Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:57:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524371.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_SRR10524371 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524371.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:57:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524371.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	617,007
Mapped reads	563,275 / 91.29%
Unmapped reads	53,732 / 8.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,625 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	13,930 / 2.26%
Duplication rate	1.85%
Clipped reads	564,467 / 91.48%

2.2. ACGT Content

Number/percentage of A's	8,502,561 / 25.68%
Number/percentage of C's	6,035,679 / 18.23%
Number/percentage of T's	10,269,969 / 31.02%
Number/percentage of G's	8,291,177 / 25.05%
Number/percentage of N's	4,772 / 0.01%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0107

Standard Deviation	0.1348

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

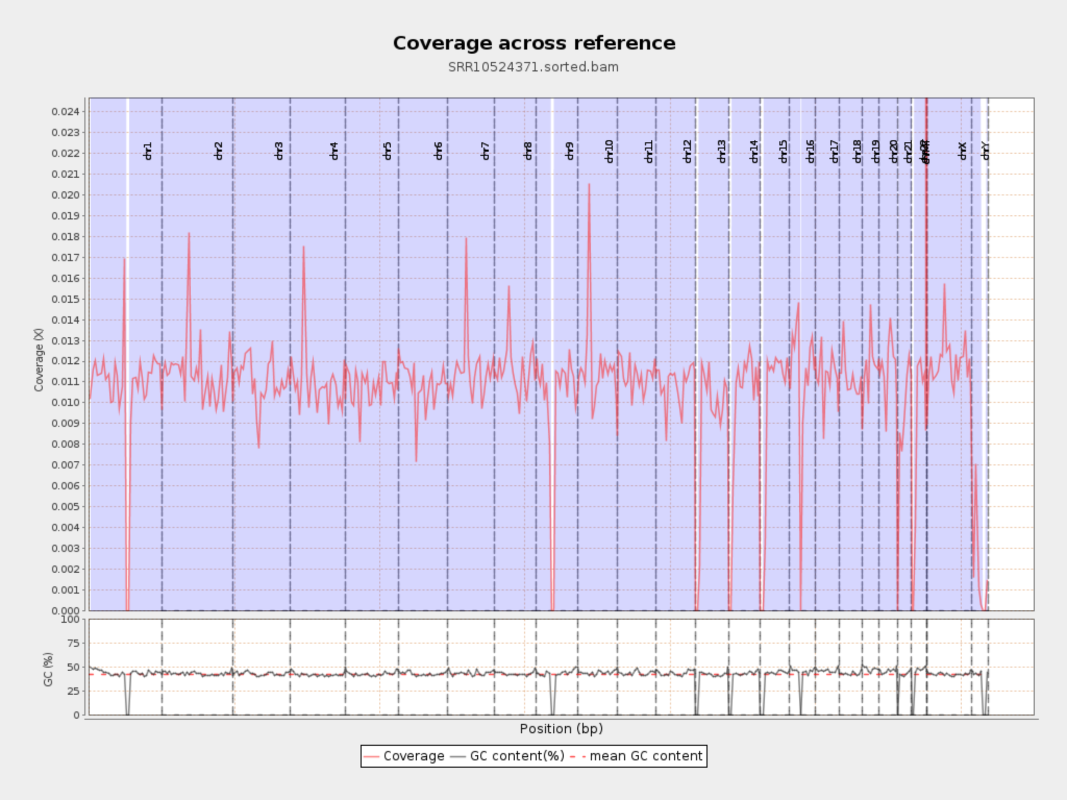
General error rate	0.53%
Mismatches	169,135
Insertions	2,403
Mapped reads with at least one insertion	0.42%
Deletions	5,973
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.08%

2.6. Chromosome stats

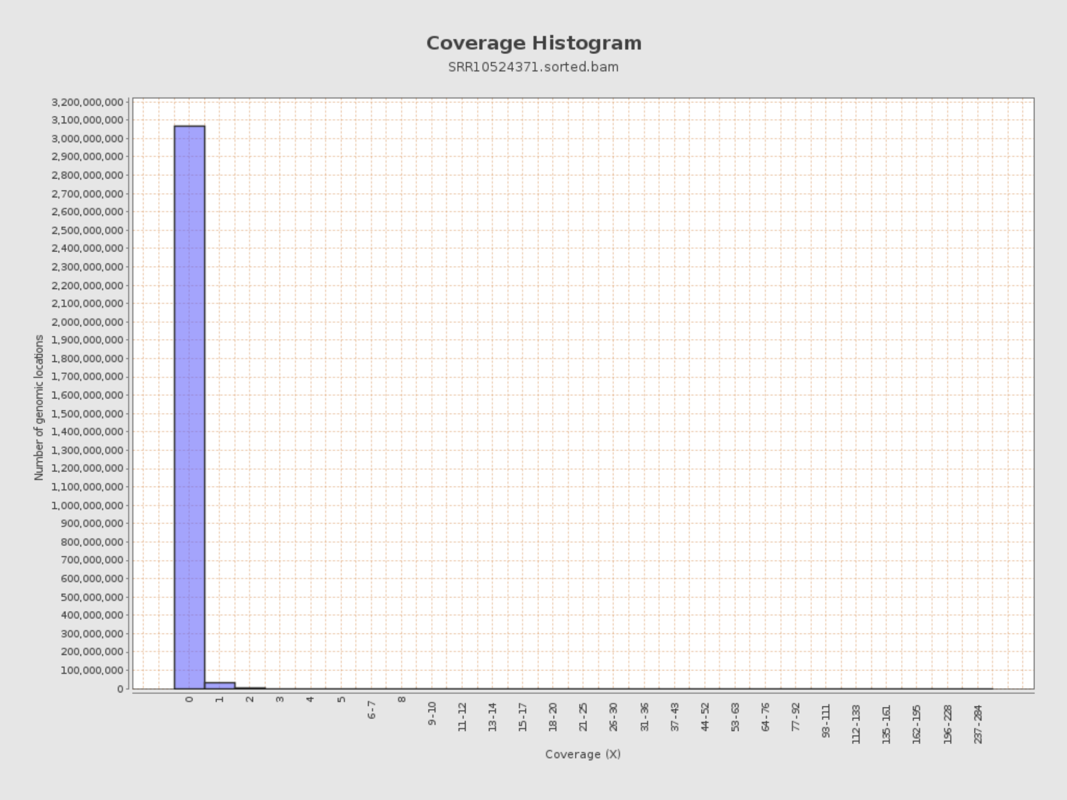
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2649190	0.0106	0.2155
chr2	243199373	2805627	0.0115	0.1654
chr3	198022430	2192722	0.0111	0.1099
chr4	191154276	2102587	0.011	0.1167
chr5	180915260	1953241	0.0108	0.1084
chr6	171115067	1866036	0.0109	0.1124
chr7	159138663	1840030	0.0116	0.1569

chr8	146364022	1702334	0.0116	0.1286
chr9	141213431	1379915	0.0098	0.12
chr10	135534747	1602741	0.0118	0.1363
chr11	135006516	1520772	0.0113	0.1228
chr12	133851895	1457043	0.0109	0.1099
chr13	115169878	1003272	0.0087	0.0972
chr14	107349540	1022510	0.0095	0.104
chr15	102531392	968254	0.0094	0.1014
chr16	90354753	1013935	0.0112	0.1146
chr17	81195210	908178	0.0112	0.1137
chr18	78077248	878072	0.0112	0.1887
chr19	59128983	698103	0.0118	0.1648
chr20	63025520	738957	0.0117	0.1149
chr21	48129895	433210	0.009	0.104
chr22	51304566	407471	0.0079	0.0928
chrMT	16571	7189	0.4338	0.7298
chrX	155270560	1851467	0.0119	0.1181
chrY	59373566	110441	0.0019	0.0698

