Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:28:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063578.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_SRR6063578 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063578.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:28:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063578.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,925,319
Mapped reads	1,654,149 / 85.92%
Unmapped reads	271,170 / 14.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,764 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	283,572 / 14.73%
Duplication rate	12.52%
Clipped reads	808,757 / 42.01%

2.2. ACGT Content

Number/percentage of A's	30,449,146 / 28.01%
Number/percentage of C's	19,877,468 / 18.28%
Number/percentage of T's	34,766,955 / 31.98%
Number/percentage of G's	23,621,763 / 21.73%
Number/percentage of N's	2,839 / 0%
GC Percentage	40.01%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.422

2.4. Mapping Quality

Mean Mapping Quality	46.64

2.5. Mismatches and indels

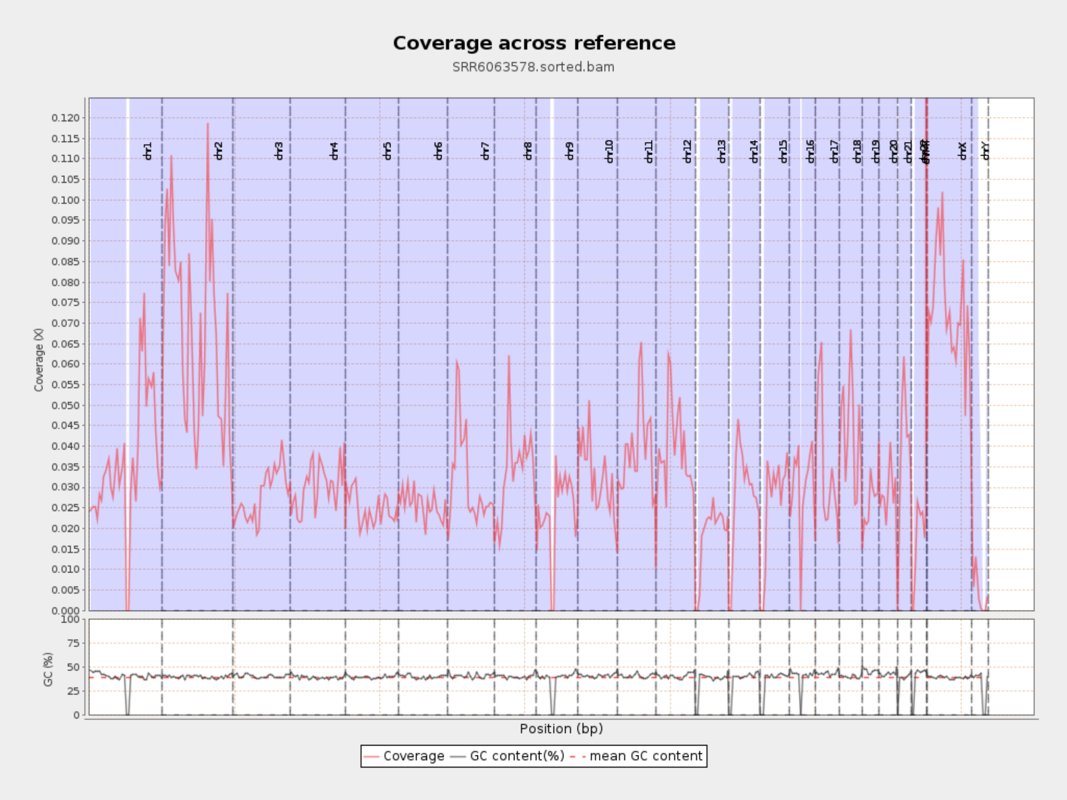
General error rate	0.8%
Mismatches	857,199
Insertions	7,615
Mapped reads with at least one insertion	0.46%
Deletions	30,395
Mapped reads with at least one deletion	1.81%
Homopolymer indels	48.77%

2.6. Chromosome stats

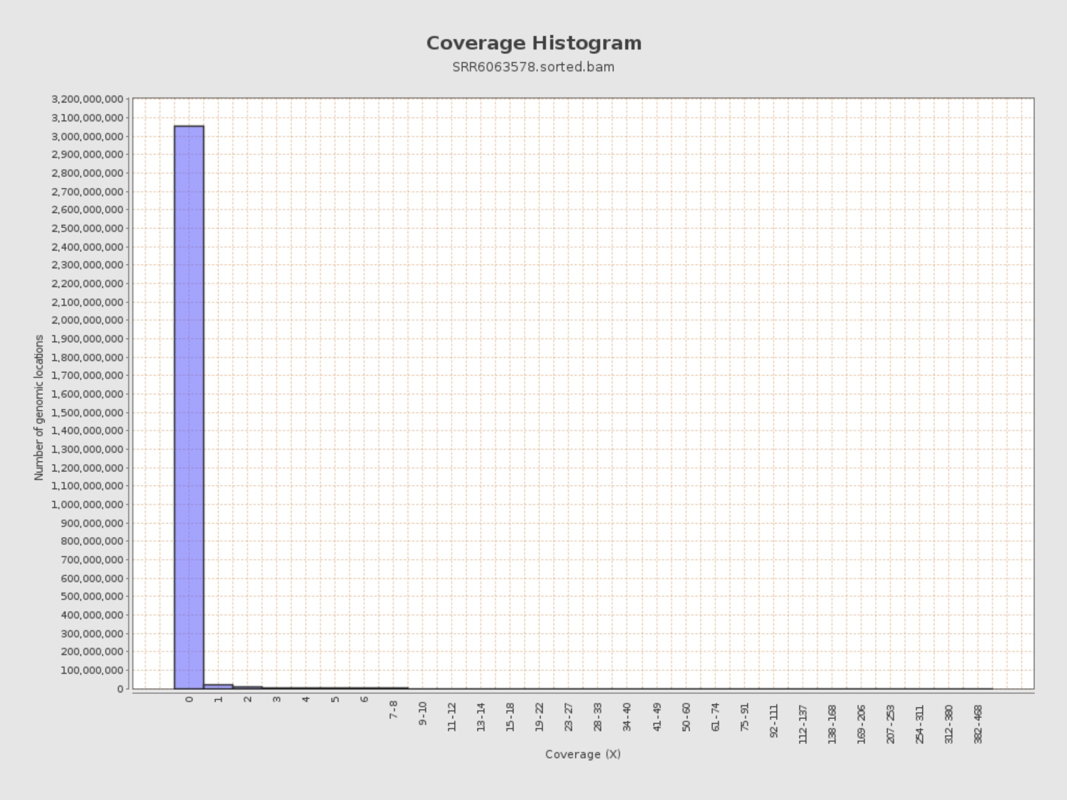
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9066656	0.0364	0.498
chr2	243199373	16654951	0.0685	0.5994
chr3	198022430	5589224	0.0282	0.3428
chr4	191154276	5793462	0.0303	0.3581
chr5	180915260	4479872	0.0248	0.3172
chr6	171115067	4382778	0.0256	0.3381
chr7	159138663	5047289	0.0317	0.4786

chr8	146364022	4981347	0.034	0.4862
chr9	141213431	3393959	0.024	0.3563
chr10	135534747	4440589	0.0328	0.4075
chr11	135006516	5256789	0.0389	0.434
chr12	133851895	5290595	0.0395	0.4068
chr13	115169878	2104417	0.0183	0.2702
chr14	107349540	3026231	0.0282	0.337
chr15	102531392	2667075	0.026	0.3256
chr16	90354753	2712897	0.03	0.3458
chr17	81195210	2755212	0.0339	0.3961
chr18	78077248	3415972	0.0438	0.5511
chr19	59128983	1569404	0.0265	0.3896
chr20	63025520	1782968	0.0283	0.3378
chr21	48129895	1874427	0.0389	0.406
chr22	51304566	838024	0.0163	0.2457
chrMT	16571	93676	5.653	4.9863
chrX	155270560	11288757	0.0727	0.5594
chrY	59373566	265462	0.0045	0.1505

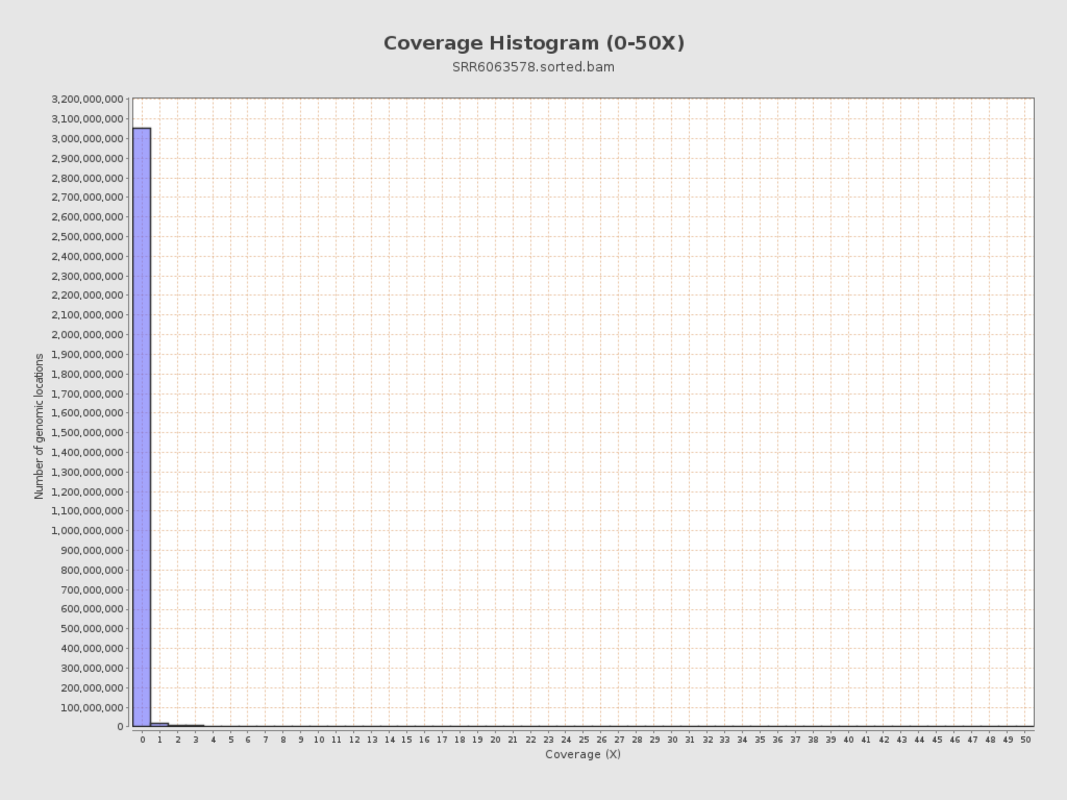
3. Results : Coverage across reference



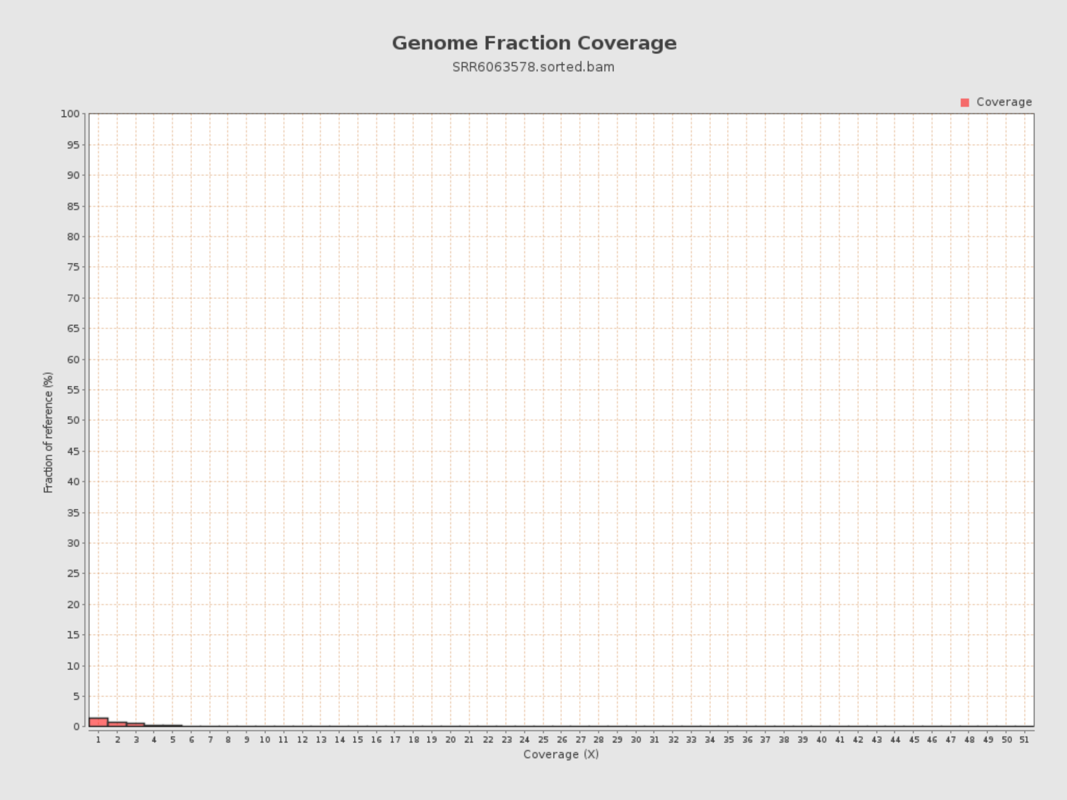
4. Results : Coverage Histogram



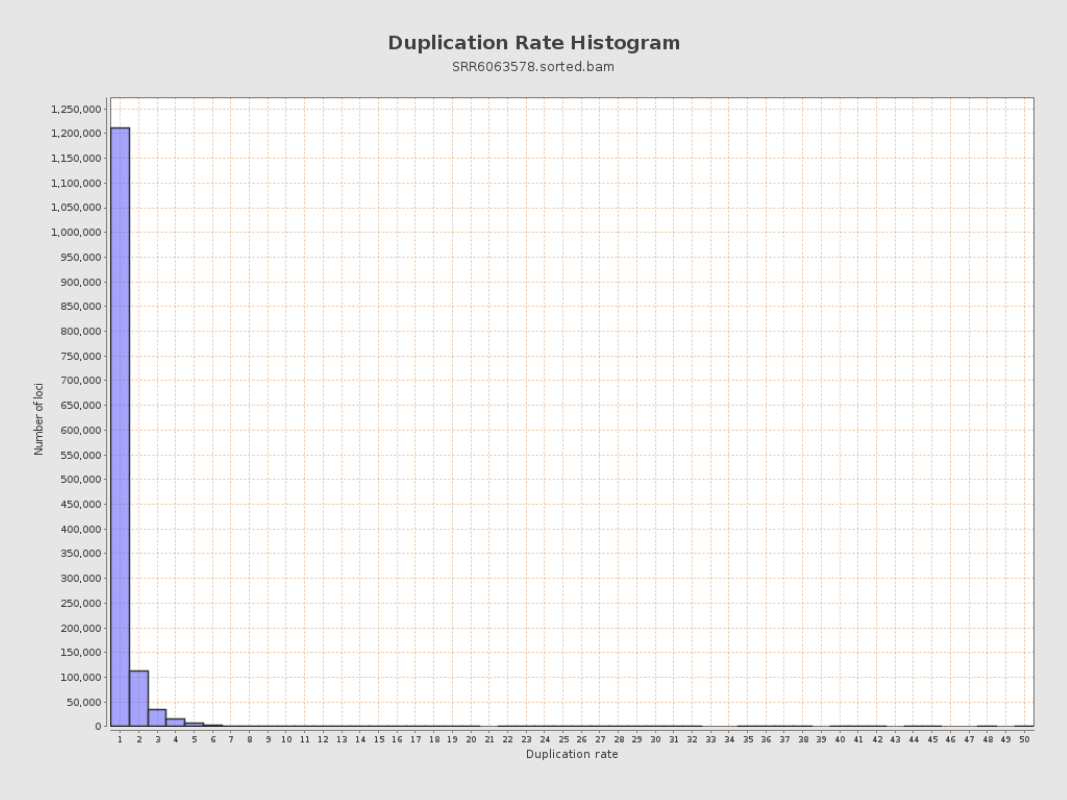
5. Results : Coverage Histogram (0-50X)



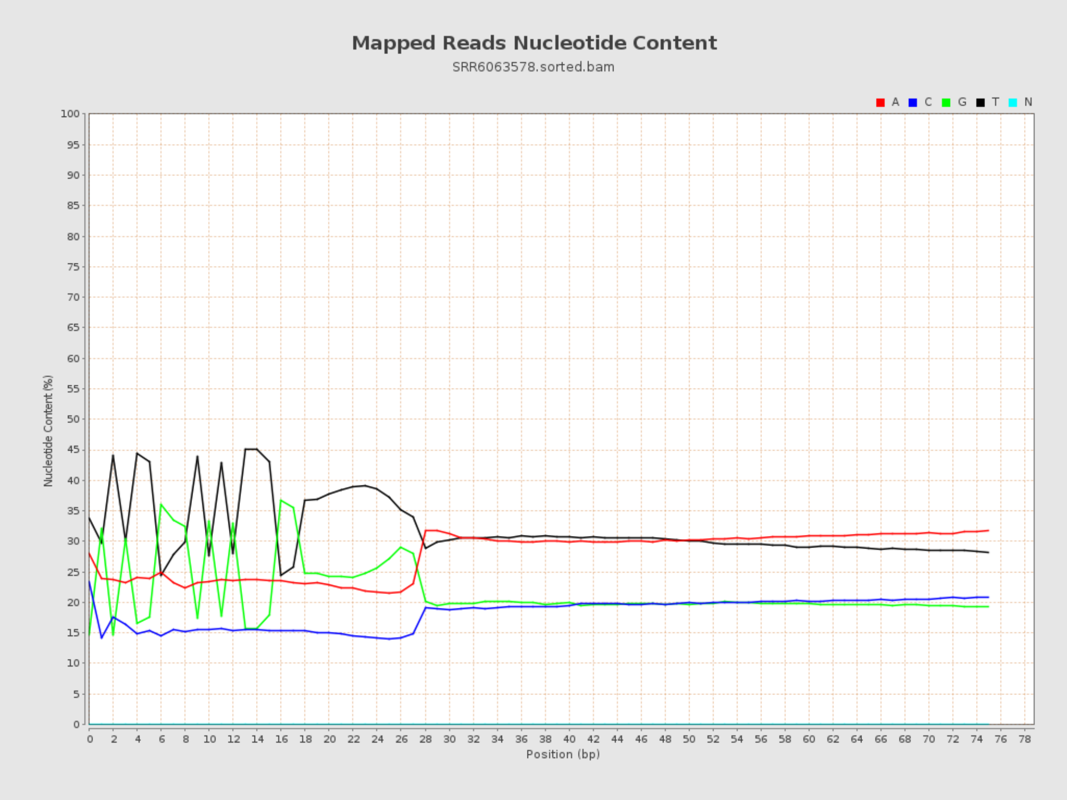
6. Results : Genome Fraction Coverage



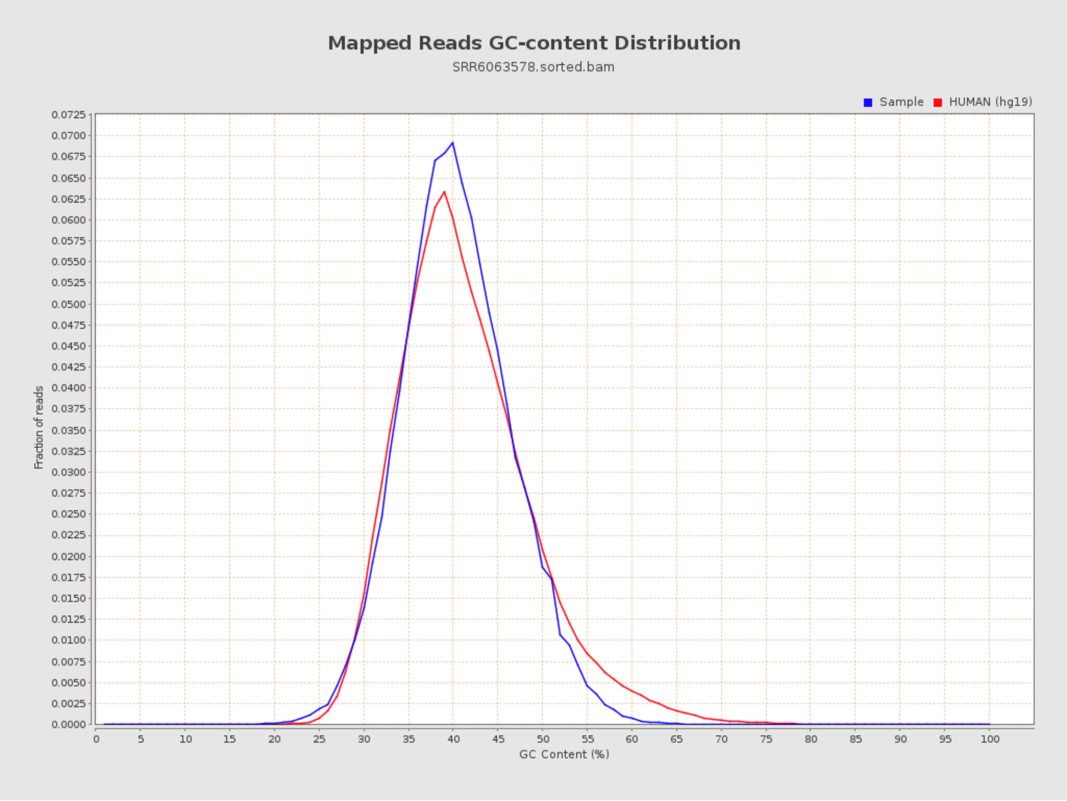
7. Results : Duplication Rate Histogram



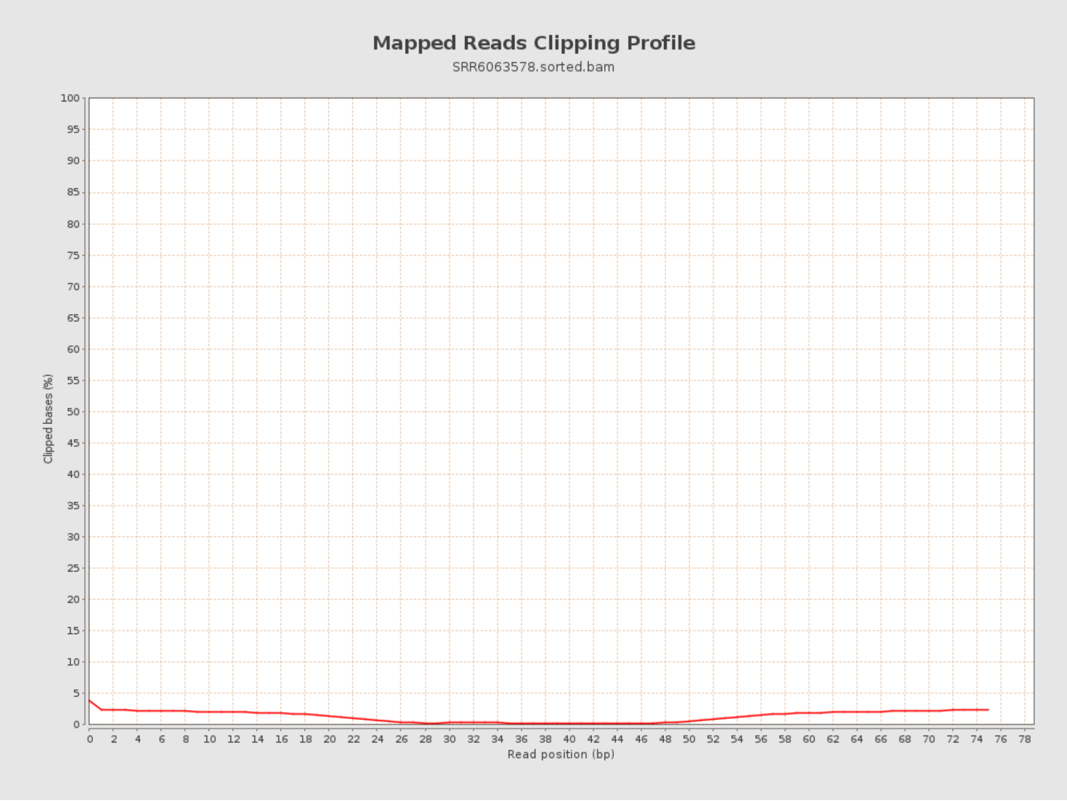
8. Results : Mapped Reads Nucleotide Content



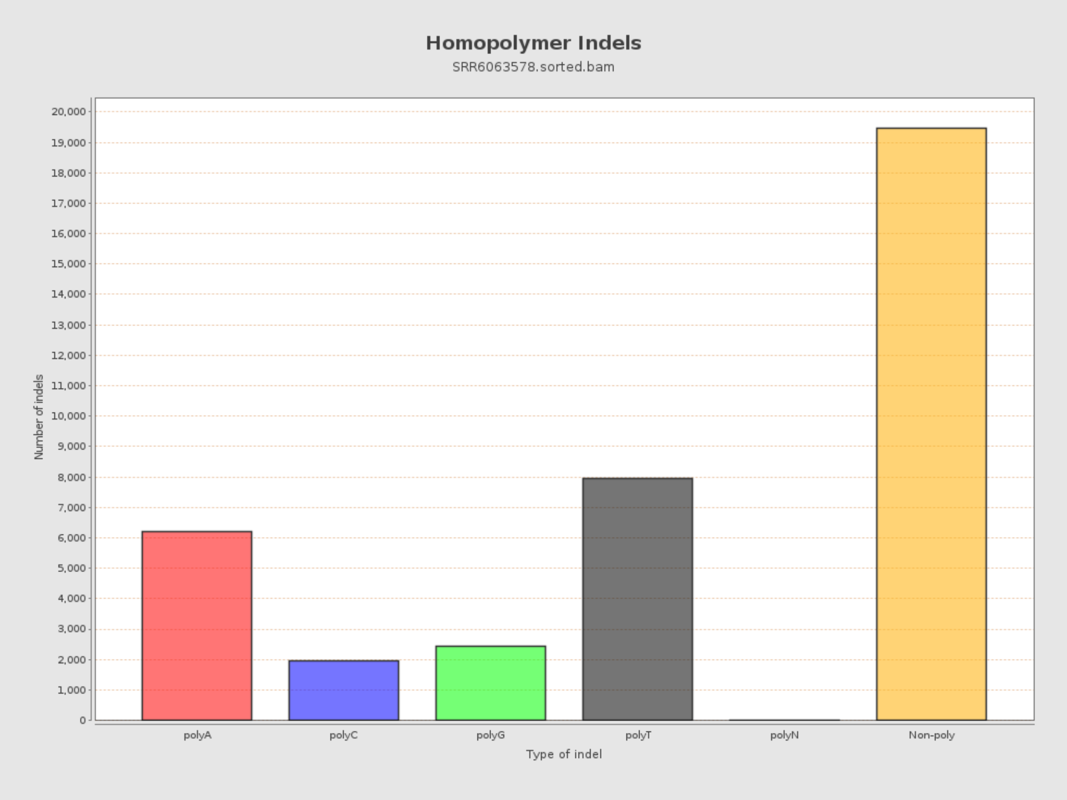
9. Results : Mapped Reads GC-content Distribution



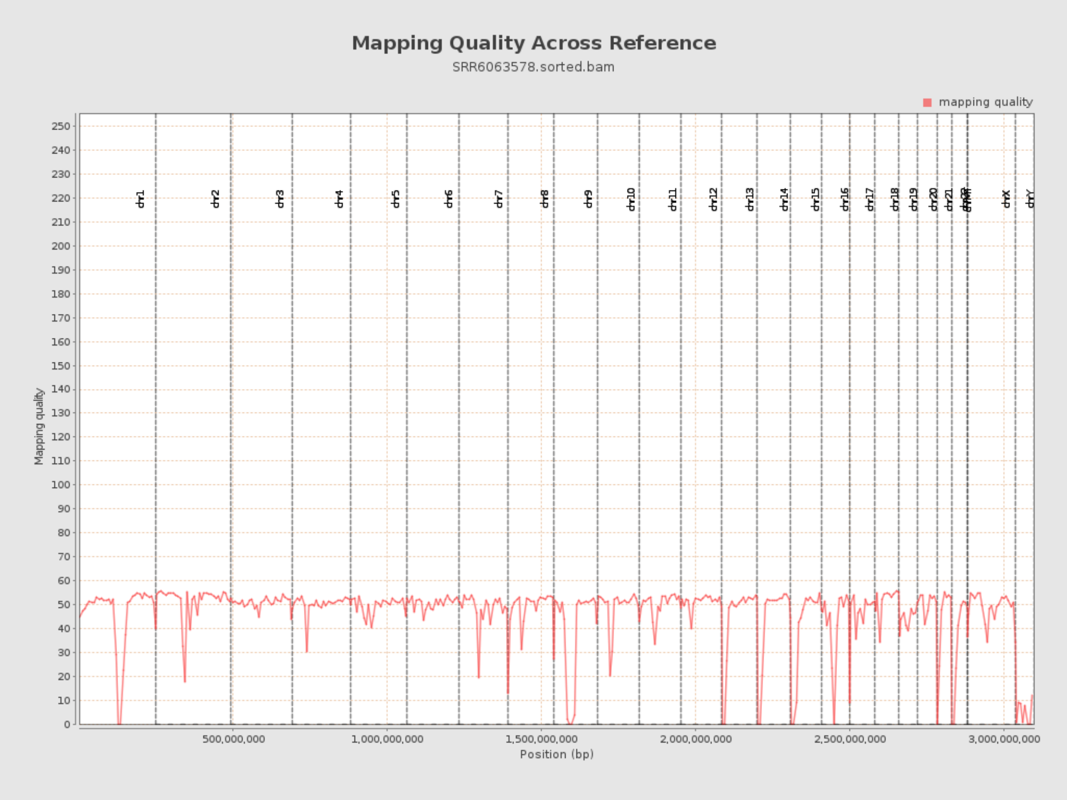
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram