

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 23:23:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038418.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_SRR5038418 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038418_1.fastq.gz SRR5038418_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 23:23:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038418.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,203,802
Mapped reads	13,928,118 / 98.06%
Unmapped reads	275,684 / 1.94%
Mapped paired reads	13,928,118 / 98.06%
Mapped reads, first in pair	7,019,526 / 49.42%
Mapped reads, second in pair	6,908,592 / 48.64%
Mapped reads, both in pair	13,804,276 / 97.19%
Mapped reads, singletons	123,842 / 0.87%
Secondary alignments	0
Supplementary alignments	186,349 / 1.31%
Read min/max/mean length	30 / 150 / 150.69
Duplicated reads (estimated)	2,043,935 / 14.39%
Duplication rate	9.6%
Clipped reads	2,725,870 / 19.19%

2.2. ACGT Content

Number/percentage of A's	596,836,214 / 29.63%
Number/percentage of C's	406,818,763 / 20.2%
Number/percentage of T's	593,845,200 / 29.48%
Number/percentage of G's	416,687,842 / 20.69%
Number/percentage of N's	43,233 / 0%

GC Percentage	40.88%
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2.3. Coverage

Mean	0.6511
Standard Deviation	9.8165

2.4. Mapping Quality

Mean Mapping Quality	53.8
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2.5. Insert size

Mean	65,866.22
Standard Deviation	2,454,012.64
P25/Median/P75	202 / 248 / 308

2.6. Mismatches and indels

General error rate	1.34%
Mismatches	26,234,226
Insertions	331,525
Mapped reads with at least one insertion	2.27%
Deletions	682,917
Mapped reads with at least one deletion	4.73%
Homopolymer indels	48.24%

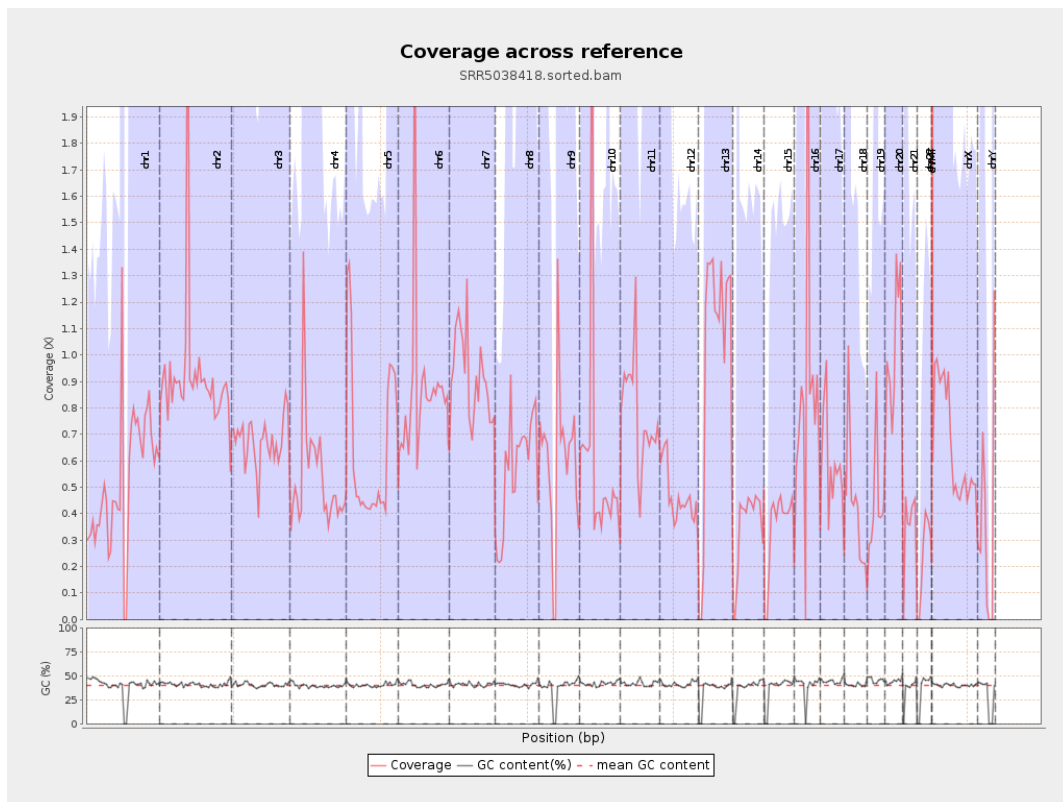
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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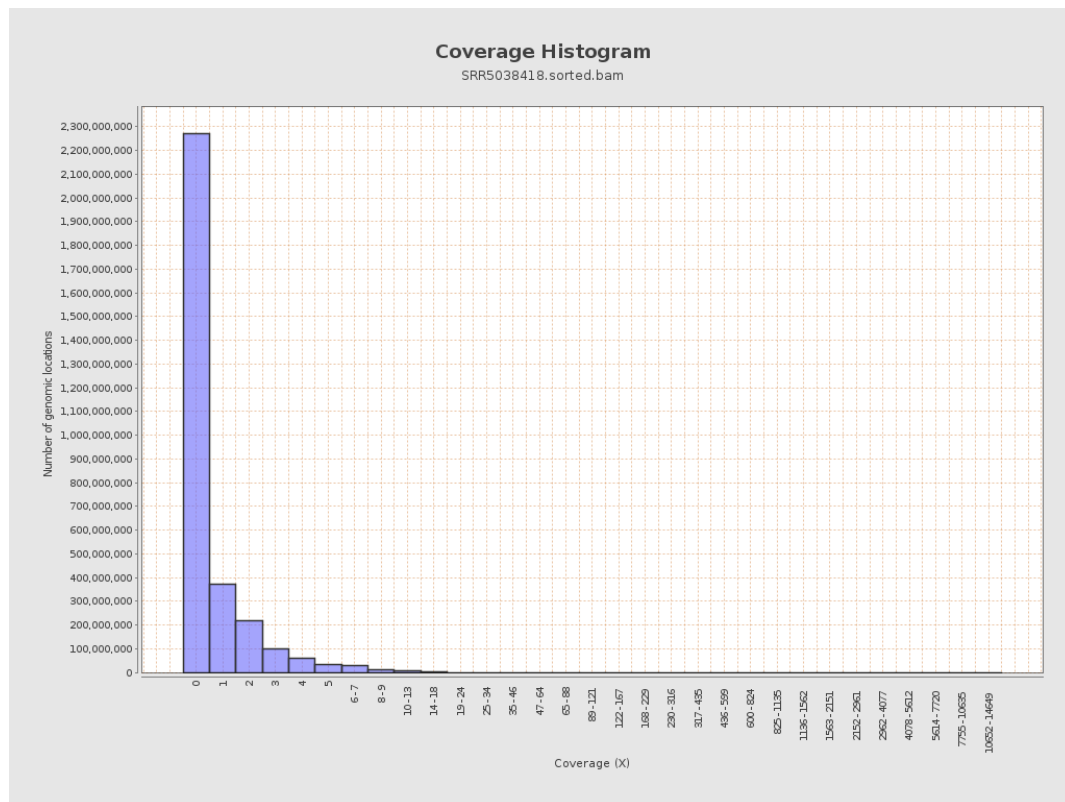
		bases	coverage	deviation
chr1	249250621	131383811	0.5271	14.8174
chr2	243199373	225654320	0.9279	10.2742
chr3	198022430	133602565	0.6747	1.4791
chr4	191154276	101472533	0.5308	6.0318
chr5	180915260	117825342	0.6513	1.5281
chr6	171115067	149923505	0.8762	17.5058
chr7	159138663	145455853	0.914	9.7921
chr8	146364022	83523413	0.5707	2.5645
chr9	141213431	83025752	0.5879	15.4432
chr10	135534747	83289605	0.6145	18.2351
chr11	135006516	102170257	0.7568	9.6893
chr12	133851895	62774923	0.469	1.2143
chr13	115169878	117803805	1.0229	1.9646
chr14	107349540	37947047	0.3535	1.1865
chr15	102531392	35490849	0.3461	0.9748
chr16	90354753	77539097	0.8582	13.3922
chr17	81195210	46691638	0.5751	9.2714
chr18	78077248	33319043	0.4267	12.6689
chr19	59128983	24971342	0.4223	8.7345
chr20	63025520	63114238	1.0014	2.6323
chr21	48129895	17185294	0.3571	2.8828
chr22	51304566	12131327	0.2365	0.8221
chrMT	16571	4625961	279.16	211.0958
chrX	155270560	101821389	0.6558	2.6946

chrY	59373566	22782140	0.3837	8.9556
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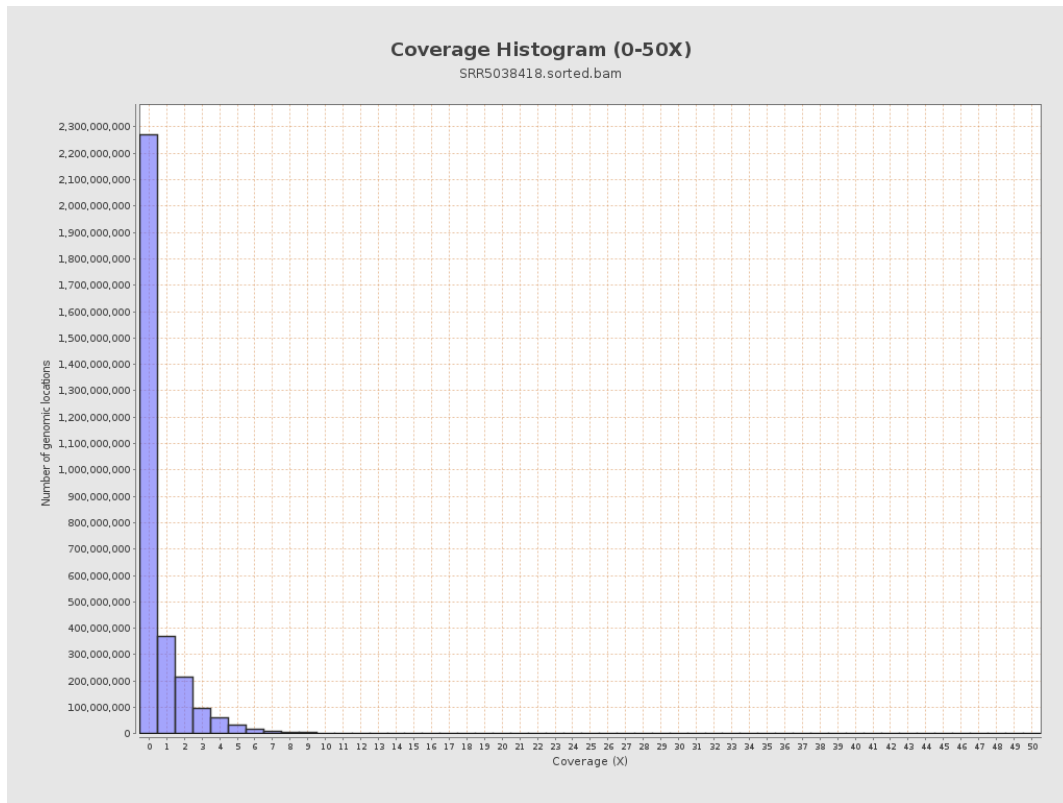
3. Results : Coverage across reference



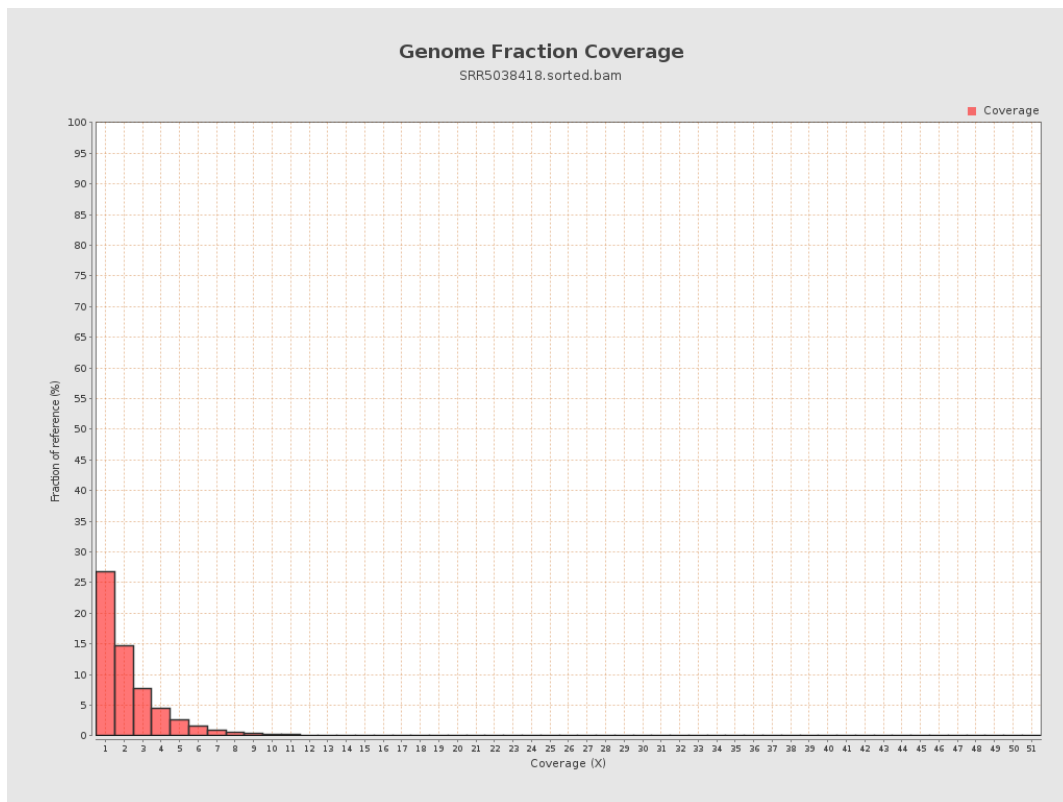
4. Results : Coverage Histogram



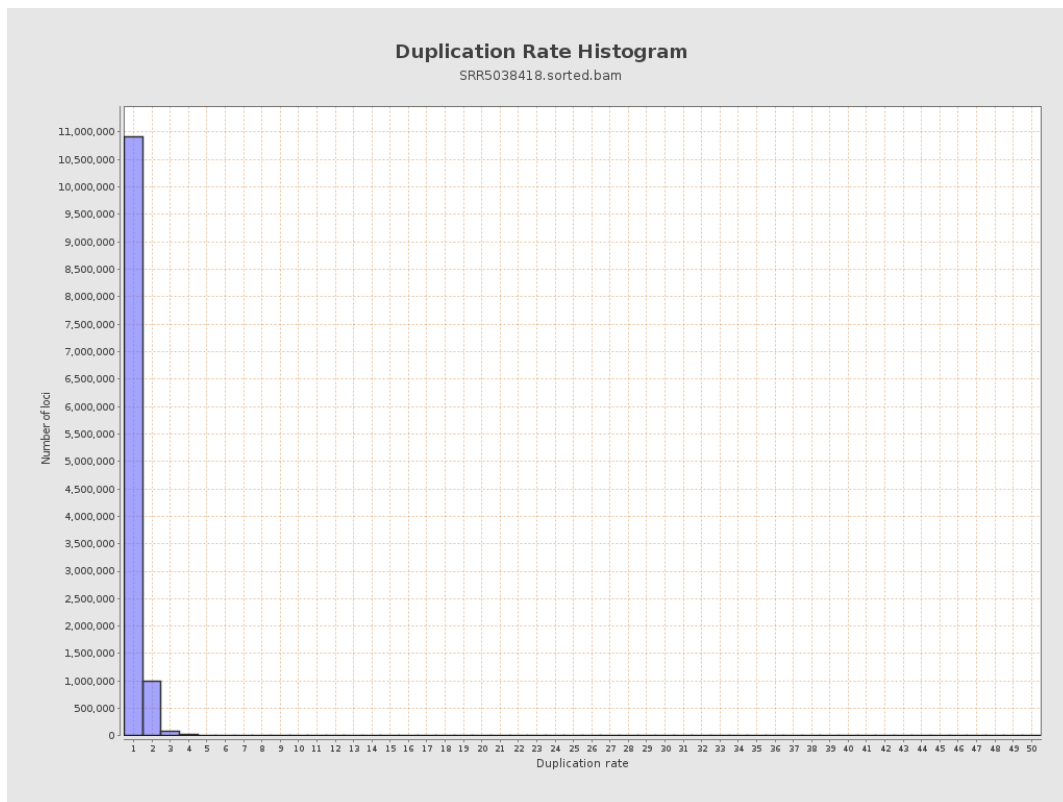
5. Results : Coverage Histogram (0-50X)



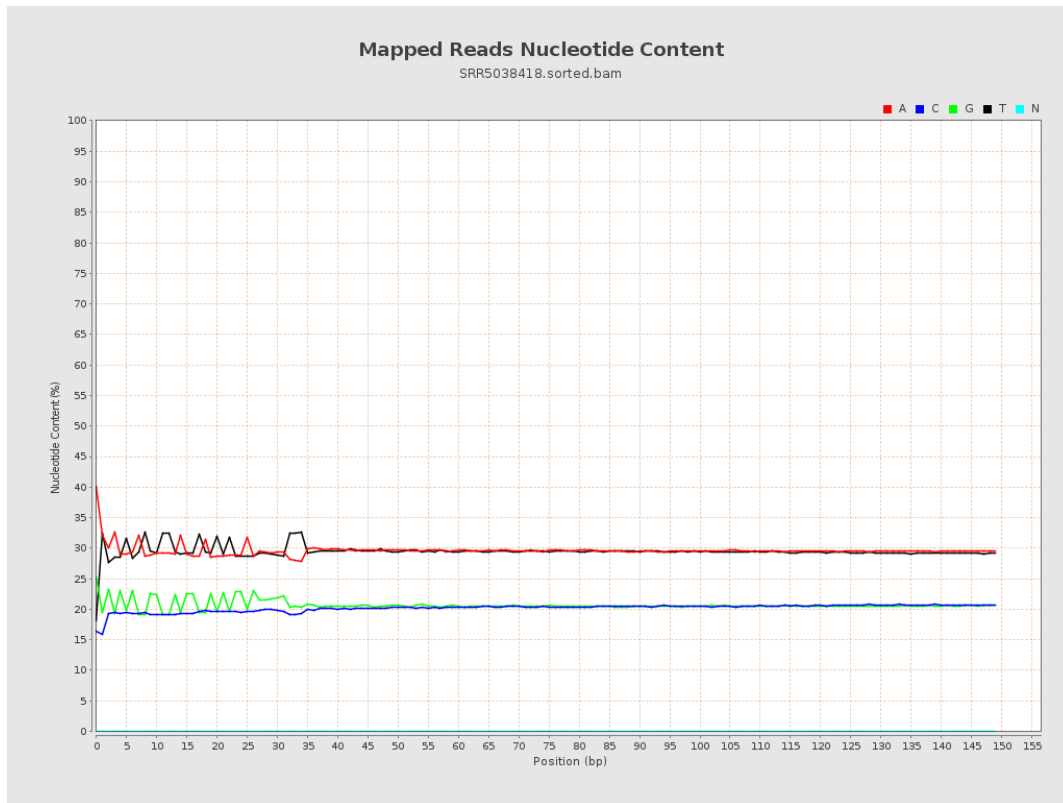
6. Results : Genome Fraction Coverage



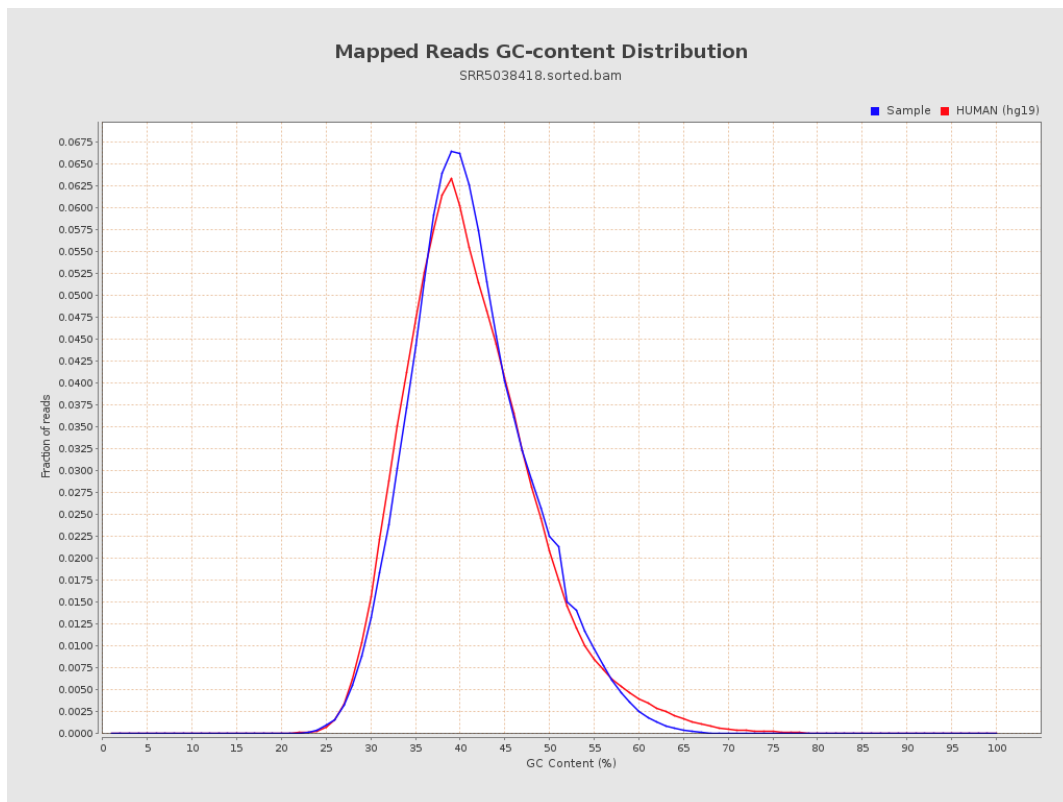
7. Results : Duplication Rate Histogram



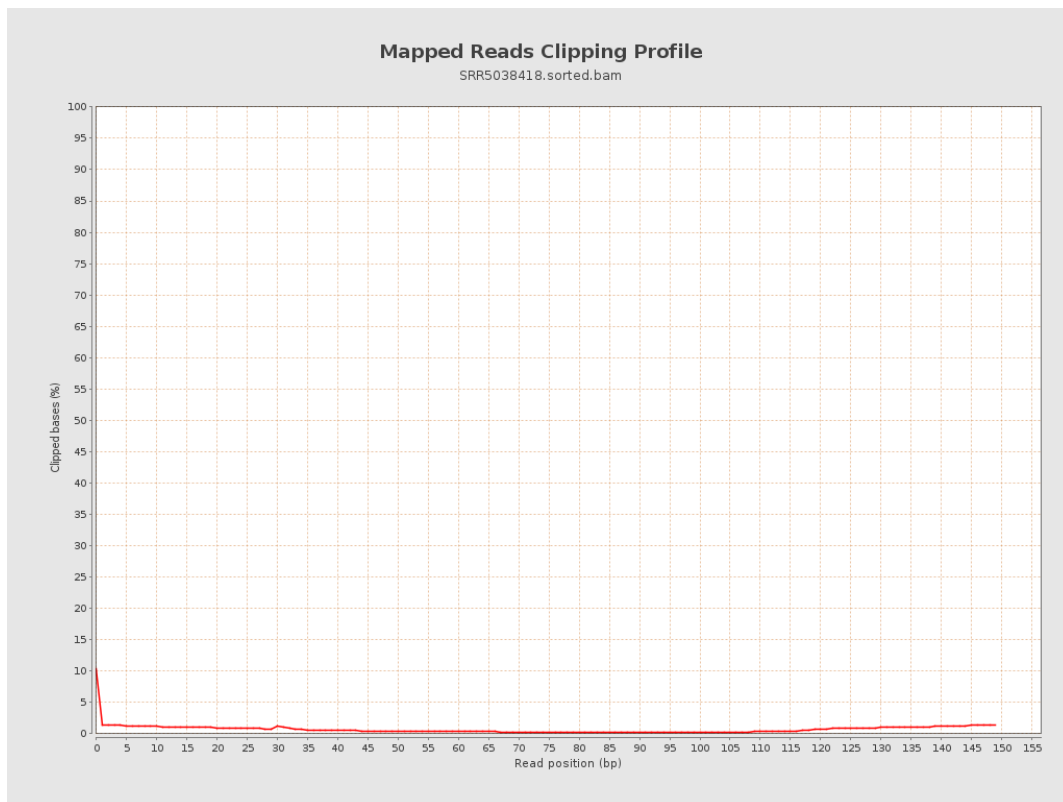
8. Results : Mapped Reads Nucleotide Content



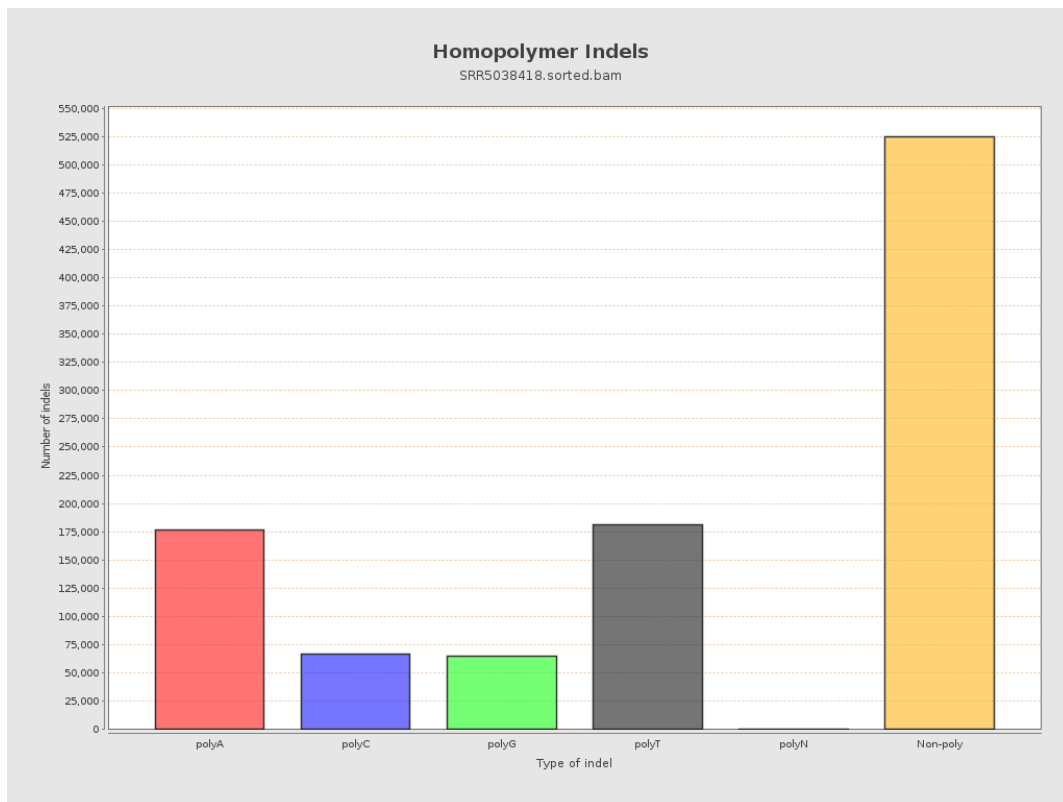
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



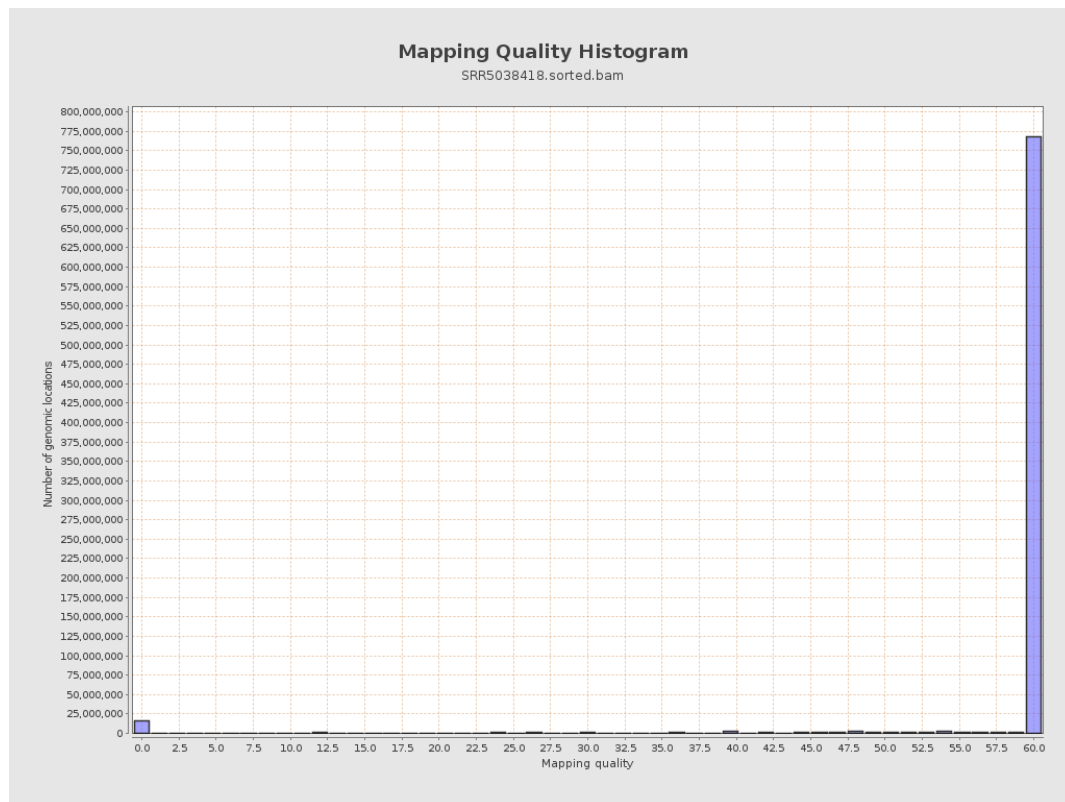
11. Results : Homopolymer Indels



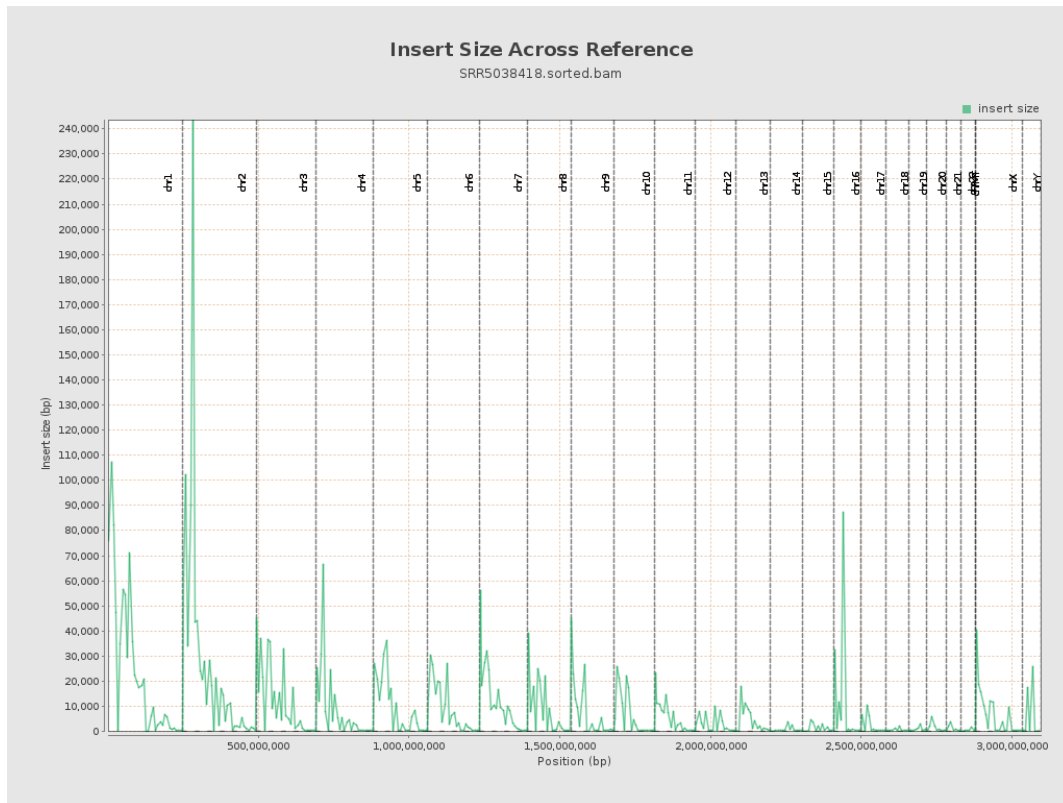
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

