

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:00:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068148.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_SRR6068148 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068148.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:00:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,065,573
Mapped reads	3,787,836 / 93.17%
Unmapped reads	277,737 / 6.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,653 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	508,411 / 12.51%
Duplication rate	11.3%
Clipped reads	1,938,210 / 47.67%

2.2. ACGT Content

Number/percentage of A's	65,714,696 / 26.76%
Number/percentage of C's	43,987,054 / 17.91%
Number/percentage of T's	80,088,754 / 32.61%
Number/percentage of G's	55,760,102 / 22.71%
Number/percentage of N's	28,820 / 0.01%
GC Percentage	40.62%

2.3. Coverage

Mean	0.0794

Standard Deviation	0.6182
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2.4. Mapping Quality

Mean Mapping Quality	45.53
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2.5. Mismatches and indels

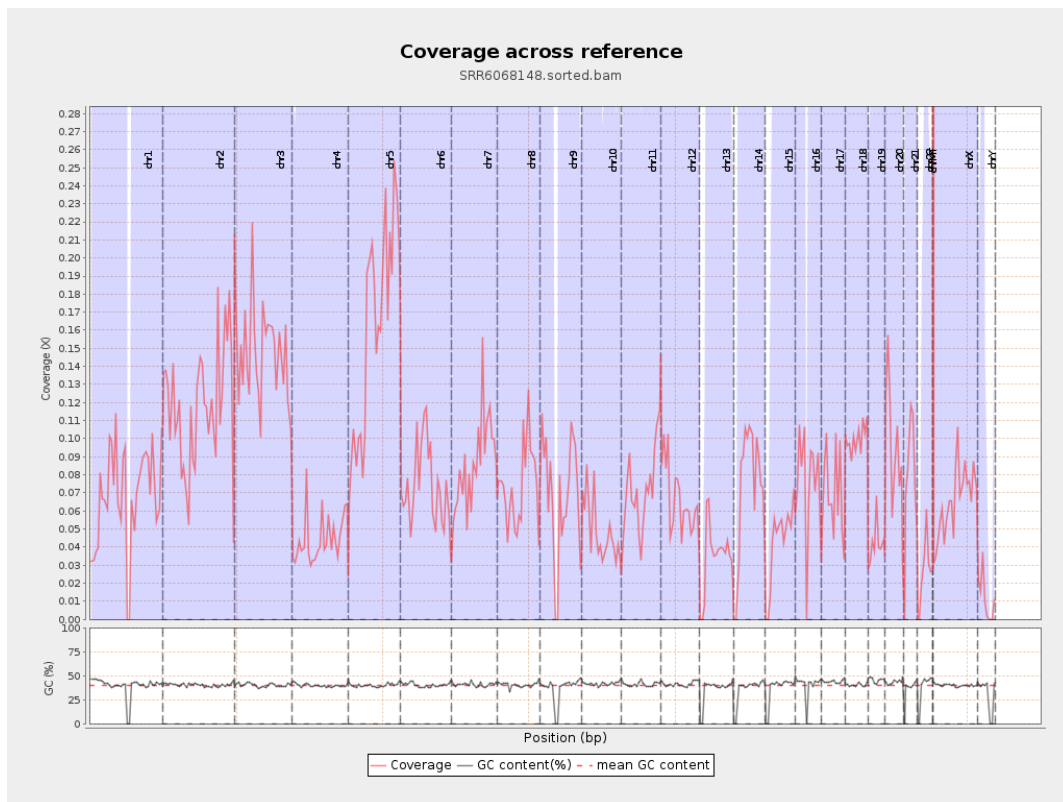
General error rate	0.54%
Mismatches	1,305,062
Insertions	15,908
Mapped reads with at least one insertion	0.42%
Deletions	54,841
Mapped reads with at least one deletion	1.43%
Homopolymer indels	45.76%

2.6. Chromosome stats

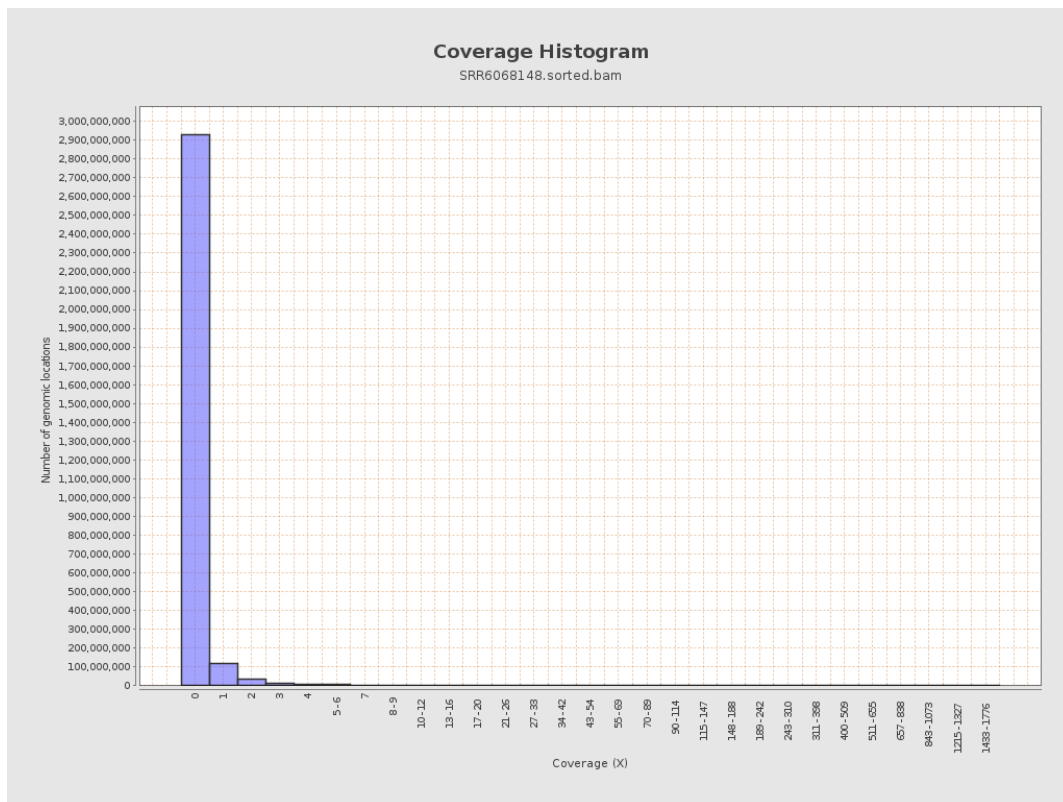
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17187148	0.069	0.9589
chr2	243199373	28603612	0.1176	0.9872
chr3	198022430	29259644	0.1478	0.5367
chr4	191154276	8515304	0.0445	0.3348
chr5	180915260	28959794	0.1601	0.5602
chr6	171115067	12722934	0.0744	0.5073
chr7	159138663	13557222	0.0852	0.5965

chr8	146364022	10703018	0.0731	0.8932
chr9	141213431	9738987	0.069	0.4812
chr10	135534747	6646553	0.049	0.5245
chr11	135006516	9596989	0.0711	0.5376
chr12	133851895	8895901	0.0665	0.3701
chr13	115169878	4070371	0.0353	0.2865
chr14	107349540	7962827	0.0742	0.3885
chr15	102531392	4364697	0.0426	0.3288
chr16	90354753	6763874	0.0749	0.4076
chr17	81195210	5706920	0.0703	0.4237
chr18	78077248	7782595	0.0997	1.0515
chr19	59128983	2518705	0.0426	0.7019
chr20	63025520	6054540	0.0961	0.4408
chr21	48129895	3761077	0.0781	0.4156
chr22	51304566	1387668	0.027	0.2237
chrMT	16571	139894	8.4421	5.8443
chrX	155270560	10078937	0.0649	0.3844
chrY	59373566	697527	0.0117	0.2482

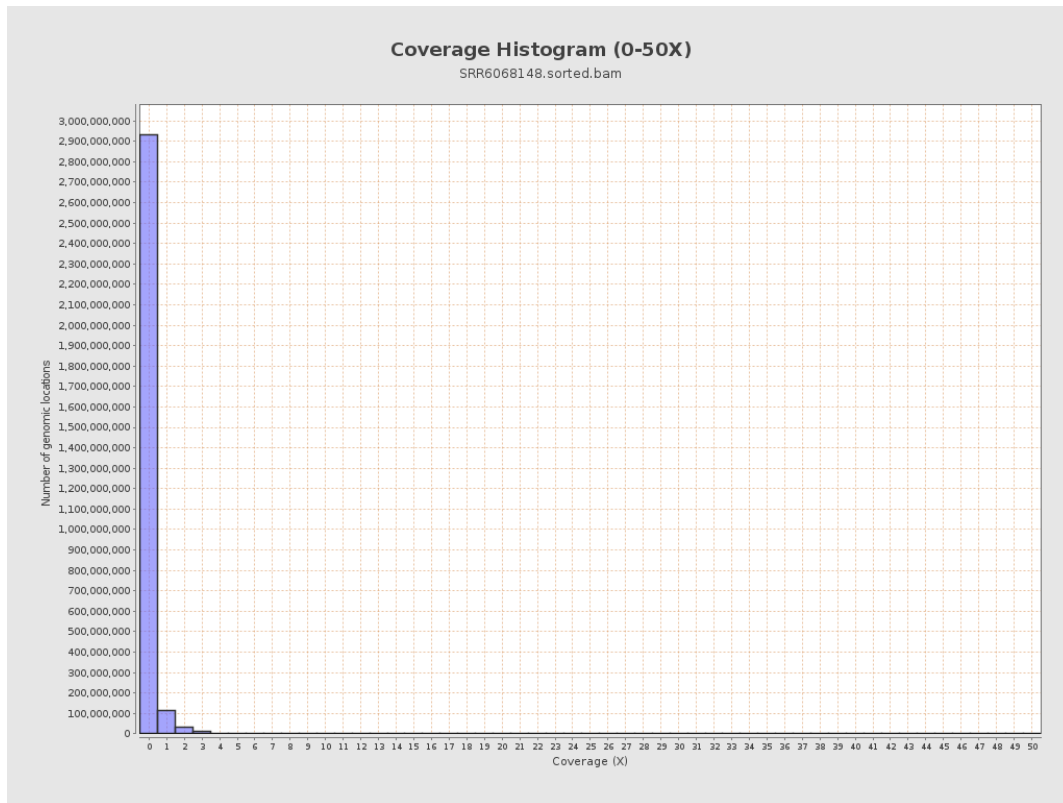
3. Results : Coverage across reference



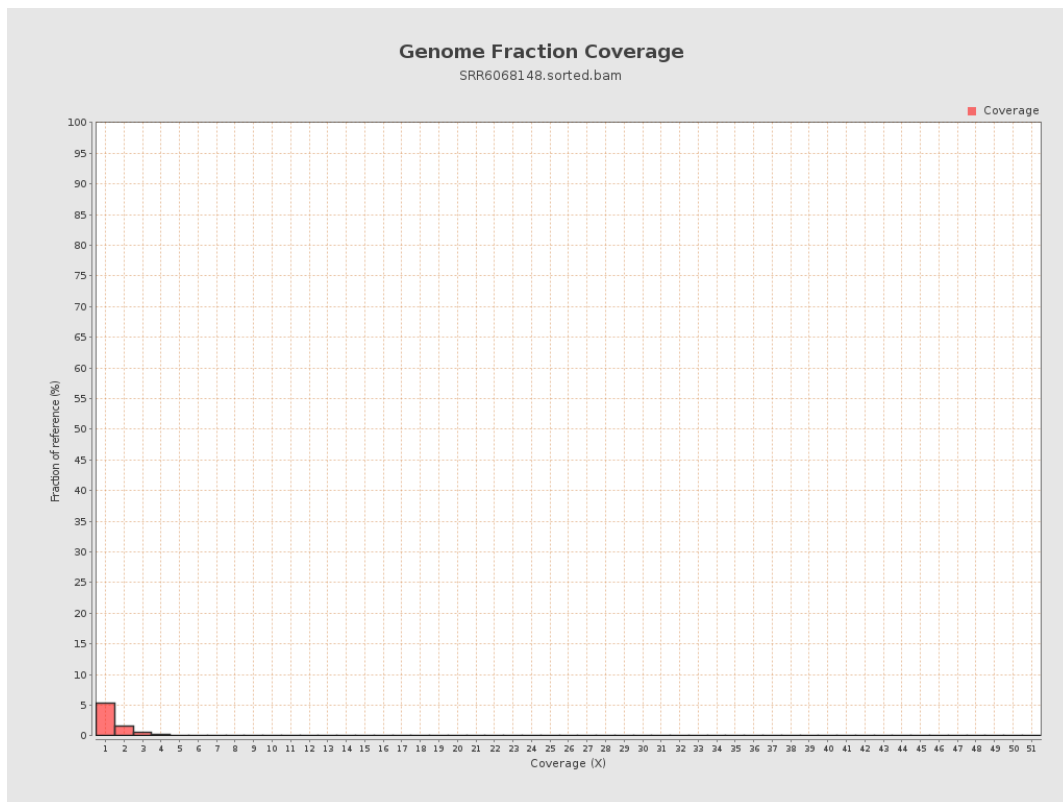
4. Results : Coverage Histogram



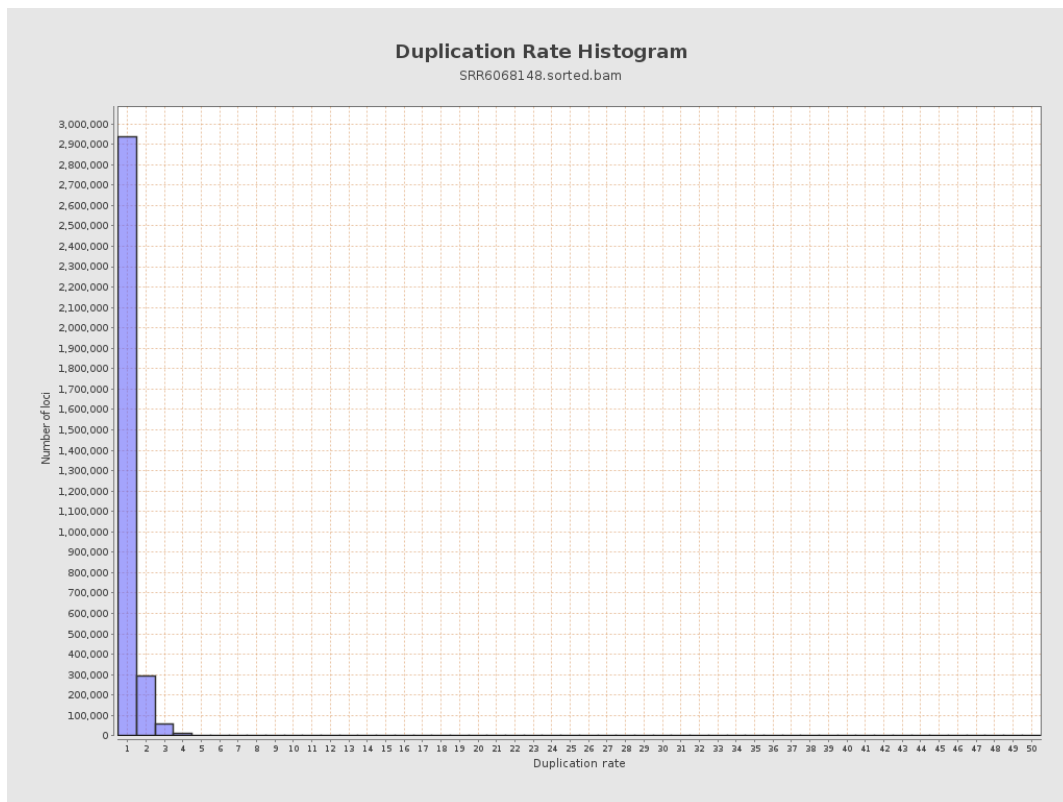
5. Results : Coverage Histogram (0-50X)



