Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:29:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063599.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_SRR6063599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063599.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:29:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063599.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,768,183
Mapped reads	857,898 / 48.52%
Unmapped reads	910,285 / 51.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,680 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	176,531 / 9.98%
Duplication rate	13.68%
Clipped reads	459,763 / 26%

2.2. ACGT Content

Number/percentage of A's	15,138,801 / 27.58%
Number/percentage of C's	9,985,492 / 18.19%
Number/percentage of T's	17,607,719 / 32.07%
Number/percentage of G's	12,164,384 / 22.16%
Number/percentage of N's	1,345 / 0%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0177

Standard Deviation	0.4172

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

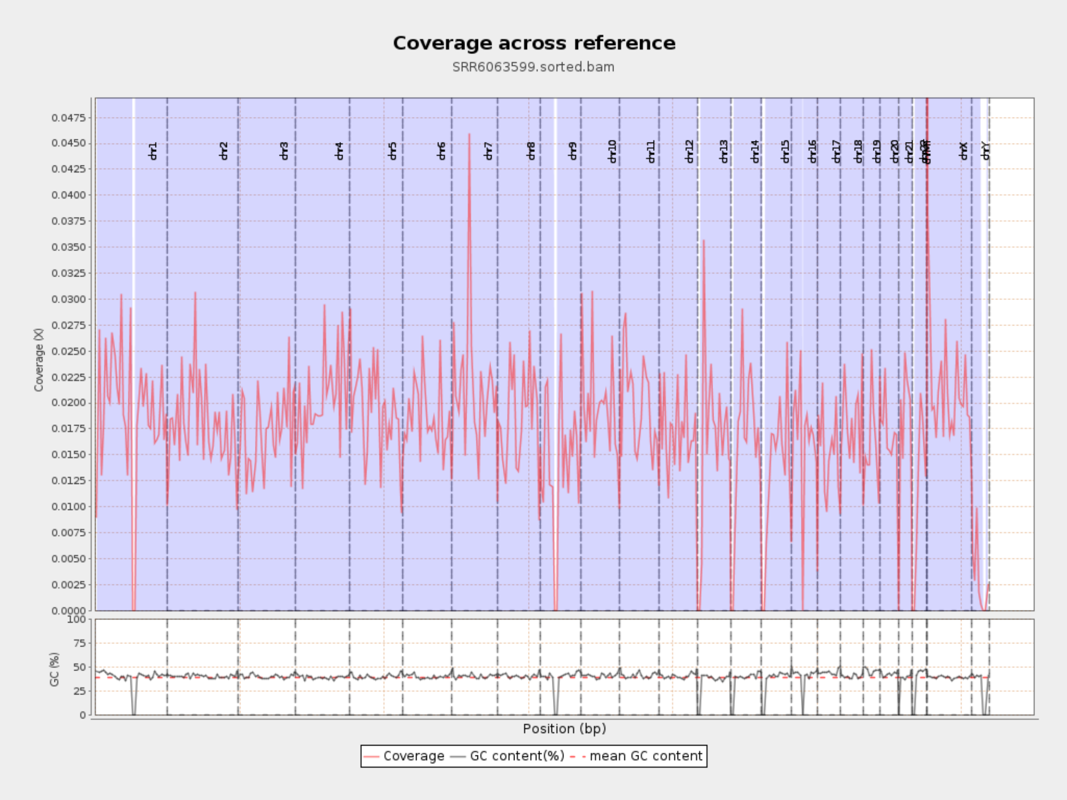
General error rate	0.83%
Mismatches	446,443
Insertions	4,393
Mapped reads with at least one insertion	0.51%
Deletions	13,360
Mapped reads with at least one deletion	1.54%
Homopolymer indels	46.33%

2.6. Chromosome stats

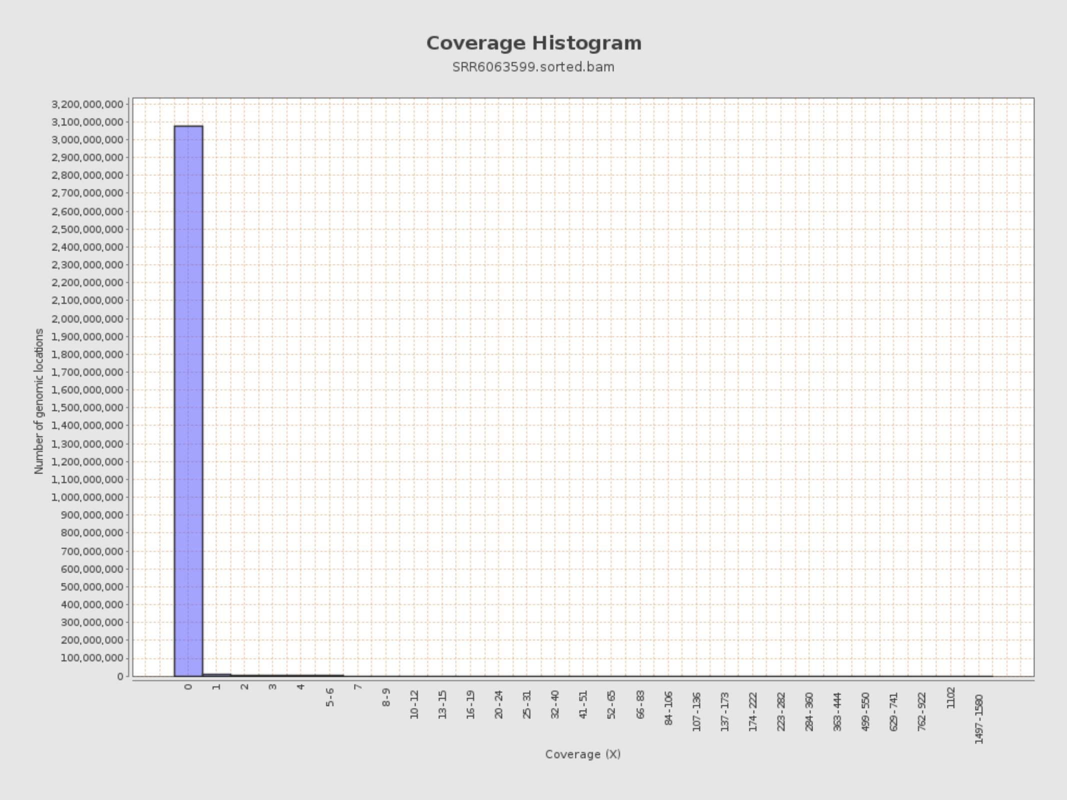
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4708378	0.0189	0.4723
chr2	243199373	4393355	0.0181	0.4011
chr3	198022430	3404358	0.0172	0.312
chr4	191154276	3906446	0.0204	0.7435
chr5	180915260	3444172	0.019	0.3392
chr6	171115067	3172205	0.0185	0.3536
chr7	159138663	3480052	0.0219	0.4849

chr8	146364022	2754323	0.0188	0.4234
chr9	141213431	1998467	0.0142	0.2917
chr10	135534747	2659120	0.0196	0.3585
chr11	135006516	2658888	0.0197	0.3446
chr12	133851895	2324327	0.0174	0.3282
chr13	115169878	1860391	0.0162	0.3403
chr14	107349540	1697479	0.0158	0.3836
chr15	102531392	1381004	0.0135	0.686
chr16	90354753	1454282	0.0161	0.3054
chr17	81195210	1240013	0.0153	0.2901
chr18	78077248	1413103	0.0181	0.4497
chr19	59128983	955009	0.0162	0.3381
chr20	63025520	1071092	0.017	0.3089
chr21	48129895	859498	0.0179	0.3333
chr22	51304566	594520	0.0116	0.2378
chrMT	16571	10198	0.6154	2.6275
chrX	155270560	3313966	0.0213	0.3753
chrY	59373566	165573	0.0028	0.1841

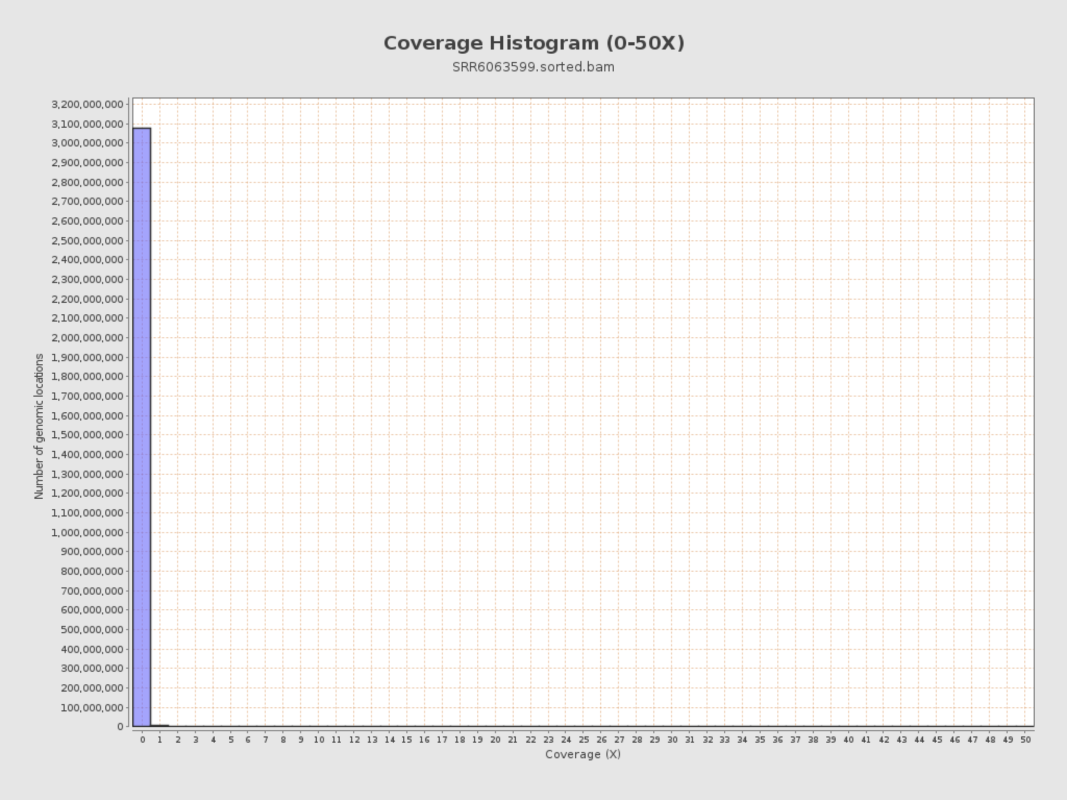
3. Results : Coverage across reference



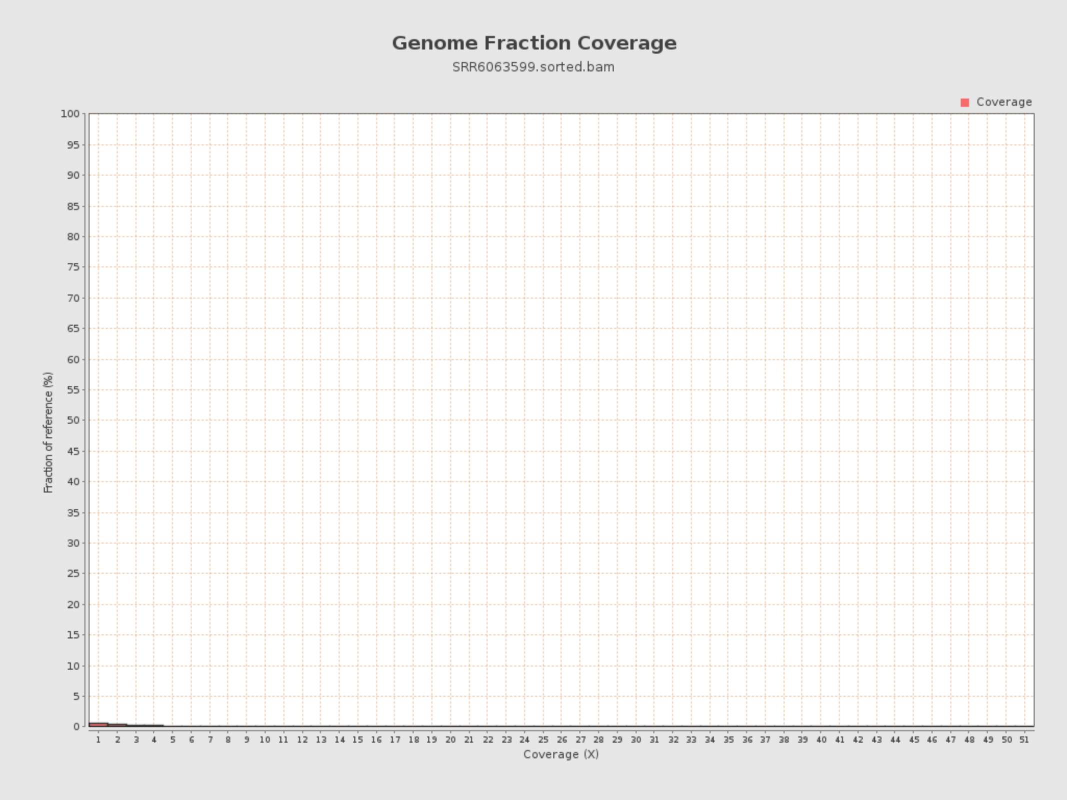
4. Results : Coverage Histogram



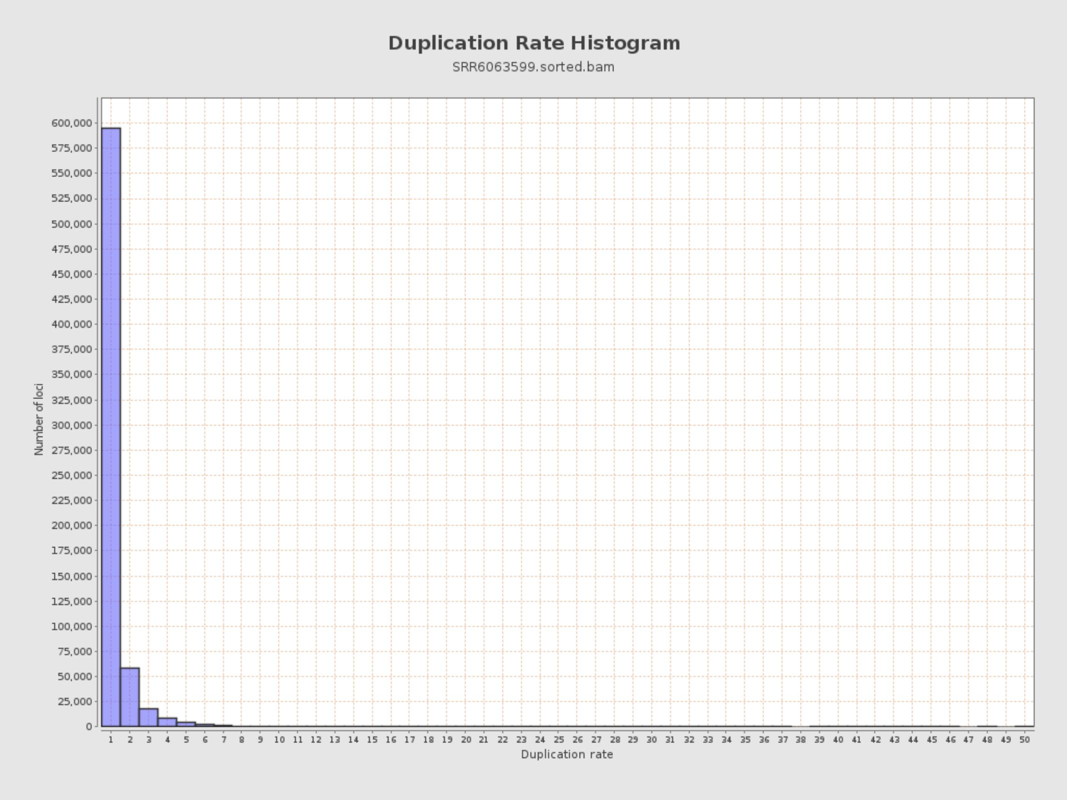
5. Results : Coverage Histogram (0-50X)



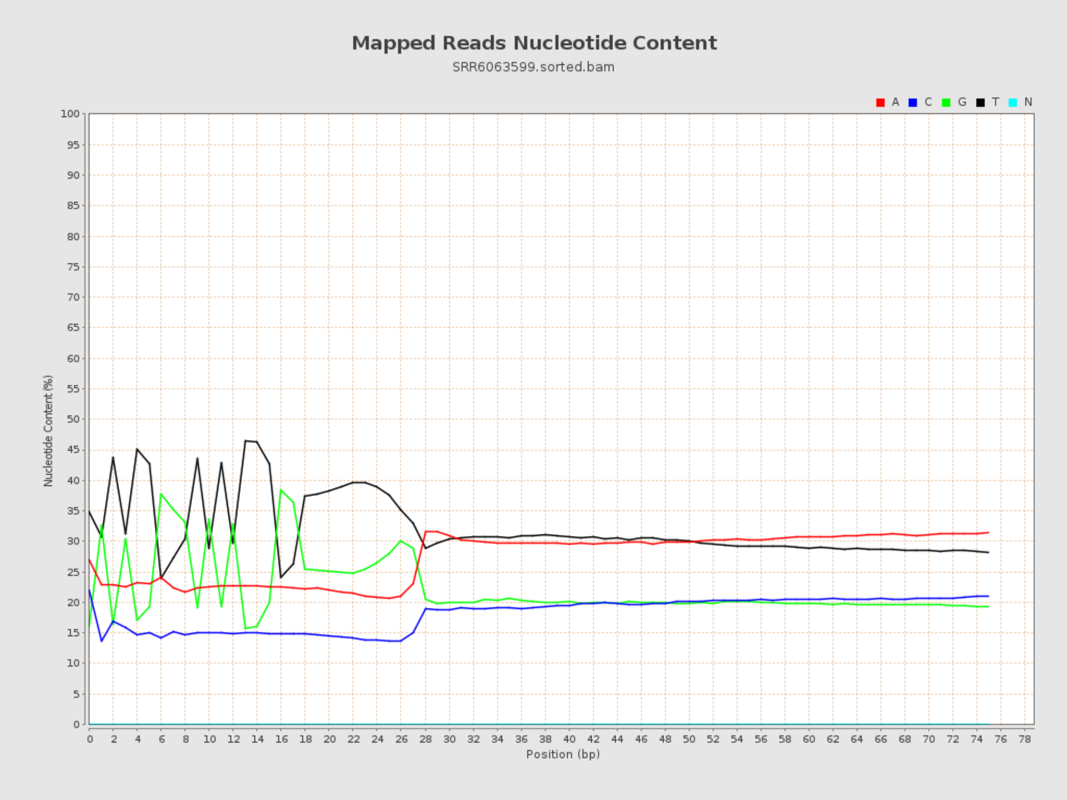
6. Results : Genome Fraction Coverage



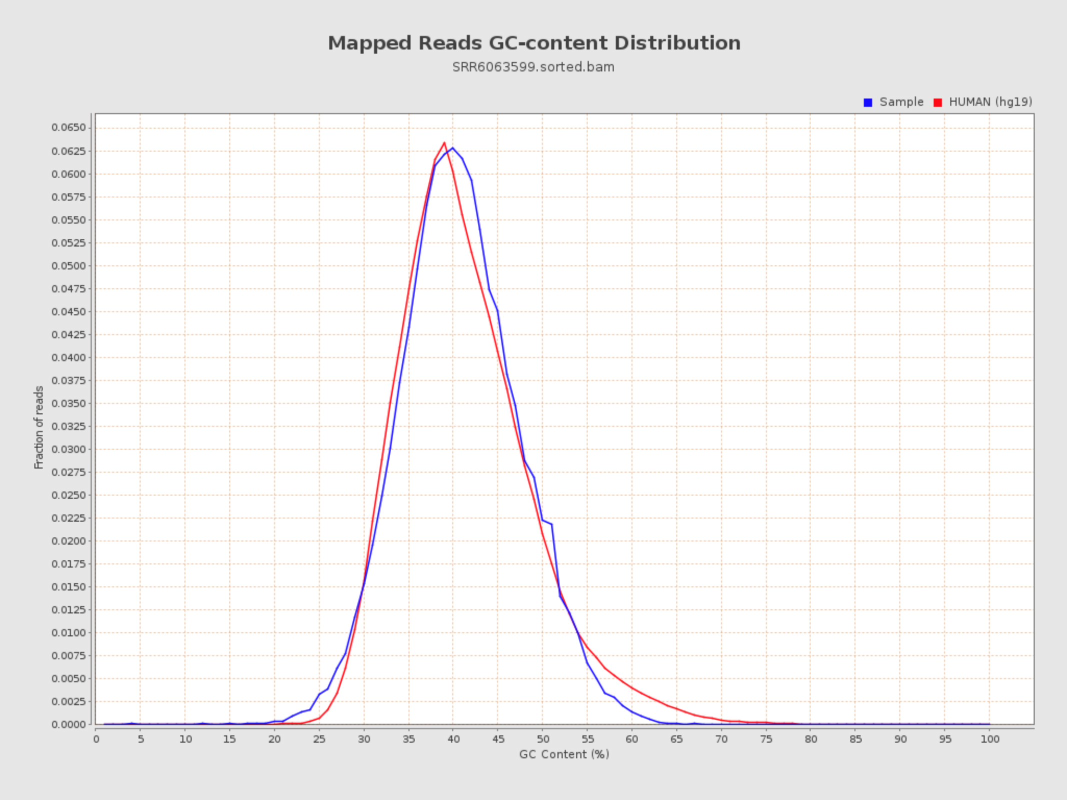
7. Results : Duplication Rate Histogram



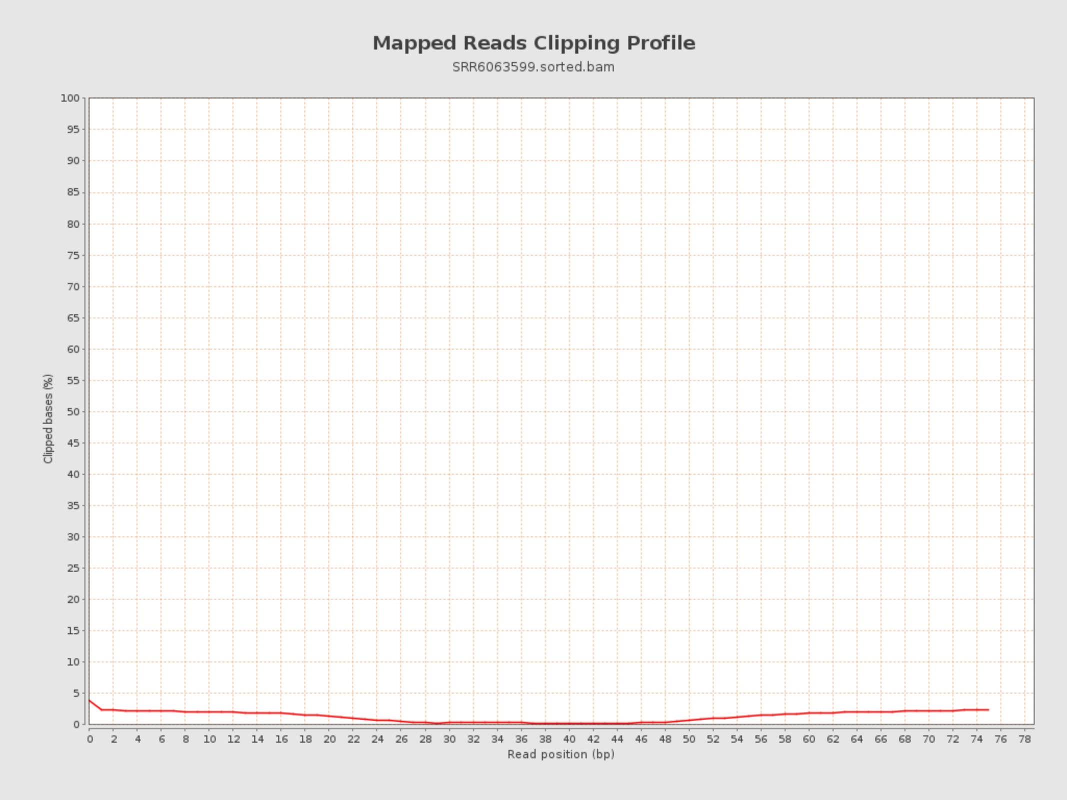
8. Results : Mapped Reads Nucleotide Content



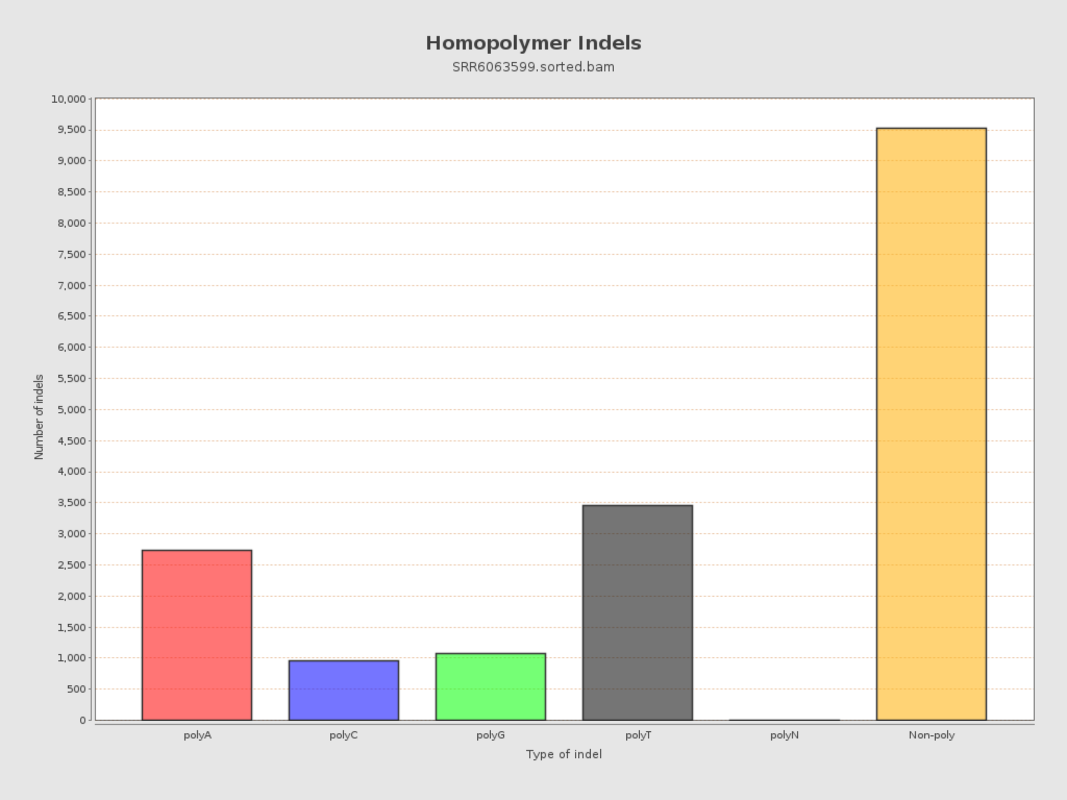
9. Results : Mapped Reads GC-content Distribution



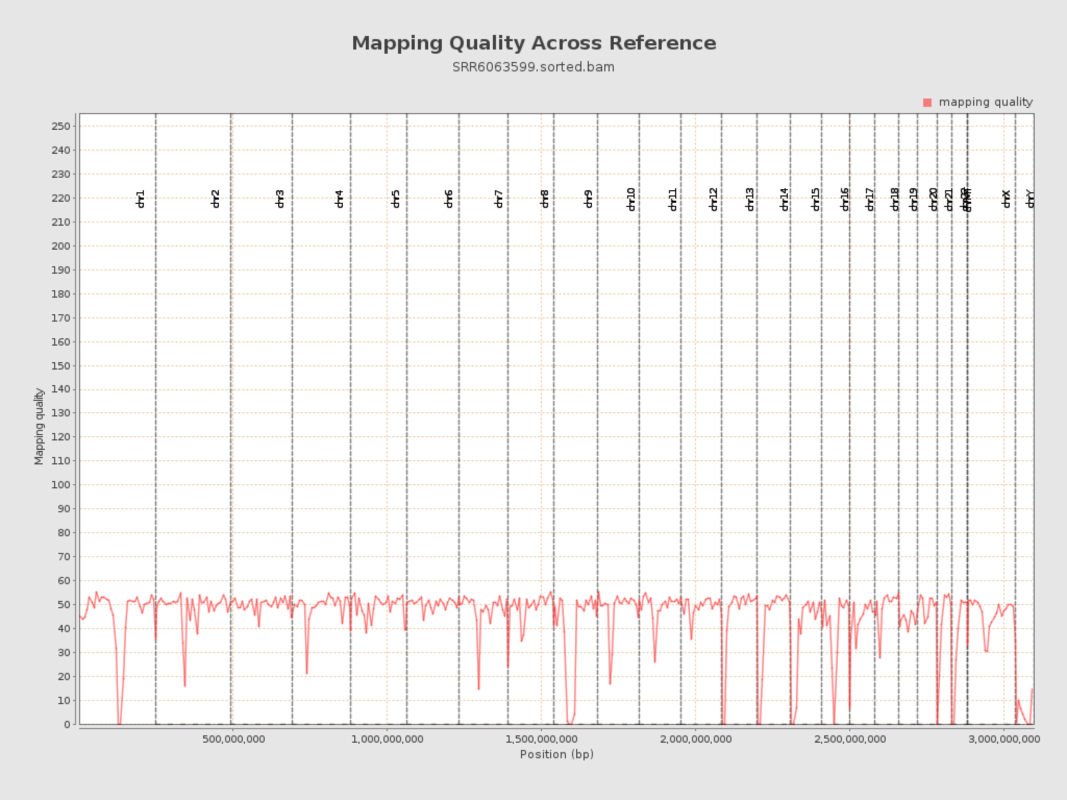
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram