Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:53:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525070.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_SRR10525070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:53:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	908,782
Mapped reads	814,214 / 89.59%
Unmapped reads	94,568 / 10.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,828 / 1.3%
Read min/max/mean length	30 / 76 / 76.44
Duplicated reads (estimated)	40,714 / 4.48%
Duplication rate	3.55%
Clipped reads	823,080 / 90.57%

2.2. ACGT Content

Number/percentage of A's	11,863,998 / 25.48%
Number/percentage of C's	8,591,521 / 18.45%
Number/percentage of T's	14,873,203 / 31.94%
Number/percentage of G's	11,227,904 / 24.11%
Number/percentage of N's	4,886 / 0.01%
GC Percentage	42.57%

2.3. Coverage

Mean	0.015

Standard Deviation	0.2092

2.4. Mapping Quality

Mean Mapping Quality	40.25

2.5. Mismatches and indels

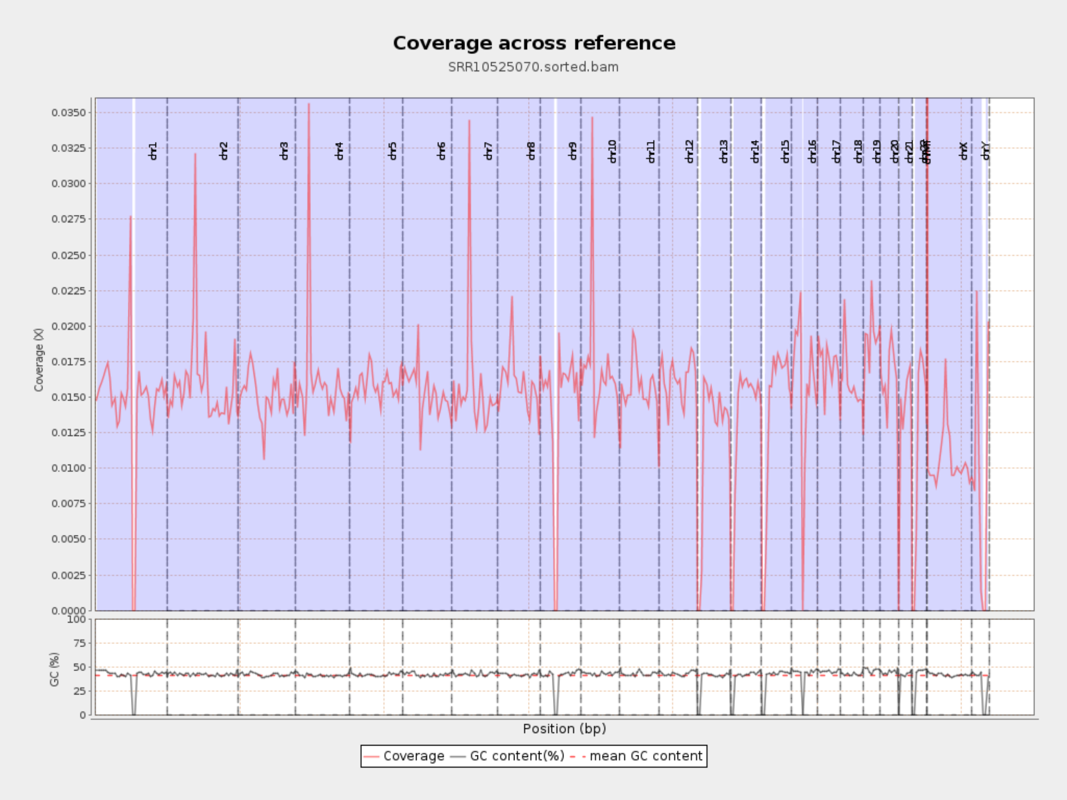
General error rate	0.56%
Mismatches	252,098
Insertions	4,444
Mapped reads with at least one insertion	0.54%
Deletions	9,551
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.71%

2.6. Chromosome stats

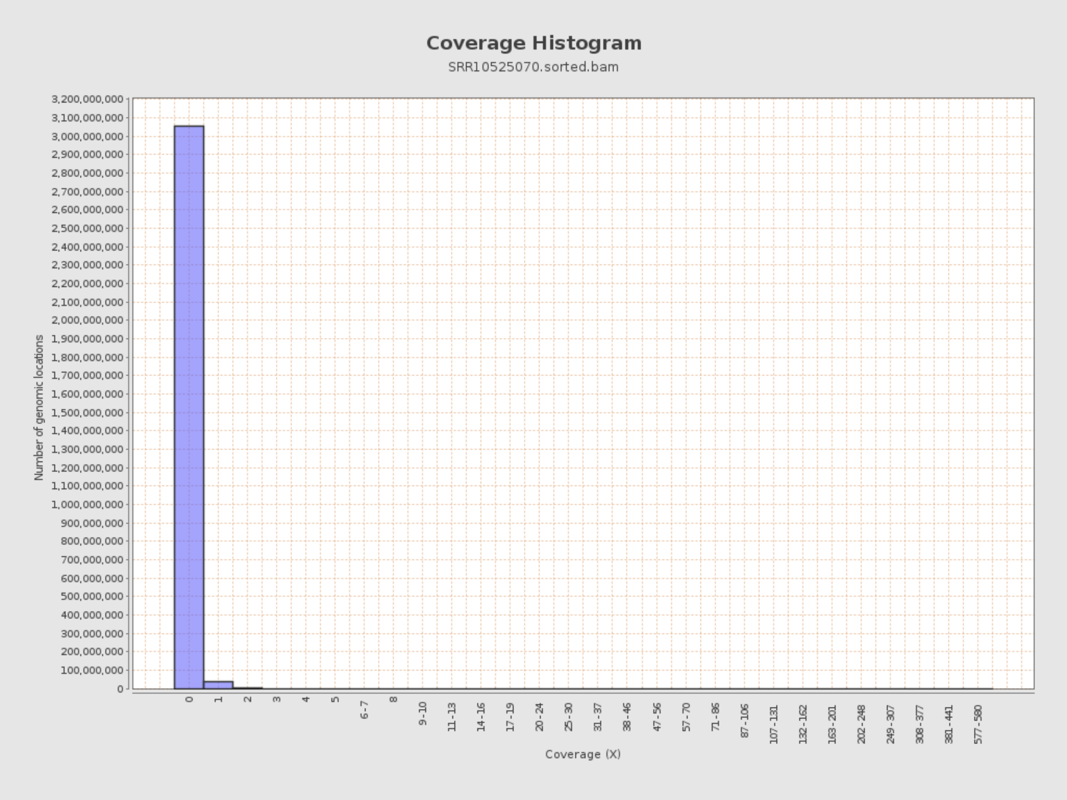
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3650422	0.0146	0.3381
chr2	243199373	3877628	0.0159	0.3048
chr3	198022430	2983747	0.0151	0.133
chr4	191154276	3084711	0.0161	0.1777
chr5	180915260	2873887	0.0159	0.1369
chr6	171115067	2629523	0.0154	0.1541
chr7	159138663	2505853	0.0157	0.2803

chr8	146364022	2334820	0.016	0.2008
chr9	141213431	2033500	0.0144	0.1762
chr10	135534747	2305324	0.017	0.2158
chr11	135006516	2135034	0.0158	0.2245
chr12	133851895	2179077	0.0163	0.1403
chr13	115169878	1388879	0.0121	0.1215
chr14	107349540	1420695	0.0132	0.1309
chr15	102531392	1399983	0.0137	0.1321
chr16	90354753	1397749	0.0155	0.1461
chr17	81195210	1399047	0.0172	0.159
chr18	78077248	1254197	0.0161	0.2903
chr19	59128983	1134239	0.0192	0.2556
chr20	63025520	1025296	0.0163	0.1448
chr21	48129895	654731	0.0136	0.145
chr22	51304566	599460	0.0117	0.1202
chrMT	16571	119861	7.2332	5.0669
chrX	155270560	1650572	0.0106	0.1403
chrY	59373566	538682	0.0091	0.1654

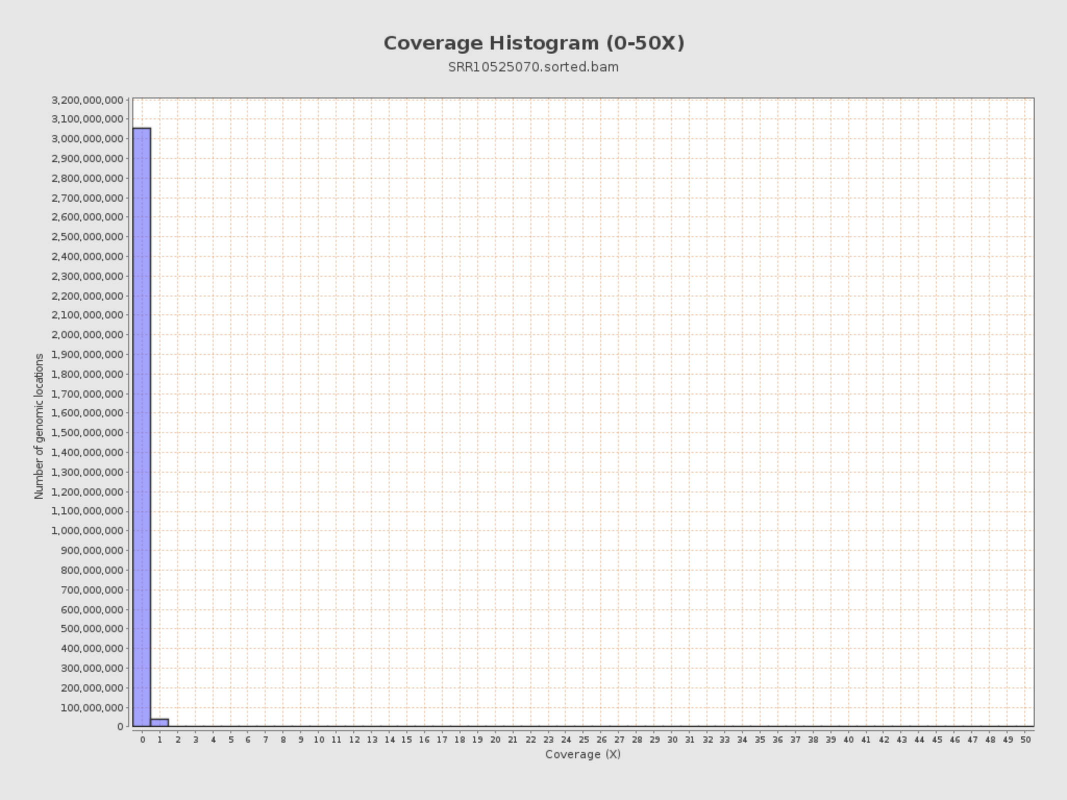
3. Results : Coverage across reference



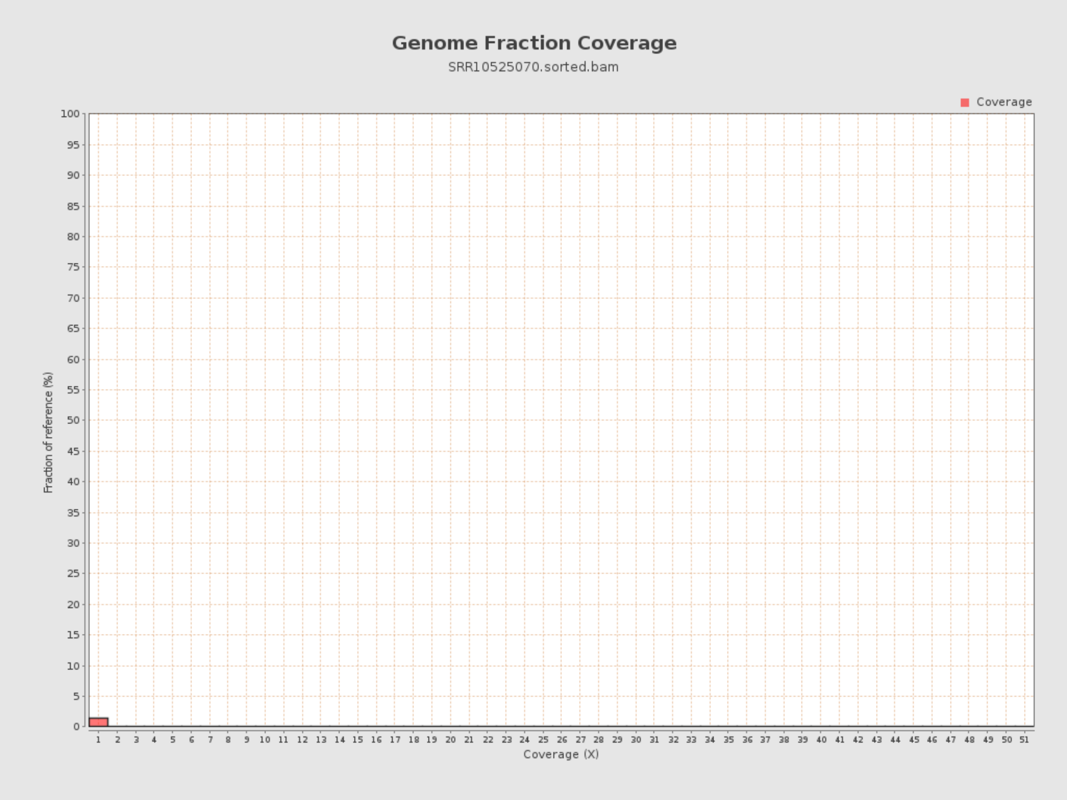
4. Results : Coverage Histogram



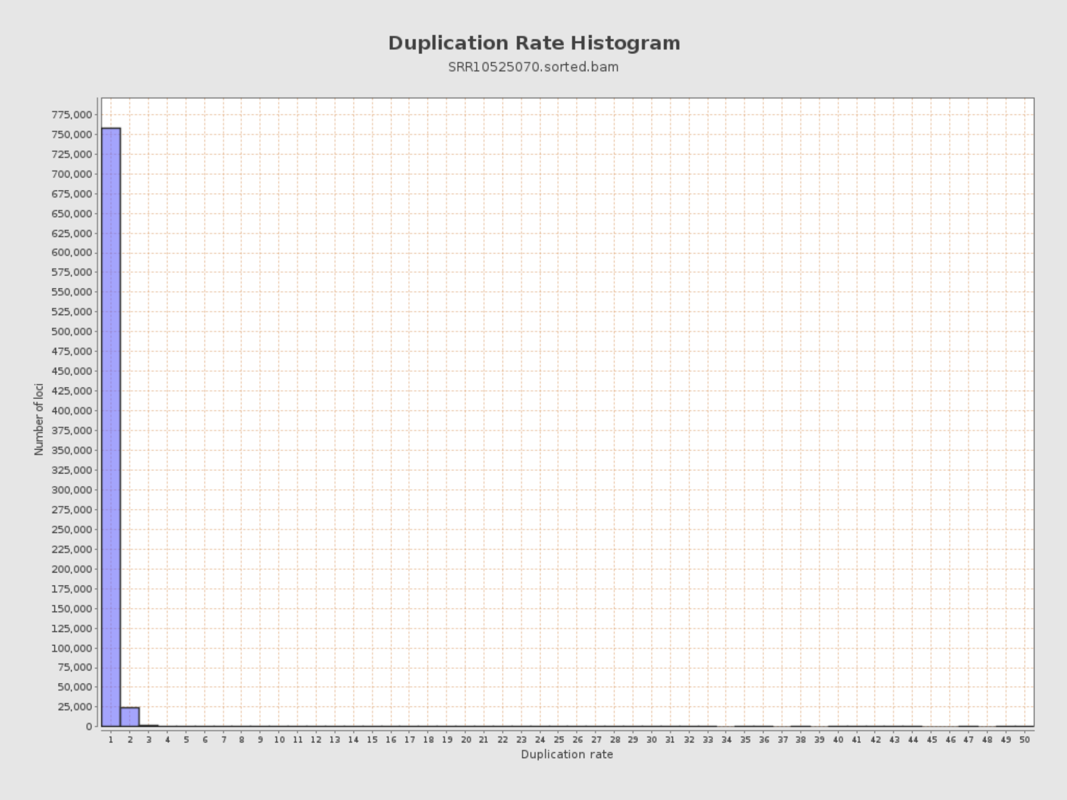
5. Results : Coverage Histogram (0-50X)



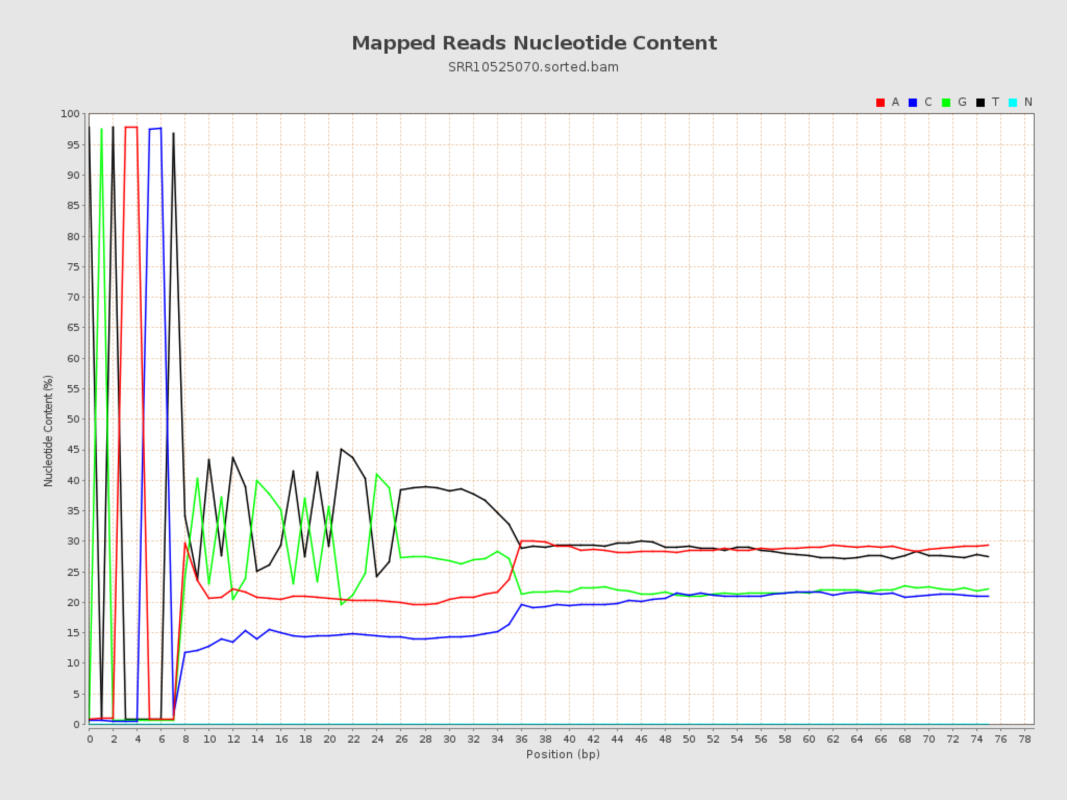
6. Results : Genome Fraction Coverage



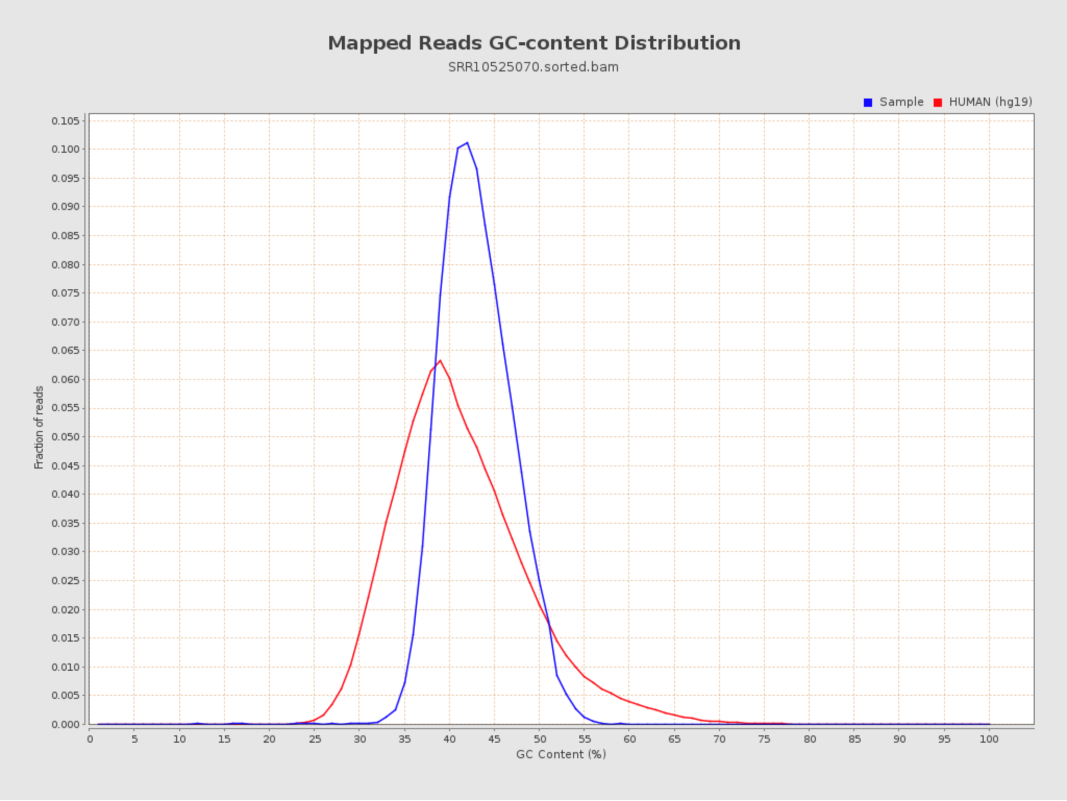
7. Results : Duplication Rate Histogram



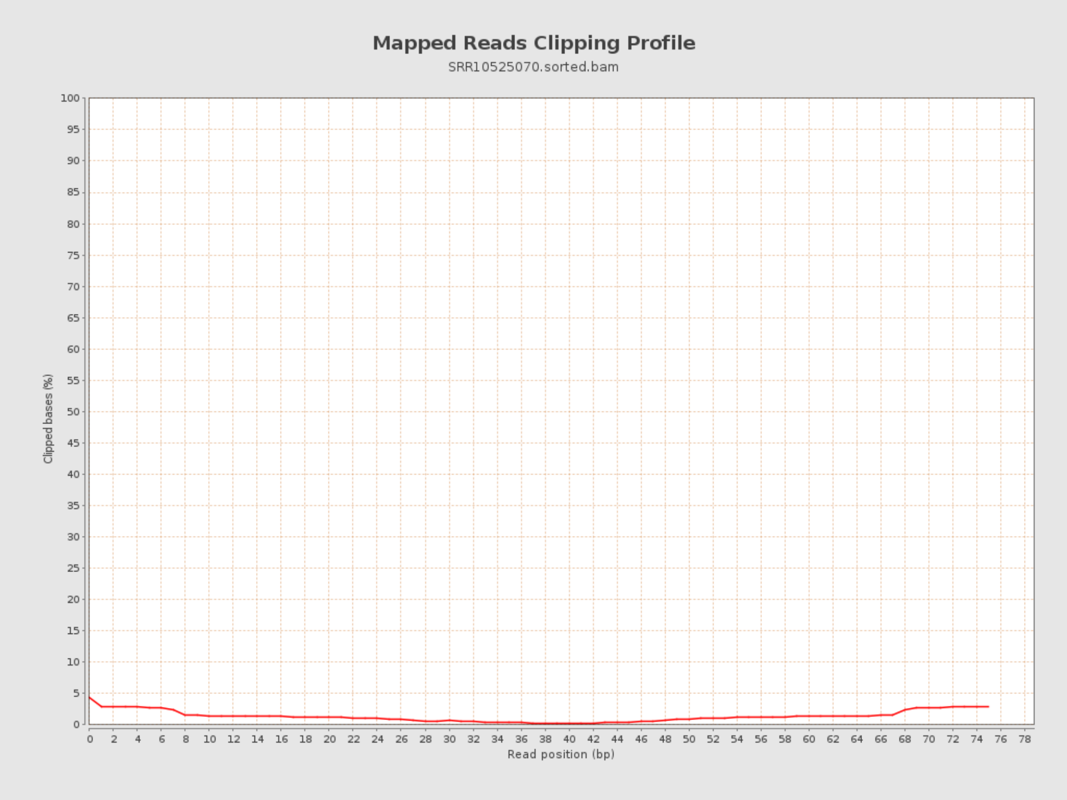
8. Results : Mapped Reads Nucleotide Content



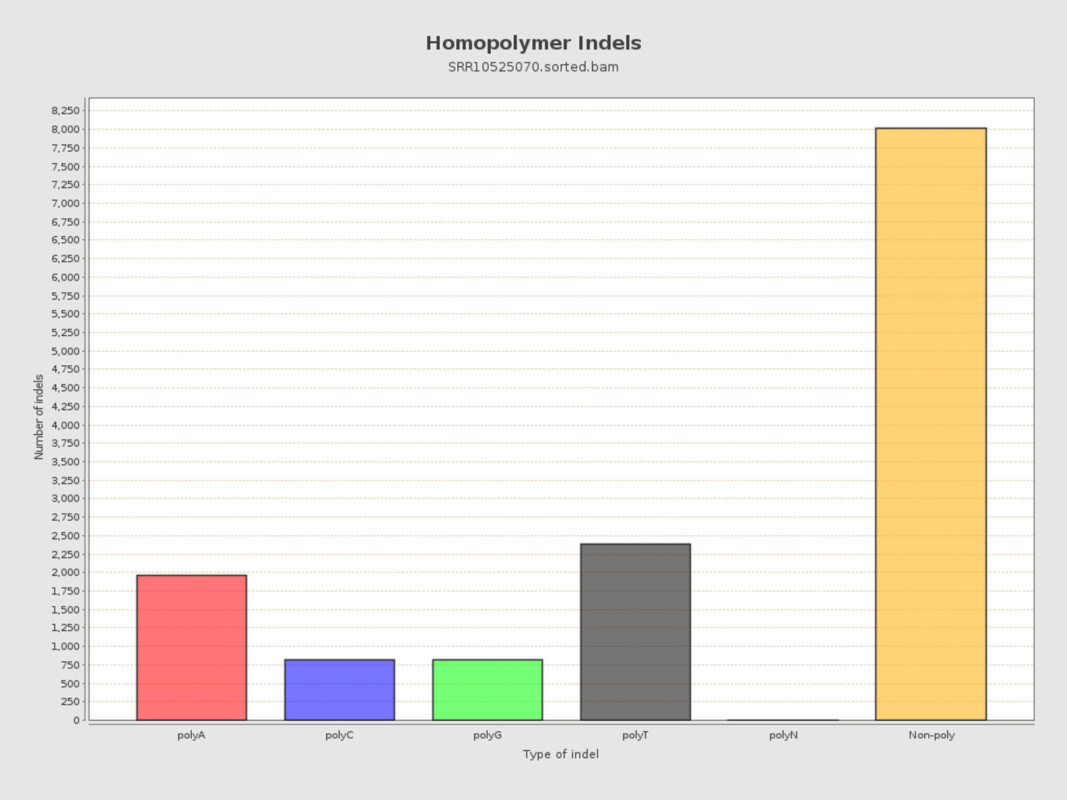
9. Results : Mapped Reads GC-content Distribution



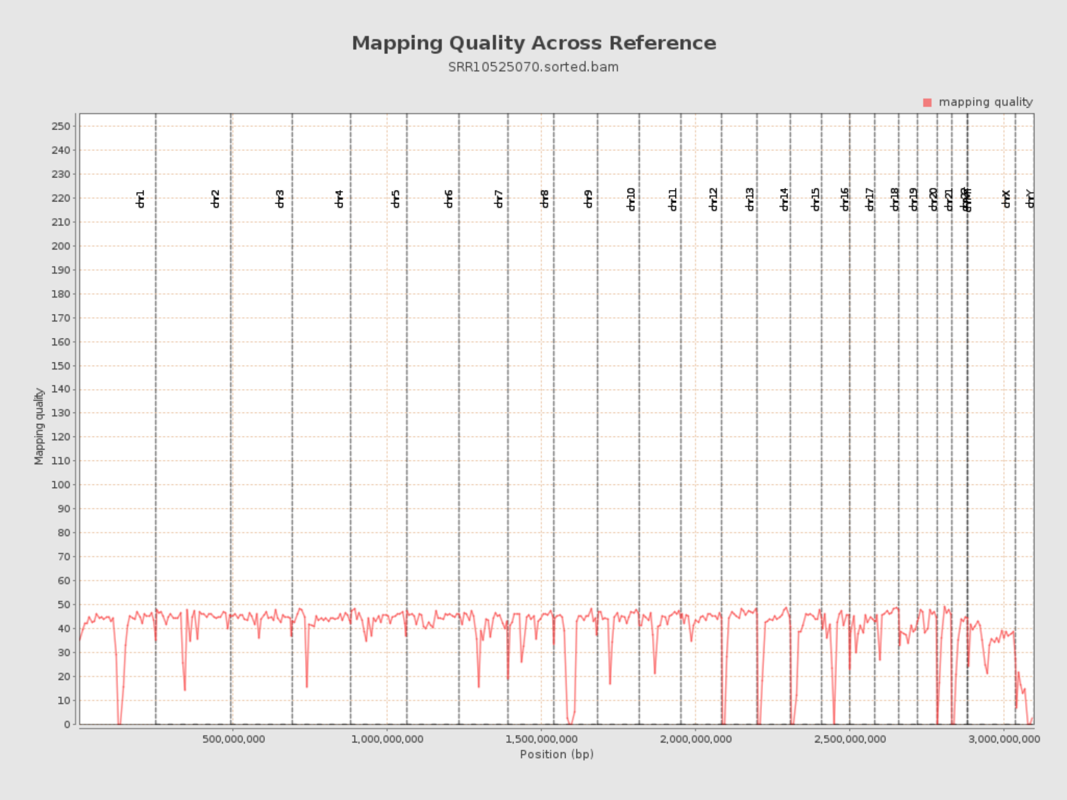
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram