Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:59:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008710.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_SRR6008710 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008710.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:59:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008710.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,459,509
Mapped reads	1,044,378 / 71.56%
Unmapped reads	415,131 / 28.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,159 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	28,672 / 1.96%
Duplication rate	2.12%
Clipped reads	421,530 / 28.88%

2.2. ACGT Content

Number/percentage of A's	21,881,045 / 31.03%
Number/percentage of C's	11,897,538 / 16.87%
Number/percentage of T's	21,024,839 / 29.82%
Number/percentage of G's	15,698,230 / 22.27%
Number/percentage of N's	3,299 / 0%
GC Percentage	39.14%

2.3. Coverage

Mean	0.0228

Standard Deviation	0.1937

2.4. Mapping Quality

Mean Mapping Quality	48.78

2.5. Mismatches and indels

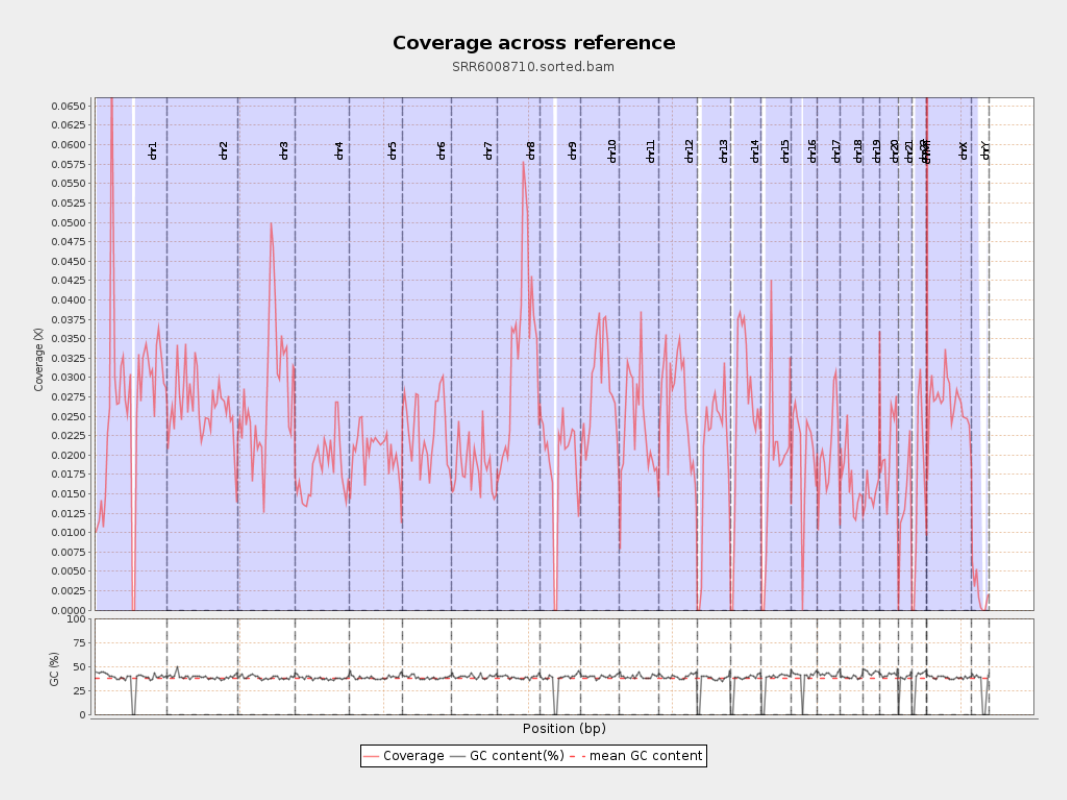
General error rate	0.95%
Mismatches	658,183
Insertions	5,344
Mapped reads with at least one insertion	0.51%
Deletions	22,622
Mapped reads with at least one deletion	2.14%
Homopolymer indels	49.21%

2.6. Chromosome stats

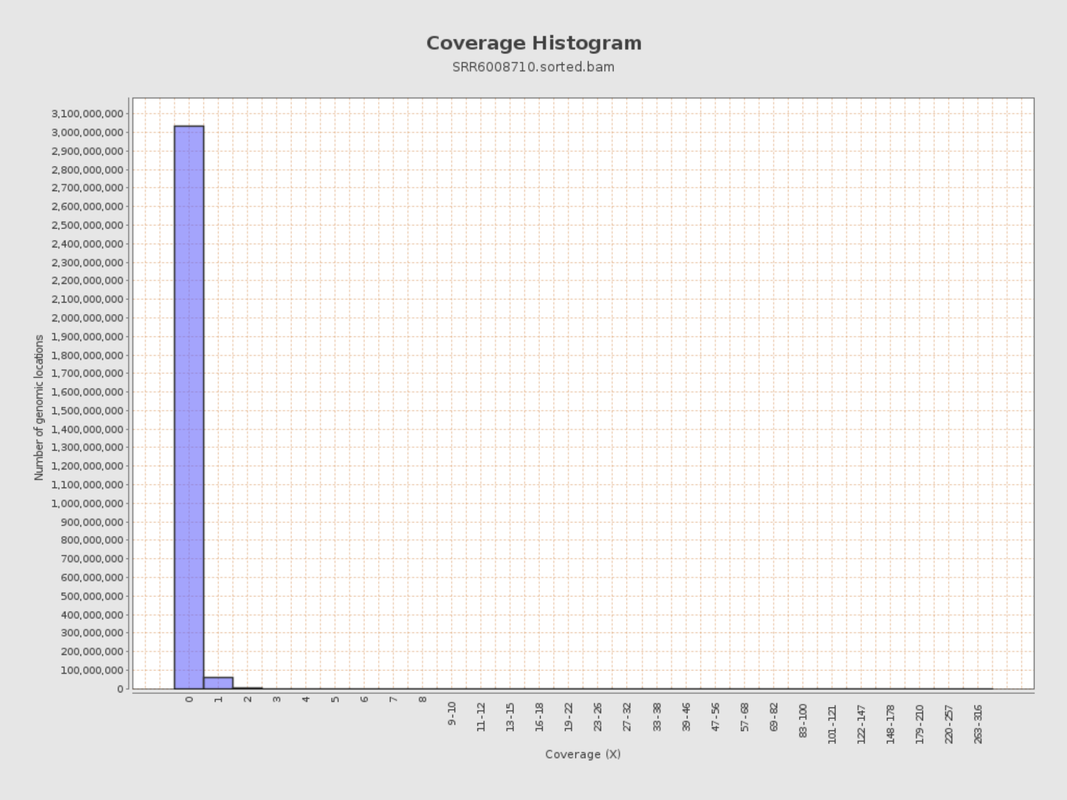
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6578973	0.0264	0.225
chr2	243199373	6372450	0.0262	0.2887
chr3	198022430	5518579	0.0279	0.1901
chr4	191154276	3496740	0.0183	0.152
chr5	180915260	3718269	0.0206	0.16
chr6	171115067	3968297	0.0232	0.1763
chr7	159138663	2928311	0.0184	0.1933

chr8	146364022	4921903	0.0336	0.2511
chr9	141213431	2653357	0.0188	0.1691
chr10	135534747	3844987	0.0284	0.1961
chr11	135006516	3224206	0.0239	0.1847
chr12	133851895	3602600	0.0269	0.1843
chr13	115169878	2349689	0.0204	0.1633
chr14	107349540	2740769	0.0255	0.1829
chr15	102531392	1893665	0.0185	0.1528
chr16	90354753	1795675	0.0199	0.1619
chr17	81195210	1659038	0.0204	0.1651
chr18	78077248	1288962	0.0165	0.2225
chr19	59128983	931432	0.0158	0.1607
chr20	63025520	1279110	0.0203	0.1573
chr21	48129895	652491	0.0136	0.1327
chr22	51304566	823534	0.0161	0.1398
chrMT	16571	22943	1.3845	1.6595
chrX	155270560	4145561	0.0267	0.185
chrY	59373566	128483	0.0022	0.0549

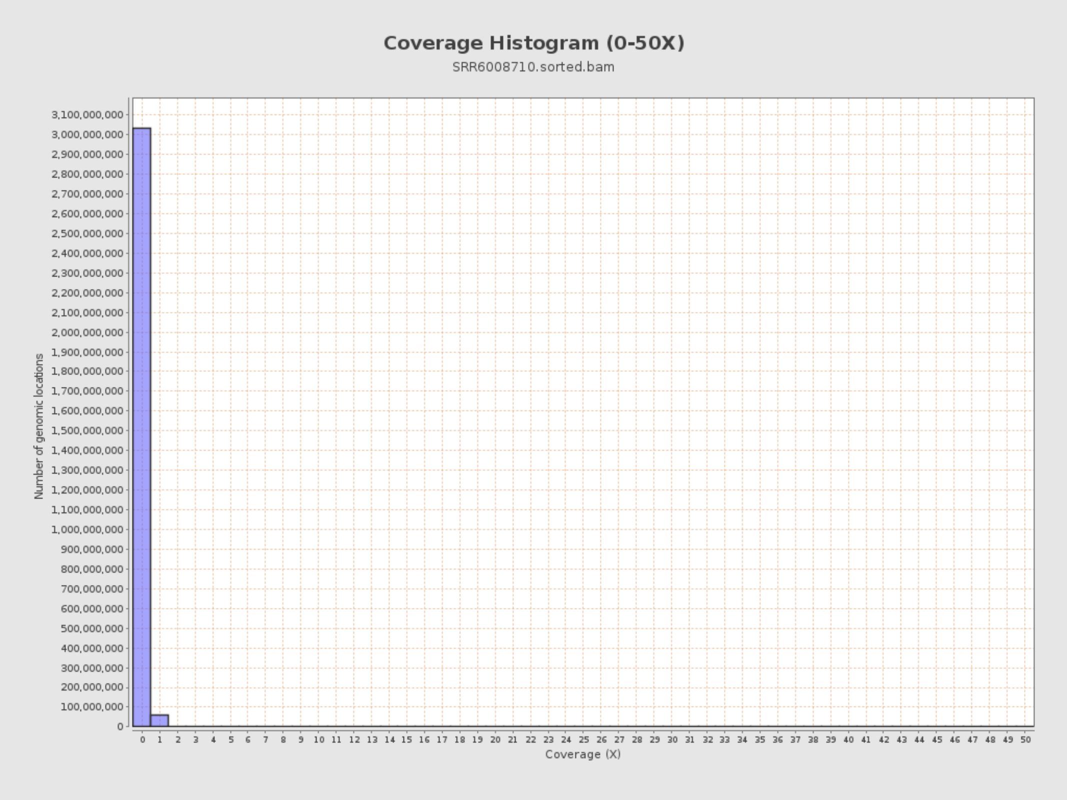
3. Results : Coverage across reference



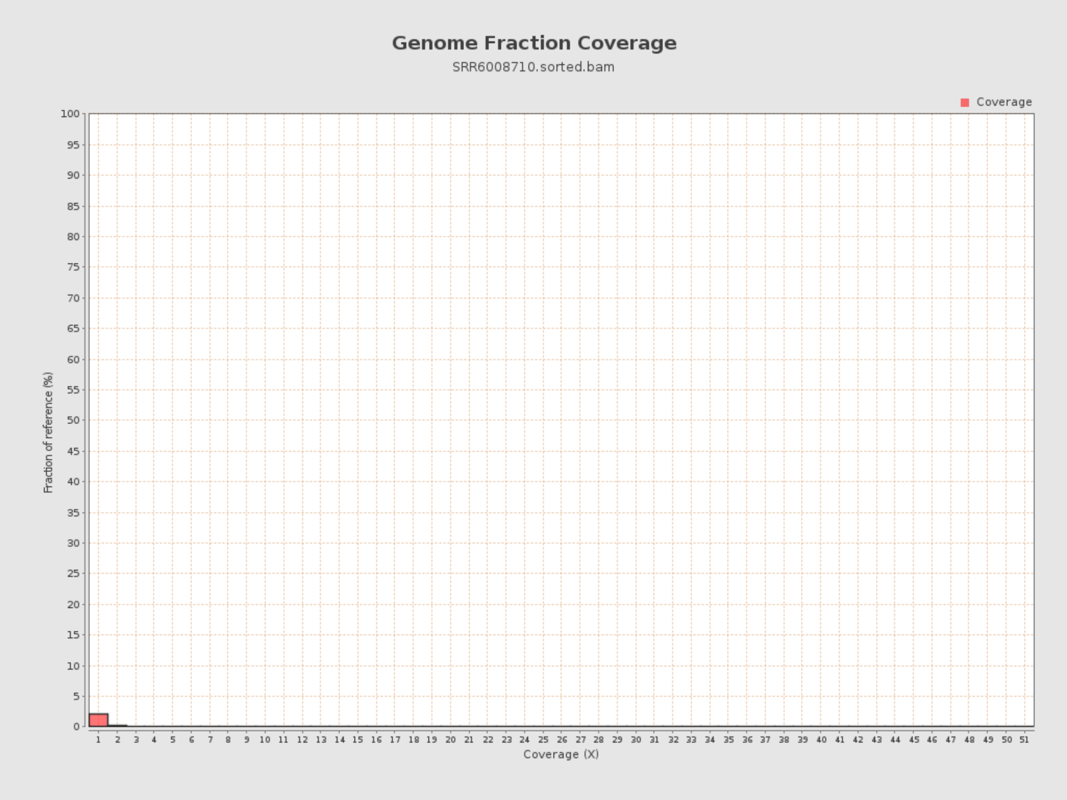
4. Results : Coverage Histogram



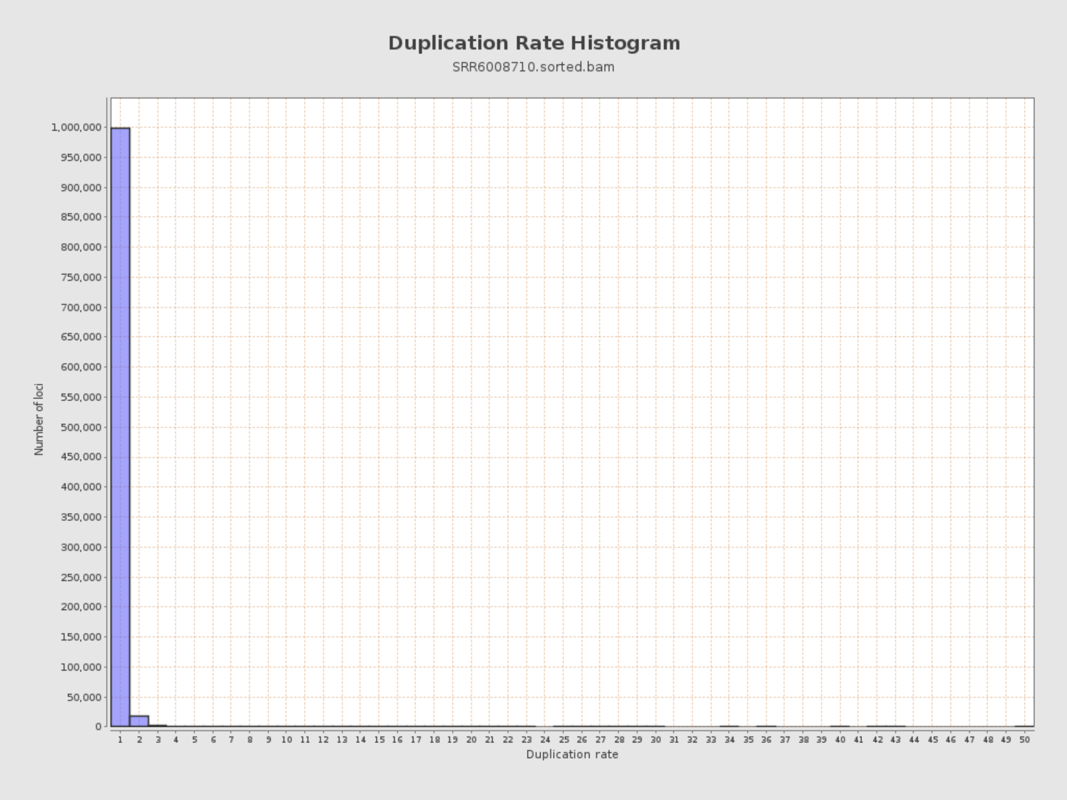
5. Results : Coverage Histogram (0-50X)



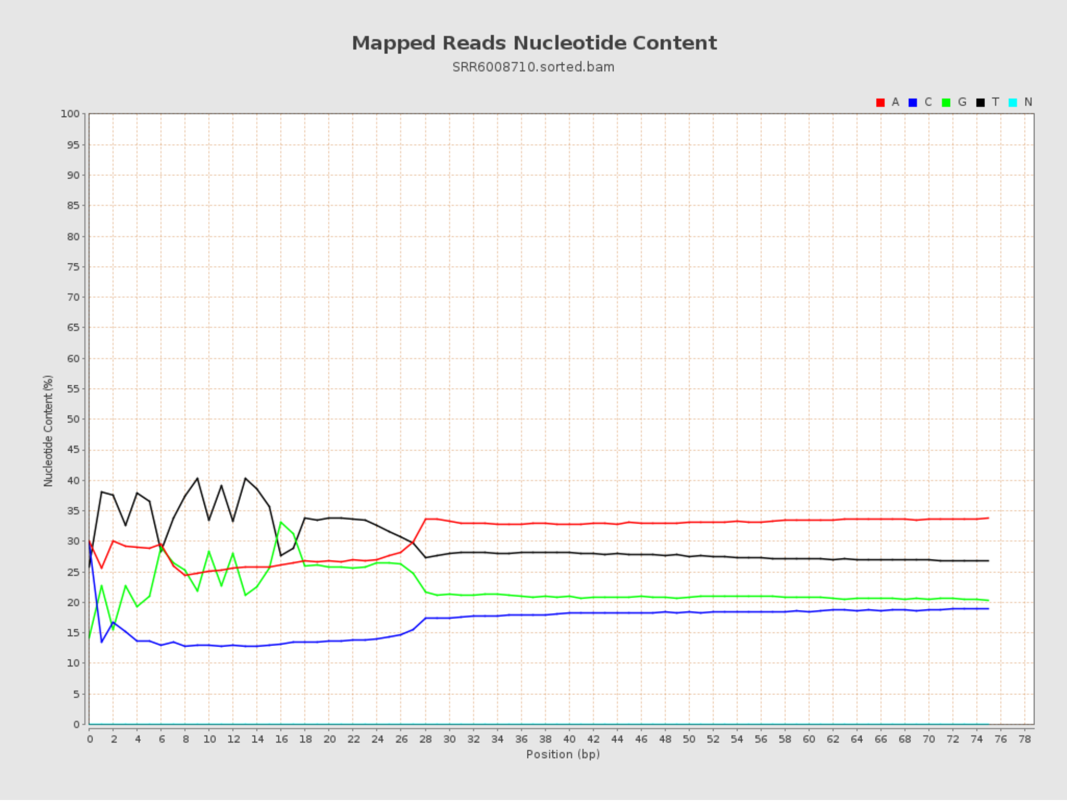
6. Results : Genome Fraction Coverage



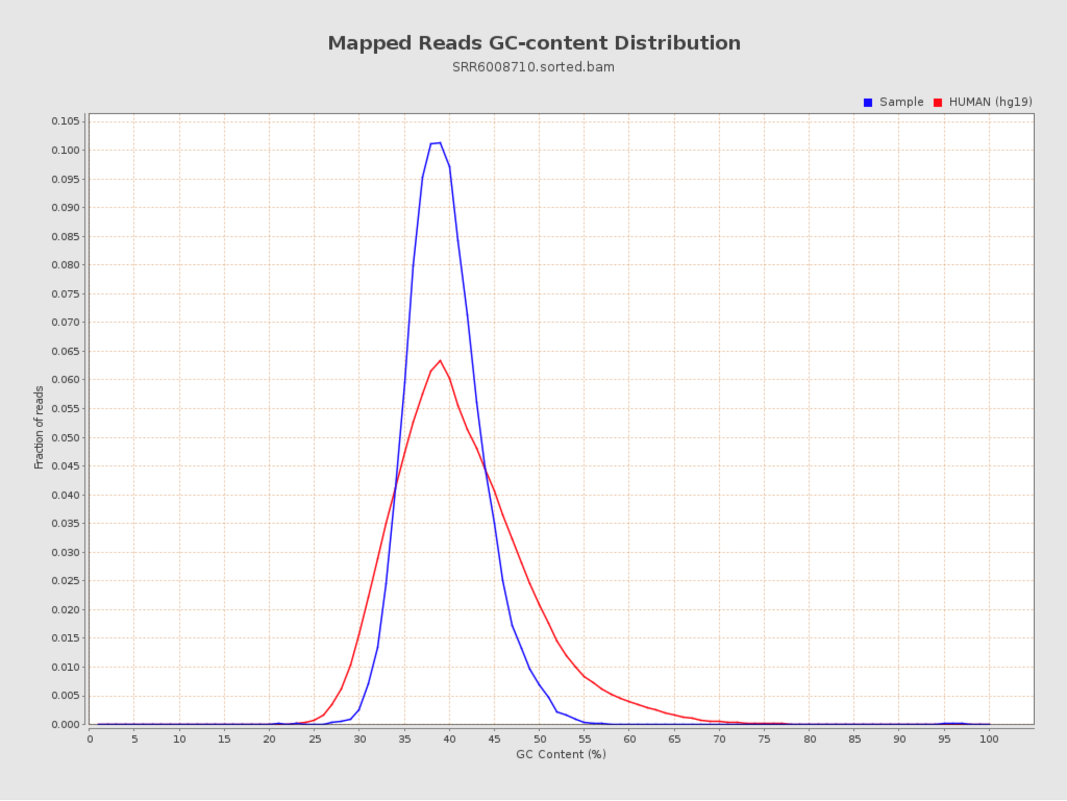
7. Results : Duplication Rate Histogram



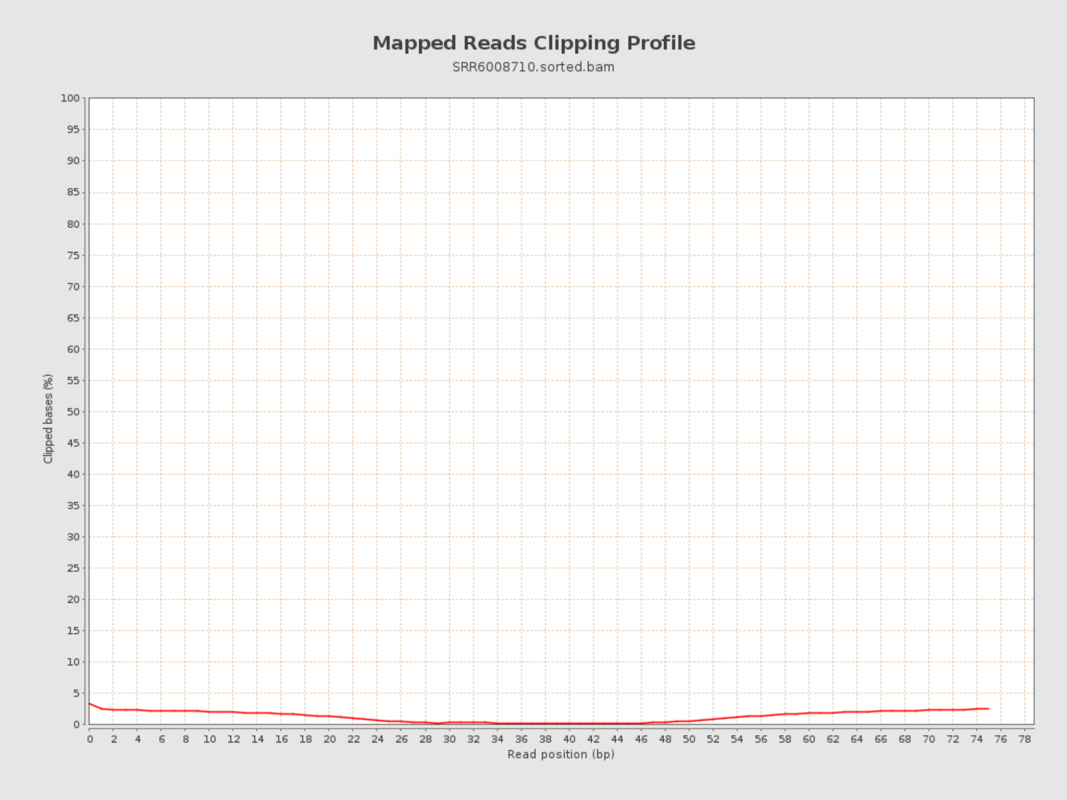
8. Results : Mapped Reads Nucleotide Content



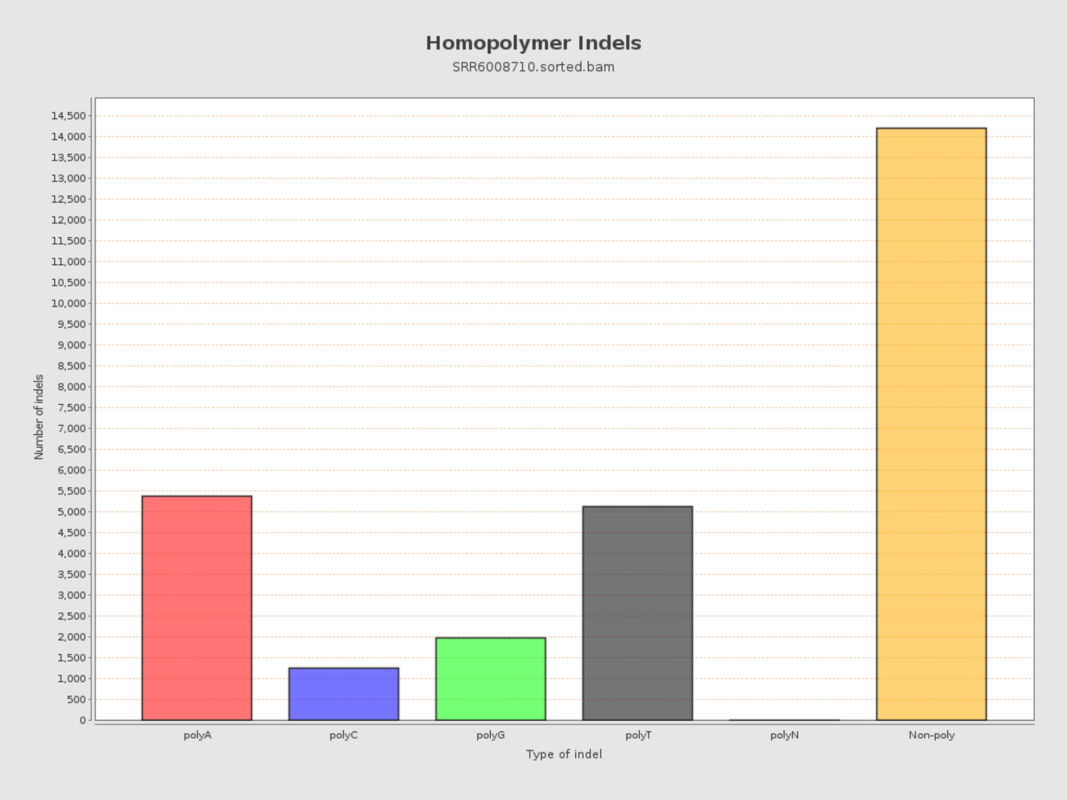
9. Results : Mapped Reads GC-content Distribution



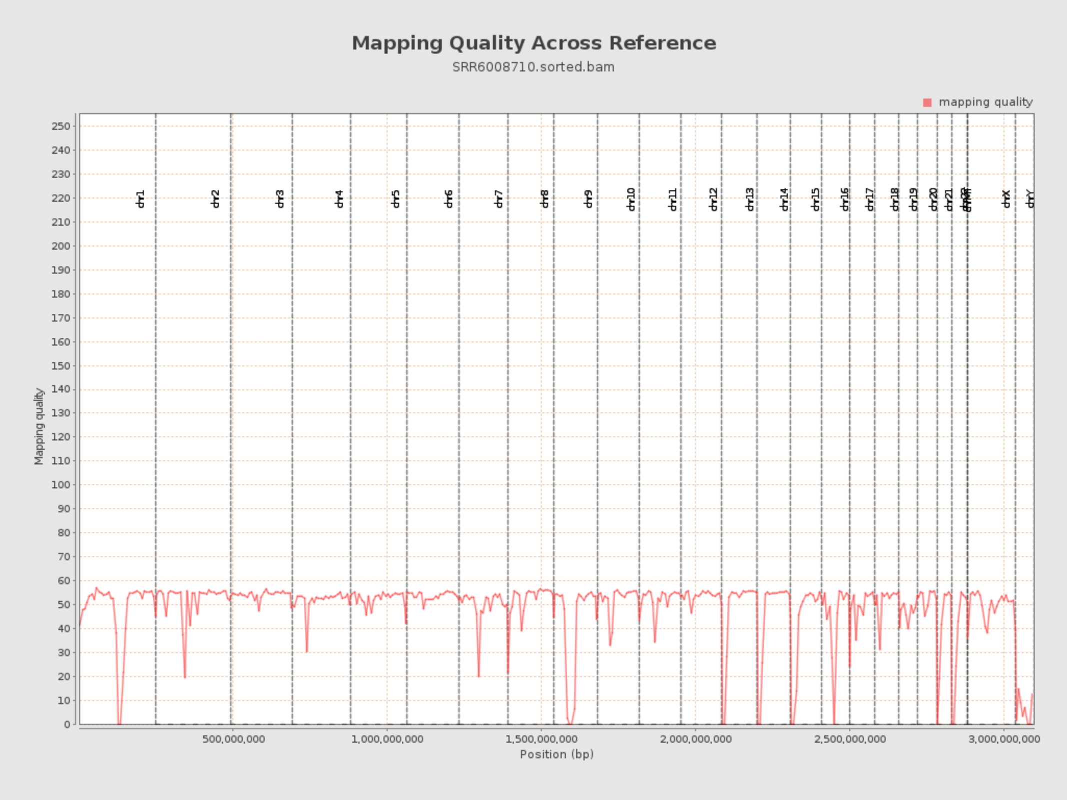
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram