

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:24:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524528.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_SRR10524528 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524528.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:24:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524528.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,067,627
Mapped reads	1,899,060 / 91.85%
Unmapped reads	168,567 / 8.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,855 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	142,491 / 6.89%
Duplication rate	5.82%
Clipped reads	1,901,942 / 91.99%

2.2. ACGT Content

Number/percentage of A's	27,973,041 / 25.36%
Number/percentage of C's	19,733,614 / 17.89%
Number/percentage of T's	34,626,727 / 31.4%
Number/percentage of G's	27,956,944 / 25.35%
Number/percentage of N's	1,468 / 0%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0356

Standard Deviation	0.3372
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2.4. Mapping Quality

Mean Mapping Quality	45.28
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2.5. Mismatches and indels

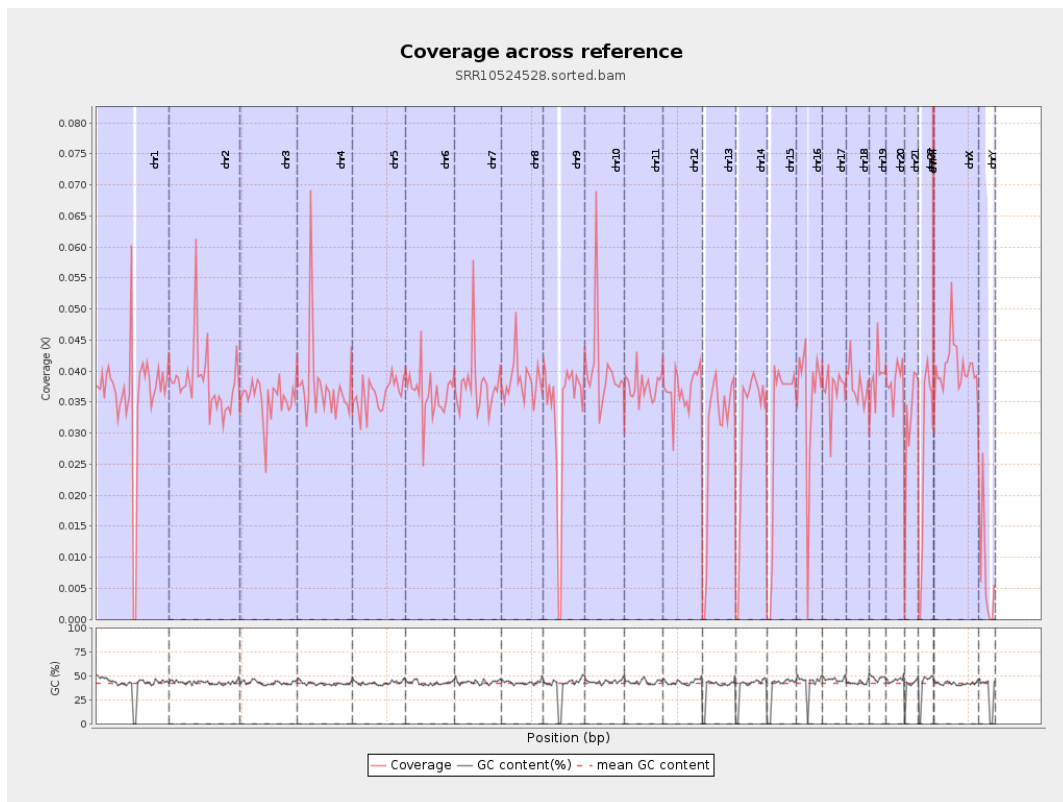
General error rate	0.52%
Mismatches	562,687
Insertions	7,166
Mapped reads with at least one insertion	0.38%
Deletions	19,820
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.34%

2.6. Chromosome stats

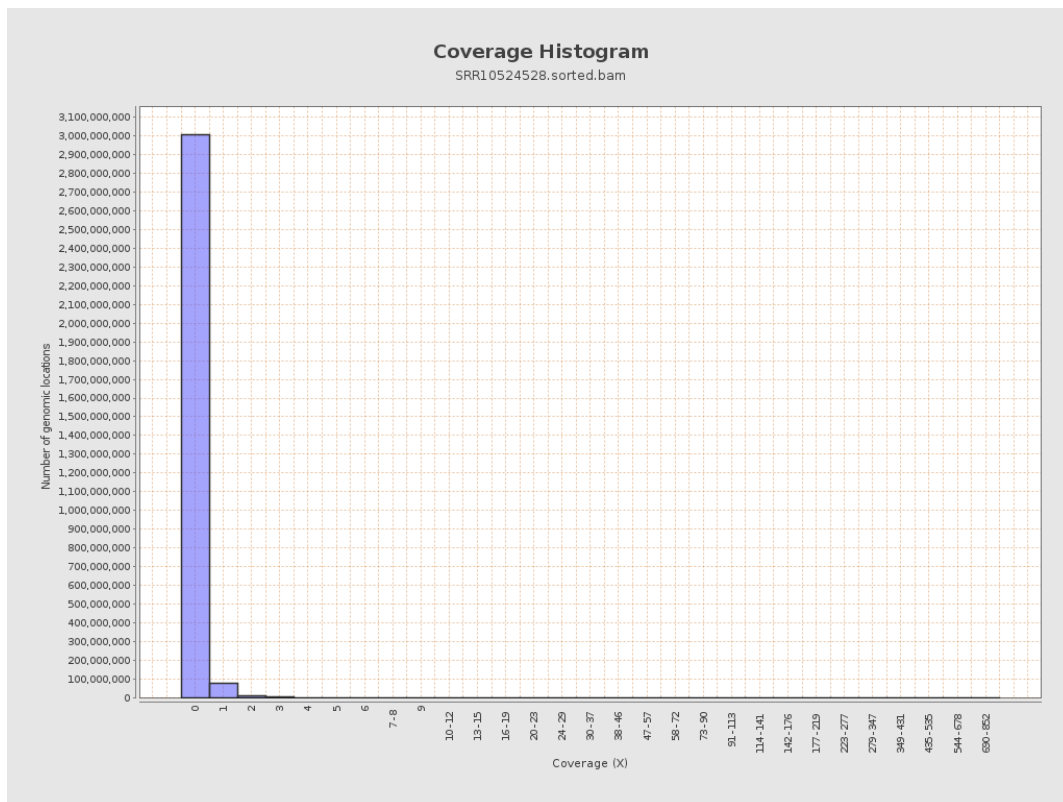
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8949504	0.0359	0.6361
chr2	243199373	9320969	0.0383	0.4177
chr3	198022430	7026659	0.0355	0.223
chr4	191154276	7172846	0.0375	0.2722
chr5	180915260	6553859	0.0362	0.2251
chr6	171115067	6250591	0.0365	0.2622
chr7	159138663	6012986	0.0378	0.3894

chr8	146364022	5618624	0.0384	0.3545
chr9	141213431	4631705	0.0328	0.2764
chr10	135534747	5412583	0.0399	0.341
chr11	135006516	5055623	0.0374	0.3007
chr12	133851895	4948629	0.037	0.2302
chr13	115169878	3395240	0.0295	0.2049
chr14	107349540	3301227	0.0308	0.213
chr15	102531392	3162568	0.0308	0.2086
chr16	90354753	3220320	0.0356	0.2391
chr17	81195210	2995293	0.0369	0.242
chr18	78077248	2952997	0.0378	0.4986
chr19	59128983	2316667	0.0392	0.4098
chr20	63025520	2412137	0.0383	0.2363
chr21	48129895	1532784	0.0318	0.2435
chr22	51304566	1348963	0.0263	0.193
chrMT	16571	18997	1.1464	1.2896
chrX	155270560	6295276	0.0405	0.26
chrY	59373566	418011	0.007	0.2285

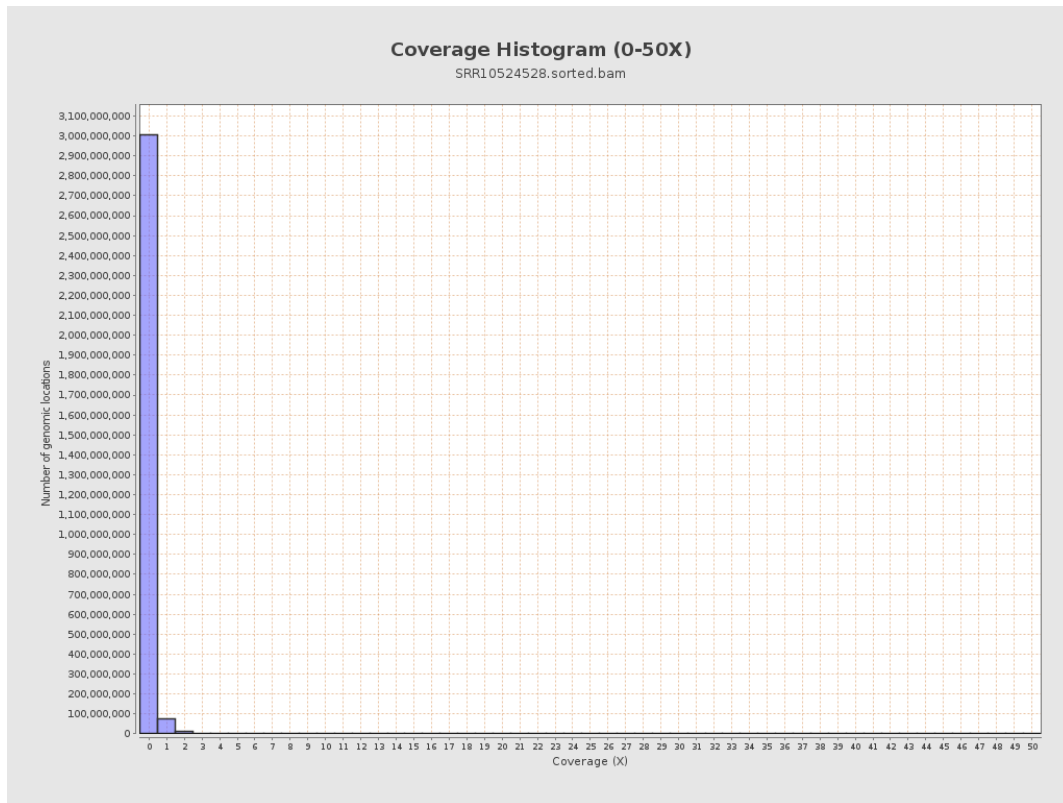
3. Results : Coverage across reference



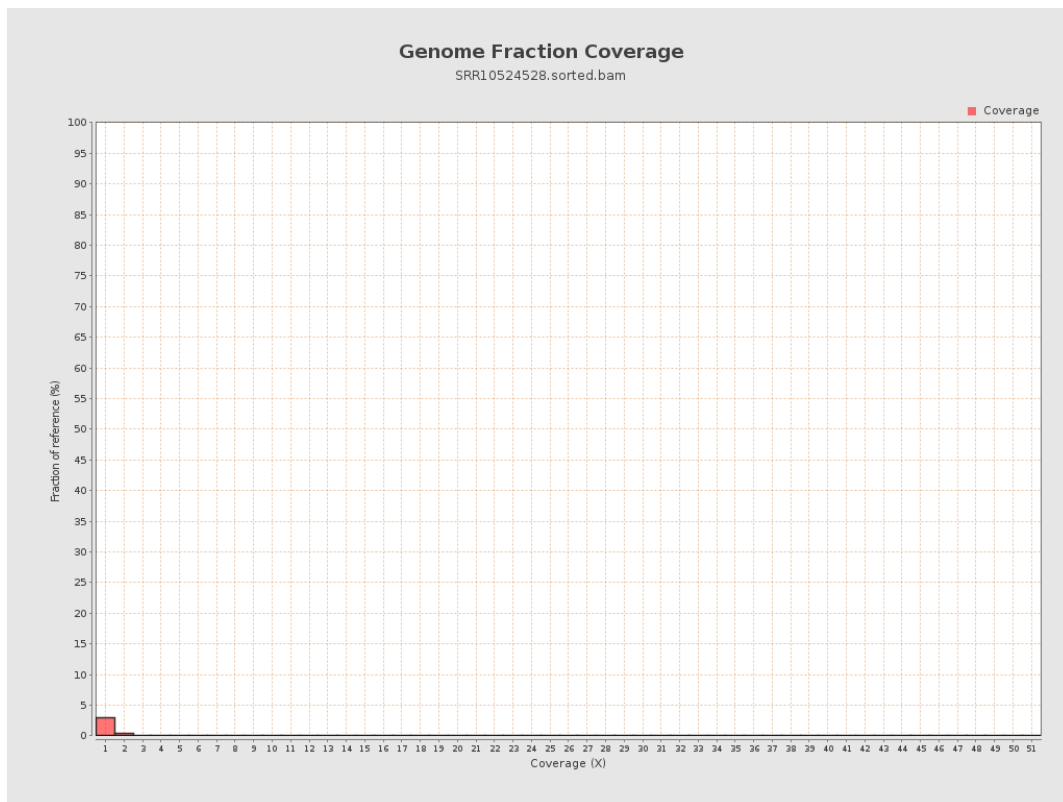
4. Results : Coverage Histogram



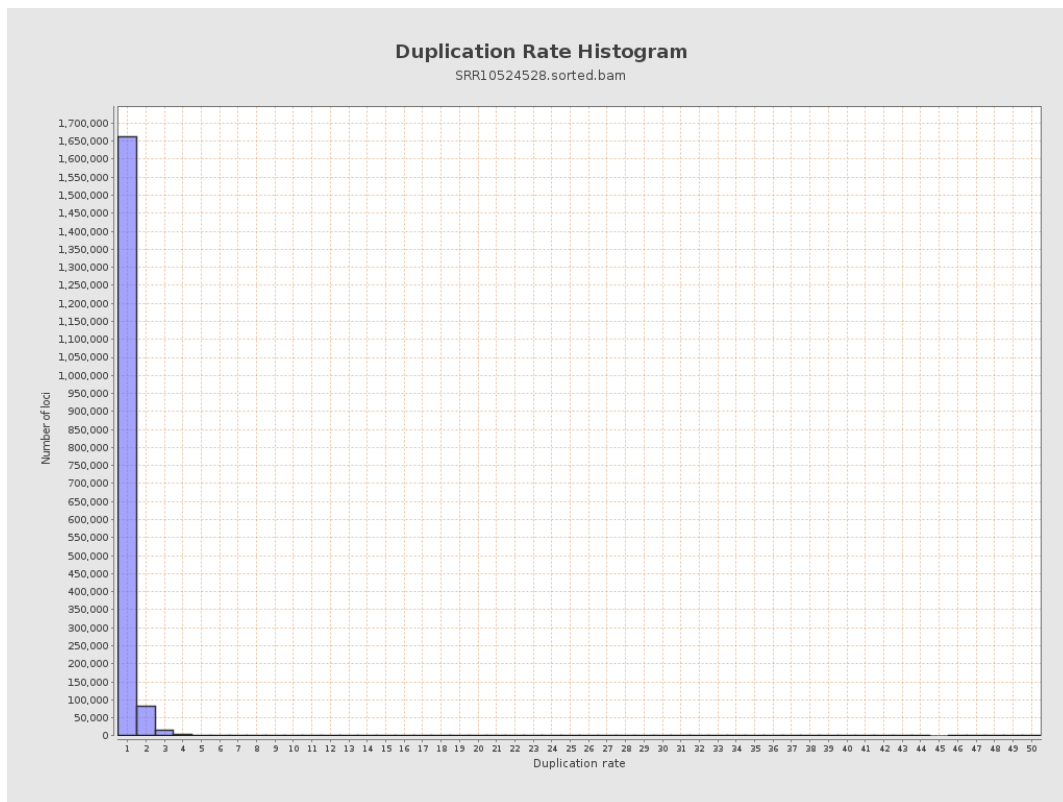
5. Results : Coverage Histogram (0-50X)



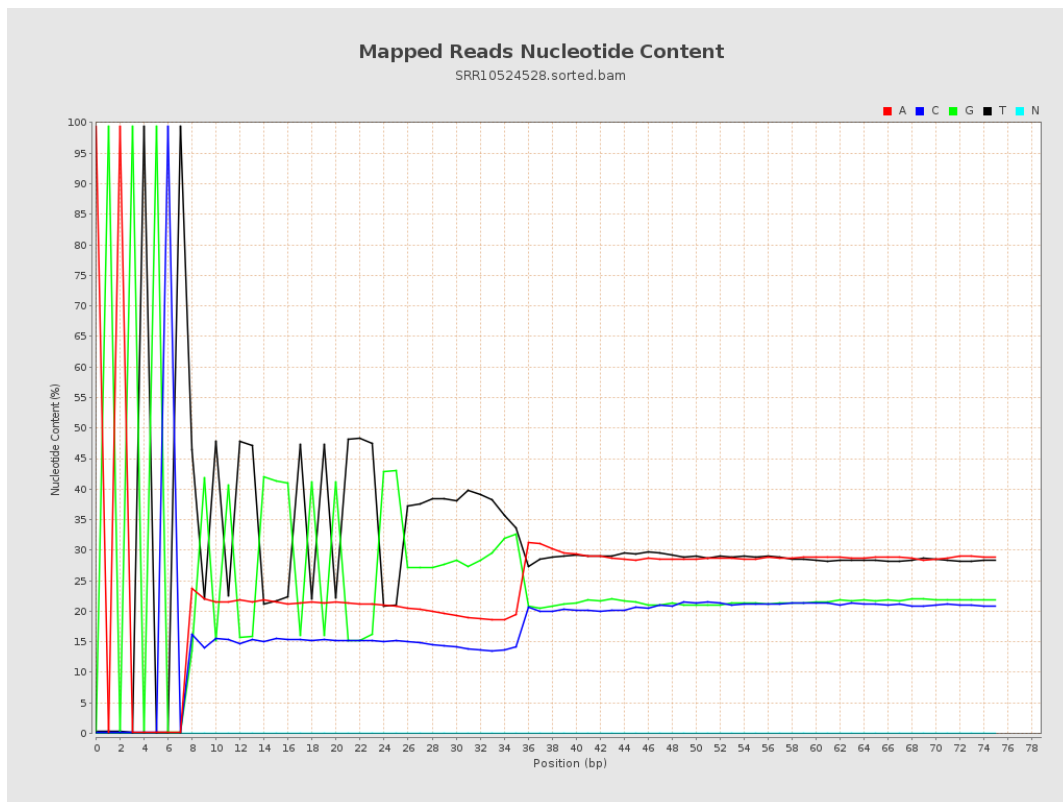
6. Results : Genome Fraction Coverage



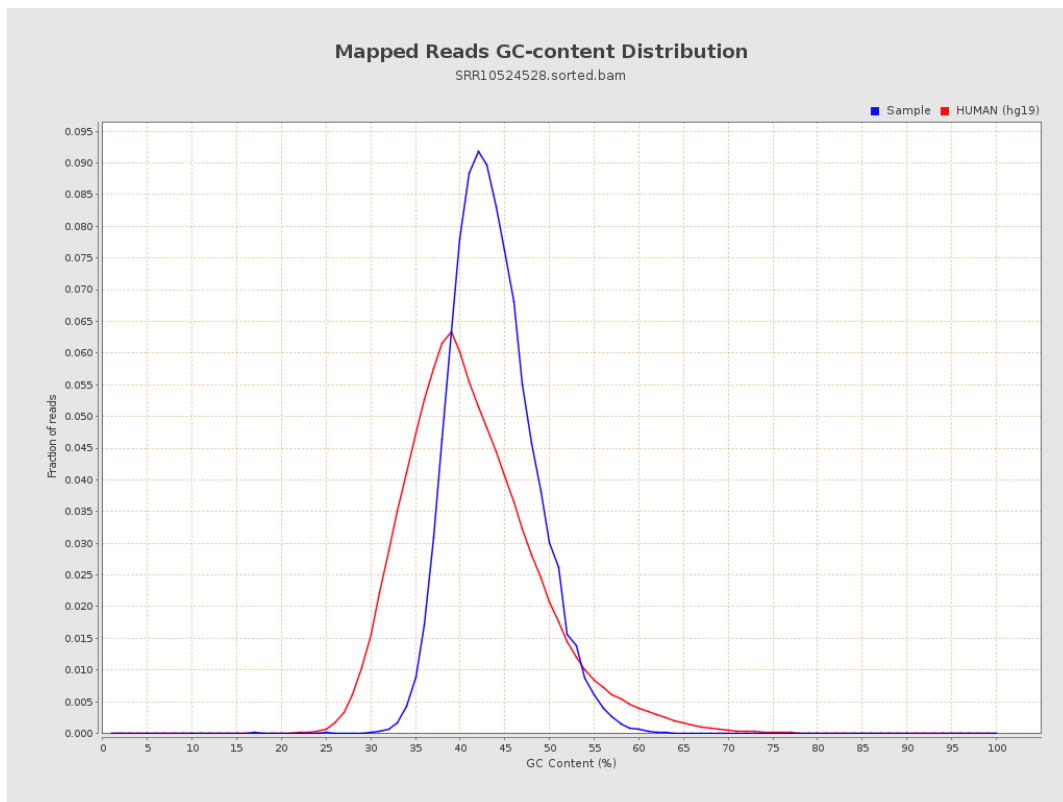
7. Results : Duplication Rate Histogram



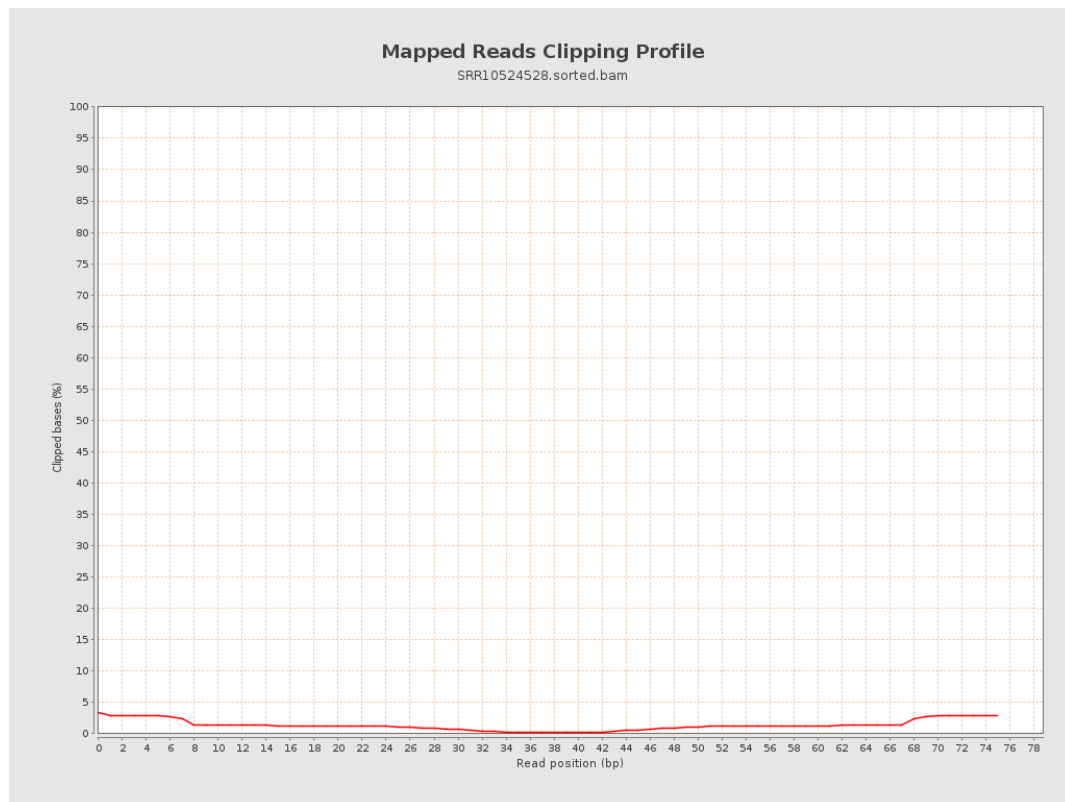
8. Results : Mapped Reads Nucleotide Content



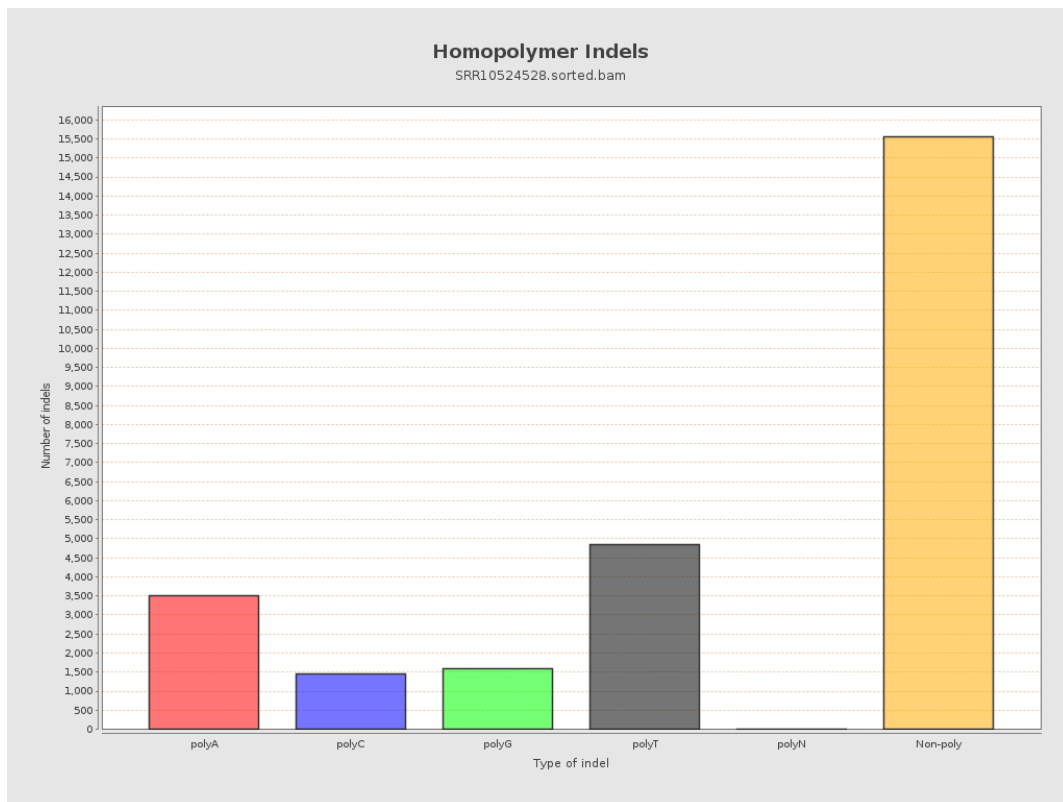
9. Results : Mapped Reads GC-content Distribution



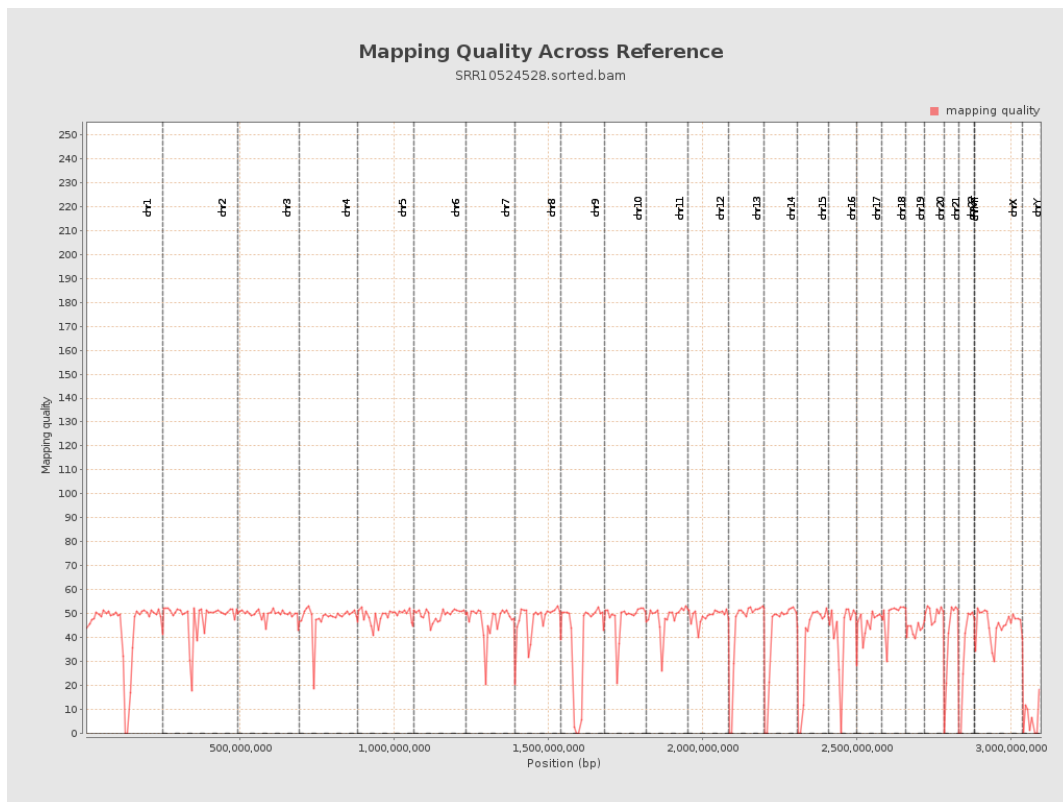
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

