Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:16:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525014.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_SRR10525014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525014.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:16:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,066,093
Mapped reads	956,636 / 89.73%
Unmapped reads	109,457 / 10.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,139 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	21,739 / 2.04%
Duplication rate	1.6%
Clipped reads	959,061 / 89.96%

2.2. ACGT Content

Number/percentage of A's	13,945,111 / 25.33%
Number/percentage of C's	10,206,014 / 18.54%
Number/percentage of T's	17,627,965 / 32.02%
Number/percentage of G's	13,271,624 / 24.11%
Number/percentage of N's	603 / 0%
GC Percentage	42.65%

2.3. Coverage

Mean	0.0178

Standard Deviation	0.1815

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Mismatches and indels

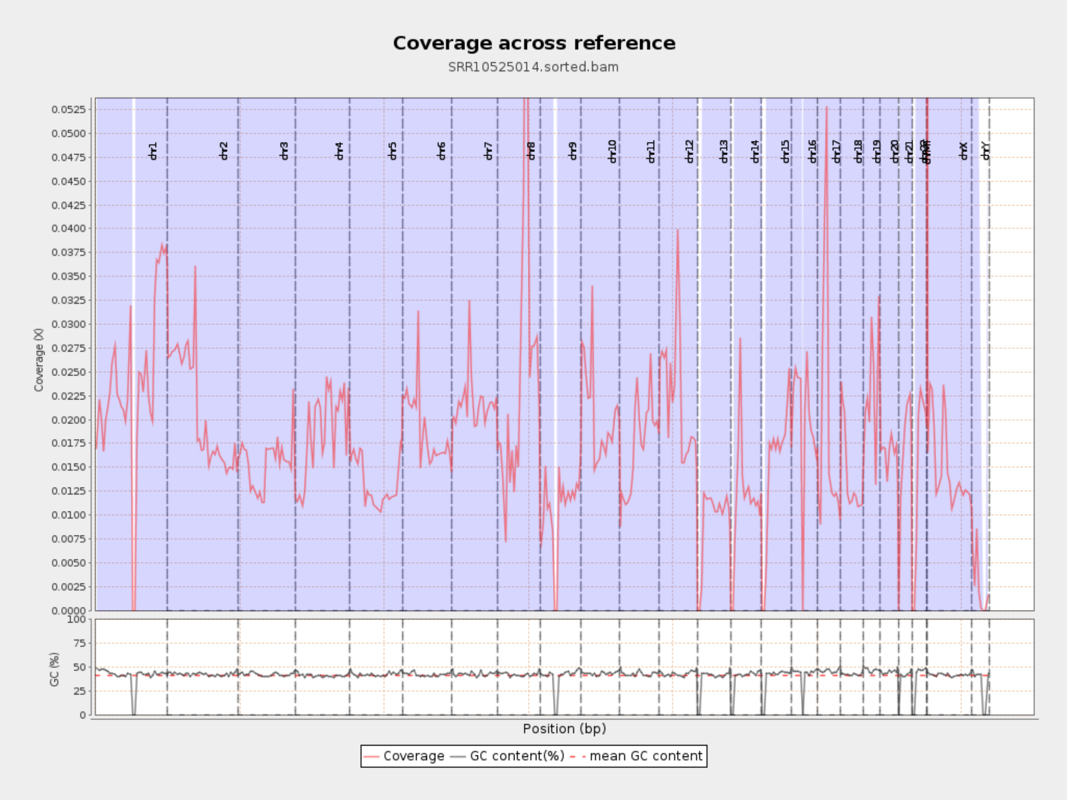
General error rate	0.52%
Mismatches	277,872
Insertions	3,264
Mapped reads with at least one insertion	0.34%
Deletions	10,464
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.11%

2.6. Chromosome stats

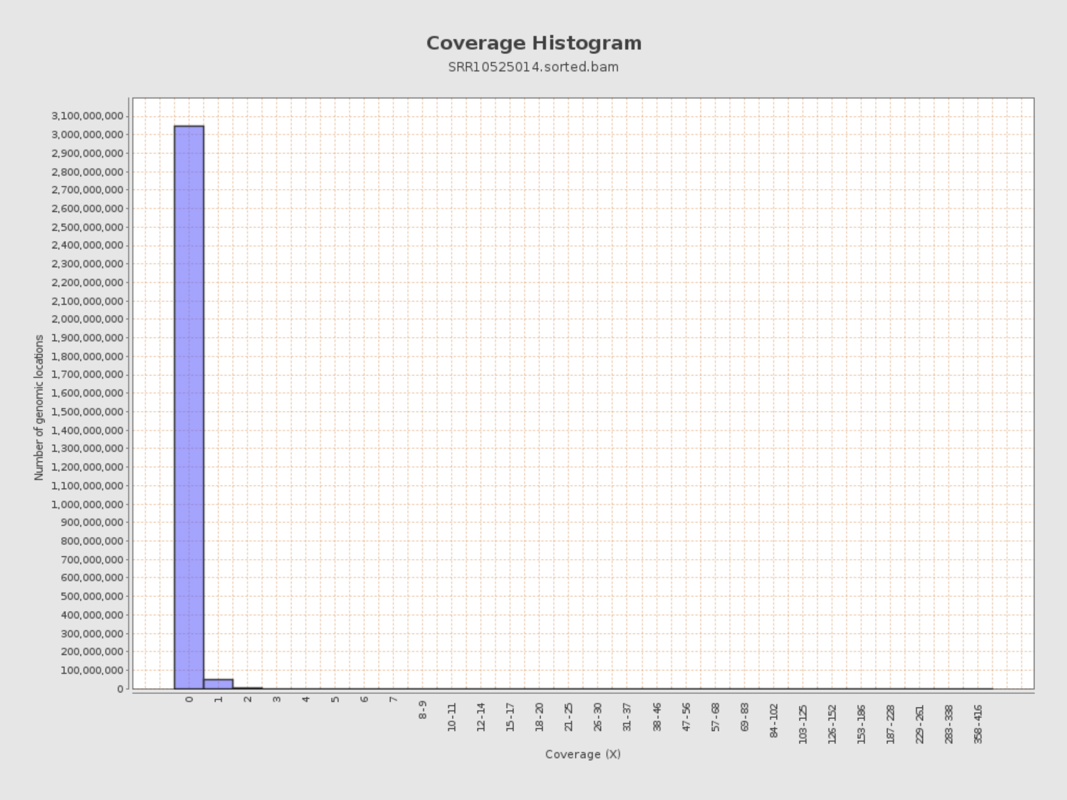
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5904315	0.0237	0.3144
chr2	243199373	5085257	0.0209	0.2043
chr3	198022430	3073389	0.0155	0.1307
chr4	191154276	3571358	0.0187	0.1504
chr5	180915260	2407190	0.0133	0.122
chr6	171115067	3245039	0.019	0.1861
chr7	159138663	3481803	0.0219	0.2282

chr8	146364022	3759248	0.0257	0.1955
chr9	141213431	1467682	0.0104	0.1376
chr10	135534747	2807284	0.0207	0.1845
chr11	135006516	2367825	0.0175	0.169
chr12	133851895	3008957	0.0225	0.1581
chr13	115169878	1076215	0.0093	0.1024
chr14	107349540	1253206	0.0117	0.1161
chr15	102531392	1548141	0.0151	0.138
chr16	90354753	1788623	0.0198	0.1518
chr17	81195210	1630427	0.0201	0.1962
chr18	78077248	1100267	0.0141	0.2052
chr19	59128983	1373951	0.0232	0.2204
chr20	63025520	1042784	0.0165	0.1353
chr21	48129895	800664	0.0166	0.1399
chr22	51304566	762669	0.0149	0.127
chrMT	16571	9372	0.5656	0.8697
chrX	155270560	2353721	0.0152	0.1449
chrY	59373566	149584	0.0025	0.0696

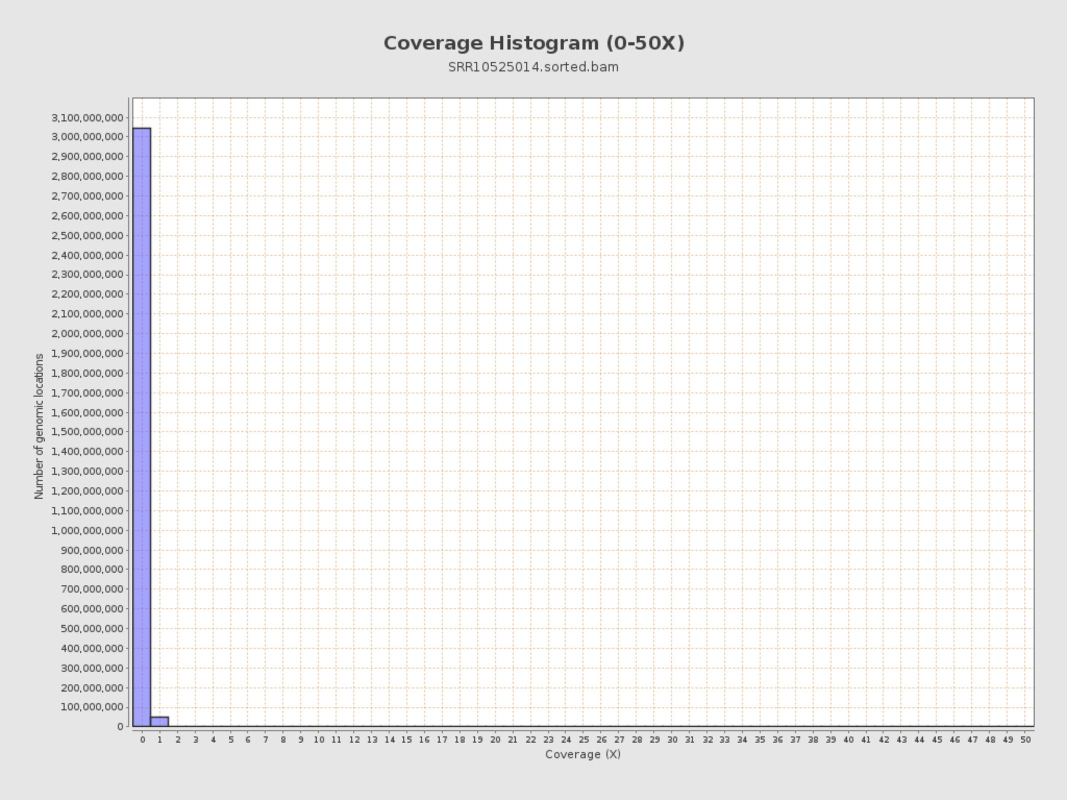
3. Results : Coverage across reference



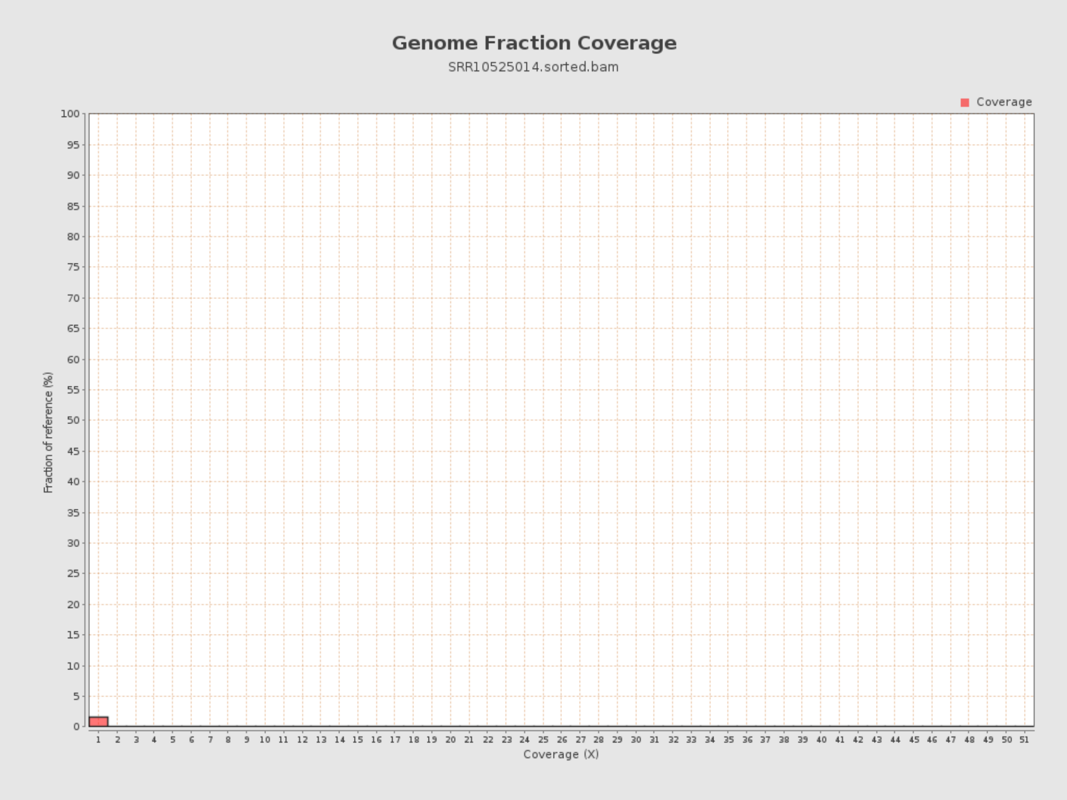
4. Results : Coverage Histogram



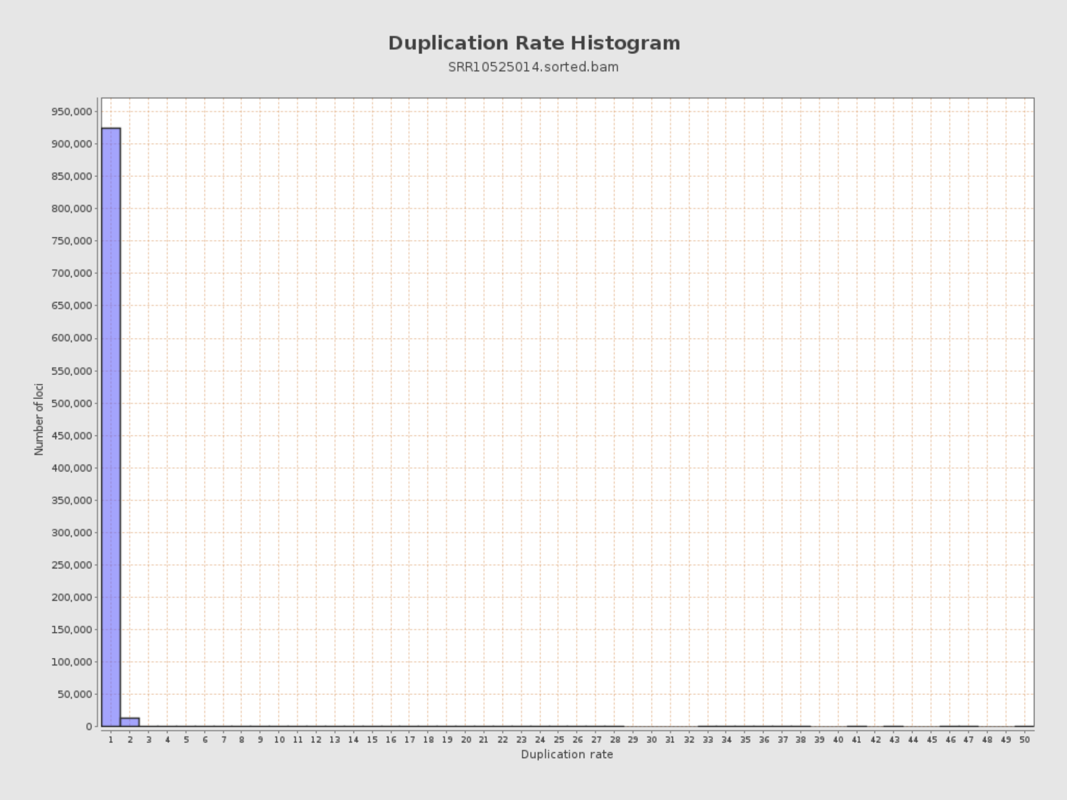
5. Results : Coverage Histogram (0-50X)



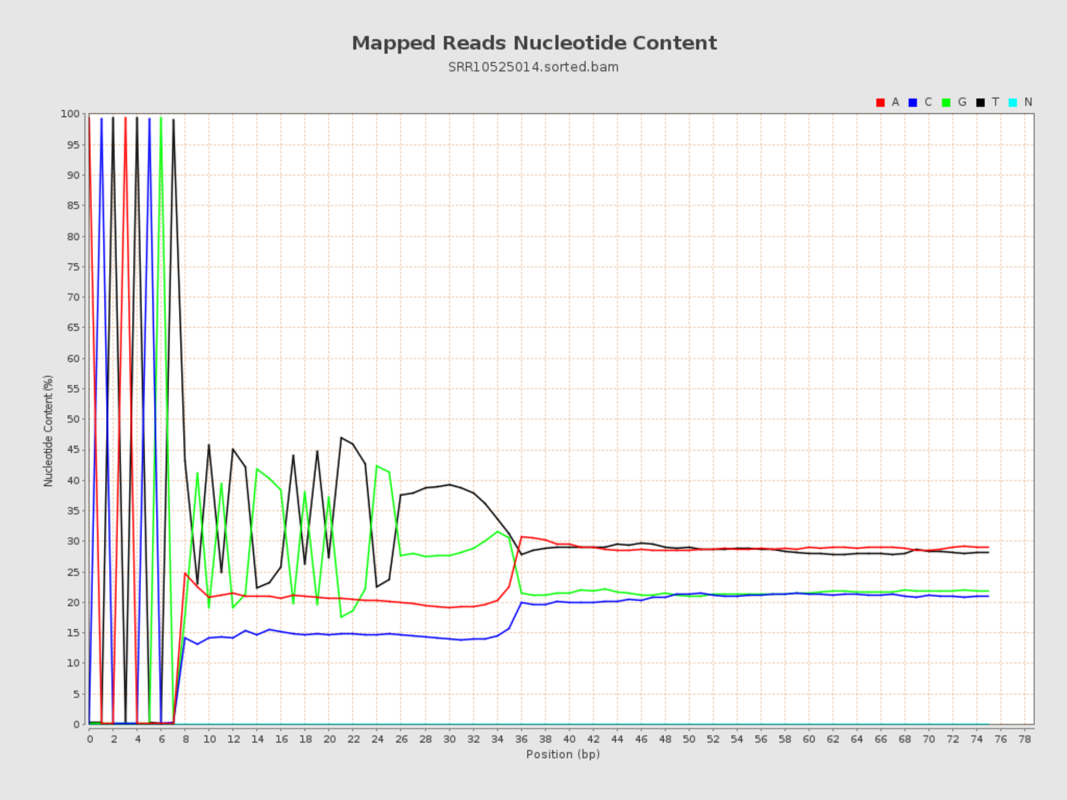
6. Results : Genome Fraction Coverage



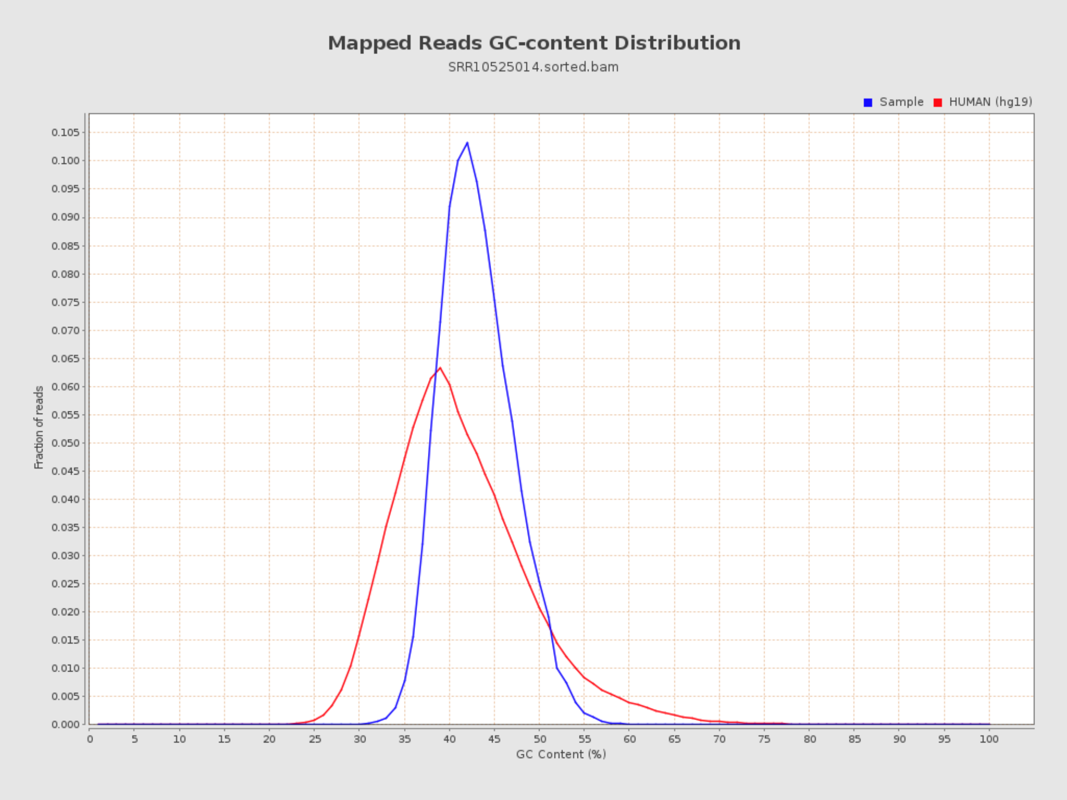
7. Results : Duplication Rate Histogram



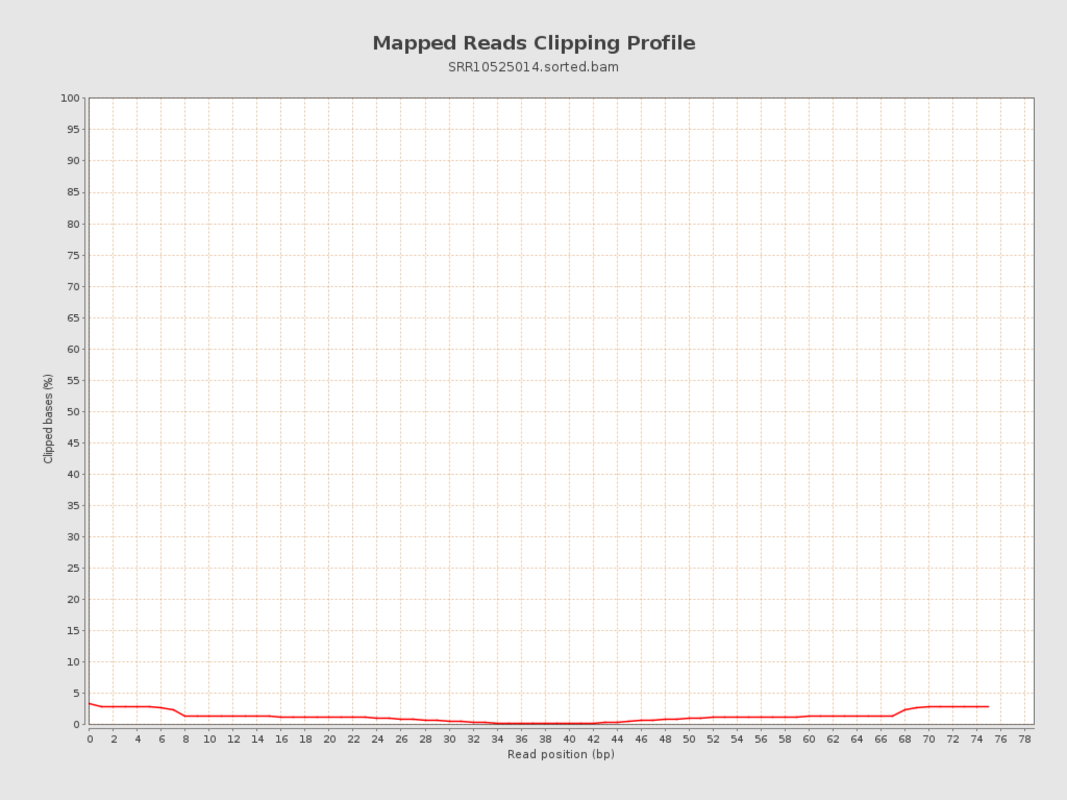
8. Results : Mapped Reads Nucleotide Content



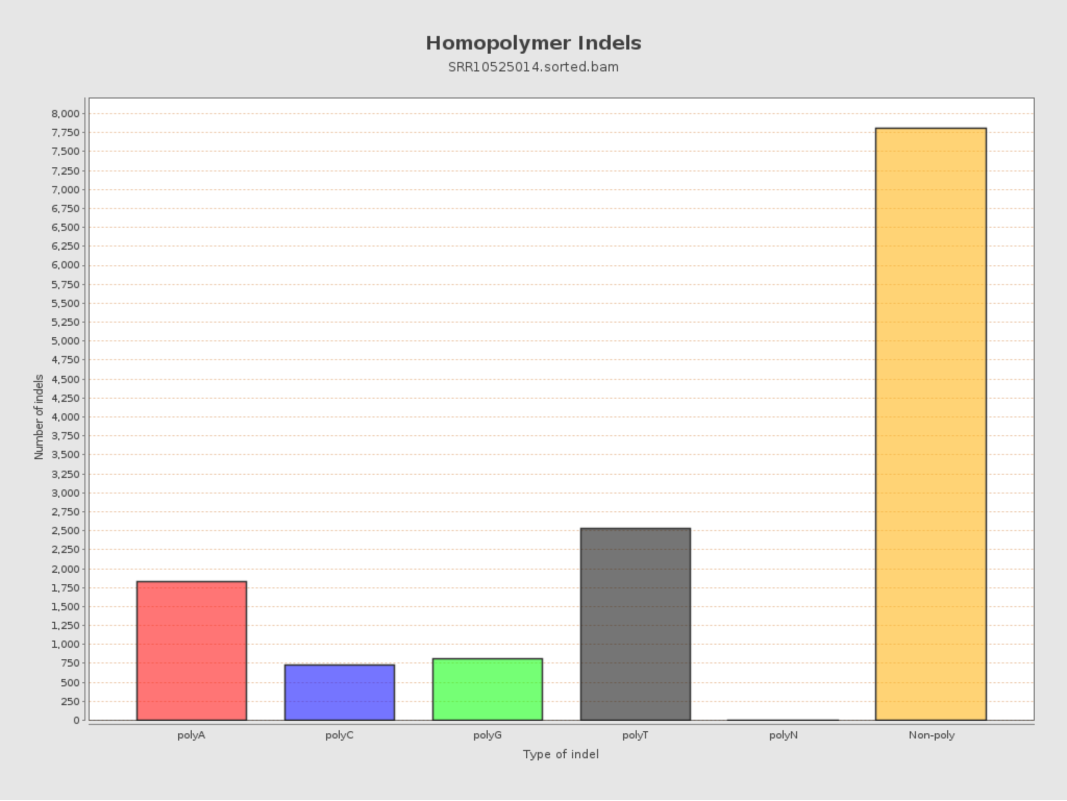
9. Results : Mapped Reads GC-content Distribution



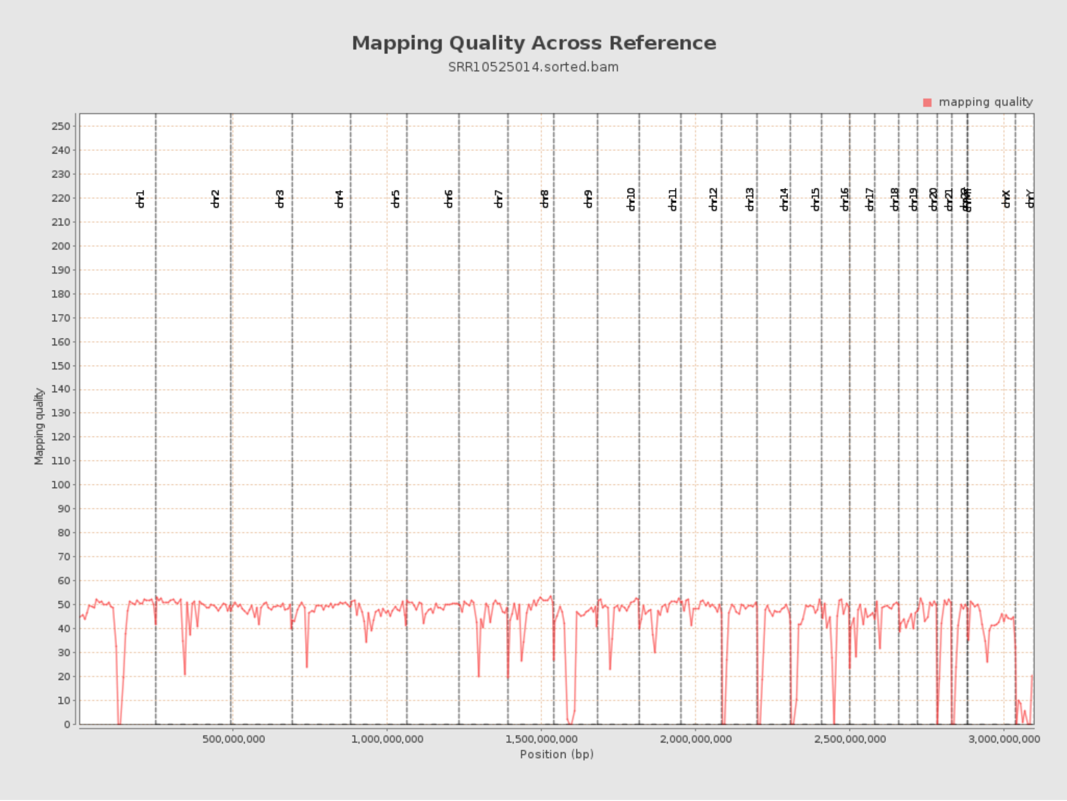
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram