Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:28:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524318.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_SRR10524318 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524318.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:28:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524318.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,139,733
Mapped reads	1,051,538 / 92.26%
Unmapped reads	88,195 / 7.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,300 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	24,306 / 2.13%
Duplication rate	1.61%
Clipped reads	1,051,523 / 92.26%

2.2. ACGT Content

Number/percentage of A's	15,821,723 / 25.57%
Number/percentage of C's	12,354,704 / 19.97%
Number/percentage of T's	19,139,616 / 30.93%
Number/percentage of G's	14,556,735 / 23.52%
Number/percentage of N's	8,266 / 0.01%
GC Percentage	43.49%

2.3. Coverage

Mean	0.02

Standard Deviation	0.2011

2.4. Mapping Quality

Mean Mapping Quality	44.33

2.5. Mismatches and indels

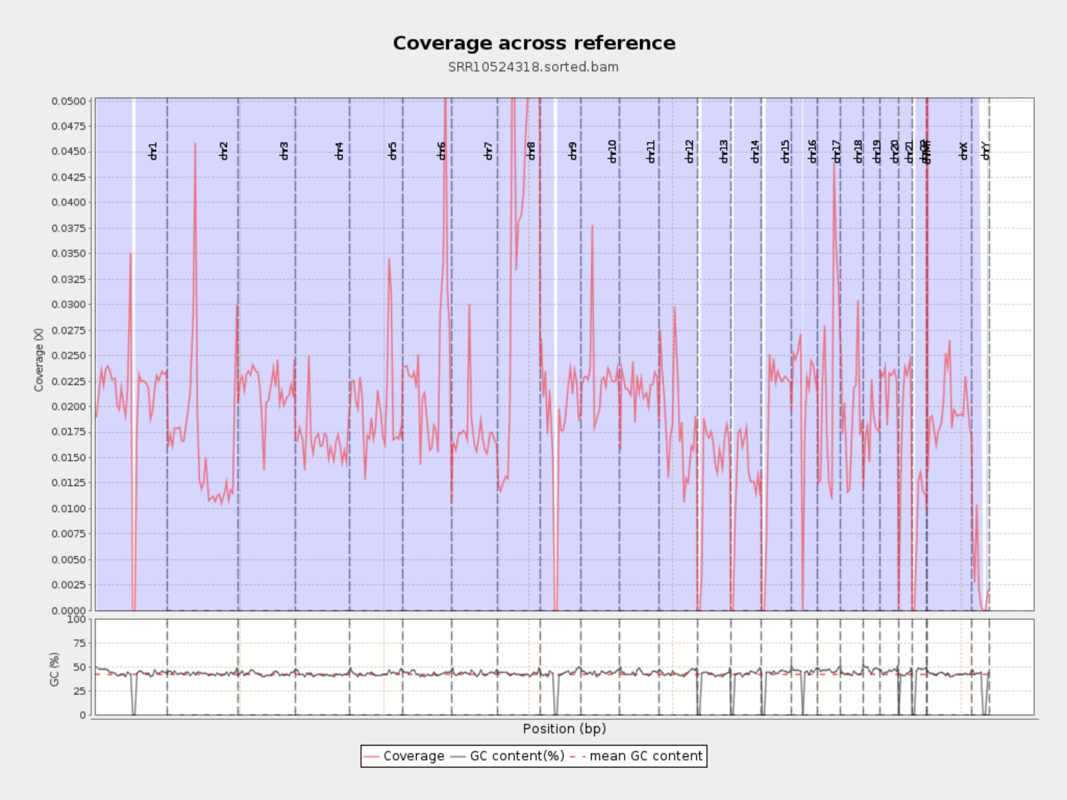
General error rate	0.52%
Mismatches	312,434
Insertions	4,968
Mapped reads with at least one insertion	0.47%
Deletions	11,322
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.04%

2.6. Chromosome stats

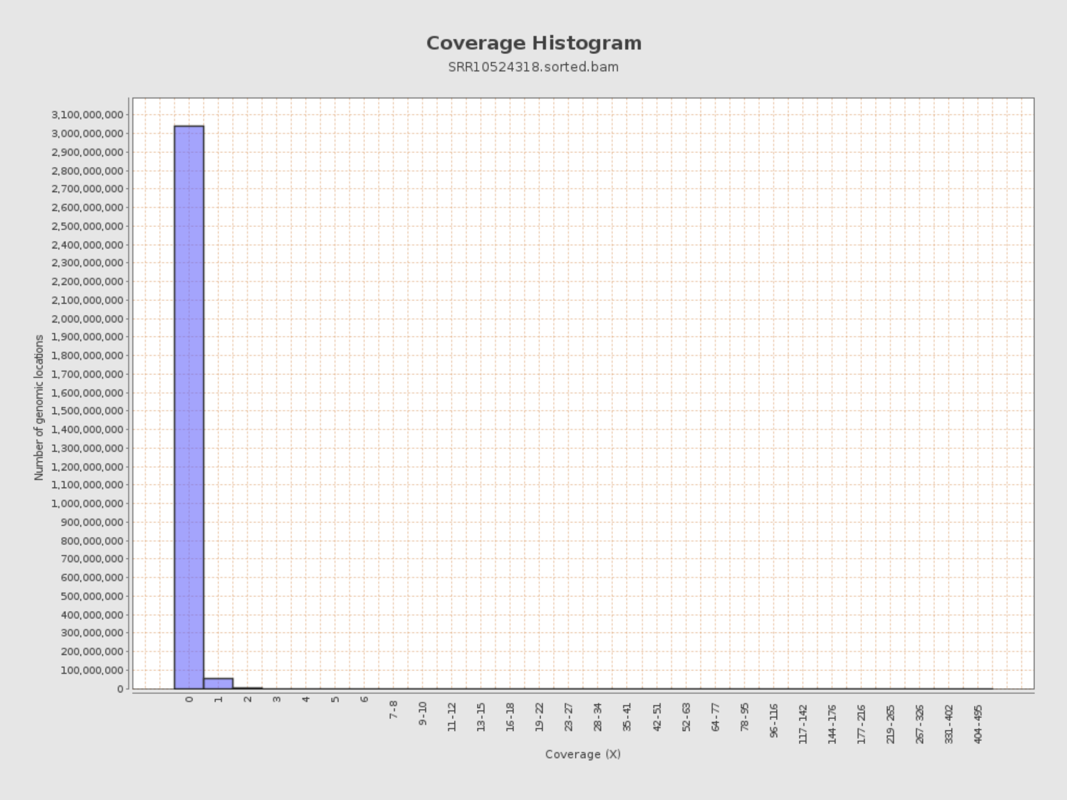
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5197200	0.0209	0.3396
chr2	243199373	3984758	0.0164	0.2475
chr3	198022430	4300092	0.0217	0.1551
chr4	191154276	3192616	0.0167	0.1474
chr5	180915260	3616804	0.02	0.1487
chr6	171115067	4017719	0.0235	0.1689
chr7	159138663	2786762	0.0175	0.2345

chr8	146364022	6500335	0.0444	0.2652
chr9	141213431	2605748	0.0185	0.1667
chr10	135534747	3113403	0.023	0.2038
chr11	135006516	2952237	0.0219	0.1812
chr12	133851895	2454340	0.0183	0.1439
chr13	115169878	1578426	0.0137	0.1239
chr14	107349540	1326269	0.0124	0.1213
chr15	102531392	1908020	0.0186	0.1451
chr16	90354753	1924354	0.0213	0.1617
chr17	81195210	1880138	0.0232	0.1708
chr18	78077248	1492265	0.0191	0.2809
chr19	59128983	1057346	0.0179	0.2525
chr20	63025520	1407773	0.0223	0.1603
chr21	48129895	907752	0.0189	0.1509
chr22	51304566	447088	0.0087	0.0982
chrMT	16571	10675	0.6442	0.8848
chrX	155270560	3060820	0.0197	0.1594
chrY	59373566	175735	0.003	0.0857

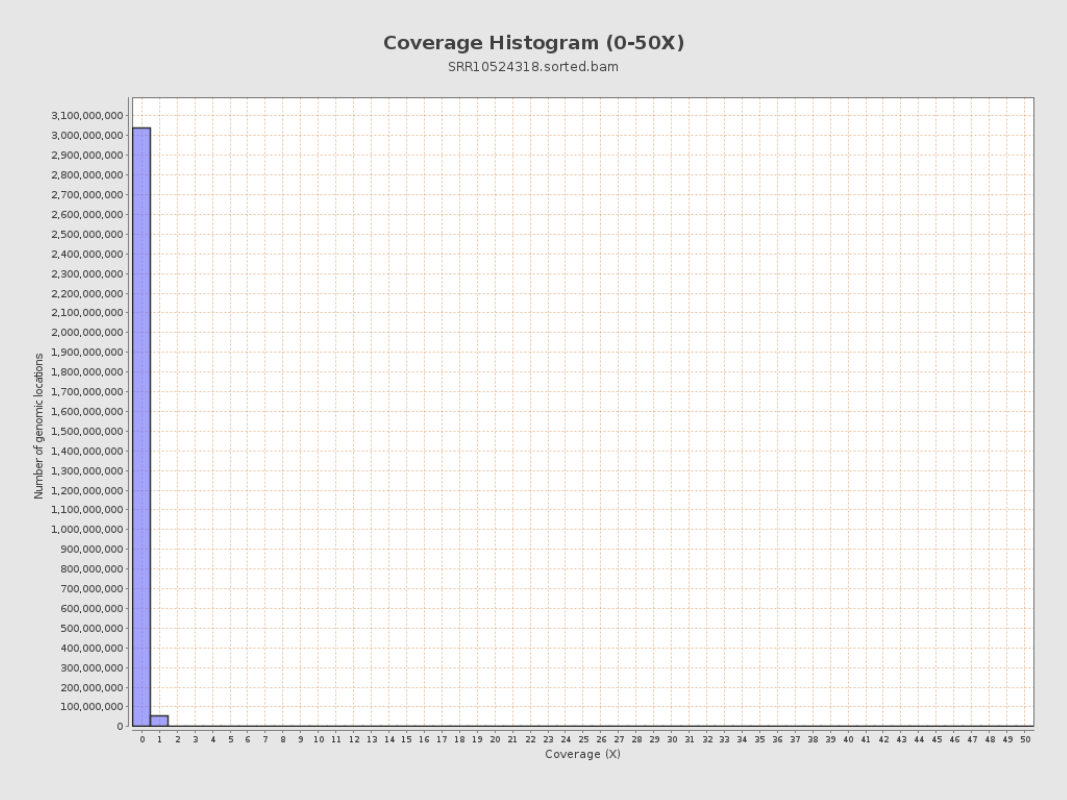
3. Results : Coverage across reference



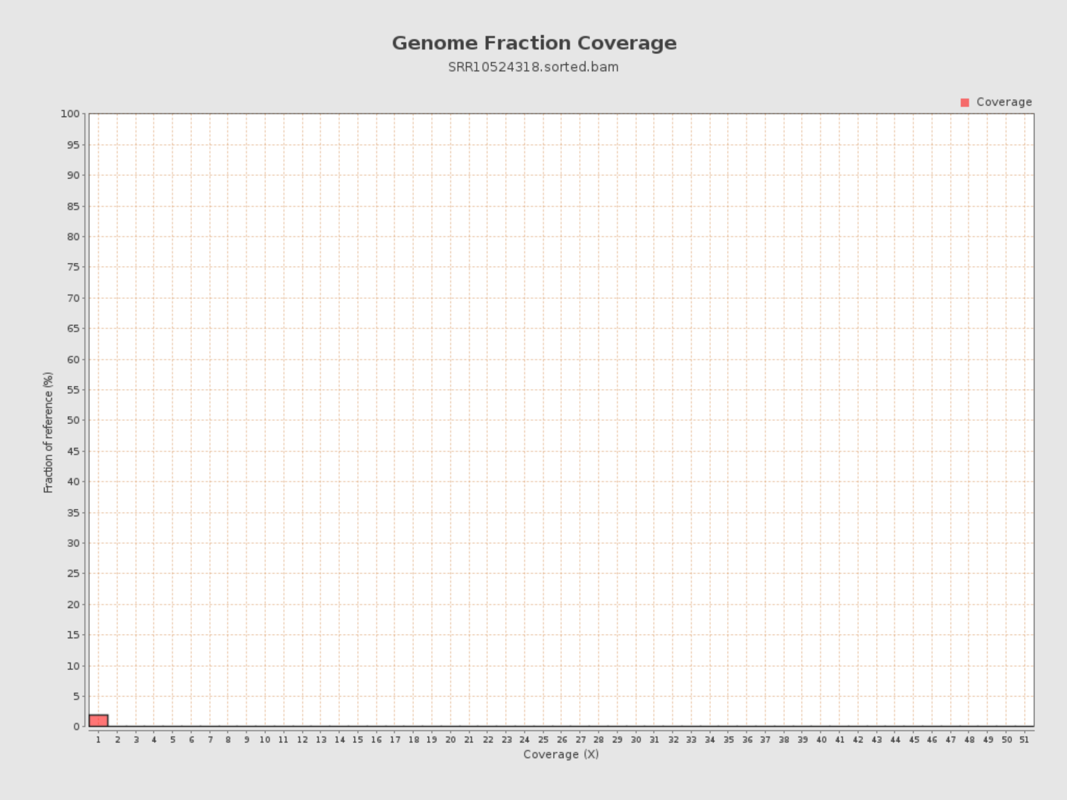
4. Results : Coverage Histogram



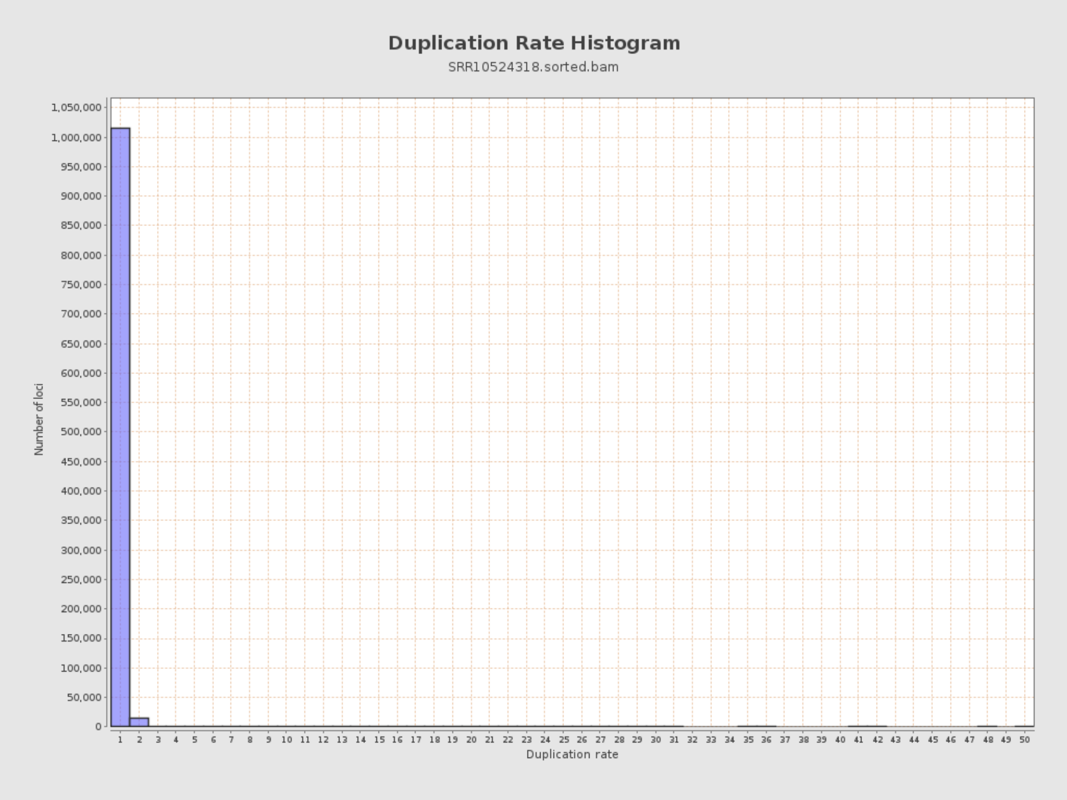
5. Results : Coverage Histogram (0-50X)



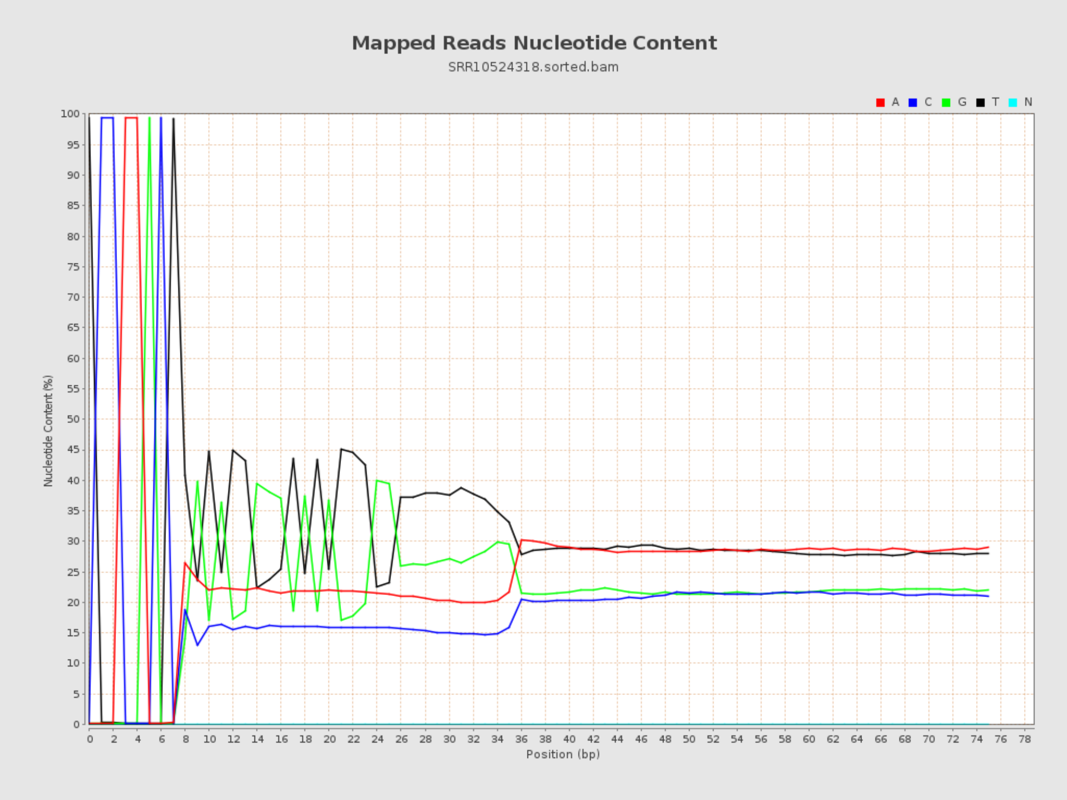
6. Results : Genome Fraction Coverage



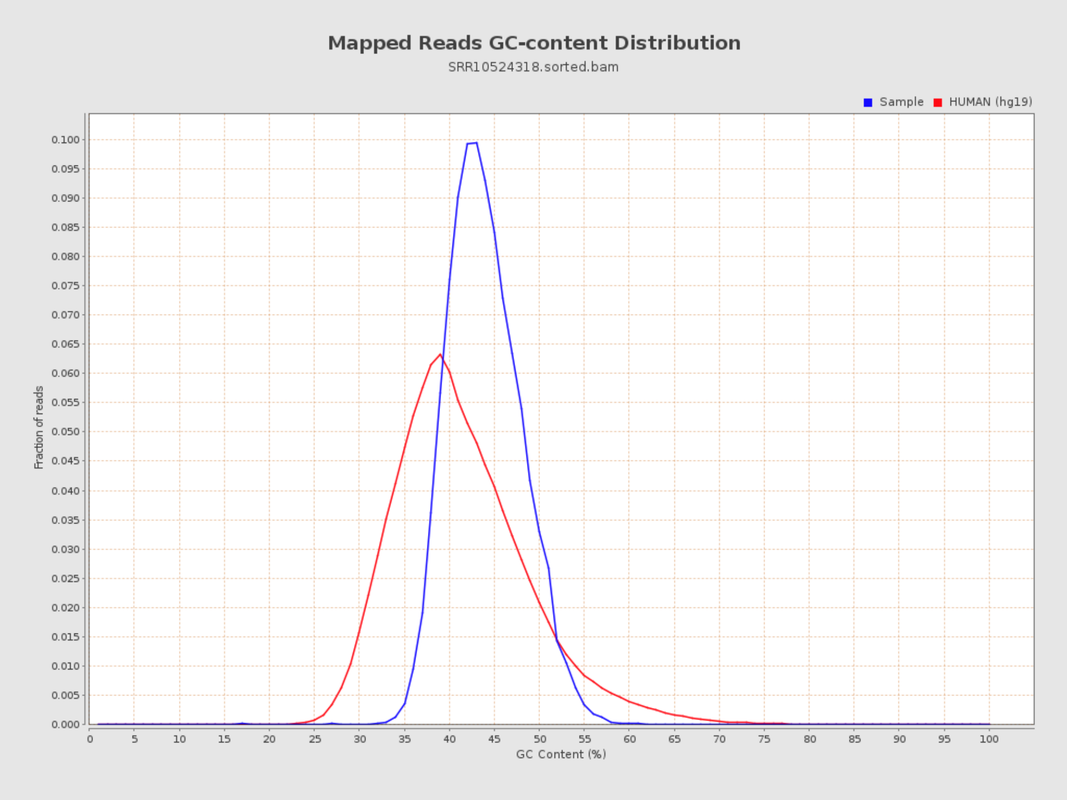
7. Results : Duplication Rate Histogram



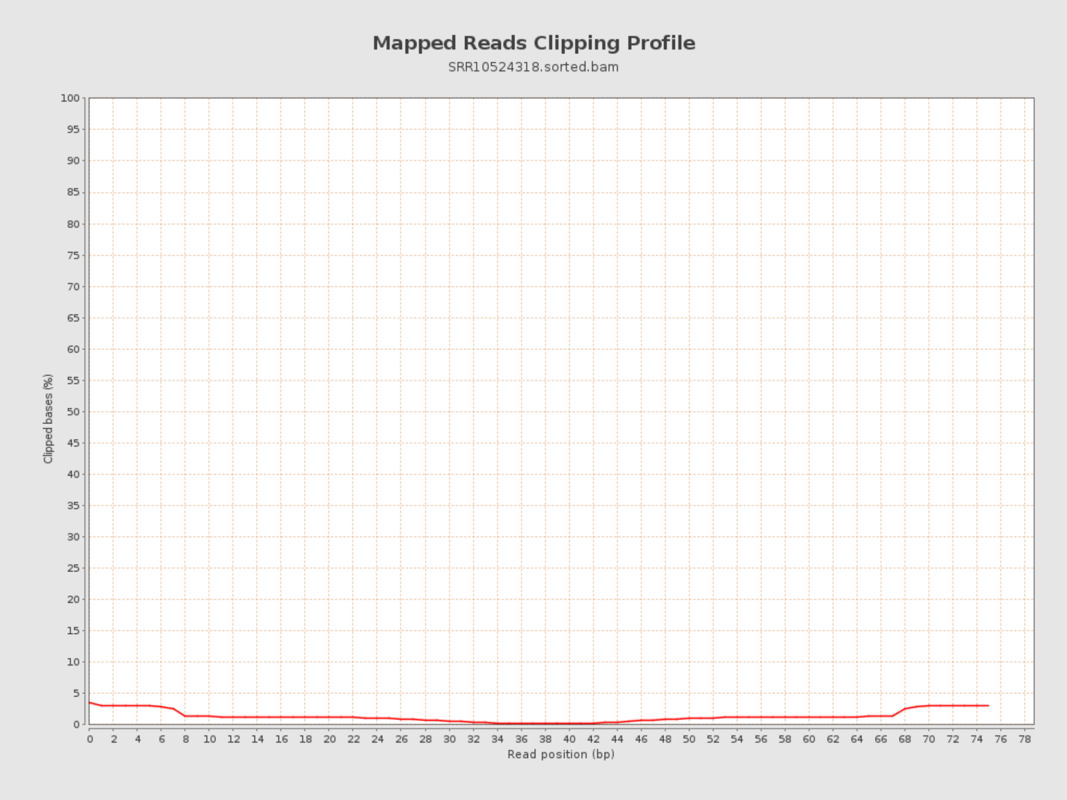
8. Results : Mapped Reads Nucleotide Content



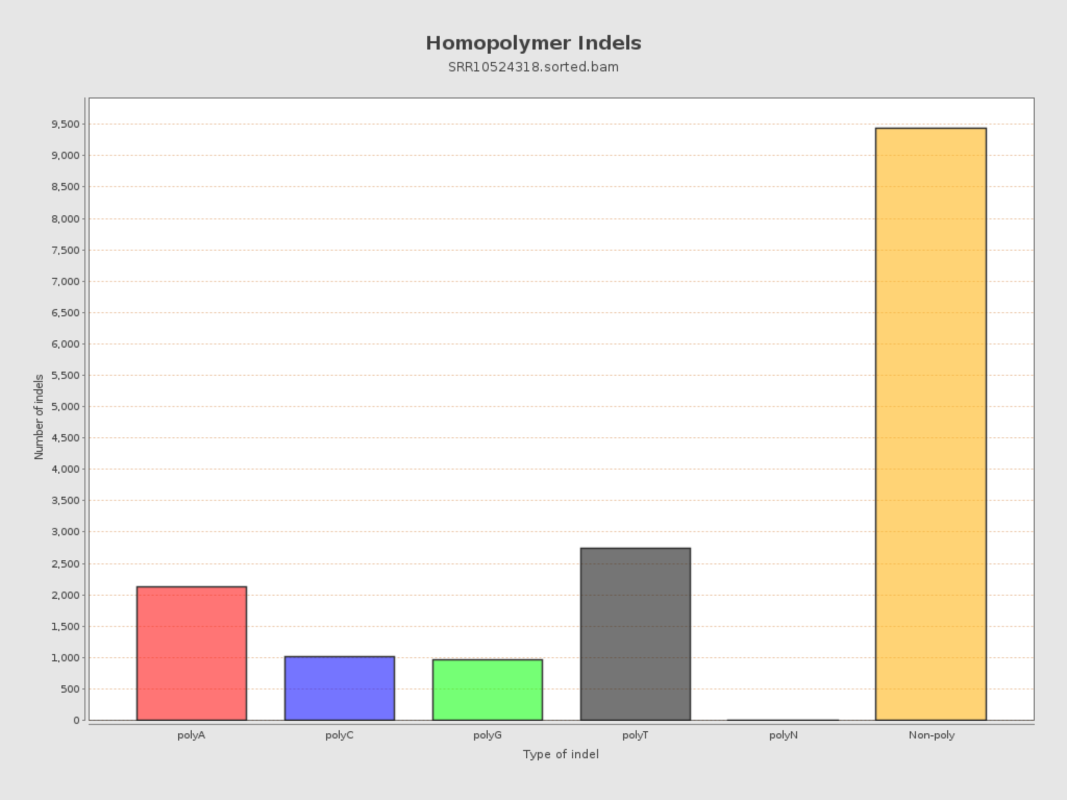
9. Results : Mapped Reads GC-content Distribution



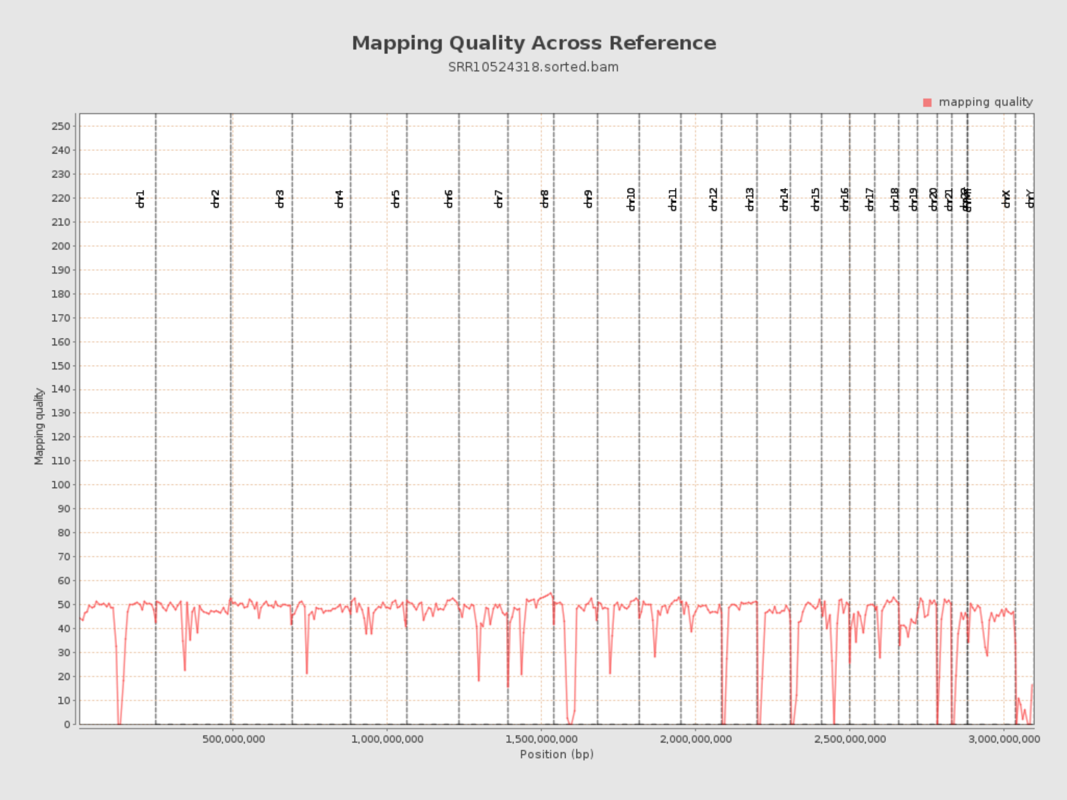
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram