Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:00:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008756.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_SRR6008756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008756.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:00:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,212,035
Mapped reads	1,075,862 / 88.76%
Unmapped reads	136,173 / 11.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,013 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	50,651 / 4.18%
Duplication rate	3.89%
Clipped reads	462,041 / 38.12%

2.2. ACGT Content

Number/percentage of A's	19,503,769 / 27.09%
Number/percentage of C's	13,904,599 / 19.32%
Number/percentage of T's	22,237,441 / 30.89%
Number/percentage of G's	16,238,329 / 22.56%
Number/percentage of N's	104,369 / 0.14%
GC Percentage	41.87%

2.3. Coverage

Mean	0.0233

Standard Deviation	0.2367

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

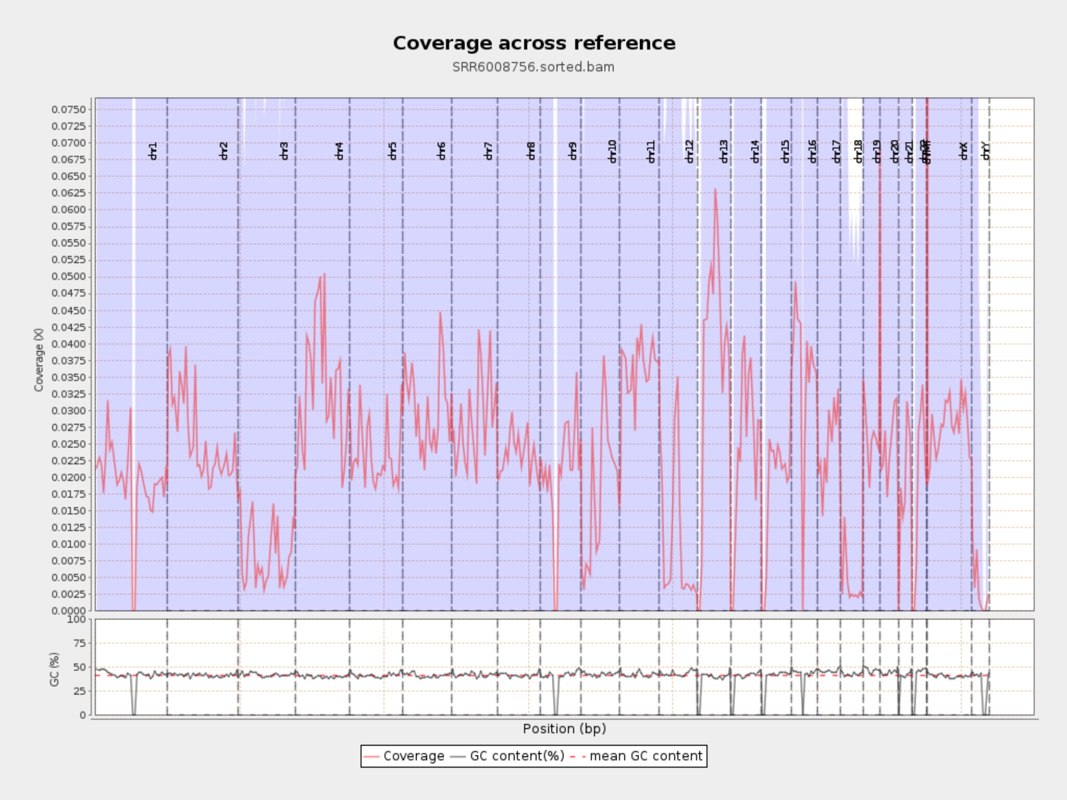
General error rate	0.87%
Mismatches	615,653
Insertions	5,056
Mapped reads with at least one insertion	0.47%
Deletions	23,294
Mapped reads with at least one deletion	2.14%
Homopolymer indels	45.1%

2.6. Chromosome stats

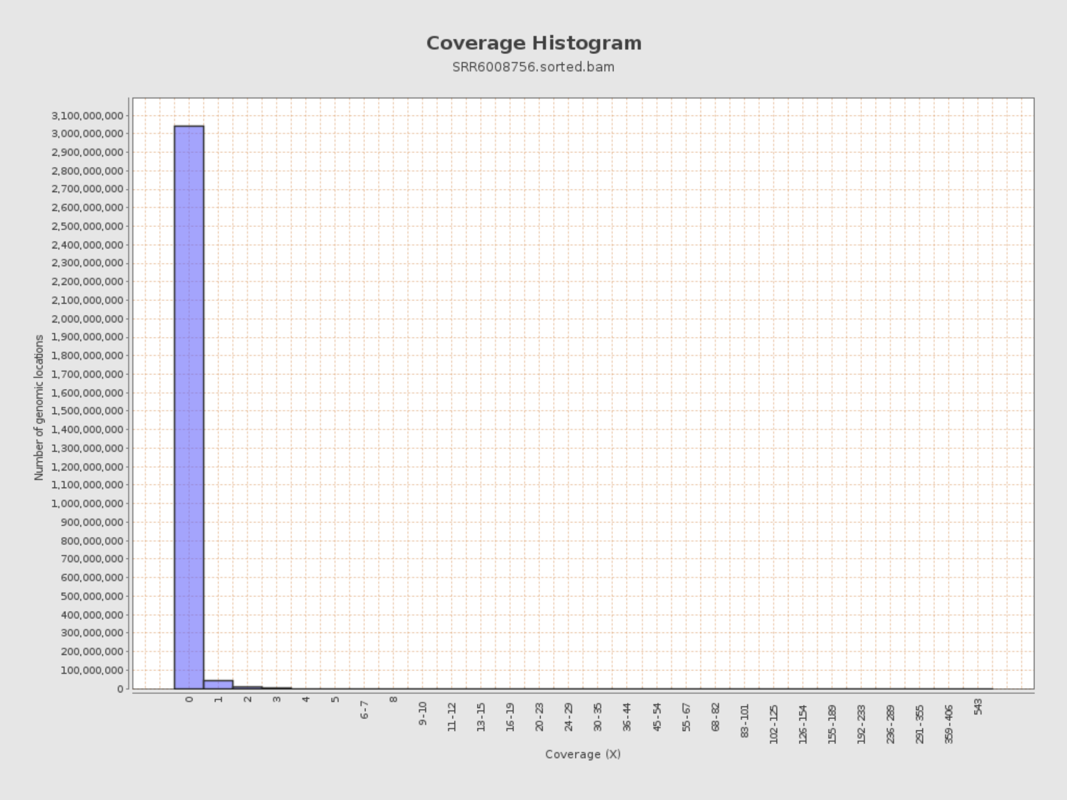
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4807302	0.0193	0.3314
chr2	243199373	6300709	0.0259	0.3192
chr3	198022430	1662380	0.0084	0.1108
chr4	191154276	6311223	0.033	0.2261
chr5	180915260	4183723	0.0231	0.1863
chr6	171115067	5165147	0.0302	0.2314
chr7	159138663	4566302	0.0287	0.3053

chr8	146364022	3429143	0.0234	0.2837
chr9	141213431	2878845	0.0204	0.2038
chr10	135534747	2450419	0.0181	0.1946
chr11	135006516	4950361	0.0367	0.2646
chr12	133851895	1373297	0.0103	0.124
chr13	115169878	4461972	0.0387	0.2425
chr14	107349540	2616788	0.0244	0.1977
chr15	102531392	1861409	0.0182	0.1652
chr16	90354753	3198439	0.0354	0.2462
chr17	81195210	1992350	0.0245	0.2019
chr18	78077248	293312	0.0038	0.2382
chr19	59128983	1612948	0.0273	0.2851
chr20	63025520	1562505	0.0248	0.1984
chr21	48129895	903936	0.0188	0.175
chr22	51304566	944002	0.0184	0.1677
chrMT	16571	17602	1.0622	1.4643
chrX	155270560	4297416	0.0277	0.2074
chrY	59373566	188407	0.0032	0.0816

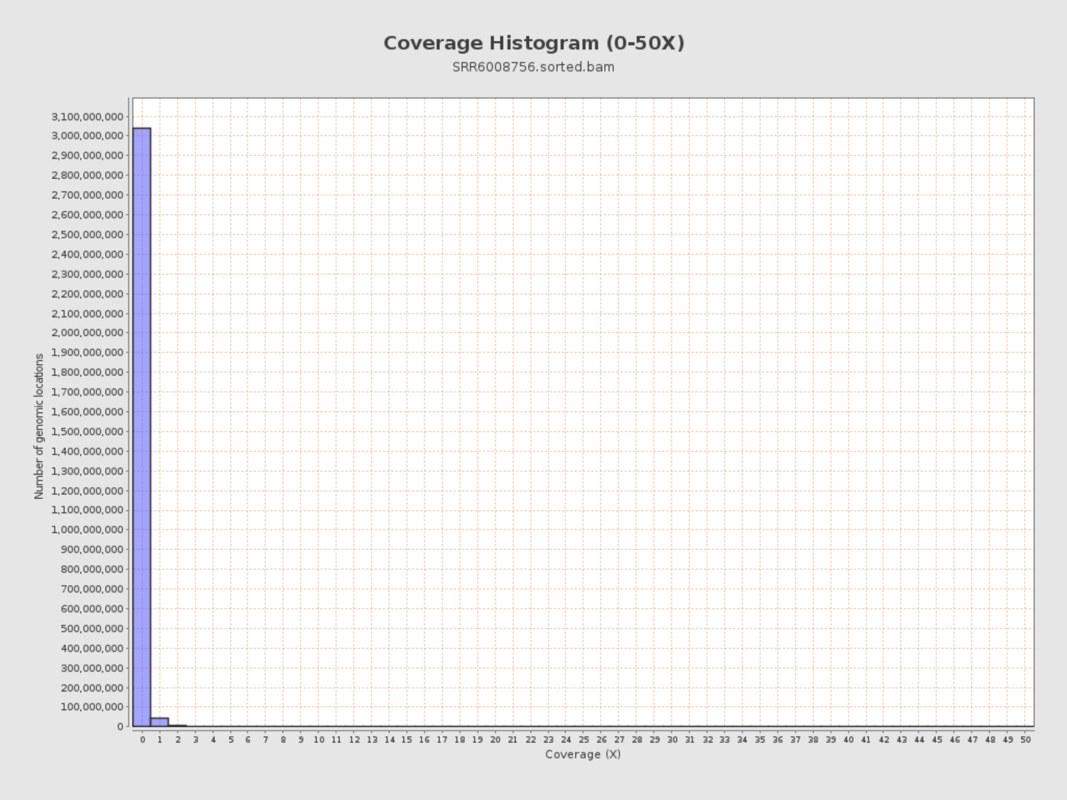
3. Results : Coverage across reference



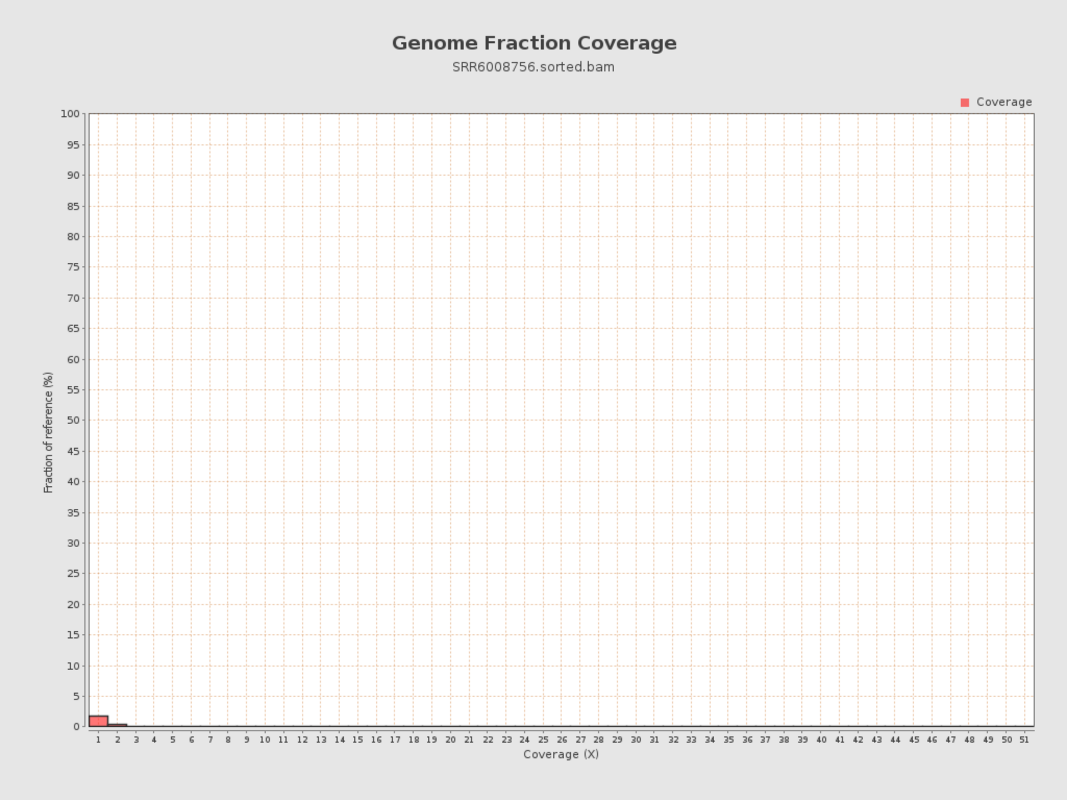
4. Results : Coverage Histogram



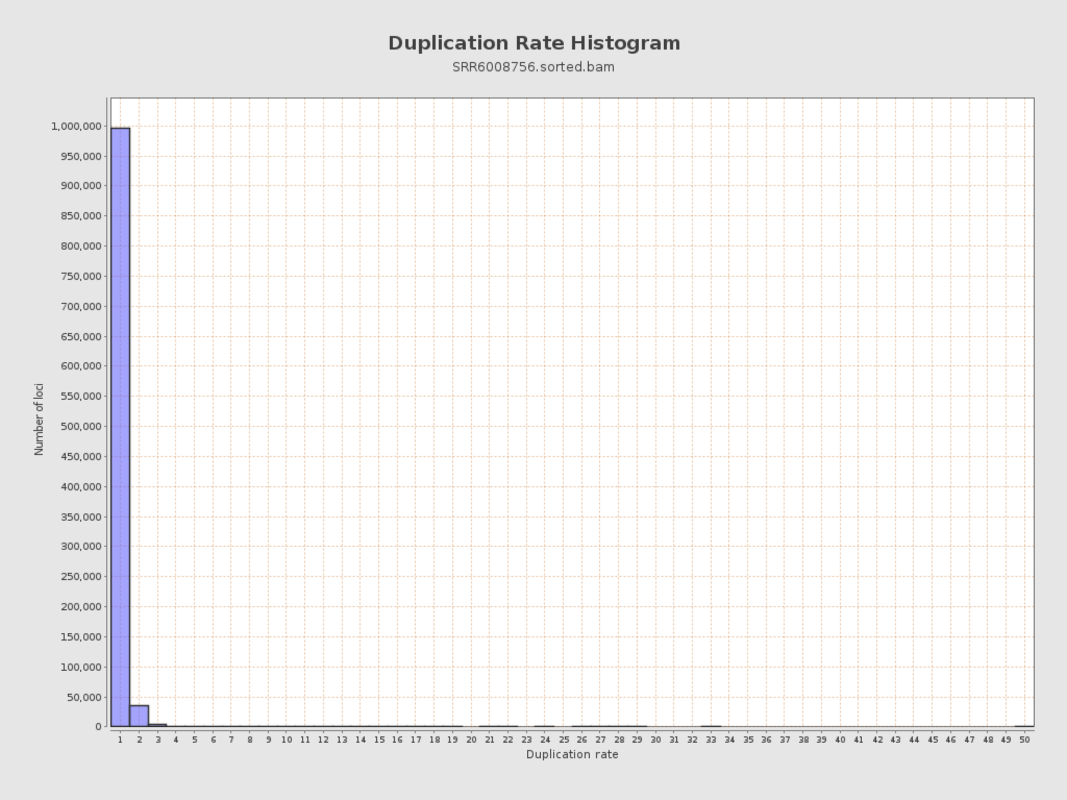
5. Results : Coverage Histogram (0-50X)



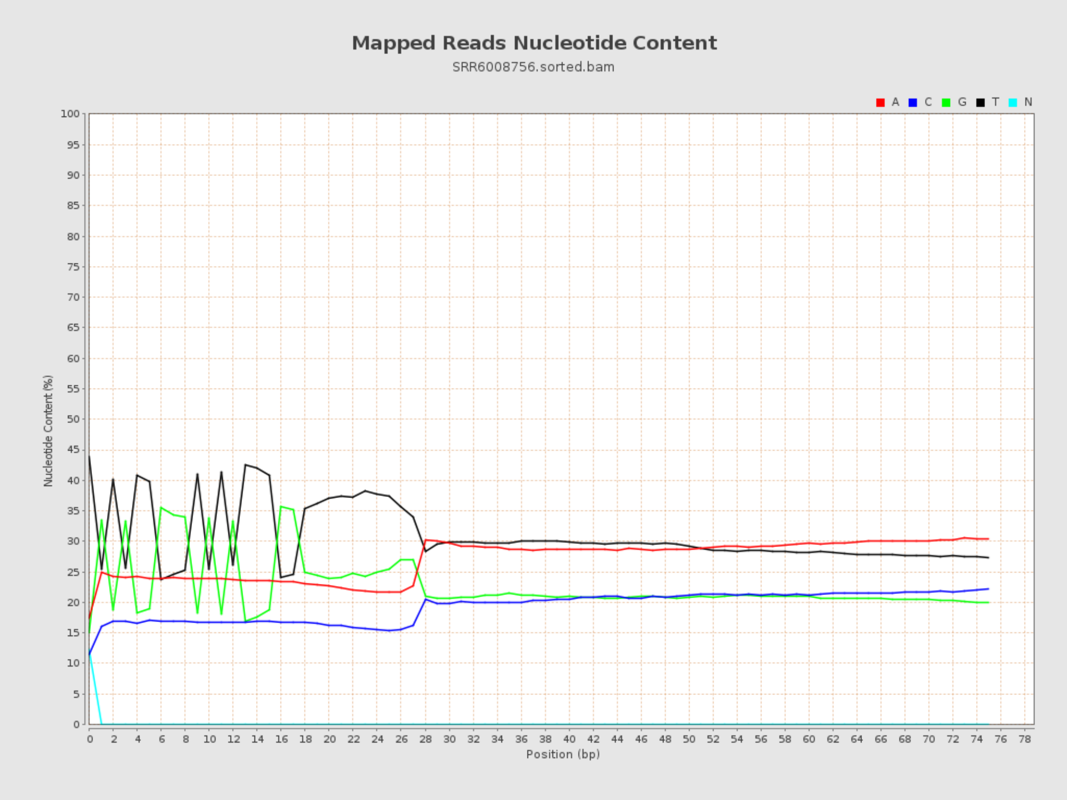
6. Results : Genome Fraction Coverage



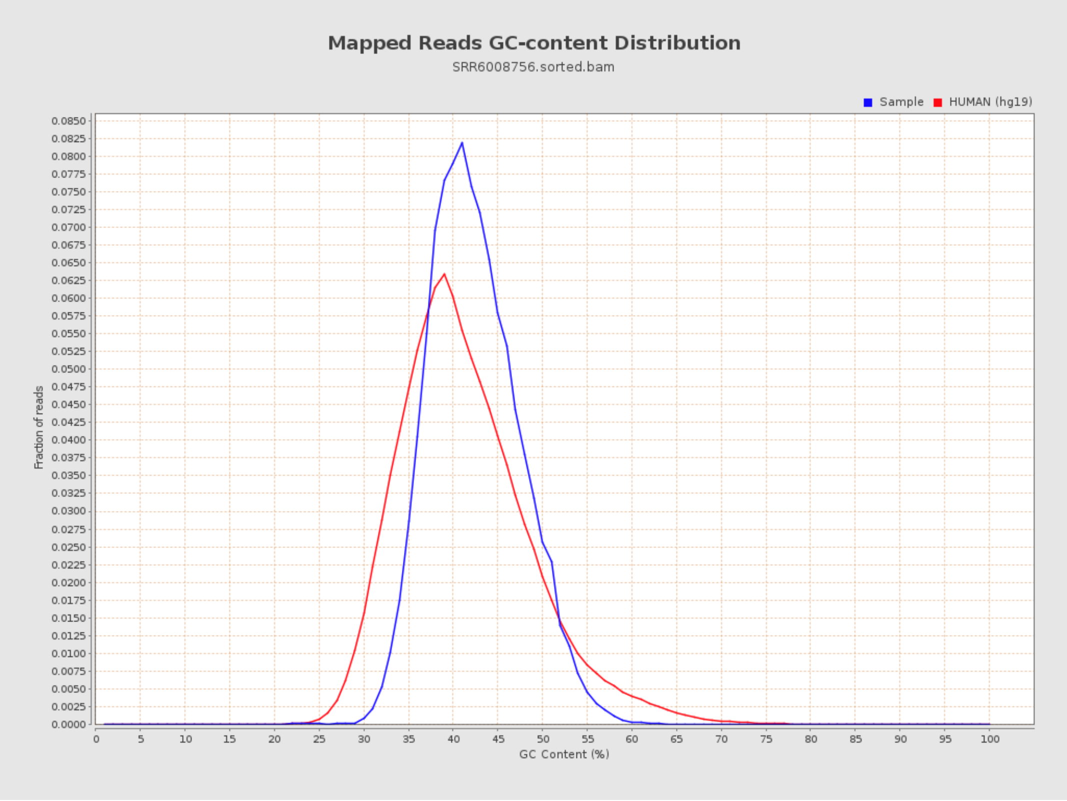
7. Results : Duplication Rate Histogram



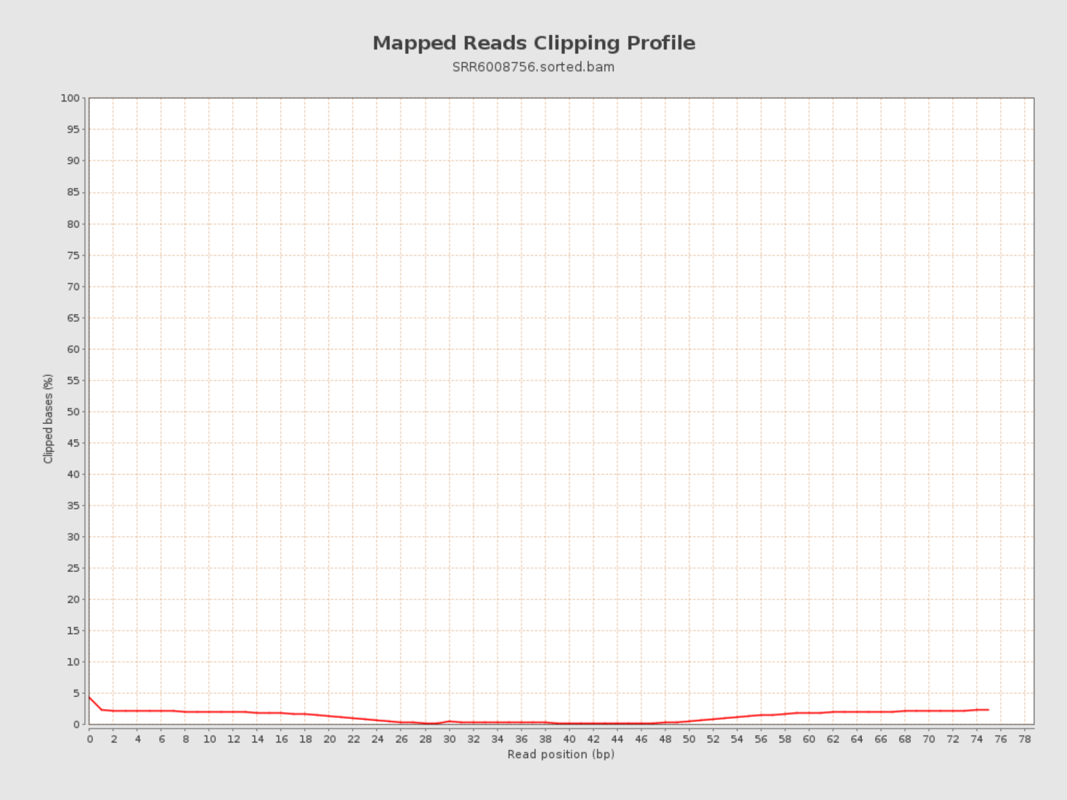
8. Results : Mapped Reads Nucleotide Content



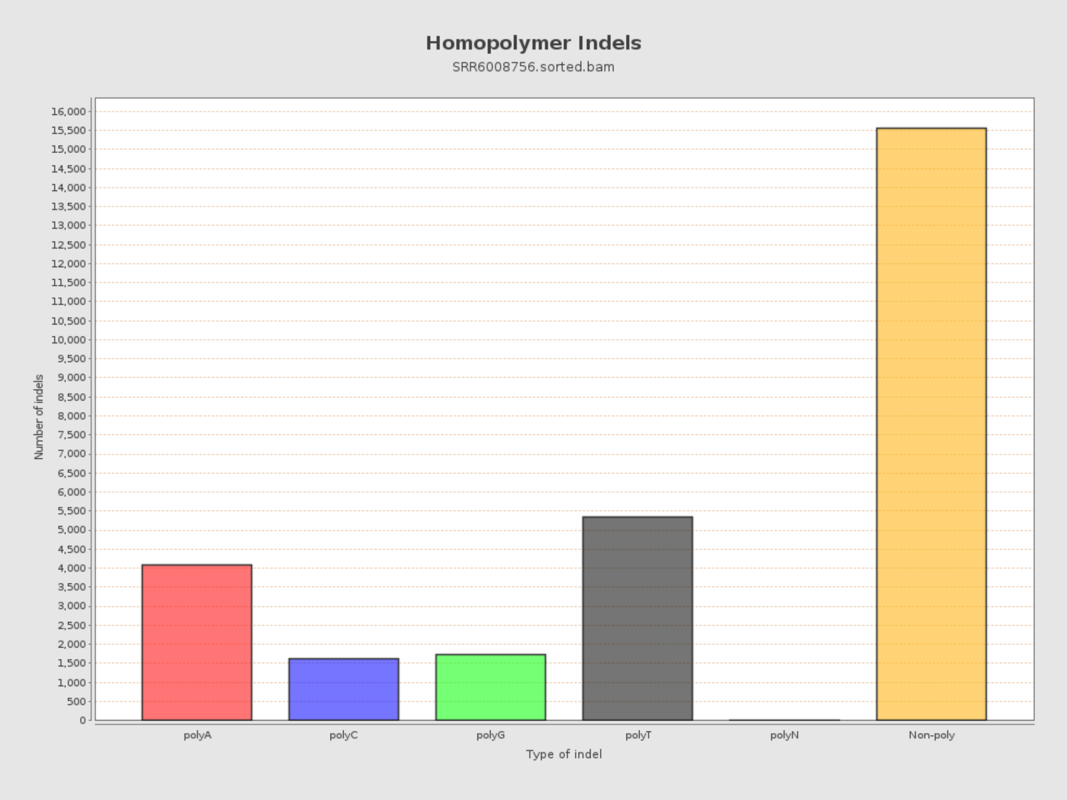
9. Results : Mapped Reads GC-content Distribution



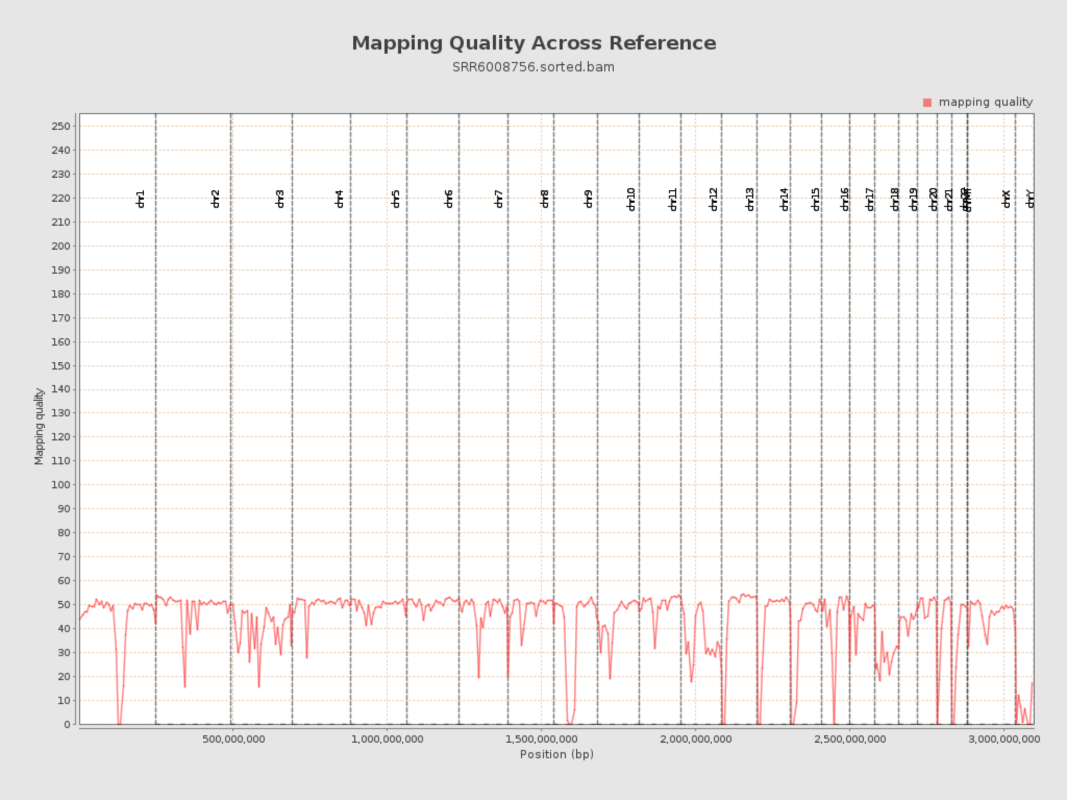
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram