Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:50:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525049.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_SRR10525049 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525049.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:50:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	805,496
Mapped reads	673,102 / 83.56%
Unmapped reads	132,394 / 16.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,872 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	28,050 / 3.48%
Duplication rate	3.51%
Clipped reads	673,426 / 83.6%

2.2. ACGT Content

Number/percentage of A's	9,924,239 / 25.58%
Number/percentage of C's	7,047,606 / 18.16%
Number/percentage of T's	12,770,708 / 32.91%
Number/percentage of G's	9,055,870 / 23.34%
Number/percentage of N's	3,926 / 0.01%
GC Percentage	41.5%

2.3. Coverage

Mean	0.0125

Standard Deviation	0.149

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

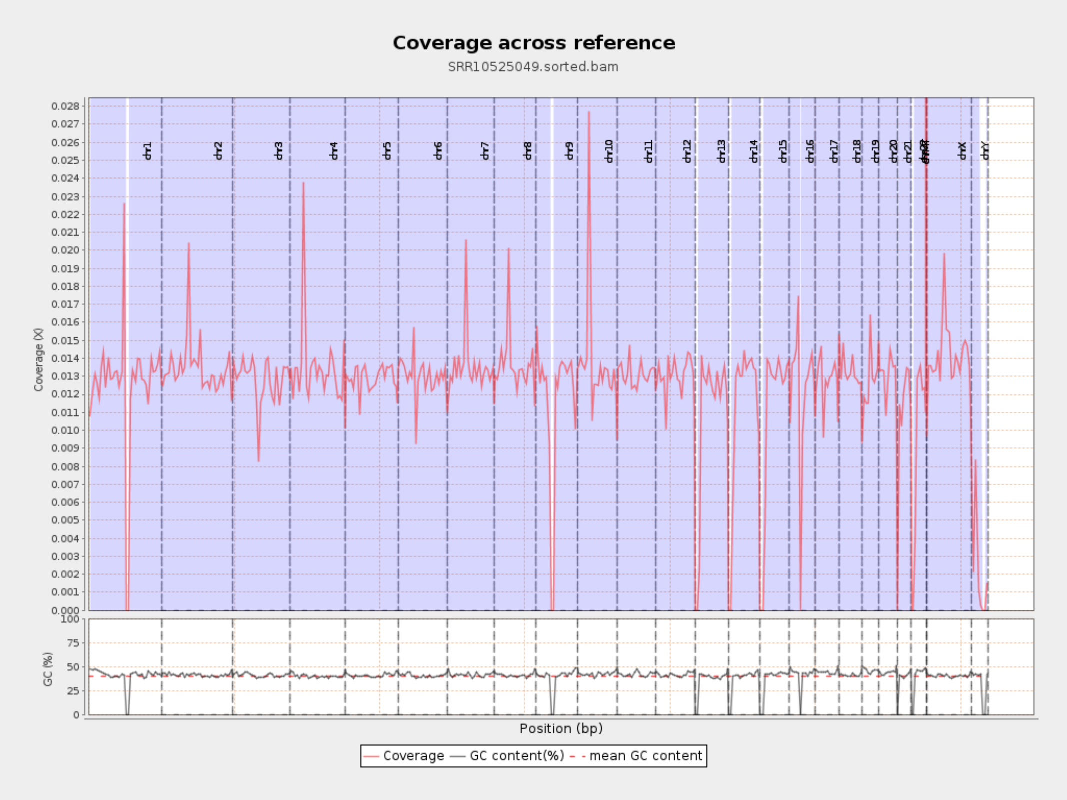
General error rate	0.51%
Mismatches	190,859
Insertions	2,994
Mapped reads with at least one insertion	0.44%
Deletions	7,698
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.05%

2.6. Chromosome stats

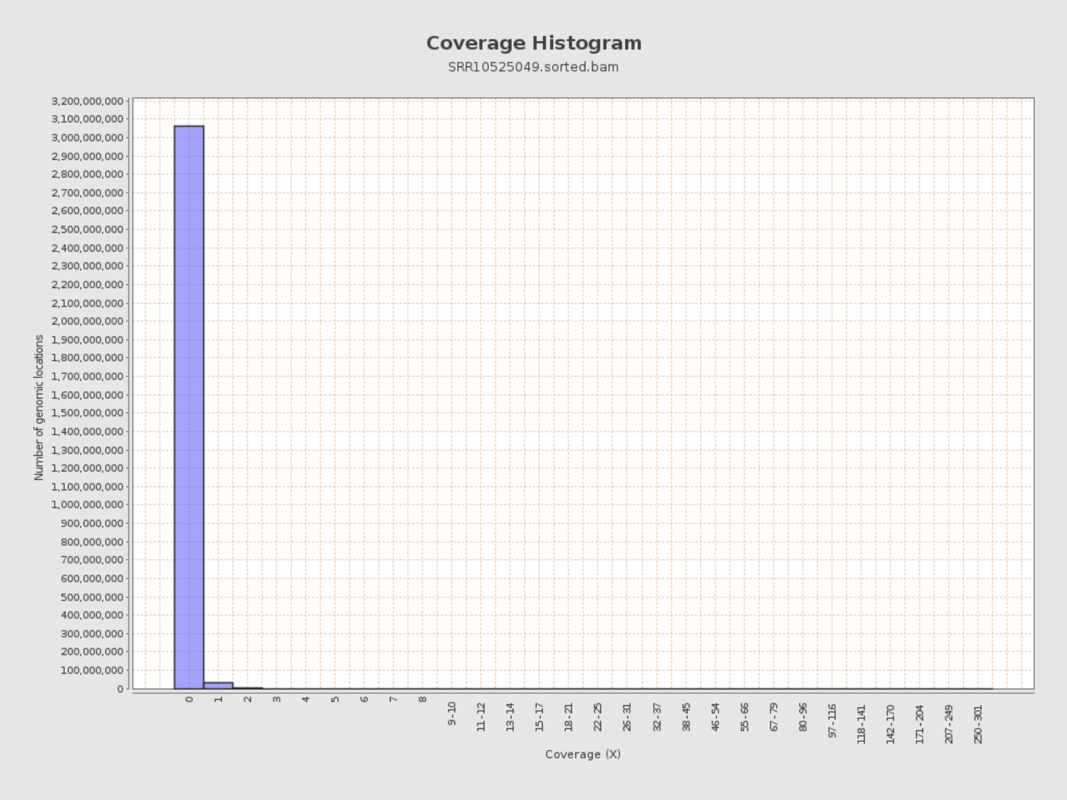
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3112833	0.0125	0.2431
chr2	243199373	3287800	0.0135	0.1757
chr3	198022430	2533507	0.0128	0.1206
chr4	191154276	2576178	0.0135	0.1333
chr5	180915260	2333001	0.0129	0.1211
chr6	171115067	2227317	0.013	0.1297
chr7	159138663	2163697	0.0136	0.1635

chr8	146364022	2001402	0.0137	0.1572
chr9	141213431	1610943	0.0114	0.1232
chr10	135534747	1871312	0.0138	0.1621
chr11	135006516	1765315	0.0131	0.1345
chr12	133851895	1745653	0.013	0.1241
chr13	115169878	1229367	0.0107	0.1103
chr14	107349540	1182814	0.011	0.1136
chr15	102531392	1108315	0.0108	0.1108
chr16	90354753	1105050	0.0122	0.1224
chr17	81195210	1030203	0.0127	0.1229
chr18	78077248	1040174	0.0133	0.187
chr19	59128983	756935	0.0128	0.1761
chr20	63025520	821198	0.013	0.1234
chr21	48129895	522200	0.0108	0.1178
chr22	51304566	448762	0.0087	0.1002
chrMT	16571	12834	0.7745	1.0573
chrX	155270560	2198036	0.0142	0.1339
chrY	59373566	129645	0.0022	0.084

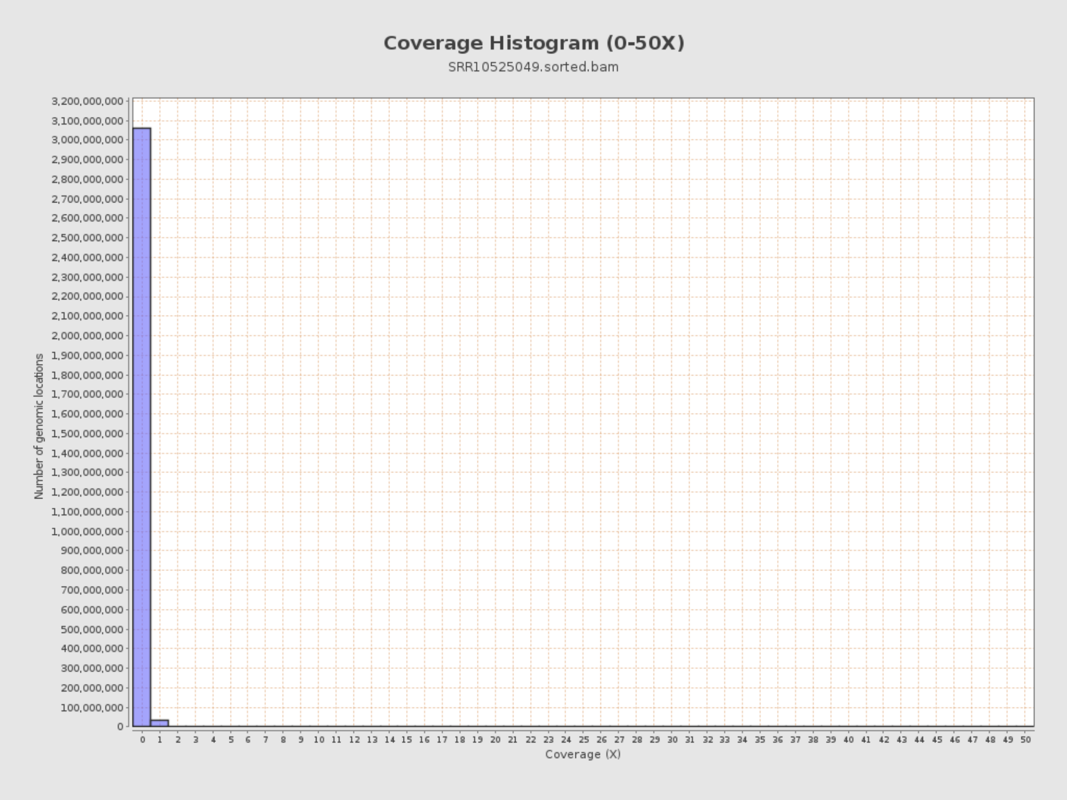
3. Results : Coverage across reference



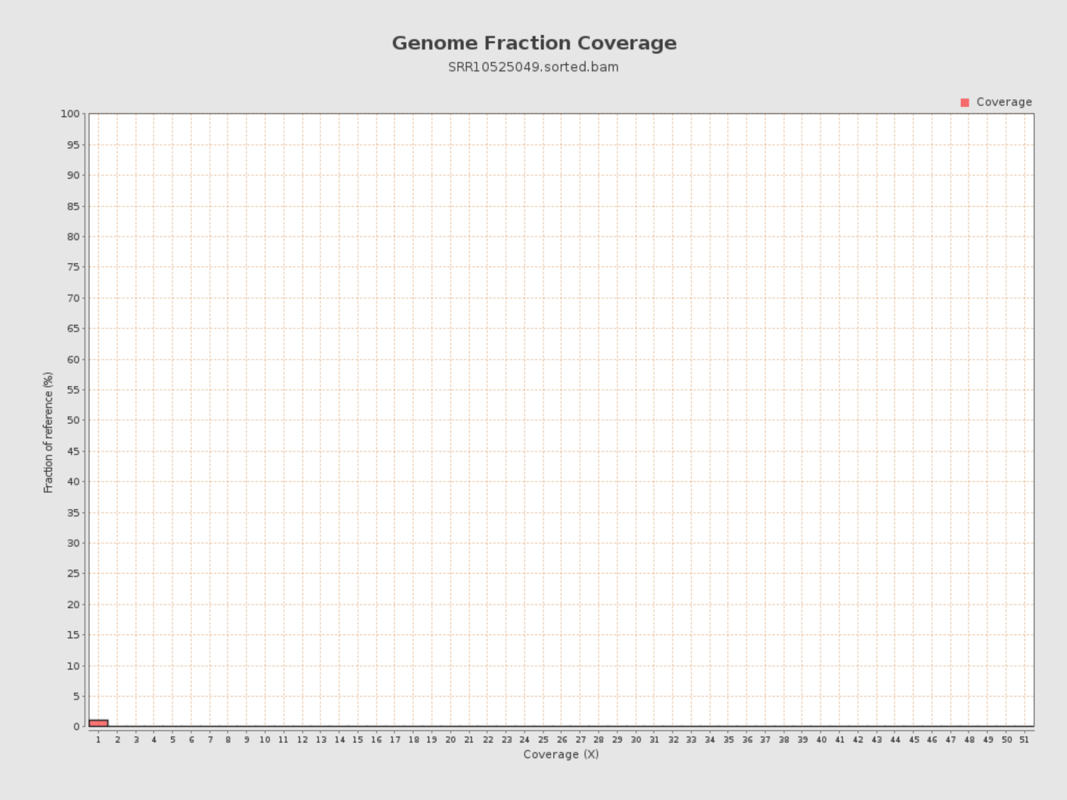
4. Results : Coverage Histogram



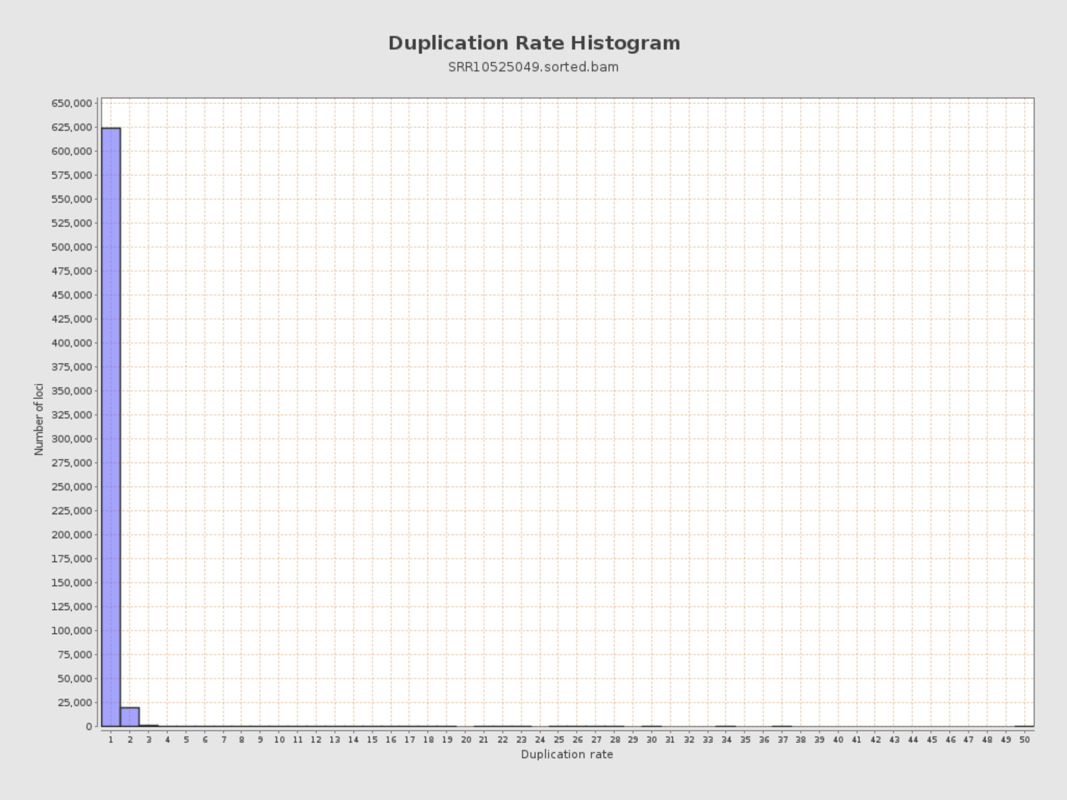
5. Results : Coverage Histogram (0-50X)



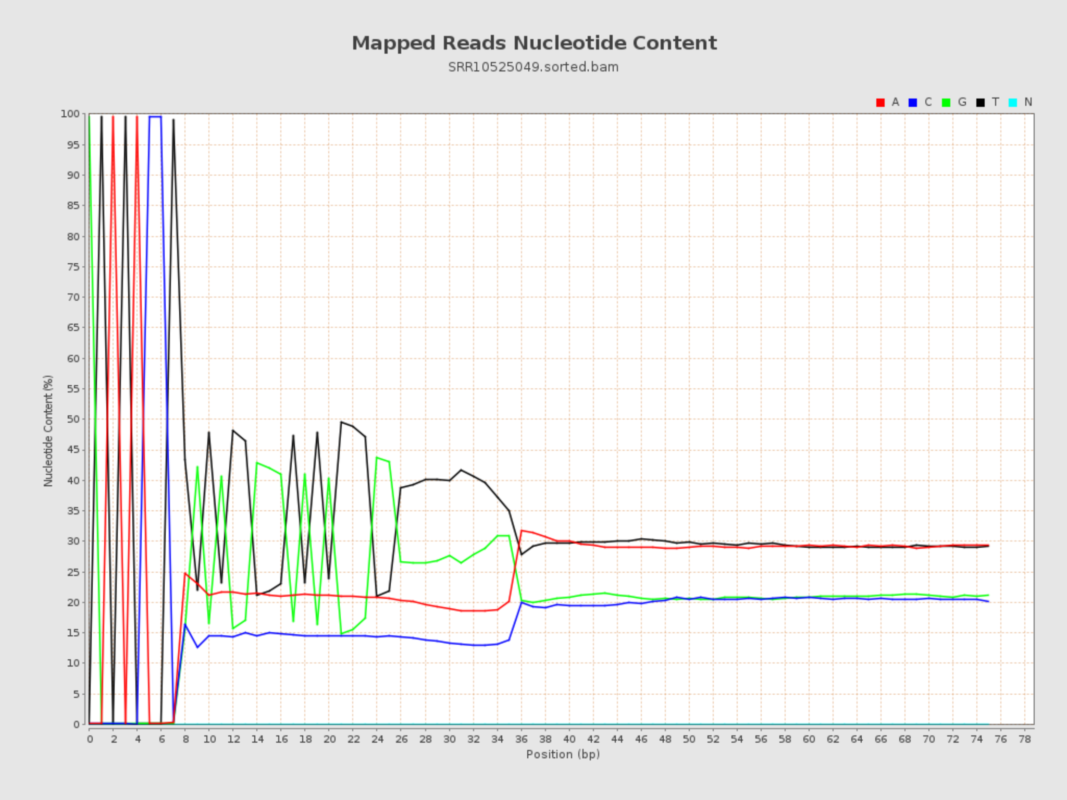
6. Results : Genome Fraction Coverage



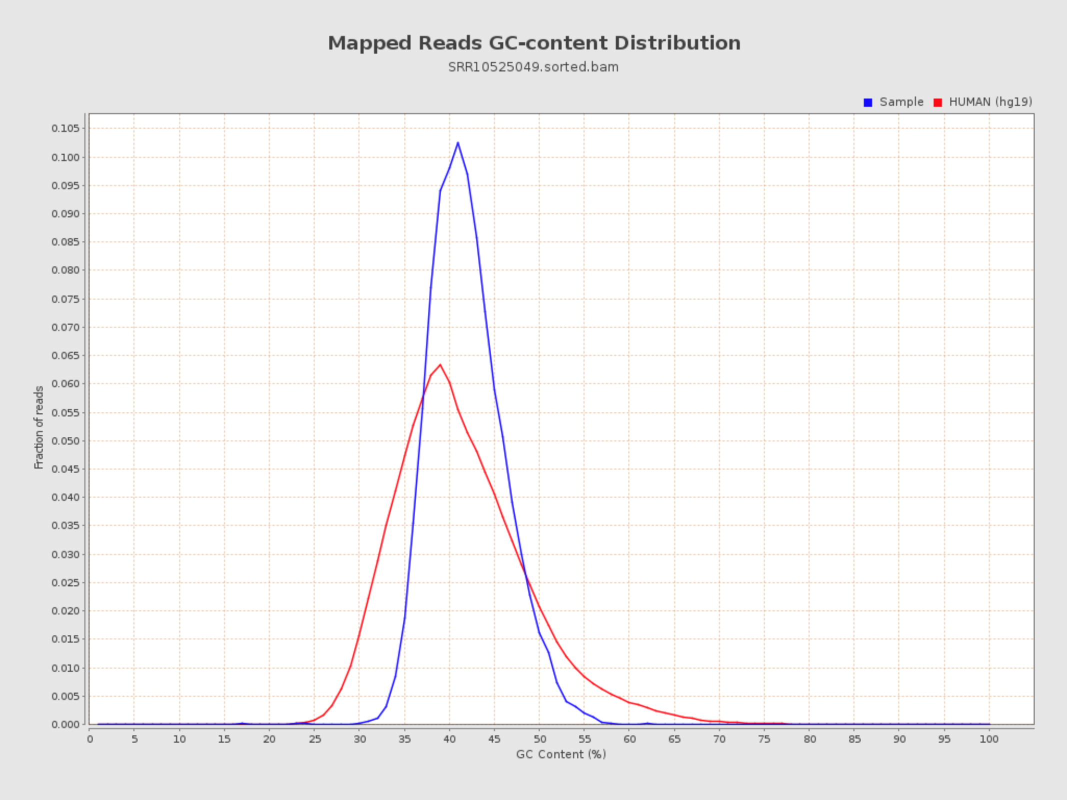
7. Results : Duplication Rate Histogram



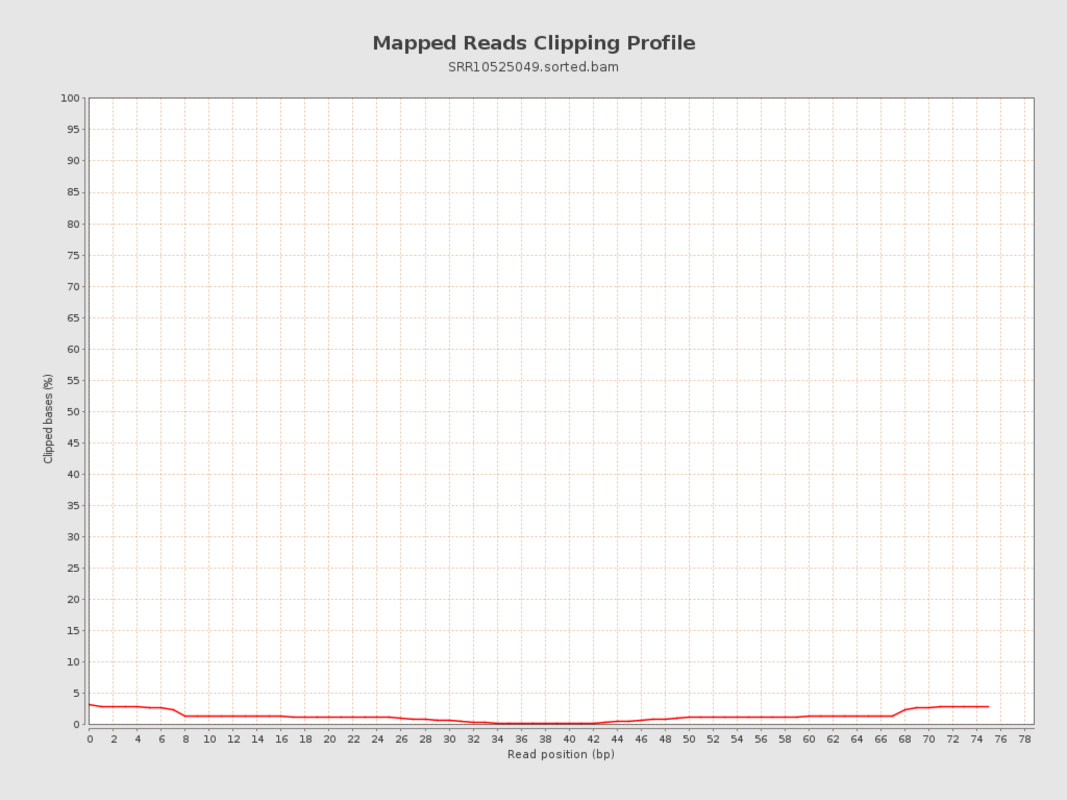
8. Results : Mapped Reads Nucleotide Content



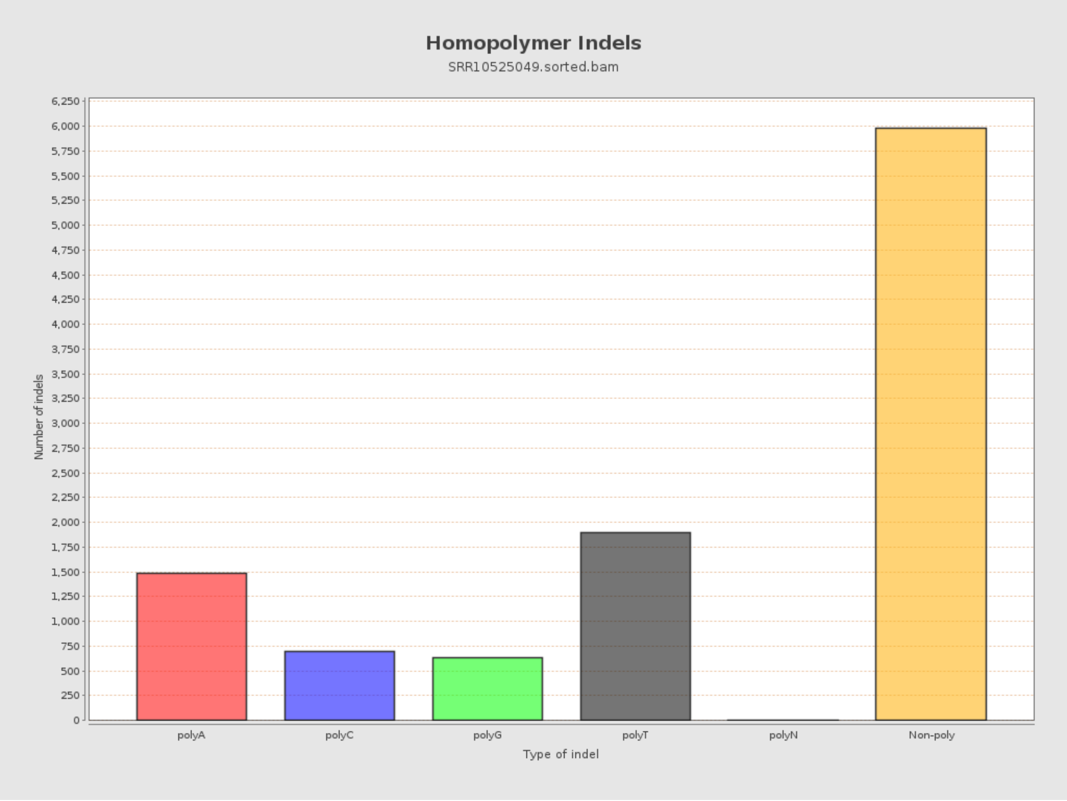
9. Results : Mapped Reads GC-content Distribution



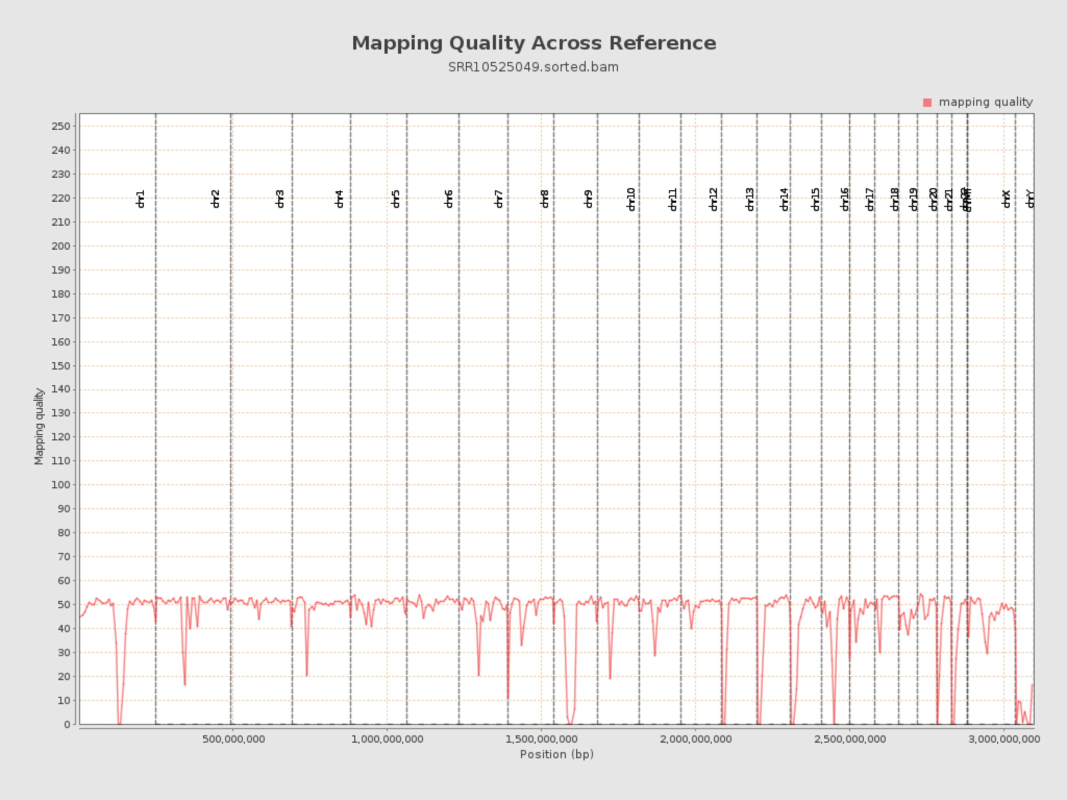
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram