Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:12:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524332.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_SRR10524332 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524332.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:12:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524332.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,934,700
Mapped reads	2,696,915 / 91.9%
Unmapped reads	237,785 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,262 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	117,882 / 4.02%
Duplication rate	3.12%
Clipped reads	2,706,929 / 92.24%

2.2. ACGT Content

Number/percentage of A's	37,000,689 / 23.51%
Number/percentage of C's	31,470,405 / 19.99%
Number/percentage of T's	48,436,345 / 30.77%
Number/percentage of G's	40,471,348 / 25.71%
Number/percentage of N's	22,094 / 0.01%
GC Percentage	45.71%

2.3. Coverage

Mean	0.0509

Standard Deviation	0.4186

2.4. Mapping Quality

Mean Mapping Quality	44.19

2.5. Mismatches and indels

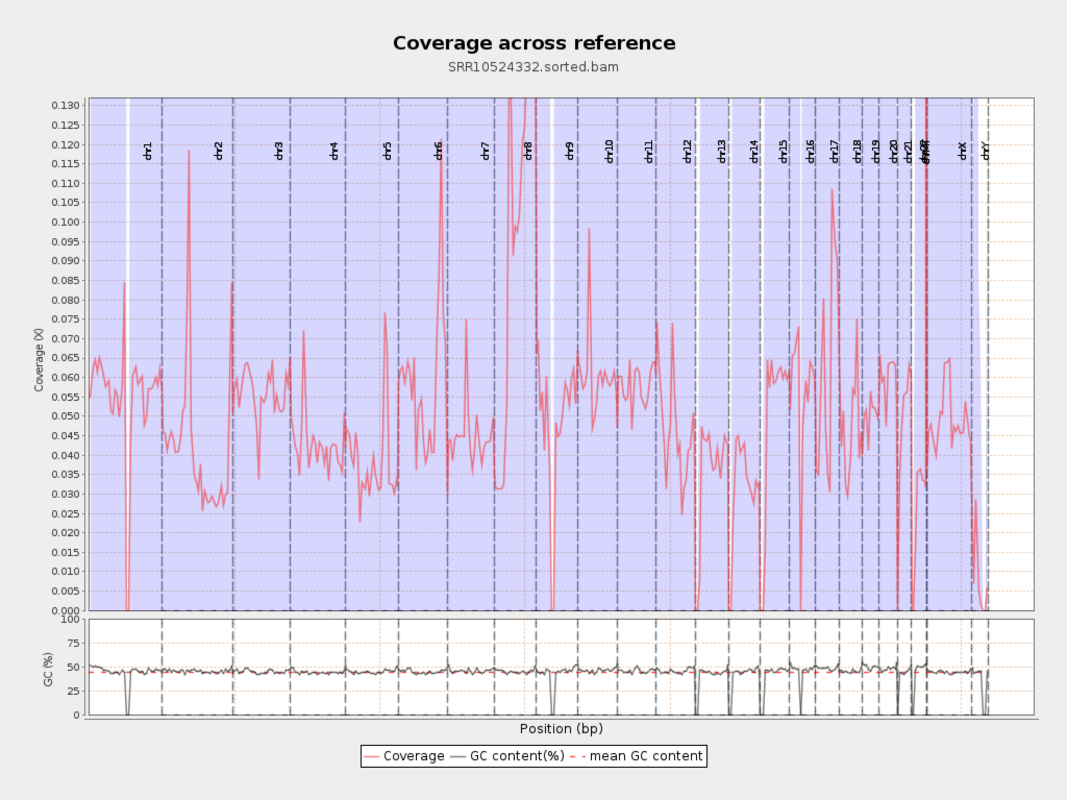
General error rate	0.51%
Mismatches	785,537
Insertions	8,604
Mapped reads with at least one insertion	0.32%
Deletions	25,250
Mapped reads with at least one deletion	0.93%
Homopolymer indels	42.85%

2.6. Chromosome stats

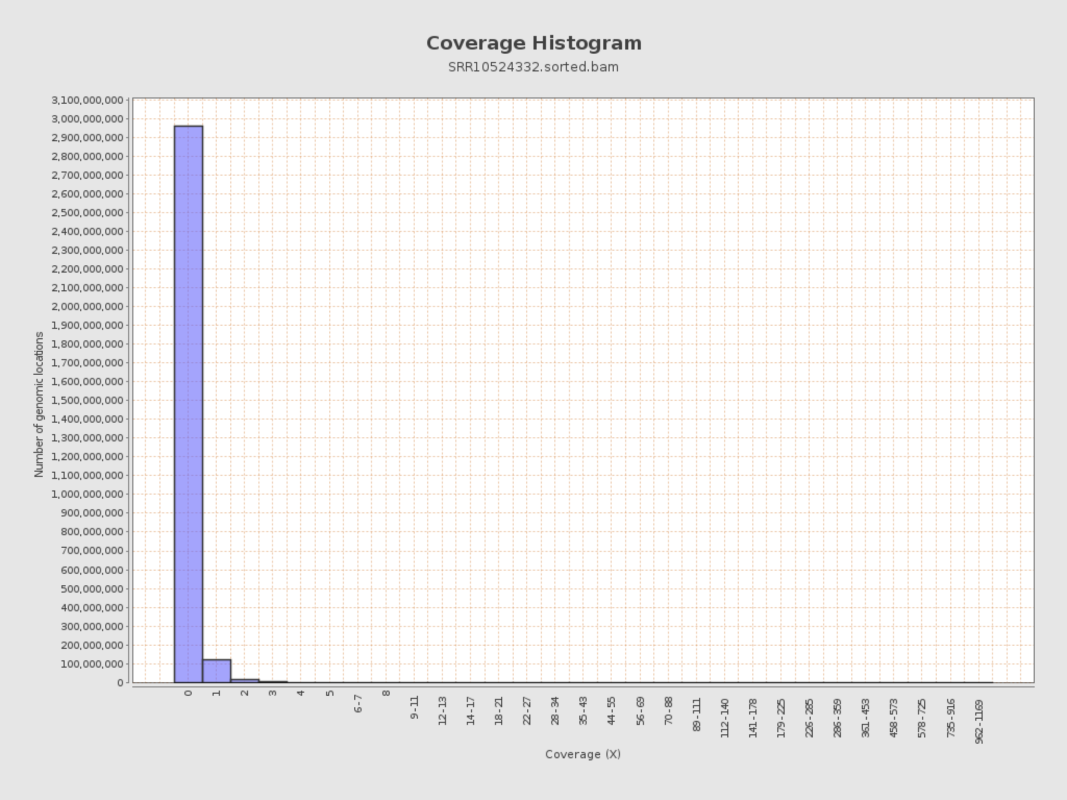
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13637557	0.0547	0.7969
chr2	243199373	10242529	0.0421	0.5534
chr3	198022430	11043523	0.0558	0.2684
chr4	191154276	8171123	0.0427	0.2825
chr5	180915260	7040113	0.0389	0.2247
chr6	171115067	10063649	0.0588	0.308
chr7	159138663	7172146	0.0451	0.5083

chr8	146364022	16492964	0.1127	0.5267
chr9	141213431	6691729	0.0474	0.3324
chr10	135534747	8177677	0.0603	0.4308
chr11	135006516	7804608	0.0578	0.3598
chr12	133851895	6236683	0.0466	0.2518
chr13	115169878	3994900	0.0347	0.2096
chr14	107349540	3330819	0.031	0.2193
chr15	102531392	5019242	0.049	0.2533
chr16	90354753	5086706	0.0563	0.29
chr17	81195210	5124375	0.0631	0.319
chr18	78077248	3723522	0.0477	0.6237
chr19	59128983	2962731	0.0501	0.5258
chr20	63025520	3798895	0.0603	0.2861
chr21	48129895	2288238	0.0475	0.28
chr22	51304566	1254116	0.0244	0.1756
chrMT	16571	11304	0.6822	0.9062
chrX	155270560	7600114	0.0489	0.286
chrY	59373566	472333	0.008	0.2195

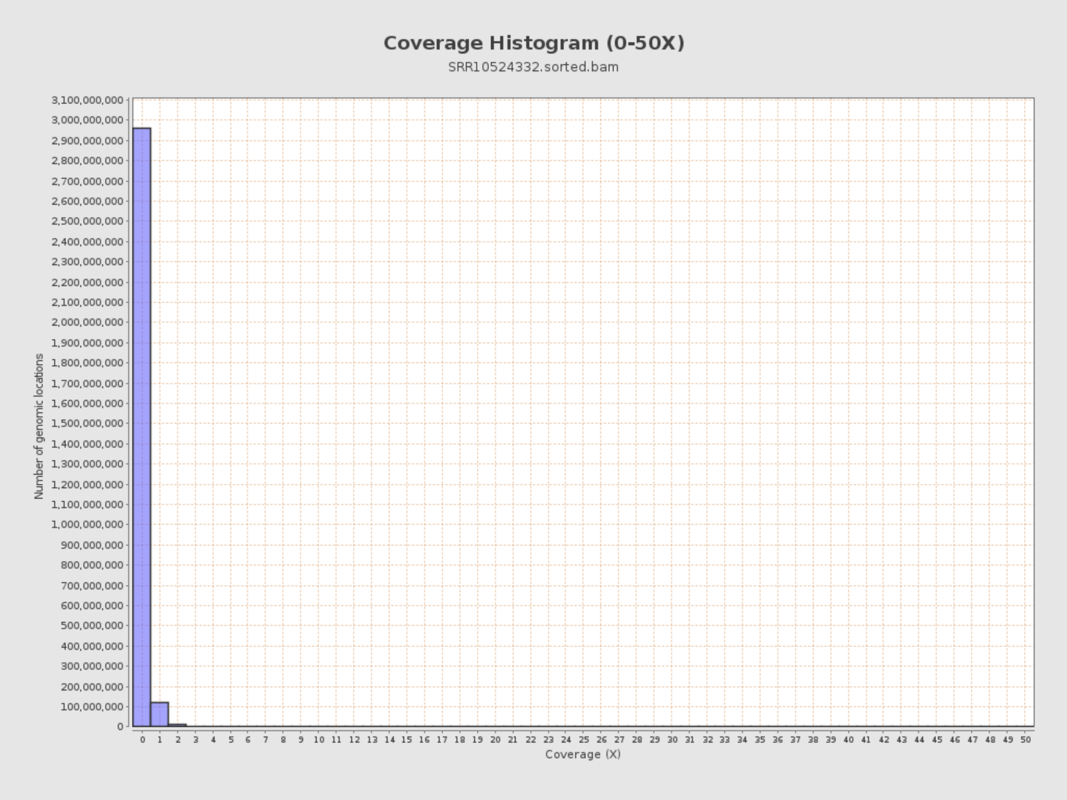
3. Results : Coverage across reference



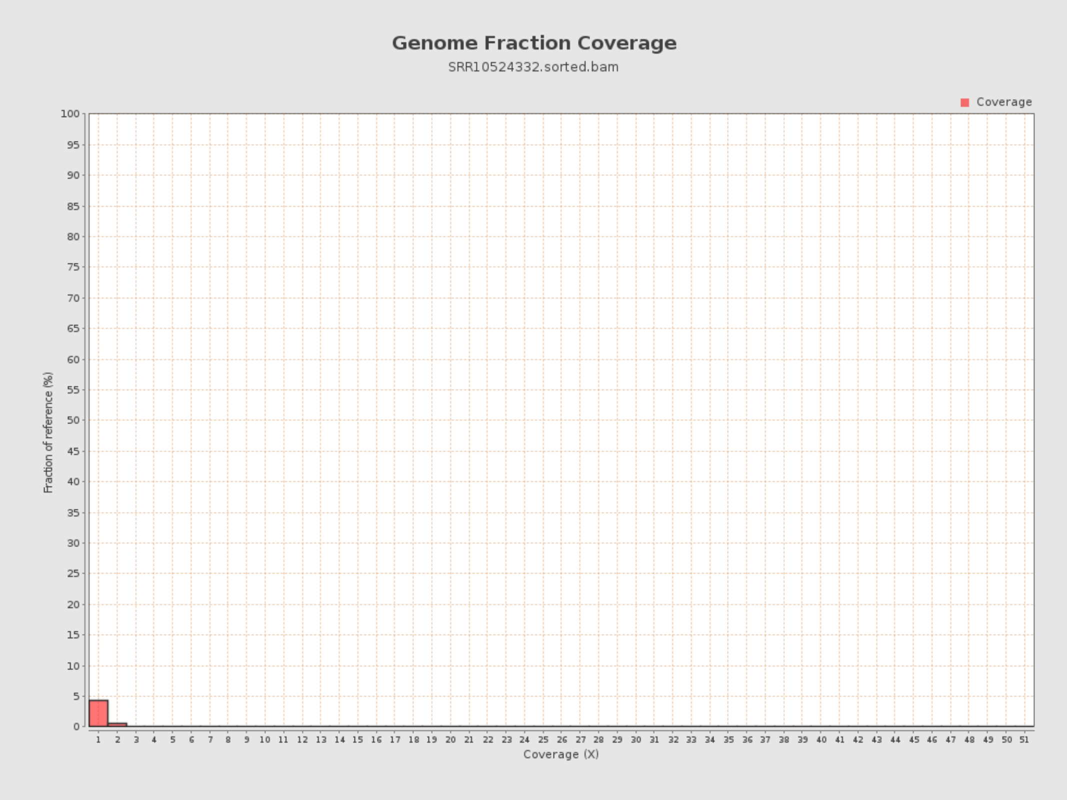
4. Results : Coverage Histogram



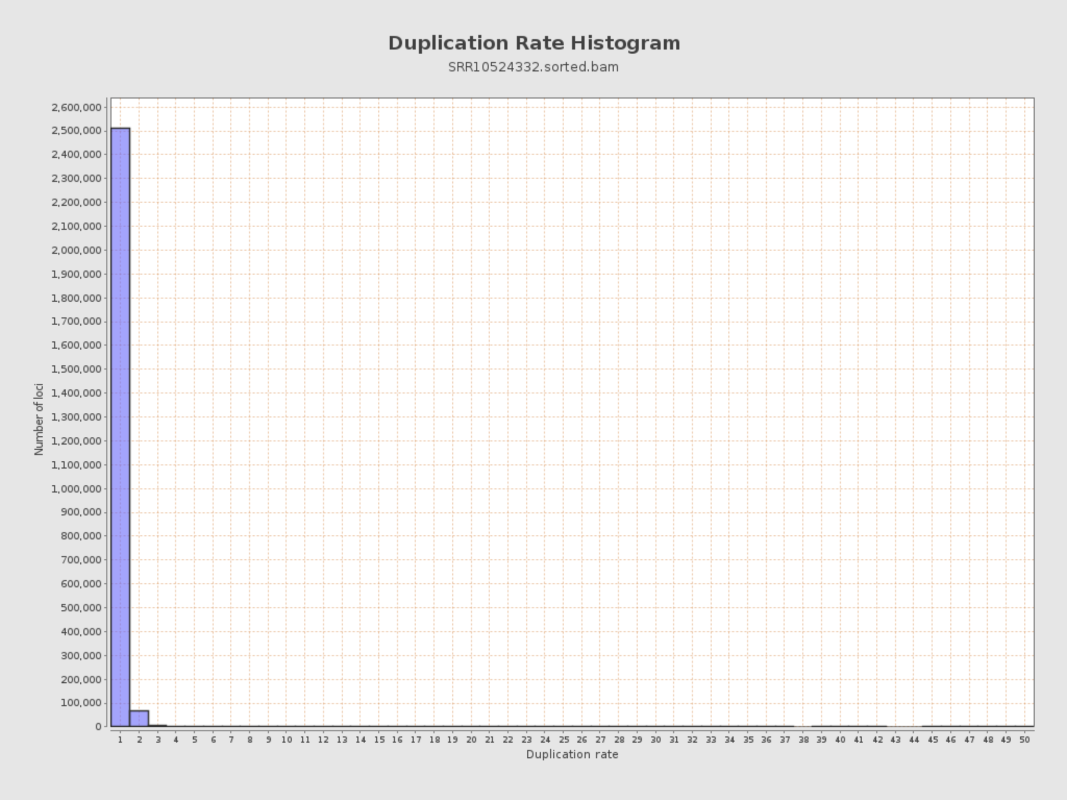
5. Results : Coverage Histogram (0-50X)



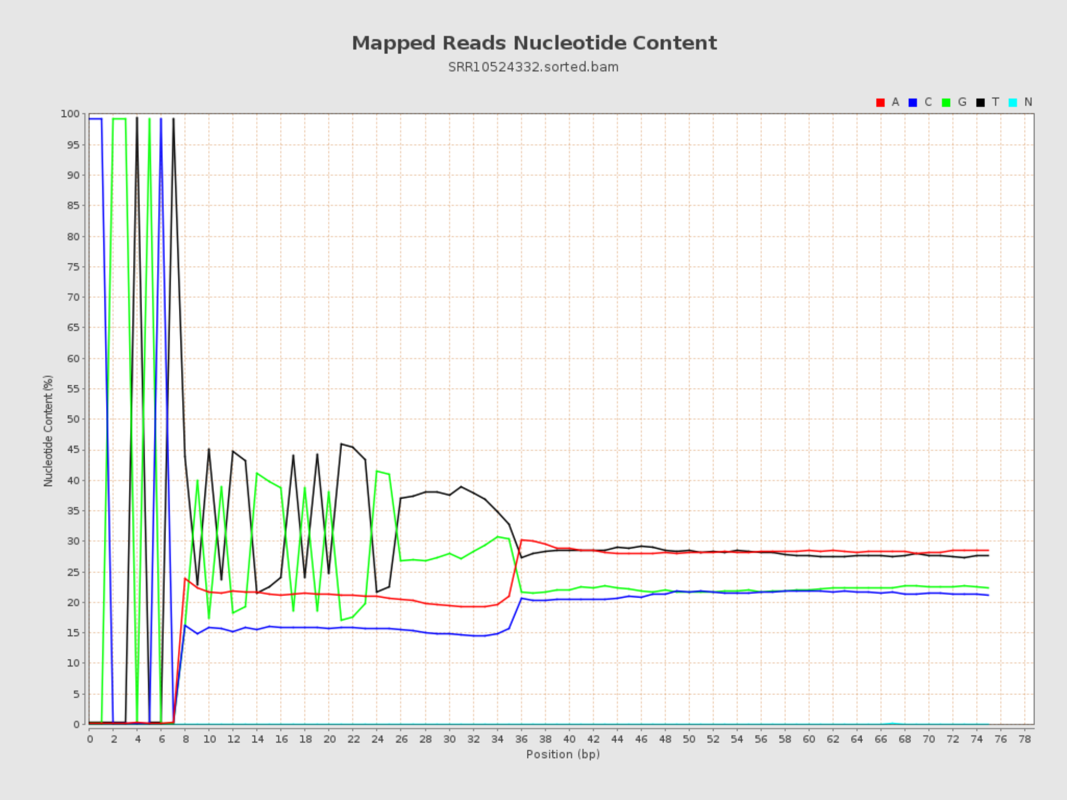
6. Results : Genome Fraction Coverage



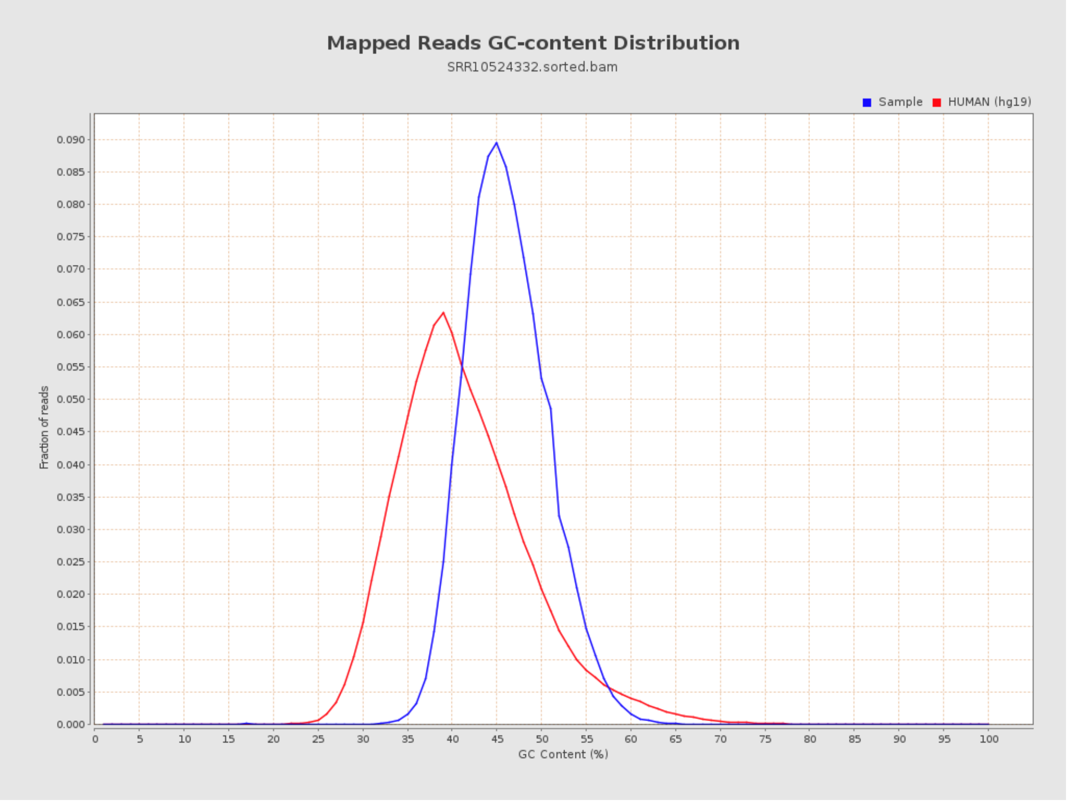
7. Results : Duplication Rate Histogram



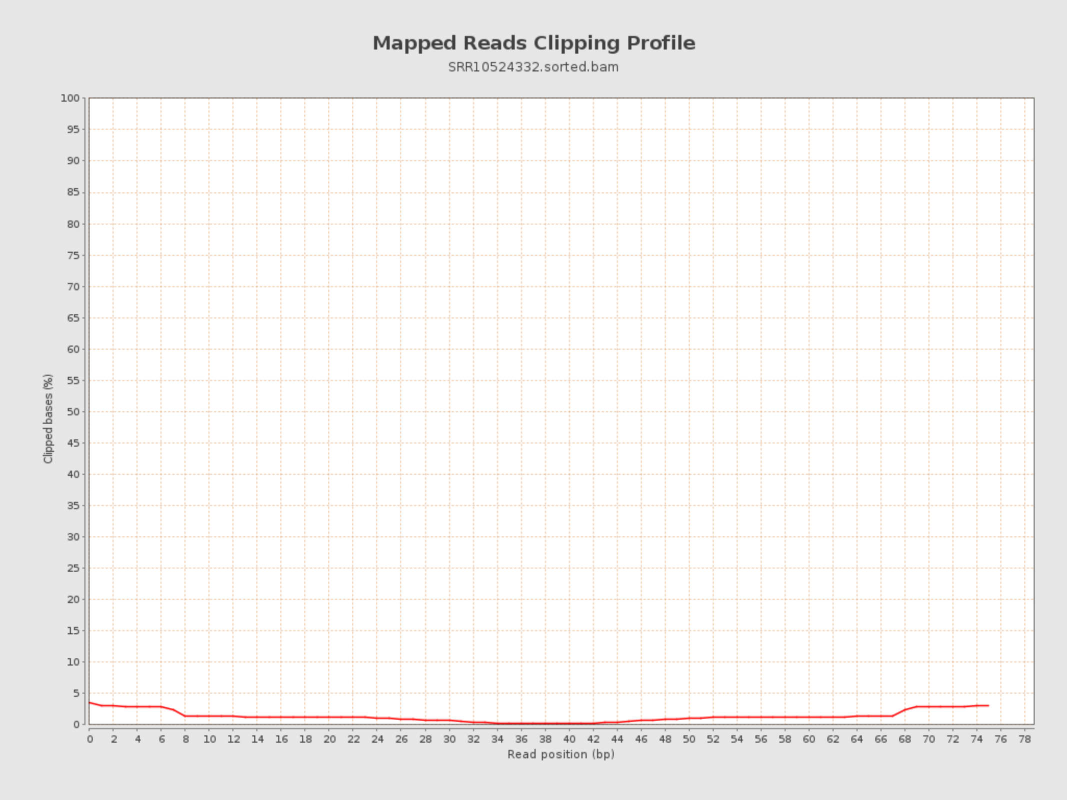
8. Results : Mapped Reads Nucleotide Content



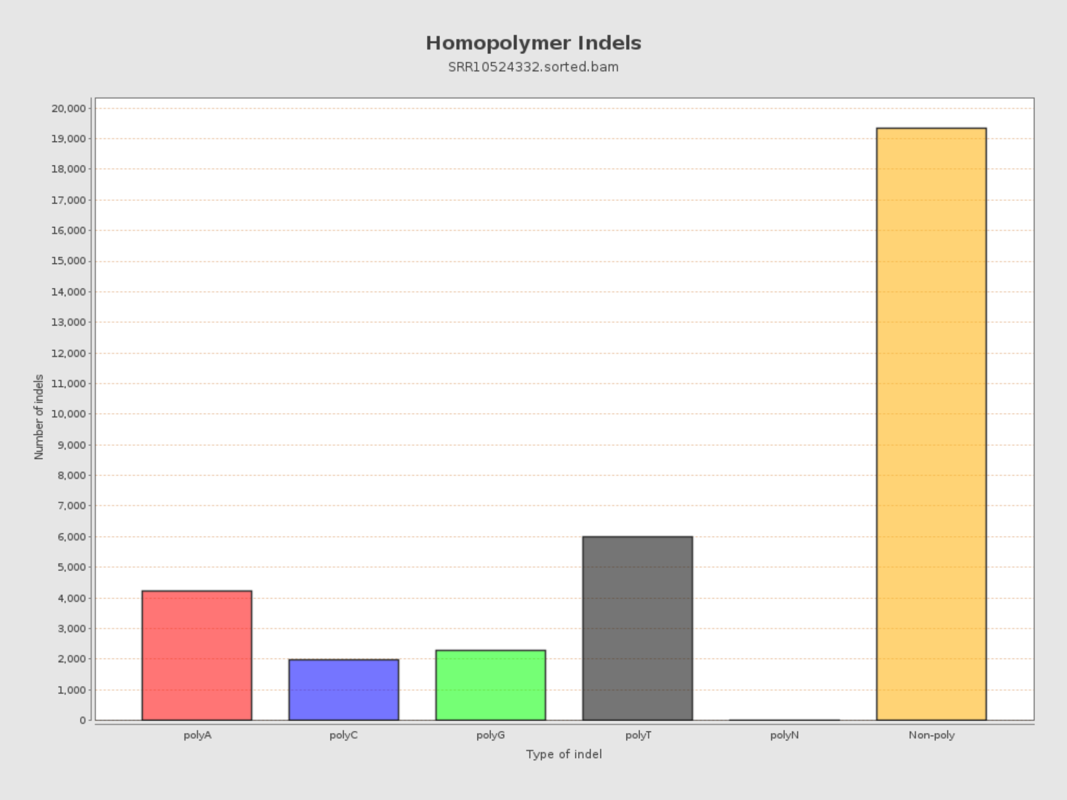
9. Results : Mapped Reads GC-content Distribution



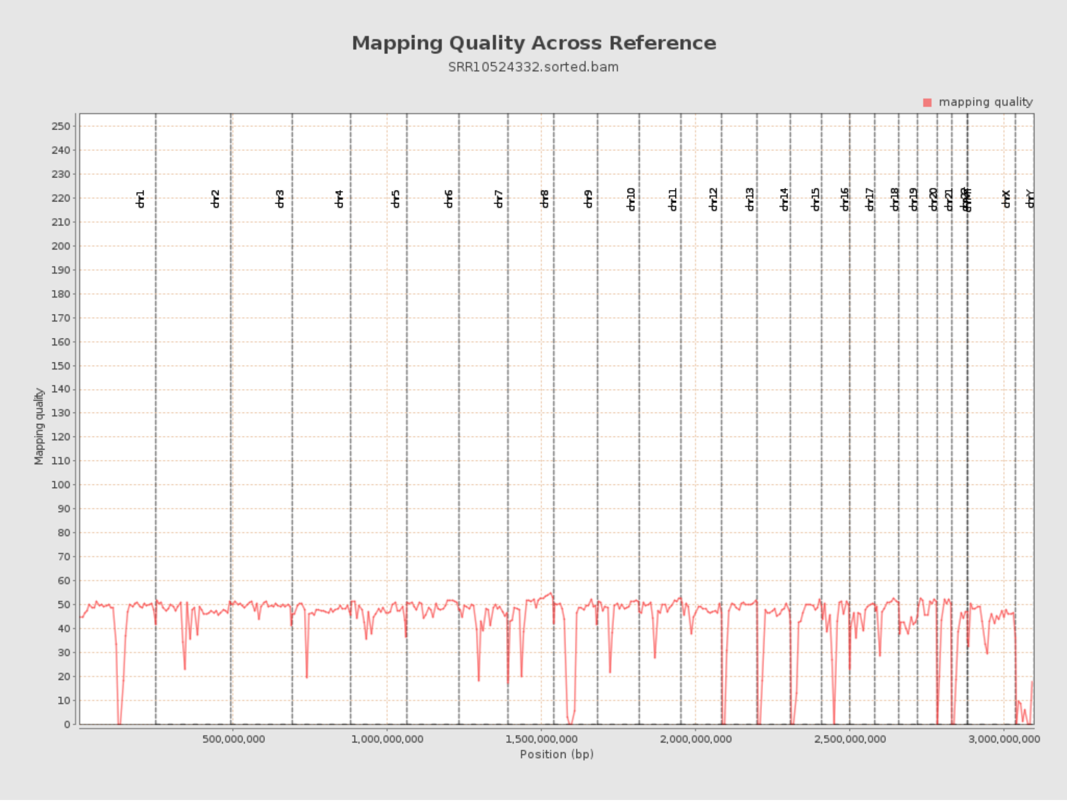
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram