Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:12:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708566.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_SRR1708566 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708566.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:12:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708566.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,049,430
Mapped reads	3,349,297 / 82.71%
Unmapped reads	700,133 / 17.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	85 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	15,990 / 0.39%
Duplication rate	0.48%
Clipped reads	44,823 / 1.11%

2.2. ACGT Content

Number/percentage of A's	51,685,028 / 30.95%
Number/percentage of C's	31,750,210 / 19.01%
Number/percentage of T's	51,512,880 / 30.84%
Number/percentage of G's	32,060,492 / 19.2%
Number/percentage of N's	7,714 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	0.054

Standard Deviation	0.2403

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

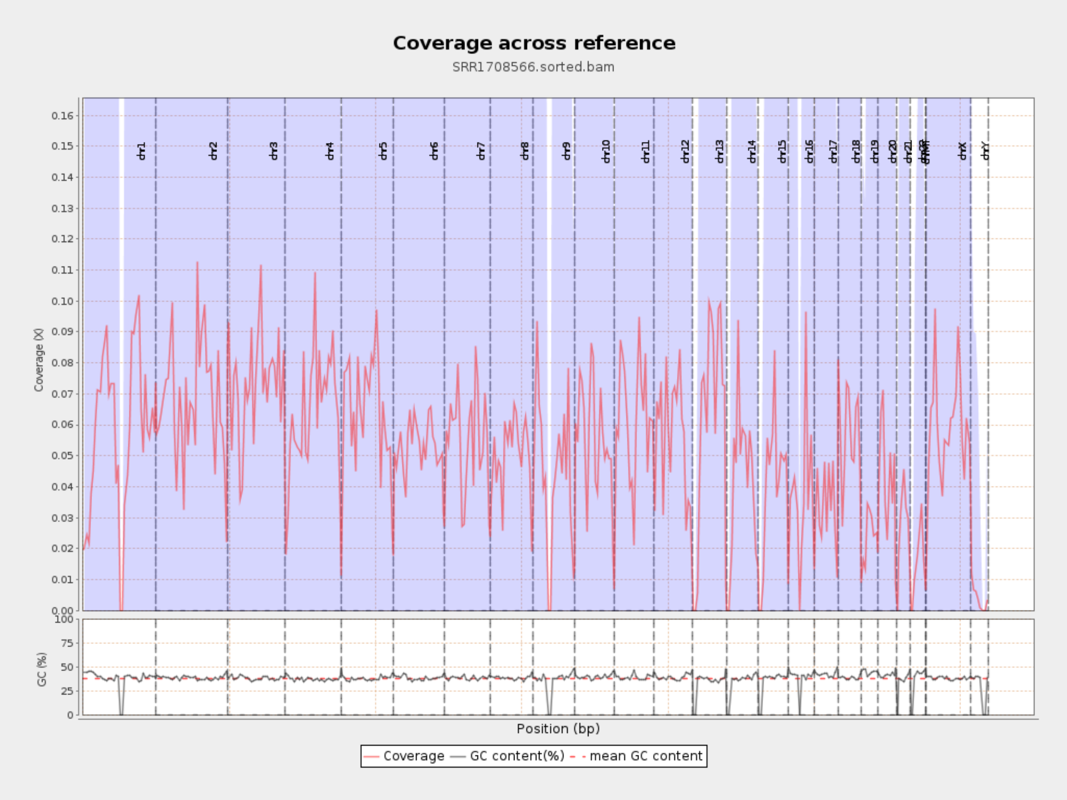
General error rate	0.16%
Mismatches	259,322
Insertions	11,006
Mapped reads with at least one insertion	0.33%
Deletions	8,786
Mapped reads with at least one deletion	0.26%
Homopolymer indels	47.56%

2.6. Chromosome stats

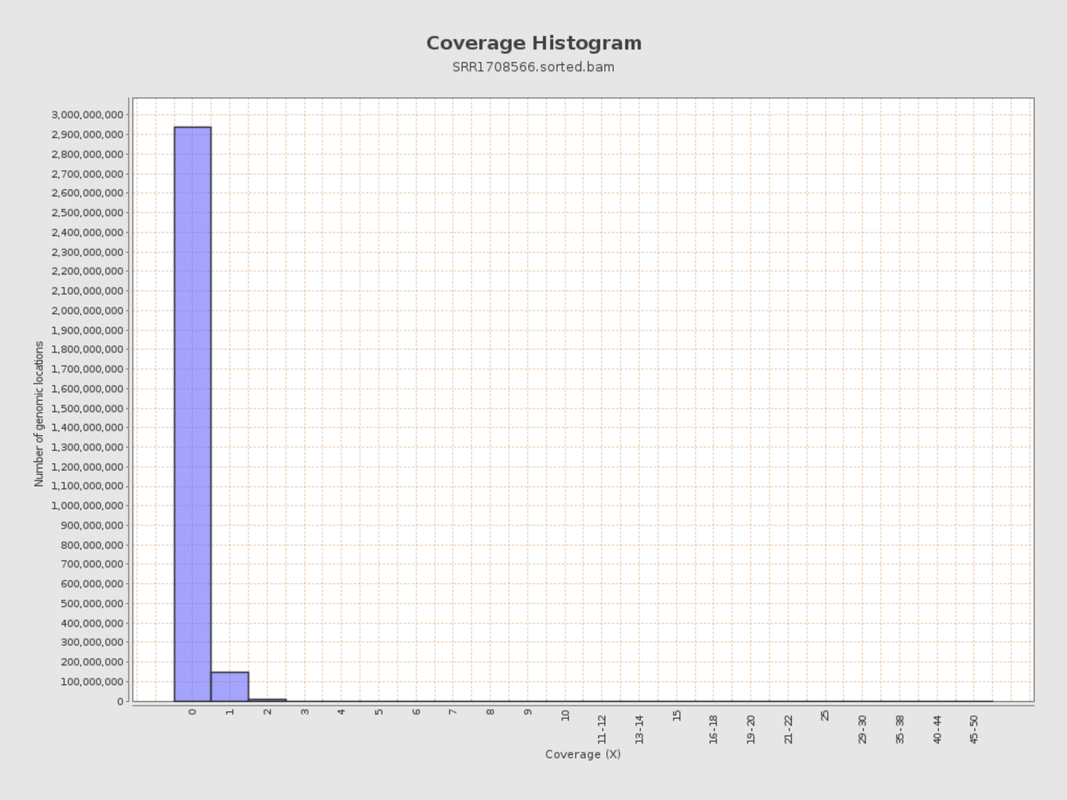
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14506955	0.0582	0.2507
chr2	243199373	16505039	0.0679	0.2688
chr3	198022430	14600694	0.0737	0.2805
chr4	191154276	12370700	0.0647	0.2626
chr5	180915260	11597788	0.0641	0.2605
chr6	171115067	9092240	0.0531	0.2368
chr7	159138663	8799311	0.0553	0.2431

chr8	146364022	7391221	0.0505	0.2309
chr9	141213431	6396331	0.0453	0.2206
chr10	135534747	7740874	0.0571	0.2466
chr11	135006516	8307492	0.0615	0.2568
chr12	133851895	7453256	0.0557	0.2433
chr13	115169878	7310936	0.0635	0.2613
chr14	107349540	4543972	0.0423	0.2127
chr15	102531392	4108523	0.0401	0.2073
chr16	90354753	3296937	0.0365	0.1969
chr17	81195210	2770048	0.0341	0.1906
chr18	78077248	4449723	0.057	0.2458
chr19	59128983	1436013	0.0243	0.1603
chr20	63025520	2804066	0.0445	0.2189
chr21	48129895	1281589	0.0266	0.1682
chr22	51304566	821210	0.016	0.13
chrMT	16571	146	0.0088	0.0935
chrX	155270560	9220895	0.0594	0.2519
chrY	59373566	225227	0.0038	0.0639

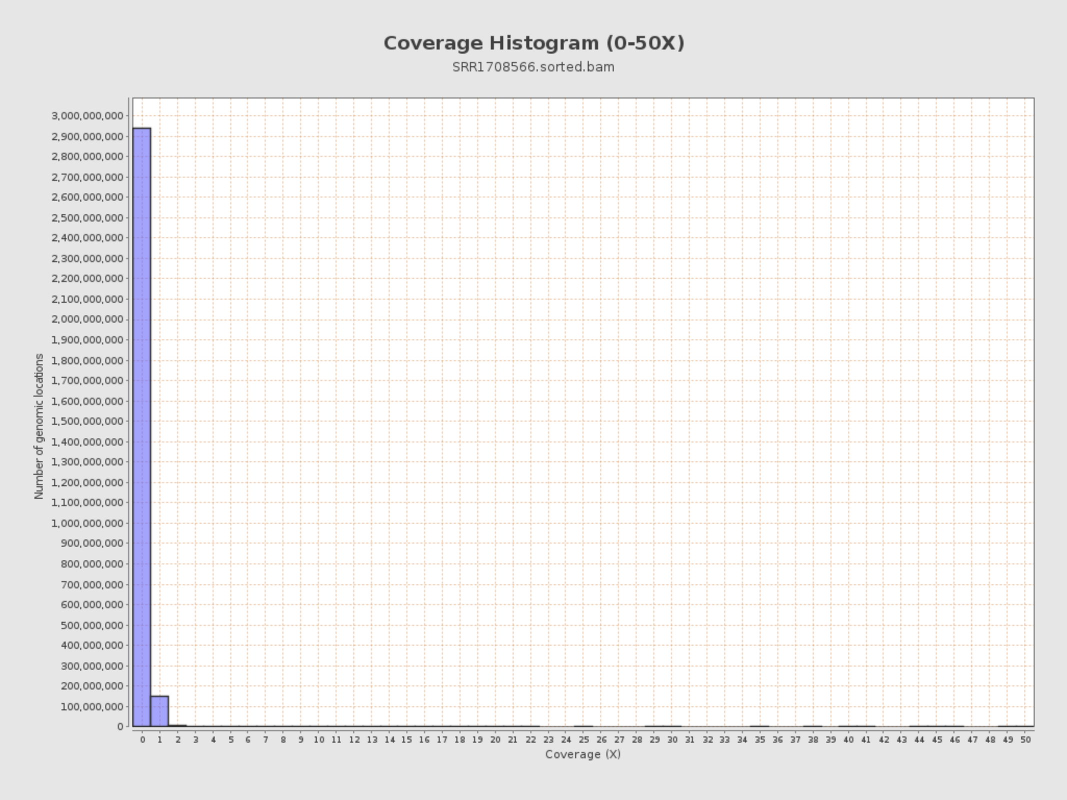
3. Results : Coverage across reference



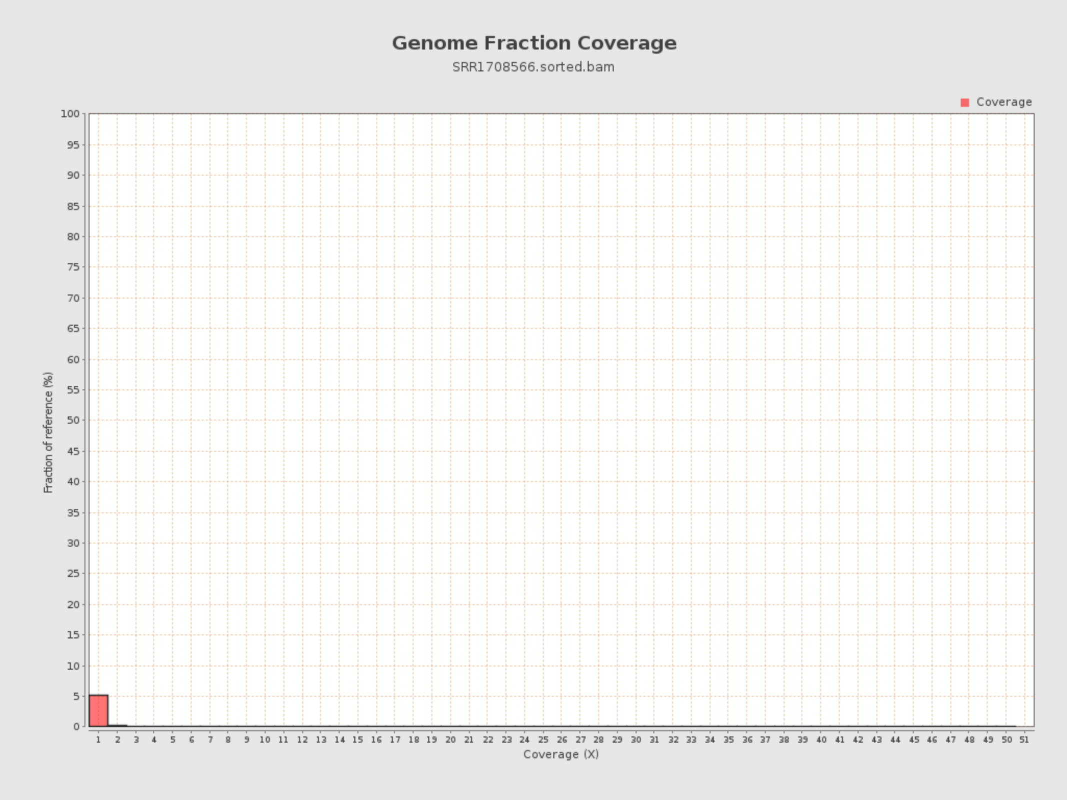
4. Results : Coverage Histogram



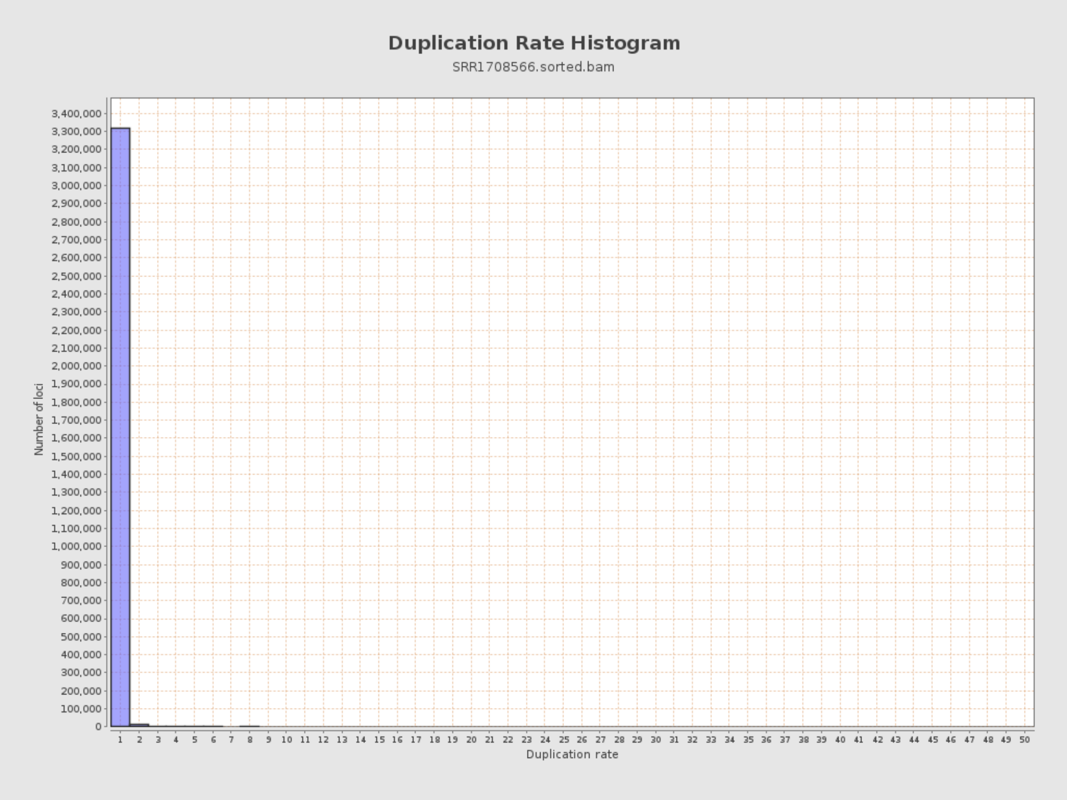
5. Results : Coverage Histogram (0-50X)



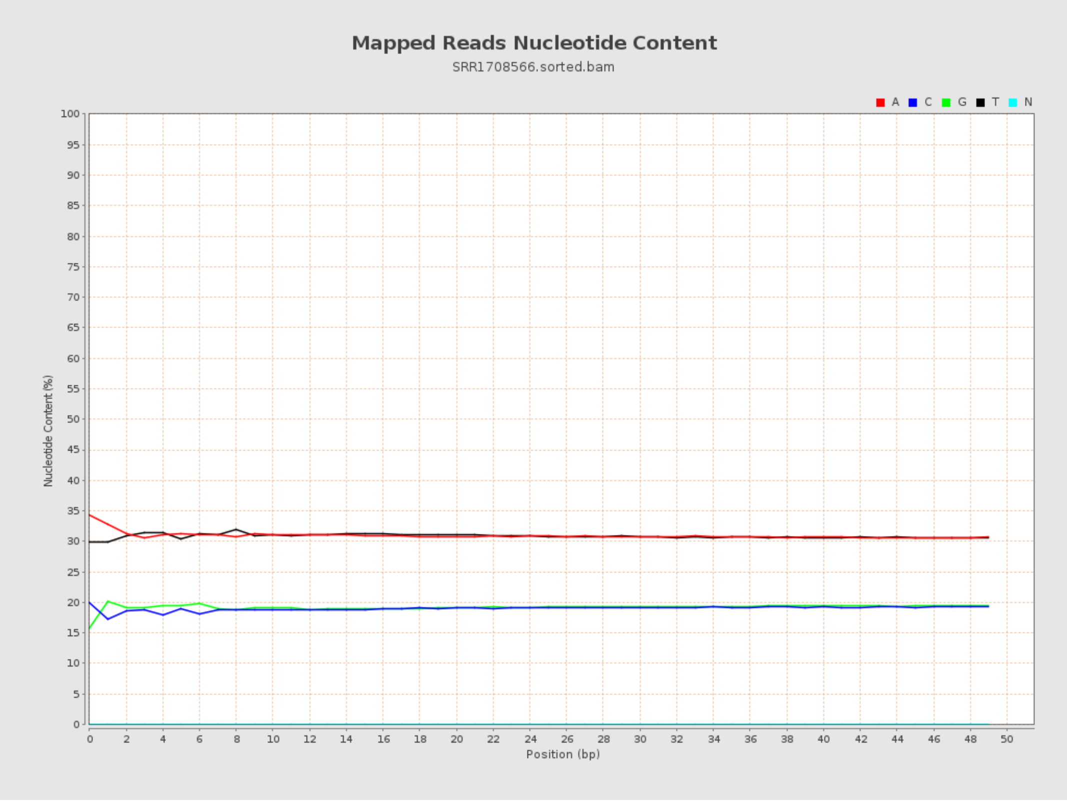
6. Results : Genome Fraction Coverage



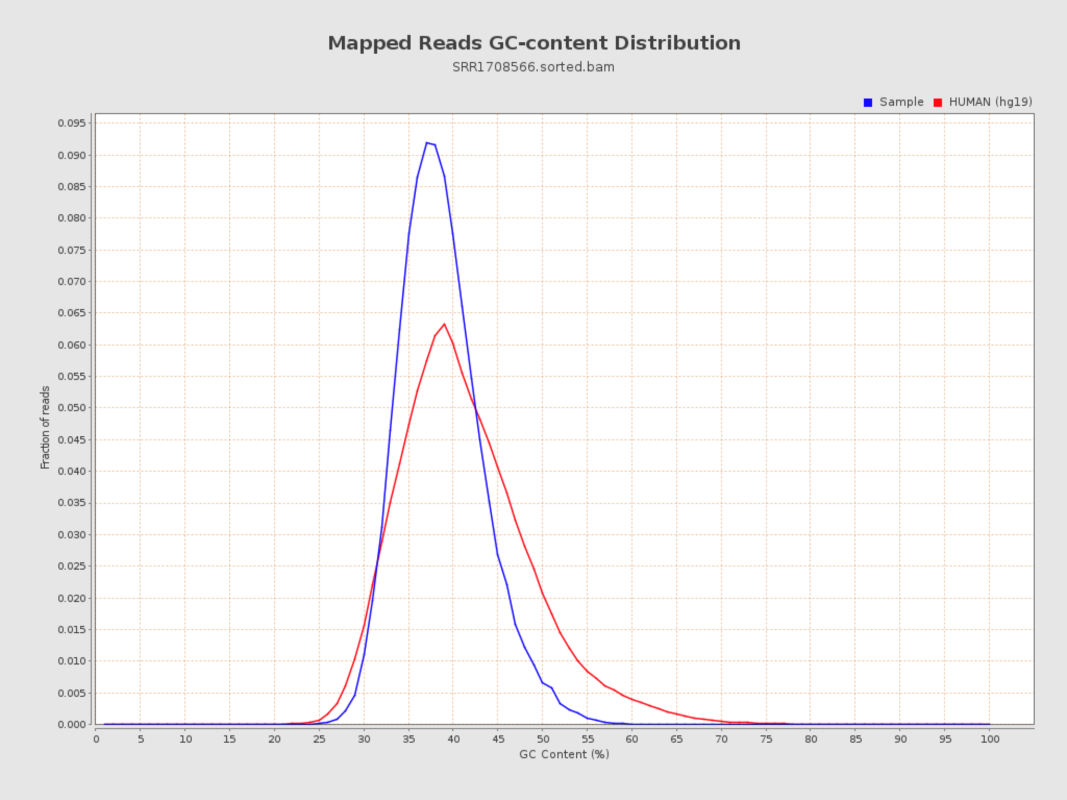
7. Results : Duplication Rate Histogram



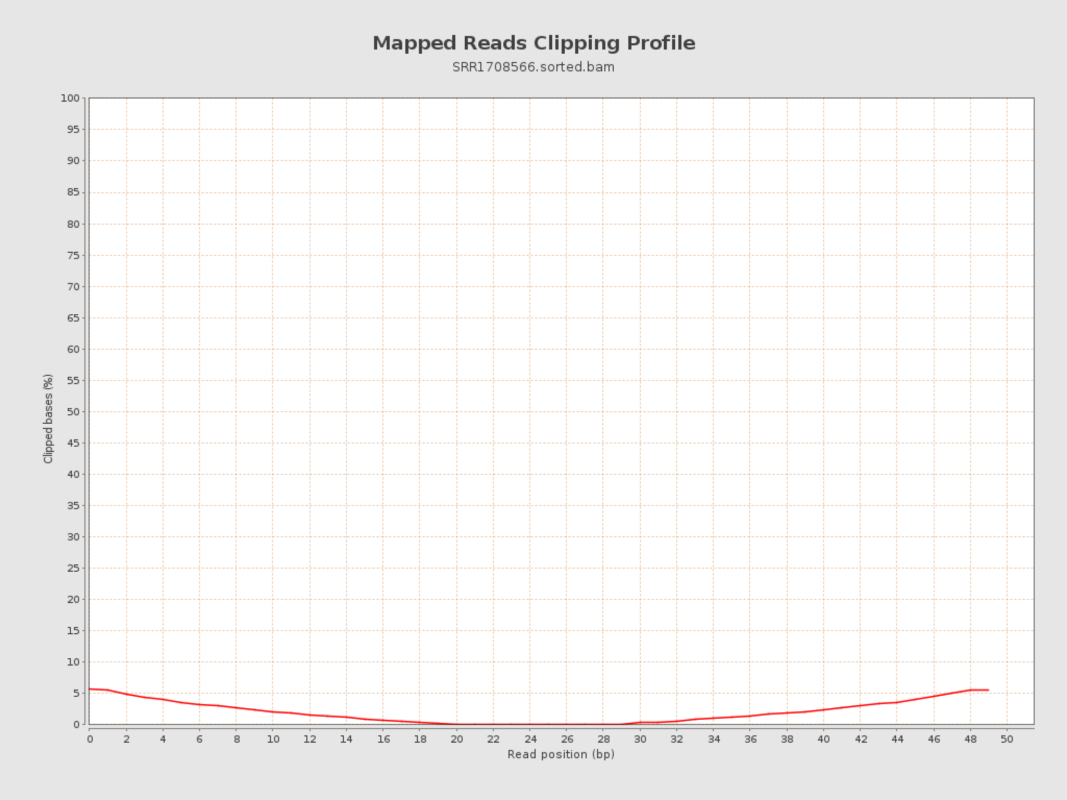
8. Results : Mapped Reads Nucleotide Content



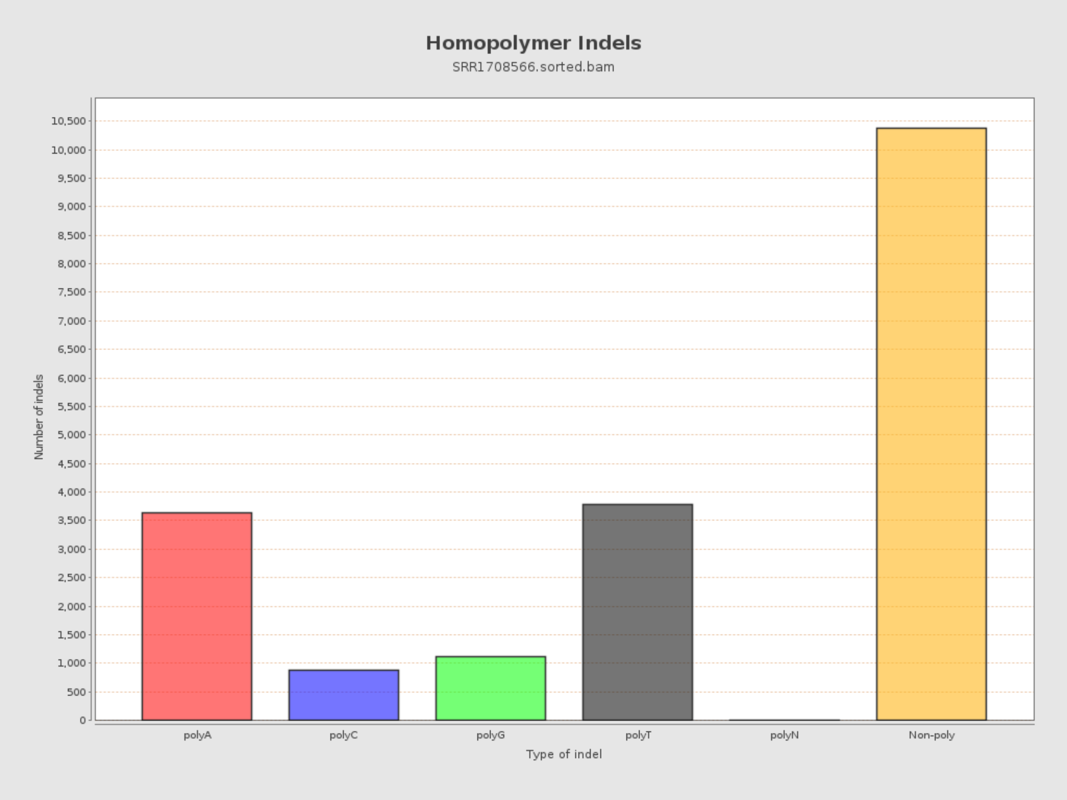
9. Results : Mapped Reads GC-content Distribution



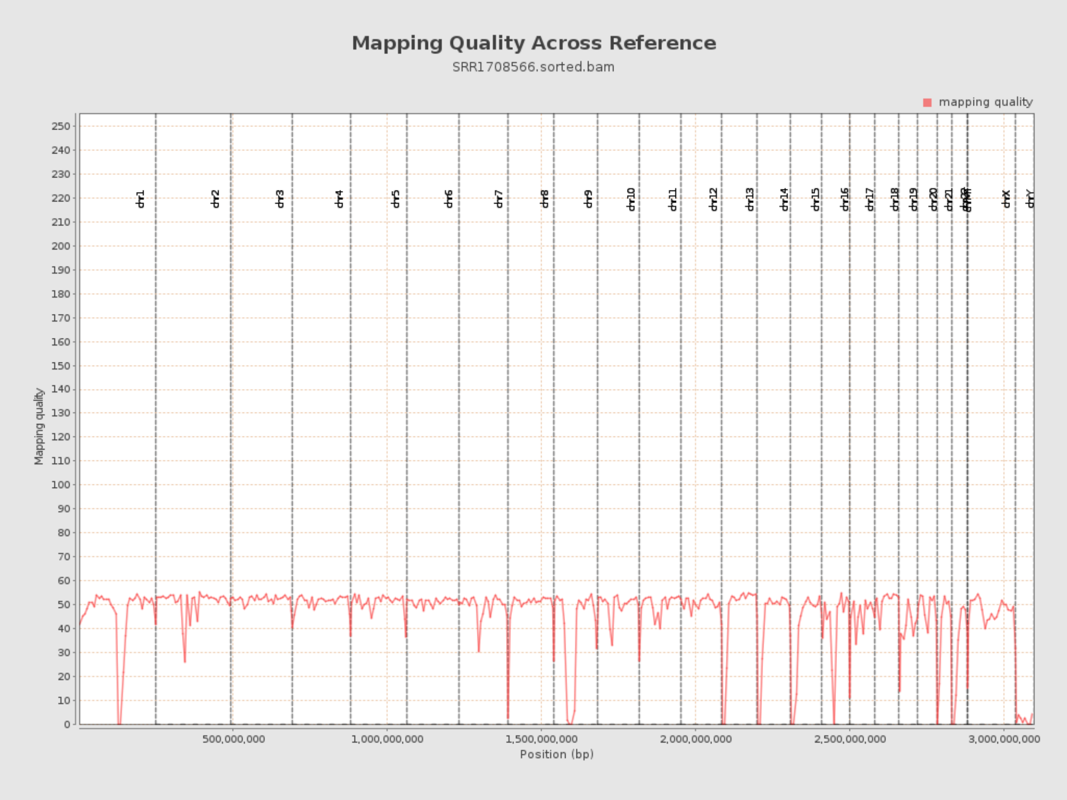
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram