Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:14:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525255.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_SRR10525255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525255.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:14:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,656,870
Mapped reads	1,518,240 / 91.63%
Unmapped reads	138,630 / 8.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,023 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	53,010 / 3.2%
Duplication rate	2.55%
Clipped reads	1,520,316 / 91.76%

2.2. ACGT Content

Number/percentage of A's	22,663,333 / 25.76%
Number/percentage of C's	15,197,434 / 17.28%
Number/percentage of T's	28,170,452 / 32.02%
Number/percentage of G's	21,938,574 / 24.94%
Number/percentage of N's	1,839 / 0%
GC Percentage	42.21%

2.3. Coverage

Mean	0.0284

Standard Deviation	0.2797

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

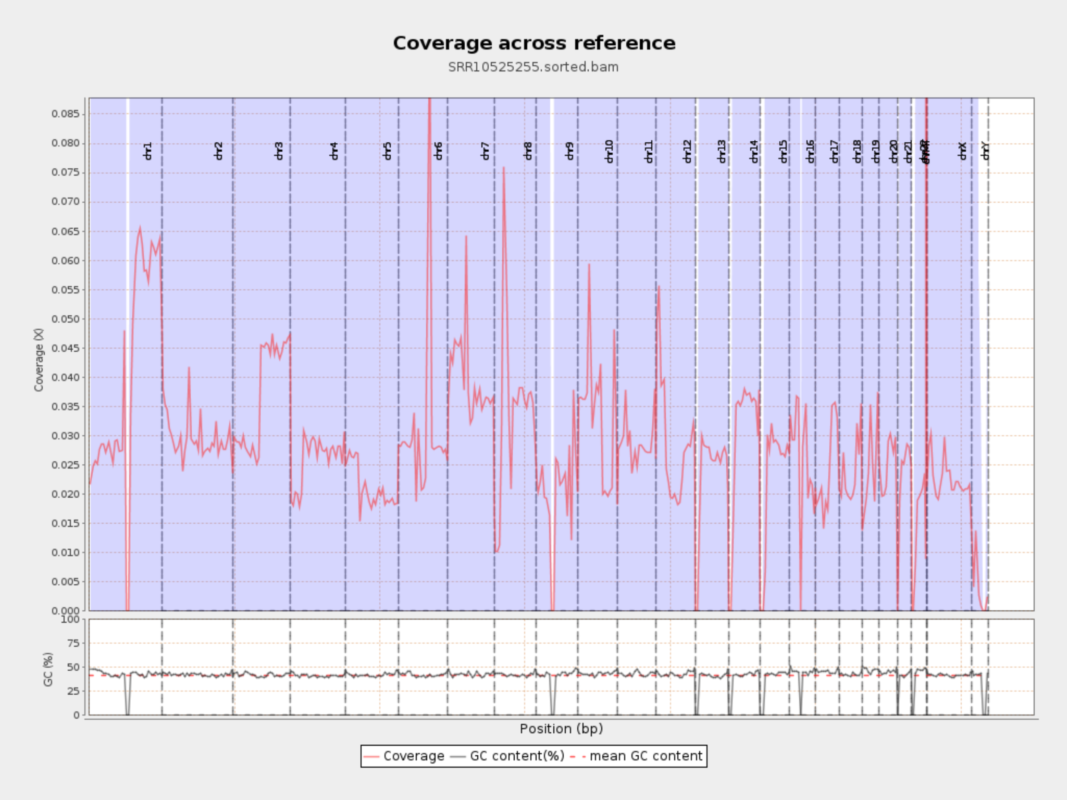
General error rate	0.51%
Mismatches	442,187
Insertions	6,022
Mapped reads with at least one insertion	0.39%
Deletions	18,593
Mapped reads with at least one deletion	1.21%
Homopolymer indels	43.43%

2.6. Chromosome stats

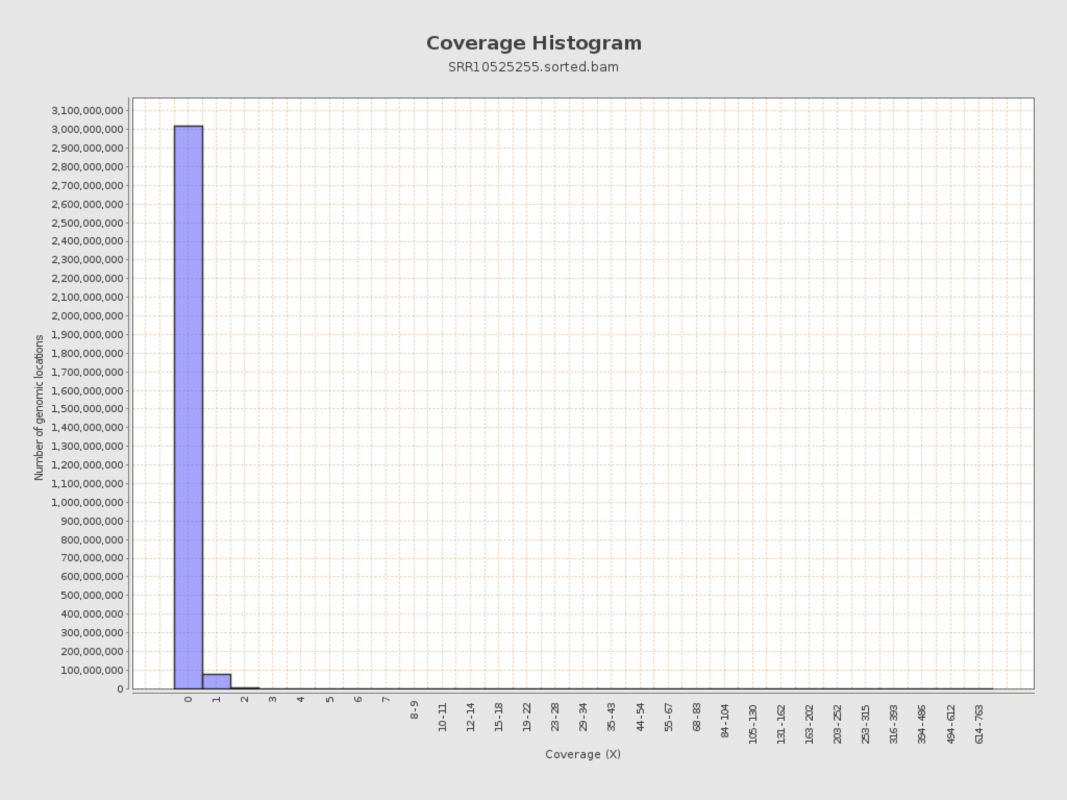
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9922938	0.0398	0.4899
chr2	243199373	7221575	0.0297	0.3636
chr3	198022430	7280321	0.0368	0.2088
chr4	191154276	4949354	0.0259	0.1813
chr5	180915260	3795079	0.021	0.157
chr6	171115067	5473309	0.032	0.2139
chr7	159138663	6356502	0.0399	0.4946

chr8	146364022	4938690	0.0337	0.2918
chr9	141213431	2847517	0.0202	0.2
chr10	135534747	4581543	0.0338	0.2882
chr11	135006516	3886858	0.0288	0.2193
chr12	133851895	3853374	0.0288	0.1872
chr13	115169878	2686154	0.0233	0.1656
chr14	107349540	3173556	0.0296	0.1903
chr15	102531392	2334685	0.0228	0.1664
chr16	90354753	2298341	0.0254	0.1864
chr17	81195210	1949247	0.024	0.1716
chr18	78077248	1844344	0.0236	0.3648
chr19	59128983	1457047	0.0246	0.357
chr20	63025520	1558357	0.0247	0.1714
chr21	48129895	1097614	0.0228	0.1683
chr22	51304566	722063	0.0141	0.127
chrMT	16571	22867	1.3799	1.2848
chrX	155270560	3518022	0.0227	0.1793
chrY	59373566	232143	0.0039	0.1203

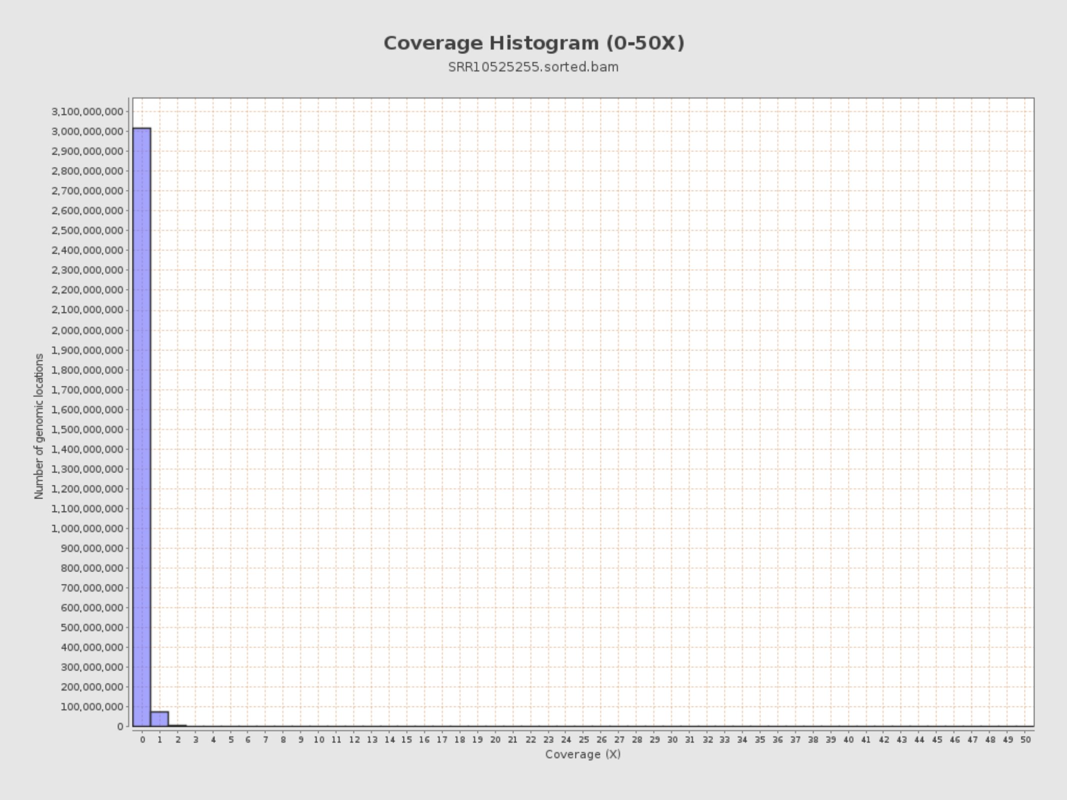
3. Results : Coverage across reference



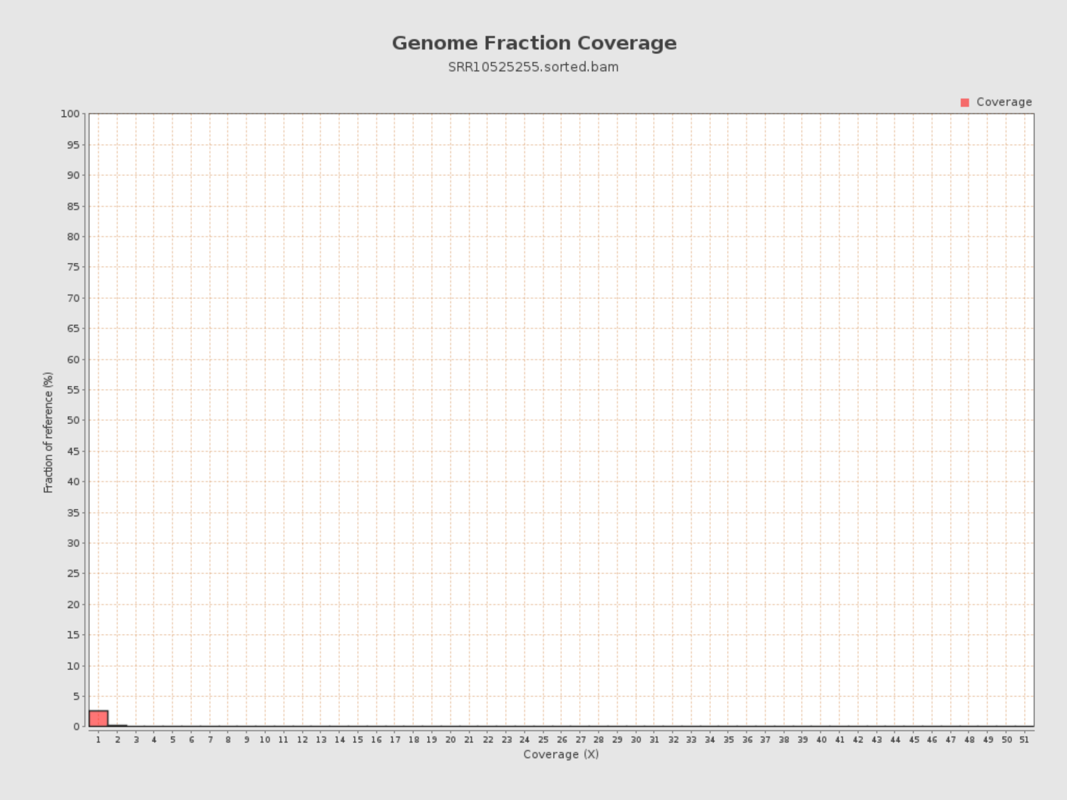
4. Results : Coverage Histogram



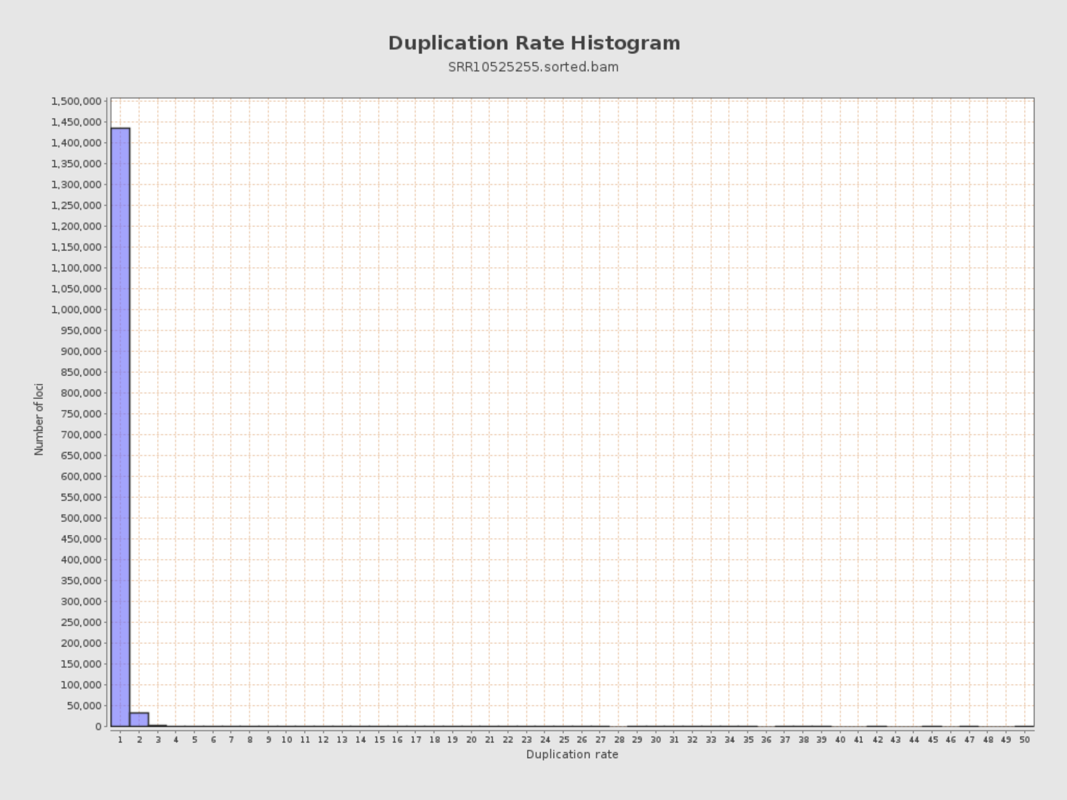
5. Results : Coverage Histogram (0-50X)



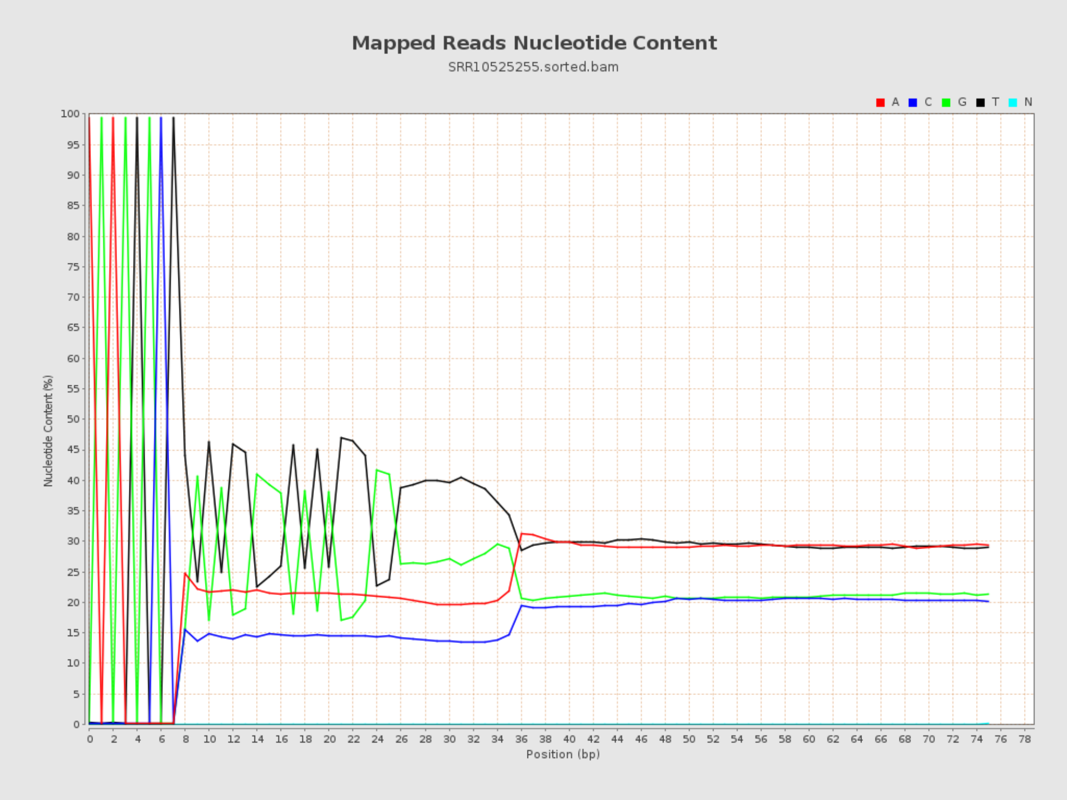
6. Results : Genome Fraction Coverage



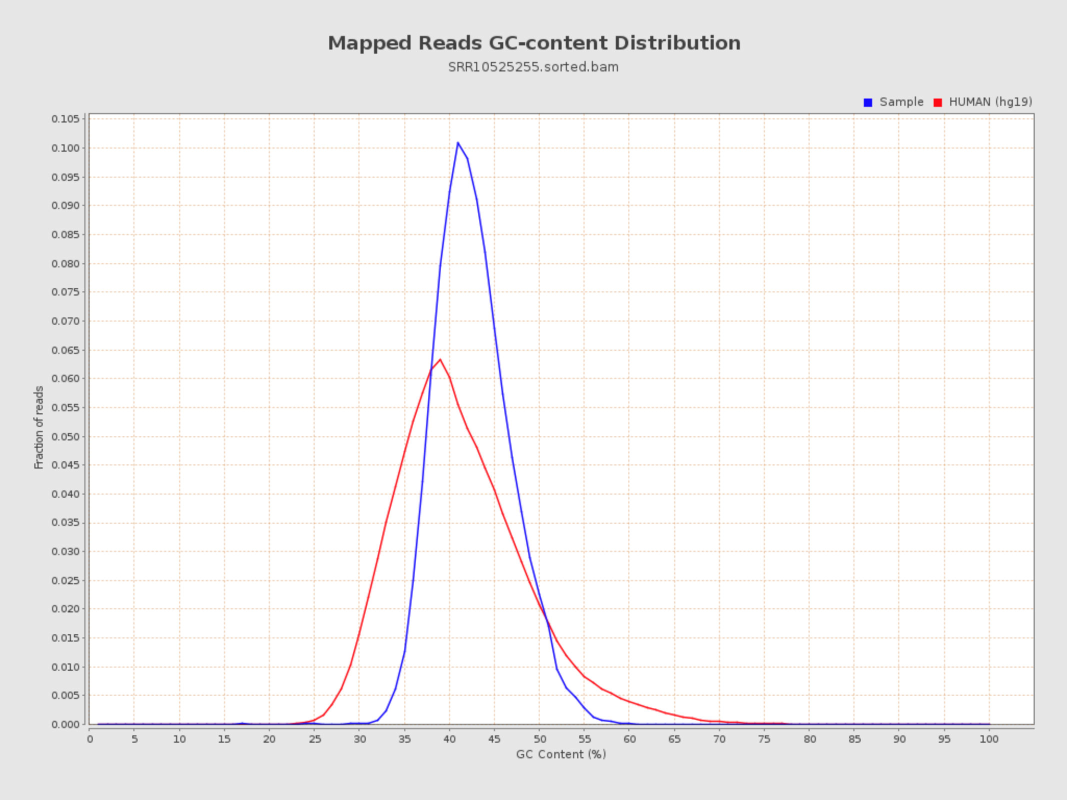
7. Results : Duplication Rate Histogram



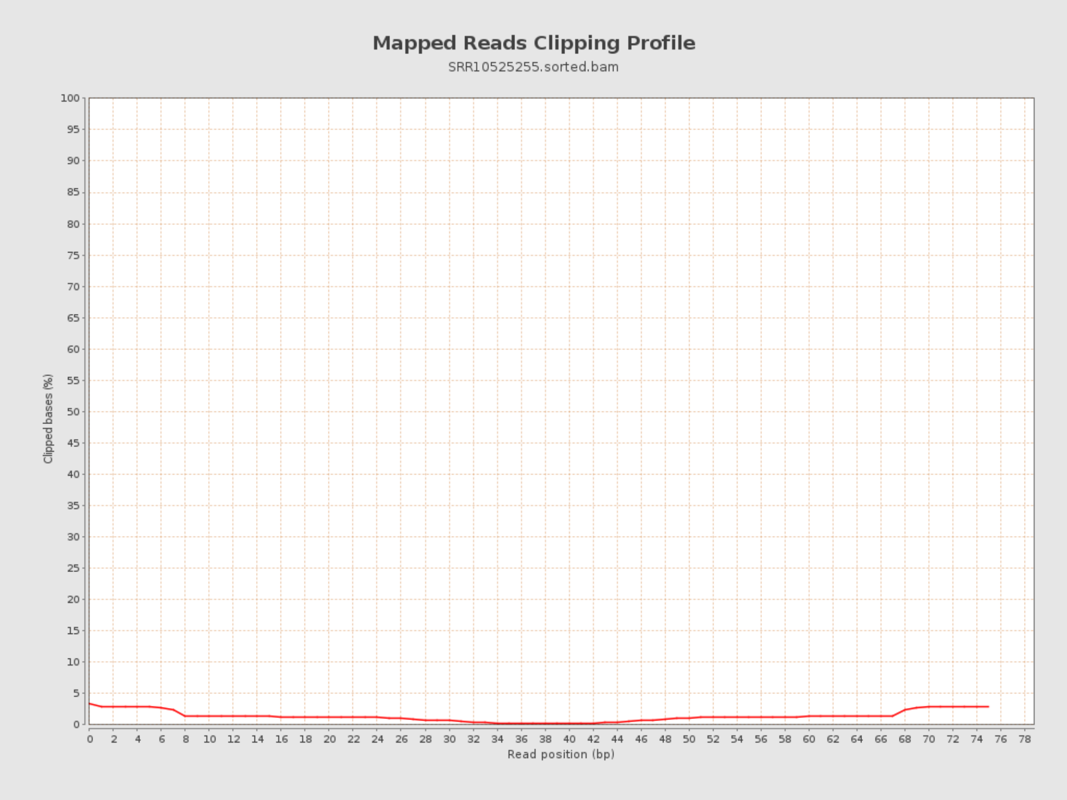
8. Results : Mapped Reads Nucleotide Content



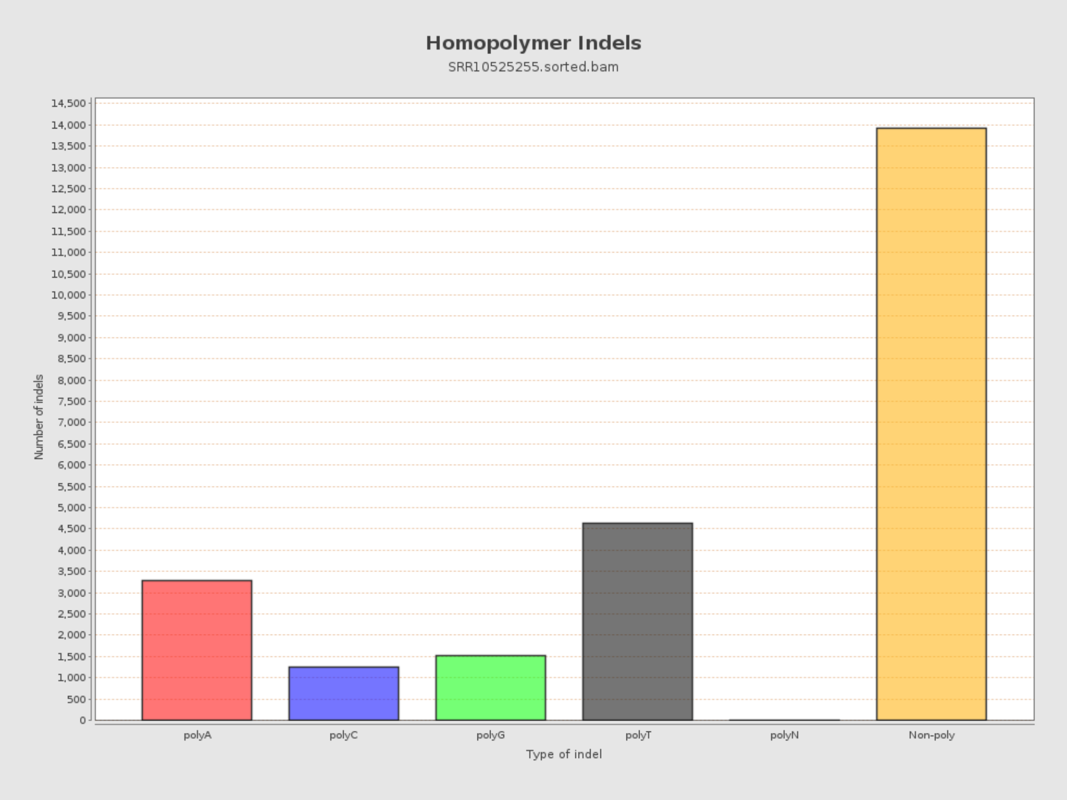
9. Results : Mapped Reads GC-content Distribution



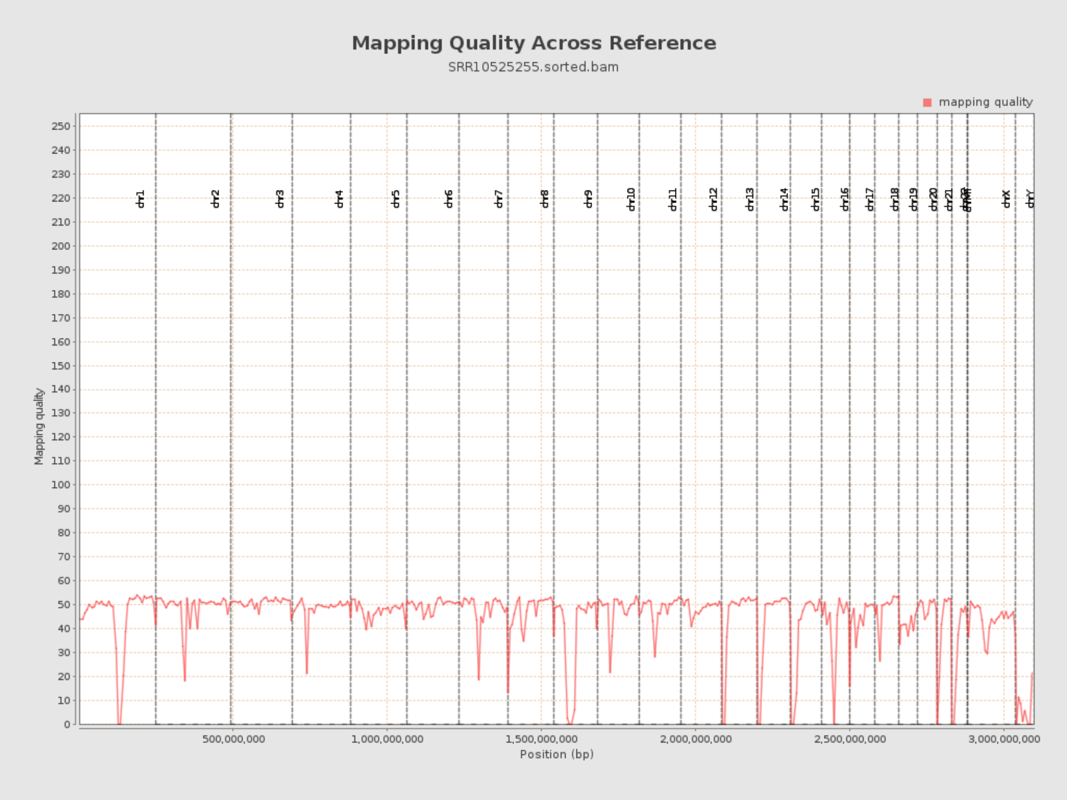
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram