Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:22:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525210.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_SRR10525210 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525210.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:22:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525210.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,047,002
Mapped reads	1,880,733 / 91.88%
Unmapped reads	166,269 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,386 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	73,042 / 3.57%
Duplication rate	2.74%
Clipped reads	1,879,203 / 91.8%

2.2. ACGT Content

Number/percentage of A's	25,698,939 / 23.69%
Number/percentage of C's	20,641,889 / 19.03%
Number/percentage of T's	36,151,559 / 33.33%
Number/percentage of G's	25,970,814 / 23.94%
Number/percentage of N's	2,614 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.035

Standard Deviation	0.3476

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

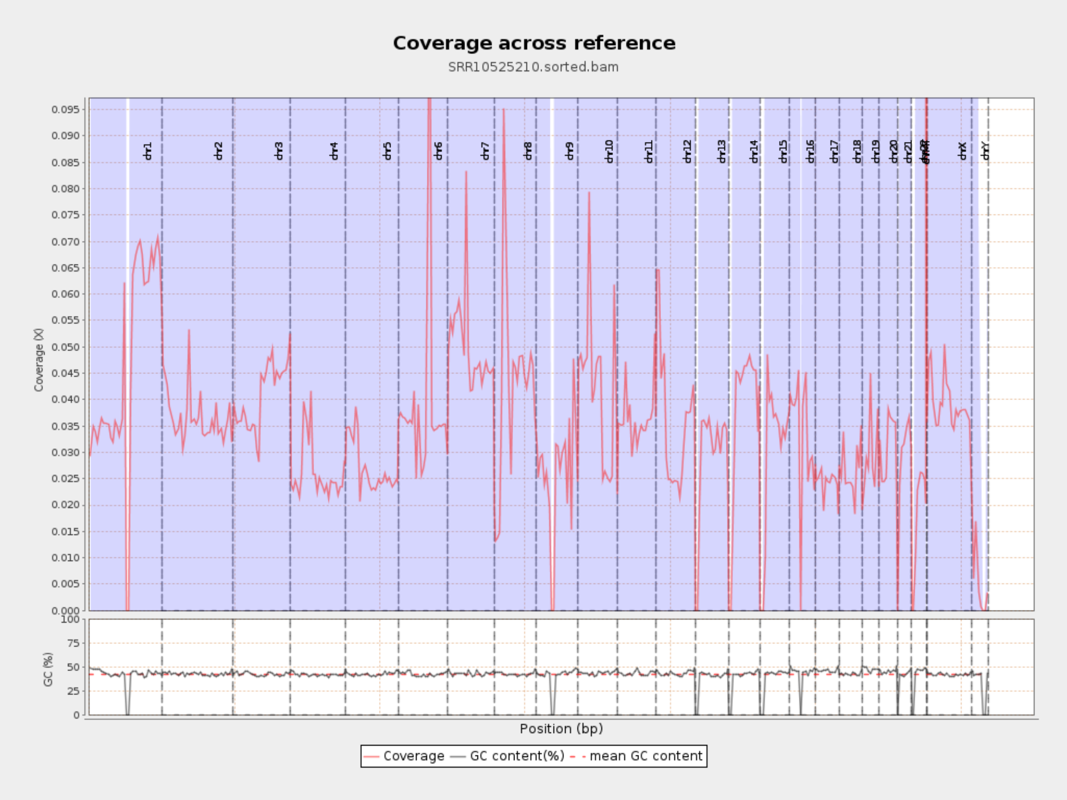
General error rate	0.52%
Mismatches	552,840
Insertions	7,791
Mapped reads with at least one insertion	0.41%
Deletions	21,235
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.89%

2.6. Chromosome stats

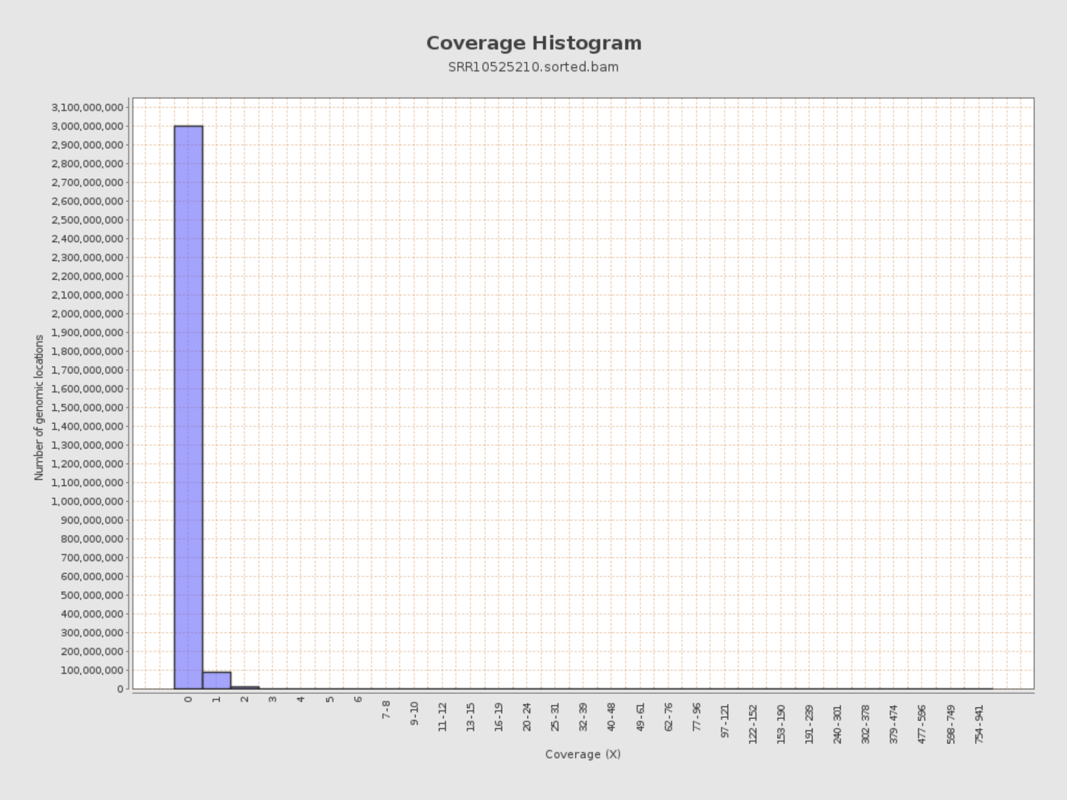
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11559005	0.0464	0.6509
chr2	243199373	8940847	0.0368	0.4389
chr3	198022430	8023588	0.0405	0.2292
chr4	191154276	4985243	0.0261	0.1906
chr5	180915260	4898038	0.0271	0.1816
chr6	171115067	6883367	0.0402	0.2503
chr7	159138663	8029255	0.0505	0.663

chr8	146364022	6191885	0.0423	0.3055
chr9	141213431	3625583	0.0257	0.2329
chr10	135534747	5787659	0.0427	0.3737
chr11	135006516	4914386	0.0364	0.2645
chr12	133851895	4776518	0.0357	0.2111
chr13	115169878	3354228	0.0291	0.1891
chr14	107349540	3975278	0.037	0.2169
chr15	102531392	3072277	0.03	0.1939
chr16	90354753	2938498	0.0325	0.2249
chr17	81195210	1962676	0.0242	0.1785
chr18	78077248	2062927	0.0264	0.4198
chr19	59128983	1757169	0.0297	0.4335
chr20	63025520	1966261	0.0312	0.1982
chr21	48129895	1375399	0.0286	0.1982
chr22	51304566	886144	0.0173	0.1427
chrMT	16571	116657	7.0398	4.5059
chrX	155270560	6095282	0.0393	0.2388
chrY	59373566	320926	0.0054	0.1427

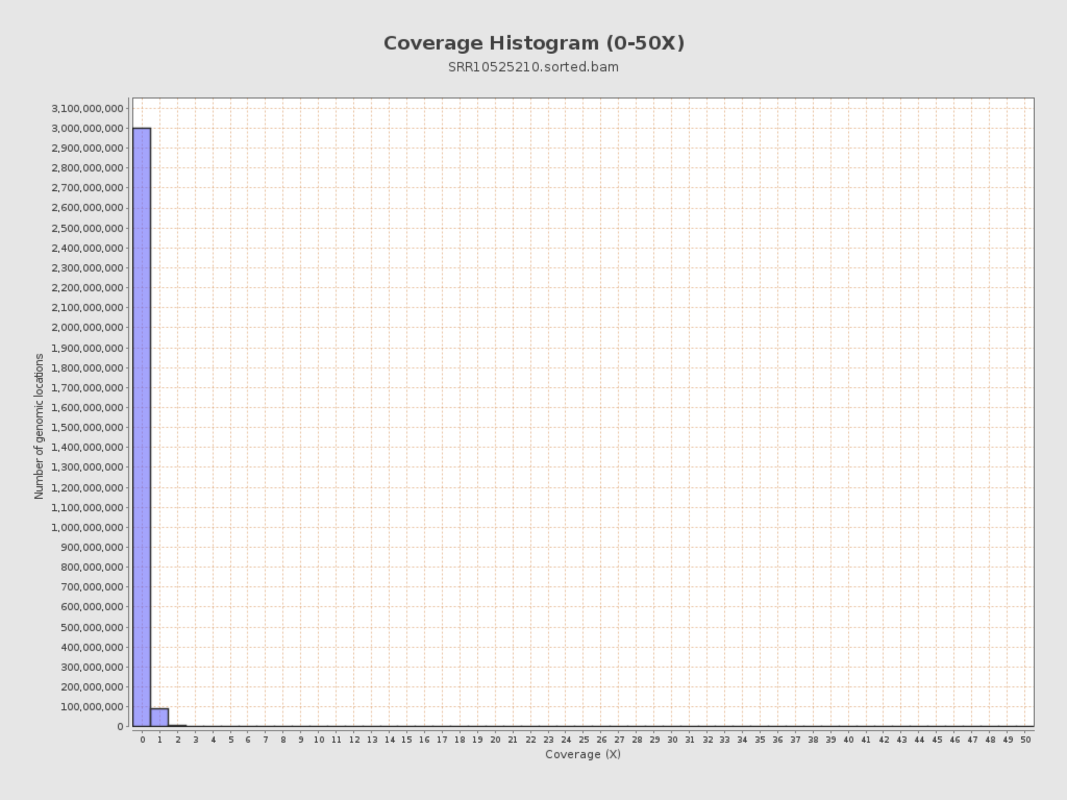
3. Results : Coverage across reference



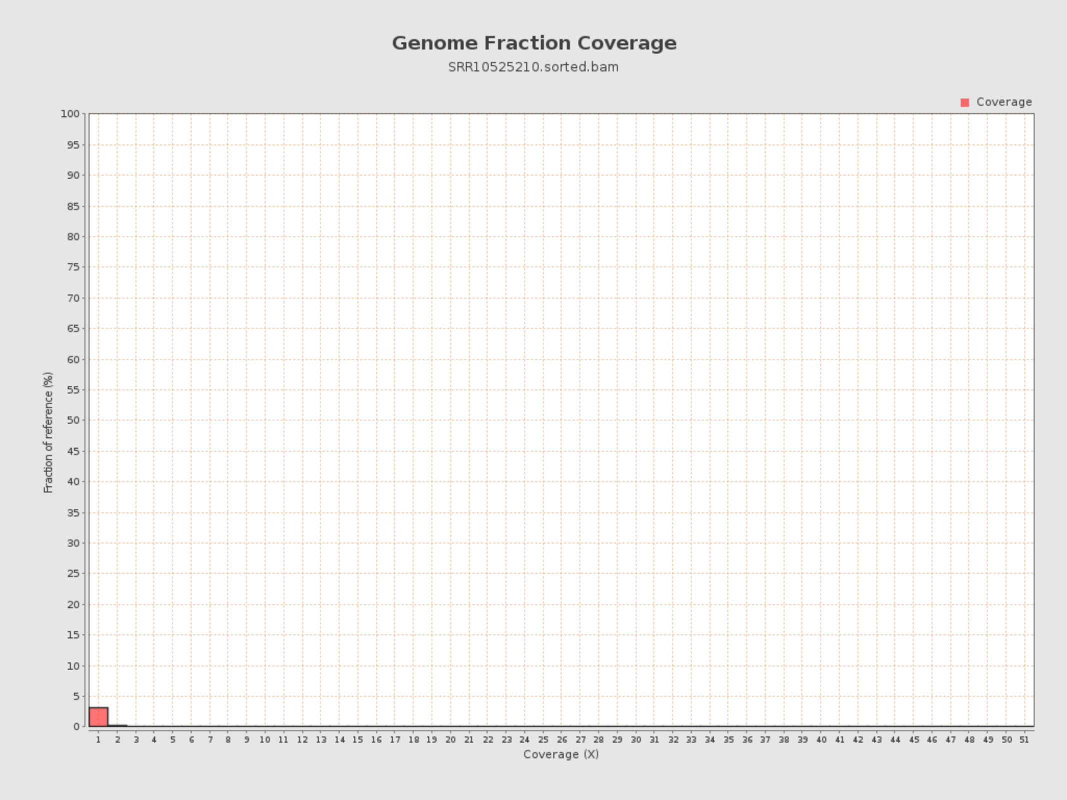
4. Results : Coverage Histogram



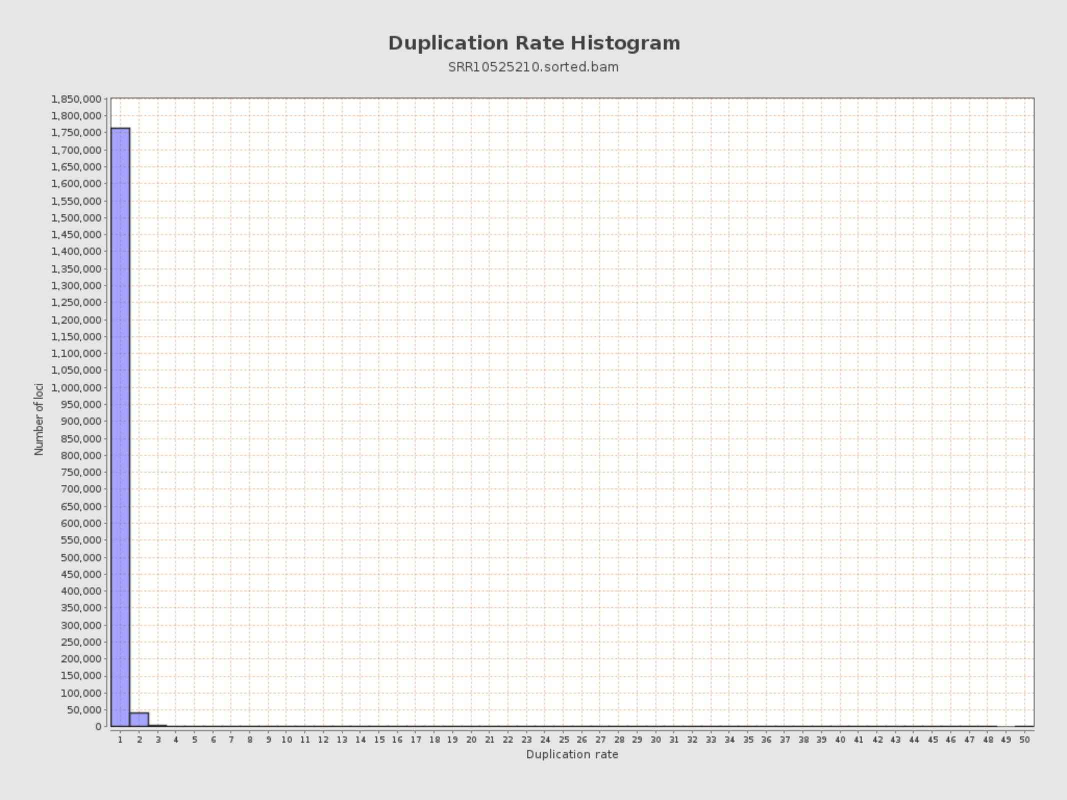
5. Results : Coverage Histogram (0-50X)



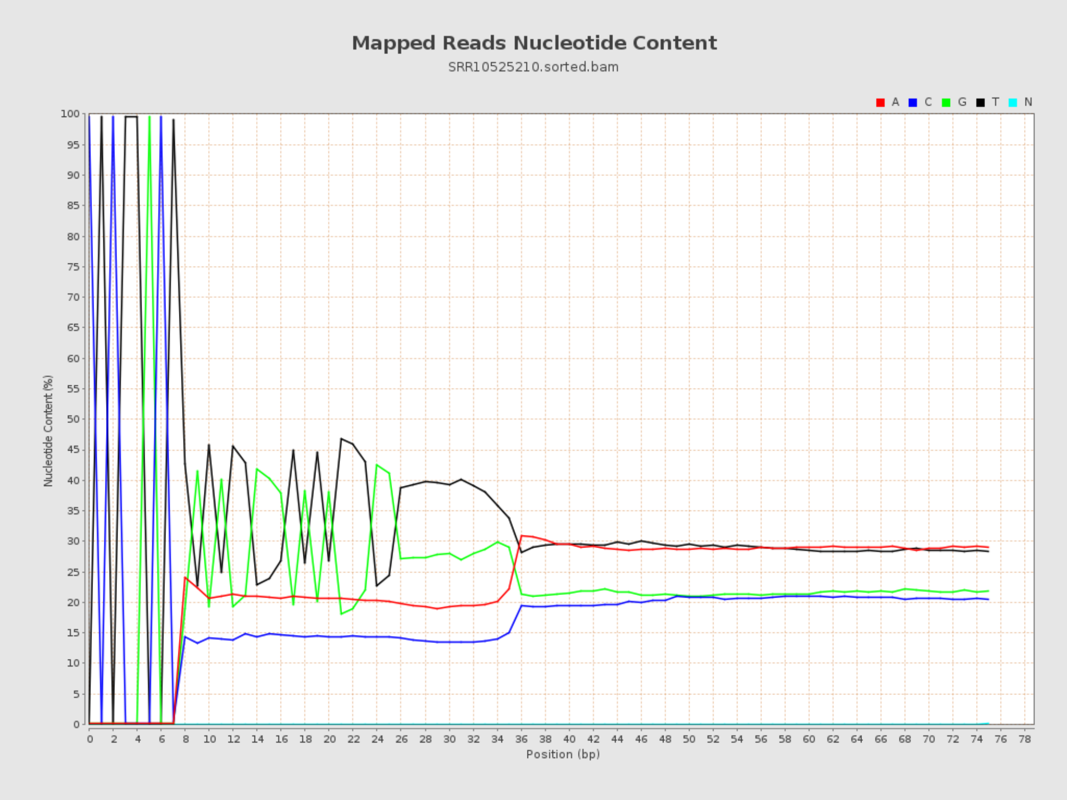
6. Results : Genome Fraction Coverage



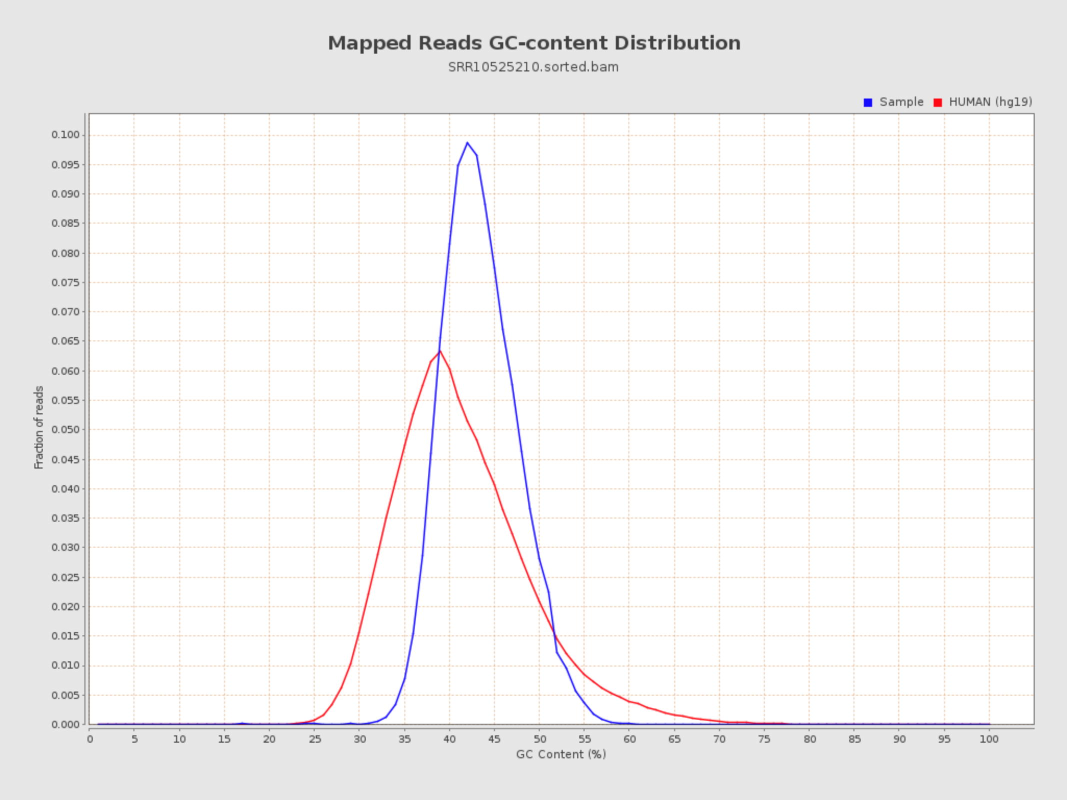
7. Results : Duplication Rate Histogram



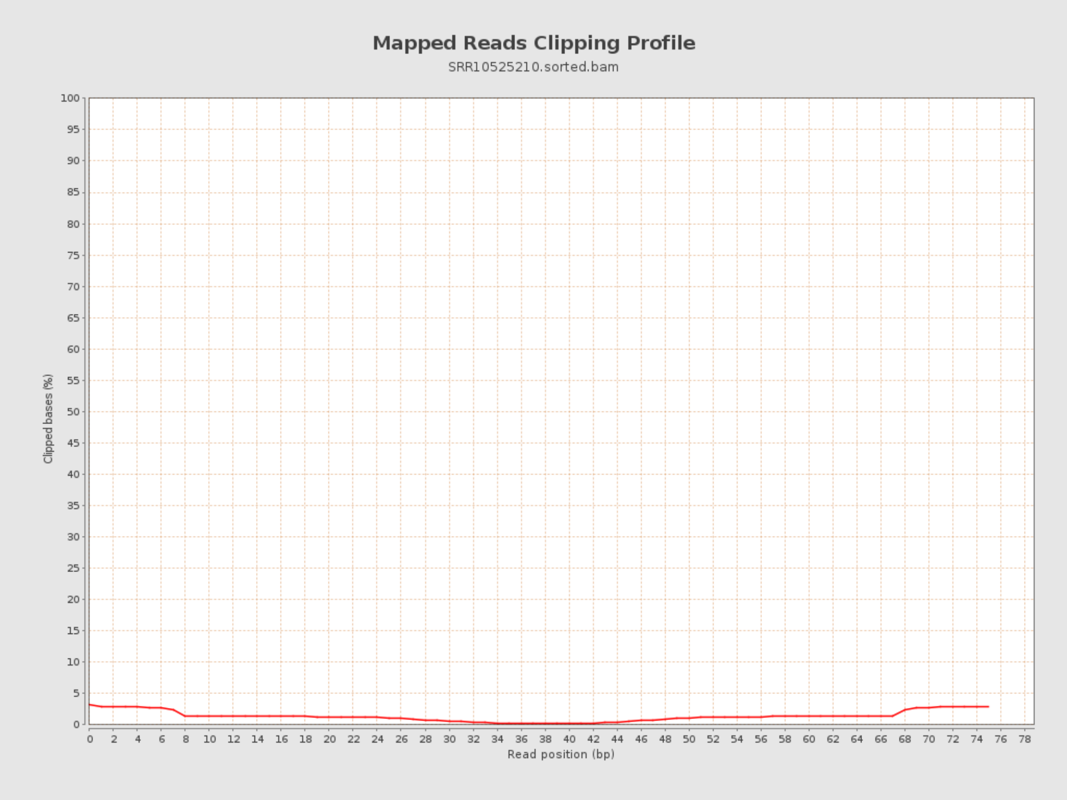
8. Results : Mapped Reads Nucleotide Content



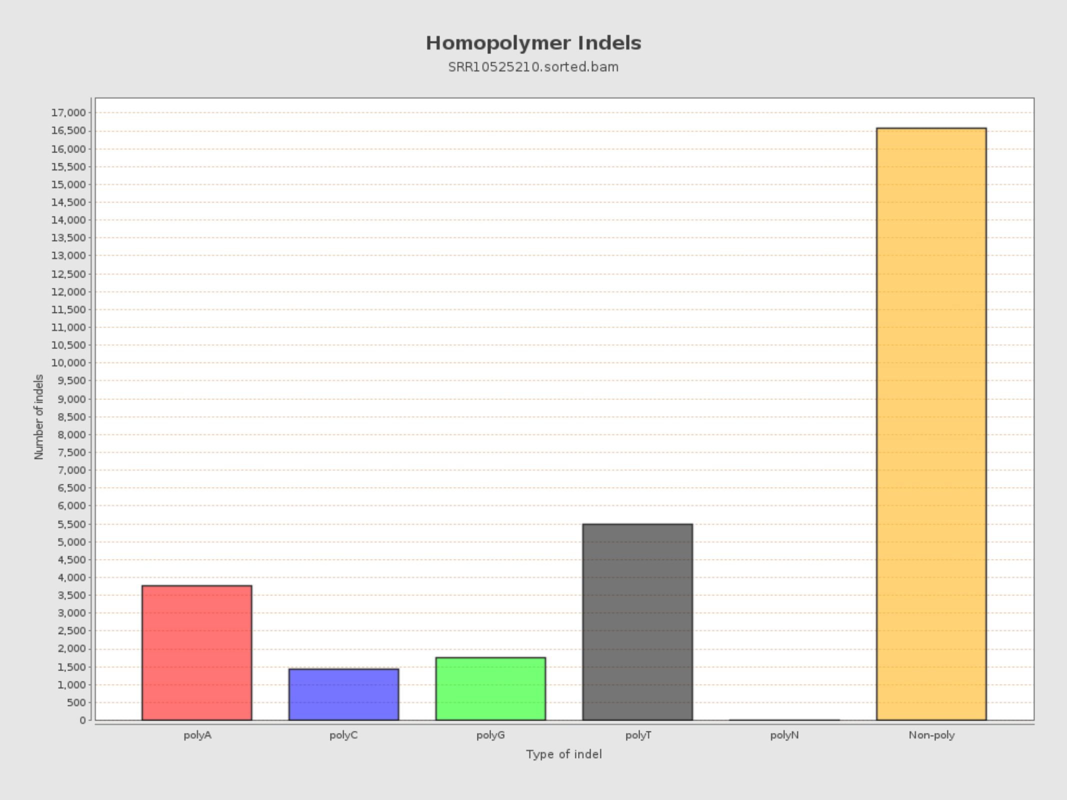
9. Results : Mapped Reads GC-content Distribution



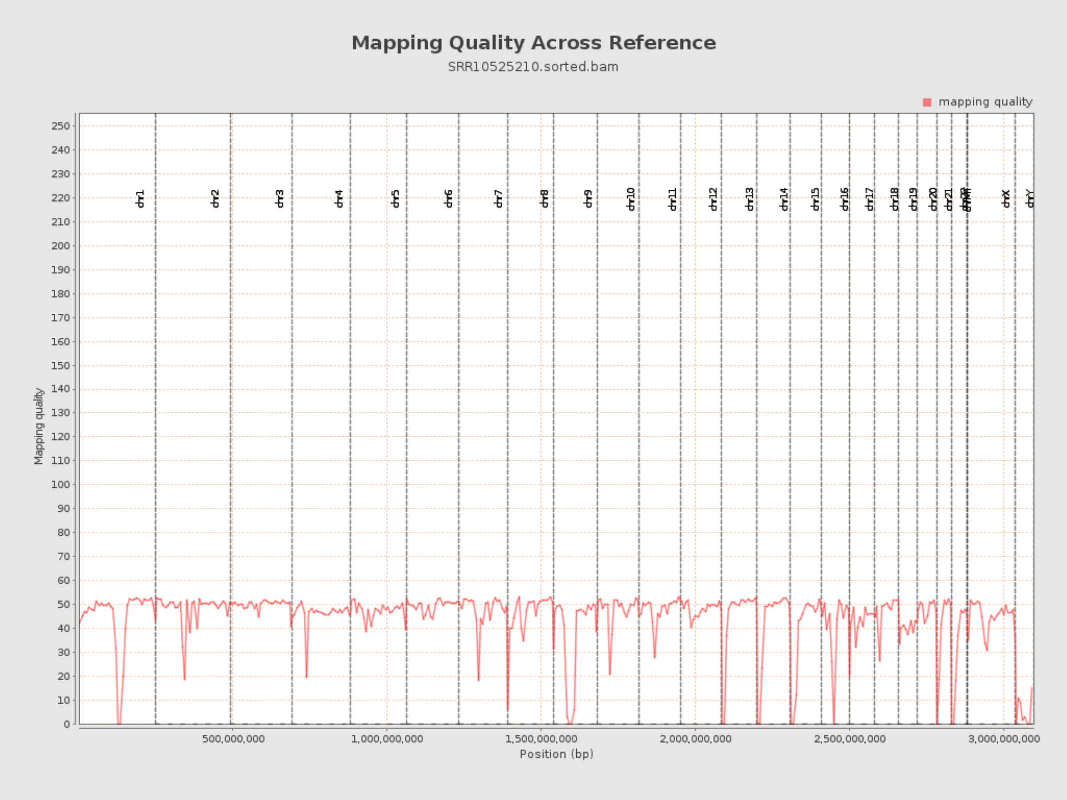
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram