Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:31:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525239.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_SRR10525239 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525239.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:31:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525239.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	939,287
Mapped reads	853,768 / 90.9%
Unmapped reads	85,519 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,122 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	23,537 / 2.51%
Duplication rate	2.05%
Clipped reads	854,411 / 90.96%

2.2. ACGT Content

Number/percentage of A's	11,657,436 / 23.87%
Number/percentage of C's	8,242,557 / 16.88%
Number/percentage of T's	16,636,205 / 34.06%
Number/percentage of G's	12,307,394 / 25.2%
Number/percentage of N's	996 / 0%
GC Percentage	42.07%

2.3. Coverage

Mean	0.0158

Standard Deviation	0.1785

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

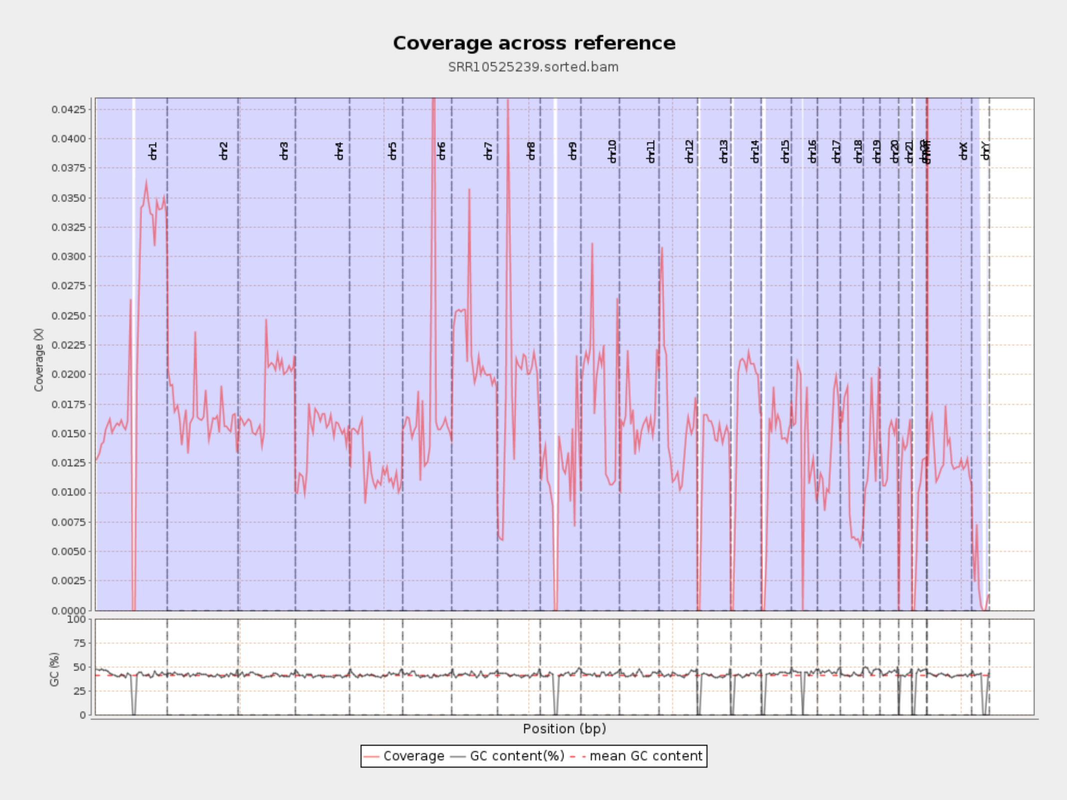
General error rate	0.52%
Mismatches	250,364
Insertions	3,408
Mapped reads with at least one insertion	0.4%
Deletions	10,635
Mapped reads with at least one deletion	1.24%
Homopolymer indels	44.39%

2.6. Chromosome stats

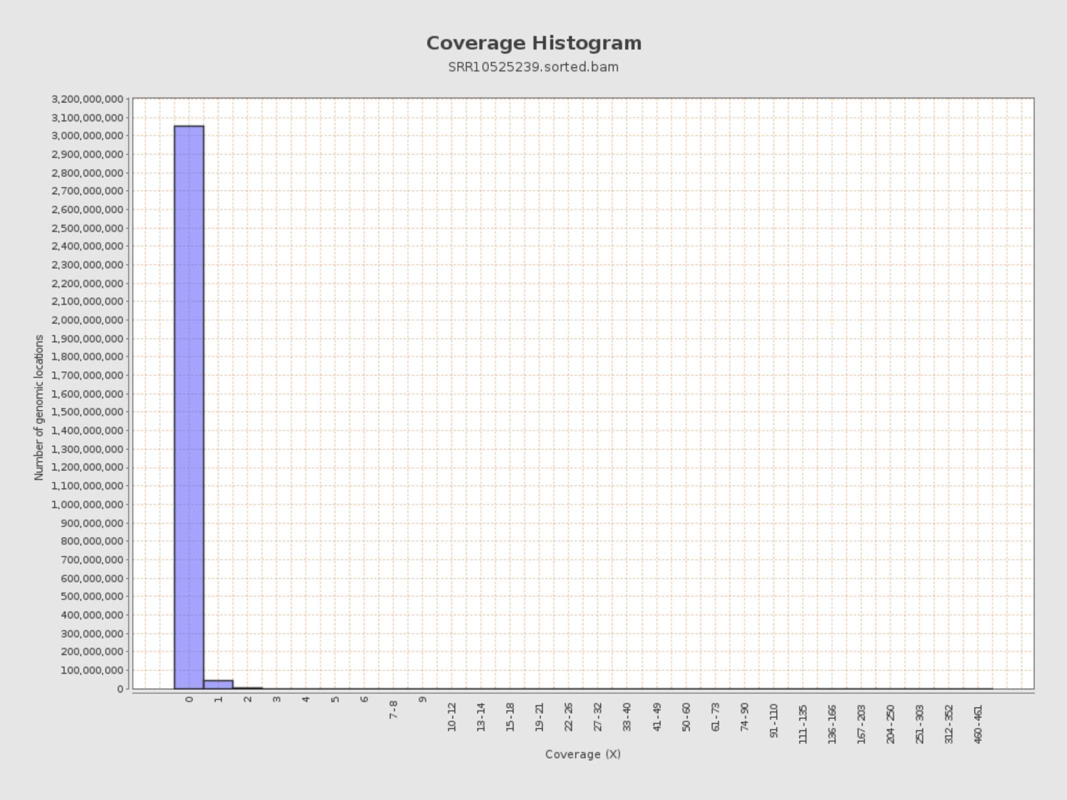
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5542127	0.0222	0.2935
chr2	243199373	4034769	0.0166	0.2294
chr3	198022430	3635257	0.0184	0.144
chr4	191154276	2806491	0.0147	0.1311
chr5	180915260	2214068	0.0122	0.116
chr6	171115067	3060636	0.0179	0.1507
chr7	159138663	3565108	0.0224	0.2885

chr8	146364022	2821728	0.0193	0.207
chr9	141213431	1588313	0.0112	0.1308
chr10	135534747	2541441	0.0188	0.1787
chr11	135006516	2188576	0.0162	0.1531
chr12	133851895	2171113	0.0162	0.1347
chr13	115169878	1529033	0.0133	0.1222
chr14	107349540	1814591	0.0169	0.1387
chr15	102531392	1299983	0.0127	0.1216
chr16	90354753	1262628	0.014	0.1307
chr17	81195210	1089547	0.0134	0.1237
chr18	78077248	795534	0.0102	0.2048
chr19	59128983	836180	0.0141	0.1933
chr20	63025520	845672	0.0134	0.1235
chr21	48129895	604020	0.0125	0.1213
chr22	51304566	404969	0.0079	0.0932
chrMT	16571	53781	3.2455	2.4986
chrX	155270560	2023582	0.013	0.1276
chrY	59373566	132209	0.0022	0.0699

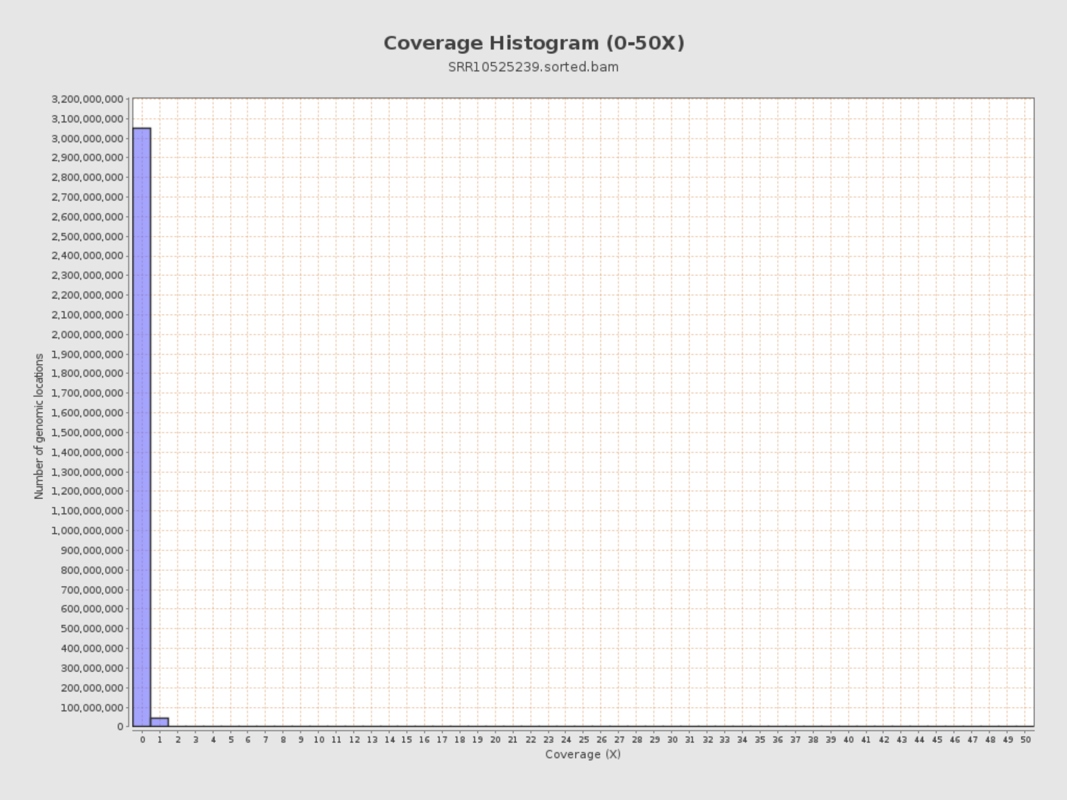
3. Results : Coverage across reference



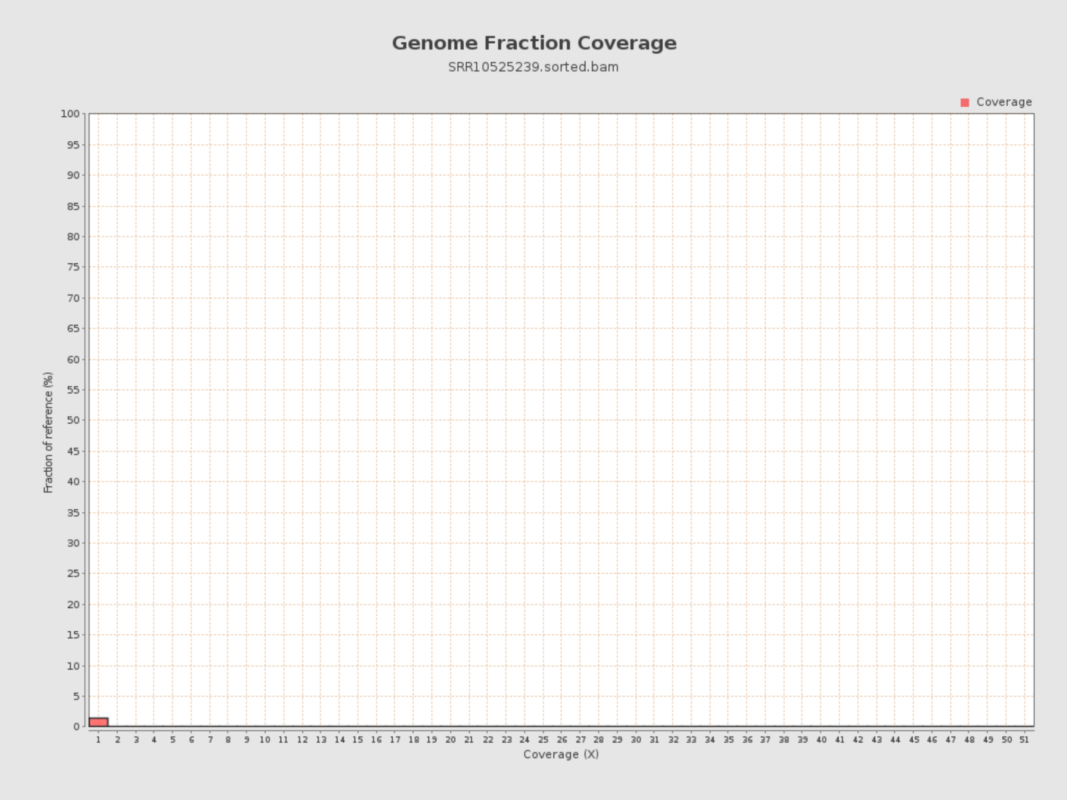
4. Results : Coverage Histogram



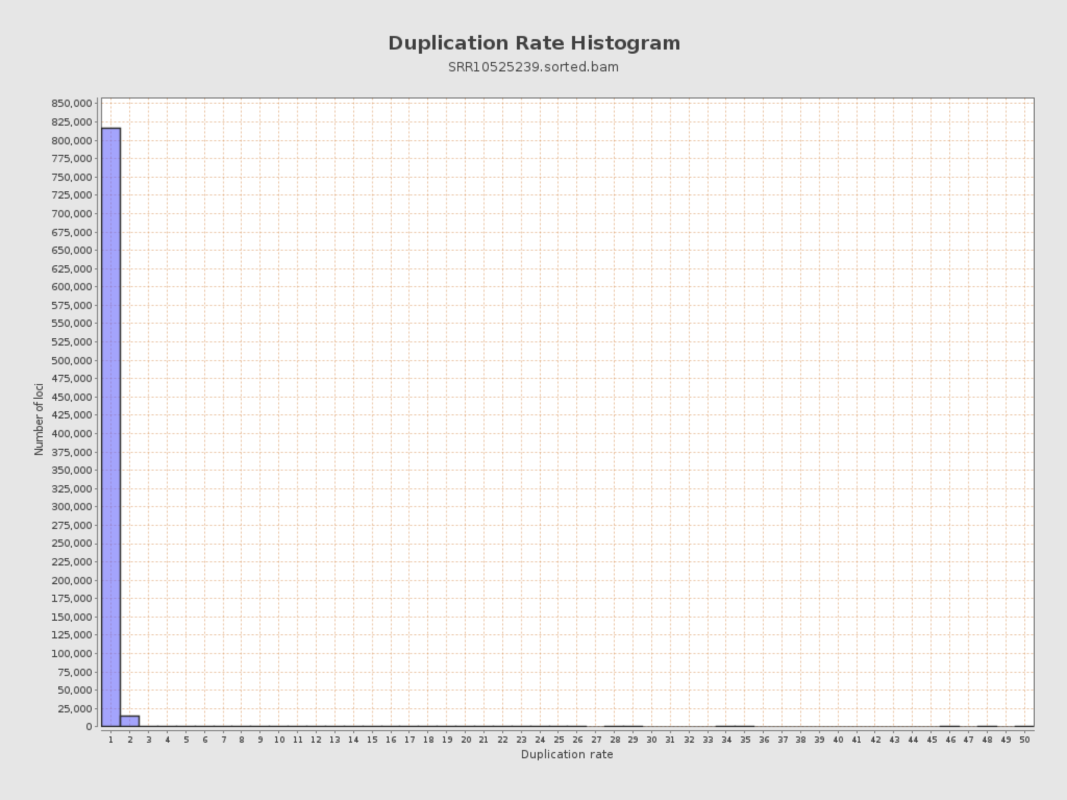
5. Results : Coverage Histogram (0-50X)



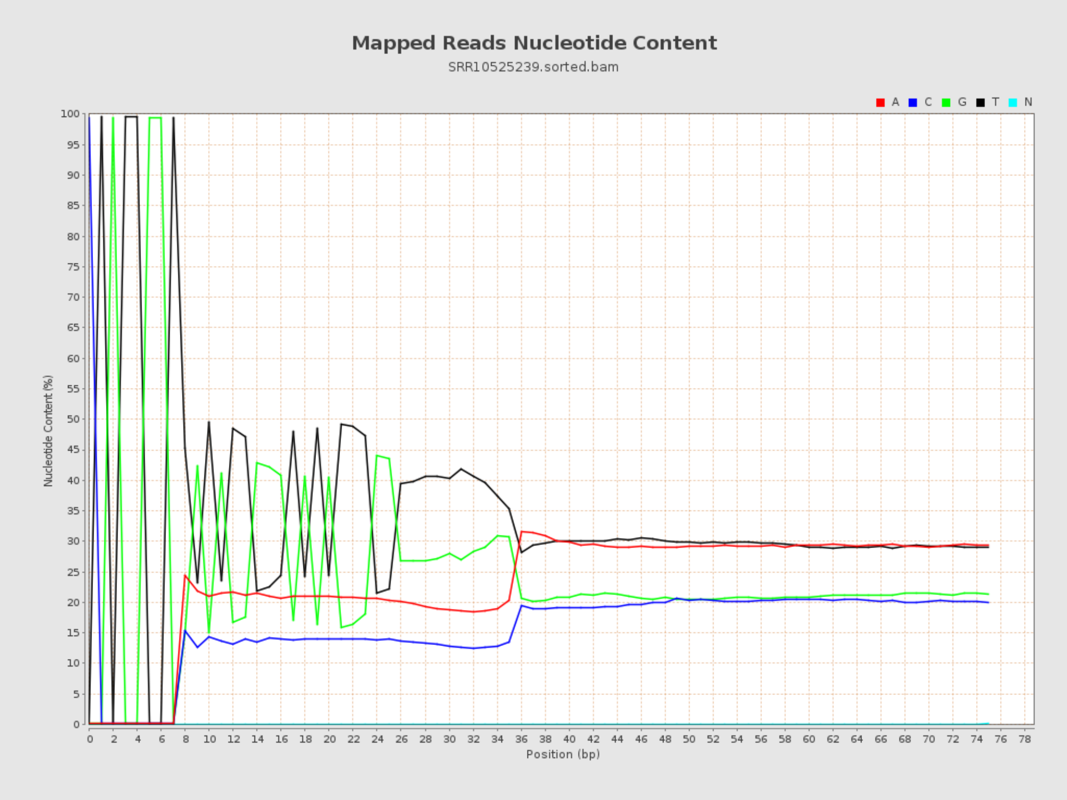
6. Results : Genome Fraction Coverage



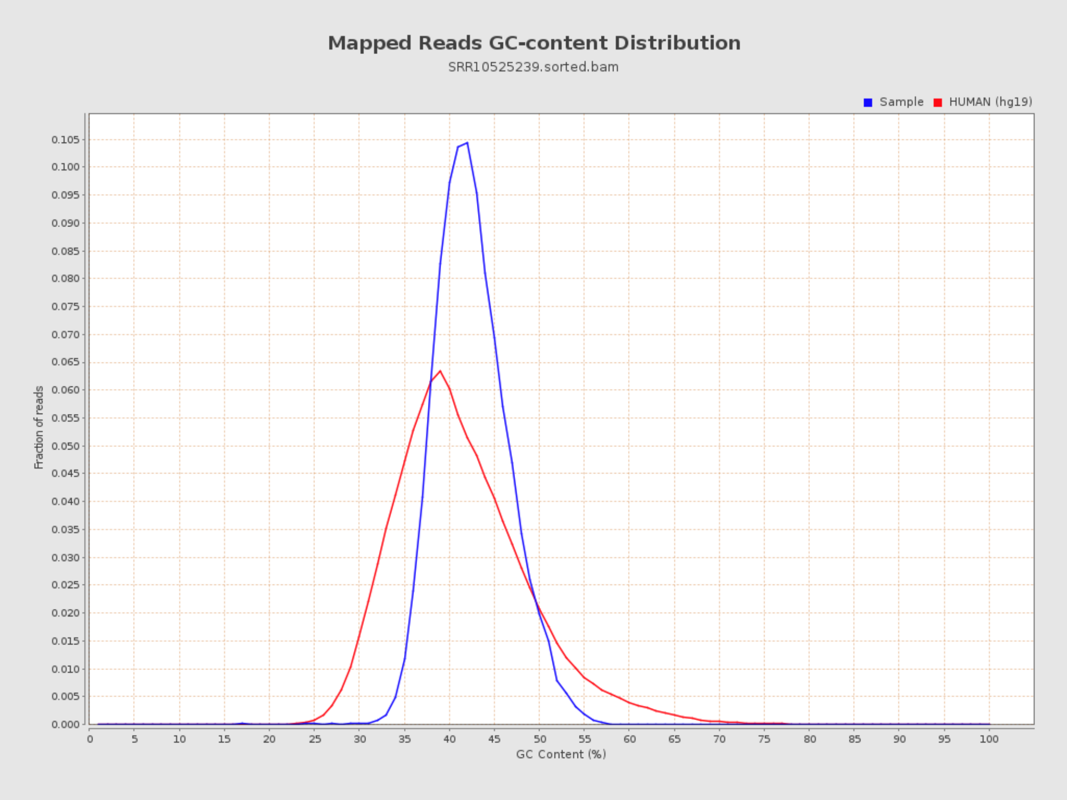
7. Results : Duplication Rate Histogram



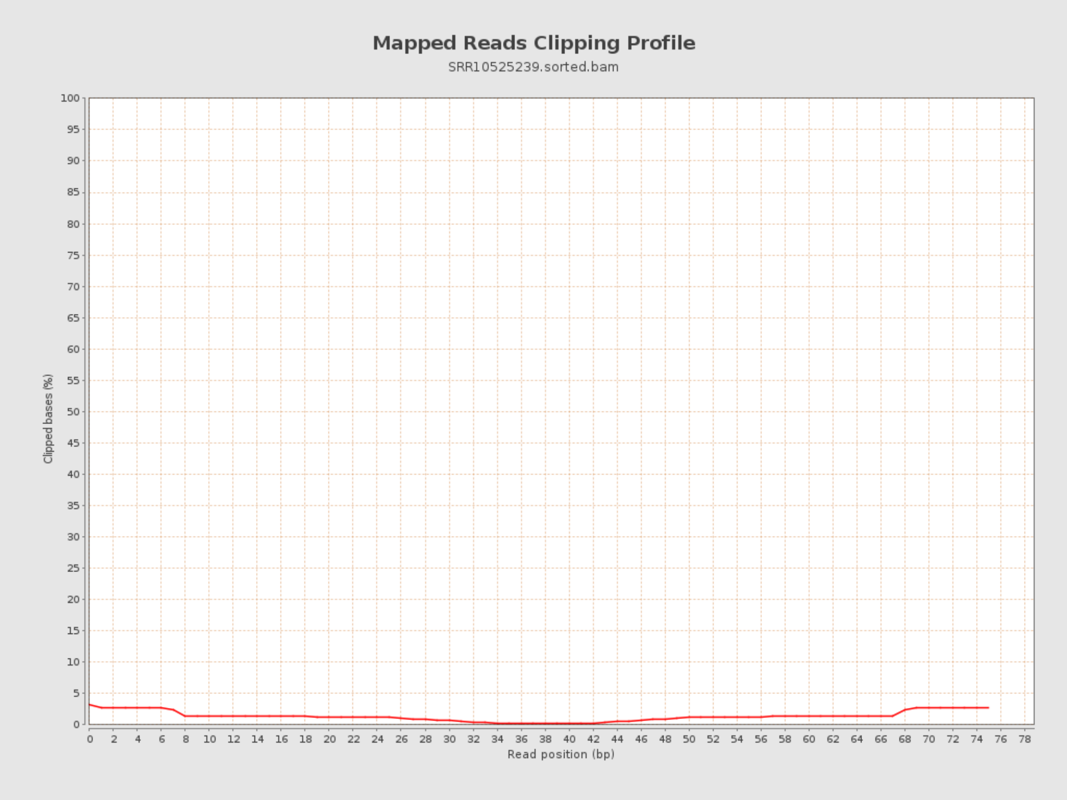
8. Results : Mapped Reads Nucleotide Content



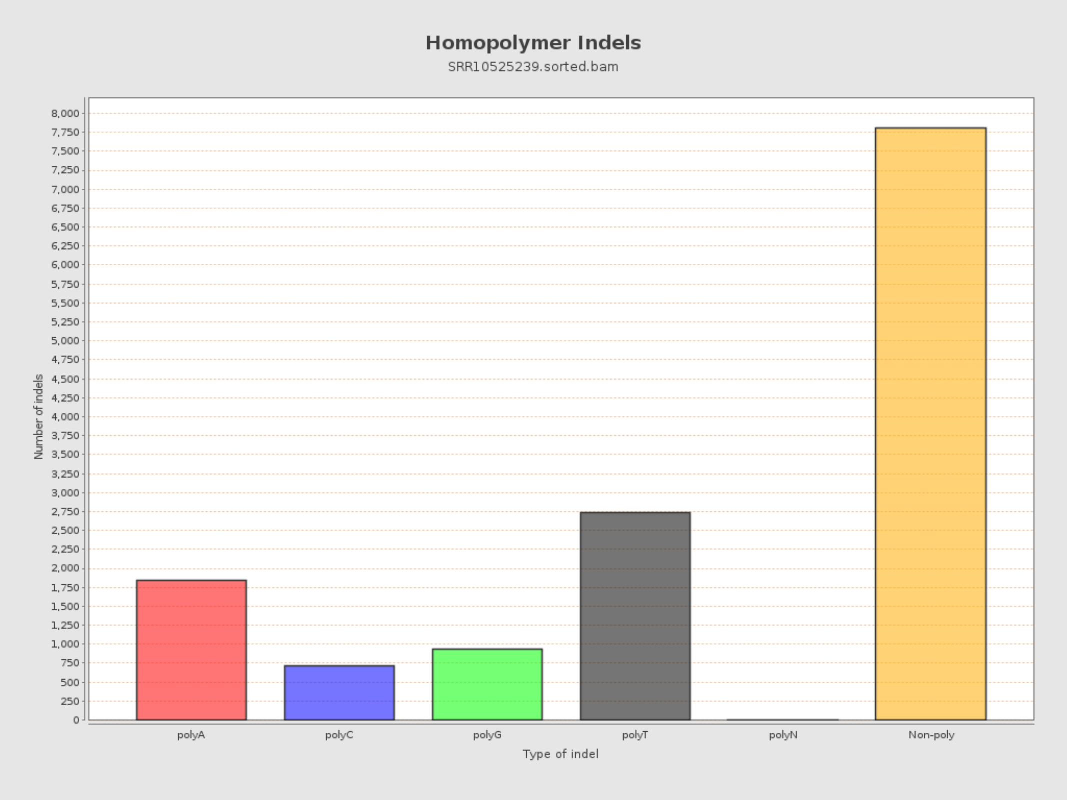
9. Results : Mapped Reads GC-content Distribution



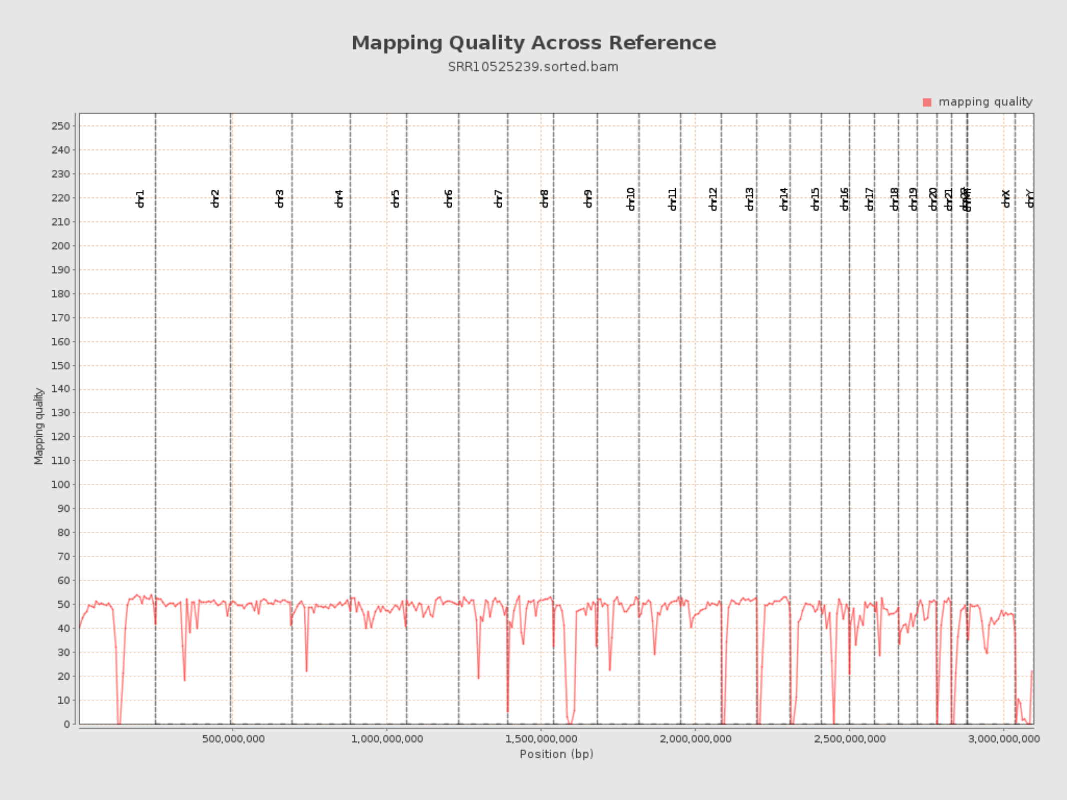
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram