Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:28:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008675.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_SRR6008675 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008675.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:28:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008675.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,609,124
Mapped reads	1,401,632 / 87.11%
Unmapped reads	207,492 / 12.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,230 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	47,797 / 2.97%
Duplication rate	2.33%
Clipped reads	730,245 / 45.38%

2.2. ACGT Content

Number/percentage of A's	24,862,078 / 27.53%
Number/percentage of C's	16,293,393 / 18.04%
Number/percentage of T's	28,113,108 / 31.12%
Number/percentage of G's	21,039,019 / 23.29%
Number/percentage of N's	16,353 / 0.02%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0292

Standard Deviation	0.3188

2.4. Mapping Quality

Mean Mapping Quality	43.71

2.5. Mismatches and indels

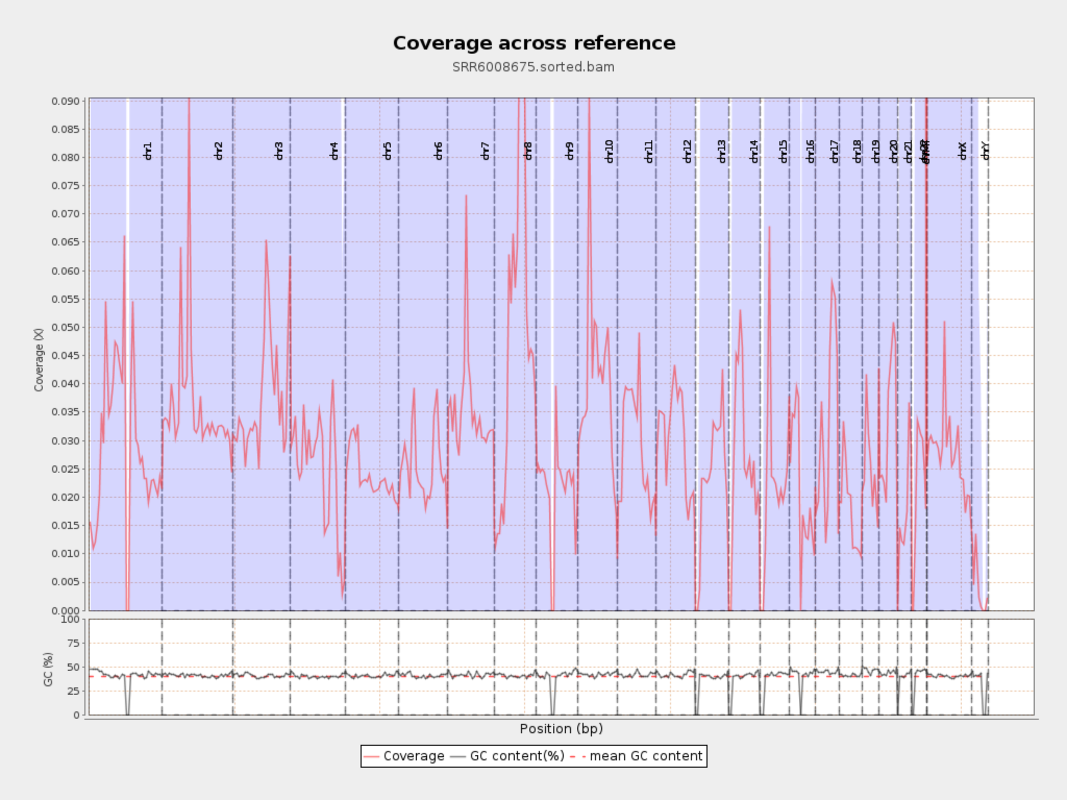
General error rate	0.8%
Mismatches	710,006
Insertions	7,835
Mapped reads with at least one insertion	0.55%
Deletions	26,015
Mapped reads with at least one deletion	1.84%
Homopolymer indels	47.07%

2.6. Chromosome stats

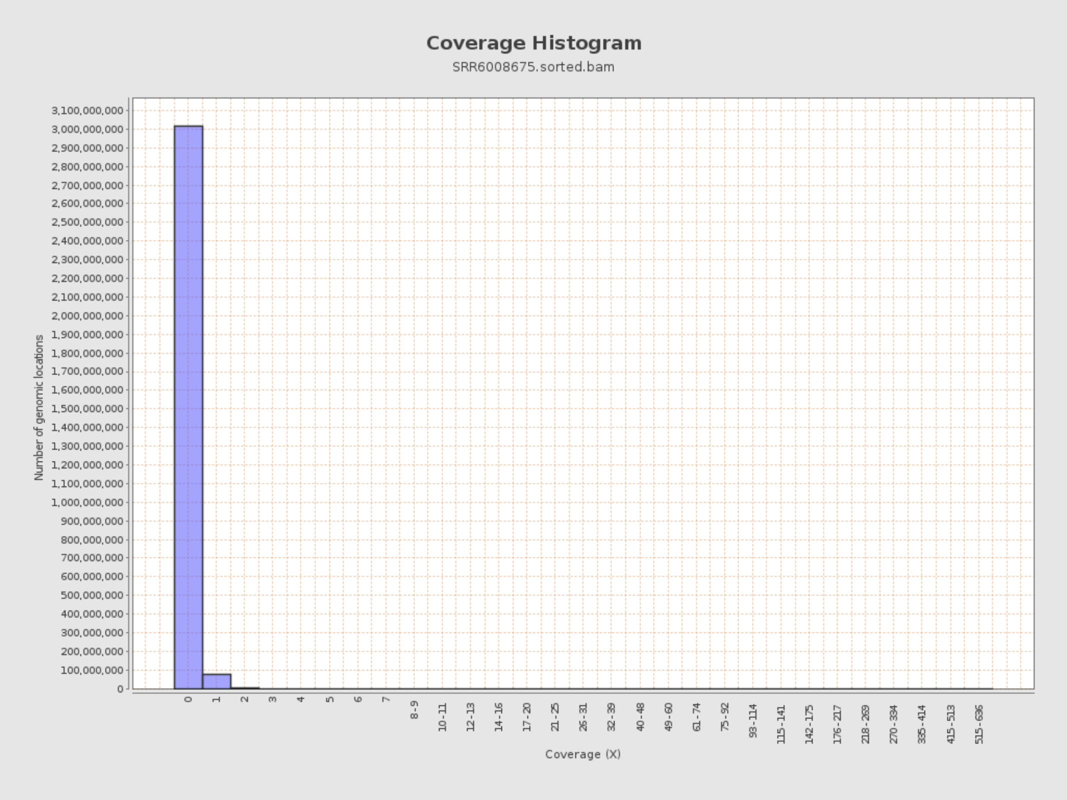
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7232593	0.029	0.5576
chr2	243199373	8885600	0.0365	0.405
chr3	198022430	7430859	0.0375	0.2175
chr4	191154276	4672141	0.0244	0.1803
chr5	180915260	4344761	0.024	0.1668
chr6	171115067	4342495	0.0254	0.2097
chr7	159138663	5705604	0.0359	0.4947

chr8	146364022	7116090	0.0486	0.3436
chr9	141213431	2989721	0.0212	0.2784
chr10	135534747	5532530	0.0408	0.461
chr11	135006516	3923420	0.0291	0.2809
chr12	133851895	4102433	0.0306	0.1897
chr13	115169878	2672172	0.0232	0.1614
chr14	107349540	2882363	0.0269	0.1869
chr15	102531392	2323254	0.0227	0.1617
chr16	90354753	1912311	0.0212	0.1885
chr17	81195210	2636605	0.0325	0.2424
chr18	78077248	1393322	0.0178	0.4683
chr19	59128983	1536254	0.026	0.3689
chr20	63025520	2122156	0.0337	0.202
chr21	48129895	859662	0.0179	0.1529
chr22	51304566	1062096	0.0207	0.152
chrMT	16571	114975	6.9383	4.7218
chrX	155270560	4333399	0.0279	0.2287
chrY	59373566	239590	0.004	0.1098

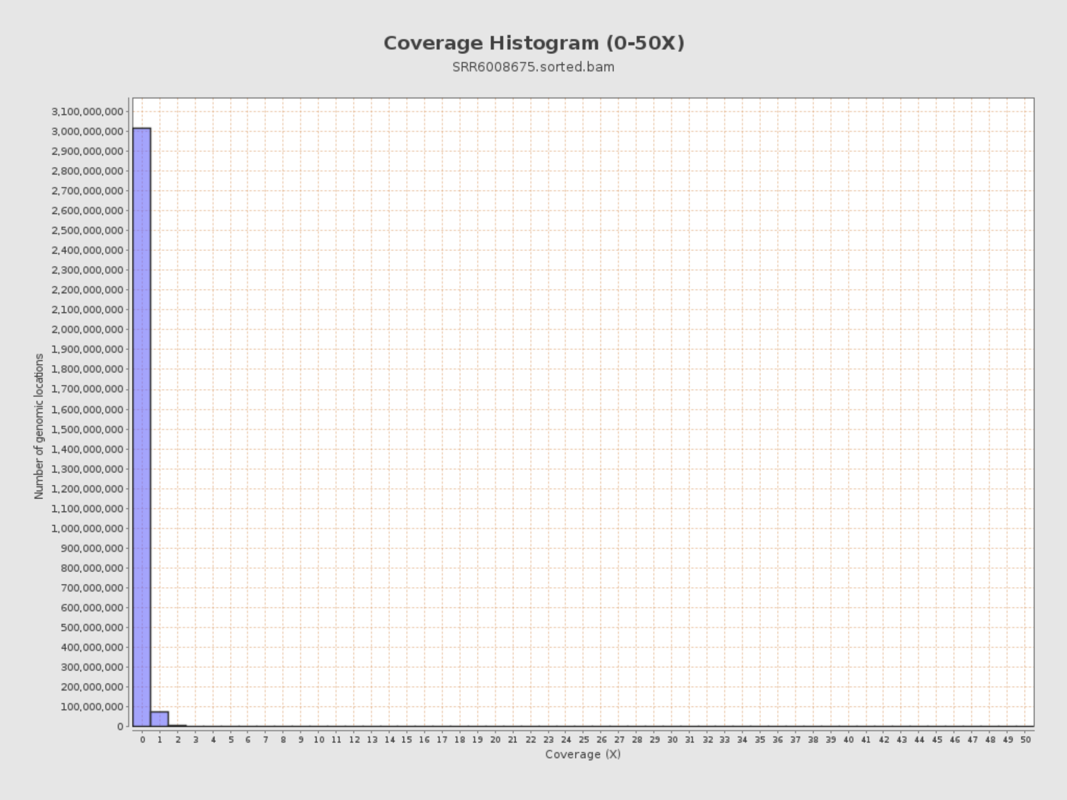
3. Results : Coverage across reference



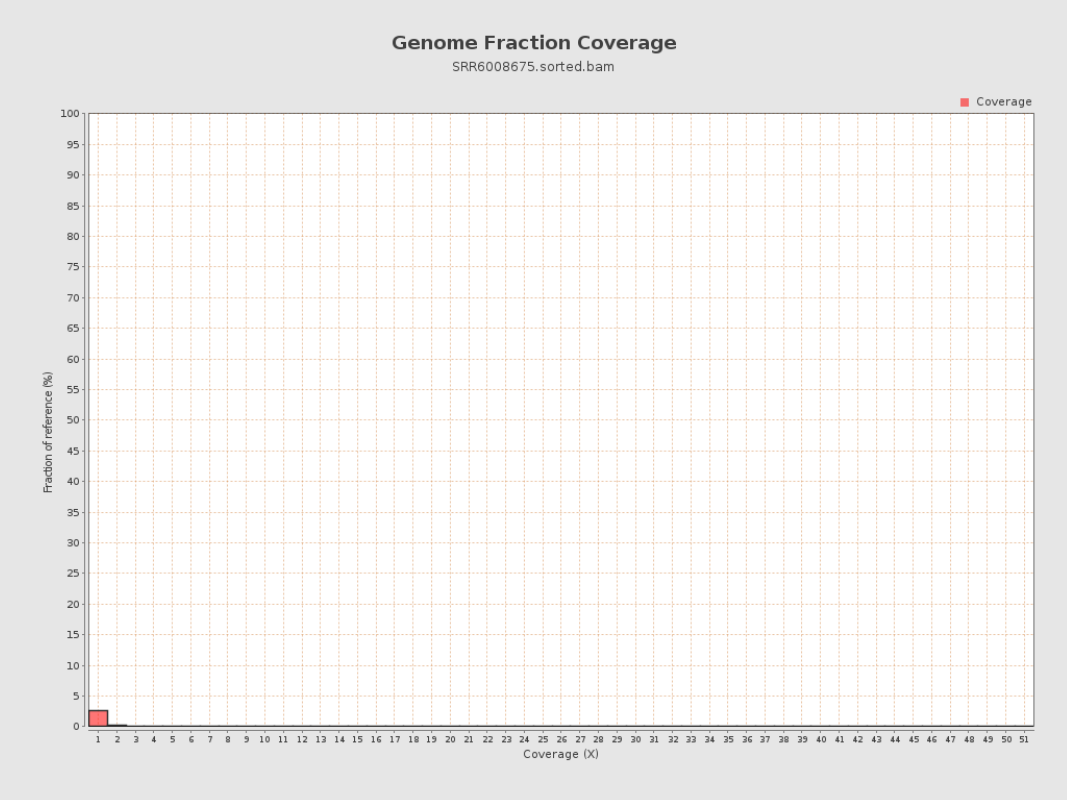
4. Results : Coverage Histogram



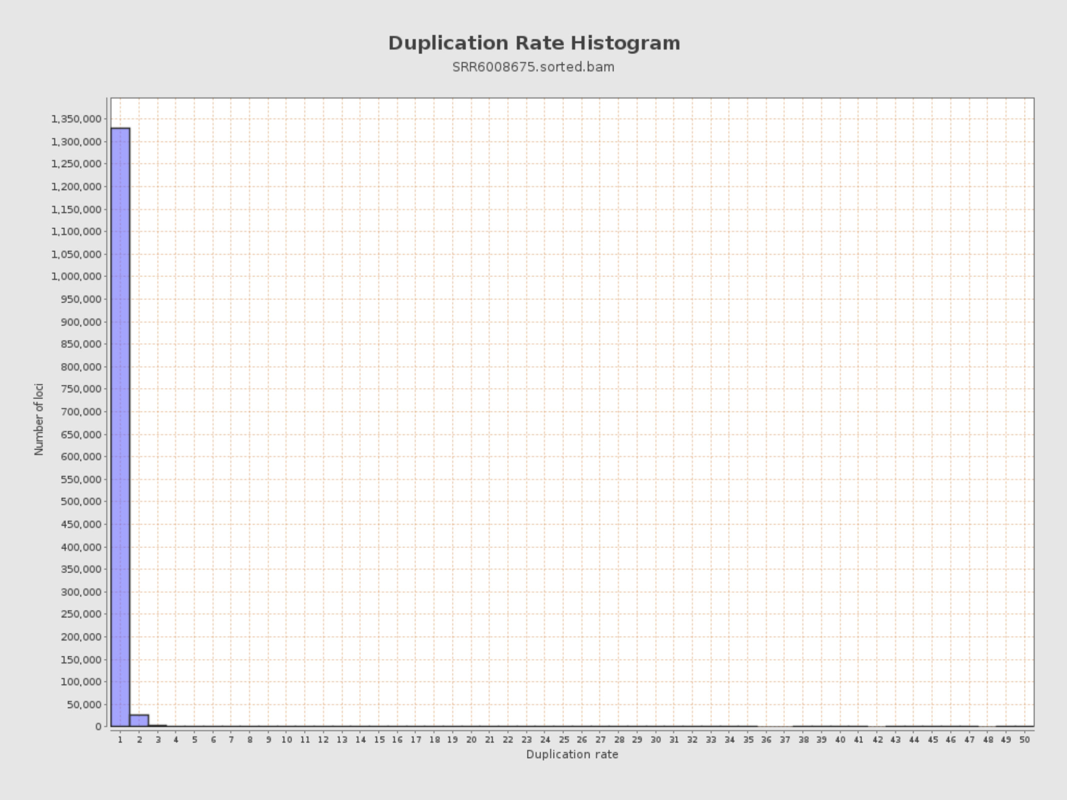
5. Results : Coverage Histogram (0-50X)



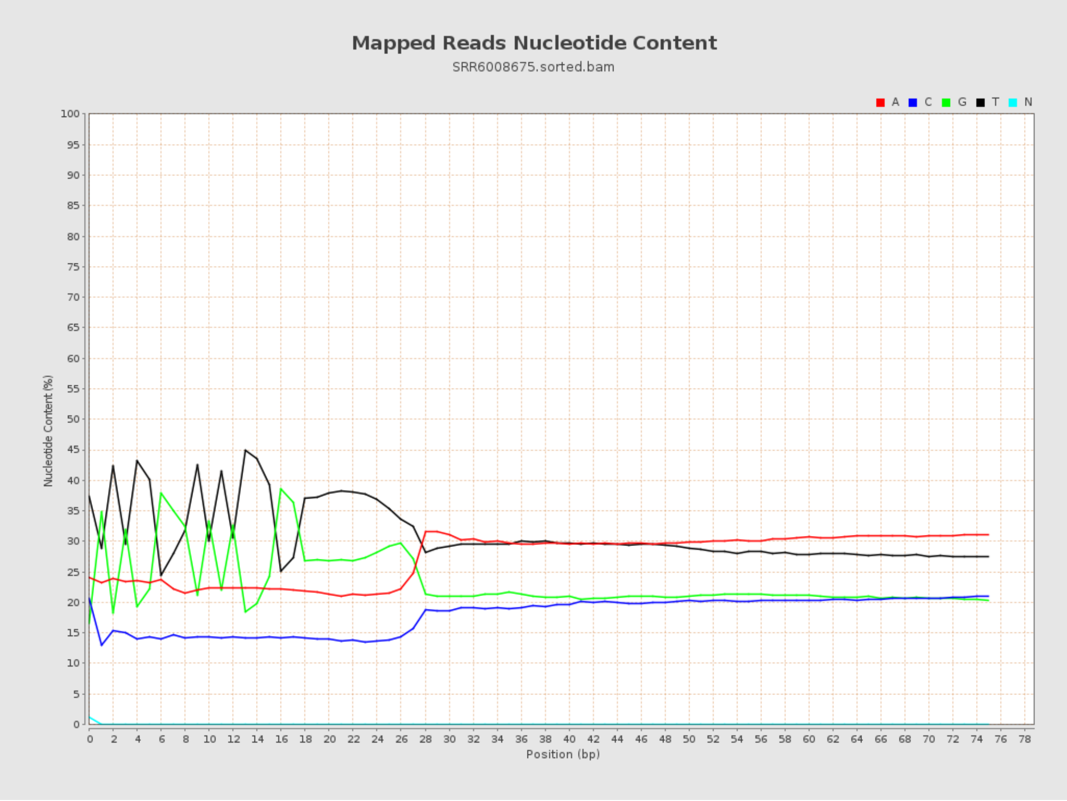
6. Results : Genome Fraction Coverage



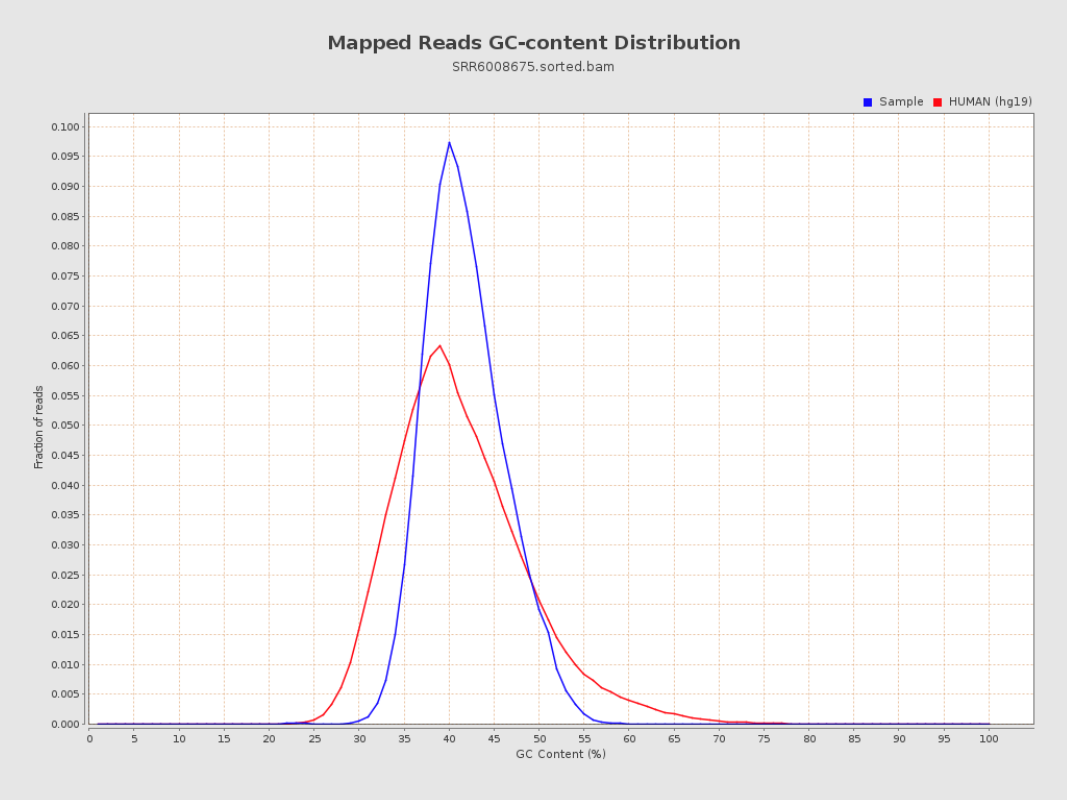
7. Results : Duplication Rate Histogram



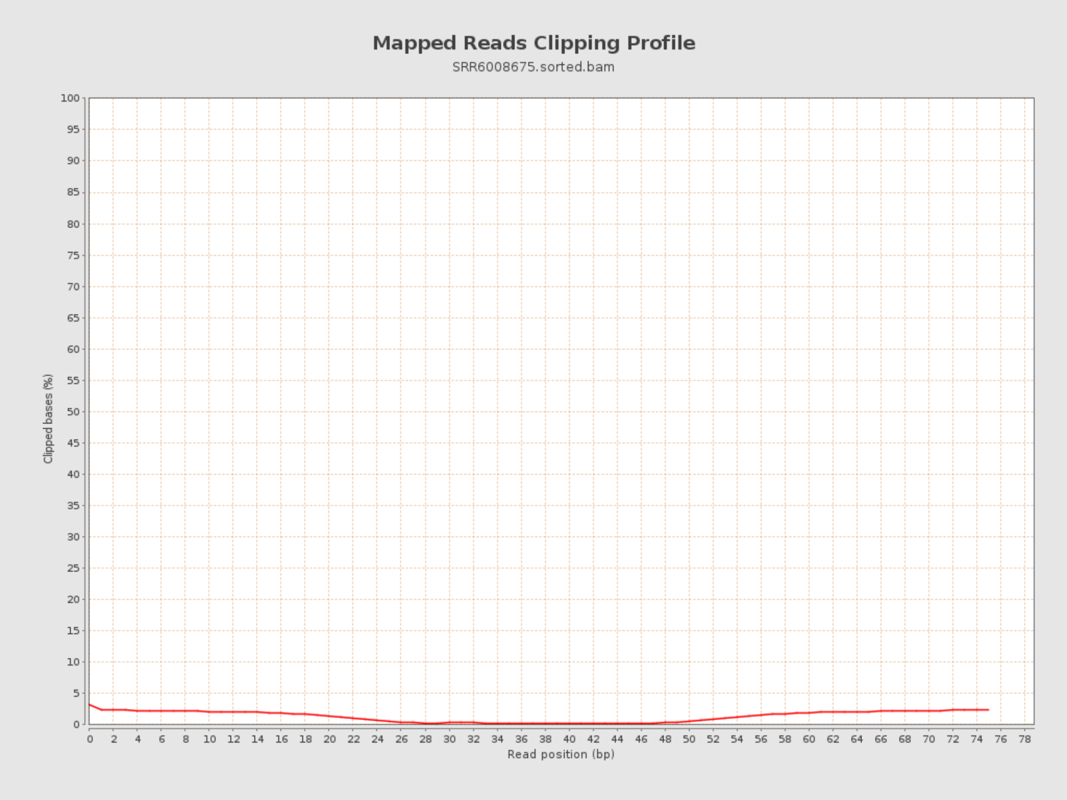
8. Results : Mapped Reads Nucleotide Content



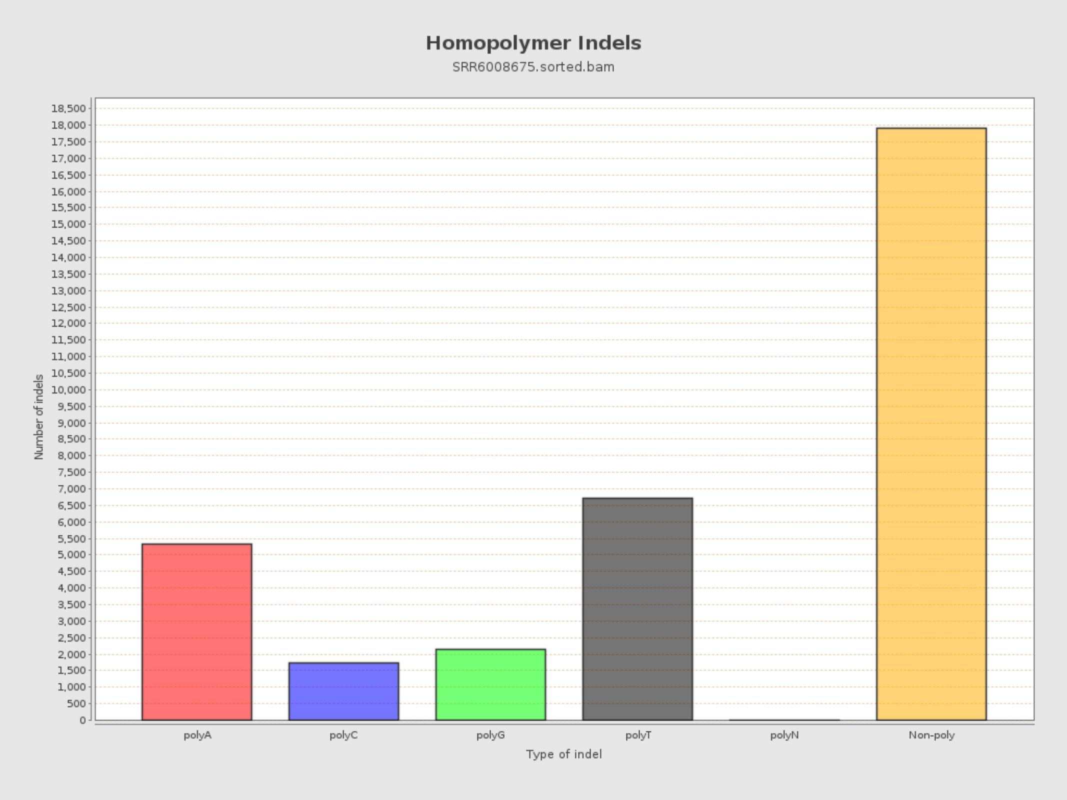
9. Results : Mapped Reads GC-content Distribution



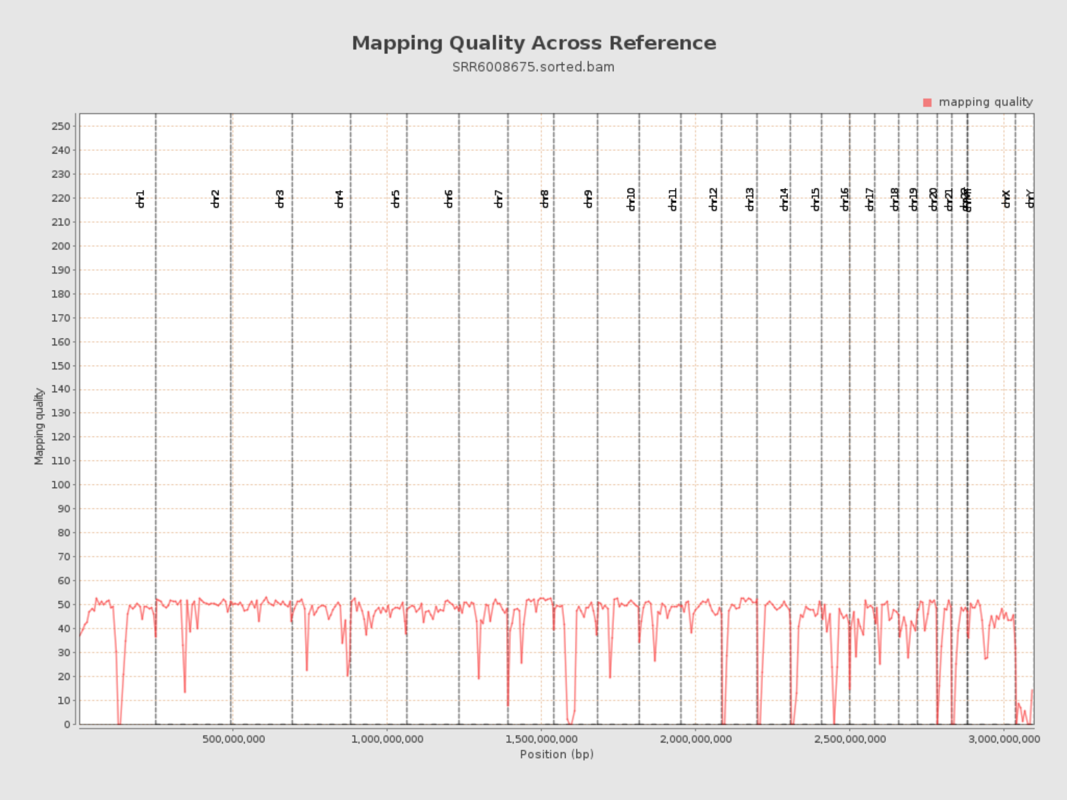
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram