Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:21:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063540.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_SRR6063540 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063540.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:20:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063540.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,563,249
Mapped reads	4,263,294 / 93.43%
Unmapped reads	299,955 / 6.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,184 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	724,143 / 15.87%
Duplication rate	13.74%
Clipped reads	2,303,542 / 50.48%

2.2. ACGT Content

Number/percentage of A's	70,050,190 / 25.65%
Number/percentage of C's	49,121,822 / 17.99%
Number/percentage of T's	89,158,906 / 32.65%
Number/percentage of G's	64,690,290 / 23.69%
Number/percentage of N's	30,475 / 0.01%
GC Percentage	41.68%

2.3. Coverage

Mean	0.0882

Standard Deviation	0.9526

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

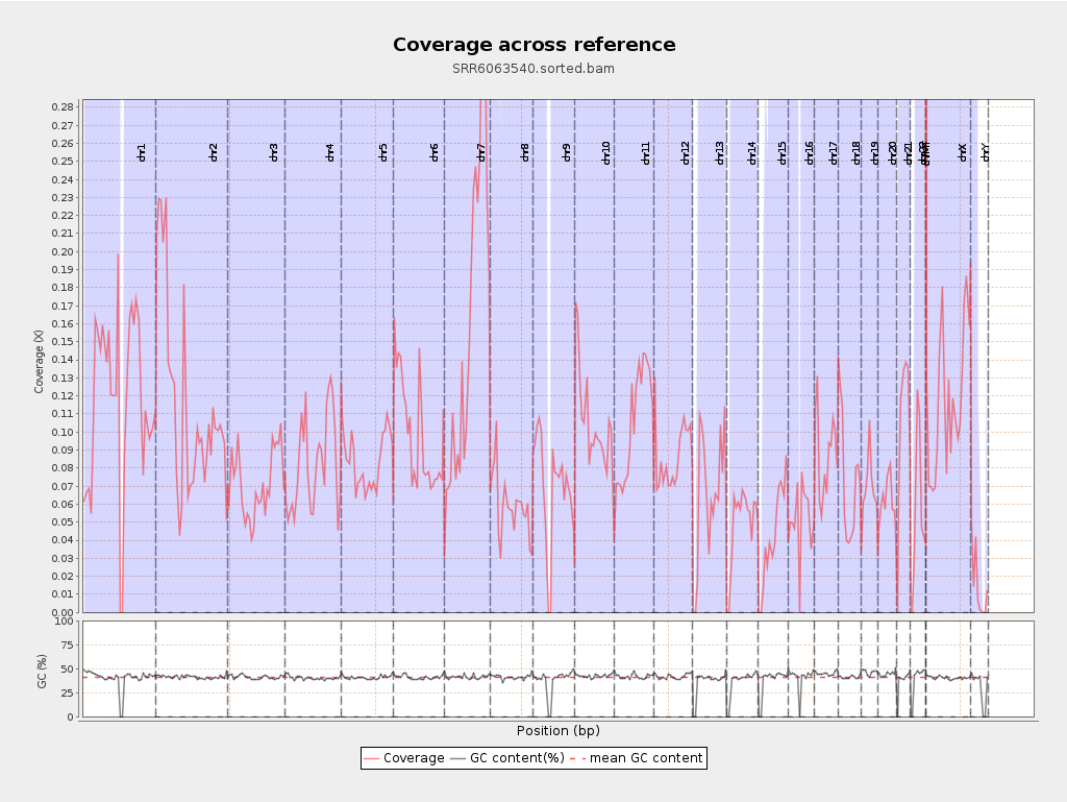
General error rate	0.54%
Mismatches	1,432,910
Insertions	17,283
Mapped reads with at least one insertion	0.4%
Deletions	58,960
Mapped reads with at least one deletion	1.37%
Homopolymer indels	44.36%

2.6. Chromosome stats

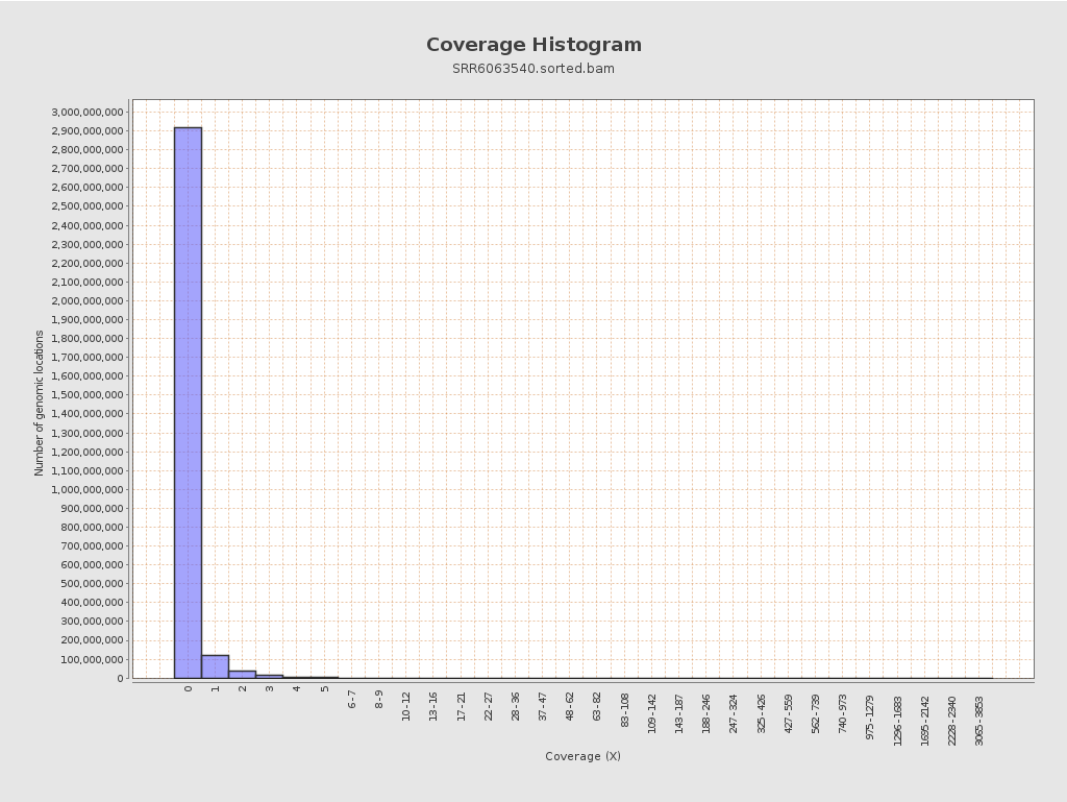
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29166761	0.117	1.9553
chr2	243199373	28223096	0.116	1.8096
chr3	198022430	14105554	0.0712	0.3874
chr4	191154276	15888300	0.0831	0.4485
chr5	180915260	15176076	0.0839	0.4202
chr6	171115067	16815467	0.0983	0.6513
chr7	159138663	25606713	0.1609	1.0218

chr8	146364022	8517320	0.0582	0.8911
chr9	141213431	9758010	0.0691	0.6875
chr10	135534747	14284291	0.1054	0.6304
chr11	135006516	14161222	0.1049	0.6389
chr12	133851895	11604095	0.0867	0.4601
chr13	115169878	7559255	0.0656	0.4365
chr14	107349540	5309374	0.0495	0.3751
chr15	102531392	4373632	0.0427	0.3493
chr16	90354753	4625509	0.0512	0.3809
chr17	81195210	7218609	0.0889	0.4841
chr18	78077248	5677133	0.0727	1.2897
chr19	59128983	4106942	0.0695	1.217
chr20	63025520	3921137	0.0622	0.4062
chr21	48129895	5001911	0.1039	0.4896
chr22	51304566	2817060	0.0549	0.3286
chrMT	16571	255022	15.3897	9.579
chrX	155270560	18131448	0.1168	0.5968
chrY	59373566	851027	0.0143	0.4269

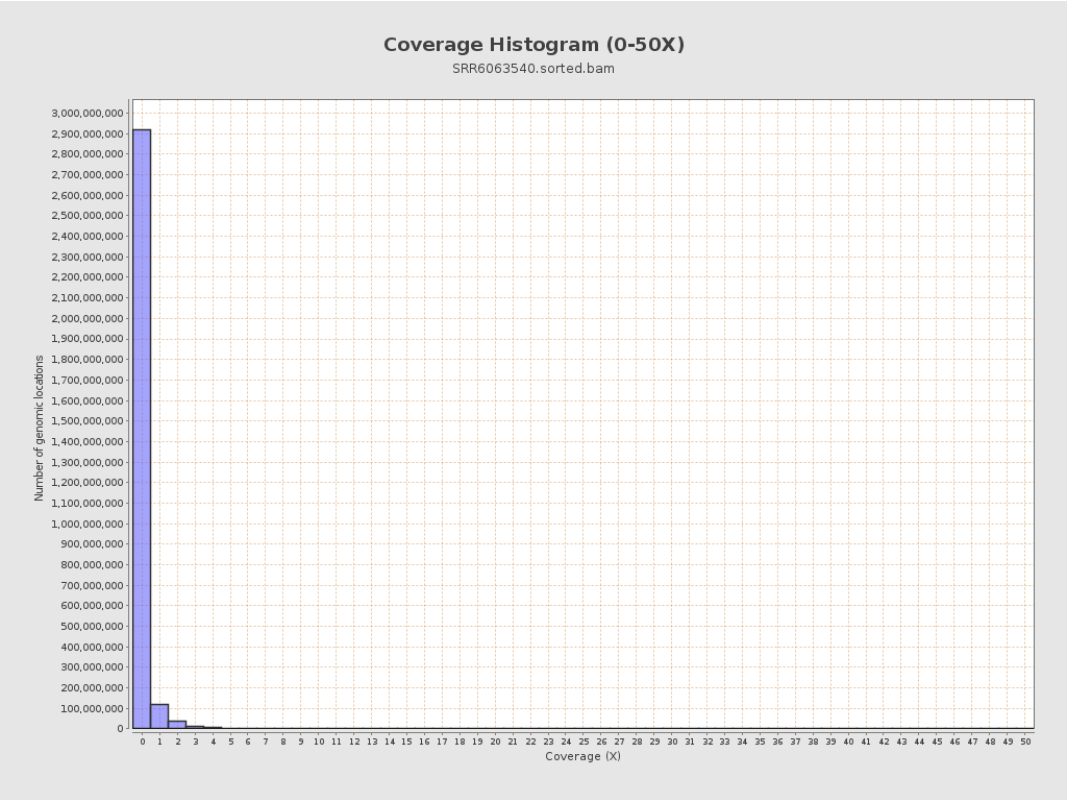
3. Results : Coverage across reference



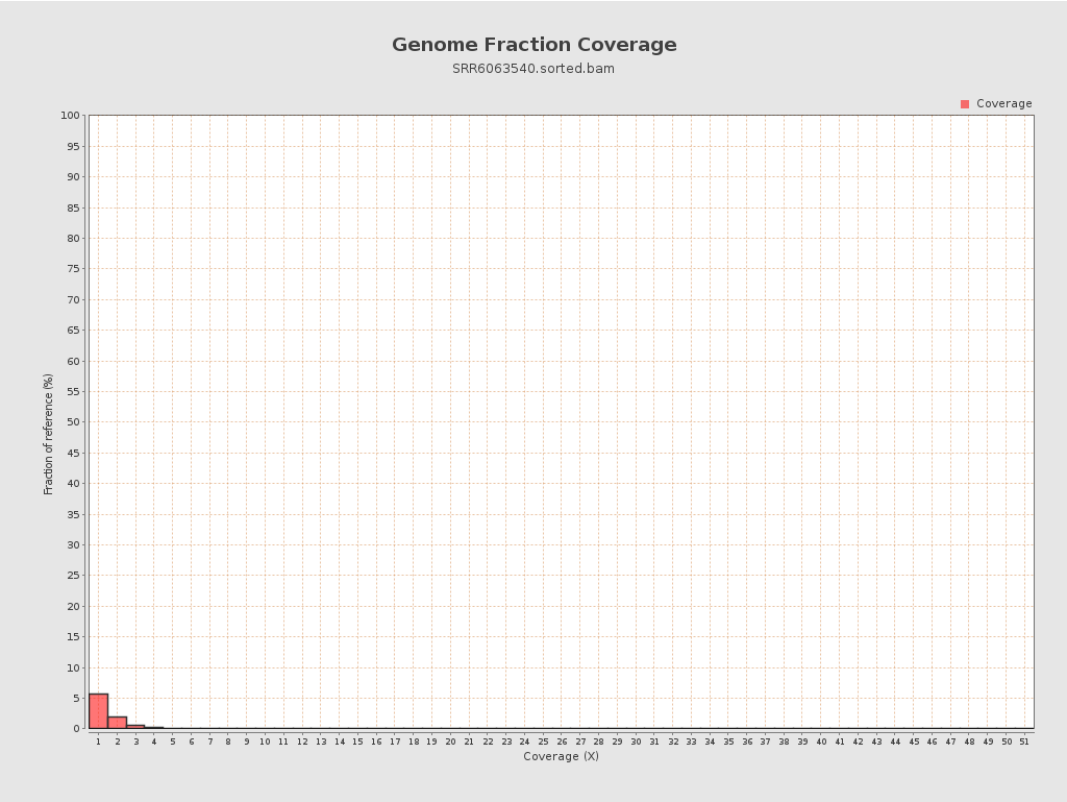
4. Results : Coverage Histogram



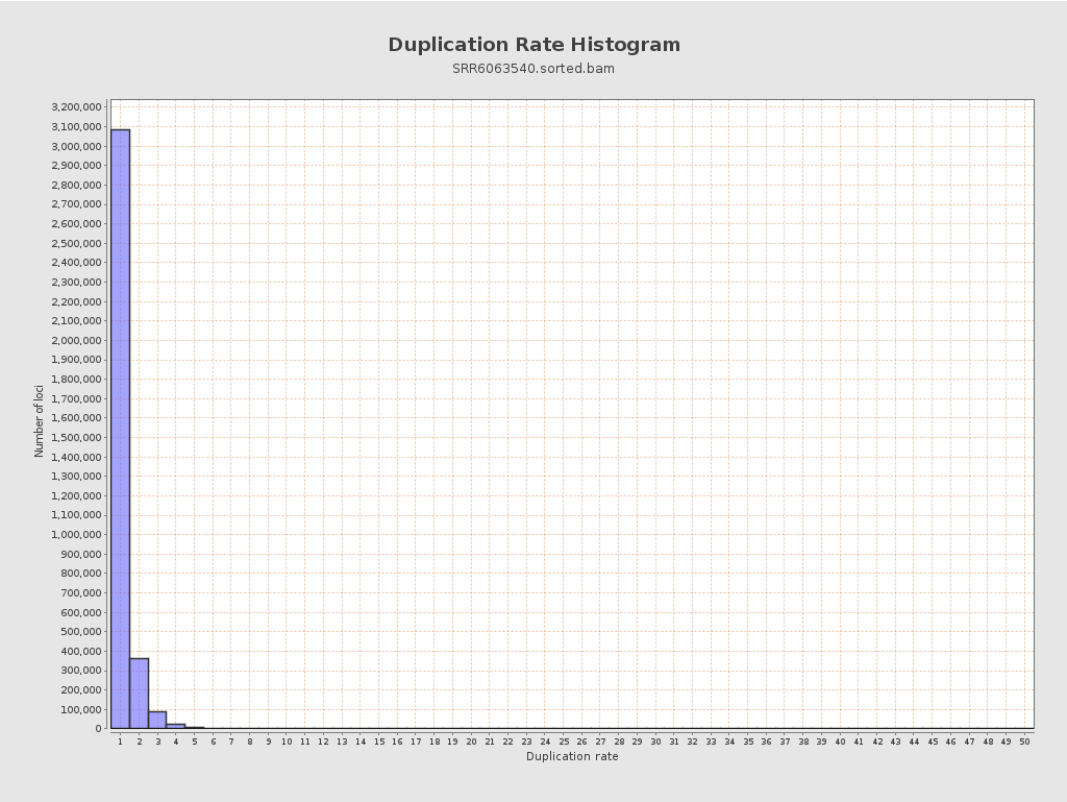
5. Results : Coverage Histogram (0-50X)



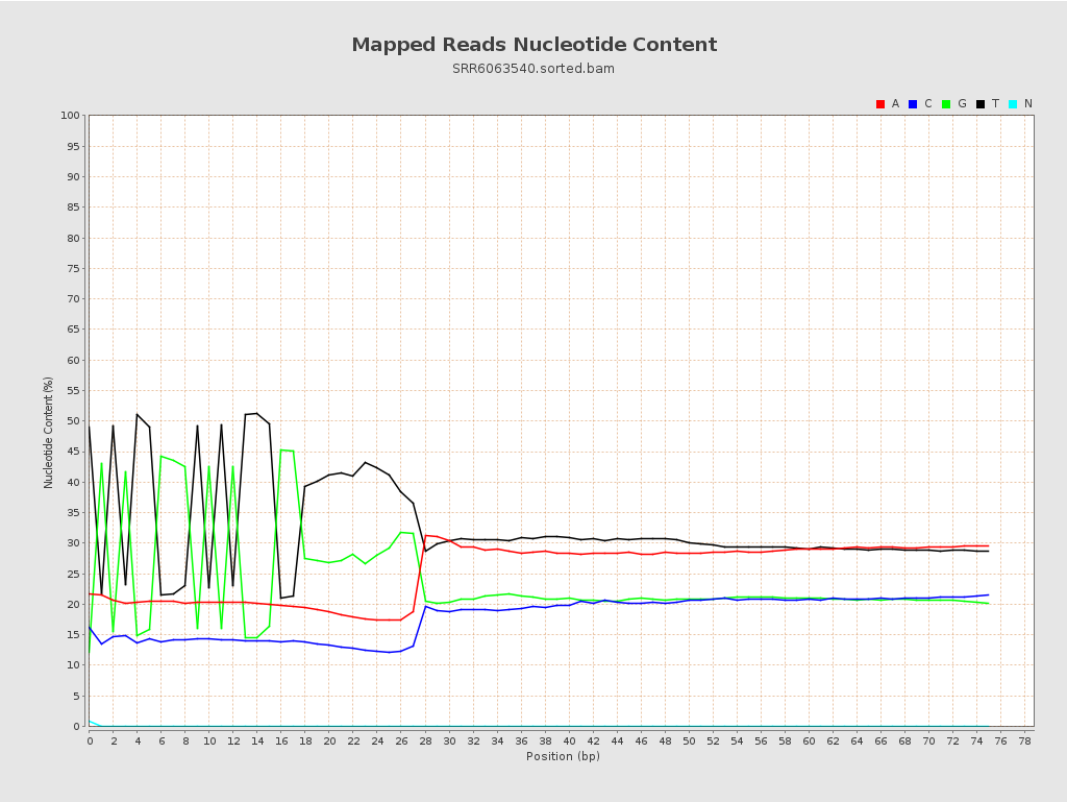
6. Results : Genome Fraction Coverage



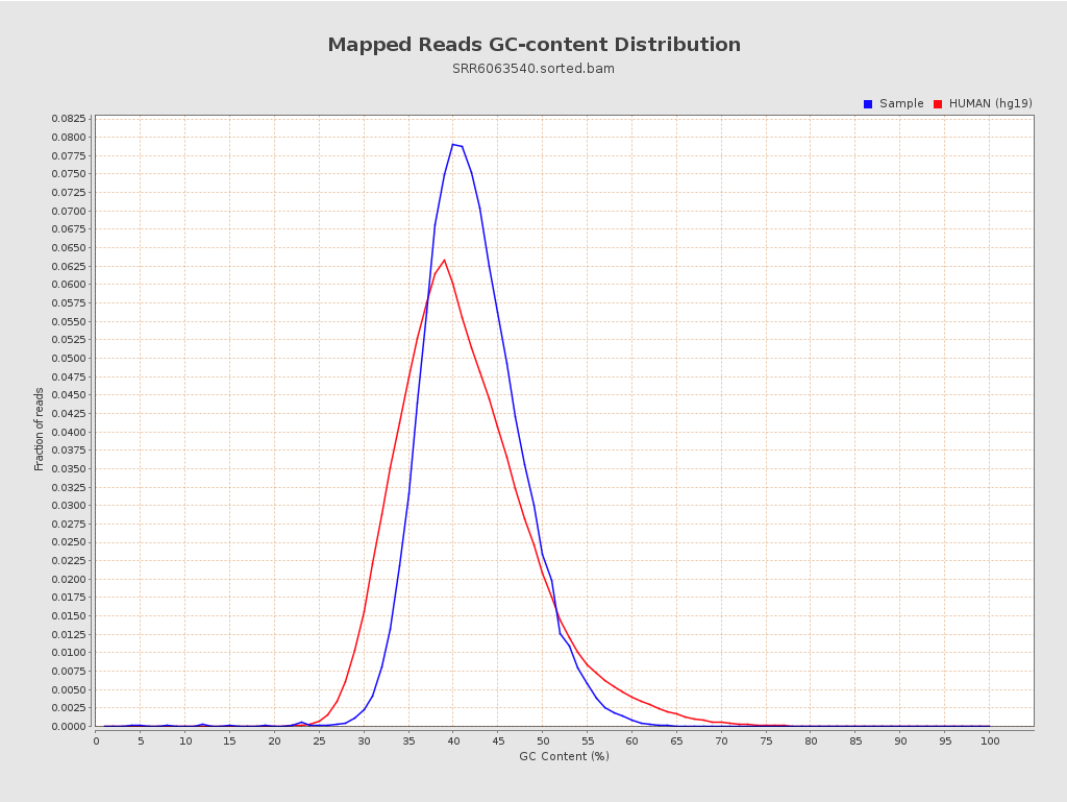
7. Results : Duplication Rate Histogram



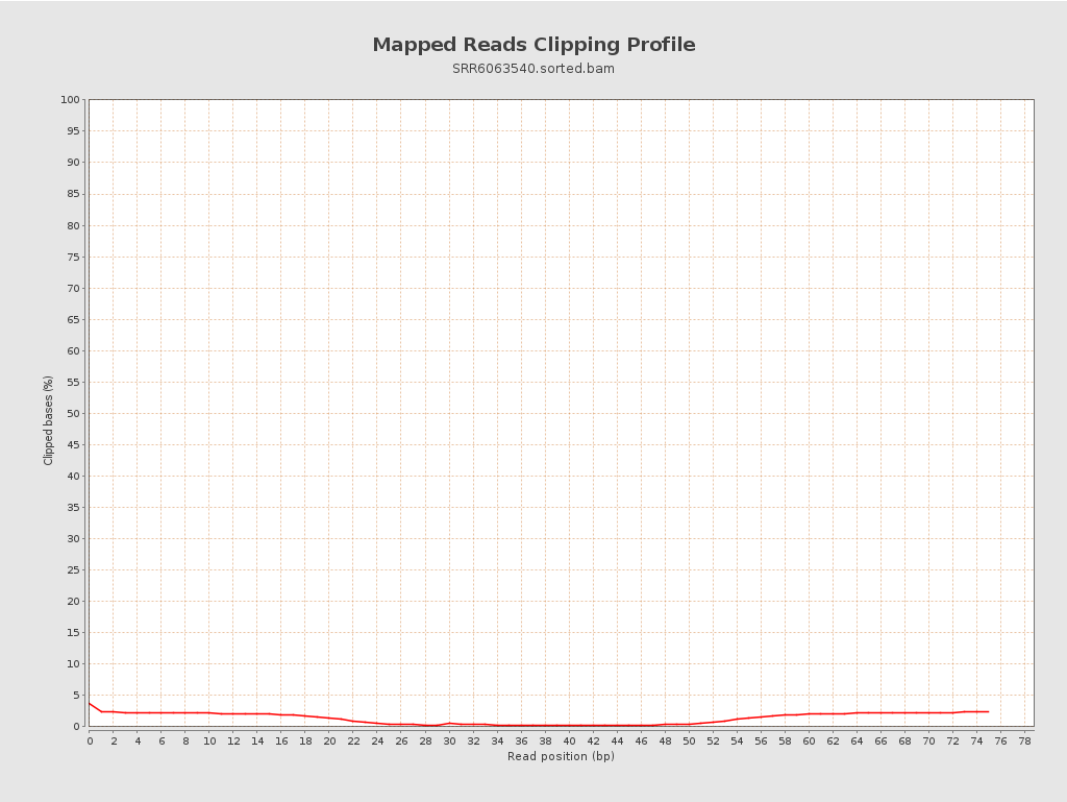
8. Results : Mapped Reads Nucleotide Content



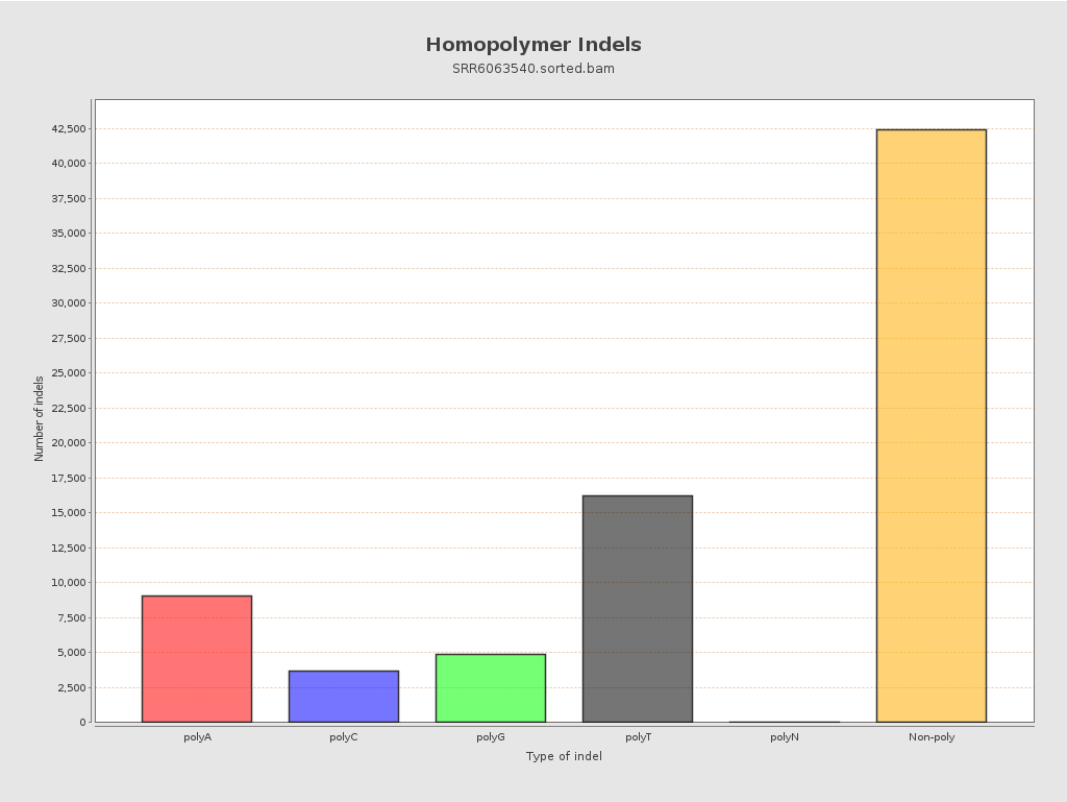
9. Results : Mapped Reads GC-content Distribution



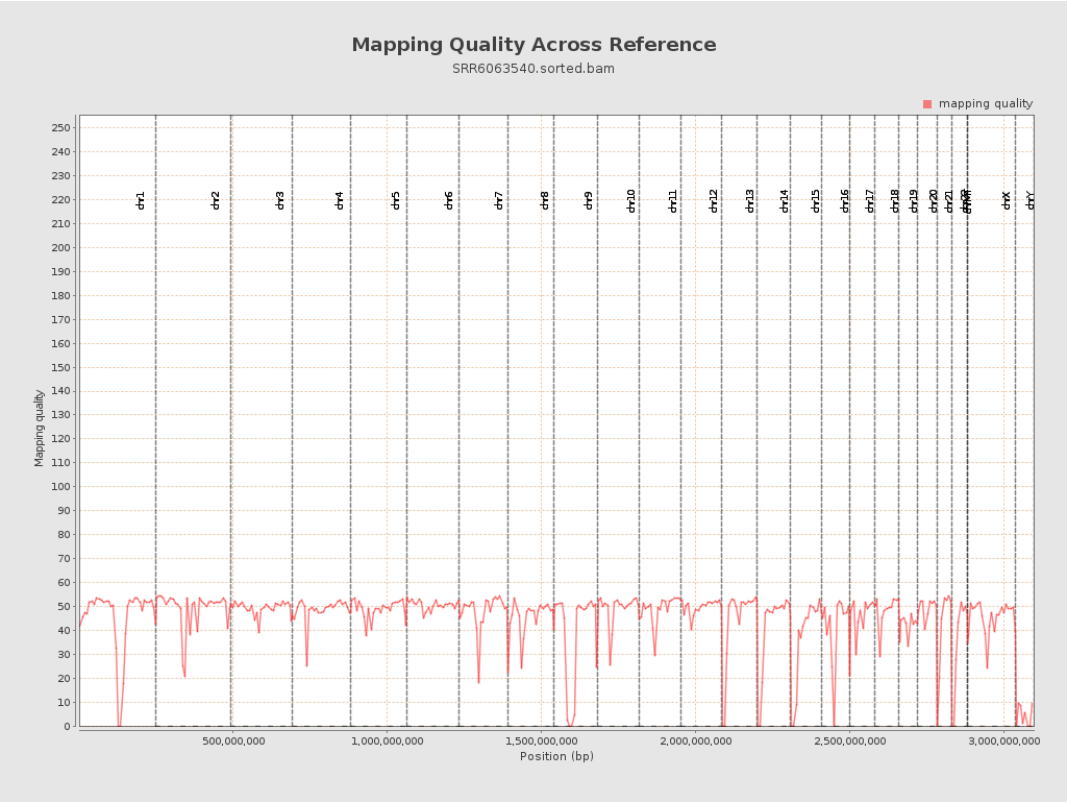
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram