Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:47:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524586.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_SRR10524586 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524586.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:47:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524586.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,803,658
Mapped reads	1,627,878 / 90.25%
Unmapped reads	175,780 / 9.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,168 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	58,699 / 3.25%
Duplication rate	2.62%
Clipped reads	1,628,101 / 90.27%

2.2. ACGT Content

Number/percentage of A's	23,398,643 / 25.09%
Number/percentage of C's	17,405,490 / 18.66%
Number/percentage of T's	29,949,582 / 32.12%
Number/percentage of G's	22,502,067 / 24.13%
Number/percentage of N's	1,297 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.2721

2.4. Mapping Quality

Mean Mapping Quality	43.82

2.5. Mismatches and indels

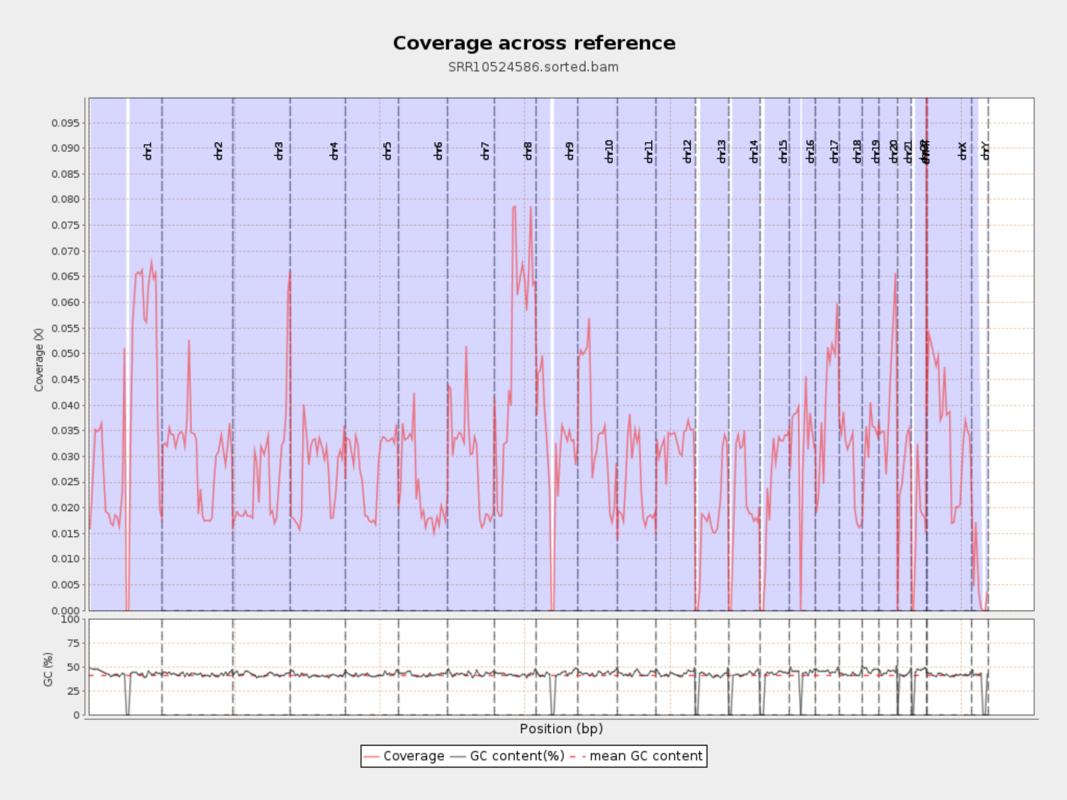
General error rate	0.53%
Mismatches	477,883
Insertions	7,269
Mapped reads with at least one insertion	0.44%
Deletions	17,631
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.94%

2.6. Chromosome stats

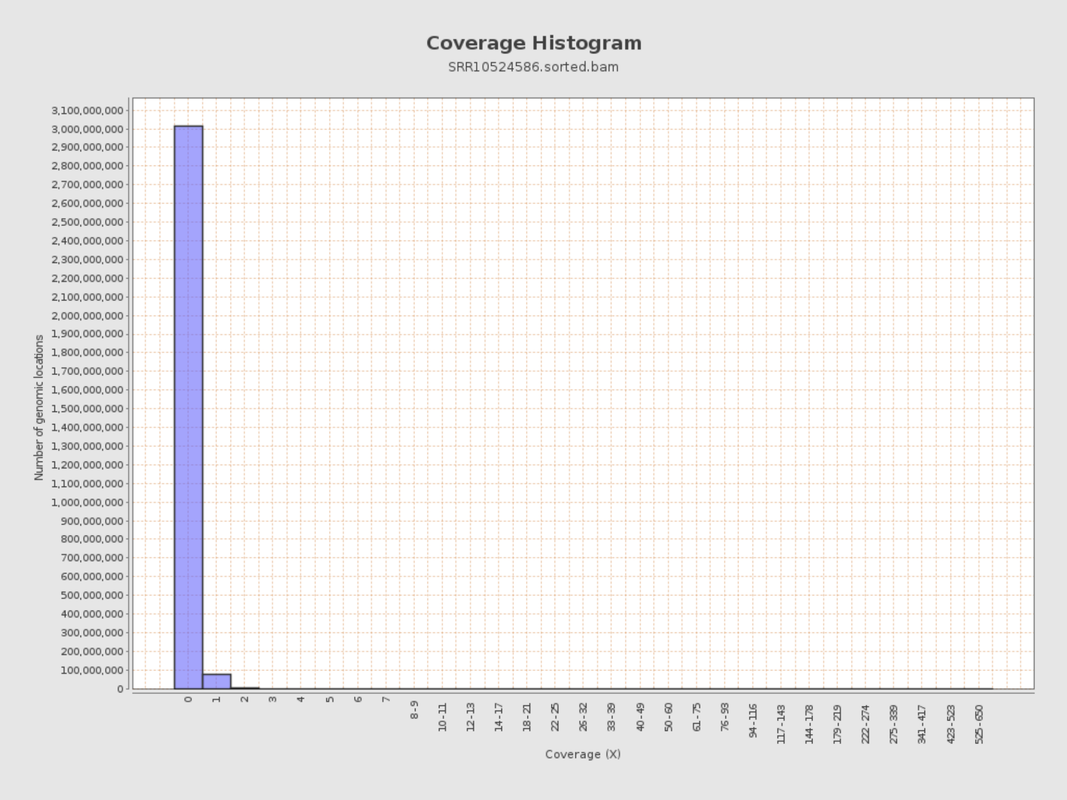
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9276977	0.0372	0.4788
chr2	243199373	7374617	0.0303	0.3211
chr3	198022430	5119502	0.0259	0.1783
chr4	191154276	5171288	0.0271	0.2041
chr5	180915260	5111780	0.0283	0.1852
chr6	171115067	4037360	0.0236	0.2111
chr7	159138663	4706533	0.0296	0.3397

chr8	146364022	7584298	0.0518	0.2899
chr9	141213431	4387109	0.0311	0.2469
chr10	135534747	4866086	0.0359	0.2884
chr11	135006516	3272348	0.0242	0.2621
chr12	133851895	4403676	0.0329	0.1992
chr13	115169878	2072512	0.018	0.1464
chr14	107349540	2251670	0.021	0.1633
chr15	102531392	2479788	0.0242	0.1806
chr16	90354753	2958471	0.0327	0.2139
chr17	81195210	3352242	0.0413	0.2331
chr18	78077248	2210415	0.0283	0.4166
chr19	59128983	1983348	0.0335	0.3382
chr20	63025520	2673636	0.0424	0.2275
chr21	48129895	1266523	0.0263	0.1905
chr22	51304566	796831	0.0155	0.1351
chrMT	16571	2370	0.143	0.3734
chrX	155270560	5617864	0.0362	0.2382
chrY	59373566	308756	0.0052	0.144

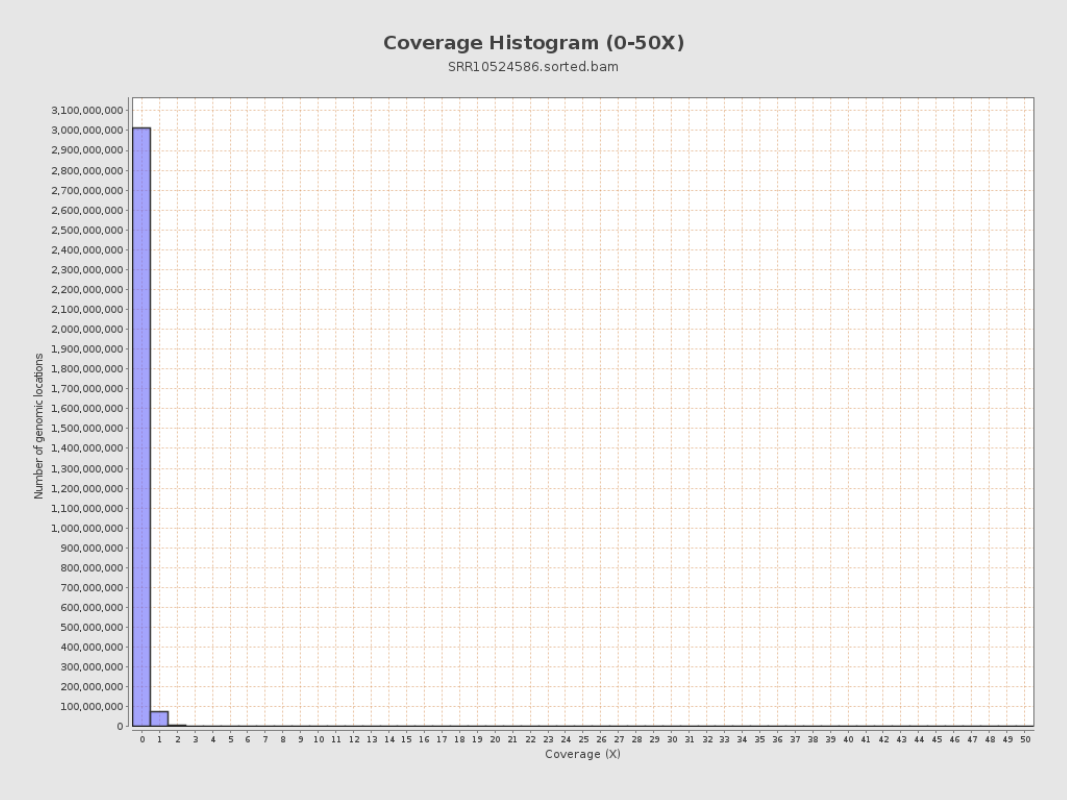
3. Results : Coverage across reference



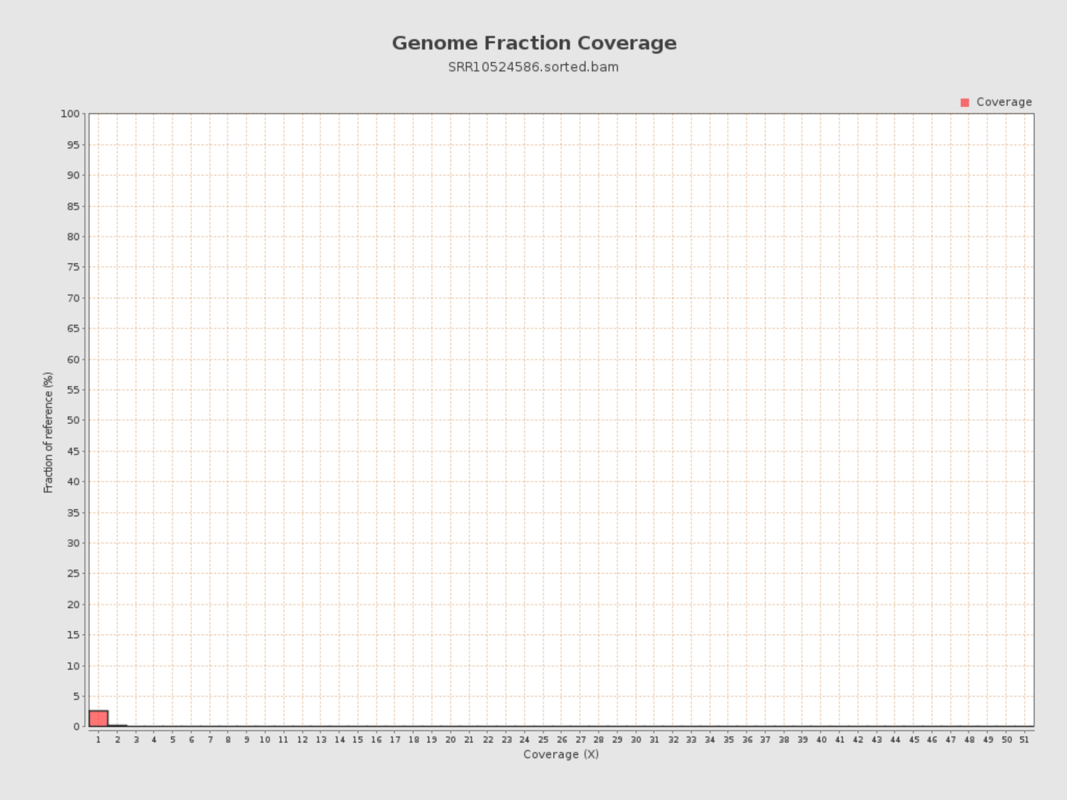
4. Results : Coverage Histogram



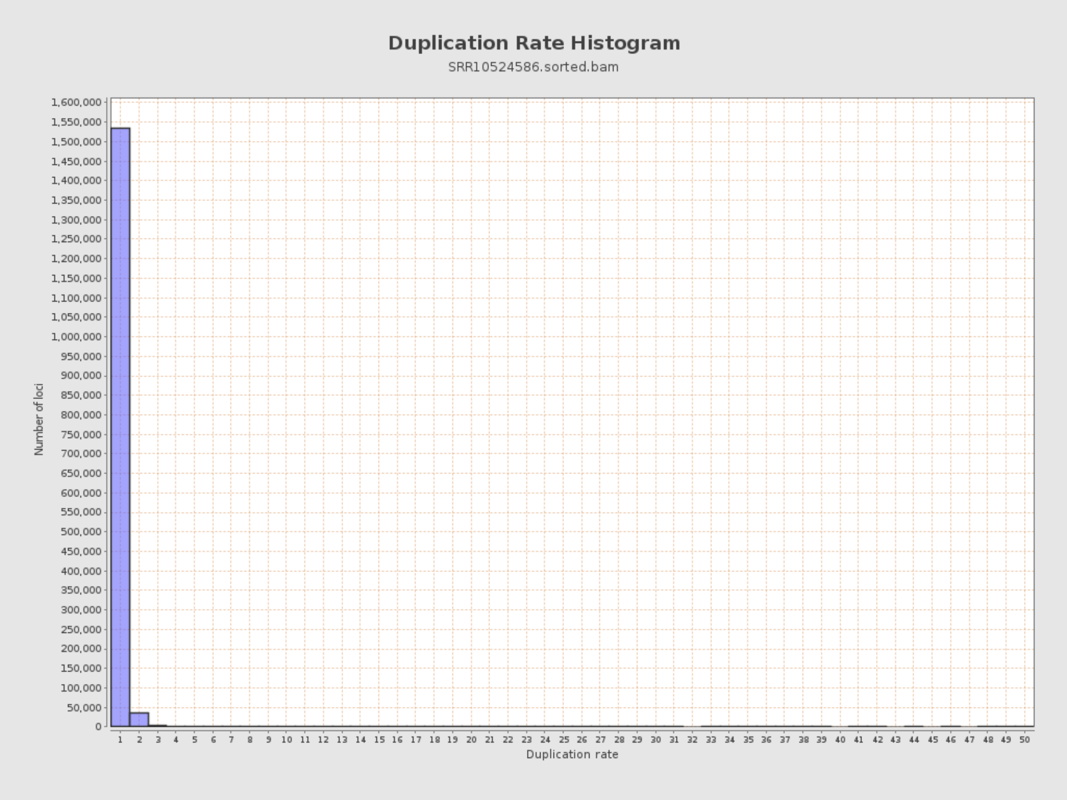
5. Results : Coverage Histogram (0-50X)



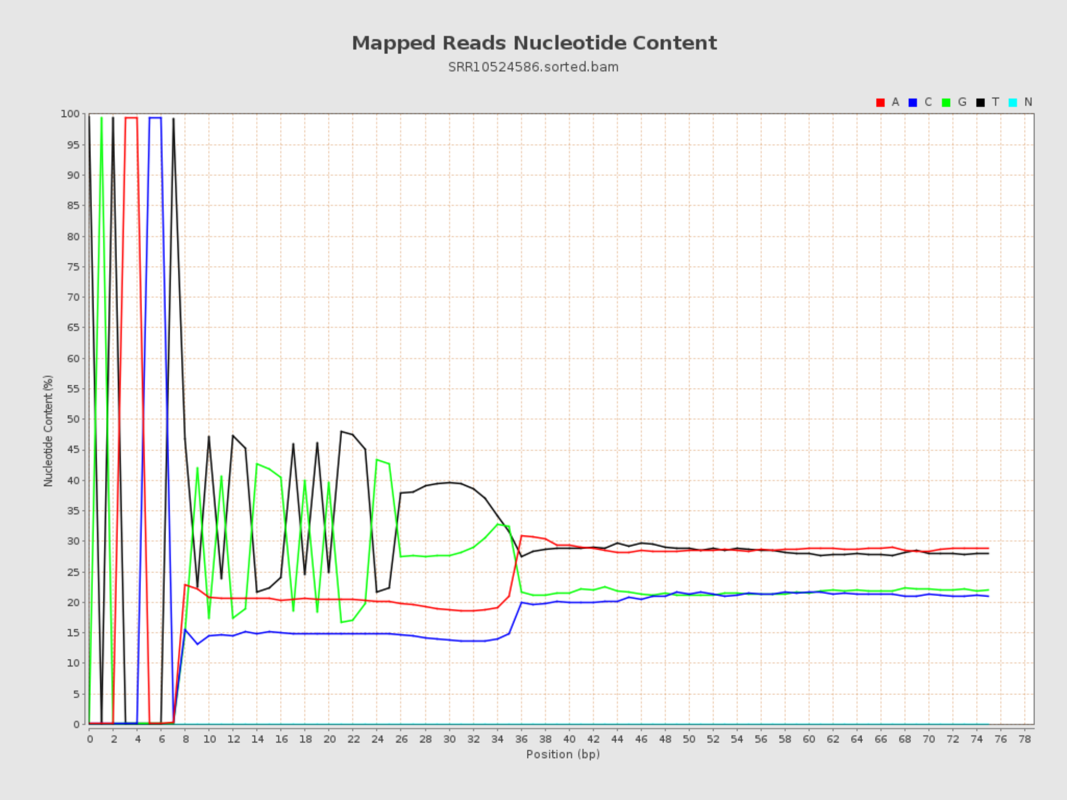
6. Results : Genome Fraction Coverage



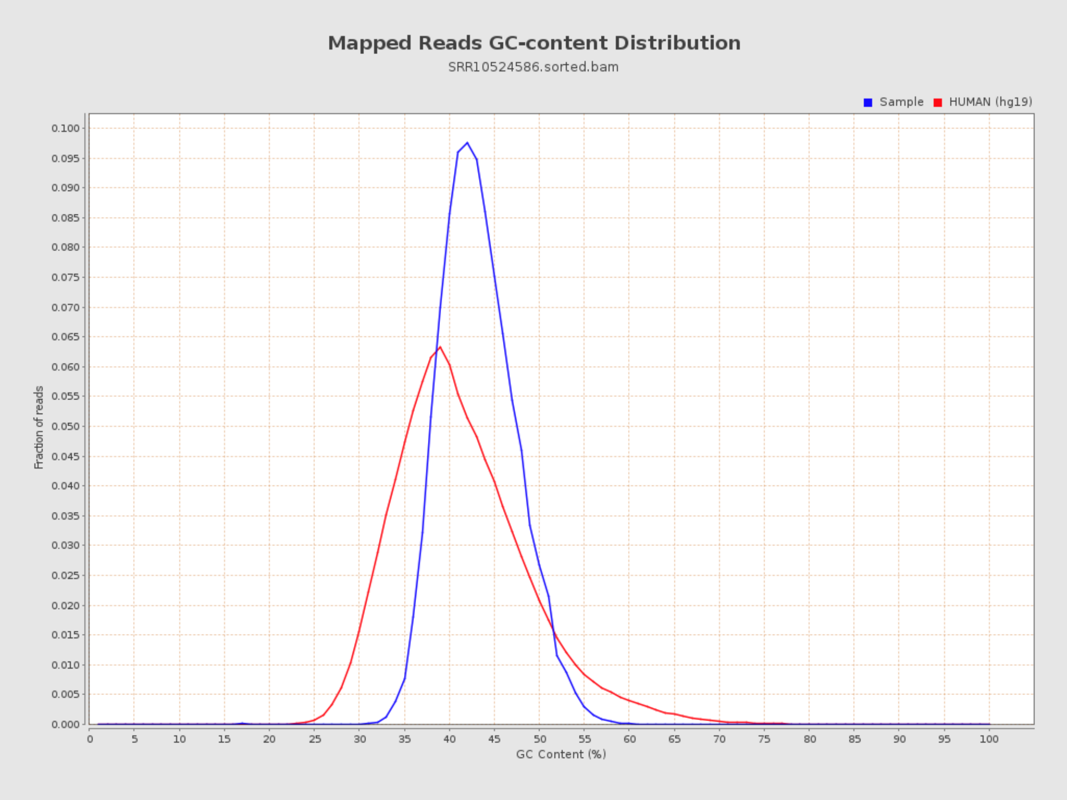
7. Results : Duplication Rate Histogram



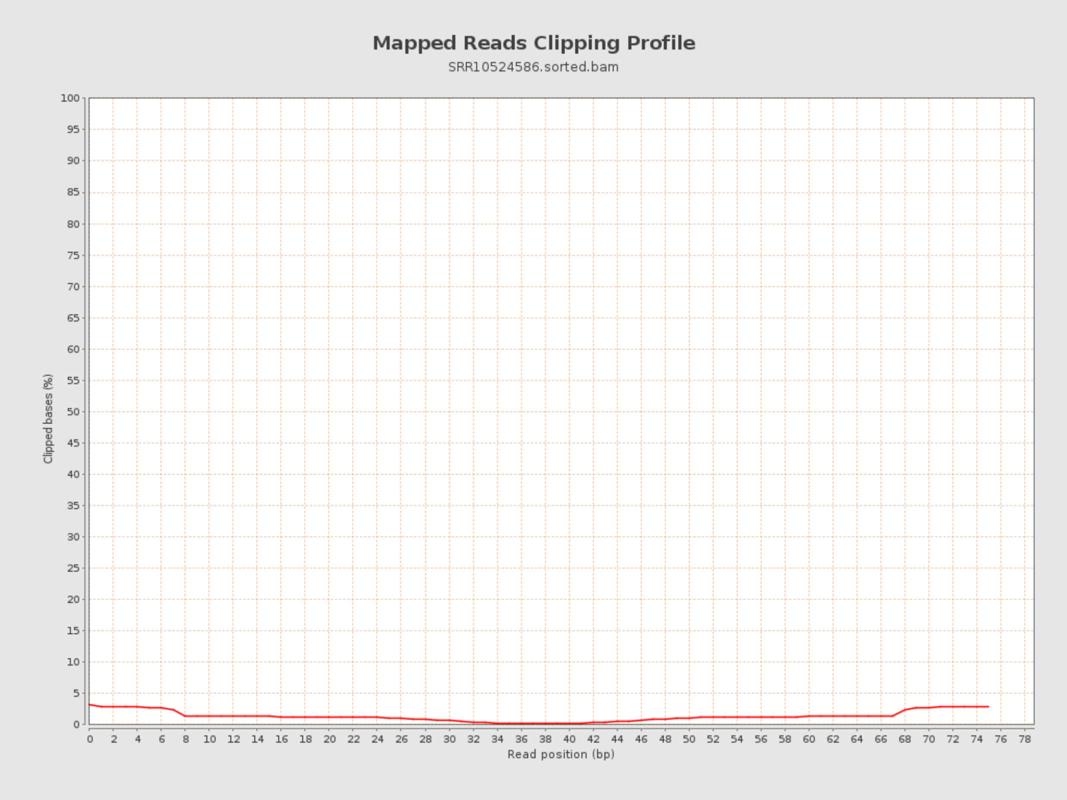
8. Results : Mapped Reads Nucleotide Content



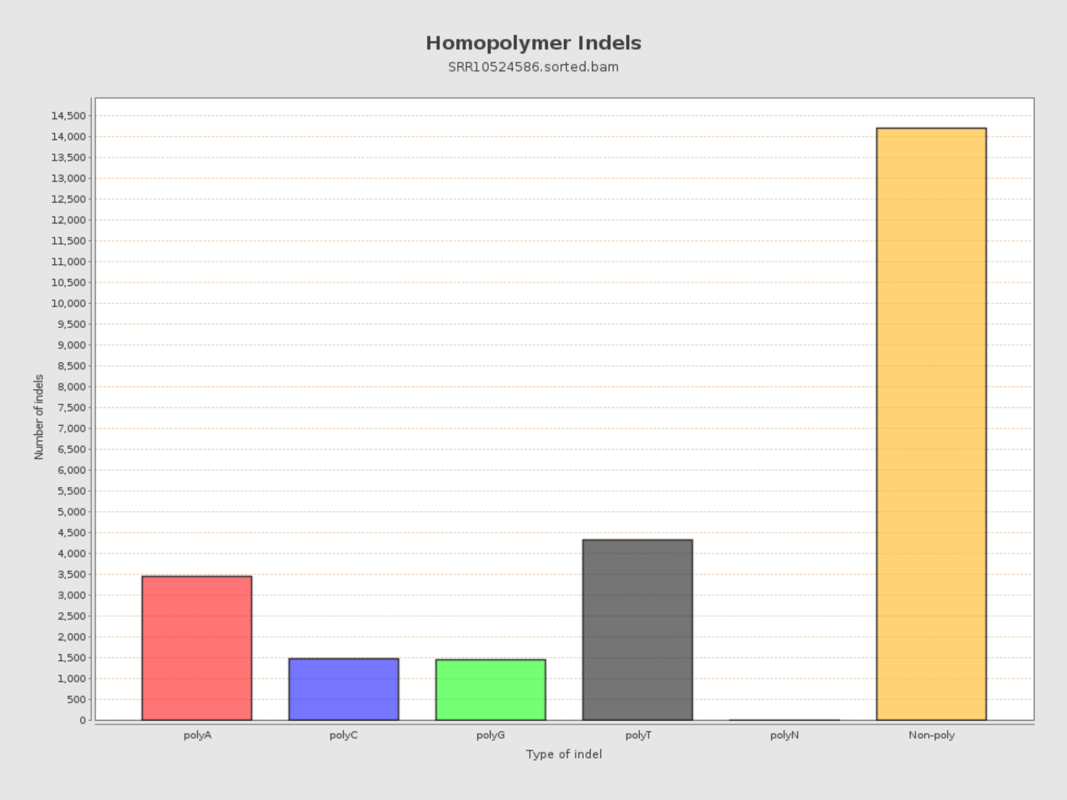
9. Results : Mapped Reads GC-content Distribution



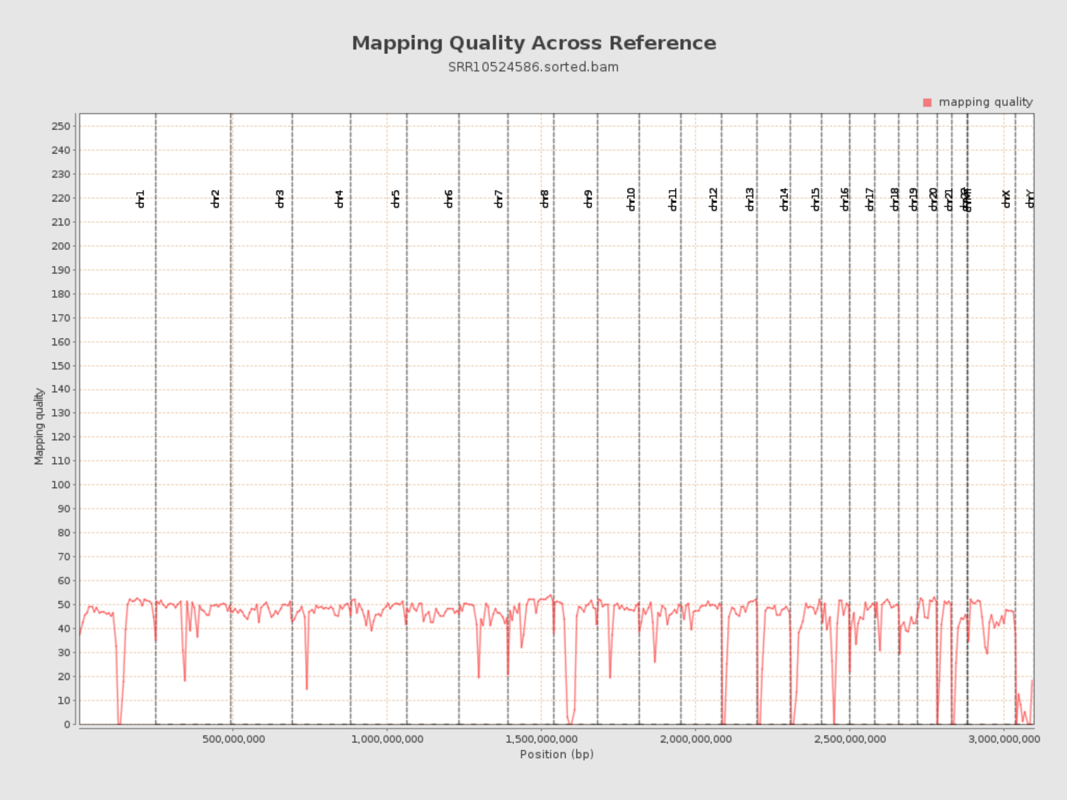
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram