

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:50:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063549.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_SRR6063549 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063549.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:50:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063549.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,769,681
Mapped reads	2,476,339 / 89.41%
Unmapped reads	293,342 / 10.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,661 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	131,905 / 4.76%
Duplication rate	4.05%
Clipped reads	1,243,887 / 44.91%

2.2. ACGT Content

Number/percentage of A's	45,129,359 / 27.84%
Number/percentage of C's	29,614,559 / 18.27%
Number/percentage of T's	51,184,694 / 31.58%
Number/percentage of G's	36,151,830 / 22.3%
Number/percentage of N's	3,217 / 0%
GC Percentage	40.58%

2.3. Coverage

Mean	0.0524

Standard Deviation	0.5324
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2.4. Mapping Quality

Mean Mapping Quality	45.57
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2.5. Mismatches and indels

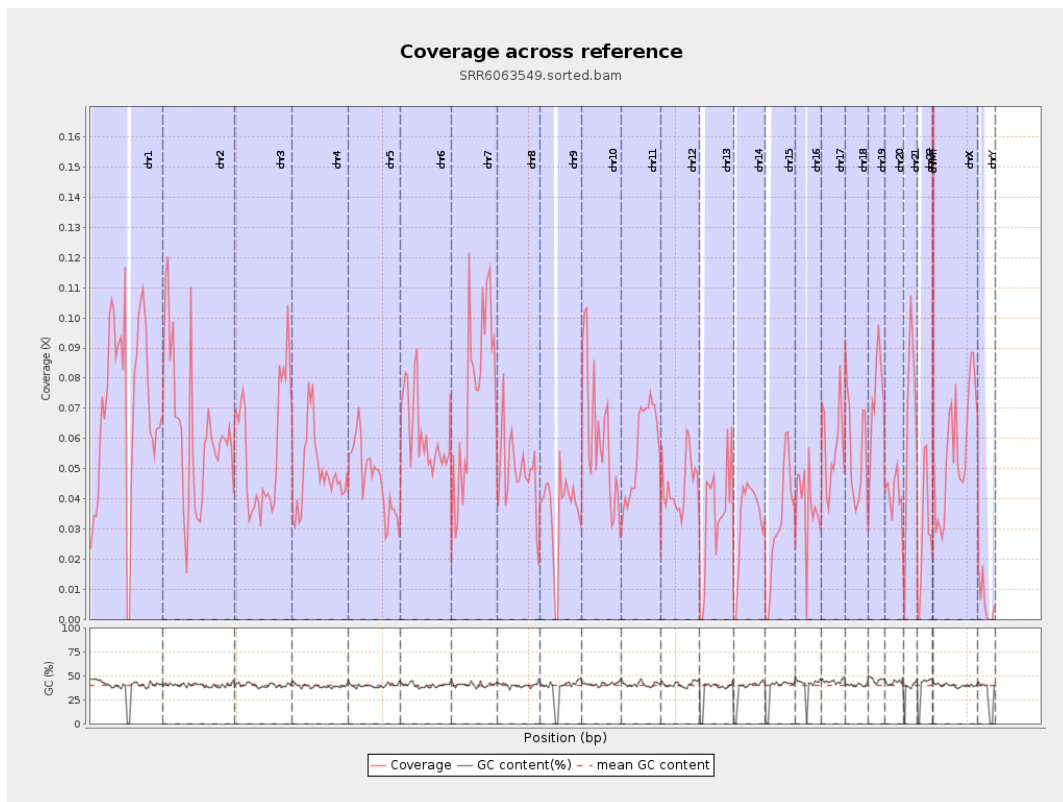
General error rate	0.81%
Mismatches	1,297,416
Insertions	12,553
Mapped reads with at least one insertion	0.5%
Deletions	46,716
Mapped reads with at least one deletion	1.87%
Homopolymer indels	45.98%

2.6. Chromosome stats

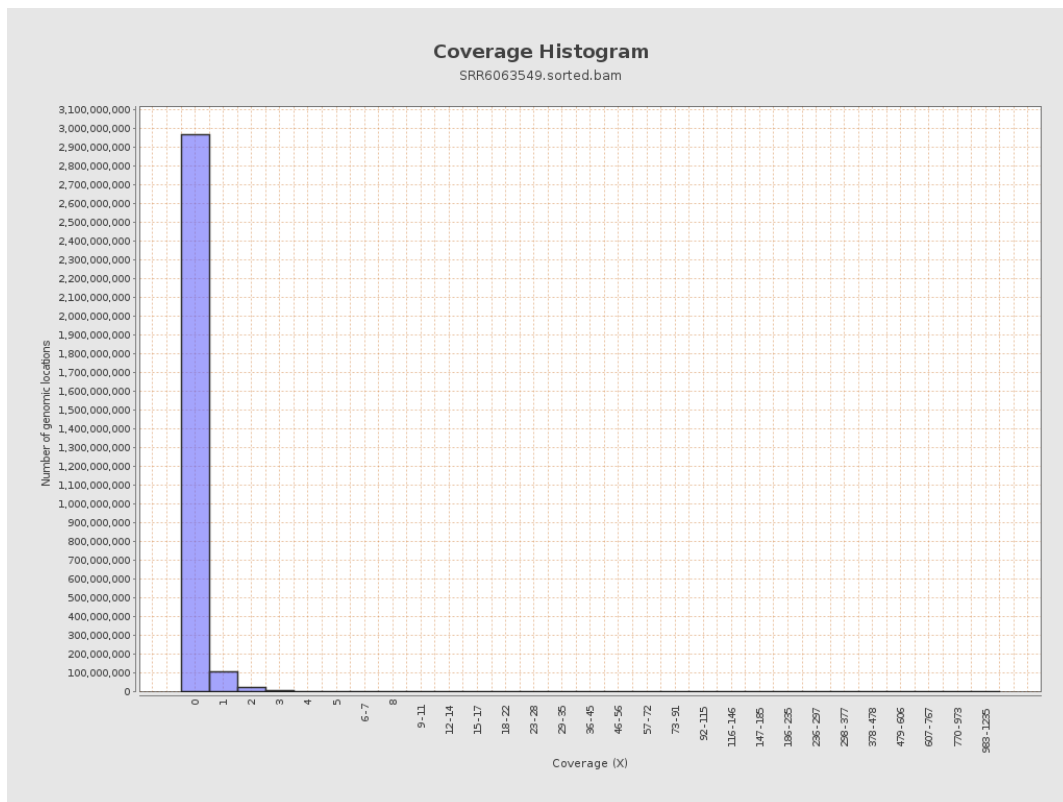
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17663555	0.0709	1.0747
chr2	243199373	15077758	0.062	0.6427
chr3	198022430	11217082	0.0566	0.2924
chr4	191154276	9374134	0.049	0.2751
chr5	180915260	8415332	0.0465	0.2622
chr6	171115067	10649197	0.0622	0.364
chr7	159138663	11829081	0.0743	0.886

chr8	146364022	7112568	0.0486	0.7278
chr9	141213431	5142661	0.0364	0.4265
chr10	135534747	8138334	0.06	0.4321
chr11	135006516	7682436	0.0569	0.381
chr12	133851895	5976882	0.0447	0.2755
chr13	115169878	4039737	0.0351	0.2287
chr14	107349540	3555012	0.0331	0.268
chr15	102531392	3237356	0.0316	0.236
chr16	90354753	3347386	0.037	0.2651
chr17	81195210	4706074	0.058	0.3181
chr18	78077248	4350880	0.0557	0.7306
chr19	59128983	4319971	0.0731	0.7342
chr20	63025520	2596874	0.0412	0.2745
chr21	48129895	3181518	0.0661	0.3305
chr22	51304566	1489234	0.029	0.2033
chrMT	16571	24783	1.4956	1.5347
chrX	155270560	8685407	0.0559	0.3352
chrY	59373566	347451	0.0059	0.1621

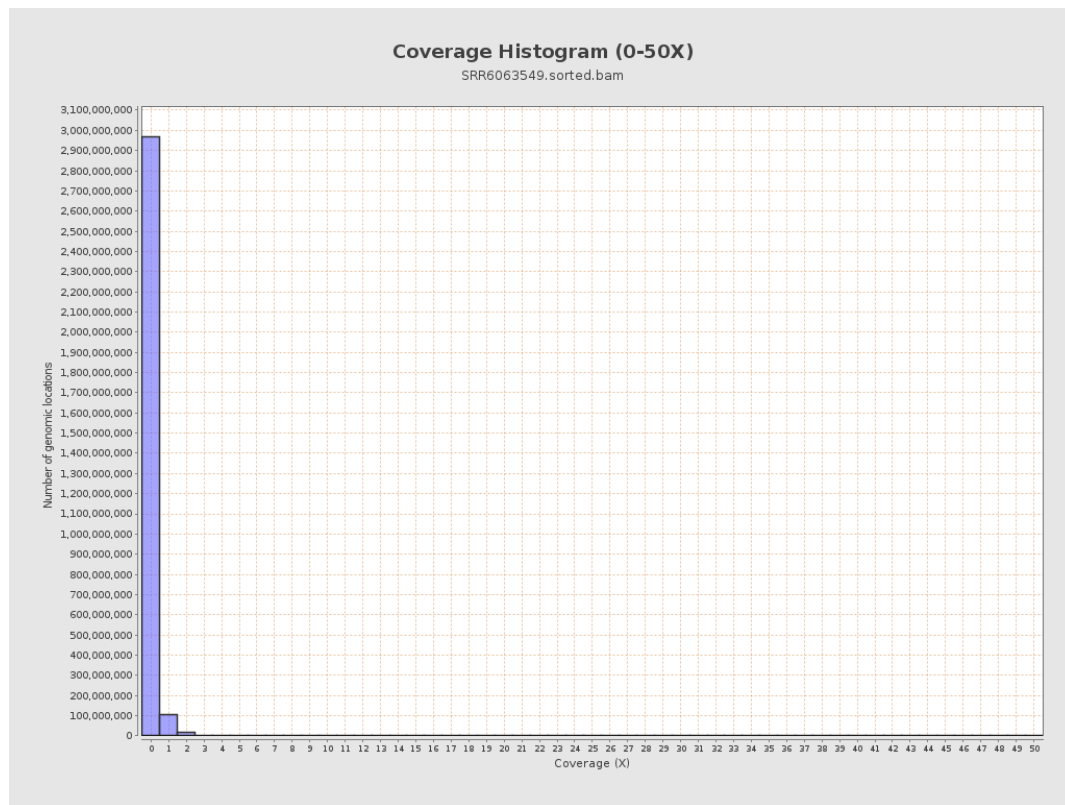
3. Results : Coverage across reference



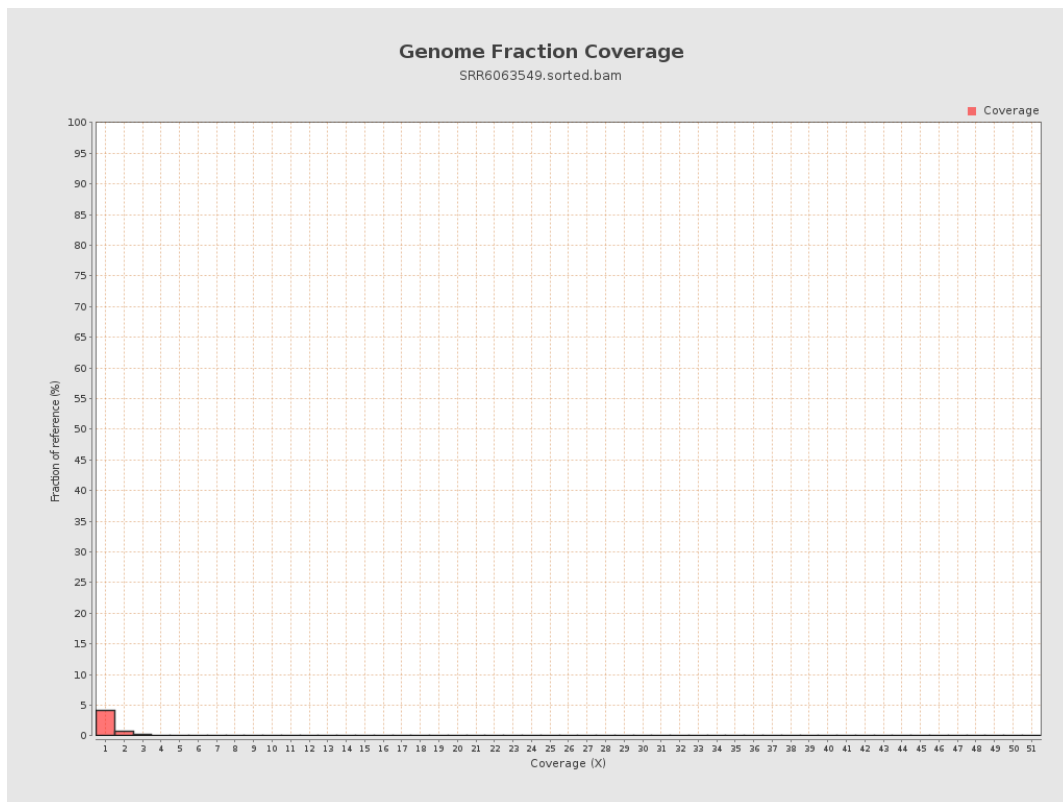
4. Results : Coverage Histogram



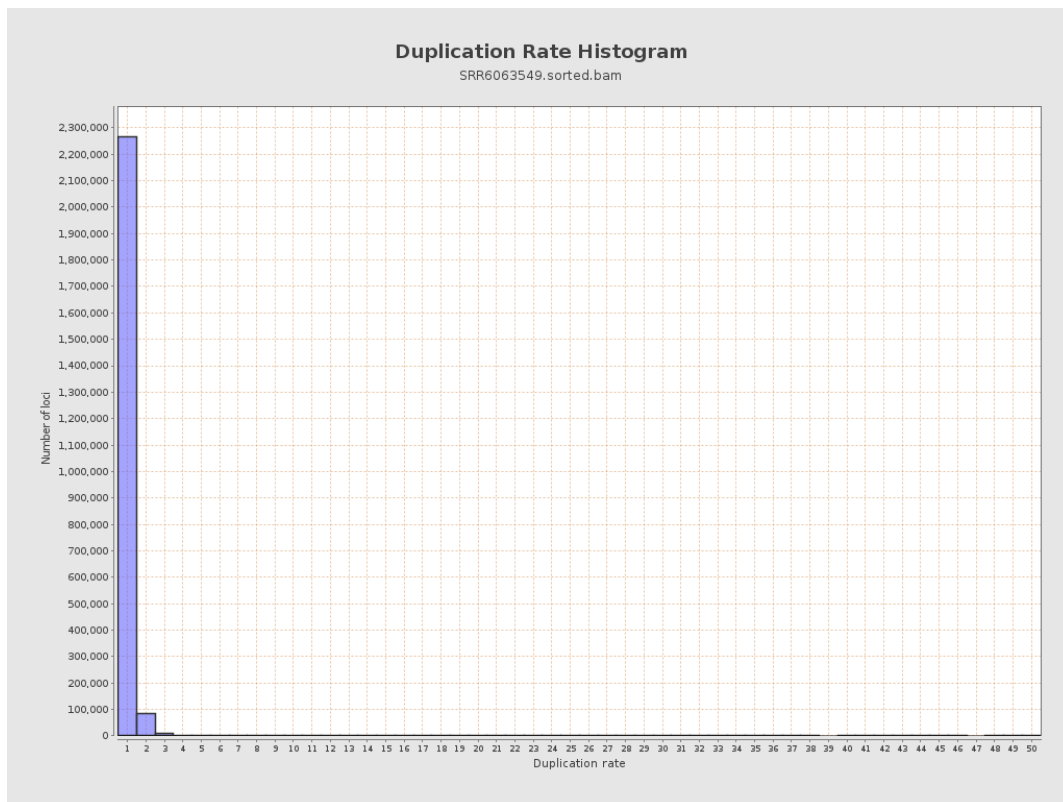
5. Results : Coverage Histogram (0-50X)



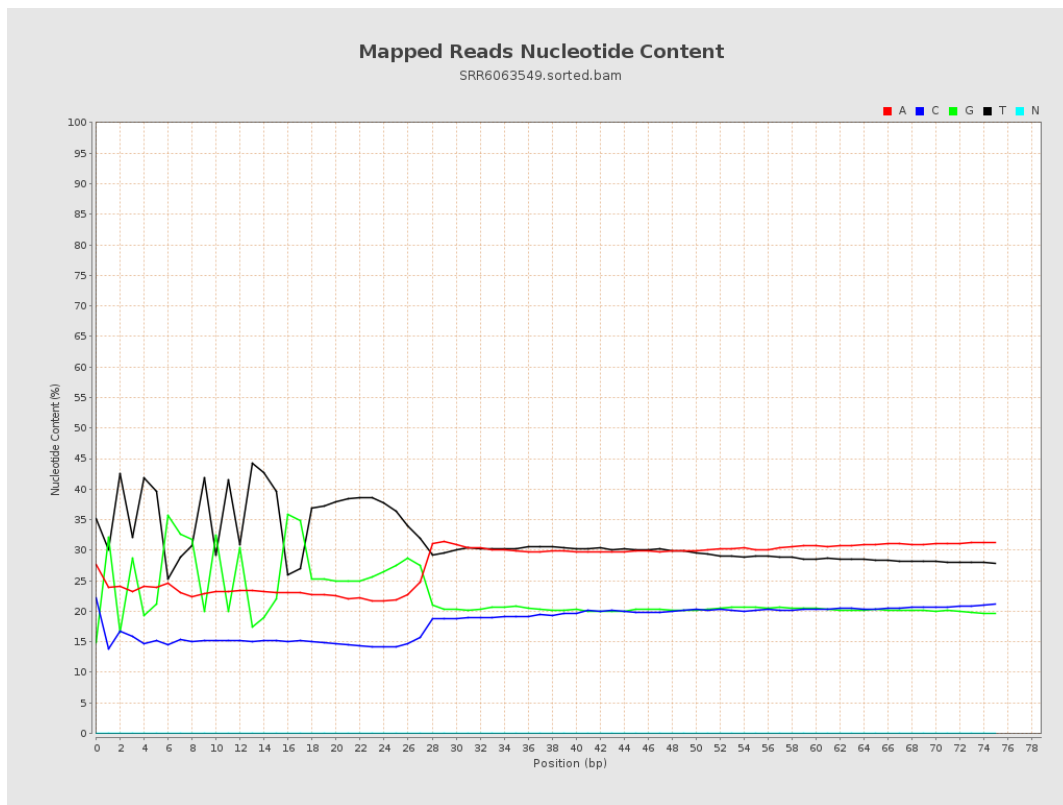
6. Results : Genome Fraction Coverage



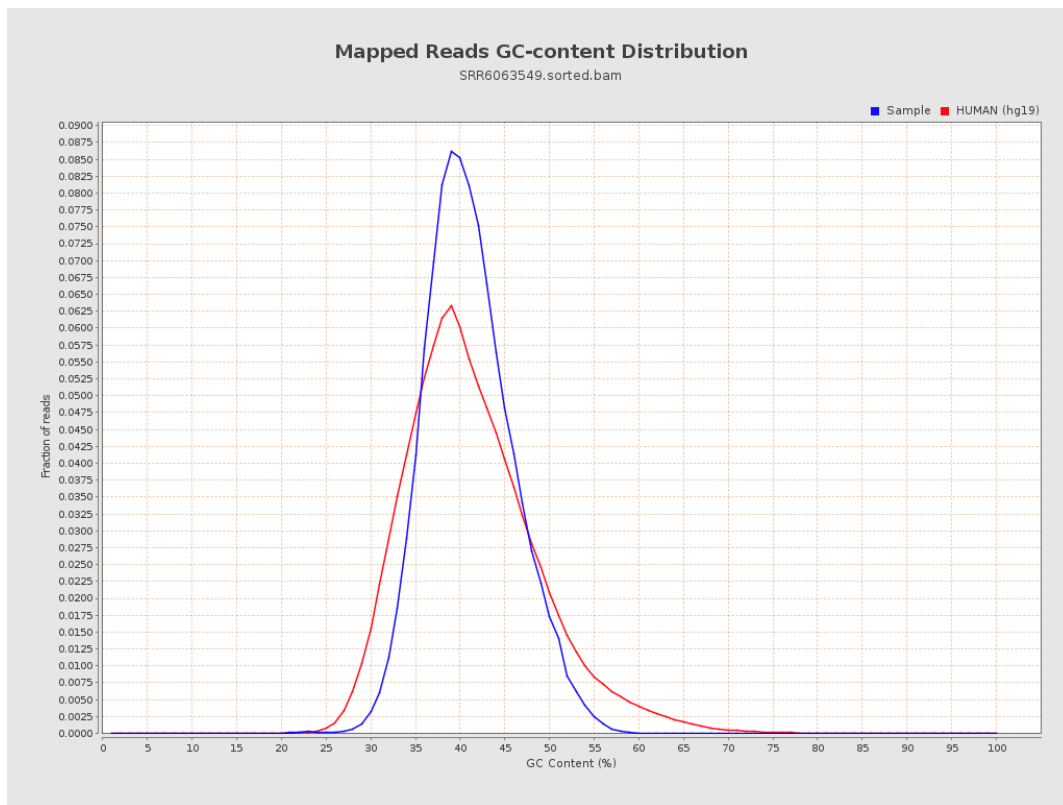
7. Results : Duplication Rate Histogram



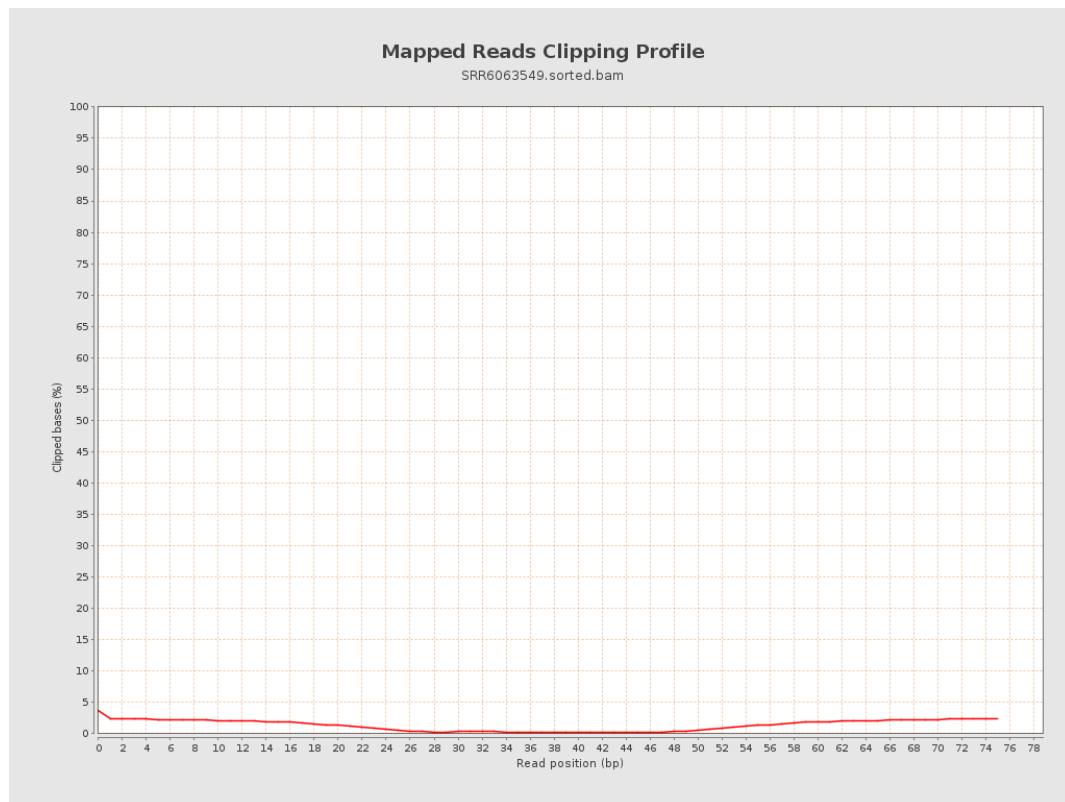
8. Results : Mapped Reads Nucleotide Content



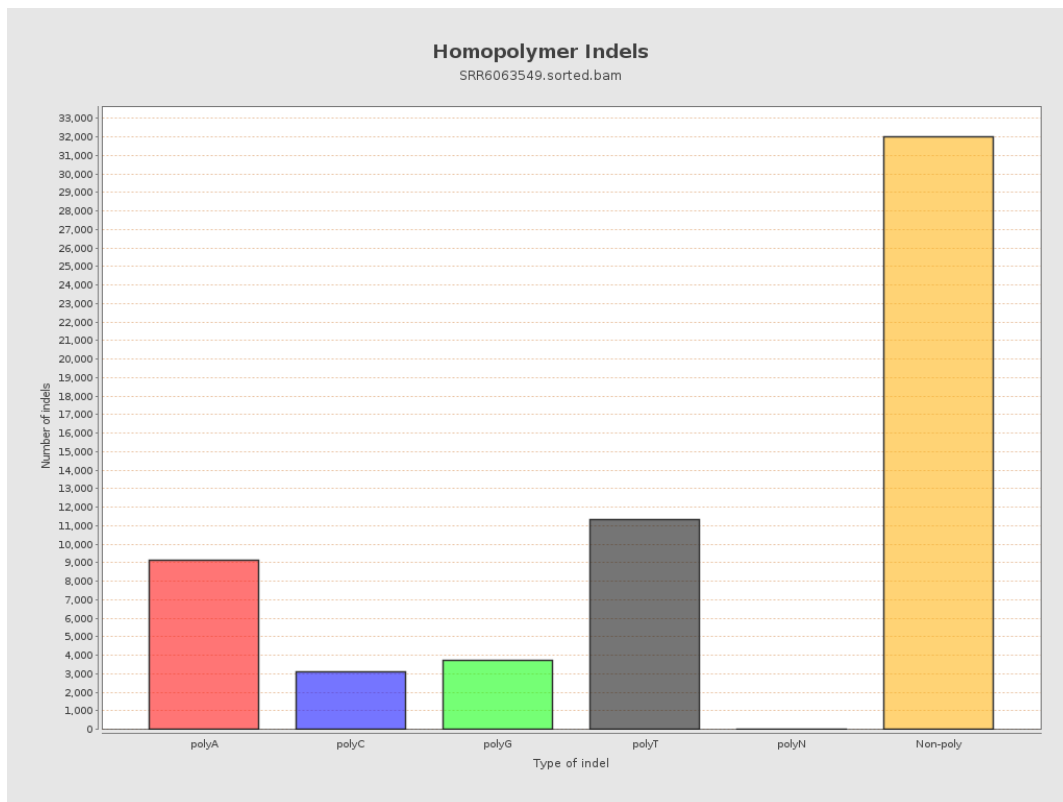
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

