Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:49:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524416.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_SRR10524416 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524416.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:49:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524416.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,401,525
Mapped reads	1,297,324 / 92.57%
Unmapped reads	104,201 / 7.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,261 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	44,361 / 3.17%
Duplication rate	2.5%
Clipped reads	1,299,056 / 92.69%

2.2. ACGT Content

Number/percentage of A's	20,016,355 / 26.15%
Number/percentage of C's	13,706,312 / 17.91%
Number/percentage of T's	23,850,714 / 31.16%
Number/percentage of G's	18,949,891 / 24.76%
Number/percentage of N's	10,223 / 0.01%
GC Percentage	42.67%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.2586

2.4. Mapping Quality

Mean Mapping Quality	46.2

2.5. Mismatches and indels

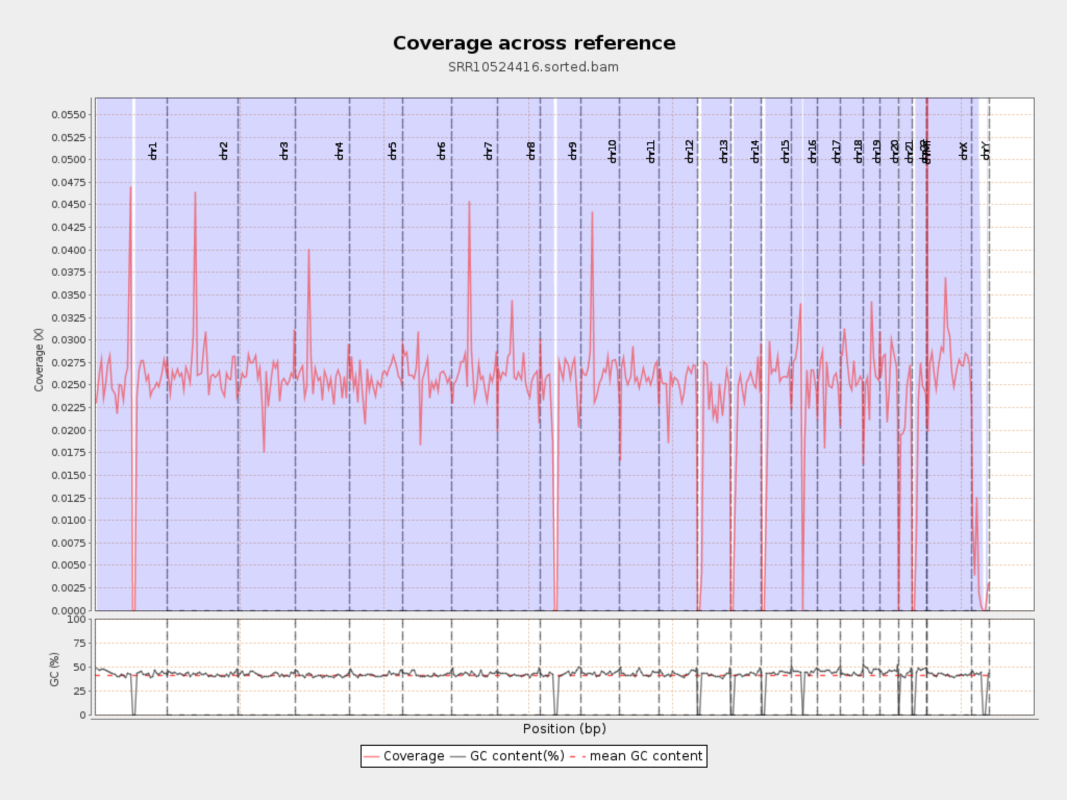
General error rate	0.5%
Mismatches	368,690
Insertions	5,751
Mapped reads with at least one insertion	0.44%
Deletions	13,920
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.46%

2.6. Chromosome stats

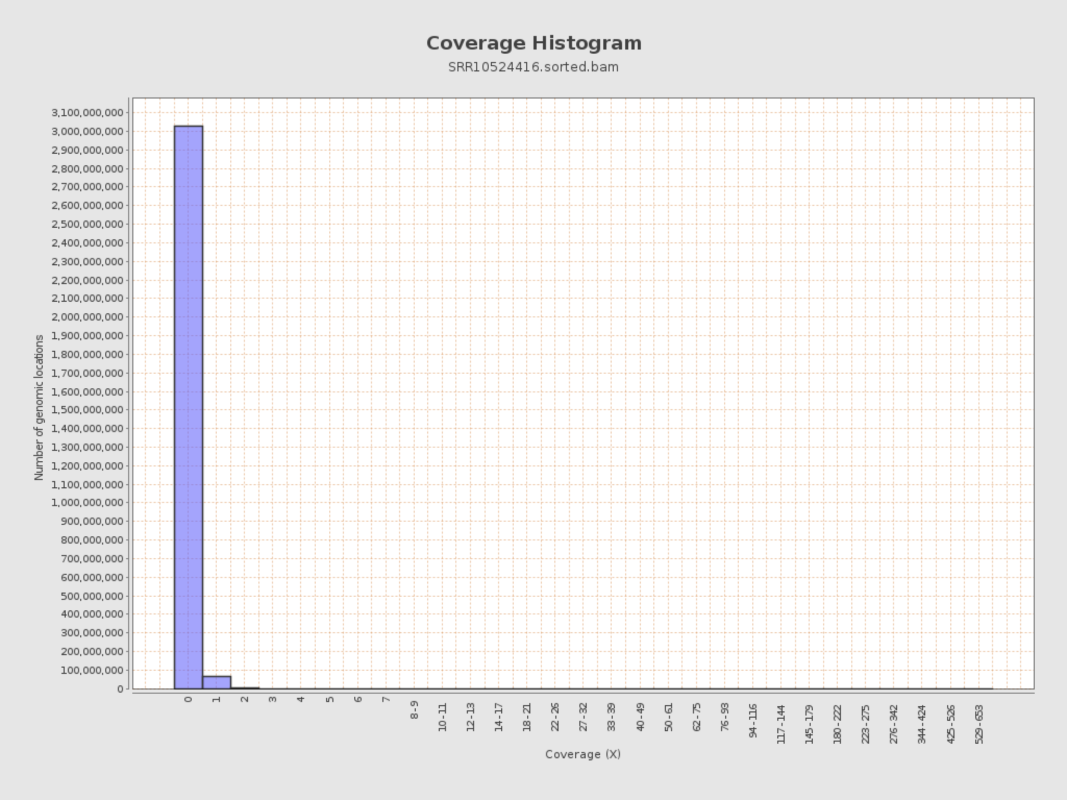
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6129859	0.0246	0.5164
chr2	243199373	6551472	0.0269	0.2844
chr3	198022430	5093039	0.0257	0.1716
chr4	191154276	5002536	0.0262	0.1943
chr5	180915260	4648587	0.0257	0.1725
chr6	171115067	4449086	0.026	0.1886
chr7	159138663	4283974	0.0269	0.3552

chr8	146364022	3856741	0.0264	0.229
chr9	141213431	3204600	0.0227	0.2126
chr10	135534747	3697323	0.0273	0.235
chr11	135006516	3520245	0.0261	0.2341
chr12	133851895	3375888	0.0252	0.1735
chr13	115169878	2328949	0.0202	0.1529
chr14	107349540	2270240	0.0211	0.1637
chr15	102531392	2238820	0.0218	0.1578
chr16	90354753	2168731	0.024	0.1758
chr17	81195210	2042571	0.0252	0.1805
chr18	78077248	2085319	0.0267	0.3854
chr19	59128983	1550111	0.0262	0.3427
chr20	63025520	1664112	0.0264	0.1784
chr21	48129895	974757	0.0203	0.1694
chr22	51304566	879565	0.0171	0.1402
chrMT	16571	2197	0.1326	0.4508
chrX	155270560	4316091	0.0278	0.1985
chrY	59373566	220913	0.0037	0.1051

3. Results : Coverage across reference



4. Results : Coverage Histogram



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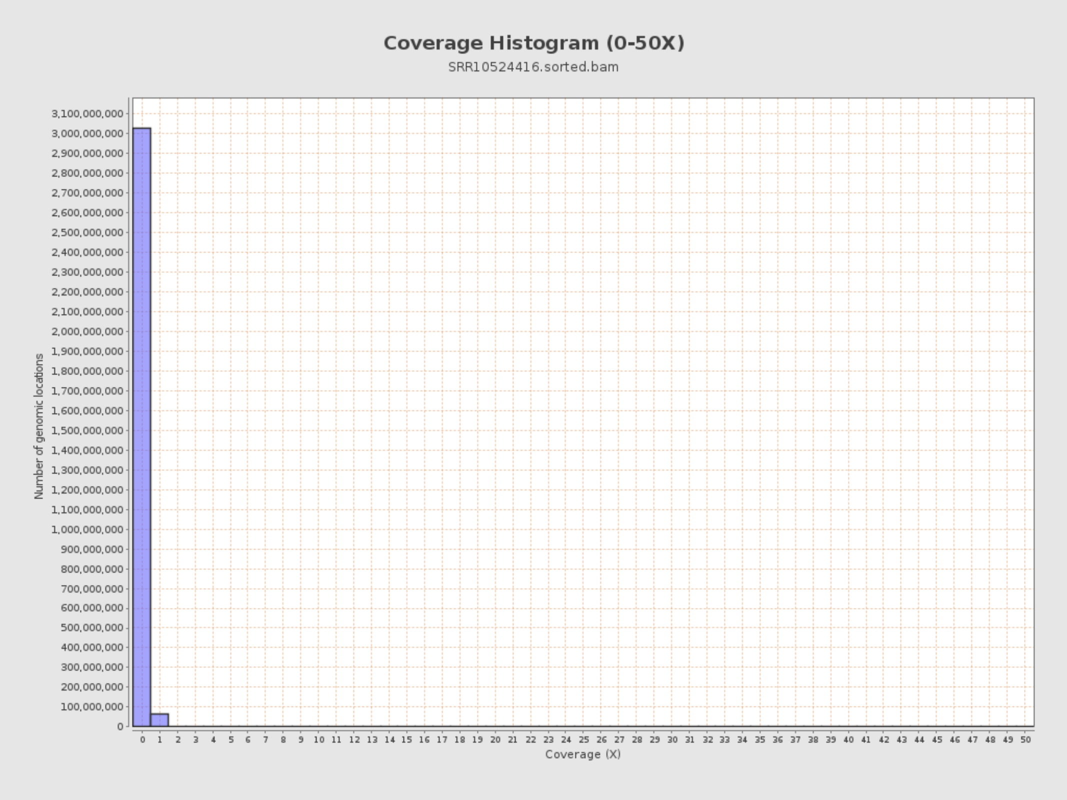
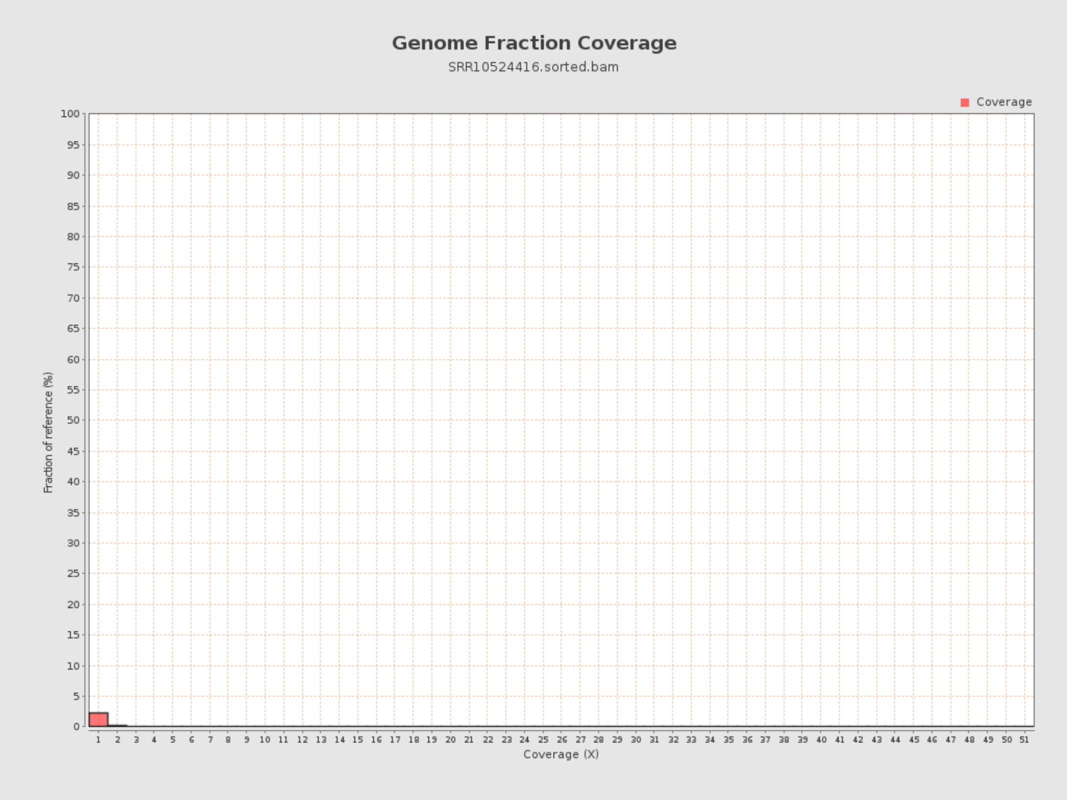
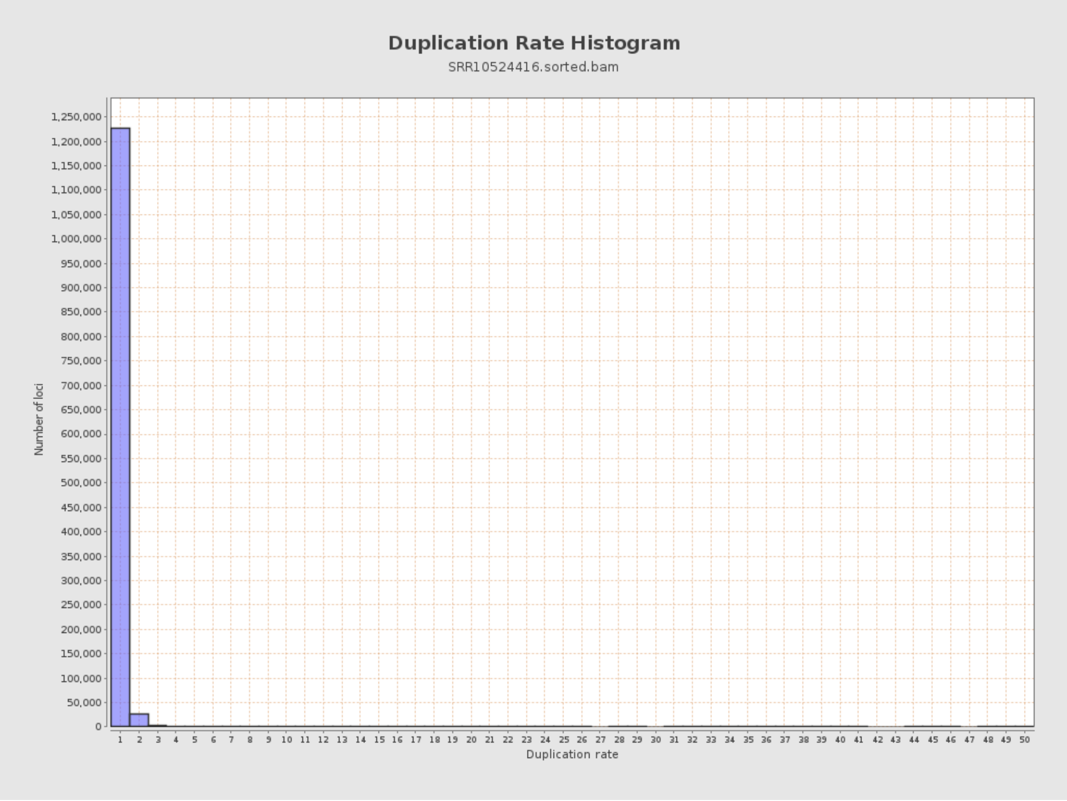
5. Results : Coverage Histogram (0-50X)



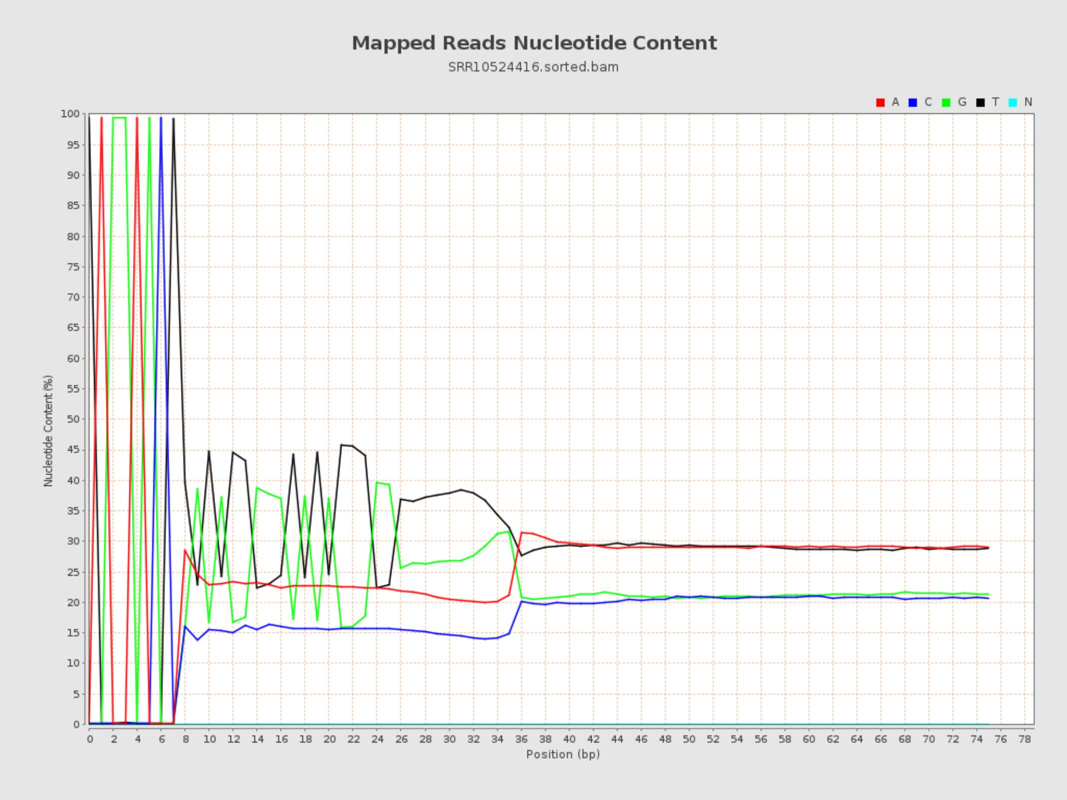
6. Results : Genome Fraction Coverage



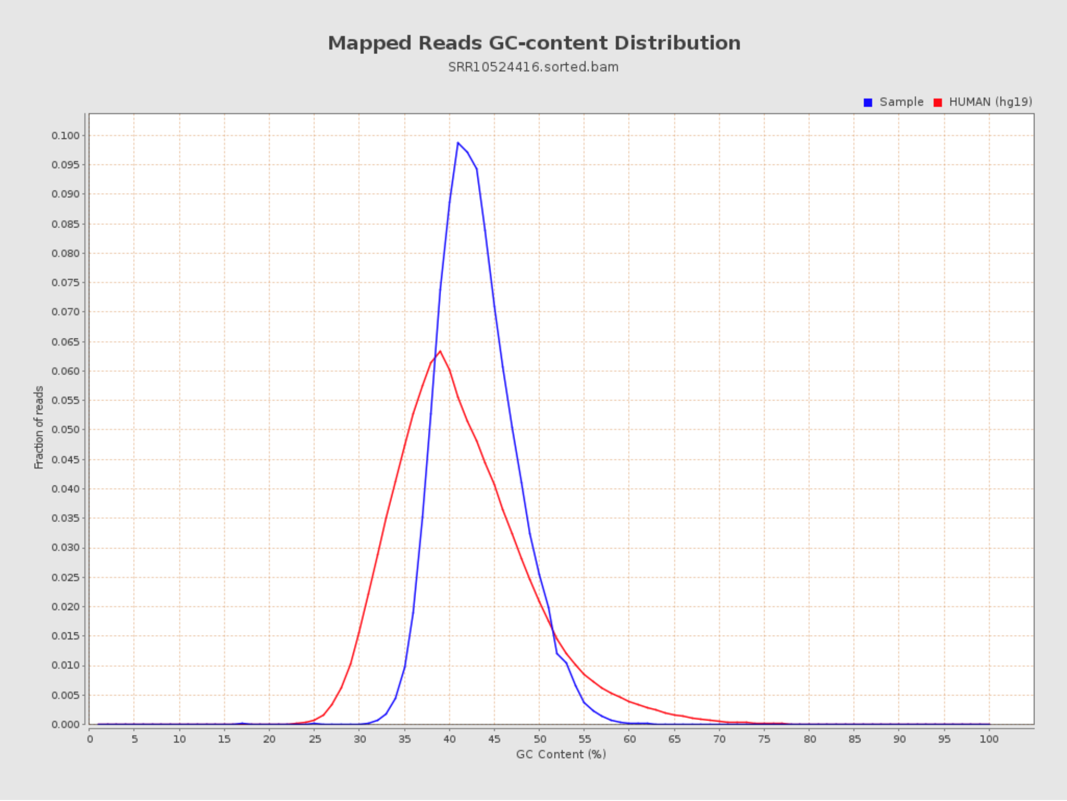
7. Results : Duplication Rate Histogram



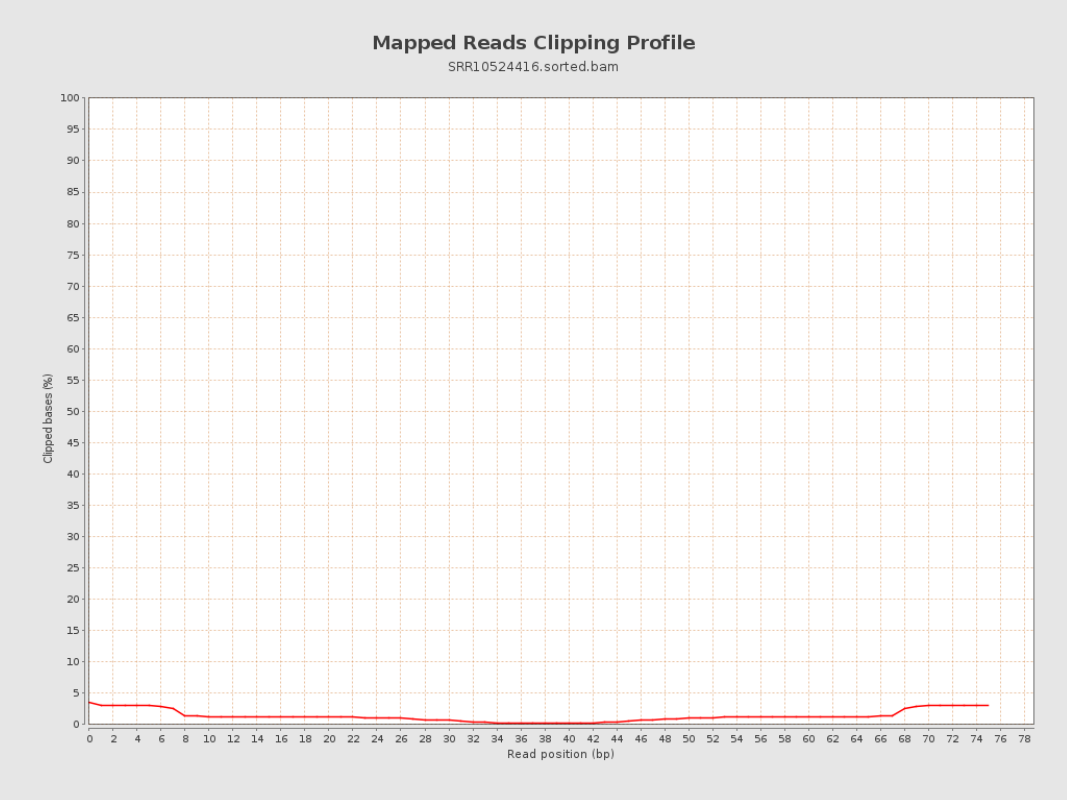
8. Results : Mapped Reads Nucleotide Content



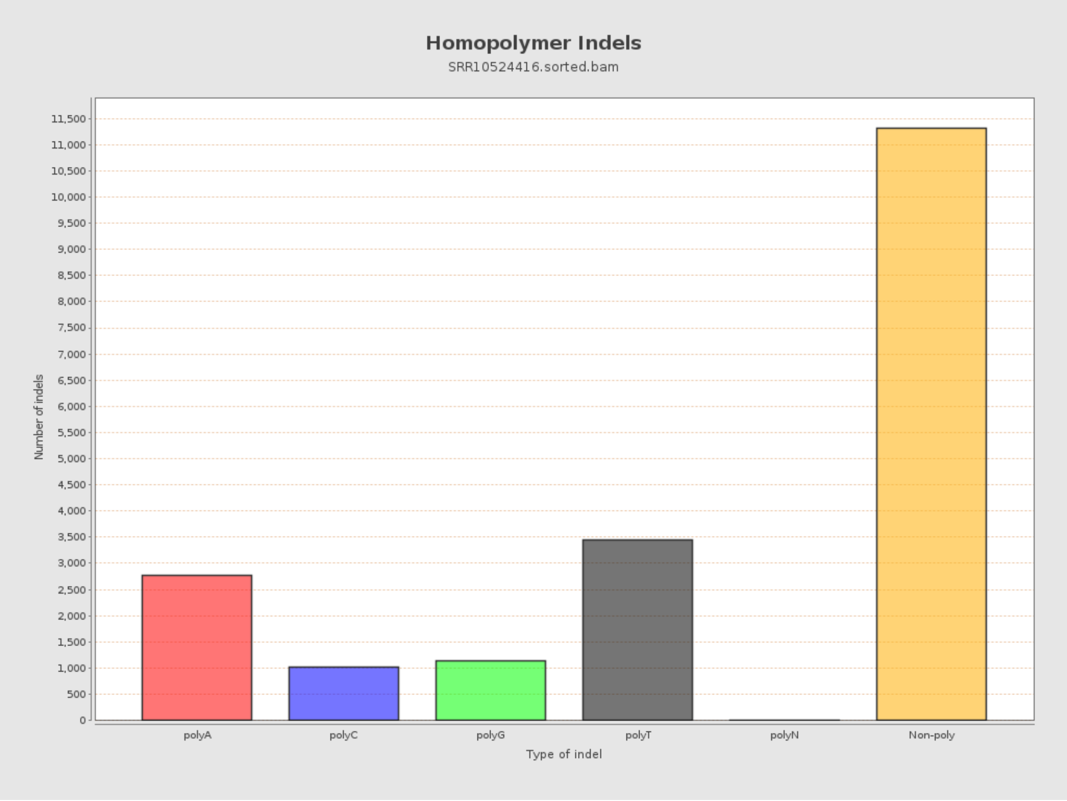
9. Results : Mapped Reads GC-content Distribution



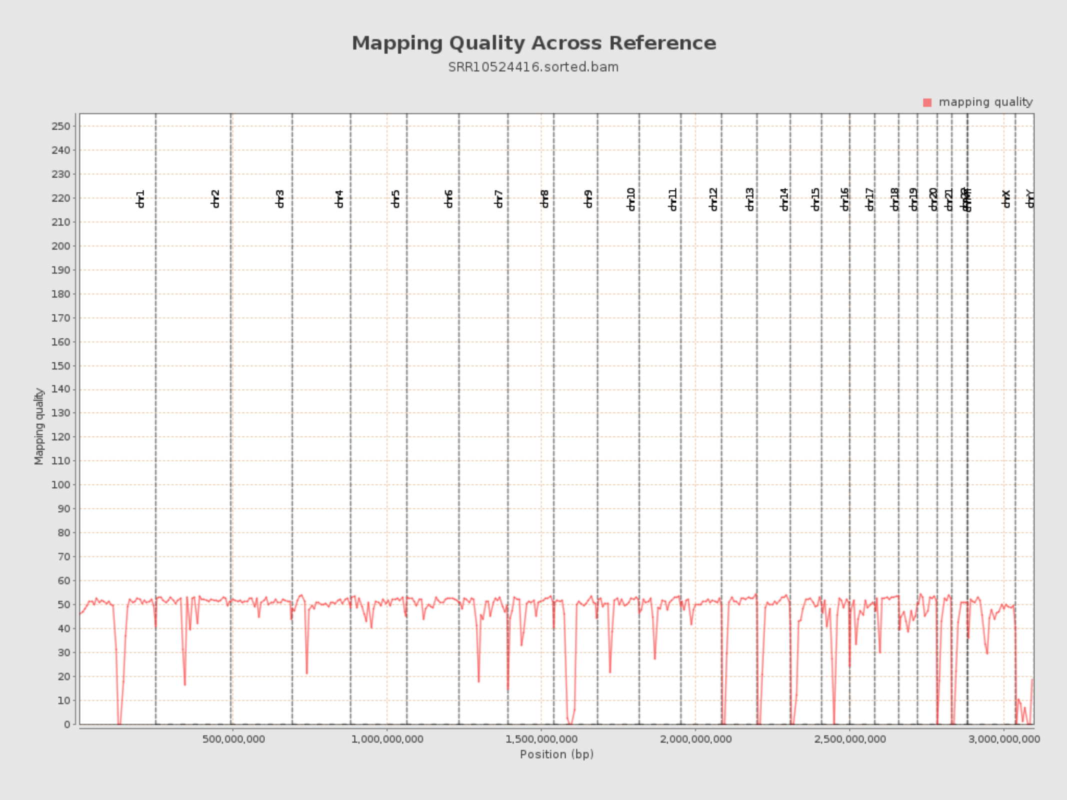
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram