Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:08:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008735.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_SRR6008735 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008735.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:08:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008735.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,589,685
Mapped reads	831,623 / 52.31%
Unmapped reads	758,062 / 47.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,148 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	34,265 / 2.16%
Duplication rate	3.03%
Clipped reads	521,587 / 32.81%

2.2. ACGT Content

Number/percentage of A's	14,635,938 / 28.22%
Number/percentage of C's	8,692,071 / 16.76%
Number/percentage of T's	15,888,178 / 30.63%
Number/percentage of G's	12,650,286 / 24.39%
Number/percentage of N's	2,259 / 0%
GC Percentage	41.15%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.1782

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

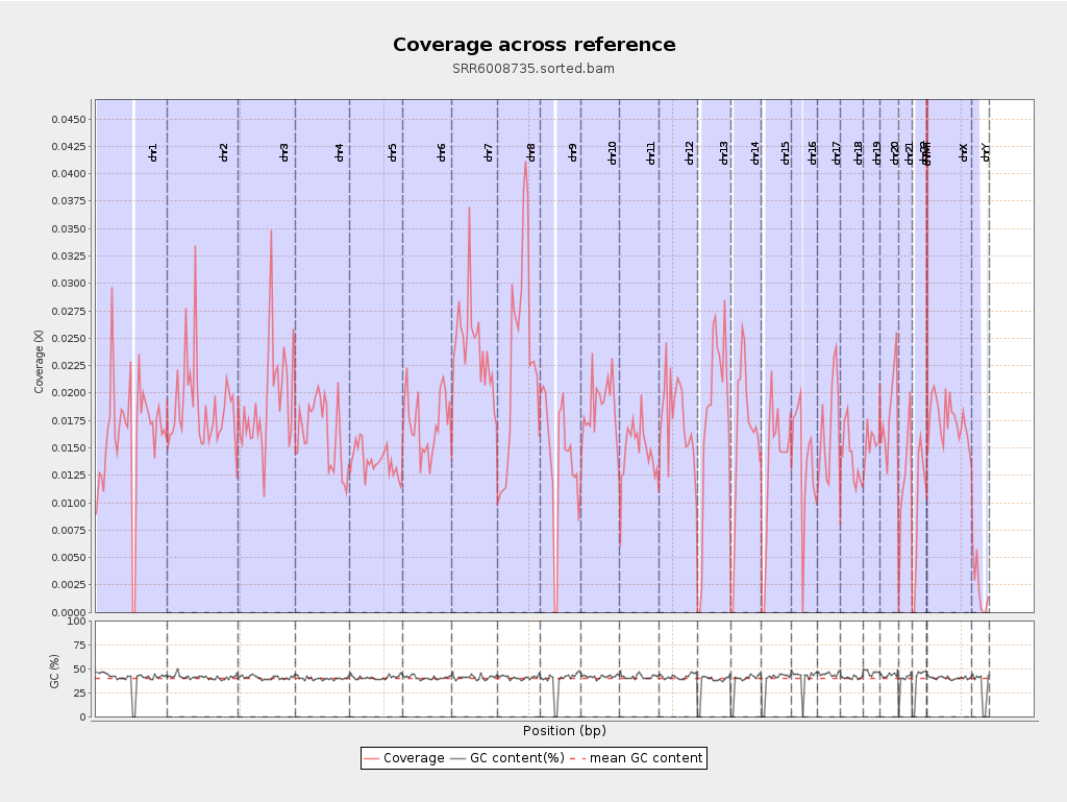
General error rate	0.99%
Mismatches	506,489
Insertions	4,405
Mapped reads with at least one insertion	0.53%
Deletions	20,147
Mapped reads with at least one deletion	2.39%
Homopolymer indels	48.85%

2.6. Chromosome stats

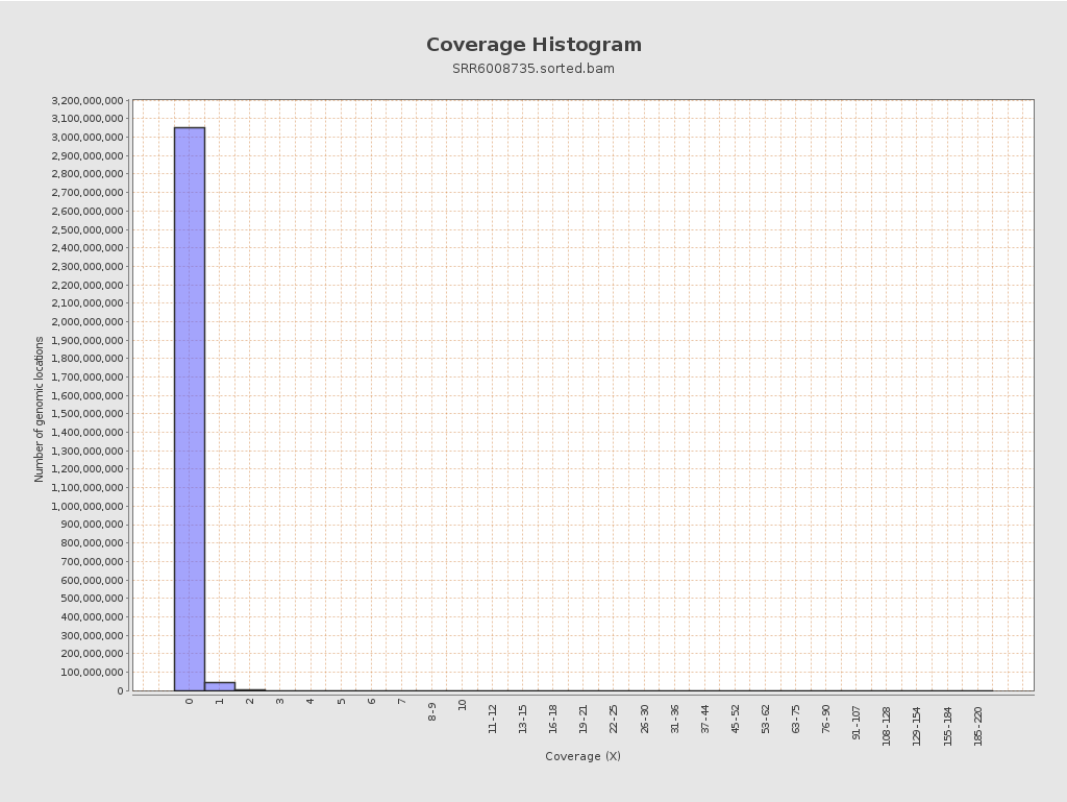
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4020801	0.0161	0.2015
chr2	243199373	4555140	0.0187	0.2387
chr3	198022430	3793557	0.0192	0.1593
chr4	191154276	3121227	0.0163	0.1457
chr5	180915260	2504285	0.0138	0.1343
chr6	171115067	2943164	0.0172	0.1596
chr7	159138663	3823269	0.024	0.2804

chr8	146364022	3366798	0.023	0.2184
chr9	141213431	1988729	0.0141	0.1633
chr10	135534747	2521075	0.0186	0.1672
chr11	135006516	2009618	0.0149	0.1703
chr12	133851895	2362932	0.0177	0.1533
chr13	115169878	2050922	0.0178	0.1524
chr14	107349540	1707348	0.0159	0.1466
chr15	102531392	1378498	0.0134	0.1348
chr16	90354753	1243153	0.0138	0.1385
chr17	81195210	1363592	0.0168	0.1535
chr18	78077248	1098961	0.0141	0.2356
chr19	59128983	926075	0.0157	0.1628
chr20	63025520	1146801	0.0182	0.1527
chr21	48129895	592760	0.0123	0.1267
chr22	51304566	495101	0.0097	0.1108
chrMT	16571	23283	1.405	2.1658
chrX	155270560	2731626	0.0176	0.1579
chrY	59373566	130789	0.0022	0.0574

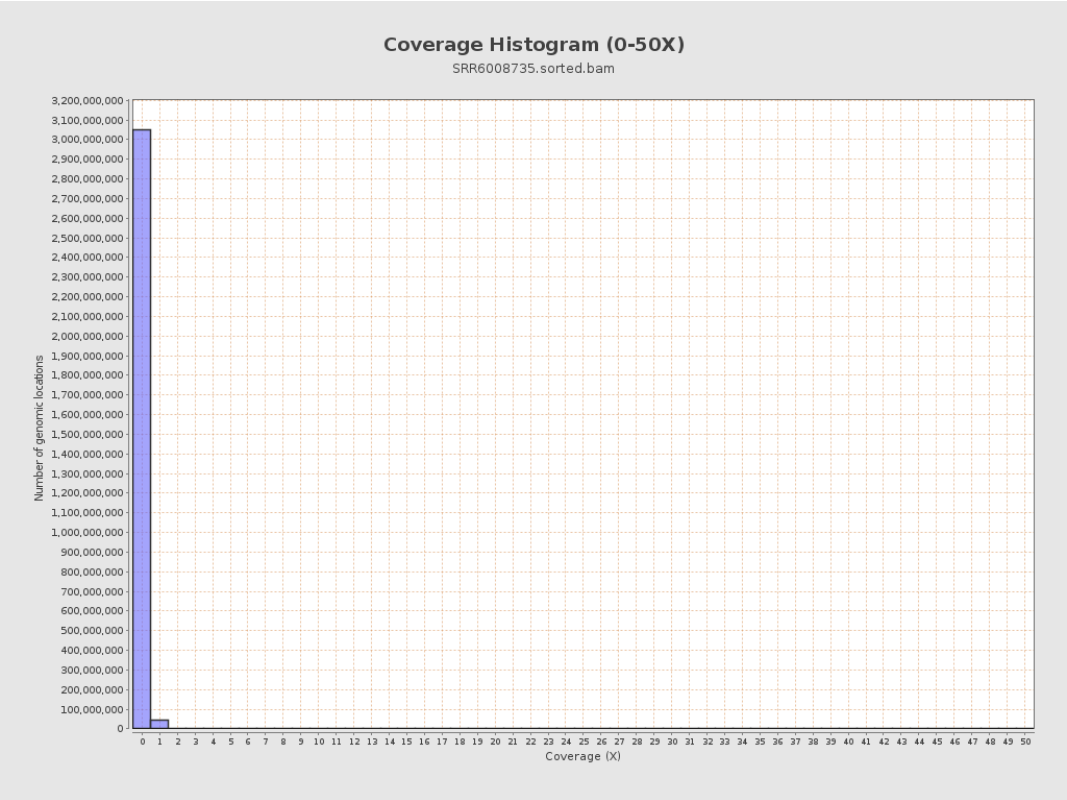
3. Results : Coverage across reference



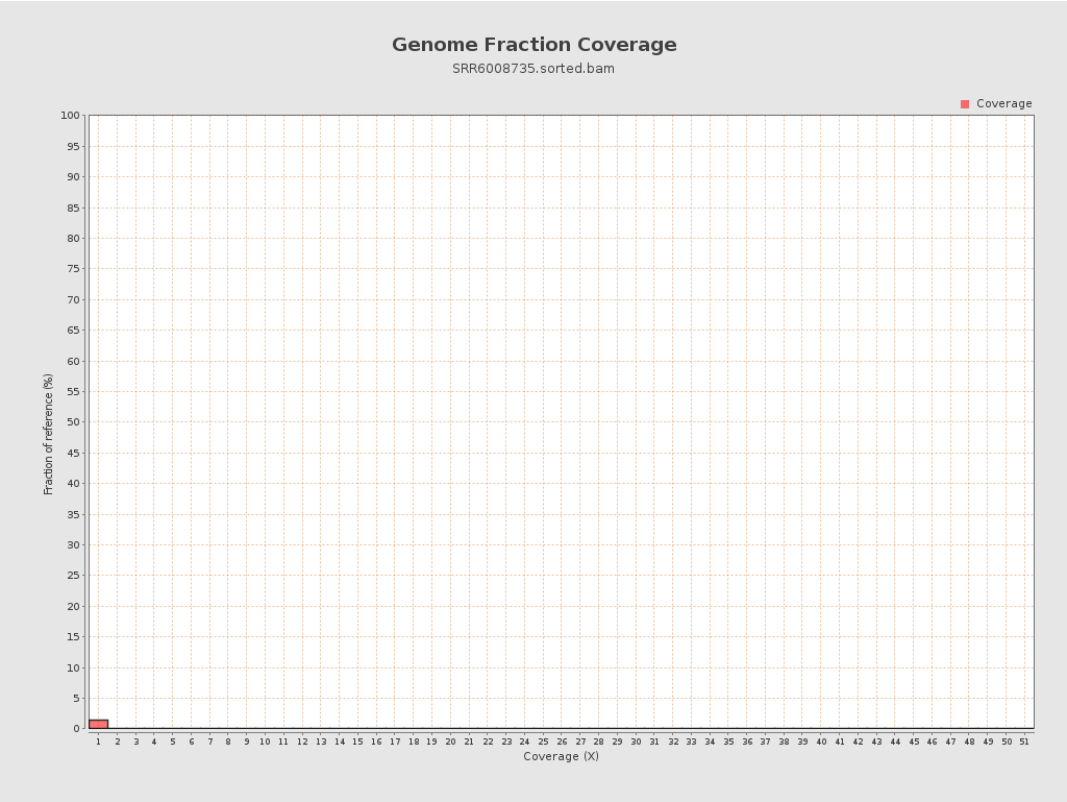
4. Results : Coverage Histogram



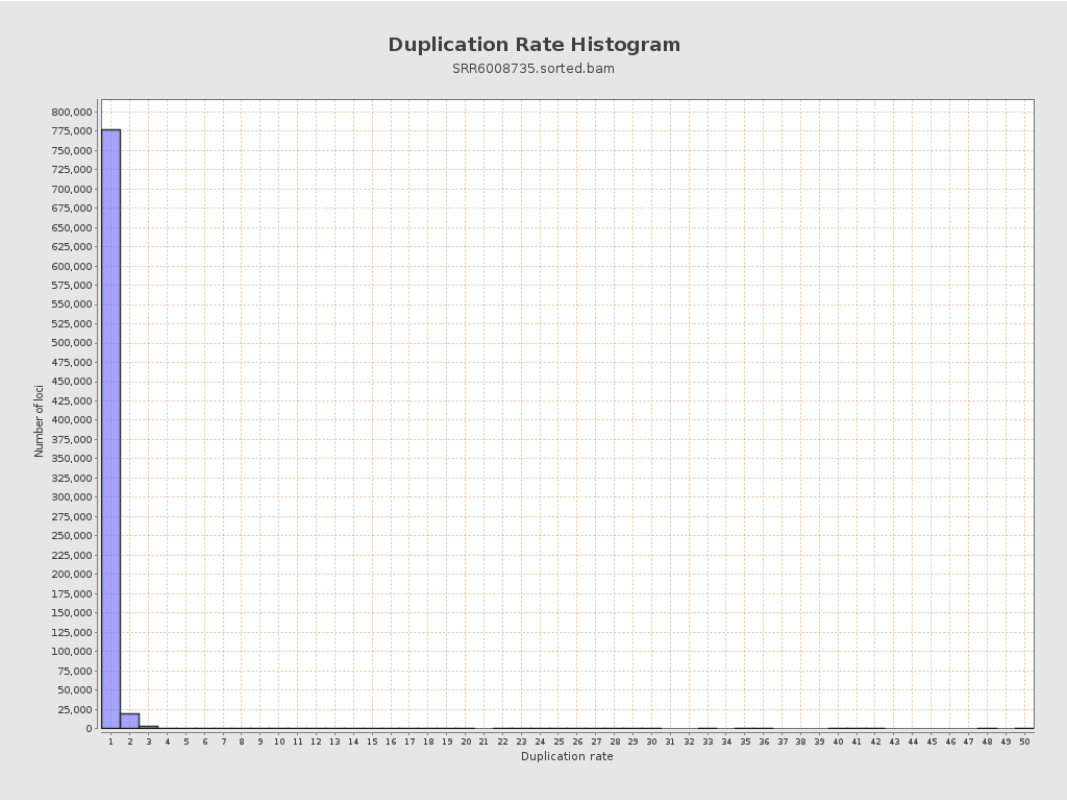
5. Results : Coverage Histogram (0-50X)



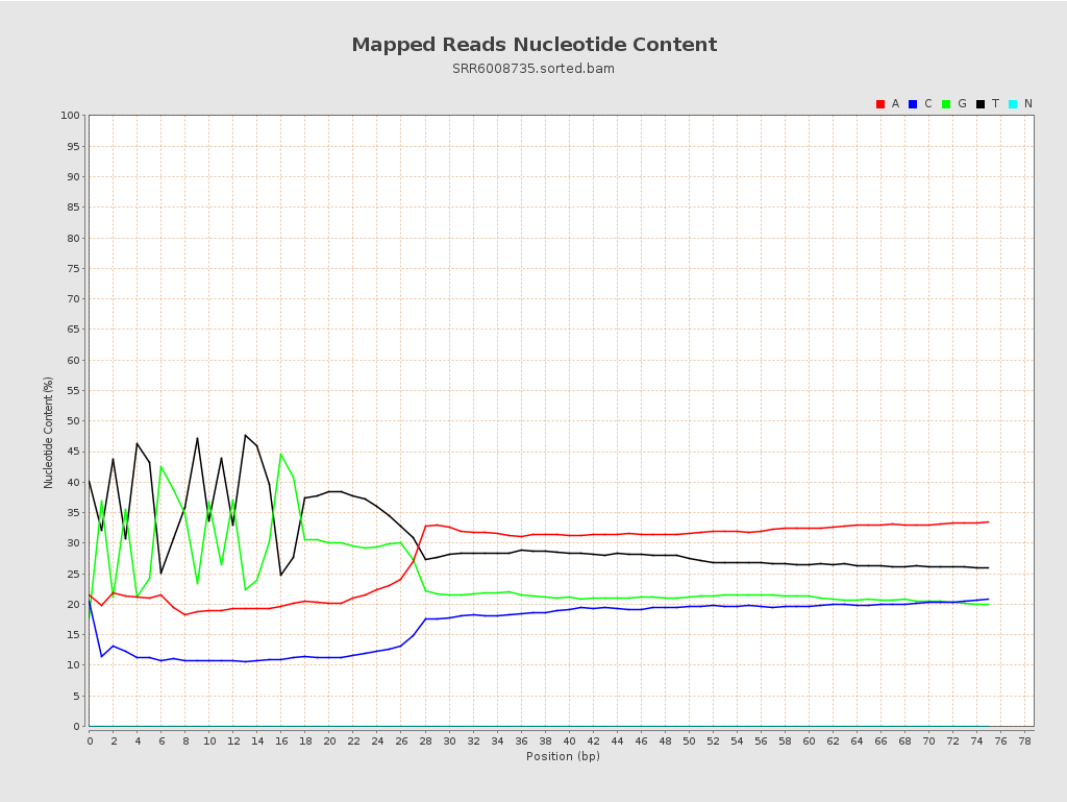
6. Results : Genome Fraction Coverage



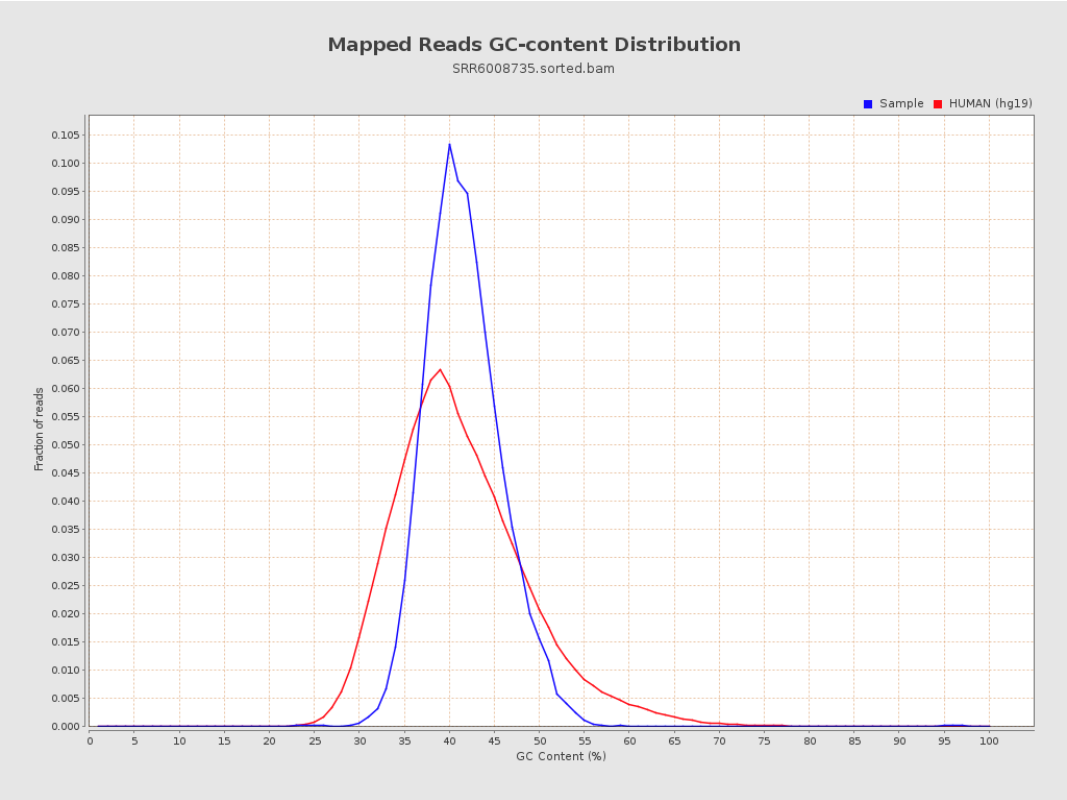
7. Results : Duplication Rate Histogram



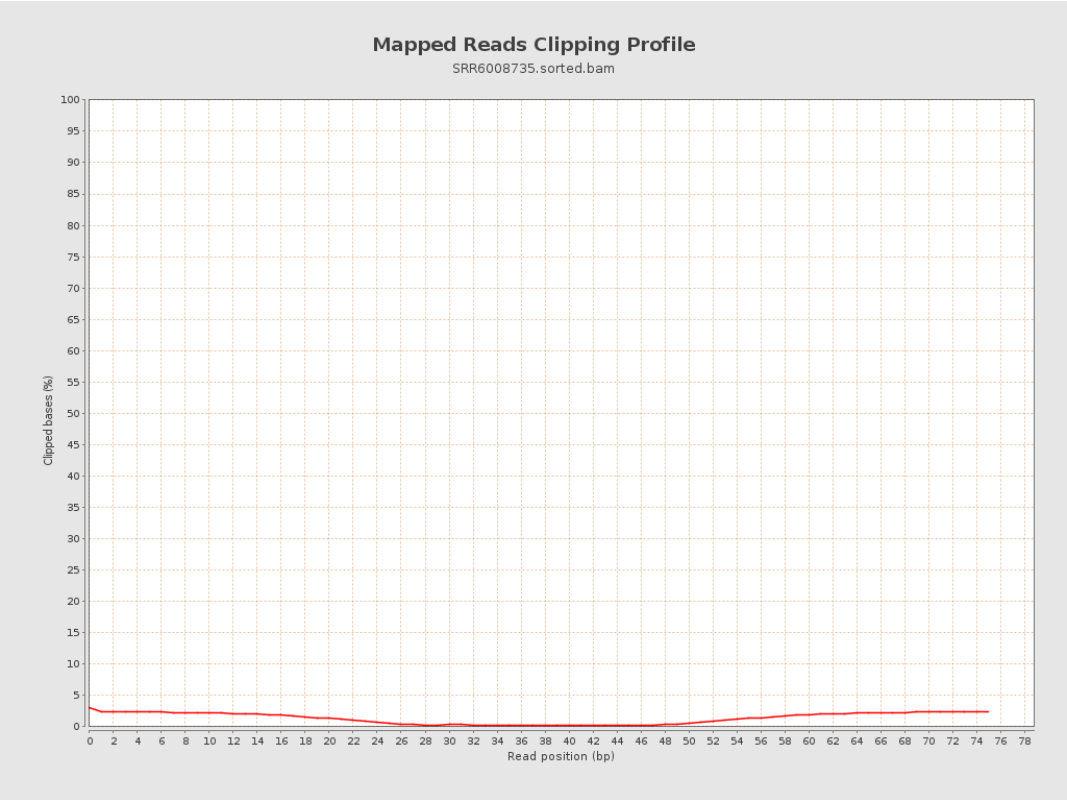
8. Results : Mapped Reads Nucleotide Content



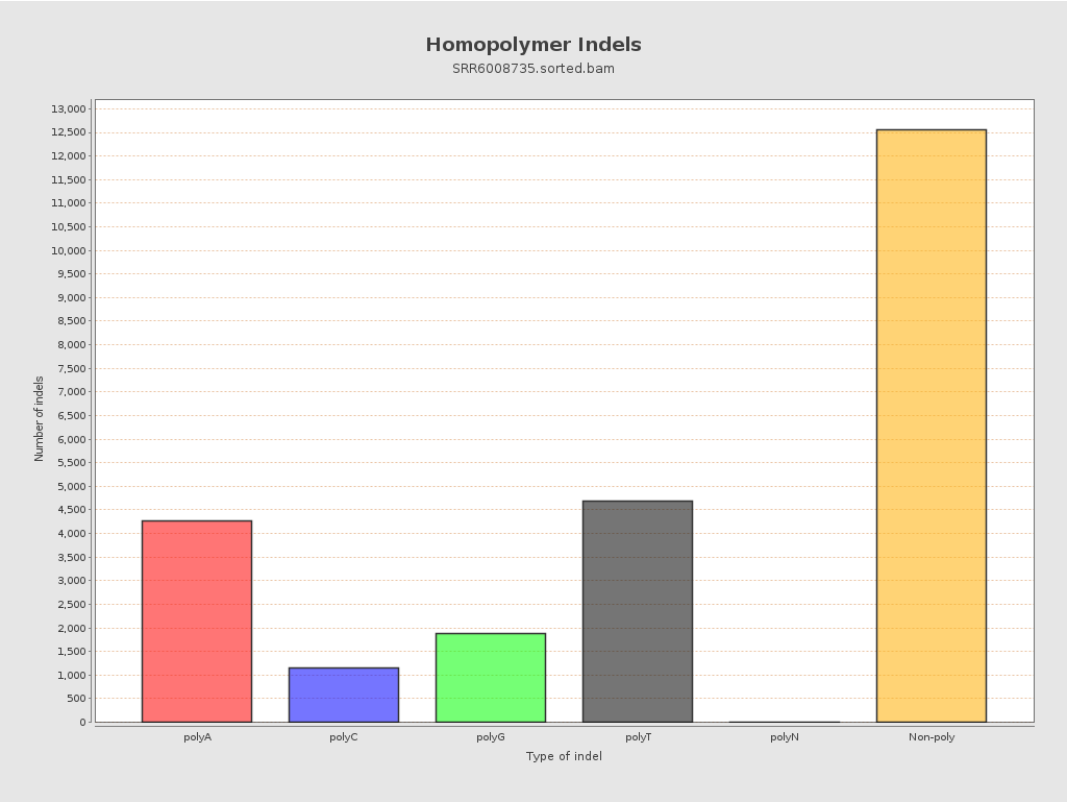
9. Results : Mapped Reads GC-content Distribution



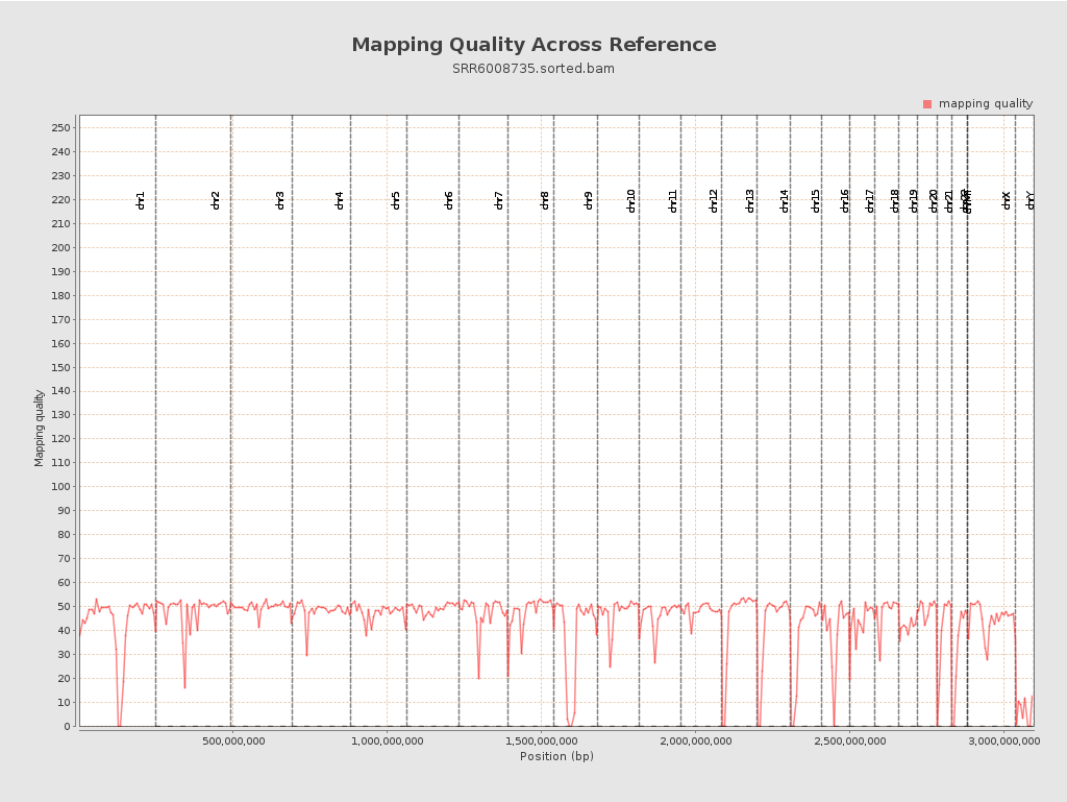
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram