Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:29:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525213.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_SRR10525213 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525213.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:29:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525213.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,137,382
Mapped reads	1,015,662 / 89.3%
Unmapped reads	121,720 / 10.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,315 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	25,034 / 2.2%
Duplication rate	1.71%
Clipped reads	1,016,141 / 89.34%

2.2. ACGT Content

Number/percentage of A's	15,969,174 / 26.39%
Number/percentage of C's	12,034,122 / 19.89%
Number/percentage of T's	18,575,262 / 30.7%
Number/percentage of G's	13,929,662 / 23.02%
Number/percentage of N's	1,351 / 0%
GC Percentage	42.91%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.2148

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

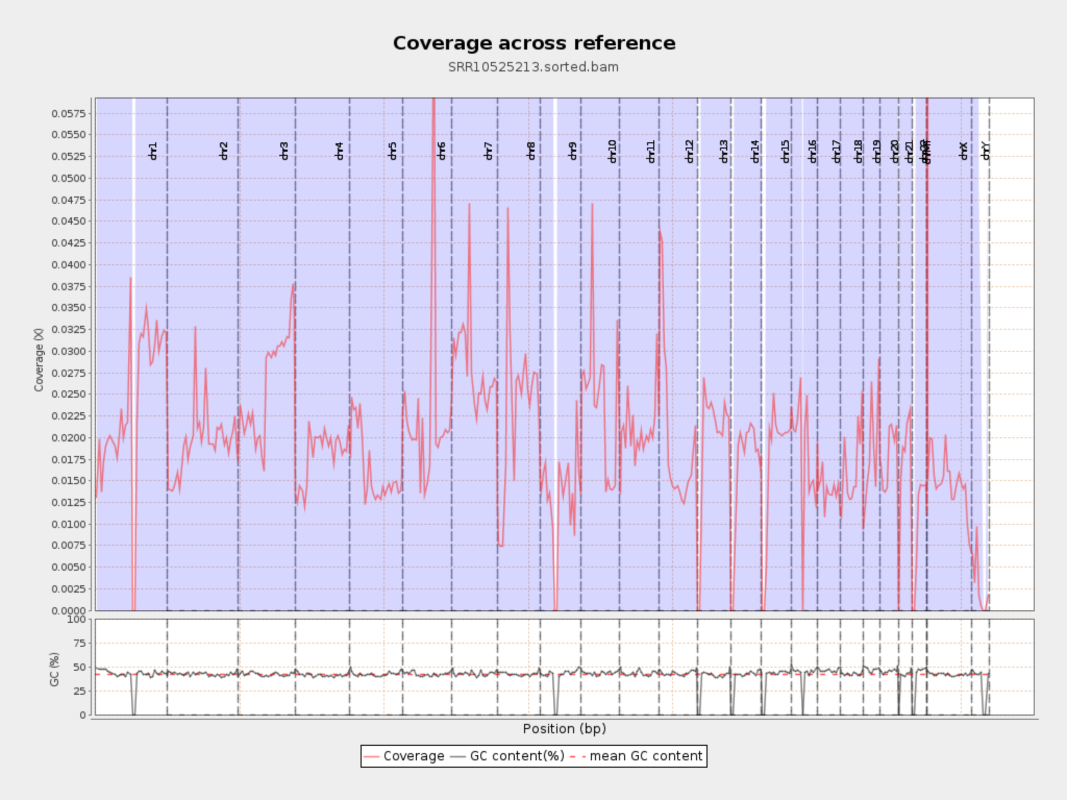
General error rate	0.51%
Mismatches	300,391
Insertions	4,490
Mapped reads with at least one insertion	0.44%
Deletions	12,279
Mapped reads with at least one deletion	1.2%
Homopolymer indels	41.76%

2.6. Chromosome stats

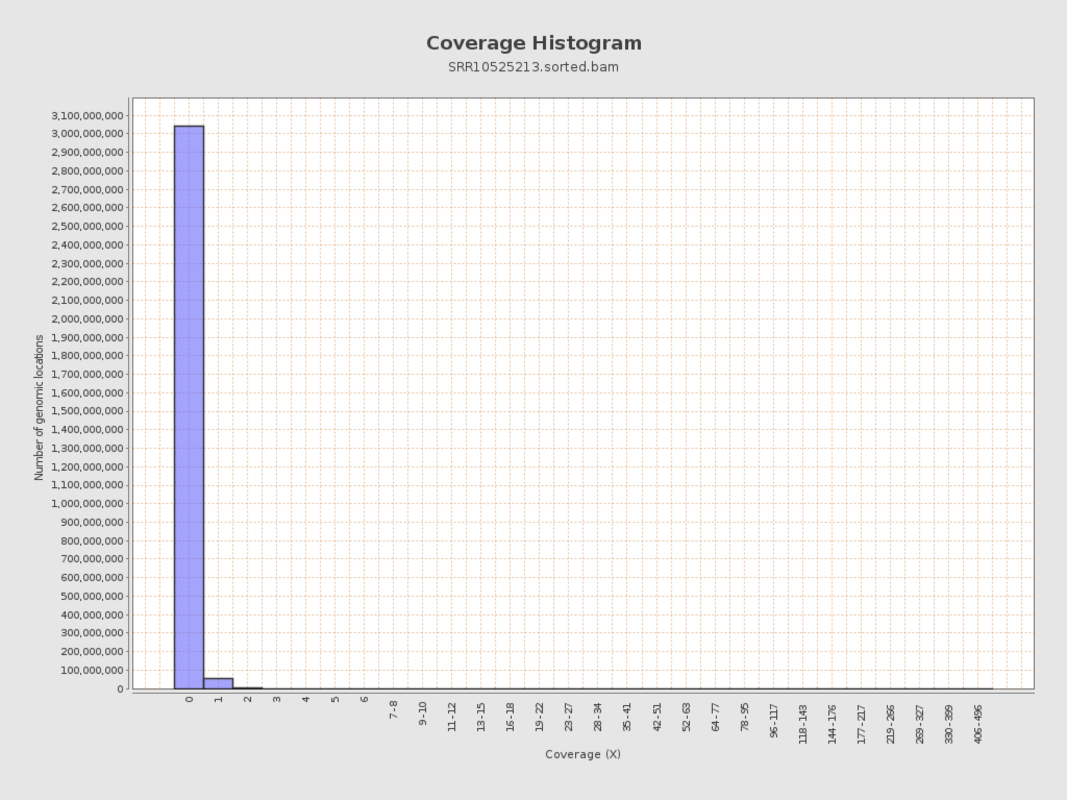
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5886875	0.0236	0.3982
chr2	243199373	4737525	0.0195	0.2251
chr3	198022430	5181469	0.0262	0.1722
chr4	191154276	3464987	0.0181	0.1455
chr5	180915260	2953384	0.0163	0.1341
chr6	171115067	3974273	0.0232	0.1708
chr7	159138663	4521521	0.0284	0.3769

chr8	146364022	3428327	0.0234	0.1938
chr9	141213431	1831060	0.013	0.1463
chr10	135534747	3297568	0.0243	0.2458
chr11	135006516	2824798	0.0209	0.1718
chr12	133851895	2665165	0.0199	0.1495
chr13	115169878	2253170	0.0196	0.1466
chr14	107349540	1745636	0.0163	0.1376
chr15	102531392	1728728	0.0169	0.1367
chr16	90354753	1608343	0.0178	0.1538
chr17	81195210	1129273	0.0139	0.1299
chr18	78077248	1271188	0.0163	0.2699
chr19	59128983	1094428	0.0185	0.2748
chr20	63025520	1112865	0.0177	0.1425
chr21	48129895	814282	0.0169	0.1423
chr22	51304566	504615	0.0098	0.1039
chrMT	16571	29809	1.7989	1.6943
chrX	155270560	2303000	0.0148	0.1372
chrY	59373566	166898	0.0028	0.0928

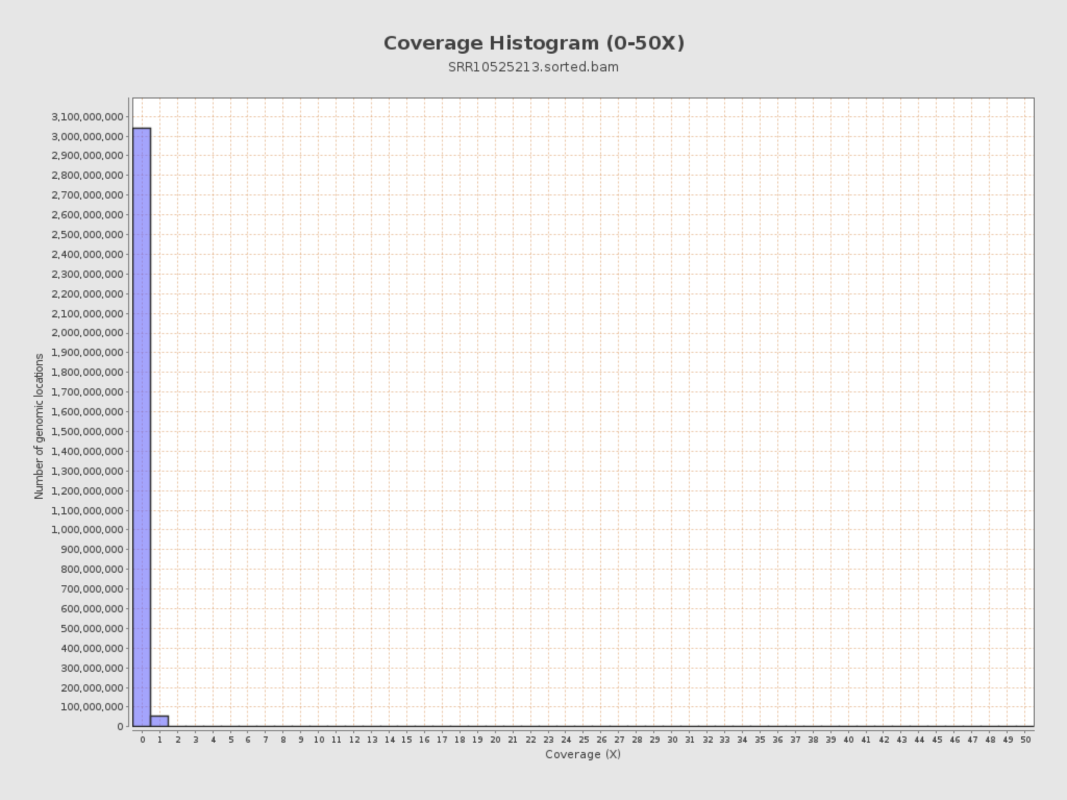
3. Results : Coverage across reference



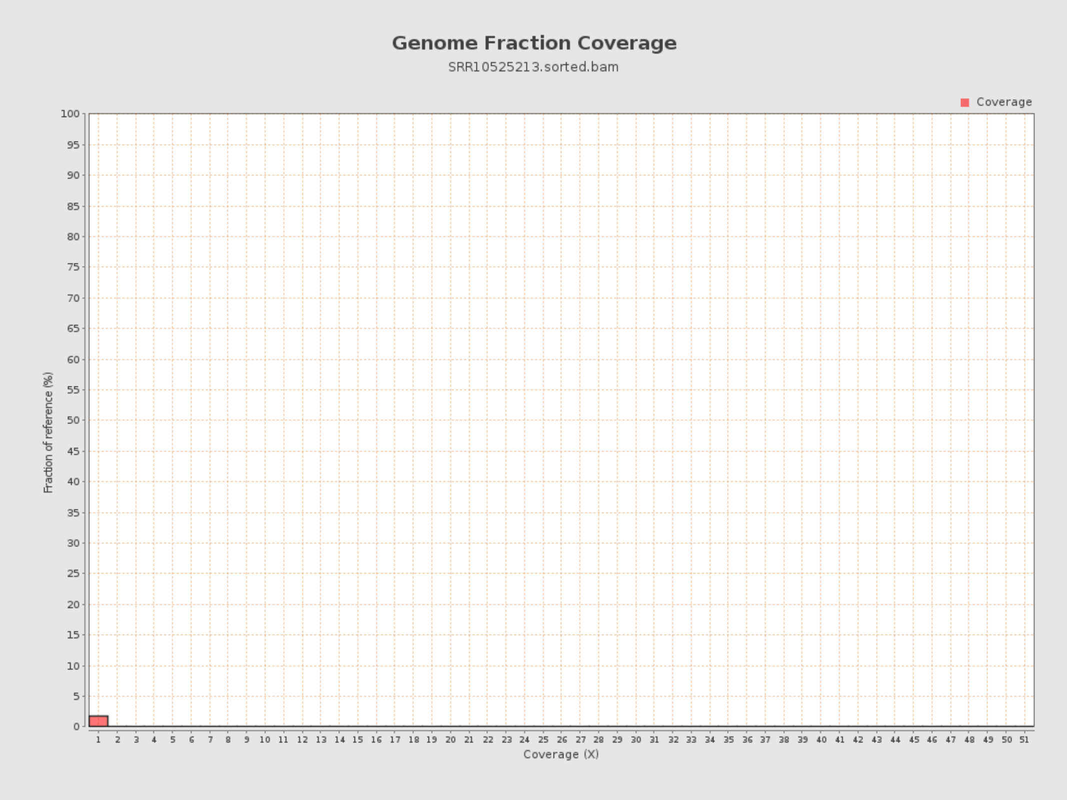
4. Results : Coverage Histogram



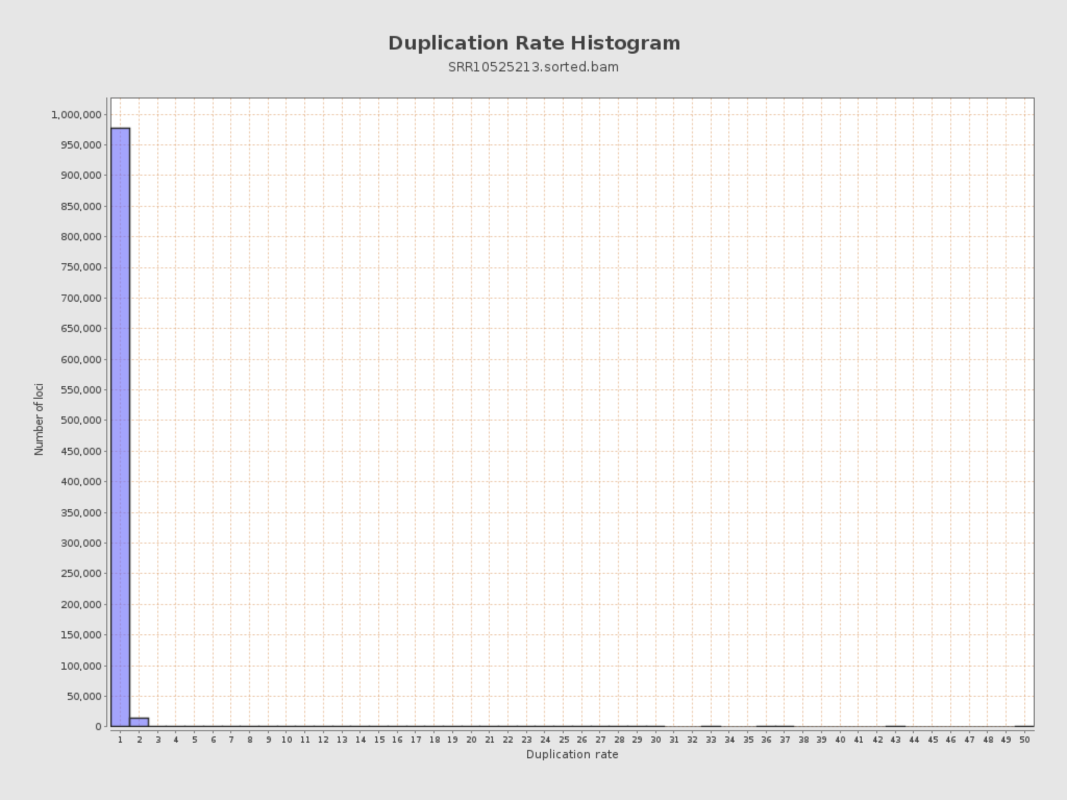
5. Results : Coverage Histogram (0-50X)



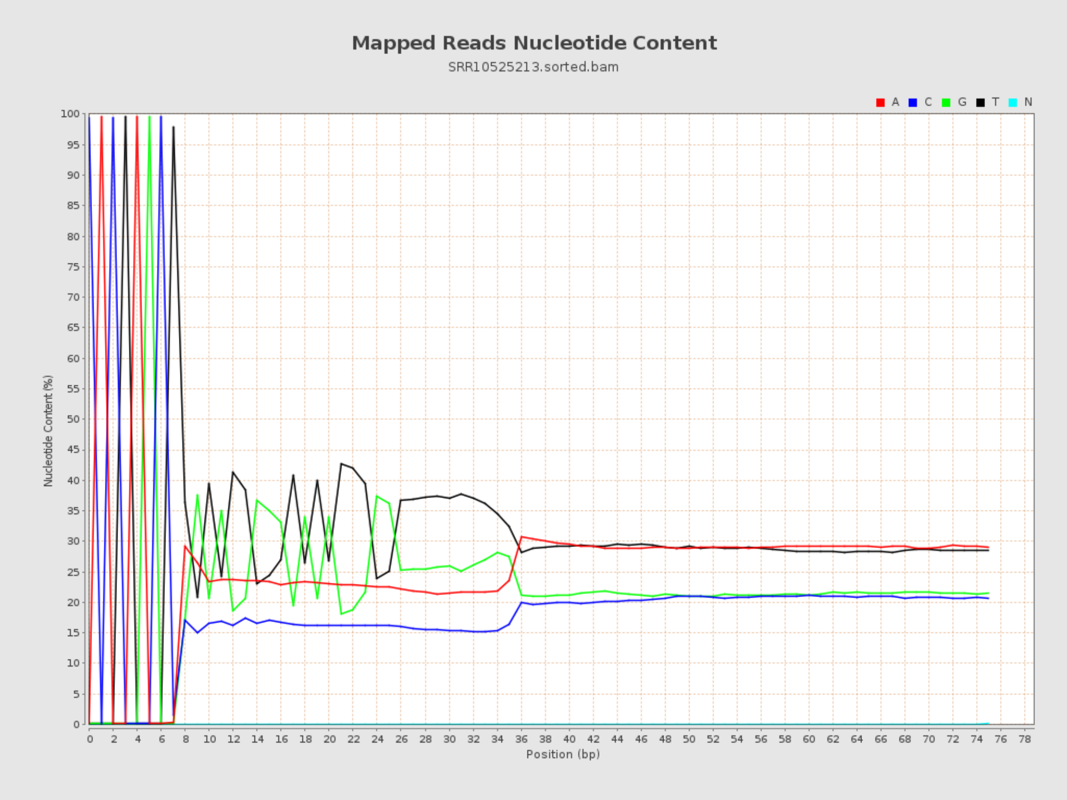
6. Results : Genome Fraction Coverage



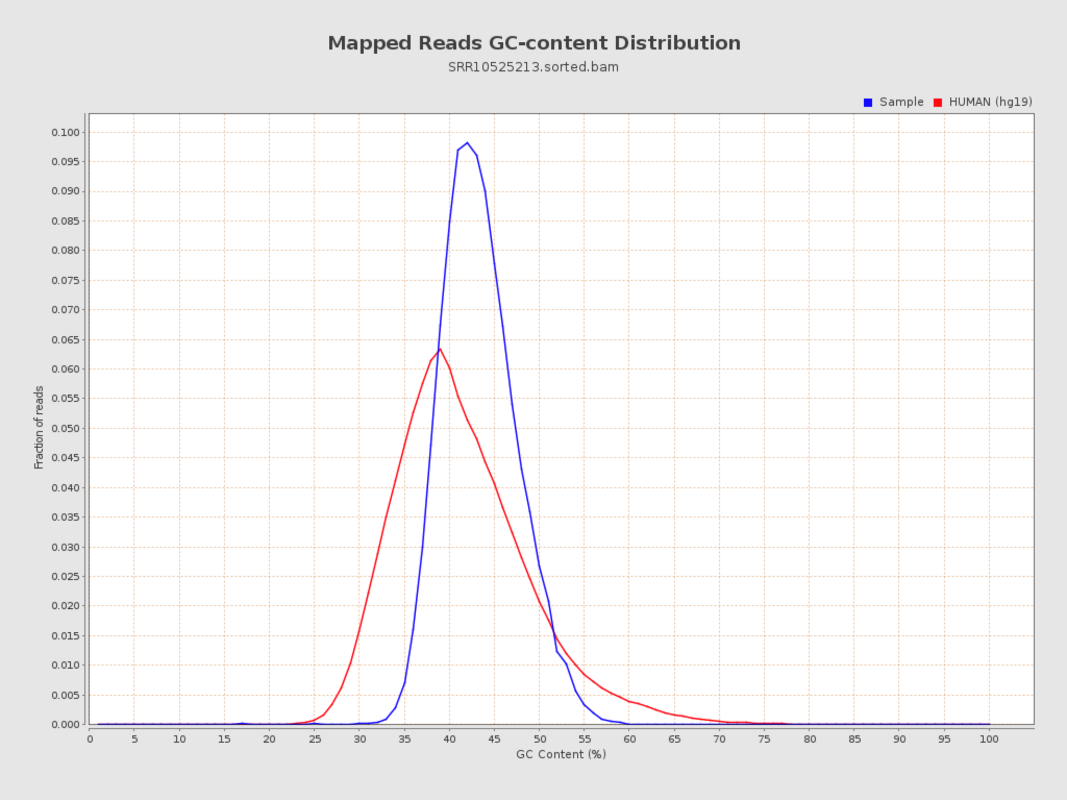
7. Results : Duplication Rate Histogram



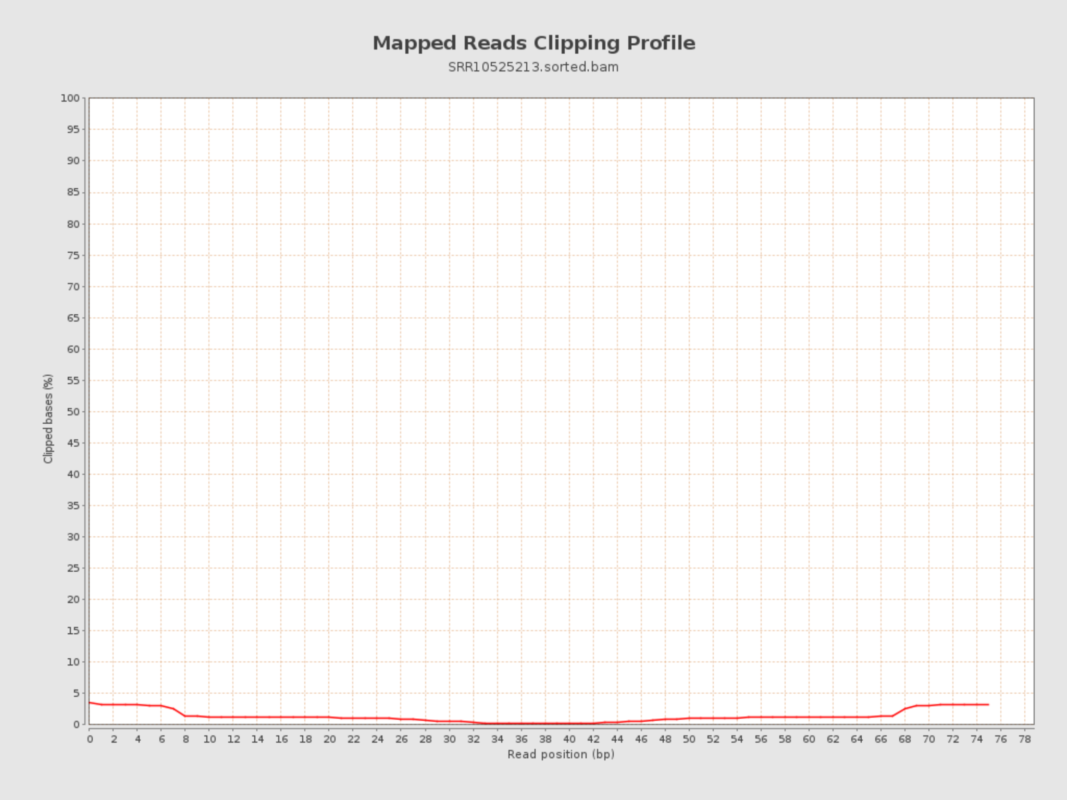
8. Results : Mapped Reads Nucleotide Content



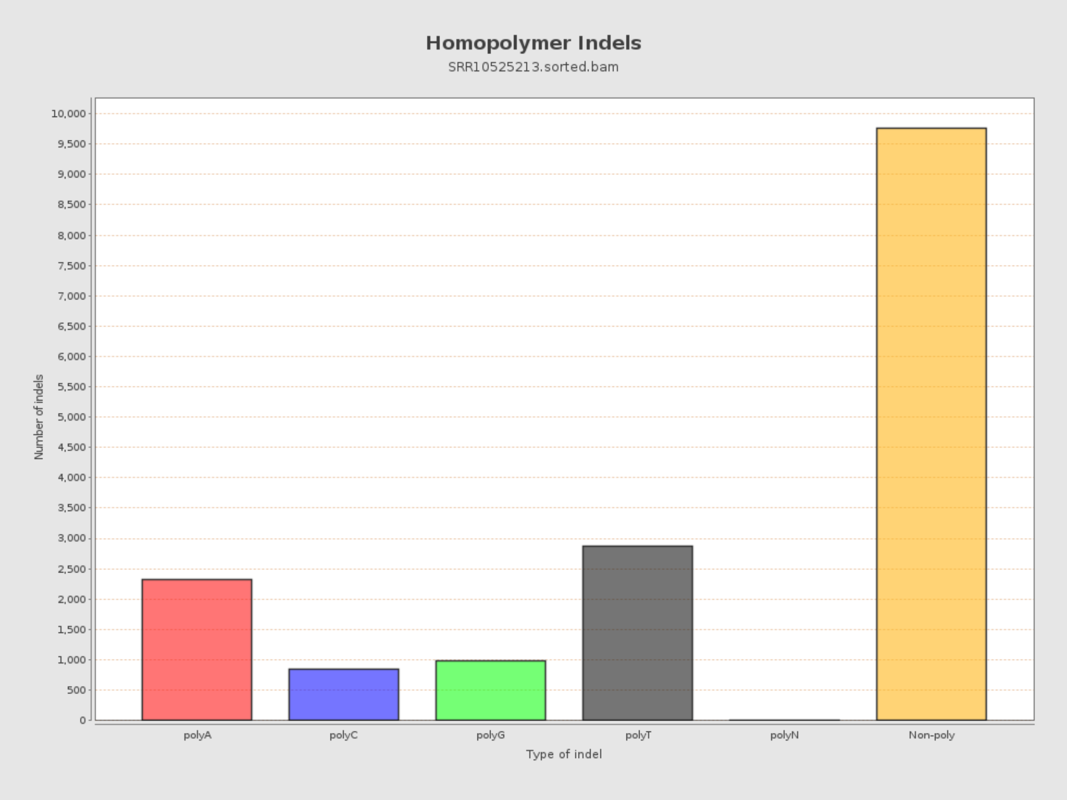
9. Results : Mapped Reads GC-content Distribution



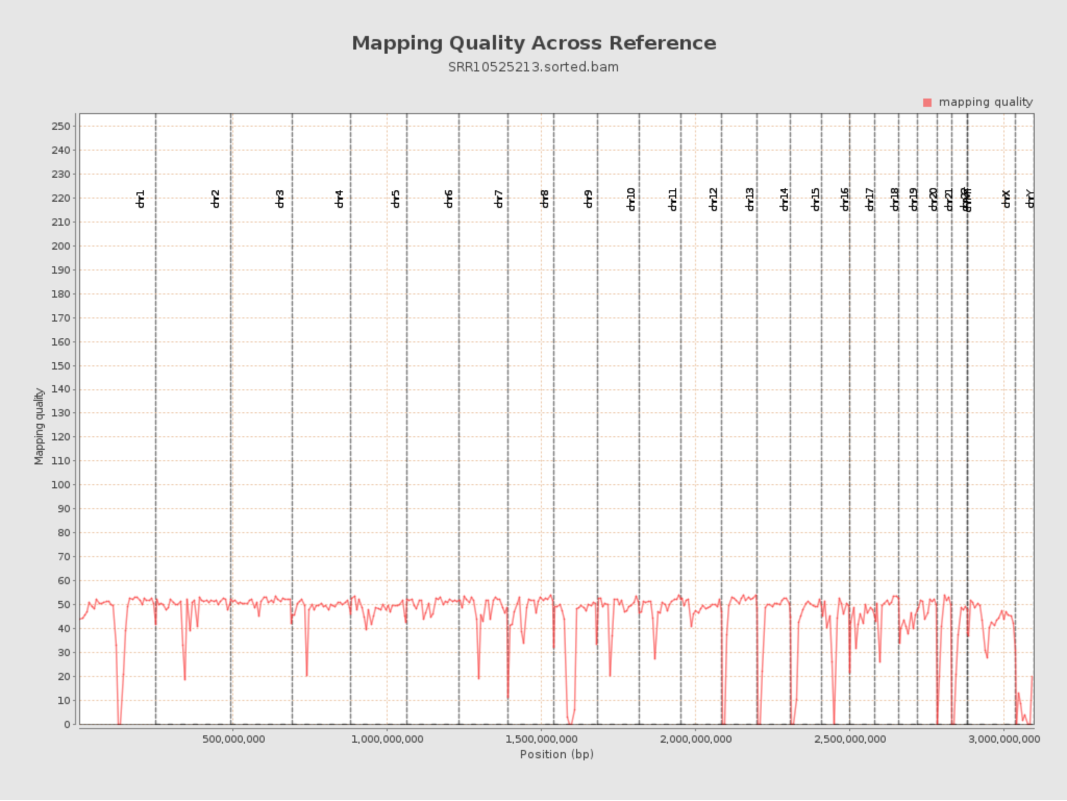
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram