Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:20:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525173.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_SRR10525173 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525173.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:20:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525173.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,676,740
Mapped reads	1,575,142 / 93.94%
Unmapped reads	101,598 / 6.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,091 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	41,401 / 2.47%
Duplication rate	1.79%
Clipped reads	1,579,178 / 94.18%

2.2. ACGT Content

Number/percentage of A's	24,802,933 / 25.93%
Number/percentage of C's	19,427,635 / 20.31%
Number/percentage of T's	28,824,804 / 30.14%
Number/percentage of G's	22,588,927 / 23.62%
Number/percentage of N's	2,231 / 0%
GC Percentage	43.93%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.2843

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

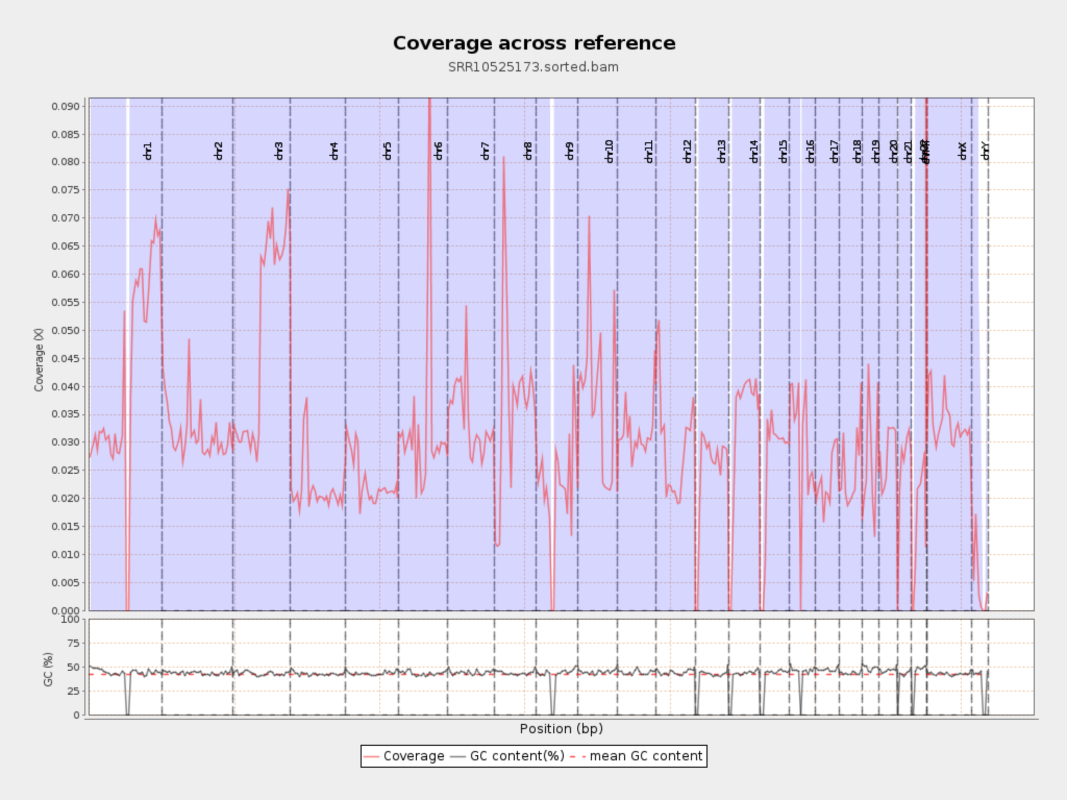
General error rate	0.5%
Mismatches	463,584
Insertions	5,413
Mapped reads with at least one insertion	0.34%
Deletions	19,005
Mapped reads with at least one deletion	1.2%
Homopolymer indels	44.37%

2.6. Chromosome stats

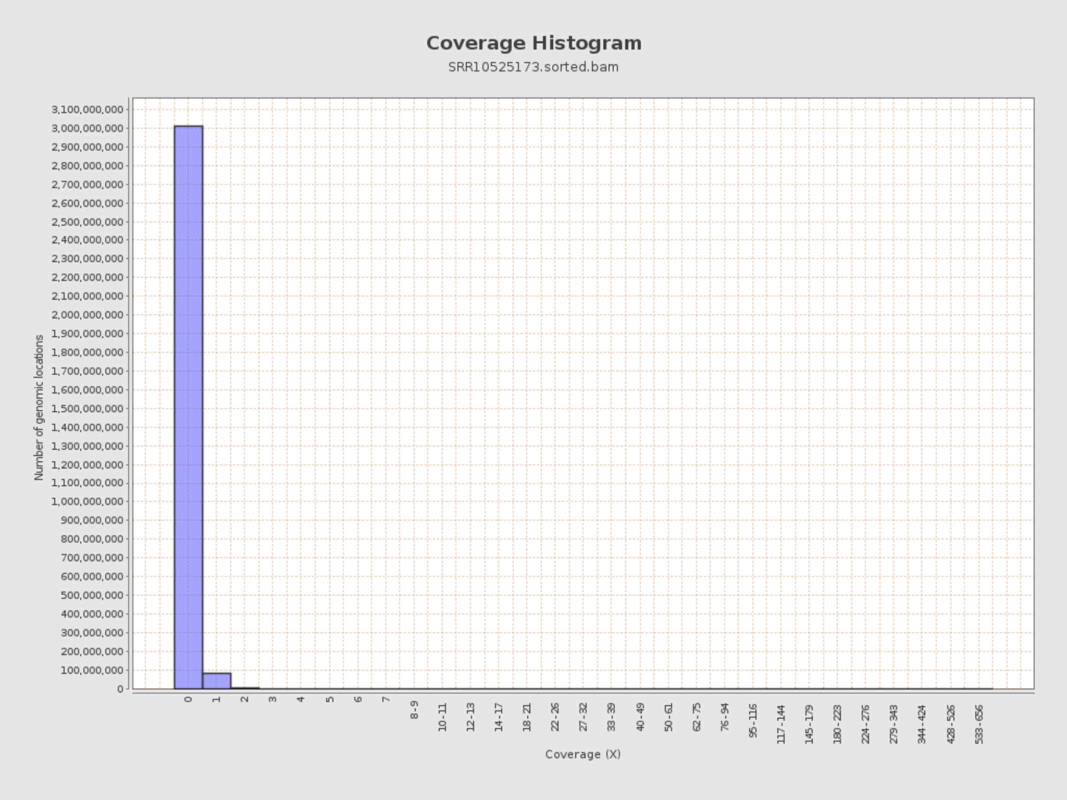
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10379937	0.0416	0.5348
chr2	243199373	7724639	0.0318	0.3379
chr3	198022430	9696563	0.049	0.2409
chr4	191154276	4137427	0.0216	0.1689
chr5	180915260	4207936	0.0233	0.1627
chr6	171115067	5761017	0.0337	0.2164
chr7	159138663	5461350	0.0343	0.4026

chr8	146364022	5356429	0.0366	0.2587
chr9	141213431	3104888	0.022	0.2072
chr10	135534747	5187667	0.0383	0.3291
chr11	135006516	4278691	0.0317	0.2283
chr12	133851895	3928963	0.0294	0.1854
chr13	115169878	2841687	0.0247	0.1688
chr14	107349540	3485827	0.0325	0.1987
chr15	102531392	2592728	0.0253	0.1708
chr16	90354753	2648730	0.0293	0.2006
chr17	81195210	1885700	0.0232	0.1707
chr18	78077248	1939651	0.0248	0.411
chr19	59128983	1601385	0.0271	0.3842
chr20	63025520	1752916	0.0278	0.1814
chr21	48129895	1224781	0.0254	0.184
chr22	51304566	842258	0.0164	0.1374
chrMT	16571	137392	8.2911	4.9329
chrX	155270560	5205082	0.0335	0.2106
chrY	59373566	293799	0.0049	0.1668

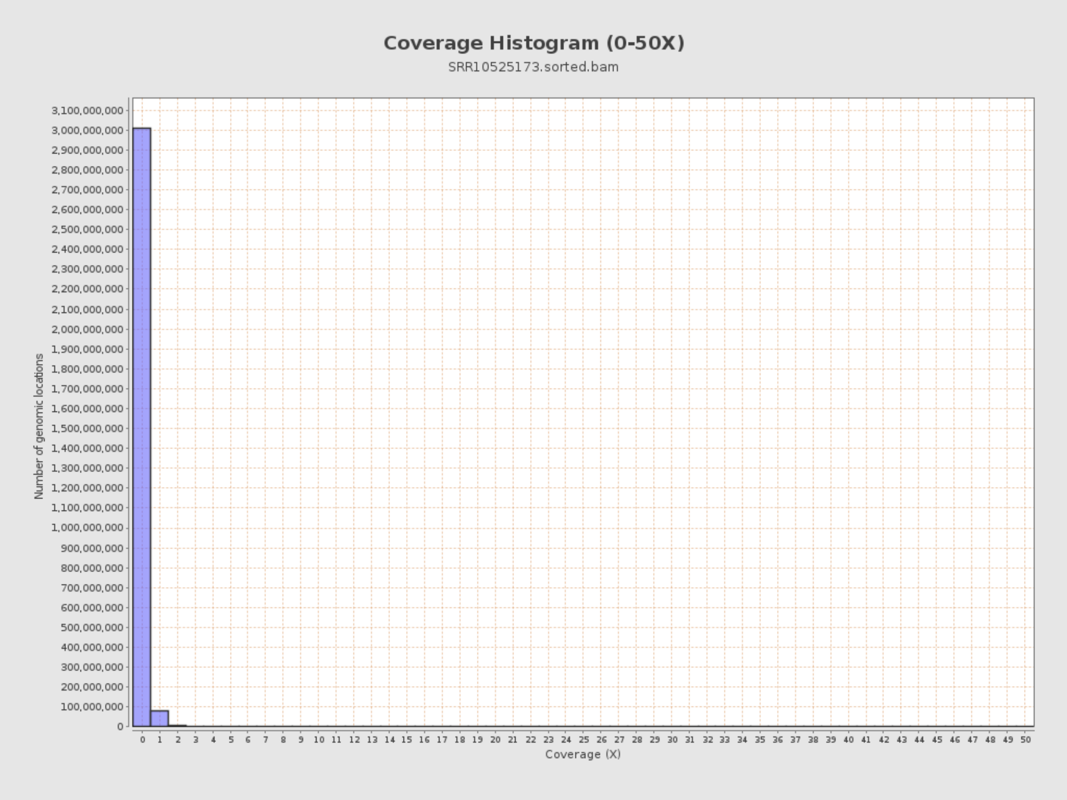
3. Results : Coverage across reference



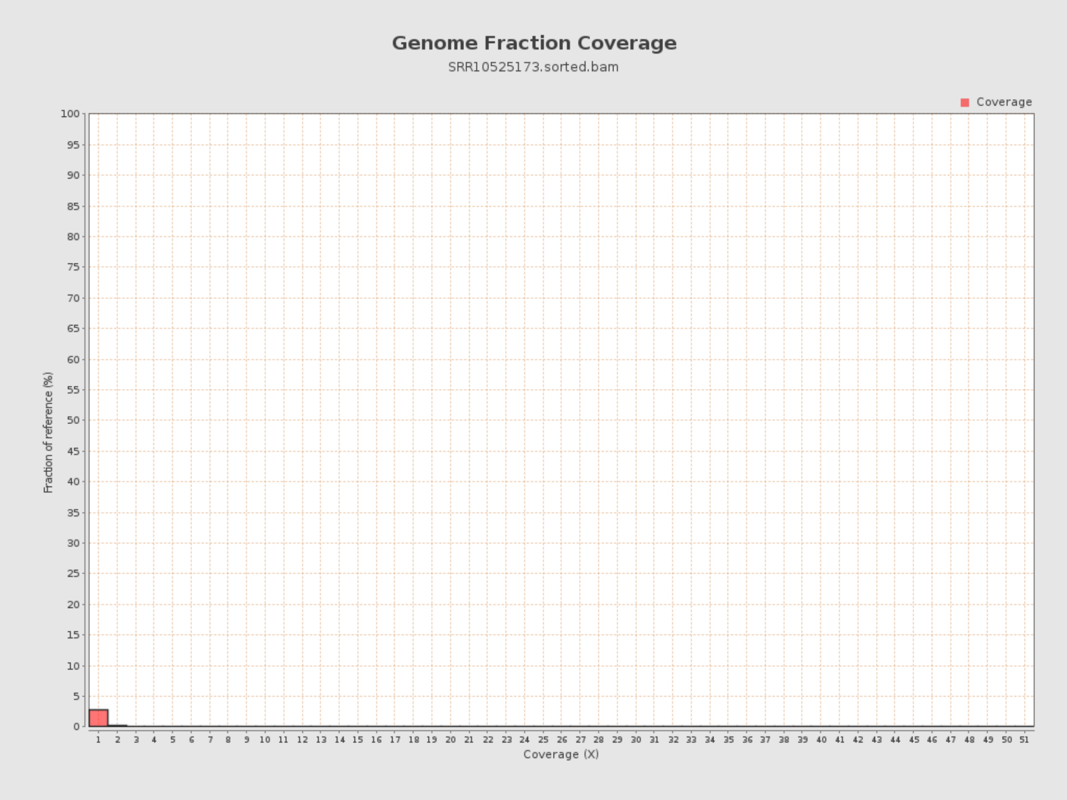
4. Results : Coverage Histogram



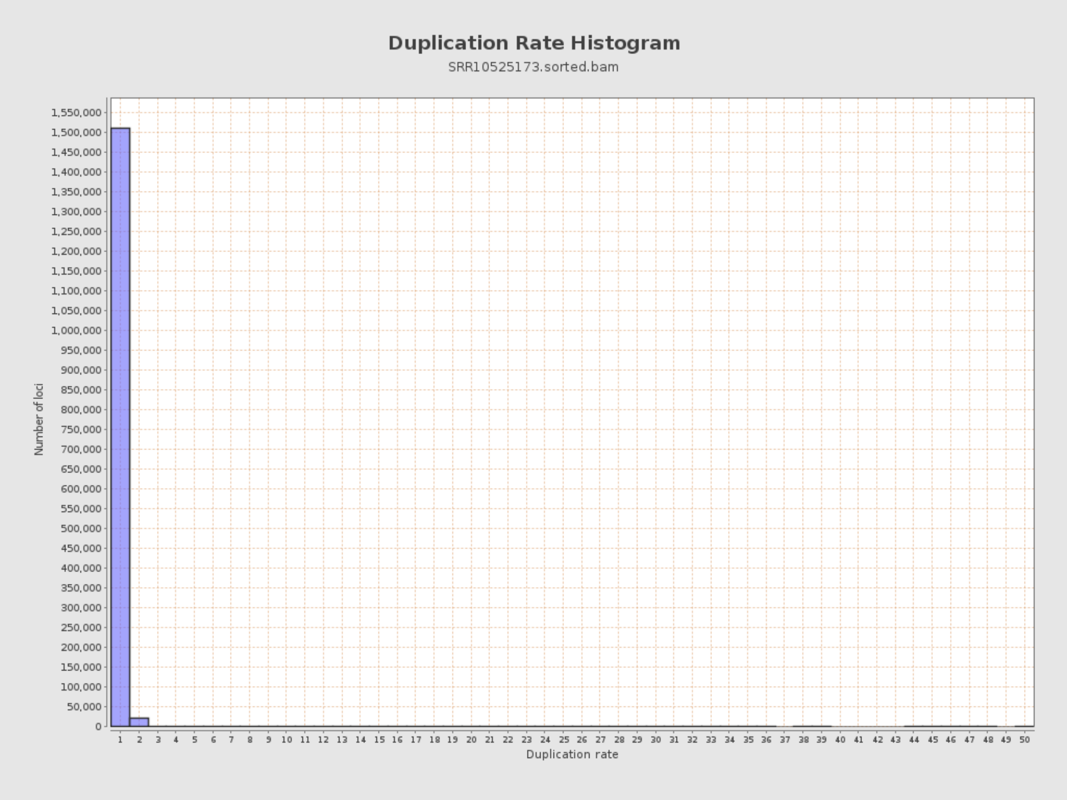
5. Results : Coverage Histogram (0-50X)



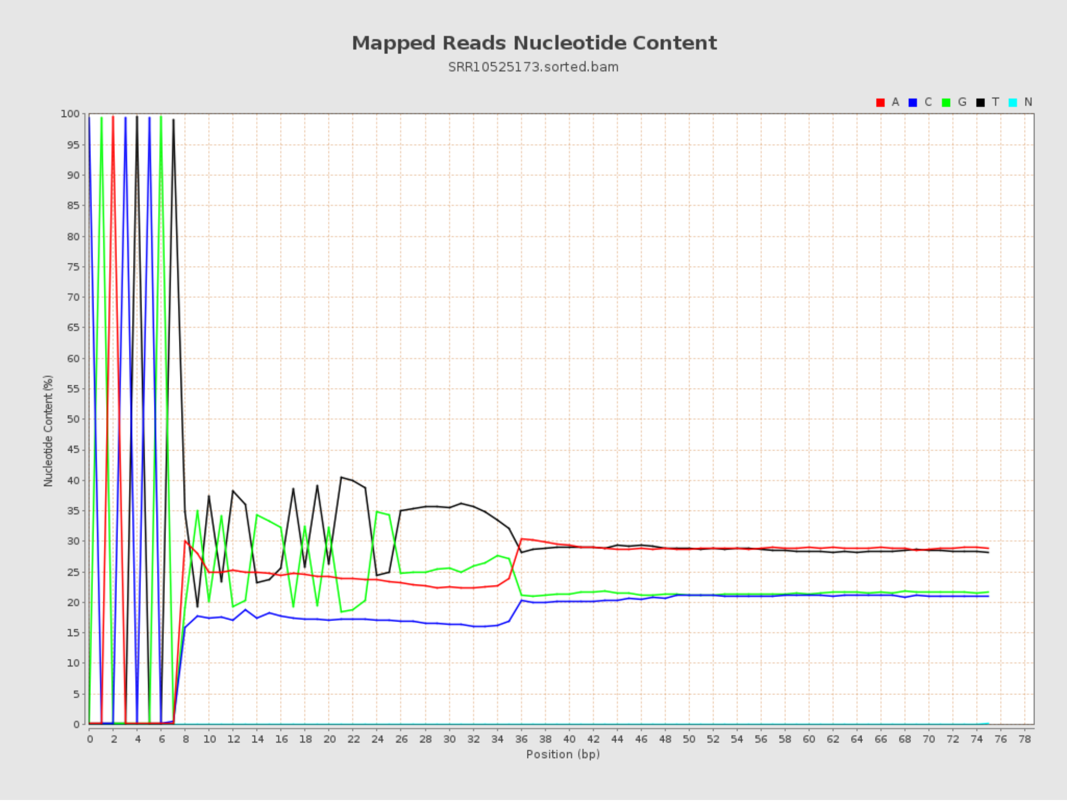
6. Results : Genome Fraction Coverage



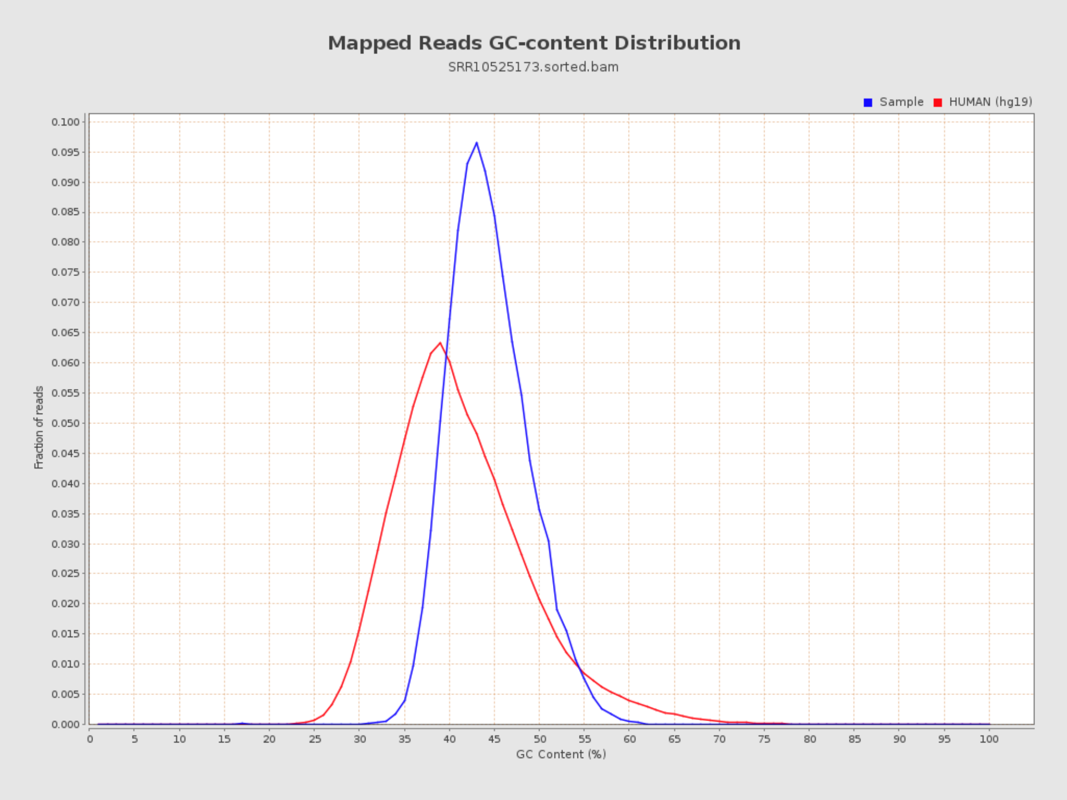
7. Results : Duplication Rate Histogram



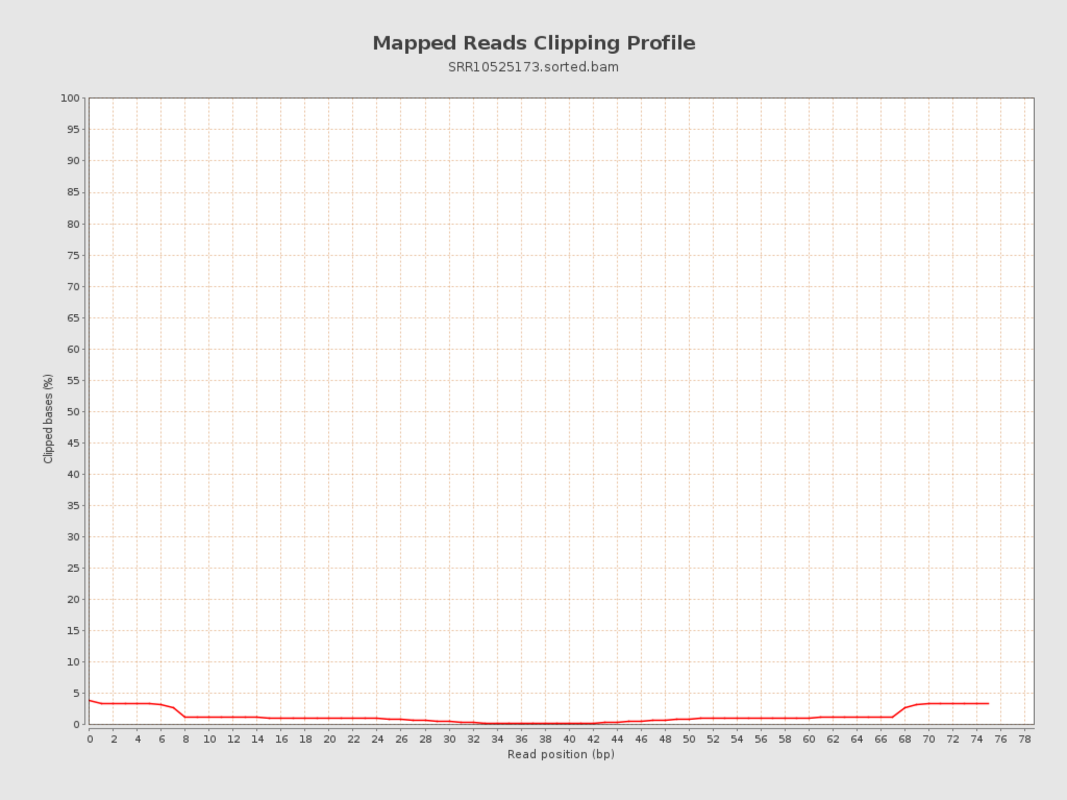
8. Results : Mapped Reads Nucleotide Content



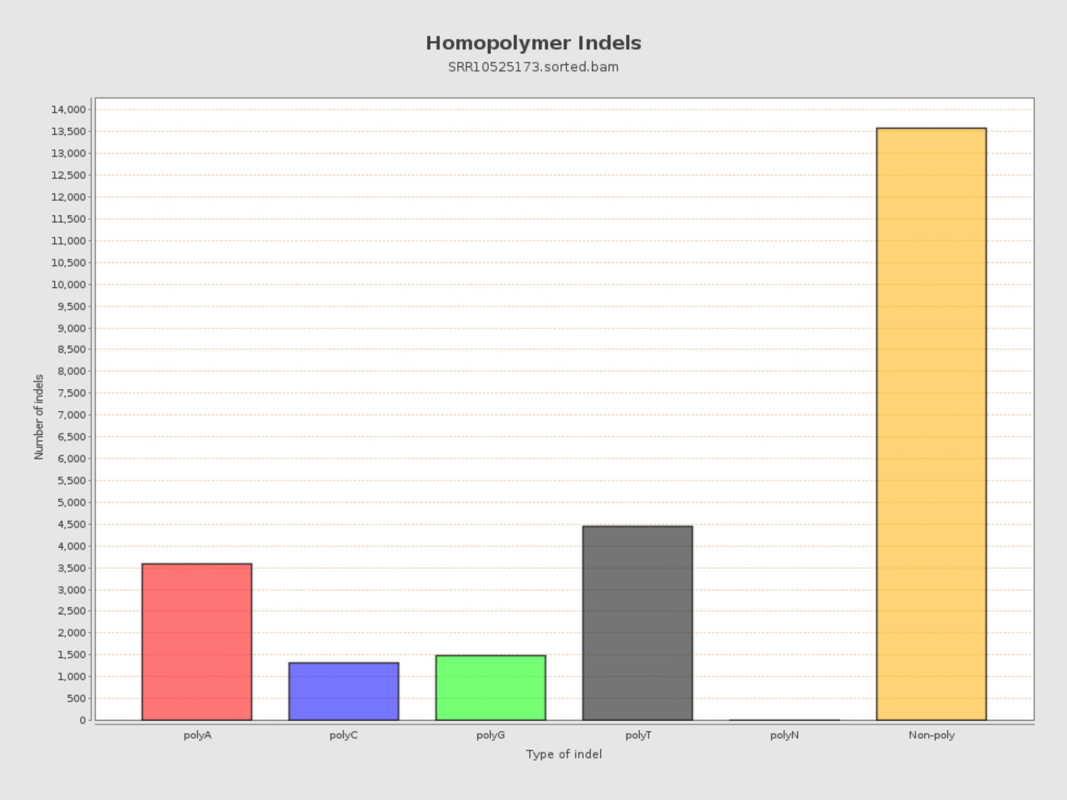
9. Results : Mapped Reads GC-content Distribution



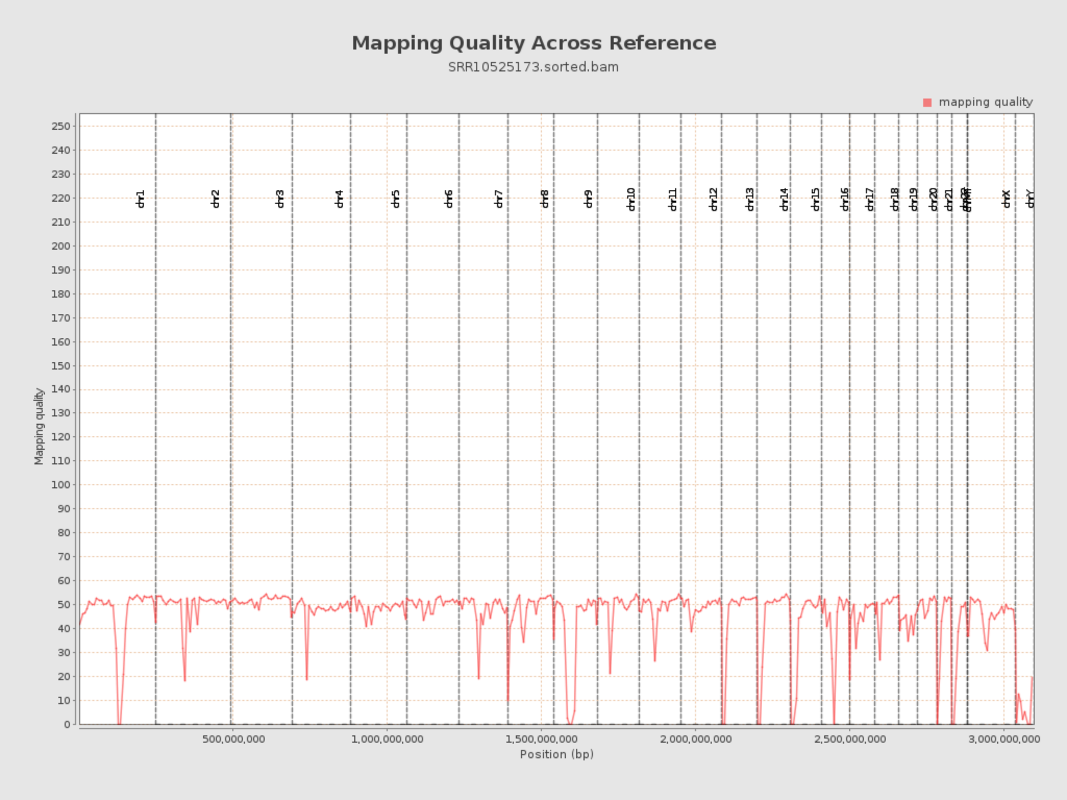
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram