Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:36:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525263.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_SRR10525263 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525263.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:36:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	497,550
Mapped reads	447,108 / 89.86%
Unmapped reads	50,442 / 10.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,877 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	8,611 / 1.73%
Duplication rate	1.44%
Clipped reads	448,019 / 90.05%

2.2. ACGT Content

Number/percentage of A's	6,541,909 / 25.52%
Number/percentage of C's	4,582,061 / 17.87%
Number/percentage of T's	8,487,753 / 33.1%
Number/percentage of G's	6,026,858 / 23.51%
Number/percentage of N's	519 / 0%
GC Percentage	41.38%

2.3. Coverage

Mean	0.0083

Standard Deviation	0.114

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

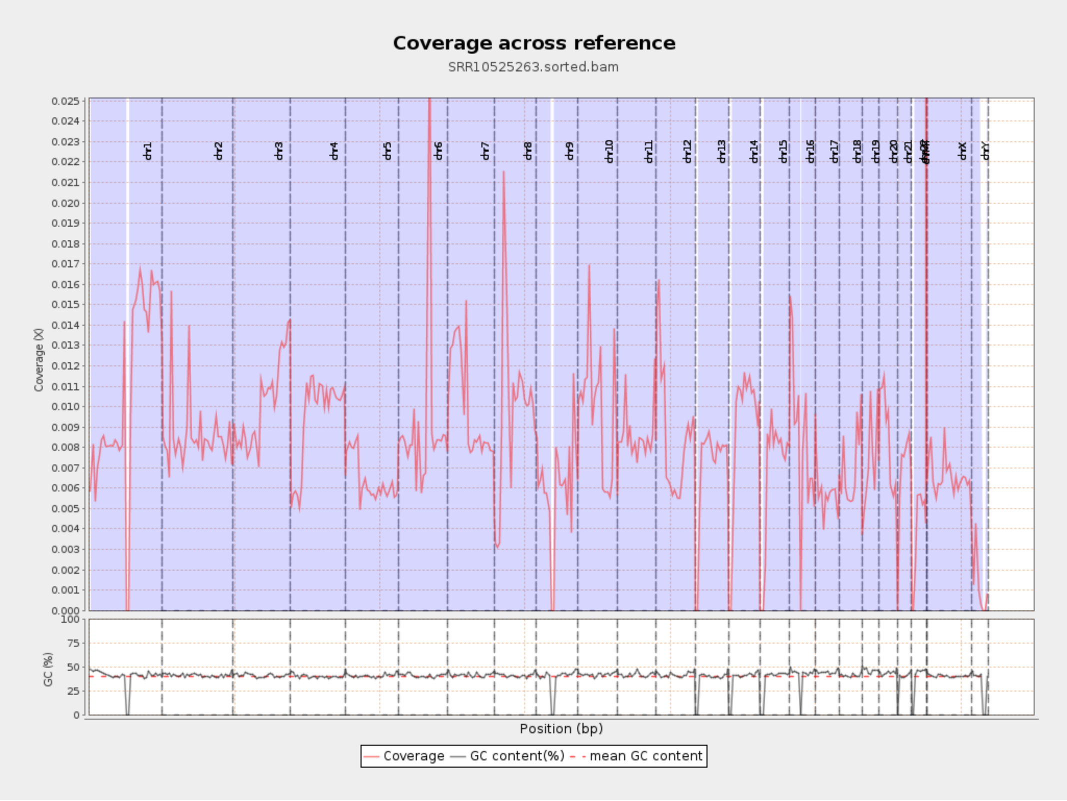
General error rate	0.53%
Mismatches	131,478
Insertions	1,904
Mapped reads with at least one insertion	0.42%
Deletions	5,206
Mapped reads with at least one deletion	1.16%
Homopolymer indels	43.21%

2.6. Chromosome stats

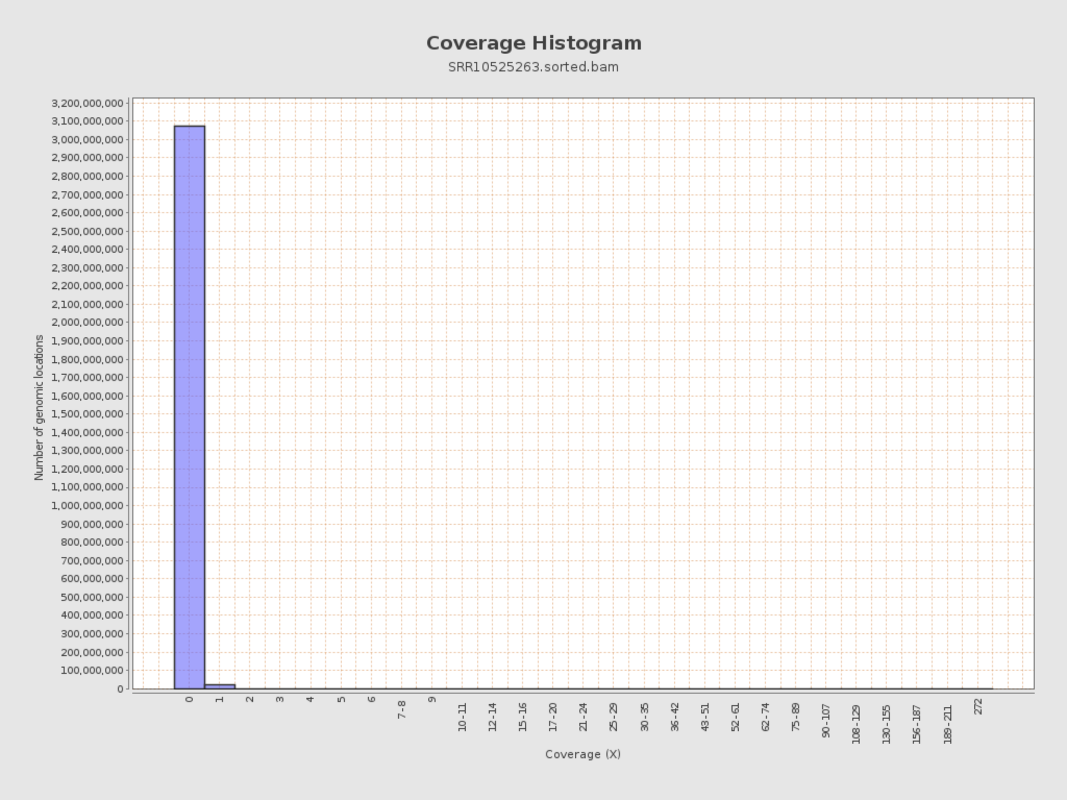
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2666574	0.0107	0.1766
chr2	243199373	2096960	0.0086	0.1472
chr3	198022430	1988102	0.01	0.1029
chr4	191154276	1802794	0.0094	0.1012
chr5	180915260	1161364	0.0064	0.0826
chr6	171115067	1604962	0.0094	0.1041
chr7	159138663	1611334	0.0101	0.146

chr8	146364022	1438865	0.0098	0.1222
chr9	141213431	838741	0.0059	0.0896
chr10	135534747	1344072	0.0099	0.118
chr11	135006516	1162249	0.0086	0.1051
chr12	133851895	1146054	0.0086	0.096
chr13	115169878	799048	0.0069	0.0858
chr14	107349540	947264	0.0088	0.0971
chr15	102531392	687203	0.0067	0.0853
chr16	90354753	737556	0.0082	0.0954
chr17	81195210	456524	0.0056	0.078
chr18	78077248	543991	0.007	0.1305
chr19	59128983	436744	0.0074	0.1275
chr20	63025520	533953	0.0085	0.0951
chr21	48129895	324608	0.0067	0.0859
chr22	51304566	195390	0.0038	0.0631
chrMT	16571	23547	1.421	1.3015
chrX	155270560	1026472	0.0066	0.0874
chrY	59373566	72989	0.0012	0.0449

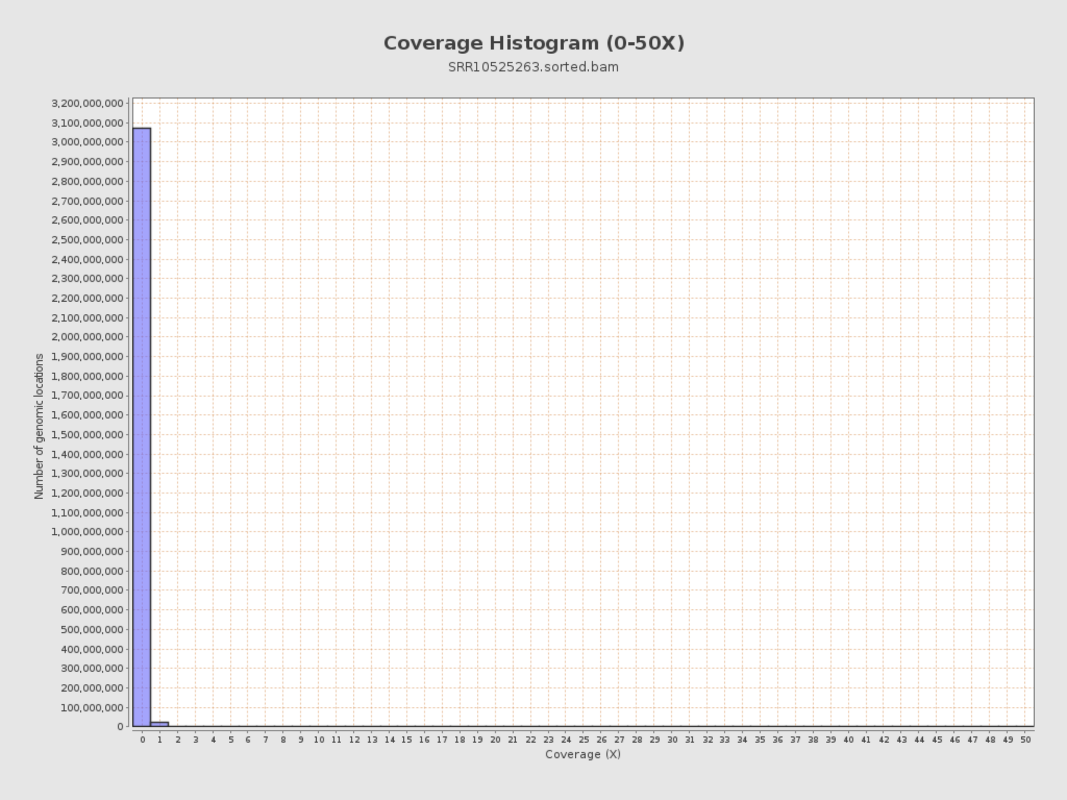
3. Results : Coverage across reference



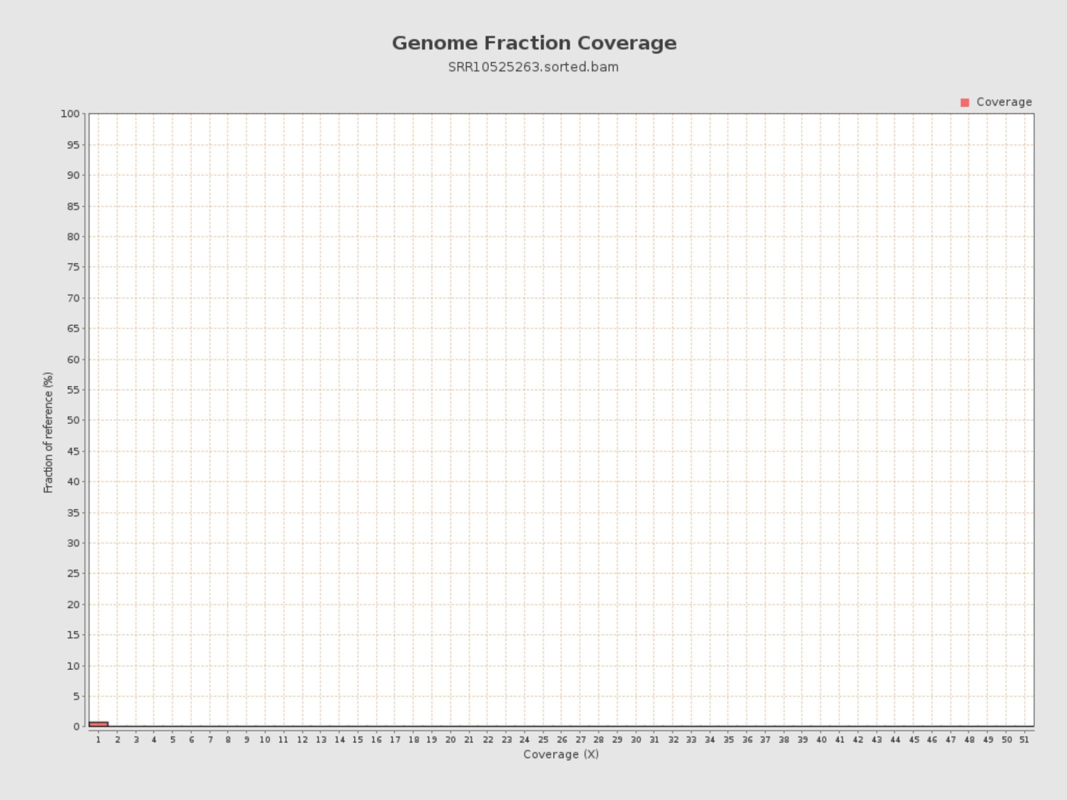
4. Results : Coverage Histogram



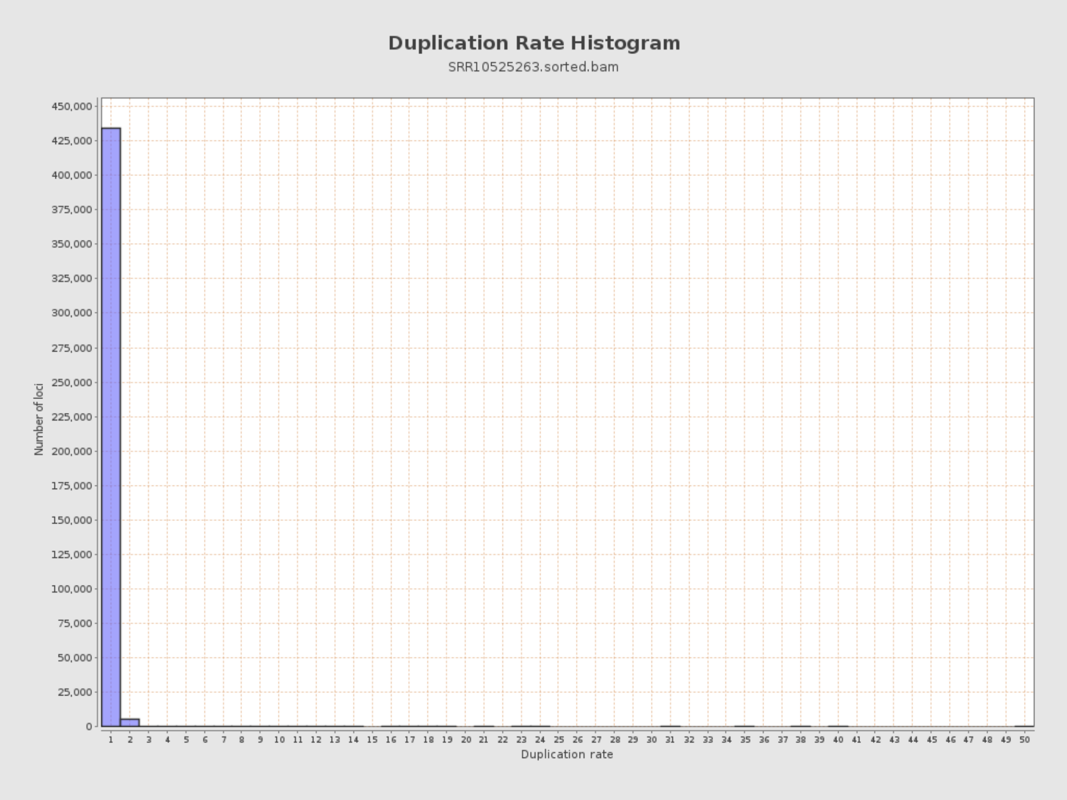
5. Results : Coverage Histogram (0-50X)



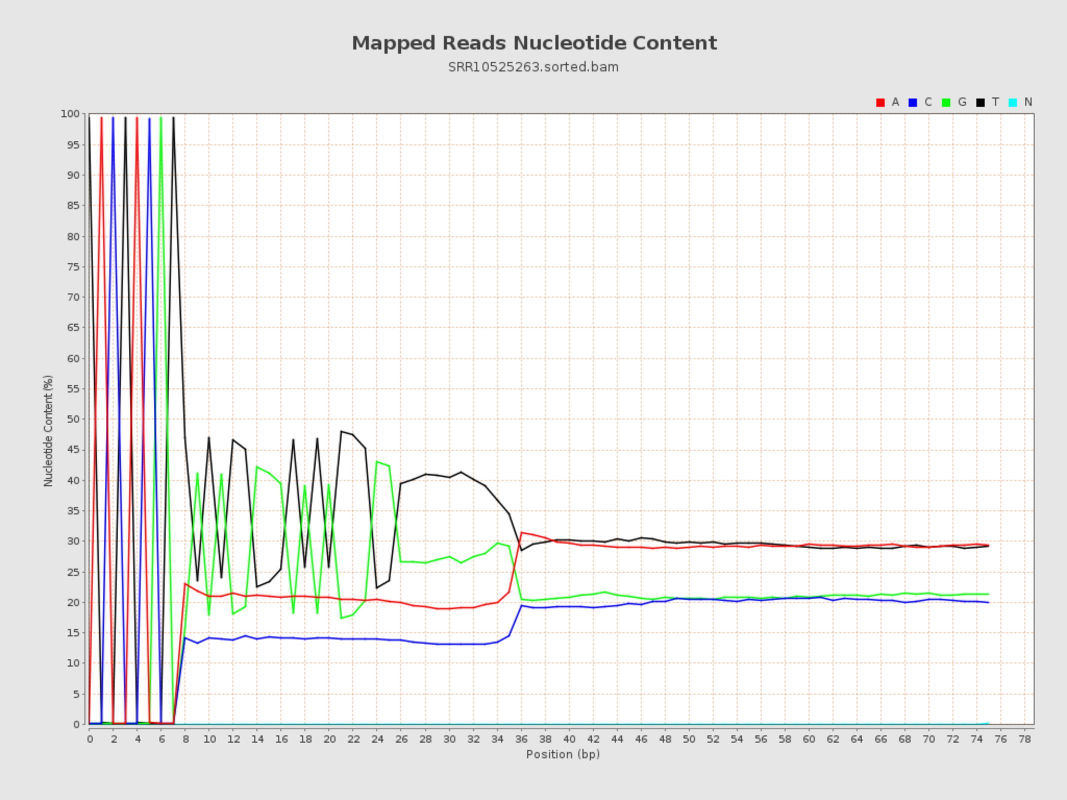
6. Results : Genome Fraction Coverage



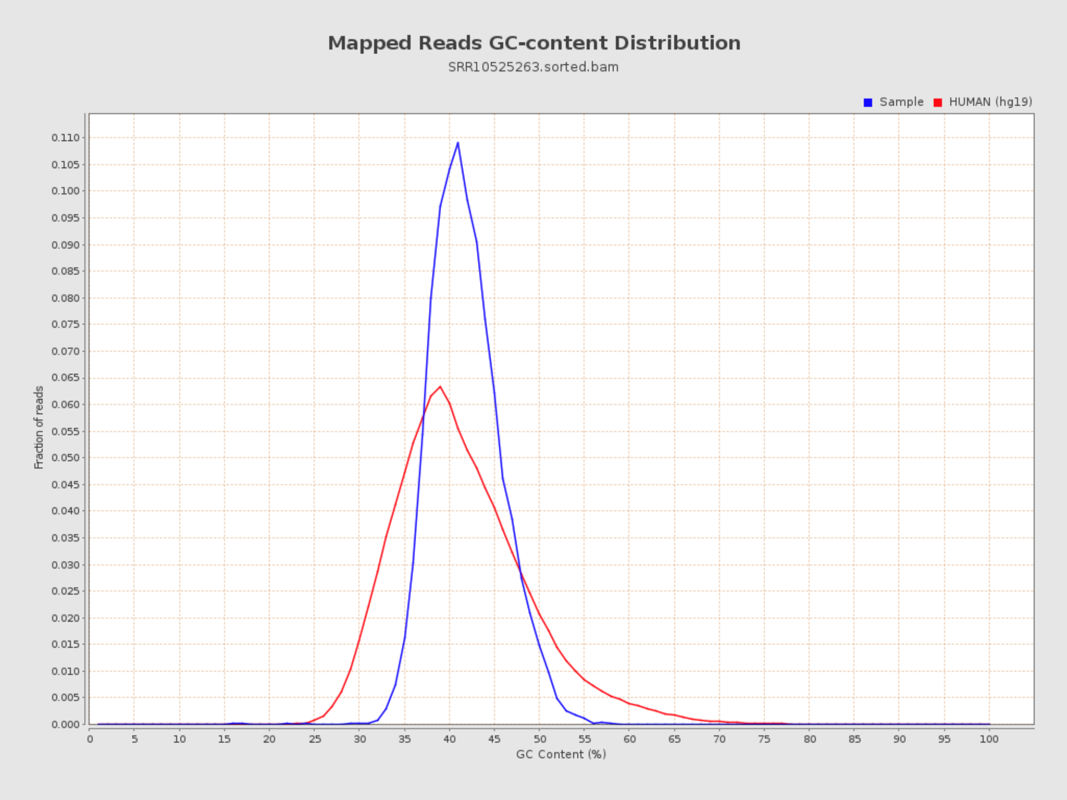
7. Results : Duplication Rate Histogram



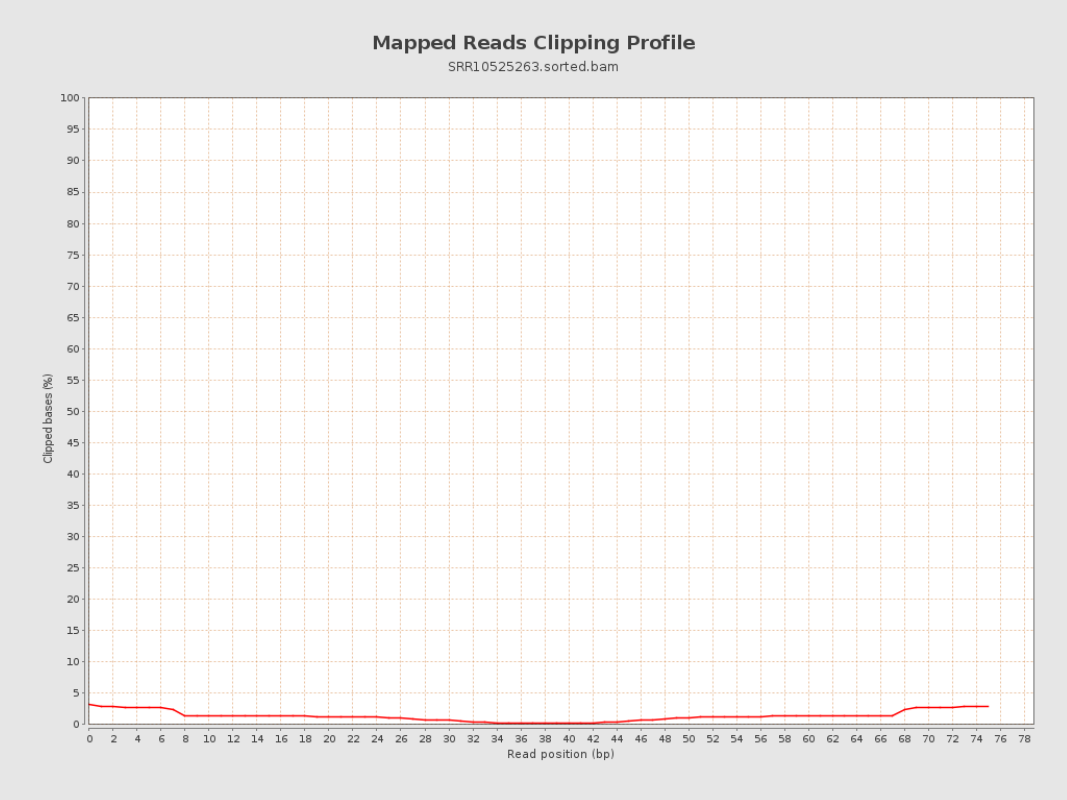
8. Results : Mapped Reads Nucleotide Content



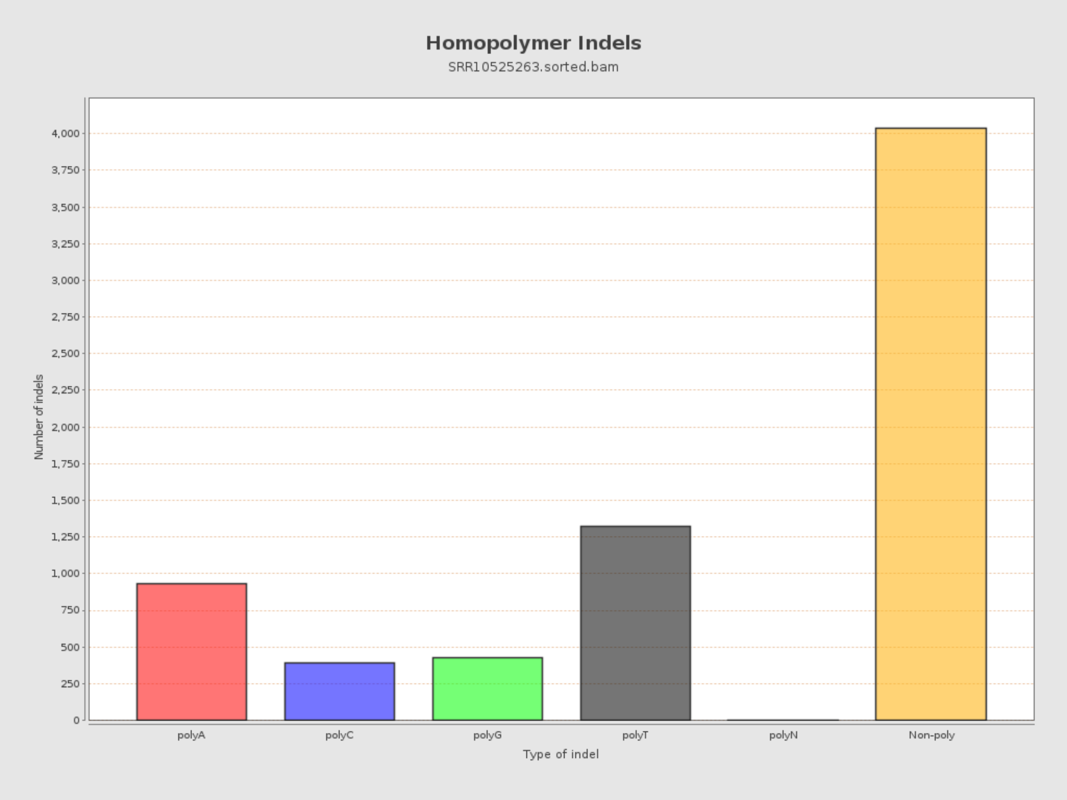
9. Results : Mapped Reads GC-content Distribution



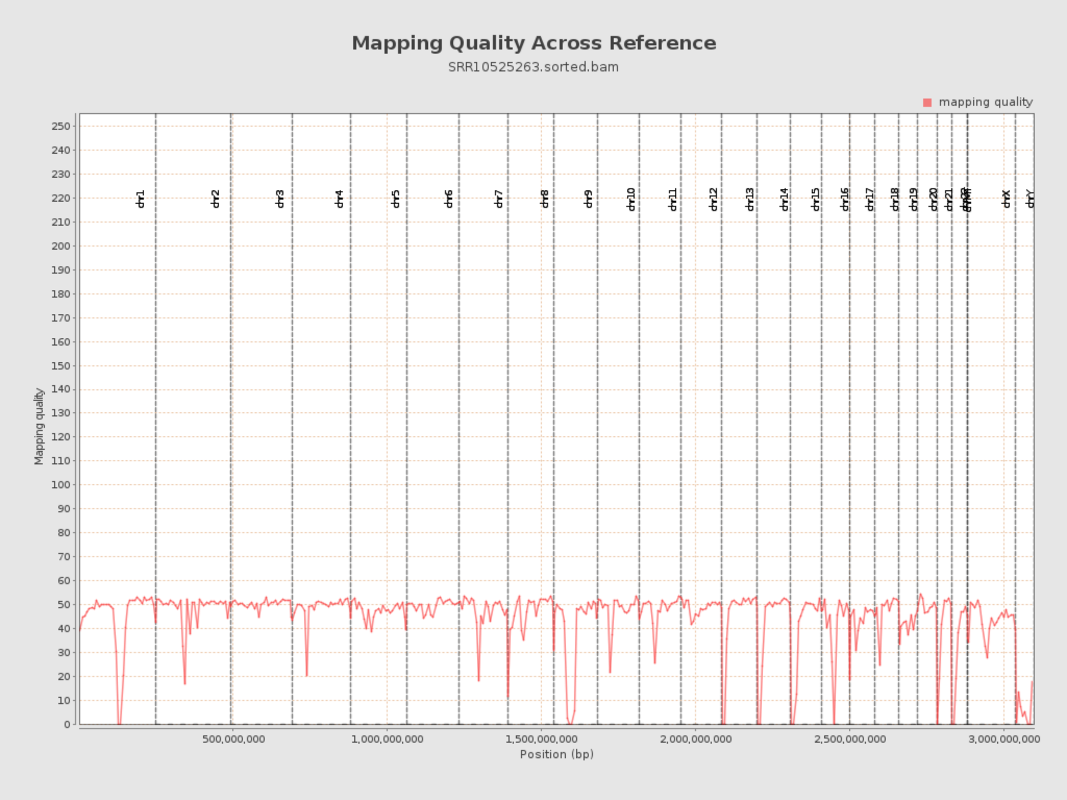
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram