Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:41:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524571.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_SRR10524571 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524571.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:41:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524571.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	907,095
Mapped reads	797,210 / 87.89%
Unmapped reads	109,885 / 12.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,656 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	62,559 / 6.9%
Duplication rate	6.24%
Clipped reads	800,519 / 88.25%

2.2. ACGT Content

Number/percentage of A's	10,803,329 / 24.05%
Number/percentage of C's	8,642,280 / 19.24%
Number/percentage of T's	14,219,883 / 31.65%
Number/percentage of G's	11,257,171 / 25.06%
Number/percentage of N's	557 / 0%
GC Percentage	44.3%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1802

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Mismatches and indels

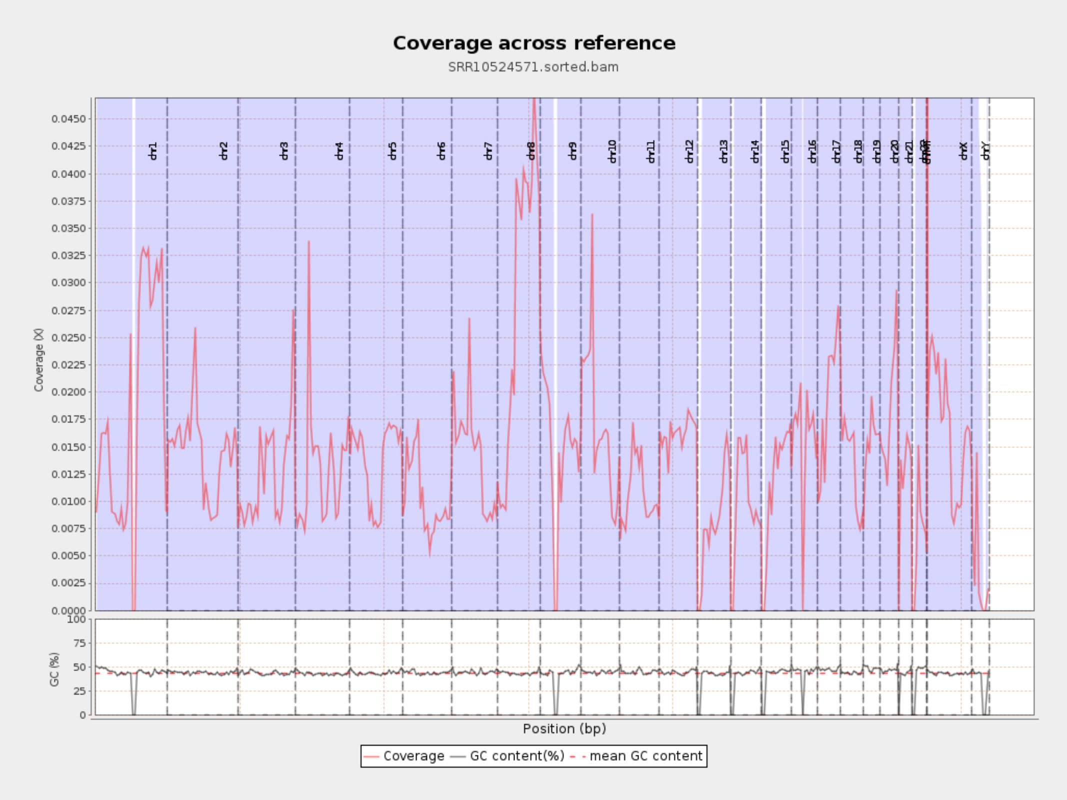
General error rate	0.57%
Mismatches	251,496
Insertions	2,675
Mapped reads with at least one insertion	0.33%
Deletions	9,460
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.37%

2.6. Chromosome stats

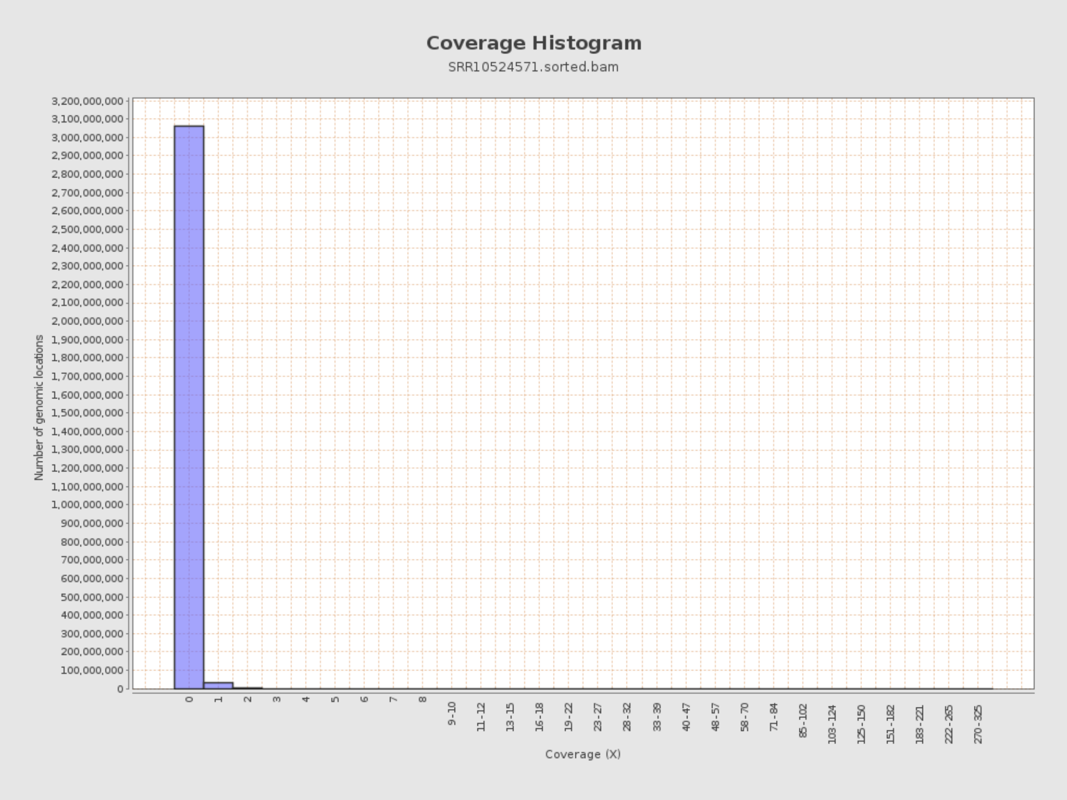
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4502013	0.0181	0.2673
chr2	243199373	3561031	0.0146	0.2183
chr3	198022430	2482058	0.0125	0.1349
chr4	191154276	2437844	0.0128	0.1661
chr5	180915260	2504279	0.0138	0.1408
chr6	171115067	1765305	0.0103	0.1316
chr7	159138663	2307966	0.0145	0.1973

chr8	146364022	4218475	0.0288	0.2309
chr9	141213431	2075427	0.0147	0.1589
chr10	135534747	2354702	0.0174	0.2267
chr11	135006516	1467384	0.0109	0.1514
chr12	133851895	2179575	0.0163	0.1542
chr13	115169878	936928	0.0081	0.1079
chr14	107349540	1055646	0.0098	0.1205
chr15	102531392	1170781	0.0114	0.1301
chr16	90354753	1393508	0.0154	0.1555
chr17	81195210	1572437	0.0194	0.1751
chr18	78077248	1047331	0.0134	0.2286
chr19	59128983	920124	0.0156	0.2012
chr20	63025520	1168634	0.0185	0.1666
chr21	48129895	603827	0.0125	0.1577
chr22	51304566	348153	0.0068	0.0991
chrMT	16571	38813	2.3422	2.173
chrX	155270560	2628364	0.0169	0.1633
chrY	59373566	198707	0.0033	0.1468

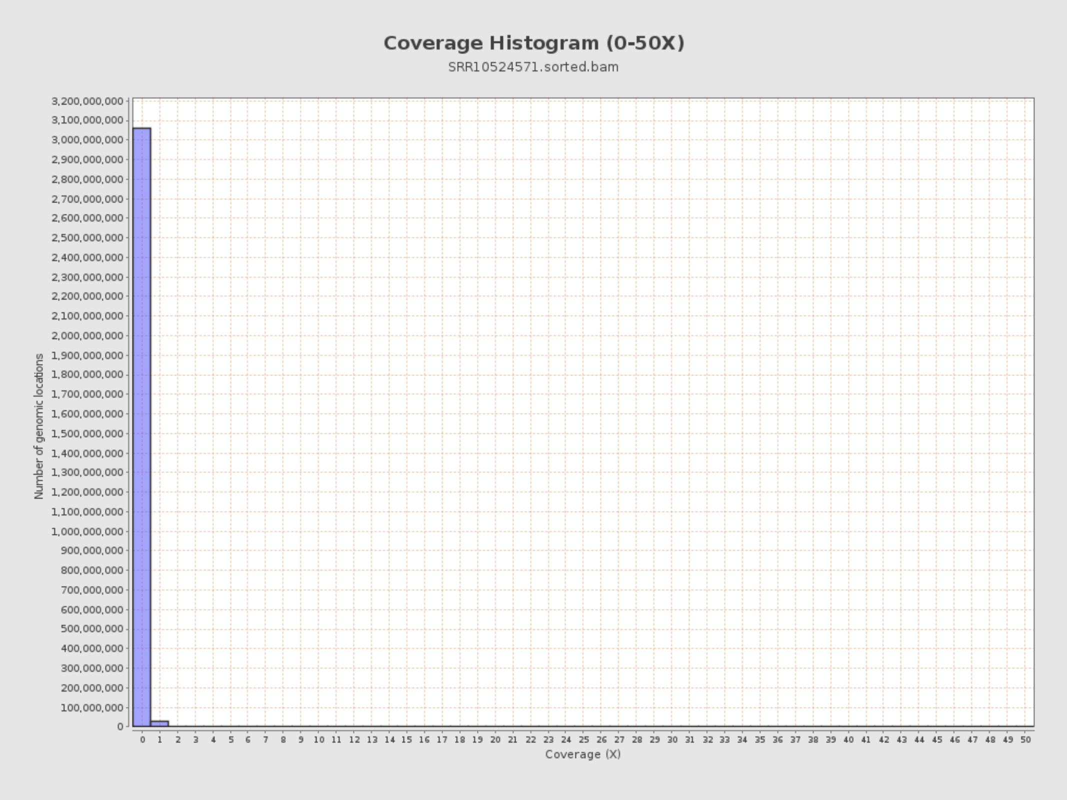
3. Results : Coverage across reference



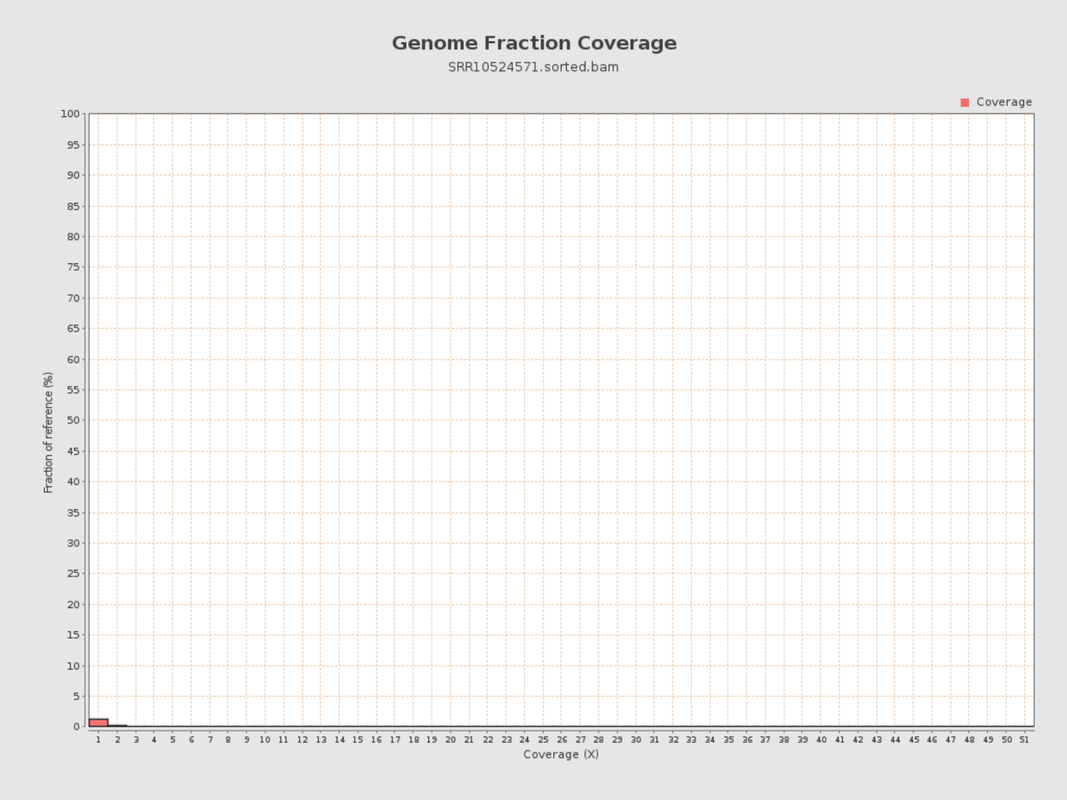
4. Results : Coverage Histogram



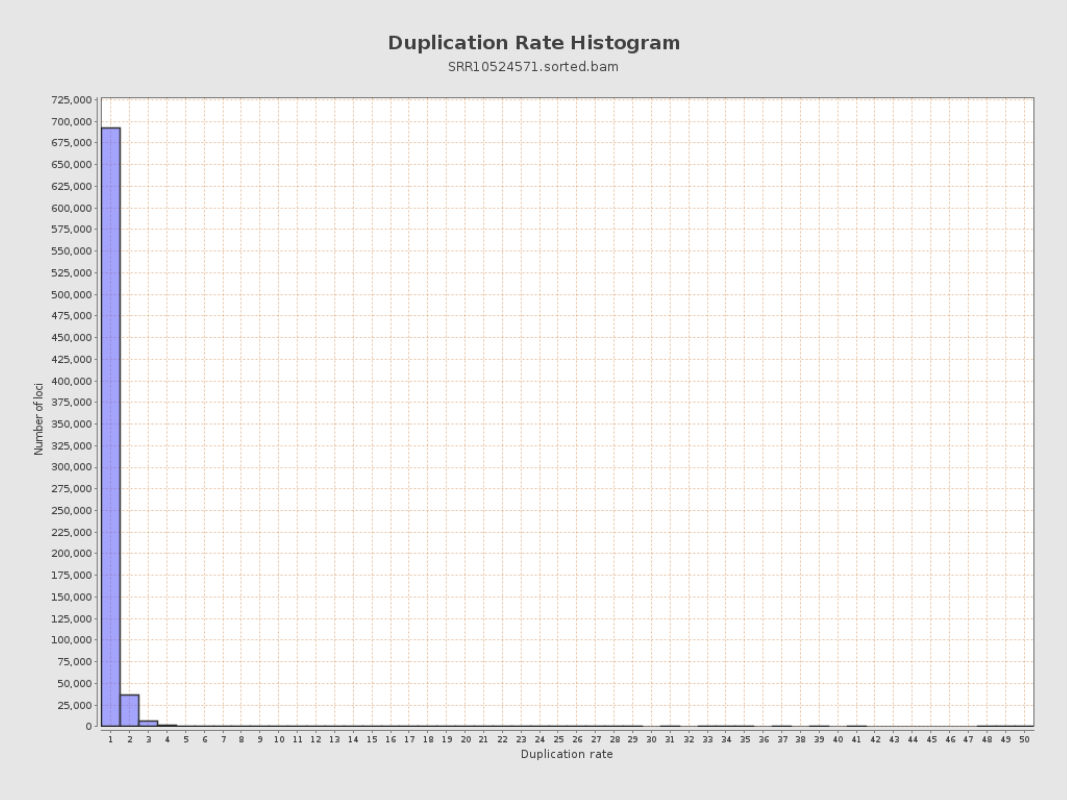
5. Results : Coverage Histogram (0-50X)



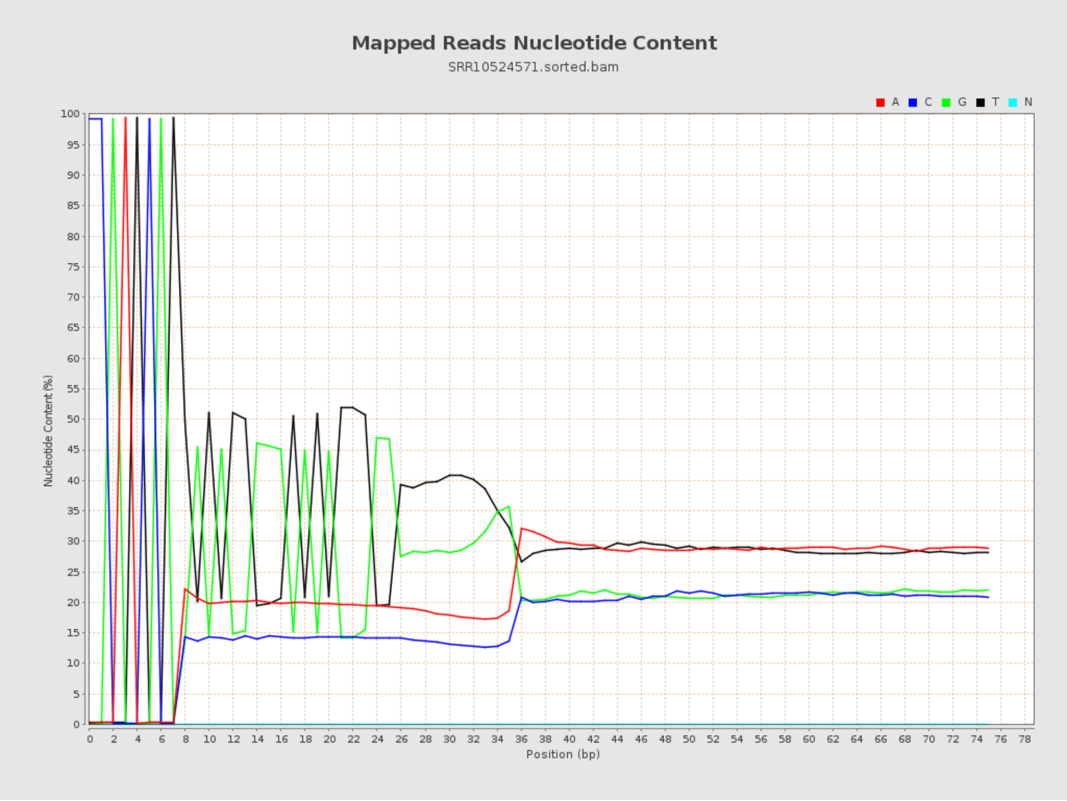
6. Results : Genome Fraction Coverage



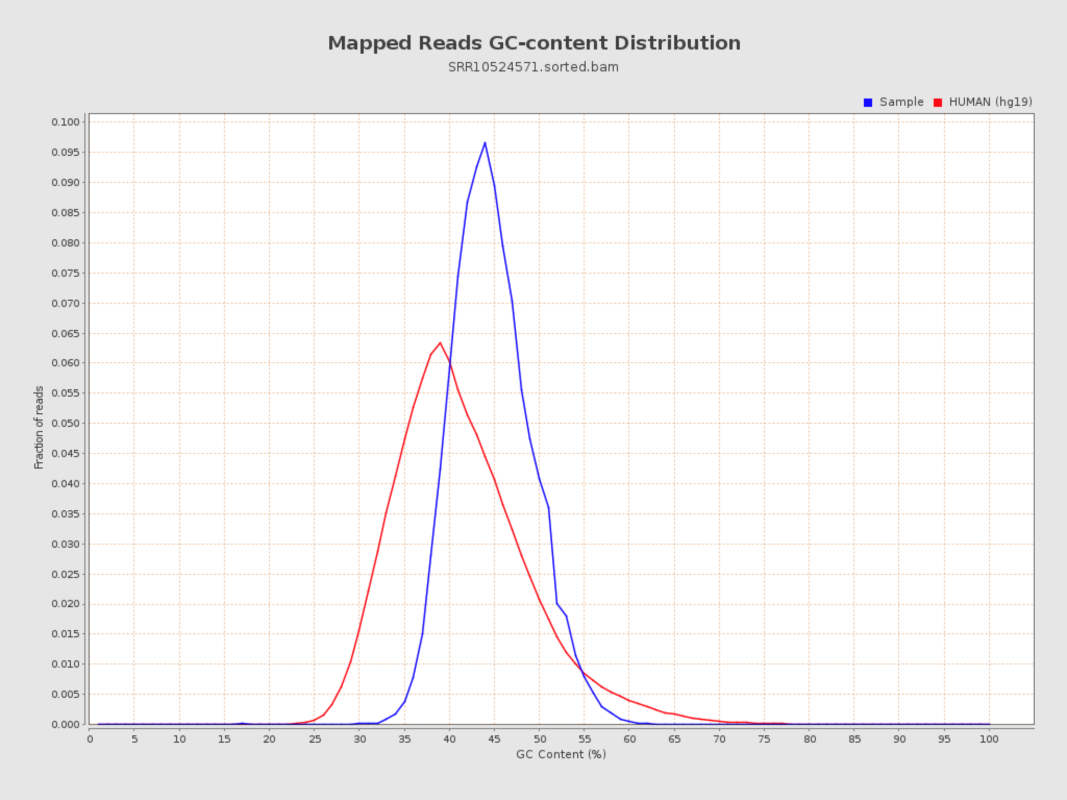
7. Results : Duplication Rate Histogram



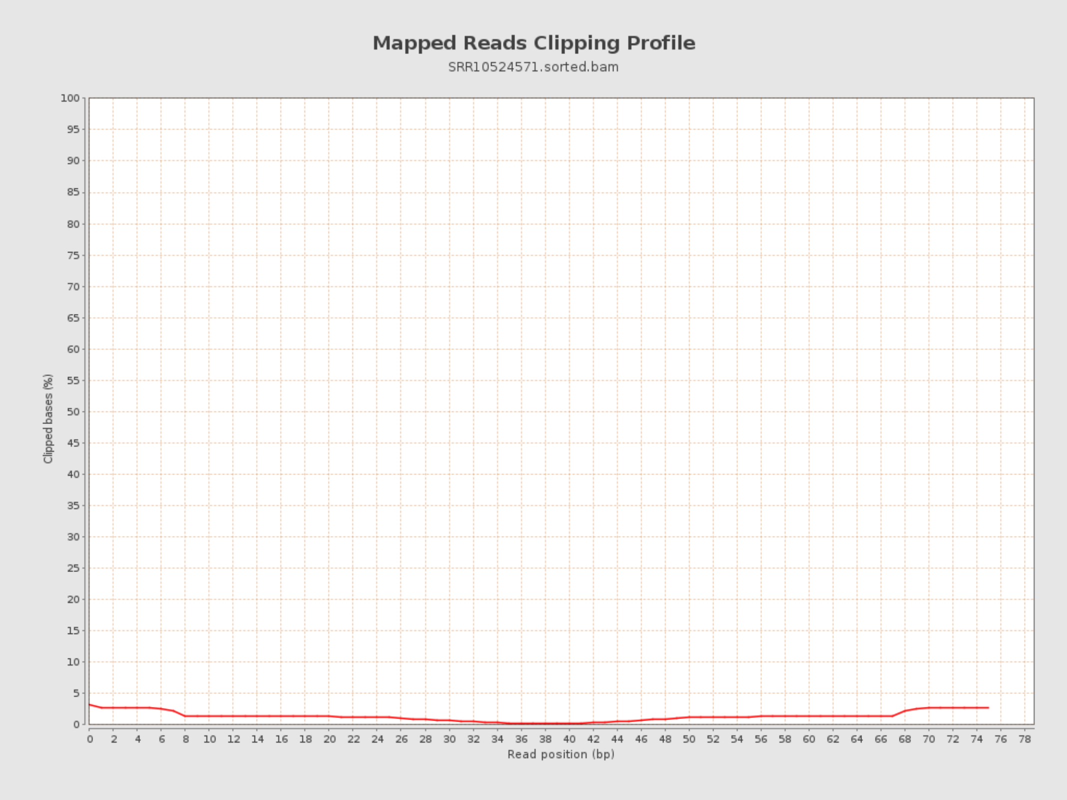
8. Results : Mapped Reads Nucleotide Content



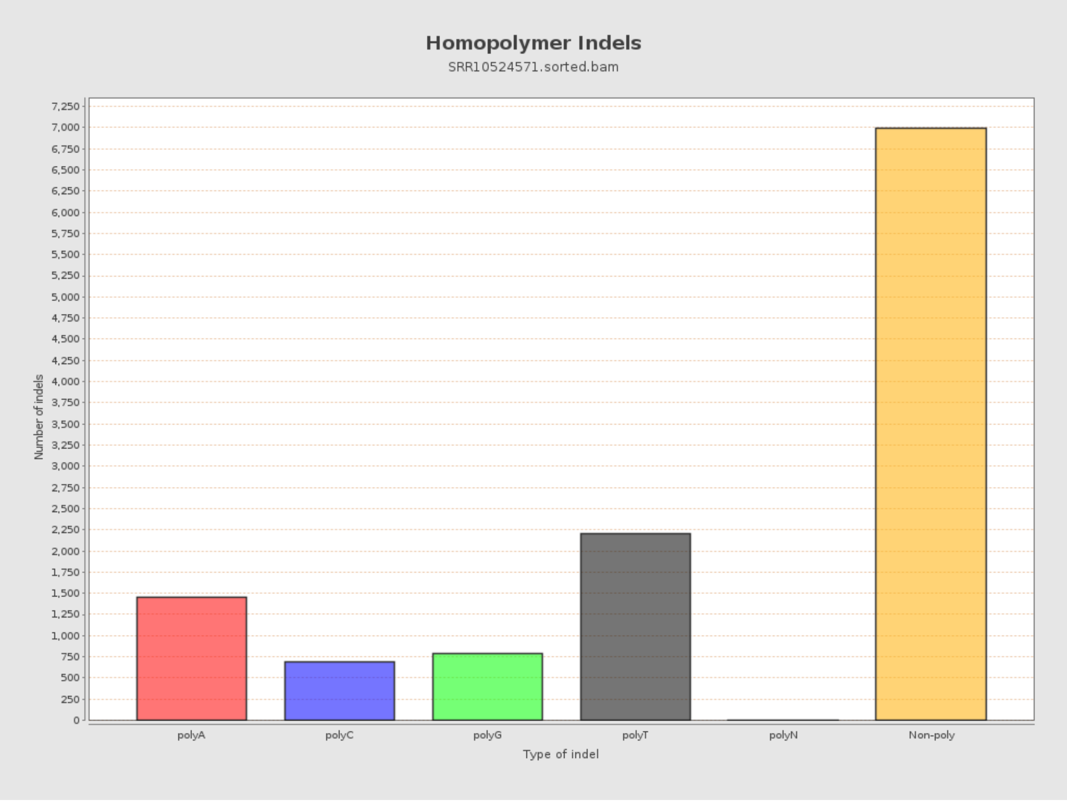
9. Results : Mapped Reads GC-content Distribution



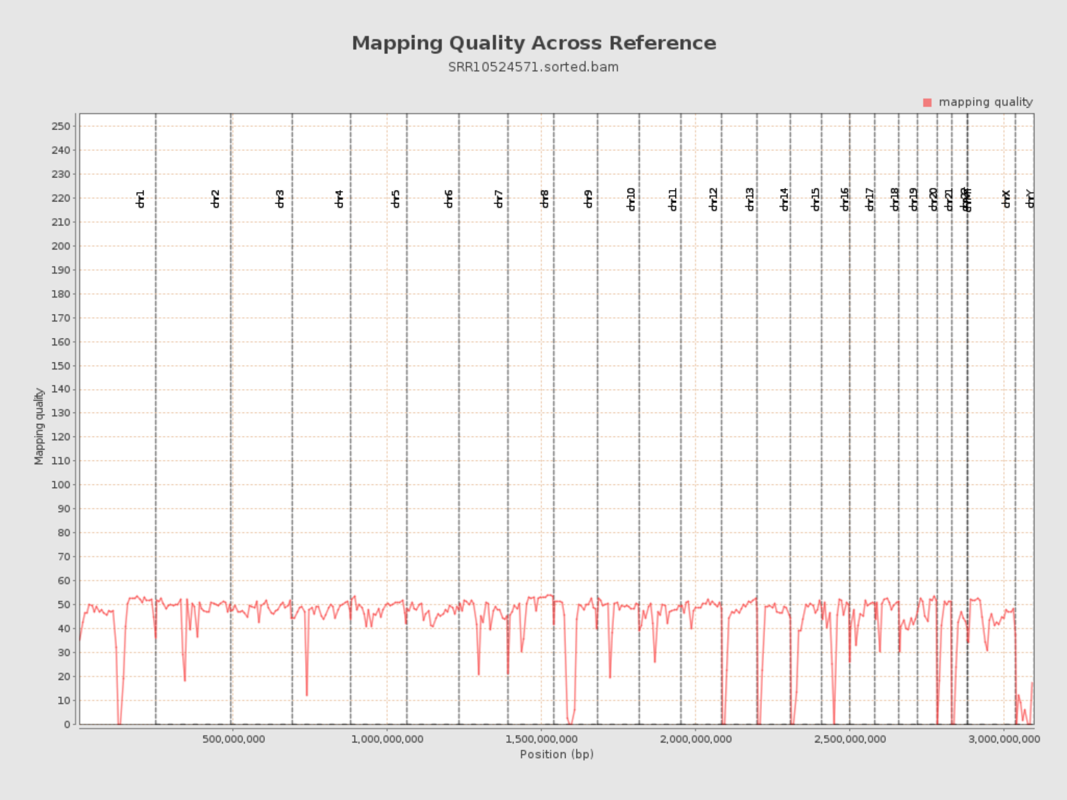
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram