Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:44:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084267.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_SRR3084267 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084267.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:44:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084267.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,731,971
Mapped reads	1,417,778 / 81.86%
Unmapped reads	314,193 / 18.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,676 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	38,613 / 2.23%
Duplication rate	2.12%
Clipped reads	718,330 / 41.47%

2.2. ACGT Content

Number/percentage of A's	27,085,096 / 29.39%
Number/percentage of C's	17,293,637 / 18.76%
Number/percentage of T's	27,599,877 / 29.95%
Number/percentage of G's	20,185,042 / 21.9%
Number/percentage of N's	1,032 / 0%
GC Percentage	40.66%

2.3. Coverage

Mean	0.0298

Standard Deviation	0.2493

2.4. Mapping Quality

Mean Mapping Quality	46.27

2.5. Mismatches and indels

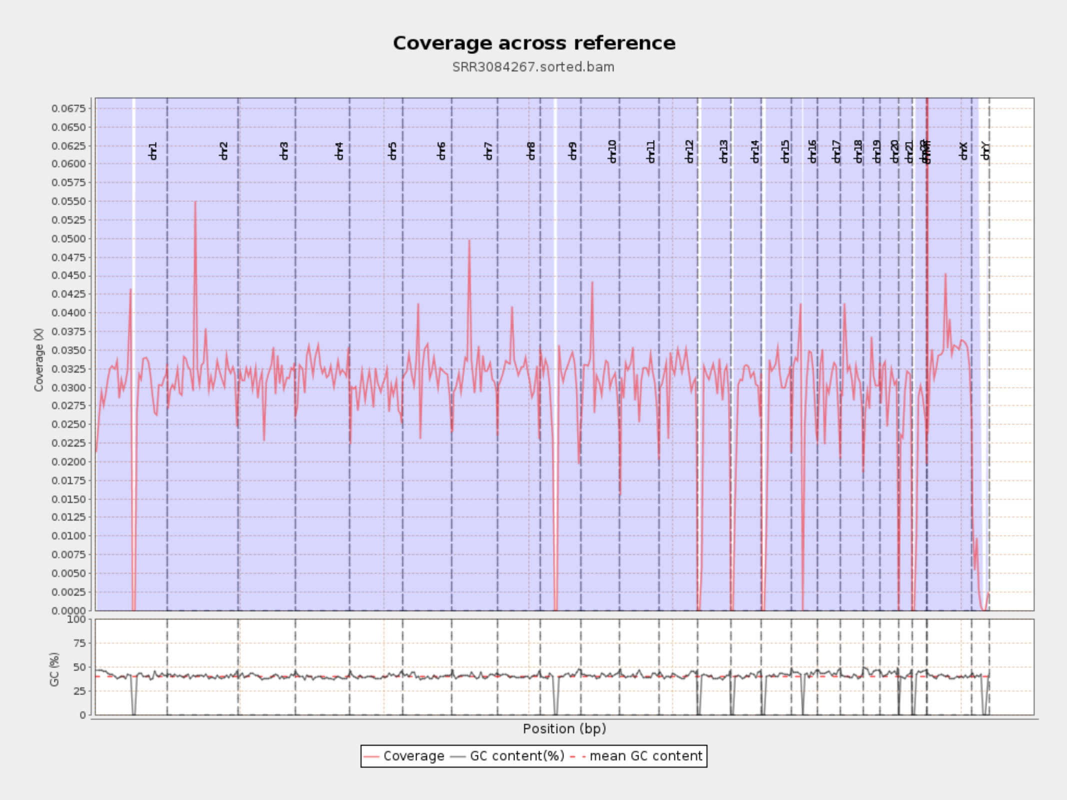
General error rate	0.88%
Mismatches	801,703
Insertions	6,989
Mapped reads with at least one insertion	0.49%
Deletions	20,328
Mapped reads with at least one deletion	1.42%
Homopolymer indels	46.65%

2.6. Chromosome stats

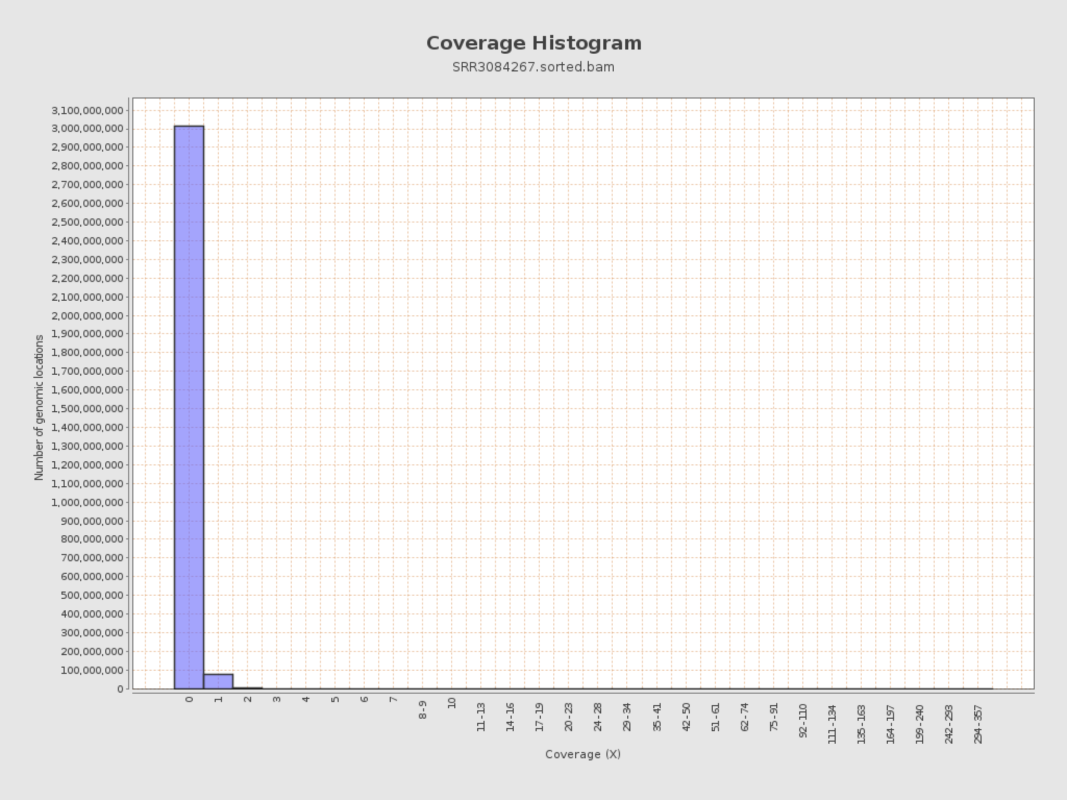
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7171863	0.0288	0.3533
chr2	243199373	7860621	0.0323	0.2988
chr3	198022430	6191768	0.0313	0.1903
chr4	191154276	6161983	0.0322	0.1975
chr5	180915260	5366336	0.0297	0.1853
chr6	171115067	5495347	0.0321	0.2203
chr7	159138663	5160846	0.0324	0.3208

chr8	146364022	4691236	0.0321	0.2669
chr9	141213431	3940806	0.0279	0.24
chr10	135534747	4288135	0.0316	0.2532
chr11	135006516	4172716	0.0309	0.2328
chr12	133851895	4242578	0.0317	0.193
chr13	115169878	3011584	0.0261	0.1737
chr14	107349540	2784608	0.0259	0.1858
chr15	102531392	2664948	0.026	0.1767
chr16	90354753	2619479	0.029	0.2039
chr17	81195210	2412238	0.0297	0.2101
chr18	78077248	2478036	0.0317	0.4931
chr19	59128983	1763997	0.0298	0.2868
chr20	63025520	1873881	0.0297	0.1942
chr21	48129895	1209621	0.0251	0.1774
chr22	51304566	990833	0.0193	0.1486
chrMT	16571	26729	1.613	1.7778
chrX	155270560	5393926	0.0347	0.2171
chrY	59373566	223055	0.0038	0.0831

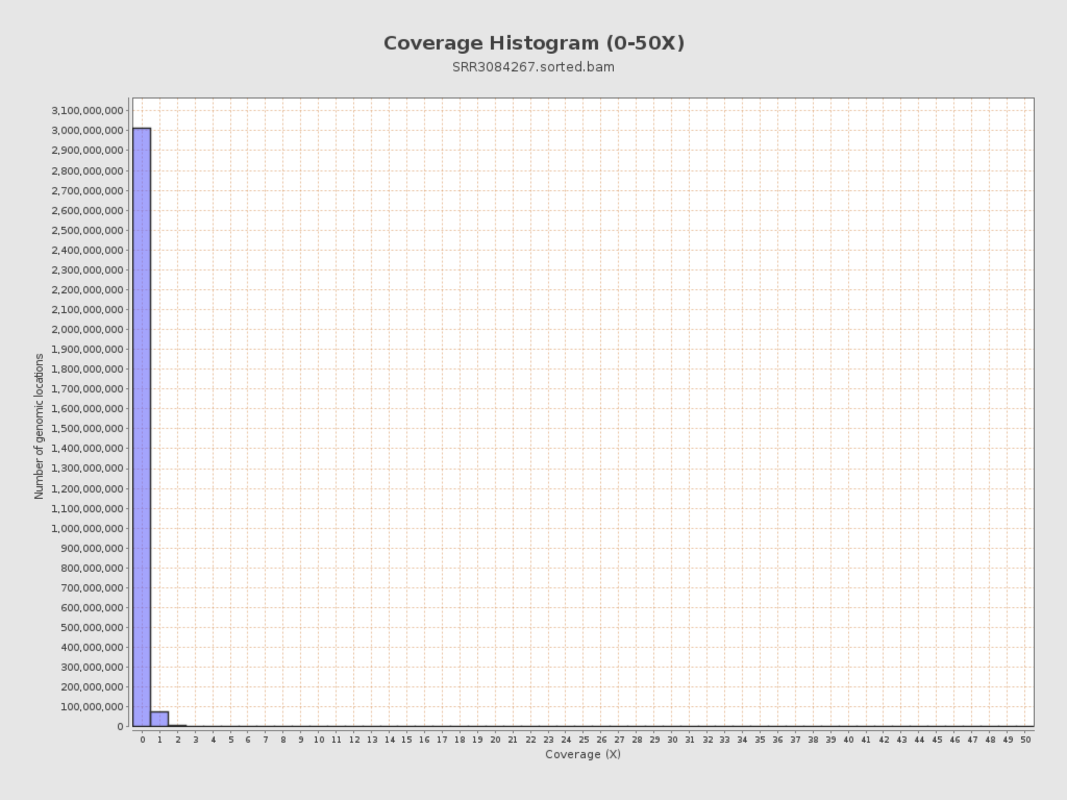
3. Results : Coverage across reference



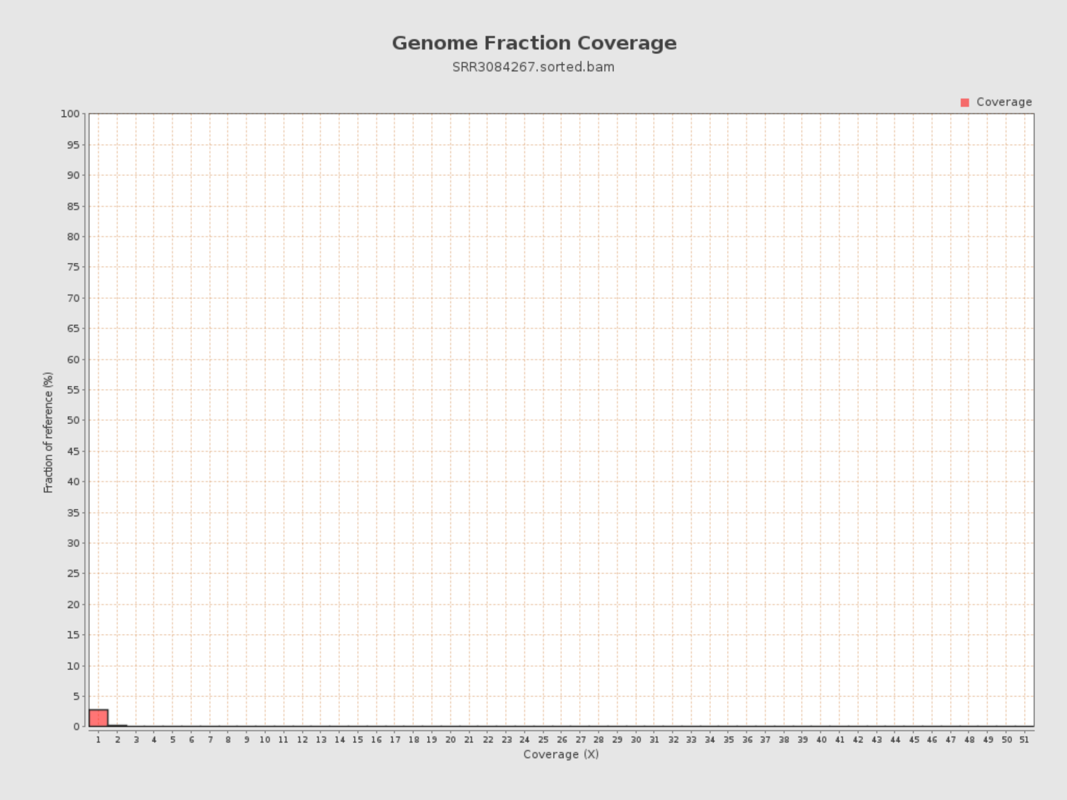
4. Results : Coverage Histogram



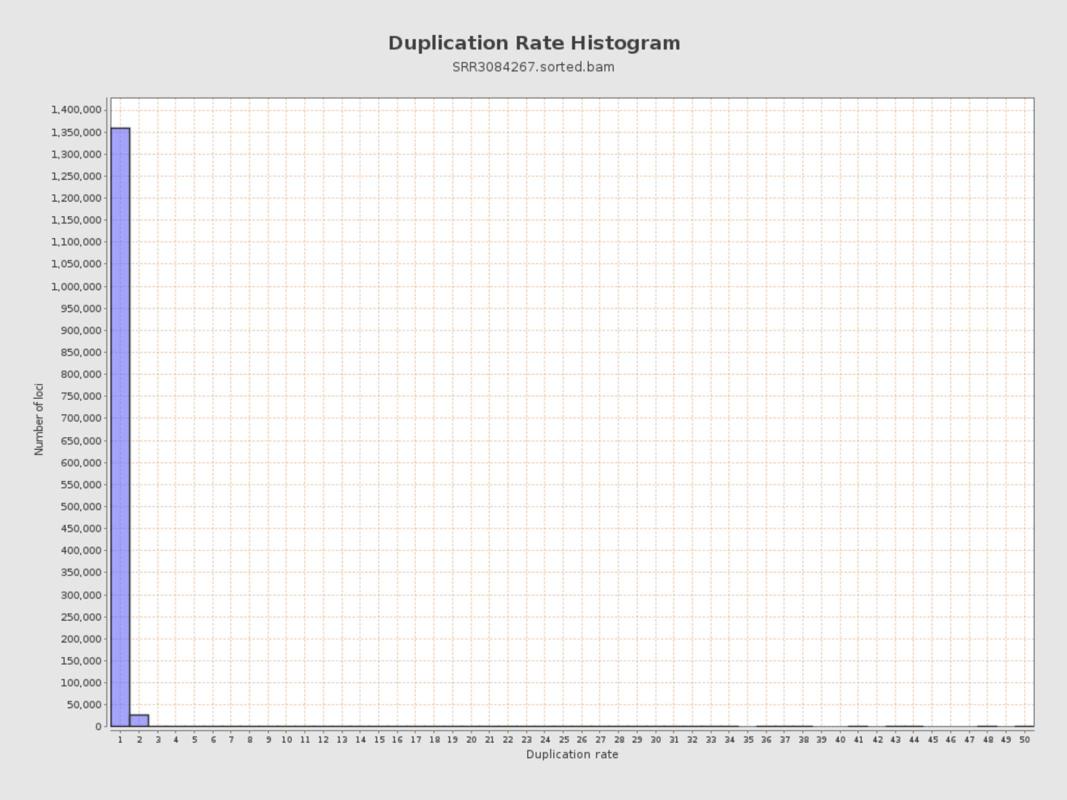
5. Results : Coverage Histogram (0-50X)



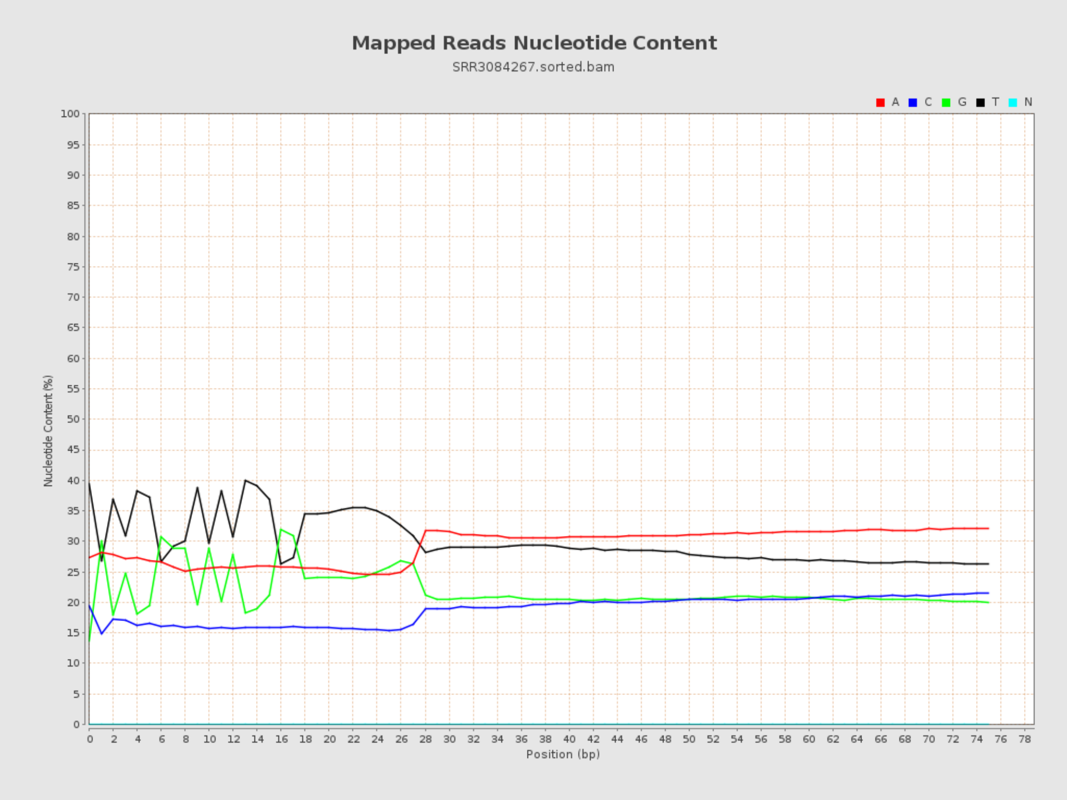
6. Results : Genome Fraction Coverage



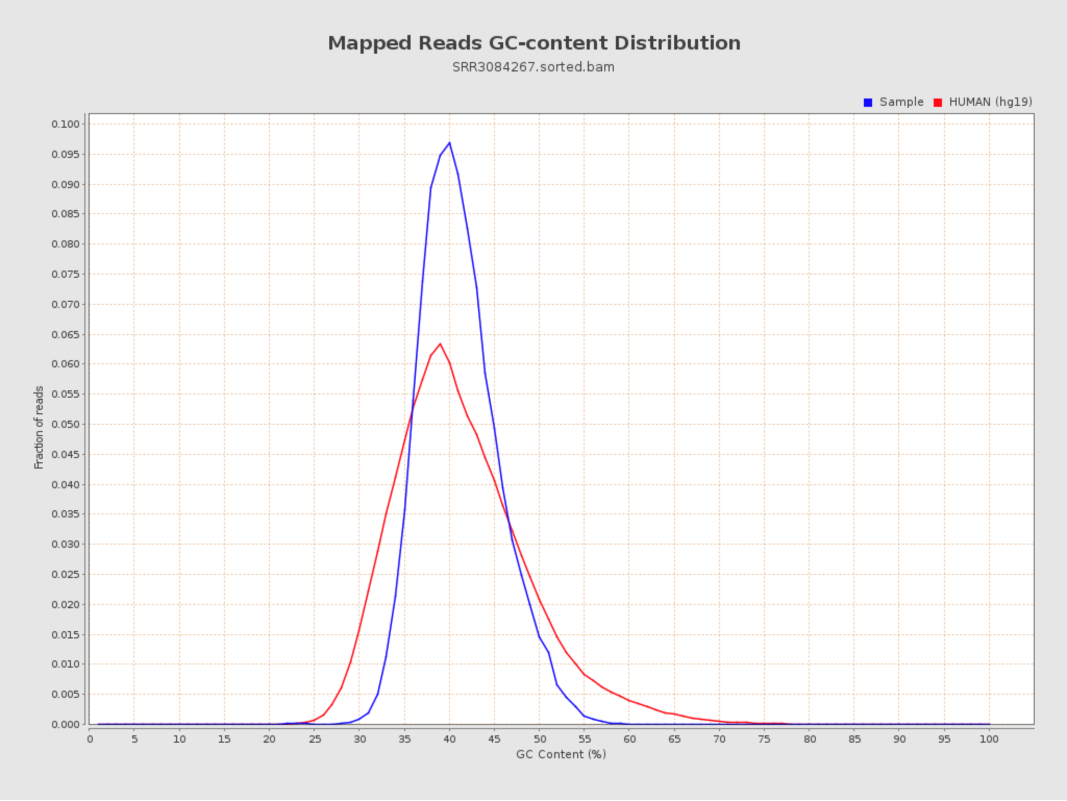
7. Results : Duplication Rate Histogram



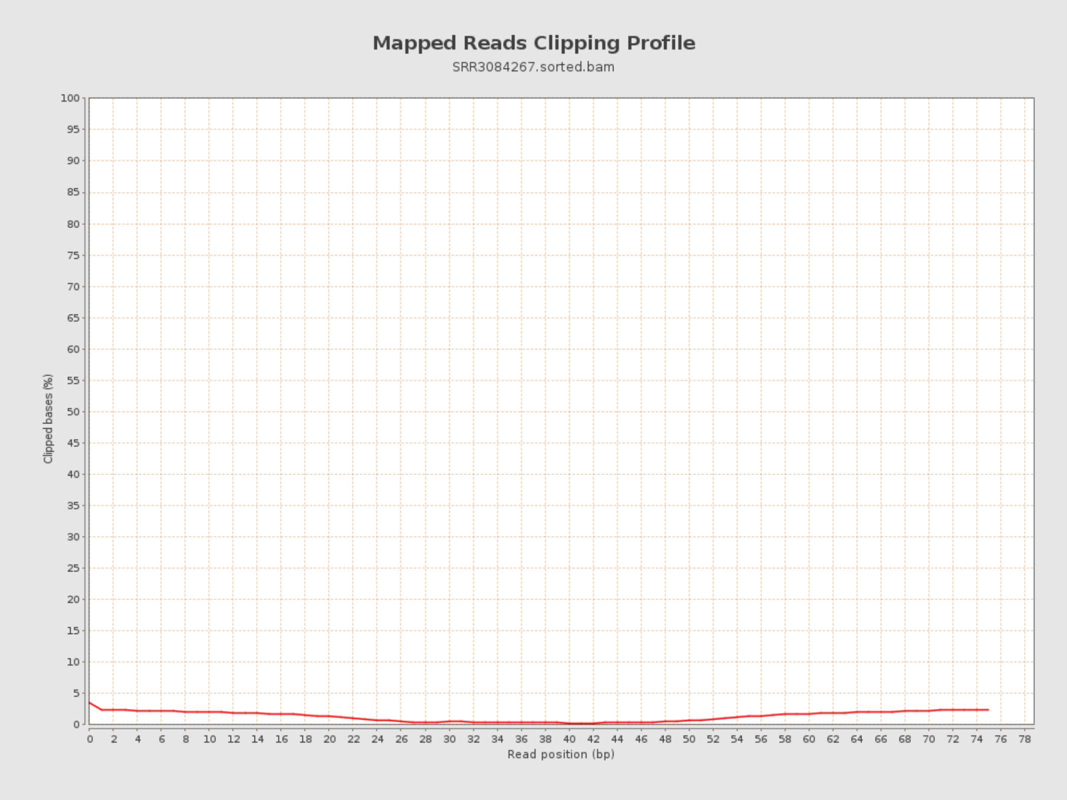
8. Results : Mapped Reads Nucleotide Content



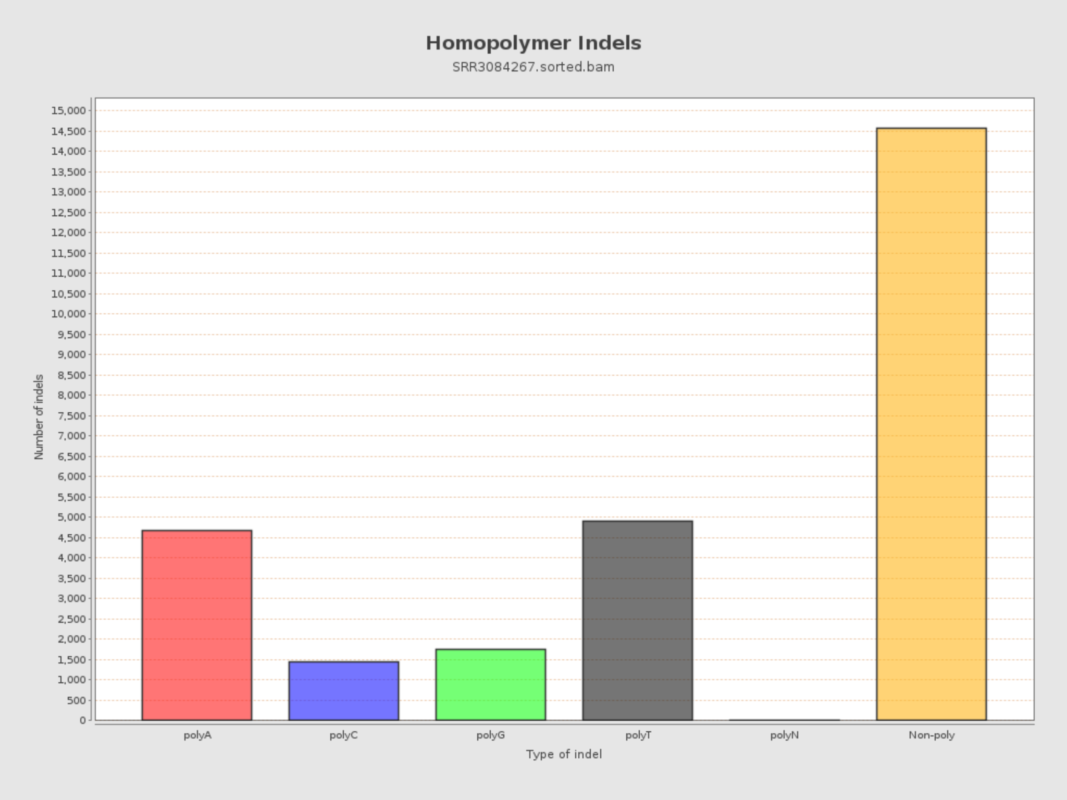
9. Results : Mapped Reads GC-content Distribution



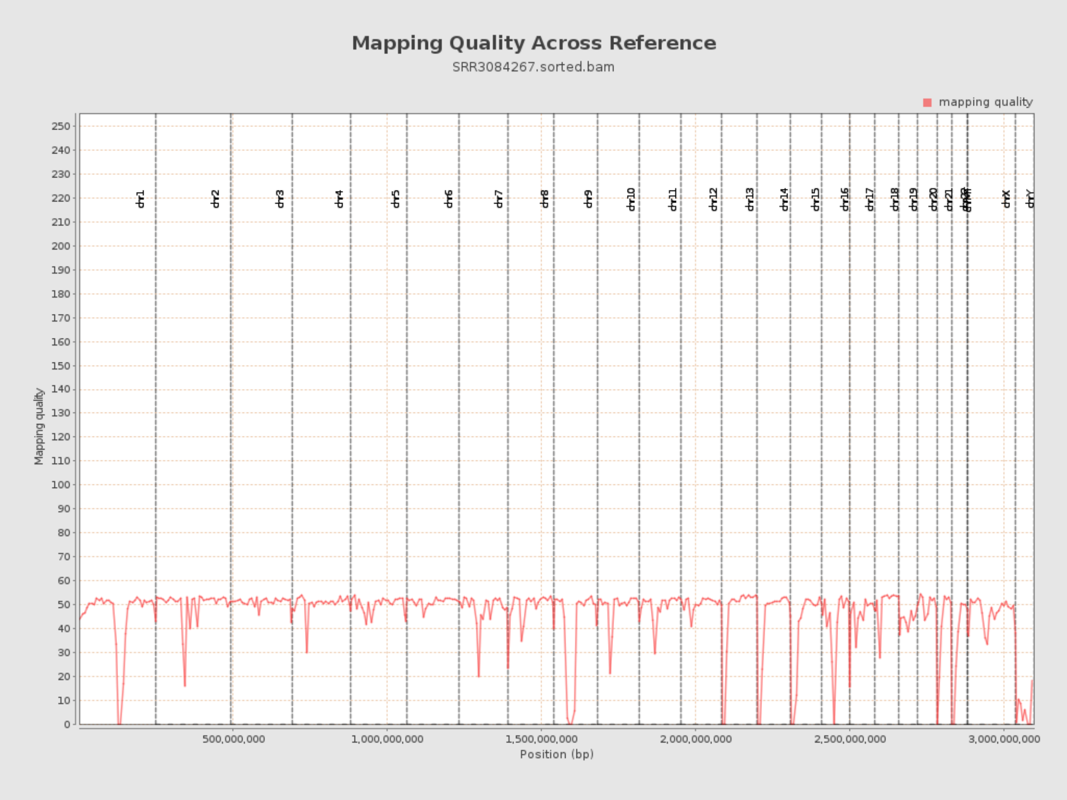
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram