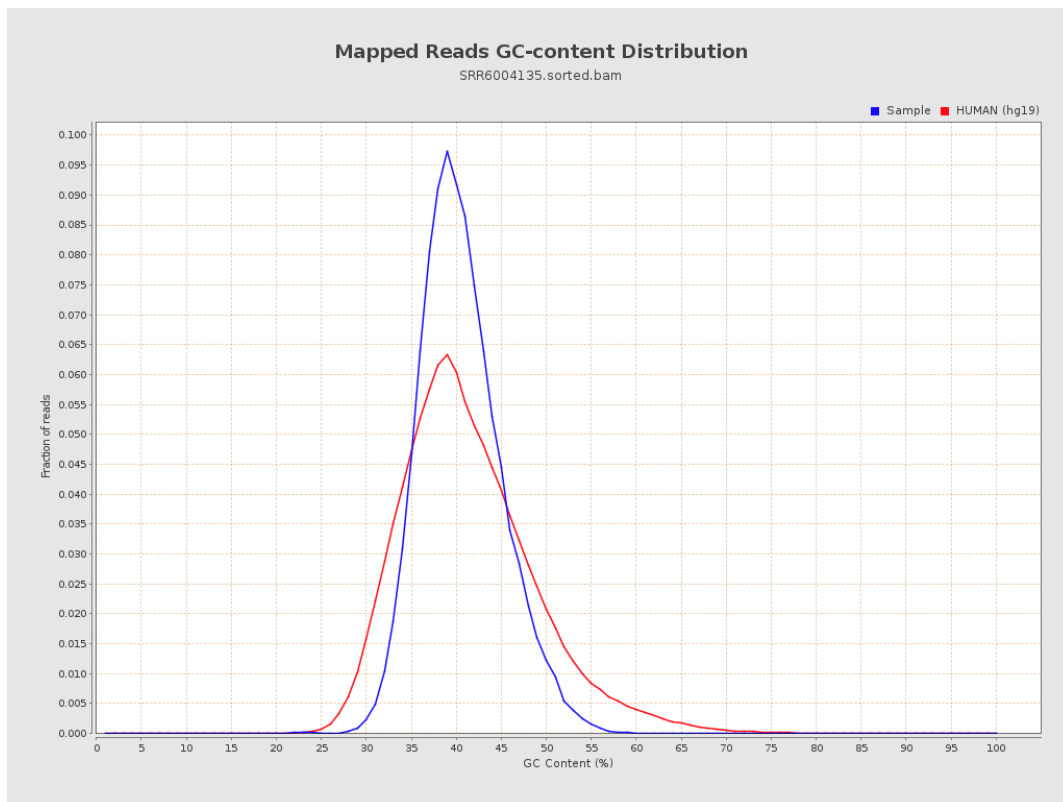
7. Results : Duplication Rate Histogram



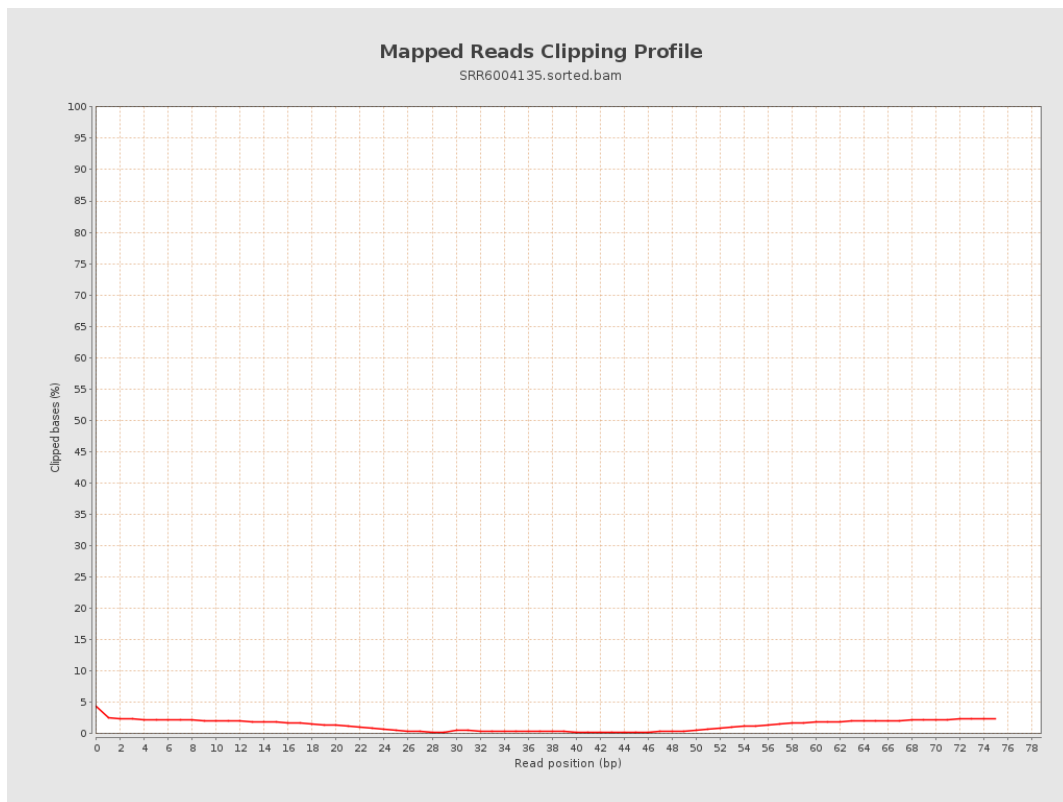
8. Results : Mapped Reads Nucleotide Content



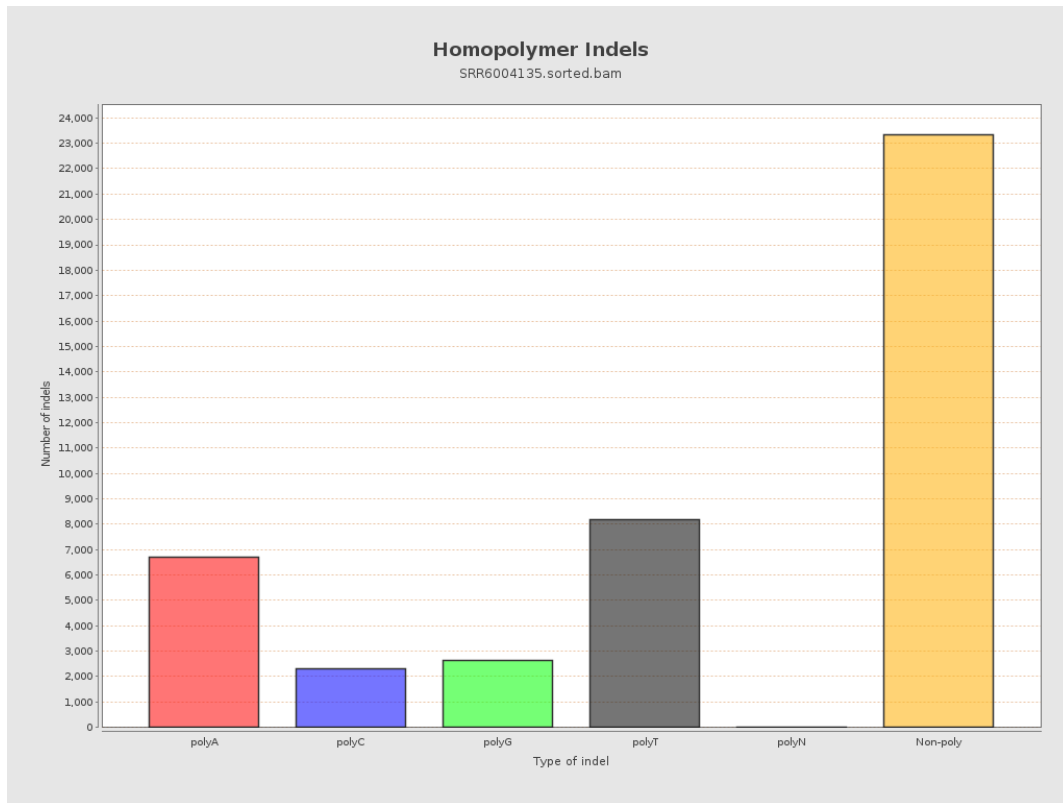
9. Results : Mapped Reads GC-content Distribution



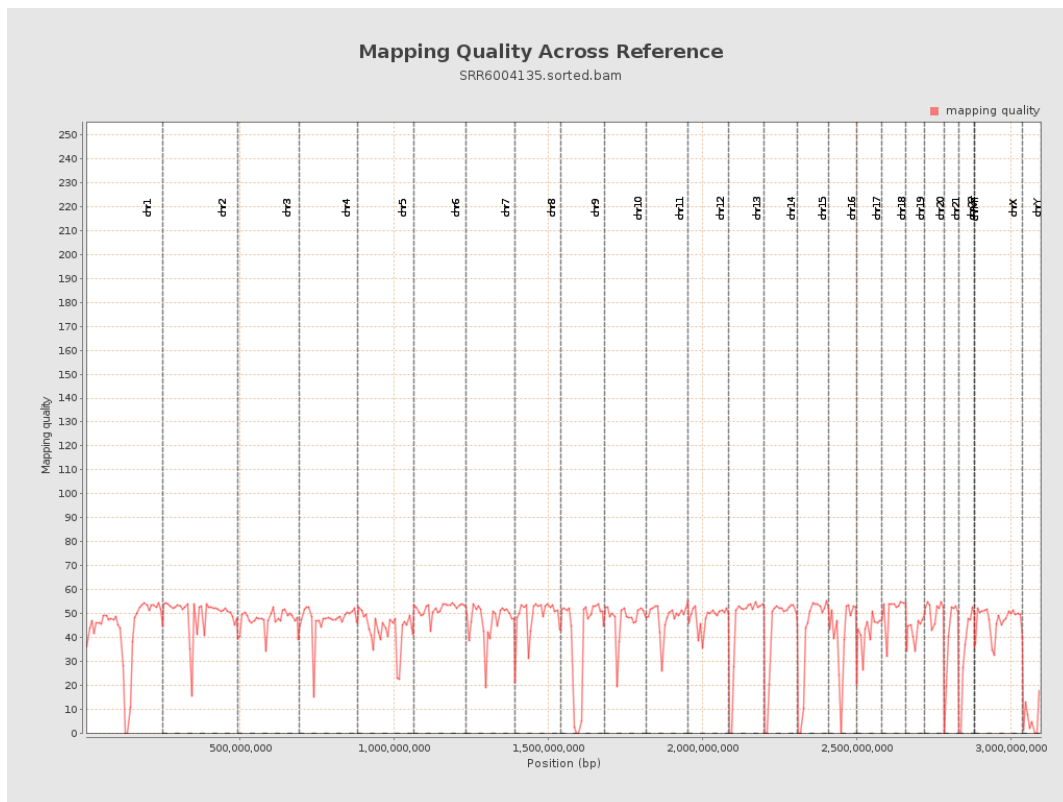
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

