

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:34:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006038.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_SRR1006038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006038_1.fastq.gz SRR1006038_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:33:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,467,438
Mapped reads	8,434,324 / 73.55%
Unmapped reads	3,033,114 / 26.45%
Mapped paired reads	8,434,324 / 73.55%
Mapped reads, first in pair	4,237,256 / 36.95%
Mapped reads, second in pair	4,197,068 / 36.6%
Mapped reads, both in pair	7,604,372 / 66.31%
Mapped reads, singletons	829,952 / 7.24%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	367,104 / 3.2%
Duplication rate	3.74%
Clipped reads	852,415 / 7.43%

2.2. ACGT Content

Number/percentage of A's	91,793,760 / 28.25%
Number/percentage of C's	69,718,906 / 21.46%
Number/percentage of T's	93,031,822 / 28.63%
Number/percentage of G's	70,360,211 / 21.65%
Number/percentage of N's	40,810 / 0.01%
GC Percentage	43.11%

2.3. Coverage

Mean	0.105
Standard Deviation	0.6452

2.4. Mapping Quality

Mean Mapping Quality	46.25
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2.5. Insert size

Mean	64,643.81
Standard Deviation	2,480,310.05
P25/Median/P75	51 / 70 / 98

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	1,983,944
Insertions	11,235
Mapped reads with at least one insertion	0.13%
Deletions	30,581
Mapped reads with at least one deletion	0.36%
Homopolymer indels	41.1%

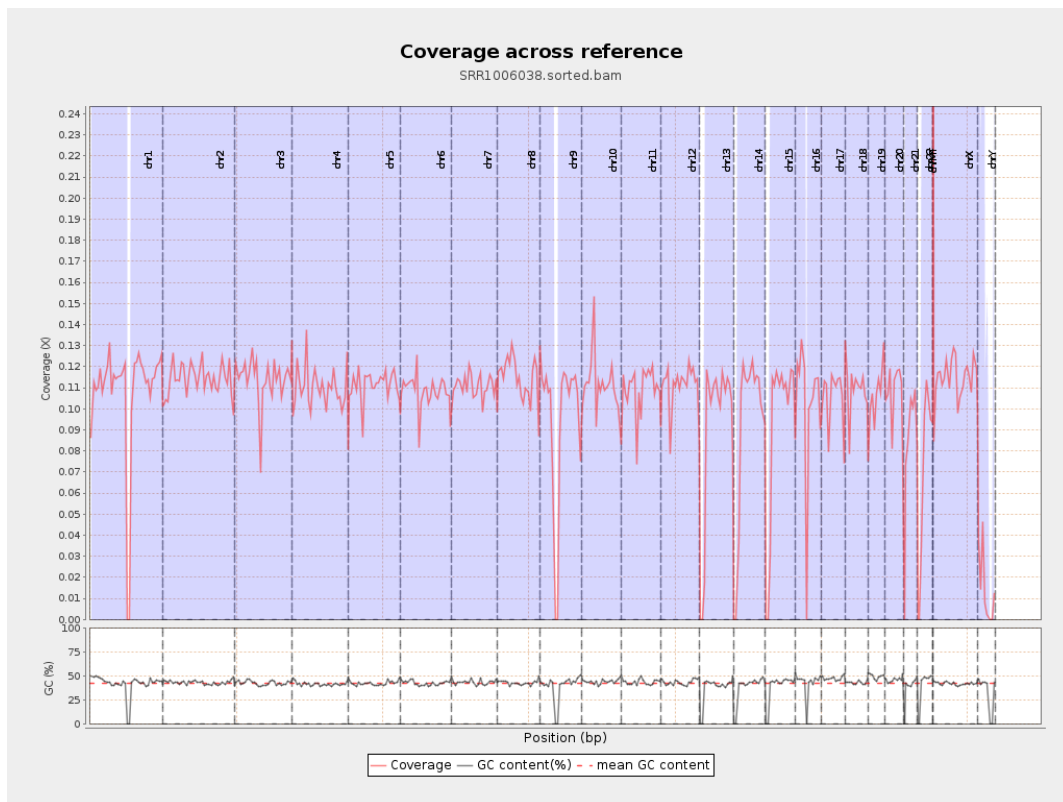
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

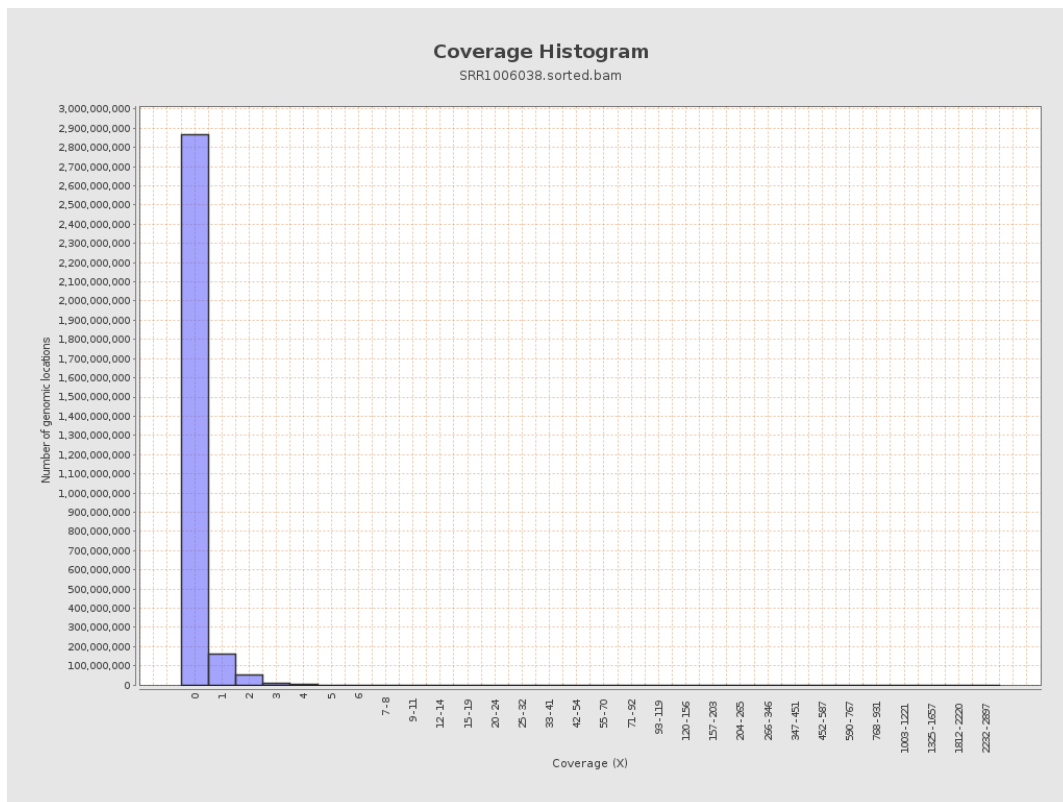
chr1	249250621	26913198	0.108	0.7911
chr2	243199373	27802541	0.1143	0.5354
chr3	198022430	22563056	0.1139	0.4408
chr4	191154276	21063565	0.1102	0.4789
chr5	180915260	20068302	0.1109	0.4341
chr6	171115067	18552293	0.1084	0.5022
chr7	159138663	17646795	0.1109	0.6095
chr8	146364022	16759891	0.1145	1.4771
chr9	141213431	13309981	0.0943	0.4531
chr10	135534747	15092432	0.1114	0.6273
chr11	135006516	14704149	0.1089	0.4712
chr12	133851895	14977163	0.1119	0.4391
chr13	115169878	10520816	0.0914	0.3948
chr14	107349540	9967032	0.0928	0.4237
chr15	102531392	9296561	0.0907	0.3936
chr16	90354753	9105234	0.1008	0.4613
chr17	81195210	8650178	0.1065	0.4347
chr18	78077248	8515710	0.1091	0.6168
chr19	59128983	6326852	0.107	1.8281
chr20	63025520	6809350	0.108	0.4439
chr21	48129895	4055917	0.0843	0.4244
chr22	51304566	3624839	0.0707	0.4694
chrMT	16571	15833	0.9555	1.3309
chrX	155270560	17801056	0.1146	0.4634

chrY	59373566	842477	0.0142	0.3014
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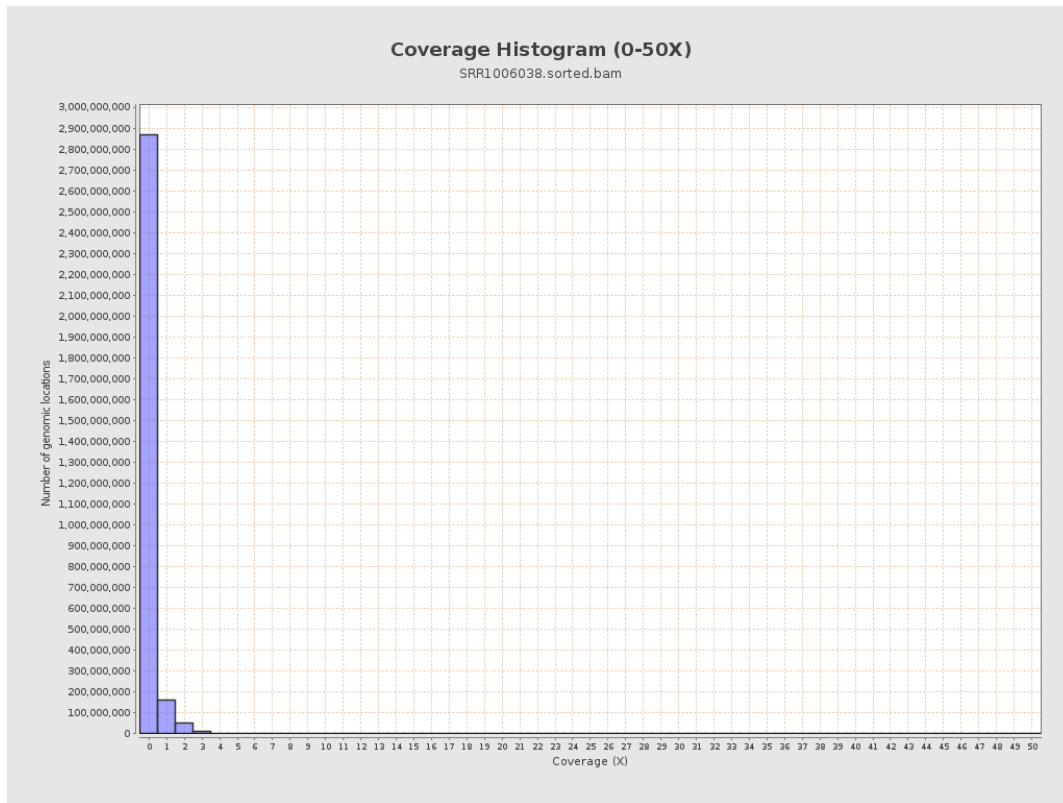
3. Results : Coverage across reference



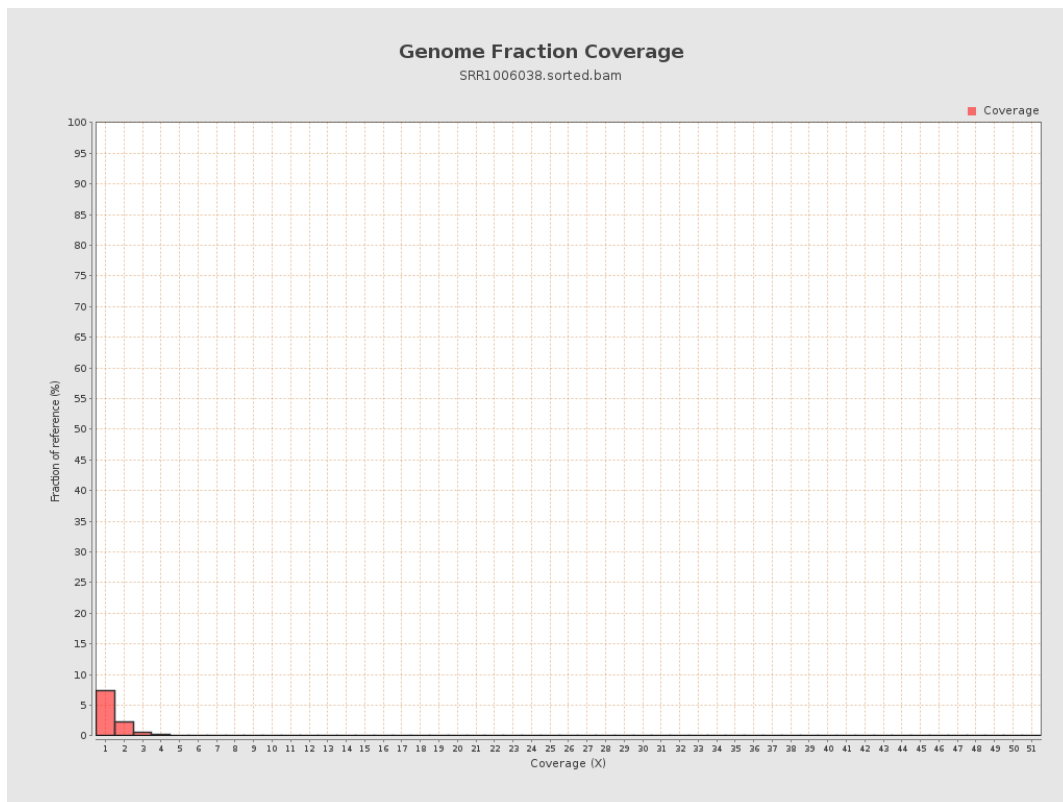
4. Results : Coverage Histogram



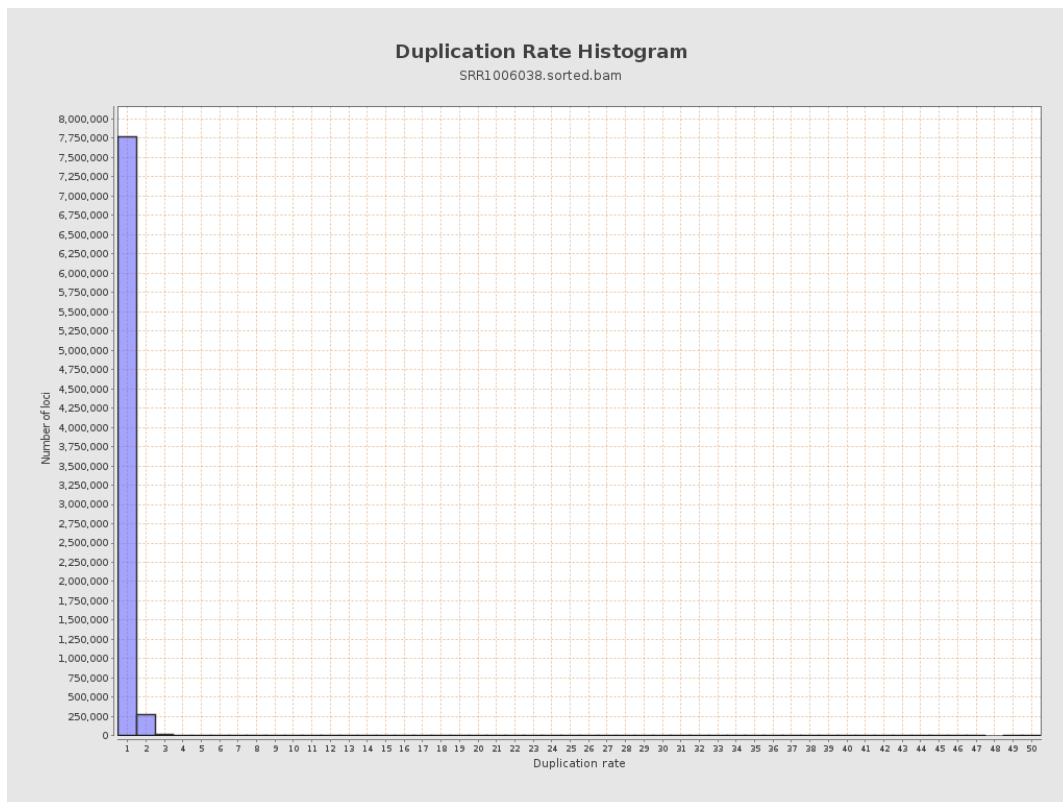
5. Results : Coverage Histogram (0-50X)



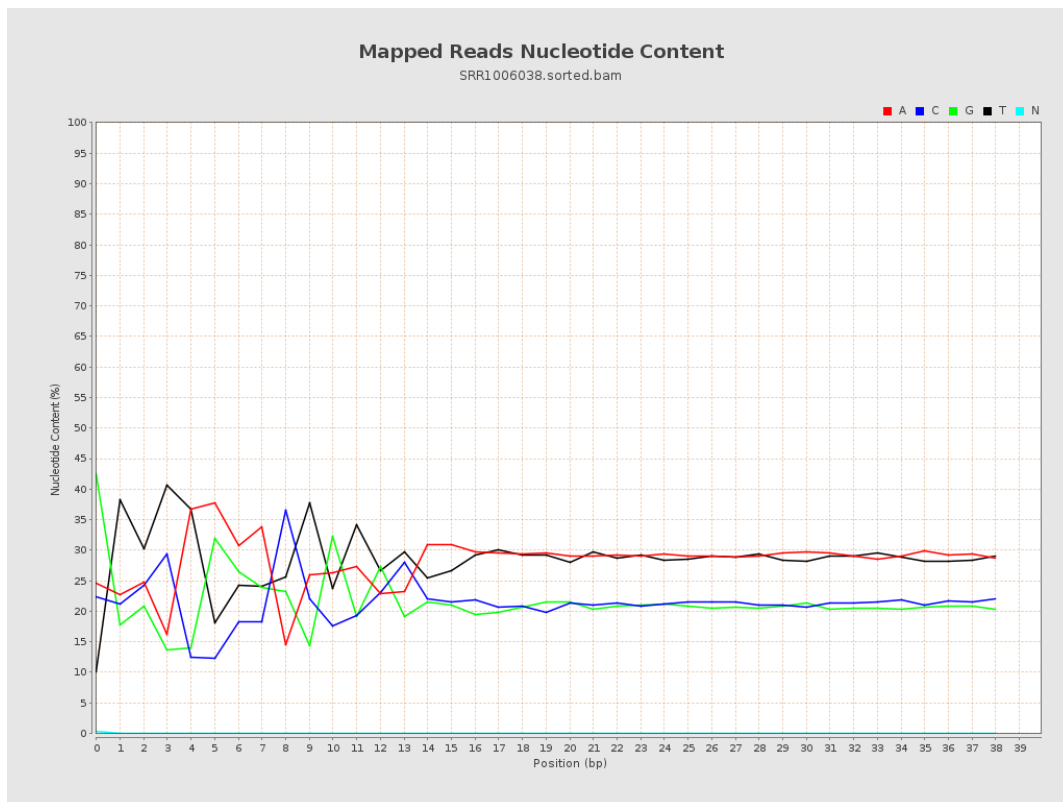
6. Results : Genome Fraction Coverage



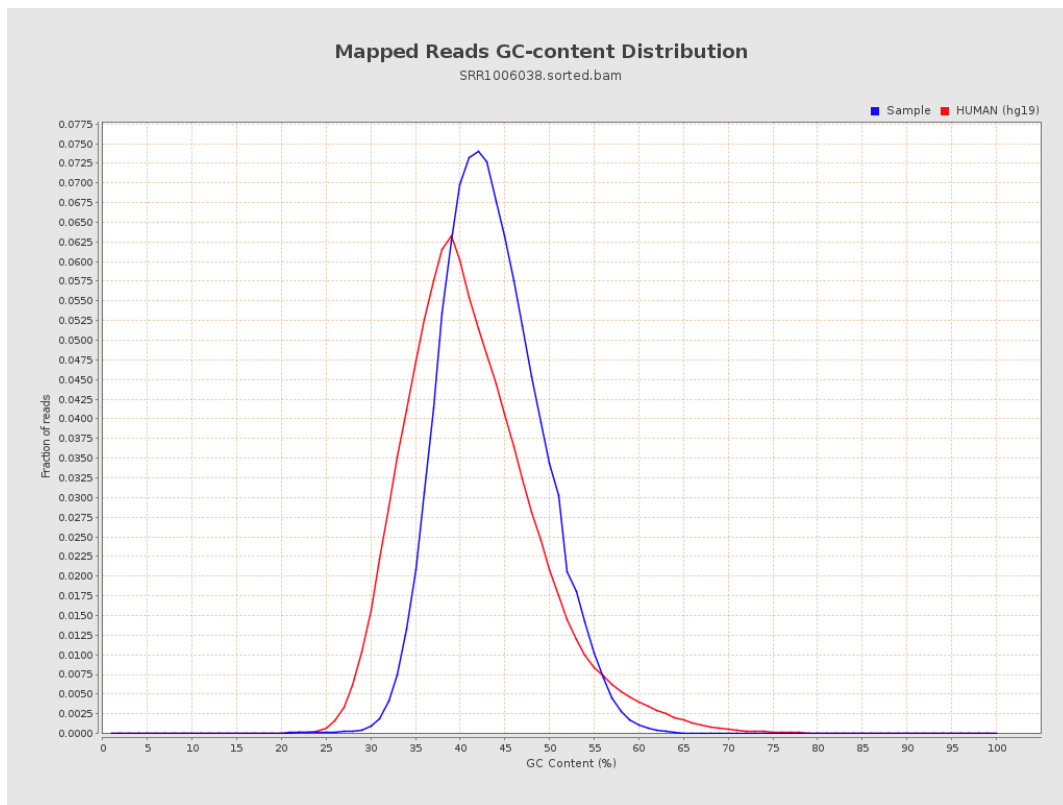
7. Results : Duplication Rate Histogram



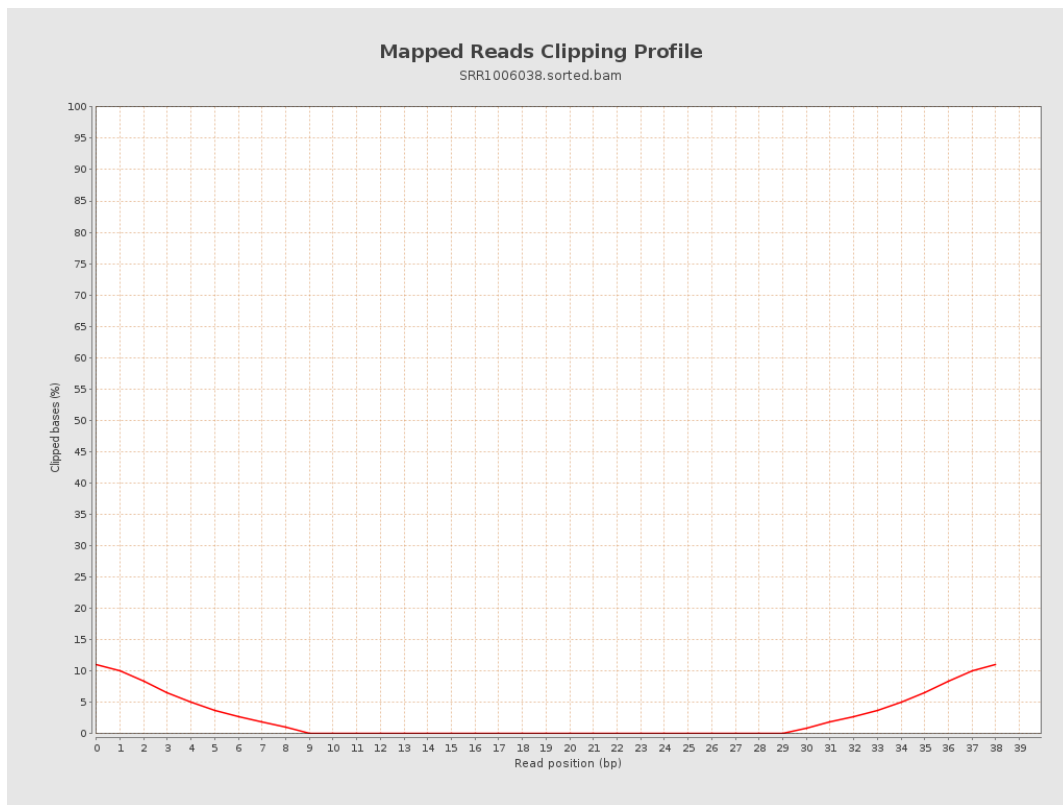
8. Results : Mapped Reads Nucleotide Content



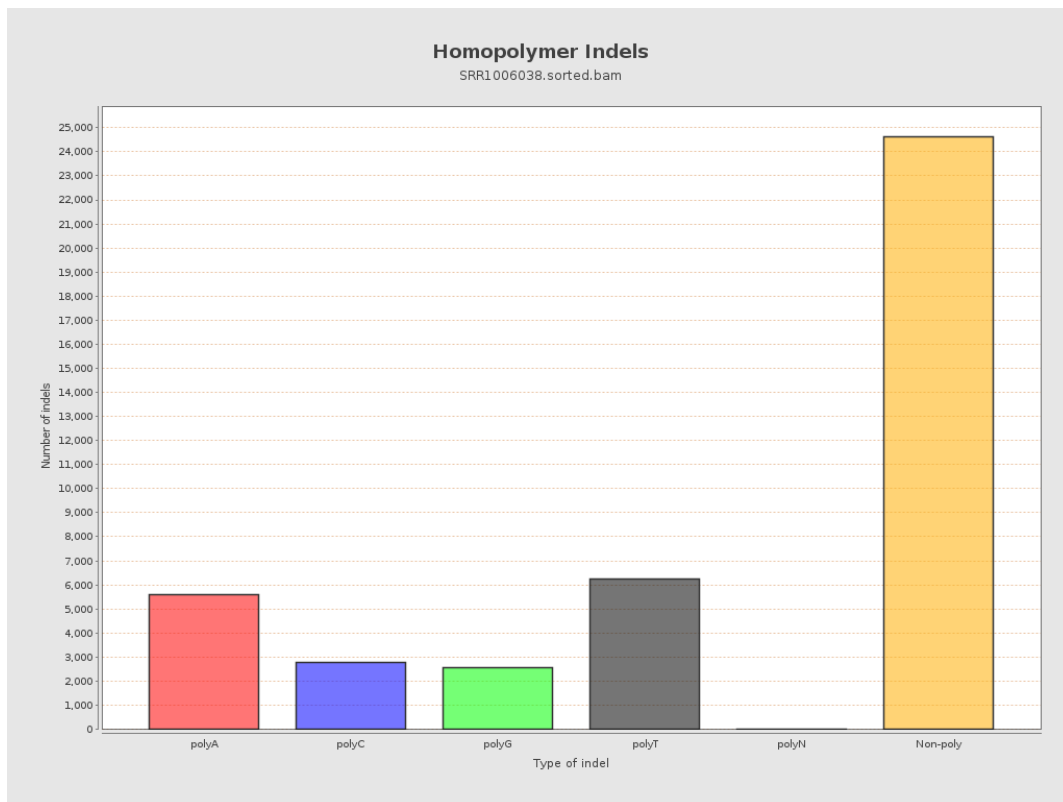
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



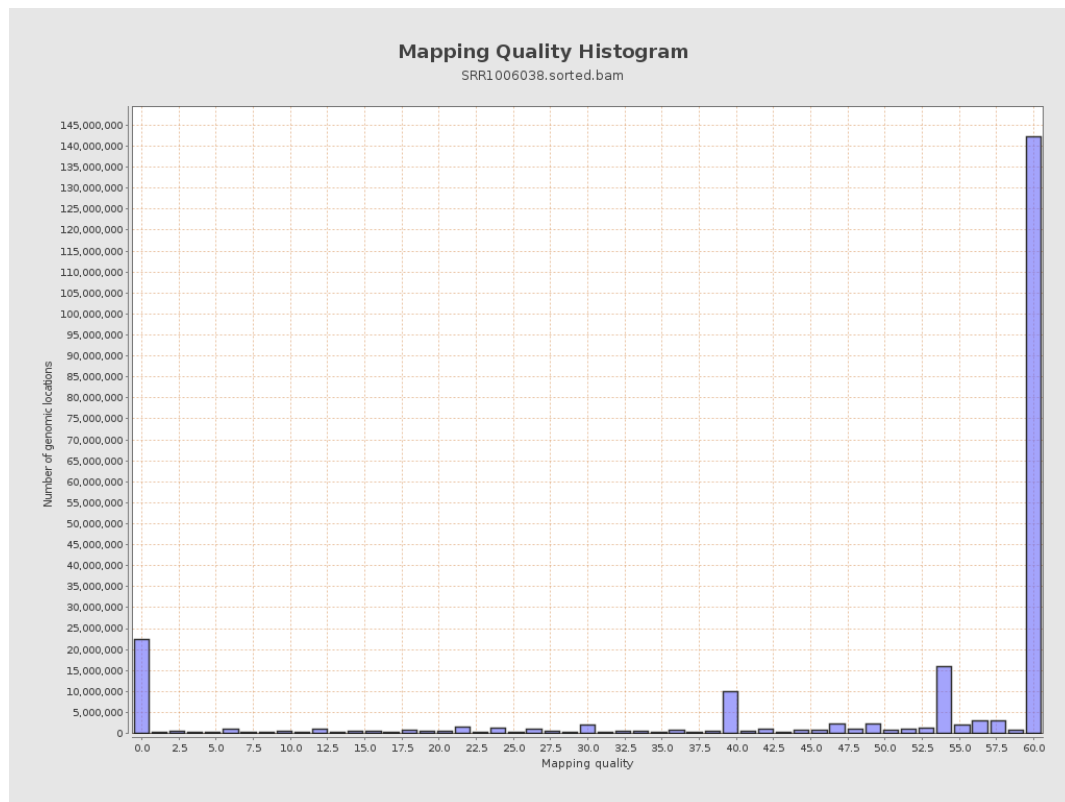
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

