Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:36:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524713.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_SRR10524713 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524713.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:36:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524713.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	531,926
Mapped reads	492,356 / 92.56%
Unmapped reads	39,570 / 7.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,885 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	9,930 / 1.87%
Duplication rate	1.44%
Clipped reads	493,220 / 92.72%

2.2. ACGT Content

Number/percentage of A's	7,629,531 / 25.87%
Number/percentage of C's	5,569,547 / 18.88%
Number/percentage of T's	9,393,323 / 31.85%
Number/percentage of G's	6,899,669 / 23.39%
Number/percentage of N's	3,924 / 0.01%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.1283

2.4. Mapping Quality

Mean Mapping Quality	46.26

2.5. Mismatches and indels

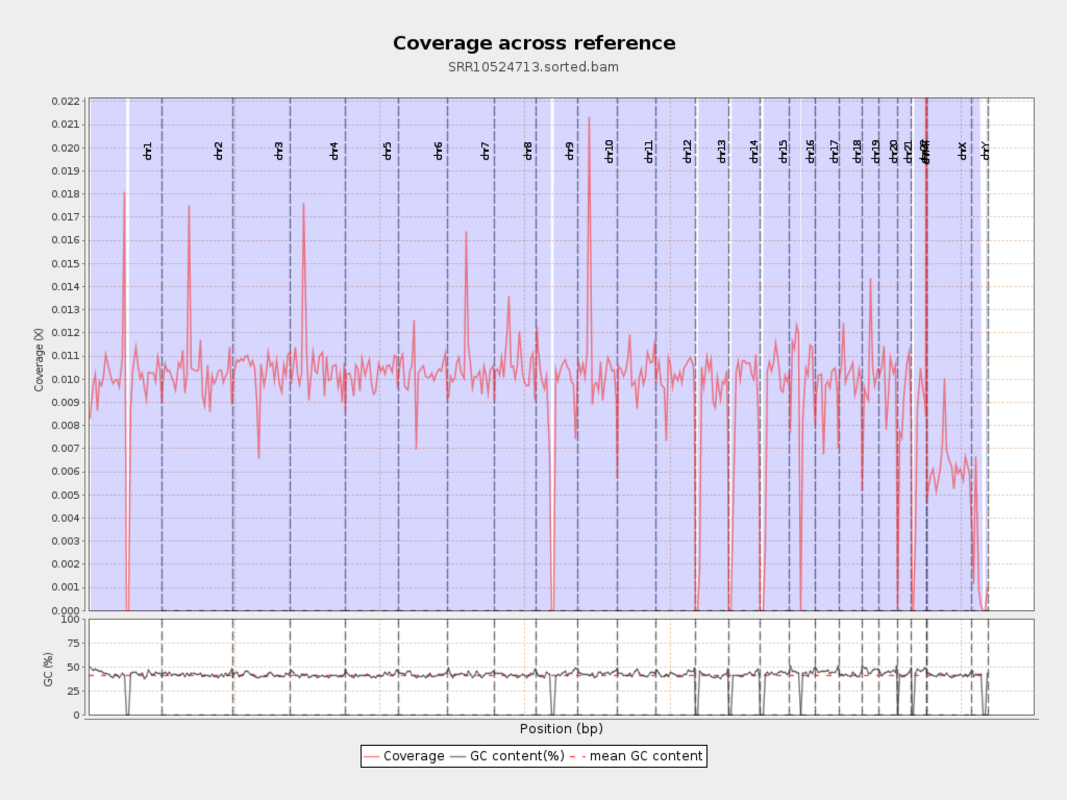
General error rate	0.51%
Mismatches	145,925
Insertions	2,226
Mapped reads with at least one insertion	0.45%
Deletions	5,443
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.98%

2.6. Chromosome stats

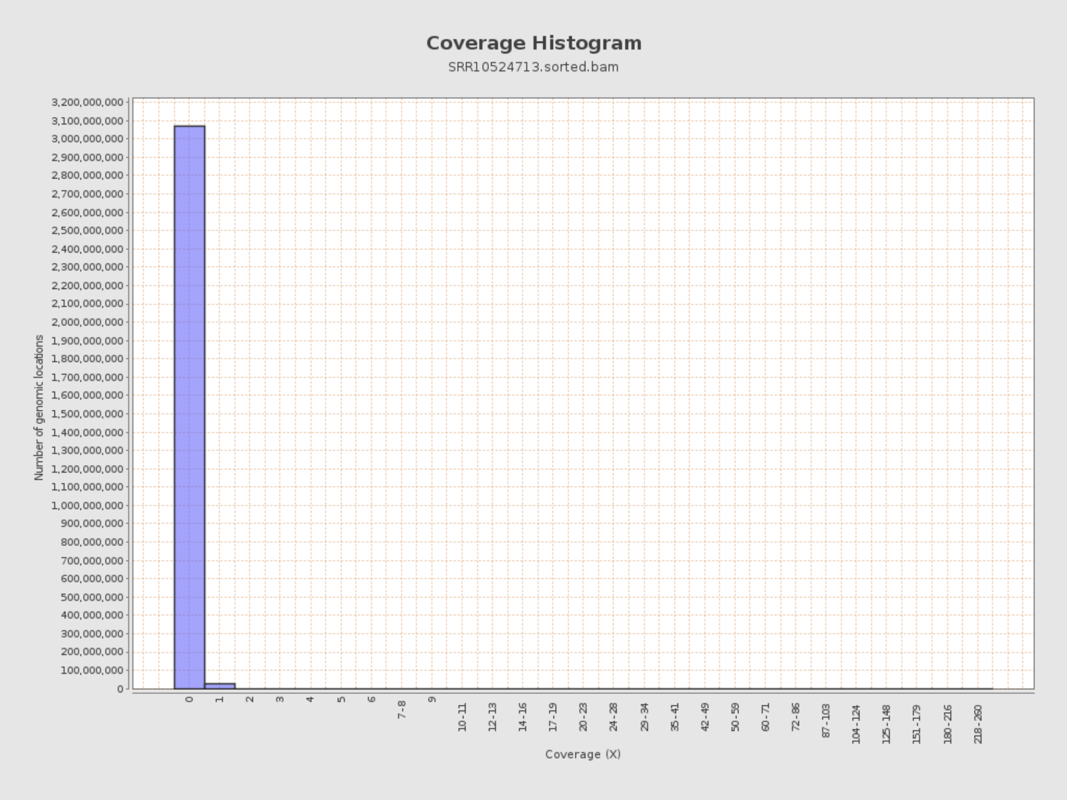
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2406185	0.0097	0.2155
chr2	243199373	2530684	0.0104	0.1475
chr3	198022430	2041792	0.0103	0.1046
chr4	191154276	2025302	0.0106	0.1111
chr5	180915260	1858109	0.0103	0.1055
chr6	171115067	1758137	0.0103	0.1098
chr7	159138663	1674470	0.0105	0.1444

chr8	146364022	1556169	0.0106	0.1417
chr9	141213431	1246149	0.0088	0.1093
chr10	135534747	1460305	0.0108	0.1345
chr11	135006516	1393428	0.0103	0.1196
chr12	133851895	1358335	0.0101	0.1044
chr13	115169878	952738	0.0083	0.0942
chr14	107349540	920399	0.0086	0.0969
chr15	102531392	851103	0.0083	0.0939
chr16	90354753	874860	0.0097	0.105
chr17	81195210	769551	0.0095	0.1027
chr18	78077248	808374	0.0104	0.1725
chr19	59128983	602213	0.0102	0.1626
chr20	63025520	628444	0.01	0.1033
chr21	48129895	399047	0.0083	0.1019
chr22	51304566	333703	0.0065	0.0839
chrMT	16571	2231	0.1346	0.3569
chrX	155270560	962152	0.0062	0.0855
chrY	59373566	91039	0.0015	0.0753

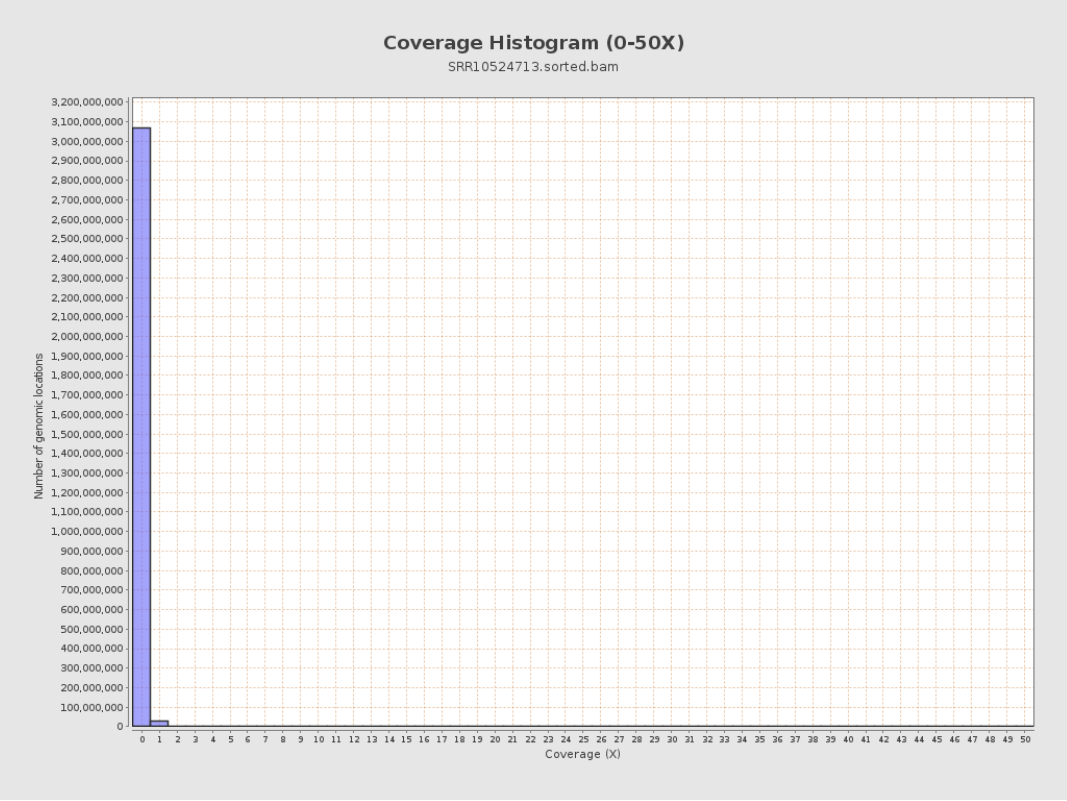
3. Results : Coverage across reference



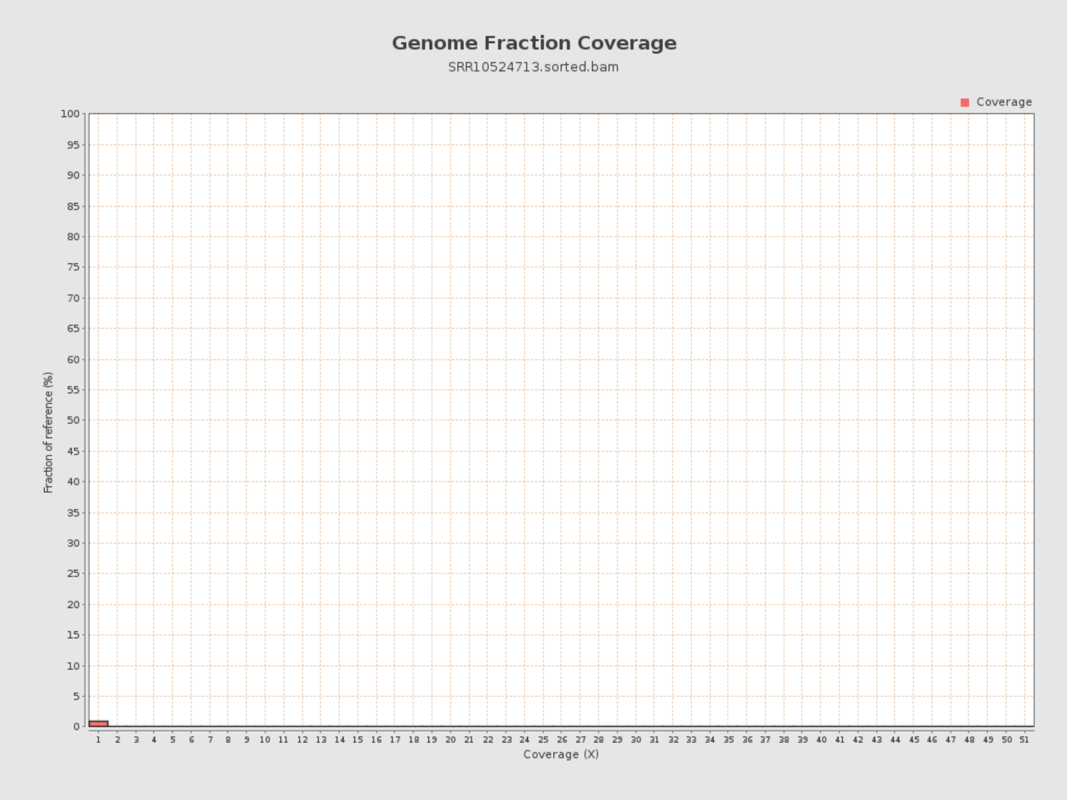
4. Results : Coverage Histogram



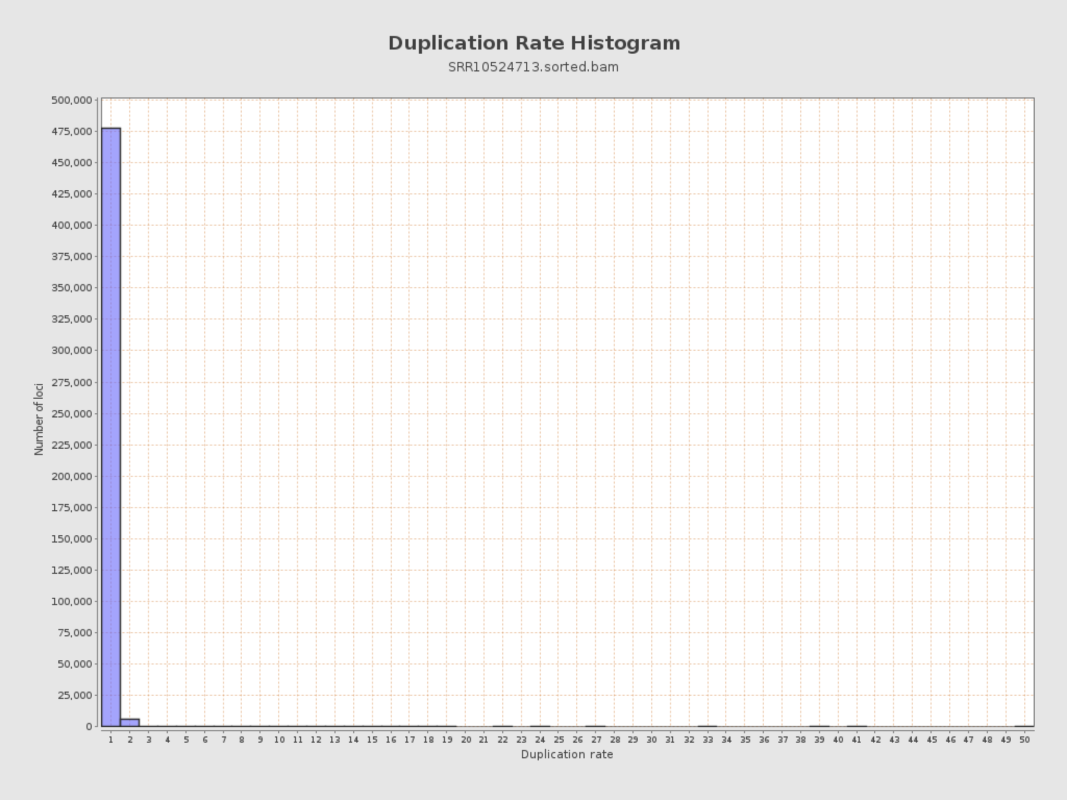
5. Results : Coverage Histogram (0-50X)



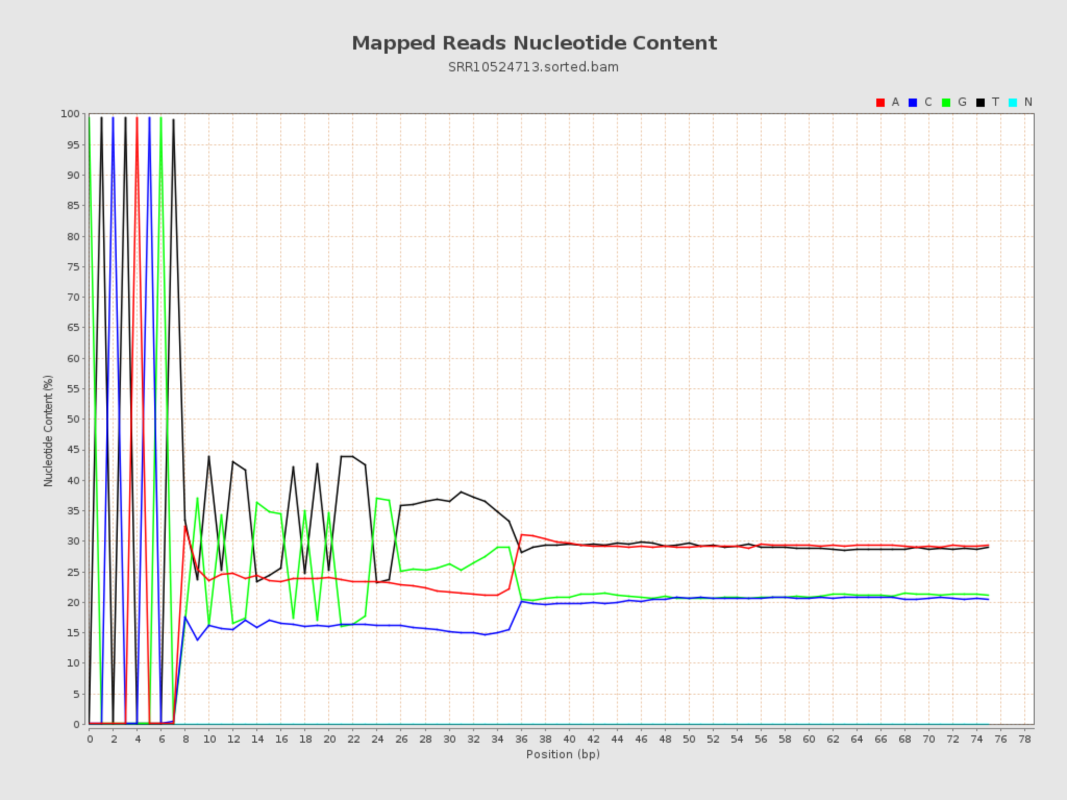
6. Results : Genome Fraction Coverage



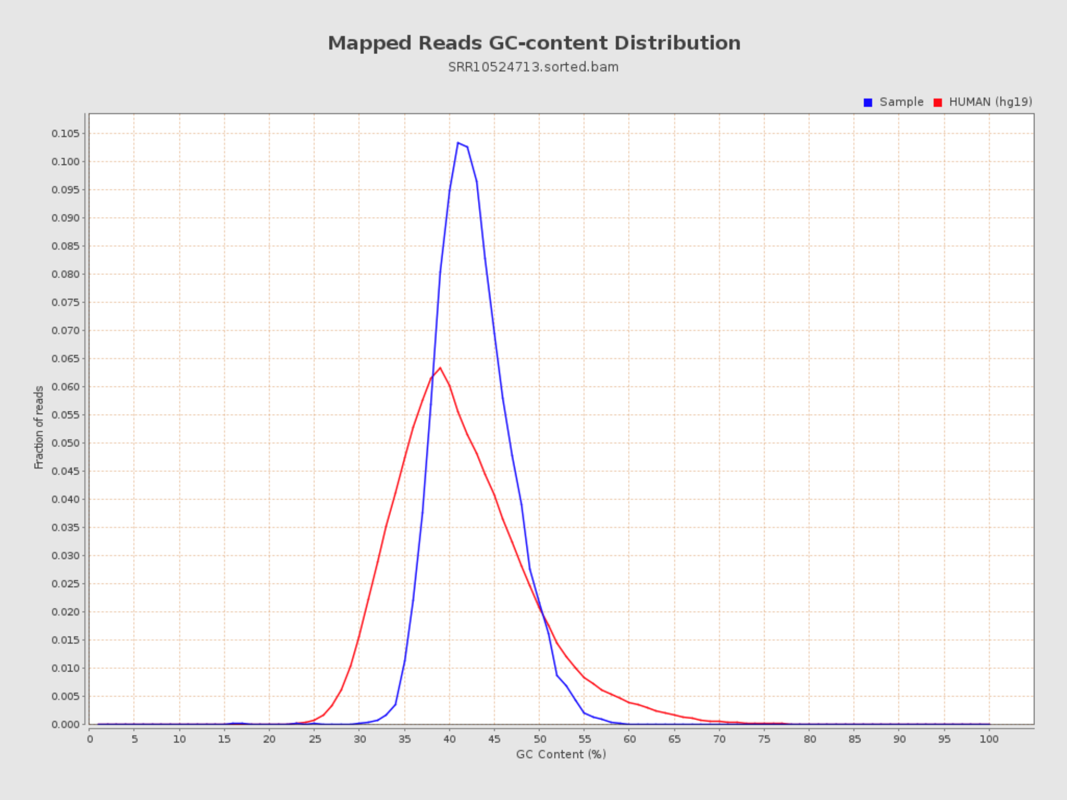
7. Results : Duplication Rate Histogram



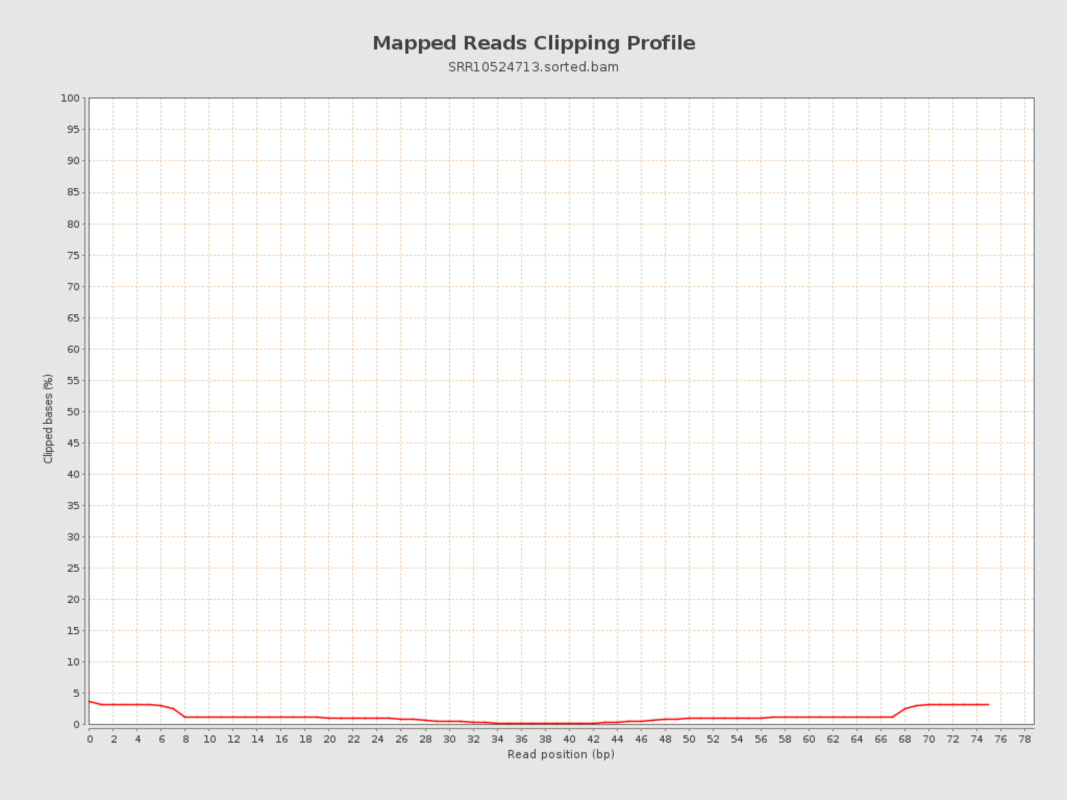
8. Results : Mapped Reads Nucleotide Content



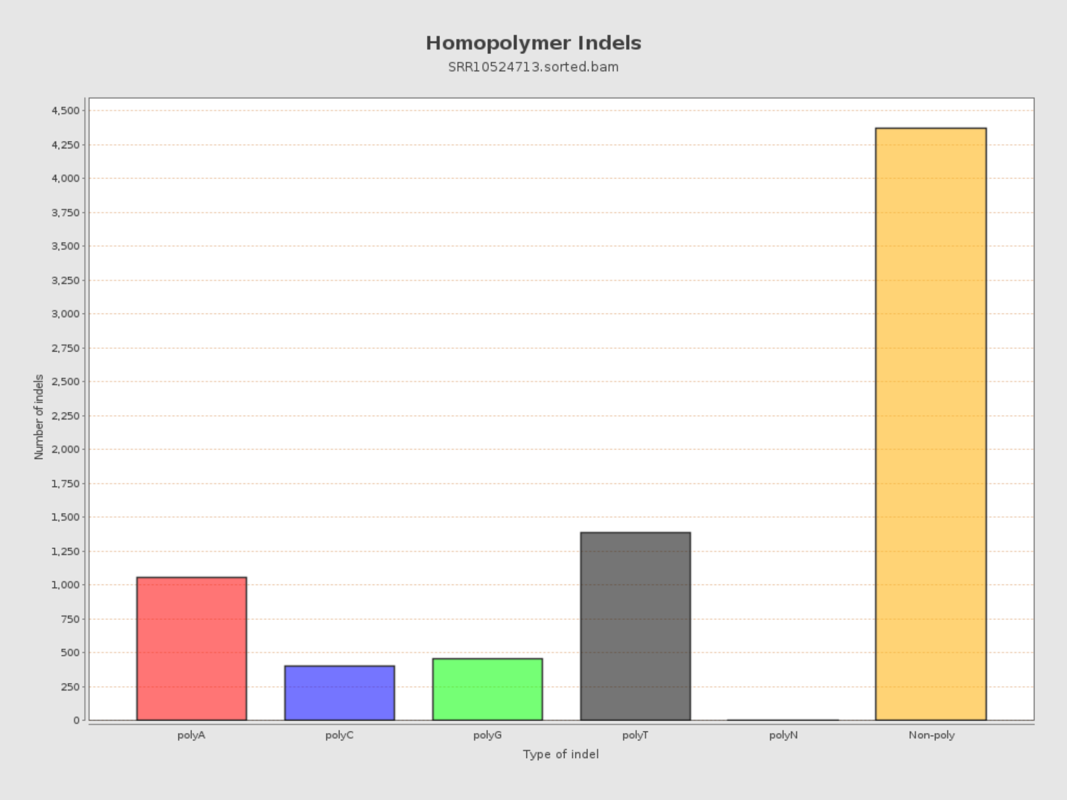
9. Results : Mapped Reads GC-content Distribution



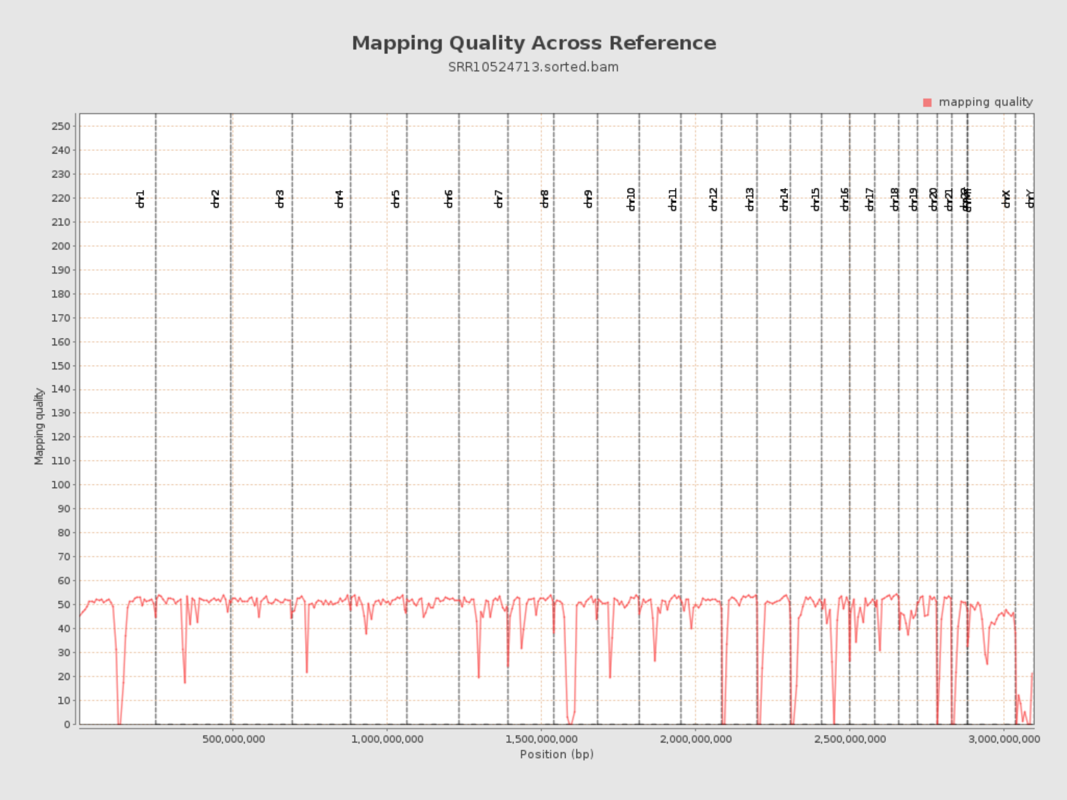
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram