Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 15:04:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124804.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_SRR3124804 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124804.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 15:04:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124804.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	179,458
Mapped reads	169,873 / 94.66%
Unmapped reads	9,585 / 5.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,738 / 3.75%
Read min/max/mean length	30 / 151 / 152.78
Duplicated reads (estimated)	71,518 / 39.85%
Duplication rate	1.54%
Clipped reads	133,373 / 74.32%

2.2. ACGT Content

Number/percentage of A's	6,719,134 / 29.51%
Number/percentage of C's	4,365,742 / 19.17%
Number/percentage of T's	6,226,565 / 27.35%
Number/percentage of G's	5,458,900 / 23.97%
Number/percentage of N's	0 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0074

Standard Deviation	7.9382

2.4. Mapping Quality

Mean Mapping Quality	50.83

2.5. Mismatches and indels

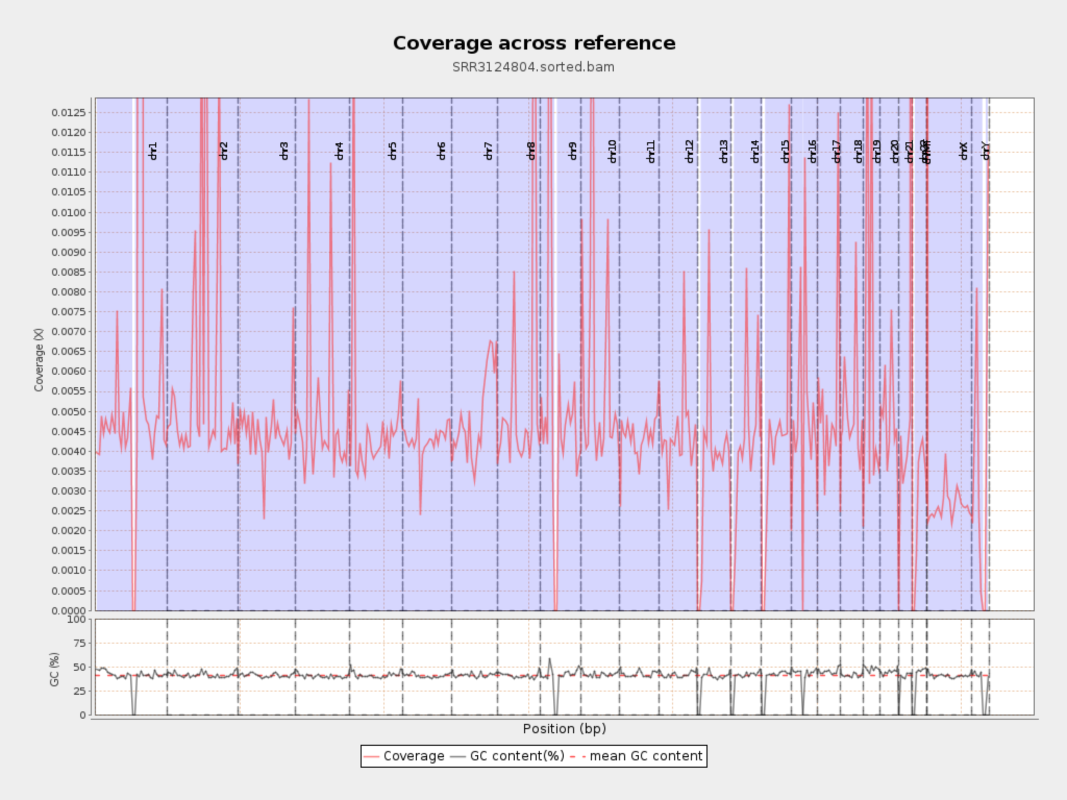
General error rate	1.36%
Mismatches	297,188
Insertions	4,848
Mapped reads with at least one insertion	2.68%
Deletions	7,215
Mapped reads with at least one deletion	4.05%
Homopolymer indels	38.47%

2.6. Chromosome stats

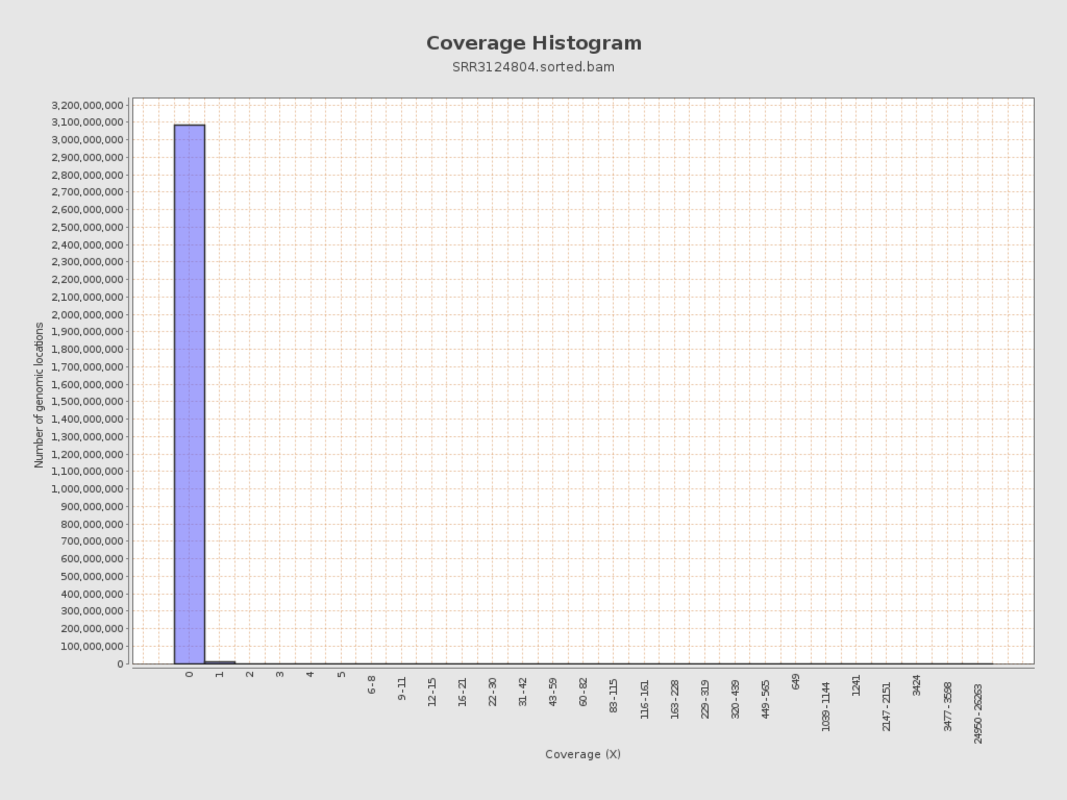
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8854491	0.0355	27.8495
chr2	243199373	1473621	0.0061	0.5751
chr3	198022430	893038	0.0045	0.1346
chr4	191154276	936523	0.0049	0.3137
chr5	180915260	853059	0.0047	0.3703
chr6	171115067	731592	0.0043	0.0694
chr7	159138663	779985	0.0049	0.0796

chr8	146364022	819262	0.0056	0.5715
chr9	141213431	715134	0.0051	0.7215
chr10	135534747	864659	0.0064	0.3644
chr11	135006516	586584	0.0043	0.0702
chr12	133851895	599165	0.0045	0.2176
chr13	115169878	430111	0.0037	0.2355
chr14	107349540	431732	0.004	0.2962
chr15	102531392	434863	0.0042	0.4488
chr16	90354753	444934	0.0049	0.1223
chr17	81195210	421309	0.0052	0.4057
chr18	78077248	396105	0.0051	0.2984
chr19	59128983	414243	0.007	0.9509
chr20	63025520	311397	0.0049	0.1886
chr21	48129895	553925	0.0115	5.3285
chr22	51304566	136836	0.0027	0.0597
chrMT	16571	67206	4.0556	2.8878
chrX	155270560	411783	0.0027	0.0542
chrY	59373566	224214	0.0038	0.1411

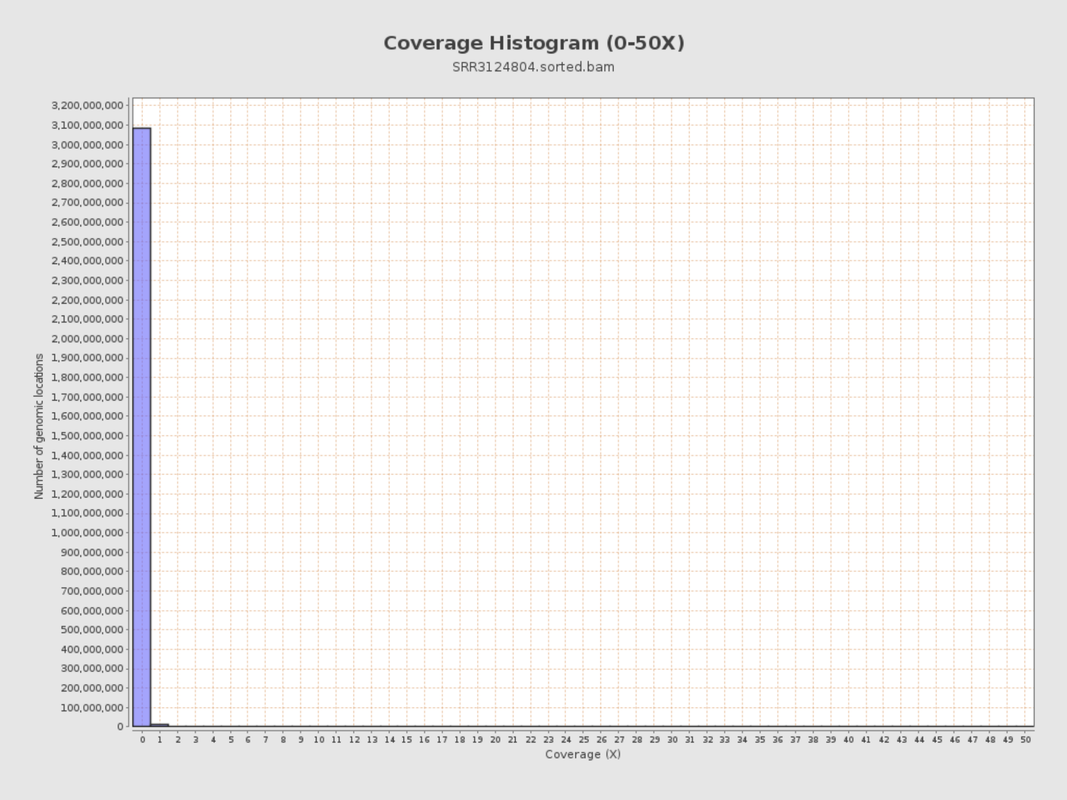
3. Results : Coverage across reference



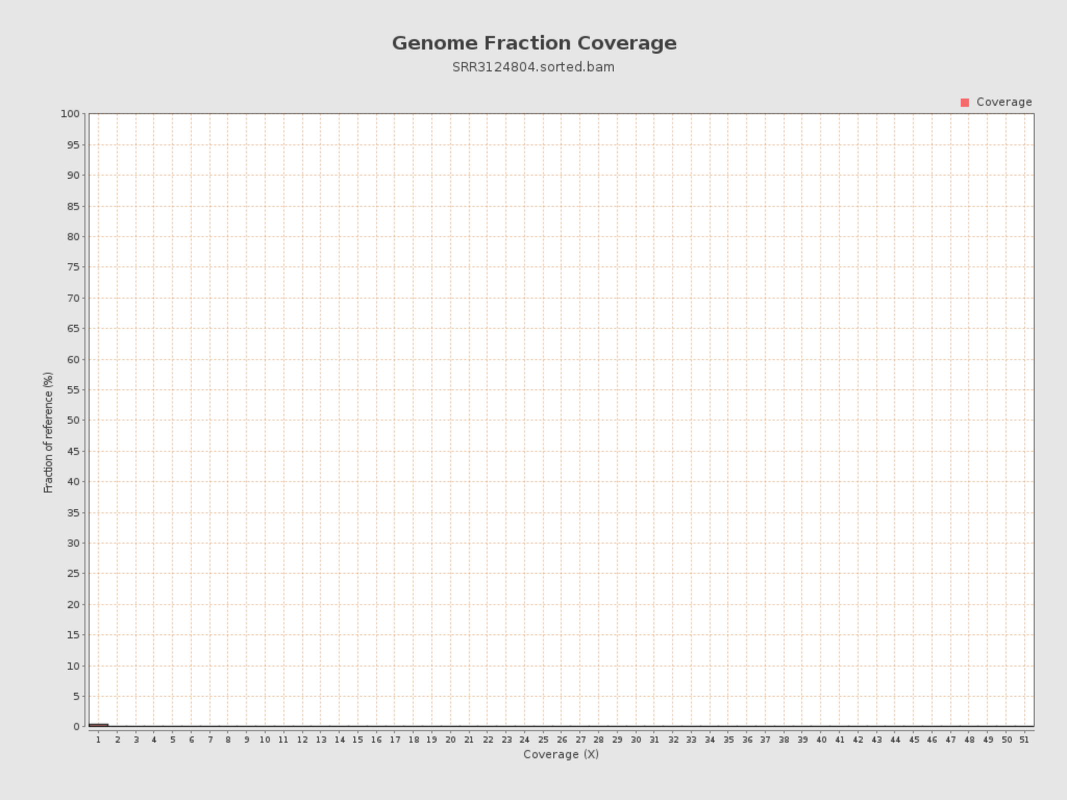
4. Results : Coverage Histogram



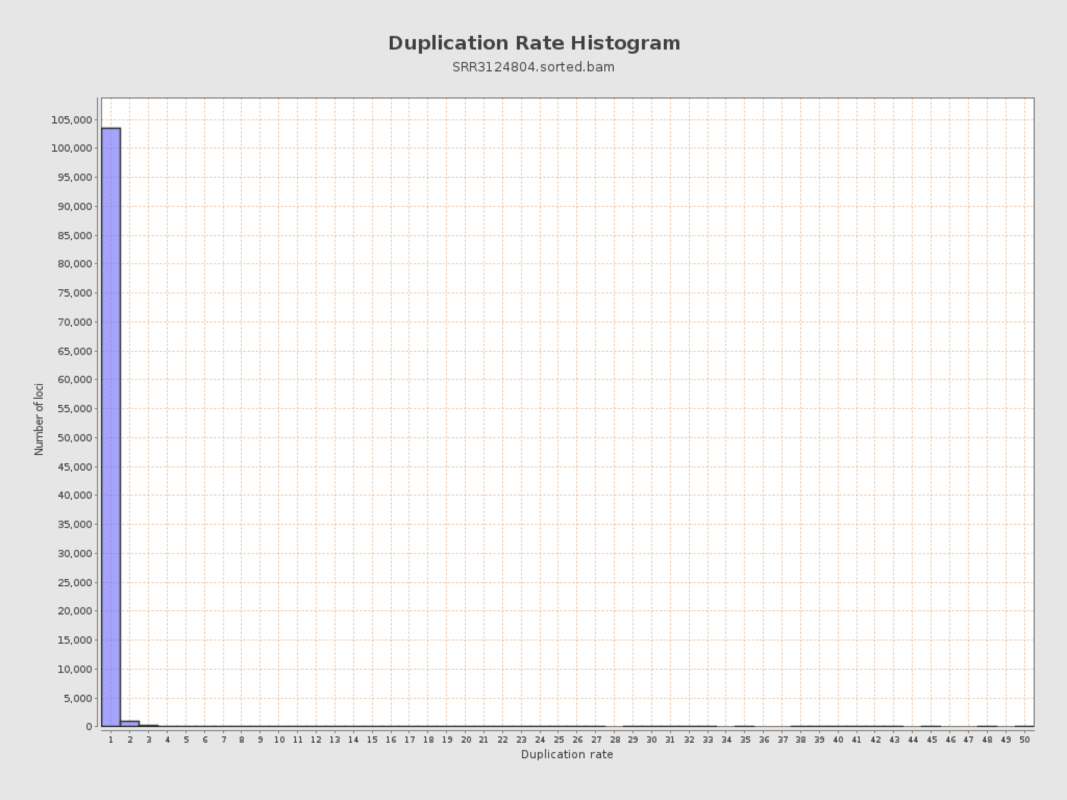
5. Results : Coverage Histogram (0-50X)



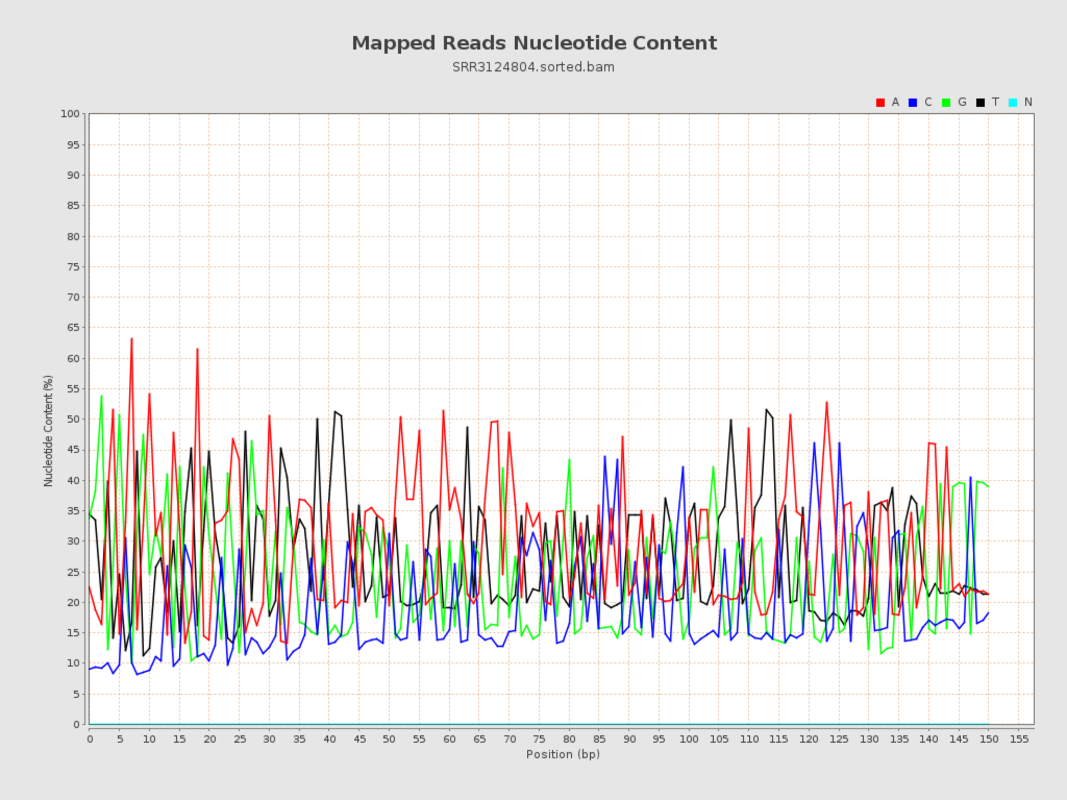
6. Results : Genome Fraction Coverage



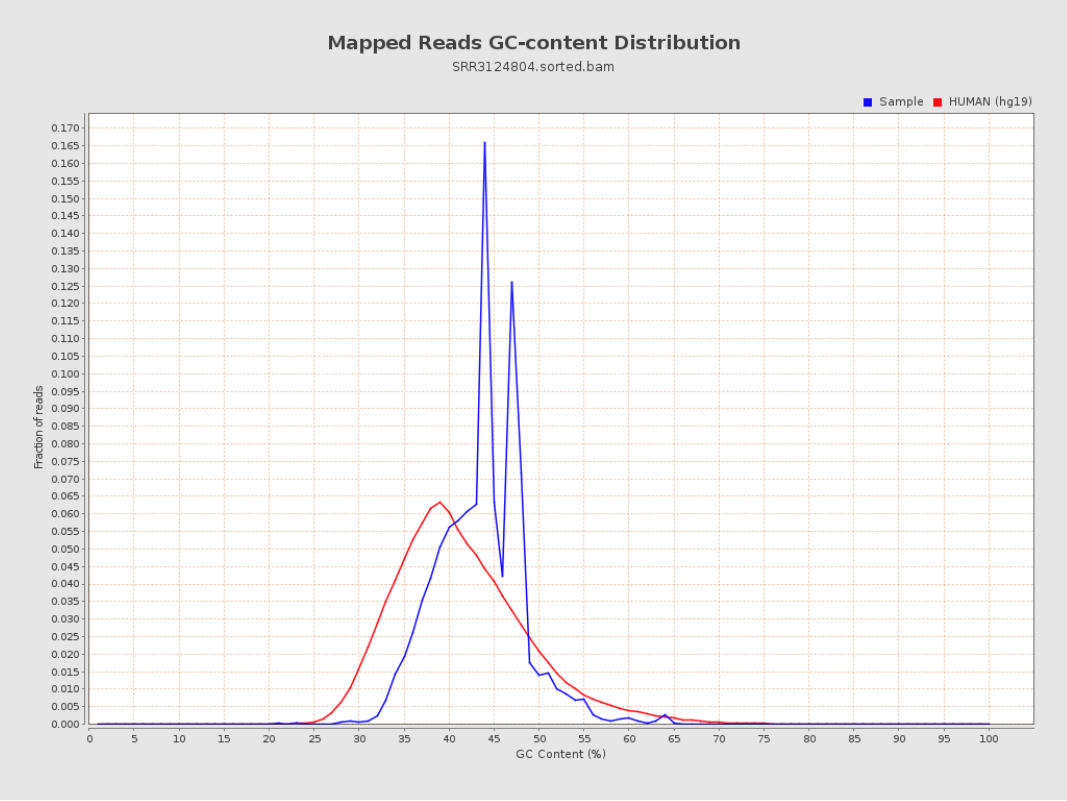
7. Results : Duplication Rate Histogram



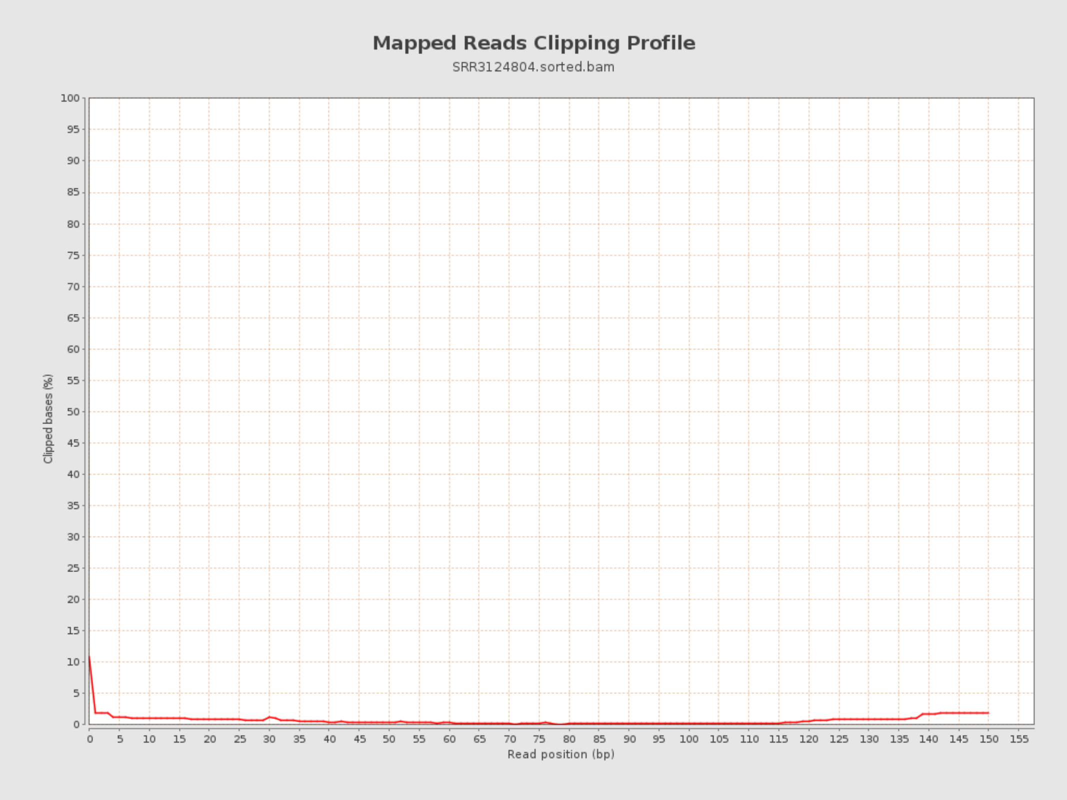
8. Results : Mapped Reads Nucleotide Content



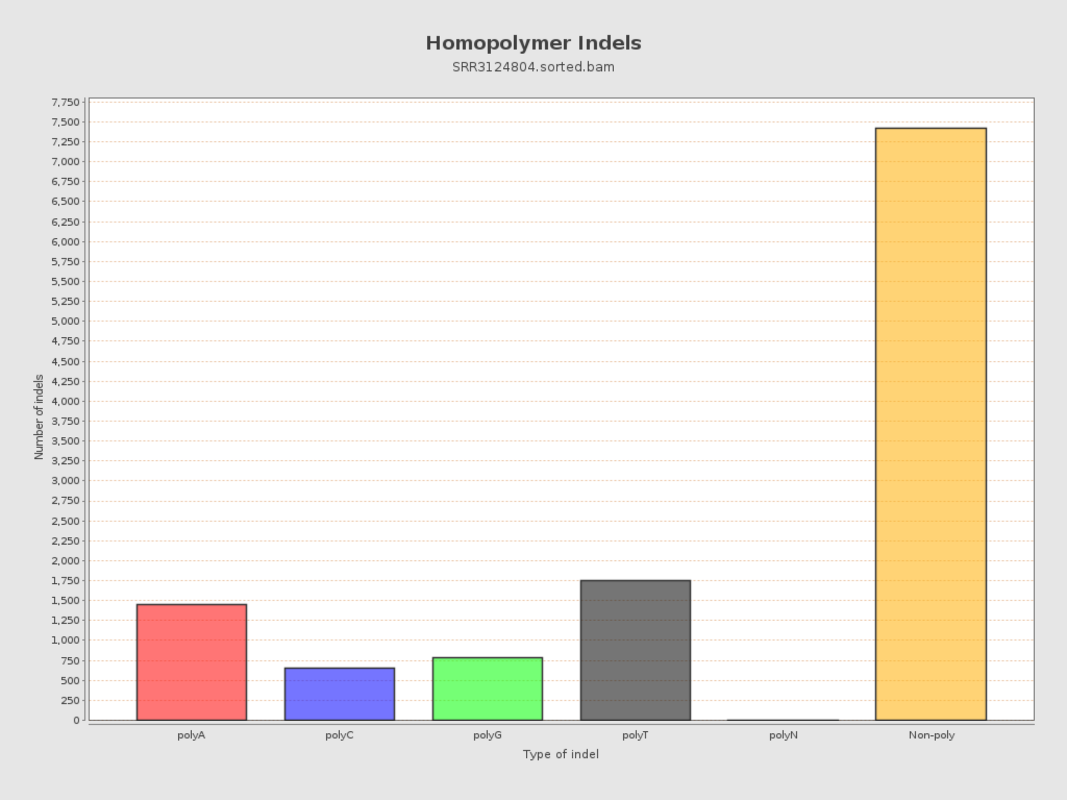
9. Results : Mapped Reads GC-content Distribution



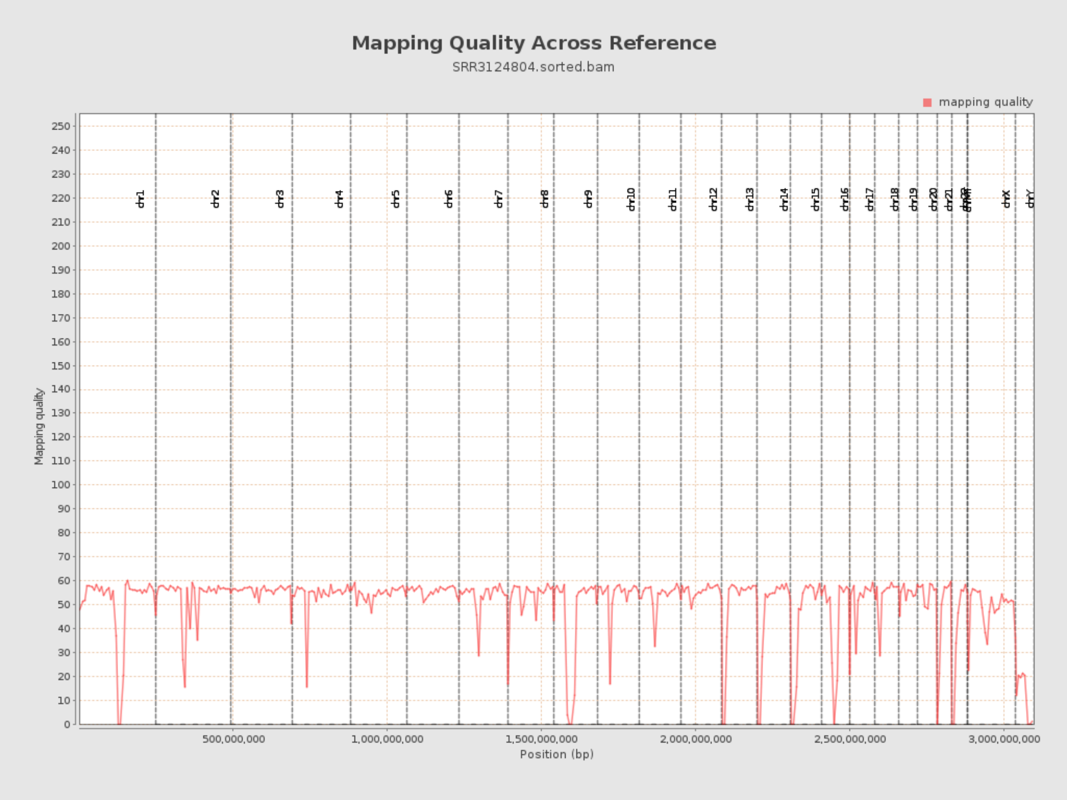
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram