Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:16:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525256.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_SRR10525256 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525256.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:16:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,366,965
Mapped reads	1,255,186 / 91.82%
Unmapped reads	111,779 / 8.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,127 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	38,149 / 2.79%
Duplication rate	2.22%
Clipped reads	1,256,658 / 91.93%

2.2. ACGT Content

Number/percentage of A's	17,656,424 / 24.18%
Number/percentage of C's	13,286,781 / 18.2%
Number/percentage of T's	23,875,372 / 32.7%
Number/percentage of G's	18,188,684 / 24.91%
Number/percentage of N's	1,357 / 0%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0236

Standard Deviation	0.236

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

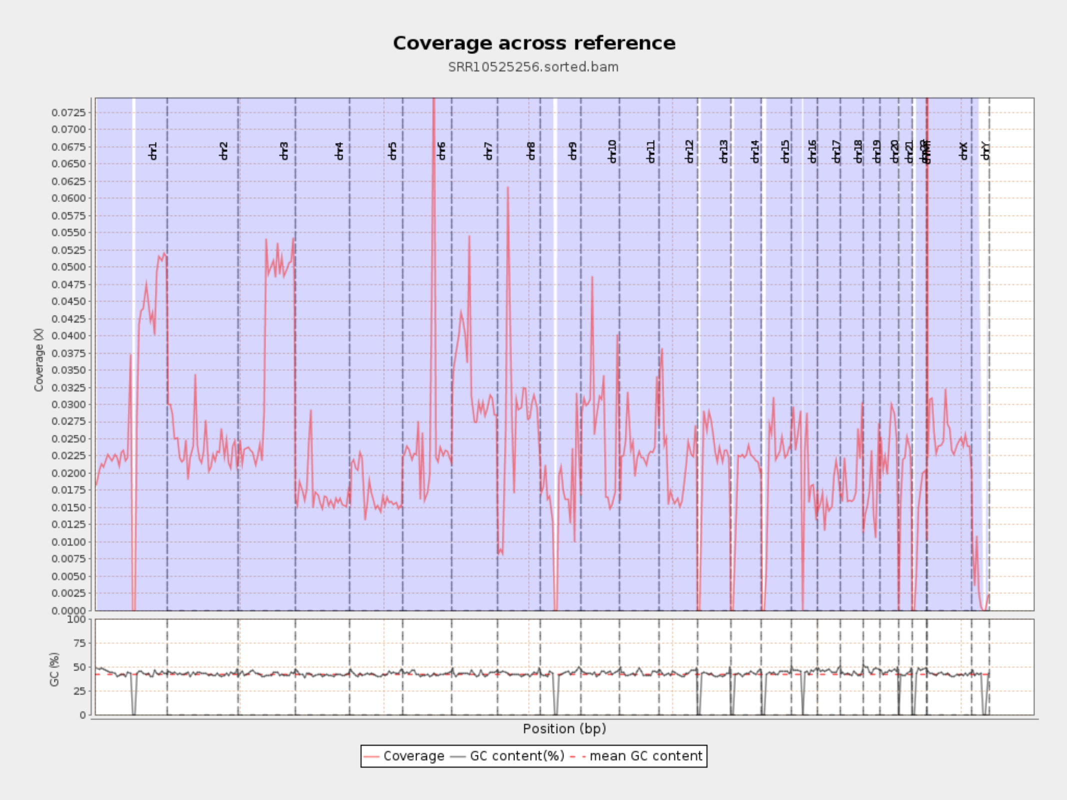
General error rate	0.51%
Mismatches	362,397
Insertions	5,032
Mapped reads with at least one insertion	0.4%
Deletions	14,680
Mapped reads with at least one deletion	1.16%
Homopolymer indels	44.88%

2.6. Chromosome stats

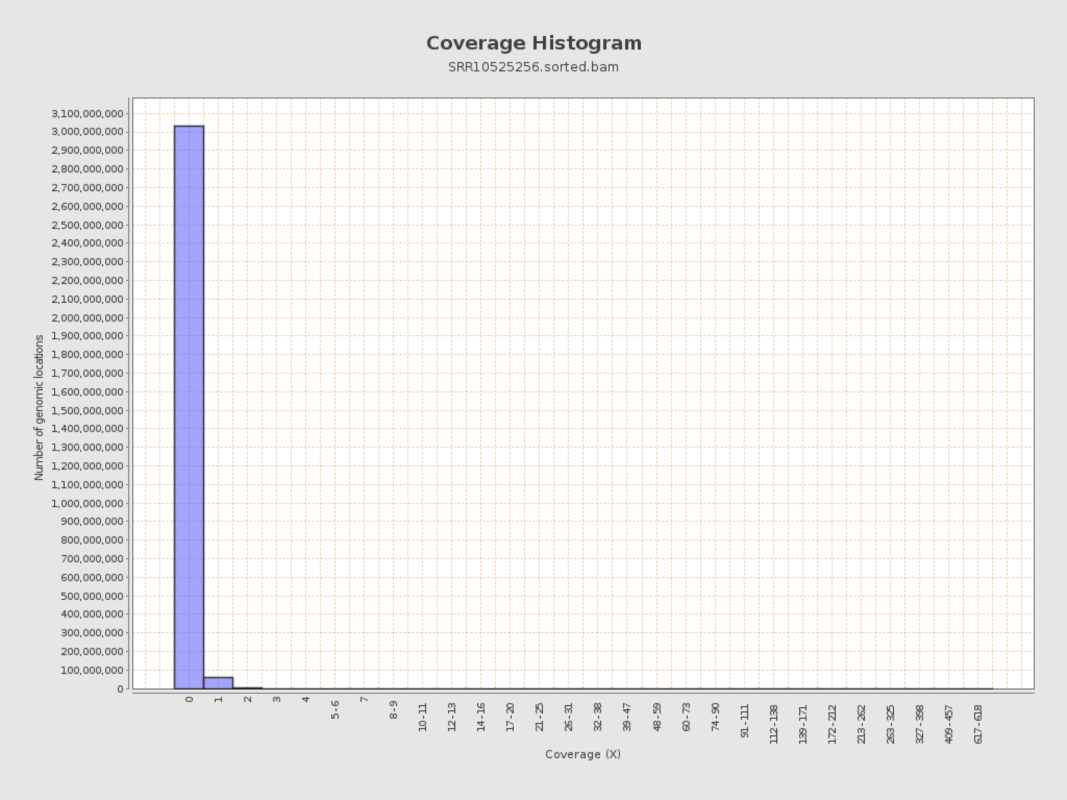
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7765561	0.0312	0.3671
chr2	243199373	5815627	0.0239	0.3016
chr3	198022430	7436119	0.0376	0.2082
chr4	191154276	3260792	0.0171	0.1455
chr5	180915260	3113347	0.0172	0.1399
chr6	171115067	4452106	0.026	0.1887
chr7	159138663	5415952	0.034	0.4489

chr8	146364022	4060033	0.0277	0.2464
chr9	141213431	2310425	0.0164	0.1639
chr10	135534747	3731378	0.0275	0.2543
chr11	135006516	3210055	0.0238	0.189
chr12	133851895	2917794	0.0218	0.1598
chr13	115169878	2443616	0.0212	0.1568
chr14	107349540	1988040	0.0185	0.1493
chr15	102531392	2015995	0.0197	0.151
chr16	90354753	1875625	0.0208	0.1656
chr17	81195210	1350630	0.0166	0.1403
chr18	78077248	1506411	0.0193	0.2849
chr19	59128983	1010838	0.0171	0.2567
chr20	63025520	1517317	0.0241	0.1688
chr21	48129895	937980	0.0195	0.153
chr22	51304566	626537	0.0122	0.1174
chrMT	16571	125392	7.567	5.0892
chrX	155270560	3941314	0.0254	0.1801
chrY	59373566	202798	0.0034	0.1004

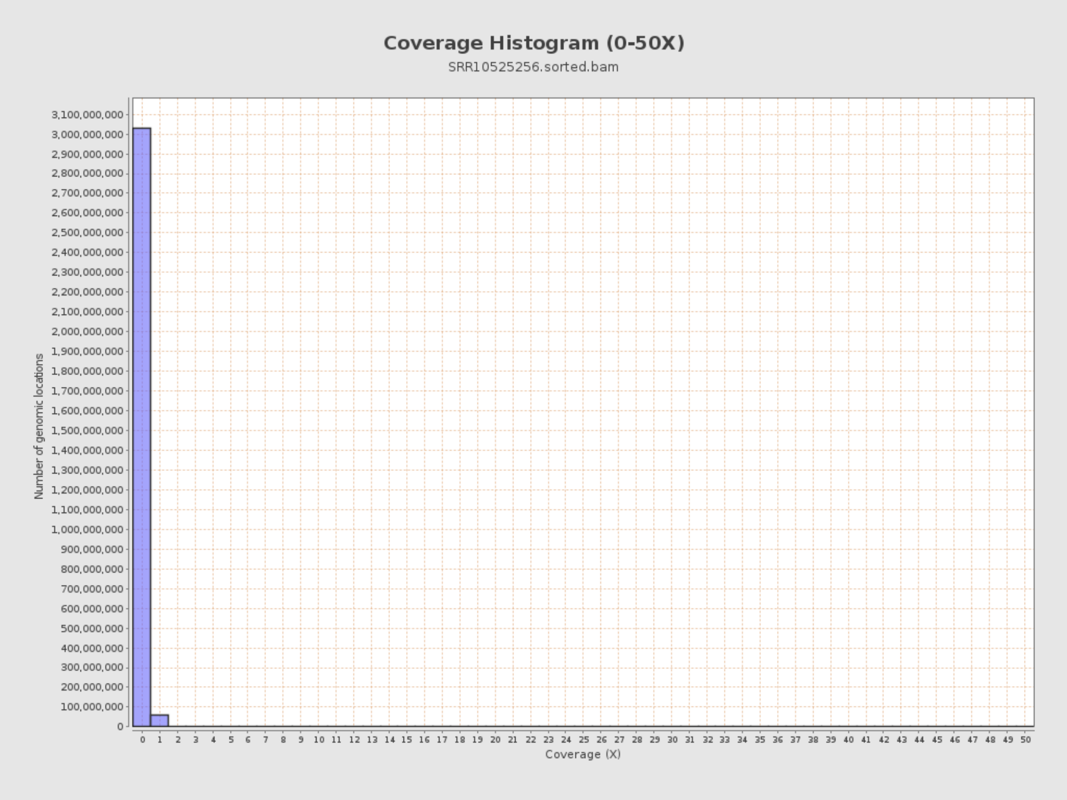
3. Results : Coverage across reference



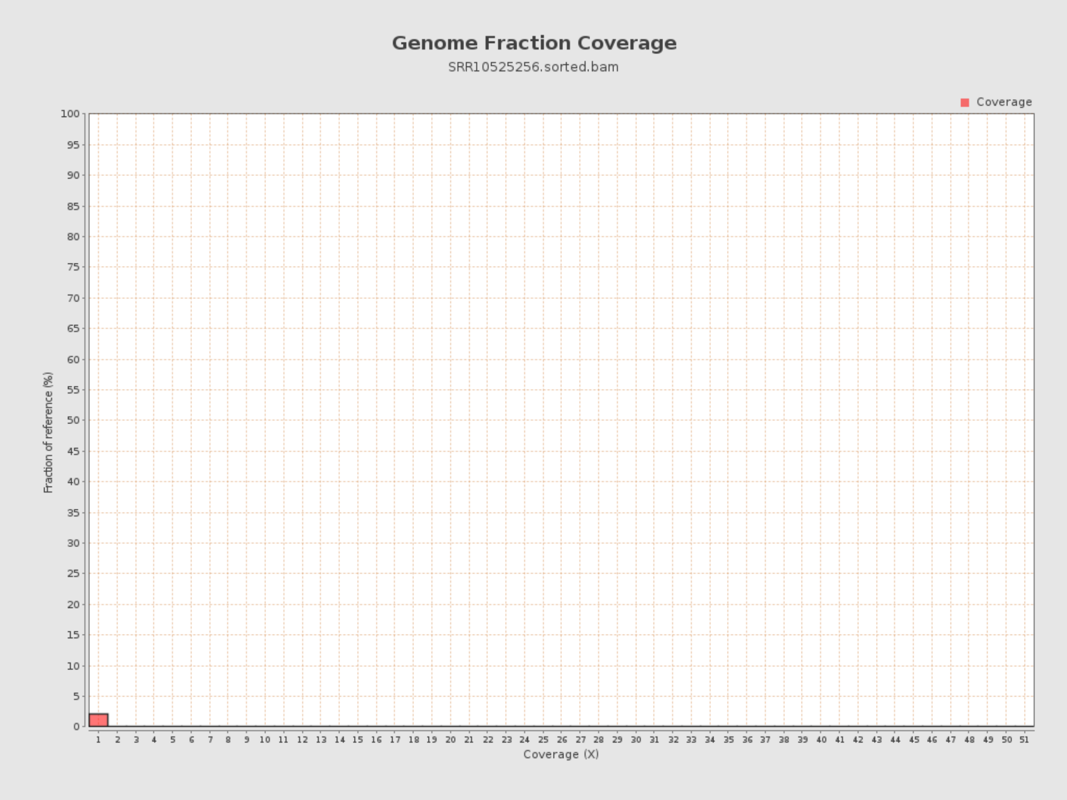
4. Results : Coverage Histogram



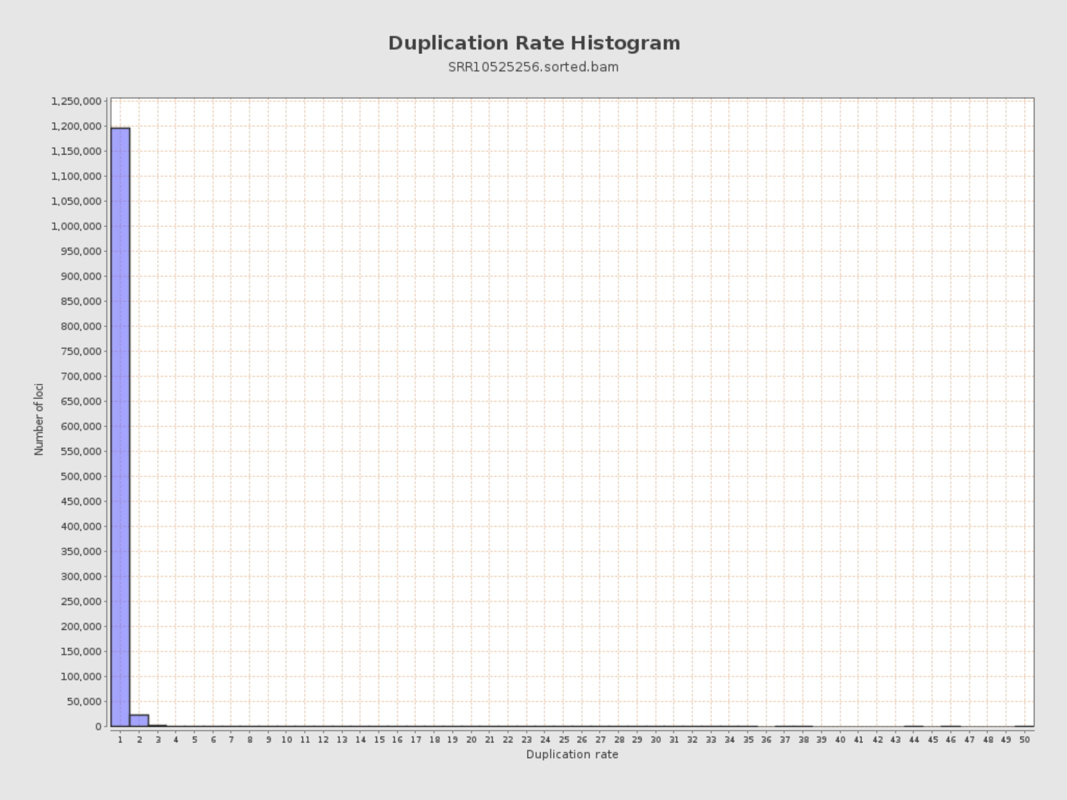
5. Results : Coverage Histogram (0-50X)



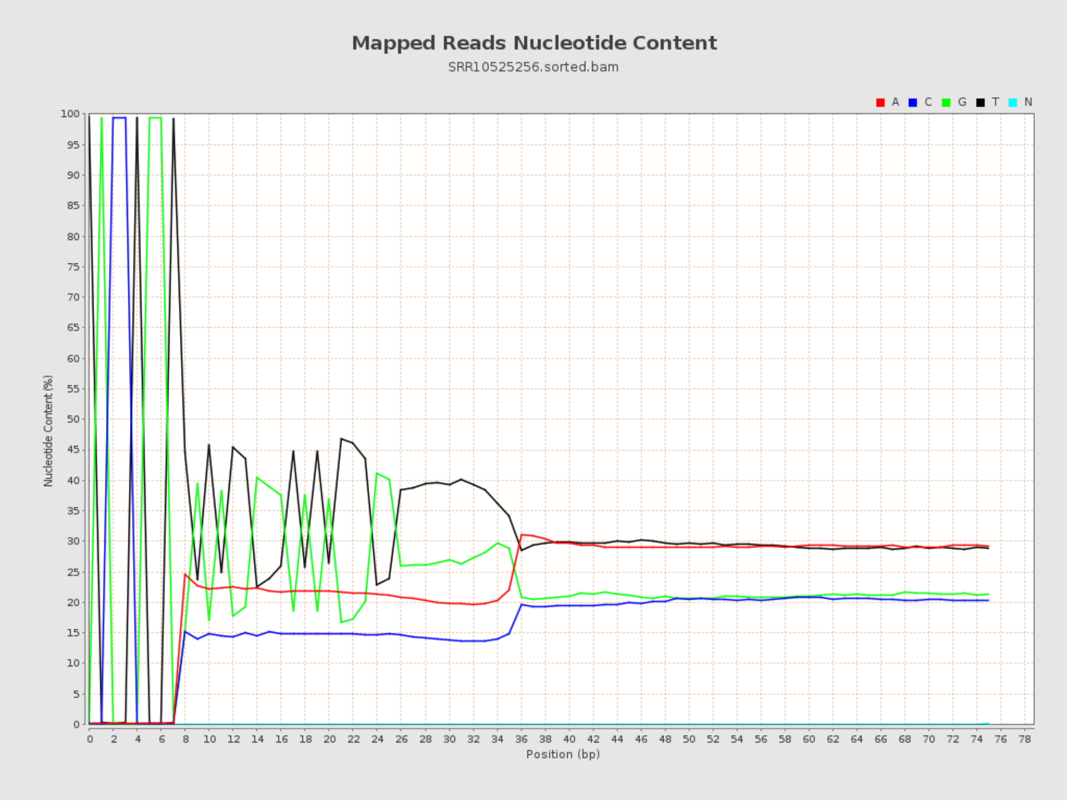
6. Results : Genome Fraction Coverage



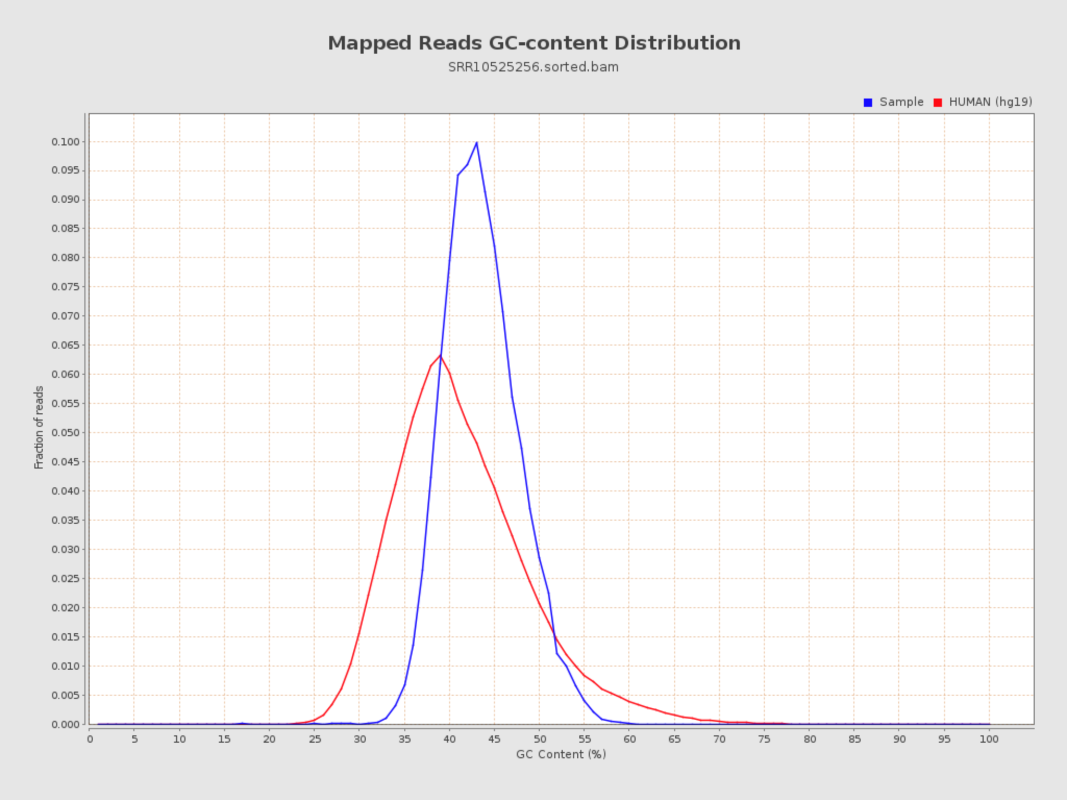
7. Results : Duplication Rate Histogram



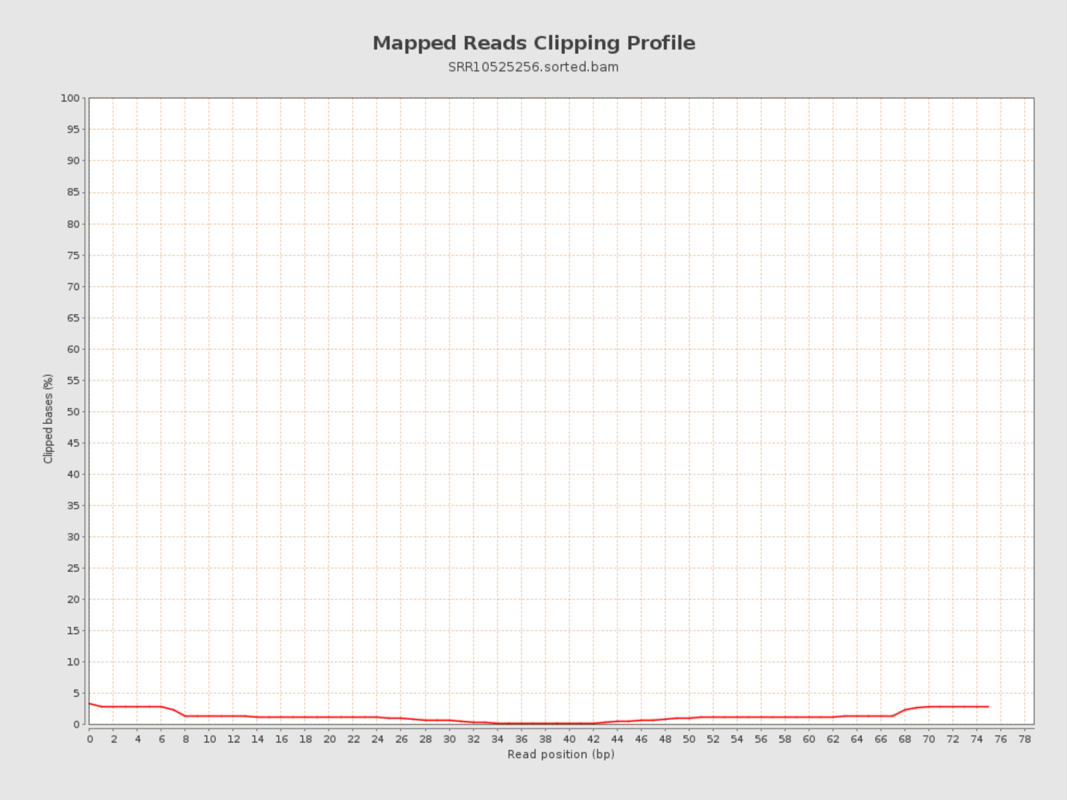
8. Results : Mapped Reads Nucleotide Content



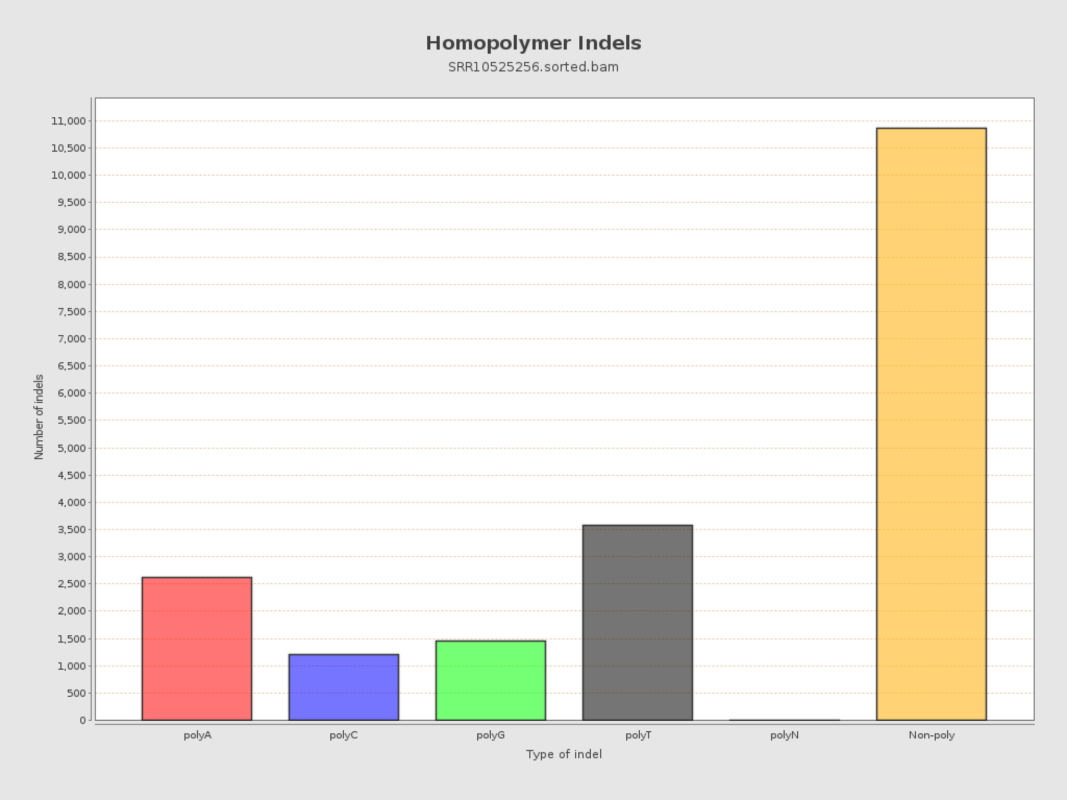
9. Results : Mapped Reads GC-content Distribution



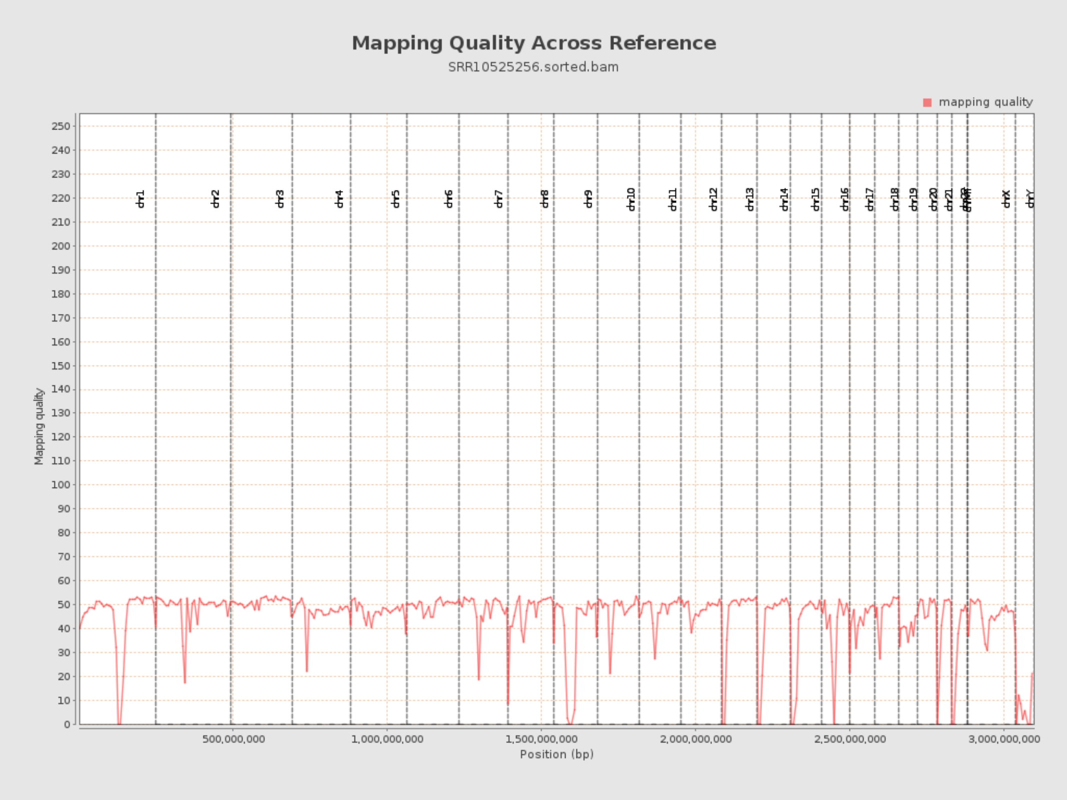
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram