

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:16:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524355.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_SRR10524355 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524355.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:16:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524355.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	724,224
Mapped reads	659,408 / 91.05%
Unmapped reads	64,816 / 8.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,301 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	16,763 / 2.31%
Duplication rate	1.92%
Clipped reads	659,382 / 91.05%

2.2. ACGT Content

Number/percentage of A's	10,201,254 / 26.68%
Number/percentage of C's	6,967,547 / 18.22%
Number/percentage of T's	11,833,990 / 30.95%
Number/percentage of G's	9,231,943 / 24.14%
Number/percentage of N's	736 / 0%
GC Percentage	42.37%

2.3. Coverage

Mean	0.0124

Standard Deviation	0.1471
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2.4. Mapping Quality

Mean Mapping Quality	45.6
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2.5. Mismatches and indels

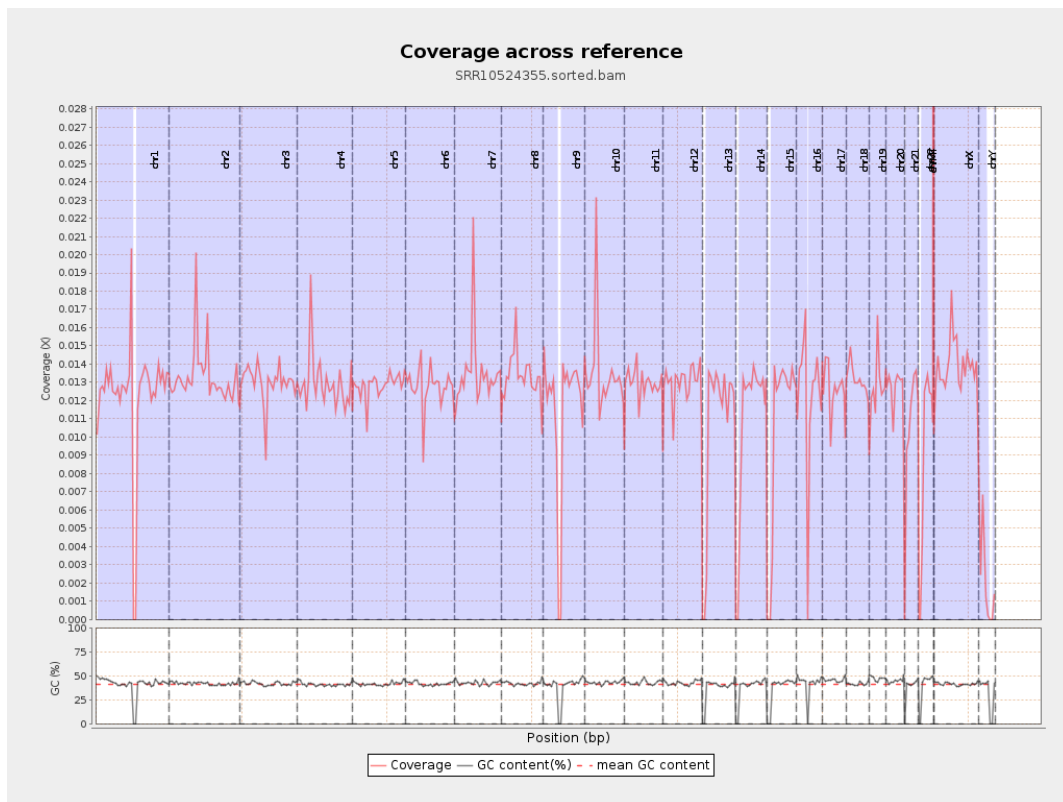
General error rate	0.53%
Mismatches	196,620
Insertions	3,245
Mapped reads with at least one insertion	0.49%
Deletions	8,033
Mapped reads with at least one deletion	1.21%
Homopolymer indels	42.4%

2.6. Chromosome stats

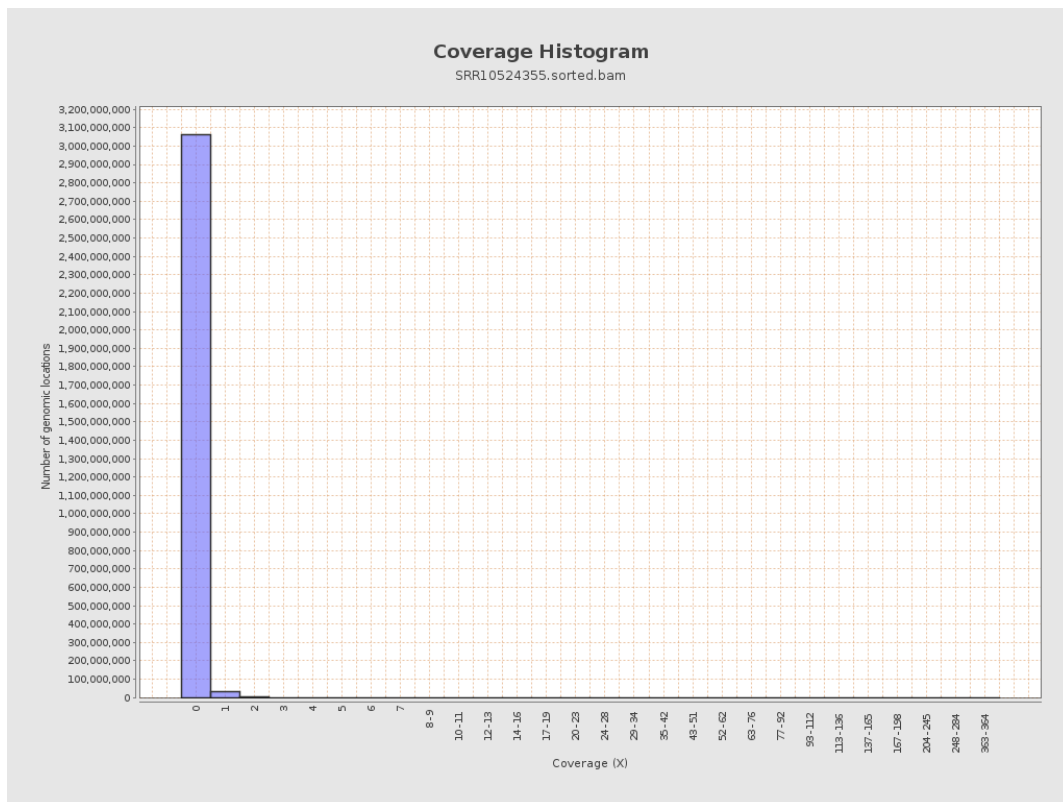
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3054789	0.0123	0.2261
chr2	243199373	3237016	0.0133	0.1917
chr3	198022430	2571059	0.013	0.119
chr4	191154276	2466049	0.0129	0.1233
chr5	180915260	2321502	0.0128	0.1179
chr6	171115067	2189221	0.0128	0.1241
chr7	159138663	2157030	0.0136	0.1828

chr8	146364022	1947946	0.0133	0.157
chr9	141213431	1602639	0.0113	0.1262
chr10	135534747	1820557	0.0134	0.1459
chr11	135006516	1745626	0.0129	0.1298
chr12	133851895	1738926	0.013	0.1199
chr13	115169878	1220886	0.0106	0.1083
chr14	107349540	1156666	0.0108	0.1097
chr15	102531392	1084375	0.0106	0.1076
chr16	90354753	1107093	0.0123	0.1217
chr17	81195210	1011835	0.0125	0.1184
chr18	78077248	1033743	0.0132	0.2023
chr19	59128983	759602	0.0128	0.1809
chr20	63025520	790871	0.0125	0.1171
chr21	48129895	507462	0.0105	0.1117
chr22	51304566	448418	0.0087	0.0971
chrMT	16571	1895	0.1144	0.3342
chrX	155270560	2152422	0.0139	0.1282
chrY	59373566	120999	0.002	0.0653

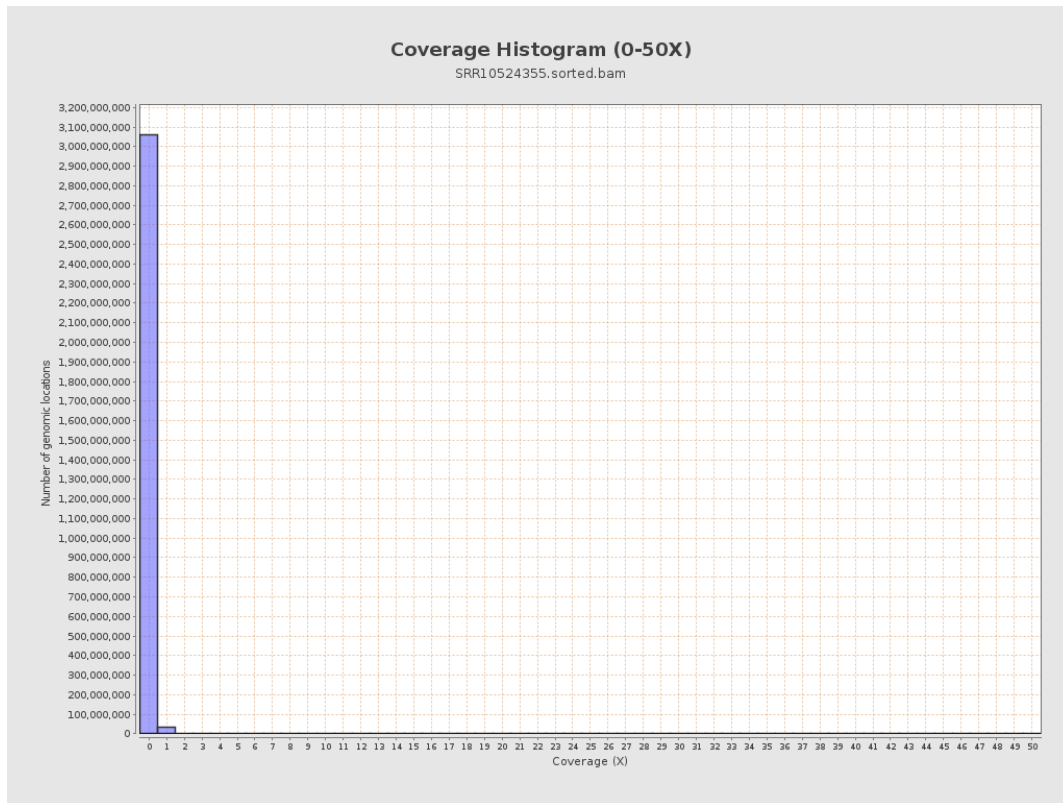
3. Results : Coverage across reference



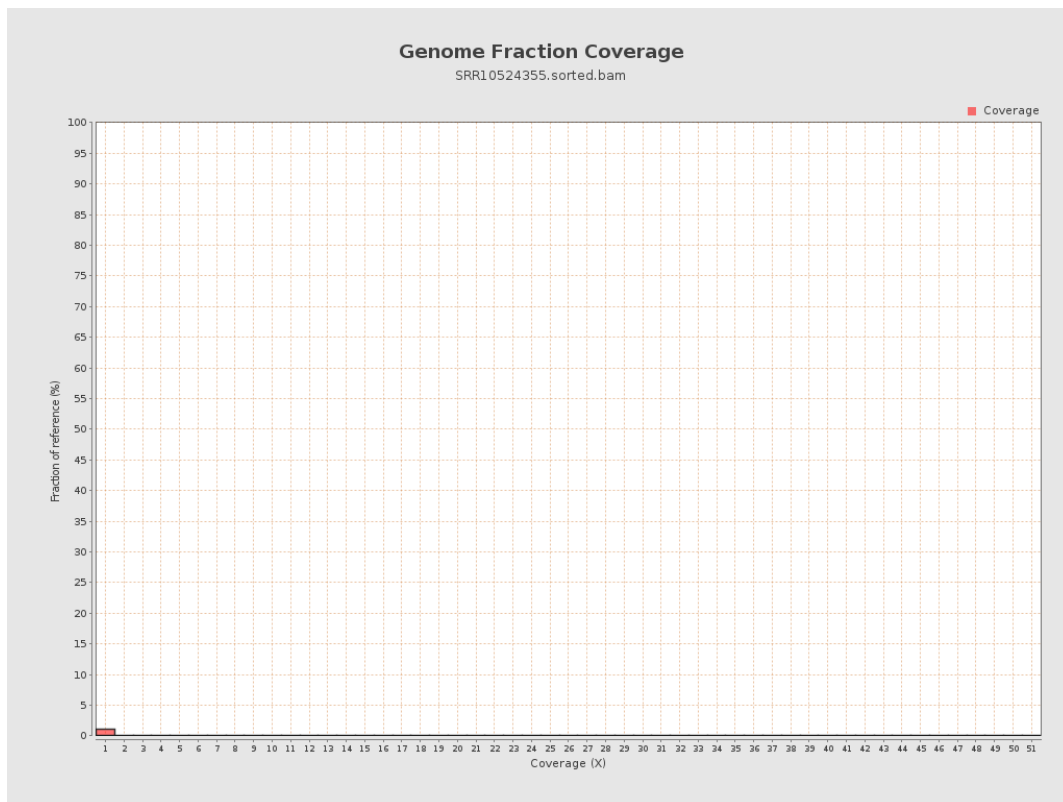
4. Results : Coverage Histogram



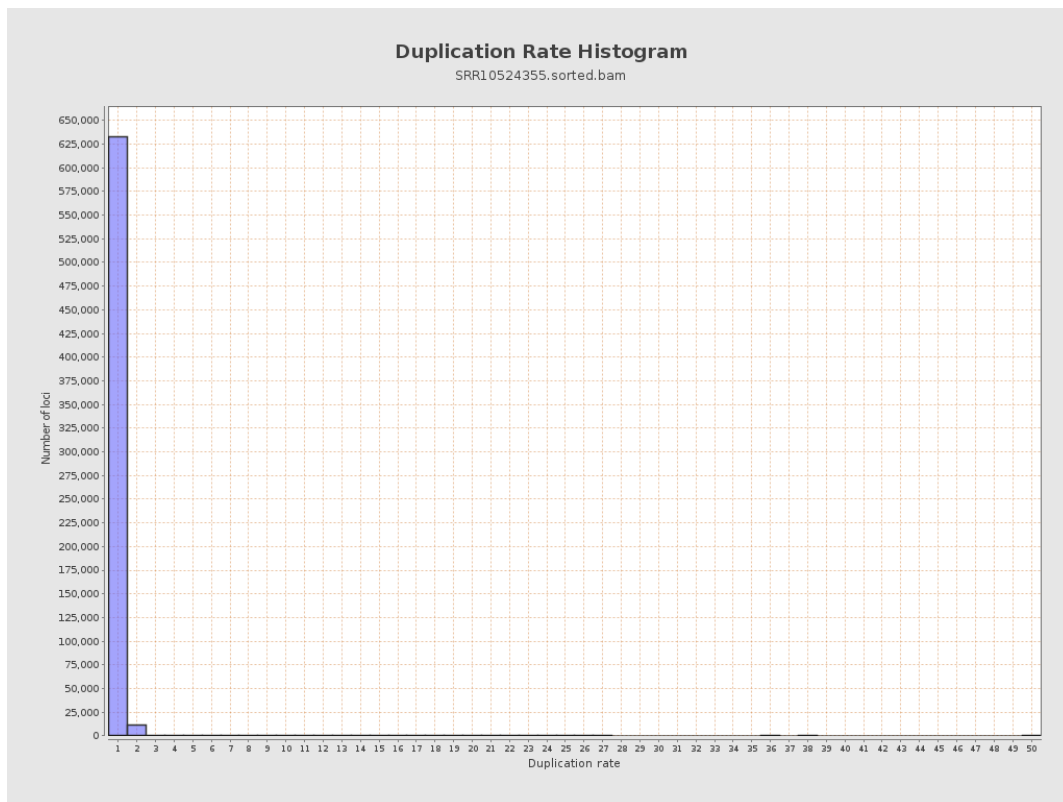
5. Results : Coverage Histogram (0-50X)



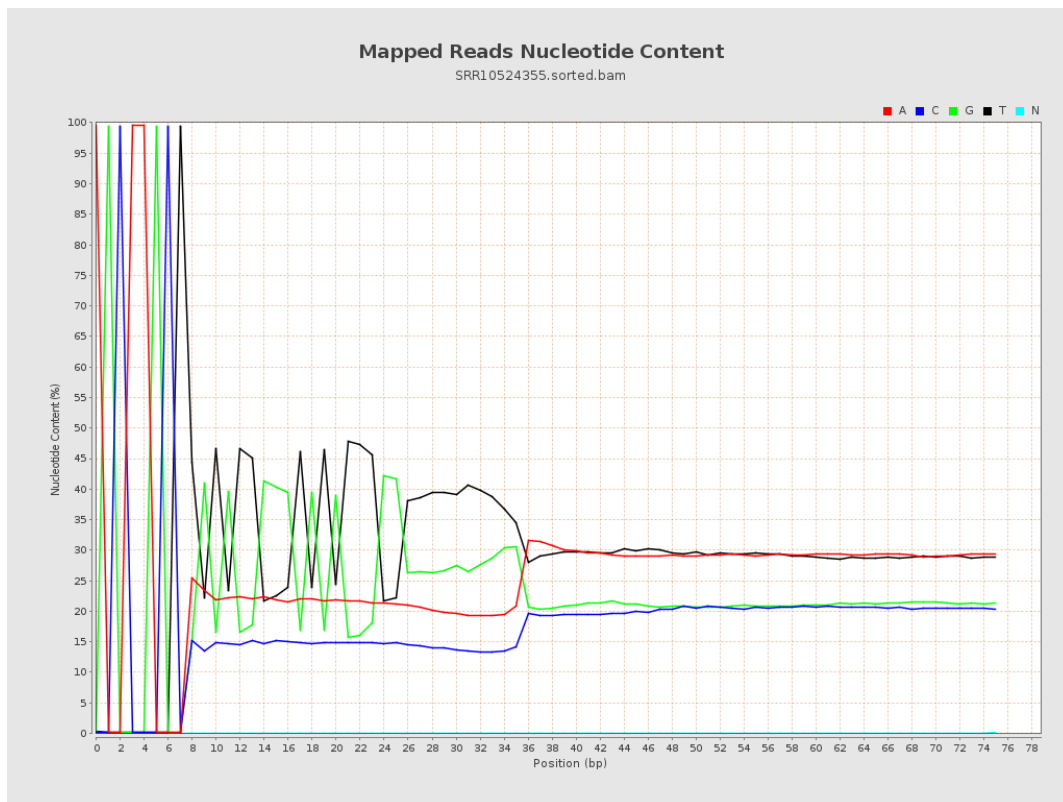
6. Results : Genome Fraction Coverage



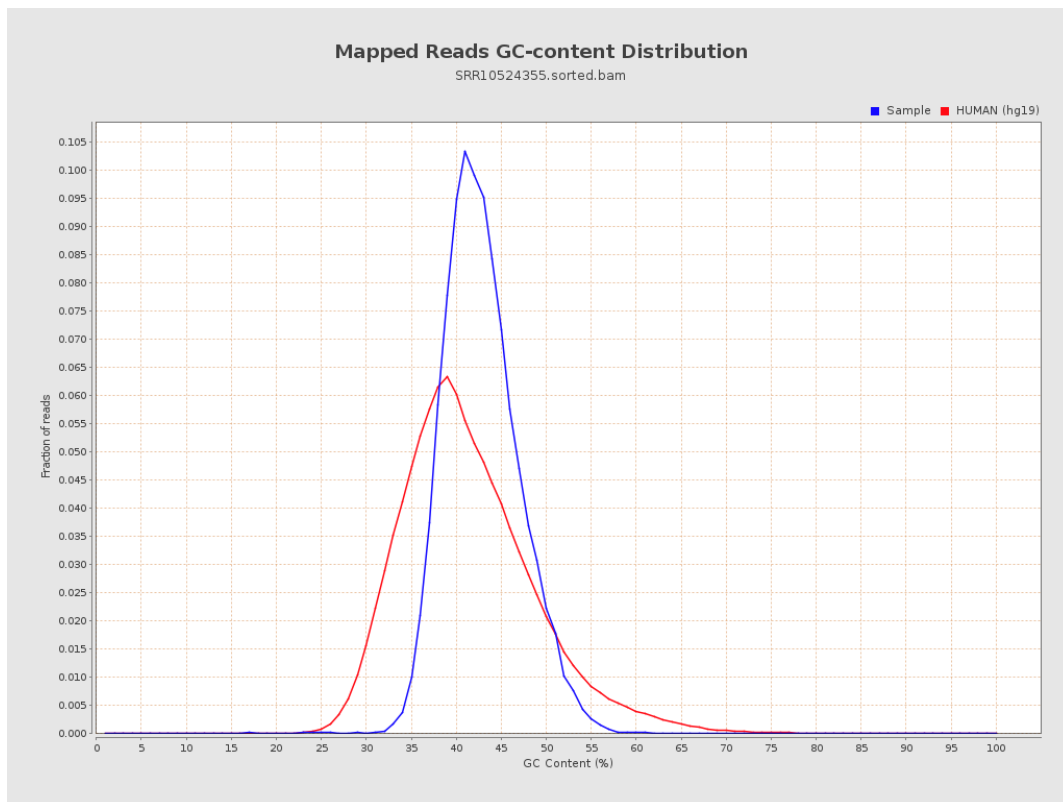
7. Results : Duplication Rate Histogram



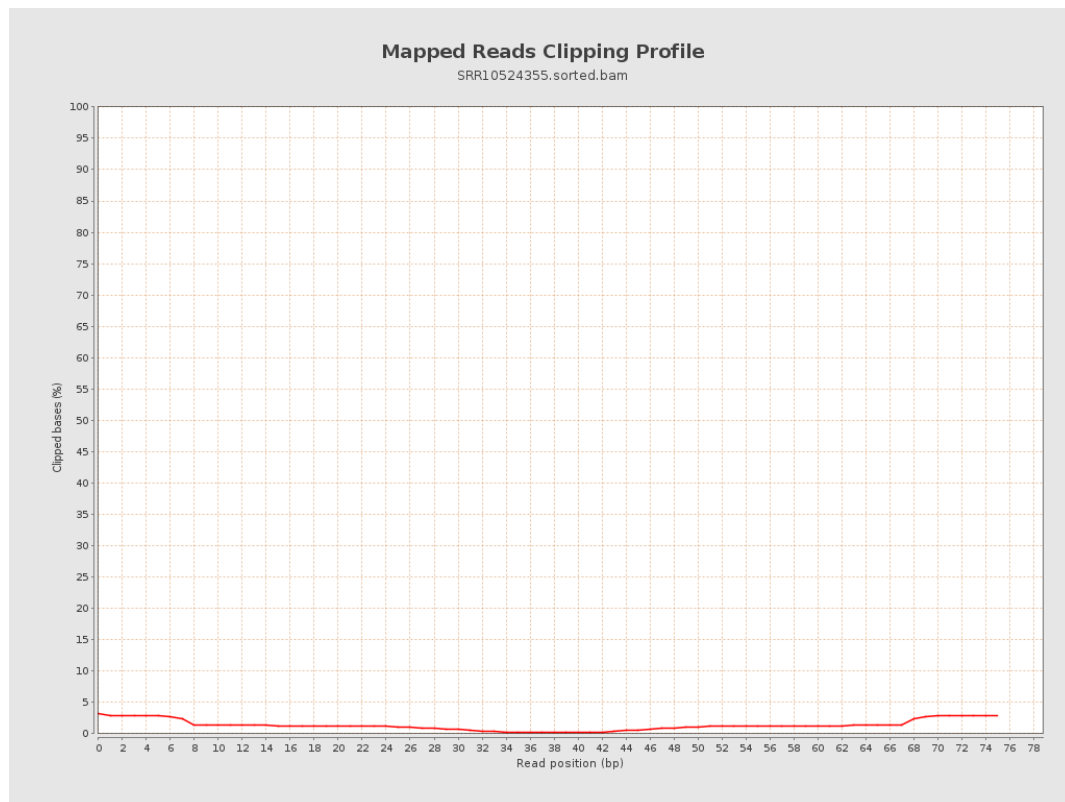
8. Results : Mapped Reads Nucleotide Content



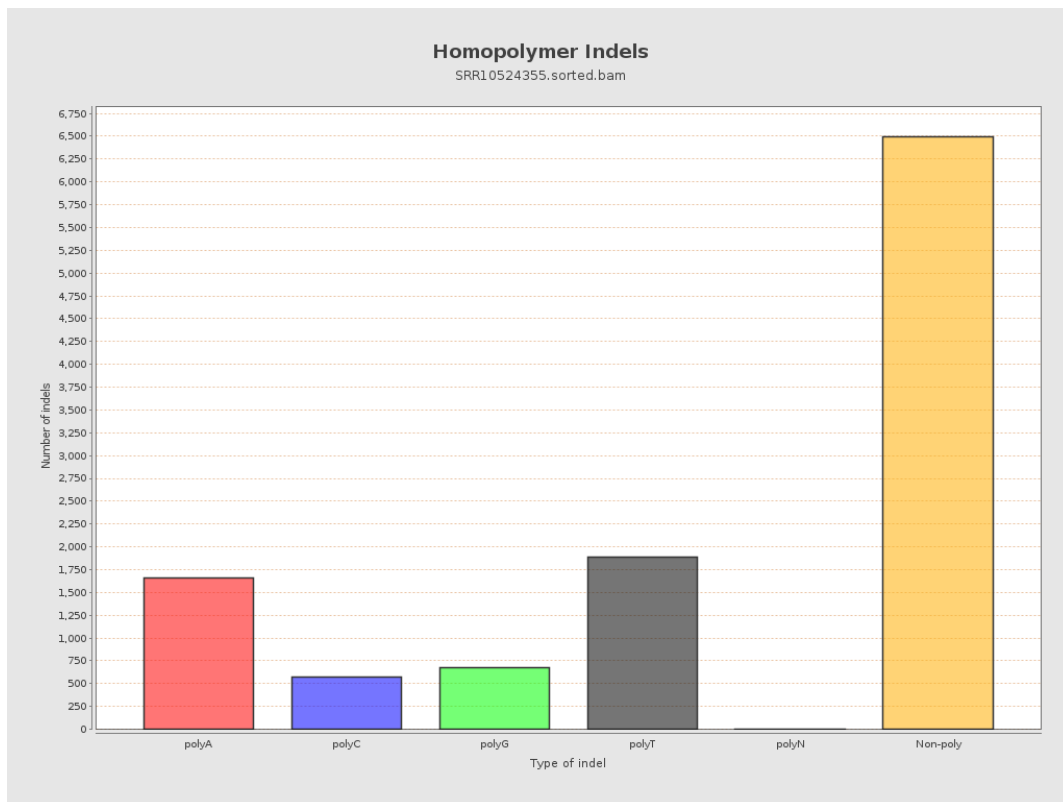
9. Results : Mapped Reads GC-content Distribution



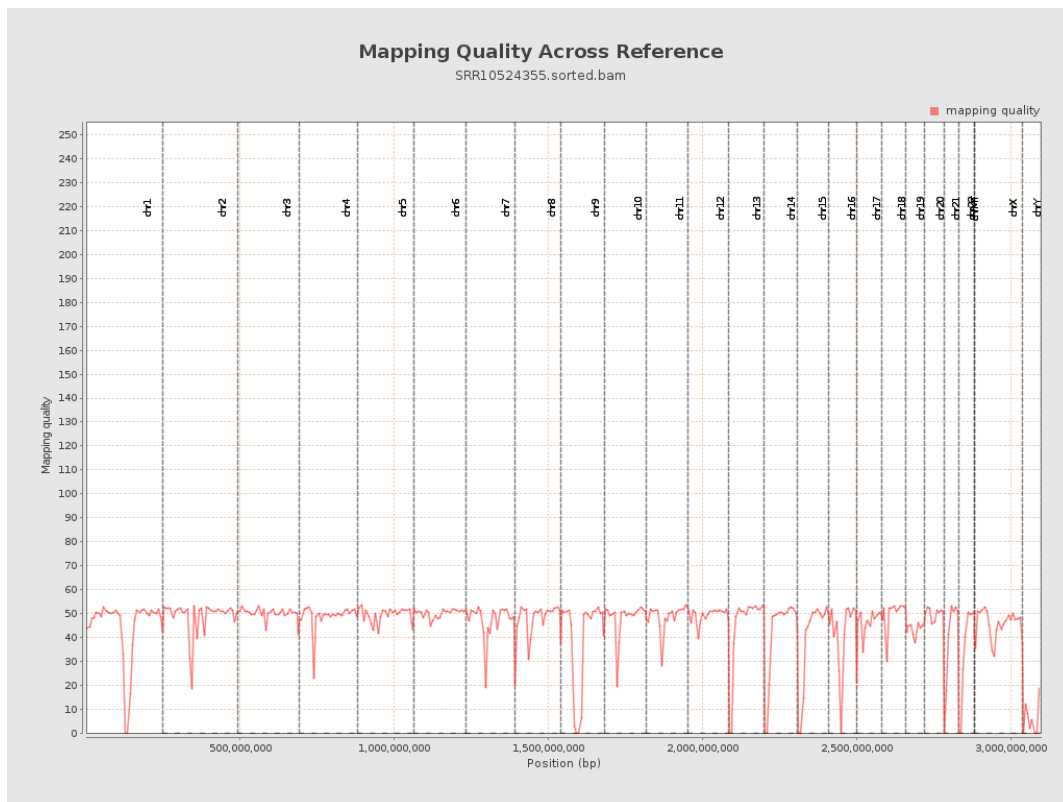
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

