Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:02:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524606.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_SRR10524606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524606.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:02:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,348,734
Mapped reads	1,250,928 / 92.75%
Unmapped reads	97,806 / 7.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,903 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	53,791 / 3.99%
Duplication rate	3.4%
Clipped reads	1,252,665 / 92.88%

2.2. ACGT Content

Number/percentage of A's	18,458,616 / 25.42%
Number/percentage of C's	14,012,822 / 19.3%
Number/percentage of T's	22,870,686 / 31.5%
Number/percentage of G's	17,264,176 / 23.78%
Number/percentage of N's	439 / 0%
GC Percentage	43.08%

2.3. Coverage

Mean	0.0235

Standard Deviation	0.2223

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

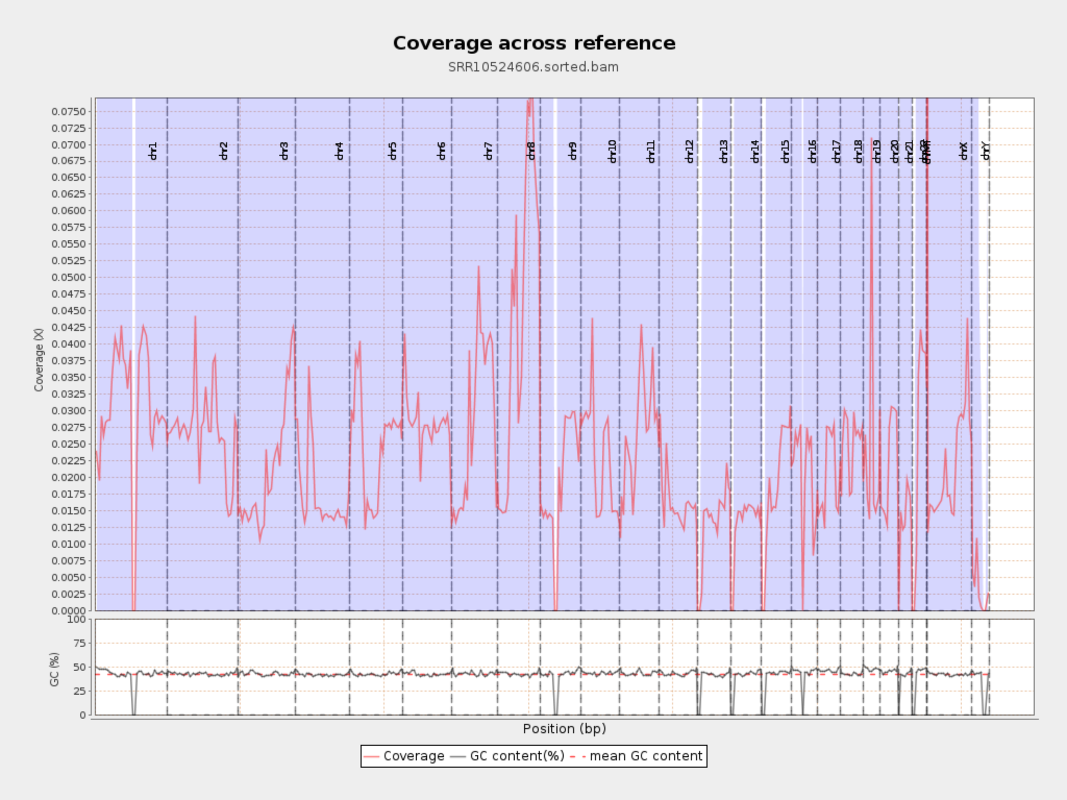
General error rate	0.48%
Mismatches	343,392
Insertions	3,872
Mapped reads with at least one insertion	0.31%
Deletions	13,629
Mapped reads with at least one deletion	1.08%
Homopolymer indels	45.03%

2.6. Chromosome stats

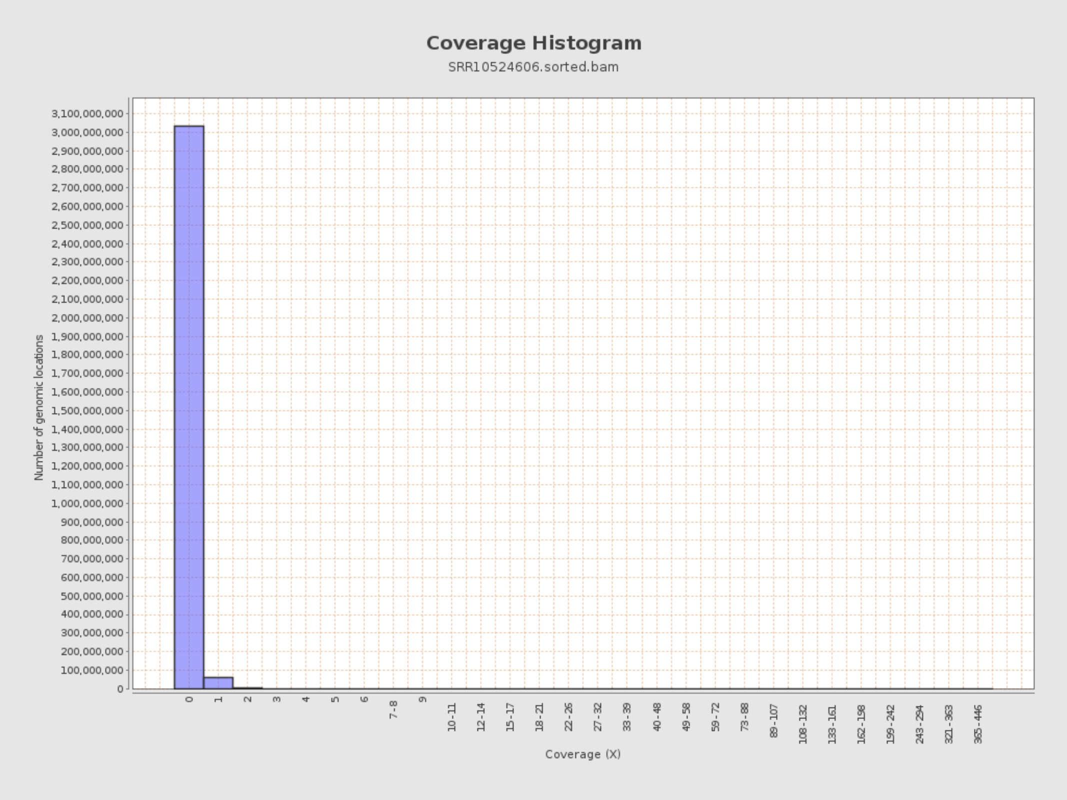
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7598795	0.0305	0.3557
chr2	243199373	6558774	0.027	0.2618
chr3	198022430	4201874	0.0212	0.1617
chr4	191154276	3383762	0.0177	0.1645
chr5	180915260	4540199	0.0251	0.1748
chr6	171115067	4838891	0.0283	0.1957
chr7	159138663	4548336	0.0286	0.3071

chr8	146364022	6652506	0.0455	0.3049
chr9	141213431	2690938	0.0191	0.2013
chr10	135534747	3181219	0.0235	0.2228
chr11	135006516	3647918	0.027	0.214
chr12	133851895	2205884	0.0165	0.1469
chr13	115169878	1489165	0.0129	0.125
chr14	107349540	1378633	0.0128	0.1305
chr15	102531392	1862500	0.0182	0.1544
chr16	90354753	1826171	0.0202	0.1639
chr17	81195210	1618176	0.0199	0.1596
chr18	78077248	1962896	0.0251	0.308
chr19	59128983	1480866	0.025	0.2597
chr20	63025520	1402125	0.0222	0.1677
chr21	48129895	658048	0.0137	0.1414
chr22	51304566	1334358	0.026	0.178
chrMT	16571	14123	0.8523	1.0772
chrX	155270560	3372448	0.0217	0.1815
chrY	59373566	181306	0.0031	0.0952

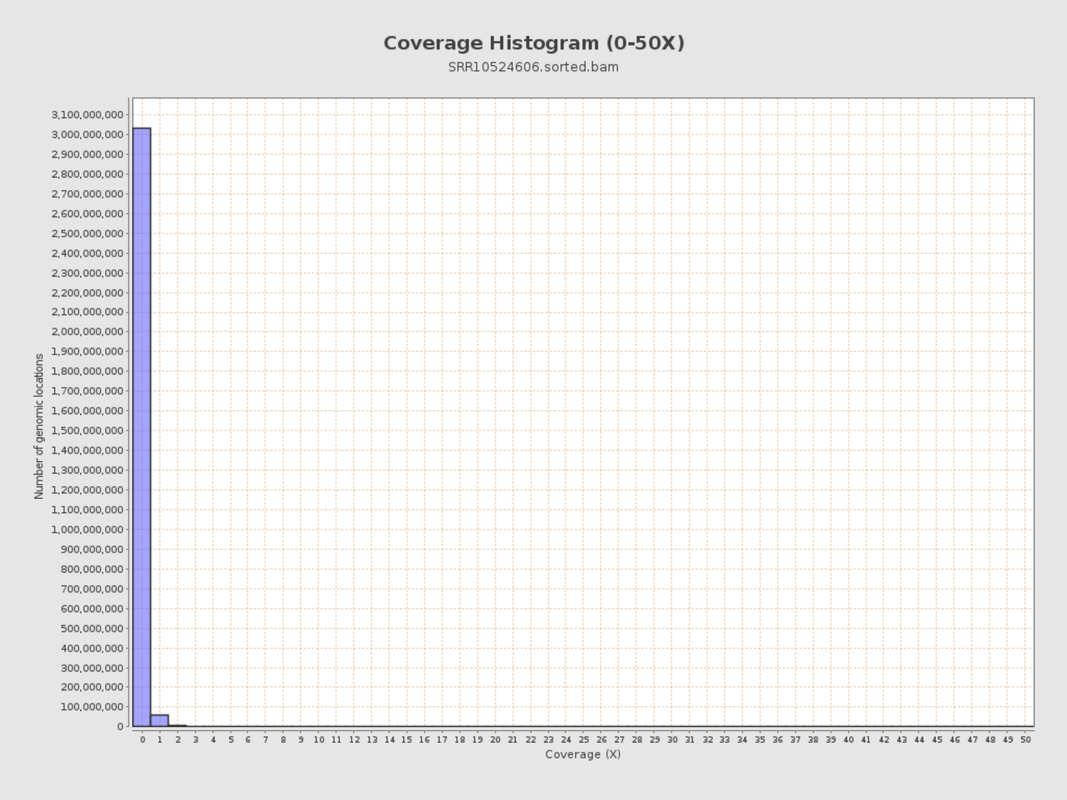
3. Results : Coverage across reference



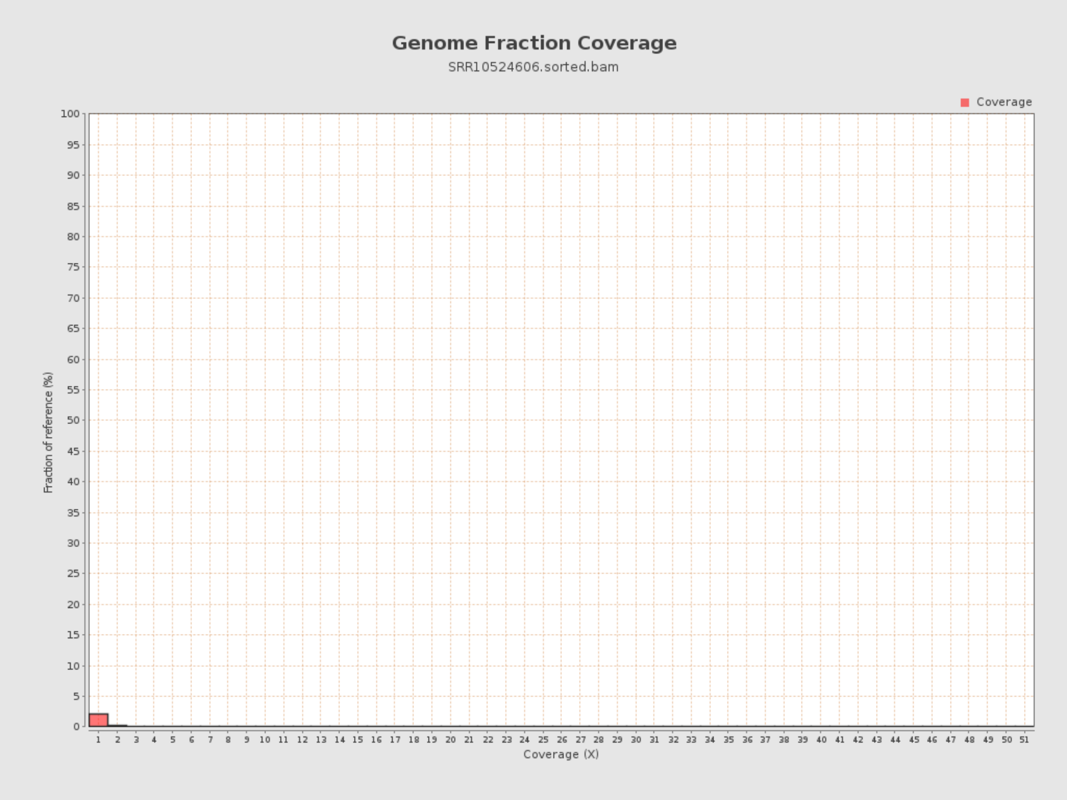
4. Results : Coverage Histogram



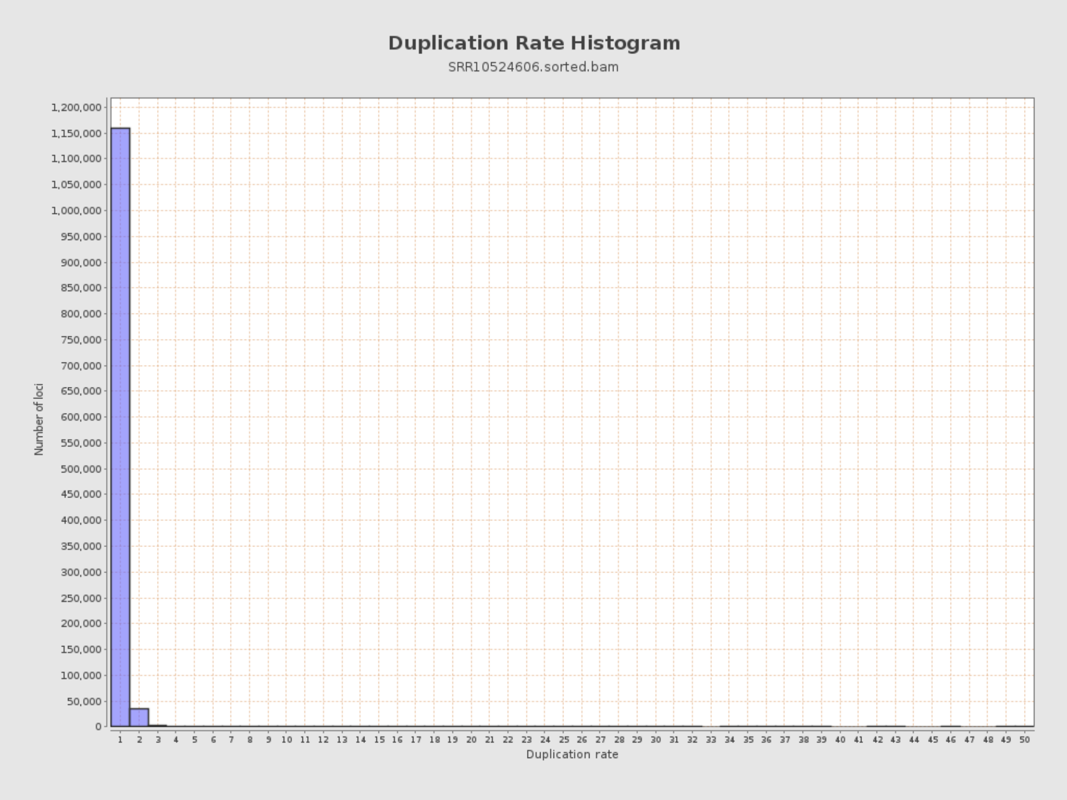
5. Results : Coverage Histogram (0-50X)



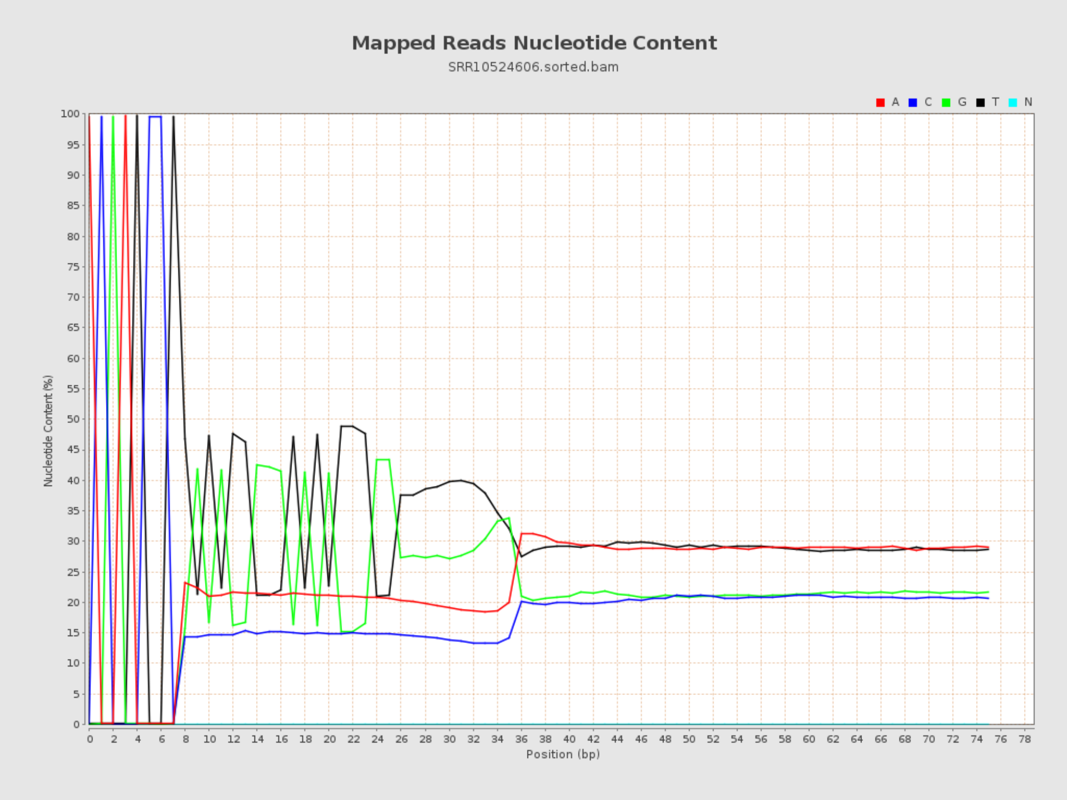
6. Results : Genome Fraction Coverage



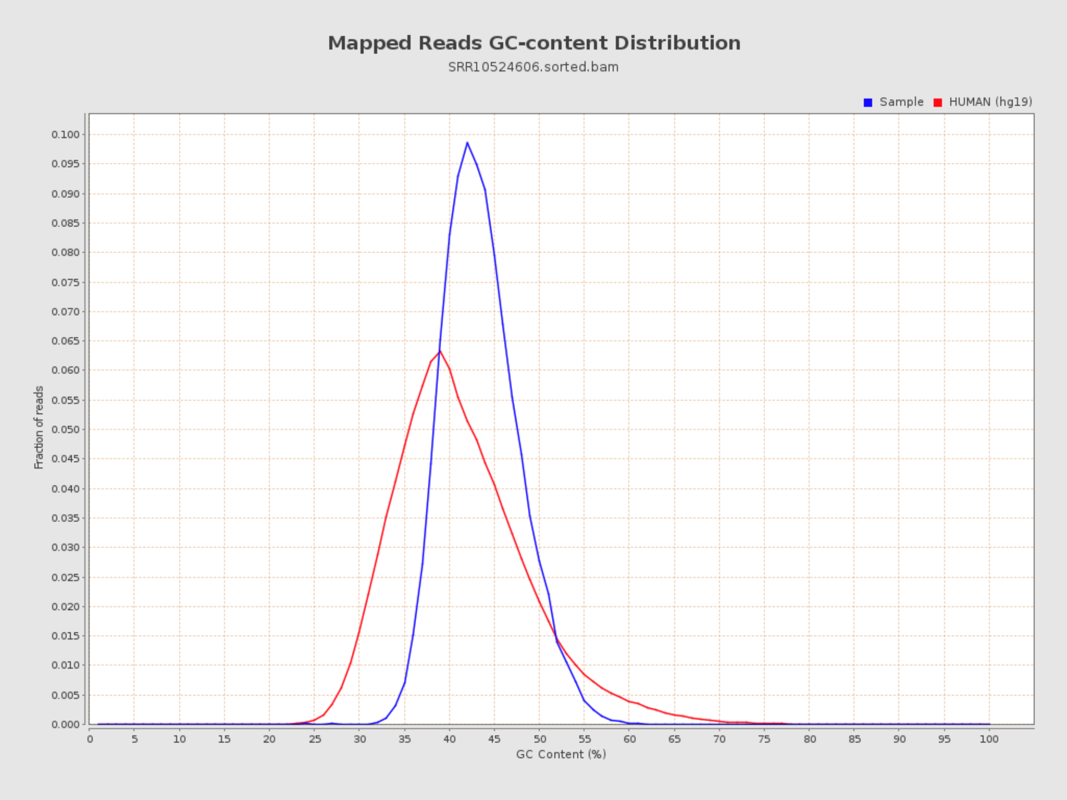
7. Results : Duplication Rate Histogram



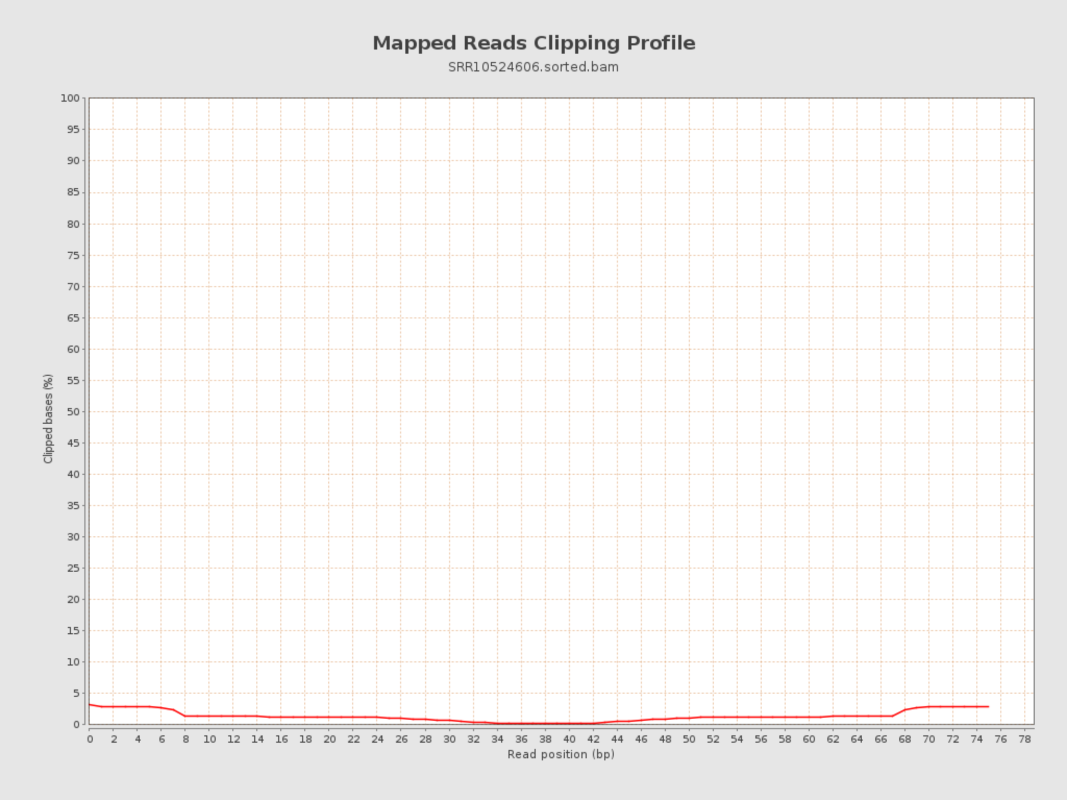
8. Results : Mapped Reads Nucleotide Content



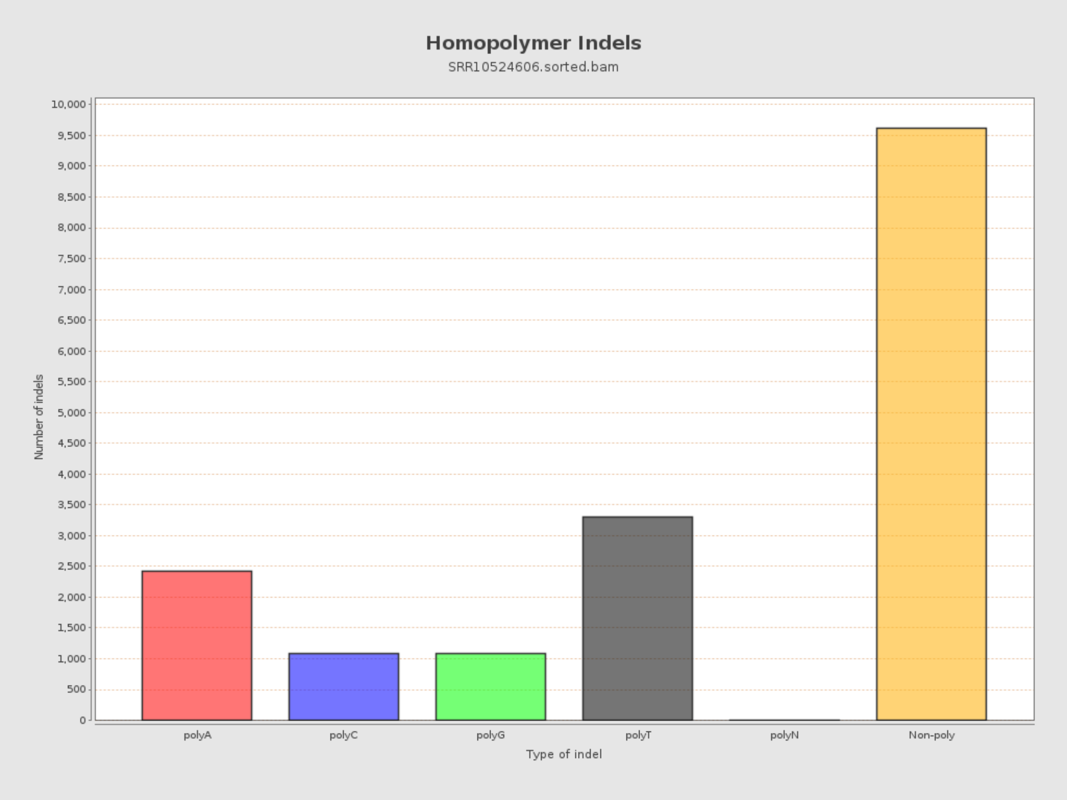
9. Results : Mapped Reads GC-content Distribution



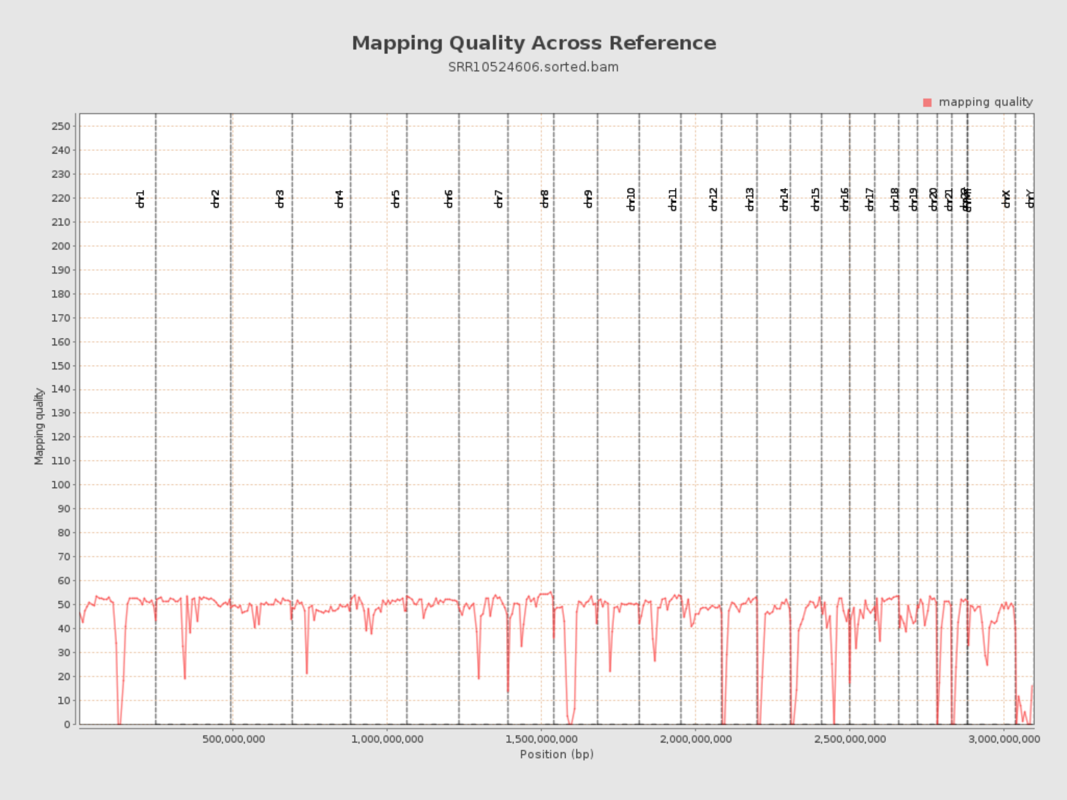
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram