Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:08:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708586.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_SRR1708586 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708586.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:08:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708586.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,782,186
Mapped reads	6,562,919 / 96.77%
Unmapped reads	219,267 / 3.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	174 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	67,922 / 1%
Duplication rate	1.03%
Clipped reads	85,527 / 1.26%

2.2. ACGT Content

Number/percentage of A's	101,370,618 / 30.97%
Number/percentage of C's	62,083,566 / 18.97%
Number/percentage of T's	100,861,626 / 30.81%
Number/percentage of G's	63,013,664 / 19.25%
Number/percentage of N's	12,012 / 0%
GC Percentage	38.22%

2.3. Coverage

Mean	0.1057

Standard Deviation	0.3426

2.4. Mapping Quality

Mean Mapping Quality	46.75

2.5. Mismatches and indels

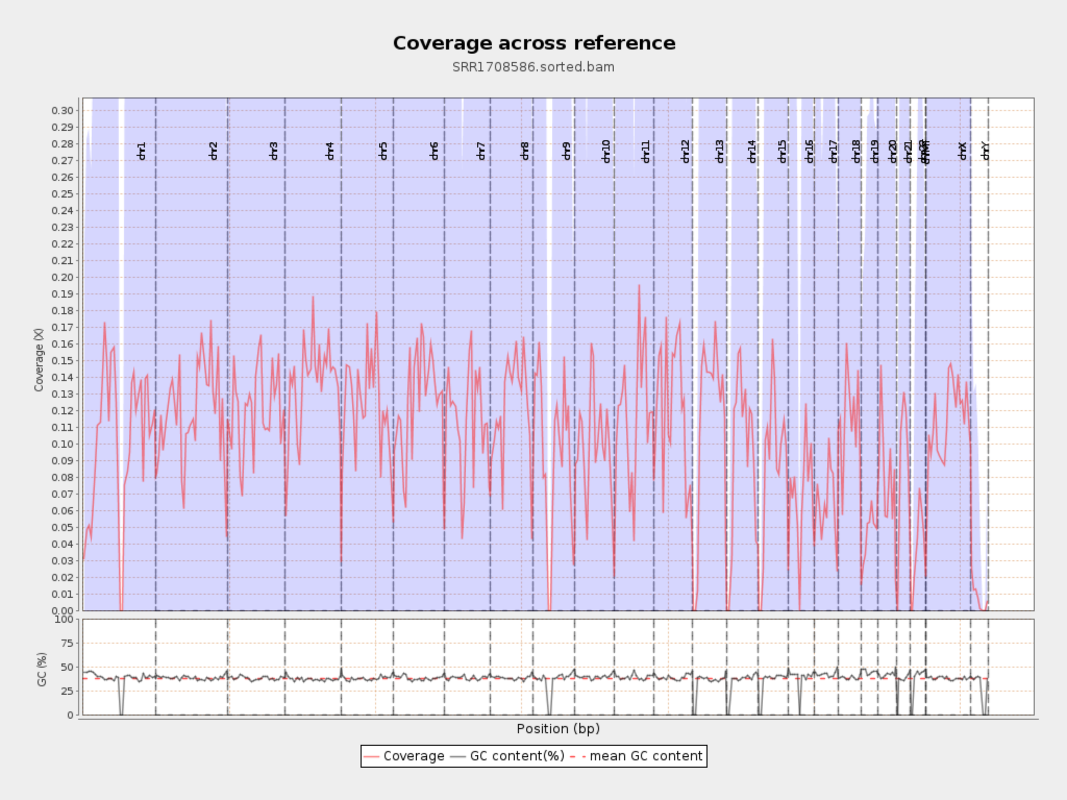
General error rate	0.15%
Mismatches	469,969
Insertions	20,410
Mapped reads with at least one insertion	0.31%
Deletions	16,602
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.87%

2.6. Chromosome stats

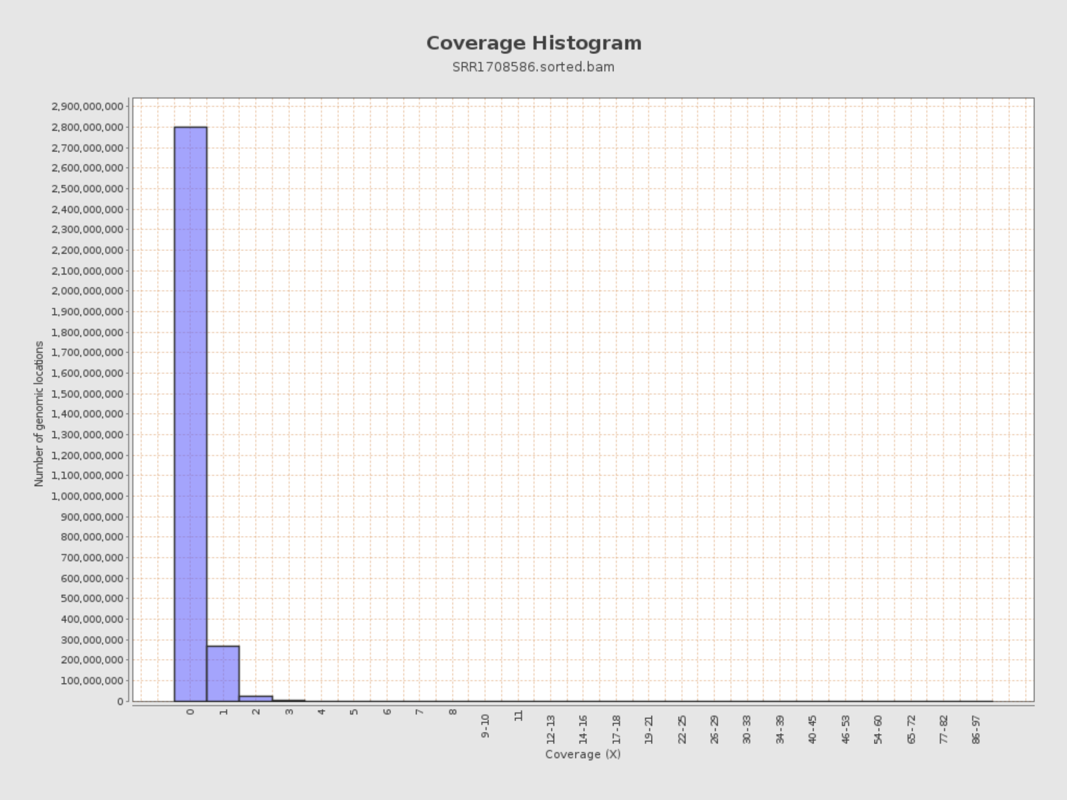
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25322156	0.1016	0.339
chr2	243199373	29001737	0.1193	0.3617
chr3	198022430	24039714	0.1214	0.3638
chr4	191154276	26074436	0.1364	0.3856
chr5	180915260	22110744	0.1222	0.3657
chr6	171115067	21780572	0.1273	0.3739
chr7	159138663	17951612	0.1128	0.3526

chr8	146364022	17947367	0.1226	0.3663
chr9	141213431	13393197	0.0948	0.3246
chr10	135534747	13672237	0.1009	0.332
chr11	135006516	15727738	0.1165	0.3624
chr12	133851895	15993410	0.1195	0.364
chr13	115169878	13121676	0.1139	0.357
chr14	107349540	10055008	0.0937	0.323
chr15	102531392	8791725	0.0857	0.3101
chr16	90354753	6113872	0.0677	0.273
chr17	81195210	5278367	0.065	0.2683
chr18	78077248	9022925	0.1156	0.3559
chr19	59128983	2784804	0.0471	0.2261
chr20	63025520	5194539	0.0824	0.302
chr21	48129895	3947247	0.082	0.3046
chr22	51304566	1948343	0.038	0.2044
chrMT	16571	432	0.0261	0.1593
chrX	155270560	17659043	0.1137	0.3531
chrY	59373566	436528	0.0074	0.0918

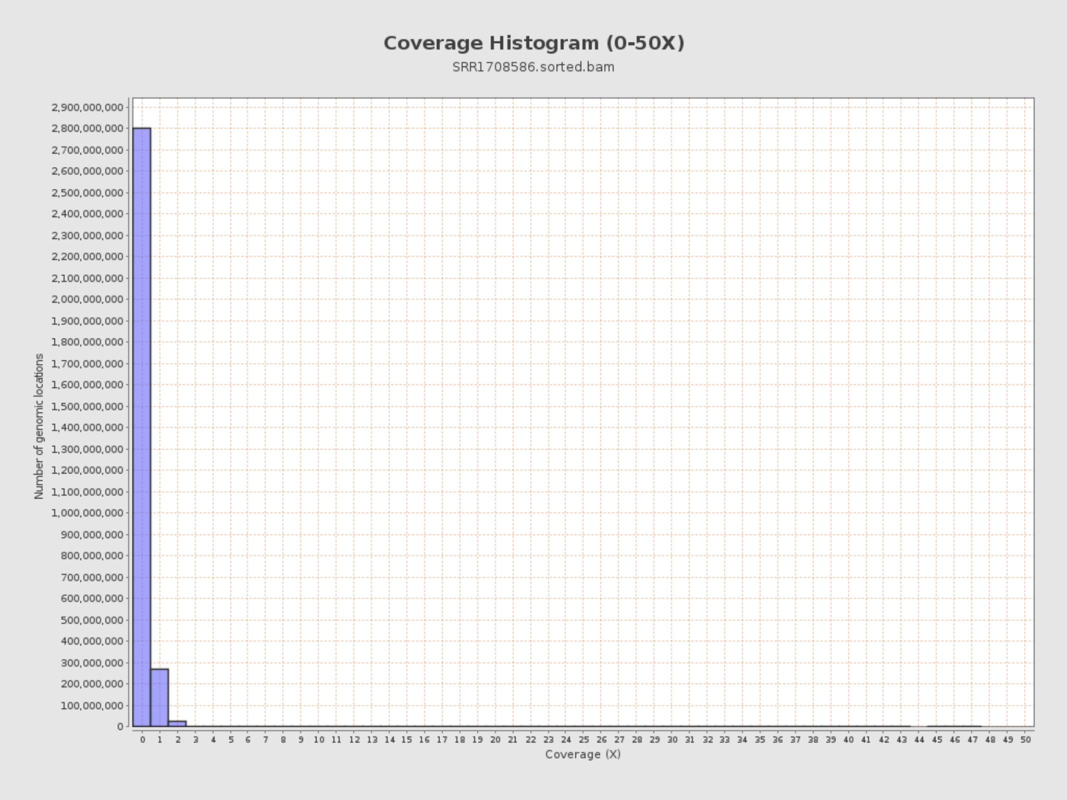
3. Results : Coverage across reference



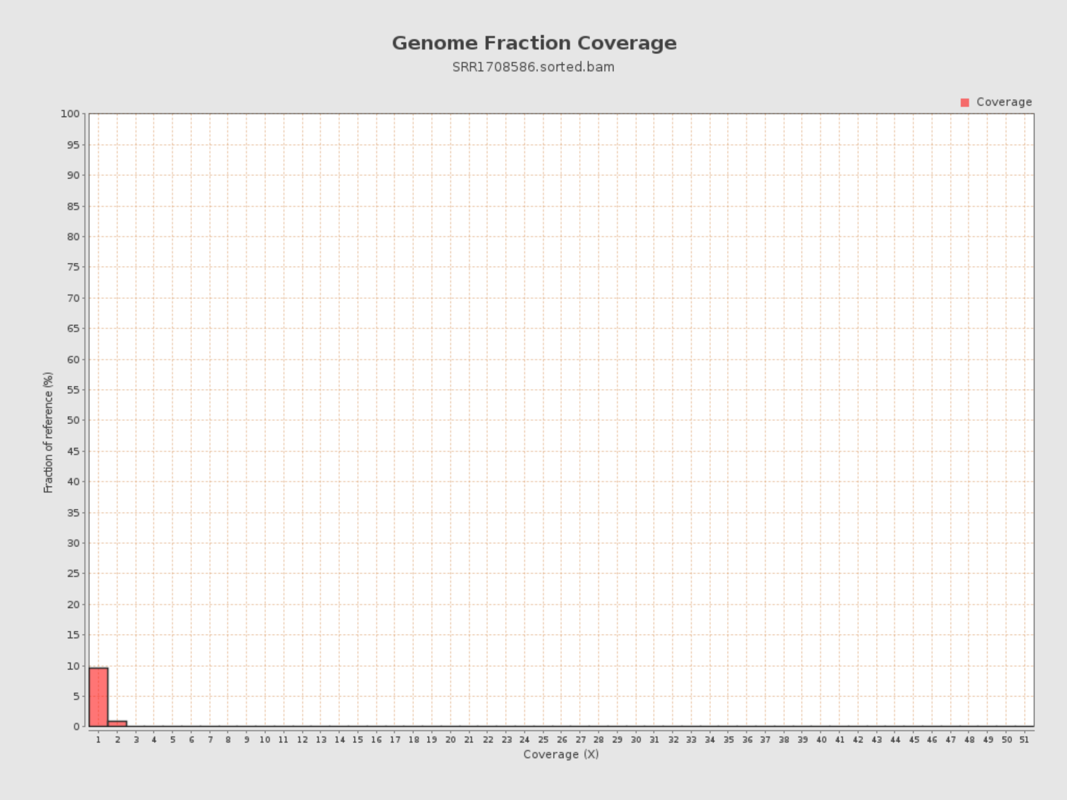
4. Results : Coverage Histogram



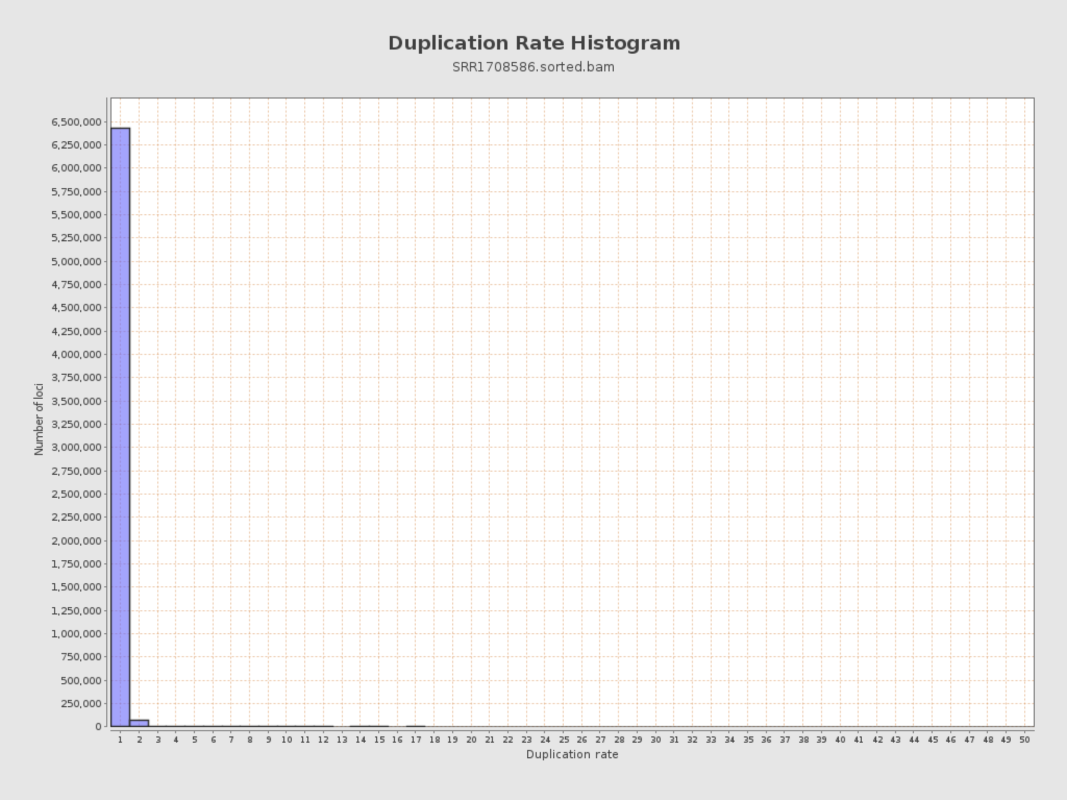
5. Results : Coverage Histogram (0-50X)



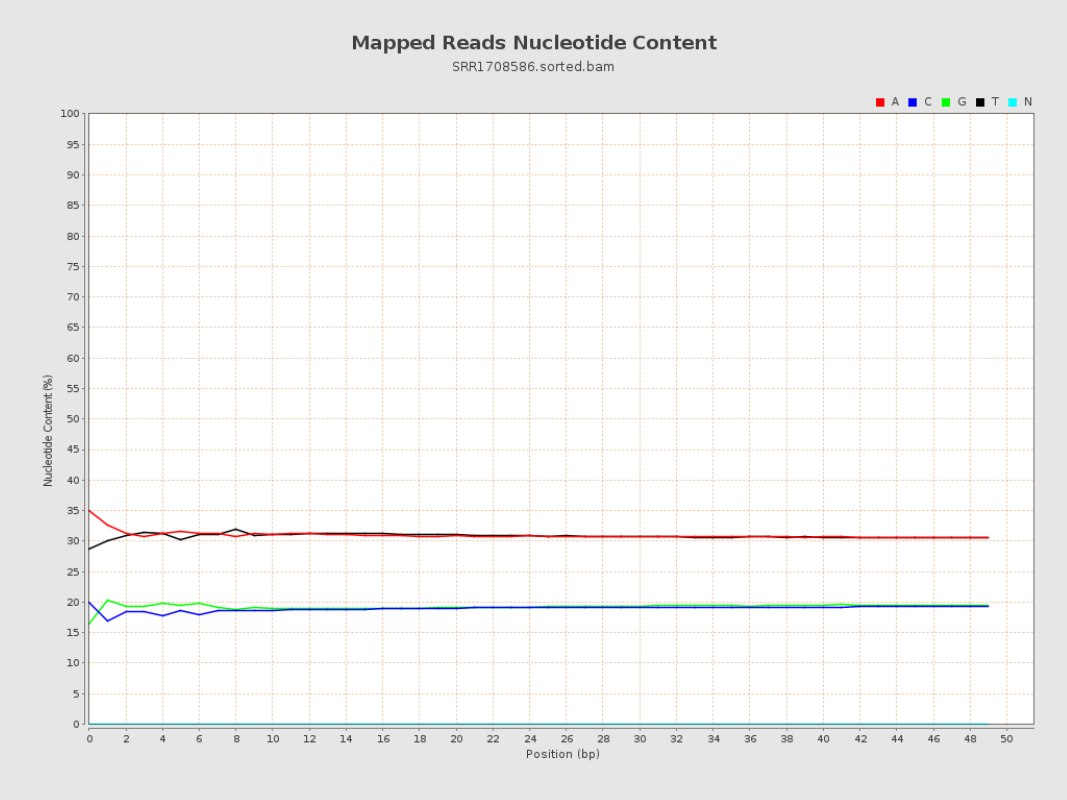
6. Results : Genome Fraction Coverage



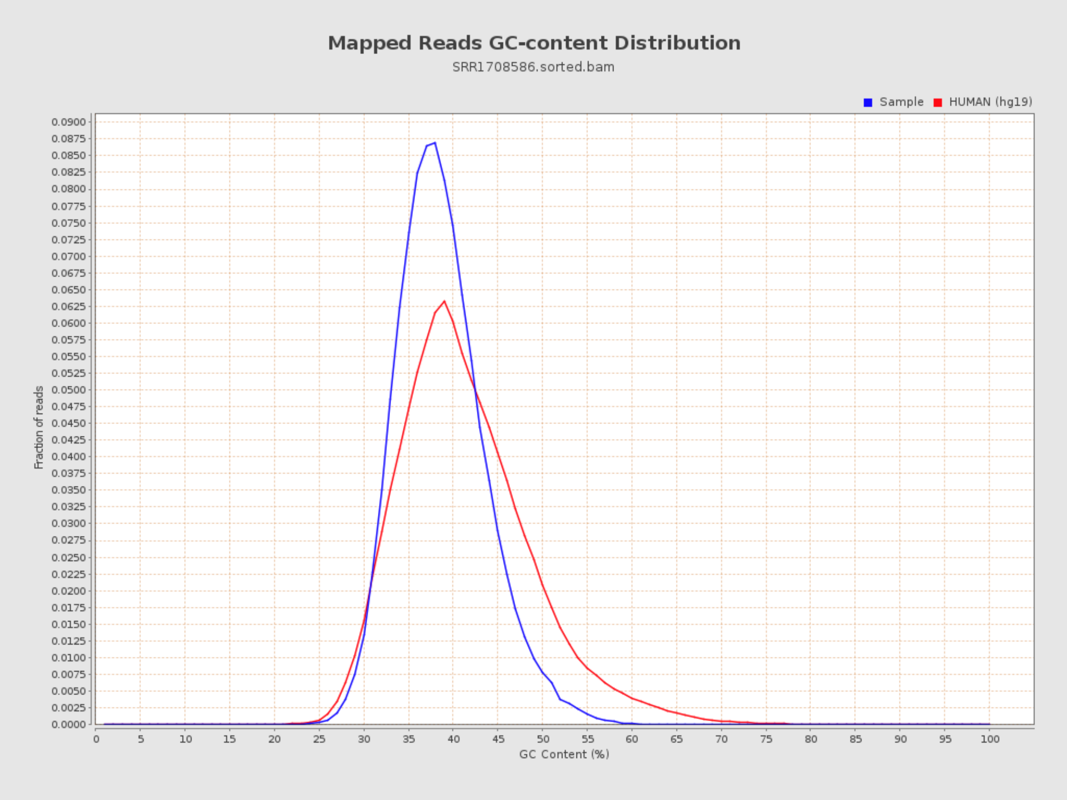
7. Results : Duplication Rate Histogram



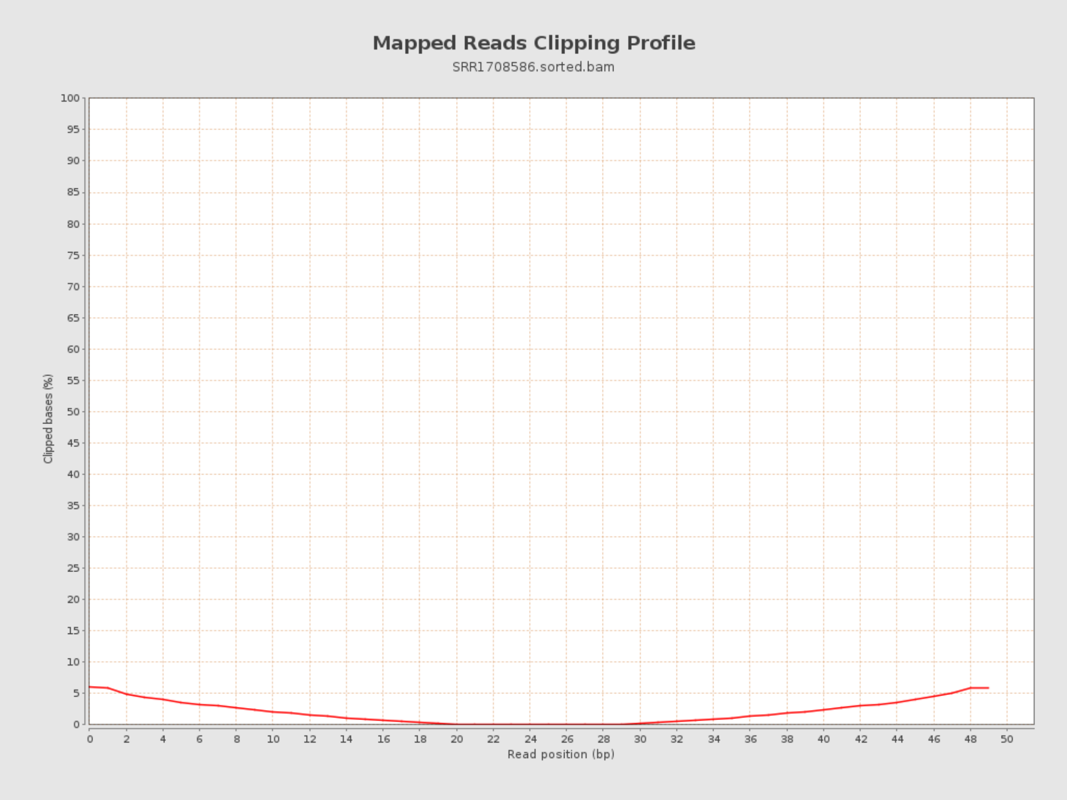
8. Results : Mapped Reads Nucleotide Content



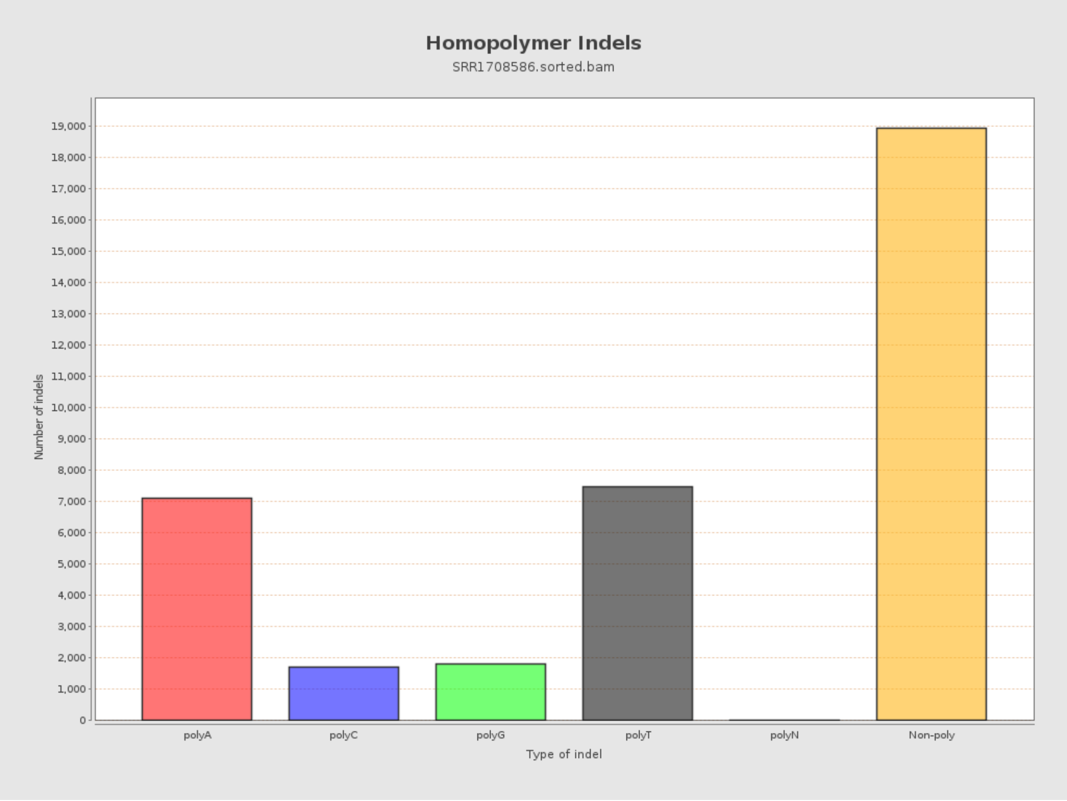
9. Results : Mapped Reads GC-content Distribution



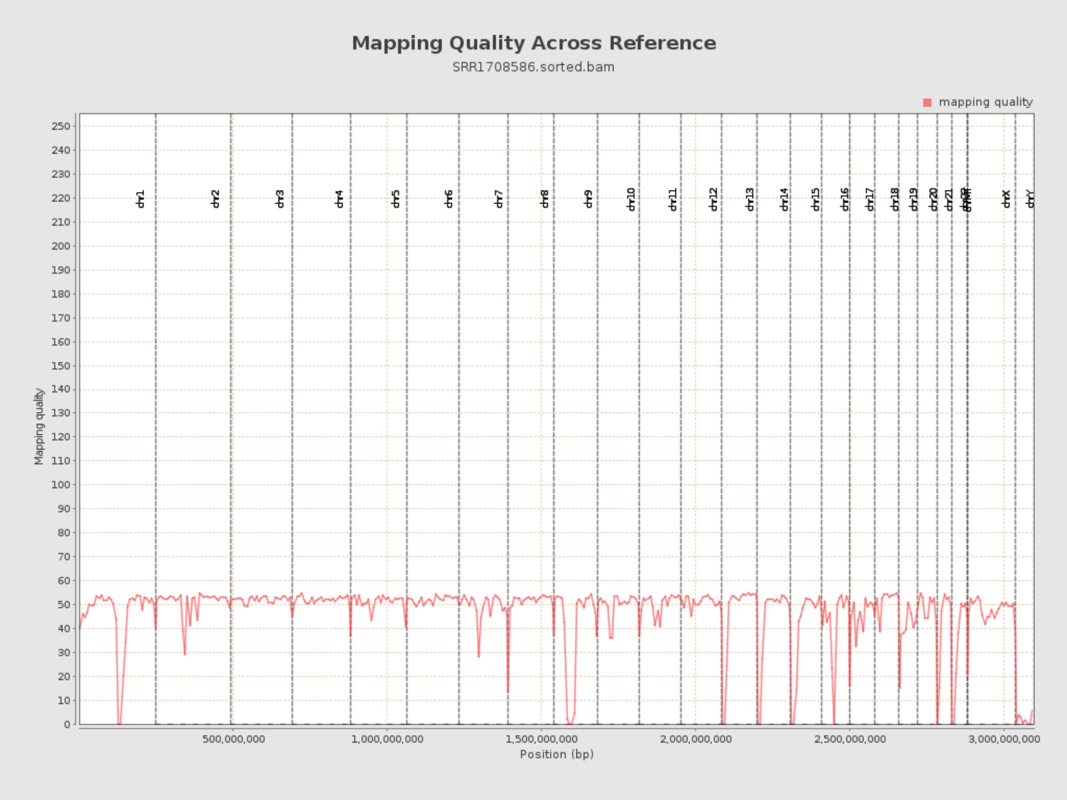
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram