Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:56:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524418.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_SRR10524418 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524418.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:56:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524418.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	709,611
Mapped reads	654,417 / 92.22%
Unmapped reads	55,194 / 7.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,905 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	22,554 / 3.18%
Duplication rate	2.61%
Clipped reads	655,191 / 92.33%

2.2. ACGT Content

Number/percentage of A's	8,881,845 / 23.13%
Number/percentage of C's	7,830,818 / 20.39%
Number/percentage of T's	12,350,765 / 32.16%
Number/percentage of G's	9,336,875 / 24.31%
Number/percentage of N's	4,393 / 0.01%
GC Percentage	44.7%

2.3. Coverage

Mean	0.0124

Standard Deviation	0.155

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

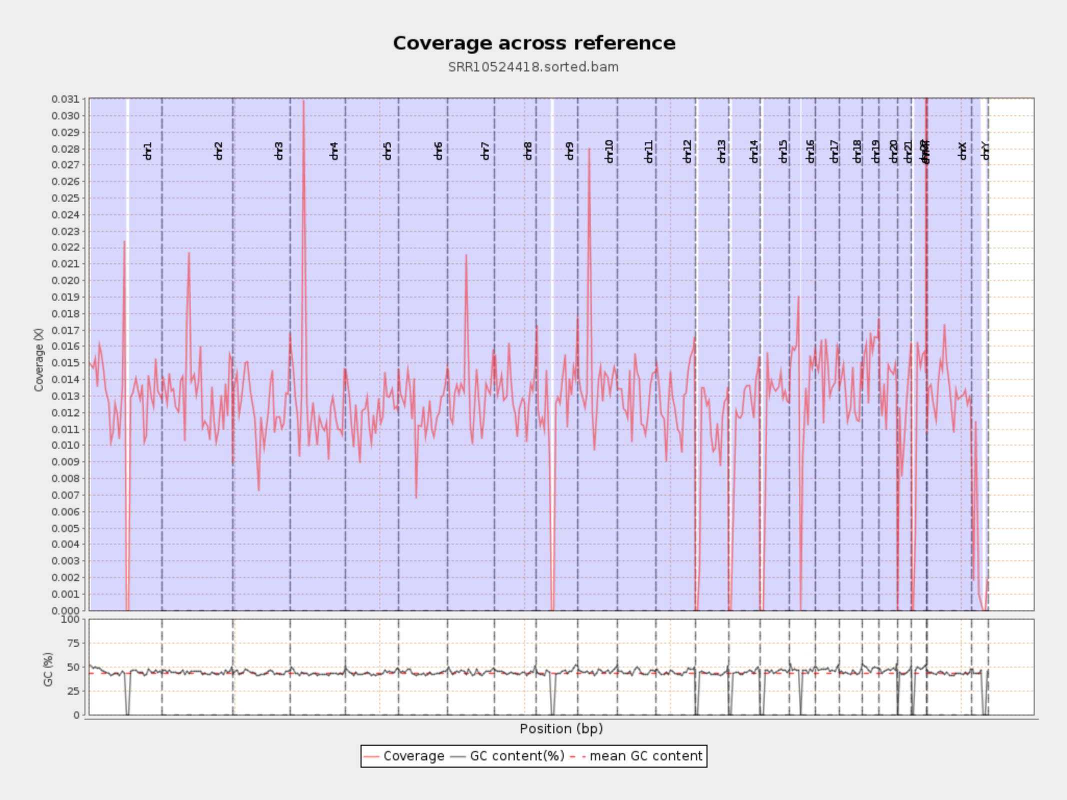
General error rate	0.52%
Mismatches	194,640
Insertions	2,891
Mapped reads with at least one insertion	0.44%
Deletions	6,395
Mapped reads with at least one deletion	0.97%
Homopolymer indels	40.91%

2.6. Chromosome stats

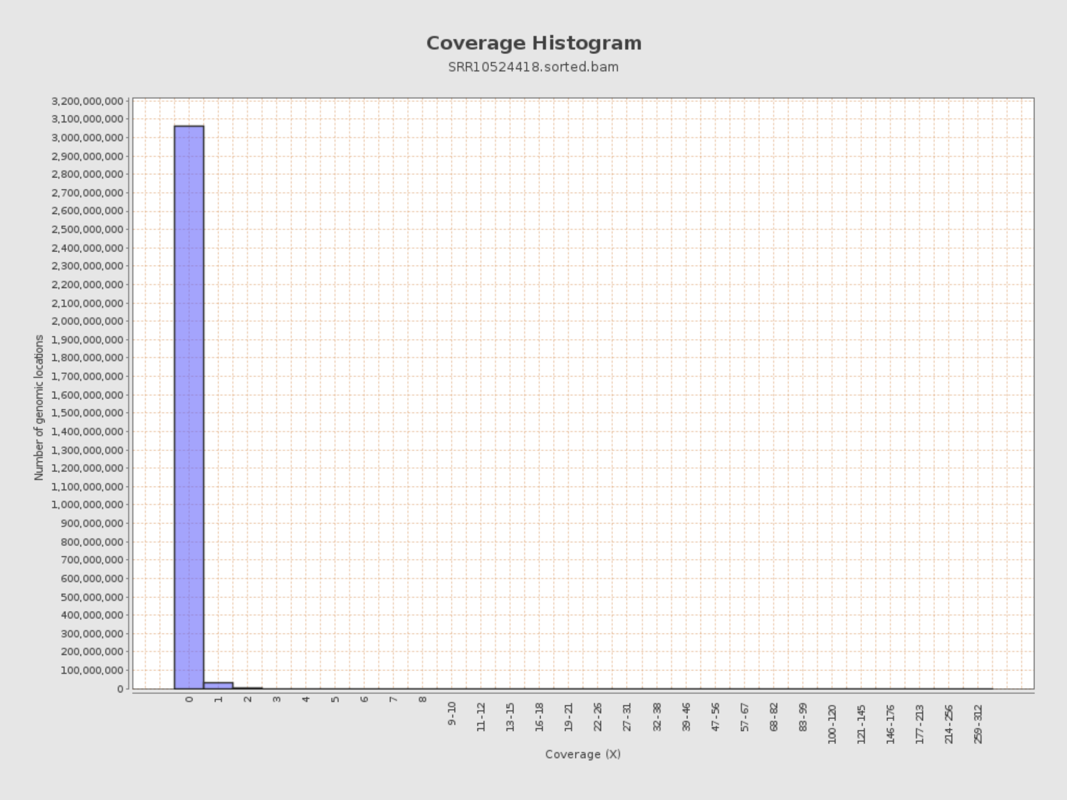
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3151746	0.0126	0.2559
chr2	243199373	3226982	0.0133	0.1965
chr3	198022430	2425332	0.0122	0.1177
chr4	191154276	2401454	0.0126	0.148
chr5	180915260	2172708	0.012	0.1162
chr6	171115067	2088030	0.0122	0.1216
chr7	159138663	2119738	0.0133	0.183

chr8	146364022	1919867	0.0131	0.1351
chr9	141213431	1615815	0.0114	0.1294
chr10	135534747	1909503	0.0141	0.1774
chr11	135006516	1743994	0.0129	0.1364
chr12	133851895	1715805	0.0128	0.1208
chr13	115169878	1127892	0.0098	0.1052
chr14	107349540	1145766	0.0107	0.1106
chr15	102531392	1144623	0.0112	0.1121
chr16	90354753	1211332	0.0134	0.1276
chr17	81195210	1183590	0.0146	0.1331
chr18	78077248	1018954	0.0131	0.1931
chr19	59128983	926607	0.0157	0.1888
chr20	63025520	858881	0.0136	0.1285
chr21	48129895	528816	0.011	0.1379
chr22	51304566	546770	0.0107	0.1103
chrMT	16571	8810	0.5317	0.7946
chrX	155270560	2063926	0.0133	0.1281
chrY	59373566	158289	0.0027	0.1073

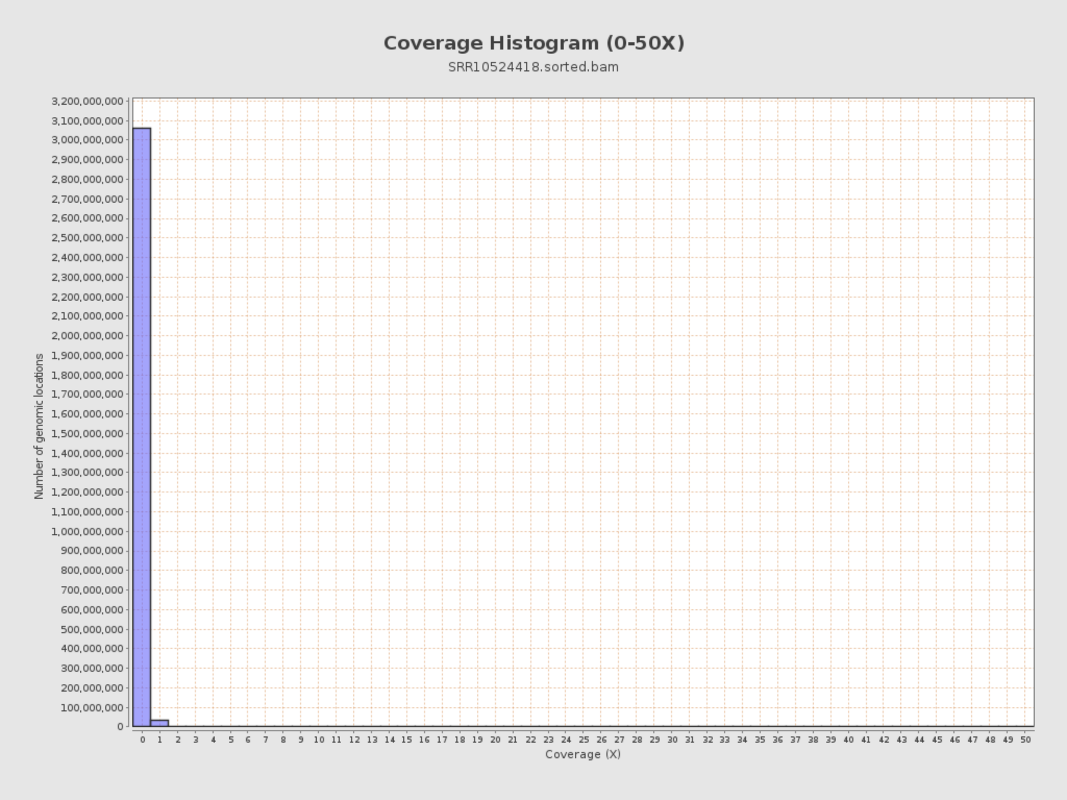
3. Results : Coverage across reference



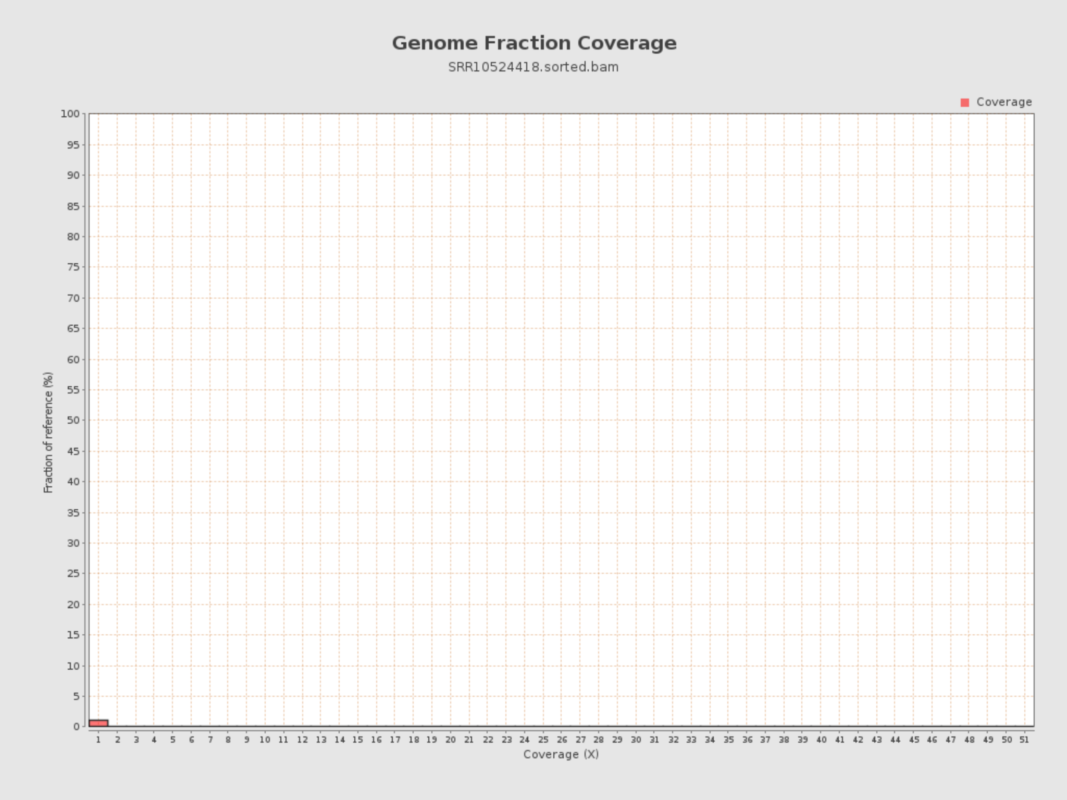
4. Results : Coverage Histogram



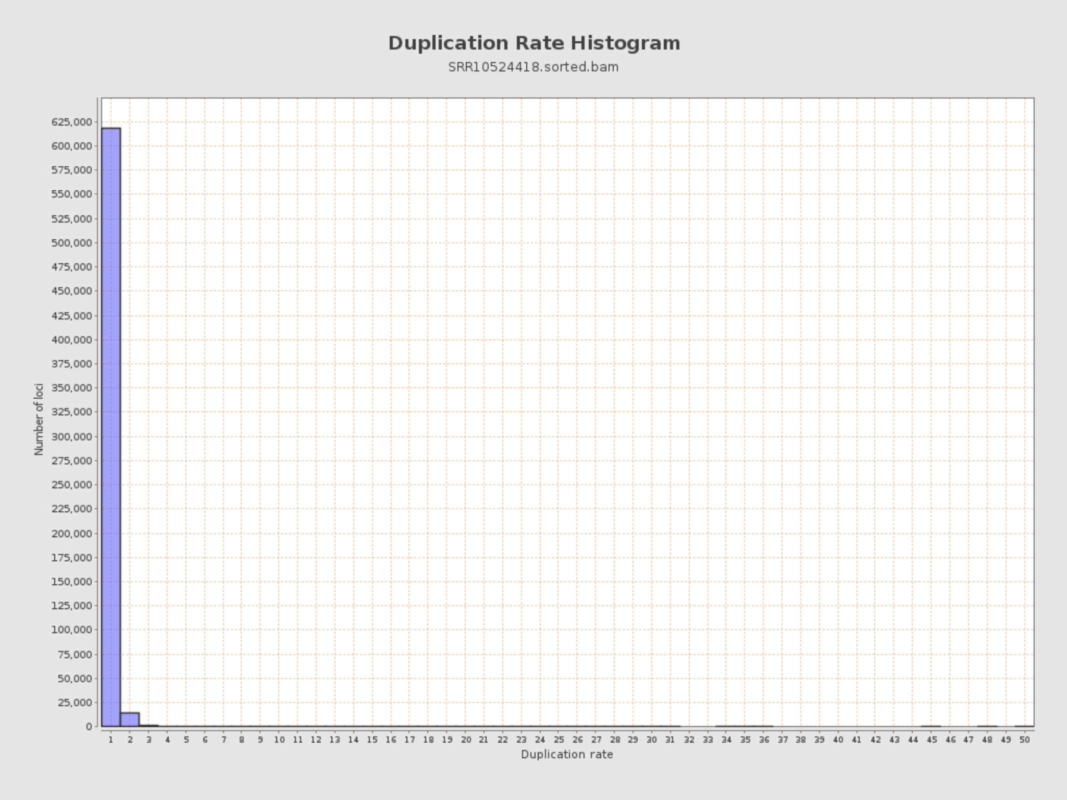
5. Results : Coverage Histogram (0-50X)



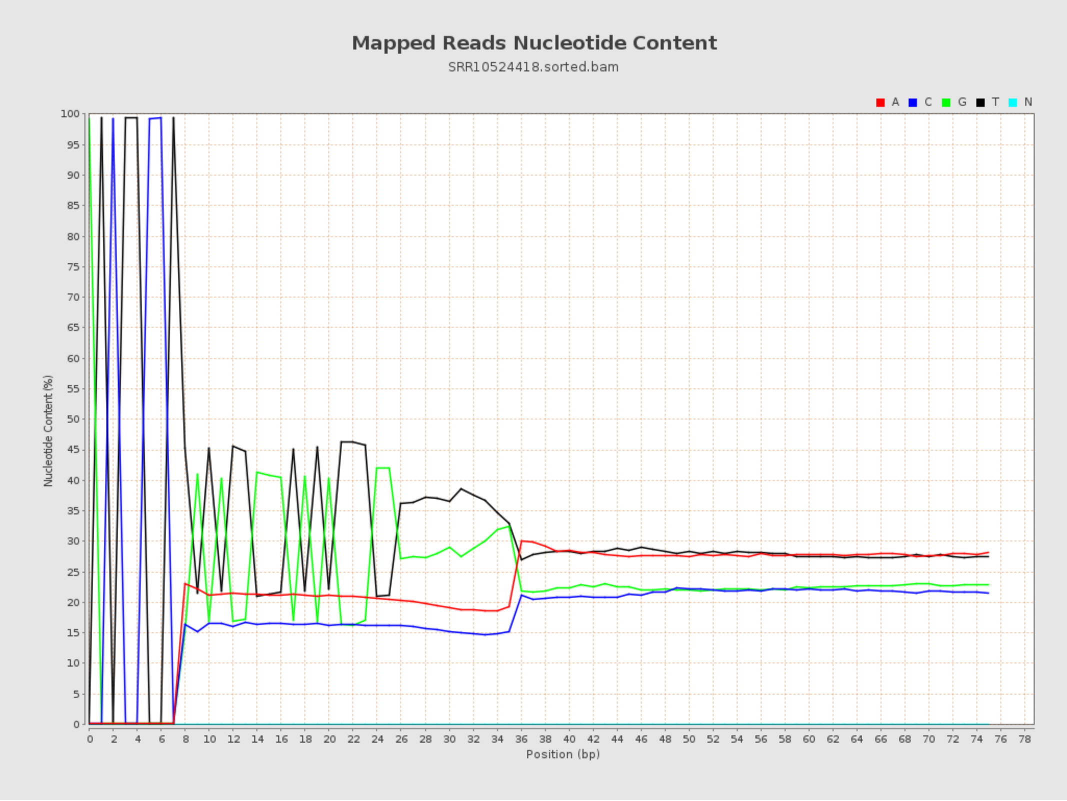
6. Results : Genome Fraction Coverage



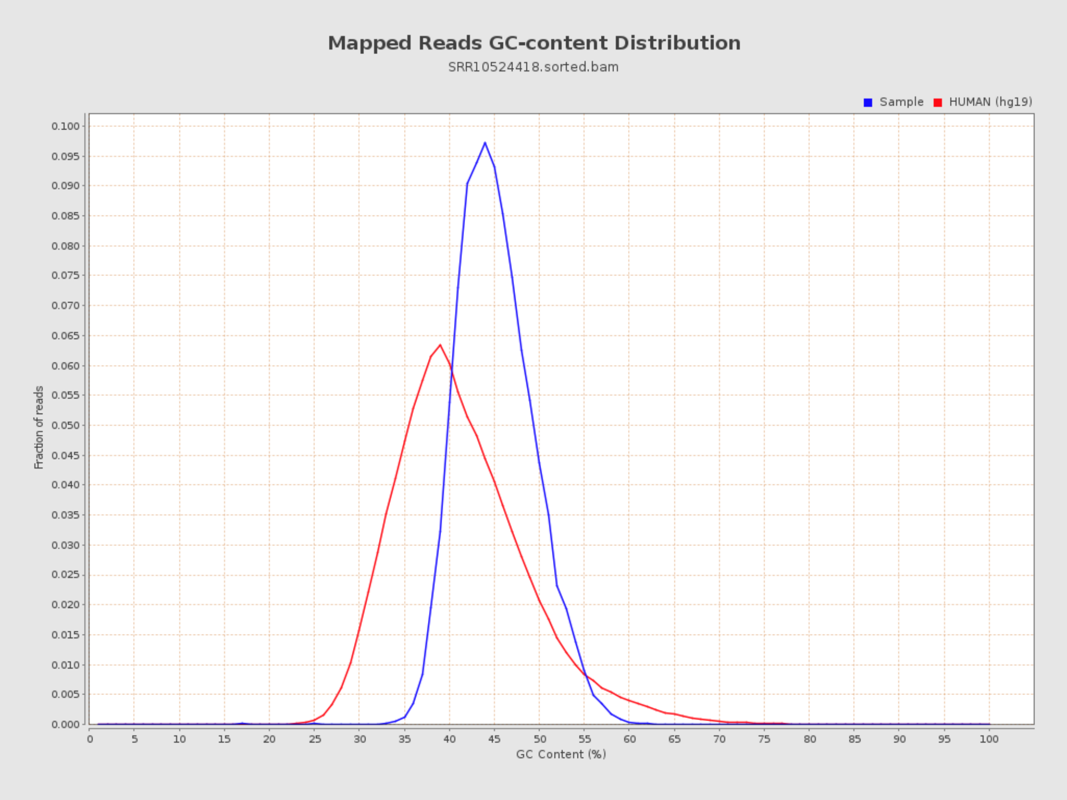
7. Results : Duplication Rate Histogram



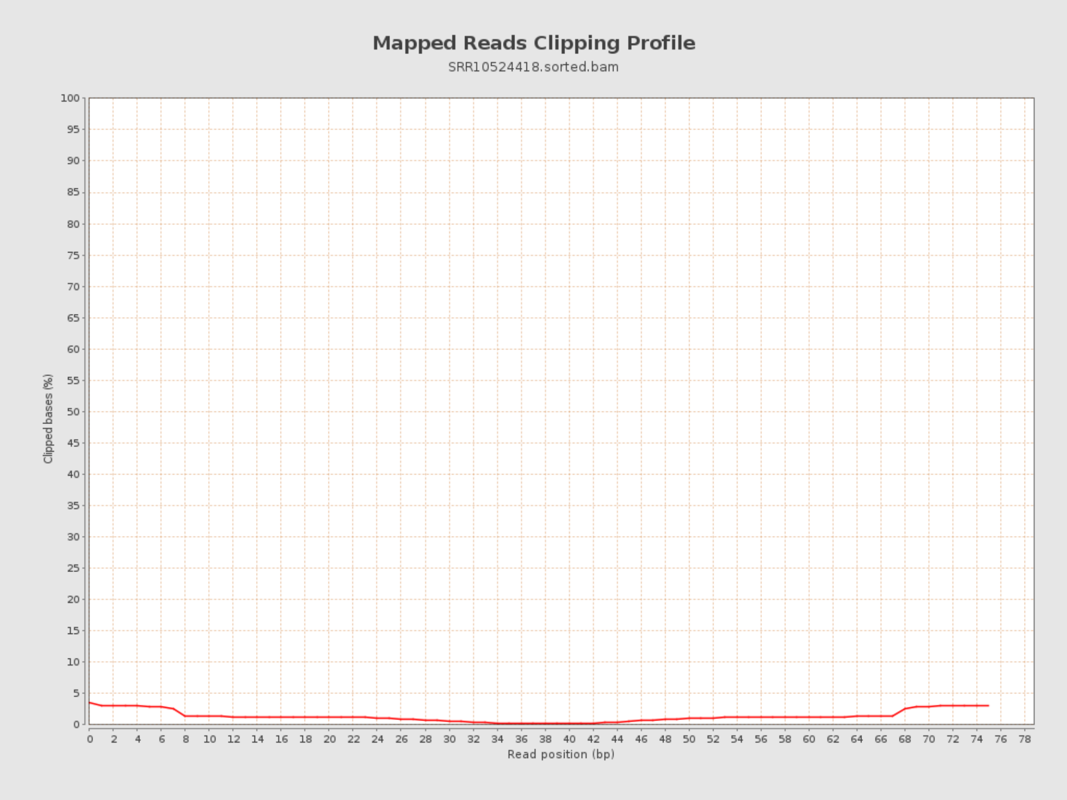
8. Results : Mapped Reads Nucleotide Content



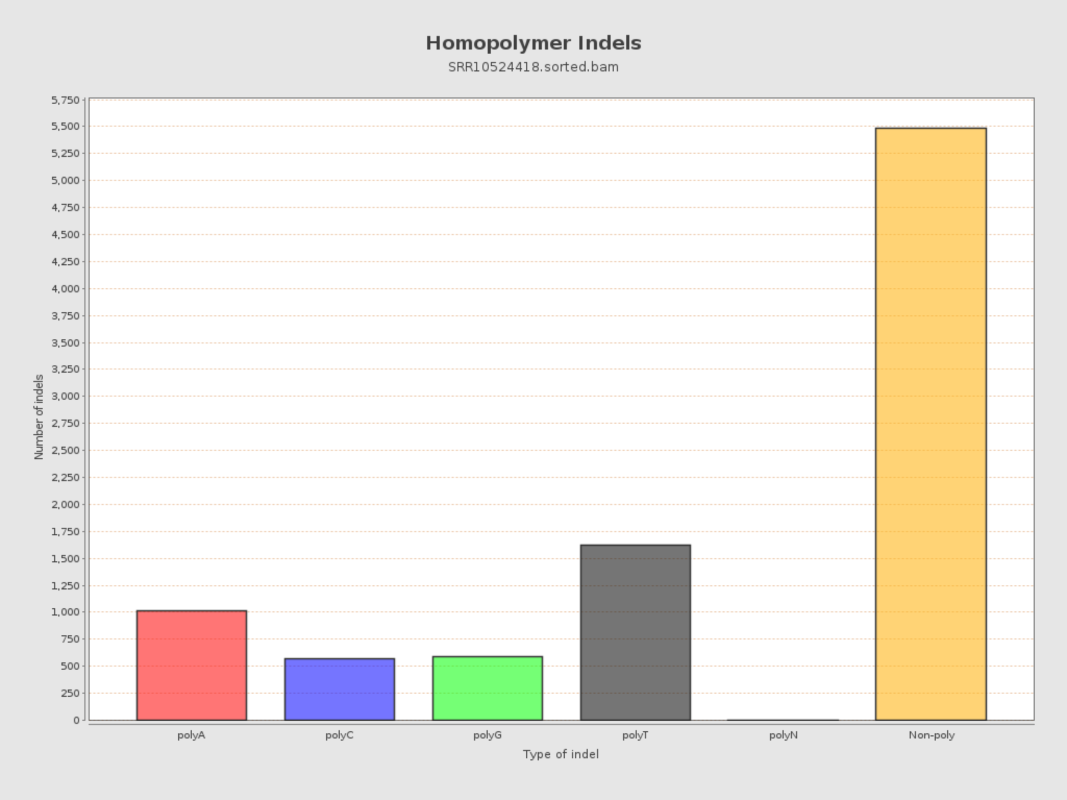
9. Results : Mapped Reads GC-content Distribution



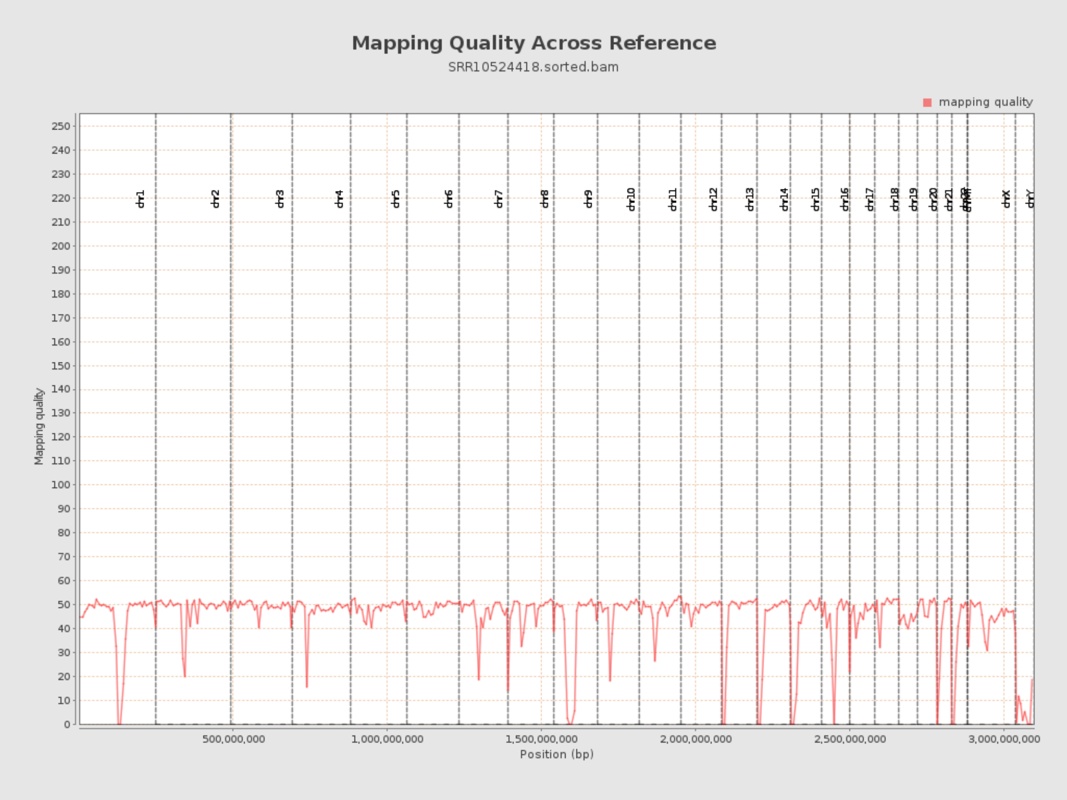
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram