Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:28:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525278.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_SRR10525278 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525278.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:28:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525278.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	855,455
Mapped reads	790,029 / 92.35%
Unmapped reads	65,426 / 7.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,096 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	20,938 / 2.45%
Duplication rate	1.95%
Clipped reads	792,163 / 92.6%

2.2. ACGT Content

Number/percentage of A's	11,245,779 / 24.32%
Number/percentage of C's	8,512,661 / 18.41%
Number/percentage of T's	15,067,781 / 32.58%
Number/percentage of G's	11,421,926 / 24.7%
Number/percentage of N's	1,025 / 0%
GC Percentage	43.1%

2.3. Coverage

Mean	0.0149

Standard Deviation	0.1734

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

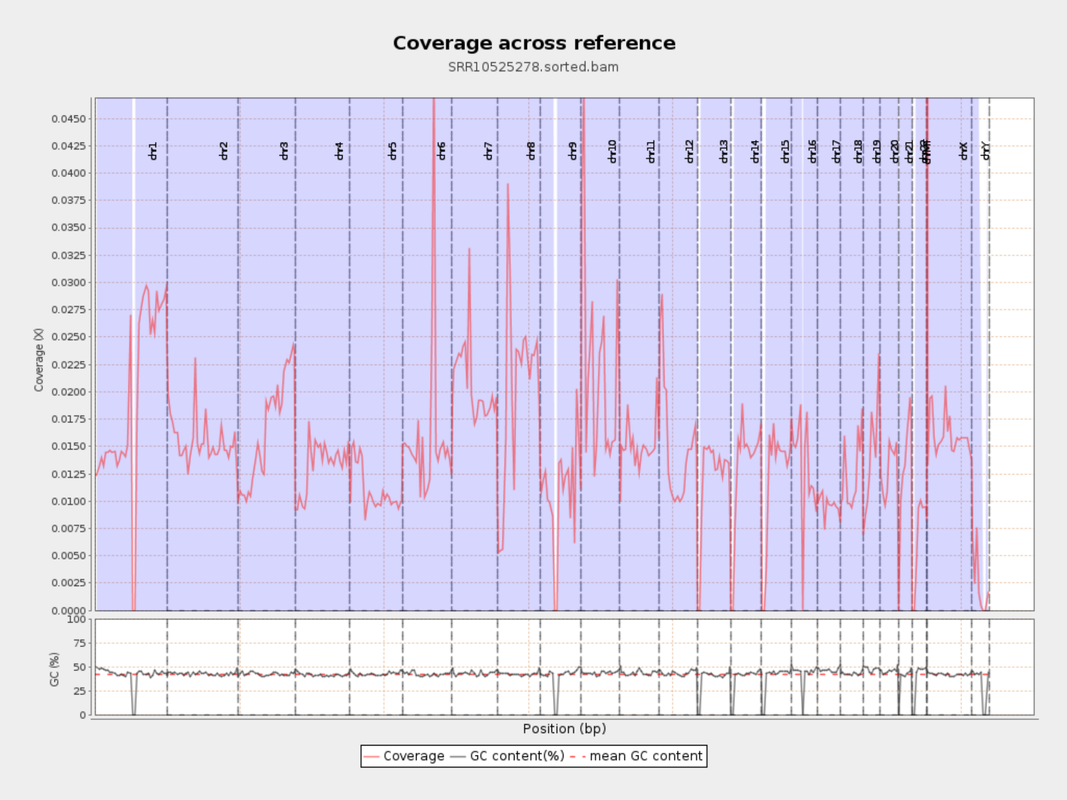
General error rate	0.51%
Mismatches	229,040
Insertions	2,842
Mapped reads with at least one insertion	0.36%
Deletions	9,606
Mapped reads with at least one deletion	1.21%
Homopolymer indels	42.83%

2.6. Chromosome stats

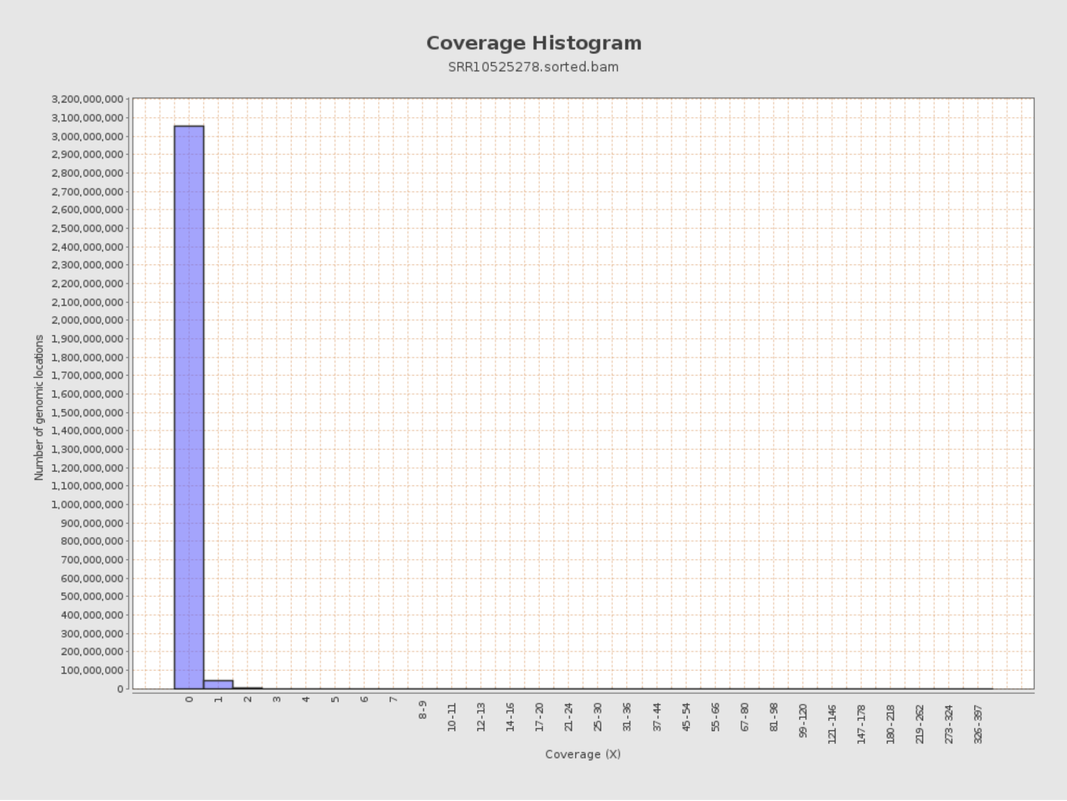
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4807207	0.0193	0.2919
chr2	243199373	3764785	0.0155	0.2107
chr3	198022430	3258333	0.0165	0.1341
chr4	191154276	2546300	0.0133	0.1258
chr5	180915260	2004831	0.0111	0.1103
chr6	171115067	2766124	0.0162	0.1401
chr7	159138663	3315856	0.0208	0.2721

chr8	146364022	2978267	0.0203	0.1962
chr9	141213431	1521361	0.0108	0.1268
chr10	135534747	3031133	0.0224	0.1848
chr11	135006516	2032562	0.0151	0.1543
chr12	133851895	2020194	0.0151	0.1293
chr13	115169878	1382029	0.012	0.1148
chr14	107349540	1388210	0.0129	0.12
chr15	102531392	1216666	0.0119	0.1145
chr16	90354753	1175390	0.013	0.1267
chr17	81195210	781546	0.0096	0.1045
chr18	78077248	961843	0.0123	0.2376
chr19	59128983	854133	0.0144	0.2043
chr20	63025520	805750	0.0128	0.1195
chr21	48129895	637676	0.0132	0.1249
chr22	51304566	344948	0.0067	0.0851
chrMT	16571	28191	1.7012	1.6627
chrX	155270560	2500977	0.0161	0.139
chrY	59373566	140192	0.0024	0.0789

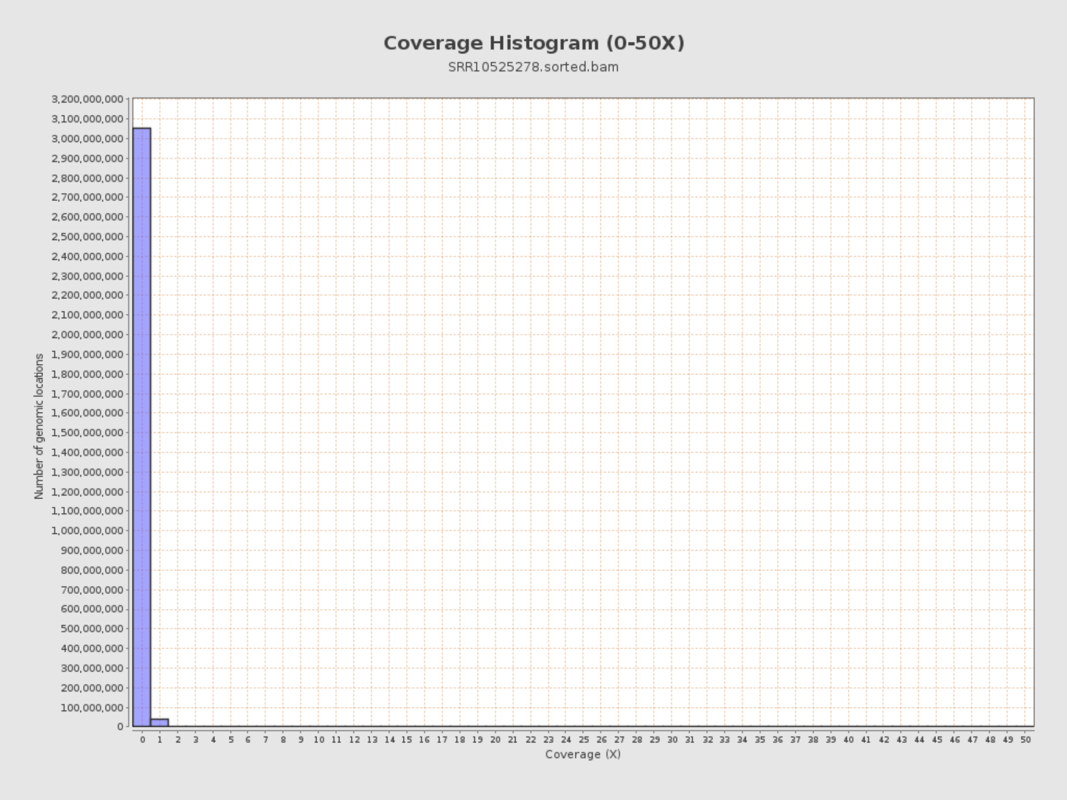
3. Results : Coverage across reference



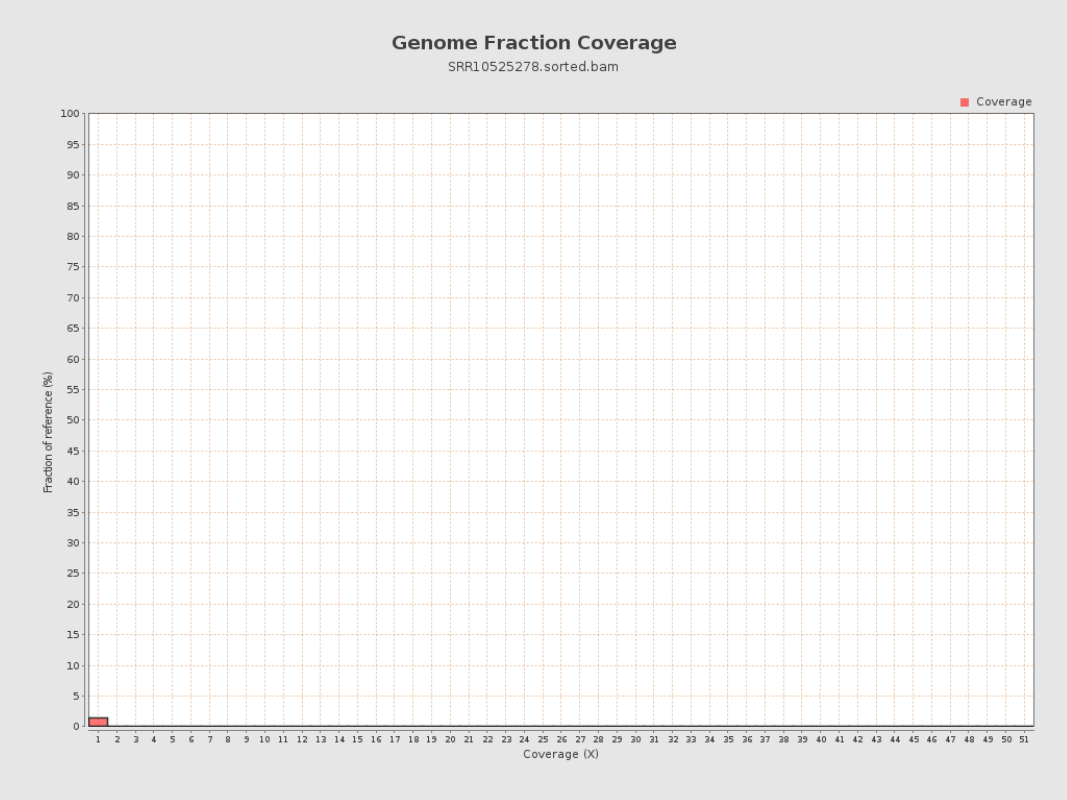
4. Results : Coverage Histogram



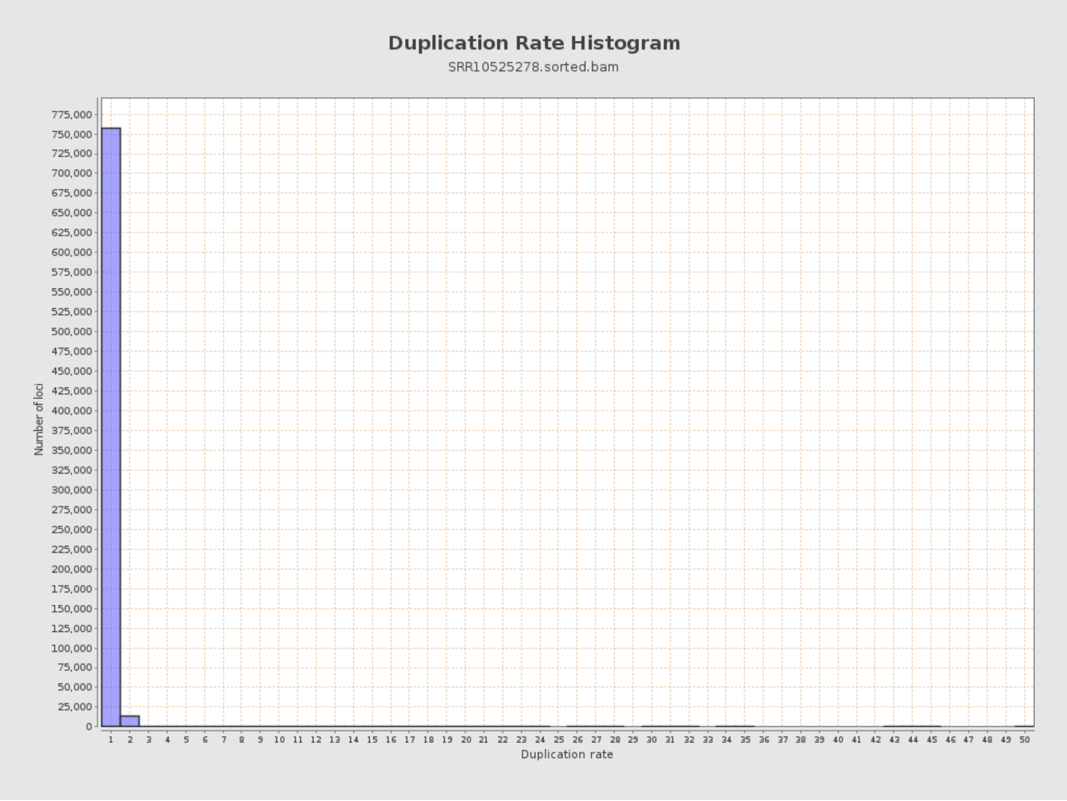
5. Results : Coverage Histogram (0-50X)



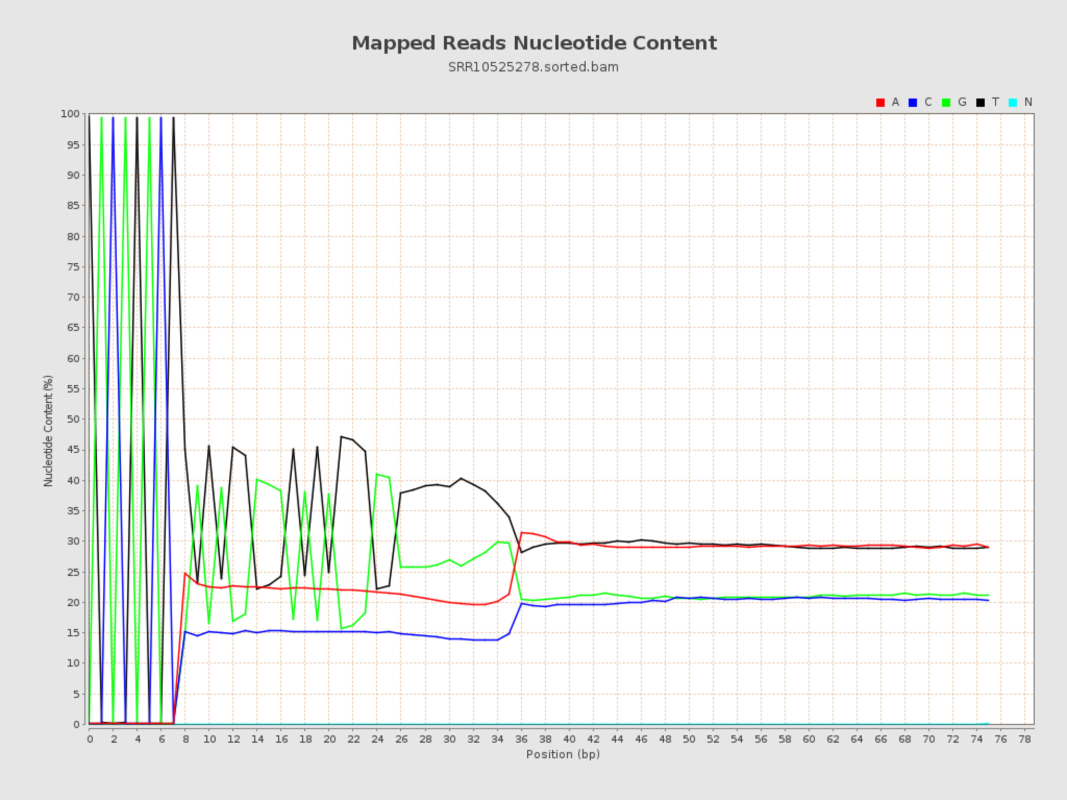
6. Results : Genome Fraction Coverage



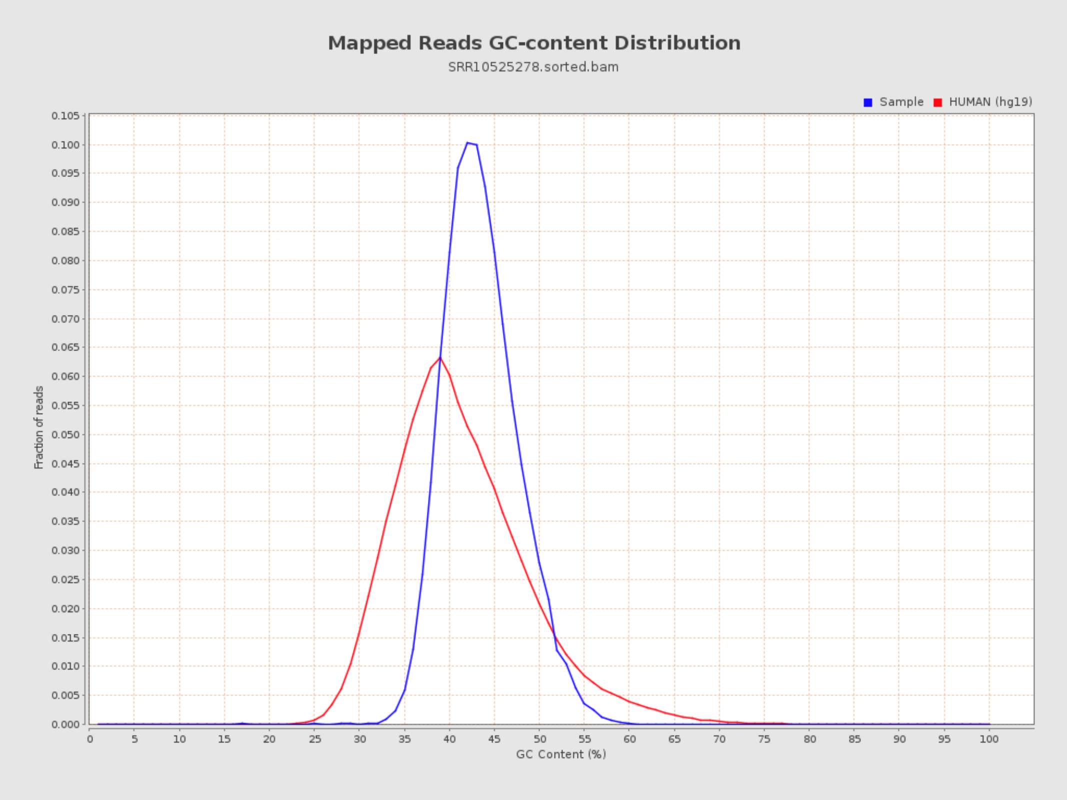
7. Results : Duplication Rate Histogram



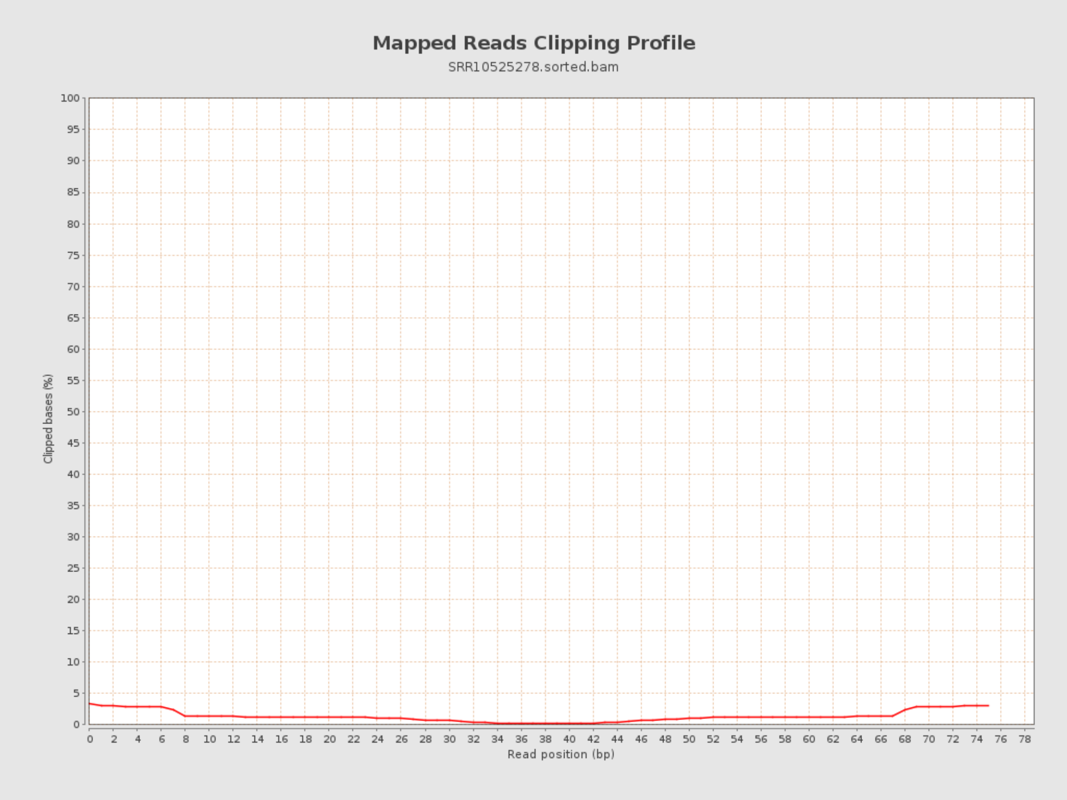
8. Results : Mapped Reads Nucleotide Content



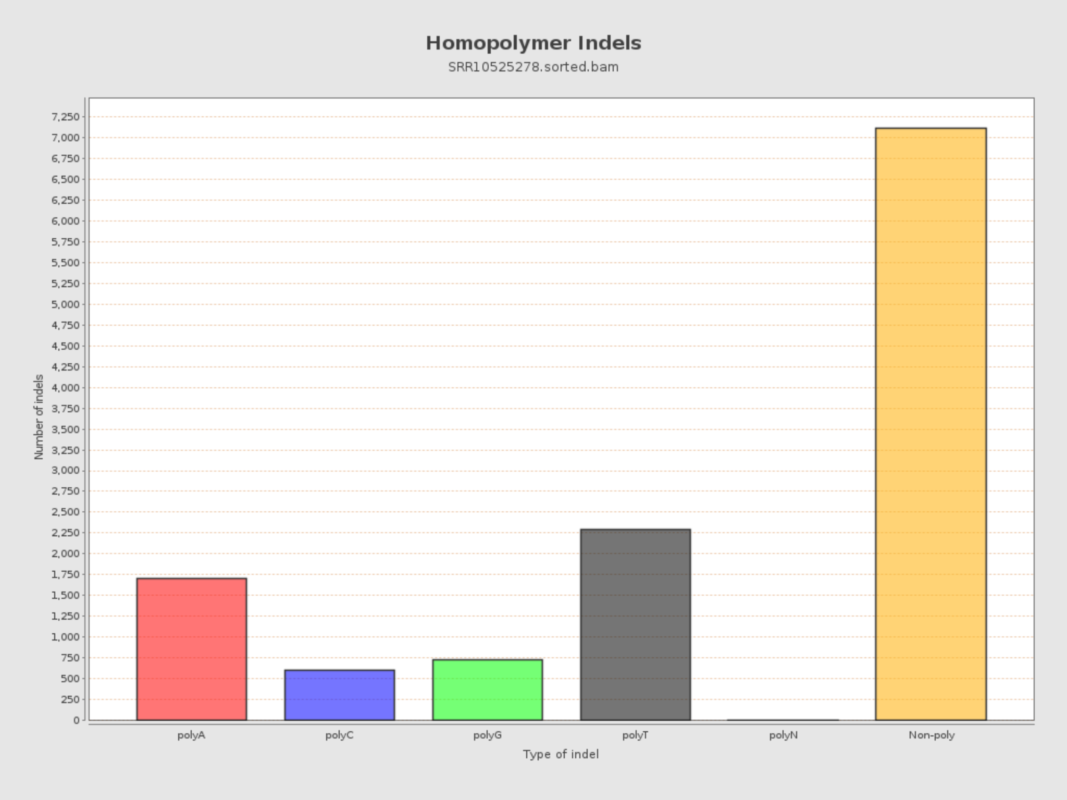
9. Results : Mapped Reads GC-content Distribution



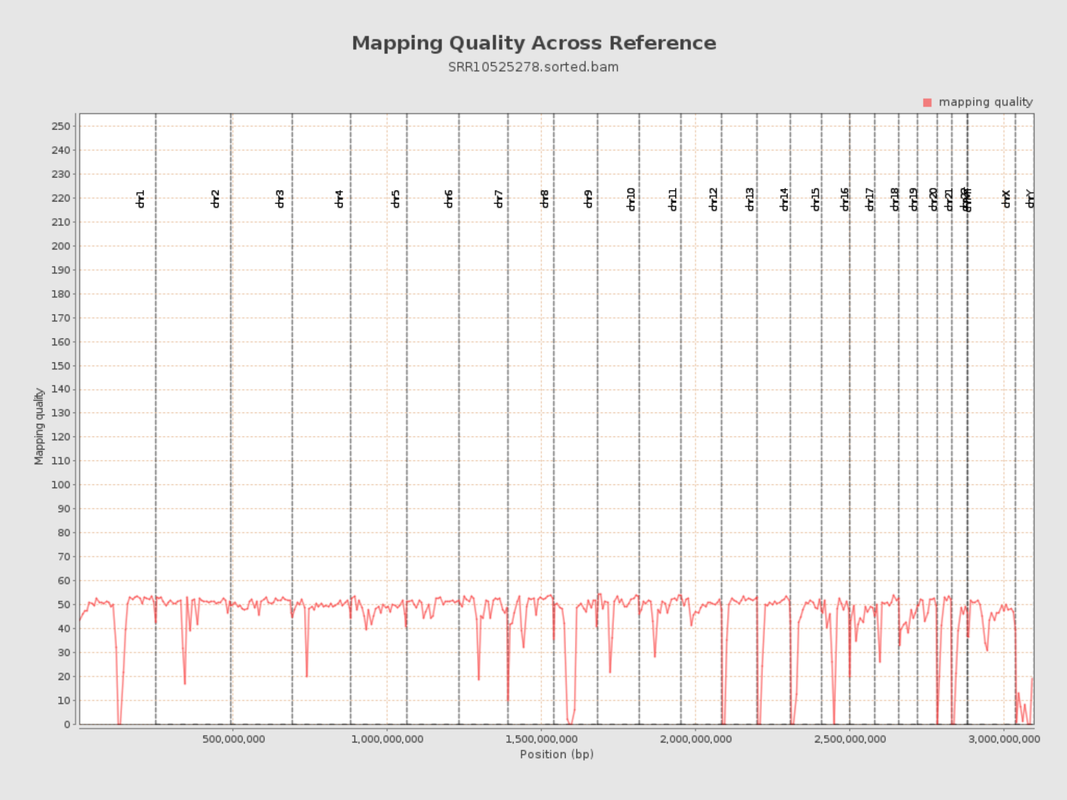
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram