Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:44:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525096.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_SRR10525096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525096.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:44:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	761,475
Mapped reads	702,095 / 92.2%
Unmapped reads	59,380 / 7.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,067 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	15,927 / 2.09%
Duplication rate	1.63%
Clipped reads	704,705 / 92.54%

2.2. ACGT Content

Number/percentage of A's	9,940,850 / 24.3%
Number/percentage of C's	7,481,411 / 18.28%
Number/percentage of T's	13,330,852 / 32.58%
Number/percentage of G's	10,162,064 / 24.84%
Number/percentage of N's	845 / 0%
GC Percentage	43.12%

2.3. Coverage

Mean	0.0132

Standard Deviation	0.1577

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

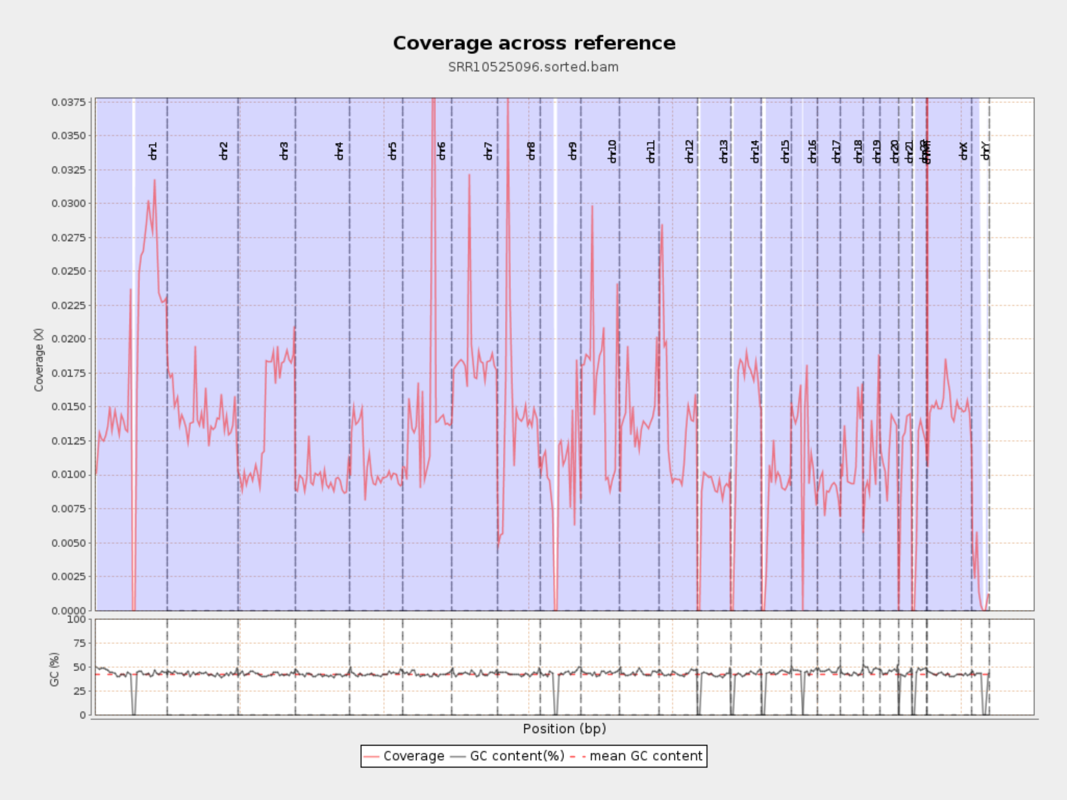
General error rate	0.51%
Mismatches	202,439
Insertions	2,457
Mapped reads with at least one insertion	0.35%
Deletions	8,426
Mapped reads with at least one deletion	1.19%
Homopolymer indels	45.89%

2.6. Chromosome stats

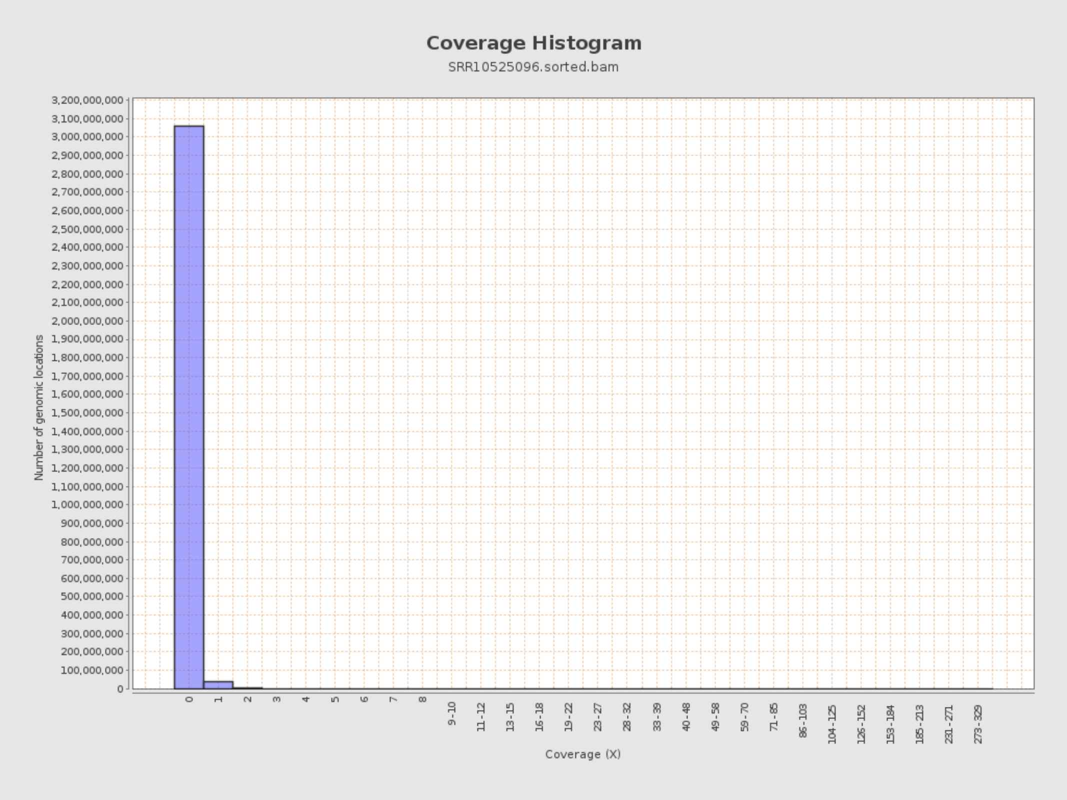
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4551957	0.0183	0.2586
chr2	243199373	3515848	0.0145	0.1853
chr3	198022430	2850929	0.0144	0.1262
chr4	191154276	1838552	0.0096	0.1045
chr5	180915260	1970422	0.0109	0.1085
chr6	171115067	2648998	0.0155	0.1385
chr7	159138663	2972865	0.0187	0.2657

chr8	146364022	2114973	0.0145	0.1432
chr9	141213431	1406421	0.01	0.1193
chr10	135534747	2261979	0.0167	0.1823
chr11	135006516	1927011	0.0143	0.1395
chr12	133851895	1930694	0.0144	0.1252
chr13	115169878	955897	0.0083	0.0951
chr14	107349540	1570530	0.0146	0.1265
chr15	102531392	816053	0.008	0.0941
chr16	90354753	1094702	0.0121	0.1197
chr17	81195210	719583	0.0089	0.1001
chr18	78077248	911549	0.0117	0.1972
chr19	59128983	669613	0.0113	0.186
chr20	63025520	737827	0.0117	0.1132
chr21	48129895	544799	0.0113	0.1141
chr22	51304566	469740	0.0092	0.0991
chrMT	16571	2874	0.1734	0.4288
chrX	155270560	2335307	0.015	0.1331
chrY	59373566	110350	0.0019	0.0599

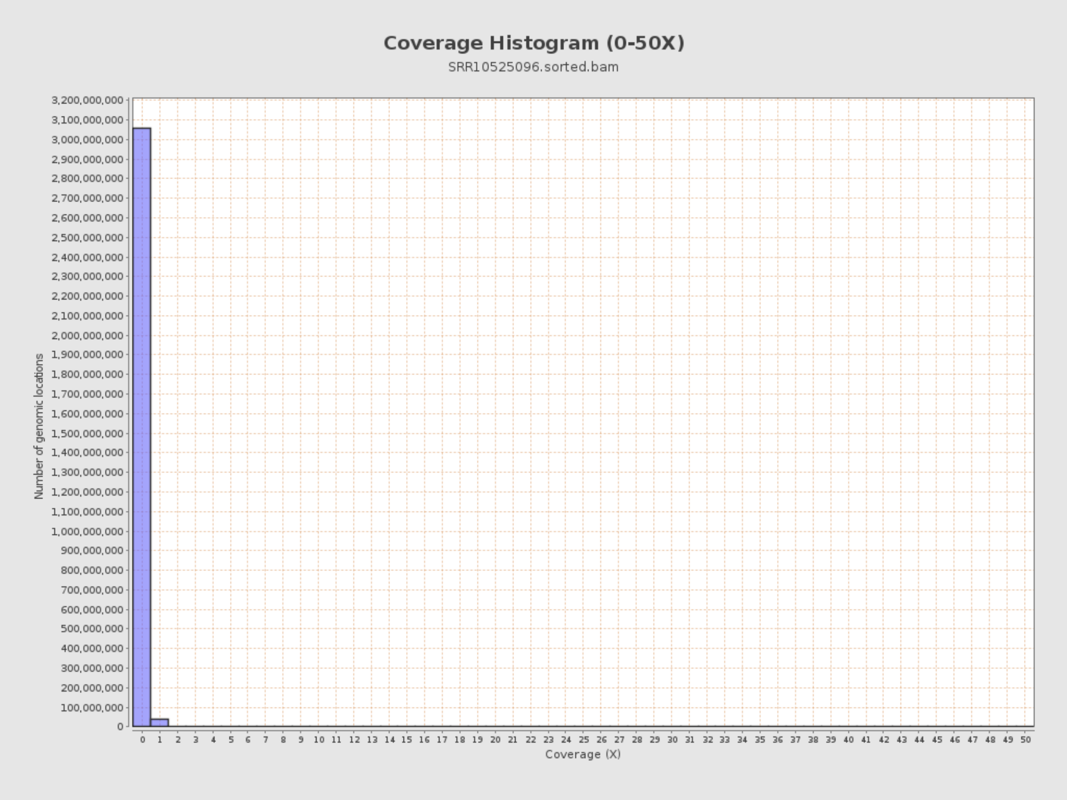
3. Results : Coverage across reference



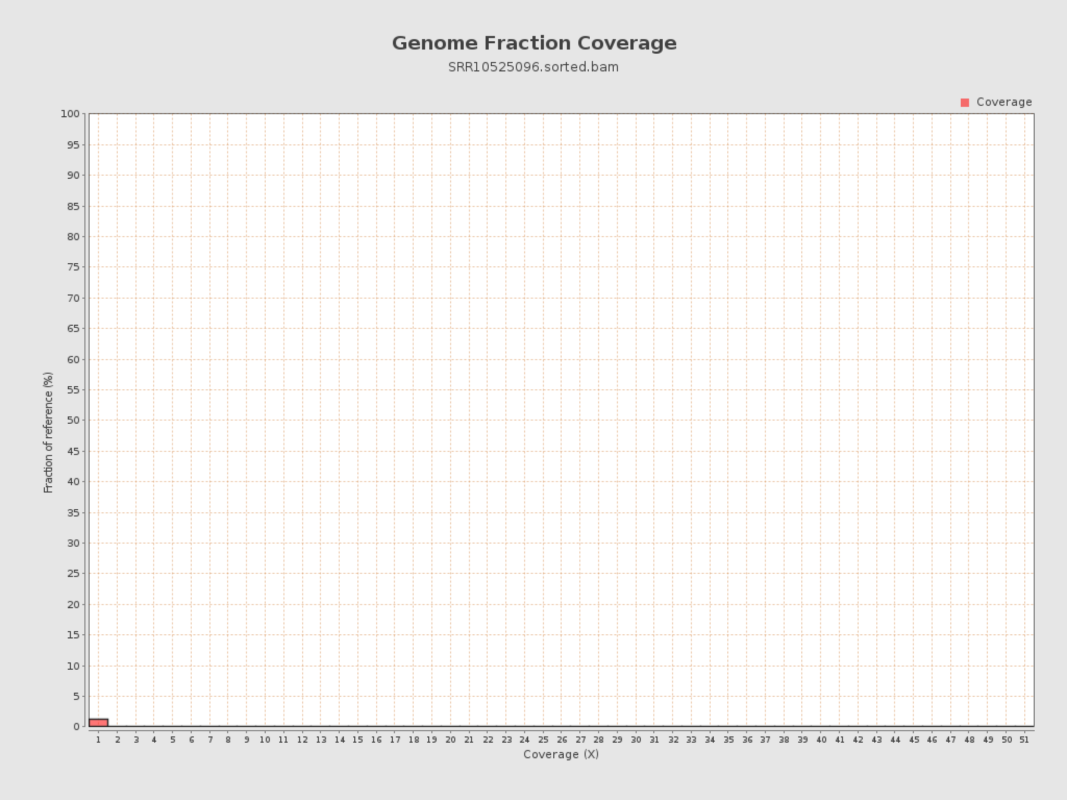
4. Results : Coverage Histogram



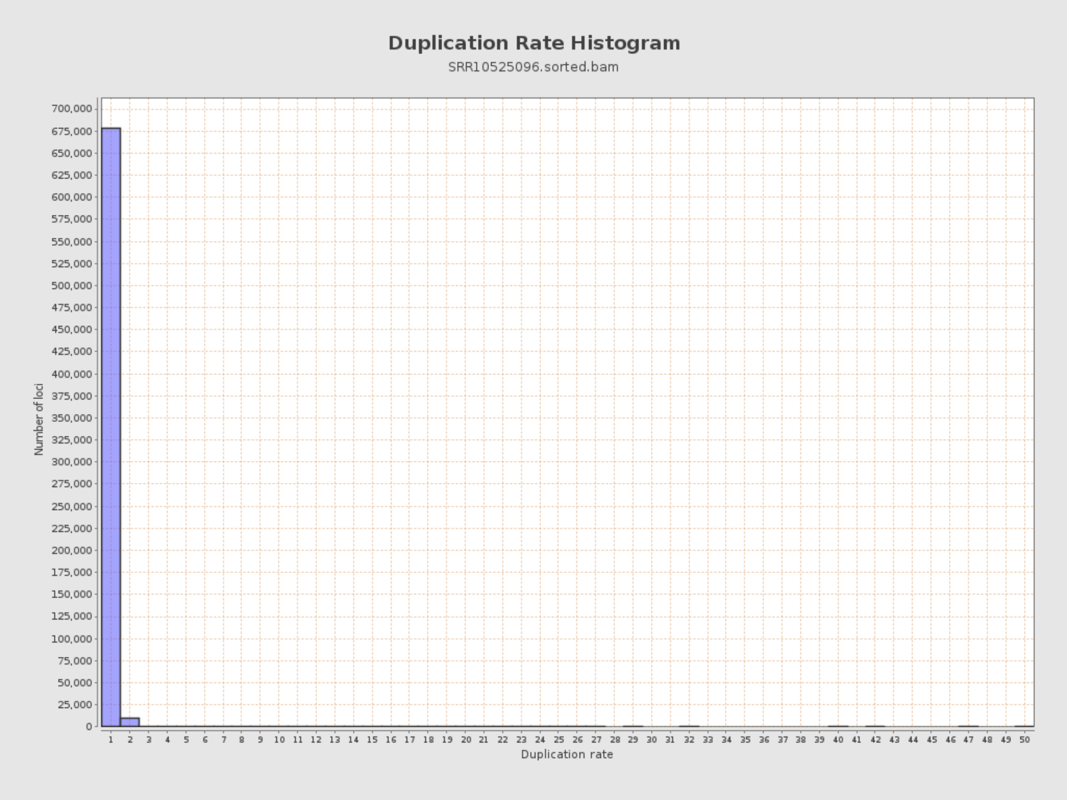
5. Results : Coverage Histogram (0-50X)



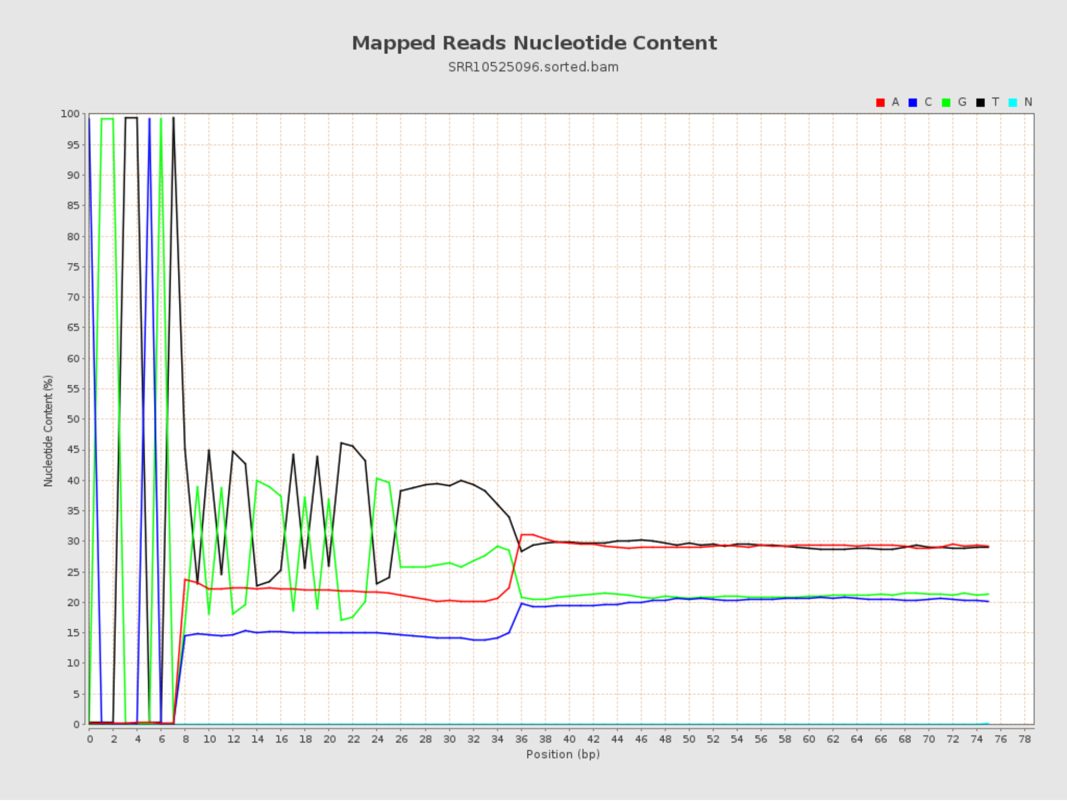
6. Results : Genome Fraction Coverage



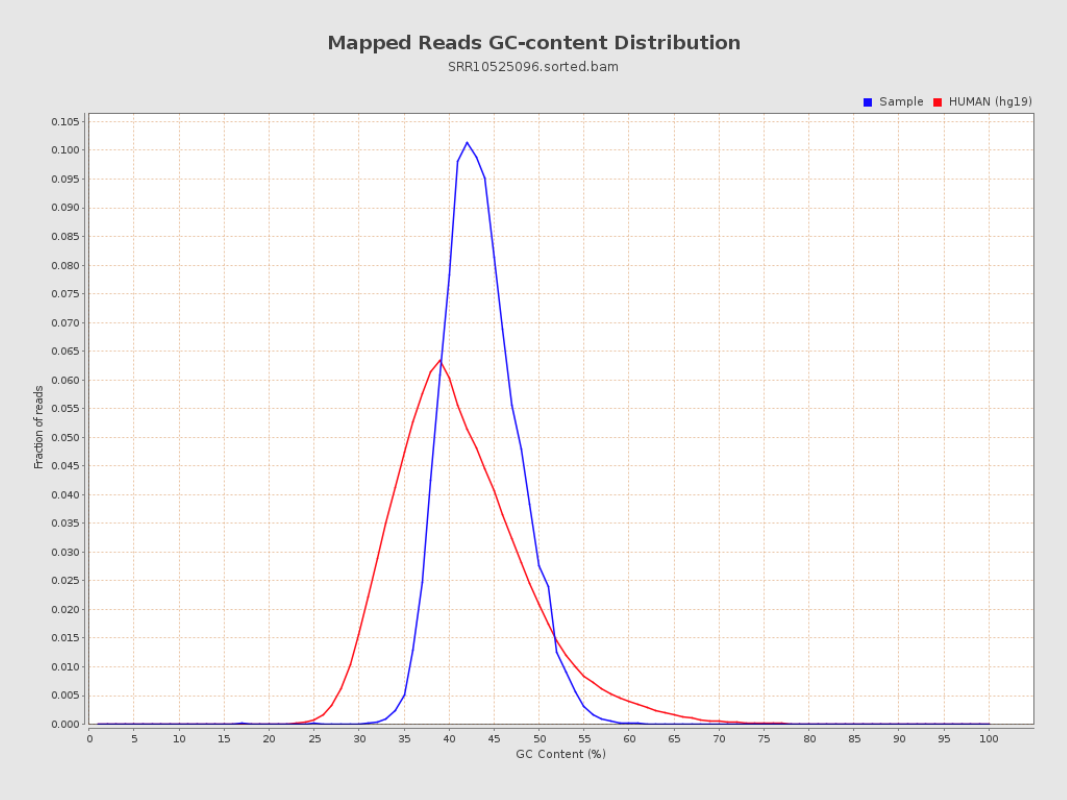
7. Results : Duplication Rate Histogram



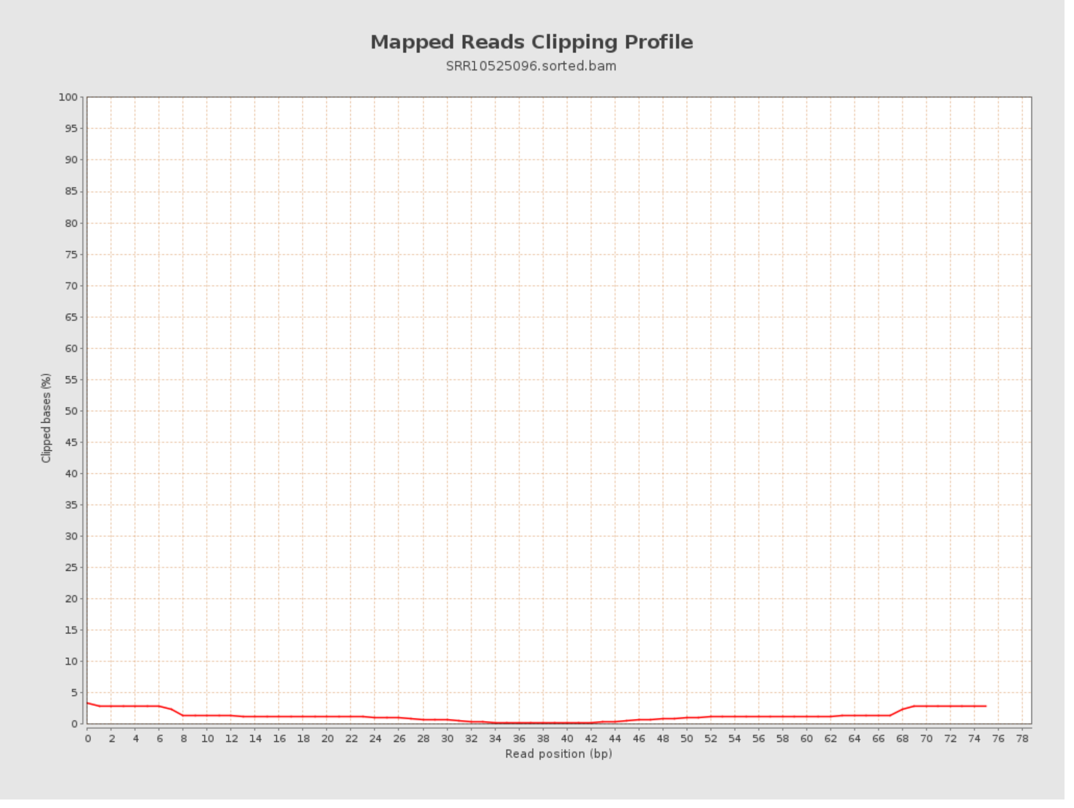
8. Results : Mapped Reads Nucleotide Content



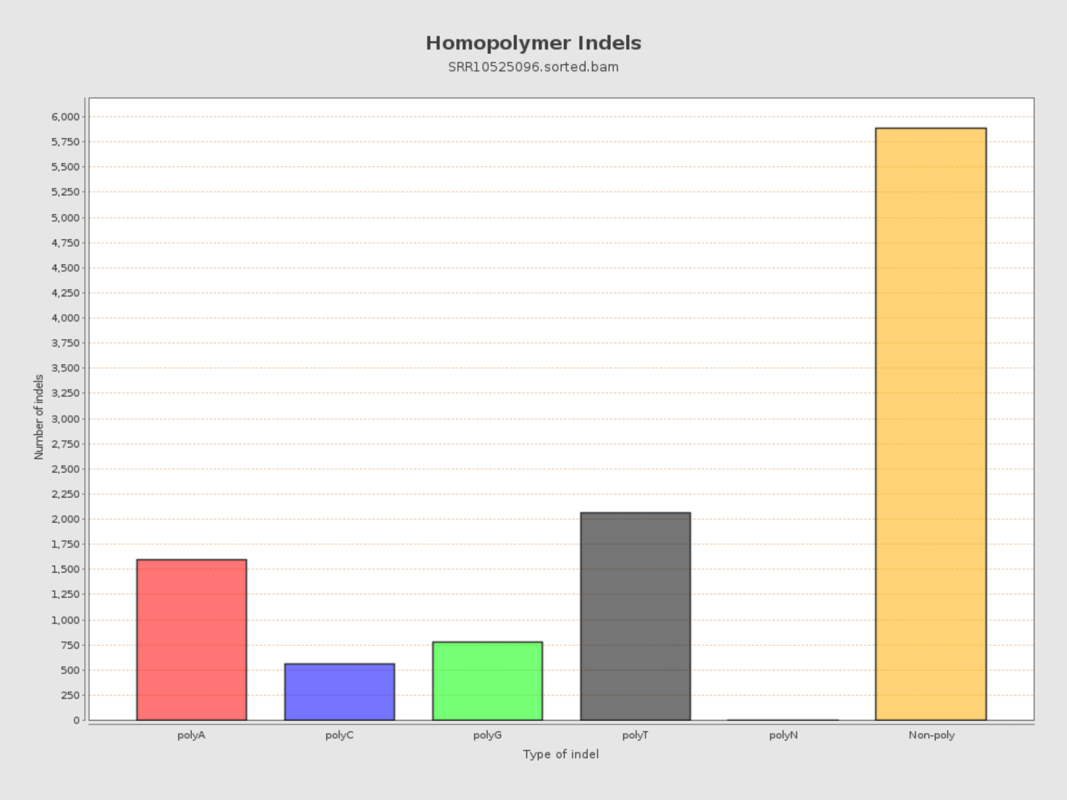
9. Results : Mapped Reads GC-content Distribution



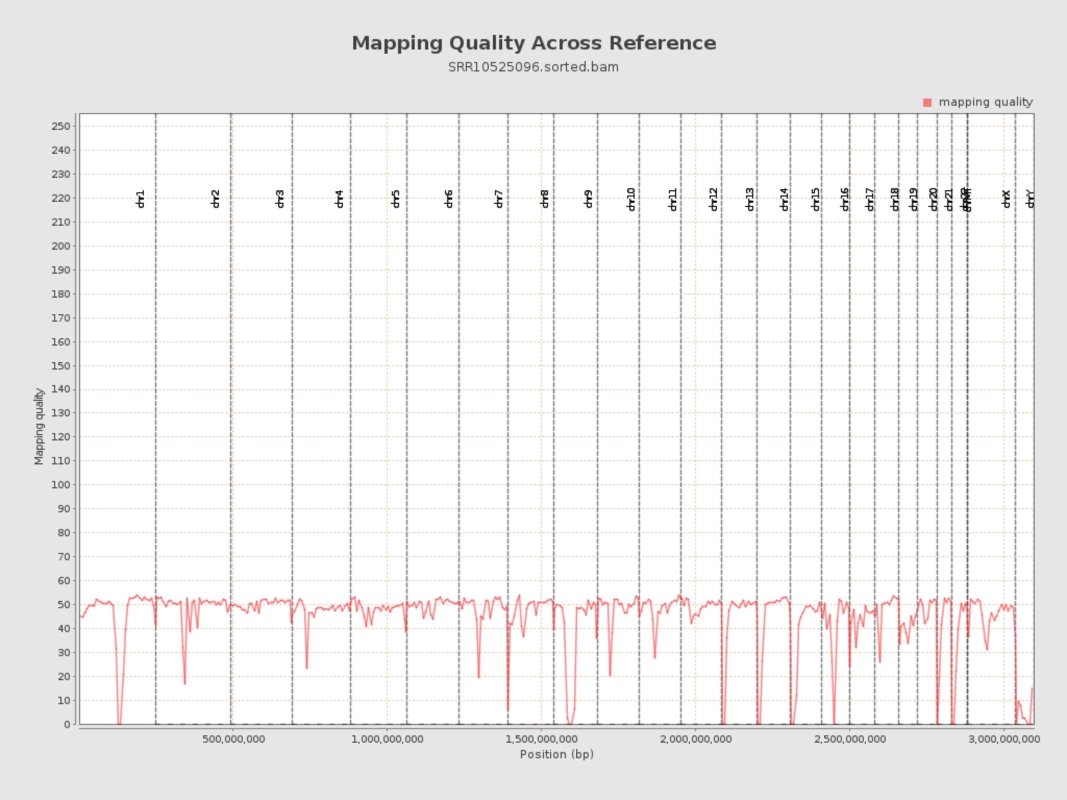
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram