Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:54:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524983.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_SRR10524983 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524983.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:54:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,386,843
Mapped reads	1,289,887 / 93.01%
Unmapped reads	96,956 / 6.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,125 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	43,491 / 3.14%
Duplication rate	2.57%
Clipped reads	1,289,275 / 92.96%

2.2. ACGT Content

Number/percentage of A's	18,791,212 / 24.95%
Number/percentage of C's	13,974,873 / 18.55%
Number/percentage of T's	24,154,597 / 32.07%
Number/percentage of G's	18,399,249 / 24.43%
Number/percentage of N's	906 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2229

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

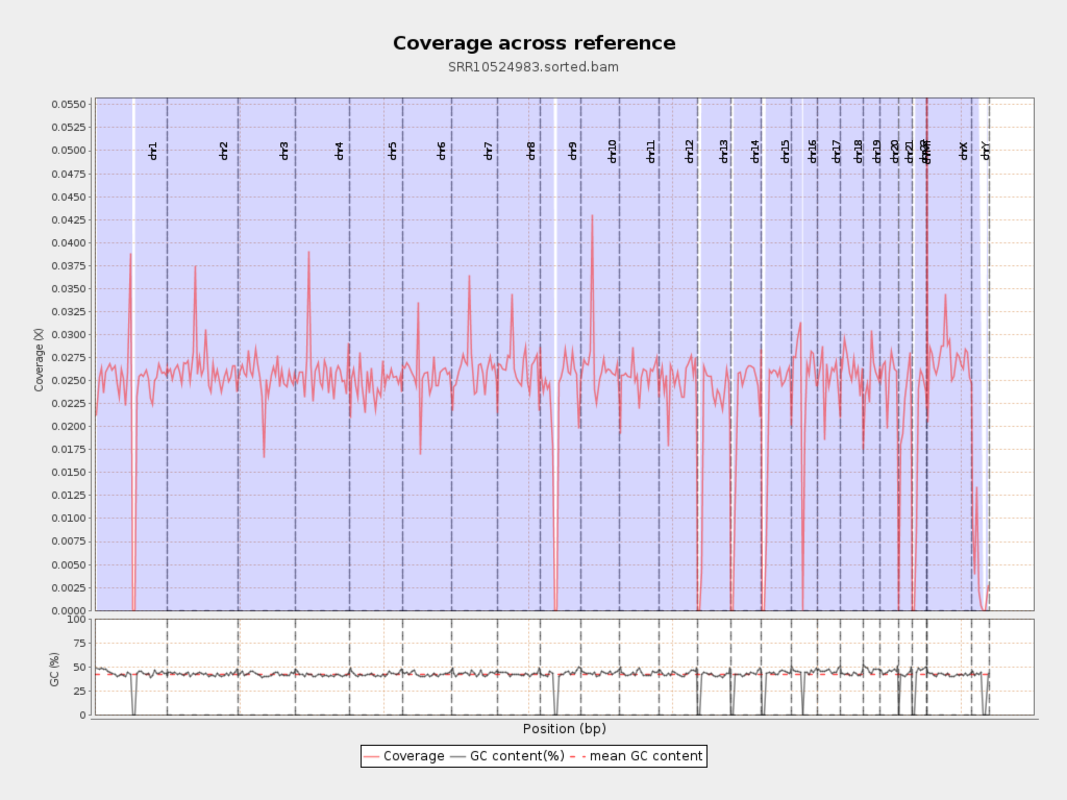
General error rate	0.49%
Mismatches	359,775
Insertions	4,822
Mapped reads with at least one insertion	0.37%
Deletions	14,399
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.64%

2.6. Chromosome stats

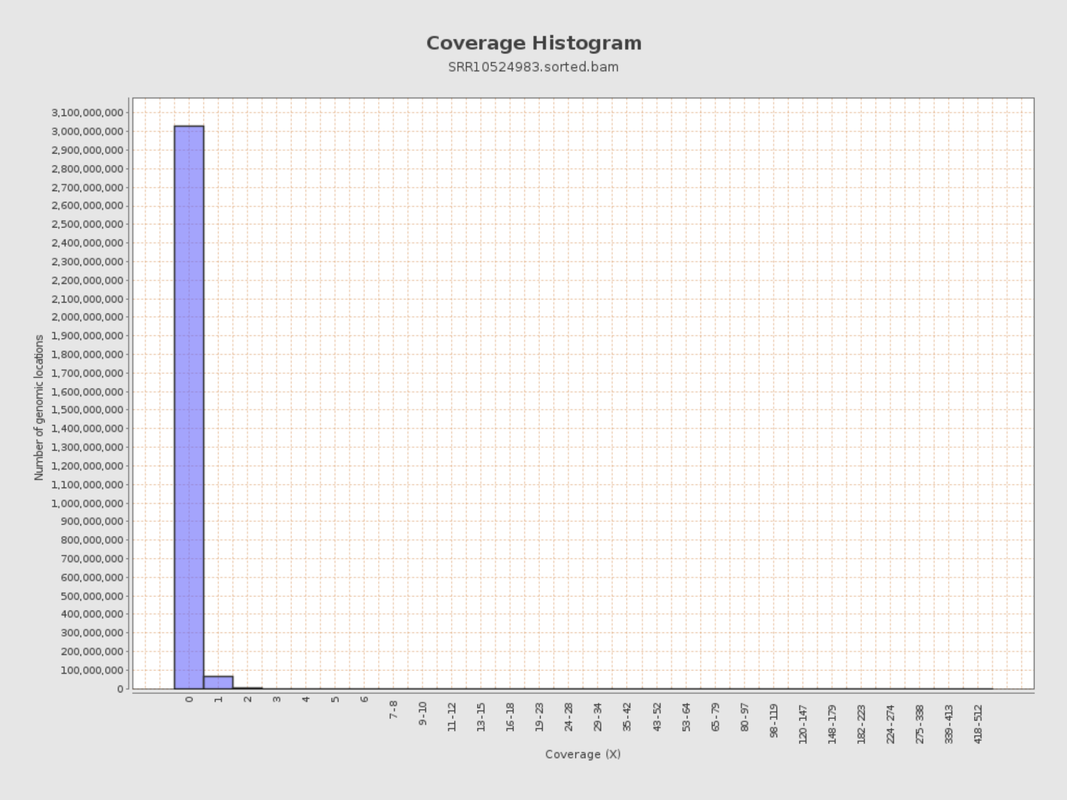
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5974111	0.024	0.3782
chr2	243199373	6402773	0.0263	0.2476
chr3	198022430	5014522	0.0253	0.1723
chr4	191154276	4972900	0.026	0.193
chr5	180915260	4492860	0.0248	0.1705
chr6	171115067	4376466	0.0256	0.1999
chr7	159138663	4188284	0.0263	0.2586

chr8	146364022	3889325	0.0266	0.2321
chr9	141213431	3129830	0.0222	0.1949
chr10	135534747	3643235	0.0269	0.2321
chr11	135006516	3451524	0.0256	0.2226
chr12	133851895	3352100	0.025	0.1732
chr13	115169878	2341899	0.0203	0.1531
chr14	107349540	2272395	0.0212	0.1612
chr15	102531392	2124044	0.0207	0.1654
chr16	90354753	2186160	0.0242	0.1737
chr17	81195210	2042284	0.0252	0.1852
chr18	78077248	2058686	0.0264	0.3143
chr19	59128983	1490580	0.0252	0.2534
chr20	63025520	1594070	0.0253	0.1741
chr21	48129895	984954	0.0205	0.1649
chr22	51304566	881685	0.0172	0.1408
chrMT	16571	1060	0.064	0.2755
chrX	155270560	4253372	0.0274	0.1935
chrY	59373566	226305	0.0038	0.115

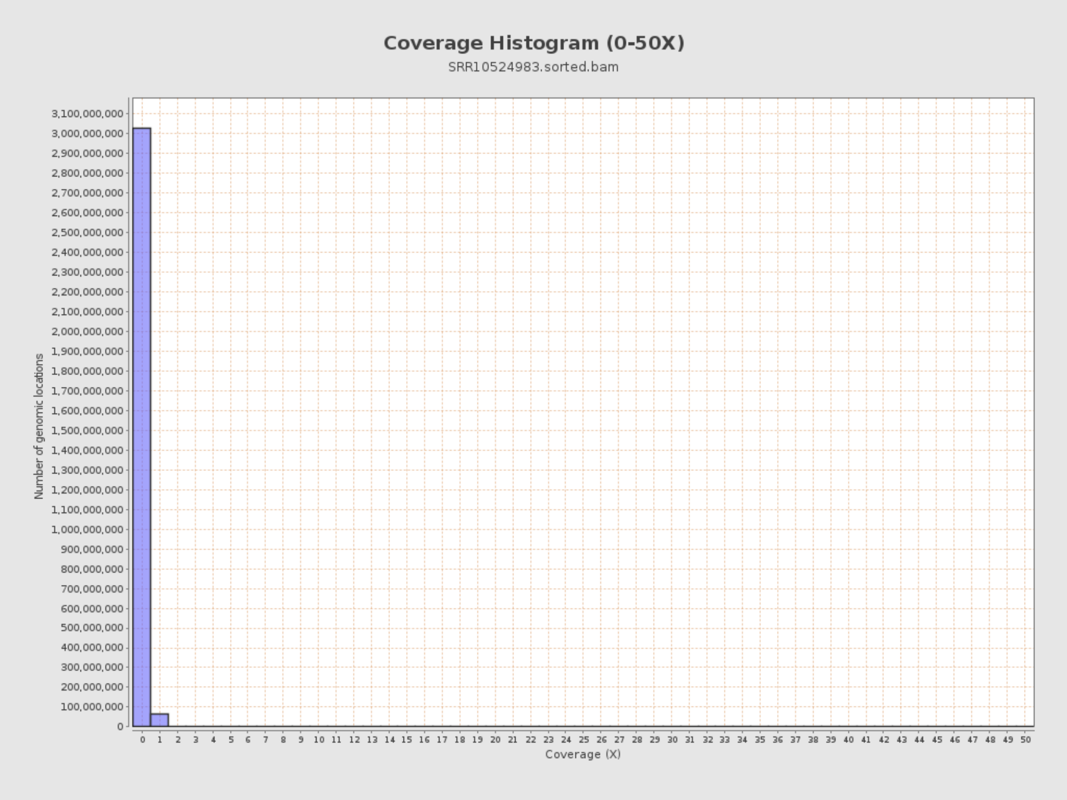
3. Results : Coverage across reference



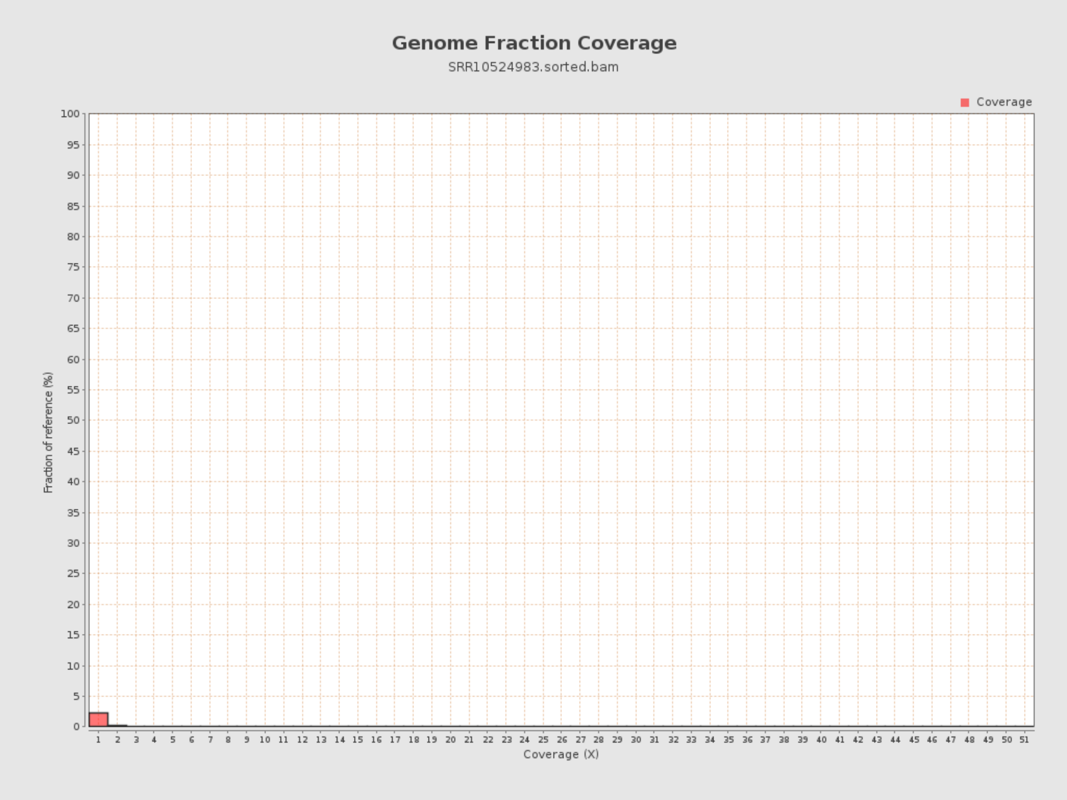
4. Results : Coverage Histogram



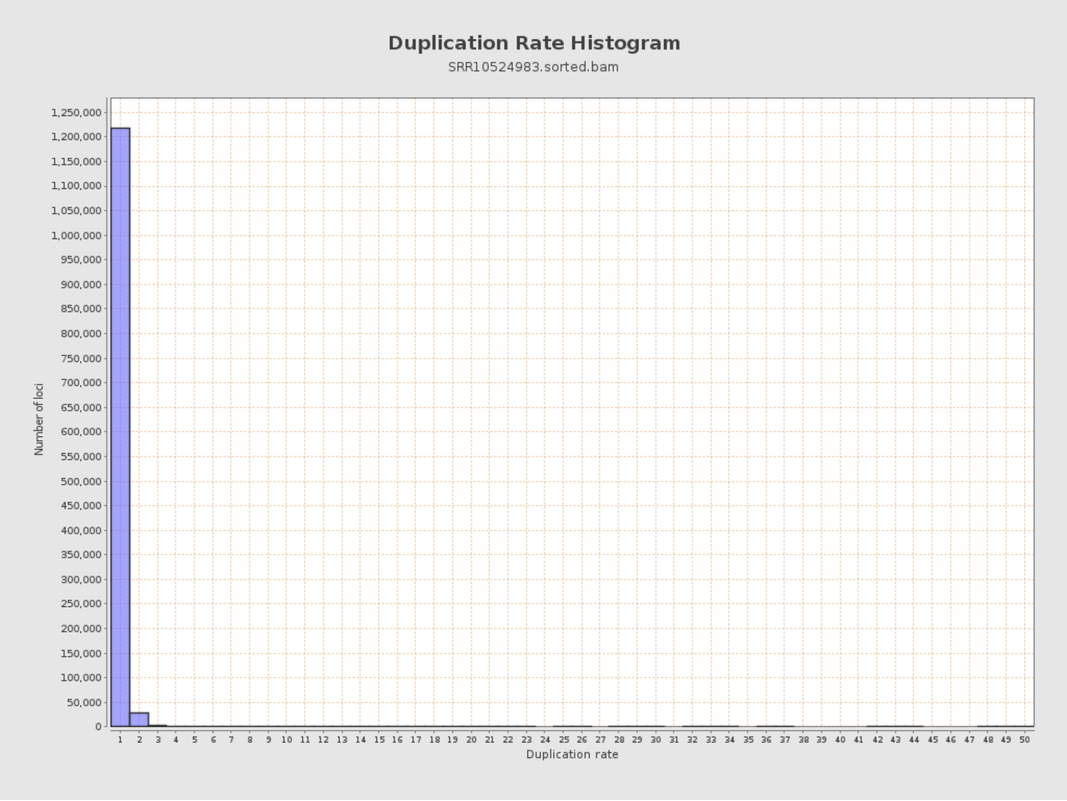
5. Results : Coverage Histogram (0-50X)



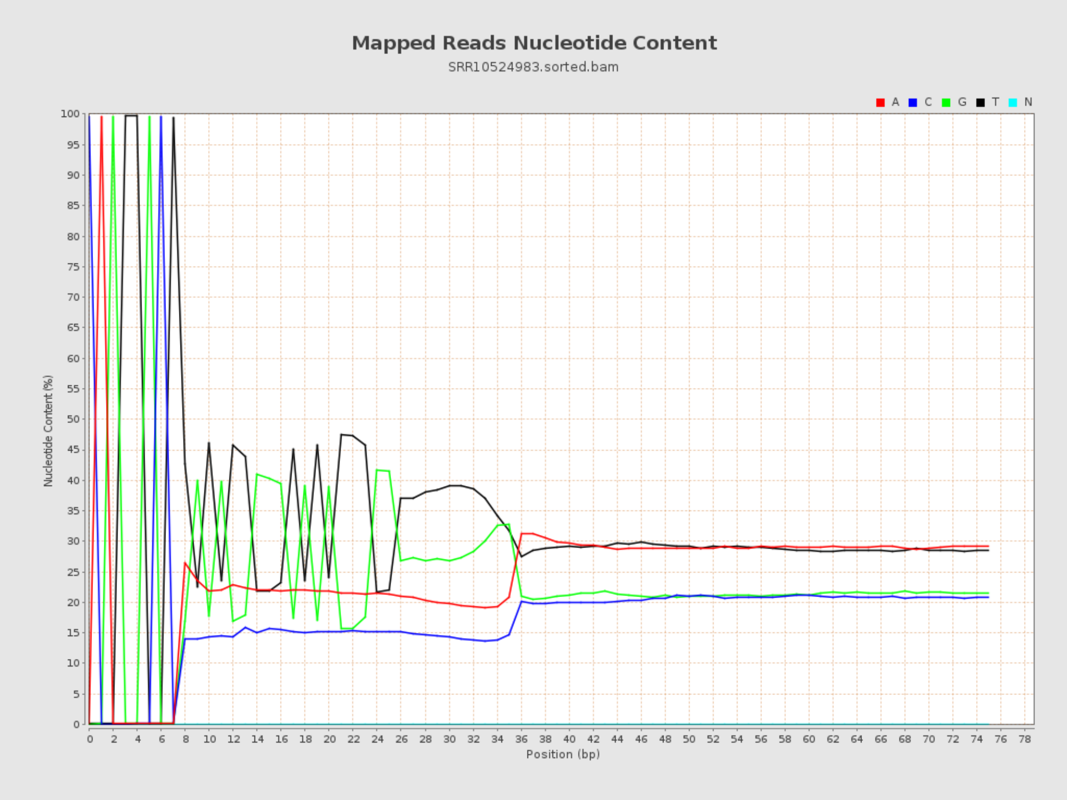
6. Results : Genome Fraction Coverage



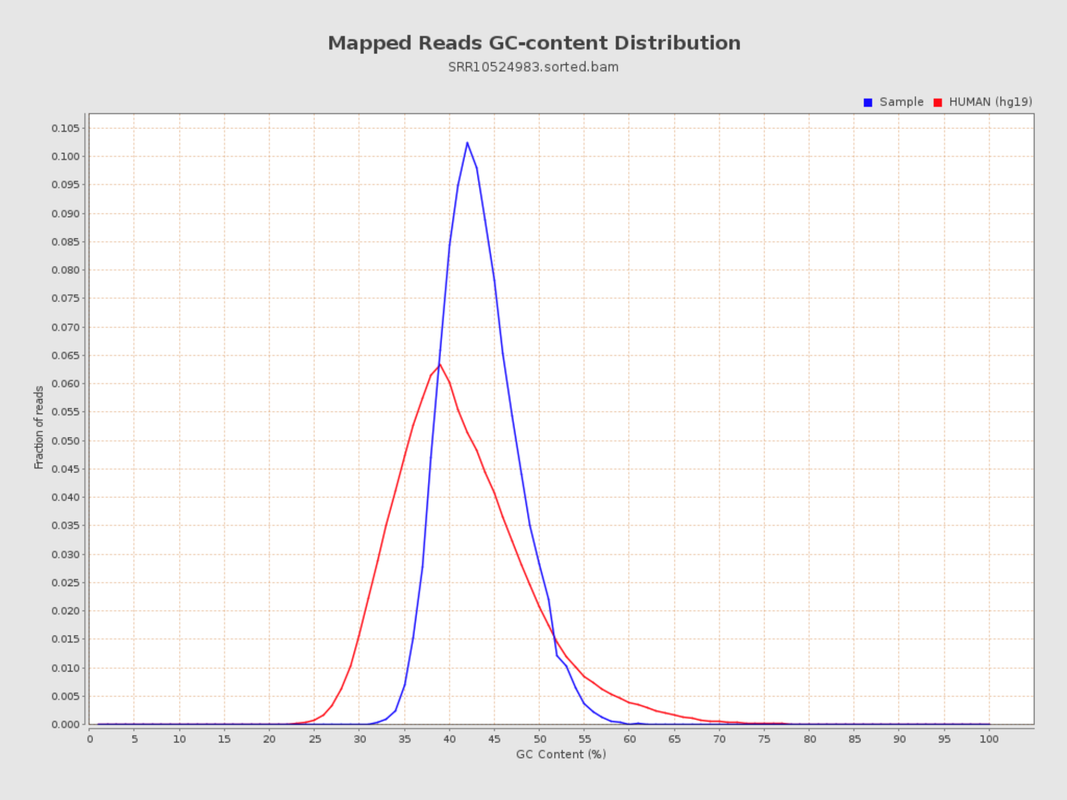
7. Results : Duplication Rate Histogram



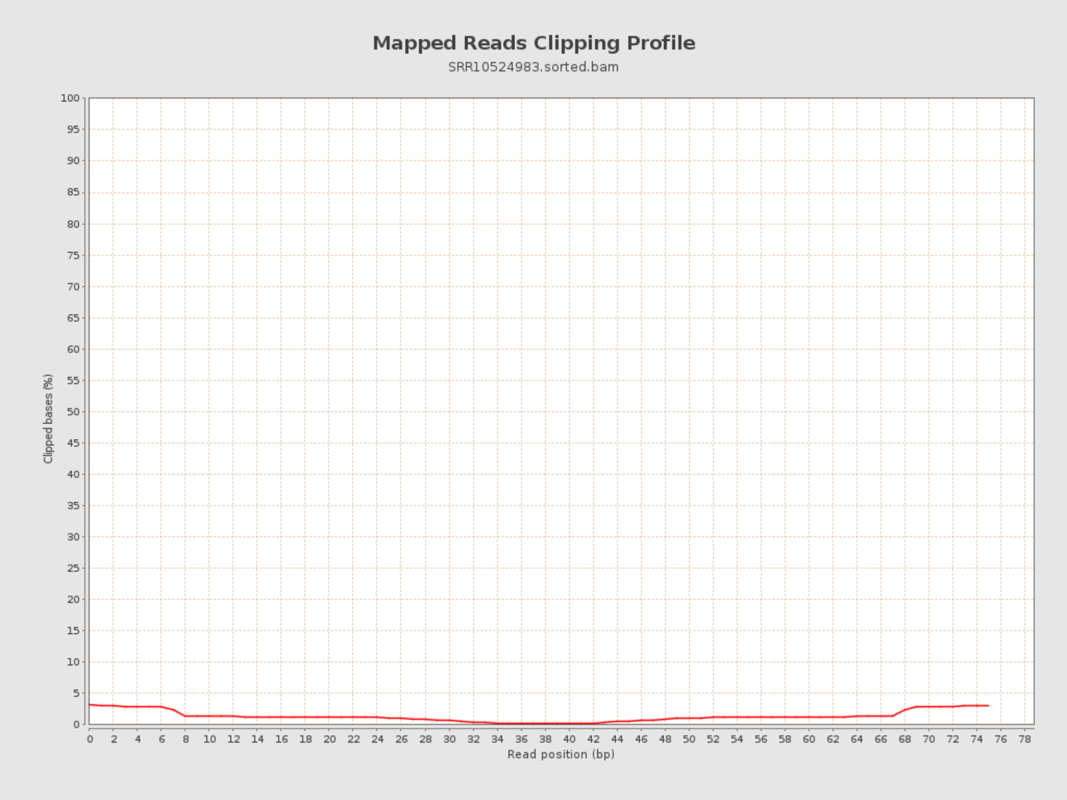
8. Results : Mapped Reads Nucleotide Content



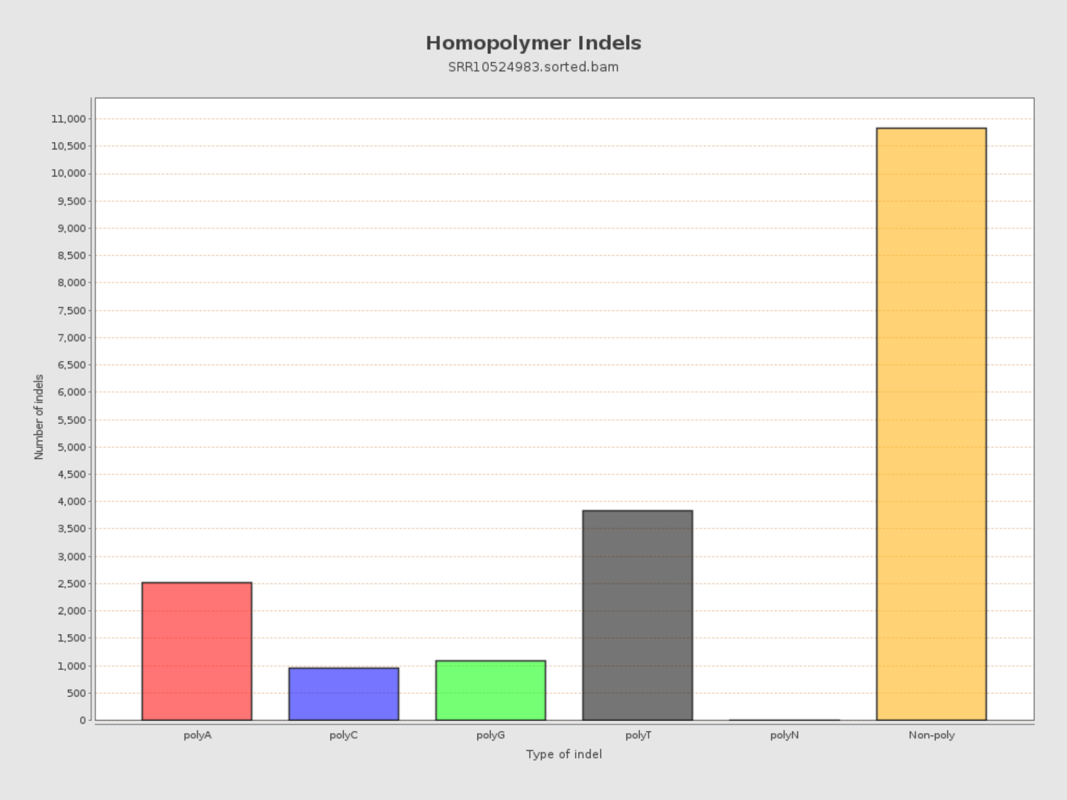
9. Results : Mapped Reads GC-content Distribution



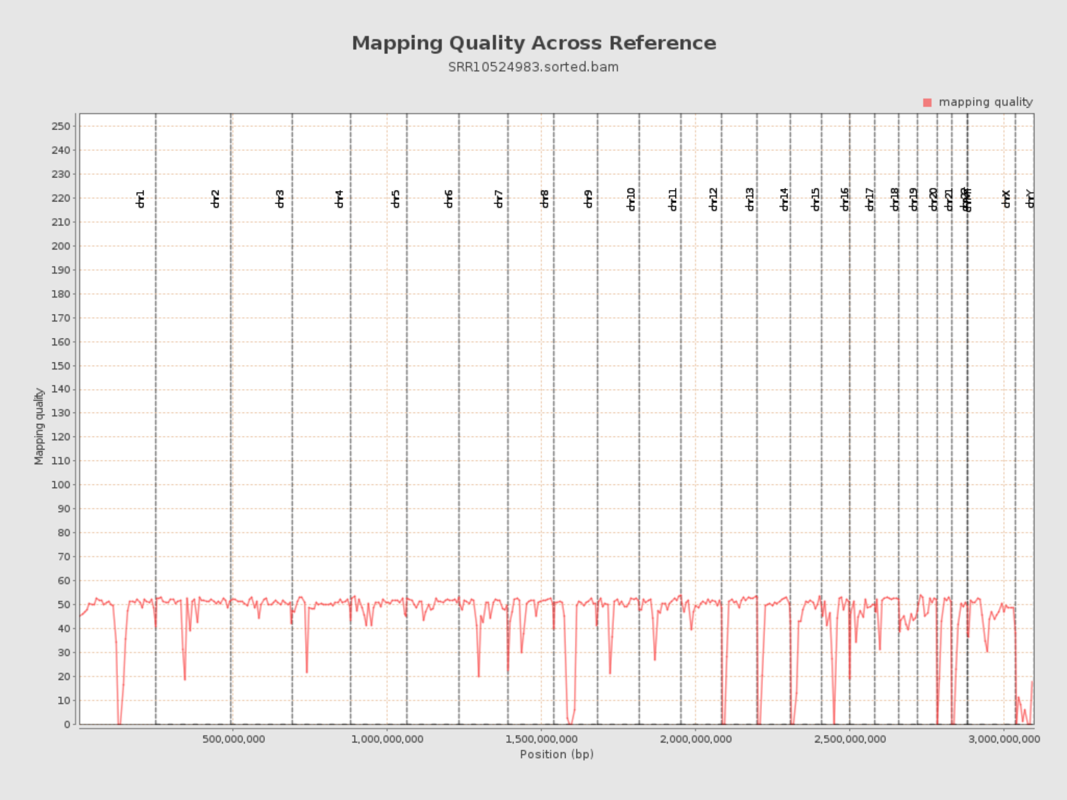
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram