Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:32:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083625.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_SRR3083625 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083625.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:32:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083625.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,744,402
Mapped reads	1,606,625 / 92.1%
Unmapped reads	137,777 / 7.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,920 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	75,396 / 4.32%
Duplication rate	3.6%
Clipped reads	662,331 / 37.97%

2.2. ACGT Content

Number/percentage of A's	30,054,614 / 27.76%
Number/percentage of C's	19,957,389 / 18.43%
Number/percentage of T's	34,438,178 / 31.81%
Number/percentage of G's	23,819,798 / 22%
Number/percentage of N's	5,447 / 0.01%
GC Percentage	40.43%

2.3. Coverage

Mean	0.035

Standard Deviation	0.4073

2.4. Mapping Quality

Mean Mapping Quality	46.34

2.5. Mismatches and indels

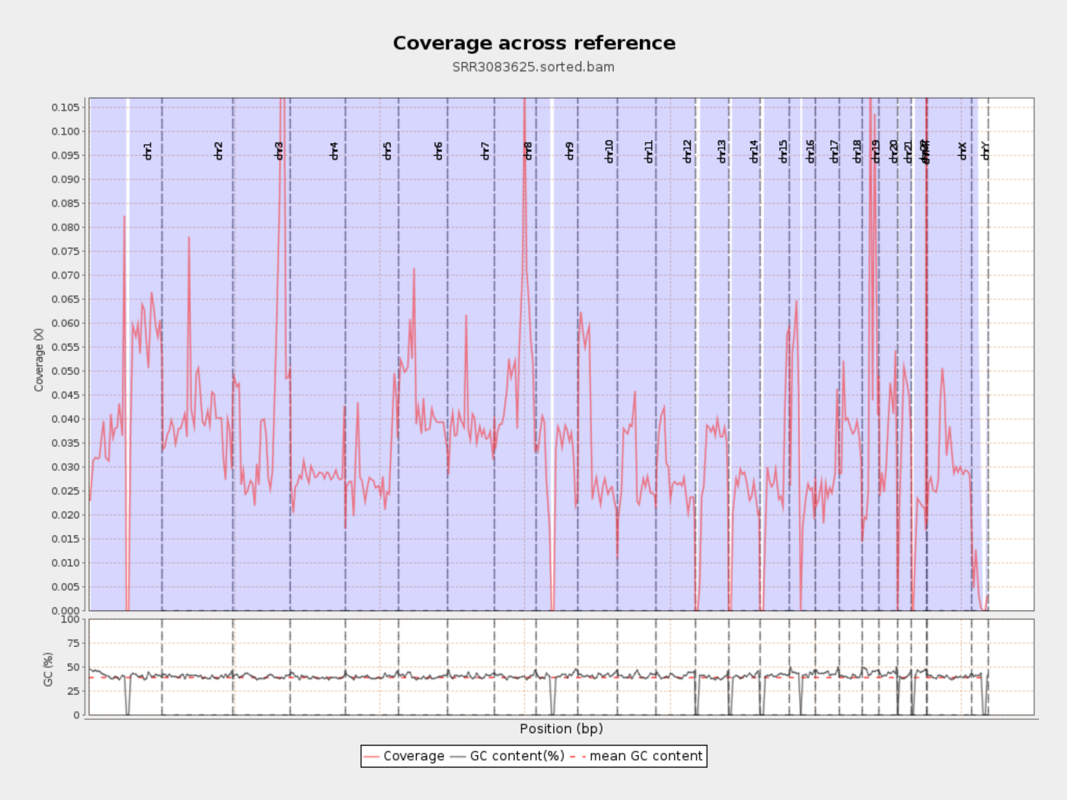
General error rate	0.73%
Mismatches	778,564
Insertions	8,524
Mapped reads with at least one insertion	0.53%
Deletions	25,887
Mapped reads with at least one deletion	1.59%
Homopolymer indels	48.46%

2.6. Chromosome stats

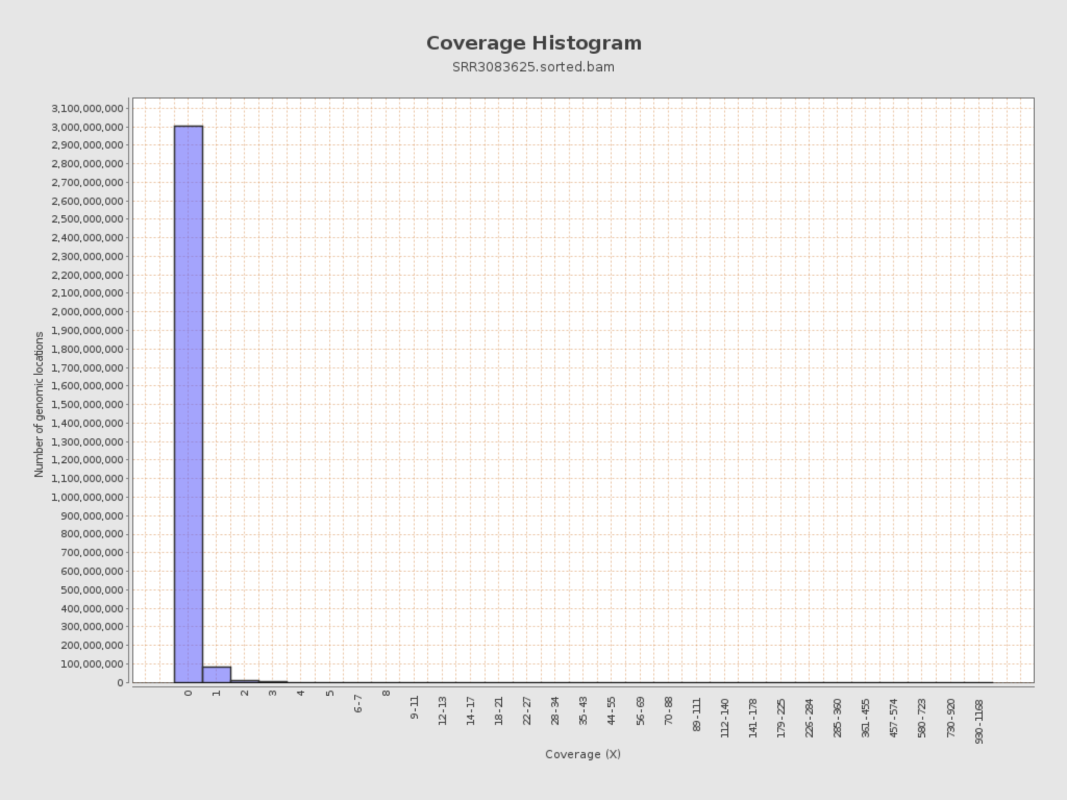
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11028692	0.0442	0.9989
chr2	243199373	9831969	0.0404	0.426
chr3	198022430	8910152	0.045	0.2407
chr4	191154276	5407748	0.0283	0.1945
chr5	180915260	5270323	0.0291	0.1934
chr6	171115067	7628588	0.0446	0.3051
chr7	159138663	6141213	0.0386	0.4464

chr8	146364022	7643510	0.0522	0.4885
chr9	141213431	4247297	0.0301	0.273
chr10	135534747	4885616	0.036	0.3065
chr11	135006516	3945545	0.0292	0.2587
chr12	133851895	3804601	0.0284	0.1909
chr13	115169878	3380369	0.0294	0.1931
chr14	107349540	2384768	0.0222	0.1748
chr15	102531392	2692776	0.0263	0.1873
chr16	90354753	2932960	0.0325	0.2182
chr17	81195210	2215168	0.0273	0.2033
chr18	78077248	2962713	0.0379	0.539
chr19	59128983	3019426	0.0511	0.5773
chr20	63025520	2299477	0.0365	0.218
chr21	48129895	1751066	0.0364	0.2171
chr22	51304566	817189	0.0159	0.1395
chrMT	16571	4687	0.2828	0.6258
chrX	155270560	4875006	0.0314	0.2149
chrY	59373566	236574	0.004	0.0999

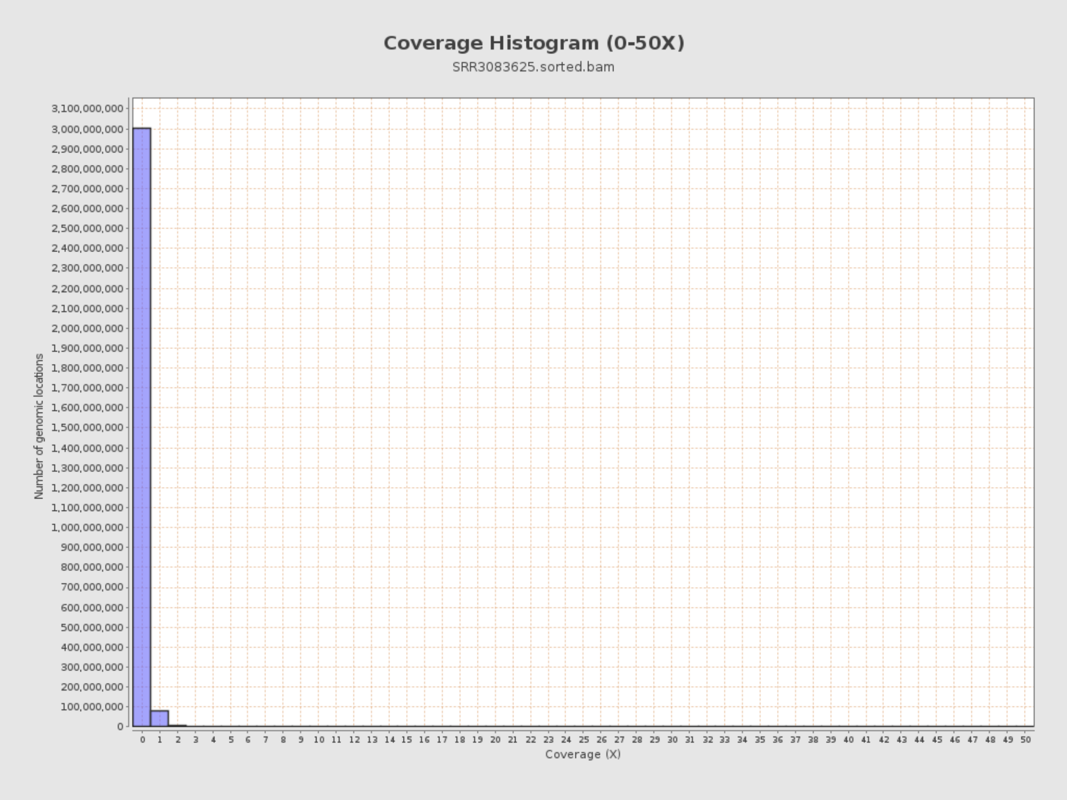
3. Results : Coverage across reference



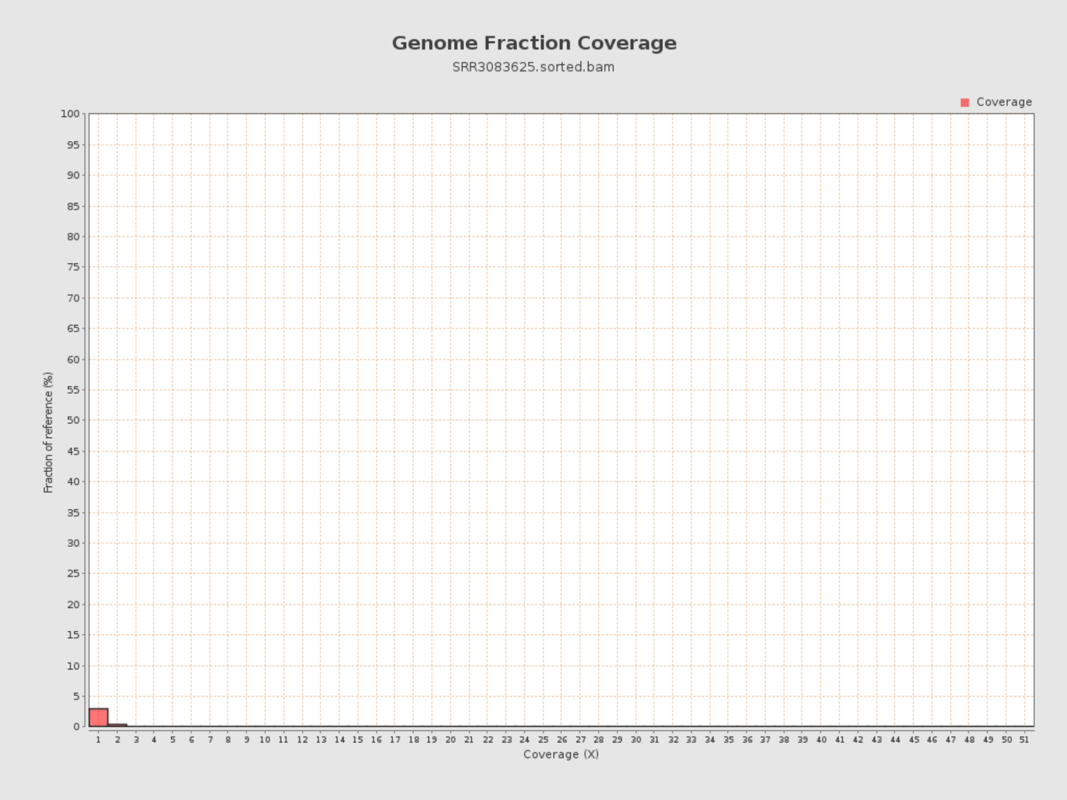
4. Results : Coverage Histogram



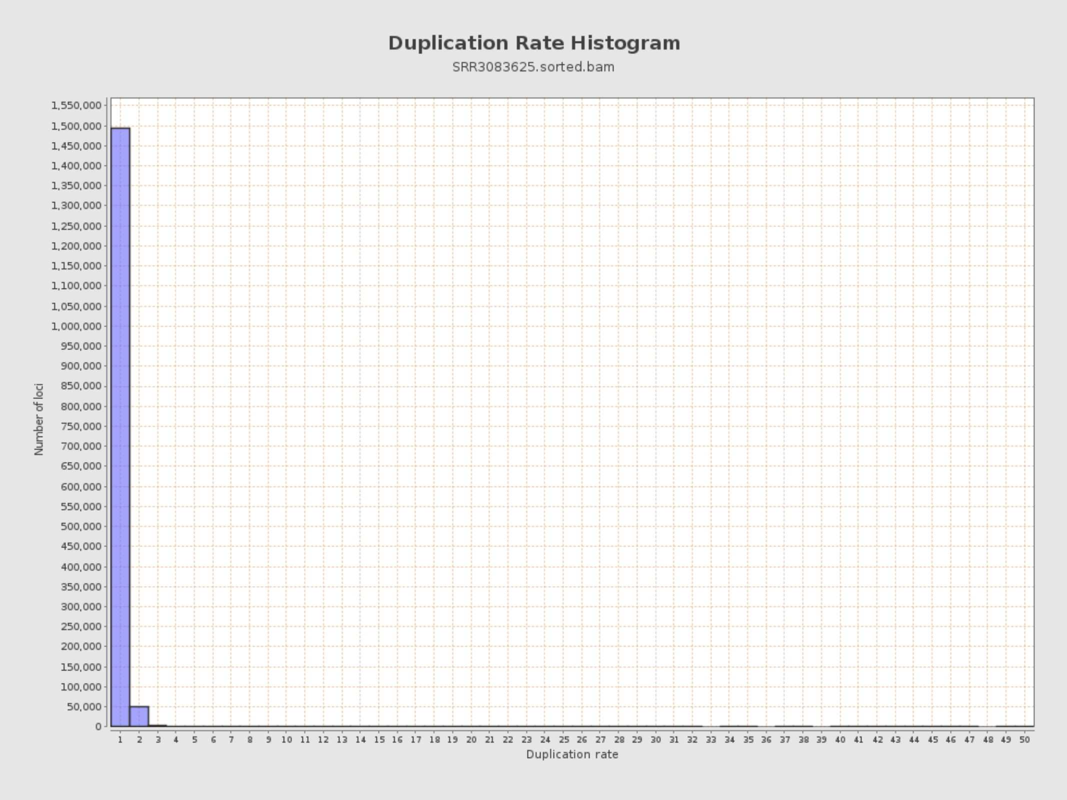
5. Results : Coverage Histogram (0-50X)



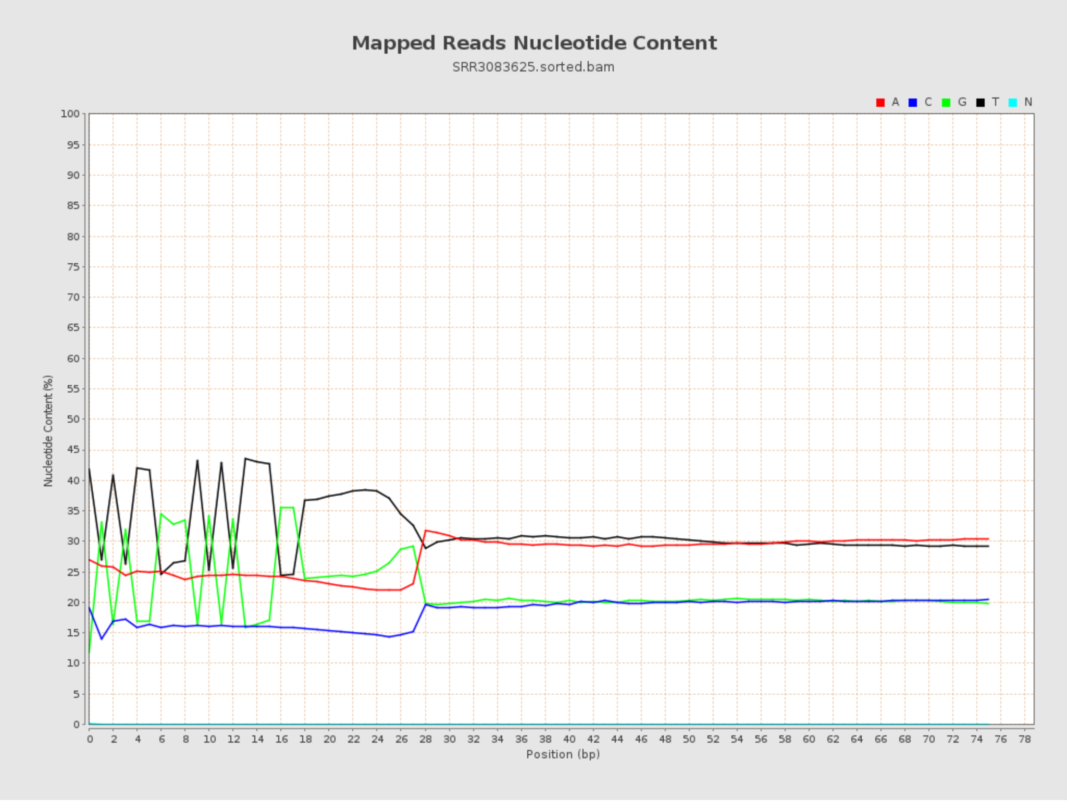
6. Results : Genome Fraction Coverage



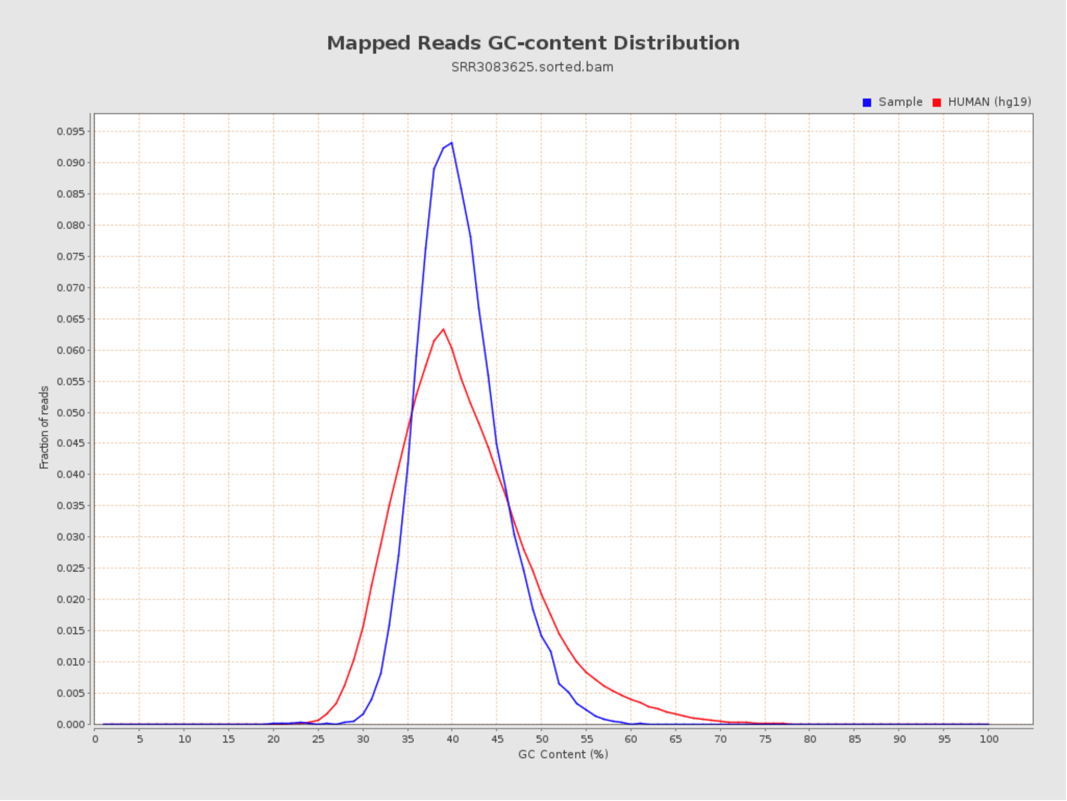
7. Results : Duplication Rate Histogram



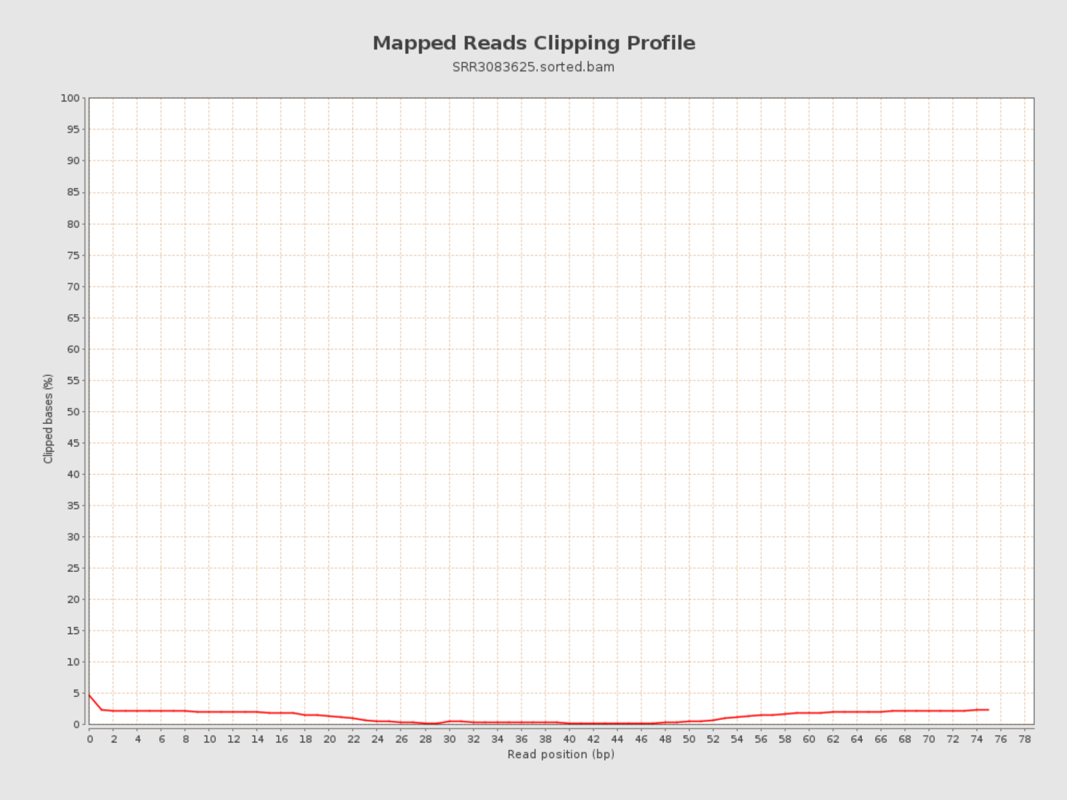
8. Results : Mapped Reads Nucleotide Content



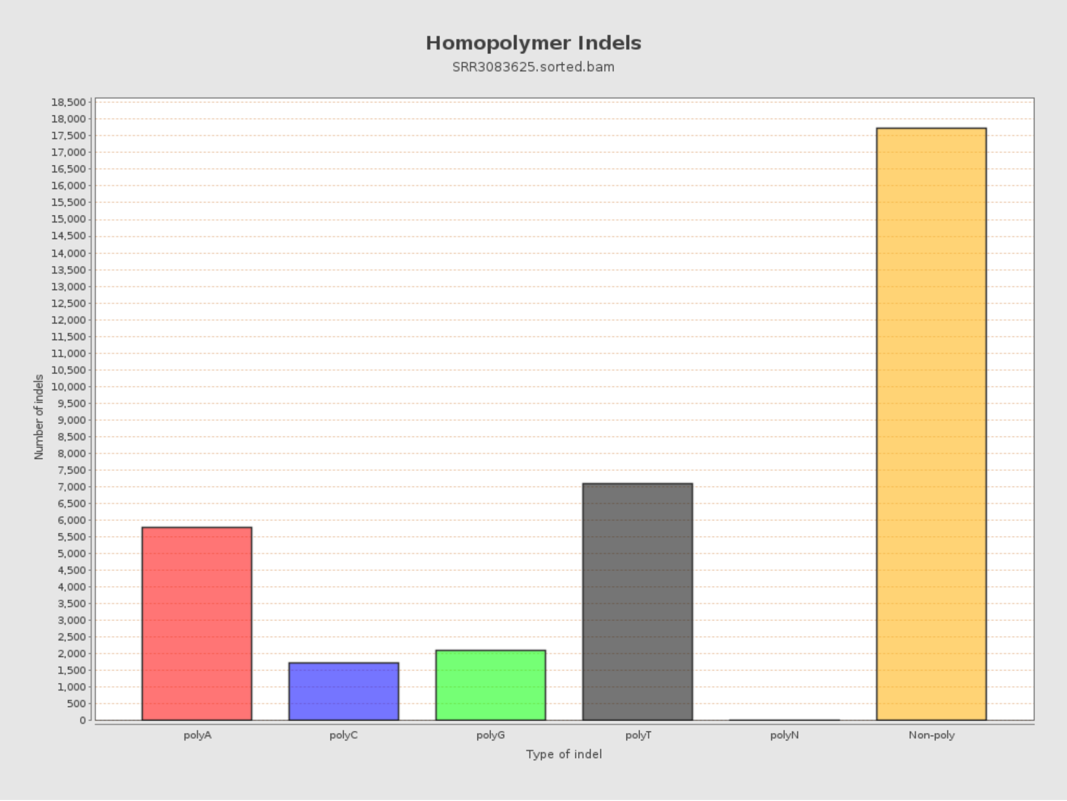
9. Results : Mapped Reads GC-content Distribution



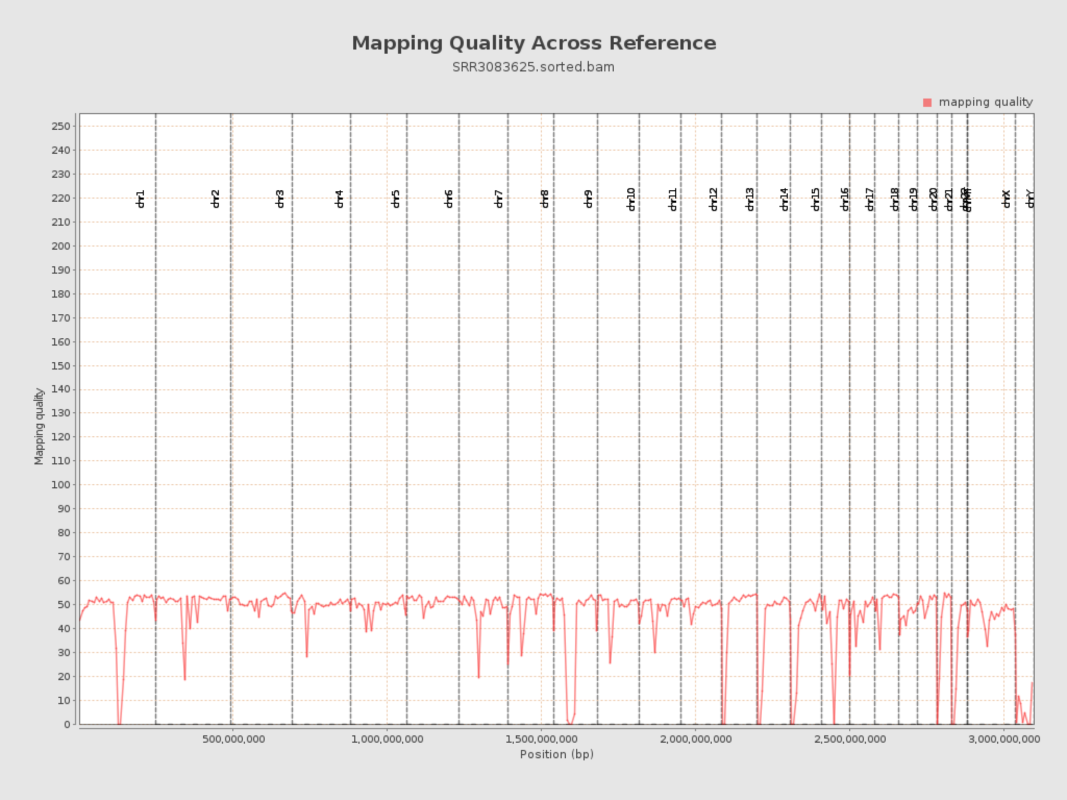
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram