Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:04:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524621.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_SRR10524621 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524621.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:04:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524621.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,022,527
Mapped reads	951,405 / 93.04%
Unmapped reads	71,122 / 6.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,183 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	30,166 / 2.95%
Duplication rate	2.47%
Clipped reads	951,907 / 93.09%

2.2. ACGT Content

Number/percentage of A's	13,804,529 / 24.89%
Number/percentage of C's	10,204,501 / 18.4%
Number/percentage of T's	17,907,308 / 32.28%
Number/percentage of G's	13,553,525 / 24.43%
Number/percentage of N's	368 / 0%
GC Percentage	42.83%

2.3. Coverage

Mean	0.0179

Standard Deviation	0.1811

2.4. Mapping Quality

Mean Mapping Quality	45.37

2.5. Mismatches and indels

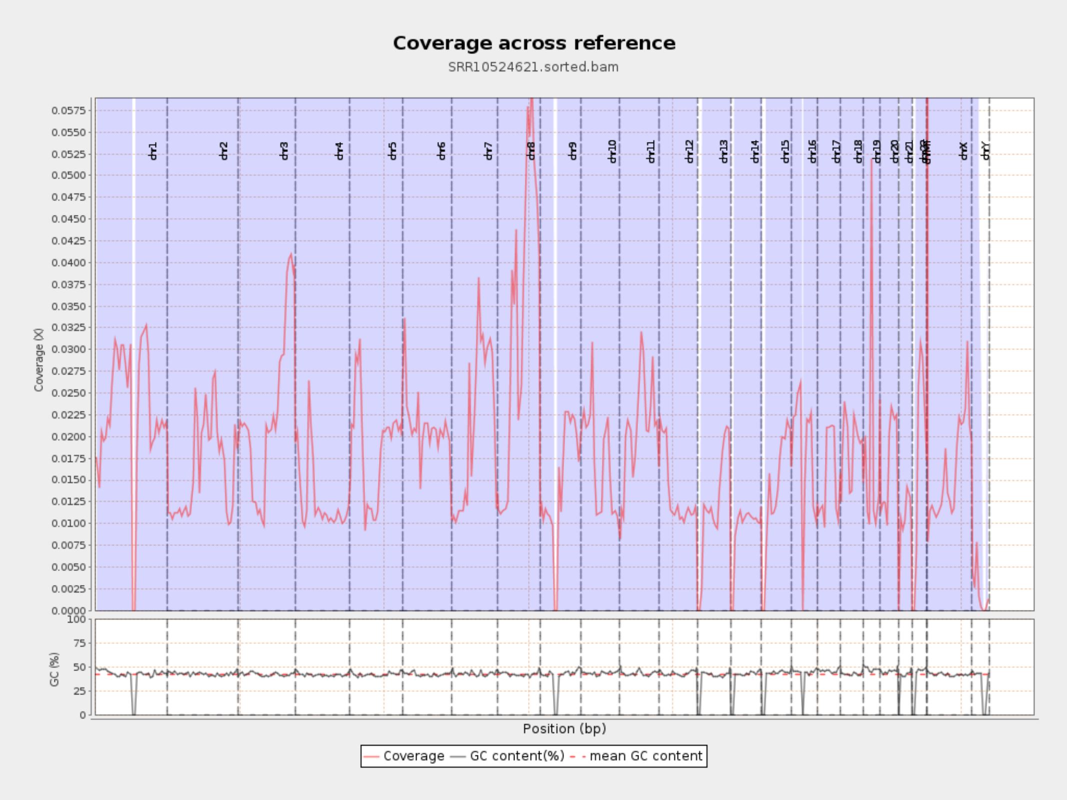
General error rate	0.47%
Mismatches	257,349
Insertions	3,071
Mapped reads with at least one insertion	0.32%
Deletions	10,553
Mapped reads with at least one deletion	1.1%
Homopolymer indels	44.14%

2.6. Chromosome stats

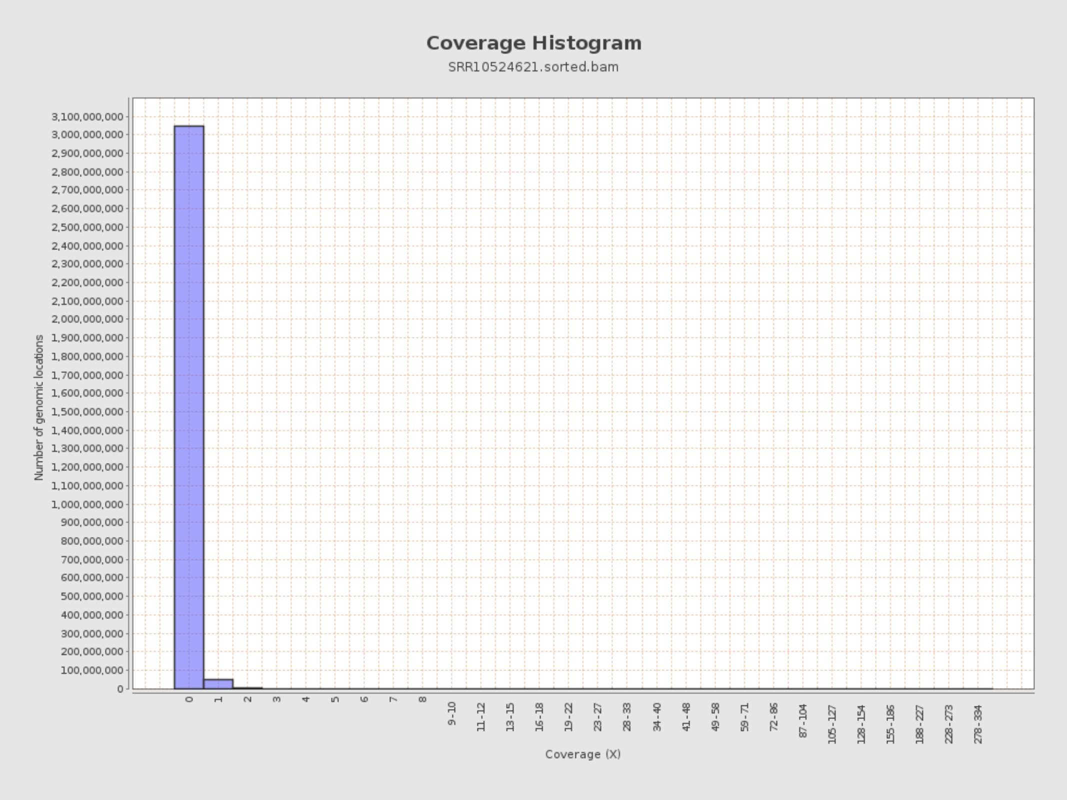
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5703590	0.0229	0.2925
chr2	243199373	3945339	0.0162	0.1903
chr3	198022430	4519368	0.0228	0.162
chr4	191154276	2486570	0.013	0.134
chr5	180915260	3438182	0.019	0.1479
chr6	171115067	3631950	0.0212	0.1646
chr7	159138663	3388786	0.0213	0.2325

chr8	146364022	4982585	0.034	0.2455
chr9	141213431	2049672	0.0145	0.1652
chr10	135534747	2362738	0.0174	0.1756
chr11	135006516	2856848	0.0212	0.1828
chr12	133851895	1820781	0.0136	0.1274
chr13	115169878	1378460	0.012	0.1174
chr14	107349540	987521	0.0092	0.1067
chr15	102531392	1389410	0.0136	0.1304
chr16	90354753	1627163	0.018	0.1501
chr17	81195210	1232045	0.0152	0.1354
chr18	78077248	1483899	0.019	0.242
chr19	59128983	1083347	0.0183	0.2116
chr20	63025520	1064374	0.0169	0.1399
chr21	48129895	496074	0.0103	0.1163
chr22	51304566	905671	0.0177	0.1419
chrMT	16571	20209	1.2195	1.2603
chrX	155270560	2503265	0.0161	0.1486
chrY	59373566	130508	0.0022	0.0714

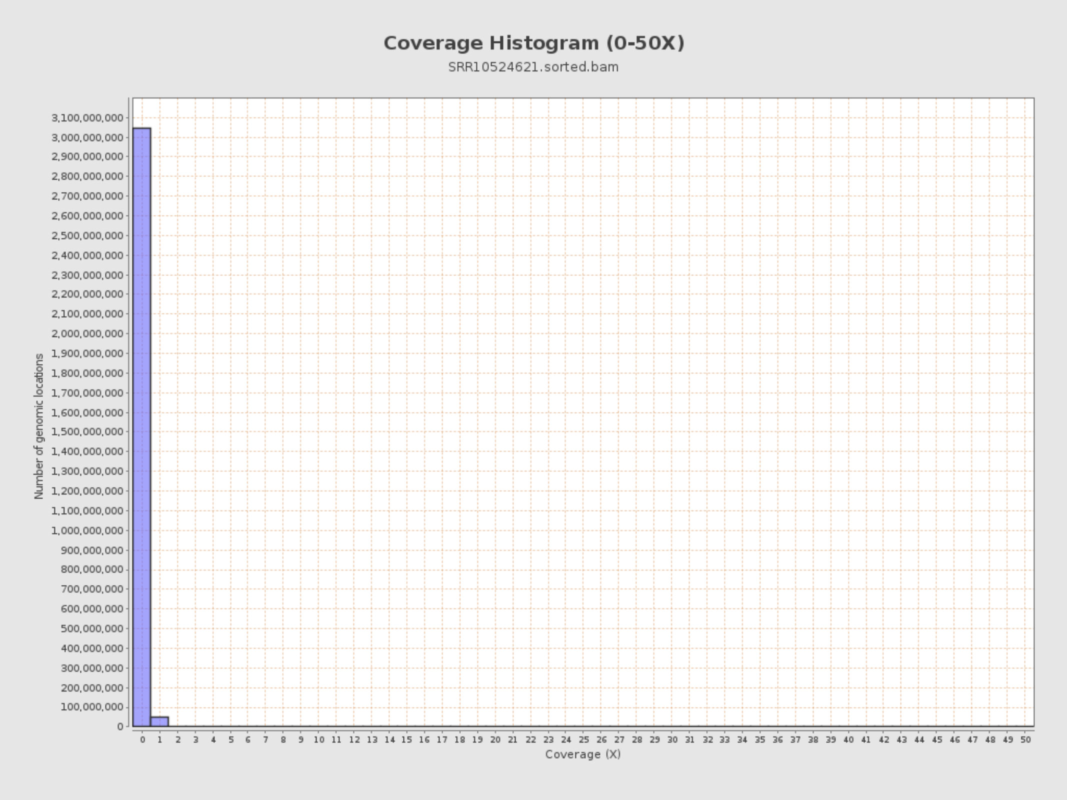
3. Results : Coverage across reference



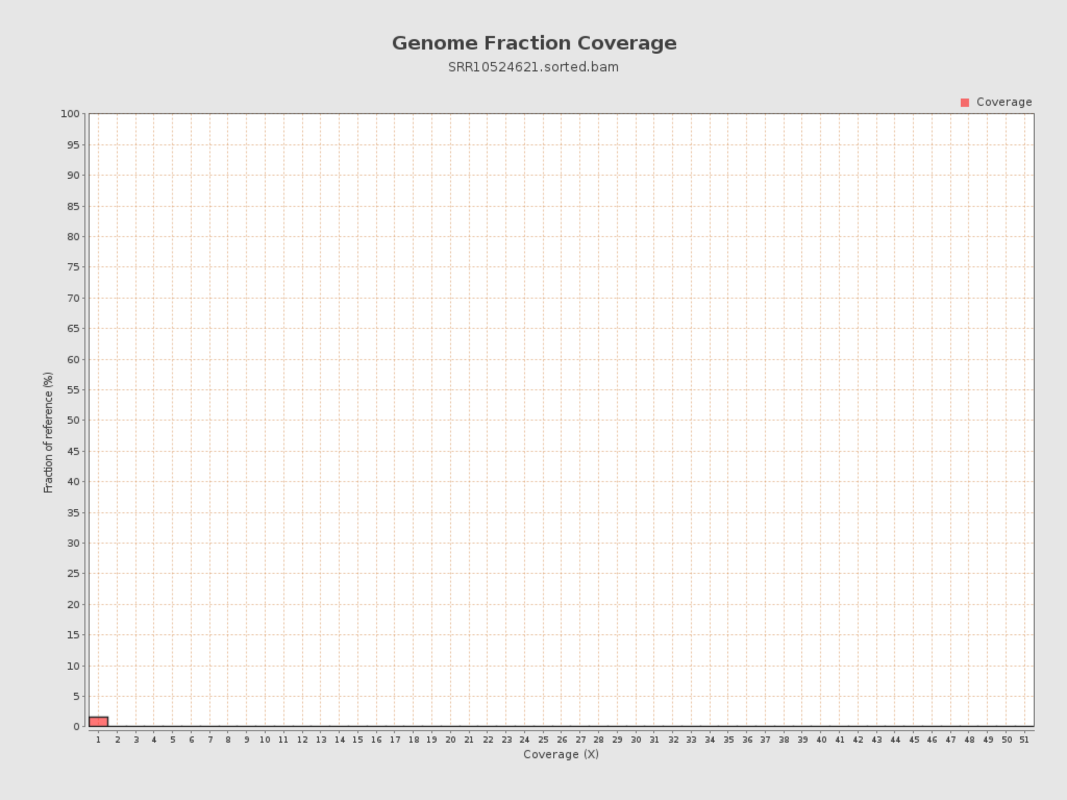
4. Results : Coverage Histogram



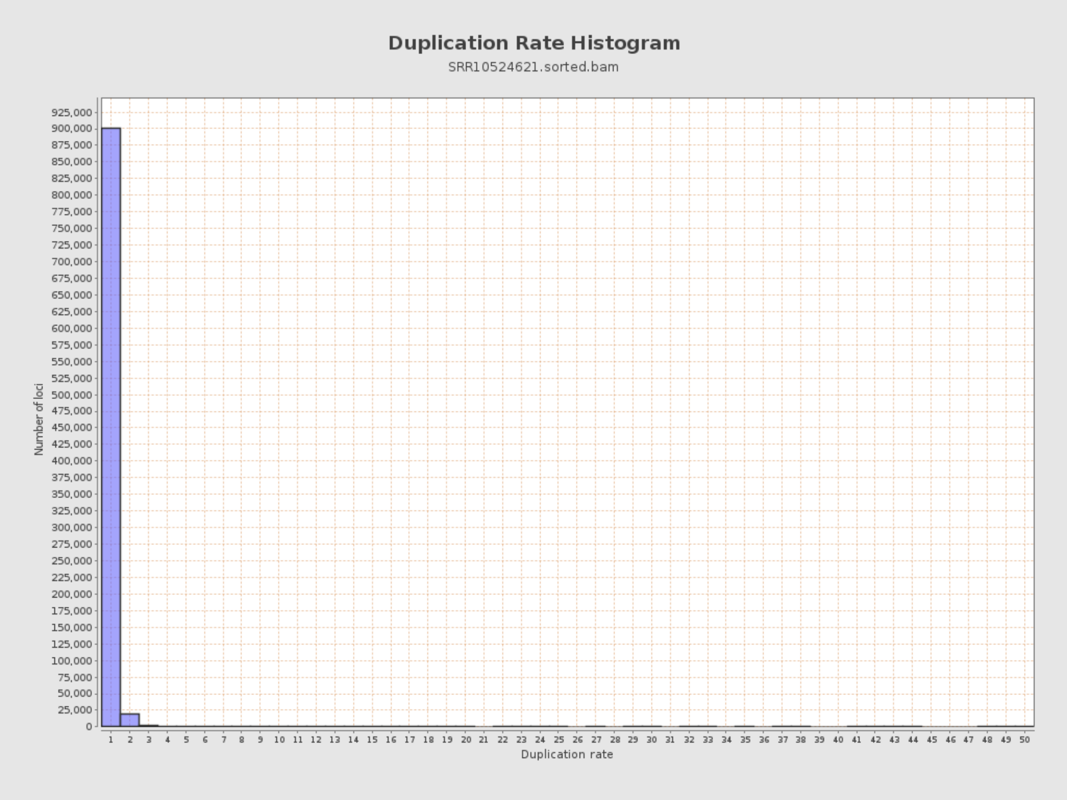
5. Results : Coverage Histogram (0-50X)



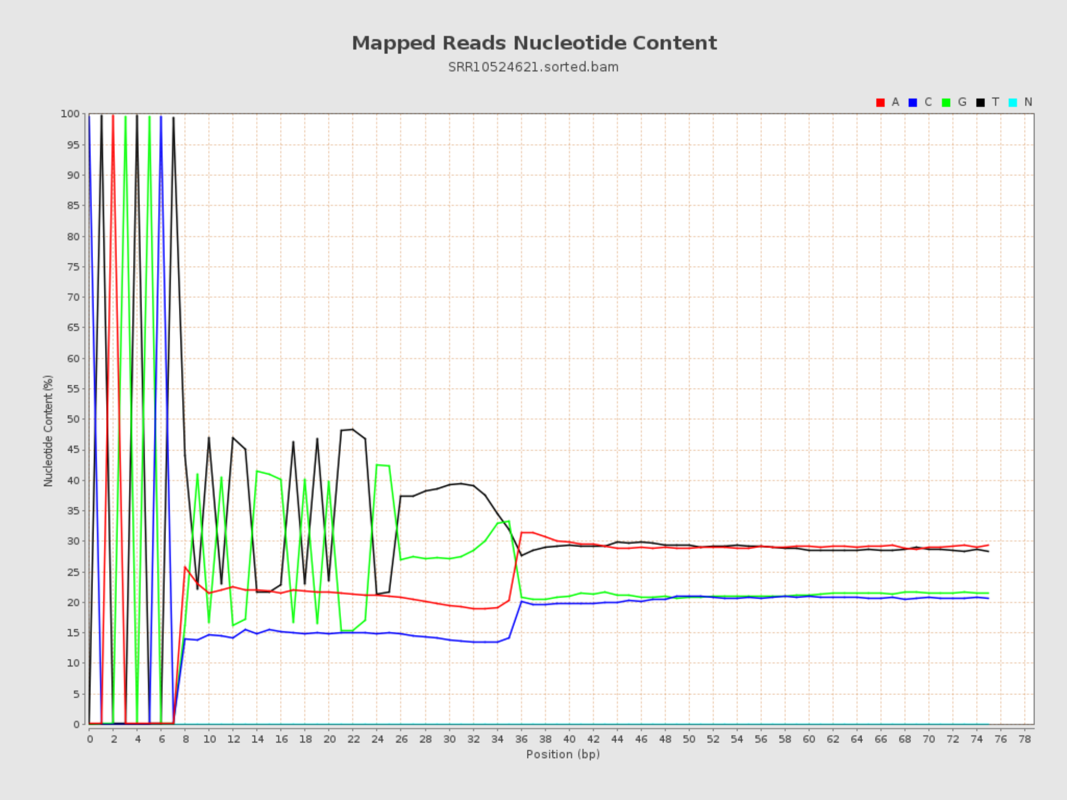
6. Results : Genome Fraction Coverage



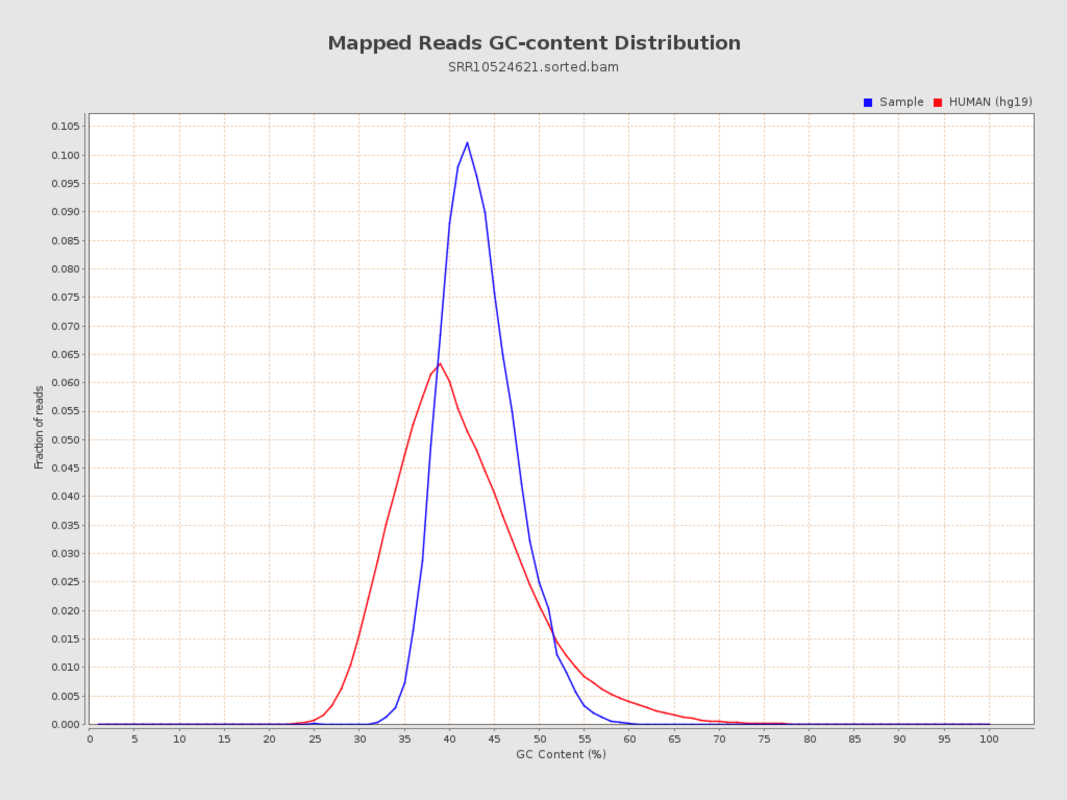
7. Results : Duplication Rate Histogram



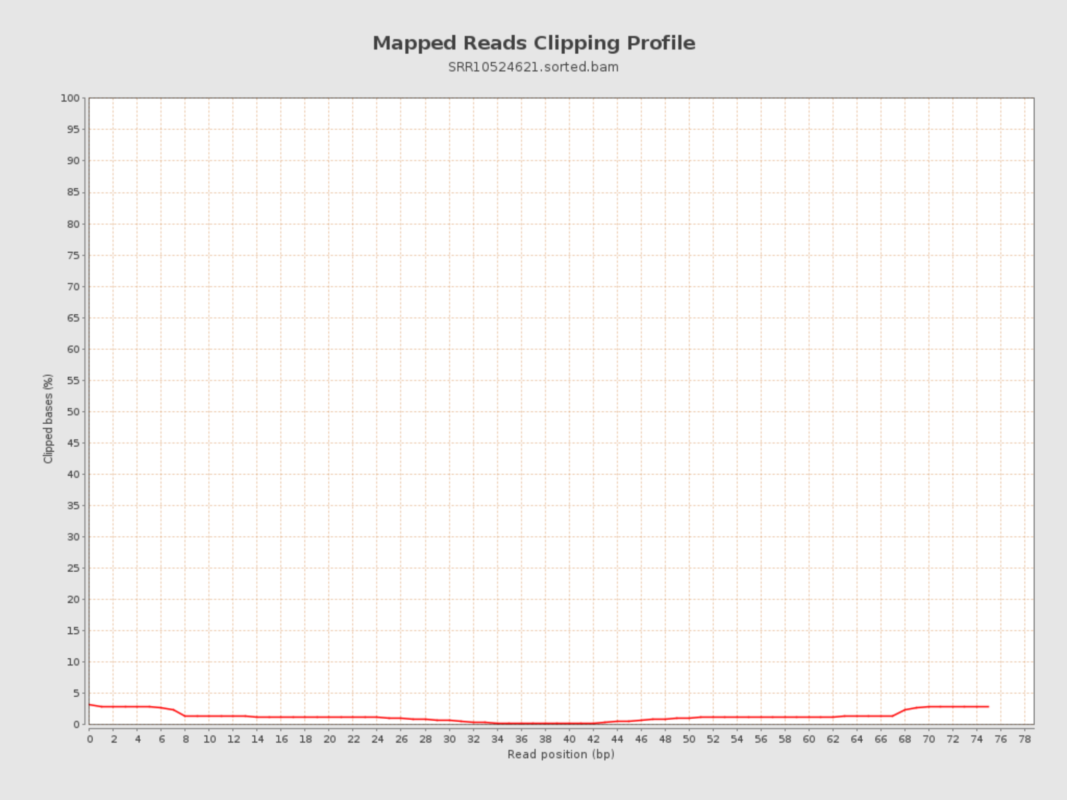
8. Results : Mapped Reads Nucleotide Content



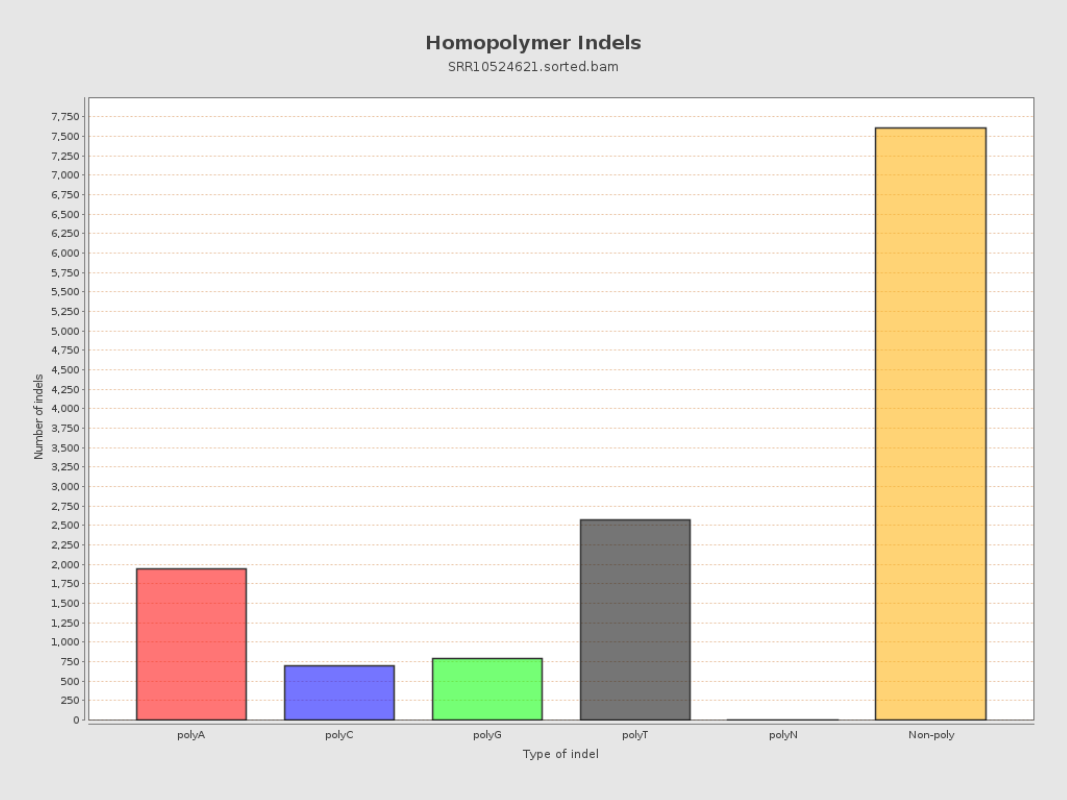
9. Results : Mapped Reads GC-content Distribution



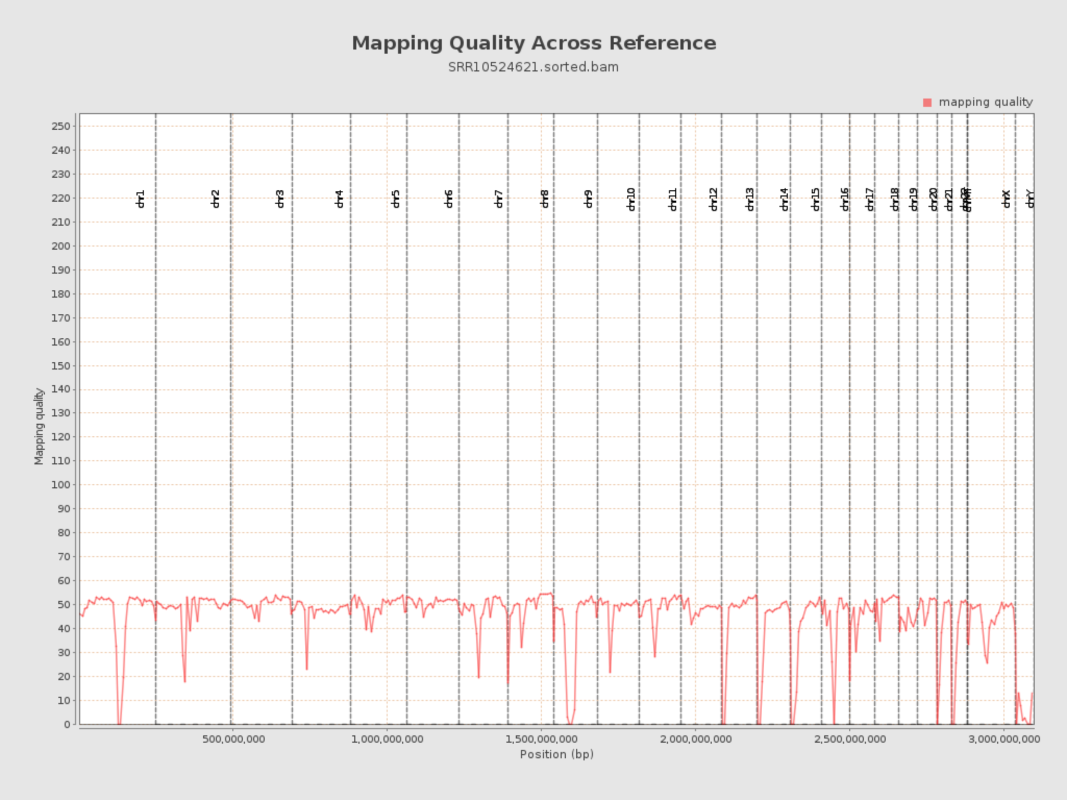
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram