

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:36:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068943.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_SRR6068943 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068943.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:36:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068943.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,229,054
Mapped reads	1,910,859 / 85.73%
Unmapped reads	318,195 / 14.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,567 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	66,231 / 2.97%
Duplication rate	2.05%
Clipped reads	958,518 / 43%

2.2. ACGT Content

Number/percentage of A's	33,812,164 / 26.96%
Number/percentage of C's	21,789,371 / 17.38%
Number/percentage of T's	41,109,543 / 32.78%
Number/percentage of G's	28,388,706 / 22.64%
Number/percentage of N's	305,366 / 0.24%
GC Percentage	40.01%

2.3. Coverage

Mean	0.0405

Standard Deviation	0.4635
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2.4. Mapping Quality

Mean Mapping Quality	45.29
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2.5. Mismatches and indels

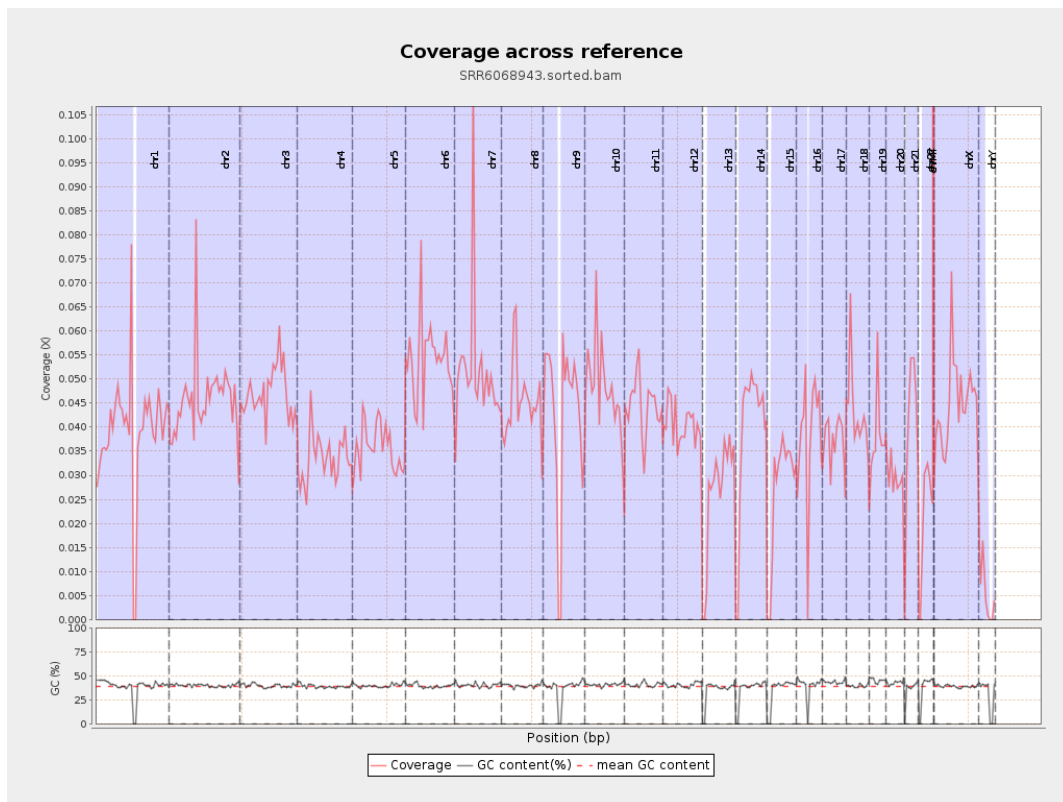
General error rate	0.98%
Mismatches	1,204,426
Insertions	12,138
Mapped reads with at least one insertion	0.63%
Deletions	32,486
Mapped reads with at least one deletion	1.68%
Homopolymer indels	48.49%

2.6. Chromosome stats

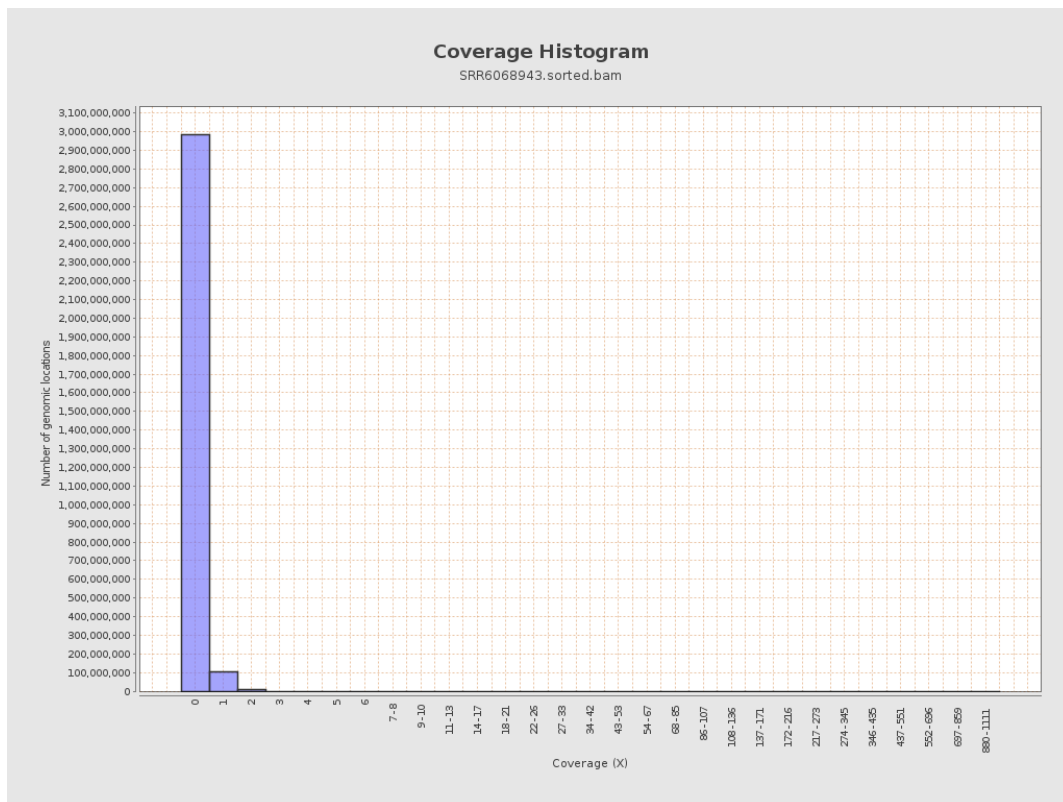
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9754126	0.0391	0.7782
chr2	243199373	11124754	0.0457	0.4971
chr3	198022430	9331918	0.0471	0.2326
chr4	191154276	6370192	0.0333	0.2256
chr5	180915260	6473850	0.0358	0.2078
chr6	171115067	9272094	0.0542	0.363
chr7	159138663	8285239	0.0521	0.8541

chr8	146364022	6581218	0.045	0.7389
chr9	141213431	6046178	0.0428	0.4968
chr10	135534747	6557352	0.0484	0.3771
chr11	135006516	5947922	0.0441	0.4614
chr12	133851895	5396293	0.0403	0.2265
chr13	115169878	3036405	0.0264	0.1732
chr14	107349540	4224897	0.0394	0.2465
chr15	102531392	2776786	0.0271	0.177
chr16	90354753	3448226	0.0382	0.2552
chr17	81195210	2983868	0.0367	0.2551
chr18	78077248	3414888	0.0437	0.8514
chr19	59128983	2262068	0.0383	0.5097
chr20	63025520	1838533	0.0292	0.1997
chr21	48129895	1929769	0.0401	0.2407
chr22	51304566	1072254	0.0209	0.1533
chrMT	16571	65568	3.9568	2.9387
chrX	155270560	6949171	0.0448	0.2895
chrY	59373566	315436	0.0053	0.1284

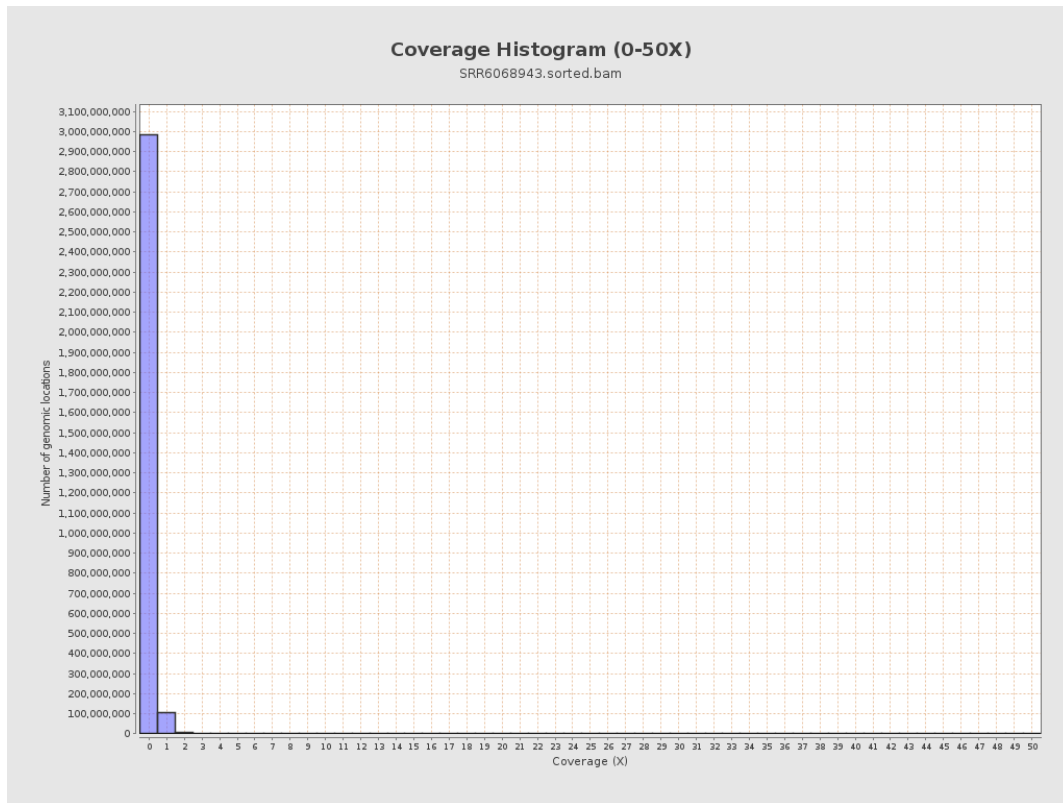
3. Results : Coverage across reference



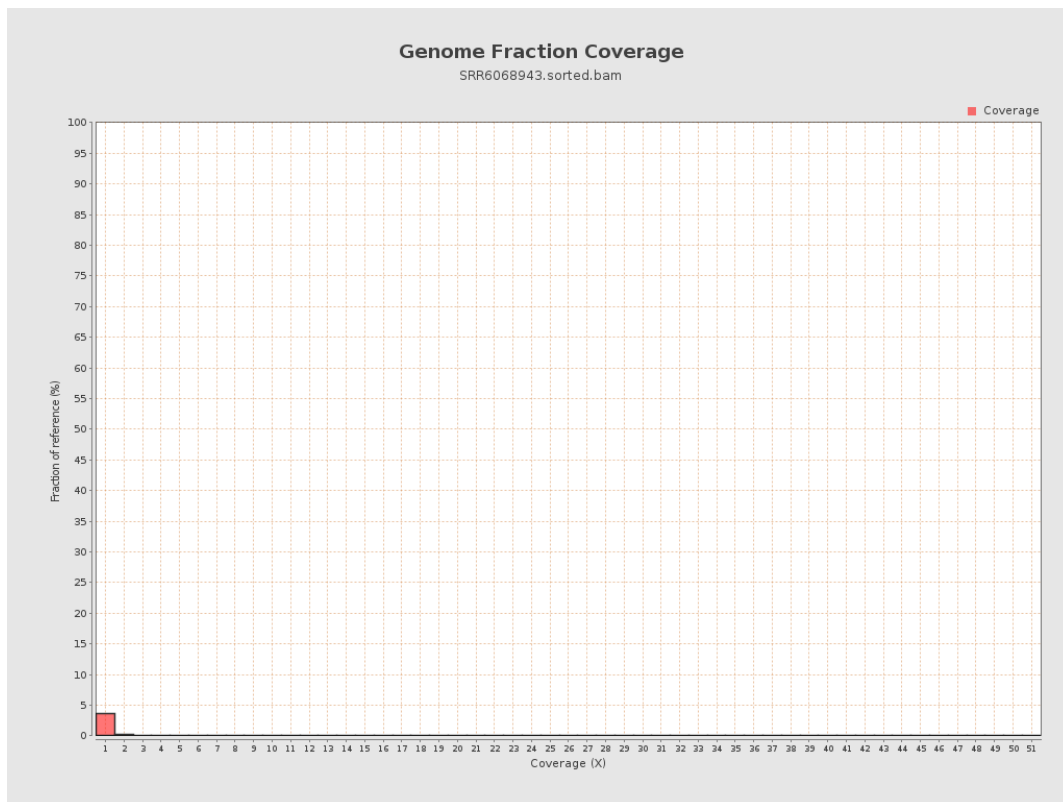
4. Results : Coverage Histogram



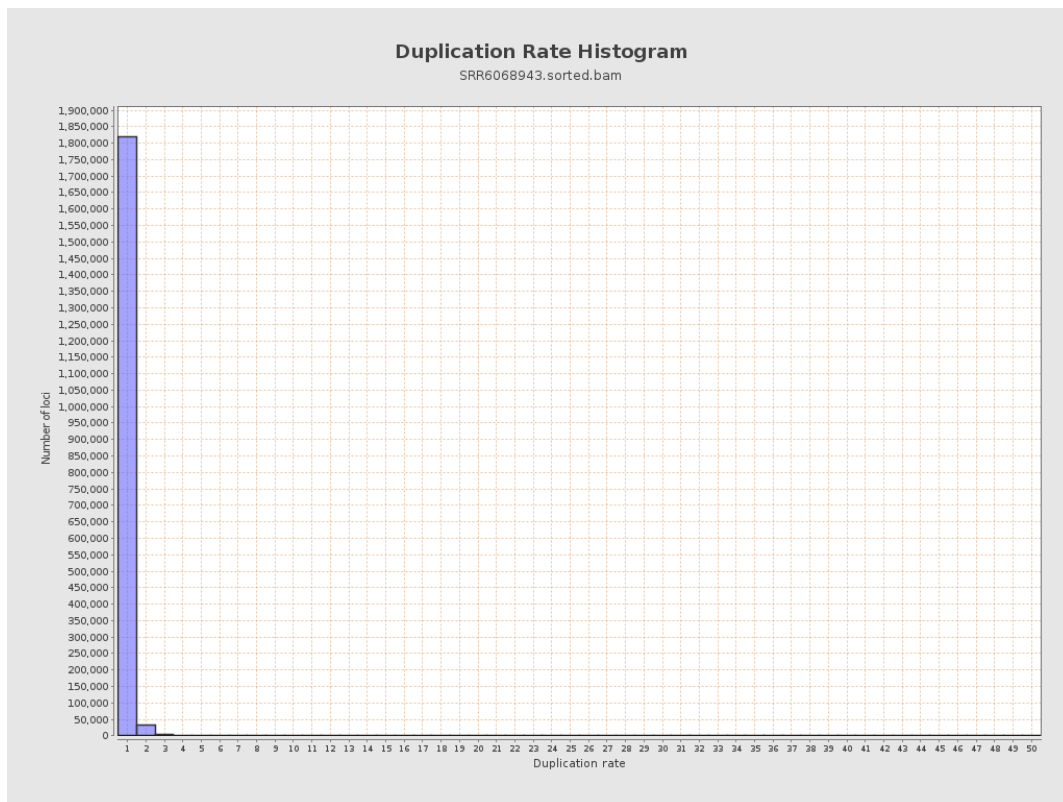
5. Results : Coverage Histogram (0-50X)



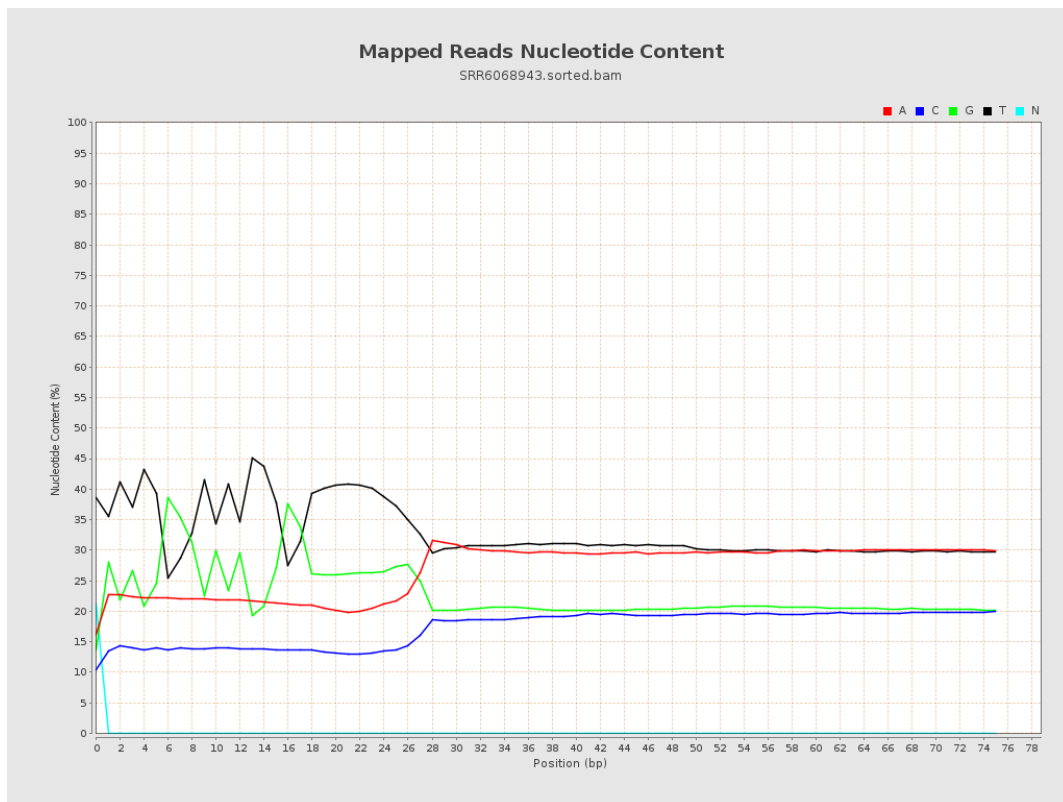
6. Results : Genome Fraction Coverage



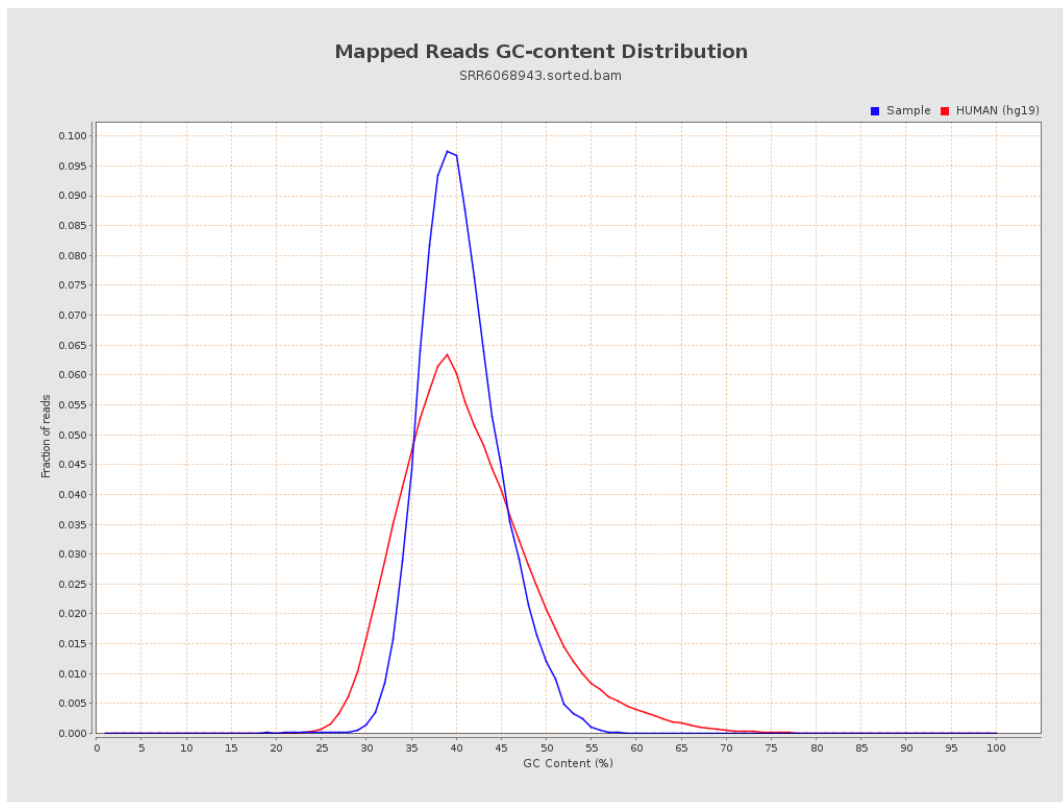
7. Results : Duplication Rate Histogram



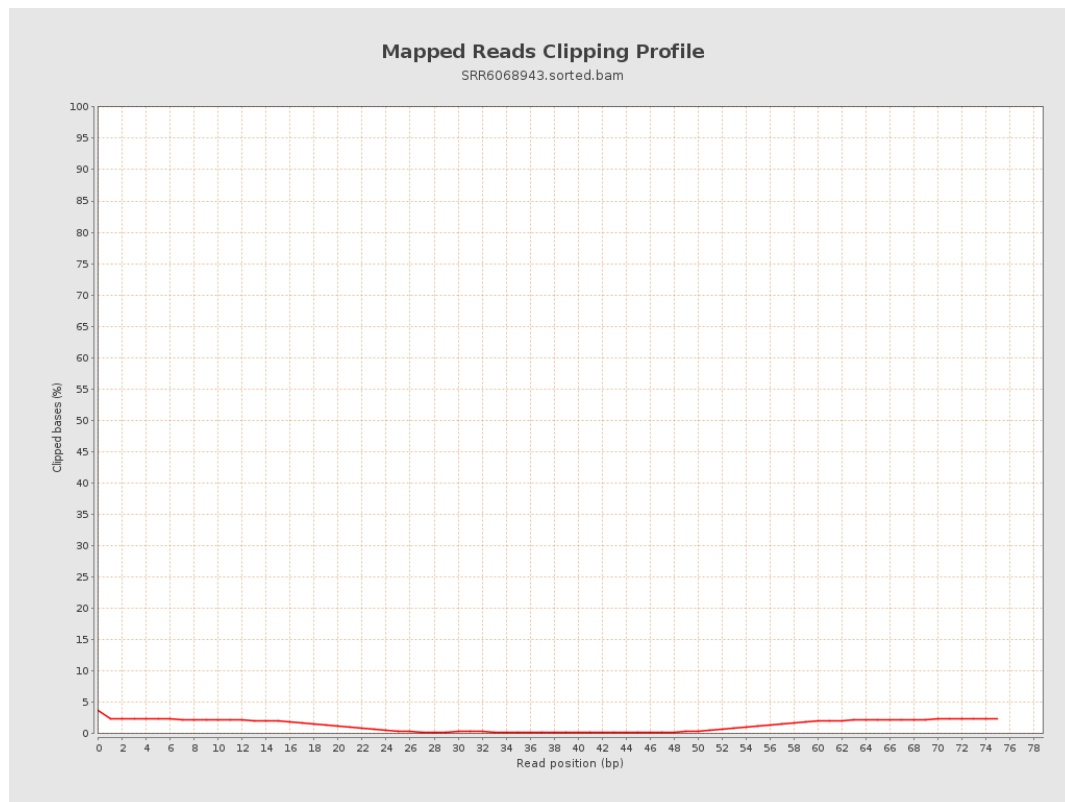
8. Results : Mapped Reads Nucleotide Content



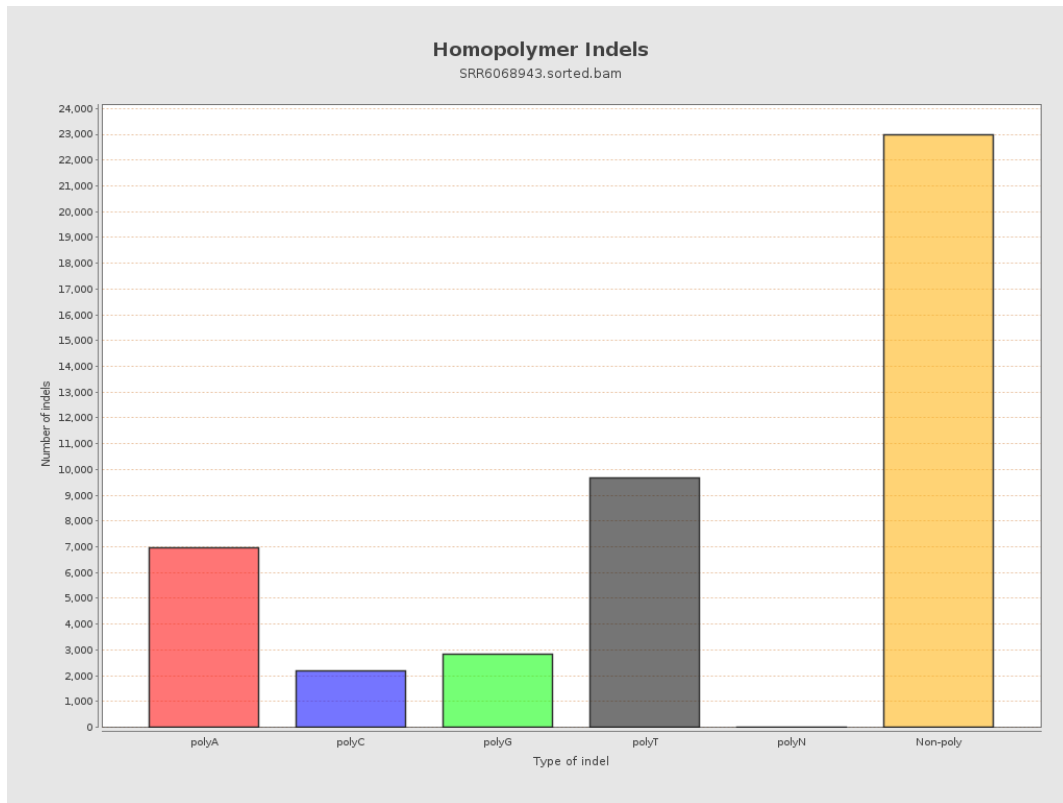
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

