

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:14:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063574.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_SRR6063574 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063574.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:14:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063574.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,702,176
Mapped reads	2,485,049 / 91.96%
Unmapped reads	217,127 / 8.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,143 / 0.67%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	205,662 / 7.61%
Duplication rate	6%
Clipped reads	1,029,310 / 38.09%

2.2. ACGT Content

Number/percentage of A's	47,213,943 / 28.23%
Number/percentage of C's	31,452,796 / 18.81%
Number/percentage of T's	52,484,800 / 31.38%
Number/percentage of G's	36,091,499 / 21.58%
Number/percentage of N's	4,757 / 0%
GC Percentage	40.39%

2.3. Coverage

Mean	0.054

Standard Deviation	0.996
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	40.97
----------------------	-------

2.5. Mismatches and indels

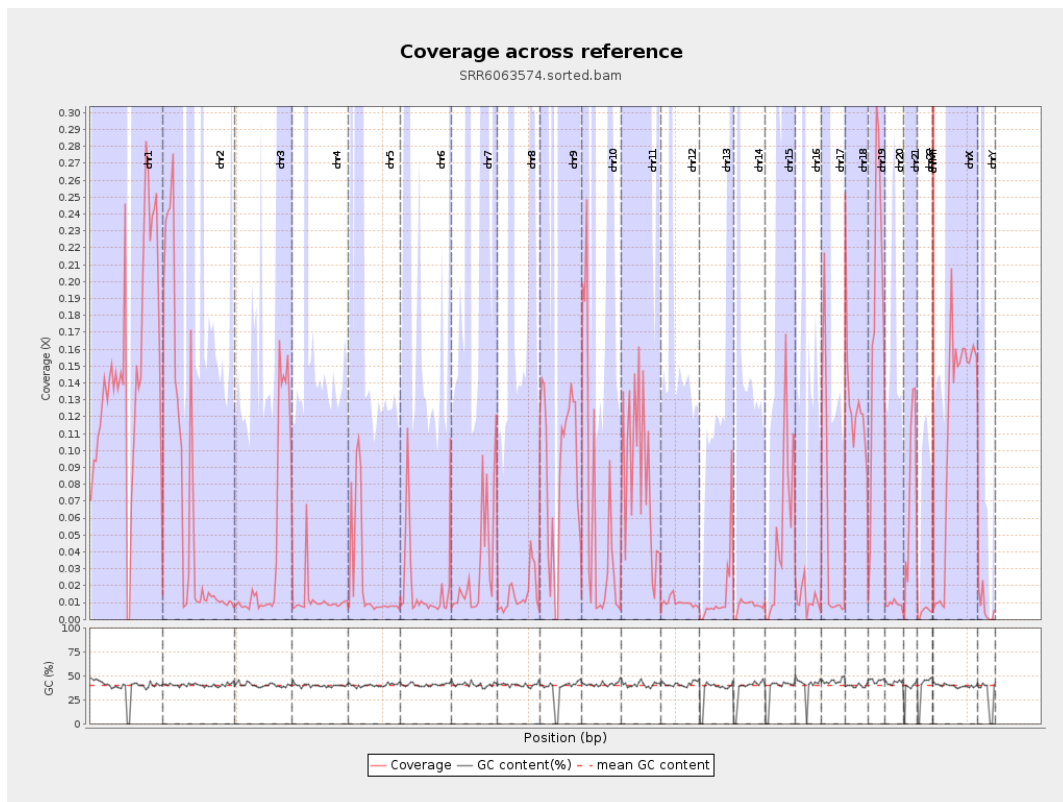
General error rate	0.76%
Mismatches	1,243,128
Insertions	12,479
Mapped reads with at least one insertion	0.5%
Deletions	39,544
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.22%

2.6. Chromosome stats

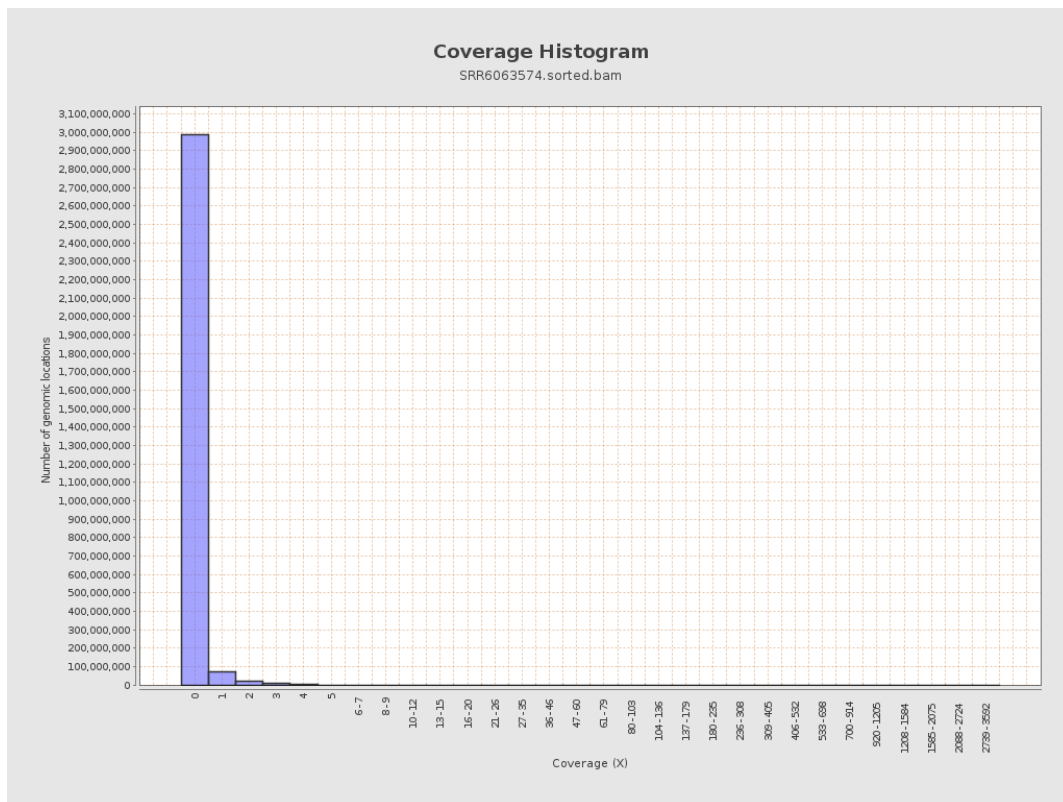
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	36257335	0.1455	2.9448
chr2	243199373	16602995	0.0683	0.8867
chr3	198022430	8283758	0.0418	0.3219
chr4	191154276	2214226	0.0116	0.2923
chr5	180915260	4199969	0.0232	0.2244
chr6	171115067	3225570	0.0189	0.2043
chr7	159138663	5087539	0.032	0.3412

chr8	146364022	2229443	0.0152	0.4099
chr9	141213431	12287604	0.087	0.6719
chr10	135534747	7930987	0.0585	0.9264
chr11	135006516	11354429	0.0841	0.7091
chr12	133851895	1341940	0.01	0.1993
chr13	115169878	1799135	0.0156	0.1735
chr14	107349540	866437	0.0081	0.2258
chr15	102531392	5483311	0.0535	0.3275
chr16	90354753	1088907	0.0121	0.2635
chr17	81195210	4110160	0.0506	0.4404
chr18	78077248	9810141	0.1256	0.9625
chr19	59128983	10983538	0.1858	1.6396
chr20	63025520	569816	0.009	0.168
chr21	48129895	3580018	0.0744	0.4846
chr22	51304566	235753	0.0046	0.0895
chrMT	16571	130497	7.875	5.6796
chrX	155270560	17227243	0.1109	0.6674
chrY	59373566	418063	0.007	0.2847

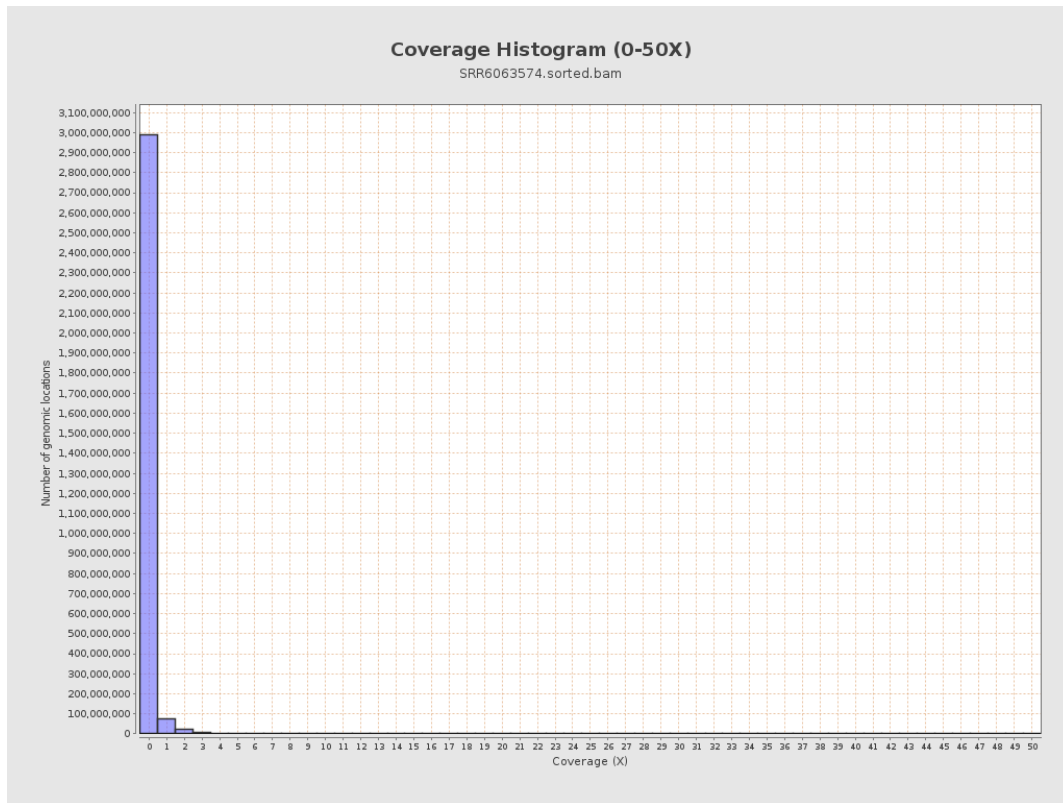
3. Results : Coverage across reference



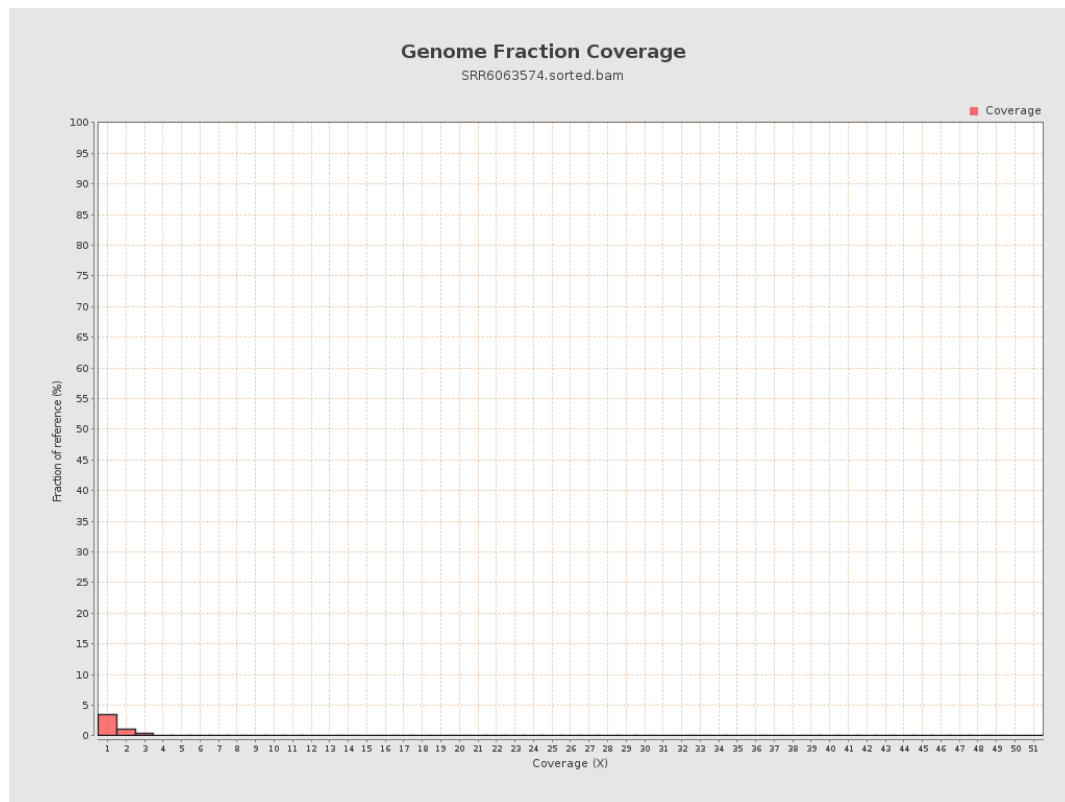
4. Results : Coverage Histogram



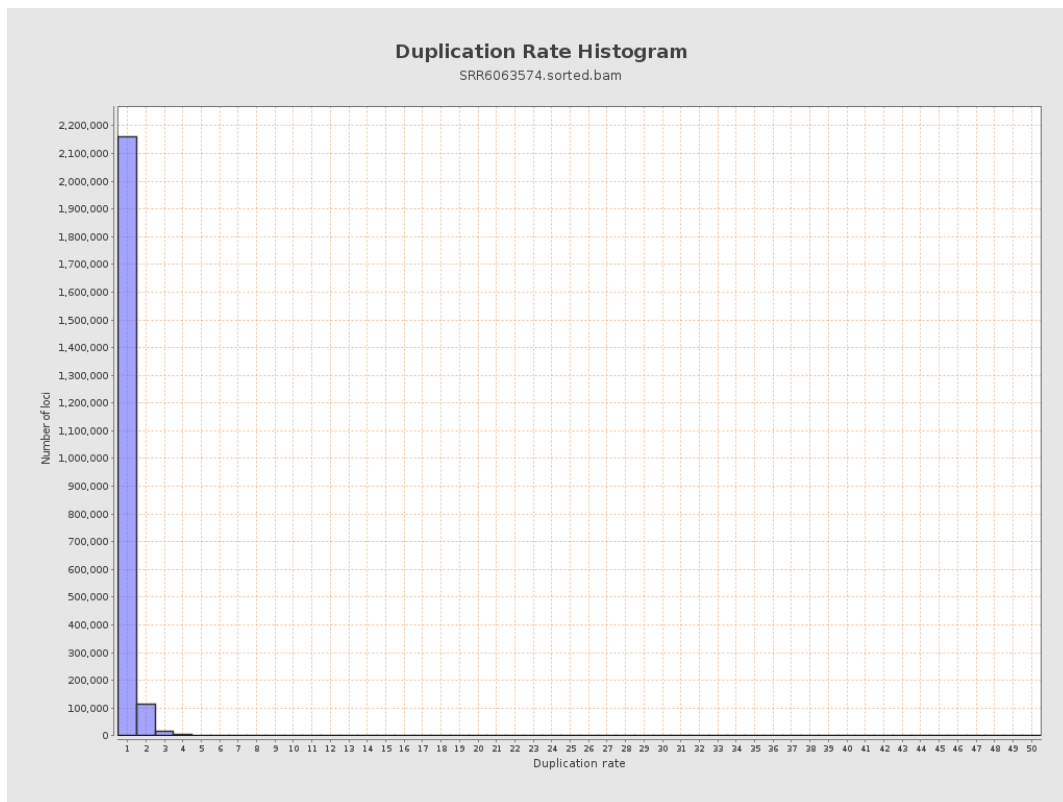
5. Results : Coverage Histogram (0-50X)



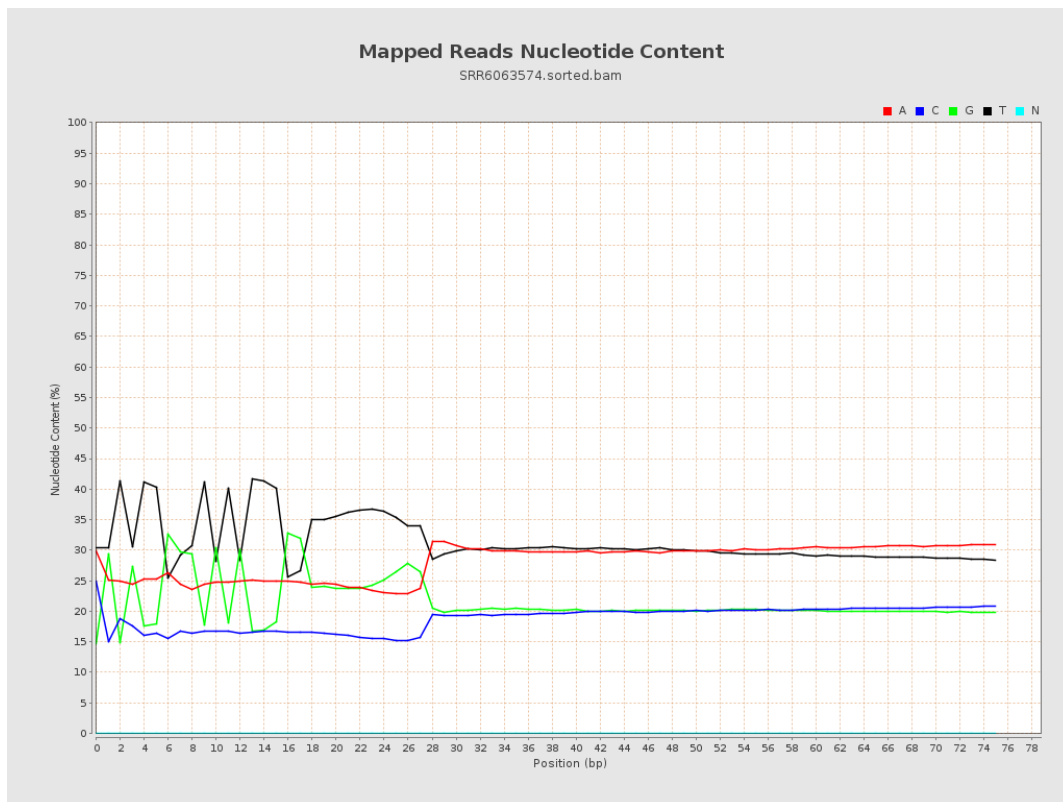
6. Results : Genome Fraction Coverage



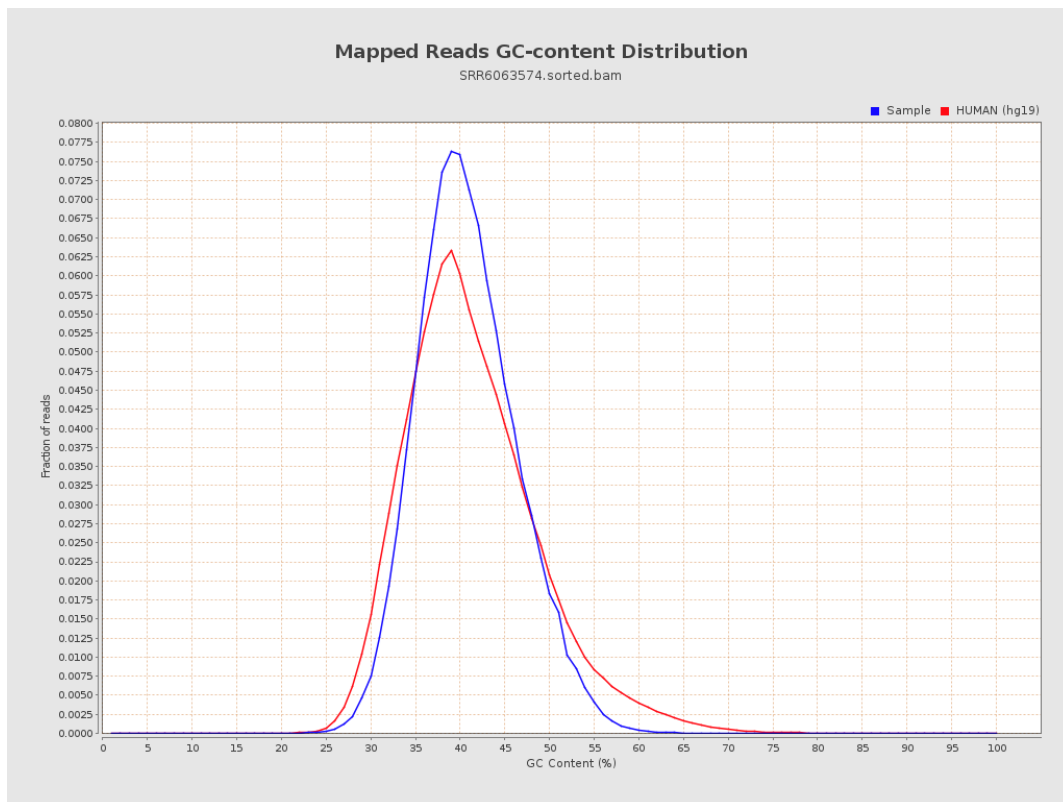
7. Results : Duplication Rate Histogram



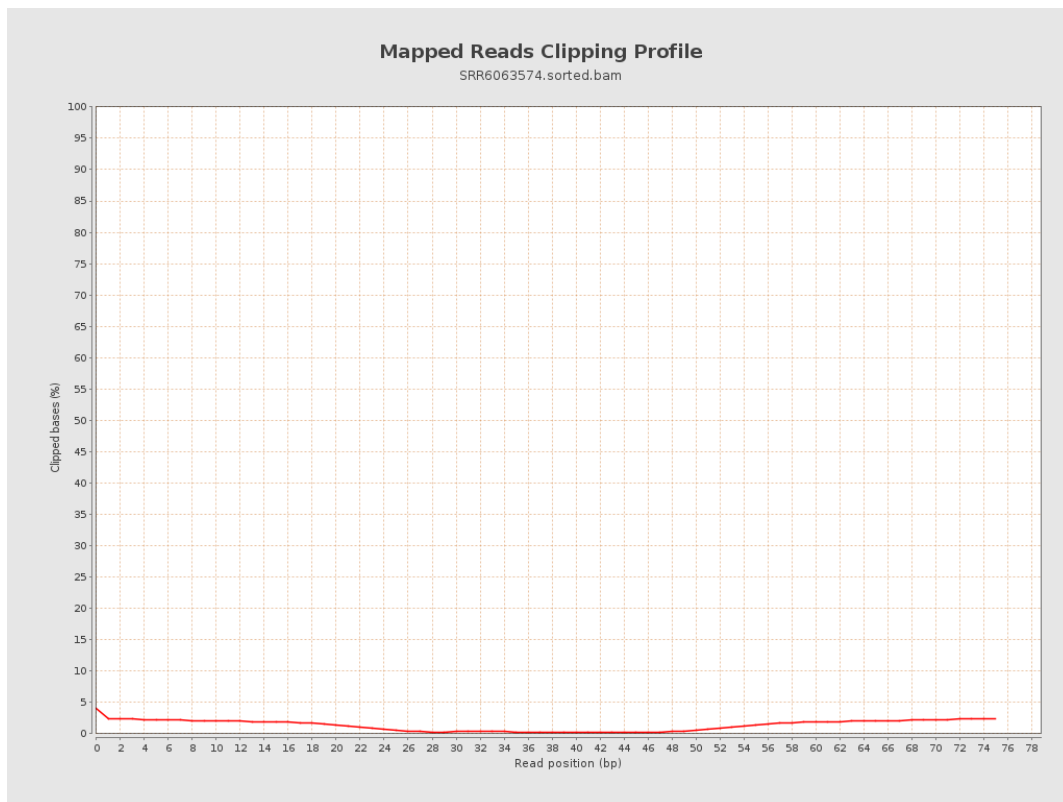
8. Results : Mapped Reads Nucleotide Content



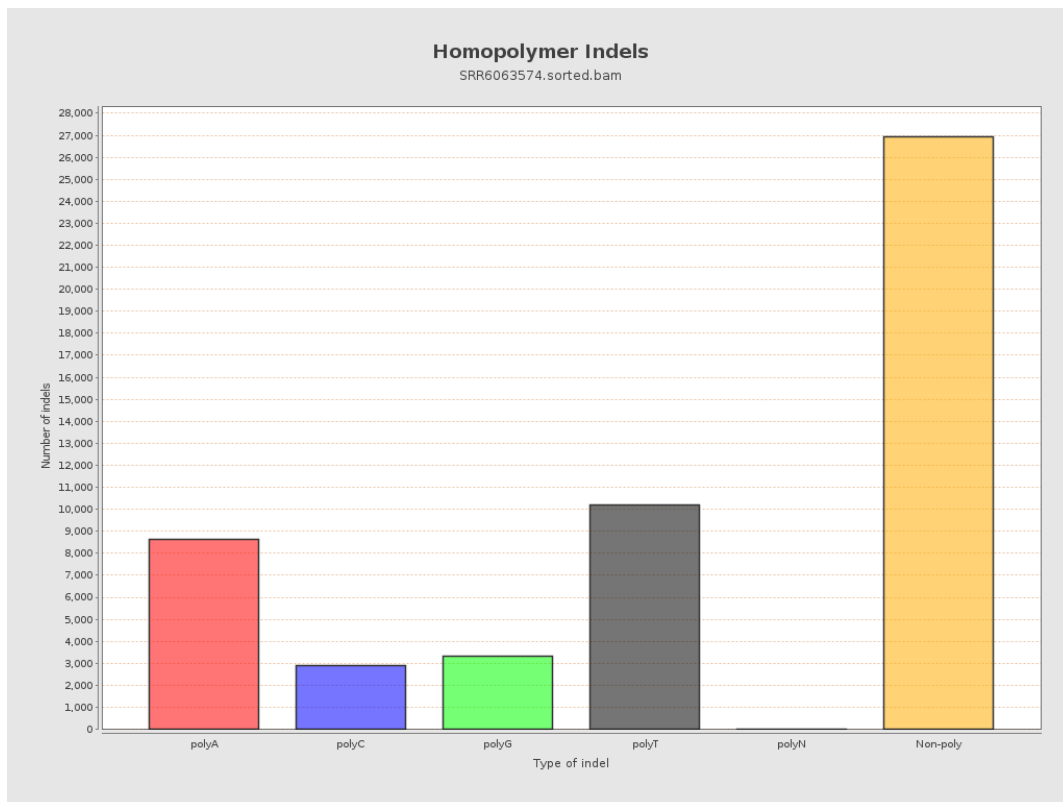
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