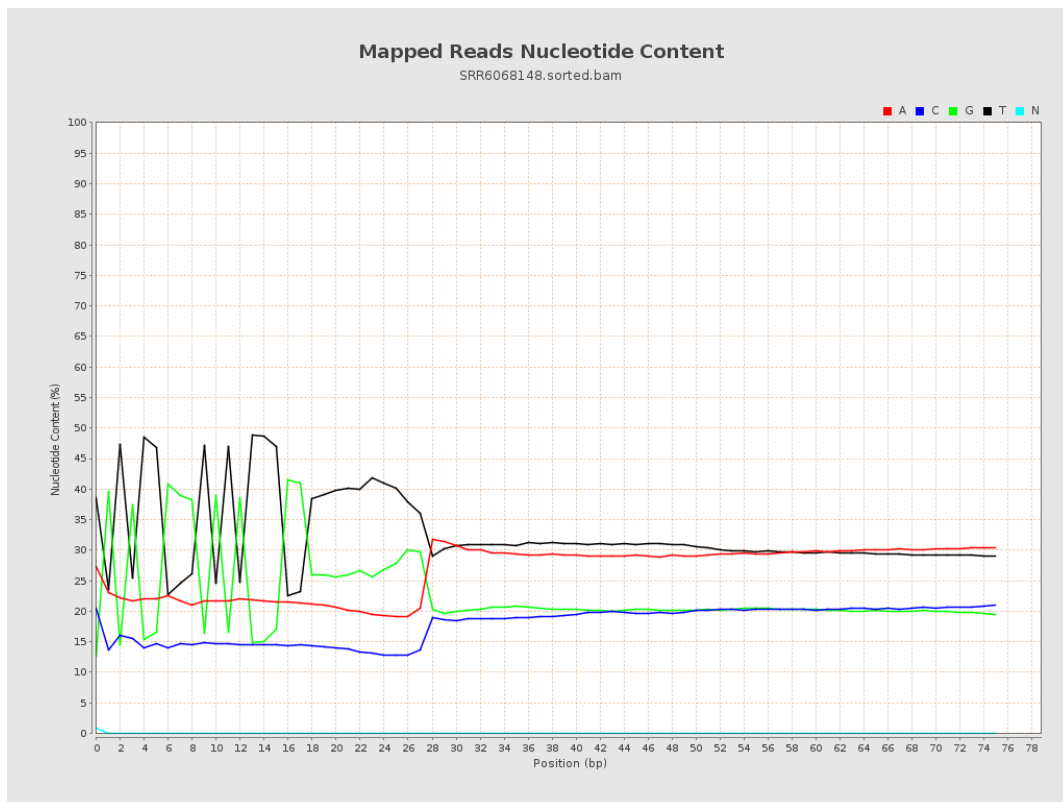
6. Results : Genome Fraction Coverage



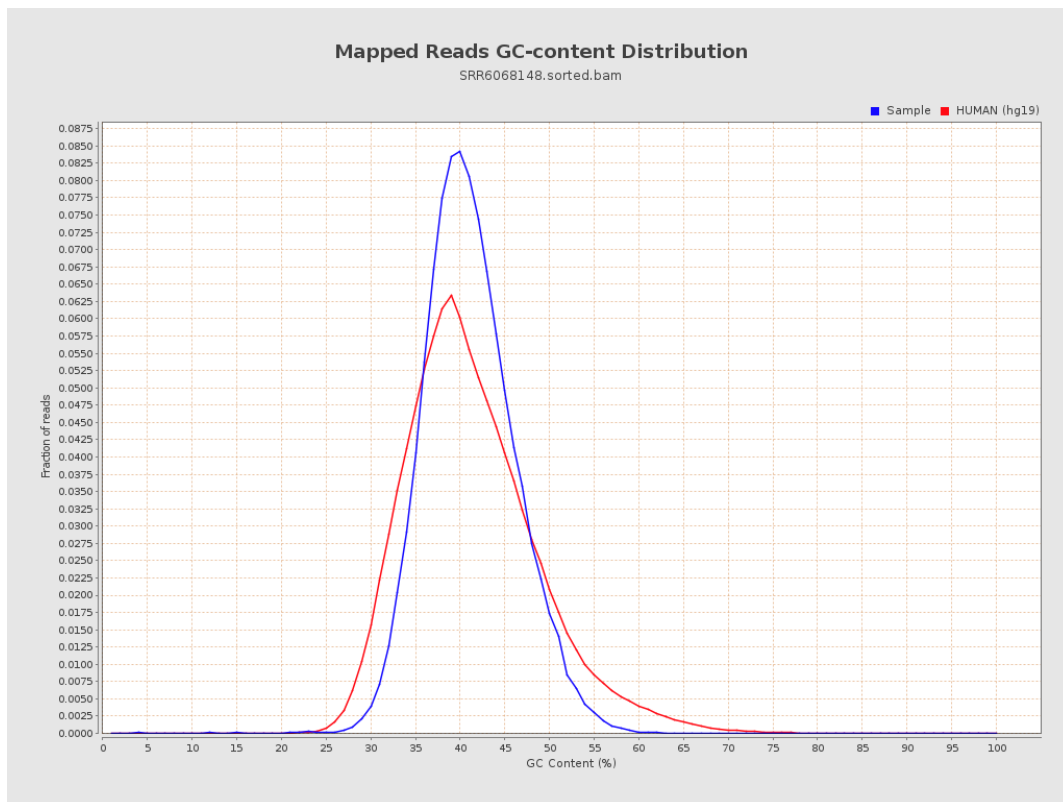
7. Results : Duplication Rate Histogram



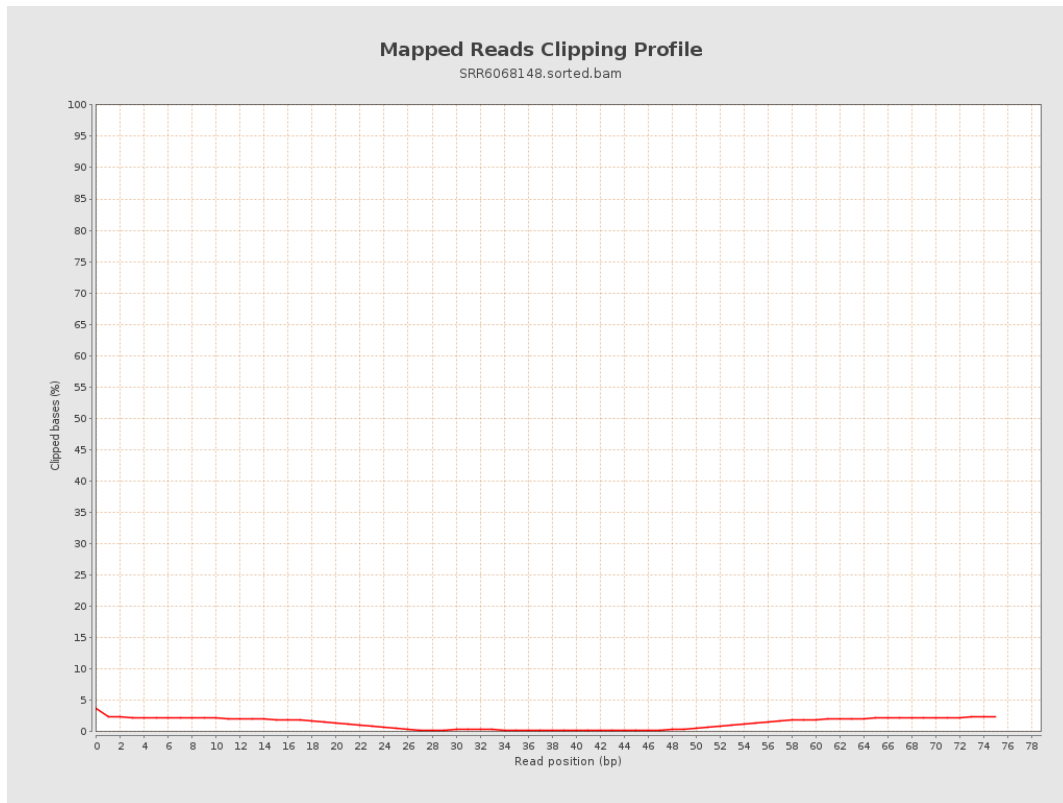
8. Results : Mapped Reads Nucleotide Content



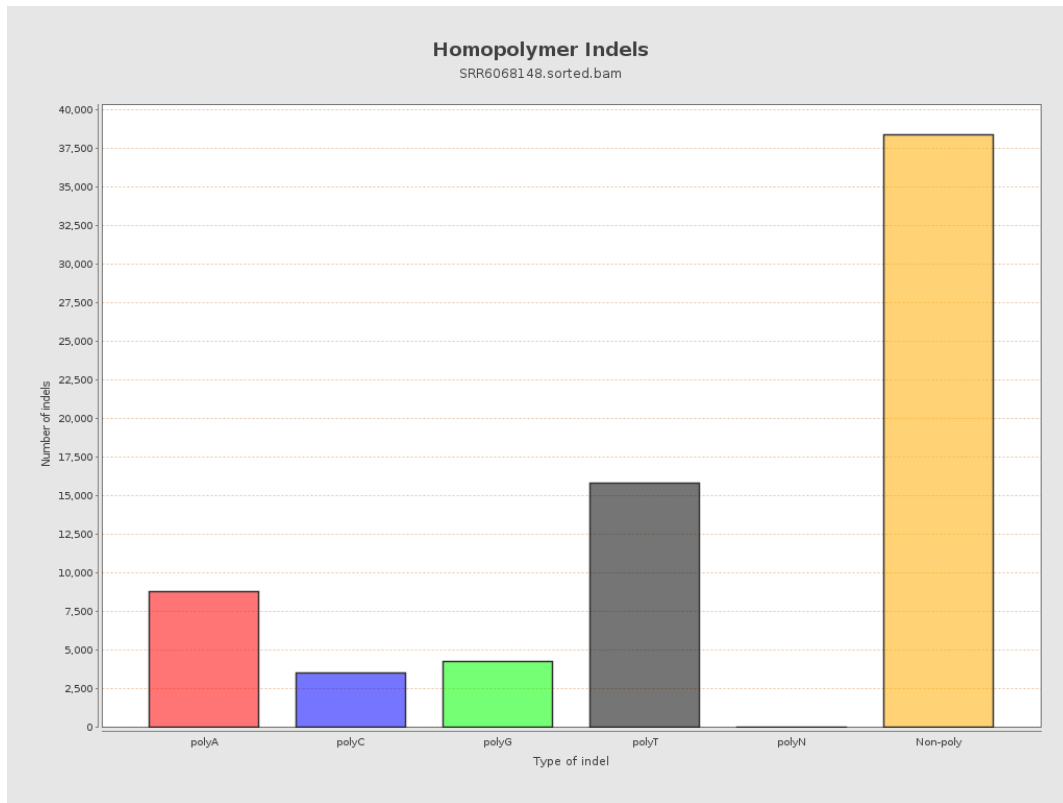
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

