Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:07:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063554.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_SRR6063554 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063554.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:07:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063554.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,759,908
Mapped reads	2,400,037 / 86.96%
Unmapped reads	359,871 / 13.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,288 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	131,077 / 4.75%
Duplication rate	4.16%
Clipped reads	1,141,526 / 41.36%

2.2. ACGT Content

Number/percentage of A's	44,596,910 / 28.09%
Number/percentage of C's	28,890,074 / 18.2%
Number/percentage of T's	50,566,041 / 31.85%
Number/percentage of G's	34,720,418 / 21.87%
Number/percentage of N's	4,192 / 0%
GC Percentage	40.06%

2.3. Coverage

Mean	0.0513

Standard Deviation	0.538

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

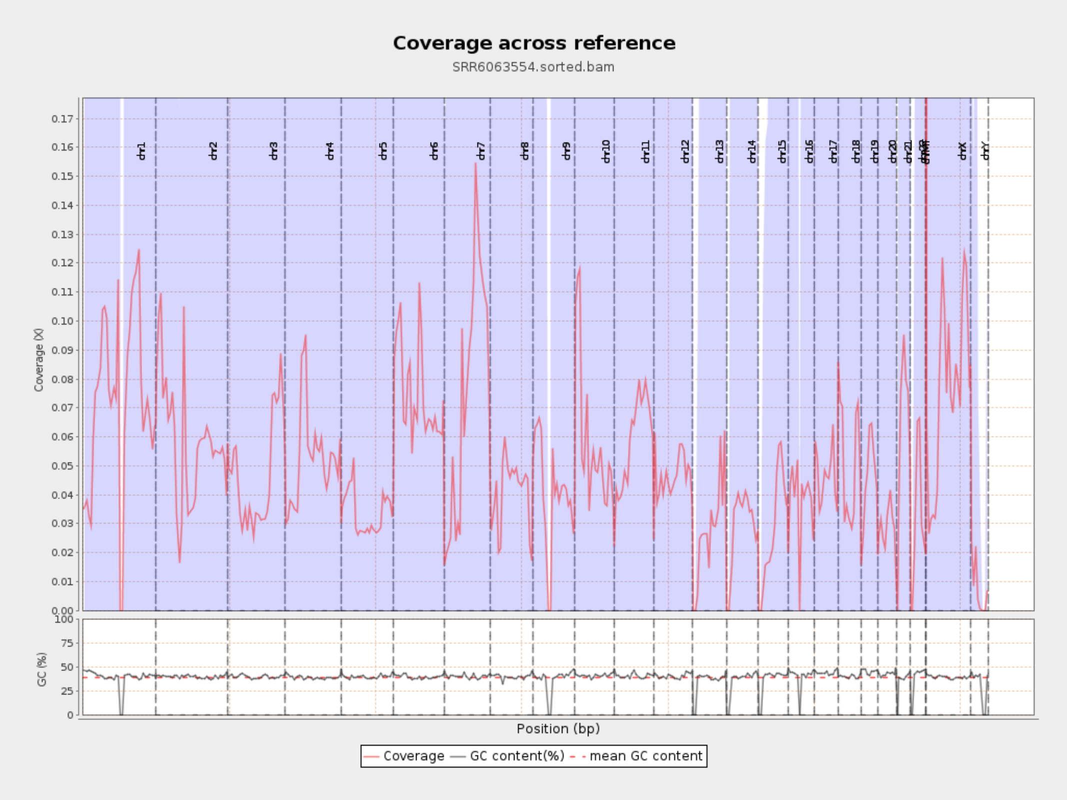
General error rate	0.83%
Mismatches	1,292,081
Insertions	12,303
Mapped reads with at least one insertion	0.51%
Deletions	42,393
Mapped reads with at least one deletion	1.75%
Homopolymer indels	46.74%

2.6. Chromosome stats

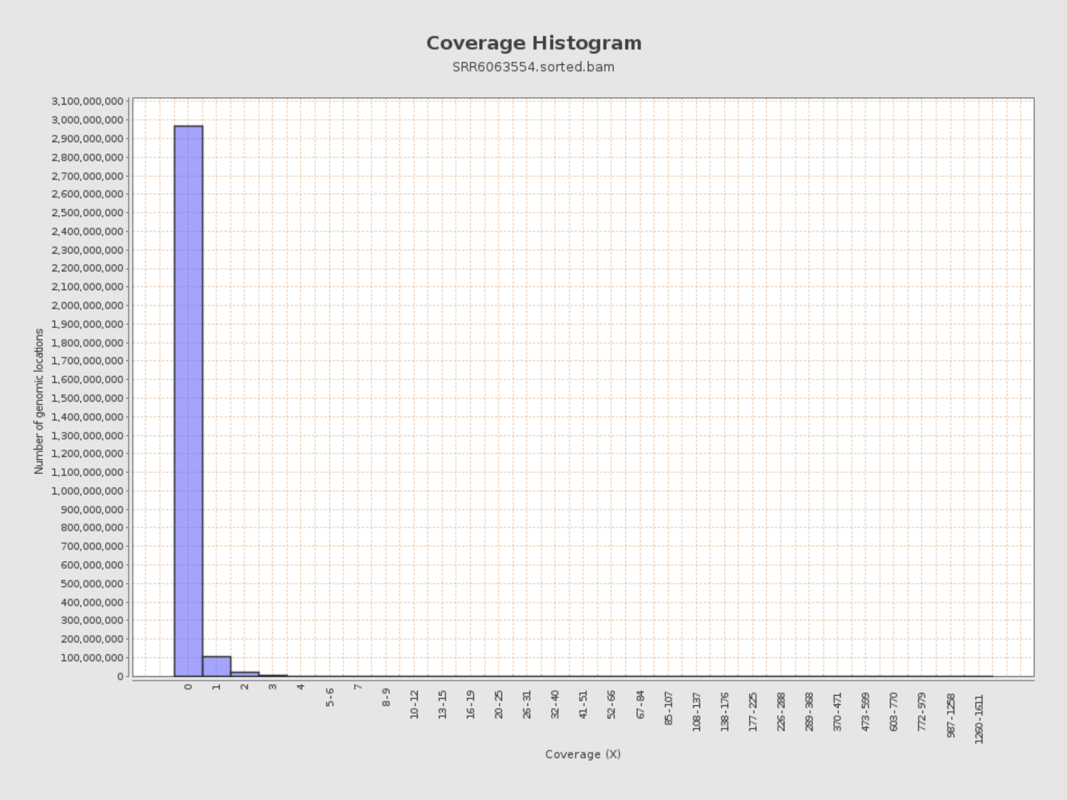
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18172239	0.0729	1.0919
chr2	243199373	14330504	0.0589	0.5997
chr3	198022430	9199021	0.0465	0.2588
chr4	191154276	10208576	0.0534	0.2896
chr5	180915260	6125139	0.0339	0.2205
chr6	171115067	12917502	0.0755	0.3901
chr7	159138663	12021925	0.0755	0.7424

chr8	146364022	5936886	0.0406	0.9797
chr9	141213431	5732282	0.0406	0.4353
chr10	135534747	8004583	0.0591	0.4043
chr11	135006516	7976896	0.0591	0.4057
chr12	133851895	6307321	0.0471	0.2756
chr13	115169878	3249137	0.0282	0.2052
chr14	107349540	3161592	0.0295	0.2573
chr15	102531392	2832448	0.0276	0.217
chr16	90354753	3341214	0.037	0.2584
chr17	81195210	3837277	0.0473	0.2899
chr18	78077248	3975616	0.0509	0.713
chr19	59128983	2721361	0.046	0.7151
chr20	63025520	1850255	0.0294	0.225
chr21	48129895	3040313	0.0632	0.3151
chr22	51304566	1620342	0.0316	0.2079
chrMT	16571	34611	2.0886	2.1783
chrX	155270560	11801785	0.076	0.4032
chrY	59373566	448315	0.0076	0.1614

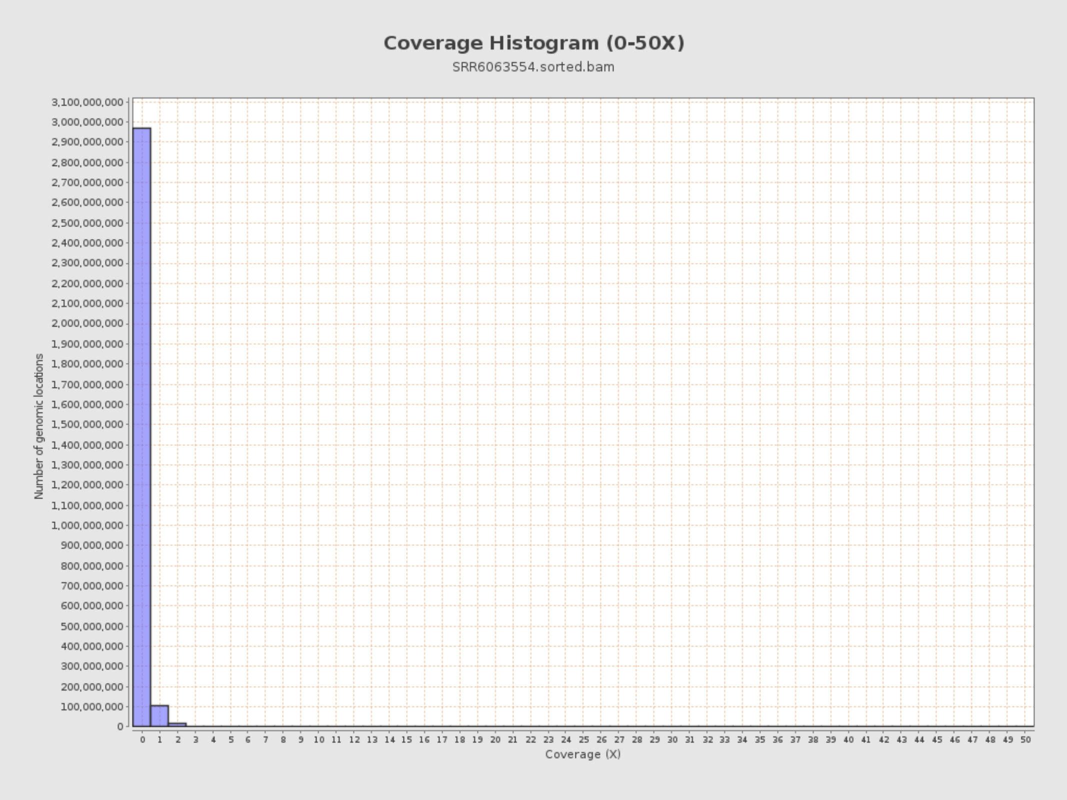
3. Results : Coverage across reference



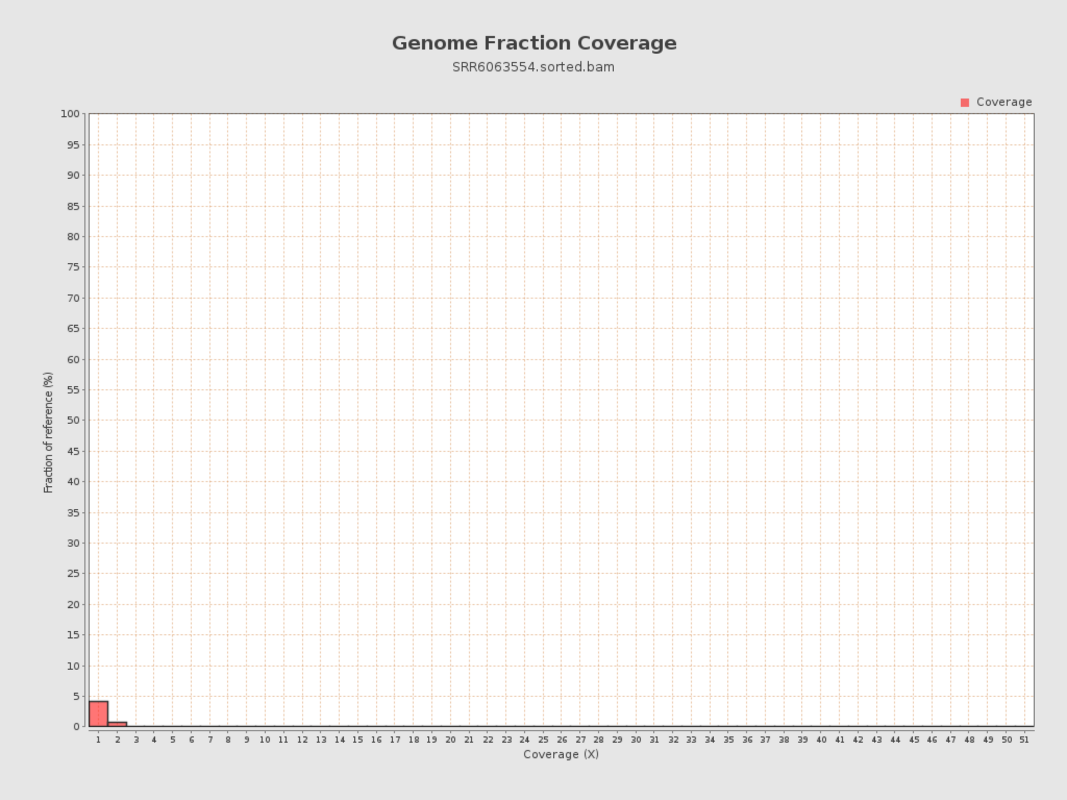
4. Results : Coverage Histogram



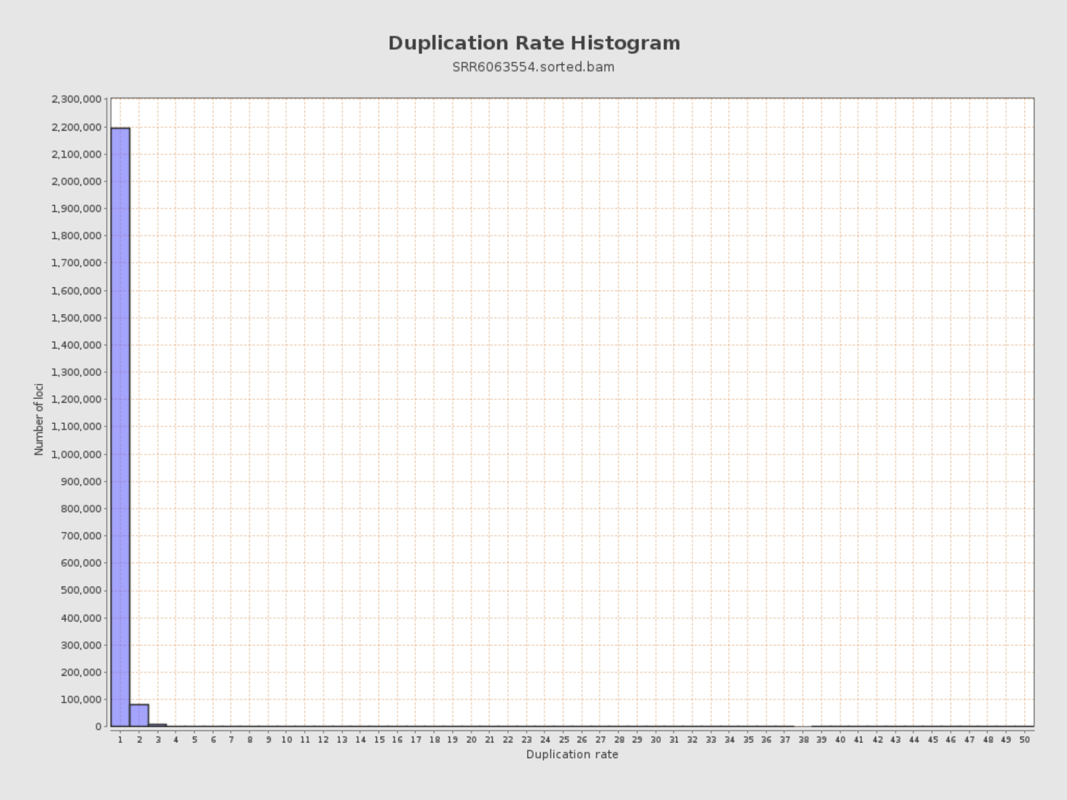
5. Results : Coverage Histogram (0-50X)



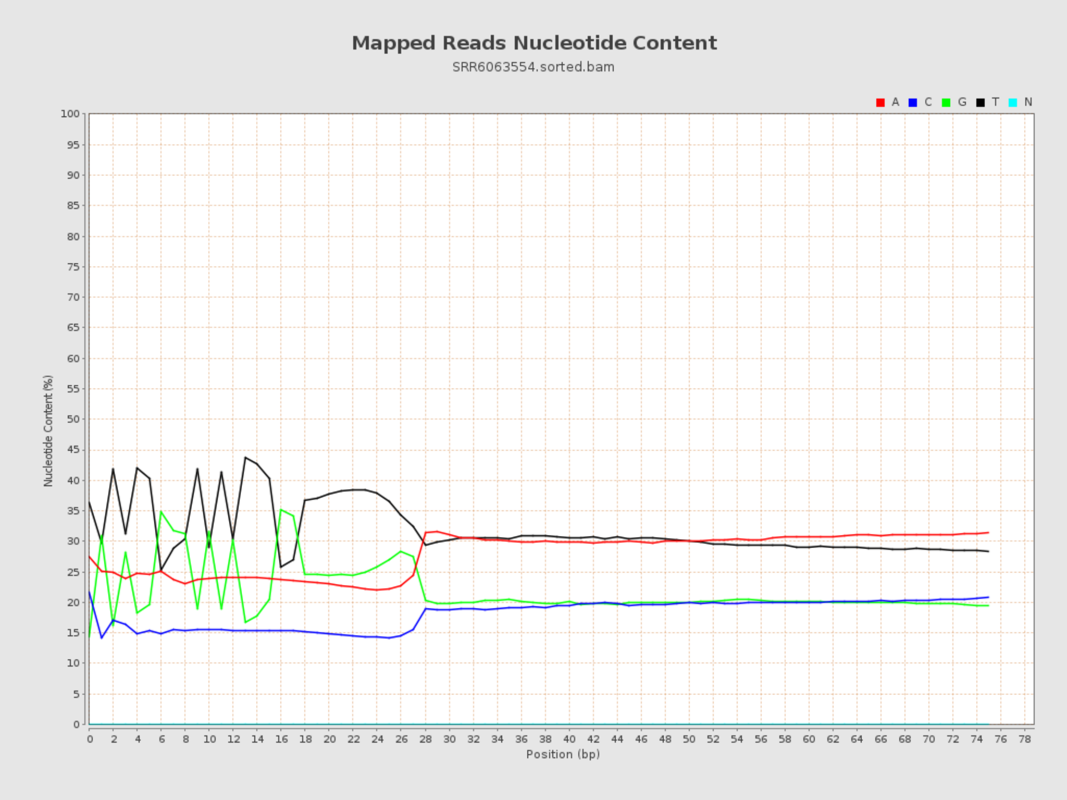
6. Results : Genome Fraction Coverage



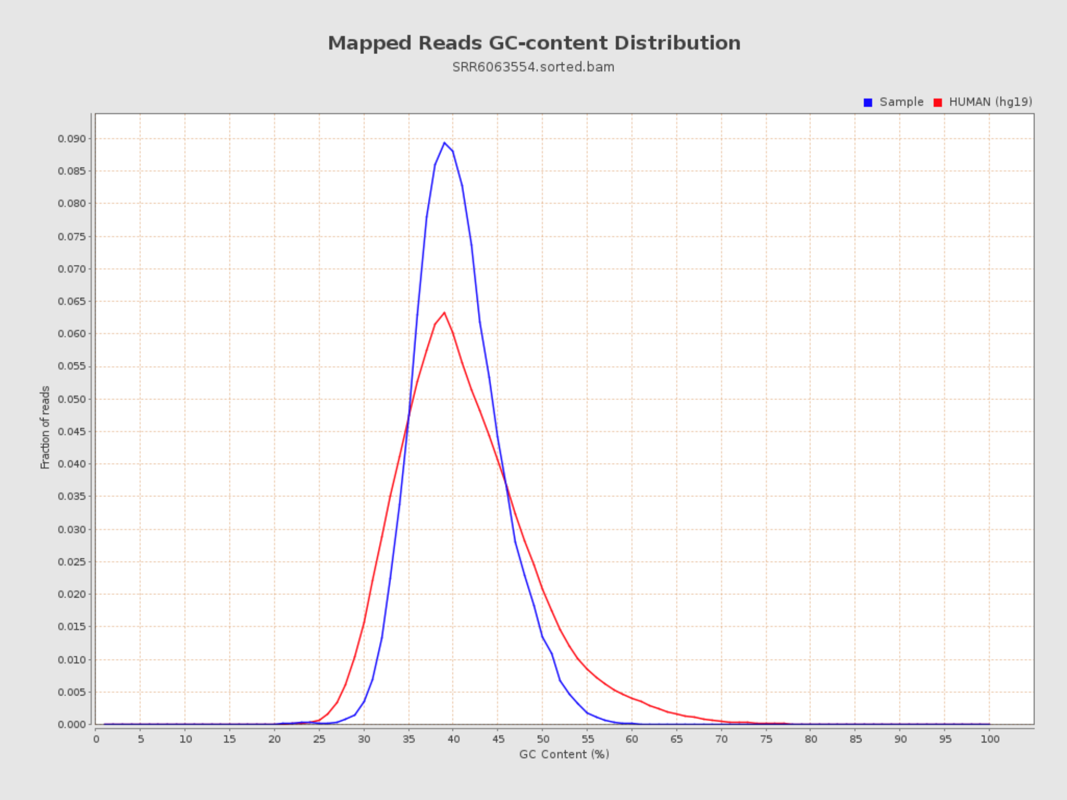
7. Results : Duplication Rate Histogram



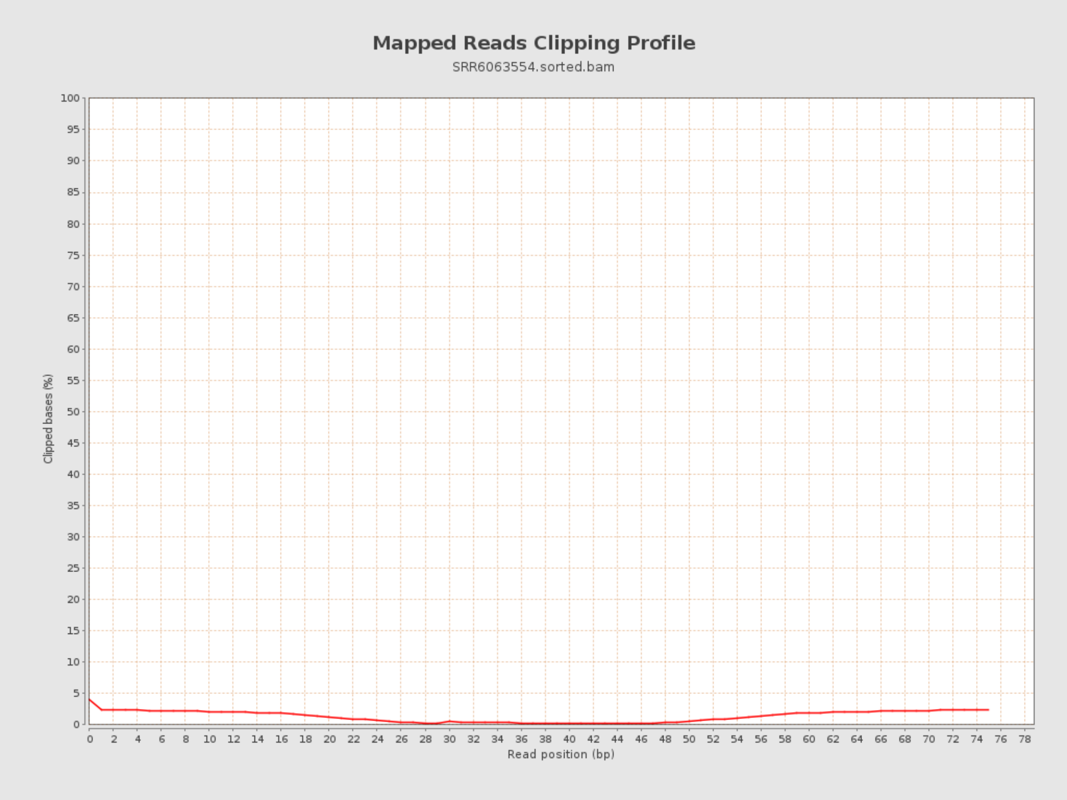
8. Results : Mapped Reads Nucleotide Content



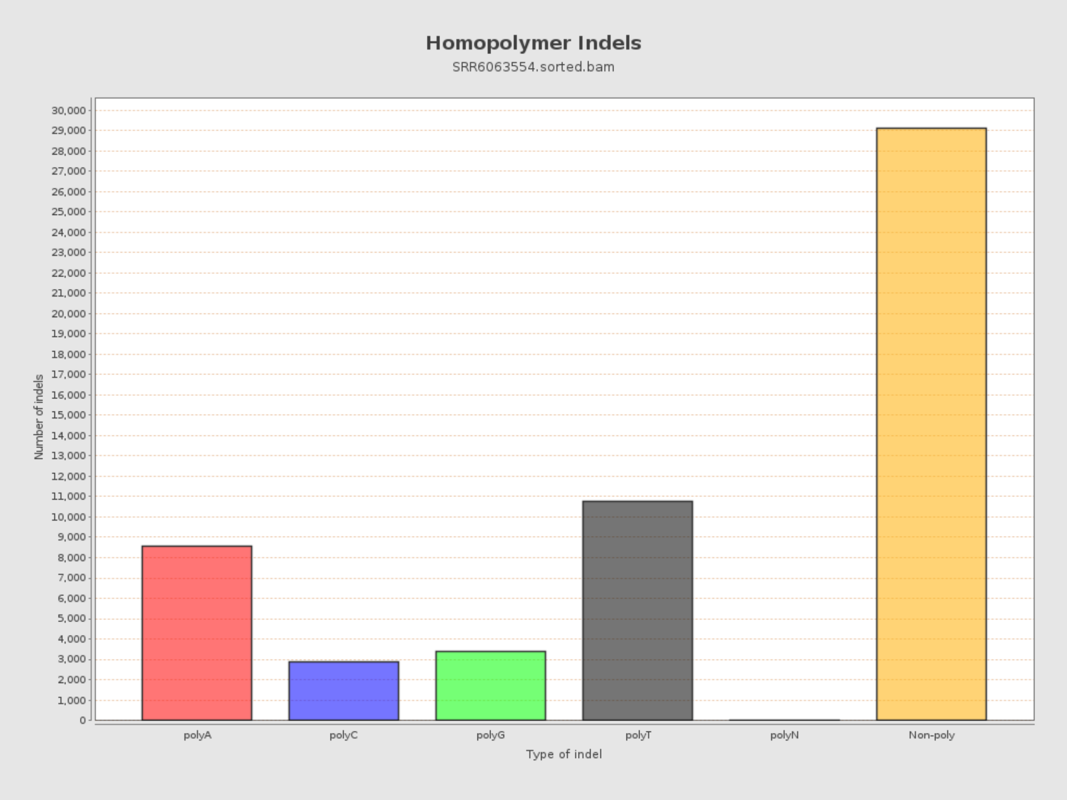
9. Results : Mapped Reads GC-content Distribution



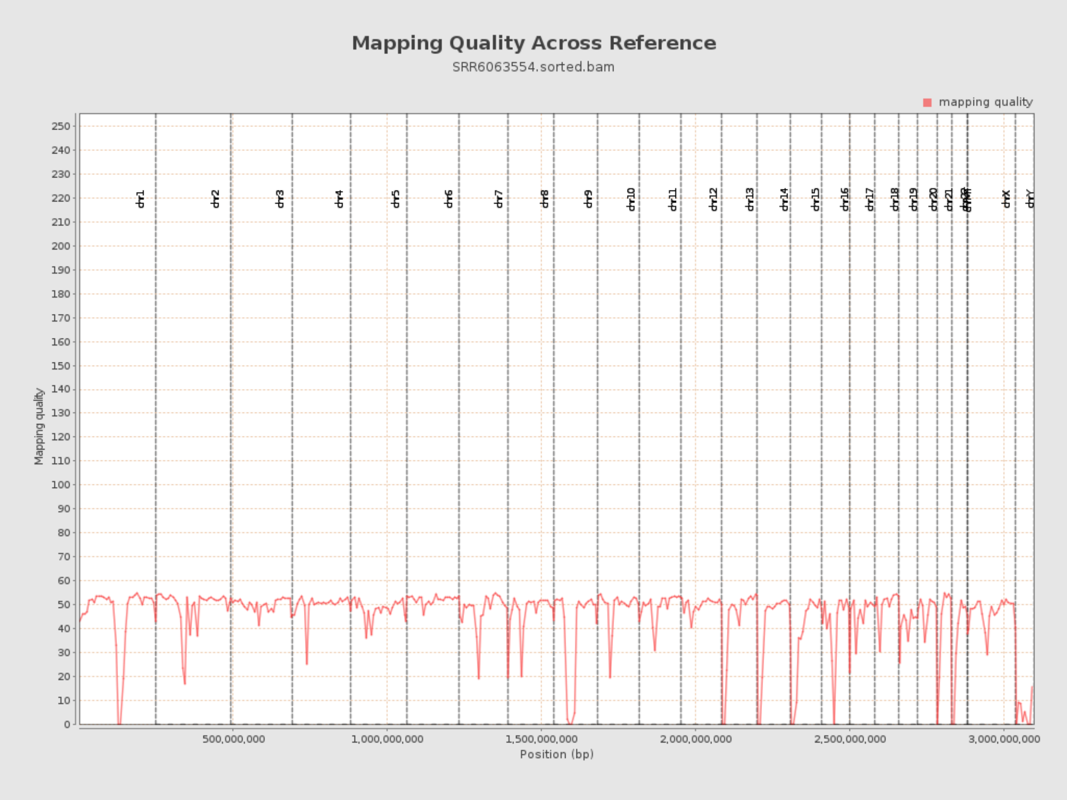
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram