Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:43:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063565.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_SRR6063565 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063565.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:43:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063565.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,983,897
Mapped reads	1,771,325 / 89.29%
Unmapped reads	212,572 / 10.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,435 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	81,775 / 4.12%
Duplication rate	3.58%
Clipped reads	847,420 / 42.71%

2.2. ACGT Content

Number/percentage of A's	32,260,847 / 27.65%
Number/percentage of C's	21,286,668 / 18.24%
Number/percentage of T's	37,334,503 / 31.99%
Number/percentage of G's	25,809,651 / 22.12%
Number/percentage of N's	2,314 / 0%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0377

Standard Deviation	0.3857

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

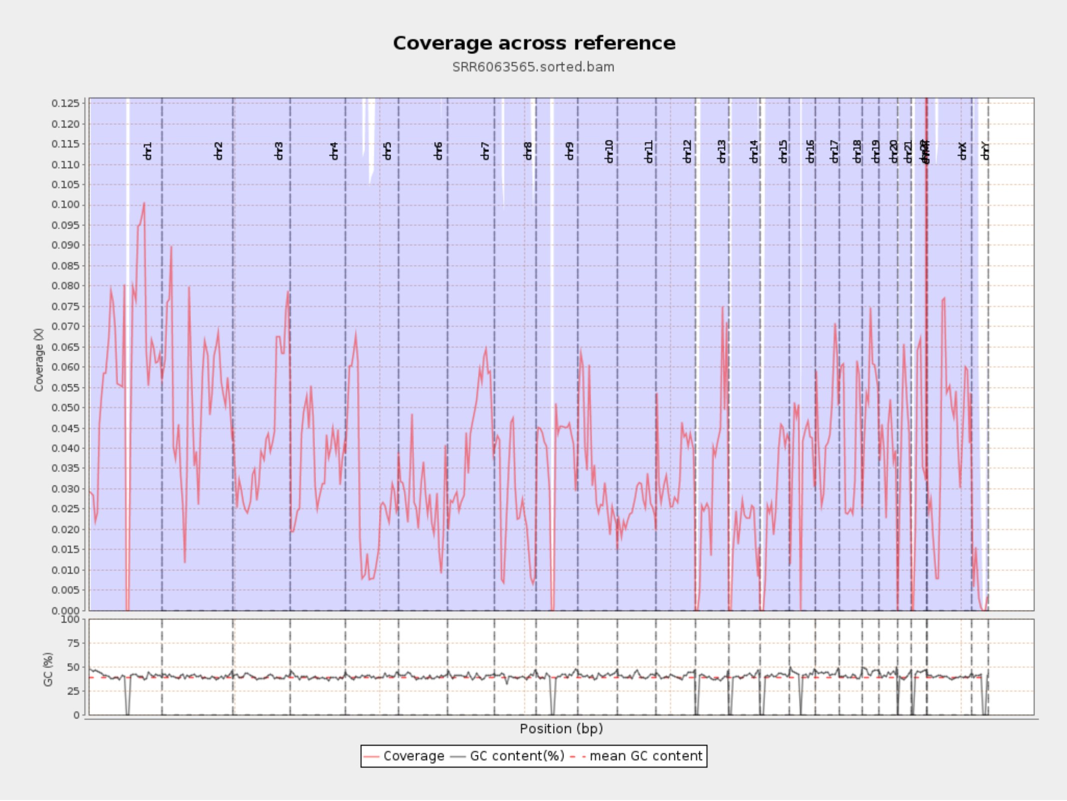
General error rate	0.79%
Mismatches	910,323
Insertions	9,142
Mapped reads with at least one insertion	0.51%
Deletions	30,462
Mapped reads with at least one deletion	1.7%
Homopolymer indels	46.92%

2.6. Chromosome stats

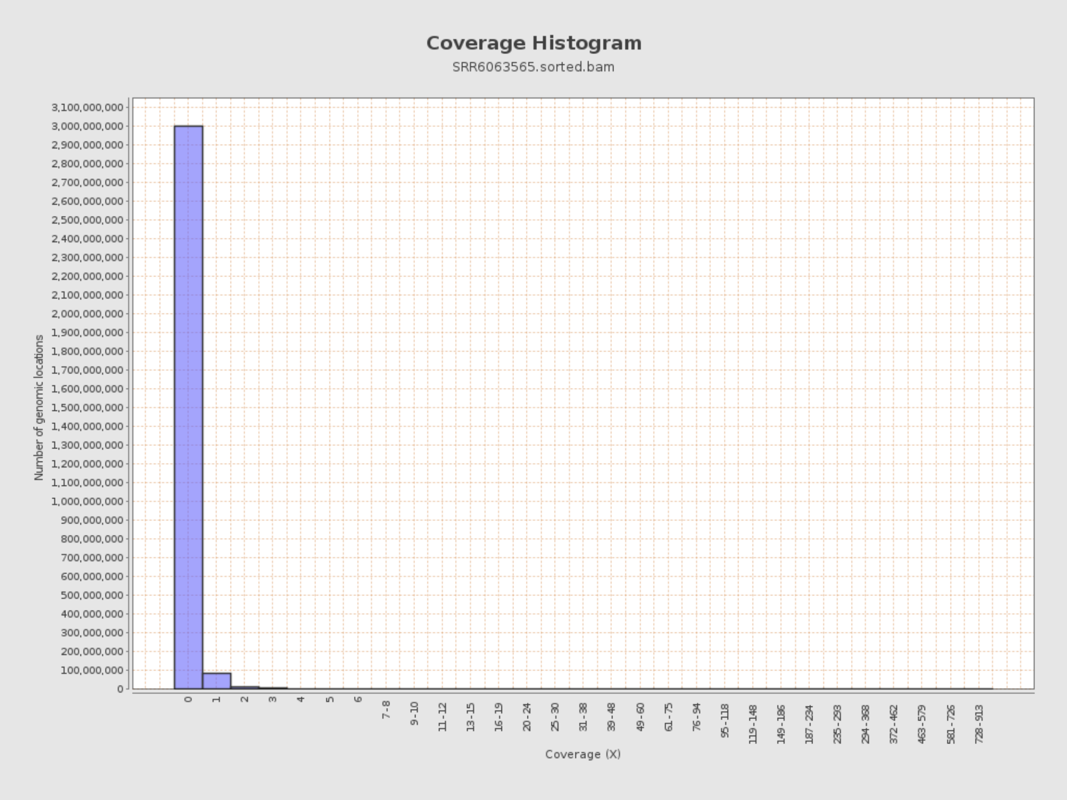
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14696857	0.059	0.8204
chr2	243199373	12752384	0.0524	0.4707
chr3	198022430	8415900	0.0425	0.2417
chr4	191154276	6980122	0.0365	0.2299
chr5	180915260	5208636	0.0288	0.1996
chr6	171115067	4709196	0.0275	0.2129
chr7	159138663	6729239	0.0423	0.3199

chr8	146364022	3727005	0.0255	0.5201
chr9	141213431	5353180	0.0379	0.3782
chr10	135534747	4732524	0.0349	0.3367
chr11	135006516	3437996	0.0255	0.2203
chr12	133851895	4693343	0.0351	0.2272
chr13	115169878	3805037	0.033	0.2106
chr14	107349540	1939802	0.0181	0.1952
chr15	102531392	2768873	0.027	0.1911
chr16	90354753	3421825	0.0379	0.2485
chr17	81195210	3782853	0.0466	0.2551
chr18	78077248	3271805	0.0419	0.6311
chr19	59128983	3249240	0.055	0.5806
chr20	63025520	2469699	0.0392	0.2364
chr21	48129895	1893885	0.0393	0.2457
chr22	51304566	1761076	0.0343	0.214
chrMT	16571	22507	1.3582	1.404
chrX	155270560	6625741	0.0427	0.2748
chrY	59373566	295153	0.005	0.1562

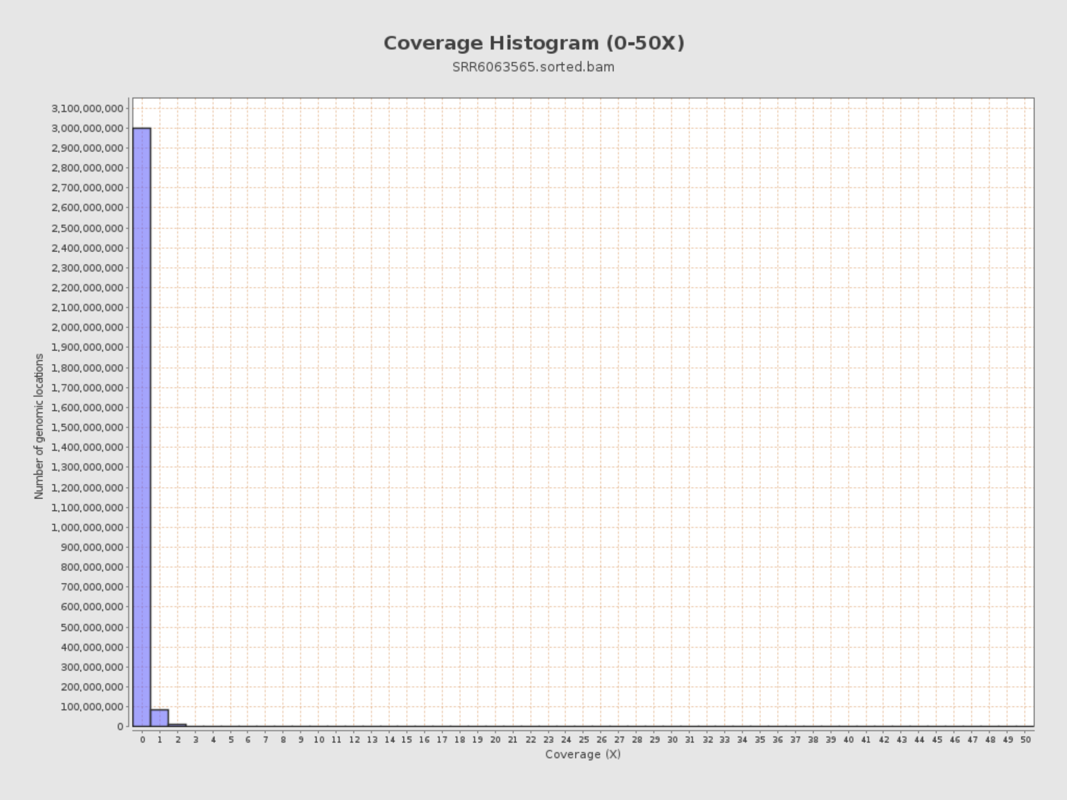
3. Results : Coverage across reference



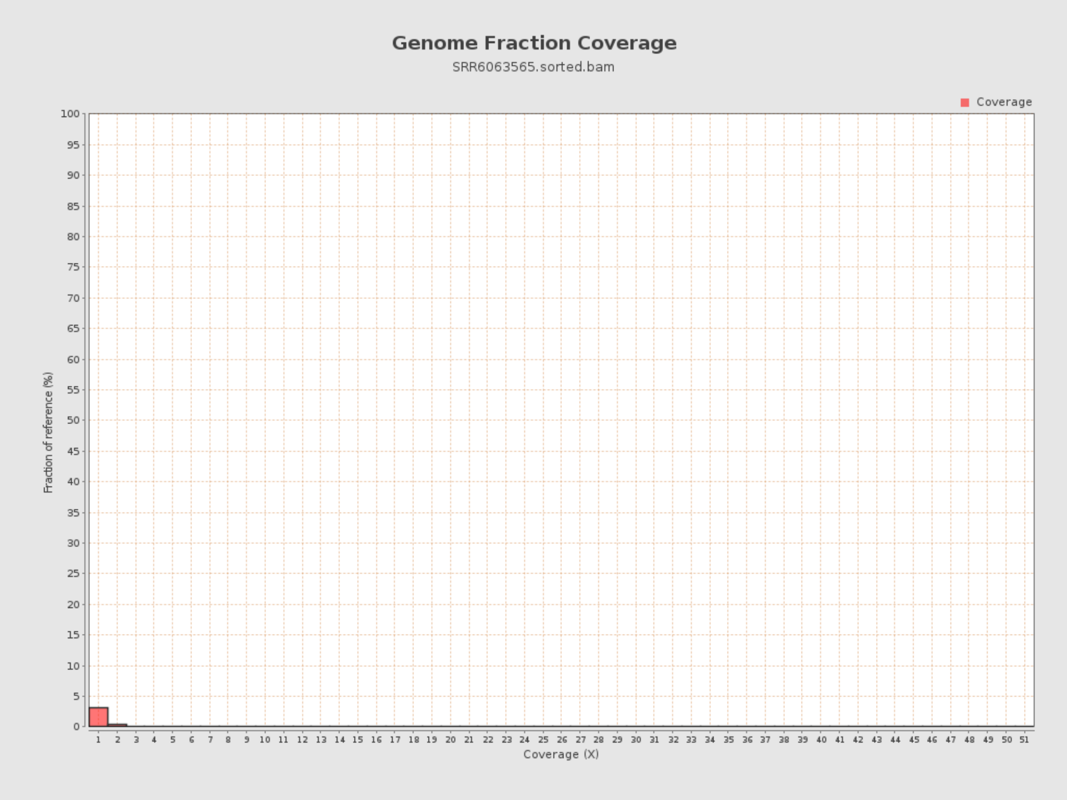
4. Results : Coverage Histogram



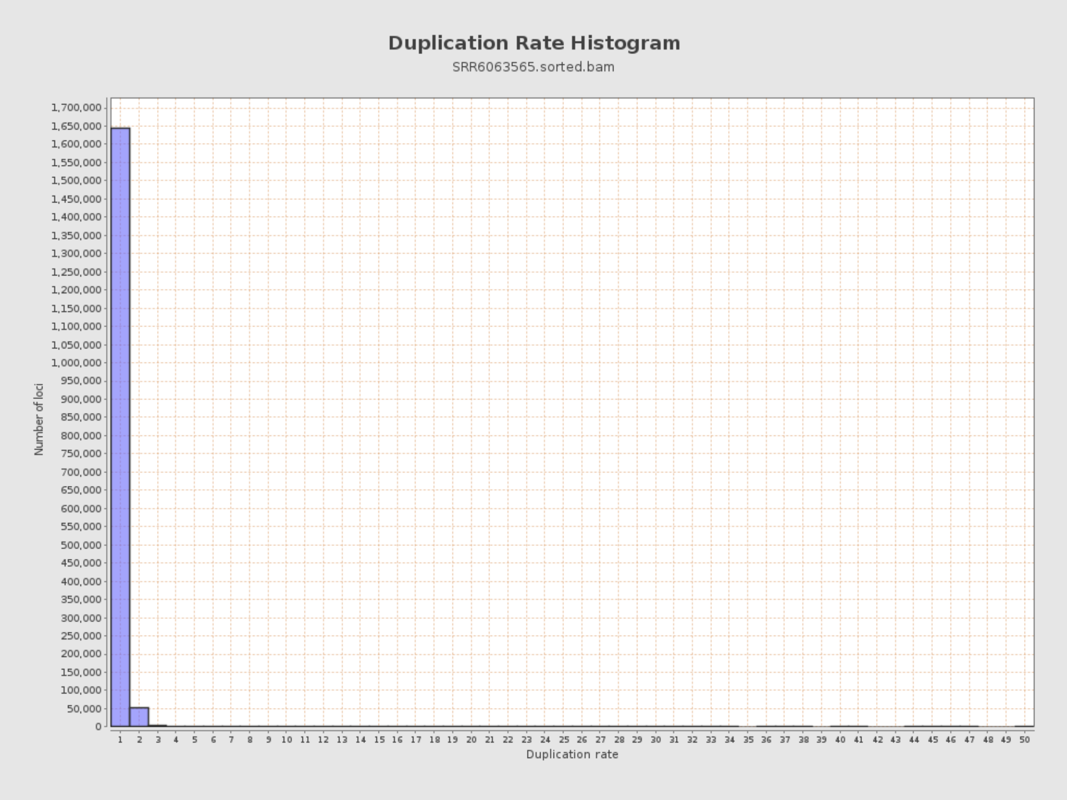
5. Results : Coverage Histogram (0-50X)



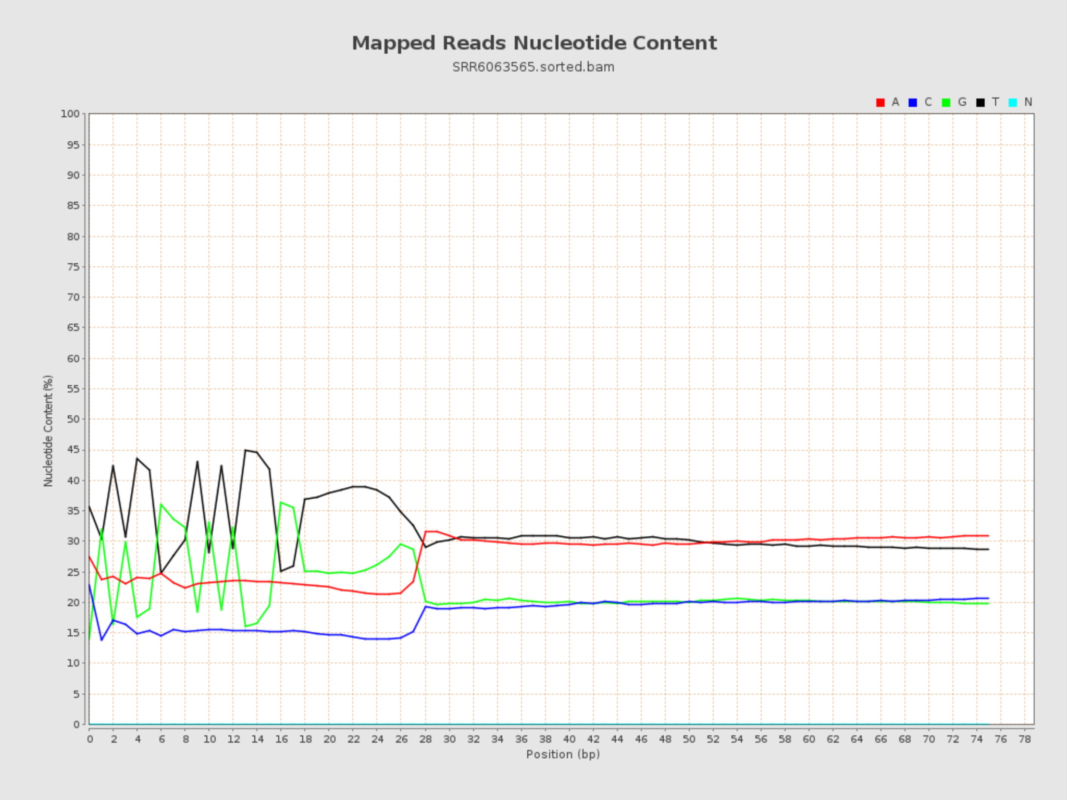
6. Results : Genome Fraction Coverage



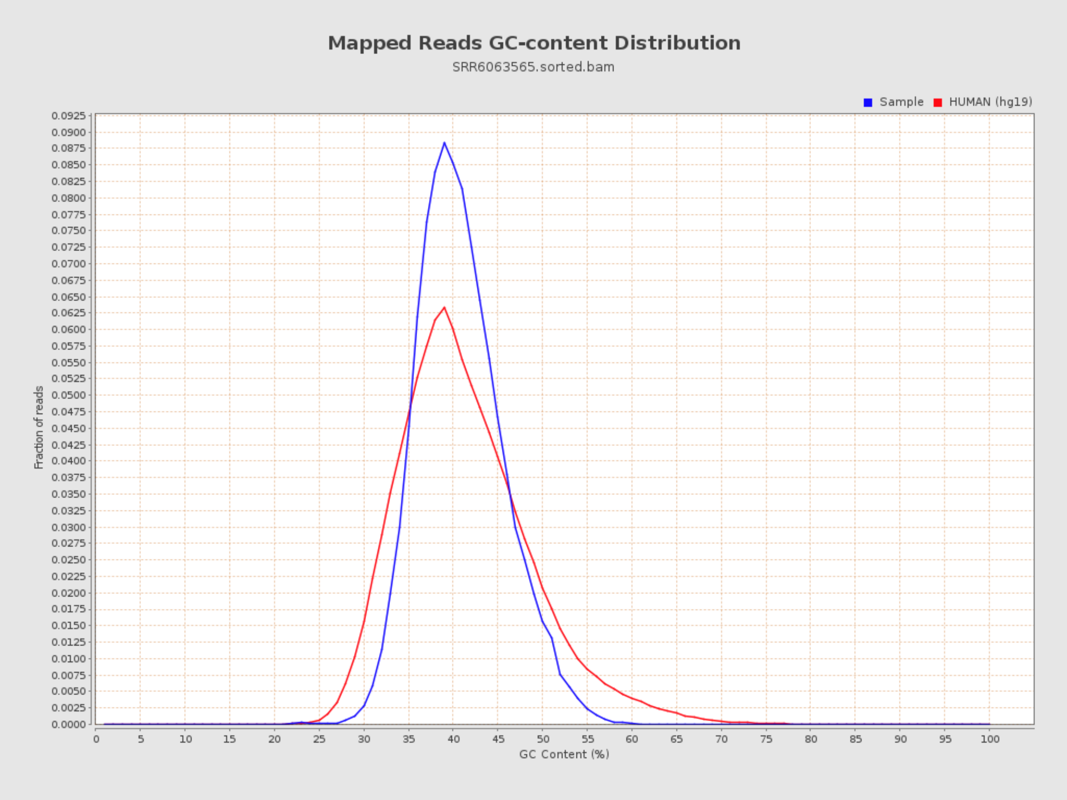
7. Results : Duplication Rate Histogram



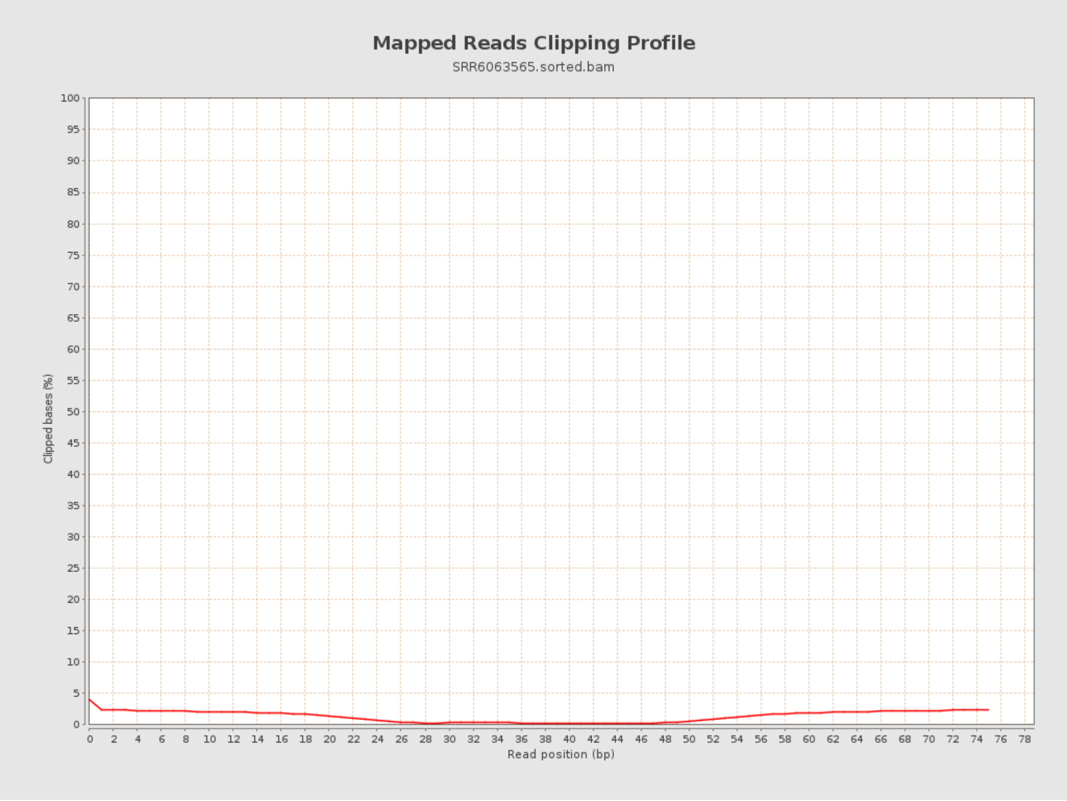
8. Results : Mapped Reads Nucleotide Content



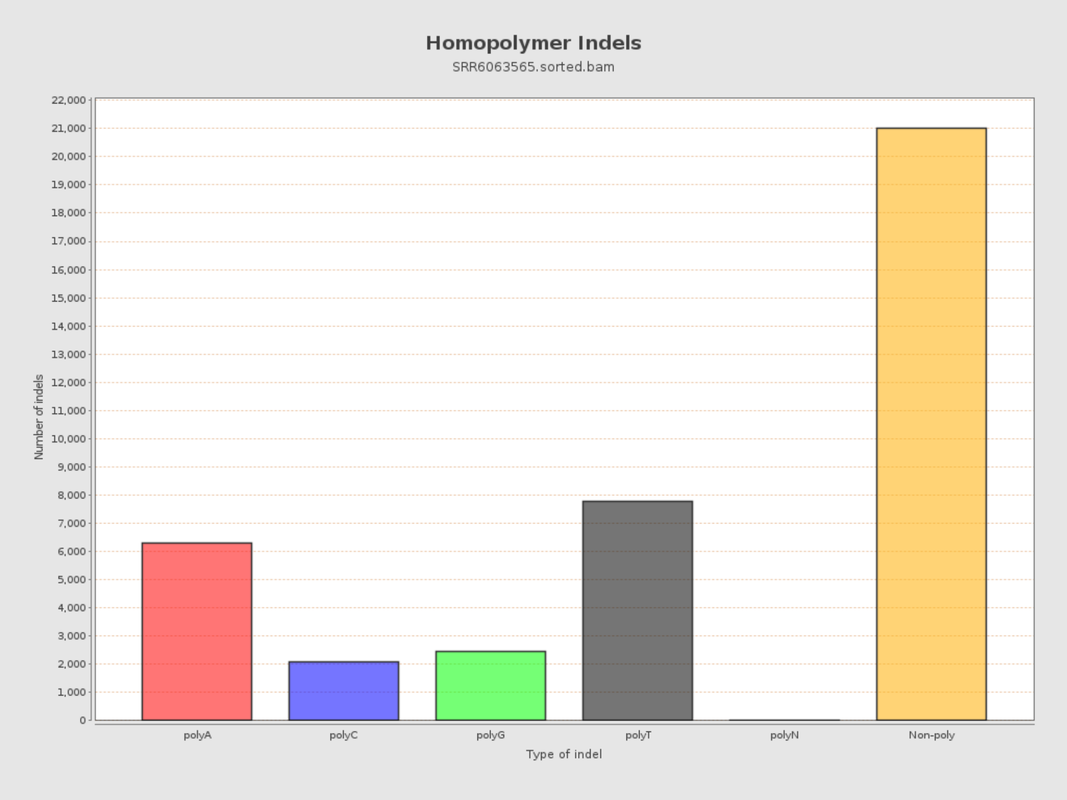
9. Results : Mapped Reads GC-content Distribution



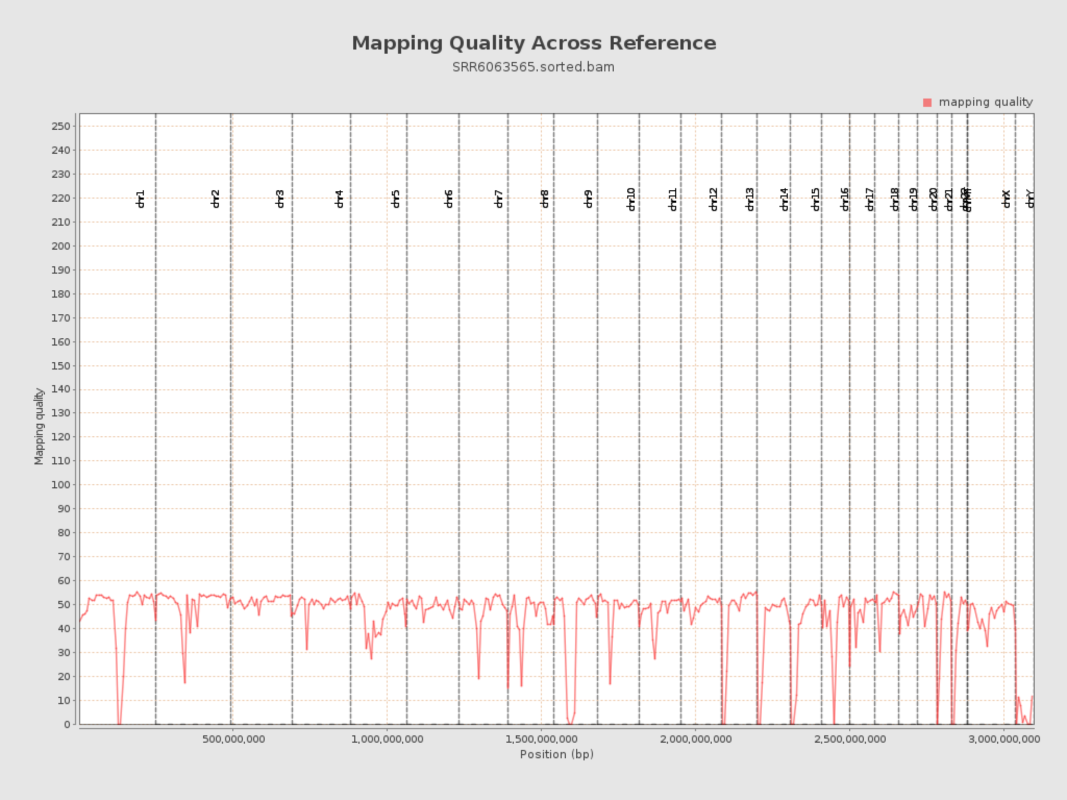
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram