Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:14:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063556.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_SRR6063556 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063556.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:14:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063556.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,931,451
Mapped reads	2,619,918 / 89.37%
Unmapped reads	311,533 / 10.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,895 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	167,744 / 5.72%
Duplication rate	5.02%
Clipped reads	1,366,456 / 46.61%

2.2. ACGT Content

Number/percentage of A's	47,271,233 / 27.72%
Number/percentage of C's	30,806,671 / 18.06%
Number/percentage of T's	54,598,724 / 32.01%
Number/percentage of G's	37,863,007 / 22.2%
Number/percentage of N's	4,534 / 0%
GC Percentage	40.27%

2.3. Coverage

Mean	0.0551

Standard Deviation	0.5789

2.4. Mapping Quality

Mean Mapping Quality	42.16

2.5. Mismatches and indels

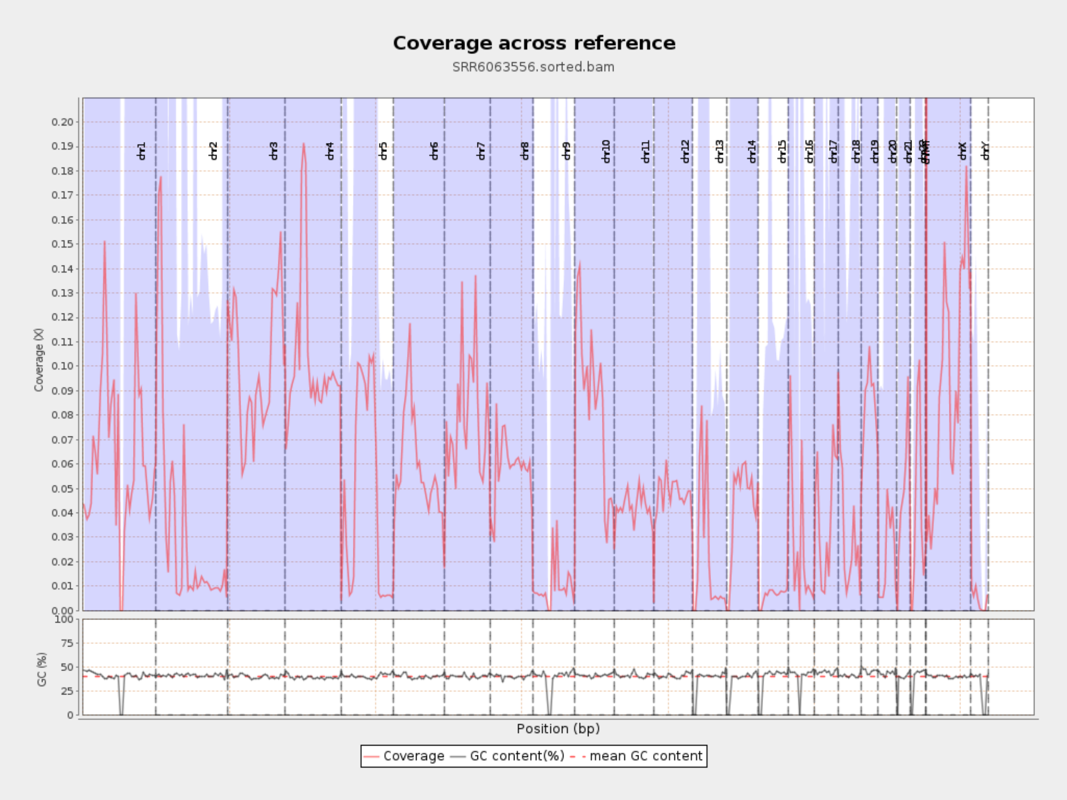
General error rate	0.81%
Mismatches	1,368,042
Insertions	12,232
Mapped reads with at least one insertion	0.46%
Deletions	45,050
Mapped reads with at least one deletion	1.7%
Homopolymer indels	46.29%

2.6. Chromosome stats

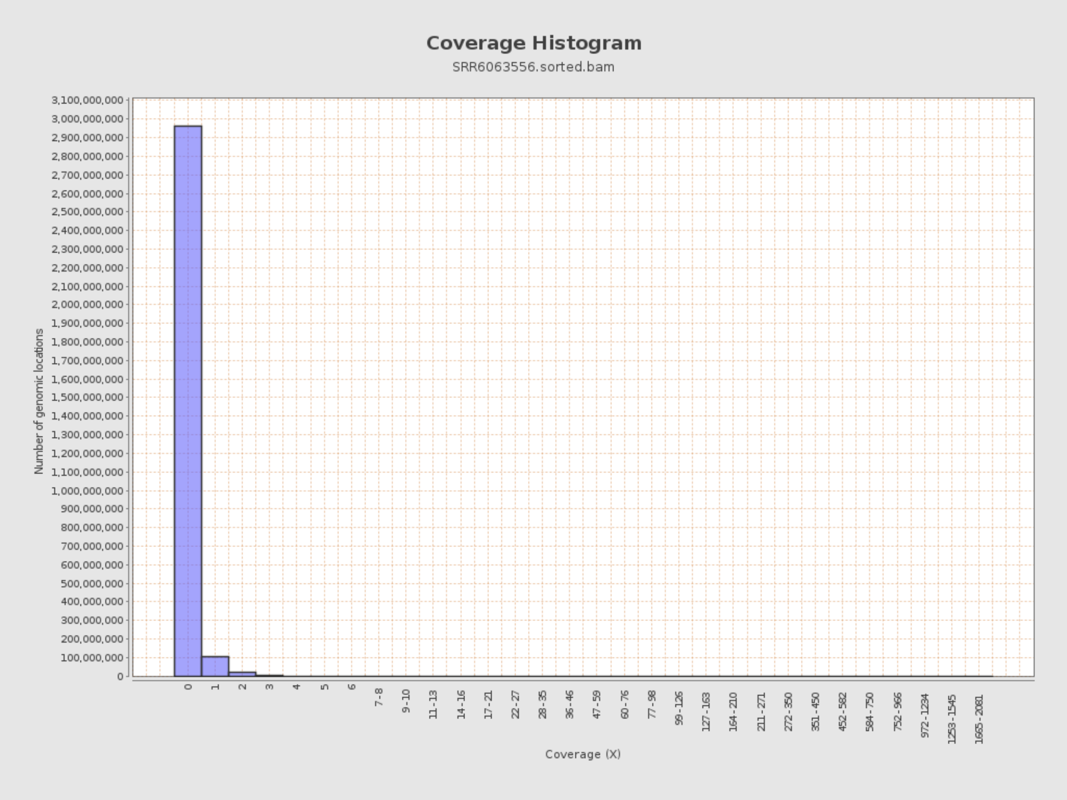
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15860551	0.0636	1.0799
chr2	243199373	8111677	0.0334	0.5748
chr3	198022430	19872090	0.1004	0.3904
chr4	191154276	19853281	0.1039	0.407
chr5	180915260	8430888	0.0466	0.2704
chr6	171115067	10403296	0.0608	0.37
chr7	159138663	12668881	0.0796	0.9408

chr8	146364022	8586690	0.0587	1.1886
chr9	141213431	1462634	0.0104	0.3696
chr10	135534747	11670399	0.0861	0.4745
chr11	135006516	5695148	0.0422	0.3624
chr12	133851895	6411493	0.0479	0.3101
chr13	115169878	2501016	0.0217	0.1903
chr14	107349540	4663966	0.0434	0.3169
chr15	102531392	624532	0.0061	0.1342
chr16	90354753	2525077	0.0279	0.2362
chr17	81195210	3185422	0.0392	0.2514
chr18	78077248	2459081	0.0315	0.6877
chr19	59128983	5058309	0.0855	0.716
chr20	63025520	1418042	0.0225	0.2356
chr21	48129895	2282599	0.0474	0.2699
chr22	51304566	2064387	0.0402	0.2452
chrMT	16571	53369	3.2206	3.1103
chrX	155270560	14494585	0.0934	0.4562
chrY	59373566	259028	0.0044	0.0835

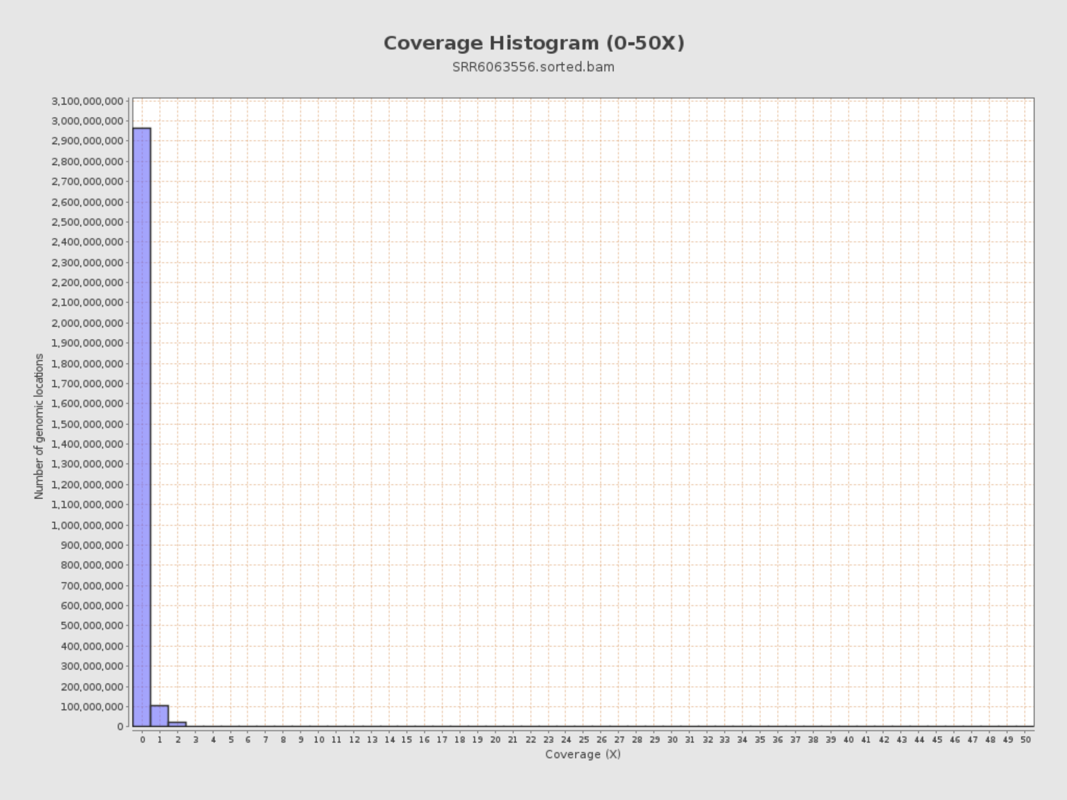
3. Results : Coverage across reference



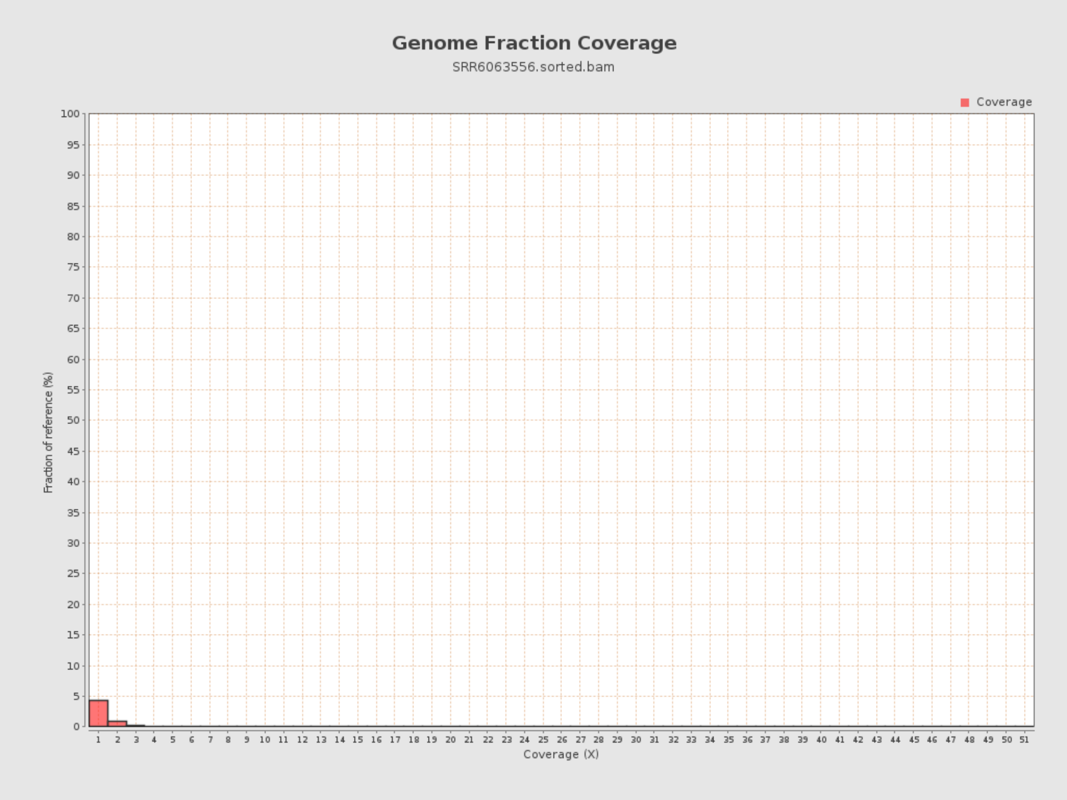
4. Results : Coverage Histogram



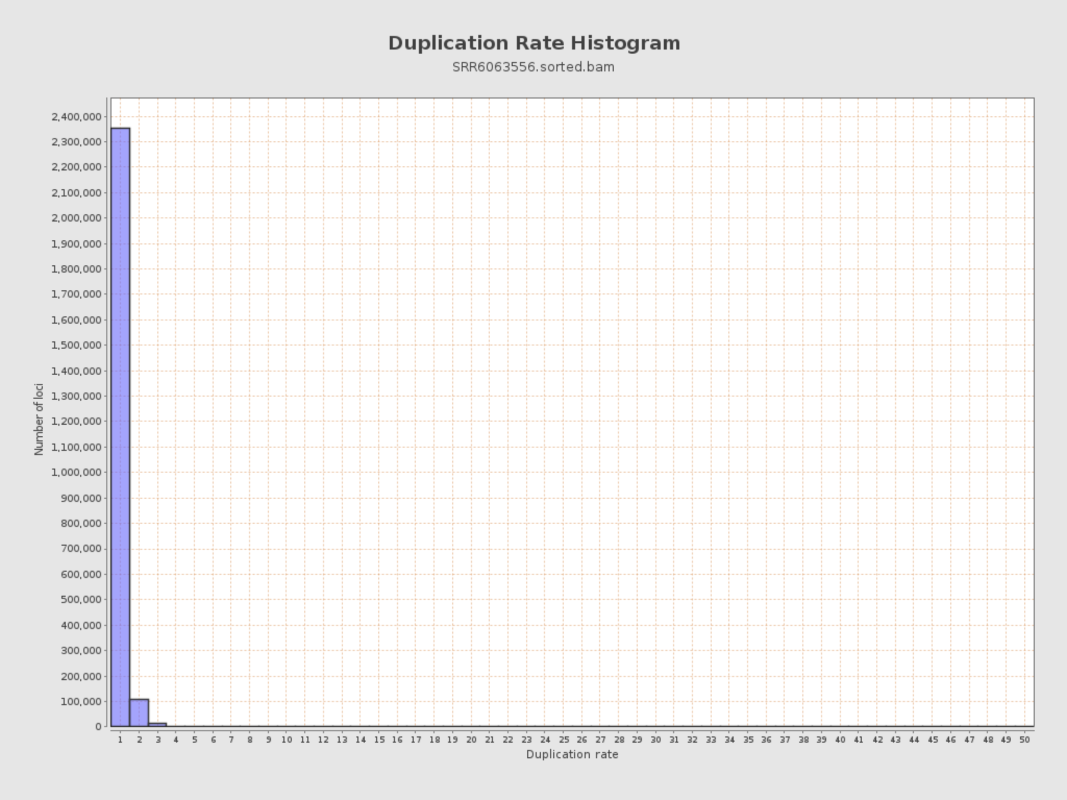
5. Results : Coverage Histogram (0-50X)



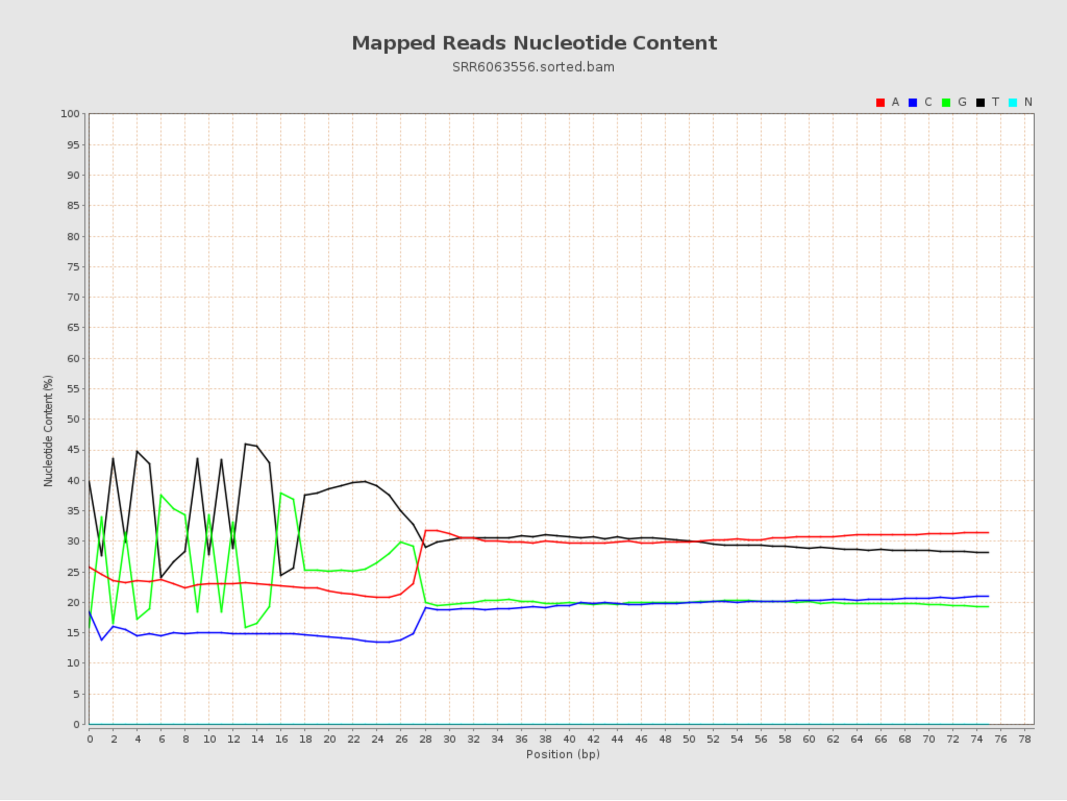
6. Results : Genome Fraction Coverage



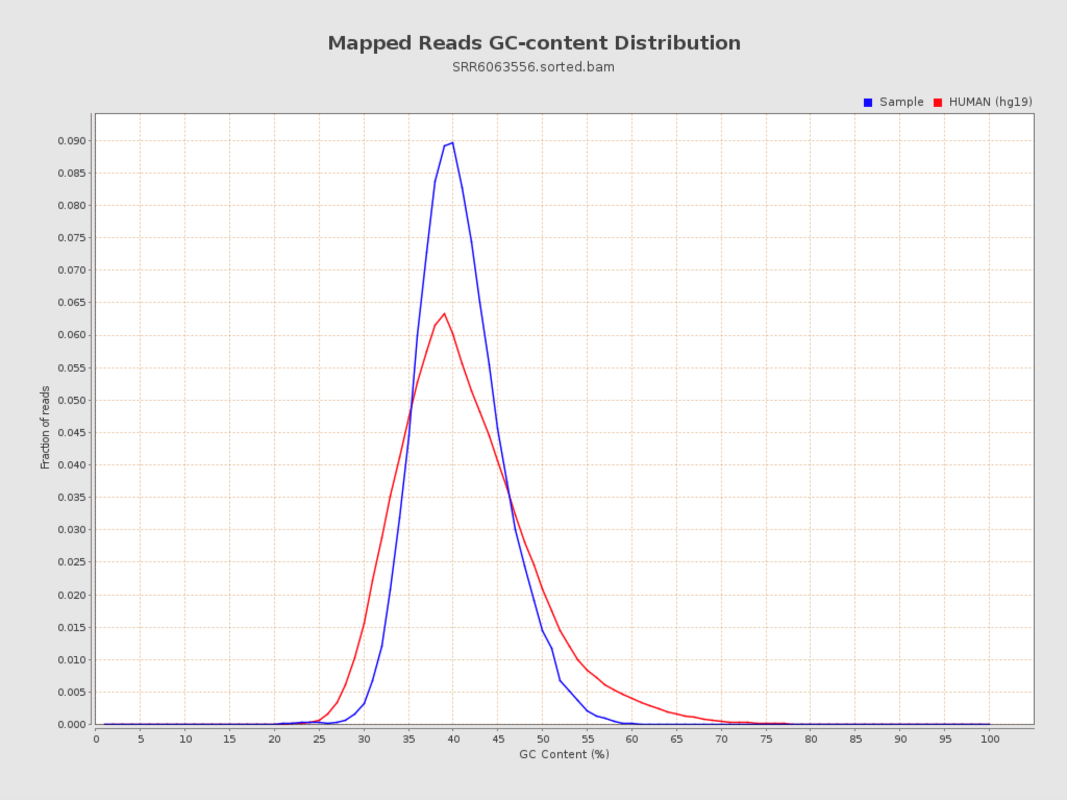
7. Results : Duplication Rate Histogram



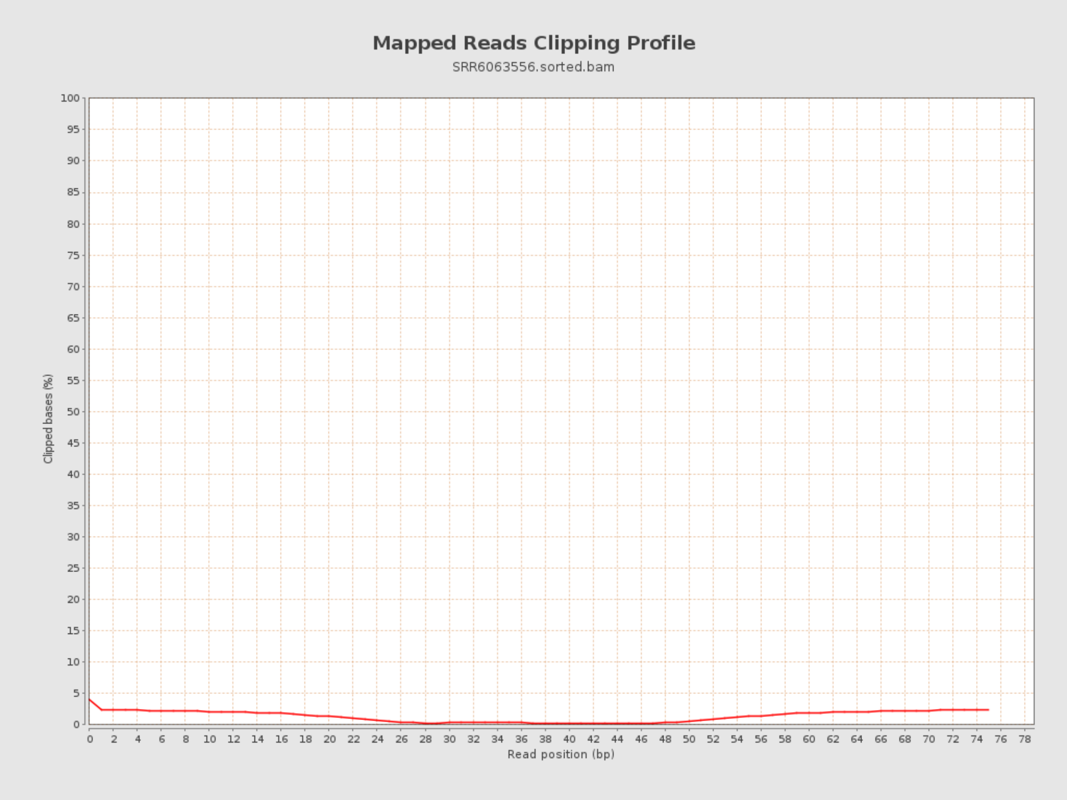
8. Results : Mapped Reads Nucleotide Content



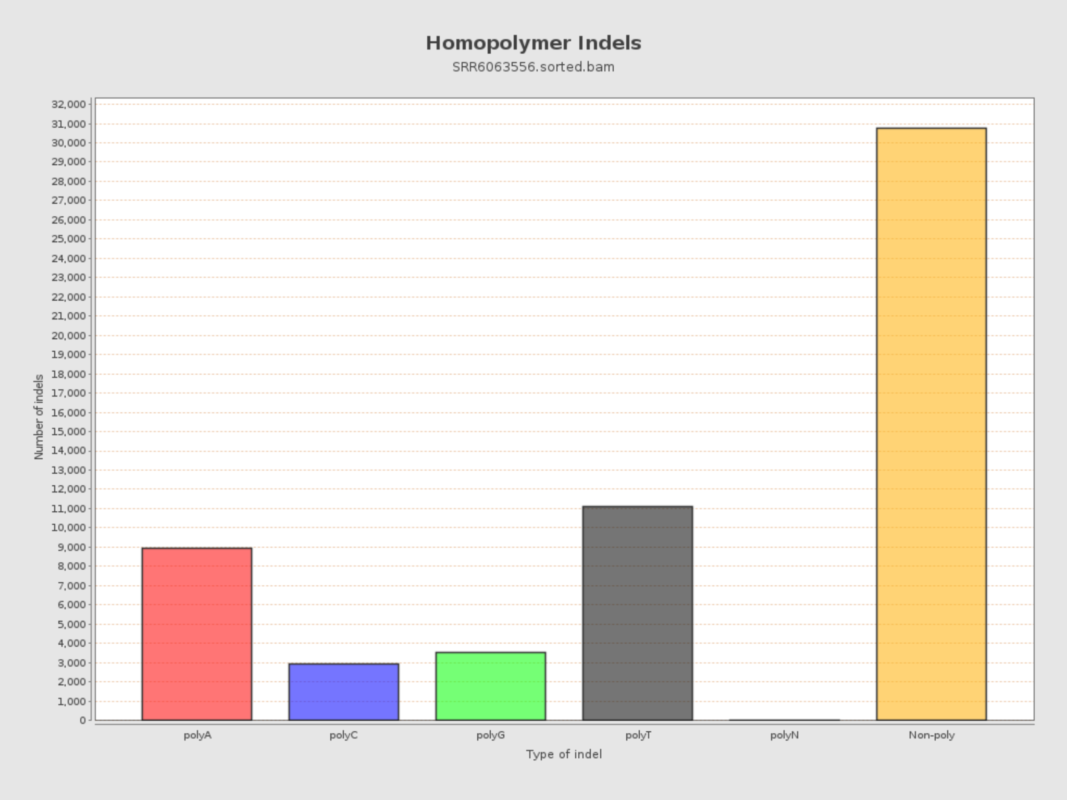
9. Results : Mapped Reads GC-content Distribution



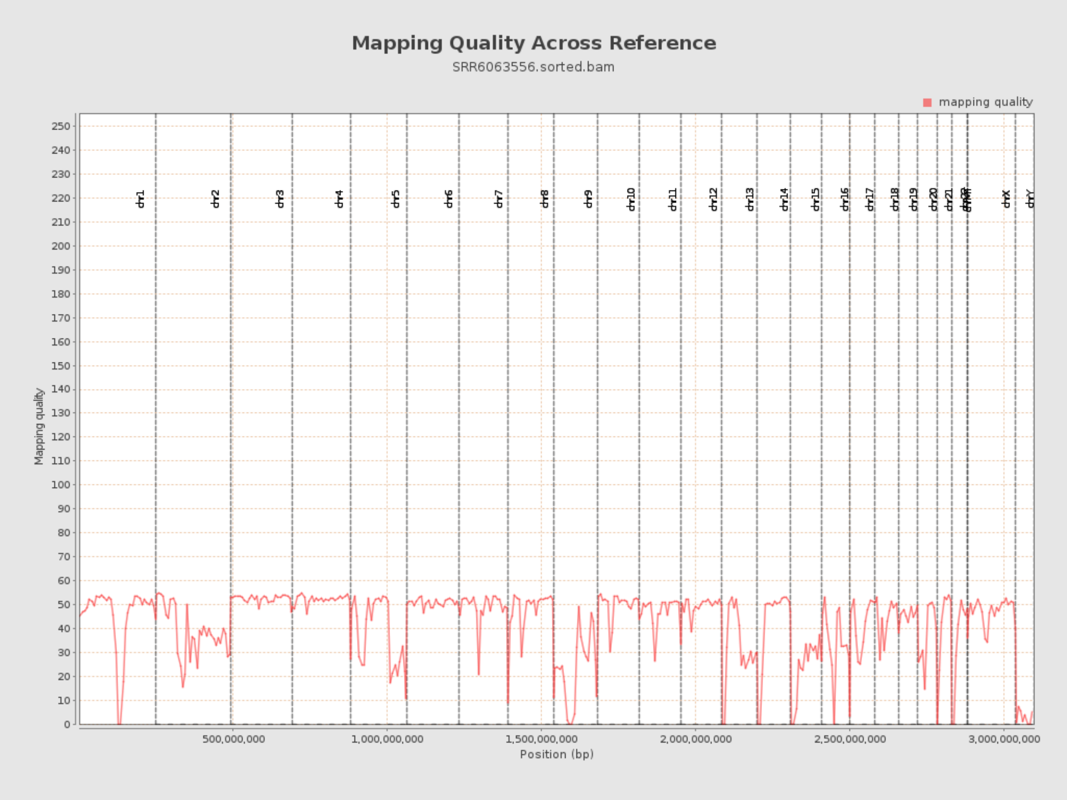
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram