Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 18:30:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524442.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_SRR10524442 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524442.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 18:30:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524442.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,209,083
Mapped reads	2,986,929 / 93.08%
Unmapped reads	222,154 / 6.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,778 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	207,336 / 6.46%
Duplication rate	5.23%
Clipped reads	2,982,721 / 92.95%

2.2. ACGT Content

Number/percentage of A's	45,450,225 / 25.9%
Number/percentage of C's	31,410,313 / 17.9%
Number/percentage of T's	54,700,821 / 31.17%
Number/percentage of G's	43,943,984 / 25.04%
Number/percentage of N's	3,624 / 0%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0567

Standard Deviation	0.4755

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

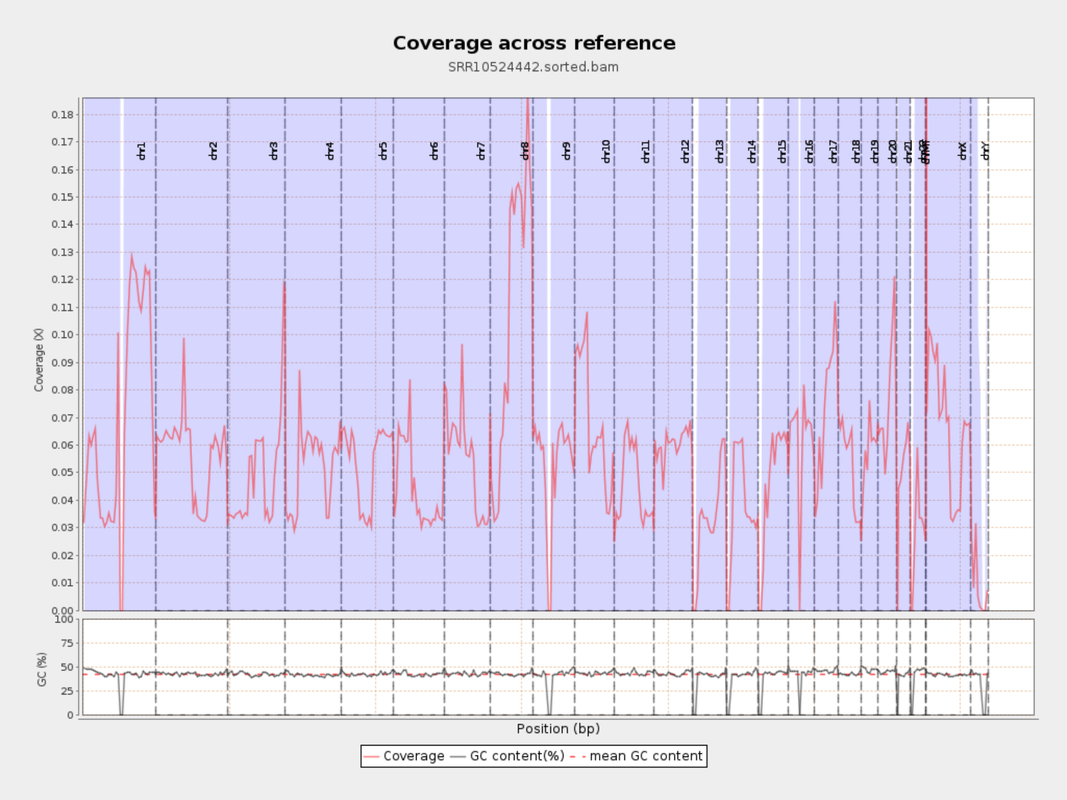
General error rate	0.48%
Mismatches	807,950
Insertions	13,555
Mapped reads with at least one insertion	0.45%
Deletions	34,561
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.8%

2.6. Chromosome stats

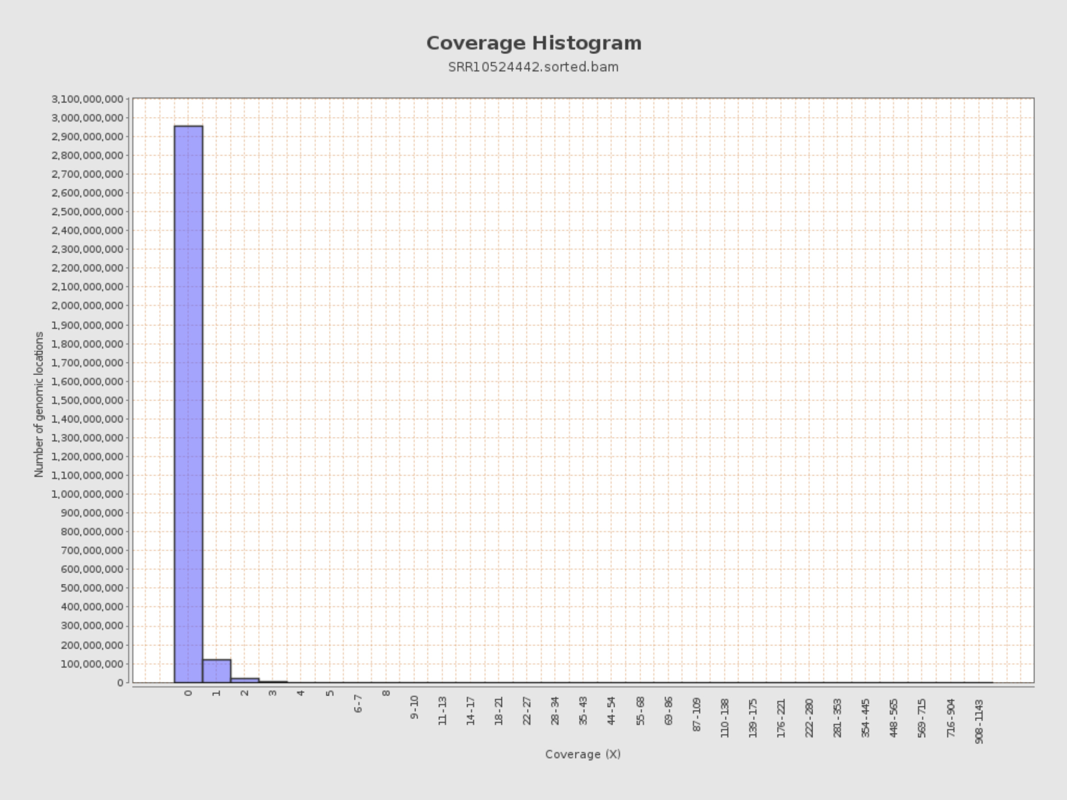
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17303149	0.0694	0.9169
chr2	243199373	13890358	0.0571	0.5122
chr3	198022430	9631178	0.0486	0.2674
chr4	191154276	9965382	0.0521	0.3418
chr5	180915260	9782277	0.0541	0.2827
chr6	171115067	7555498	0.0442	0.3644
chr7	159138663	8687969	0.0546	0.6638

chr8	146364022	16241012	0.111	0.5019
chr9	141213431	7423383	0.0526	0.4104
chr10	135534747	9162630	0.0676	0.5027
chr11	135006516	6069838	0.045	0.4605
chr12	133851895	8138838	0.0608	0.2982
chr13	115169878	3889563	0.0338	0.2241
chr14	107349540	4140717	0.0386	0.2455
chr15	102531392	4654576	0.0454	0.2793
chr16	90354753	5484572	0.0607	0.3233
chr17	81195210	6031069	0.0743	0.354
chr18	78077248	4162544	0.0533	0.7602
chr19	59128983	3424229	0.0579	0.6226
chr20	63025520	4966340	0.0788	0.3481
chr21	48129895	2422825	0.0503	0.3066
chr22	51304566	1417656	0.0276	0.1998
chrMT	16571	14302	0.8631	1.0859
chrX	155270560	10559728	0.068	0.3689
chrY	59373566	548910	0.0092	0.2357

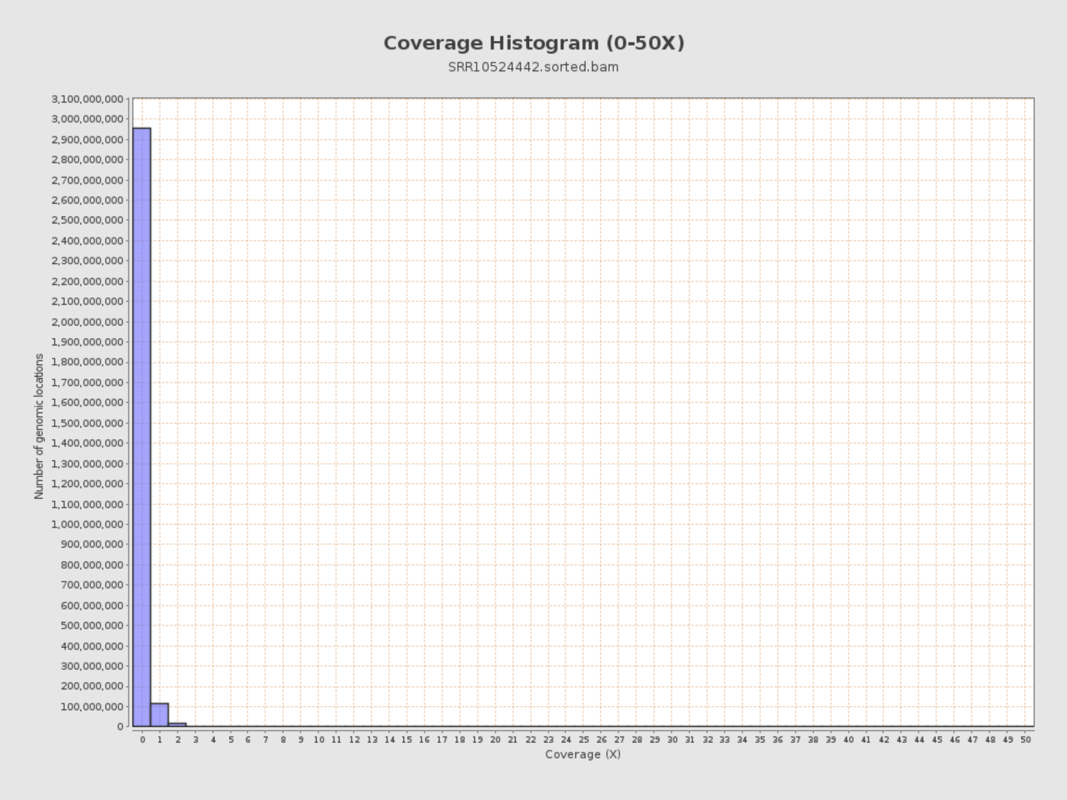
3. Results : Coverage across reference



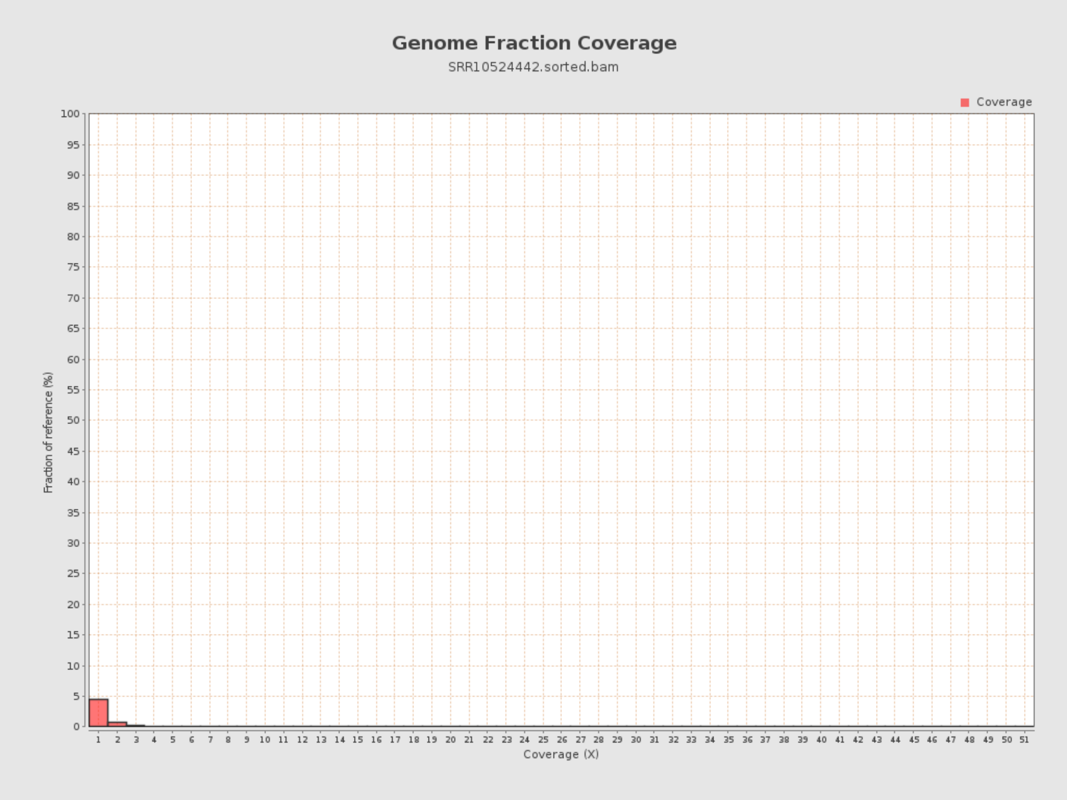
4. Results : Coverage Histogram



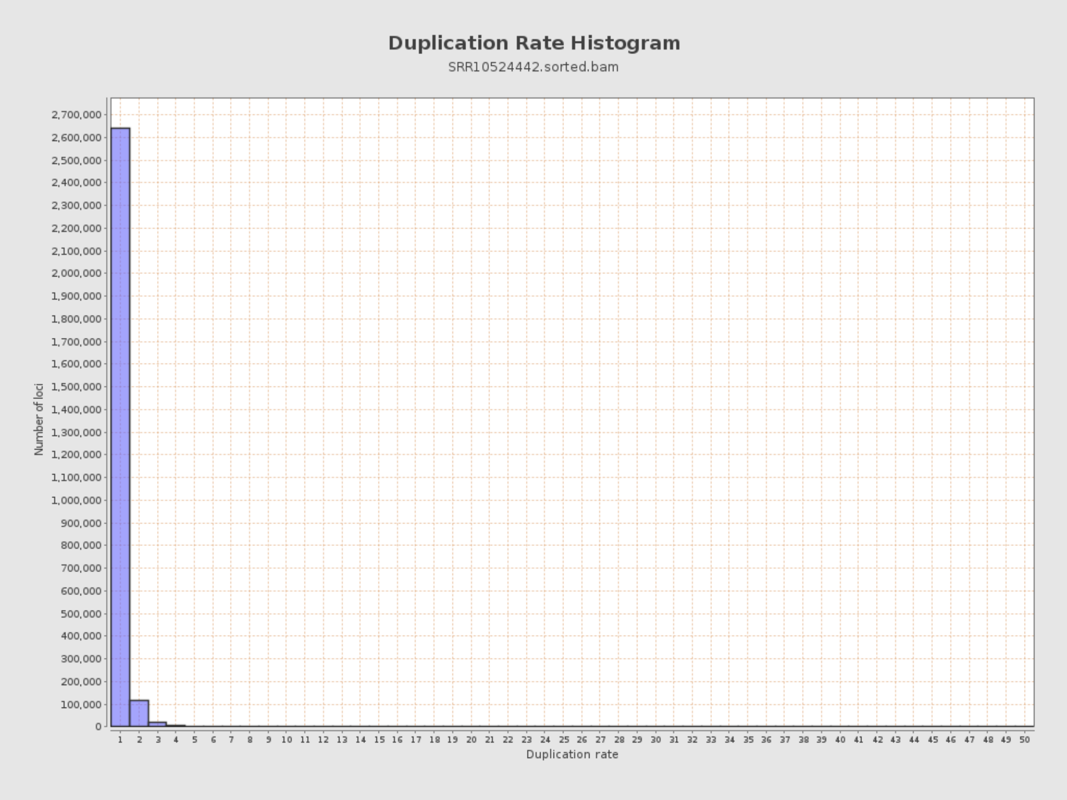
5. Results : Coverage Histogram (0-50X)



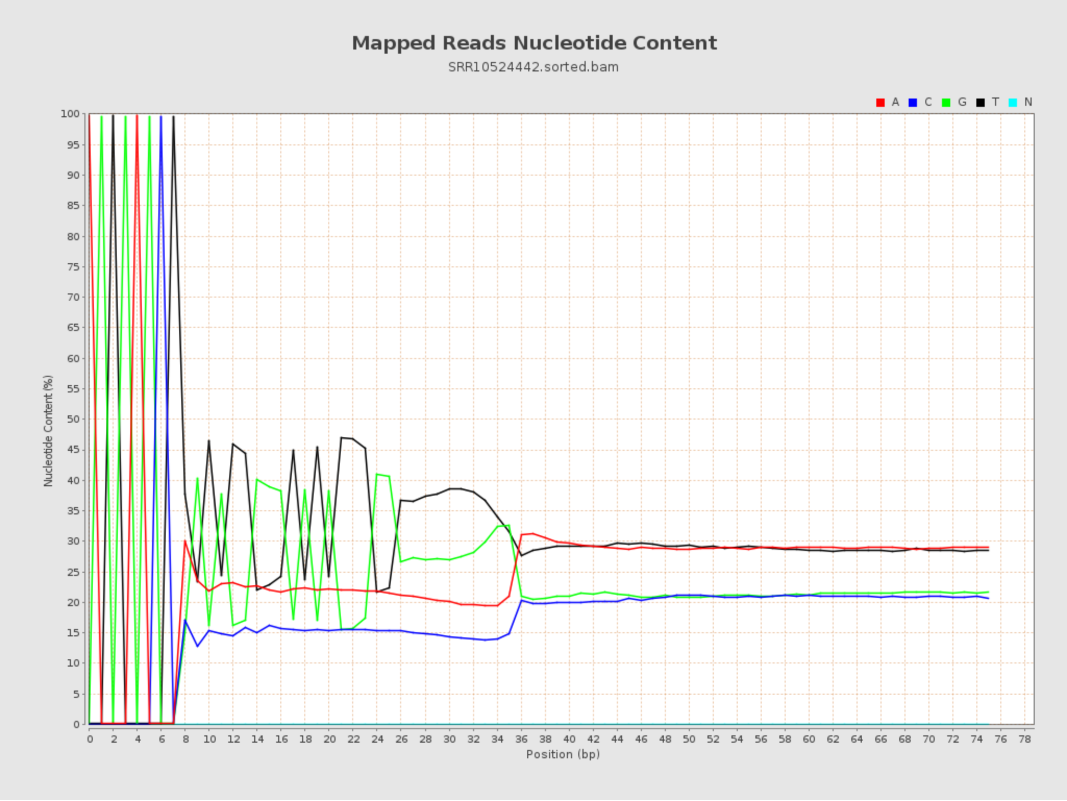
6. Results : Genome Fraction Coverage



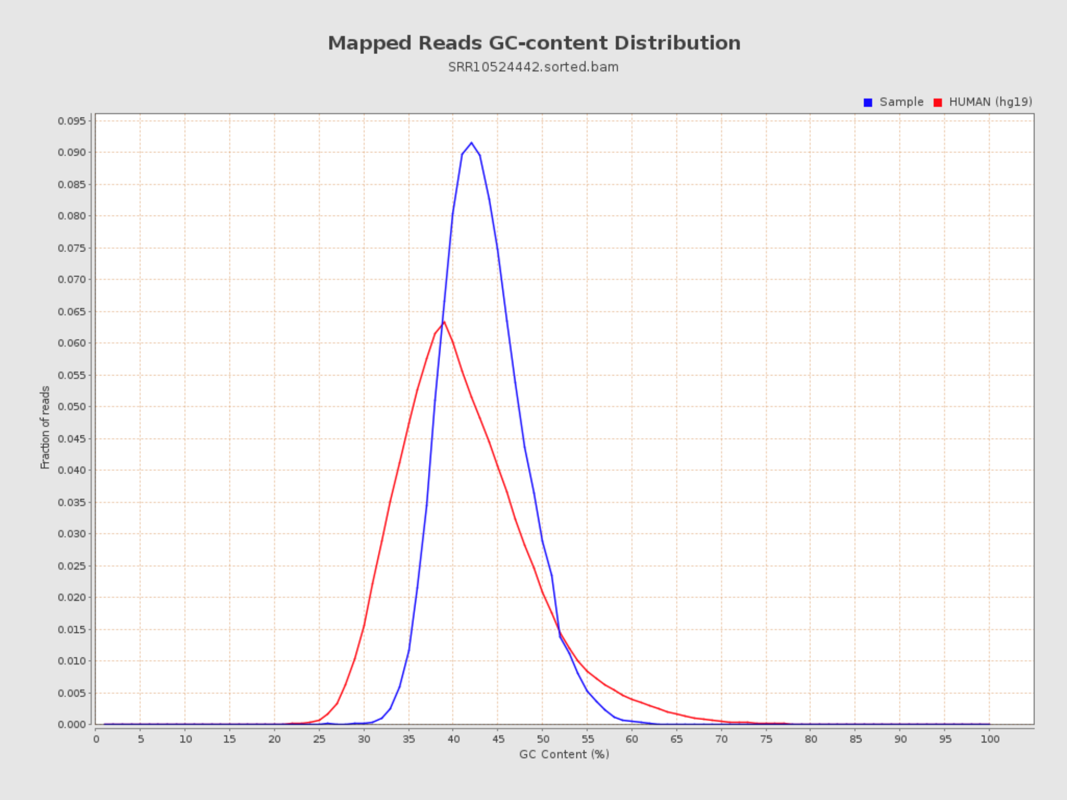
7. Results : Duplication Rate Histogram



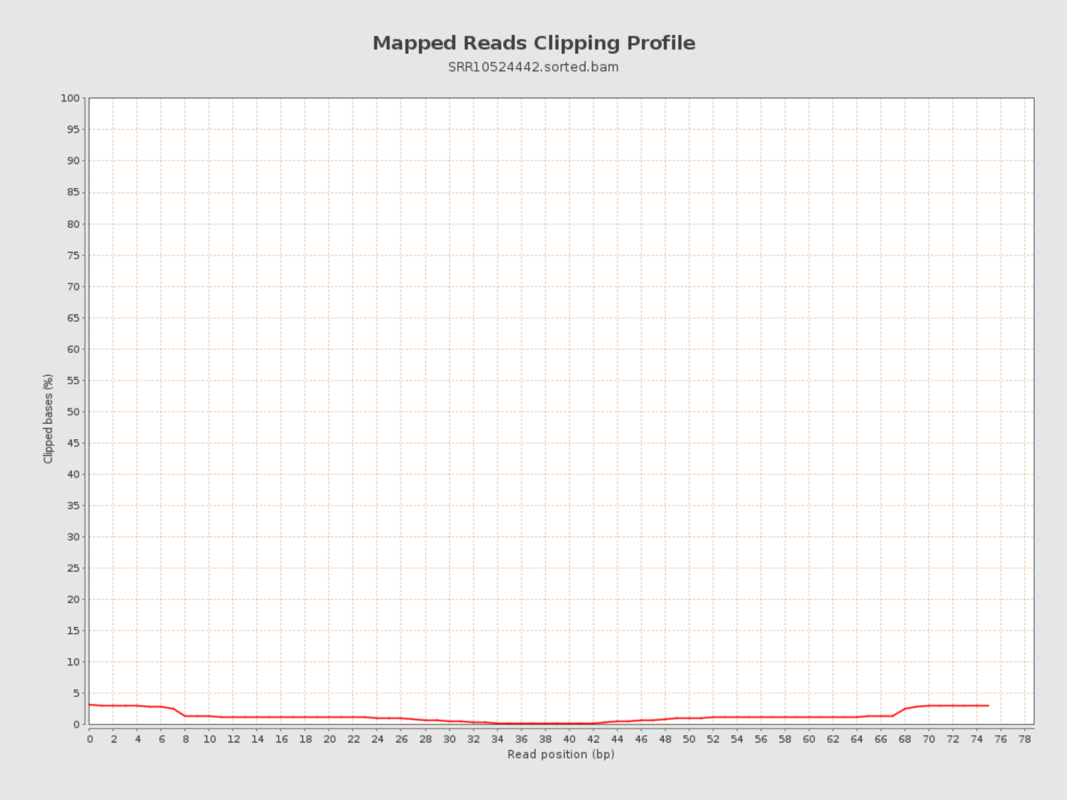
8. Results : Mapped Reads Nucleotide Content



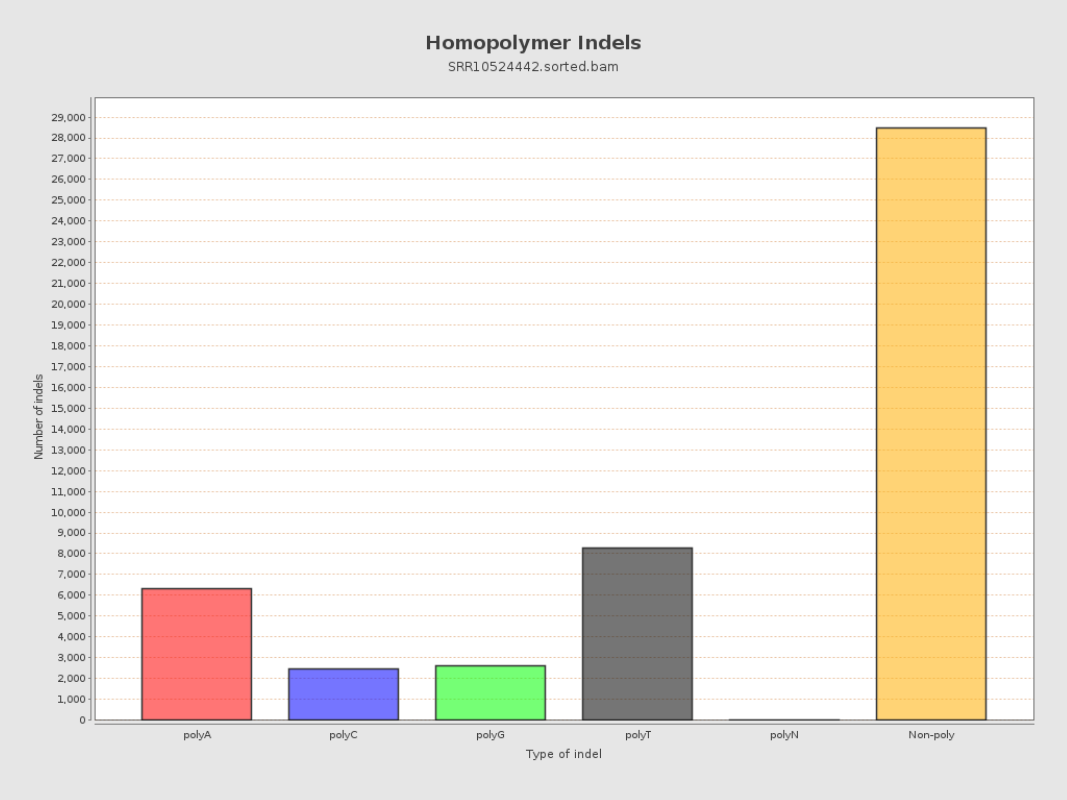
9. Results : Mapped Reads GC-content Distribution



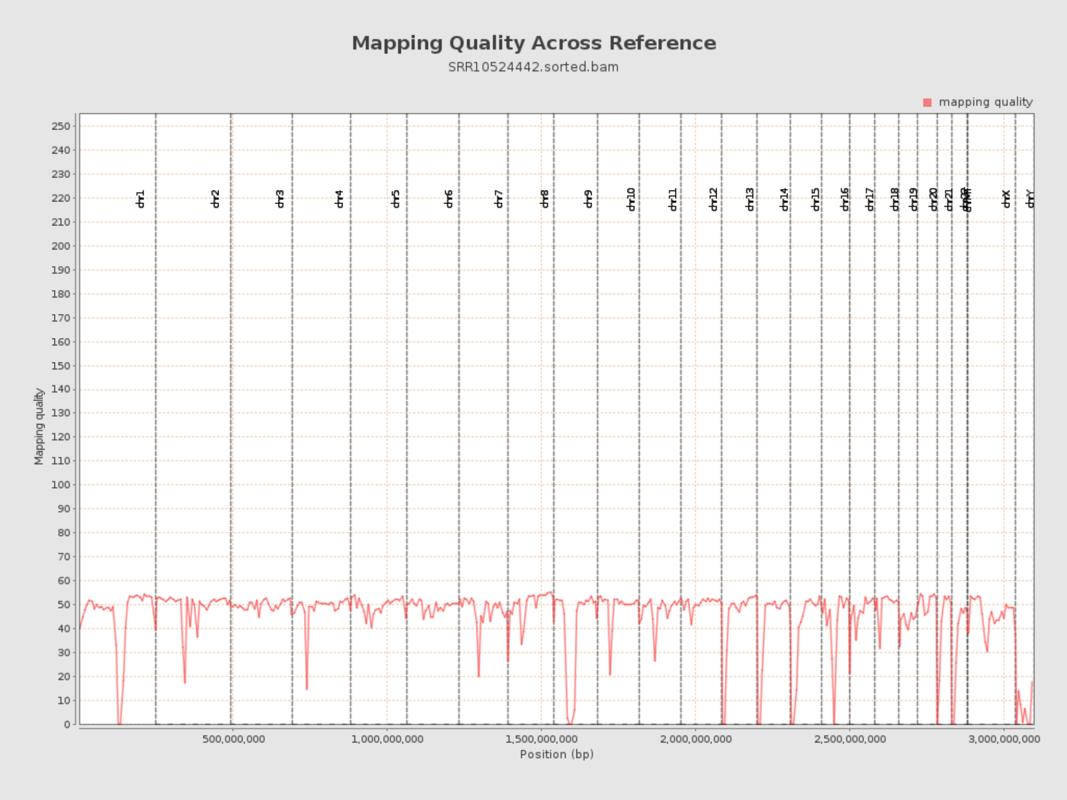
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram