Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 03:46:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524913.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_SRR10524913 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524913.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 03:45:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524913.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,064,043
Mapped reads	986,475 / 92.71%
Unmapped reads	77,568 / 7.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,589 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	41,910 / 3.94%
Duplication rate	3.36%
Clipped reads	988,659 / 92.92%

2.2. ACGT Content

Number/percentage of A's	14,200,901 / 24.64%
Number/percentage of C's	11,373,928 / 19.74%
Number/percentage of T's	18,018,007 / 31.27%
Number/percentage of G's	14,035,445 / 24.35%
Number/percentage of N's	486 / 0%
GC Percentage	44.09%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.1959

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

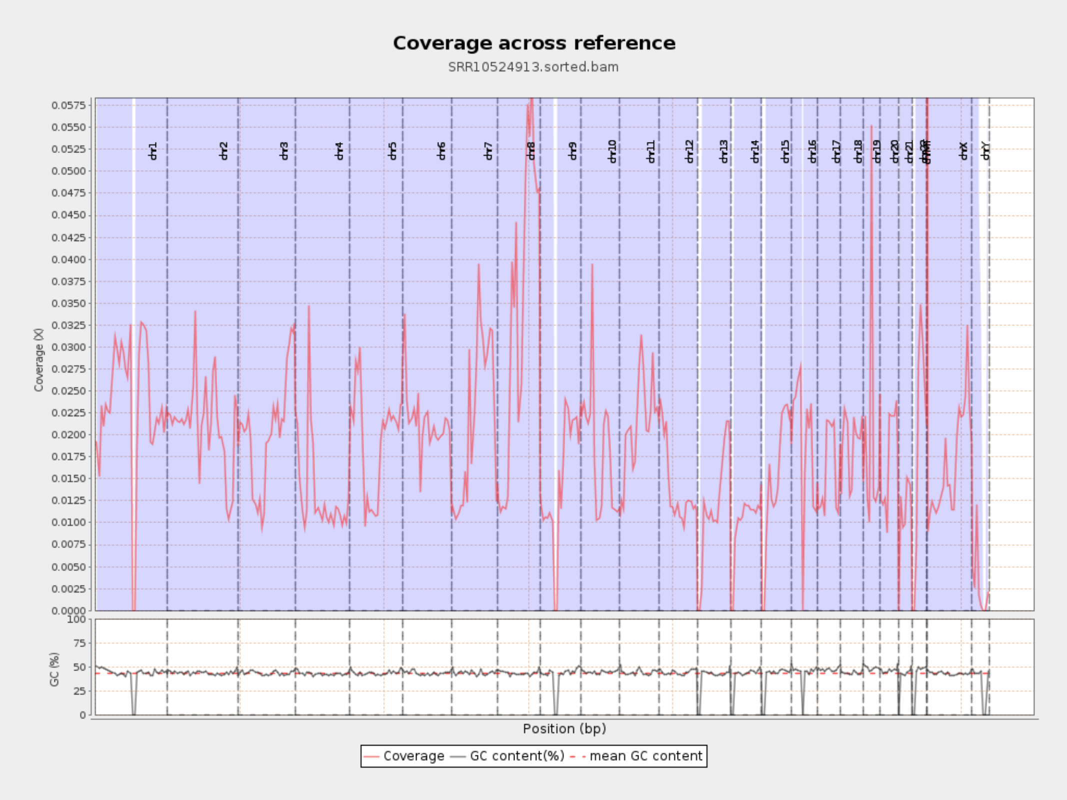
General error rate	0.52%
Mismatches	291,068
Insertions	3,836
Mapped reads with at least one insertion	0.39%
Deletions	10,946
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.04%

2.6. Chromosome stats

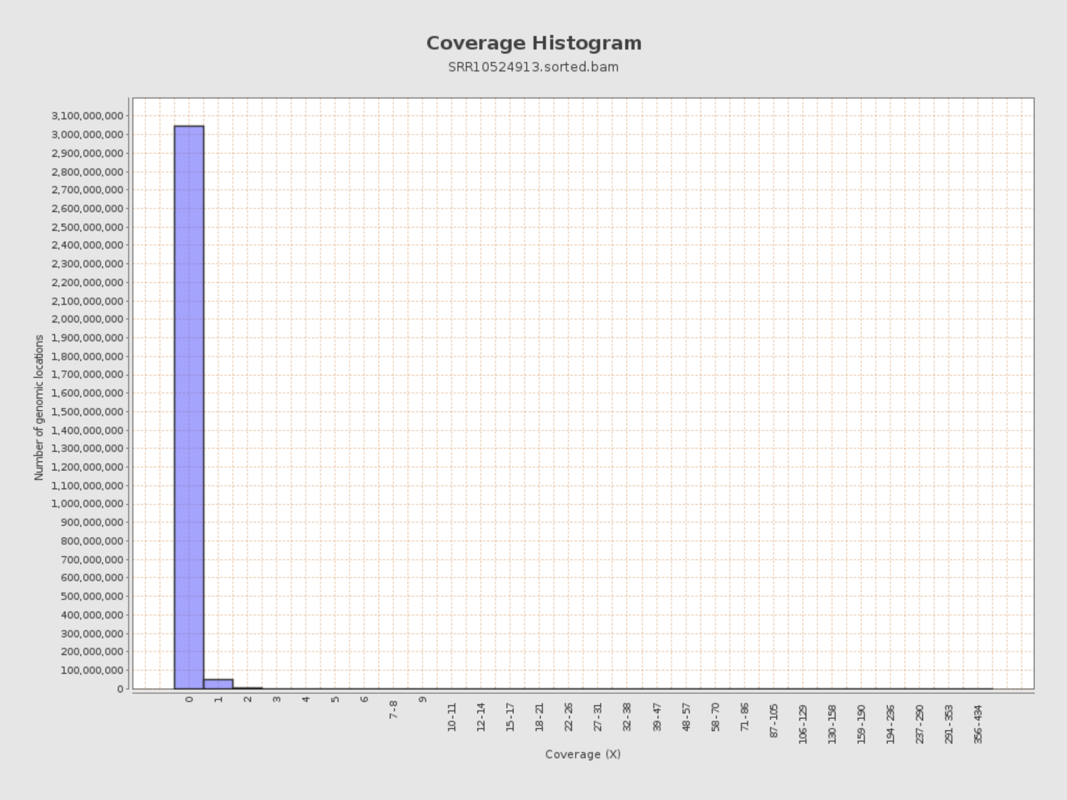
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5843783	0.0234	0.3409
chr2	243199373	5118328	0.021	0.2266
chr3	198022430	4039816	0.0204	0.1554
chr4	191154276	2599805	0.0136	0.1509
chr5	180915260	3513039	0.0194	0.1517
chr6	171115067	3682075	0.0215	0.1669
chr7	159138663	3476155	0.0218	0.2319

chr8	146364022	5058391	0.0346	0.2609
chr9	141213431	2049092	0.0145	0.1605
chr10	135534747	2509916	0.0185	0.2097
chr11	135006516	2886679	0.0214	0.1813
chr12	133851895	1891624	0.0141	0.1333
chr13	115169878	1362924	0.0118	0.1186
chr14	107349540	1046825	0.0098	0.1107
chr15	102531392	1504475	0.0147	0.1319
chr16	90354753	1708384	0.0189	0.1547
chr17	81195210	1279744	0.0158	0.1405
chr18	78077248	1481555	0.019	0.2422
chr19	59128983	1174081	0.0199	0.241
chr20	63025520	1093259	0.0173	0.1467
chr21	48129895	533747	0.0111	0.1372
chr22	51304566	1002082	0.0195	0.154
chrMT	16571	13024	0.786	1.1097
chrX	155270560	2605163	0.0168	0.1504
chrY	59373566	173352	0.0029	0.1095

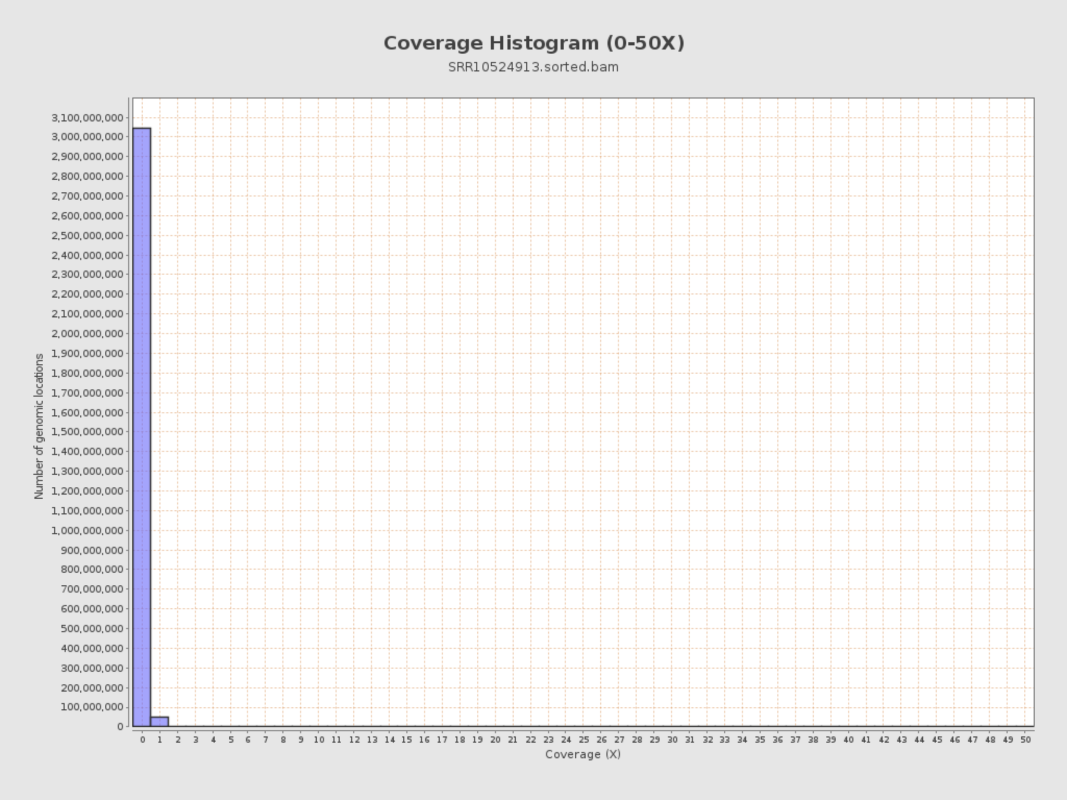
3. Results : Coverage across reference



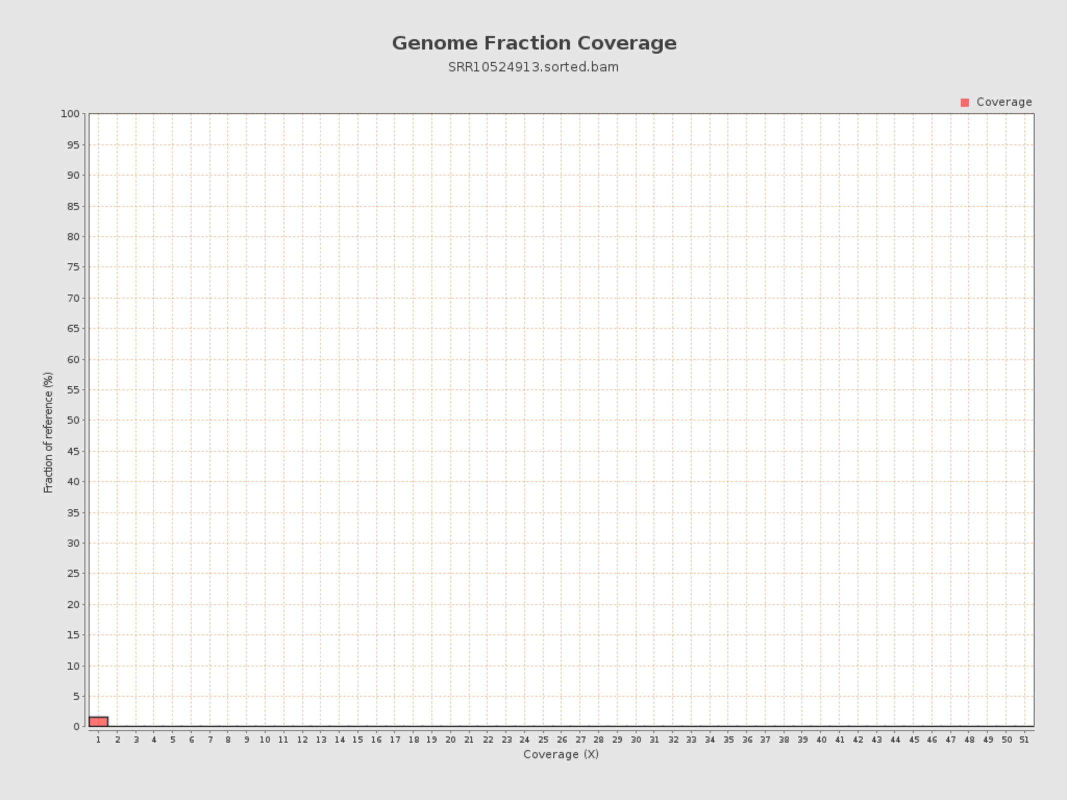
4. Results : Coverage Histogram



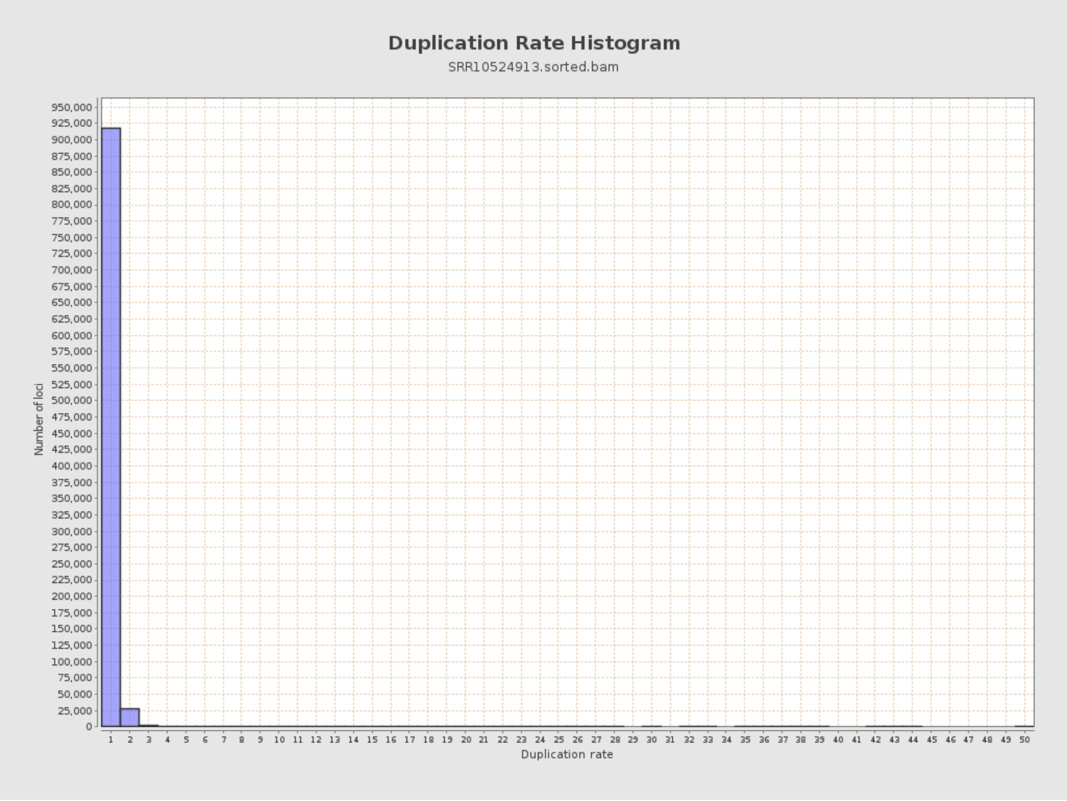
5. Results : Coverage Histogram (0-50X)



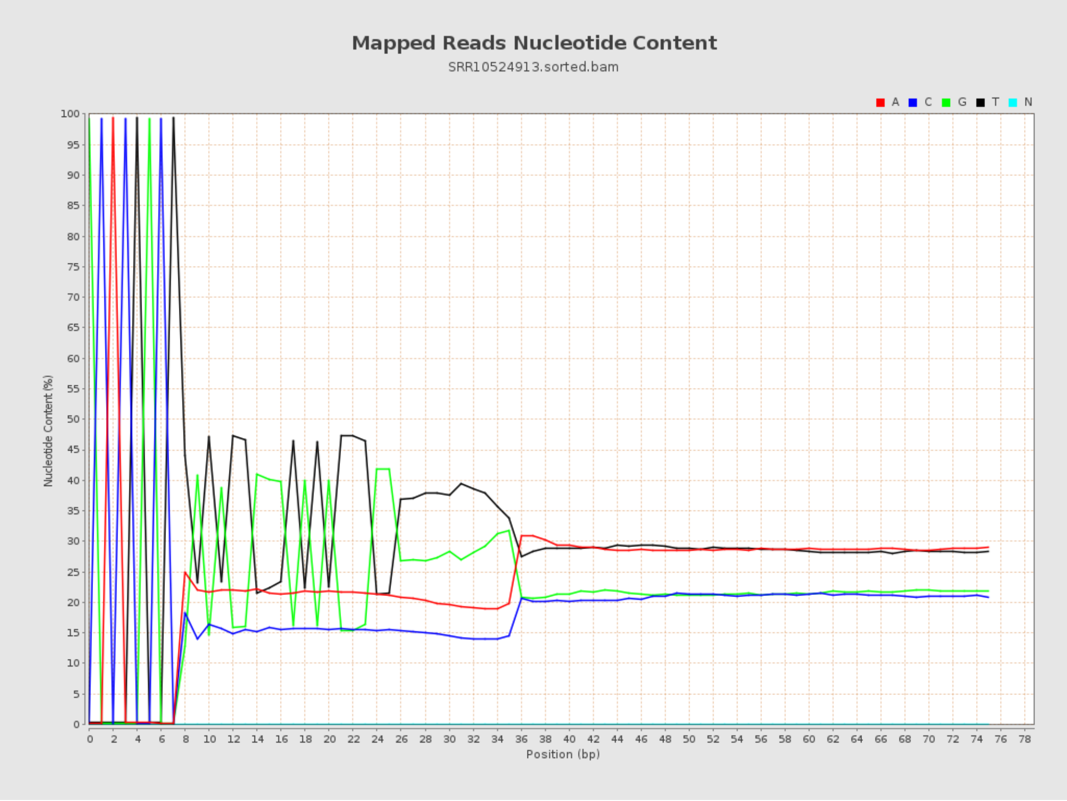
6. Results : Genome Fraction Coverage



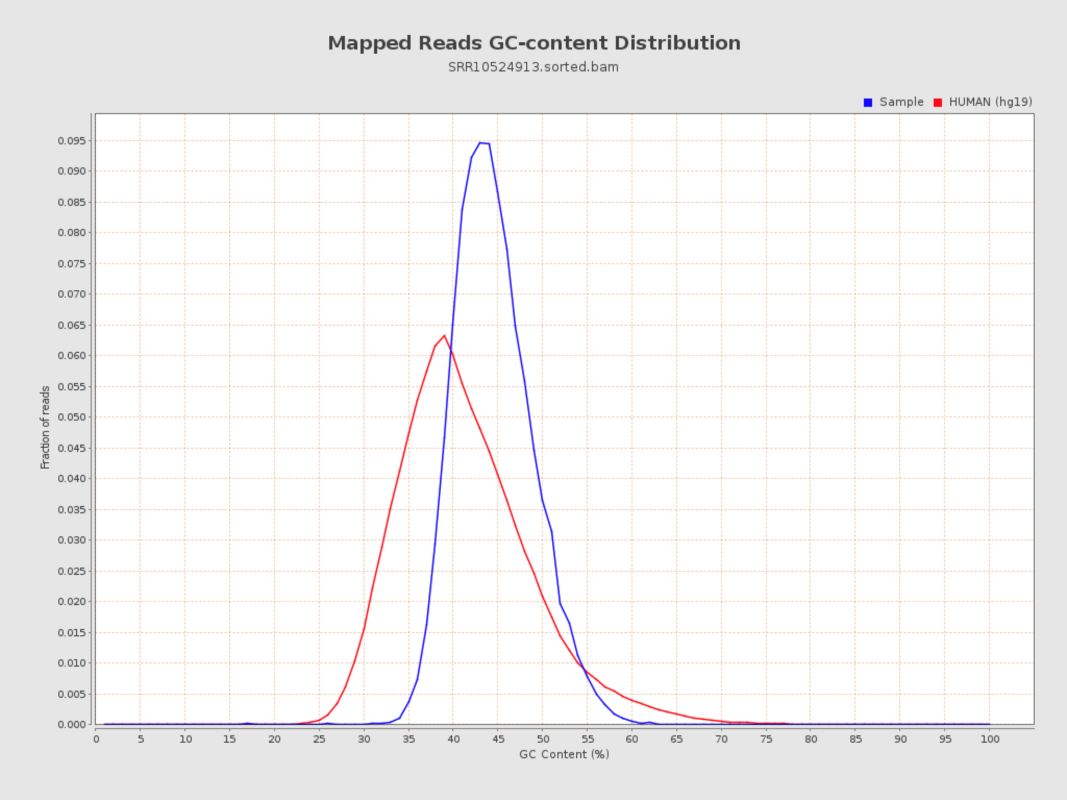
7. Results : Duplication Rate Histogram



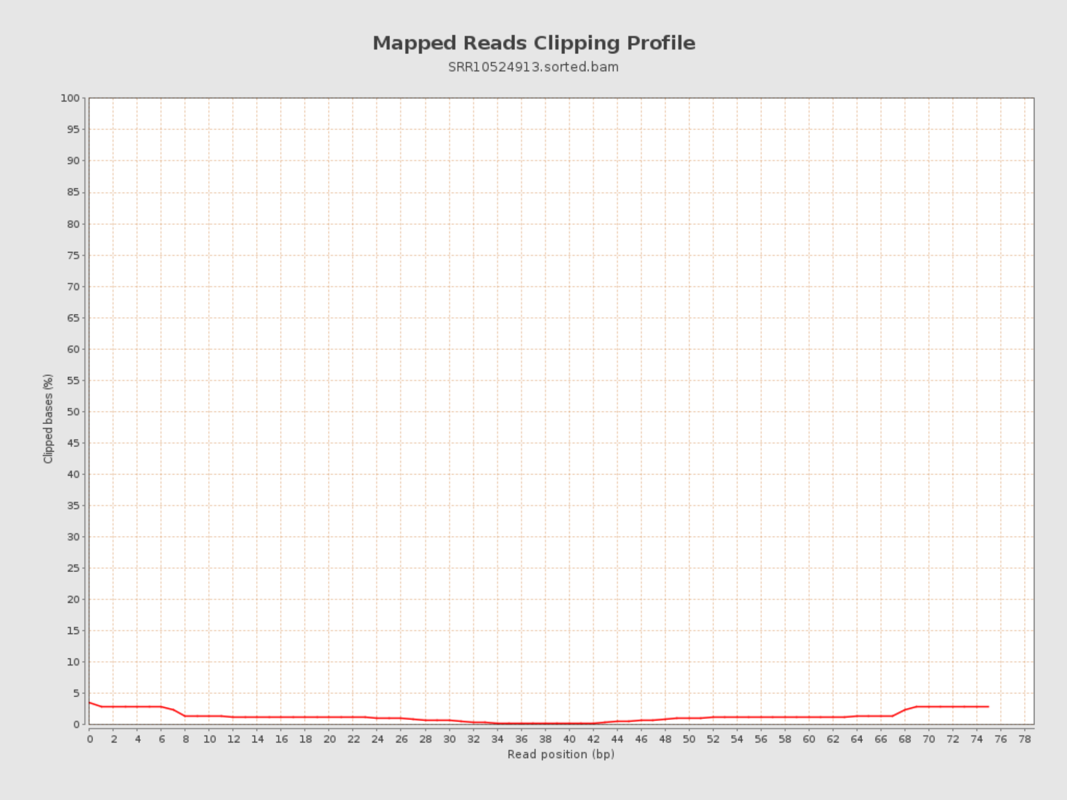
8. Results : Mapped Reads Nucleotide Content



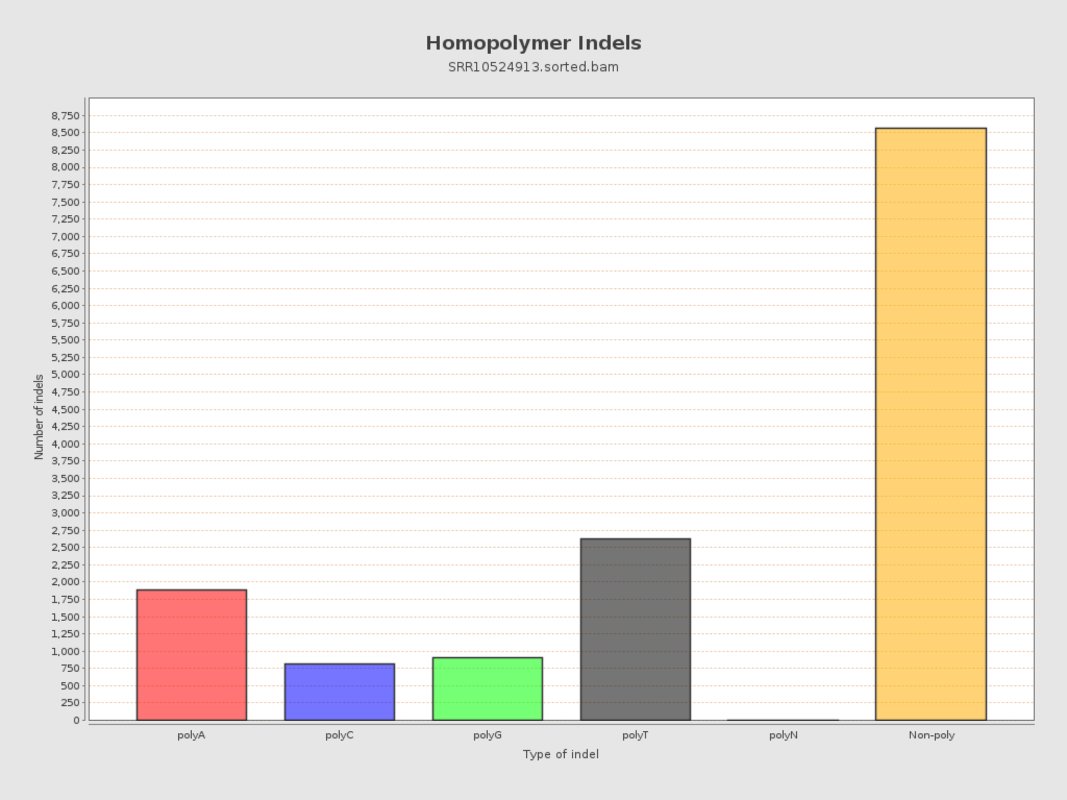
9. Results : Mapped Reads GC-content Distribution



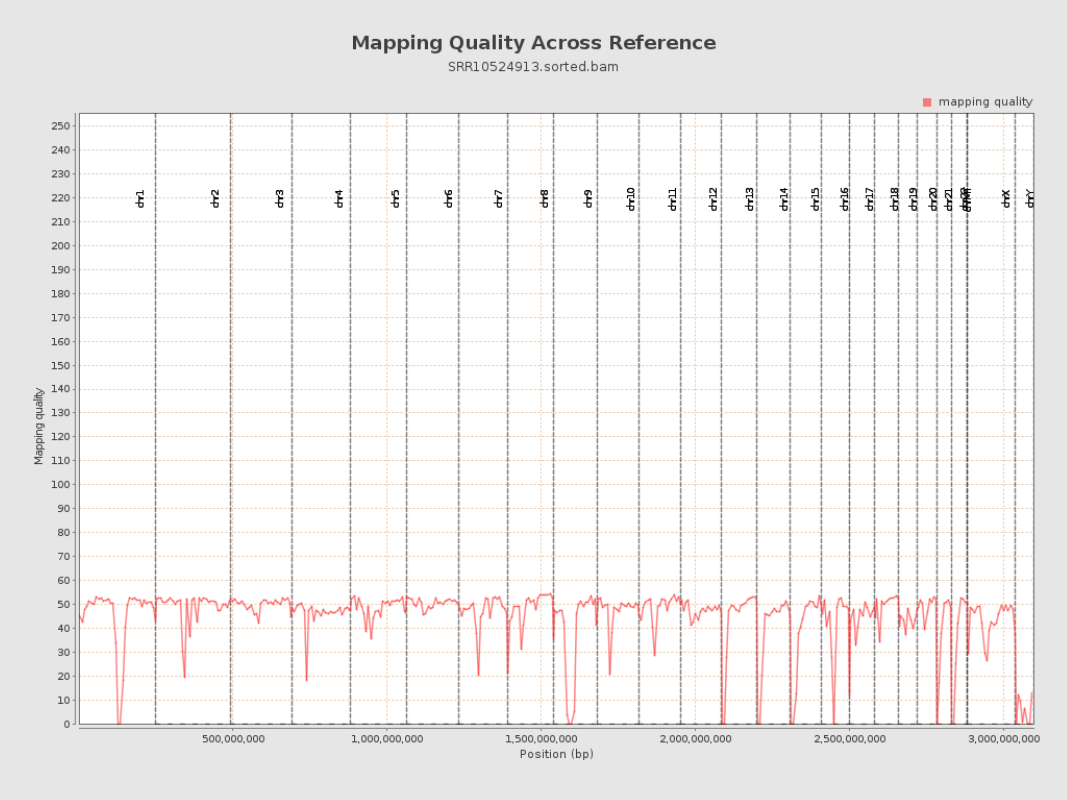
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram