Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 03:51:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524914.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_SRR10524914 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524914.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 03:51:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524914.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,151,113
Mapped reads	1,060,850 / 92.16%
Unmapped reads	90,263 / 7.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,966 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	41,284 / 3.59%
Duplication rate	3.02%
Clipped reads	1,061,884 / 92.25%

2.2. ACGT Content

Number/percentage of A's	15,568,872 / 25.31%
Number/percentage of C's	11,999,887 / 19.51%
Number/percentage of T's	19,348,075 / 31.46%
Number/percentage of G's	14,591,139 / 23.72%
Number/percentage of N's	507 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0199

Standard Deviation	0.203

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

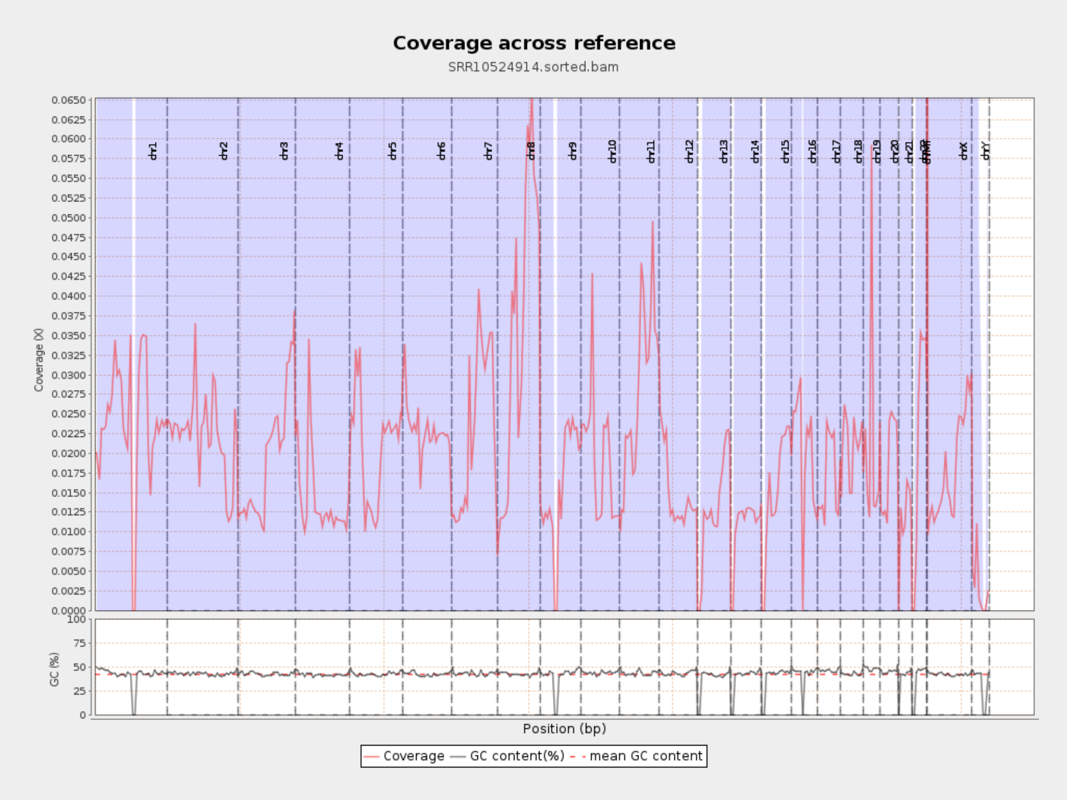
General error rate	0.52%
Mismatches	311,138
Insertions	4,047
Mapped reads with at least one insertion	0.38%
Deletions	11,693
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.13%

2.6. Chromosome stats

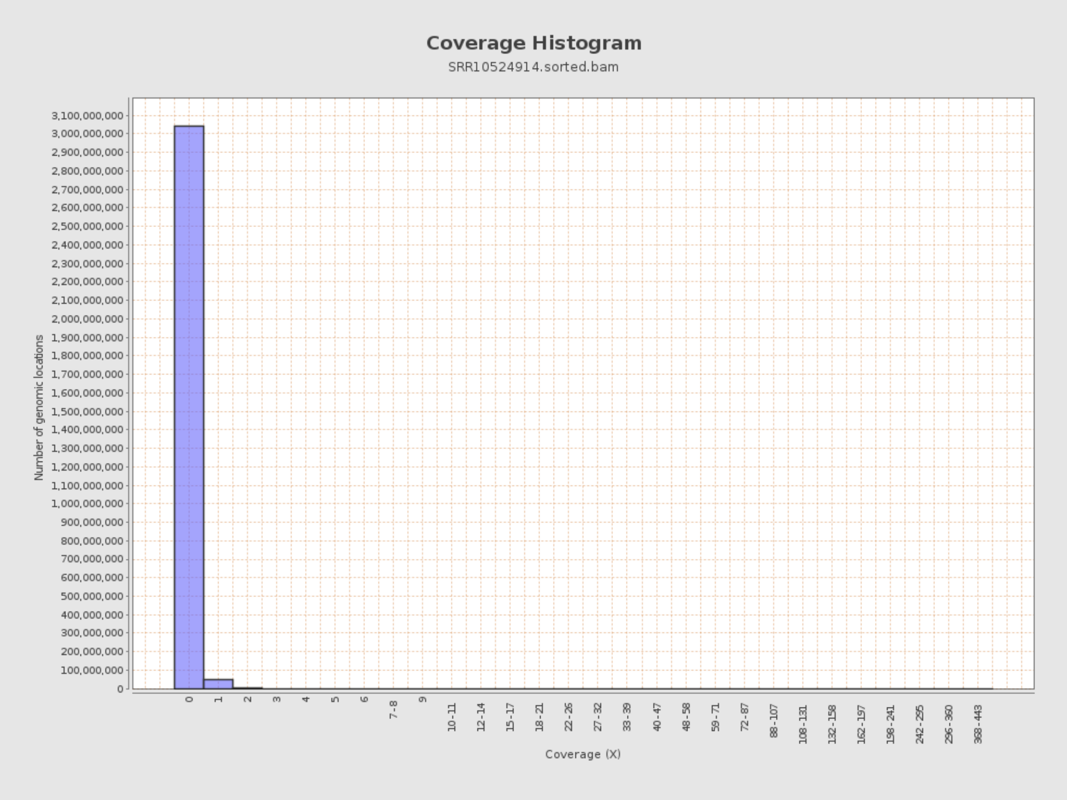
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5932292	0.0238	0.3479
chr2	243199373	5423035	0.0223	0.2428
chr3	198022430	3818943	0.0193	0.1515
chr4	191154276	2760233	0.0144	0.1519
chr5	180915260	3779050	0.0209	0.1564
chr6	171115067	3934811	0.023	0.1717
chr7	159138663	3714039	0.0233	0.2476

chr8	146364022	5357997	0.0366	0.2647
chr9	141213431	2189086	0.0155	0.1596
chr10	135534747	2685041	0.0198	0.2237
chr11	135006516	3842410	0.0285	0.2023
chr12	133851895	2020884	0.0151	0.1359
chr13	115169878	1468047	0.0127	0.1226
chr14	107349540	1137553	0.0106	0.1165
chr15	102531392	1535063	0.015	0.133
chr16	90354753	1811940	0.0201	0.1611
chr17	81195210	1368877	0.0169	0.1465
chr18	78077248	1634350	0.0209	0.2533
chr19	59128983	1270643	0.0215	0.2602
chr20	63025520	1173939	0.0186	0.1514
chr21	48129895	564202	0.0117	0.1339
chr22	51304566	1137188	0.0222	0.1623
chrMT	16571	7300	0.4405	0.6871
chrX	155270560	2788249	0.018	0.1577
chrY	59373566	172570	0.0029	0.0975

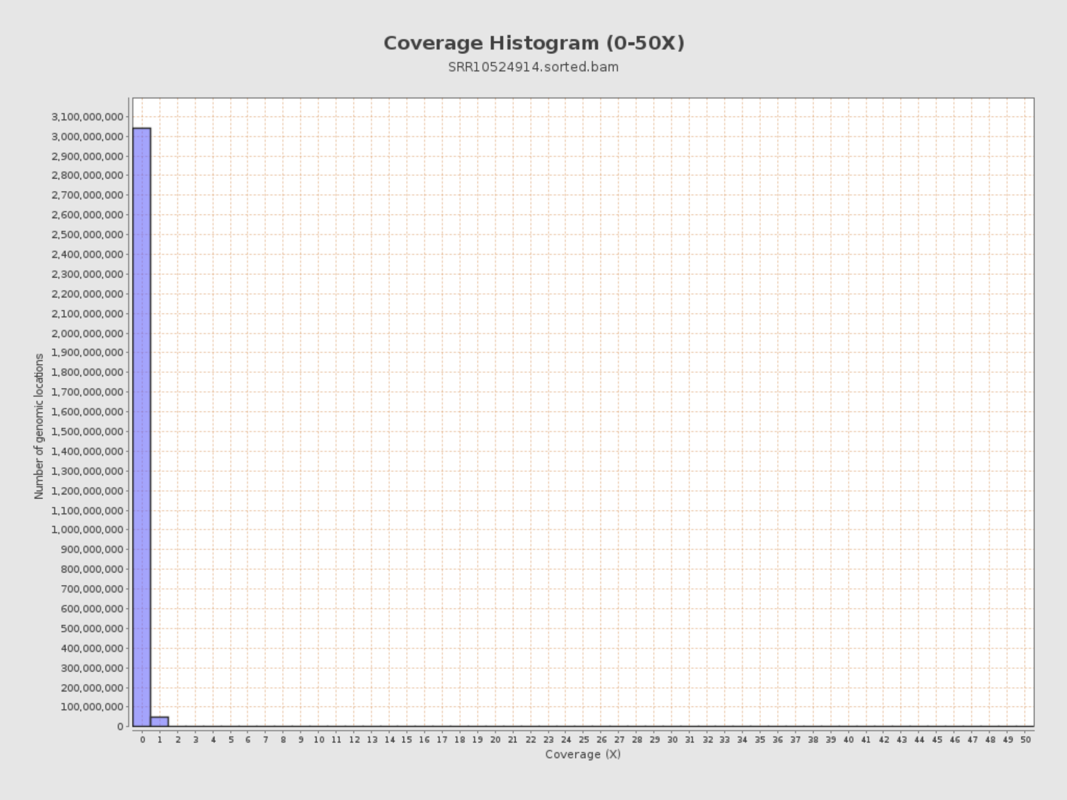
3. Results : Coverage across reference



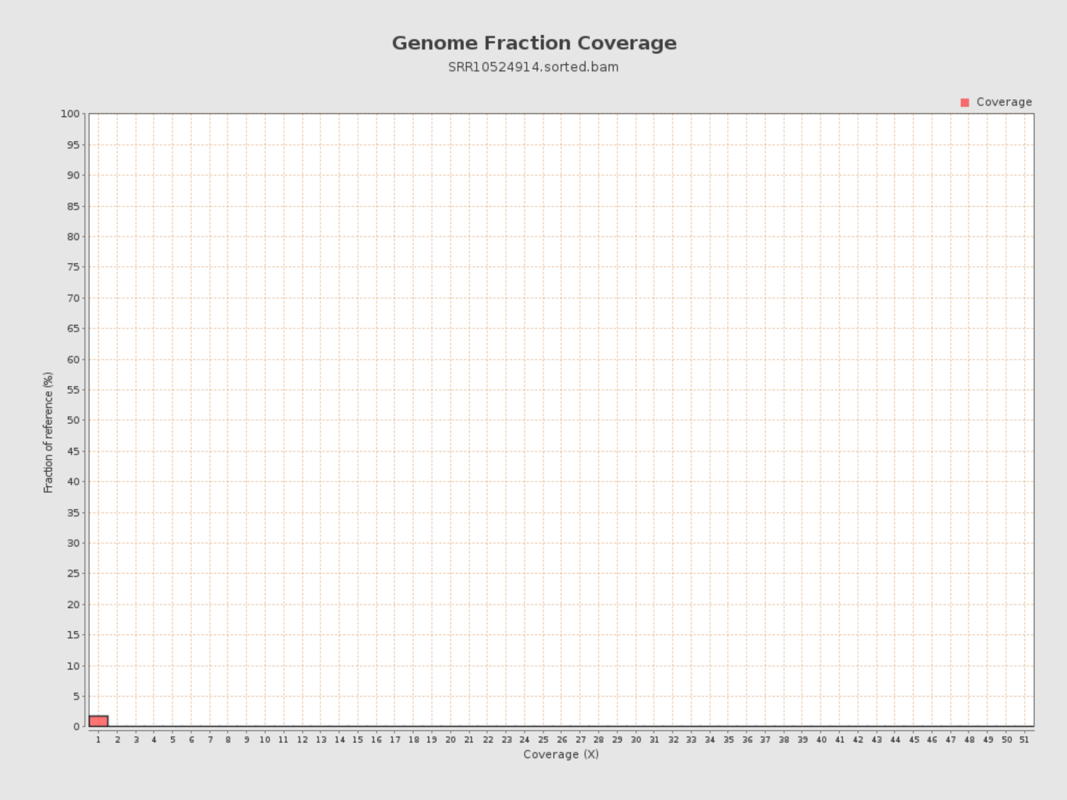
4. Results : Coverage Histogram



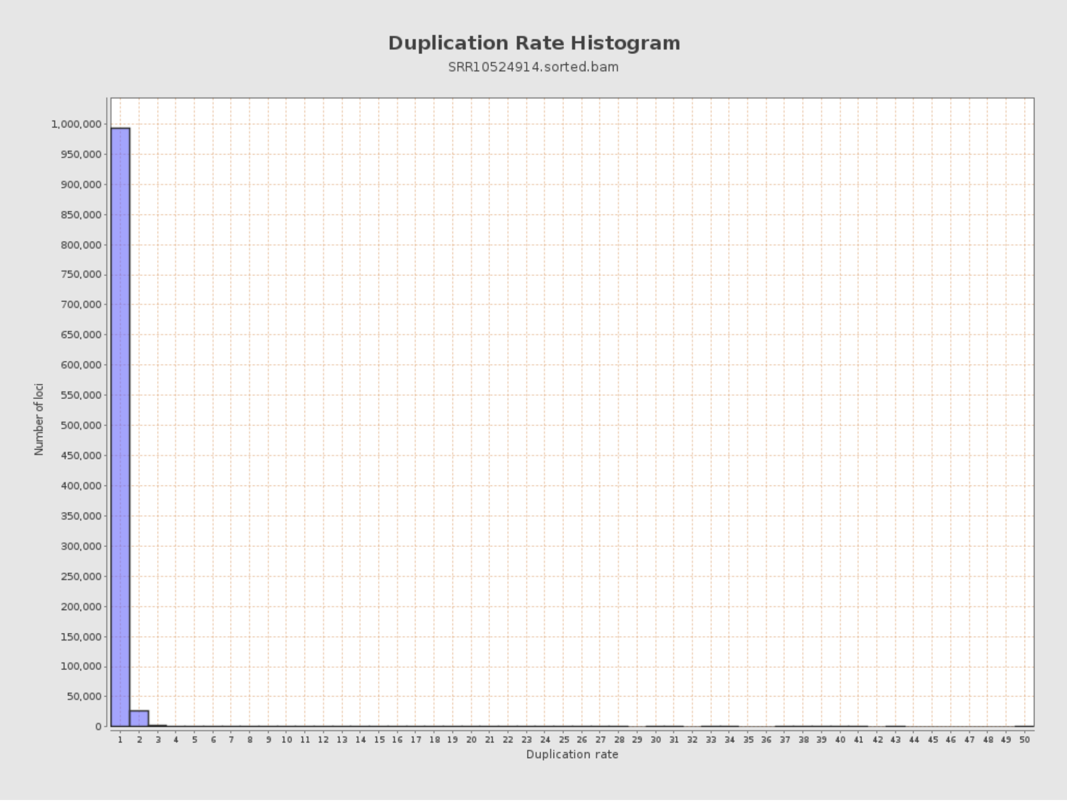
5. Results : Coverage Histogram (0-50X)



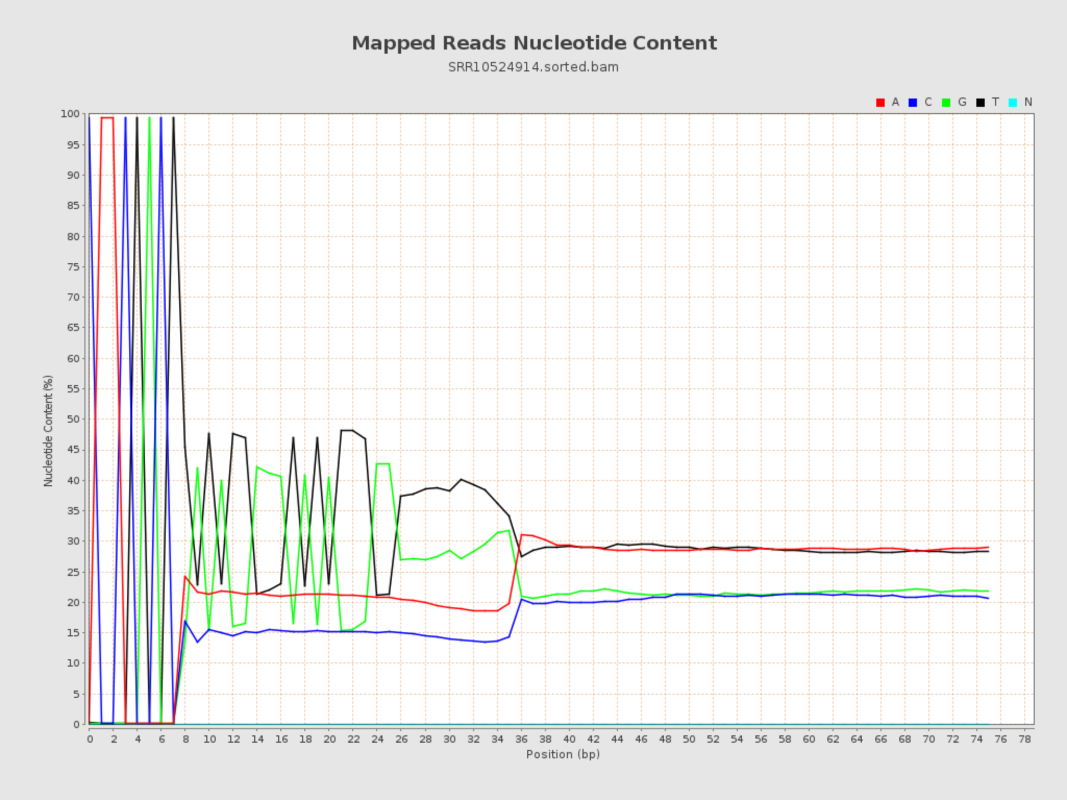
6. Results : Genome Fraction Coverage



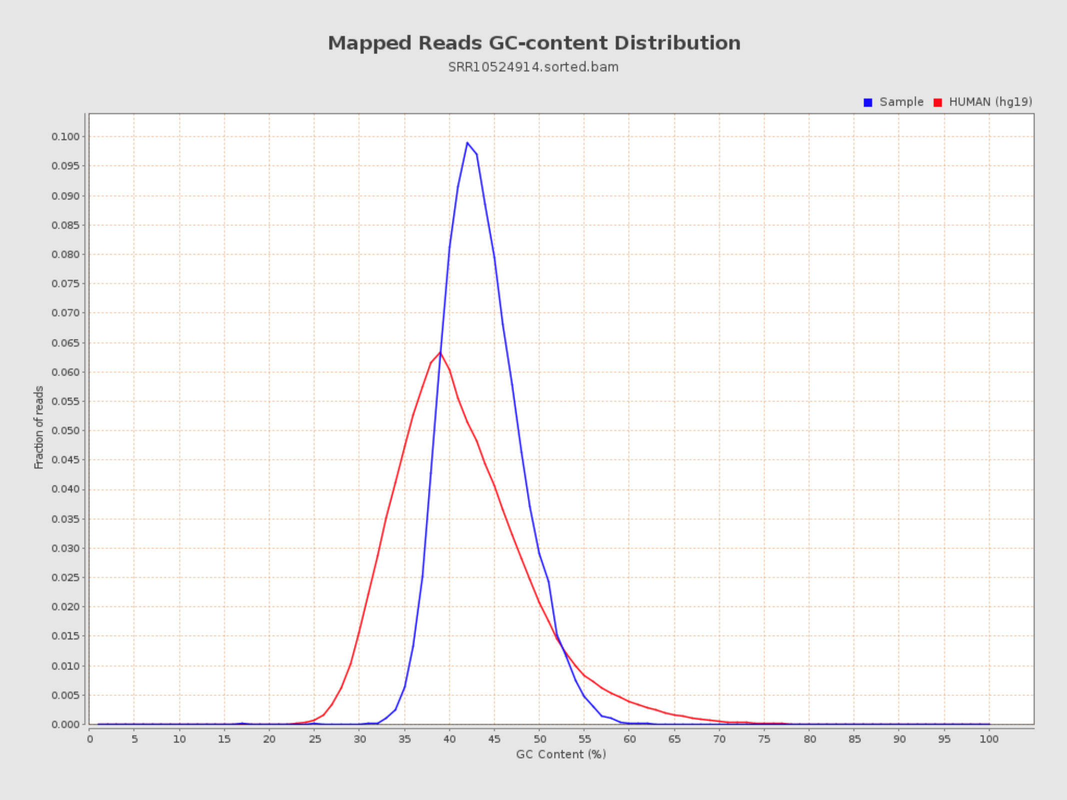
7. Results : Duplication Rate Histogram



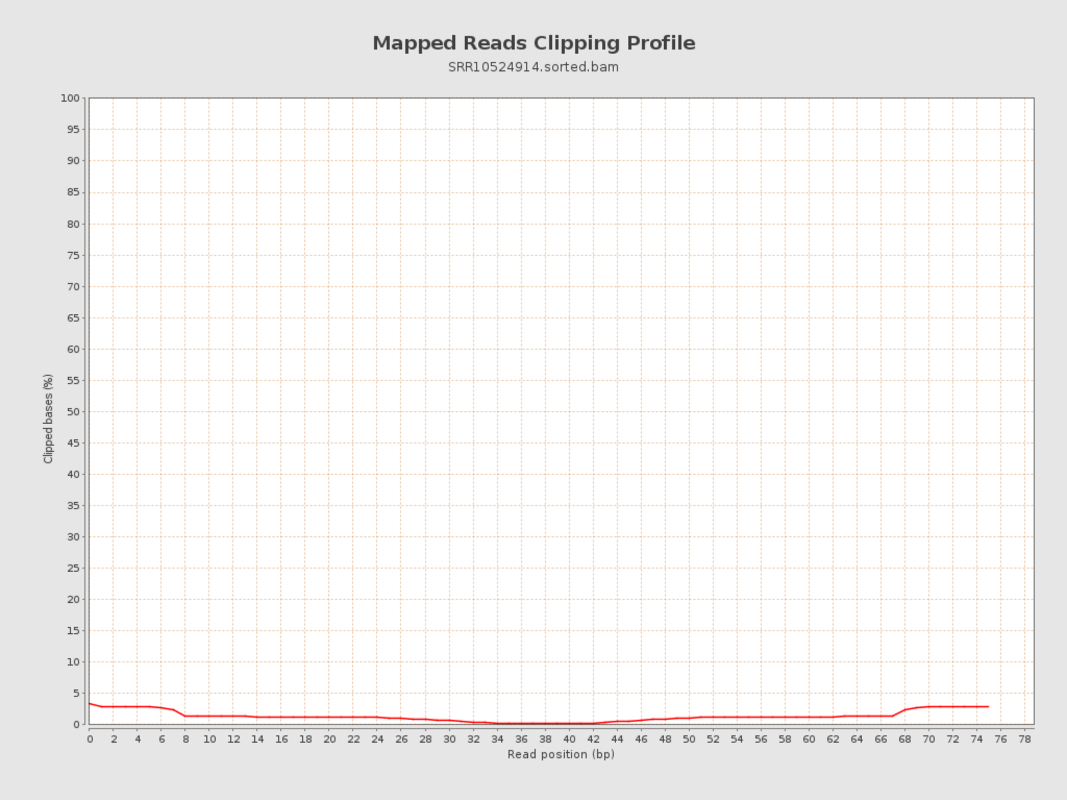
8. Results : Mapped Reads Nucleotide Content



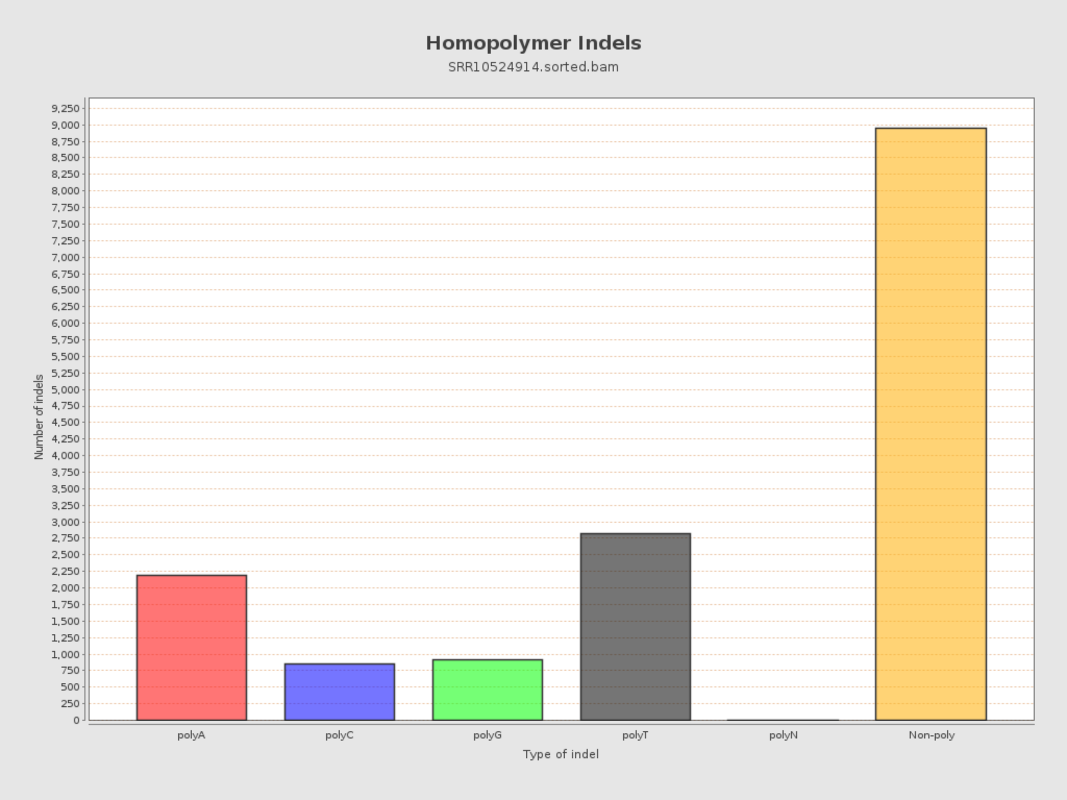
9. Results : Mapped Reads GC-content Distribution



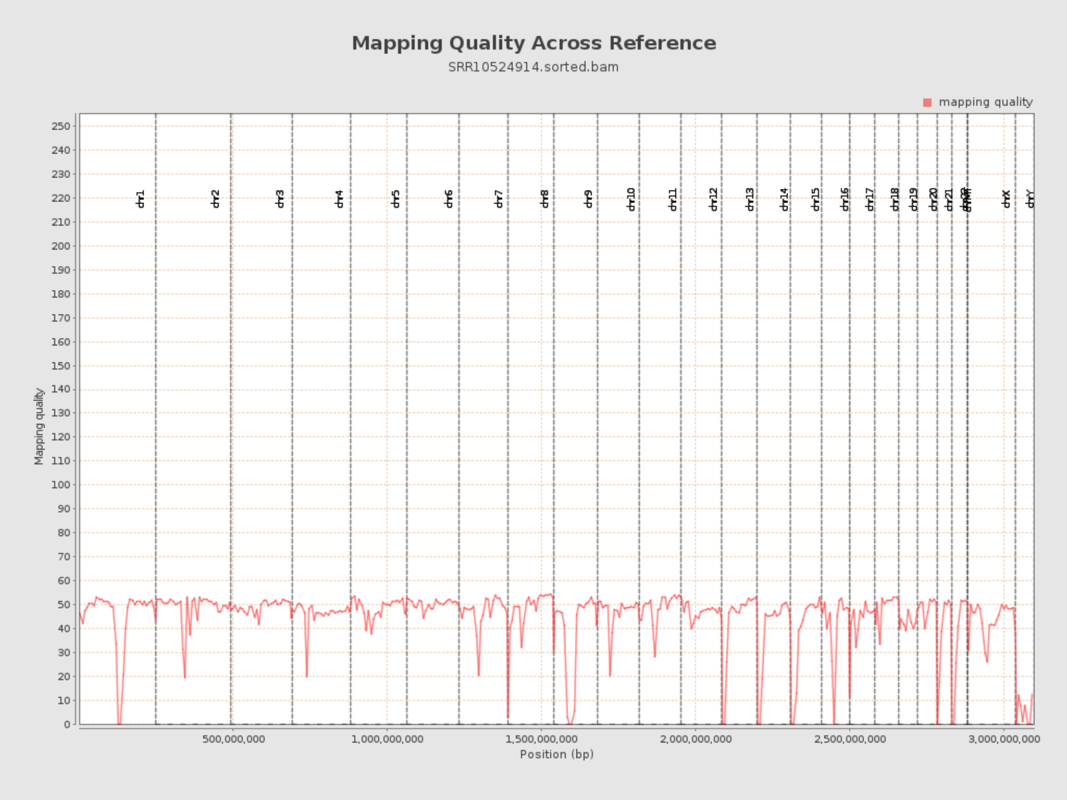
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram