Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:58:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008755.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_SRR6008755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008755.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:58:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,484,064
Mapped reads	1,278,416 / 86.14%
Unmapped reads	205,648 / 13.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,920 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	127,919 / 8.62%
Duplication rate	7.73%
Clipped reads	605,715 / 40.81%

2.2. ACGT Content

Number/percentage of A's	22,487,307 / 26.77%
Number/percentage of C's	16,252,491 / 19.35%
Number/percentage of T's	25,913,301 / 30.85%
Number/percentage of G's	19,234,508 / 22.9%
Number/percentage of N's	121,314 / 0.14%
GC Percentage	42.24%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.3561

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

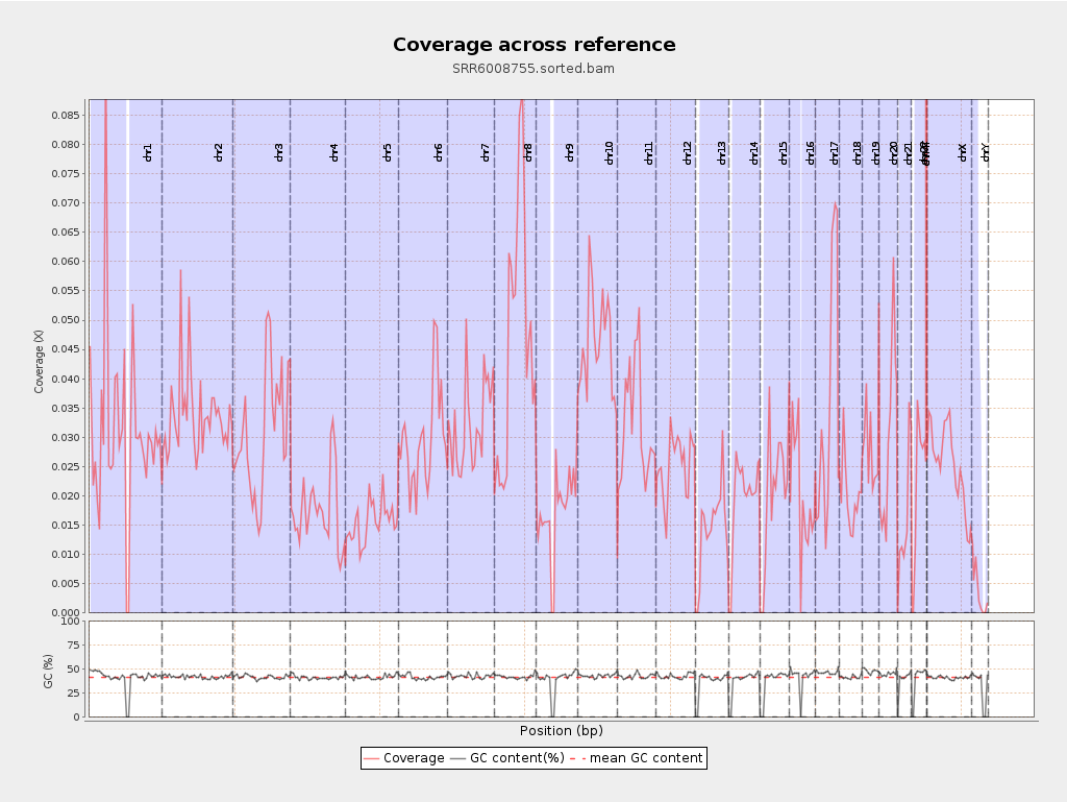
General error rate	0.86%
Mismatches	707,877
Insertions	6,029
Mapped reads with at least one insertion	0.47%
Deletions	22,004
Mapped reads with at least one deletion	1.7%
Homopolymer indels	45.37%

2.6. Chromosome stats

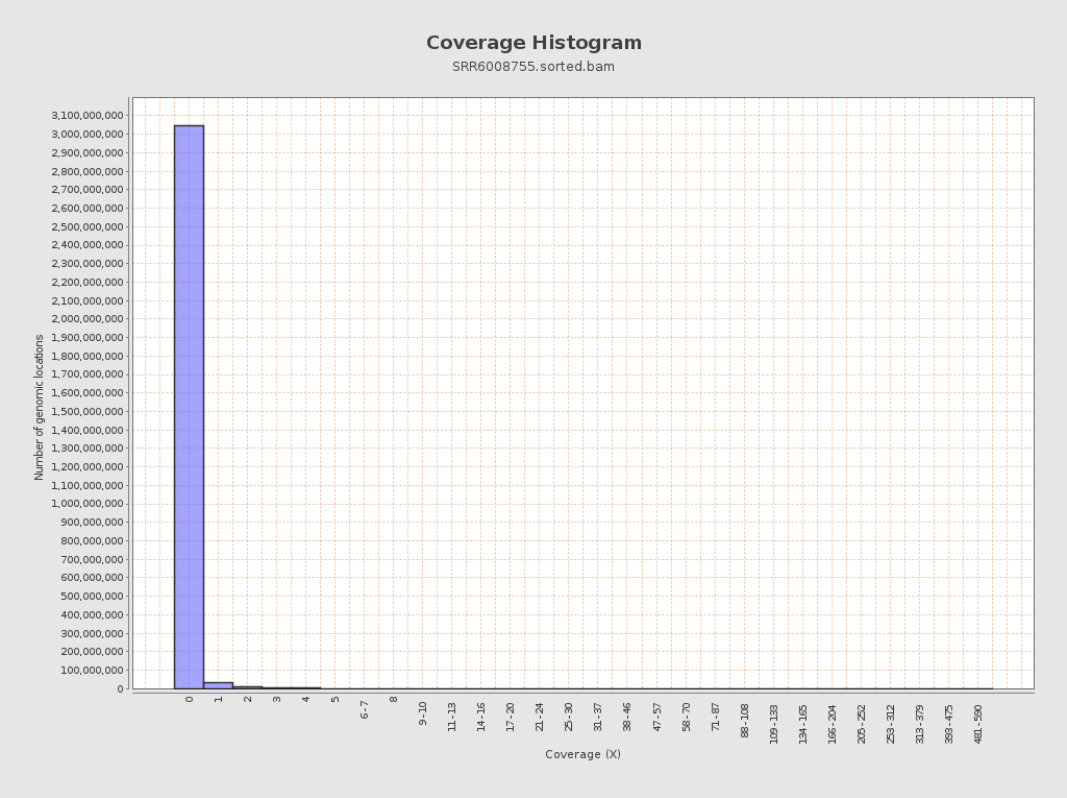
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7611072	0.0305	0.4199
chr2	243199373	8207462	0.0337	0.4135
chr3	198022430	6094699	0.0308	0.2634
chr4	191154276	3271408	0.0171	0.1944
chr5	180915260	2824568	0.0156	0.19
chr6	171115067	5016793	0.0293	0.2667
chr7	159138663	5135323	0.0323	0.4067

chr8	146364022	6851888	0.0468	0.345
chr9	141213431	2402251	0.017	0.2737
chr10	135534747	6228271	0.046	0.3841
chr11	135006516	4308932	0.0319	0.3417
chr12	133851895	3375457	0.0252	0.2391
chr13	115169878	1648023	0.0143	0.1875
chr14	107349540	2068429	0.0193	0.2077
chr15	102531392	2092703	0.0204	0.2126
chr16	90354753	1826899	0.0202	0.2729
chr17	81195210	2868559	0.0353	0.3031
chr18	78077248	1574742	0.0202	0.5883
chr19	59128983	1683732	0.0285	0.3257
chr20	63025520	1858913	0.0295	0.2585
chr21	48129895	783852	0.0163	0.1972
chr22	51304566	1093148	0.0213	0.2193
chrMT	16571	1087314	65.6155	33.4484
chrX	155270560	3923839	0.0253	0.248
chrY	59373566	209723	0.0035	0.1158

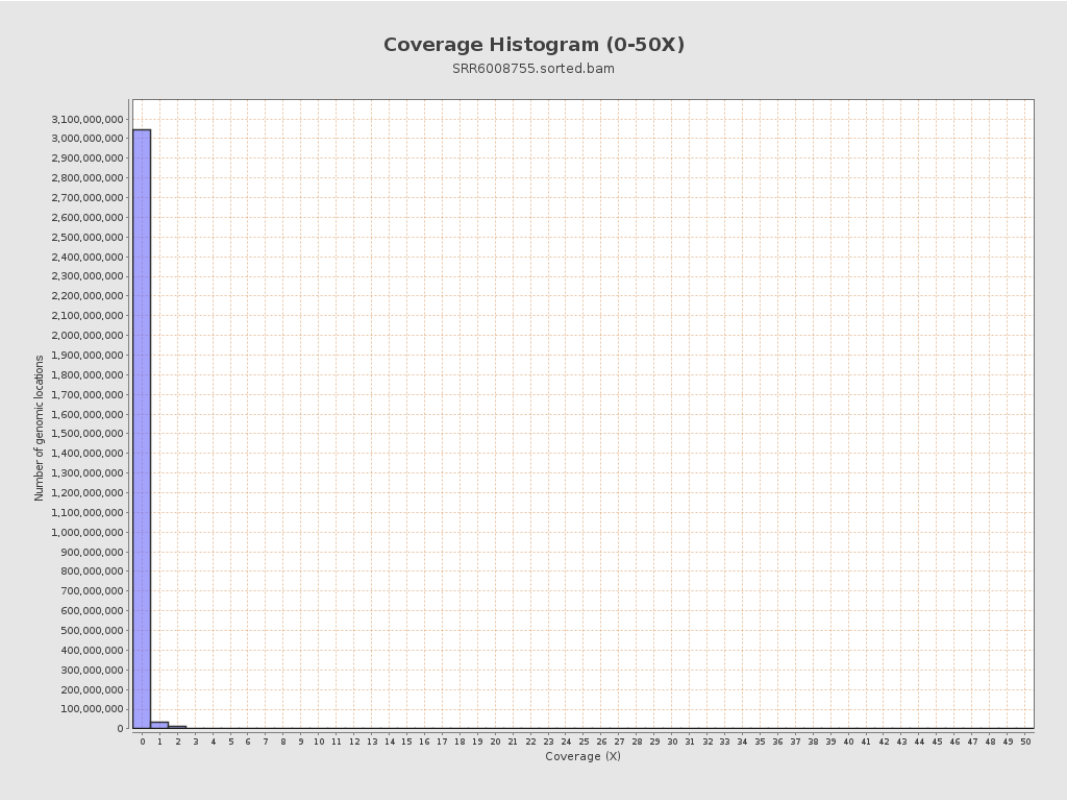
3. Results : Coverage across reference



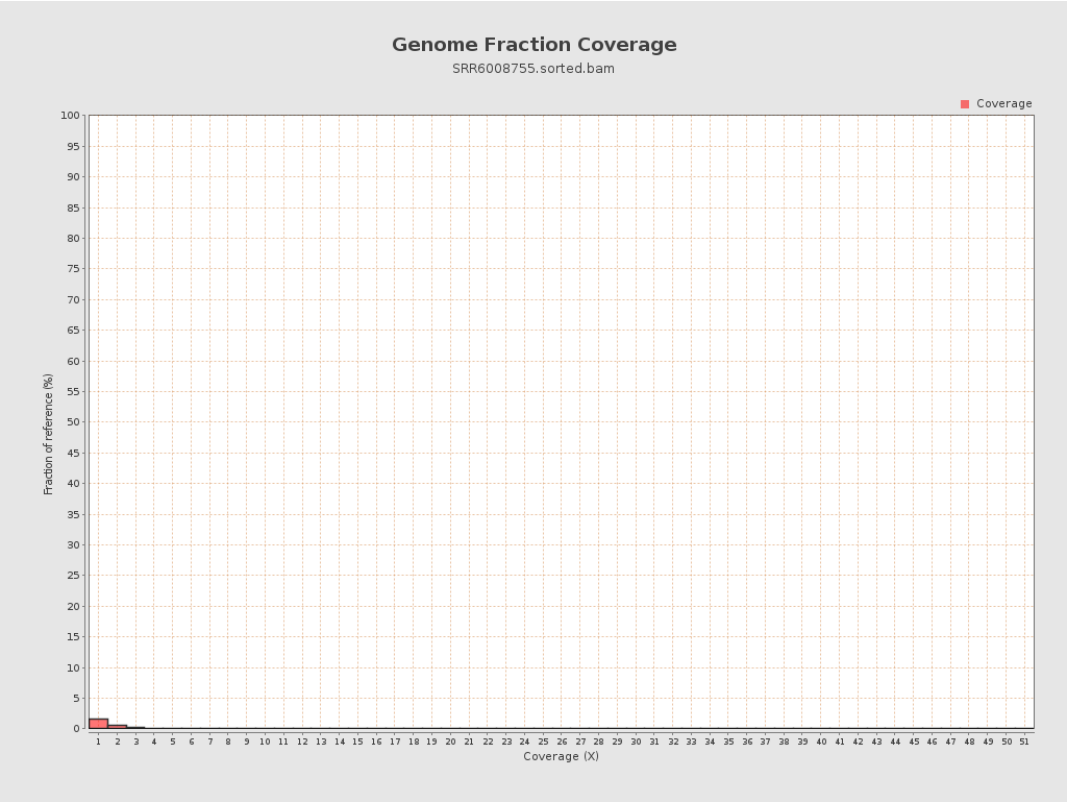
4. Results : Coverage Histogram



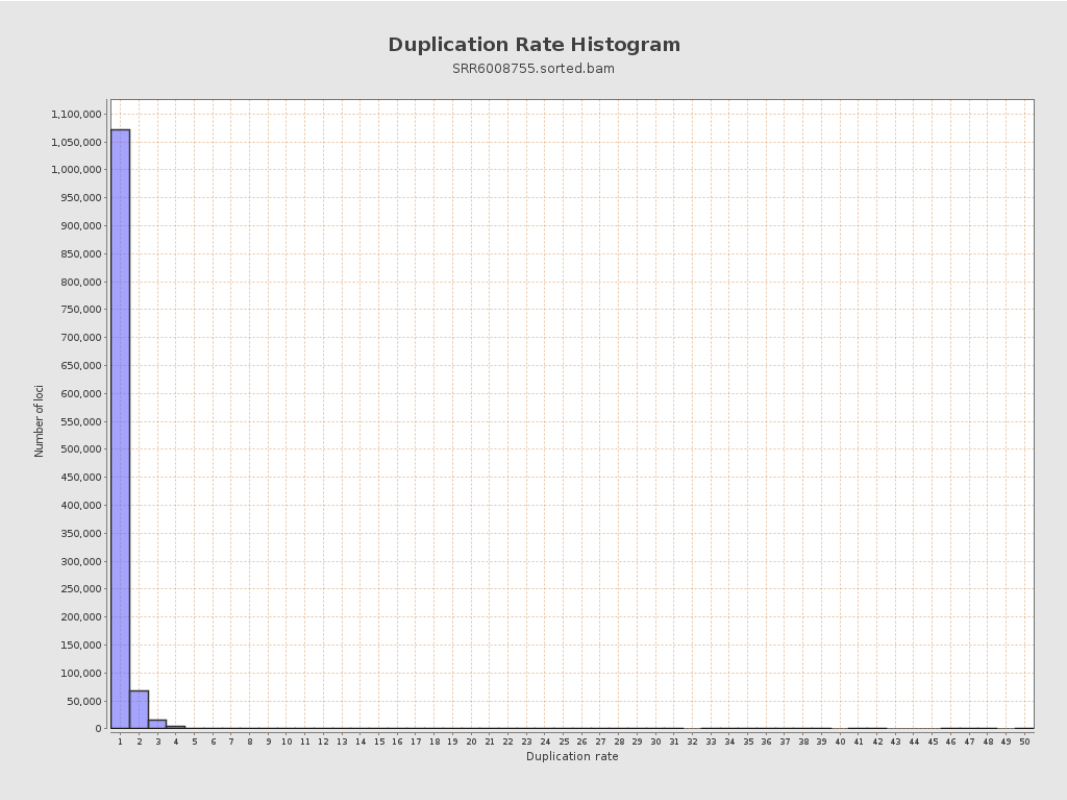
5. Results : Coverage Histogram (0-50X)



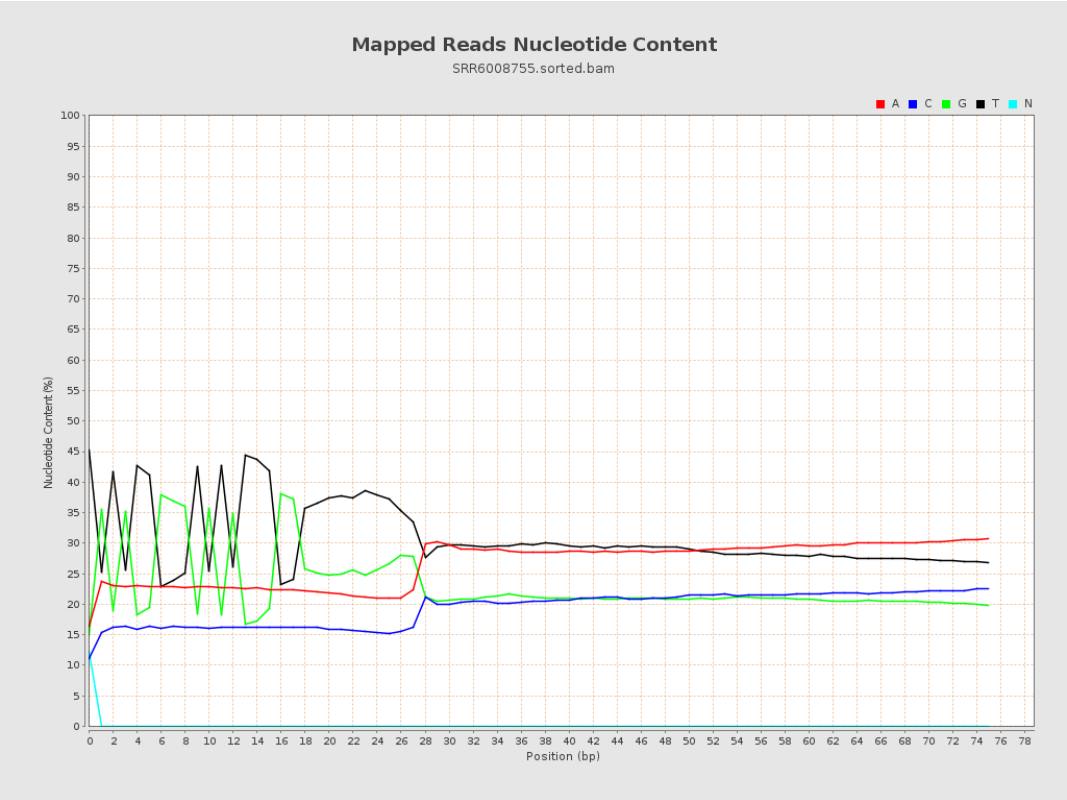
6. Results : Genome Fraction Coverage



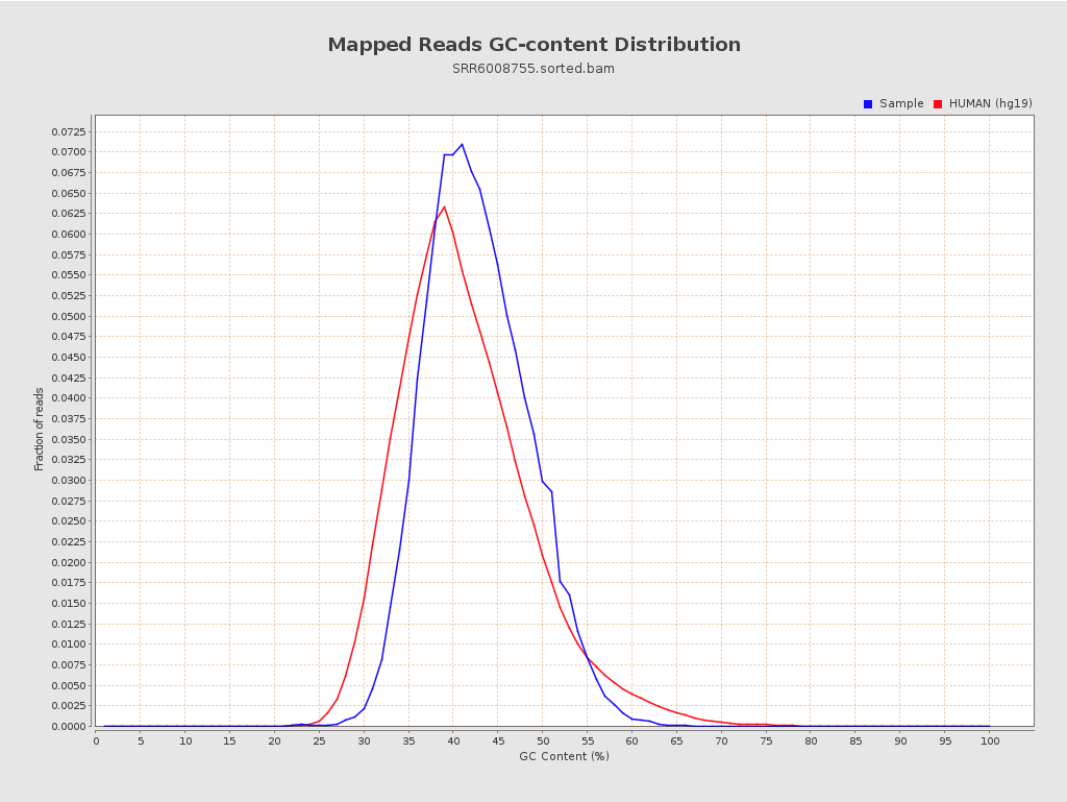
7. Results : Duplication Rate Histogram



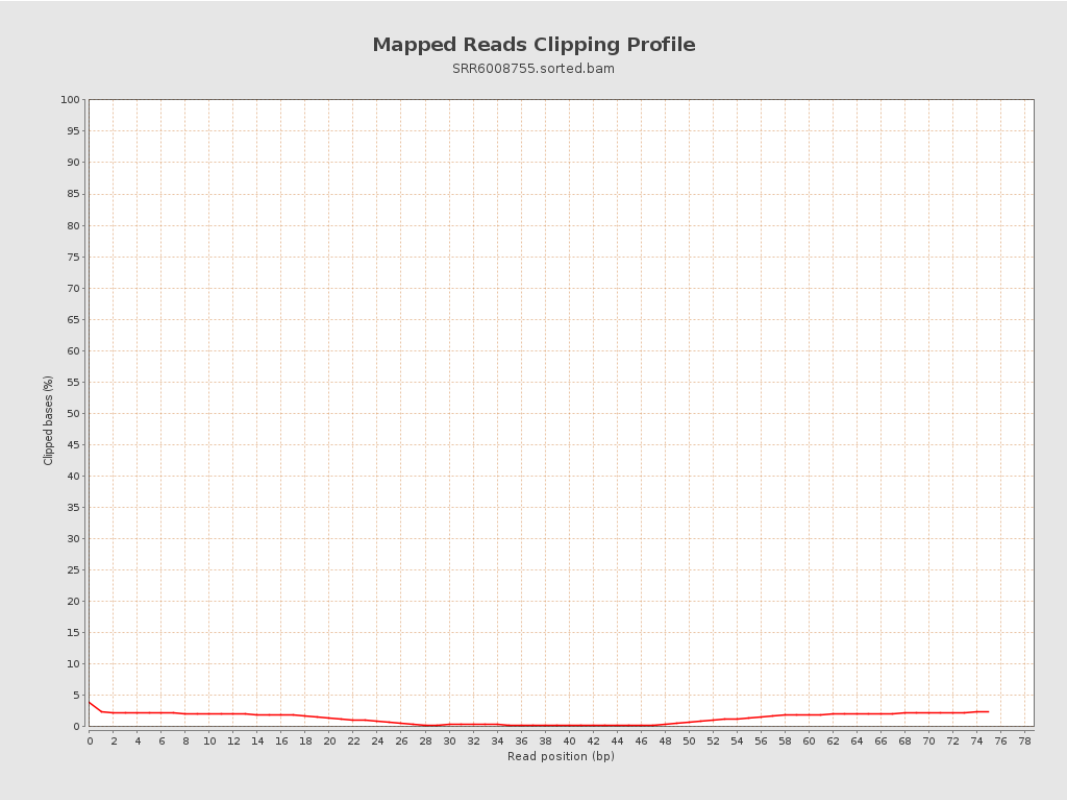
8. Results : Mapped Reads Nucleotide Content



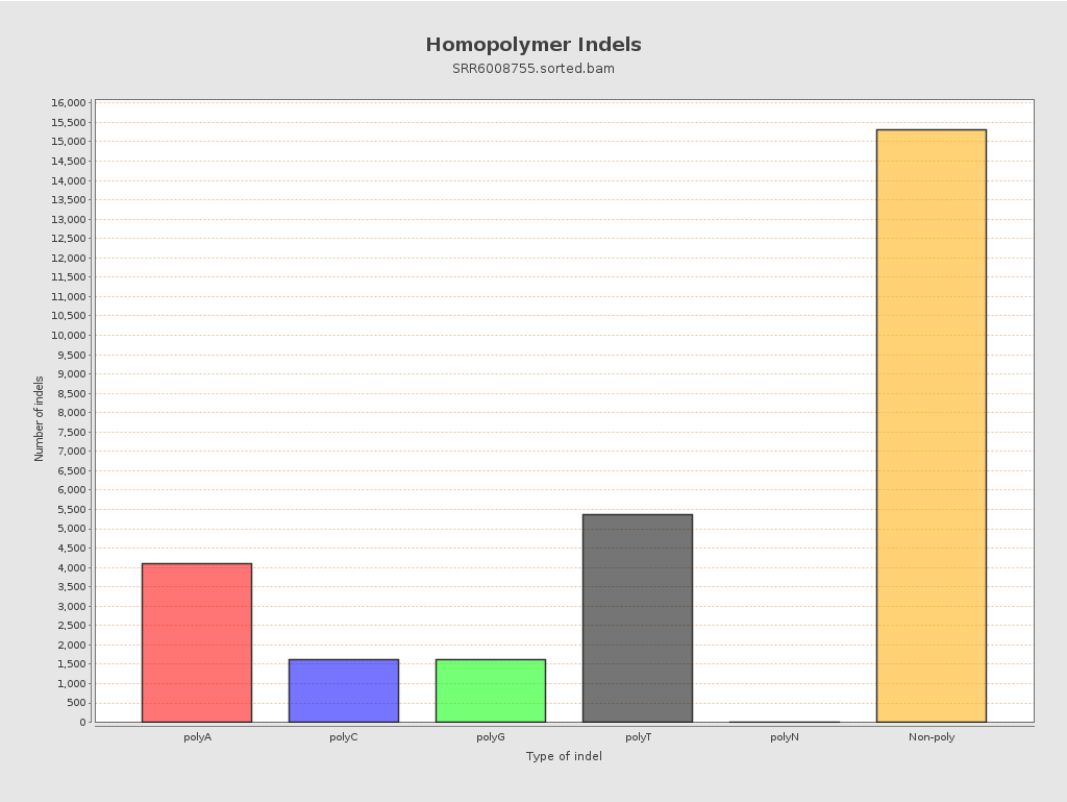
9. Results : Mapped Reads GC-content Distribution



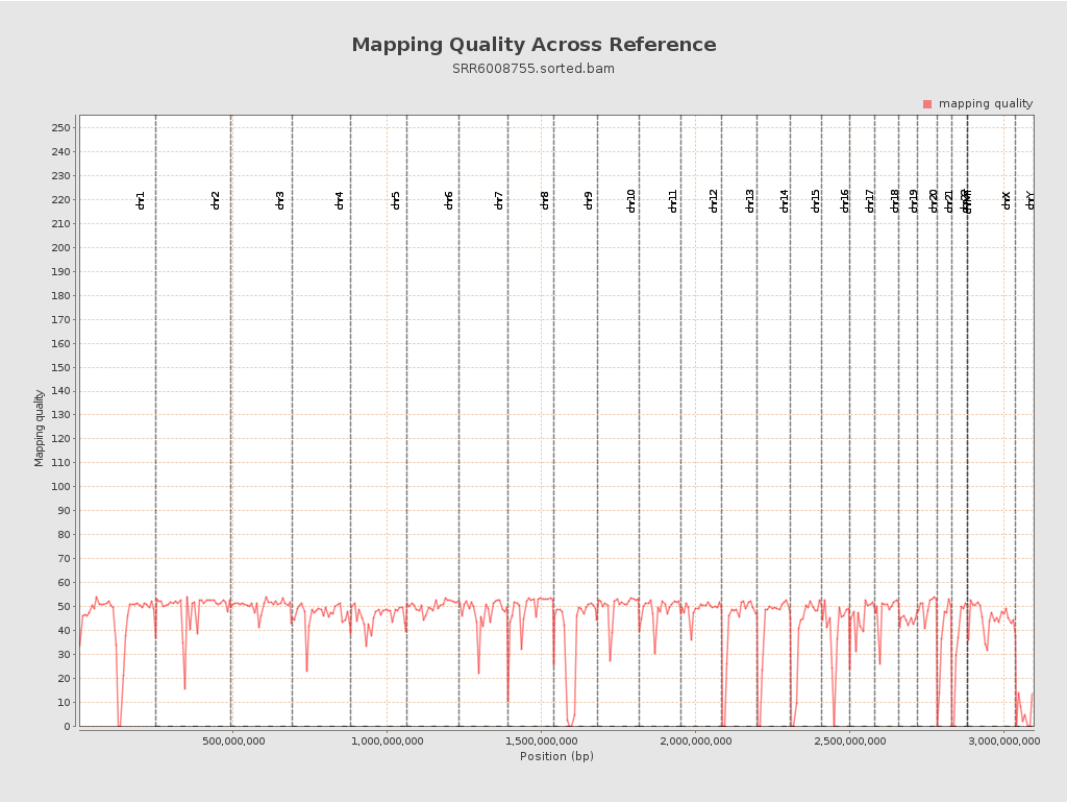
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram