Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:08:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525229.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_SRR10525229 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525229.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:08:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525229.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	533,912
Mapped reads	503,087 / 94.23%
Unmapped reads	30,825 / 5.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,059 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	8,228 / 1.54%
Duplication rate	1.2%
Clipped reads	502,933 / 94.2%

2.2. ACGT Content

Number/percentage of A's	8,586,375 / 27%
Number/percentage of C's	6,518,749 / 20.49%
Number/percentage of T's	9,483,686 / 29.82%
Number/percentage of G's	7,217,453 / 22.69%
Number/percentage of N's	839 / 0%
GC Percentage	43.19%

2.3. Coverage

Mean	0.0103

Standard Deviation	0.1303

2.4. Mapping Quality

Mean Mapping Quality	46.91

2.5. Mismatches and indels

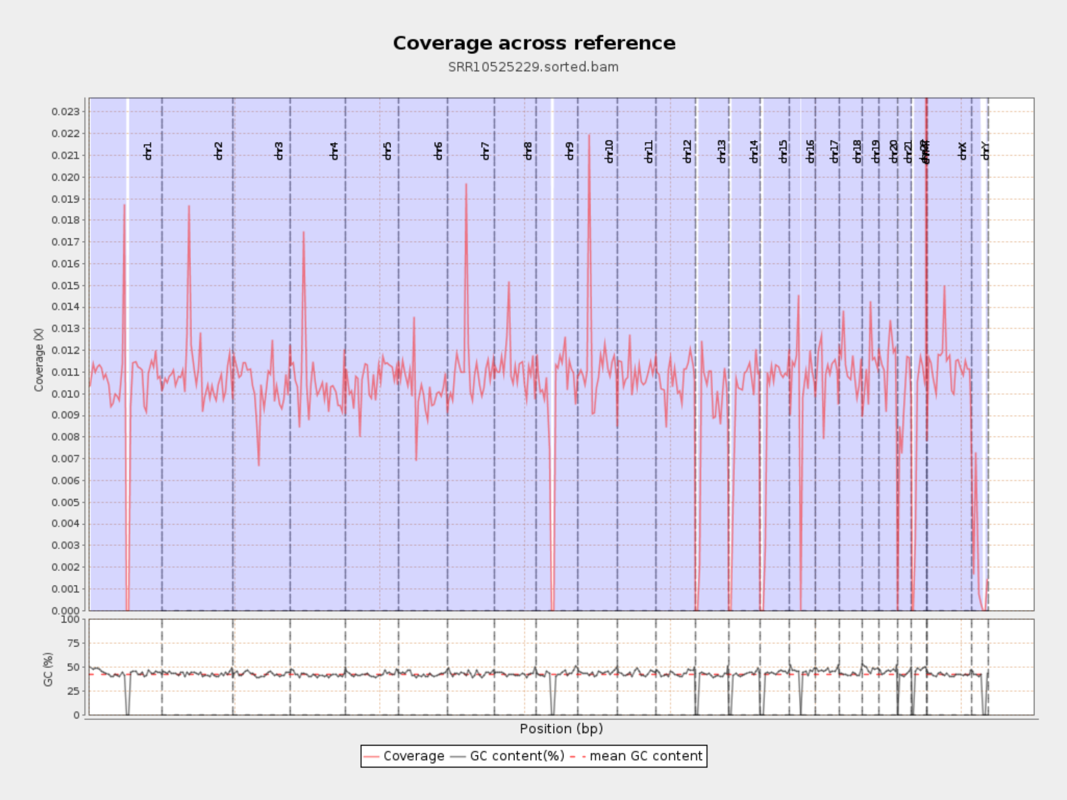
General error rate	0.49%
Mismatches	152,845
Insertions	2,403
Mapped reads with at least one insertion	0.48%
Deletions	6,923
Mapped reads with at least one deletion	1.36%
Homopolymer indels	43.26%

2.6. Chromosome stats

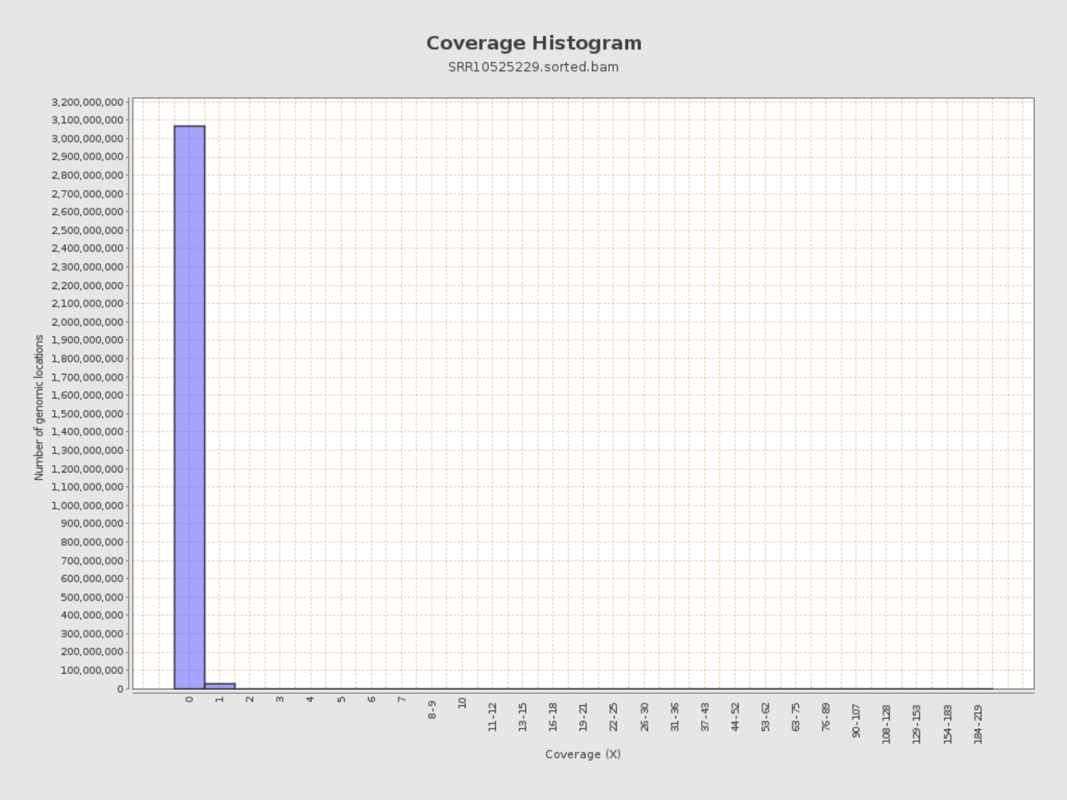
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2562007	0.0103	0.21
chr2	243199373	2665922	0.011	0.1386
chr3	198022430	2053061	0.0104	0.1053
chr4	191154276	2010936	0.0105	0.1113
chr5	180915260	1922452	0.0106	0.1066
chr6	171115067	1744089	0.0102	0.109
chr7	159138663	1786843	0.0112	0.1734

chr8	146364022	1645787	0.0112	0.1242
chr9	141213431	1343211	0.0095	0.1143
chr10	135534747	1559794	0.0115	0.1401
chr11	135006516	1472972	0.0109	0.117
chr12	133851895	1431096	0.0107	0.1073
chr13	115169878	992730	0.0086	0.0958
chr14	107349540	964609	0.009	0.1003
chr15	102531392	903267	0.0088	0.0968
chr16	90354753	928040	0.0103	0.1094
chr17	81195210	889480	0.011	0.1118
chr18	78077248	881478	0.0113	0.1783
chr19	59128983	664825	0.0112	0.1651
chr20	63025520	719173	0.0114	0.1117
chr21	48129895	422772	0.0088	0.1037
chr22	51304566	388121	0.0076	0.0902
chrMT	16571	8388	0.5062	0.7966
chrX	155270560	1746891	0.0113	0.1121
chrY	59373566	110555	0.0019	0.0749

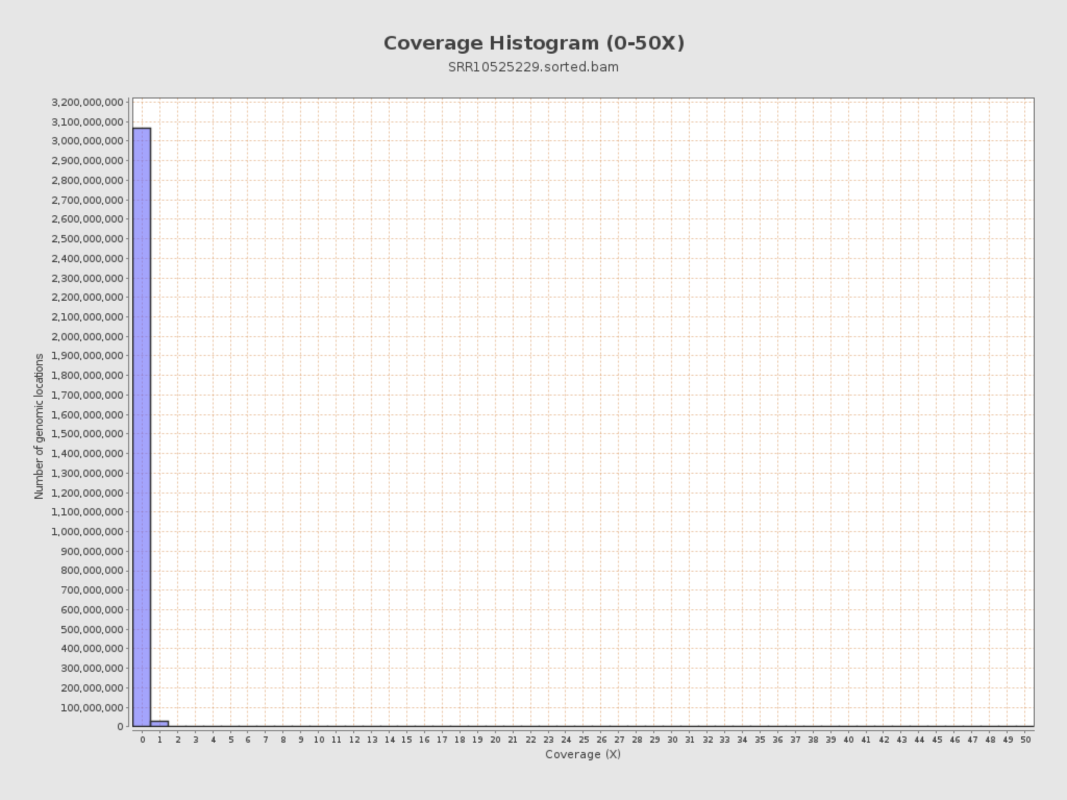
3. Results : Coverage across reference



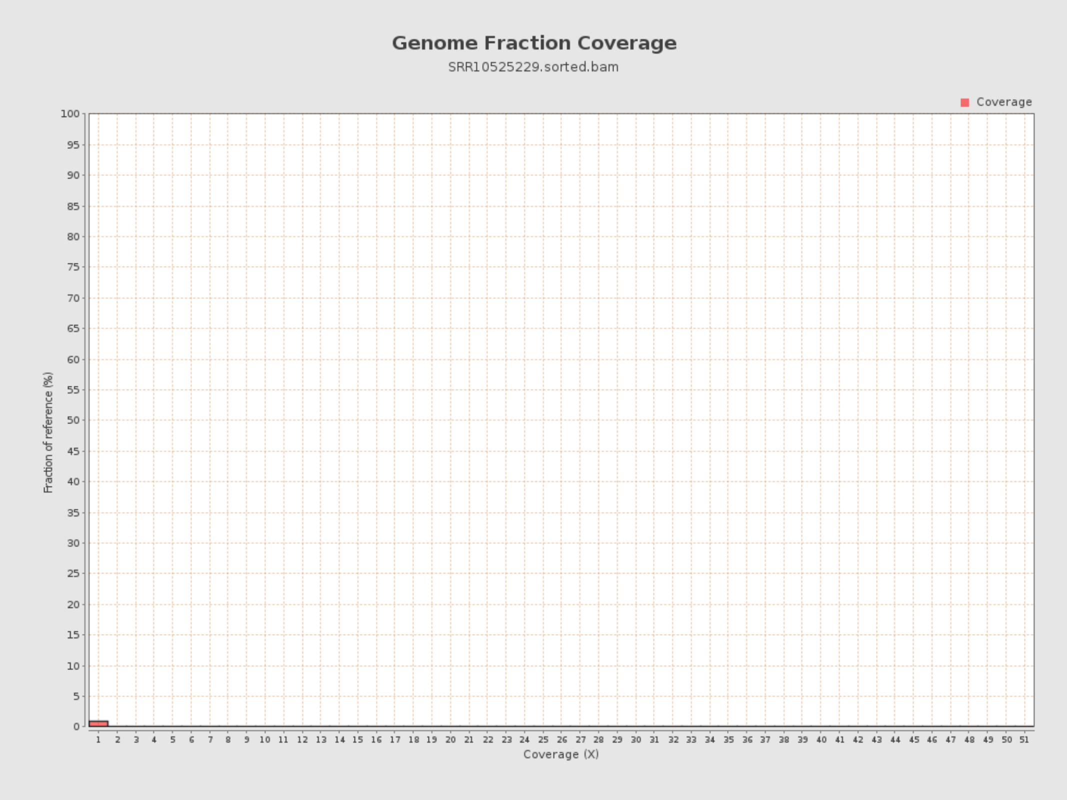
4. Results : Coverage Histogram



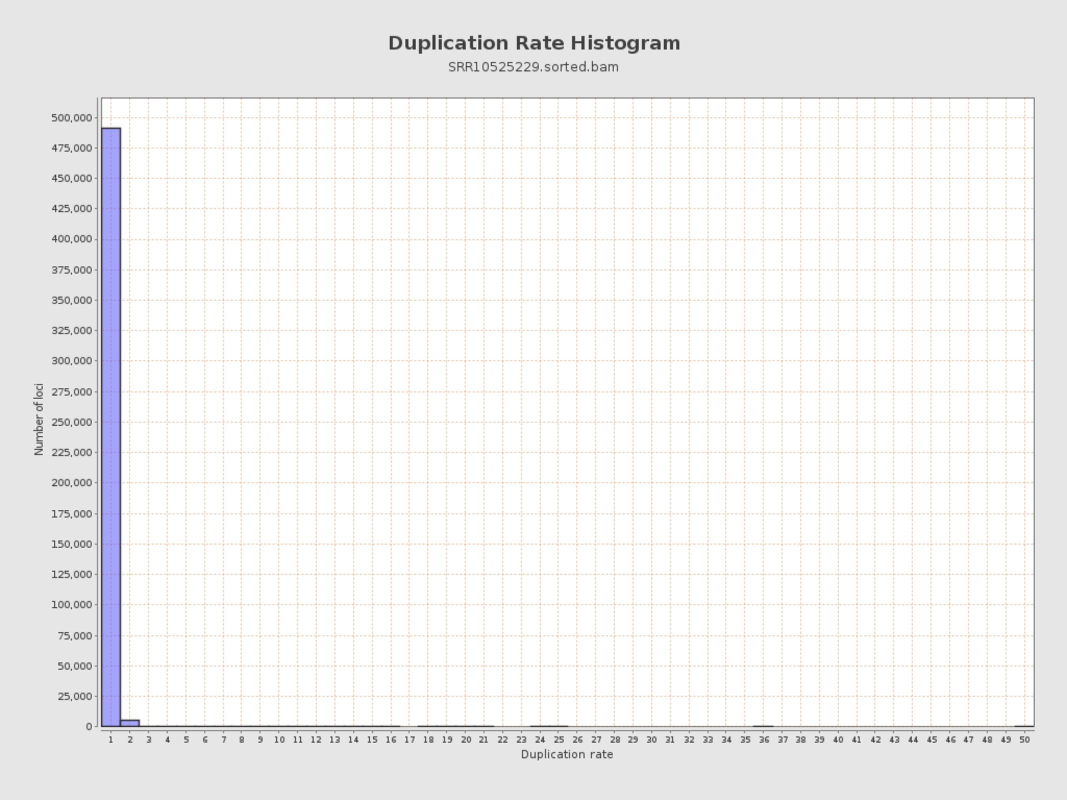
5. Results : Coverage Histogram (0-50X)



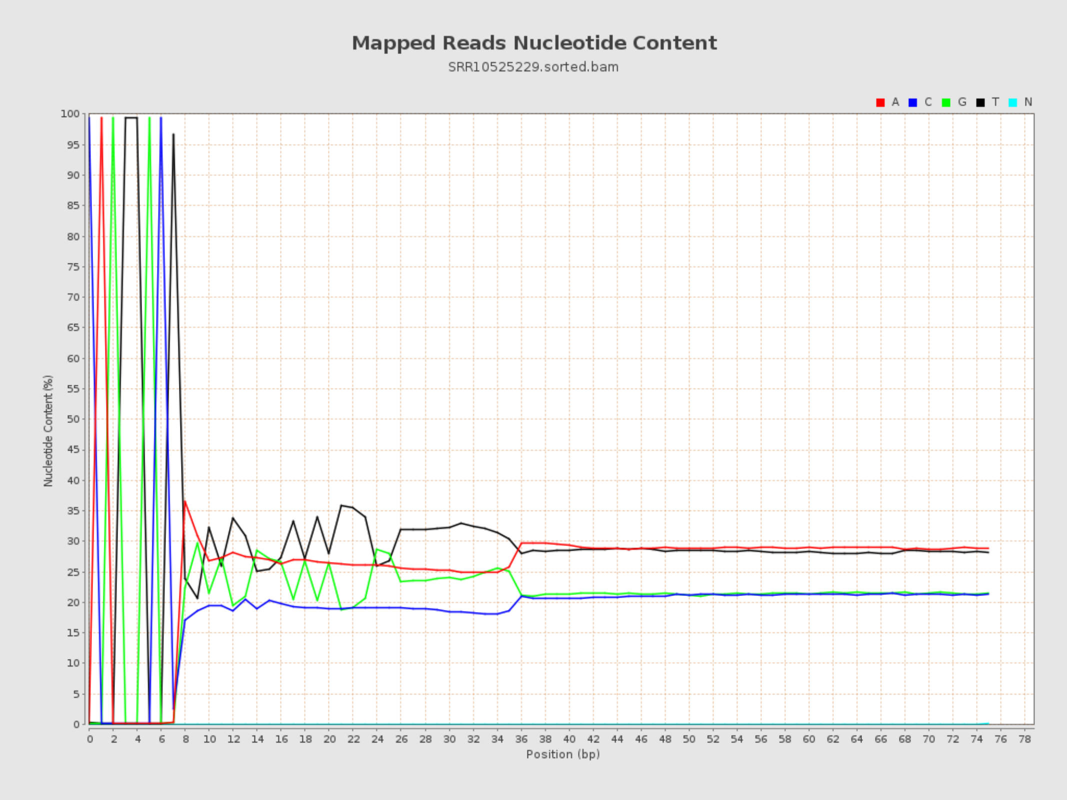
6. Results : Genome Fraction Coverage



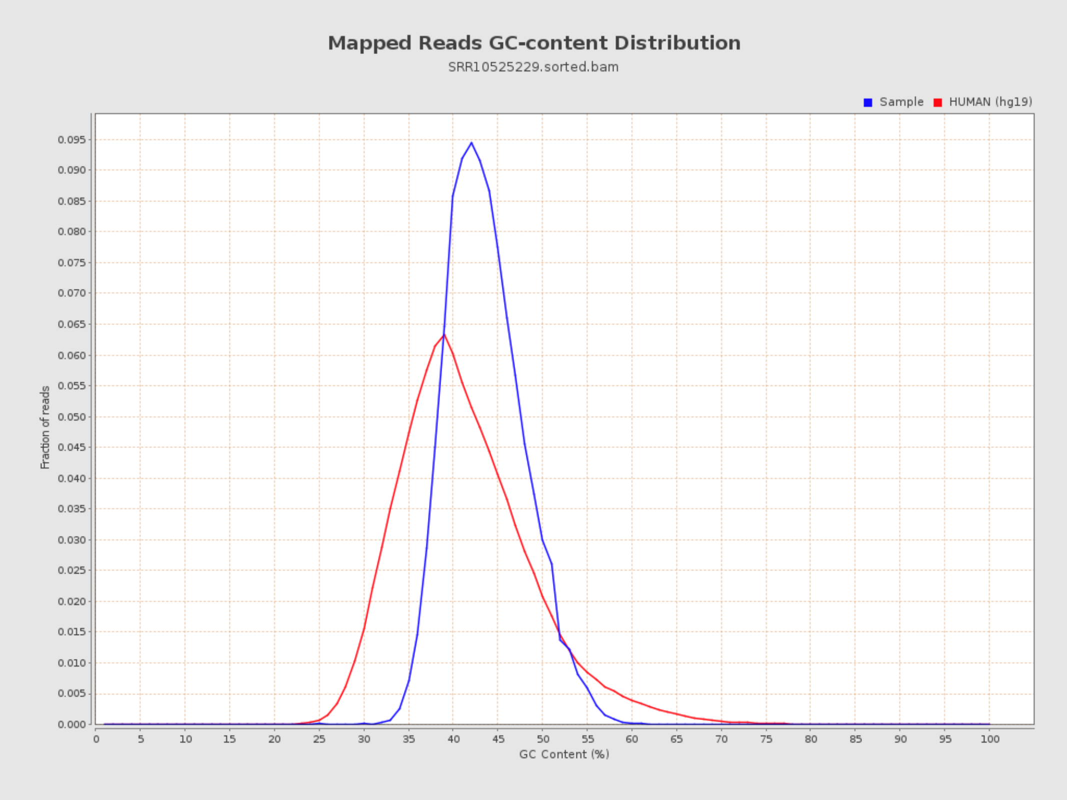
7. Results : Duplication Rate Histogram



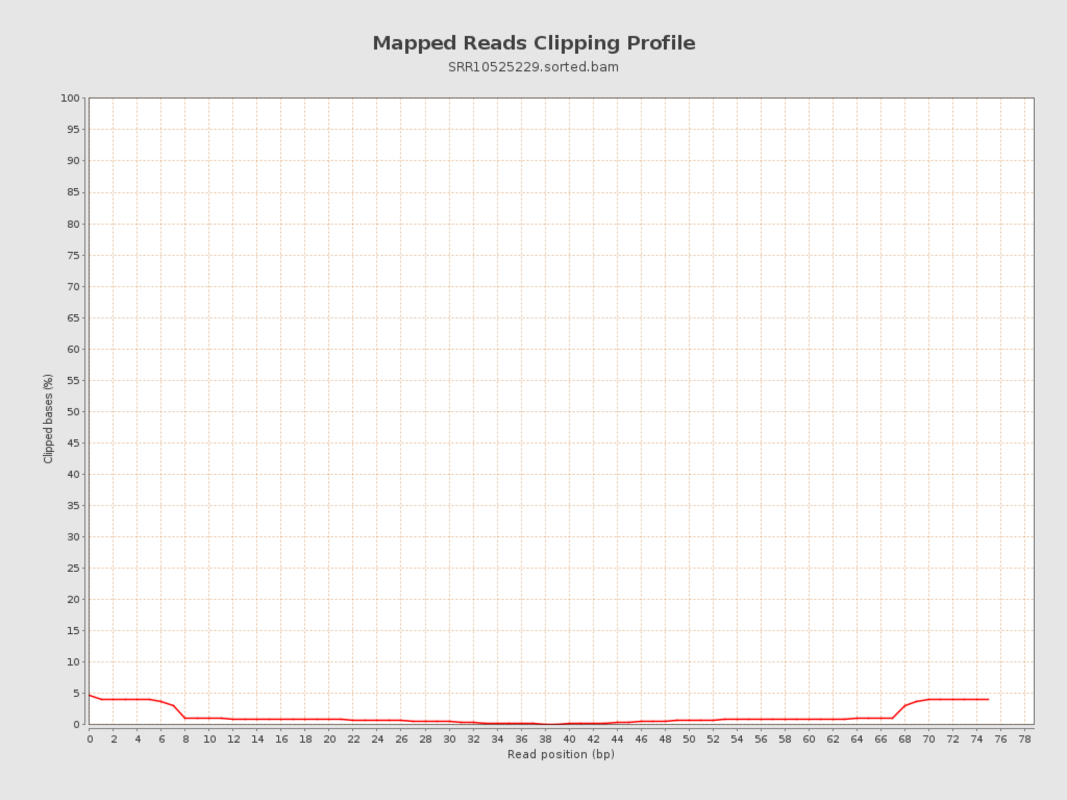
8. Results : Mapped Reads Nucleotide Content



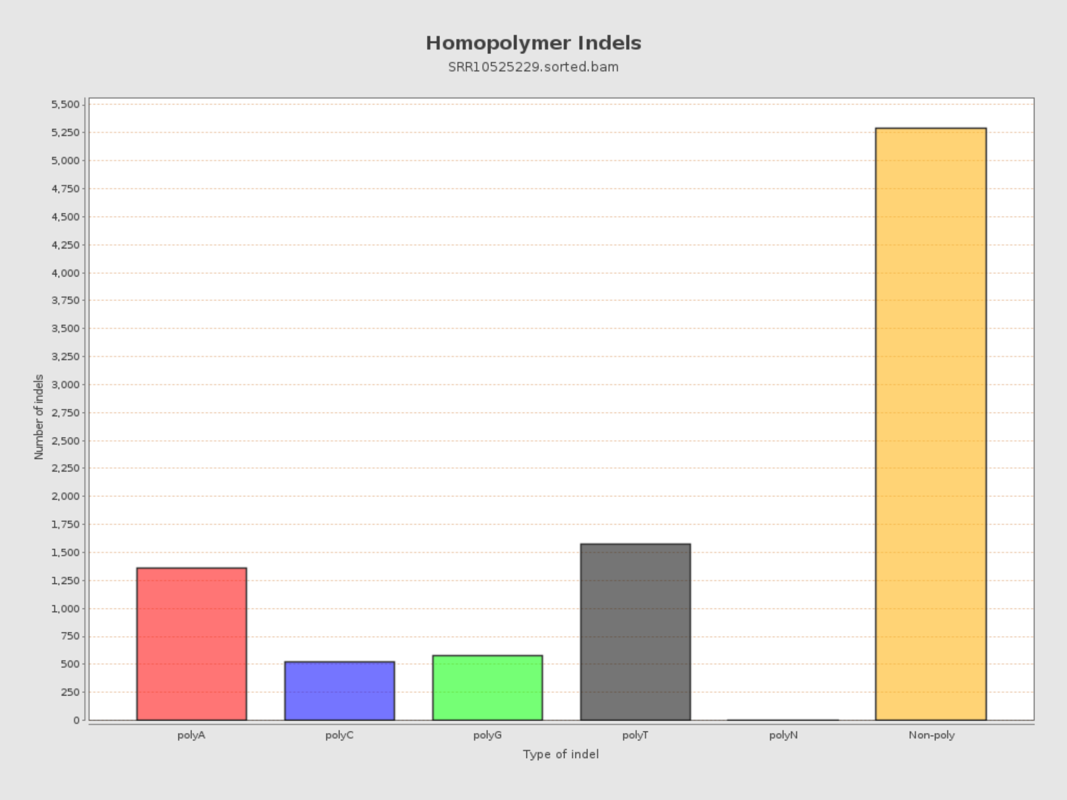
9. Results : Mapped Reads GC-content Distribution



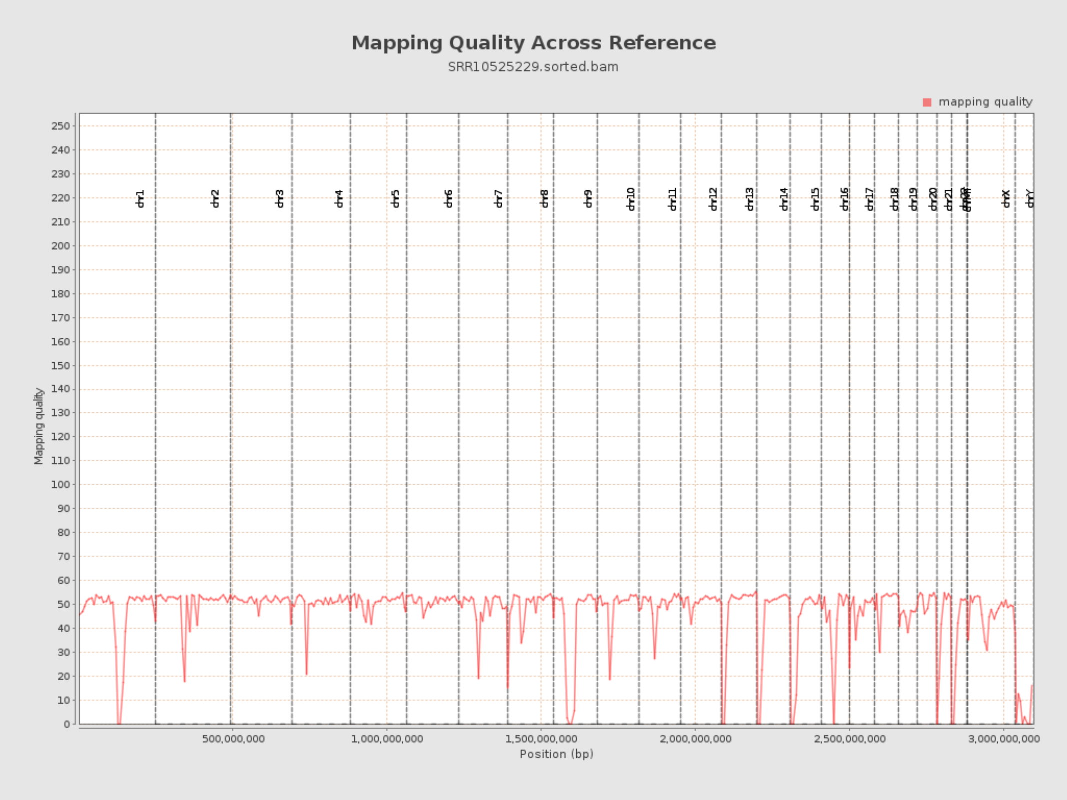
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram