Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:10:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063555.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_SRR6063555 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063555.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:10:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063555.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,780,061
Mapped reads	2,529,307 / 90.98%
Unmapped reads	250,754 / 9.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,838 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	152,388 / 5.48%
Duplication rate	4.69%
Clipped reads	1,211,087 / 43.56%

2.2. ACGT Content

Number/percentage of A's	46,584,948 / 27.87%
Number/percentage of C's	30,385,209 / 18.18%
Number/percentage of T's	53,476,043 / 31.99%
Number/percentage of G's	36,716,601 / 21.96%
Number/percentage of N's	4,138 / 0%
GC Percentage	40.14%

2.3. Coverage

Mean	0.054

Standard Deviation	0.5688

2.4. Mapping Quality

Mean Mapping Quality	42.27

2.5. Mismatches and indels

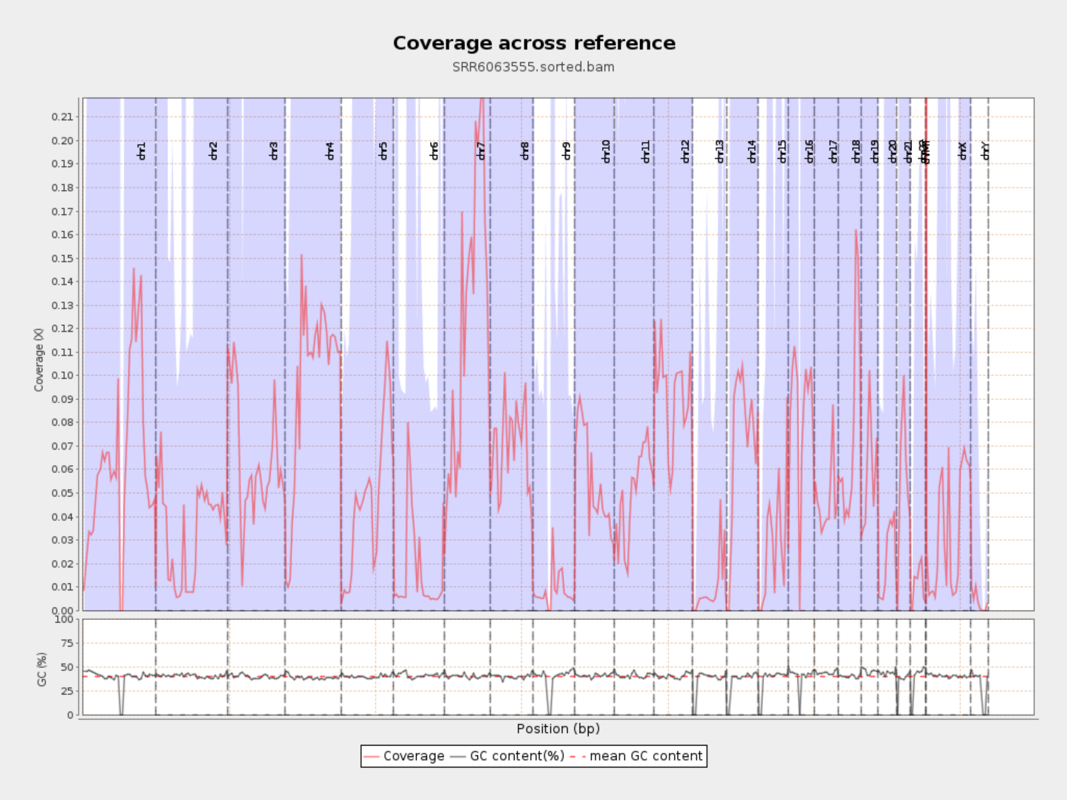
General error rate	0.82%
Mismatches	1,345,825
Insertions	12,340
Mapped reads with at least one insertion	0.48%
Deletions	45,352
Mapped reads with at least one deletion	1.77%
Homopolymer indels	46.7%

2.6. Chromosome stats

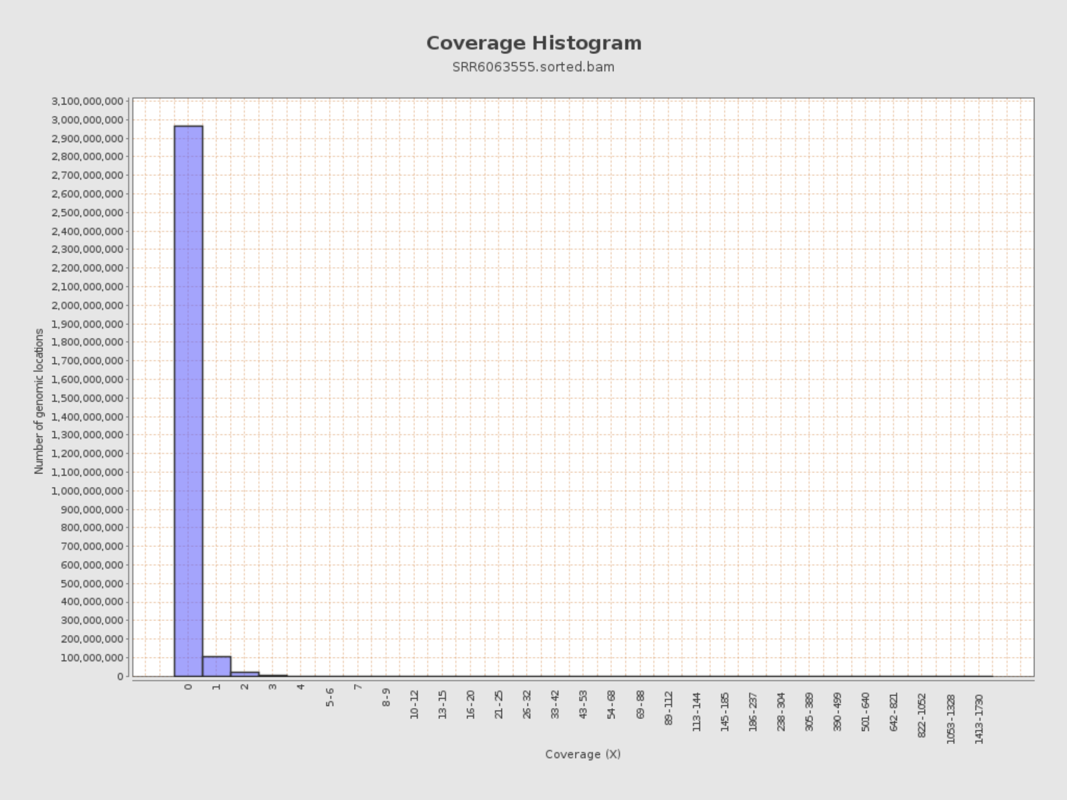
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15868891	0.0637	1.0425
chr2	243199373	8216715	0.0338	0.5195
chr3	198022430	12808935	0.0647	0.3118
chr4	191154276	18700749	0.0978	0.394
chr5	180915260	8640148	0.0478	0.2714
chr6	171115067	2934549	0.0171	0.2173
chr7	159138663	19511921	0.1226	1.1599

chr8	146364022	10211726	0.0698	1.0348
chr9	141213431	1186418	0.0084	0.362
chr10	135534747	7569003	0.0558	0.4613
chr11	135006516	6815291	0.0505	0.3402
chr12	133851895	12283949	0.0918	0.3999
chr13	115169878	1180077	0.0102	0.1344
chr14	107349540	7771481	0.0724	0.3756
chr15	102531392	2809584	0.0274	0.2155
chr16	90354753	7321493	0.081	0.3661
chr17	81195210	3881429	0.0478	0.2745
chr18	78077248	5981524	0.0766	0.7225
chr19	59128983	3534861	0.0598	0.7817
chr20	63025520	1412541	0.0224	0.222
chr21	48129895	2587867	0.0538	0.2873
chr22	51304566	593656	0.0116	0.1258
chrMT	16571	54917	3.314	3.0088
chrX	155270560	5128421	0.033	0.2641
chrY	59373566	234655	0.004	0.0795

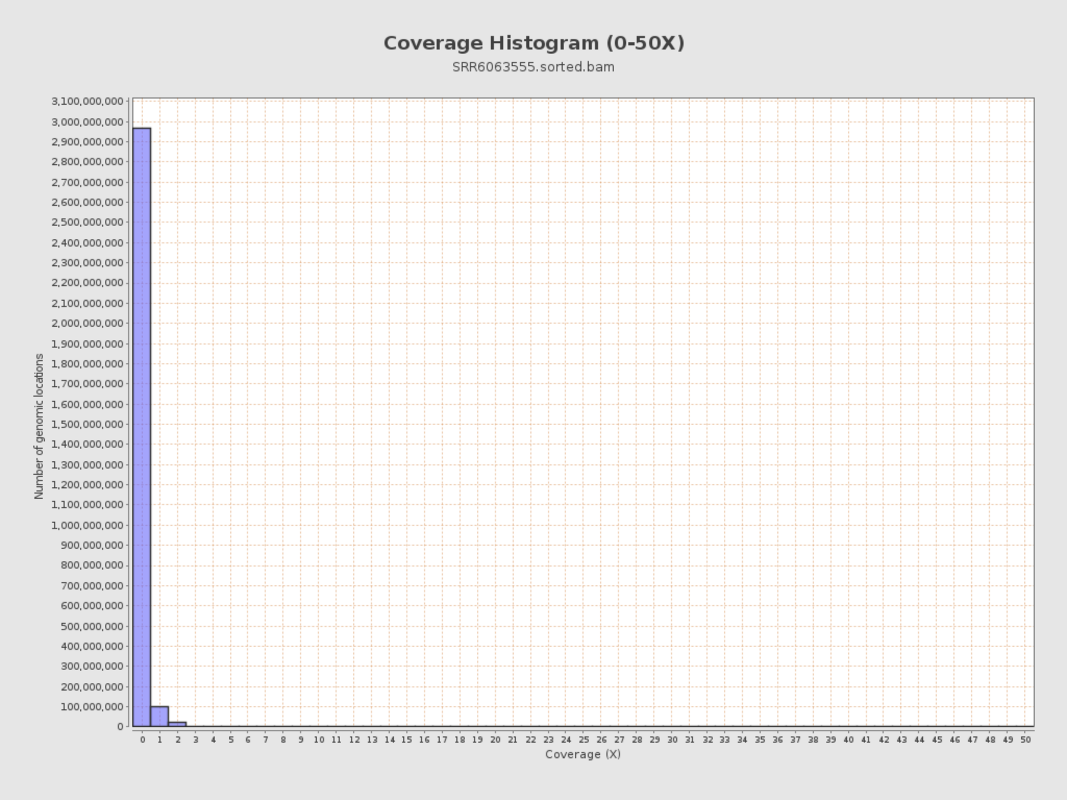
3. Results : Coverage across reference



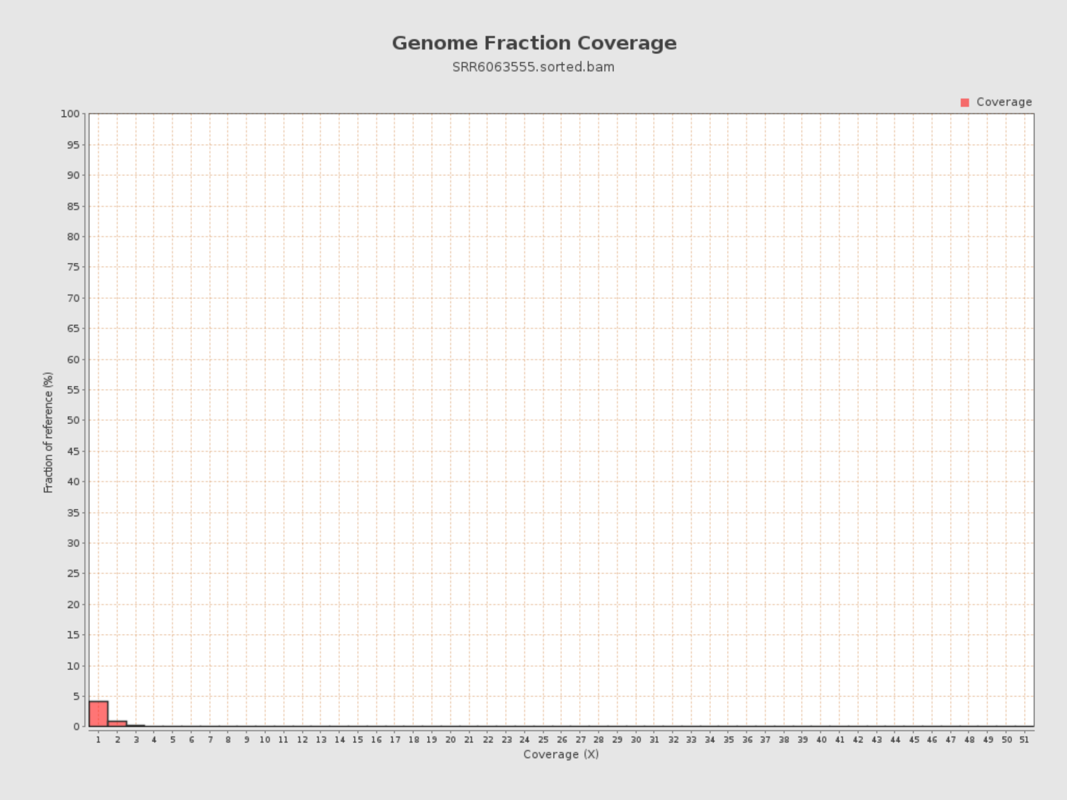
4. Results : Coverage Histogram



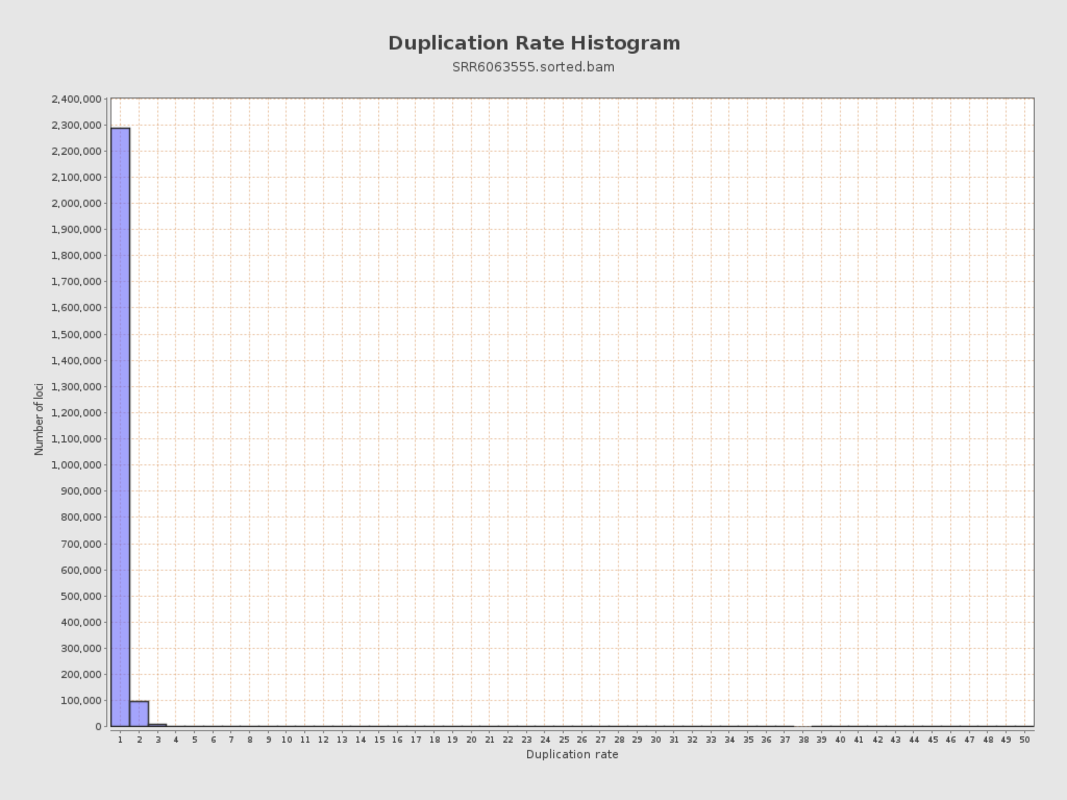
5. Results : Coverage Histogram (0-50X)



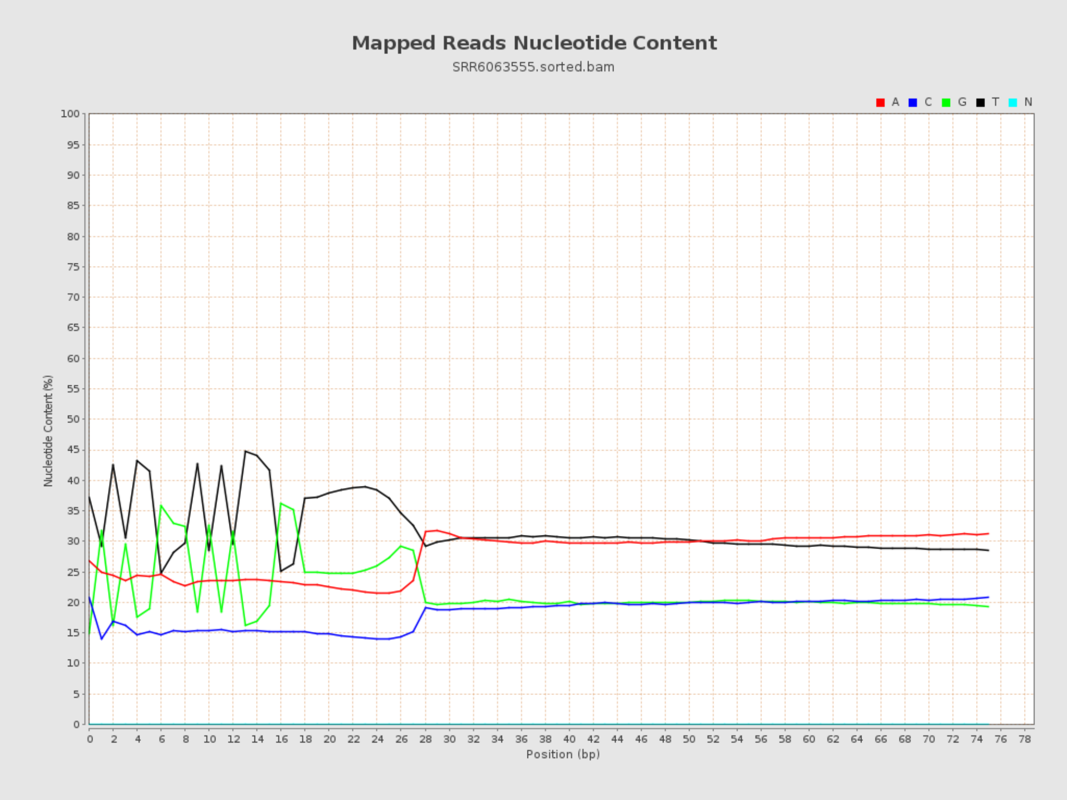
6. Results : Genome Fraction Coverage



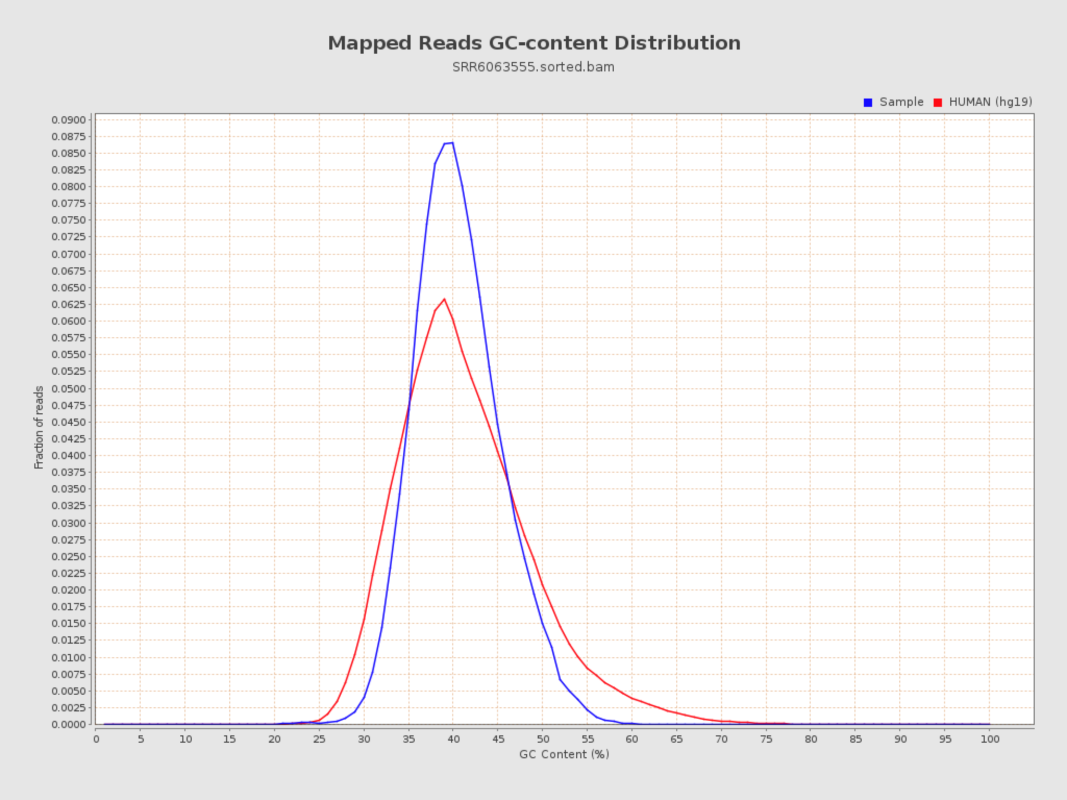
7. Results : Duplication Rate Histogram



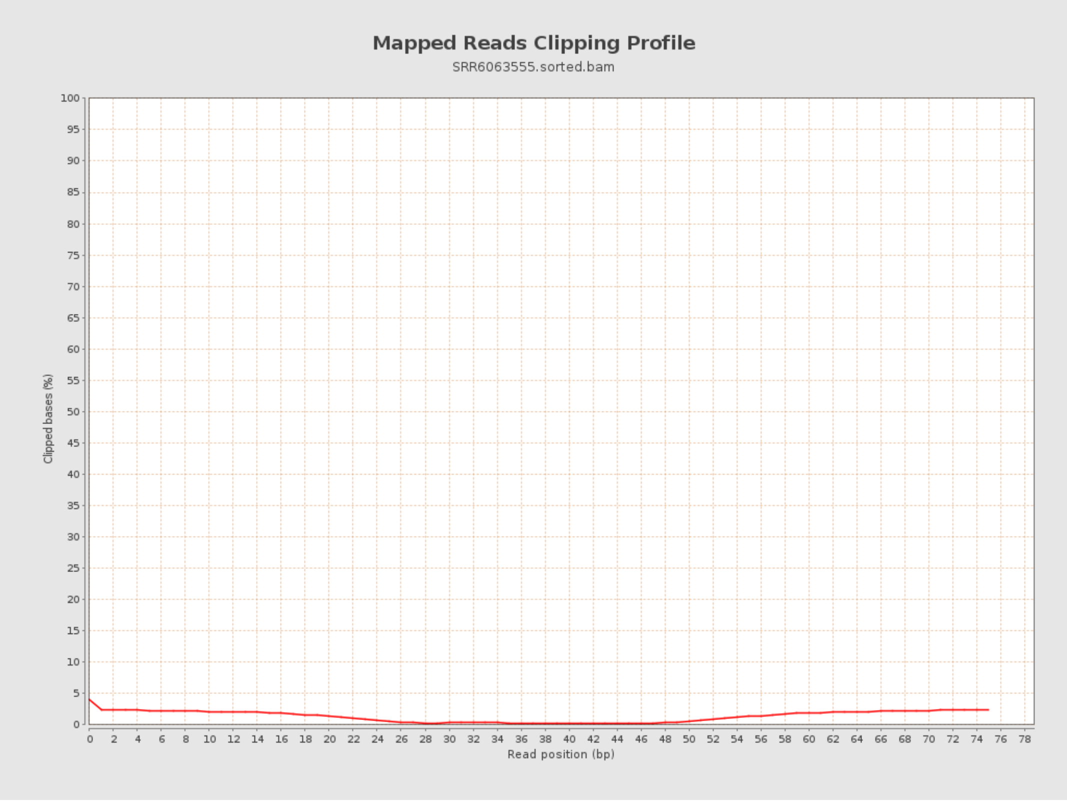
8. Results : Mapped Reads Nucleotide Content



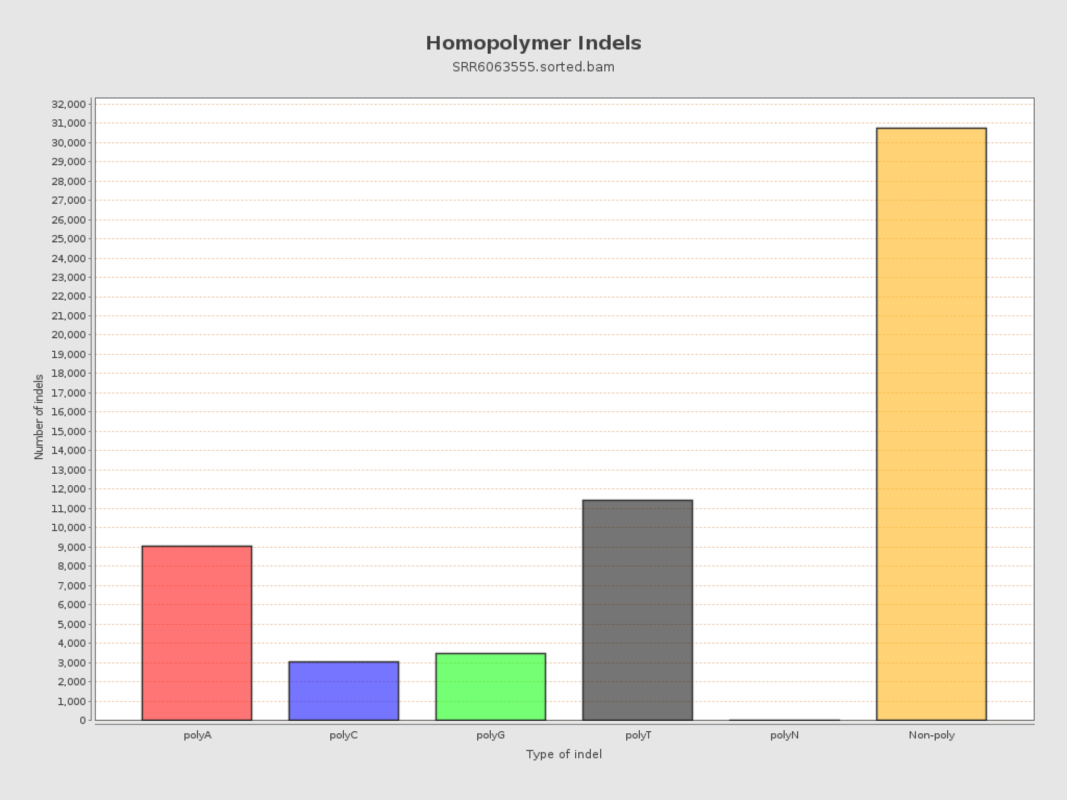
9. Results : Mapped Reads GC-content Distribution



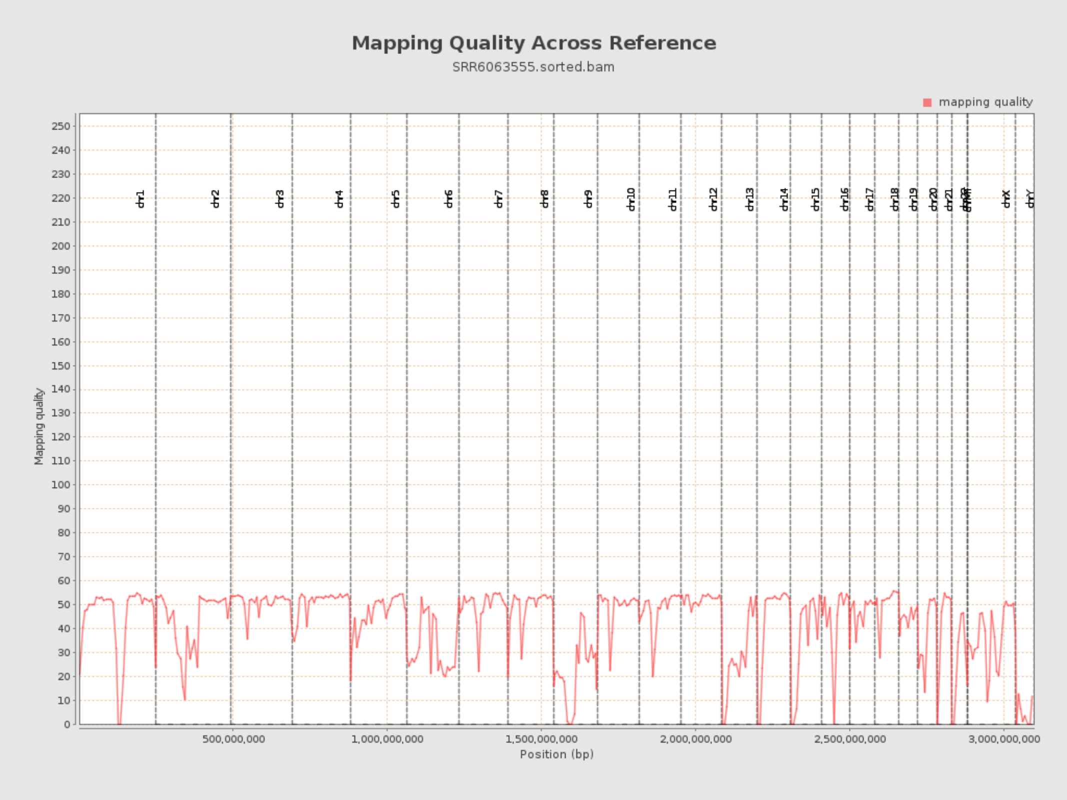
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram