Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:14:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524681.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_SRR10524681 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524681.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:14:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524681.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,225,390
Mapped reads	1,120,002 / 91.4%
Unmapped reads	105,388 / 8.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,187 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	35,463 / 2.89%
Duplication rate	2.31%
Clipped reads	1,120,627 / 91.45%

2.2. ACGT Content

Number/percentage of A's	16,605,228 / 25.26%
Number/percentage of C's	13,261,871 / 20.17%
Number/percentage of T's	21,182,310 / 32.22%
Number/percentage of G's	14,689,156 / 22.34%
Number/percentage of N's	8,661 / 0.01%
GC Percentage	42.51%

2.3. Coverage

Mean	0.0212

Standard Deviation	0.2201

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

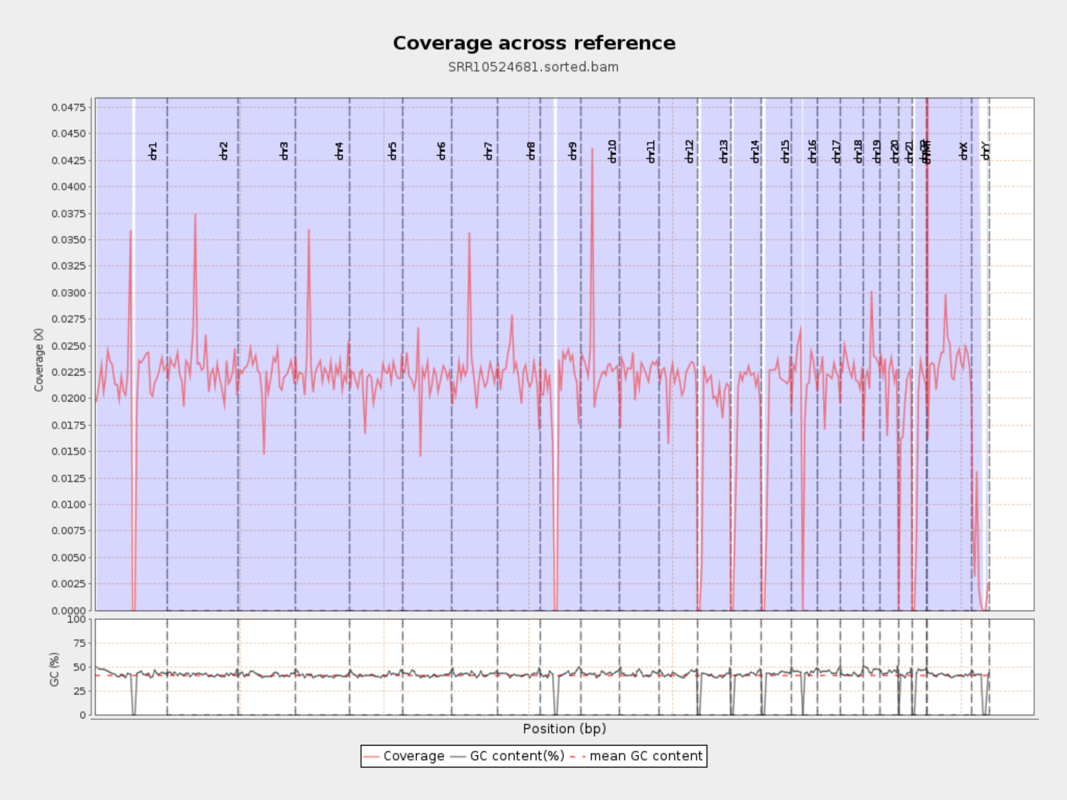
General error rate	0.53%
Mismatches	337,081
Insertions	4,605
Mapped reads with at least one insertion	0.41%
Deletions	12,762
Mapped reads with at least one deletion	1.13%
Homopolymer indels	44.07%

2.6. Chromosome stats

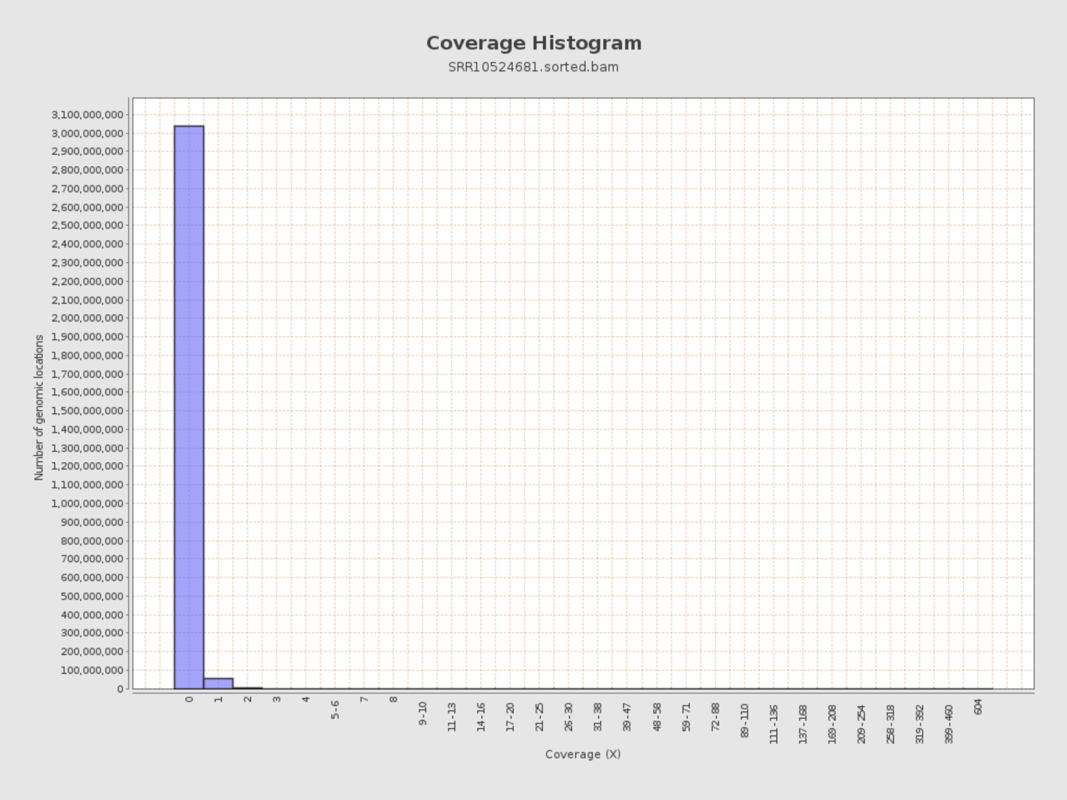
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5283163	0.0212	0.3732
chr2	243199373	5623265	0.0231	0.3073
chr3	198022430	4426932	0.0224	0.1594
chr4	191154276	4402979	0.023	0.177
chr5	180915260	3950113	0.0218	0.1575
chr6	171115067	3767482	0.022	0.1757
chr7	159138663	3603959	0.0226	0.2505

chr8	146364022	3291508	0.0225	0.2392
chr9	141213431	2746807	0.0195	0.1839
chr10	135534747	3212420	0.0237	0.2242
chr11	135006516	3051324	0.0226	0.1919
chr12	133851895	2925473	0.0219	0.1593
chr13	115169878	2015423	0.0175	0.1417
chr14	107349540	1937869	0.0181	0.1481
chr15	102531392	1849184	0.018	0.1437
chr16	90354753	1863223	0.0206	0.1642
chr17	81195210	1778662	0.0219	0.1639
chr18	78077248	1767846	0.0226	0.3087
chr19	59128983	1386058	0.0234	0.29
chr20	63025520	1376443	0.0218	0.1589
chr21	48129895	850804	0.0177	0.153
chr22	51304566	768847	0.015	0.1308
chrMT	16571	15978	0.9642	1.0679
chrX	155270560	3661121	0.0236	0.1746
chrY	59373566	210630	0.0035	0.1252

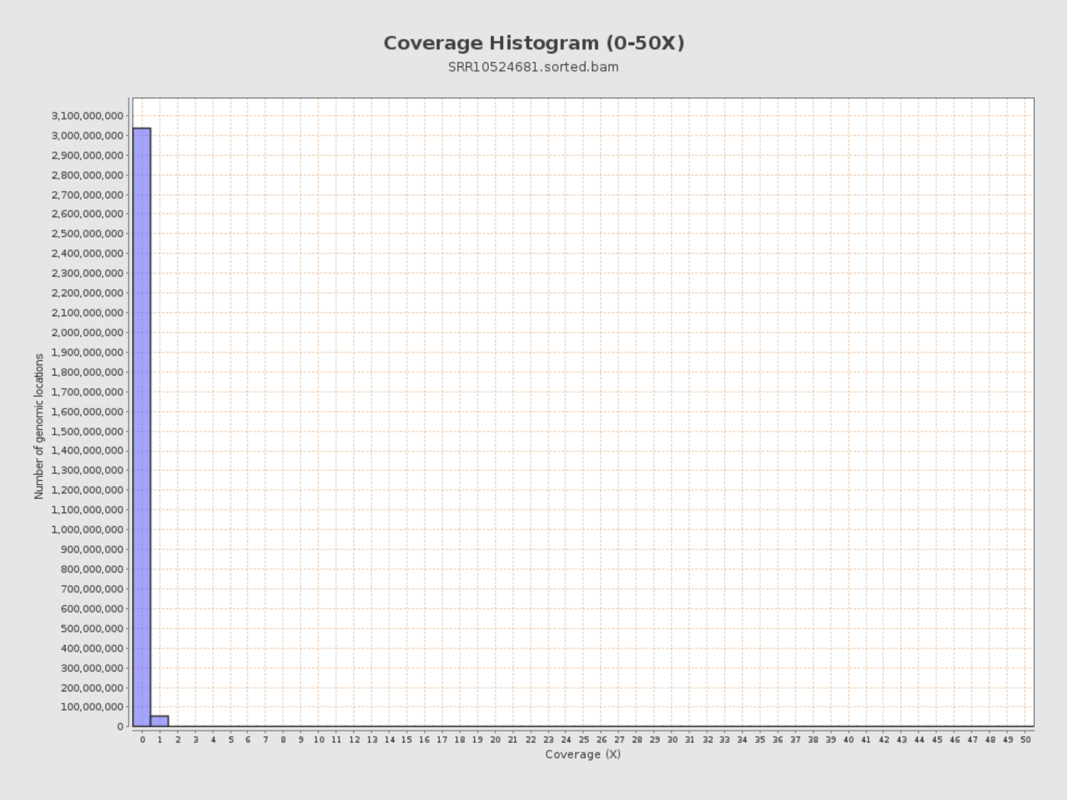
3. Results : Coverage across reference



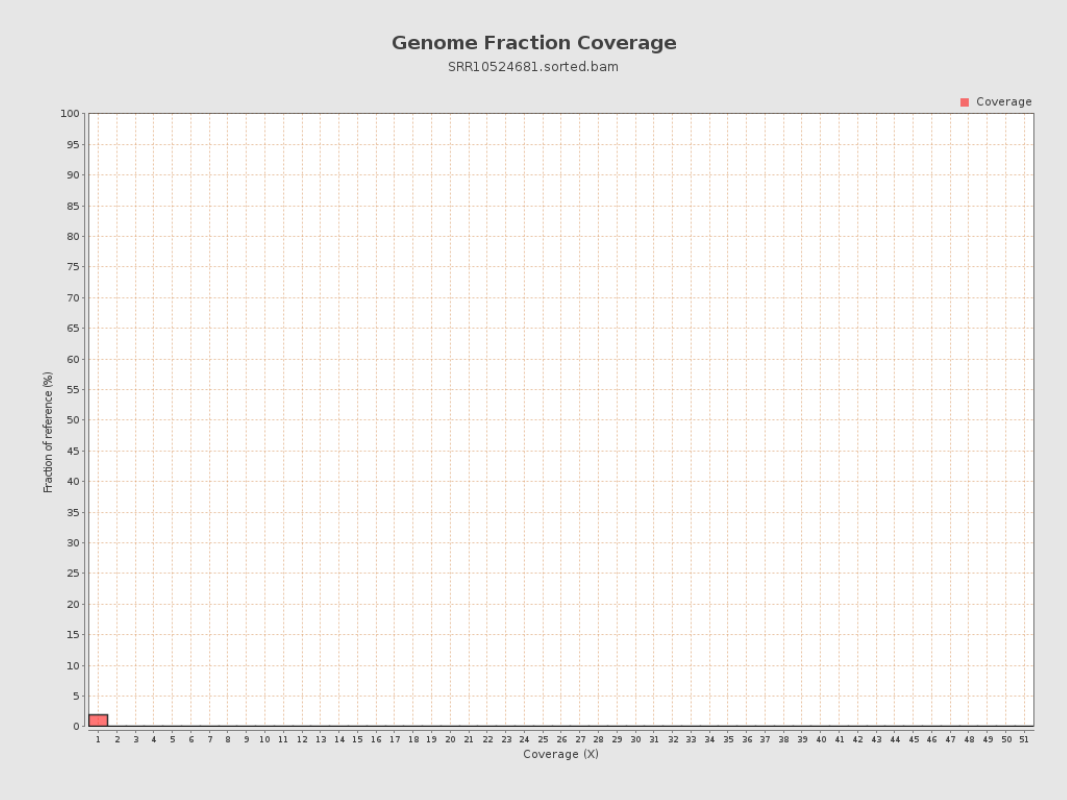
4. Results : Coverage Histogram



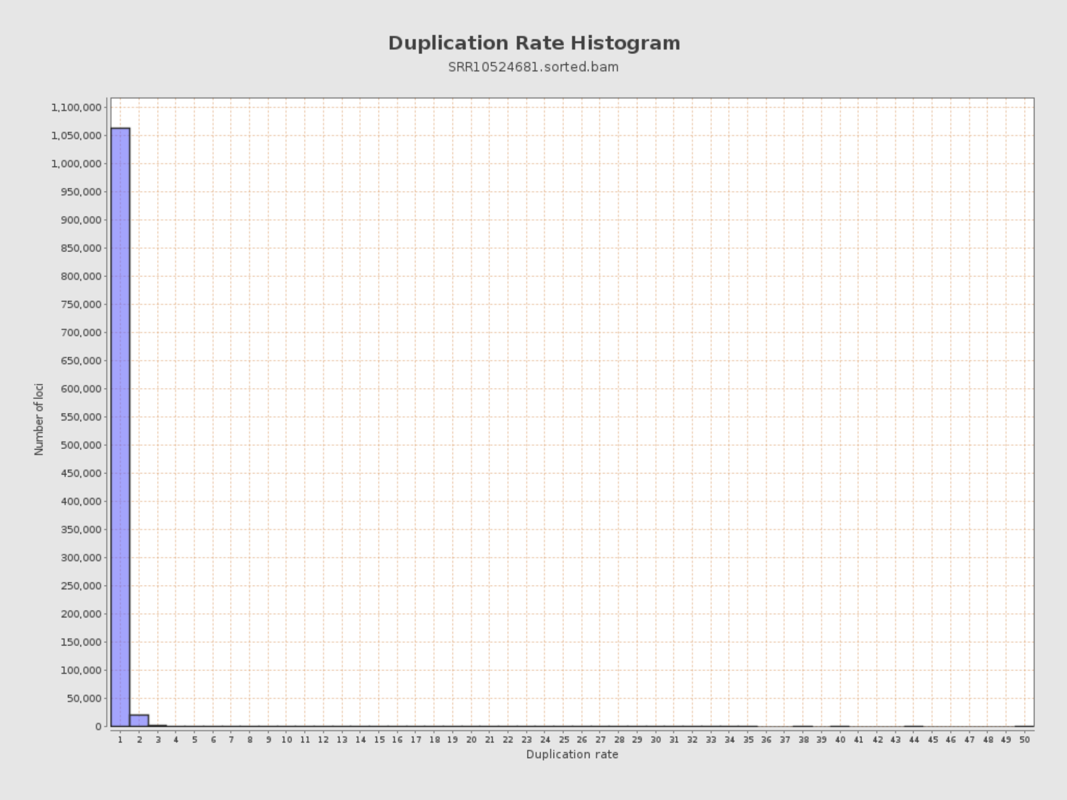
5. Results : Coverage Histogram (0-50X)



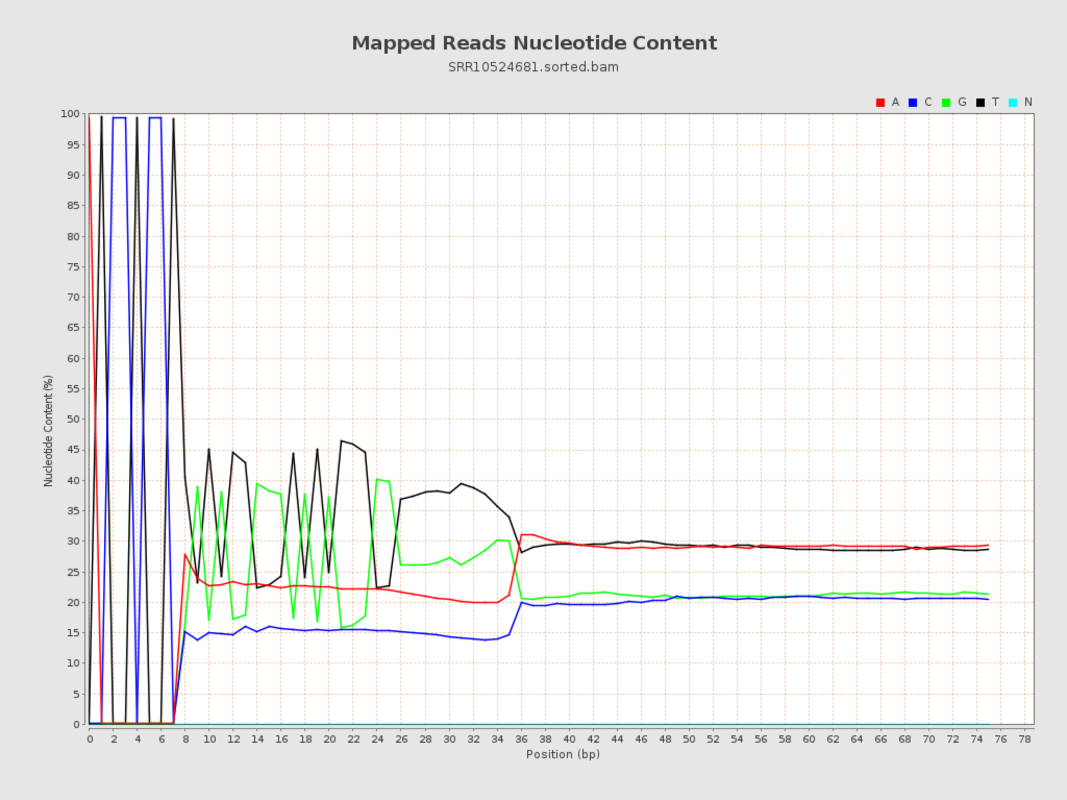
6. Results : Genome Fraction Coverage



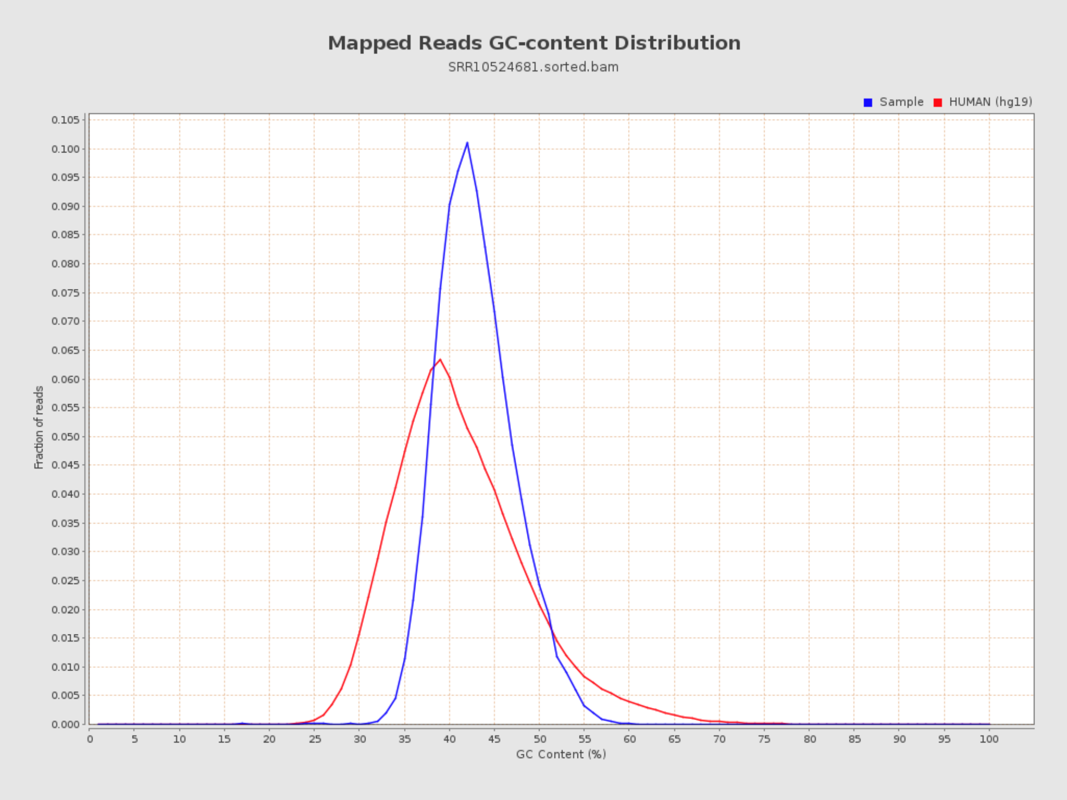
7. Results : Duplication Rate Histogram



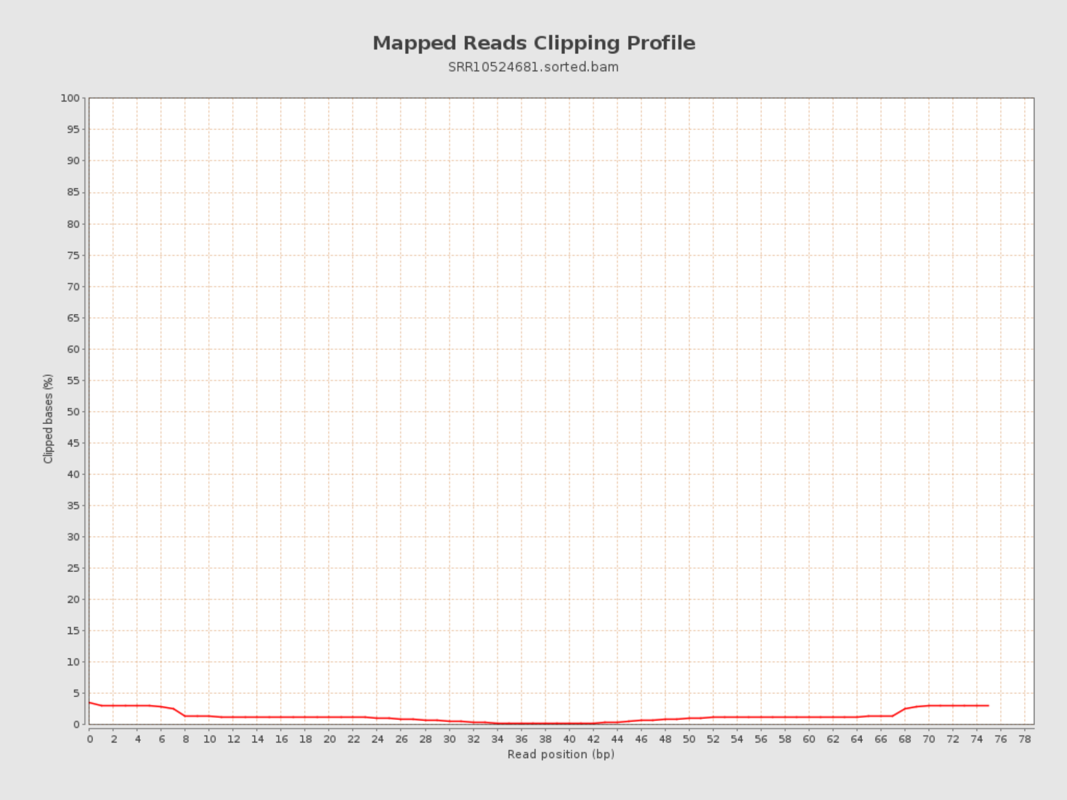
8. Results : Mapped Reads Nucleotide Content



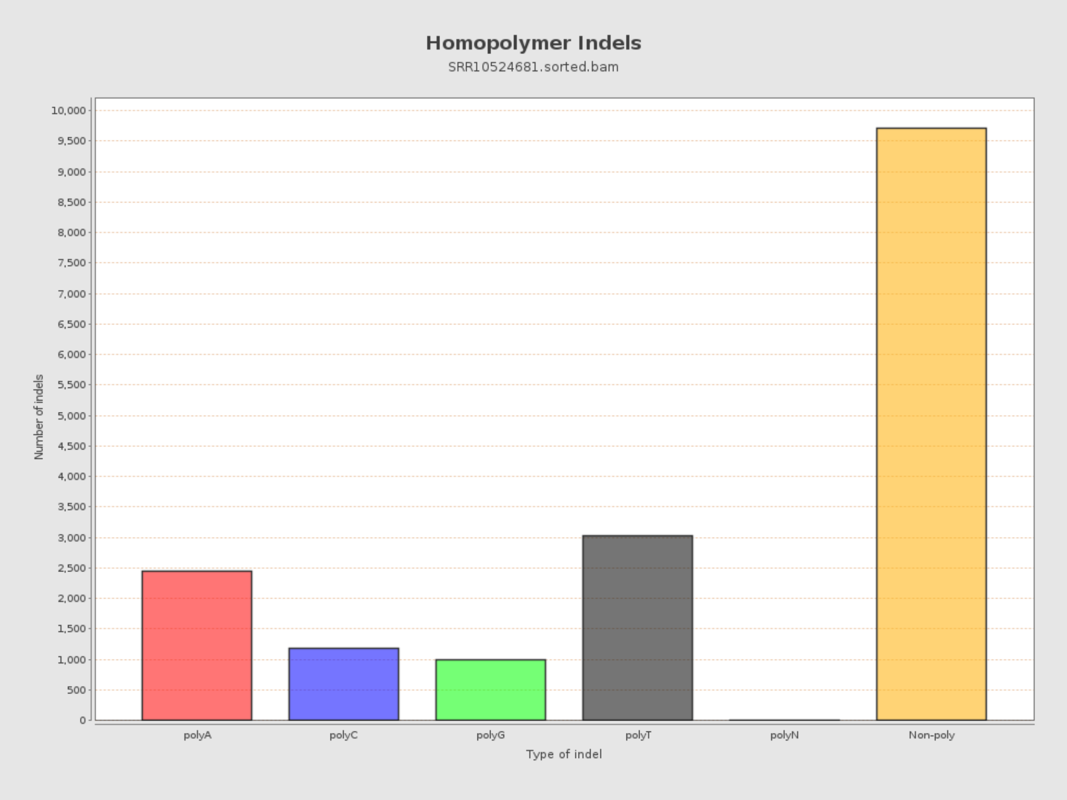
9. Results : Mapped Reads GC-content Distribution



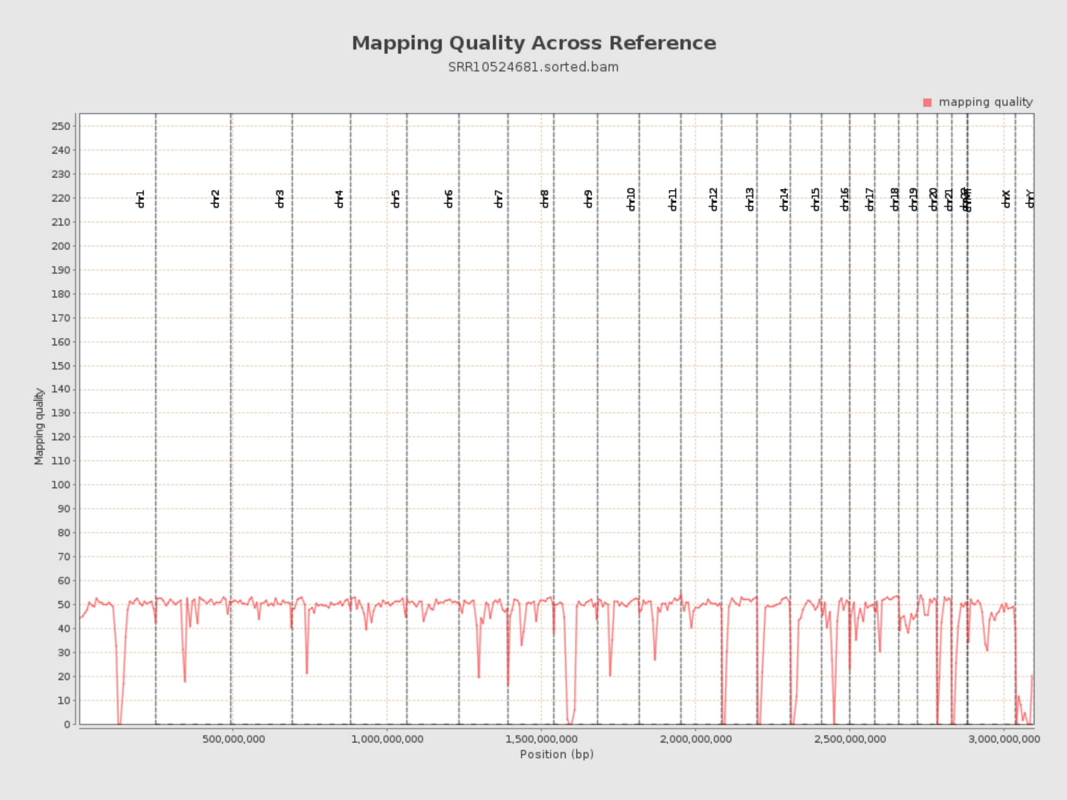
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram