Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:48:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083641.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_SRR3083641 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083641.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:48:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083641.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,124,738
Mapped reads	1,680,627 / 79.1%
Unmapped reads	444,111 / 20.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,318 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	60,415 / 2.84%
Duplication rate	2.97%
Clipped reads	1,185,153 / 55.78%

2.2. ACGT Content

Number/percentage of A's	29,364,696 / 29.27%
Number/percentage of C's	19,483,174 / 19.42%
Number/percentage of T's	29,388,523 / 29.3%
Number/percentage of G's	22,065,222 / 22%
Number/percentage of N's	13,671 / 0.01%
GC Percentage	41.42%

2.3. Coverage

Mean	0.0324

Standard Deviation	0.2748

2.4. Mapping Quality

Mean Mapping Quality	45.01

2.5. Mismatches and indels

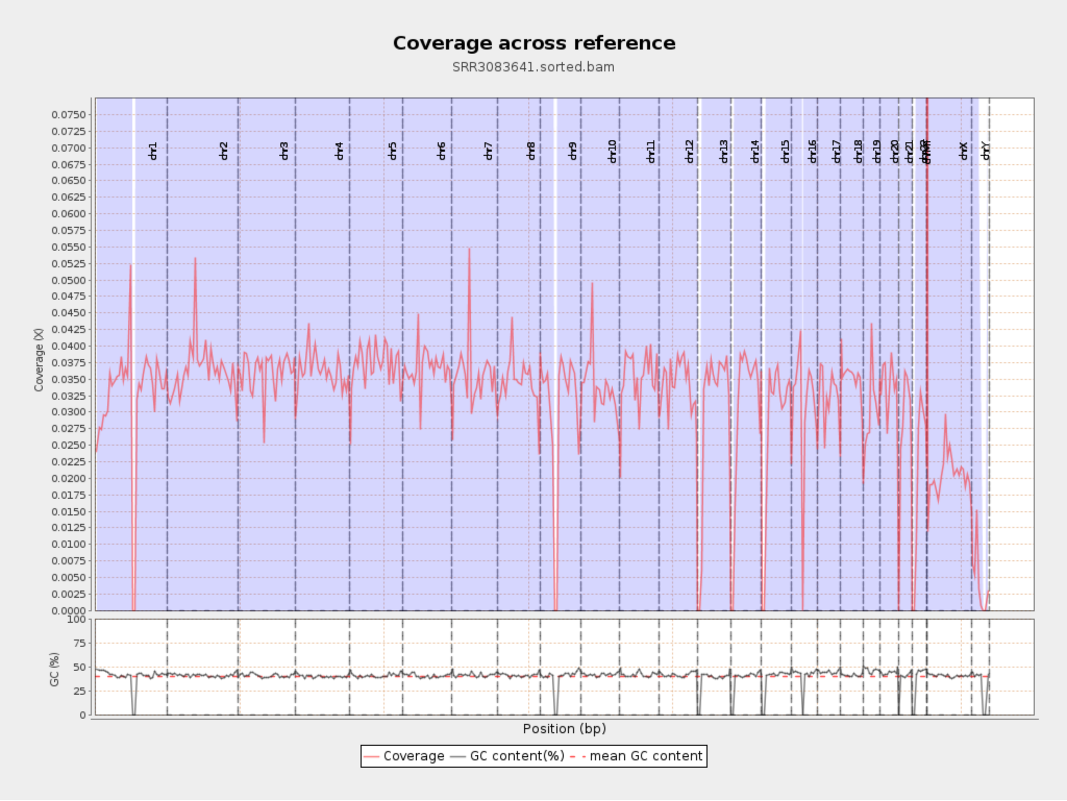
General error rate	0.84%
Mismatches	834,071
Insertions	7,196
Mapped reads with at least one insertion	0.42%
Deletions	20,579
Mapped reads with at least one deletion	1.21%
Homopolymer indels	45.47%

2.6. Chromosome stats

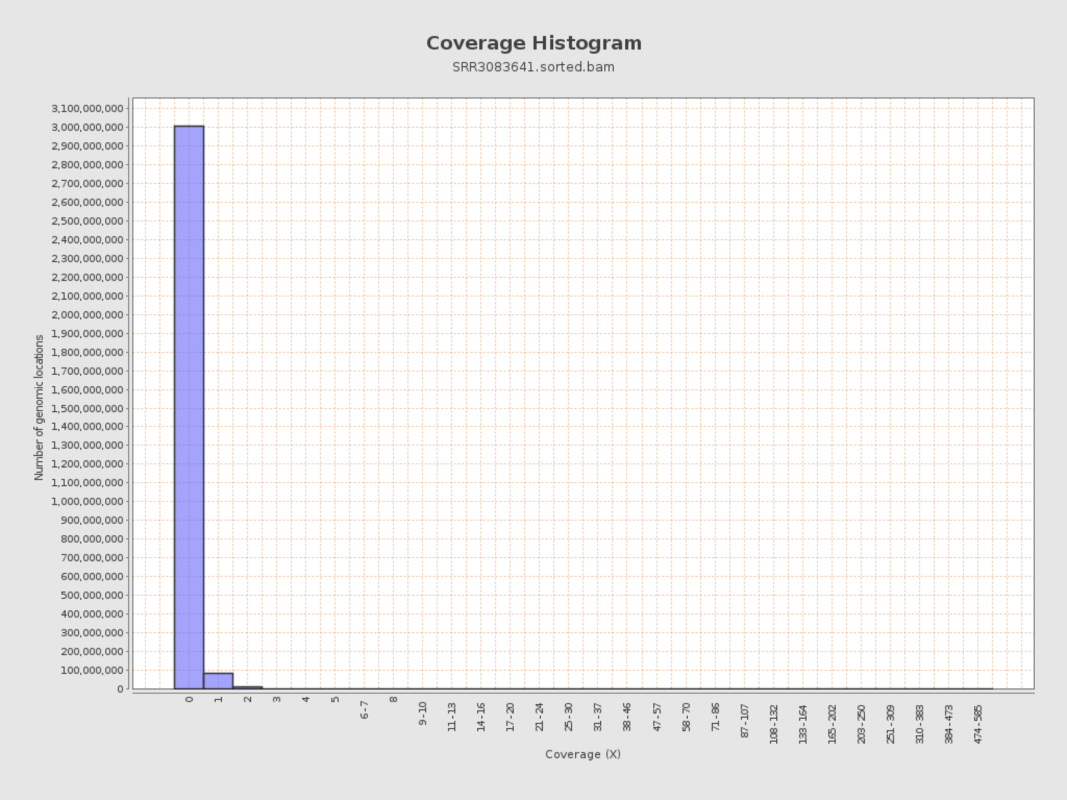
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8038509	0.0323	0.4882
chr2	243199373	8843688	0.0364	0.2649
chr3	198022430	7151000	0.0361	0.2055
chr4	191154276	6907895	0.0361	0.2138
chr5	180915260	6781511	0.0375	0.21
chr6	171115067	6262427	0.0366	0.2305
chr7	159138663	5663207	0.0356	0.3712

chr8	146364022	5066334	0.0346	0.3745
chr9	141213431	4270199	0.0302	0.2401
chr10	135534747	4595467	0.0339	0.2703
chr11	135006516	4786484	0.0355	0.2297
chr12	133851895	4604562	0.0344	0.2041
chr13	115169878	3406100	0.0296	0.186
chr14	107349540	3202645	0.0298	0.1926
chr15	102531392	2849666	0.0278	0.1811
chr16	90354753	2764113	0.0306	0.2016
chr17	81195210	2618801	0.0323	0.2081
chr18	78077248	2767576	0.0354	0.4089
chr19	59128983	1794230	0.0303	0.3542
chr20	63025520	2129125	0.0338	0.2055
chr21	48129895	1328699	0.0276	0.1882
chr22	51304566	1050836	0.0205	0.1539
chrMT	16571	13249	0.7995	0.9557
chrX	155270560	3201027	0.0206	0.1713
chrY	59373566	250490	0.0042	0.1125

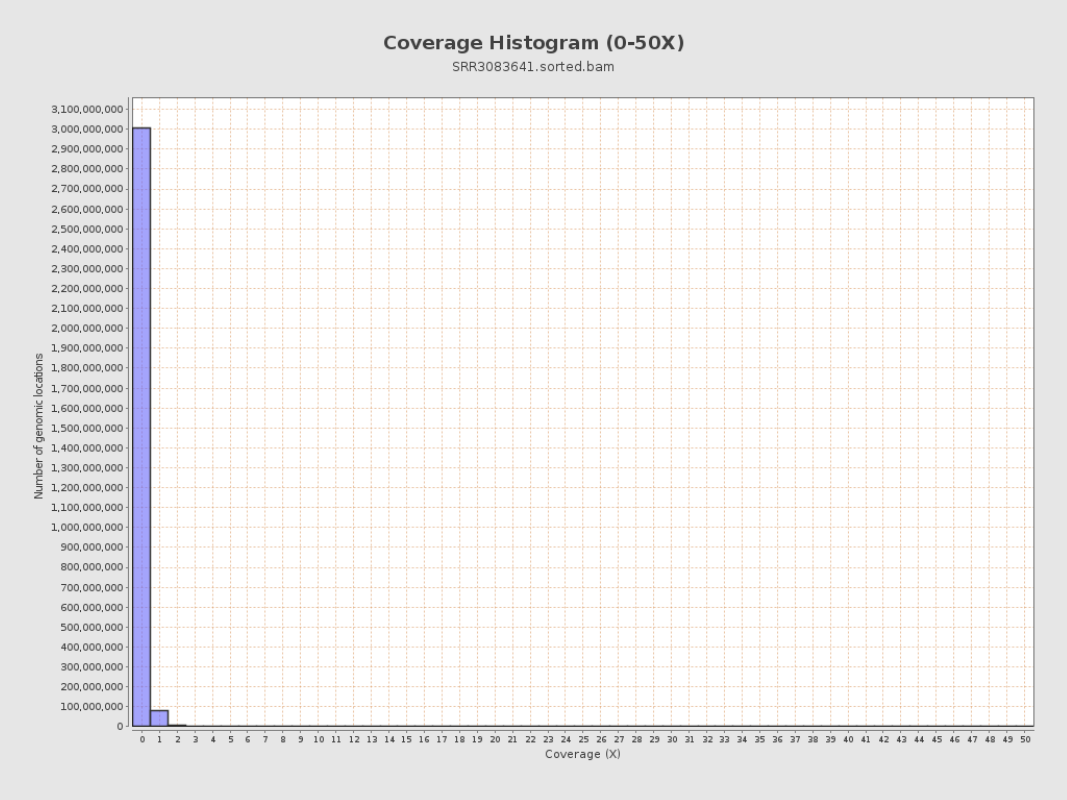
3. Results : Coverage across reference



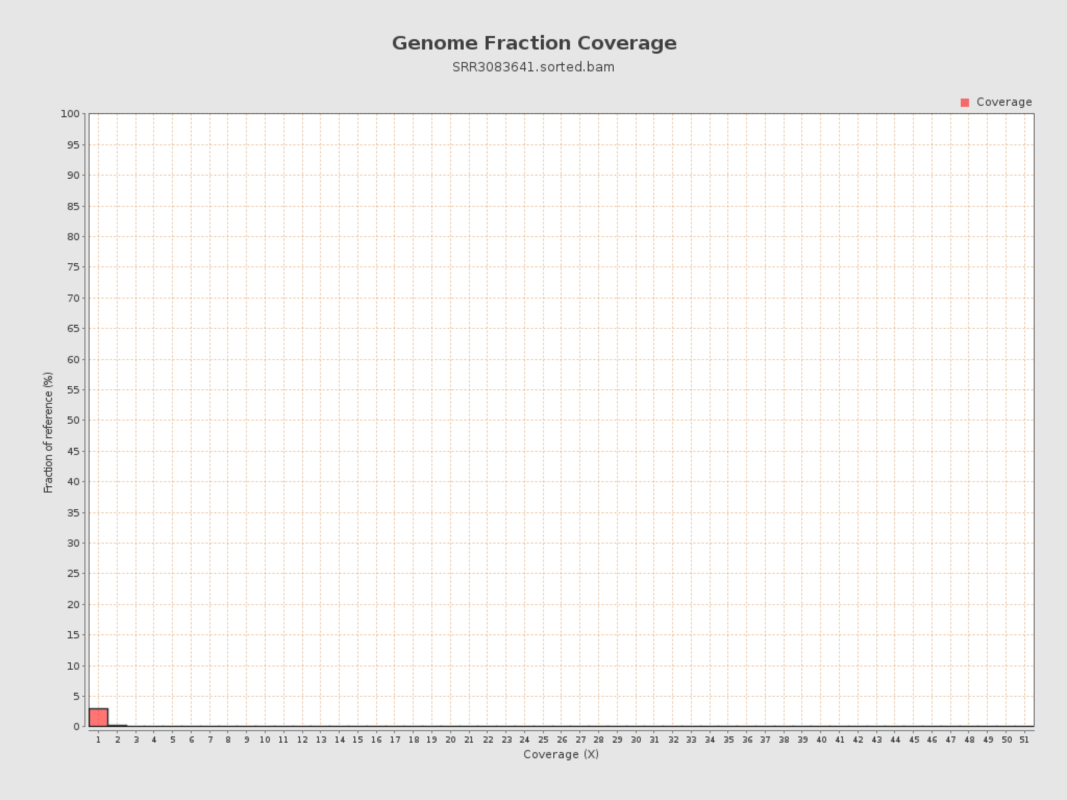
4. Results : Coverage Histogram



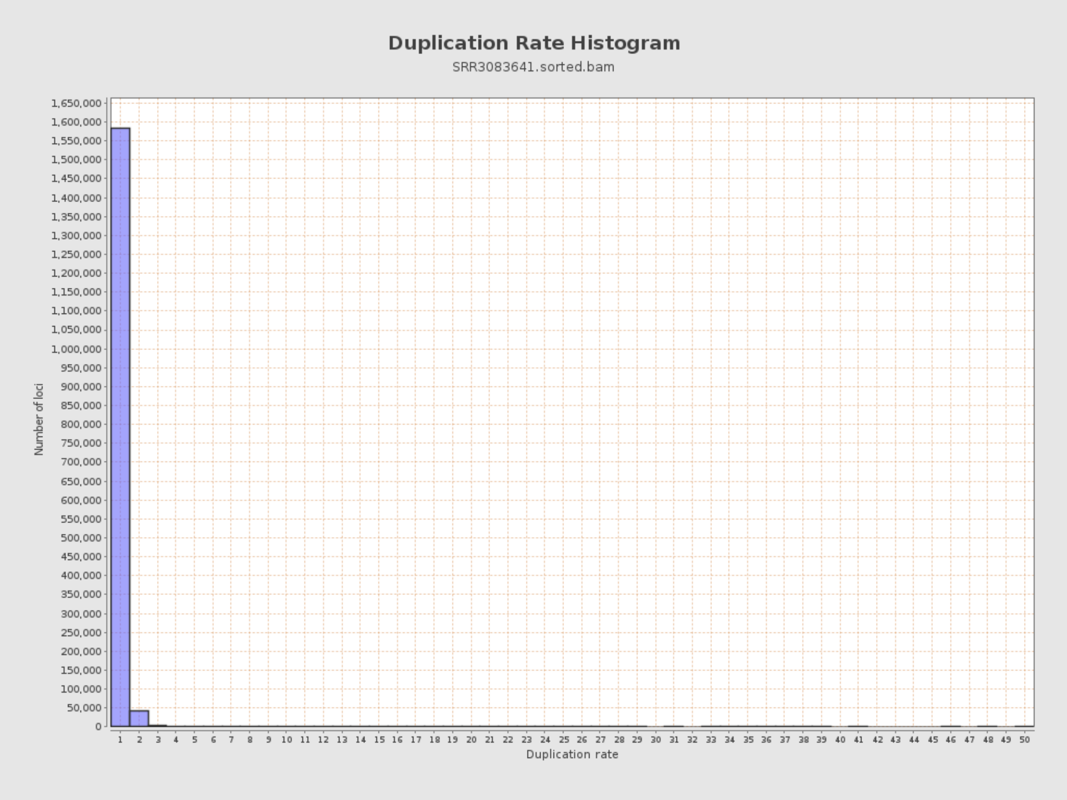
5. Results : Coverage Histogram (0-50X)



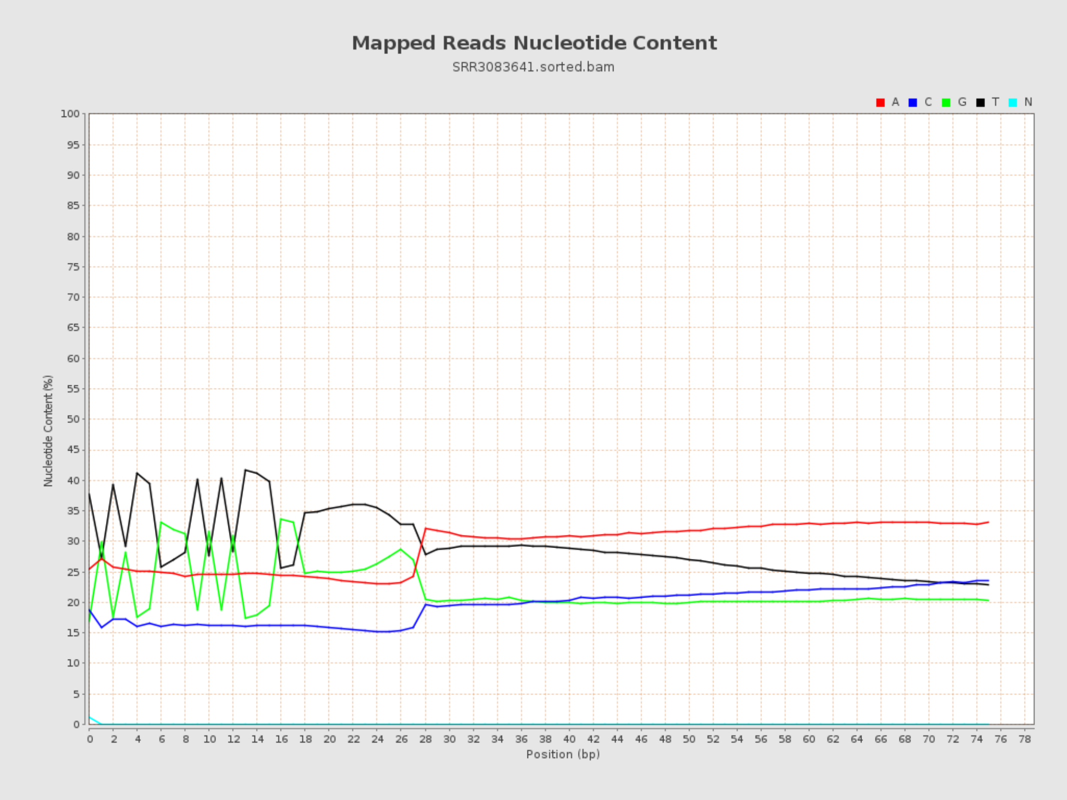
6. Results : Genome Fraction Coverage



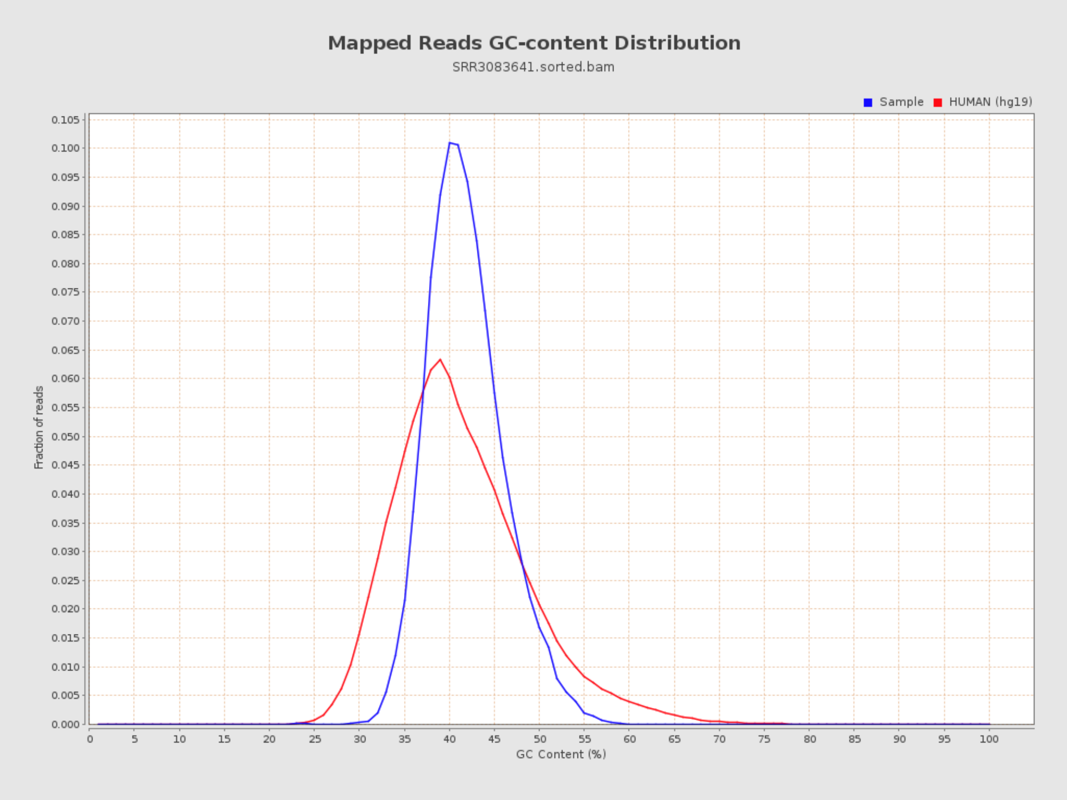
7. Results : Duplication Rate Histogram



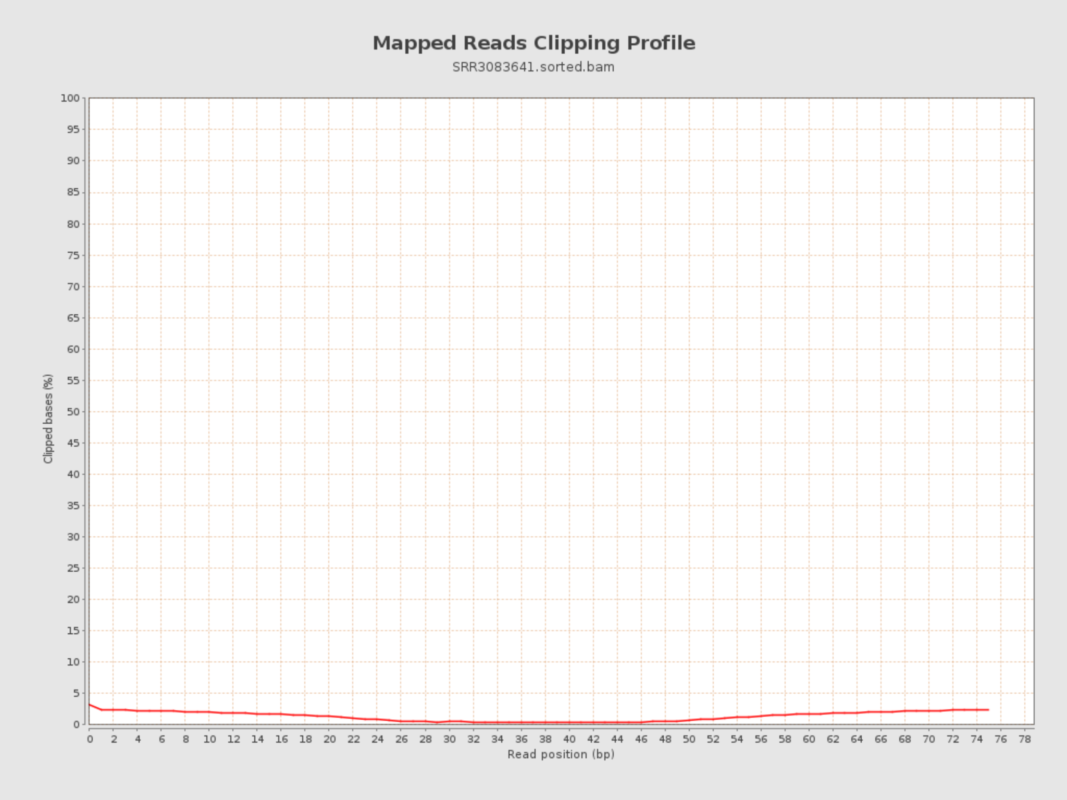
8. Results : Mapped Reads Nucleotide Content



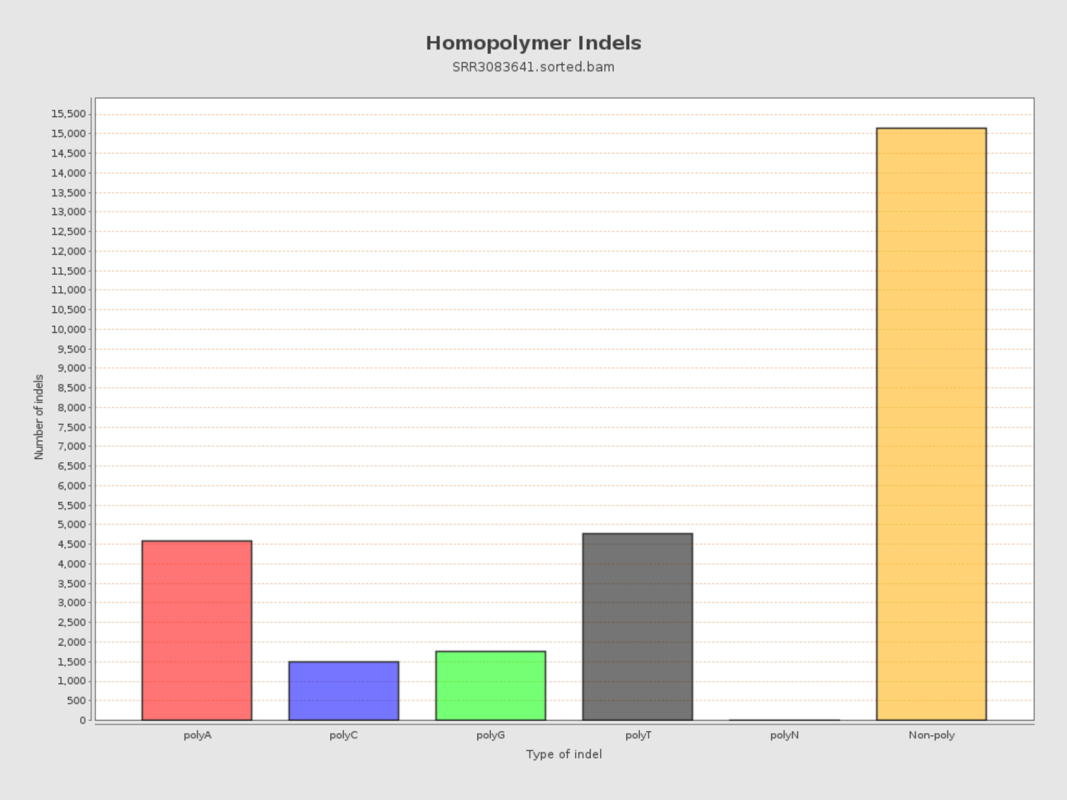
9. Results : Mapped Reads GC-content Distribution



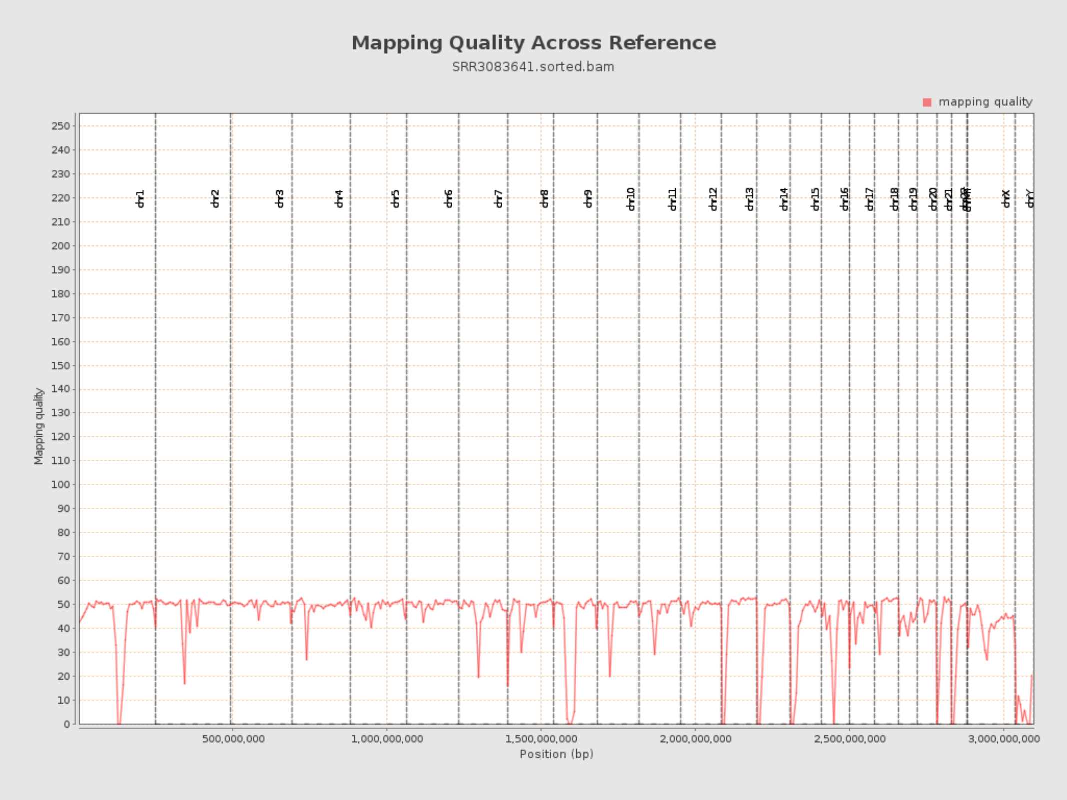
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram