Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:31:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524758.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_SRR10524758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524758.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:31:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,528,145
Mapped reads	1,386,911 / 90.76%
Unmapped reads	141,234 / 9.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,415 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	47,415 / 3.1%
Duplication rate	2.59%
Clipped reads	1,388,478 / 90.86%

2.2. ACGT Content

Number/percentage of A's	18,921,915 / 23.89%
Number/percentage of C's	14,743,396 / 18.62%
Number/percentage of T's	25,452,450 / 32.14%
Number/percentage of G's	20,067,031 / 25.34%
Number/percentage of N's	9,387 / 0.01%
GC Percentage	43.96%

2.3. Coverage

Mean	0.0256

Standard Deviation	0.2246

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Mismatches and indels

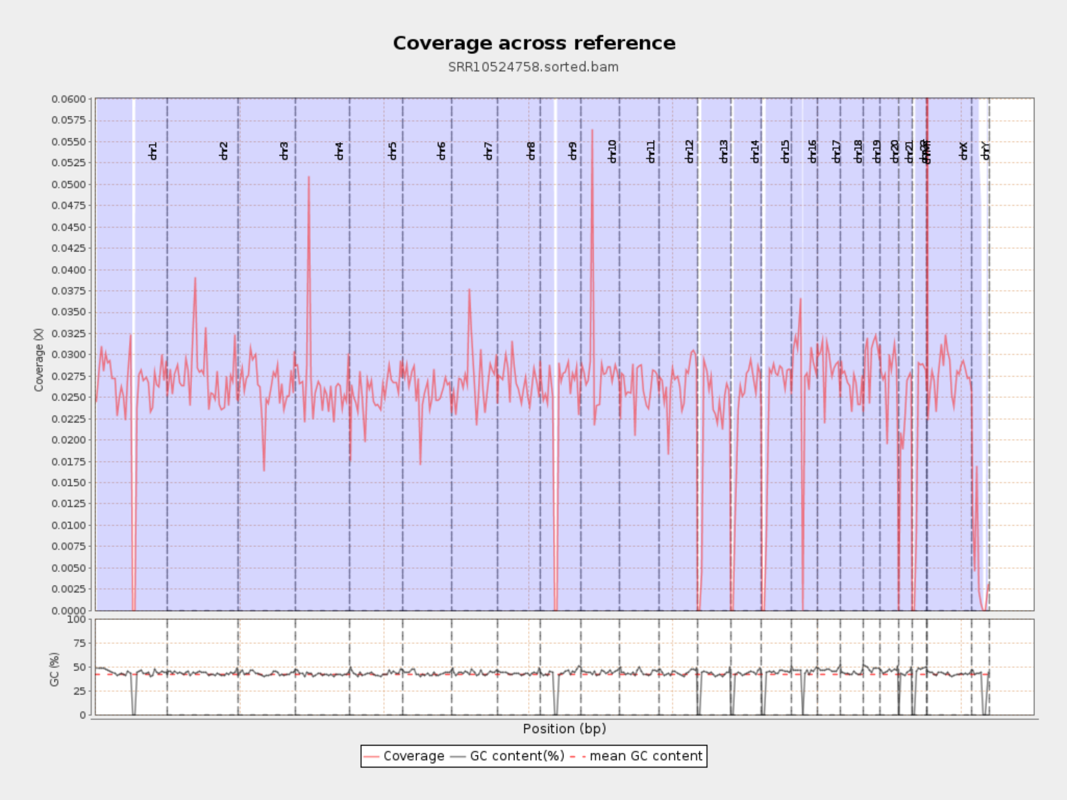
General error rate	0.52%
Mismatches	400,786
Insertions	5,530
Mapped reads with at least one insertion	0.4%
Deletions	15,079
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.6%

2.6. Chromosome stats

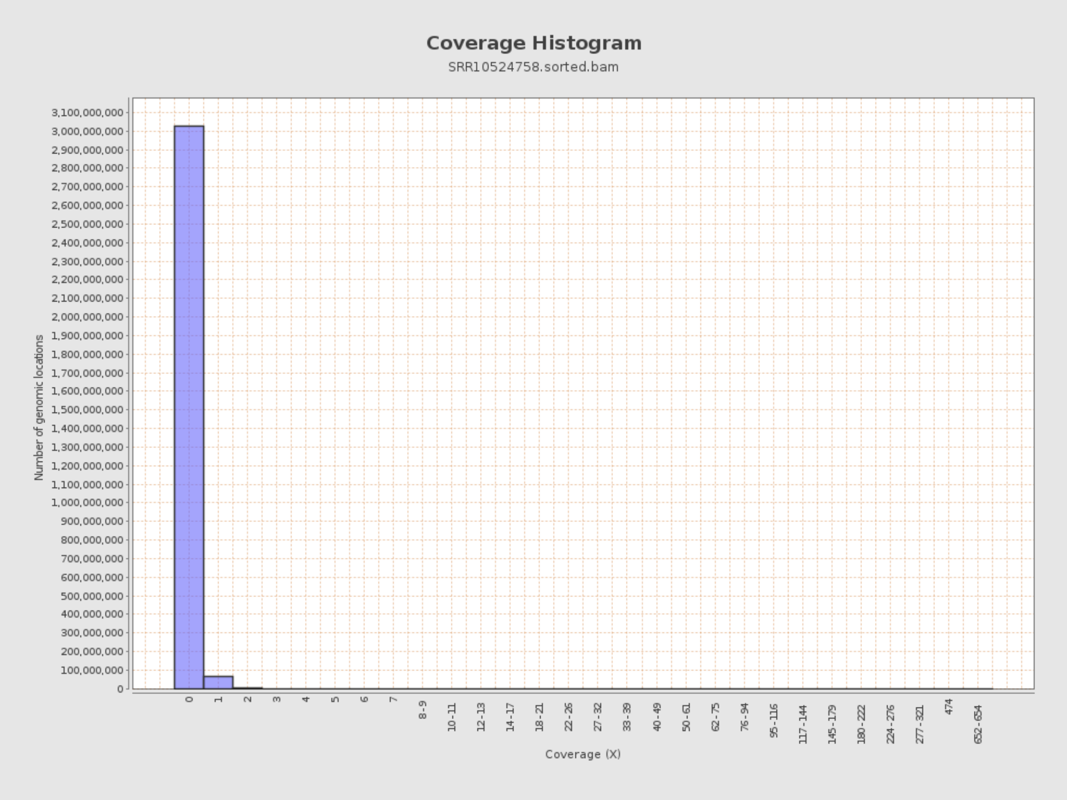
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6322976	0.0254	0.2729
chr2	243199373	6682356	0.0275	0.3448
chr3	198022430	5202397	0.0263	0.1792
chr4	191154276	5124536	0.0268	0.2097
chr5	180915260	4653532	0.0257	0.1752
chr6	171115067	4429310	0.0259	0.1897
chr7	159138663	4348036	0.0273	0.2656

chr8	146364022	3936318	0.0269	0.2024
chr9	141213431	3366605	0.0238	0.1995
chr10	135534747	3909635	0.0288	0.2896
chr11	135006516	3567123	0.0264	0.2051
chr12	133851895	3573670	0.0267	0.1803
chr13	115169878	2423423	0.021	0.1593
chr14	107349540	2390342	0.0223	0.1671
chr15	102531392	2316794	0.0226	0.1662
chr16	90354753	2451270	0.0271	0.2042
chr17	81195210	2335822	0.0288	0.1931
chr18	78077248	2059570	0.0264	0.294
chr19	59128983	1767849	0.0299	0.2392
chr20	63025520	1712965	0.0272	0.1898
chr21	48129895	1040865	0.0216	0.1844
chr22	51304566	1009579	0.0197	0.1546
chrMT	16571	25050	1.5117	1.4466
chrX	155270560	4294486	0.0277	0.1941
chrY	59373566	274551	0.0046	0.1407

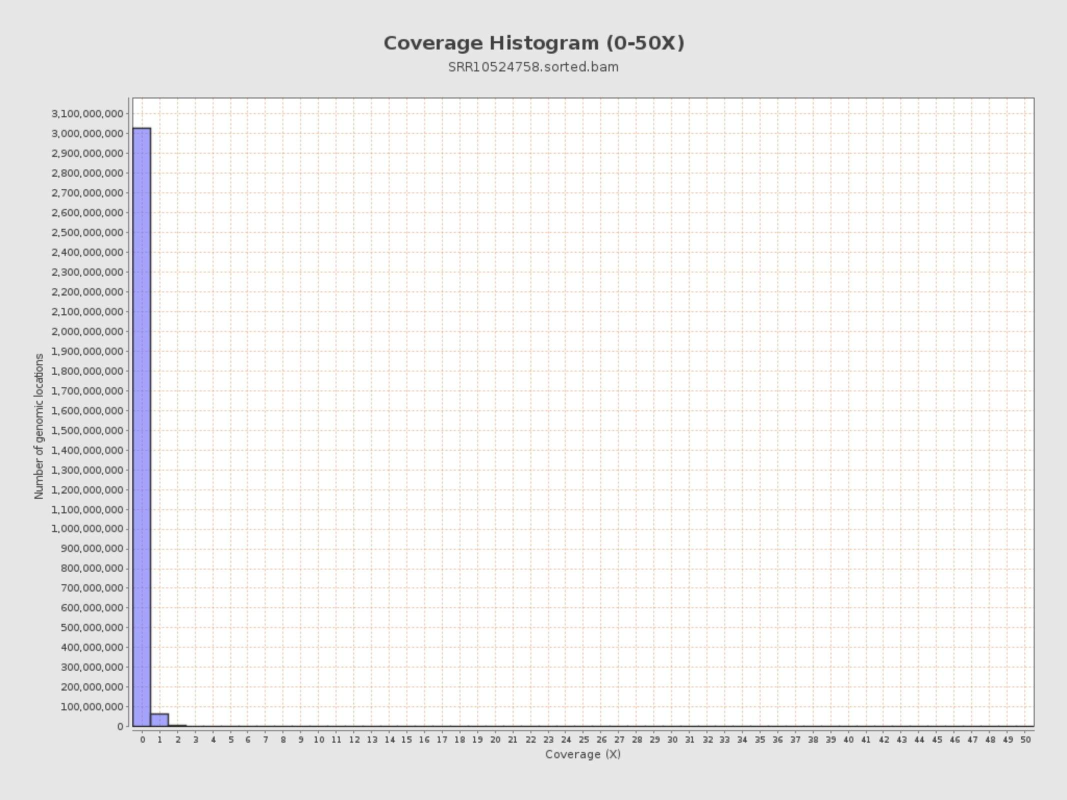
3. Results : Coverage across reference



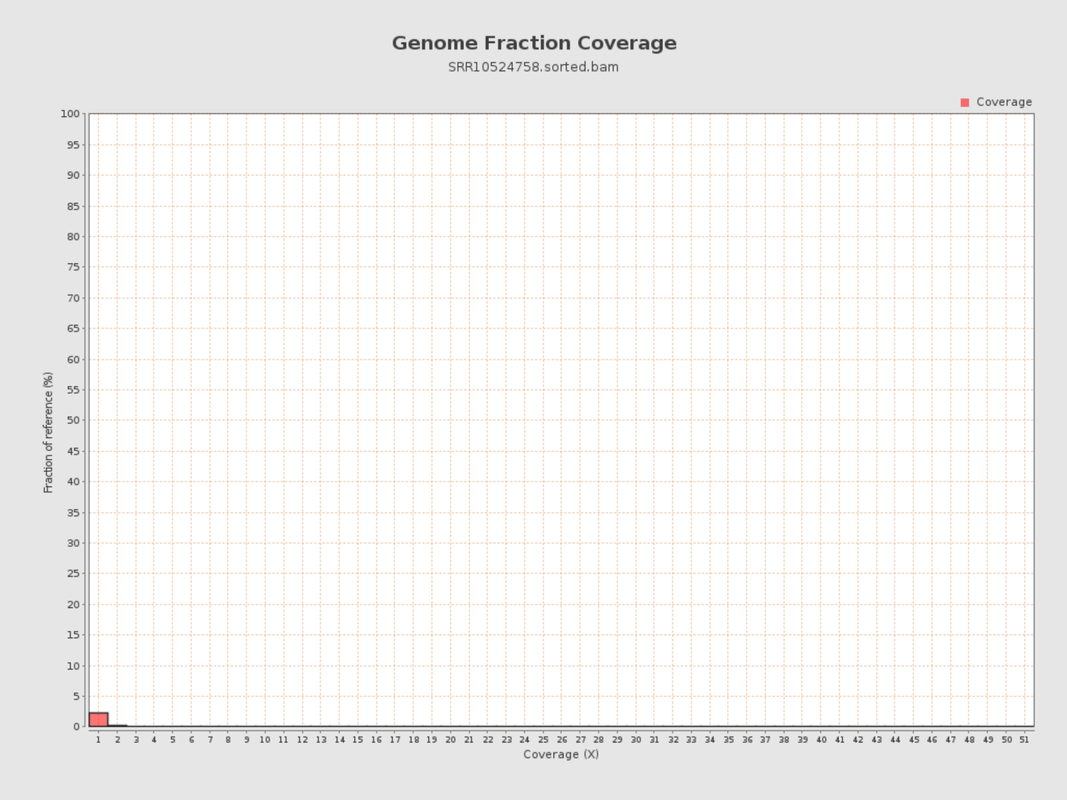
4. Results : Coverage Histogram



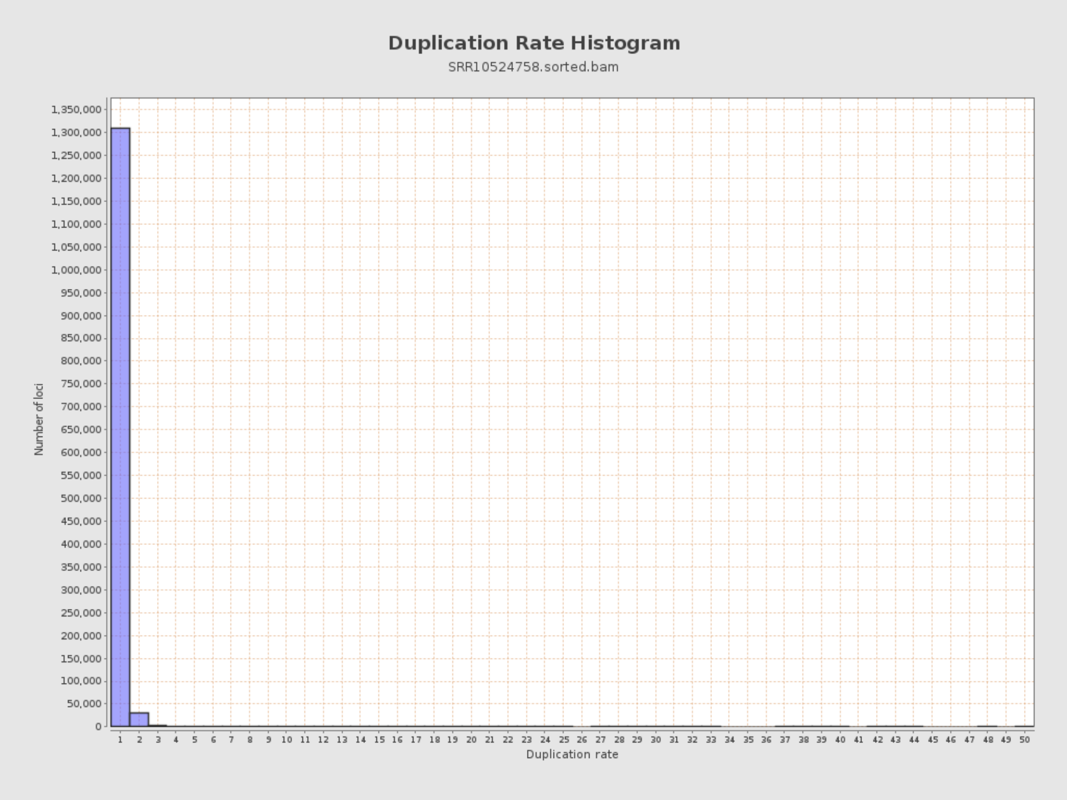
5. Results : Coverage Histogram (0-50X)



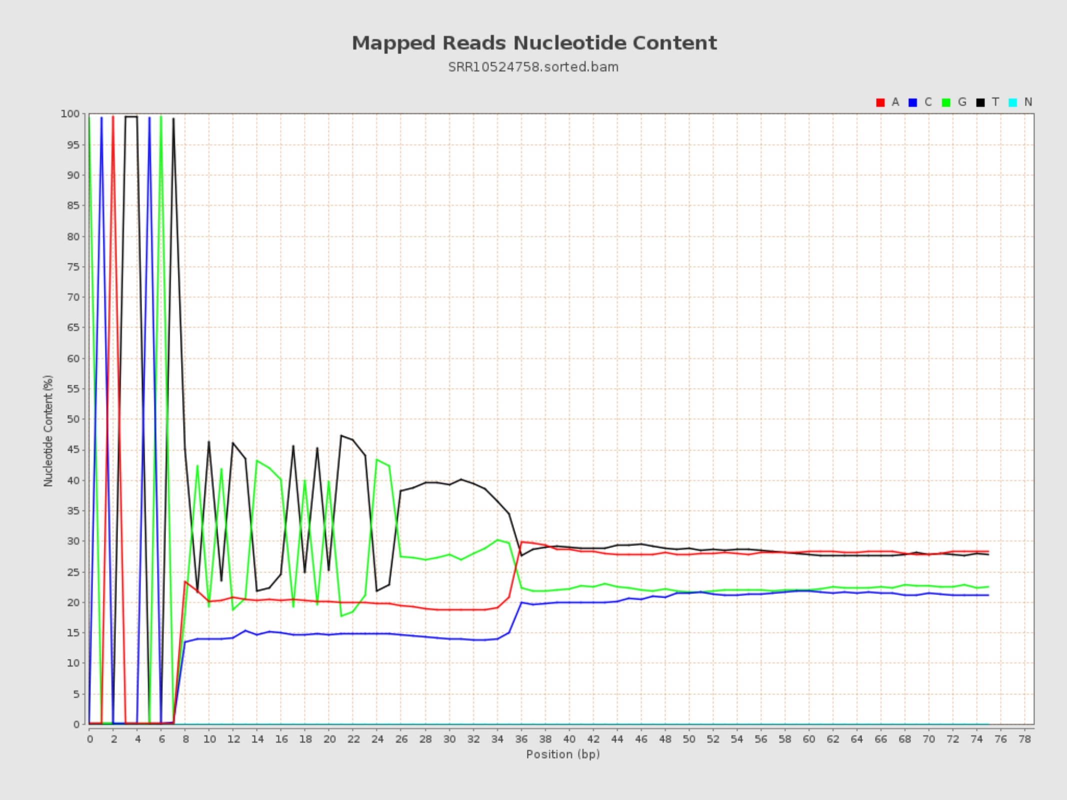
6. Results : Genome Fraction Coverage



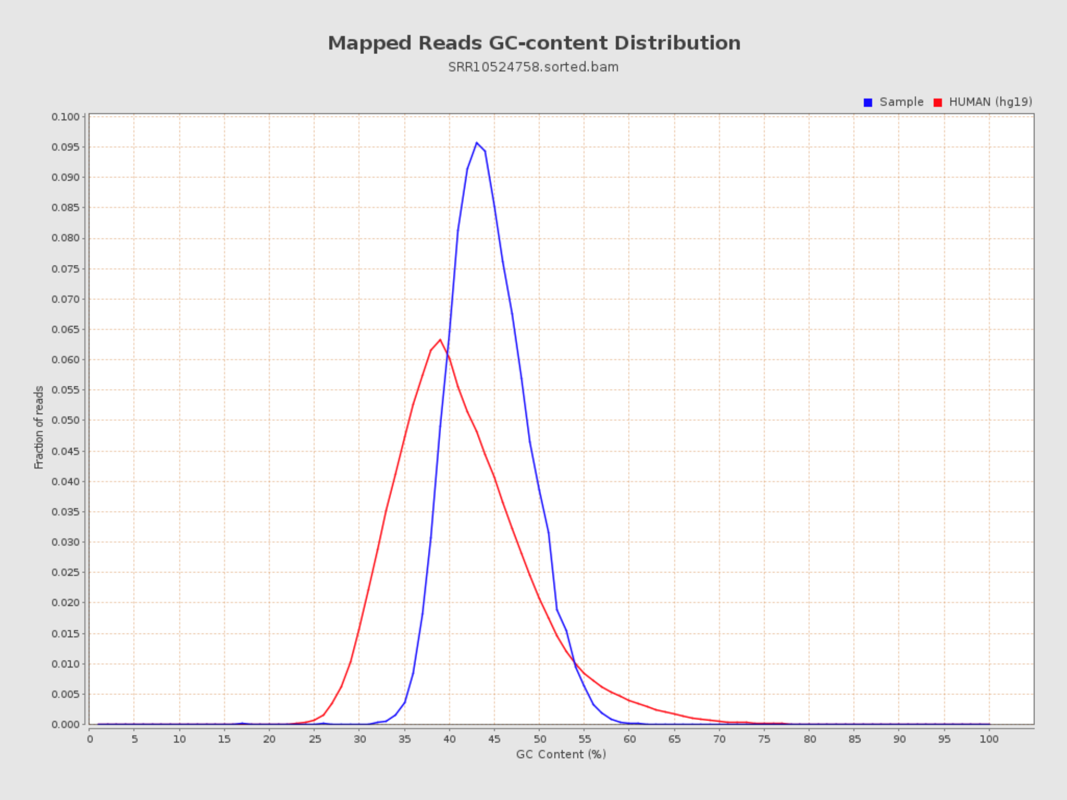
7. Results : Duplication Rate Histogram



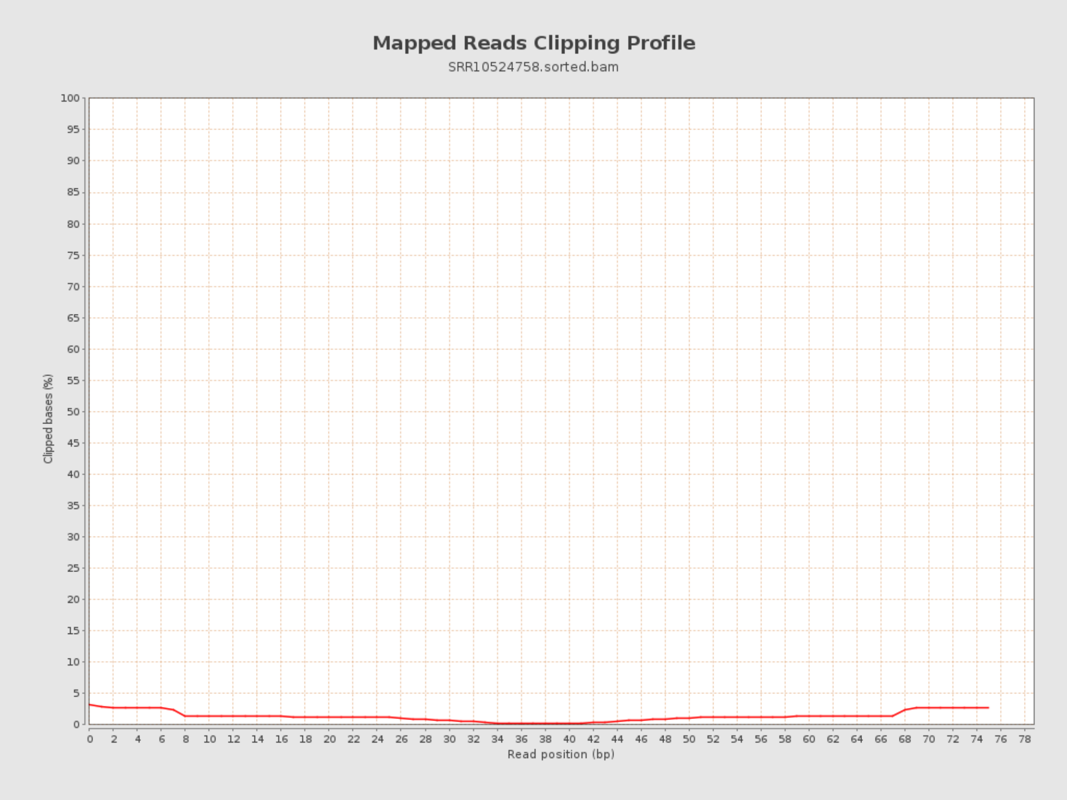
8. Results : Mapped Reads Nucleotide Content



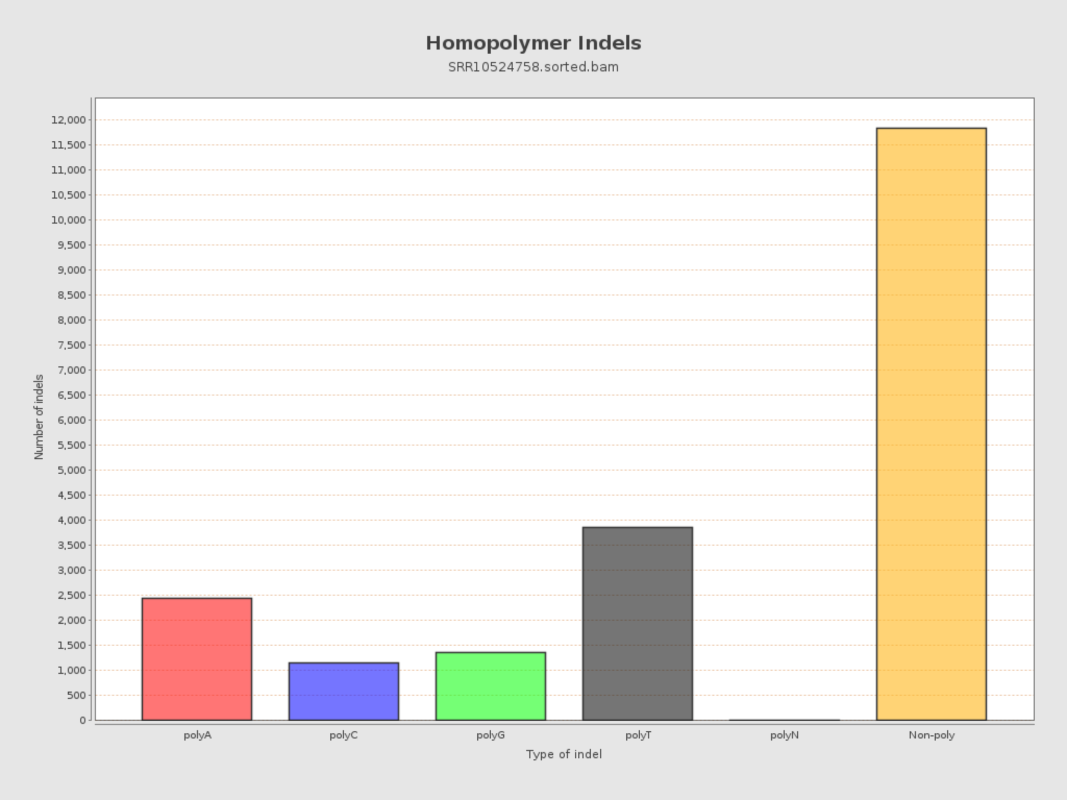
9. Results : Mapped Reads GC-content Distribution



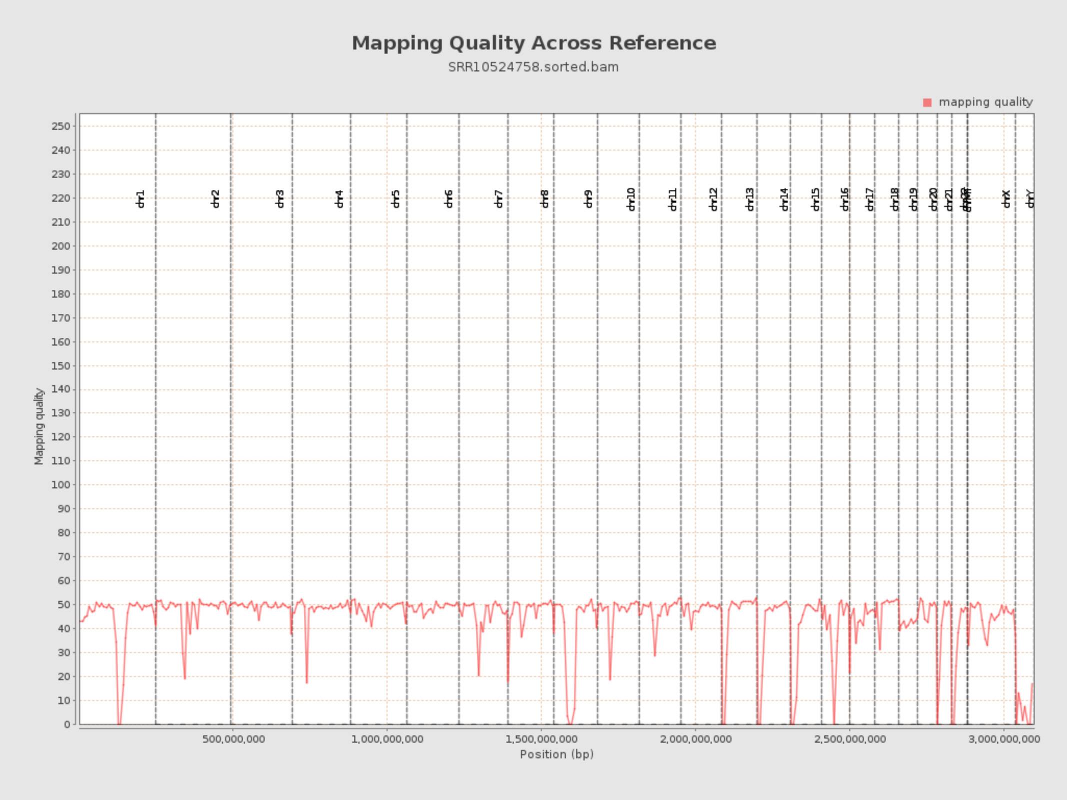
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram