Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:36:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084263.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_SRR3084263 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084263.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:36:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,056,835
Mapped reads	1,723,307 / 83.78%
Unmapped reads	333,528 / 16.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,070 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	52,128 / 2.53%
Duplication rate	2.53%
Clipped reads	952,759 / 46.32%

2.2. ACGT Content

Number/percentage of A's	32,097,464 / 29.12%
Number/percentage of C's	20,642,398 / 18.73%
Number/percentage of T's	33,546,339 / 30.44%
Number/percentage of G's	23,928,214 / 21.71%
Number/percentage of N's	1,199 / 0%
GC Percentage	40.44%

2.3. Coverage

Mean	0.0356

Standard Deviation	0.2577

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

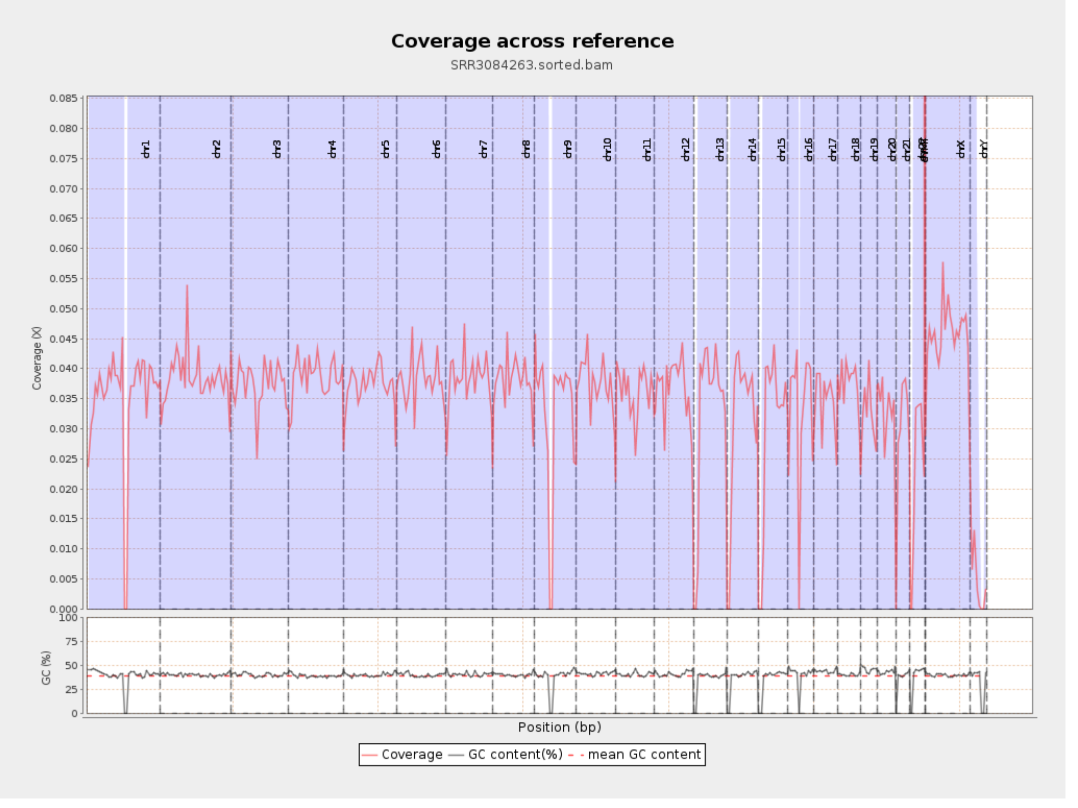
General error rate	0.86%
Mismatches	929,556
Insertions	8,659
Mapped reads with at least one insertion	0.5%
Deletions	23,627
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.28%

2.6. Chromosome stats

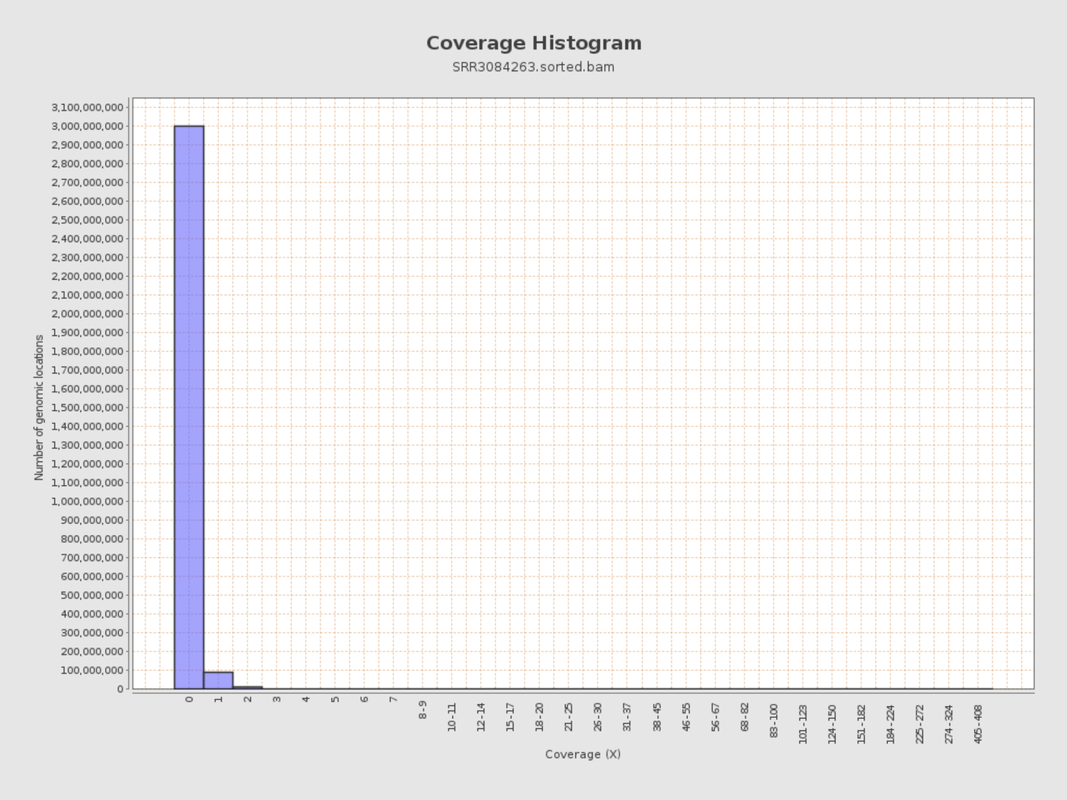
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8754785	0.0351	0.3411
chr2	243199373	9368783	0.0385	0.3144
chr3	198022430	7440187	0.0376	0.2127
chr4	191154276	7392309	0.0387	0.2201
chr5	180915260	6788962	0.0375	0.2127
chr6	171115067	6557010	0.0383	0.2428
chr7	159138663	6122759	0.0385	0.2943

chr8	146364022	5584853	0.0382	0.296
chr9	141213431	4566177	0.0323	0.2441
chr10	135534747	5125505	0.0378	0.2633
chr11	135006516	4865789	0.036	0.2359
chr12	133851895	4901793	0.0366	0.2118
chr13	115169878	3712440	0.0322	0.1983
chr14	107349540	3342912	0.0311	0.2034
chr15	102531392	3080582	0.03	0.1943
chr16	90354753	2987031	0.0331	0.2171
chr17	81195210	2774615	0.0342	0.2143
chr18	78077248	2952901	0.0378	0.4577
chr19	59128983	1933664	0.0327	0.2811
chr20	63025520	2069873	0.0328	0.2022
chr21	48129895	1427765	0.0297	0.1957
chr22	51304566	1131738	0.0221	0.1619
chrMT	16571	8560	0.5166	0.7606
chrX	155270560	7085687	0.0456	0.2503
chrY	59373566	276451	0.0047	0.0983

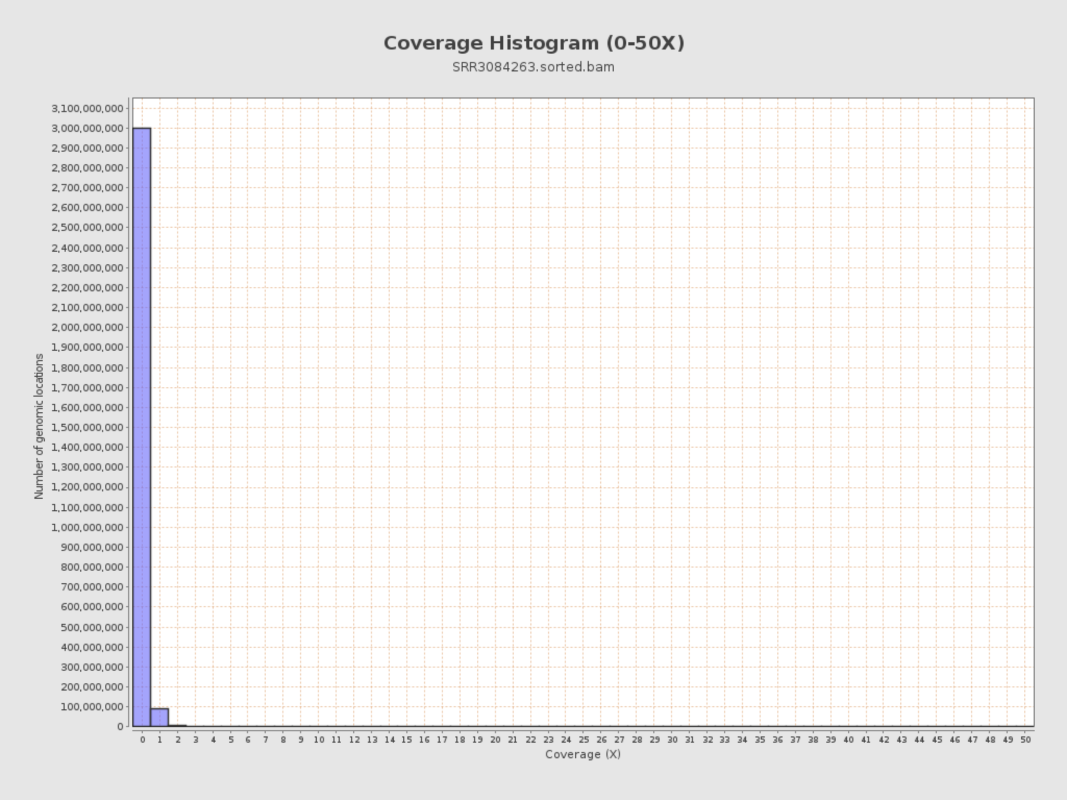
3. Results : Coverage across reference



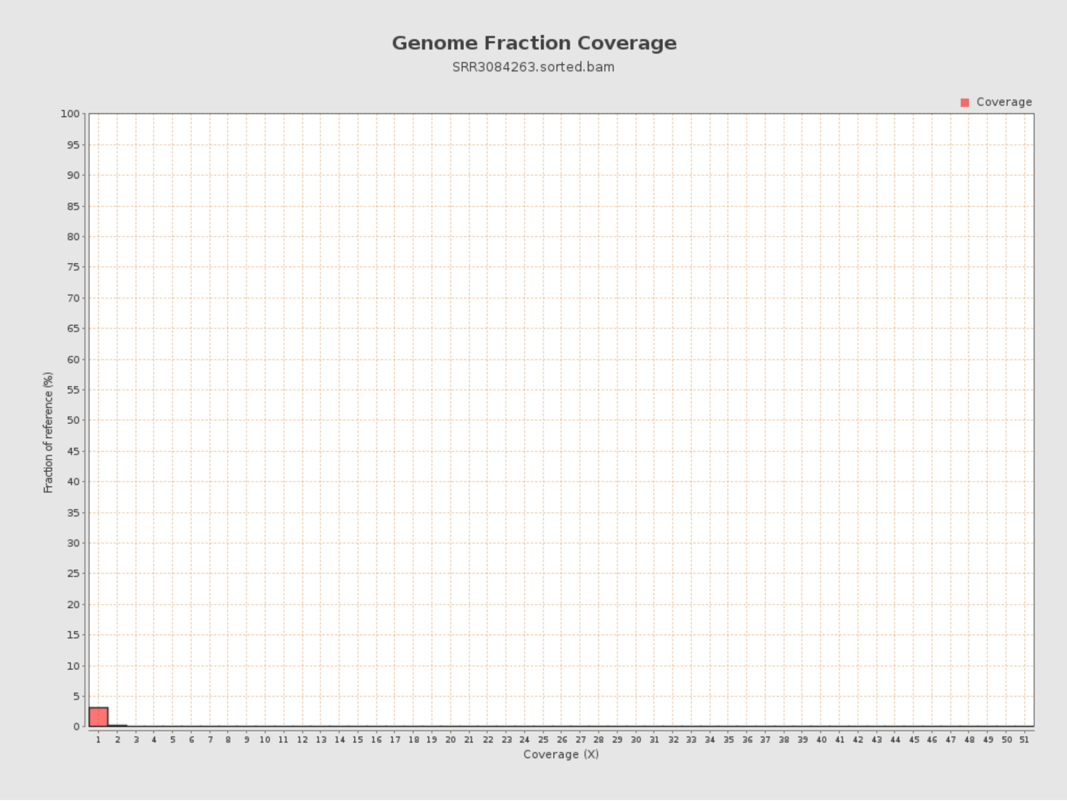
4. Results : Coverage Histogram



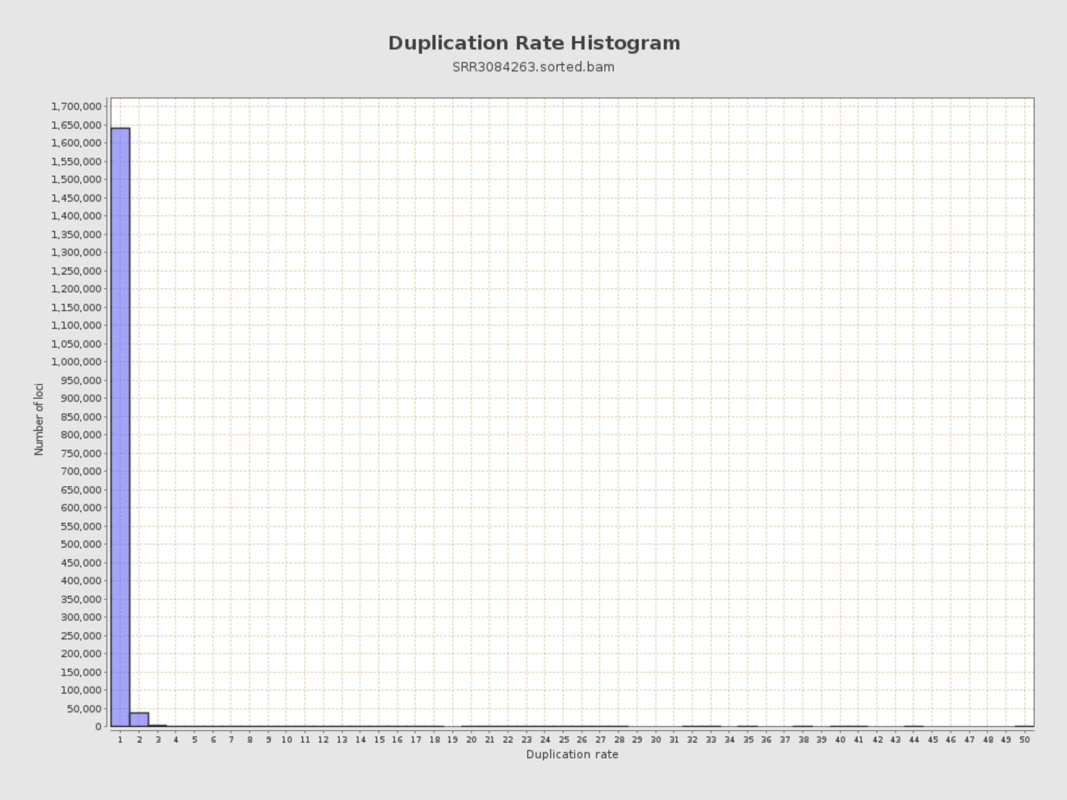
5. Results : Coverage Histogram (0-50X)



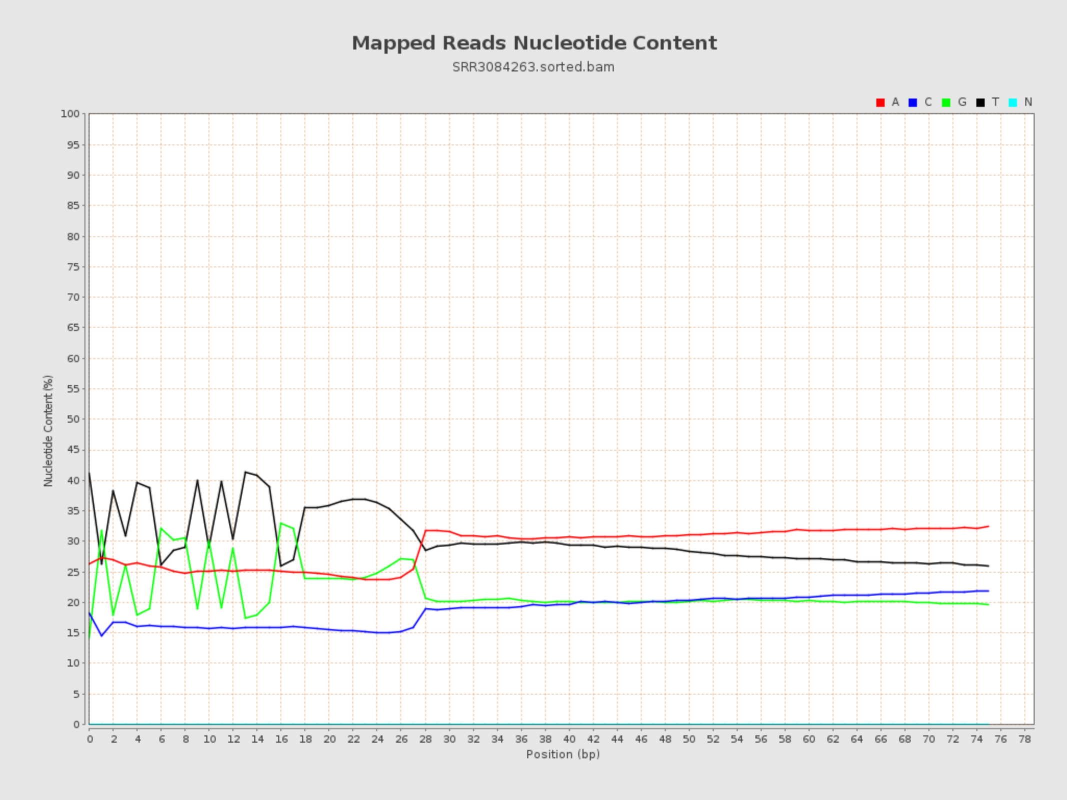
6. Results : Genome Fraction Coverage



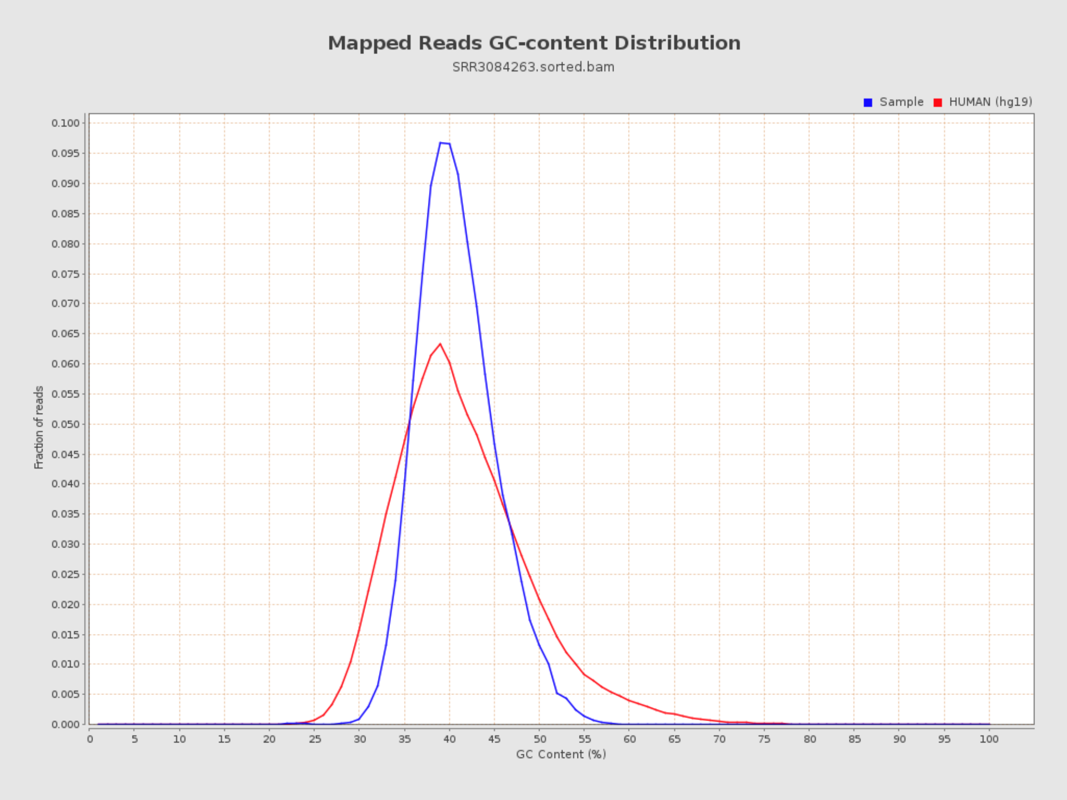
7. Results : Duplication Rate Histogram



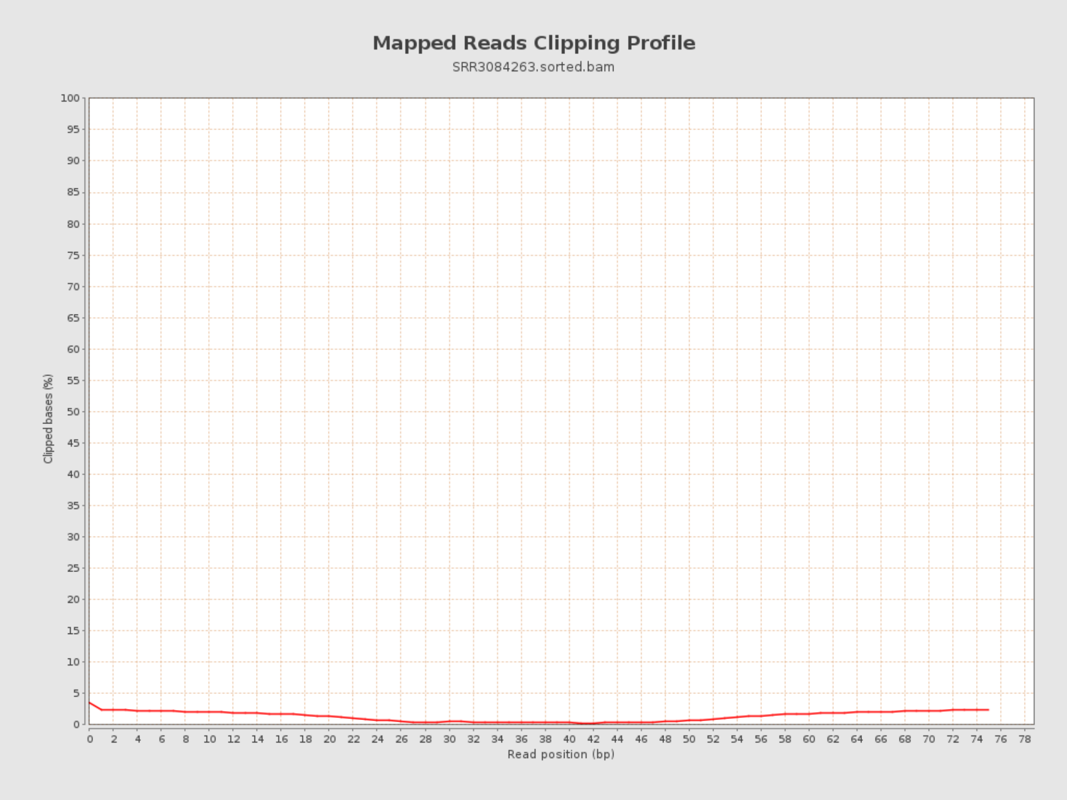
8. Results : Mapped Reads Nucleotide Content



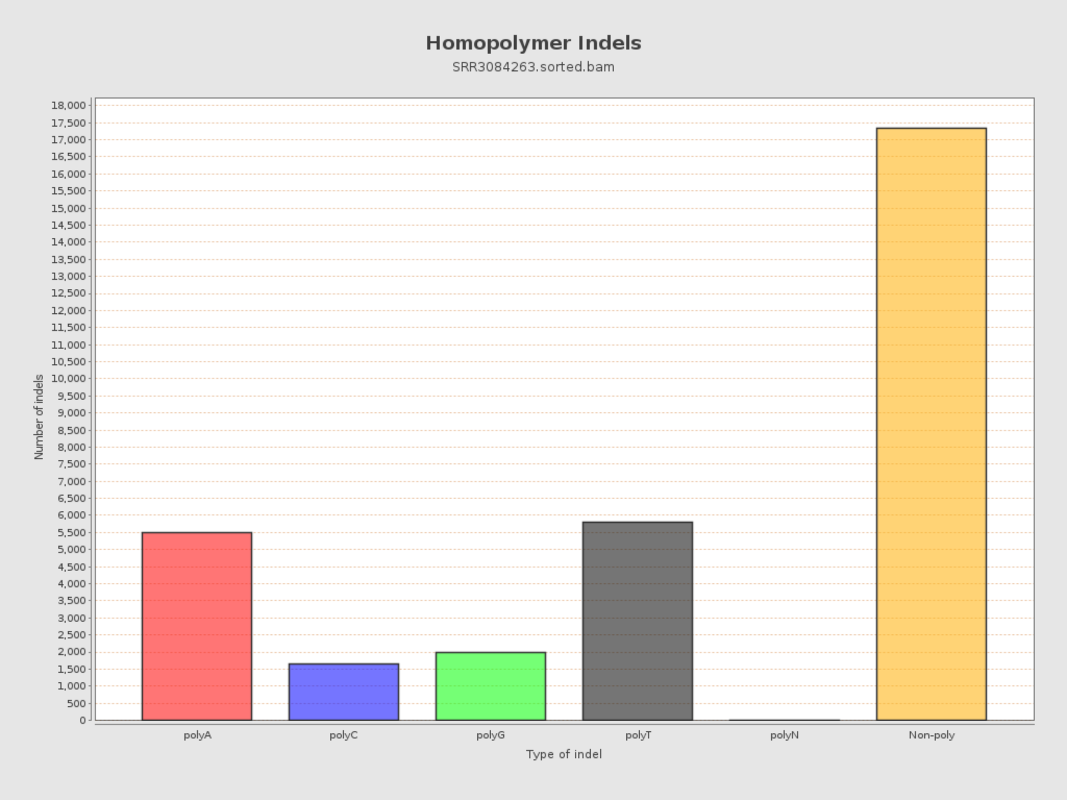
9. Results : Mapped Reads GC-content Distribution



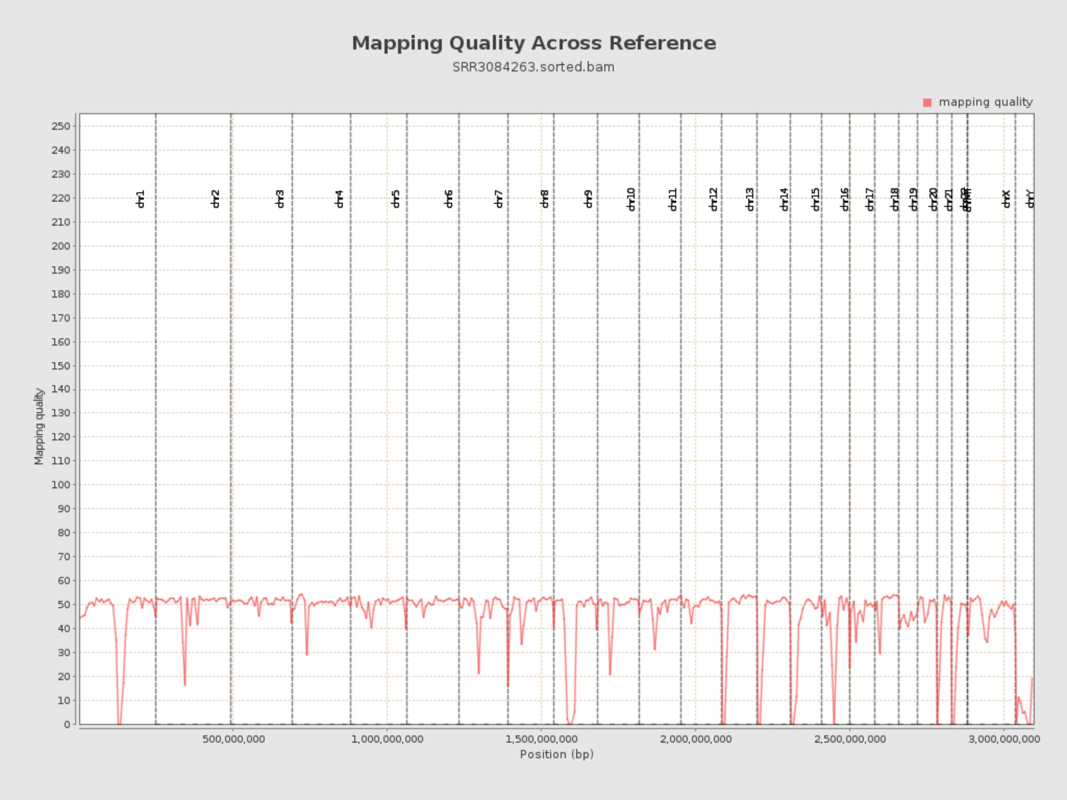
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram