Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 15:09:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124807.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_SRR3124807 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124807.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 15:09:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124807.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	686,414
Mapped reads	685,609 / 99.88%
Unmapped reads	805 / 0.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	314,847 / 45.87%
Read min/max/mean length	30 / 151 / 181.73
Duplicated reads (estimated)	999,039 / 145.54%
Duplication rate	34.93%
Clipped reads	651,795 / 94.96%

2.2. ACGT Content

Number/percentage of A's	27,861,919 / 26.97%
Number/percentage of C's	19,797,448 / 19.17%
Number/percentage of T's	33,421,180 / 32.35%
Number/percentage of G's	22,215,519 / 21.51%
Number/percentage of N's	1 / 0%
GC Percentage	40.67%

2.3. Coverage

Mean	0.0334

Standard Deviation	68.3193

2.4. Mapping Quality

Mean Mapping Quality	36.75

2.5. Mismatches and indels

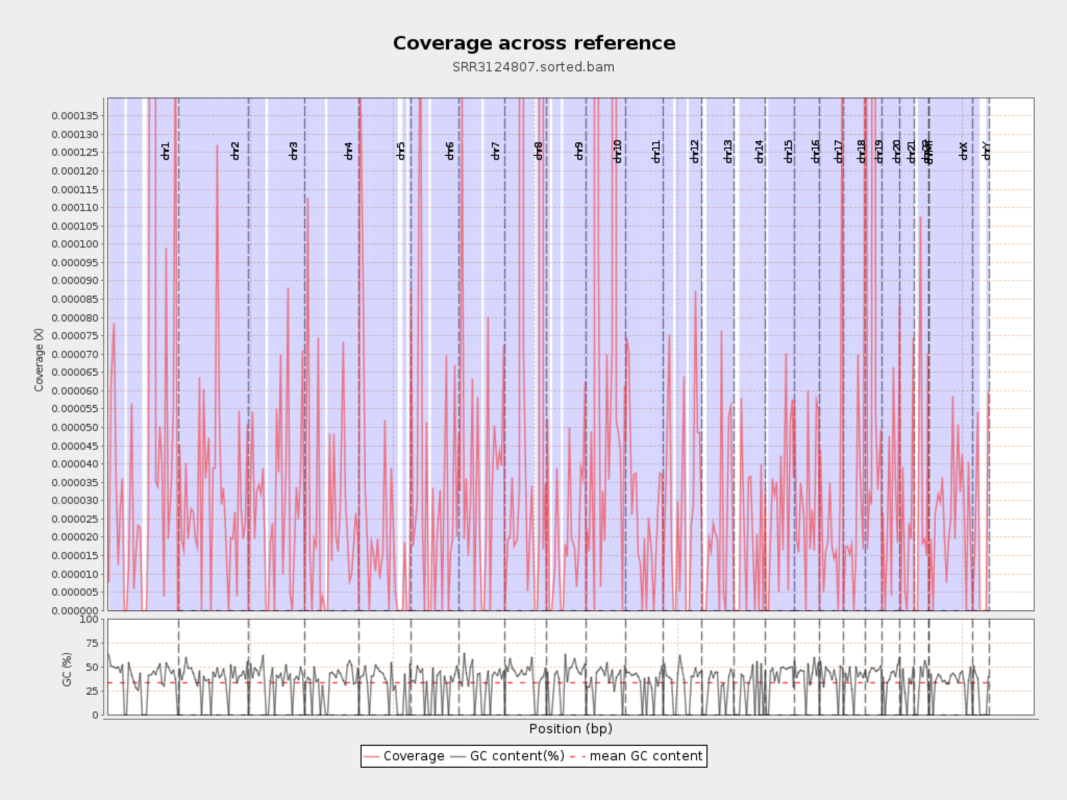
General error rate	0.72%
Mismatches	733,870
Insertions	13,491
Mapped reads with at least one insertion	1.95%
Deletions	41,097
Mapped reads with at least one deletion	5.85%
Homopolymer indels	84.4%

2.6. Chromosome stats

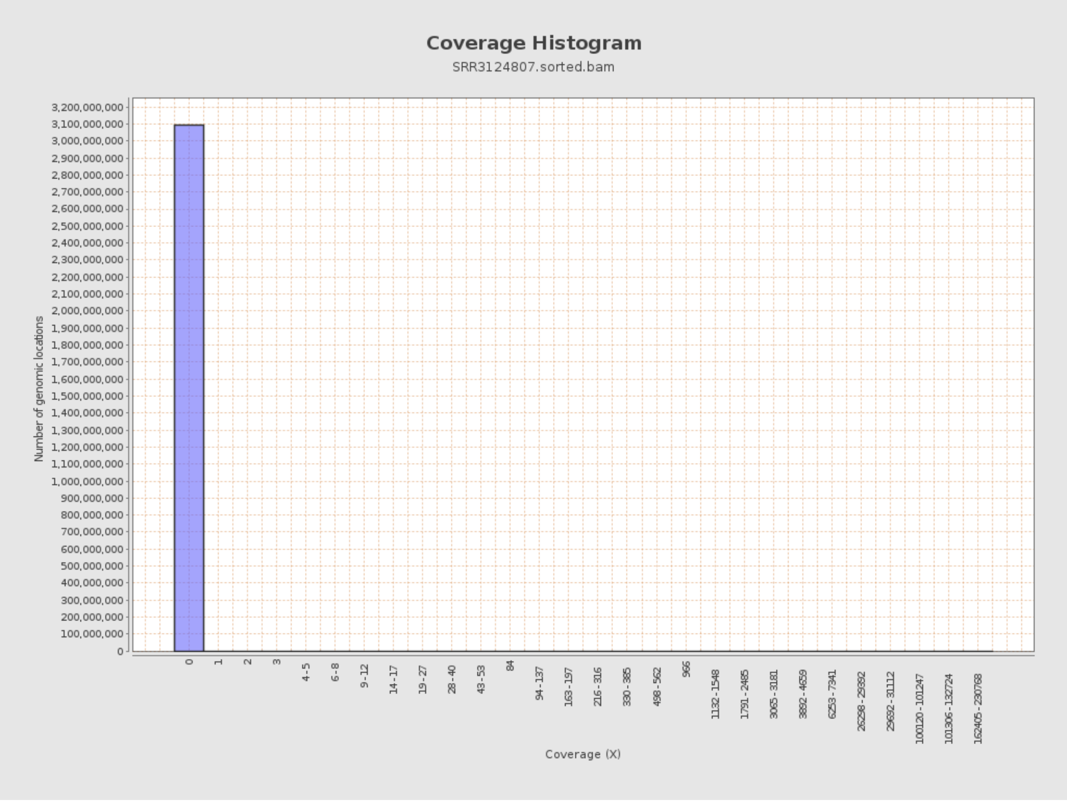
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	61758	0.0002	0.1904
chr2	243199373	7757	0	0.0062
chr3	198022430	6008	0	0.0055
chr4	191154276	4961	0	0.0054
chr5	180915260	4209	0	0.0087
chr6	171115067	5611	0	0.0097
chr7	159138663	6030	0	0.0141

chr8	146364022	93213852	0.6369	311.0293
chr9	141213431	3082	0	0.0047
chr10	135534747	9987477	0.0737	46.2594
chr11	135006516	3627	0	0.0053
chr12	133851895	4035	0	0.0061
chr13	115169878	2389	0	0.0074
chr14	107349540	1906	0	0.005
chr15	102531392	2977	0	0.0056
chr16	90354753	2827	0	0.0058
chr17	81195210	2244	0	0.0053
chr18	78077248	2061	0	0.0051
chr19	59128983	7511	0.0001	0.0512
chr20	63025520	1894	0	0.0055
chr21	48129895	1045	0	0.0047
chr22	51304566	1385	0	0.0057
chrMT	16571	0	0	0
chrX	155270560	3908	0	0.0062
chrY	59373566	1048	0	0.0042

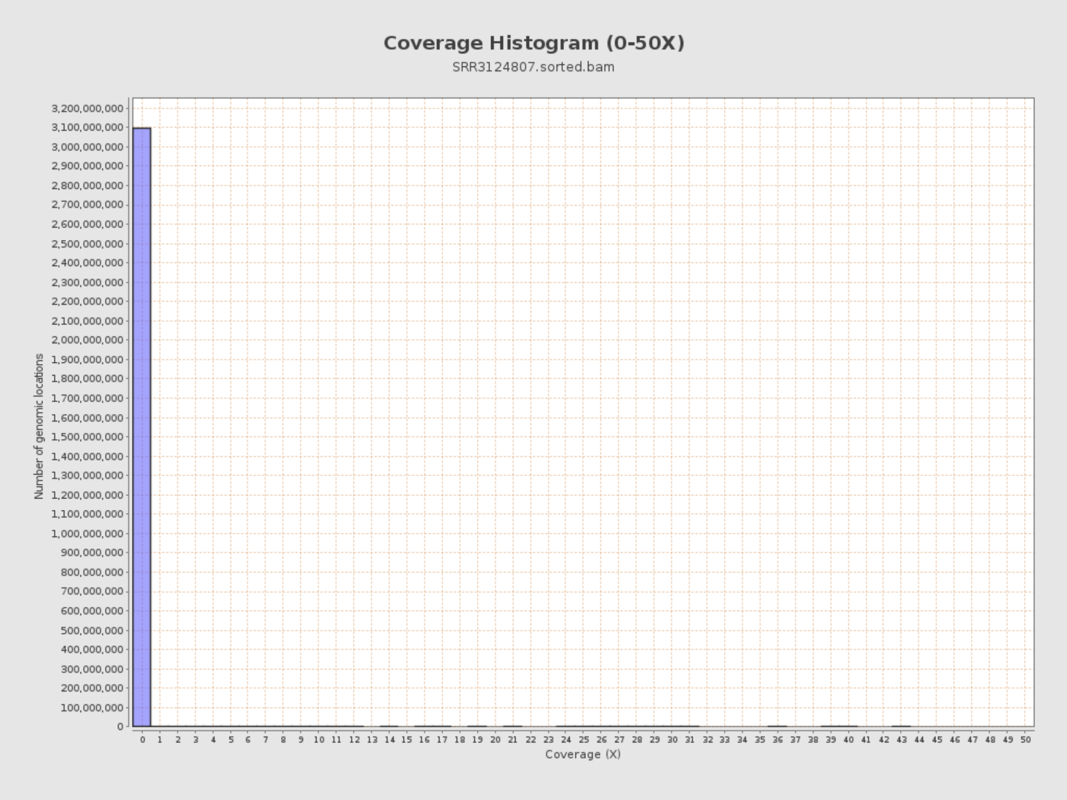
3. Results : Coverage across reference



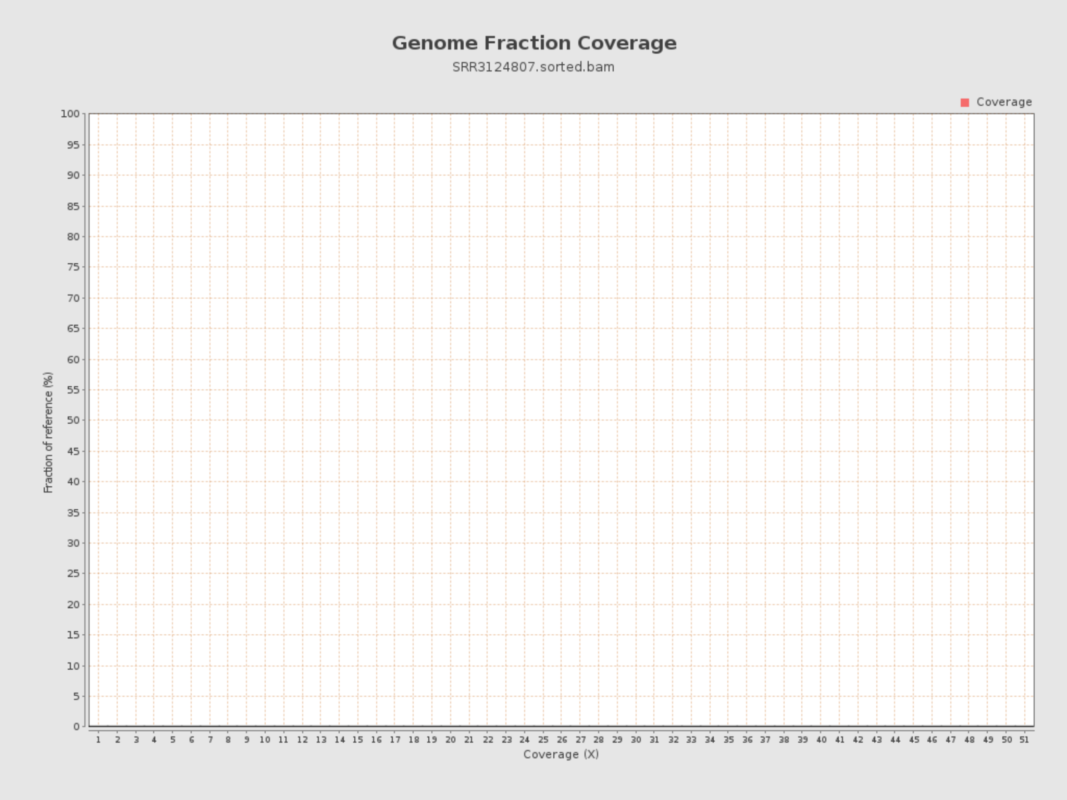
4. Results : Coverage Histogram



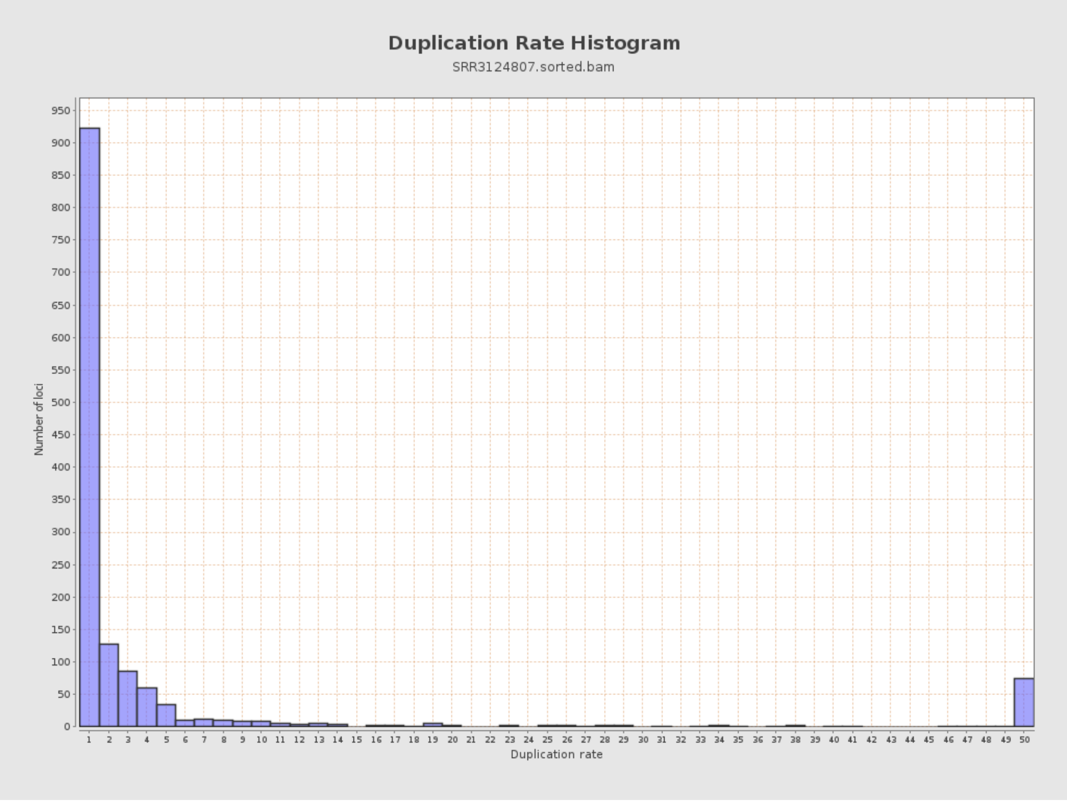
5. Results : Coverage Histogram (0-50X)



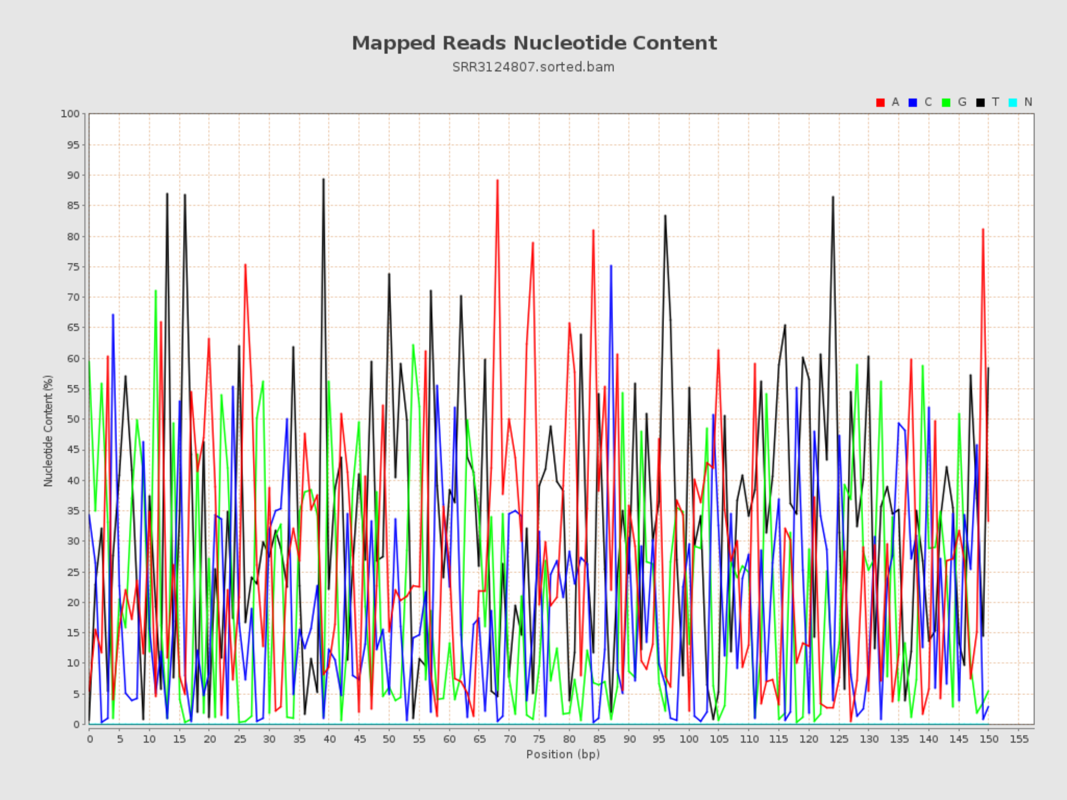
6. Results : Genome Fraction Coverage



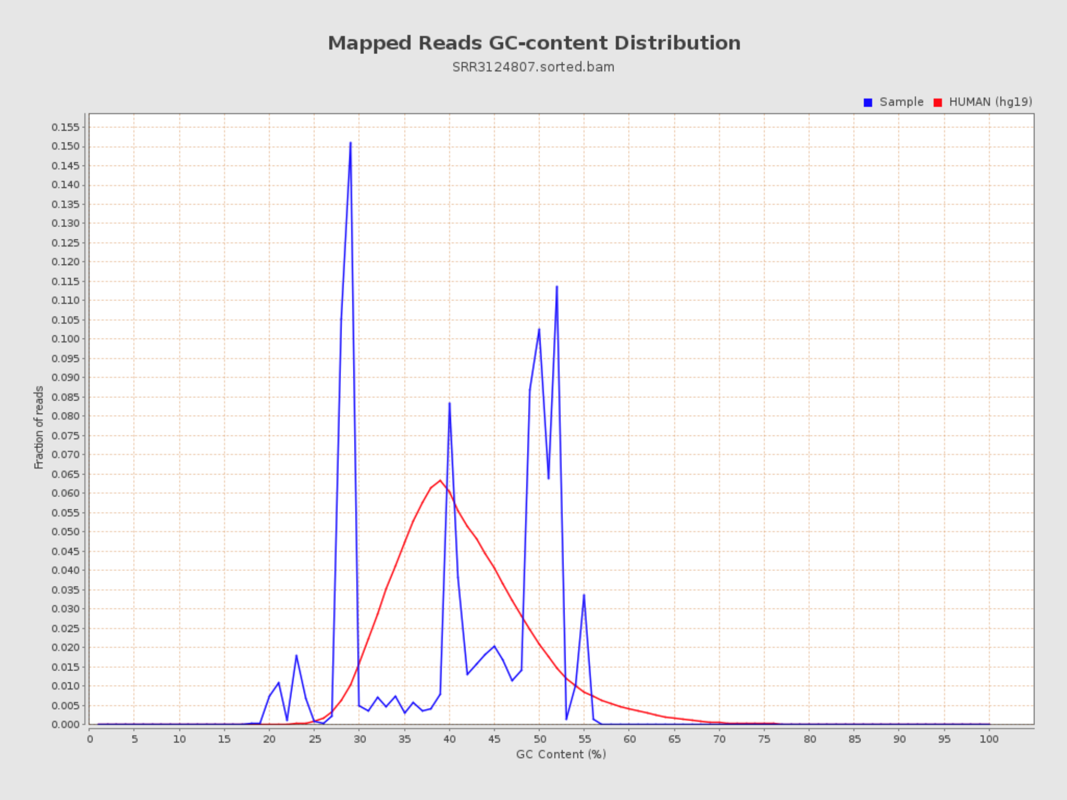
7. Results : Duplication Rate Histogram



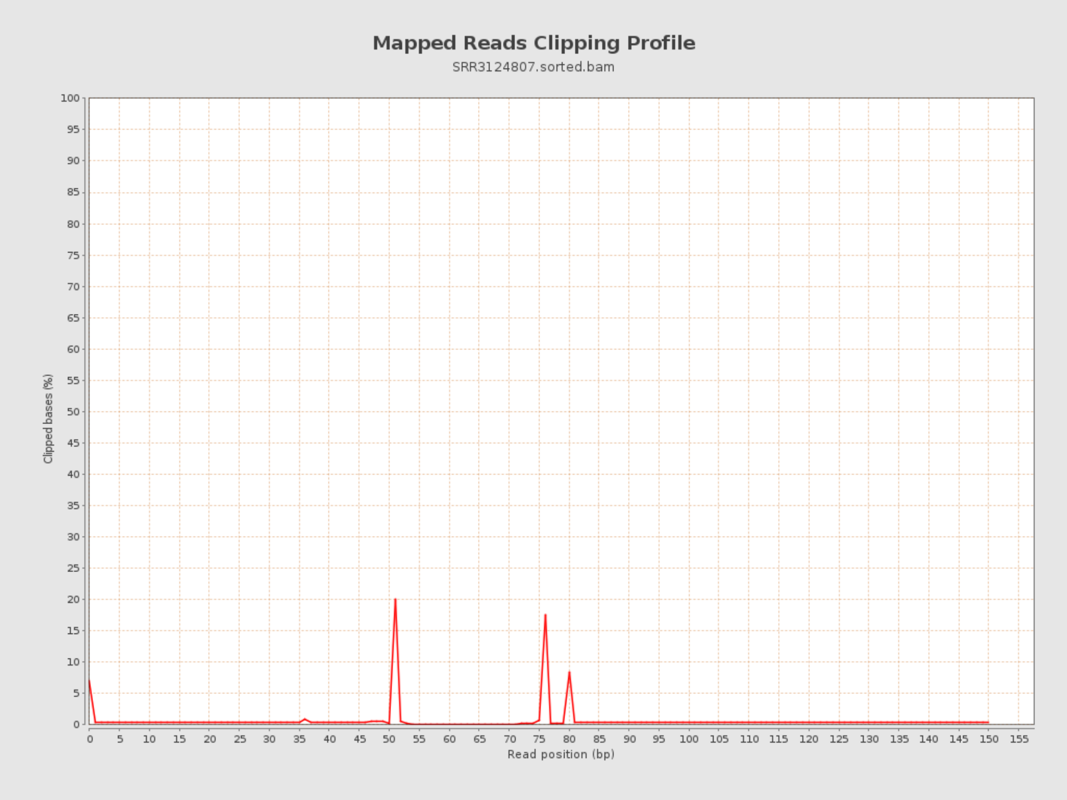
8. Results : Mapped Reads Nucleotide Content



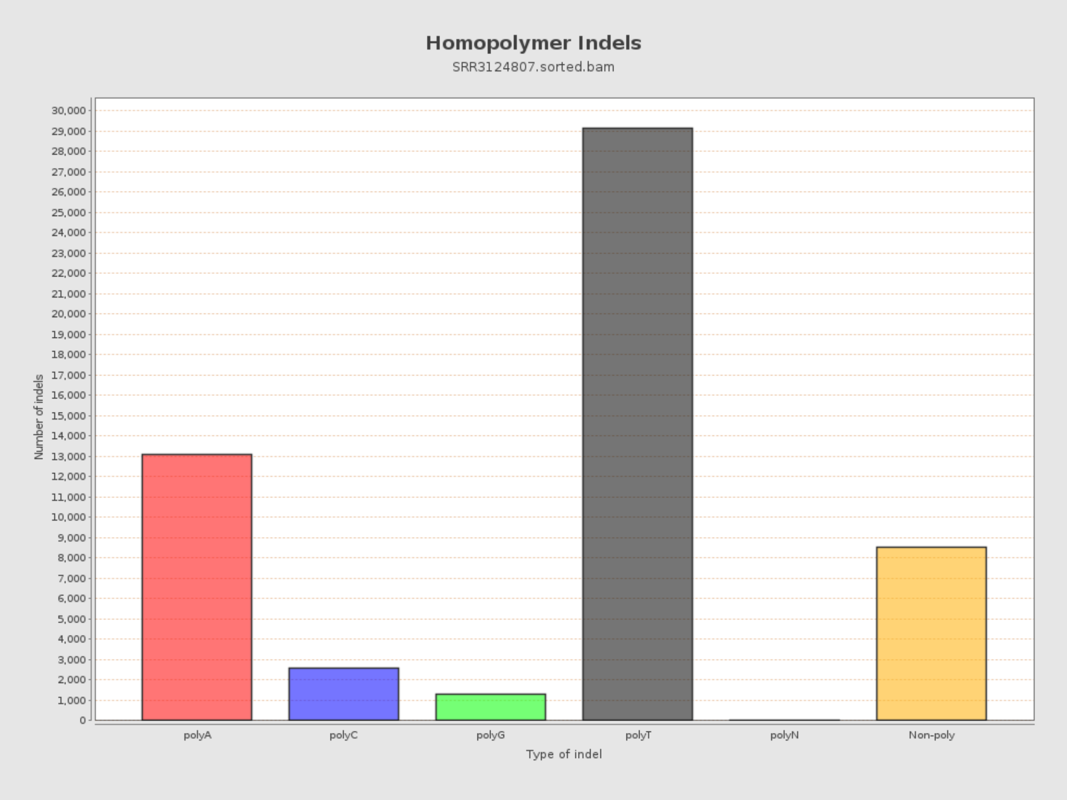
9. Results : Mapped Reads GC-content Distribution



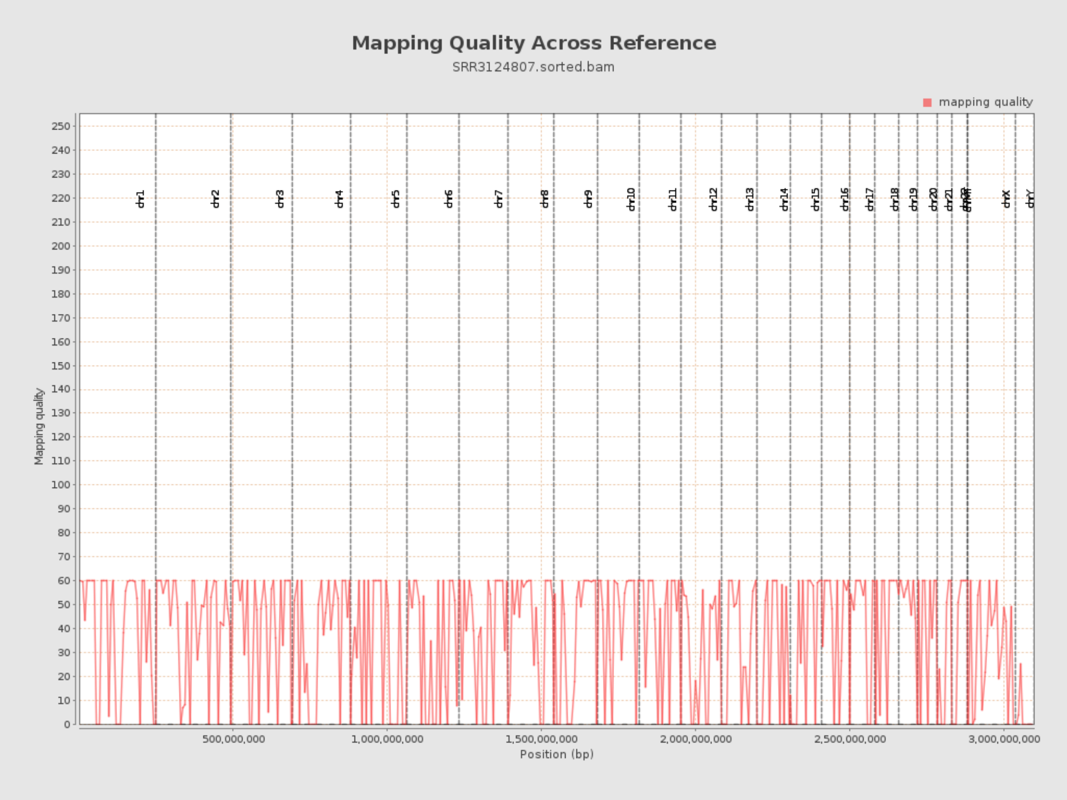
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram