Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:48:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524648.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_SRR10524648 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524648.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:48:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524648.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,325,372
Mapped reads	1,222,668 / 92.25%
Unmapped reads	102,704 / 7.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,434 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	59,828 / 4.51%
Duplication rate	3.87%
Clipped reads	1,225,132 / 92.44%

2.2. ACGT Content

Number/percentage of A's	17,974,527 / 25.27%
Number/percentage of C's	13,945,343 / 19.61%
Number/percentage of T's	22,298,681 / 31.35%
Number/percentage of G's	16,903,776 / 23.77%
Number/percentage of N's	605 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.023

Standard Deviation	0.2253

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

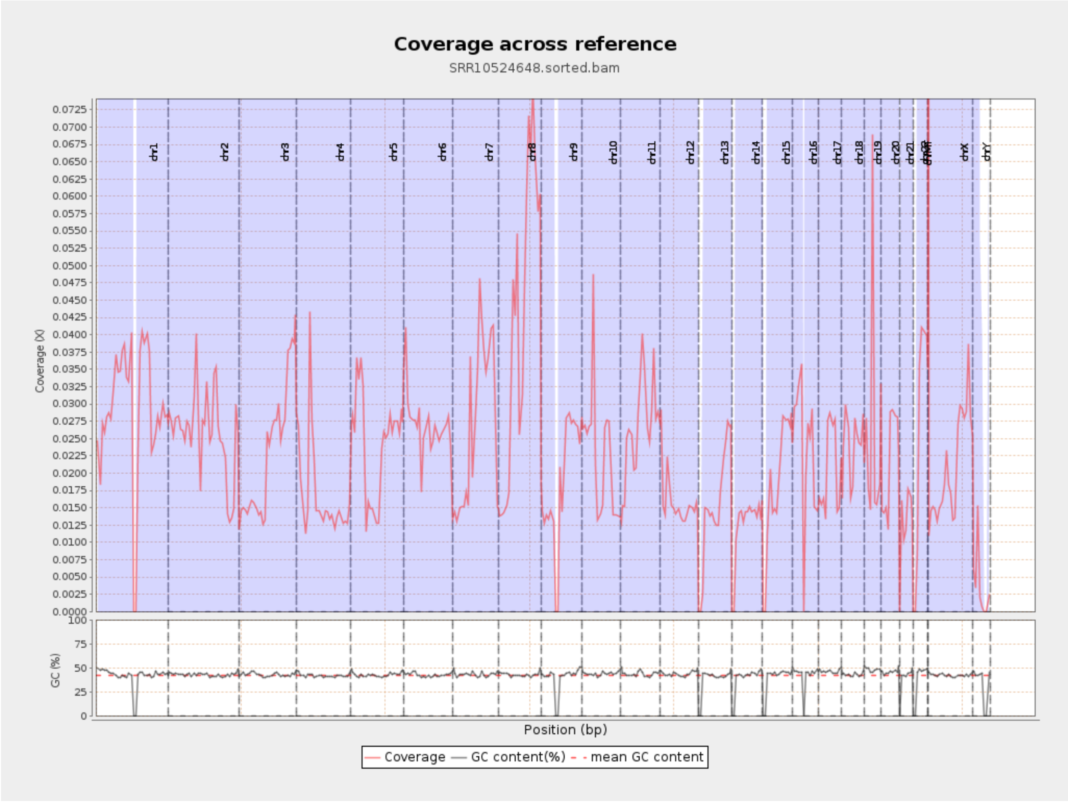
General error rate	0.53%
Mismatches	364,787
Insertions	4,576
Mapped reads with at least one insertion	0.37%
Deletions	14,061
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.85%

2.6. Chromosome stats

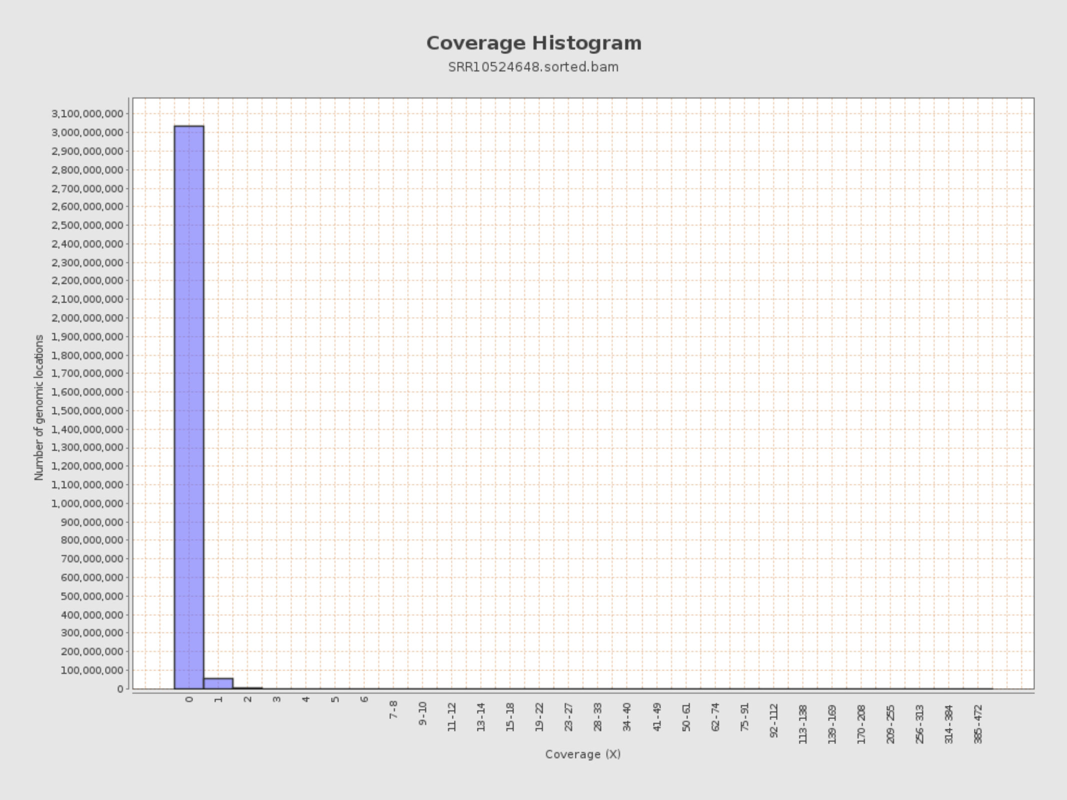
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7275240	0.0292	0.3855
chr2	243199373	6283506	0.0258	0.2701
chr3	198022430	4514885	0.0228	0.1672
chr4	191154276	3259653	0.0171	0.1754
chr5	180915260	4377993	0.0242	0.1715
chr6	171115067	4603937	0.0269	0.1899
chr7	159138663	4317635	0.0271	0.2646

chr8	146364022	6247752	0.0427	0.2995
chr9	141213431	2582072	0.0183	0.1828
chr10	135534747	3061225	0.0226	0.2516
chr11	135006516	3627318	0.0269	0.2075
chr12	133851895	2134426	0.0159	0.1439
chr13	115169878	1729658	0.015	0.1352
chr14	107349540	1312610	0.0122	0.1259
chr15	102531392	1846111	0.018	0.1489
chr16	90354753	2131018	0.0236	0.178
chr17	81195210	1650081	0.0203	0.163
chr18	78077248	1874565	0.024	0.2932
chr19	59128983	1515074	0.0256	0.2843
chr20	63025520	1358597	0.0216	0.1655
chr21	48129895	626843	0.013	0.155
chr22	51304566	1352748	0.0264	0.1804
chrMT	16571	9790	0.5908	0.8872
chrX	155270560	3236742	0.0208	0.1723
chrY	59373566	216910	0.0037	0.1507

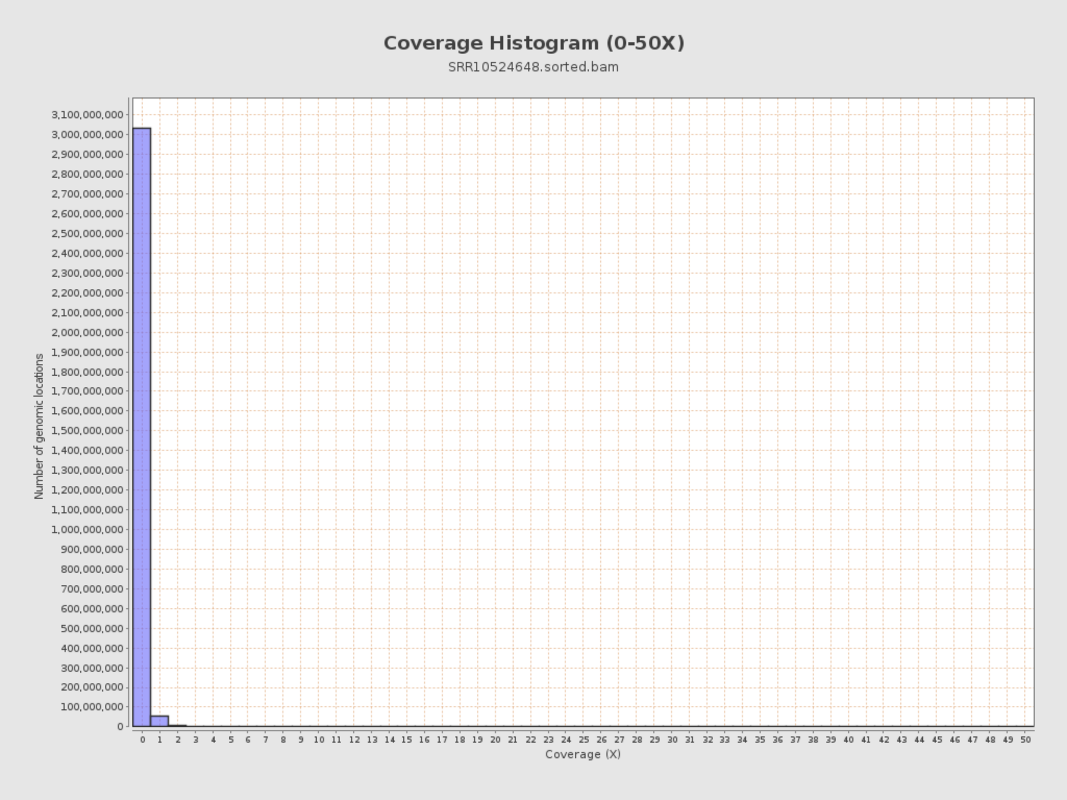
3. Results : Coverage across reference



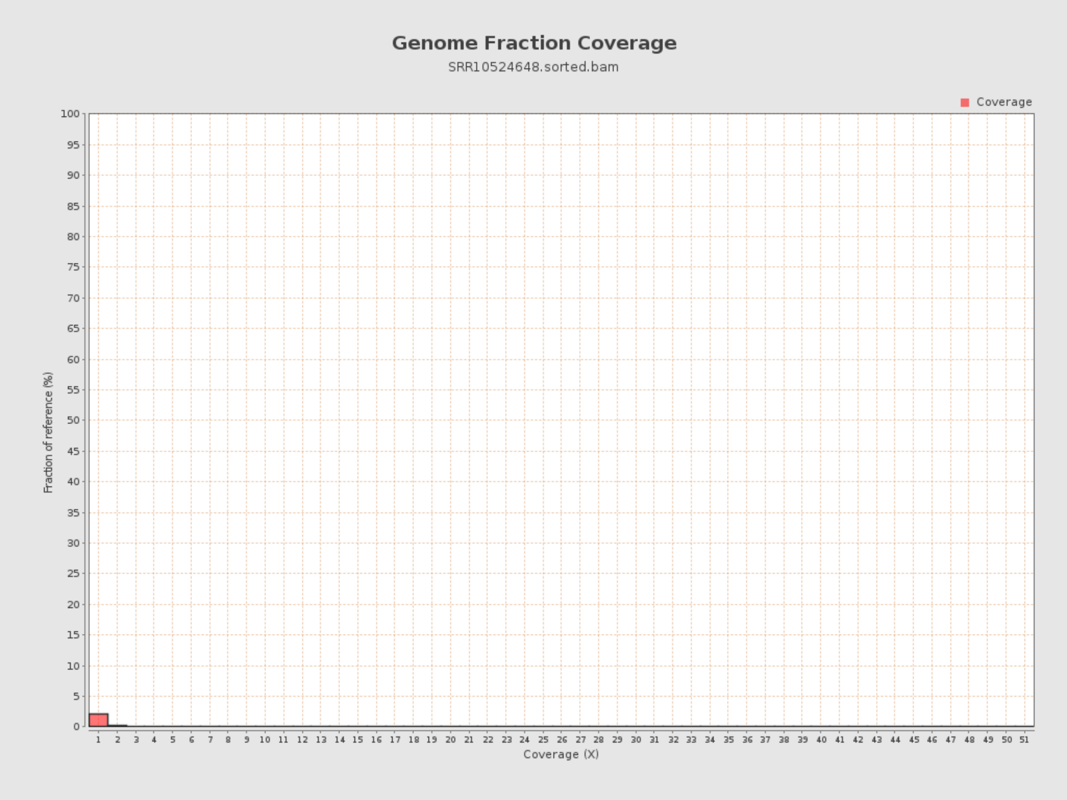
4. Results : Coverage Histogram



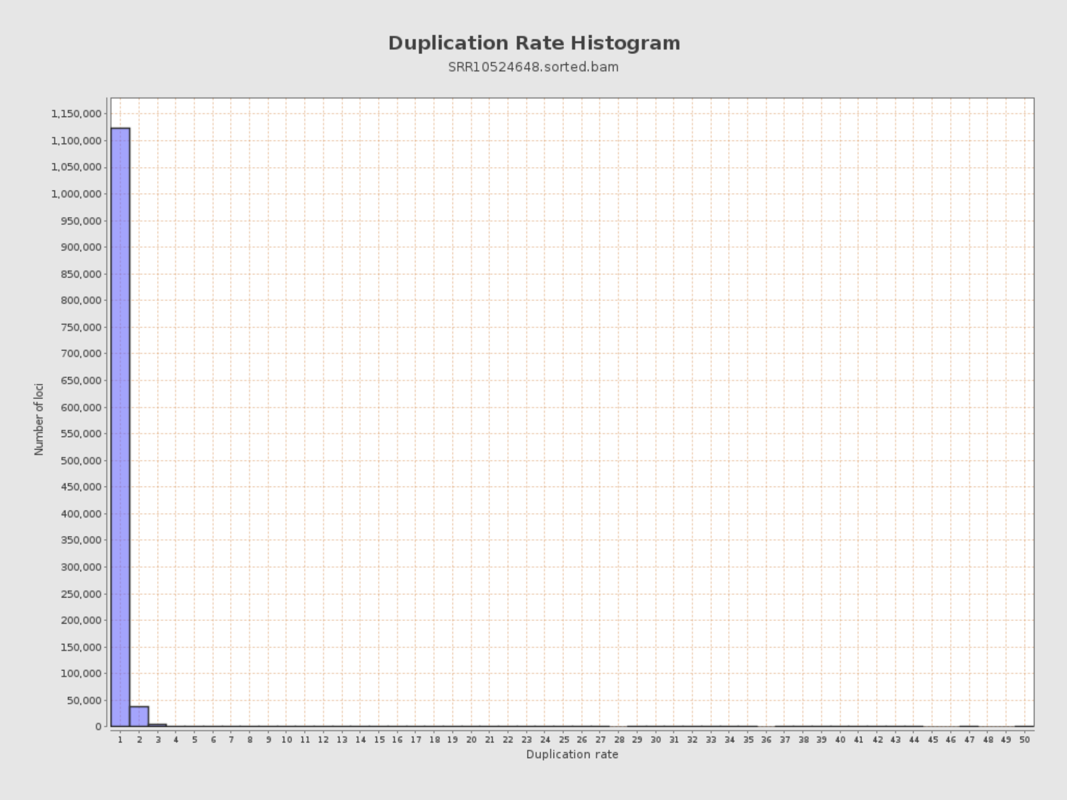
5. Results : Coverage Histogram (0-50X)



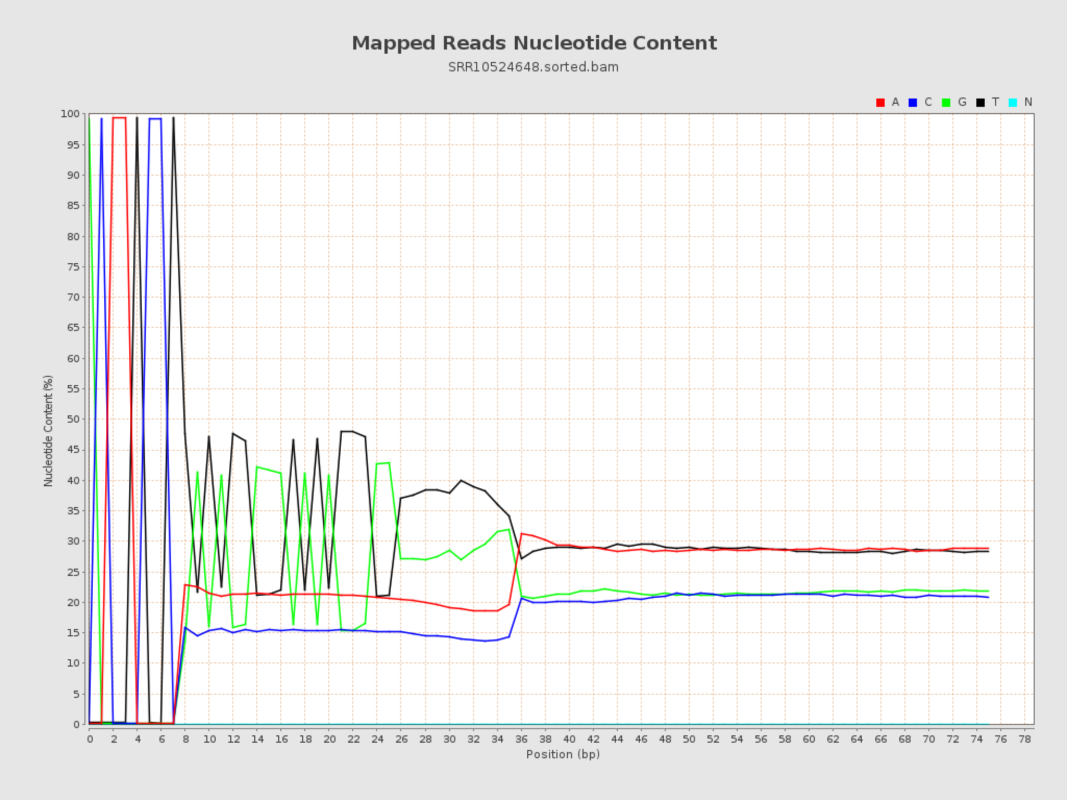
6. Results : Genome Fraction Coverage



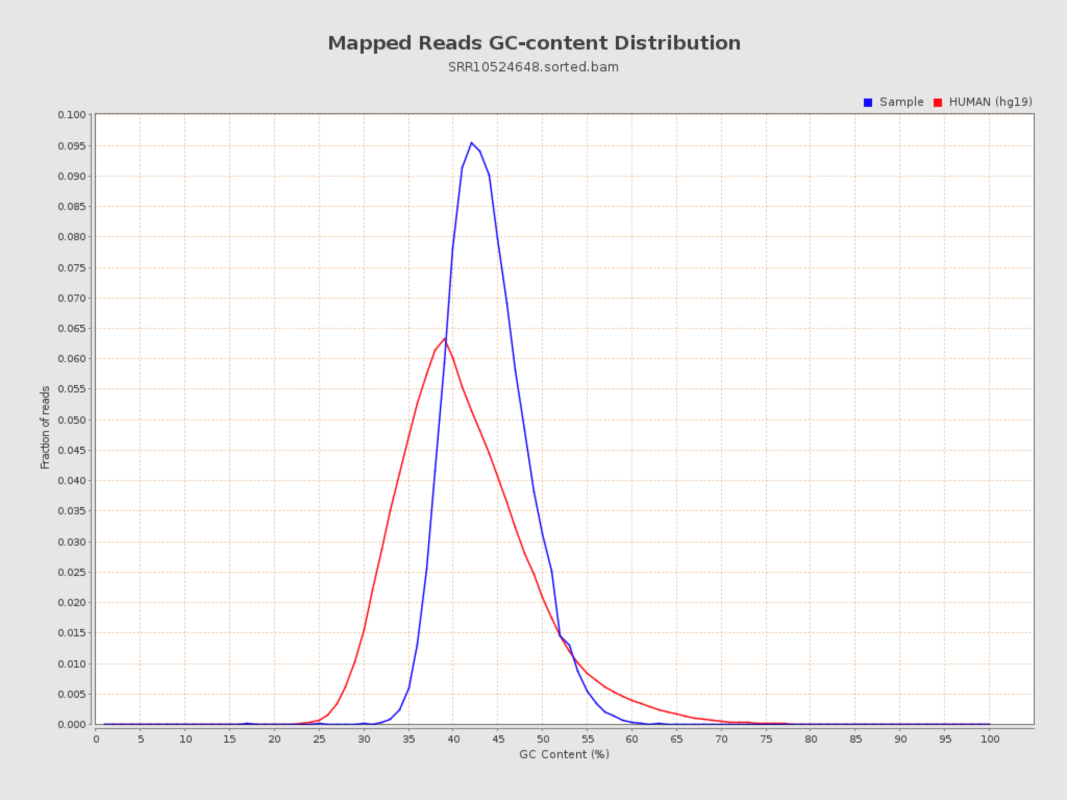
7. Results : Duplication Rate Histogram



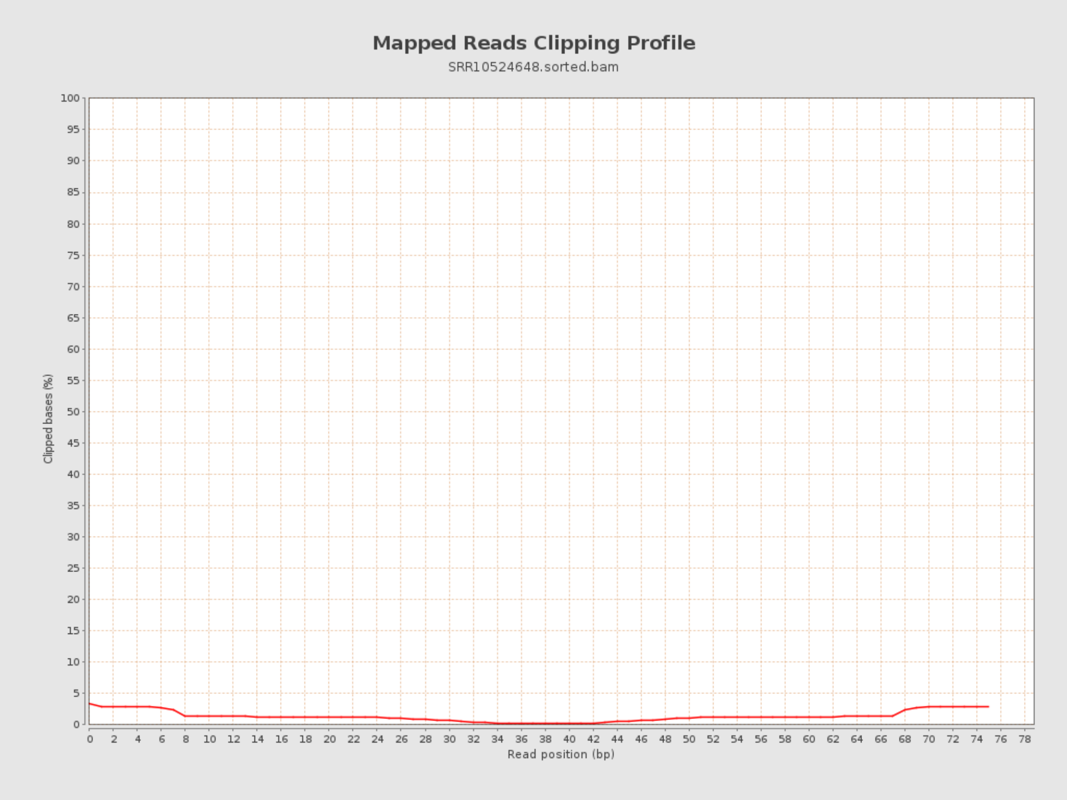
8. Results : Mapped Reads Nucleotide Content



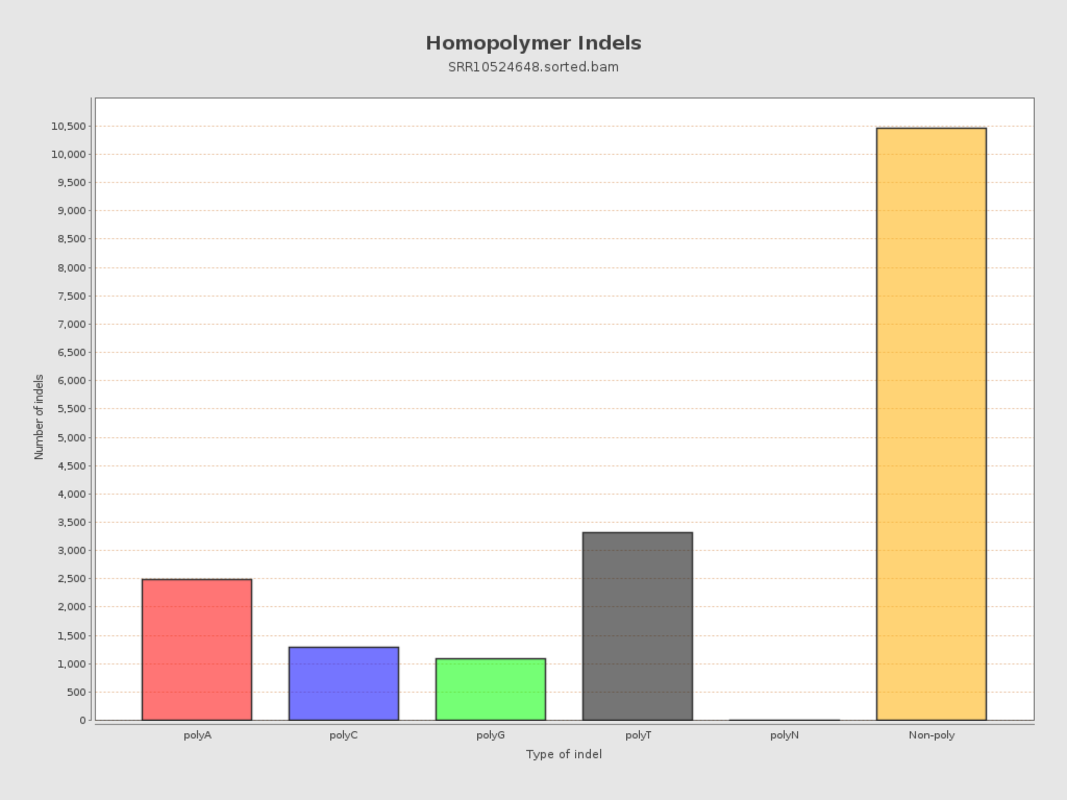
9. Results : Mapped Reads GC-content Distribution



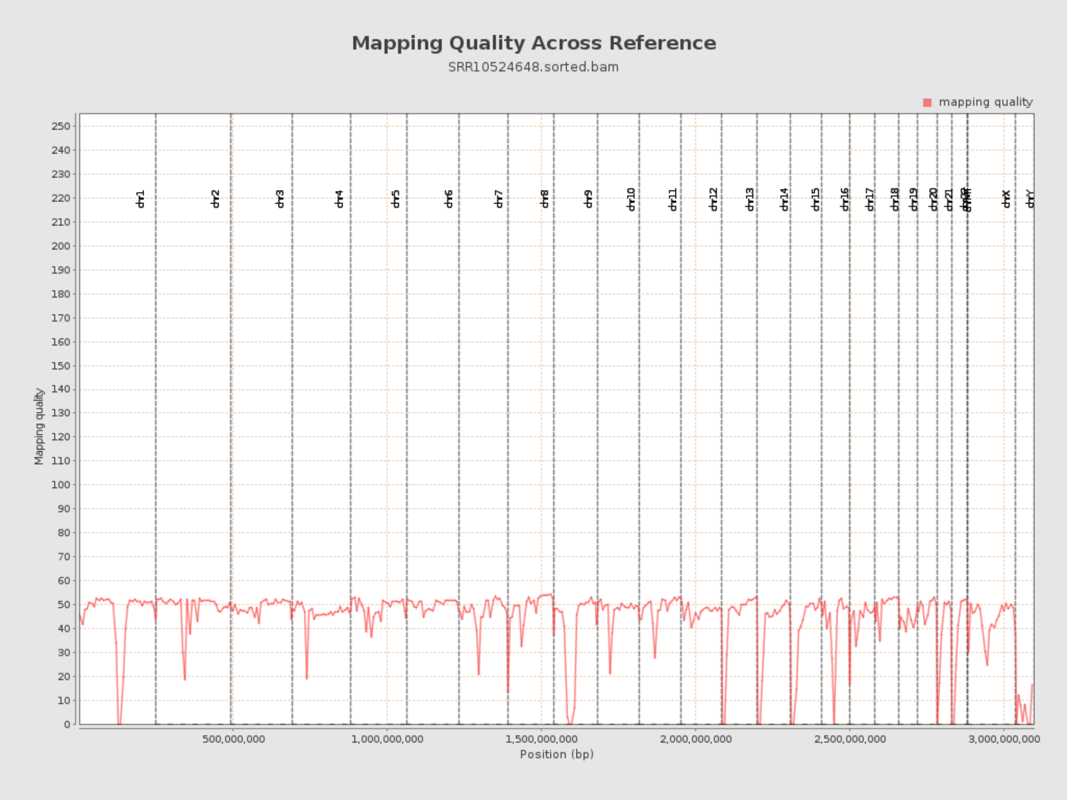
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram