Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:56:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008685.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_SRR6008685 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008685.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:56:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008685.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,372,473
Mapped reads	1,100,809 / 80.21%
Unmapped reads	271,664 / 19.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,655 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	47,816 / 3.48%
Duplication rate	3.76%
Clipped reads	591,940 / 43.13%

2.2. ACGT Content

Number/percentage of A's	19,224,778 / 27.26%
Number/percentage of C's	12,703,867 / 18.02%
Number/percentage of T's	22,677,099 / 32.16%
Number/percentage of G's	15,889,629 / 22.53%
Number/percentage of N's	22,302 / 0.03%
GC Percentage	40.55%

2.3. Coverage

Mean	0.0228

Standard Deviation	0.2127

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

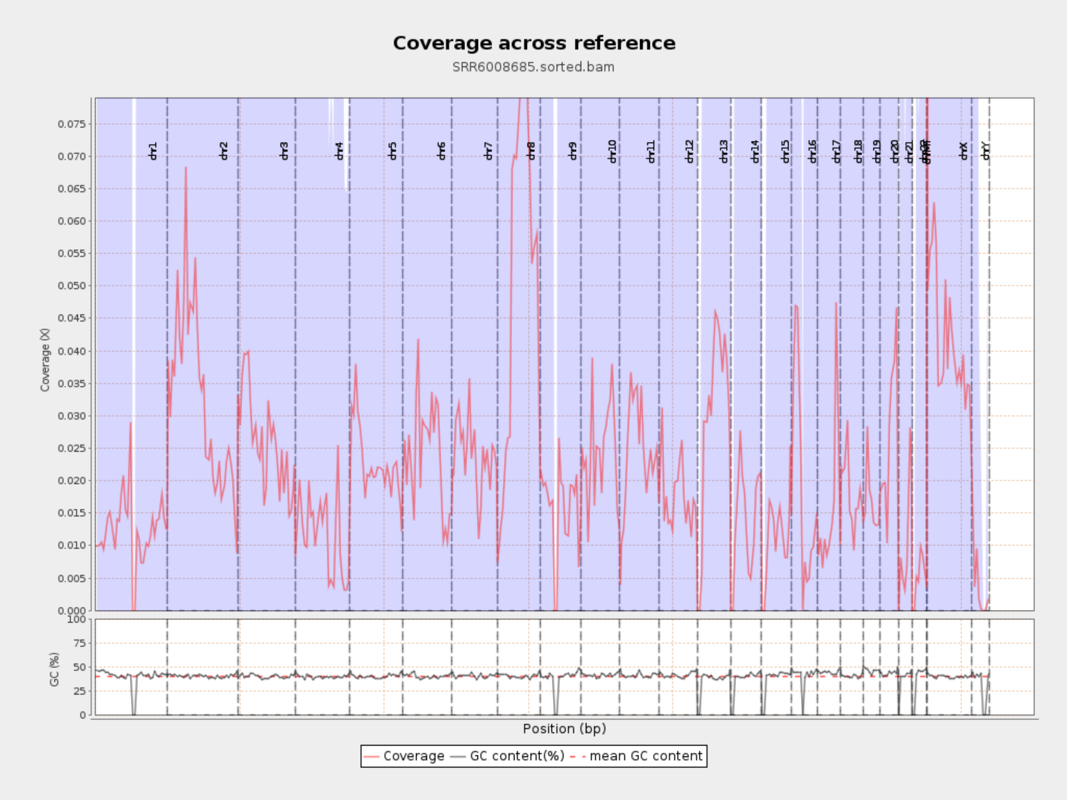
General error rate	0.84%
Mismatches	585,344
Insertions	4,300
Mapped reads with at least one insertion	0.39%
Deletions	25,775
Mapped reads with at least one deletion	2.31%
Homopolymer indels	43.01%

2.6. Chromosome stats

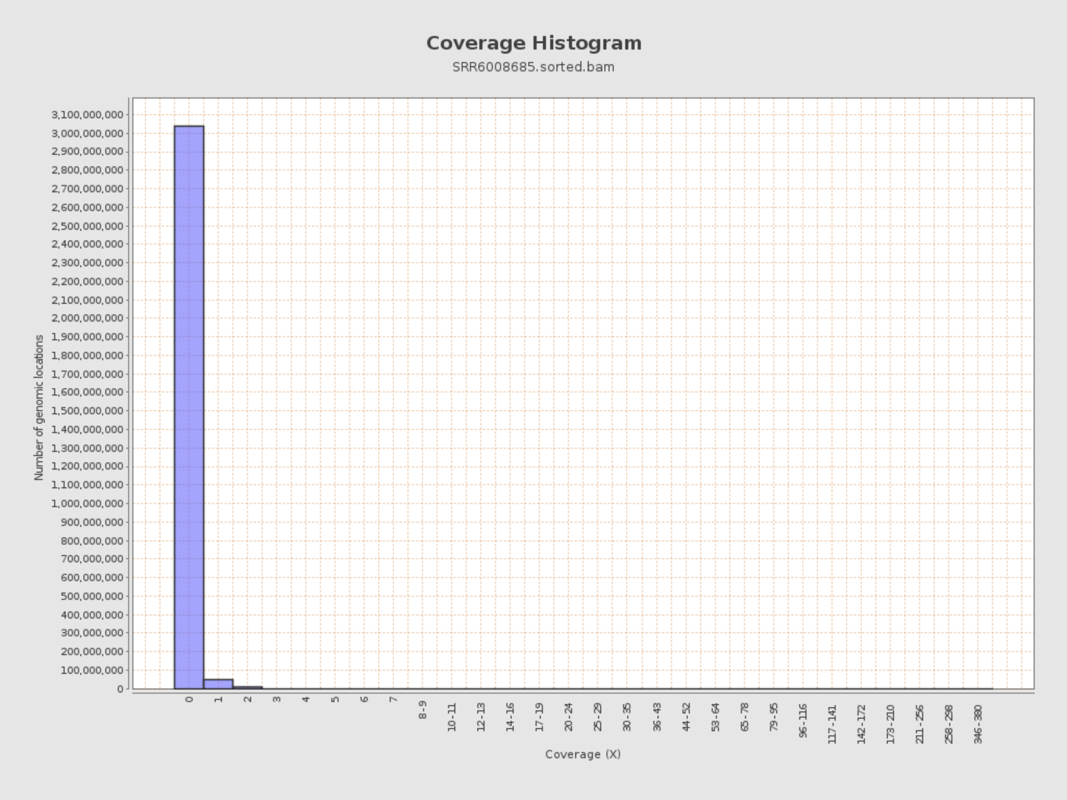
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3103024	0.0124	0.302
chr2	243199373	7934566	0.0326	0.2612
chr3	198022430	5160987	0.0261	0.1855
chr4	191154276	2238883	0.0117	0.1302
chr5	180915260	4155886	0.023	0.1736
chr6	171115067	4105020	0.024	0.1997
chr7	159138663	3803420	0.0239	0.2314

chr8	146364022	8000016	0.0547	0.3118
chr9	141213431	2233702	0.0158	0.1622
chr10	135534747	3312525	0.0244	0.2234
chr11	135006516	3310765	0.0245	0.2346
chr12	133851895	2392961	0.0179	0.153
chr13	115169878	3530890	0.0307	0.201
chr14	107349540	1499248	0.014	0.1399
chr15	102531392	1114718	0.0109	0.1197
chr16	90354753	1669396	0.0185	0.1629
chr17	81195210	1298489	0.016	0.1581
chr18	78077248	1402767	0.018	0.2441
chr19	59128983	999809	0.0169	0.2308
chr20	63025520	1719164	0.0273	0.1905
chr21	48129895	525331	0.0109	0.1258
chr22	51304566	263243	0.0051	0.0799
chrMT	16571	9572	0.5776	0.881
chrX	155270560	6562406	0.0423	0.2512
chrY	59373566	216452	0.0036	0.0962

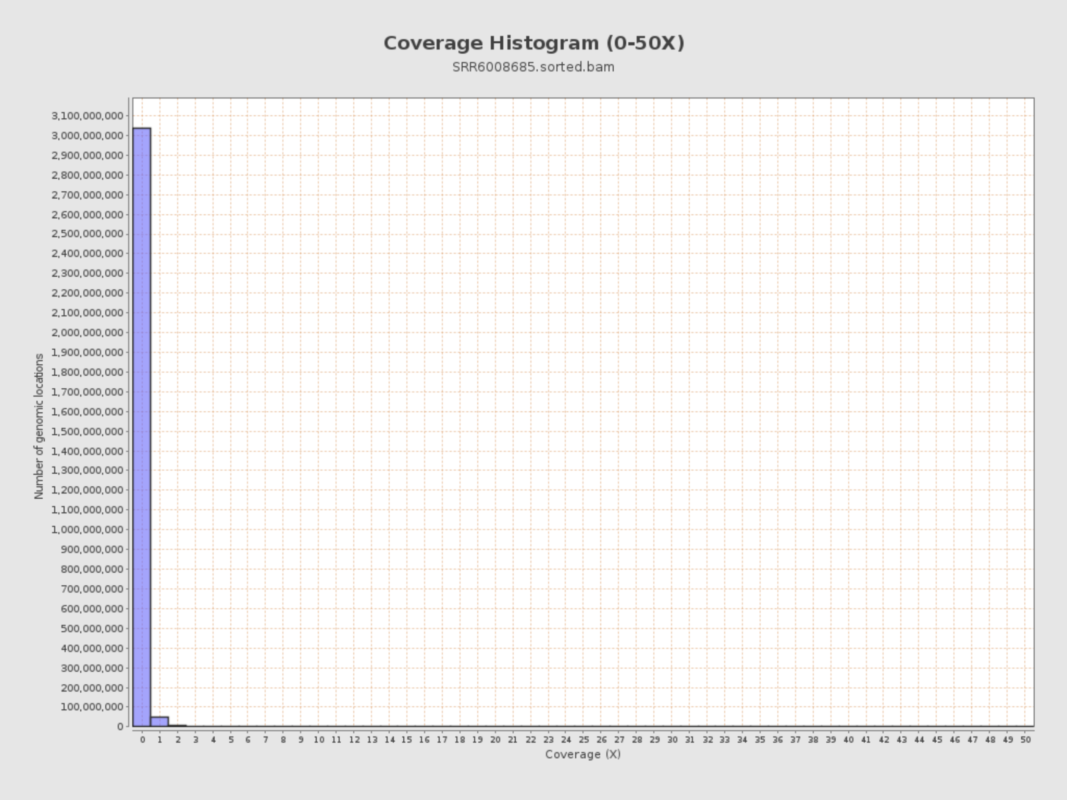
3. Results : Coverage across reference



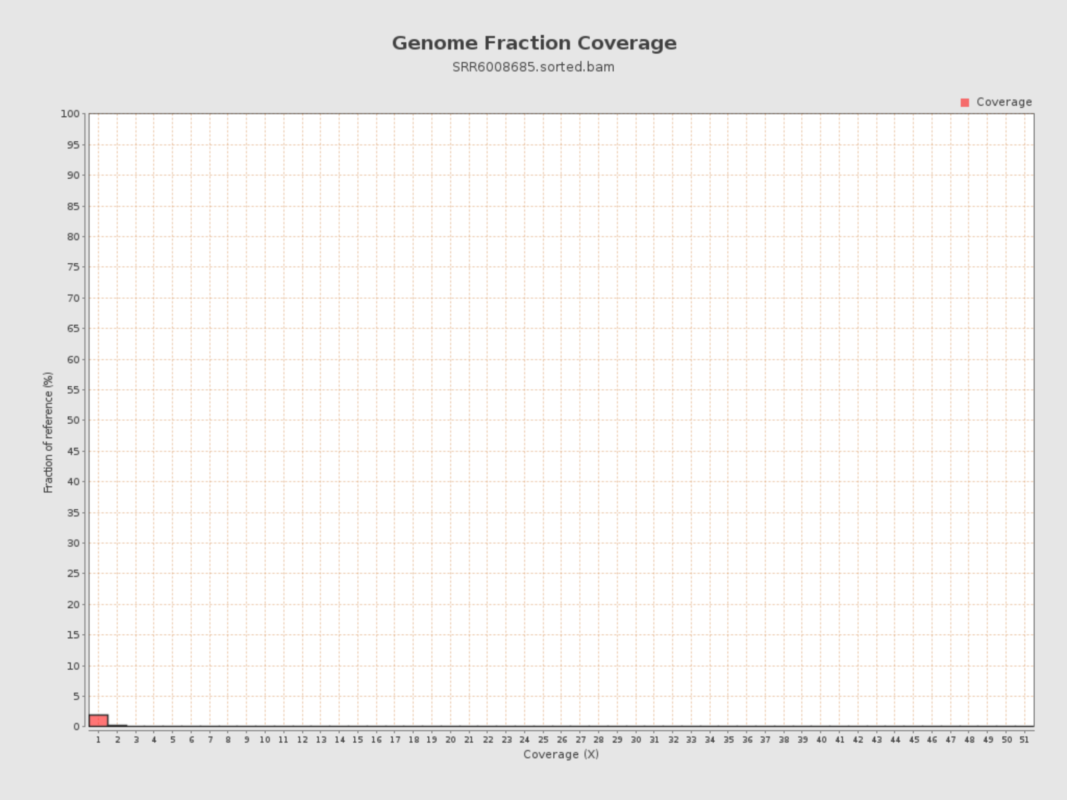
4. Results : Coverage Histogram



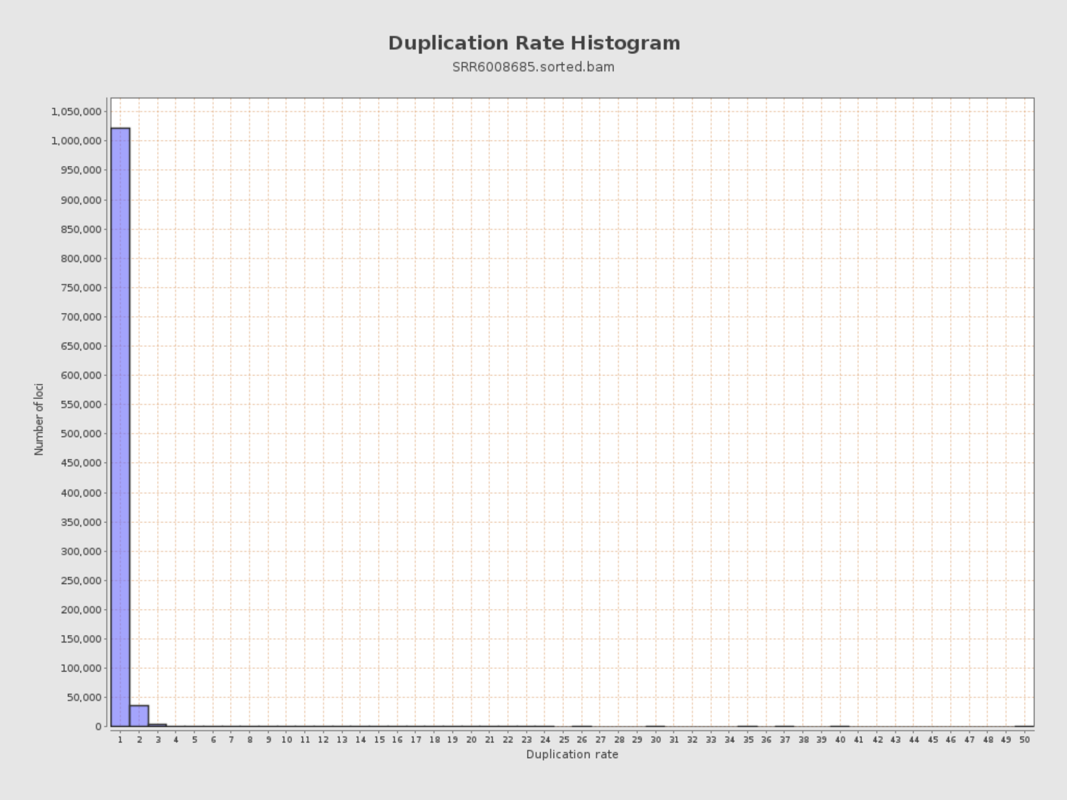
5. Results : Coverage Histogram (0-50X)



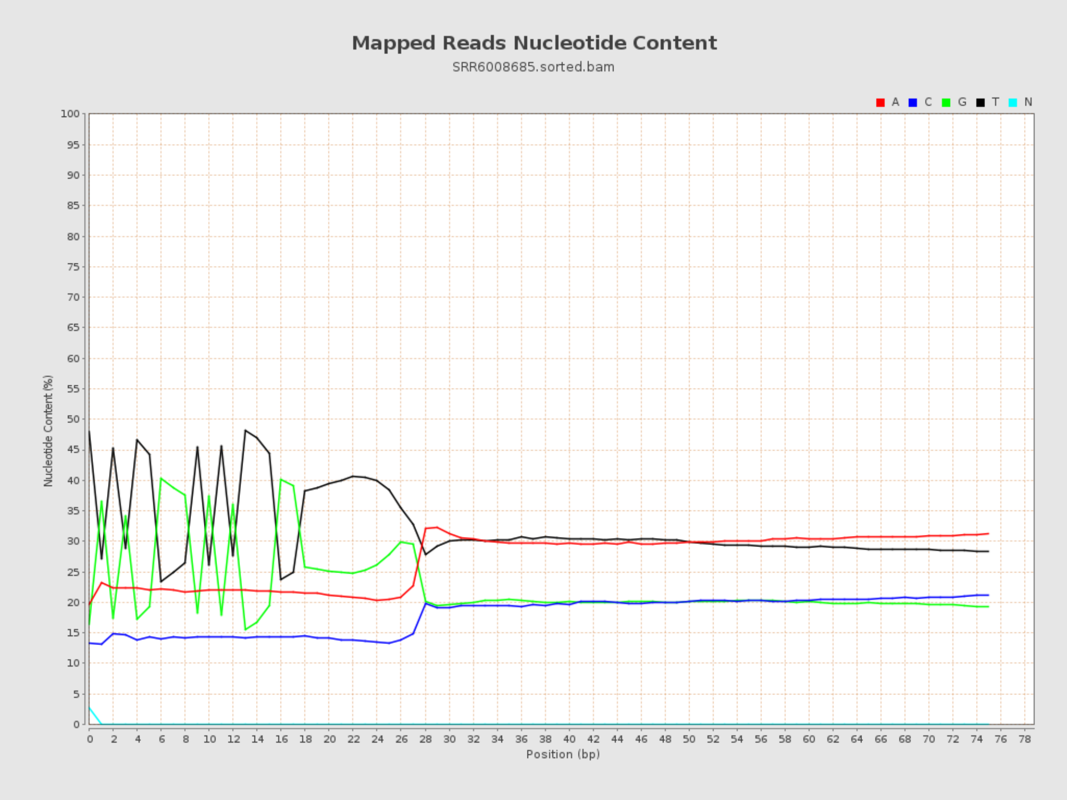
6. Results : Genome Fraction Coverage



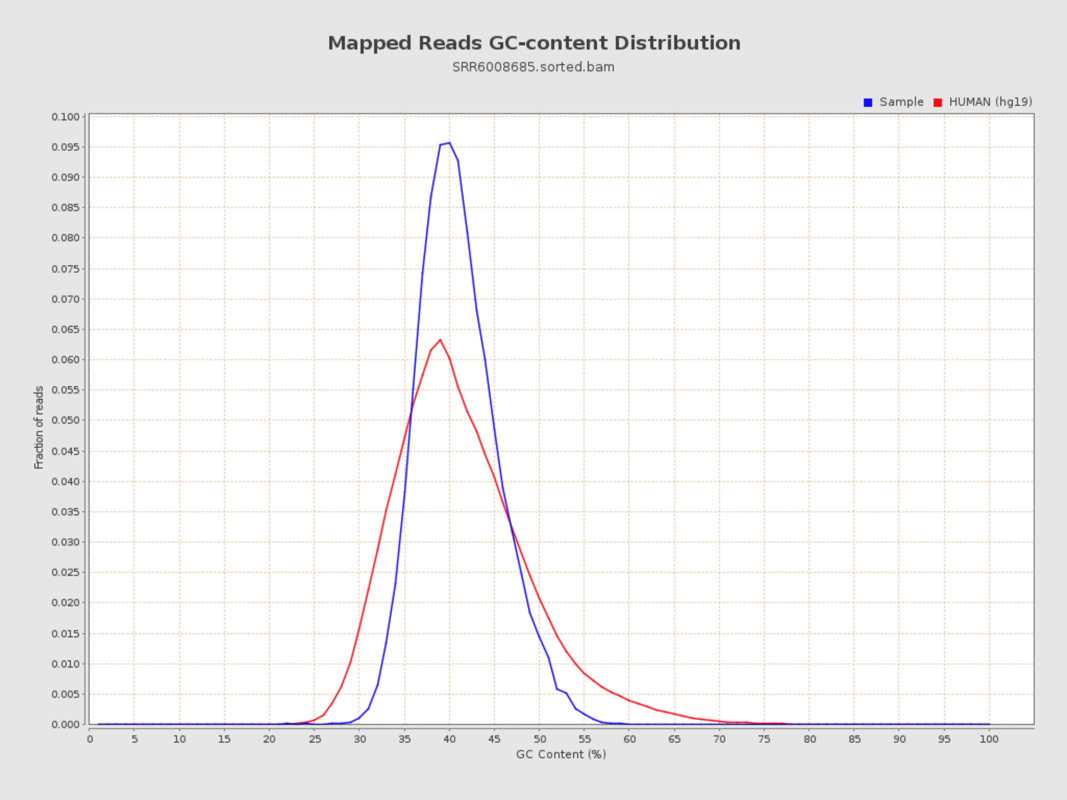
7. Results : Duplication Rate Histogram



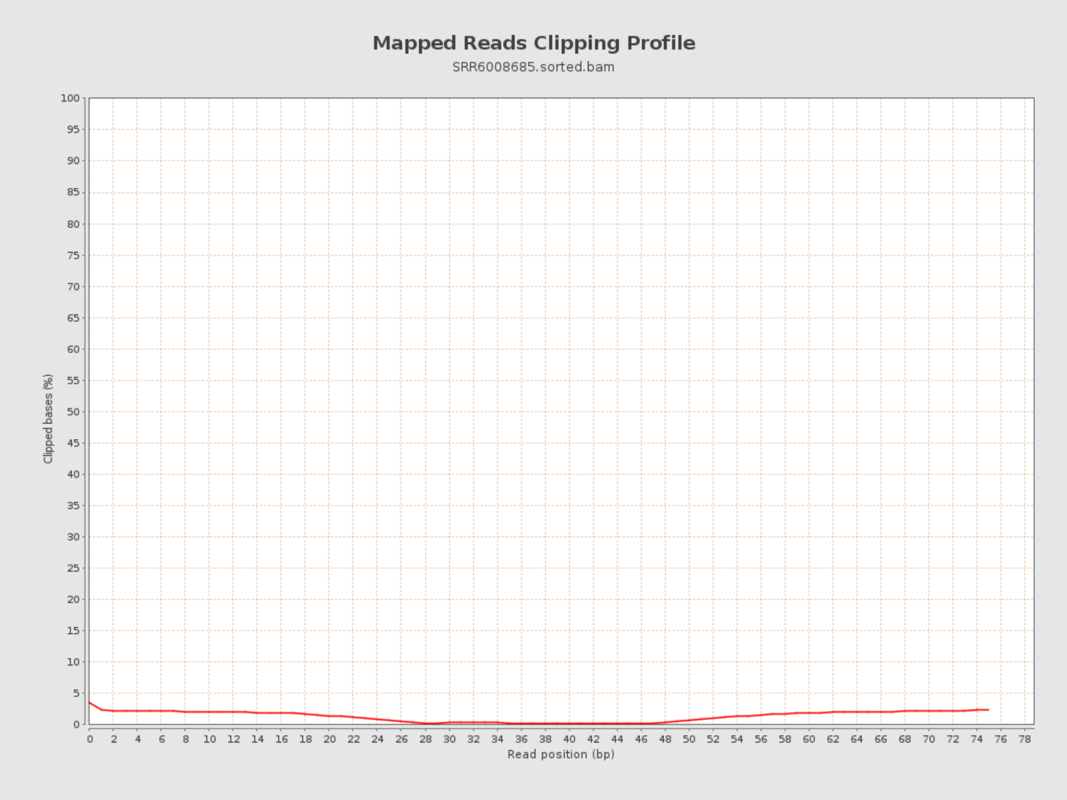
8. Results : Mapped Reads Nucleotide Content



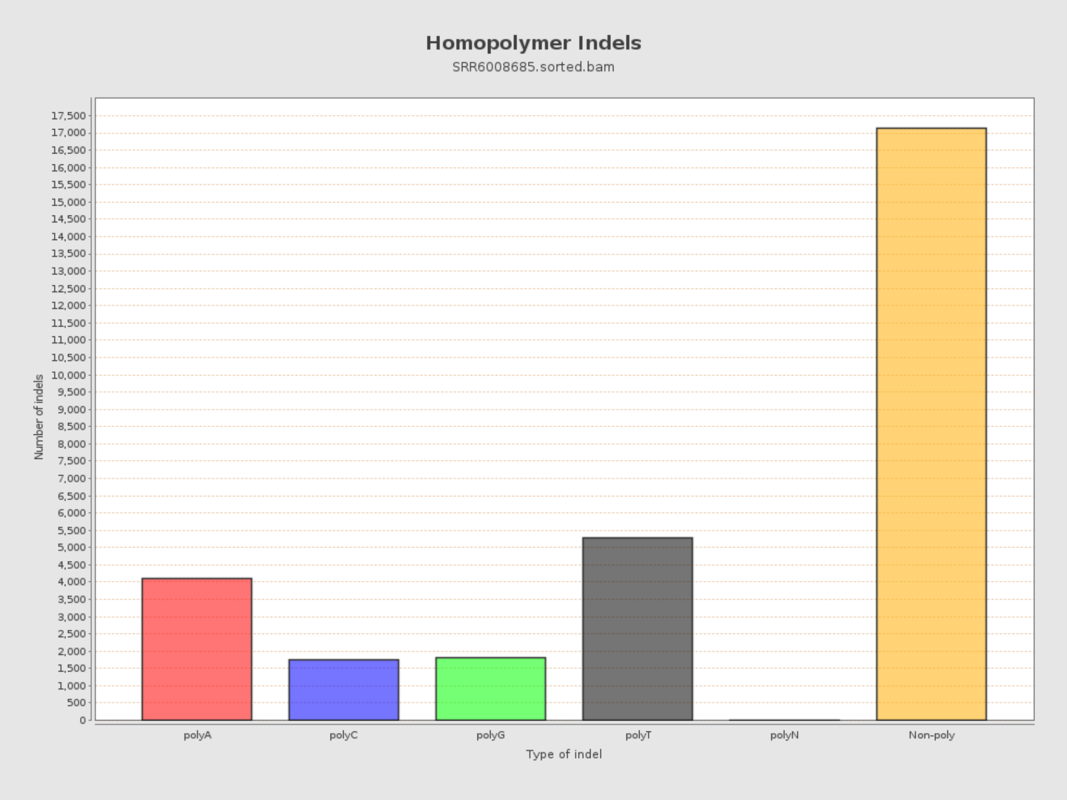
9. Results : Mapped Reads GC-content Distribution



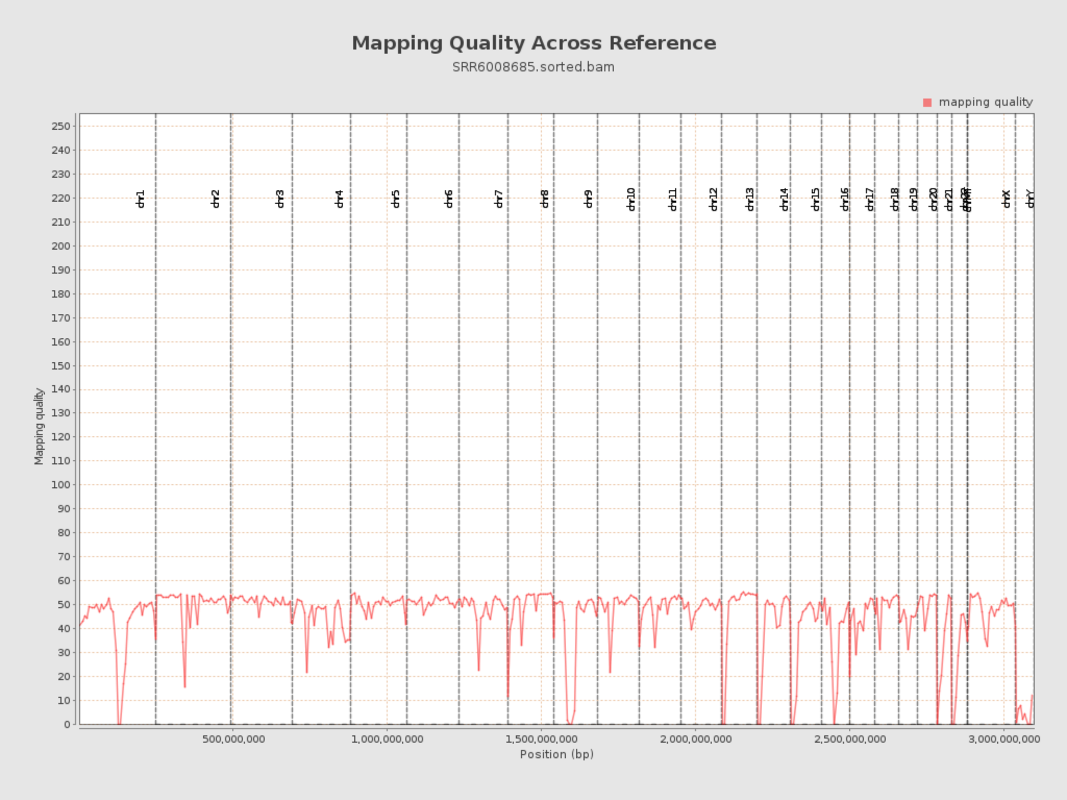
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram