

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:30:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524542.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_SRR10524542 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524542.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:30:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524542.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,461,909
Mapped reads	2,235,377 / 90.8%
Unmapped reads	226,532 / 9.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,416 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	96,526 / 3.92%
Duplication rate	3.14%
Clipped reads	2,237,647 / 90.89%

2.2. ACGT Content

Number/percentage of A's	32,624,752 / 25.25%
Number/percentage of C's	23,042,533 / 17.83%
Number/percentage of T's	40,505,850 / 31.35%
Number/percentage of G's	33,030,687 / 25.56%
Number/percentage of N's	1,663 / 0%
GC Percentage	43.4%

2.3. Coverage

Mean	0.0418

Standard Deviation	0.3543
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.96
----------------------	-------

2.5. Mismatches and indels

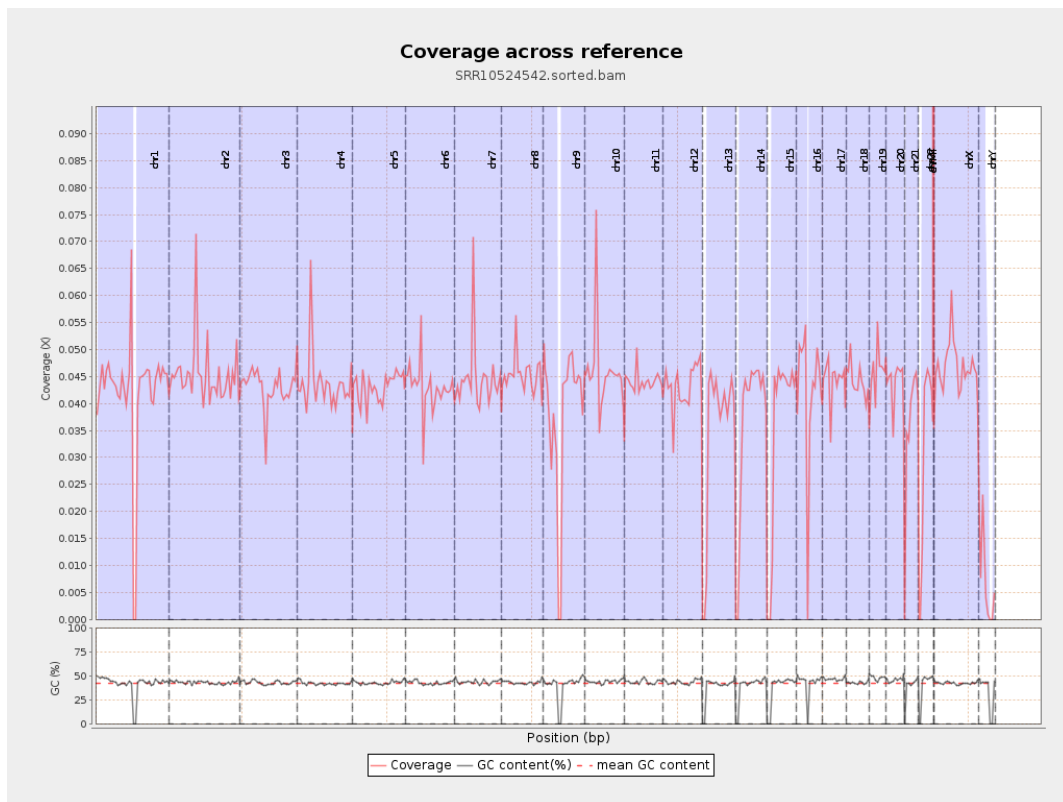
General error rate	0.52%
Mismatches	654,075
Insertions	8,234
Mapped reads with at least one insertion	0.37%
Deletions	24,475
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.42%

2.6. Chromosome stats

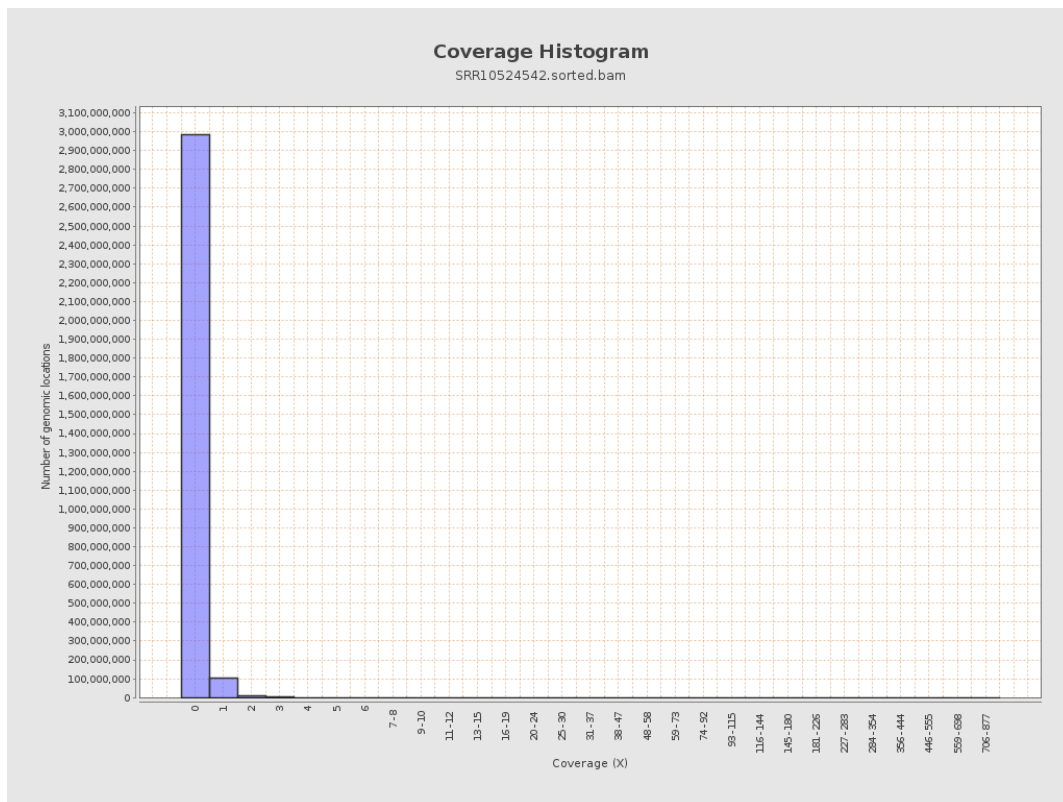
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10467377	0.042	0.6522
chr2	243199373	11024562	0.0453	0.4167
chr3	198022430	8507652	0.043	0.2352
chr4	191154276	8322010	0.0435	0.2626
chr5	180915260	7776950	0.043	0.2325
chr6	171115067	7349710	0.043	0.2826
chr7	159138663	7112309	0.0447	0.4757

chr8	146364022	6619879	0.0452	0.3145
chr9	141213431	5270805	0.0373	0.3031
chr10	135534747	6224399	0.0459	0.3507
chr11	135006516	5916048	0.0438	0.3532
chr12	133851895	5773679	0.0431	0.2366
chr13	115169878	3992921	0.0347	0.2087
chr14	107349540	3922957	0.0365	0.2214
chr15	102531392	3650580	0.0356	0.2273
chr16	90354753	3818071	0.0423	0.2614
chr17	81195210	3577934	0.0441	0.2539
chr18	78077248	3463838	0.0444	0.5648
chr19	59128983	2726776	0.0461	0.4847
chr20	63025520	2752409	0.0437	0.2383
chr21	48129895	1736773	0.0361	0.2328
chr22	51304566	1548985	0.0302	0.1936
chrMT	16571	23664	1.428	1.4563
chrX	155270560	7265762	0.0468	0.2816
chrY	59373566	399923	0.0067	0.1835

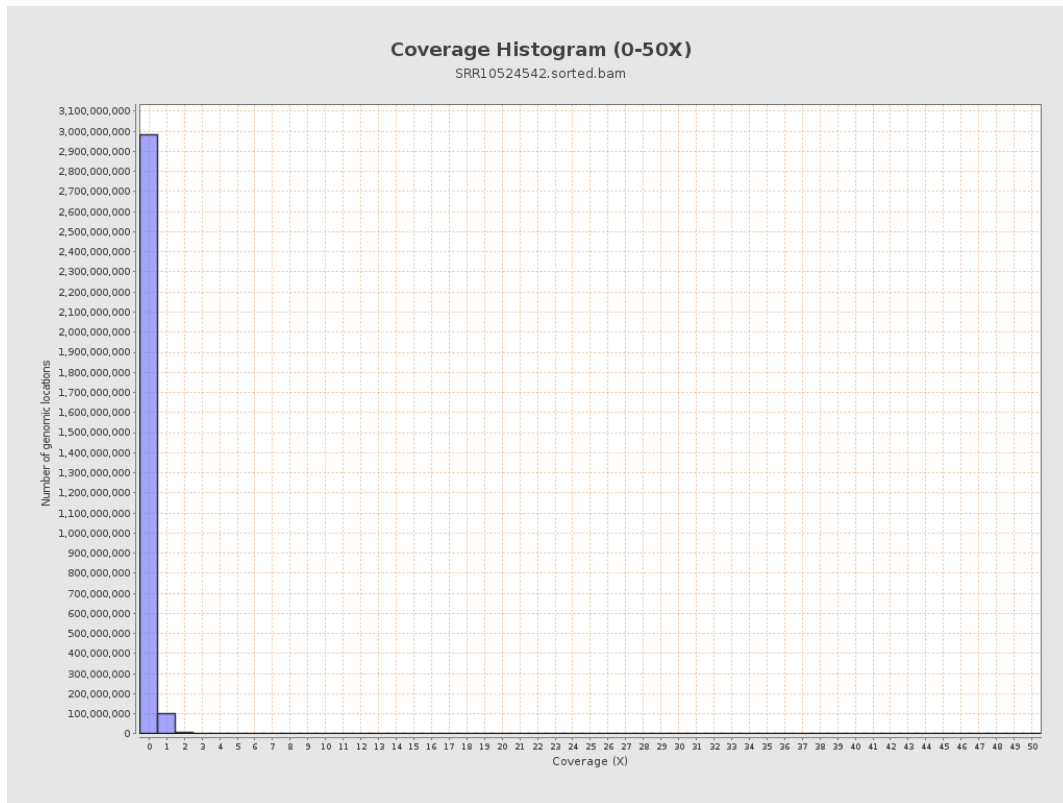
3. Results : Coverage across reference



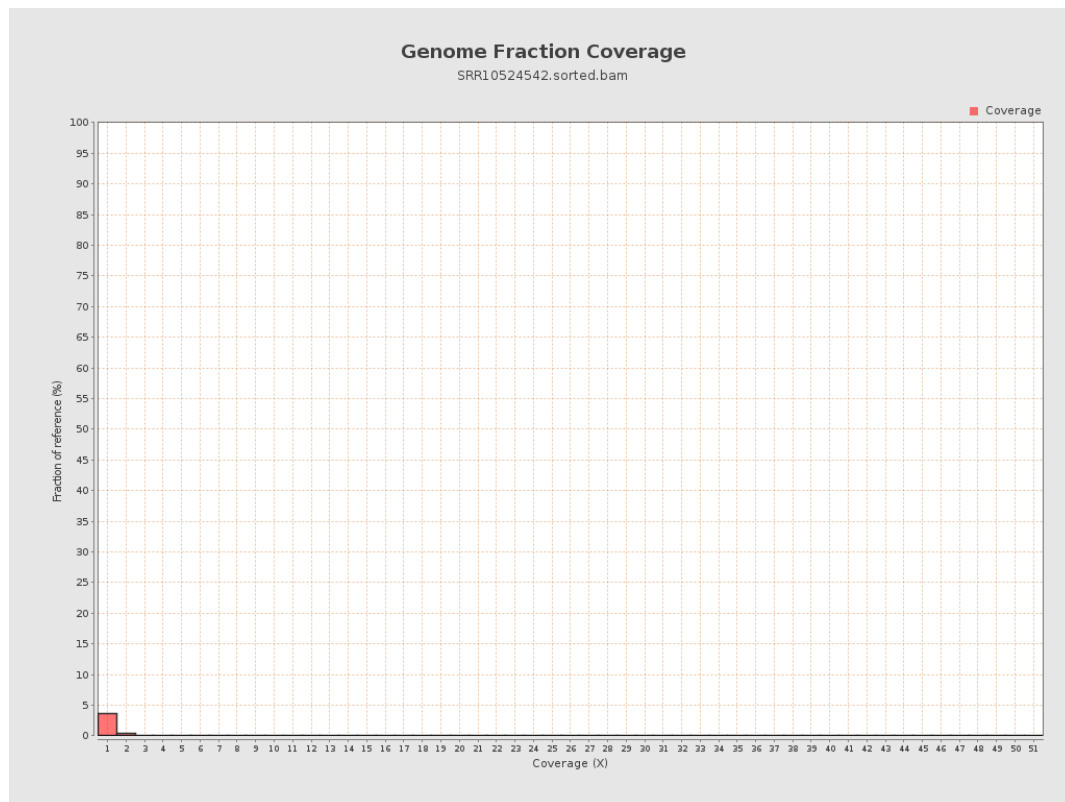
4. Results : Coverage Histogram



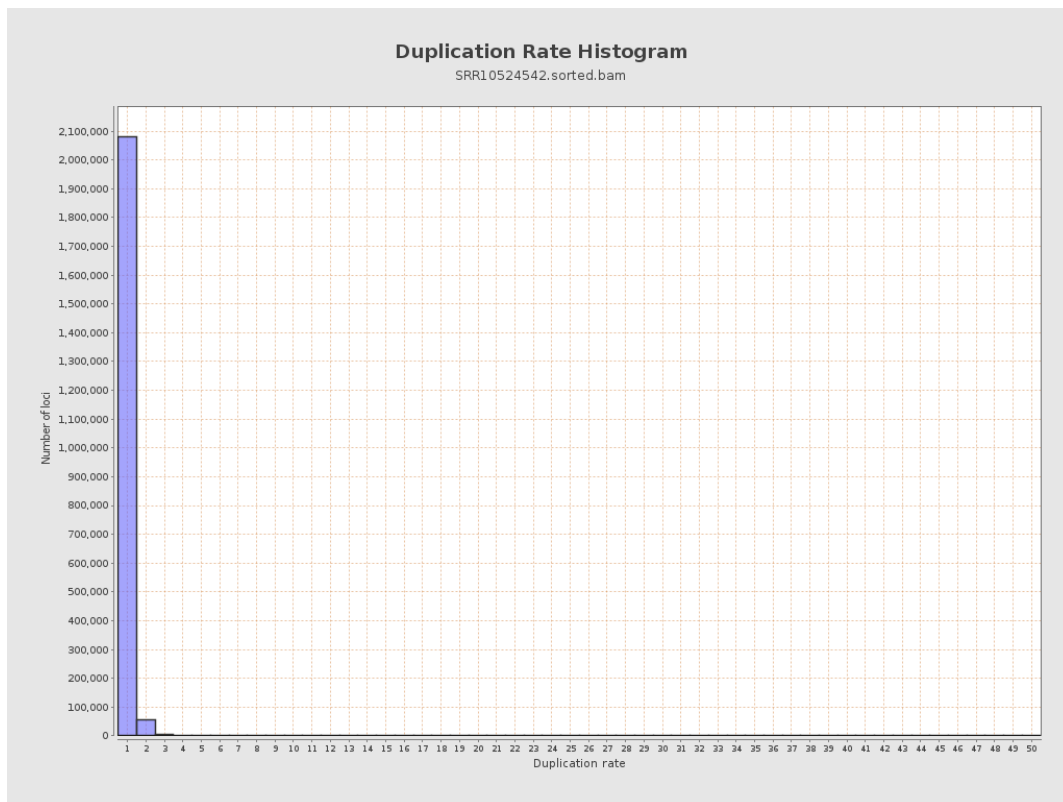
5. Results : Coverage Histogram (0-50X)



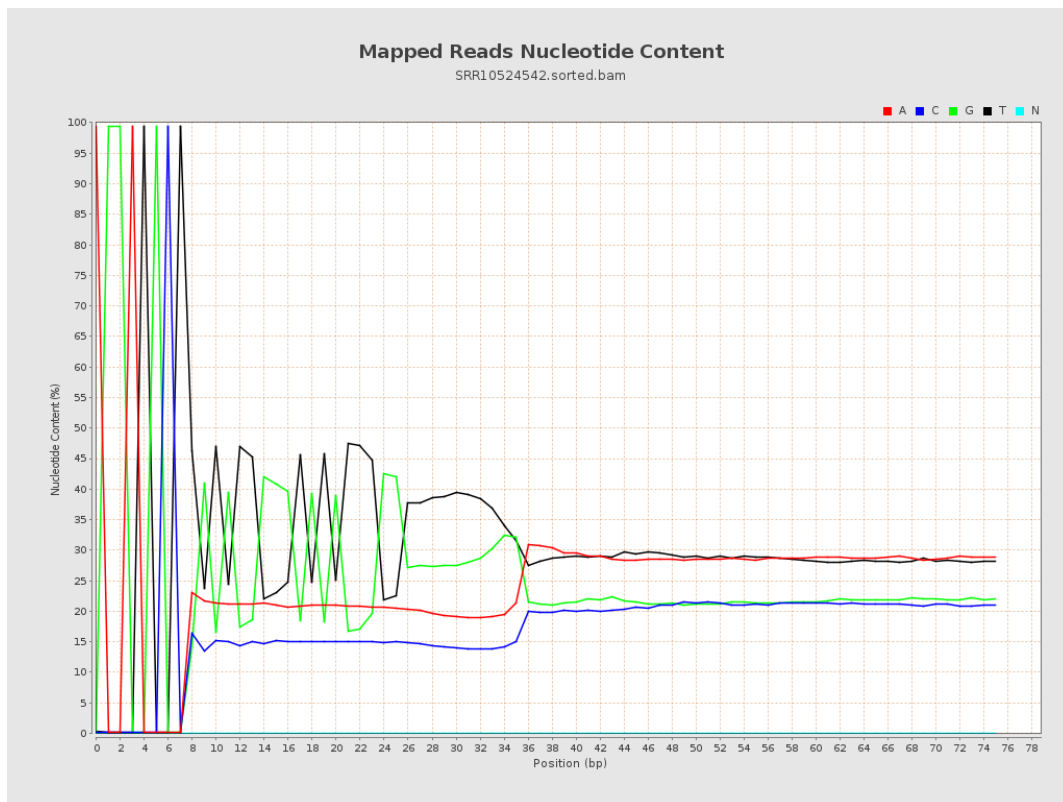
6. Results : Genome Fraction Coverage



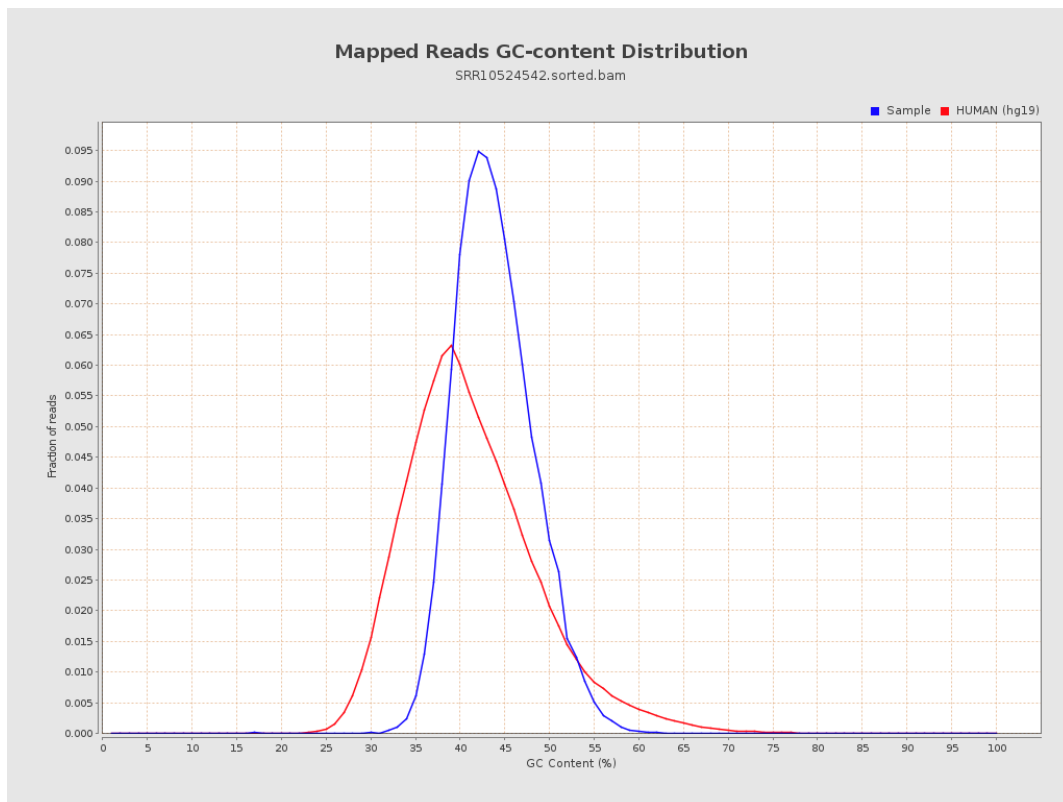
7. Results : Duplication Rate Histogram



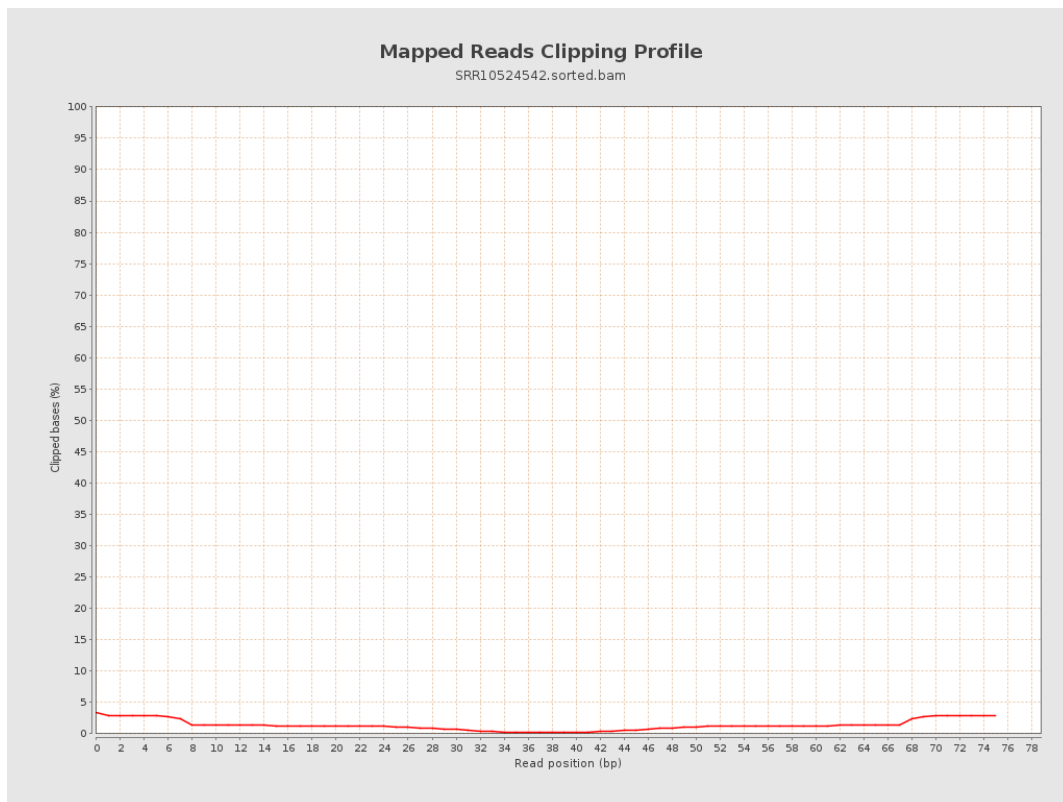
8. Results : Mapped Reads Nucleotide Content



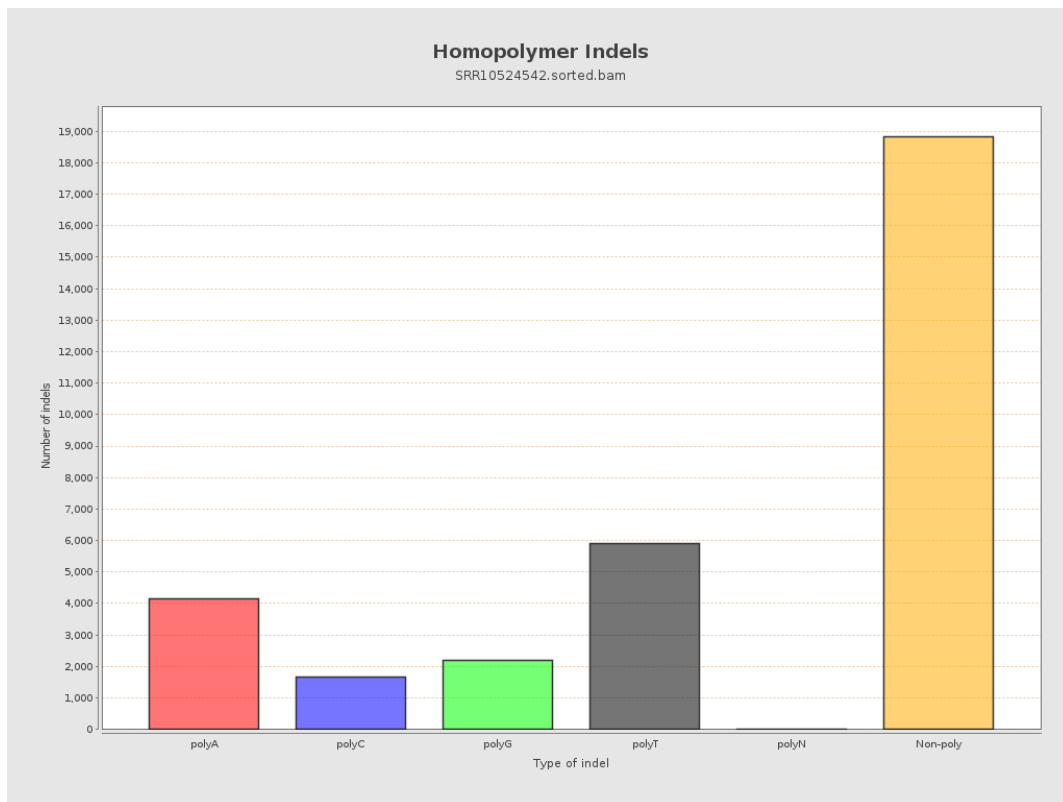
9. Results : Mapped Reads GC-content Distribution



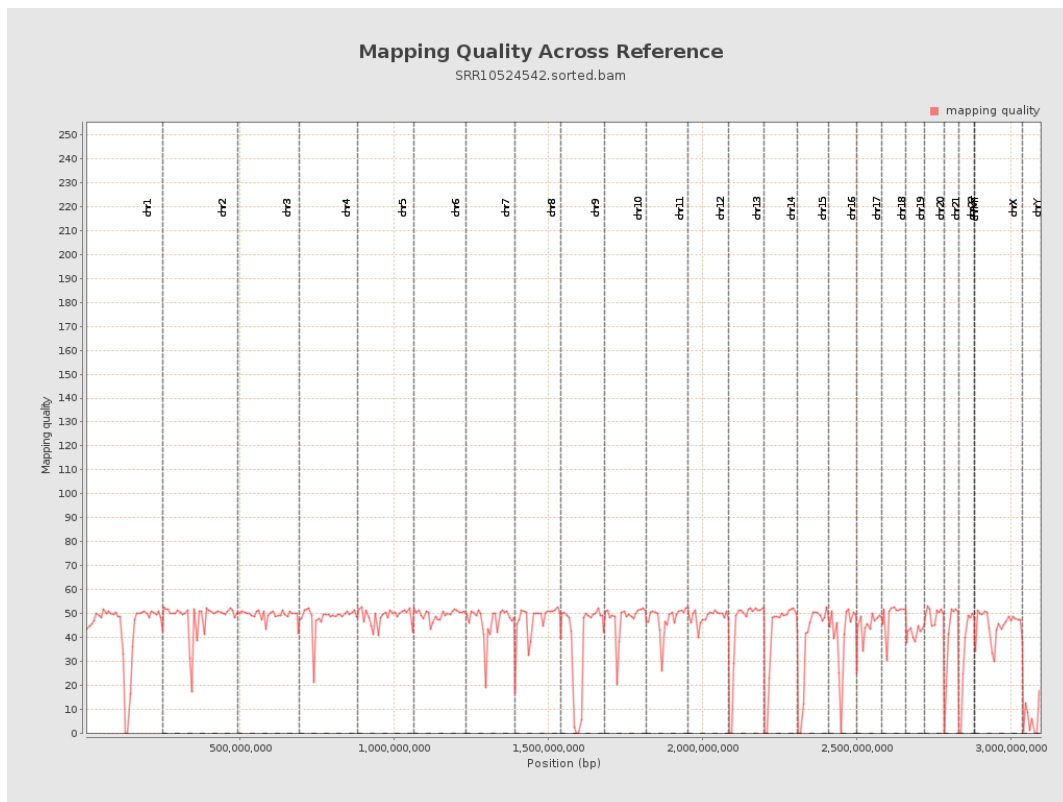
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

