

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:23:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068139.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_SRR6068139 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068139.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:23:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068139.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,681,154
Mapped reads	1,494,438 / 88.89%
Unmapped reads	186,716 / 11.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,138 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	123,589 / 7.35%
Duplication rate	6.55%
Clipped reads	552,044 / 32.84%

2.2. ACGT Content

Number/percentage of A's	29,061,151 / 28.5%
Number/percentage of C's	18,541,738 / 18.18%
Number/percentage of T's	32,788,945 / 32.15%
Number/percentage of G's	21,522,299 / 21.11%
Number/percentage of N's	60,814 / 0.06%
GC Percentage	39.29%

2.3. Coverage

Mean	0.033

Standard Deviation	0.3954
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2.4. Mapping Quality

Mean Mapping Quality	44.75
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2.5. Mismatches and indels

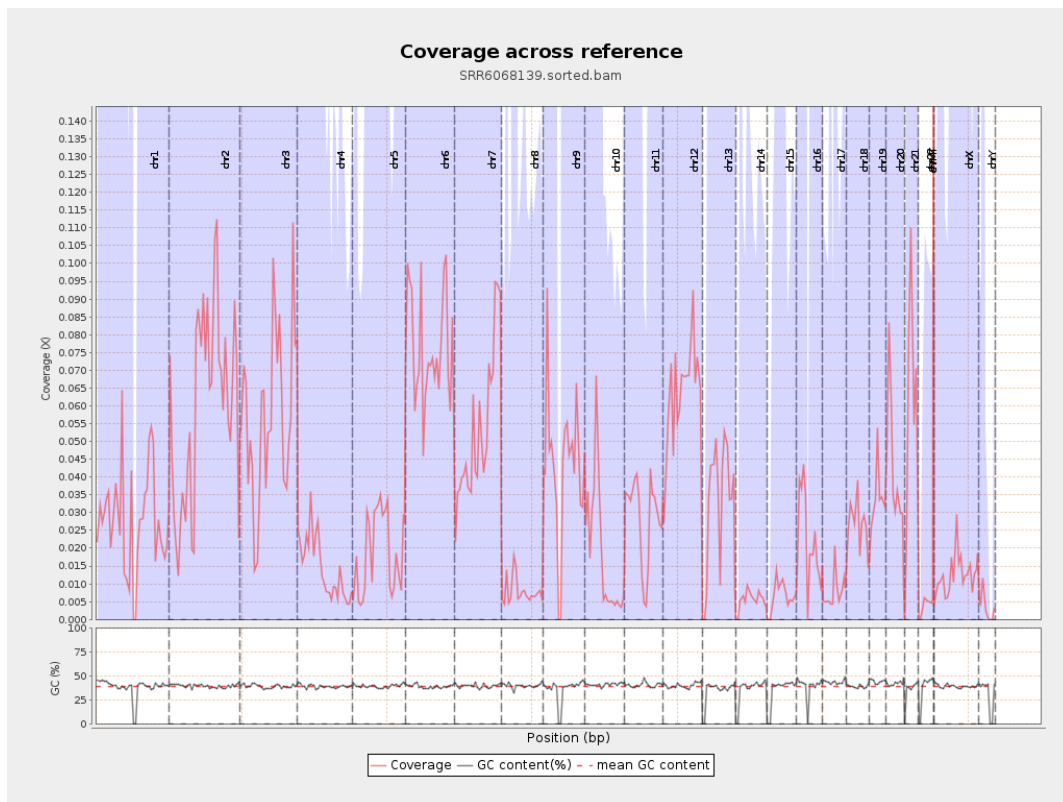
General error rate	0.87%
Mismatches	869,360
Insertions	7,887
Mapped reads with at least one insertion	0.52%
Deletions	27,783
Mapped reads with at least one deletion	1.84%
Homopolymer indels	47.71%

2.6. Chromosome stats

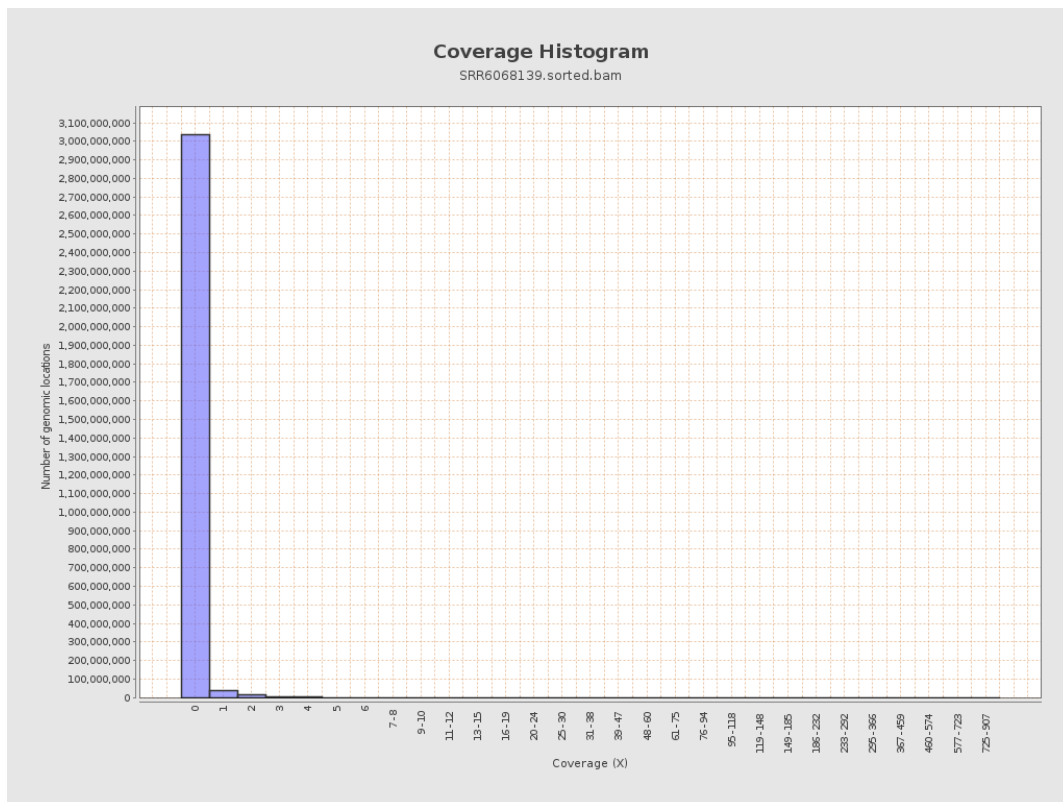
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6918887	0.0278	0.7532
chr2	243199373	14466612	0.0595	0.5116
chr3	198022430	11466421	0.0579	0.3576
chr4	191154276	2747179	0.0144	0.1973
chr5	180915260	3398469	0.0188	0.2038
chr6	171115067	12936186	0.0756	0.518
chr7	159138663	8616991	0.0541	0.4654

chr8	146364022	1157218	0.0079	0.3327
chr9	141213431	6105475	0.0432	0.3855
chr10	135534747	2450431	0.0181	0.3848
chr11	135006516	3804268	0.0282	0.3125
chr12	133851895	8446358	0.0631	0.3904
chr13	115169878	3718827	0.0323	0.2731
chr14	107349540	596078	0.0056	0.1246
chr15	102531392	674374	0.0066	0.1203
chr16	90354753	2024121	0.0224	0.2311
chr17	81195210	647670	0.008	0.136
chr18	78077248	2098748	0.0269	0.4207
chr19	59128983	2009258	0.034	0.4865
chr20	63025520	2683188	0.0426	0.3258
chr21	48129895	2761052	0.0574	0.3737
chr22	51304566	192533	0.0038	0.0814
chrMT	16571	4060	0.245	0.6553
chrX	155270560	1901703	0.0122	0.1872
chrY	59373566	194693	0.0033	0.1199

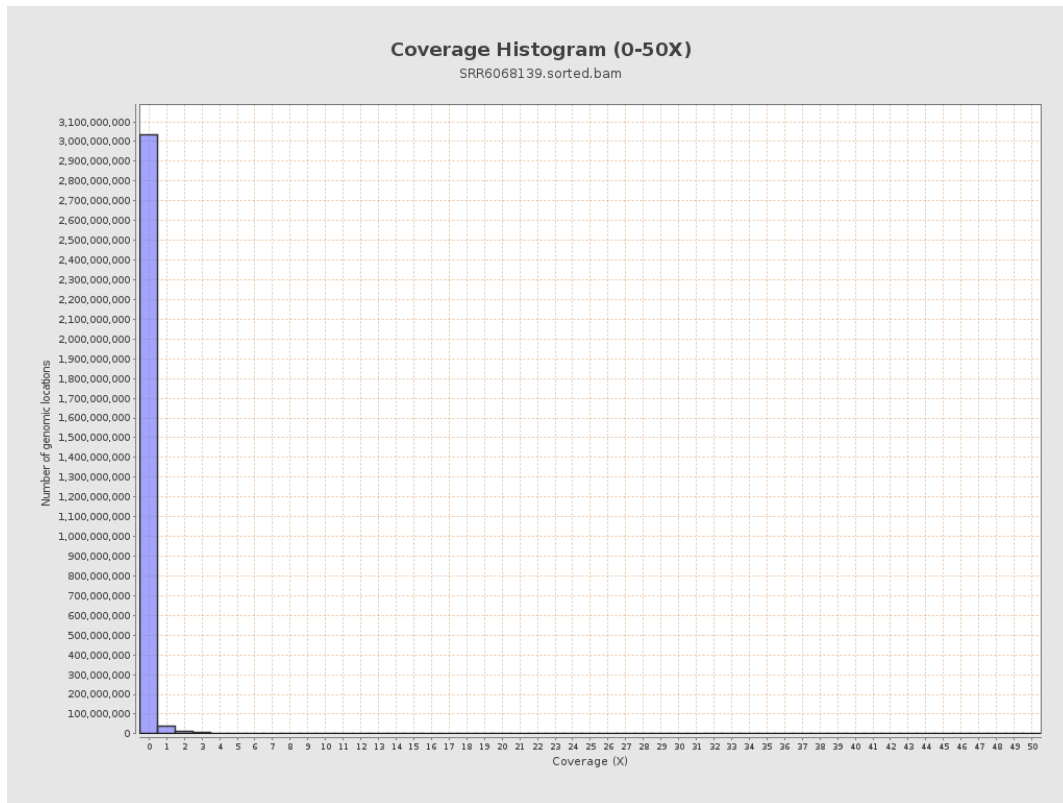
3. Results : Coverage across reference



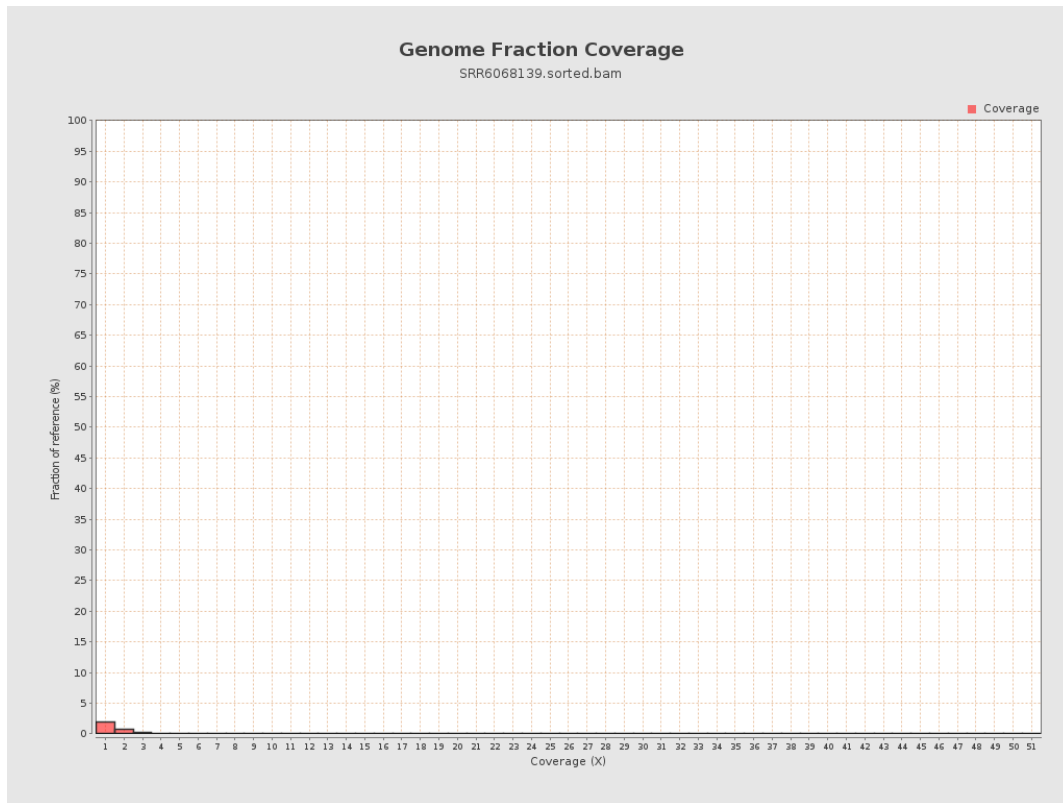
4. Results : Coverage Histogram



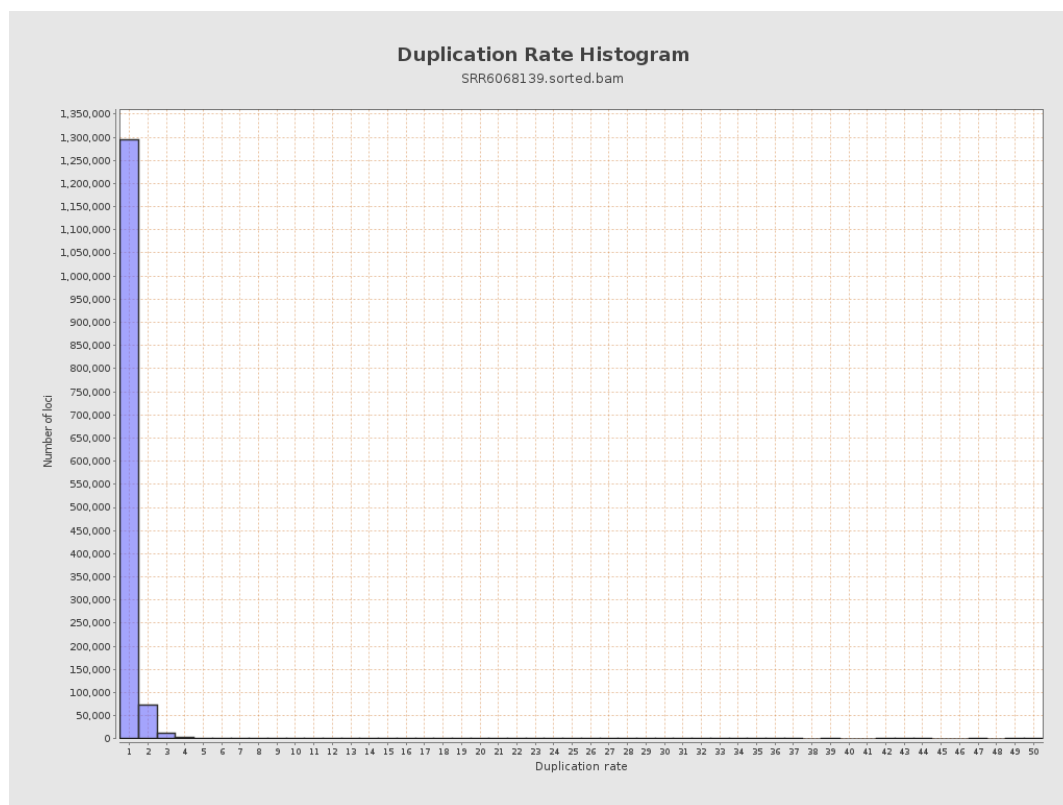
5. Results : Coverage Histogram (0-50X)



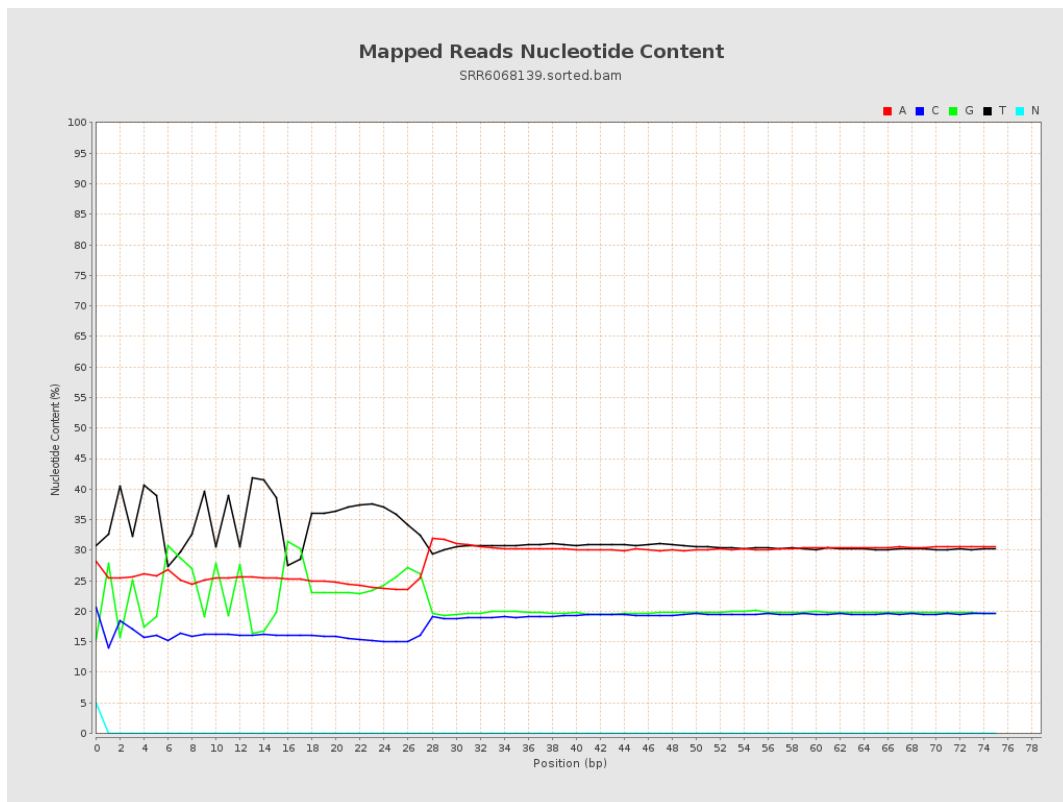
6. Results : Genome Fraction Coverage



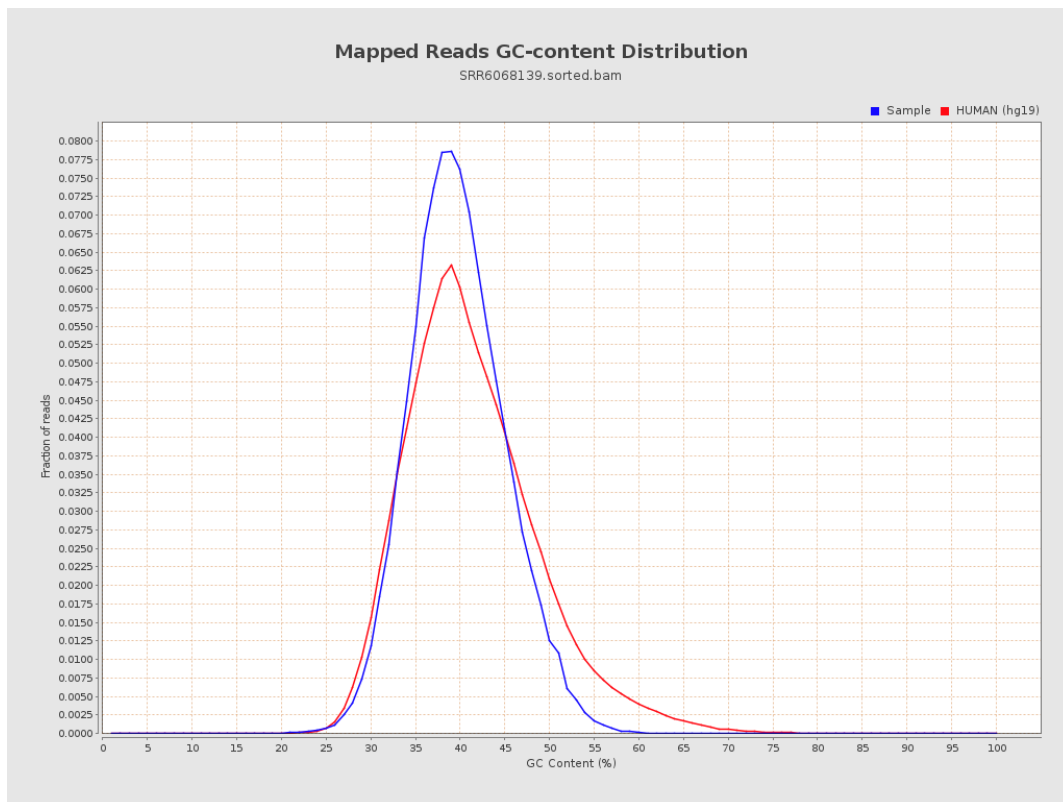
7. Results : Duplication Rate Histogram



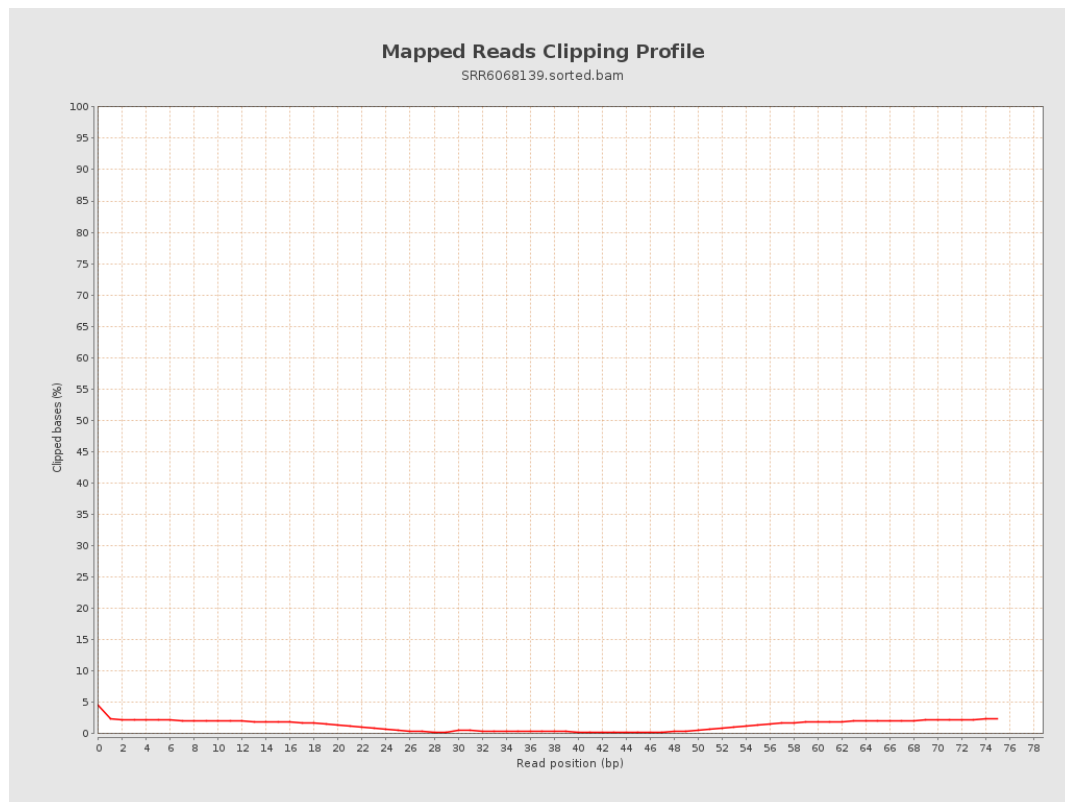
8. Results : Mapped Reads Nucleotide Content



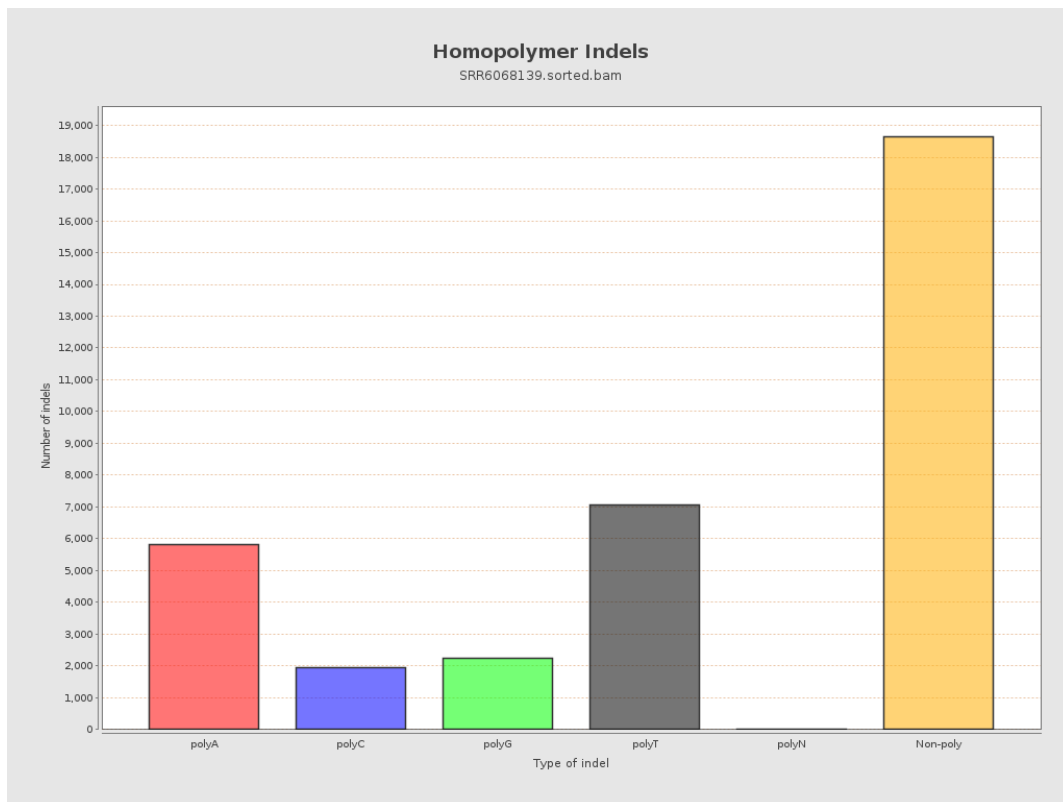
9. Results : Mapped Reads GC-content Distribution



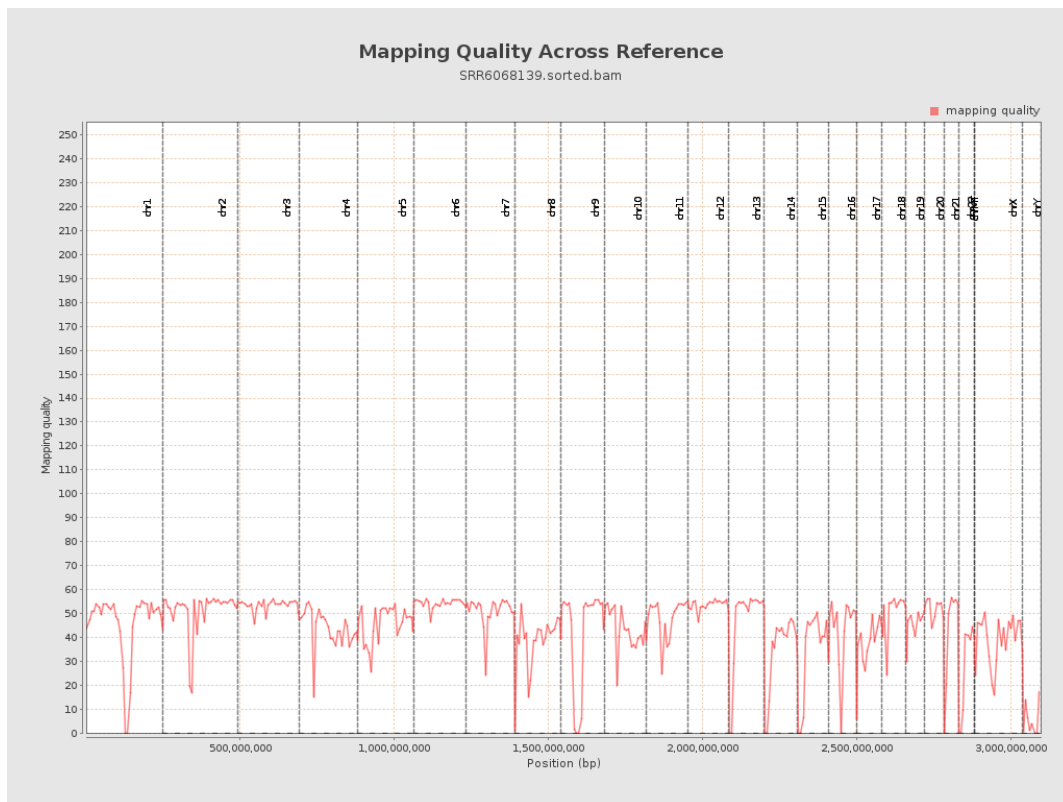
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

