Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:42:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708584.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_SRR1708584 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708584.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:42:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708584.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,814,182
Mapped reads	5,561,275 / 95.65%
Unmapped reads	252,907 / 4.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	163 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	57,100 / 0.98%
Duplication rate	1.03%
Clipped reads	72,918 / 1.25%

2.2. ACGT Content

Number/percentage of A's	85,774,777 / 30.92%
Number/percentage of C's	52,793,308 / 19.03%
Number/percentage of T's	85,277,305 / 30.74%
Number/percentage of G's	53,521,936 / 19.3%
Number/percentage of N's	9,596 / 0%
GC Percentage	38.33%

2.3. Coverage

Mean	0.0896

Standard Deviation	0.3138

2.4. Mapping Quality

Mean Mapping Quality	46.78

2.5. Mismatches and indels

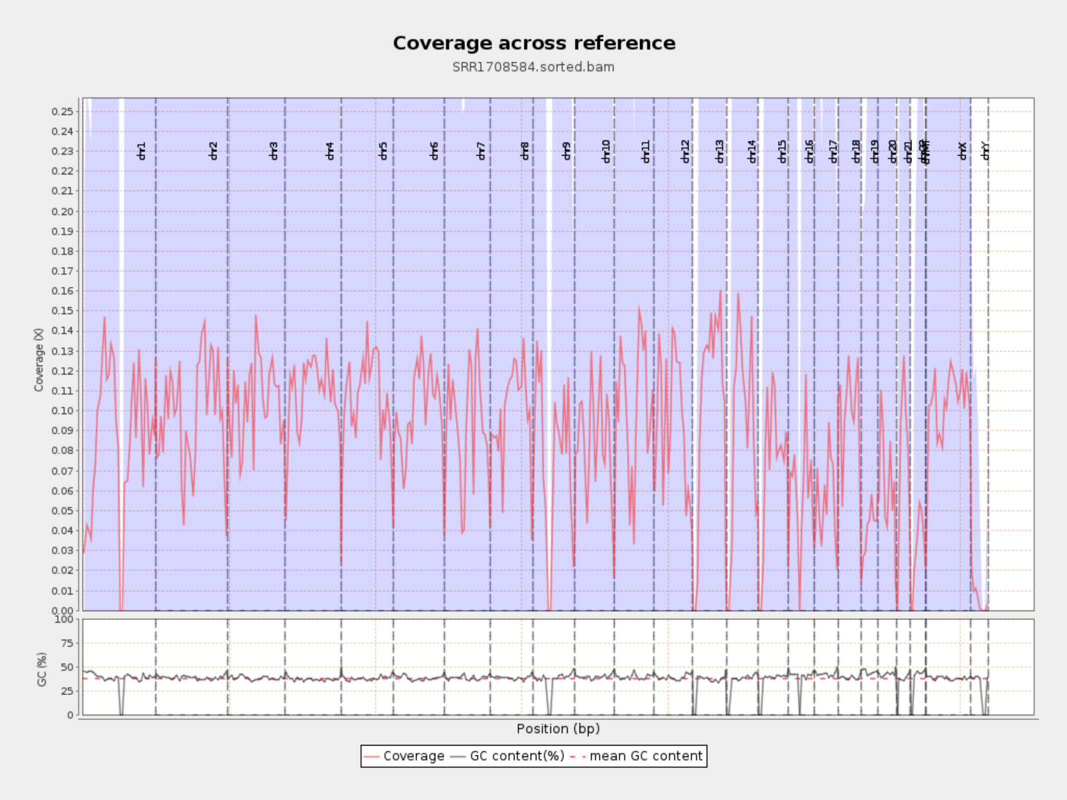
General error rate	0.15%
Mismatches	401,820
Insertions	17,347
Mapped reads with at least one insertion	0.31%
Deletions	14,015
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.49%

2.6. Chromosome stats

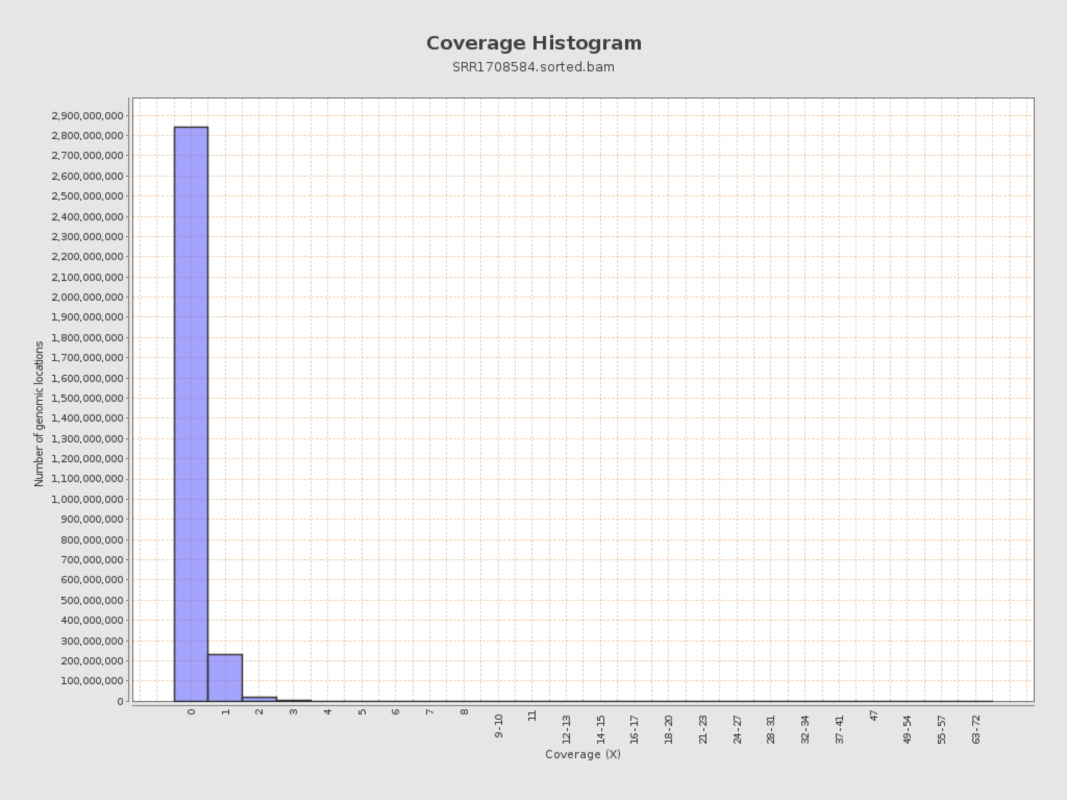
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21444231	0.086	0.3097
chr2	243199373	23966271	0.0985	0.3278
chr3	198022430	20950028	0.1058	0.339
chr4	191154276	20862000	0.1091	0.3436
chr5	180915260	19039968	0.1052	0.3378
chr6	171115067	17486235	0.1022	0.3322
chr7	159138663	14660498	0.0921	0.317

chr8	146364022	14647252	0.1001	0.3294
chr9	141213431	10974583	0.0777	0.293
chr10	135534747	11756577	0.0867	0.3067
chr11	135006516	13702036	0.1015	0.3358
chr12	133851895	12666703	0.0946	0.3219
chr13	115169878	12033483	0.1045	0.3404
chr14	107349540	9889498	0.0921	0.3205
chr15	102531392	7407533	0.0722	0.2828
chr16	90354753	5247308	0.0581	0.2516
chr17	81195210	4577305	0.0564	0.2483
chr18	78077248	7850296	0.1005	0.3305
chr19	59128983	2429067	0.0411	0.2107
chr20	63025520	4155965	0.0659	0.2684
chr21	48129895	3520037	0.0731	0.2866
chr22	51304566	1602402	0.0312	0.1839
chrMT	16571	350	0.0211	0.157
chrX	155270560	16174632	0.1042	0.3374
chrY	59373566	356336	0.006	0.0815

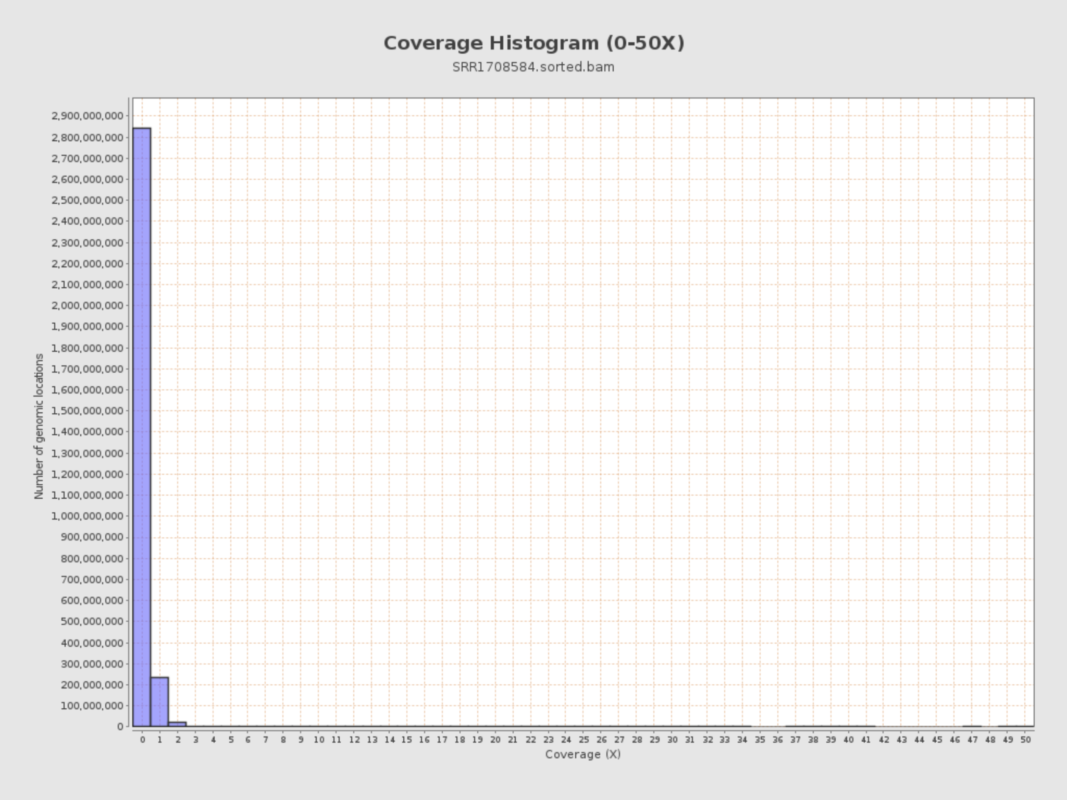
3. Results : Coverage across reference



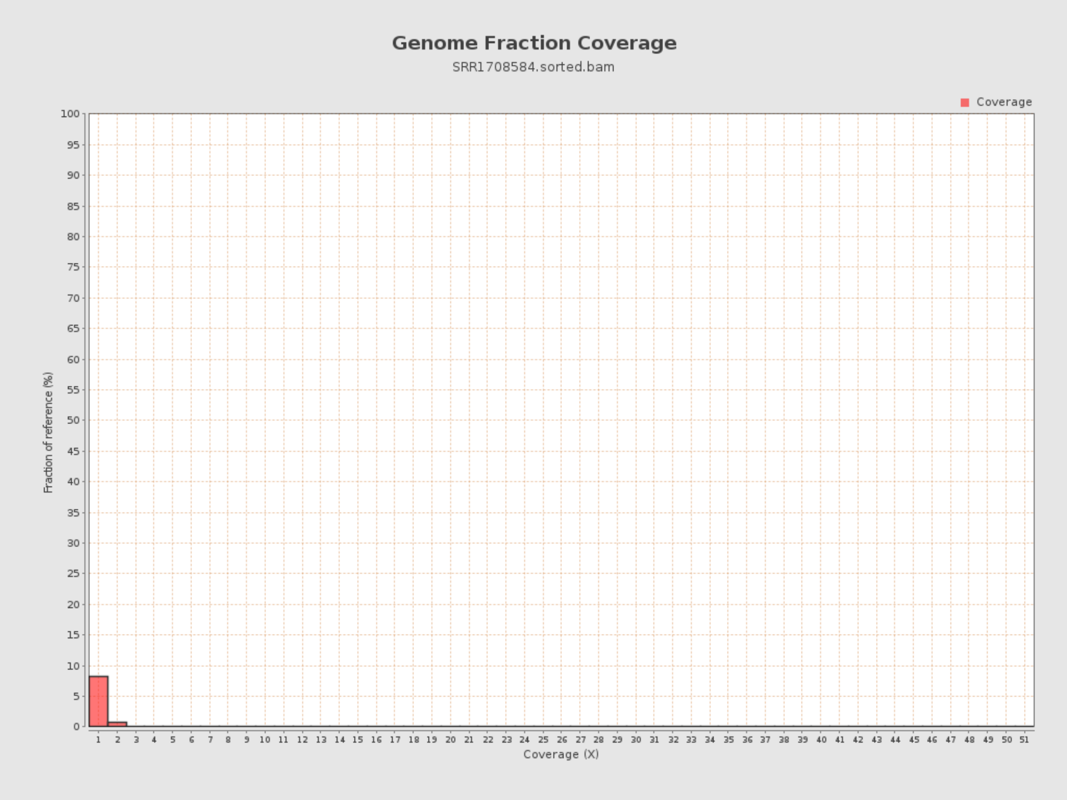
4. Results : Coverage Histogram



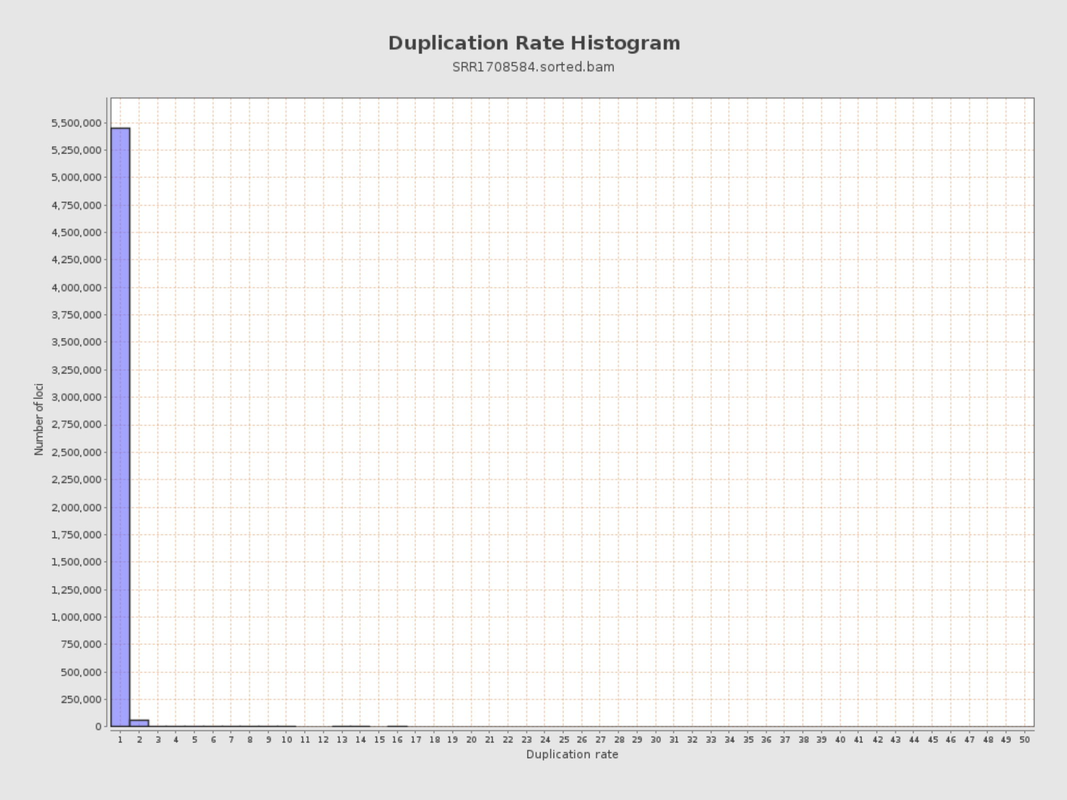
5. Results : Coverage Histogram (0-50X)



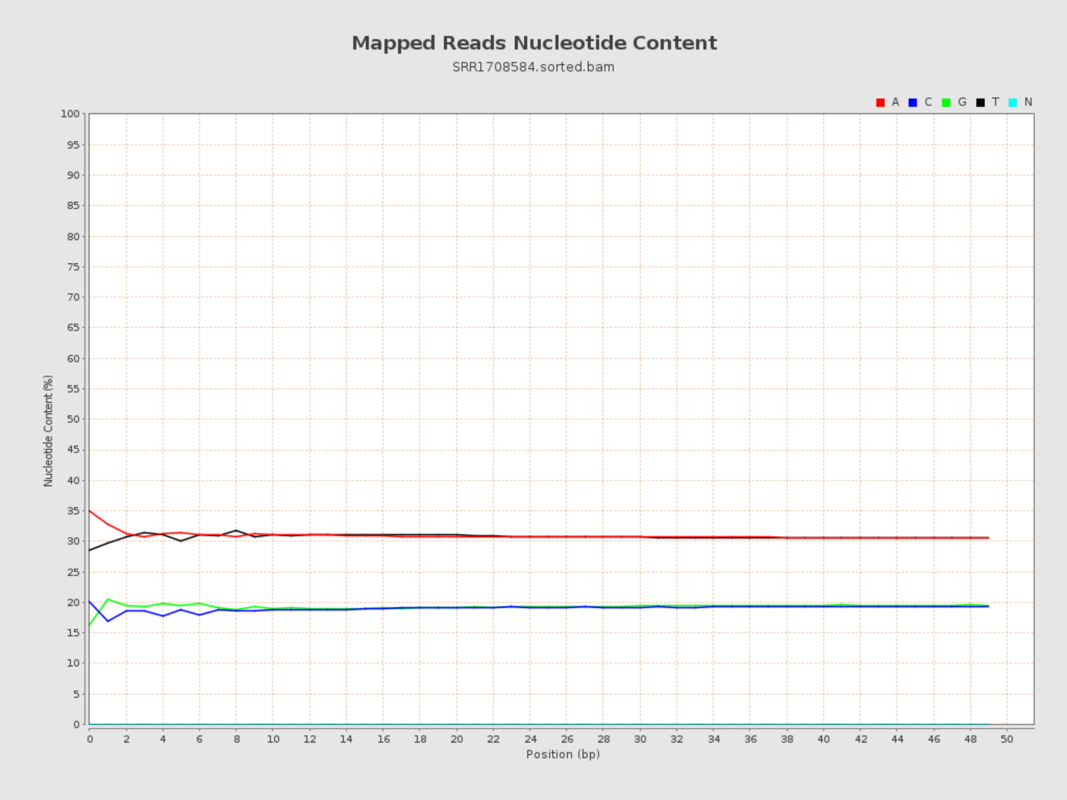
6. Results : Genome Fraction Coverage



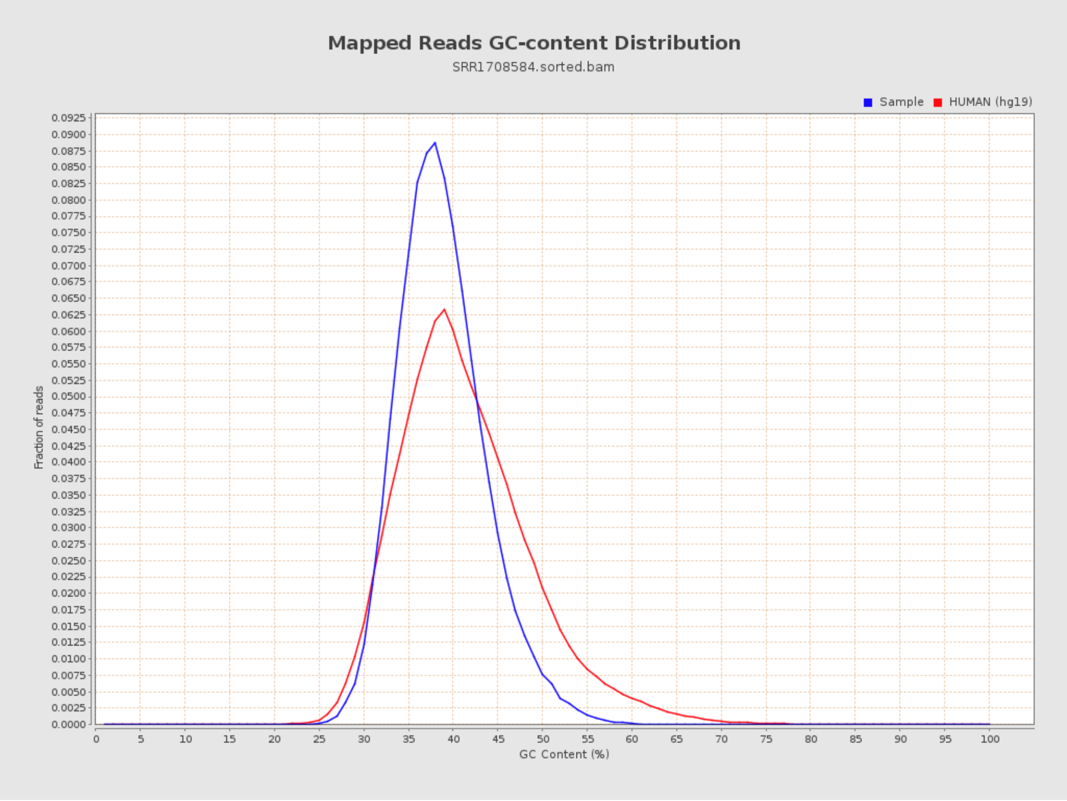
7. Results : Duplication Rate Histogram



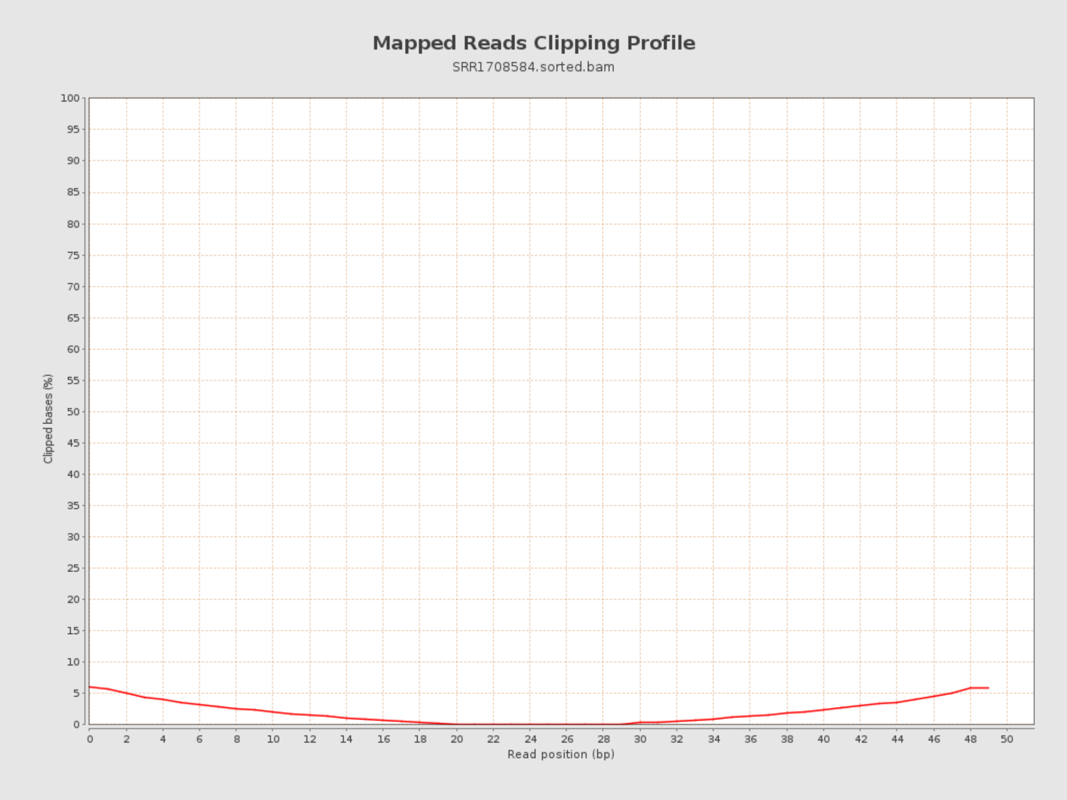
8. Results : Mapped Reads Nucleotide Content



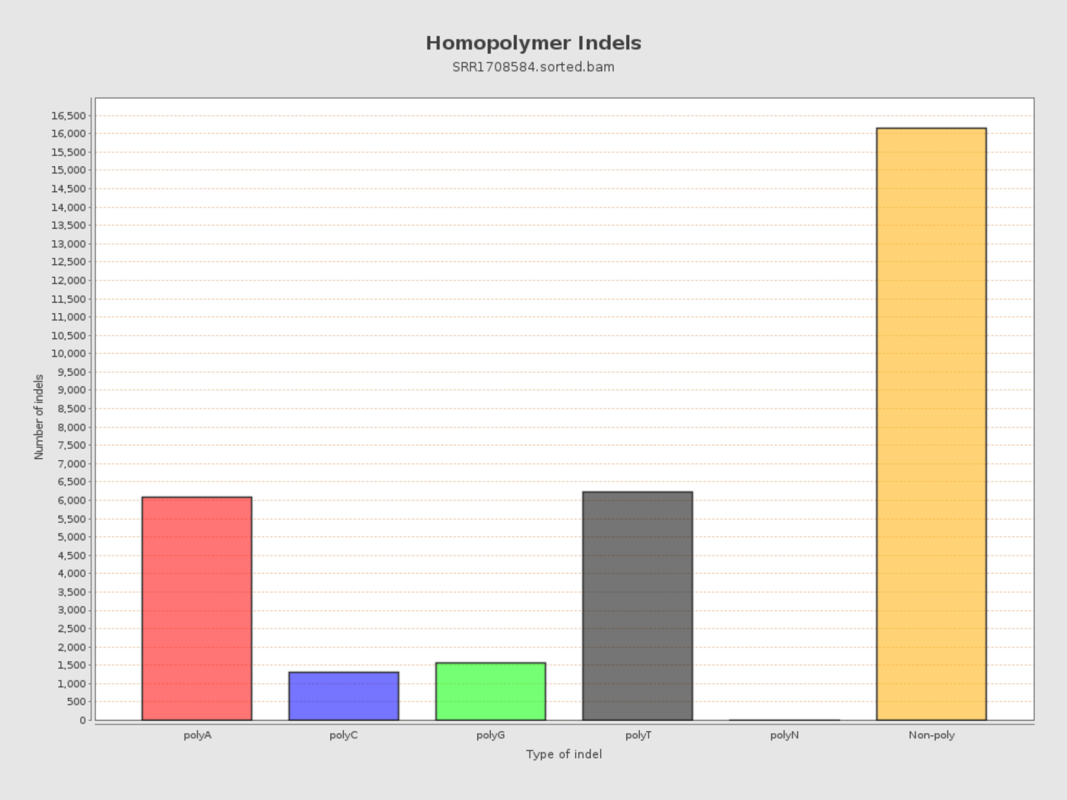
9. Results : Mapped Reads GC-content Distribution



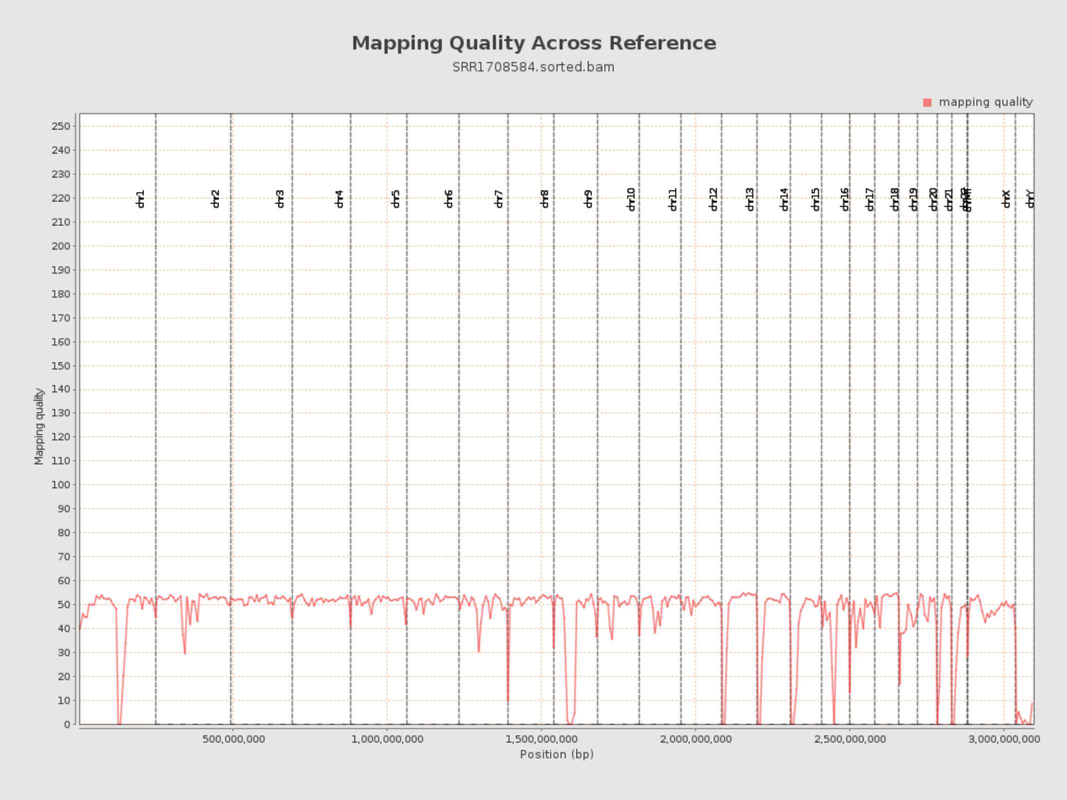
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram