Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:58:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063551.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_SRR6063551 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063551.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:58:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063551.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,709,303
Mapped reads	2,374,719 / 87.65%
Unmapped reads	334,584 / 12.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,352 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	121,162 / 4.47%
Duplication rate	3.78%
Clipped reads	1,430,399 / 52.8%

2.2. ACGT Content

Number/percentage of A's	38,289,784 / 25.61%
Number/percentage of C's	27,002,221 / 18.06%
Number/percentage of T's	47,125,961 / 31.52%
Number/percentage of G's	37,072,473 / 24.8%
Number/percentage of N's	2,667 / 0%
GC Percentage	42.86%

2.3. Coverage

Mean	0.0483

Standard Deviation	0.4839

2.4. Mapping Quality

Mean Mapping Quality	42.11

2.5. Mismatches and indels

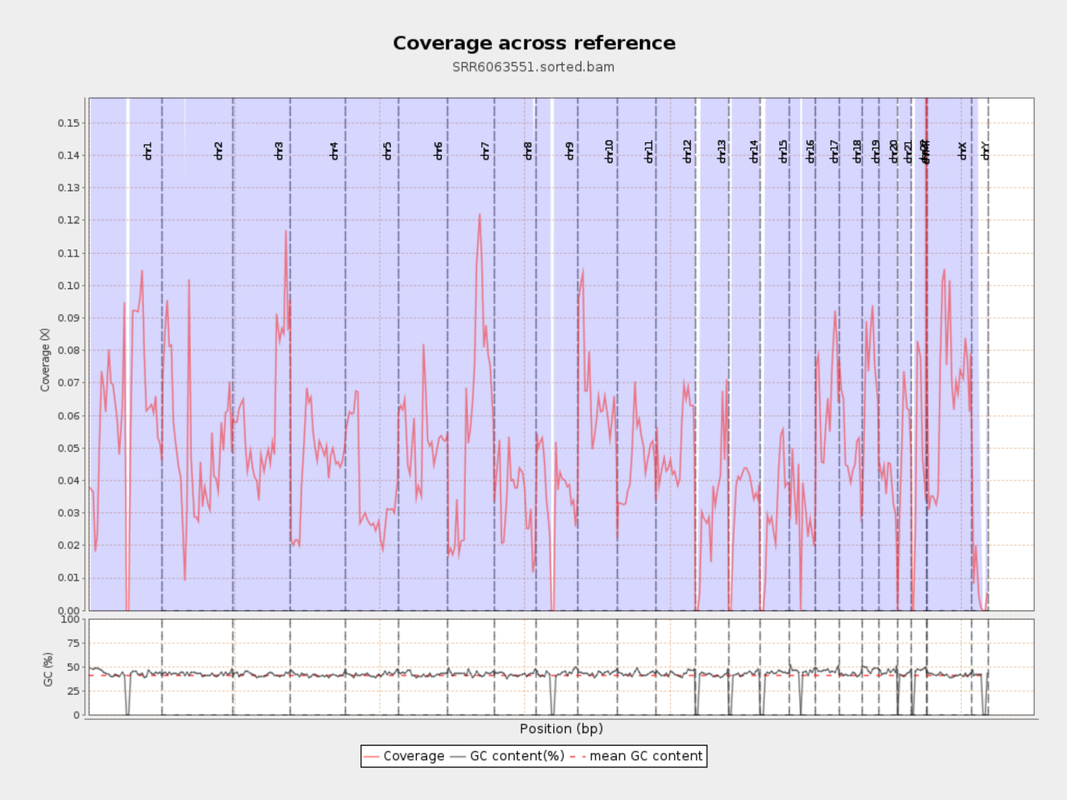
General error rate	0.82%
Mismatches	1,206,749
Insertions	11,355
Mapped reads with at least one insertion	0.47%
Deletions	38,638
Mapped reads with at least one deletion	1.61%
Homopolymer indels	45.31%

2.6. Chromosome stats

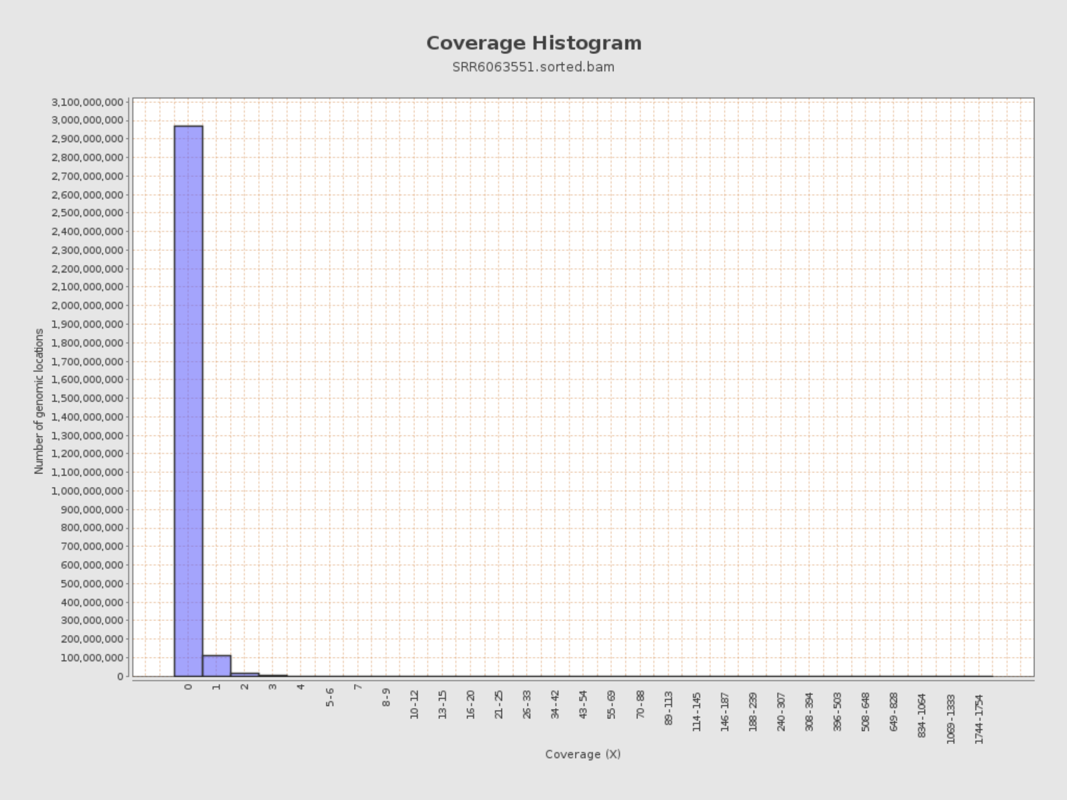
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15167851	0.0609	0.8956
chr2	243199373	12235849	0.0503	0.8885
chr3	198022430	11860137	0.0599	0.2859
chr4	191154276	8529507	0.0446	0.2682
chr5	180915260	6658717	0.0368	0.2262
chr6	171115067	9059678	0.0529	0.3337
chr7	159138663	9210890	0.0579	0.5266

chr8	146364022	5071196	0.0346	0.4522
chr9	141213431	5048302	0.0357	0.4337
chr10	135534747	9194160	0.0678	0.4024
chr11	135006516	6143802	0.0455	0.3367
chr12	133851895	6829267	0.051	0.2811
chr13	115169878	3716246	0.0323	0.2115
chr14	107349540	3551321	0.0331	0.2604
chr15	102531392	2973689	0.029	0.2414
chr16	90354753	2643639	0.0293	0.238
chr17	81195210	5429648	0.0669	0.3223
chr18	78077248	3936235	0.0504	0.648
chr19	59128983	4353050	0.0736	0.6682
chr20	63025520	2444348	0.0388	0.2425
chr21	48129895	2383976	0.0495	0.2758
chr22	51304566	2162107	0.0421	0.2384
chrMT	16571	17746	1.0709	1.3692
chrX	155270560	10458539	0.0674	0.3833
chrY	59373566	474703	0.008	0.1627

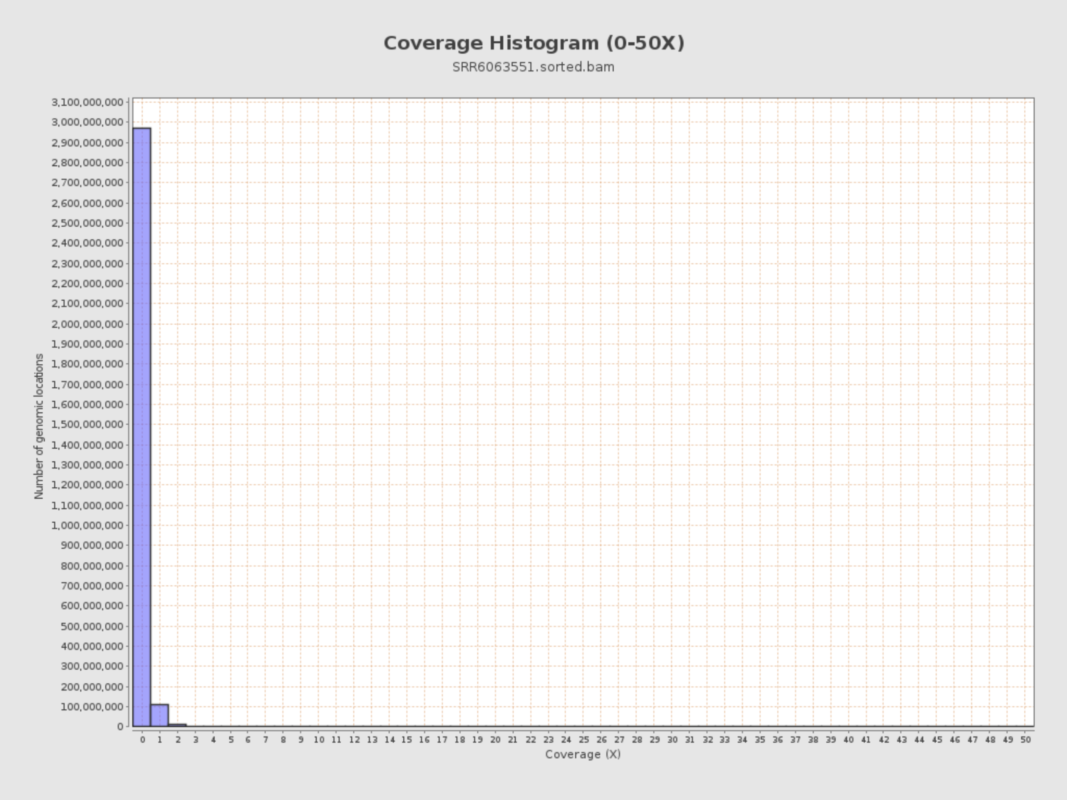
3. Results : Coverage across reference



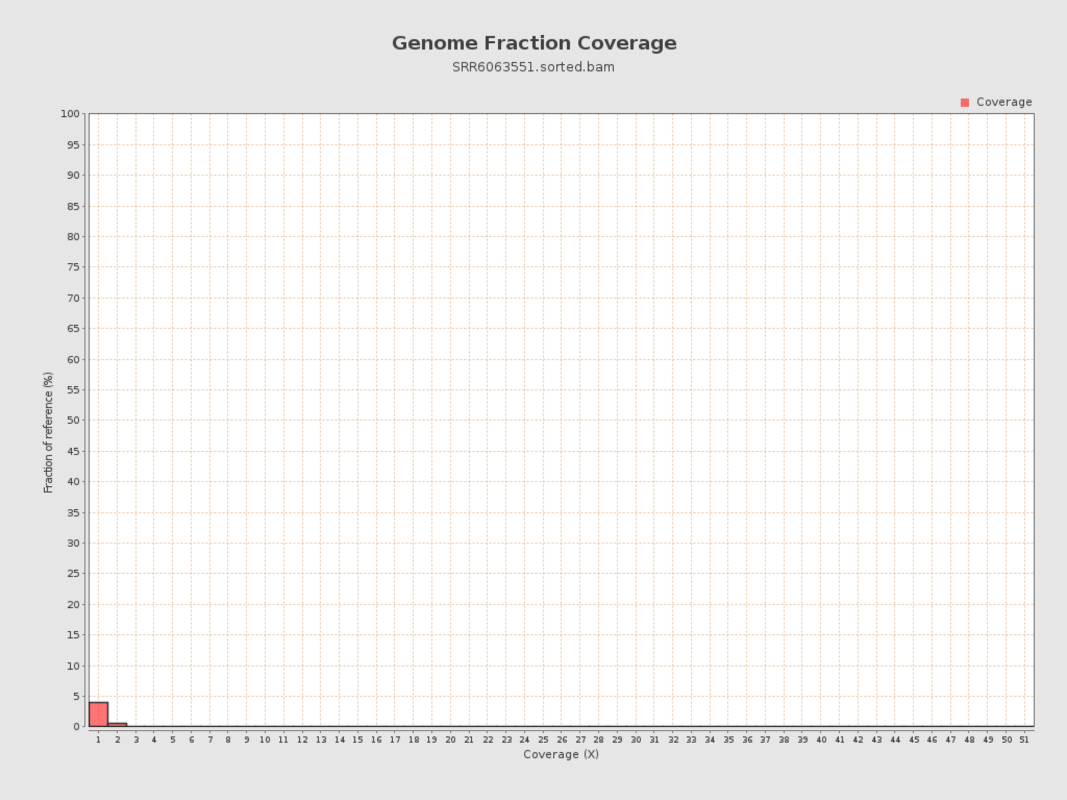
4. Results : Coverage Histogram



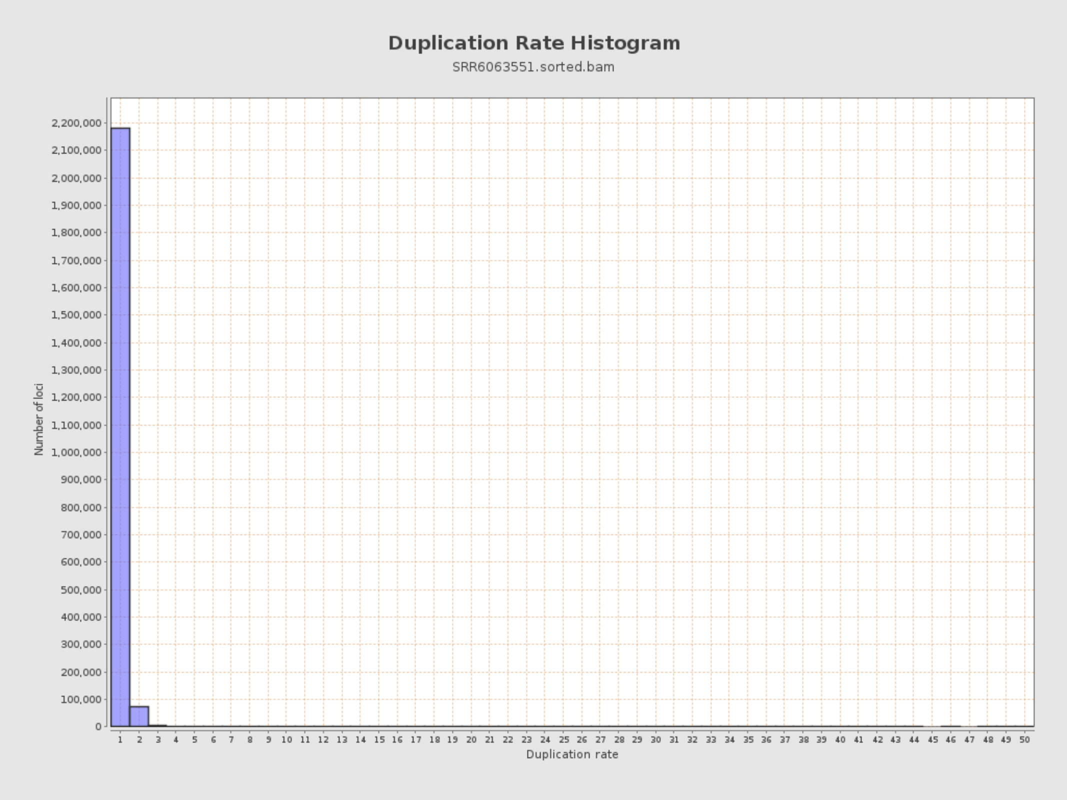
5. Results : Coverage Histogram (0-50X)



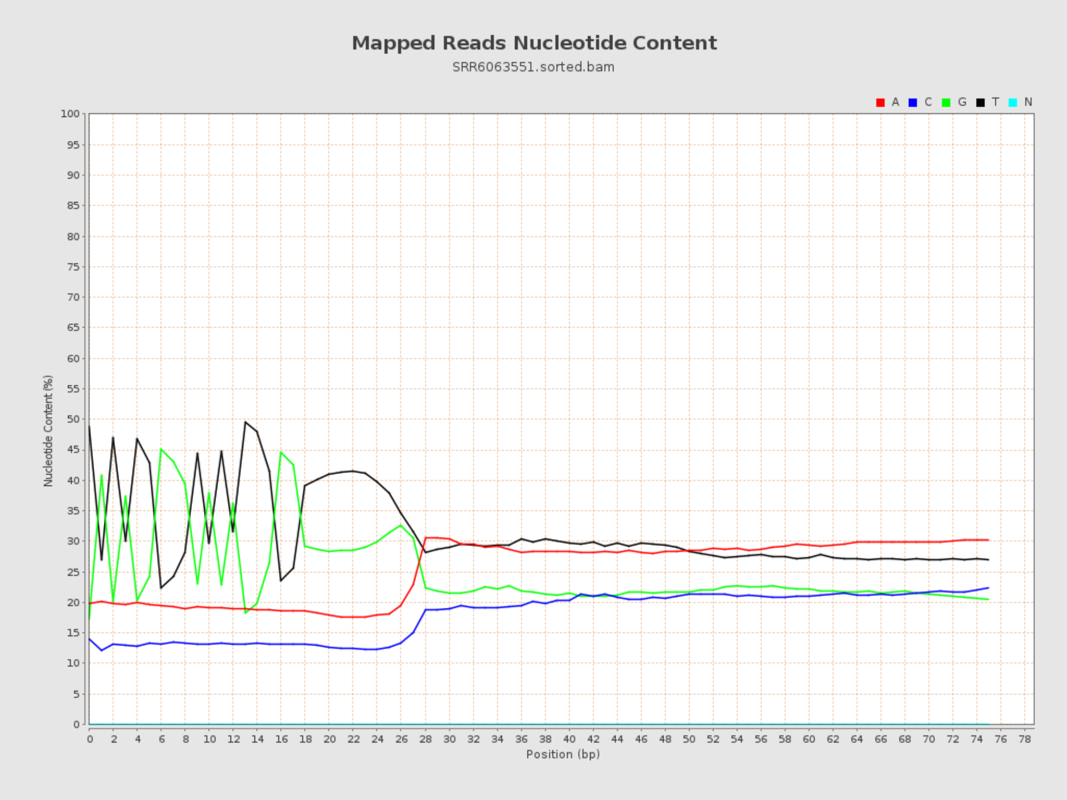
6. Results : Genome Fraction Coverage



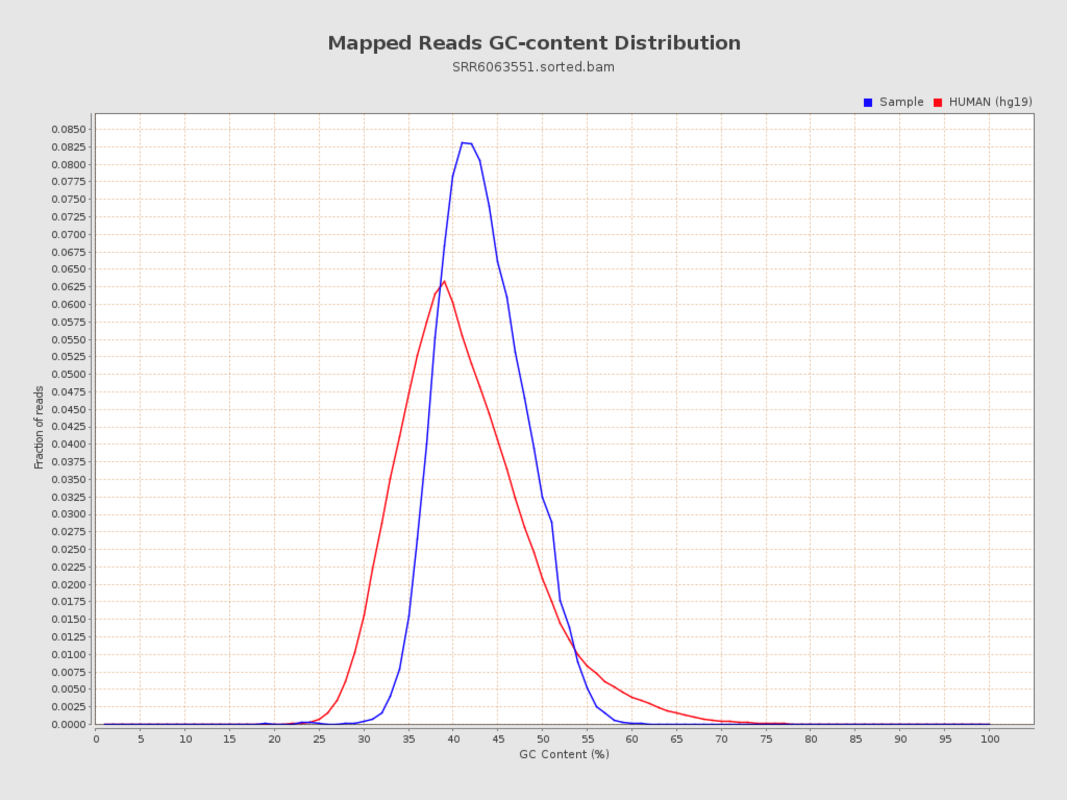
7. Results : Duplication Rate Histogram



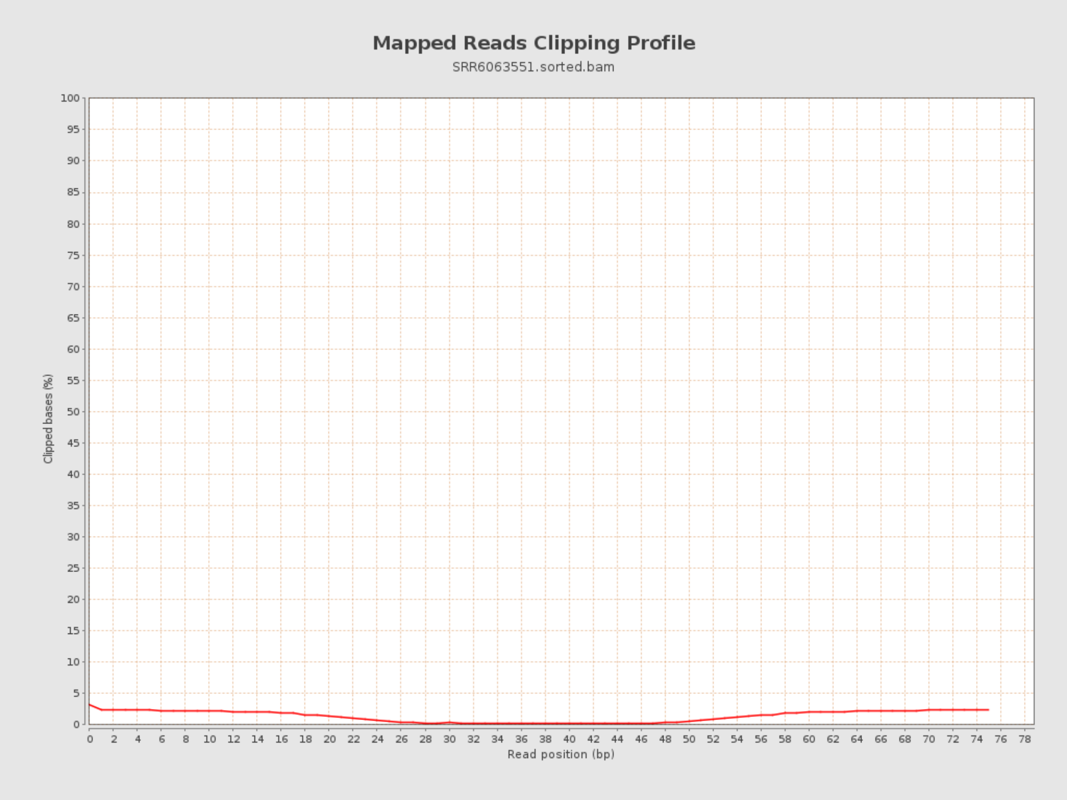
8. Results : Mapped Reads Nucleotide Content



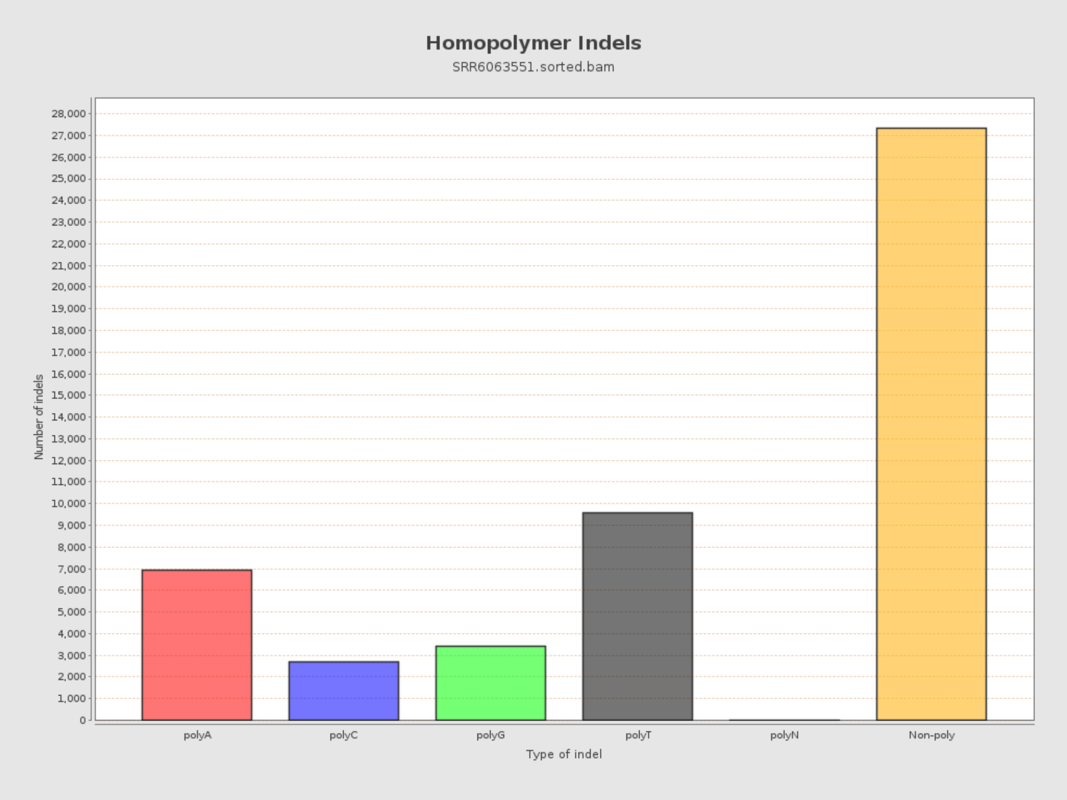
9. Results : Mapped Reads GC-content Distribution



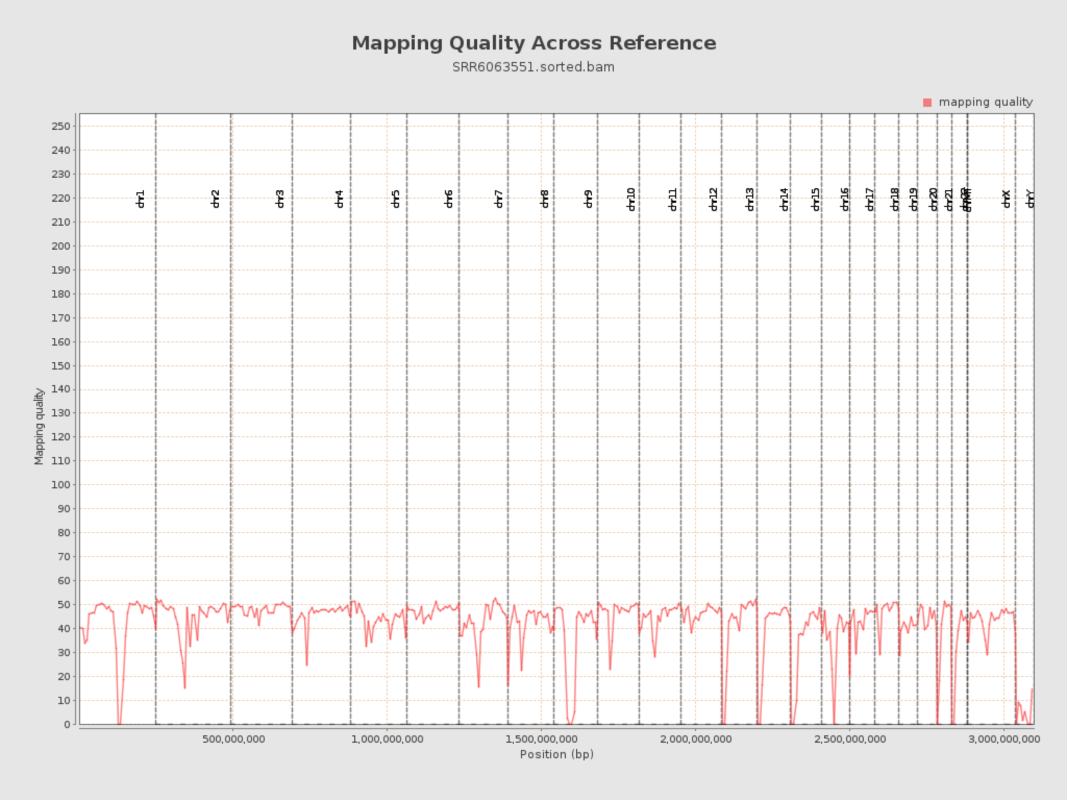
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram