

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:09:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524312.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_SRR10524312 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524312.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:09:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524312.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	707,815
Mapped reads	646,288 / 91.31%
Unmapped reads	61,527 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,603 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	11,689 / 1.65%
Duplication rate	1.27%
Clipped reads	646,984 / 91.41%

2.2. ACGT Content

Number/percentage of A's	8,851,883 / 23.52%
Number/percentage of C's	6,886,018 / 18.3%
Number/percentage of T's	12,240,636 / 32.52%
Number/percentage of G's	9,654,909 / 25.65%
Number/percentage of N's	4,863 / 0.01%
GC Percentage	43.95%

2.3. Coverage

Mean	0.0122

Standard Deviation	0.1423
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2.4. Mapping Quality

Mean Mapping Quality	43.89
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2.5. Mismatches and indels

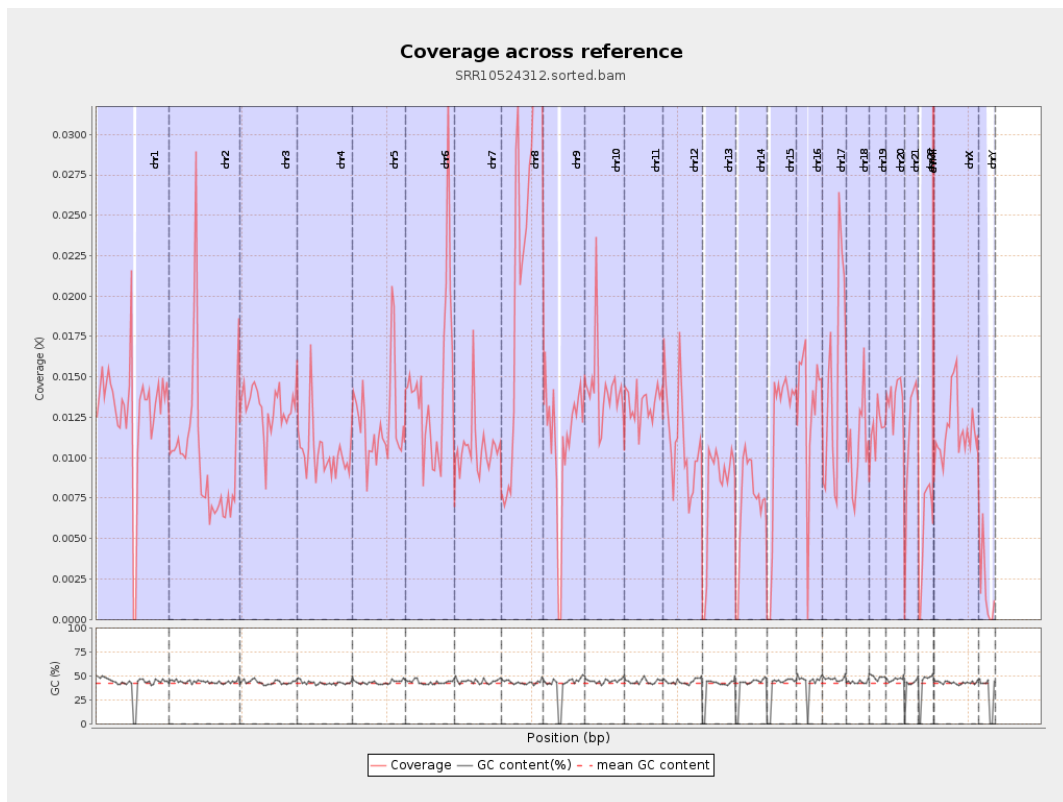
General error rate	0.52%
Mismatches	190,916
Insertions	2,613
Mapped reads with at least one insertion	0.4%
Deletions	5,981
Mapped reads with at least one deletion	0.92%
Homopolymer indels	40.41%

2.6. Chromosome stats

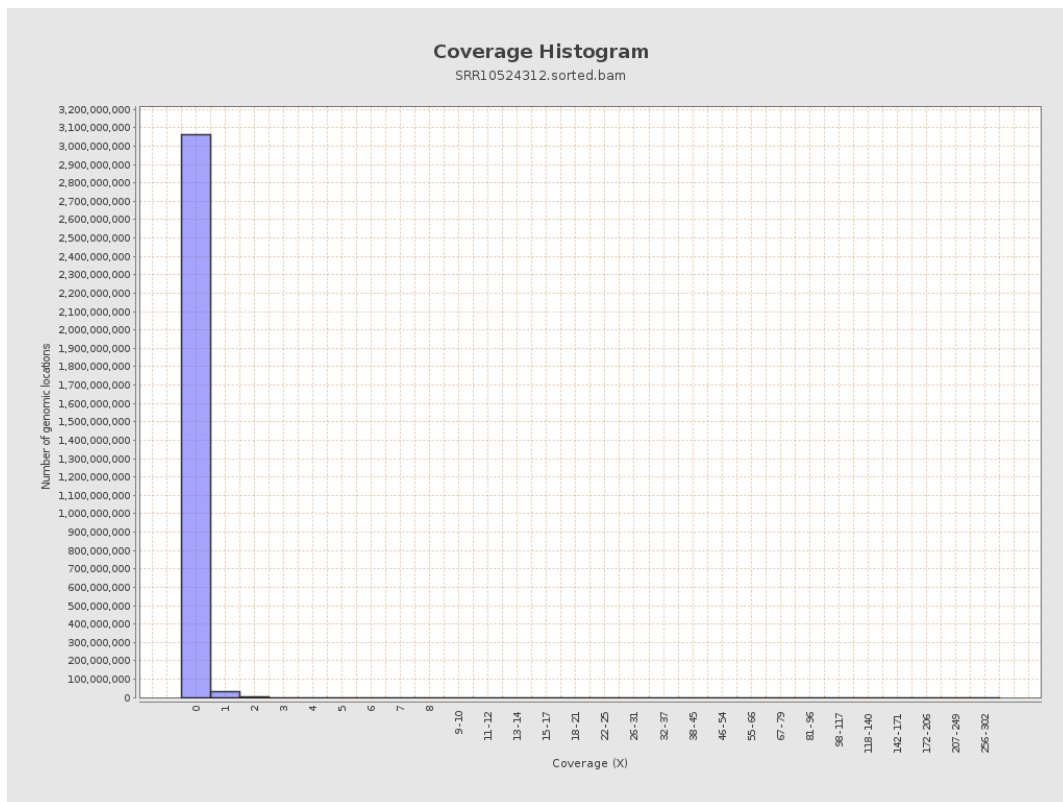
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3222249	0.0129	0.2331
chr2	243199373	2455000	0.0101	0.1642
chr3	198022430	2583410	0.013	0.1189
chr4	191154276	1963545	0.0103	0.1104
chr5	180915260	2213856	0.0122	0.1143
chr6	171115067	2426898	0.0142	0.1271
chr7	159138663	1699148	0.0107	0.1545

chr8	146364022	3876175	0.0265	0.1871
chr9	141213431	1553657	0.011	0.1213
chr10	135534747	1928929	0.0142	0.1482
chr11	135006516	1793155	0.0133	0.1317
chr12	133851895	1476646	0.011	0.109
chr13	115169878	925288	0.008	0.0926
chr14	107349540	778275	0.0072	0.0912
chr15	102531392	1168204	0.0114	0.1103
chr16	90354753	1213372	0.0134	0.124
chr17	81195210	1197879	0.0148	0.1306
chr18	78077248	859663	0.011	0.1773
chr19	59128983	698444	0.0118	0.171
chr20	63025520	860991	0.0137	0.1218
chr21	48129895	544946	0.0113	0.1149
chr22	51304566	281854	0.0055	0.0765
chrMT	16571	3244	0.1958	0.4883
chrX	155270560	1814553	0.0117	0.1166
chrY	59373566	108471	0.0018	0.0659

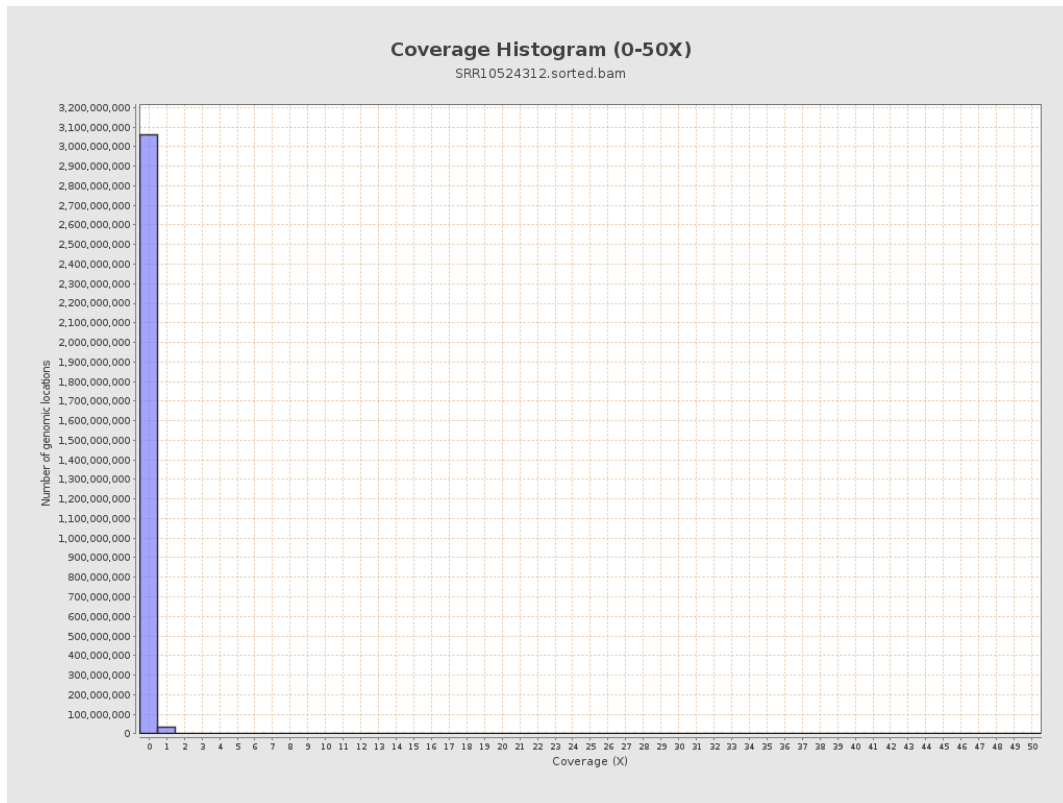
3. Results : Coverage across reference



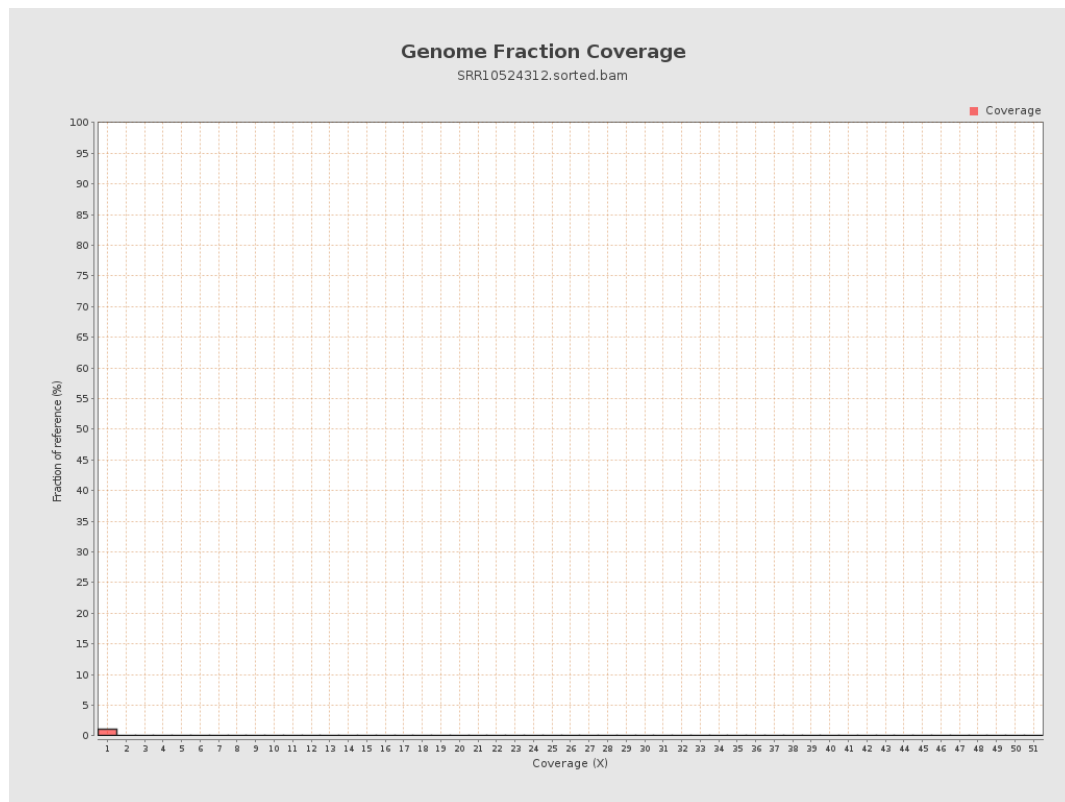
4. Results : Coverage Histogram



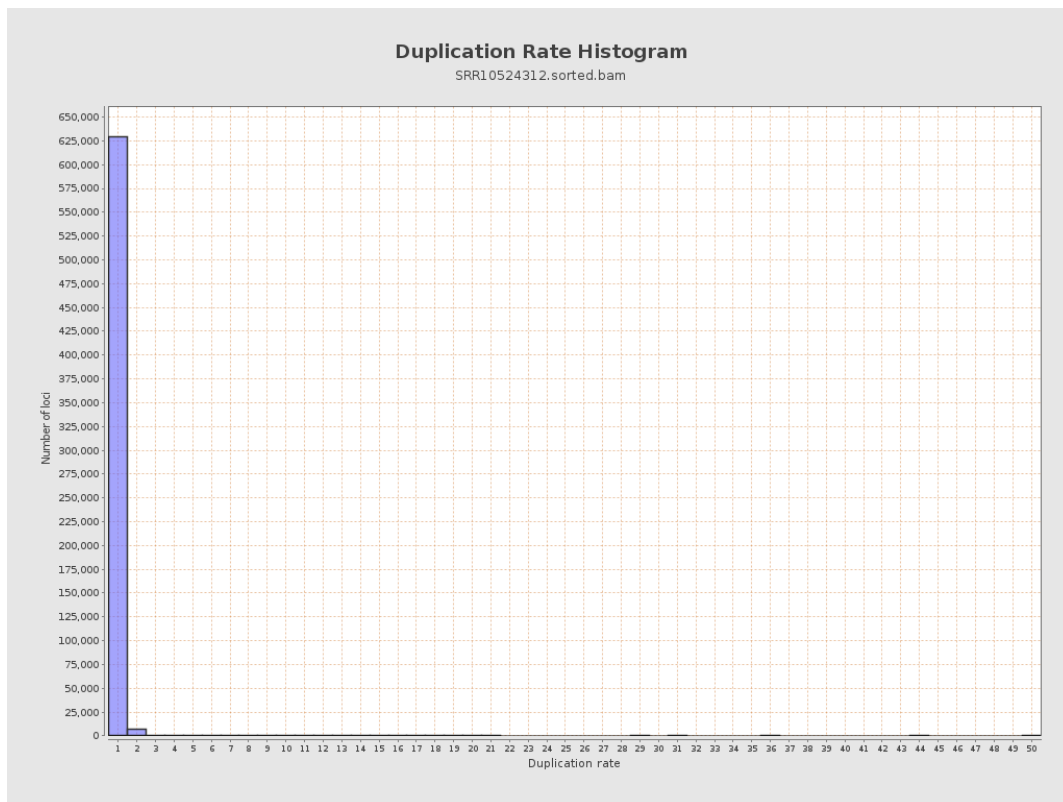
5. Results : Coverage Histogram (0-50X)



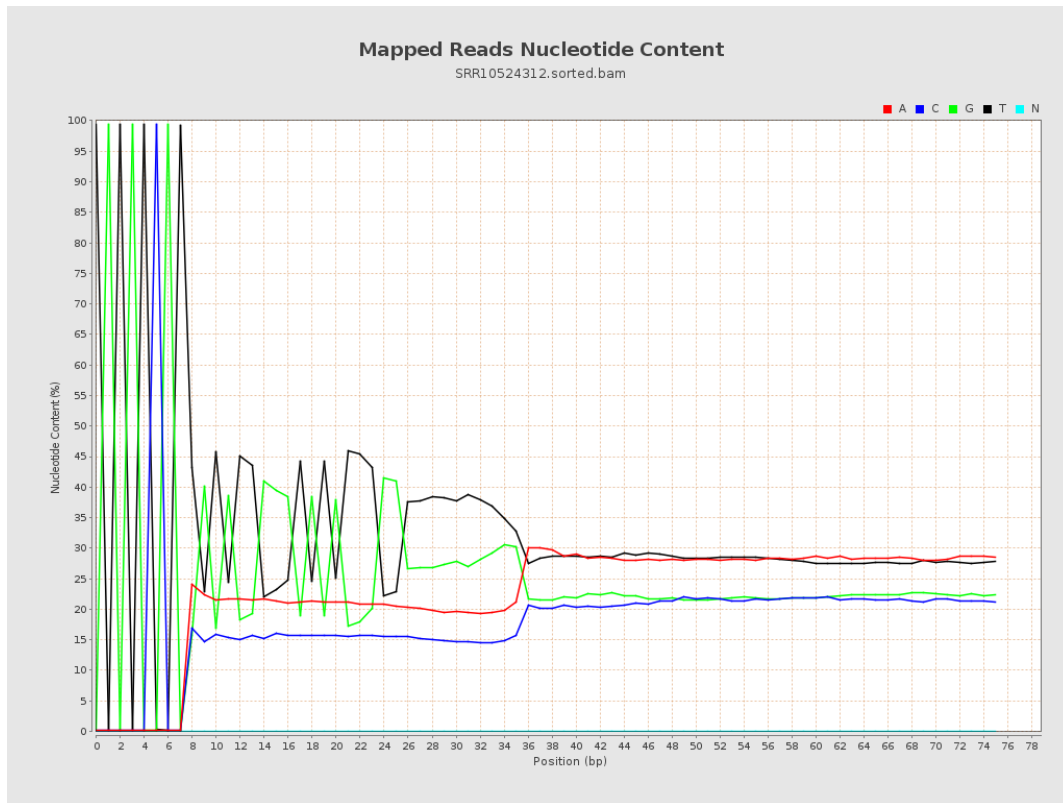
6. Results : Genome Fraction Coverage



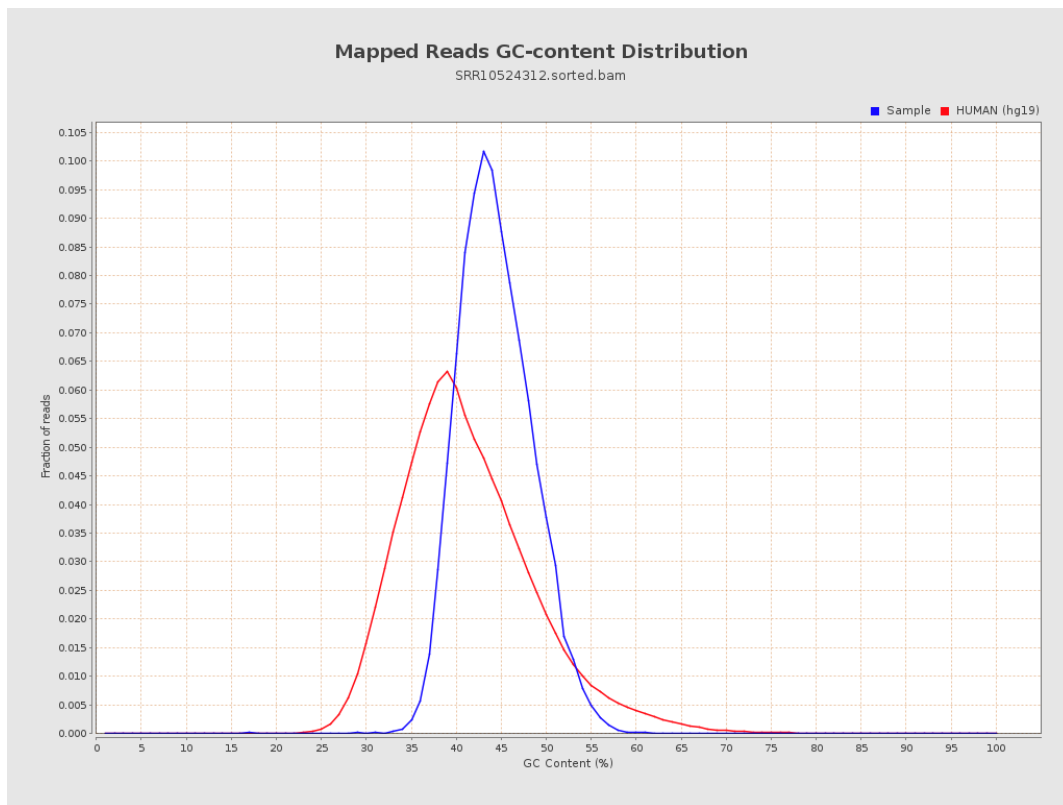
7. Results : Duplication Rate Histogram



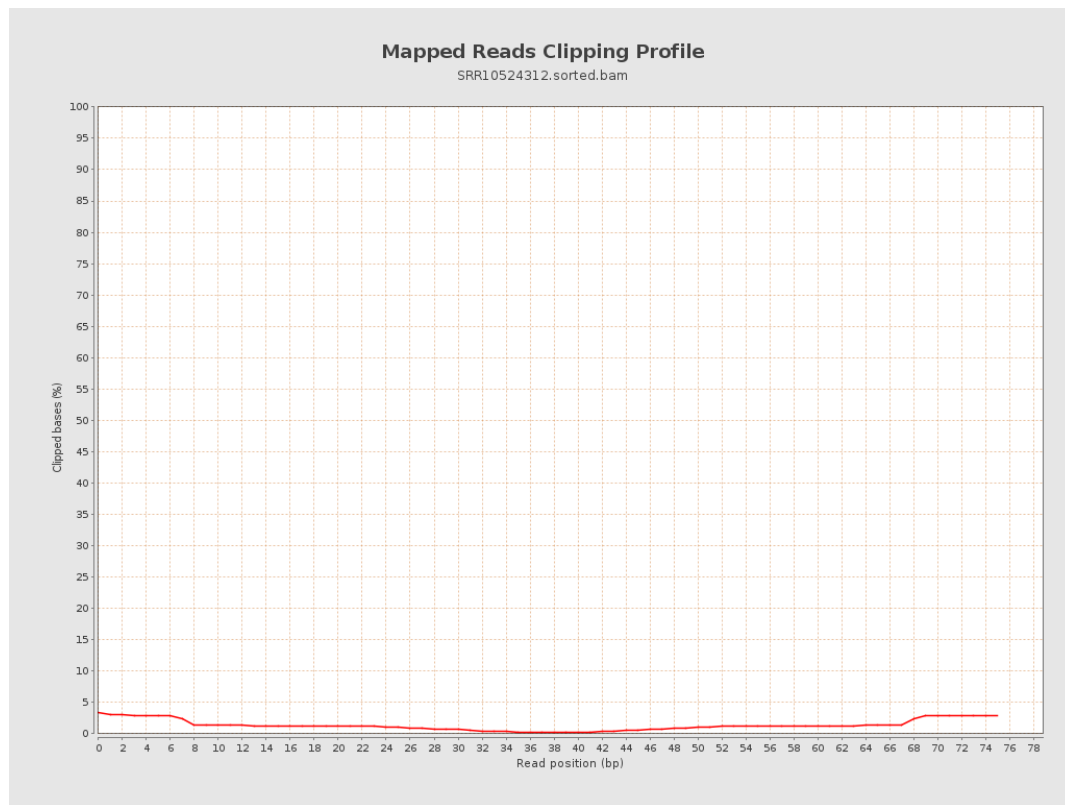
8. Results : Mapped Reads Nucleotide Content



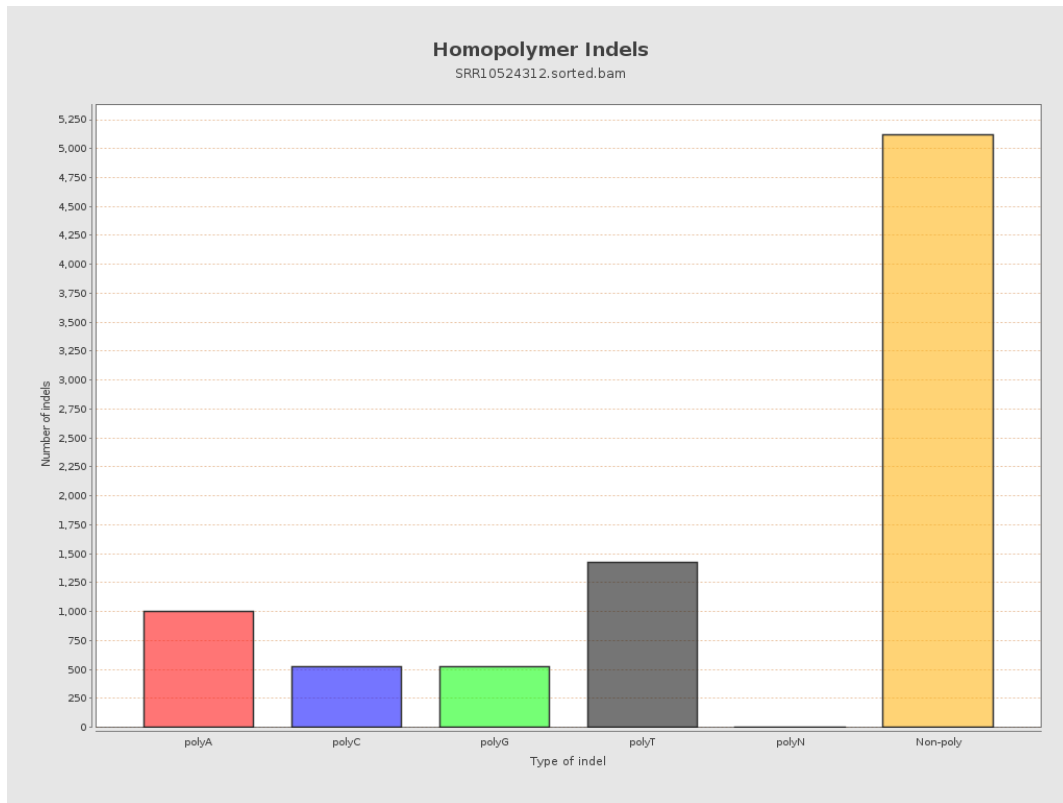
9. Results : Mapped Reads GC-content Distribution



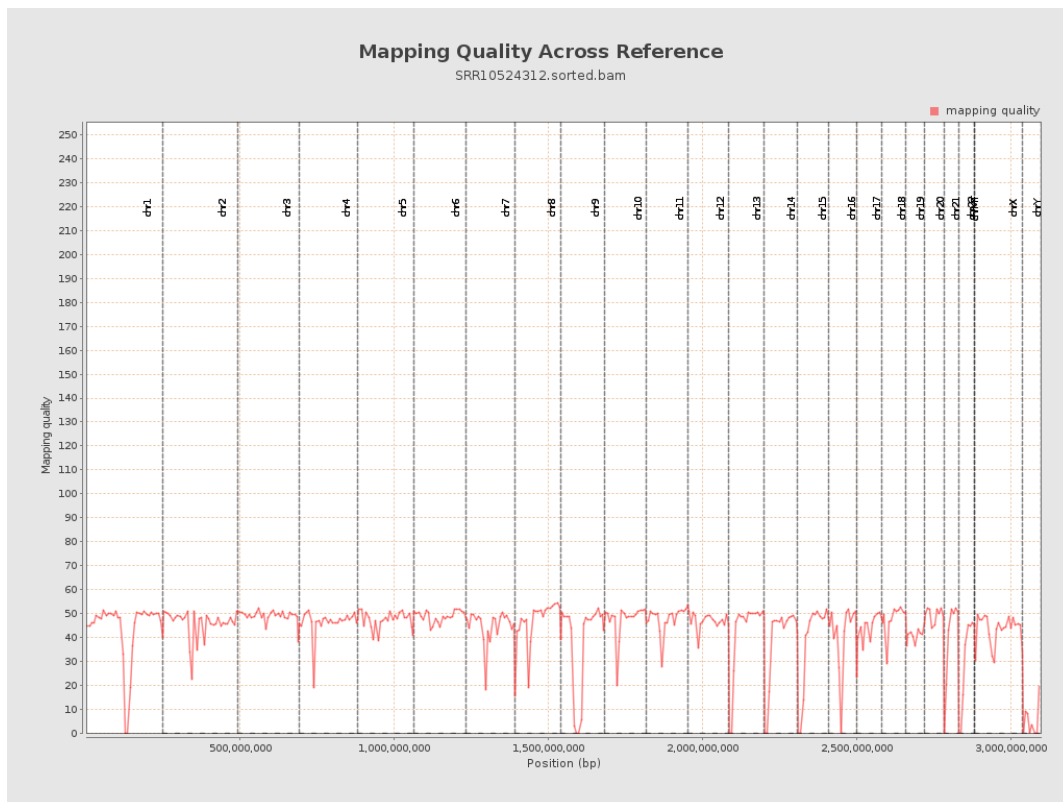
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

