Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:34:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525020.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_SRR10525020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525020.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:34:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	986,864
Mapped reads	905,343 / 91.74%
Unmapped reads	81,521 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,363 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	19,392 / 1.97%
Duplication rate	1.5%
Clipped reads	907,580 / 91.97%

2.2. ACGT Content

Number/percentage of A's	13,198,512 / 24.97%
Number/percentage of C's	9,932,082 / 18.79%
Number/percentage of T's	15,980,696 / 30.24%
Number/percentage of G's	13,740,082 / 26%
Number/percentage of N's	487 / 0%
GC Percentage	44.79%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.1757

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

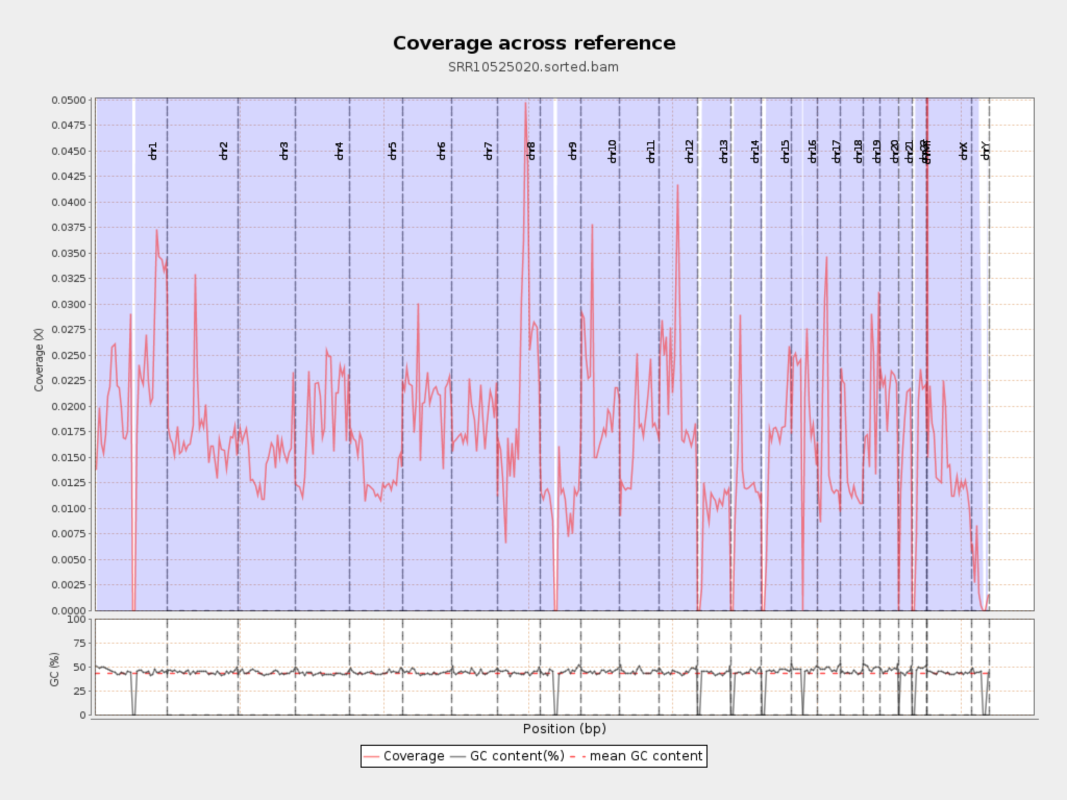
General error rate	0.5%
Mismatches	258,913
Insertions	2,929
Mapped reads with at least one insertion	0.32%
Deletions	10,168
Mapped reads with at least one deletion	1.11%
Homopolymer indels	45.31%

2.6. Chromosome stats

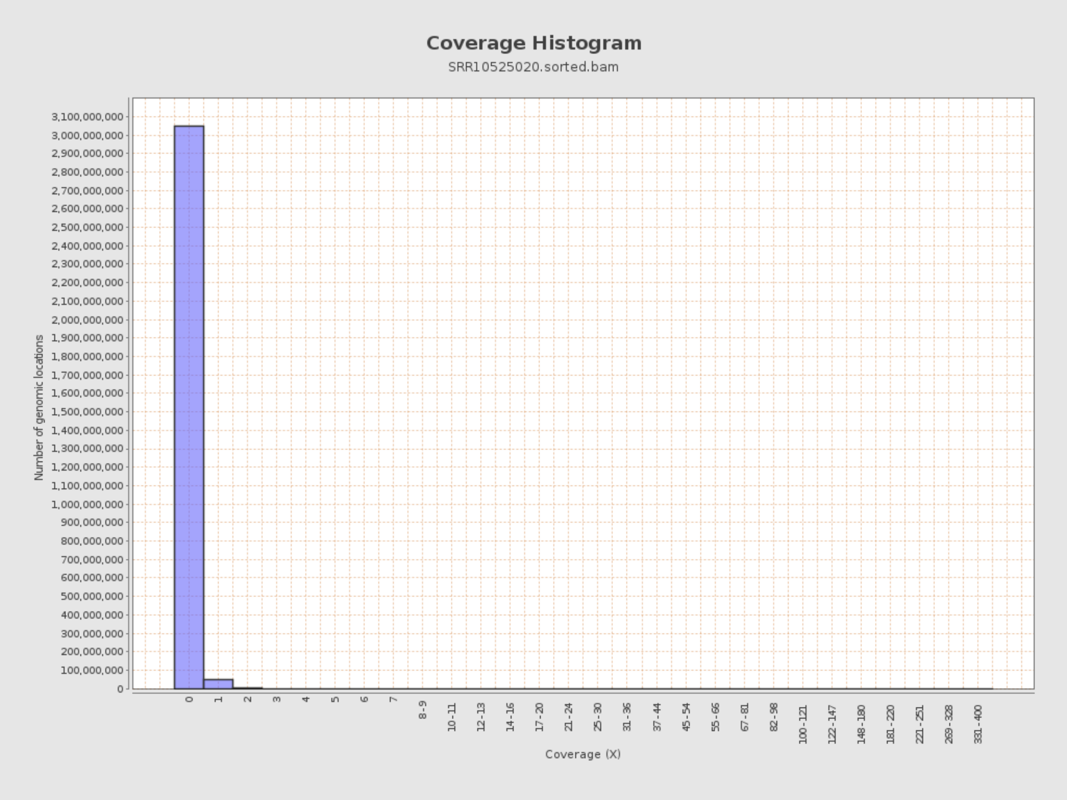
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5470410	0.0219	0.3086
chr2	243199373	4167938	0.0171	0.1972
chr3	198022430	3002487	0.0152	0.1292
chr4	191154276	3673566	0.0192	0.1515
chr5	180915260	2433732	0.0135	0.1224
chr6	171115067	3622712	0.0212	0.1834
chr7	159138663	2942745	0.0185	0.1663

chr8	146364022	3348143	0.0229	0.1902
chr9	141213431	1390349	0.0098	0.1359
chr10	135534747	2891488	0.0213	0.1961
chr11	135006516	2313757	0.0171	0.1678
chr12	133851895	3032997	0.0227	0.1587
chr13	115169878	1043367	0.0091	0.0992
chr14	107349540	1274200	0.0119	0.1169
chr15	102531392	1559462	0.0152	0.1306
chr16	90354753	1769395	0.0196	0.154
chr17	81195210	1325880	0.0163	0.1602
chr18	78077248	1101690	0.0141	0.2263
chr19	59128983	1223830	0.0207	0.2011
chr20	63025520	1364084	0.0216	0.1538
chr21	48129895	771332	0.016	0.1359
chr22	51304566	772874	0.0151	0.1278
chrMT	16571	16401	0.9897	1.1518
chrX	155270560	2209716	0.0142	0.1381
chrY	59373566	146205	0.0025	0.0712

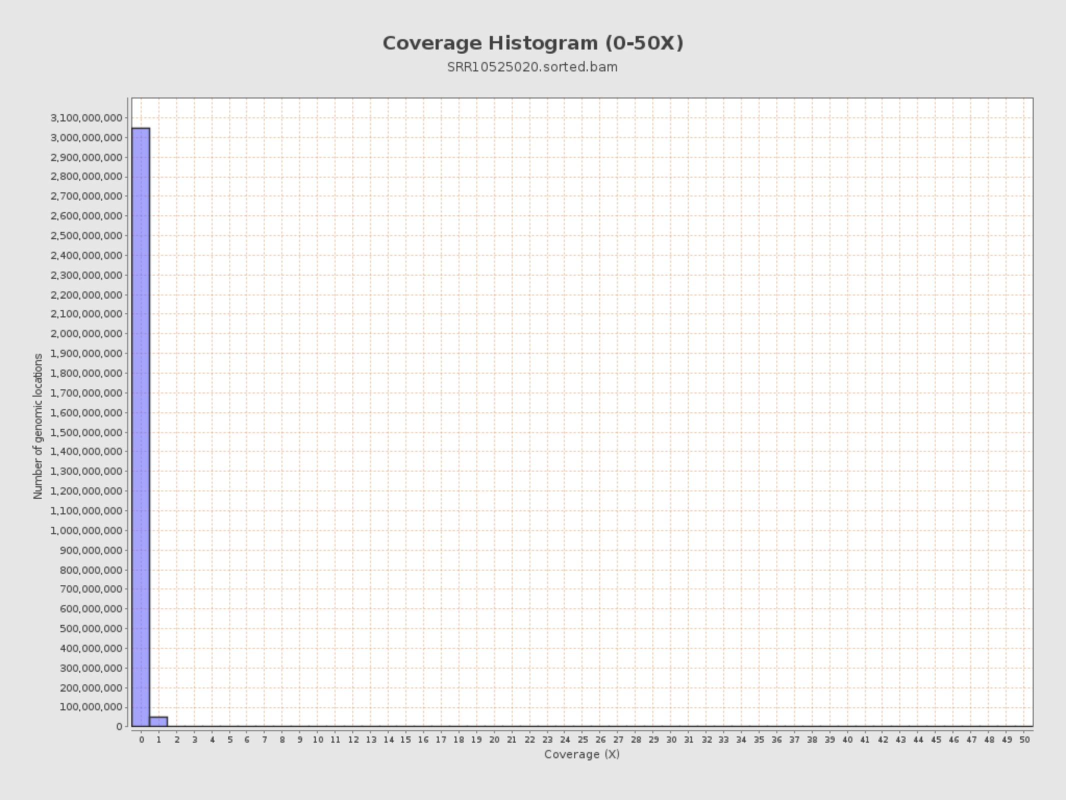
3. Results : Coverage across reference



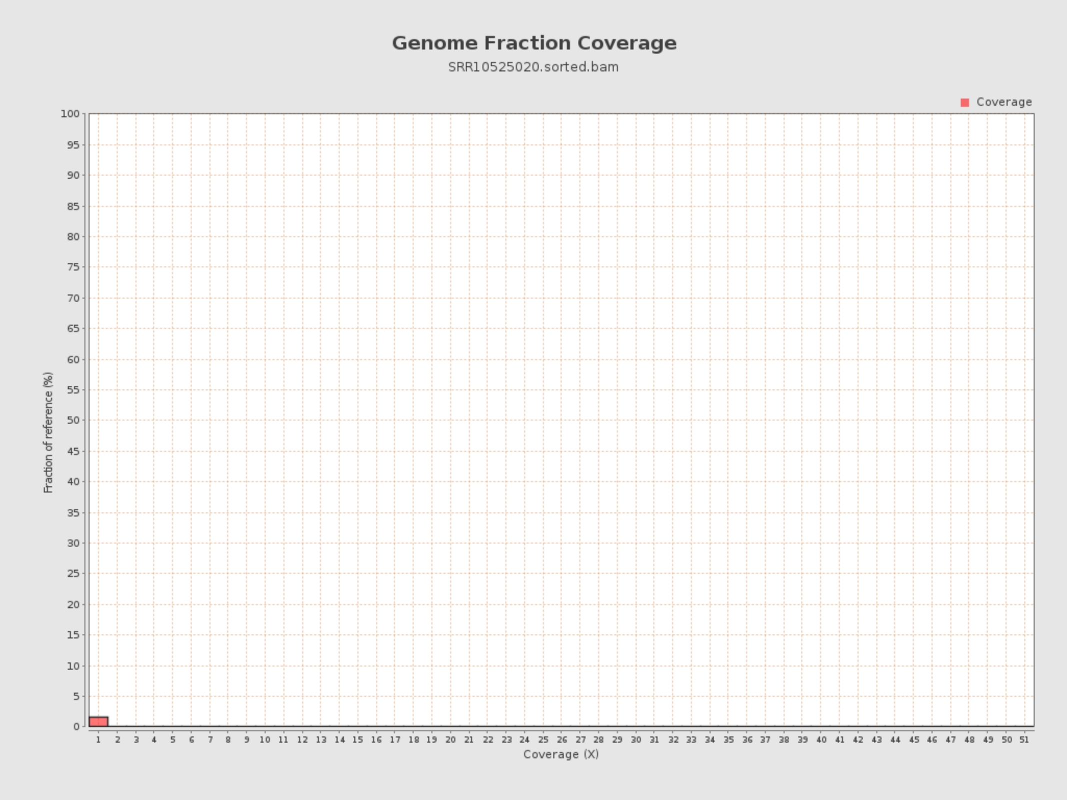
4. Results : Coverage Histogram



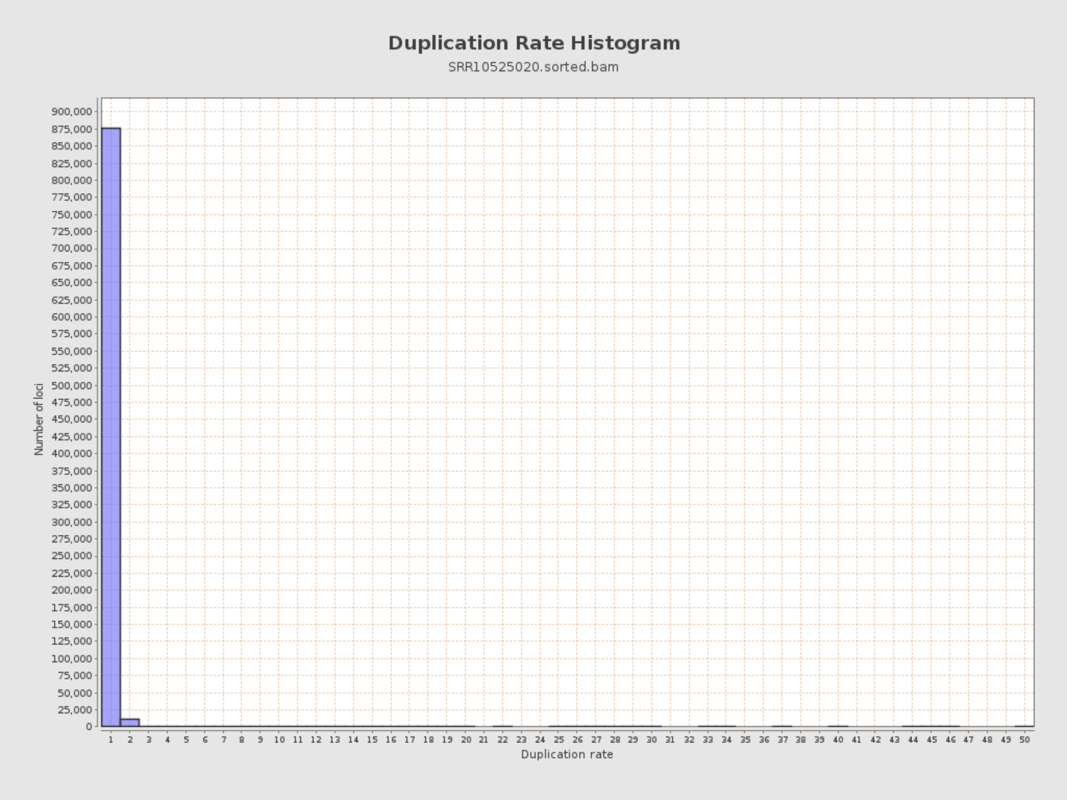
5. Results : Coverage Histogram (0-50X)



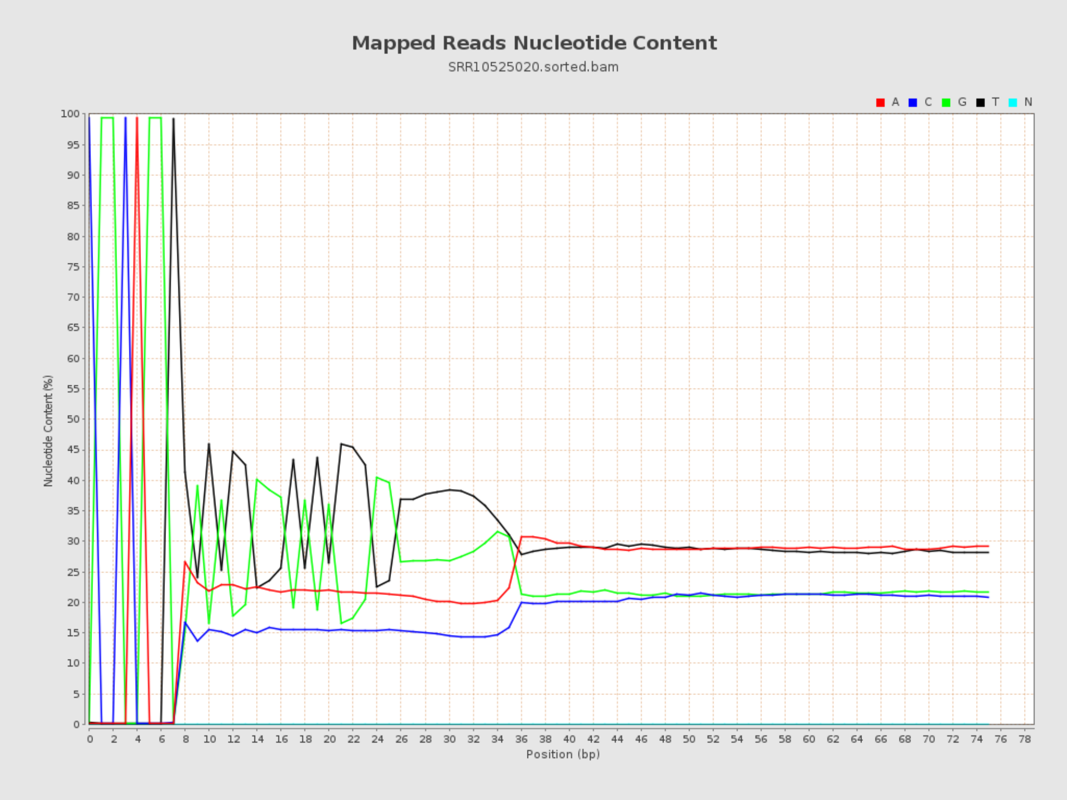
6. Results : Genome Fraction Coverage



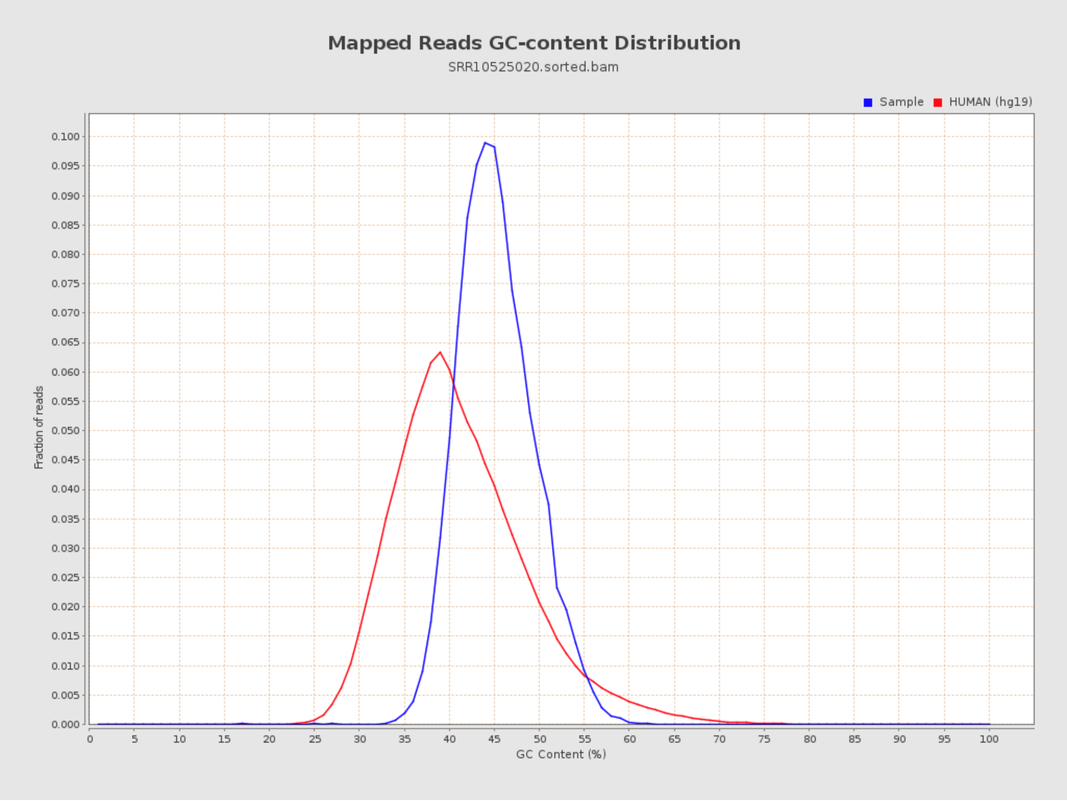
7. Results : Duplication Rate Histogram



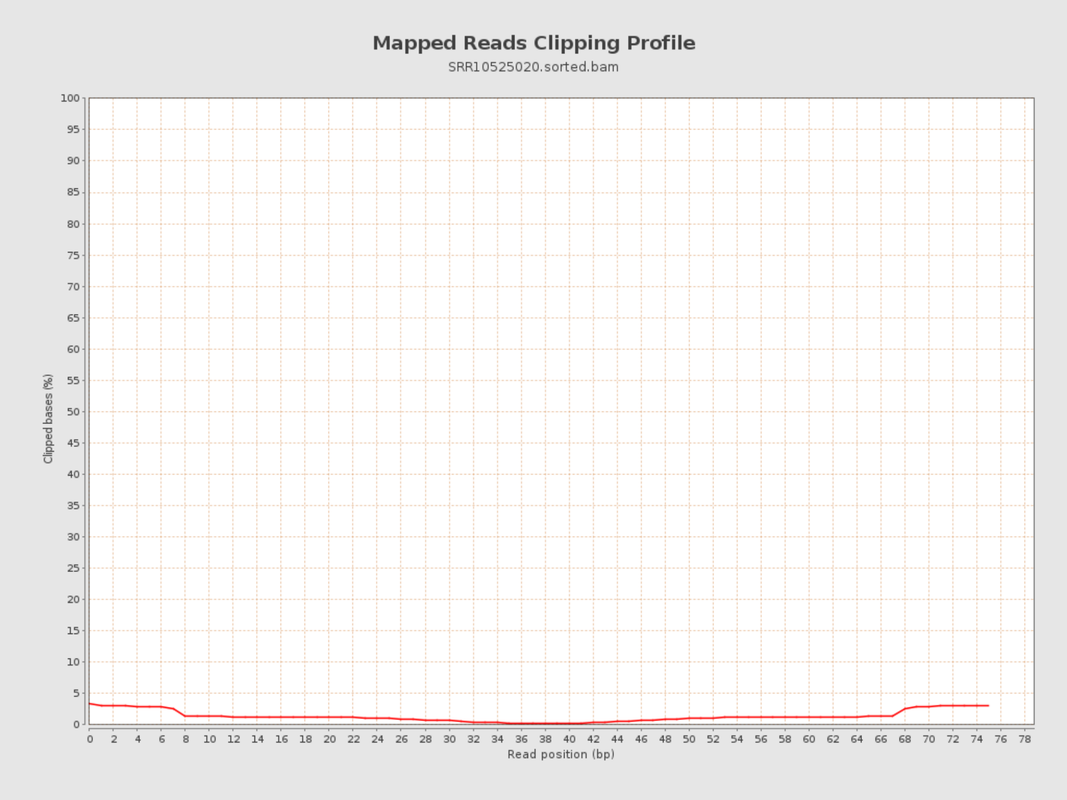
8. Results : Mapped Reads Nucleotide Content



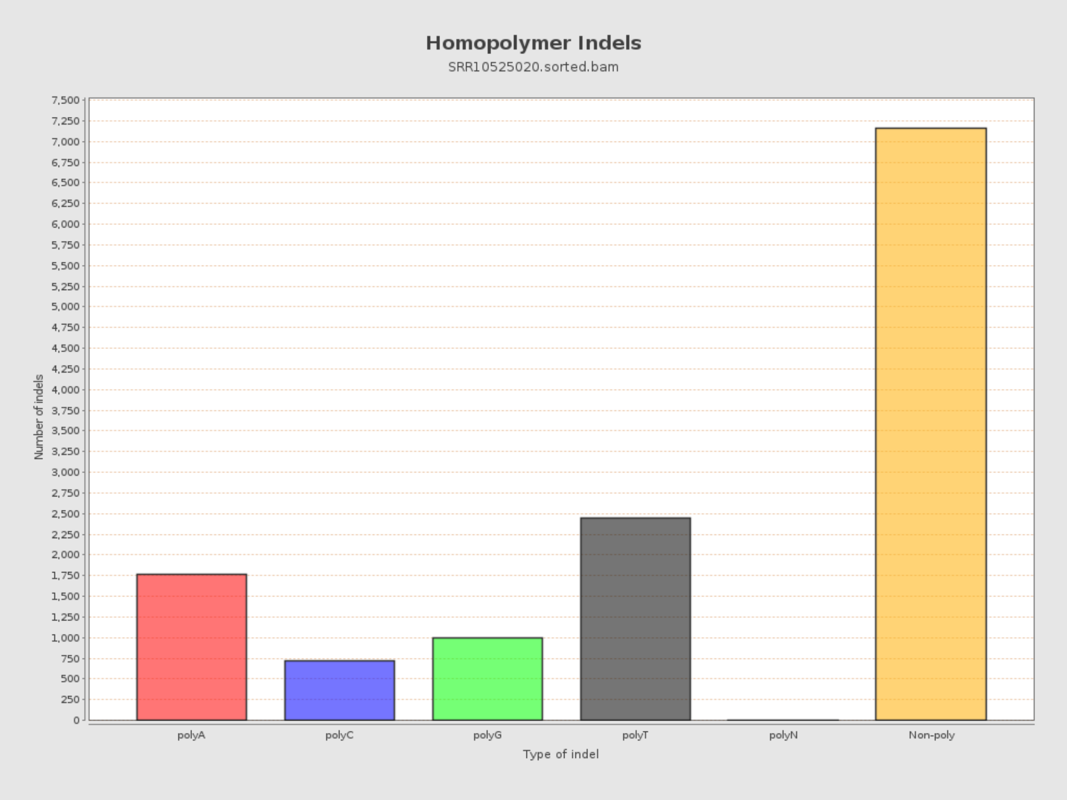
9. Results : Mapped Reads GC-content Distribution



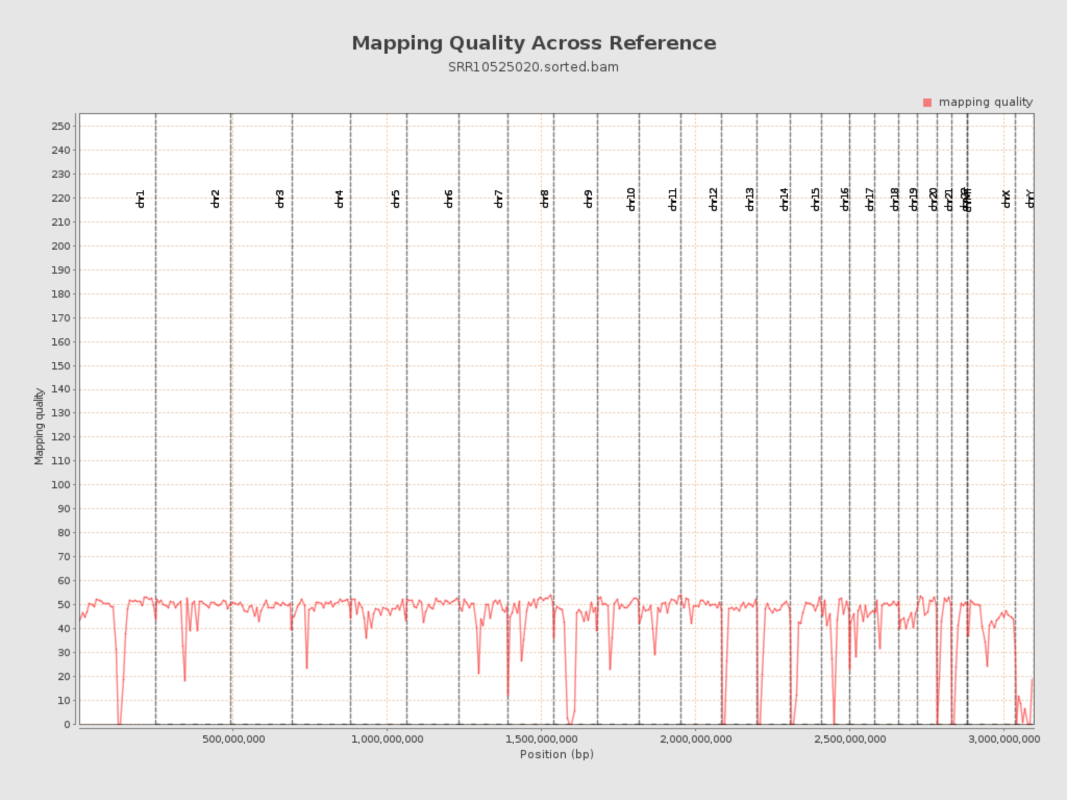
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram