Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:58:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525053.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_SRR10525053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:58:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,089,198
Mapped reads	942,632 / 86.54%
Unmapped reads	146,566 / 13.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,946 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	41,443 / 3.8%
Duplication rate	3.53%
Clipped reads	942,866 / 86.57%

2.2. ACGT Content

Number/percentage of A's	15,742,704 / 27.47%
Number/percentage of C's	9,941,703 / 17.35%
Number/percentage of T's	17,978,496 / 31.37%
Number/percentage of G's	13,646,507 / 23.81%
Number/percentage of N's	6,536 / 0.01%
GC Percentage	41.15%

2.3. Coverage

Mean	0.0185

Standard Deviation	0.202

2.4. Mapping Quality

Mean Mapping Quality	46.85

2.5. Mismatches and indels

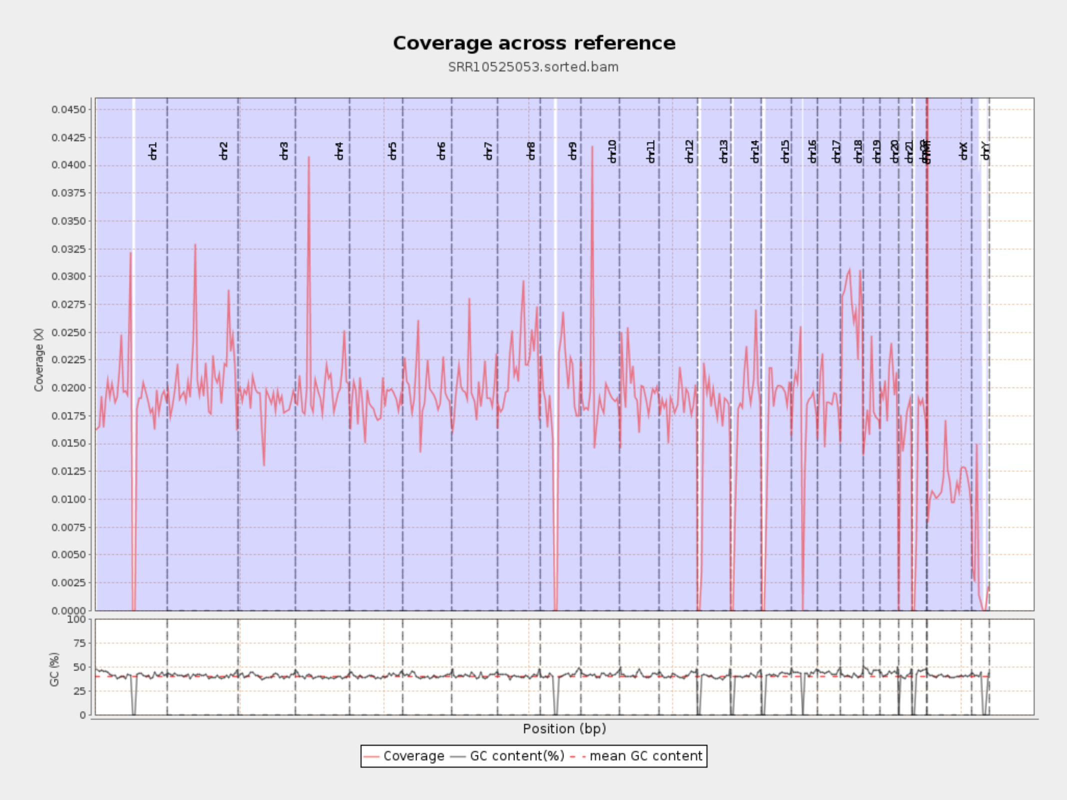
General error rate	0.49%
Mismatches	272,305
Insertions	4,978
Mapped reads with at least one insertion	0.53%
Deletions	11,873
Mapped reads with at least one deletion	1.25%
Homopolymer indels	43.67%

2.6. Chromosome stats

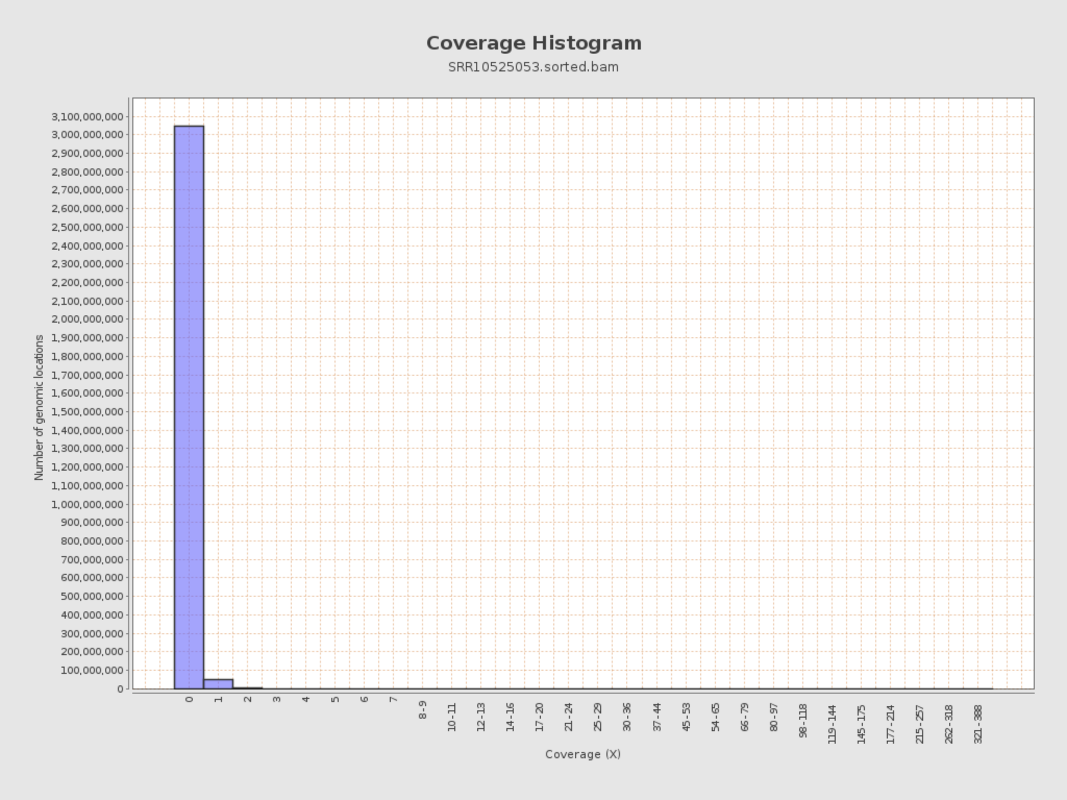
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4561092	0.0183	0.3375
chr2	243199373	5121613	0.0211	0.2356
chr3	198022430	3733808	0.0189	0.1493
chr4	191154276	3951123	0.0207	0.1894
chr5	180915260	3397584	0.0188	0.1499
chr6	171115067	3387674	0.0198	0.1623
chr7	159138663	3172605	0.0199	0.2071

chr8	146364022	3253581	0.0222	0.2624
chr9	141213431	2584158	0.0183	0.1779
chr10	135534747	2682003	0.0198	0.2422
chr11	135006516	2689925	0.0199	0.1765
chr12	133851895	2506853	0.0187	0.1525
chr13	115169878	1832435	0.0159	0.1371
chr14	107349540	1827862	0.017	0.1453
chr15	102531392	1675328	0.0163	0.1384
chr16	90354753	1582074	0.0175	0.1504
chr17	81195210	1524662	0.0188	0.158
chr18	78077248	2143045	0.0274	0.2805
chr19	59128983	1055932	0.0179	0.2409
chr20	63025520	1264396	0.0201	0.1601
chr21	48129895	731732	0.0152	0.1682
chr22	51304566	646441	0.0126	0.122
chrMT	16571	59775	3.6072	2.6983
chrX	155270560	1761335	0.0113	0.1242
chrY	59373566	188001	0.0032	0.1543

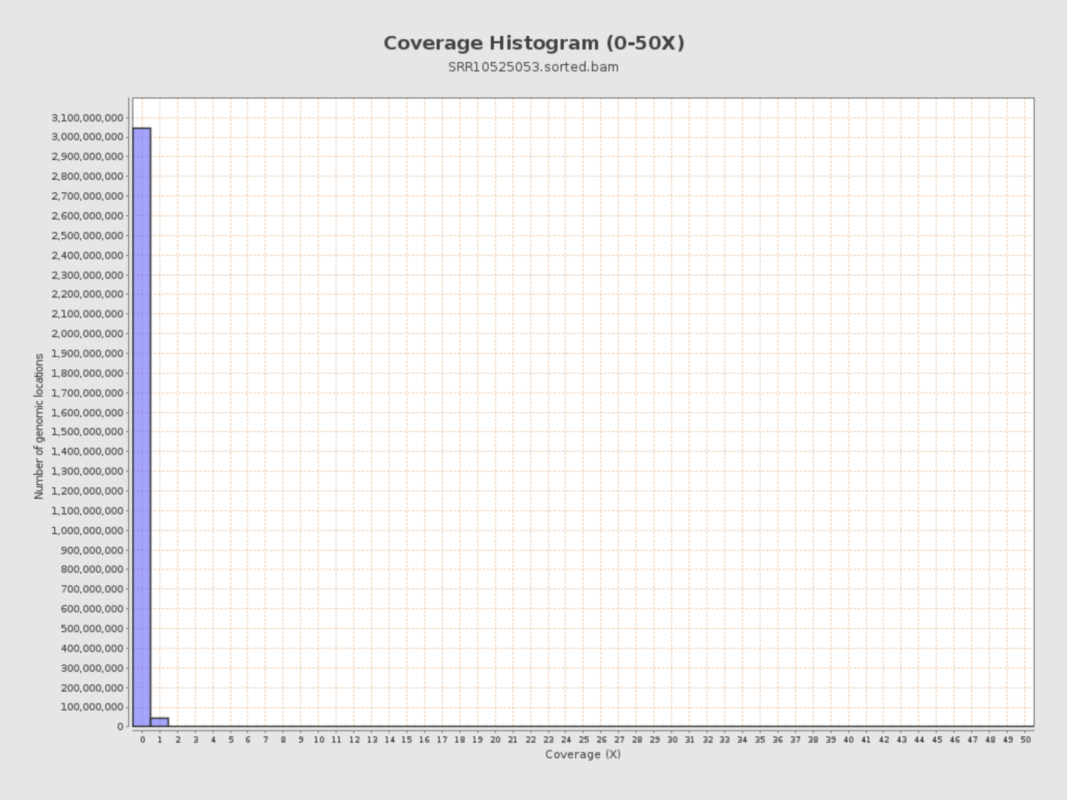
3. Results : Coverage across reference



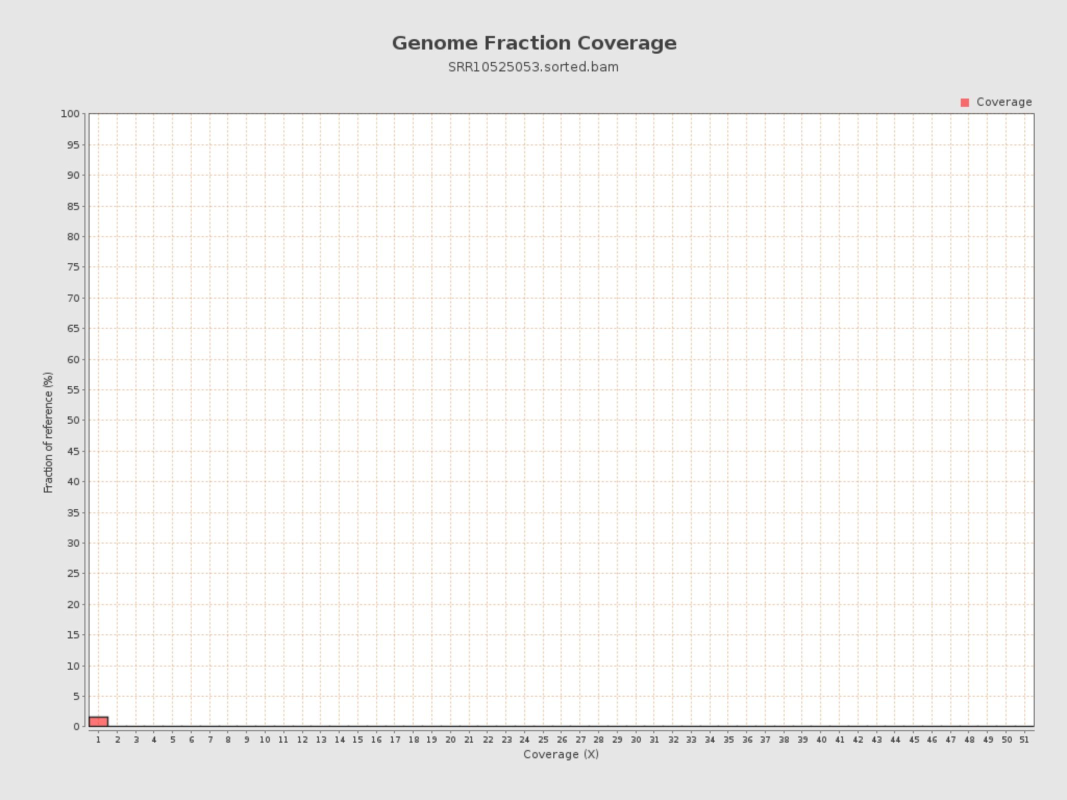
4. Results : Coverage Histogram



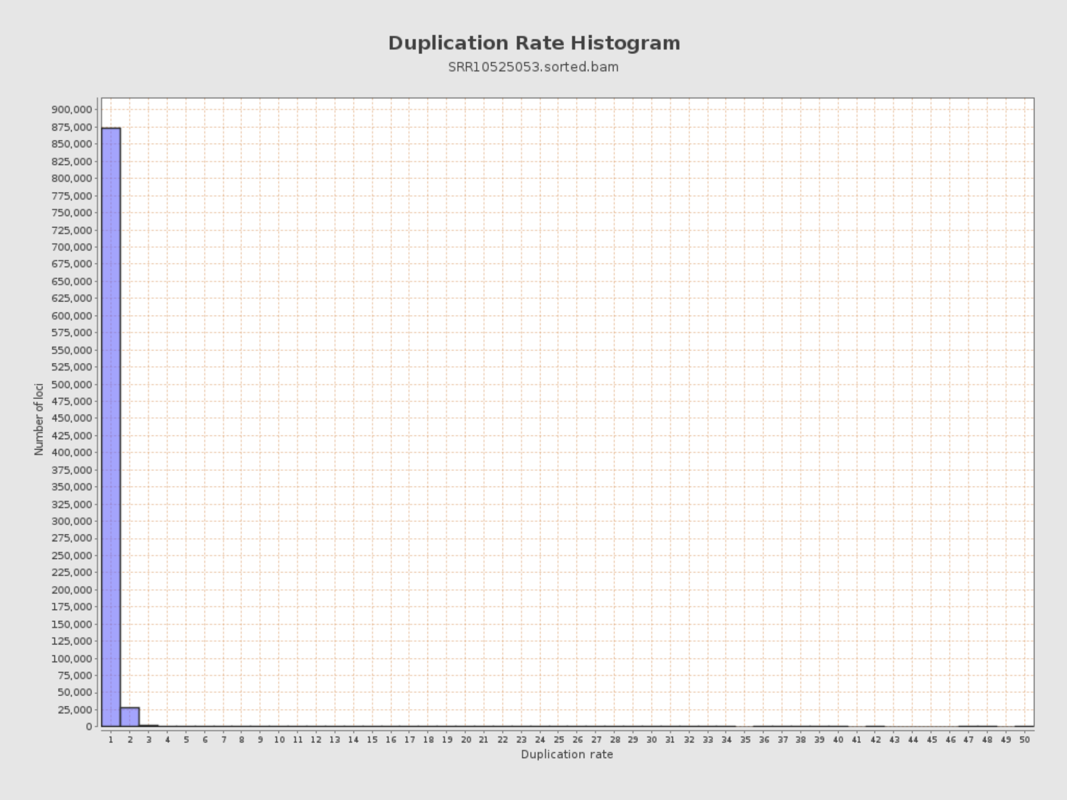
5. Results : Coverage Histogram (0-50X)



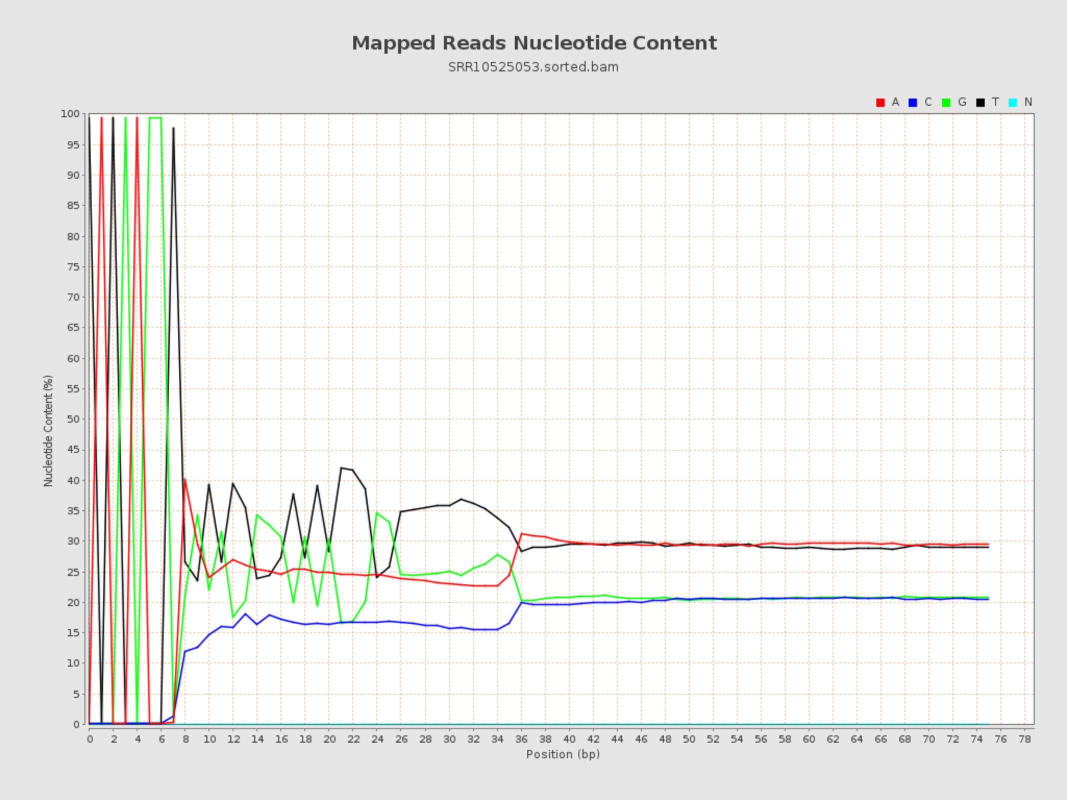
6. Results : Genome Fraction Coverage



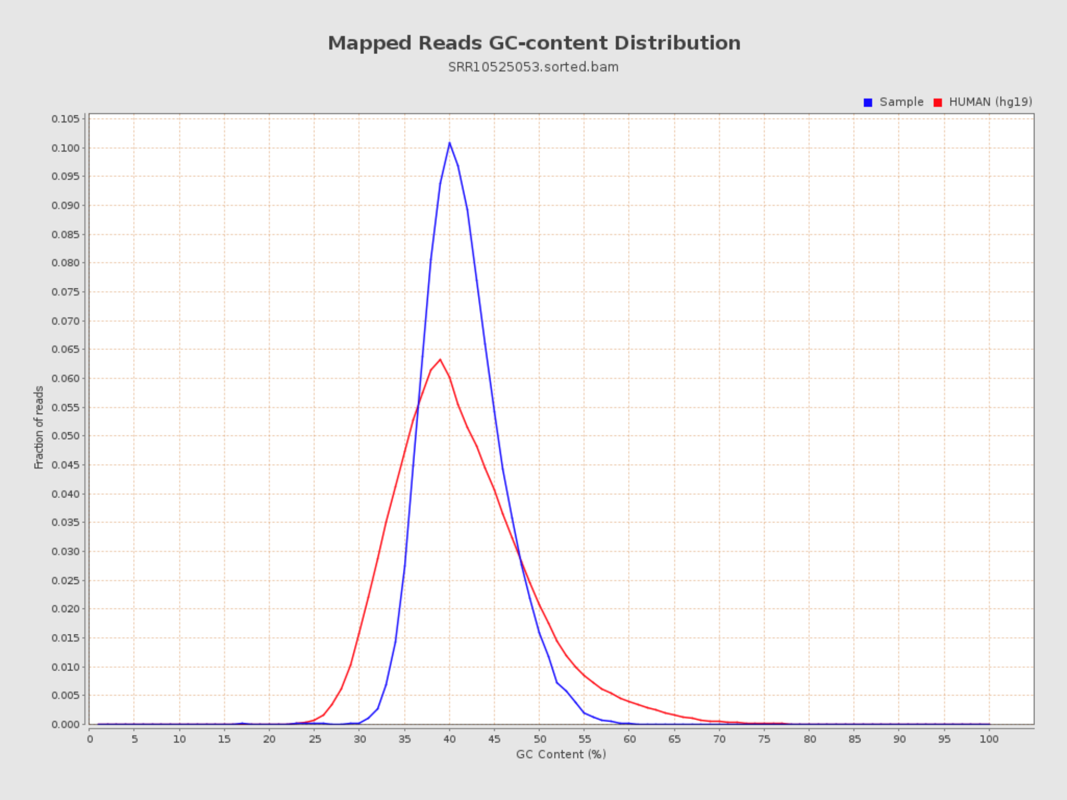
7. Results : Duplication Rate Histogram



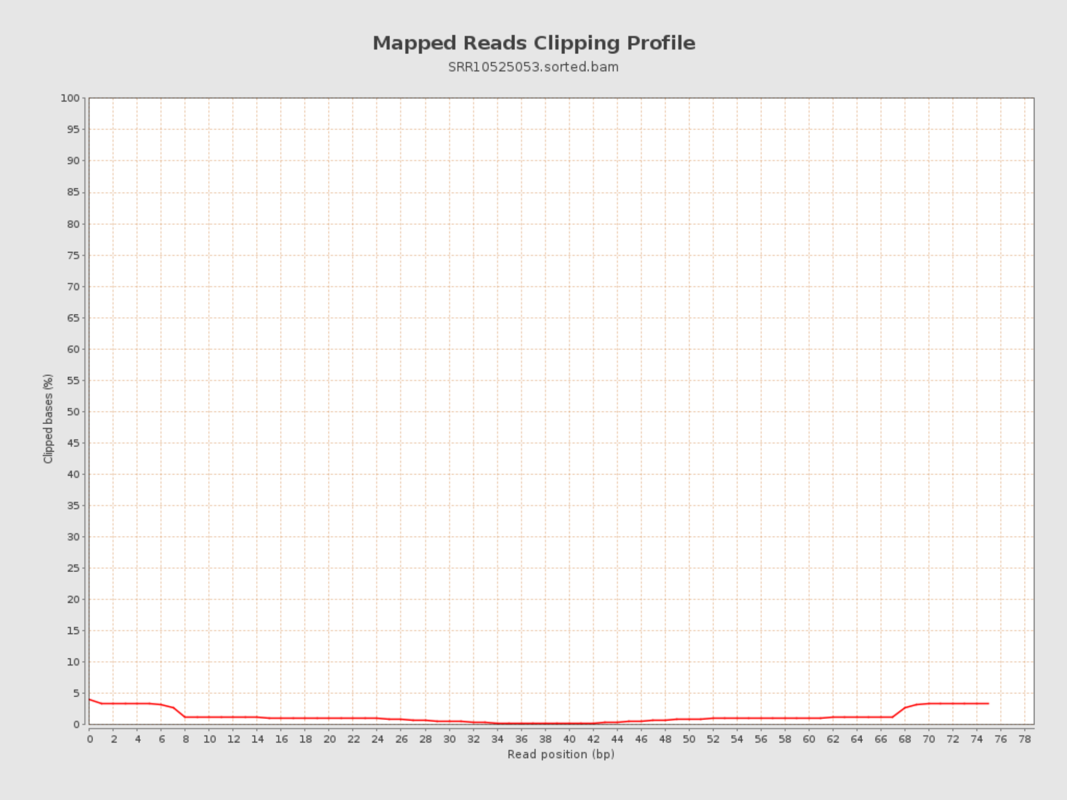
8. Results : Mapped Reads Nucleotide Content



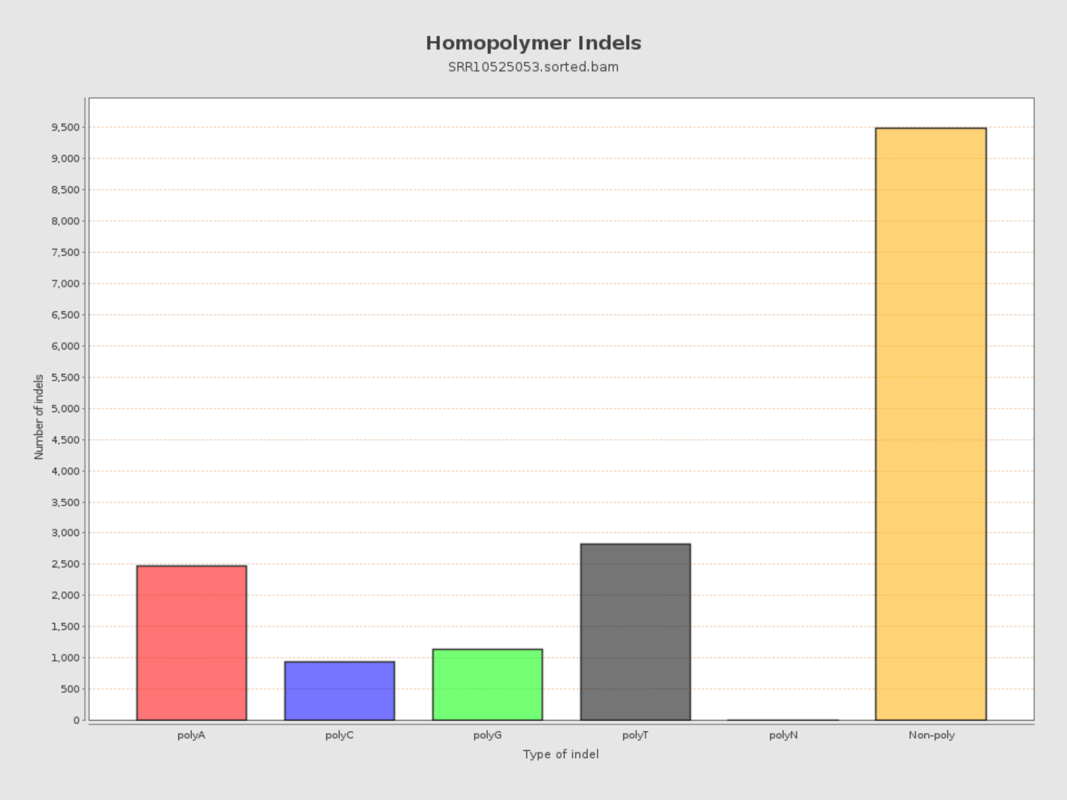
9. Results : Mapped Reads GC-content Distribution



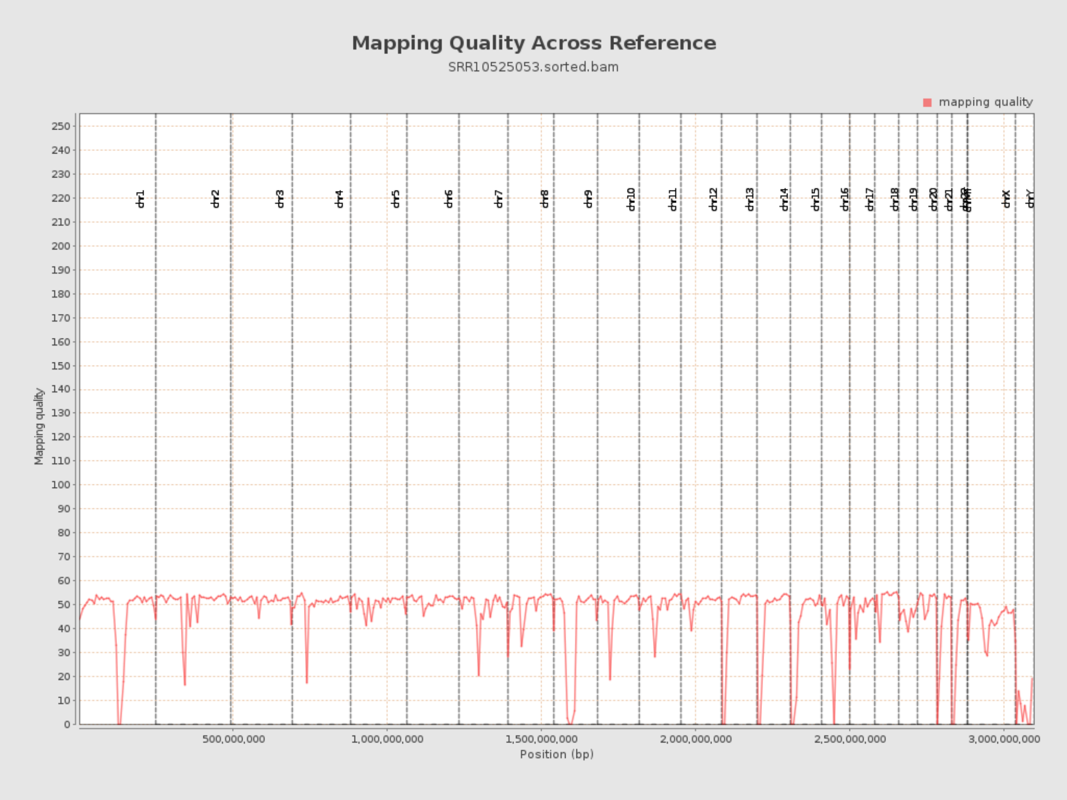
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram