Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:31:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525018.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_SRR10525018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525018.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:31:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,043,350
Mapped reads	958,889 / 91.9%
Unmapped reads	84,461 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,930 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	22,614 / 2.17%
Duplication rate	1.66%
Clipped reads	961,845 / 92.19%

2.2. ACGT Content

Number/percentage of A's	14,096,959 / 25.37%
Number/percentage of C's	10,455,840 / 18.82%
Number/percentage of T's	16,800,187 / 30.24%
Number/percentage of G's	14,211,444 / 25.58%
Number/percentage of N's	562 / 0%
GC Percentage	44.39%

2.3. Coverage

Mean	0.018

Standard Deviation	0.1844

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

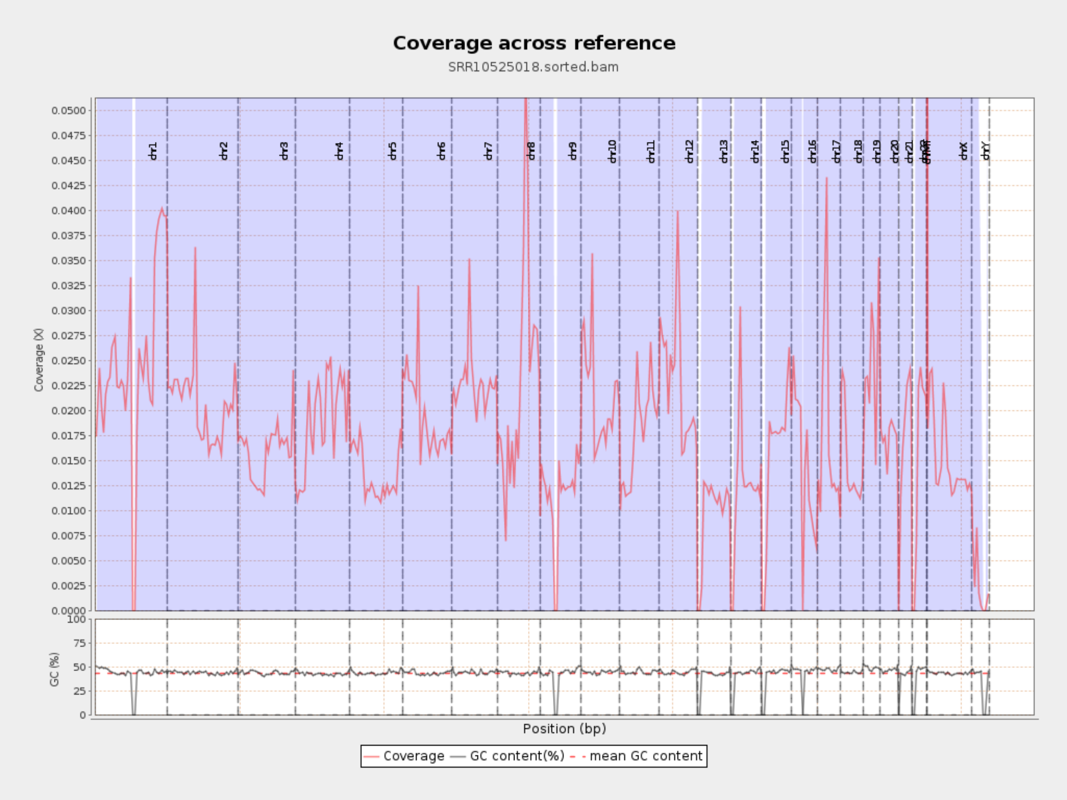
General error rate	0.49%
Mismatches	268,486
Insertions	3,311
Mapped reads with at least one insertion	0.34%
Deletions	10,302
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.94%

2.6. Chromosome stats

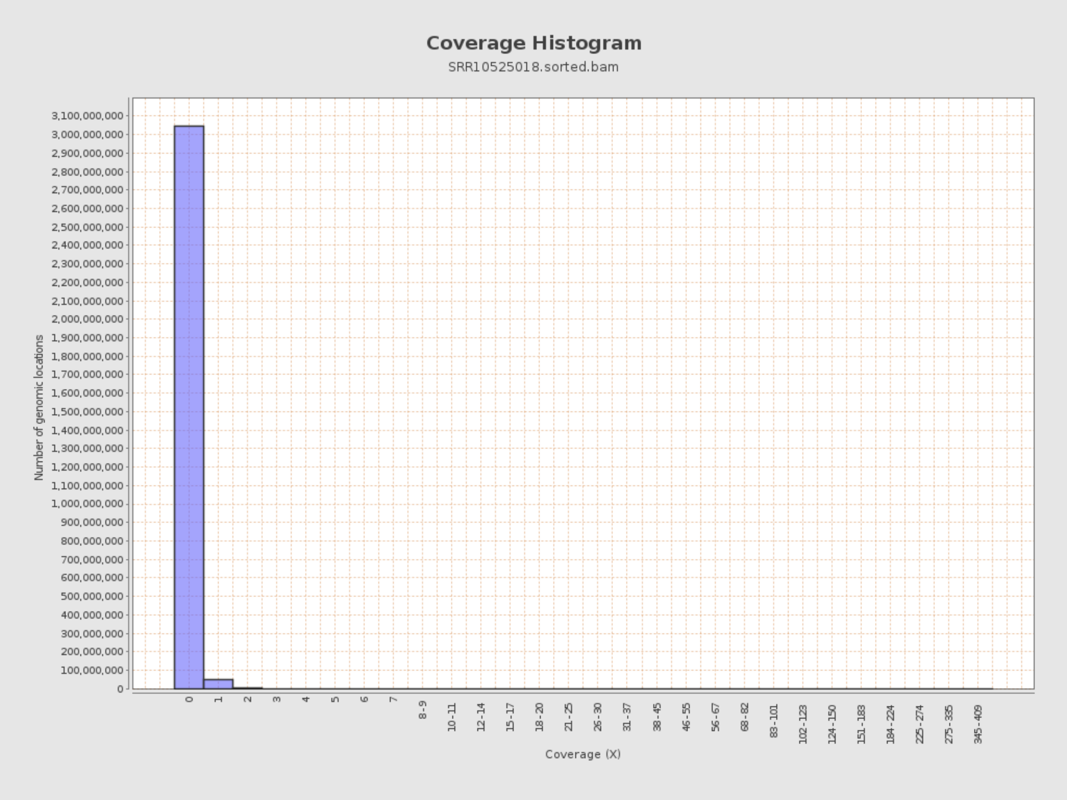
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6129001	0.0246	0.3259
chr2	243199373	5013350	0.0206	0.2087
chr3	198022430	3157599	0.0159	0.1337
chr4	191154276	3649254	0.0191	0.1523
chr5	180915260	2472756	0.0137	0.1243
chr6	171115067	3351233	0.0196	0.1849
chr7	159138663	3644806	0.0229	0.245

chr8	146364022	3413793	0.0233	0.1874
chr9	141213431	1614302	0.0114	0.1375
chr10	135534747	2927554	0.0216	0.191
chr11	135006516	2423525	0.018	0.1692
chr12	133851895	3107000	0.0232	0.1601
chr13	115169878	1111966	0.0097	0.1045
chr14	107349540	1309003	0.0122	0.1185
chr15	102531392	1603550	0.0156	0.1344
chr16	90354753	1304003	0.0144	0.1324
chr17	81195210	1482682	0.0183	0.1741
chr18	78077248	1157125	0.0148	0.2188
chr19	59128983	1461129	0.0247	0.2191
chr20	63025520	1083286	0.0172	0.1387
chr21	48129895	832756	0.0173	0.1427
chr22	51304566	790027	0.0154	0.1301
chrMT	16571	4450	0.2685	0.5315
chrX	155270560	2385698	0.0154	0.144
chrY	59373566	152384	0.0026	0.0747

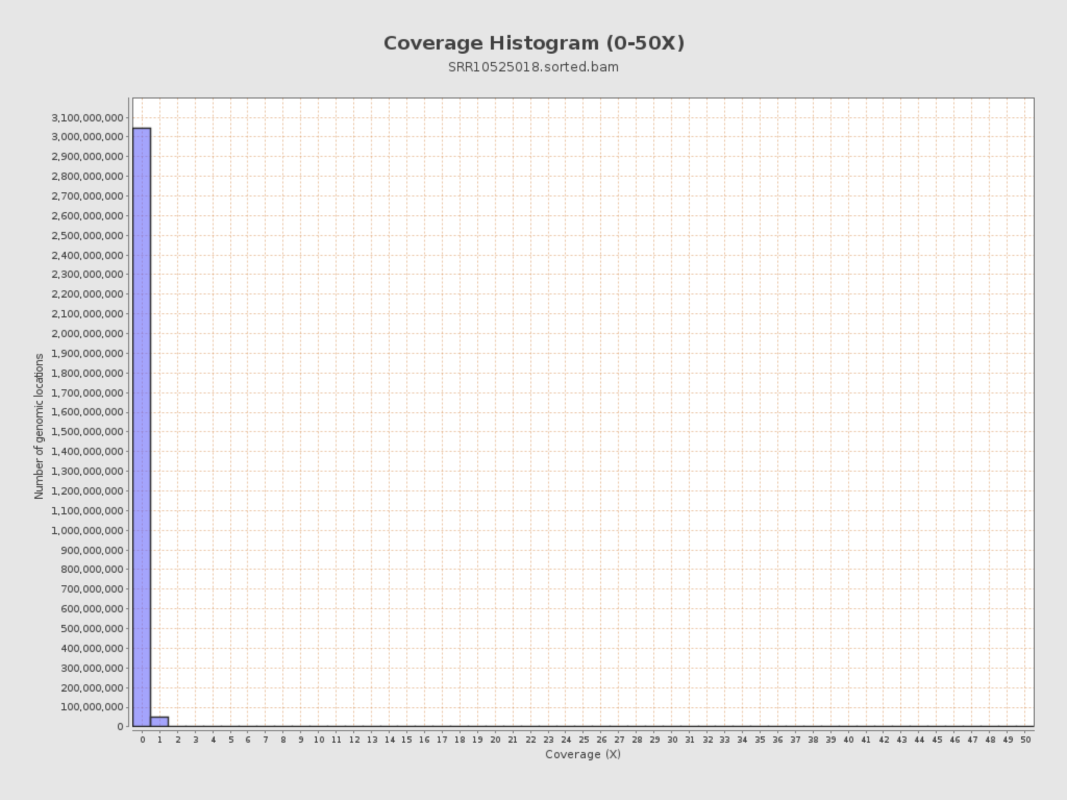
3. Results : Coverage across reference



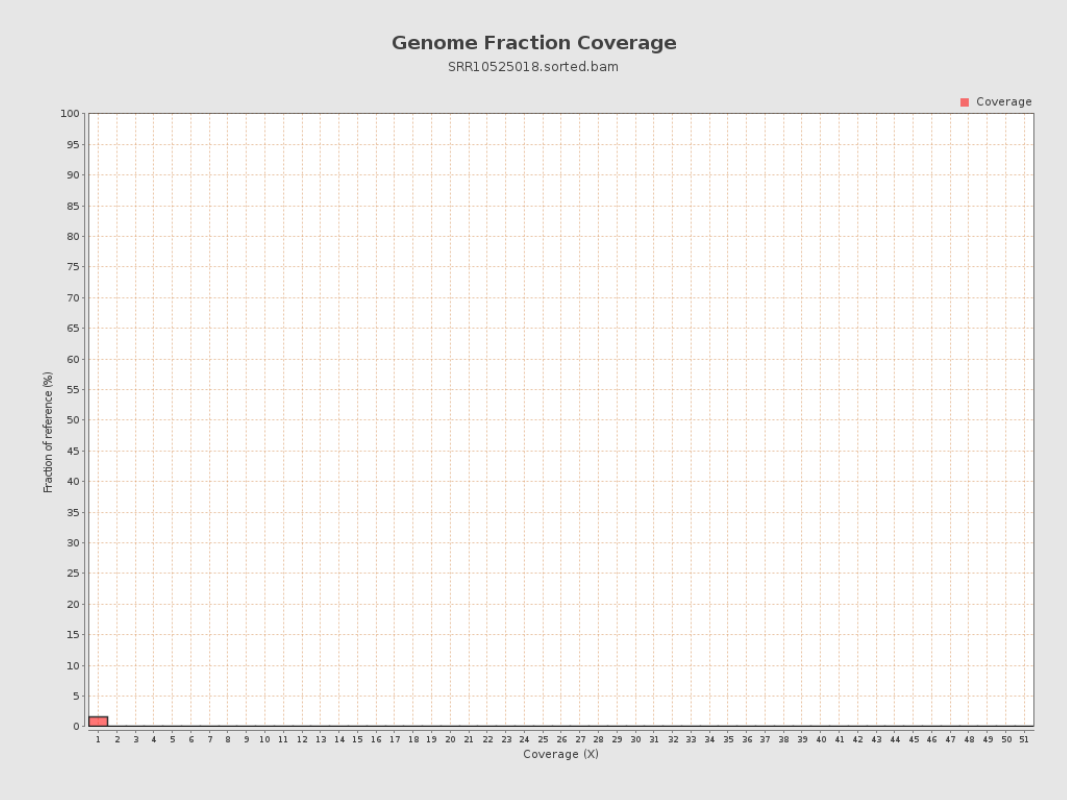
4. Results : Coverage Histogram



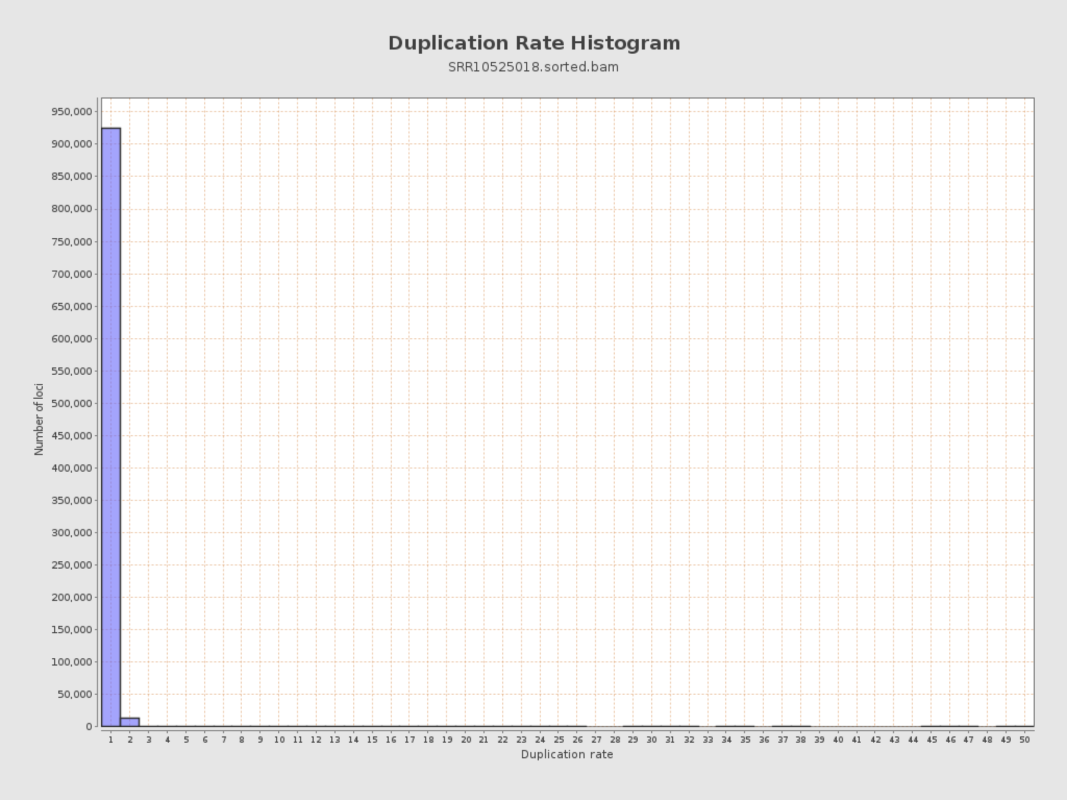
5. Results : Coverage Histogram (0-50X)



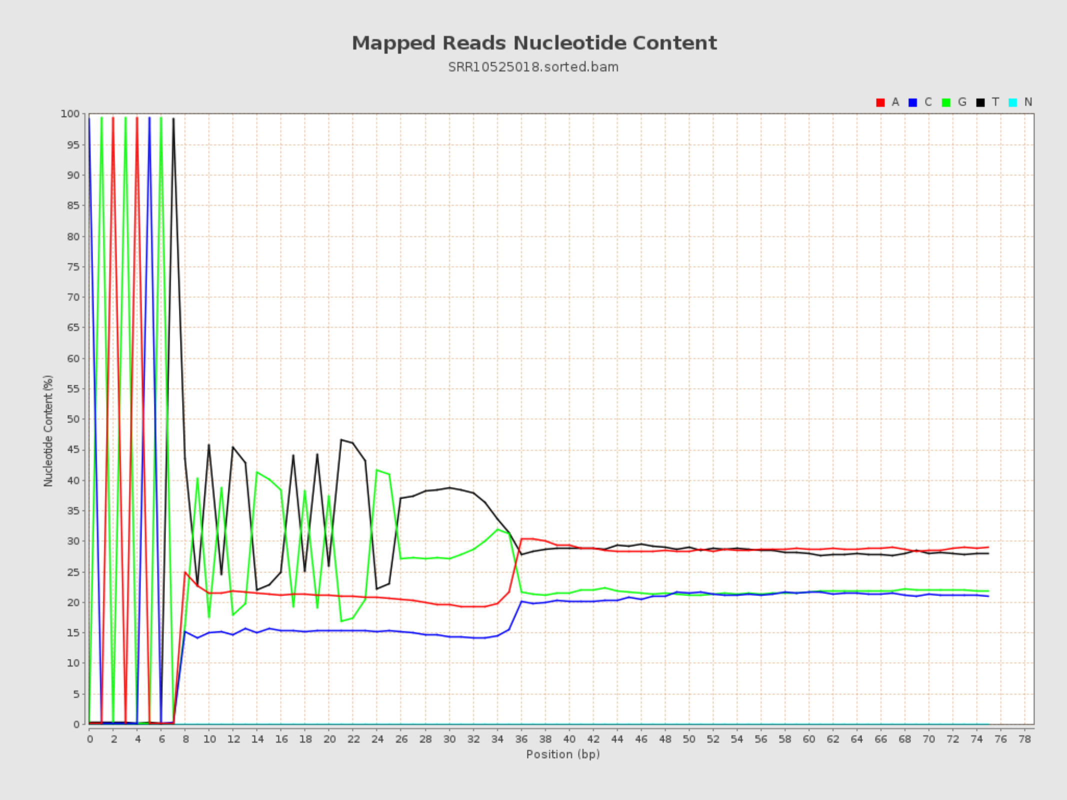
6. Results : Genome Fraction Coverage



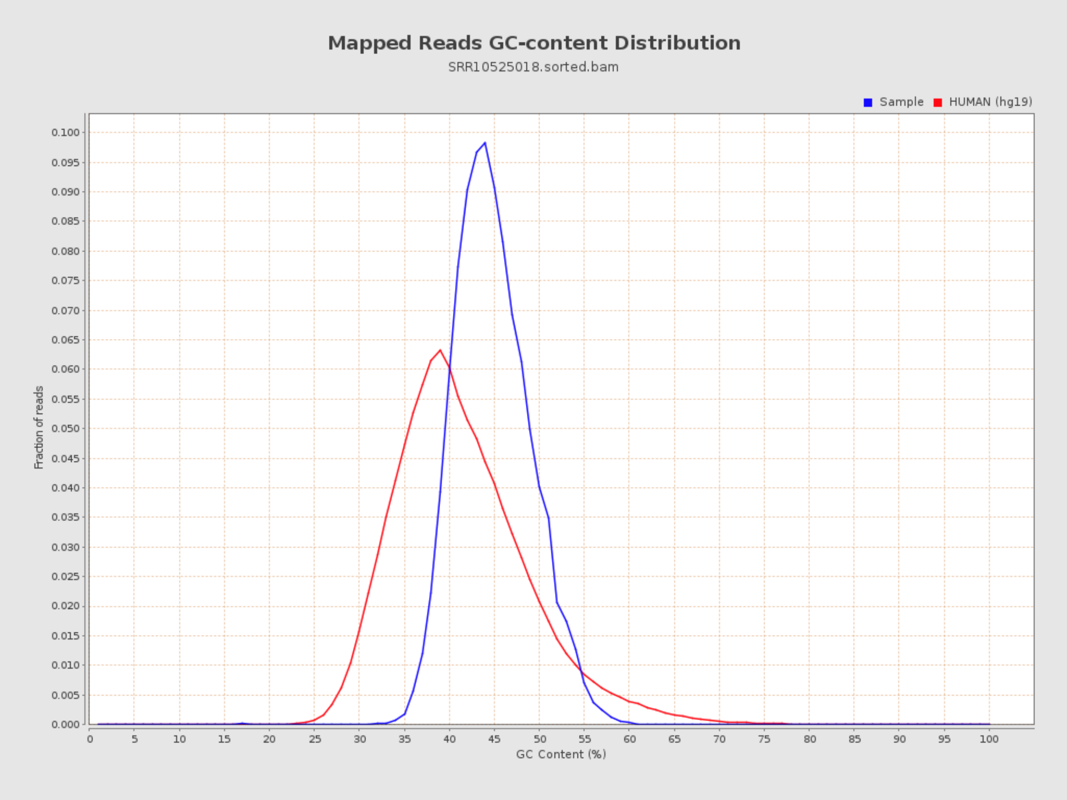
7. Results : Duplication Rate Histogram



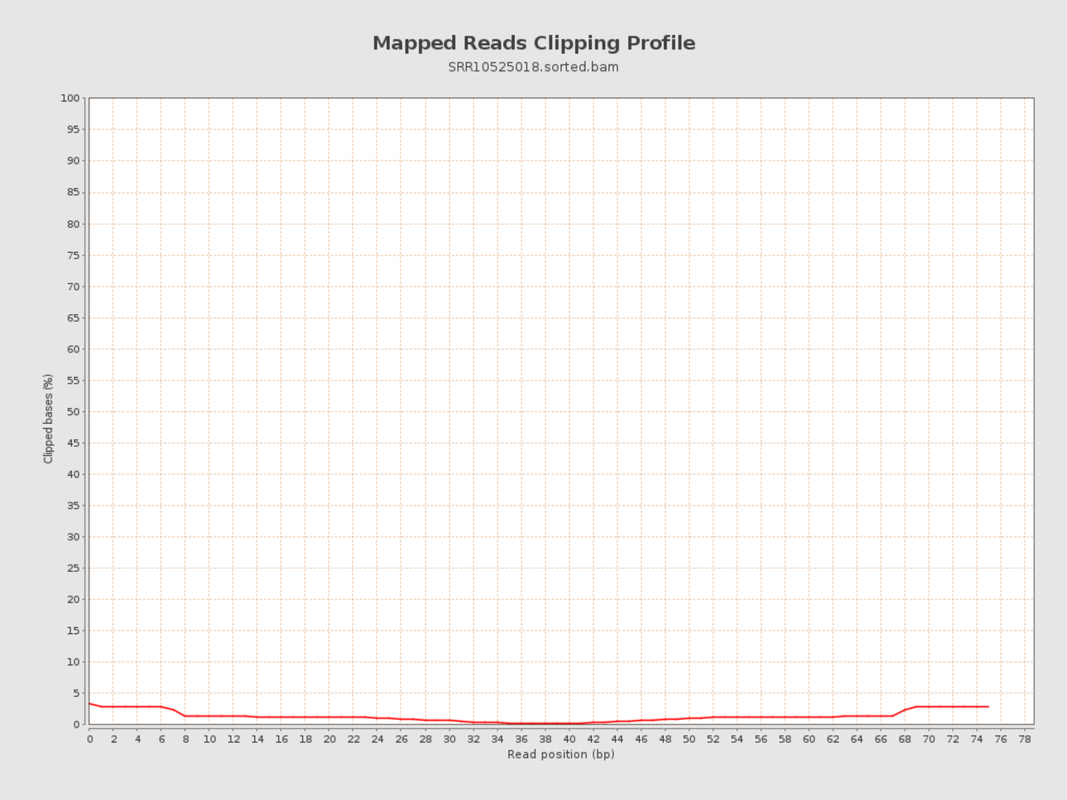
8. Results : Mapped Reads Nucleotide Content



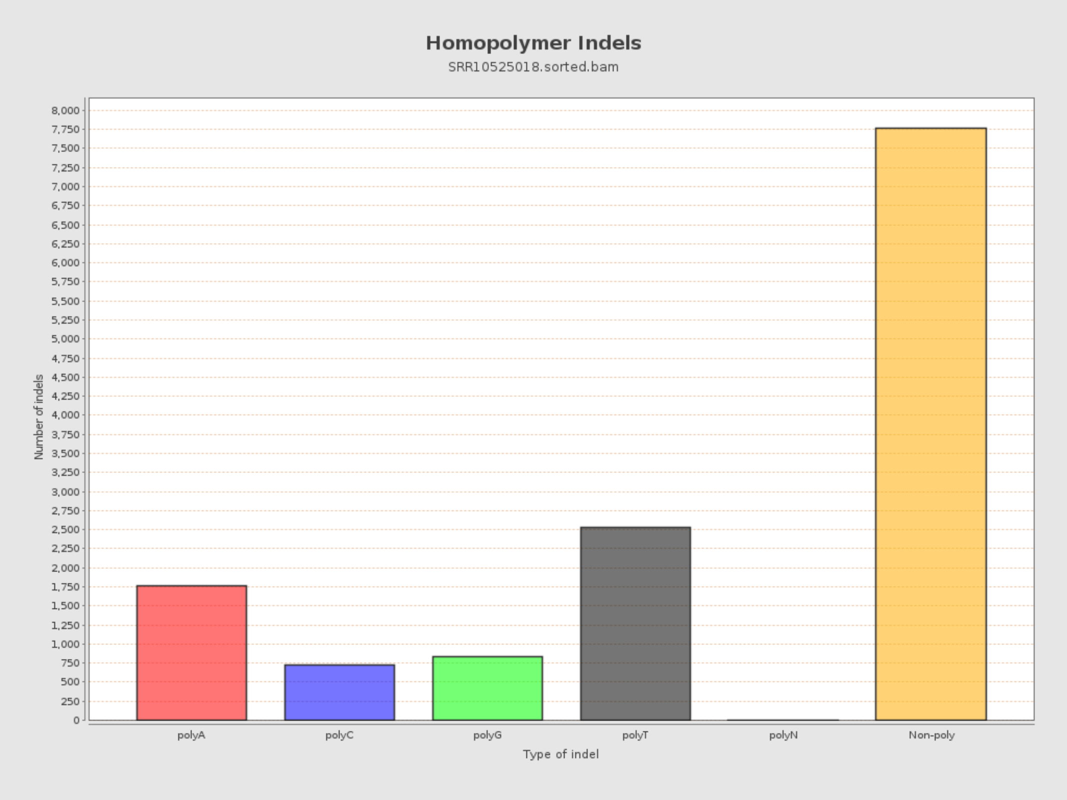
9. Results : Mapped Reads GC-content Distribution



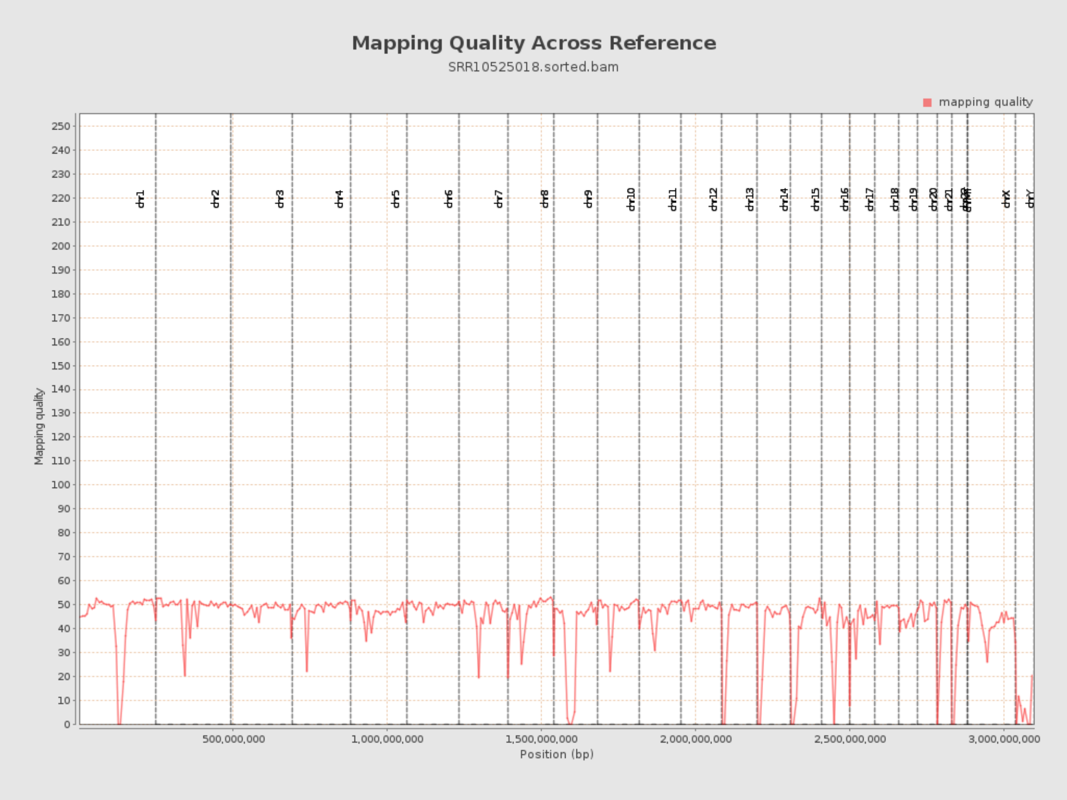
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram