Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:26:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524628.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_SRR10524628 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524628.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:25:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524628.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,147,987
Mapped reads	2,001,128 / 93.16%
Unmapped reads	146,859 / 6.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,825 / 0.22%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	98,510 / 4.59%
Duplication rate	3.79%
Clipped reads	1,999,828 / 93.1%

2.2. ACGT Content

Number/percentage of A's	30,007,175 / 25.7%
Number/percentage of C's	21,490,158 / 18.4%
Number/percentage of T's	37,762,176 / 32.34%
Number/percentage of G's	27,504,949 / 23.56%
Number/percentage of N's	761 / 0%
GC Percentage	41.96%

2.3. Coverage

Mean	0.0377

Standard Deviation	0.3171

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

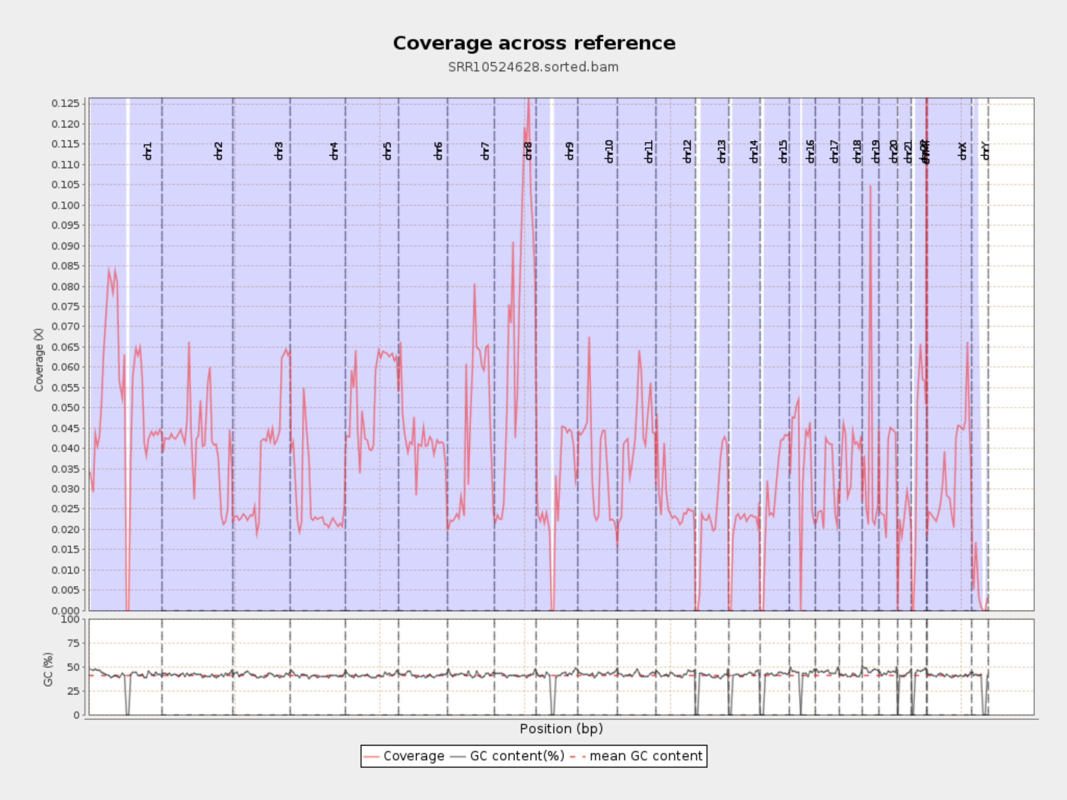
General error rate	0.48%
Mismatches	548,598
Insertions	7,389
Mapped reads with at least one insertion	0.37%
Deletions	22,458
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.69%

2.6. Chromosome stats

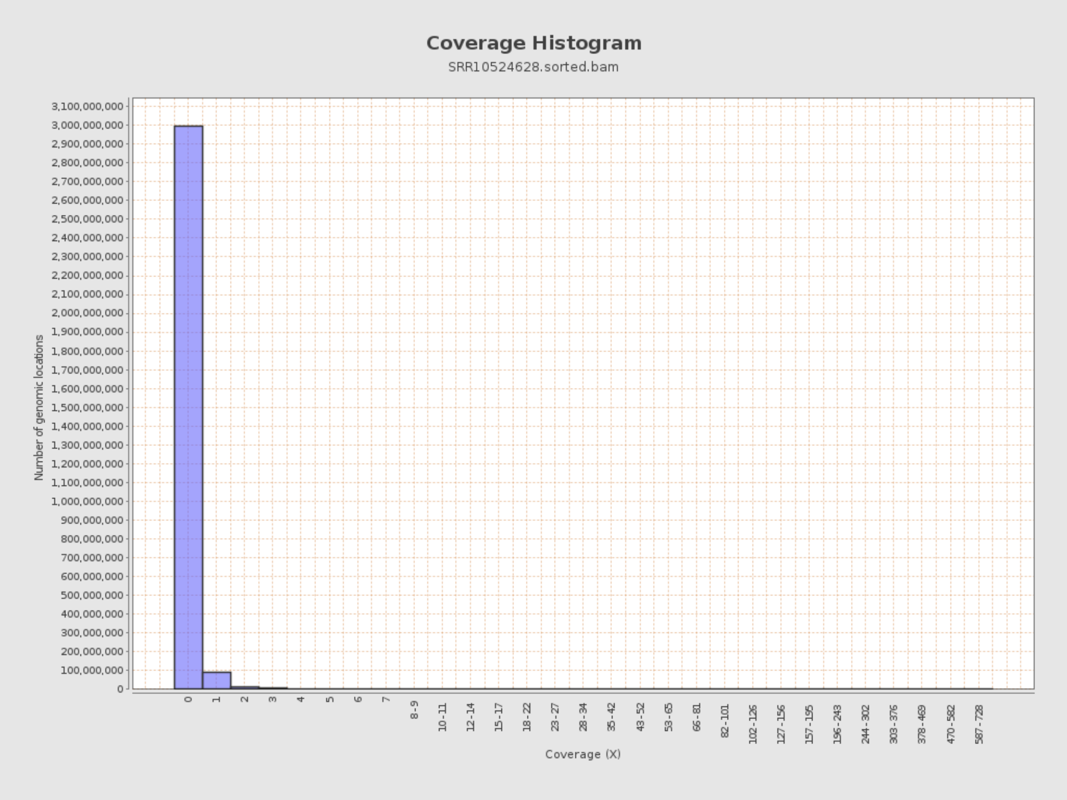
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12790324	0.0513	0.5668
chr2	243199373	10055168	0.0413	0.3614
chr3	198022430	7223171	0.0365	0.217
chr4	191154276	5085986	0.0266	0.2182
chr5	180915260	9623896	0.0532	0.2599
chr6	171115067	7249271	0.0424	0.2527
chr7	159138663	7017293	0.0441	0.4195

chr8	146364022	10131909	0.0692	0.4129
chr9	141213431	4079818	0.0289	0.2754
chr10	135534747	4868832	0.0359	0.3253
chr11	135006516	5717635	0.0424	0.3003
chr12	133851895	3542561	0.0265	0.1902
chr13	115169878	2769305	0.024	0.1762
chr14	107349540	2123489	0.0198	0.1684
chr15	102531392	2903947	0.0283	0.201
chr16	90354753	3340774	0.037	0.2302
chr17	81195210	2454022	0.0302	0.2056
chr18	78077248	3030642	0.0388	0.4637
chr19	59128983	2177233	0.0368	0.4034
chr20	63025520	2100413	0.0333	0.2126
chr21	48129895	1014973	0.0211	0.1872
chr22	51304566	1997570	0.0389	0.2233
chrMT	16571	3467	0.2092	0.5667
chrX	155270560	5230672	0.0337	0.2379
chrY	59373566	271307	0.0046	0.138

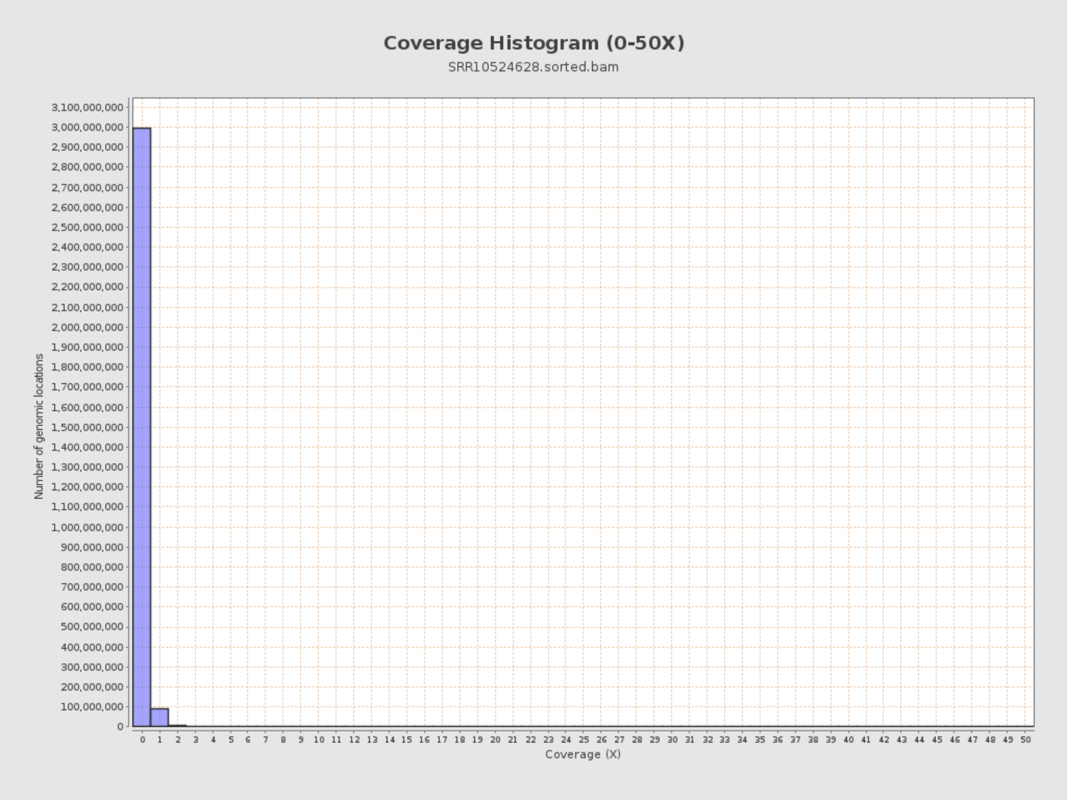
3. Results : Coverage across reference



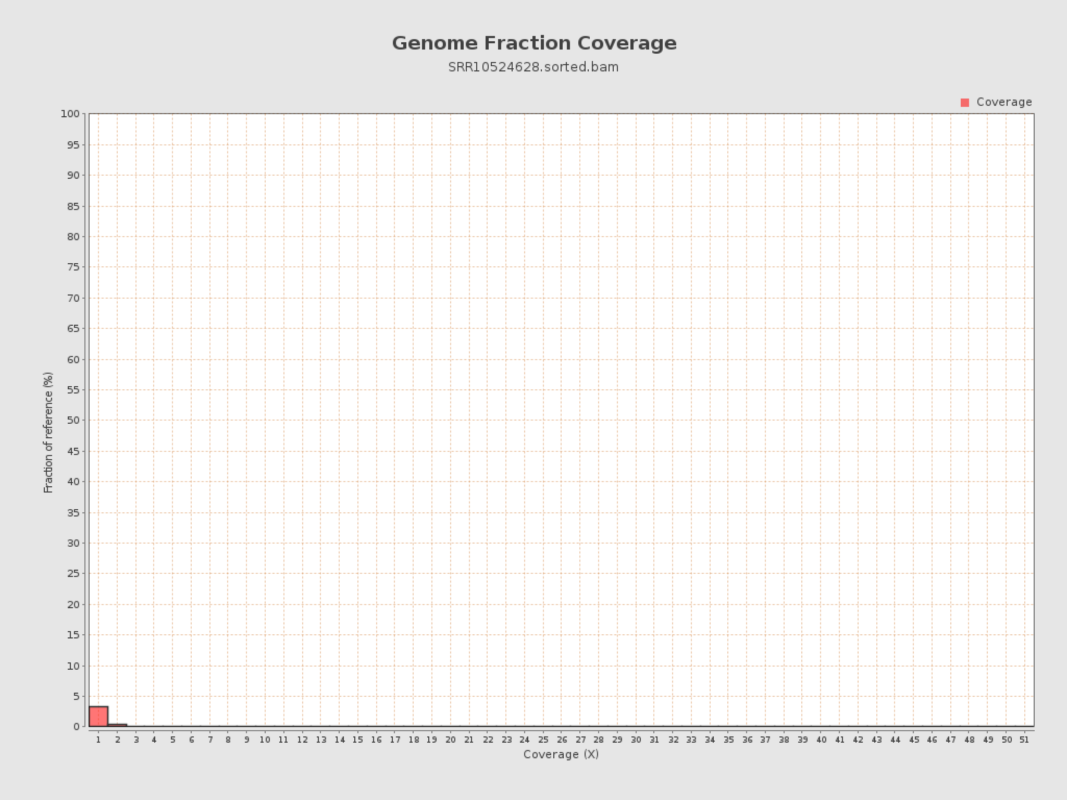
4. Results : Coverage Histogram



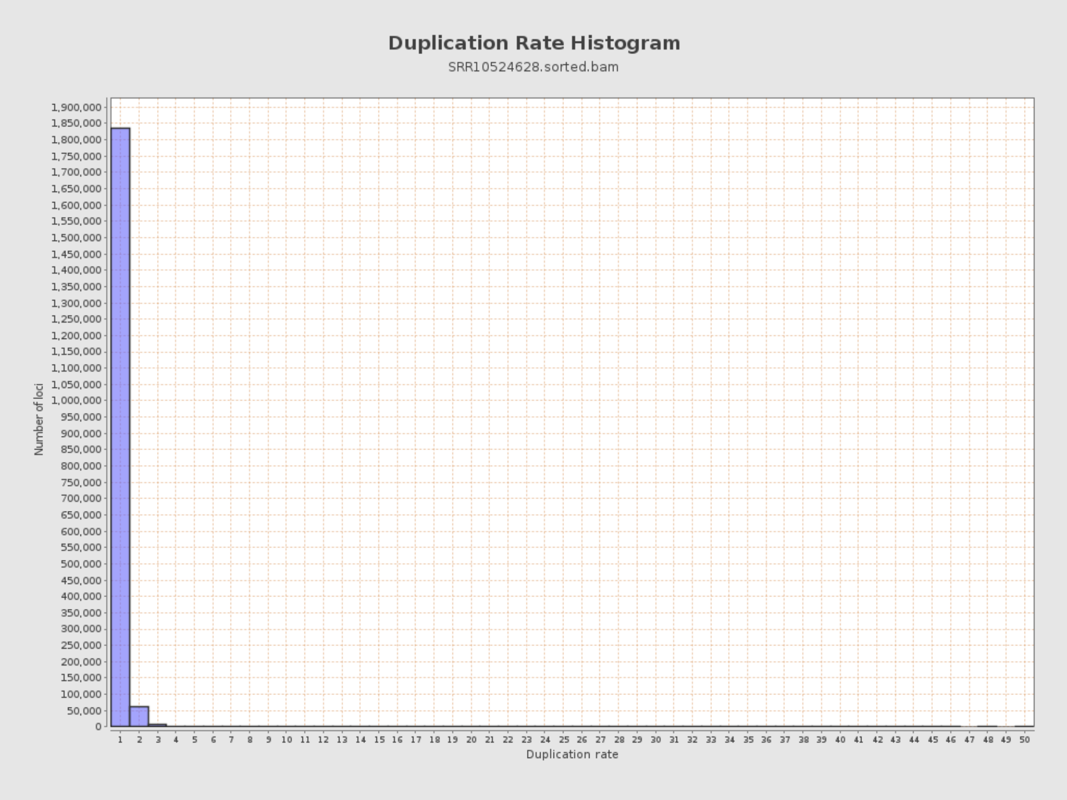
5. Results : Coverage Histogram (0-50X)



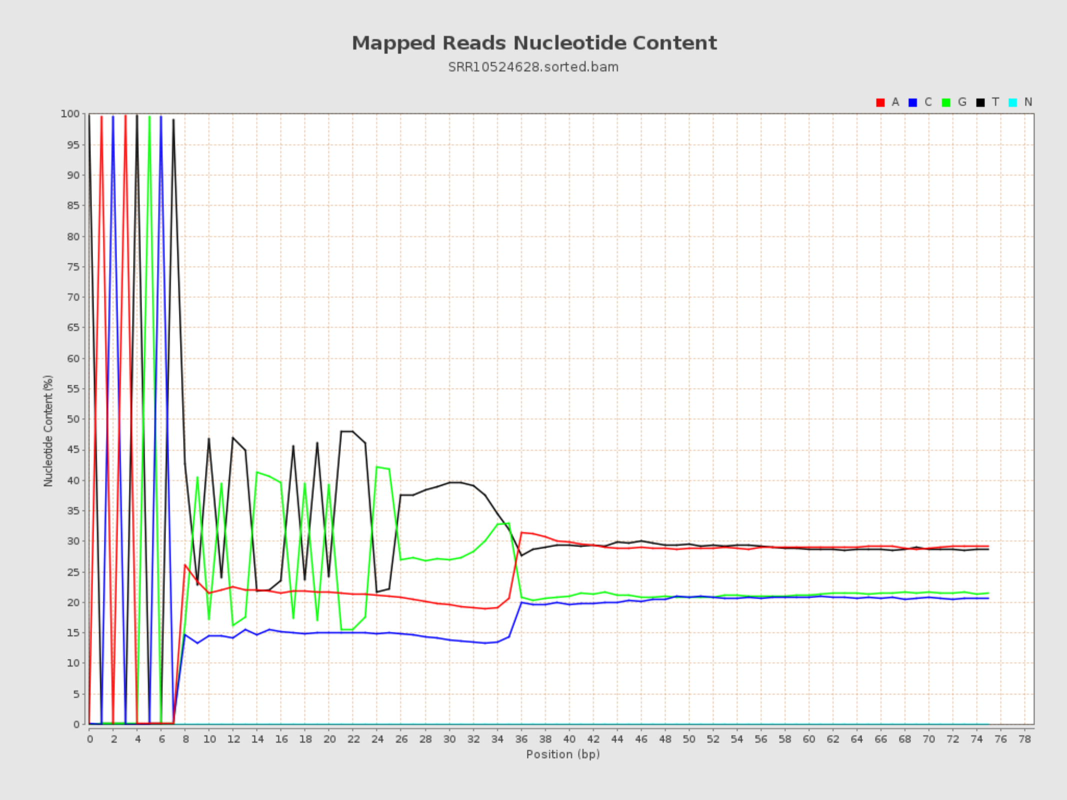
6. Results : Genome Fraction Coverage



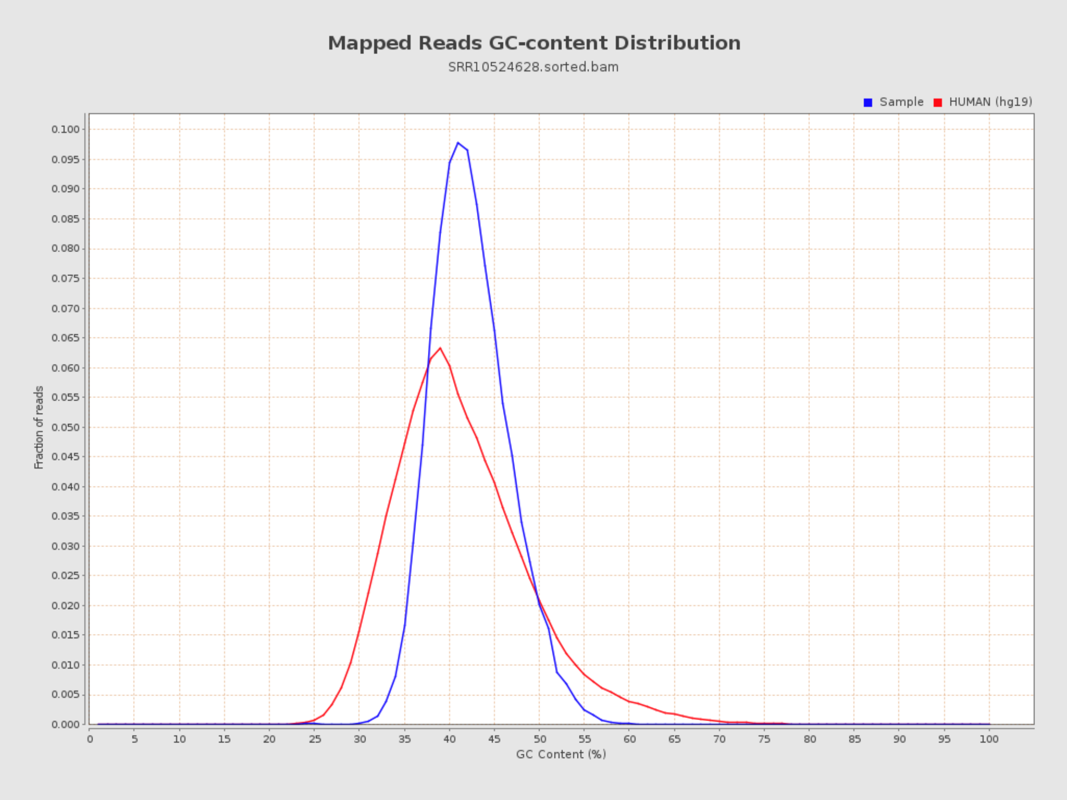
7. Results : Duplication Rate Histogram



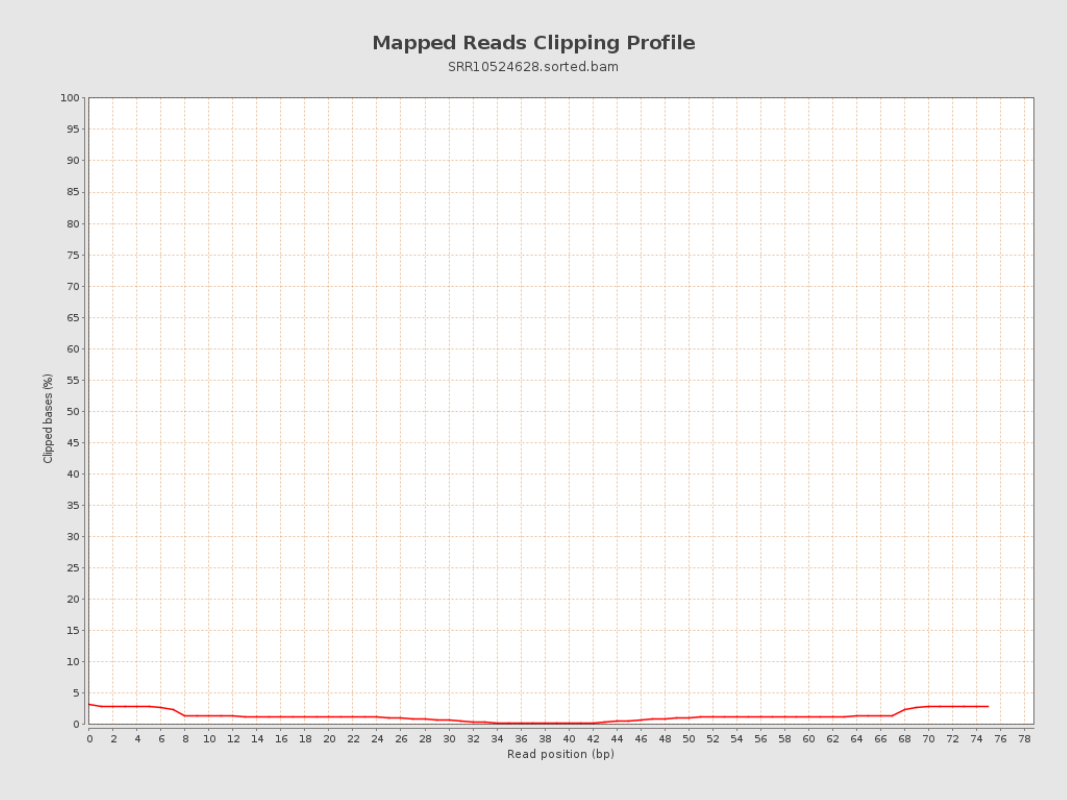
8. Results : Mapped Reads Nucleotide Content



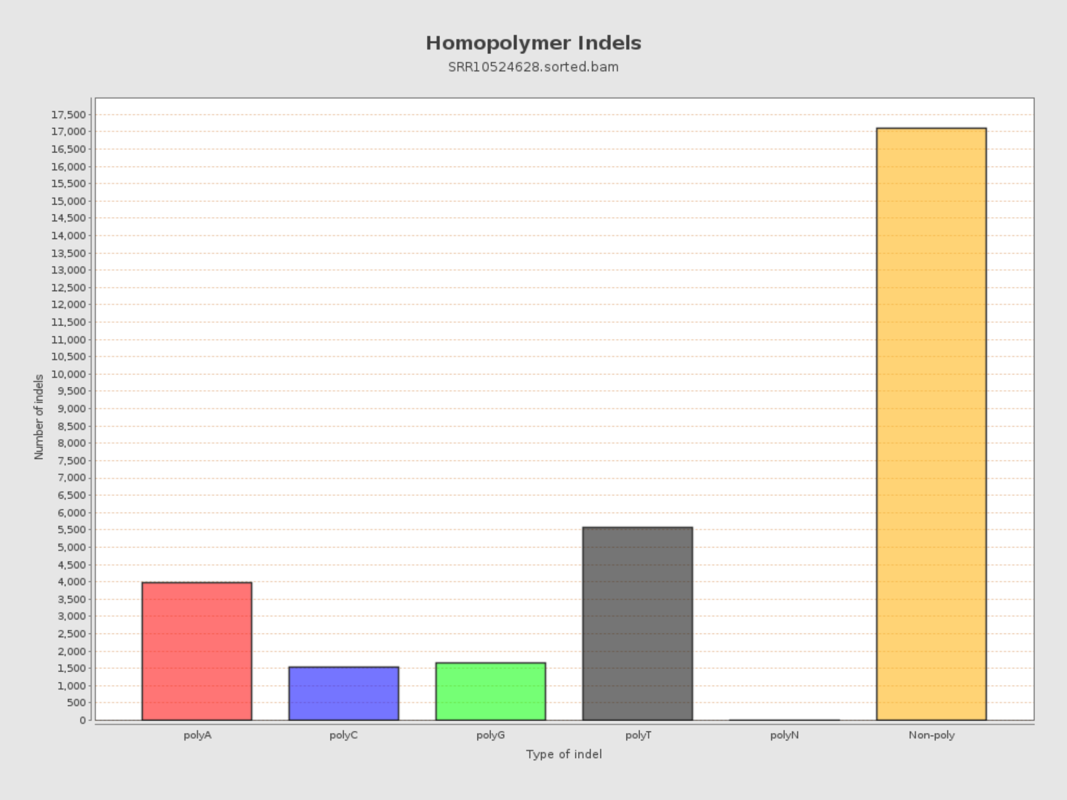
9. Results : Mapped Reads GC-content Distribution



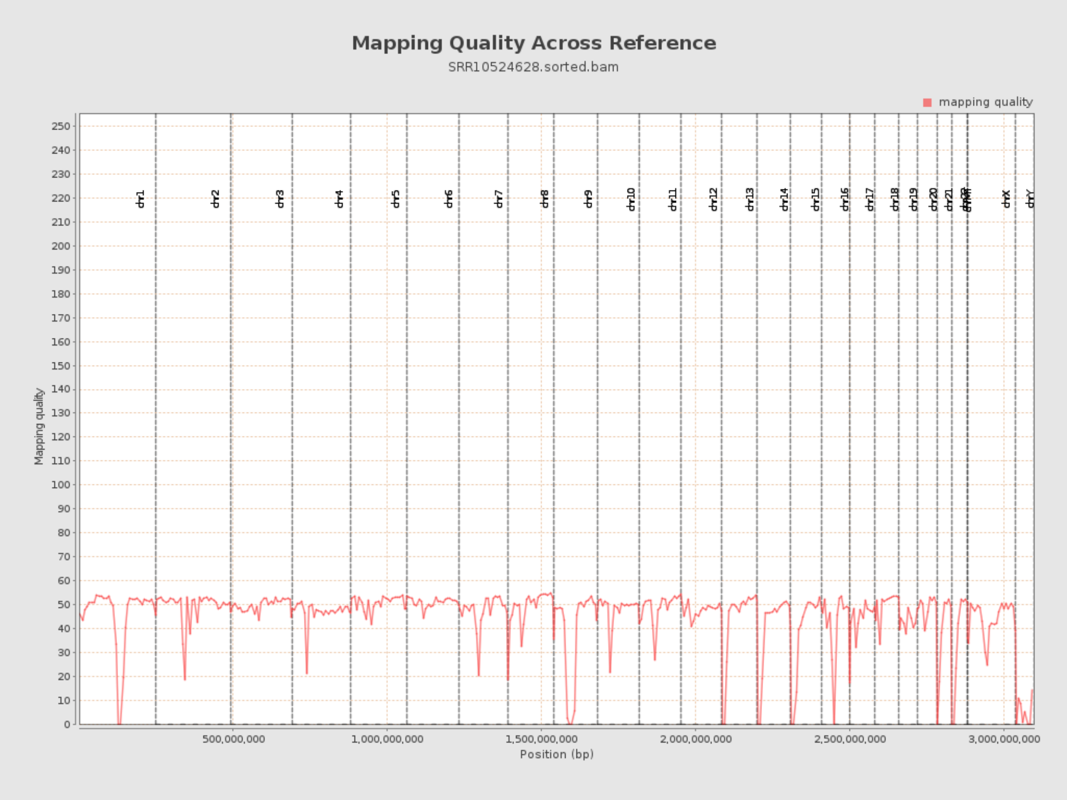
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram