Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 03:09:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083671.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_SRR3083671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083671.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 03:09:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083671.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,154,485
Mapped reads	907,024 / 78.57%
Unmapped reads	247,461 / 21.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,932 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	15,740 / 1.36%
Duplication rate	1.41%
Clipped reads	422,544 / 36.6%

2.2. ACGT Content

Number/percentage of A's	18,482,141 / 30.7%
Number/percentage of C's	11,130,168 / 18.49%
Number/percentage of T's	17,746,921 / 29.48%
Number/percentage of G's	12,830,784 / 21.32%
Number/percentage of N's	3,738 / 0.01%
GC Percentage	39.81%

2.3. Coverage

Mean	0.0195

Standard Deviation	0.1921

2.4. Mapping Quality

Mean Mapping Quality	47.27

2.5. Mismatches and indels

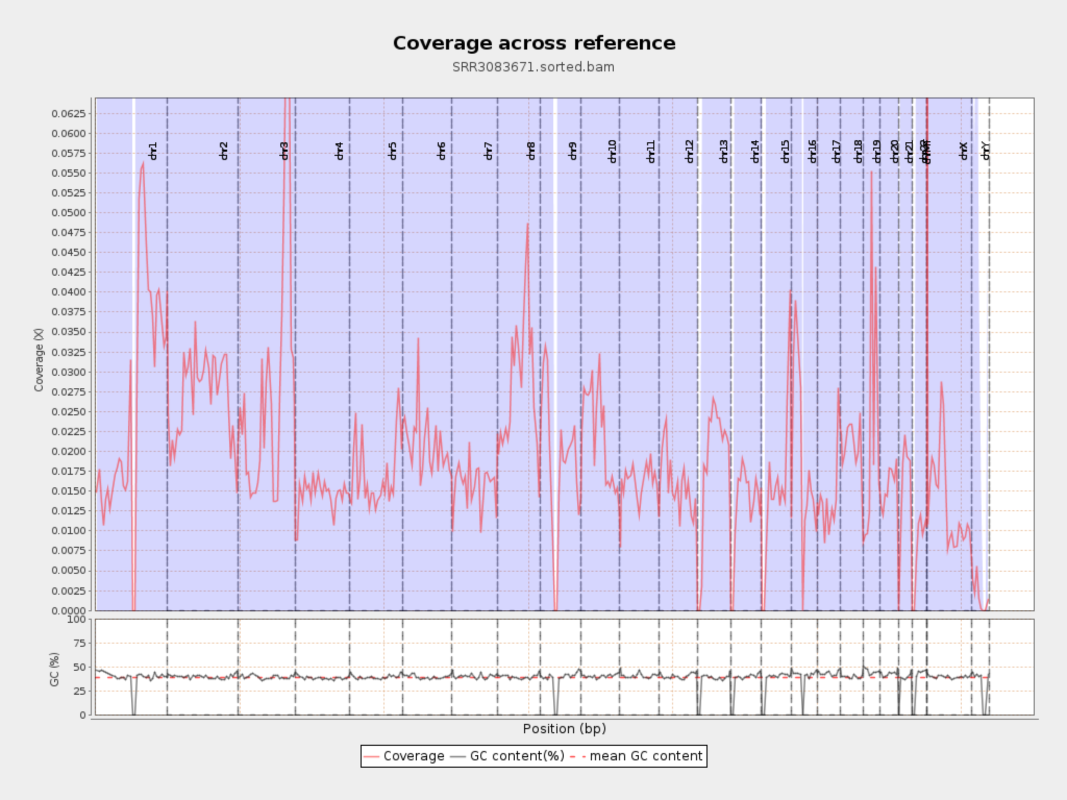
General error rate	0.95%
Mismatches	562,488
Insertions	4,593
Mapped reads with at least one insertion	0.5%
Deletions	13,281
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.36%

2.6. Chromosome stats

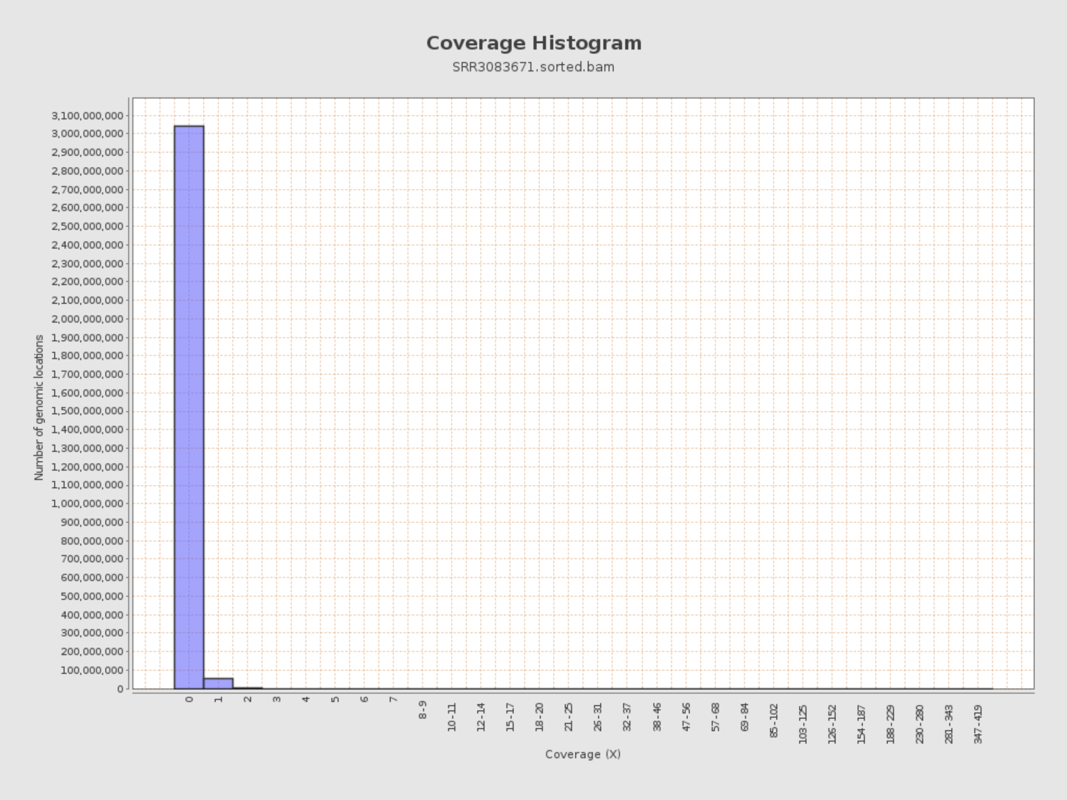
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6525543	0.0262	0.3967
chr2	243199373	6583148	0.0271	0.1952
chr3	198022430	5570109	0.0281	0.1768
chr4	191154276	2785563	0.0146	0.1264
chr5	180915260	3108200	0.0172	0.1372
chr6	171115067	3586041	0.021	0.1668
chr7	159138663	2489319	0.0156	0.1604

chr8	146364022	4250413	0.029	0.2523
chr9	141213431	2658919	0.0188	0.1551
chr10	135534747	2997927	0.0221	0.1921
chr11	135006516	2189268	0.0162	0.1443
chr12	133851895	2135715	0.016	0.1325
chr13	115169878	2148256	0.0187	0.1422
chr14	107349540	1413675	0.0132	0.1209
chr15	102531392	1604245	0.0156	0.1305
chr16	90354753	1724567	0.0191	0.1475
chr17	81195210	1160424	0.0143	0.1311
chr18	78077248	1632090	0.0209	0.2235
chr19	59128983	1327226	0.0224	0.2427
chr20	63025520	979215	0.0155	0.1319
chr21	48129895	743158	0.0154	0.1305
chr22	51304566	408704	0.008	0.0927
chrMT	16571	3706	0.2236	0.4693
chrX	155270560	2084591	0.0134	0.1239
chrY	59373566	104924	0.0018	0.0489

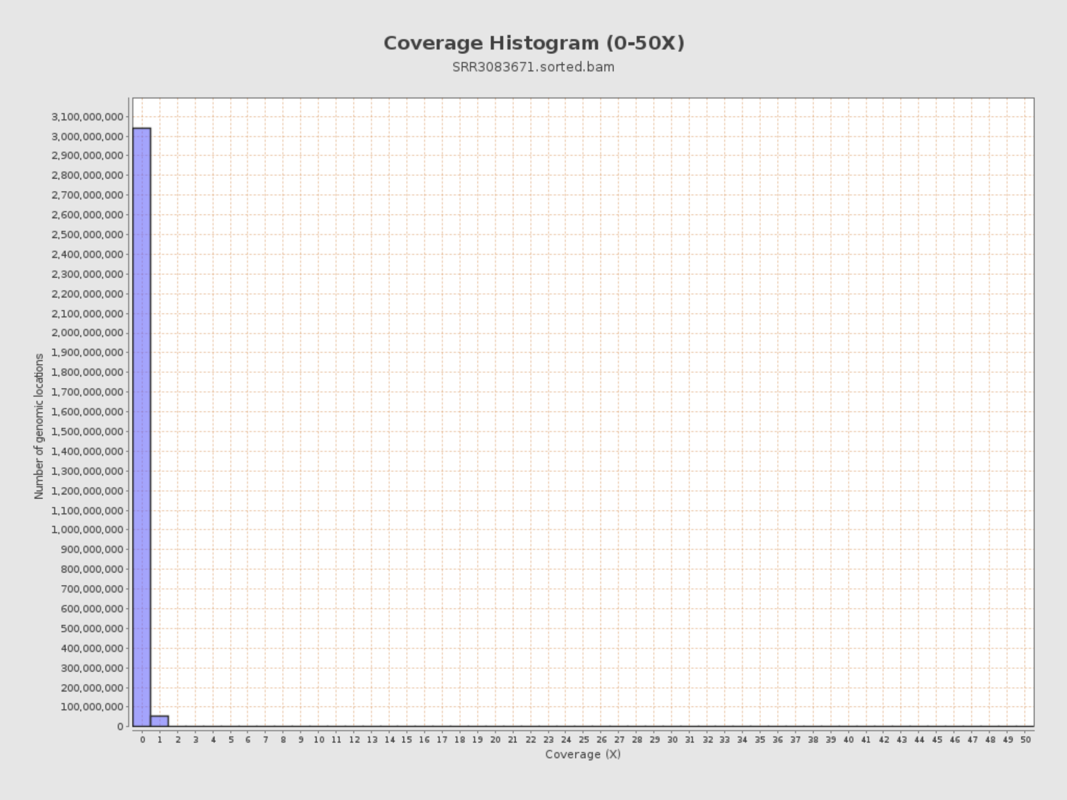
3. Results : Coverage across reference



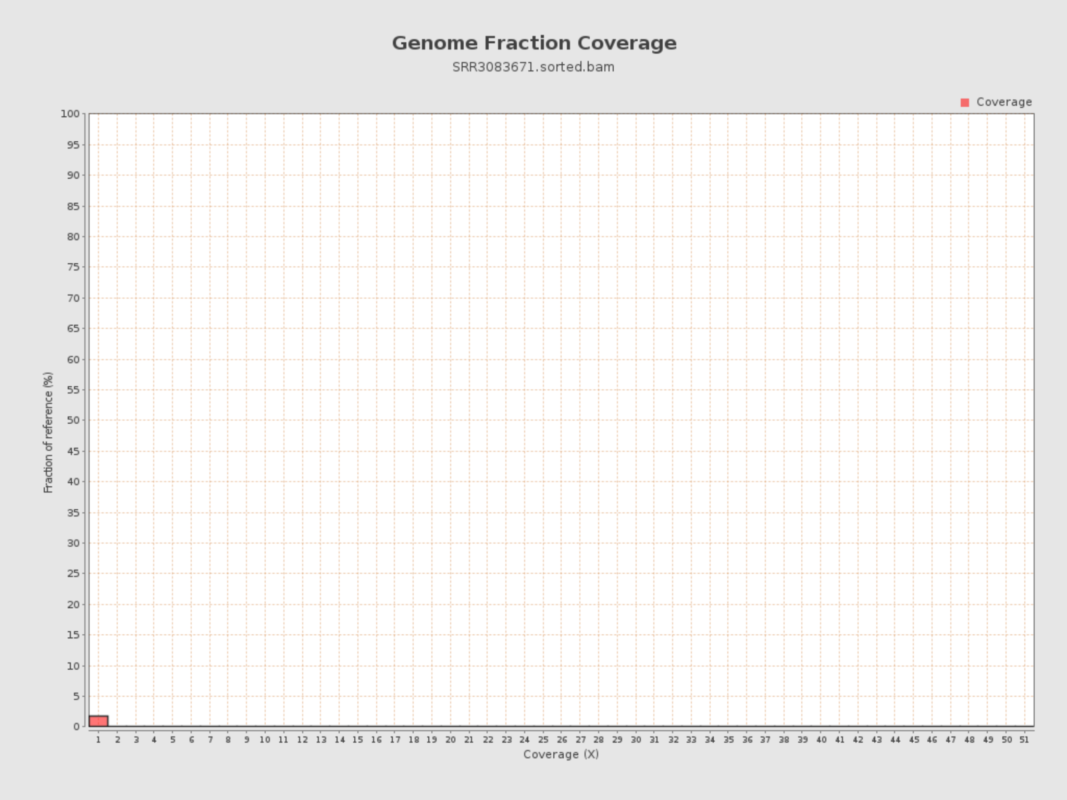
4. Results : Coverage Histogram



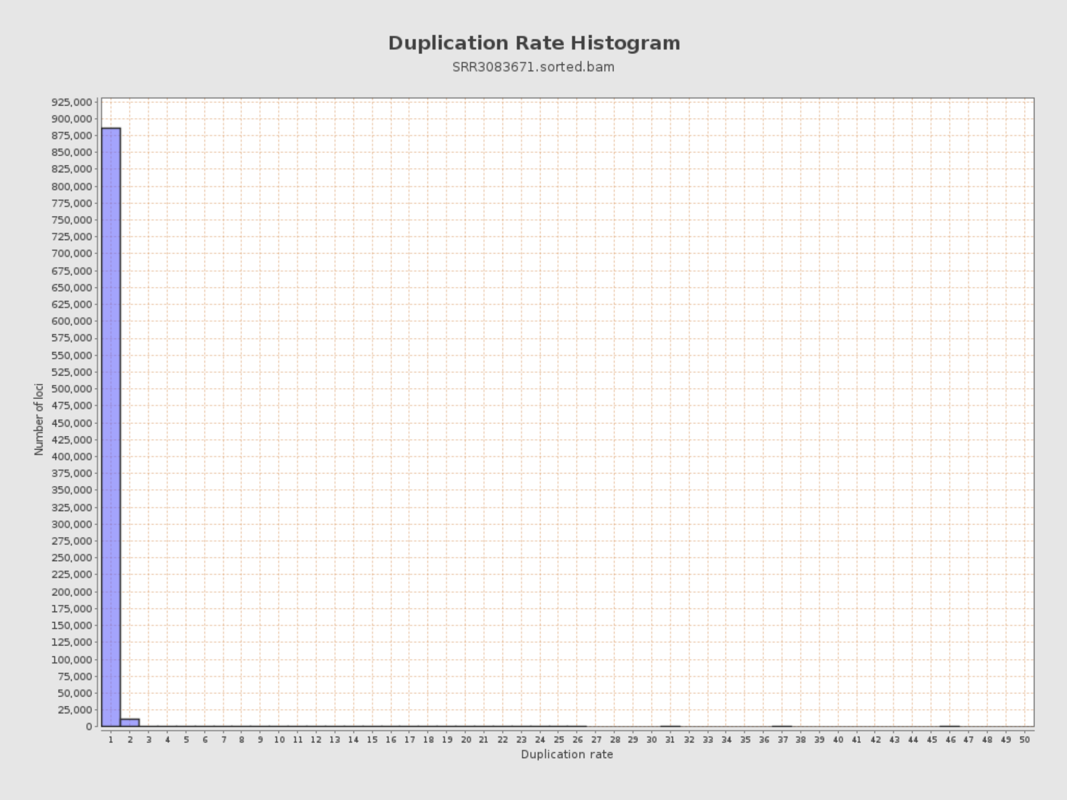
5. Results : Coverage Histogram (0-50X)



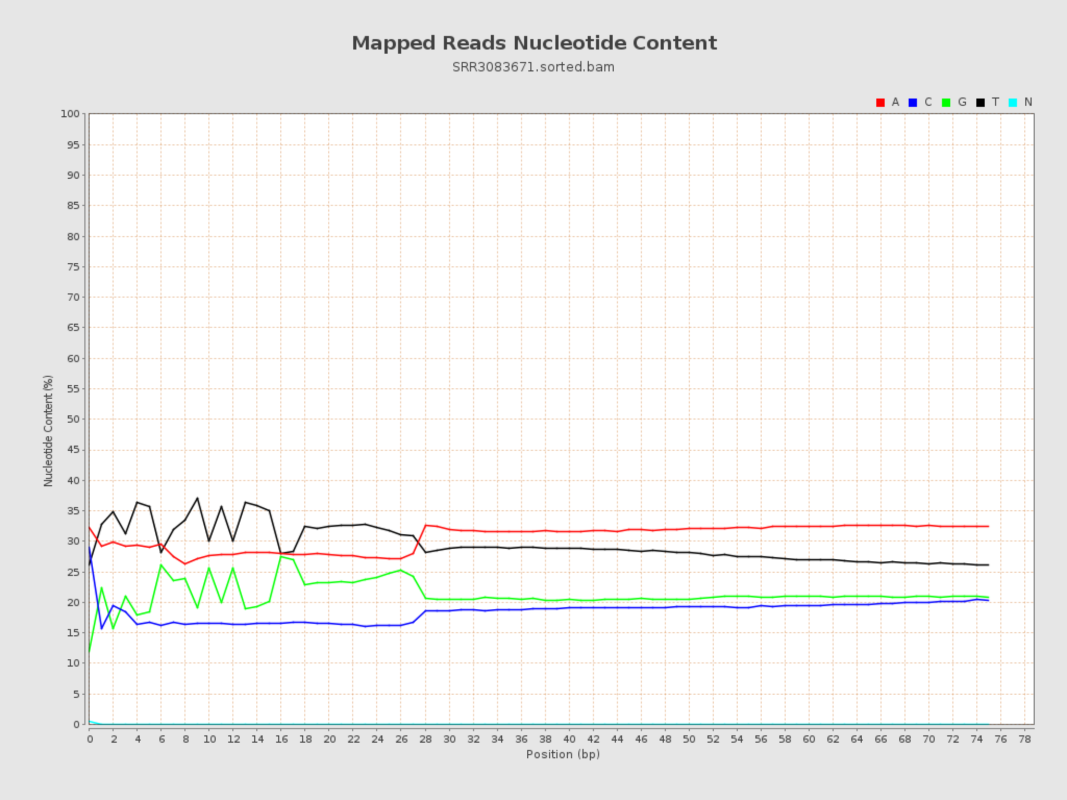
6. Results : Genome Fraction Coverage



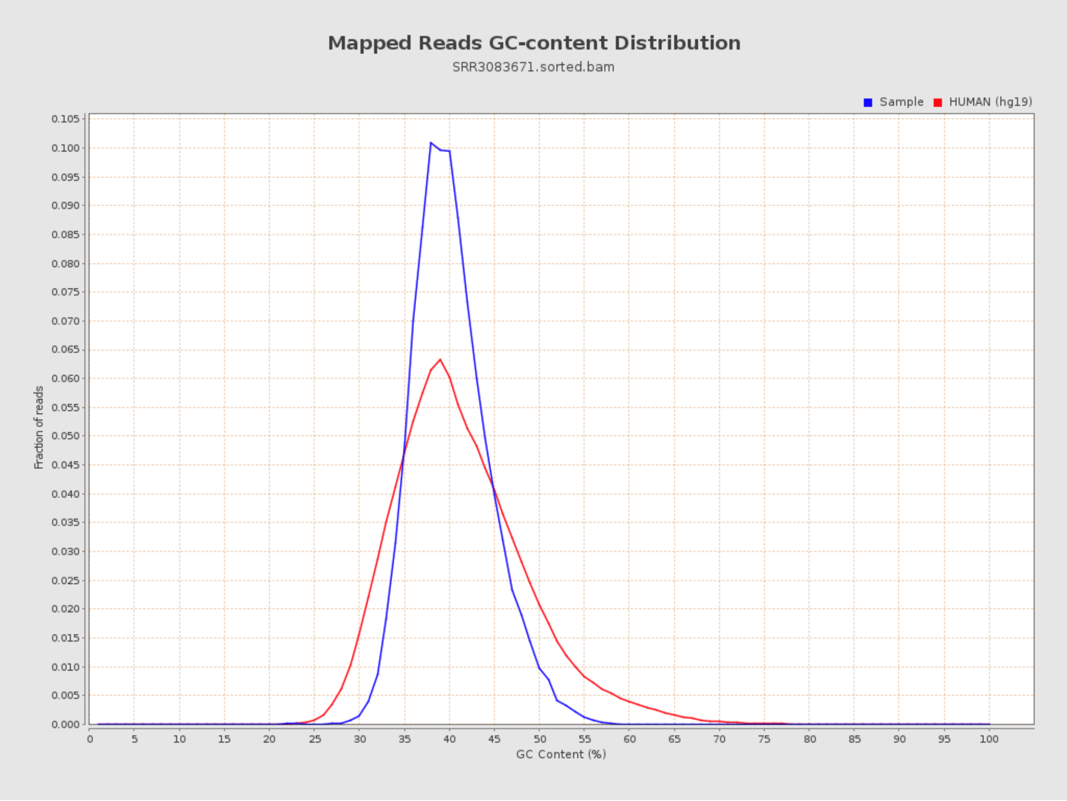
7. Results : Duplication Rate Histogram



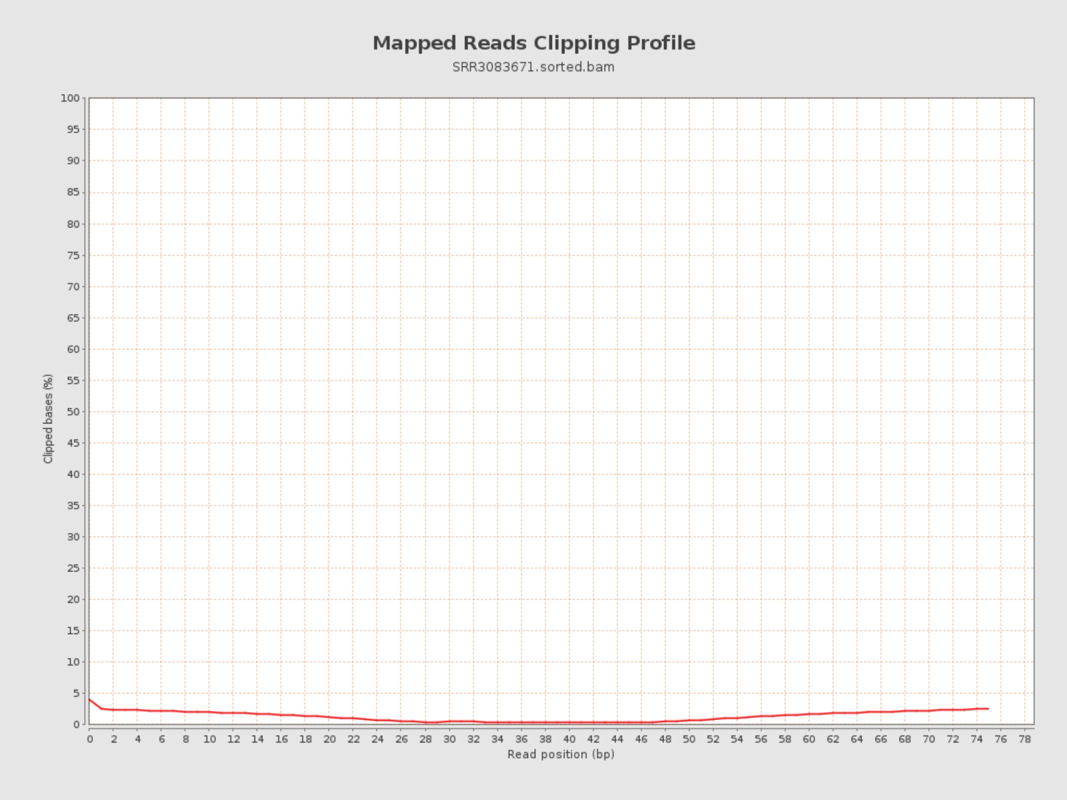
8. Results : Mapped Reads Nucleotide Content



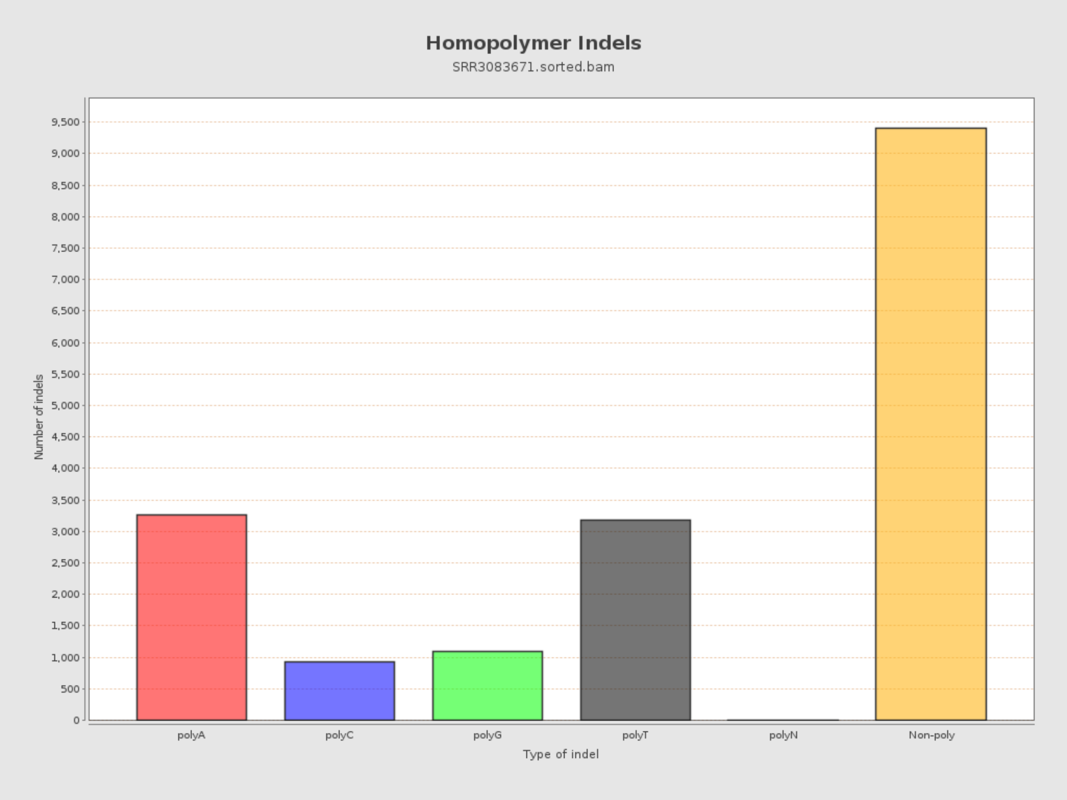
9. Results : Mapped Reads GC-content Distribution



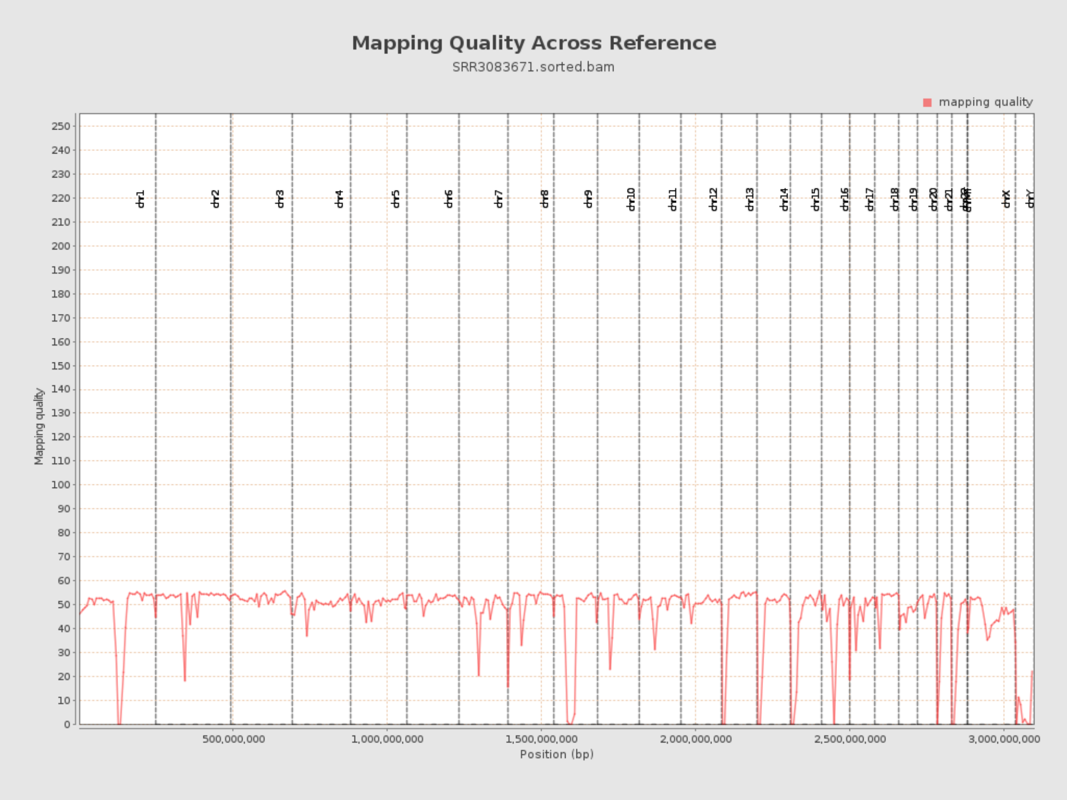
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram