Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 05:44:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524926.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_SRR10524926 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524926.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 05:44:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	670,173
Mapped reads	620,932 / 92.65%
Unmapped reads	49,241 / 7.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,658 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	15,274 / 2.28%
Duplication rate	1.93%
Clipped reads	621,873 / 92.79%

2.2. ACGT Content

Number/percentage of A's	8,677,410 / 23.94%
Number/percentage of C's	6,484,866 / 17.89%
Number/percentage of T's	11,951,647 / 32.97%
Number/percentage of G's	9,138,256 / 25.21%
Number/percentage of N's	237 / 0%
GC Percentage	43.1%

2.3. Coverage

Mean	0.0117

Standard Deviation	0.1369

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

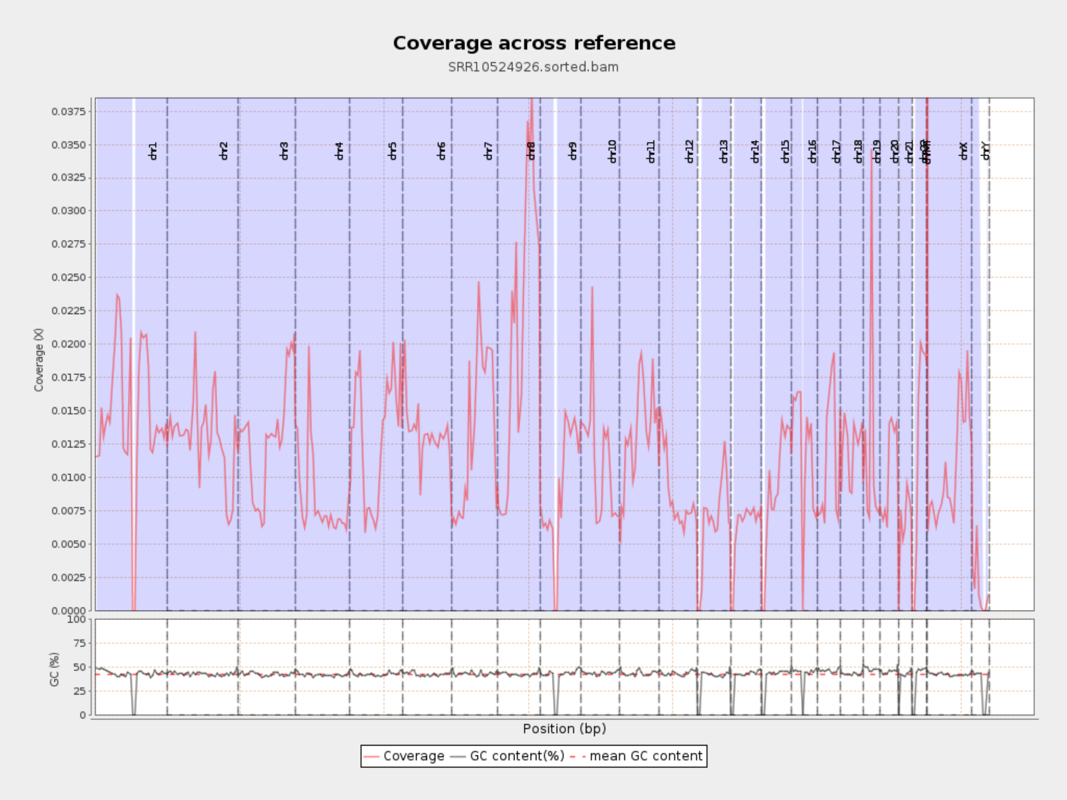
General error rate	0.51%
Mismatches	179,070
Insertions	2,464
Mapped reads with at least one insertion	0.39%
Deletions	6,801
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.59%

2.6. Chromosome stats

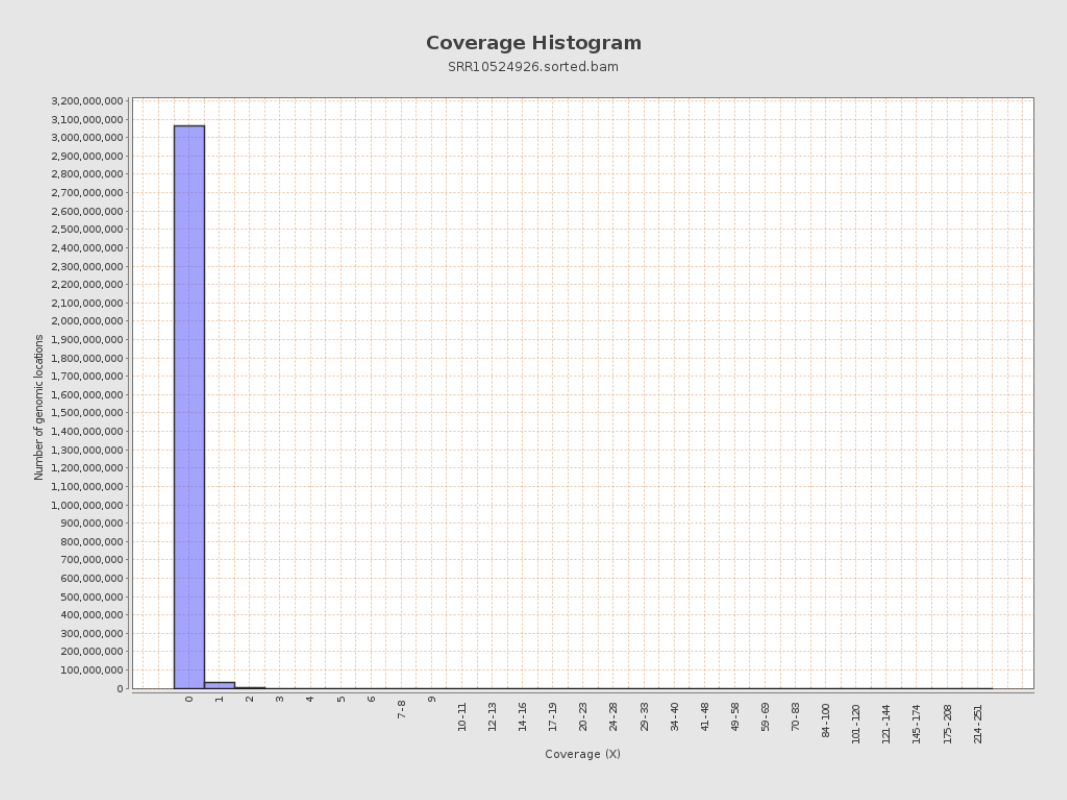
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3665519	0.0147	0.2196
chr2	243199373	3155443	0.013	0.1532
chr3	198022430	2556743	0.0129	0.1188
chr4	191154276	1615507	0.0085	0.1054
chr5	180915260	2398788	0.0133	0.1206
chr6	171115067	2292029	0.0134	0.1251
chr7	159138663	2168008	0.0136	0.1582

chr8	146364022	3138755	0.0214	0.1806
chr9	141213431	1279960	0.0091	0.1146
chr10	135534747	1552470	0.0115	0.145
chr11	135006516	1817952	0.0135	0.1345
chr12	133851895	1176270	0.0088	0.0995
chr13	115169878	772863	0.0067	0.0858
chr14	107349540	658476	0.0061	0.0824
chr15	102531392	929663	0.0091	0.1002
chr16	90354753	1069934	0.0118	0.1166
chr17	81195210	927095	0.0114	0.1132
chr18	78077248	958876	0.0123	0.1659
chr19	59128983	718807	0.0122	0.1686
chr20	63025520	669869	0.0106	0.1094
chr21	48129895	318516	0.0066	0.0908
chr22	51304566	650735	0.0127	0.118
chrMT	16571	8604	0.5192	0.7648
chrX	155270560	1664445	0.0107	0.1131
chrY	59373566	98675	0.0017	0.0641

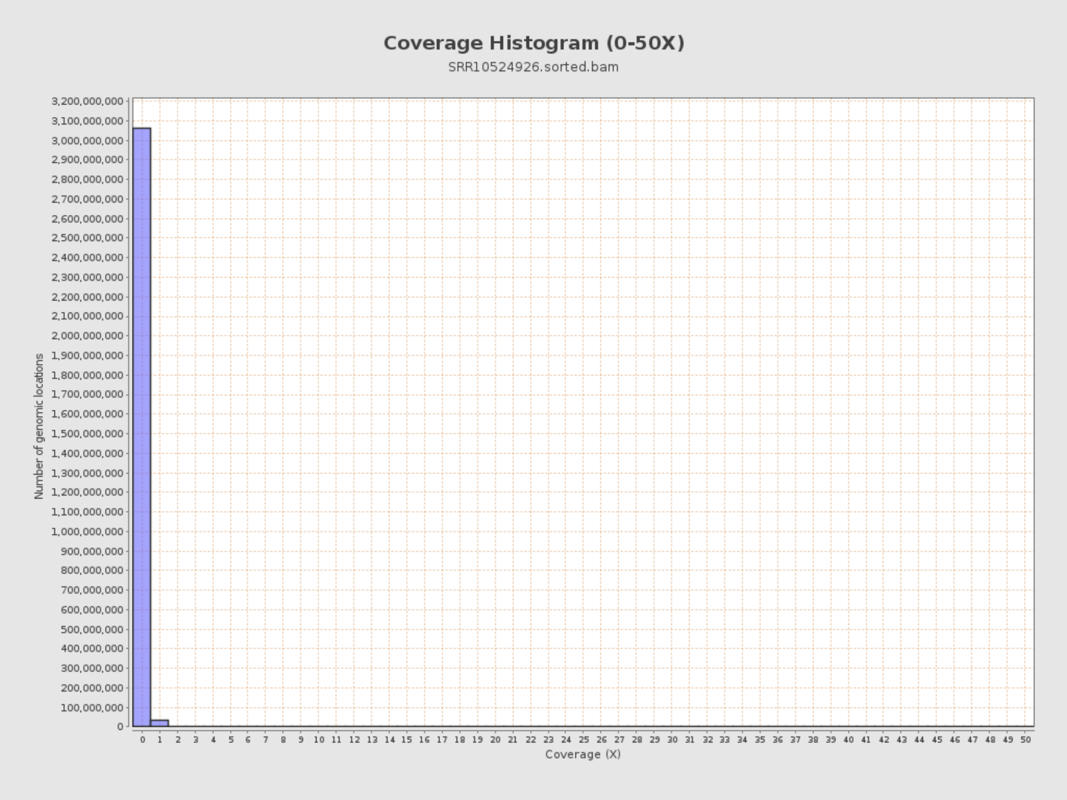
3. Results : Coverage across reference



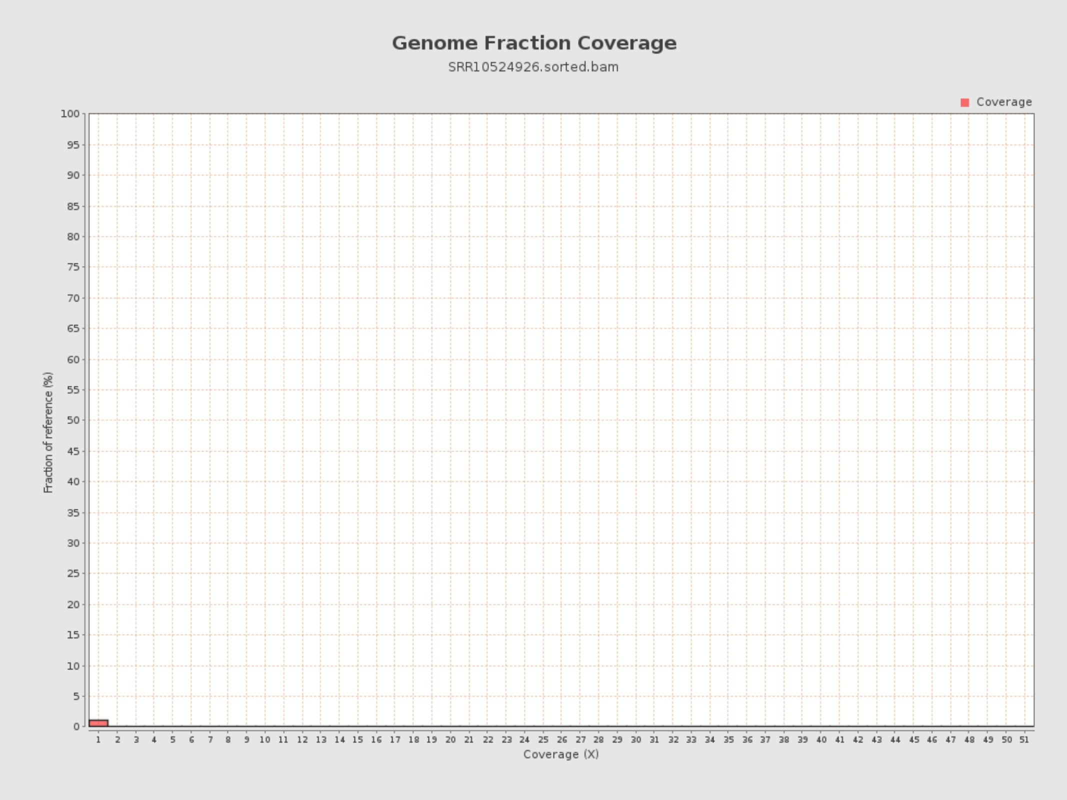
4. Results : Coverage Histogram



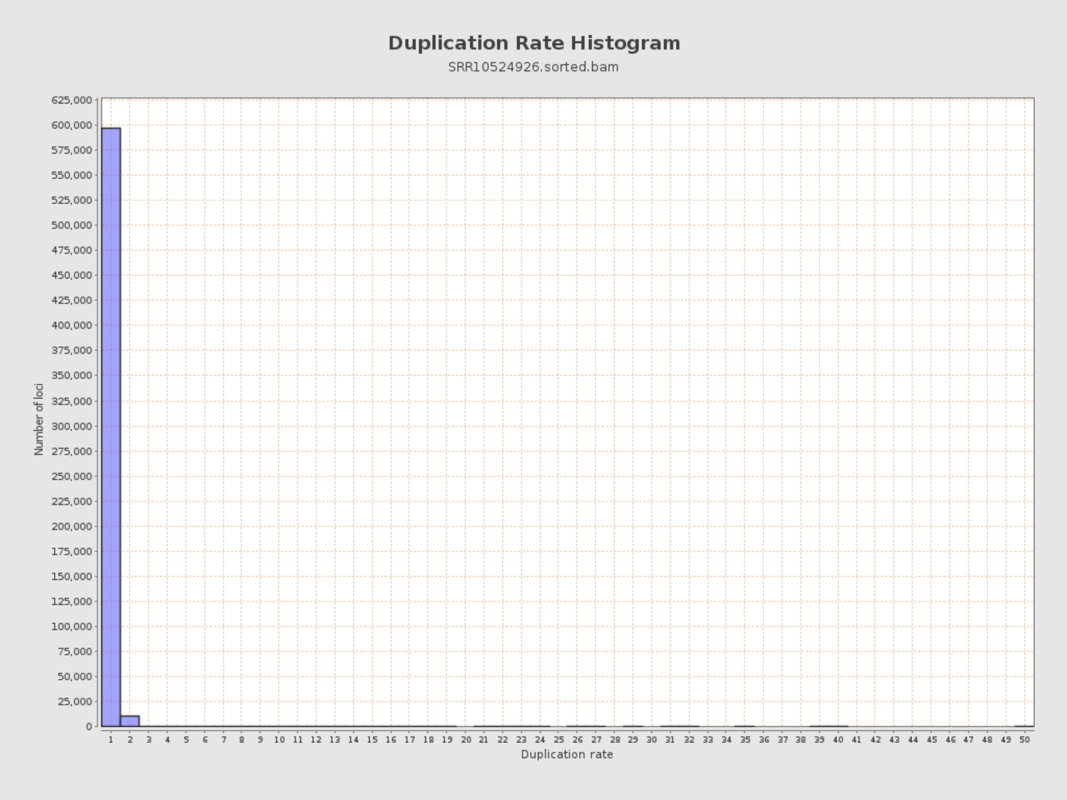
5. Results : Coverage Histogram (0-50X)



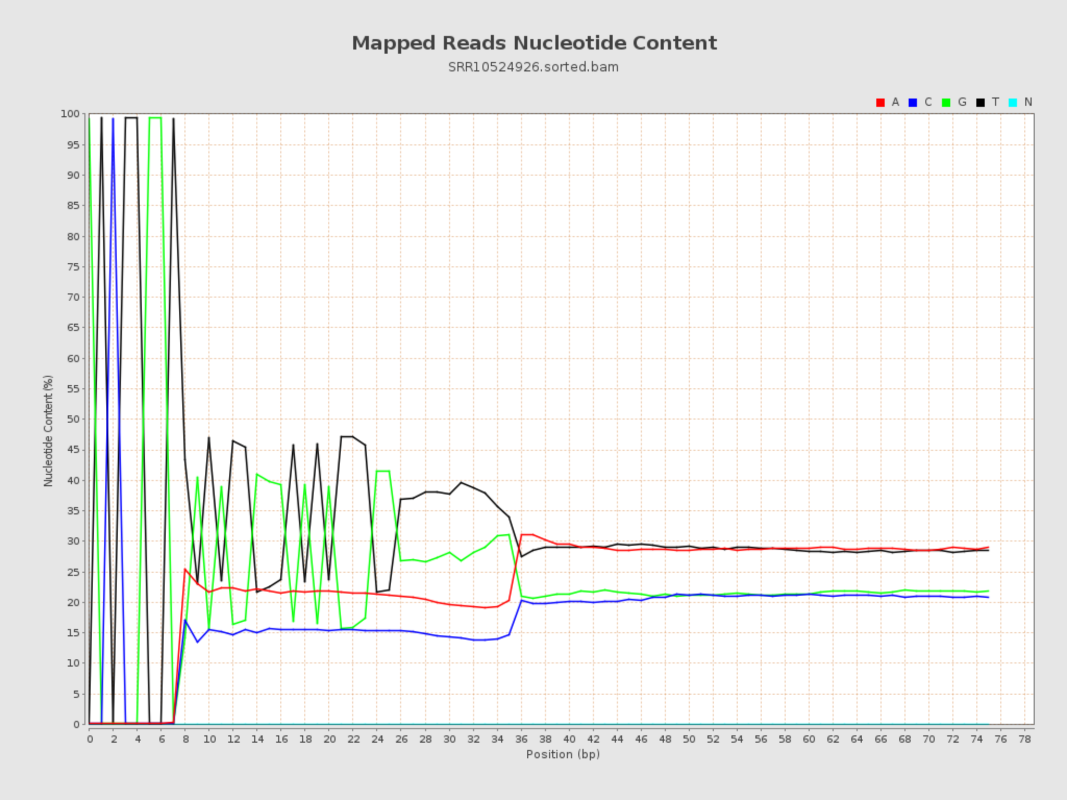
6. Results : Genome Fraction Coverage



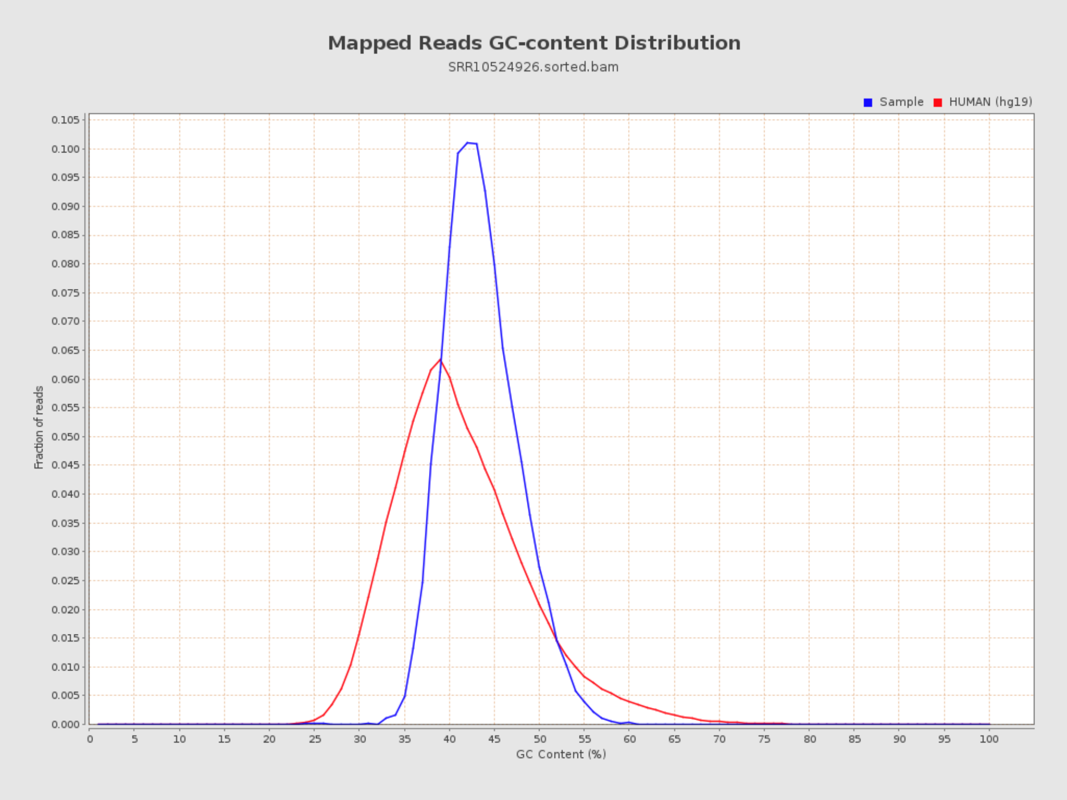
7. Results : Duplication Rate Histogram



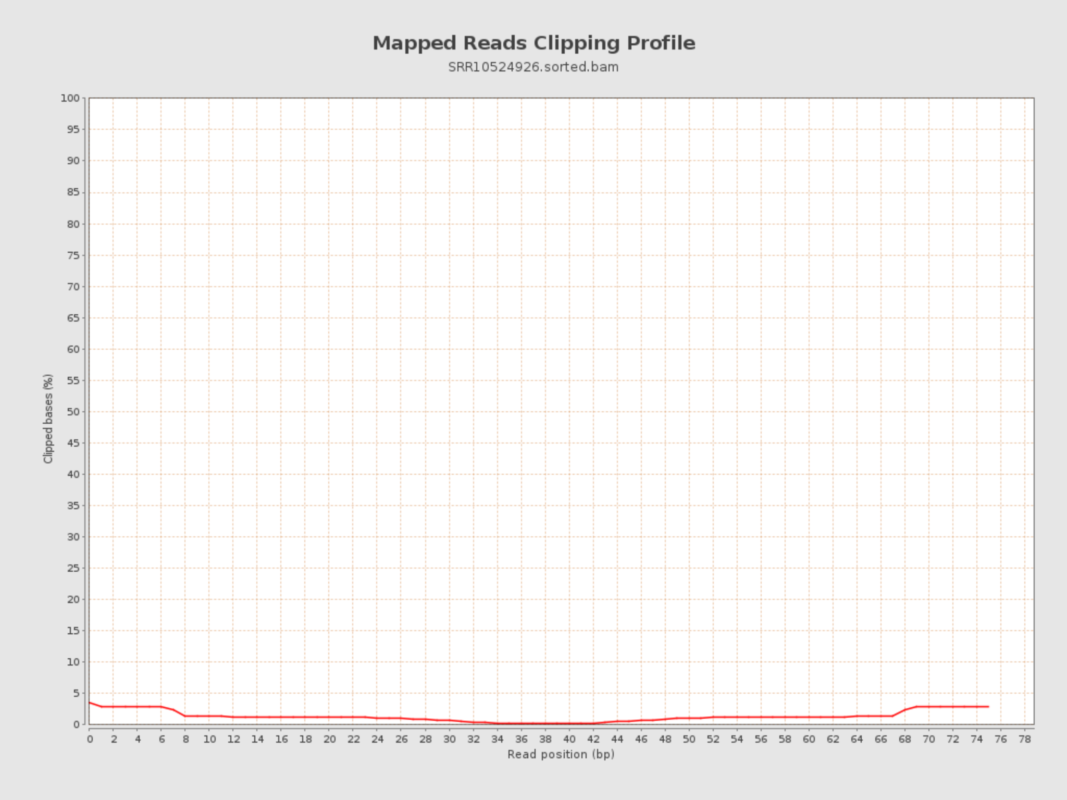
8. Results : Mapped Reads Nucleotide Content



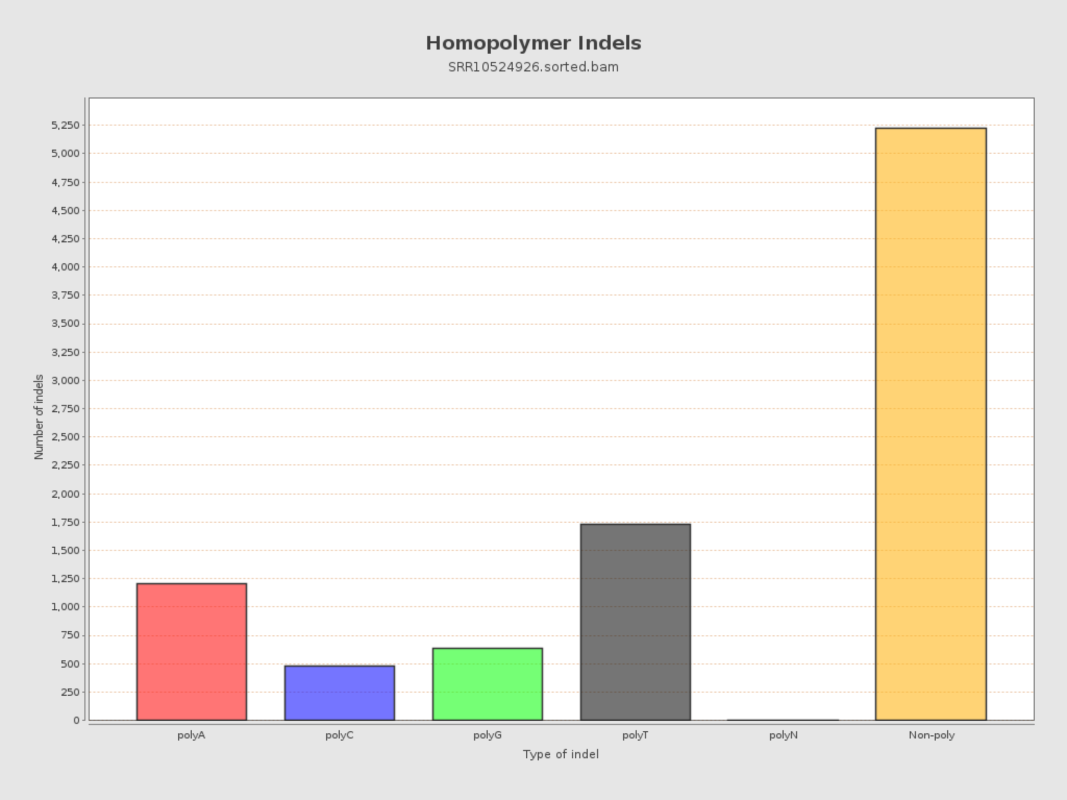
9. Results : Mapped Reads GC-content Distribution



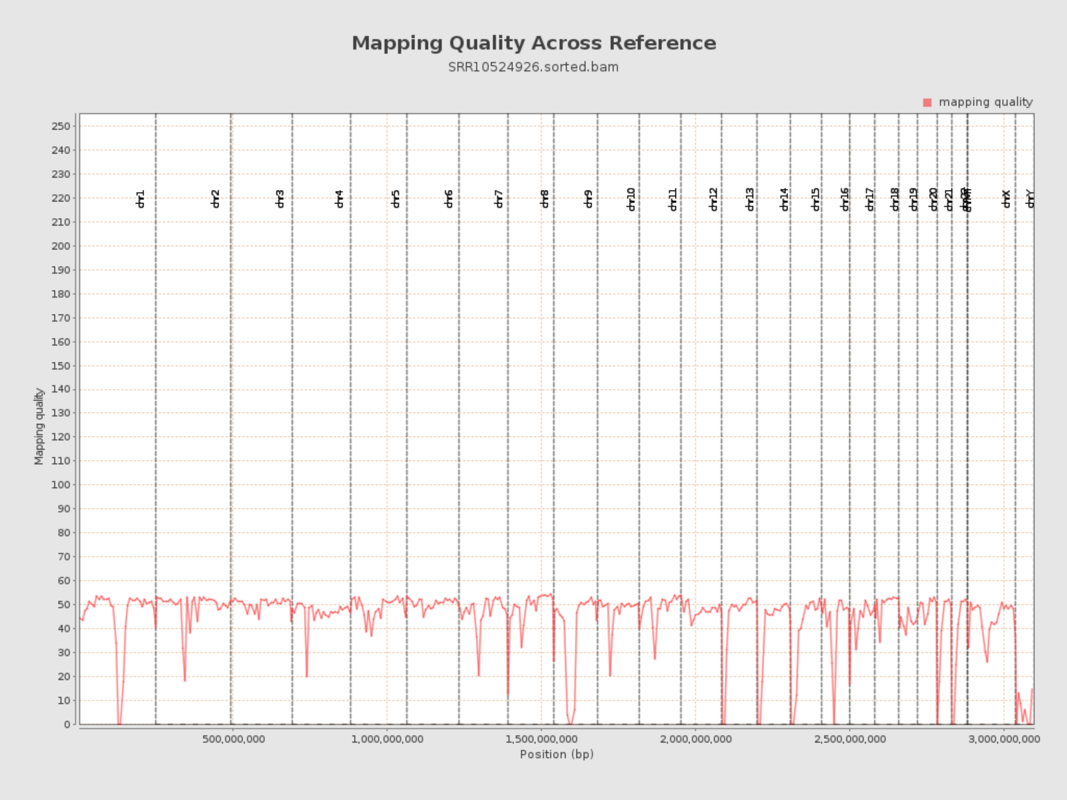
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram