Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:11:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524656.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_SRR10524656 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524656.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:11:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524656.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,270,729
Mapped reads	3,025,529 / 92.5%
Unmapped reads	245,200 / 7.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,350 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	244,193 / 7.47%
Duplication rate	6.07%
Clipped reads	3,029,921 / 92.64%

2.2. ACGT Content

Number/percentage of A's	43,541,861 / 24.67%
Number/percentage of C's	36,034,993 / 20.42%
Number/percentage of T's	53,814,931 / 30.5%
Number/percentage of G's	43,071,113 / 24.41%
Number/percentage of N's	1,514 / 0%
GC Percentage	44.83%

2.3. Coverage

Mean	0.057

Standard Deviation	0.4827

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

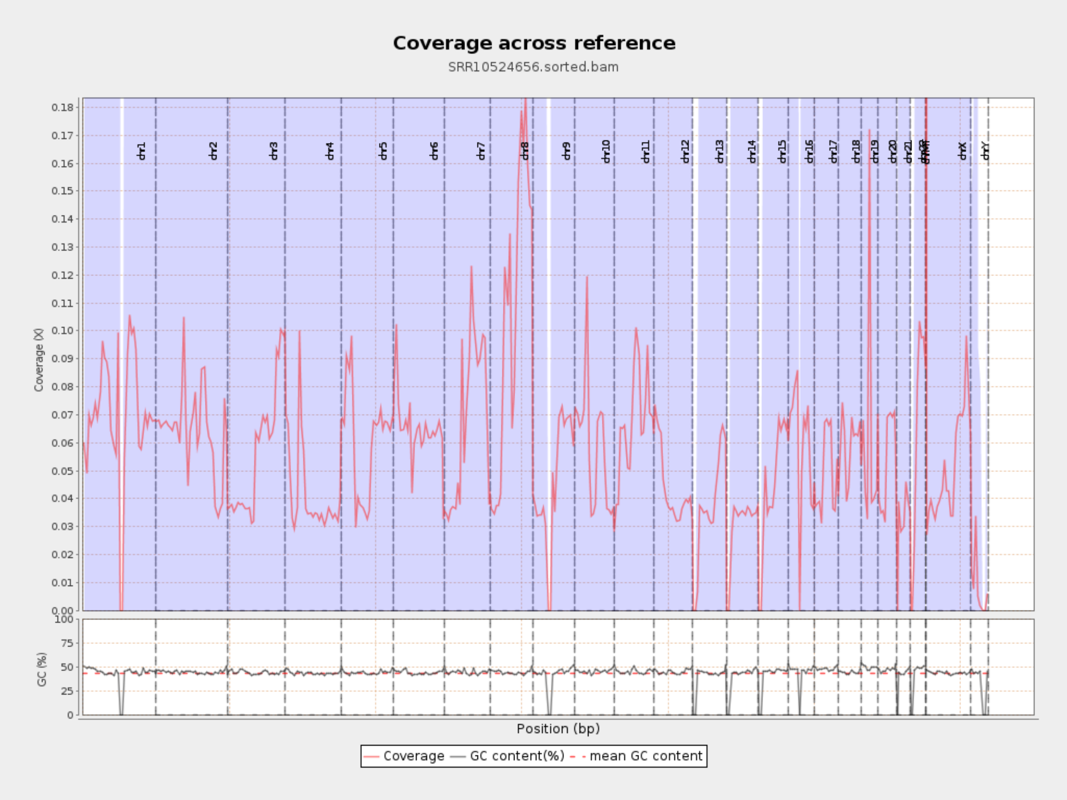
General error rate	0.52%
Mismatches	897,437
Insertions	12,042
Mapped reads with at least one insertion	0.4%
Deletions	34,269
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.91%

2.6. Chromosome stats

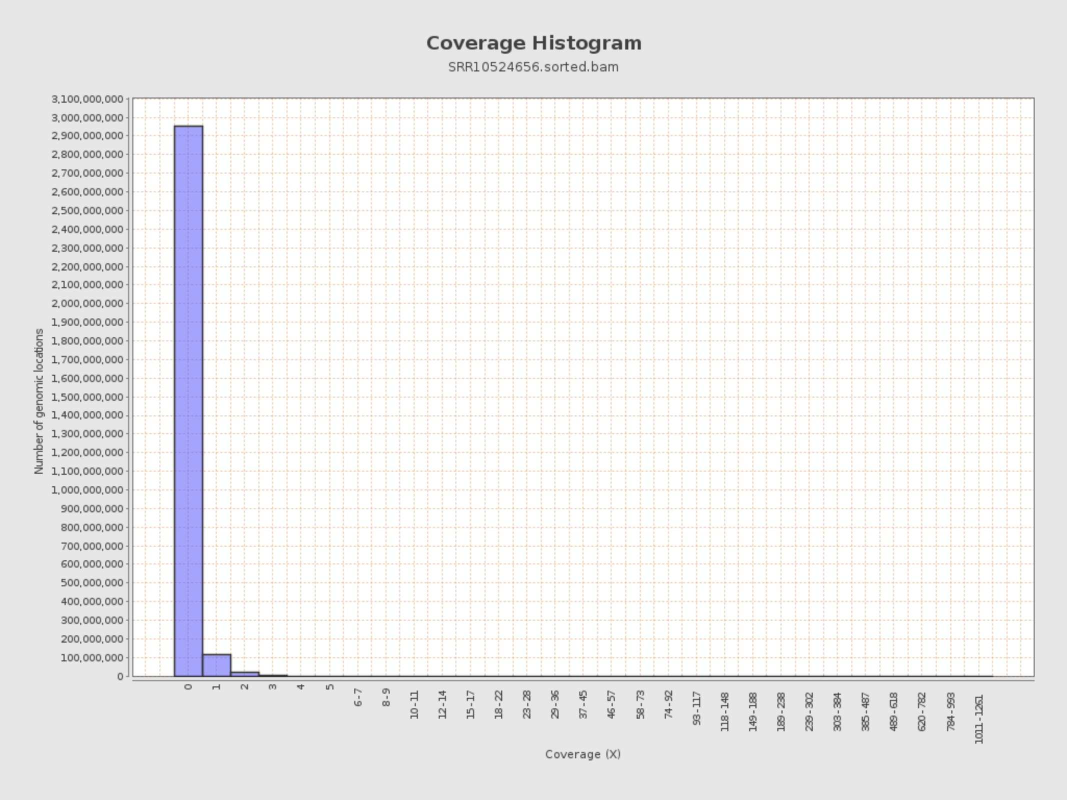
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17464089	0.0701	0.9371
chr2	243199373	15659250	0.0644	0.5949
chr3	198022430	11152143	0.0563	0.287
chr4	191154276	8046967	0.0421	0.3357
chr5	180915260	10949493	0.0605	0.2961
chr6	171115067	11215119	0.0655	0.342
chr7	159138663	10787319	0.0678	0.6312

chr8	146364022	15521910	0.1061	0.6222
chr9	141213431	6454942	0.0457	0.3763
chr10	135534747	7816647	0.0577	0.5309
chr11	135006516	9096579	0.0674	0.4023
chr12	133851895	5924213	0.0443	0.27
chr13	115169878	4247657	0.0369	0.234
chr14	107349540	3258787	0.0304	0.2235
chr15	102531392	4490671	0.0438	0.2545
chr16	90354753	5265439	0.0583	0.3208
chr17	81195210	3991666	0.0492	0.2845
chr18	78077248	4625300	0.0592	0.6706
chr19	59128983	3676735	0.0622	0.6536
chr20	63025520	3378063	0.0536	0.2943
chr21	48129895	1588147	0.033	0.2874
chr22	51304566	3294755	0.0642	0.3111
chrMT	16571	175963	10.6187	6.6272
chrX	155270560	7942153	0.0512	0.3137
chrY	59373566	497956	0.0084	0.2908

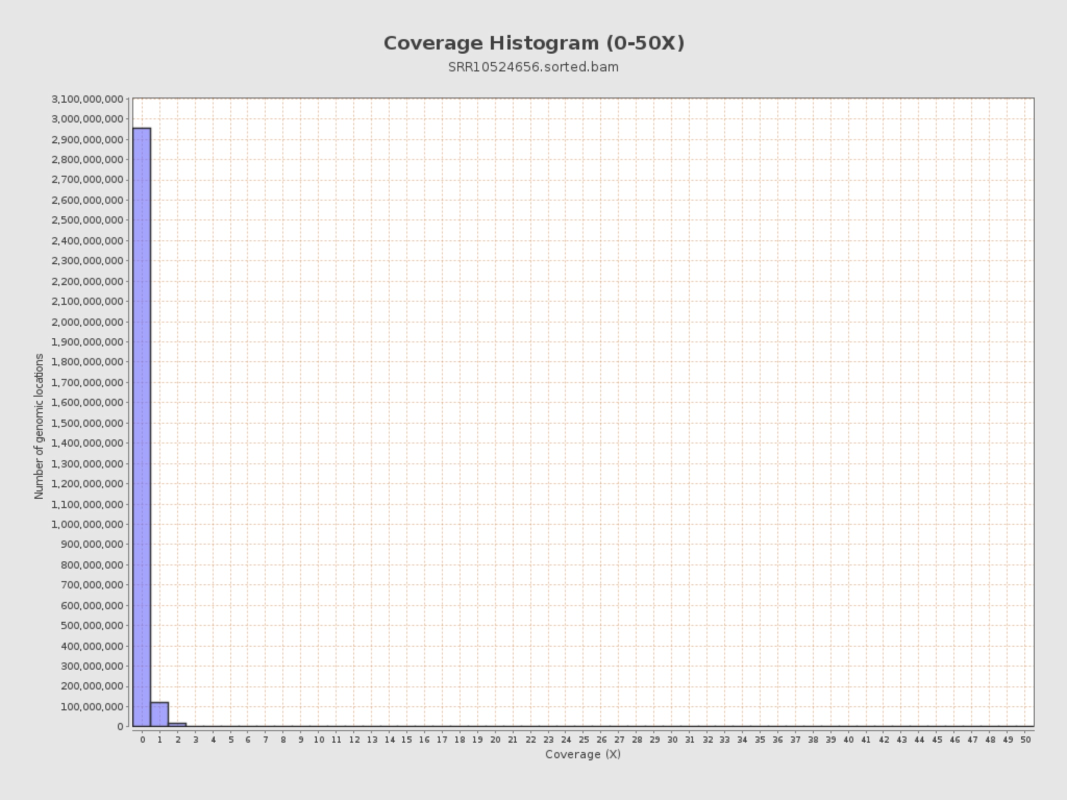
3. Results : Coverage across reference



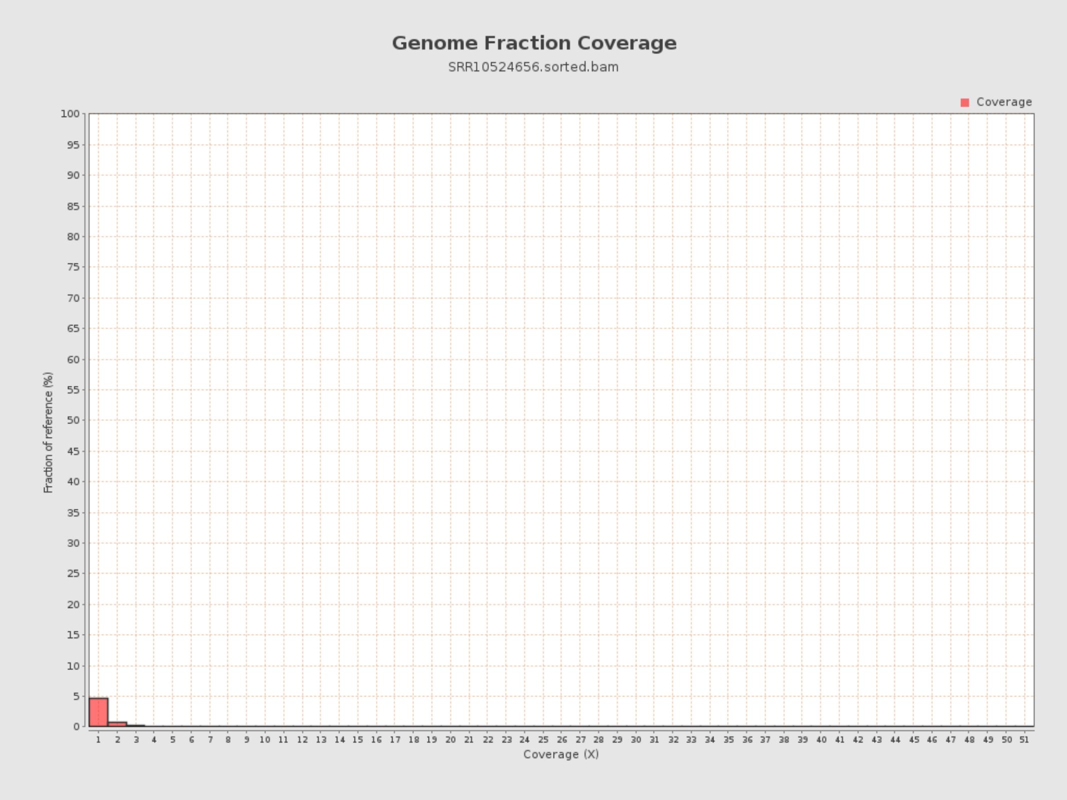
4. Results : Coverage Histogram



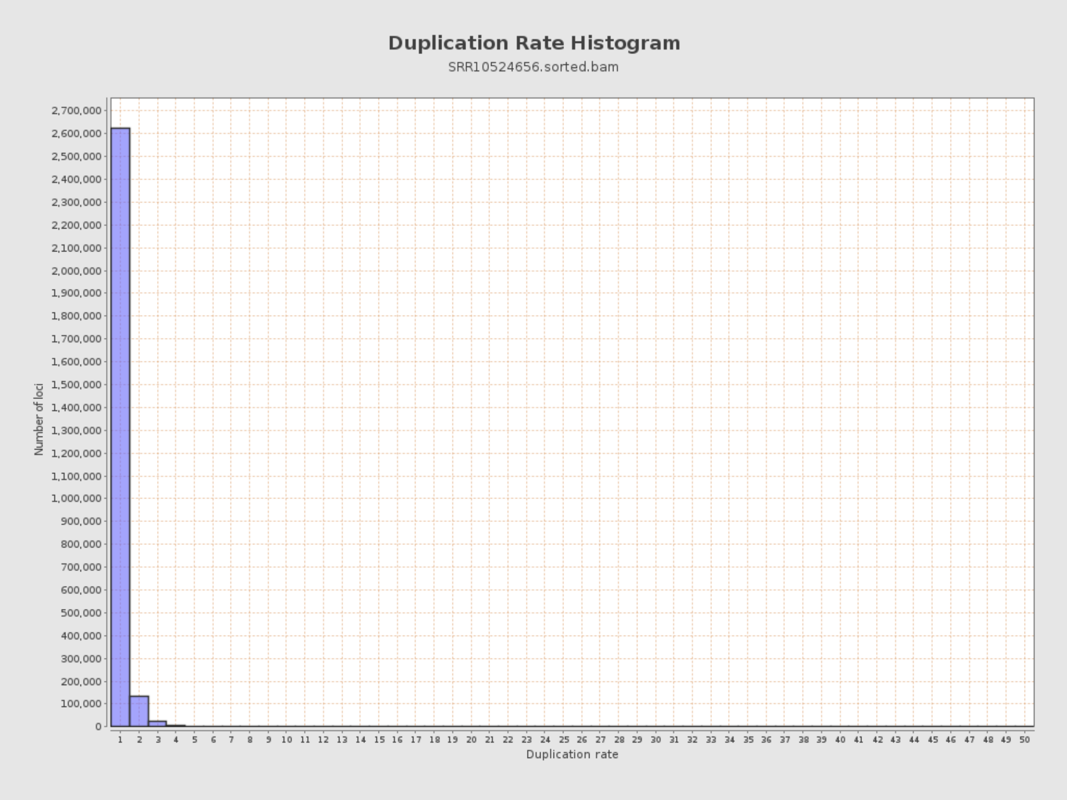
5. Results : Coverage Histogram (0-50X)



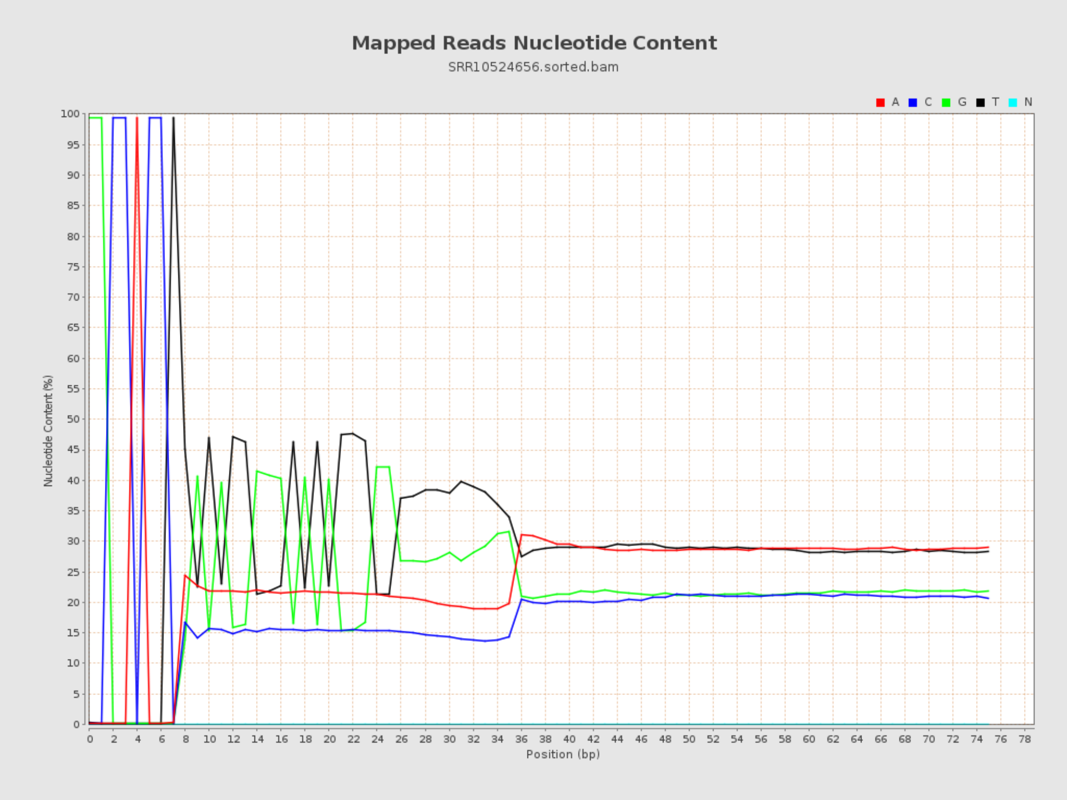
6. Results : Genome Fraction Coverage



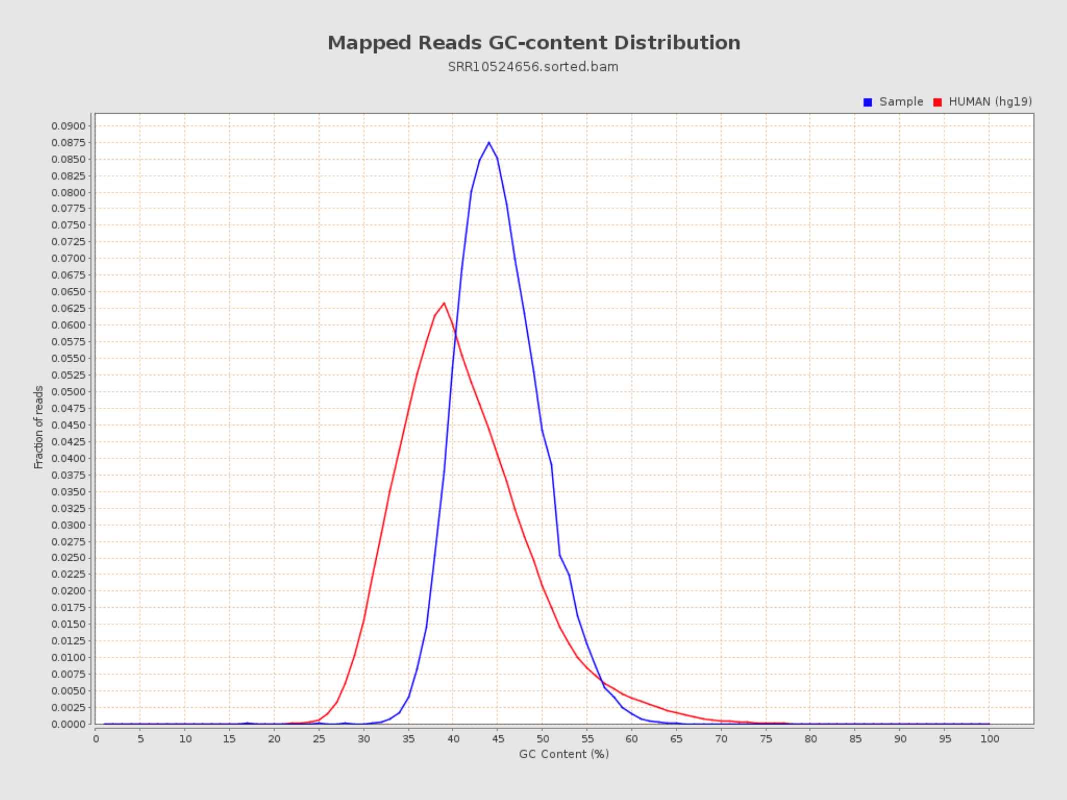
7. Results : Duplication Rate Histogram



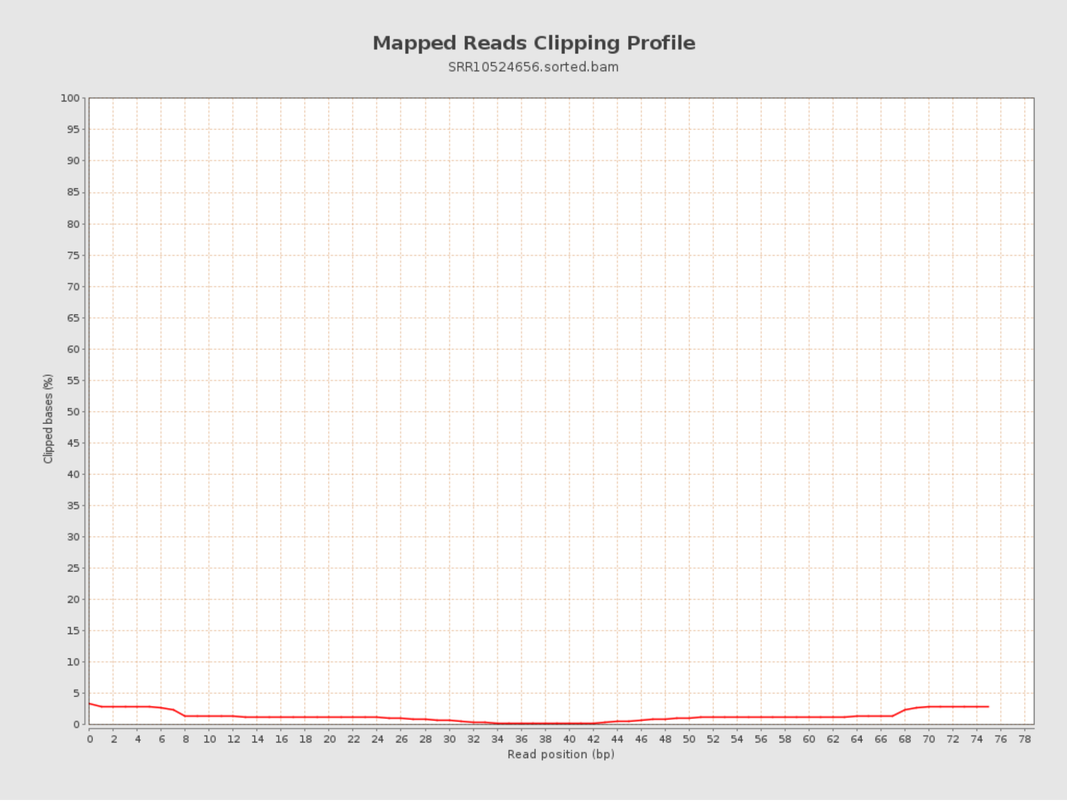
8. Results : Mapped Reads Nucleotide Content



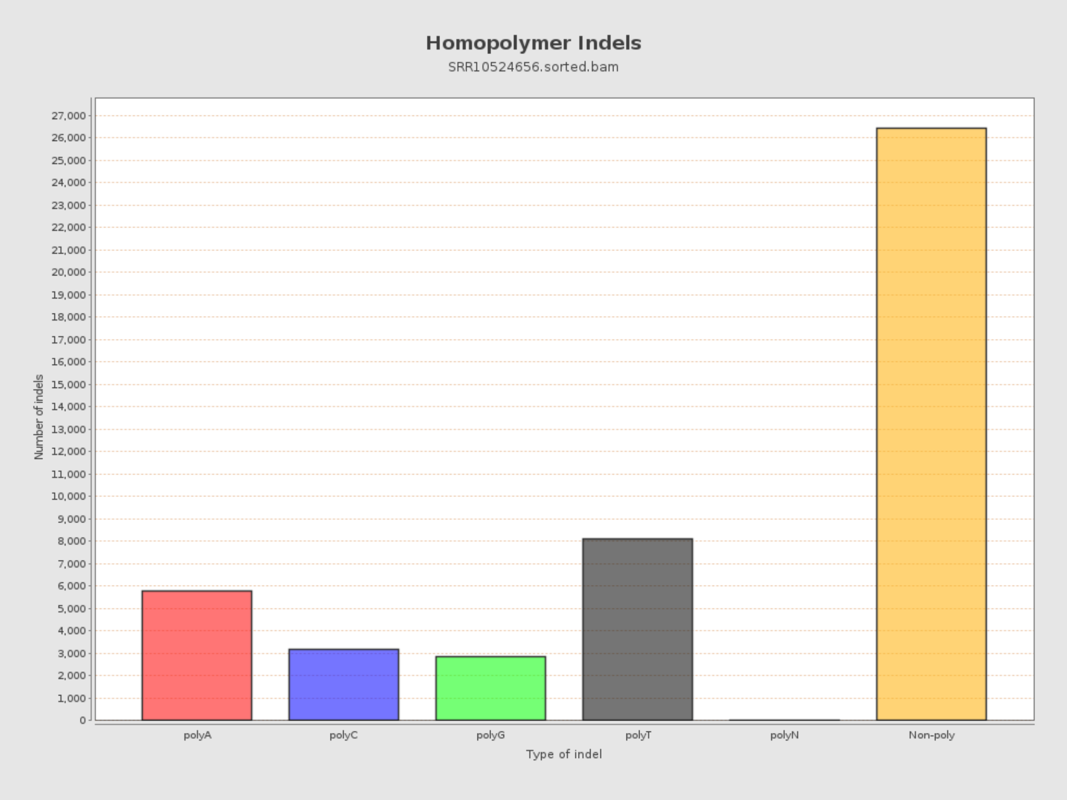
9. Results : Mapped Reads GC-content Distribution



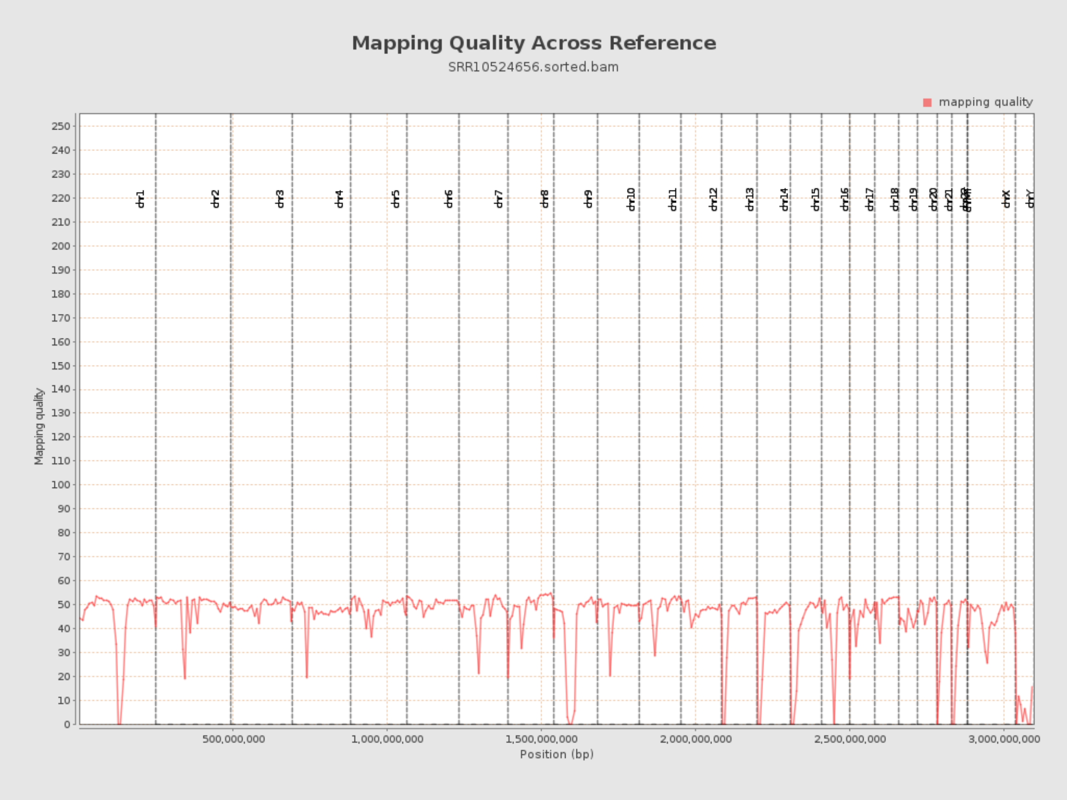
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram