

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:15:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068120.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_SRR6068120 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068120.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:15:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,593,841
Mapped reads	960,580 / 60.27%
Unmapped reads	633,261 / 39.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,887 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	161,360 / 10.12%
Duplication rate	11.7%
Clipped reads	425,643 / 26.71%

2.2. ACGT Content

Number/percentage of A's	17,705,222 / 27.81%
Number/percentage of C's	11,519,940 / 18.09%
Number/percentage of T's	20,500,520 / 32.2%
Number/percentage of G's	13,884,614 / 21.81%
Number/percentage of N's	63,079 / 0.1%
GC Percentage	39.9%

2.3. Coverage

Mean	0.0206

Standard Deviation	0.3679
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2.4. Mapping Quality

Mean Mapping Quality	46.53
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2.5. Mismatches and indels

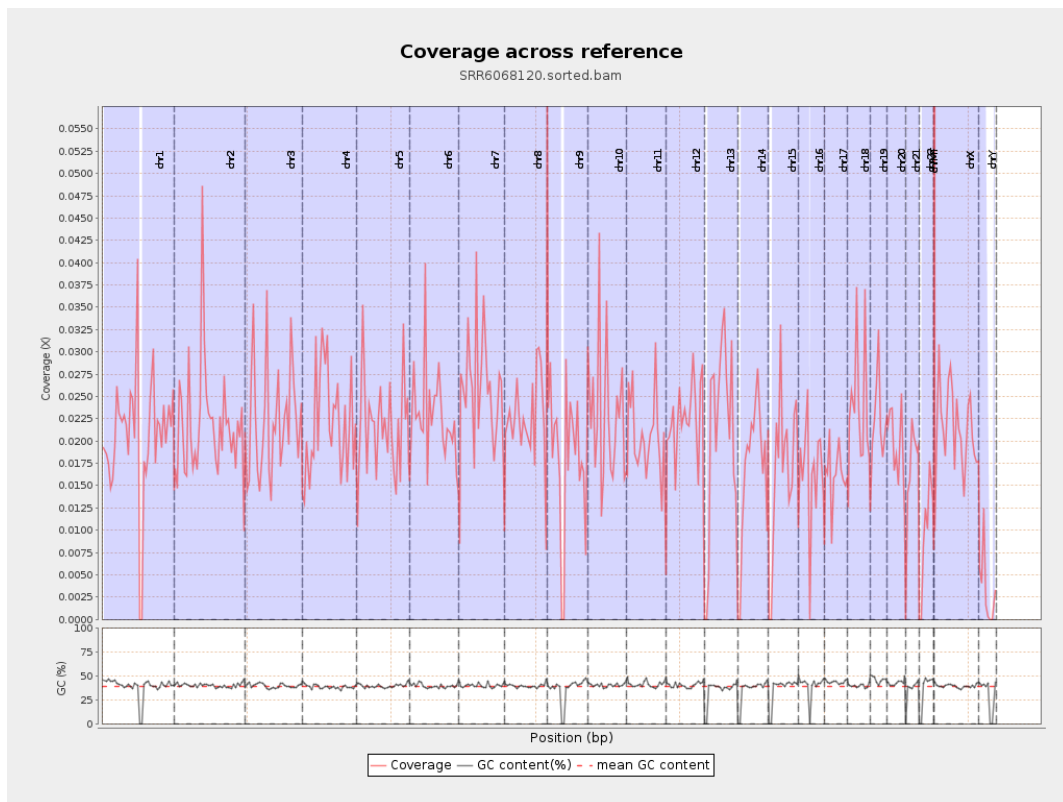
General error rate	0.89%
Mismatches	558,919
Insertions	5,255
Mapped reads with at least one insertion	0.54%
Deletions	14,555
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.84%

2.6. Chromosome stats

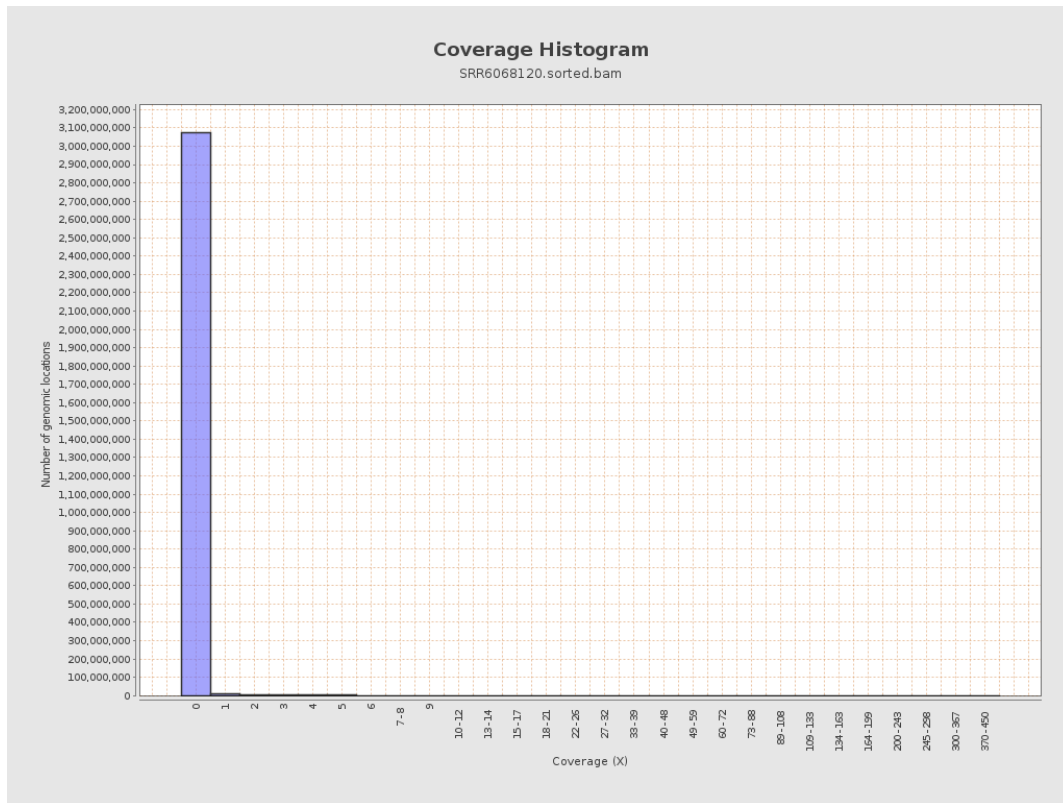
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5086381	0.0204	0.5019
chr2	243199373	5334555	0.0219	0.3934
chr3	198022430	4397847	0.0222	0.3382
chr4	191154276	4200135	0.022	0.3612
chr5	180915260	3965074	0.0219	0.3377
chr6	171115067	3878187	0.0227	0.3544
chr7	159138663	4106705	0.0258	0.4551

chr8	146364022	3283462	0.0224	0.4223
chr9	141213431	2589140	0.0183	0.3249
chr10	135534747	3057087	0.0226	0.38
chr11	135006516	2790920	0.0207	0.3348
chr12	133851895	3014931	0.0225	0.3476
chr13	115169878	2399060	0.0208	0.3413
chr14	107349540	1794770	0.0167	0.2919
chr15	102531392	1735158	0.0169	0.3271
chr16	90354753	1443569	0.016	0.2816
chr17	81195210	1324157	0.0163	0.287
chr18	78077248	1881636	0.0241	0.4403
chr19	59128983	1335890	0.0226	0.4056
chr20	63025520	1229505	0.0195	0.3209
chr21	48129895	803510	0.0167	0.2919
chr22	51304566	496044	0.0097	0.2094
chrMT	16571	17858	1.0777	2.1107
chrX	155270560	3334094	0.0215	0.3384
chrY	59373566	197484	0.0033	0.1318

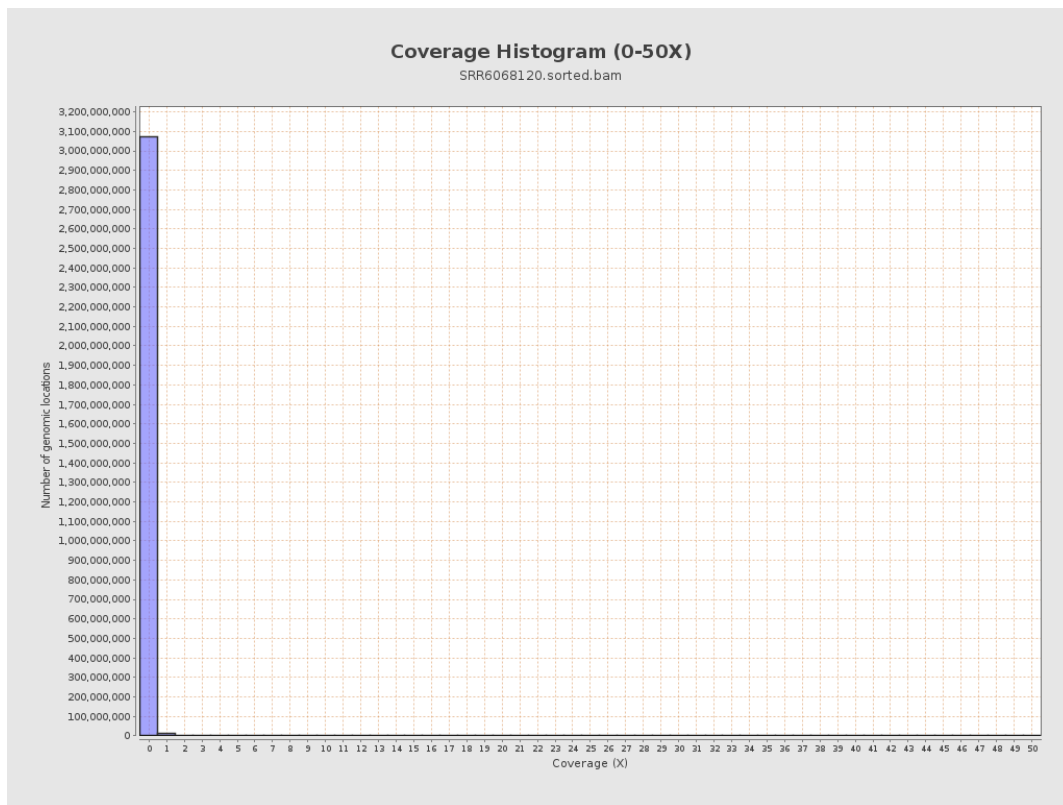
3. Results : Coverage across reference



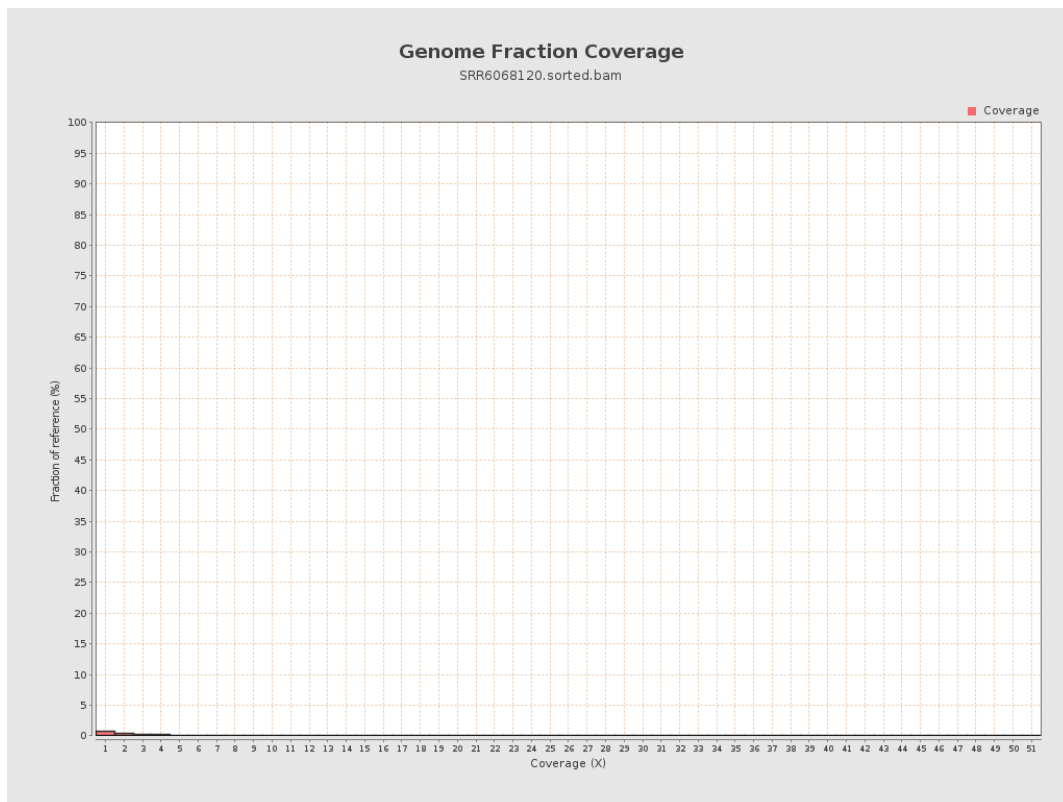
4. Results : Coverage Histogram



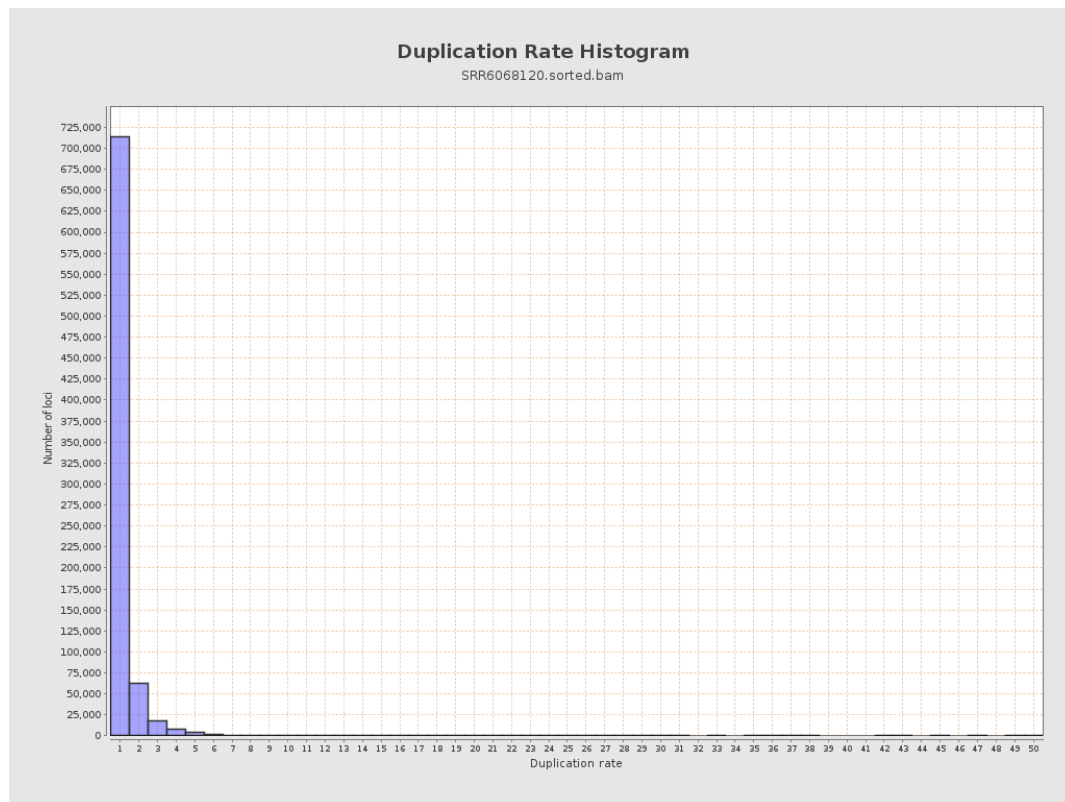
5. Results : Coverage Histogram (0-50X)



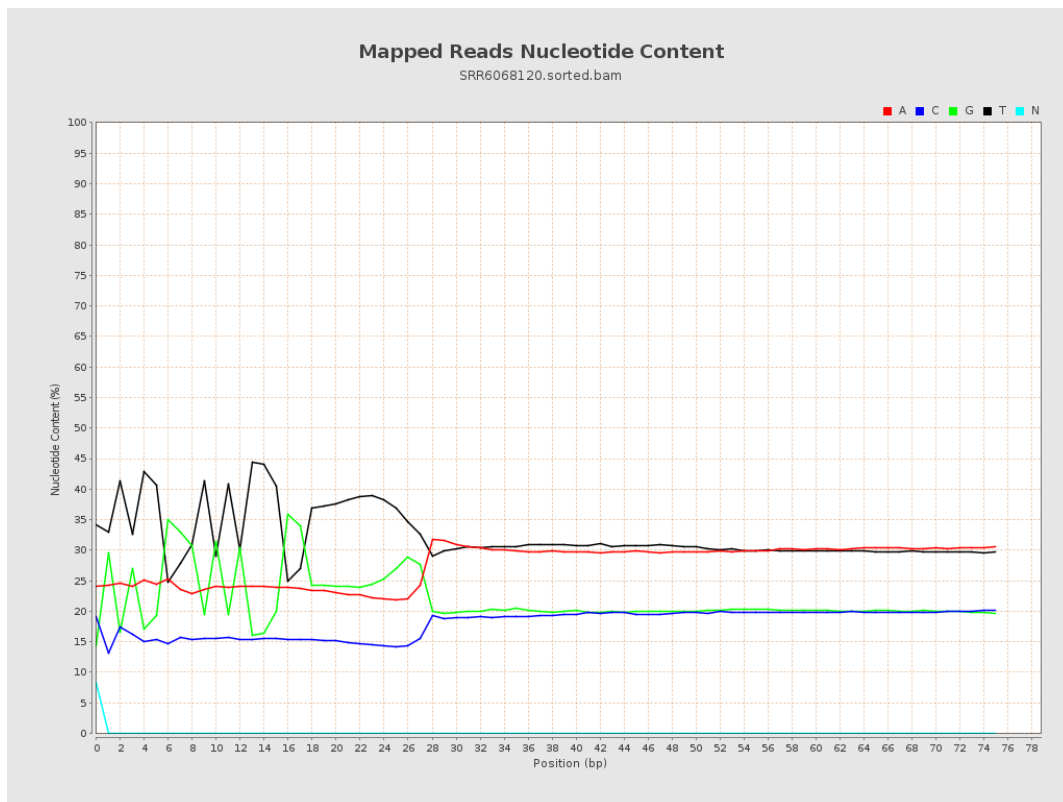
6. Results : Genome Fraction Coverage



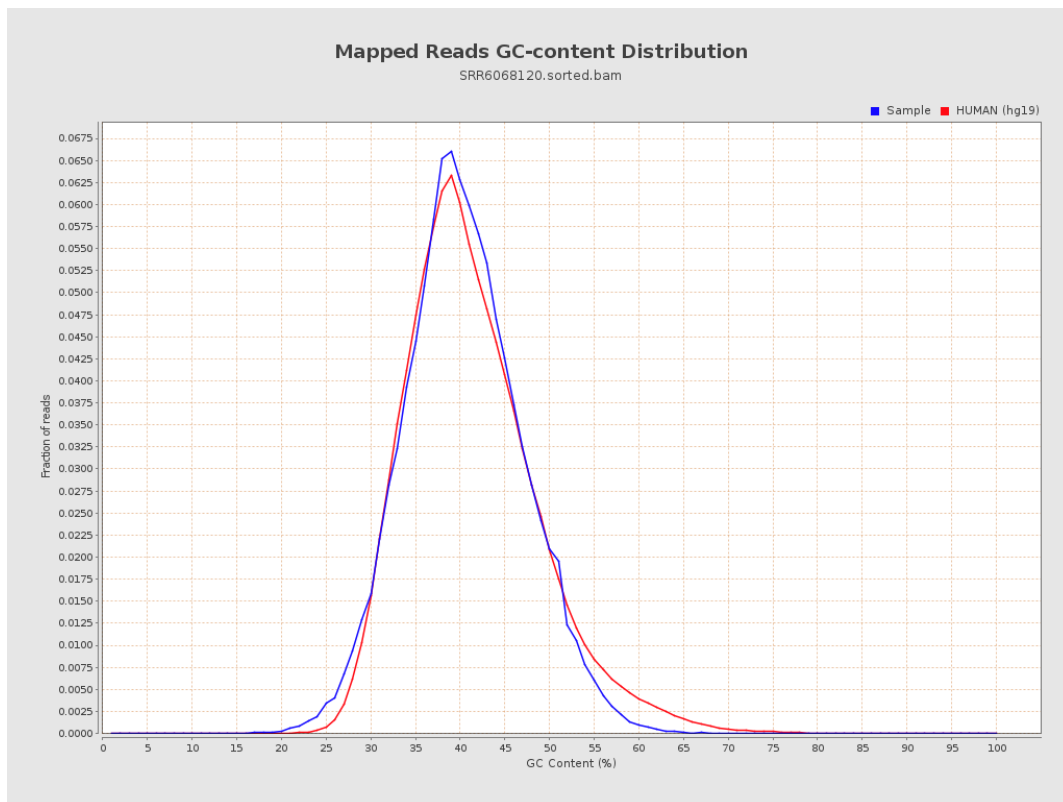
7. Results : Duplication Rate Histogram



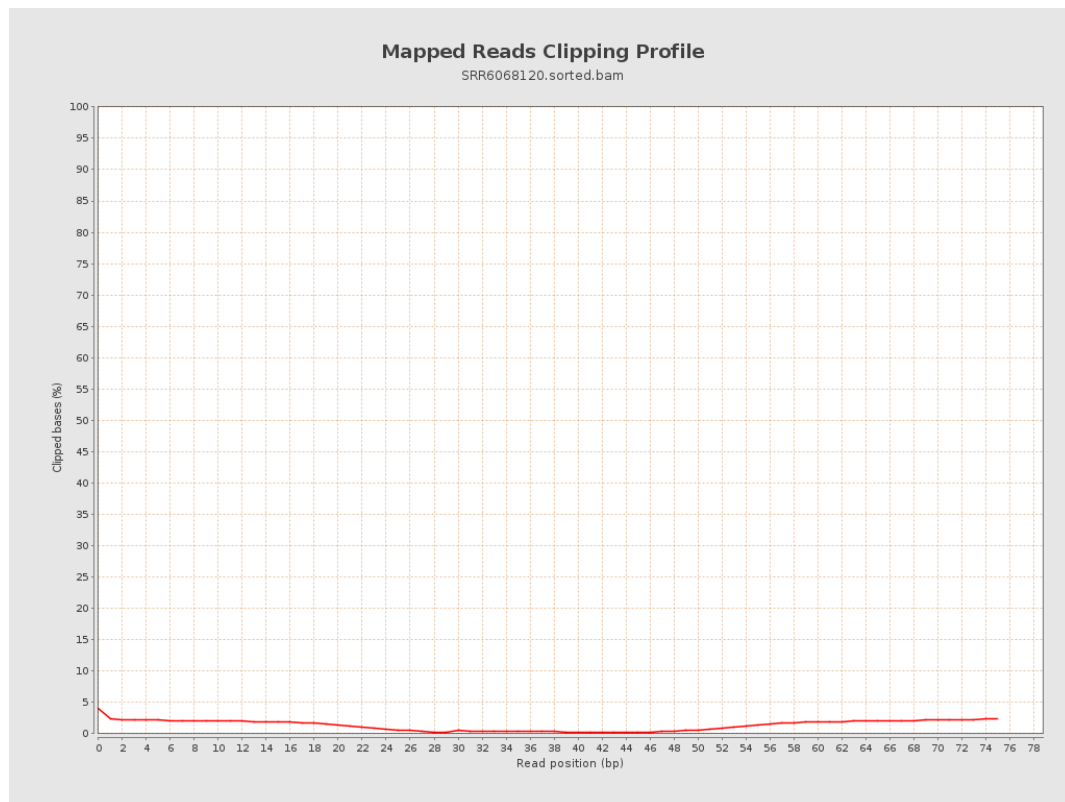
8. Results : Mapped Reads Nucleotide Content



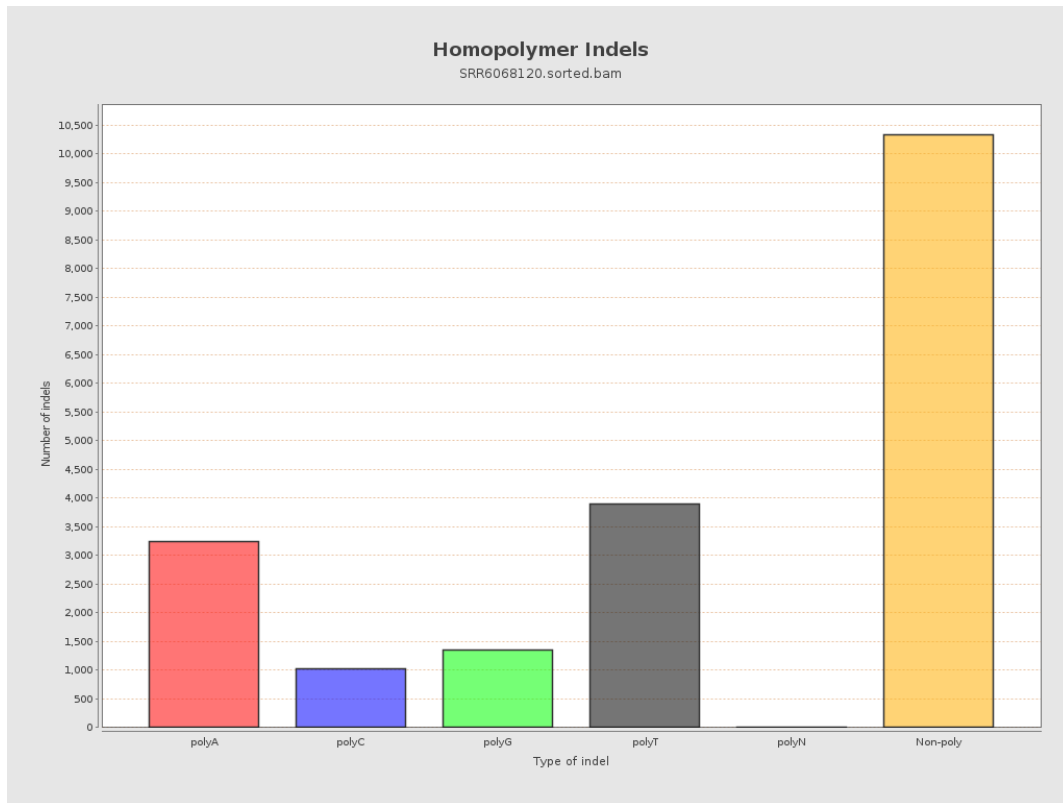
9. Results : Mapped Reads GC-content Distribution



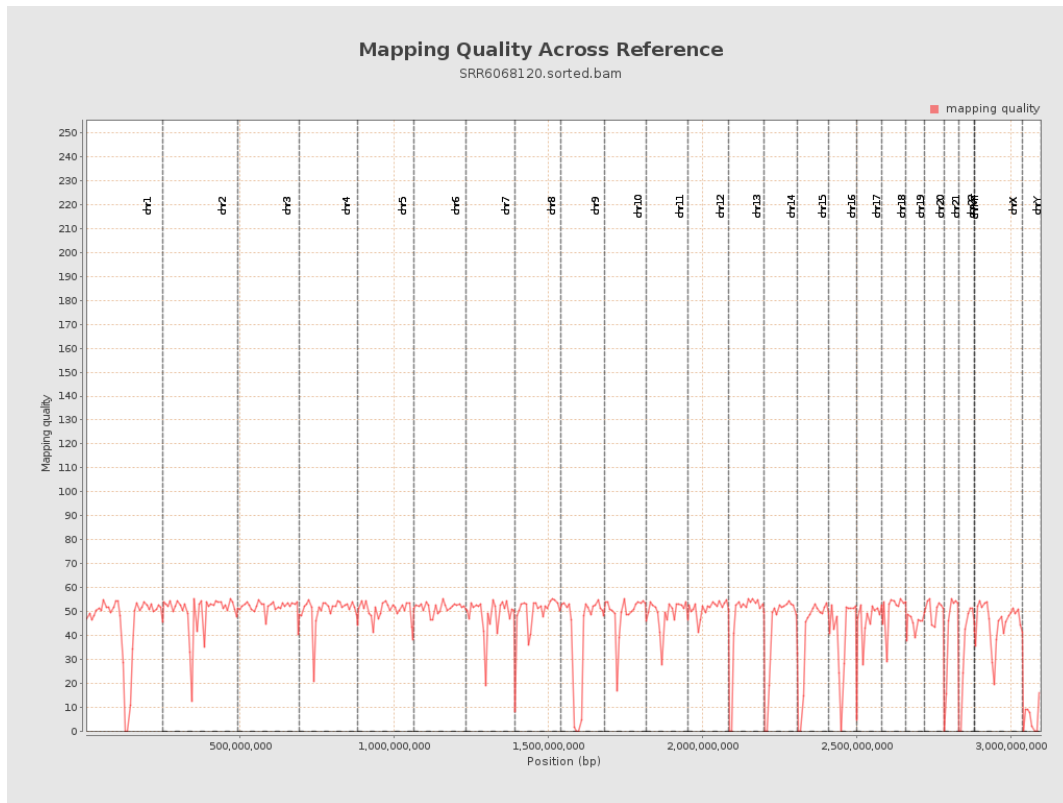
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

