Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:48:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524479.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_SRR10524479 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524479.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:48:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524479.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,533,543
Mapped reads	1,410,338 / 91.97%
Unmapped reads	123,205 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,096 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	59,806 / 3.9%
Duplication rate	3.24%
Clipped reads	1,409,416 / 91.91%

2.2. ACGT Content

Number/percentage of A's	20,811,525 / 25.46%
Number/percentage of C's	15,837,951 / 19.38%
Number/percentage of T's	25,605,817 / 31.33%
Number/percentage of G's	19,485,310 / 23.84%
Number/percentage of N's	1,643 / 0%
GC Percentage	43.21%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.2491

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

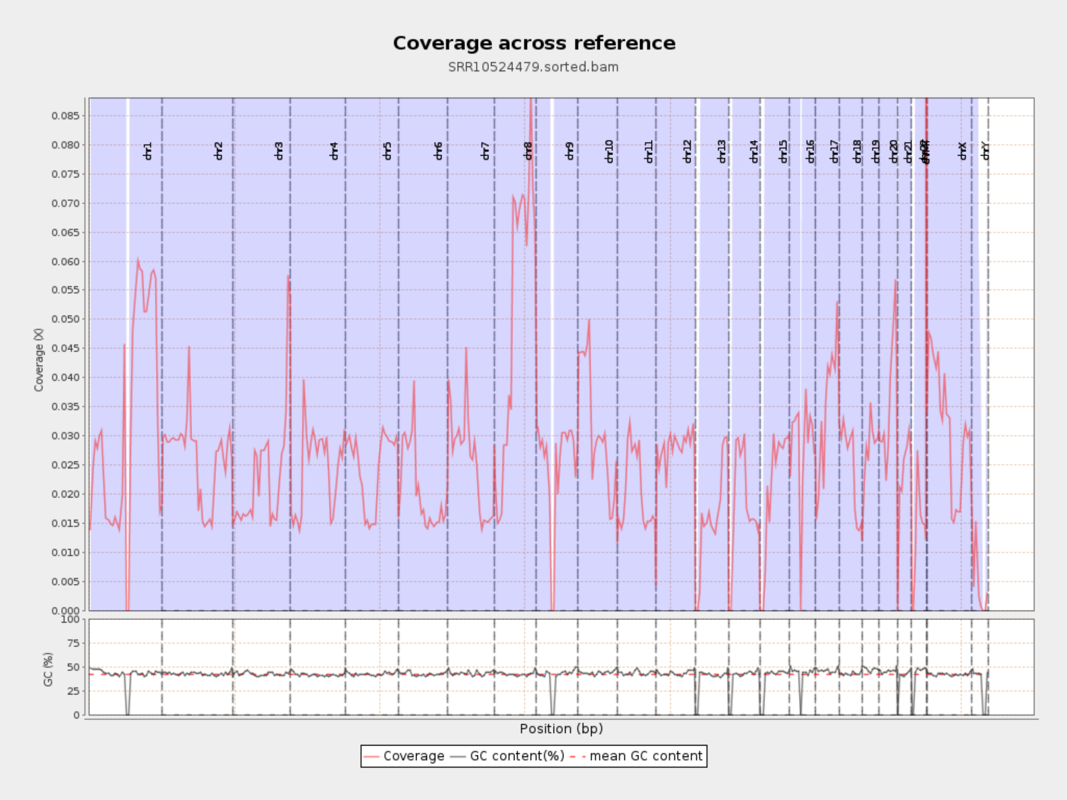
General error rate	0.48%
Mismatches	381,700
Insertions	6,017
Mapped reads with at least one insertion	0.43%
Deletions	15,070
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.95%

2.6. Chromosome stats

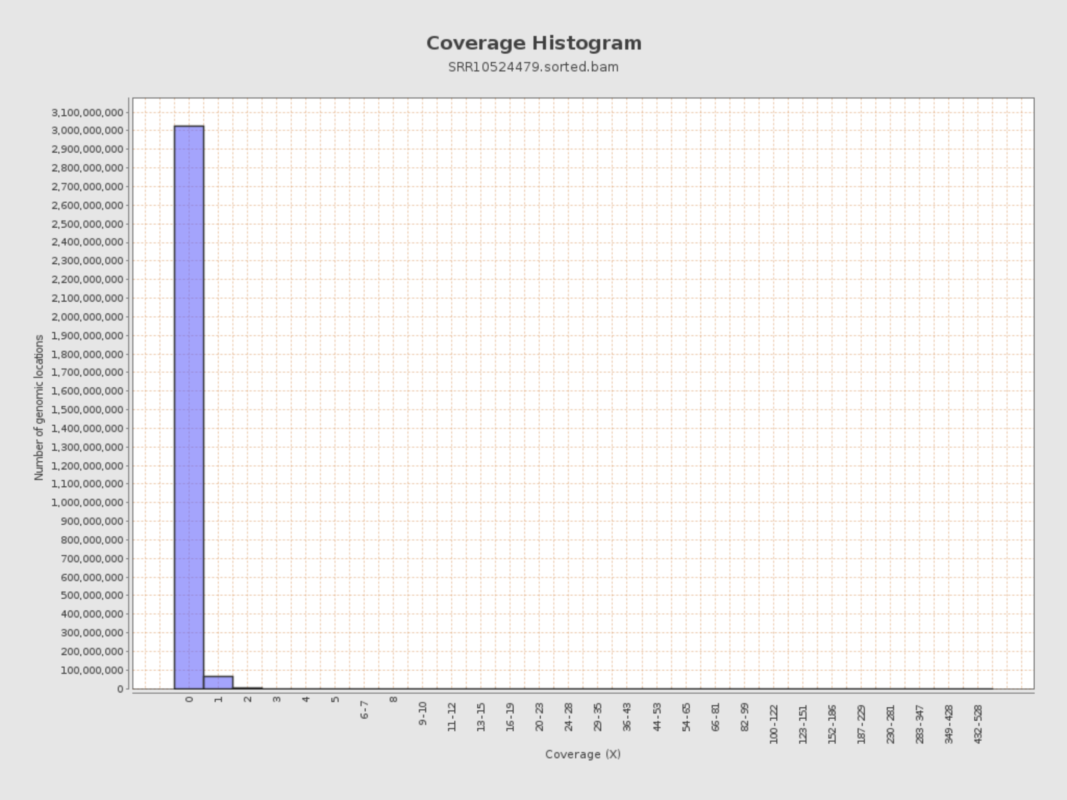
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8088800	0.0325	0.4311
chr2	243199373	6419335	0.0264	0.2813
chr3	198022430	4503865	0.0227	0.1677
chr4	191154276	4642857	0.0243	0.1939
chr5	180915260	4455170	0.0246	0.1725
chr6	171115067	3543689	0.0207	0.2017
chr7	159138663	4088933	0.0257	0.3224

chr8	146364022	7503655	0.0513	0.2832
chr9	141213431	3483878	0.0247	0.2273
chr10	135534747	4292341	0.0317	0.2594
chr11	135006516	2759631	0.0204	0.2422
chr12	133851895	3778625	0.0282	0.1852
chr13	115169878	1839109	0.016	0.1405
chr14	107349540	1935900	0.018	0.1504
chr15	102531392	2148870	0.021	0.1689
chr16	90354753	2556959	0.0283	0.1973
chr17	81195210	2855740	0.0352	0.215
chr18	78077248	1938650	0.0248	0.3547
chr19	59128983	1655452	0.028	0.3117
chr20	63025520	2285395	0.0363	0.2154
chr21	48129895	1117435	0.0232	0.1789
chr22	51304566	666305	0.013	0.1245
chrMT	16571	16538	0.998	1.3277
chrX	155270560	4924861	0.0317	0.2163
chrY	59373566	265760	0.0045	0.1259

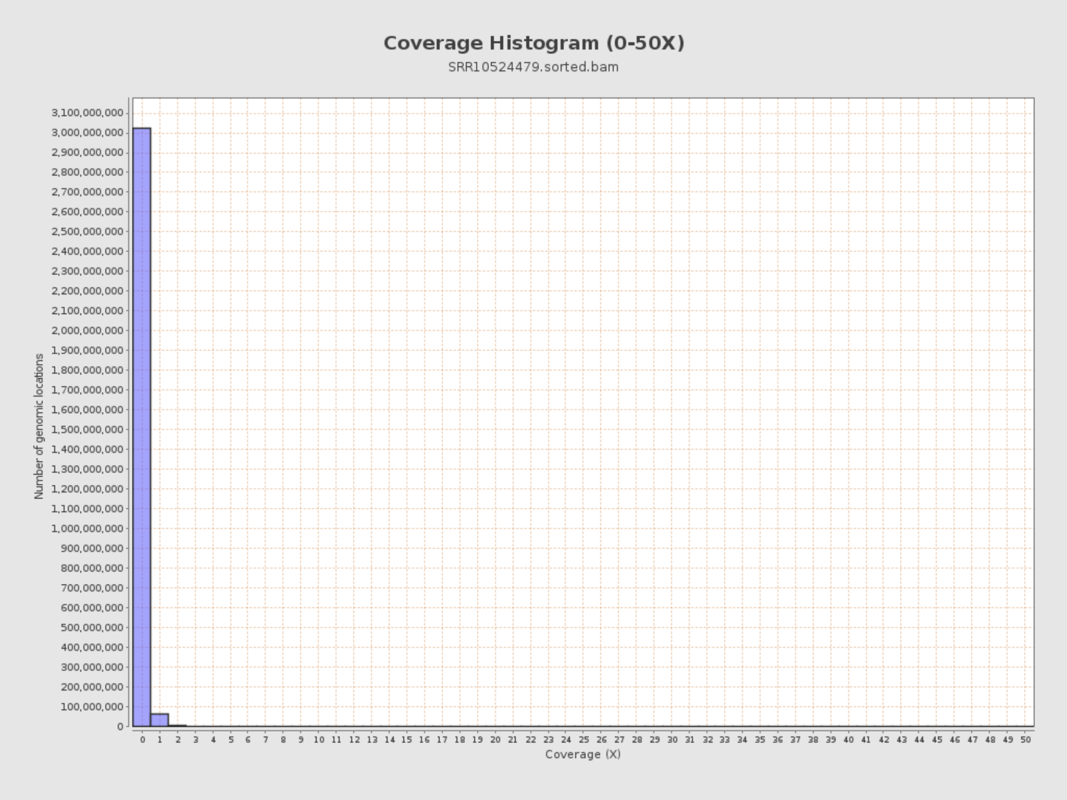
3. Results : Coverage across reference



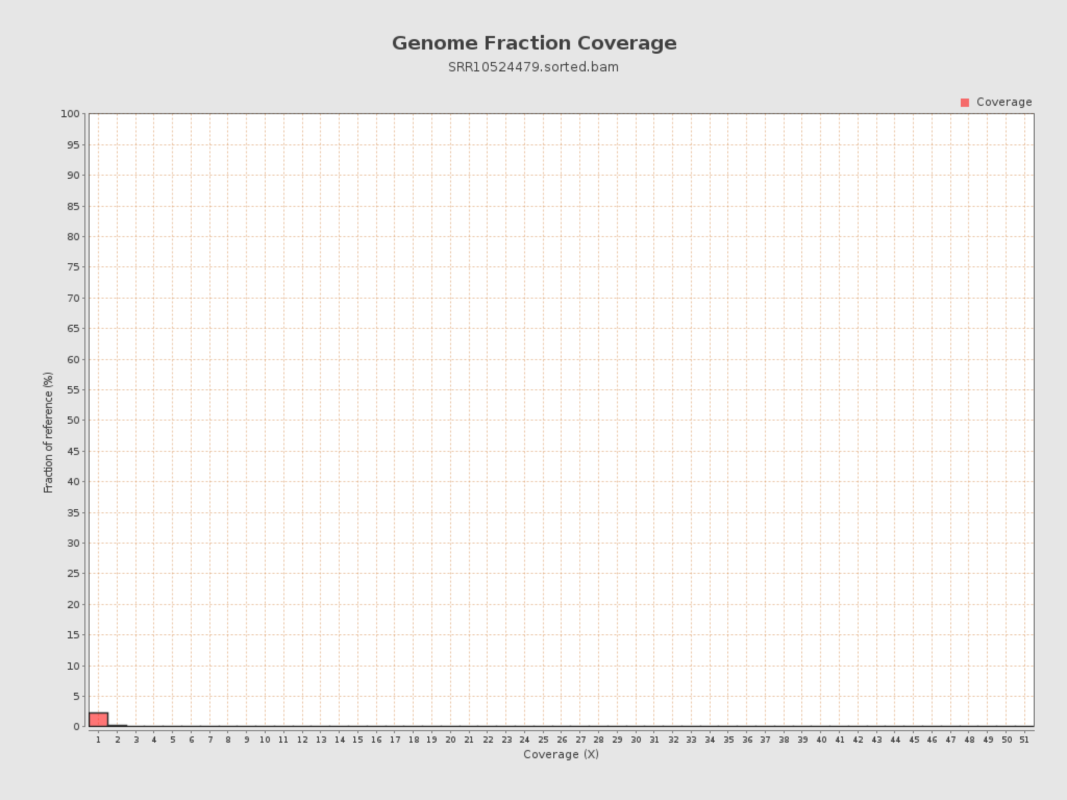
4. Results : Coverage Histogram



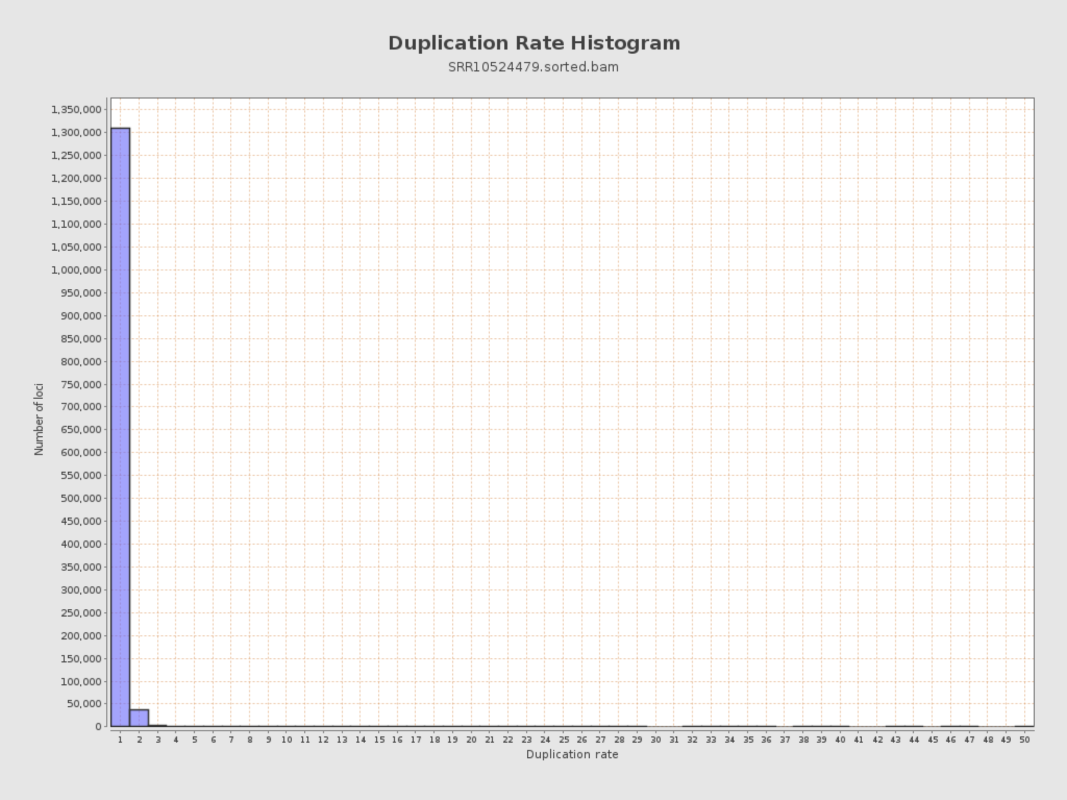
5. Results : Coverage Histogram (0-50X)



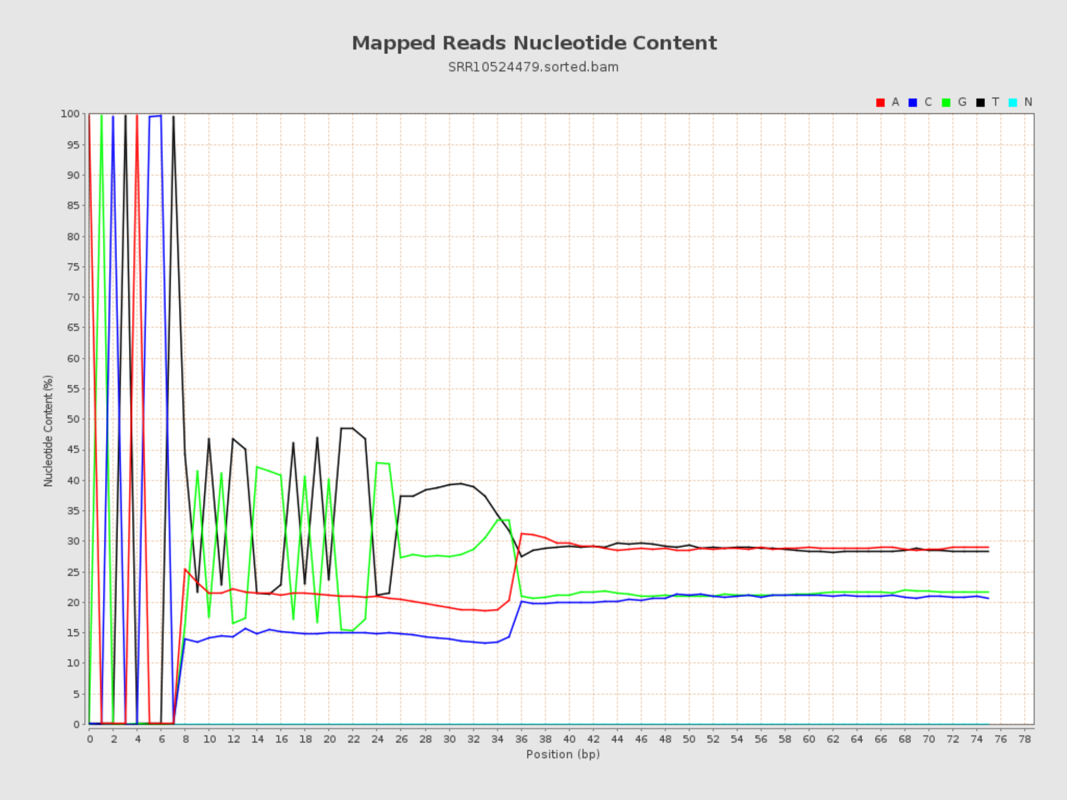
6. Results : Genome Fraction Coverage



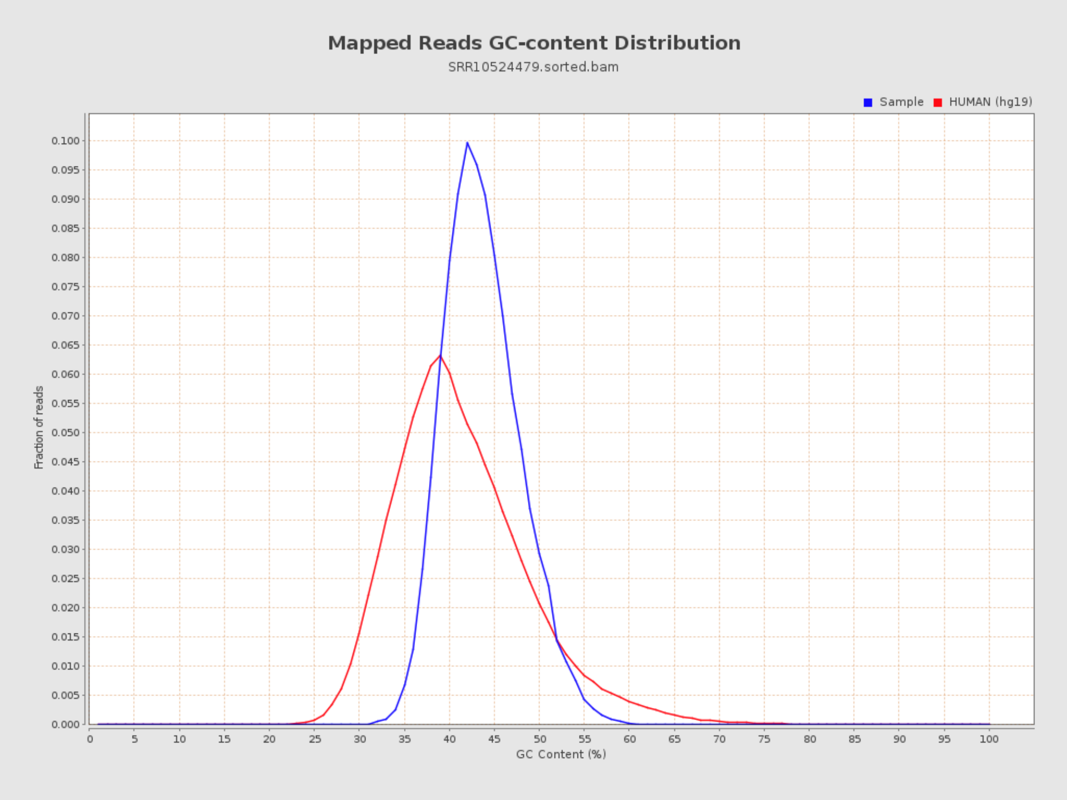
7. Results : Duplication Rate Histogram



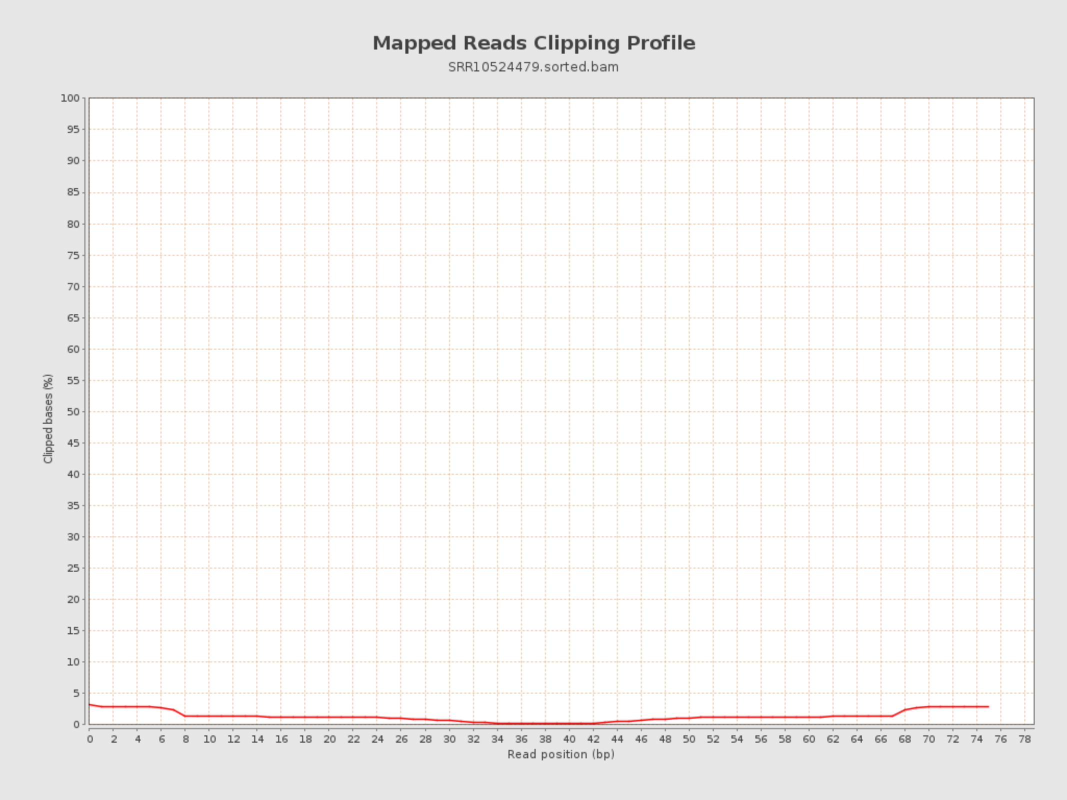
8. Results : Mapped Reads Nucleotide Content



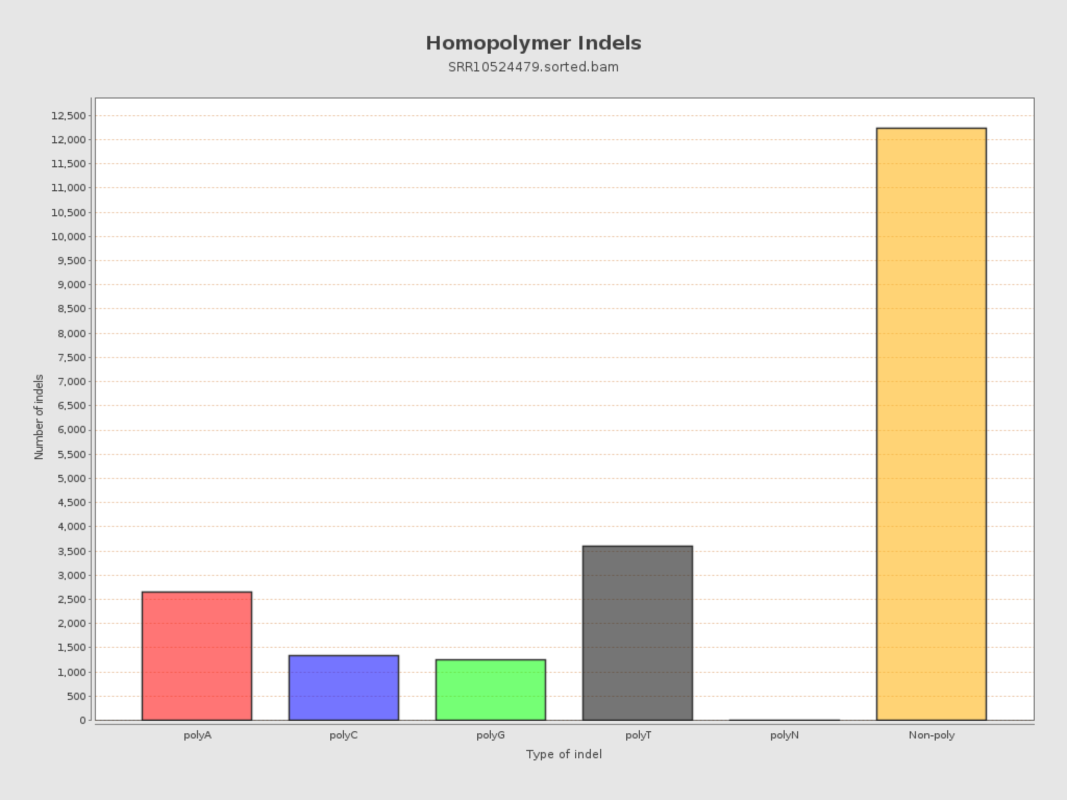
9. Results : Mapped Reads GC-content Distribution



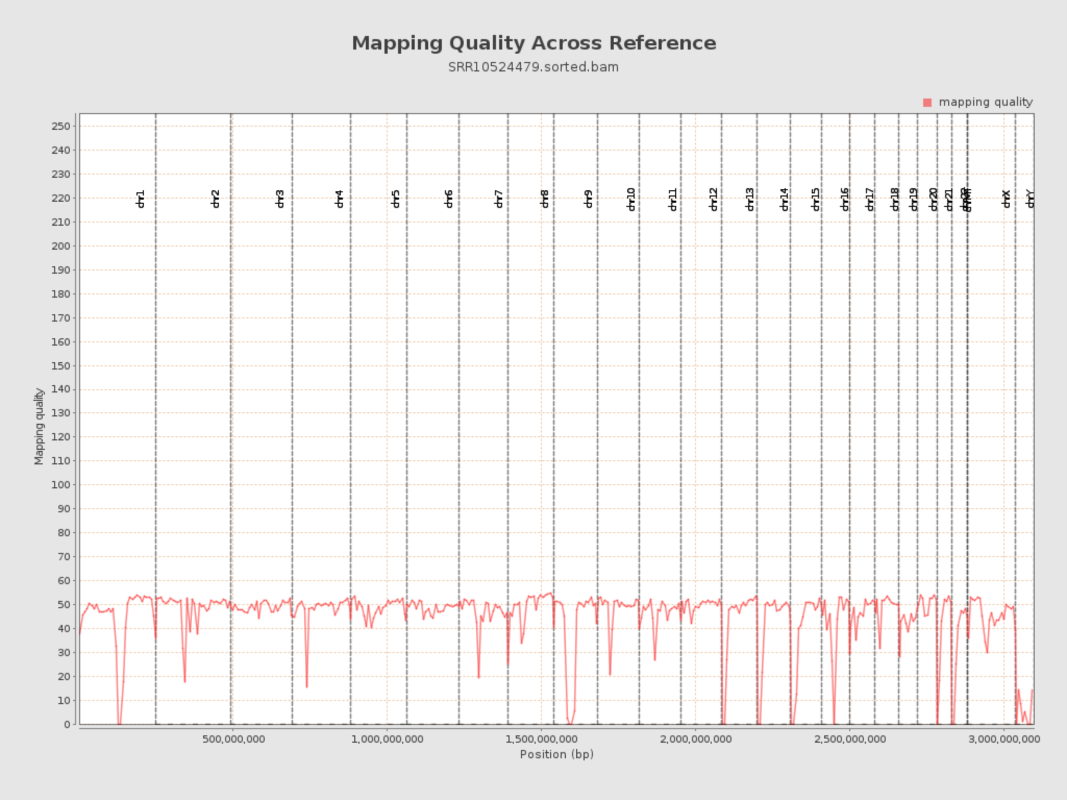
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram