Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:21:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708649.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_SRR1708649 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708649.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:21:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708649.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,074,405
Mapped reads	4,881,861 / 96.21%
Unmapped reads	192,544 / 3.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	184 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	207,717 / 4.09%
Duplication rate	4.13%
Clipped reads	72,627 / 1.43%

2.2. ACGT Content

Number/percentage of A's	75,306,011 / 30.94%
Number/percentage of C's	46,202,196 / 18.98%
Number/percentage of T's	75,232,683 / 30.91%
Number/percentage of G's	46,643,308 / 19.16%
Number/percentage of N's	7,844 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	0.0786

Standard Deviation	0.6198

2.4. Mapping Quality

Mean Mapping Quality	41.38

2.5. Mismatches and indels

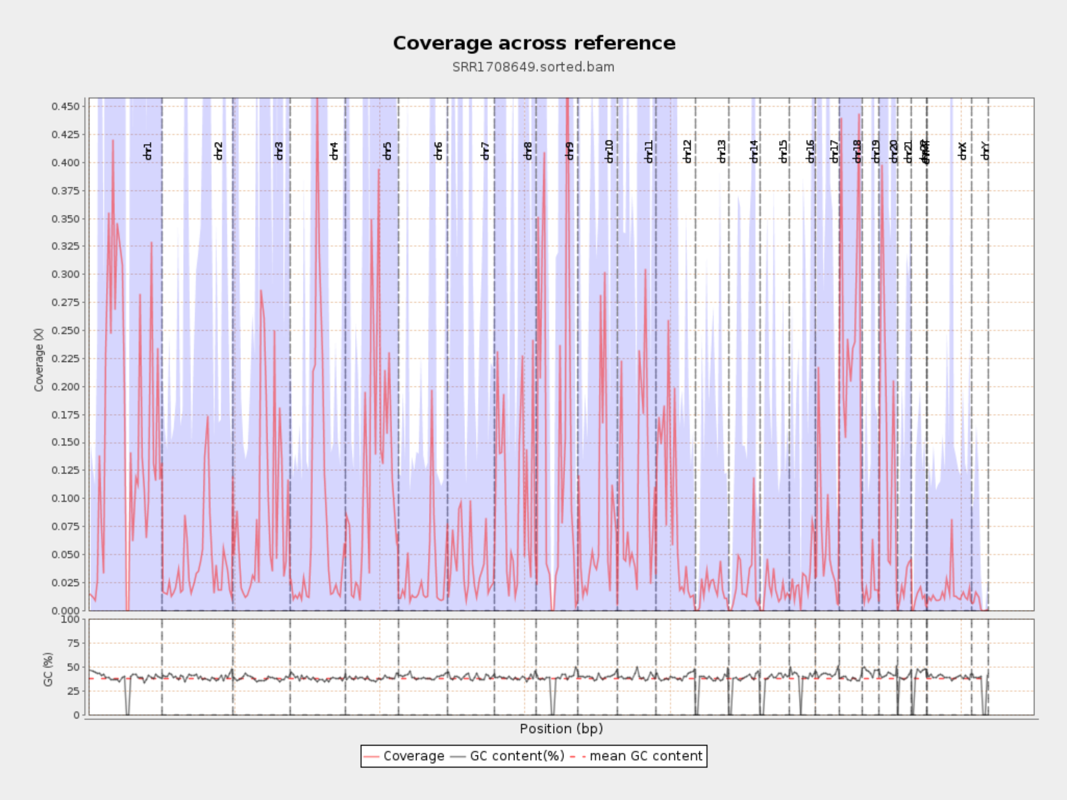
General error rate	0.18%
Mismatches	407,361
Insertions	18,249
Mapped reads with at least one insertion	0.37%
Deletions	13,607
Mapped reads with at least one deletion	0.28%
Homopolymer indels	48.86%

2.6. Chromosome stats

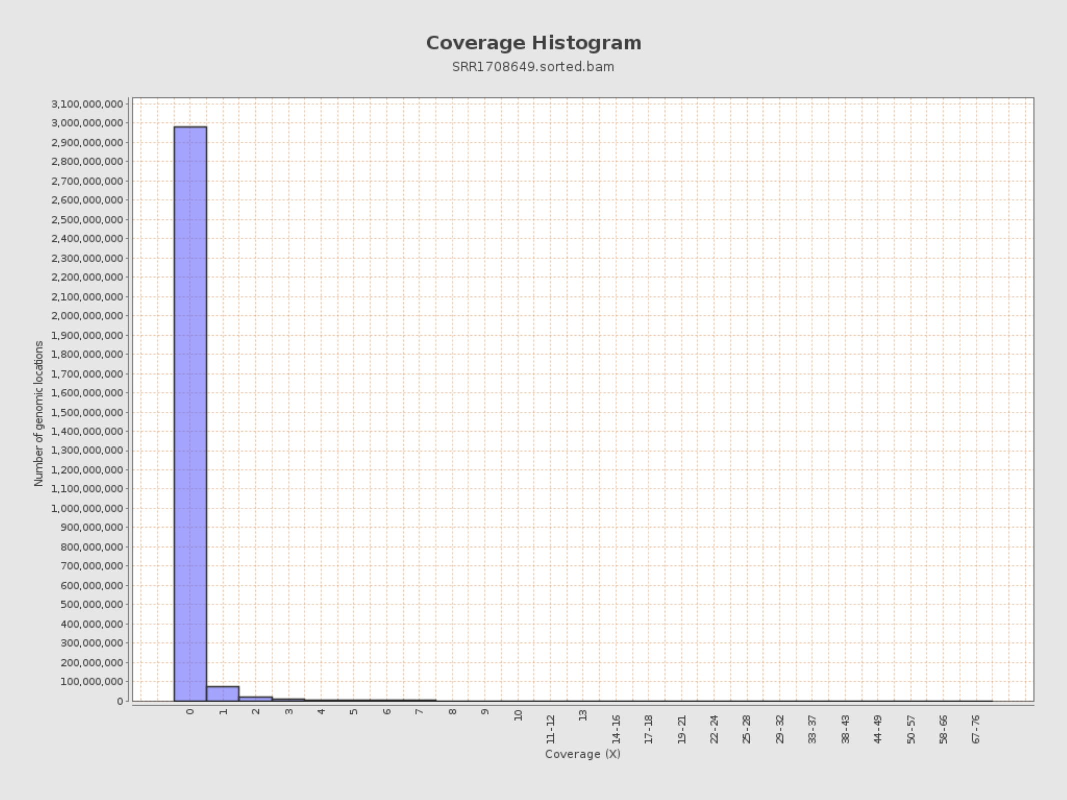
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39402173	0.1581	0.8983
chr2	243199373	9843202	0.0405	0.3344
chr3	198022430	17161415	0.0867	0.6484
chr4	191154276	15854455	0.0829	0.6253
chr5	180915260	22806259	0.1261	0.7846
chr6	171115067	5277468	0.0308	0.3033
chr7	159138663	6677132	0.042	0.3897

chr8	146364022	14877506	0.1016	0.6659
chr9	141213431	22527262	0.1595	1.0746
chr10	135534747	11300847	0.0834	0.5516
chr11	135006516	14585277	0.108	0.7648
chr12	133851895	11983497	0.0895	0.6087
chr13	115169878	2104876	0.0183	0.1805
chr14	107349540	2888808	0.0269	0.3388
chr15	102531392	1828454	0.0178	0.1864
chr16	90354753	2736143	0.0303	0.2668
chr17	81195210	4795701	0.0591	0.457
chr18	78077248	20192860	0.2586	1.2995
chr19	59128983	1210454	0.0205	0.3245
chr20	63025520	10781345	0.1711	0.909
chr21	48129895	1188712	0.0247	0.2035
chr22	51304566	548498	0.0107	0.1255
chrMT	16571	50	0.003	0.0548
chrX	155270560	2528509	0.0163	0.2188
chrY	59373566	314174	0.0053	0.0812

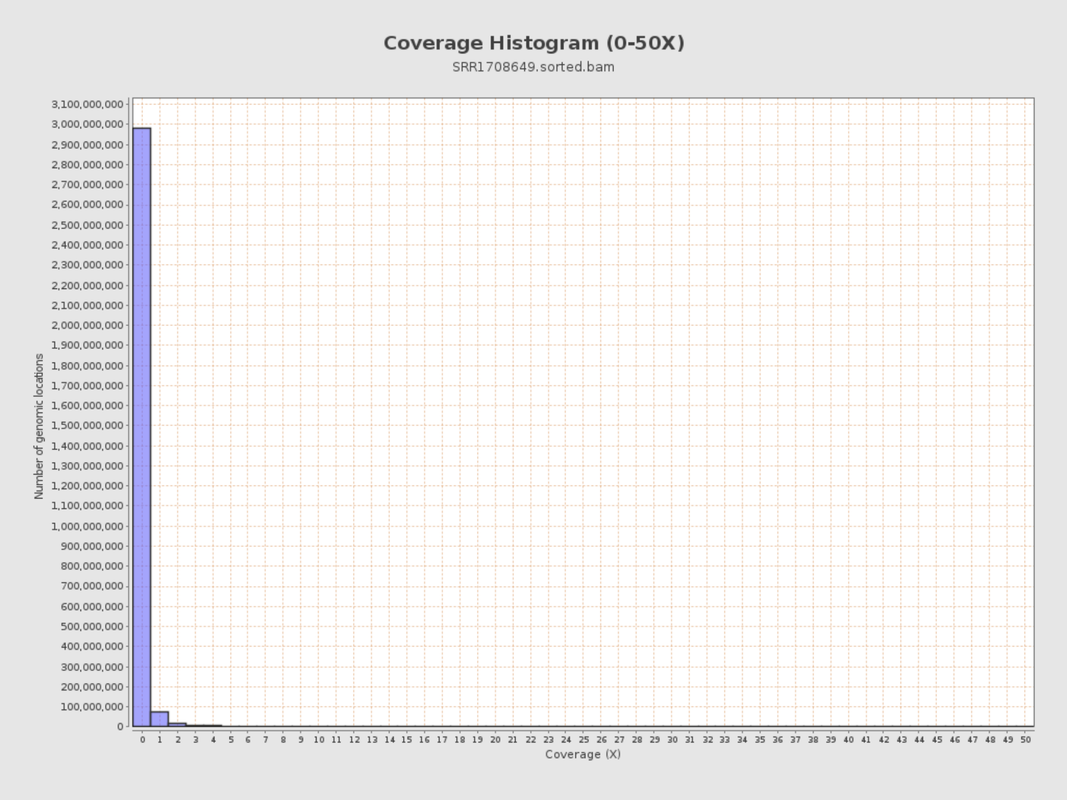
3. Results : Coverage across reference



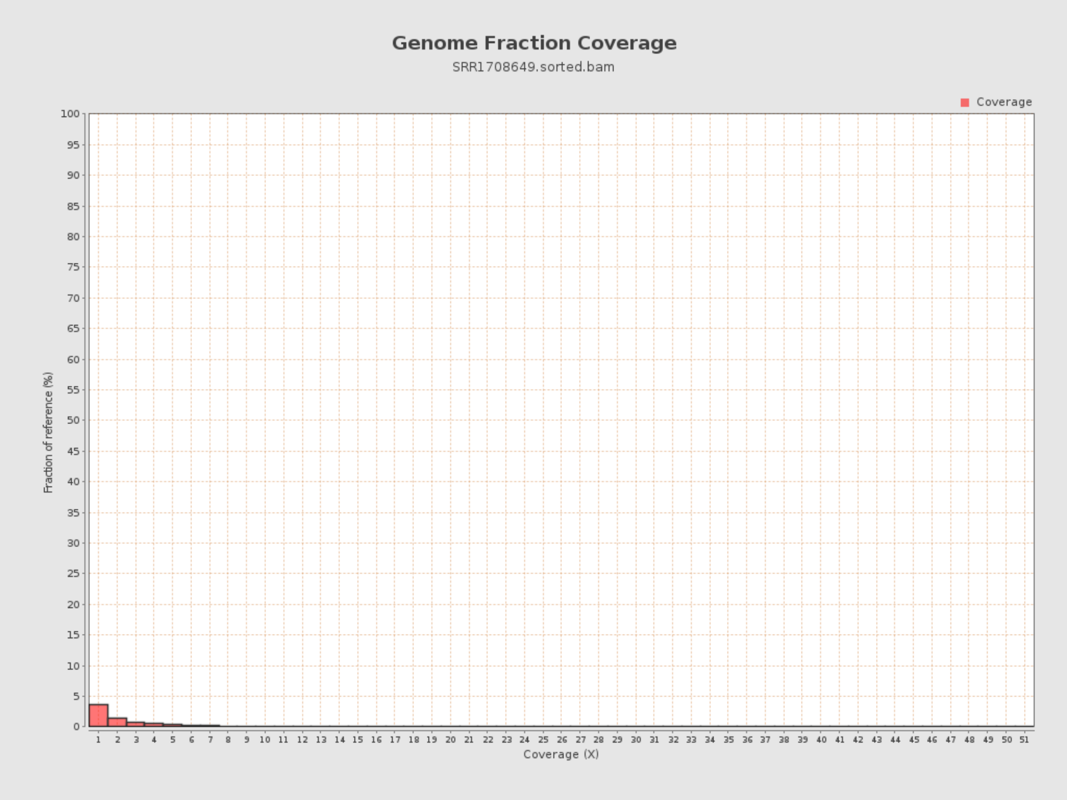
4. Results : Coverage Histogram



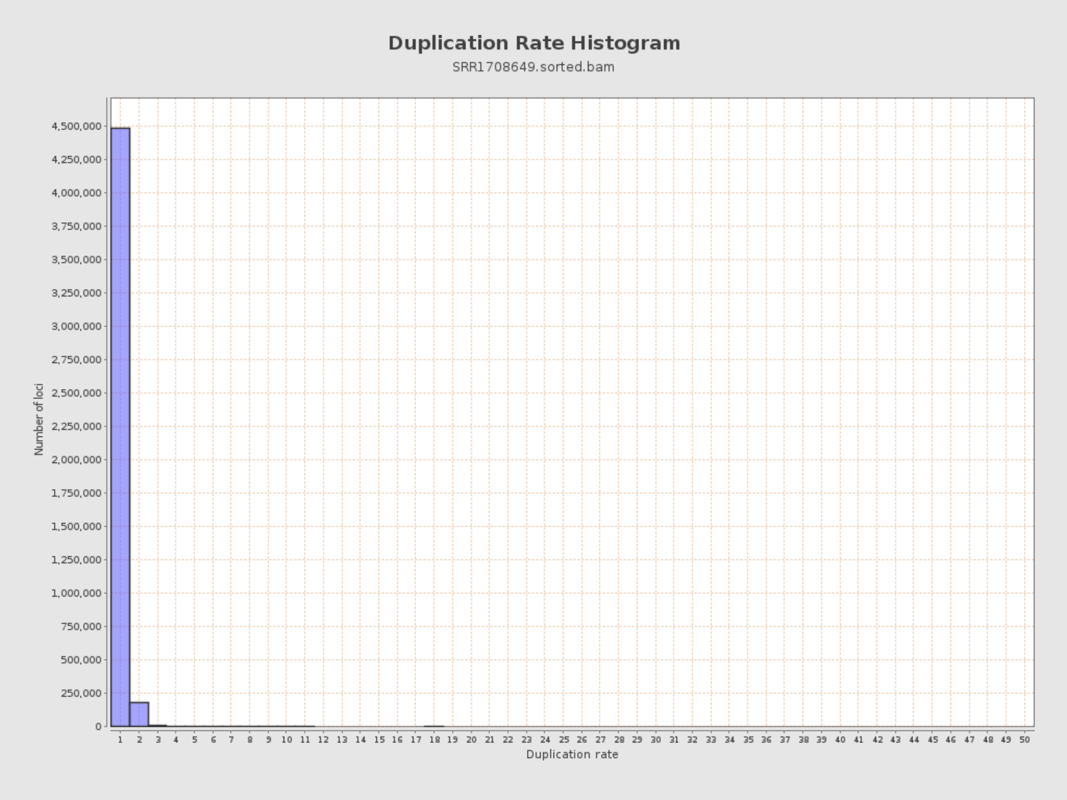
5. Results : Coverage Histogram (0-50X)



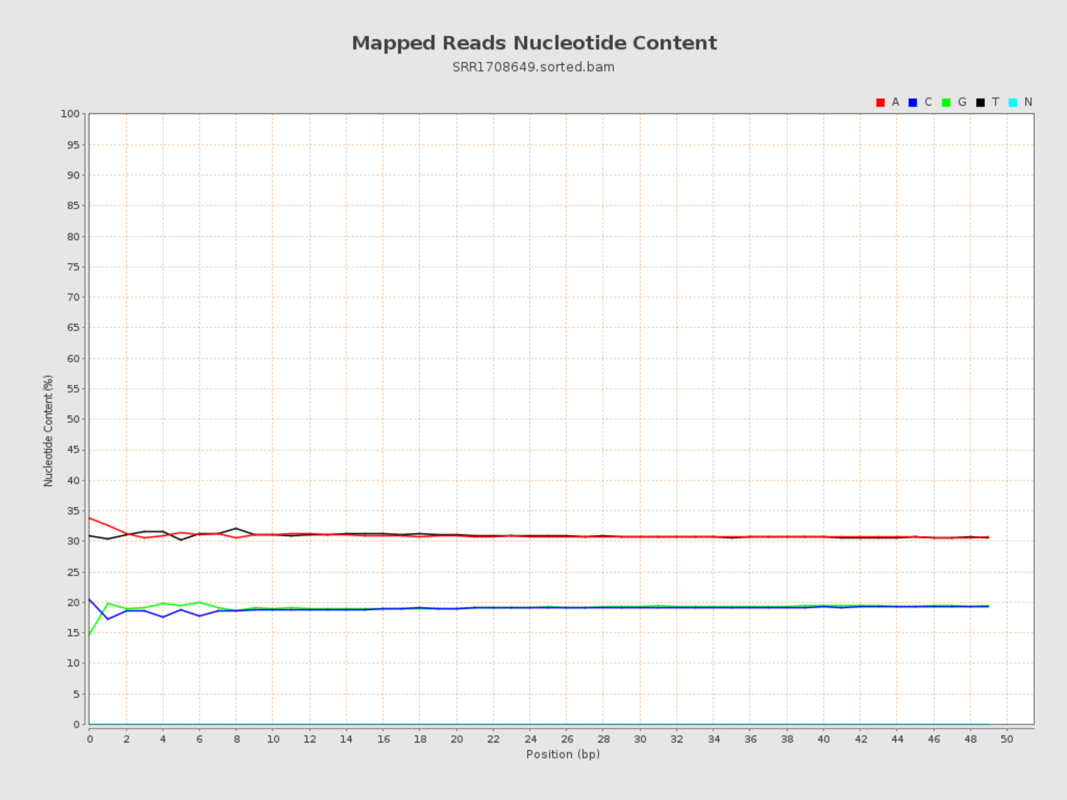
6. Results : Genome Fraction Coverage



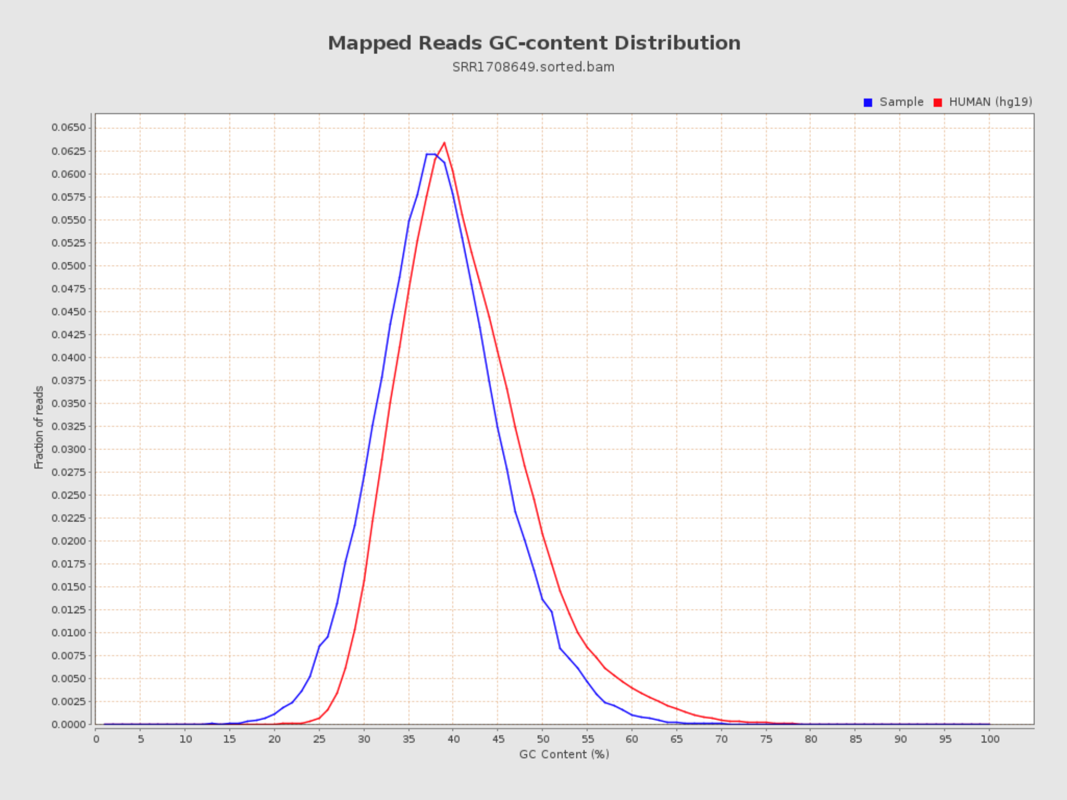
7. Results : Duplication Rate Histogram



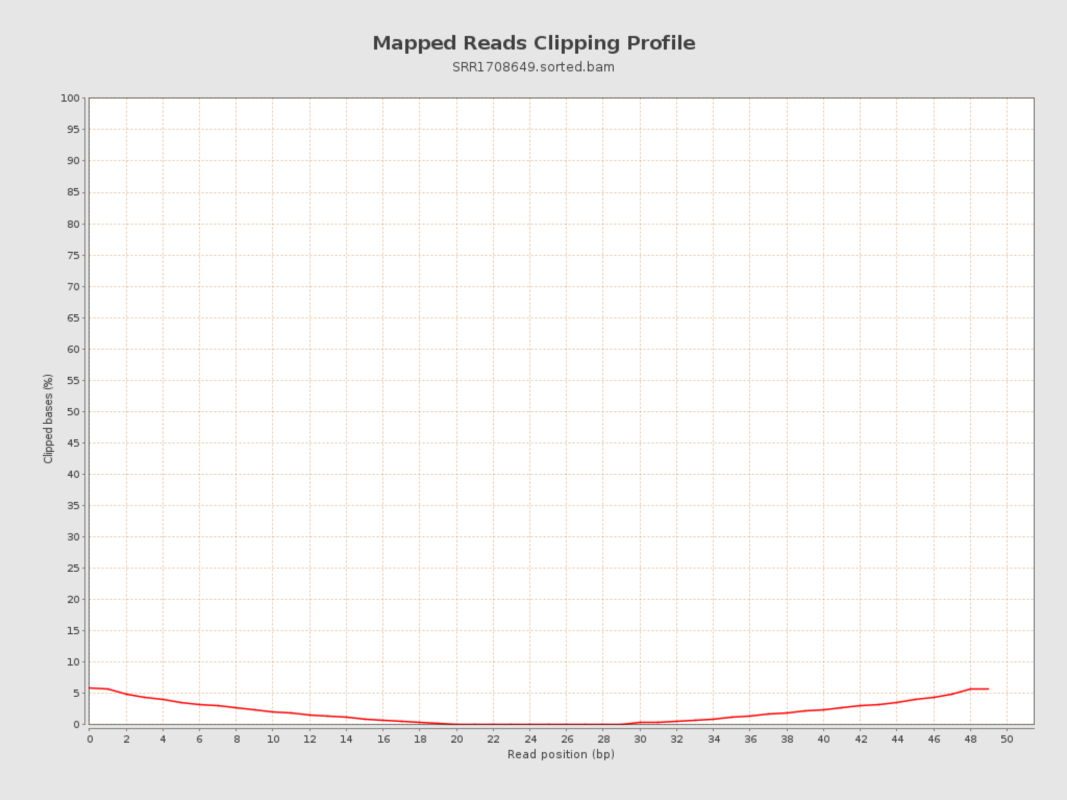
8. Results : Mapped Reads Nucleotide Content



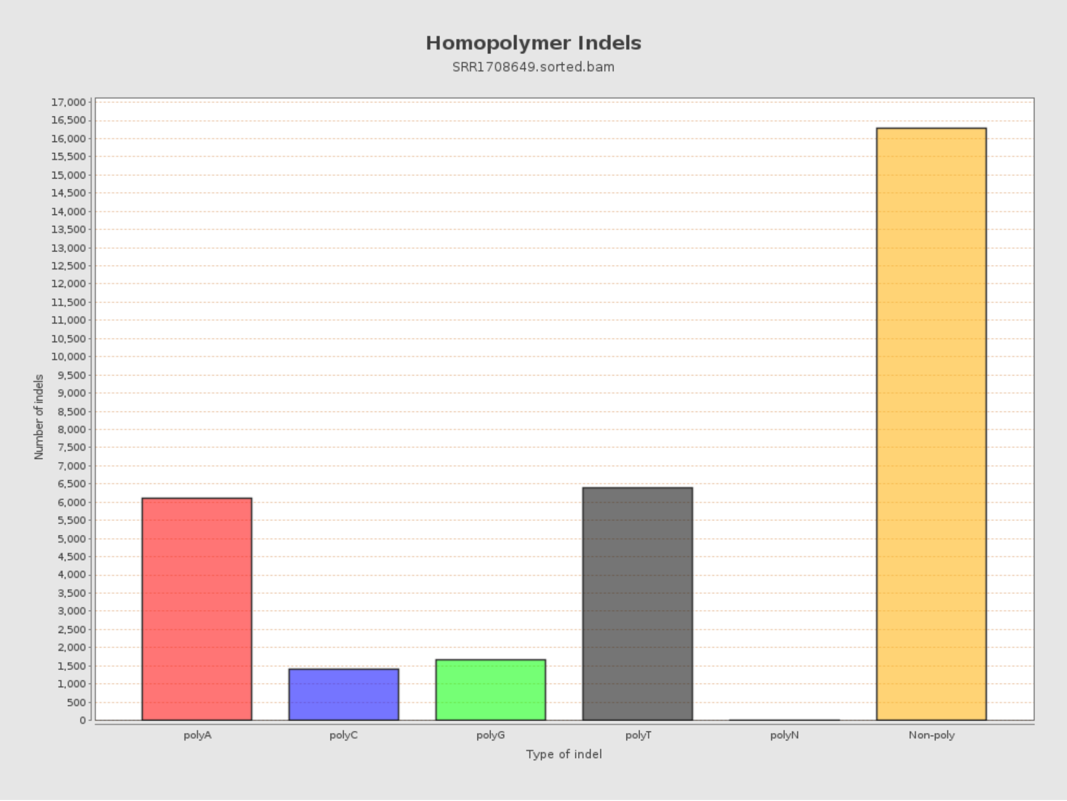
9. Results : Mapped Reads GC-content Distribution



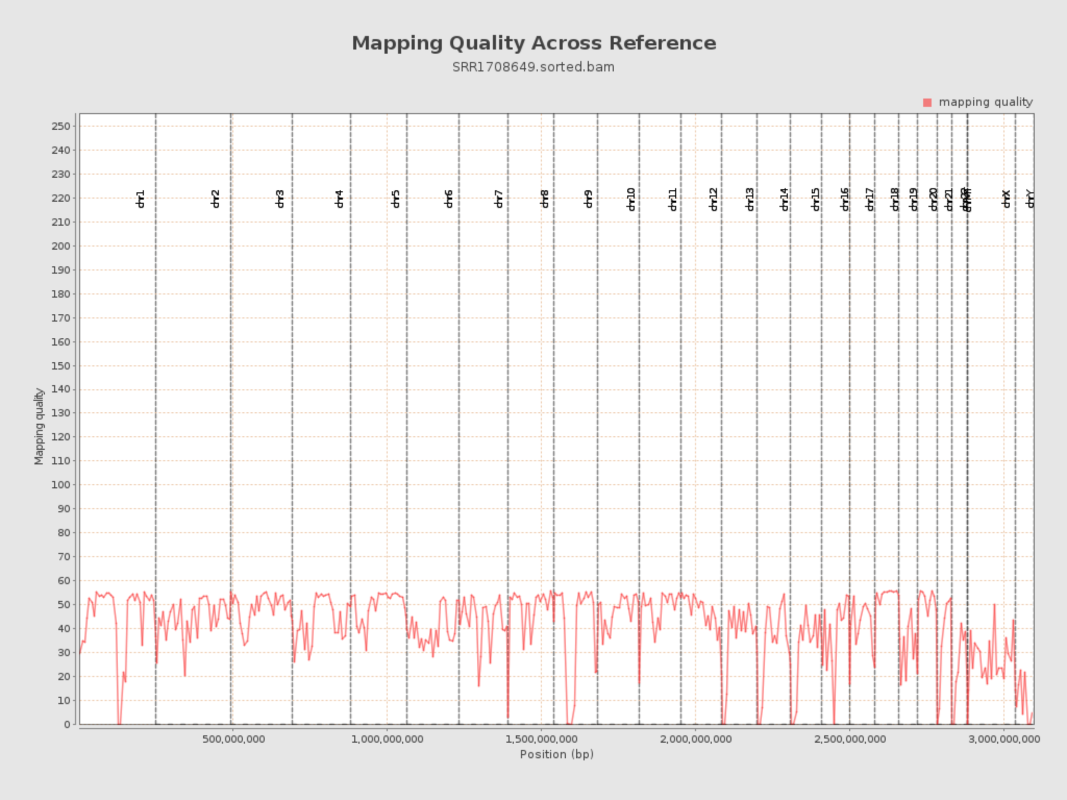
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram