Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:33:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708602.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_SRR1708602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708602.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:33:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,280,159
Mapped reads	5,181,642 / 98.13%
Unmapped reads	98,517 / 1.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	179 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	52,489 / 0.99%
Duplication rate	1.01%
Clipped reads	71,336 / 1.35%

2.2. ACGT Content

Number/percentage of A's	80,071,676 / 30.99%
Number/percentage of C's	48,940,577 / 18.94%
Number/percentage of T's	79,706,910 / 30.85%
Number/percentage of G's	49,680,162 / 19.23%
Number/percentage of N's	9,073 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	0.0835

Standard Deviation	0.3029

2.4. Mapping Quality

Mean Mapping Quality	46.69

2.5. Mismatches and indels

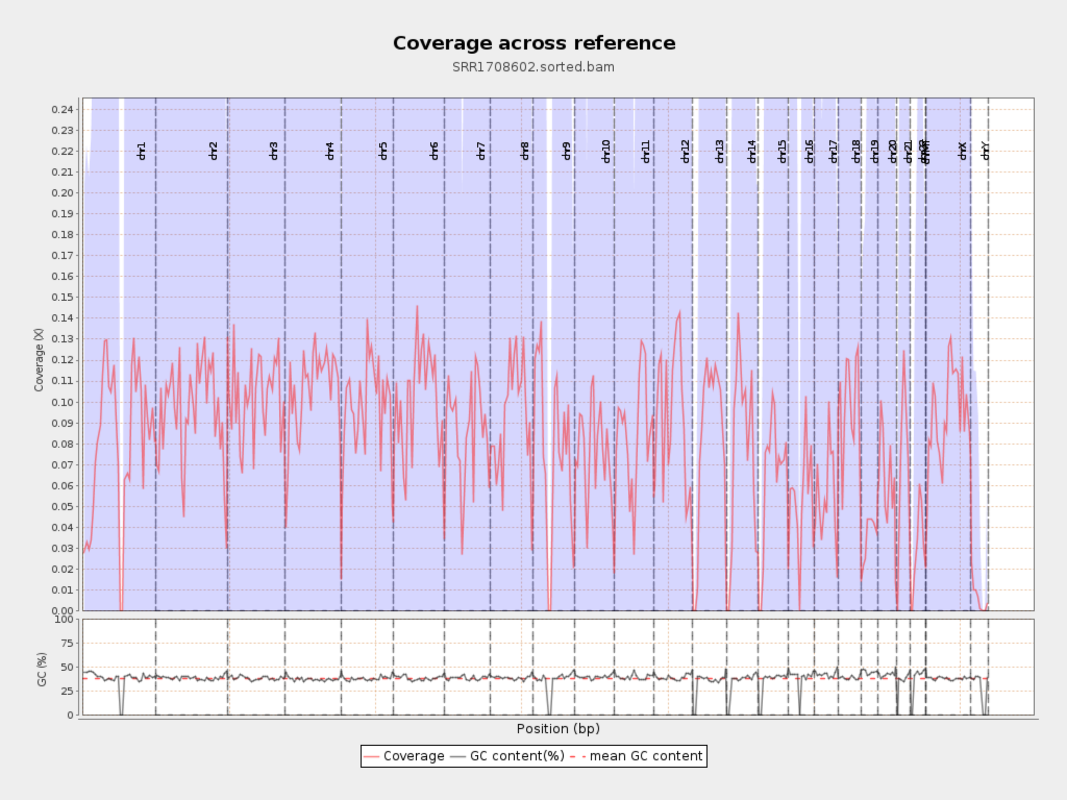
General error rate	0.15%
Mismatches	377,078
Insertions	16,328
Mapped reads with at least one insertion	0.31%
Deletions	13,268
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.5%

2.6. Chromosome stats

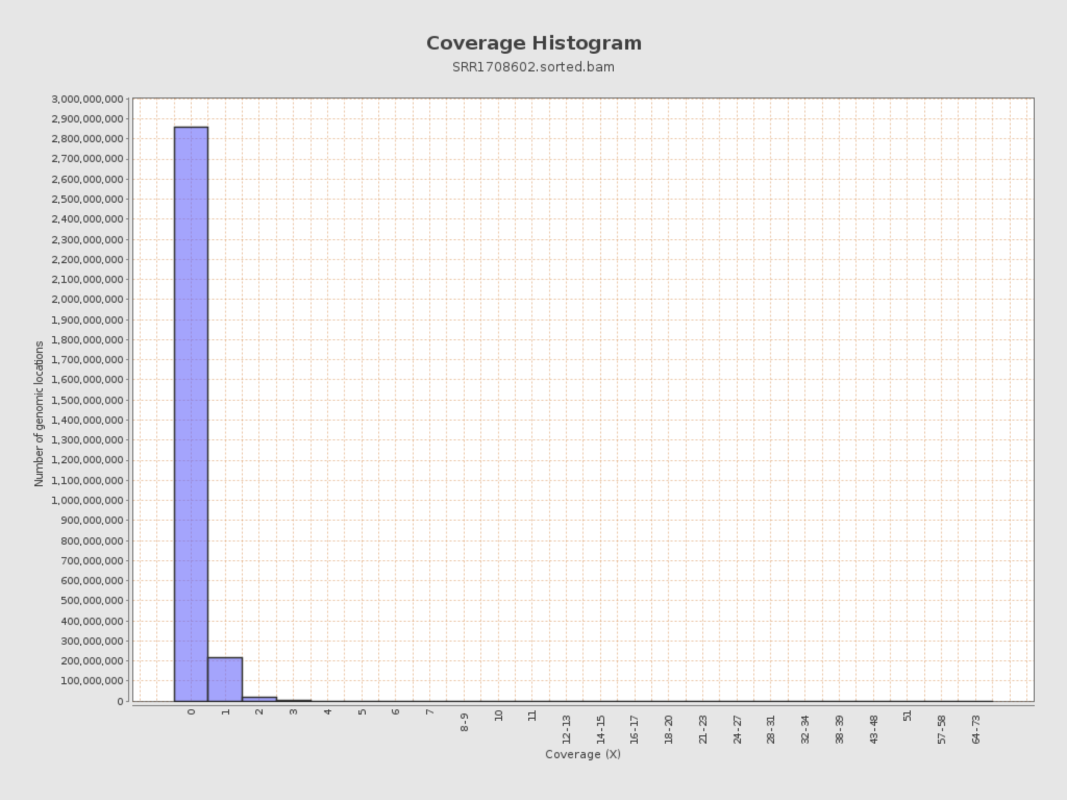
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20013310	0.0803	0.299
chr2	243199373	23309303	0.0958	0.3227
chr3	198022430	20428812	0.1032	0.3351
chr4	191154276	20238725	0.1059	0.3392
chr5	180915260	17533480	0.0969	0.3244
chr6	171115067	17342975	0.1014	0.3324
chr7	159138663	13558612	0.0852	0.3054

chr8	146364022	13550030	0.0926	0.3172
chr9	141213431	10964601	0.0776	0.2931
chr10	135534747	10373674	0.0765	0.2882
chr11	135006516	11481974	0.085	0.3062
chr12	133851895	12355980	0.0923	0.3186
chr13	115169878	9460475	0.0821	0.3006
chr14	107349540	8315144	0.0775	0.2931
chr15	102531392	6468216	0.0631	0.2647
chr16	90354753	4740422	0.0525	0.2396
chr17	81195210	4587879	0.0565	0.2492
chr18	78077248	7657372	0.0981	0.3263
chr19	59128983	2151749	0.0364	0.1979
chr20	63025520	4046349	0.0642	0.265
chr21	48129895	3219526	0.0669	0.274
chr22	51304566	1549218	0.0302	0.1818
chrMT	16571	500	0.0302	0.1711
chrX	155270560	14729218	0.0949	0.322
chrY	59373566	353496	0.006	0.0811

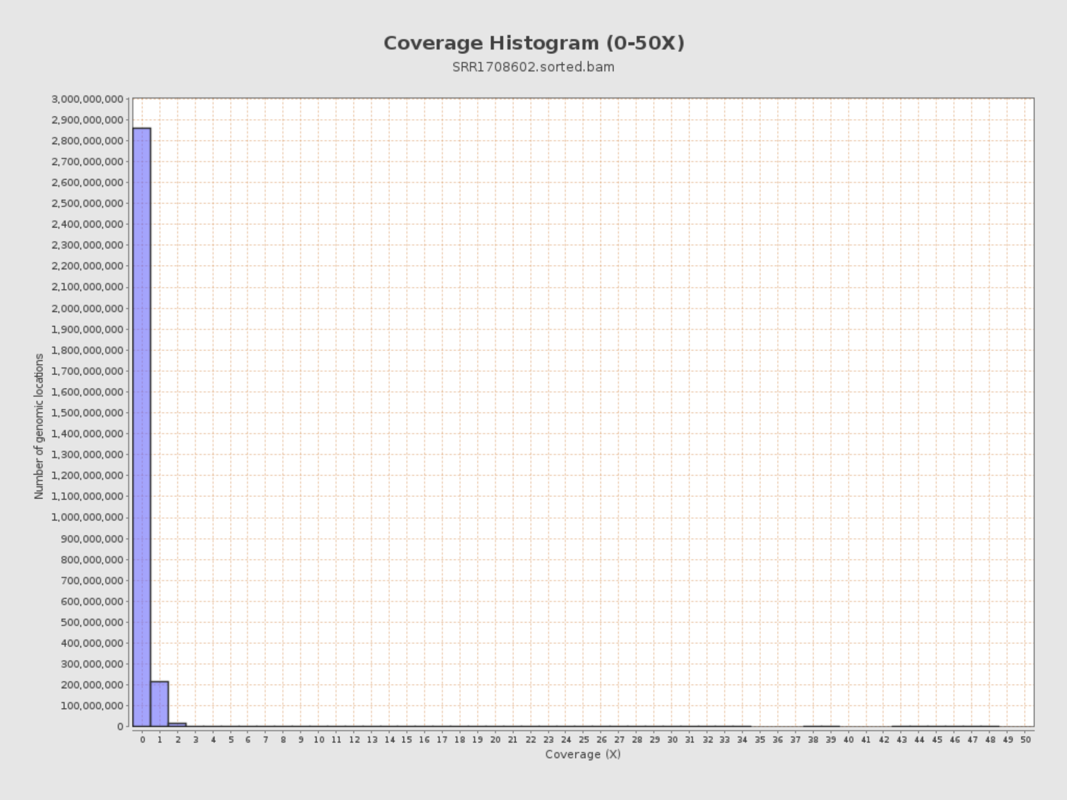
3. Results : Coverage across reference



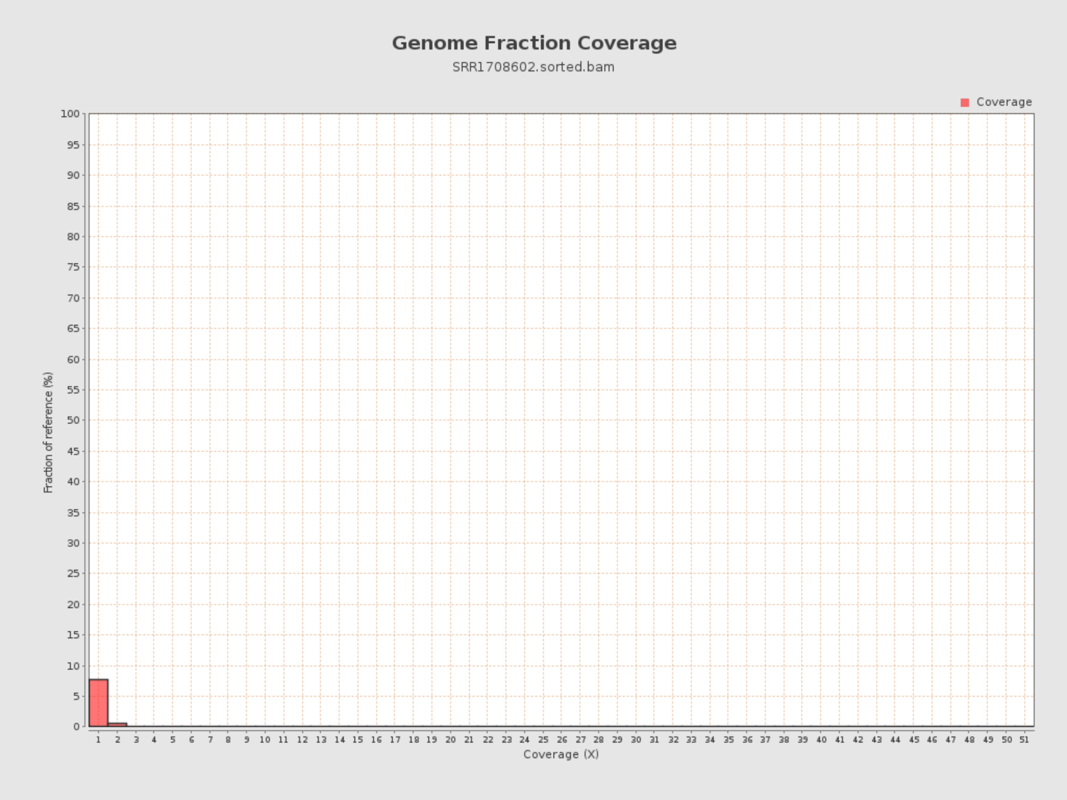
4. Results : Coverage Histogram



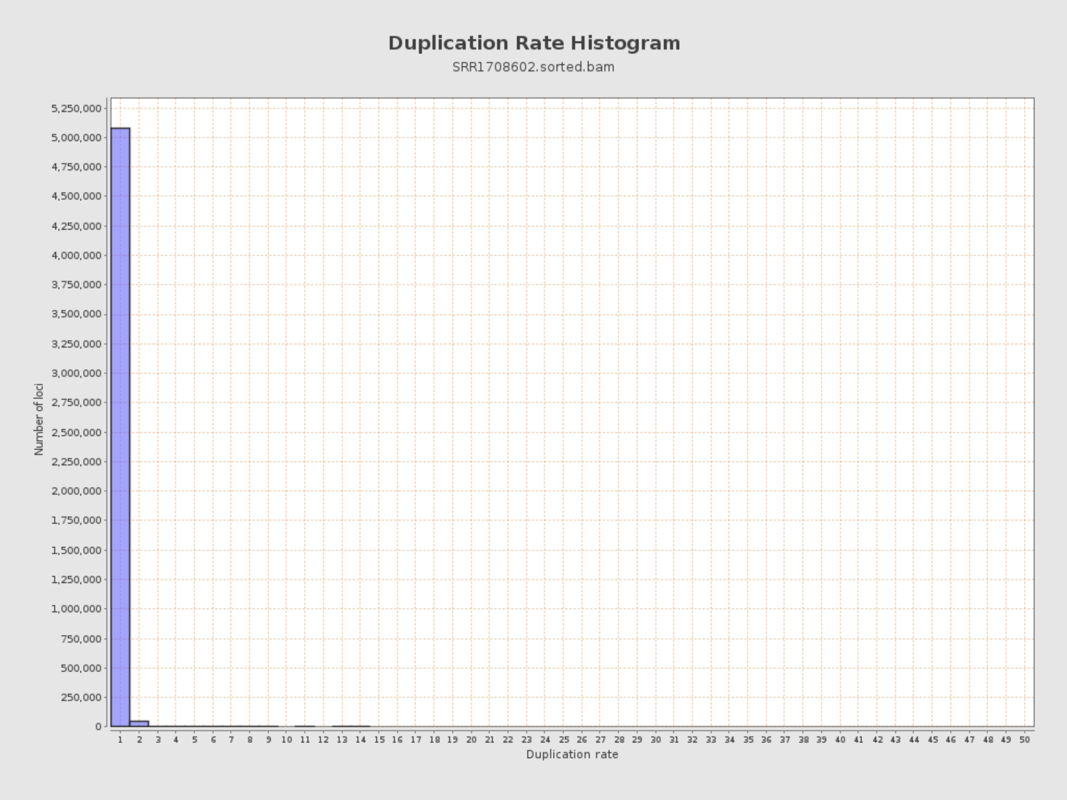
5. Results : Coverage Histogram (0-50X)



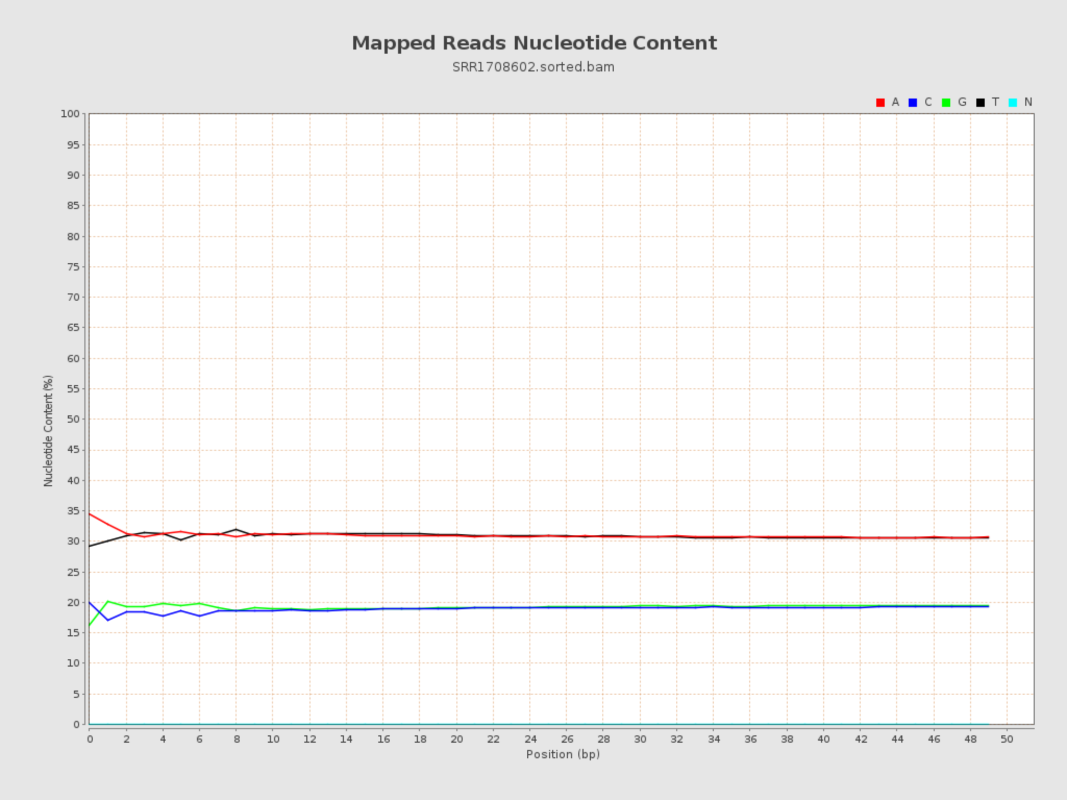
6. Results : Genome Fraction Coverage



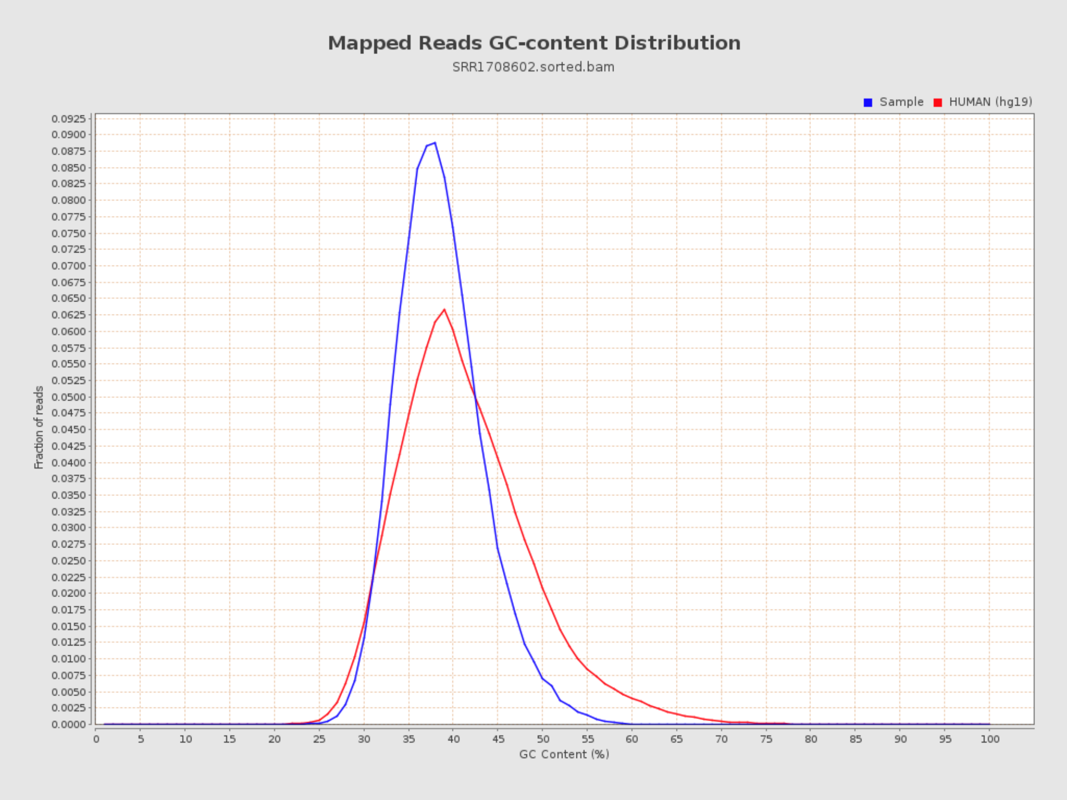
7. Results : Duplication Rate Histogram



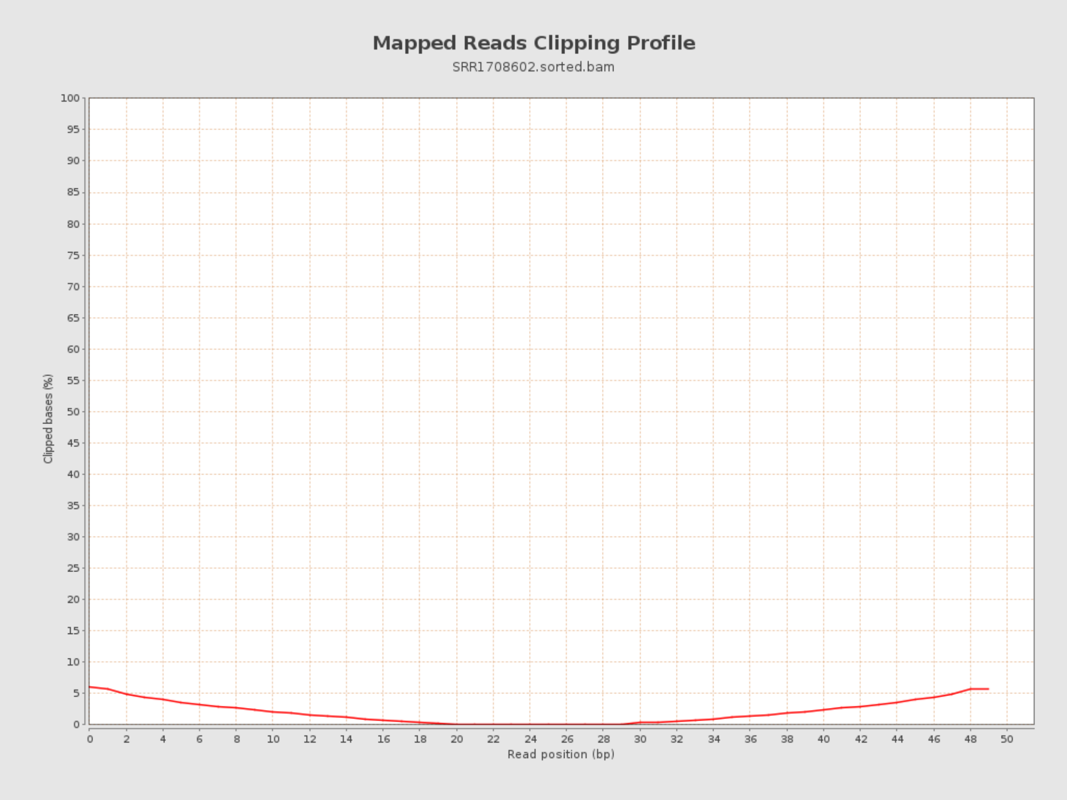
8. Results : Mapped Reads Nucleotide Content



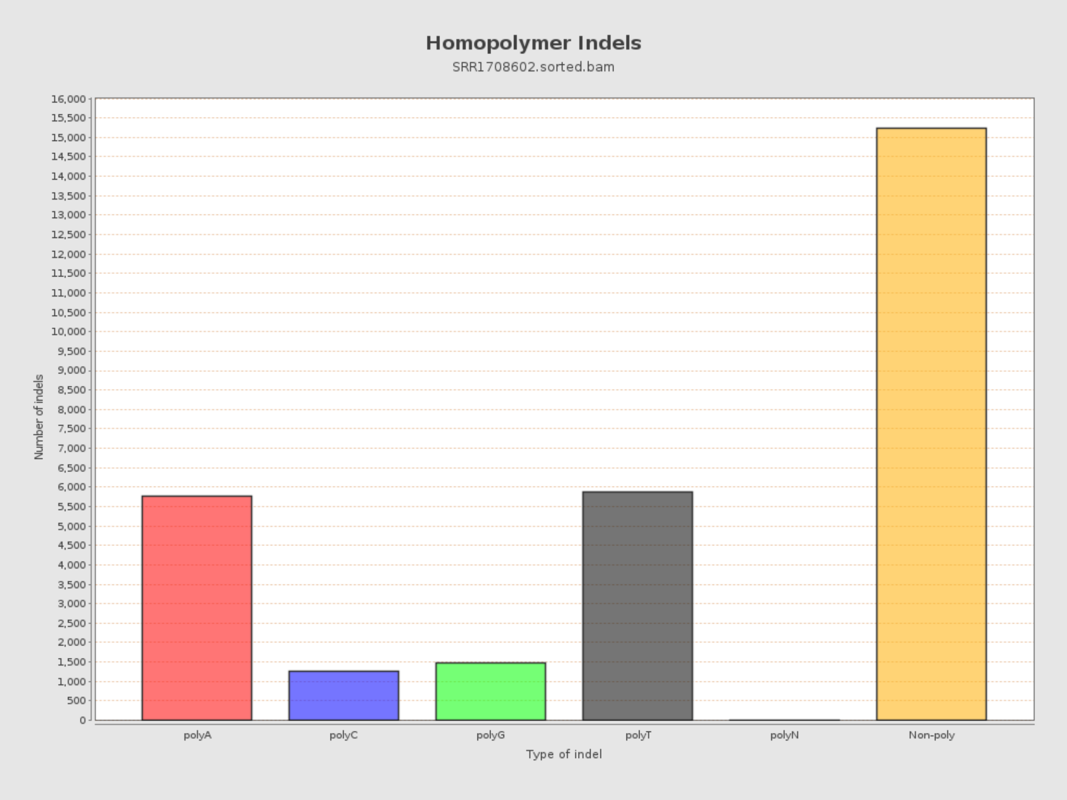
9. Results : Mapped Reads GC-content Distribution



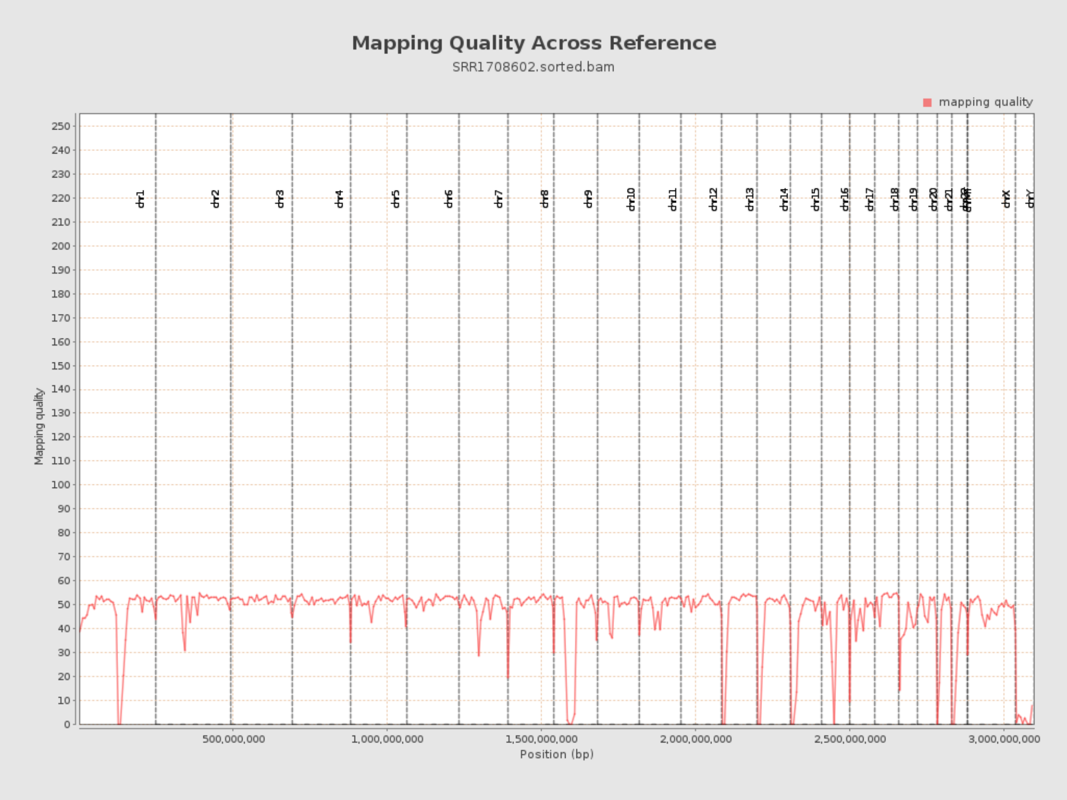
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram