Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:15:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525073.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_SRR10525073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525073.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:15:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,431,594
Mapped reads	1,322,336 / 92.37%
Unmapped reads	109,258 / 7.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,652 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	78,313 / 5.47%
Duplication rate	4.78%
Clipped reads	1,325,487 / 92.59%

2.2. ACGT Content

Number/percentage of A's	19,734,577 / 25.55%
Number/percentage of C's	14,480,316 / 18.75%
Number/percentage of T's	23,468,236 / 30.39%
Number/percentage of G's	19,535,009 / 25.3%
Number/percentage of N's	8,636 / 0.01%
GC Percentage	44.05%

2.3. Coverage

Mean	0.025

Standard Deviation	0.2433

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

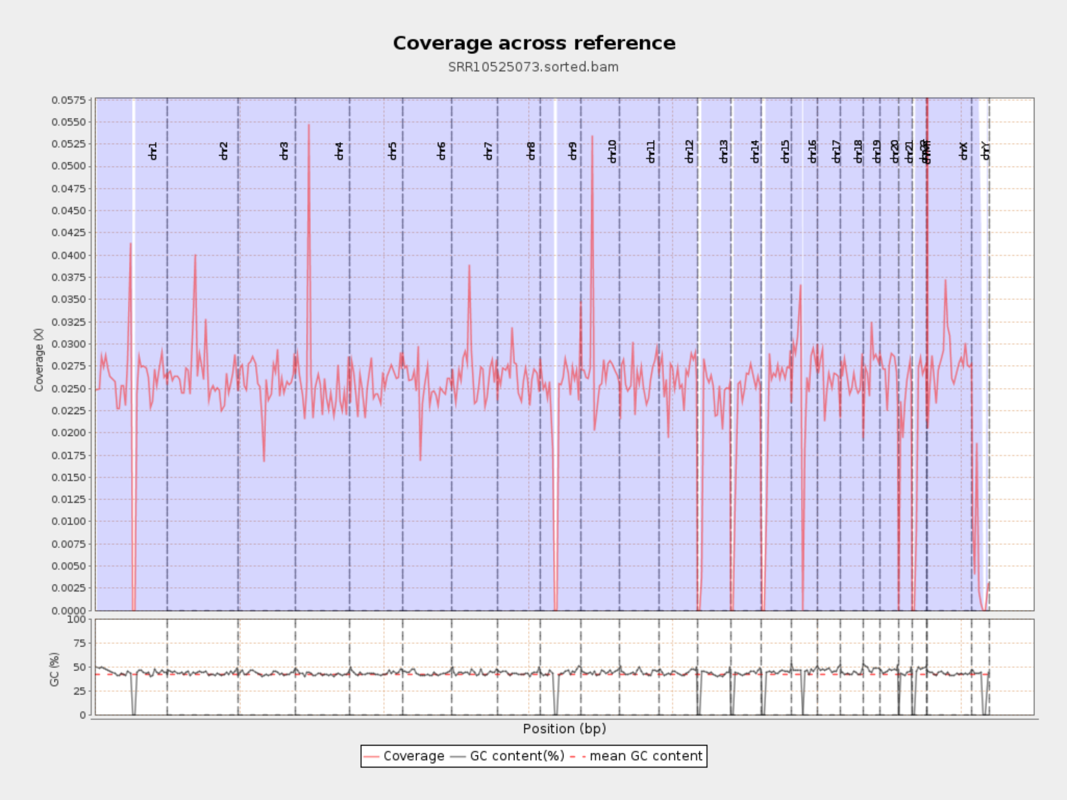
General error rate	0.48%
Mismatches	360,603
Insertions	5,091
Mapped reads with at least one insertion	0.38%
Deletions	14,574
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.1%

2.6. Chromosome stats

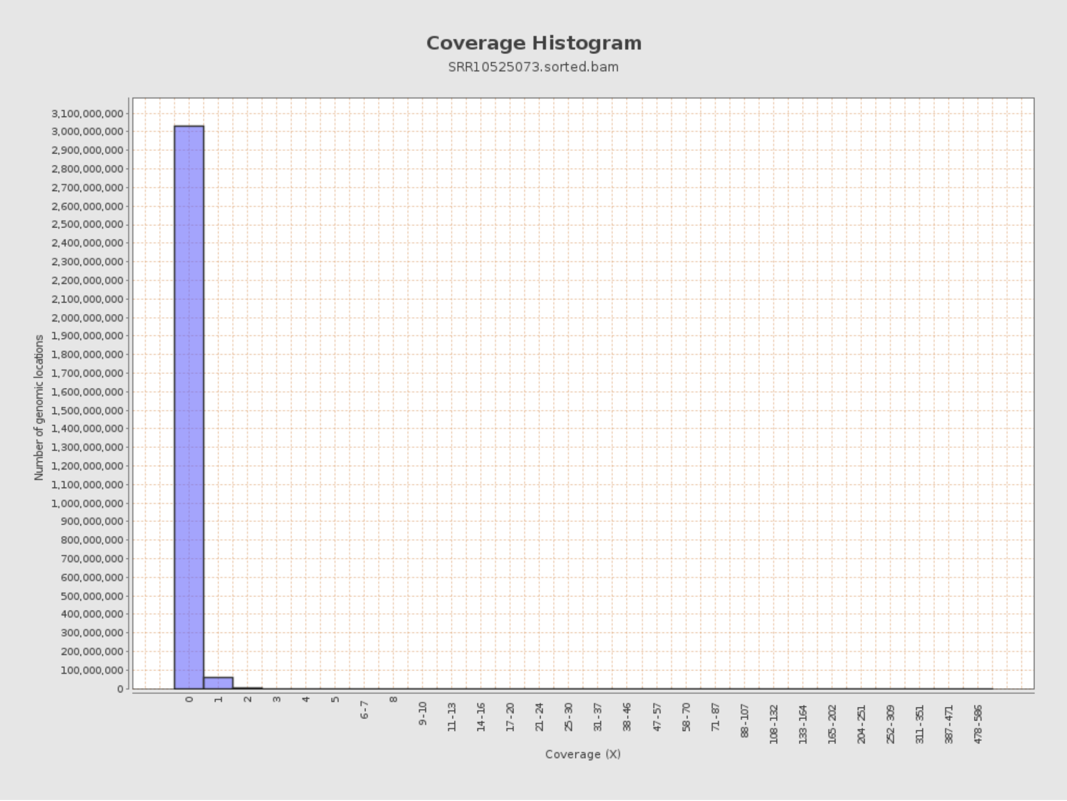
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6217397	0.0249	0.4244
chr2	243199373	6487651	0.0267	0.298
chr3	198022430	5092468	0.0257	0.1795
chr4	191154276	4941386	0.0259	0.2161
chr5	180915260	4659992	0.0258	0.1806
chr6	171115067	4318541	0.0252	0.1869
chr7	159138663	4284304	0.0269	0.2772

chr8	146364022	3869005	0.0264	0.2368
chr9	141213431	3204285	0.0227	0.207
chr10	135534747	3749754	0.0277	0.2733
chr11	135006516	3535491	0.0262	0.2067
chr12	133851895	3508733	0.0262	0.1856
chr13	115169878	2375660	0.0206	0.1611
chr14	107349540	2297361	0.0214	0.1657
chr15	102531392	2254301	0.022	0.1669
chr16	90354753	2303535	0.0255	0.1916
chr17	81195210	2105499	0.0259	0.1883
chr18	78077248	2030528	0.026	0.3104
chr19	59128983	1631966	0.0276	0.3212
chr20	63025520	1696510	0.0269	0.1917
chr21	48129895	1060989	0.022	0.1932
chr22	51304566	964538	0.0188	0.1548
chrMT	16571	45706	2.7582	2.2225
chrX	155270560	4337645	0.0279	0.2067
chrY	59373566	277313	0.0047	0.1699

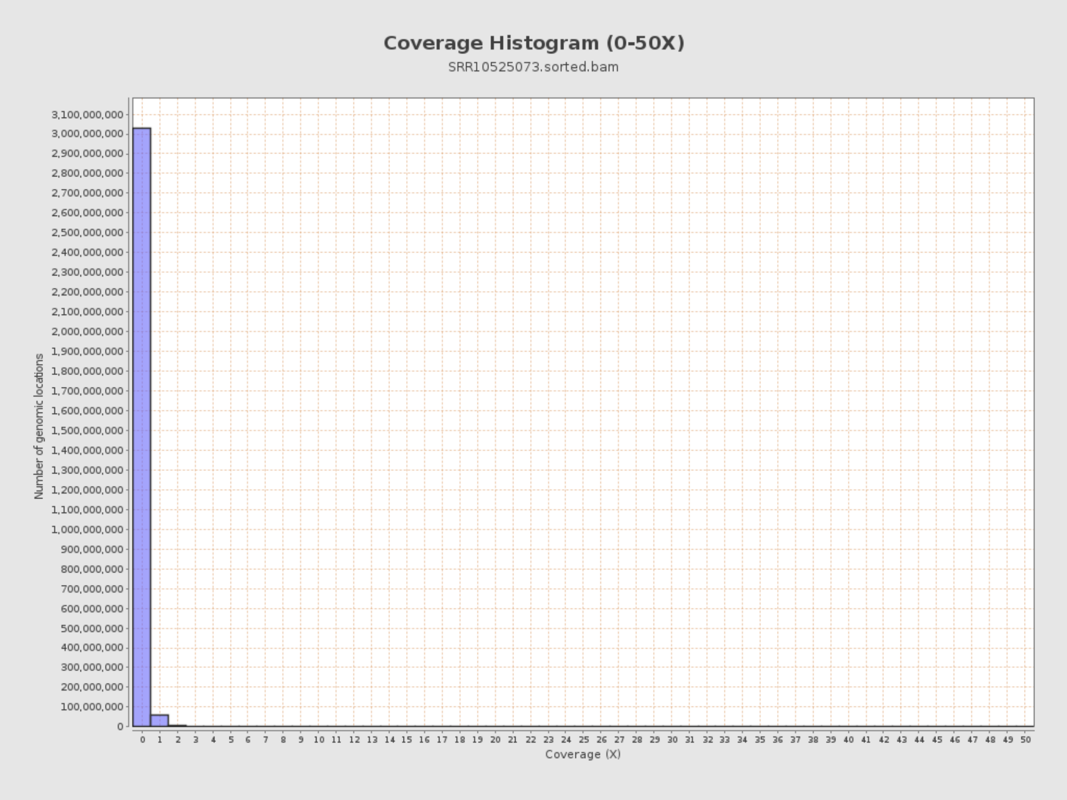
3. Results : Coverage across reference



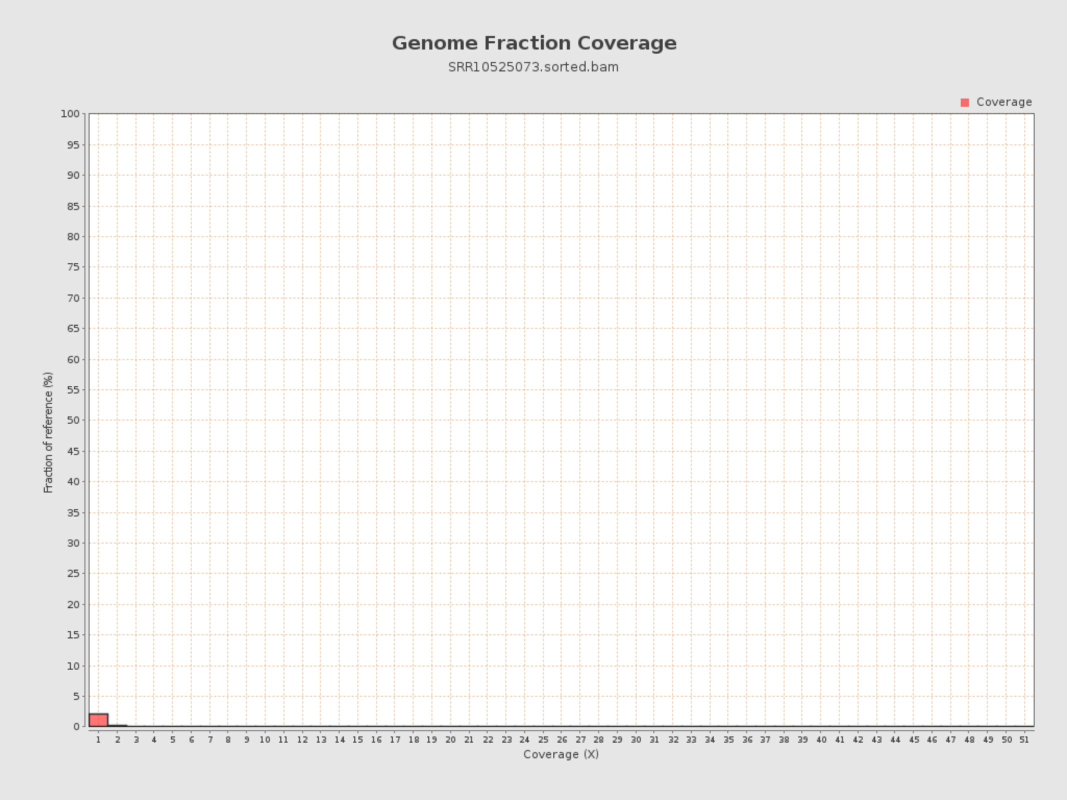
4. Results : Coverage Histogram



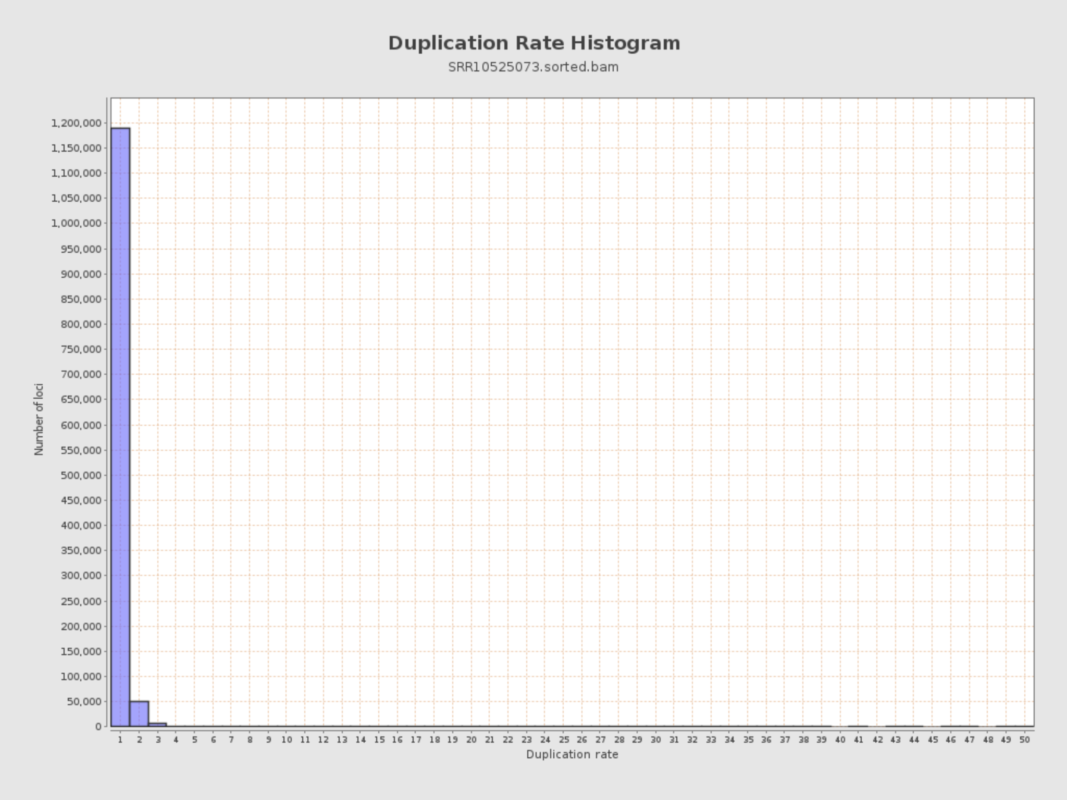
5. Results : Coverage Histogram (0-50X)



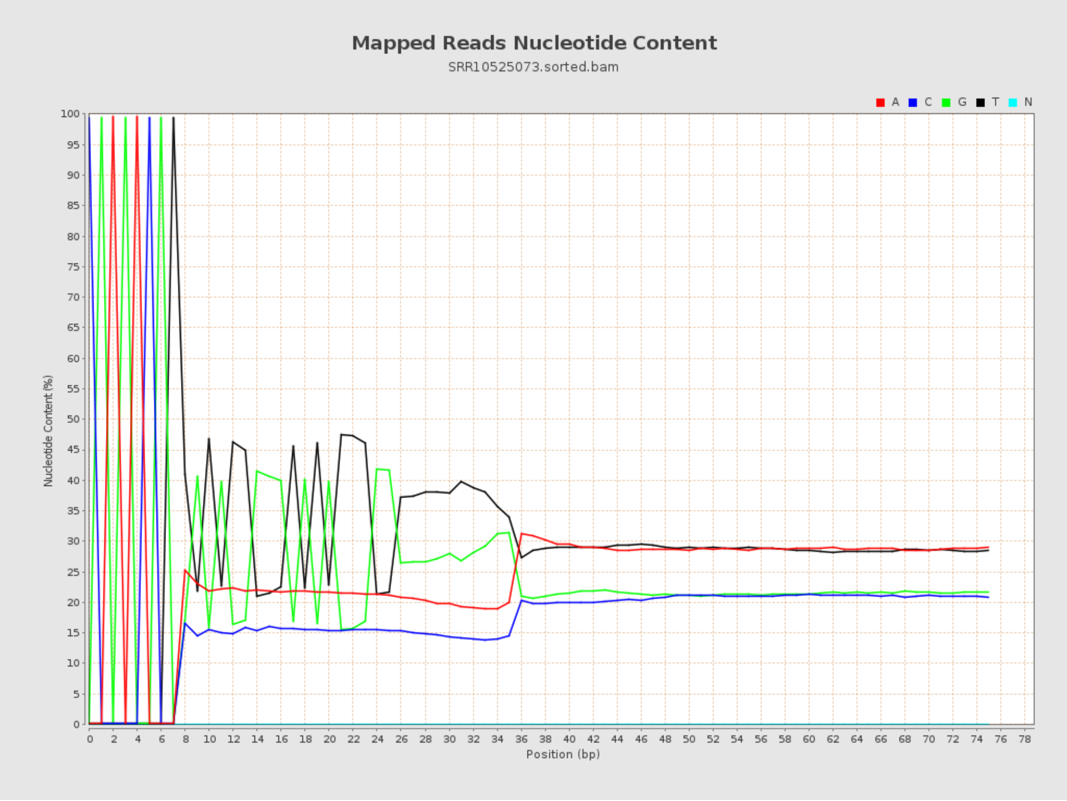
6. Results : Genome Fraction Coverage



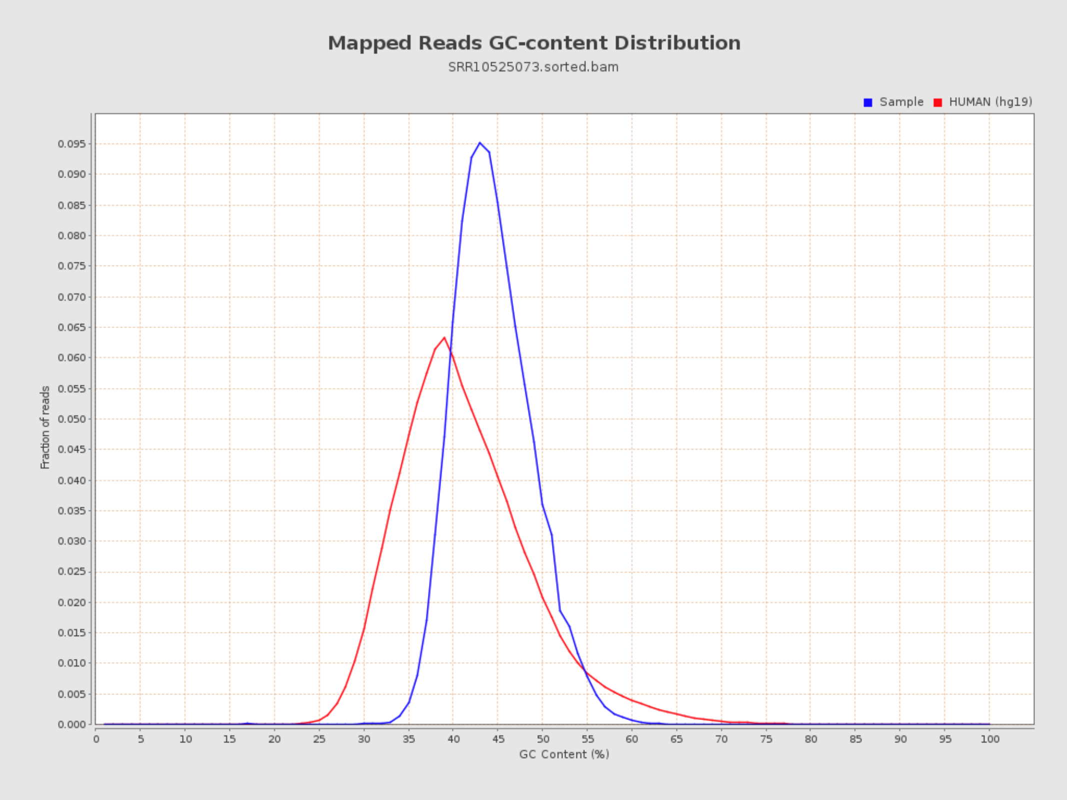
7. Results : Duplication Rate Histogram



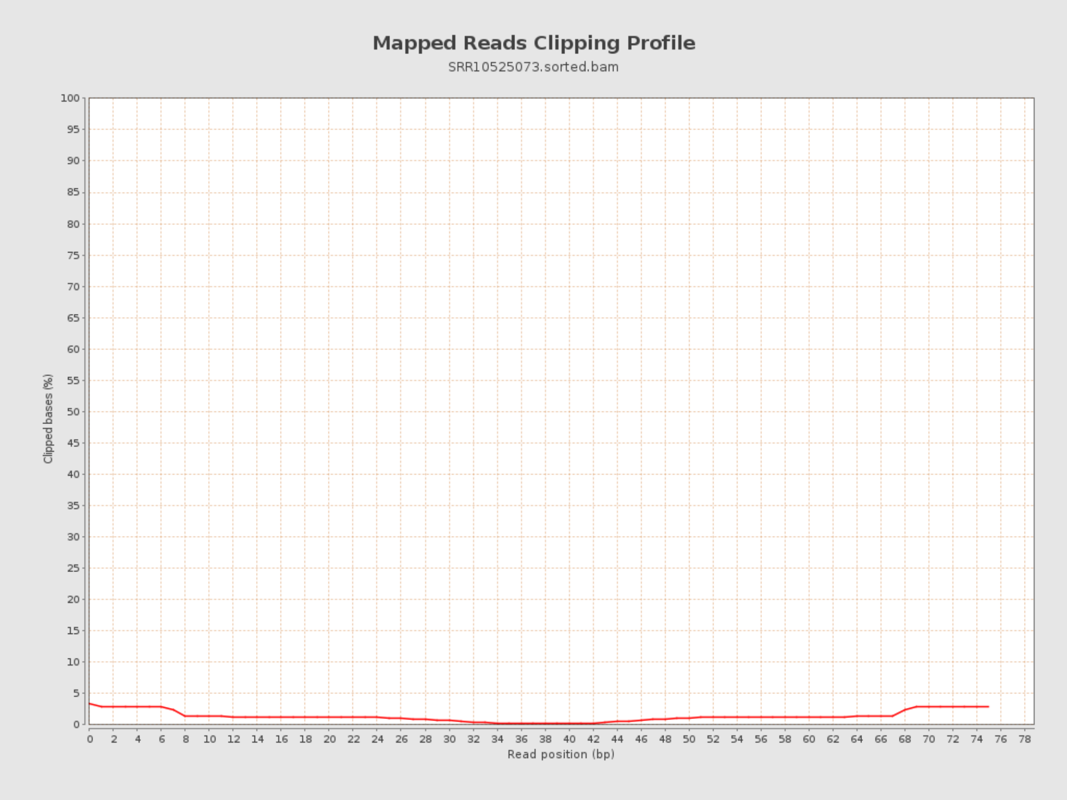
8. Results : Mapped Reads Nucleotide Content



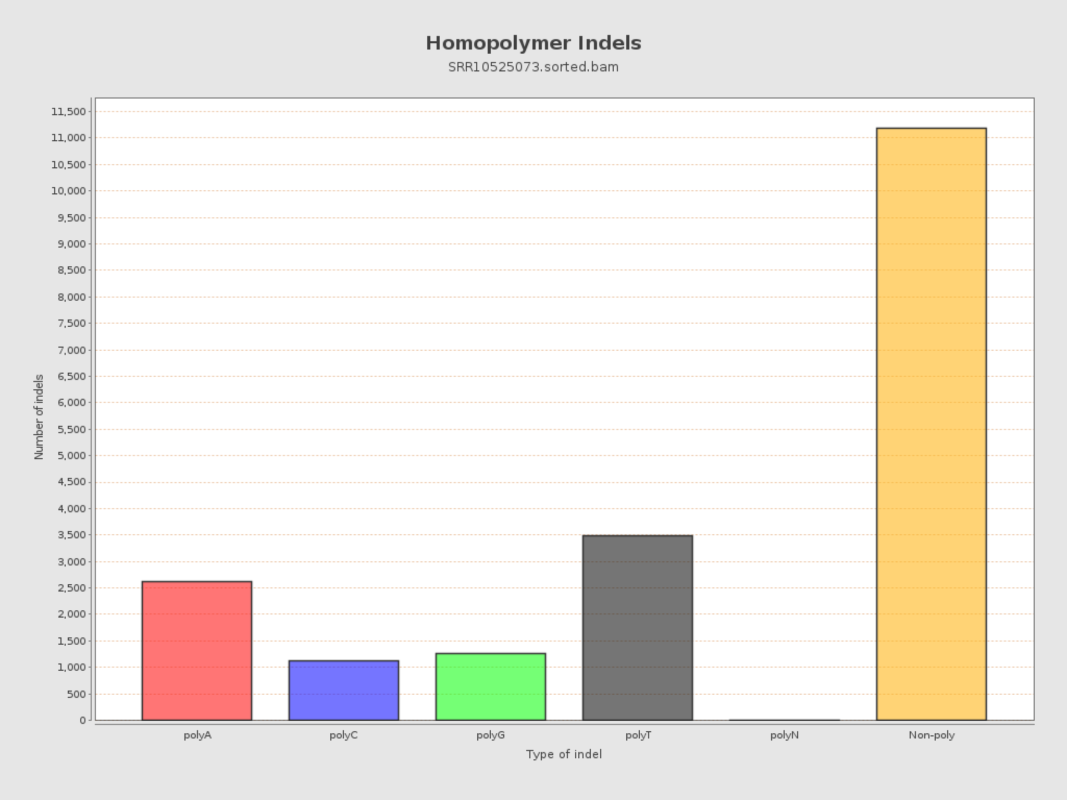
9. Results : Mapped Reads GC-content Distribution



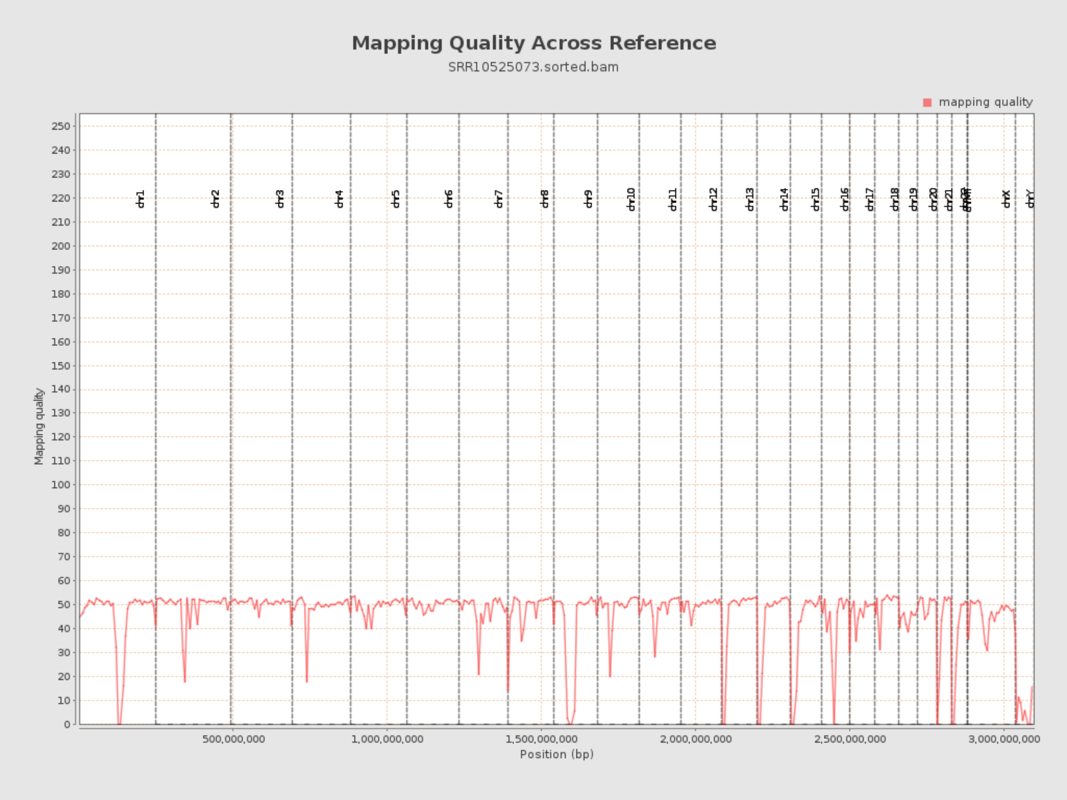
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram