Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:54:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083644.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_SRR3083644 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083644.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:54:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083644.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,502,198
Mapped reads	1,228,177 / 81.76%
Unmapped reads	274,021 / 18.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,865 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	29,755 / 1.98%
Duplication rate	1.99%
Clipped reads	793,173 / 52.8%

2.2. ACGT Content

Number/percentage of A's	22,457,645 / 29.74%
Number/percentage of C's	14,342,768 / 18.99%
Number/percentage of T's	22,265,348 / 29.48%
Number/percentage of G's	16,449,725 / 21.78%
Number/percentage of N's	10,074 / 0.01%
GC Percentage	40.77%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.216

2.4. Mapping Quality

Mean Mapping Quality	45.55

2.5. Mismatches and indels

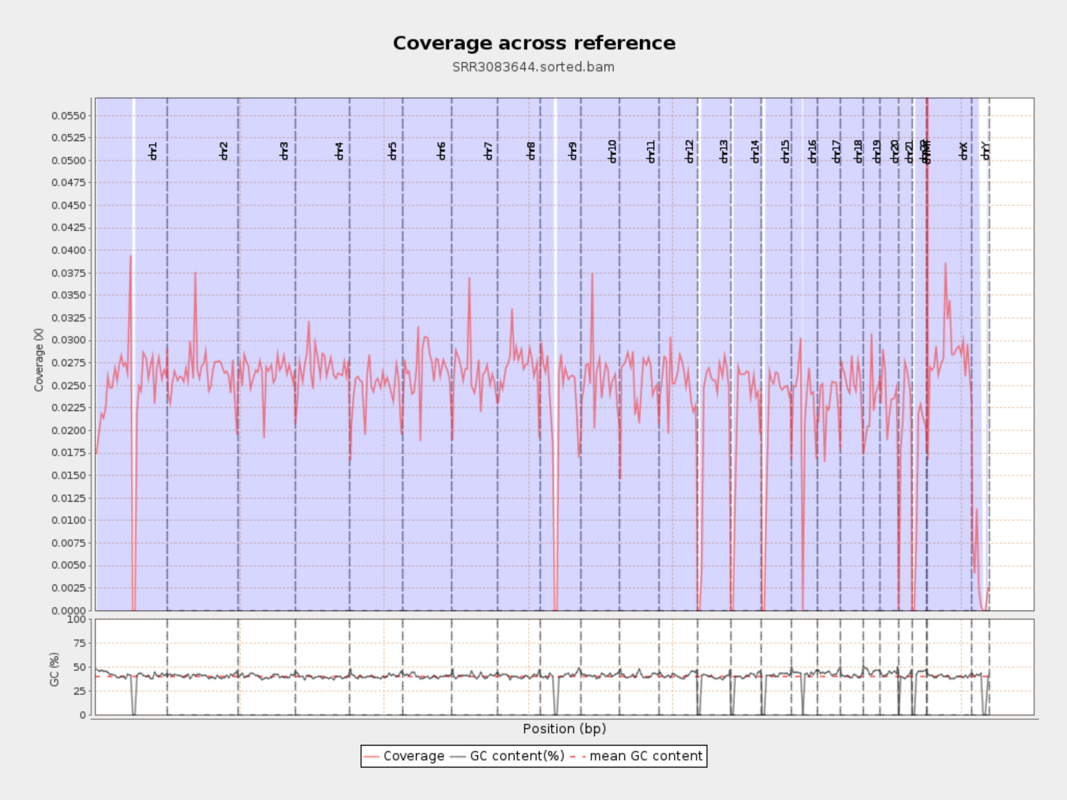
General error rate	0.9%
Mismatches	669,837
Insertions	5,821
Mapped reads with at least one insertion	0.47%
Deletions	17,155
Mapped reads with at least one deletion	1.38%
Homopolymer indels	45.58%

2.6. Chromosome stats

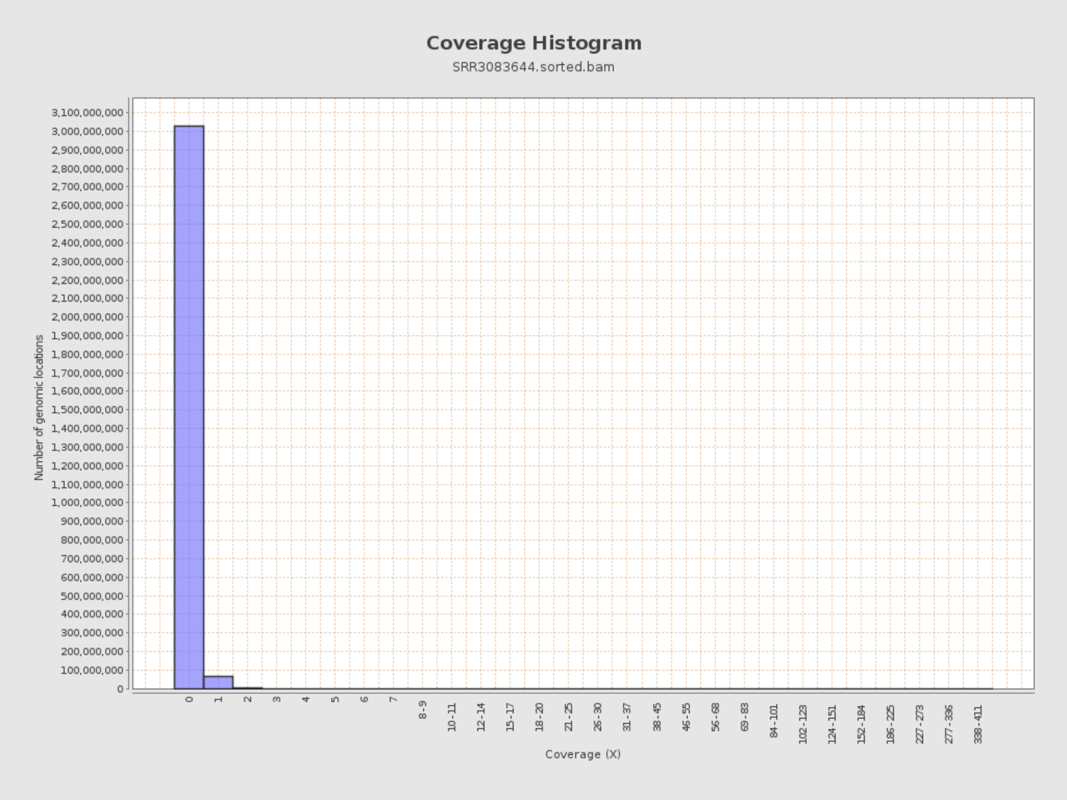
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6029647	0.0242	0.3822
chr2	243199373	6437416	0.0265	0.207
chr3	198022430	5226071	0.0264	0.1705
chr4	191154276	5127567	0.0268	0.1774
chr5	180915260	4476547	0.0247	0.1657
chr6	171115067	4571147	0.0267	0.1844
chr7	159138663	4188176	0.0263	0.2506

chr8	146364022	3970055	0.0271	0.2839
chr9	141213431	3173075	0.0225	0.1871
chr10	135534747	3502582	0.0258	0.2142
chr11	135006516	3467314	0.0257	0.1808
chr12	133851895	3404479	0.0254	0.1692
chr13	115169878	2486702	0.0216	0.1539
chr14	107349540	2258078	0.021	0.1595
chr15	102531392	2122130	0.0207	0.1516
chr16	90354753	1973885	0.0218	0.164
chr17	81195210	1854550	0.0228	0.1672
chr18	78077248	2011802	0.0258	0.2921
chr19	59128983	1357615	0.023	0.2889
chr20	63025520	1484895	0.0236	0.1647
chr21	48129895	1015823	0.0211	0.1584
chr22	51304566	771571	0.015	0.1286
chrMT	16571	6439	0.3886	0.6725
chrX	155270560	4434912	0.0286	0.1884
chrY	59373566	200604	0.0034	0.0903

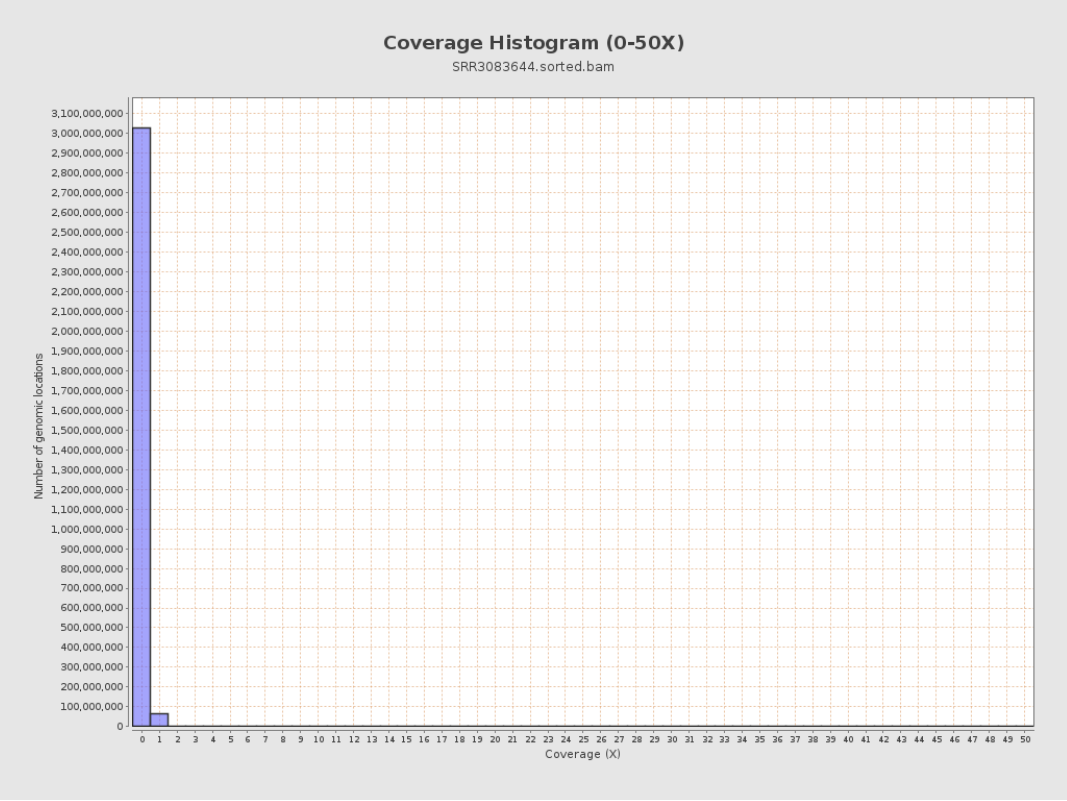
3. Results : Coverage across reference



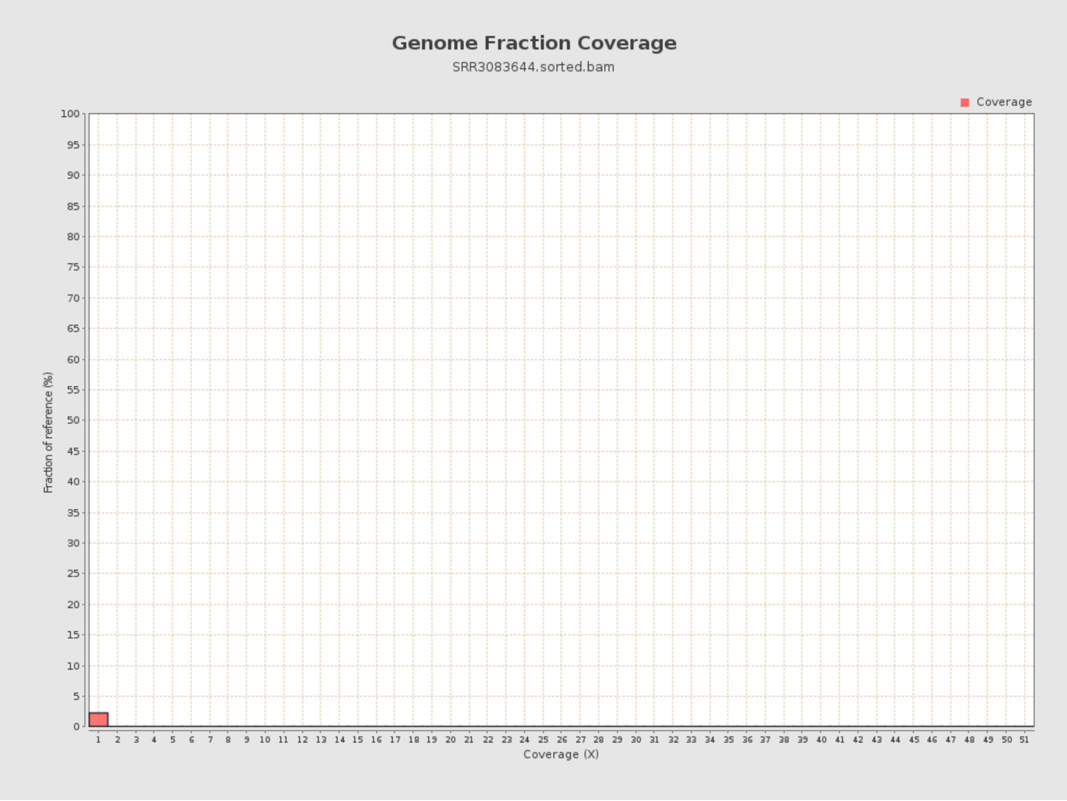
4. Results : Coverage Histogram



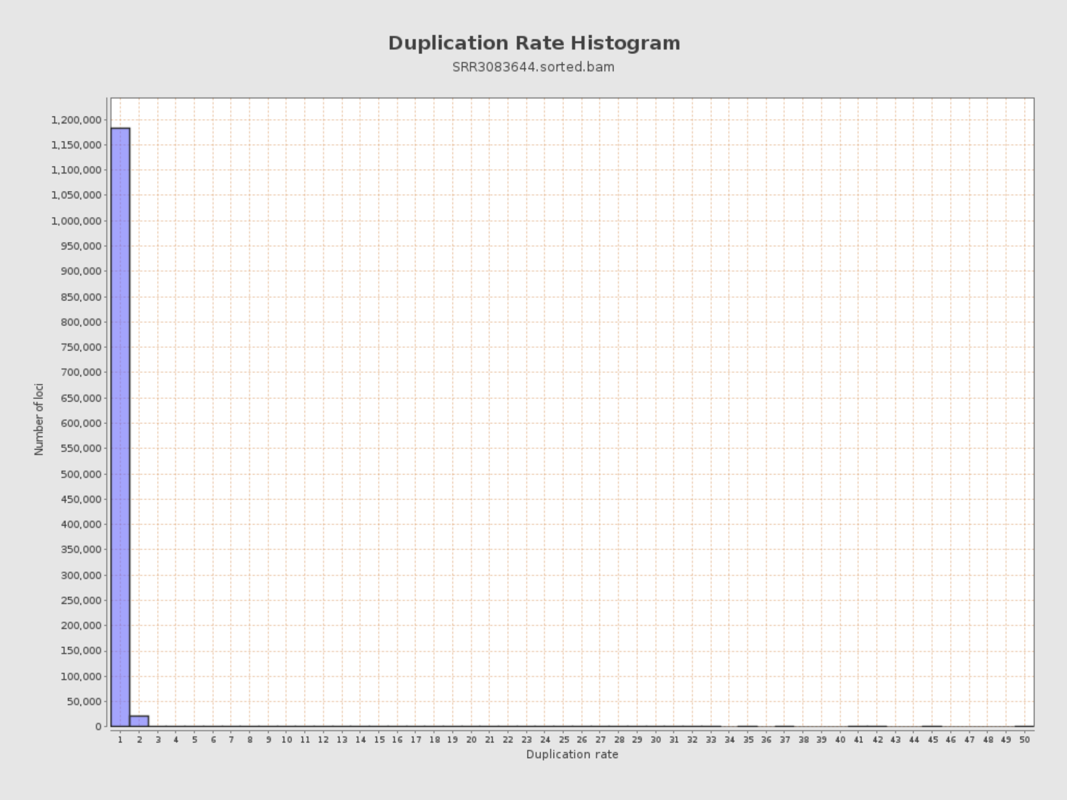
5. Results : Coverage Histogram (0-50X)



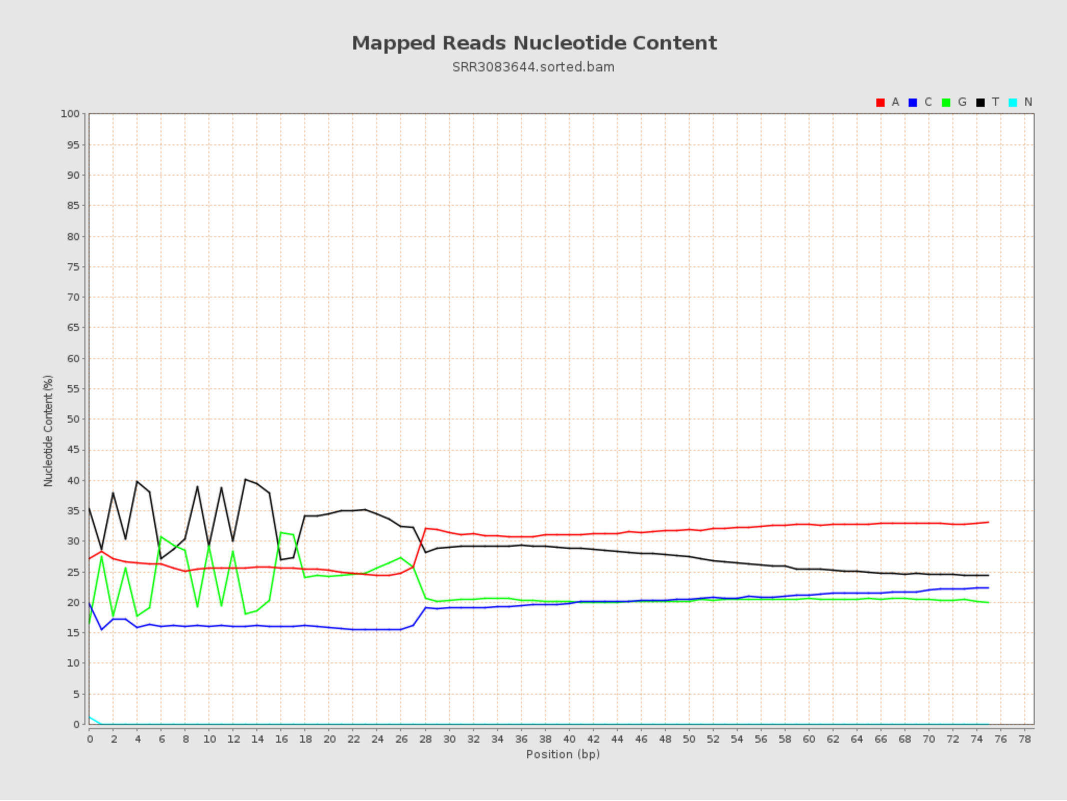
6. Results : Genome Fraction Coverage



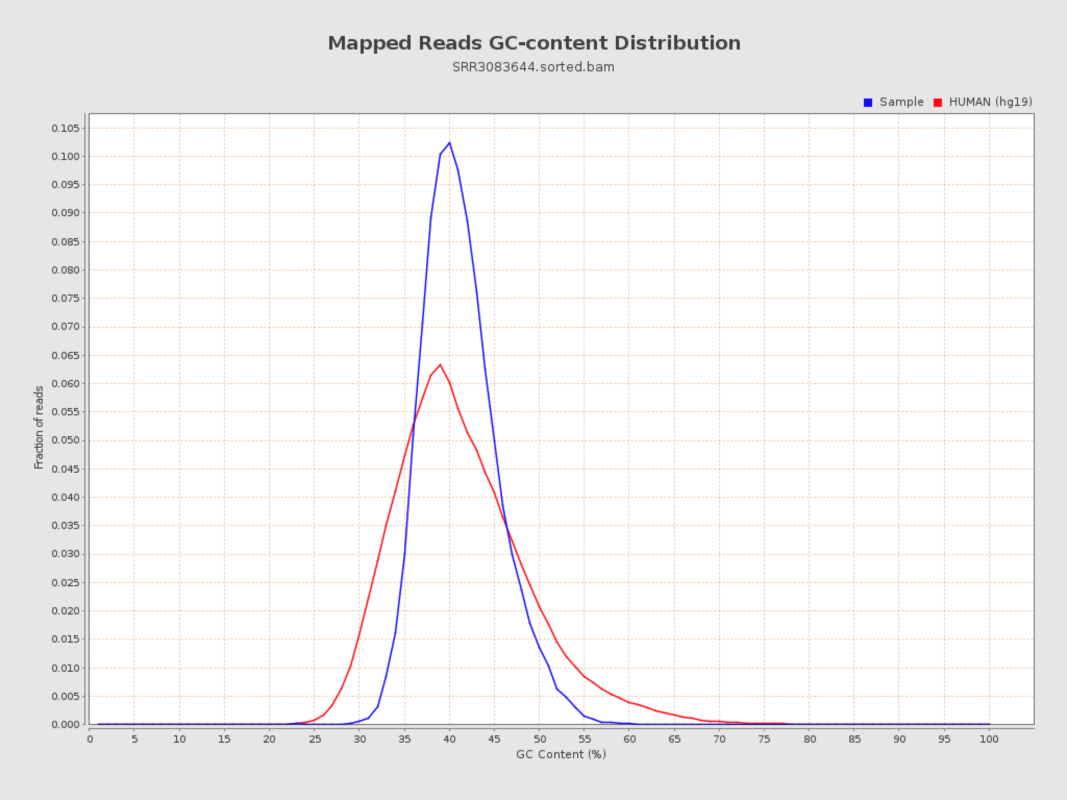
7. Results : Duplication Rate Histogram



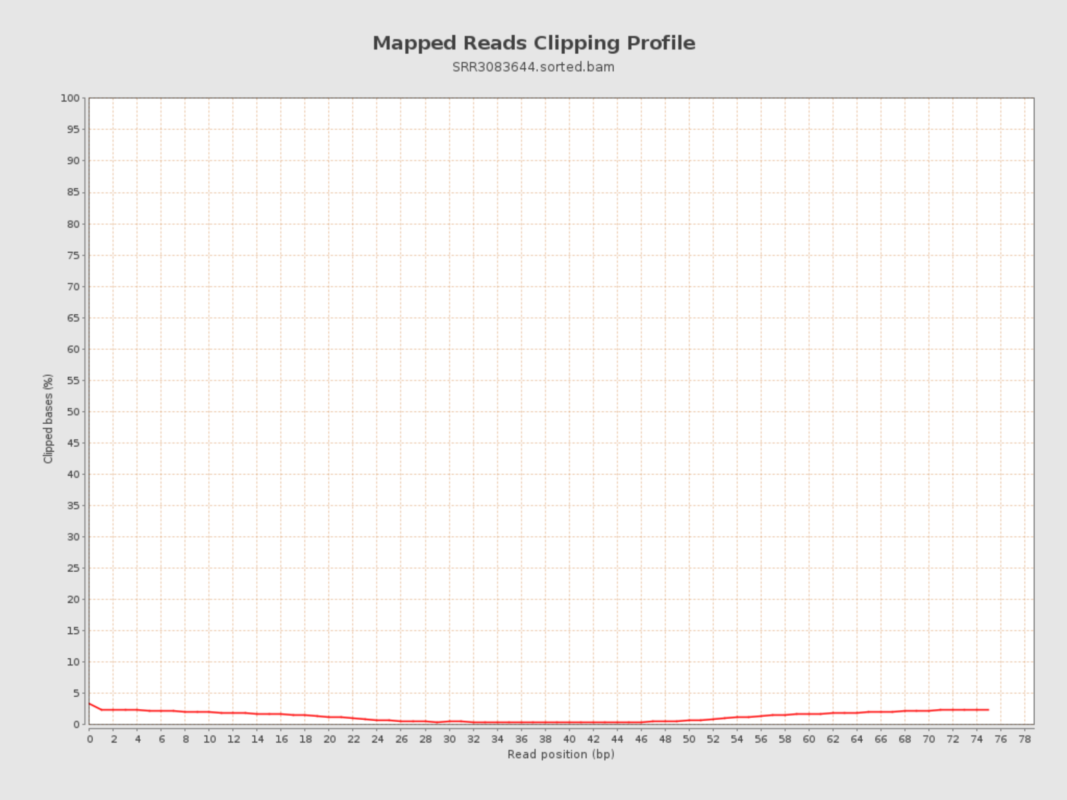
8. Results : Mapped Reads Nucleotide Content



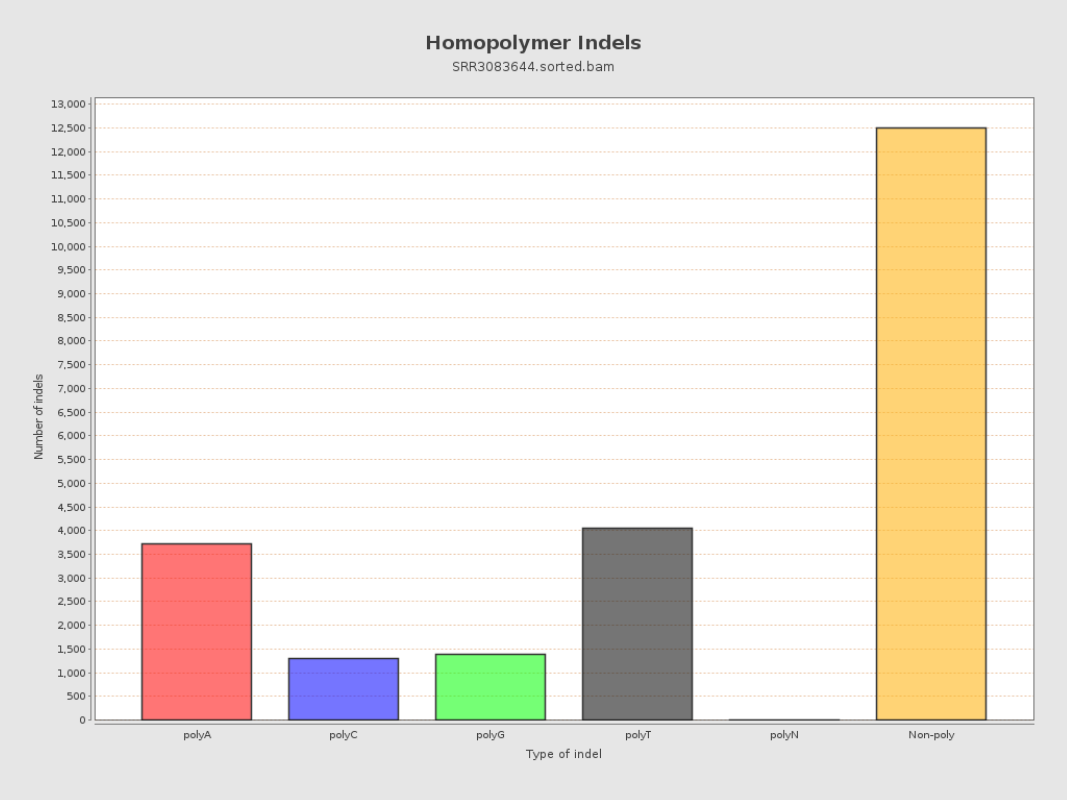
9. Results : Mapped Reads GC-content Distribution



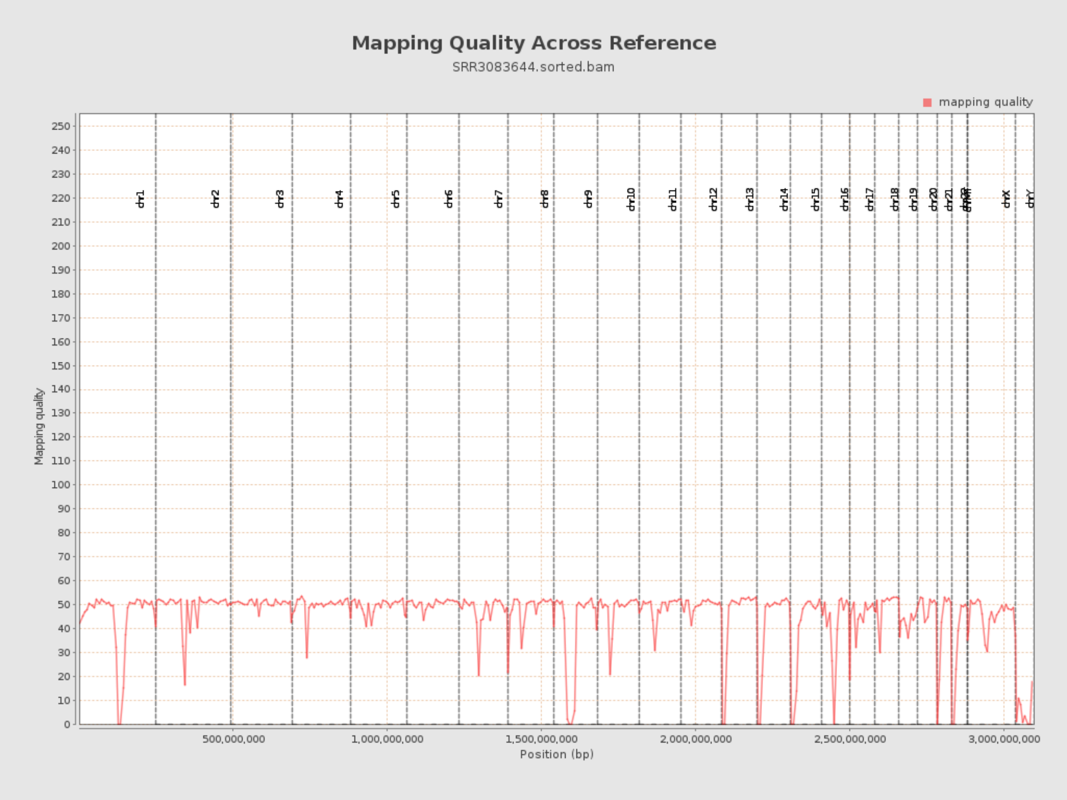
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram