Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:31:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525040.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_SRR10525040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525040.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:31:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	875,048
Mapped reads	810,373 / 92.61%
Unmapped reads	64,675 / 7.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,106 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	20,355 / 2.33%
Duplication rate	1.87%
Clipped reads	812,587 / 92.86%

2.2. ACGT Content

Number/percentage of A's	11,707,736 / 24.77%
Number/percentage of C's	8,484,243 / 17.95%
Number/percentage of T's	14,730,279 / 31.16%
Number/percentage of G's	12,342,808 / 26.11%
Number/percentage of N's	482 / 0%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1623

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

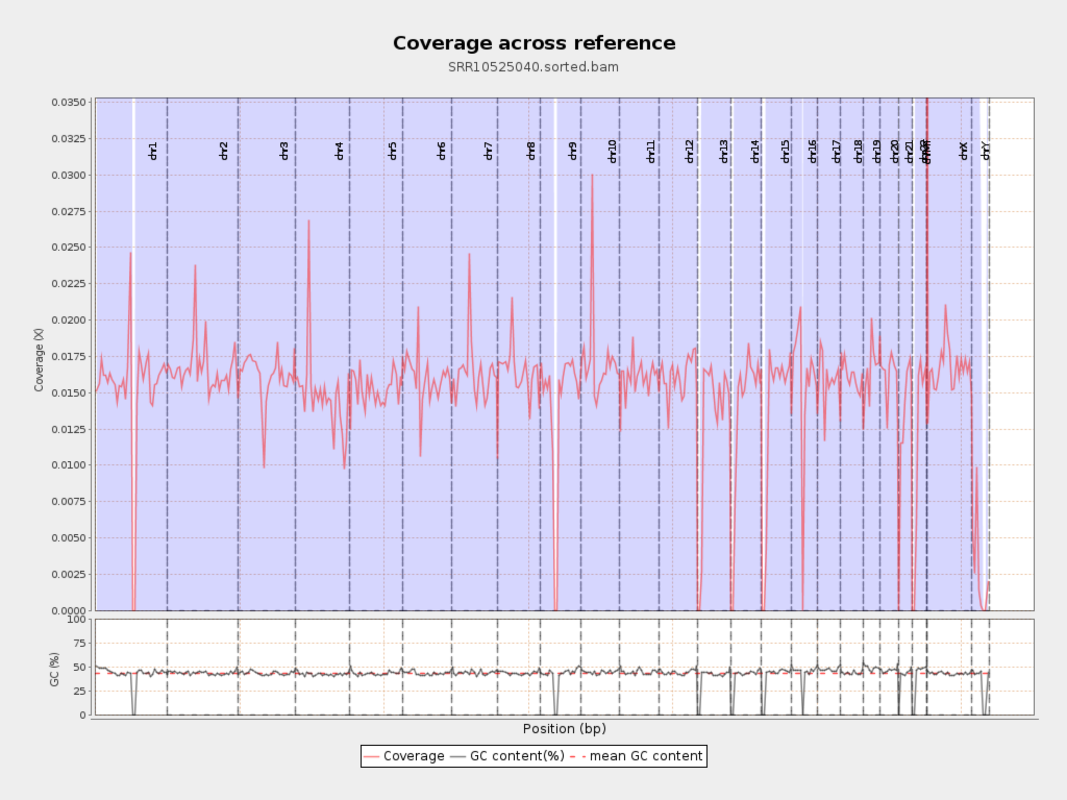
General error rate	0.5%
Mismatches	229,327
Insertions	2,761
Mapped reads with at least one insertion	0.34%
Deletions	8,995
Mapped reads with at least one deletion	1.1%
Homopolymer indels	45.12%

2.6. Chromosome stats

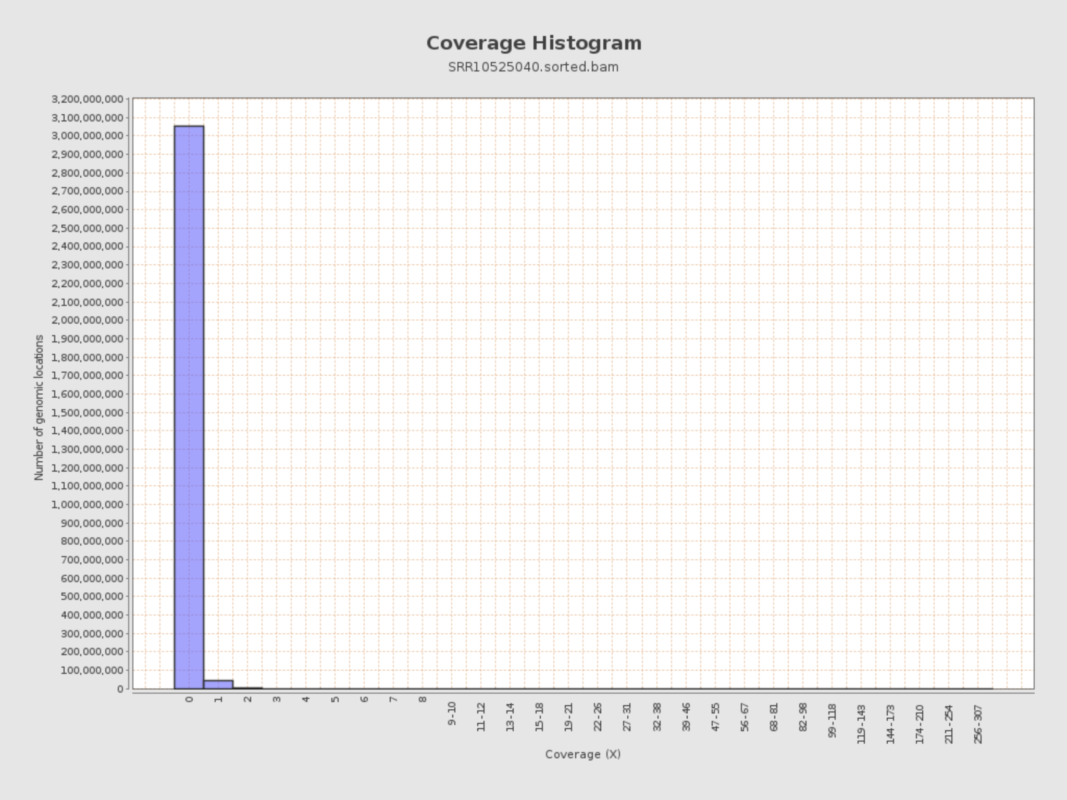
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3794350	0.0152	0.2591
chr2	243199373	4053658	0.0167	0.1786
chr3	198022430	3187717	0.0161	0.1335
chr4	191154276	2840680	0.0149	0.1415
chr5	180915260	2778273	0.0154	0.1302
chr6	171115067	2734241	0.016	0.1486
chr7	159138663	2608614	0.0164	0.181

chr8	146364022	2417951	0.0165	0.1755
chr9	141213431	1983624	0.014	0.1456
chr10	135534747	2337098	0.0172	0.1794
chr11	135006516	2177684	0.0161	0.1585
chr12	133851895	2165779	0.0162	0.1353
chr13	115169878	1471752	0.0128	0.1182
chr14	107349540	1449747	0.0135	0.1236
chr15	102531392	1367578	0.0133	0.1233
chr16	90354753	1398956	0.0155	0.1346
chr17	81195210	1283554	0.0158	0.1404
chr18	78077248	1257773	0.0161	0.2117
chr19	59128983	988238	0.0167	0.1879
chr20	63025520	1016955	0.0161	0.1348
chr21	48129895	629784	0.0131	0.1292
chr22	51304566	580896	0.0113	0.1115
chrMT	16571	4367	0.2635	0.5599
chrX	155270560	2598154	0.0167	0.1427
chrY	59373566	153296	0.0026	0.0913

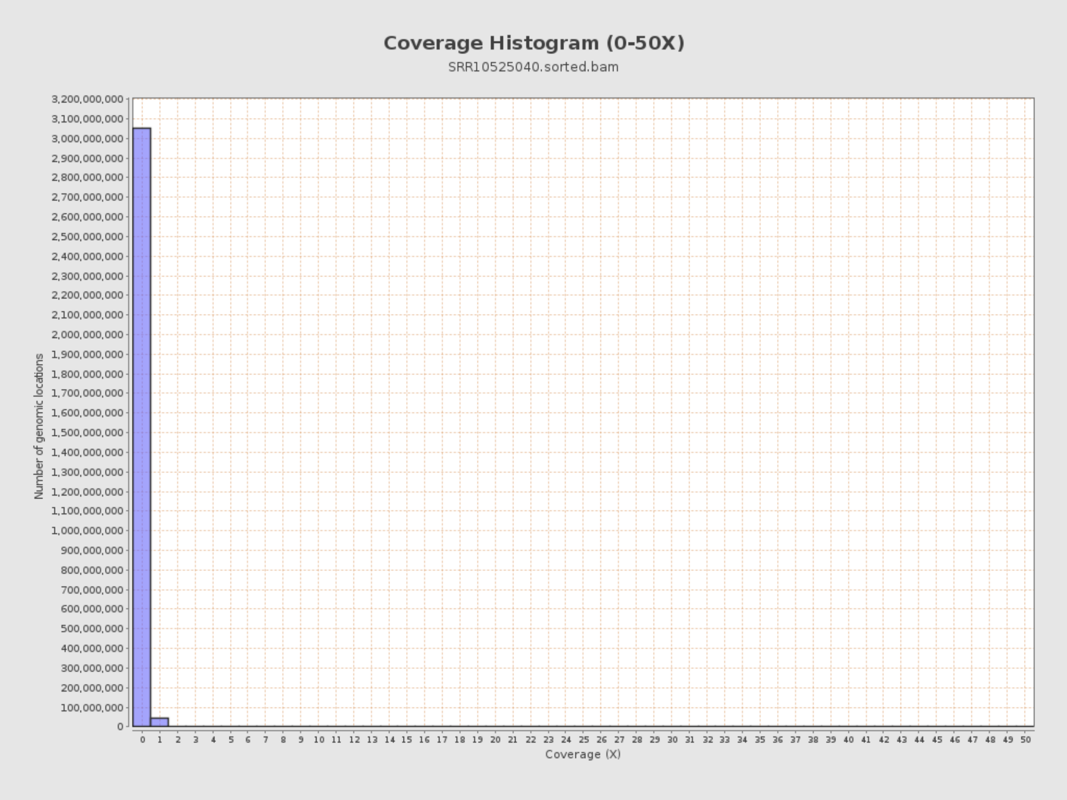
3. Results : Coverage across reference



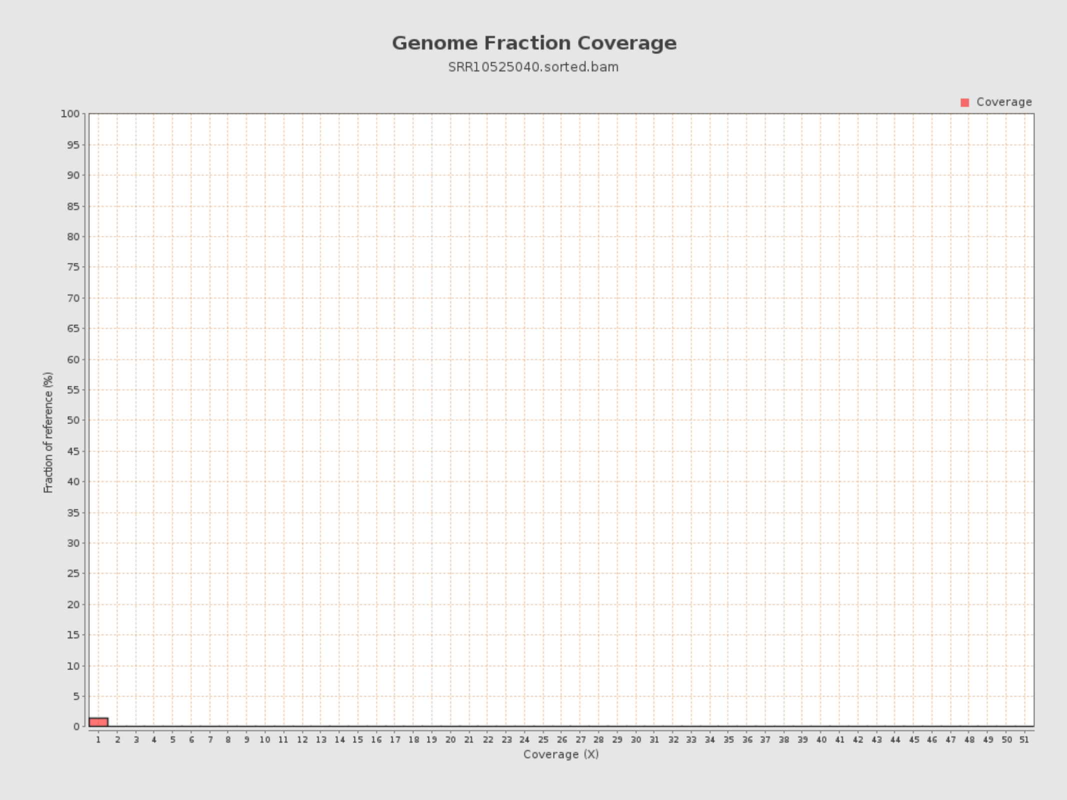
4. Results : Coverage Histogram



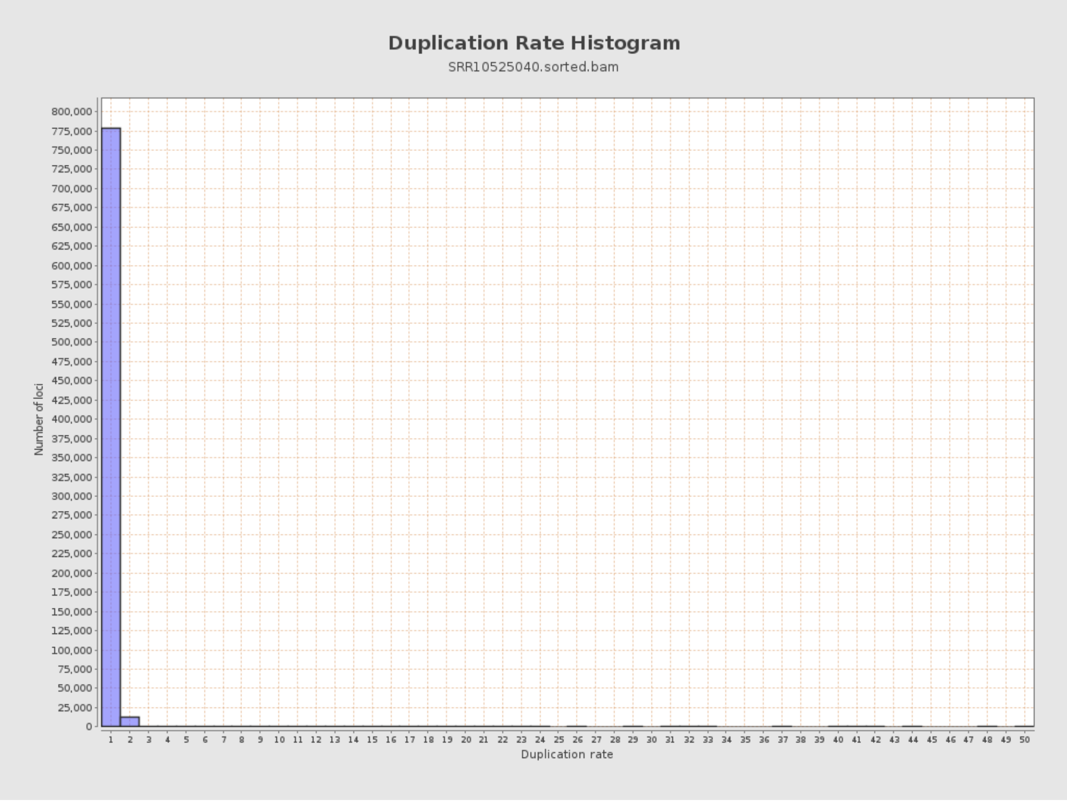
5. Results : Coverage Histogram (0-50X)



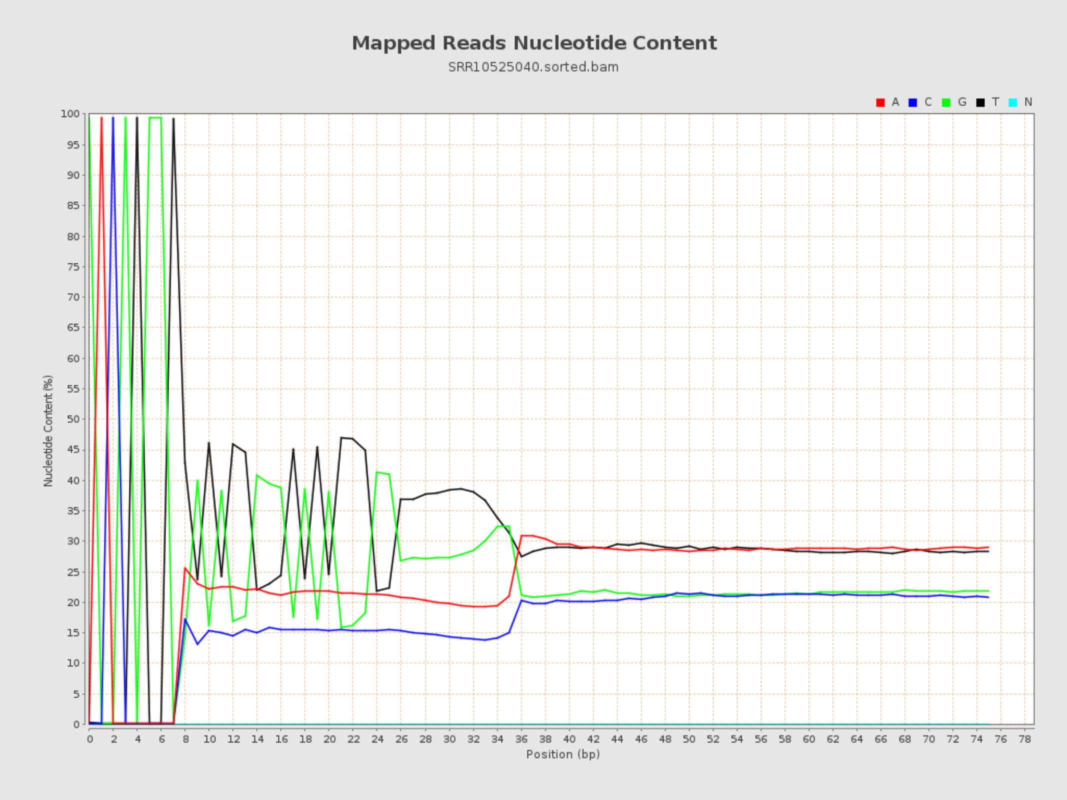
6. Results : Genome Fraction Coverage



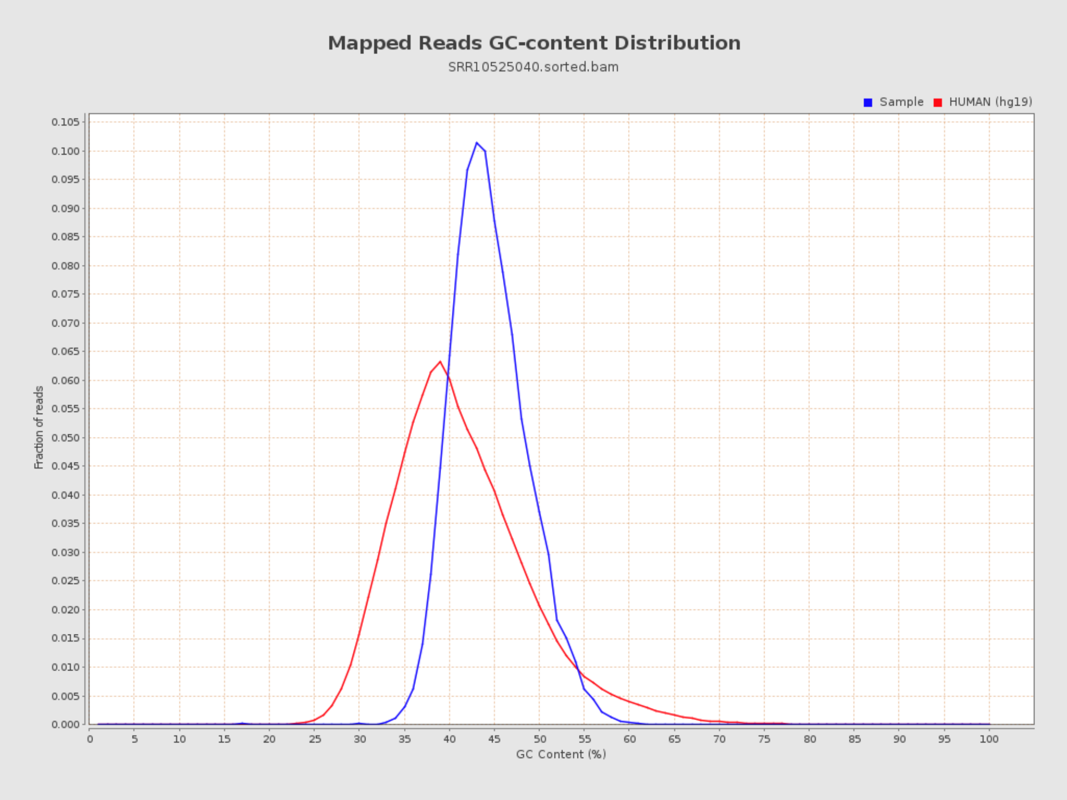
7. Results : Duplication Rate Histogram



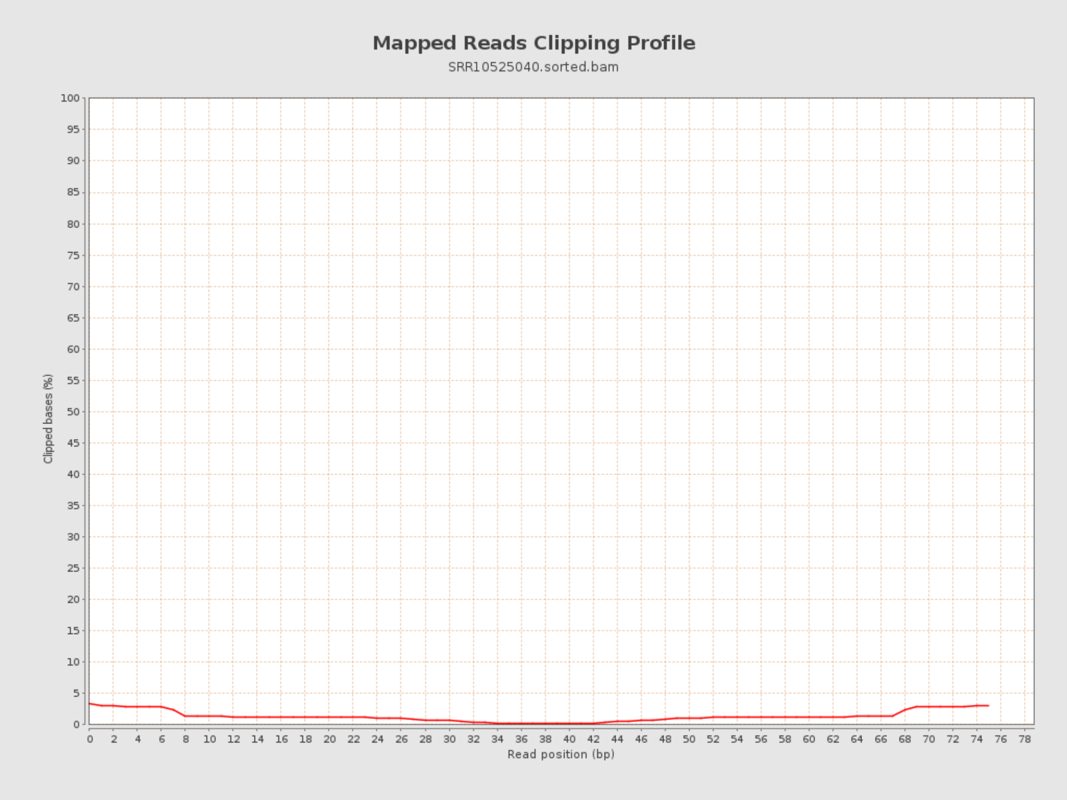
8. Results : Mapped Reads Nucleotide Content



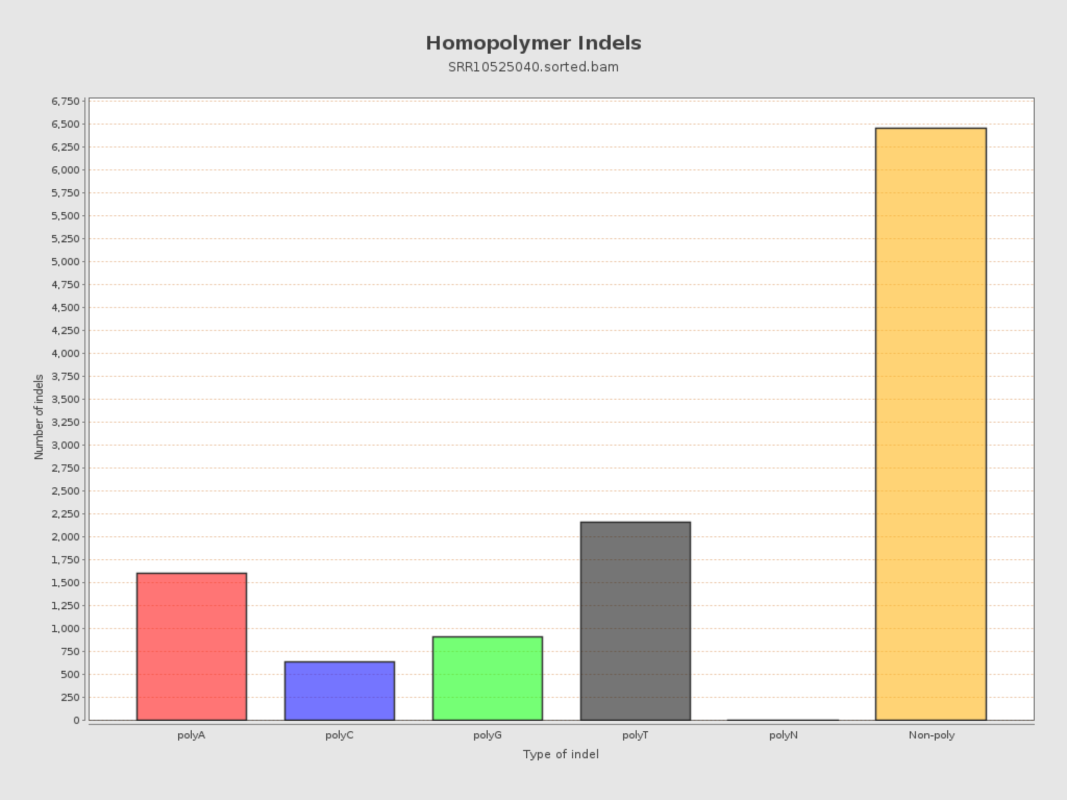
9. Results : Mapped Reads GC-content Distribution



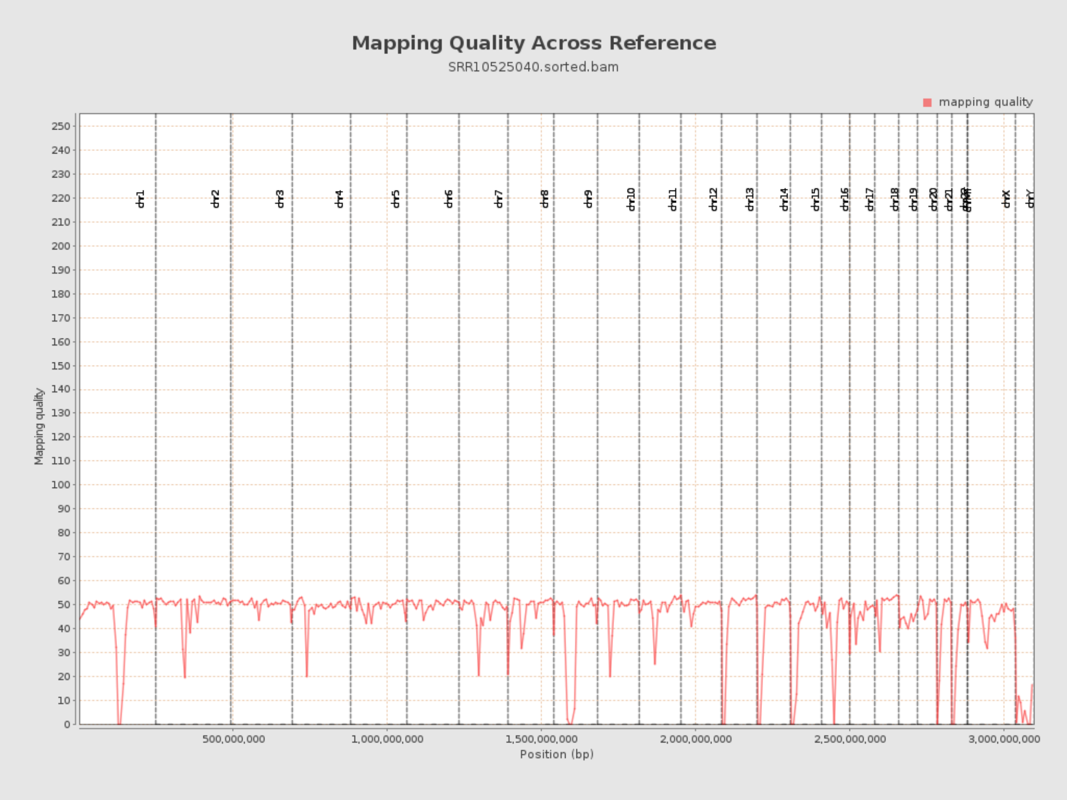
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram