Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:46:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524301.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_SRR10524301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524301.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:46:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524301.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,327,725
Mapped reads	1,167,176 / 87.91%
Unmapped reads	160,549 / 12.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,587 / 0.8%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	32,461 / 2.44%
Duplication rate	1.41%
Clipped reads	1,175,035 / 88.5%

2.2. ACGT Content

Number/percentage of A's	16,034,836 / 24.1%
Number/percentage of C's	13,962,310 / 20.98%
Number/percentage of T's	20,866,361 / 31.36%
Number/percentage of G's	15,672,621 / 23.55%
Number/percentage of N's	9,200 / 0.01%
GC Percentage	44.53%

2.3. Coverage

Mean	0.0215

Standard Deviation	0.2886

2.4. Mapping Quality

Mean Mapping Quality	39.48

2.5. Mismatches and indels

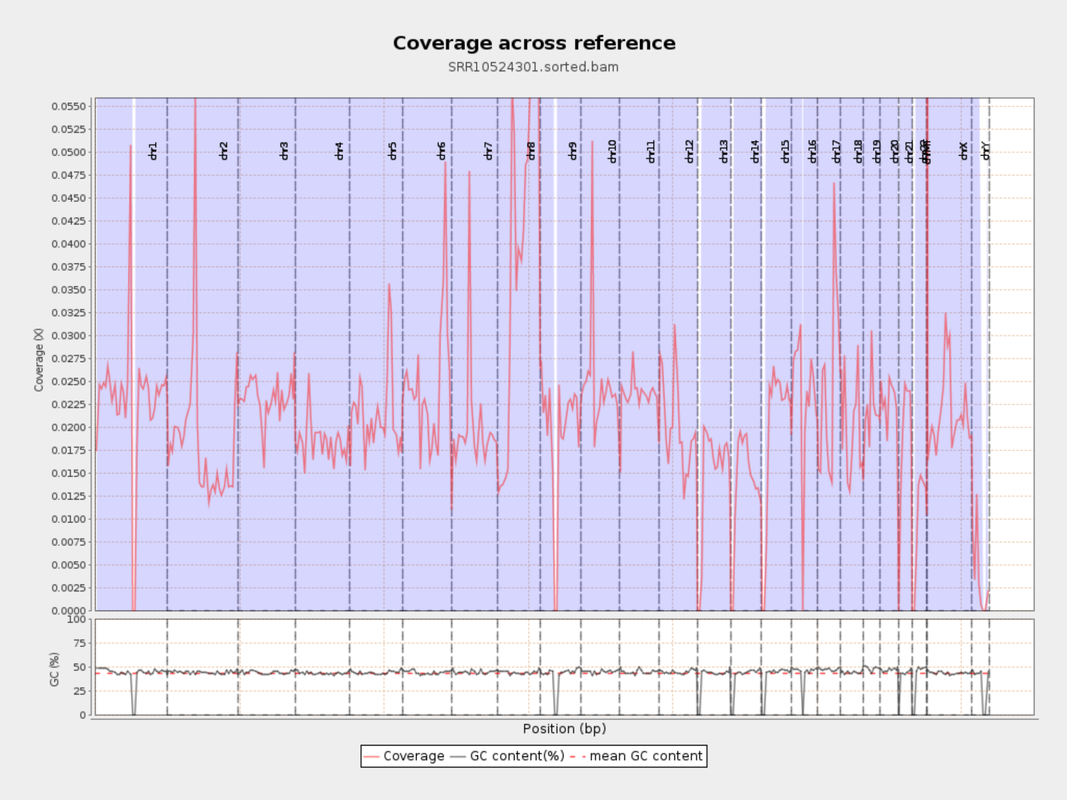
General error rate	0.53%
Mismatches	347,735
Insertions	4,501
Mapped reads with at least one insertion	0.38%
Deletions	9,607
Mapped reads with at least one deletion	0.82%
Homopolymer indels	39.34%

2.6. Chromosome stats

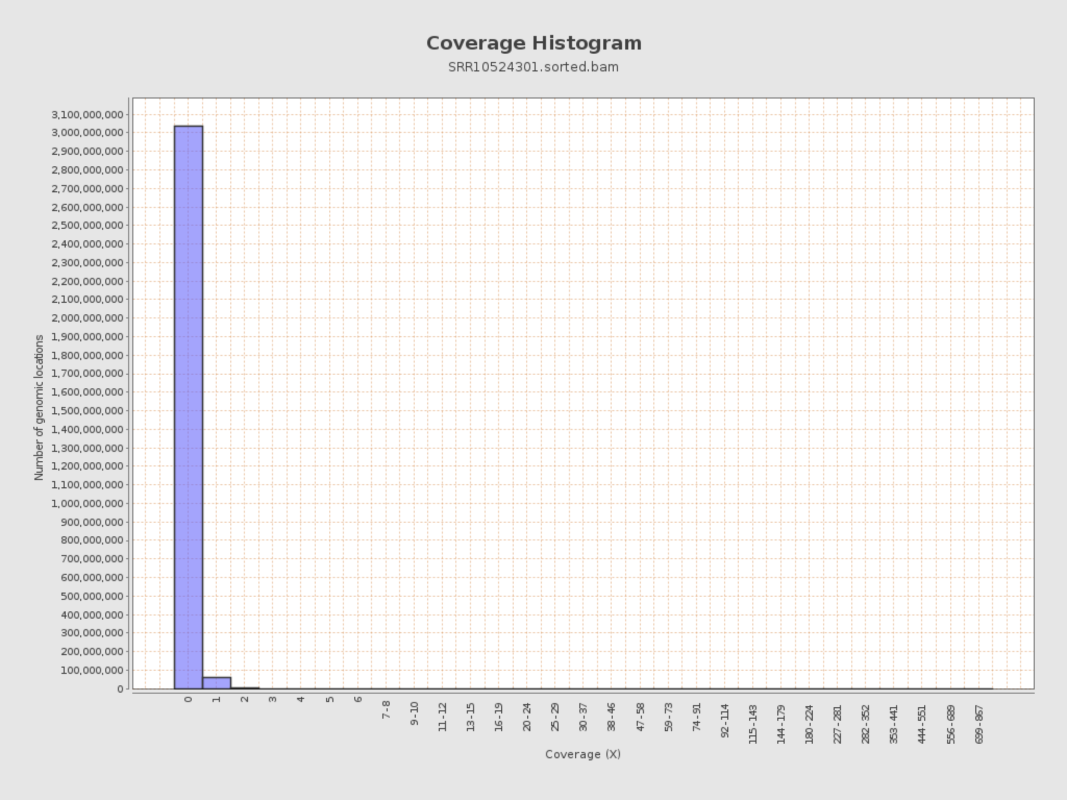
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5703701	0.0229	0.6471
chr2	243199373	4463676	0.0184	0.3042
chr3	198022430	4579235	0.0231	0.1633
chr4	191154276	3544528	0.0185	0.157
chr5	180915260	3921039	0.0217	0.1598
chr6	171115067	4162182	0.0243	0.1809
chr7	159138663	3205091	0.0201	0.4001

chr8	146364022	6459177	0.0441	0.3095
chr9	141213431	2723873	0.0193	0.2095
chr10	135534747	3373205	0.0249	0.2697
chr11	135006516	3198222	0.0237	0.22
chr12	133851895	2685084	0.0201	0.1578
chr13	115169878	1682384	0.0146	0.1268
chr14	107349540	1474599	0.0137	0.1397
chr15	102531392	1999350	0.0195	0.1557
chr16	90354753	2078208	0.023	0.1827
chr17	81195210	2017114	0.0248	0.1853
chr18	78077248	1547928	0.0198	0.4012
chr19	59128983	1296382	0.0219	0.4218
chr20	63025520	1424025	0.0226	0.1641
chr21	48129895	913087	0.019	0.1564
chr22	51304566	501911	0.0098	0.1042
chrMT	16571	27660	1.6692	1.6211
chrX	155270560	3366277	0.0217	0.1916
chrY	59373566	212902	0.0036	0.1023

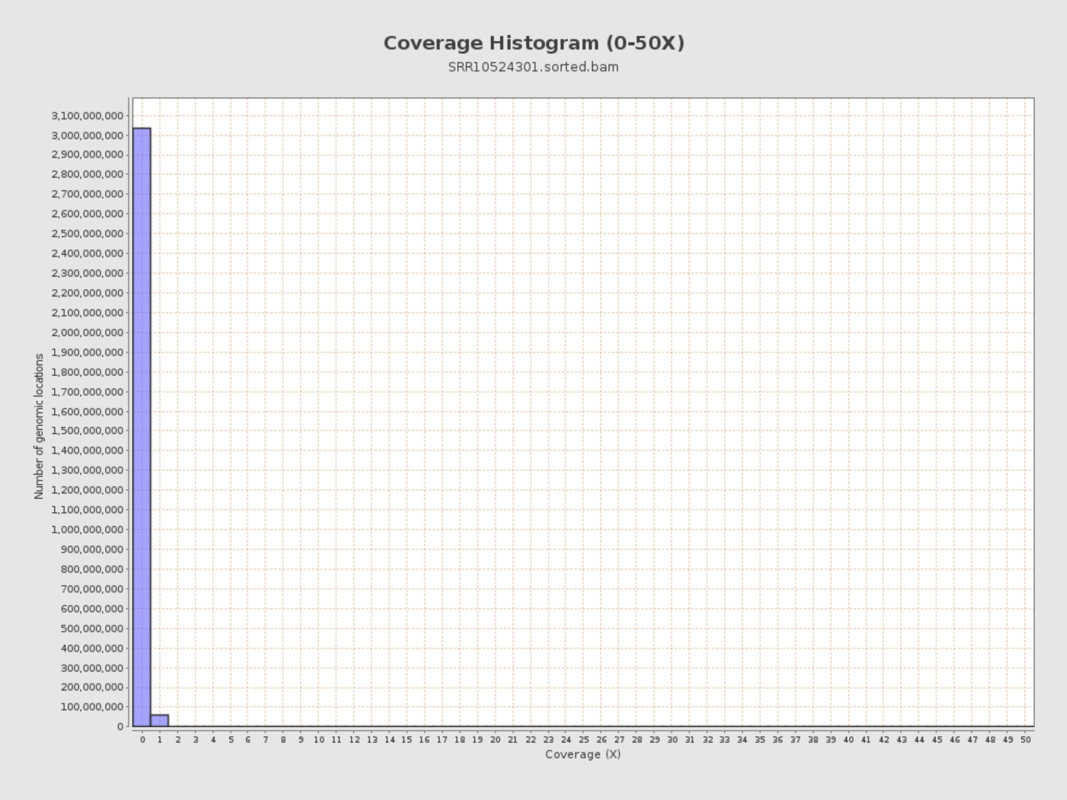
3. Results : Coverage across reference



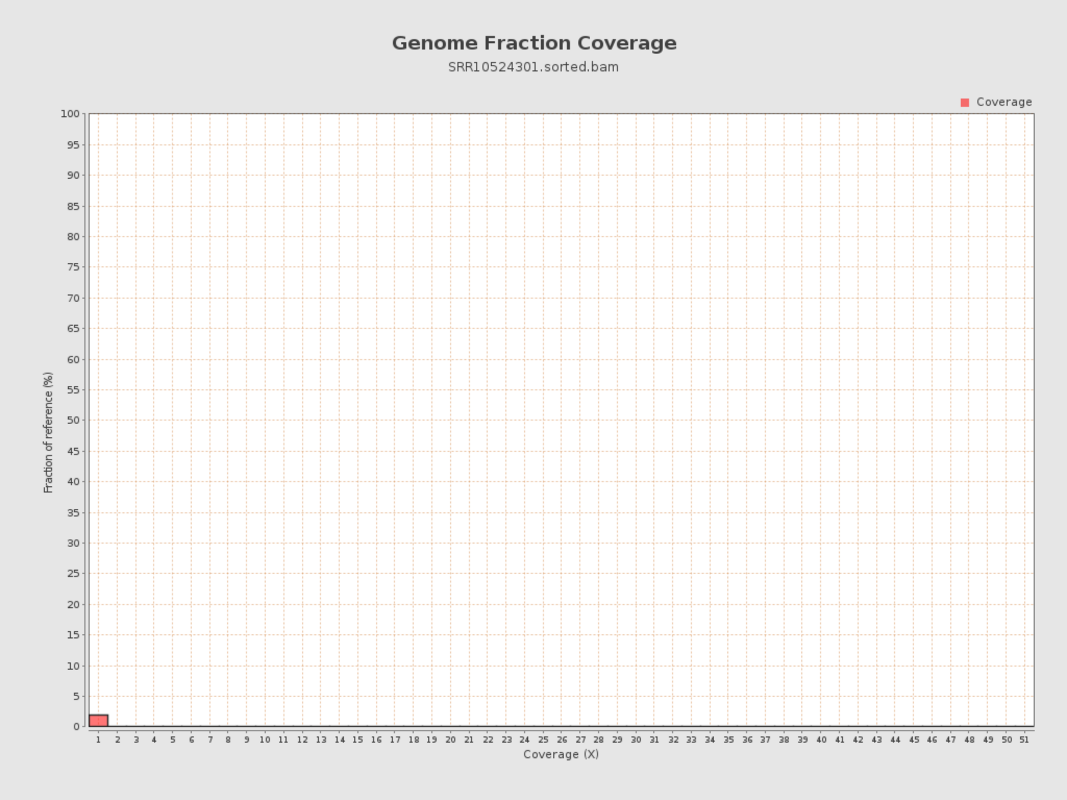
4. Results : Coverage Histogram



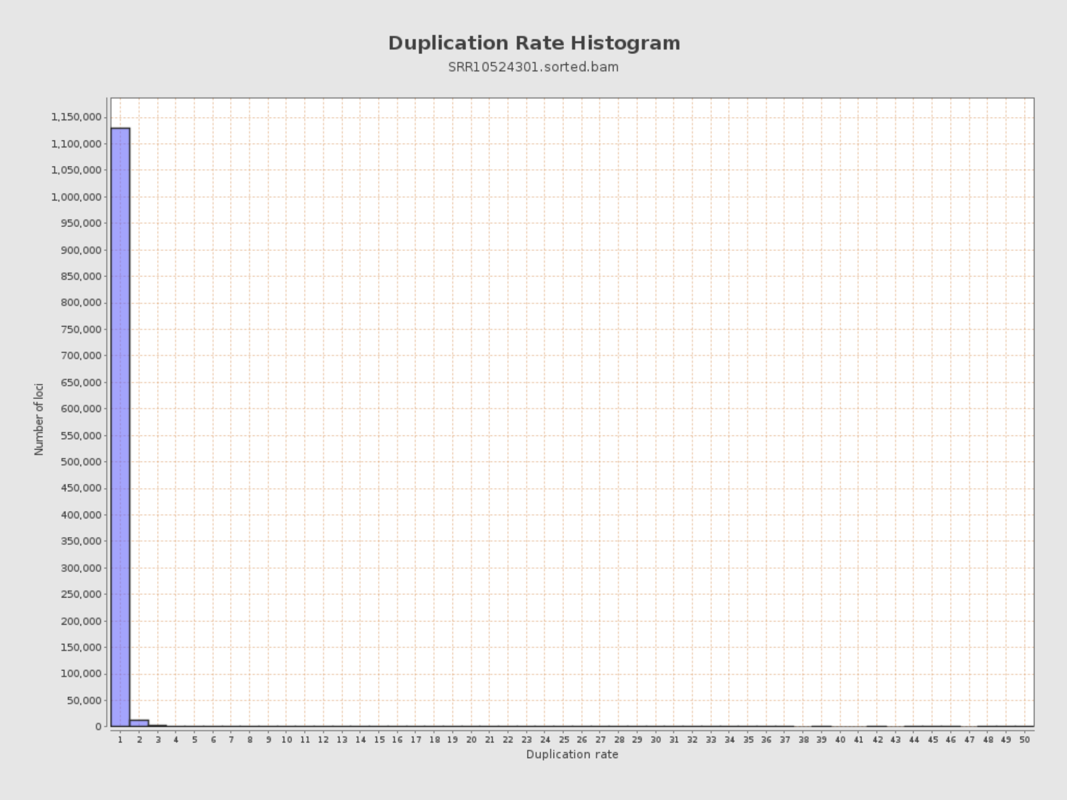
5. Results : Coverage Histogram (0-50X)



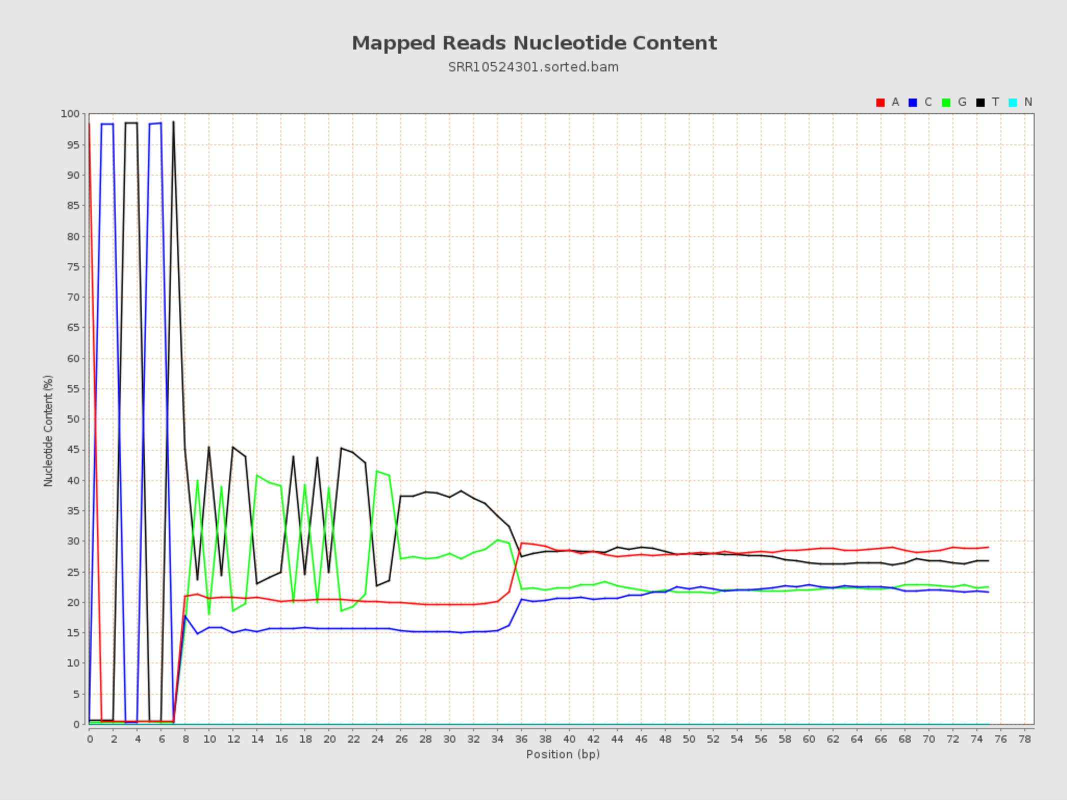
6. Results : Genome Fraction Coverage



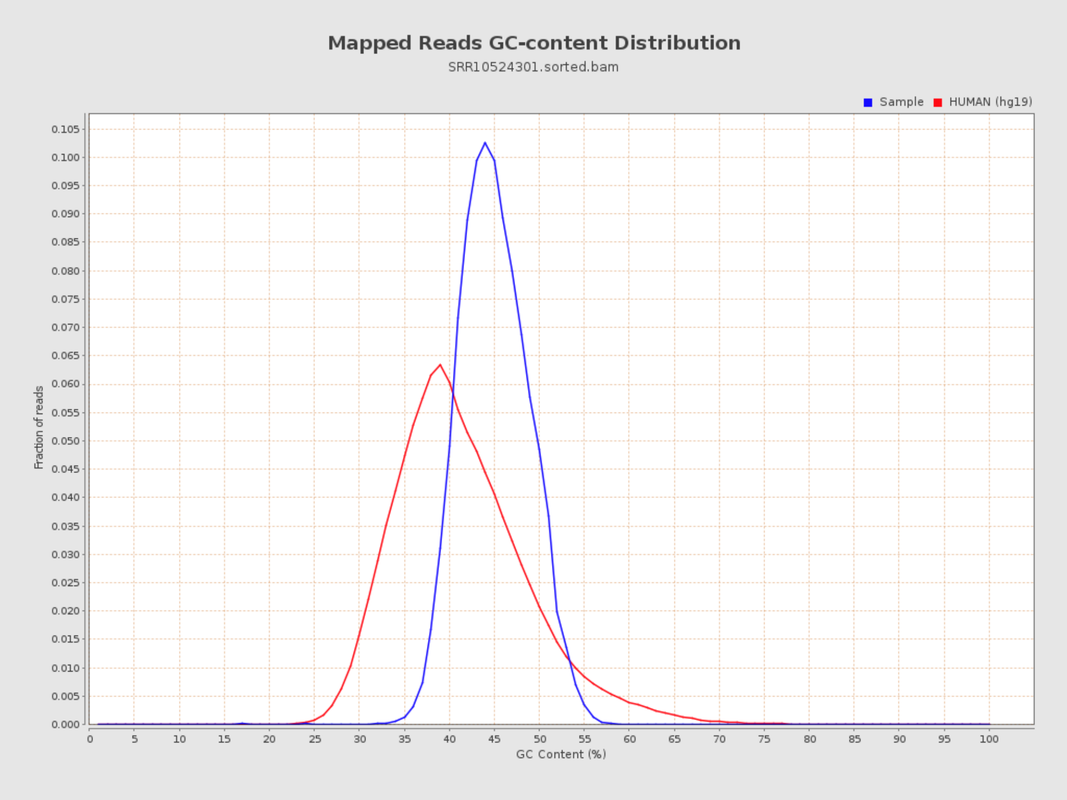
7. Results : Duplication Rate Histogram



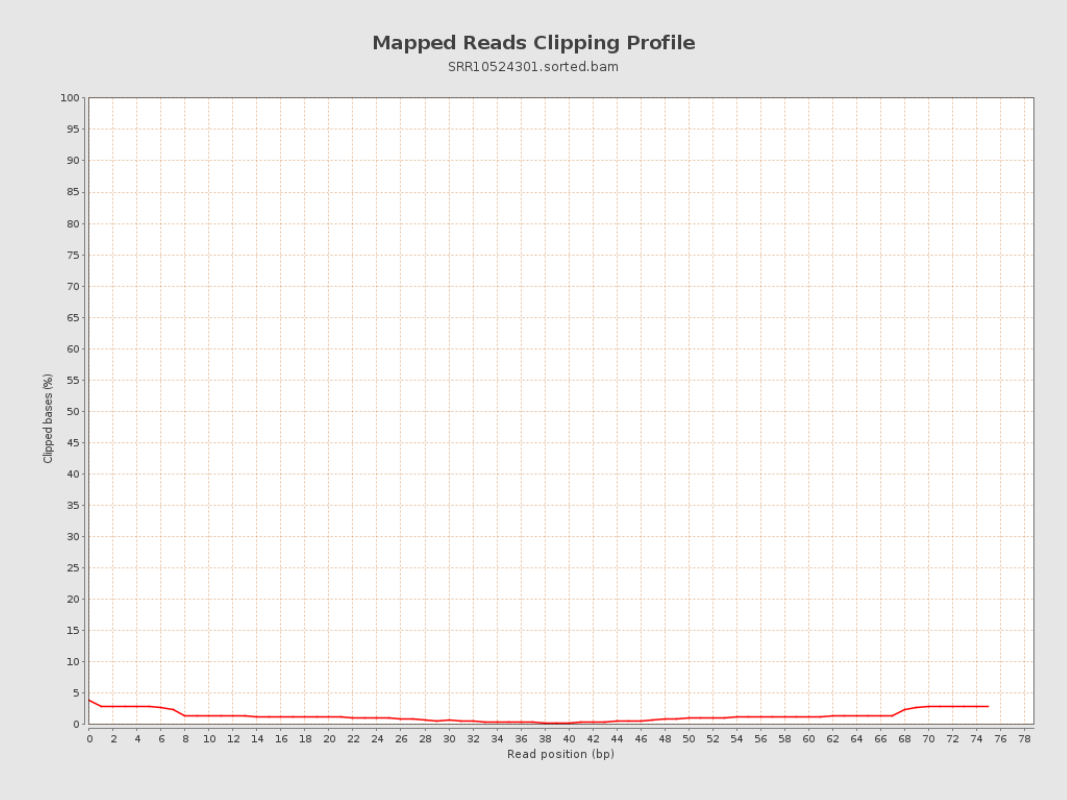
8. Results : Mapped Reads Nucleotide Content



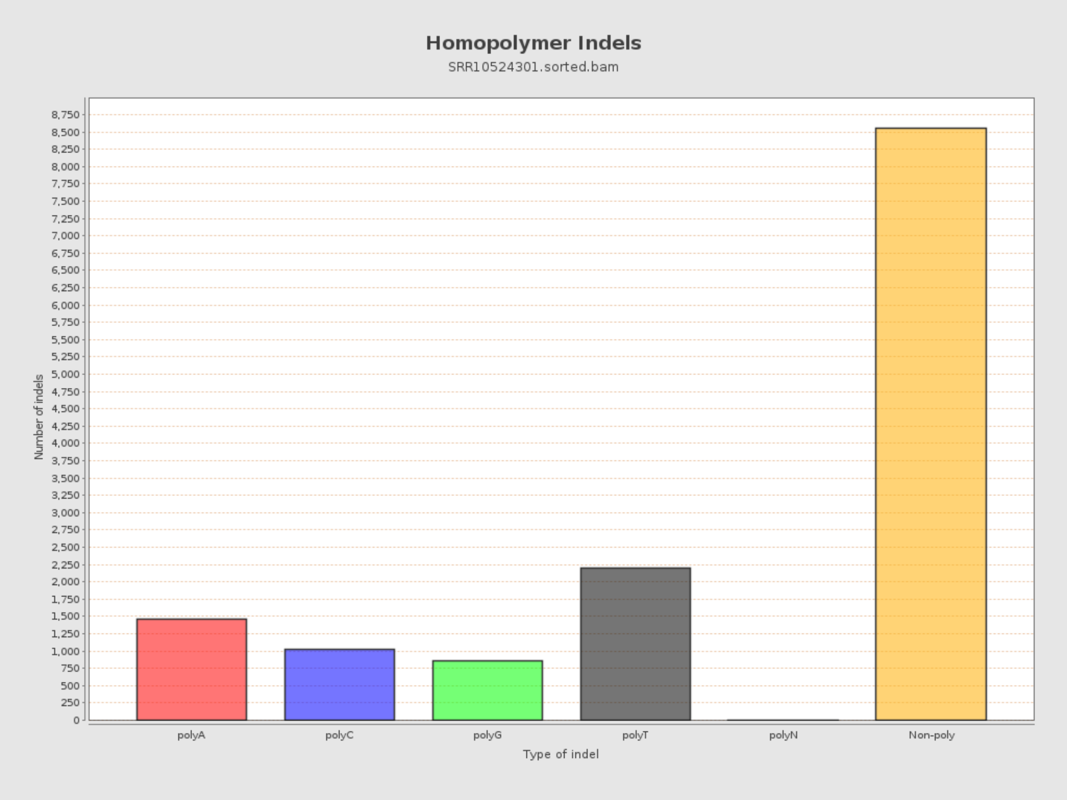
9. Results : Mapped Reads GC-content Distribution



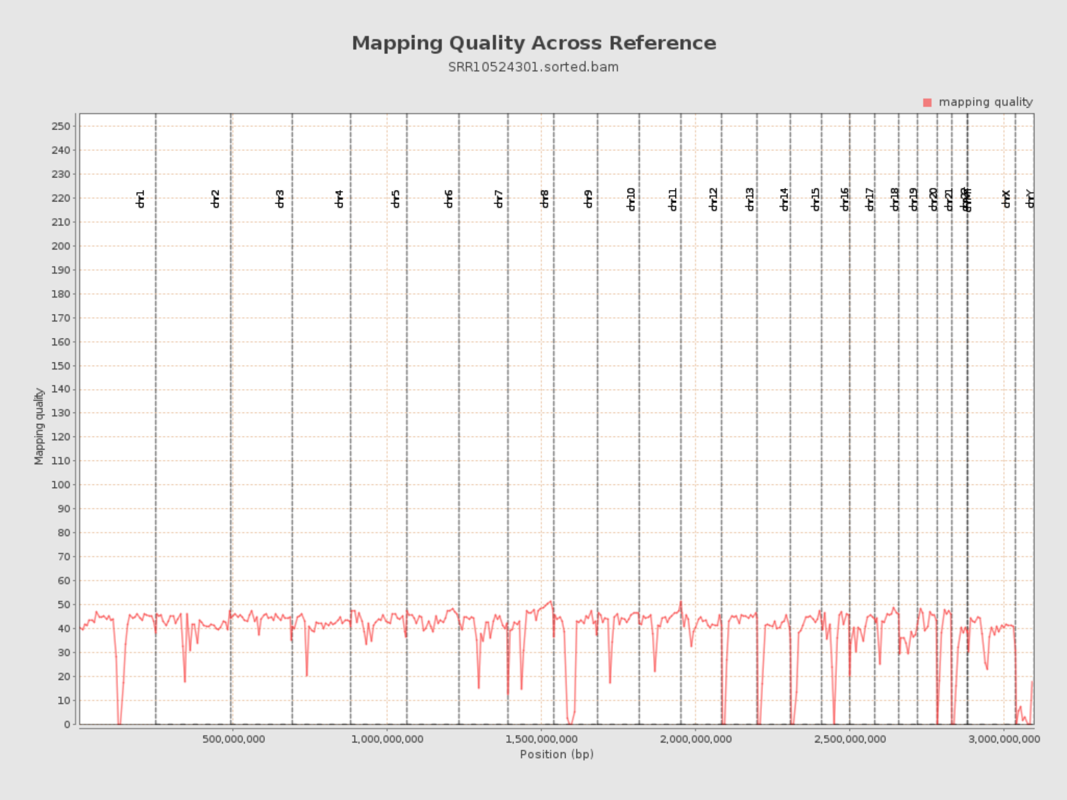
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram