Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:25:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063577.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_SRR6063577 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063577.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:25:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063577.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,372,915
Mapped reads	1,819,436 / 76.68%
Unmapped reads	553,479 / 23.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,919 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	281,598 / 11.87%
Duplication rate	11.76%
Clipped reads	868,382 / 36.6%

2.2. ACGT Content

Number/percentage of A's	33,150,825 / 27.69%
Number/percentage of C's	21,751,885 / 18.17%
Number/percentage of T's	38,525,207 / 32.17%
Number/percentage of G's	26,306,310 / 21.97%
Number/percentage of N's	3,044 / 0%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0387

Standard Deviation	0.4292

2.4. Mapping Quality

Mean Mapping Quality	46.94

2.5. Mismatches and indels

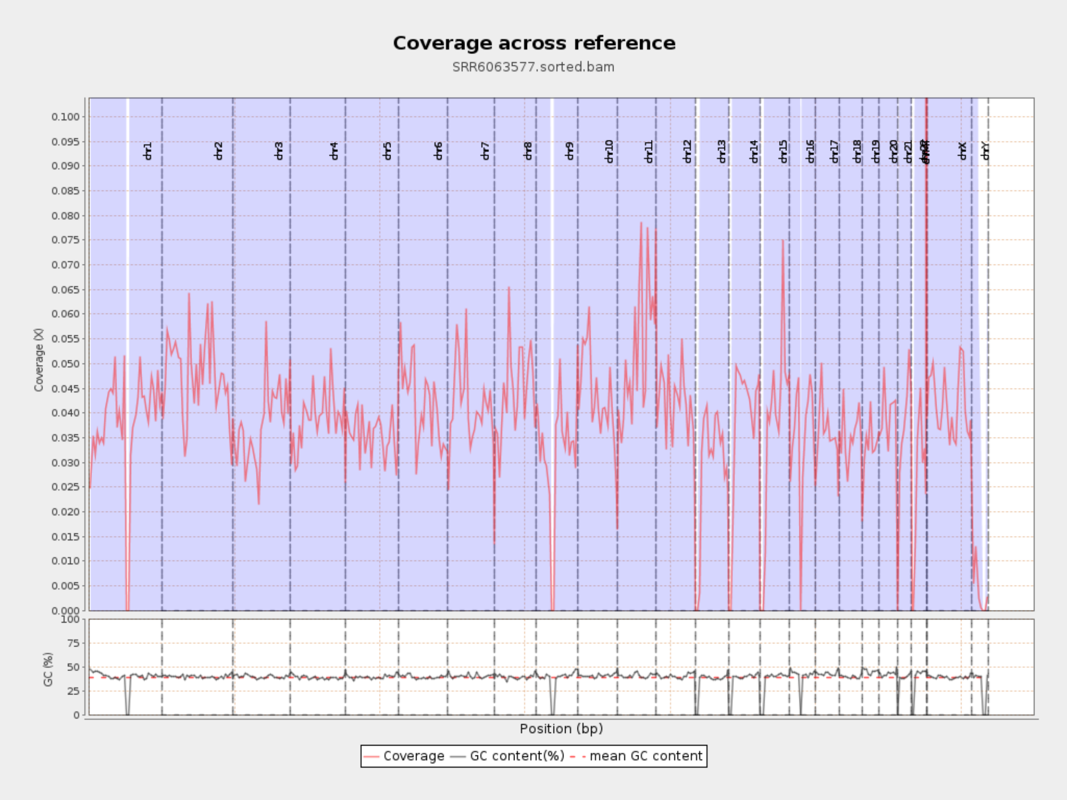
General error rate	0.79%
Mismatches	929,876
Insertions	8,777
Mapped reads with at least one insertion	0.48%
Deletions	32,378
Mapped reads with at least one deletion	1.76%
Homopolymer indels	48.8%

2.6. Chromosome stats

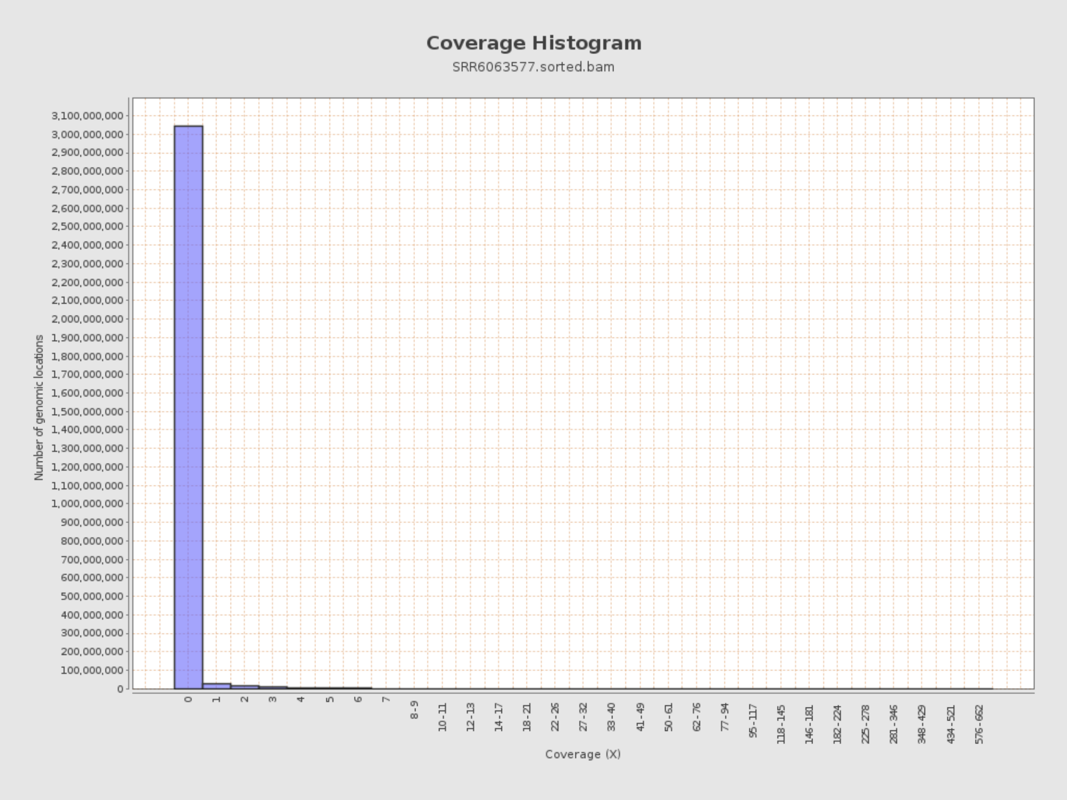
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9430116	0.0378	0.5211
chr2	243199373	11632985	0.0478	0.4893
chr3	198022430	7462879	0.0377	0.3648
chr4	191154276	7475257	0.0391	0.3761
chr5	180915260	6400802	0.0354	0.355
chr6	171115067	7157870	0.0418	0.4101
chr7	159138663	6693279	0.0421	0.5606

chr8	146364022	6489144	0.0443	0.5747
chr9	141213431	4389338	0.0311	0.3795
chr10	135534747	5956607	0.0439	0.4479
chr11	135006516	6953871	0.0515	0.4718
chr12	133851895	5622126	0.042	0.3876
chr13	115169878	3275345	0.0284	0.3312
chr14	107349540	3984178	0.0371	0.3705
chr15	102531392	3796026	0.037	0.3655
chr16	90354753	3182129	0.0352	0.3509
chr17	81195210	2894601	0.0356	0.3641
chr18	78077248	2786528	0.0357	0.5664
chr19	59128983	1984194	0.0336	0.4154
chr20	63025520	2473561	0.0392	0.3769
chr21	48129895	1723202	0.0358	0.3604
chr22	51304566	1255904	0.0245	0.2944
chrMT	16571	26988	1.6286	2.5202
chrX	155270560	6479850	0.0417	0.3949
chrY	59373566	267505	0.0045	0.1214

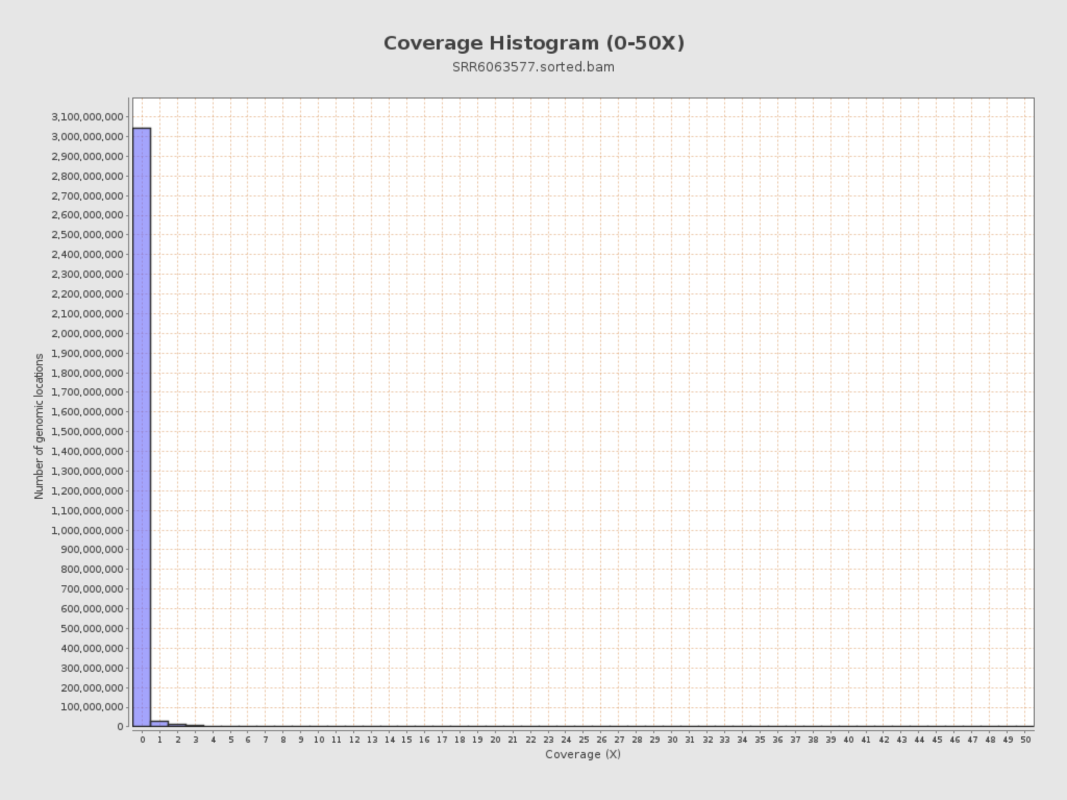
3. Results : Coverage across reference



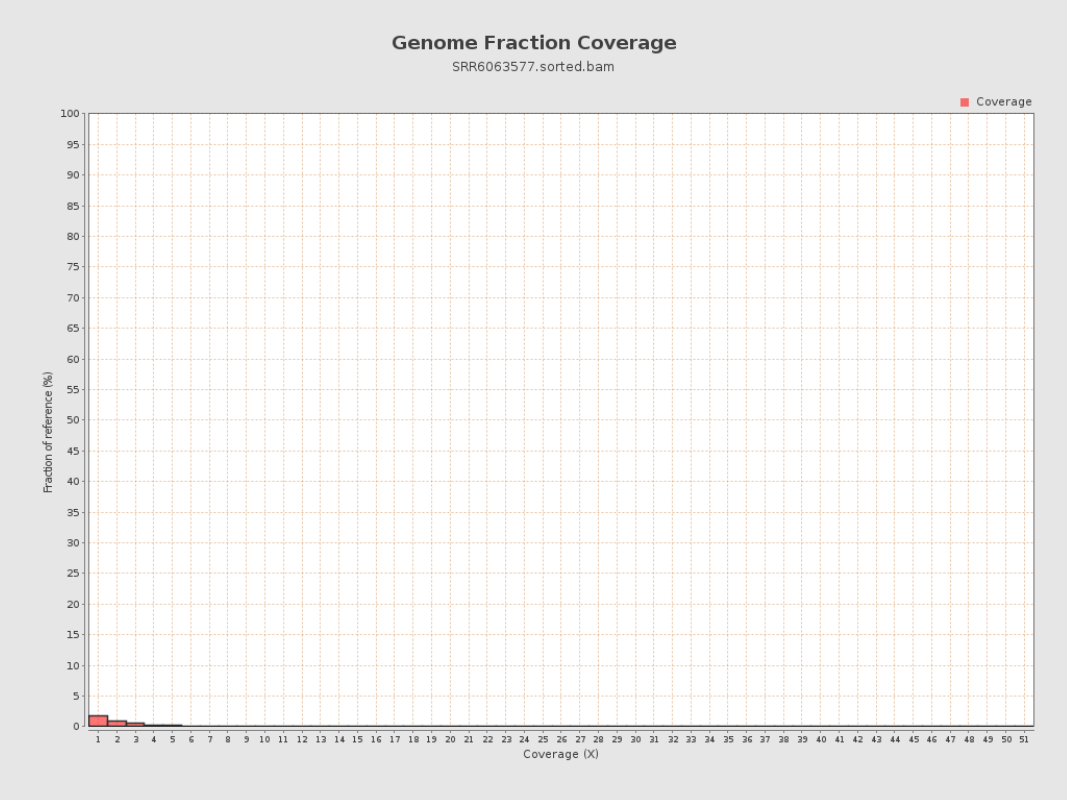
4. Results : Coverage Histogram



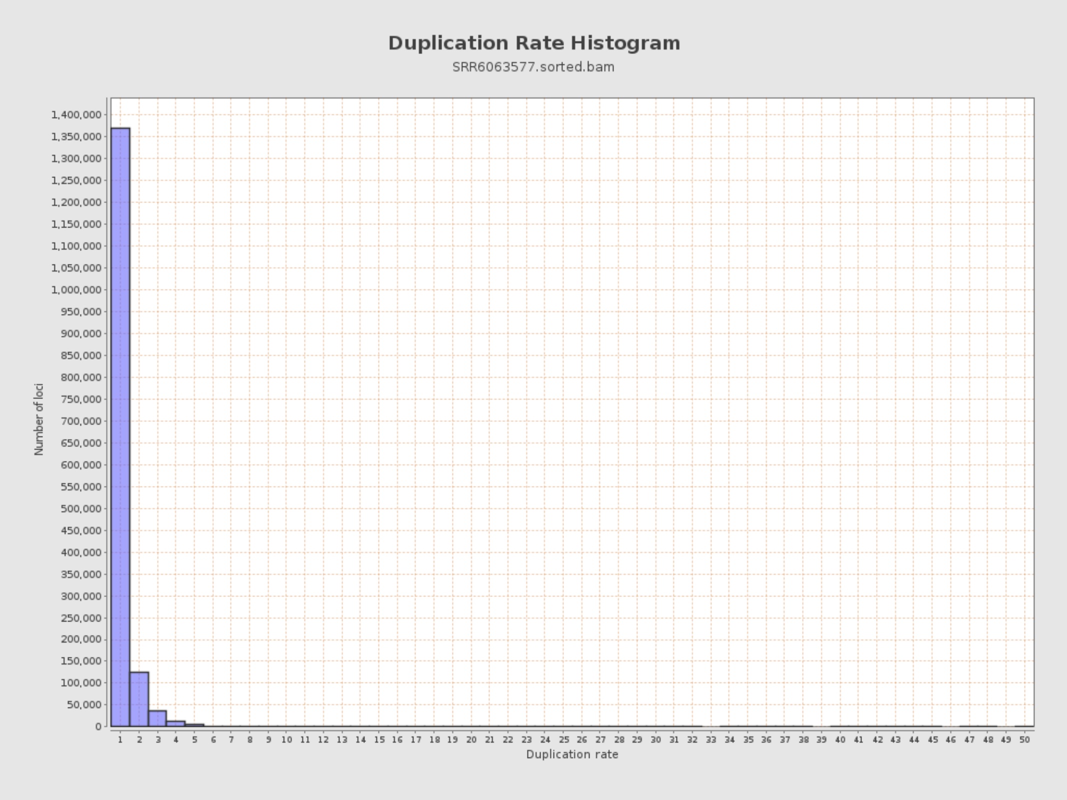
5. Results : Coverage Histogram (0-50X)



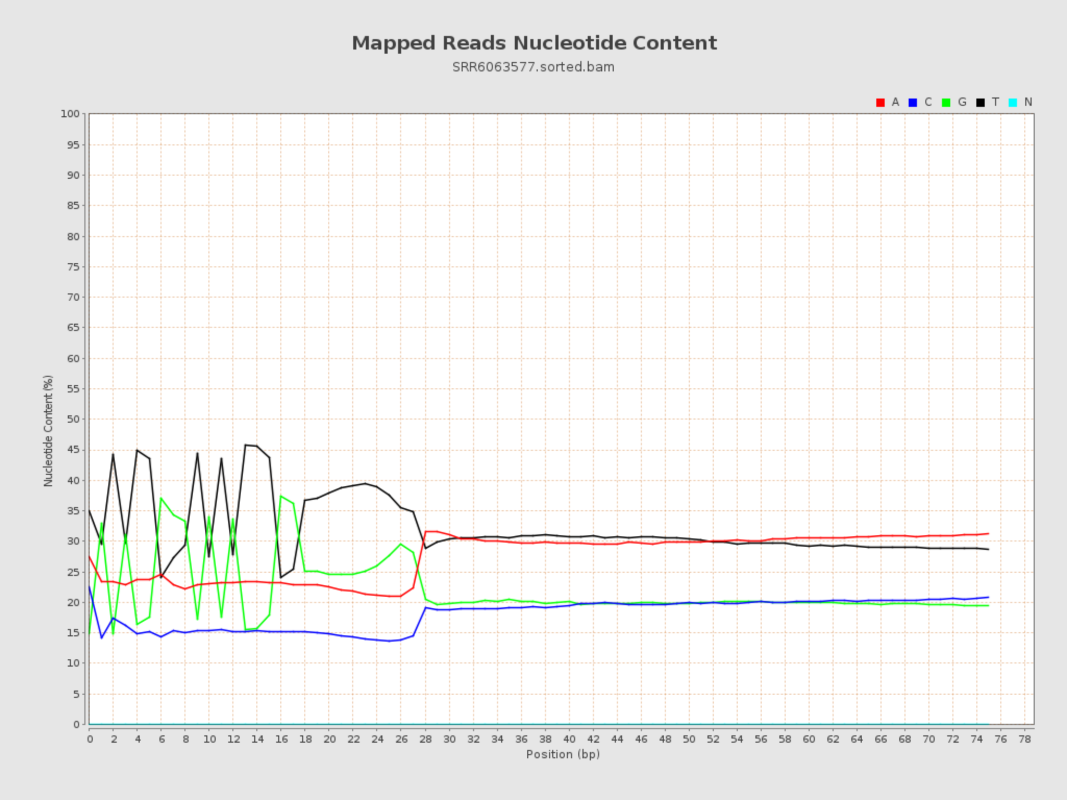
6. Results : Genome Fraction Coverage



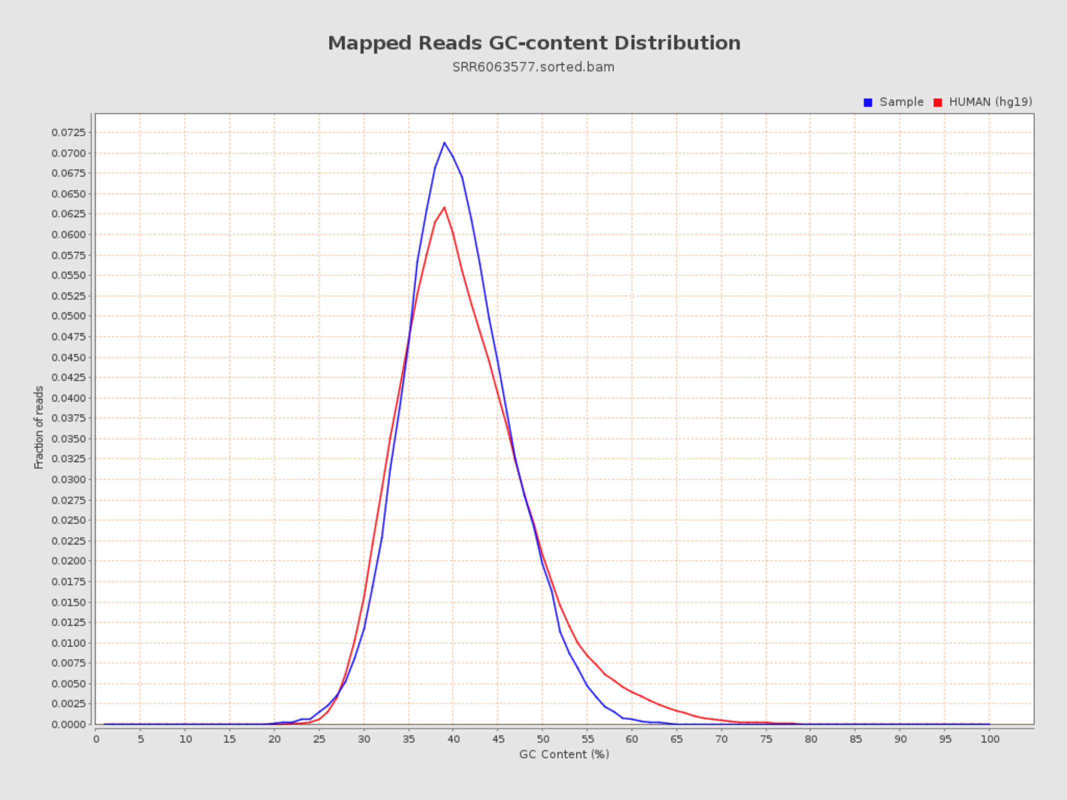
7. Results : Duplication Rate Histogram



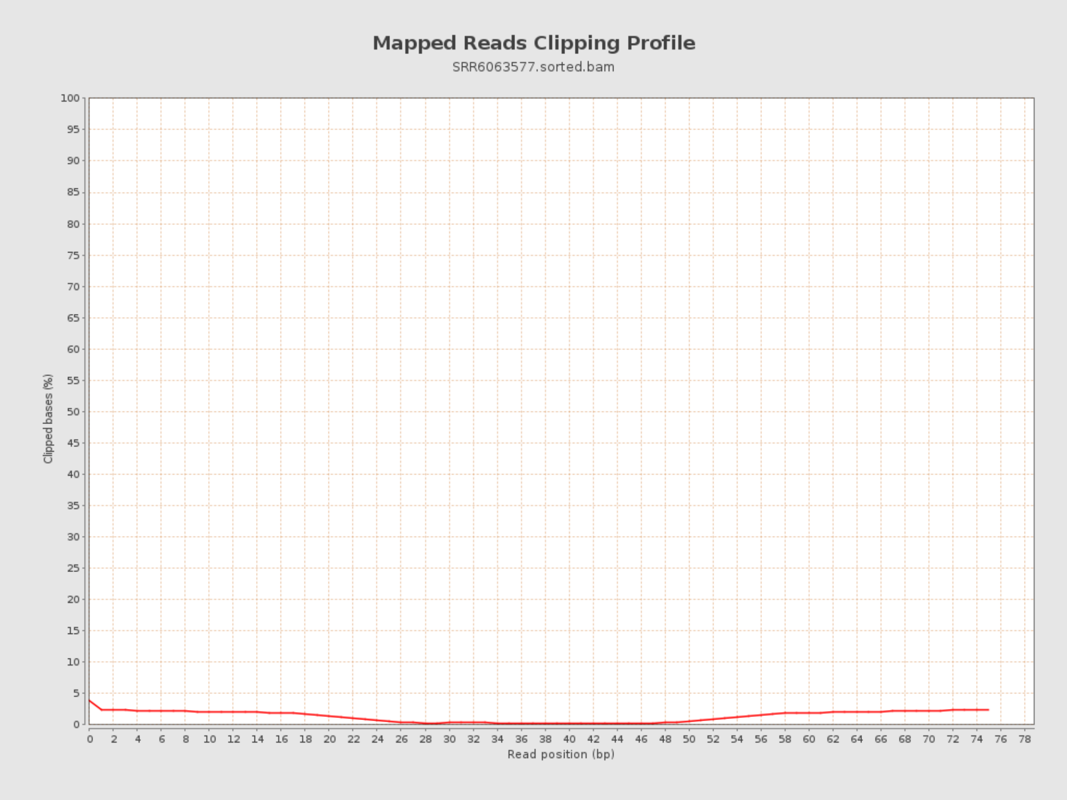
8. Results : Mapped Reads Nucleotide Content



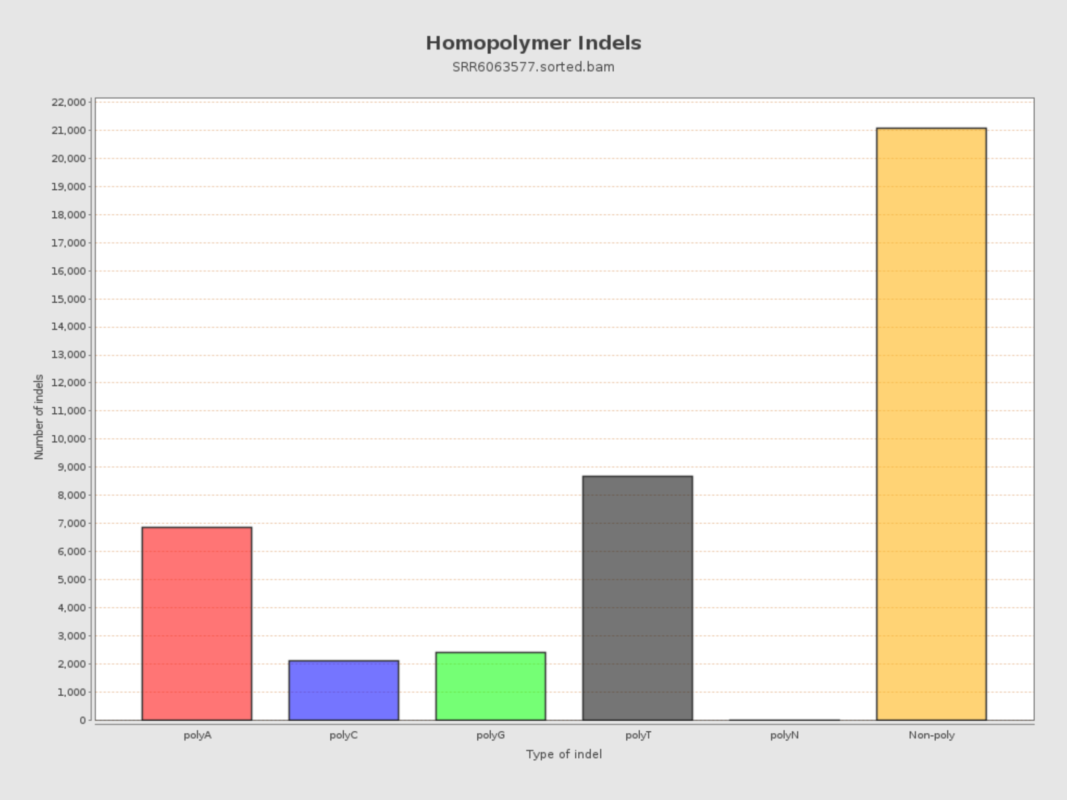
9. Results : Mapped Reads GC-content Distribution



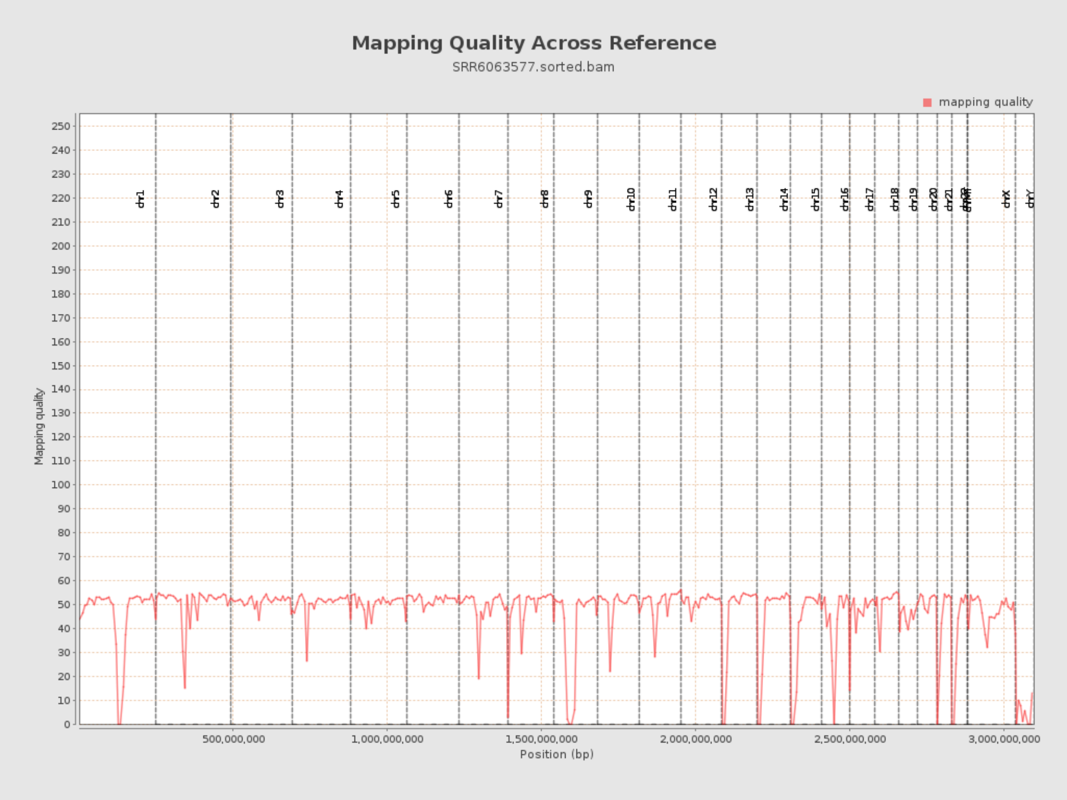
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram