Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 03:02:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524909.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_SRR10524909 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524909.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 03:02:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524909.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,113,438
Mapped reads	1,034,677 / 92.93%
Unmapped reads	78,761 / 7.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,127 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	41,228 / 3.7%
Duplication rate	3.13%
Clipped reads	1,038,129 / 93.24%

2.2. ACGT Content

Number/percentage of A's	14,509,406 / 23.96%
Number/percentage of C's	11,378,229 / 18.79%
Number/percentage of T's	19,395,517 / 32.03%
Number/percentage of G's	15,276,497 / 25.23%
Number/percentage of N's	488 / 0%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.2008

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

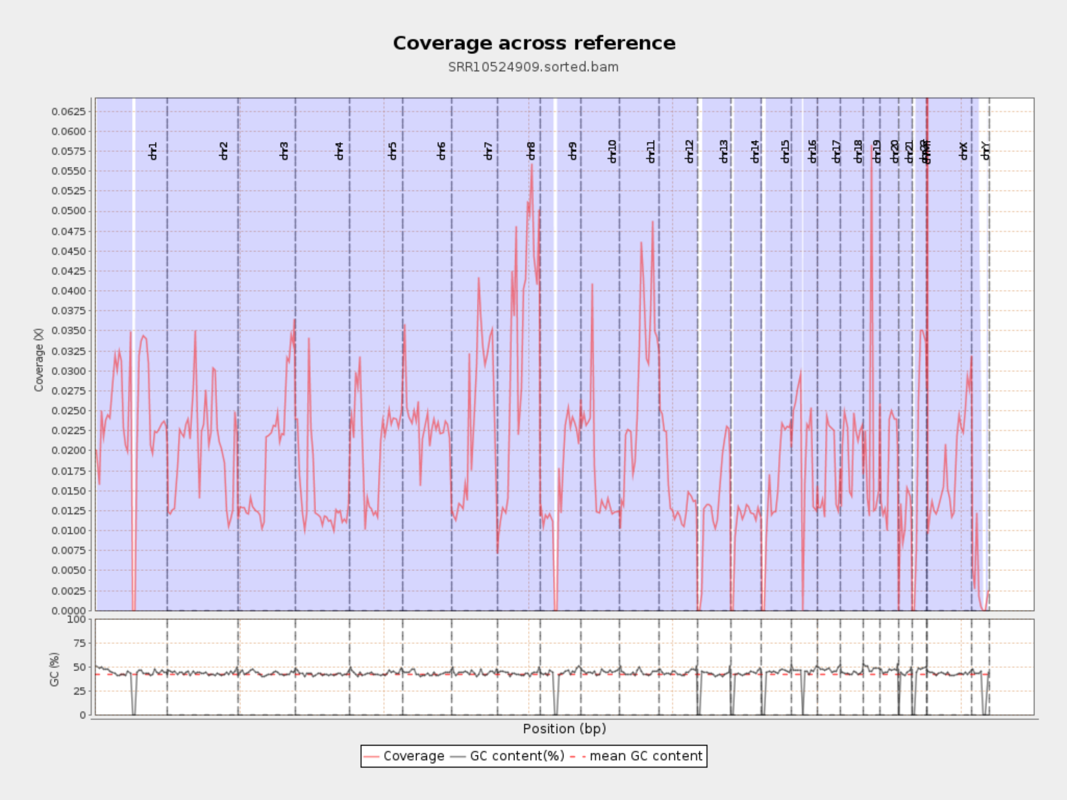
General error rate	0.51%
Mismatches	299,591
Insertions	3,407
Mapped reads with at least one insertion	0.33%
Deletions	11,691
Mapped reads with at least one deletion	1.12%
Homopolymer indels	45.03%

2.6. Chromosome stats

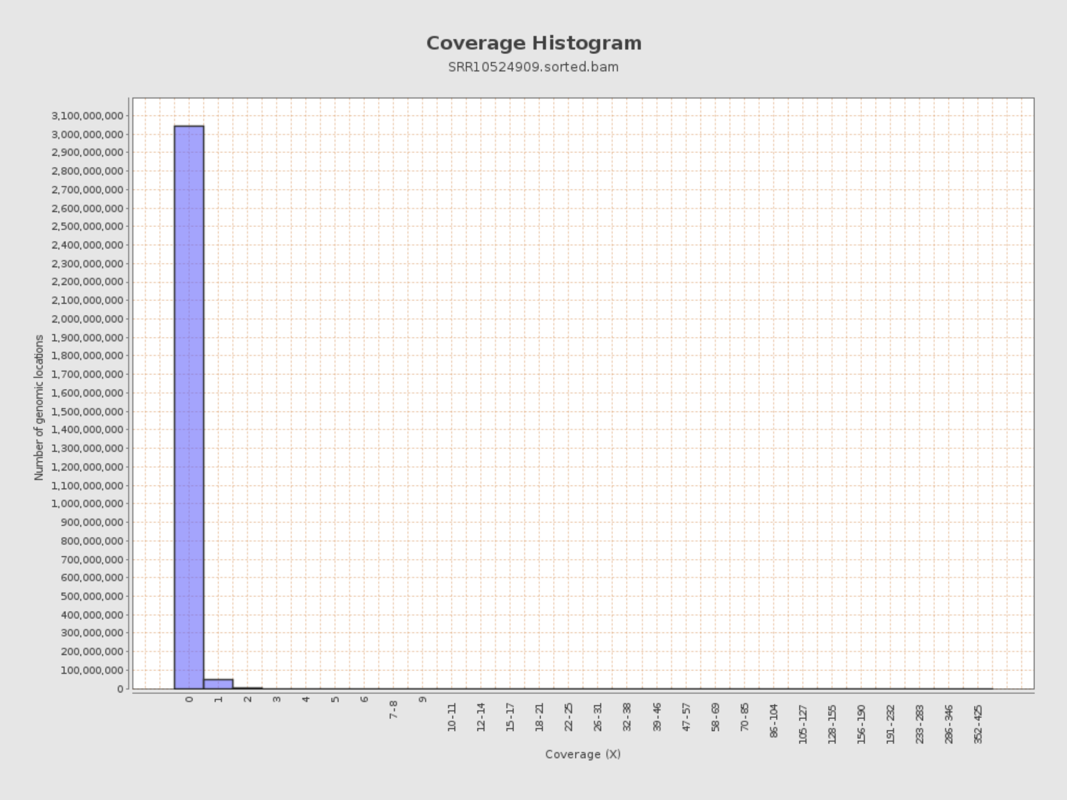
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5995409	0.0241	0.3435
chr2	243199373	5006340	0.0206	0.2323
chr3	198022430	3818222	0.0193	0.1505
chr4	191154276	2758921	0.0144	0.1516
chr5	180915260	3774830	0.0209	0.1564
chr6	171115067	4026518	0.0235	0.1733
chr7	159138663	3772809	0.0237	0.2406

chr8	146364022	4889911	0.0334	0.2689
chr9	141213431	2213520	0.0157	0.1649
chr10	135534747	2406168	0.0178	0.2073
chr11	135006516	3852474	0.0285	0.2033
chr12	133851895	2045704	0.0153	0.1363
chr13	115169878	1501274	0.013	0.1232
chr14	107349540	1132252	0.0105	0.1151
chr15	102531392	1535574	0.015	0.1324
chr16	90354753	1820692	0.0202	0.1589
chr17	81195210	1384642	0.0171	0.1474
chr18	78077248	1621438	0.0208	0.2637
chr19	59128983	1239368	0.021	0.2506
chr20	63025520	1160036	0.0184	0.1507
chr21	48129895	539201	0.0112	0.1339
chr22	51304566	1122015	0.0219	0.1609
chrMT	16571	9347	0.5641	0.8587
chrX	155270560	2773613	0.0179	0.1543
chrY	59373566	179838	0.003	0.1137

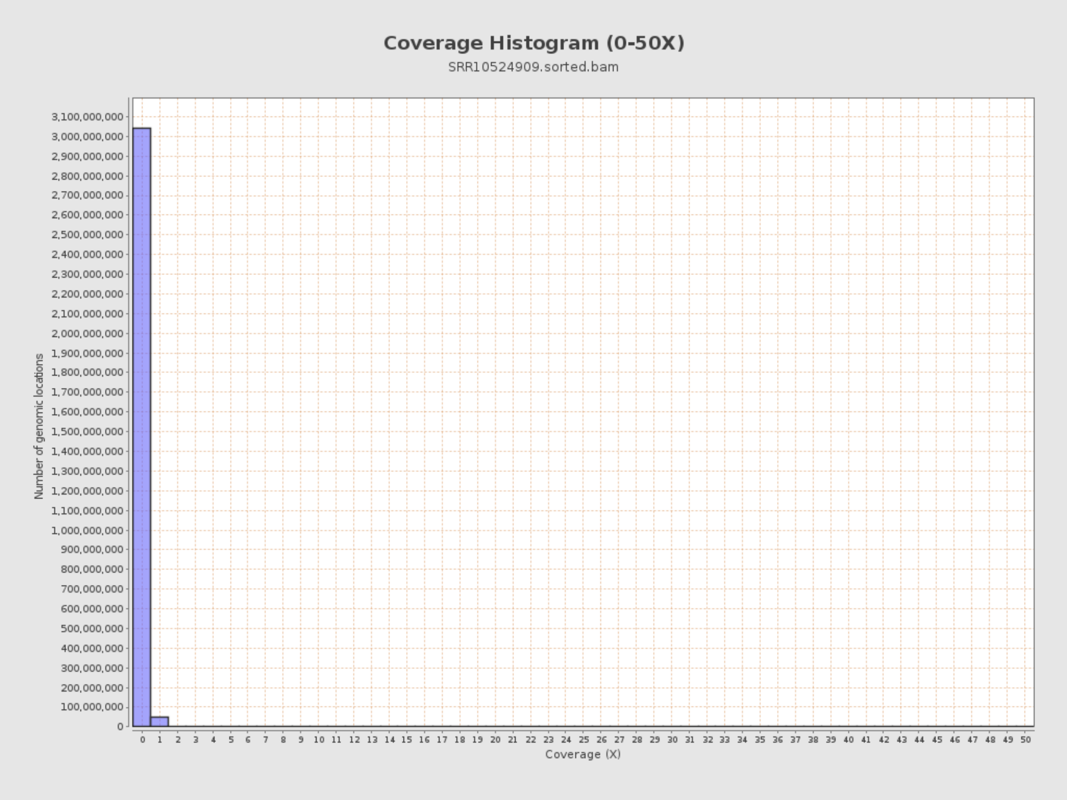
3. Results : Coverage across reference



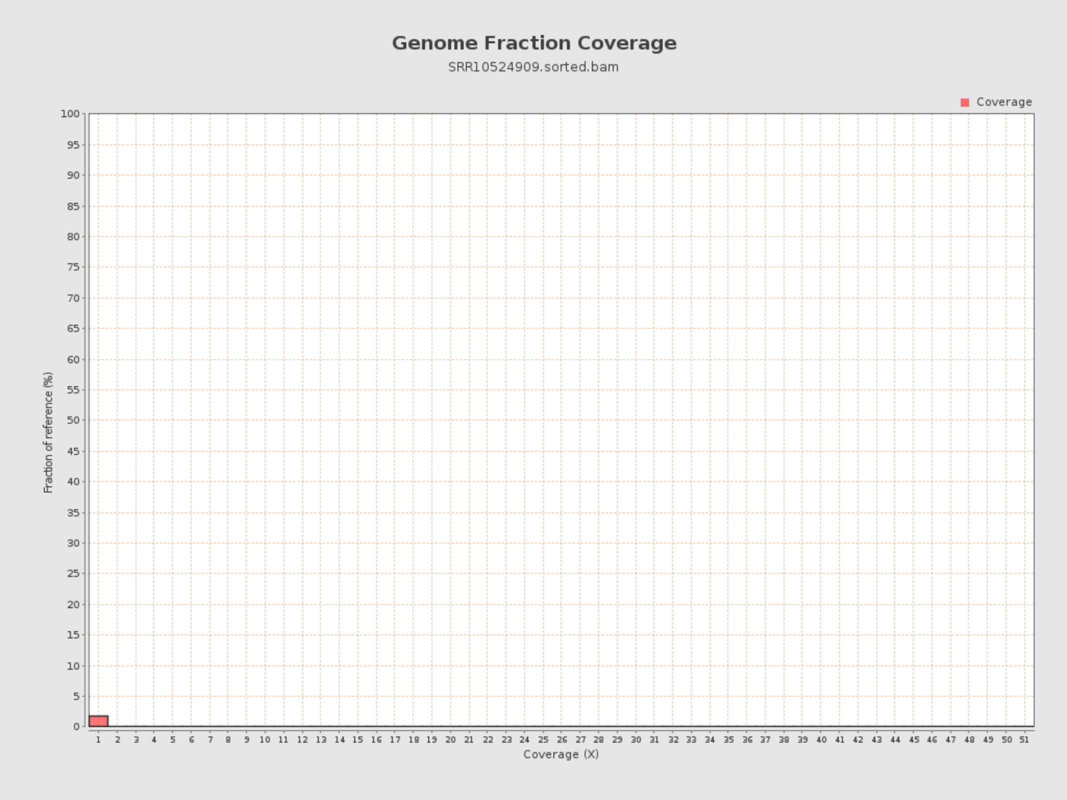
4. Results : Coverage Histogram



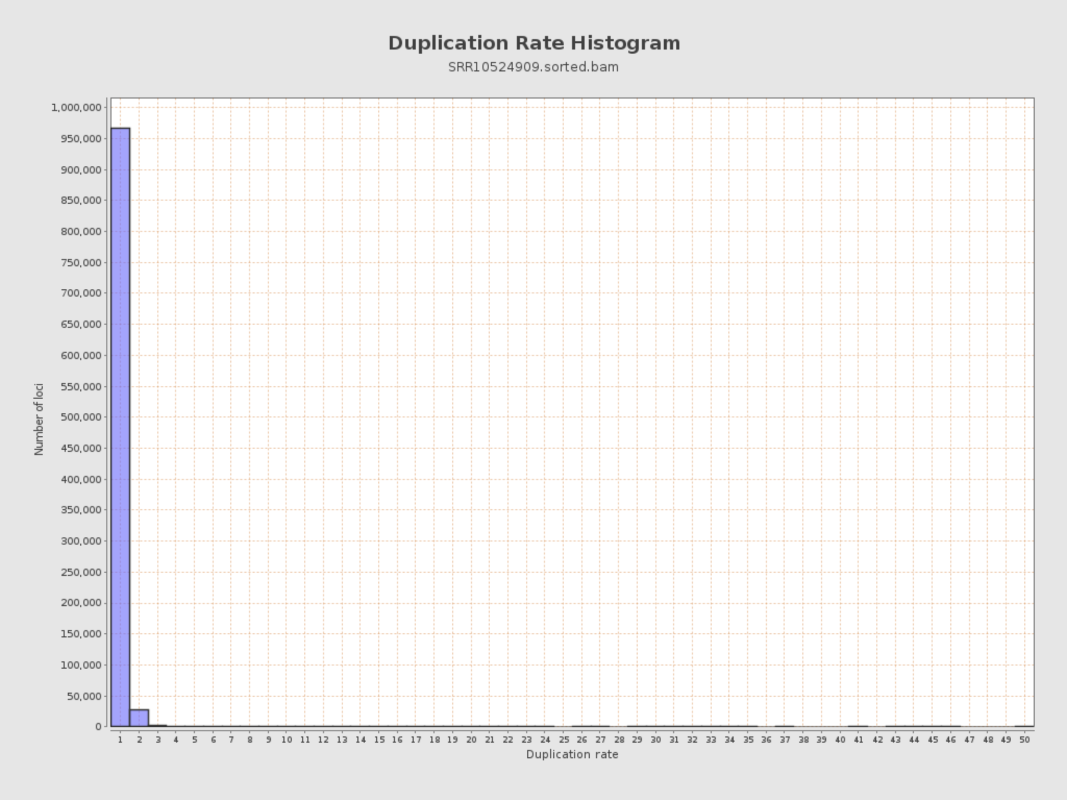
5. Results : Coverage Histogram (0-50X)



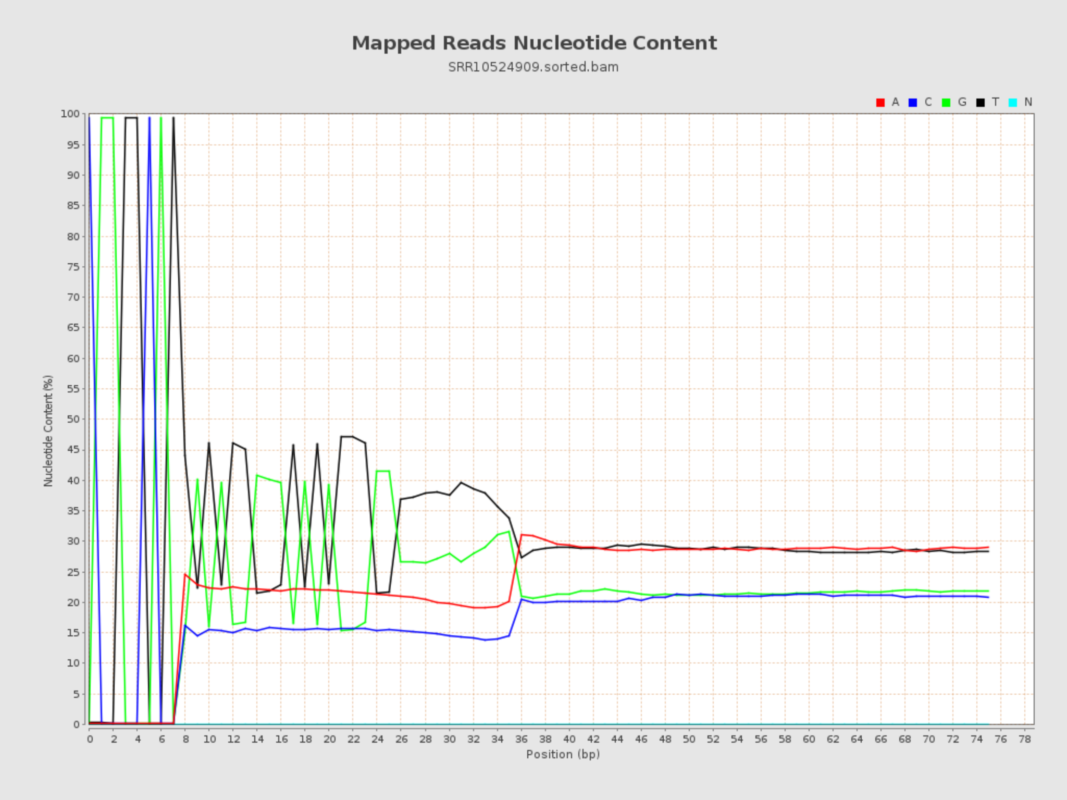
6. Results : Genome Fraction Coverage



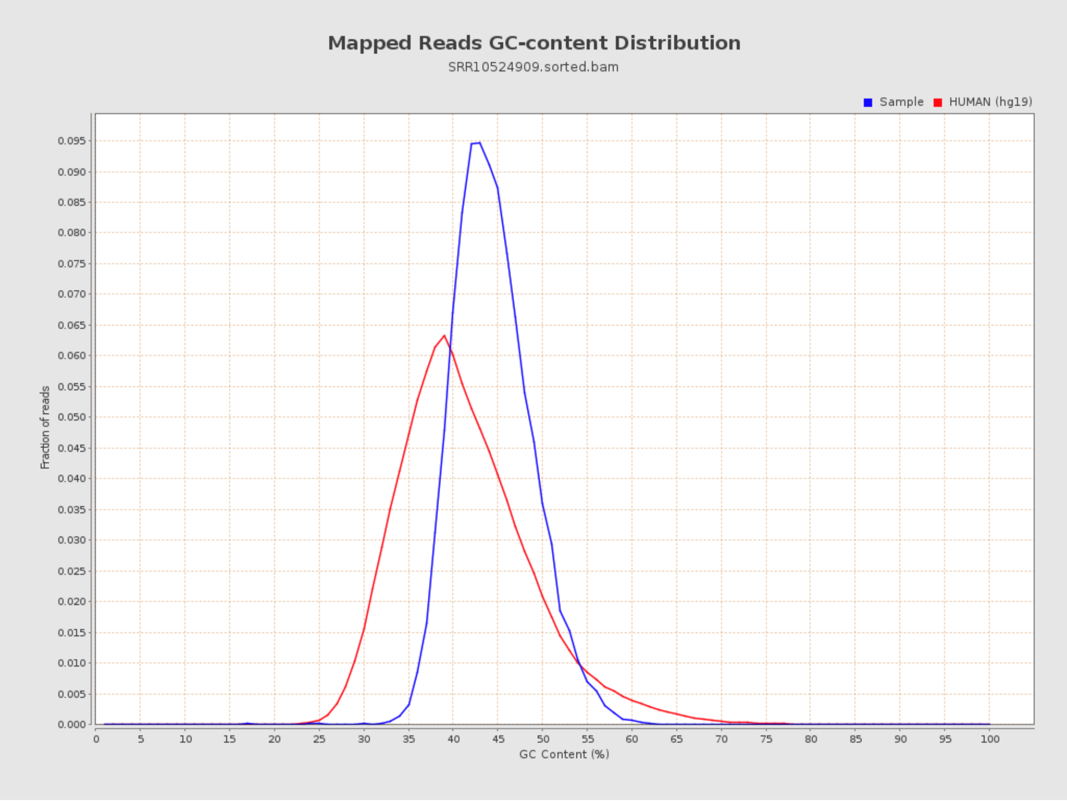
7. Results : Duplication Rate Histogram



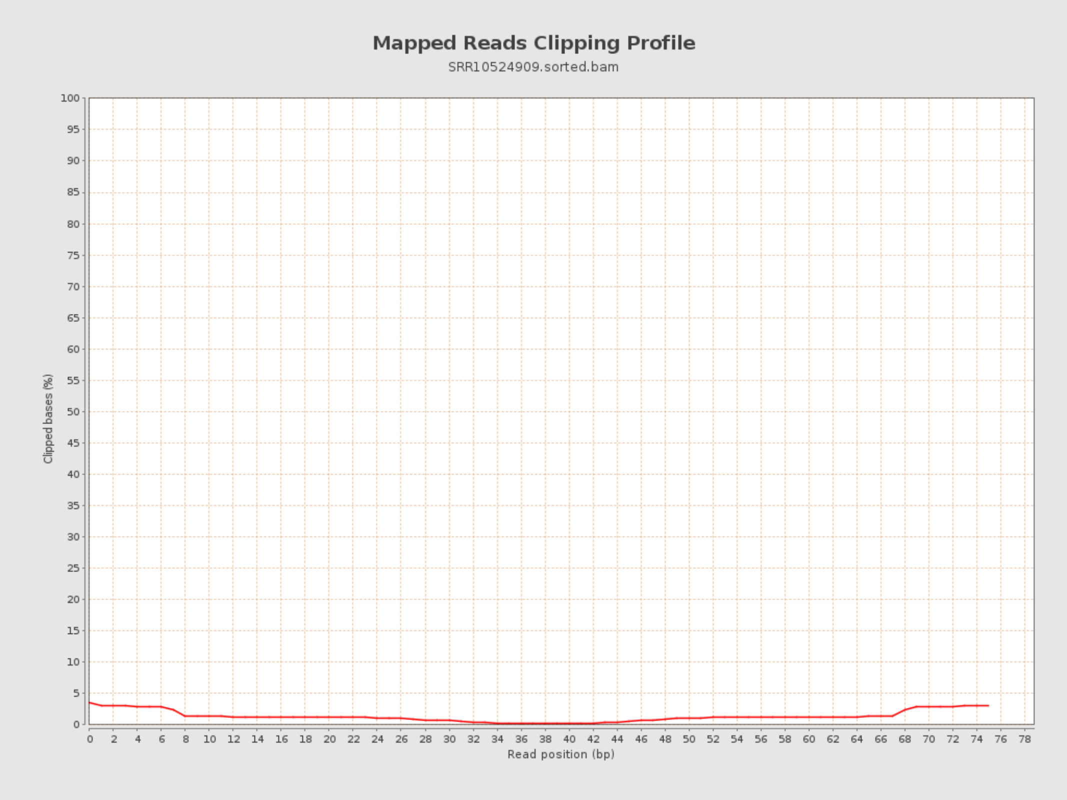
8. Results : Mapped Reads Nucleotide Content



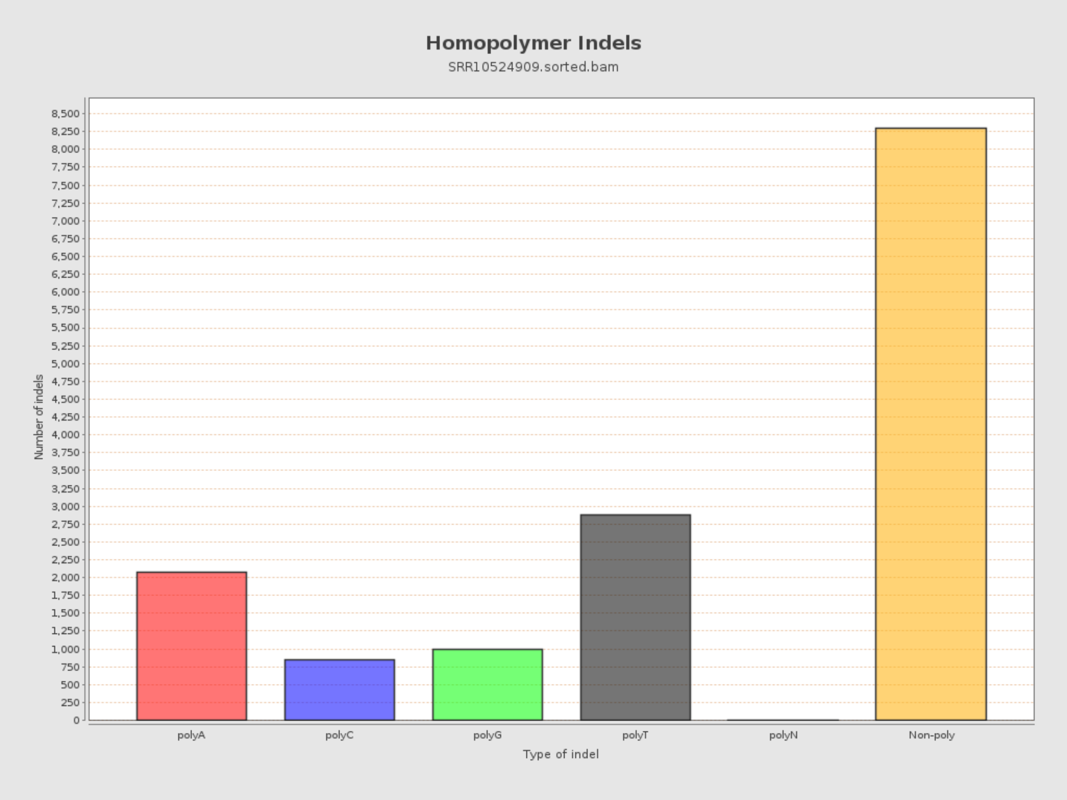
9. Results : Mapped Reads GC-content Distribution



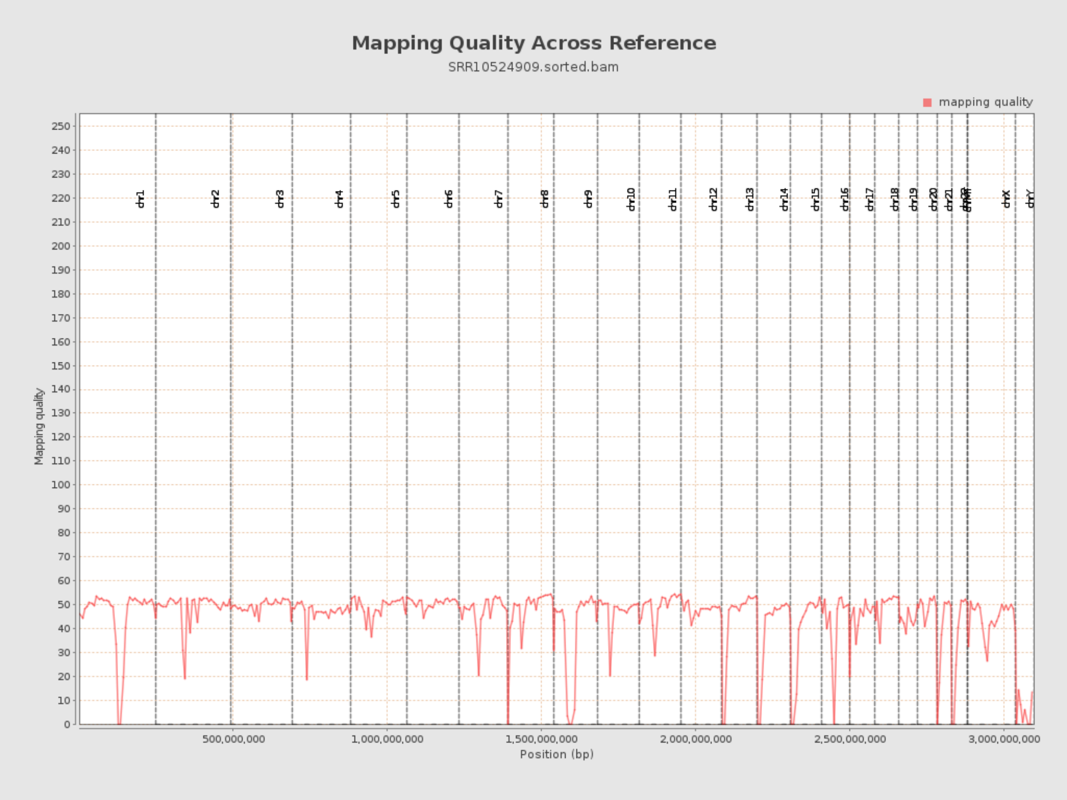
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram