

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:55:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068949.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_SRR6068949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068949.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:55:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,460,474
Mapped reads	1,974,752 / 80.26%
Unmapped reads	485,722 / 19.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,897 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	86,964 / 3.53%
Duplication rate	3.59%
Clipped reads	889,697 / 36.16%

2.2. ACGT Content

Number/percentage of A's	36,113,477 / 27.6%
Number/percentage of C's	22,656,836 / 17.31%
Number/percentage of T's	43,778,076 / 33.45%
Number/percentage of G's	28,000,370 / 21.4%
Number/percentage of N's	319,766 / 0.24%
GC Percentage	38.71%

2.3. Coverage

Mean	0.0423

Standard Deviation	0.3463
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.93
----------------------	-------

2.5. Mismatches and indels

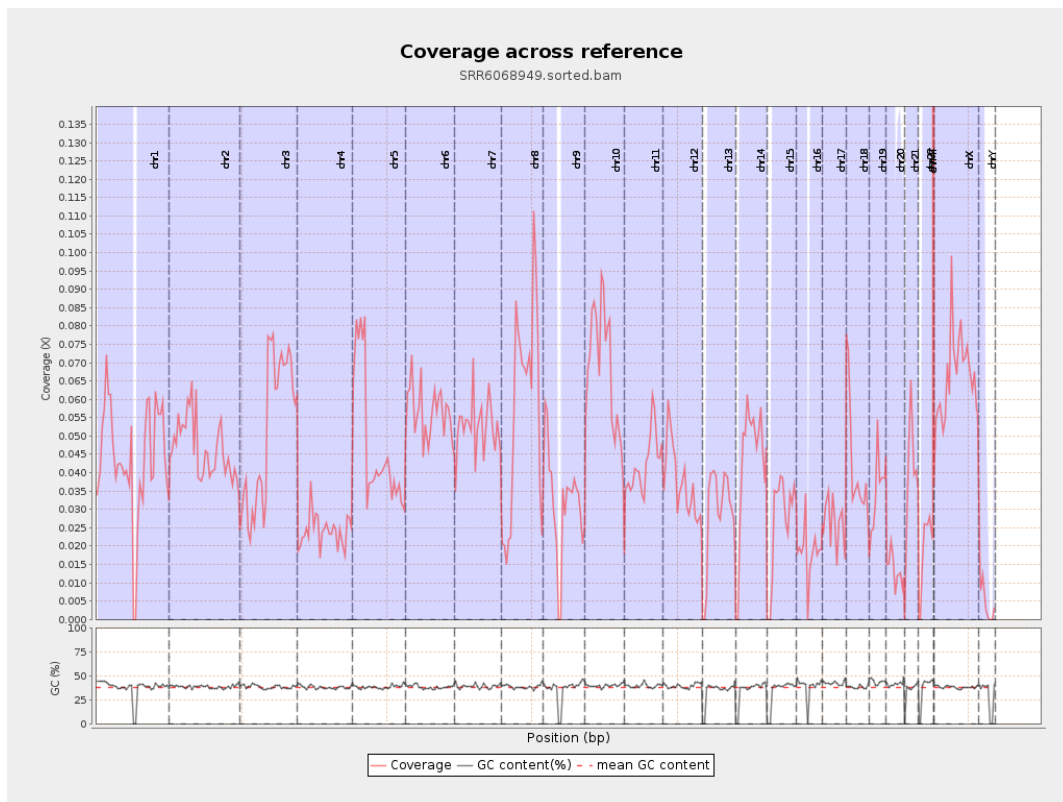
General error rate	1%
Mismatches	1,294,570
Insertions	11,668
Mapped reads with at least one insertion	0.59%
Deletions	33,394
Mapped reads with at least one deletion	1.67%
Homopolymer indels	48.56%

2.6. Chromosome stats

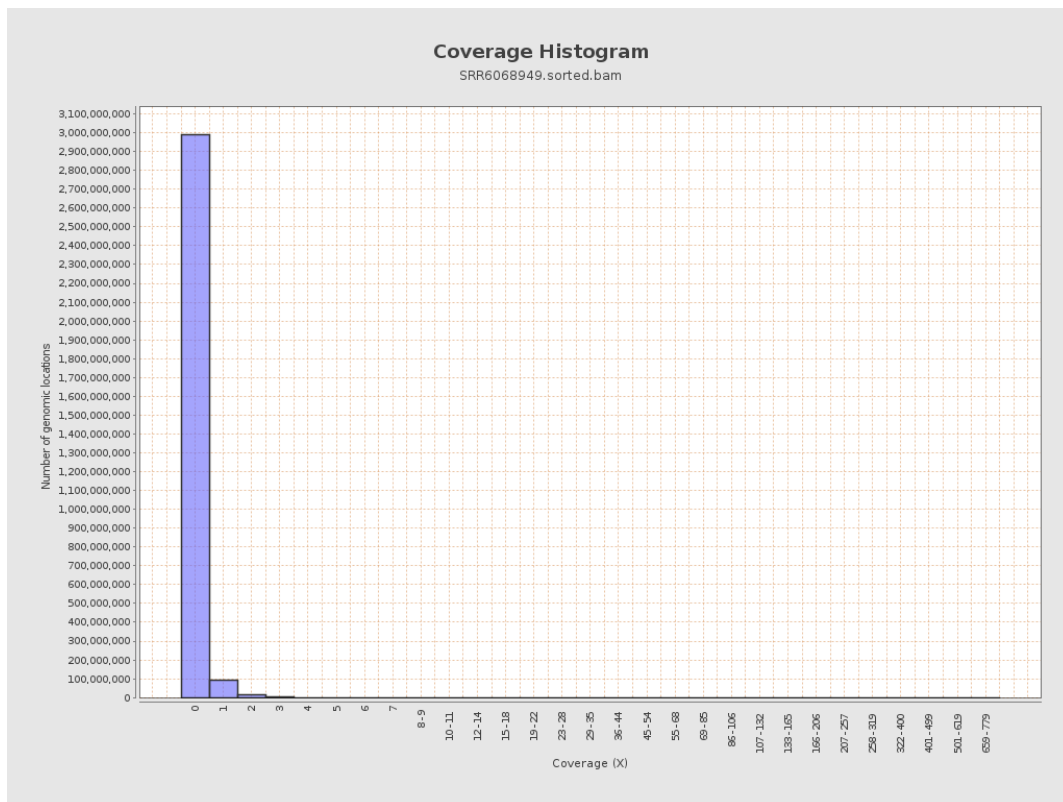
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11046360	0.0443	0.5296
chr2	243199373	11385435	0.0468	0.3429
chr3	198022430	10062915	0.0508	0.2627
chr4	191154276	4599738	0.0241	0.1933
chr5	180915260	8590730	0.0475	0.2552
chr6	171115067	9651543	0.0564	0.3351
chr7	159138663	8405461	0.0528	0.5098

chr8	146364022	8367476	0.0572	0.5599
chr9	141213431	4530193	0.0321	0.2785
chr10	135534747	9392783	0.0693	0.3907
chr11	135006516	5703194	0.0422	0.319
chr12	133851895	4948044	0.037	0.2263
chr13	115169878	3281162	0.0285	0.1973
chr14	107349540	4601457	0.0429	0.2492
chr15	102531392	2764782	0.027	0.1893
chr16	90354753	1668452	0.0185	0.1839
chr17	81195210	2088053	0.0257	0.1959
chr18	78077248	3245783	0.0416	0.5156
chr19	59128983	2077849	0.0351	0.3497
chr20	63025520	843420	0.0134	0.1426
chr21	48129895	1858067	0.0386	0.2439
chr22	51304566	955460	0.0186	0.1581
chrMT	16571	323409	19.5166	11.6132
chrX	155270560	10229205	0.0659	0.3331
chrY	59373566	302173	0.0051	0.1032

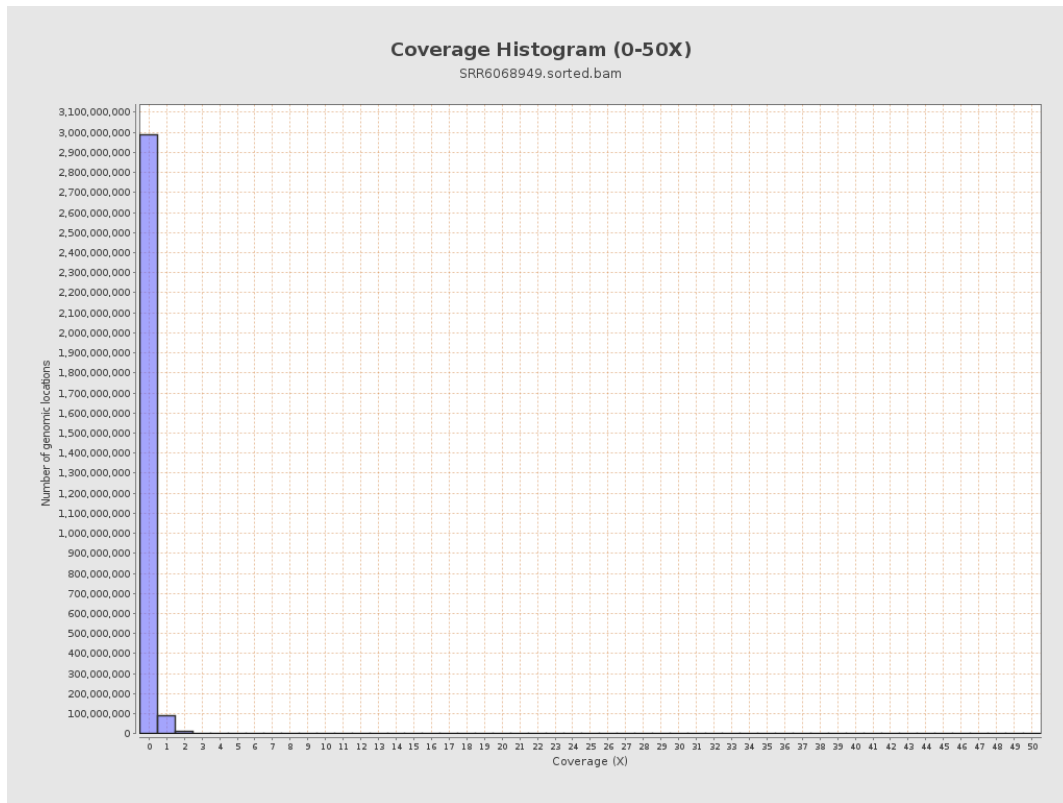
3. Results : Coverage across reference



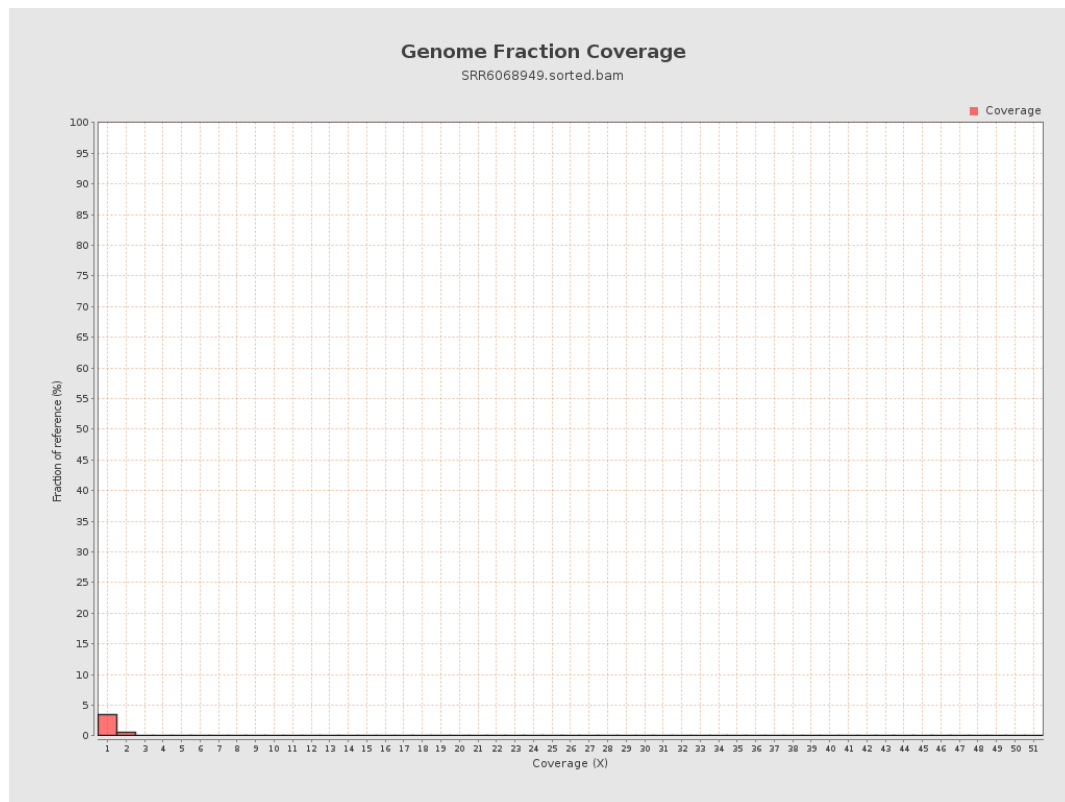
4. Results : Coverage Histogram



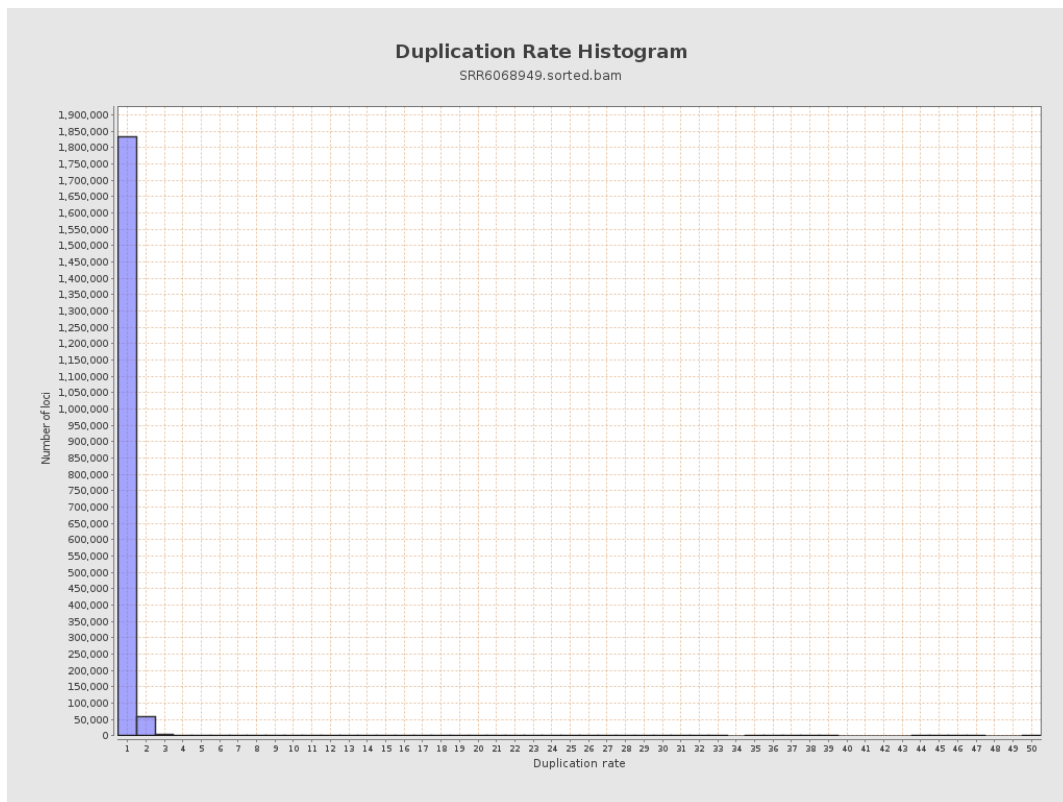
5. Results : Coverage Histogram (0-50X)



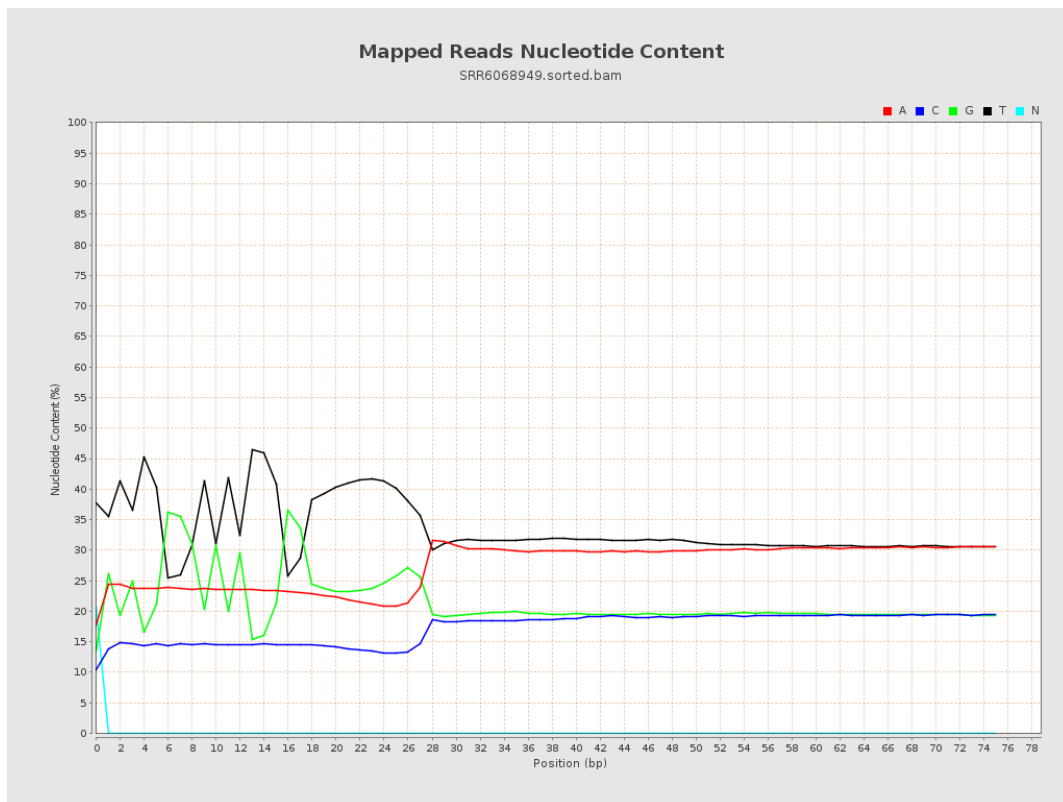
6. Results : Genome Fraction Coverage



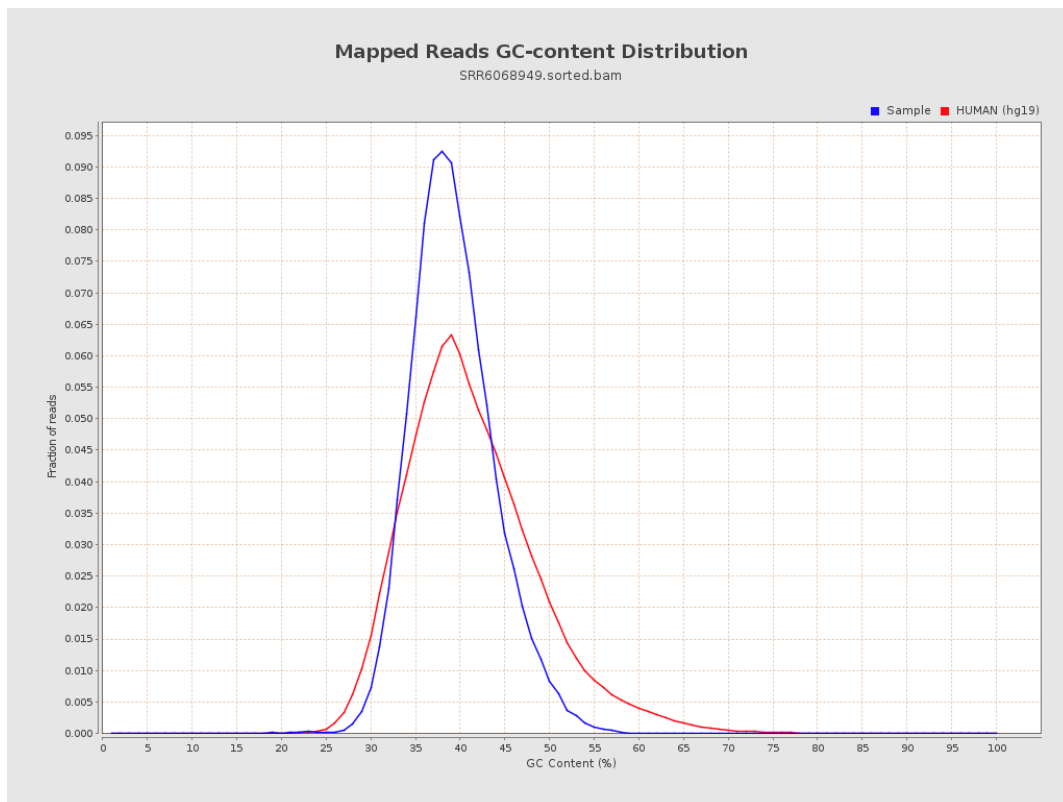
7. Results : Duplication Rate Histogram



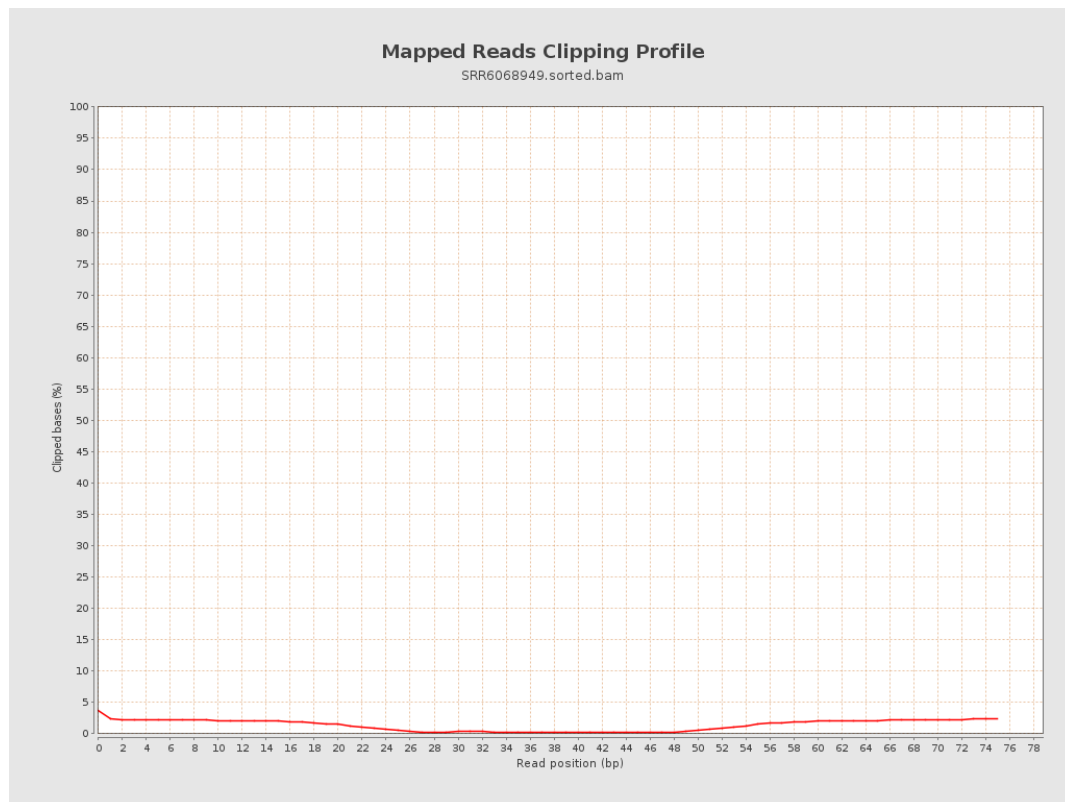
8. Results : Mapped Reads Nucleotide Content



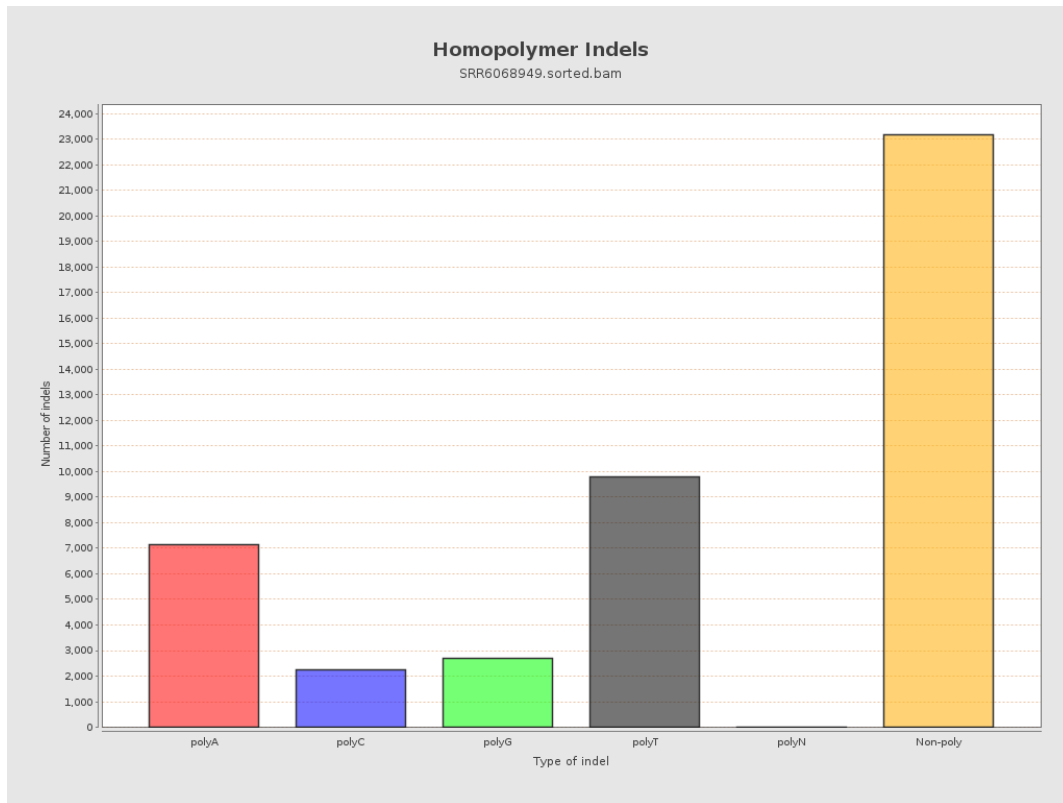
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

