Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:00:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525250.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_SRR10525250 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525250.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:00:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	783,492
Mapped reads	718,674 / 91.73%
Unmapped reads	64,818 / 8.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,730 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	17,383 / 2.22%
Duplication rate	1.73%
Clipped reads	719,702 / 91.86%

2.2. ACGT Content

Number/percentage of A's	10,270,398 / 24.83%
Number/percentage of C's	7,398,722 / 17.89%
Number/percentage of T's	13,662,643 / 33.03%
Number/percentage of G's	10,031,771 / 24.25%
Number/percentage of N's	822 / 0%
GC Percentage	42.14%

2.3. Coverage

Mean	0.0134

Standard Deviation	0.1629

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

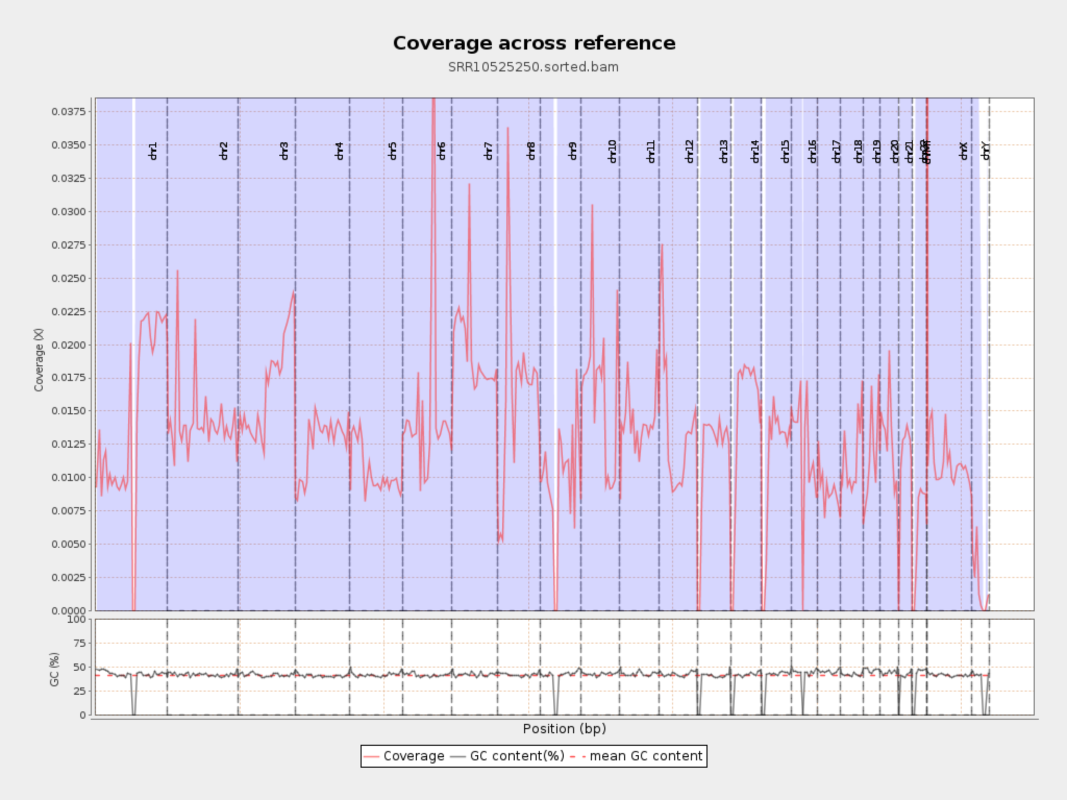
General error rate	0.51%
Mismatches	206,704
Insertions	2,947
Mapped reads with at least one insertion	0.41%
Deletions	8,186
Mapped reads with at least one deletion	1.13%
Homopolymer indels	44.7%

2.6. Chromosome stats

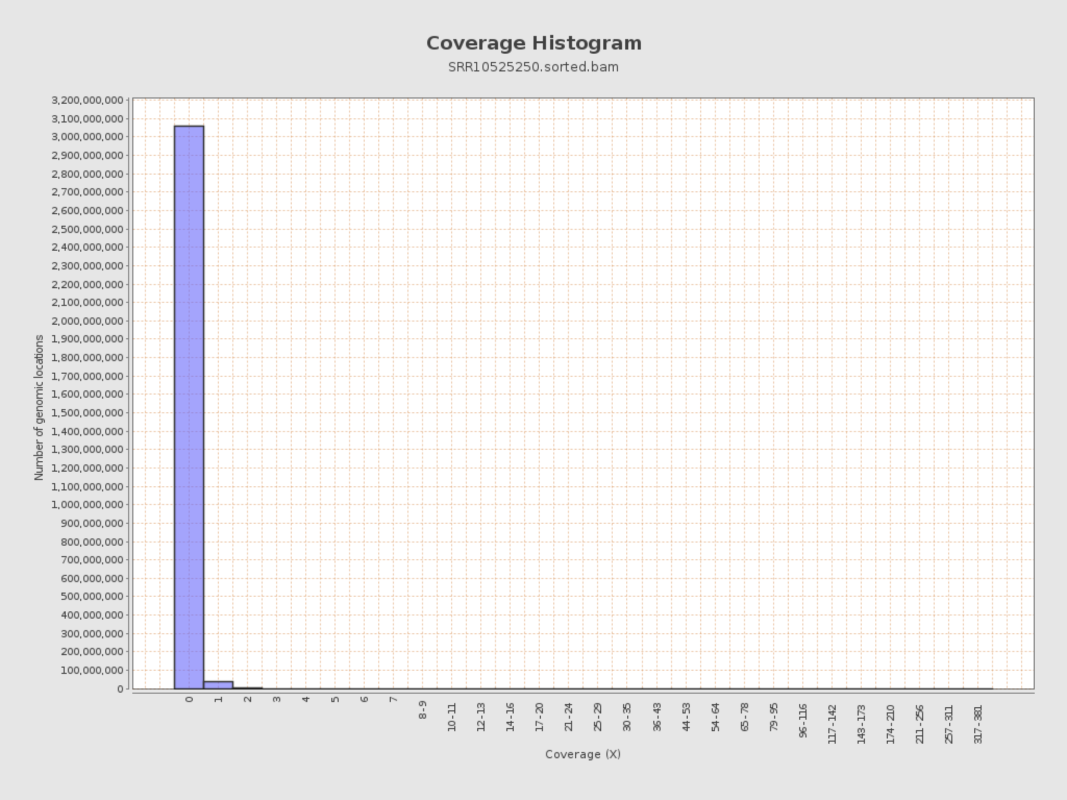
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3617018	0.0145	0.2577
chr2	243199373	3454563	0.0142	0.2025
chr3	198022430	3329545	0.0168	0.1357
chr4	191154276	2412255	0.0126	0.1198
chr5	180915260	1908483	0.0105	0.1071
chr6	171115067	2664973	0.0156	0.1383
chr7	159138663	3121915	0.0196	0.2725

chr8	146364022	2415733	0.0165	0.1671
chr9	141213431	1383778	0.0098	0.1243
chr10	135534747	2230002	0.0165	0.177
chr11	135006516	1907125	0.0141	0.1388
chr12	133851895	1858438	0.0139	0.1233
chr13	115169878	1333384	0.0116	0.1137
chr14	107349540	1558050	0.0145	0.1262
chr15	102531392	1140909	0.0111	0.1116
chr16	90354753	1087696	0.012	0.1224
chr17	81195210	740596	0.0091	0.1013
chr18	78077248	891261	0.0114	0.1937
chr19	59128983	694863	0.0118	0.1874
chr20	63025520	813782	0.0129	0.1197
chr21	48129895	546236	0.0113	0.1134
chr22	51304566	313271	0.0061	0.0809
chrMT	16571	109672	6.6183	4.5567
chrX	155270560	1731464	0.0112	0.1152
chrY	59373566	112279	0.0019	0.0644

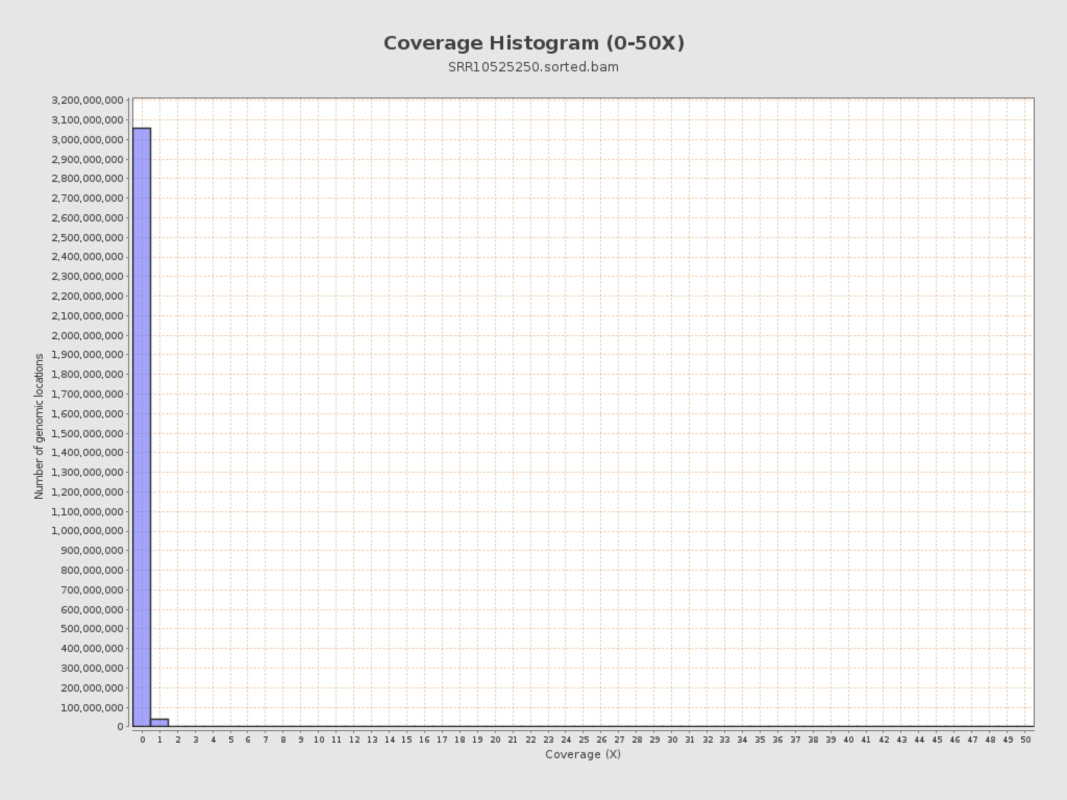
3. Results : Coverage across reference



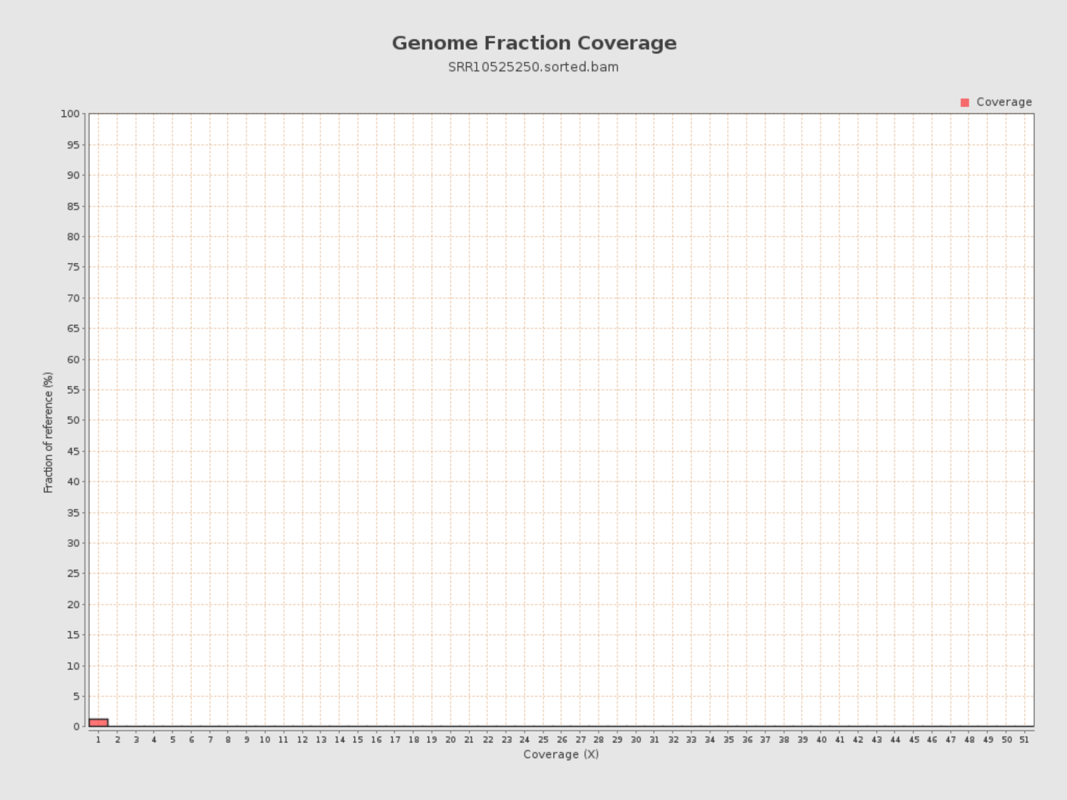
4. Results : Coverage Histogram



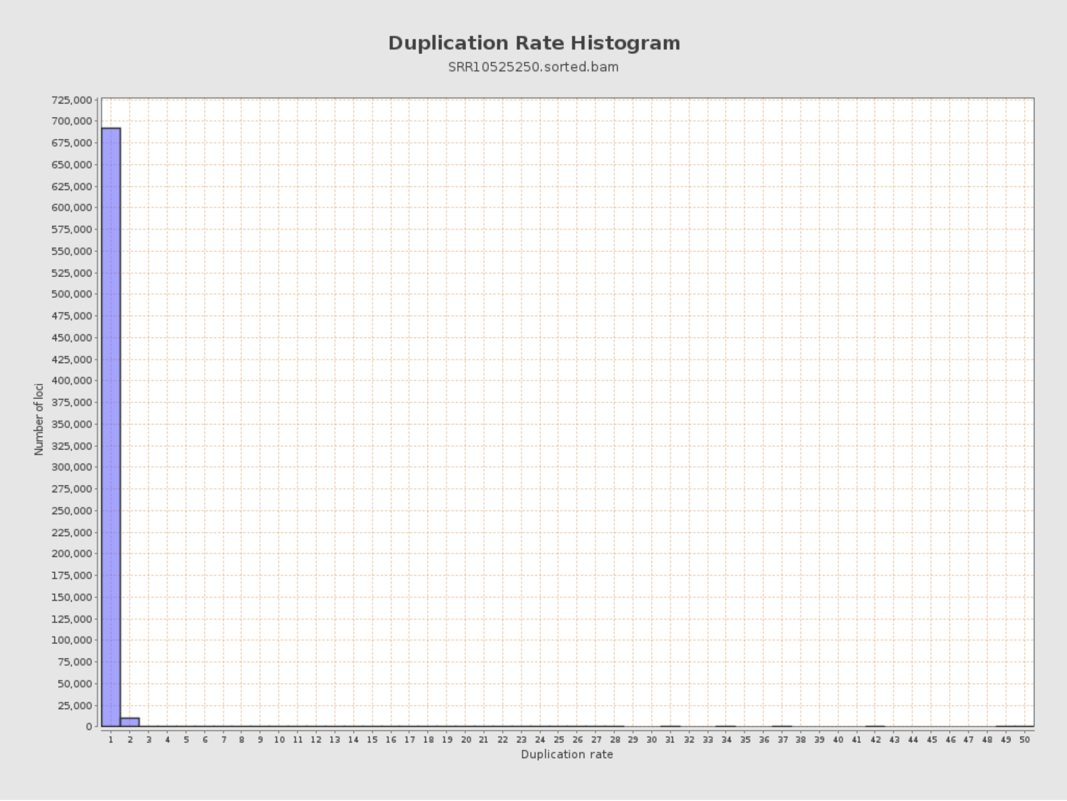
5. Results : Coverage Histogram (0-50X)



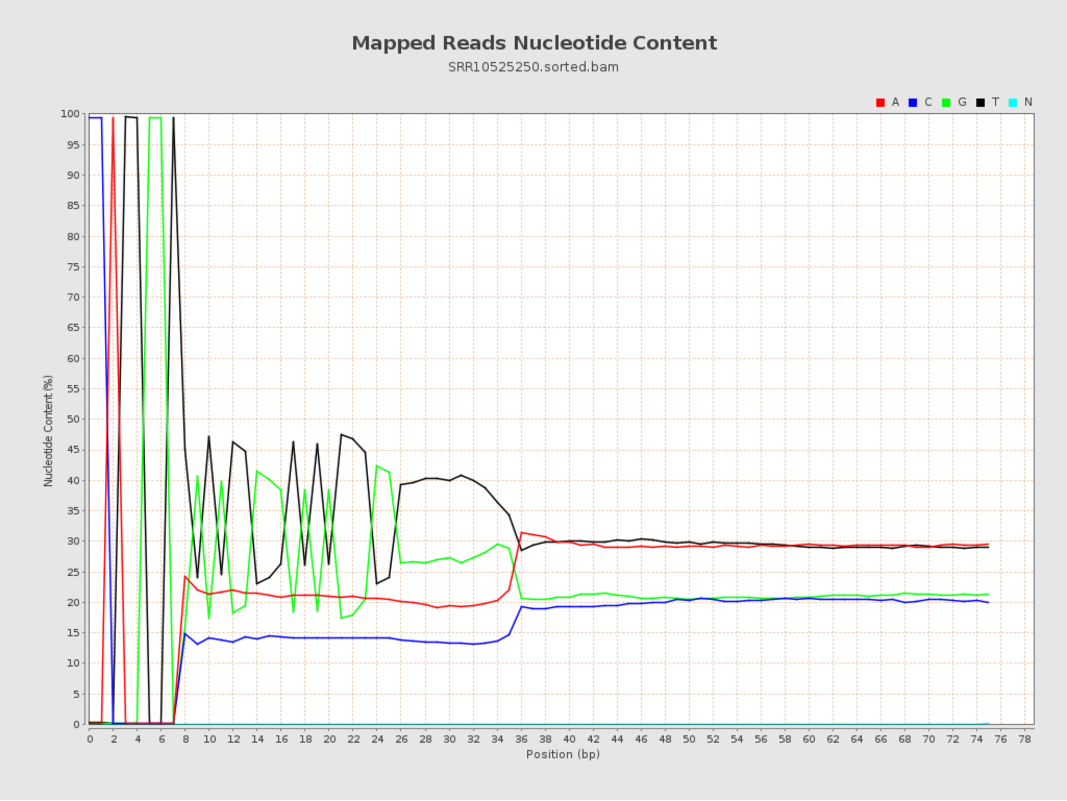
6. Results : Genome Fraction Coverage



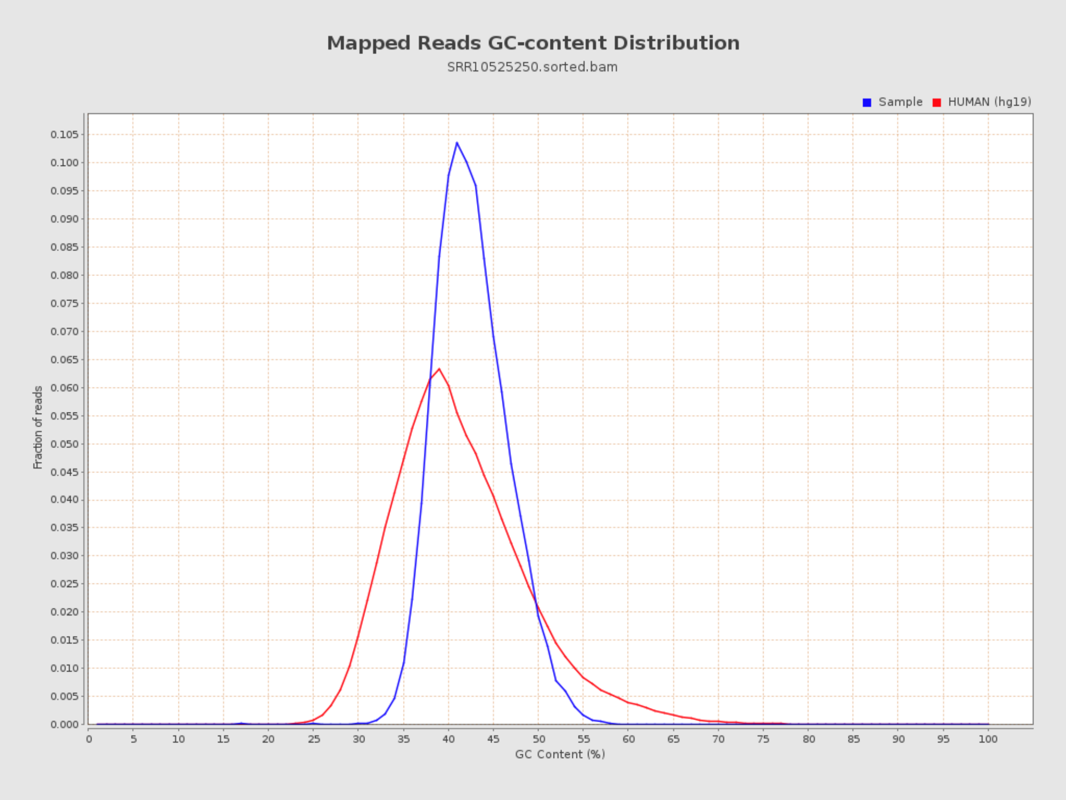
7. Results : Duplication Rate Histogram



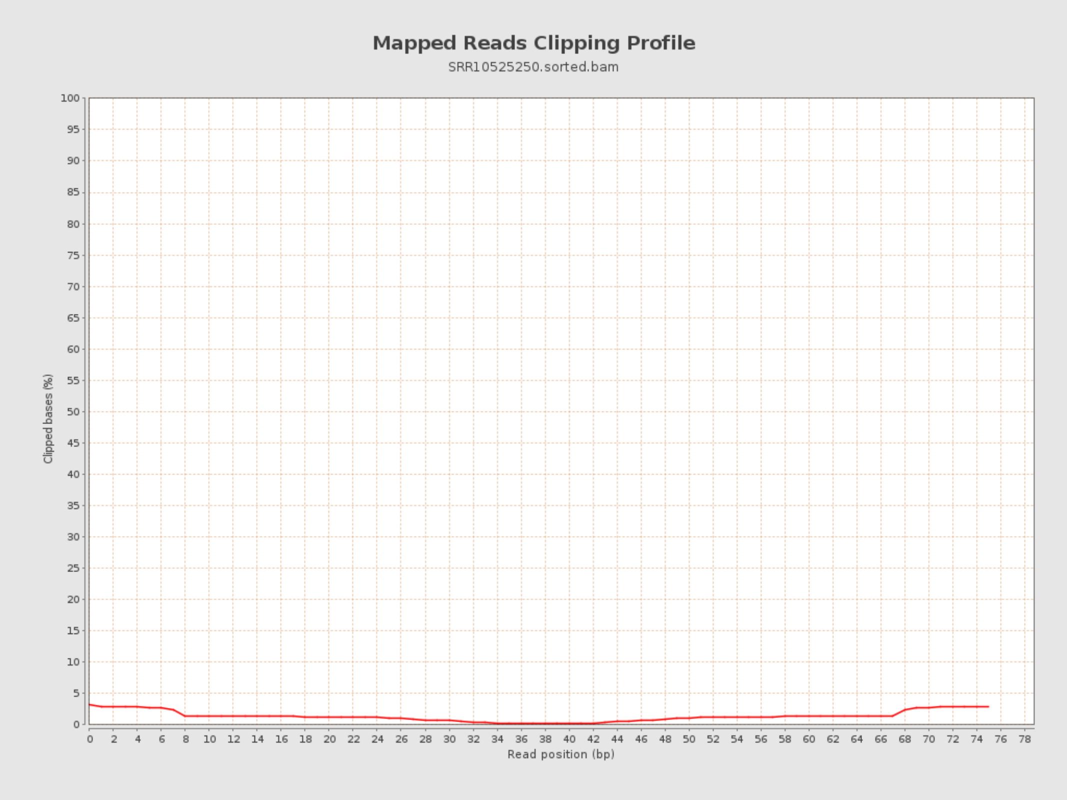
8. Results : Mapped Reads Nucleotide Content



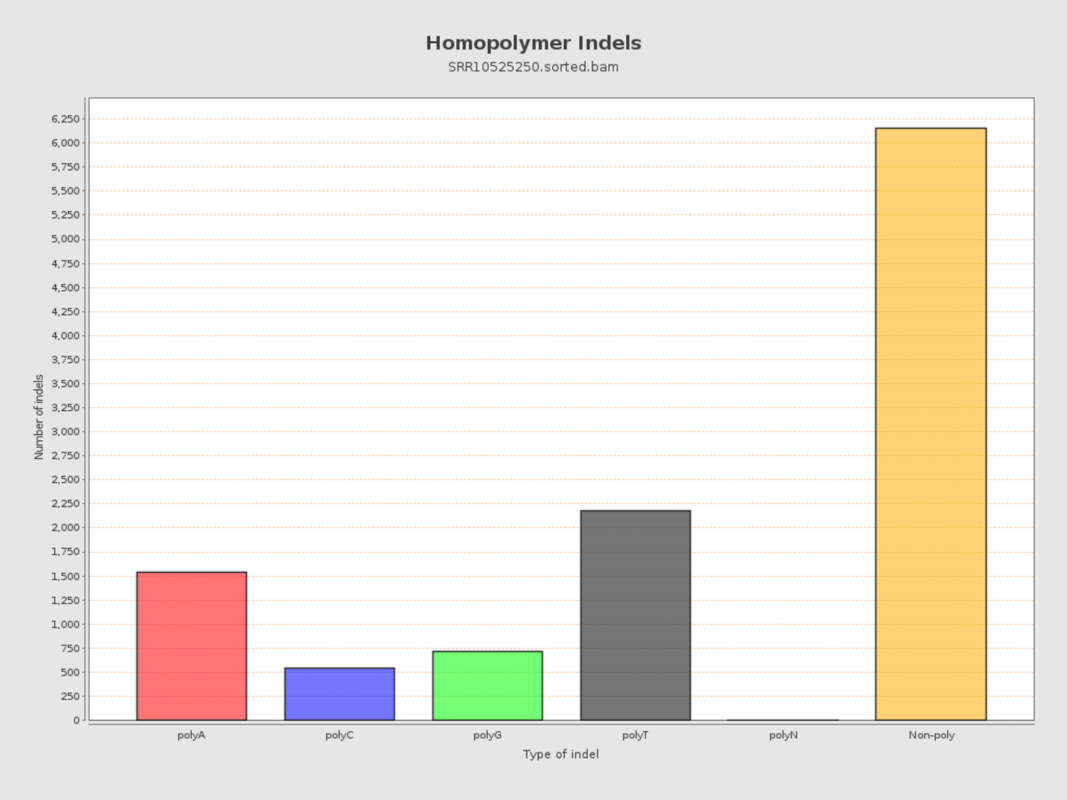
9. Results : Mapped Reads GC-content Distribution



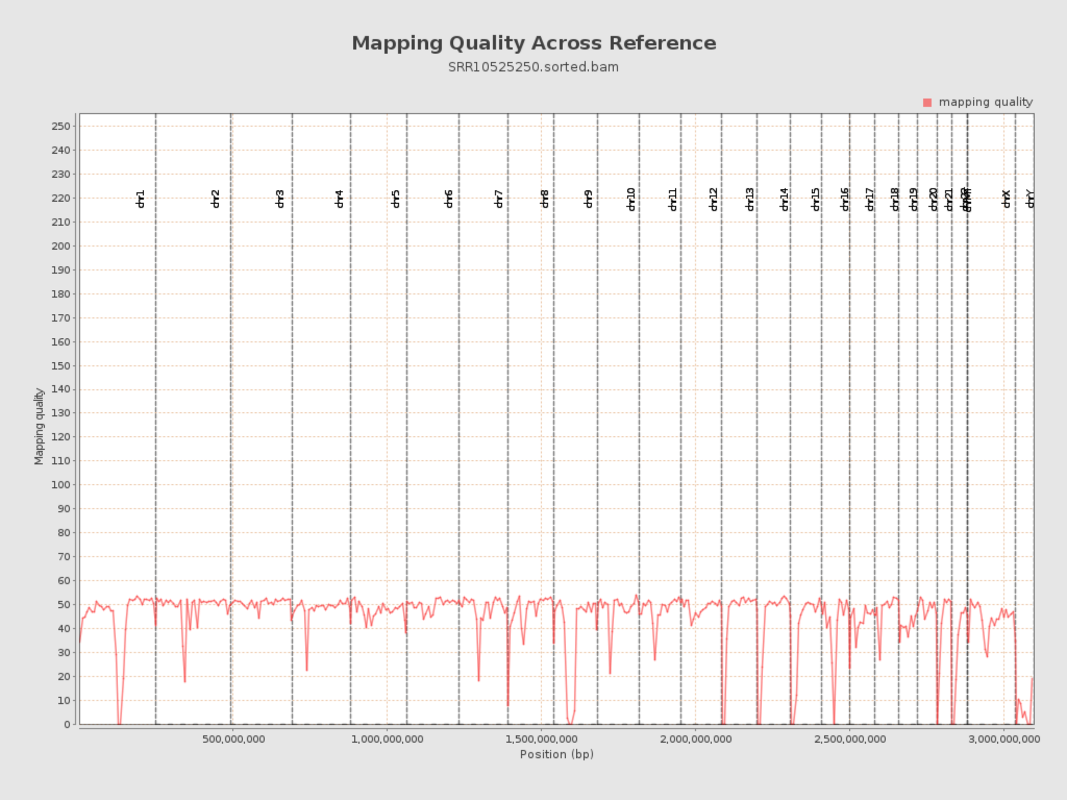
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram