Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:21:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819108.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_SRR1819108 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:21:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,285,587
Mapped reads	1,180,801 / 91.85%
Unmapped reads	104,786 / 8.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,705 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	39,597 / 3.08%
Duplication rate	2.49%
Clipped reads	1,182,652 / 91.99%

2.2. ACGT Content

Number/percentage of A's	16,889,292 / 24.56%
Number/percentage of C's	13,513,562 / 19.65%
Number/percentage of T's	21,466,636 / 31.22%
Number/percentage of G's	16,894,605 / 24.57%
Number/percentage of N's	1,084 / 0%
GC Percentage	44.22%

2.3. Coverage

Mean	0.0222

Standard Deviation	0.2205

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

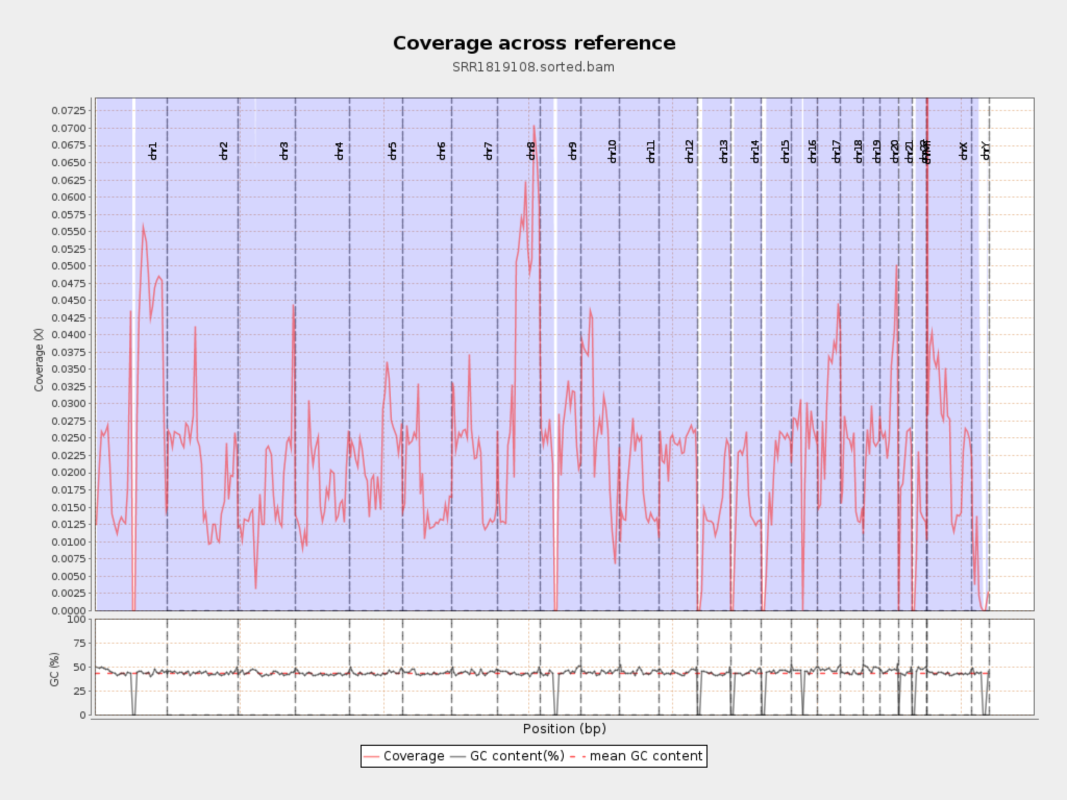
General error rate	0.52%
Mismatches	347,515
Insertions	4,200
Mapped reads with at least one insertion	0.35%
Deletions	12,701
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.66%

2.6. Chromosome stats

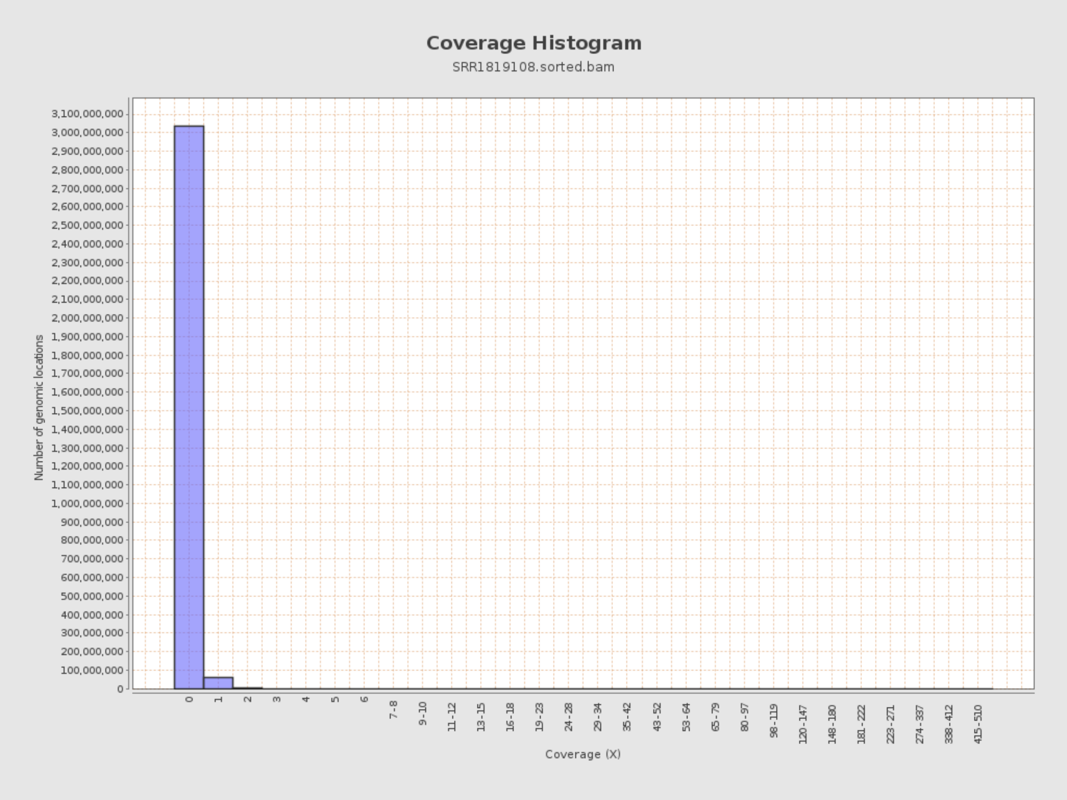
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7045207	0.0283	0.396
chr2	243199373	5070471	0.0208	0.2384
chr3	198022430	3380201	0.0171	0.1411
chr4	191154276	3271611	0.0171	0.1577
chr5	180915260	4235389	0.0234	0.165
chr6	171115067	2990703	0.0175	0.1738
chr7	159138663	3478011	0.0219	0.2612

chr8	146364022	6013691	0.0411	0.2545
chr9	141213431	3347612	0.0237	0.2002
chr10	135534747	3740627	0.0276	0.2302
chr11	135006516	2409276	0.0178	0.1988
chr12	133851895	3230735	0.0241	0.1677
chr13	115169878	1541982	0.0134	0.1246
chr14	107349540	1641250	0.0153	0.1361
chr15	102531392	1843313	0.018	0.1465
chr16	90354753	2169127	0.024	0.1775
chr17	81195210	2492042	0.0307	0.2006
chr18	78077248	1556159	0.0199	0.3368
chr19	59128983	1423597	0.0241	0.2811
chr20	63025520	2004038	0.0318	0.1933
chr21	48129895	974234	0.0202	0.1635
chr22	51304566	574722	0.0112	0.1133
chrMT	16571	16377	0.9883	1.2179
chrX	155270560	4100704	0.0264	0.1909
chrY	59373566	234999	0.004	0.1171

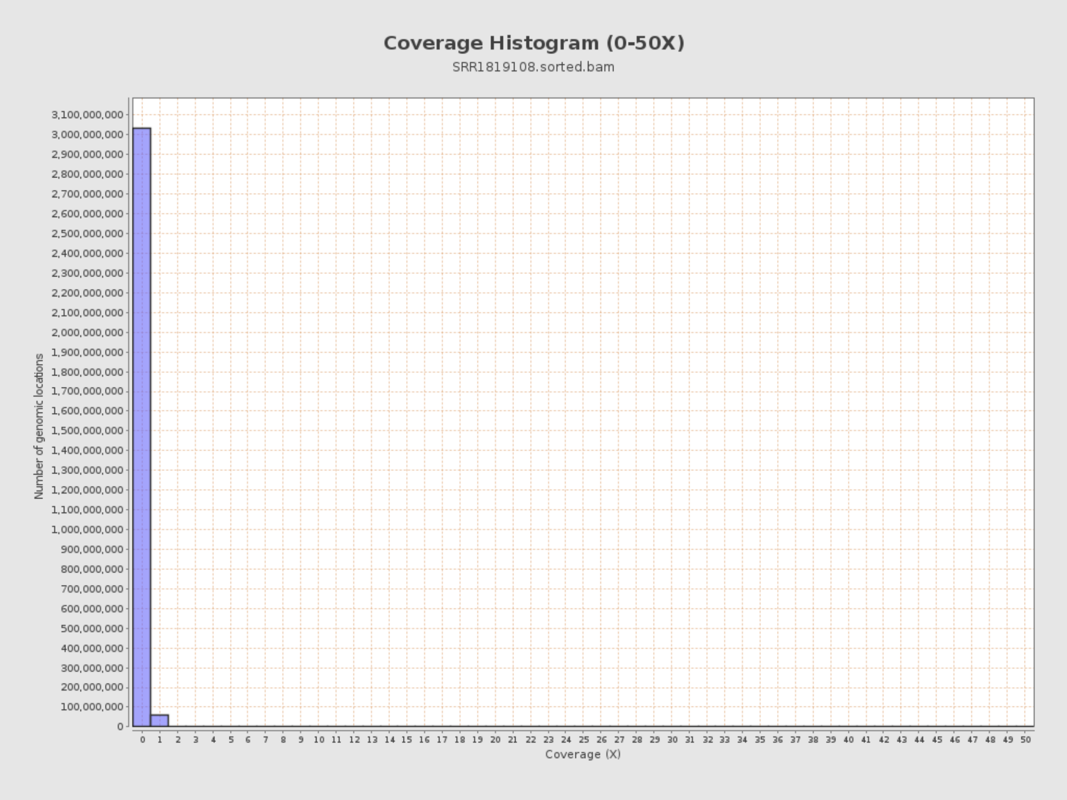
3. Results : Coverage across reference



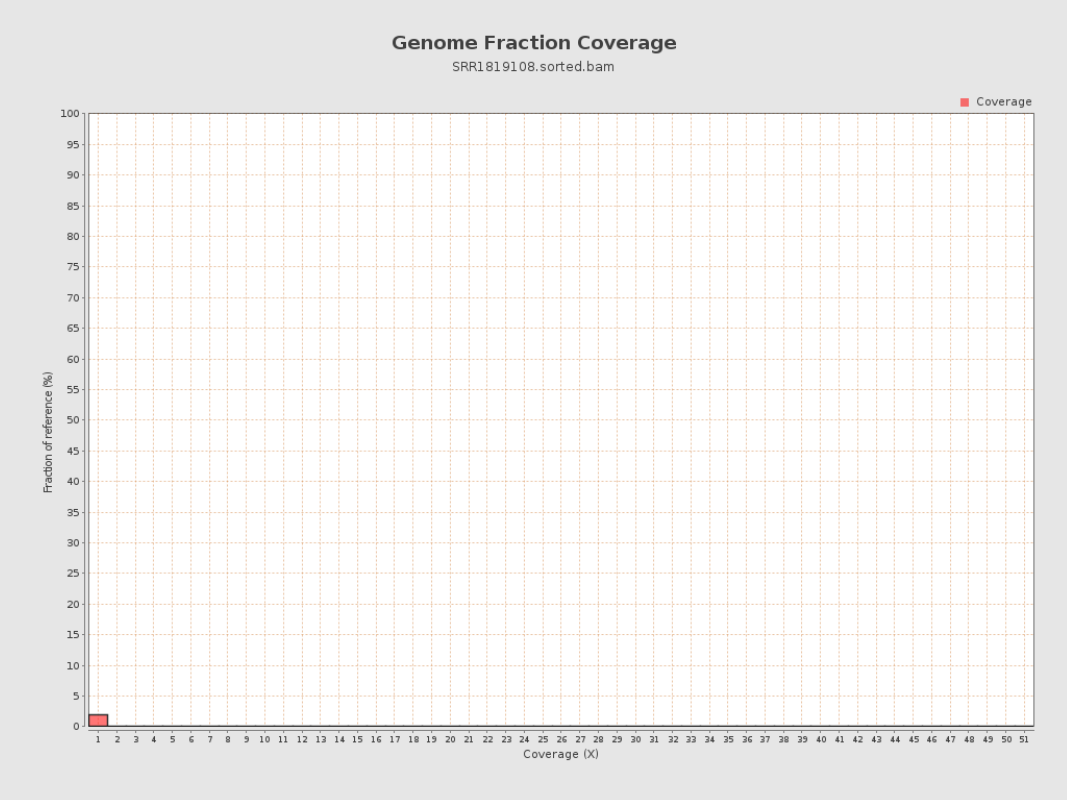
4. Results : Coverage Histogram



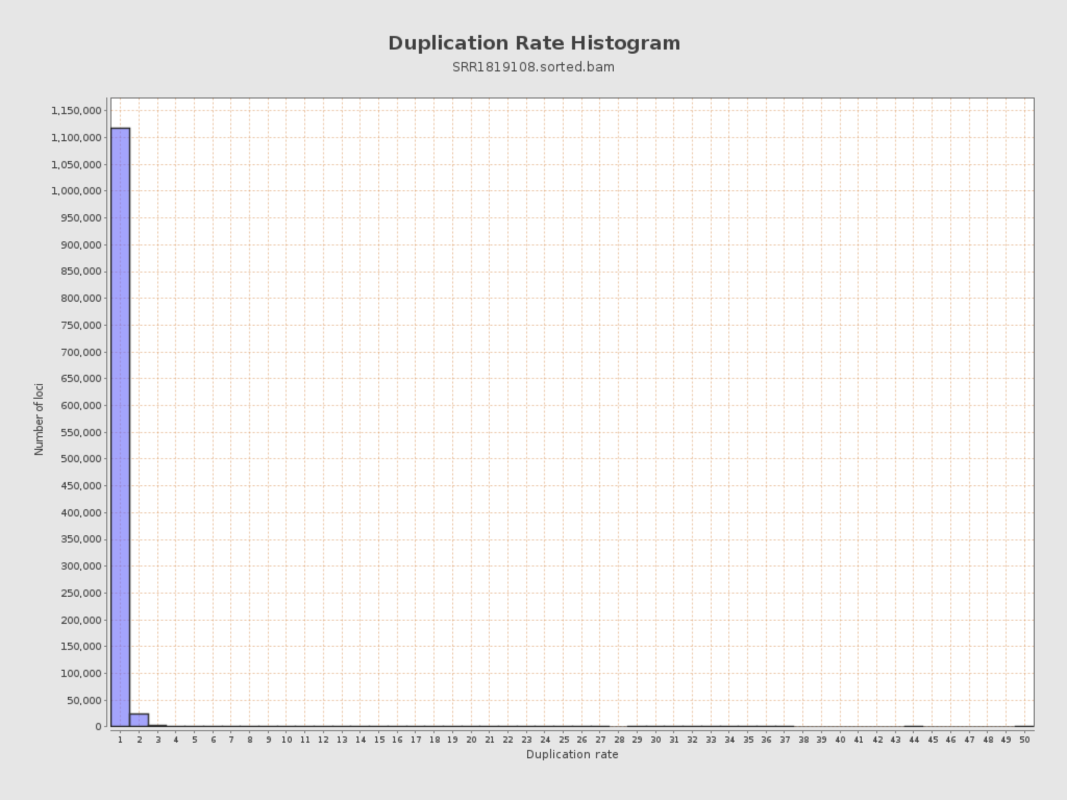
5. Results : Coverage Histogram (0-50X)



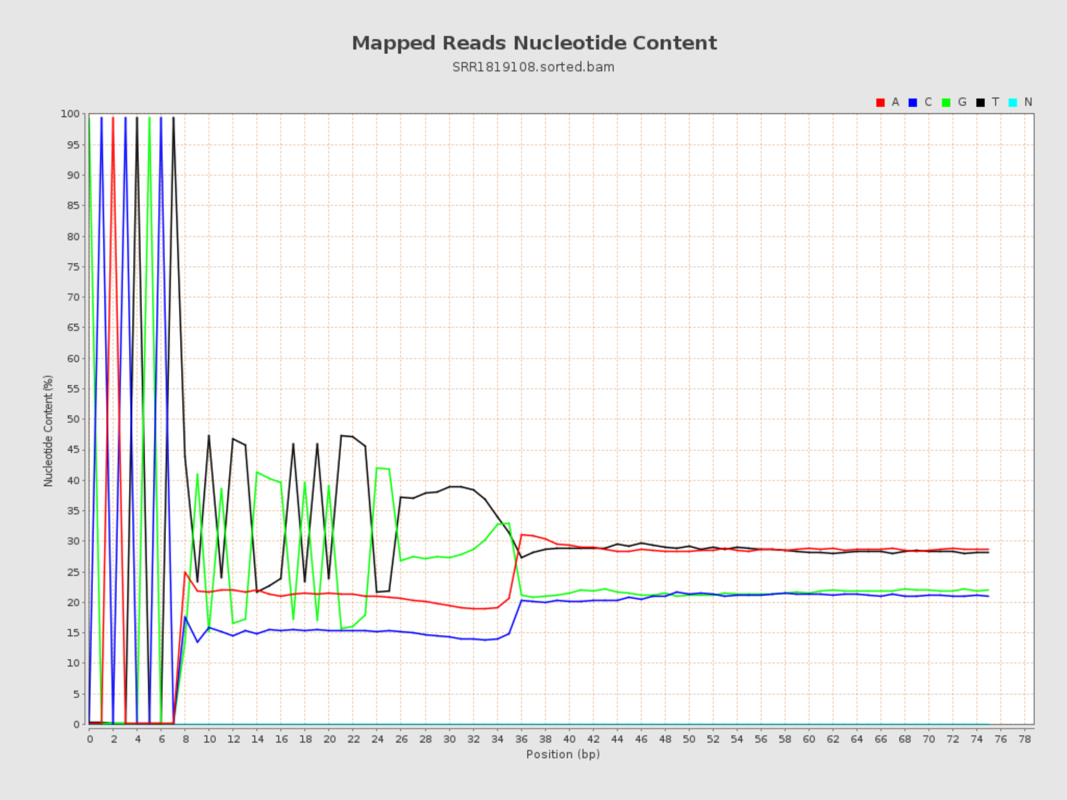
6. Results : Genome Fraction Coverage



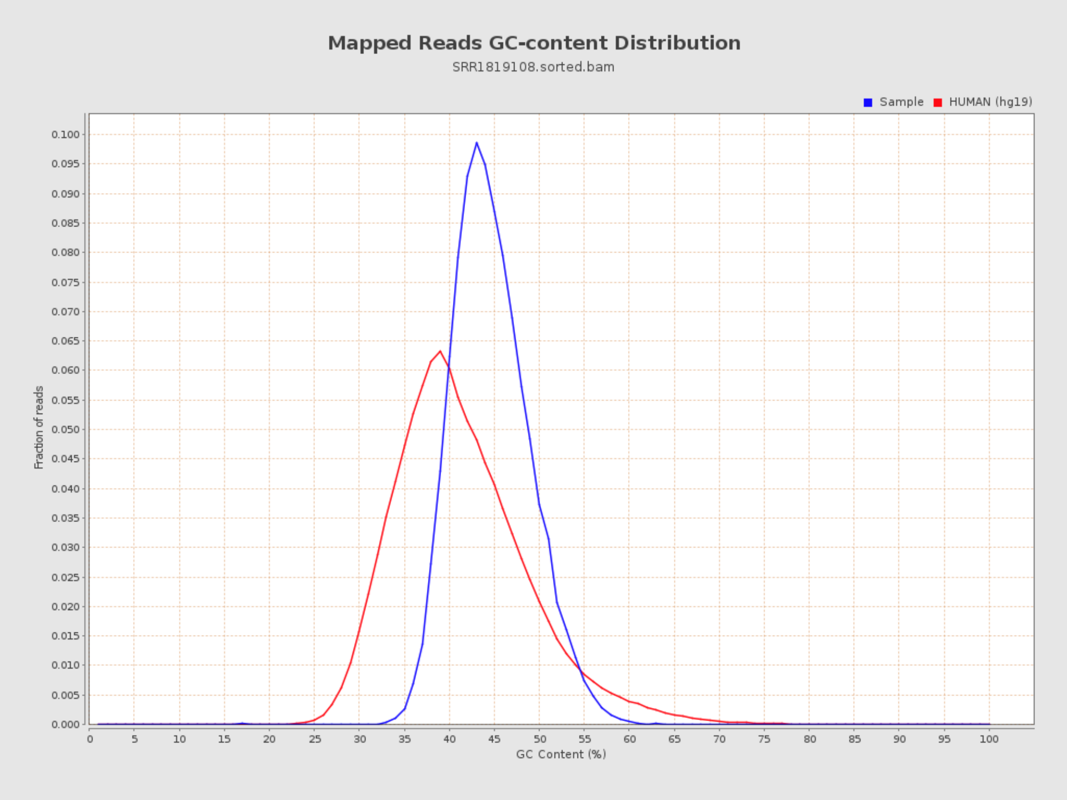
7. Results : Duplication Rate Histogram



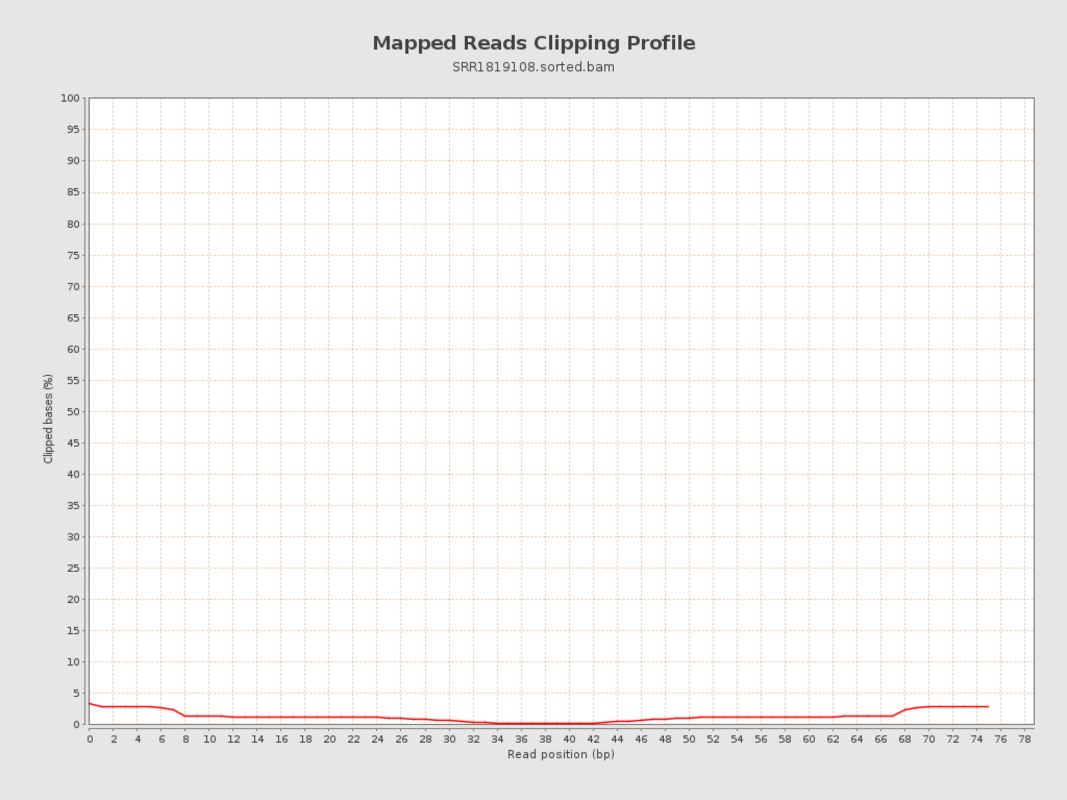
8. Results : Mapped Reads Nucleotide Content



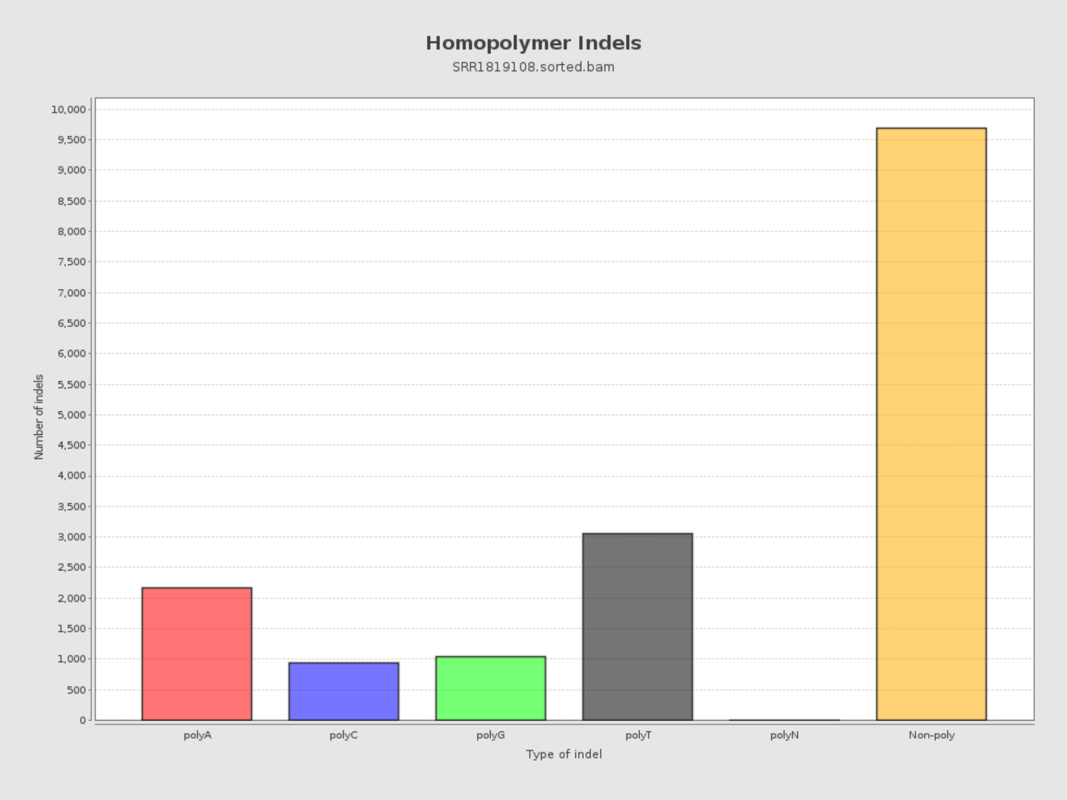
9. Results : Mapped Reads GC-content Distribution



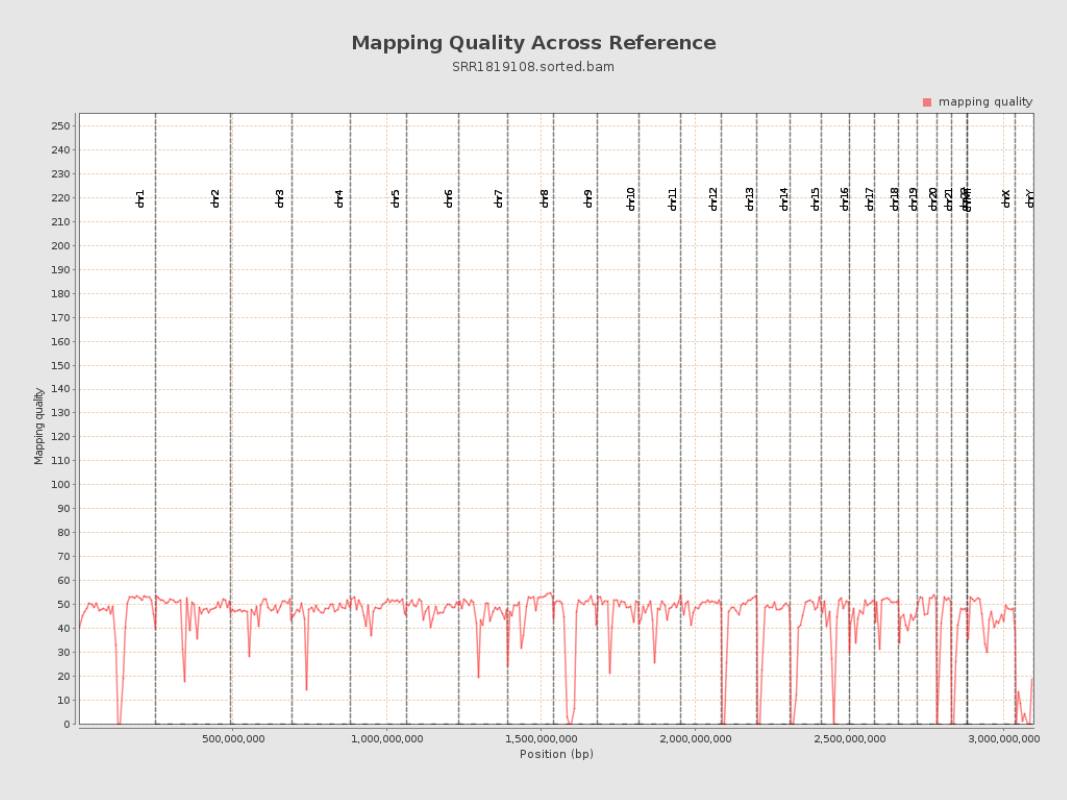
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram