Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:24:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524385.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_SRR10524385 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524385.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:24:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524385.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,184,321
Mapped reads	1,095,220 / 92.48%
Unmapped reads	89,101 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,468 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	34,068 / 2.88%
Duplication rate	2.29%
Clipped reads	1,096,586 / 92.59%

2.2. ACGT Content

Number/percentage of A's	16,635,900 / 25.84%
Number/percentage of C's	12,622,763 / 19.6%
Number/percentage of T's	19,996,444 / 31.06%
Number/percentage of G's	15,122,392 / 23.49%
Number/percentage of N's	8,727 / 0.01%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0208

Standard Deviation	0.2278

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

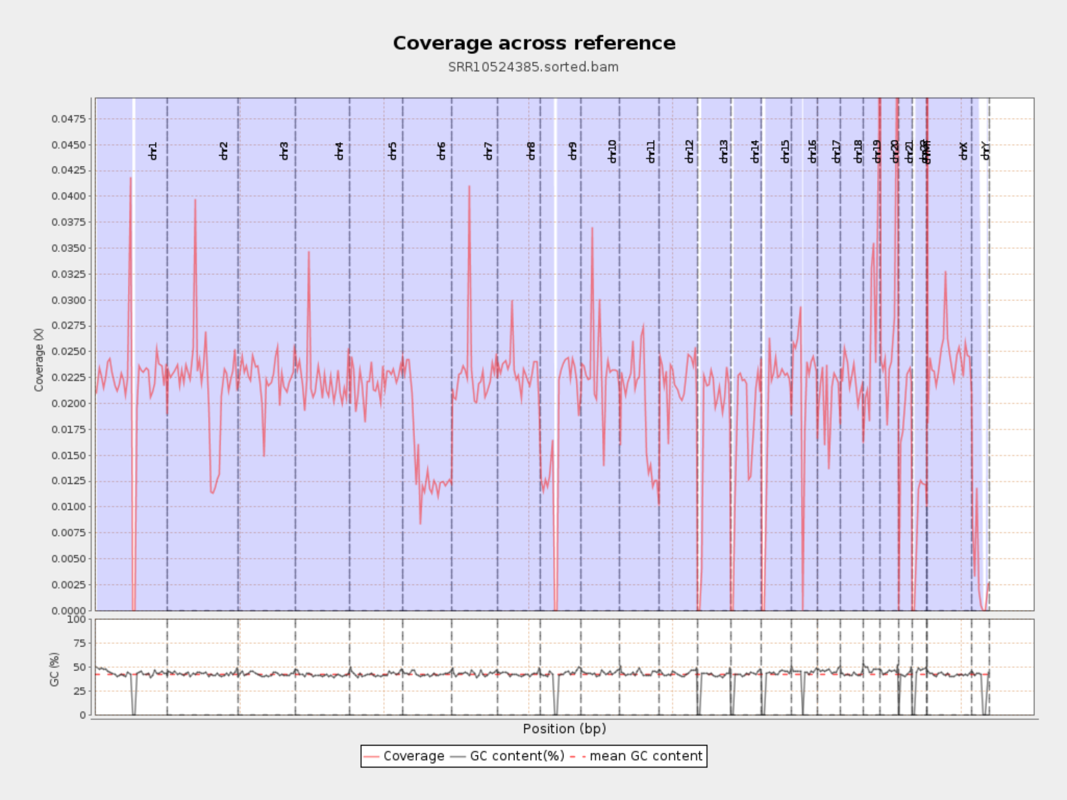
General error rate	0.5%
Mismatches	312,174
Insertions	4,744
Mapped reads with at least one insertion	0.43%
Deletions	11,093
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.22%

2.6. Chromosome stats

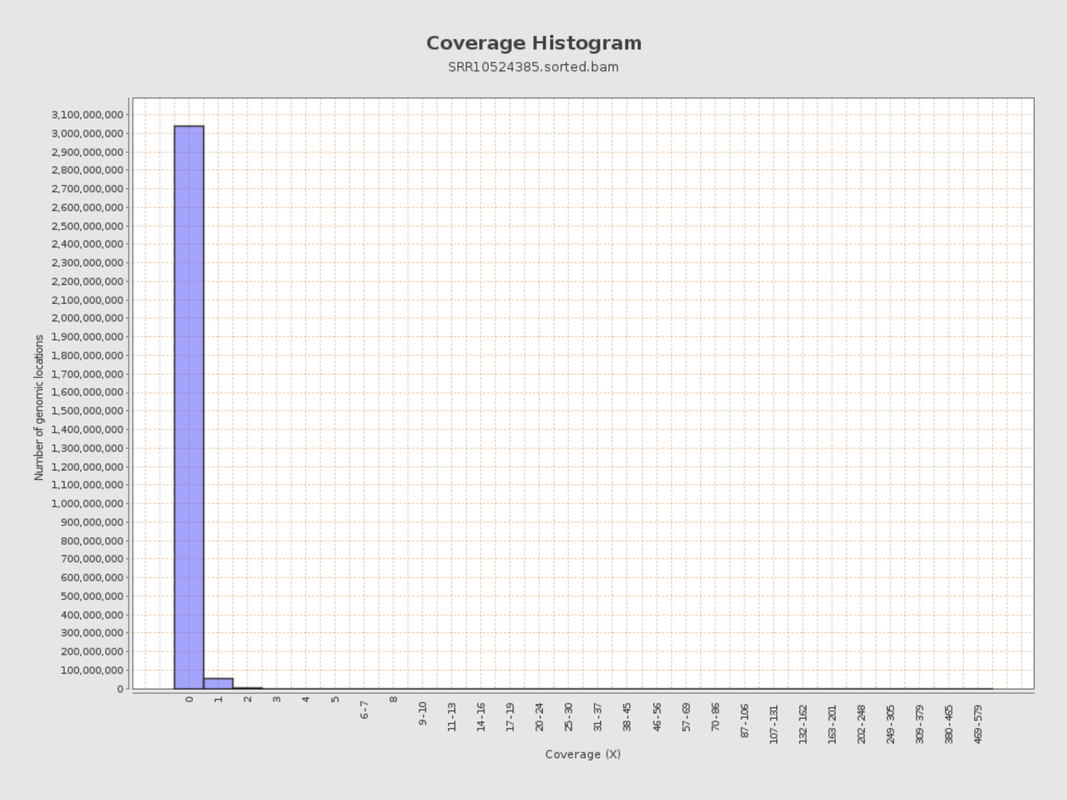
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5413171	0.0217	0.4679
chr2	243199373	5296971	0.0218	0.2434
chr3	198022430	4436865	0.0224	0.1587
chr4	191154276	4278061	0.0224	0.1717
chr5	180915260	4013667	0.0222	0.1586
chr6	171115067	2519429	0.0147	0.139
chr7	159138663	3678686	0.0231	0.3124

chr8	146364022	3402403	0.0232	0.2077
chr9	141213431	2414704	0.0171	0.1711
chr10	135534747	3170804	0.0234	0.2079
chr11	135006516	2655463	0.0197	0.193
chr12	133851895	3001108	0.0224	0.1623
chr13	115169878	2068425	0.018	0.1417
chr14	107349540	1823944	0.017	0.141
chr15	102531392	1946066	0.019	0.1457
chr16	90354753	1977010	0.0219	0.1628
chr17	81195210	1672585	0.0206	0.163
chr18	78077248	1752719	0.0224	0.2899
chr19	59128983	1748554	0.0296	0.3075
chr20	63025520	1801786	0.0286	0.184
chr21	48129895	880934	0.0183	0.1566
chr22	51304566	440970	0.0086	0.0983
chrMT	16571	27188	1.6407	1.5744
chrX	155270560	3783522	0.0244	0.1799
chrY	59373566	198754	0.0033	0.0969

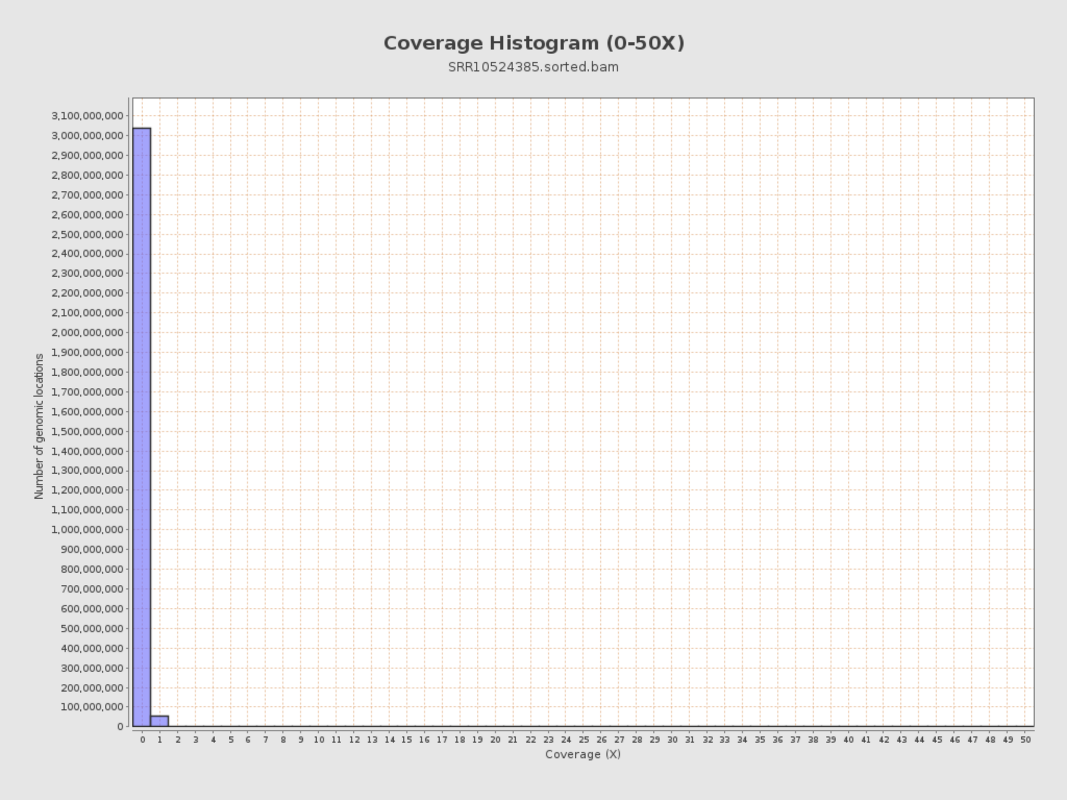
3. Results : Coverage across reference



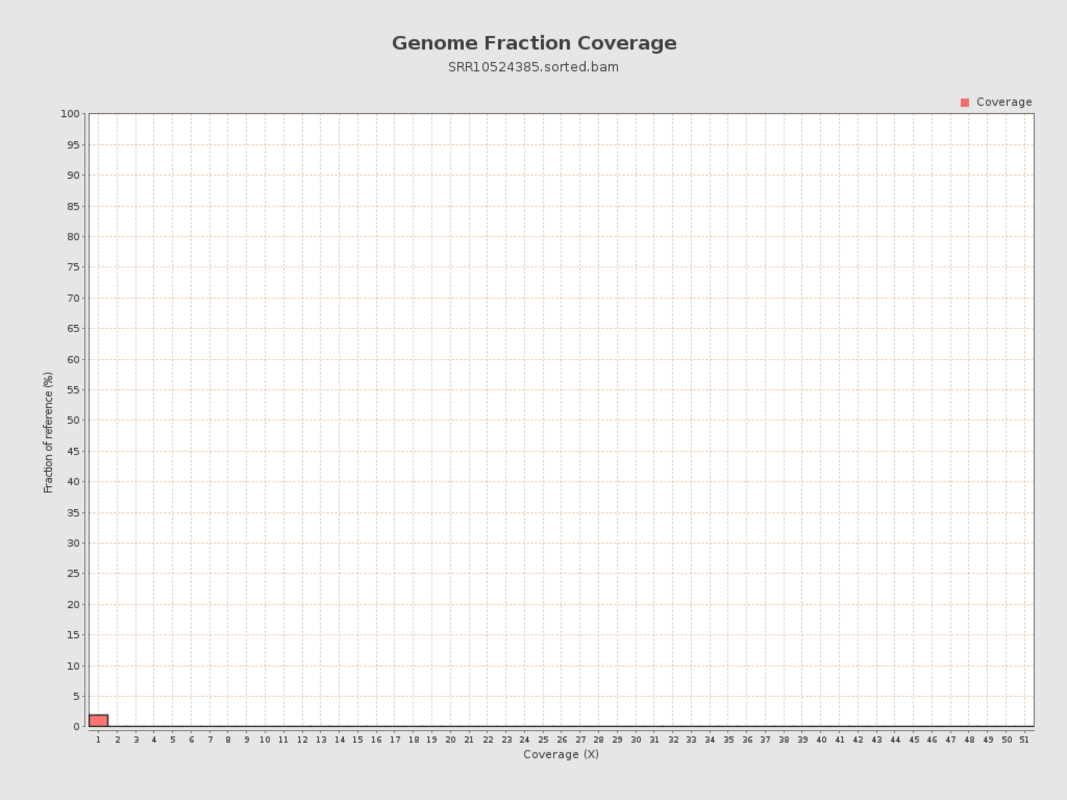
4. Results : Coverage Histogram



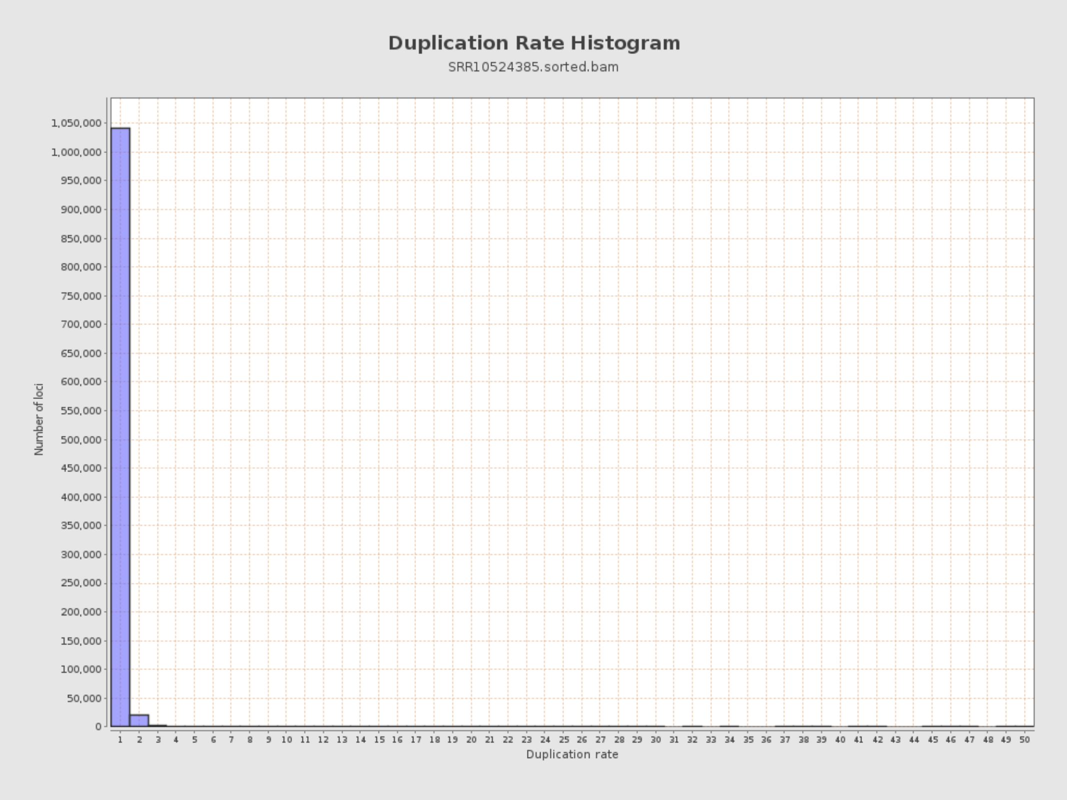
5. Results : Coverage Histogram (0-50X)



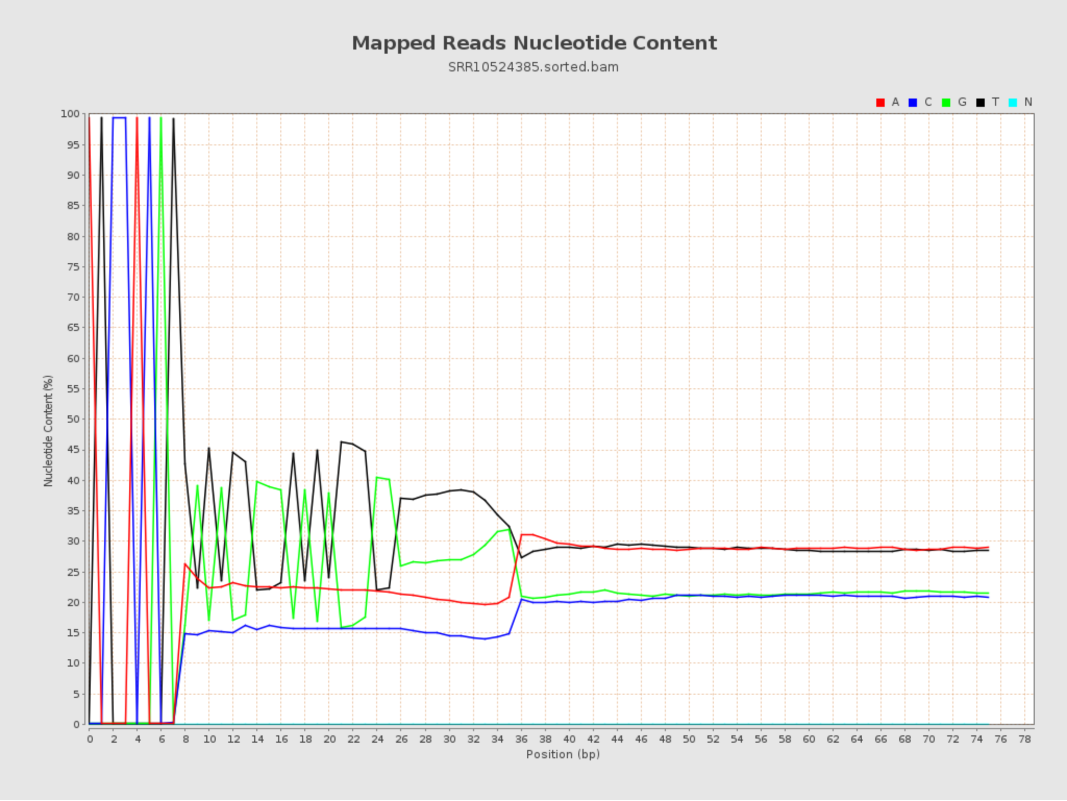
6. Results : Genome Fraction Coverage



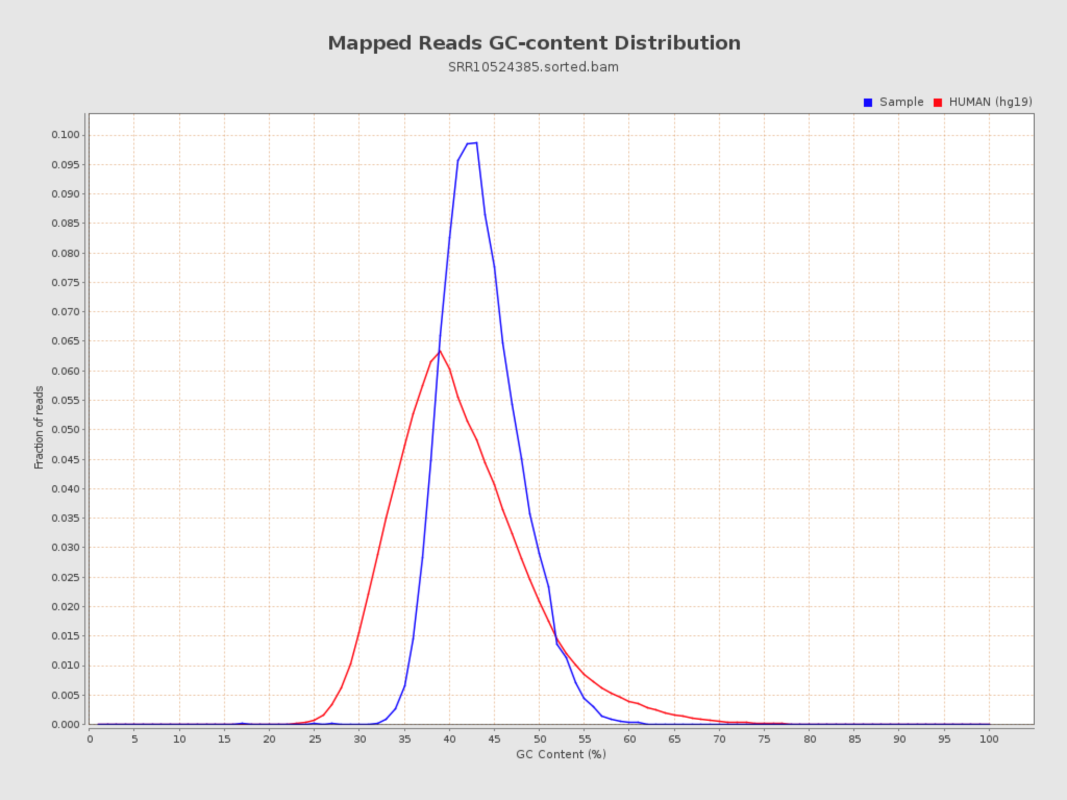
7. Results : Duplication Rate Histogram



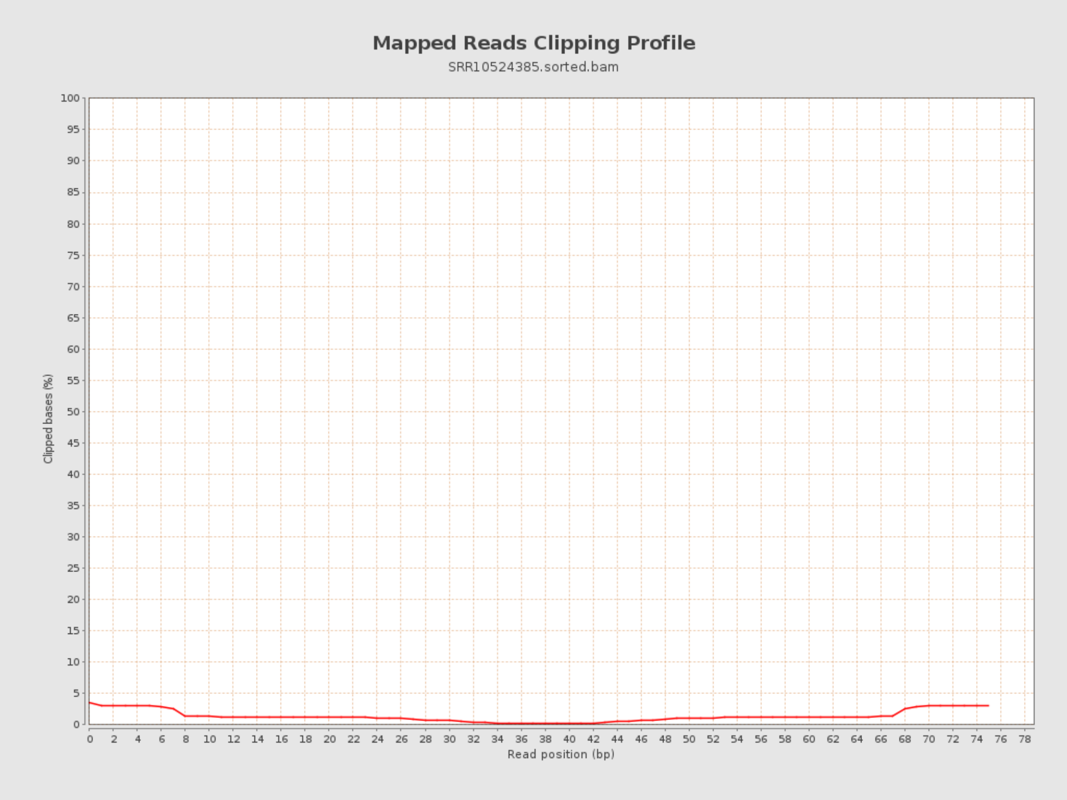
8. Results : Mapped Reads Nucleotide Content



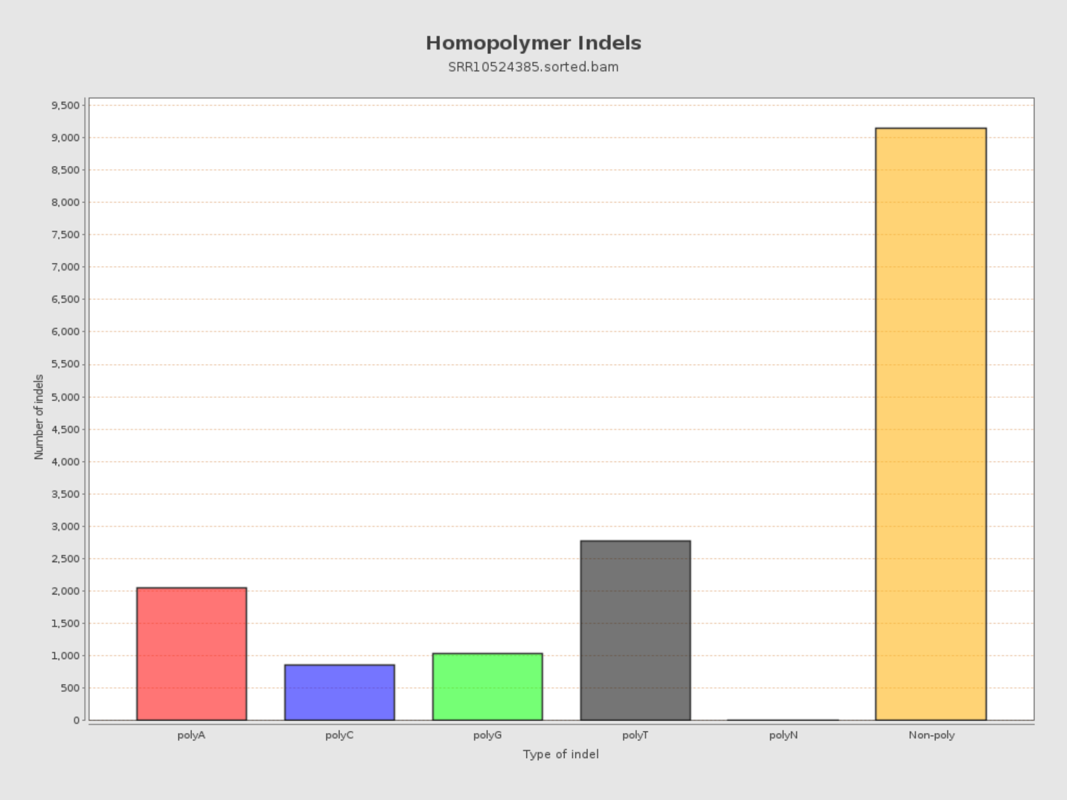
9. Results : Mapped Reads GC-content Distribution



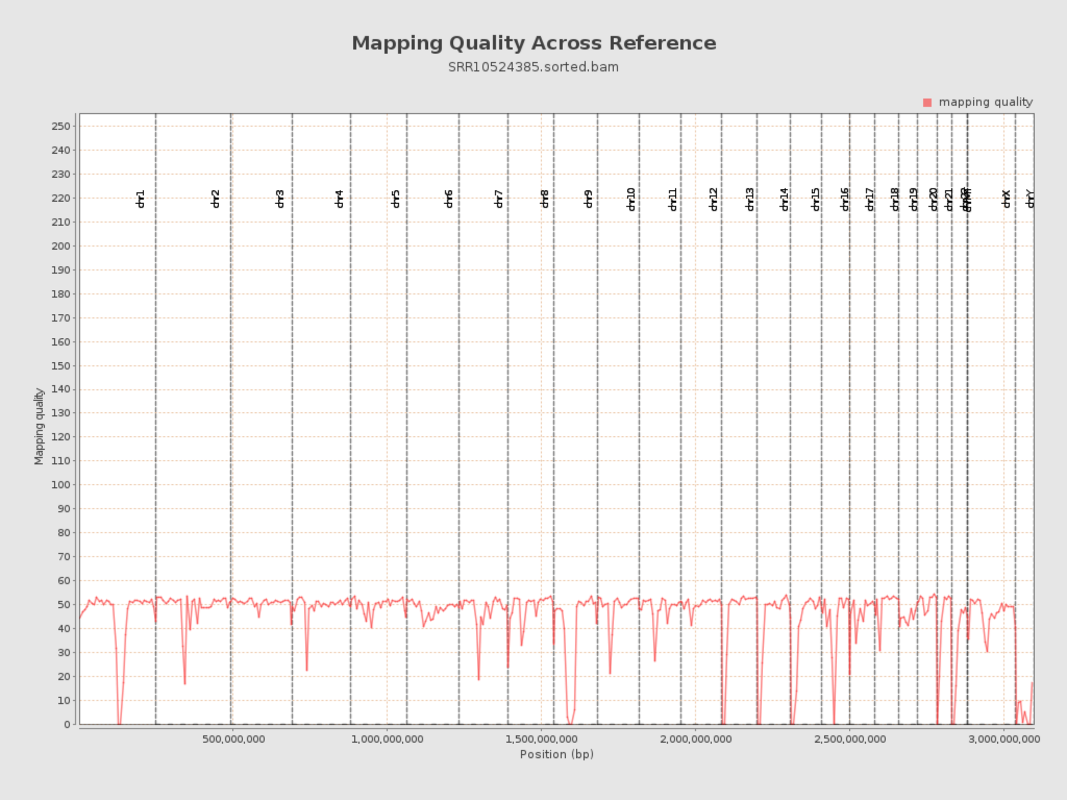
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram