Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 04:38:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524923.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_SRR10524923 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524923.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 04:38:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	771,952
Mapped reads	702,379 / 90.99%
Unmapped reads	69,573 / 9.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,940 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	34,831 / 4.51%
Duplication rate	4.05%
Clipped reads	704,964 / 91.32%

2.2. ACGT Content

Number/percentage of A's	9,715,603 / 24.16%
Number/percentage of C's	7,815,258 / 19.44%
Number/percentage of T's	12,659,564 / 31.49%
Number/percentage of G's	10,015,631 / 24.91%
Number/percentage of N's	309 / 0%
GC Percentage	44.35%

2.3. Coverage

Mean	0.013

Standard Deviation	0.1531

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

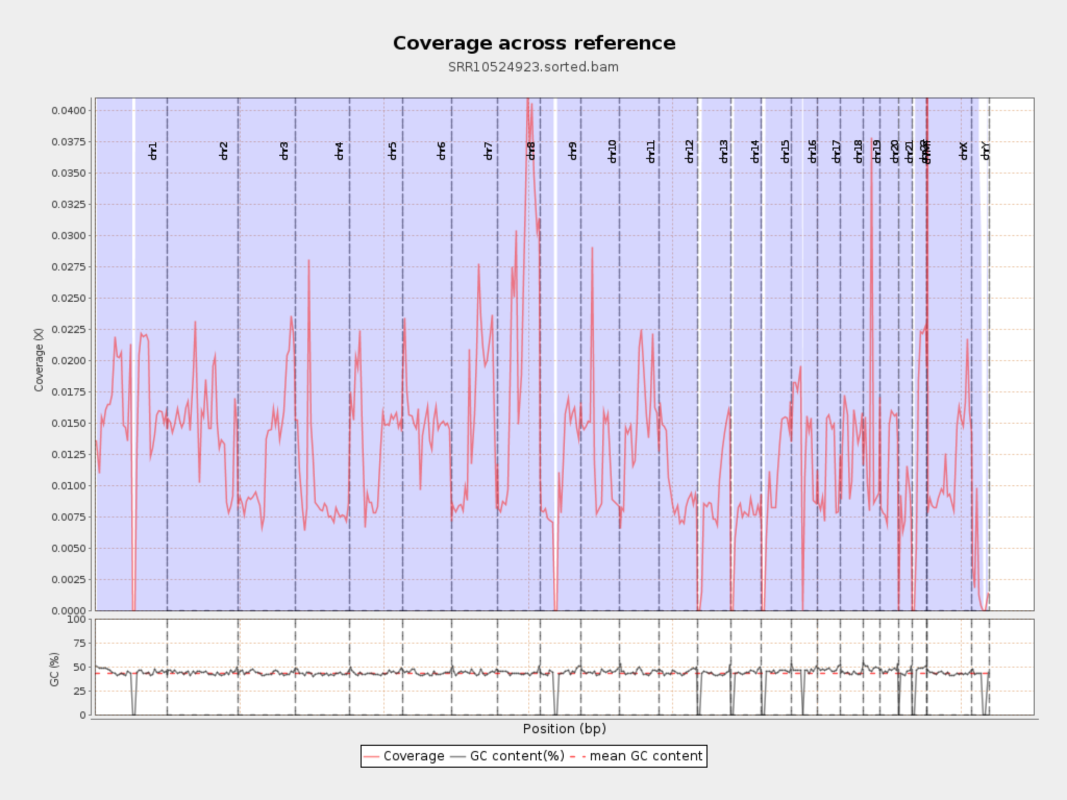
General error rate	0.56%
Mismatches	218,521
Insertions	2,351
Mapped reads with at least one insertion	0.33%
Deletions	9,054
Mapped reads with at least one deletion	1.28%
Homopolymer indels	42.42%

2.6. Chromosome stats

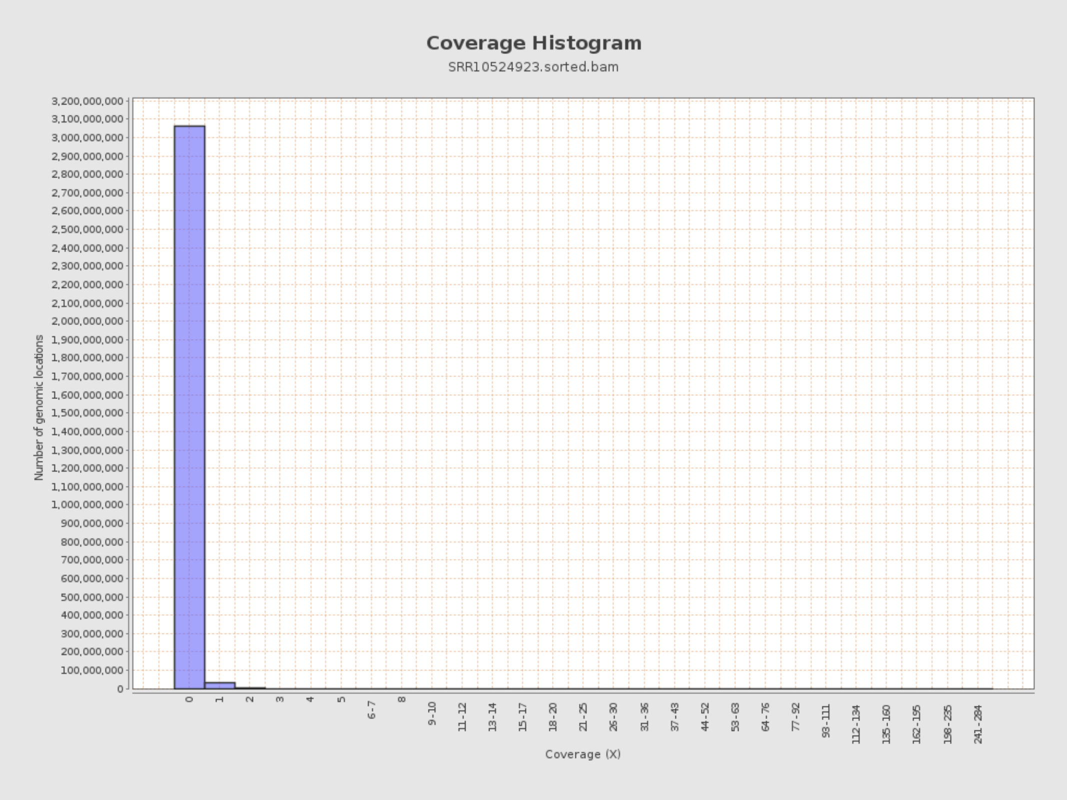
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3951713	0.0159	0.2216
chr2	243199373	3620068	0.0149	0.1963
chr3	198022430	2557211	0.0129	0.1264
chr4	191154276	1873793	0.0098	0.1281
chr5	180915260	2493147	0.0138	0.1294
chr6	171115067	2602033	0.0152	0.1416
chr7	159138663	2434002	0.0153	0.1768

chr8	146364022	3481622	0.0238	0.2018
chr9	141213431	1453104	0.0103	0.1262
chr10	135534747	1766333	0.013	0.178
chr11	135006516	2057813	0.0152	0.1468
chr12	133851895	1339625	0.01	0.113
chr13	115169878	1005580	0.0087	0.1035
chr14	107349540	733926	0.0068	0.0924
chr15	102531392	1030248	0.01	0.1109
chr16	90354753	1207763	0.0134	0.133
chr17	81195210	894638	0.011	0.1187
chr18	78077248	1067192	0.0137	0.1807
chr19	59128983	830326	0.014	0.178
chr20	63025520	744856	0.0118	0.1241
chr21	48129895	373200	0.0078	0.1122
chr22	51304566	743681	0.0145	0.1342
chrMT	16571	4202	0.2536	0.6229
chrX	155270560	1823644	0.0117	0.1247
chrY	59373566	131872	0.0022	0.0967

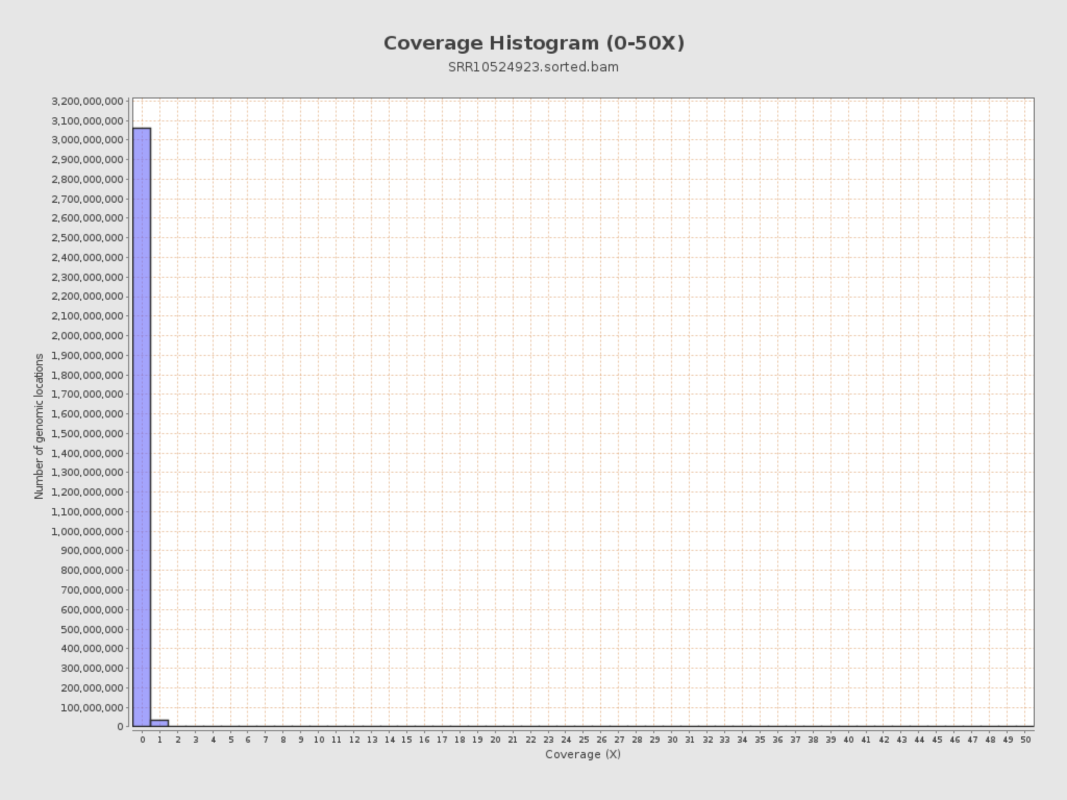
3. Results : Coverage across reference



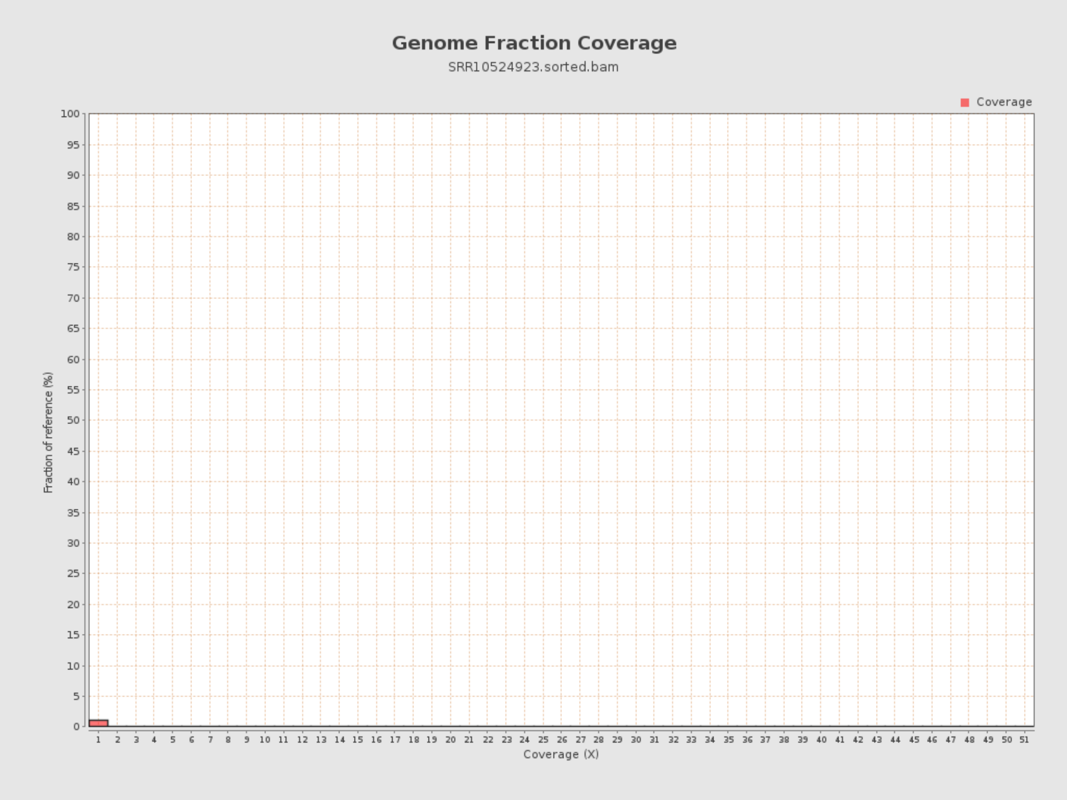
4. Results : Coverage Histogram



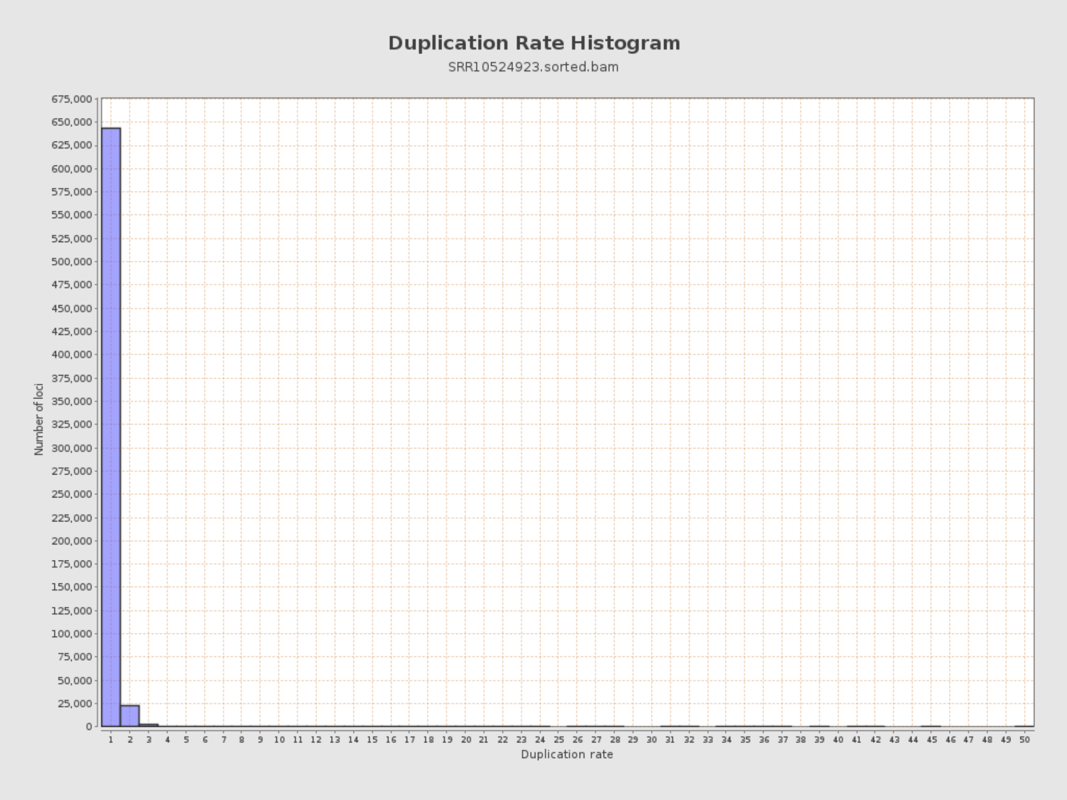
5. Results : Coverage Histogram (0-50X)



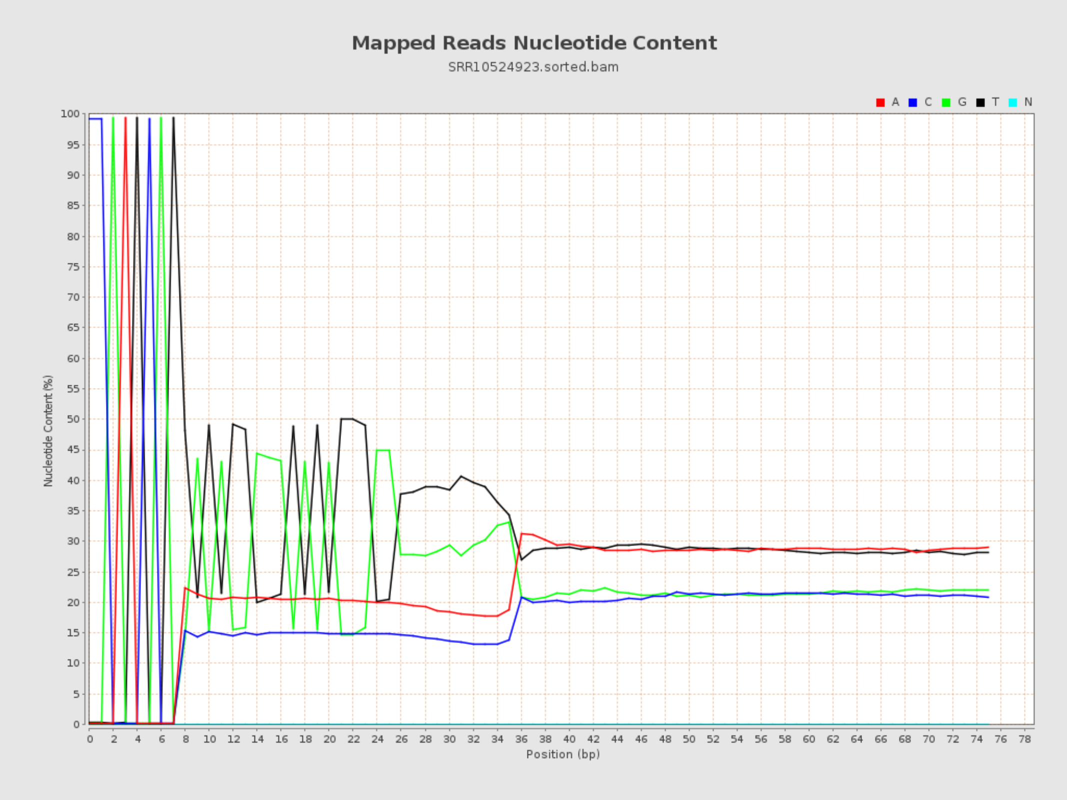
6. Results : Genome Fraction Coverage



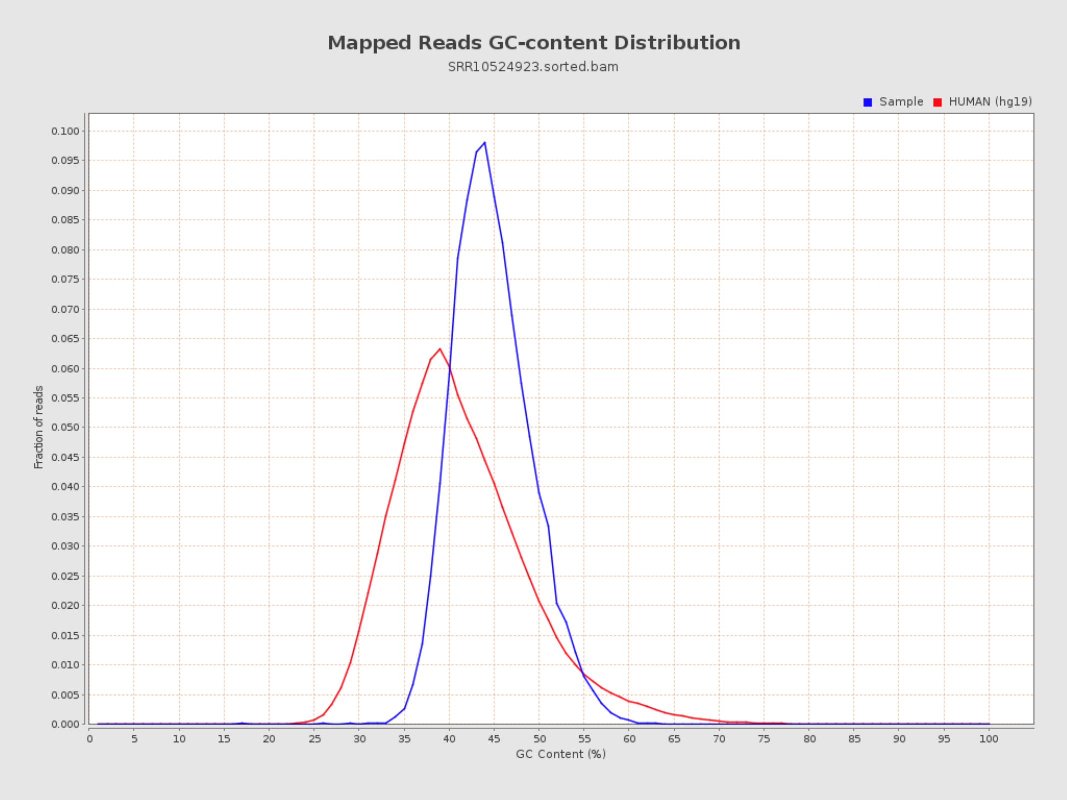
7. Results : Duplication Rate Histogram



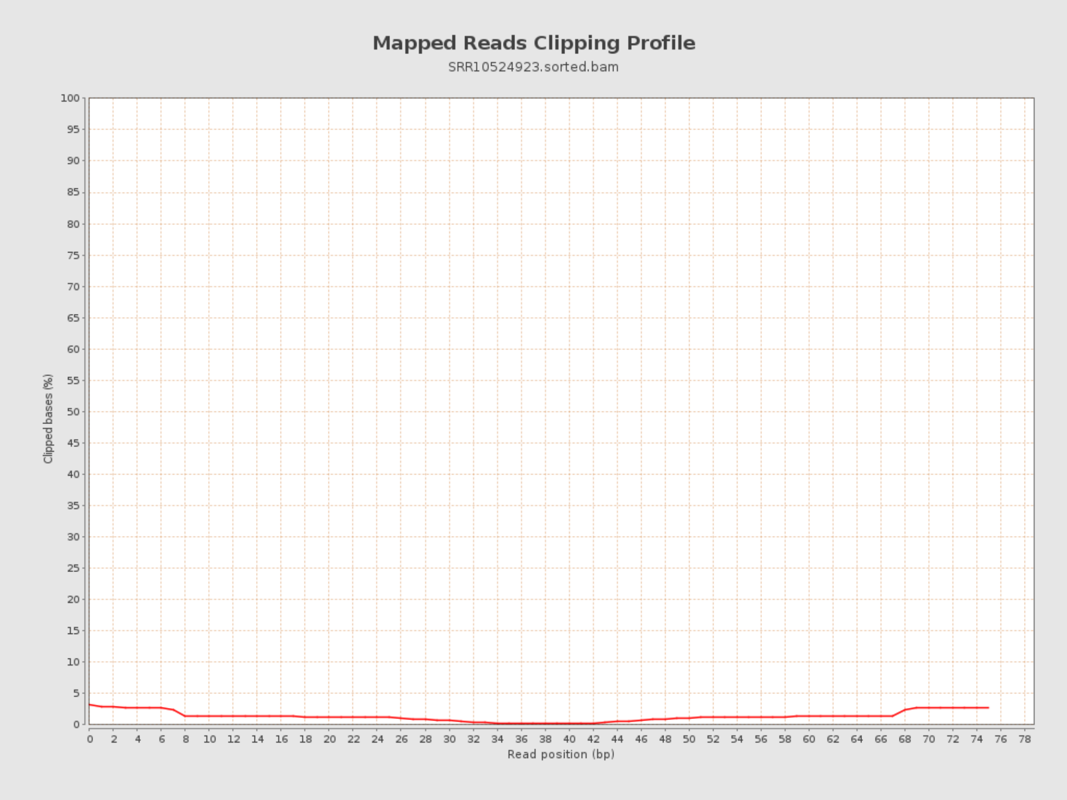
8. Results : Mapped Reads Nucleotide Content



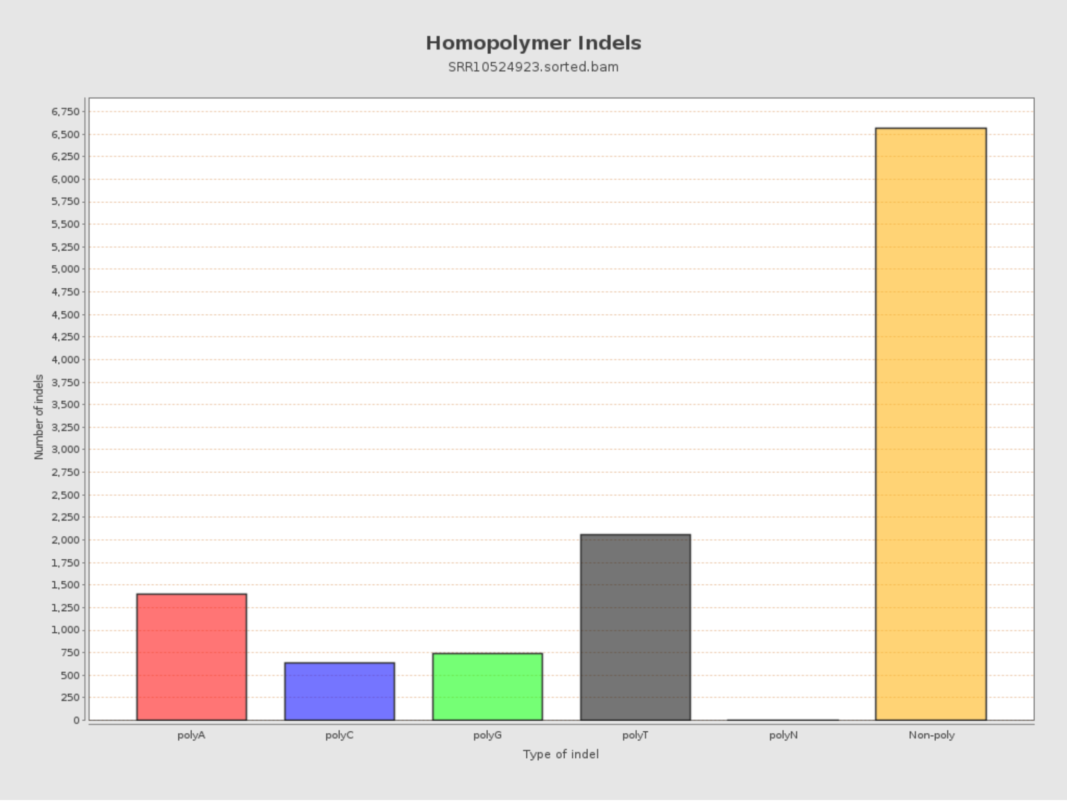
9. Results : Mapped Reads GC-content Distribution



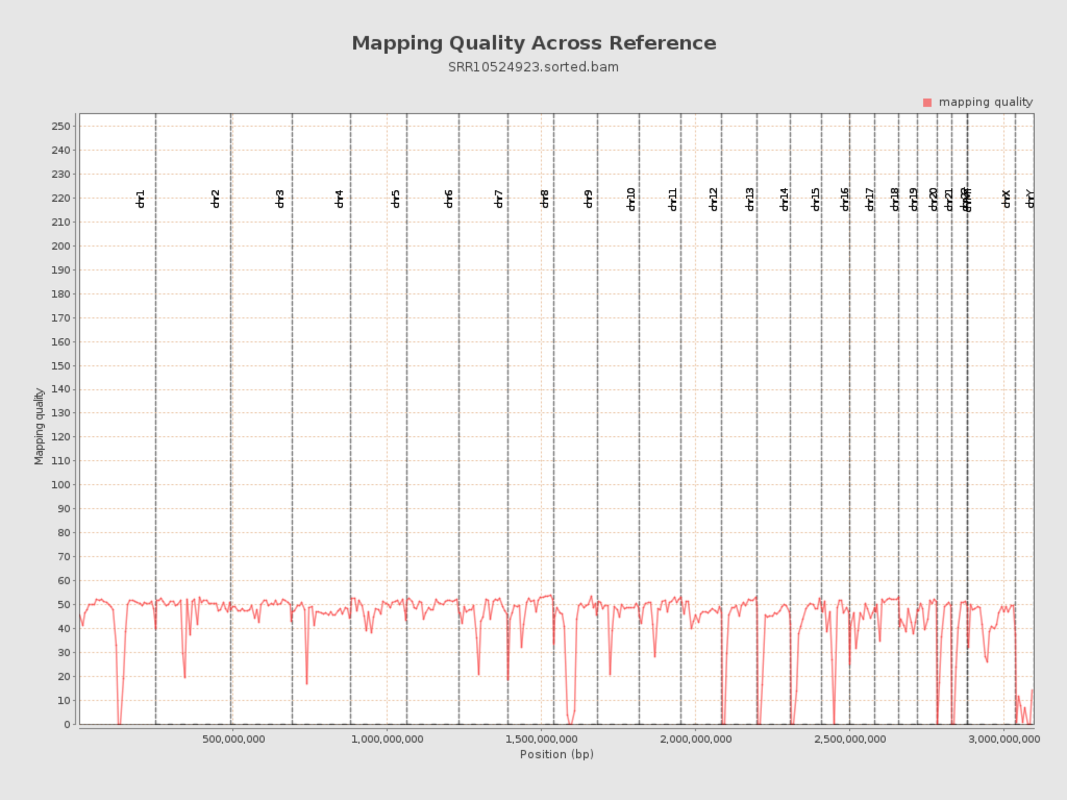
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram