Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:18:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524753.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_SRR10524753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524753.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:18:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524753.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,277,810
Mapped reads	1,152,631 / 90.2%
Unmapped reads	125,179 / 9.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,424 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	34,813 / 2.72%
Duplication rate	2.3%
Clipped reads	1,153,800 / 90.3%

2.2. ACGT Content

Number/percentage of A's	16,019,310 / 24.53%
Number/percentage of C's	11,964,252 / 18.32%
Number/percentage of T's	21,264,810 / 32.56%
Number/percentage of G's	16,044,812 / 24.57%
Number/percentage of N's	8,556 / 0.01%
GC Percentage	42.89%

2.3. Coverage

Mean	0.0211

Standard Deviation	0.1946

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

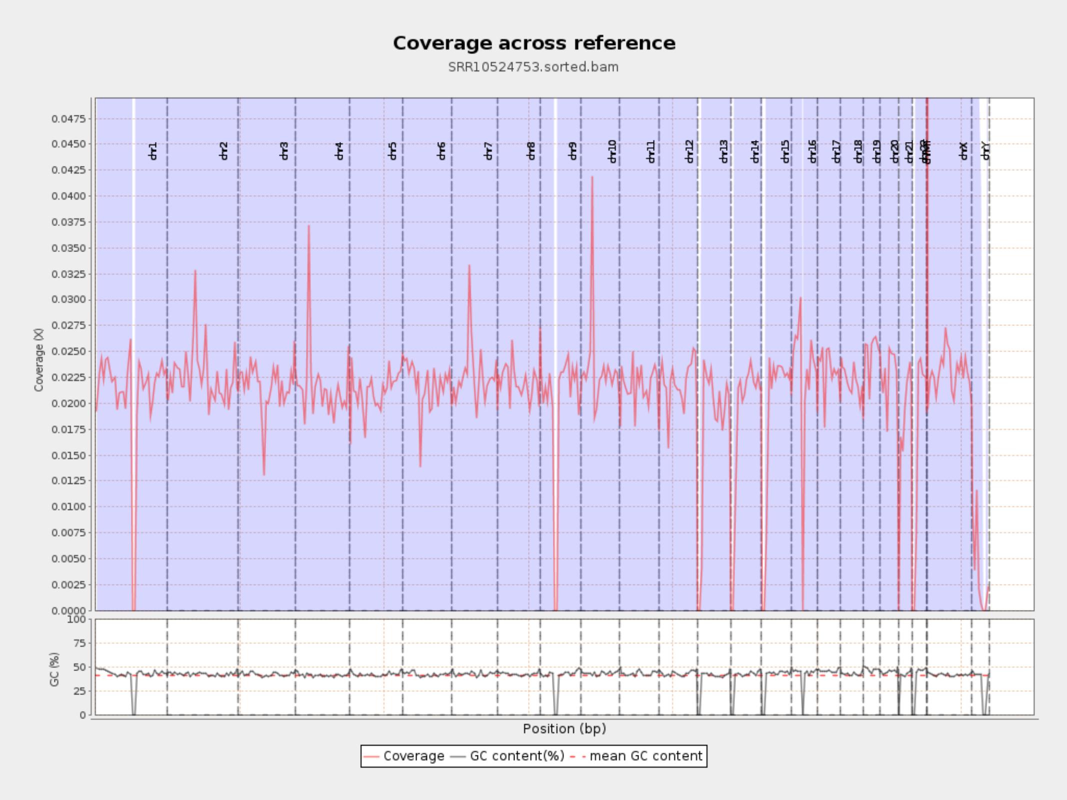
General error rate	0.52%
Mismatches	332,642
Insertions	4,223
Mapped reads with at least one insertion	0.36%
Deletions	12,510
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.01%

2.6. Chromosome stats

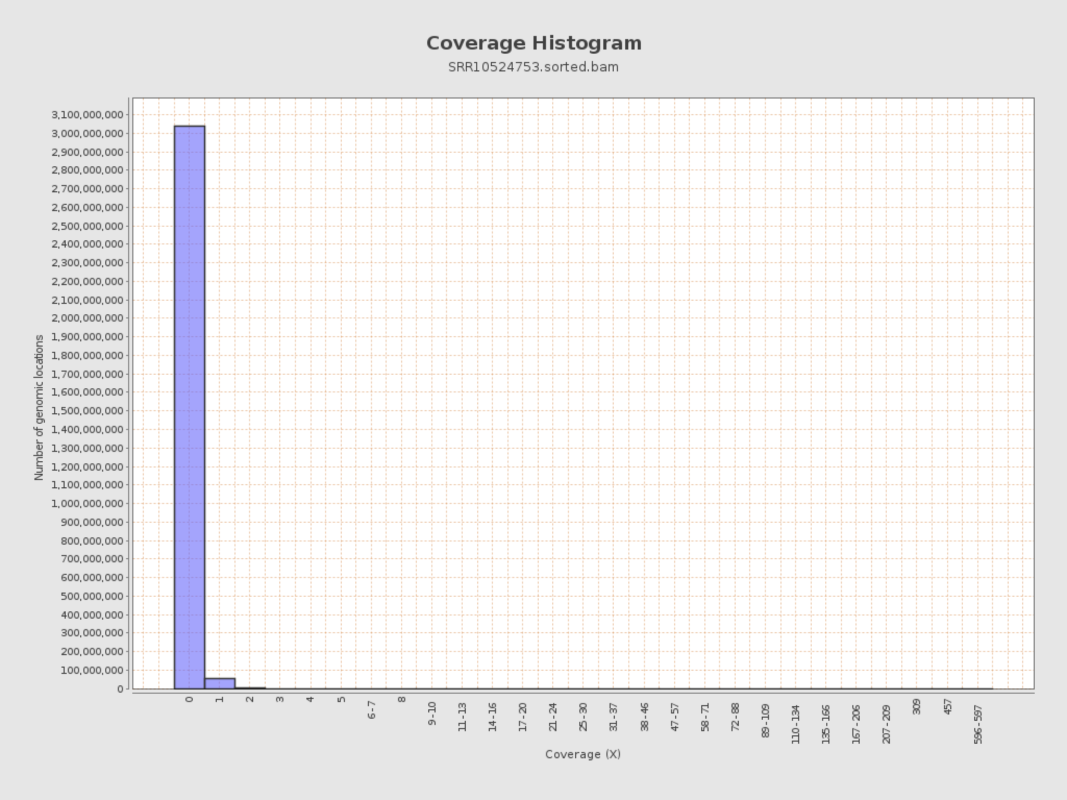
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5186893	0.0208	0.2249
chr2	243199373	5518661	0.0227	0.3074
chr3	198022430	4273808	0.0216	0.1609
chr4	191154276	4140732	0.0217	0.1742
chr5	180915260	3871086	0.0214	0.1573
chr6	171115067	3732594	0.0218	0.1722
chr7	159138663	3622718	0.0228	0.2333

chr8	146364022	3223702	0.022	0.1778
chr9	141213431	2777218	0.0197	0.175
chr10	135534747	3186256	0.0235	0.2231
chr11	135006516	2960306	0.0219	0.182
chr12	133851895	2946813	0.022	0.1613
chr13	115169878	1999802	0.0174	0.1428
chr14	107349540	1961458	0.0183	0.1489
chr15	102531392	1906041	0.0186	0.1475
chr16	90354753	2015523	0.0223	0.1741
chr17	81195210	1884179	0.0232	0.1695
chr18	78077248	1730559	0.0222	0.2502
chr19	59128983	1461595	0.0247	0.2121
chr20	63025520	1420484	0.0225	0.1686
chr21	48129895	863212	0.0179	0.1552
chr22	51304566	820142	0.016	0.137
chrMT	16571	25716	1.5519	1.4192
chrX	155270560	3583488	0.0231	0.174
chrY	59373566	208661	0.0035	0.1009

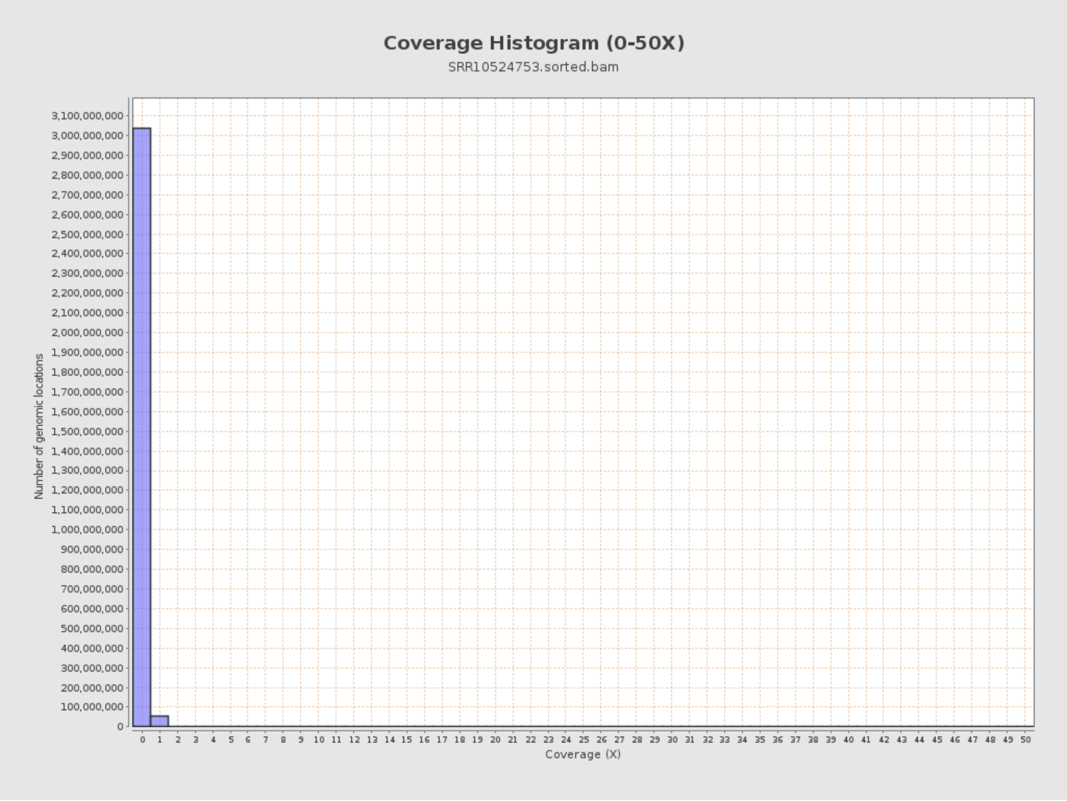
3. Results : Coverage across reference



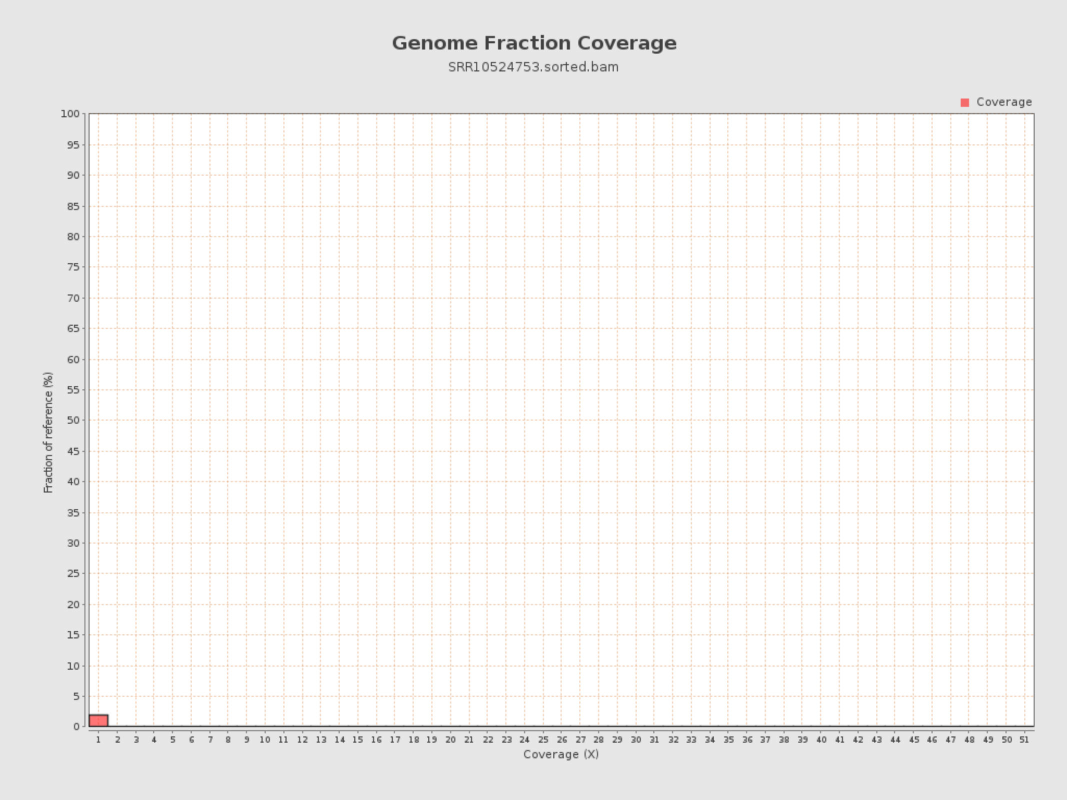
4. Results : Coverage Histogram



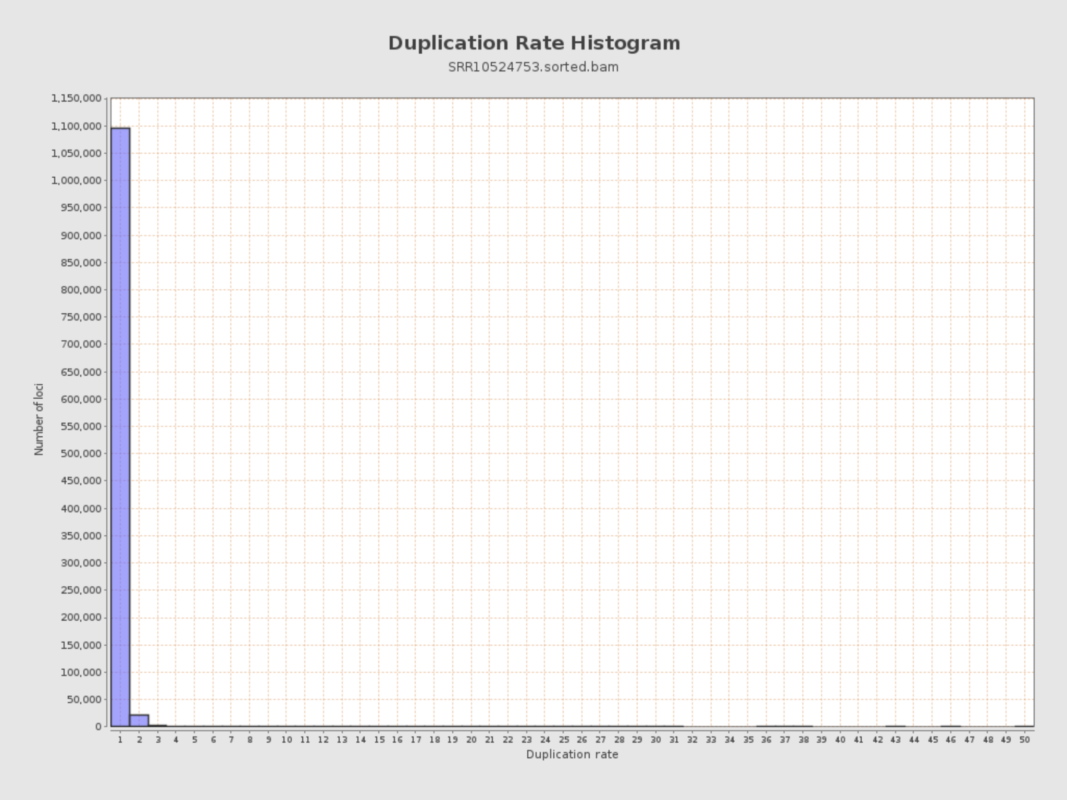
5. Results : Coverage Histogram (0-50X)



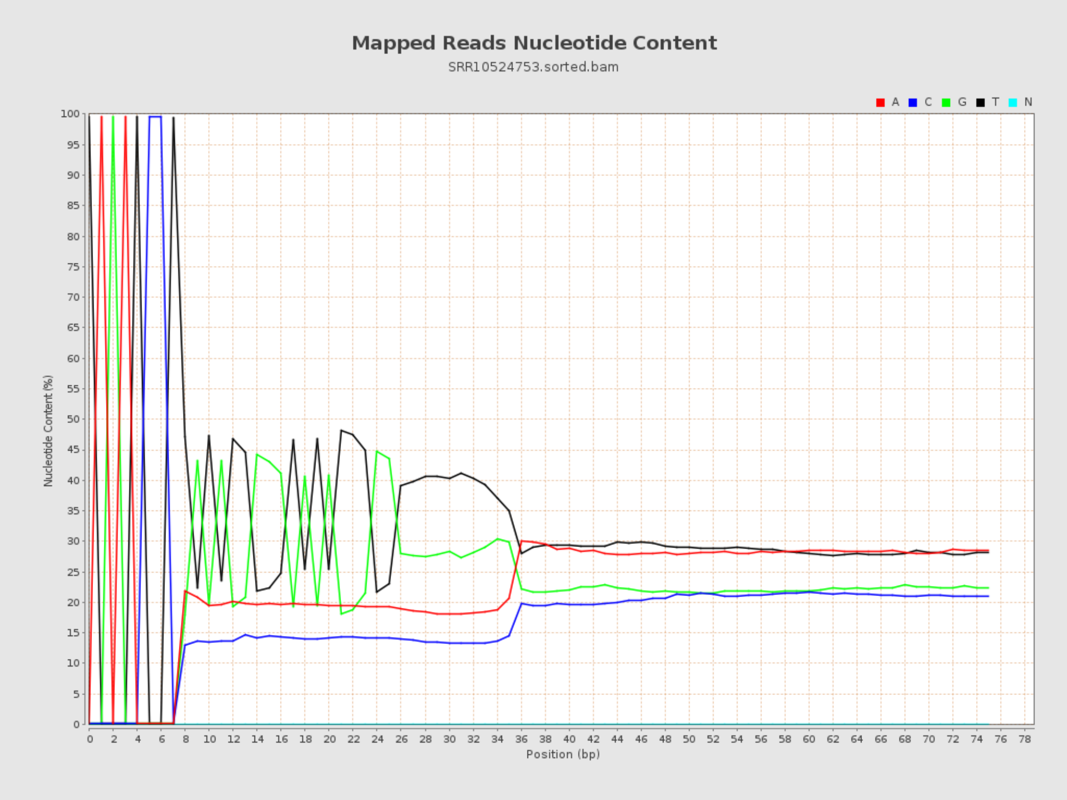
6. Results : Genome Fraction Coverage



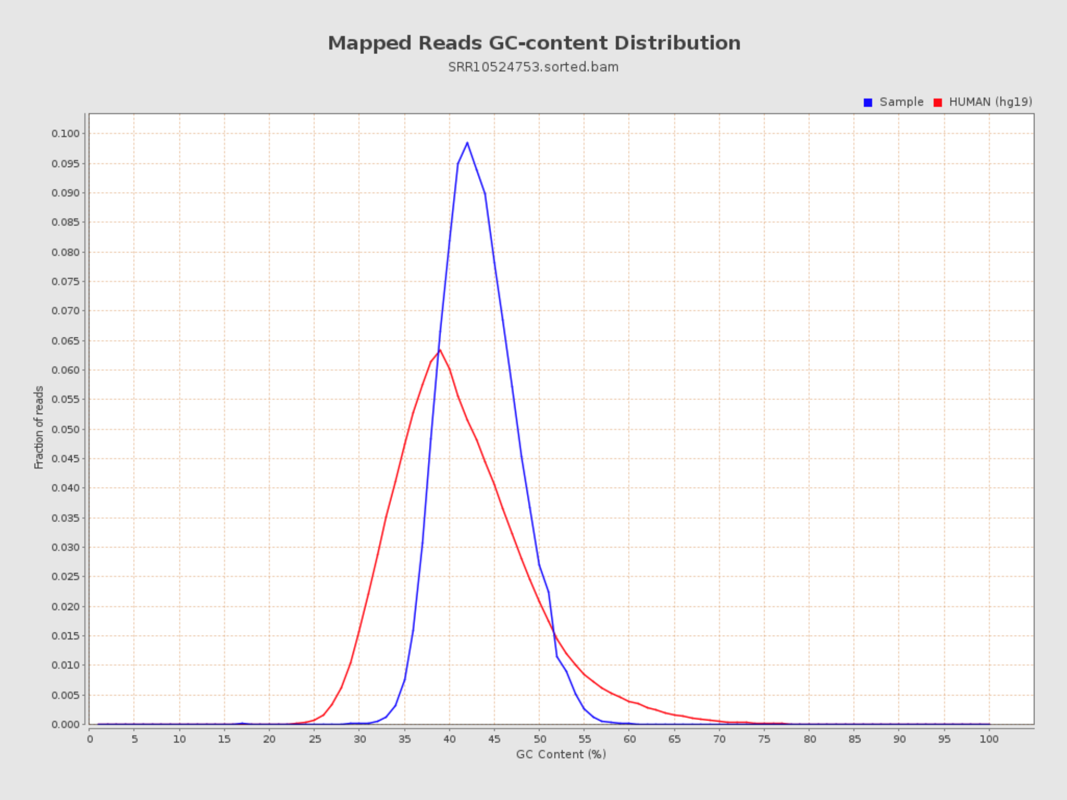
7. Results : Duplication Rate Histogram



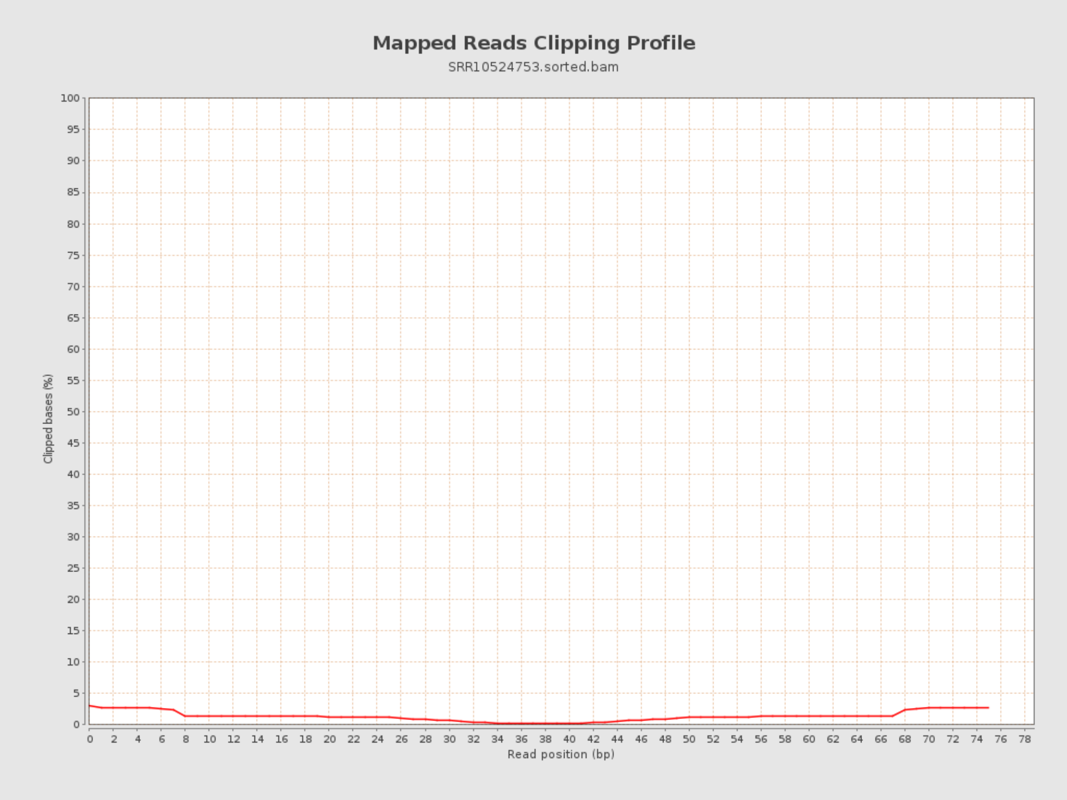
8. Results : Mapped Reads Nucleotide Content



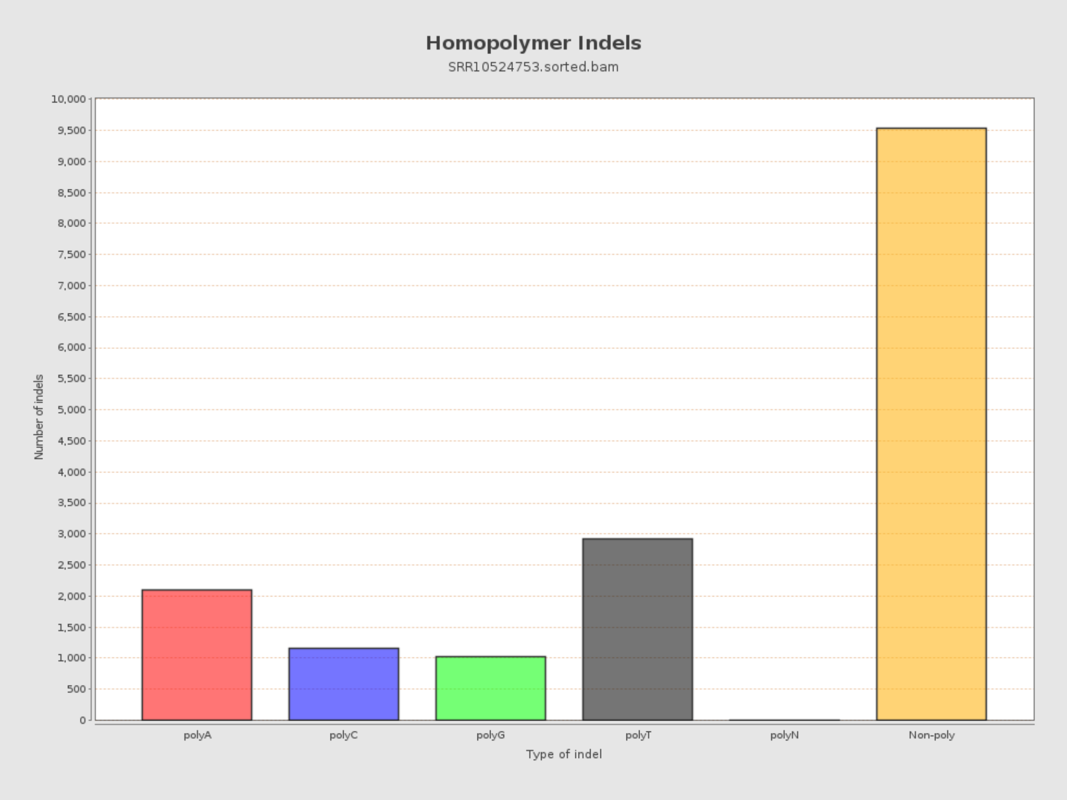
9. Results : Mapped Reads GC-content Distribution



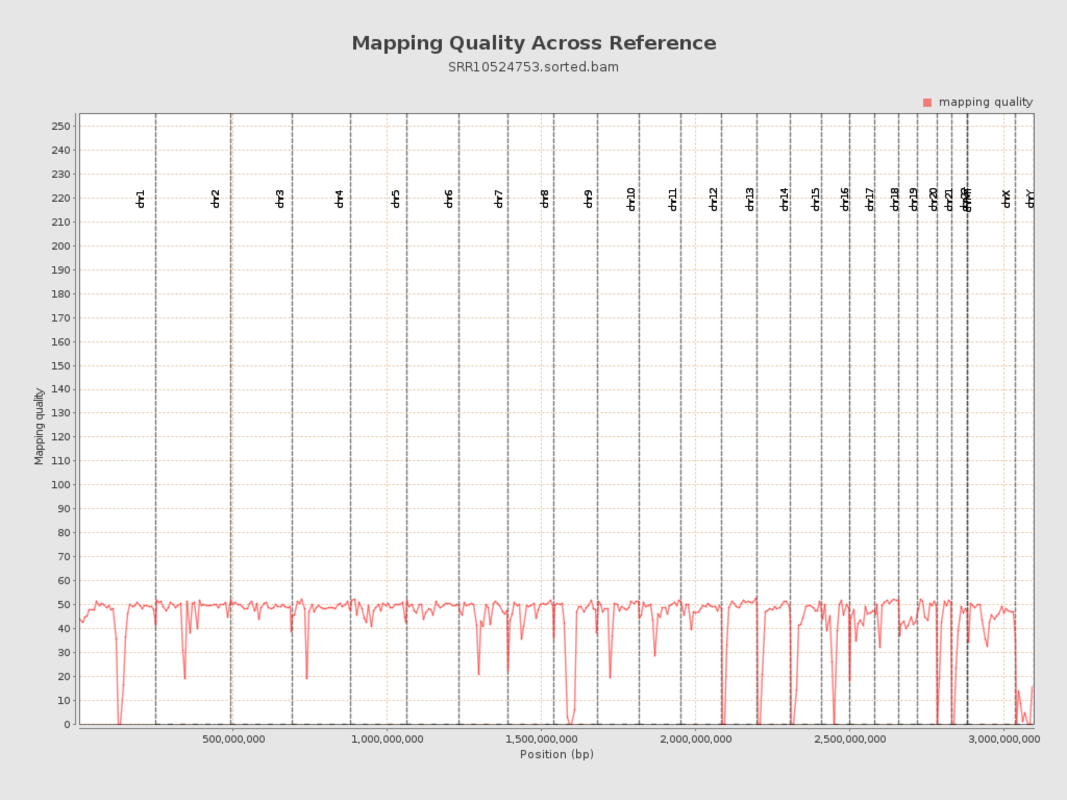
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram