Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:19:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524383.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_SRR10524383 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524383.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:19:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524383.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,046,998
Mapped reads	963,911 / 92.06%
Unmapped reads	83,087 / 7.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,729 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	26,203 / 2.5%
Duplication rate	1.94%
Clipped reads	964,677 / 92.14%

2.2. ACGT Content

Number/percentage of A's	14,691,964 / 25.91%
Number/percentage of C's	10,148,327 / 17.9%
Number/percentage of T's	17,620,430 / 31.07%
Number/percentage of G's	14,237,704 / 25.11%
Number/percentage of N's	7,345 / 0.01%
GC Percentage	43%

2.3. Coverage

Mean	0.0183

Standard Deviation	0.2036

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

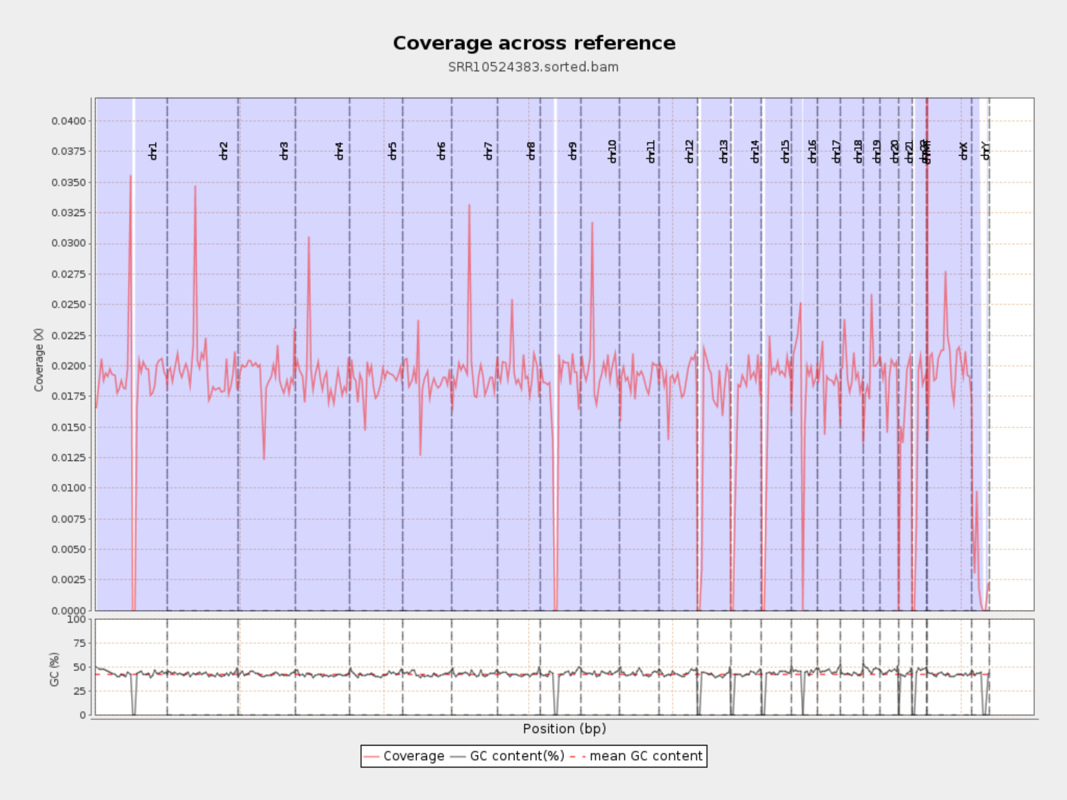
General error rate	0.5%
Mismatches	276,819
Insertions	3,810
Mapped reads with at least one insertion	0.39%
Deletions	10,362
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.99%

2.6. Chromosome stats

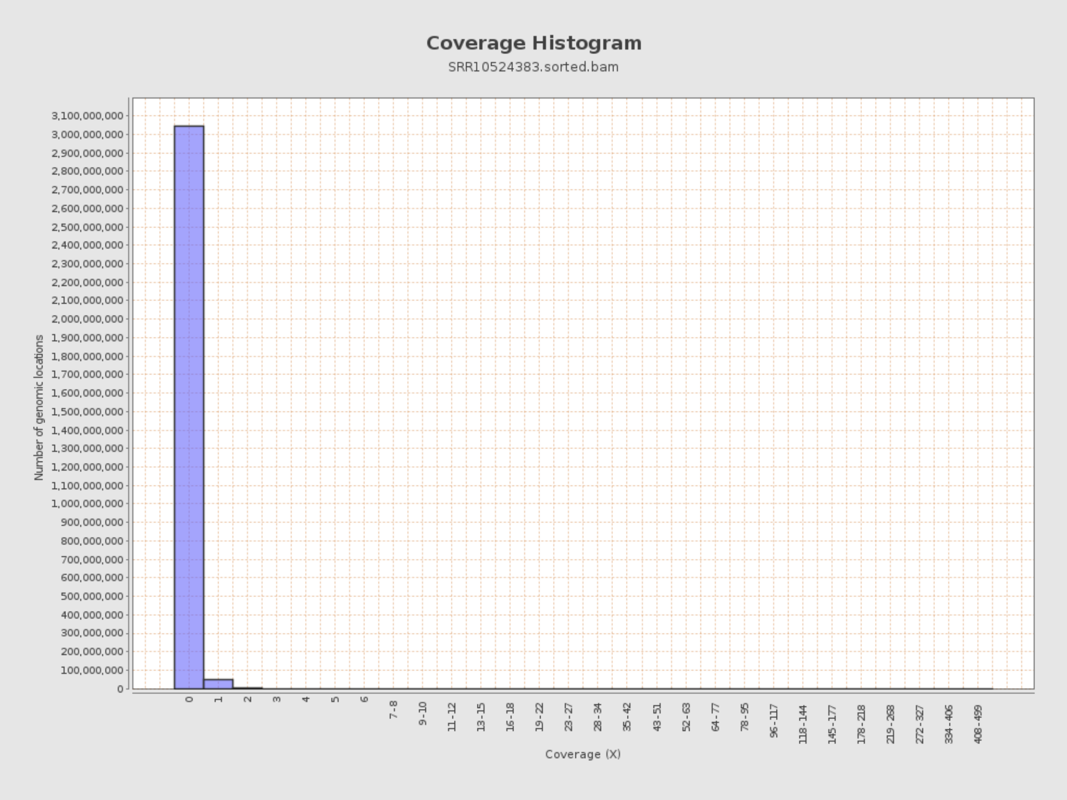
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4578401	0.0184	0.3985
chr2	243199373	4823740	0.0198	0.2192
chr3	198022430	3768247	0.019	0.1447
chr4	191154276	3682935	0.0193	0.1576
chr5	180915260	3412857	0.0189	0.1445
chr6	171115067	3221708	0.0188	0.1557
chr7	159138663	3128143	0.0197	0.2614

chr8	146364022	2866151	0.0196	0.1772
chr9	141213431	2388563	0.0169	0.1761
chr10	135534747	2724891	0.0201	0.1855
chr11	135006516	2575239	0.0191	0.1835
chr12	133851895	2533862	0.0189	0.1476
chr13	115169878	1804681	0.0157	0.1309
chr14	107349540	1711036	0.0159	0.1377
chr15	102531392	1681568	0.0164	0.1342
chr16	90354753	1651423	0.0183	0.1459
chr17	81195210	1514538	0.0187	0.1552
chr18	78077248	1526140	0.0195	0.2947
chr19	59128983	1162544	0.0197	0.2636
chr20	63025520	1198889	0.019	0.146
chr21	48129895	752653	0.0156	0.1415
chr22	51304566	690577	0.0135	0.1216
chrMT	16571	1745	0.1053	0.3353
chrX	155270560	3150622	0.0203	0.1624
chrY	59373566	170923	0.0029	0.0861

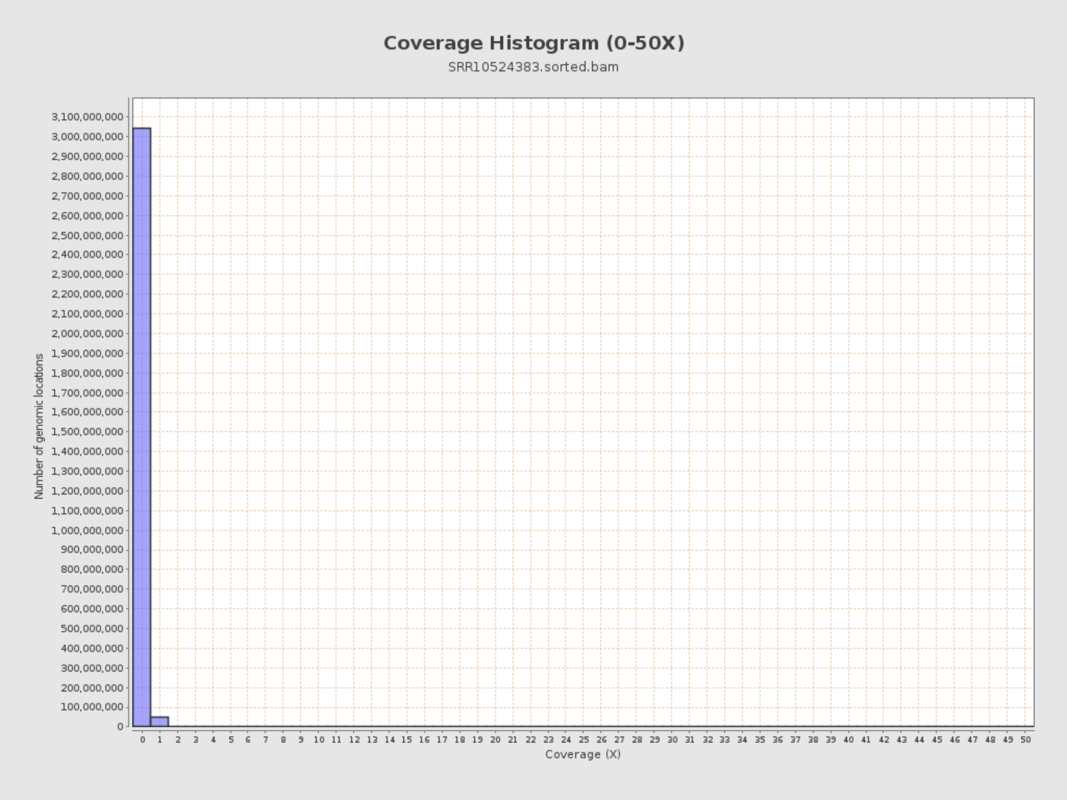
3. Results : Coverage across reference



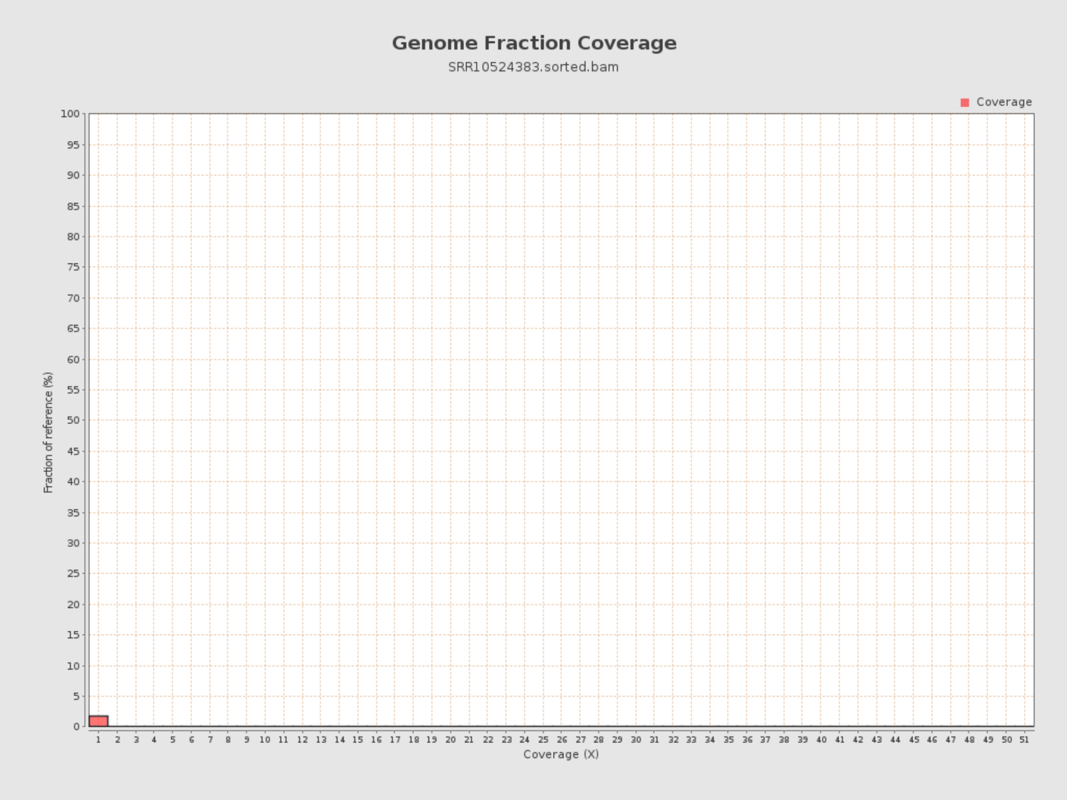
4. Results : Coverage Histogram



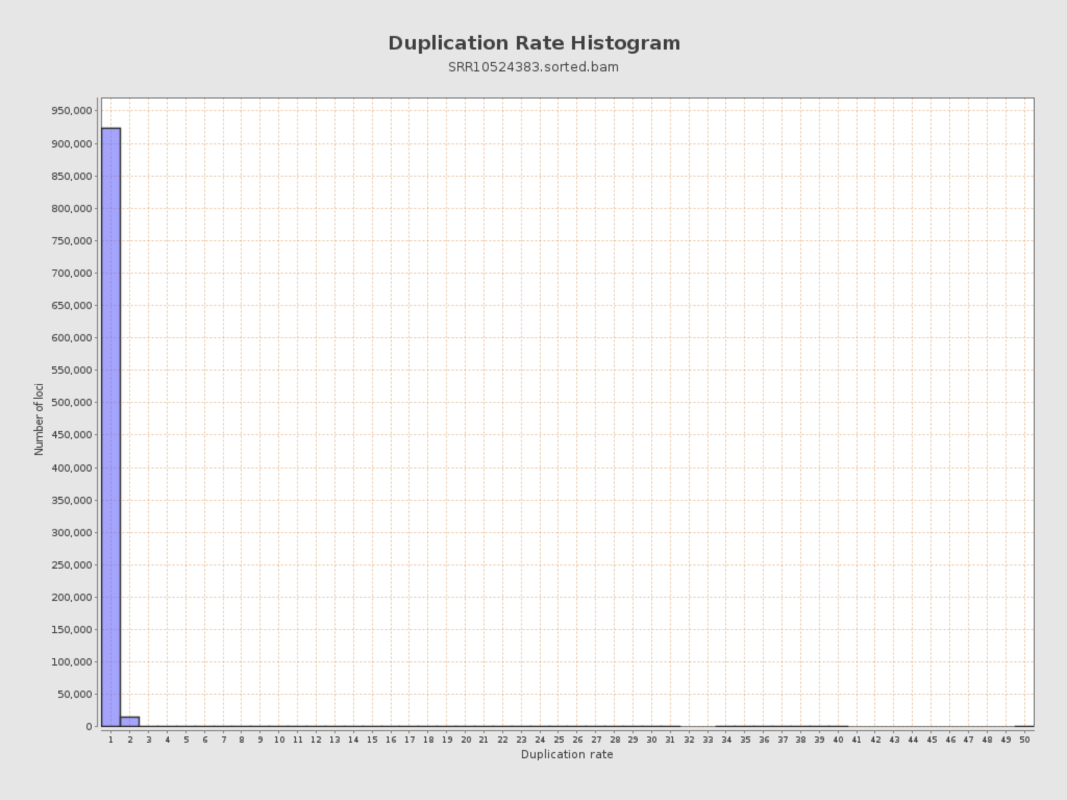
5. Results : Coverage Histogram (0-50X)



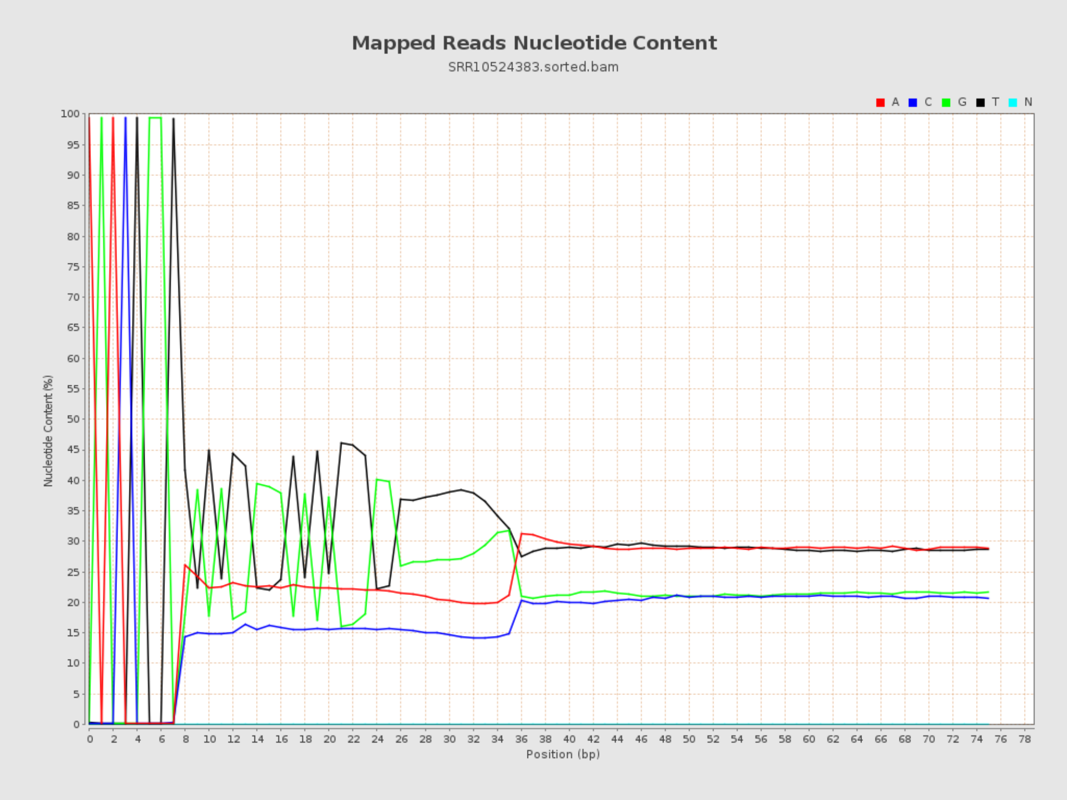
6. Results : Genome Fraction Coverage



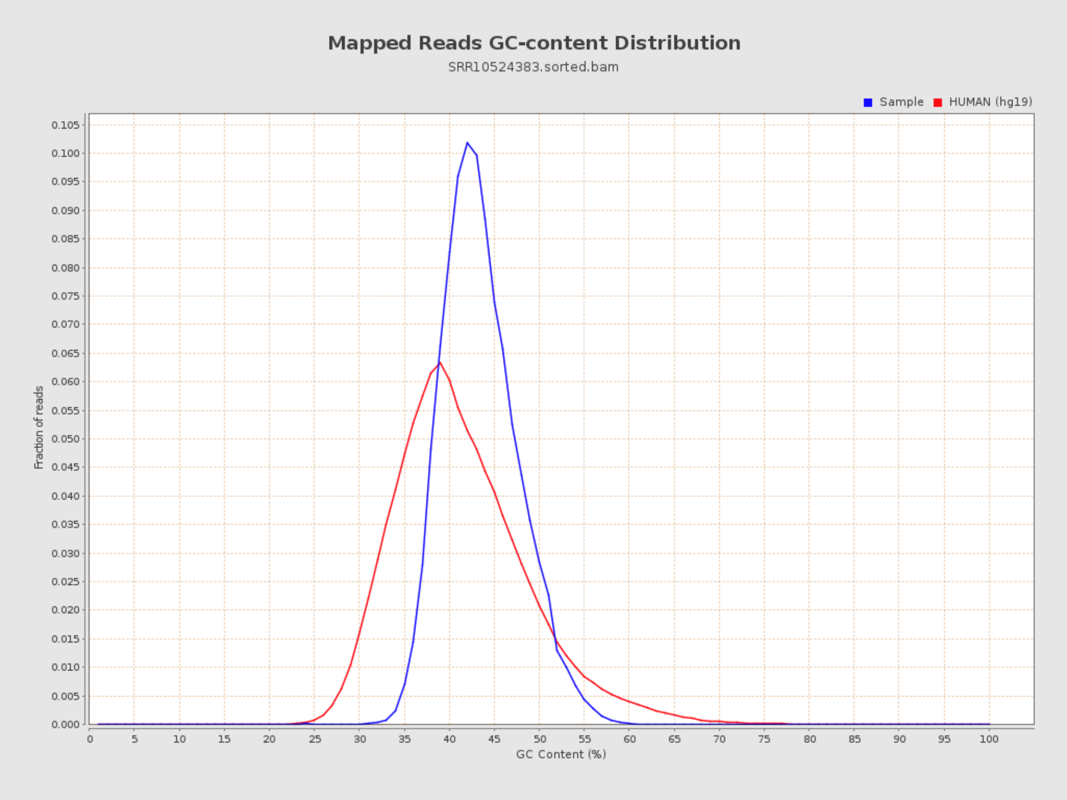
7. Results : Duplication Rate Histogram



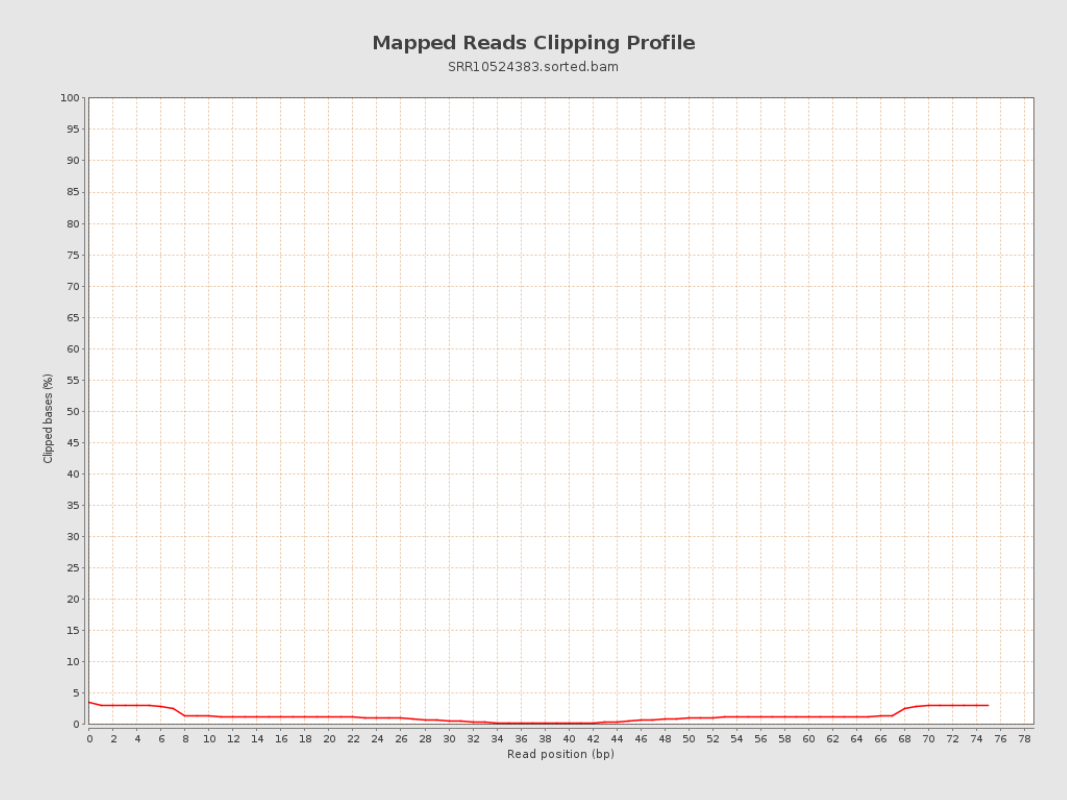
8. Results : Mapped Reads Nucleotide Content



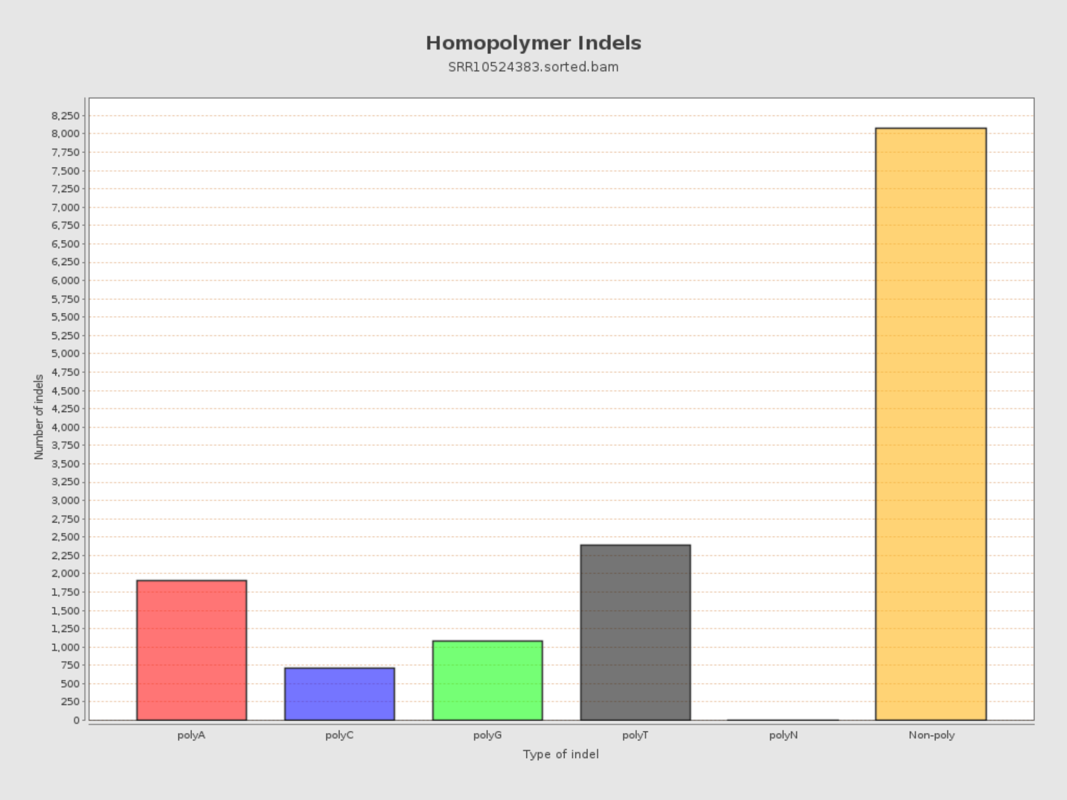
9. Results : Mapped Reads GC-content Distribution



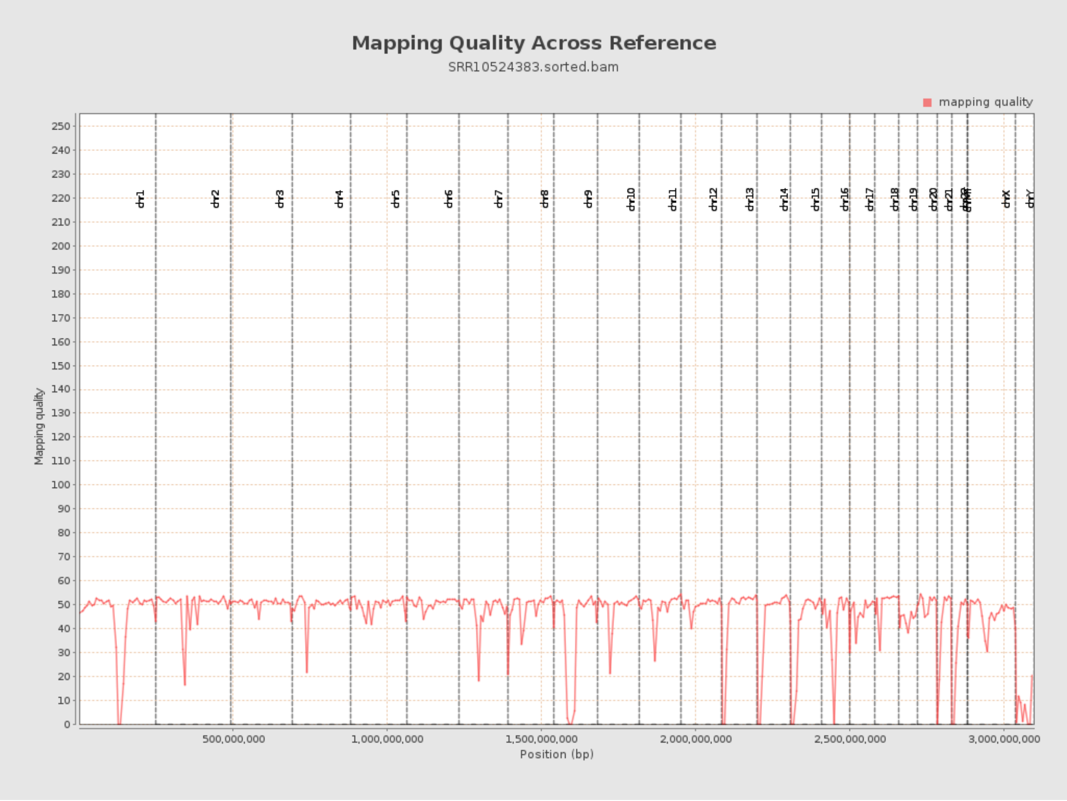
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram