Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:31:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524319.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_SRR10524319 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524319.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:31:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524319.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,984,628
Mapped reads	3,623,851 / 90.95%
Unmapped reads	360,777 / 9.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,451 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	208,386 / 5.23%
Duplication rate	4.16%
Clipped reads	3,631,495 / 91.14%

2.2. ACGT Content

Number/percentage of A's	52,500,003 / 25.01%
Number/percentage of C's	39,603,611 / 18.86%
Number/percentage of T's	67,224,940 / 32.02%
Number/percentage of G's	50,582,650 / 24.09%
Number/percentage of N's	28,745 / 0.01%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0678

Standard Deviation	0.5706

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Mismatches and indels

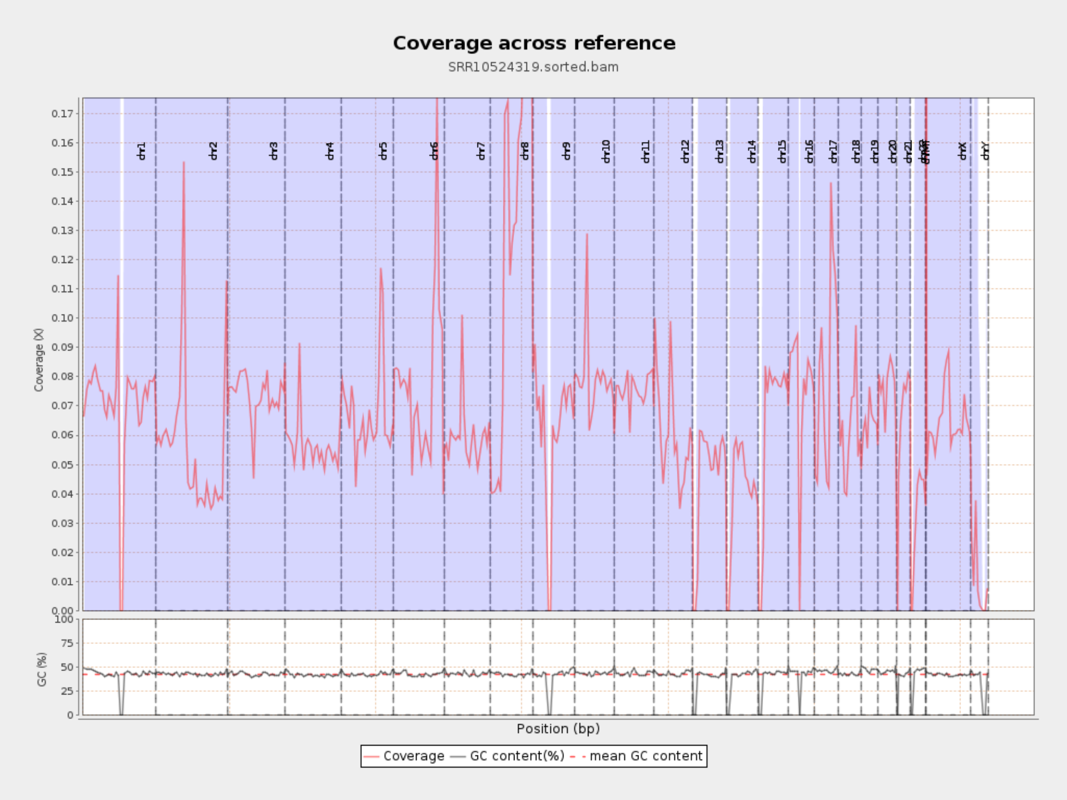
General error rate	0.53%
Mismatches	1,078,226
Insertions	13,132
Mapped reads with at least one insertion	0.36%
Deletions	35,772
Mapped reads with at least one deletion	0.98%
Homopolymer indels	43.25%

2.6. Chromosome stats

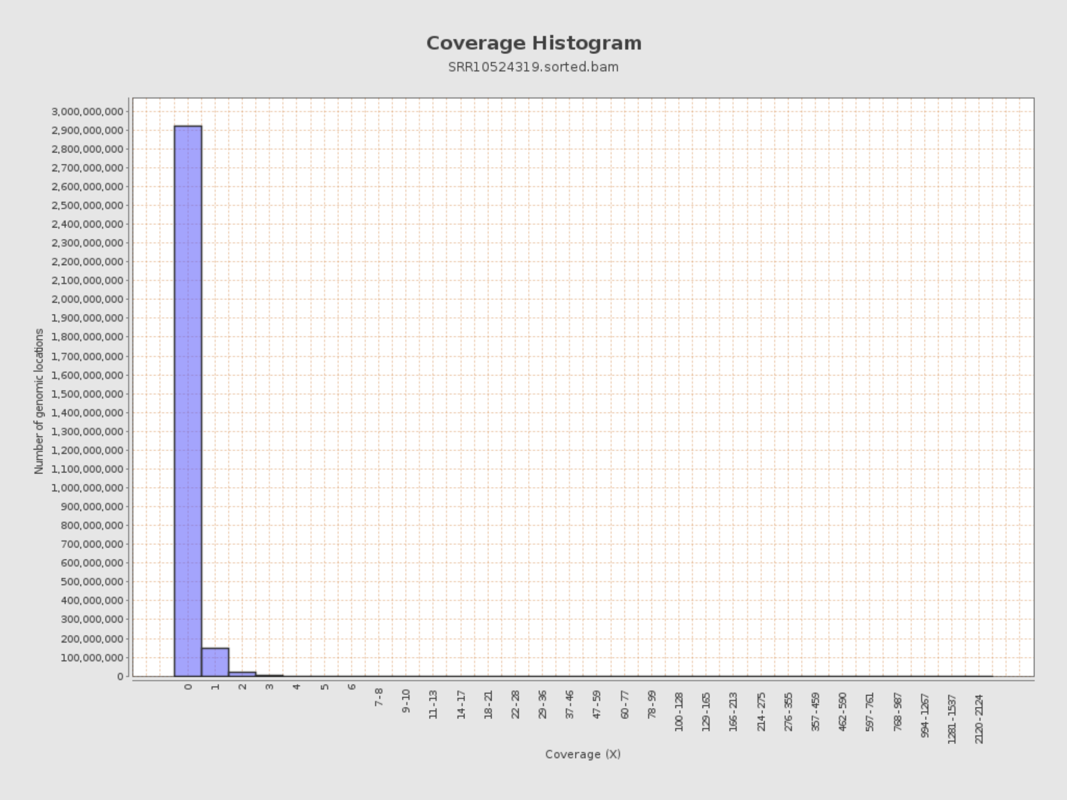
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17639095	0.0708	1.115
chr2	243199373	13659275	0.0562	0.8929
chr3	198022430	14573489	0.0736	0.321
chr4	191154276	10824783	0.0566	0.3437
chr5	180915260	12282283	0.0679	0.3093
chr6	171115067	13451097	0.0786	0.3855
chr7	159138663	9529911	0.0599	0.7007

chr8	146364022	21825759	0.1491	0.6805
chr9	141213431	8632150	0.0611	0.4063
chr10	135534747	10746627	0.0793	0.5402
chr11	135006516	10187271	0.0755	0.4381
chr12	133851895	8196769	0.0612	0.3006
chr13	115169878	5308563	0.0461	0.2558
chr14	107349540	4404666	0.041	0.2626
chr15	102531392	6505160	0.0634	0.3072
chr16	90354753	6729492	0.0745	0.354
chr17	81195210	6622542	0.0816	0.3909
chr18	78077248	4855708	0.0622	0.7829
chr19	59128983	3781215	0.0639	0.7554
chr20	63025520	4881513	0.0775	0.3398
chr21	48129895	3055821	0.0635	0.3386
chr22	51304566	1621950	0.0316	0.2087
chrMT	16571	18190	1.0977	1.3204
chrX	155270560	10053809	0.0648	0.3576
chrY	59373566	609482	0.0103	0.2919

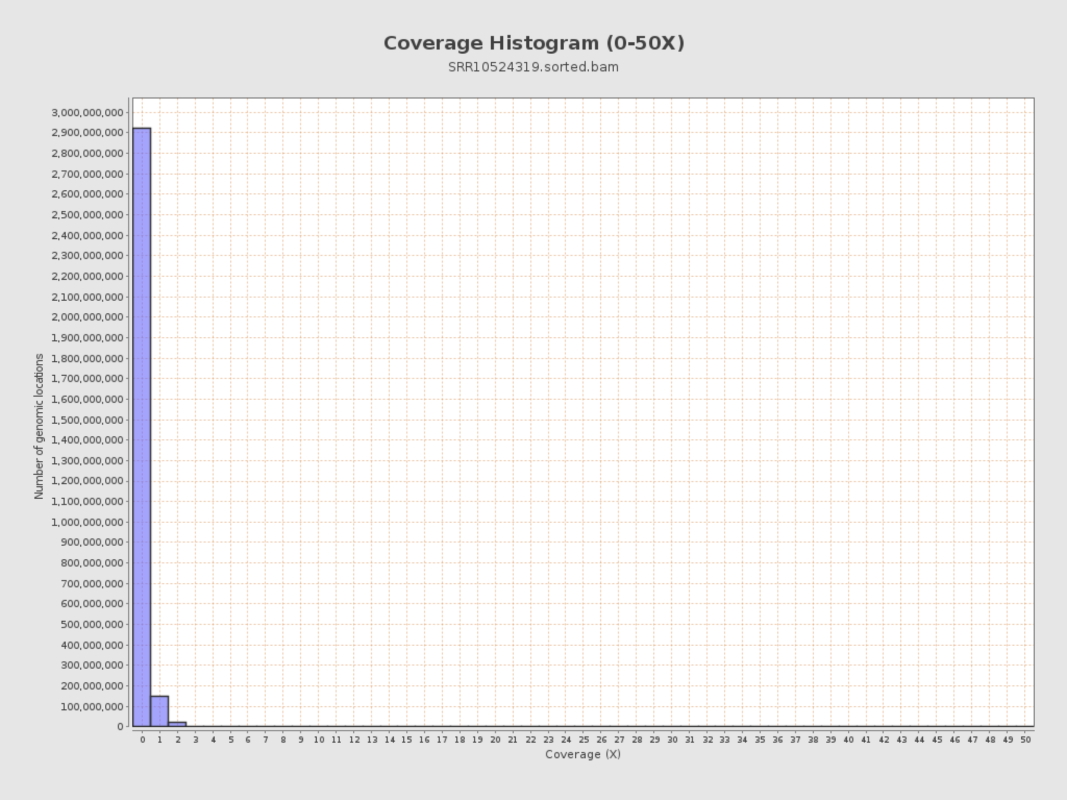
3. Results : Coverage across reference



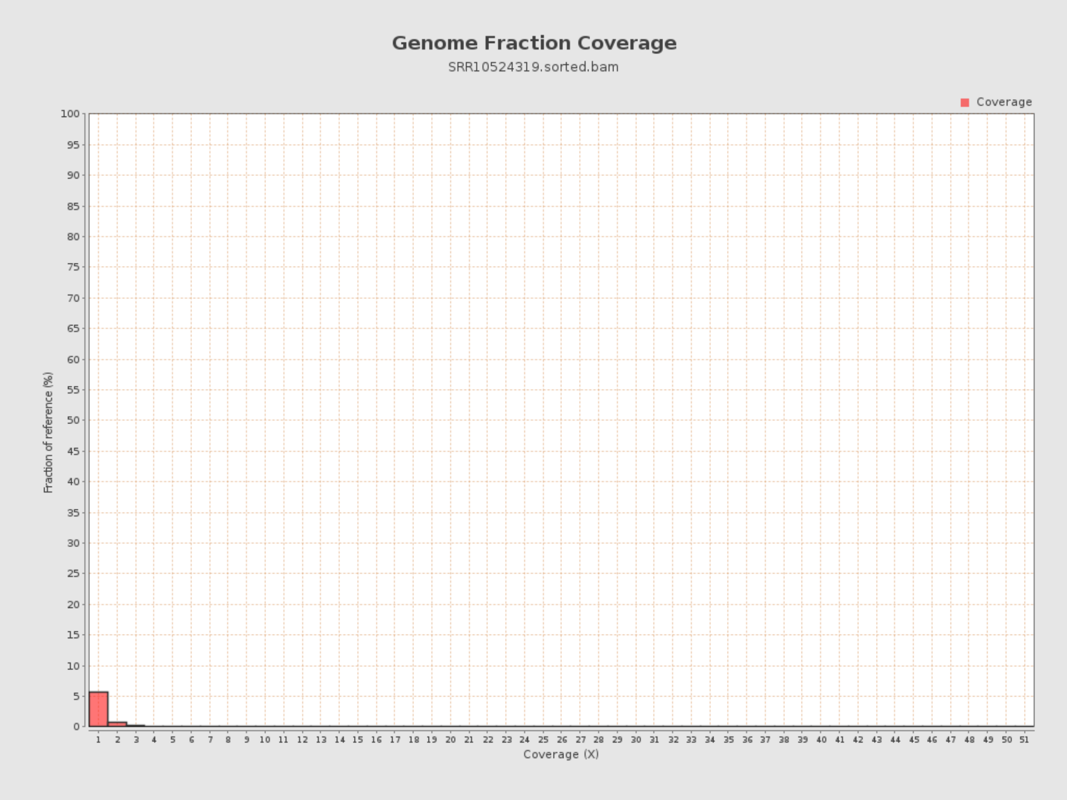
4. Results : Coverage Histogram



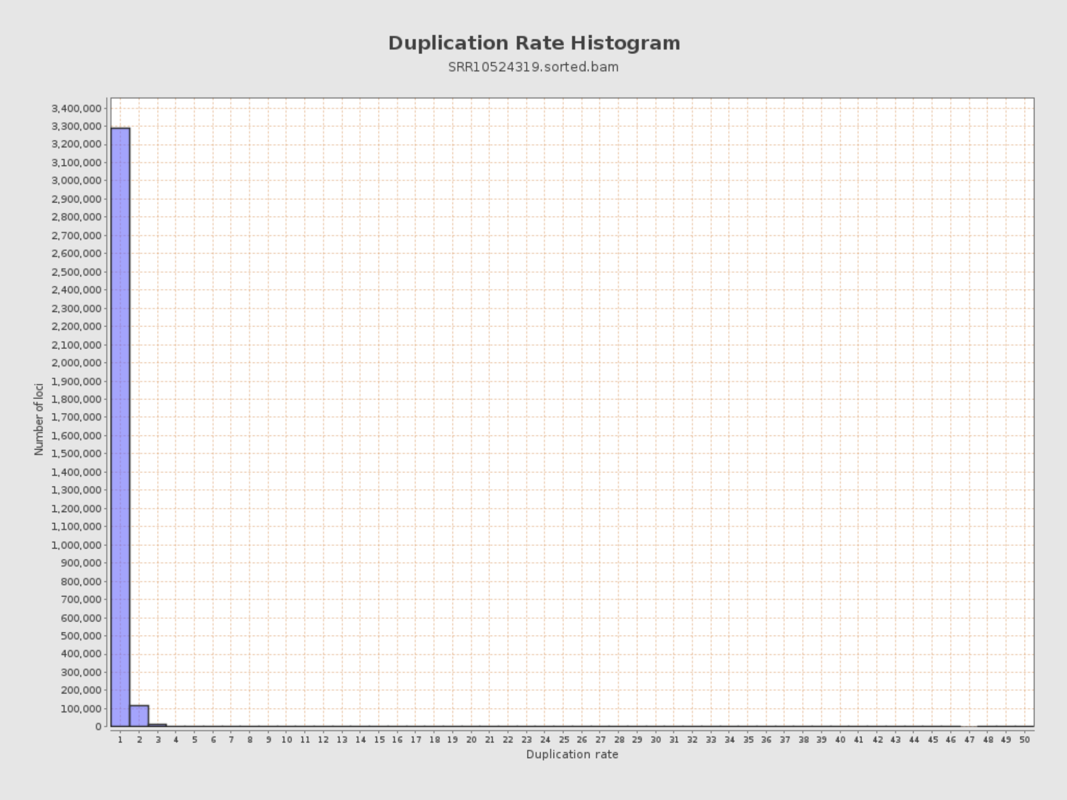
5. Results : Coverage Histogram (0-50X)



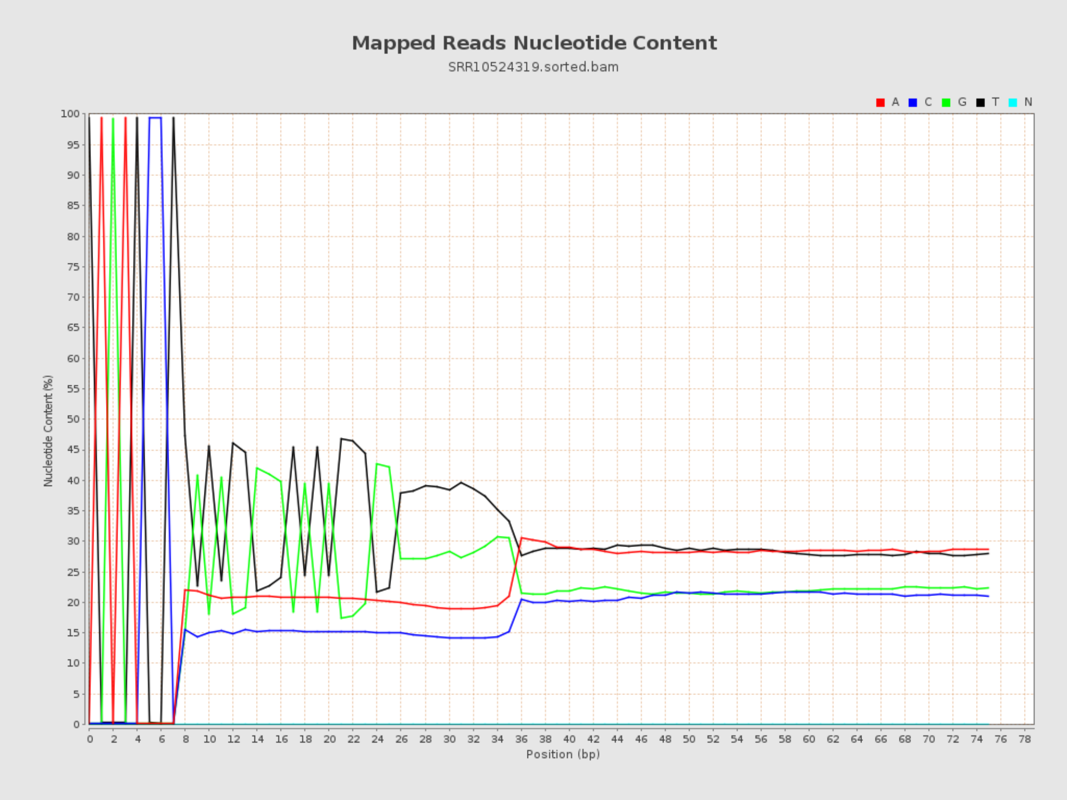
6. Results : Genome Fraction Coverage



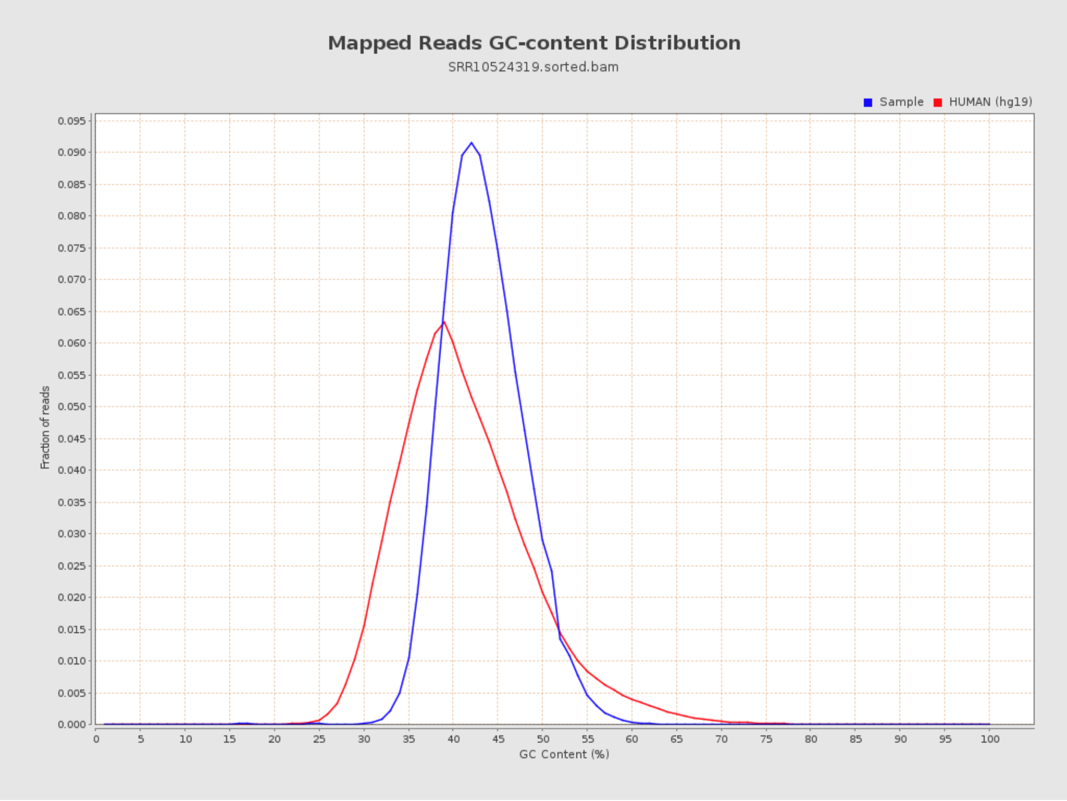
7. Results : Duplication Rate Histogram



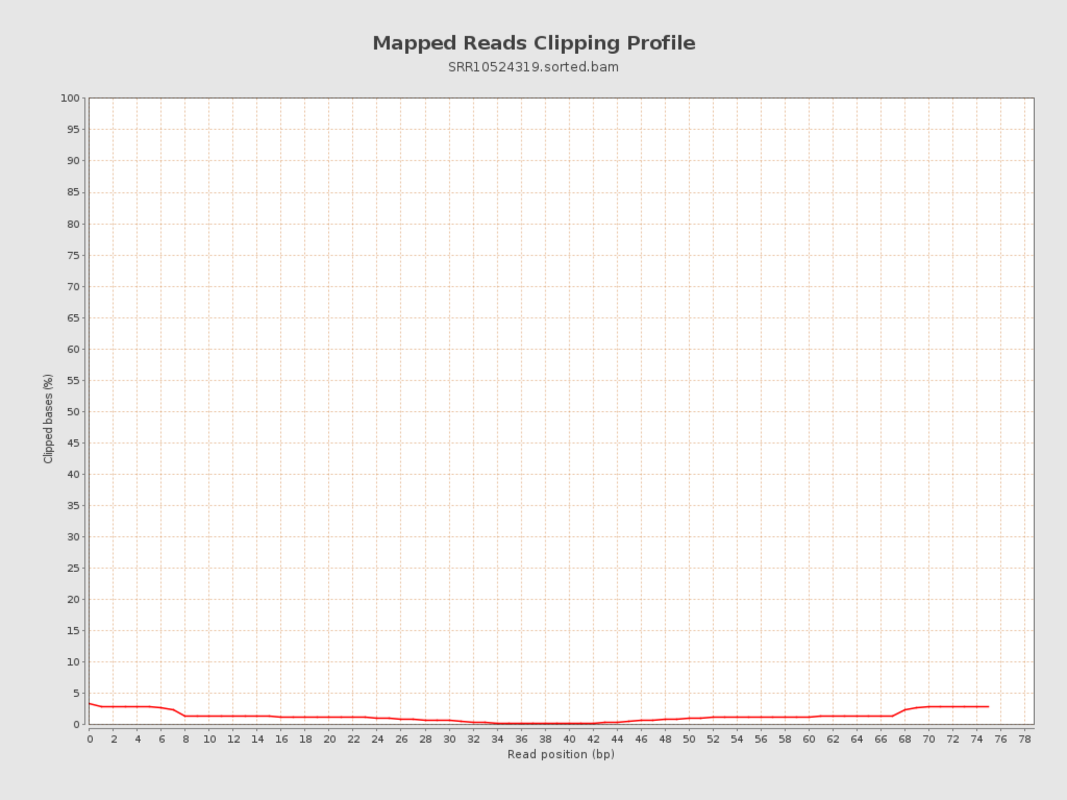
8. Results : Mapped Reads Nucleotide Content



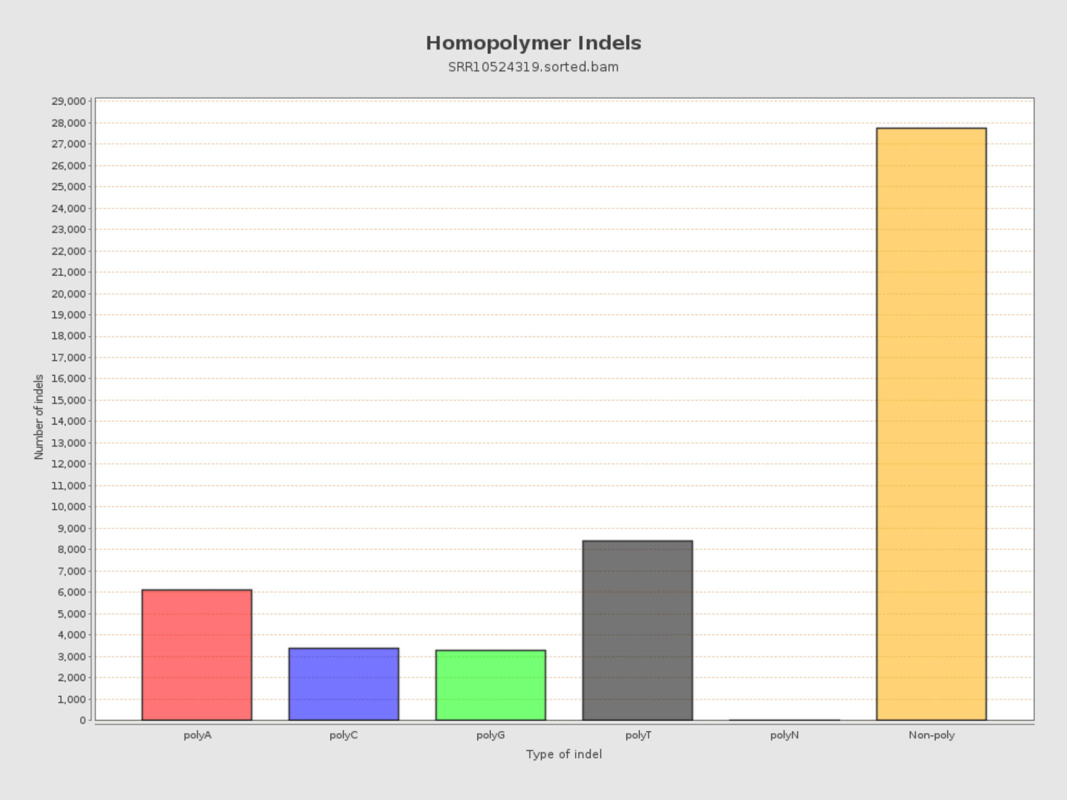
9. Results : Mapped Reads GC-content Distribution



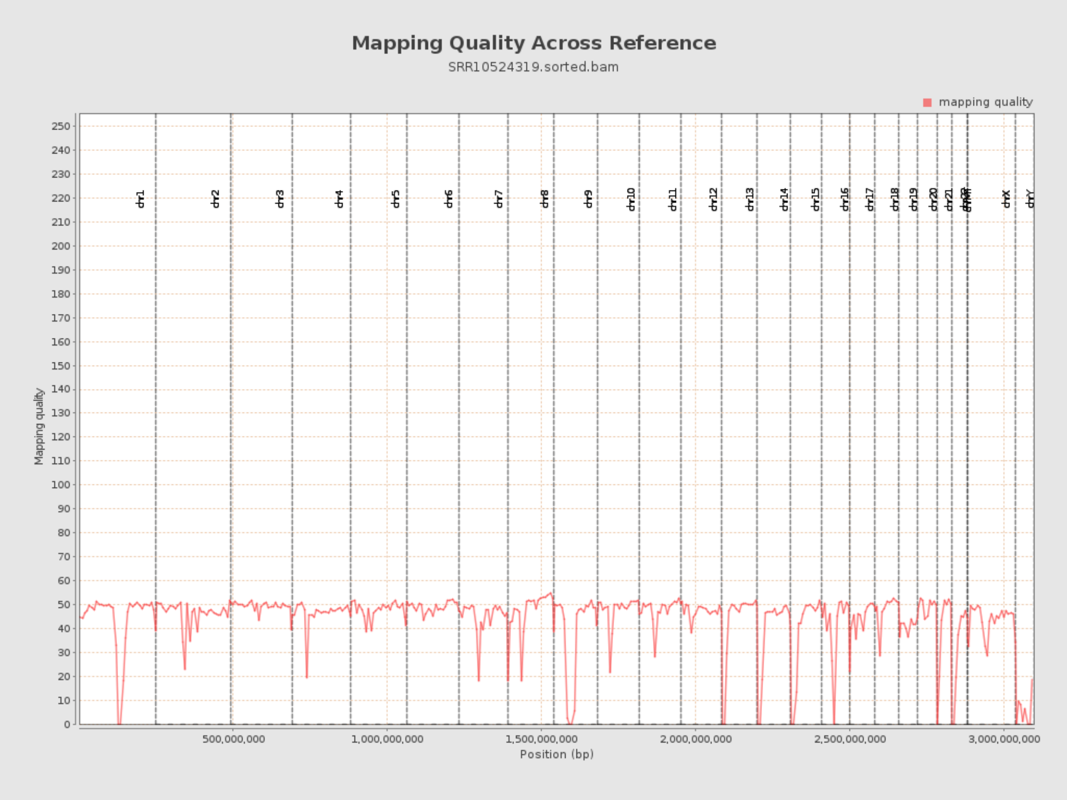
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram