Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:47:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708524.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_SRR1708524 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708524.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:47:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708524.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,305,801
Mapped reads	2,084,609 / 63.06%
Unmapped reads	1,221,192 / 36.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	597 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	98,248 / 2.97%
Duplication rate	3.35%
Clipped reads	503,151 / 15.22%

2.2. ACGT Content

Number/percentage of A's	27,775,620 / 28.21%
Number/percentage of C's	18,215,877 / 18.5%
Number/percentage of T's	31,526,066 / 32.02%
Number/percentage of G's	20,931,068 / 21.26%
Number/percentage of N's	1,227 / 0%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0318

Standard Deviation	0.3232

2.4. Mapping Quality

Mean Mapping Quality	39.13

2.5. Mismatches and indels

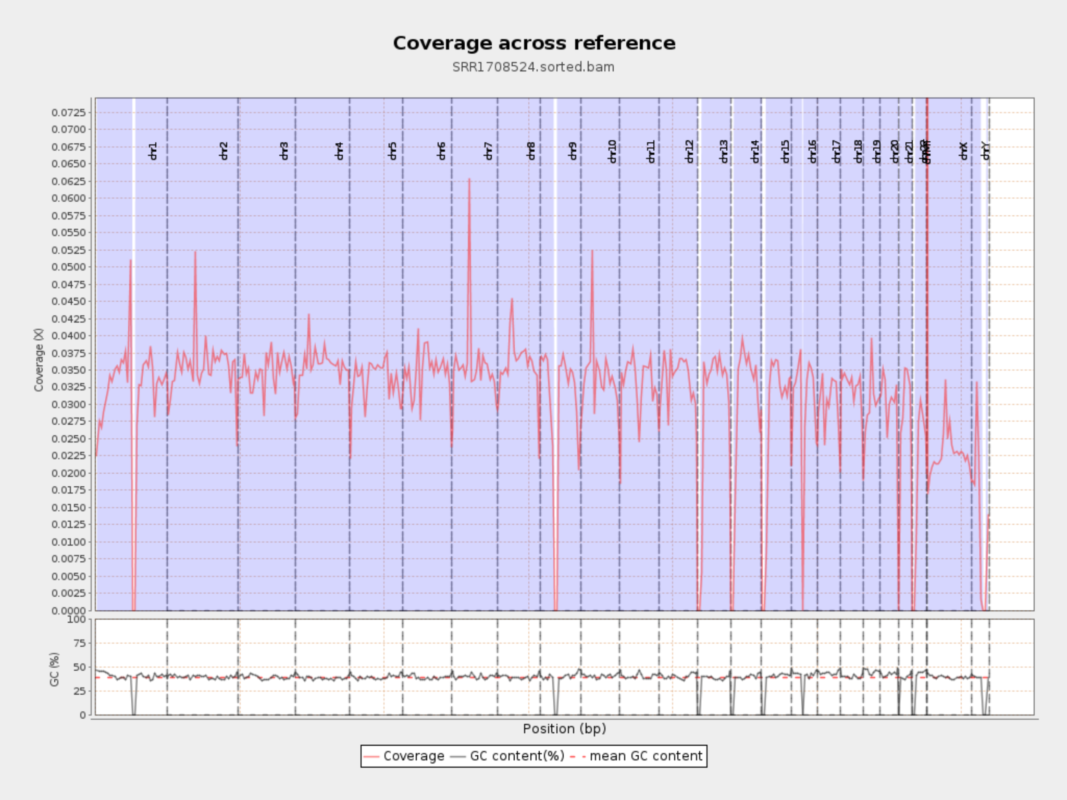
General error rate	0.54%
Mismatches	521,218
Insertions	5,497
Mapped reads with at least one insertion	0.26%
Deletions	15,012
Mapped reads with at least one deletion	0.72%
Homopolymer indels	47.61%

2.6. Chromosome stats

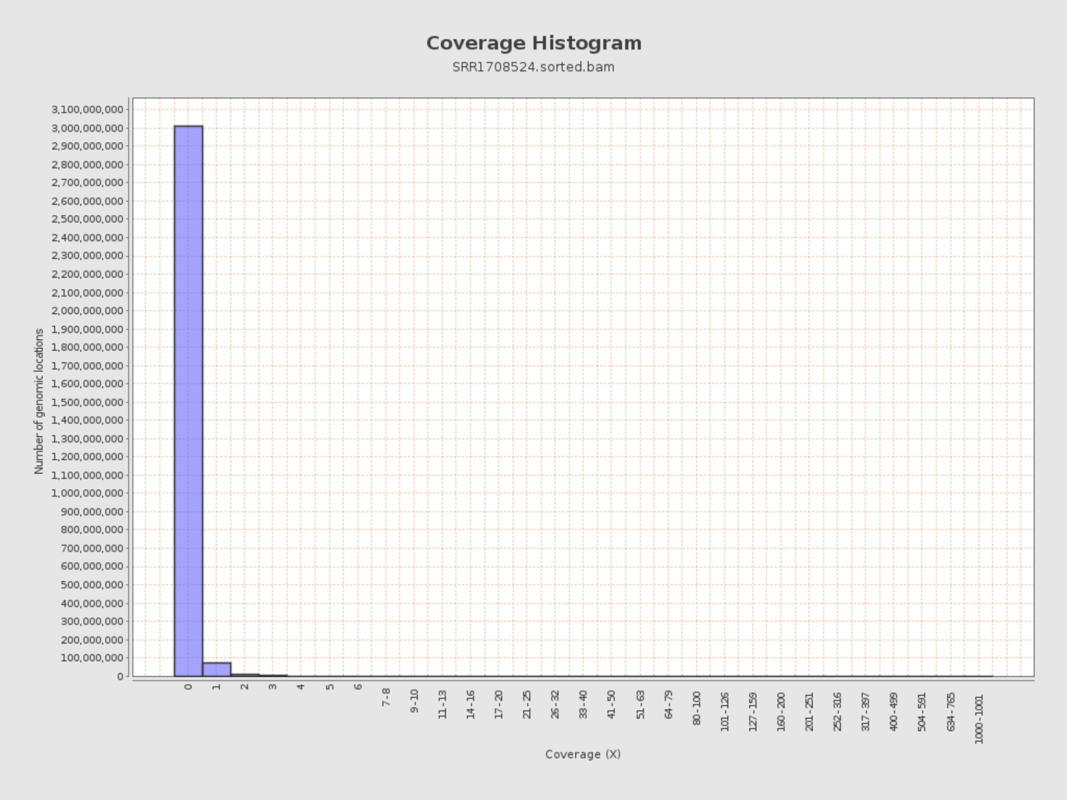
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7840814	0.0315	0.4671
chr2	243199373	8670439	0.0357	0.4903
chr3	198022430	6884916	0.0348	0.2251
chr4	191154276	6805809	0.0356	0.2311
chr5	180915260	6111756	0.0338	0.2157
chr6	171115067	5931874	0.0347	0.3275
chr7	159138663	5723199	0.036	0.427

chr8	146364022	5255708	0.0359	0.4771
chr9	141213431	4180208	0.0296	0.2712
chr10	135534747	4646575	0.0343	0.2776
chr11	135006516	4496503	0.0333	0.2901
chr12	133851895	4535271	0.0339	0.2215
chr13	115169878	3327501	0.0289	0.2674
chr14	107349540	3111822	0.029	0.2092
chr15	102531392	2785857	0.0272	0.2047
chr16	90354753	2655608	0.0294	0.2148
chr17	81195210	2455090	0.0302	0.2455
chr18	78077248	2567362	0.0329	0.399
chr19	59128983	1784080	0.0302	0.3536
chr20	63025520	1917024	0.0304	0.2097
chr21	48129895	1330199	0.0276	0.2258
chr22	51304566	991412	0.0193	0.1809
chrMT	16571	102108	6.1618	4.2237
chrX	155270560	3574592	0.023	0.2121
chrY	59373566	786935	0.0133	0.1556

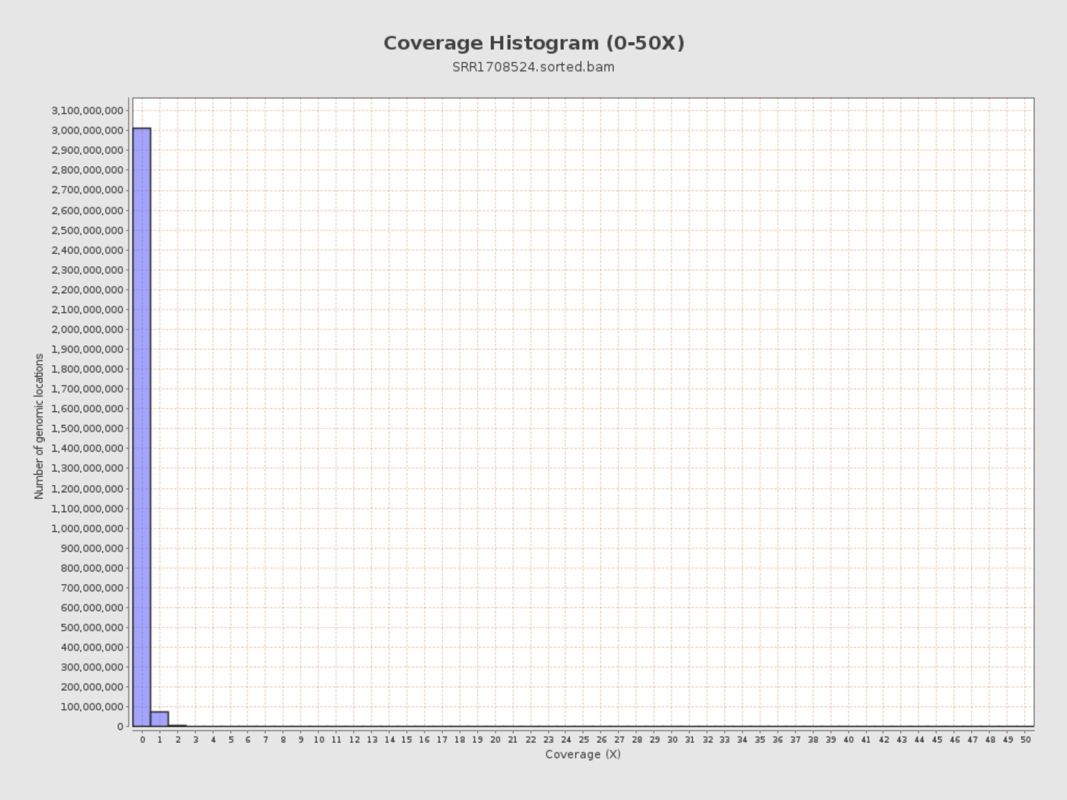
3. Results : Coverage across reference



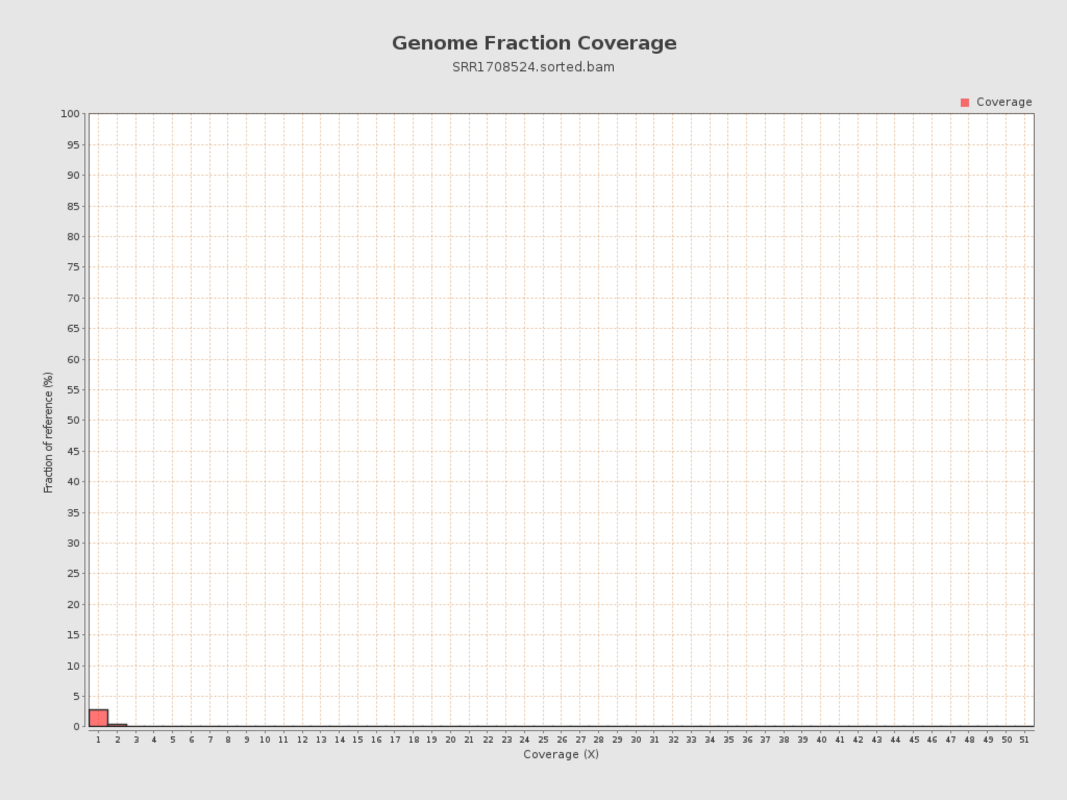
4. Results : Coverage Histogram



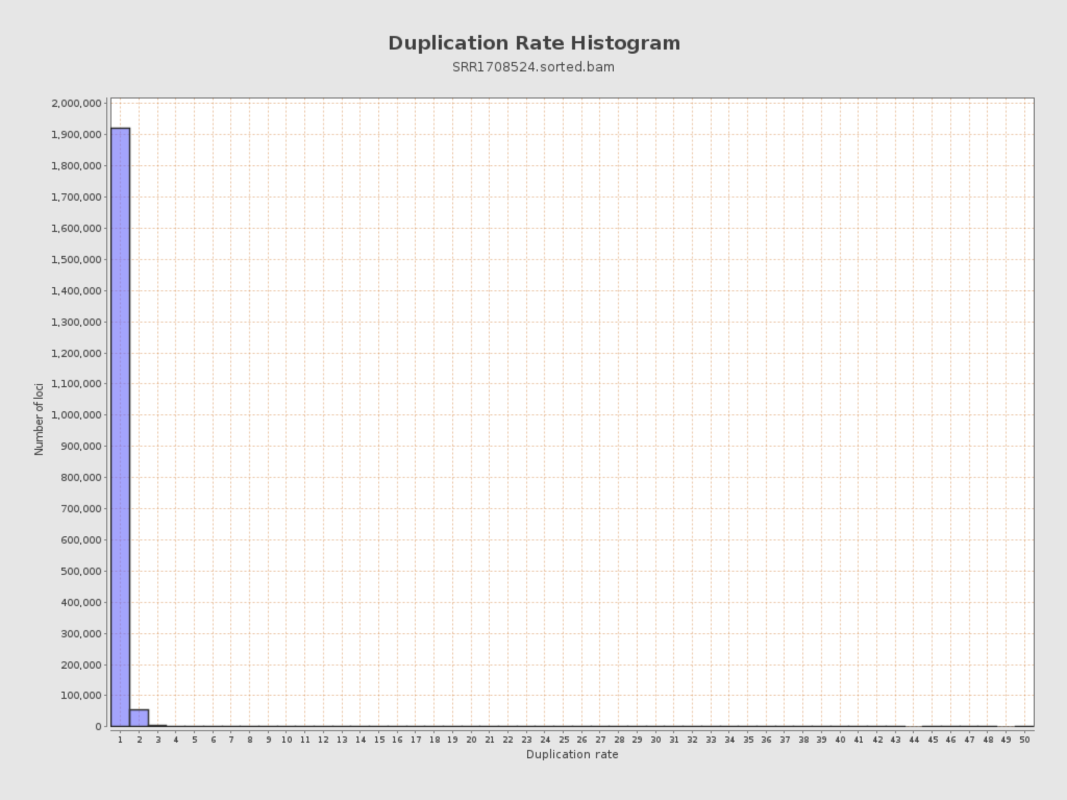
5. Results : Coverage Histogram (0-50X)



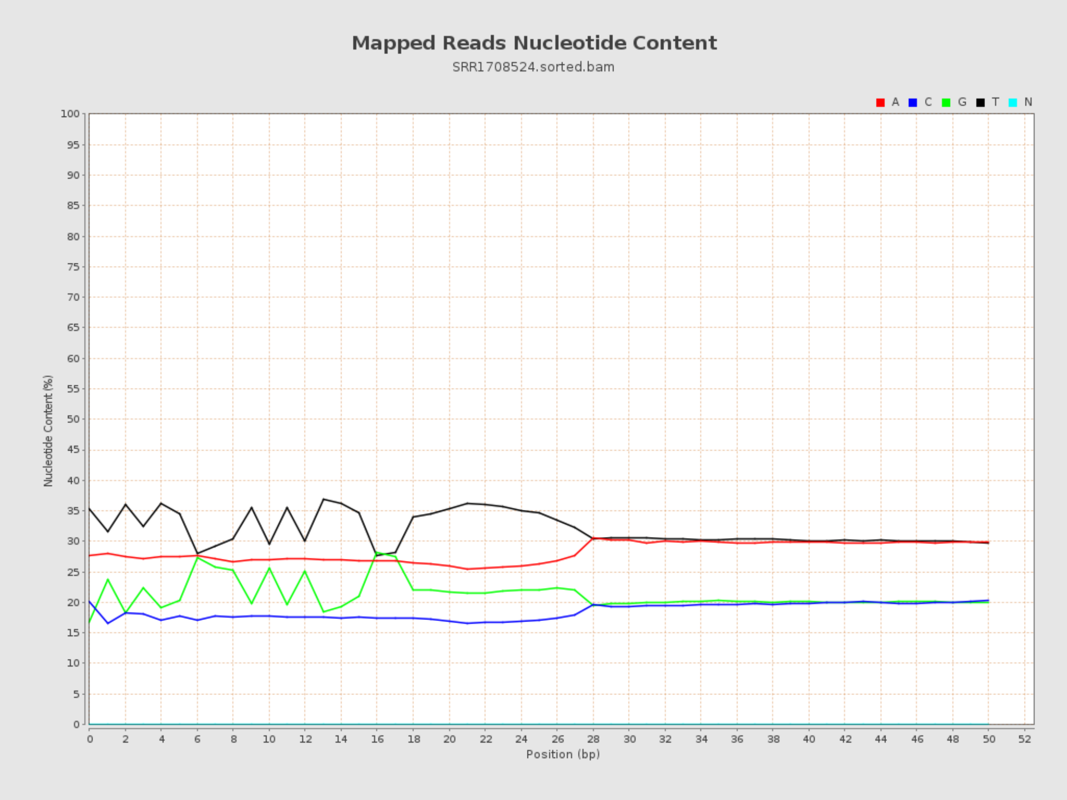
6. Results : Genome Fraction Coverage



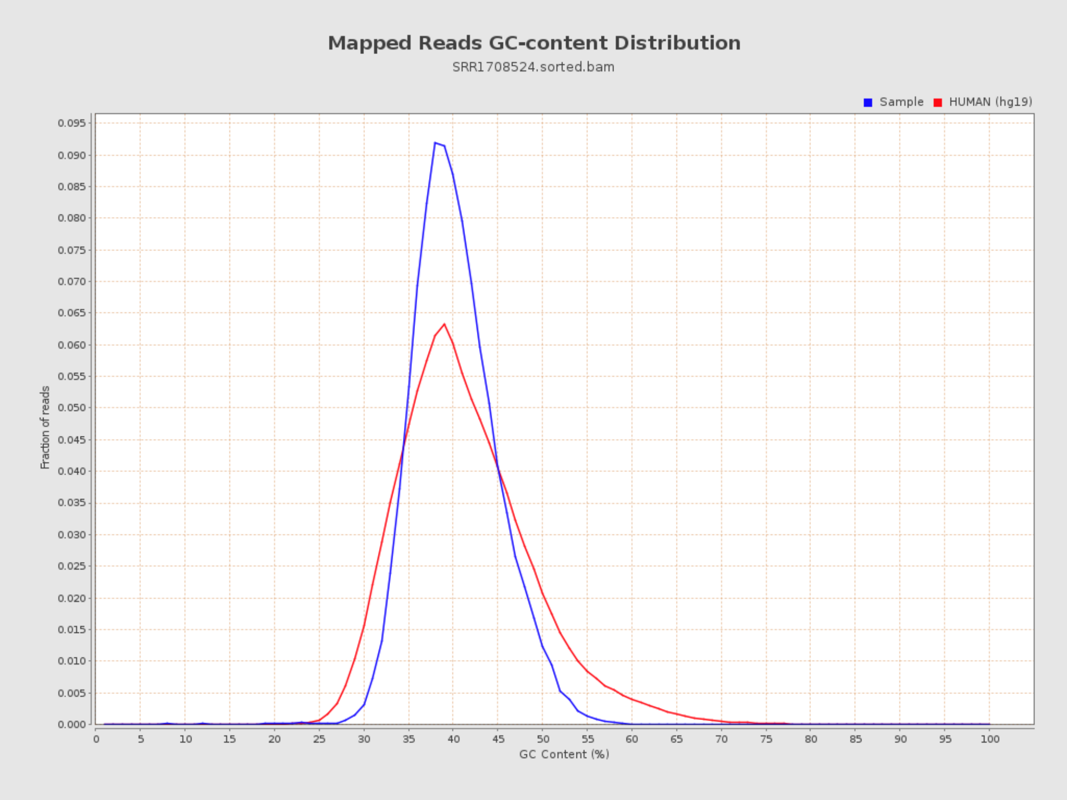
7. Results : Duplication Rate Histogram



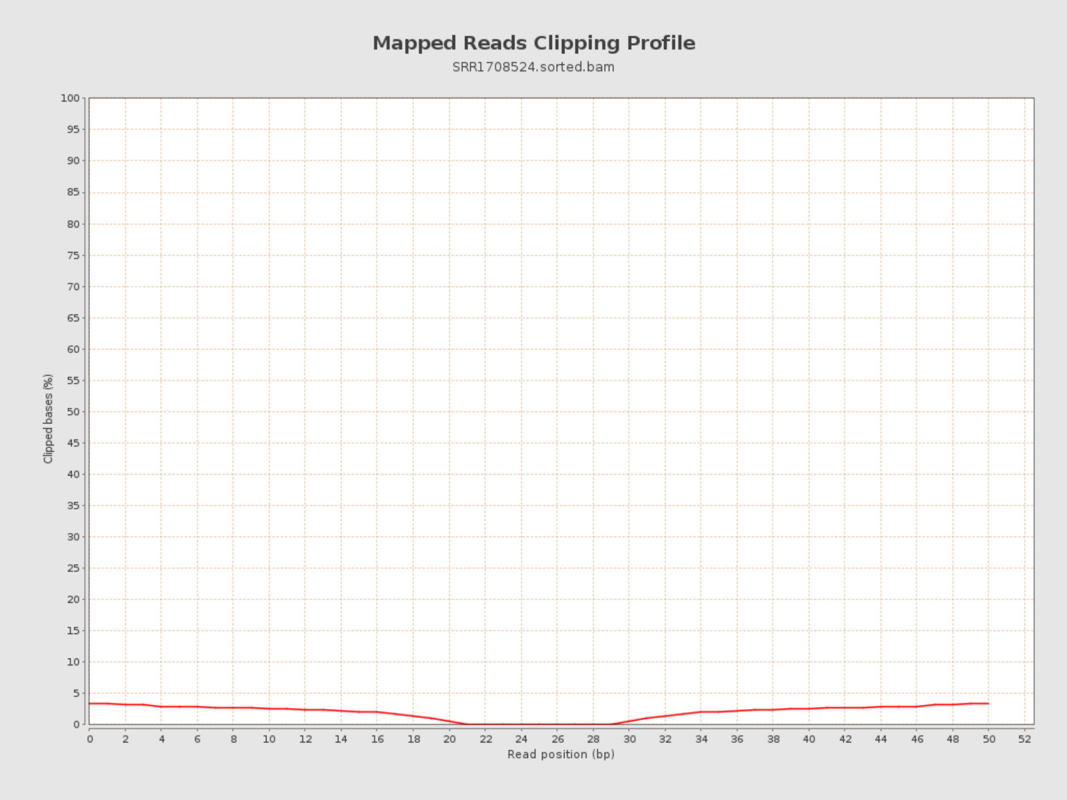
8. Results : Mapped Reads Nucleotide Content



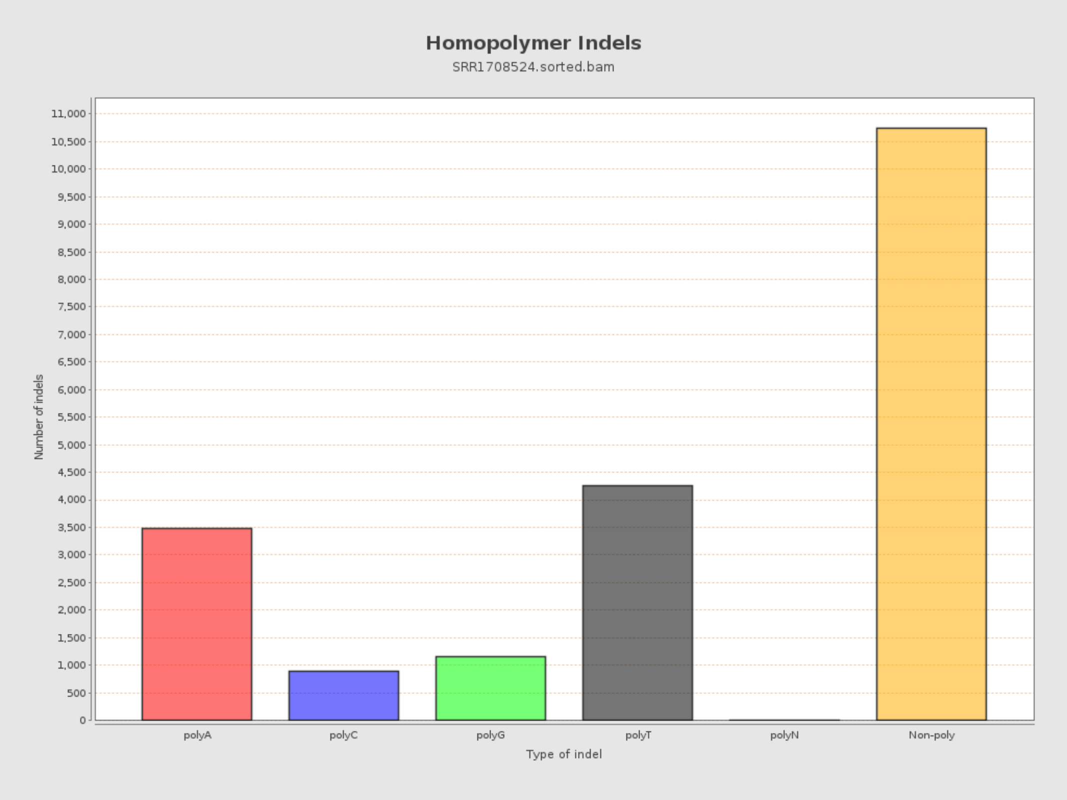
9. Results : Mapped Reads GC-content Distribution



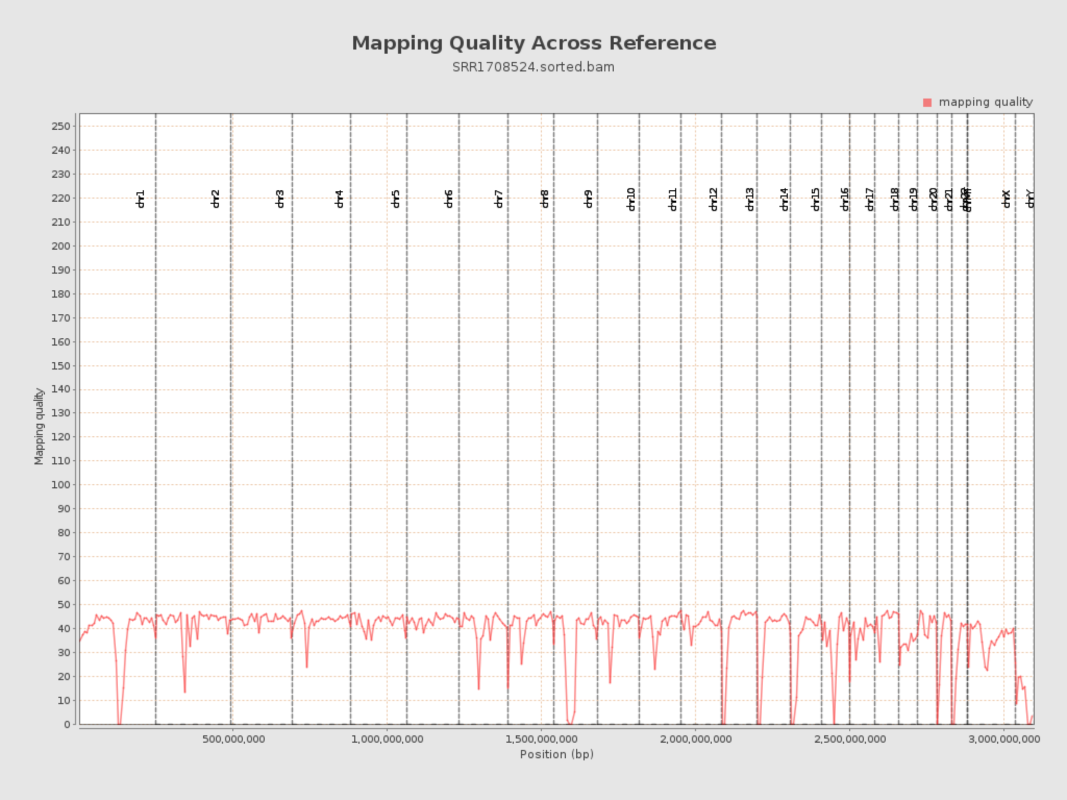
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram