Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:58:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708606.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_SRR1708606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708606.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:58:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,182,410
Mapped reads	5,085,868 / 98.14%
Unmapped reads	96,542 / 1.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	151 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	50,961 / 0.98%
Duplication rate	1%
Clipped reads	68,004 / 1.31%

2.2. ACGT Content

Number/percentage of A's	78,756,455 / 31.05%
Number/percentage of C's	47,969,495 / 18.91%
Number/percentage of T's	78,177,968 / 30.82%
Number/percentage of G's	48,740,966 / 19.22%
Number/percentage of N's	9,250 / 0%
GC Percentage	38.13%

2.3. Coverage

Mean	0.0819

Standard Deviation	0.3003

2.4. Mapping Quality

Mean Mapping Quality	46.86

2.5. Mismatches and indels

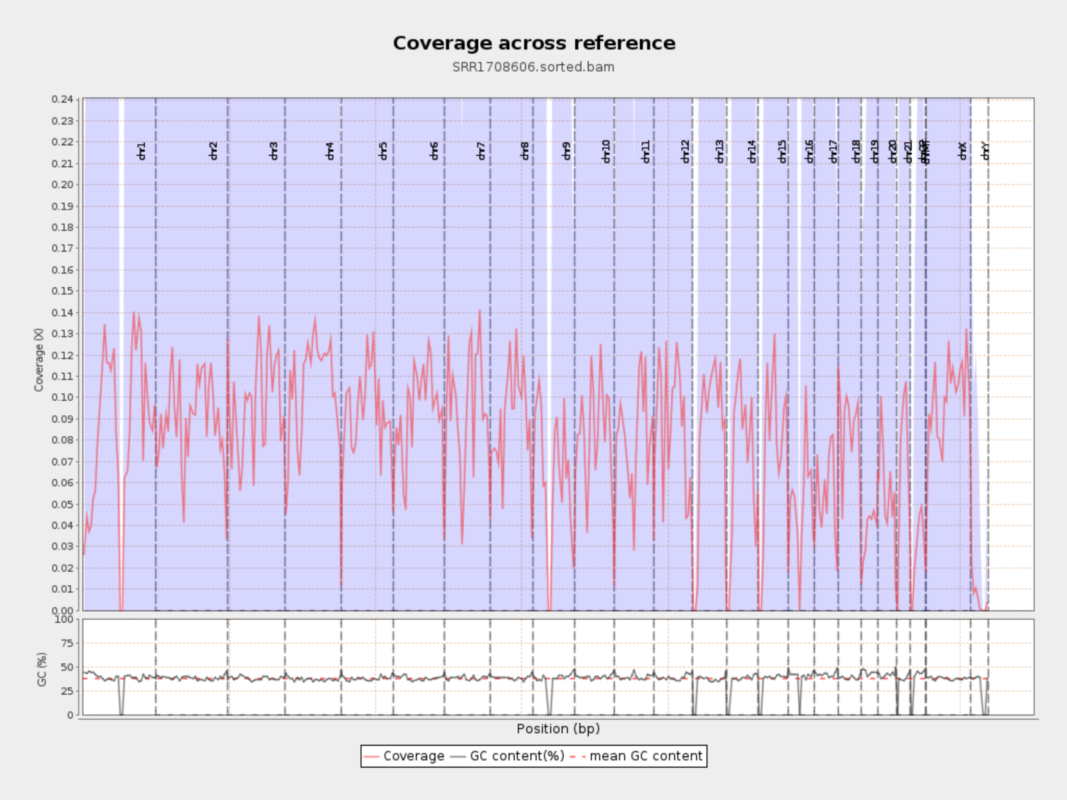
General error rate	0.16%
Mismatches	373,813
Insertions	15,843
Mapped reads with at least one insertion	0.31%
Deletions	12,903
Mapped reads with at least one deletion	0.25%
Homopolymer indels	49.04%

2.6. Chromosome stats

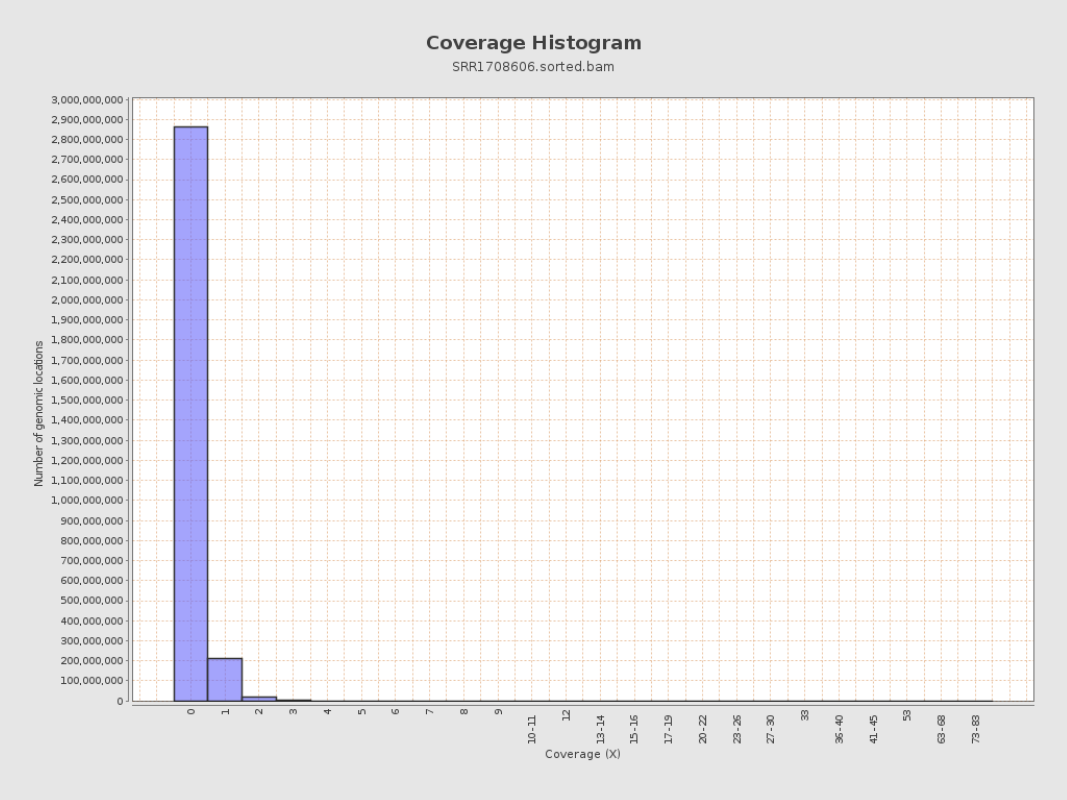
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21256770	0.0853	0.3092
chr2	243199373	21883676	0.09	0.3132
chr3	198022430	19315610	0.0975	0.3256
chr4	191154276	20126485	0.1053	0.3392
chr5	180915260	16751419	0.0926	0.3167
chr6	171115067	16122000	0.0942	0.3201
chr7	159138663	14844149	0.0933	0.3206

chr8	146364022	13281108	0.0907	0.314
chr9	141213431	9039312	0.064	0.2646
chr10	135534747	11496231	0.0848	0.3039
chr11	135006516	10909520	0.0808	0.2982
chr12	133851895	11694937	0.0874	0.3094
chr13	115169878	9513652	0.0826	0.3015
chr14	107349540	7610881	0.0709	0.2803
chr15	102531392	7657848	0.0747	0.2891
chr16	90354753	4460389	0.0494	0.2317
chr17	81195210	4574993	0.0563	0.2483
chr18	78077248	6769671	0.0867	0.3059
chr19	59128983	2255879	0.0382	0.2028
chr20	63025520	3696574	0.0587	0.2537
chr21	48129895	3193240	0.0663	0.2732
chr22	51304566	1458059	0.0284	0.1757
chrMT	16571	300	0.0181	0.1543
chrX	155270560	15422157	0.0993	0.33
chrY	59373566	341386	0.0057	0.08

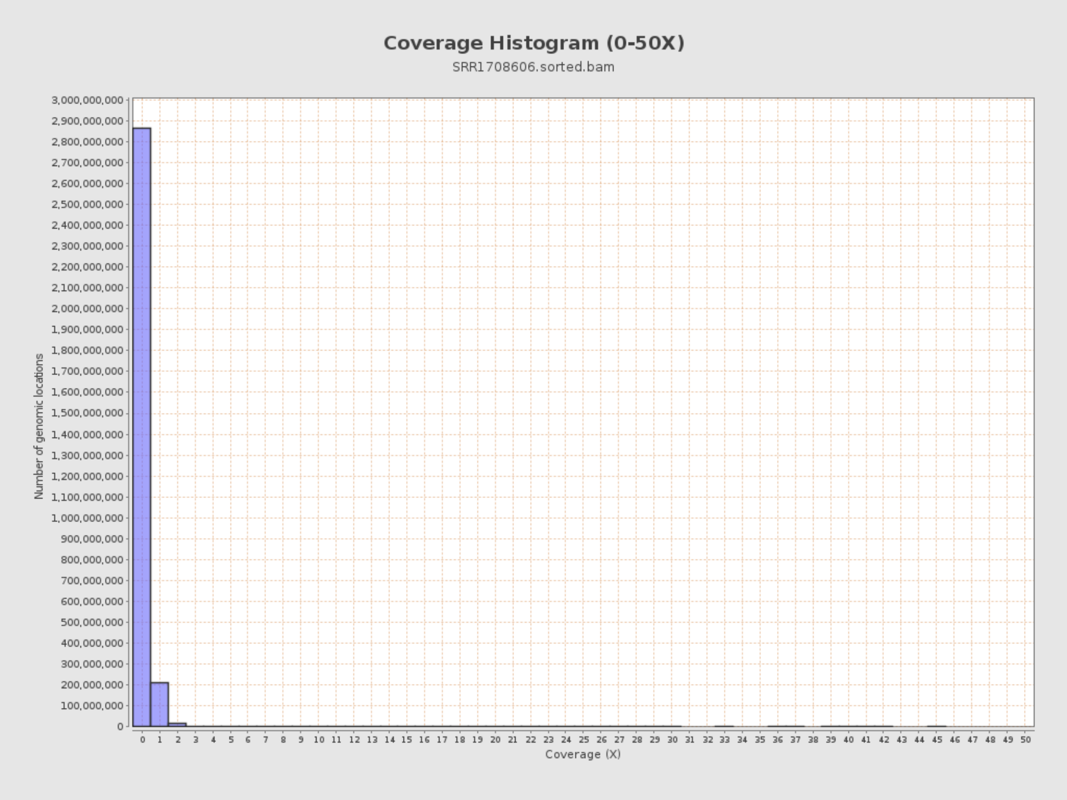
3. Results : Coverage across reference



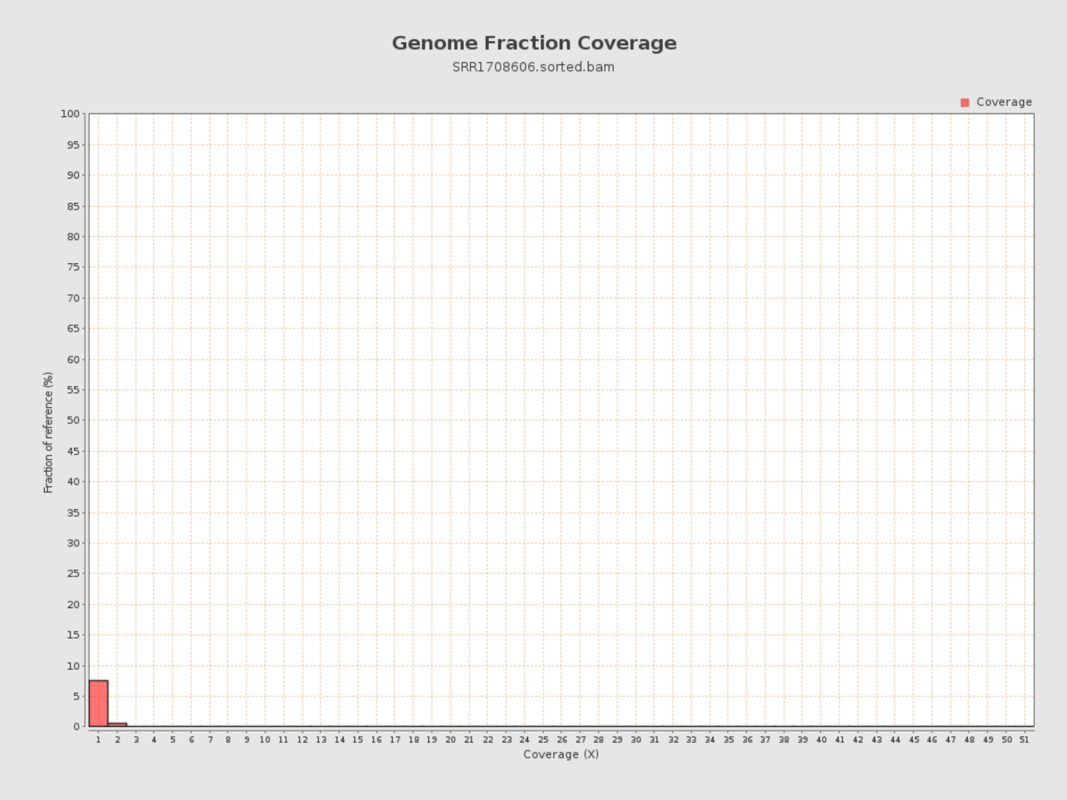
4. Results : Coverage Histogram



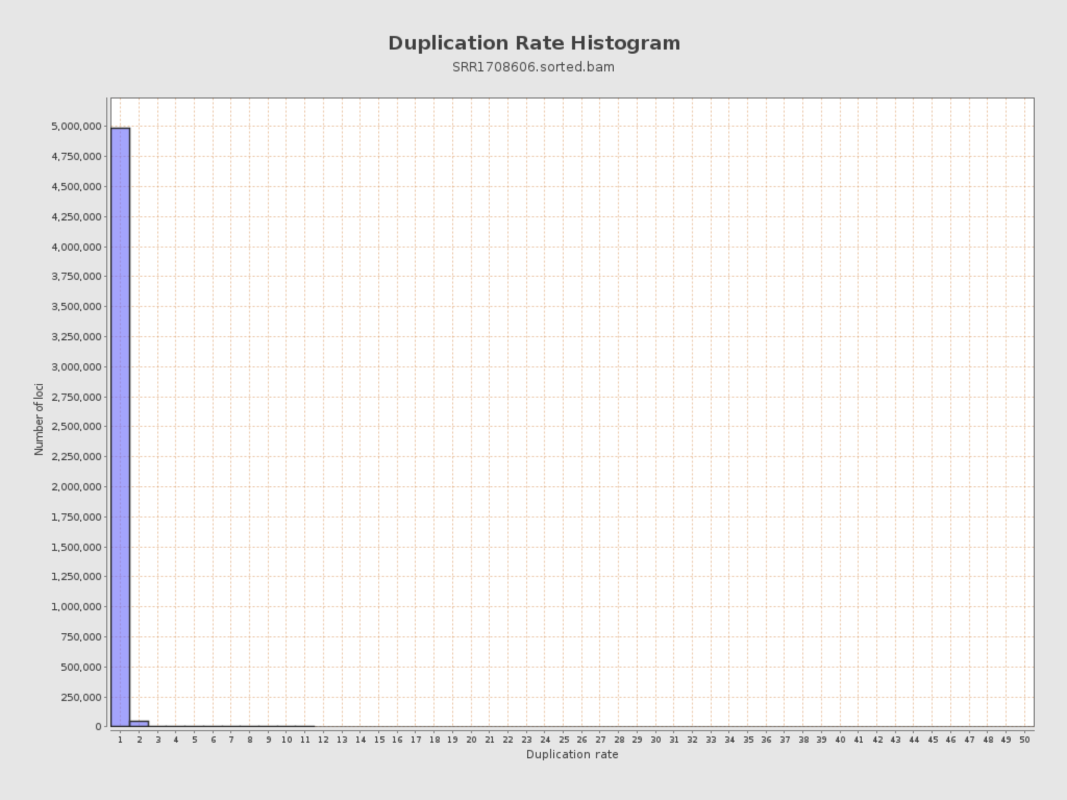
5. Results : Coverage Histogram (0-50X)



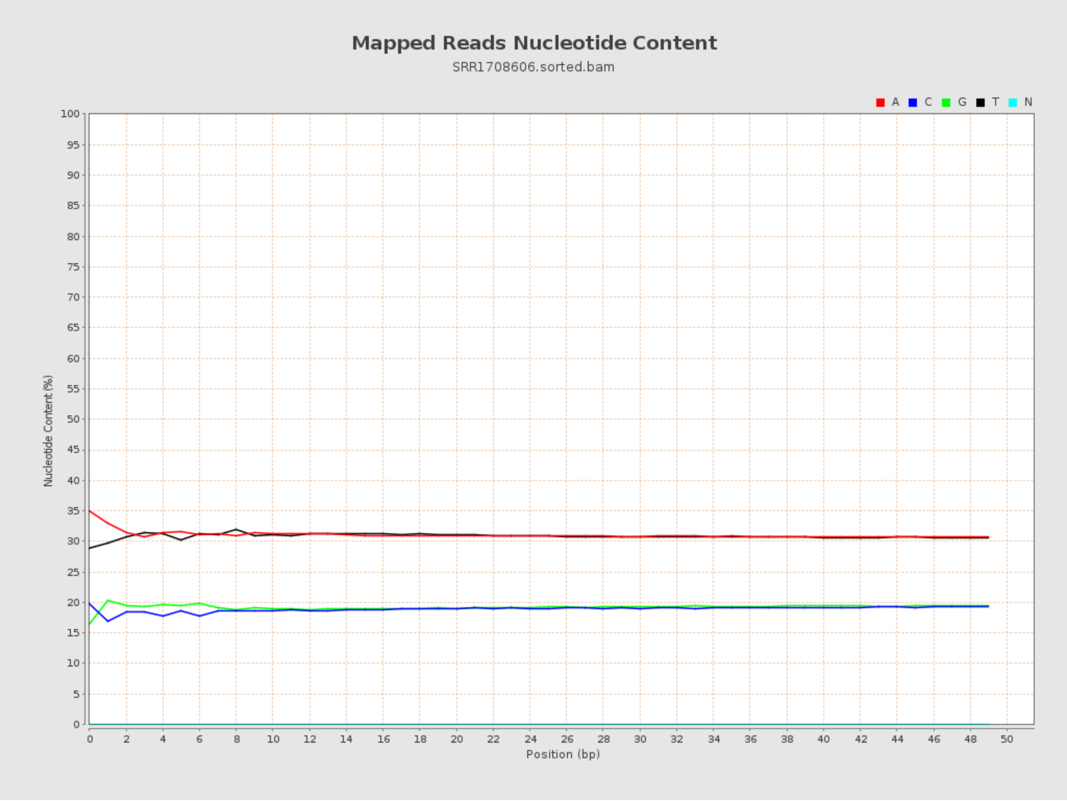
6. Results : Genome Fraction Coverage



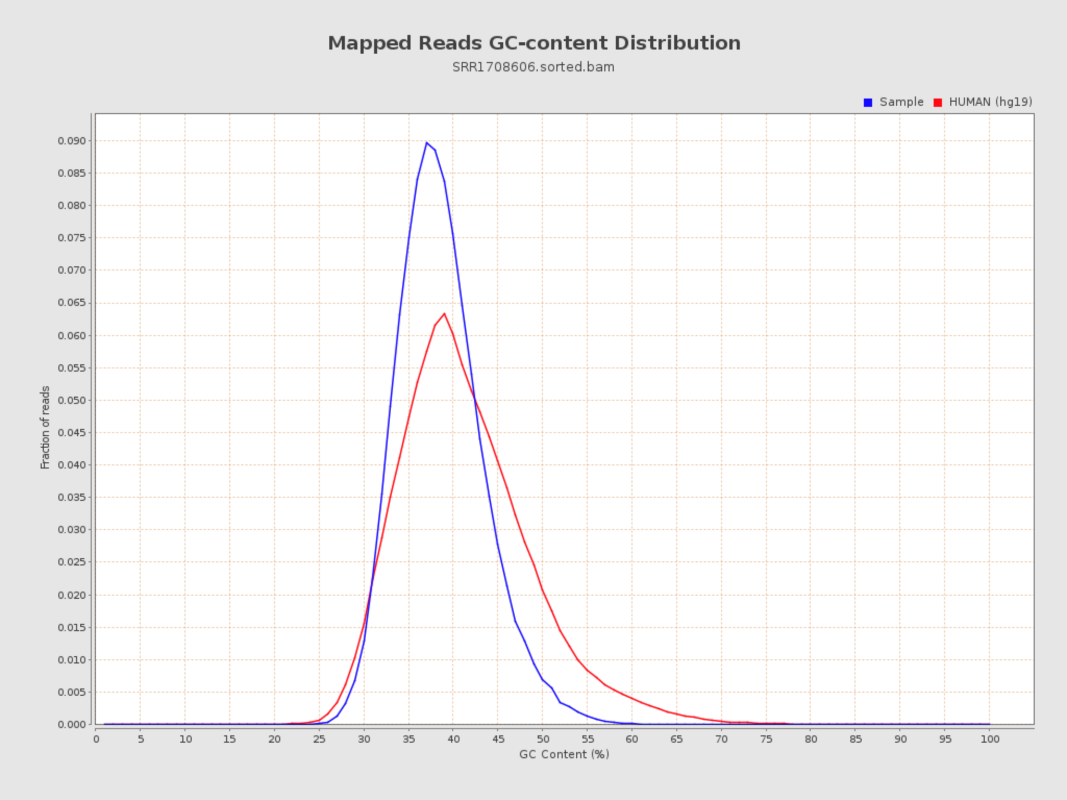
7. Results : Duplication Rate Histogram



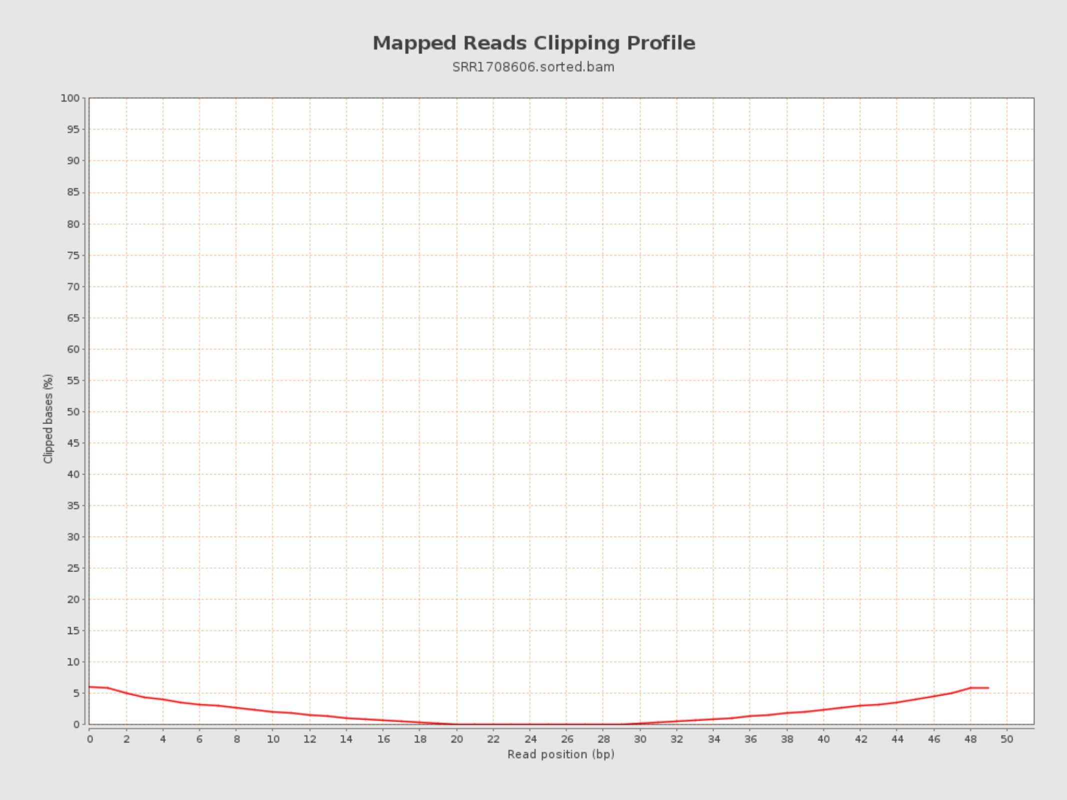
8. Results : Mapped Reads Nucleotide Content



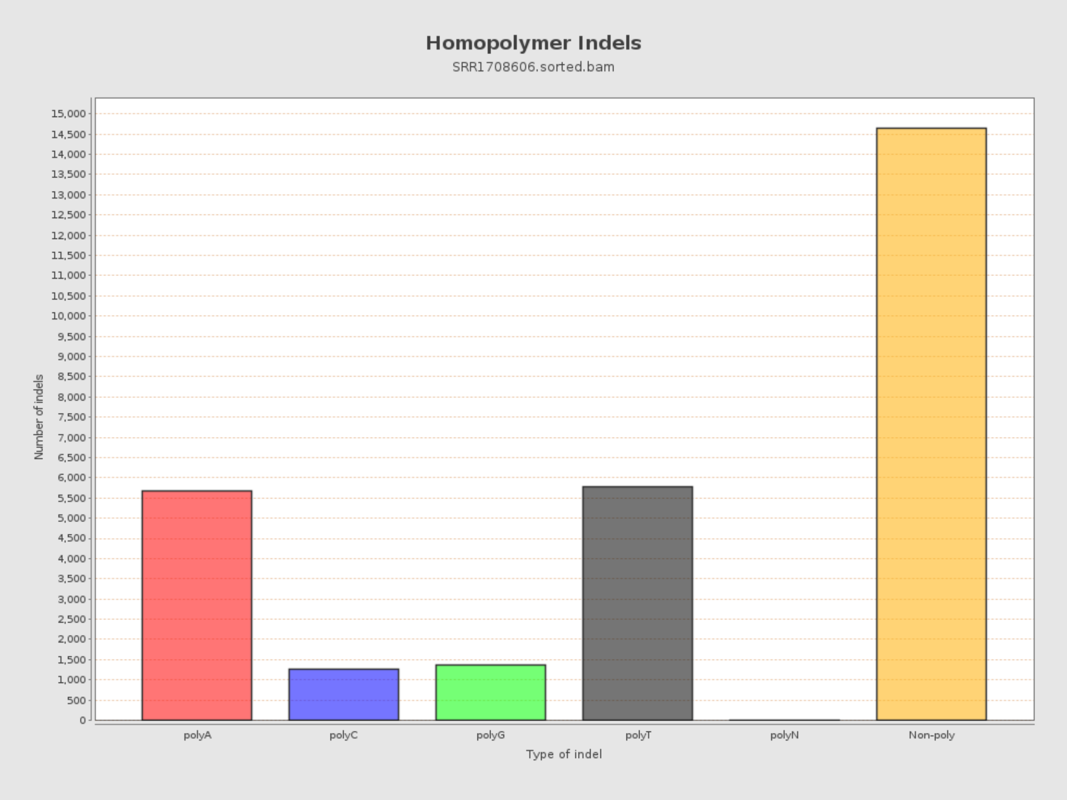
9. Results : Mapped Reads GC-content Distribution



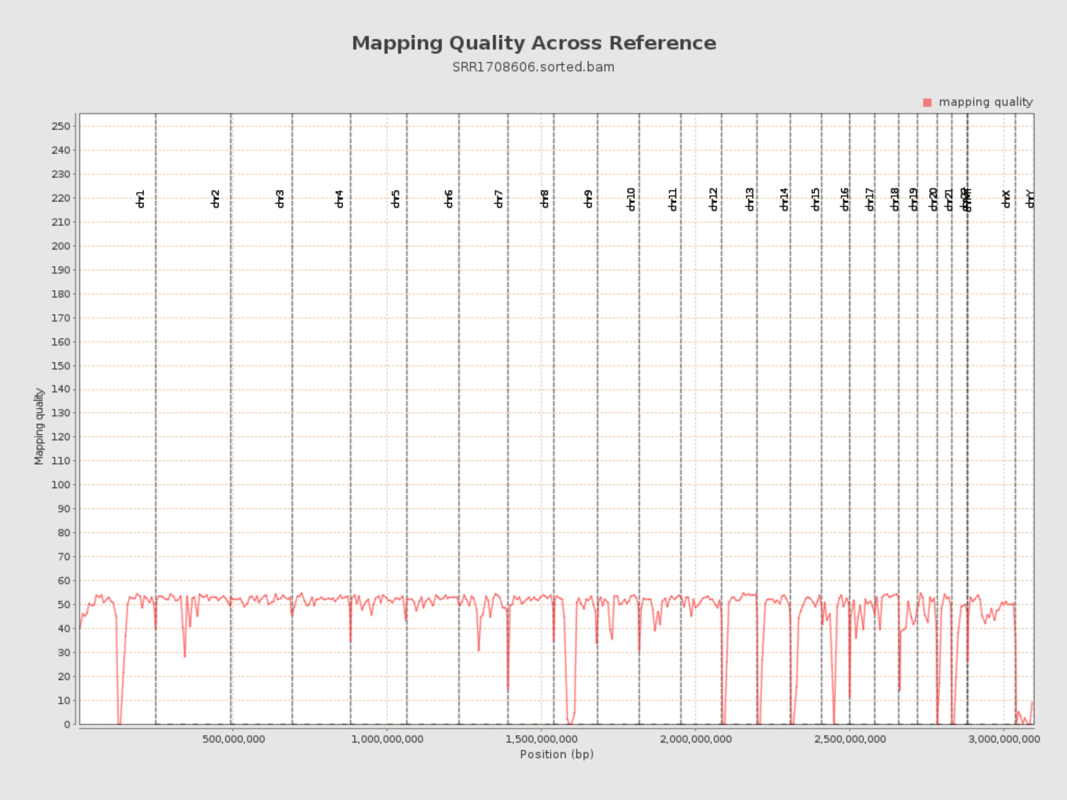
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram