Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:19:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525090.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_SRR10525090 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525090.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:19:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525090.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	464,032
Mapped reads	404,076 / 87.08%
Unmapped reads	59,956 / 12.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,465 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	11,298 / 2.43%
Duplication rate	2.42%
Clipped reads	404,227 / 87.11%

2.2. ACGT Content

Number/percentage of A's	6,115,409 / 25.74%
Number/percentage of C's	4,467,810 / 18.81%
Number/percentage of T's	7,203,643 / 30.32%
Number/percentage of G's	5,967,191 / 25.12%
Number/percentage of N's	2,826 / 0.01%
GC Percentage	43.92%

2.3. Coverage

Mean	0.0077

Standard Deviation	0.103

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

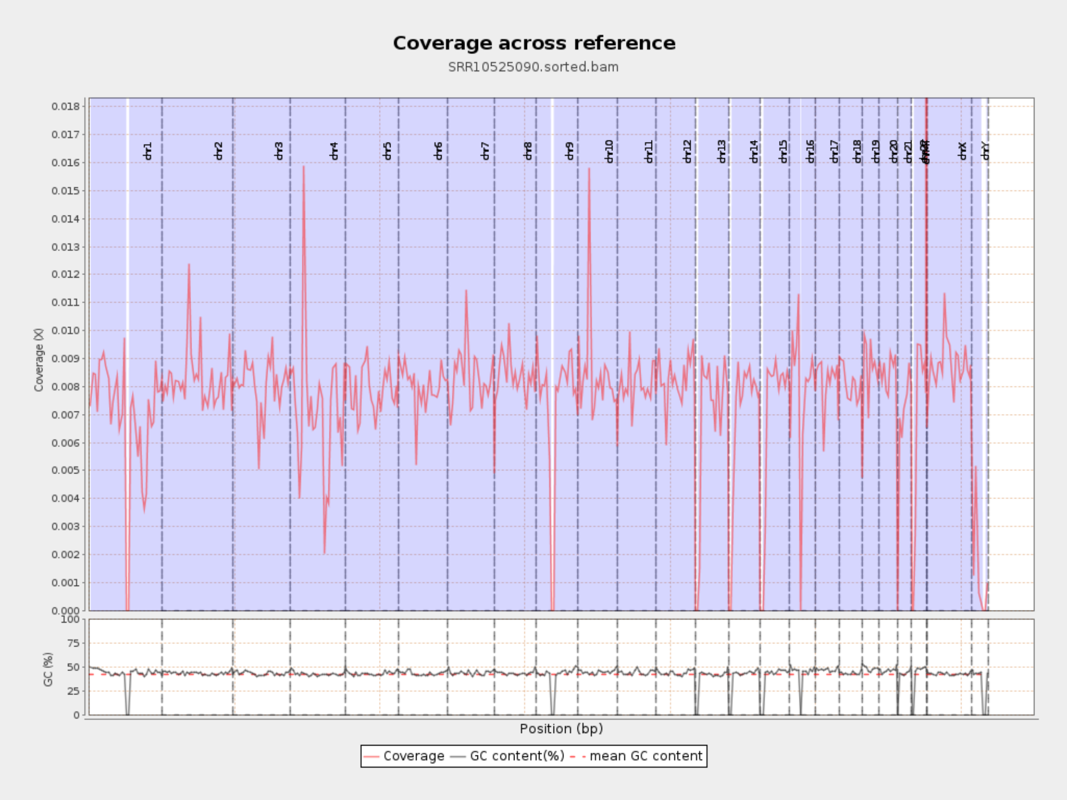
General error rate	0.47%
Mismatches	108,878
Insertions	1,801
Mapped reads with at least one insertion	0.44%
Deletions	4,276
Mapped reads with at least one deletion	1.05%
Homopolymer indels	44.15%

2.6. Chromosome stats

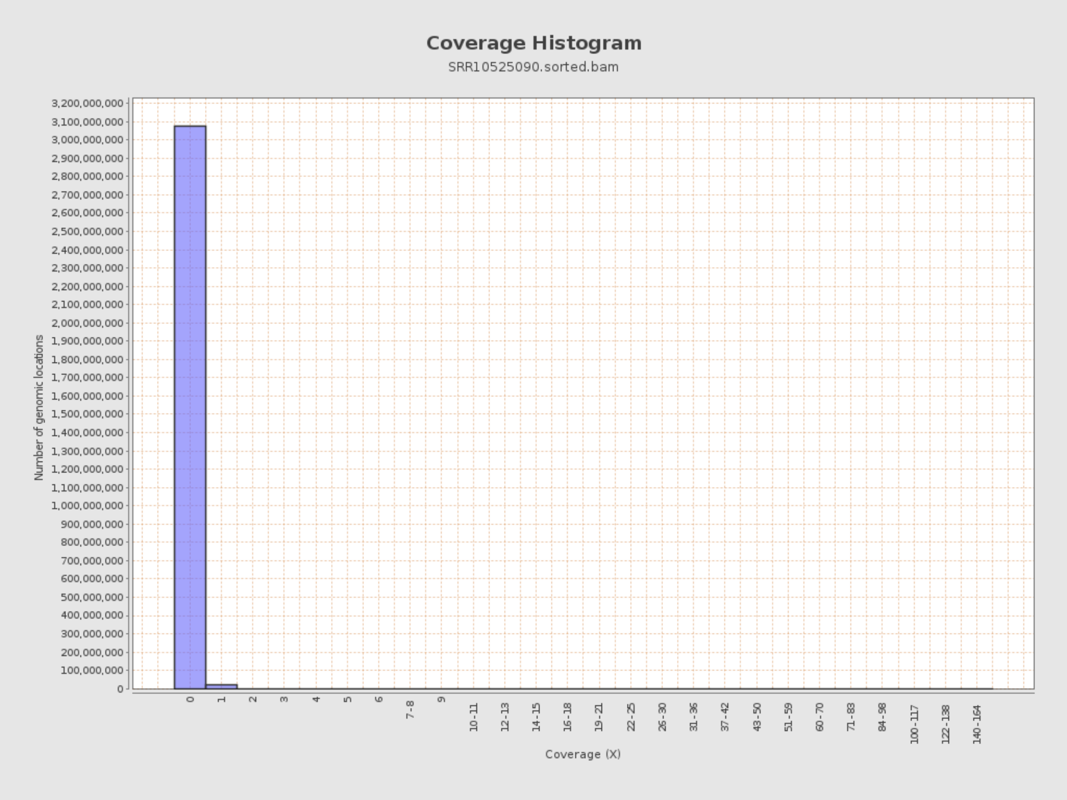
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1716018	0.0069	0.1363
chr2	243199373	2017736	0.0083	0.1149
chr3	198022430	1599147	0.0081	0.0937
chr4	191154276	1349774	0.0071	0.0952
chr5	180915260	1425731	0.0079	0.0928
chr6	171115067	1375266	0.008	0.0958
chr7	159138663	1330734	0.0084	0.1106

chr8	146364022	1228378	0.0084	0.1097
chr9	141213431	1023494	0.0072	0.0947
chr10	135534747	1149355	0.0085	0.1145
chr11	135006516	1094717	0.0081	0.099
chr12	133851895	1107349	0.0083	0.0954
chr13	115169878	770744	0.0067	0.0855
chr14	107349540	725025	0.0068	0.0873
chr15	102531392	697850	0.0068	0.0861
chr16	90354753	713859	0.0079	0.0952
chr17	81195210	659944	0.0081	0.0946
chr18	78077248	635651	0.0081	0.1232
chr19	59128983	509366	0.0086	0.1181
chr20	63025520	533672	0.0085	0.0972
chr21	48129895	324792	0.0067	0.0913
chr22	51304566	319323	0.0062	0.0826
chrMT	16571	14745	0.8898	1.047
chrX	155270560	1358538	0.0087	0.0999
chrY	59373566	82593	0.0014	0.0531

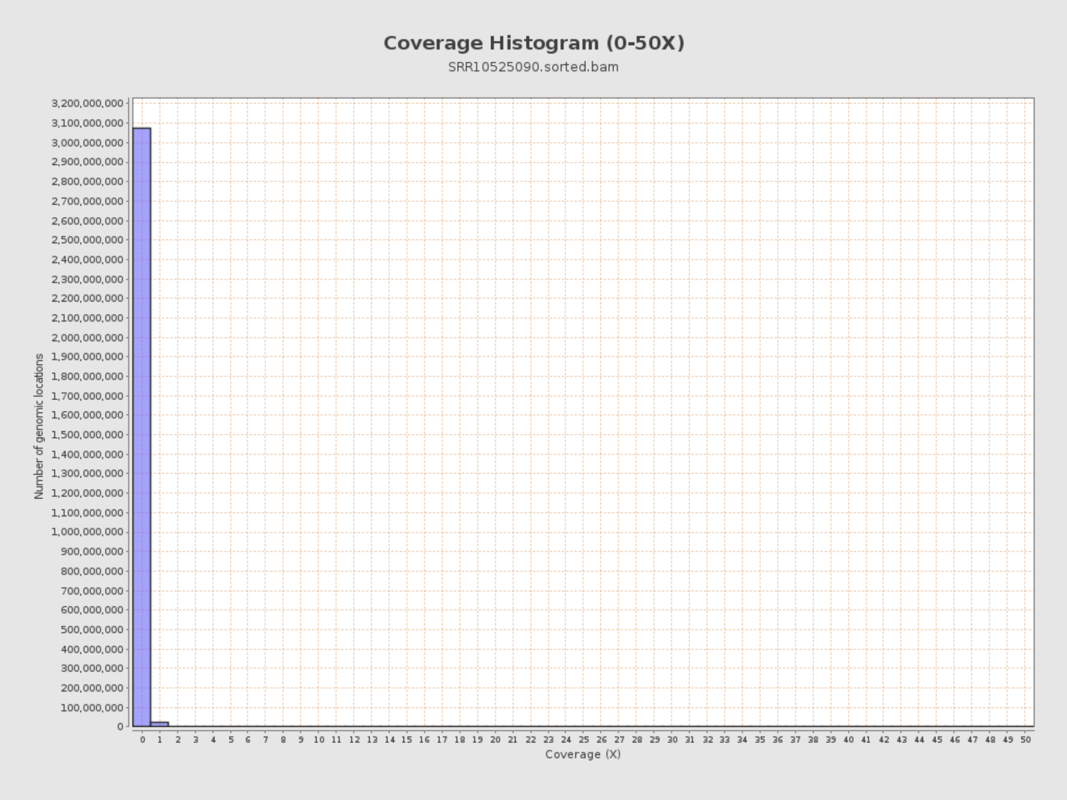
3. Results : Coverage across reference



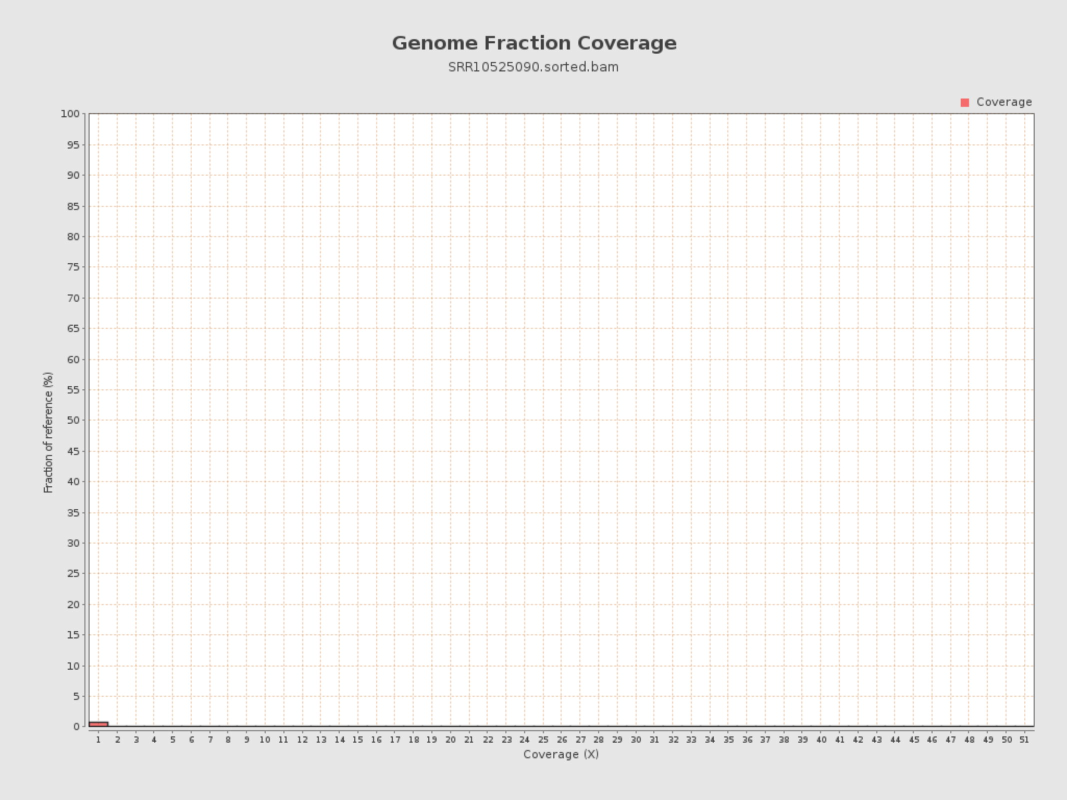
4. Results : Coverage Histogram



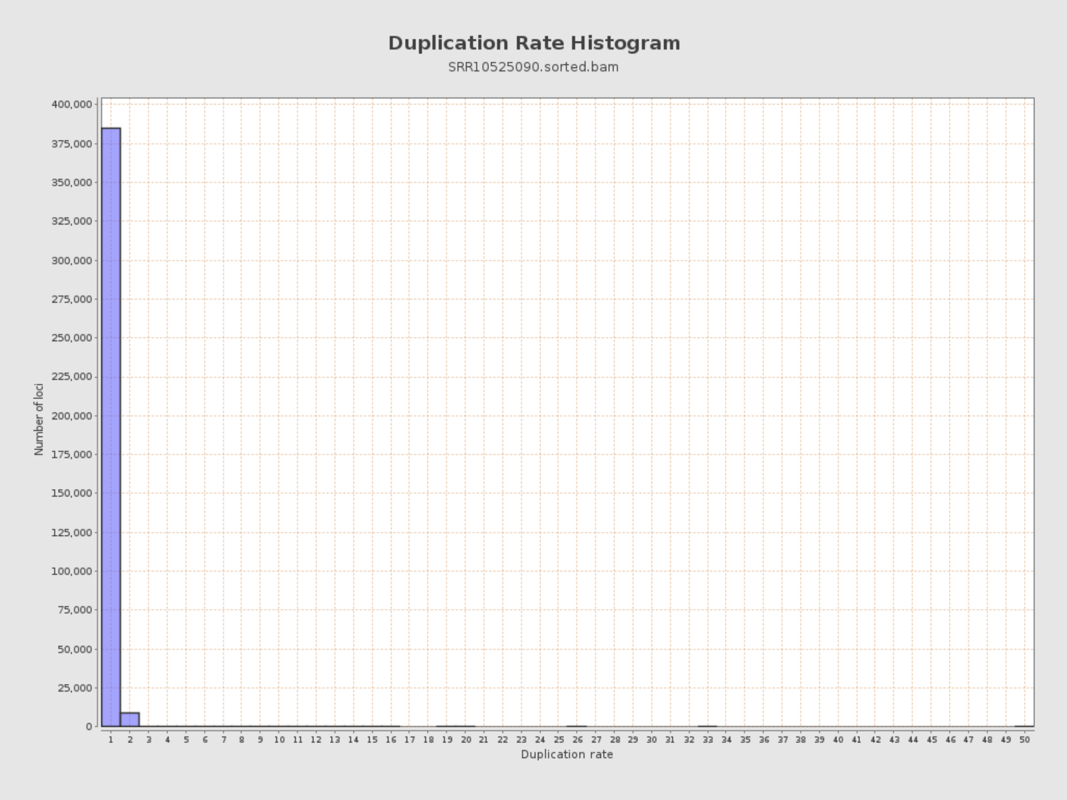
5. Results : Coverage Histogram (0-50X)



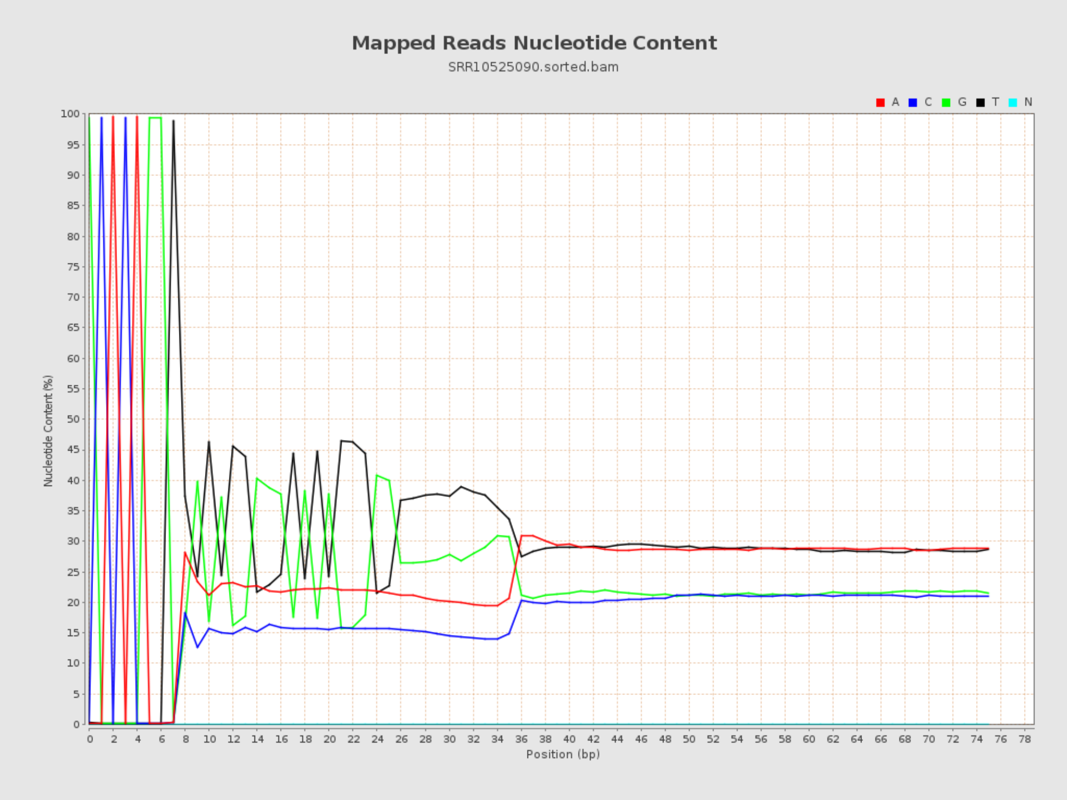
6. Results : Genome Fraction Coverage



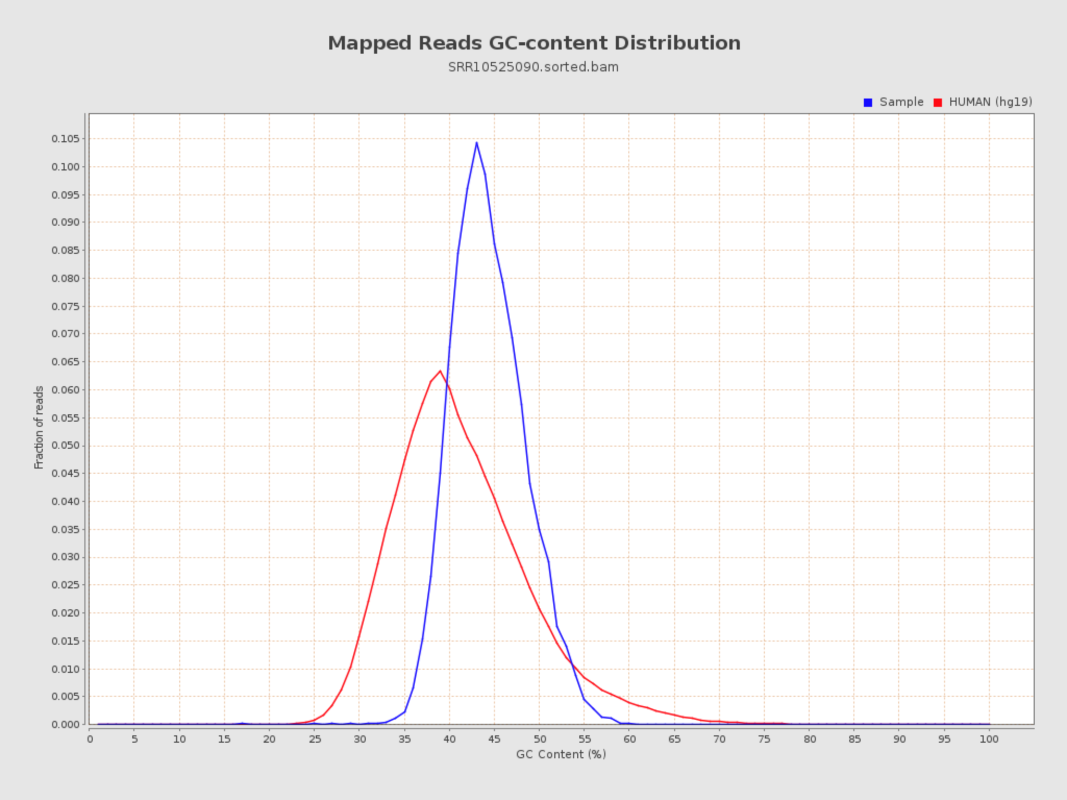
7. Results : Duplication Rate Histogram



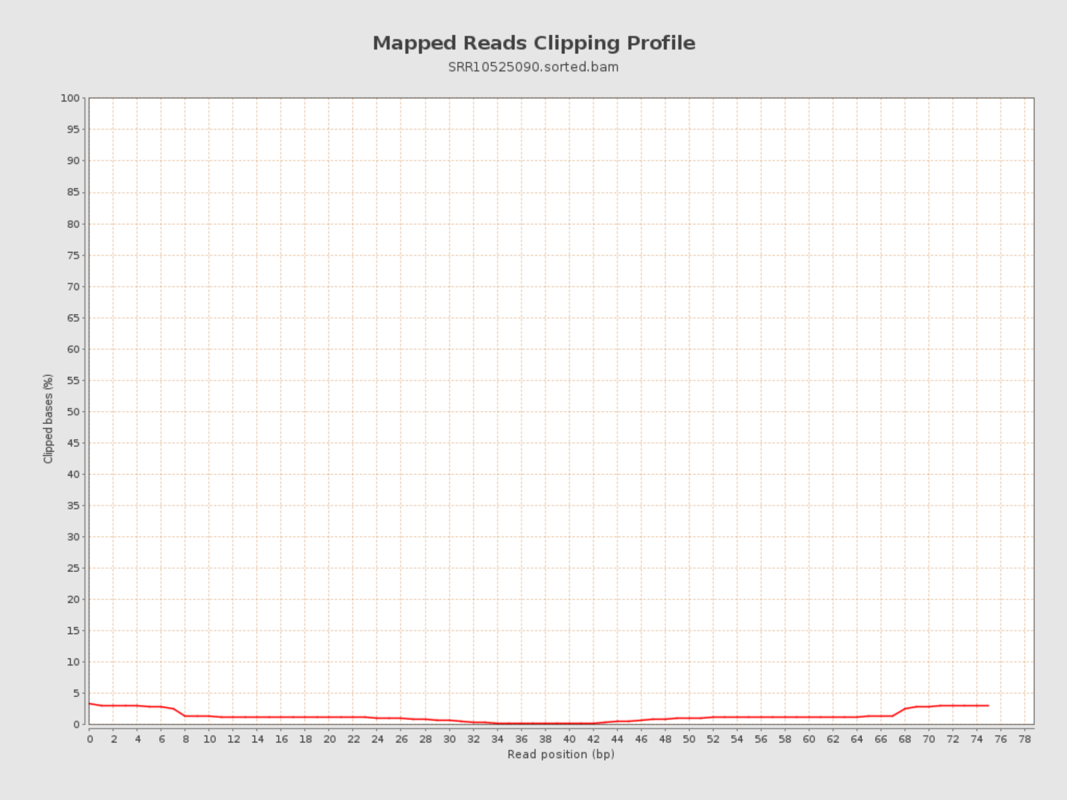
8. Results : Mapped Reads Nucleotide Content



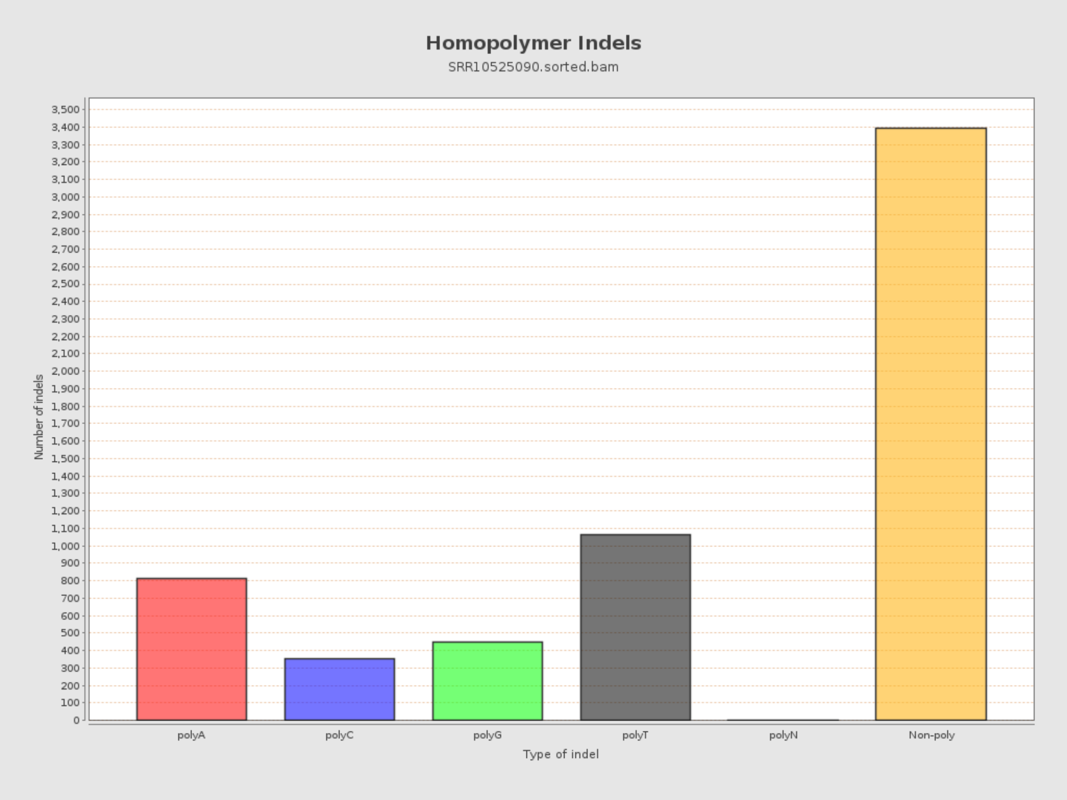
9. Results : Mapped Reads GC-content Distribution



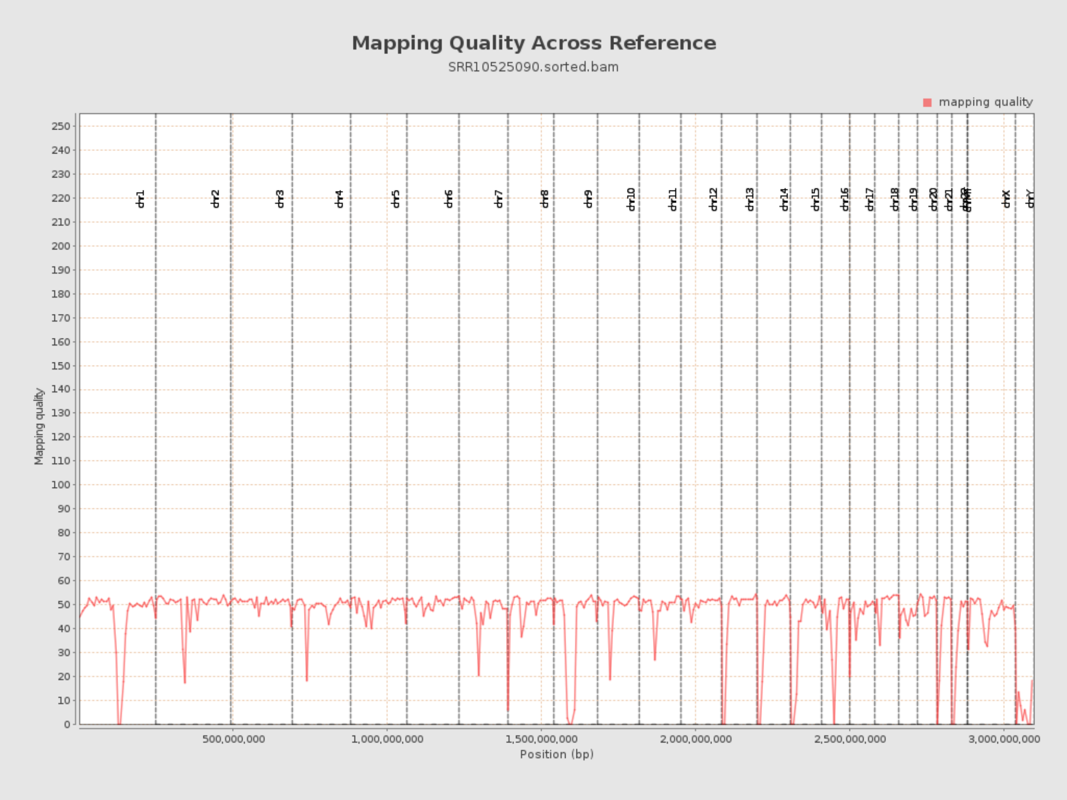
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram