Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:52:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525082.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_SRR10525082 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525082.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:52:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525082.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	524,755
Mapped reads	482,555 / 91.96%
Unmapped reads	42,200 / 8.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,631 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	13,867 / 2.64%
Duplication rate	2.44%
Clipped reads	483,152 / 92.07%

2.2. ACGT Content

Number/percentage of A's	6,979,380 / 24.83%
Number/percentage of C's	5,000,469 / 17.79%
Number/percentage of T's	8,805,364 / 31.33%
Number/percentage of G's	7,321,387 / 26.05%
Number/percentage of N's	2,724 / 0.01%
GC Percentage	43.84%

2.3. Coverage

Mean	0.0091

Standard Deviation	0.1152

2.4. Mapping Quality

Mean Mapping Quality	45.83

2.5. Mismatches and indels

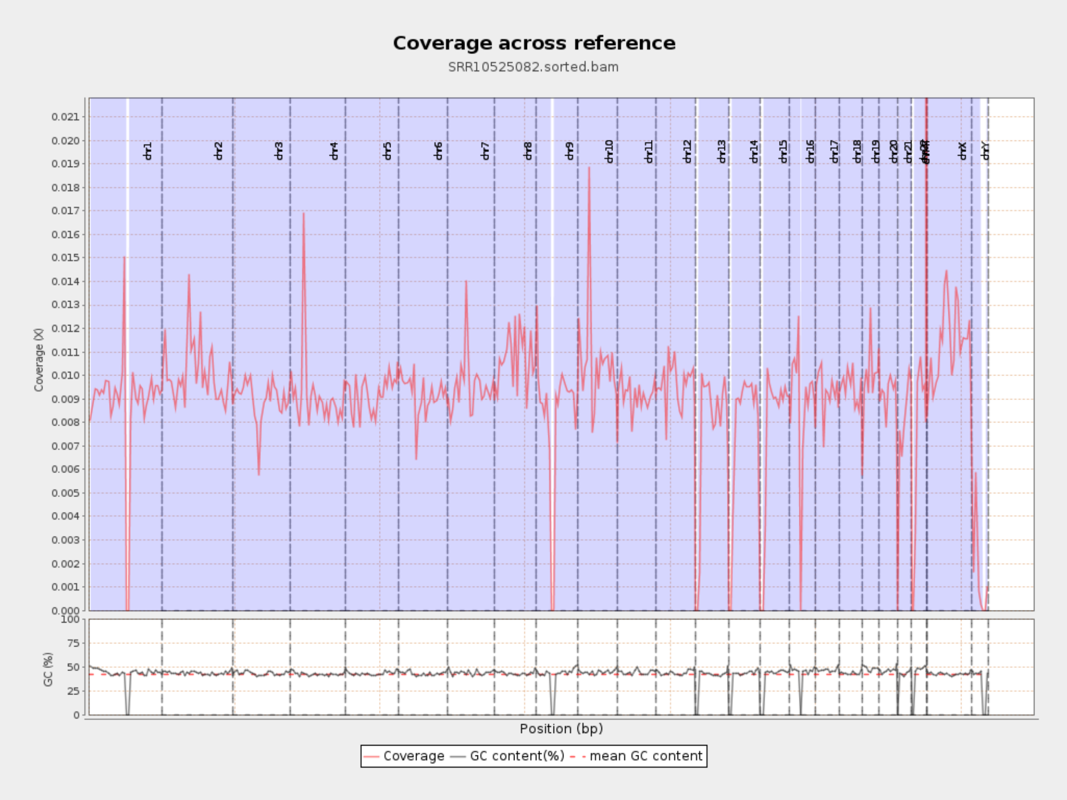
General error rate	0.48%
Mismatches	131,424
Insertions	2,024
Mapped reads with at least one insertion	0.42%
Deletions	5,338
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.66%

2.6. Chromosome stats

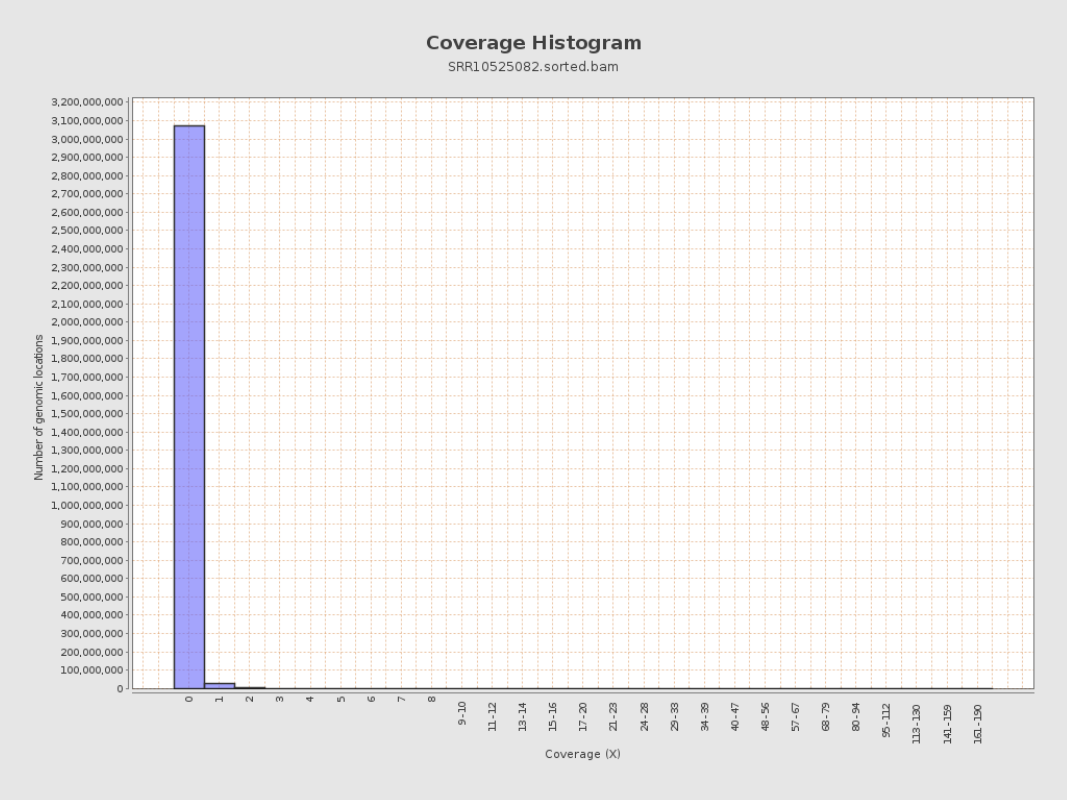
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2190373	0.0088	0.1685
chr2	243199373	2460812	0.0101	0.1312
chr3	198022430	1777430	0.009	0.0989
chr4	191154276	1748058	0.0091	0.1053
chr5	180915260	1663281	0.0092	0.1002
chr6	171115067	1576676	0.0092	0.1028
chr7	159138663	1525025	0.0096	0.1262

chr8	146364022	1566297	0.0107	0.1222
chr9	141213431	1136904	0.0081	0.1007
chr10	135534747	1443973	0.0107	0.1301
chr11	135006516	1235425	0.0092	0.1054
chr12	133851895	1293464	0.0097	0.1032
chr13	115169878	863692	0.0075	0.0906
chr14	107349540	820670	0.0076	0.0921
chr15	102531392	774496	0.0076	0.0915
chr16	90354753	795164	0.0088	0.1011
chr17	81195210	755378	0.0093	0.1024
chr18	78077248	741442	0.0095	0.1334
chr19	59128983	592415	0.01	0.138
chr20	63025520	580419	0.0092	0.101
chr21	48129895	368205	0.0077	0.0977
chr22	51304566	347046	0.0068	0.0865
chrMT	16571	3869	0.2335	0.5335
chrX	155270560	1763421	0.0114	0.1148
chrY	59373566	94037	0.0016	0.0643

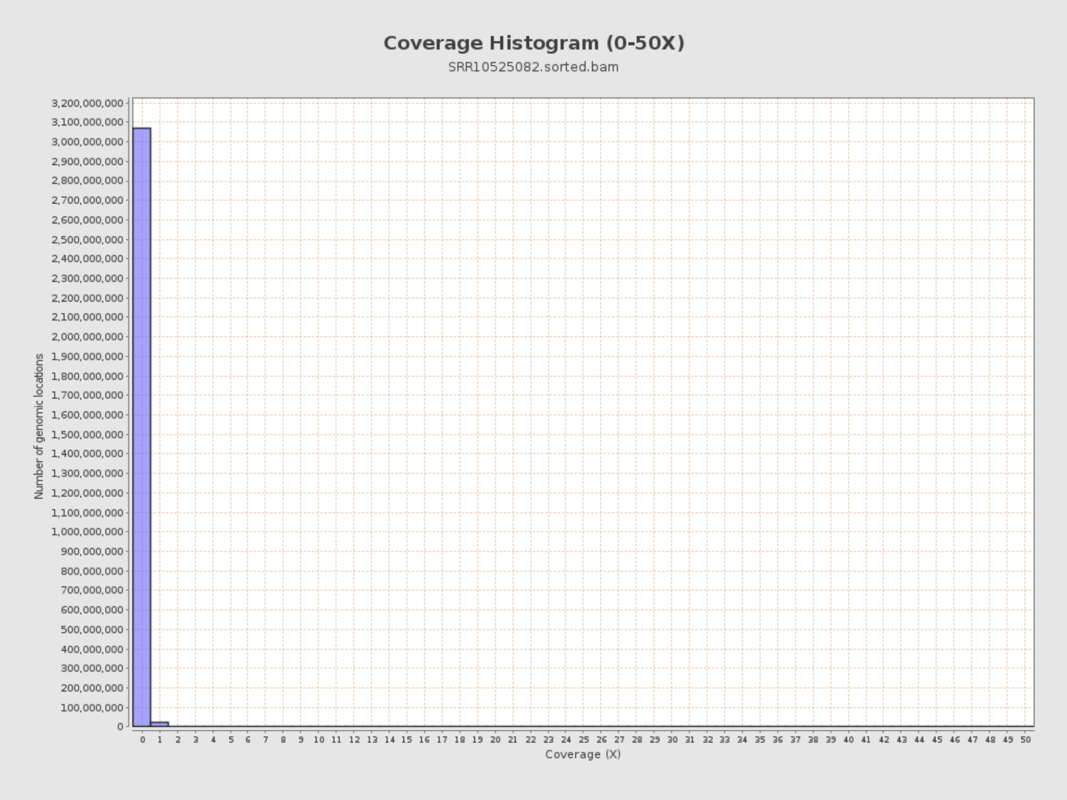
3. Results : Coverage across reference



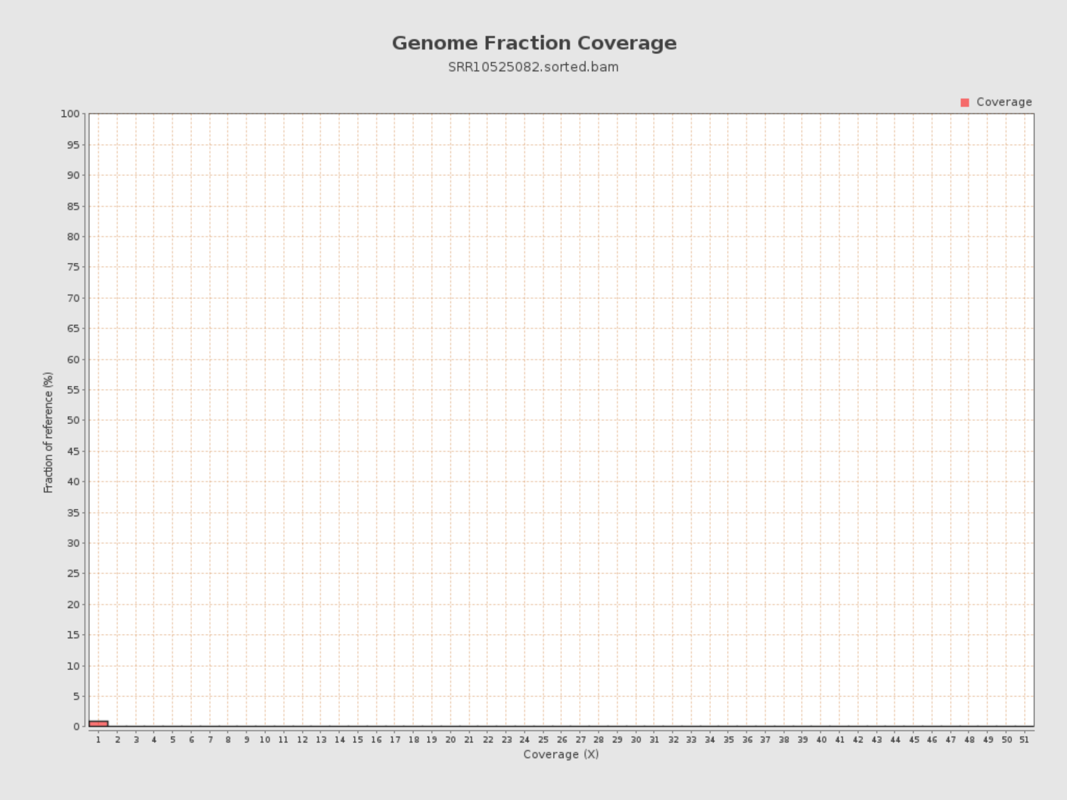
4. Results : Coverage Histogram



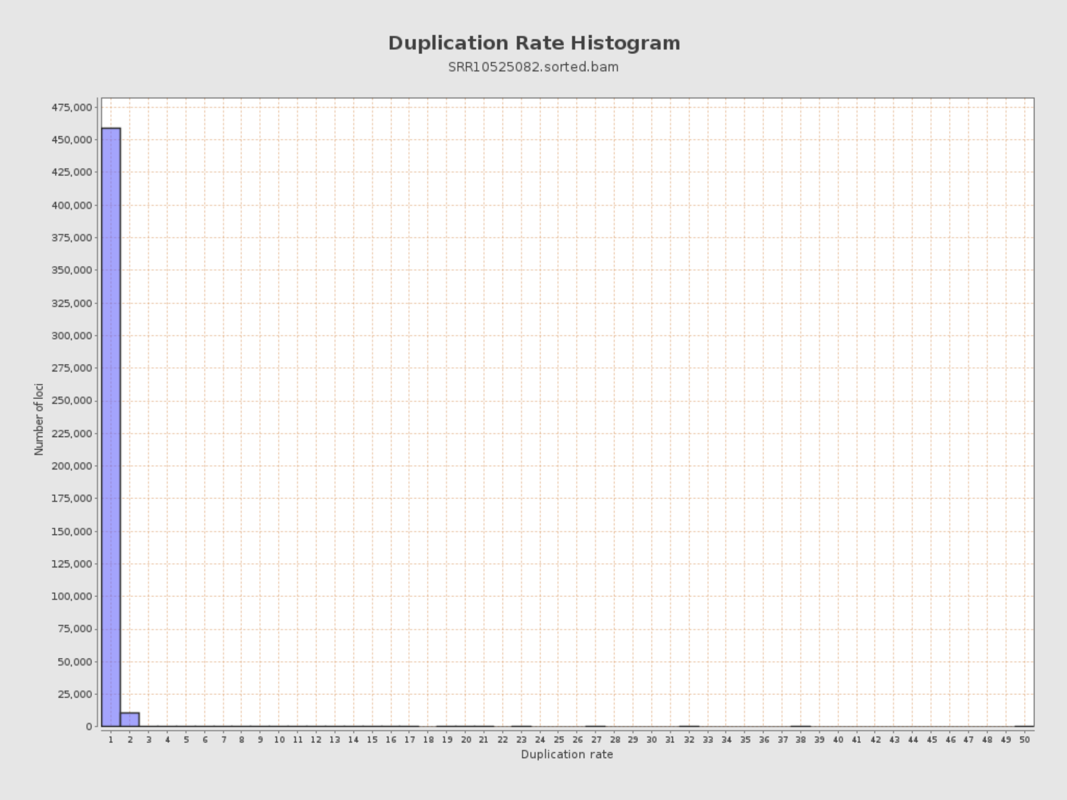
5. Results : Coverage Histogram (0-50X)



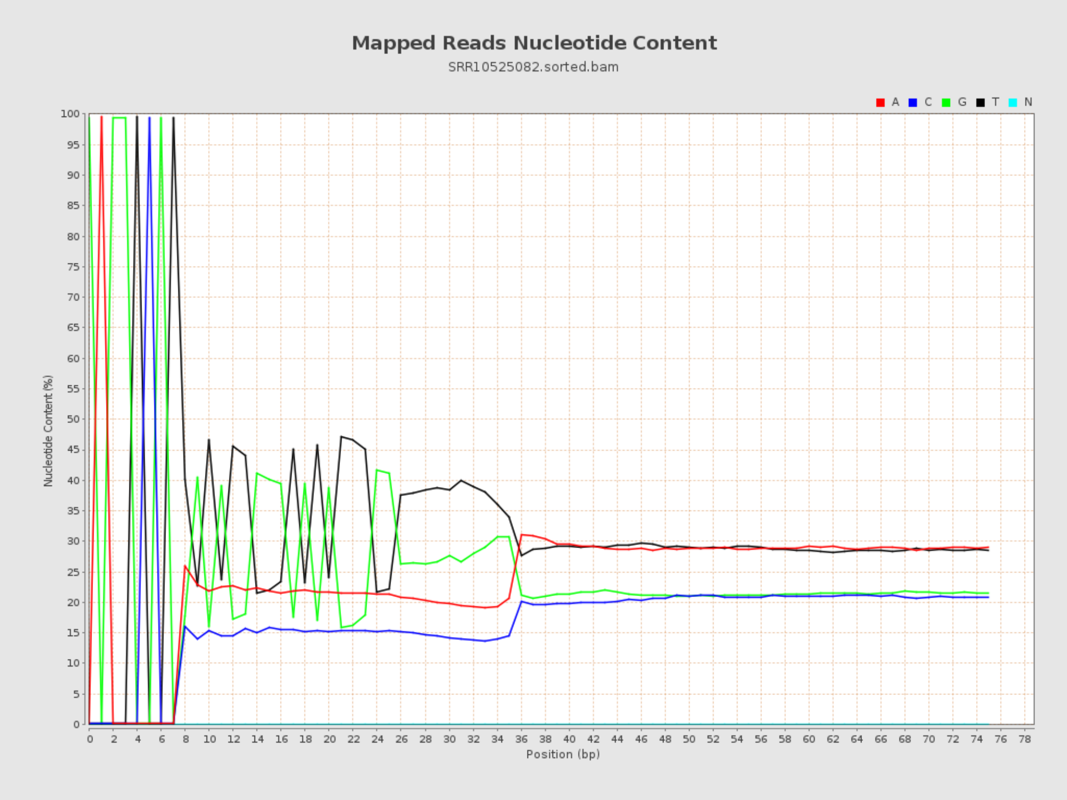
6. Results : Genome Fraction Coverage



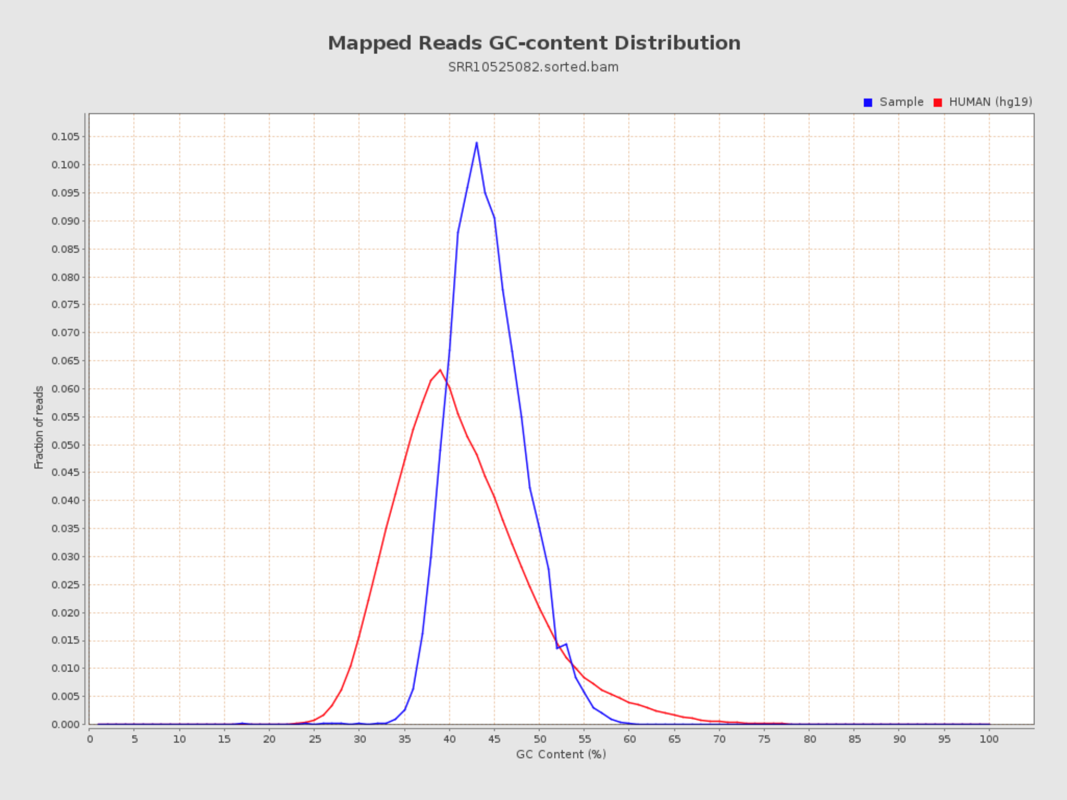
7. Results : Duplication Rate Histogram



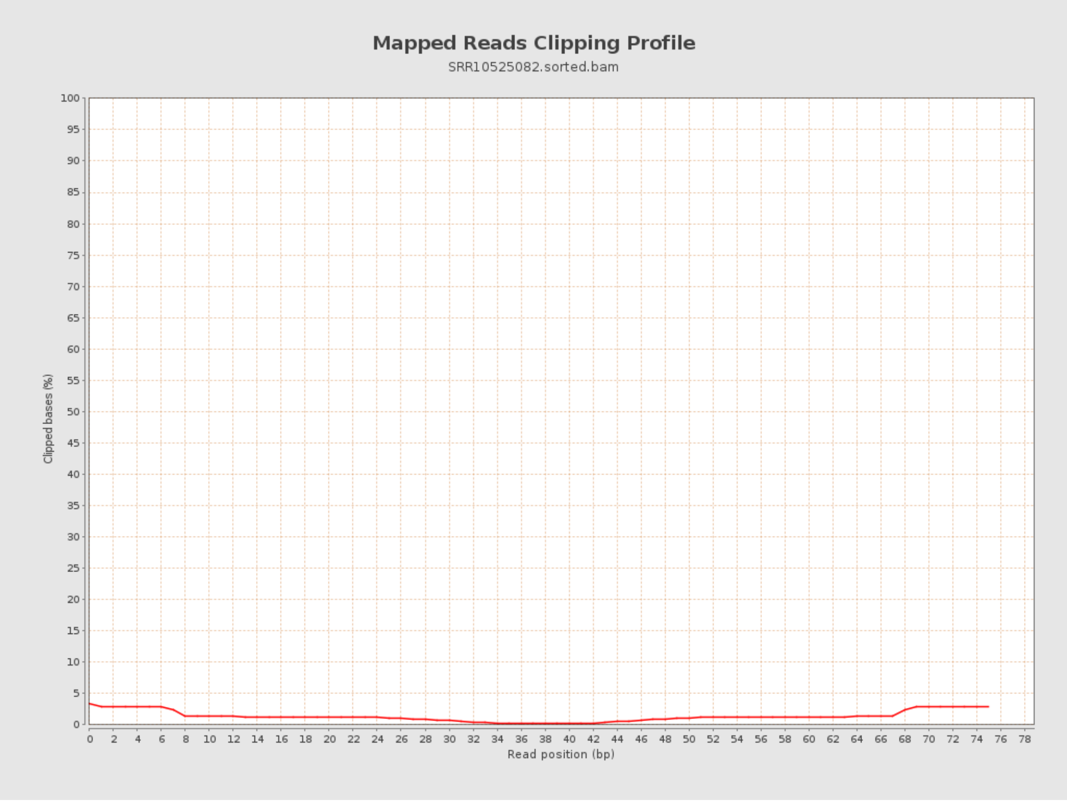
8. Results : Mapped Reads Nucleotide Content



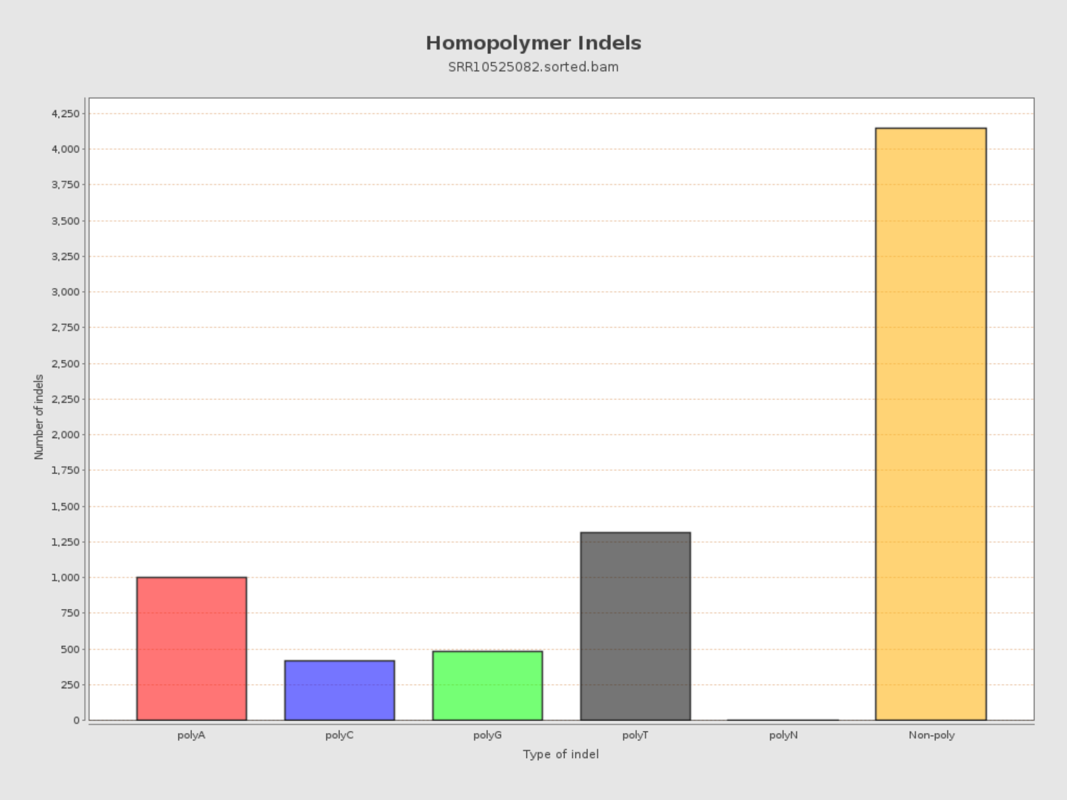
9. Results : Mapped Reads GC-content Distribution



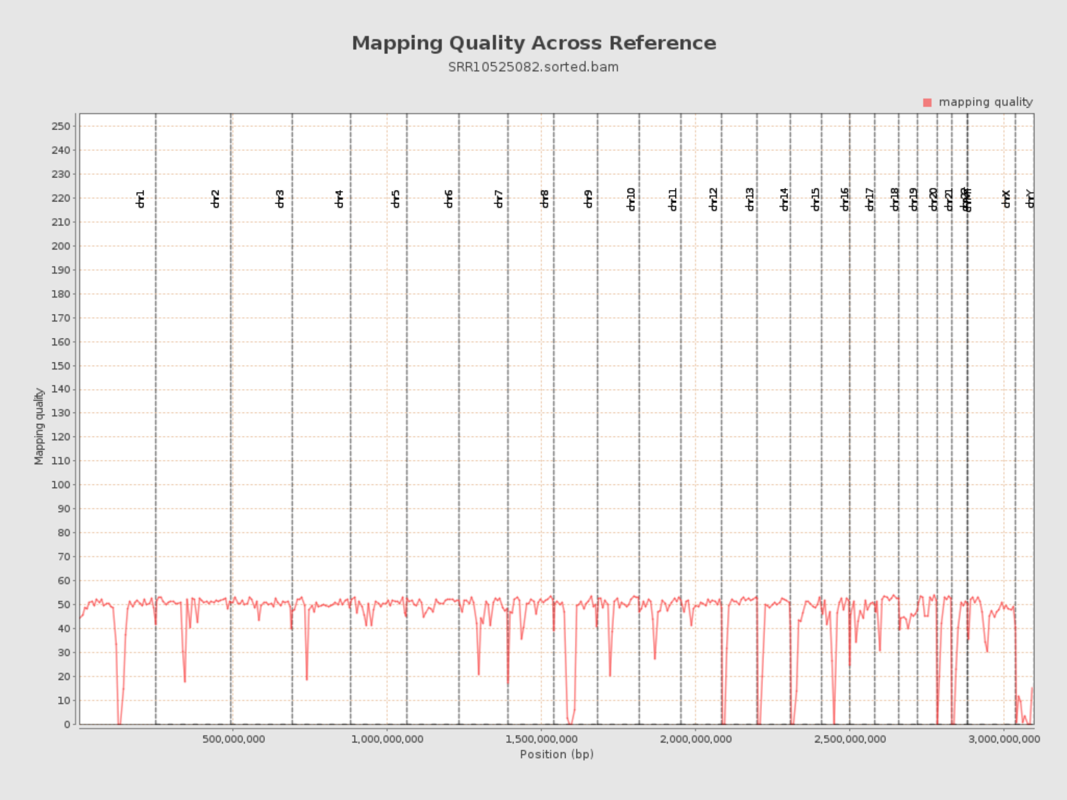
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram