Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 18:17:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524381.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_SRR10524381 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524381.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 18:17:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524381.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,268,159
Mapped reads	1,155,074 / 91.08%
Unmapped reads	113,085 / 8.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,992 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	30,220 / 2.38%
Duplication rate	1.84%
Clipped reads	1,154,493 / 91.04%

2.2. ACGT Content

Number/percentage of A's	16,307,206 / 24.2%
Number/percentage of C's	13,130,176 / 19.48%
Number/percentage of T's	22,000,491 / 32.65%
Number/percentage of G's	15,946,060 / 23.66%
Number/percentage of N's	8,635 / 0.01%
GC Percentage	43.14%

2.3. Coverage

Mean	0.0218

Standard Deviation	0.2255

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

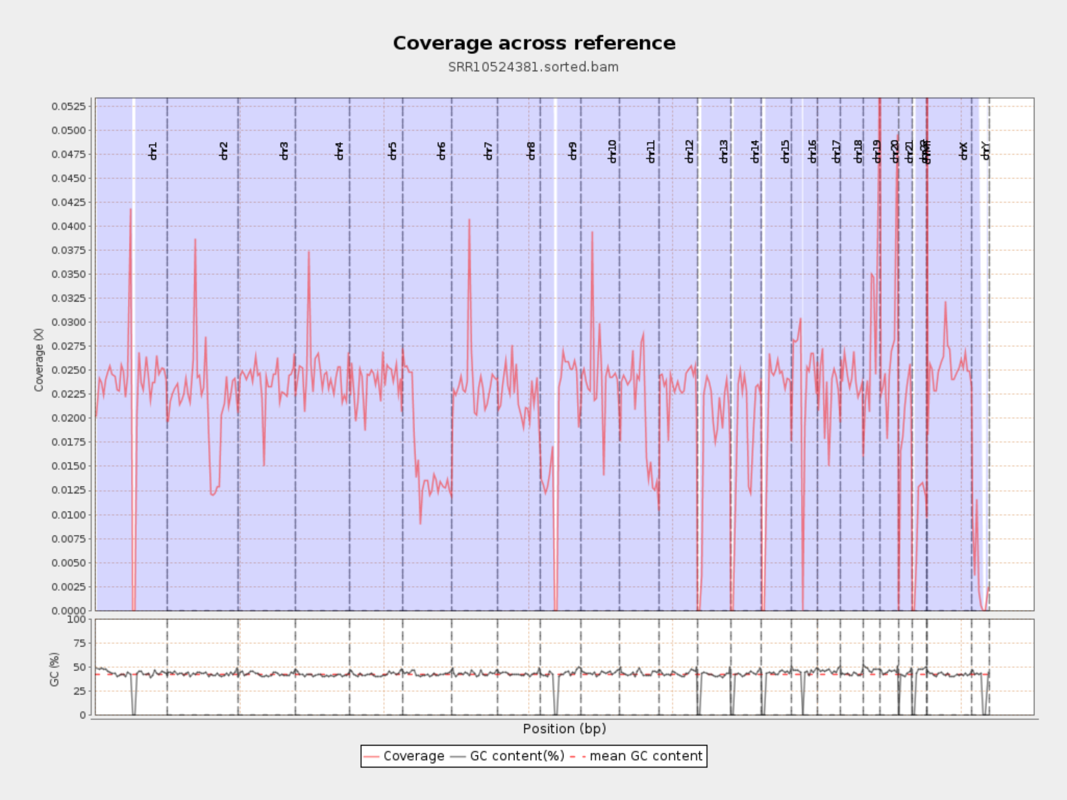
General error rate	0.5%
Mismatches	329,436
Insertions	5,276
Mapped reads with at least one insertion	0.45%
Deletions	12,421
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.68%

2.6. Chromosome stats

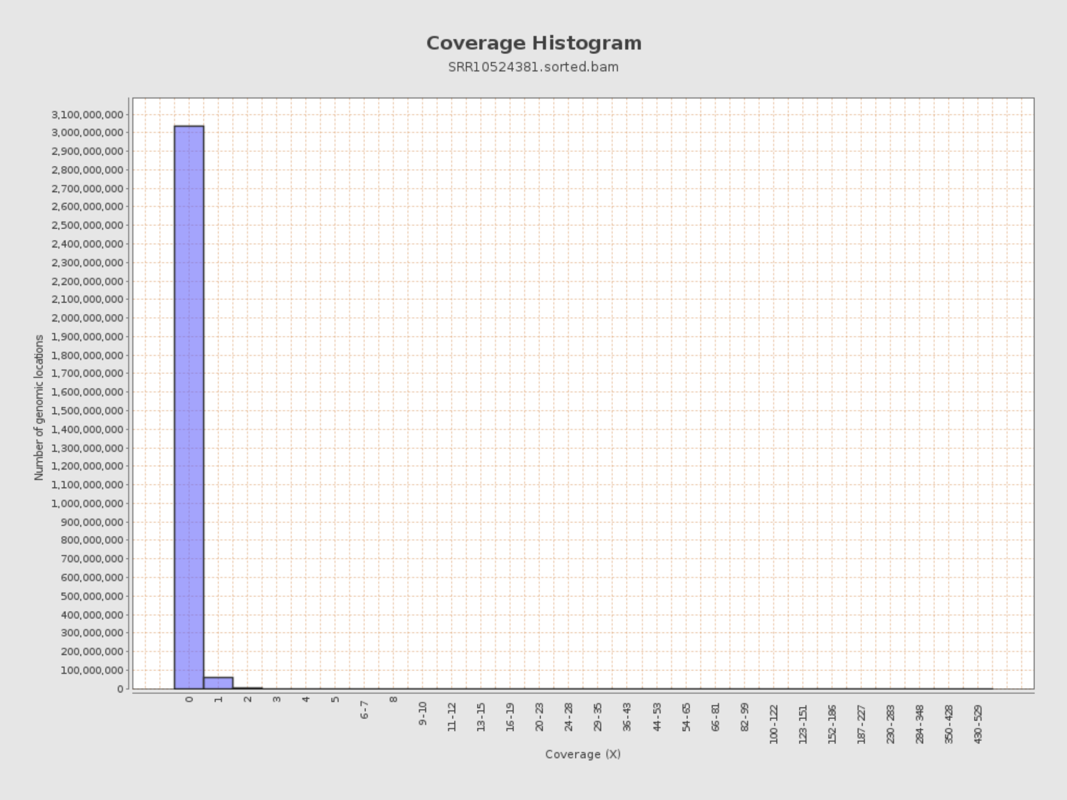
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5749745	0.0231	0.4342
chr2	243199373	5265073	0.0216	0.2507
chr3	198022430	4704610	0.0238	0.1643
chr4	191154276	4714567	0.0247	0.1797
chr5	180915260	4318813	0.0239	0.1641
chr6	171115067	2715337	0.0159	0.142
chr7	159138663	3808480	0.0239	0.3168

chr8	146364022	3274710	0.0224	0.1947
chr9	141213431	2588026	0.0183	0.1771
chr10	135534747	3315287	0.0245	0.2146
chr11	135006516	2819268	0.0209	0.1907
chr12	133851895	3159612	0.0236	0.1652
chr13	115169878	2068791	0.018	0.142
chr14	107349540	1897175	0.0177	0.1527
chr15	102531392	2077671	0.0203	0.1523
chr16	90354753	2110719	0.0234	0.1677
chr17	81195210	1830501	0.0225	0.1707
chr18	78077248	1898721	0.0243	0.2938
chr19	59128983	1820735	0.0308	0.3241
chr20	63025520	1761892	0.028	0.182
chr21	48129895	917646	0.0191	0.1563
chr22	51304566	455904	0.0089	0.1002
chrMT	16571	2064	0.1246	0.3975
chrX	155270560	3932488	0.0253	0.1824
chrY	59373566	204457	0.0034	0.0922

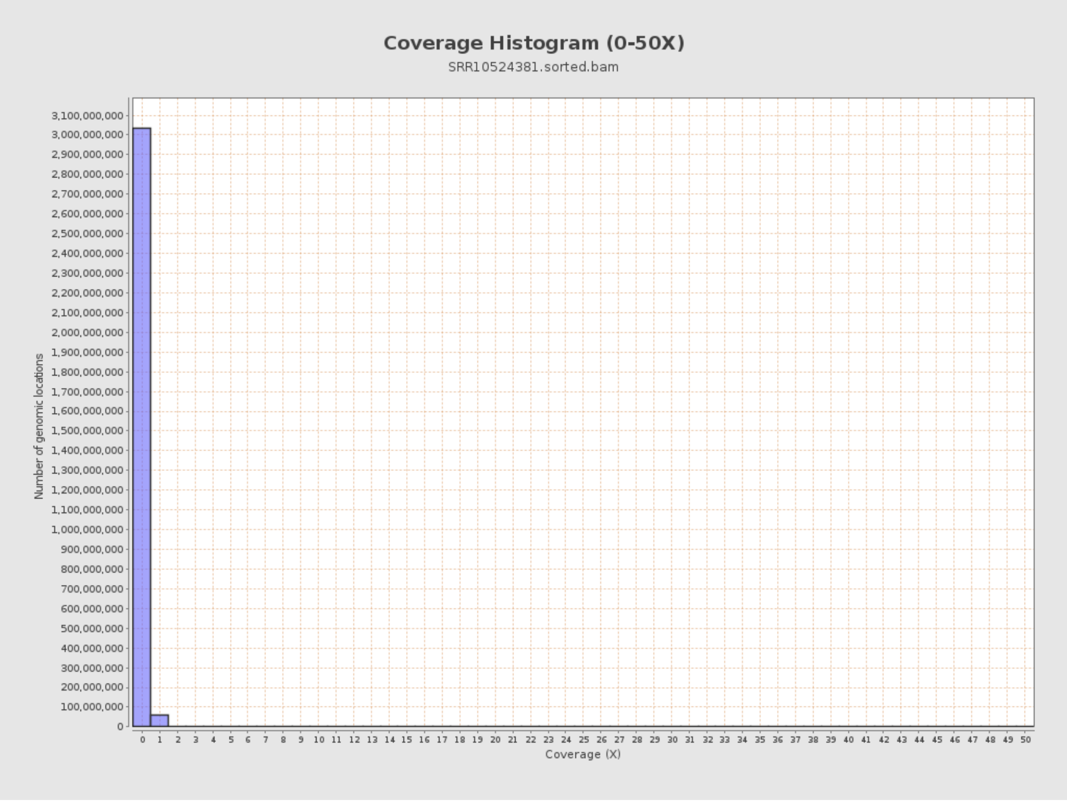
3. Results : Coverage across reference



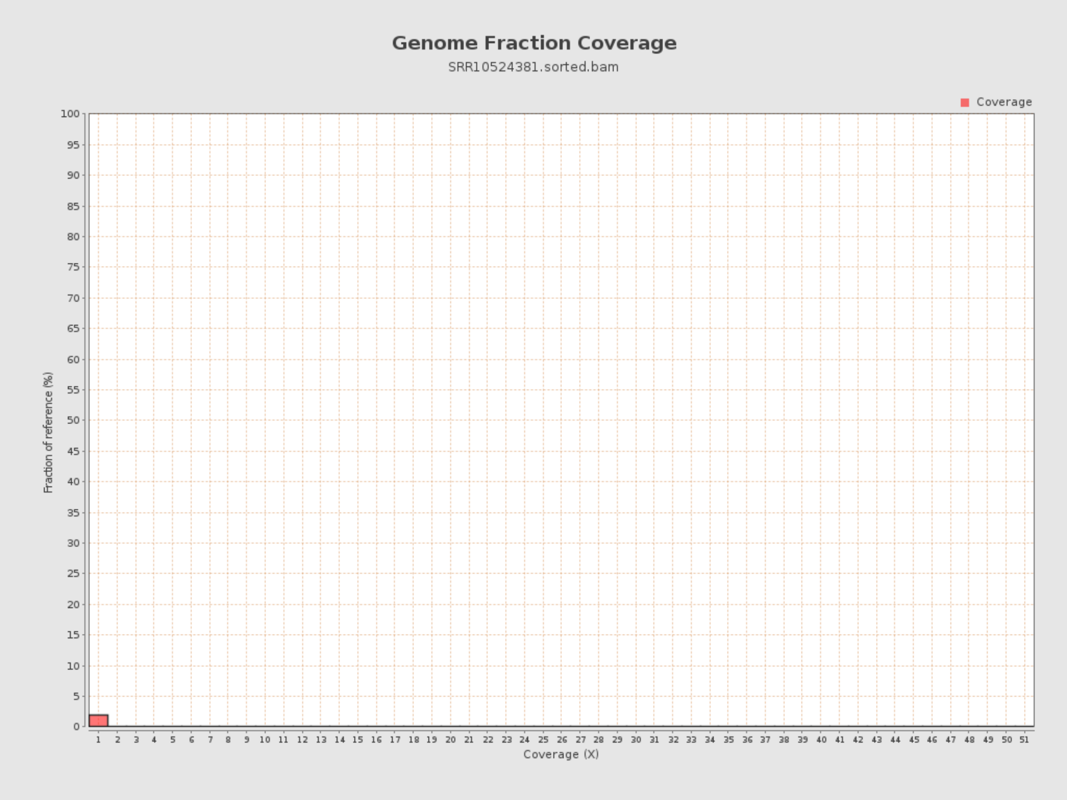
4. Results : Coverage Histogram



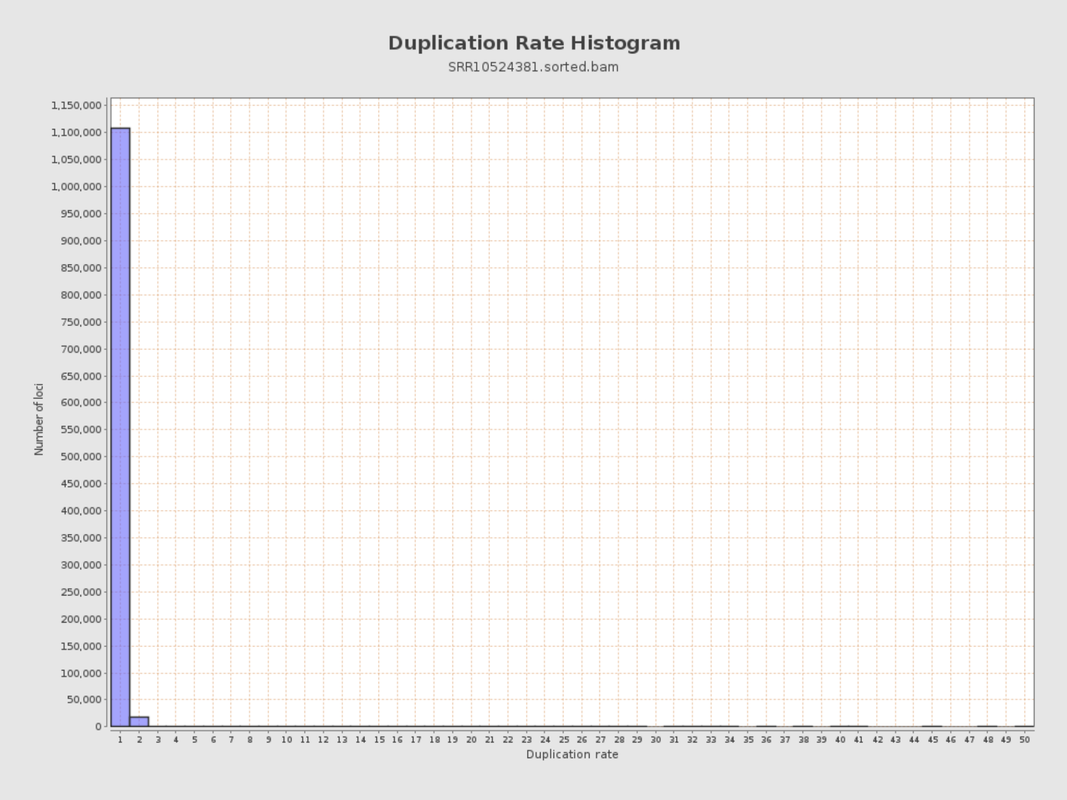
5. Results : Coverage Histogram (0-50X)



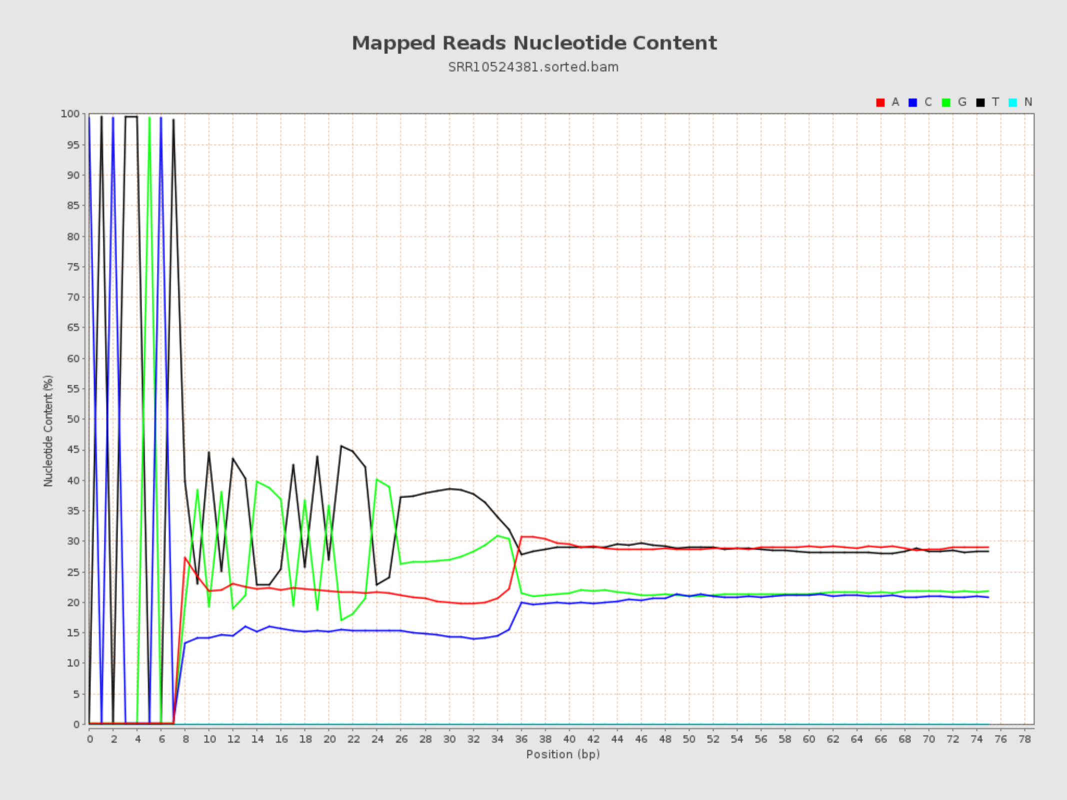
6. Results : Genome Fraction Coverage



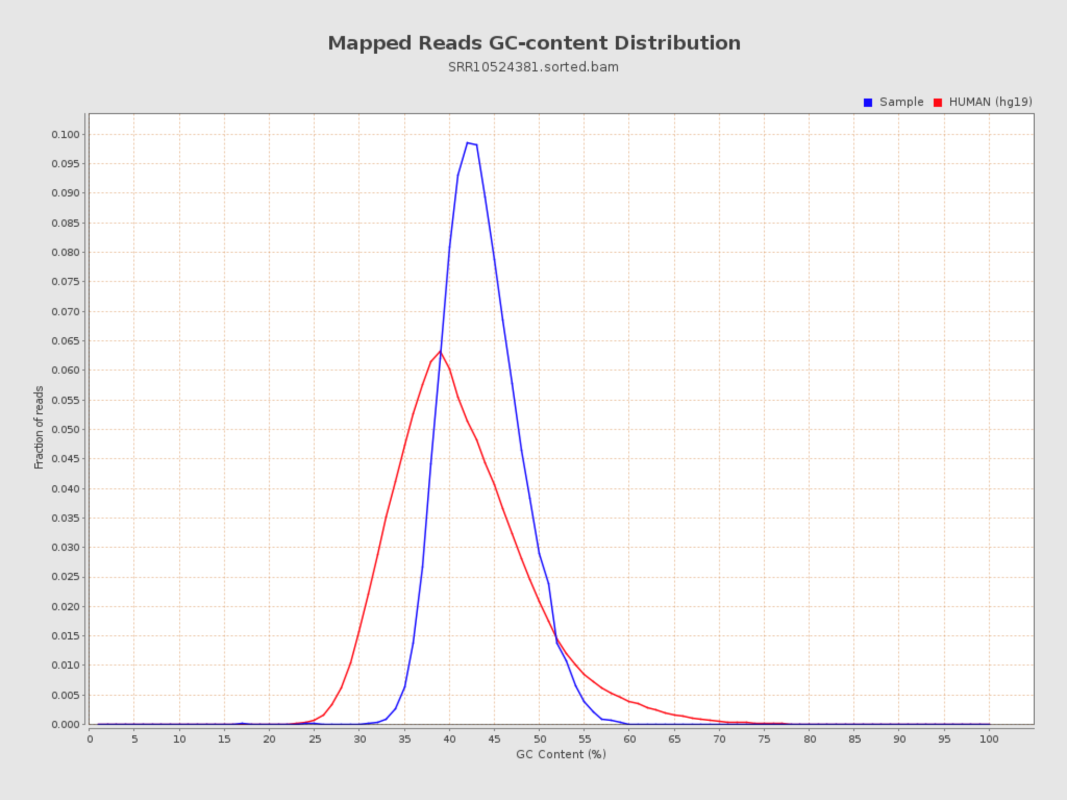
7. Results : Duplication Rate Histogram



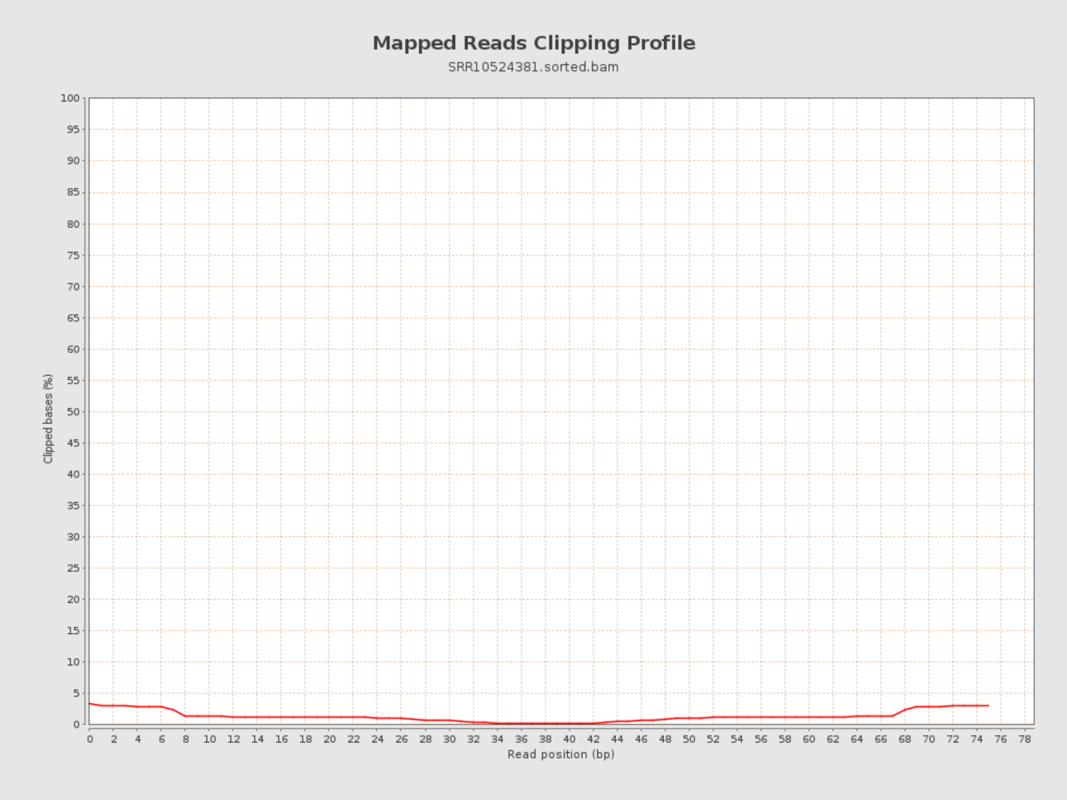
8. Results : Mapped Reads Nucleotide Content



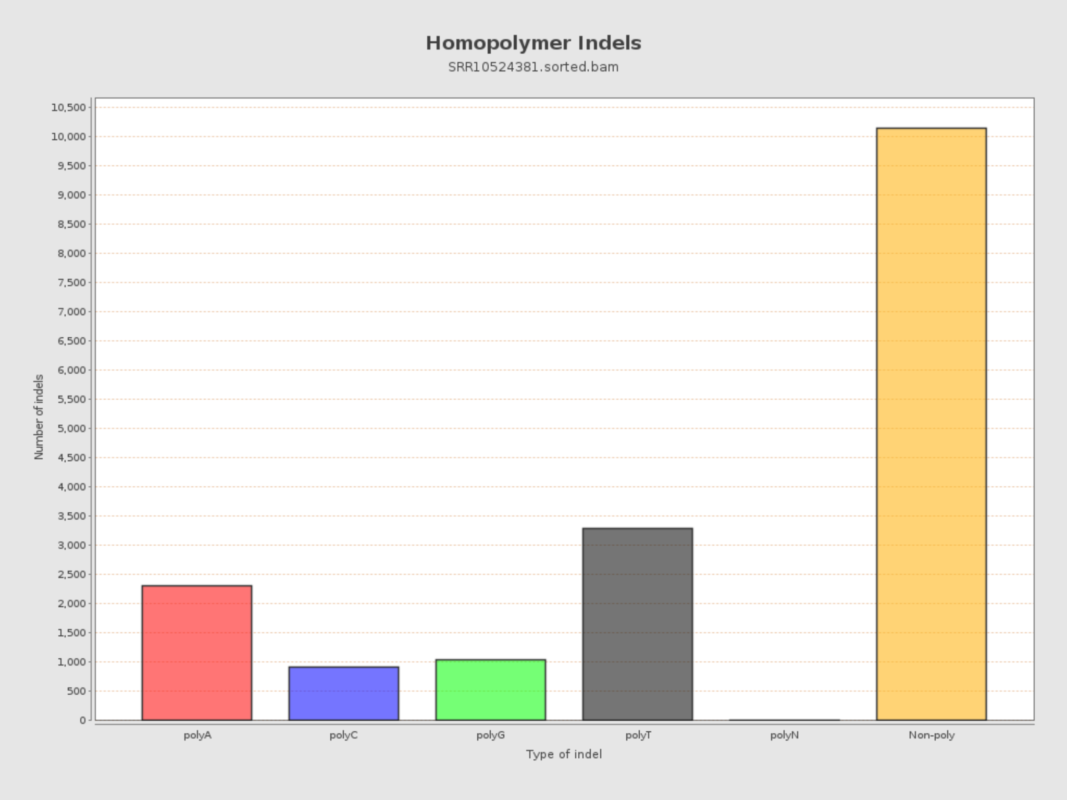
9. Results : Mapped Reads GC-content Distribution



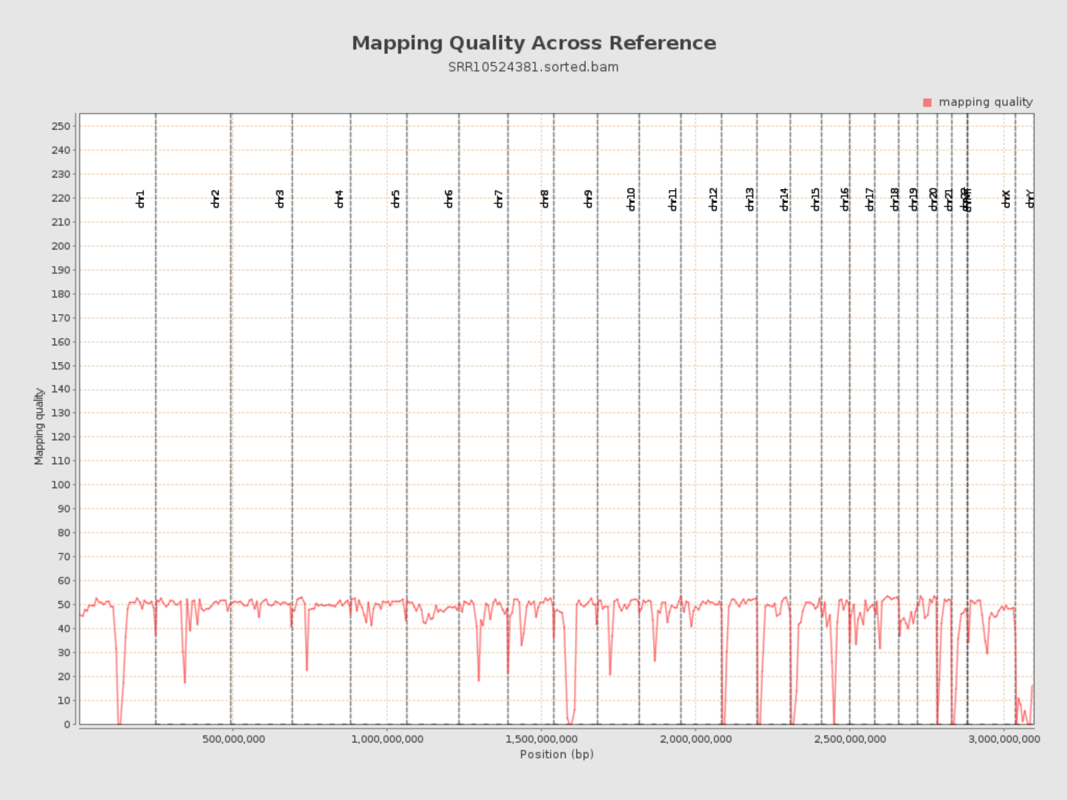
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram