Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:11:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525150.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_SRR10525150 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525150.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:11:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525150.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,529,180
Mapped reads	1,228,211 / 80.32%
Unmapped reads	300,969 / 19.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,894 / 0.25%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	37,213 / 2.43%
Duplication rate	2.2%
Clipped reads	1,228,567 / 80.34%

2.2. ACGT Content

Number/percentage of A's	18,007,419 / 24.94%
Number/percentage of C's	13,643,071 / 18.89%
Number/percentage of T's	22,798,022 / 31.57%
Number/percentage of G's	17,755,942 / 24.59%
Number/percentage of N's	1,643 / 0%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0233

Standard Deviation	0.2376

2.4. Mapping Quality

Mean Mapping Quality	45.03

2.5. Mismatches and indels

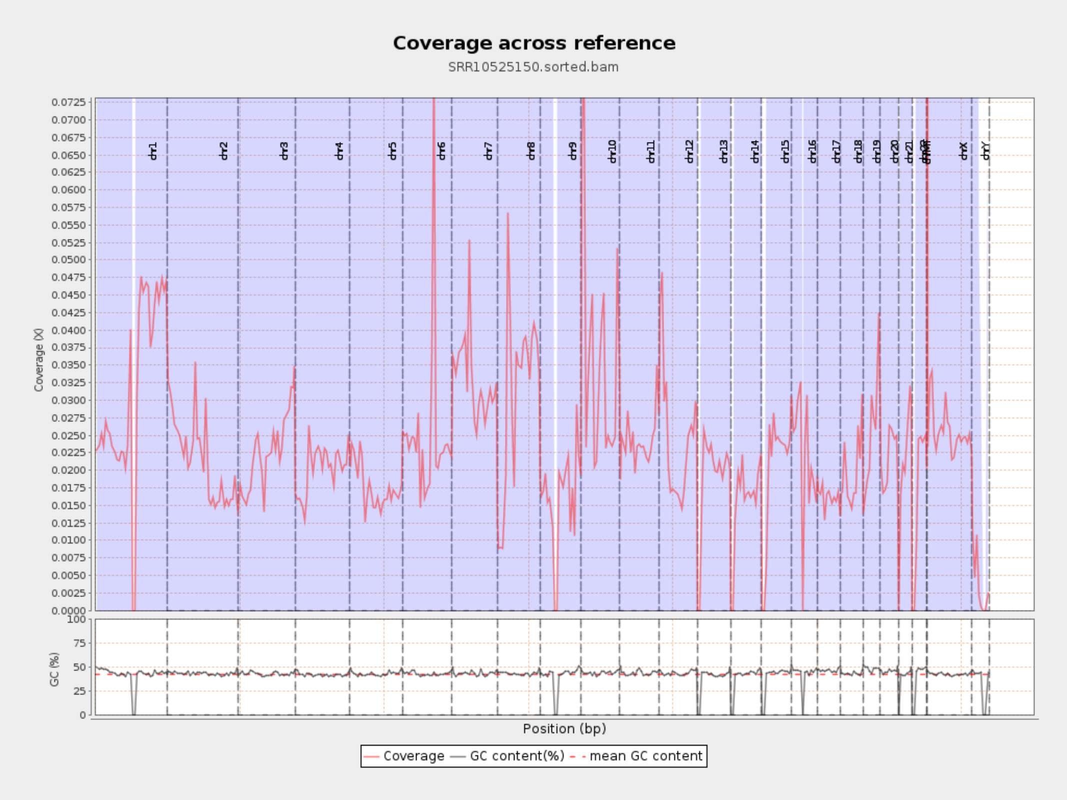
General error rate	0.51%
Mismatches	359,967
Insertions	5,803
Mapped reads with at least one insertion	0.47%
Deletions	13,670
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.16%

2.6. Chromosome stats

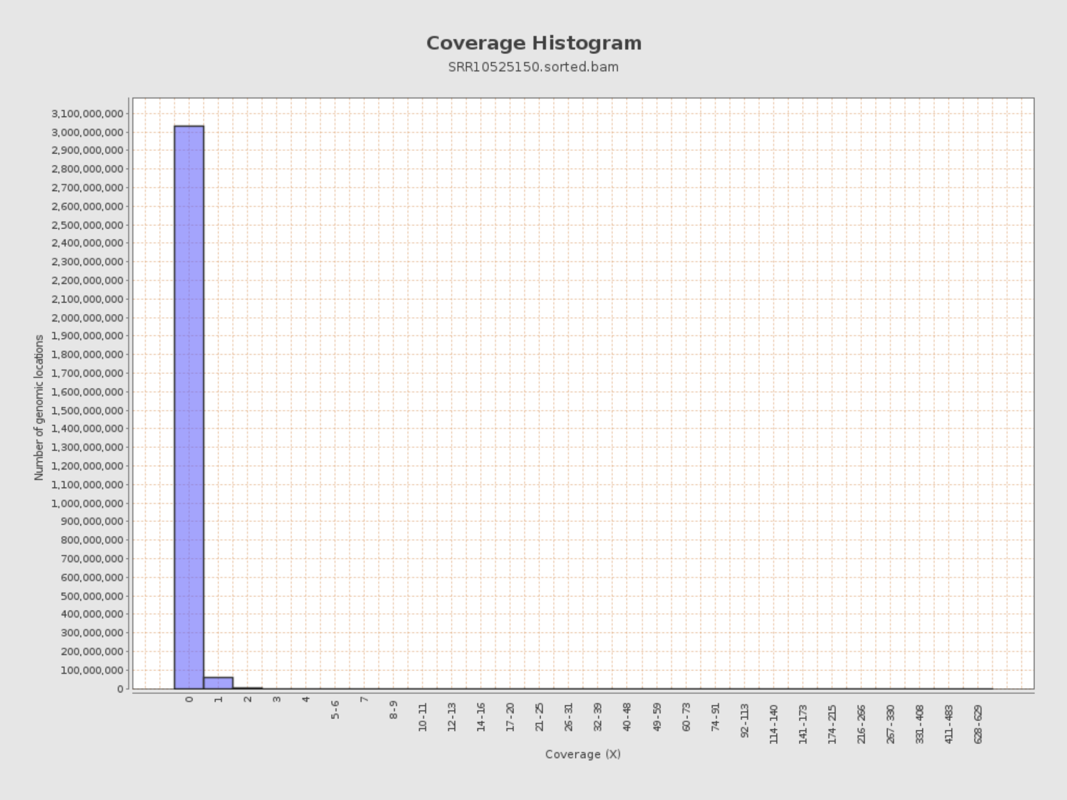
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7823578	0.0314	0.4087
chr2	243199373	5214706	0.0214	0.3021
chr3	198022430	4418056	0.0223	0.1603
chr4	191154276	3885166	0.0203	0.1579
chr5	180915260	3181564	0.0176	0.1414
chr6	171115067	4343838	0.0254	0.1883
chr7	159138663	5281676	0.0332	0.4071

chr8	146364022	4597154	0.0314	0.2217
chr9	141213431	2239958	0.0159	0.1676
chr10	135534747	4930903	0.0364	0.255
chr11	135006516	3265726	0.0242	0.2032
chr12	133851895	3291315	0.0246	0.1692
chr13	115169878	2176274	0.0189	0.1481
chr14	107349540	1658854	0.0155	0.1389
chr15	102531392	2009476	0.0196	0.1514
chr16	90354753	1999096	0.0221	0.1835
chr17	81195210	1307159	0.0161	0.1406
chr18	78077248	1517993	0.0194	0.3353
chr19	59128983	1513997	0.0256	0.2928
chr20	63025520	1369120	0.0217	0.1584
chr21	48129895	1030626	0.0214	0.1602
chr22	51304566	871237	0.017	0.1385
chrMT	16571	83744	5.0536	3.2462
chrX	155270560	3996500	0.0257	0.181
chrY	59373566	220900	0.0037	0.0943

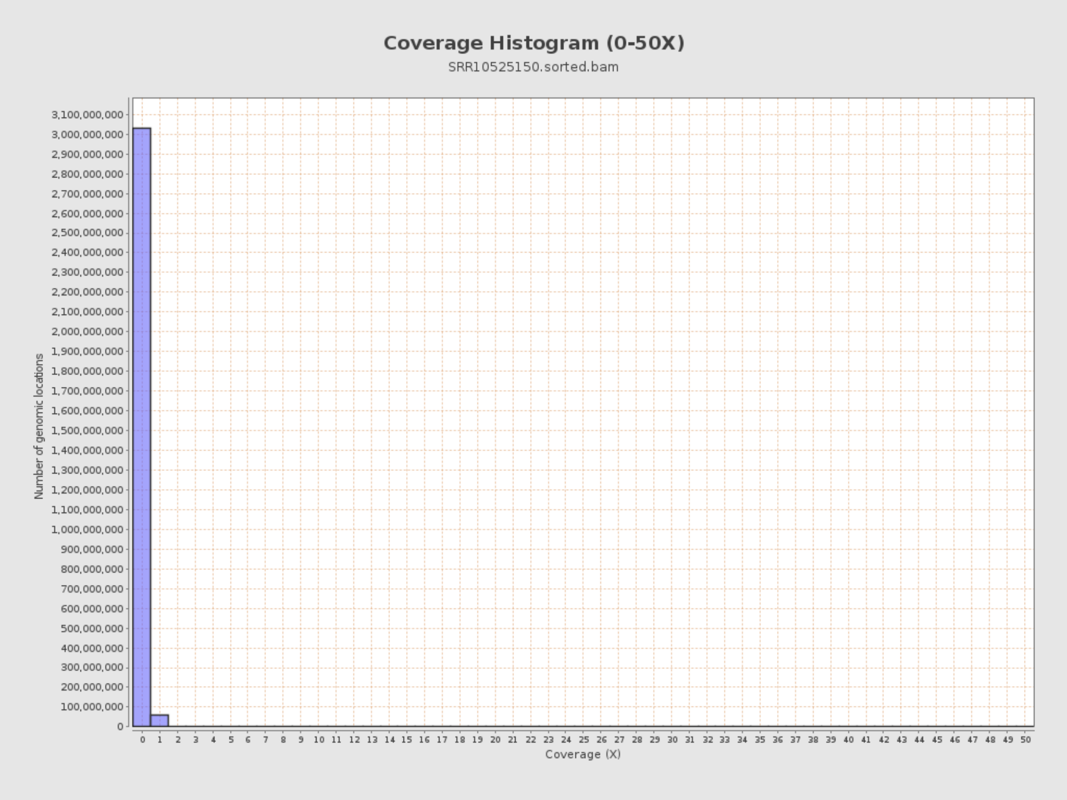
3. Results : Coverage across reference



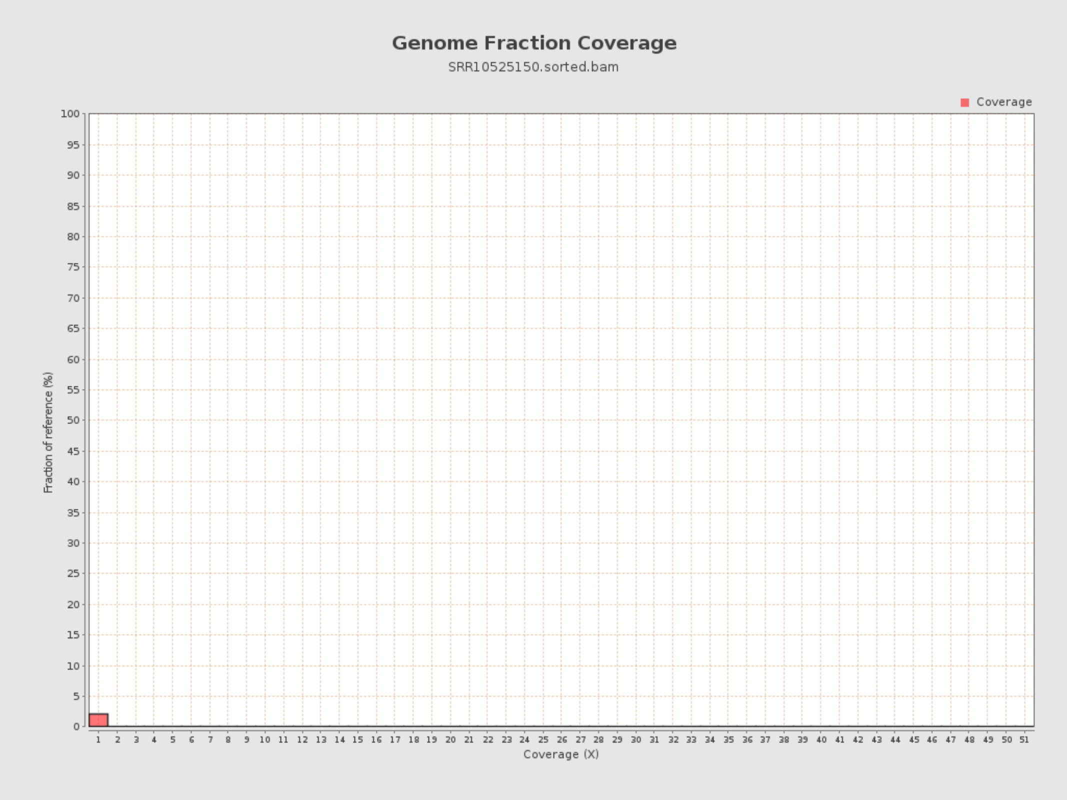
4. Results : Coverage Histogram



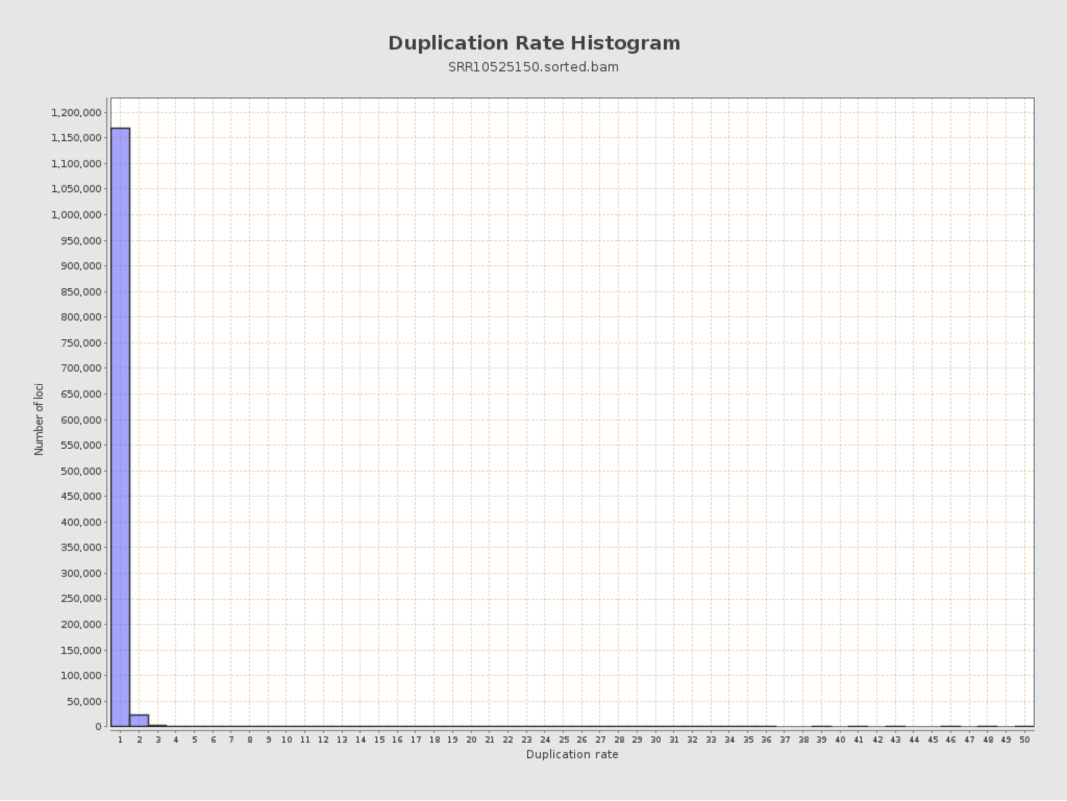
5. Results : Coverage Histogram (0-50X)



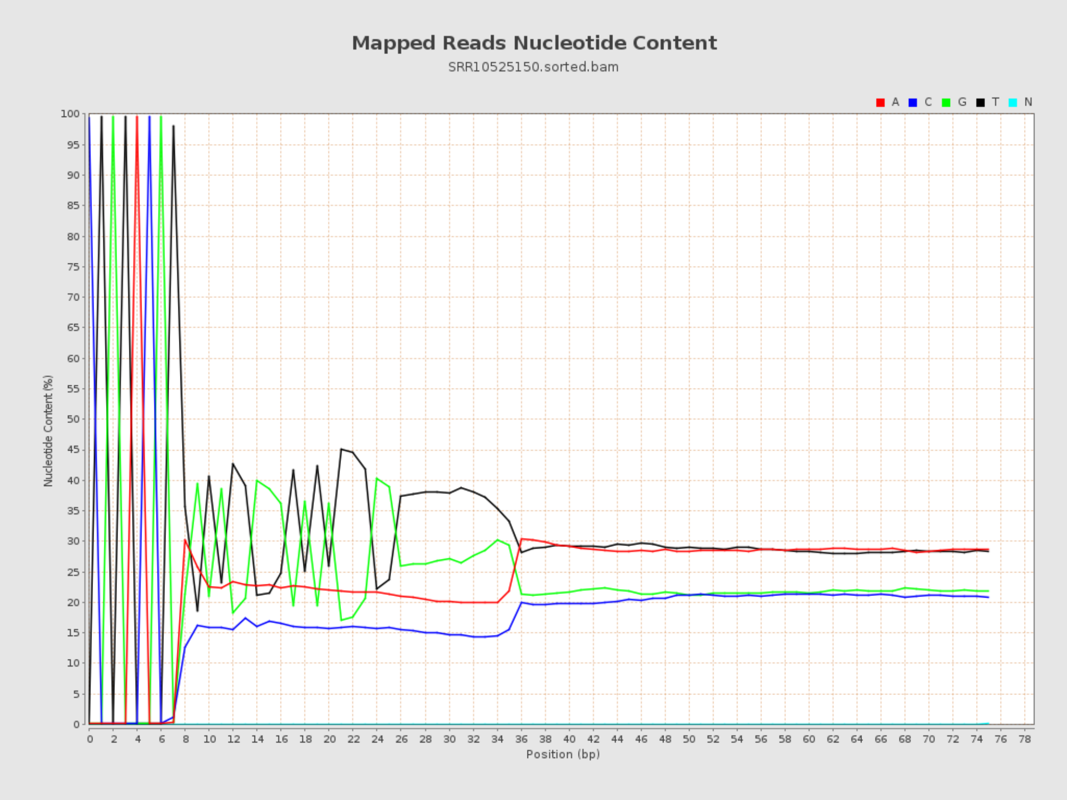
6. Results : Genome Fraction Coverage



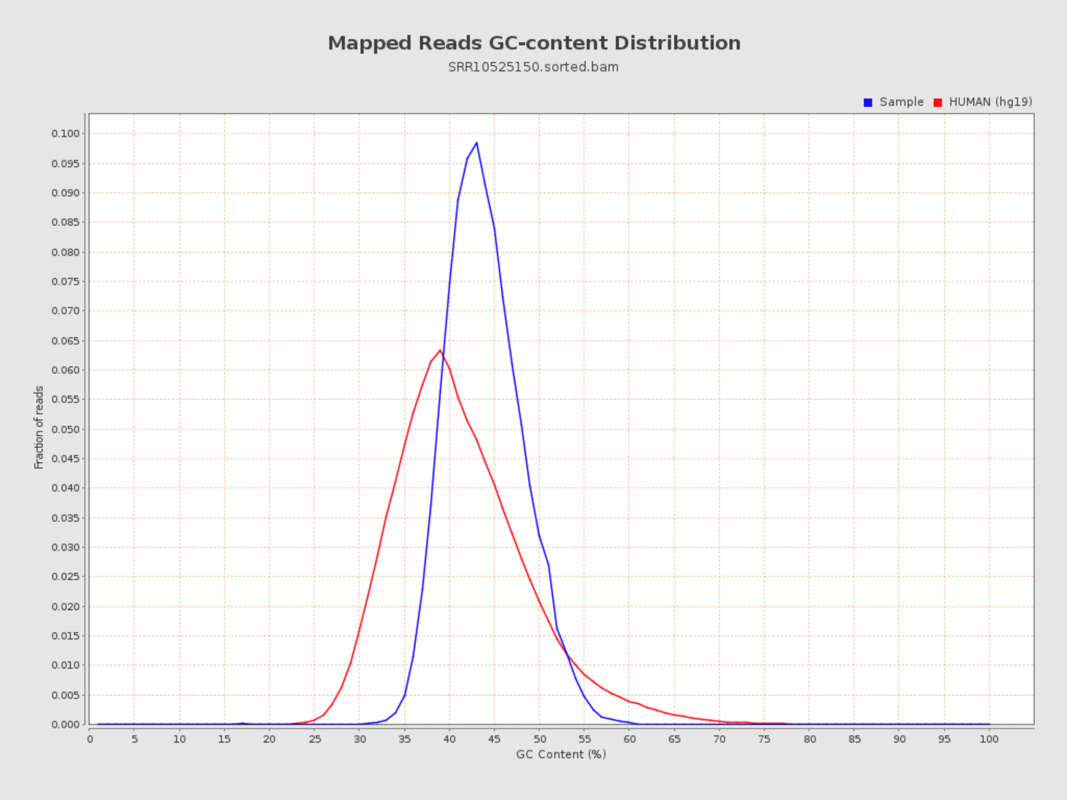
7. Results : Duplication Rate Histogram



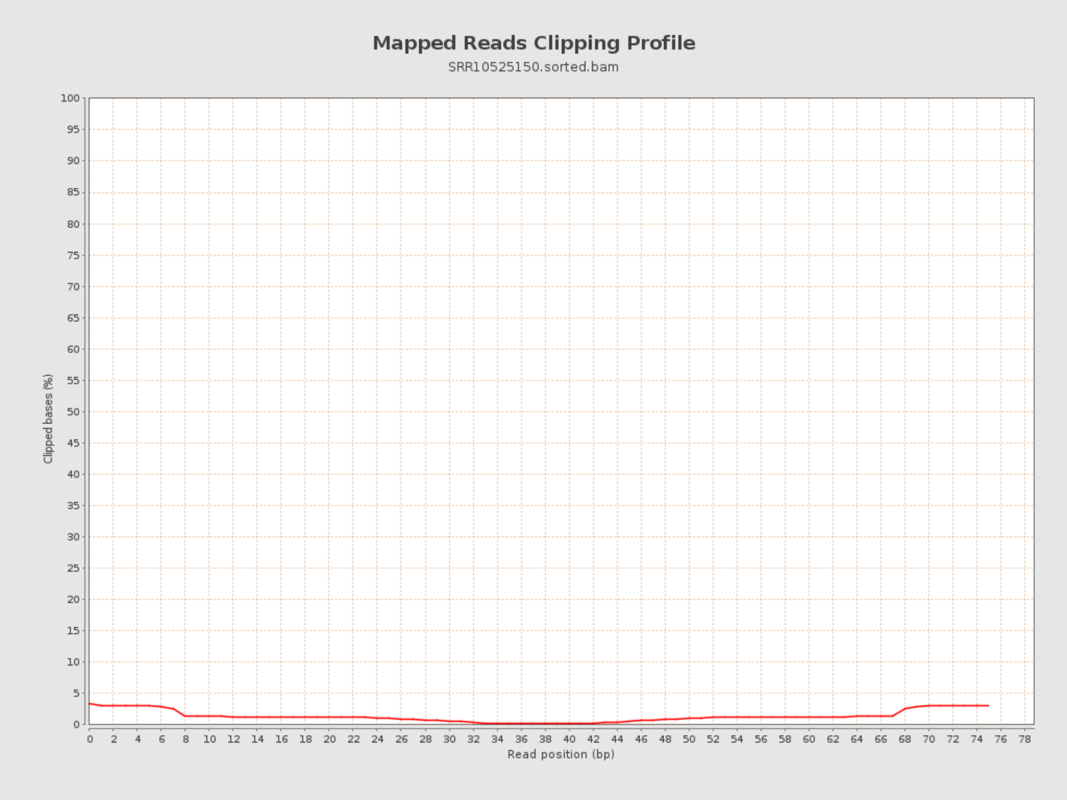
8. Results : Mapped Reads Nucleotide Content



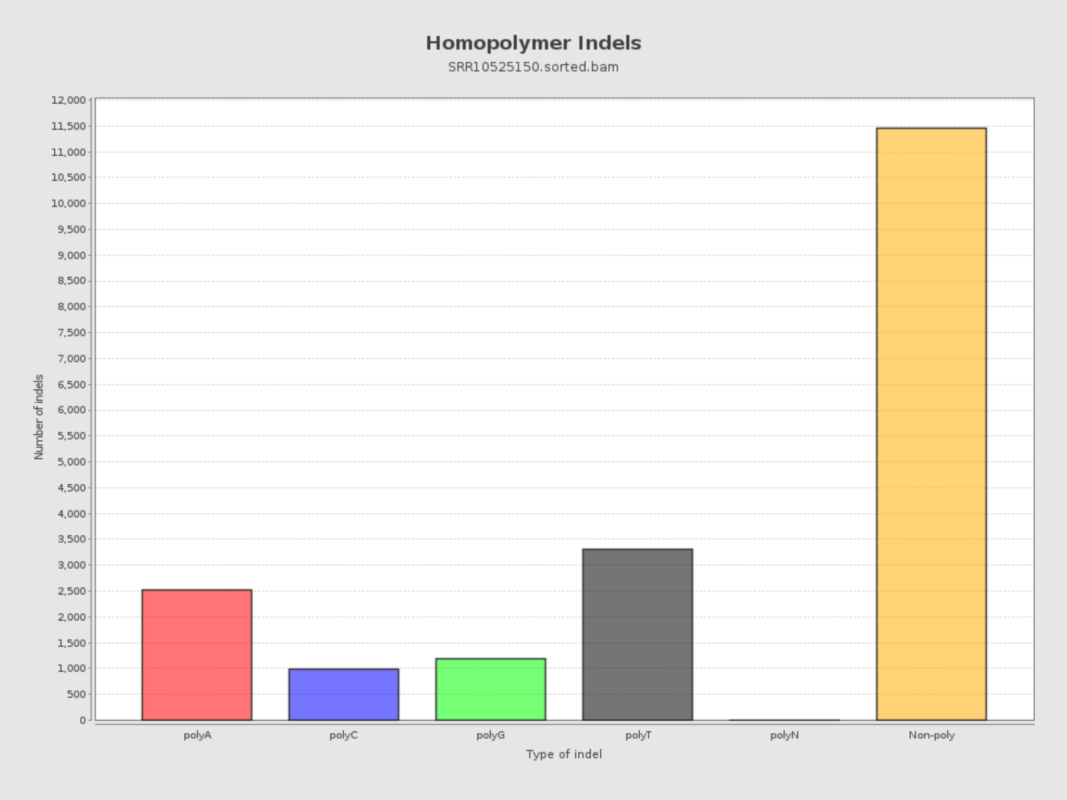
9. Results : Mapped Reads GC-content Distribution



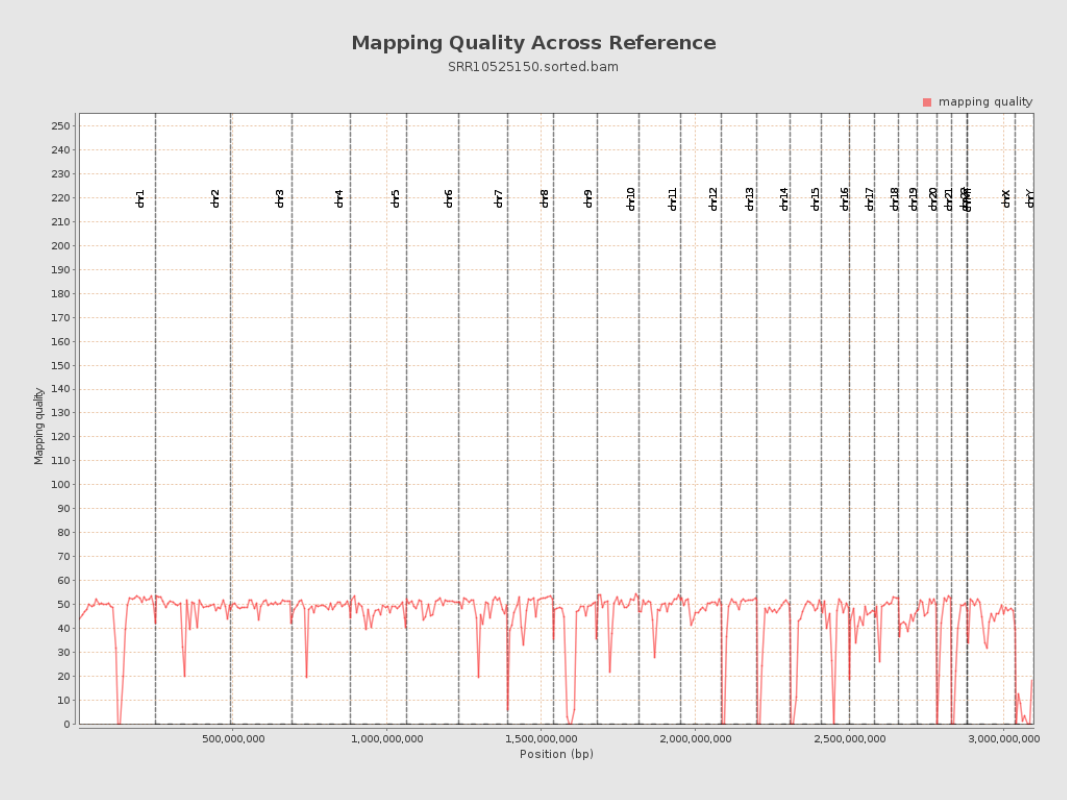
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram