Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:41:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063546.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_SRR6063546 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063546.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:41:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063546.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,148,447
Mapped reads	1,950,527 / 90.79%
Unmapped reads	197,920 / 9.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,594 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	105,397 / 4.91%
Duplication rate	4.23%
Clipped reads	896,889 / 41.75%

2.2. ACGT Content

Number/percentage of A's	36,018,613 / 27.8%
Number/percentage of C's	23,593,947 / 18.21%
Number/percentage of T's	41,549,537 / 32.07%
Number/percentage of G's	28,382,584 / 21.91%
Number/percentage of N's	3,420 / 0%
GC Percentage	40.12%

2.3. Coverage

Mean	0.0419

Standard Deviation	0.444

2.4. Mapping Quality

Mean Mapping Quality	46.5

2.5. Mismatches and indels

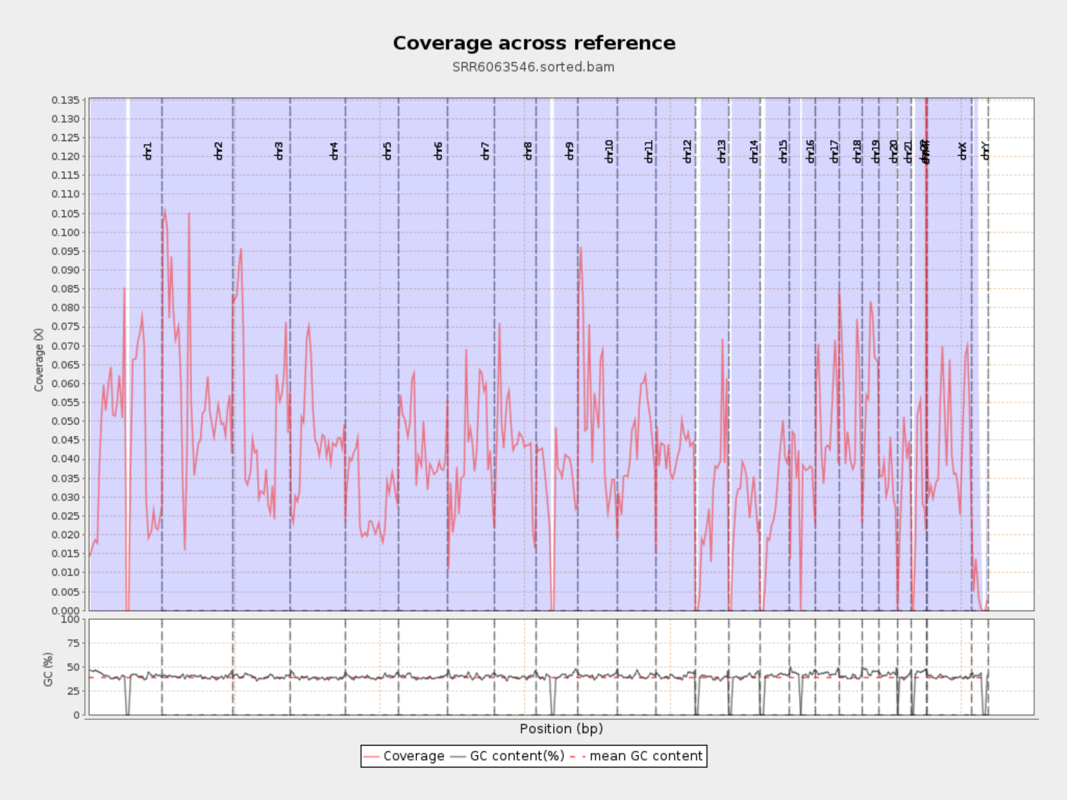
General error rate	0.83%
Mismatches	1,054,846
Insertions	10,130
Mapped reads with at least one insertion	0.51%
Deletions	36,216
Mapped reads with at least one deletion	1.83%
Homopolymer indels	46.73%

2.6. Chromosome stats

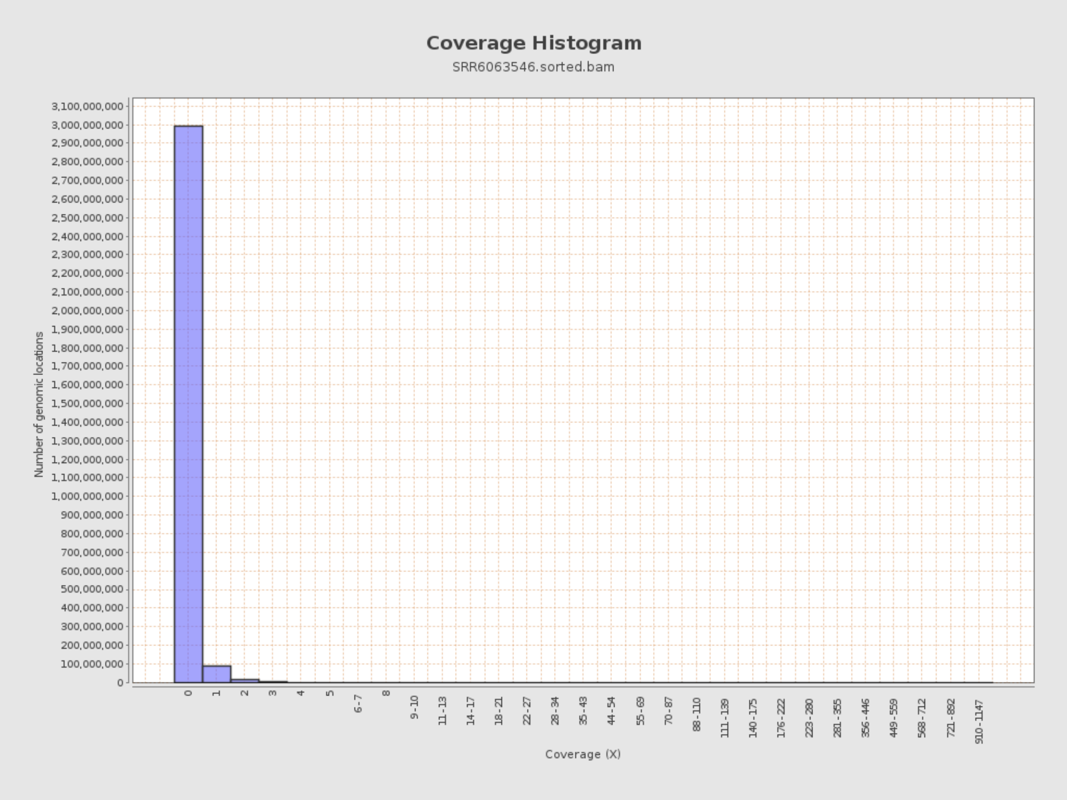
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10735038	0.0431	0.9171
chr2	243199373	14411008	0.0593	0.5486
chr3	198022430	10095959	0.051	0.2717
chr4	191154276	8643020	0.0452	0.2614
chr5	180915260	5189305	0.0287	0.203
chr6	171115067	7523404	0.044	0.2849
chr7	159138663	6584273	0.0414	0.4852

chr8	146364022	6568798	0.0449	0.7157
chr9	141213431	4688641	0.0332	0.4002
chr10	135534747	7225422	0.0533	0.3838
chr11	135006516	5973747	0.0442	0.3437
chr12	133851895	5678154	0.0424	0.2608
chr13	115169878	3335771	0.029	0.2049
chr14	107349540	2819589	0.0263	0.2345
chr15	102531392	2691410	0.0262	0.1987
chr16	90354753	3060828	0.0339	0.2385
chr17	81195210	4154024	0.0512	0.2943
chr18	78077248	4200617	0.0538	0.5853
chr19	59128983	3603869	0.0609	0.6164
chr20	63025520	2114090	0.0335	0.2257
chr21	48129895	1590670	0.033	0.2287
chr22	51304566	1424111	0.0278	0.1943
chrMT	16571	20772	1.2535	1.4636
chrX	155270560	7007733	0.0451	0.2895
chrY	59373566	267198	0.0045	0.1276

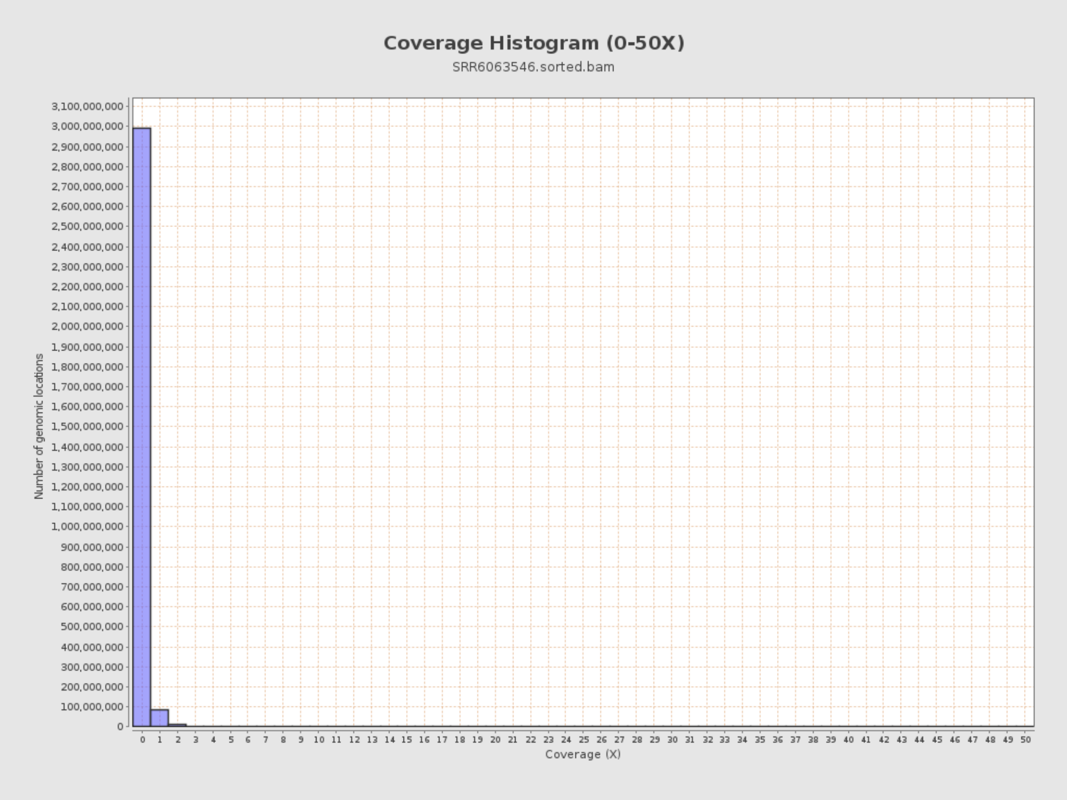
3. Results : Coverage across reference



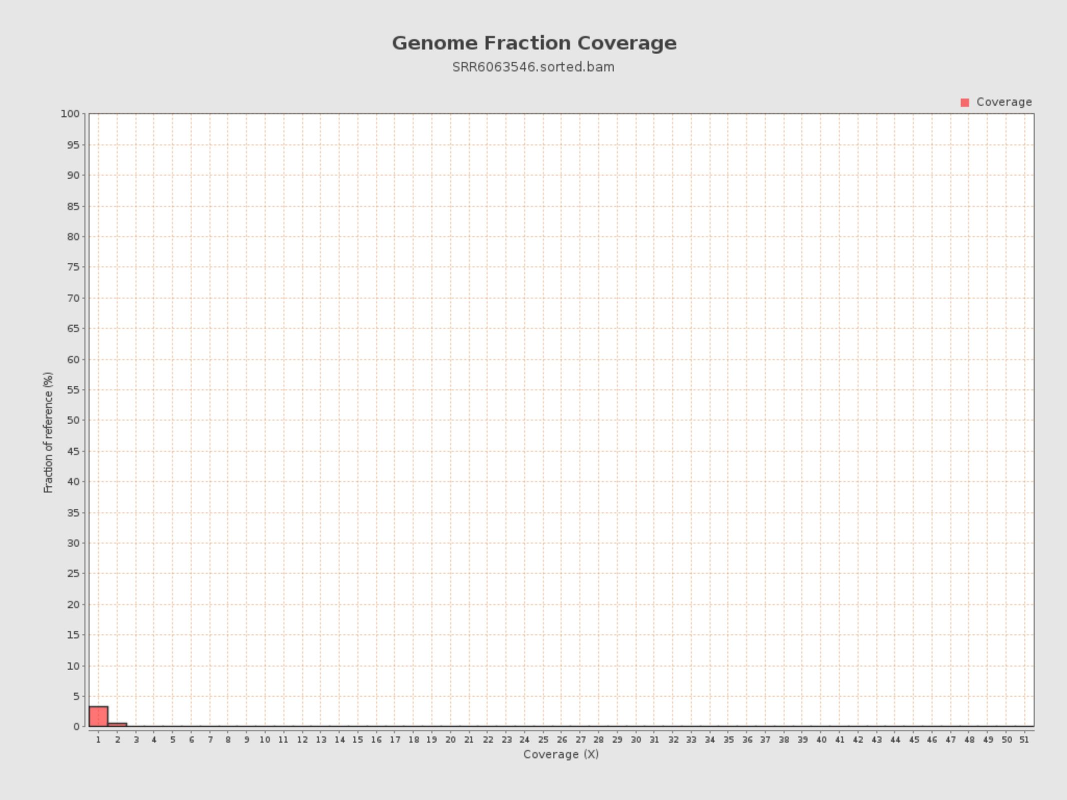
4. Results : Coverage Histogram



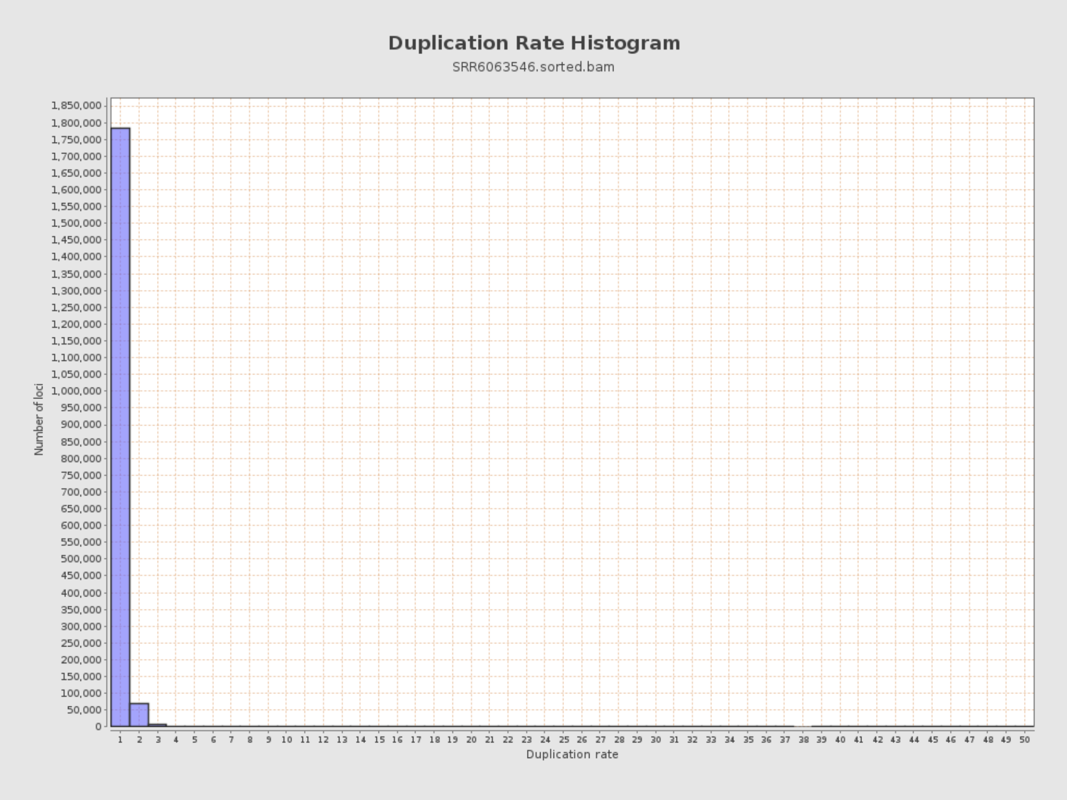
5. Results : Coverage Histogram (0-50X)



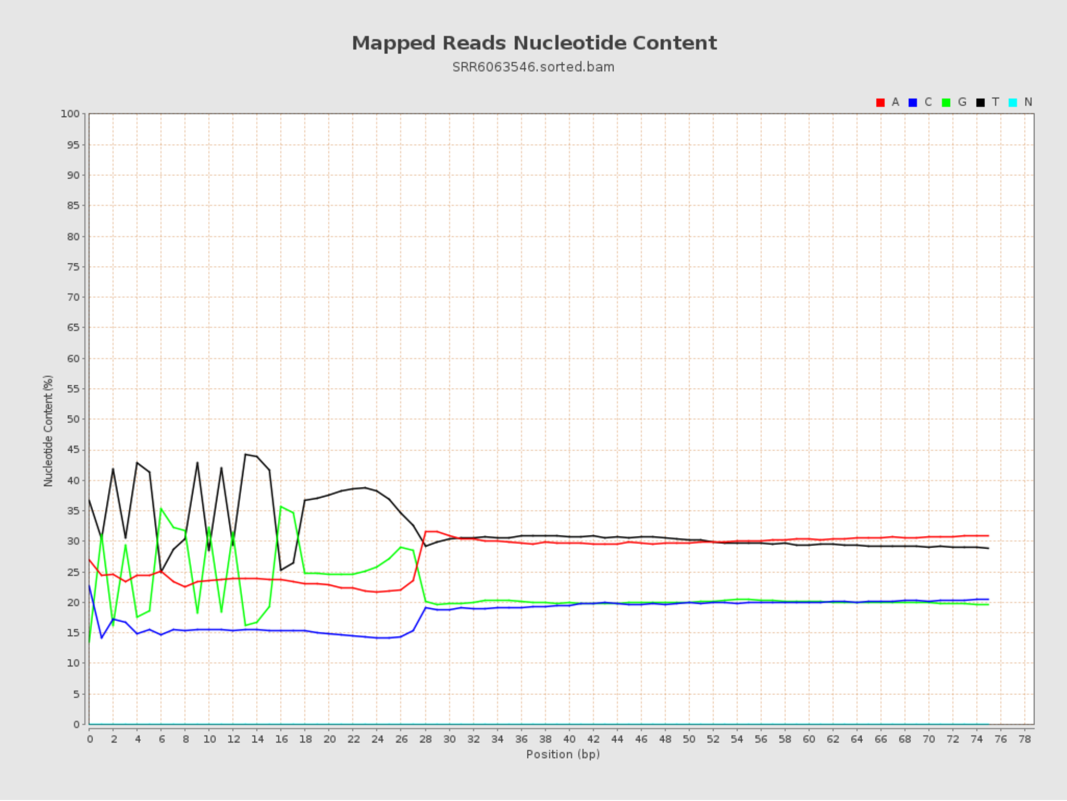
6. Results : Genome Fraction Coverage



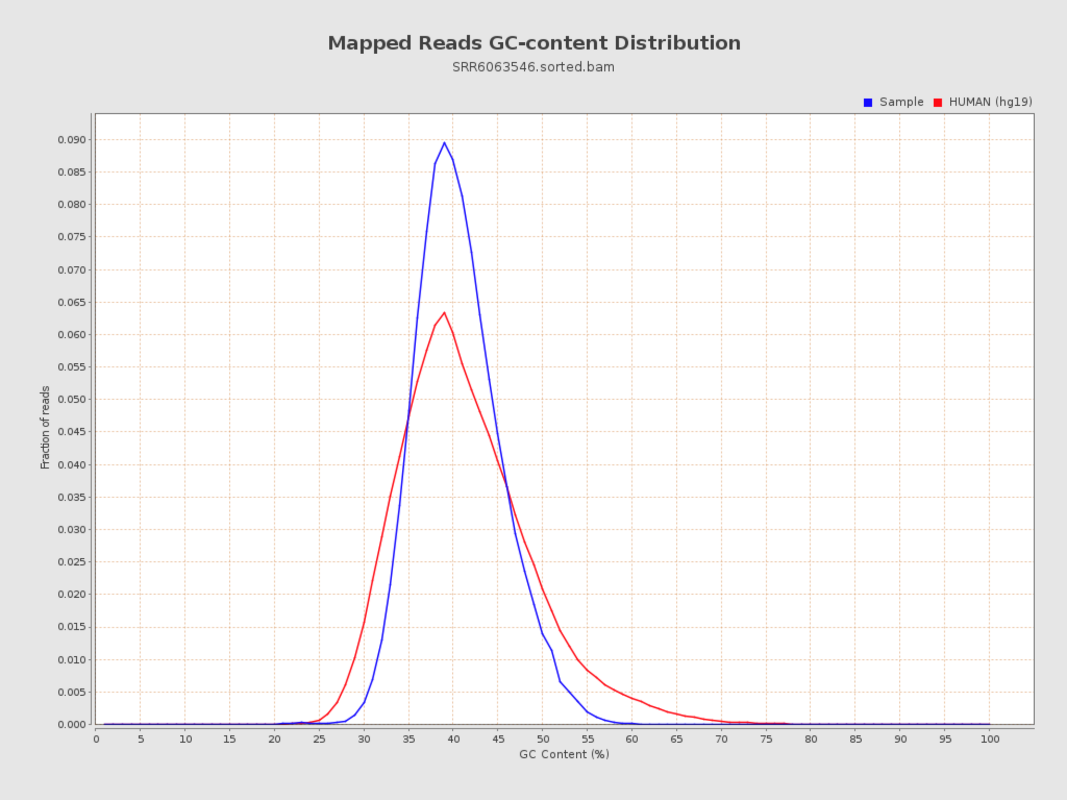
7. Results : Duplication Rate Histogram



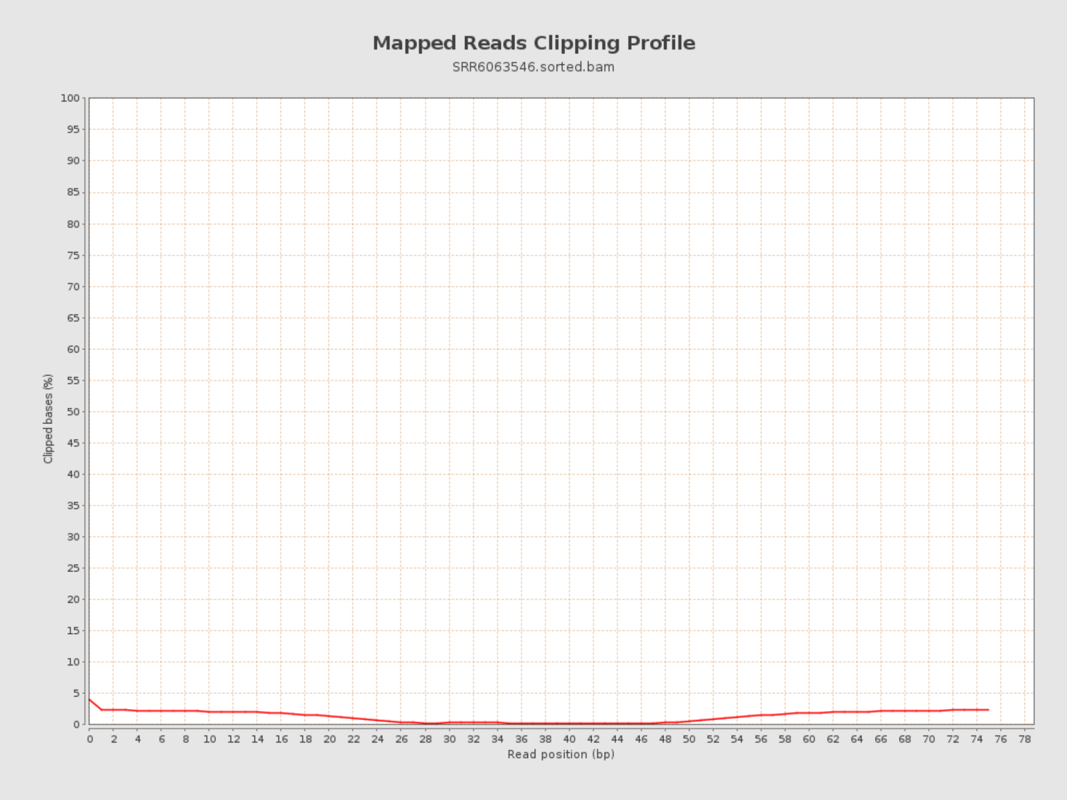
8. Results : Mapped Reads Nucleotide Content



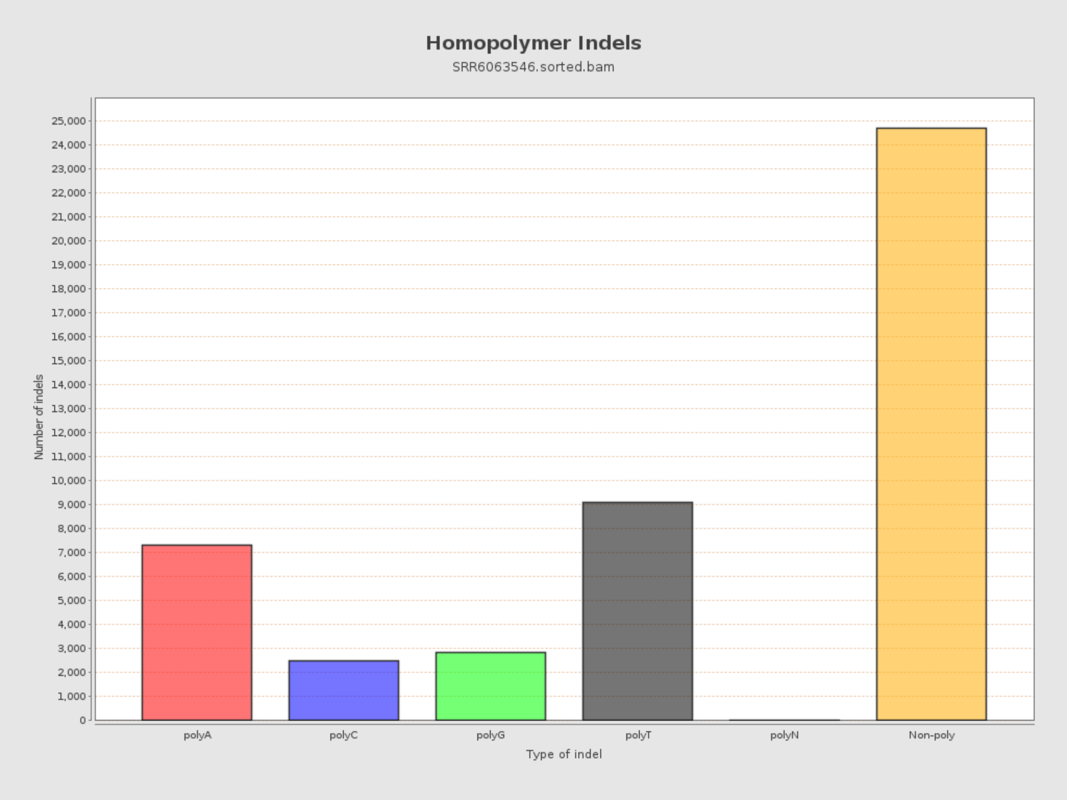
9. Results : Mapped Reads GC-content Distribution



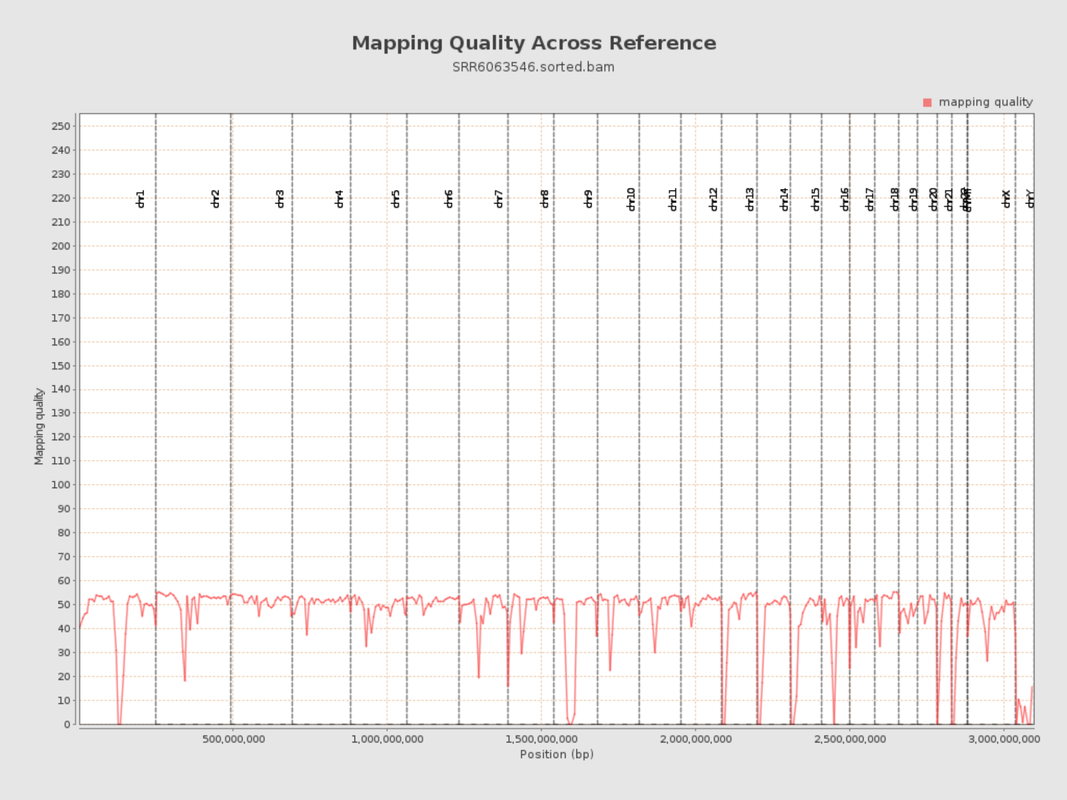
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram