Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:14:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080669.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_SRR3080669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080669.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:14:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,634,706
Mapped reads	1,474,668 / 90.21%
Unmapped reads	160,038 / 9.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,869 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	59,148 / 3.62%
Duplication rate	3.39%
Clipped reads	718,874 / 43.98%

2.2. ACGT Content

Number/percentage of A's	25,807,927 / 26.64%
Number/percentage of C's	18,164,847 / 18.75%
Number/percentage of T's	30,351,681 / 31.33%
Number/percentage of G's	22,544,999 / 23.27%
Number/percentage of N's	4,595 / 0%
GC Percentage	42.02%

2.3. Coverage

Mean	0.0313

Standard Deviation	0.2696

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

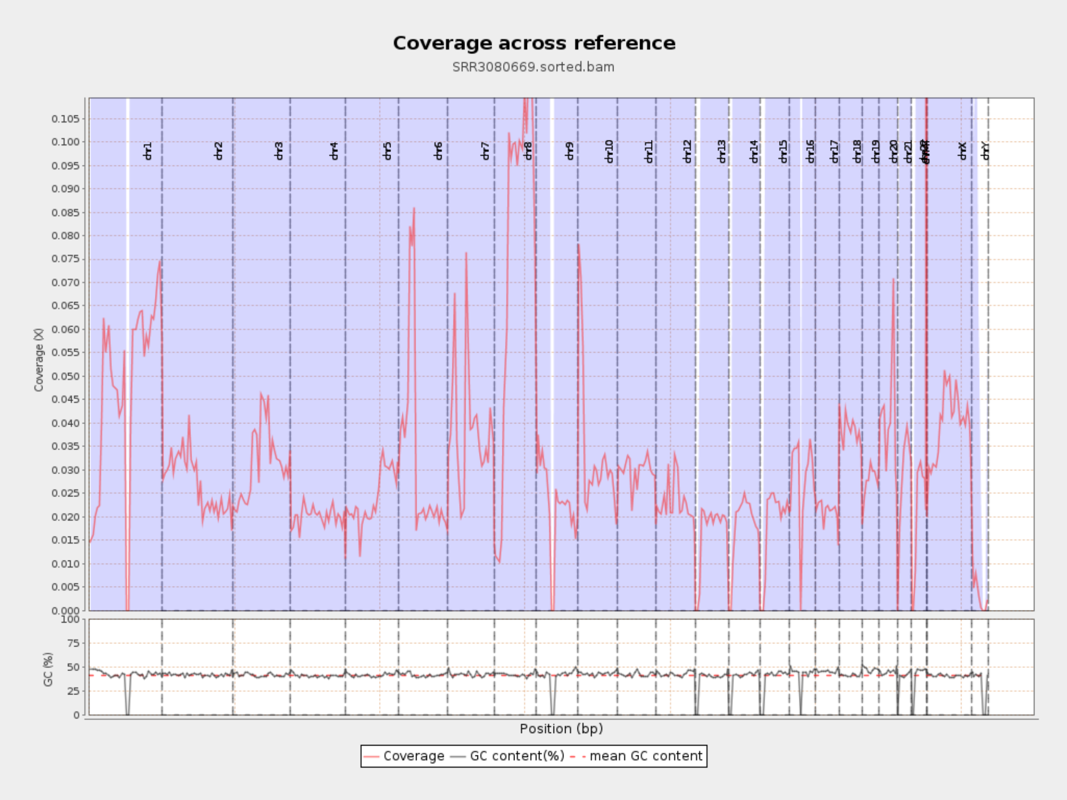
General error rate	0.71%
Mismatches	672,966
Insertions	7,319
Mapped reads with at least one insertion	0.49%
Deletions	22,419
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.79%

2.6. Chromosome stats

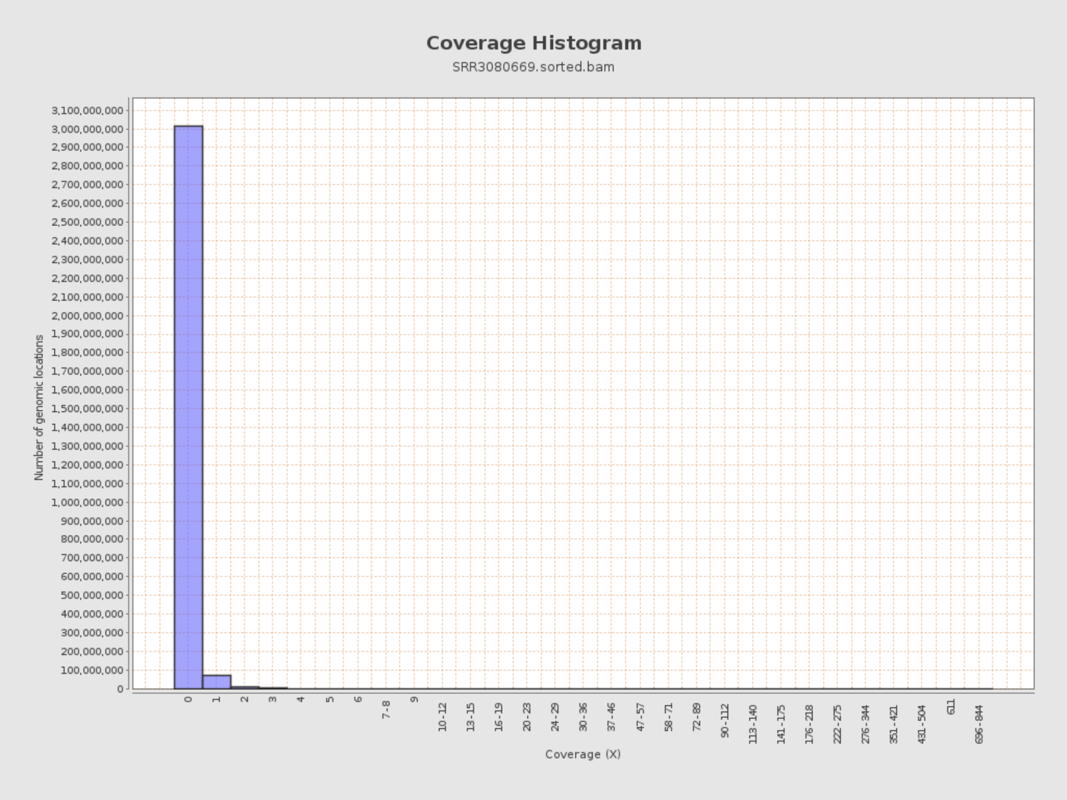
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11748231	0.0471	0.3128
chr2	243199373	6620769	0.0272	0.401
chr3	198022430	6234107	0.0315	0.1997
chr4	191154276	3847371	0.0201	0.164
chr5	180915260	4352132	0.0241	0.1743
chr6	171115067	5567510	0.0325	0.2486
chr7	159138663	6299447	0.0396	0.5731

chr8	146364022	11326066	0.0774	0.3531
chr9	141213431	3162583	0.0224	0.2044
chr10	135534747	4648835	0.0343	0.2223
chr11	135006516	4027028	0.0298	0.2098
chr12	133851895	3103773	0.0232	0.1738
chr13	115169878	1905796	0.0165	0.1456
chr14	107349540	1907377	0.0178	0.1568
chr15	102531392	1887628	0.0184	0.1605
chr16	90354753	2557258	0.0283	0.197
chr17	81195210	1711612	0.0211	0.1688
chr18	78077248	3012275	0.0386	0.2939
chr19	59128983	1642951	0.0278	0.2224
chr20	63025520	2600065	0.0413	0.2324
chr21	48129895	1346551	0.028	0.1935
chr22	51304566	1022670	0.0199	0.1584
chrMT	16571	13558	0.8182	1.0755
chrX	155270560	6162223	0.0397	0.235
chrY	59373566	201948	0.0034	0.0744

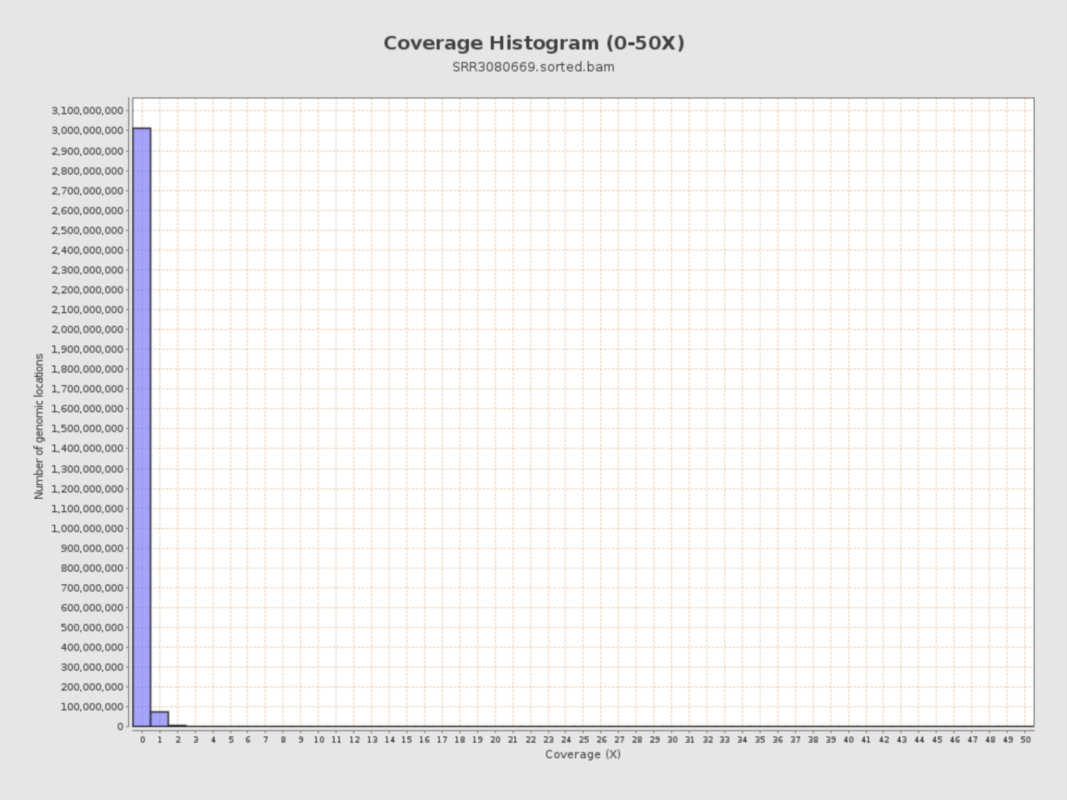
3. Results : Coverage across reference



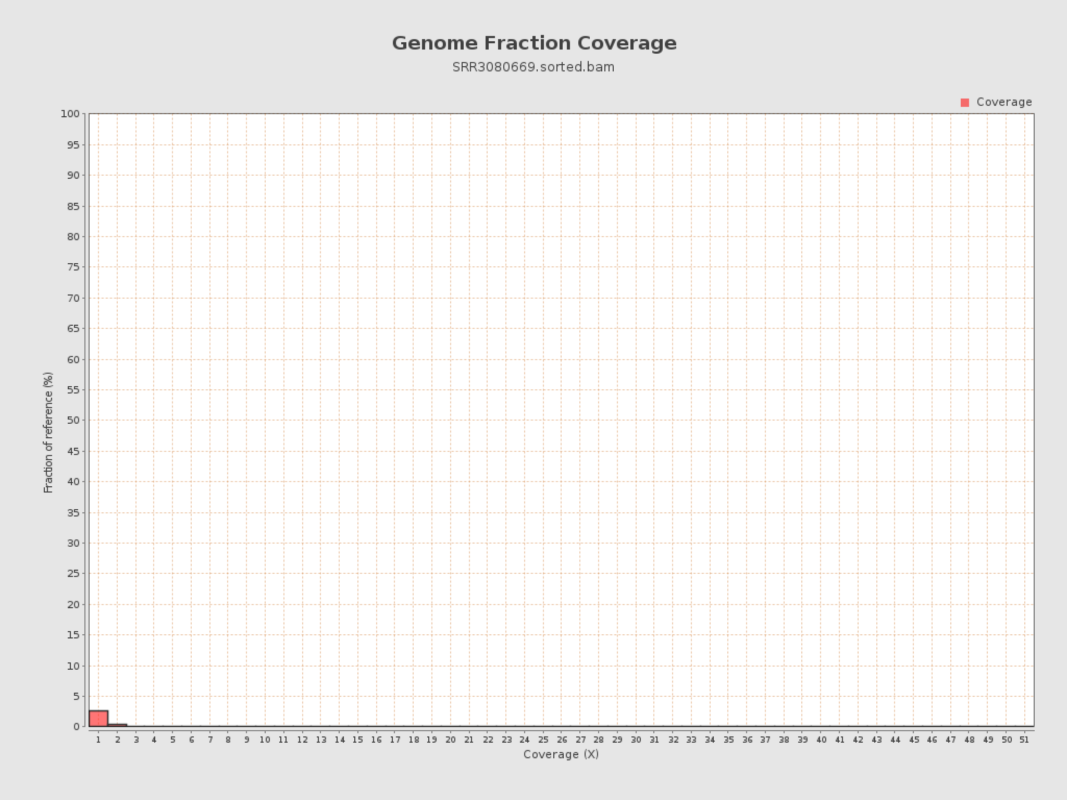
4. Results : Coverage Histogram



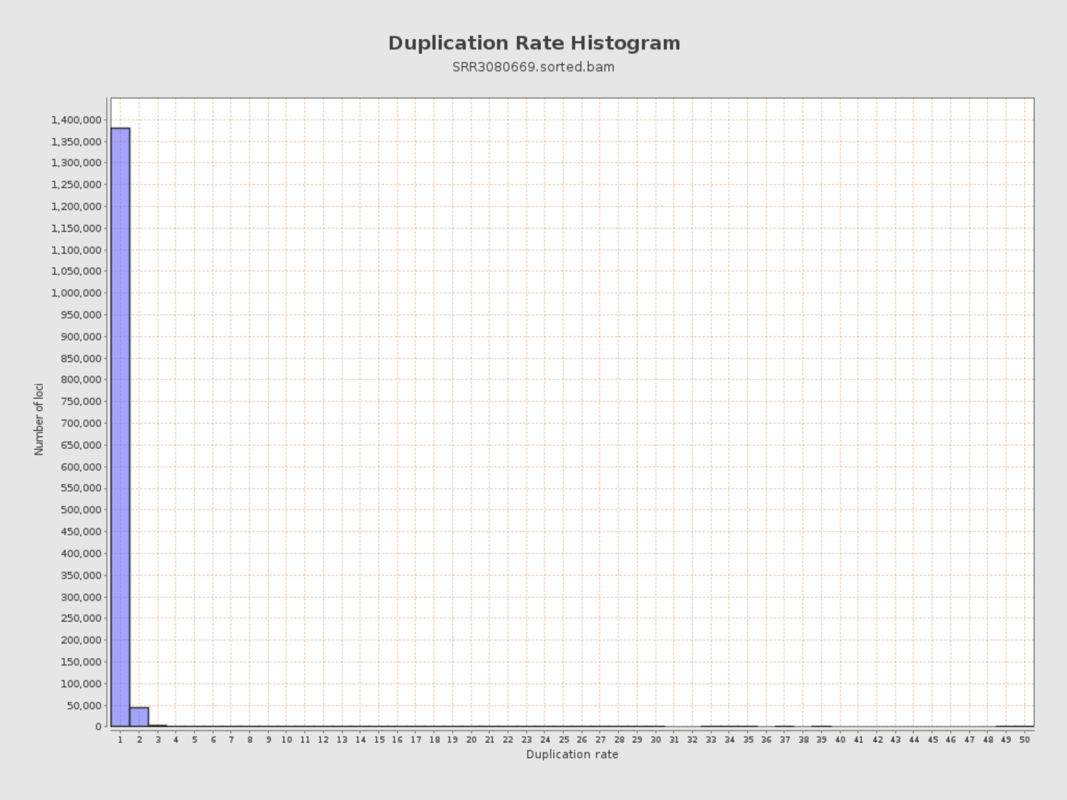
5. Results : Coverage Histogram (0-50X)



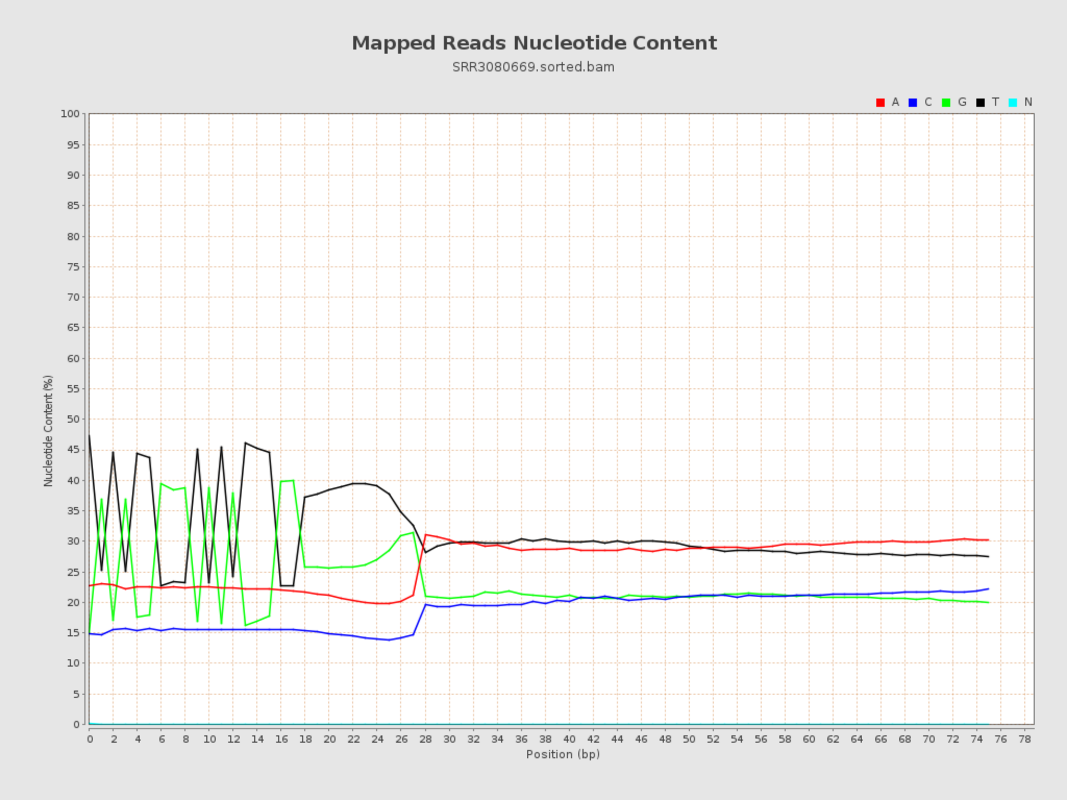
6. Results : Genome Fraction Coverage



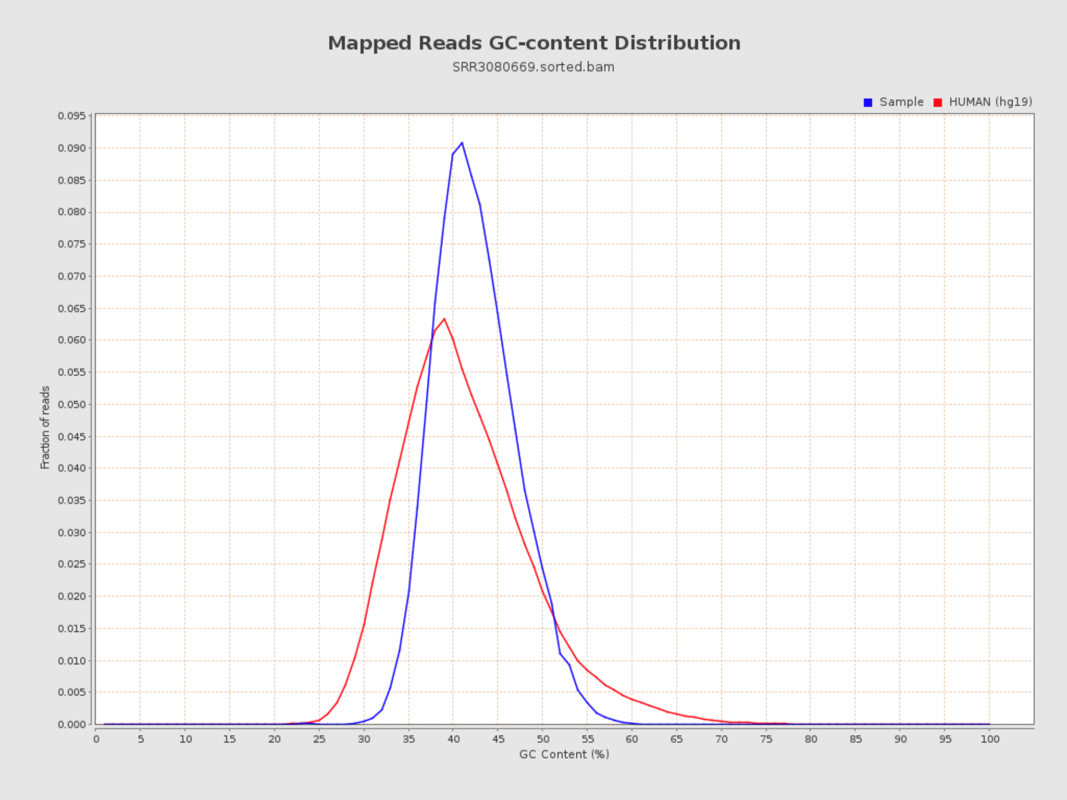
7. Results : Duplication Rate Histogram



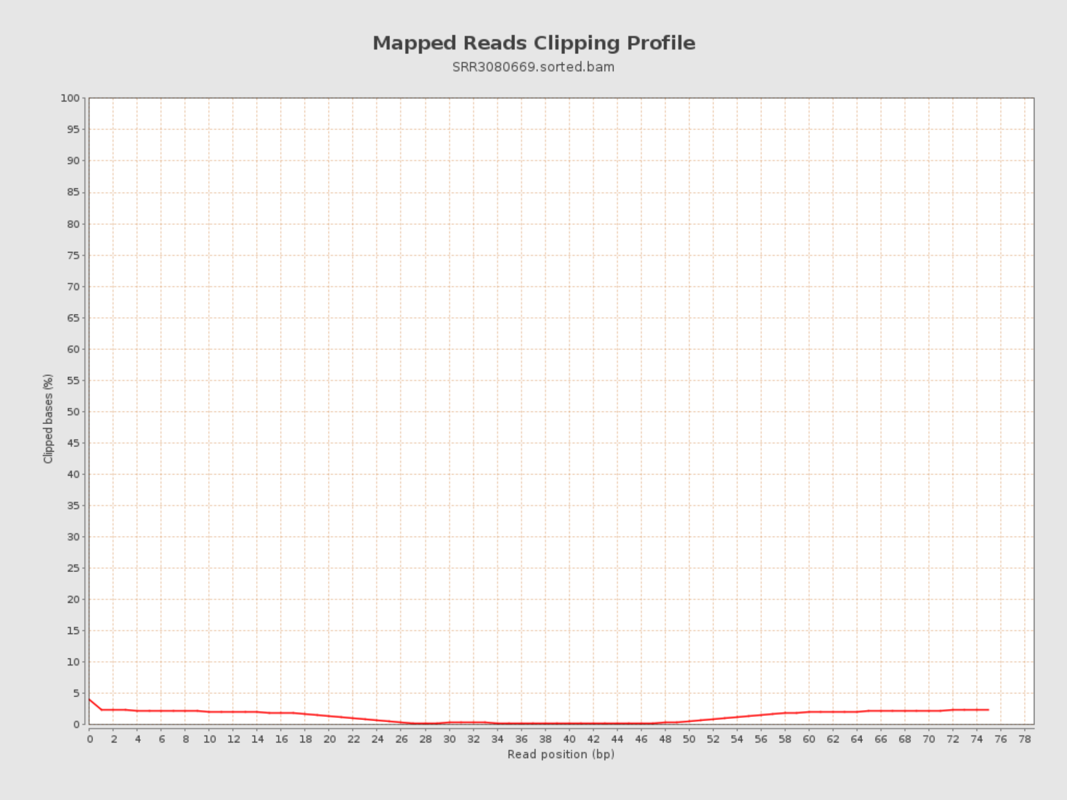
8. Results : Mapped Reads Nucleotide Content



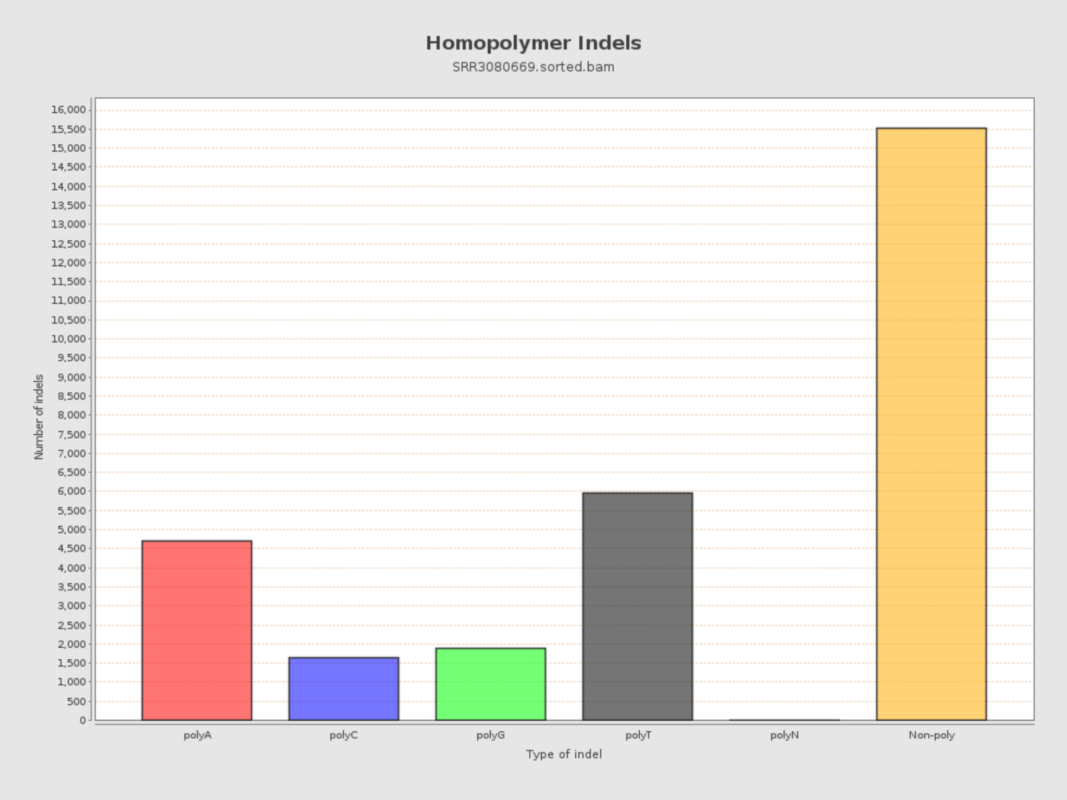
9. Results : Mapped Reads GC-content Distribution



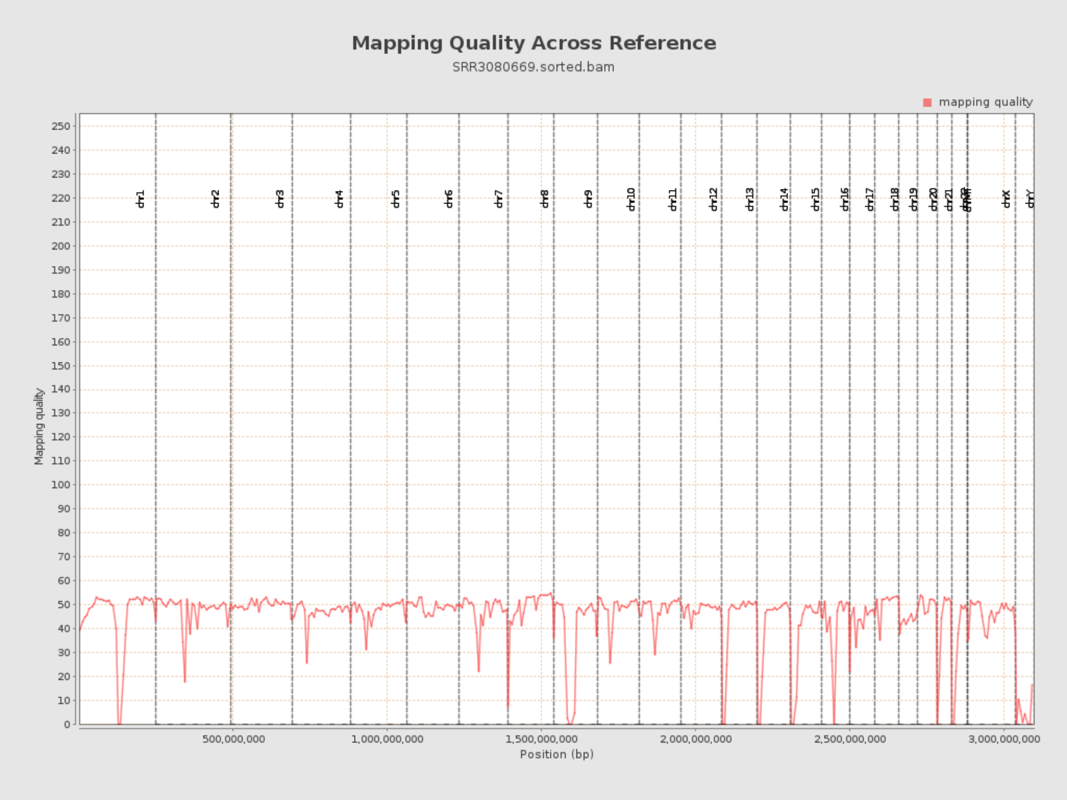
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram