Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 04:09:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063590.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_SRR6063590 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063590.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 04:09:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063590.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,191,351
Mapped reads	4,604,259 / 88.69%
Unmapped reads	587,092 / 11.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,287 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	309,663 / 5.96%
Duplication rate	5.19%
Clipped reads	2,142,110 / 41.26%

2.2. ACGT Content

Number/percentage of A's	84,616,400 / 27.72%
Number/percentage of C's	57,727,931 / 18.91%
Number/percentage of T's	94,338,009 / 30.9%
Number/percentage of G's	68,298,679 / 22.37%
Number/percentage of N's	307,462 / 0.1%
GC Percentage	41.28%

2.3. Coverage

Mean	0.0987

Standard Deviation	0.7981

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

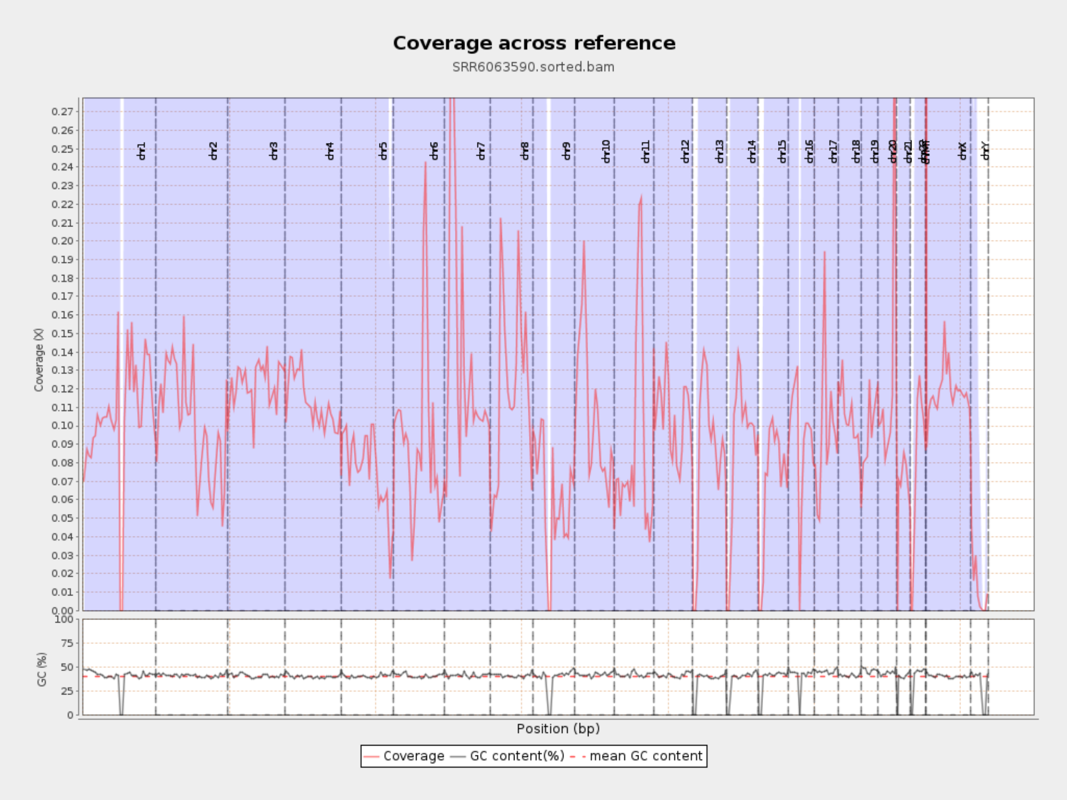
General error rate	0.83%
Mismatches	2,500,006
Insertions	21,261
Mapped reads with at least one insertion	0.46%
Deletions	74,274
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.44%

2.6. Chromosome stats

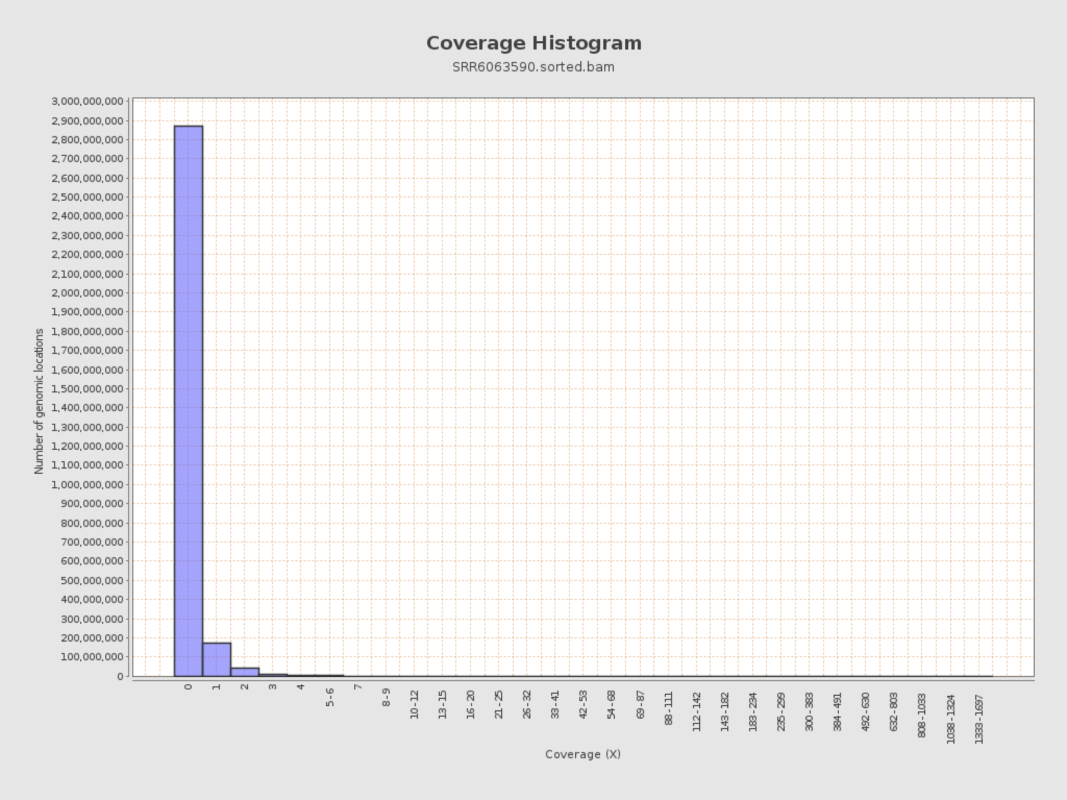
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26039577	0.1045	1.4732
chr2	243199373	24563025	0.101	0.9081
chr3	198022430	24275439	0.1226	0.4458
chr4	191154276	21658834	0.1133	0.4539
chr5	180915260	13742103	0.076	0.3568
chr6	171115067	15985996	0.0934	0.4455
chr7	159138663	21586943	0.1356	1.4753

chr8	146364022	17768435	0.1214	1.1127
chr9	141213431	8428204	0.0597	0.6424
chr10	135534747	14383562	0.1061	0.686
chr11	135006516	11738303	0.0869	0.5375
chr12	133851895	14055085	0.105	0.4291
chr13	115169878	9760328	0.0847	0.3793
chr14	107349540	9702540	0.0904	0.4385
chr15	102531392	6943432	0.0677	0.3452
chr16	90354753	8255519	0.0914	0.4515
chr17	81195210	7699889	0.0948	0.4566
chr18	78077248	8194546	0.105	1.4423
chr19	59128983	5747434	0.0972	0.9977
chr20	63025520	8527166	0.1353	0.5173
chr21	48129895	3139502	0.0652	0.3594
chr22	51304566	4044628	0.0788	0.3563
chrMT	16571	51692	3.1194	3.0081
chrX	155270560	18397139	0.1185	0.517
chrY	59373566	728200	0.0123	0.1895

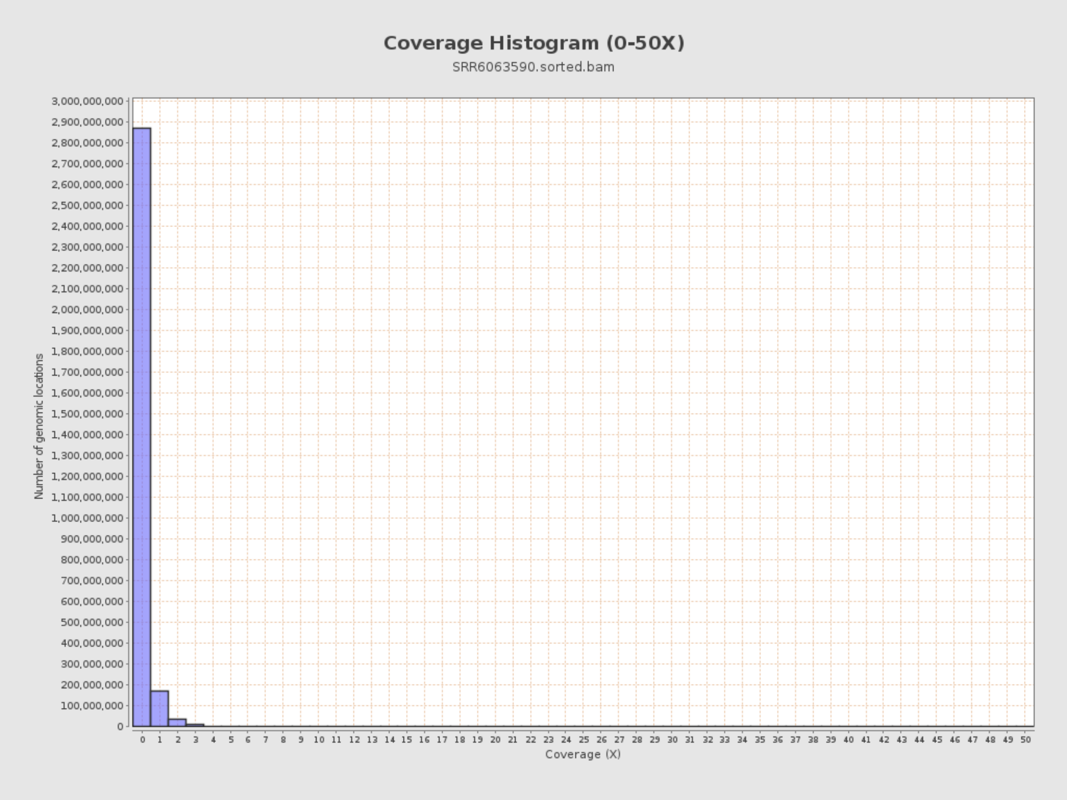
3. Results : Coverage across reference



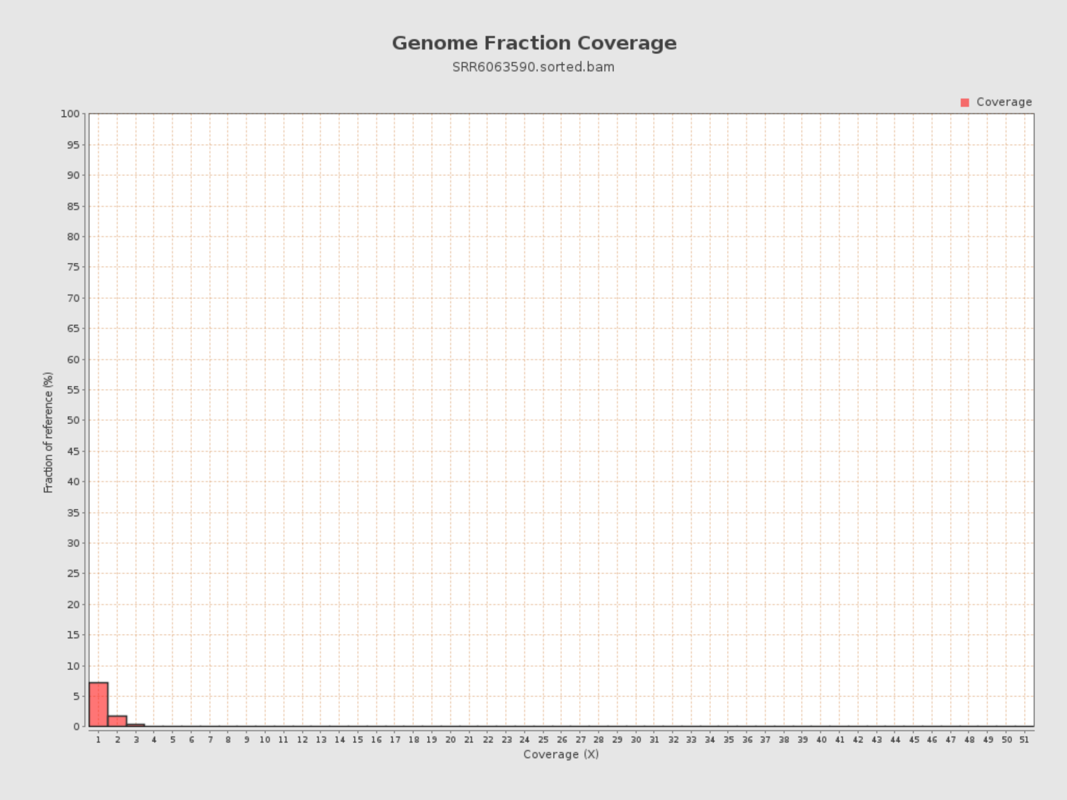
4. Results : Coverage Histogram



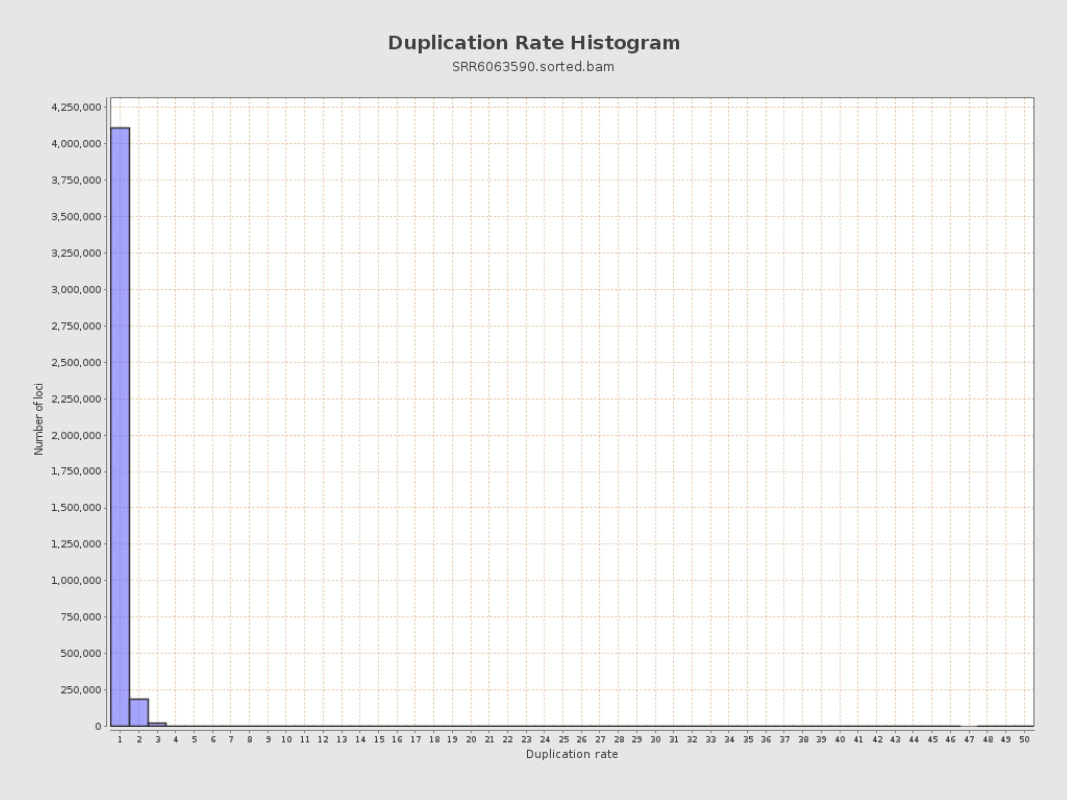
5. Results : Coverage Histogram (0-50X)



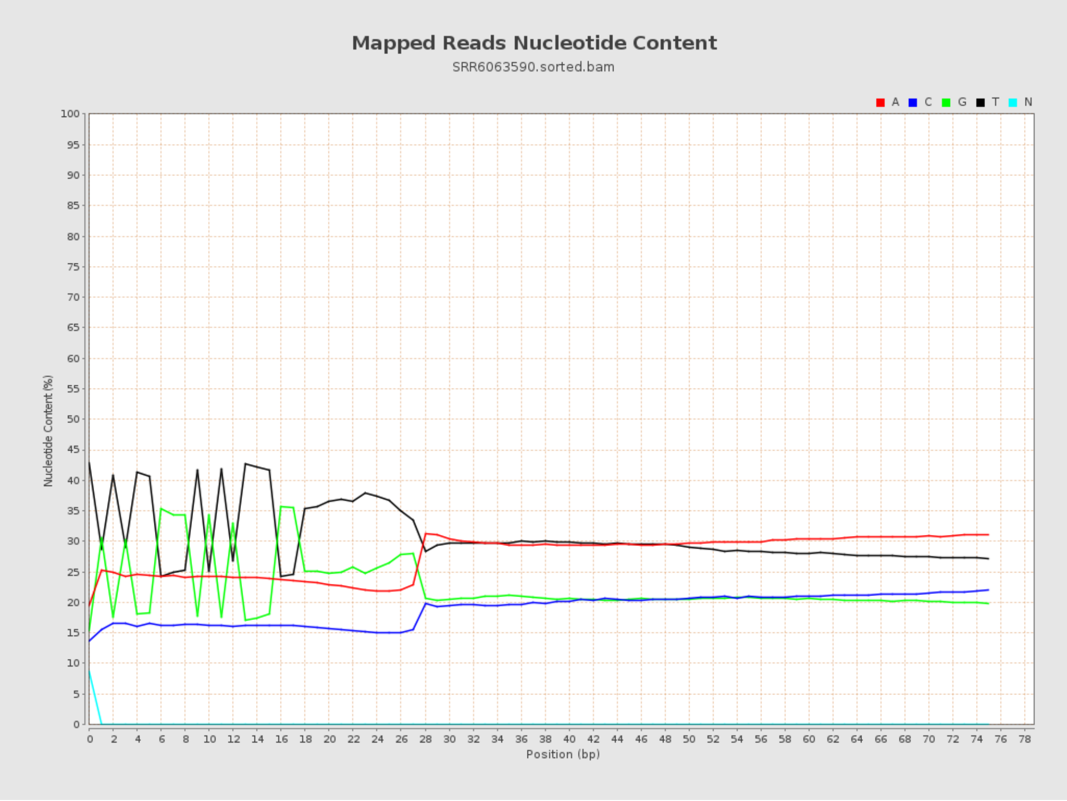
6. Results : Genome Fraction Coverage



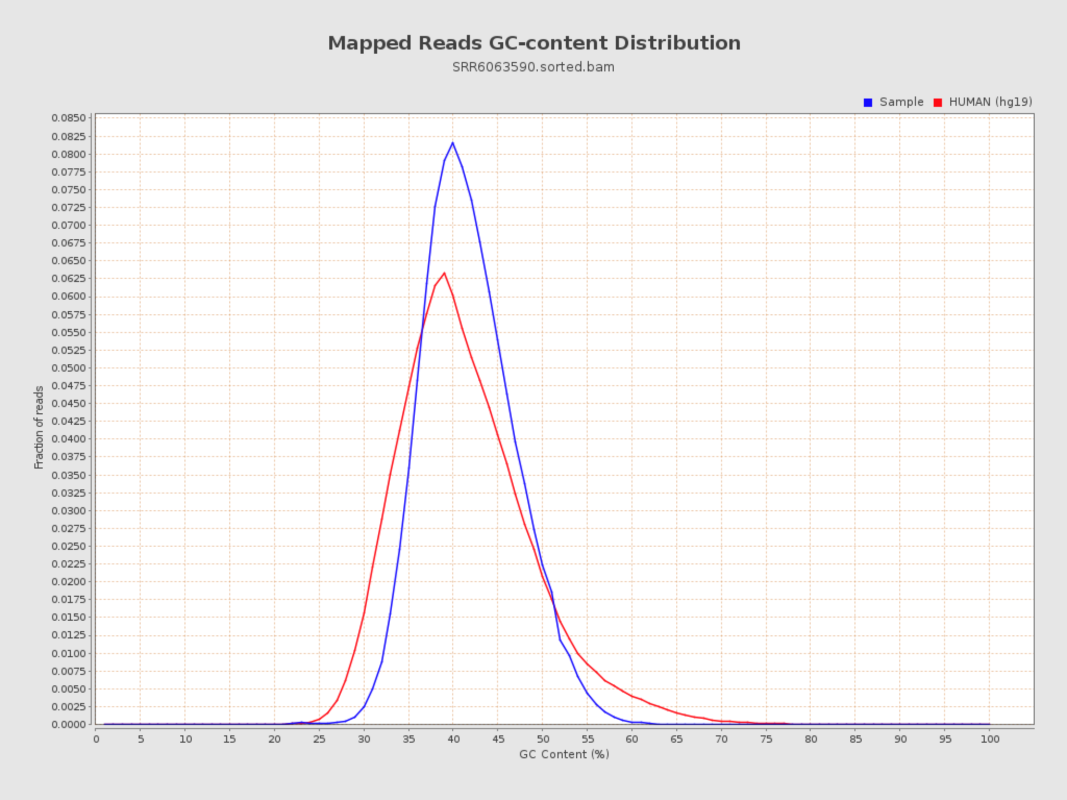
7. Results : Duplication Rate Histogram



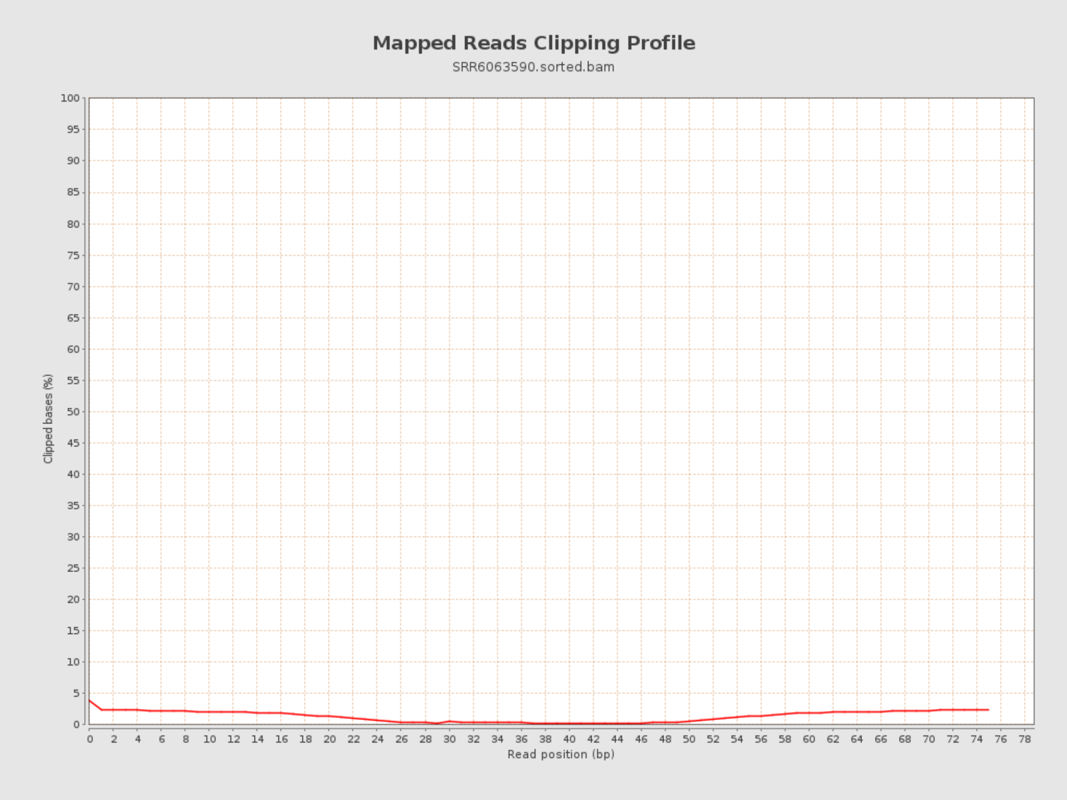
8. Results : Mapped Reads Nucleotide Content



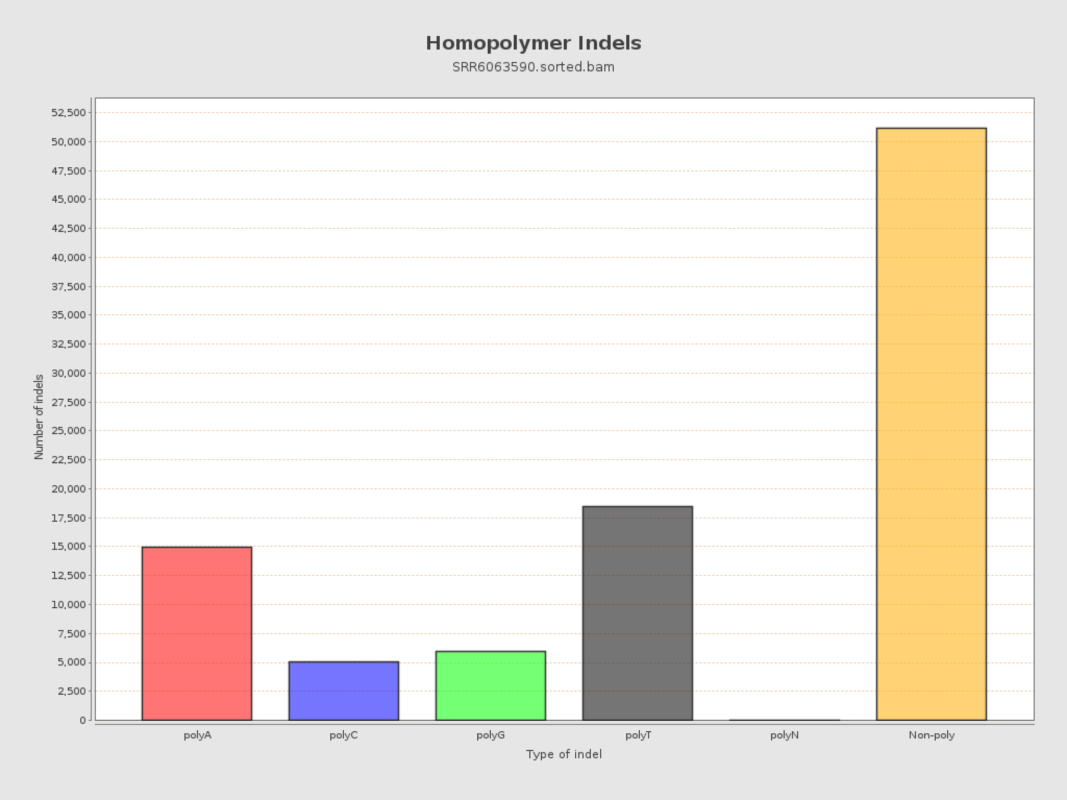
9. Results : Mapped Reads GC-content Distribution



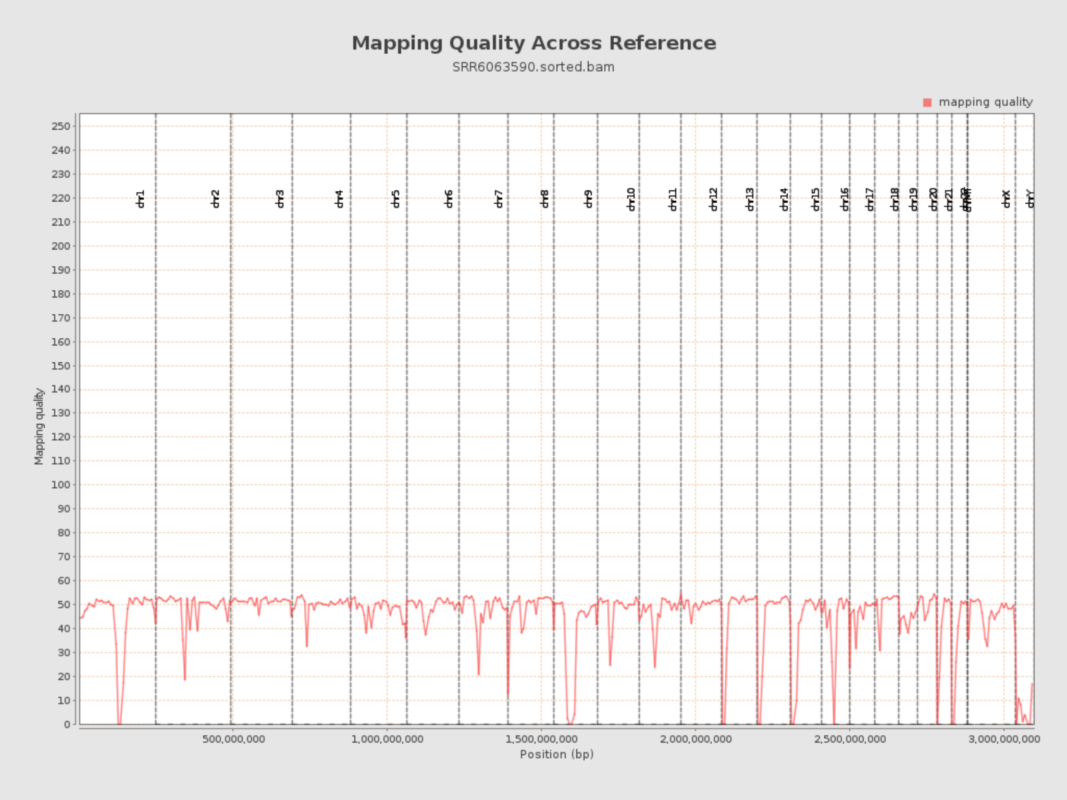
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram