Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:15:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708593.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_SRR1708593 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708593.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:15:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708593.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,337,258
Mapped reads	6,023,838 / 95.05%
Unmapped reads	313,420 / 4.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	142 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	61,374 / 0.97%
Duplication rate	1.02%
Clipped reads	77,706 / 1.23%

2.2. ACGT Content

Number/percentage of A's	93,193,167 / 31.02%
Number/percentage of C's	56,963,513 / 18.96%
Number/percentage of T's	92,546,957 / 30.8%
Number/percentage of G's	57,749,544 / 19.22%
Number/percentage of N's	8,462 / 0%
GC Percentage	38.18%

2.3. Coverage

Mean	0.0971

Standard Deviation	0.3282

2.4. Mapping Quality

Mean Mapping Quality	46.65

2.5. Mismatches and indels

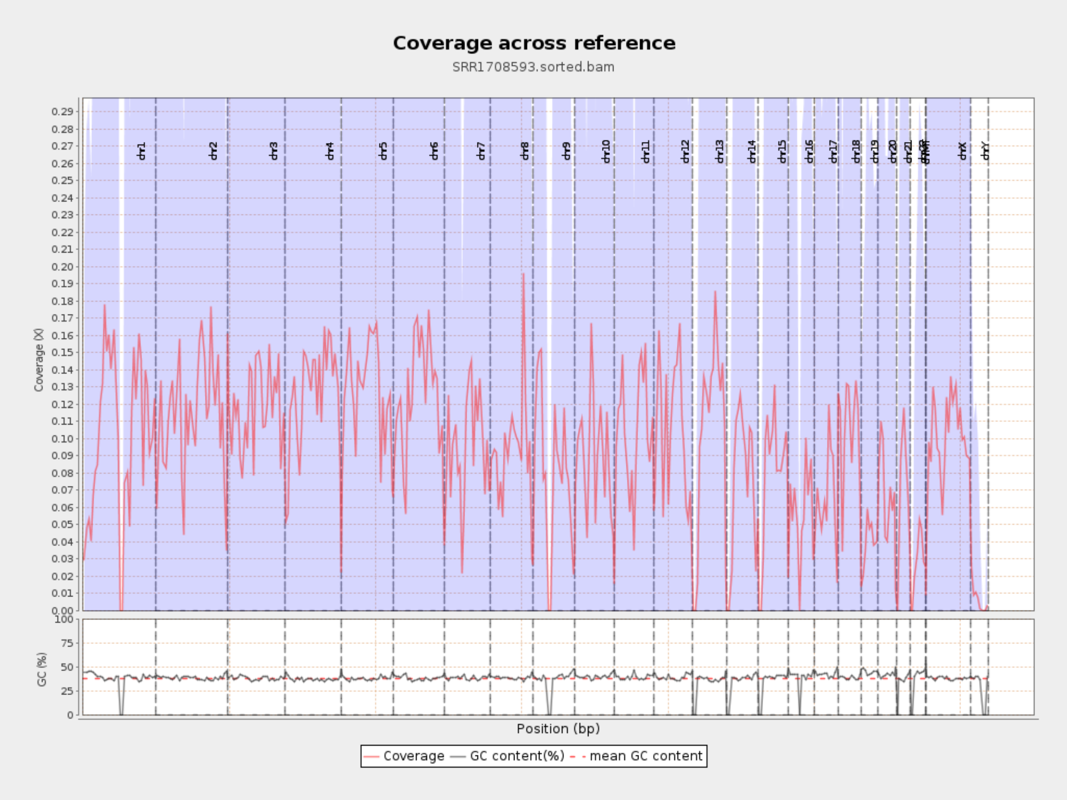
General error rate	0.15%
Mismatches	429,495
Insertions	19,093
Mapped reads with at least one insertion	0.32%
Deletions	15,216
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.82%

2.6. Chromosome stats

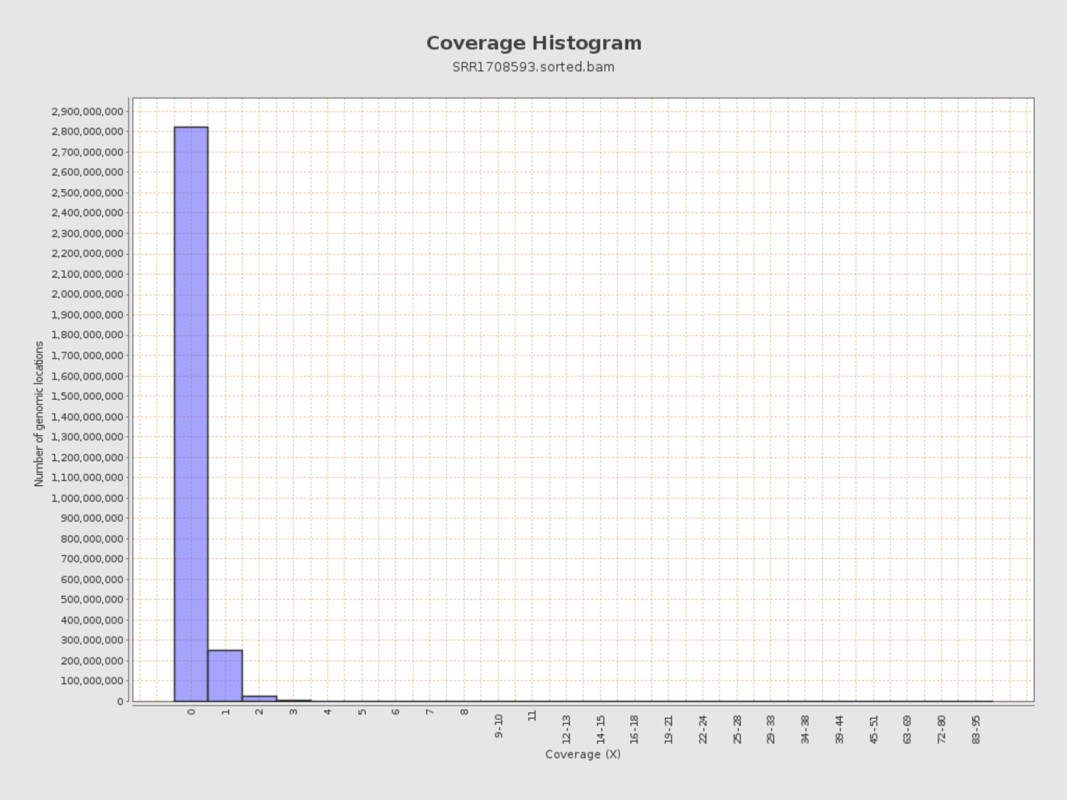
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25240086	0.1013	0.3383
chr2	243199373	27847374	0.1145	0.3546
chr3	198022430	23469835	0.1185	0.3602
chr4	191154276	24100698	0.1261	0.3713
chr5	180915260	22976893	0.127	0.3726
chr6	171115067	21635883	0.1264	0.3726
chr7	159138663	15017857	0.0944	0.3232

chr8	146364022	13817301	0.0944	0.3216
chr9	141213431	11599845	0.0821	0.3022
chr10	135534747	12413845	0.0916	0.3167
chr11	135006516	14057528	0.1041	0.3402
chr12	133851895	13918820	0.104	0.339
chr13	115169878	12260840	0.1065	0.3439
chr14	107349540	7987287	0.0744	0.287
chr15	102531392	8095787	0.079	0.298
chr16	90354753	4983460	0.0552	0.2458
chr17	81195210	5418322	0.0667	0.2735
chr18	78077248	8256731	0.1058	0.3392
chr19	59128983	2402735	0.0406	0.2094
chr20	63025520	4324082	0.0686	0.275
chr21	48129895	3172593	0.0659	0.271
chr22	51304566	1452691	0.0283	0.1743
chrMT	16571	150	0.0091	0.0947
chrX	155270560	15668567	0.1009	0.3332
chrY	59373566	368277	0.0062	0.083

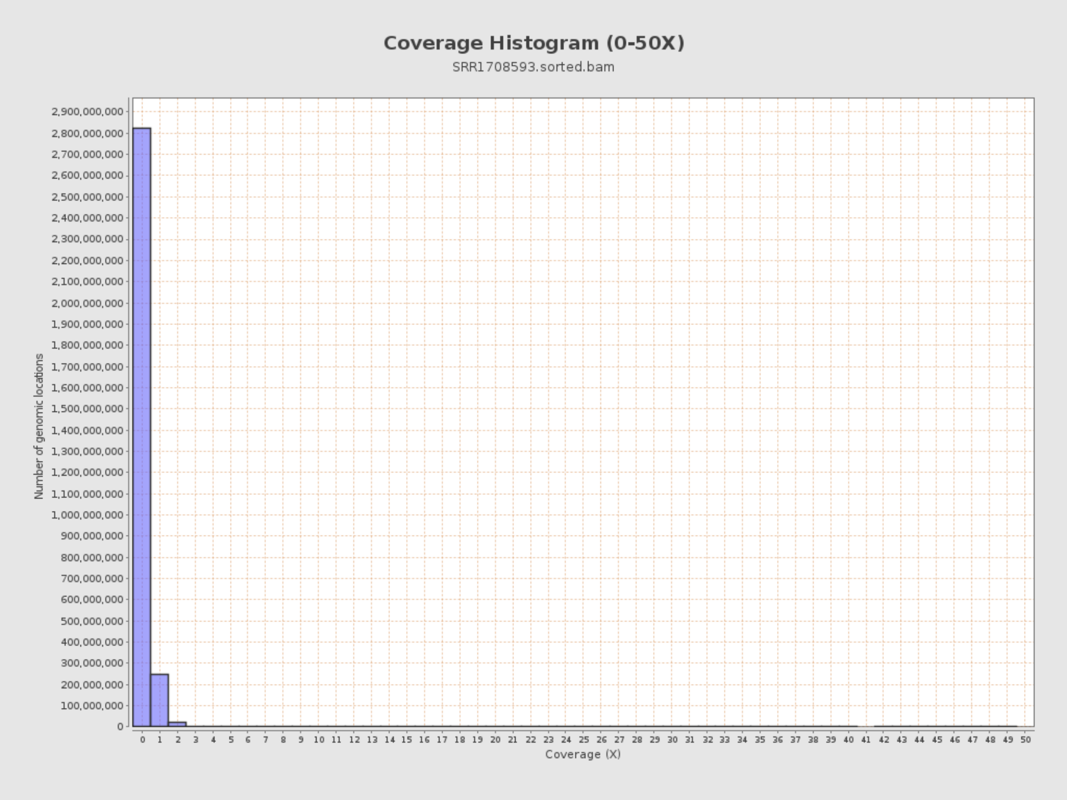
3. Results : Coverage across reference



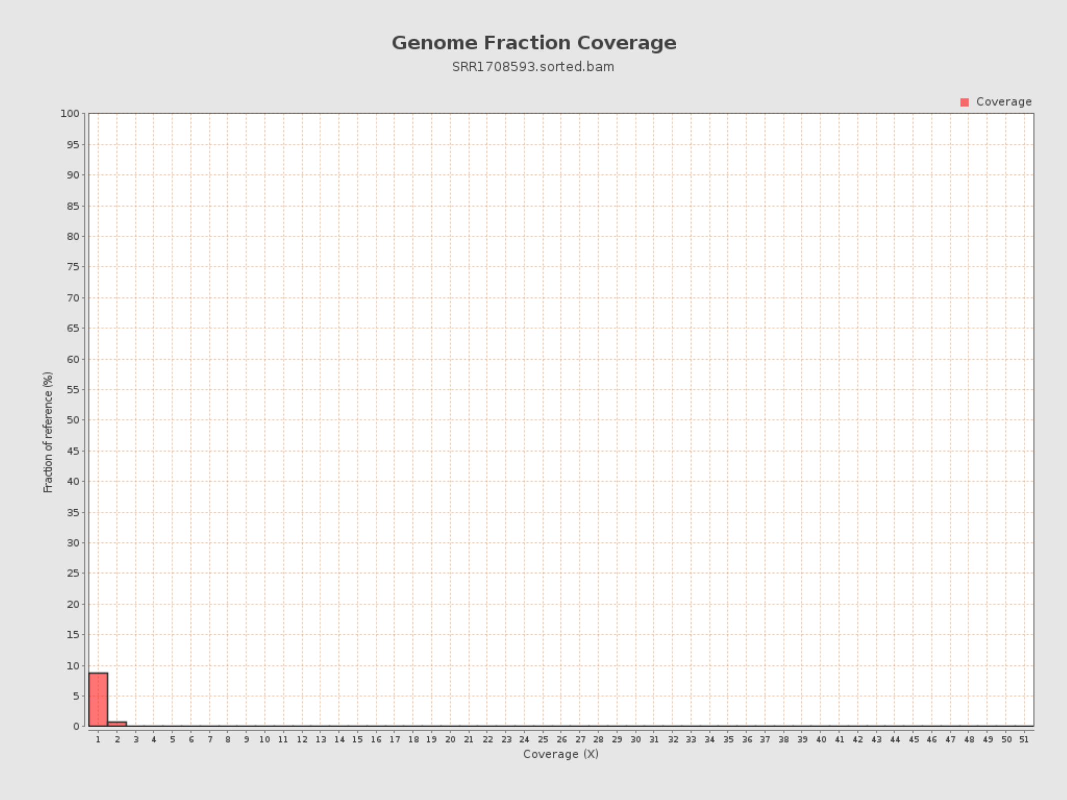
4. Results : Coverage Histogram



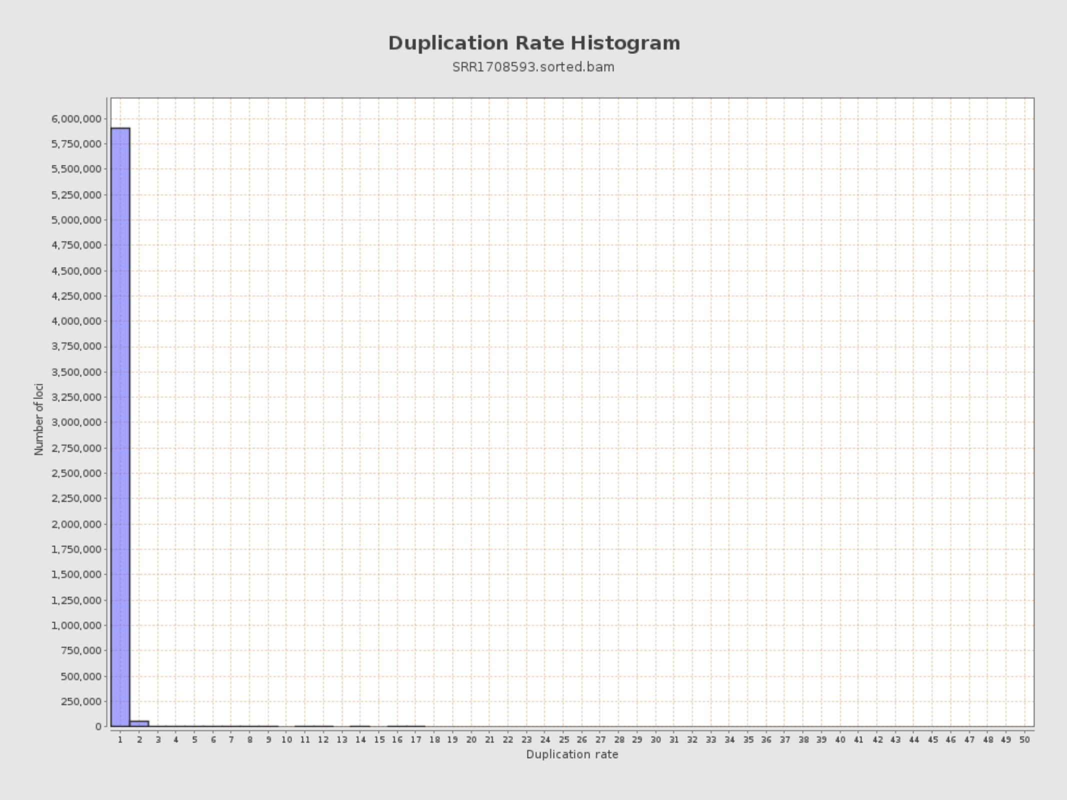
5. Results : Coverage Histogram (0-50X)



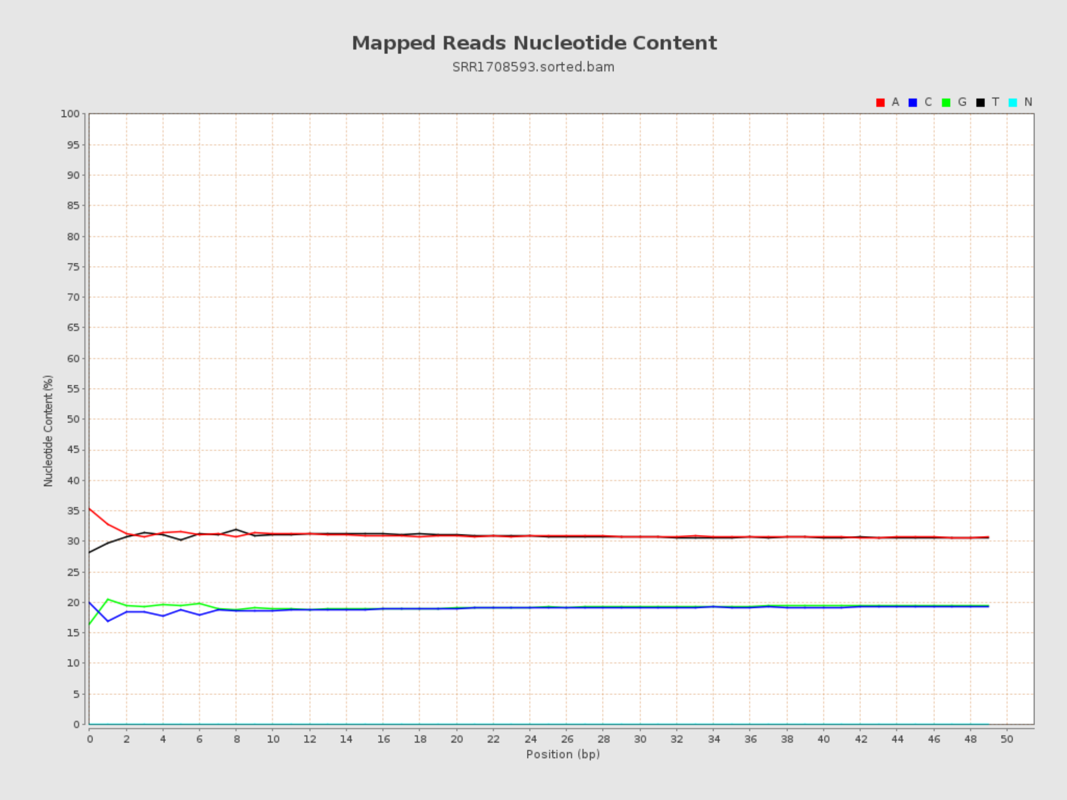
6. Results : Genome Fraction Coverage



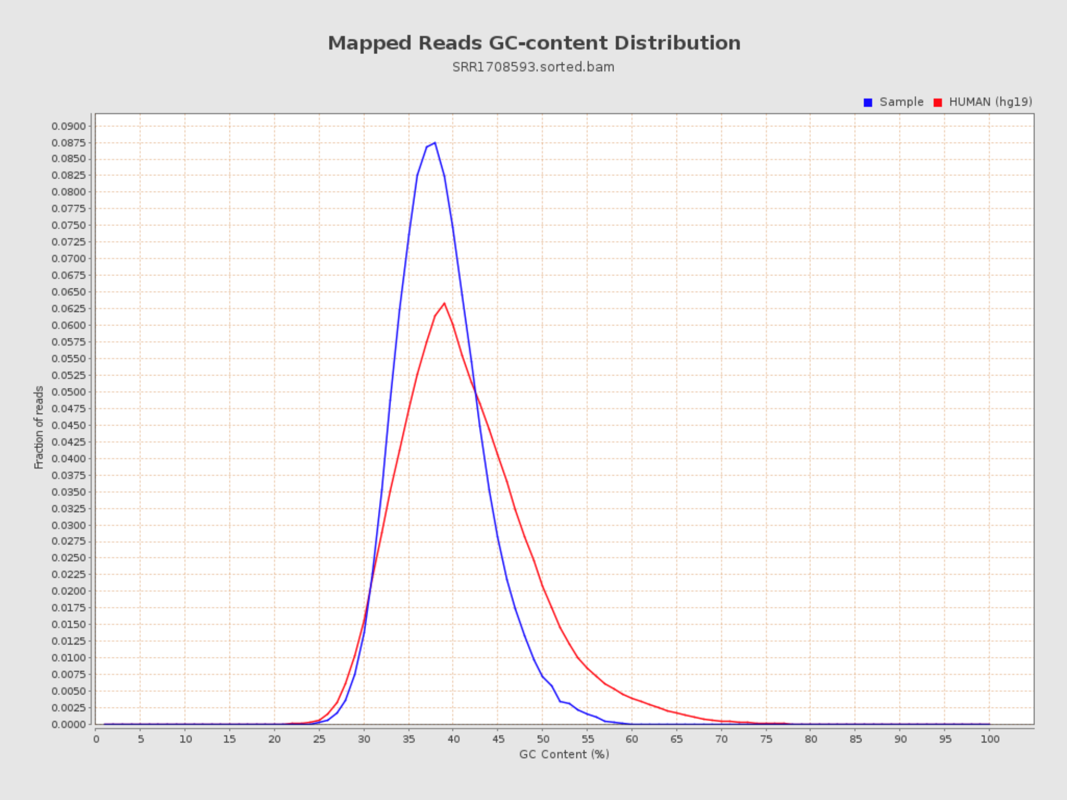
7. Results : Duplication Rate Histogram



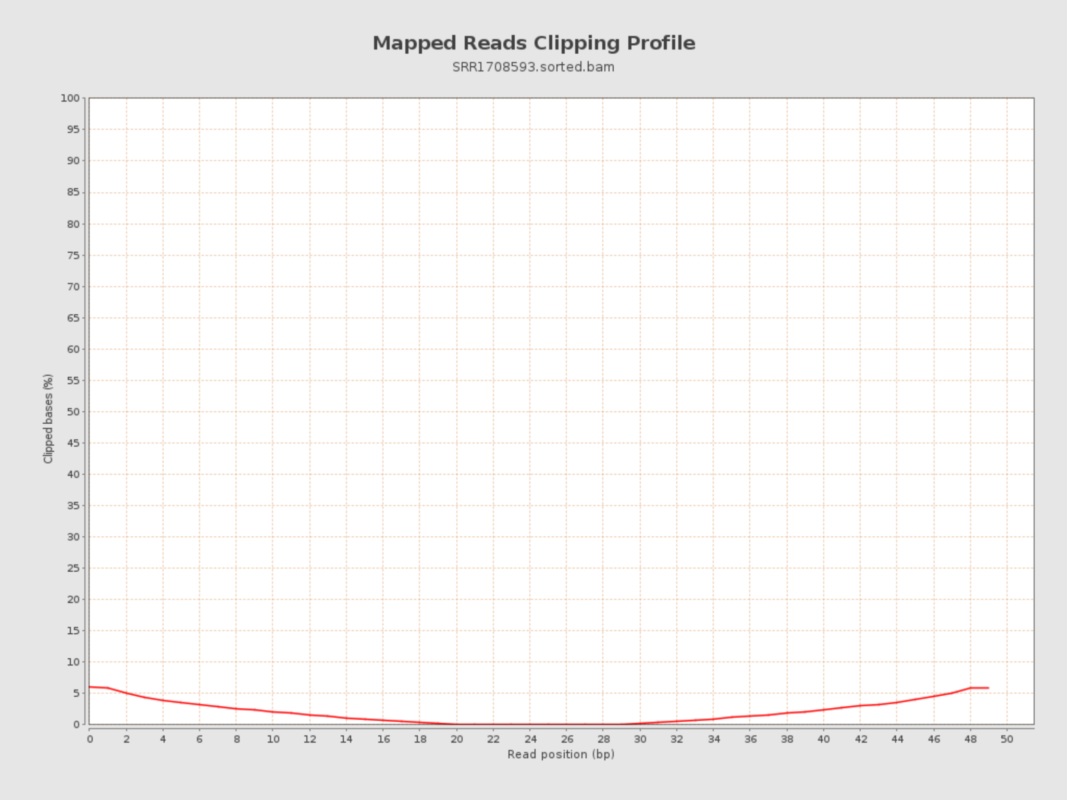
8. Results : Mapped Reads Nucleotide Content



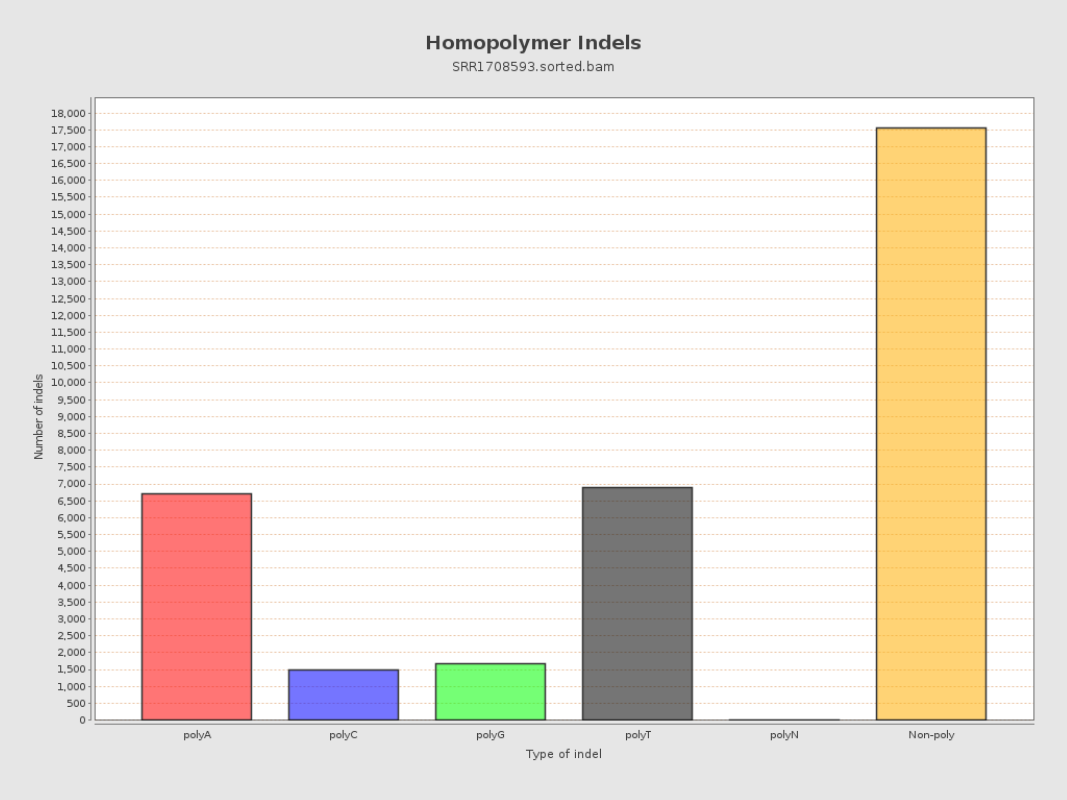
9. Results : Mapped Reads GC-content Distribution



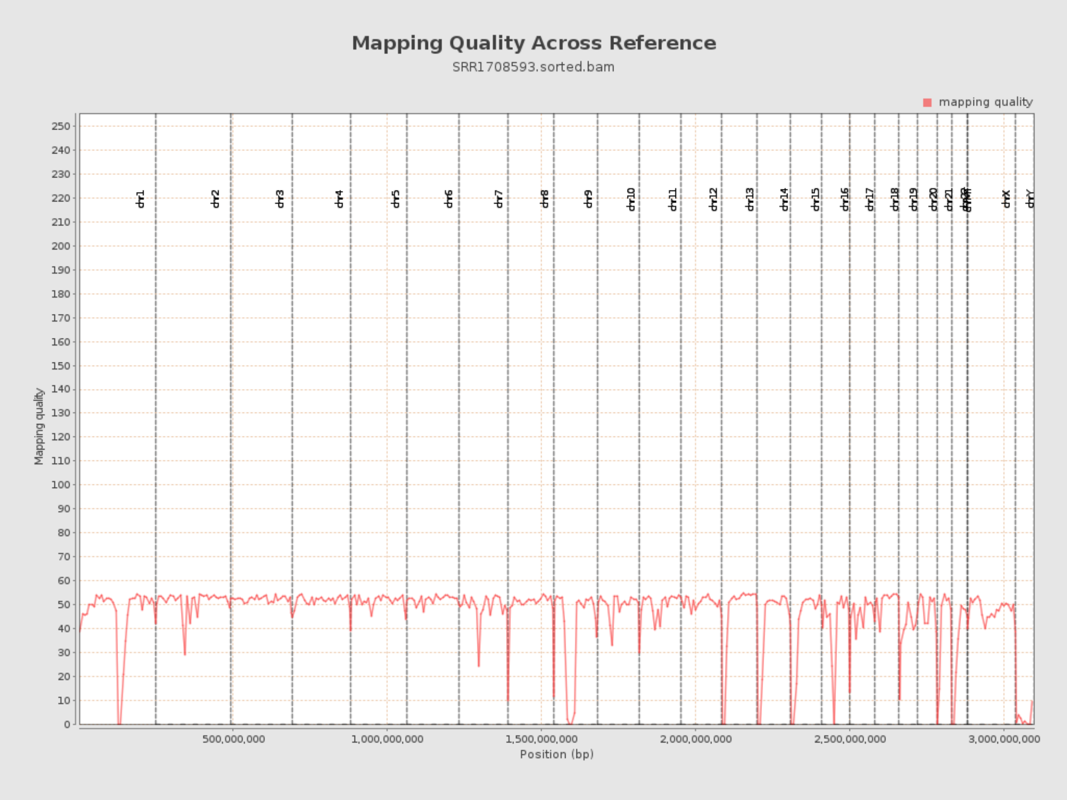
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram