Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:00:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063552.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_SRR6063552 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063552.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:00:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063552.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,975,263
Mapped reads	242,596 / 12.28%
Unmapped reads	1,732,667 / 87.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,614 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	14,113 / 0.71%
Duplication rate	5.14%
Clipped reads	115,181 / 5.83%

2.2. ACGT Content

Number/percentage of A's	4,418,963 / 27.61%
Number/percentage of C's	2,946,909 / 18.41%
Number/percentage of T's	5,132,016 / 32.07%
Number/percentage of G's	3,505,637 / 21.9%
Number/percentage of N's	369 / 0%
GC Percentage	40.32%

2.3. Coverage

Mean	0.0052

Standard Deviation	0.0975

2.4. Mapping Quality

Mean Mapping Quality	46.43

2.5. Mismatches and indels

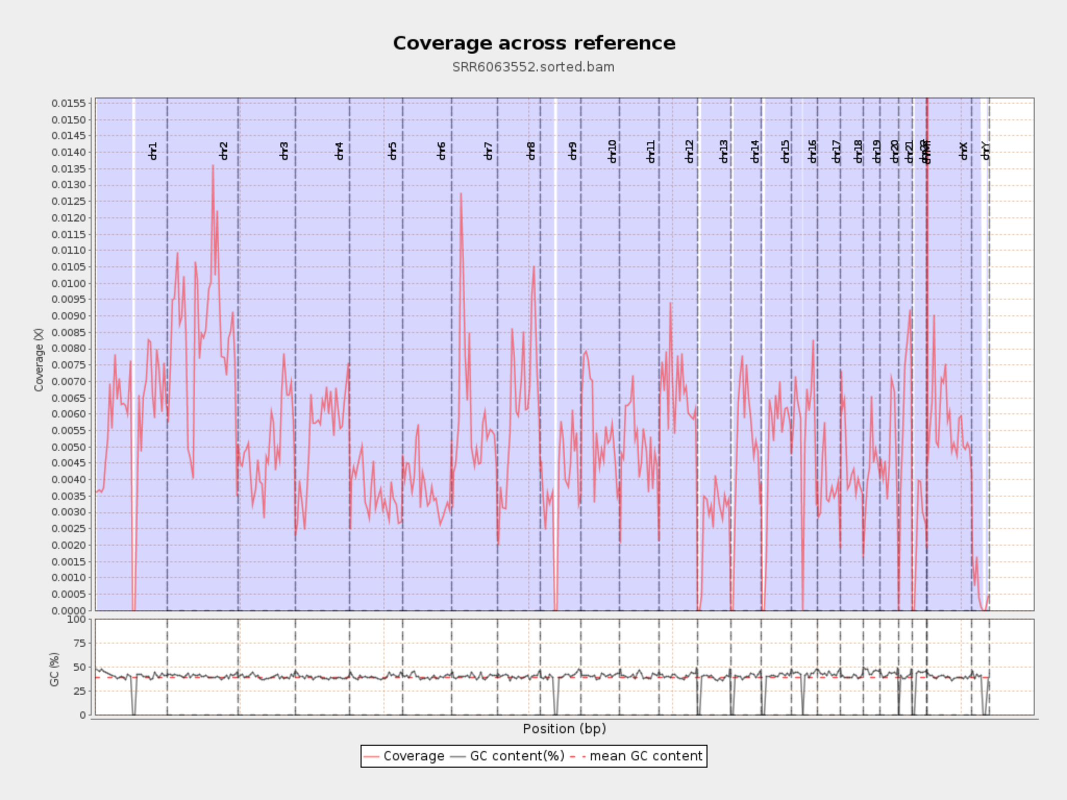
General error rate	0.89%
Mismatches	140,011
Insertions	1,278
Mapped reads with at least one insertion	0.52%
Deletions	5,170
Mapped reads with at least one deletion	2.1%
Homopolymer indels	48.46%

2.6. Chromosome stats

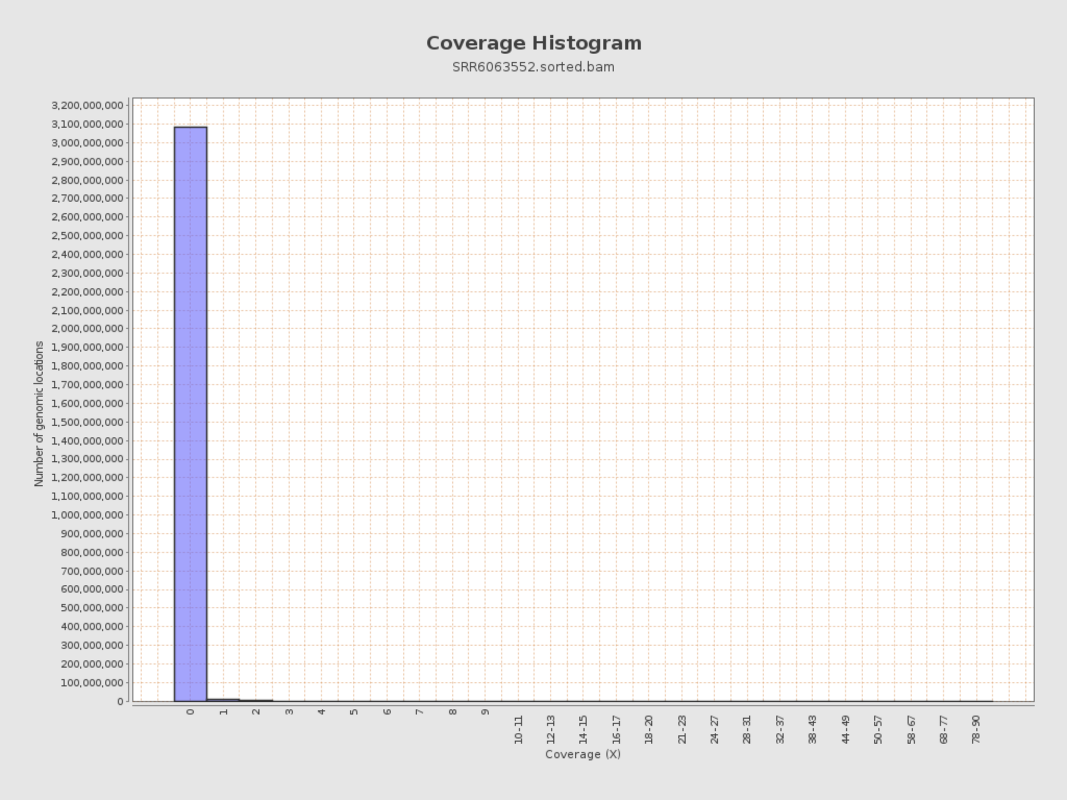
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1429613	0.0057	0.12
chr2	243199373	2088847	0.0086	0.1278
chr3	198022430	994274	0.005	0.0906
chr4	191154276	1036420	0.0054	0.096
chr5	180915260	648874	0.0036	0.0761
chr6	171115067	646594	0.0038	0.0782
chr7	159138663	956281	0.006	0.1123

chr8	146364022	910606	0.0062	0.1138
chr9	141213431	536672	0.0038	0.0806
chr10	135534747	759087	0.0056	0.0981
chr11	135006516	681718	0.005	0.0937
chr12	133851895	902683	0.0067	0.1062
chr13	115169878	313558	0.0027	0.0661
chr14	107349540	531965	0.005	0.0929
chr15	102531392	499809	0.0049	0.0916
chr16	90354753	499311	0.0055	0.096
chr17	81195210	300316	0.0037	0.0758
chr18	78077248	353433	0.0045	0.0996
chr19	59128983	257167	0.0043	0.0873
chr20	63025520	300730	0.0048	0.0886
chr21	48129895	299402	0.0062	0.102
chr22	51304566	123603	0.0024	0.0614
chrMT	16571	10716	0.6467	1.111
chrX	155270560	896663	0.0058	0.0969
chrY	59373566	34401	0.0006	0.028

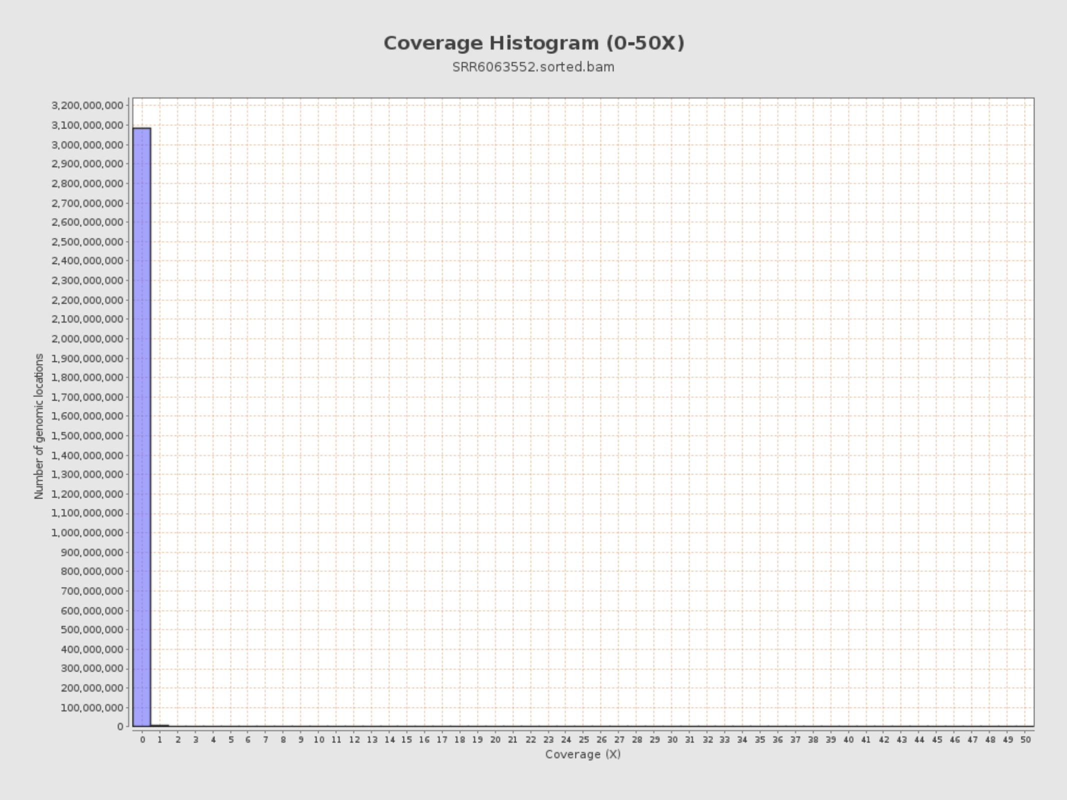
3. Results : Coverage across reference



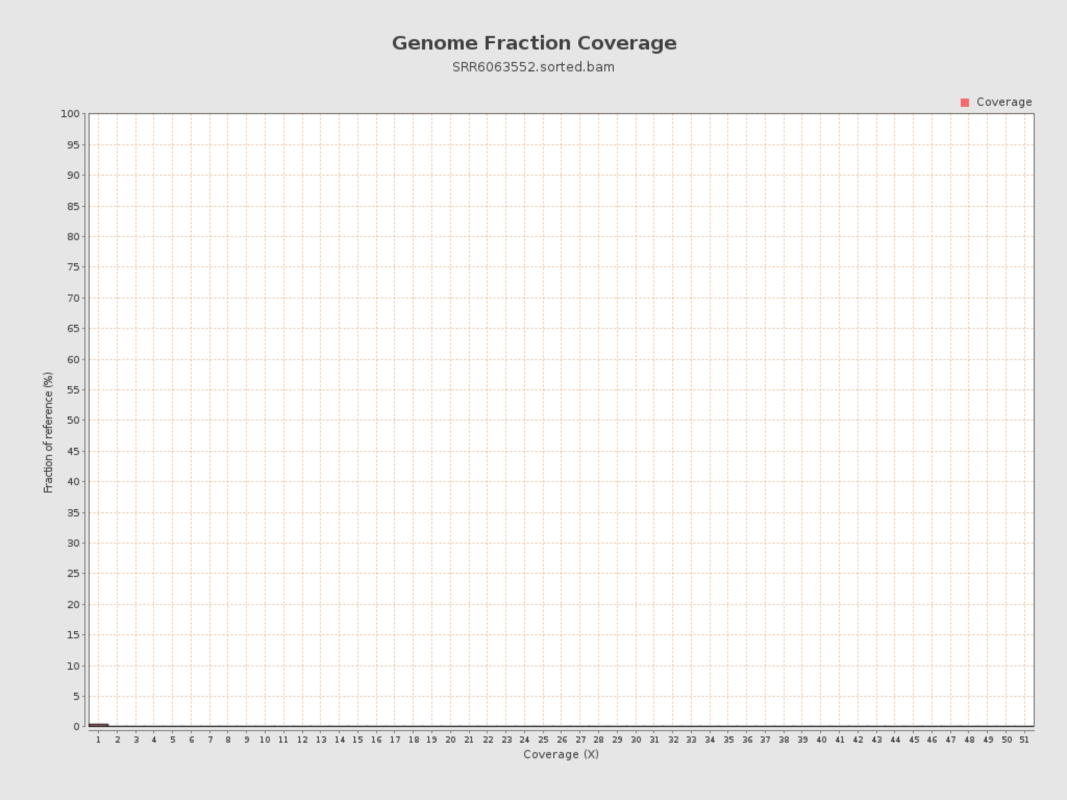
4. Results : Coverage Histogram



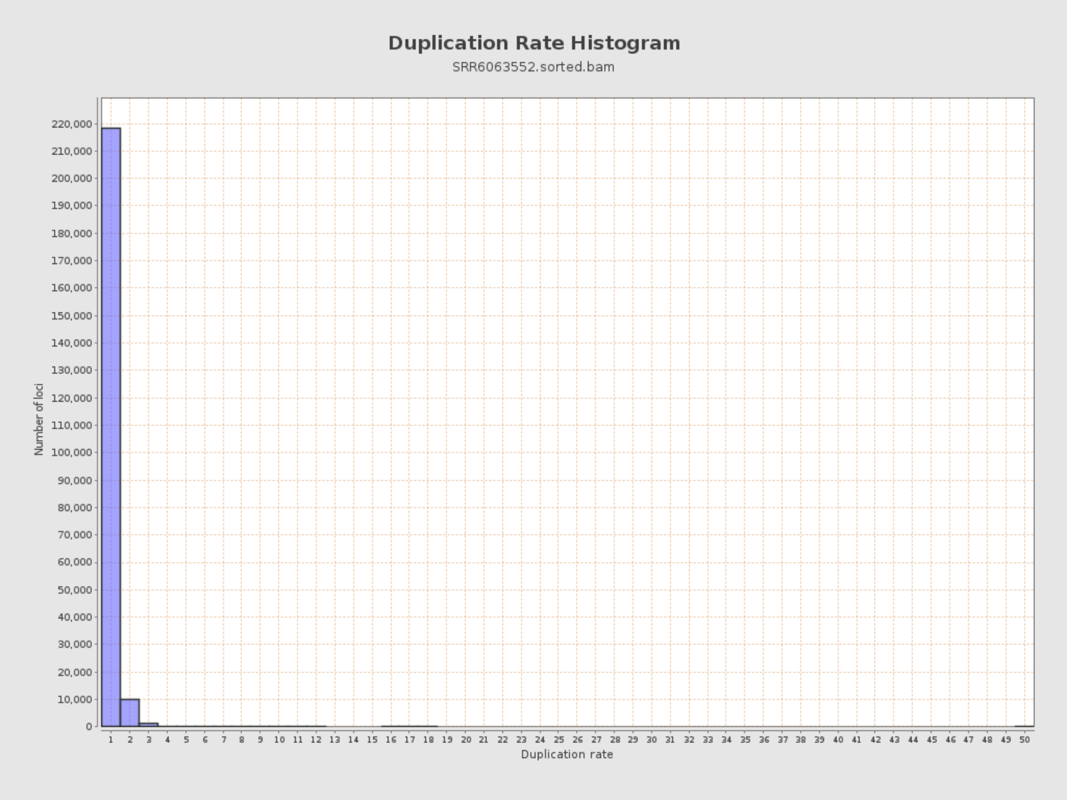
5. Results : Coverage Histogram (0-50X)



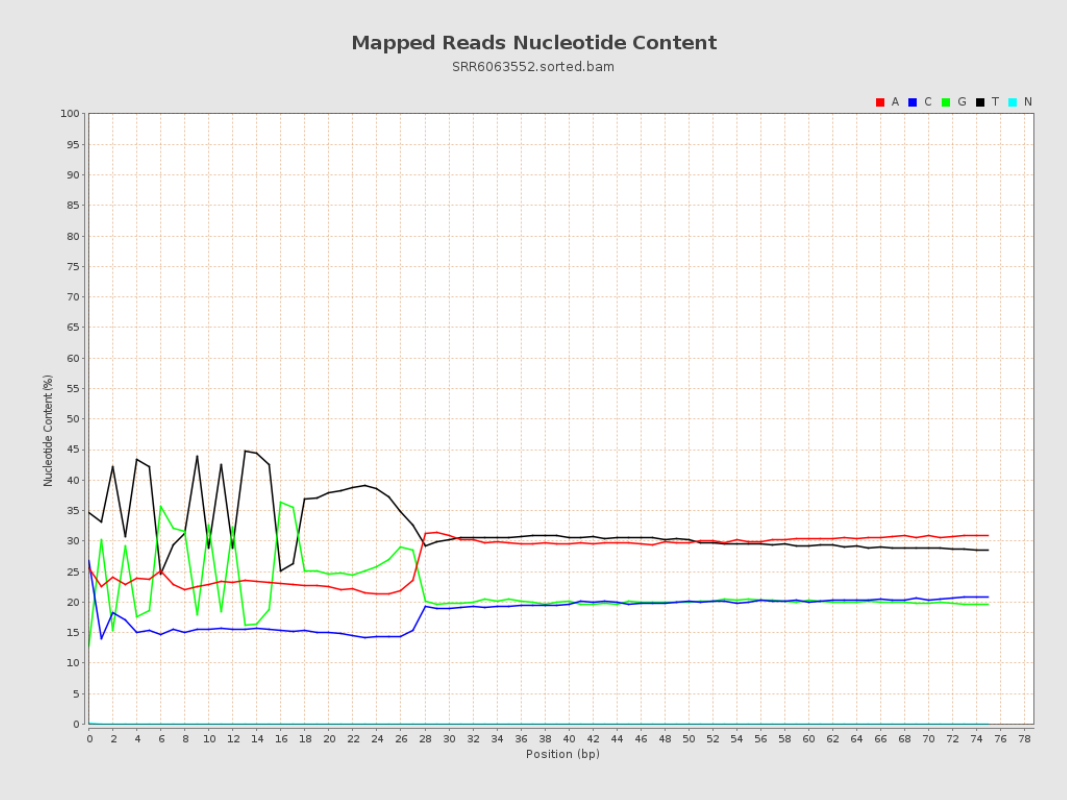
6. Results : Genome Fraction Coverage



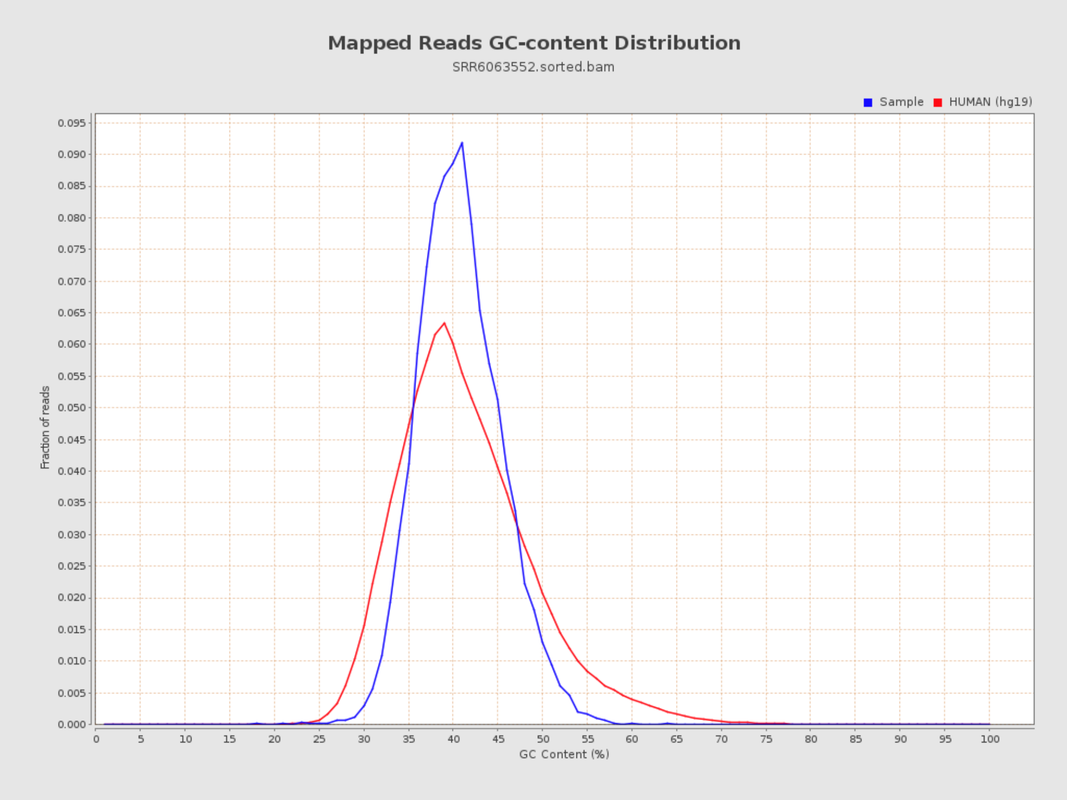
7. Results : Duplication Rate Histogram



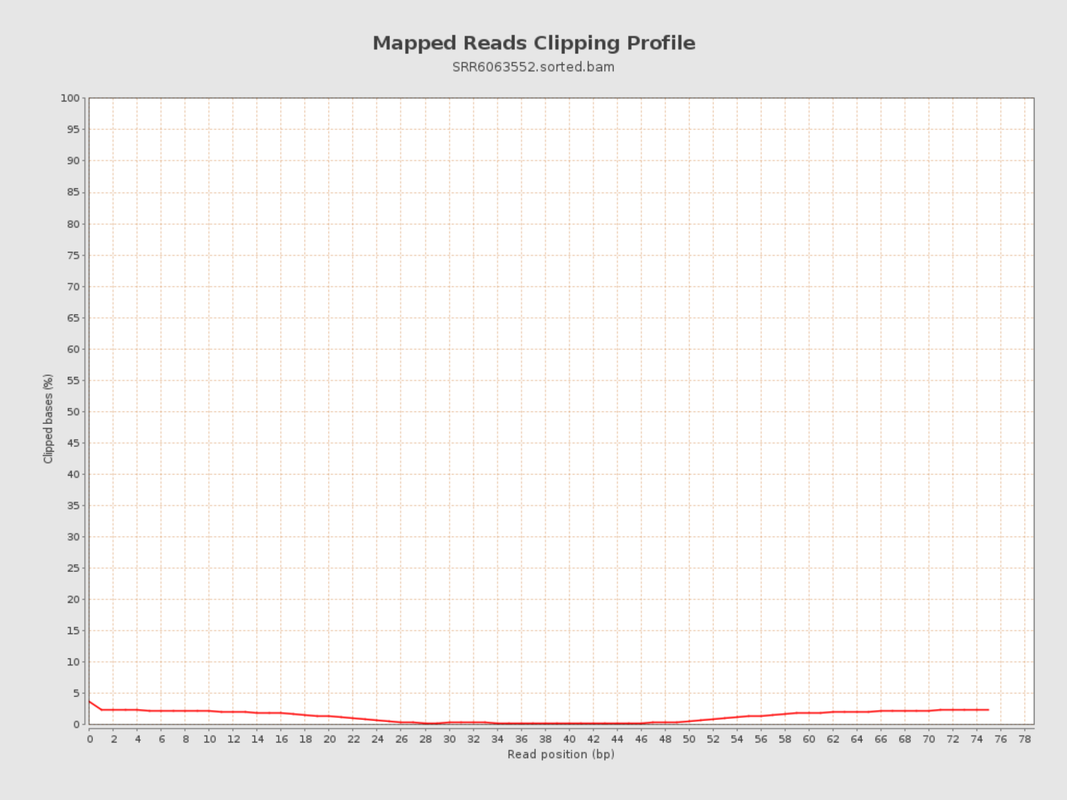
8. Results : Mapped Reads Nucleotide Content



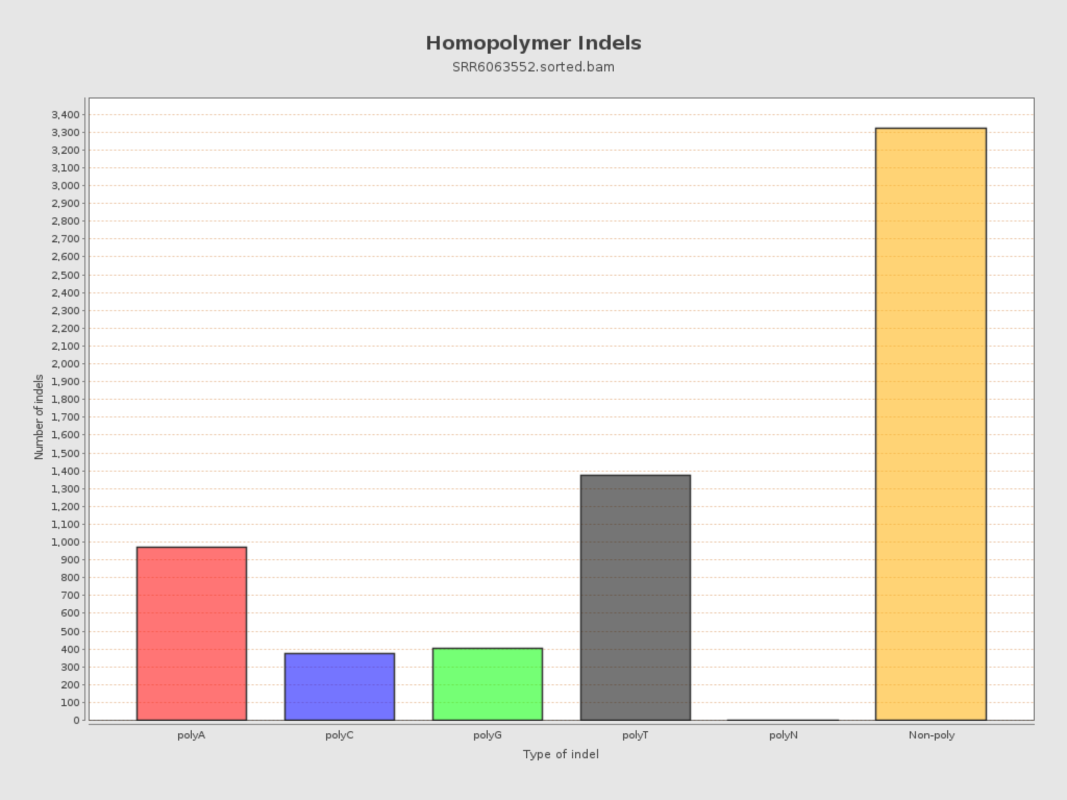
9. Results : Mapped Reads GC-content Distribution



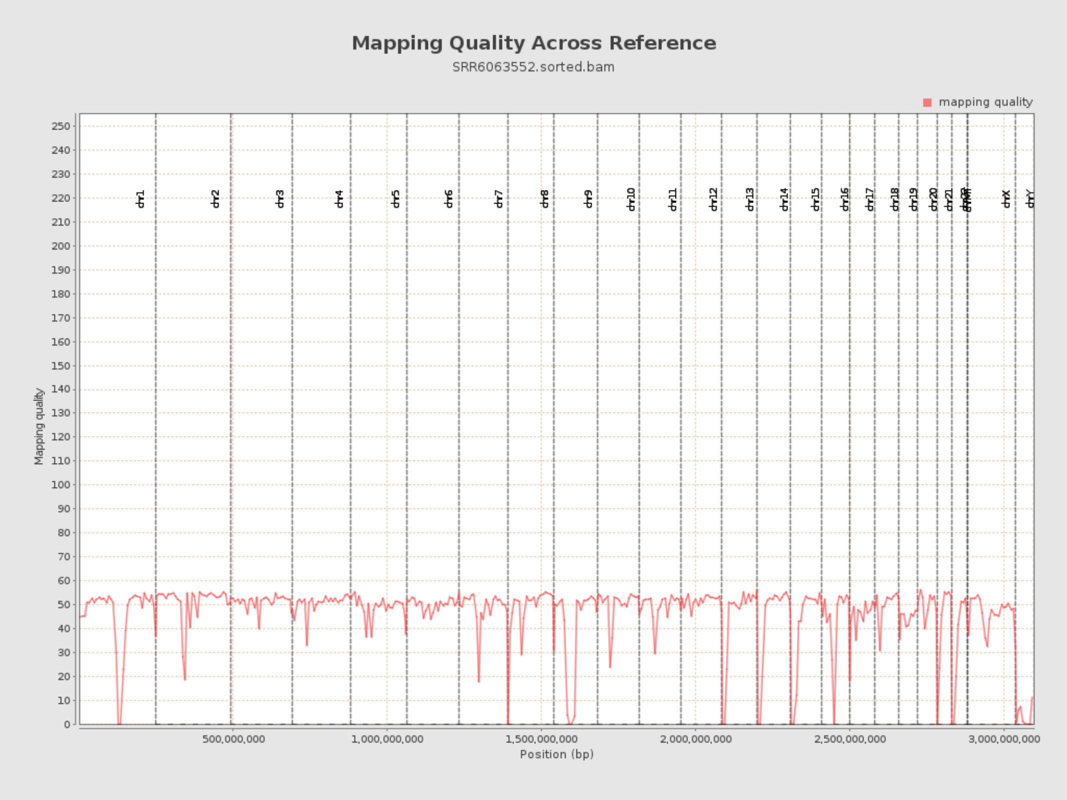
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram