

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:33:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068942.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_SRR6068942 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068942.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:32:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068942.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,171,896
Mapped reads	1,792,920 / 82.55%
Unmapped reads	378,976 / 17.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,969 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	70,580 / 3.25%
Duplication rate	2.92%
Clipped reads	783,331 / 36.07%

2.2. ACGT Content

Number/percentage of A's	33,116,408 / 27.7%
Number/percentage of C's	21,025,847 / 17.59%
Number/percentage of T's	39,489,075 / 33.04%
Number/percentage of G's	25,607,362 / 21.42%
Number/percentage of N's	295,689 / 0.25%
GC Percentage	39.01%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.3722
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2.4. Mapping Quality

Mean Mapping Quality	47.48
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2.5. Mismatches and indels

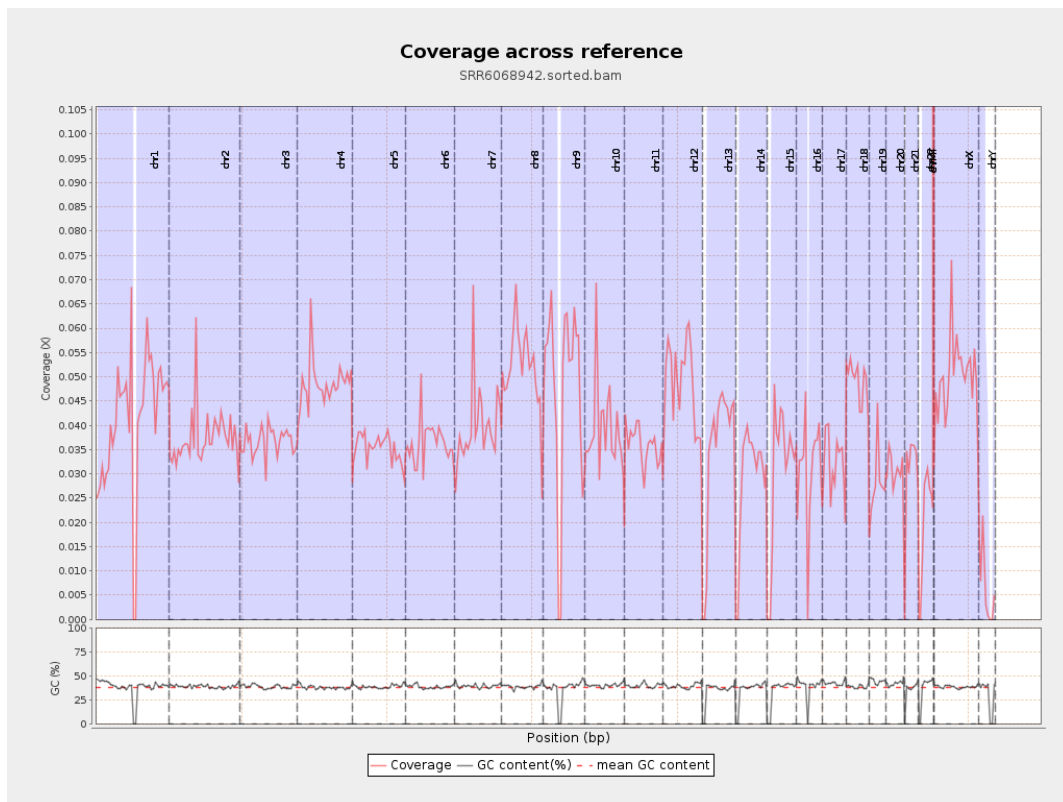
General error rate	1.13%
Mismatches	1,326,908
Insertions	11,348
Mapped reads with at least one insertion	0.63%
Deletions	30,950
Mapped reads with at least one deletion	1.71%
Homopolymer indels	47.87%

2.6. Chromosome stats

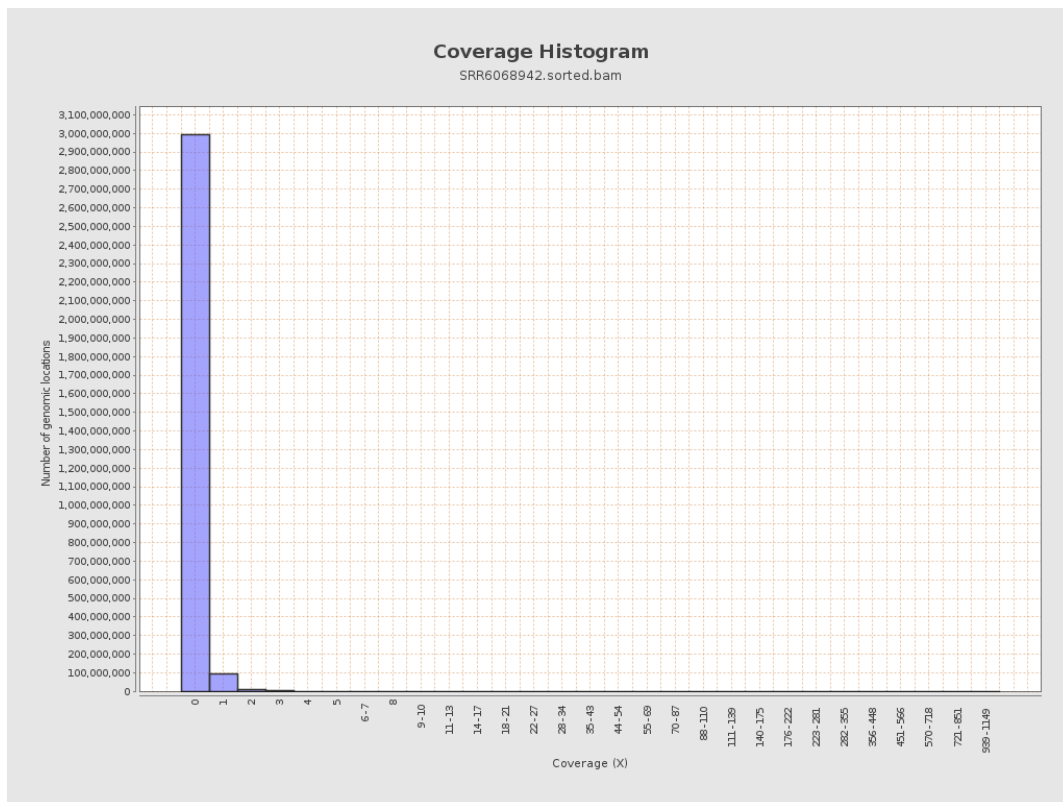
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10296557	0.0413	0.6209
chr2	243199373	9115663	0.0375	0.3699
chr3	198022430	7263404	0.0367	0.2116
chr4	191154276	9267117	0.0485	0.2775
chr5	180915260	6399931	0.0354	0.212
chr6	171115067	6215012	0.0363	0.2626
chr7	159138663	6338826	0.0398	0.4749

chr8	146364022	7595796	0.0519	0.7506
chr9	141213431	6745569	0.0478	0.3738
chr10	135534747	5323499	0.0393	0.3626
chr11	135006516	4820305	0.0357	0.3057
chr12	133851895	6491669	0.0485	0.2498
chr13	115169878	3984025	0.0346	0.2065
chr14	107349540	3111716	0.029	0.2013
chr15	102531392	3160373	0.0308	0.1942
chr16	90354753	2788594	0.0309	0.2257
chr17	81195210	2572666	0.0317	0.2172
chr18	78077248	3835352	0.0491	0.5879
chr19	59128983	1676664	0.0284	0.3936
chr20	63025520	1927485	0.0306	0.2067
chr21	48129895	1454807	0.0302	0.22
chr22	51304566	1002184	0.0195	0.1524
chrMT	16571	61373	3.7036	2.7535
chrX	155270560	7771227	0.05	0.2884
chrY	59373566	366004	0.0062	0.1683

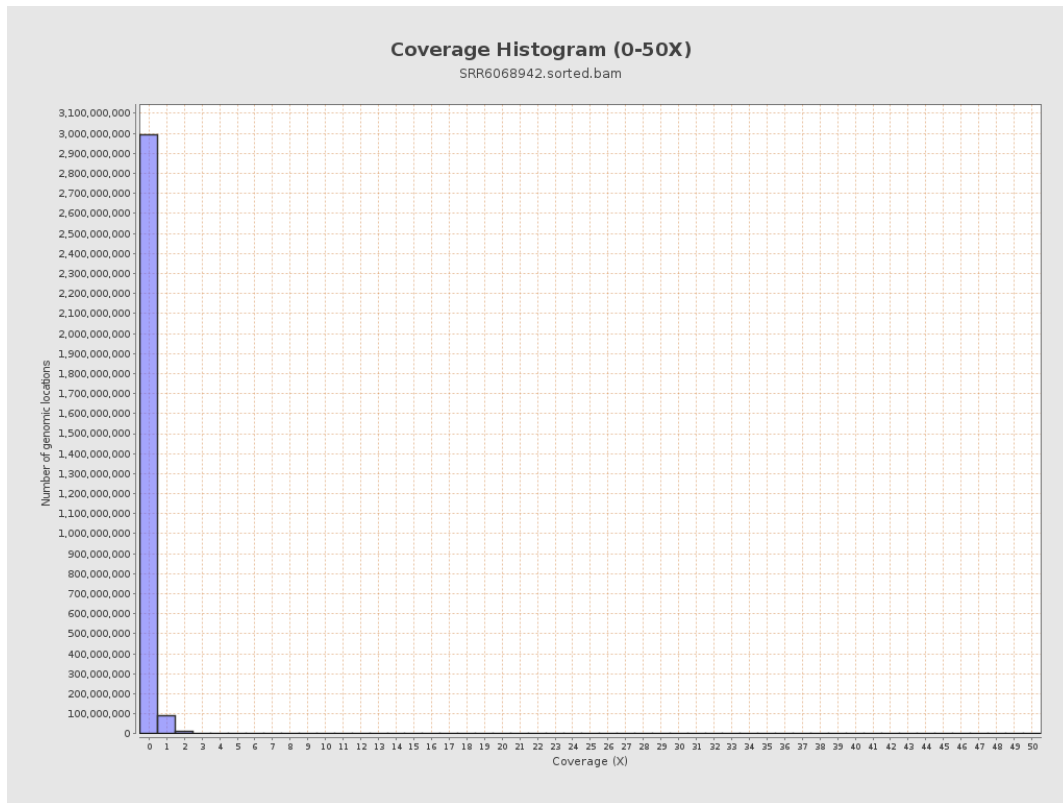
3. Results : Coverage across reference



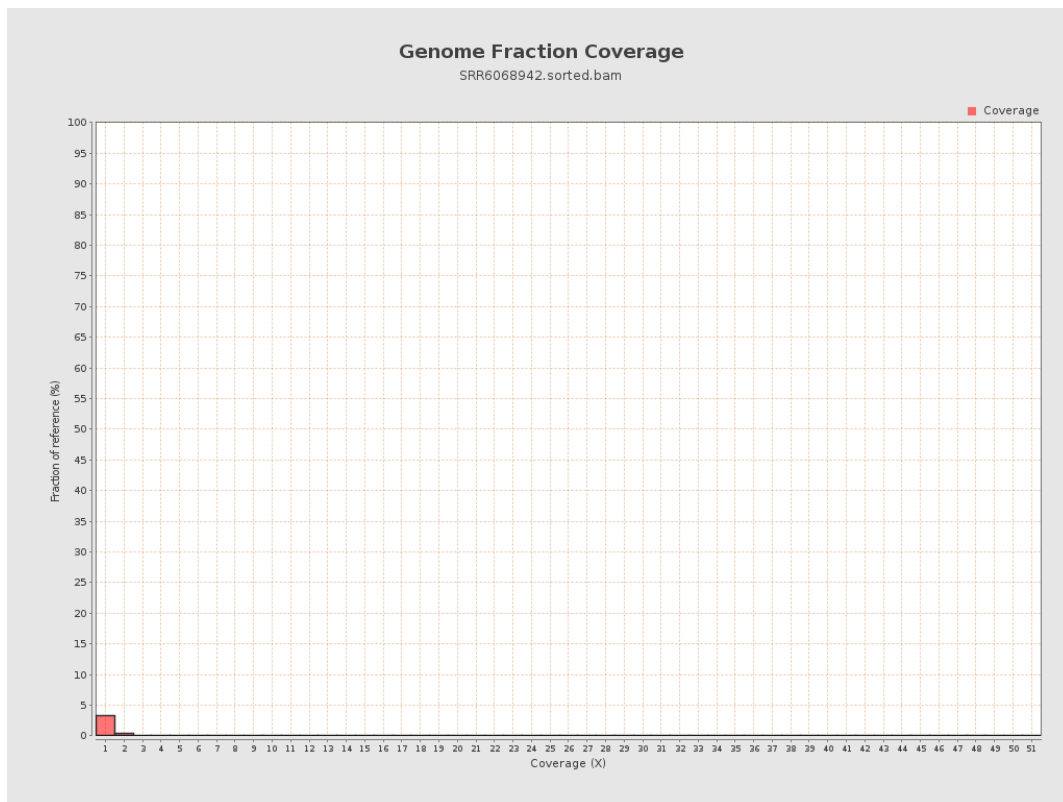
4. Results : Coverage Histogram



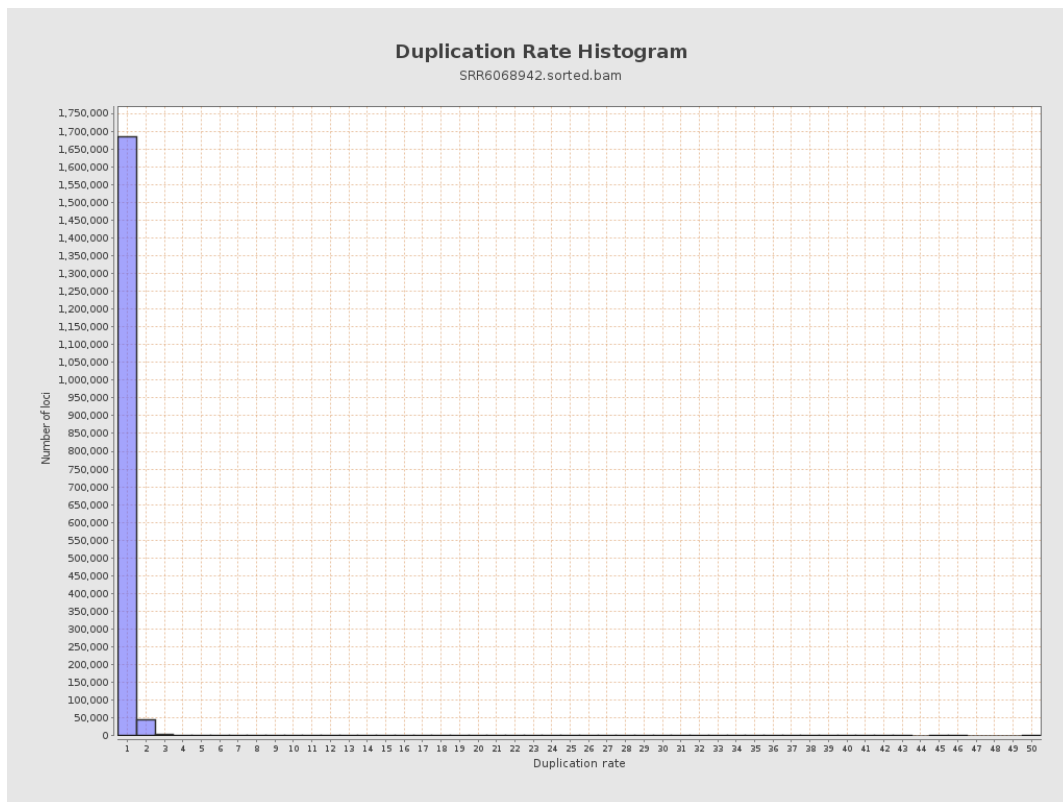
5. Results : Coverage Histogram (0-50X)



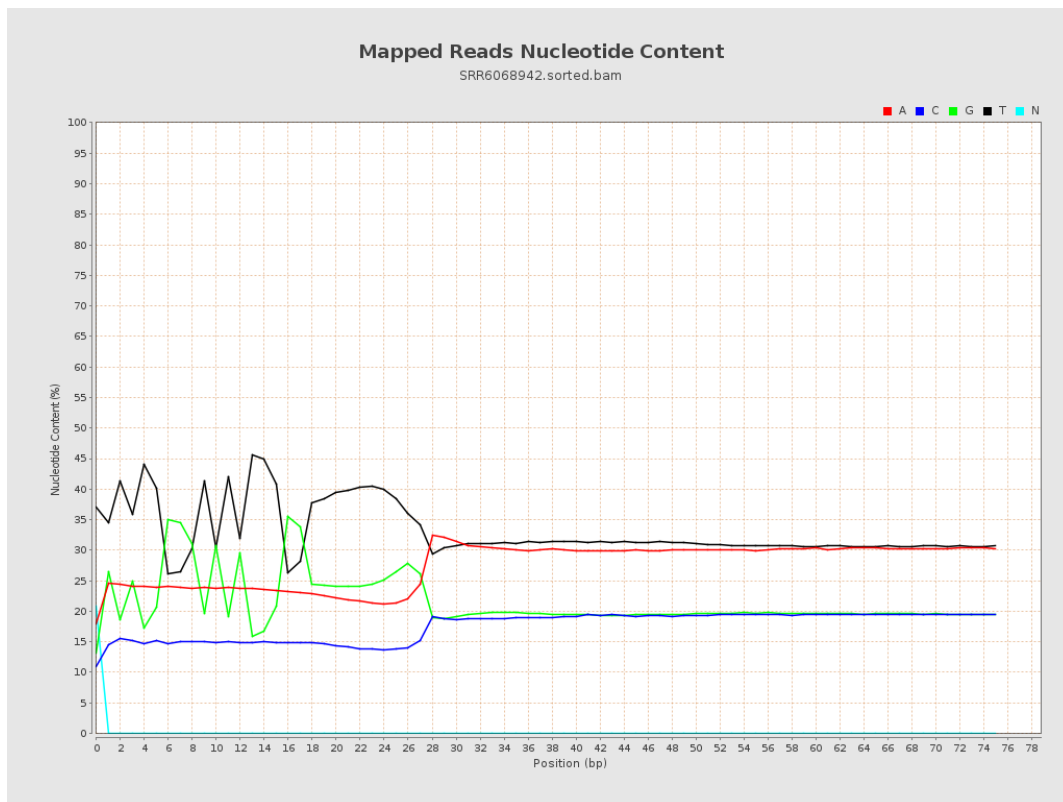
6. Results : Genome Fraction Coverage



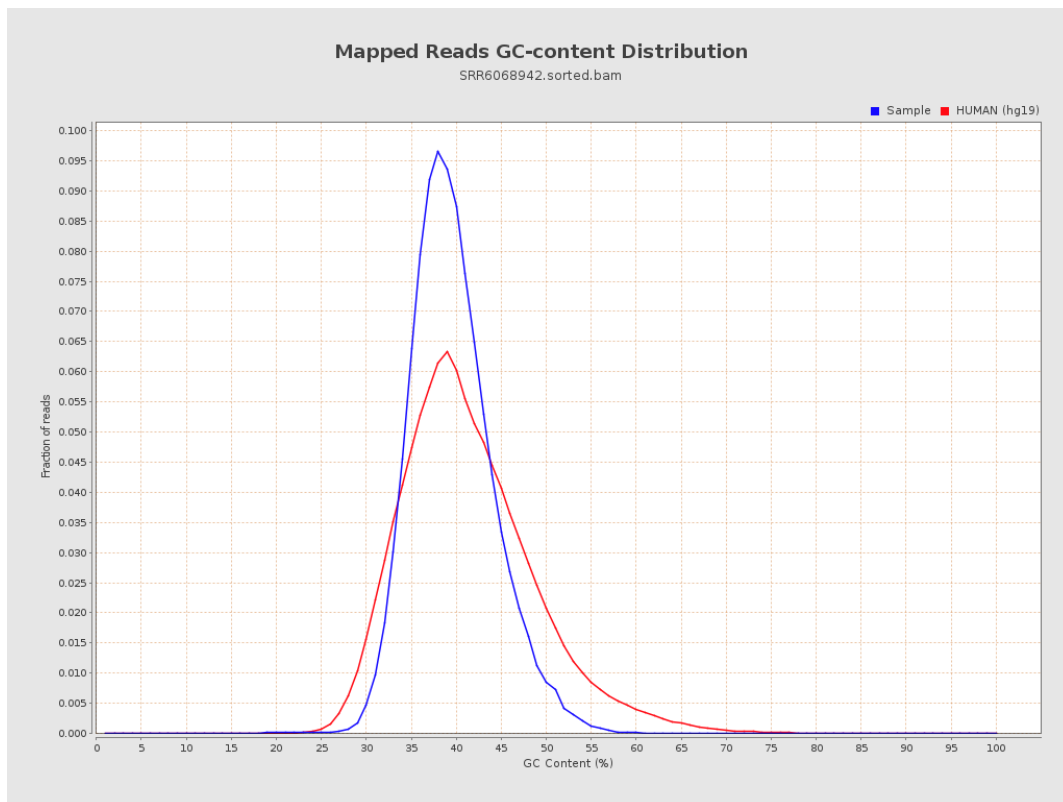
7. Results : Duplication Rate Histogram



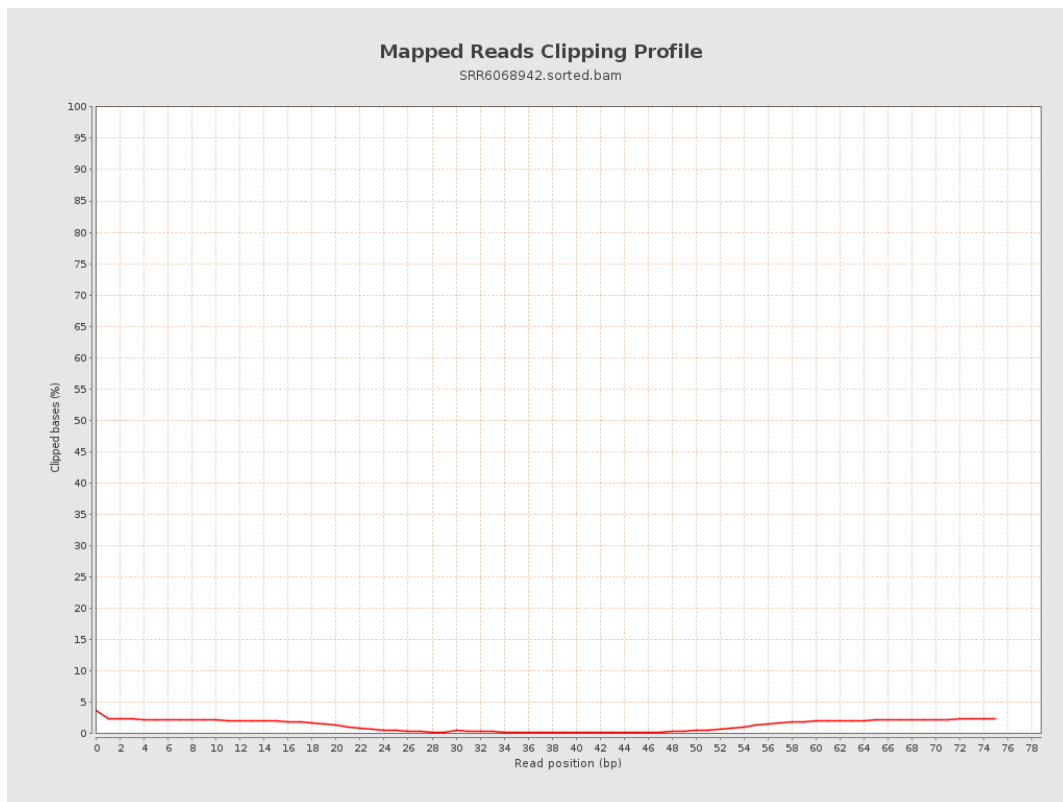
8. Results : Mapped Reads Nucleotide Content



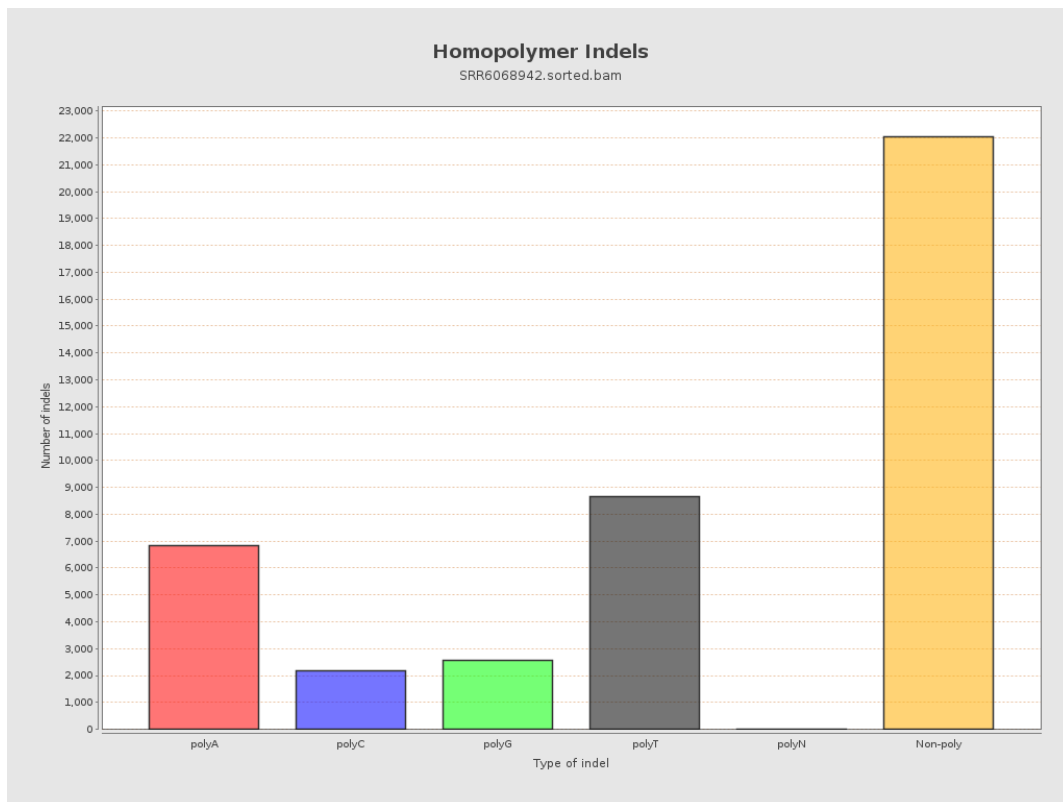
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