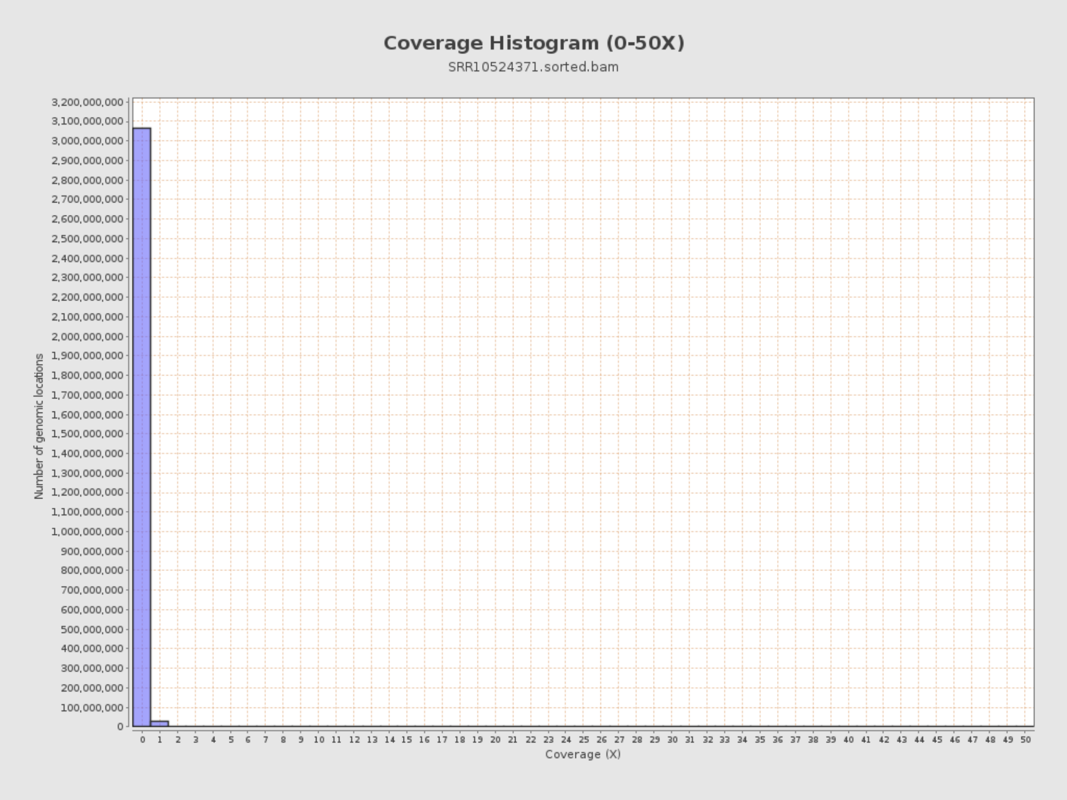
3. Results : Coverage across reference



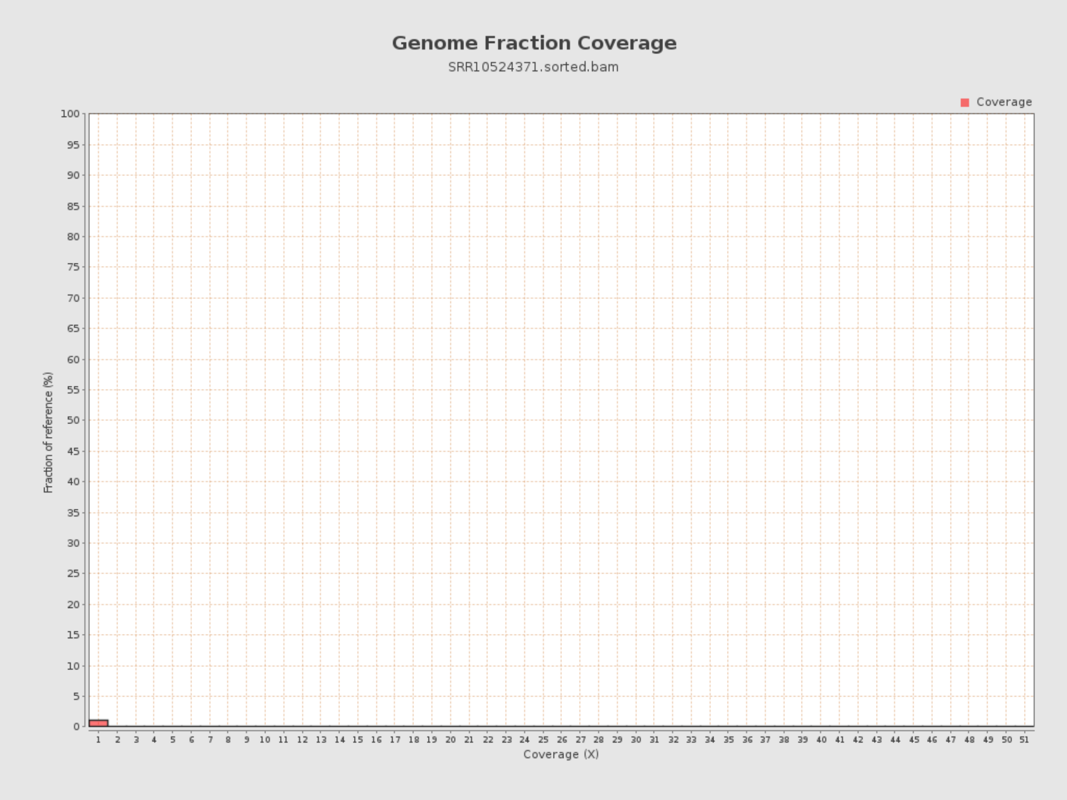
4. Results : Coverage Histogram



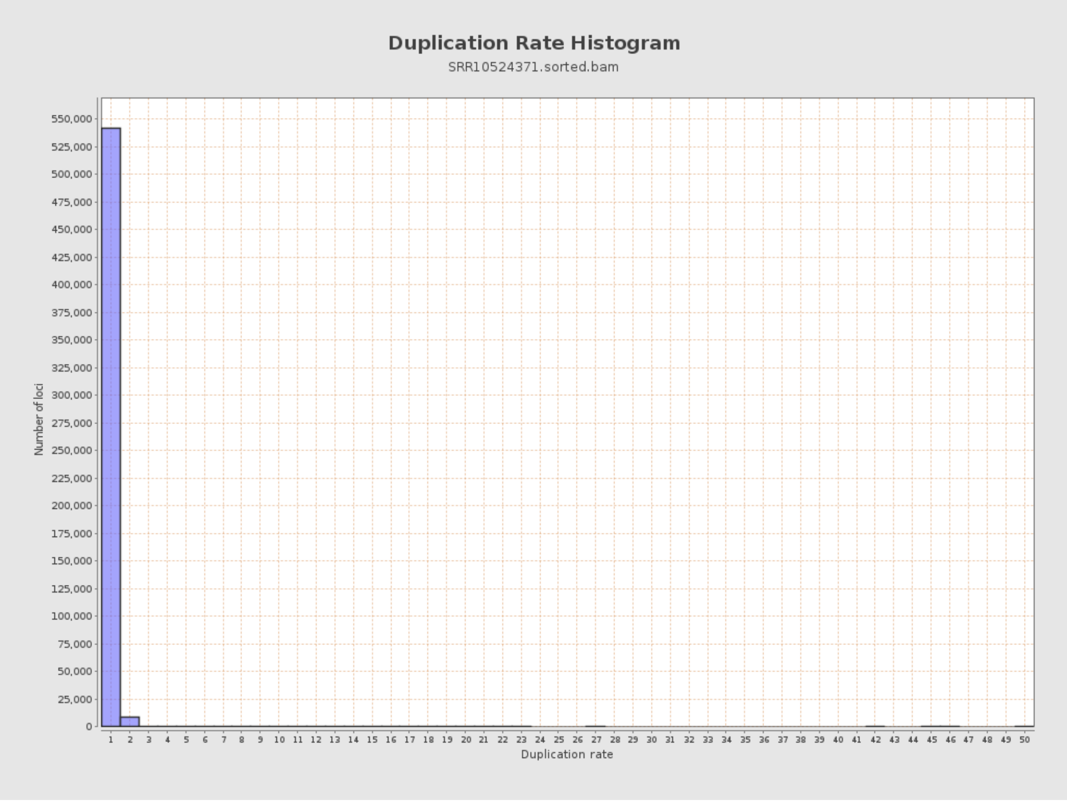
5. Results : Coverage Histogram (0-50X)



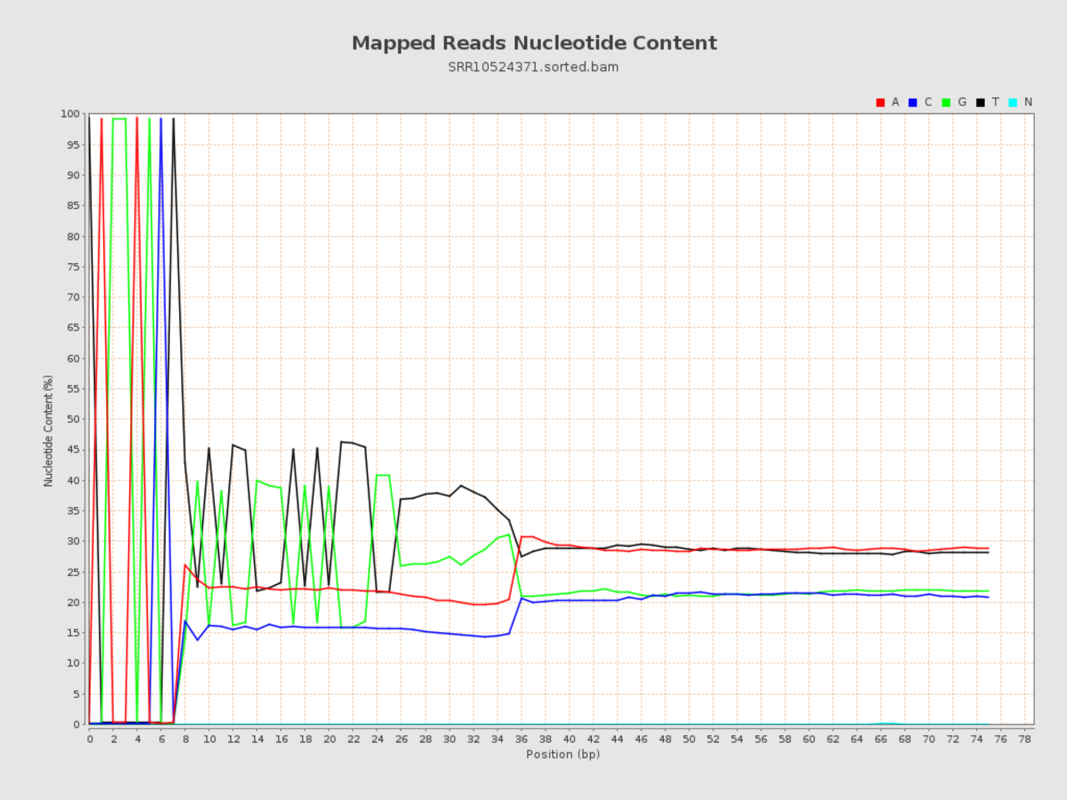
6. Results : Genome Fraction Coverage



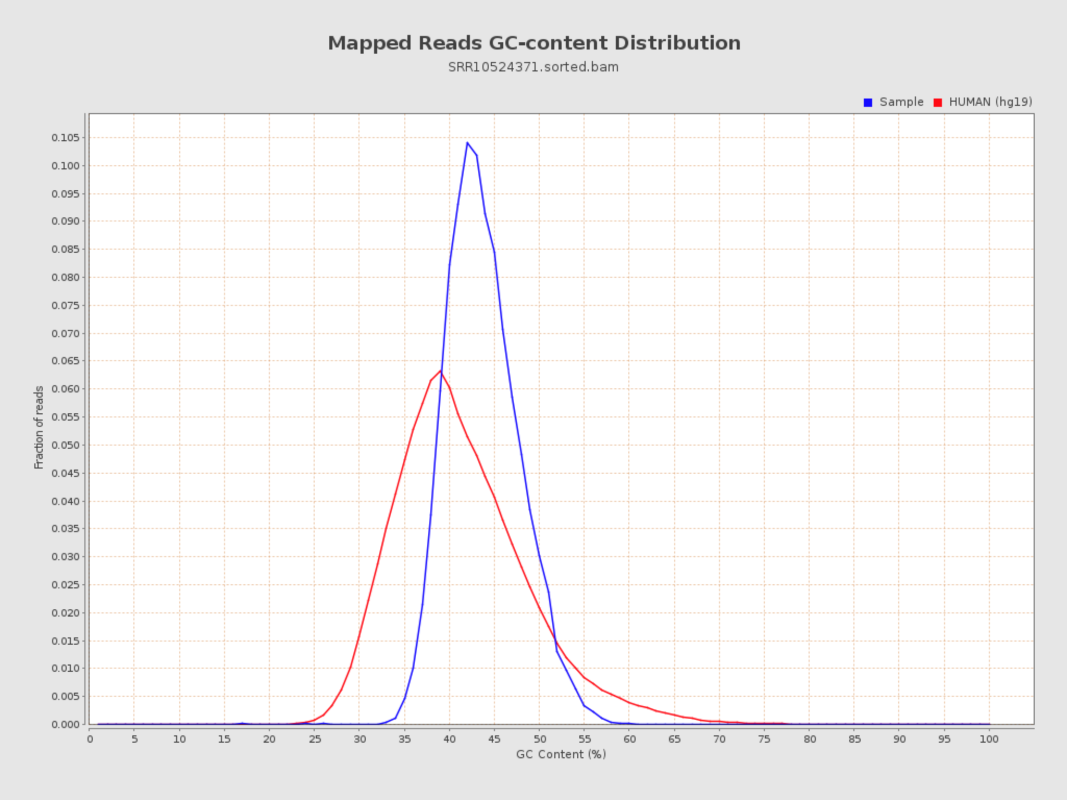
7. Results : Duplication Rate Histogram



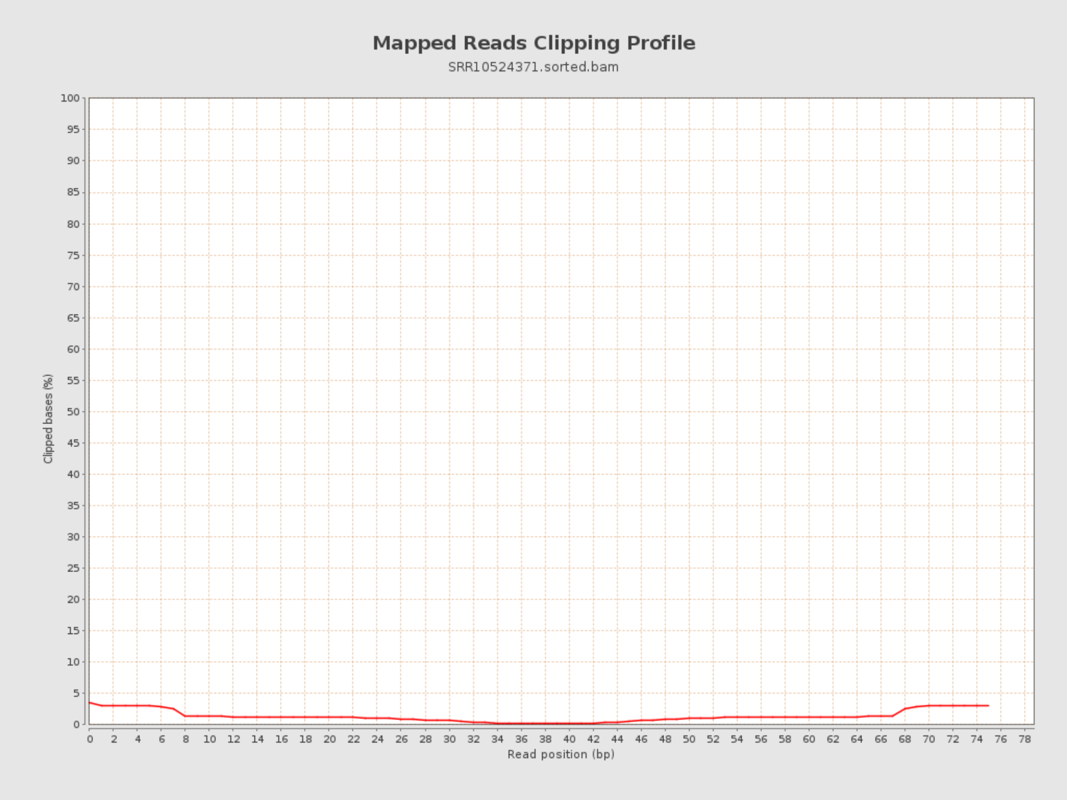
8. Results : Mapped Reads Nucleotide Content



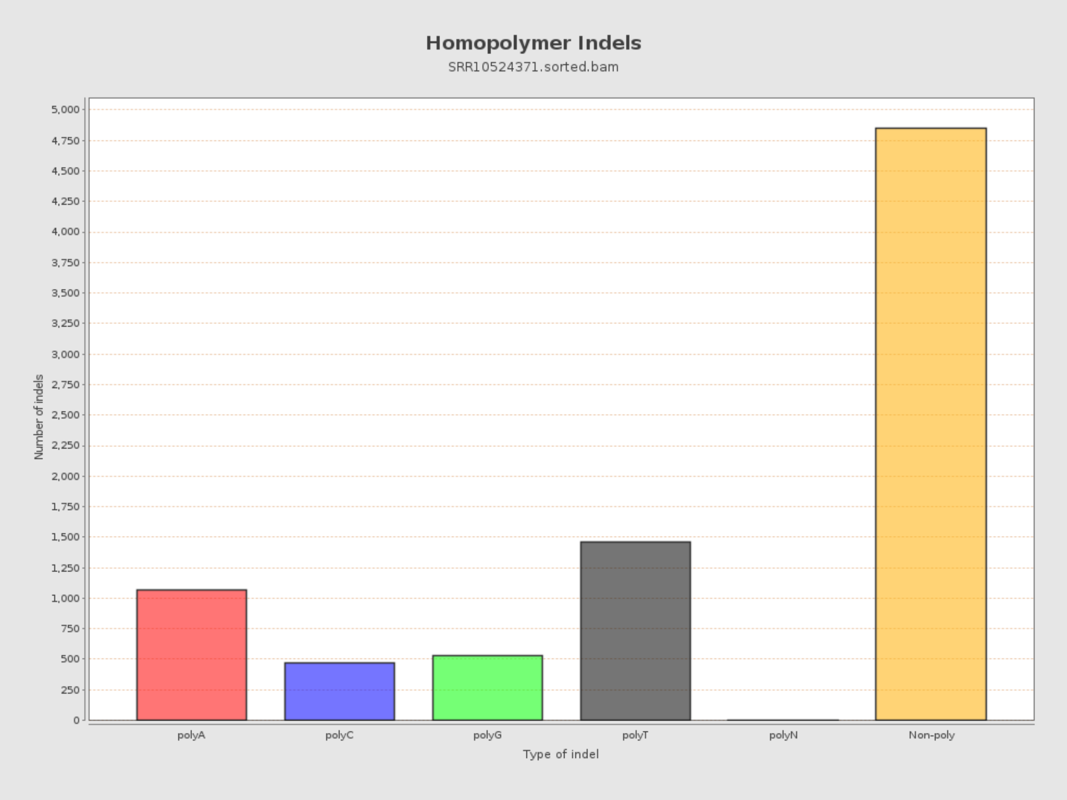
9. Results : Mapped Reads GC-content Distribution



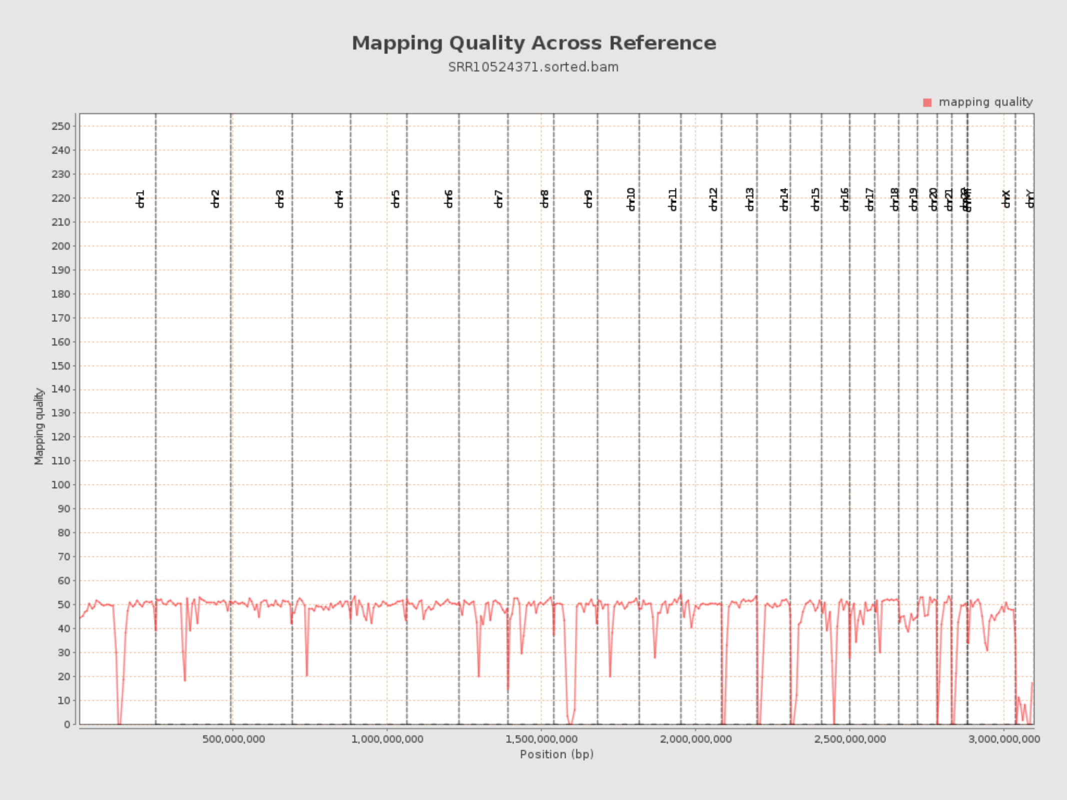
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram