Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:23:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524638.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_SRR10524638 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524638.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:23:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524638.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,444,504
Mapped reads	3,107,407 / 90.21%
Unmapped reads	337,097 / 9.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,198 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	305,463 / 8.87%
Duplication rate	7.25%
Clipped reads	3,109,826 / 90.28%

2.2. ACGT Content

Number/percentage of A's	43,184,071 / 23.88%
Number/percentage of C's	32,233,492 / 17.82%
Number/percentage of T's	59,826,308 / 33.08%
Number/percentage of G's	45,619,319 / 25.22%
Number/percentage of N's	1,413 / 0%
GC Percentage	43.04%

2.3. Coverage

Mean	0.0584

Standard Deviation	0.517

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

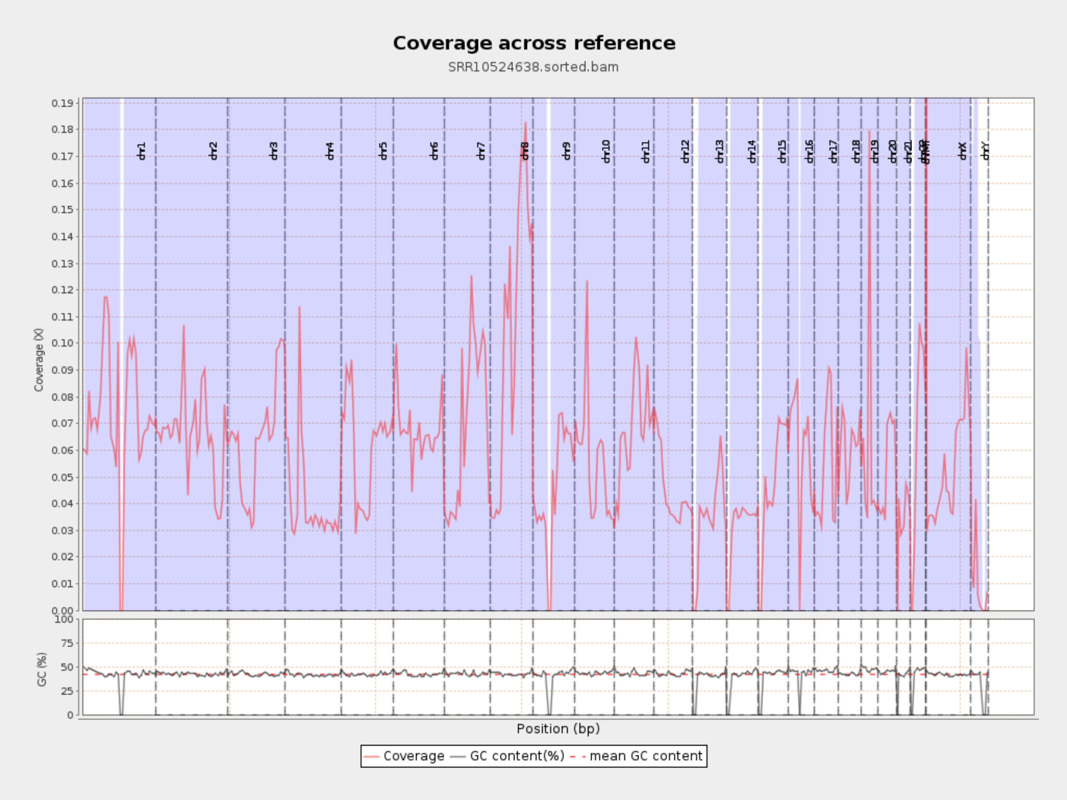
General error rate	0.52%
Mismatches	908,076
Insertions	13,159
Mapped reads with at least one insertion	0.42%
Deletions	35,797
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.04%

2.6. Chromosome stats

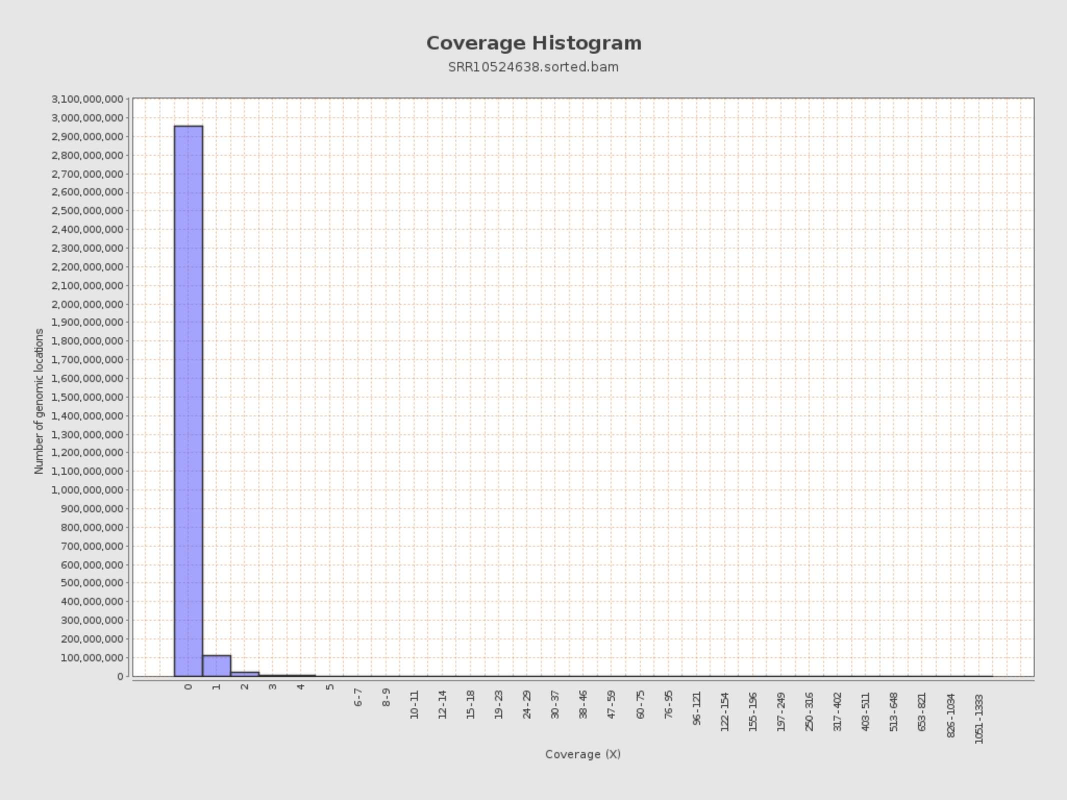
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18419701	0.0739	1.0211
chr2	243199373	16002840	0.0658	0.6334
chr3	198022430	12723109	0.0643	0.3184
chr4	191154276	7874077	0.0412	0.3794
chr5	180915260	11090448	0.0613	0.3108
chr6	171115067	11599782	0.0678	0.3542
chr7	159138663	11043758	0.0694	0.6334

chr8	146364022	15416822	0.1053	0.676
chr9	141213431	6423138	0.0455	0.399
chr10	135534747	7483104	0.0552	0.5812
chr11	135006516	9218616	0.0683	0.418
chr12	133851895	6052511	0.0452	0.2809
chr13	115169878	3981840	0.0346	0.2374
chr14	107349540	3373808	0.0314	0.2356
chr15	102531392	4746439	0.0463	0.2745
chr16	90354753	5351179	0.0592	0.3374
chr17	81195210	4428637	0.0545	0.312
chr18	78077248	4785086	0.0613	0.7098
chr19	59128983	3631287	0.0614	0.6815
chr20	63025520	3454466	0.0548	0.312
chr21	48129895	1676933	0.0348	0.3382
chr22	51304566	3323101	0.0648	0.3253
chrMT	16571	96076	5.7978	4.4359
chrX	155270560	8144865	0.0525	0.3363
chrY	59373566	583268	0.0098	0.3823

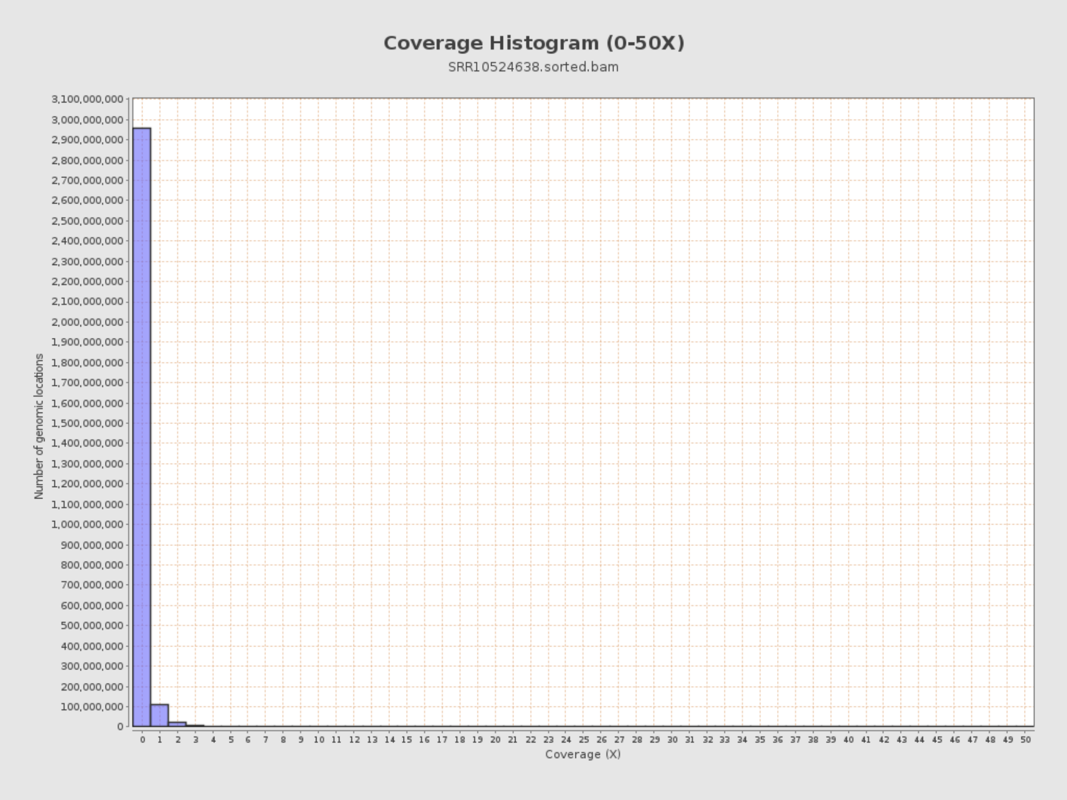
3. Results : Coverage across reference



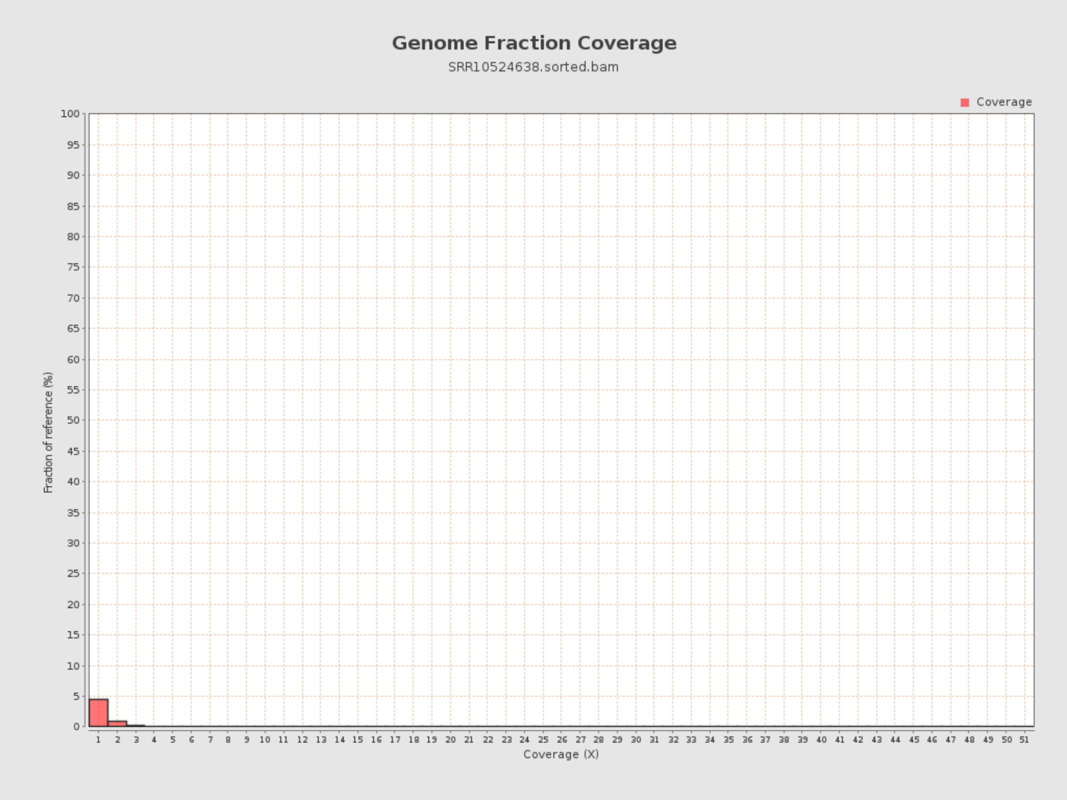
4. Results : Coverage Histogram



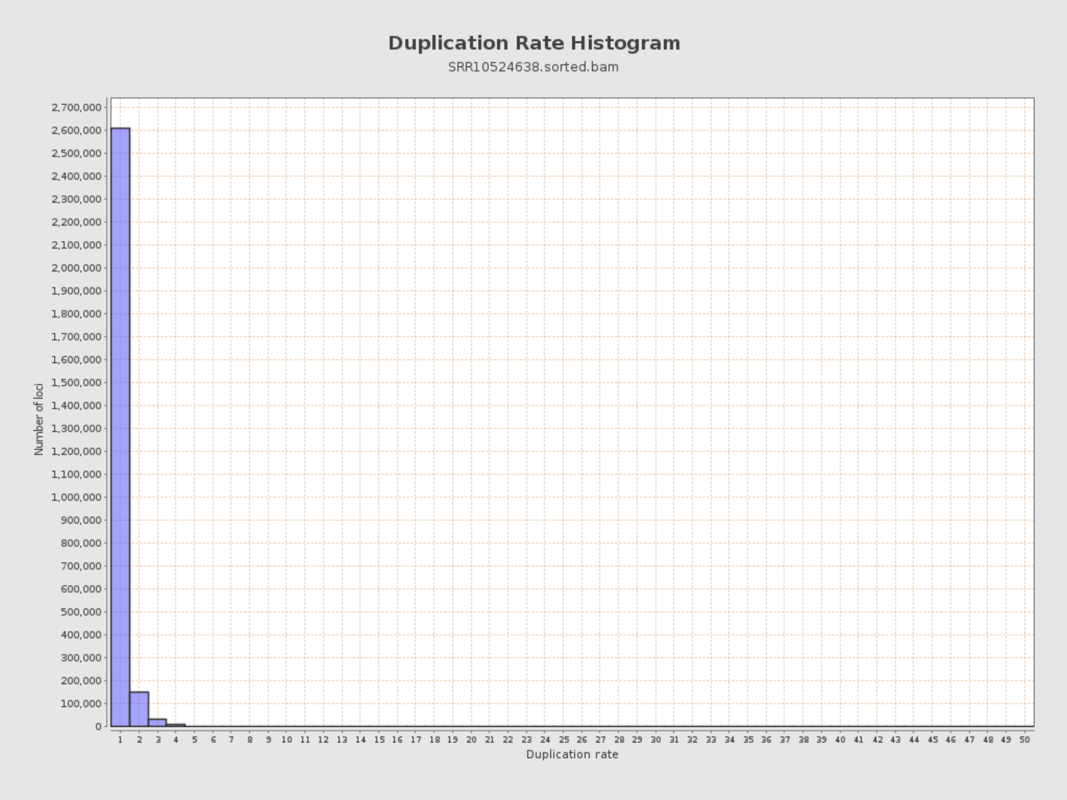
5. Results : Coverage Histogram (0-50X)



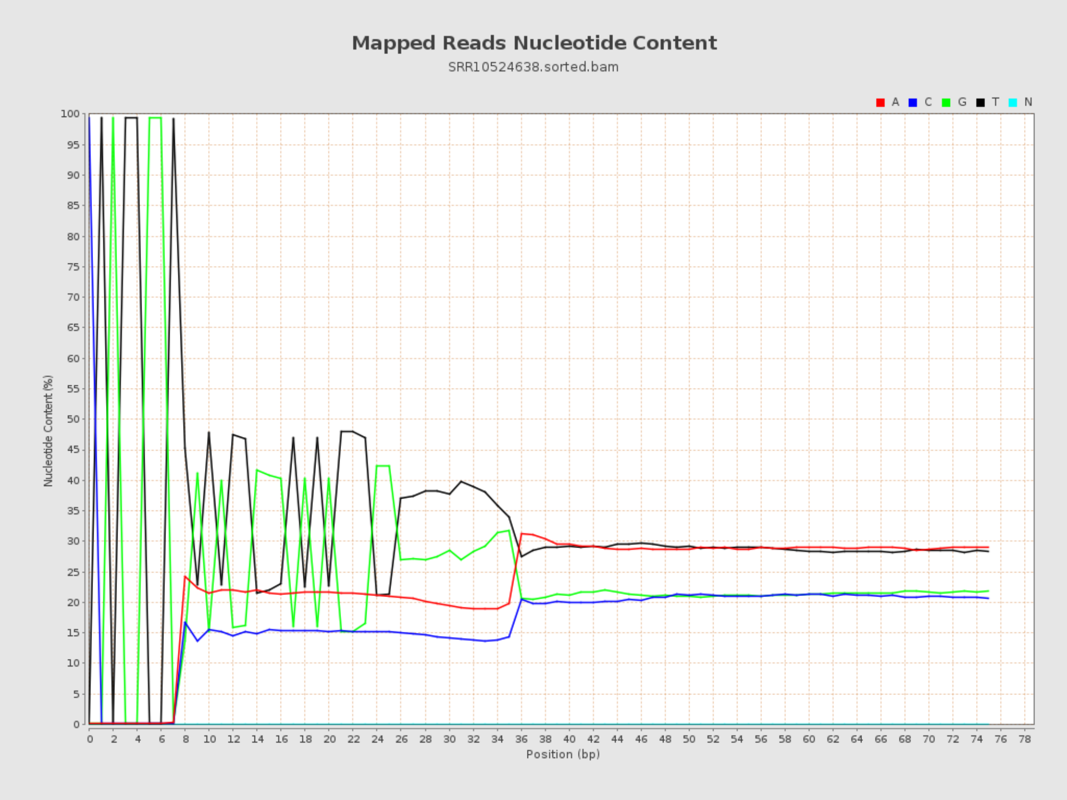
6. Results : Genome Fraction Coverage



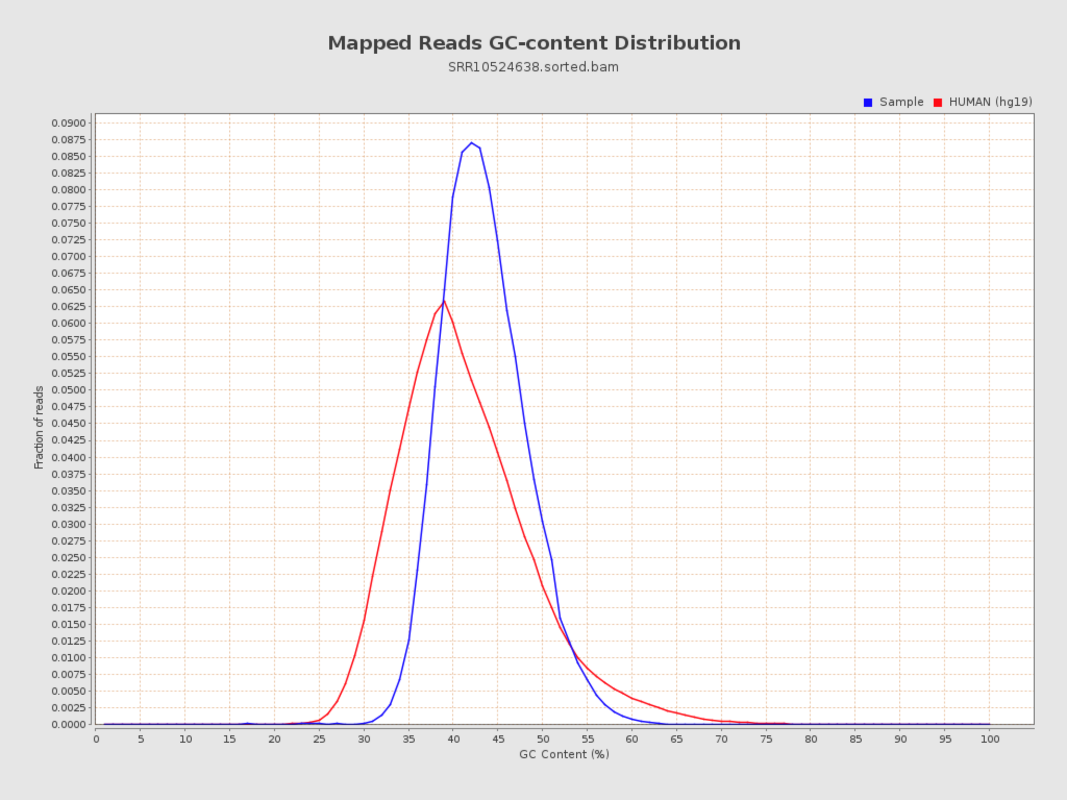
7. Results : Duplication Rate Histogram



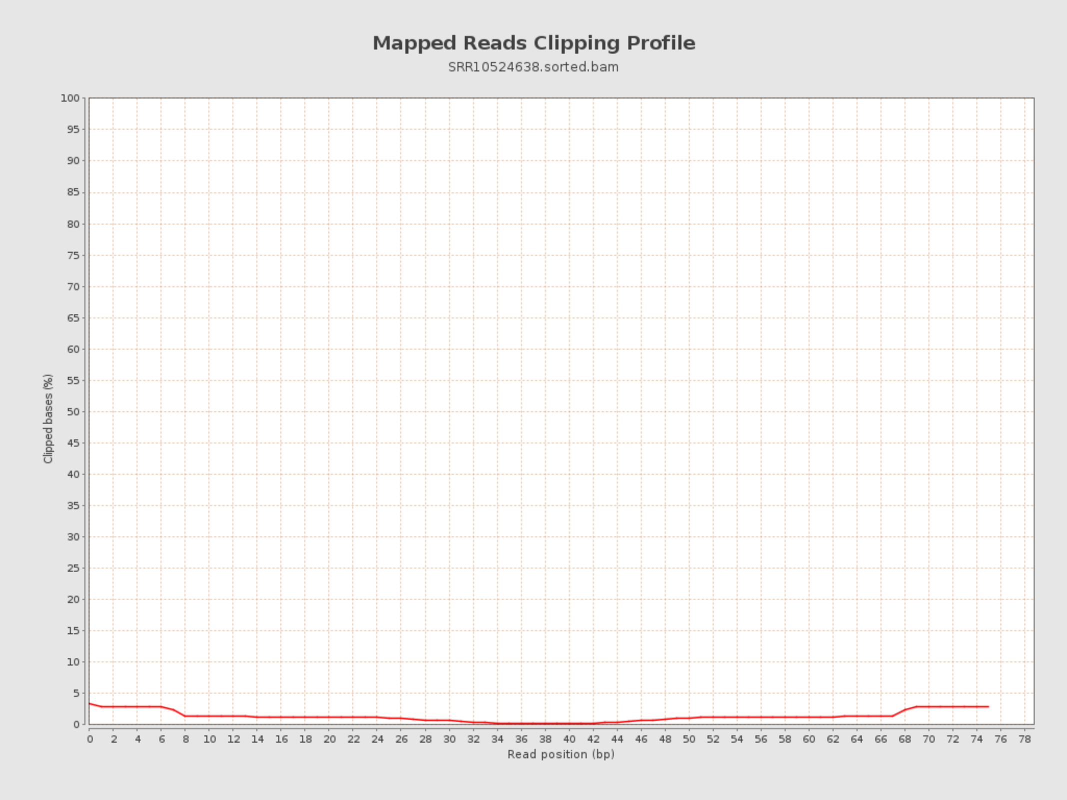
8. Results : Mapped Reads Nucleotide Content



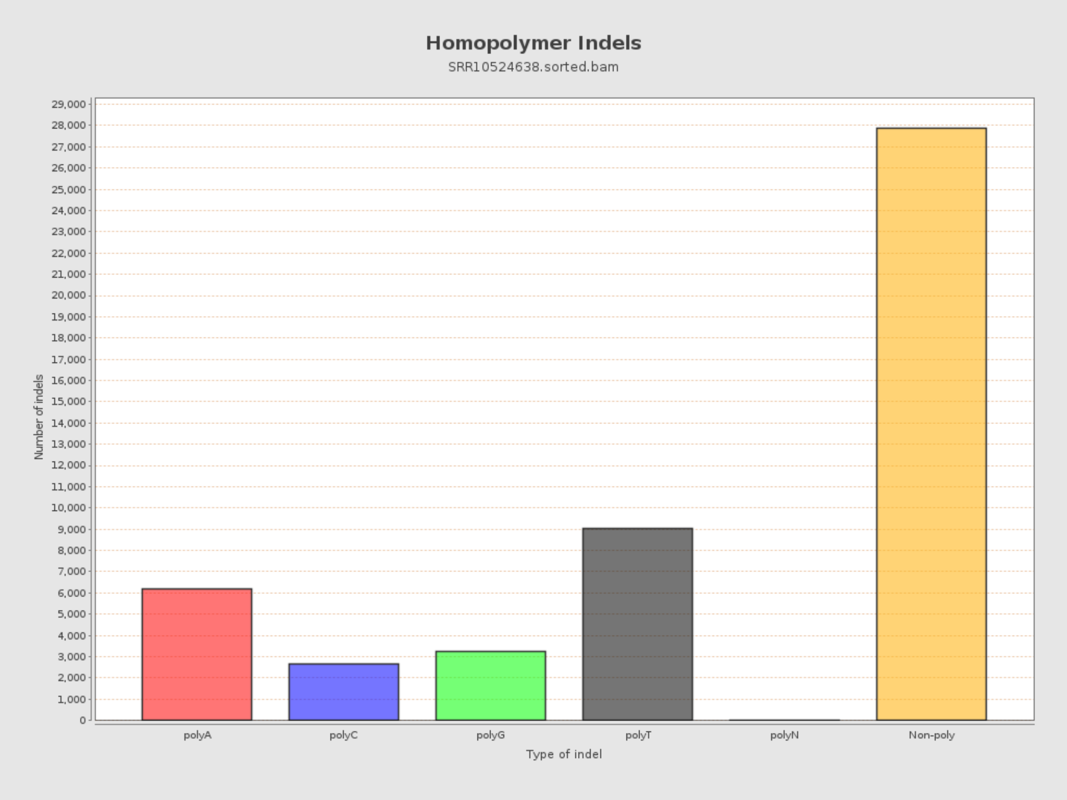
9. Results : Mapped Reads GC-content Distribution



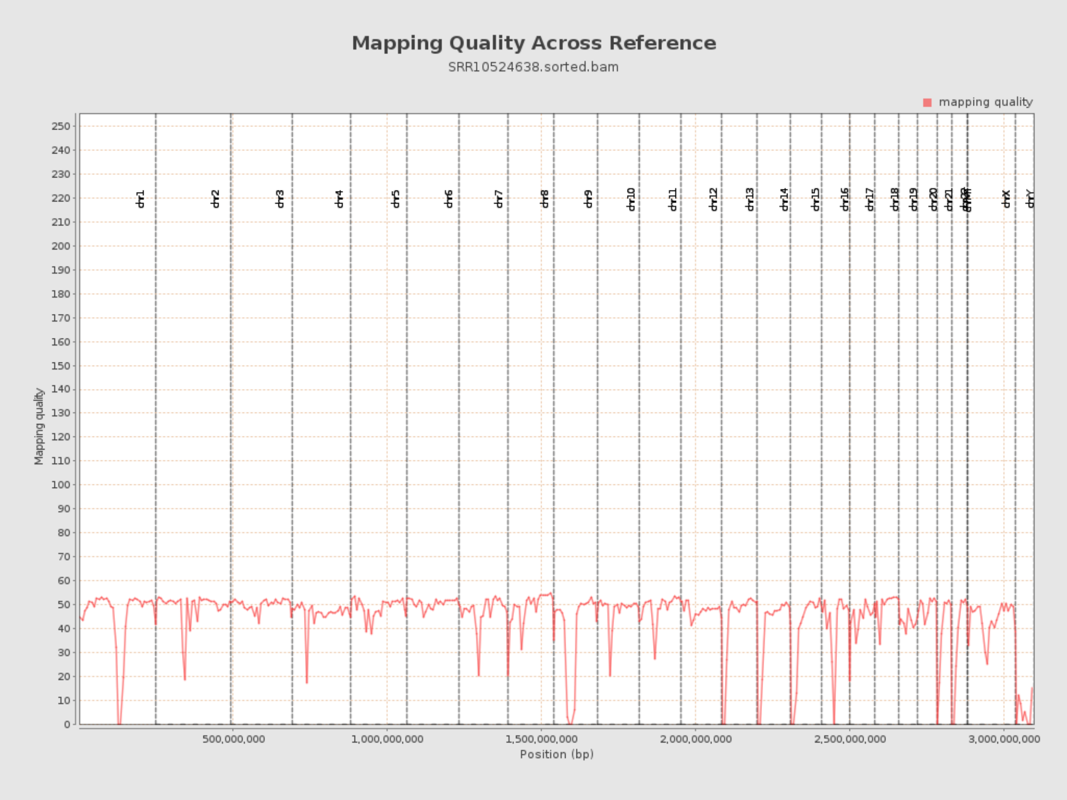
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram