Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:20:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524437.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_SRR10524437 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524437.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:20:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524437.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,037,878
Mapped reads	2,733,301 / 89.97%
Unmapped reads	304,577 / 10.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,964 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	207,430 / 6.83%
Duplication rate	5.6%
Clipped reads	2,743,743 / 90.32%

2.2. ACGT Content

Number/percentage of A's	39,628,911 / 24.83%
Number/percentage of C's	32,453,361 / 20.34%
Number/percentage of T's	48,843,950 / 30.61%
Number/percentage of G's	38,628,433 / 24.21%
Number/percentage of N's	16,488 / 0.01%
GC Percentage	44.55%

2.3. Coverage

Mean	0.0516

Standard Deviation	0.4898

2.4. Mapping Quality

Mean Mapping Quality	44.63

2.5. Mismatches and indels

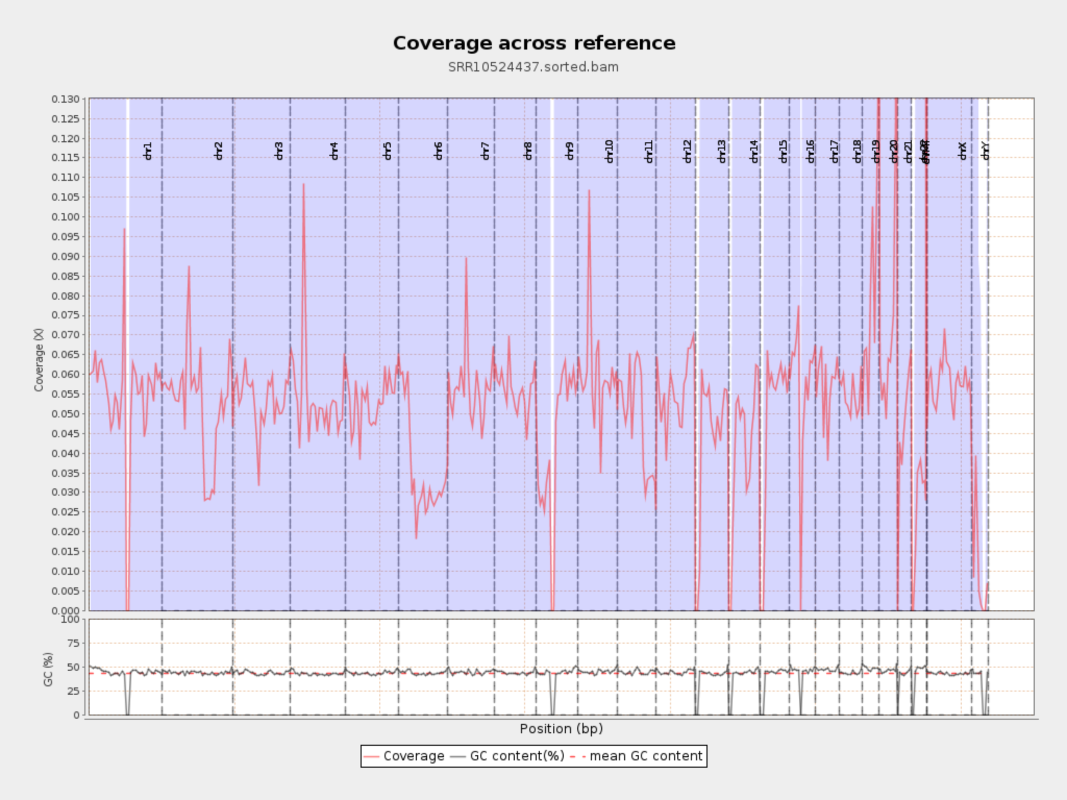
General error rate	0.52%
Mismatches	807,128
Insertions	9,731
Mapped reads with at least one insertion	0.35%
Deletions	26,000
Mapped reads with at least one deletion	0.94%
Homopolymer indels	42.22%

2.6. Chromosome stats

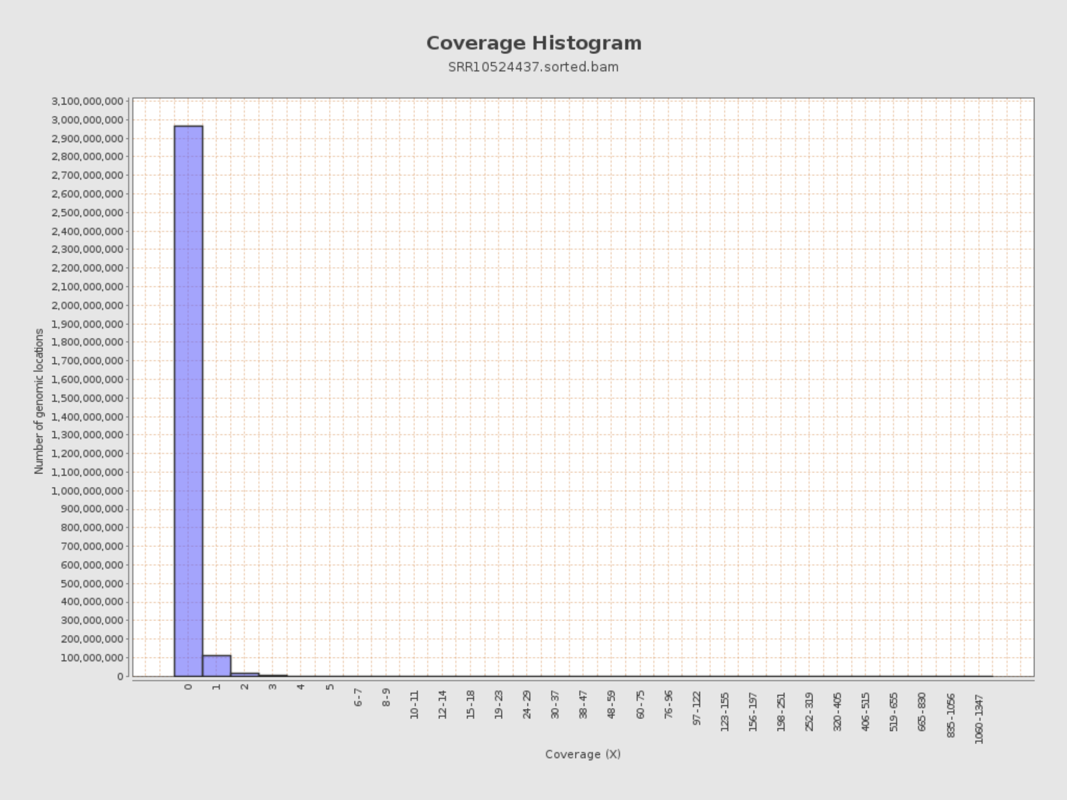
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13501431	0.0542	1.0628
chr2	243199373	12871539	0.0529	0.6393
chr3	198022430	10594805	0.0535	0.2777
chr4	191154276	10337735	0.0541	0.3935
chr5	180915260	9608387	0.0531	0.2754
chr6	171115067	6179044	0.0361	0.251
chr7	159138663	9027796	0.0567	0.6243

chr8	146364022	8232681	0.0562	0.3671
chr9	141213431	5914075	0.0419	0.3157
chr10	135534747	8146340	0.0601	0.5065
chr11	135006516	6585039	0.0488	0.359
chr12	133851895	7517143	0.0562	0.2937
chr13	115169878	4966498	0.0431	0.2476
chr14	107349540	4416791	0.0411	0.2552
chr15	102531392	4972129	0.0485	0.2645
chr16	90354753	5160396	0.0571	0.313
chr17	81195210	4596990	0.0566	0.3226
chr18	78077248	4279945	0.0548	0.5982
chr19	59128983	4925461	0.0833	0.6793
chr20	63025520	4691124	0.0744	0.3584
chr21	48129895	2205573	0.0458	0.3488
chr22	51304566	1241721	0.0242	0.188
chrMT	16571	34742	2.0966	2.1137
chrX	155270560	9007641	0.058	0.3225
chrY	59373566	599168	0.0101	0.3387

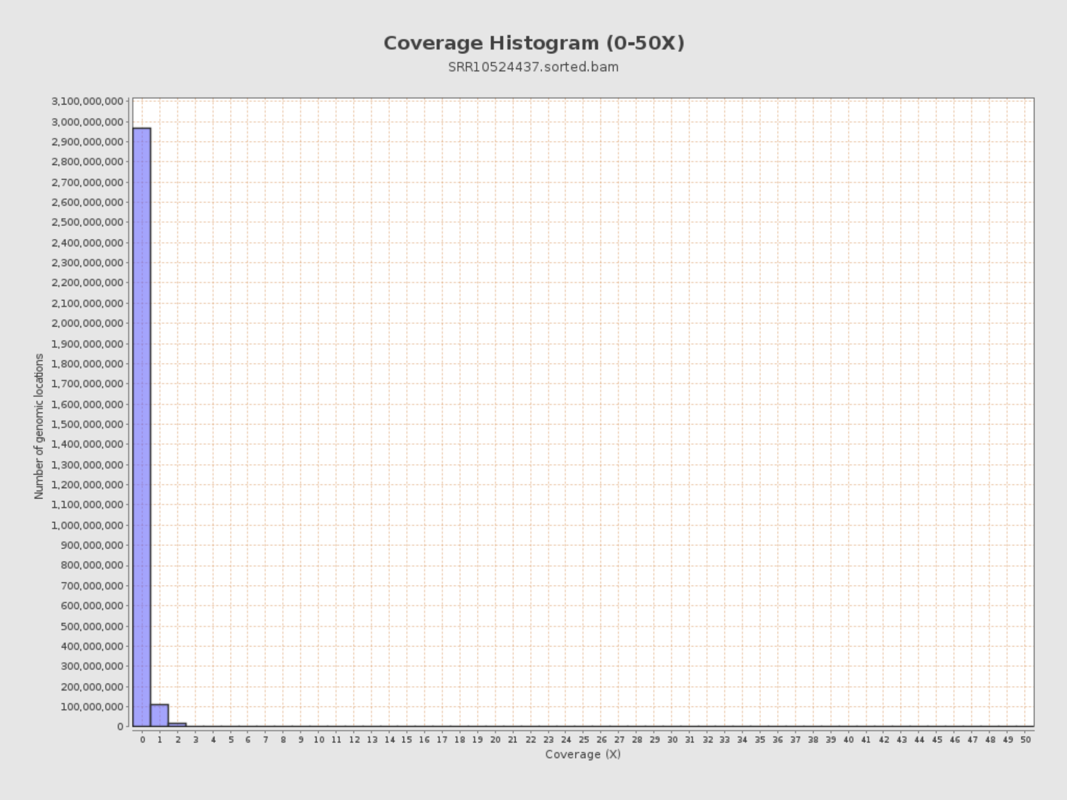
3. Results : Coverage across reference



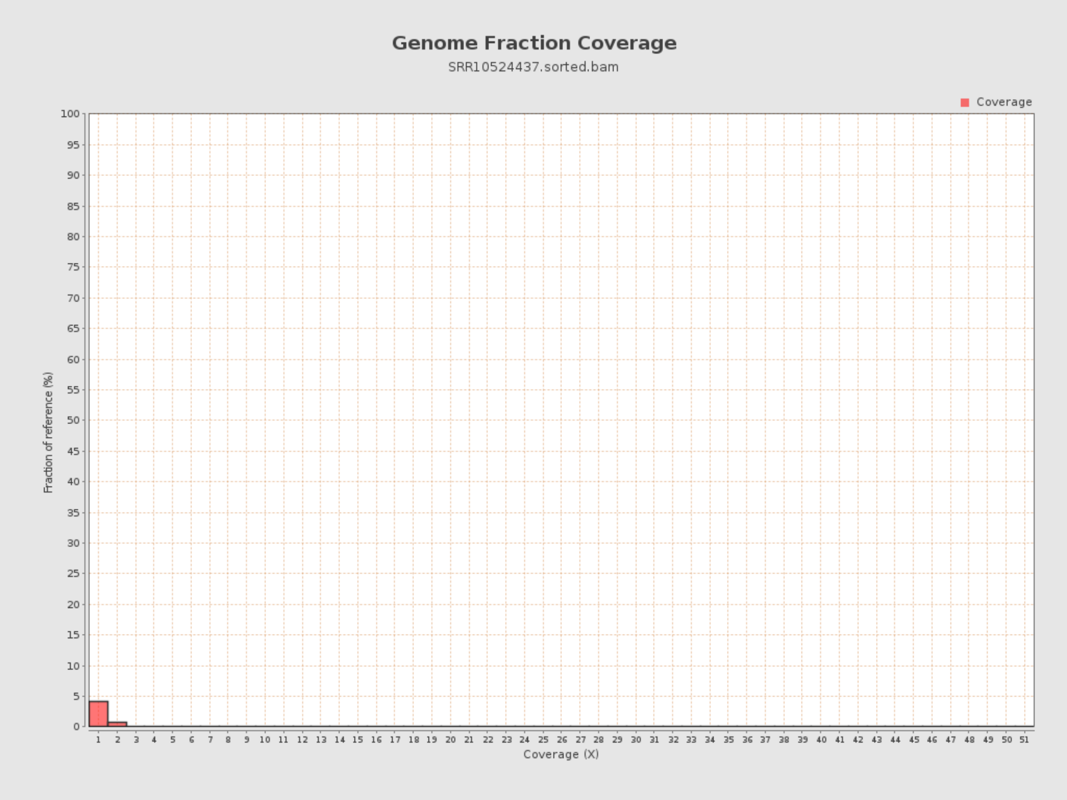
4. Results : Coverage Histogram



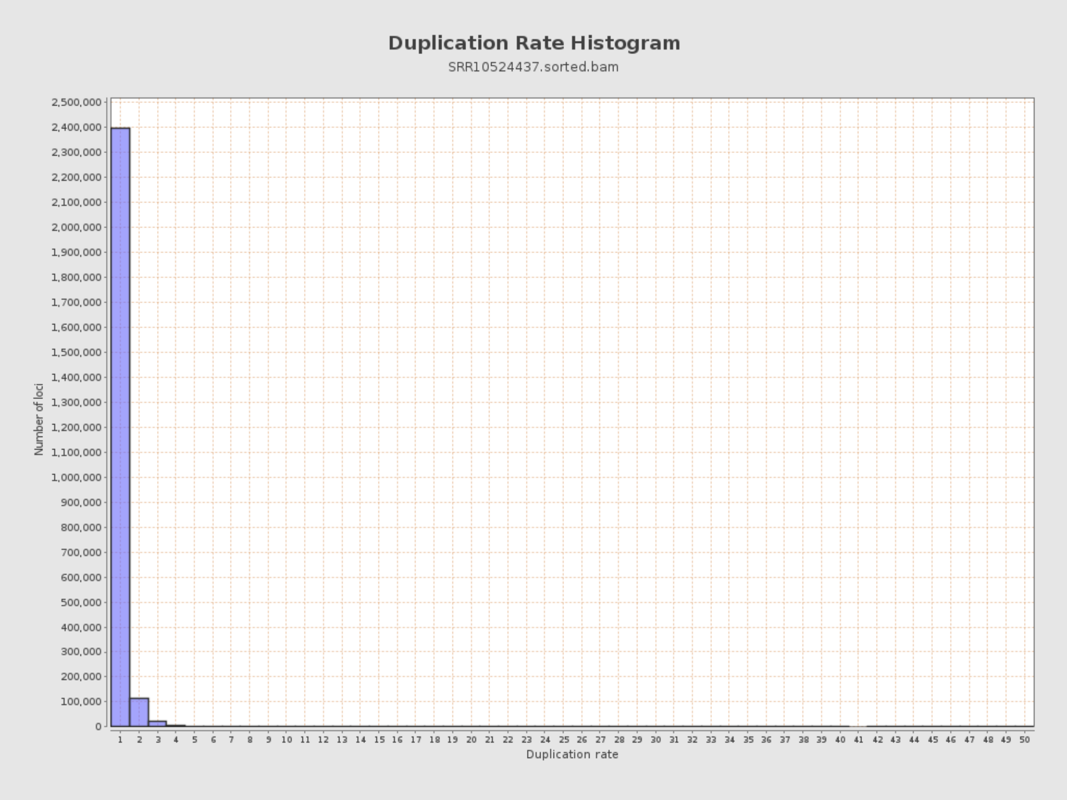
5. Results : Coverage Histogram (0-50X)



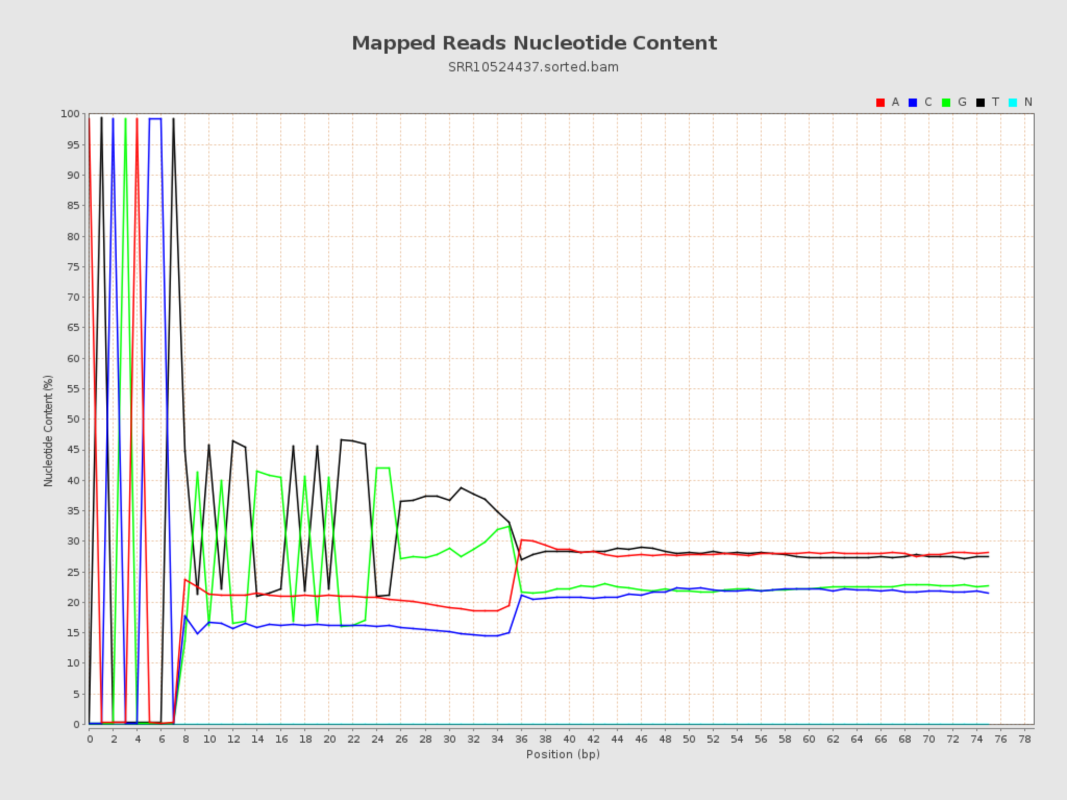
6. Results : Genome Fraction Coverage



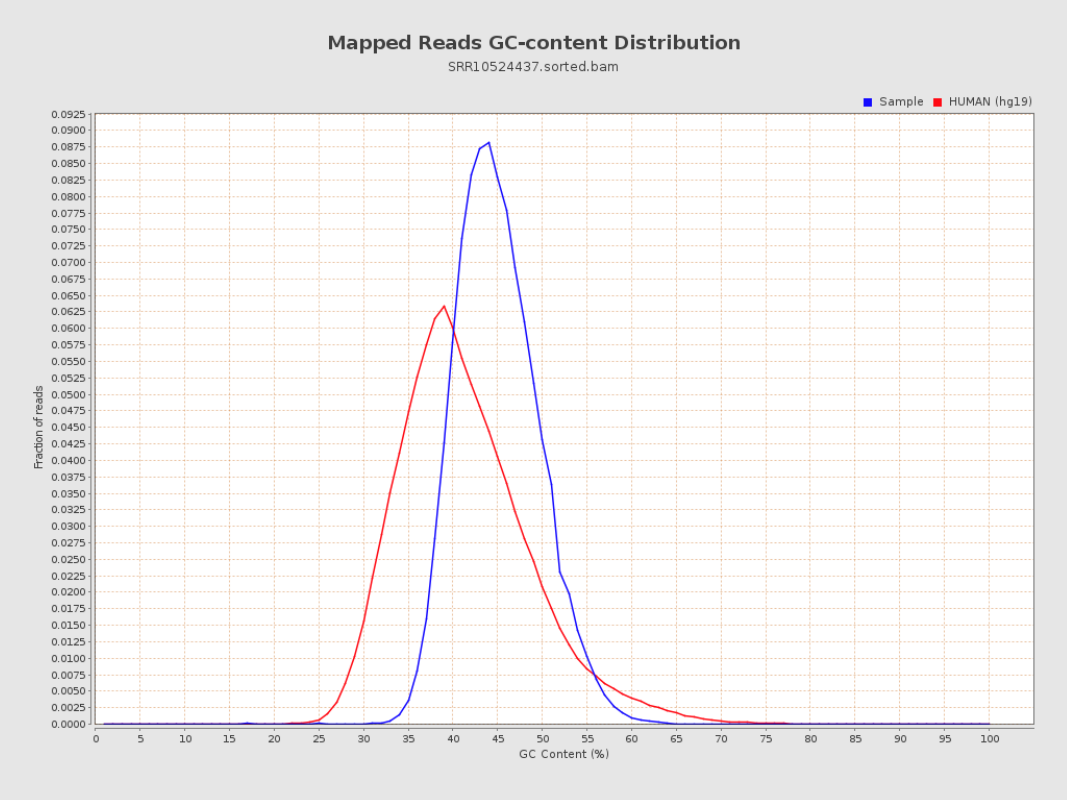
7. Results : Duplication Rate Histogram



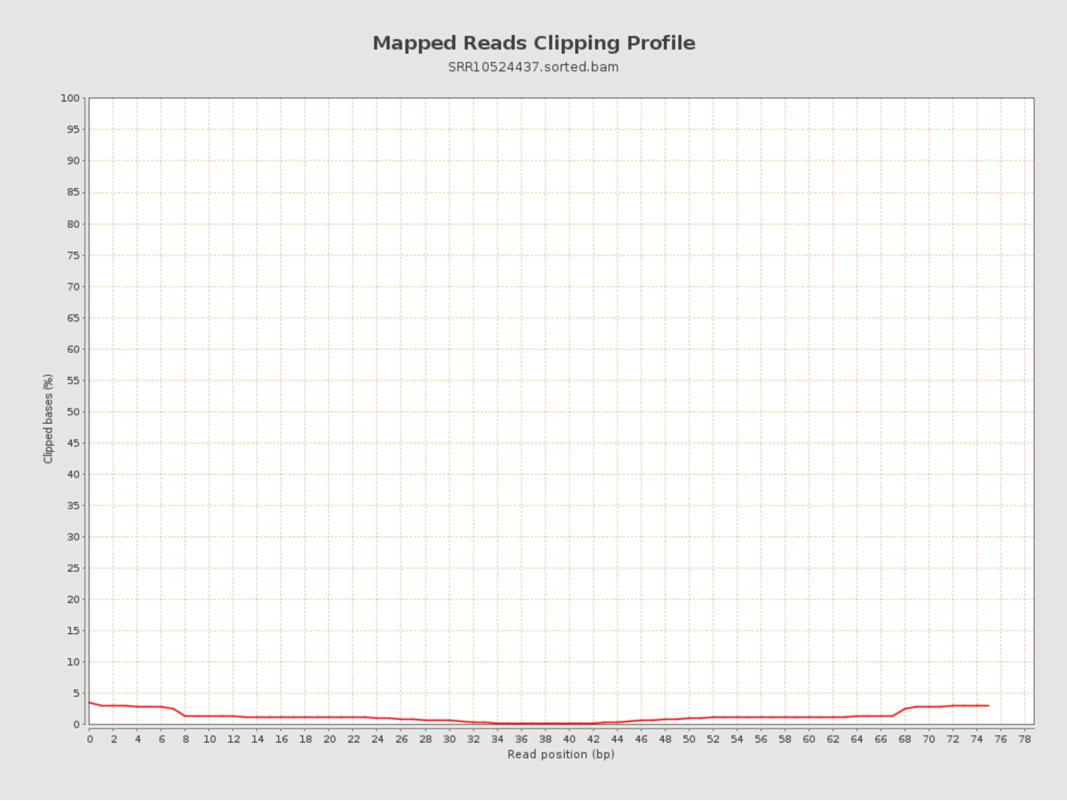
8. Results : Mapped Reads Nucleotide Content



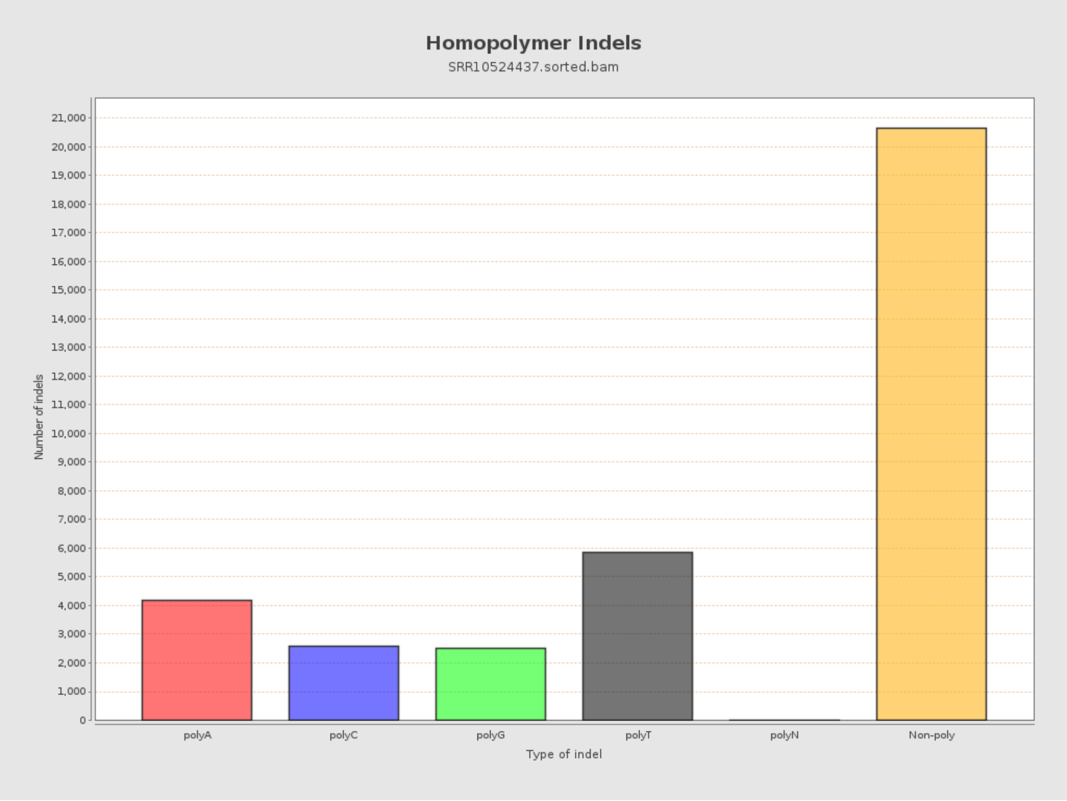
9. Results : Mapped Reads GC-content Distribution



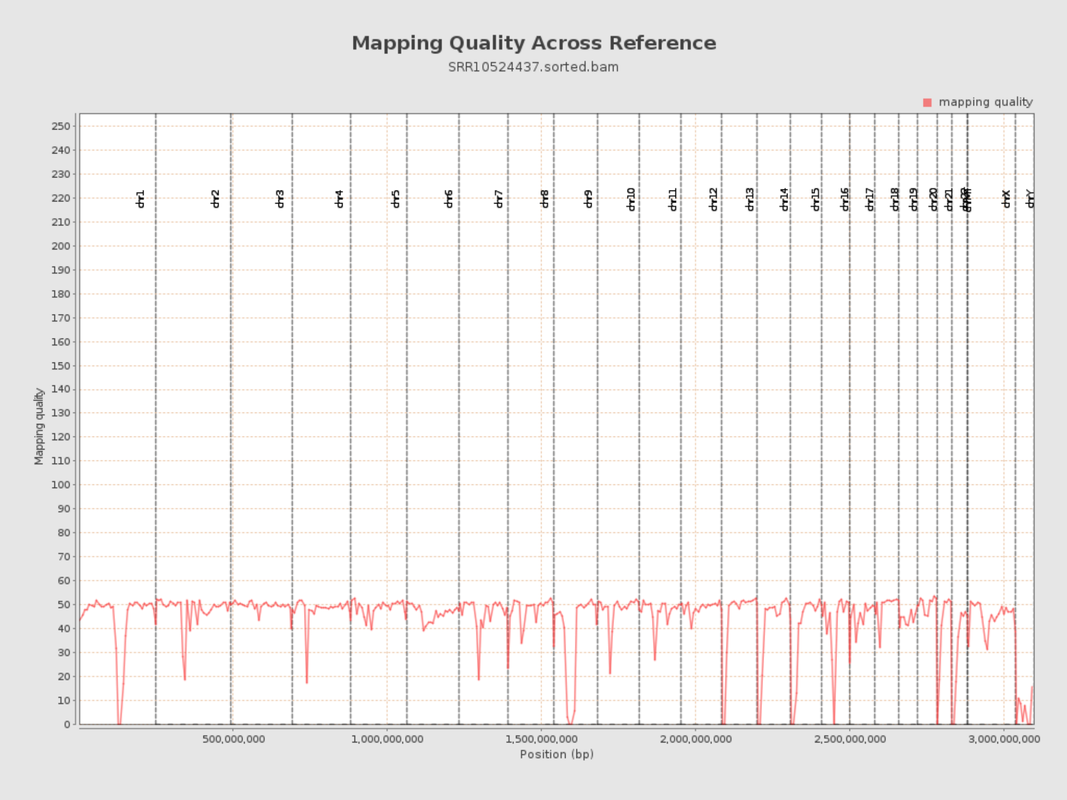
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram