Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:20:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063595.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_SRR6063595 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063595.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:20:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063595.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,947,506
Mapped reads	1,610,275 / 82.68%
Unmapped reads	337,231 / 17.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,253 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	257,437 / 13.22%
Duplication rate	12.64%
Clipped reads	916,750 / 47.07%

2.2. ACGT Content

Number/percentage of A's	27,746,931 / 27.09%
Number/percentage of C's	18,237,117 / 17.81%
Number/percentage of T's	33,555,973 / 32.77%
Number/percentage of G's	22,867,694 / 22.33%
Number/percentage of N's	2,496 / 0%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0331

Standard Deviation	0.3891

2.4. Mapping Quality

Mean Mapping Quality	46.3

2.5. Mismatches and indels

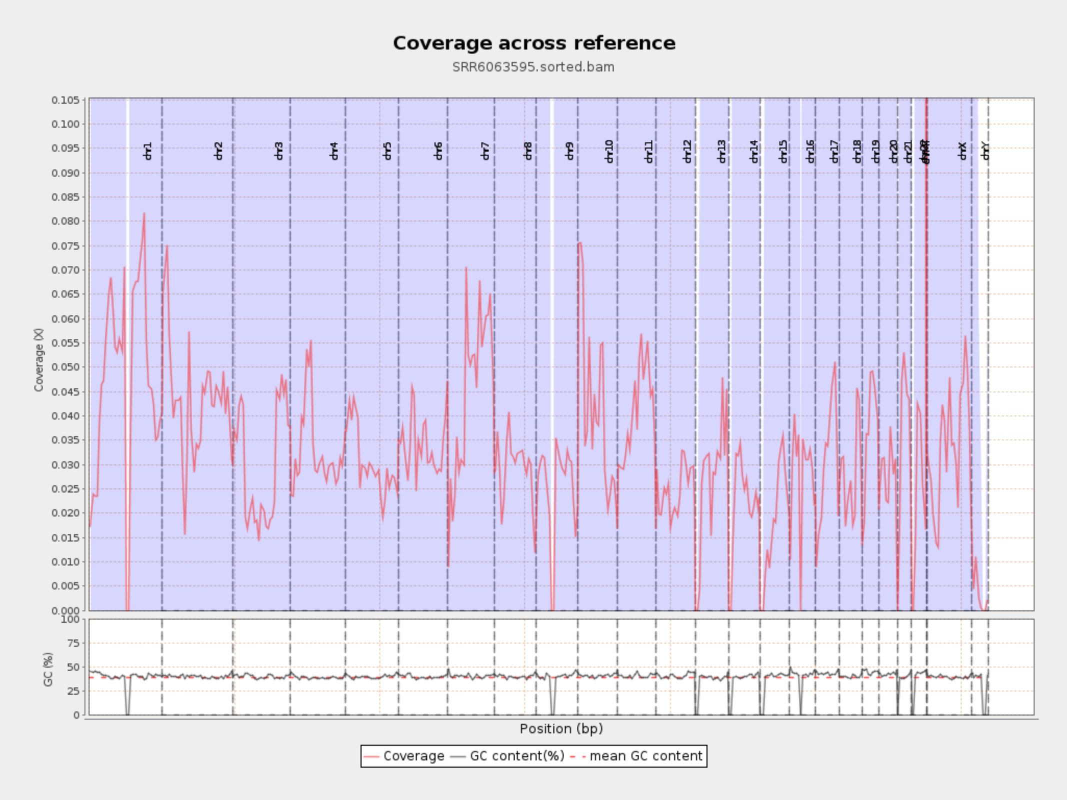
General error rate	0.94%
Mismatches	946,847
Insertions	7,037
Mapped reads with at least one insertion	0.43%
Deletions	31,147
Mapped reads with at least one deletion	1.91%
Homopolymer indels	49.26%

2.6. Chromosome stats

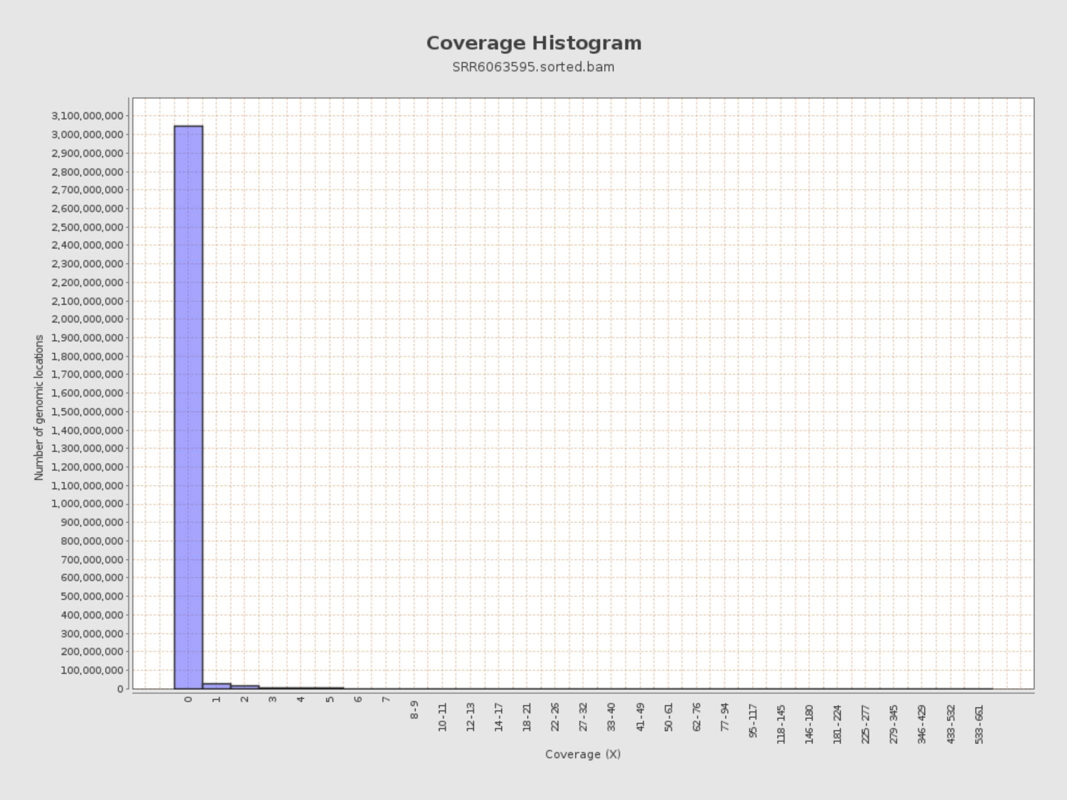
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11887765	0.0477	0.6577
chr2	243199373	10626032	0.0437	0.4001
chr3	198022430	5851427	0.0295	0.2907
chr4	191154276	6274701	0.0328	0.3072
chr5	180915260	5512627	0.0305	0.2929
chr6	171115067	5823737	0.034	0.3293
chr7	159138663	7233899	0.0455	0.627

chr8	146364022	4286416	0.0293	0.4576
chr9	141213431	3577712	0.0253	0.3168
chr10	135534747	5761236	0.0425	0.4052
chr11	135006516	5478513	0.0406	0.3852
chr12	133851895	3338698	0.0249	0.2668
chr13	115169878	3045222	0.0264	0.2743
chr14	107349540	2337582	0.0218	0.2655
chr15	102531392	1859282	0.0181	0.2227
chr16	90354753	2544735	0.0282	0.2851
chr17	81195210	2475794	0.0305	0.2993
chr18	78077248	2202526	0.0282	0.44
chr19	59128983	2202583	0.0373	0.4605
chr20	63025520	1769716	0.0281	0.2854
chr21	48129895	1699634	0.0353	0.324
chr22	51304566	1132610	0.0221	0.2454
chrMT	16571	51615	3.1148	4.0387
chrX	155270560	5286296	0.034	0.3192
chrY	59373566	204412	0.0034	0.0989

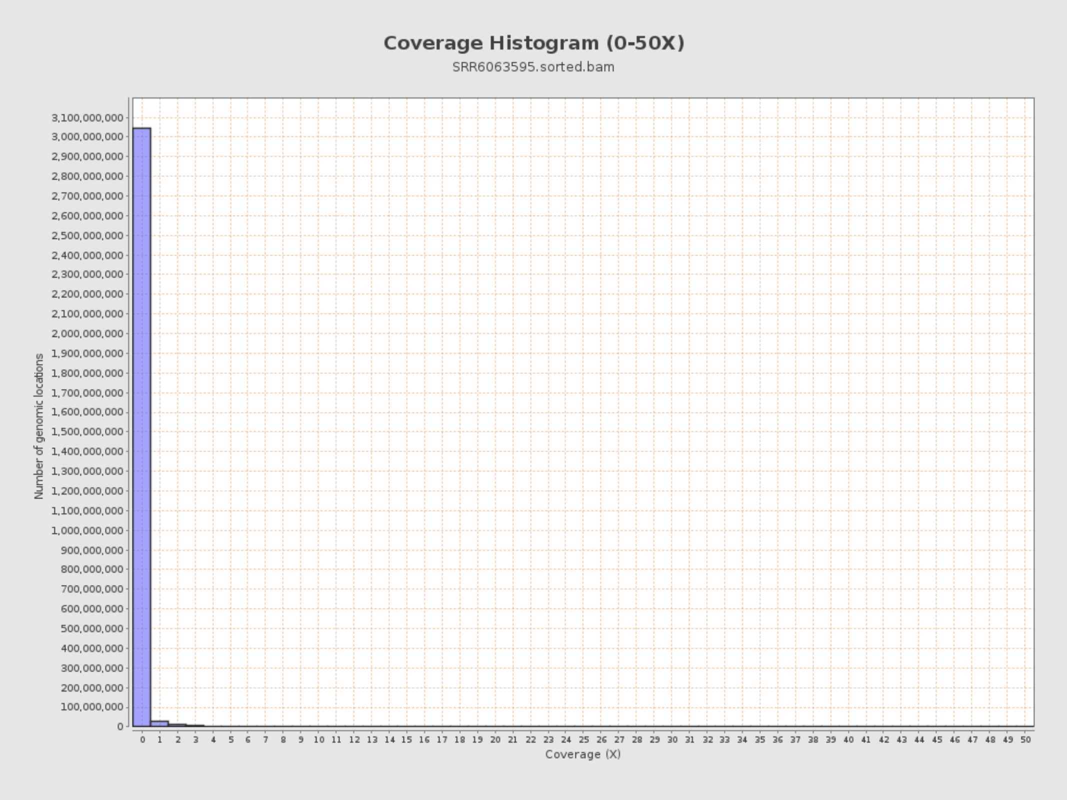
3. Results : Coverage across reference



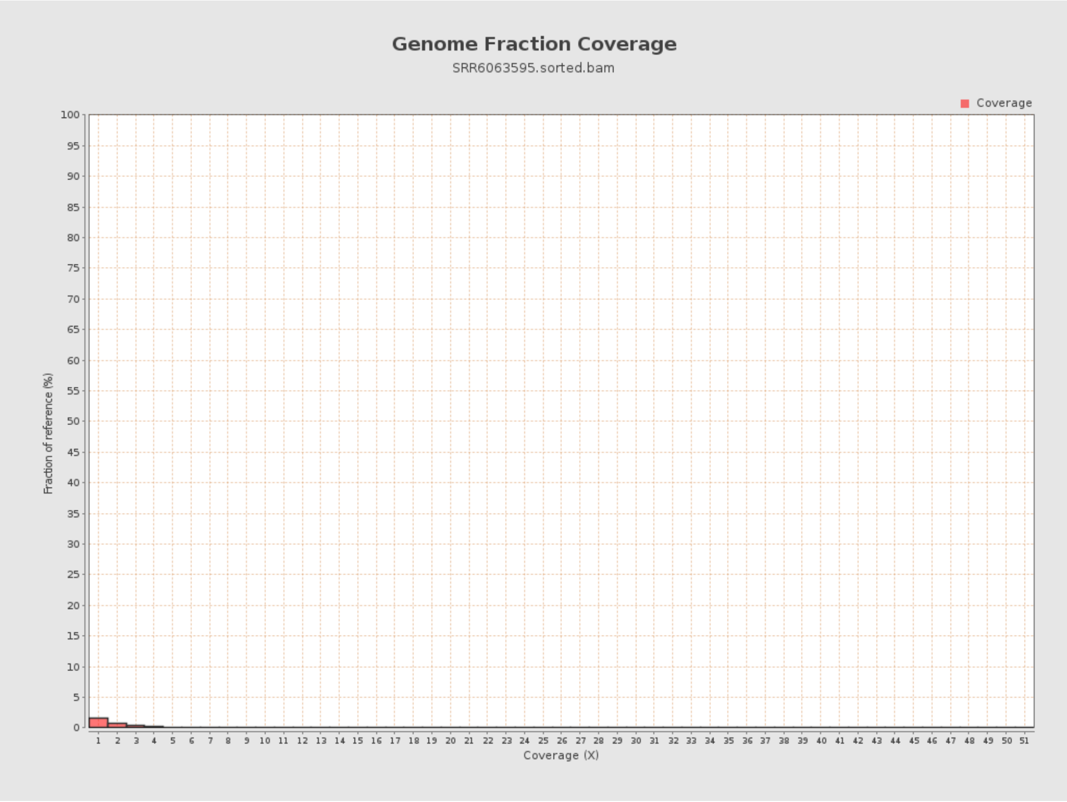
4. Results : Coverage Histogram



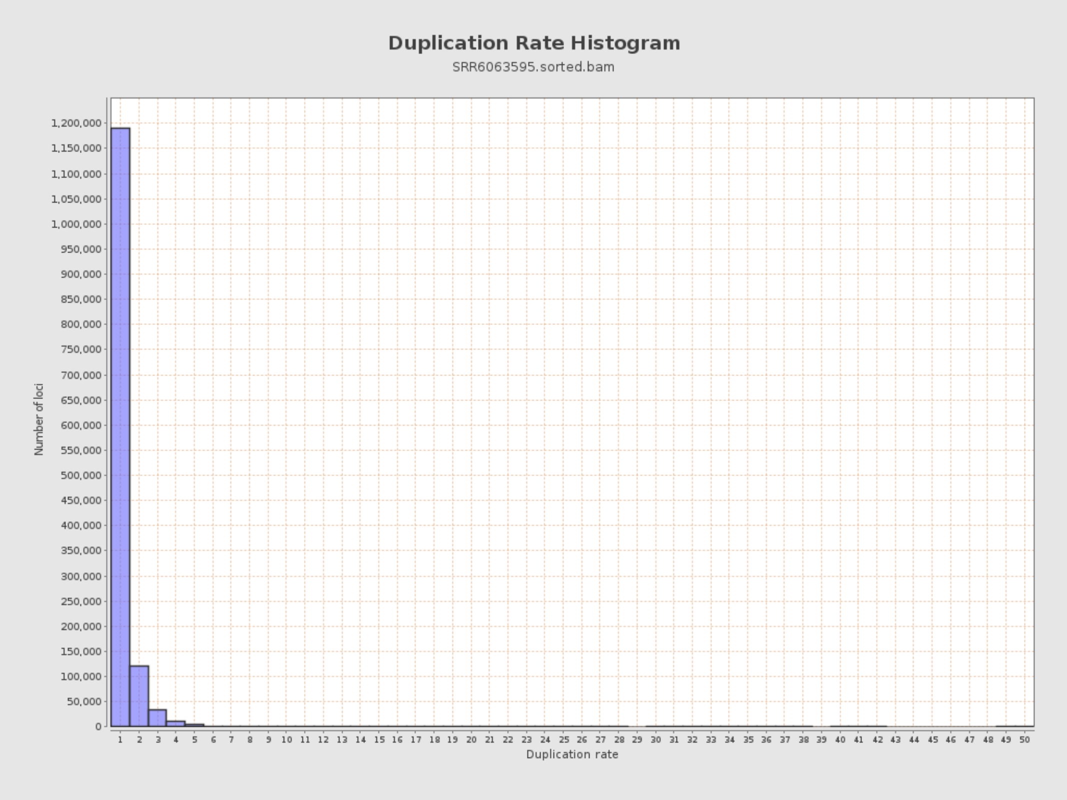
5. Results : Coverage Histogram (0-50X)



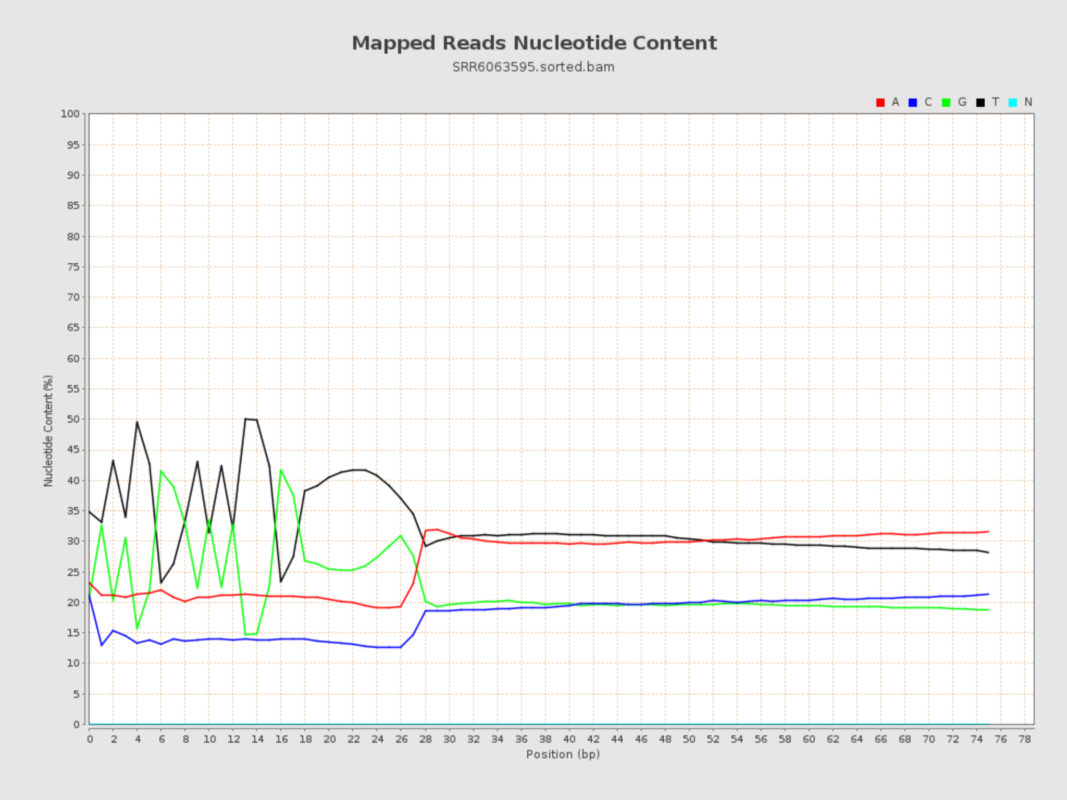
6. Results : Genome Fraction Coverage



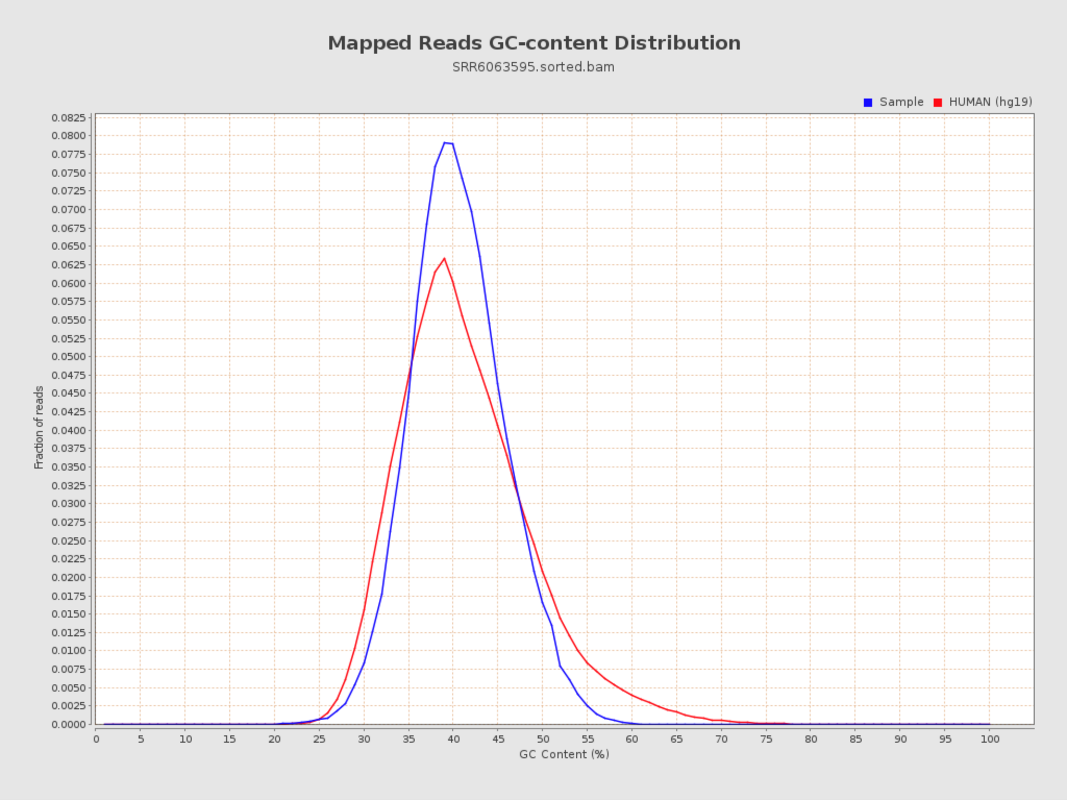
7. Results : Duplication Rate Histogram



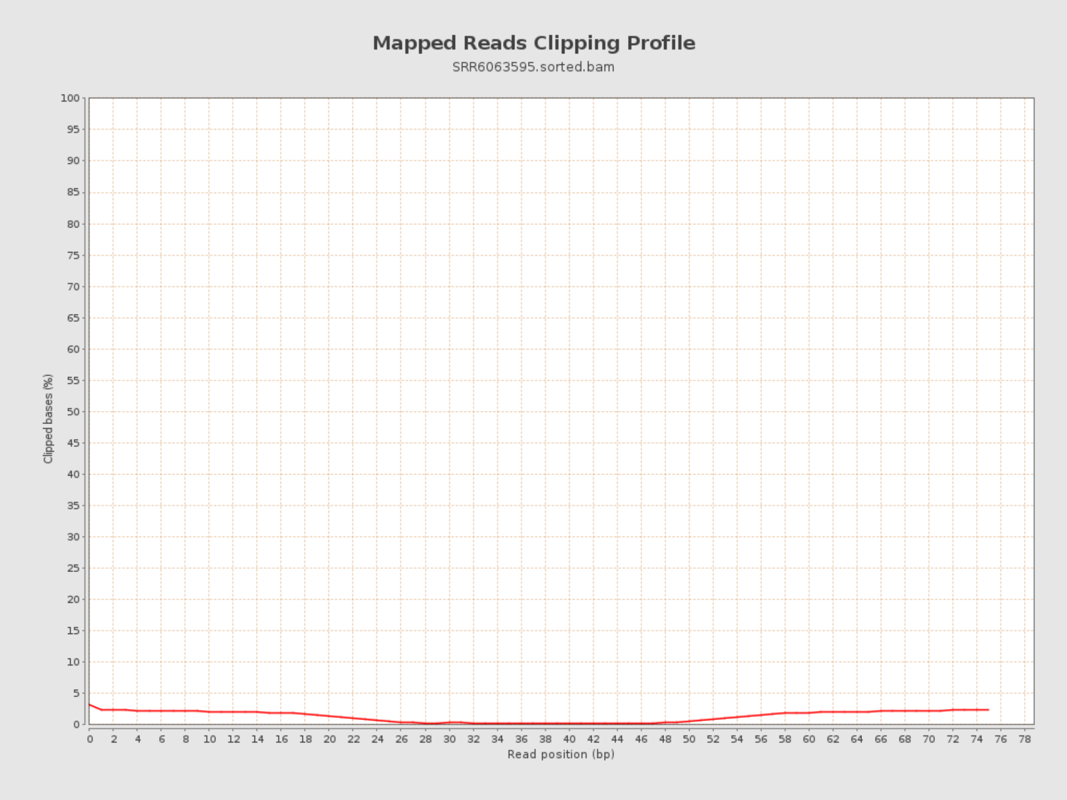
8. Results : Mapped Reads Nucleotide Content



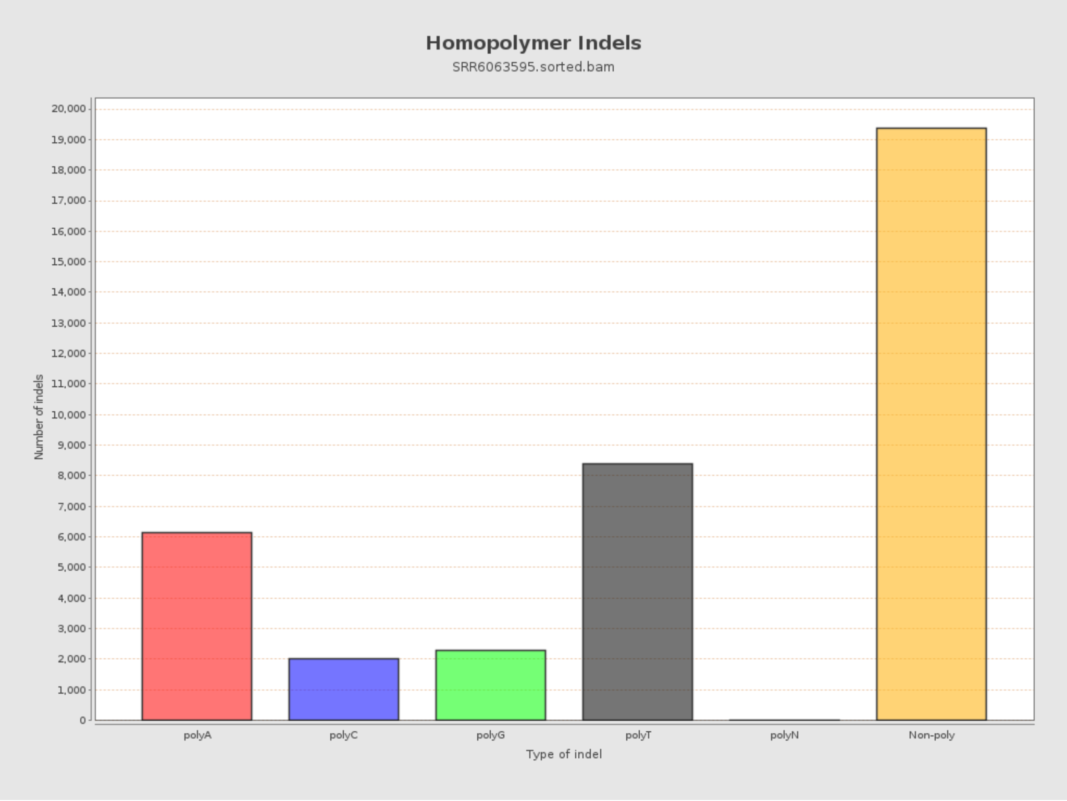
9. Results : Mapped Reads GC-content Distribution



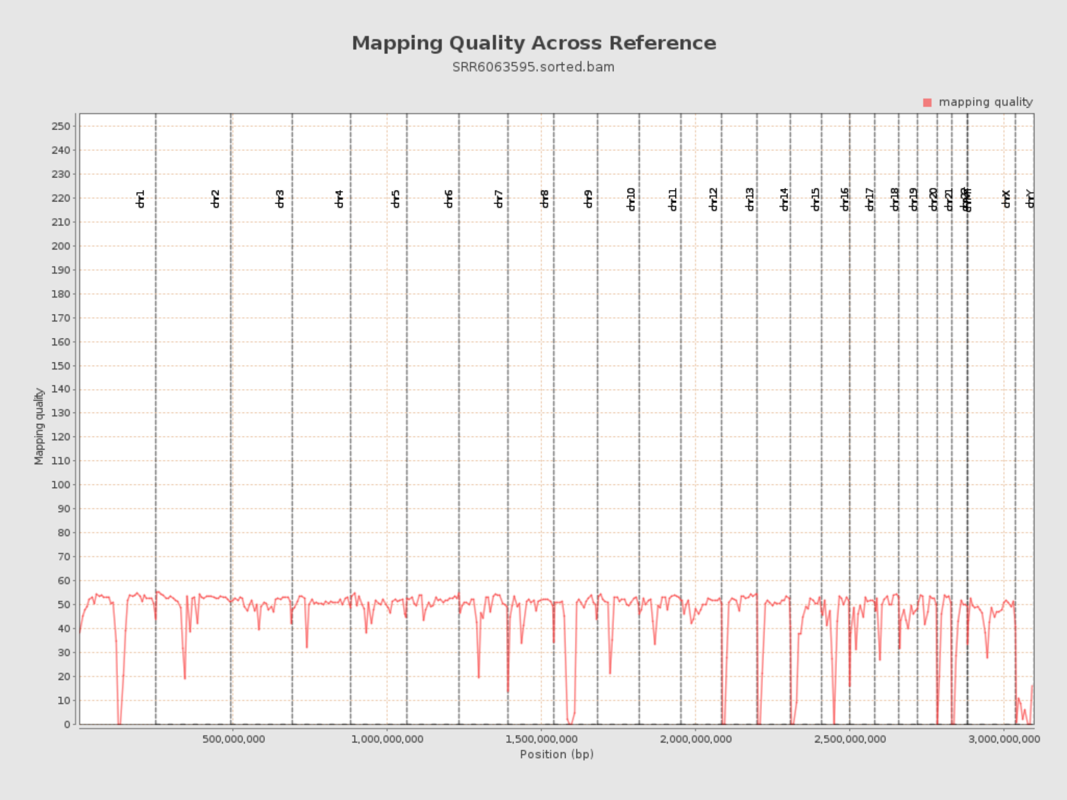
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram