Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:41:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063602.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_SRR6063602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063602.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:41:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,844,283
Mapped reads	6,902,961 / 88%
Unmapped reads	941,322 / 12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	58,239 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,085,357 / 13.84%
Duplication rate	12.88%
Clipped reads	3,696,246 / 47.12%

2.2. ACGT Content

Number/percentage of A's	116,161,938 / 26.2%
Number/percentage of C's	79,520,883 / 17.93%
Number/percentage of T's	144,288,645 / 32.54%
Number/percentage of G's	103,396,409 / 23.32%
Number/percentage of N's	51,493 / 0.01%
GC Percentage	41.25%

2.3. Coverage

Mean	0.1433

Standard Deviation	1.4997

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

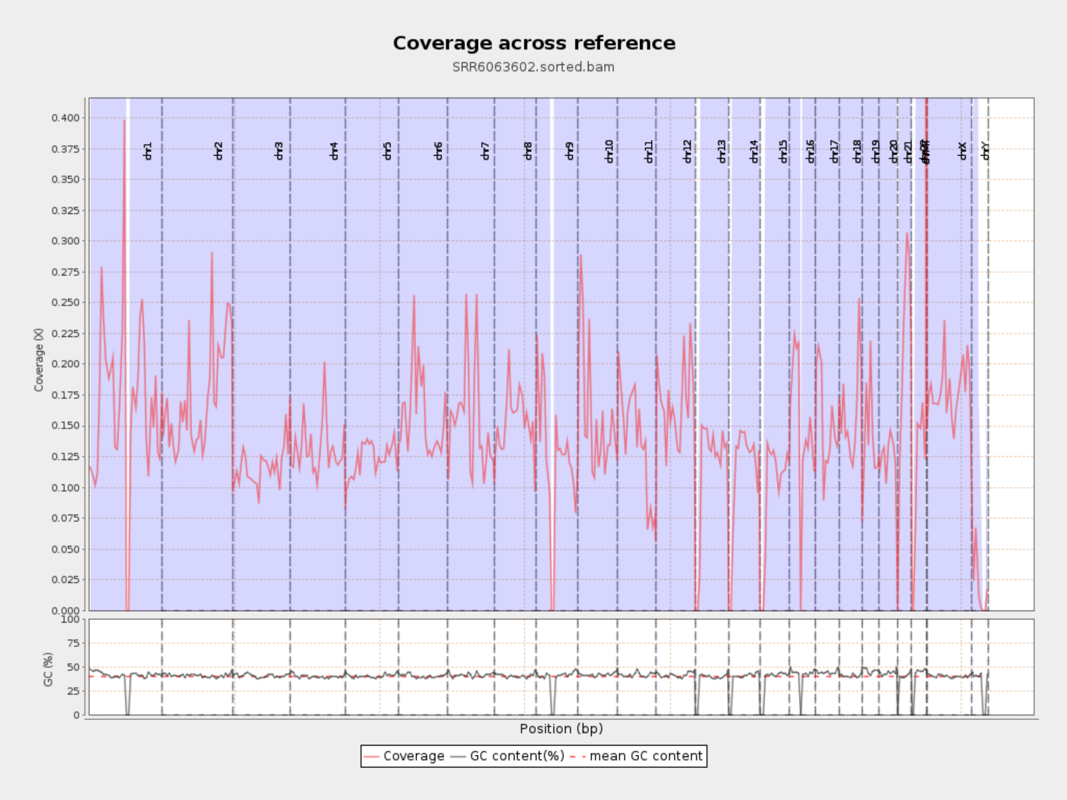
General error rate	0.56%
Mismatches	2,419,190
Insertions	29,340
Mapped reads with at least one insertion	0.42%
Deletions	98,519
Mapped reads with at least one deletion	1.41%
Homopolymer indels	44.92%

2.6. Chromosome stats

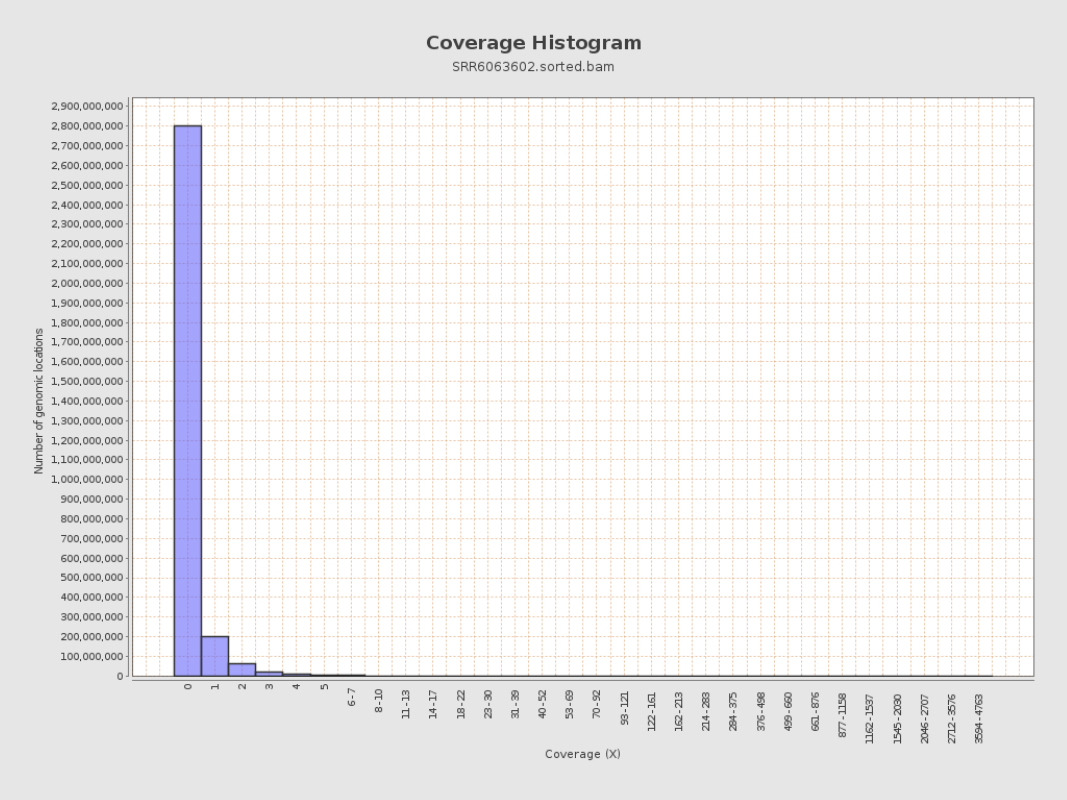
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	41917835	0.1682	3.7317
chr2	243199373	42155366	0.1733	2.0455
chr3	198022430	23056485	0.1164	0.4876
chr4	191154276	25235948	0.132	0.5974
chr5	180915260	22372104	0.1237	0.5075
chr6	171115067	27127151	0.1585	0.8681
chr7	159138663	24768940	0.1556	1.5403

chr8	146364022	22505126	0.1538	1.4133
chr9	141213431	17173022	0.1216	0.9697
chr10	135534747	21688860	0.16	1.0638
chr11	135006516	18611688	0.1379	1.0297
chr12	133851895	22678839	0.1694	0.6147
chr13	115169878	13042750	0.1132	0.5297
chr14	107349540	11778001	0.1097	0.5565
chr15	102531392	9987668	0.0974	0.4991
chr16	90354753	13608037	0.1506	0.6525
chr17	81195210	12241115	0.1508	0.6909
chr18	78077248	12531804	0.1605	2.1587
chr19	59128983	8498210	0.1437	2.3141
chr20	63025520	7796022	0.1237	0.5678
chr21	48129895	9825844	0.2042	0.7079
chr22	51304566	5378399	0.1048	0.4462
chrMT	16571	606181	36.5808	19.442
chrX	155270560	27772855	0.1789	0.7191
chrY	59373566	1234242	0.0208	0.5566

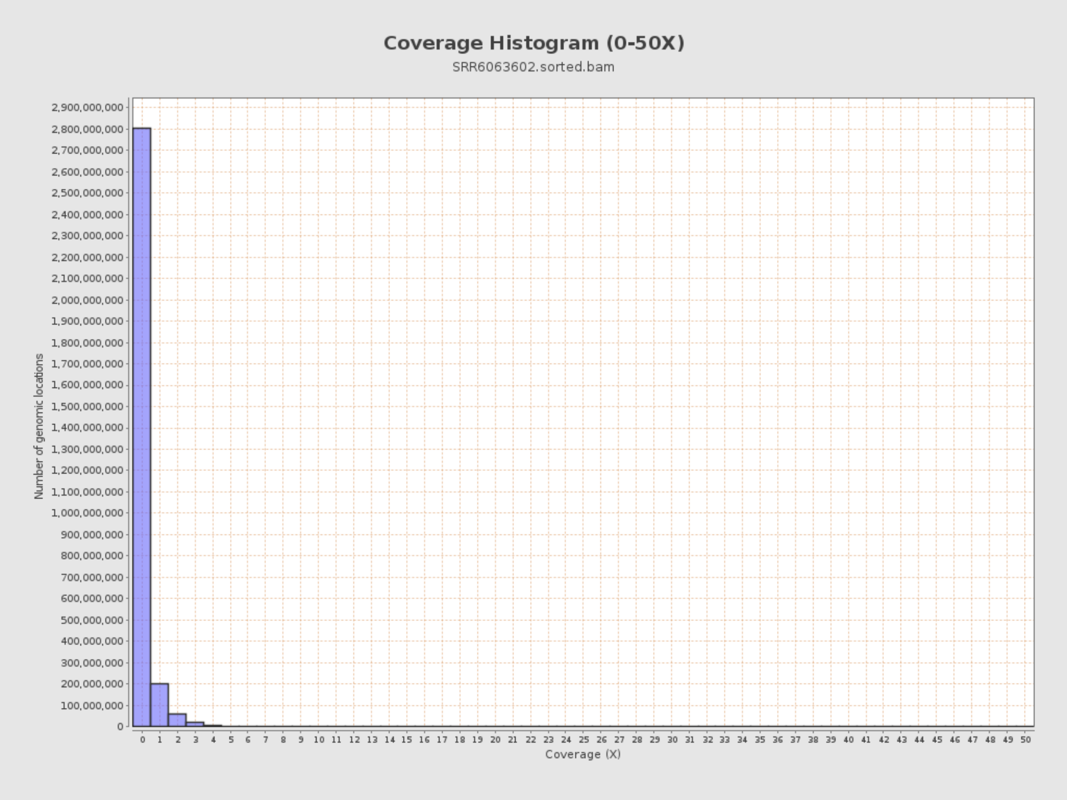
3. Results : Coverage across reference



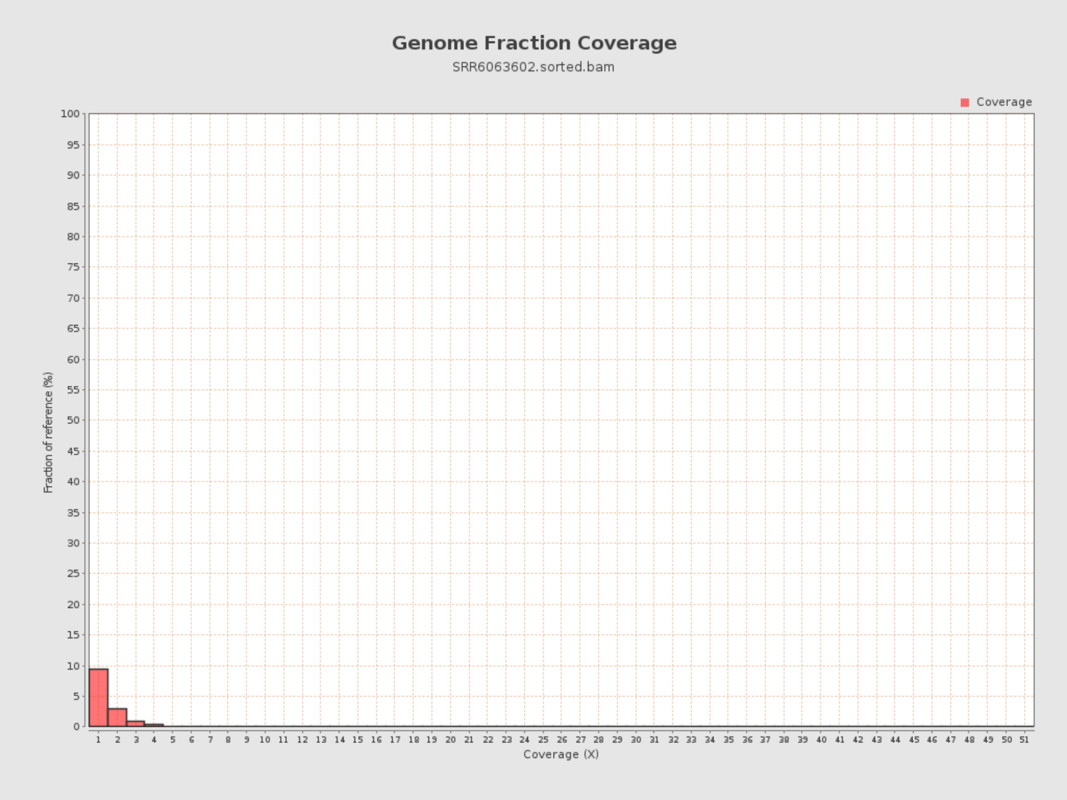
4. Results : Coverage Histogram



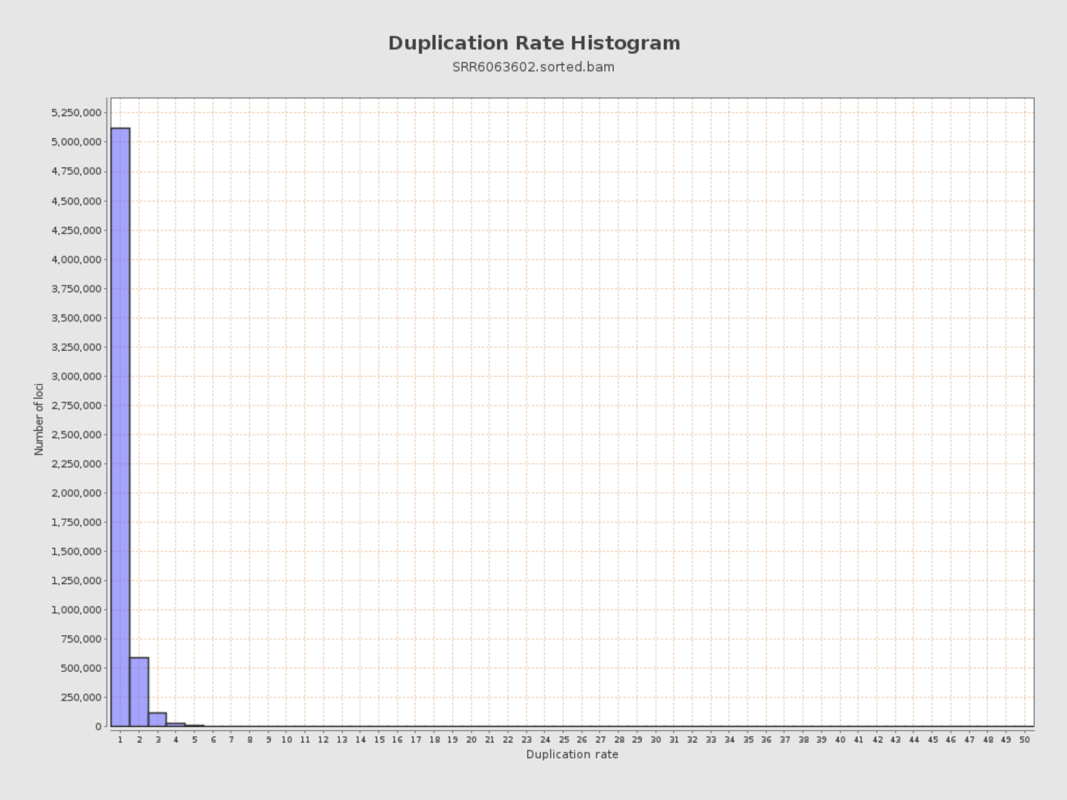
5. Results : Coverage Histogram (0-50X)



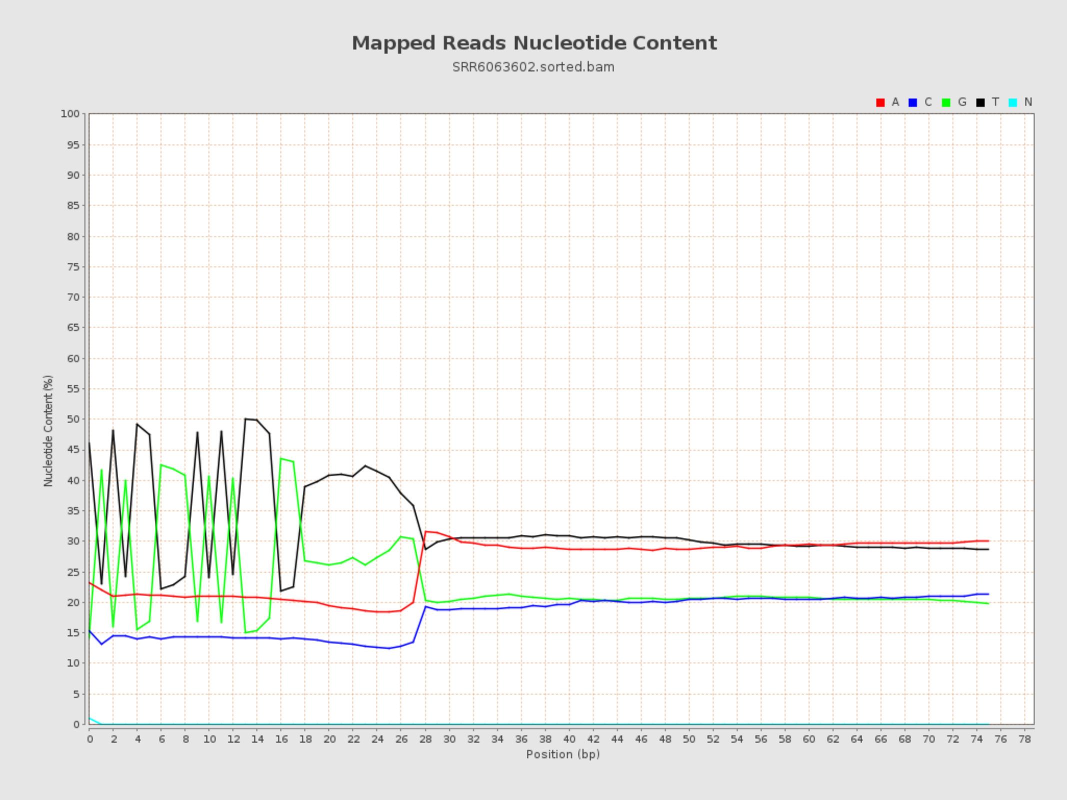
6. Results : Genome Fraction Coverage



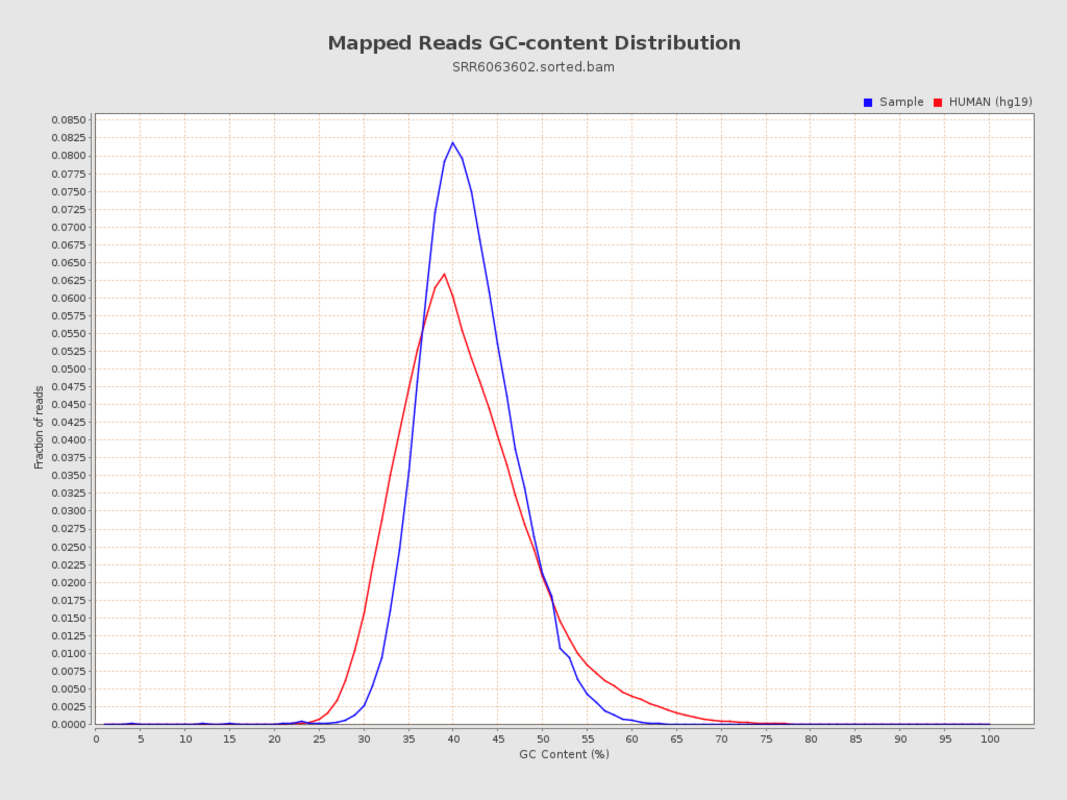
7. Results : Duplication Rate Histogram



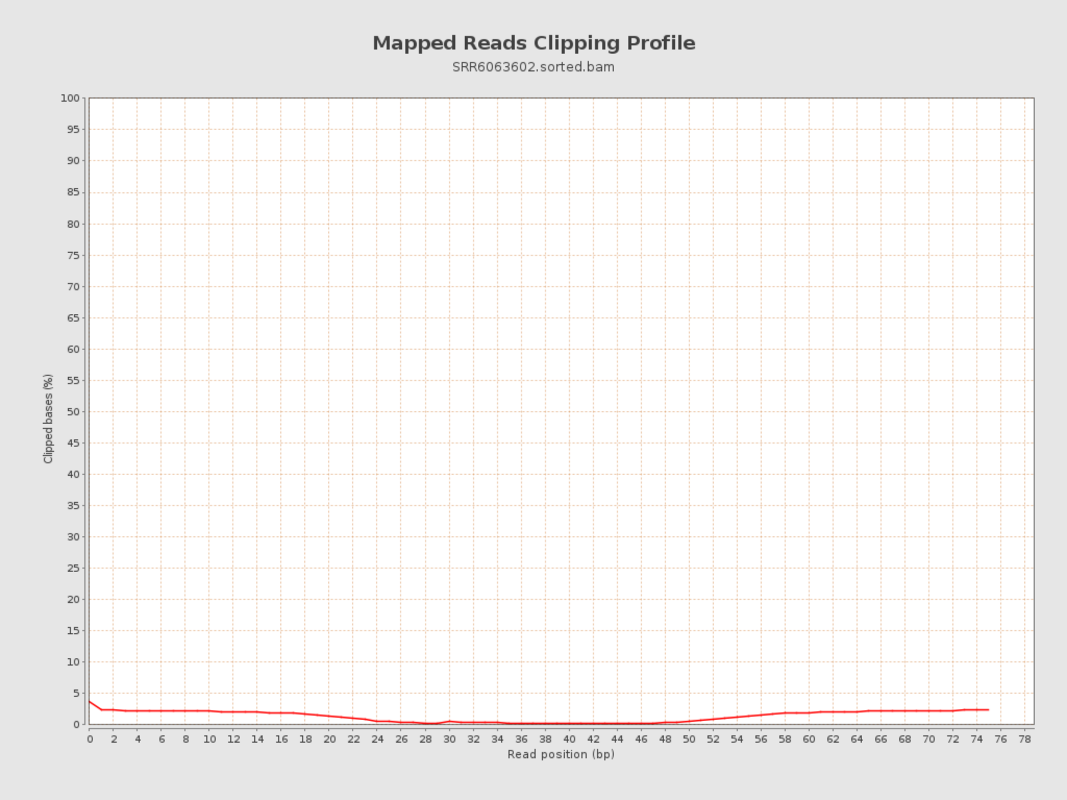
8. Results : Mapped Reads Nucleotide Content



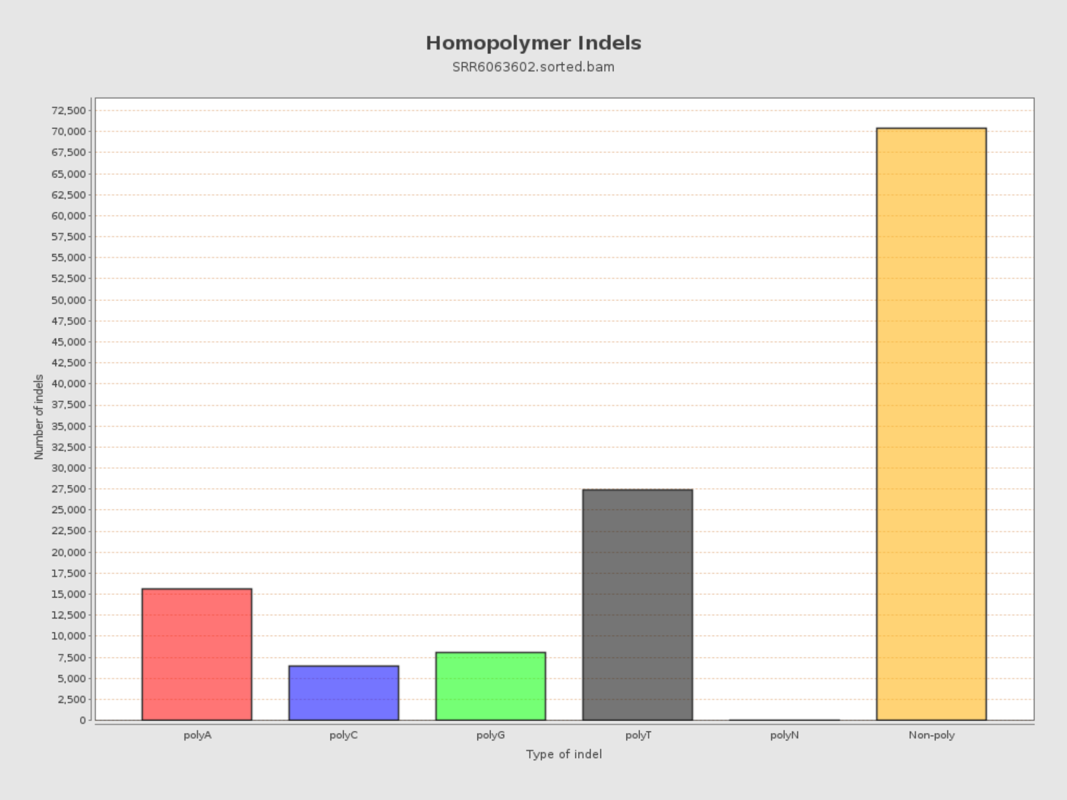
9. Results : Mapped Reads GC-content Distribution



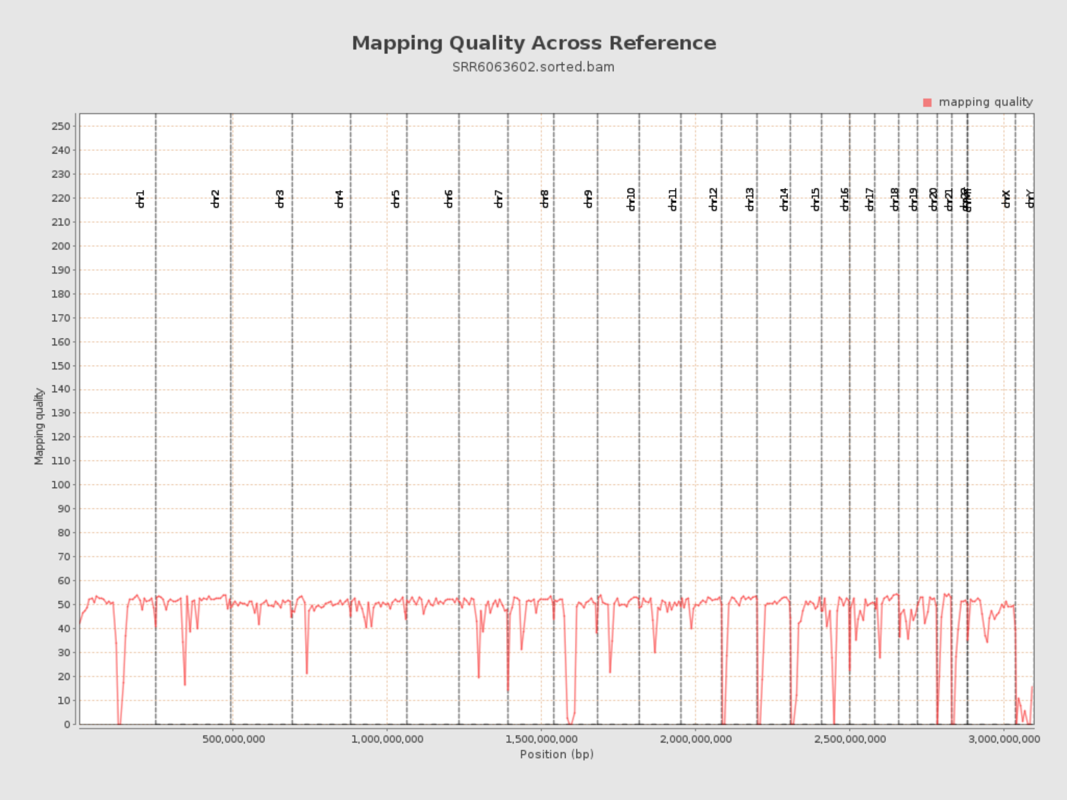
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram