Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:57:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525265.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_SRR10525265 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525265.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:56:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525265.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,025,076
Mapped reads	942,013 / 91.9%
Unmapped reads	83,063 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,759 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	27,538 / 2.69%
Duplication rate	2.14%
Clipped reads	943,758 / 92.07%

2.2. ACGT Content

Number/percentage of A's	13,724,992 / 25.02%
Number/percentage of C's	10,009,671 / 18.25%
Number/percentage of T's	17,897,153 / 32.62%
Number/percentage of G's	13,225,132 / 24.11%
Number/percentage of N's	1,273 / 0%
GC Percentage	42.35%

2.3. Coverage

Mean	0.0177

Standard Deviation	0.2029

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

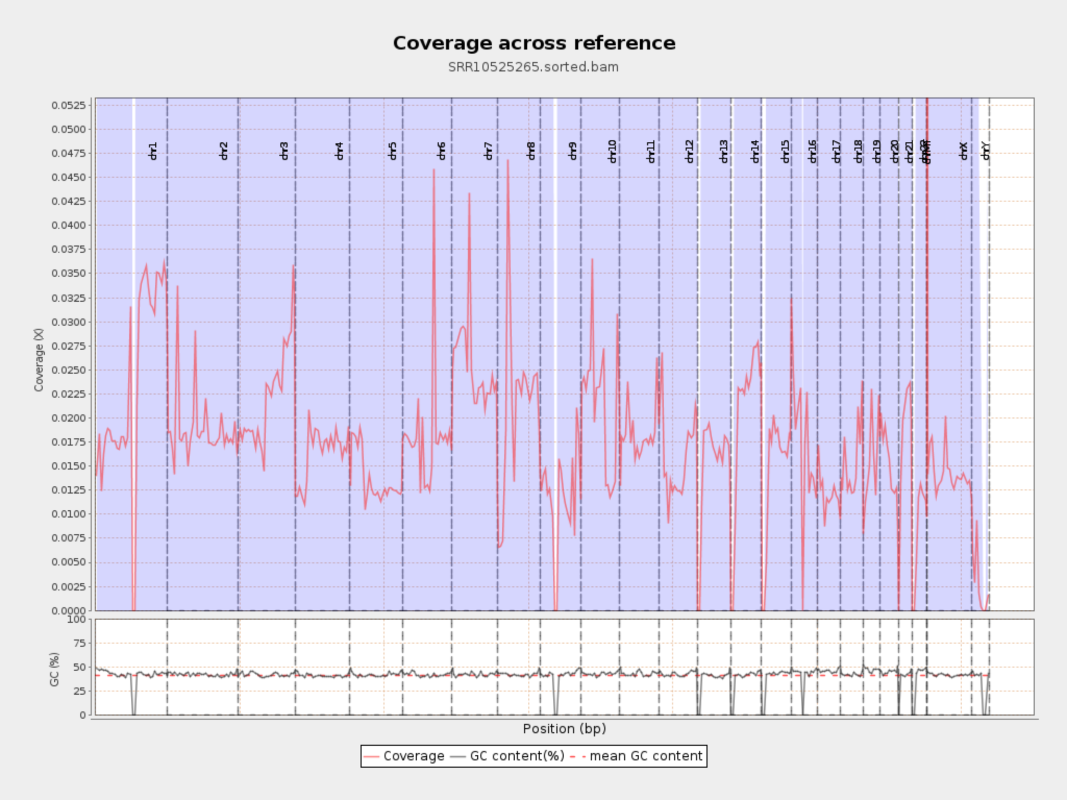
General error rate	0.52%
Mismatches	276,698
Insertions	3,746
Mapped reads with at least one insertion	0.4%
Deletions	11,294
Mapped reads with at least one deletion	1.19%
Homopolymer indels	44.53%

2.6. Chromosome stats

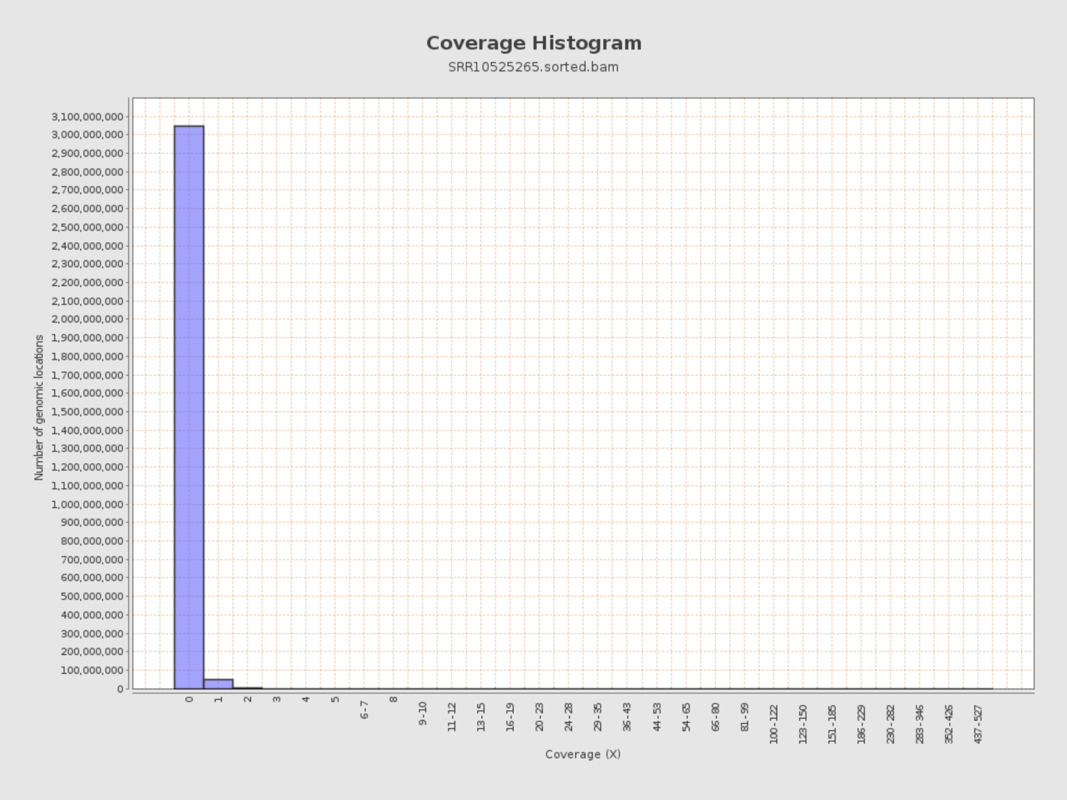
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5841700	0.0234	0.354
chr2	243199373	4569053	0.0188	0.2613
chr3	198022430	4375954	0.0221	0.1573
chr4	191154276	3139914	0.0164	0.1405
chr5	180915260	2493932	0.0138	0.1242
chr6	171115067	3126948	0.0183	0.1549
chr7	159138663	4092019	0.0257	0.3468

chr8	146364022	3157606	0.0216	0.2033
chr9	141213431	1662292	0.0118	0.1357
chr10	135534747	2946246	0.0217	0.1966
chr11	135006516	2471313	0.0183	0.1626
chr12	133851895	2120967	0.0158	0.1345
chr13	115169878	1733619	0.0151	0.1294
chr14	107349540	2180403	0.0203	0.152
chr15	102531392	1470297	0.0143	0.1278
chr16	90354753	1548489	0.0171	0.1462
chr17	81195210	987396	0.0122	0.1186
chr18	78077248	1195917	0.0153	0.2558
chr19	59128983	934371	0.0158	0.2263
chr20	63025520	976408	0.0155	0.1326
chr21	48129895	881570	0.0183	0.1465
chr22	51304566	434977	0.0085	0.0964
chrMT	16571	145121	8.7575	5.4706
chrX	155270560	2232302	0.0144	0.1342
chrY	59373566	157634	0.0027	0.0904

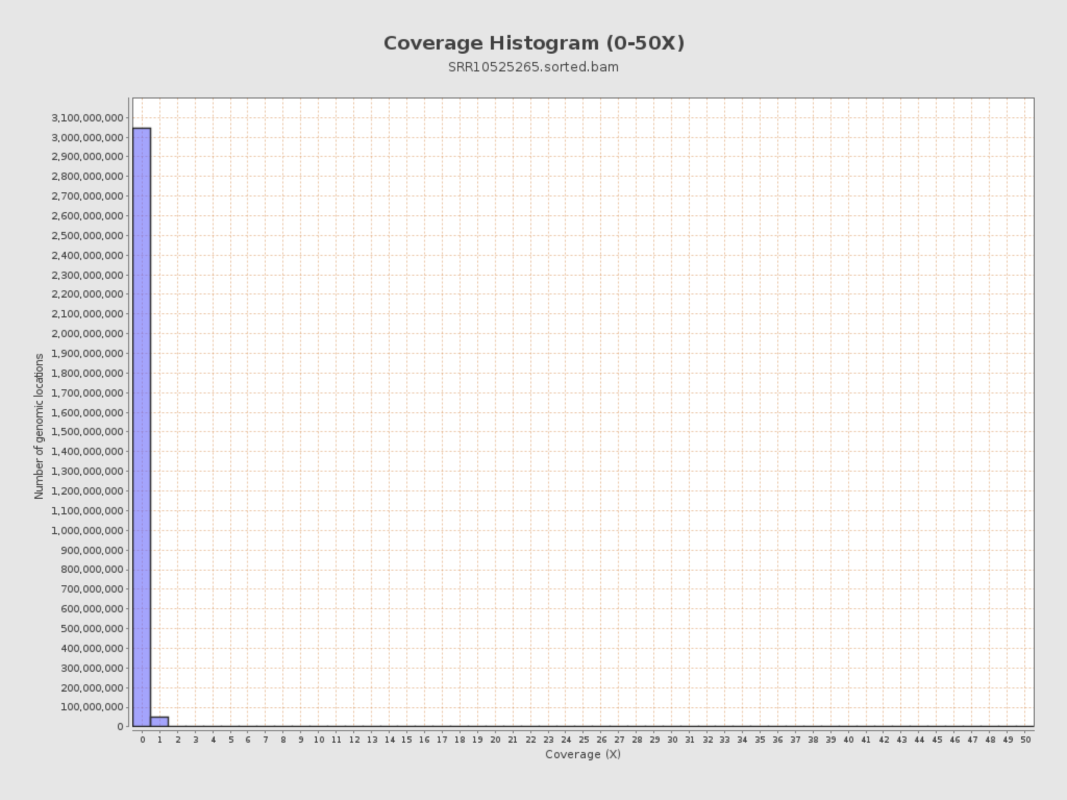
3. Results : Coverage across reference



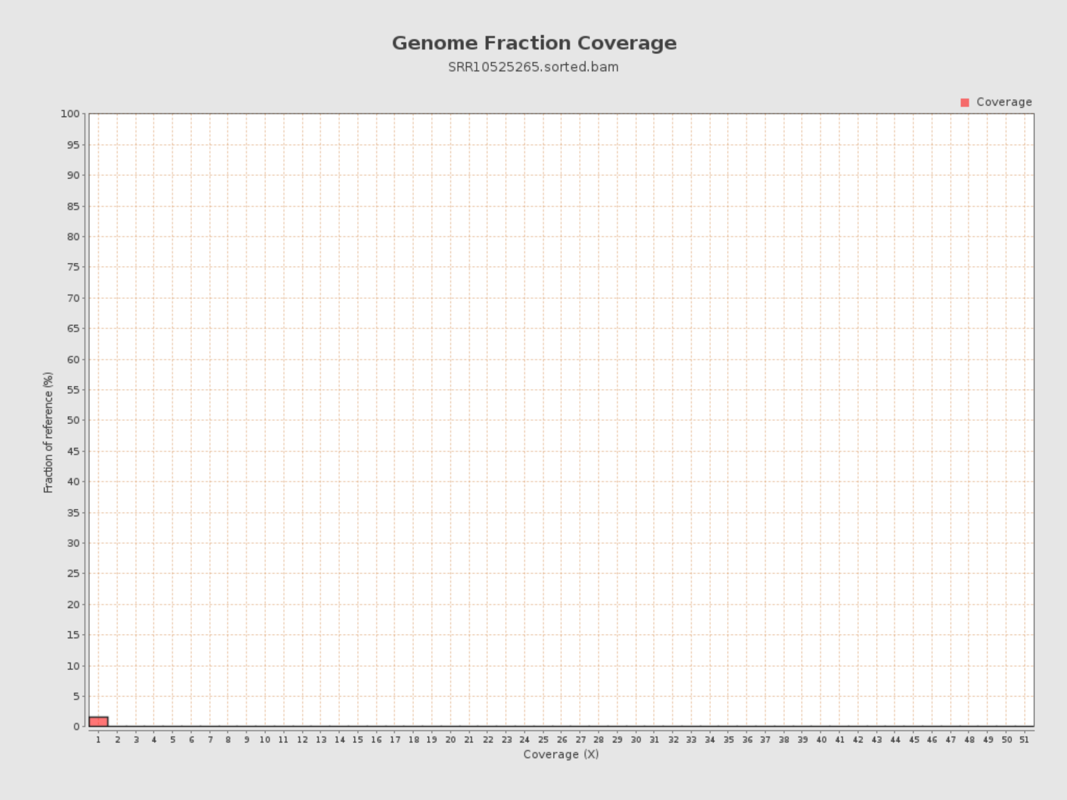
4. Results : Coverage Histogram



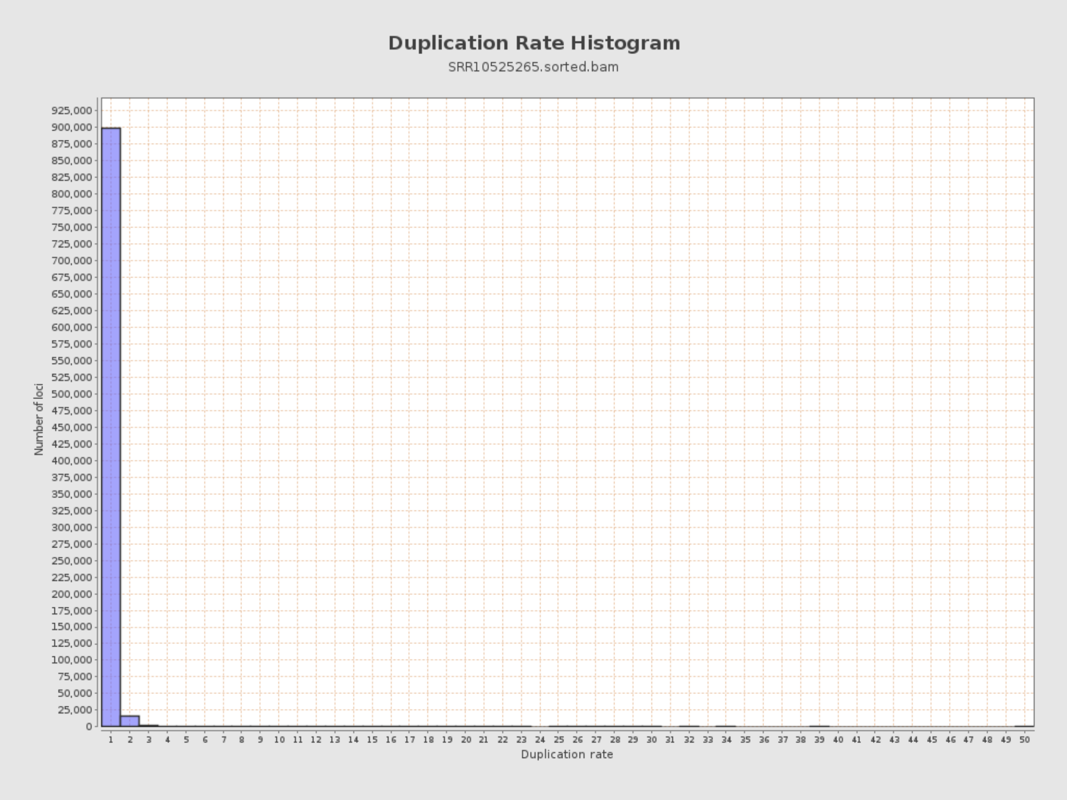
5. Results : Coverage Histogram (0-50X)



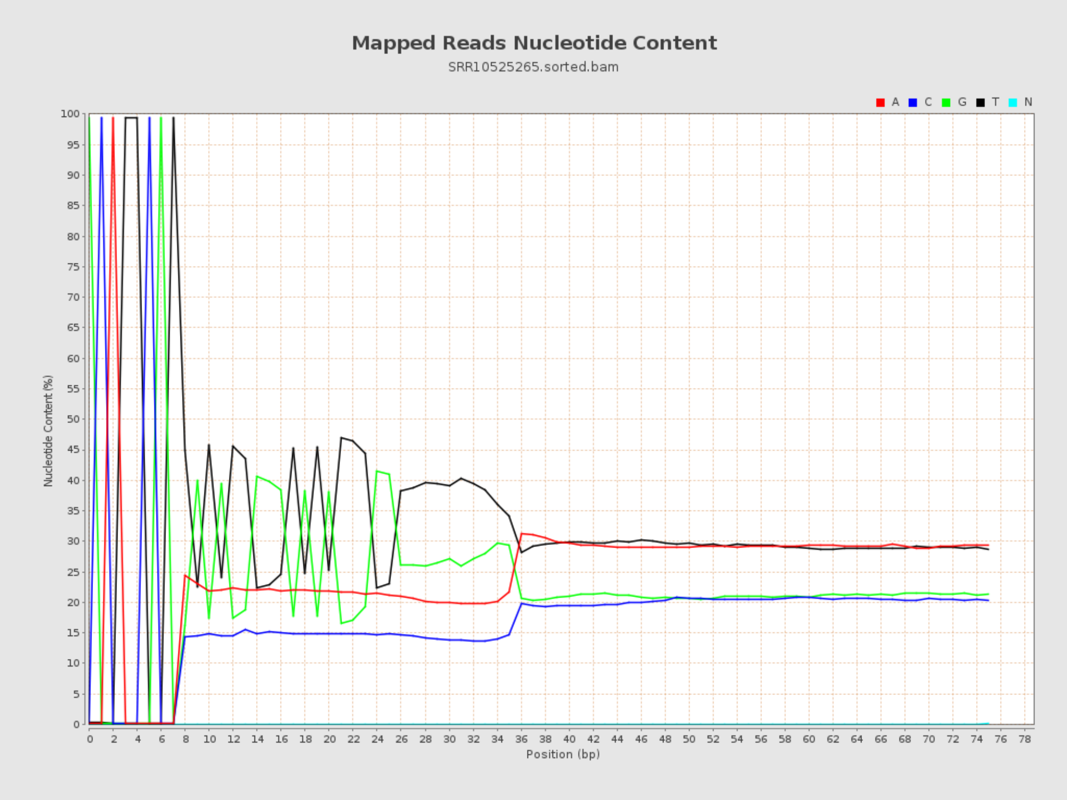
6. Results : Genome Fraction Coverage



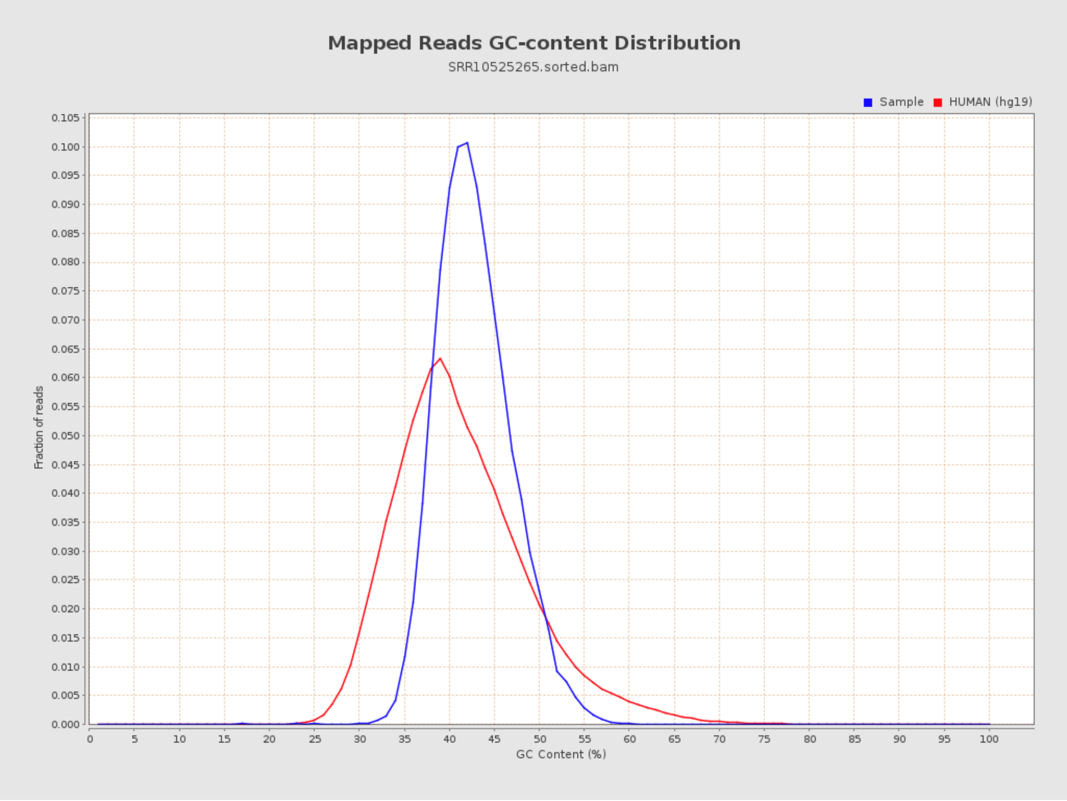
7. Results : Duplication Rate Histogram



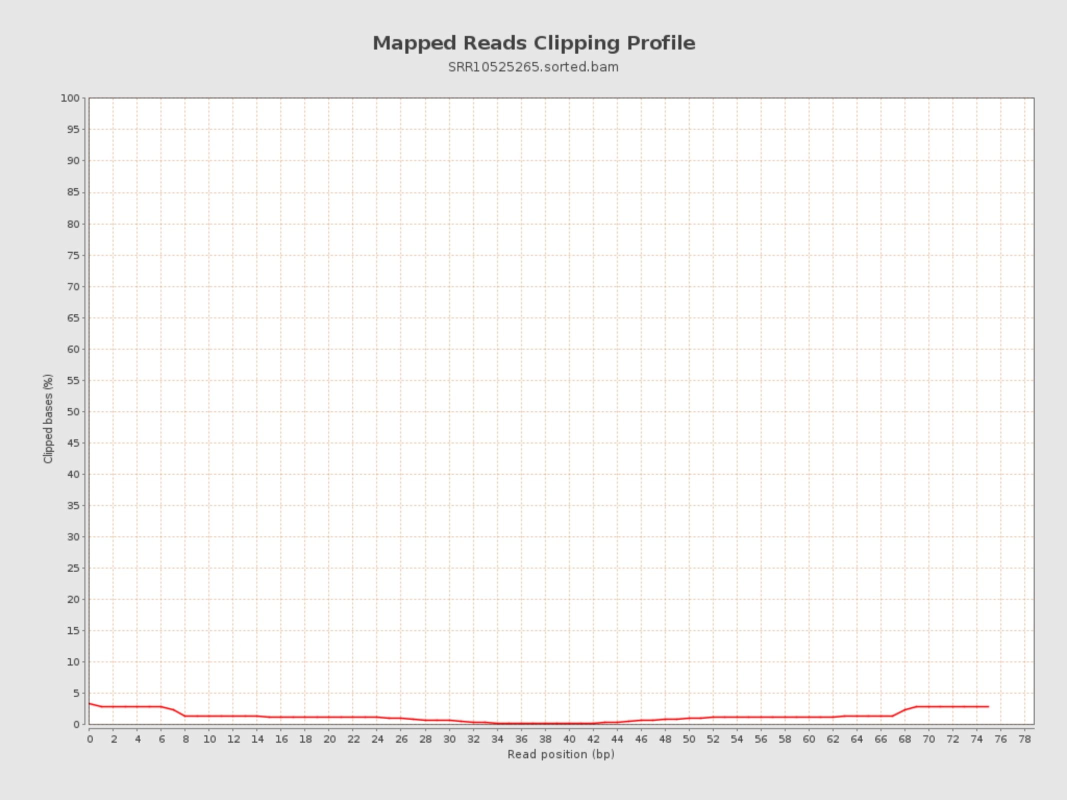
8. Results : Mapped Reads Nucleotide Content



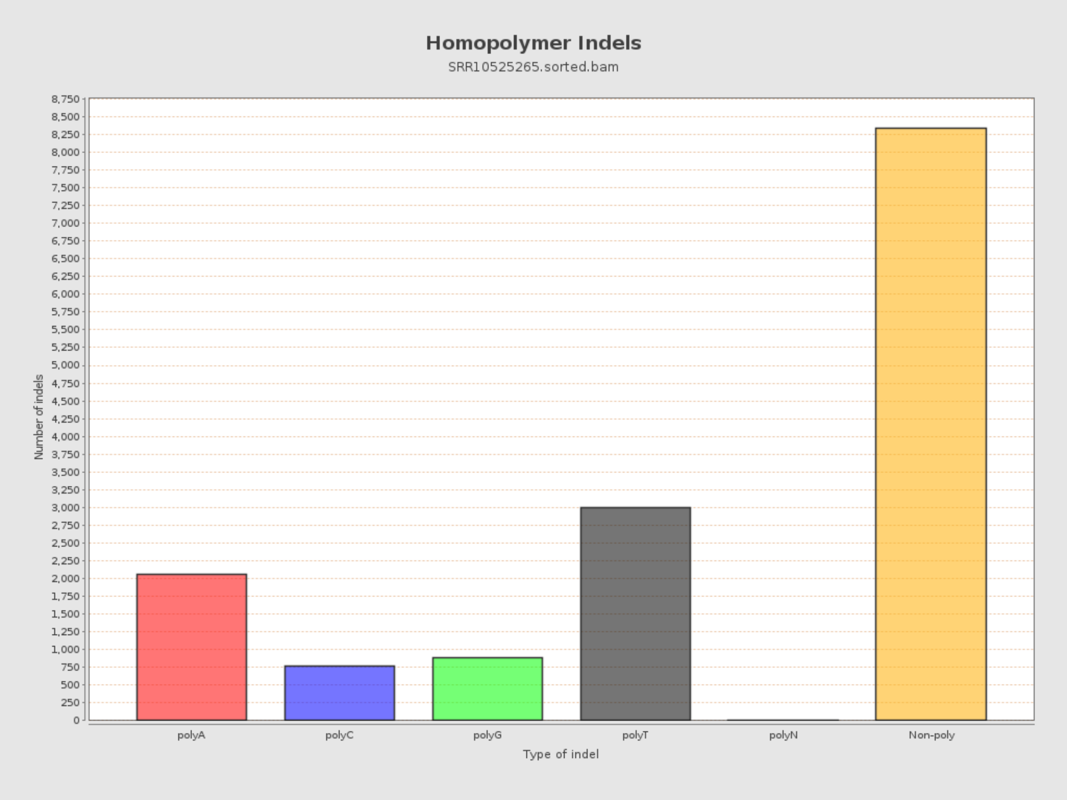
9. Results : Mapped Reads GC-content Distribution



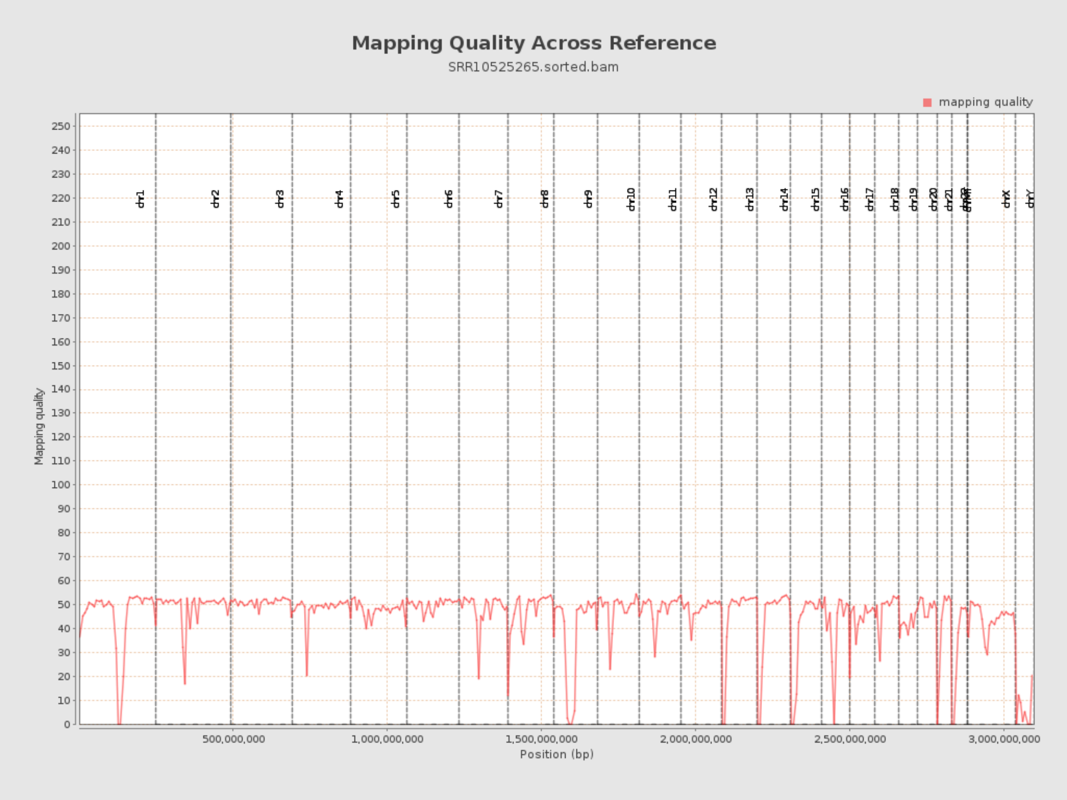
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram