Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 04:11:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524918.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_SRR10524918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524918.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 04:11:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	873,507
Mapped reads	807,788 / 92.48%
Unmapped reads	65,719 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,020 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	29,156 / 3.34%
Duplication rate	2.84%
Clipped reads	808,766 / 92.59%

2.2. ACGT Content

Number/percentage of A's	12,172,767 / 25.67%
Number/percentage of C's	9,383,108 / 19.78%
Number/percentage of T's	14,781,849 / 31.17%
Number/percentage of G's	11,088,719 / 23.38%
Number/percentage of N's	342 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1701

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

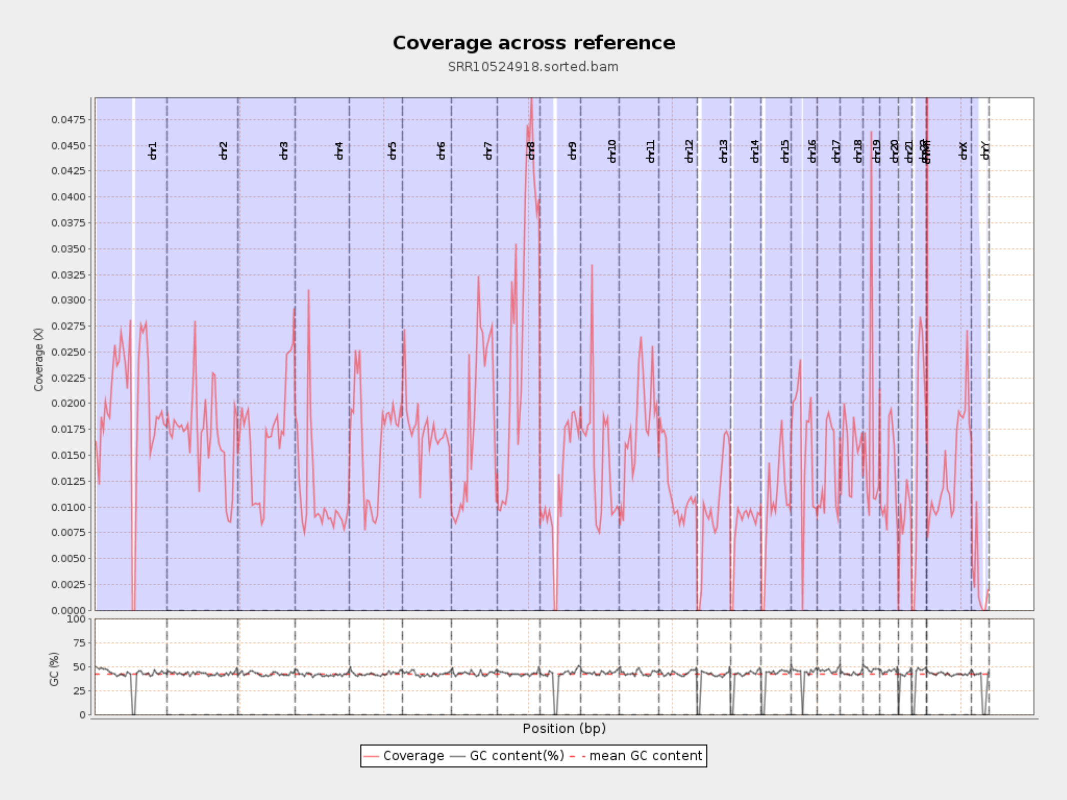
General error rate	0.52%
Mismatches	240,246
Insertions	3,461
Mapped reads with at least one insertion	0.43%
Deletions	9,372
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.96%

2.6. Chromosome stats

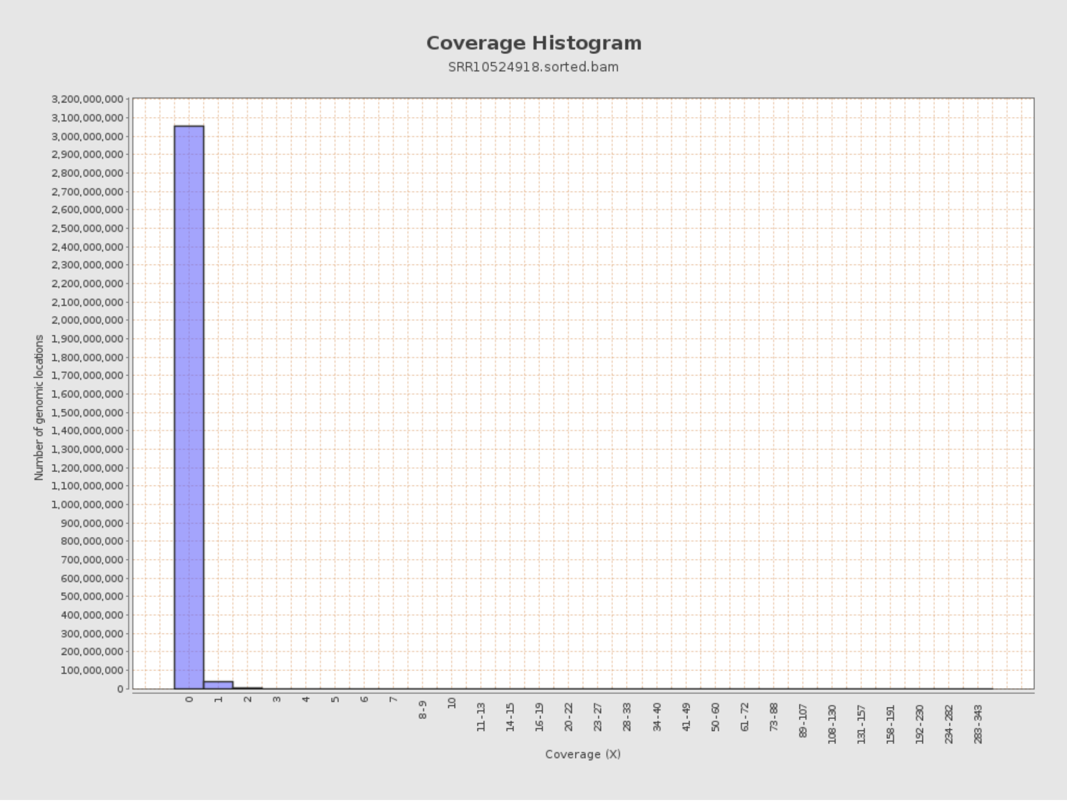
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4908720	0.0197	0.2847
chr2	243199373	4134383	0.017	0.2028
chr3	198022430	3378595	0.0171	0.1395
chr4	191154276	2156820	0.0113	0.1364
chr5	180915260	2985997	0.0165	0.1374
chr6	171115067	2992490	0.0175	0.1468
chr7	159138663	2903301	0.0182	0.2015

chr8	146364022	4126319	0.0282	0.2209
chr9	141213431	1706253	0.0121	0.1404
chr10	135534747	2027902	0.015	0.185
chr11	135006516	2407804	0.0178	0.1584
chr12	133851895	1577445	0.0118	0.1176
chr13	115169878	1119168	0.0097	0.1051
chr14	107349540	853018	0.0079	0.0982
chr15	102531392	1030390	0.01	0.1078
chr16	90354753	1451039	0.0161	0.1403
chr17	81195210	1093000	0.0135	0.1276
chr18	78077248	1215361	0.0156	0.2069
chr19	59128983	994199	0.0168	0.2051
chr20	63025520	786499	0.0125	0.123
chr21	48129895	429664	0.0089	0.1179
chr22	51304566	849055	0.0165	0.1384
chrMT	16571	17272	1.0423	1.2213
chrX	155270560	2147207	0.0138	0.1319
chrY	59373566	150686	0.0025	0.1103

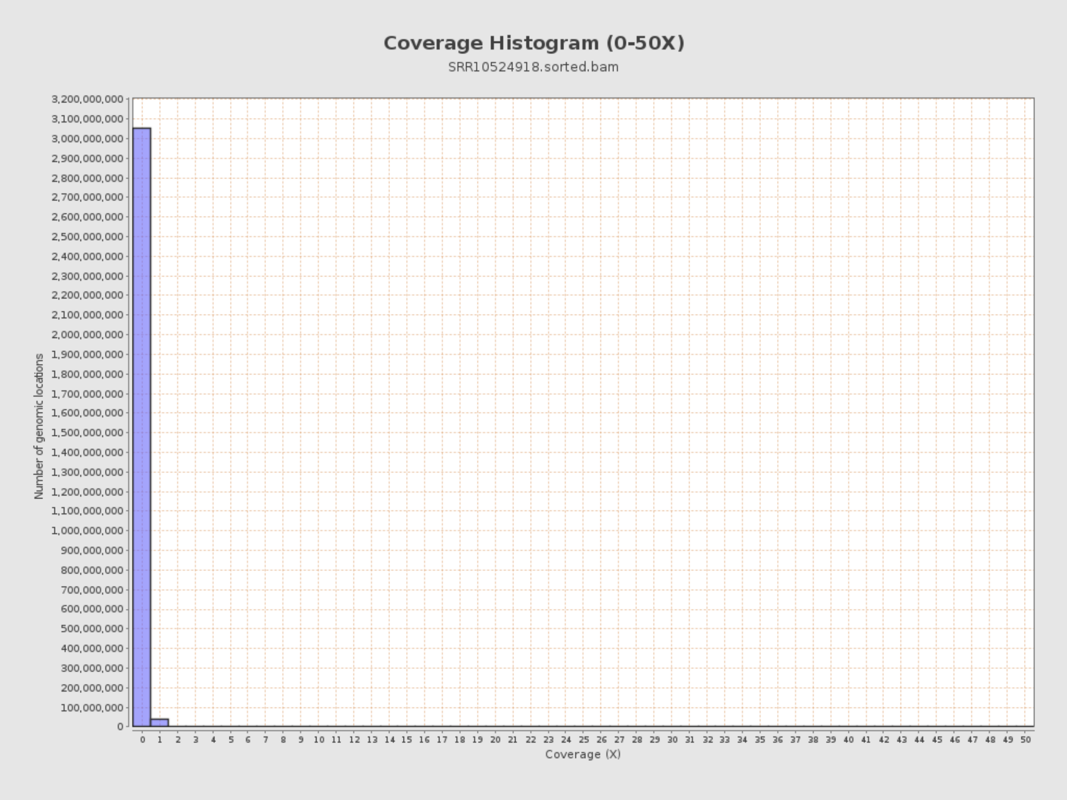
3. Results : Coverage across reference



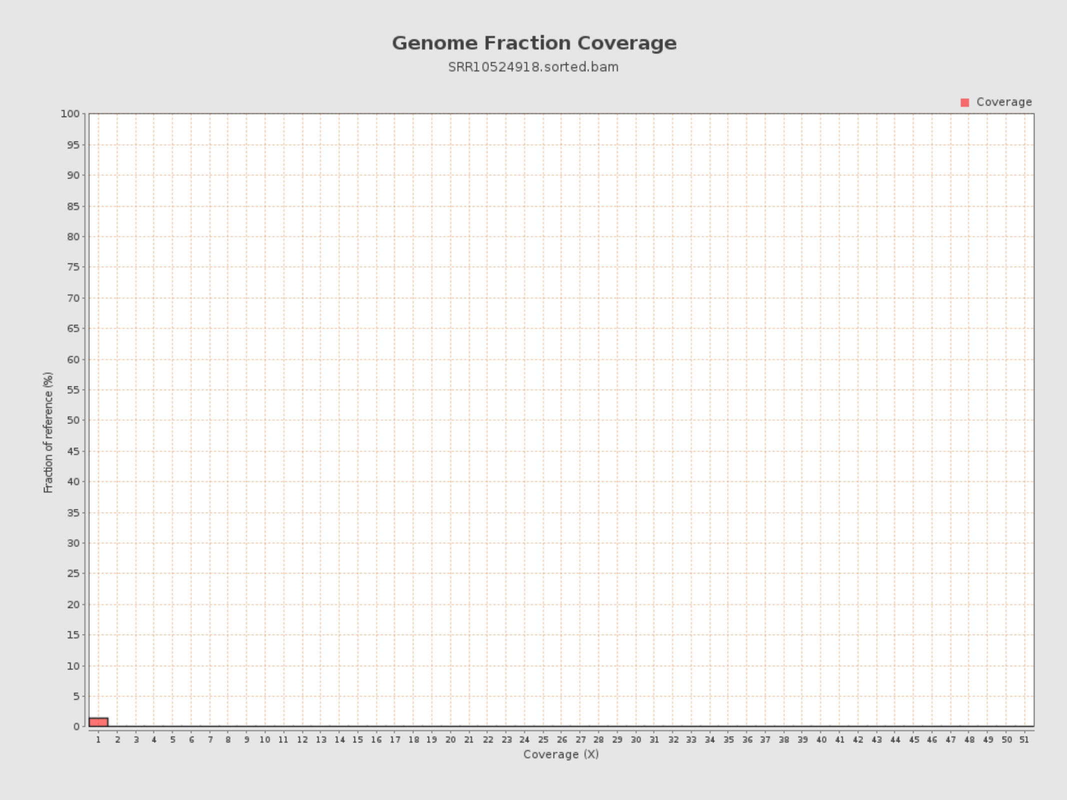
4. Results : Coverage Histogram



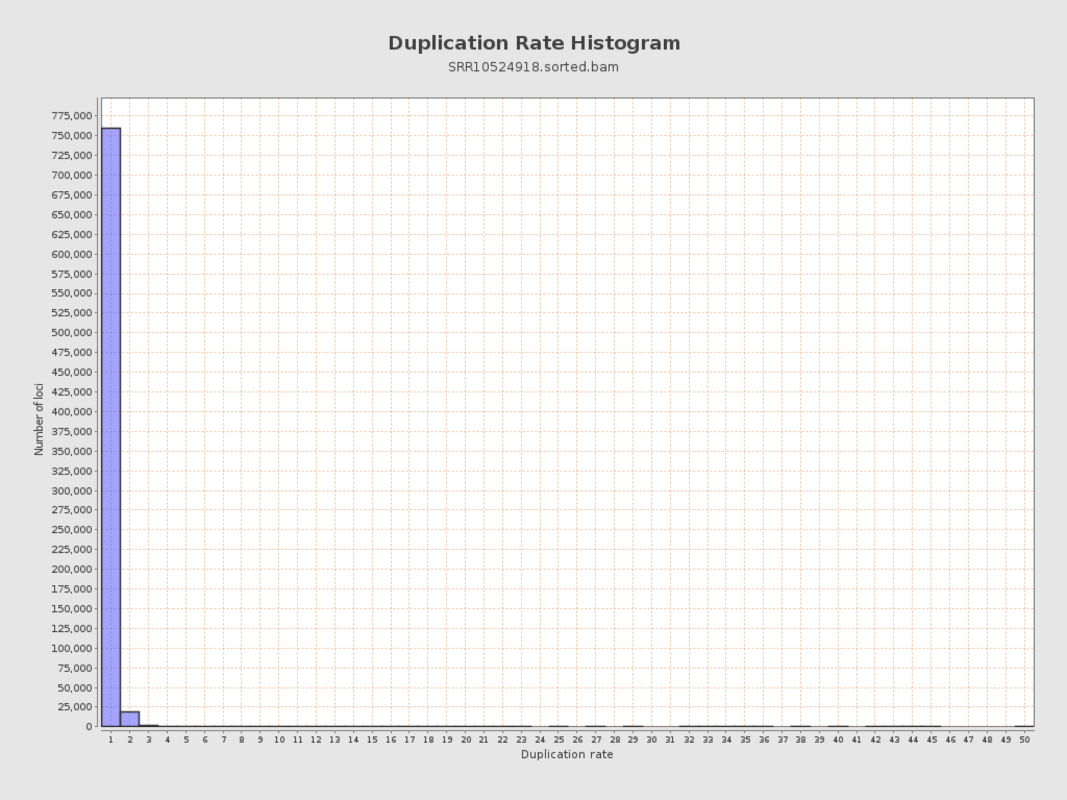
5. Results : Coverage Histogram (0-50X)



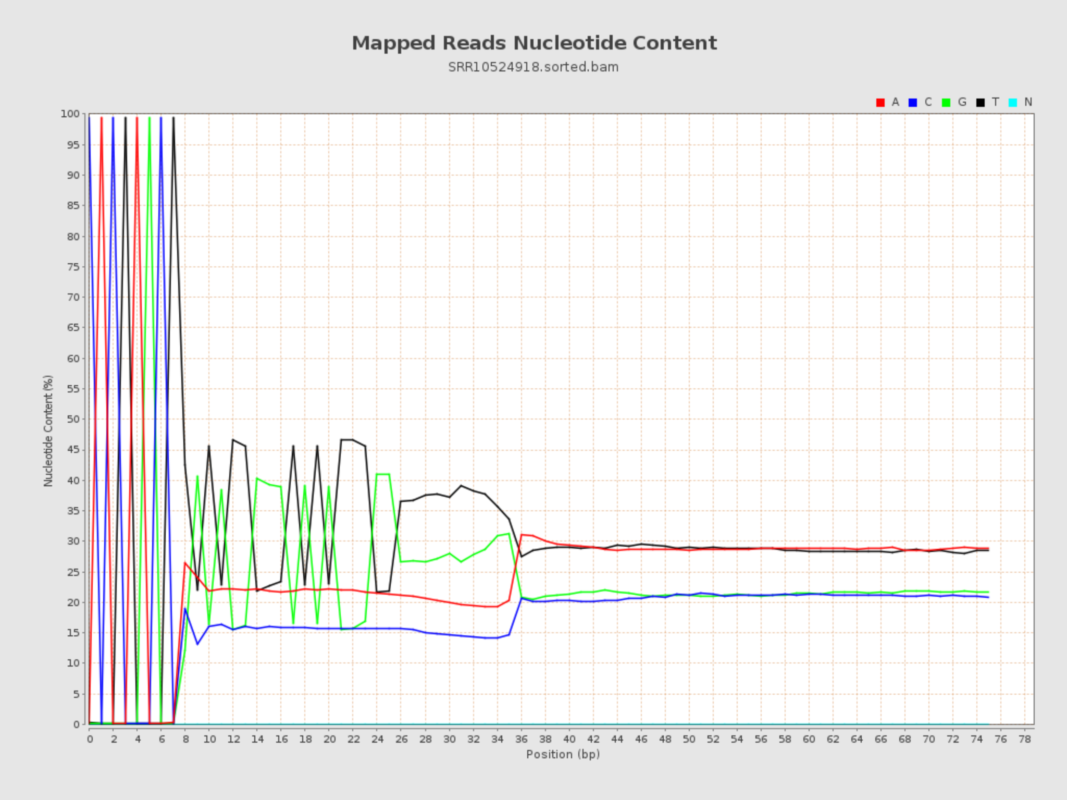
6. Results : Genome Fraction Coverage



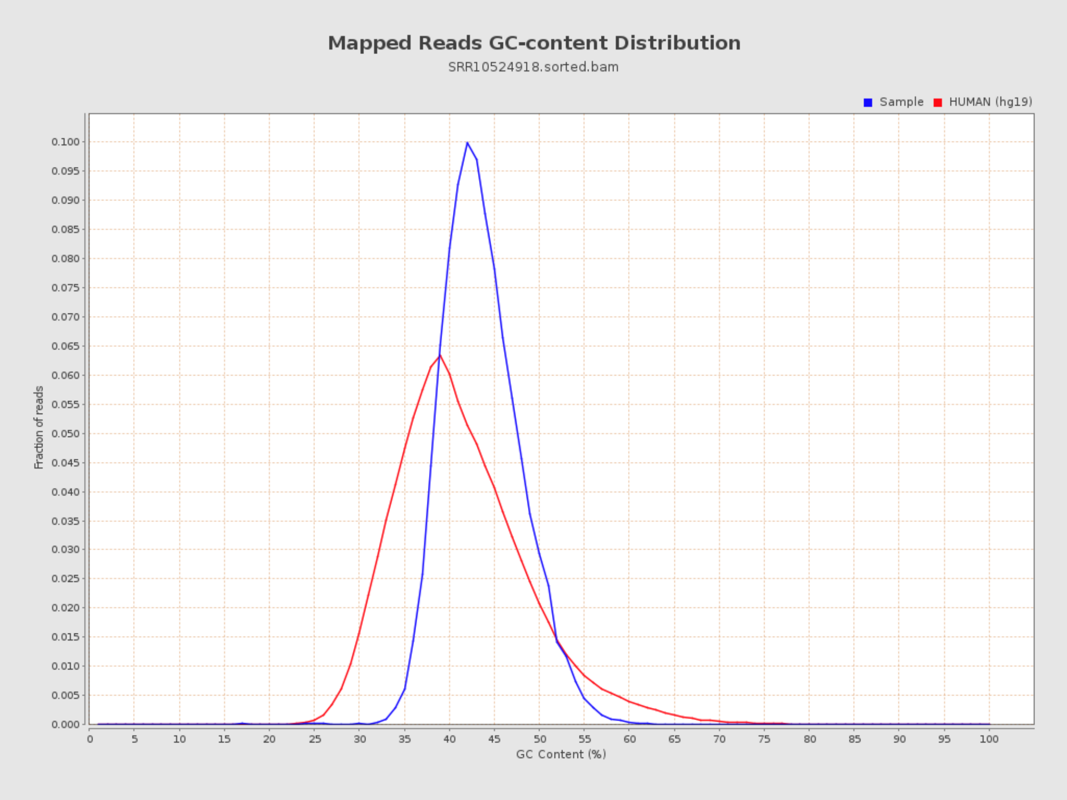
7. Results : Duplication Rate Histogram



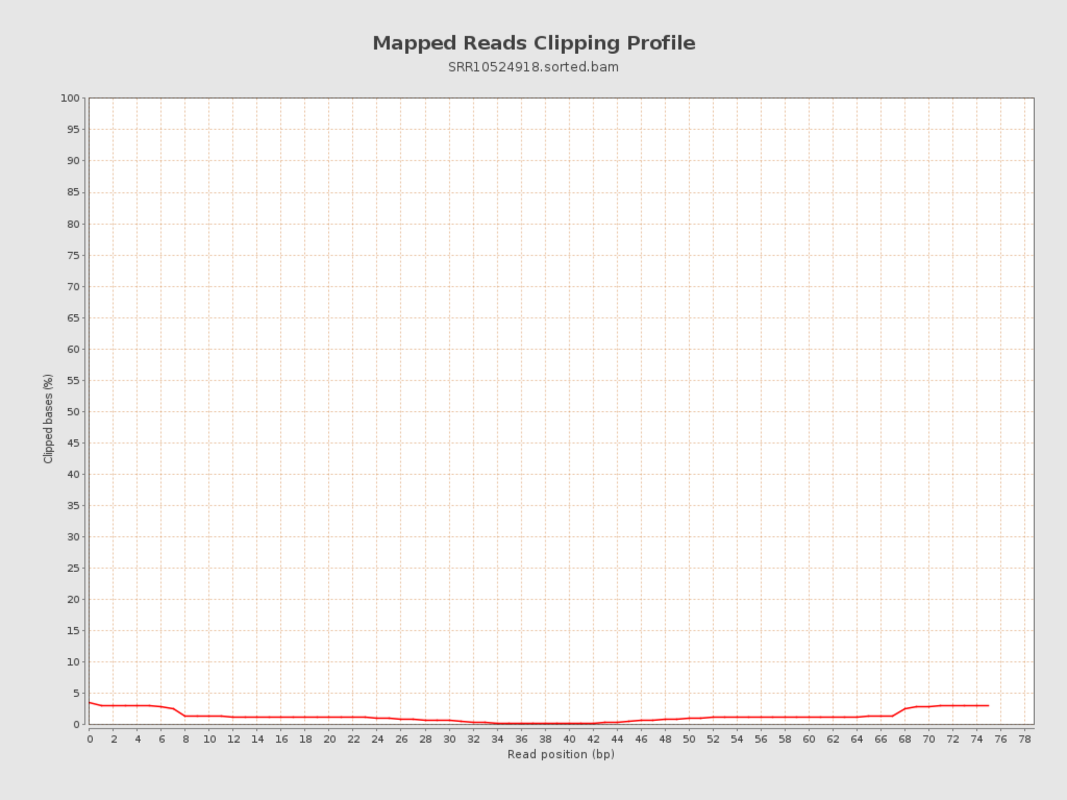
8. Results : Mapped Reads Nucleotide Content



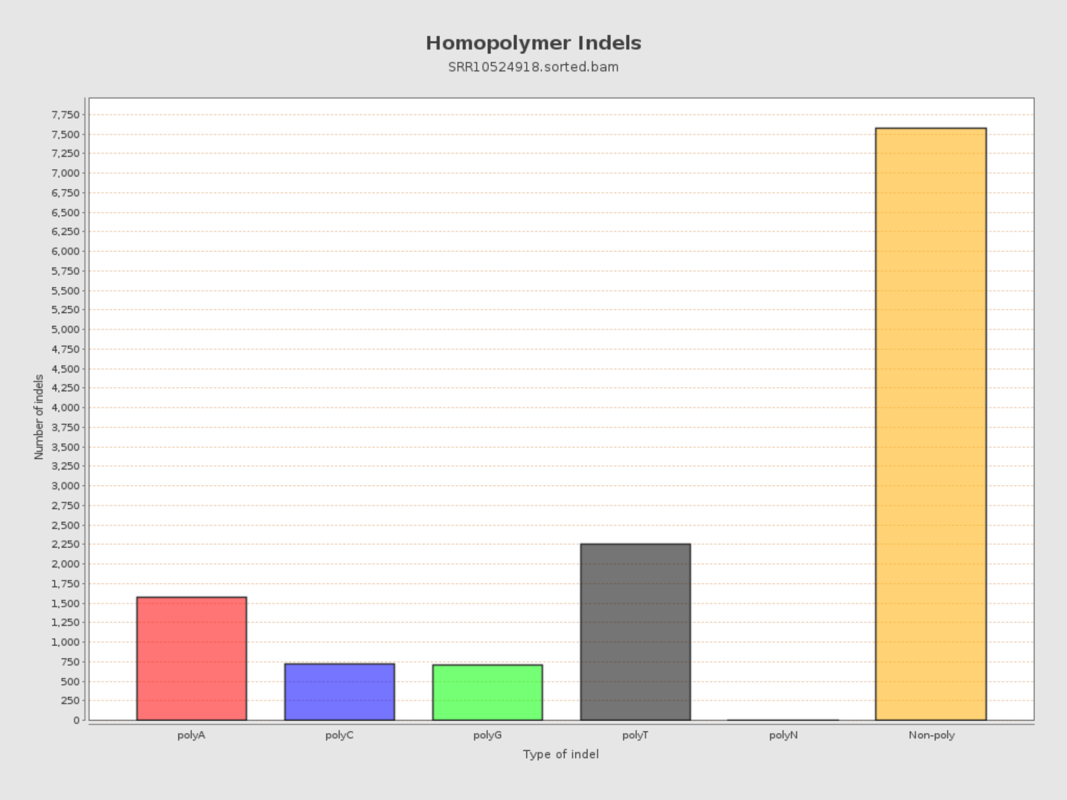
9. Results : Mapped Reads GC-content Distribution



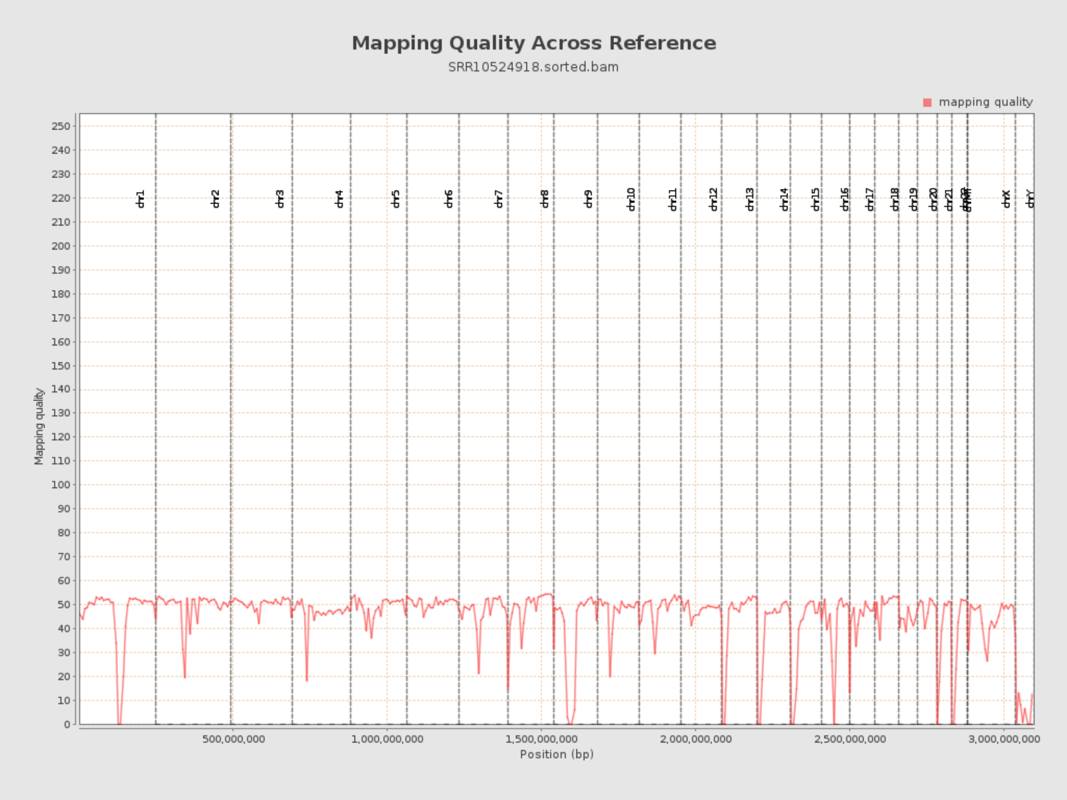
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram