Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:25:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008808.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_SRR6008808 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008808.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:25:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008808.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,357,718
Mapped reads	1,069,032 / 78.74%
Unmapped reads	288,686 / 21.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,956 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	98,059 / 7.22%
Duplication rate	6.86%
Clipped reads	466,626 / 34.37%

2.2. ACGT Content

Number/percentage of A's	19,596,644 / 27.44%
Number/percentage of C's	13,848,791 / 19.39%
Number/percentage of T's	21,937,213 / 30.71%
Number/percentage of G's	15,944,375 / 22.32%
Number/percentage of N's	96,885 / 0.14%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.4623

2.4. Mapping Quality

Mean Mapping Quality	43.09

2.5. Mismatches and indels

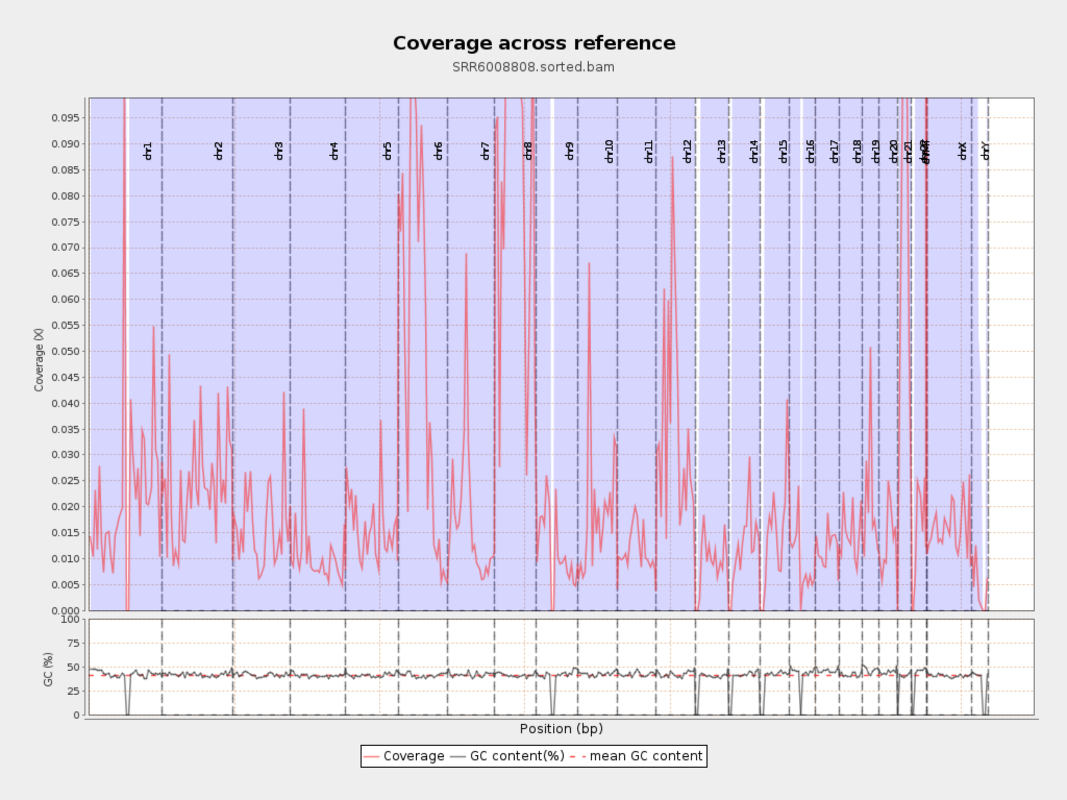
General error rate	0.88%
Mismatches	614,270
Insertions	5,358
Mapped reads with at least one insertion	0.5%
Deletions	18,952
Mapped reads with at least one deletion	1.75%
Homopolymer indels	44.97%

2.6. Chromosome stats

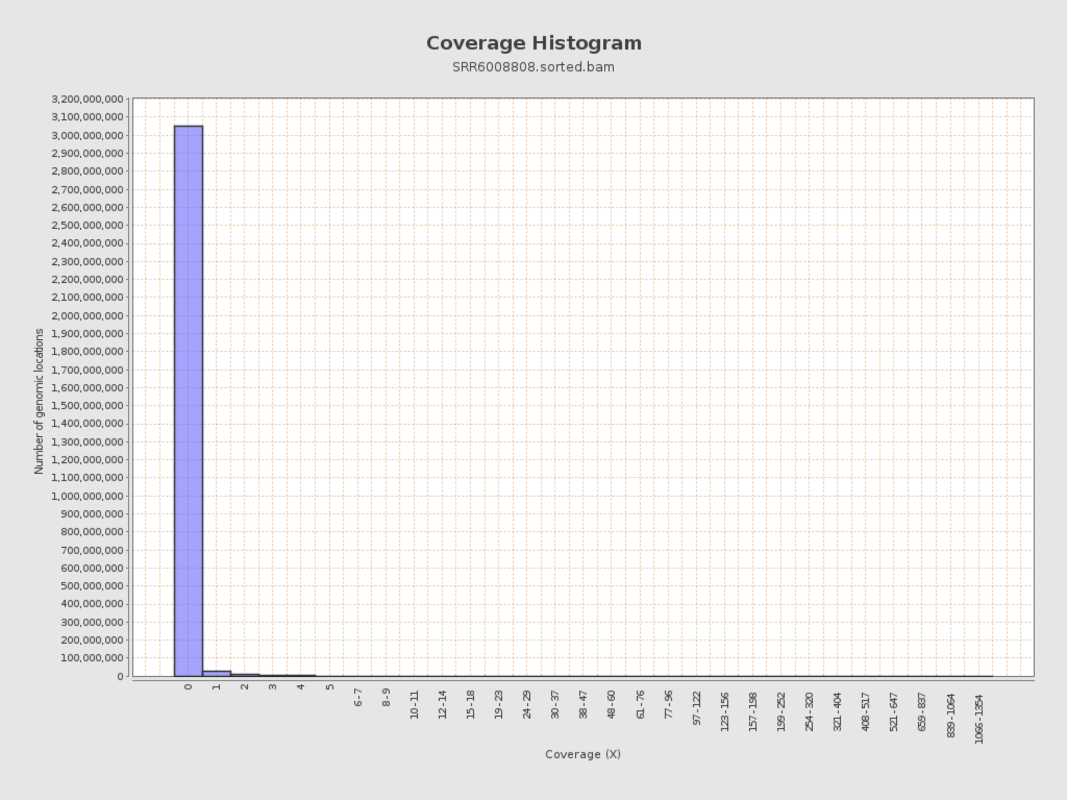
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5624497	0.0226	1.2155
chr2	243199373	5881027	0.0242	0.3137
chr3	198022430	3229284	0.0163	0.2004
chr4	191154276	2029175	0.0106	0.1741
chr5	180915260	2970762	0.0164	0.1886
chr6	171115067	8848947	0.0517	0.5038
chr7	159138663	2866216	0.018	0.5262

chr8	146364022	13553252	0.0926	0.575
chr9	141213431	1615620	0.0114	0.1671
chr10	135534747	2595279	0.0191	0.4393
chr11	135006516	1590799	0.0118	0.1613
chr12	133851895	4804666	0.0359	0.2881
chr13	115169878	1067746	0.0093	0.1407
chr14	107349540	1300832	0.0121	0.1702
chr15	102531392	1522662	0.0149	0.1818
chr16	90354753	832119	0.0092	0.1726
chr17	81195210	989634	0.0122	0.1625
chr18	78077248	1152628	0.0148	0.3288
chr19	59128983	1259866	0.0213	0.6748
chr20	63025520	867308	0.0138	0.1868
chr21	48129895	3266738	0.0679	0.4027
chr22	51304566	762758	0.0149	0.1816
chrMT	16571	82840	4.9991	4.1833
chrX	155270560	2486877	0.016	0.1875
chrY	59373566	256815	0.0043	0.1131

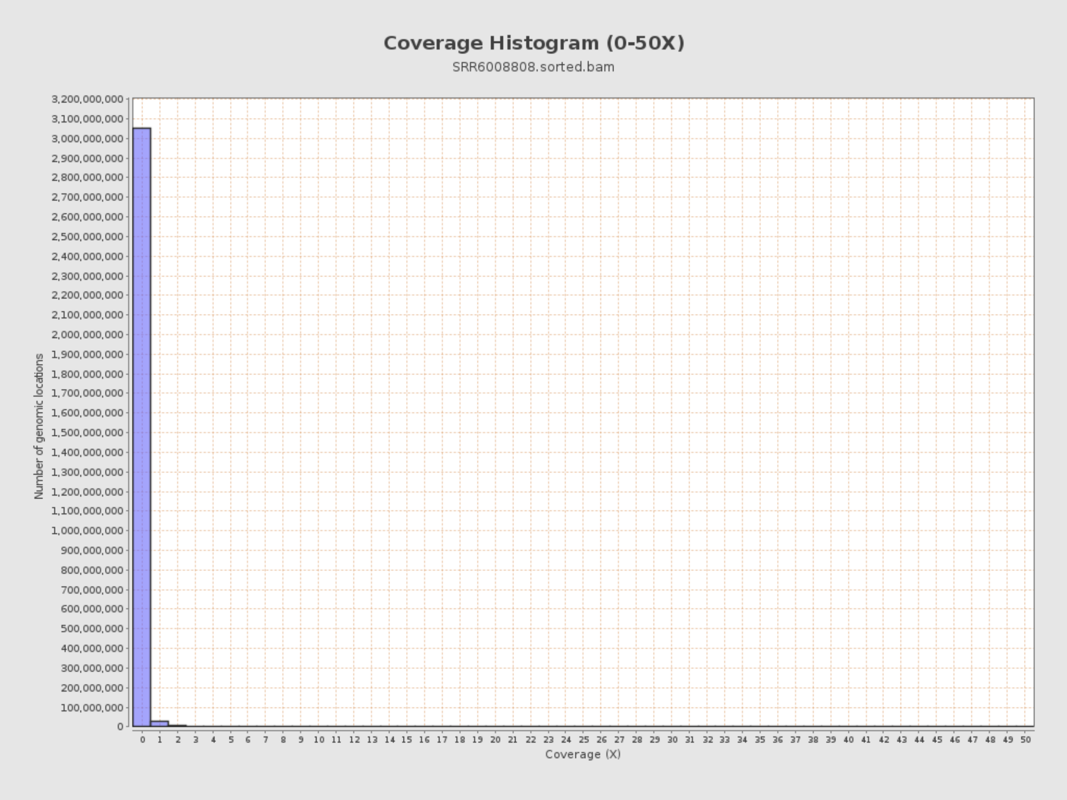
3. Results : Coverage across reference



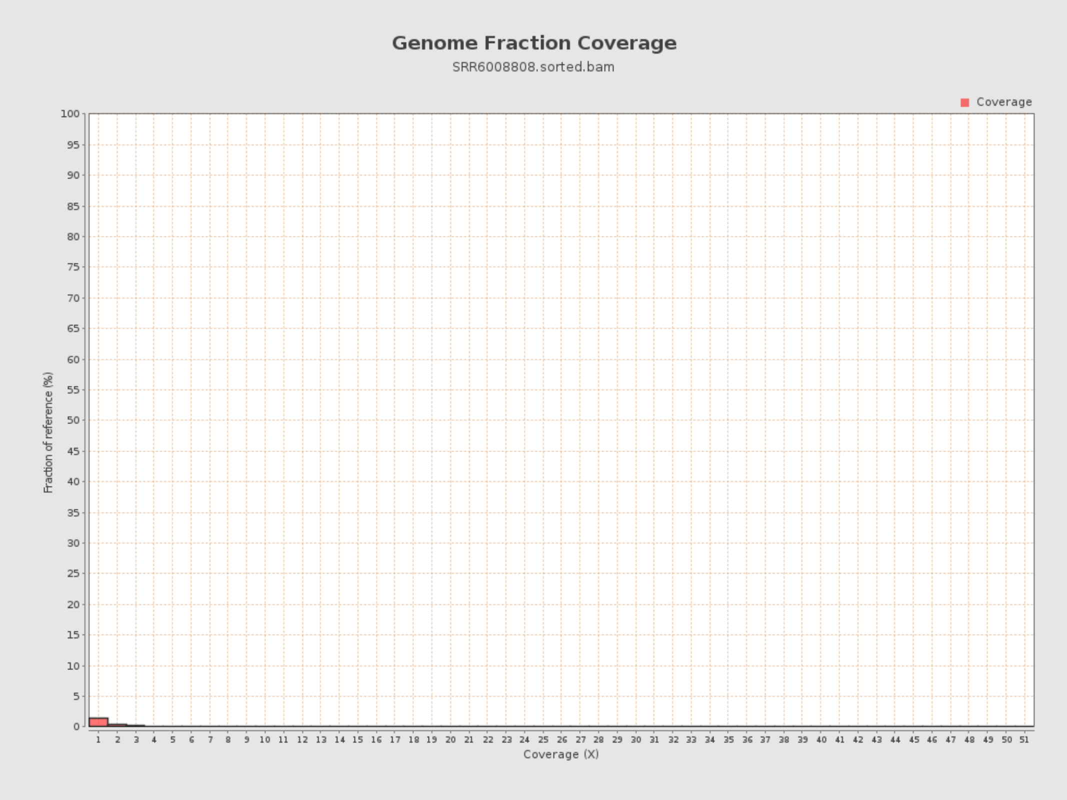
4. Results : Coverage Histogram



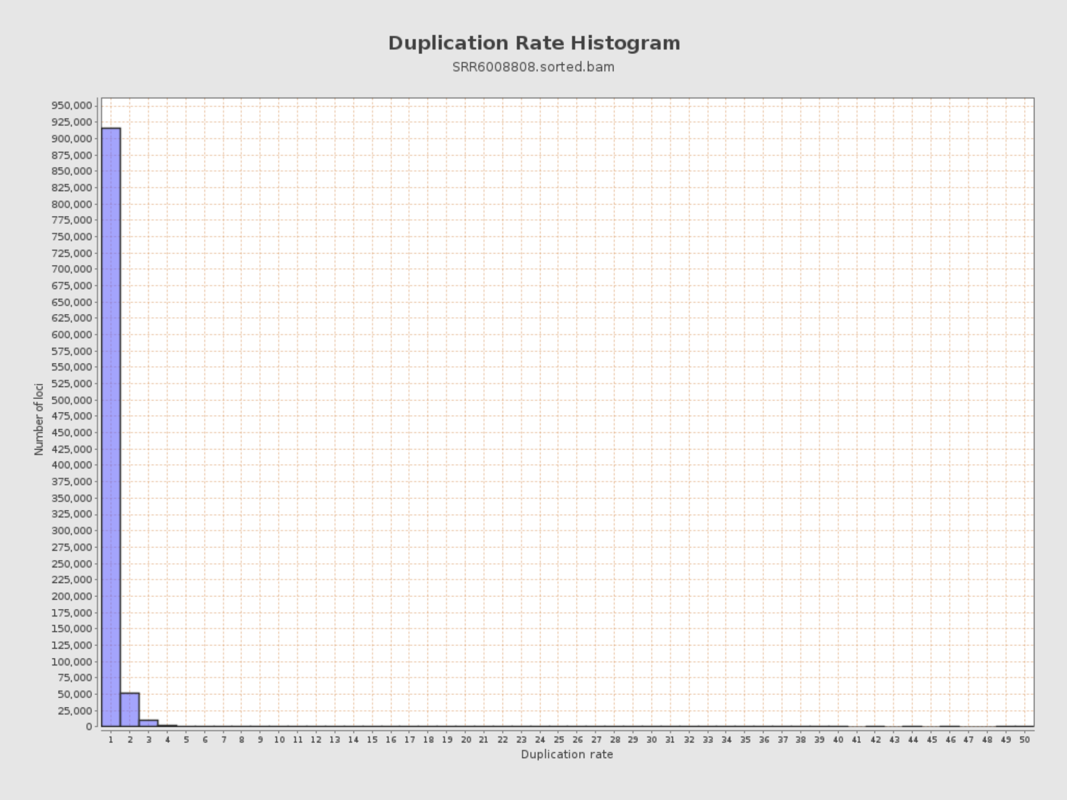
5. Results : Coverage Histogram (0-50X)



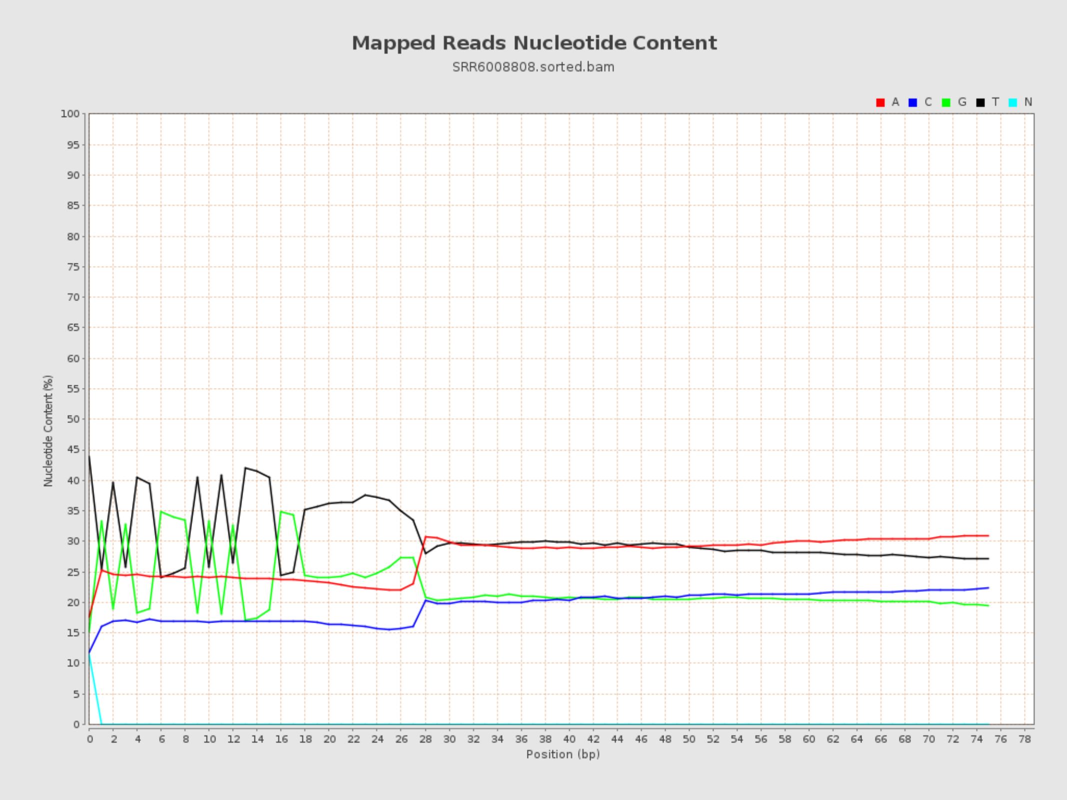
6. Results : Genome Fraction Coverage



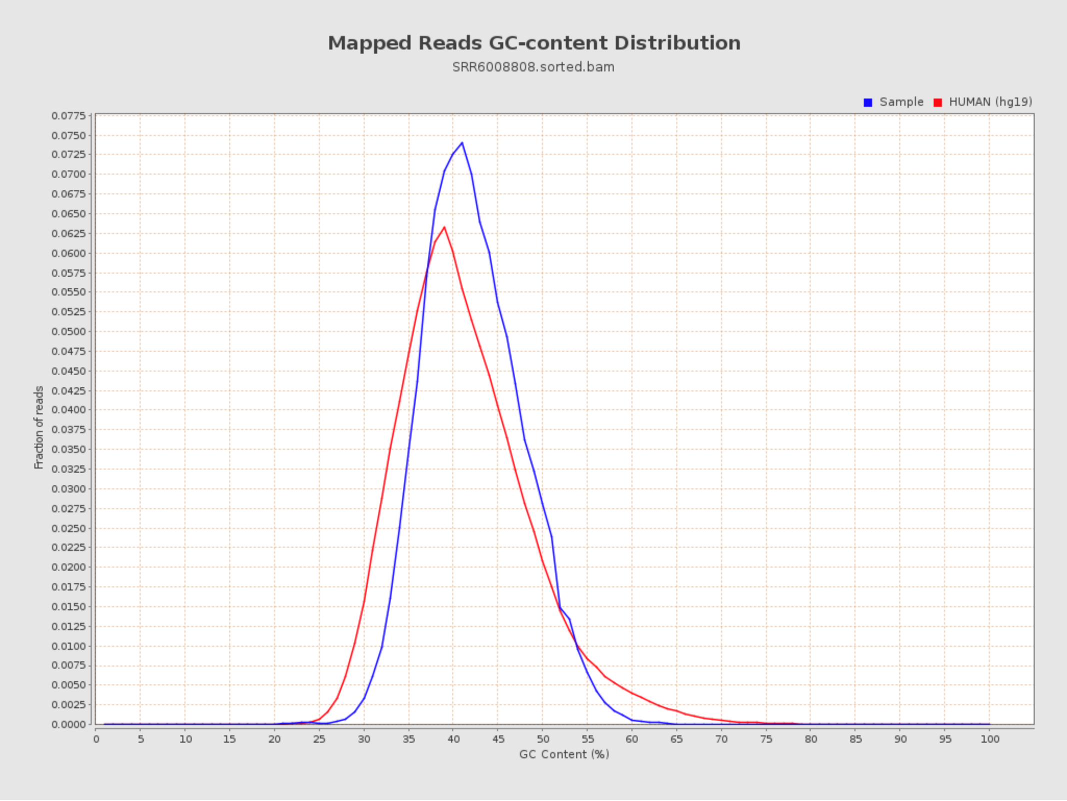
7. Results : Duplication Rate Histogram



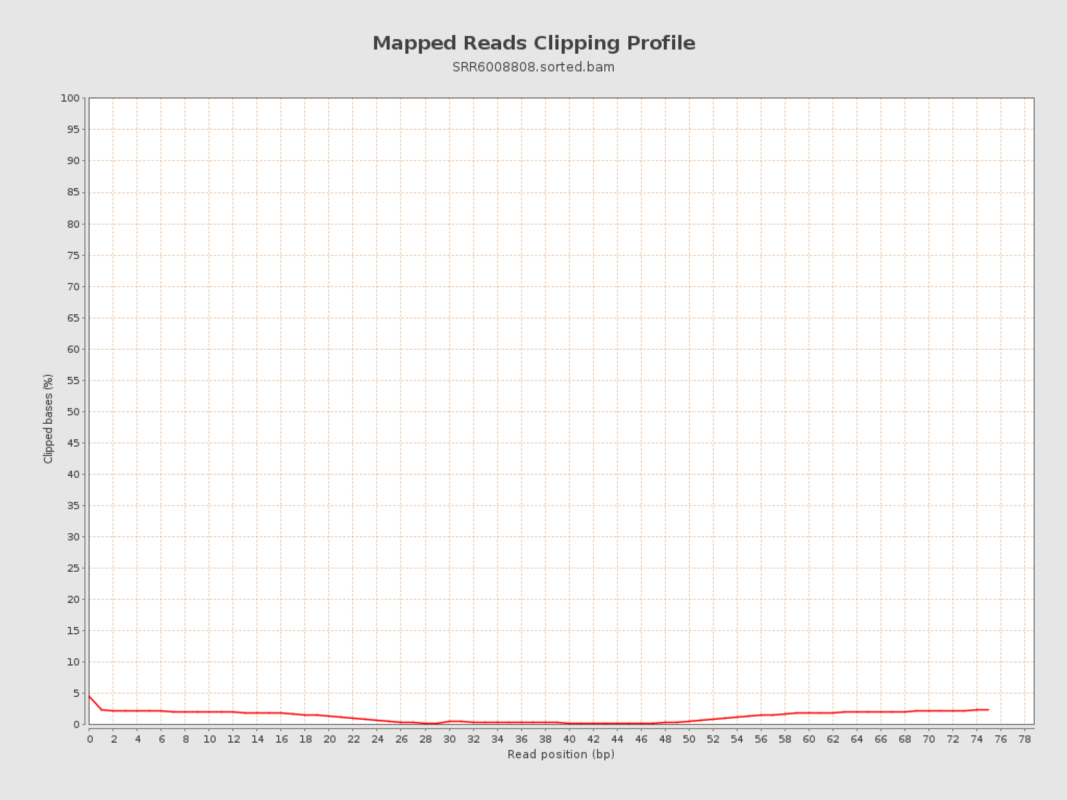
8. Results : Mapped Reads Nucleotide Content



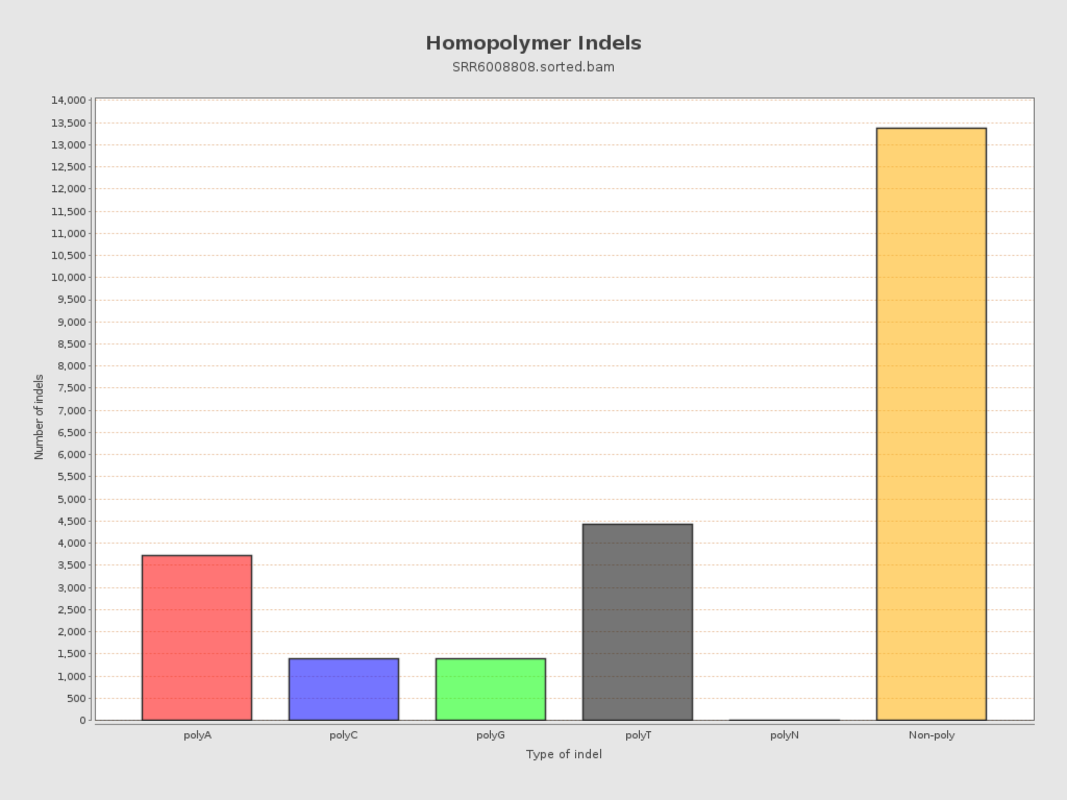
9. Results : Mapped Reads GC-content Distribution



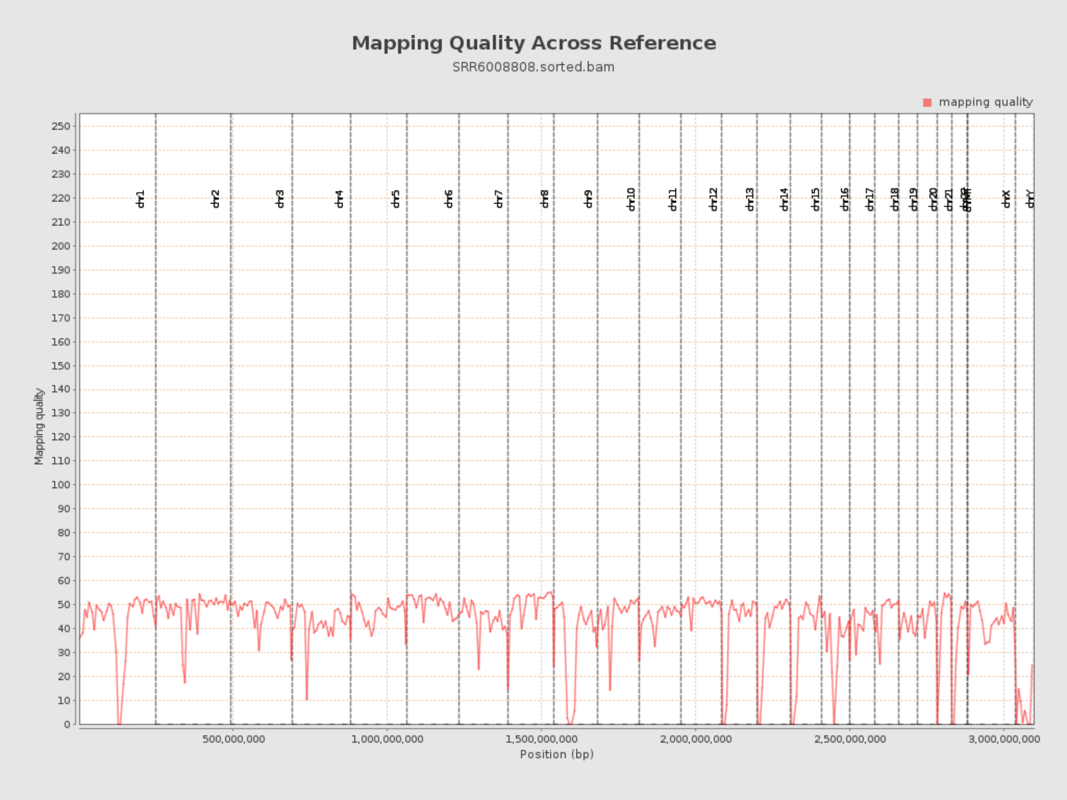
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram