Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:12:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008760.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_SRR6008760 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008760.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:12:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008760.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,172,535
Mapped reads	1,041,192 / 88.8%
Unmapped reads	131,343 / 11.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,215 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	55,573 / 4.74%
Duplication rate	4.3%
Clipped reads	473,397 / 40.37%

2.2. ACGT Content

Number/percentage of A's	18,433,187 / 26.76%
Number/percentage of C's	13,466,265 / 19.55%
Number/percentage of T's	21,077,126 / 30.6%
Number/percentage of G's	15,793,759 / 22.93%
Number/percentage of N's	103,809 / 0.15%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0223

Standard Deviation	0.2456

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

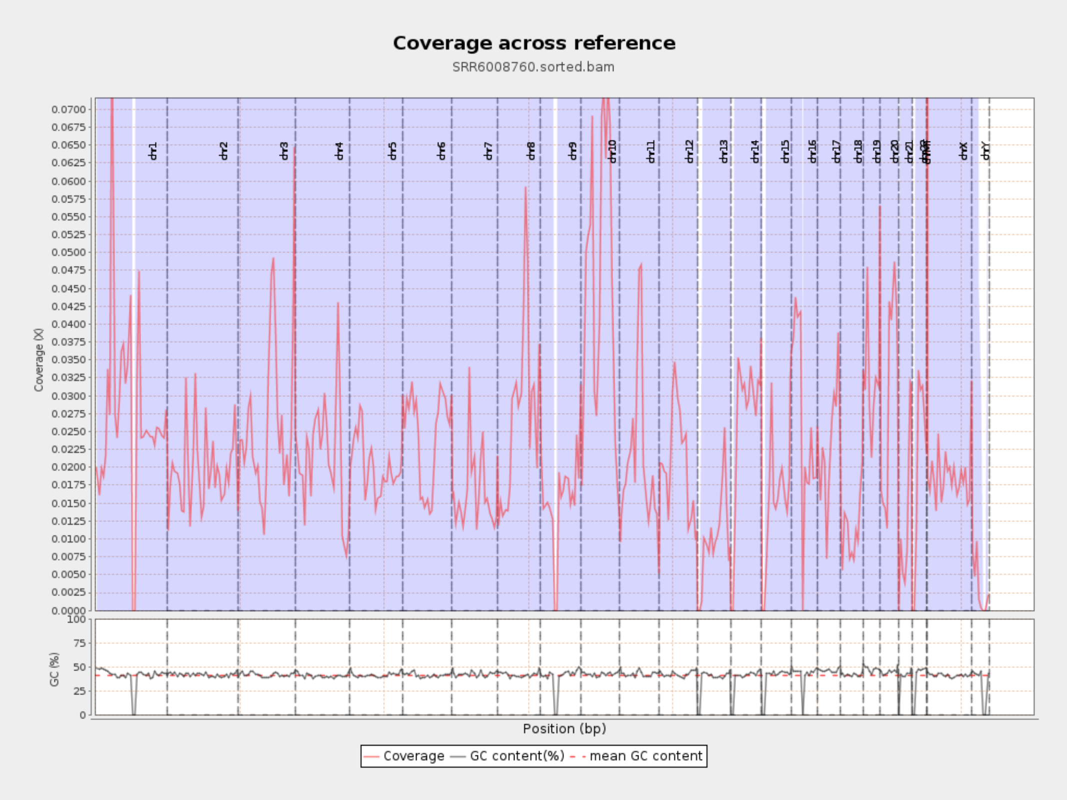
General error rate	0.85%
Mismatches	576,178
Insertions	5,059
Mapped reads with at least one insertion	0.48%
Deletions	19,276
Mapped reads with at least one deletion	1.83%
Homopolymer indels	44.57%

2.6. Chromosome stats

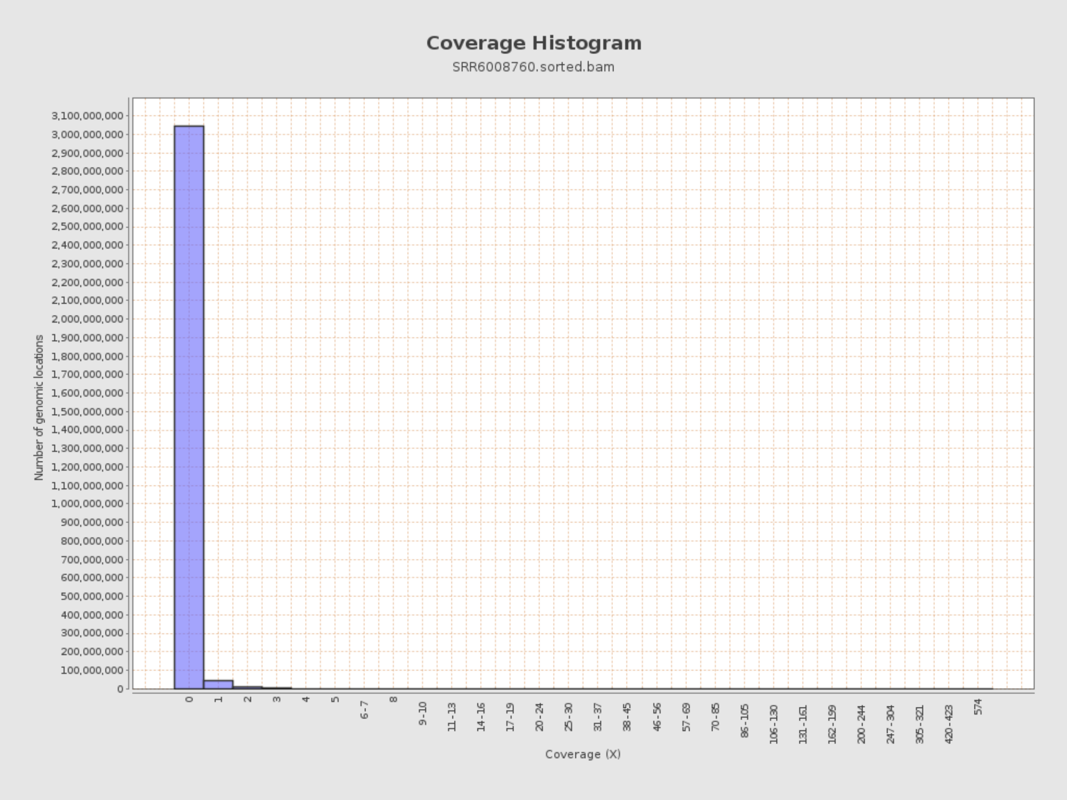
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6859820	0.0275	0.3187
chr2	243199373	4788592	0.0197	0.3121
chr3	198022430	5064376	0.0256	0.2073
chr4	191154276	4127984	0.0216	0.1856
chr5	180915260	3655316	0.0202	0.1751
chr6	171115067	4163585	0.0243	0.2078
chr7	159138663	2621747	0.0165	0.2944

chr8	146364022	4061254	0.0277	0.2747
chr9	141213431	2152872	0.0152	0.1707
chr10	135534747	6288585	0.0464	0.4266
chr11	135006516	2944405	0.0218	0.2026
chr12	133851895	2785733	0.0208	0.1788
chr13	115169878	1147582	0.01	0.1258
chr14	107349540	2800210	0.0261	0.2014
chr15	102531392	1536827	0.015	0.1498
chr16	90354753	2373870	0.0263	0.2805
chr17	81195210	1867883	0.023	0.2027
chr18	78077248	844535	0.0108	0.2276
chr19	59128983	1924750	0.0326	0.2877
chr20	63025520	1875032	0.0298	0.217
chr21	48129895	613220	0.0127	0.1459
chr22	51304566	1054099	0.0205	0.18
chrMT	16571	300272	18.1203	10.6085
chrX	155270560	2867688	0.0185	0.1696
chrY	59373566	188577	0.0032	0.1144

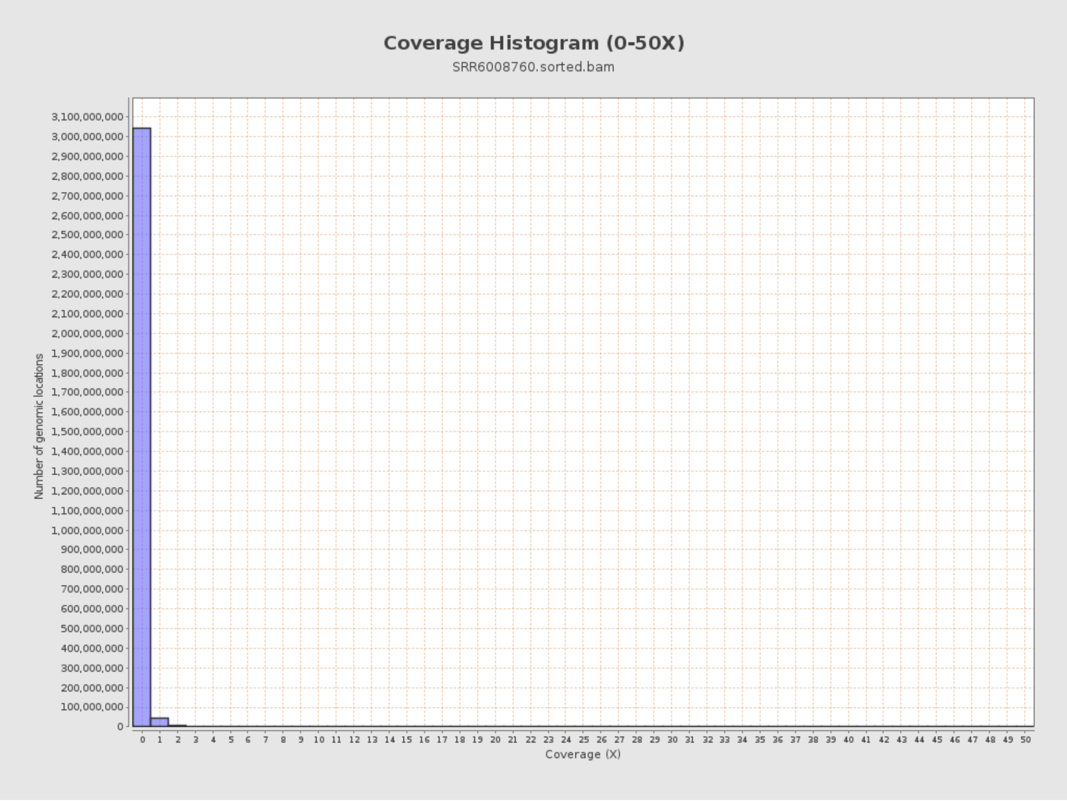
3. Results : Coverage across reference



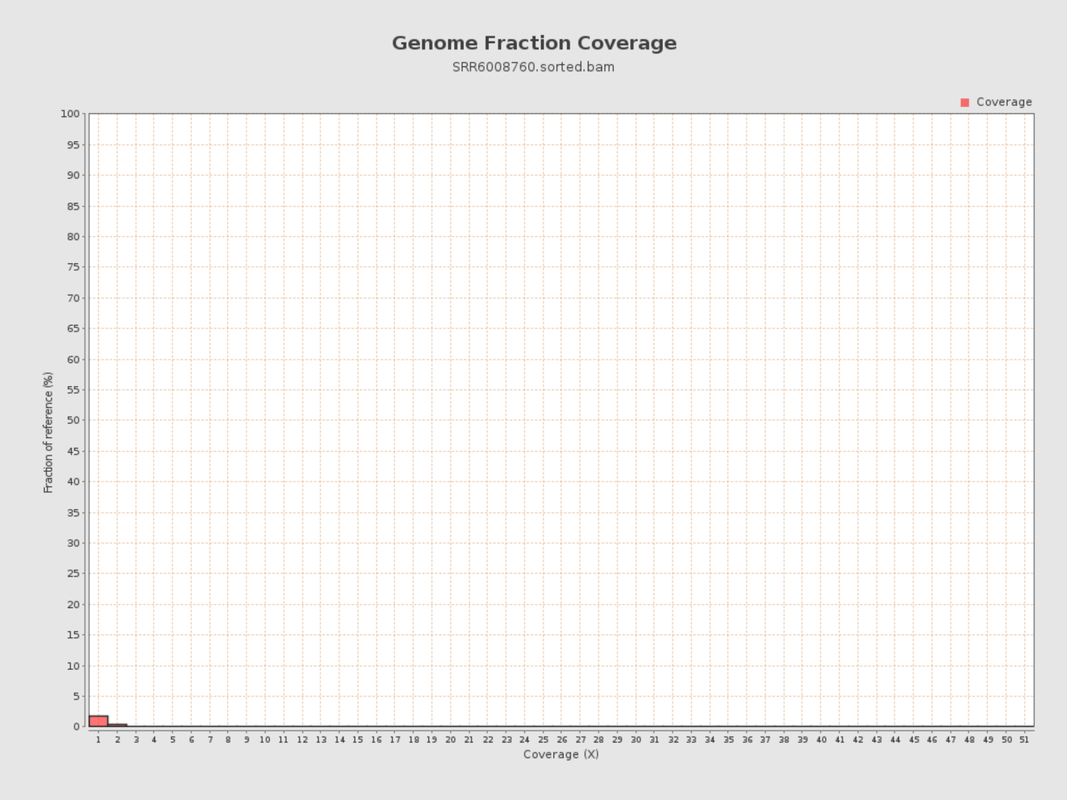
4. Results : Coverage Histogram



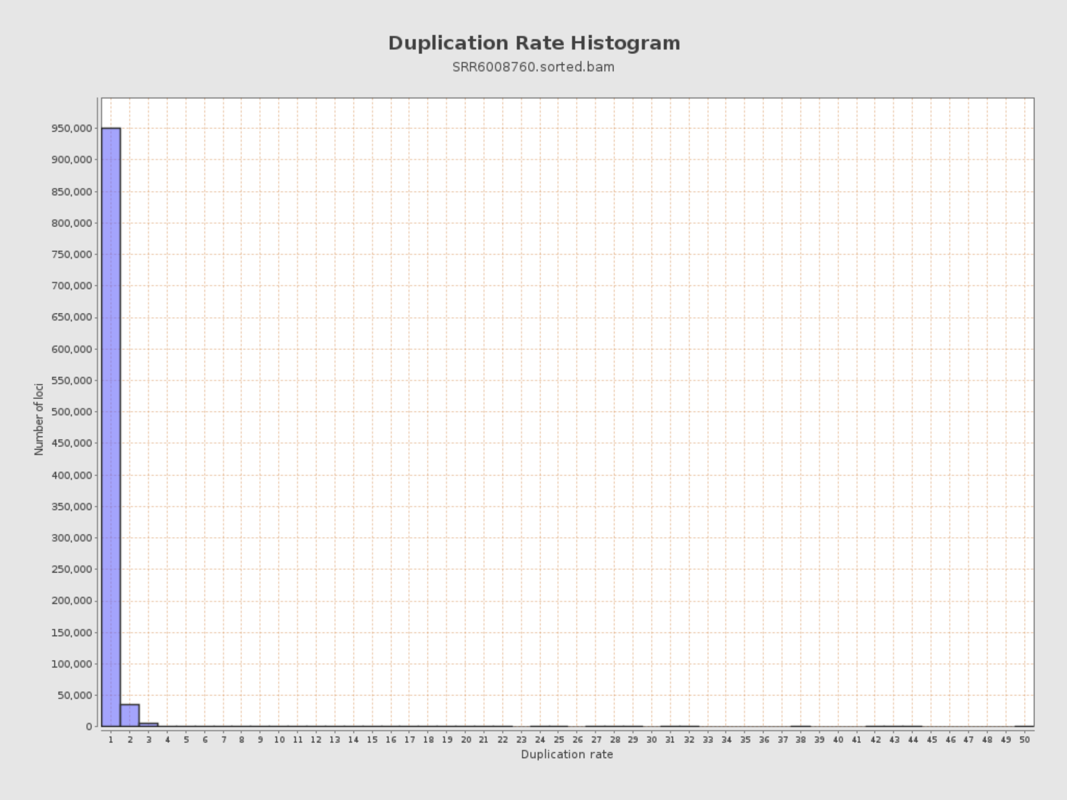
5. Results : Coverage Histogram (0-50X)



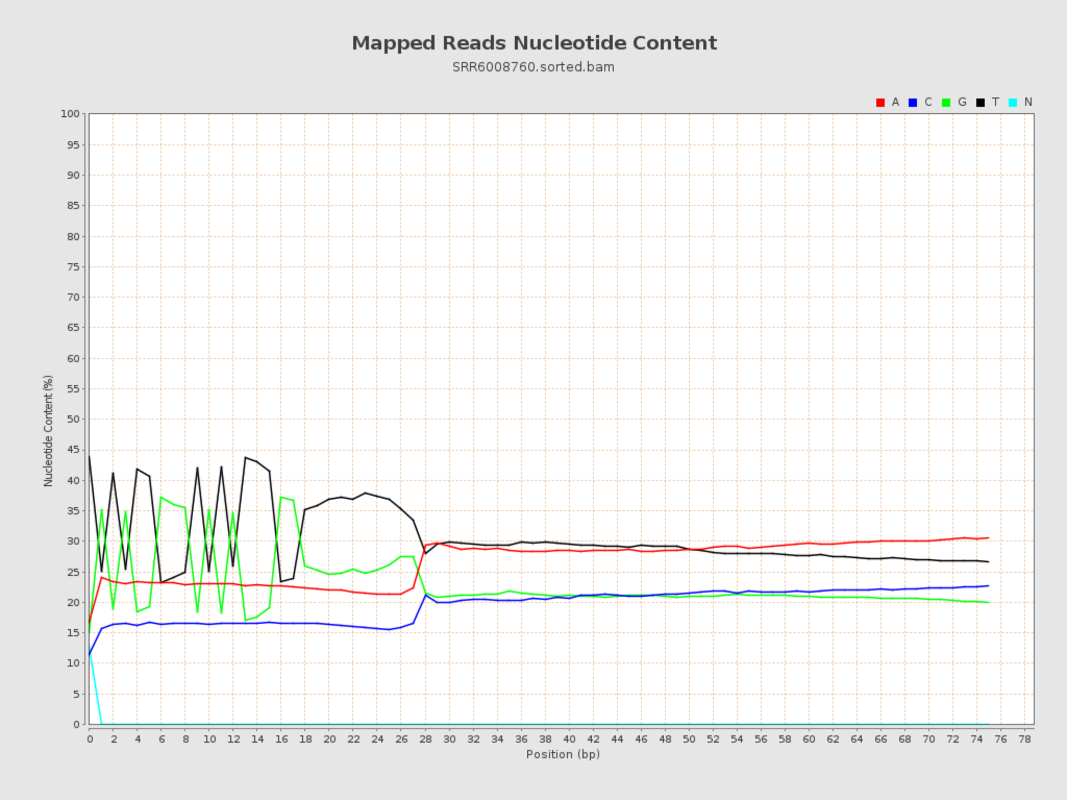
6. Results : Genome Fraction Coverage



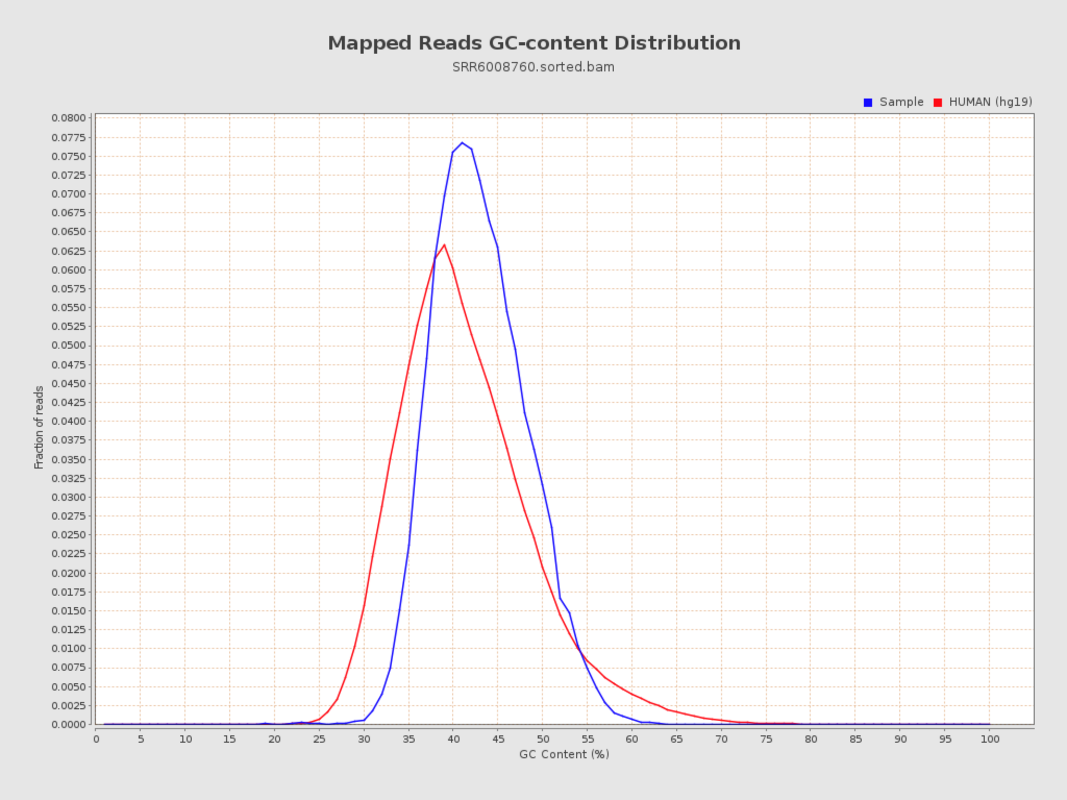
7. Results : Duplication Rate Histogram



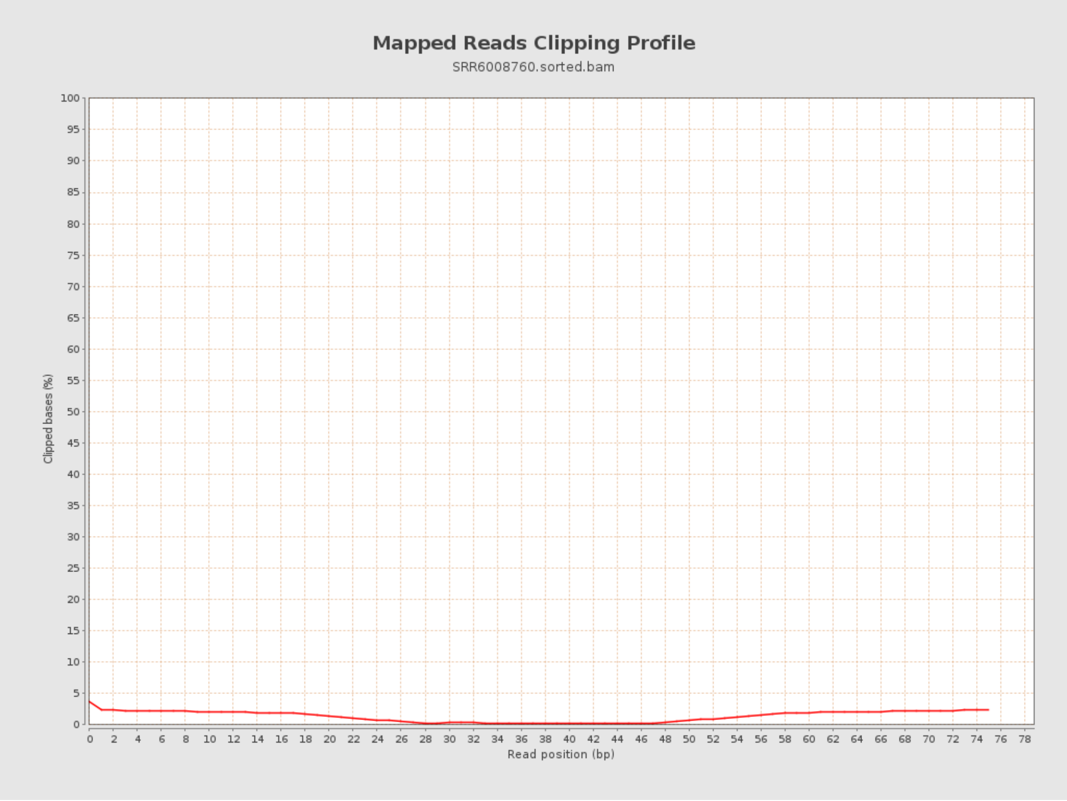
8. Results : Mapped Reads Nucleotide Content



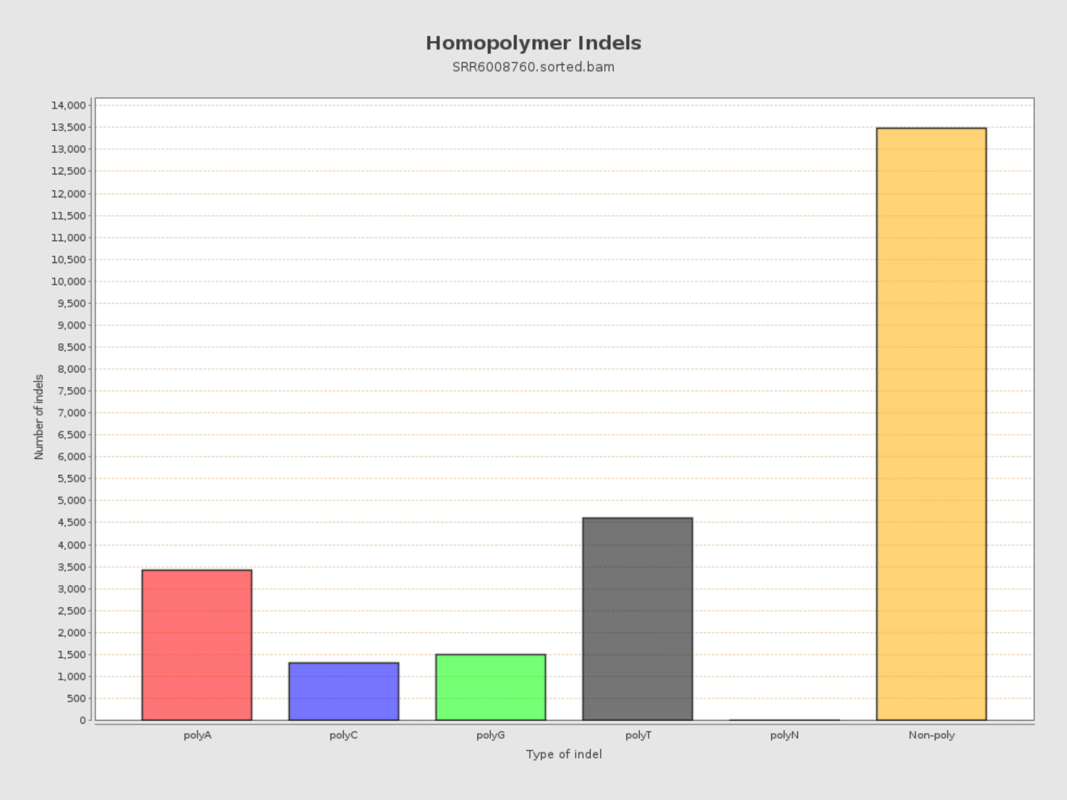
9. Results : Mapped Reads GC-content Distribution



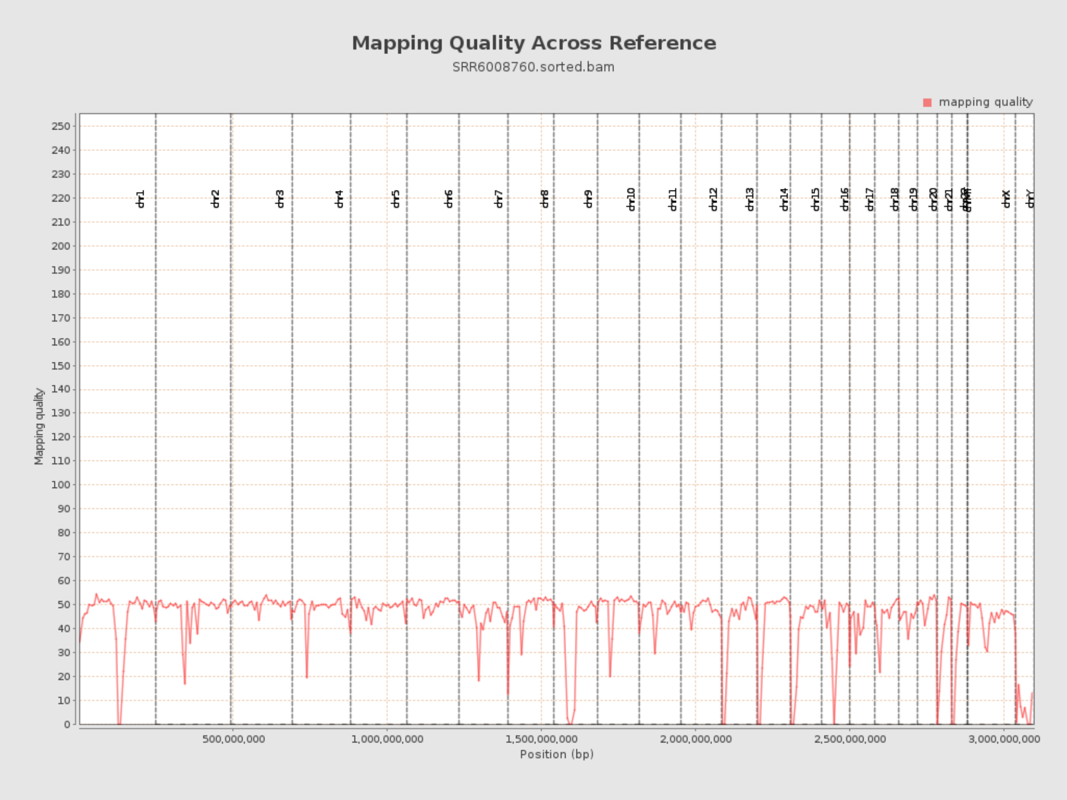
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram