Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:21:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708625.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_SRR1708625 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708625.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:21:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708625.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,835,272
Mapped reads	1,851,104 / 65.29%
Unmapped reads	984,168 / 34.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	600 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	93,021 / 3.28%
Duplication rate	3.55%
Clipped reads	333,529 / 11.76%

2.2. ACGT Content

Number/percentage of A's	26,692,763 / 29.84%
Number/percentage of C's	16,349,156 / 18.28%
Number/percentage of T's	28,827,758 / 32.22%
Number/percentage of G's	17,583,352 / 19.65%
Number/percentage of N's	7,403 / 0.01%
GC Percentage	37.93%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.3862

2.4. Mapping Quality

Mean Mapping Quality	41.3

2.5. Mismatches and indels

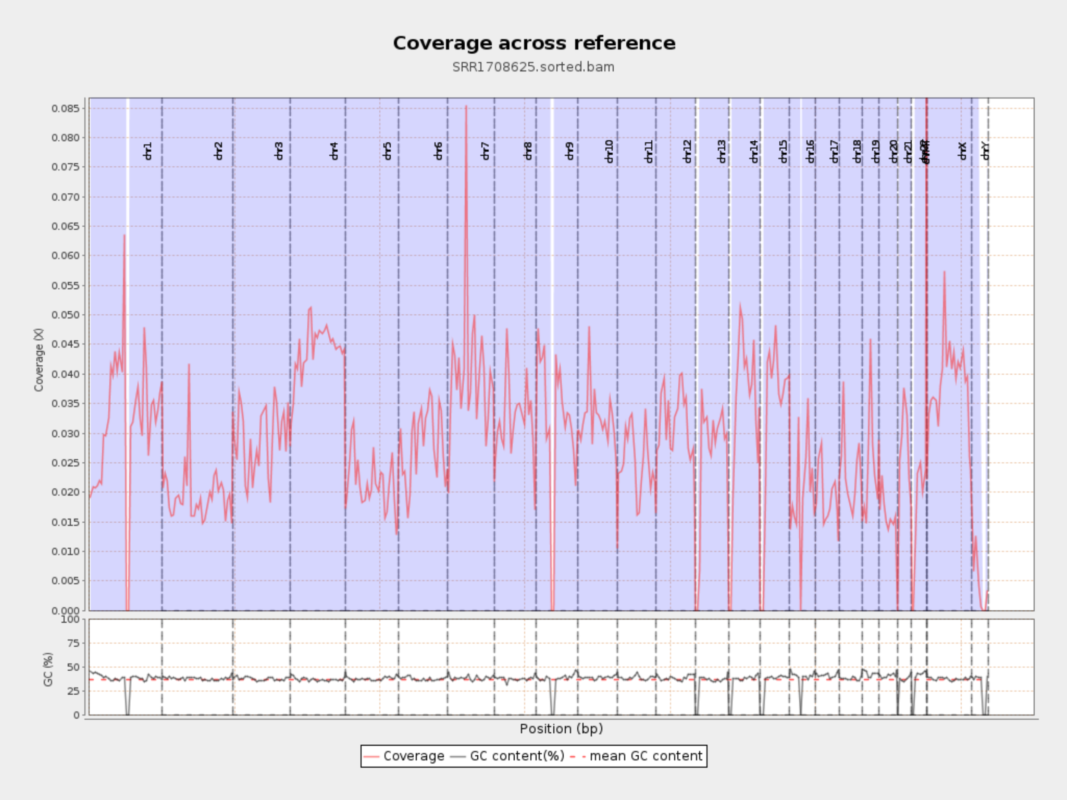
General error rate	0.73%
Mismatches	645,977
Insertions	4,654
Mapped reads with at least one insertion	0.25%
Deletions	15,671
Mapped reads with at least one deletion	0.84%
Homopolymer indels	44.36%

2.6. Chromosome stats

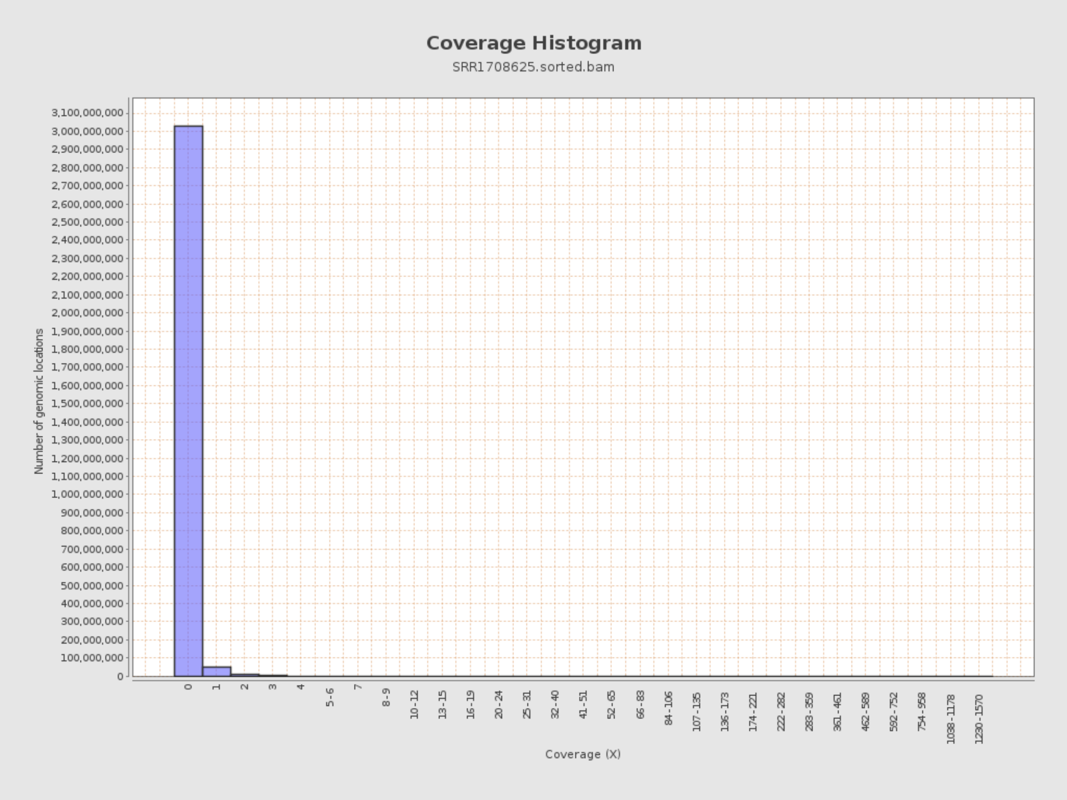
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7935286	0.0318	0.6579
chr2	243199373	4795989	0.0197	0.3141
chr3	198022430	5751187	0.029	0.2218
chr4	191154276	8463224	0.0443	0.2781
chr5	180915260	3903829	0.0216	0.1928
chr6	171115067	4853261	0.0284	0.269
chr7	159138663	6505892	0.0409	0.5961

chr8	146364022	4737215	0.0324	0.8674
chr9	141213431	4496437	0.0318	0.2816
chr10	135534747	4436569	0.0327	0.2975
chr11	135006516	3373966	0.025	0.2699
chr12	133851895	4282060	0.032	0.2374
chr13	115169878	2969653	0.0258	0.2097
chr14	107349540	3592085	0.0335	0.255
chr15	102531392	3369333	0.0329	0.2344
chr16	90354753	1794258	0.0199	0.1993
chr17	81195210	1549323	0.0191	0.2013
chr18	78077248	1841525	0.0236	0.5671
chr19	59128983	1467532	0.0248	0.4333
chr20	63025520	1018204	0.0162	0.1771
chr21	48129895	1233009	0.0256	0.2191
chr22	51304566	838937	0.0164	0.1627
chrMT	16571	2786	0.1681	0.5709
chrX	155270560	5991499	0.0386	0.2764
chrY	59373566	281244	0.0047	0.0953

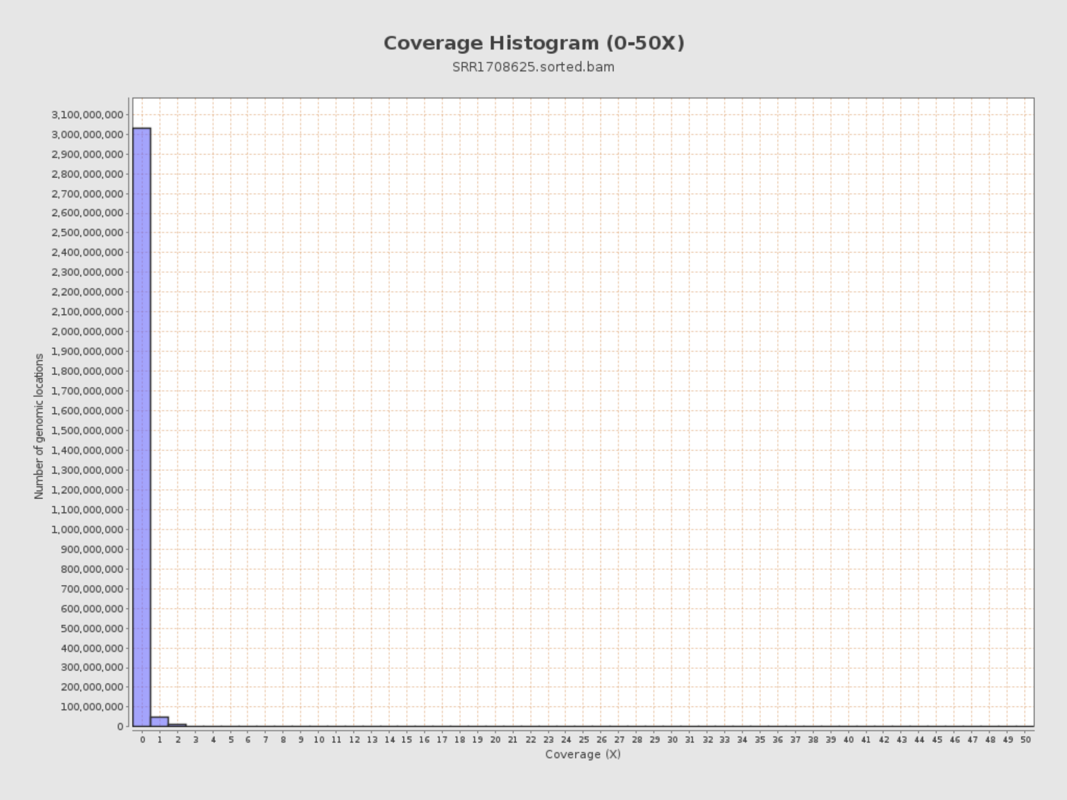
3. Results : Coverage across reference



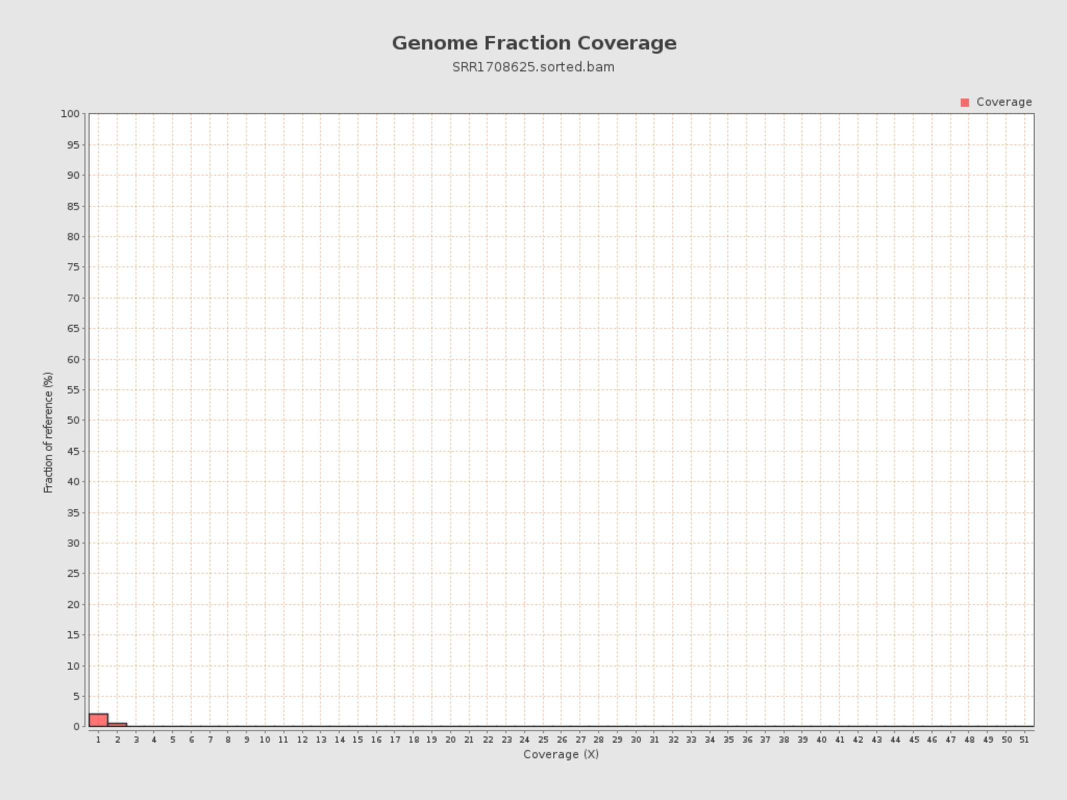
4. Results : Coverage Histogram



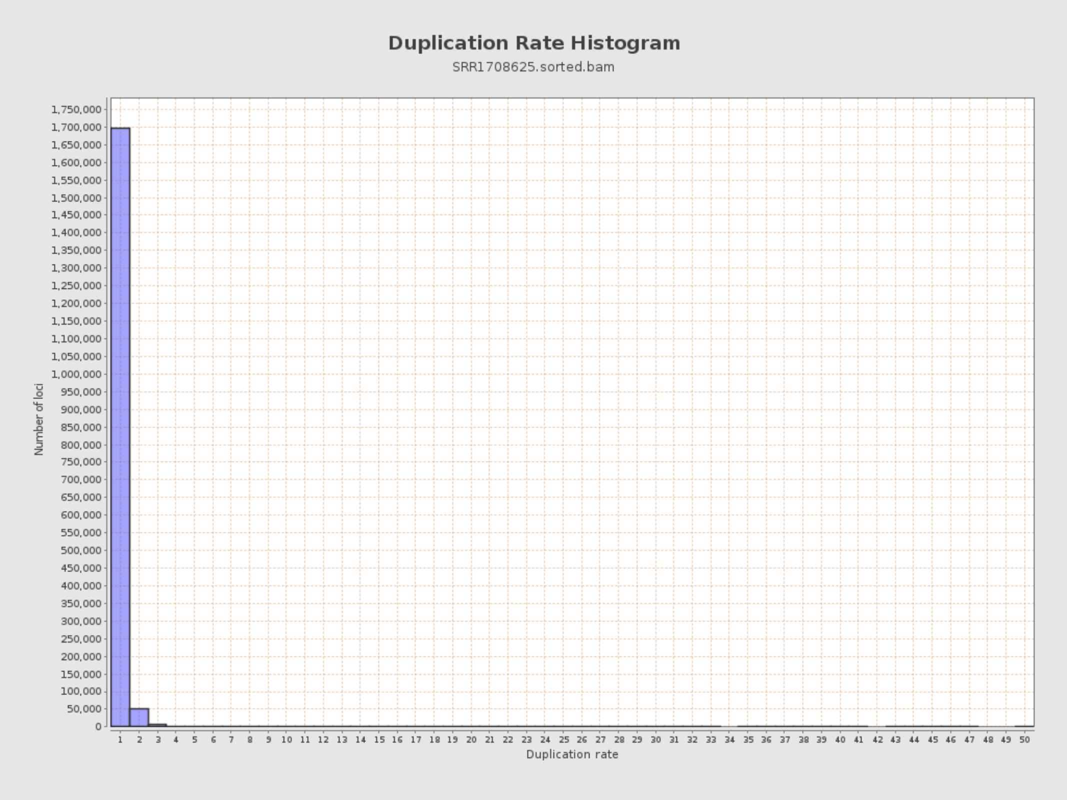
5. Results : Coverage Histogram (0-50X)



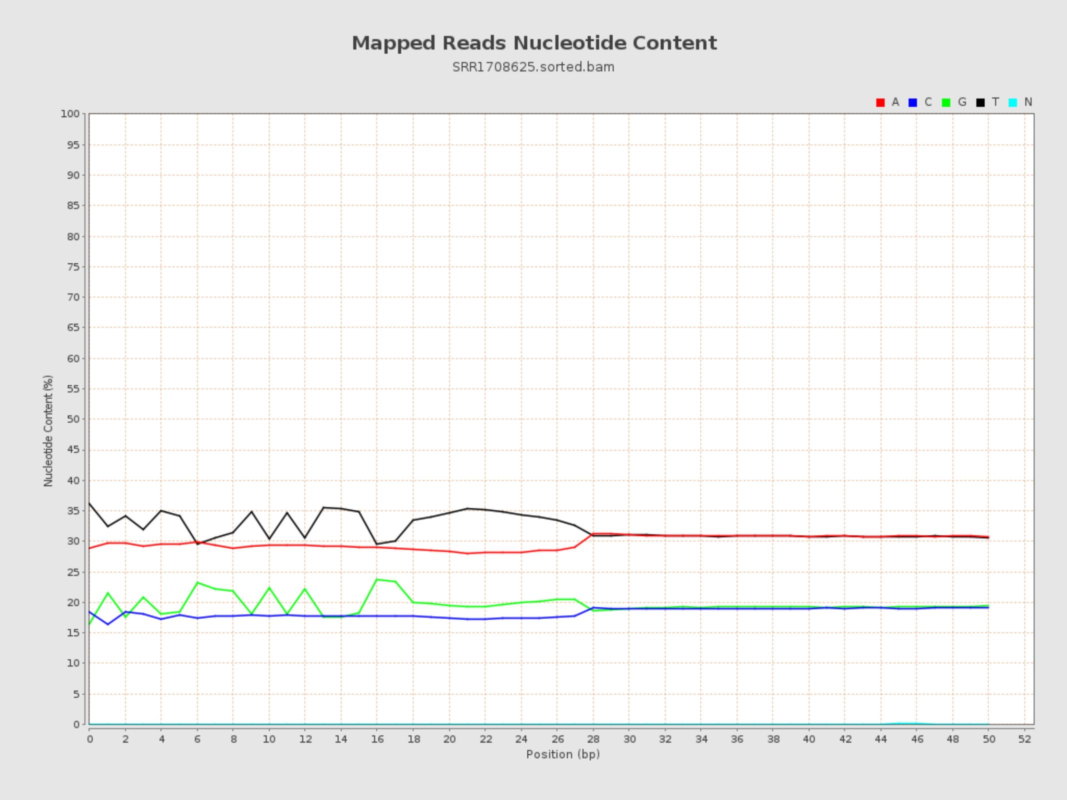
6. Results : Genome Fraction Coverage



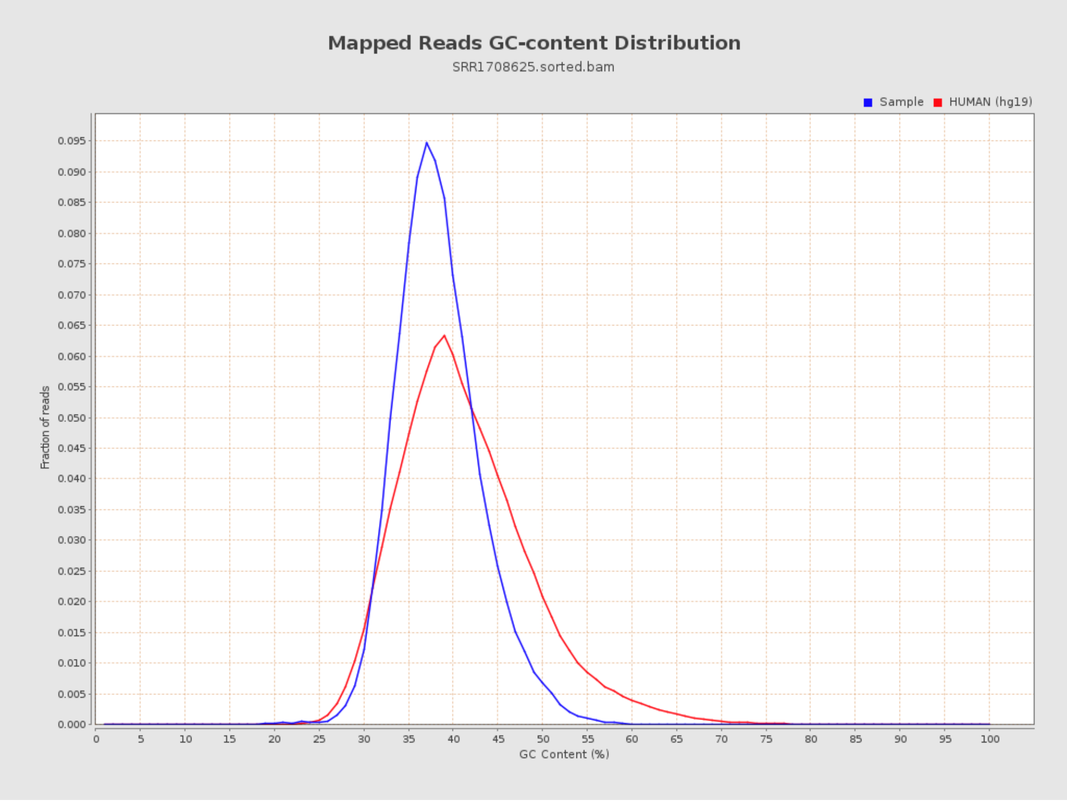
7. Results : Duplication Rate Histogram



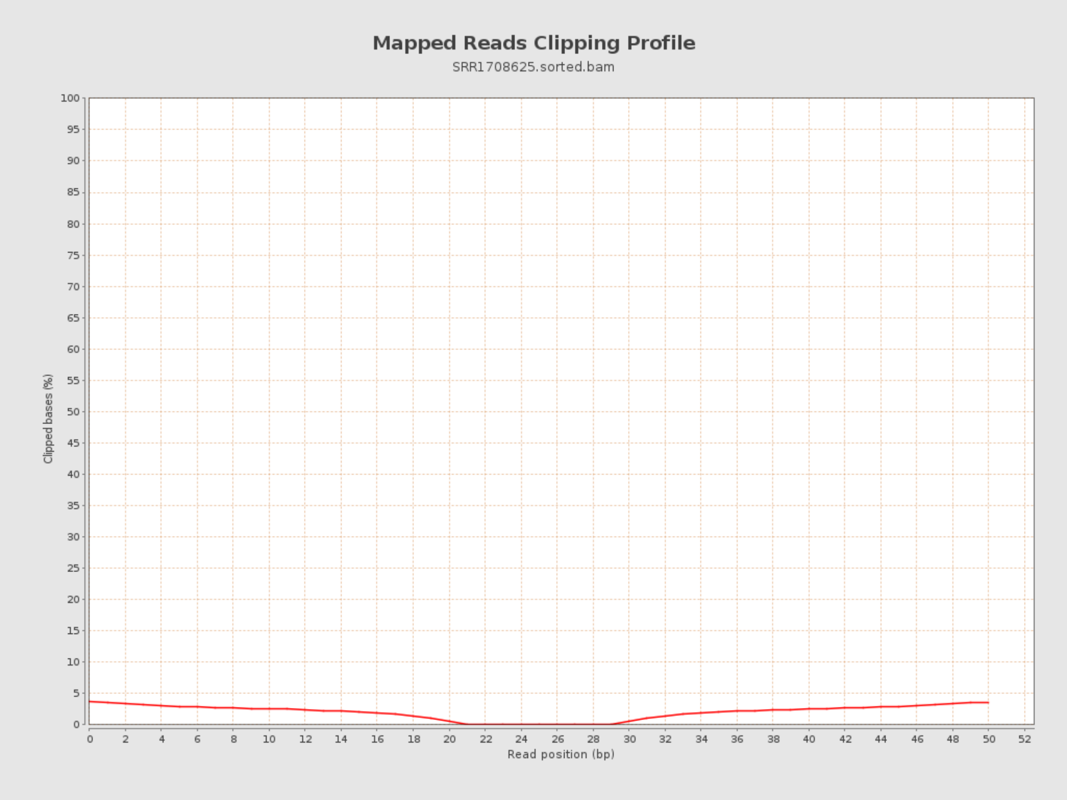
8. Results : Mapped Reads Nucleotide Content



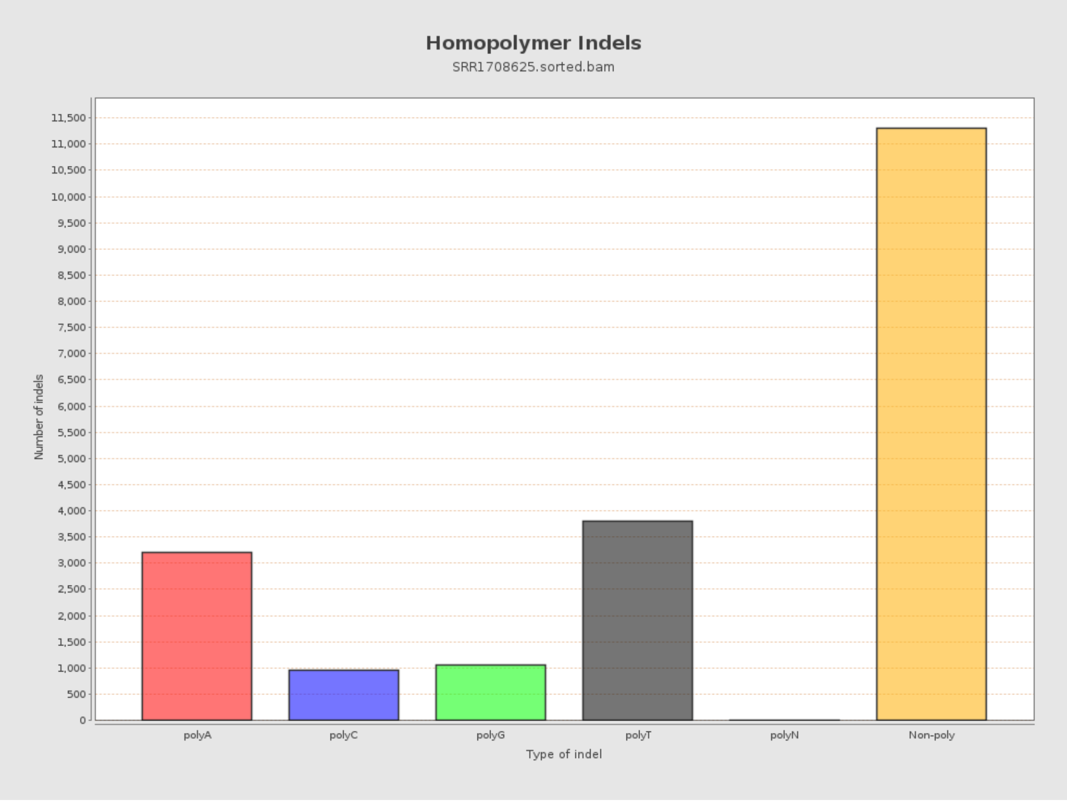
9. Results : Mapped Reads GC-content Distribution



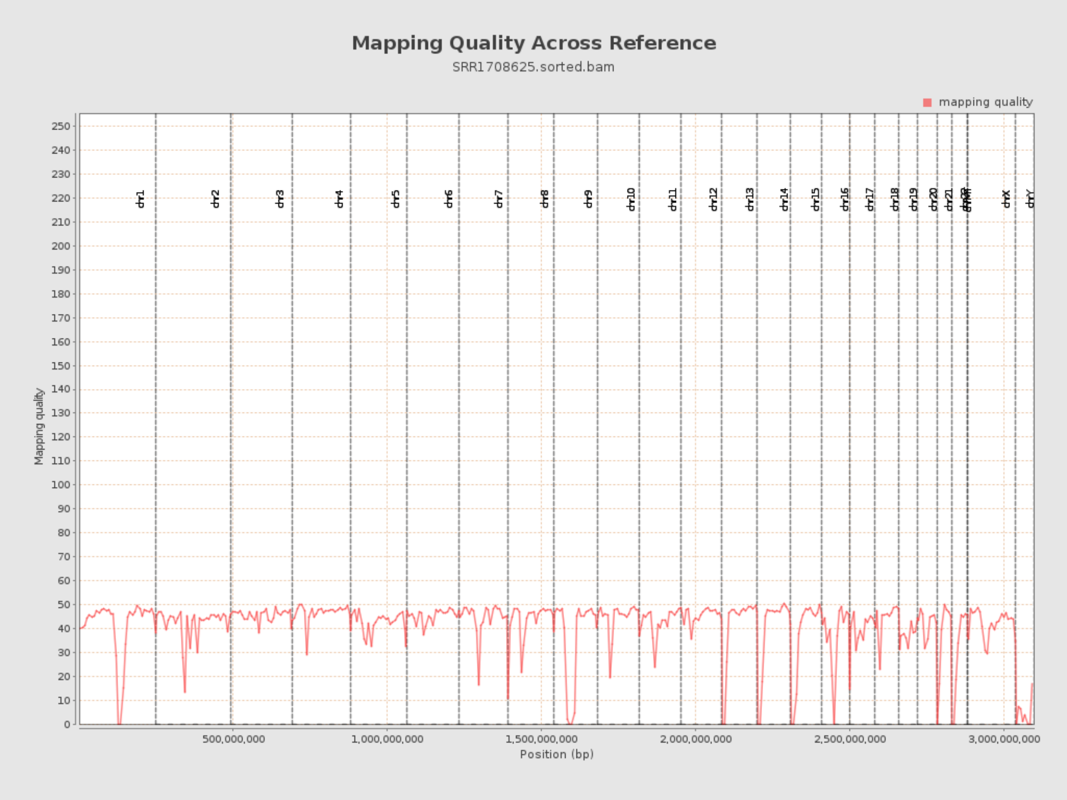
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram