Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:29:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008810.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_SRR6008810 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008810.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:29:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008810.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,272,724
Mapped reads	1,100,452 / 86.46%
Unmapped reads	172,272 / 13.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,568 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	34,640 / 2.72%
Duplication rate	2.17%
Clipped reads	539,351 / 42.38%

2.2. ACGT Content

Number/percentage of A's	20,105,430 / 28.06%
Number/percentage of C's	13,037,318 / 18.2%
Number/percentage of T's	22,294,639 / 31.12%
Number/percentage of G's	16,193,203 / 22.6%
Number/percentage of N's	14,308 / 0.02%
GC Percentage	40.8%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2823

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

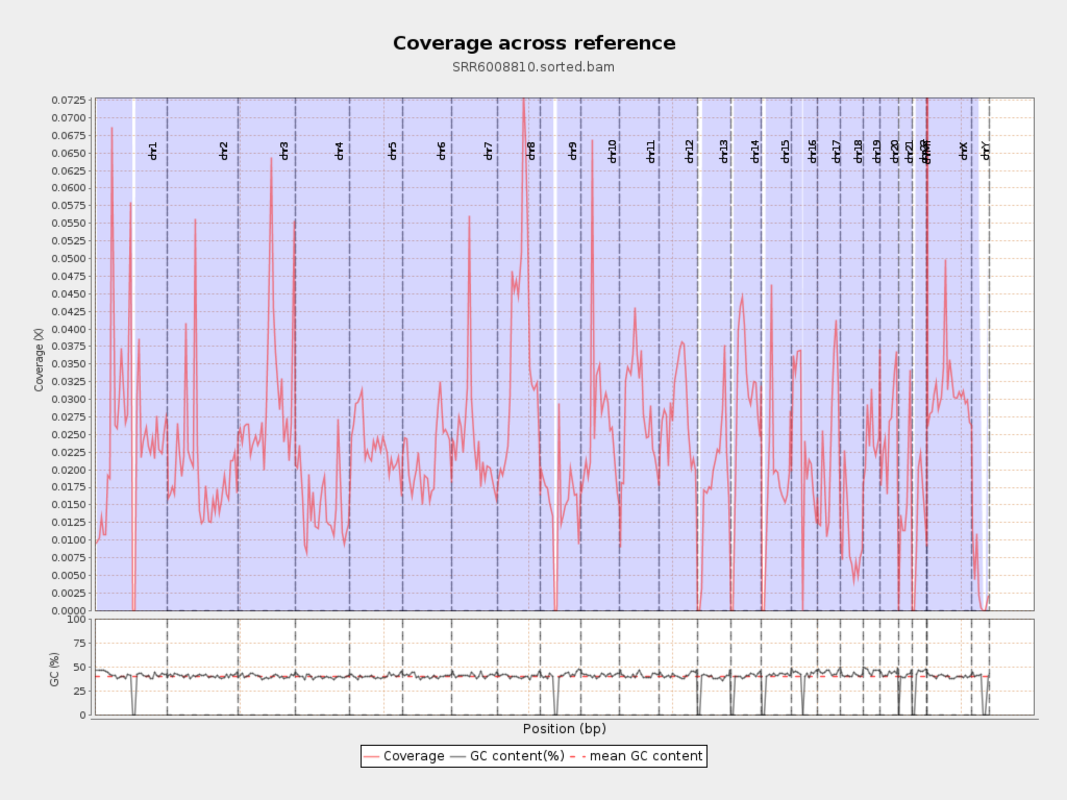
General error rate	0.81%
Mismatches	565,735
Insertions	6,402
Mapped reads with at least one insertion	0.58%
Deletions	23,154
Mapped reads with at least one deletion	2.08%
Homopolymer indels	46.47%

2.6. Chromosome stats

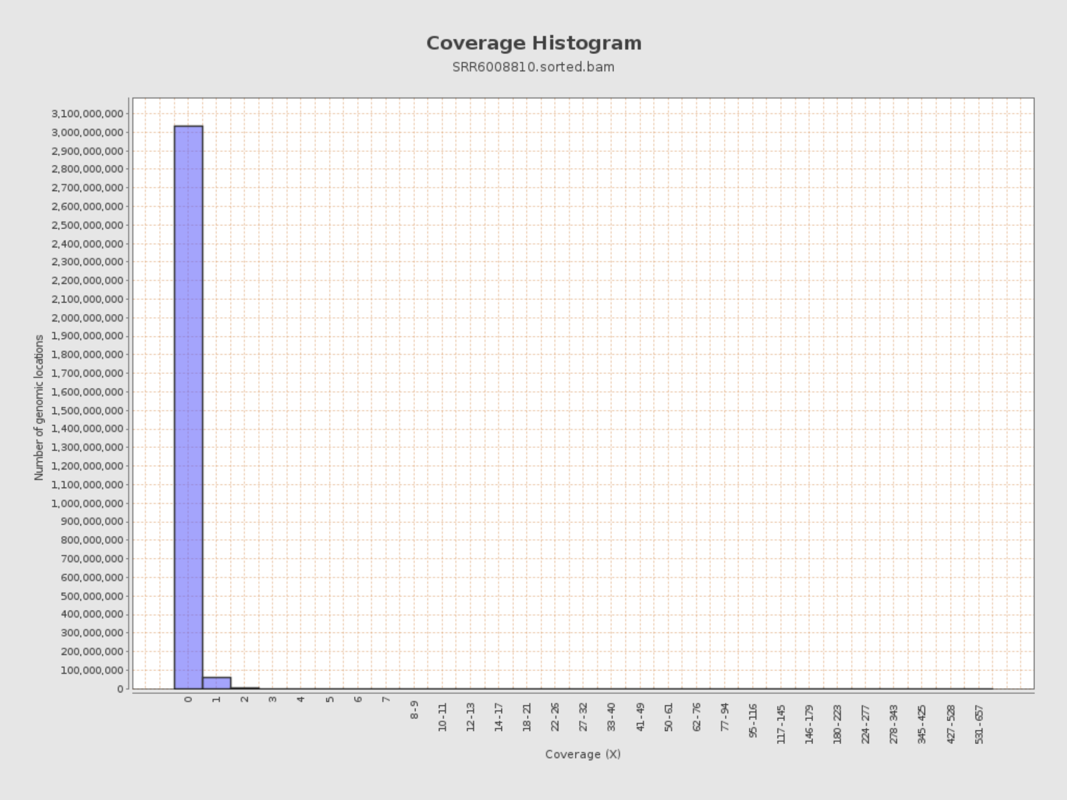
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6106983	0.0245	0.5622
chr2	243199373	4823838	0.0198	0.2733
chr3	198022430	5926536	0.0299	0.192
chr4	191154276	2859748	0.015	0.1358
chr5	180915260	4272102	0.0236	0.1637
chr6	171115067	3690241	0.0216	0.1704
chr7	159138663	3842594	0.0241	0.3988

chr8	146364022	5536846	0.0378	0.3101
chr9	141213431	2117073	0.015	0.2216
chr10	135534747	3647432	0.0269	0.3648
chr11	135006516	3859292	0.0286	0.2945
chr12	133851895	3776935	0.0282	0.1807
chr13	115169878	2054110	0.0178	0.1398
chr14	107349540	3080333	0.0287	0.1842
chr15	102531392	1822748	0.0178	0.141
chr16	90354753	2095833	0.0232	0.1939
chr17	81195210	1838625	0.0226	0.2028
chr18	78077248	715080	0.0092	0.4225
chr19	59128983	1479526	0.025	0.3639
chr20	63025520	1616672	0.0257	0.1722
chr21	48129895	755991	0.0157	0.1477
chr22	51304566	640742	0.0125	0.1169
chrMT	16571	40898	2.468	2.0298
chrX	155270560	4871345	0.0314	0.2229
chrY	59373566	211895	0.0036	0.0955

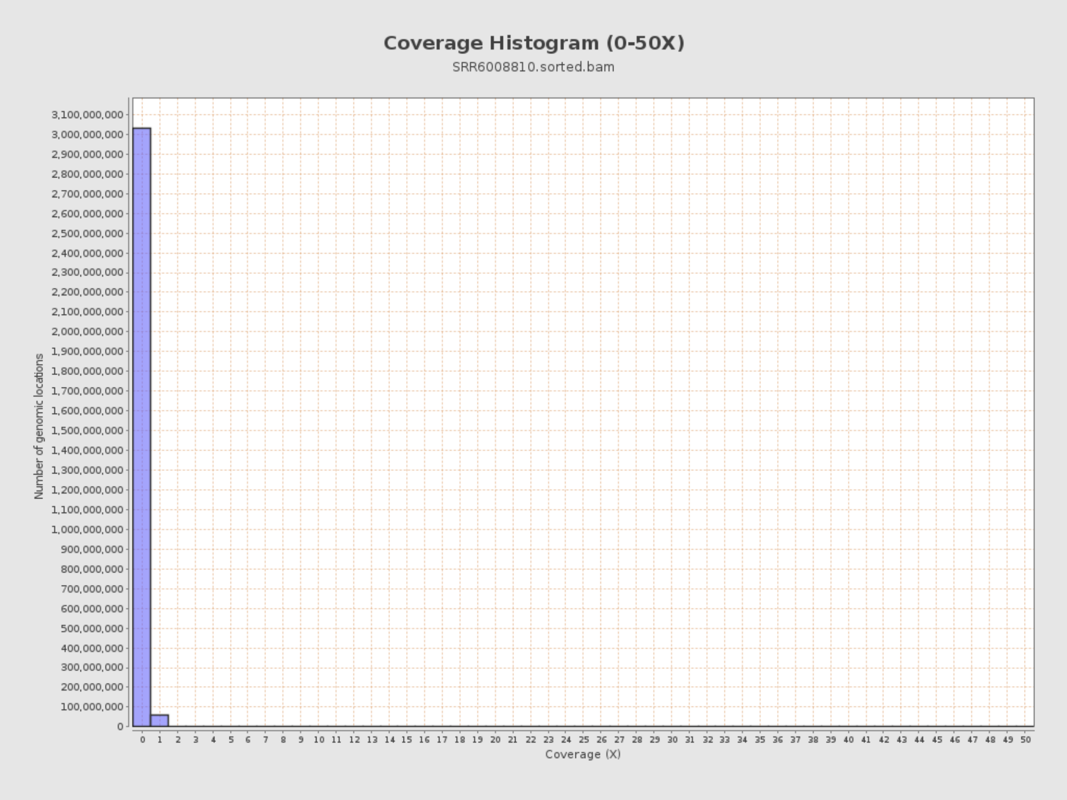
3. Results : Coverage across reference



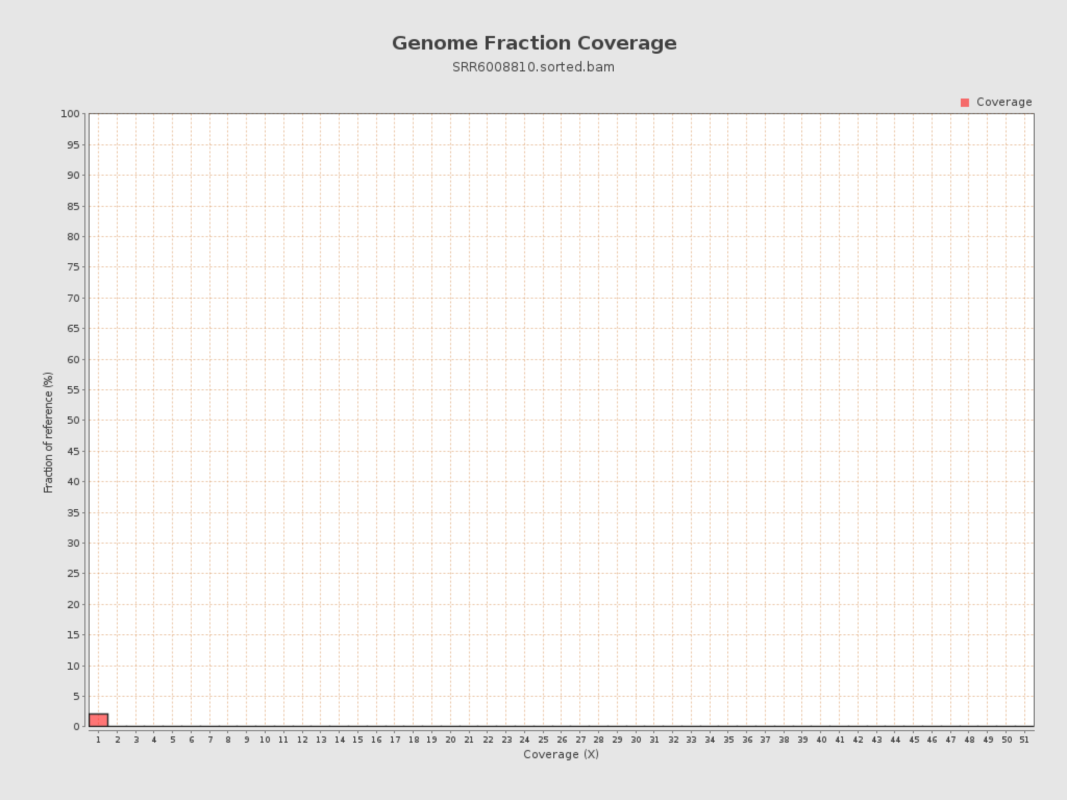
4. Results : Coverage Histogram



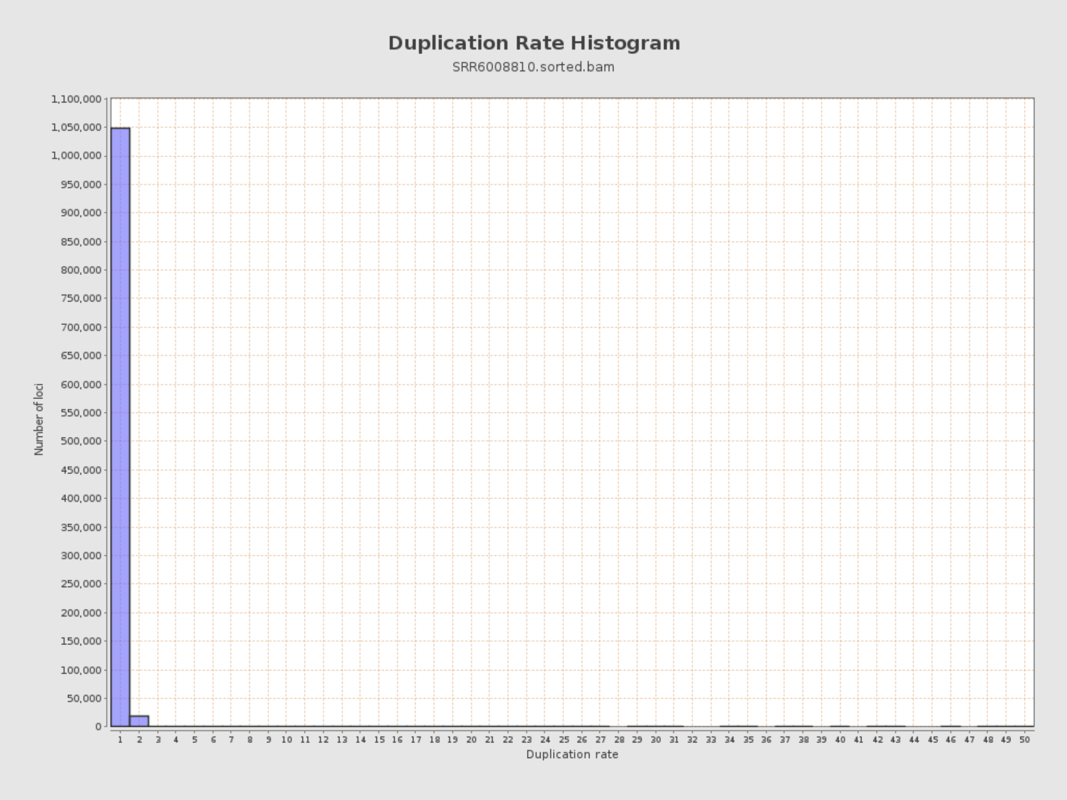
5. Results : Coverage Histogram (0-50X)



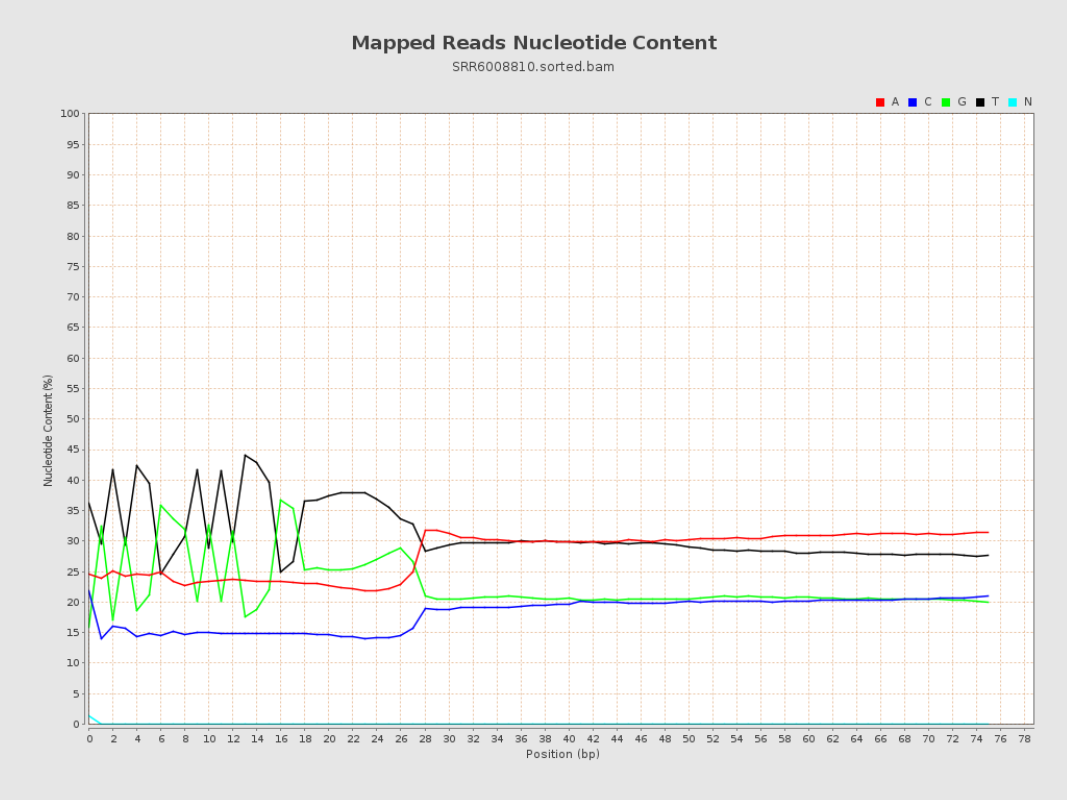
6. Results : Genome Fraction Coverage



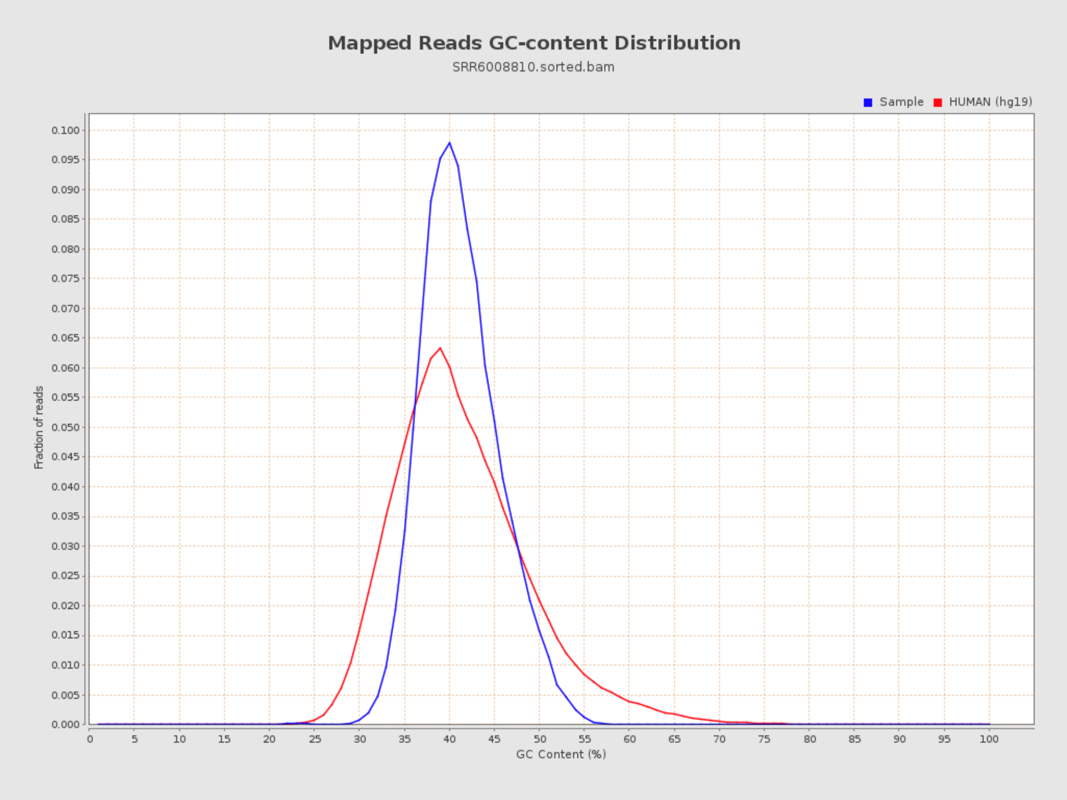
7. Results : Duplication Rate Histogram



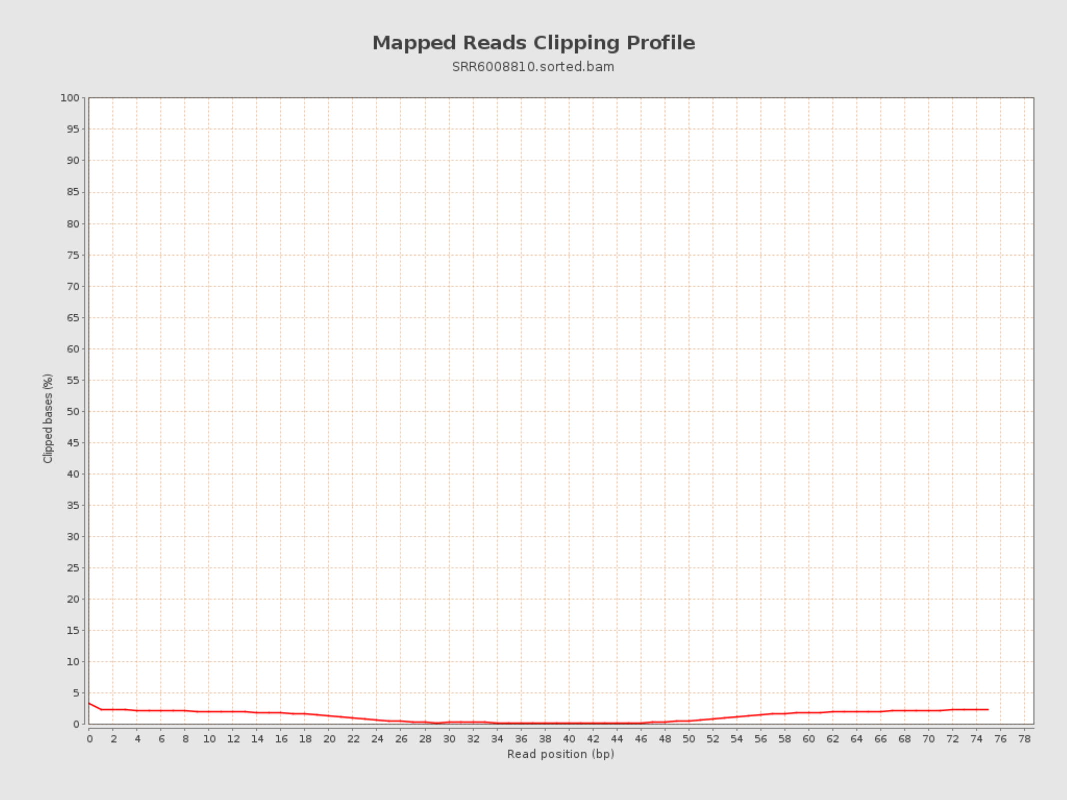
8. Results : Mapped Reads Nucleotide Content



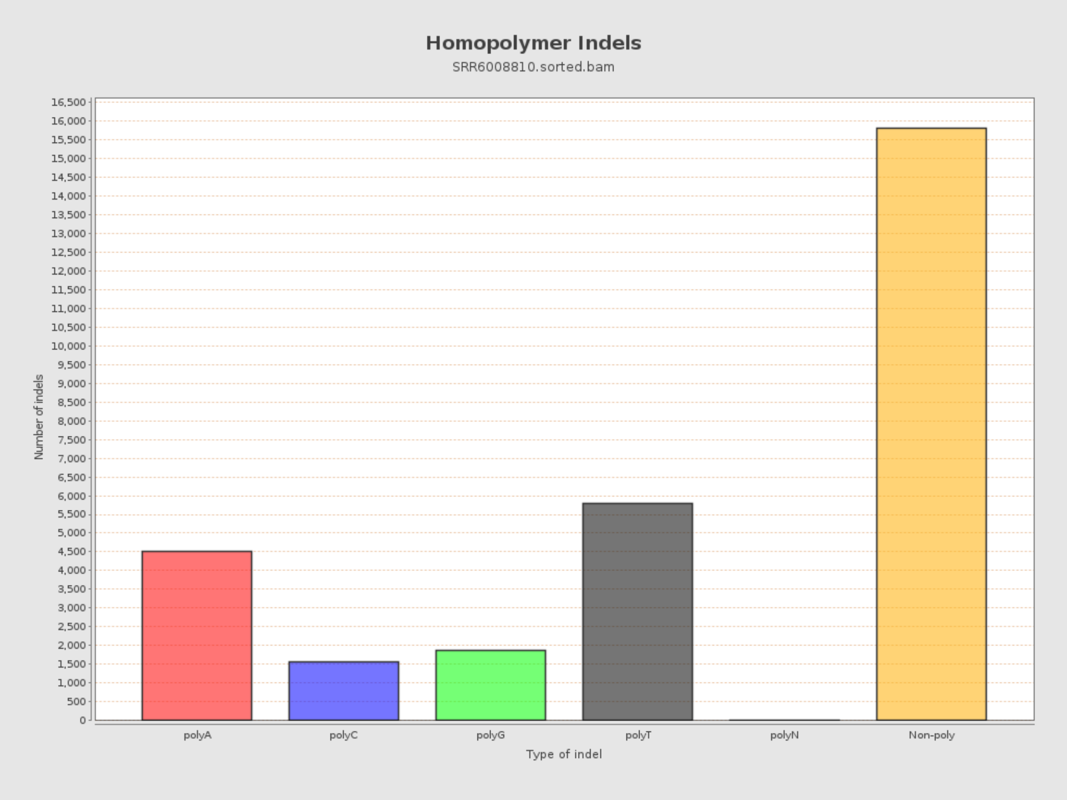
9. Results : Mapped Reads GC-content Distribution



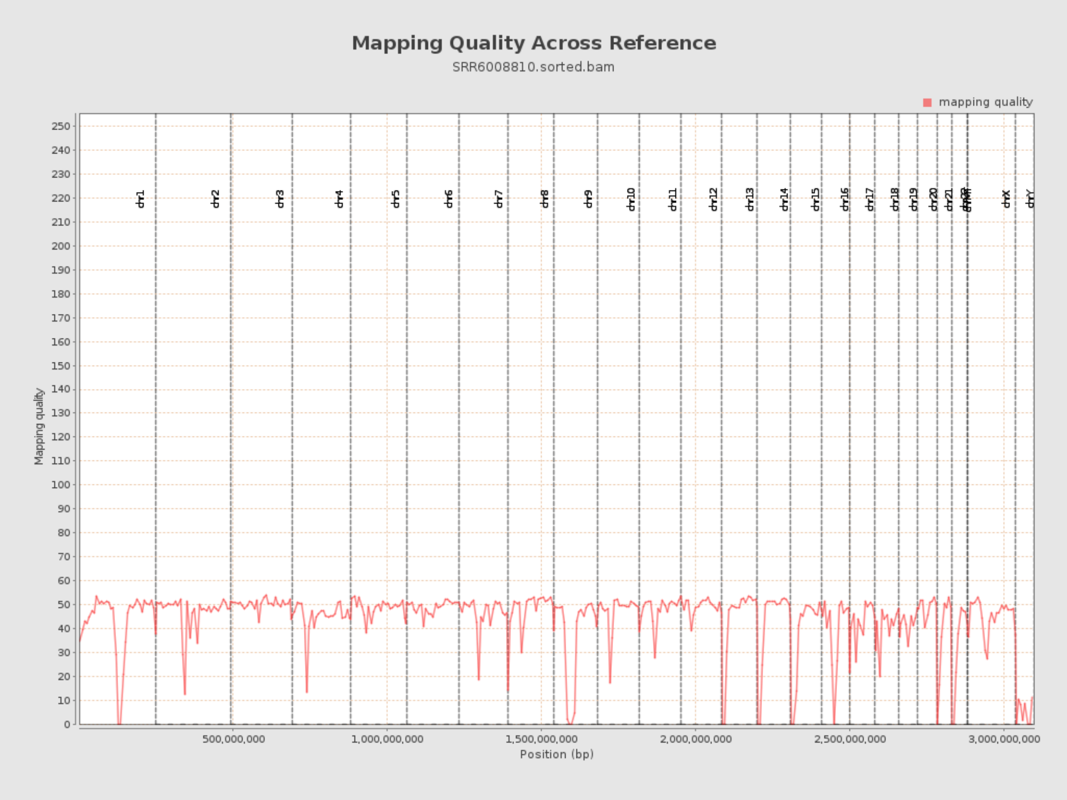
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram