Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:37:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008789.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_SRR6008789 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008789.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:37:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008789.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,437,033
Mapped reads	1,119,346 / 77.89%
Unmapped reads	317,687 / 22.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,477 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	26,889 / 1.87%
Duplication rate	1.94%
Clipped reads	457,266 / 31.82%

2.2. ACGT Content

Number/percentage of A's	22,494,032 / 29.77%
Number/percentage of C's	13,205,576 / 17.48%
Number/percentage of T's	23,358,707 / 30.92%
Number/percentage of G's	16,477,496 / 21.81%
Number/percentage of N's	13,937 / 0.02%
GC Percentage	39.29%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2157

2.4. Mapping Quality

Mean Mapping Quality	47.06

2.5. Mismatches and indels

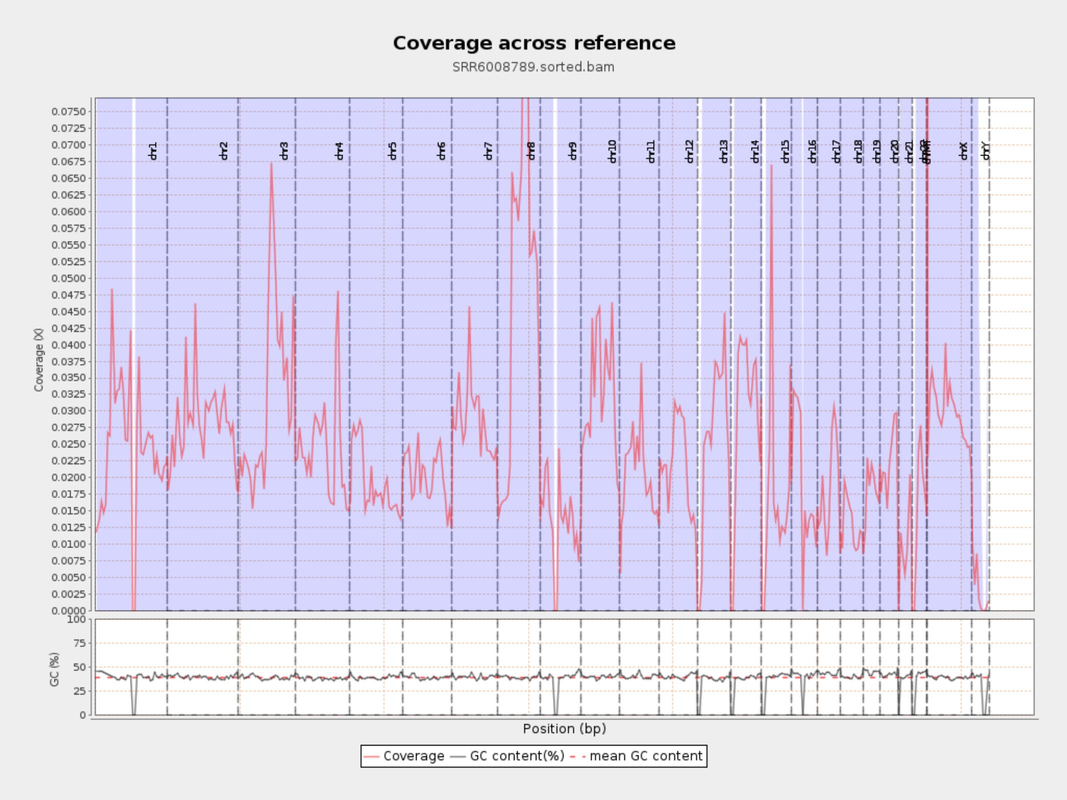
General error rate	0.9%
Mismatches	668,951
Insertions	6,322
Mapped reads with at least one insertion	0.56%
Deletions	22,326
Mapped reads with at least one deletion	1.97%
Homopolymer indels	47.56%

2.6. Chromosome stats

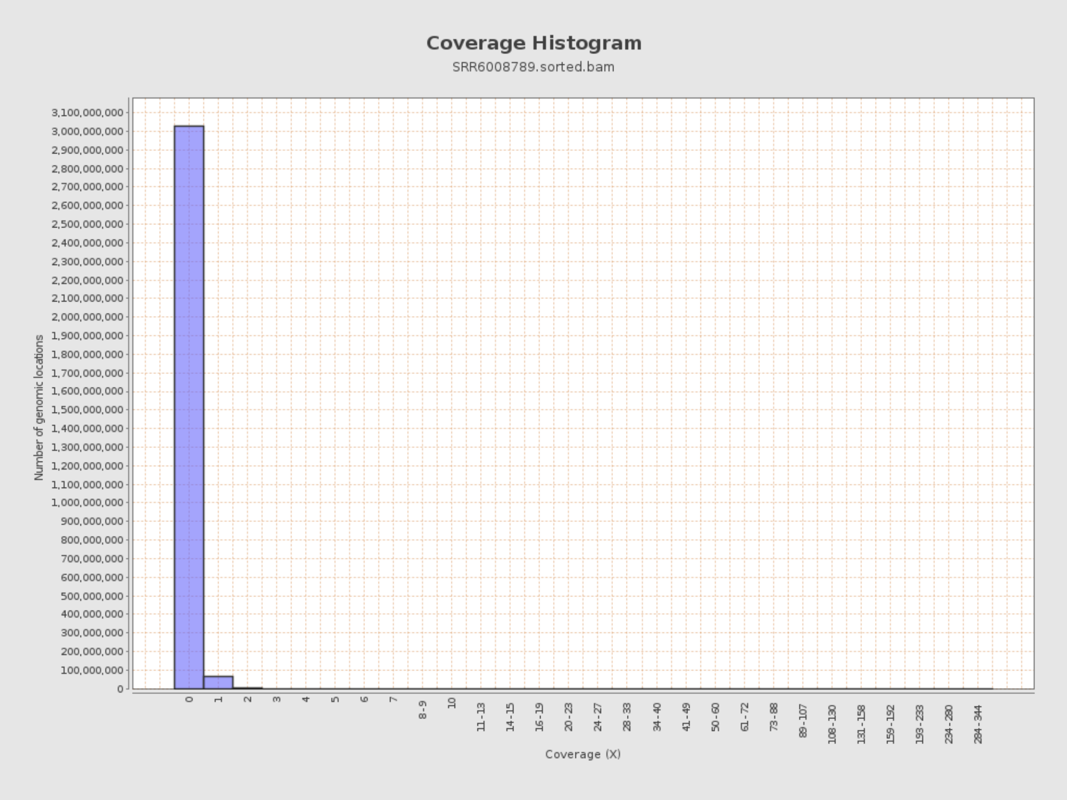
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6079966	0.0244	0.3318
chr2	243199373	6918537	0.0284	0.2416
chr3	198022430	6354527	0.0321	0.189
chr4	191154276	4676317	0.0245	0.1664
chr5	180915260	3498271	0.0193	0.1462
chr6	171115067	3472229	0.0203	0.1609
chr7	159138663	4604528	0.0289	0.3031

chr8	146364022	7247309	0.0495	0.3091
chr9	141213431	1906147	0.0135	0.1724
chr10	135534747	4418666	0.0326	0.2399
chr11	135006516	2795916	0.0207	0.196
chr12	133851895	2912446	0.0218	0.1556
chr13	115169878	2972897	0.0258	0.1686
chr14	107349540	3160879	0.0294	0.1834
chr15	102531392	1763420	0.0172	0.1394
chr16	90354753	1686548	0.0187	0.1578
chr17	81195210	1495057	0.0184	0.1567
chr18	78077248	999952	0.0128	0.3048
chr19	59128983	1080081	0.0183	0.2175
chr20	63025520	1409836	0.0224	0.1596
chr21	48129895	488990	0.0102	0.11
chr22	51304566	792569	0.0154	0.1297
chrMT	16571	24968	1.5067	1.3965
chrX	155270560	4651610	0.03	0.1934
chrY	59373566	174410	0.0029	0.0762

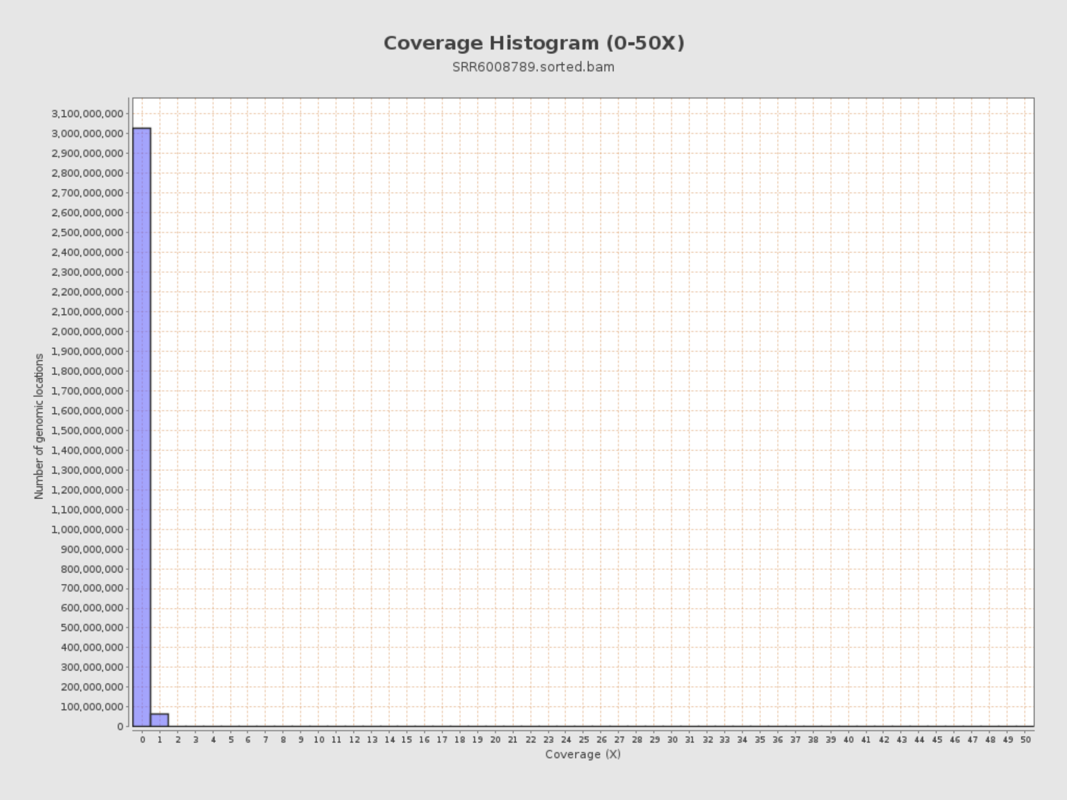
3. Results : Coverage across reference



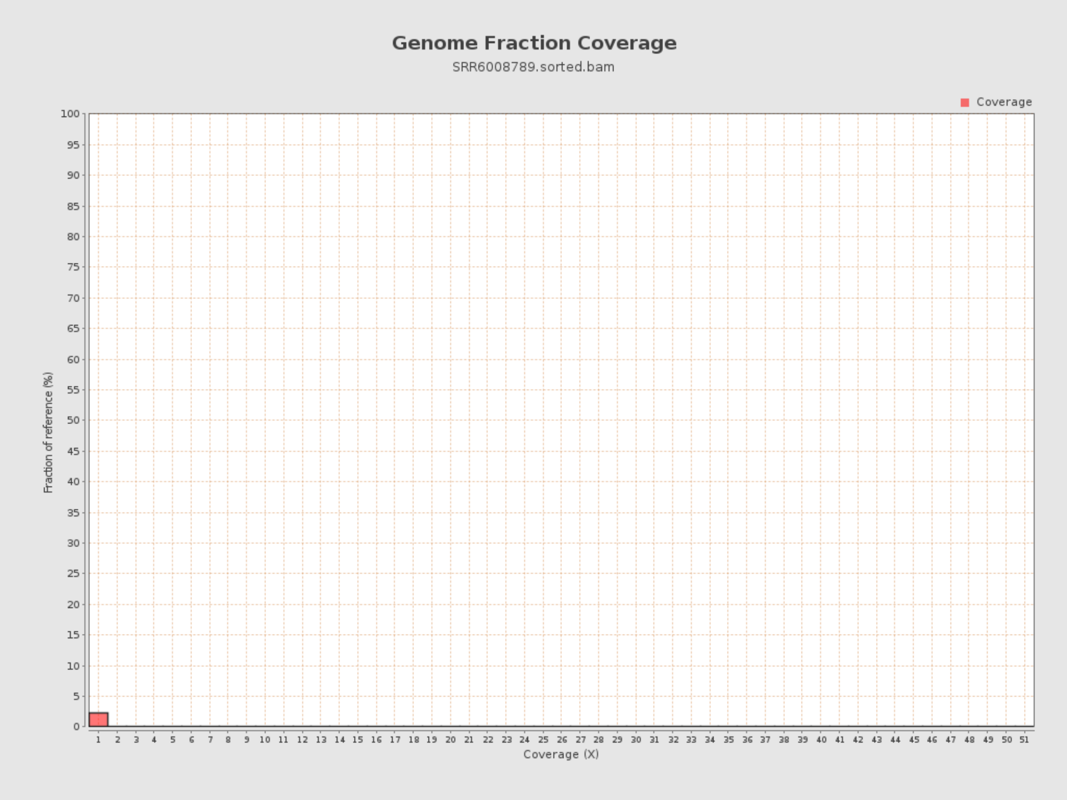
4. Results : Coverage Histogram



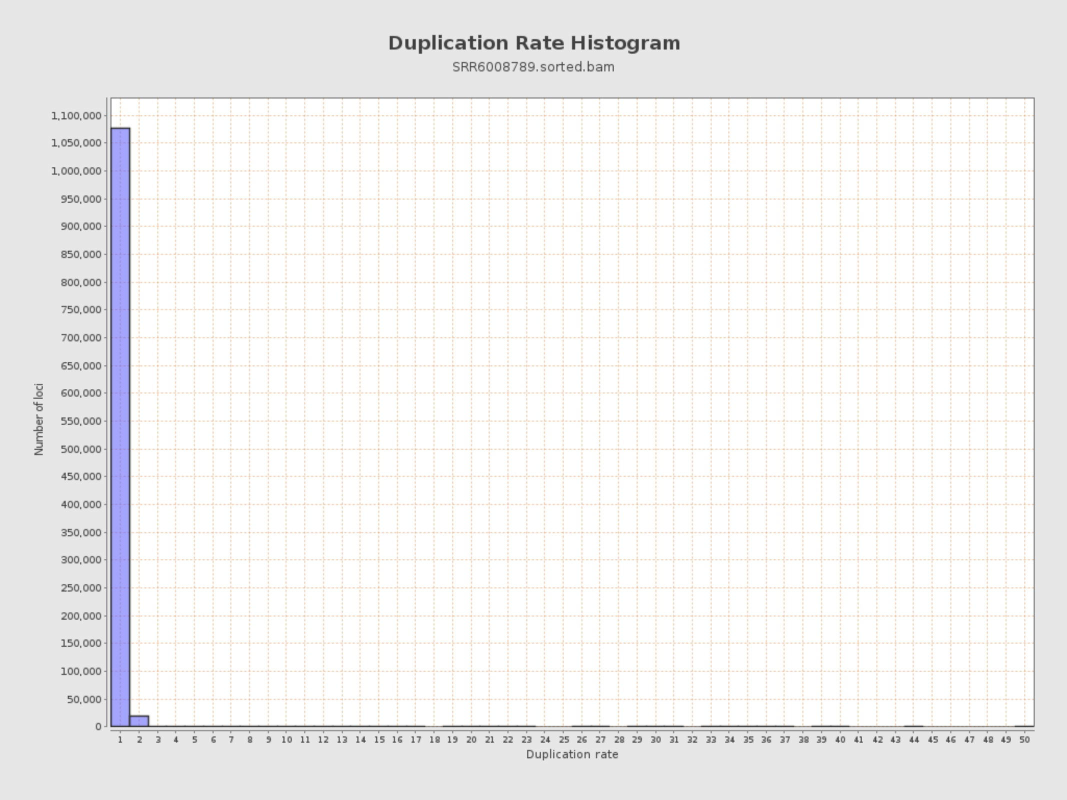
5. Results : Coverage Histogram (0-50X)



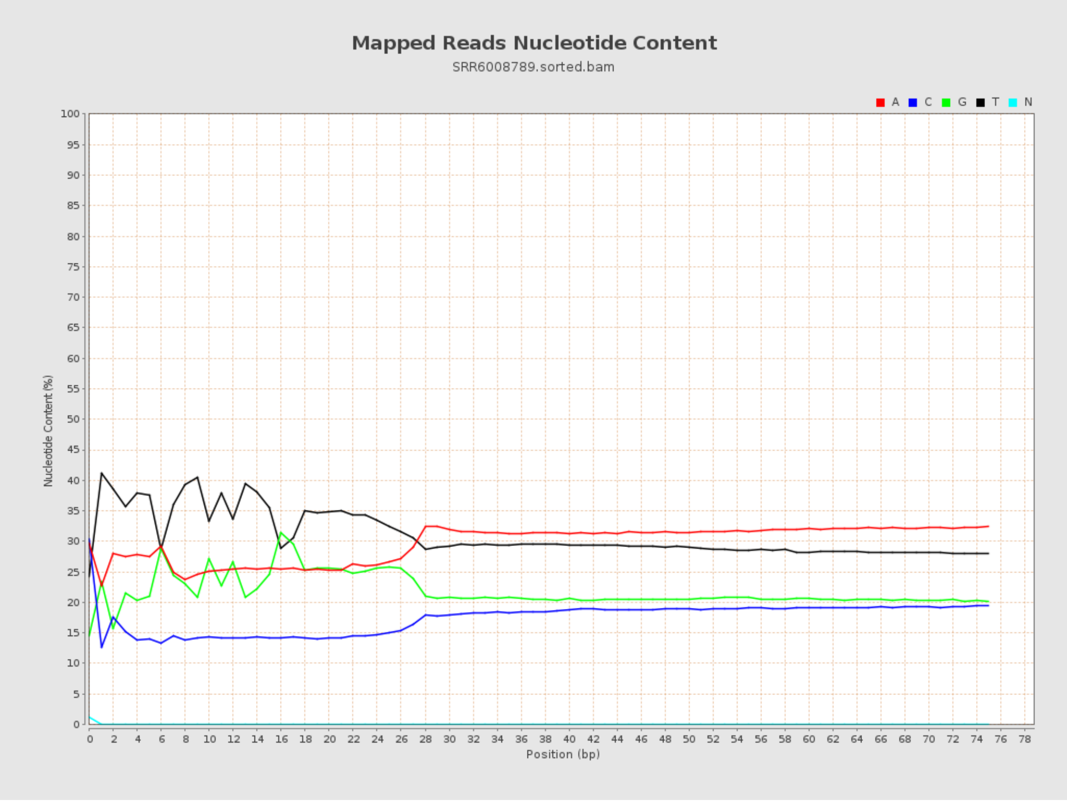
6. Results : Genome Fraction Coverage



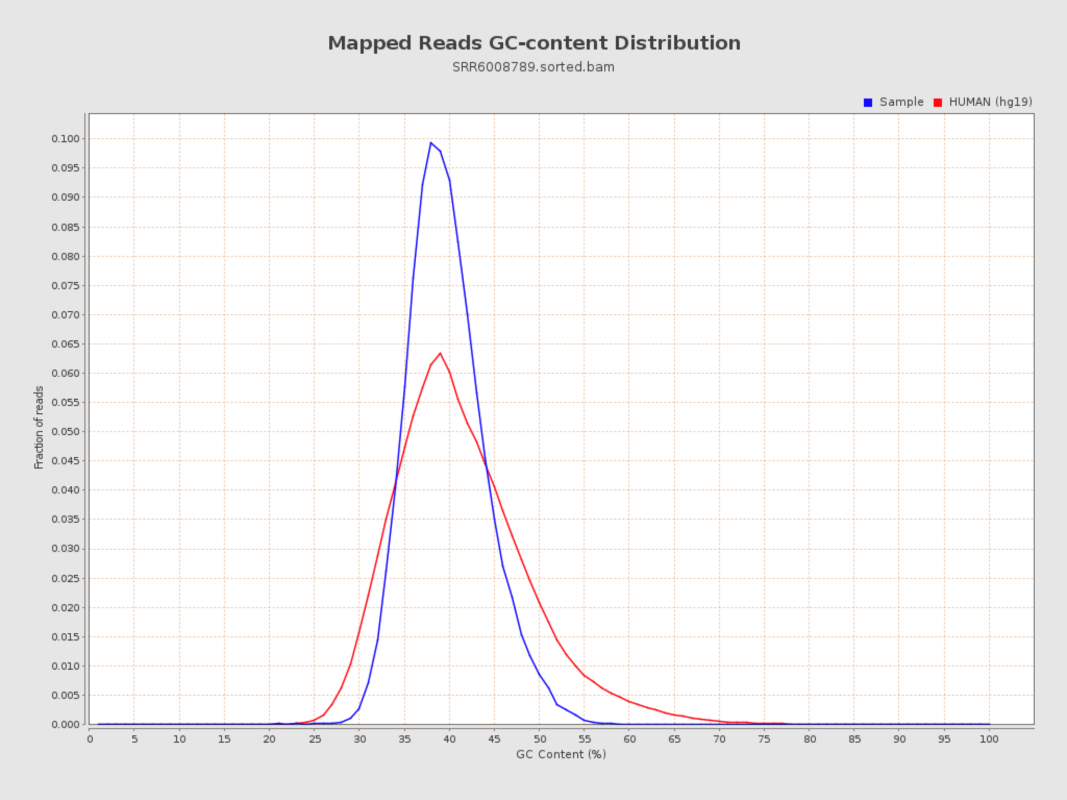
7. Results : Duplication Rate Histogram



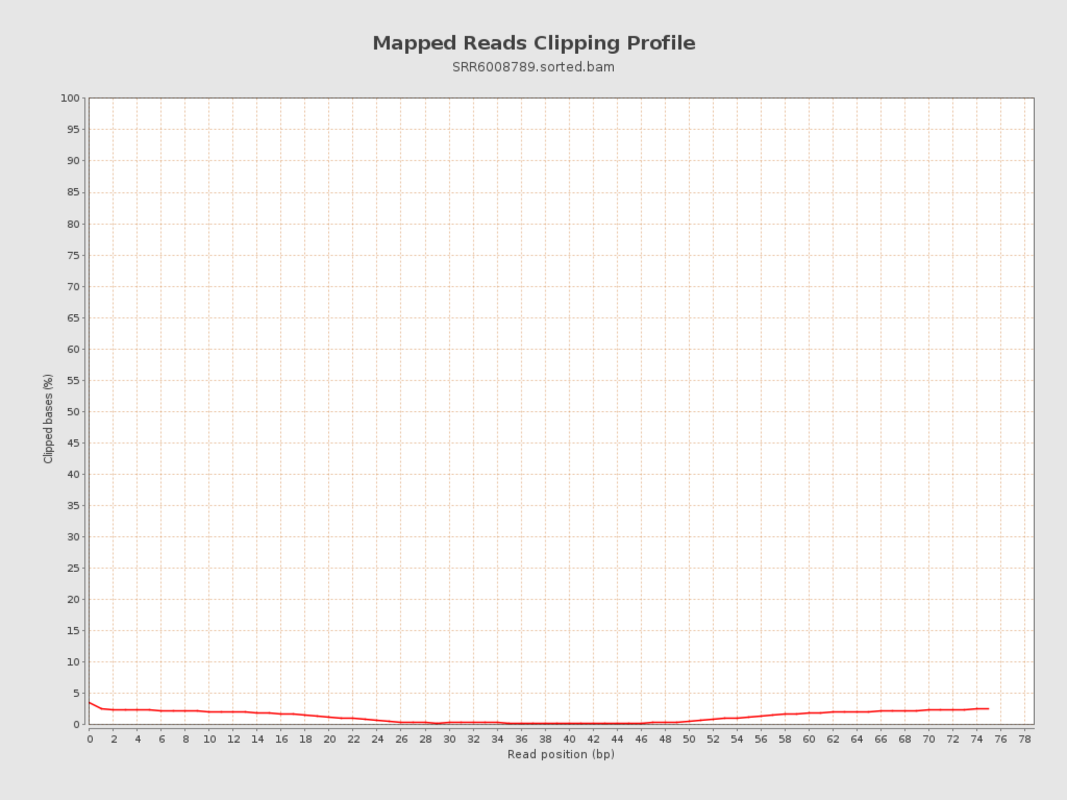
8. Results : Mapped Reads Nucleotide Content



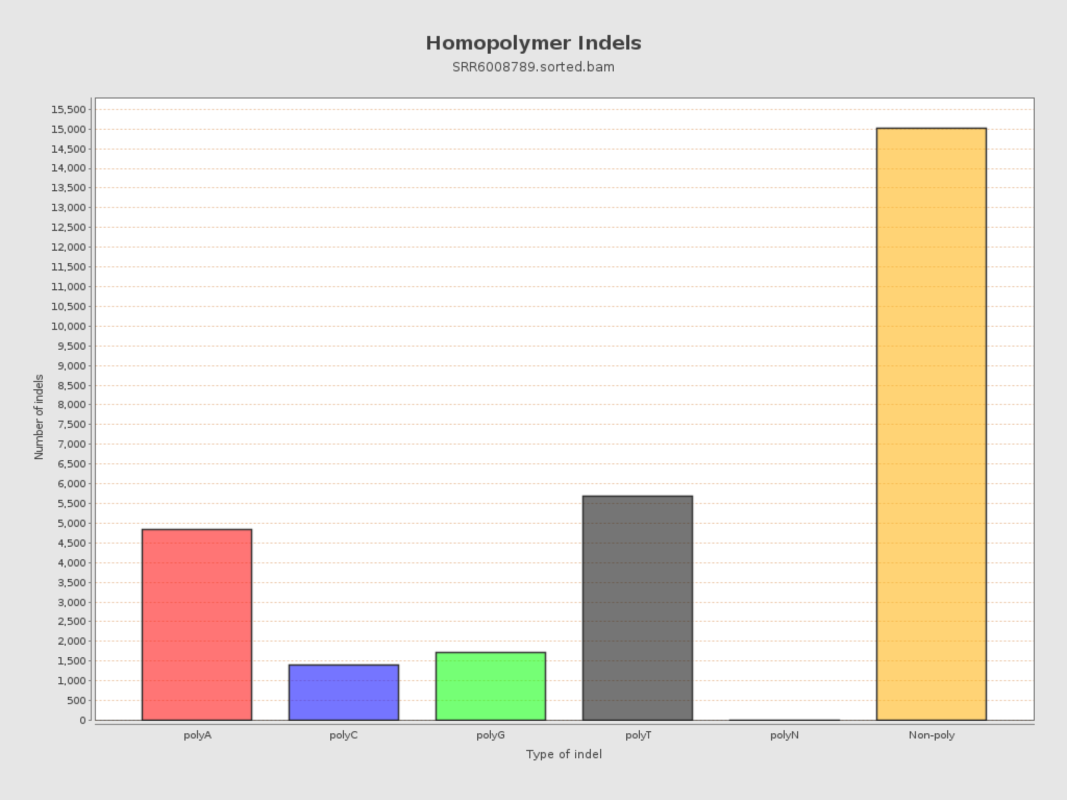
9. Results : Mapped Reads GC-content Distribution



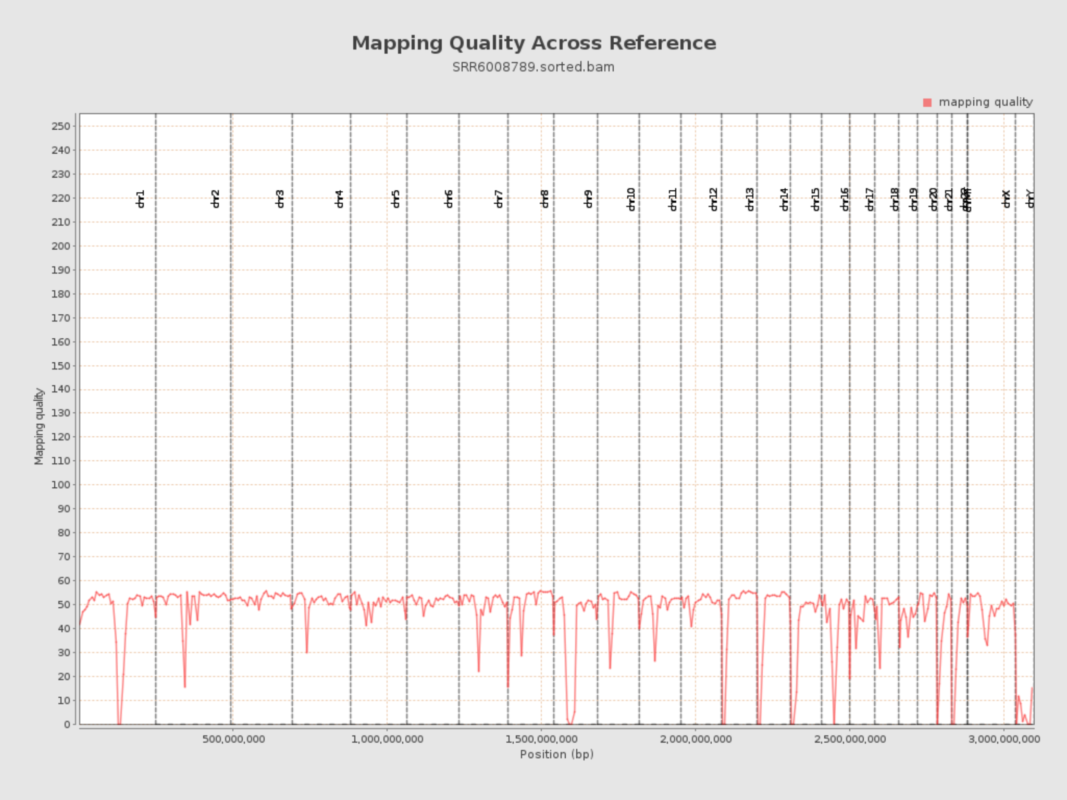
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram