Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:10:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524969.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_SRR10524969 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524969.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:10:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524969.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	535,555
Mapped reads	493,515 / 92.15%
Unmapped reads	42,040 / 7.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,305 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	7,745 / 1.45%
Duplication rate	1.16%
Clipped reads	493,464 / 92.14%

2.2. ACGT Content

Number/percentage of A's	7,468,943 / 25.85%
Number/percentage of C's	5,375,473 / 18.6%
Number/percentage of T's	9,136,852 / 31.62%
Number/percentage of G's	6,911,267 / 23.92%
Number/percentage of N's	362 / 0%
GC Percentage	42.53%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.117

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Mismatches and indels

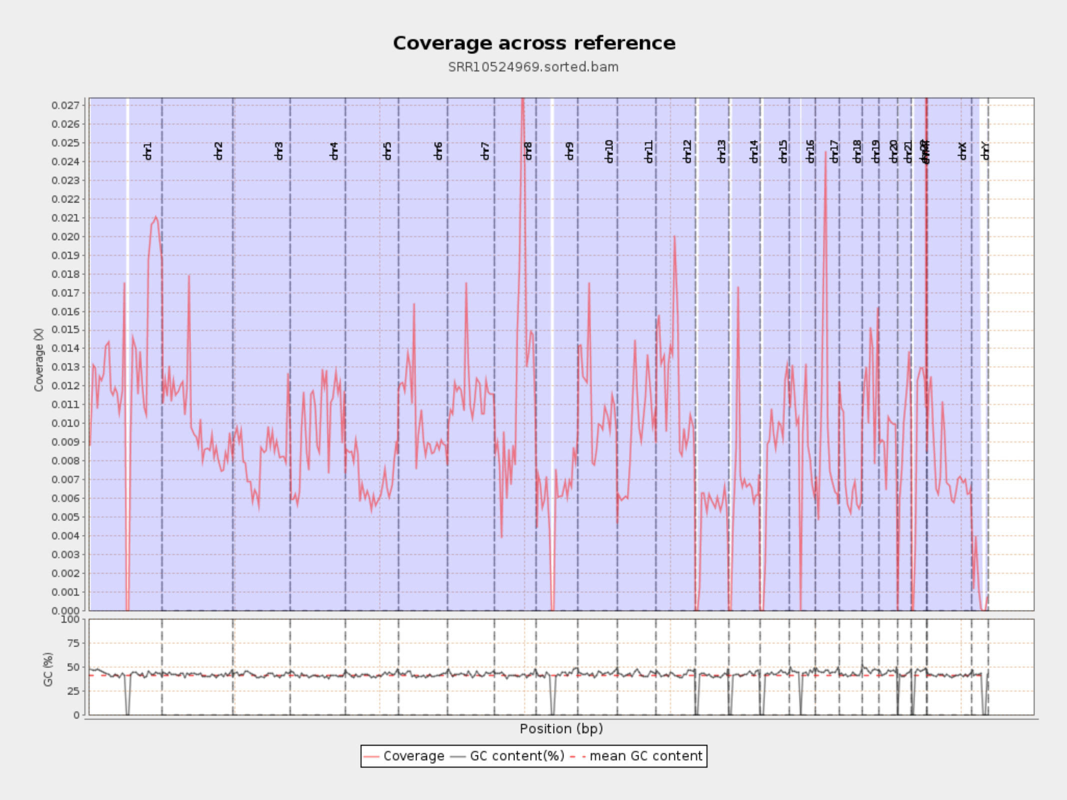
General error rate	0.51%
Mismatches	141,884
Insertions	2,189
Mapped reads with at least one insertion	0.44%
Deletions	5,670
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.94%

2.6. Chromosome stats

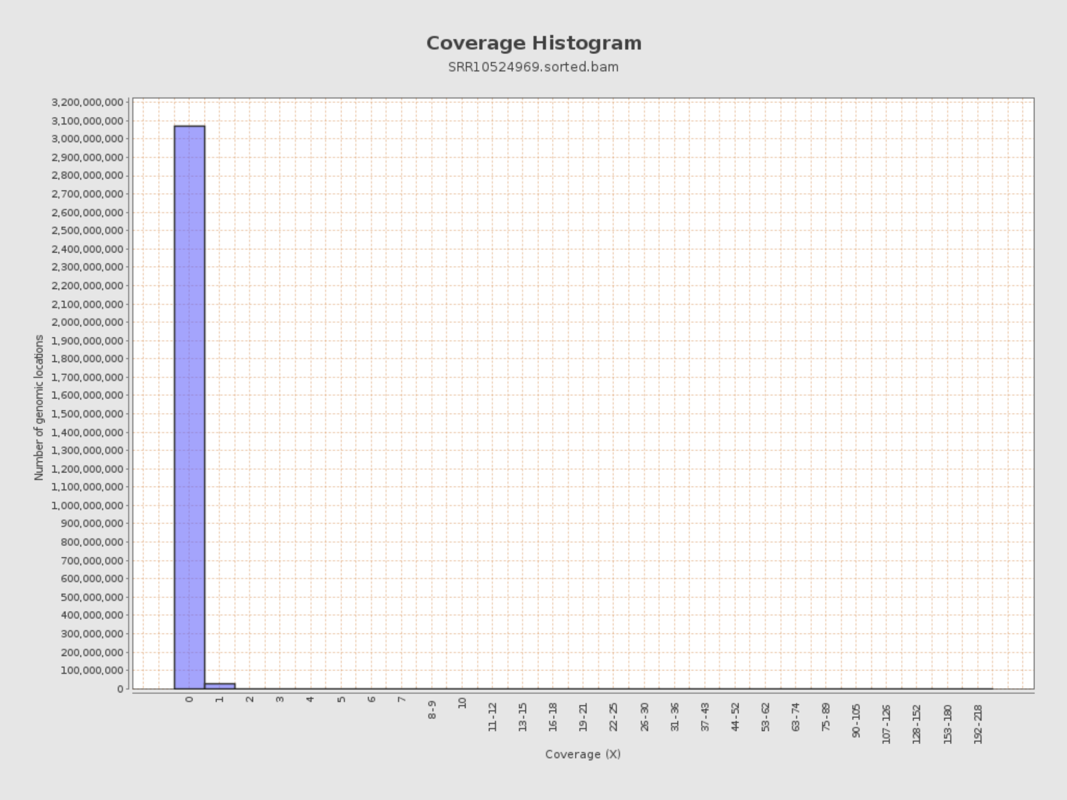
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3258069	0.0131	0.191
chr2	243199373	2468367	0.0101	0.128
chr3	198022430	1650669	0.0083	0.0939
chr4	191154276	1868923	0.0098	0.1034
chr5	180915260	1279966	0.0071	0.0866
chr6	171115067	1750020	0.0102	0.1178
chr7	159138663	1864077	0.0117	0.1464

chr8	146364022	1780297	0.0122	0.1249
chr9	141213431	833943	0.0059	0.0898
chr10	135534747	1505004	0.0111	0.1219
chr11	135006516	1261402	0.0093	0.1105
chr12	133851895	1628842	0.0122	0.1134
chr13	115169878	562024	0.0049	0.0719
chr14	107349540	698067	0.0065	0.0832
chr15	102531392	839042	0.0082	0.095
chr16	90354753	809764	0.009	0.0989
chr17	81195210	815105	0.01	0.1142
chr18	78077248	562947	0.0072	0.1205
chr19	59128983	736117	0.0124	0.1397
chr20	63025520	575088	0.0091	0.0985
chr21	48129895	434196	0.009	0.0991
chr22	51304566	439284	0.0086	0.0952
chrMT	16571	10030	0.6053	0.8592
chrX	155270560	1200111	0.0077	0.0949
chrY	59373566	71315	0.0012	0.0412

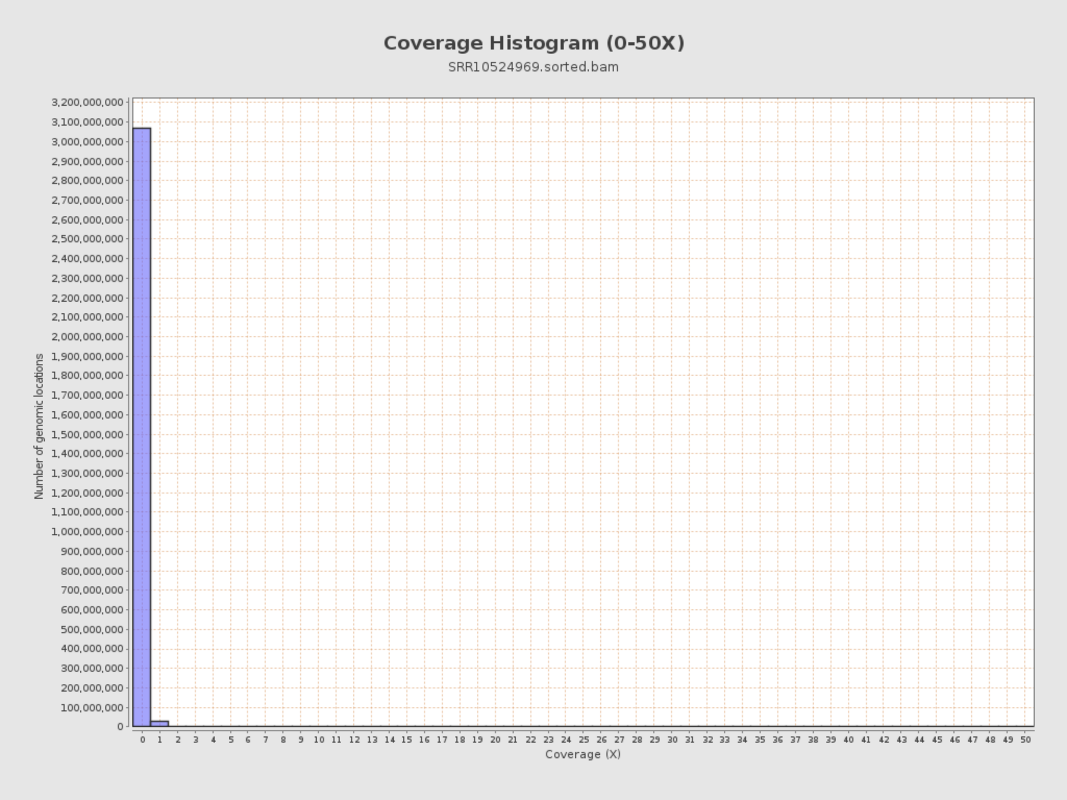
3. Results : Coverage across reference



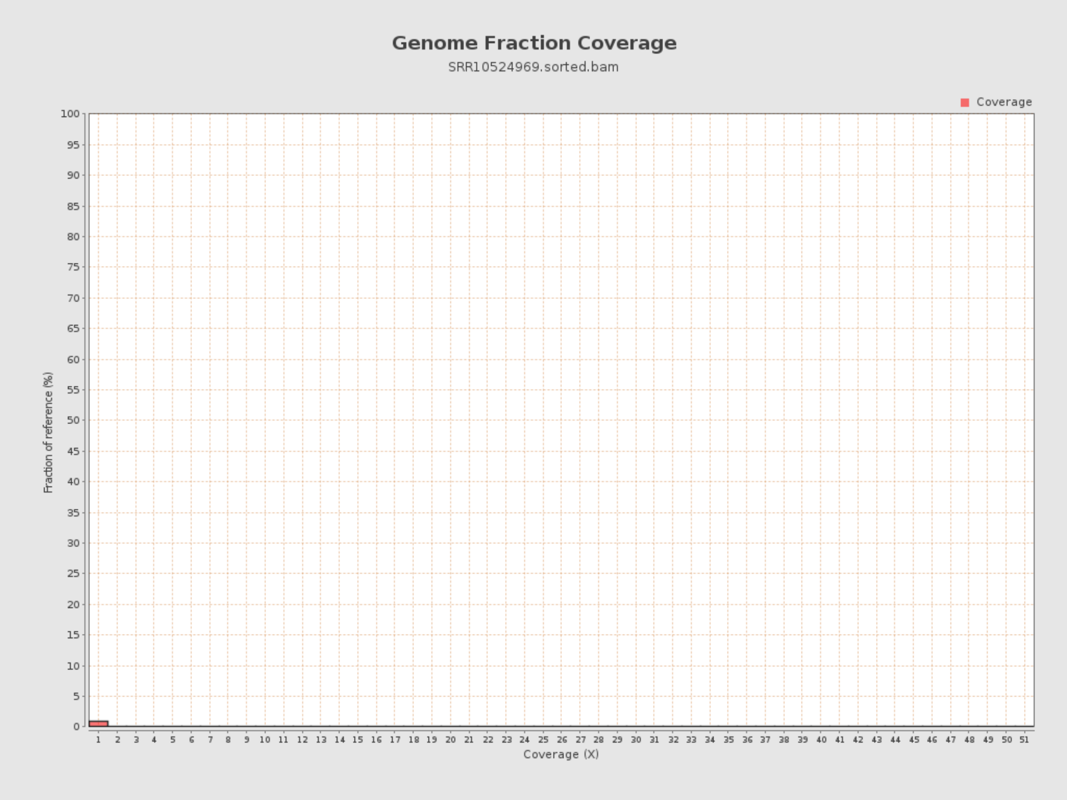
4. Results : Coverage Histogram



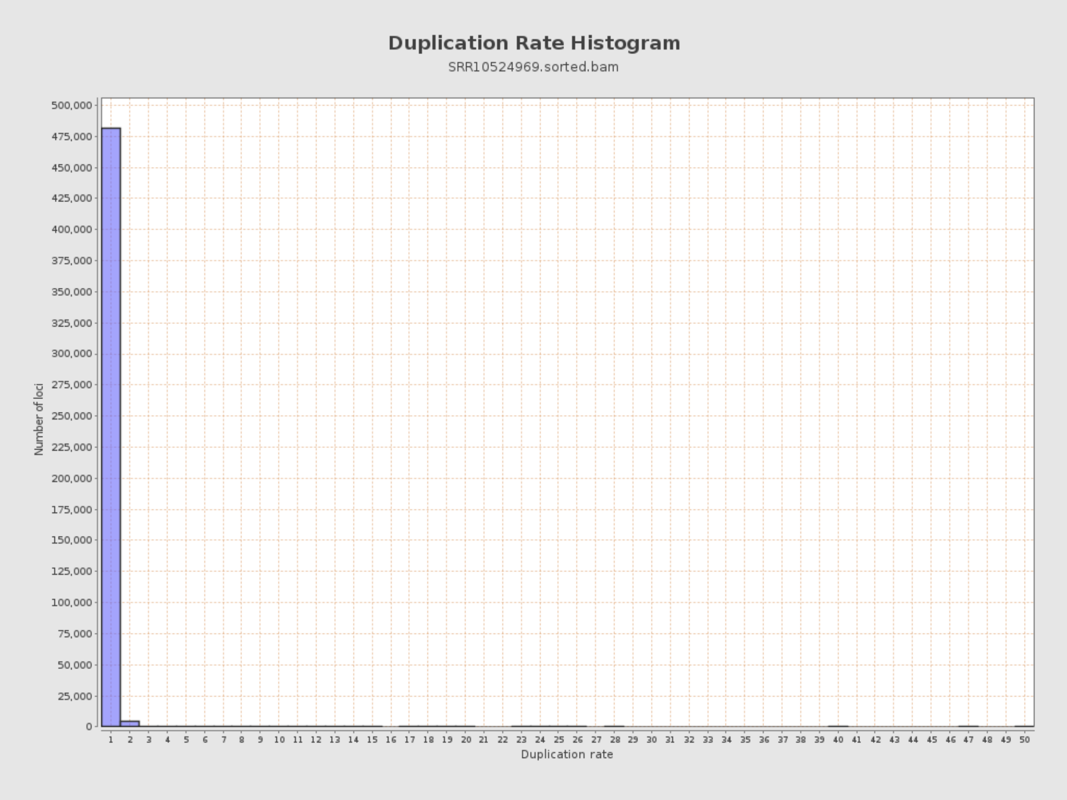
5. Results : Coverage Histogram (0-50X)



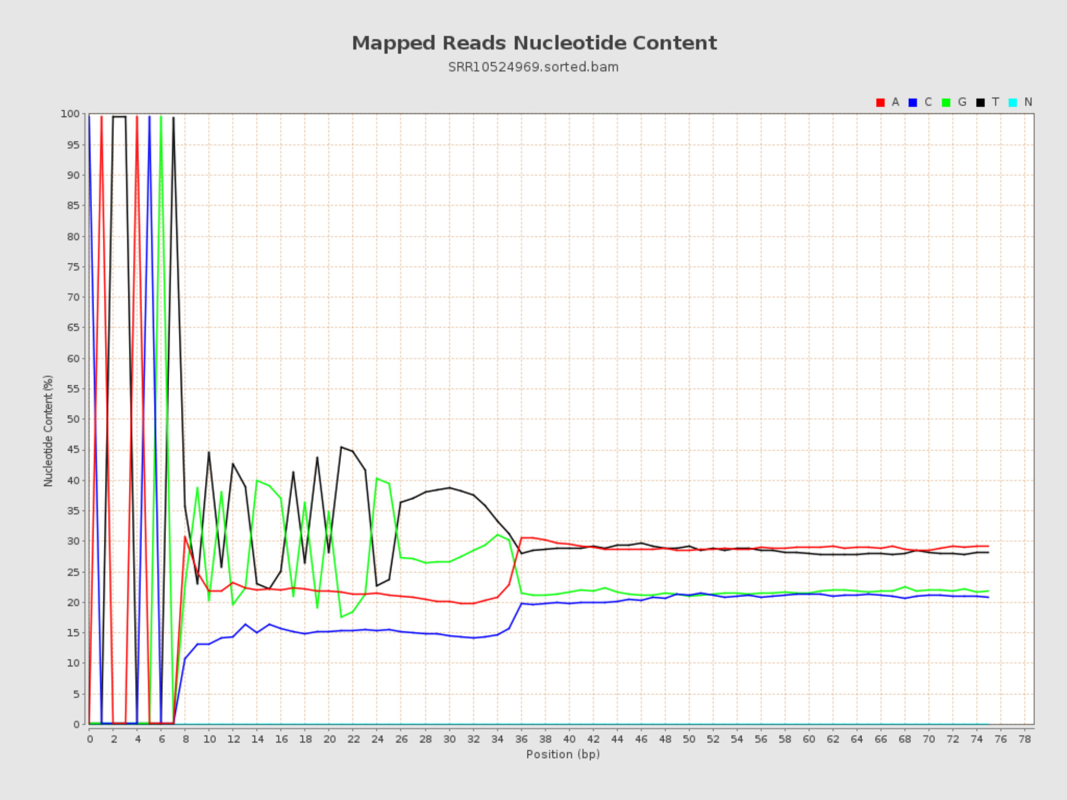
6. Results : Genome Fraction Coverage



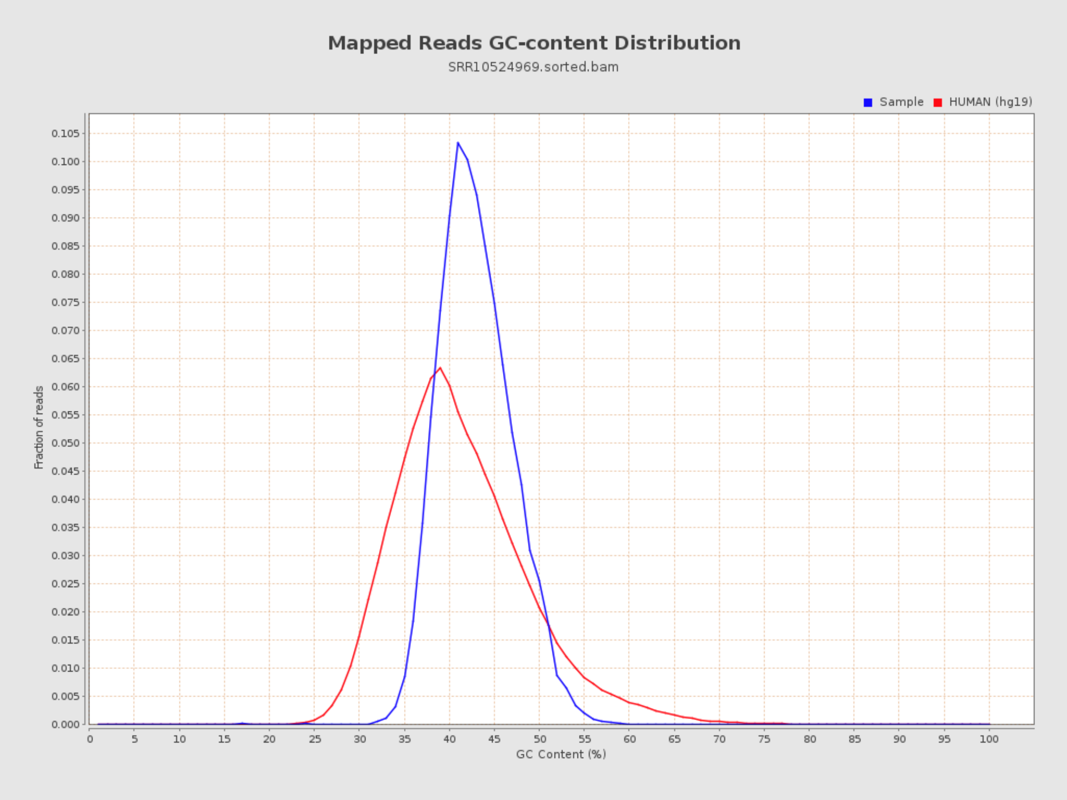
7. Results : Duplication Rate Histogram



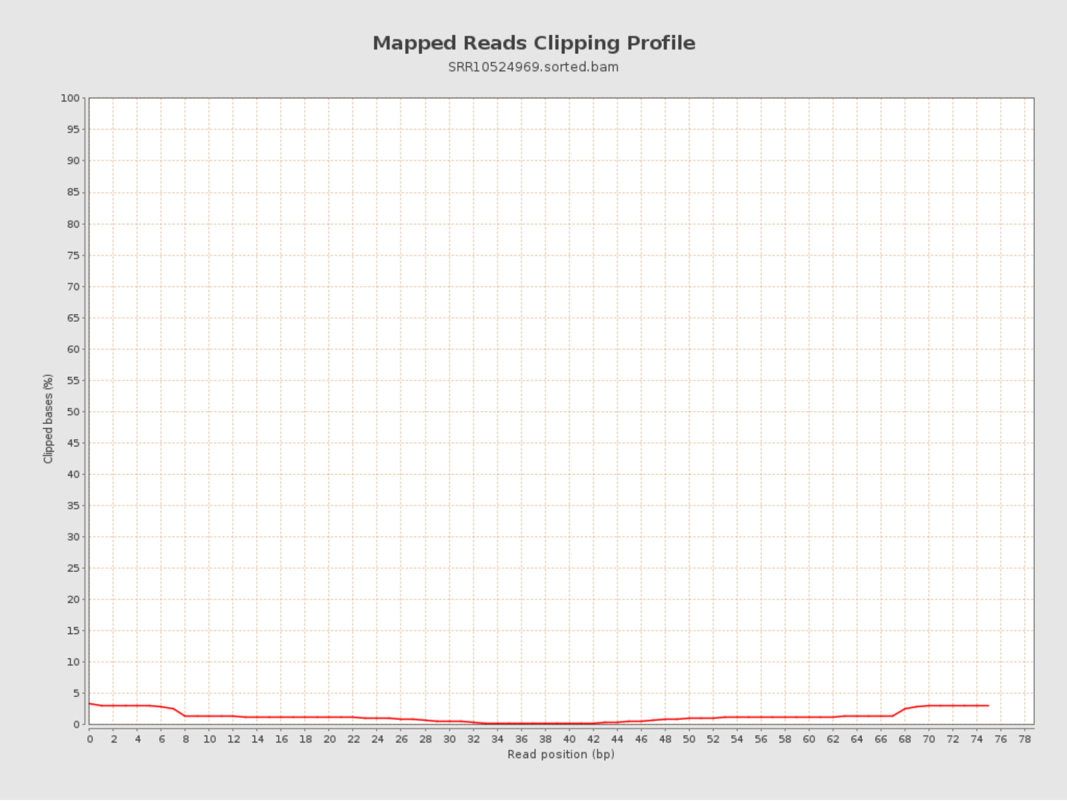
8. Results : Mapped Reads Nucleotide Content



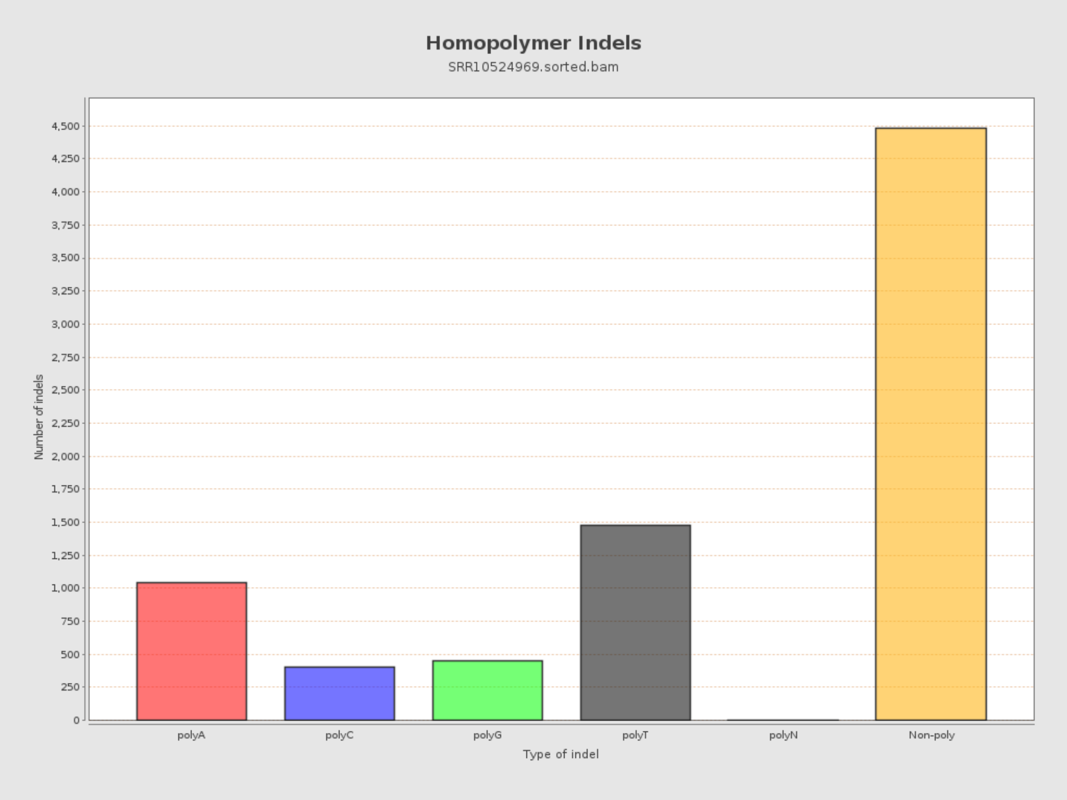
9. Results : Mapped Reads GC-content Distribution



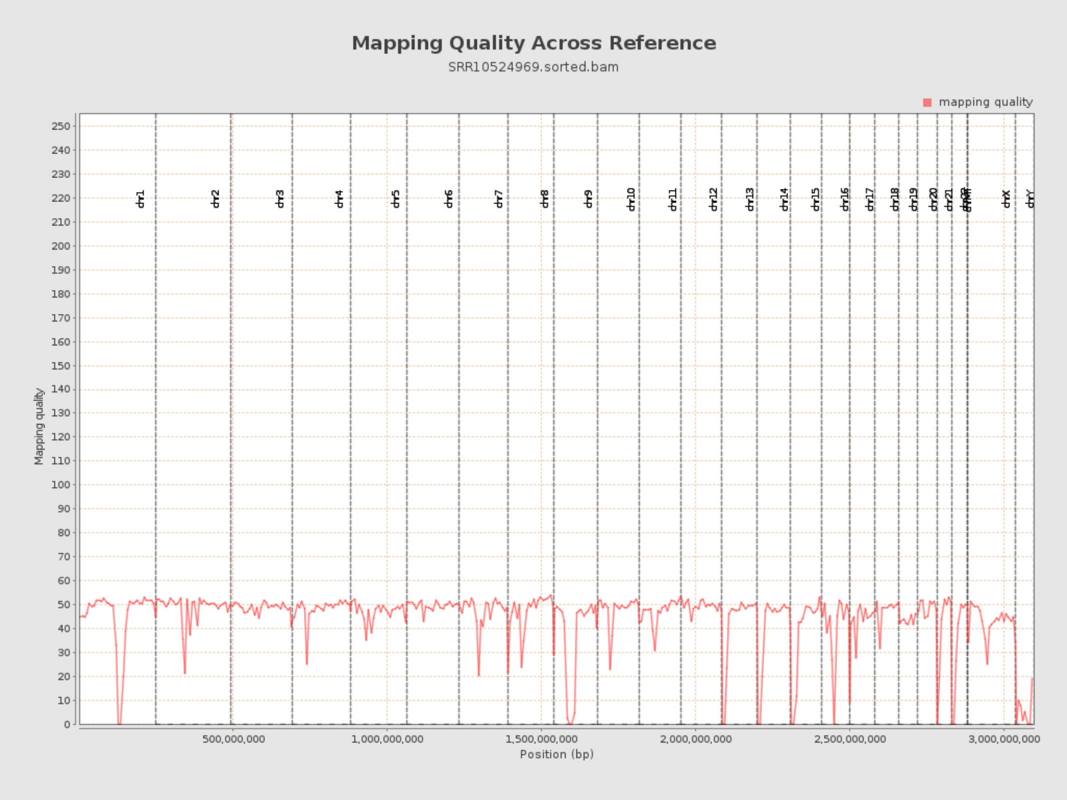
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram