Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:35:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708557.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_SRR1708557 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708557.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:35:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708557.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,177,906
Mapped reads	3,440,023 / 82.34%
Unmapped reads	737,883 / 17.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	93 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	16,798 / 0.4%
Duplication rate	0.49%
Clipped reads	47,795 / 1.14%

2.2. ACGT Content

Number/percentage of A's	53,208,776 / 31.02%
Number/percentage of C's	32,499,813 / 18.95%
Number/percentage of T's	52,989,781 / 30.89%
Number/percentage of G's	32,819,117 / 19.13%
Number/percentage of N's	7,142 / 0%
GC Percentage	38.08%

2.3. Coverage

Mean	0.0554

Standard Deviation	0.2446

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

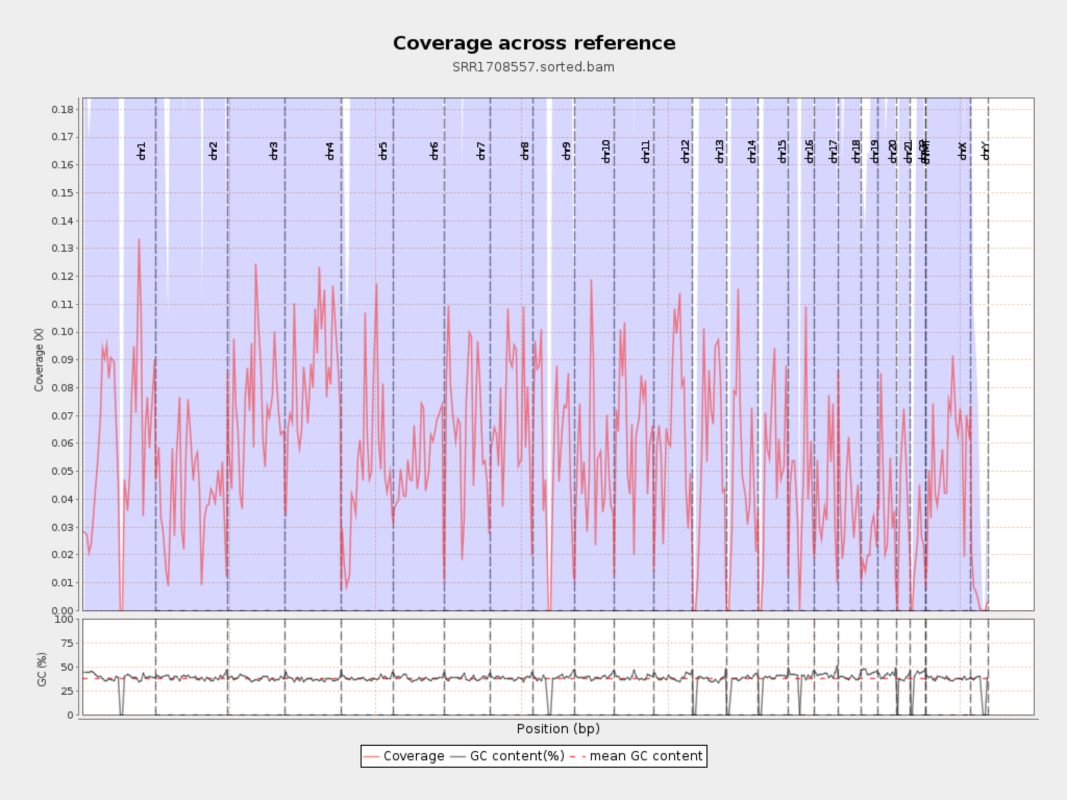
General error rate	0.17%
Mismatches	271,000
Insertions	11,409
Mapped reads with at least one insertion	0.33%
Deletions	9,330
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.16%

2.6. Chromosome stats

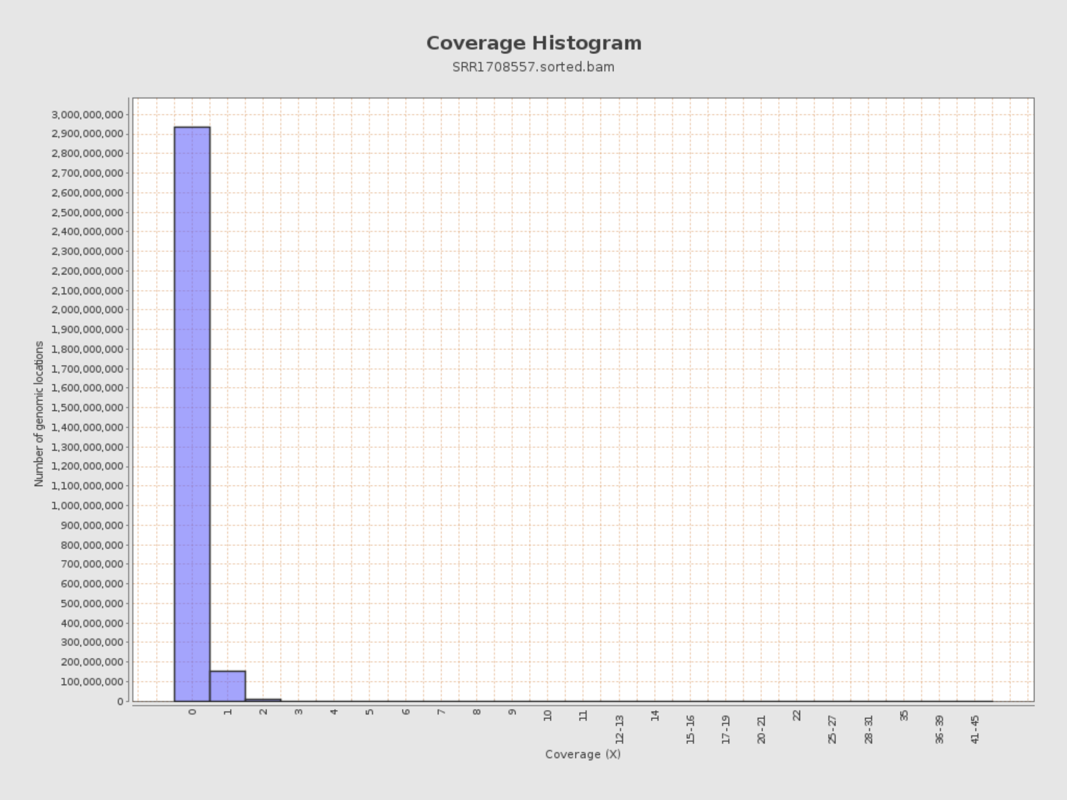
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15318136	0.0615	0.2588
chr2	243199373	10144261	0.0417	0.2109
chr3	198022430	14483686	0.0731	0.2804
chr4	191154276	16213027	0.0848	0.3016
chr5	180915260	9203012	0.0509	0.2337
chr6	171115067	9242093	0.054	0.2395
chr7	159138663	10404603	0.0654	0.2652

chr8	146364022	10231437	0.0699	0.2732
chr9	141213431	8234570	0.0583	0.2516
chr10	135534747	7205752	0.0532	0.2386
chr11	135006516	8898488	0.0659	0.2672
chr12	133851895	8662934	0.0647	0.2633
chr13	115169878	6504643	0.0565	0.2467
chr14	107349540	5231808	0.0487	0.2302
chr15	102531392	5329831	0.052	0.2377
chr16	90354753	3952708	0.0437	0.2174
chr17	81195210	3434154	0.0423	0.2134
chr18	78077248	3080198	0.0395	0.2046
chr19	59128983	1339038	0.0226	0.1542
chr20	63025520	2552825	0.0405	0.2088
chr21	48129895	1897477	0.0394	0.2067
chr22	51304566	1043881	0.0203	0.1471
chrMT	16571	250	0.0151	0.1407
chrX	155270560	8642116	0.0557	0.245
chrY	59373566	289679	0.0049	0.0729

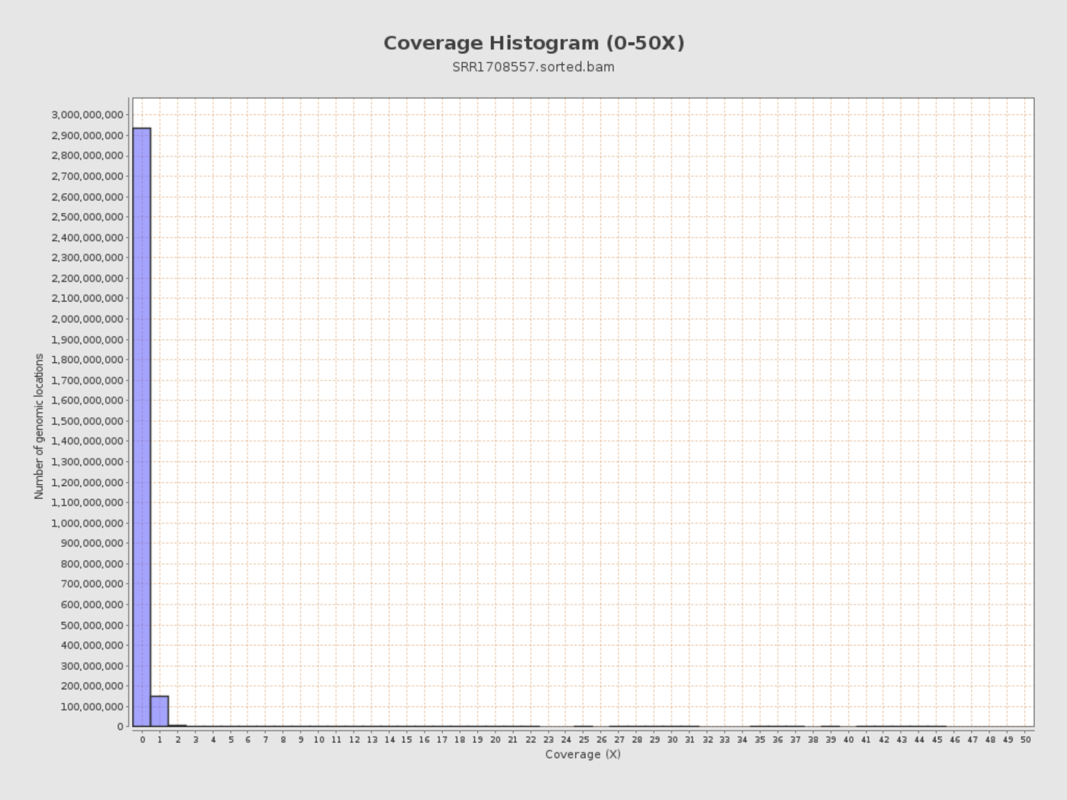
3. Results : Coverage across reference



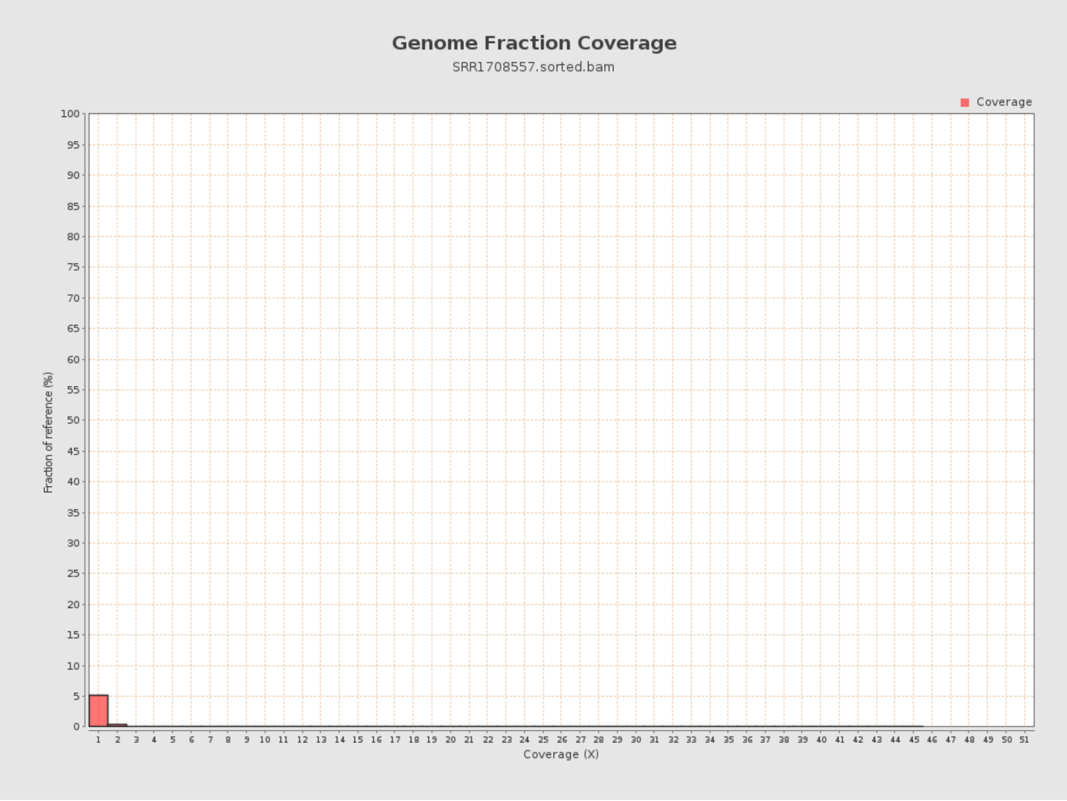
4. Results : Coverage Histogram



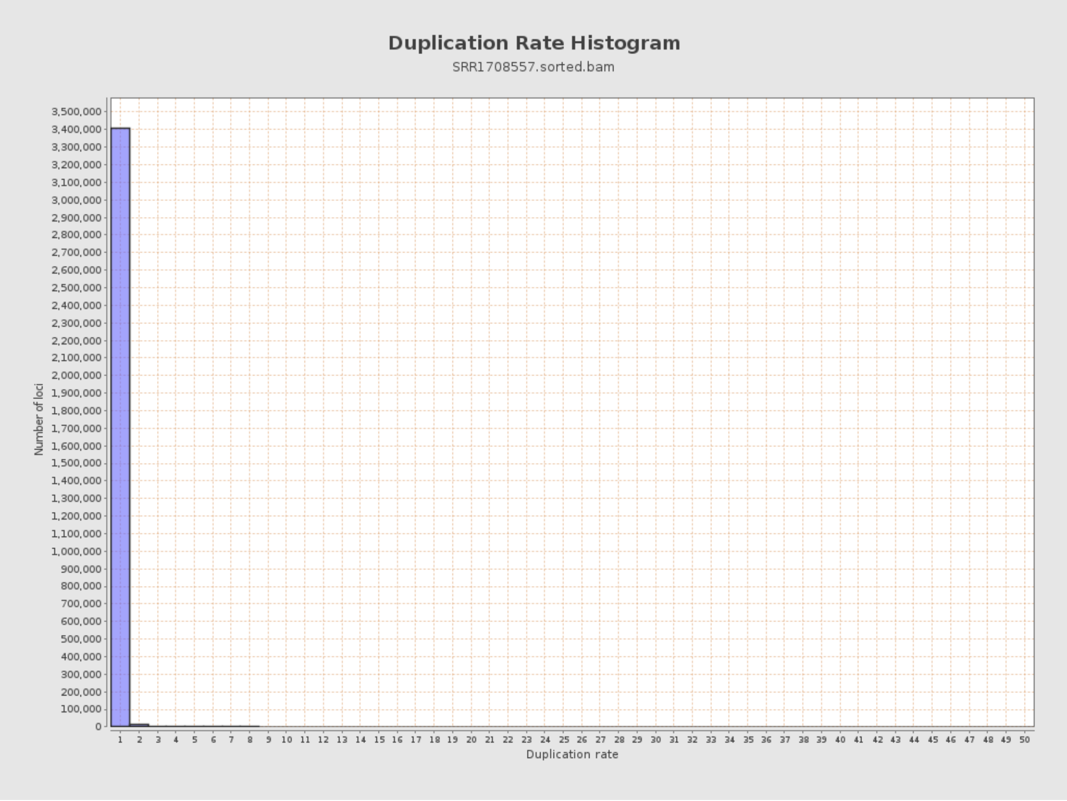
5. Results : Coverage Histogram (0-50X)



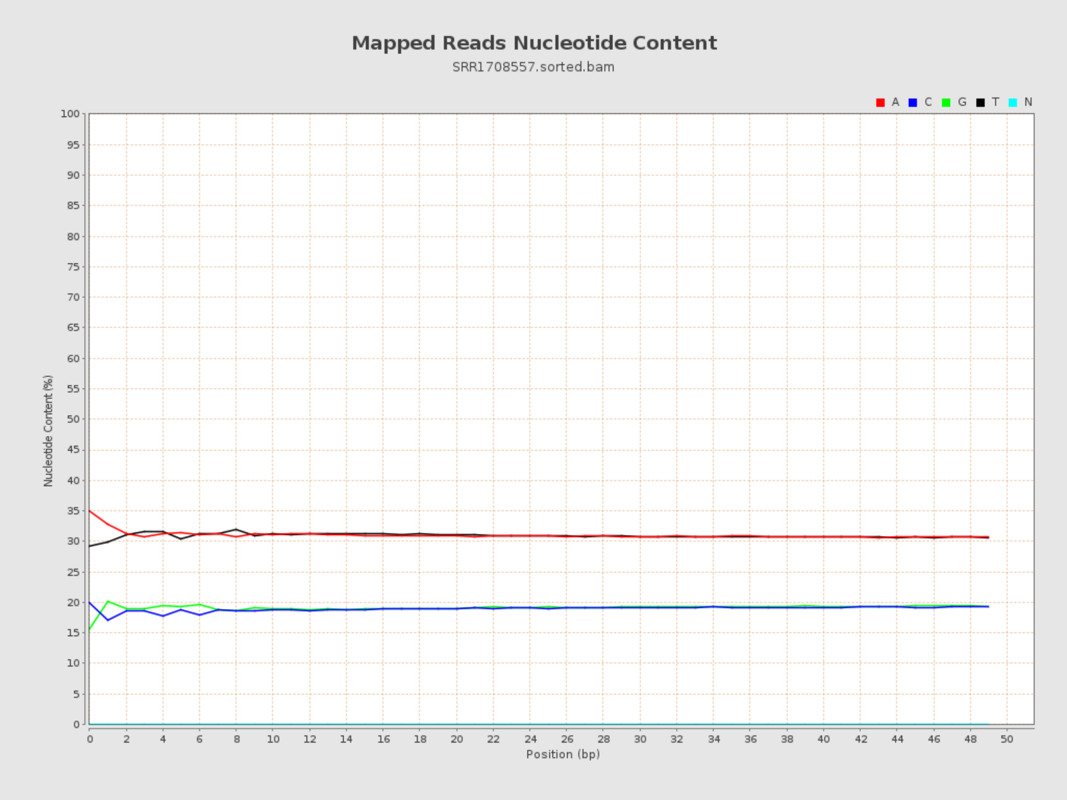
6. Results : Genome Fraction Coverage



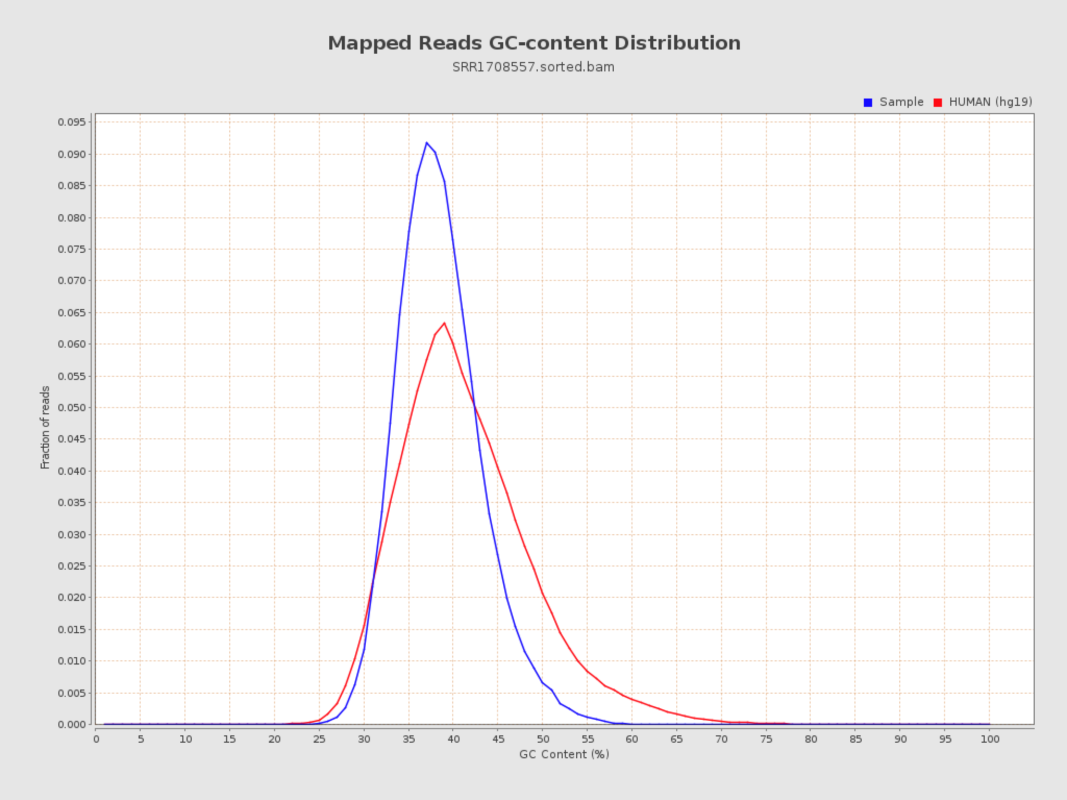
7. Results : Duplication Rate Histogram



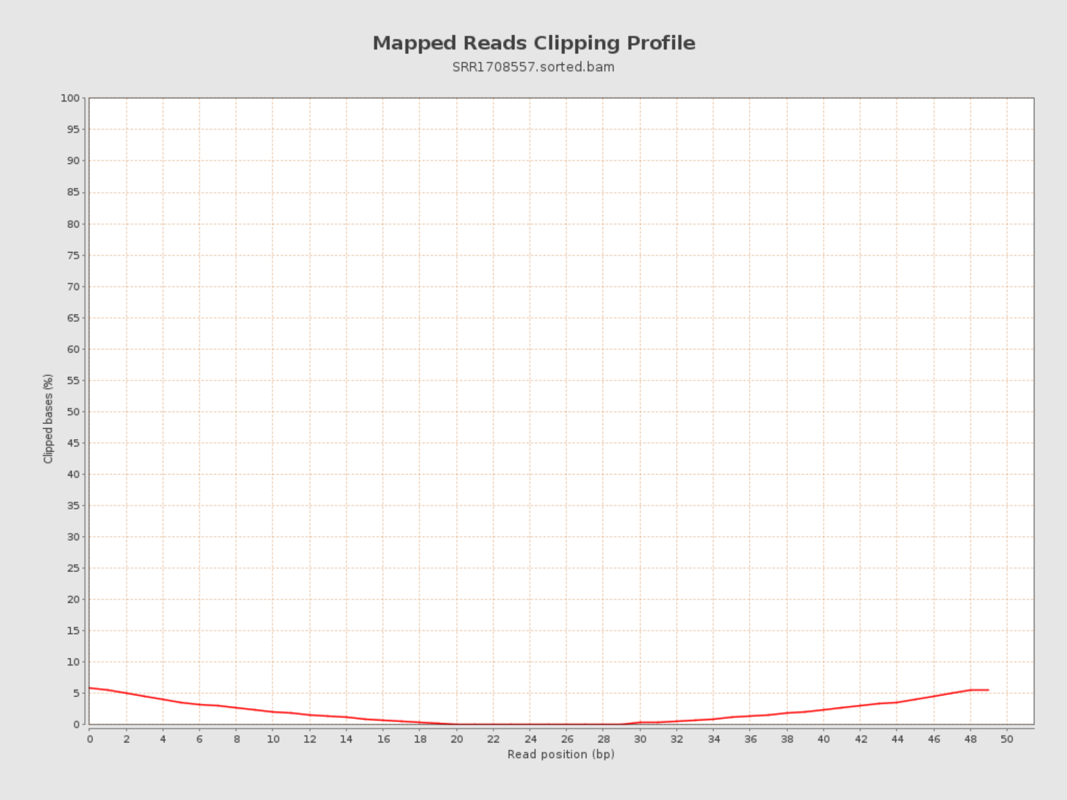
8. Results : Mapped Reads Nucleotide Content



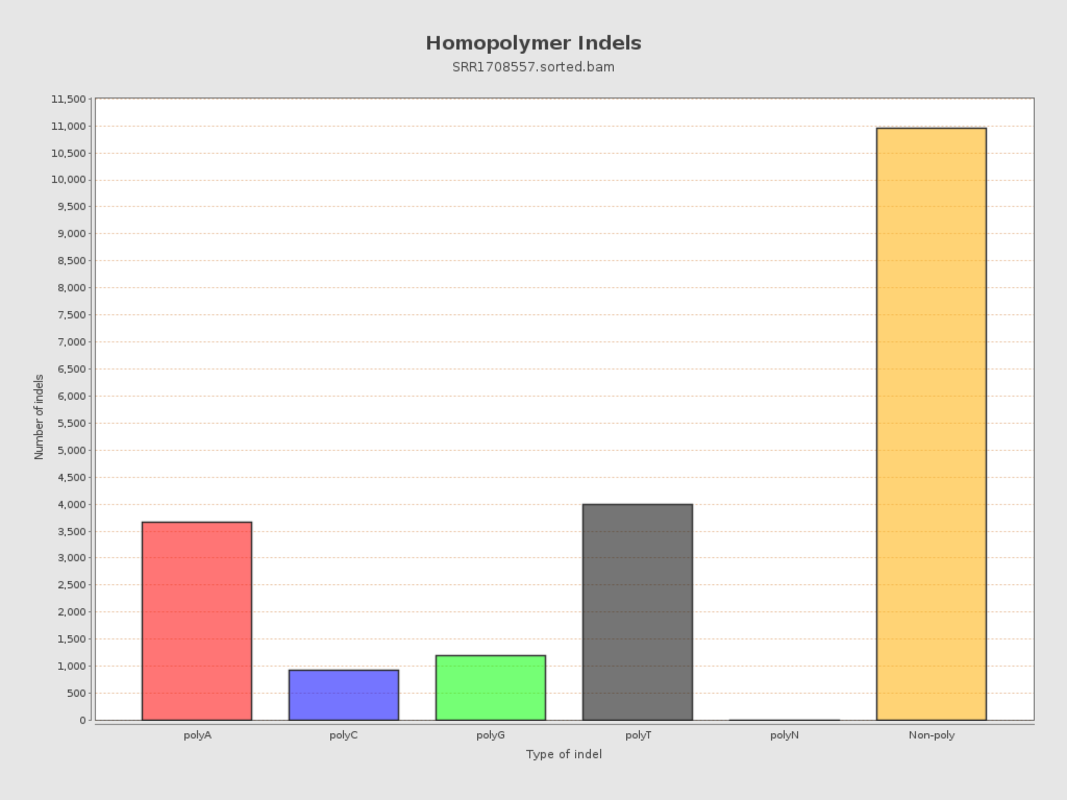
9. Results : Mapped Reads GC-content Distribution



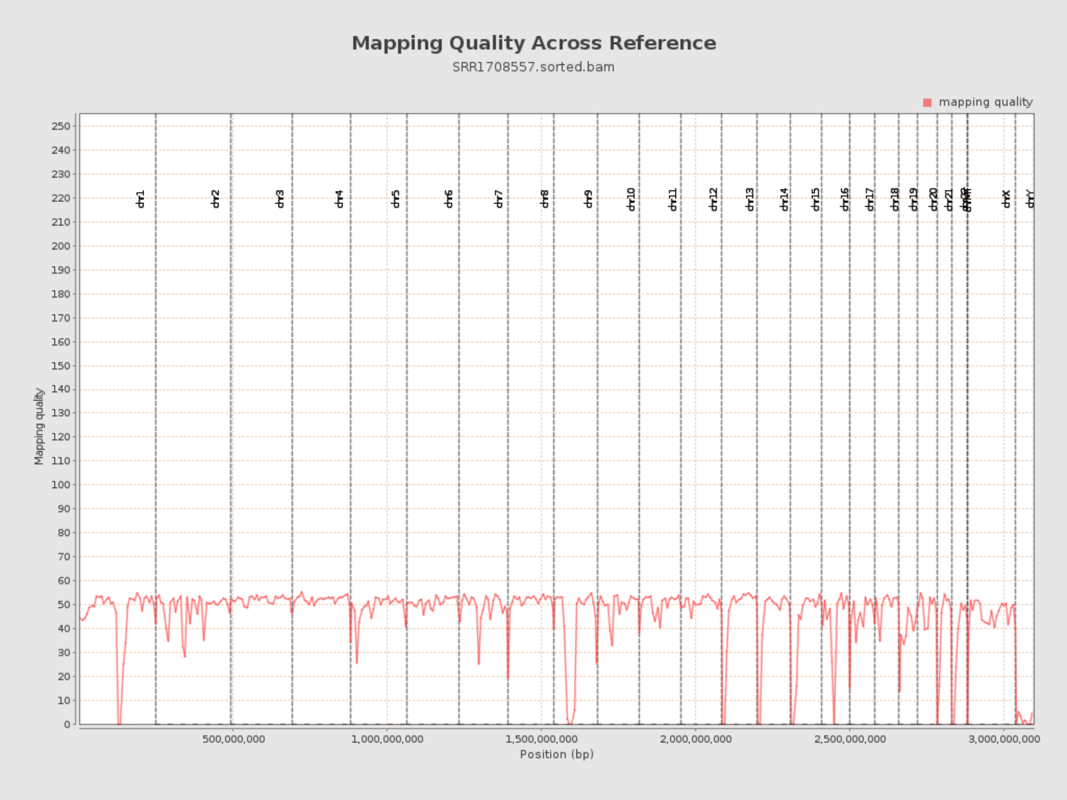
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram