

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:56:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549061.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_SRR1549061 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549061.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:56:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549061.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,659,987
Mapped reads	7,449,714 / 86.02%
Unmapped reads	1,210,273 / 13.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	312,836 / 3.61%
Duplication rate	2.97%
Clipped reads	304,962 / 3.52%

2.2. ACGT Content

Number/percentage of A's	86,800,869 / 29.31%
Number/percentage of C's	61,259,191 / 20.68%
Number/percentage of T's	86,858,270 / 29.33%
Number/percentage of G's	61,235,660 / 20.68%
Number/percentage of N's	5,443 / 0%
GC Percentage	41.36%

2.3. Coverage

Mean	0.0957
Standard Deviation	1.0183

2.4. Mapping Quality

Mean Mapping Quality	44.74
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2.5. Mismatches and indels

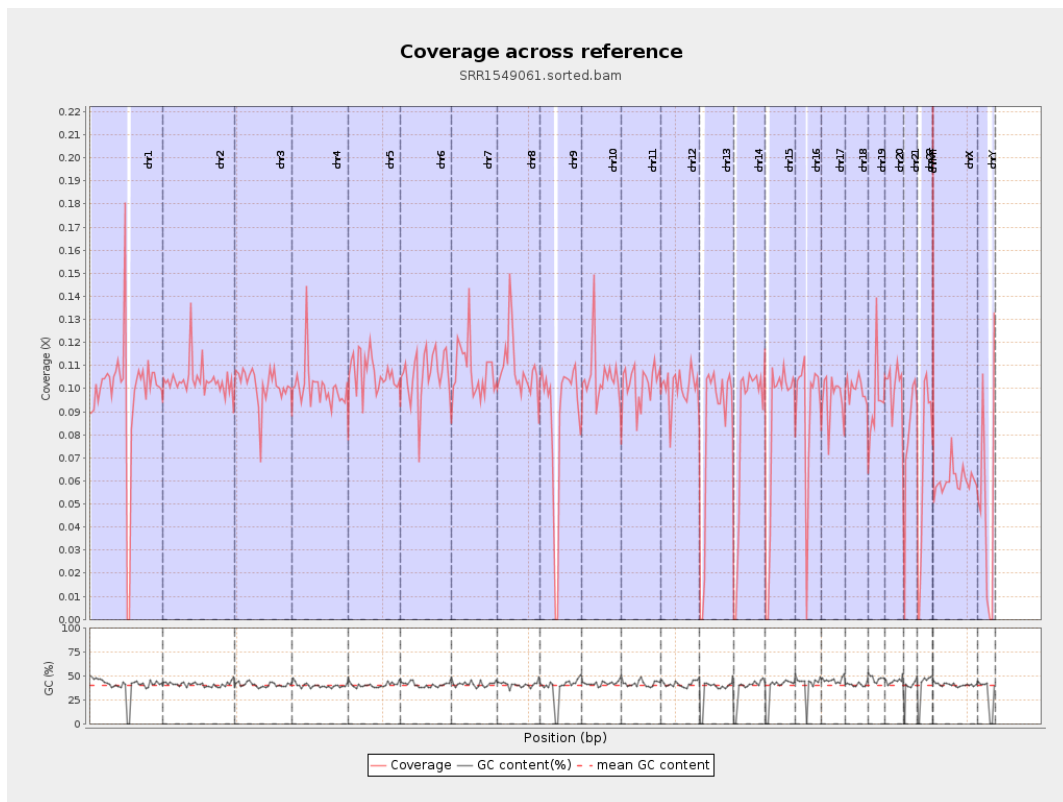
General error rate	0.31%
Mismatches	897,627
Insertions	6,873
Mapped reads with at least one insertion	0.09%
Deletions	22,844
Mapped reads with at least one deletion	0.31%
Homopolymer indels	45.19%

2.6. Chromosome stats

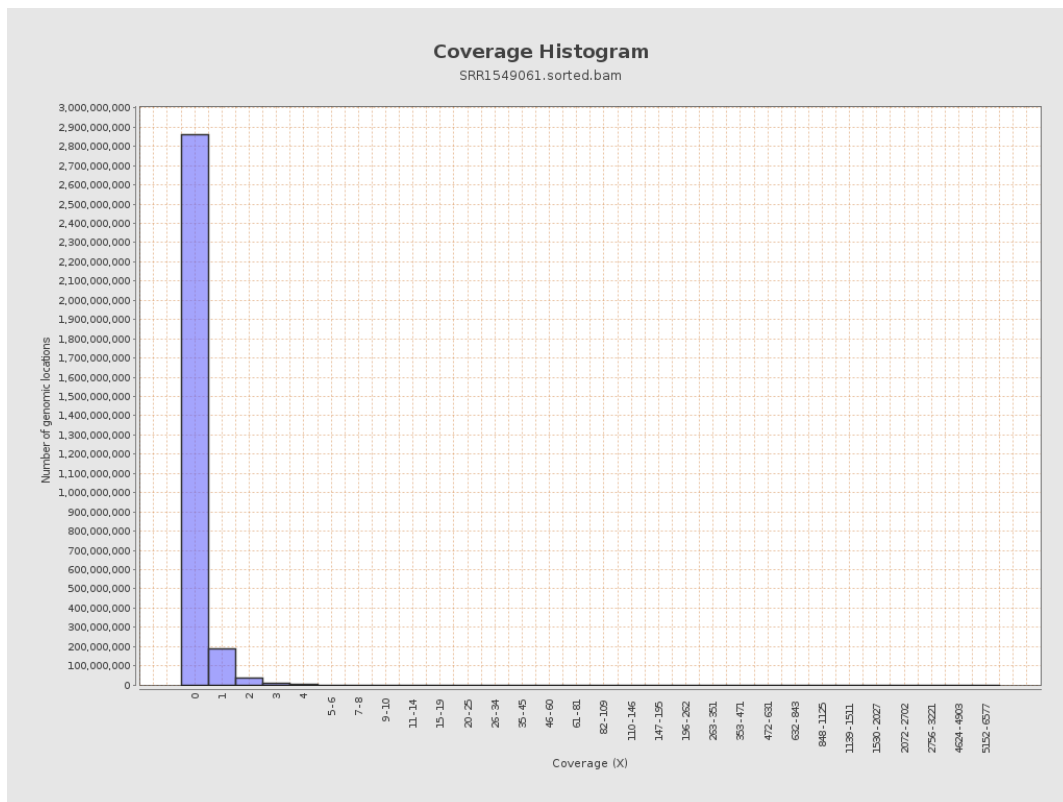
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24420482	0.098	1.9256
chr2	243199373	25240639	0.1038	0.5505
chr3	198022430	20047346	0.1012	0.3858
chr4	191154276	19311052	0.101	0.4513
chr5	180915260	19266730	0.1065	0.405
chr6	171115067	18179735	0.1062	0.4375
chr7	159138663	17126819	0.1076	0.7541
chr8	146364022	15883498	0.1085	3.2236

chr9	141213431	12421701	0.088	0.4809
chr10	135534747	14221035	0.1049	0.6453
chr11	135006516	13744620	0.1018	0.5295
chr12	133851895	13474395	0.1007	0.3972
chr13	115169878	9591208	0.0833	0.3423
chr14	107349540	9111050	0.0849	0.3889
chr15	102531392	8588380	0.0838	0.3427
chr16	90354753	8200040	0.0908	0.4116
chr17	81195210	7825871	0.0964	0.4129
chr18	78077248	7808435	0.1	0.9749
chr19	59128983	5627103	0.0952	1.3336
chr20	63025520	6379452	0.1012	0.403
chr21	48129895	3863853	0.0803	0.4346
chr22	51304566	3469570	0.0676	0.3254
chrMT	16571	4253	0.2567	0.5777
chrX	155270560	9351486	0.0602	0.3587
chrY	59373566	3029453	0.051	0.6634

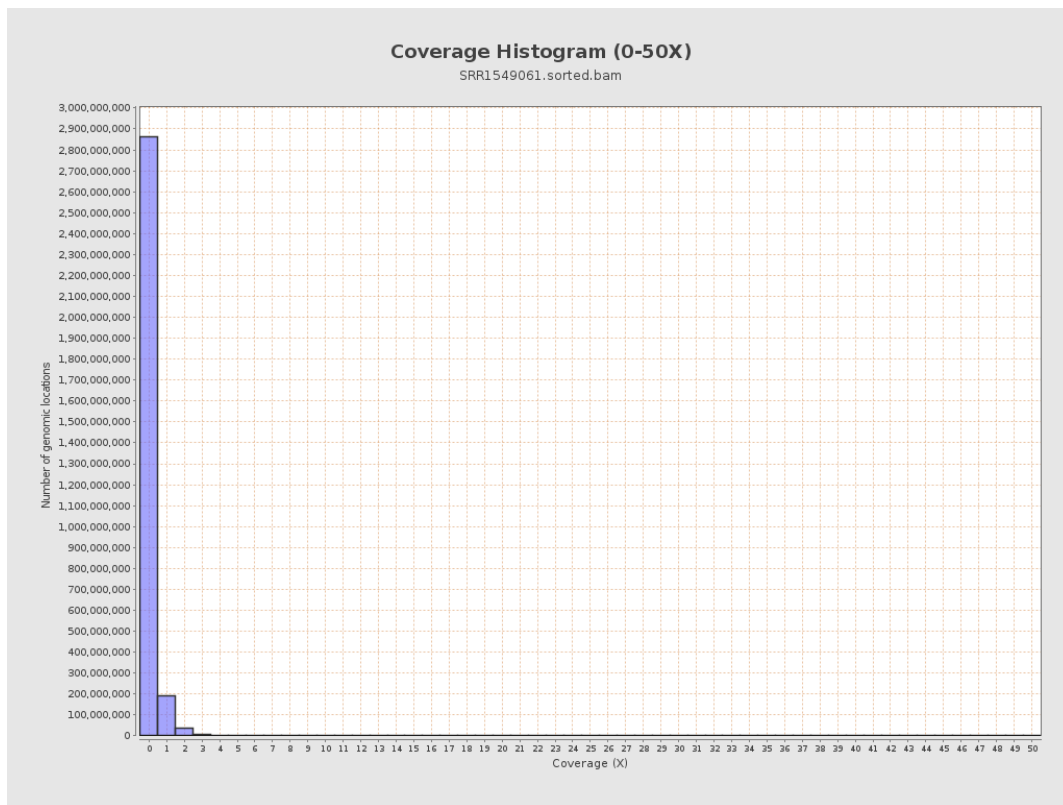
3. Results : Coverage across reference



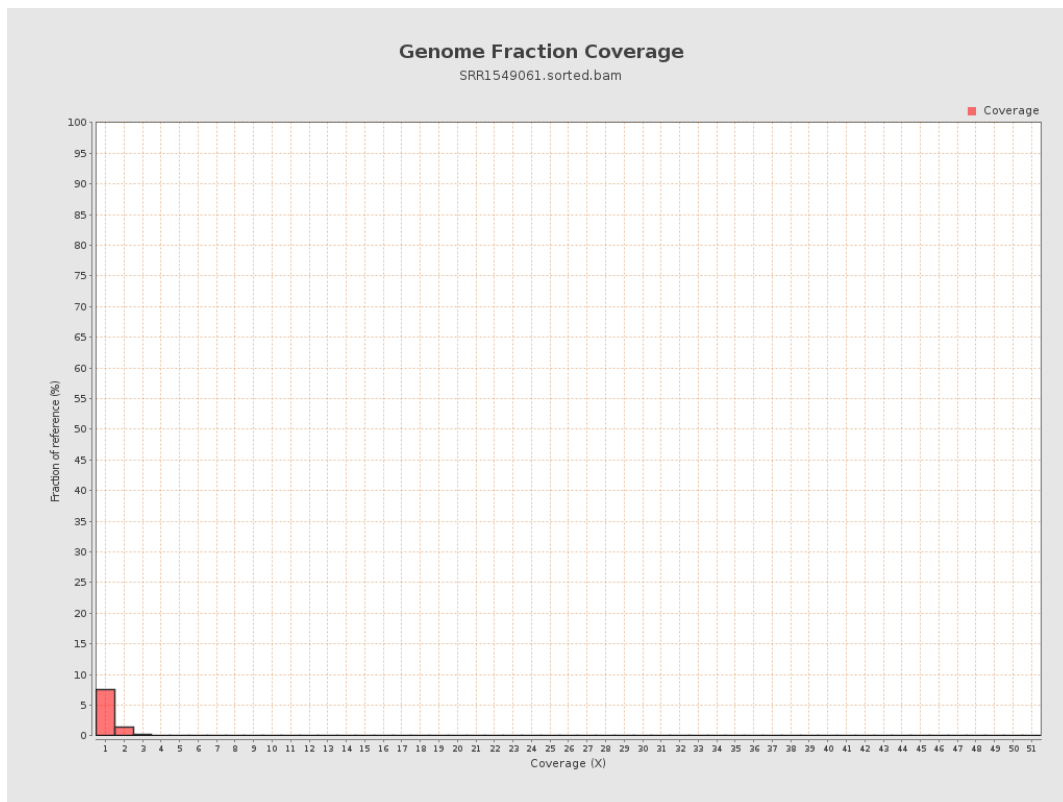
4. Results : Coverage Histogram



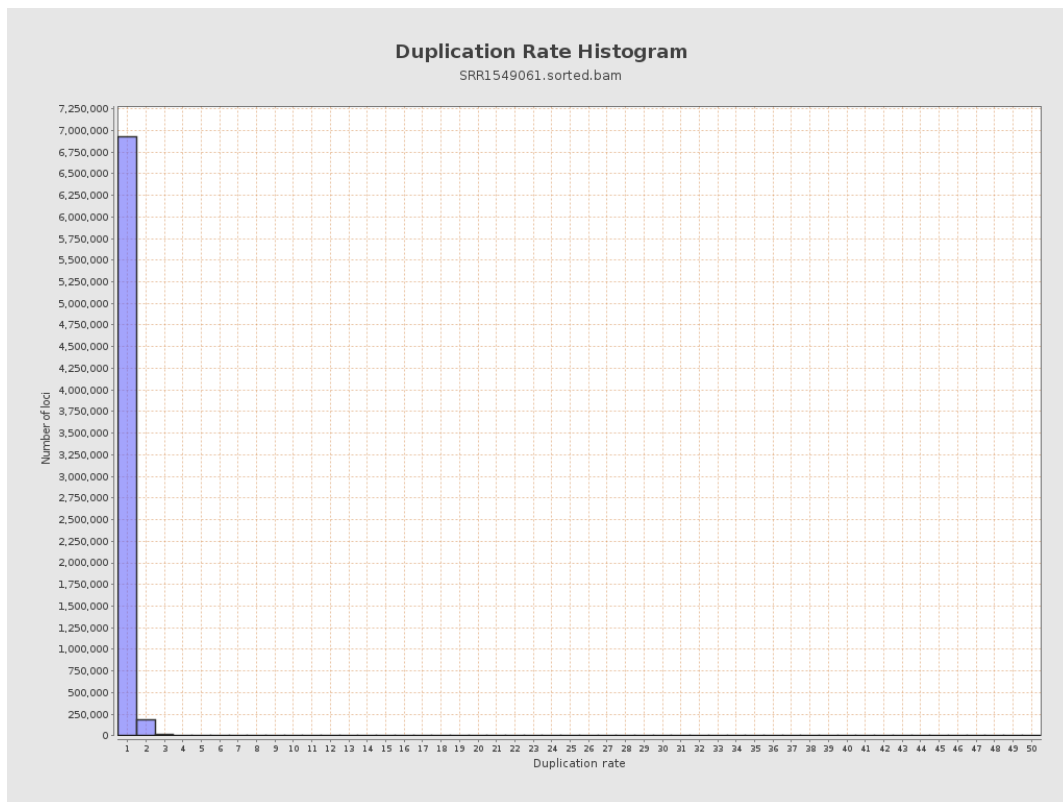
5. Results : Coverage Histogram (0-50X)



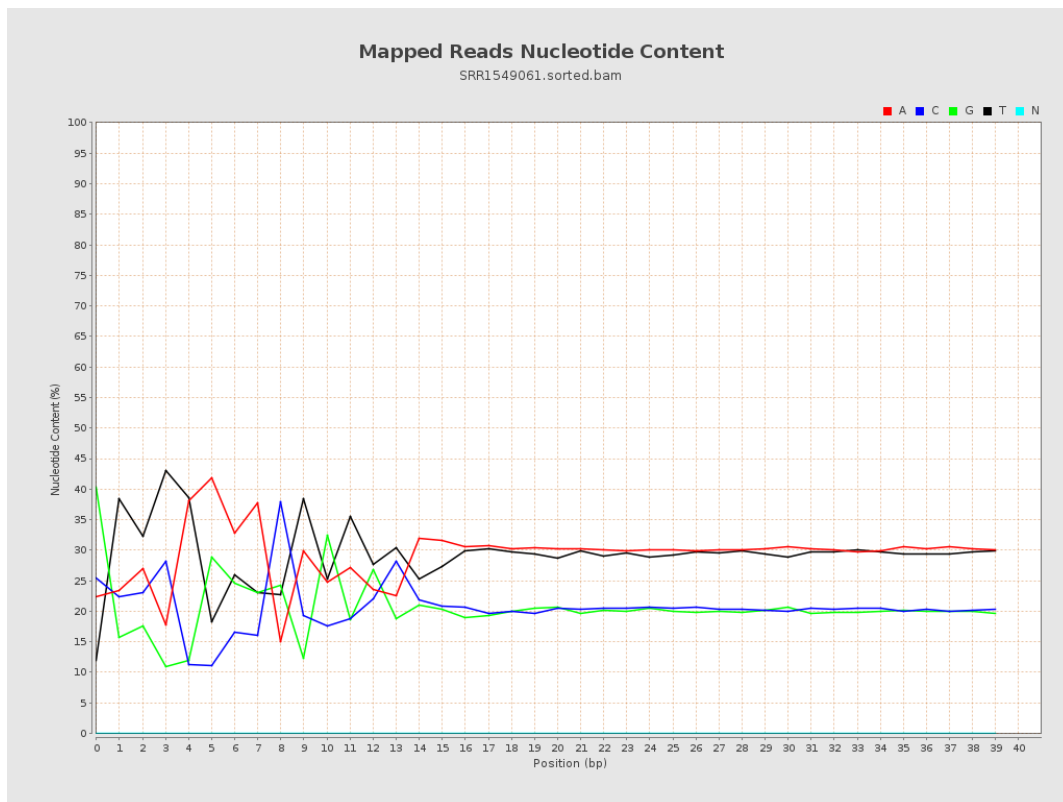
6. Results : Genome Fraction Coverage



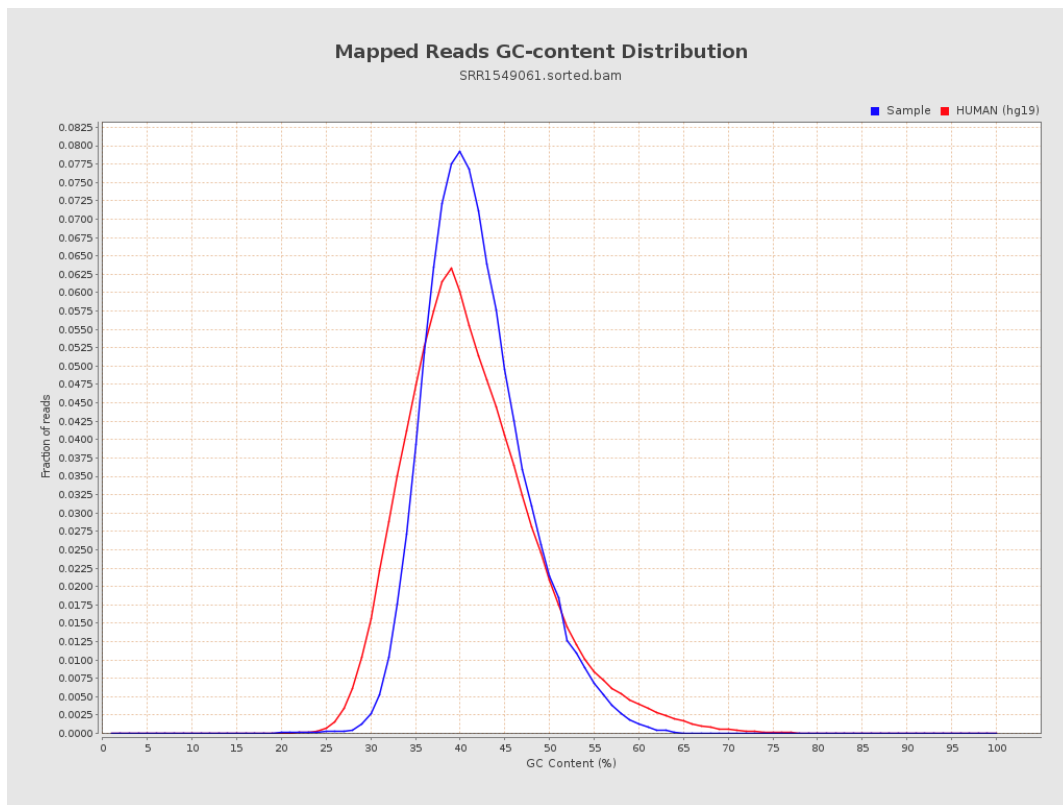
7. Results : Duplication Rate Histogram



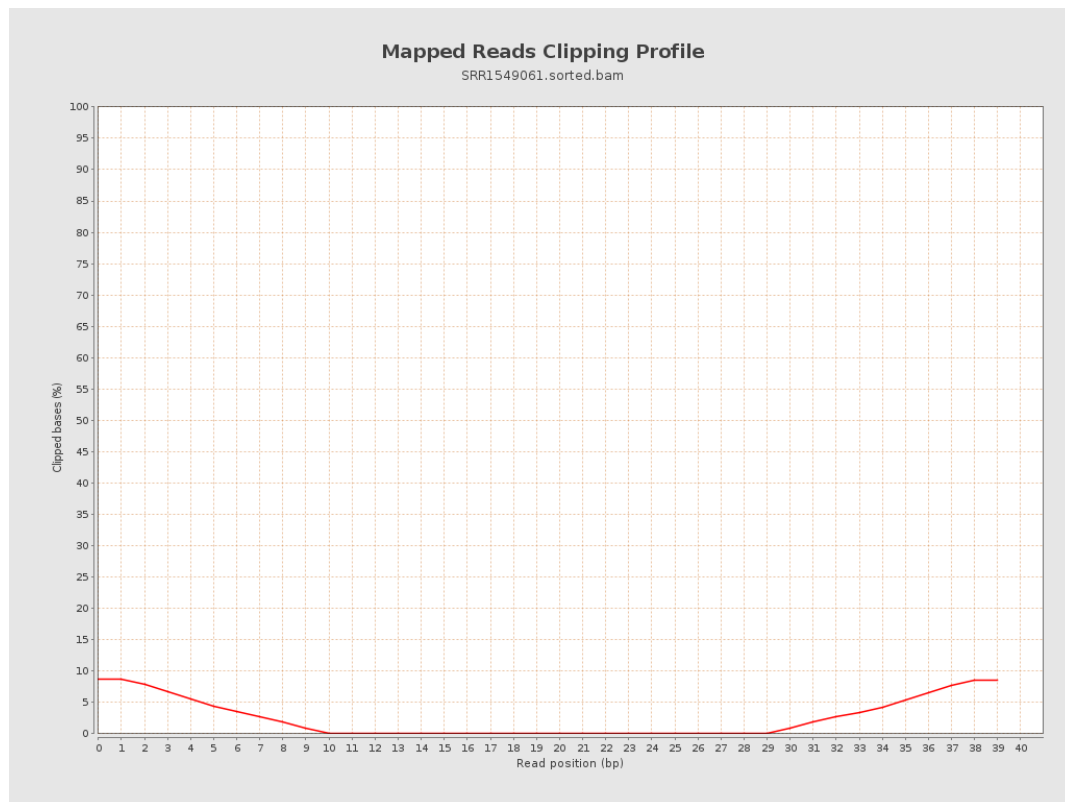
8. Results : Mapped Reads Nucleotide Content



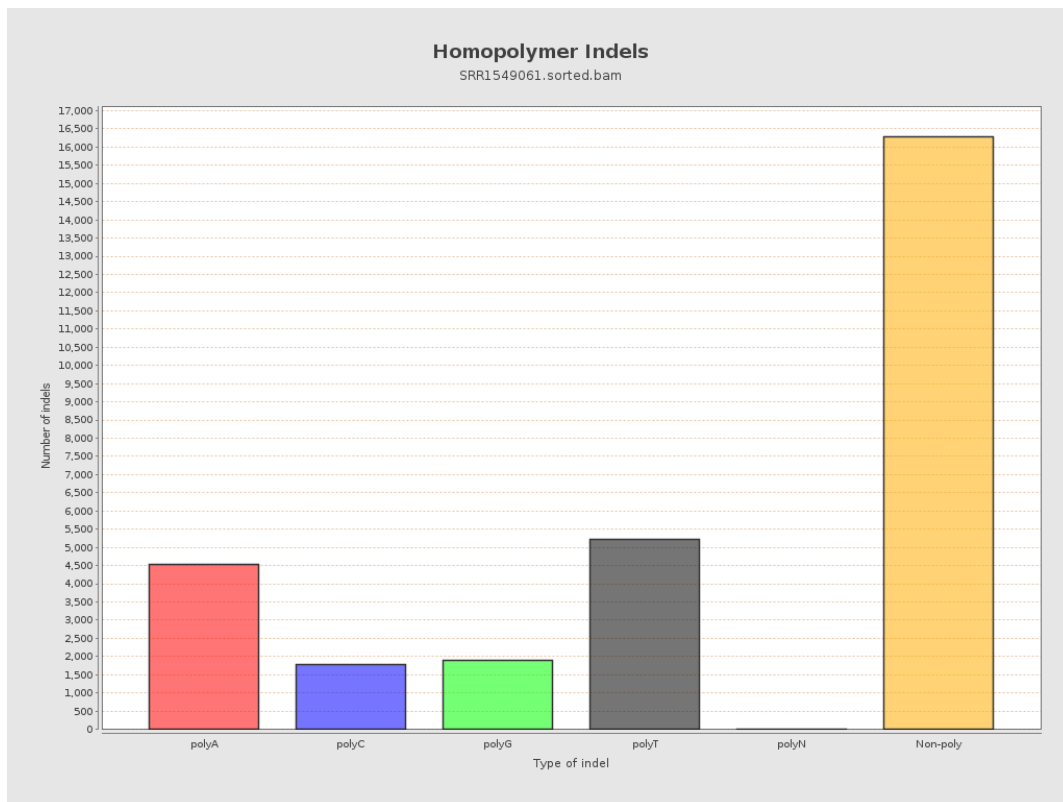
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

