Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:36:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063544.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_SRR6063544 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063544.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:36:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063544.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,556,556
Mapped reads	3,192,394 / 89.76%
Unmapped reads	364,162 / 10.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,789 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	211,229 / 5.94%
Duplication rate	5.17%
Clipped reads	1,648,601 / 46.35%

2.2. ACGT Content

Number/percentage of A's	57,091,823 / 27.46%
Number/percentage of C's	37,343,456 / 17.96%
Number/percentage of T's	66,627,311 / 32.05%
Number/percentage of G's	46,839,886 / 22.53%
Number/percentage of N's	4,382 / 0%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0672

Standard Deviation	0.5889

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

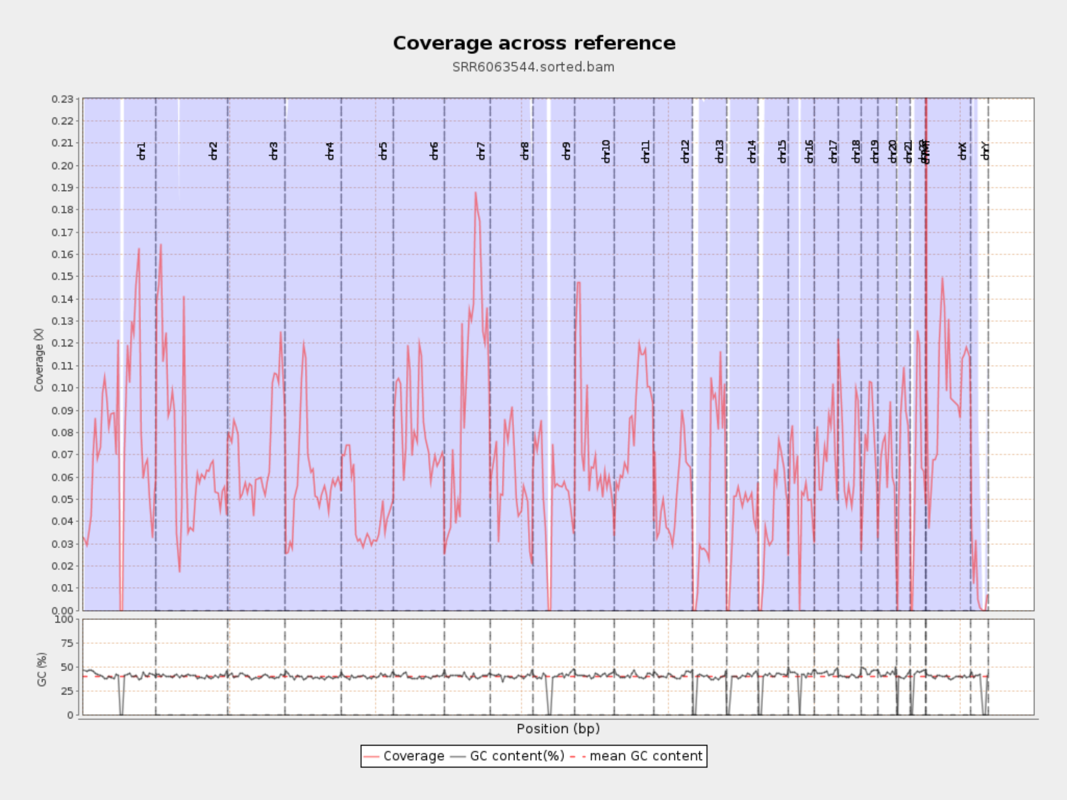
General error rate	0.8%
Mismatches	1,642,159
Insertions	15,965
Mapped reads with at least one insertion	0.5%
Deletions	56,074
Mapped reads with at least one deletion	1.74%
Homopolymer indels	46.39%

2.6. Chromosome stats

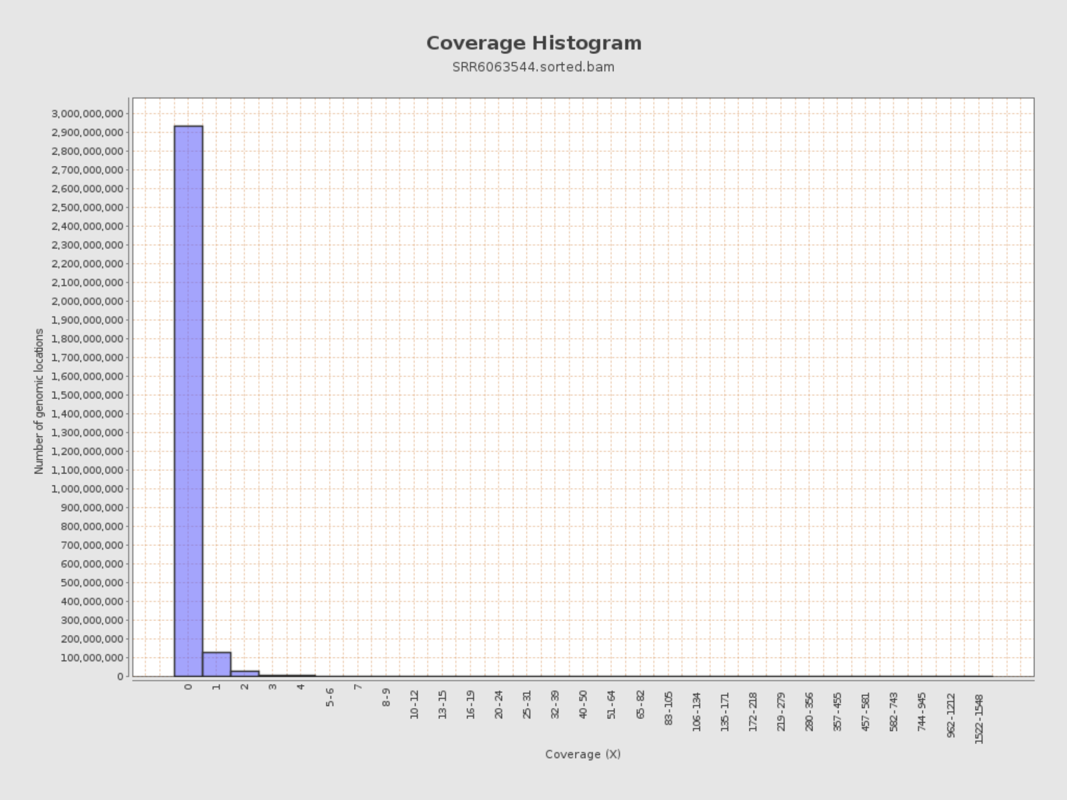
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19087226	0.0766	1.0418
chr2	243199373	17633774	0.0725	0.8556
chr3	198022430	14435118	0.0729	0.3366
chr4	191154276	11270121	0.059	0.3272
chr5	180915260	8099936	0.0448	0.2661
chr6	171115067	14288132	0.0835	0.4673
chr7	159138663	15925343	0.1001	0.8926

chr8	146364022	8477601	0.0579	0.7775
chr9	141213431	7453690	0.0528	0.5183
chr10	135534747	10187887	0.0752	0.4753
chr11	135006516	11480444	0.085	0.4964
chr12	133851895	7041011	0.0526	0.307
chr13	115169878	6446596	0.056	0.2994
chr14	107349540	4455068	0.0415	0.3045
chr15	102531392	4252732	0.0415	0.2706
chr16	90354753	4644934	0.0514	0.3185
chr17	81195210	5943962	0.0732	0.3877
chr18	78077248	5719072	0.0732	0.8747
chr19	59128983	4397556	0.0744	0.7606
chr20	63025520	4144387	0.0658	0.3437
chr21	48129895	3505656	0.0728	0.3622
chr22	51304566	3256217	0.0635	0.3133
chrMT	16571	65821	3.9721	3.1827
chrX	155270560	15153956	0.0976	0.4666
chrY	59373566	631924	0.0106	0.2899

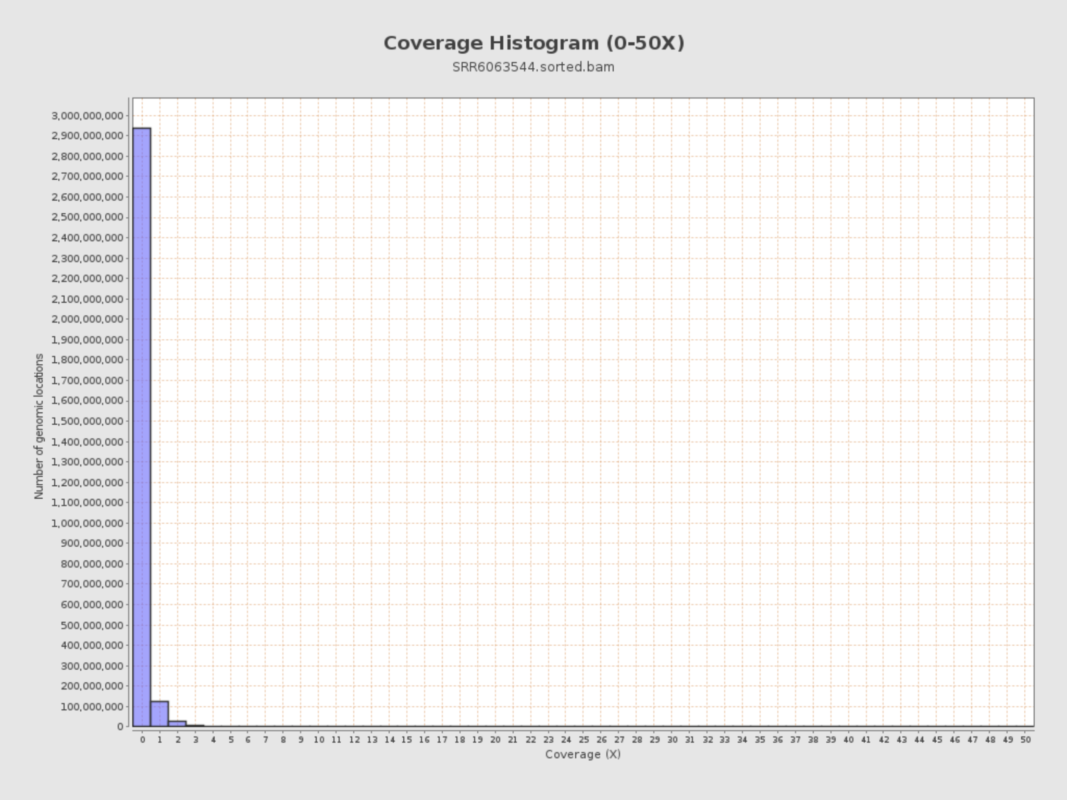
3. Results : Coverage across reference



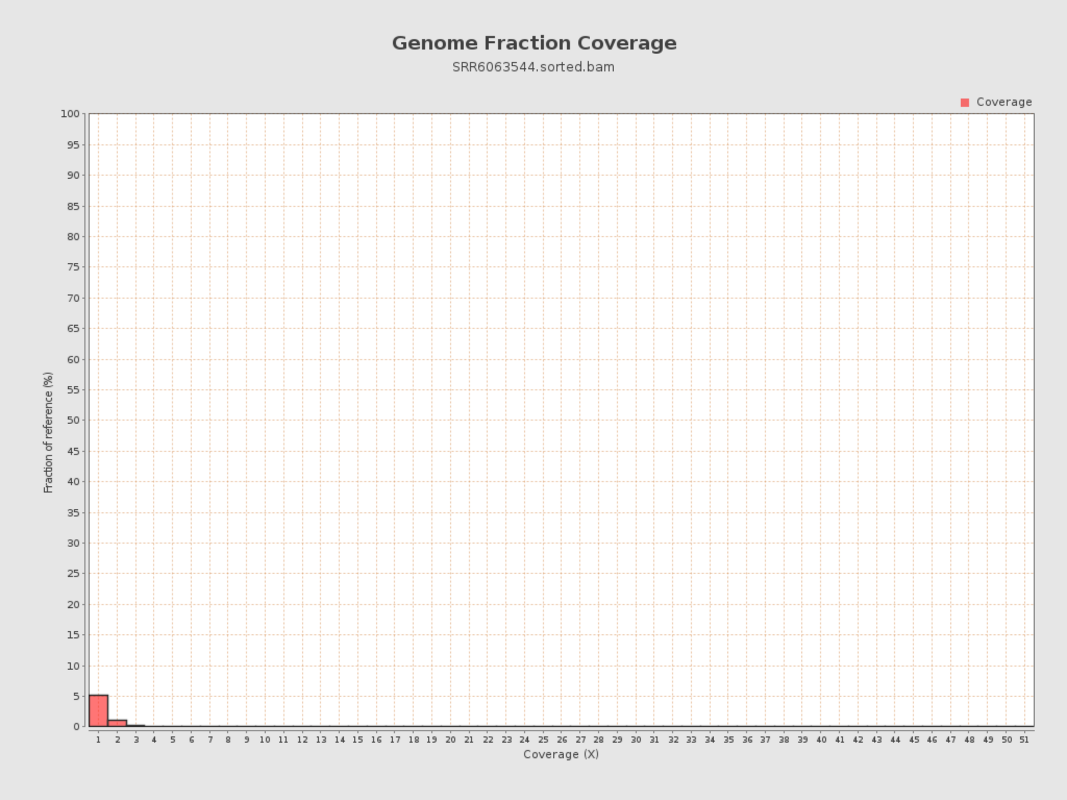
4. Results : Coverage Histogram



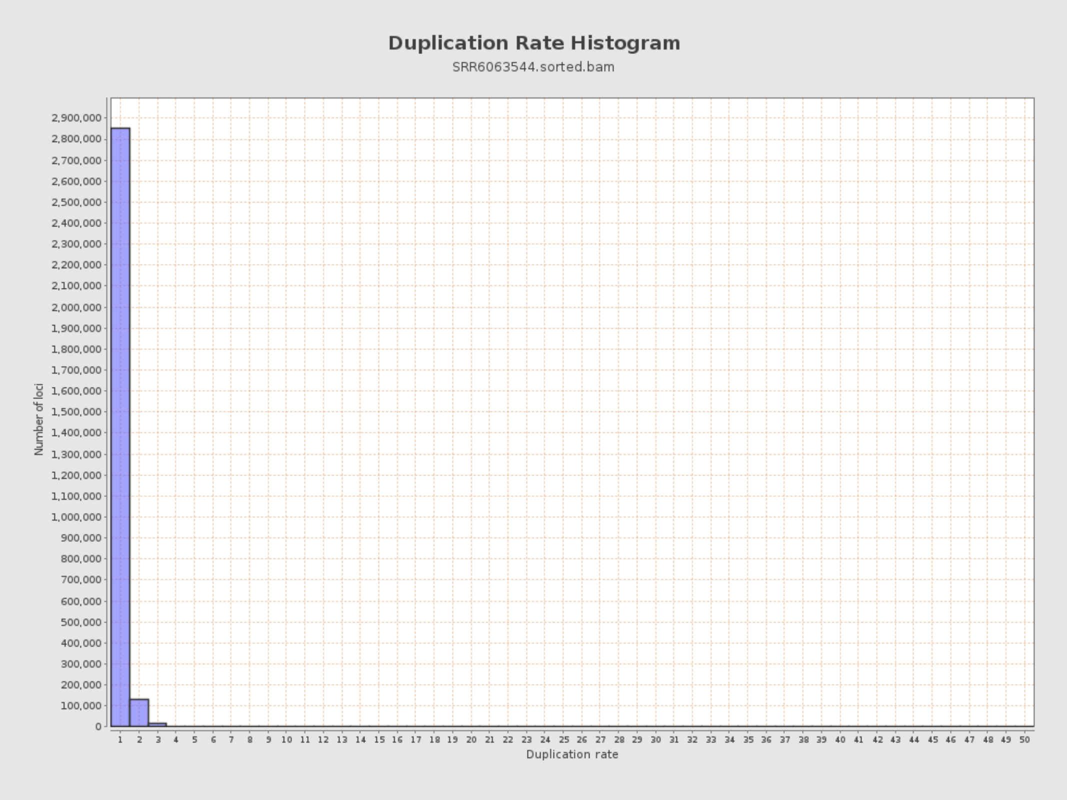
5. Results : Coverage Histogram (0-50X)



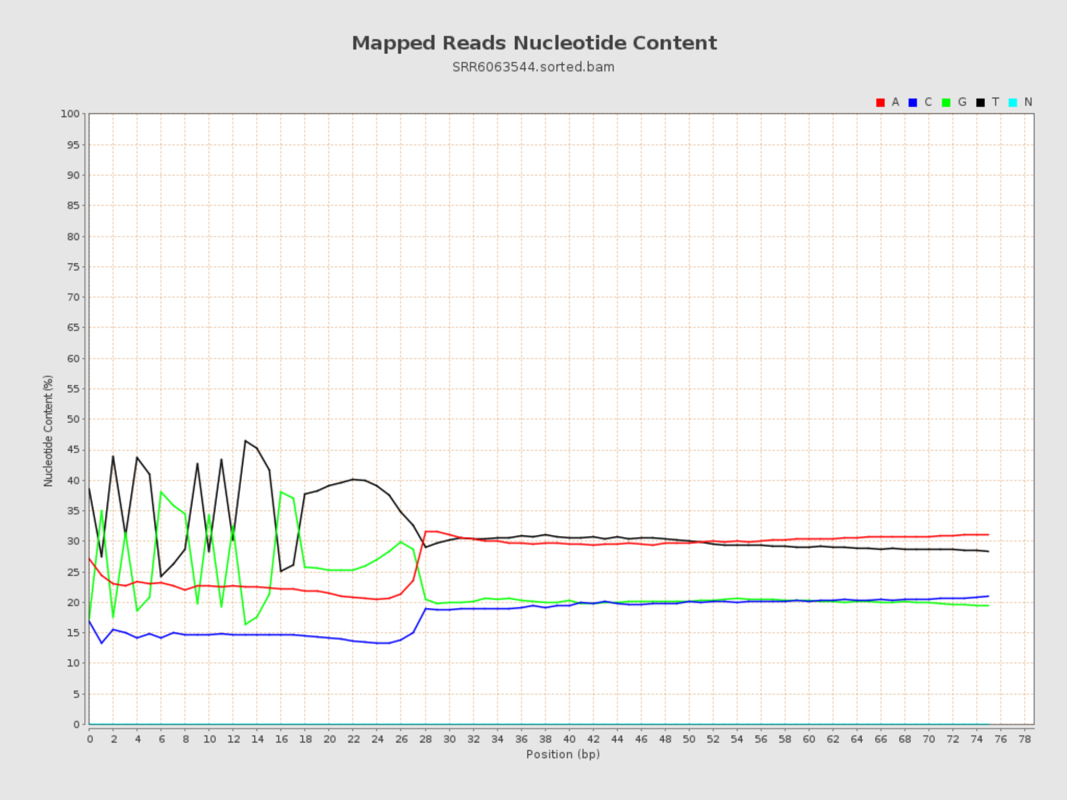
6. Results : Genome Fraction Coverage



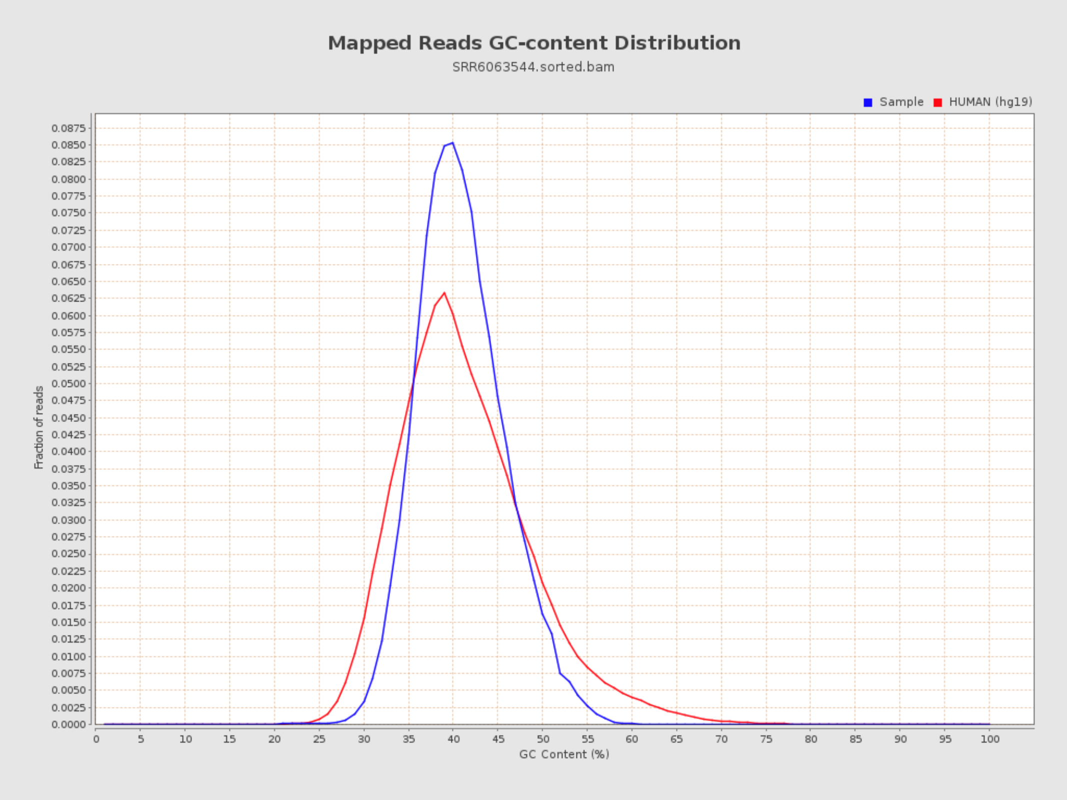
7. Results : Duplication Rate Histogram



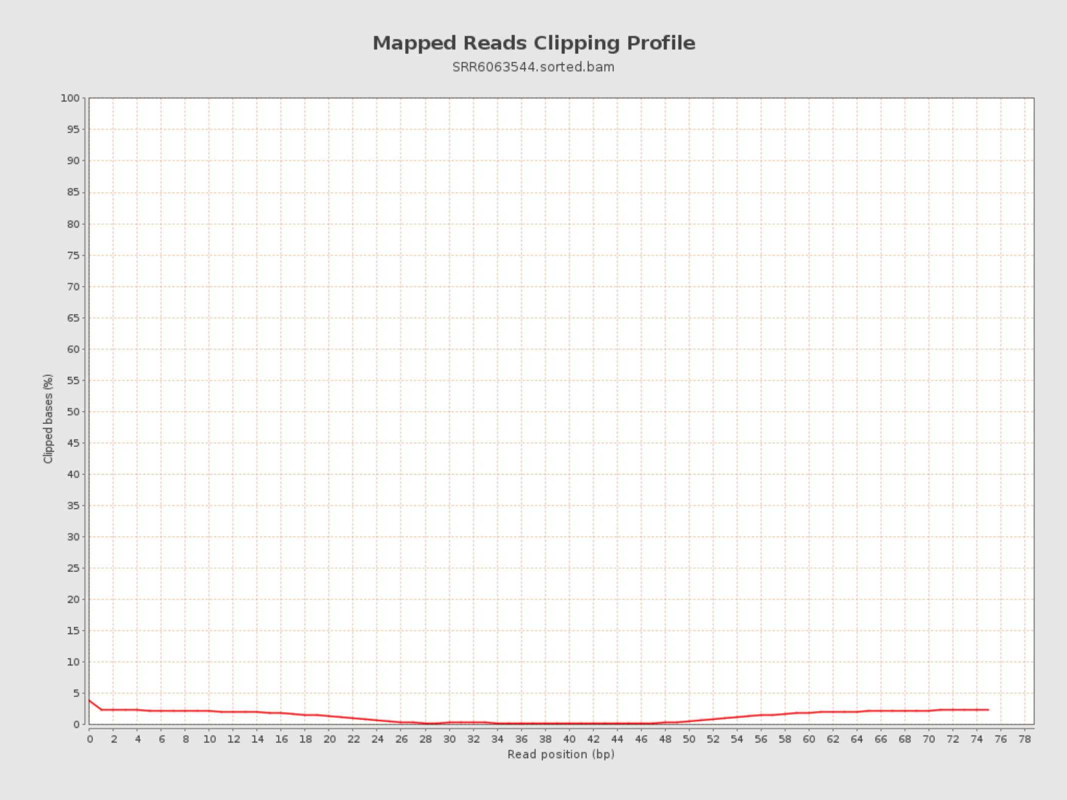
8. Results : Mapped Reads Nucleotide Content



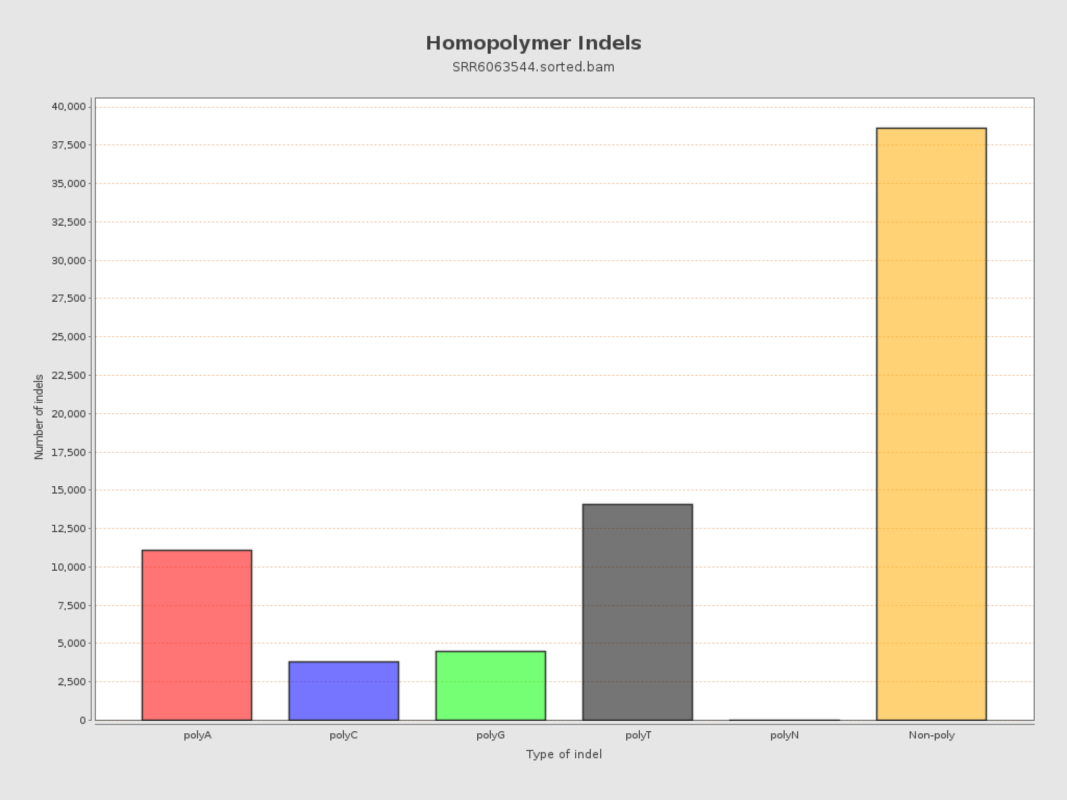
9. Results : Mapped Reads GC-content Distribution



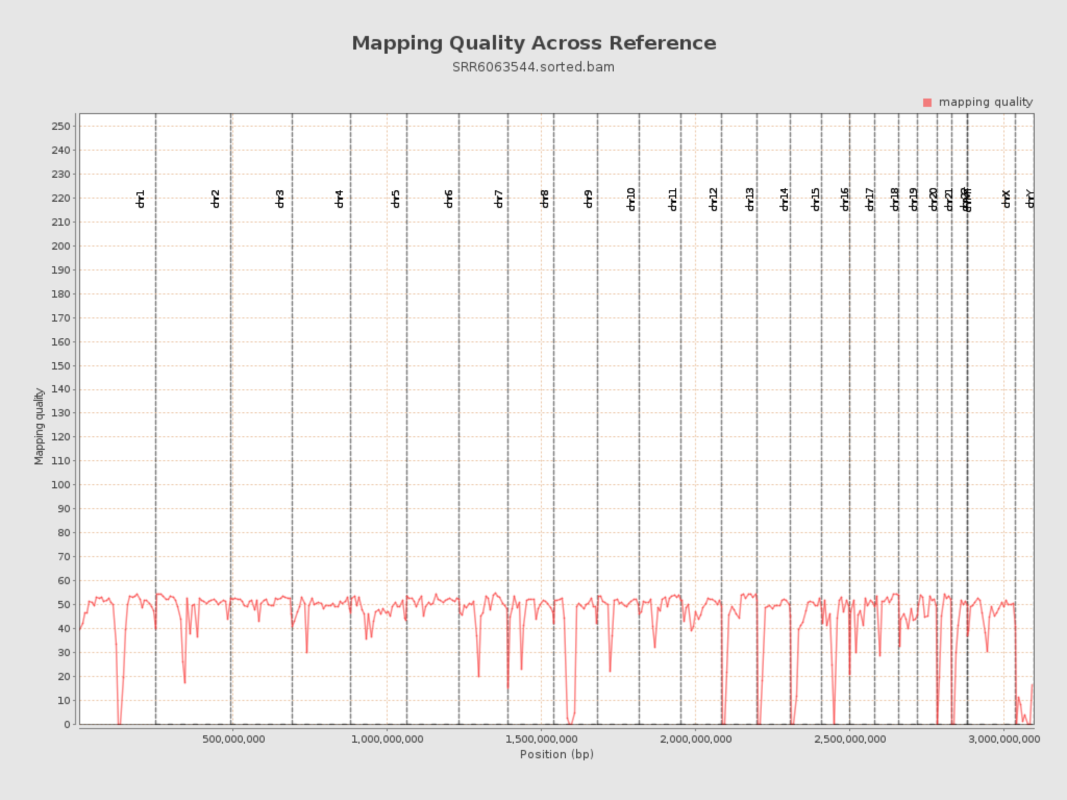
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram