Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:13:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524751.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_SRR10524751 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524751.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:13:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524751.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,270,385
Mapped reads	1,136,240 / 89.44%
Unmapped reads	134,145 / 10.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,671 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	31,662 / 2.49%
Duplication rate	2.08%
Clipped reads	1,136,281 / 89.44%

2.2. ACGT Content

Number/percentage of A's	16,249,401 / 24.91%
Number/percentage of C's	12,745,136 / 19.54%
Number/percentage of T's	20,351,650 / 31.19%
Number/percentage of G's	15,886,535 / 24.35%
Number/percentage of N's	7,848 / 0.01%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0211

Standard Deviation	0.1941

2.4. Mapping Quality

Mean Mapping Quality	44.41

2.5. Mismatches and indels

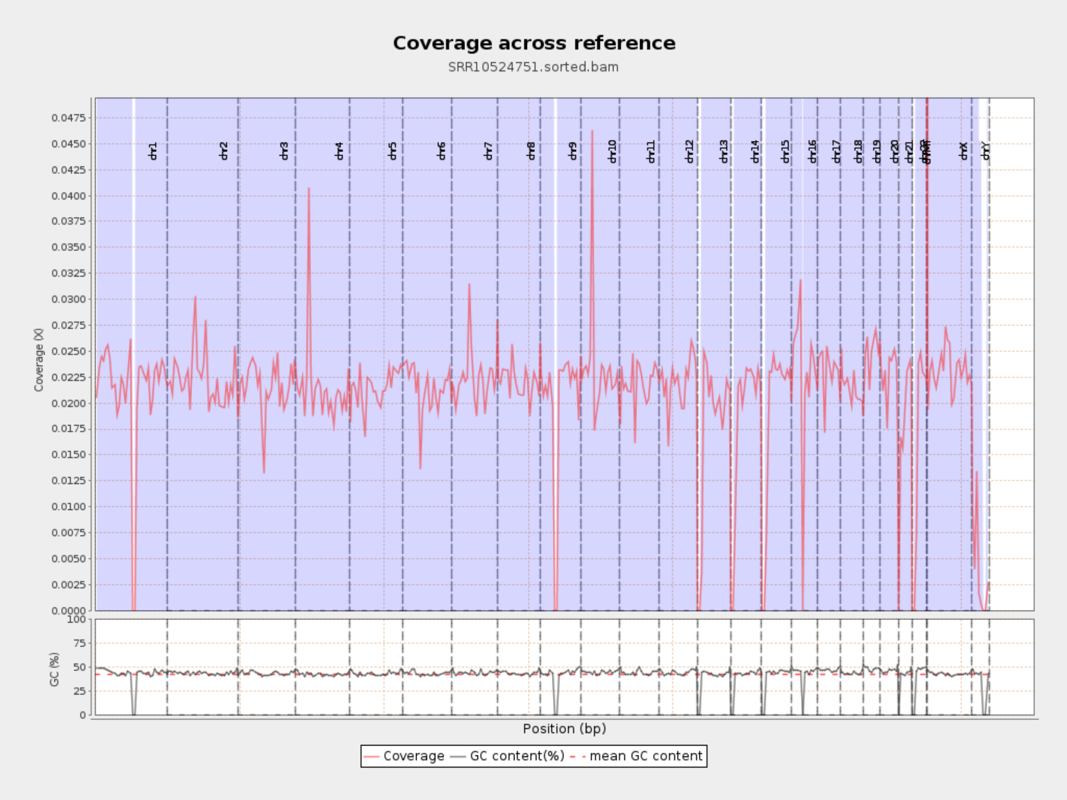
General error rate	0.52%
Mismatches	328,891
Insertions	5,456
Mapped reads with at least one insertion	0.48%
Deletions	12,781
Mapped reads with at least one deletion	1.12%
Homopolymer indels	40.92%

2.6. Chromosome stats

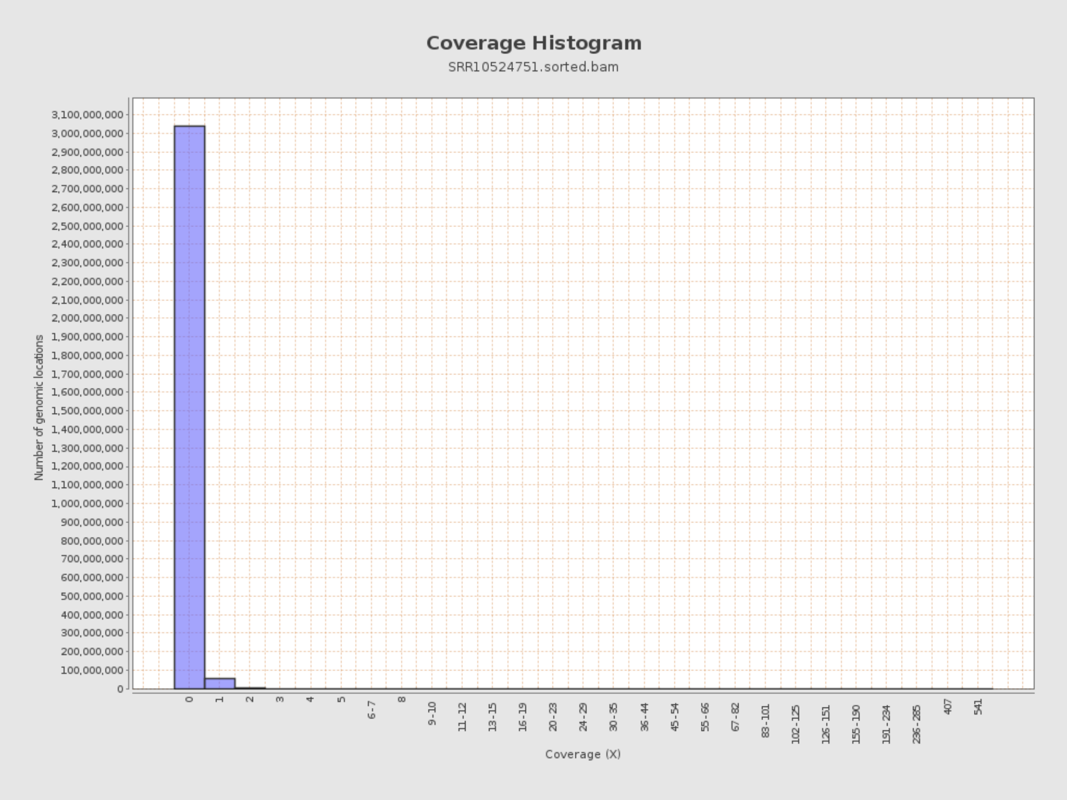
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5260694	0.0211	0.2387
chr2	243199373	5423521	0.0223	0.2839
chr3	198022430	4265135	0.0215	0.1599
chr4	191154276	4130900	0.0216	0.1793
chr5	180915260	3906016	0.0216	0.1576
chr6	171115067	3671571	0.0215	0.1704
chr7	159138663	3560616	0.0224	0.2337

chr8	146364022	3225241	0.022	0.1754
chr9	141213431	2790192	0.0198	0.1723
chr10	135534747	3175463	0.0234	0.2428
chr11	135006516	2965656	0.022	0.1796
chr12	133851895	2949267	0.022	0.1607
chr13	115169878	2024220	0.0176	0.1417
chr14	107349540	1970669	0.0184	0.1477
chr15	102531392	1914066	0.0187	0.148
chr16	90354753	2029525	0.0225	0.1752
chr17	81195210	1883093	0.0232	0.1688
chr18	78077248	1672849	0.0214	0.2434
chr19	59128983	1464753	0.0248	0.2188
chr20	63025520	1422210	0.0226	0.1675
chr21	48129895	878669	0.0183	0.16
chr22	51304566	826872	0.0161	0.137
chrMT	16571	22672	1.3682	1.3568
chrX	155270560	3603910	0.0232	0.1738
chrY	59373566	223504	0.0038	0.1141

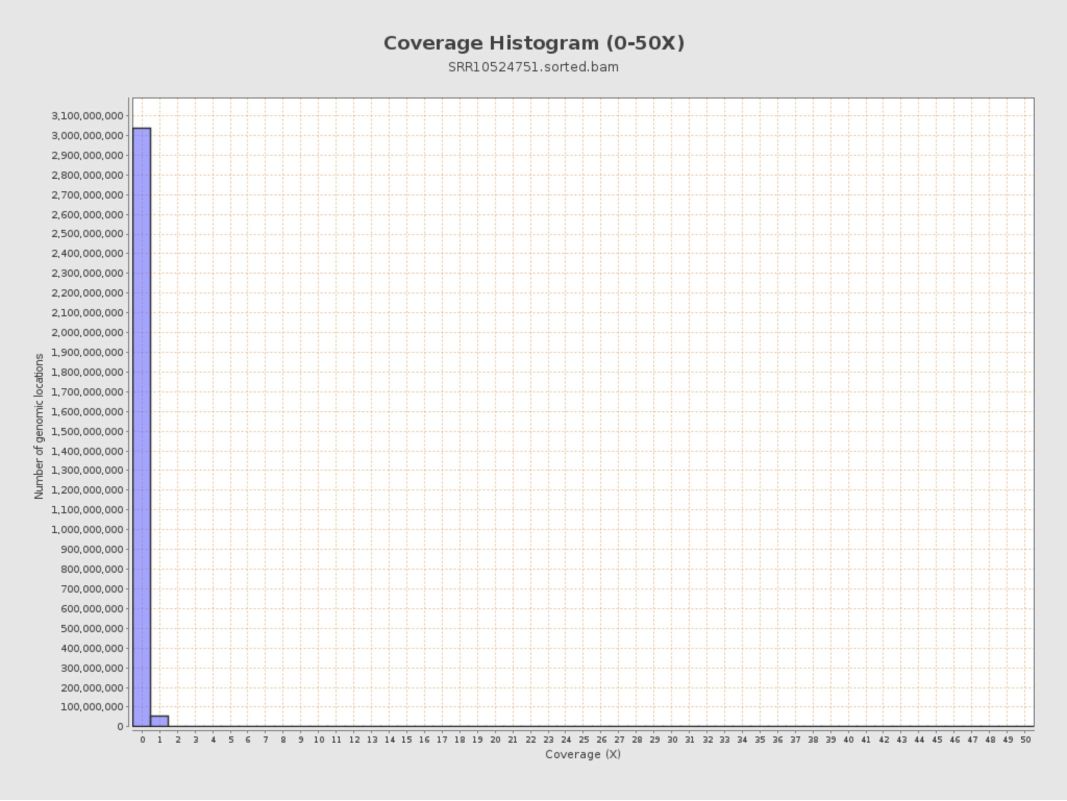
3. Results : Coverage across reference



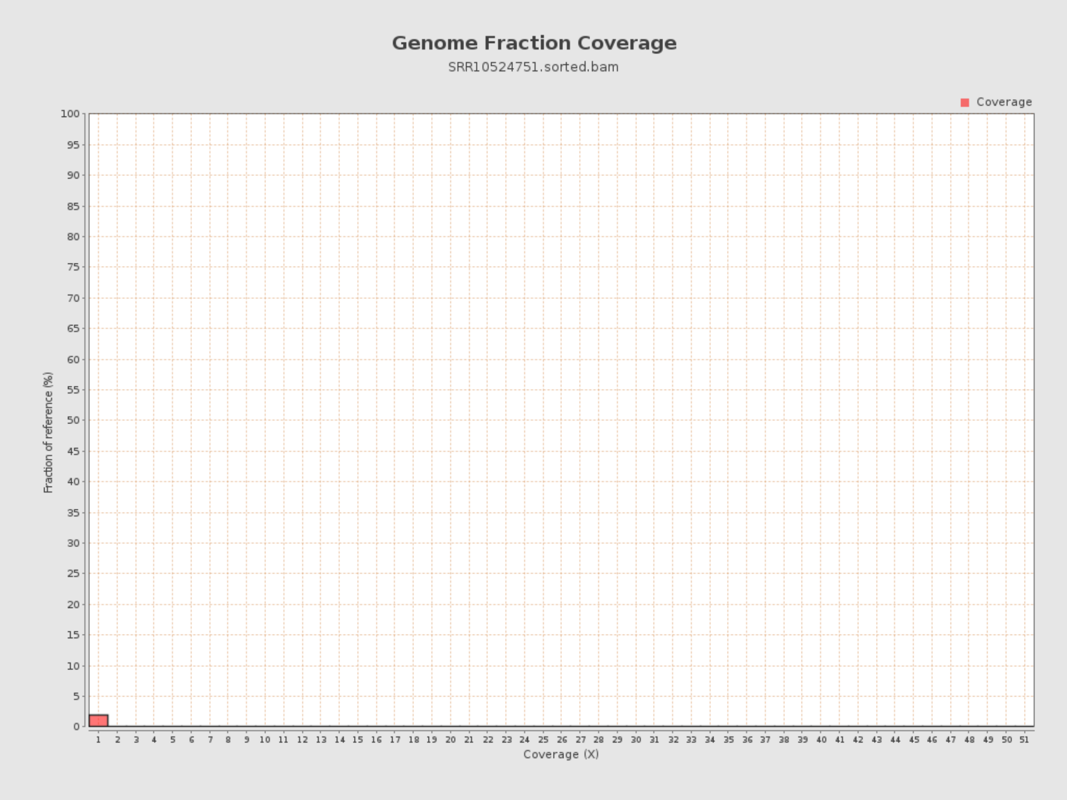
4. Results : Coverage Histogram



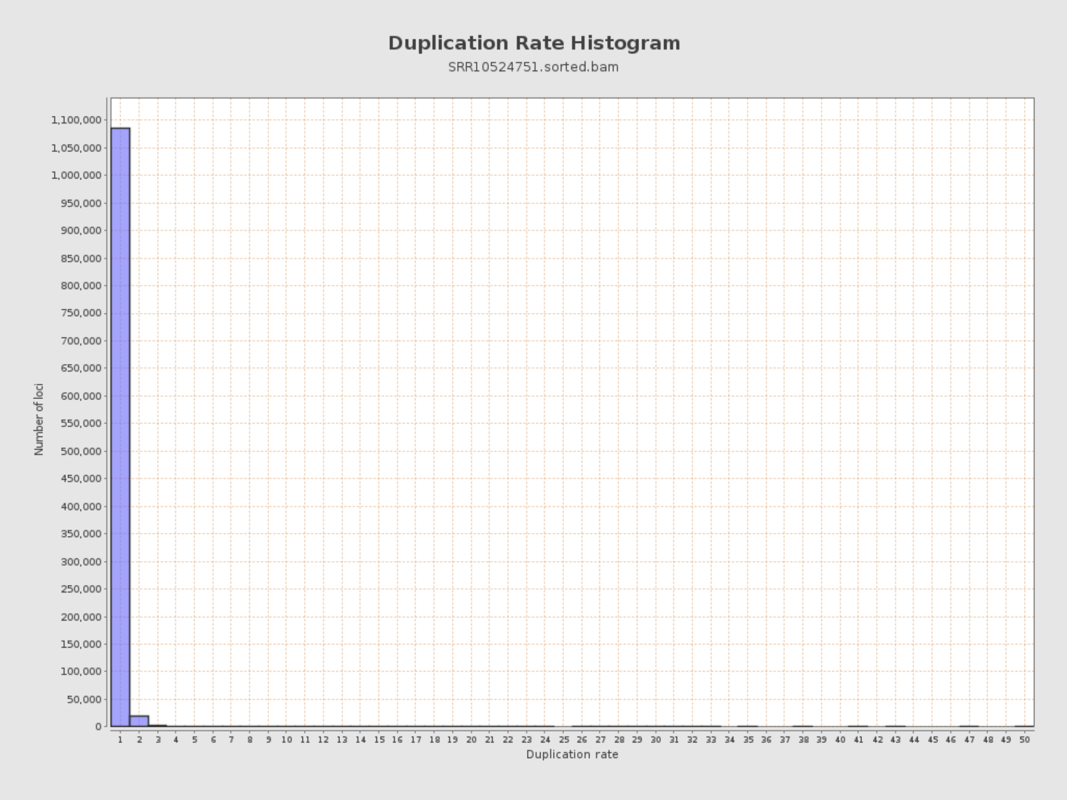
5. Results : Coverage Histogram (0-50X)



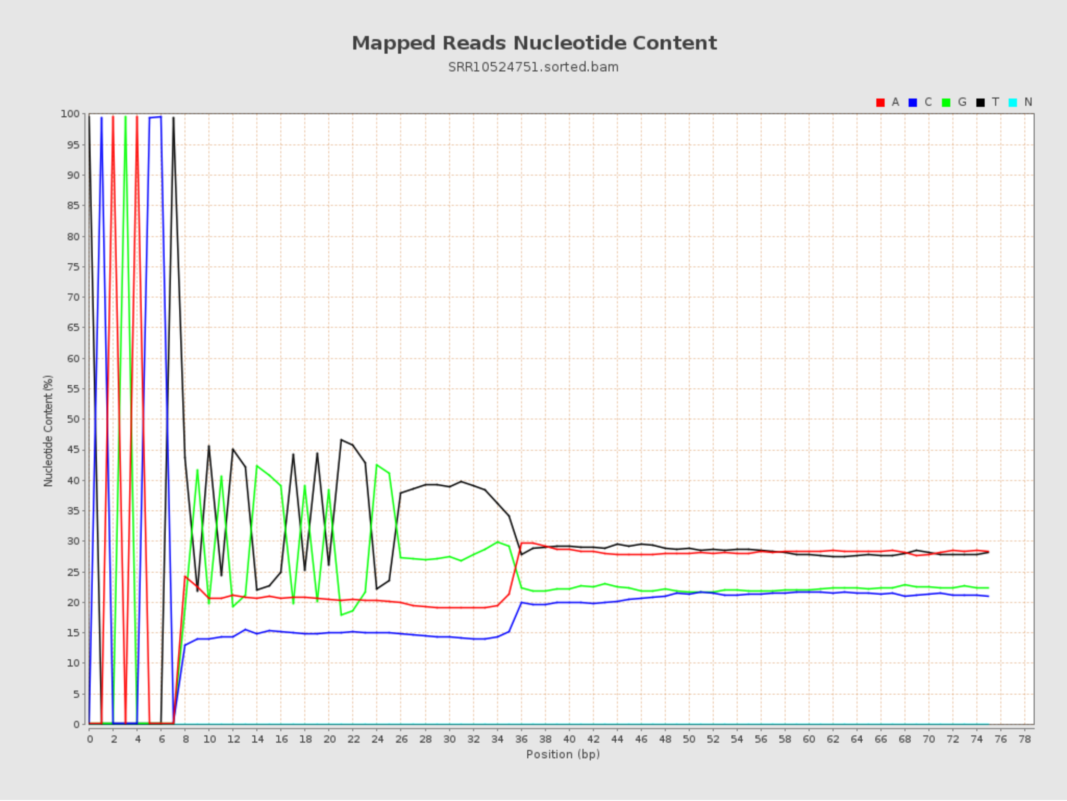
6. Results : Genome Fraction Coverage



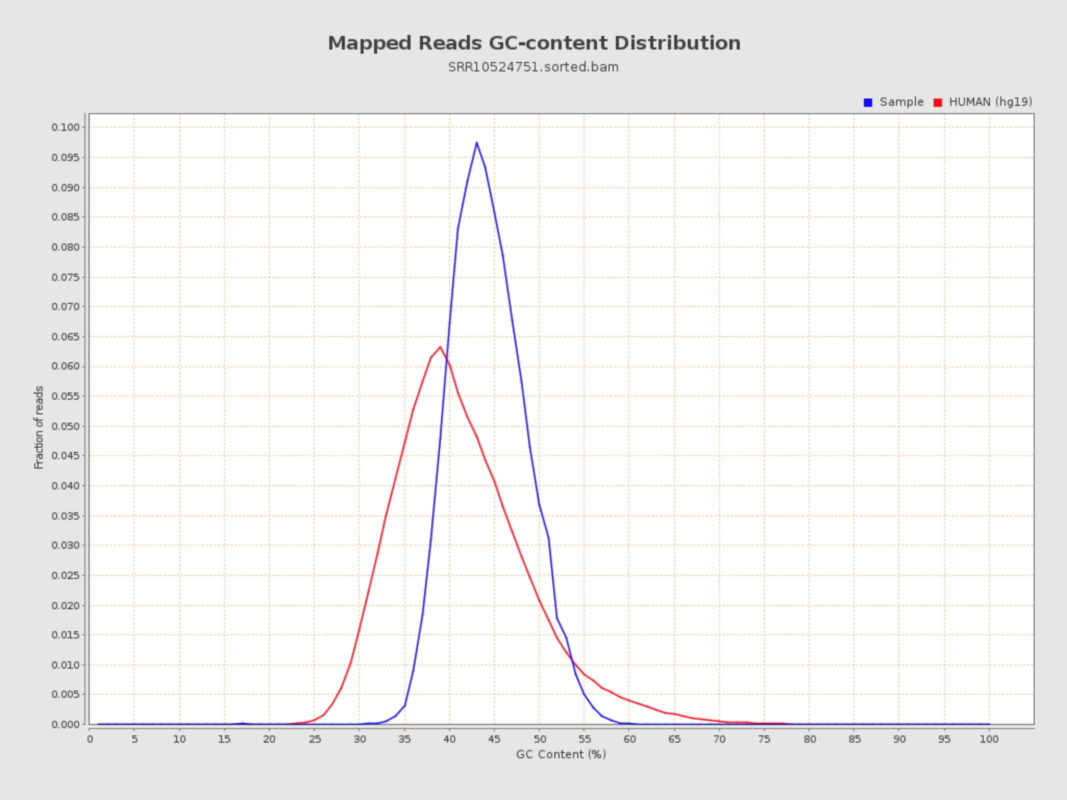
7. Results : Duplication Rate Histogram



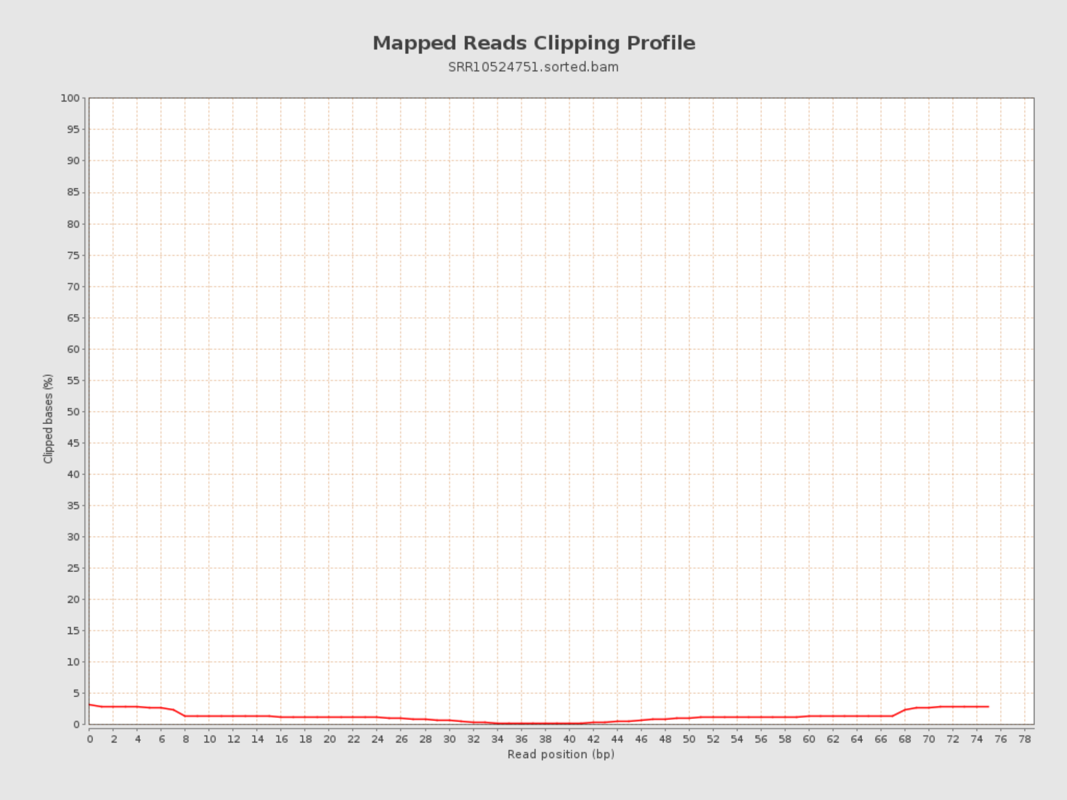
8. Results : Mapped Reads Nucleotide Content



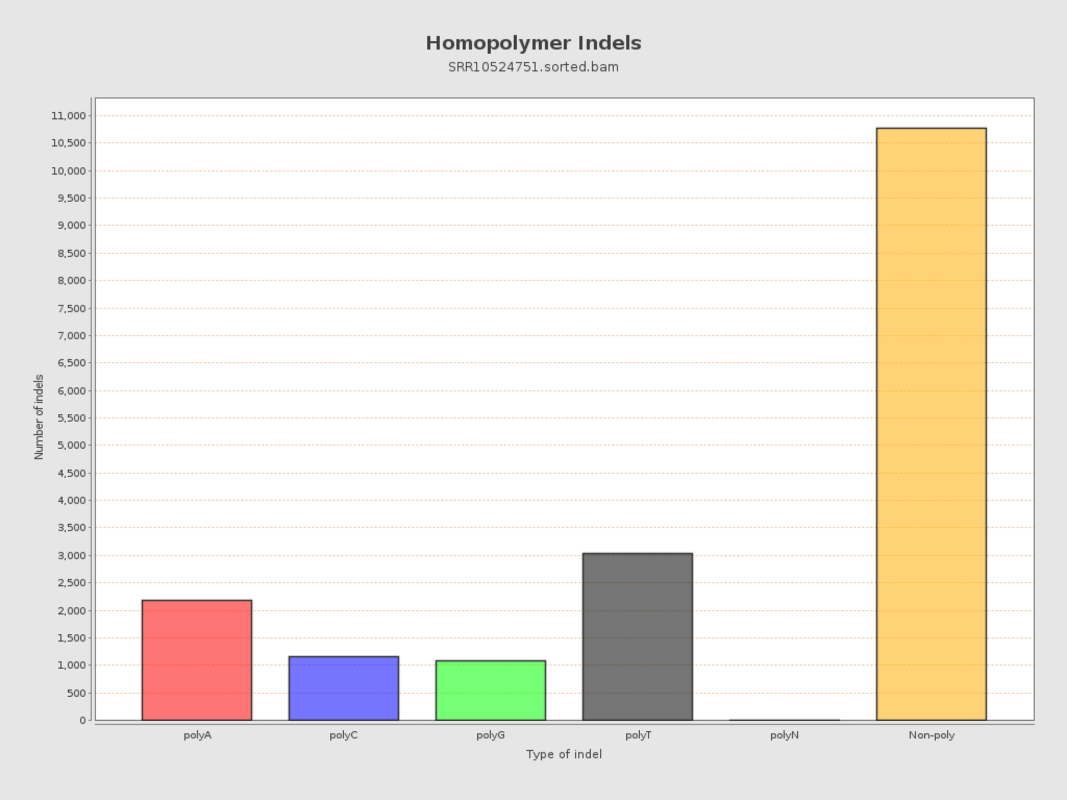
9. Results : Mapped Reads GC-content Distribution



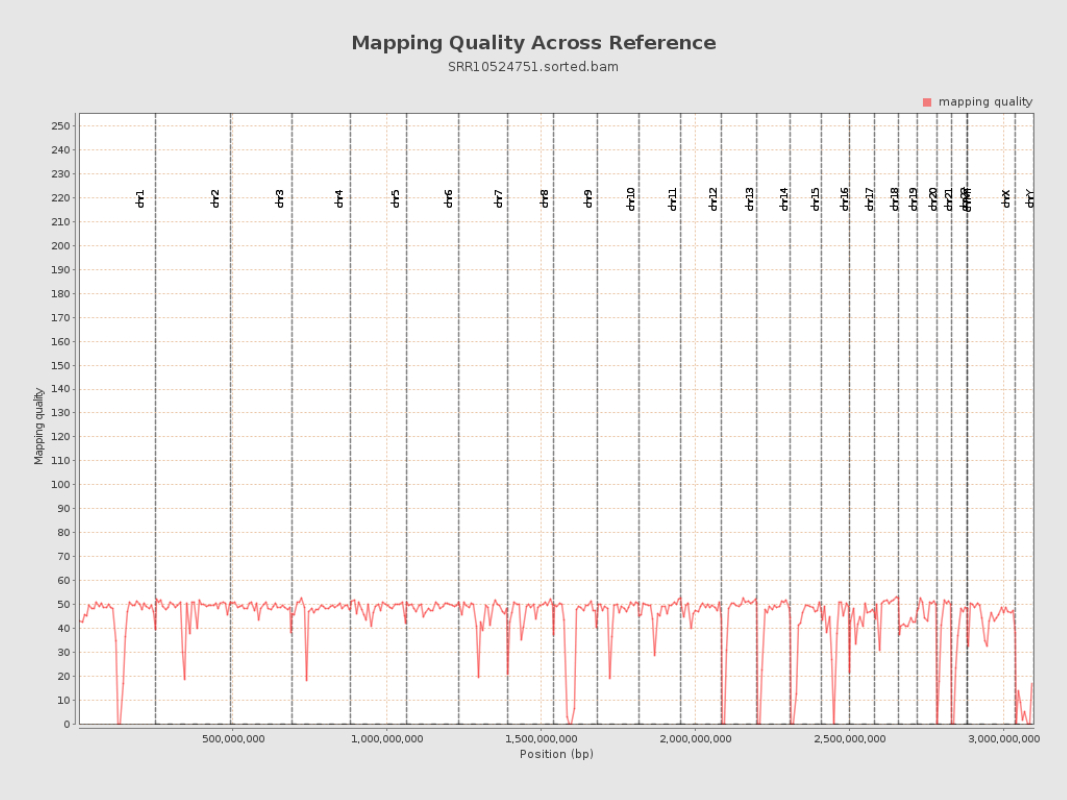
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram