Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:39:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063545.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_SRR6063545 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063545.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:39:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063545.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,058,143
Mapped reads	945,621 / 89.37%
Unmapped reads	112,522 / 10.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,698 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	38,562 / 3.64%
Duplication rate	3.36%
Clipped reads	474,320 / 44.83%

2.2. ACGT Content

Number/percentage of A's	16,821,133 / 27.27%
Number/percentage of C's	10,906,935 / 17.68%
Number/percentage of T's	20,102,684 / 32.59%
Number/percentage of G's	13,854,406 / 22.46%
Number/percentage of N's	1,572 / 0%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0199

Standard Deviation	0.2214

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

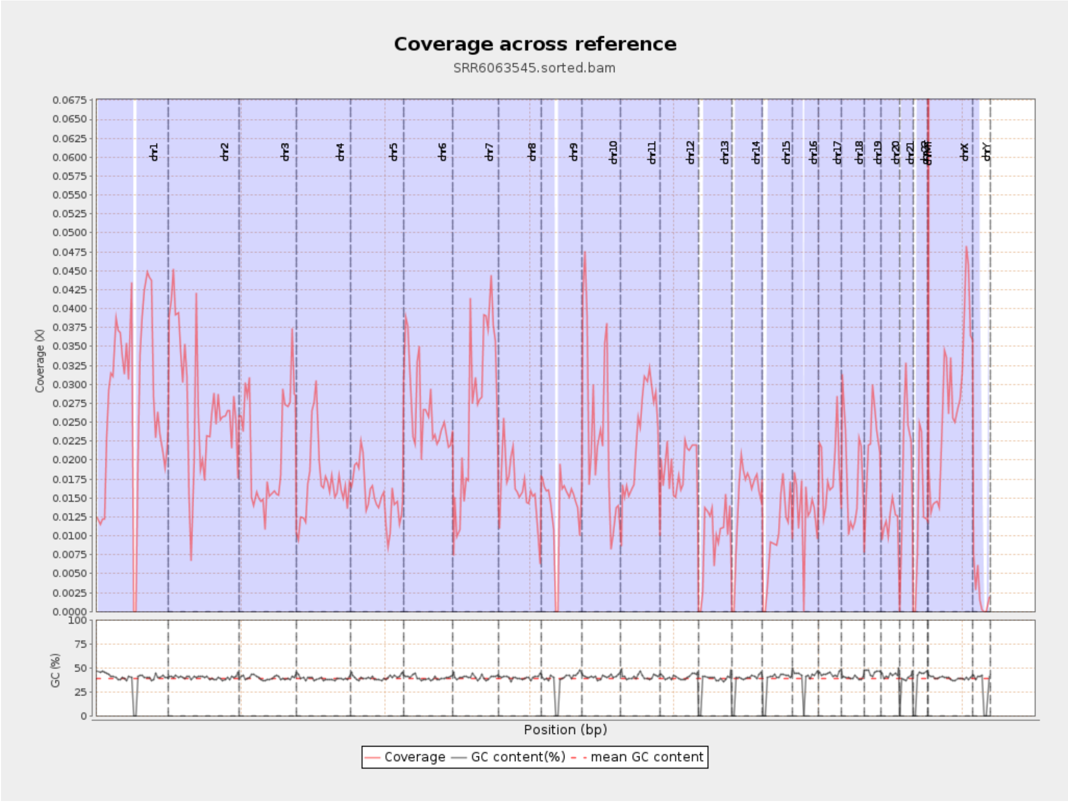
General error rate	0.82%
Mismatches	497,021
Insertions	4,622
Mapped reads with at least one insertion	0.49%
Deletions	16,751
Mapped reads with at least one deletion	1.75%
Homopolymer indels	47.62%

2.6. Chromosome stats

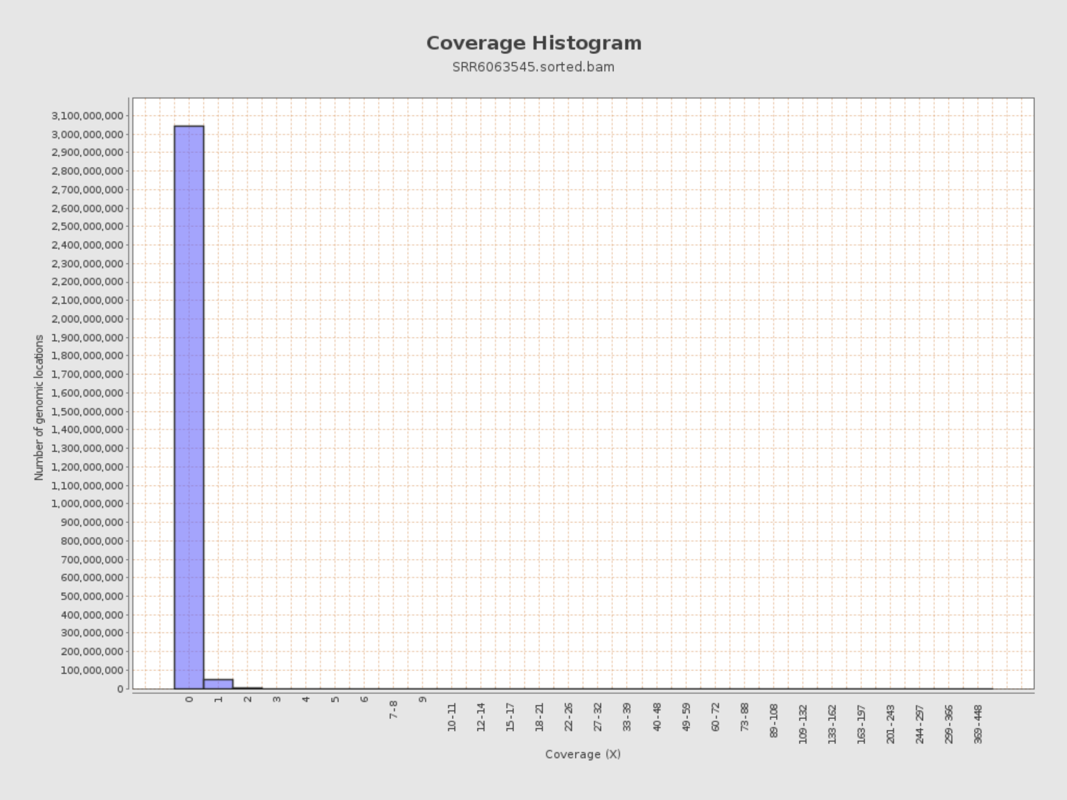
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6856361	0.0275	0.3968
chr2	243199373	6691801	0.0275	0.2807
chr3	198022430	4221953	0.0213	0.161
chr4	191154276	3262896	0.0171	0.1466
chr5	180915260	2770232	0.0153	0.1355
chr6	171115067	4551698	0.0266	0.1946
chr7	159138663	4263288	0.0268	0.325

chr8	146364022	2359355	0.0161	0.2736
chr9	141213431	1927297	0.0136	0.1845
chr10	135534747	3249403	0.024	0.1973
chr11	135006516	3131694	0.0232	0.1907
chr12	133851895	2568175	0.0192	0.1564
chr13	115169878	1121108	0.0097	0.1104
chr14	107349540	1567785	0.0146	0.1392
chr15	102531392	1007418	0.0098	0.1156
chr16	90354753	1164045	0.0129	0.1321
chr17	81195210	1505156	0.0185	0.1544
chr18	78077248	1391352	0.0178	0.2826
chr19	59128983	1304546	0.0221	0.2731
chr20	63025520	744336	0.0118	0.1232
chr21	48129895	963009	0.02	0.1575
chr22	51304566	648583	0.0126	0.1222
chrMT	16571	10545	0.6364	1.0301
chrX	155270560	4294812	0.0277	0.1962
chrY	59373566	136990	0.0023	0.0641

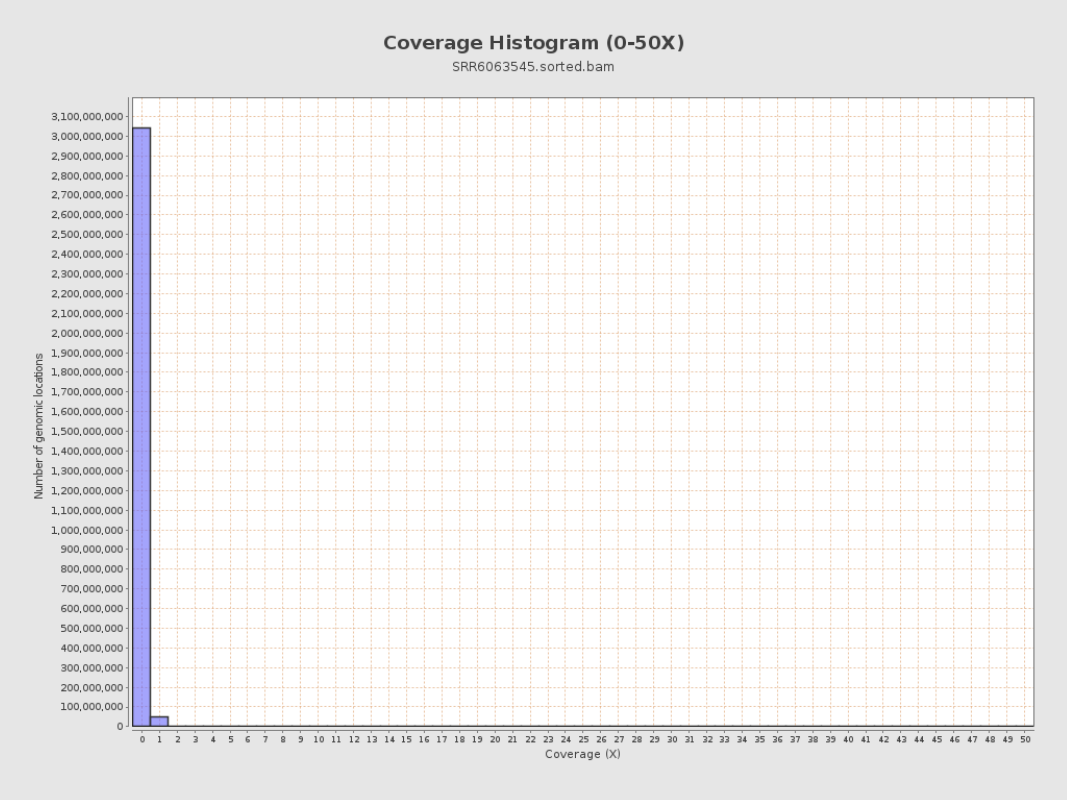
3. Results : Coverage across reference



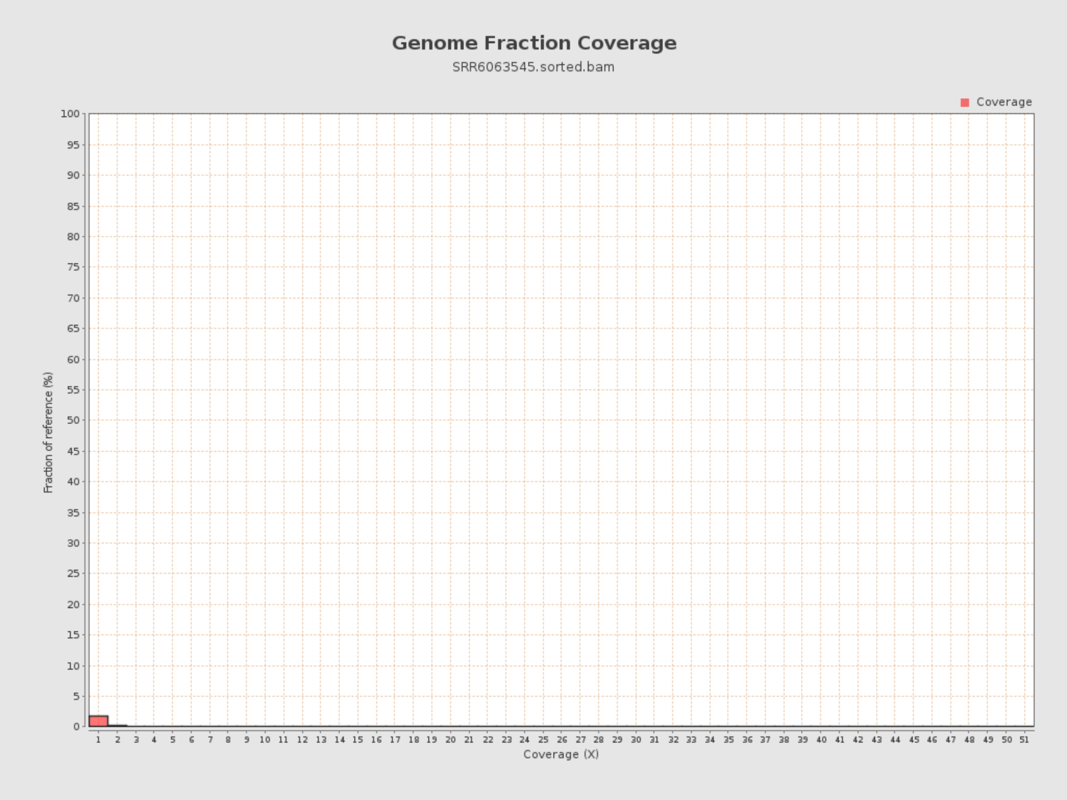
4. Results : Coverage Histogram



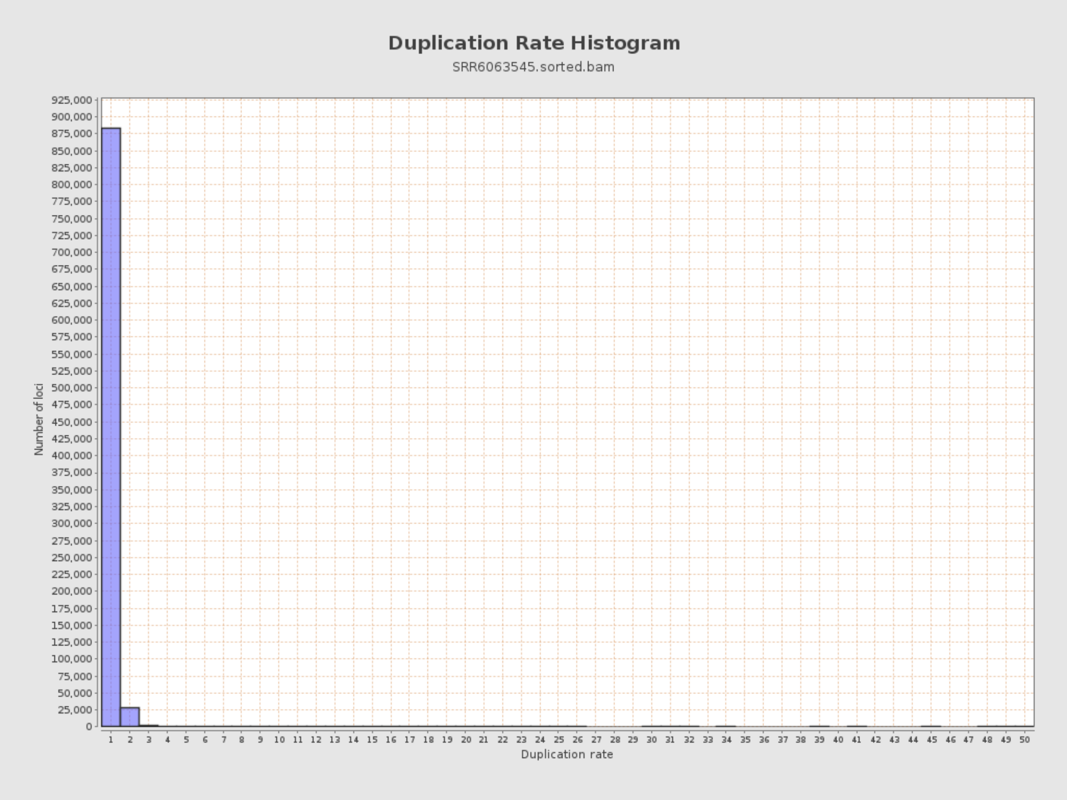
5. Results : Coverage Histogram (0-50X)



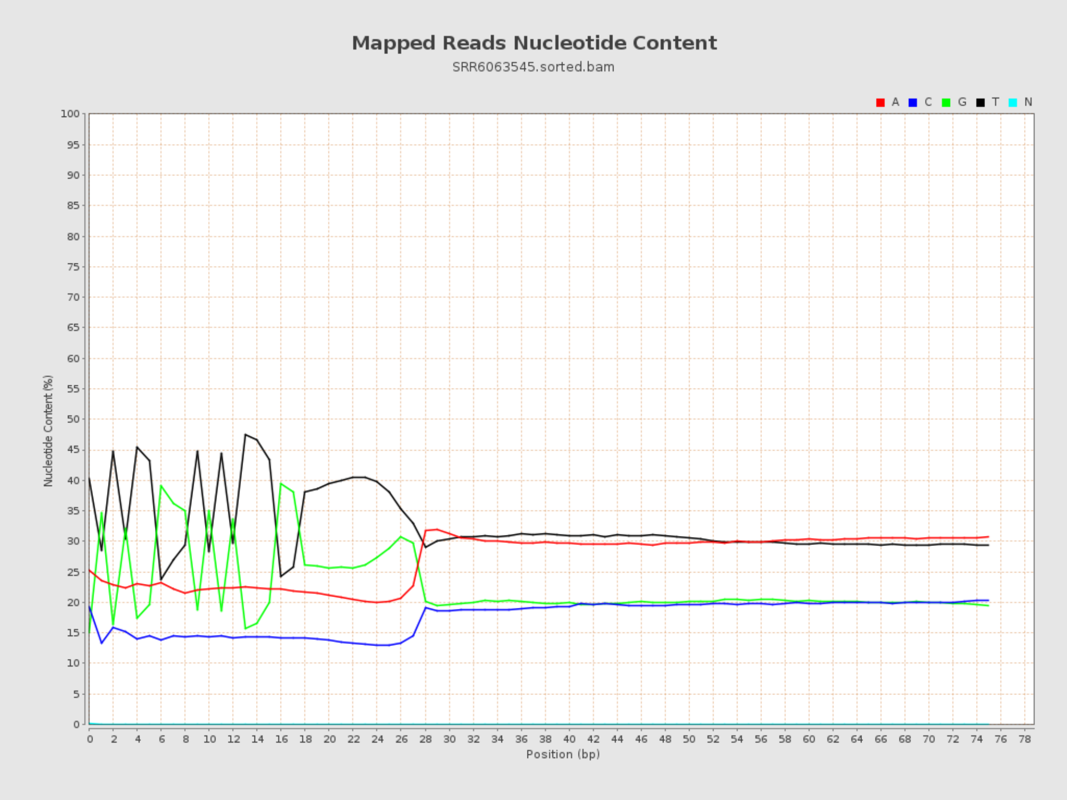
6. Results : Genome Fraction Coverage



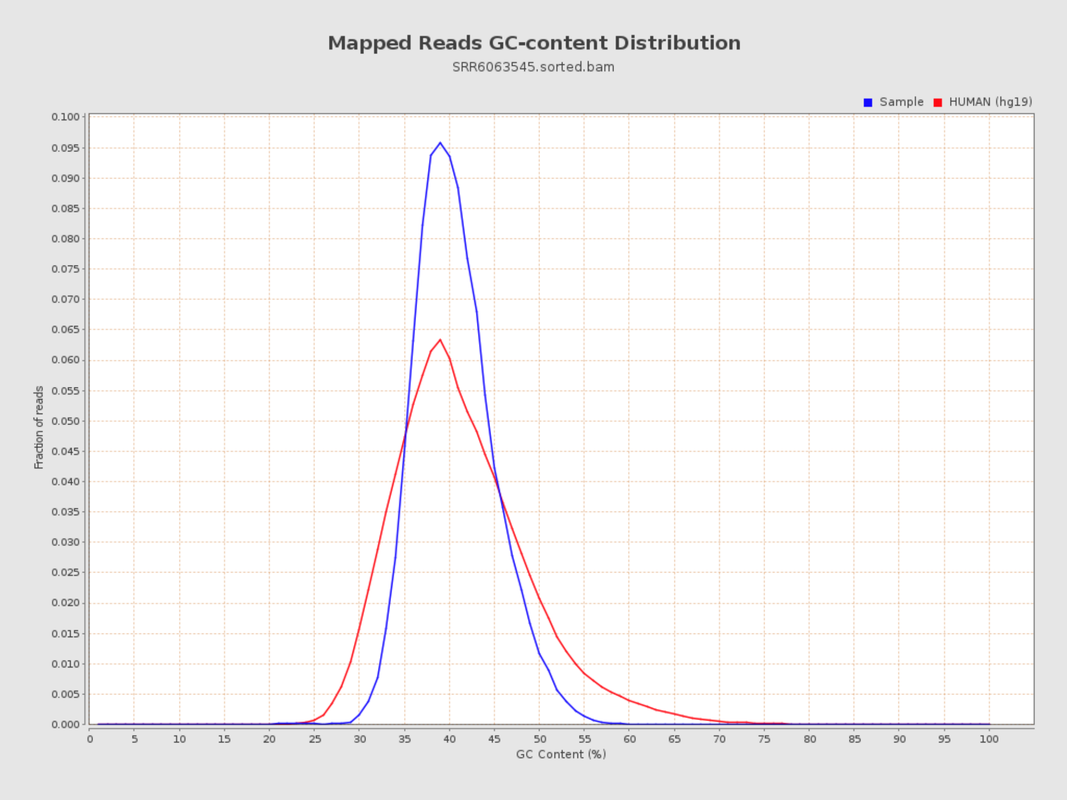
7. Results : Duplication Rate Histogram



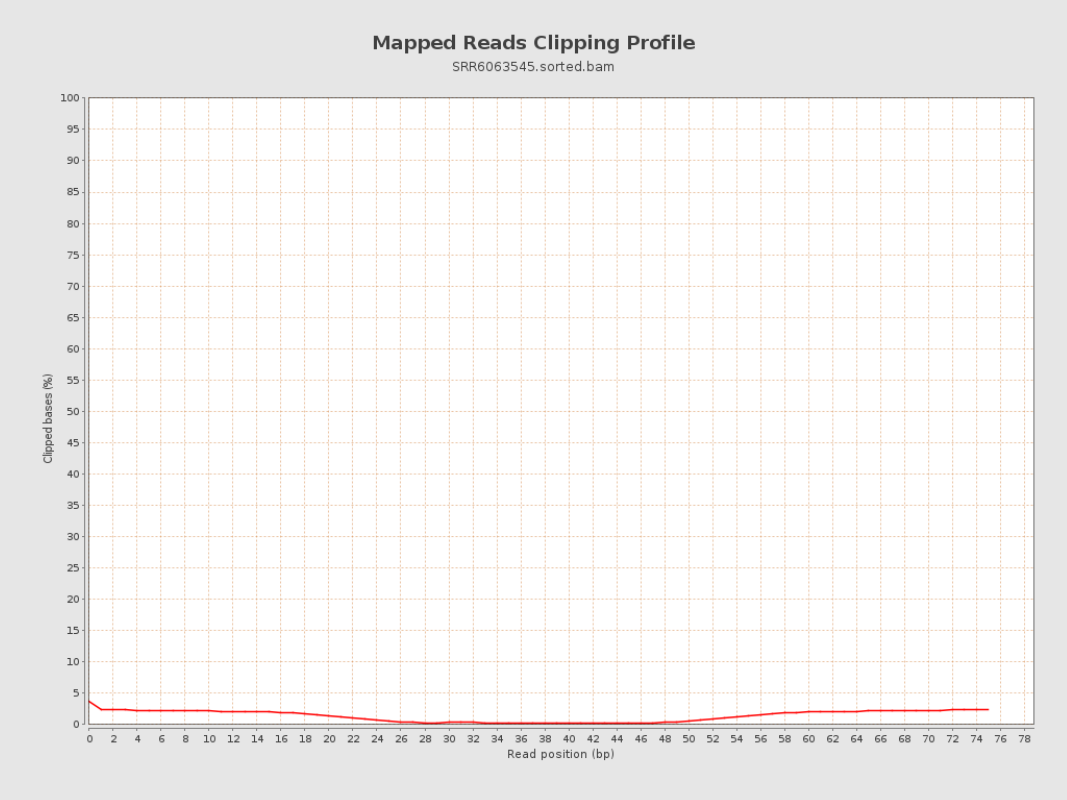
8. Results : Mapped Reads Nucleotide Content



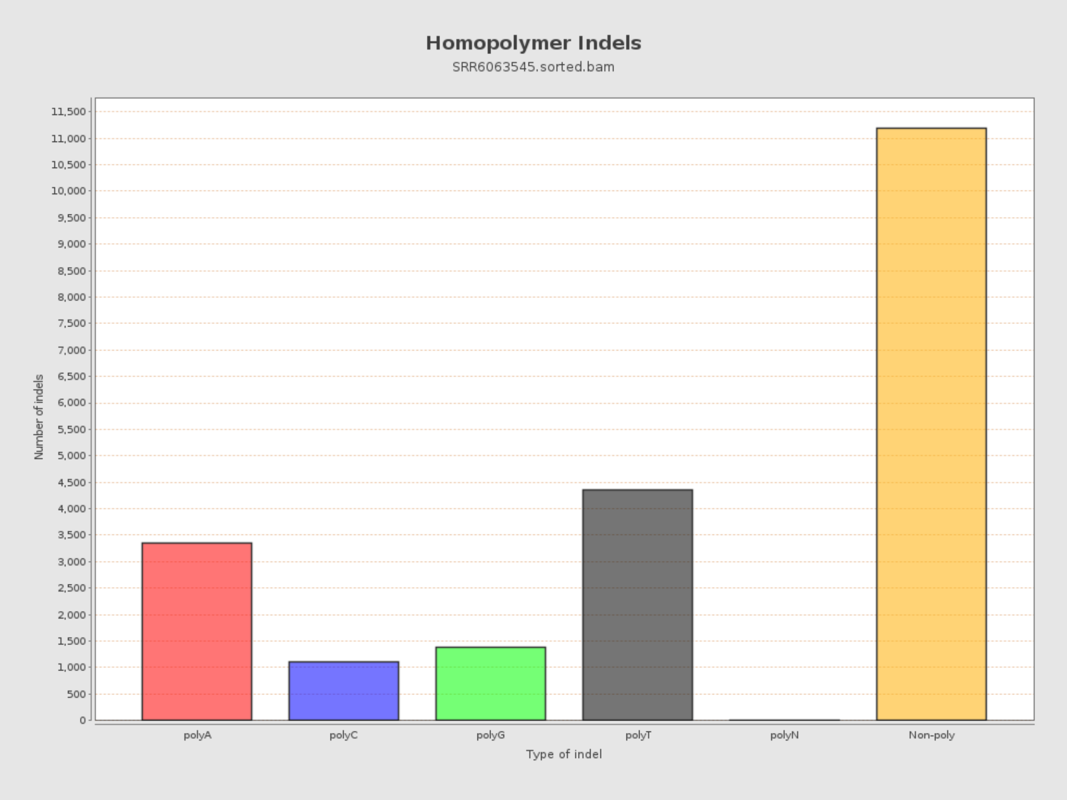
9. Results : Mapped Reads GC-content Distribution



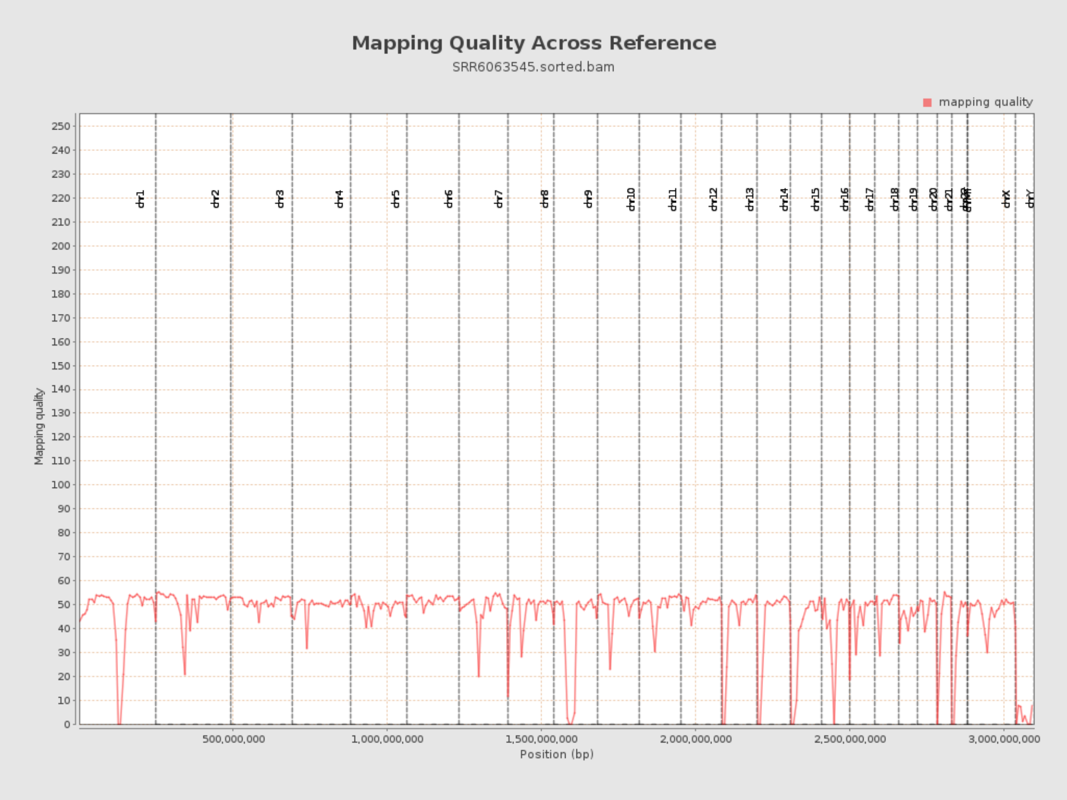
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram