

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 14:29:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038447.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_SRR5038447 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038447_1.fastq.gz SRR5038447_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 14:29:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038447.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,499,644
Mapped reads	14,603,532 / 94.22%
Unmapped reads	896,112 / 5.78%
Mapped paired reads	14,603,532 / 94.22%
Mapped reads, first in pair	7,377,262 / 47.6%
Mapped reads, second in pair	7,226,270 / 46.62%
Mapped reads, both in pair	14,430,572 / 93.1%
Mapped reads, singletons	172,960 / 1.12%
Secondary alignments	0
Supplementary alignments	209,120 / 1.35%
Read min/max/mean length	30 / 150 / 150.68
Duplicated reads (estimated)	2,072,443 / 13.37%
Duplication rate	10.01%
Clipped reads	2,935,167 / 18.94%

2.2. ACGT Content

Number/percentage of A's	608,999,334 / 28.91%
Number/percentage of C's	440,202,566 / 20.9%
Number/percentage of T's	607,358,701 / 28.83%
Number/percentage of G's	450,048,899 / 21.36%
Number/percentage of N's	44,309 / 0%

GC Percentage	42.26%
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2.3. Coverage

Mean	0.681
Standard Deviation	7.7201

2.4. Mapping Quality

Mean Mapping Quality	53.95
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2.5. Insert size

Mean	79,256.32
Standard Deviation	2,737,626.34
P25/Median/P75	198 / 241 / 296

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	27,923,687
Insertions	367,894
Mapped reads with at least one insertion	2.34%
Deletions	731,643
Mapped reads with at least one deletion	4.8%
Homopolymer indels	46.59%

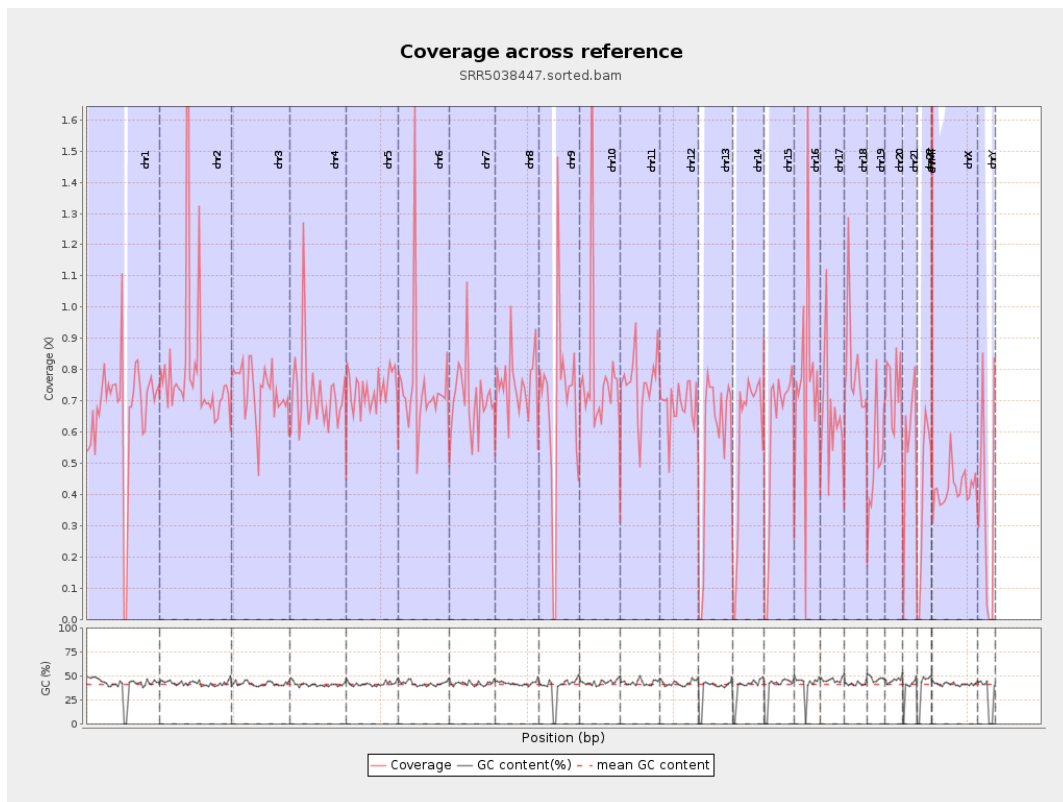
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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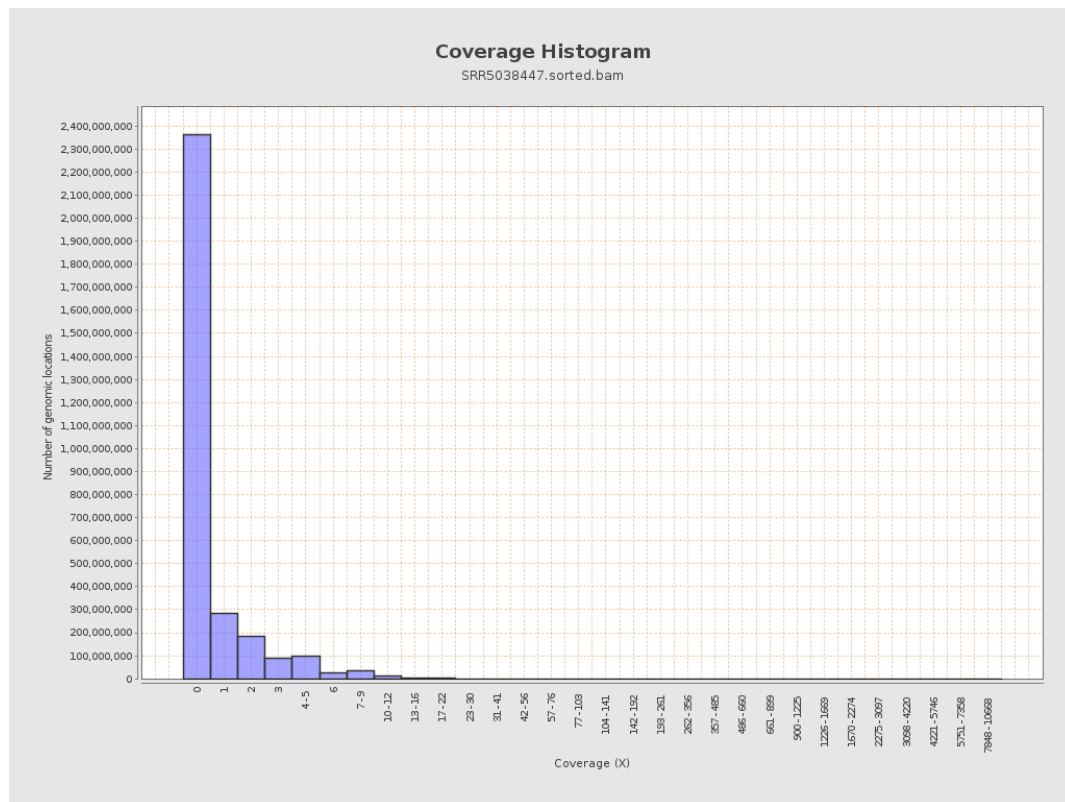
		bases	coverage	deviation
chr1	249250621	167259341	0.671	7.2429
chr2	243199373	195637233	0.8044	11.6343
chr3	198022430	144998994	0.7322	1.7937
chr4	191154276	137420418	0.7189	4.6271
chr5	180915260	132726657	0.7336	1.9493
chr6	171115067	127849543	0.7472	10.7335
chr7	159138663	112394885	0.7063	8.4424
chr8	146364022	110227033	0.7531	2.9178
chr9	141213431	94667721	0.6704	17.2698
chr10	135534747	107551625	0.7935	11.0483
chr11	135006516	100907654	0.7474	5.5553
chr12	133851895	91406950	0.6829	1.7926
chr13	115169878	65437643	0.5682	1.5658
chr14	107349540	63202559	0.5888	1.8062
chr15	102531392	60827125	0.5933	1.6282
chr16	90354753	67701877	0.7493	9.2213
chr17	81195210	52022378	0.6407	7.5777
chr18	78077248	62556265	0.8012	14.9165
chr19	59128983	29312507	0.4957	4.1729
chr20	63025520	46002808	0.7299	2.2332
chr21	48129895	27879173	0.5792	2.9979
chr22	51304566	20823868	0.4059	1.5553
chrMT	16571	2767009	166.979	99.6711
chrX	155270560	64895735	0.418	2.0167

chrY	59373566	21600594	0.3638	7.915
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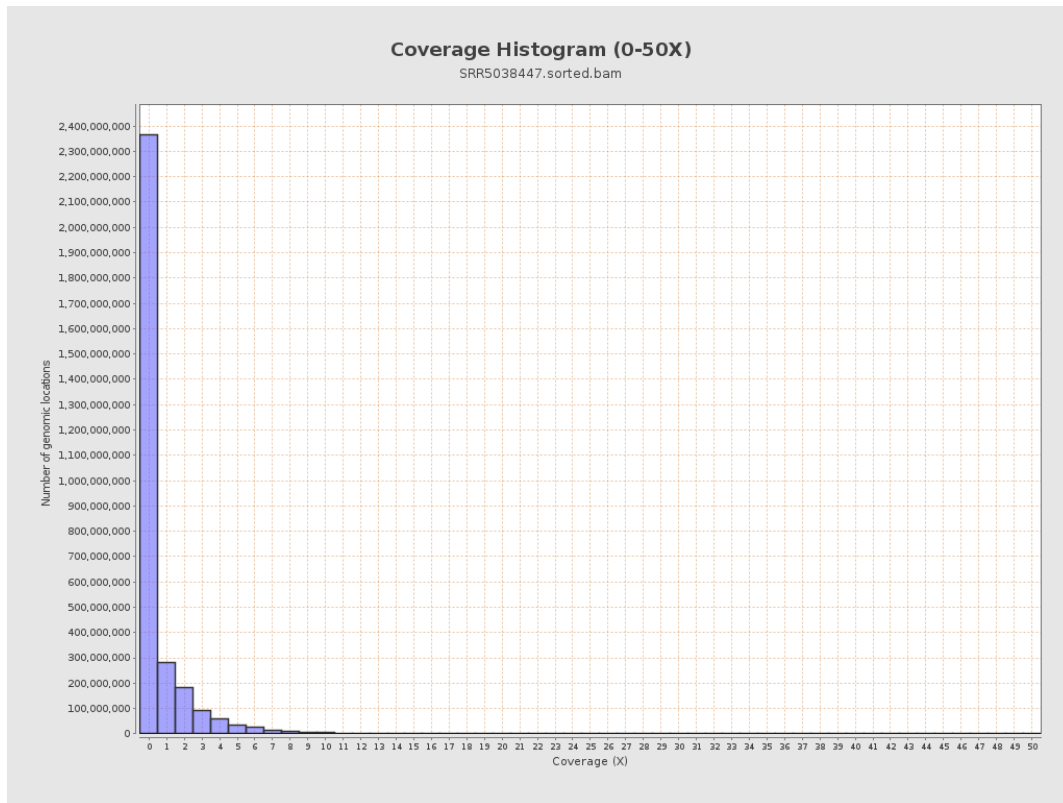
3. Results : Coverage across reference



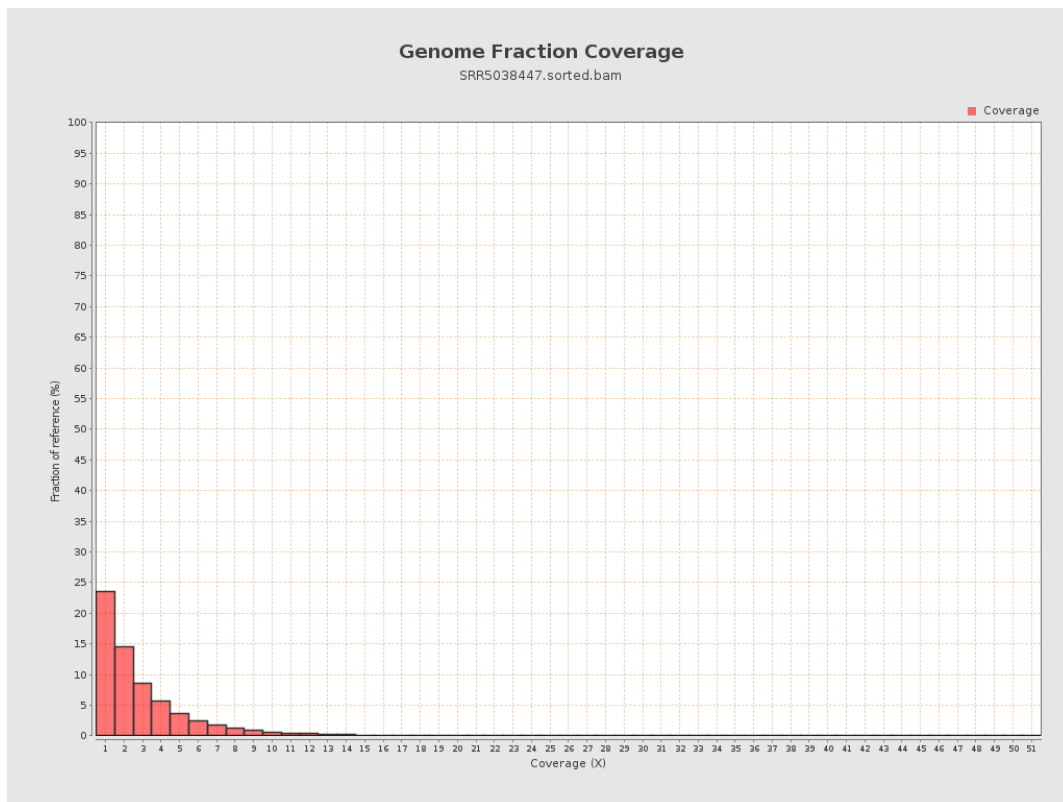
4. Results : Coverage Histogram



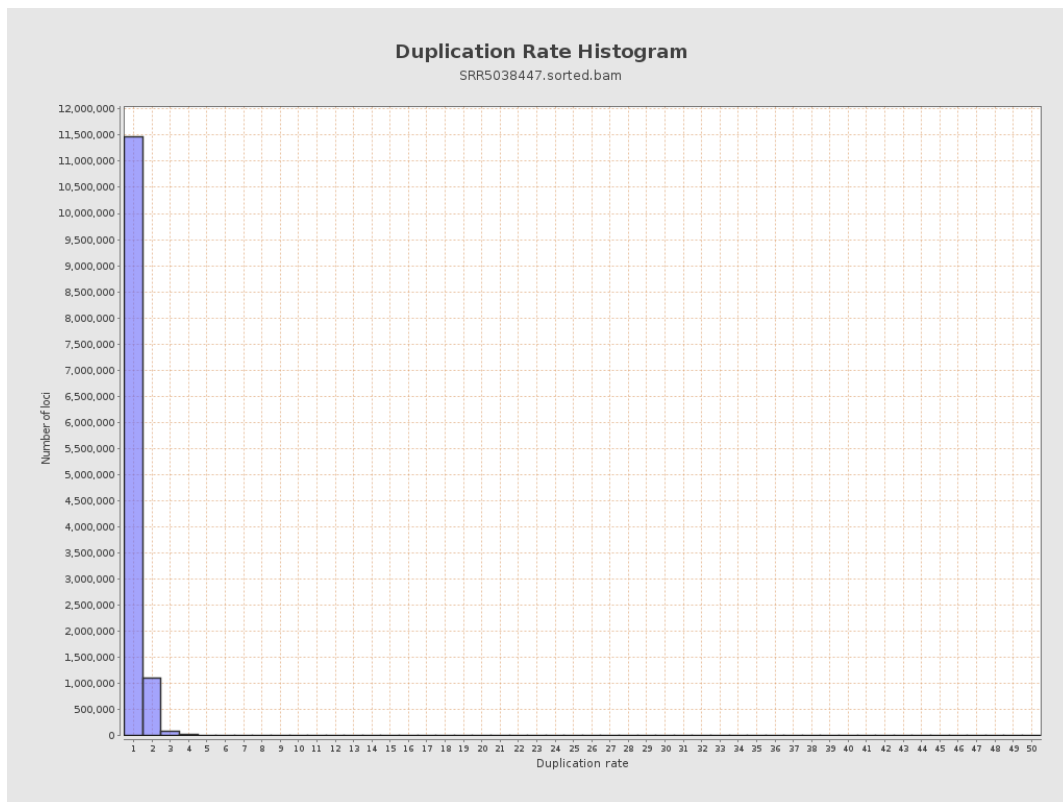
5. Results : Coverage Histogram (0-50X)



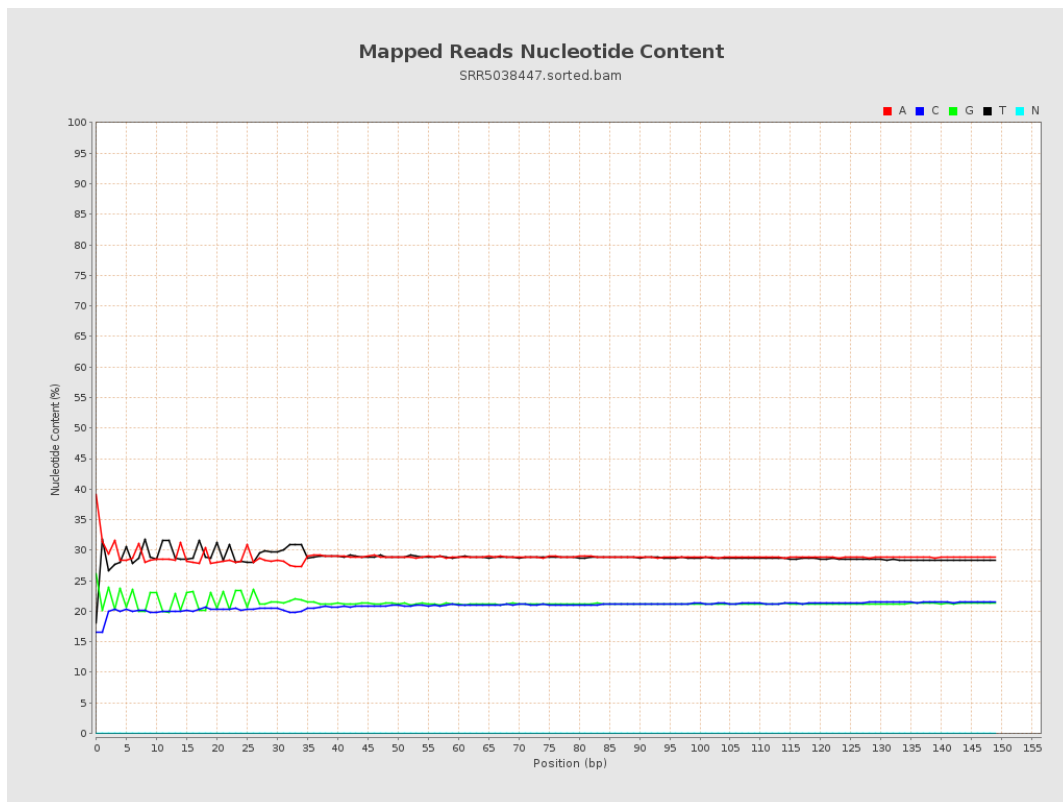
6. Results : Genome Fraction Coverage



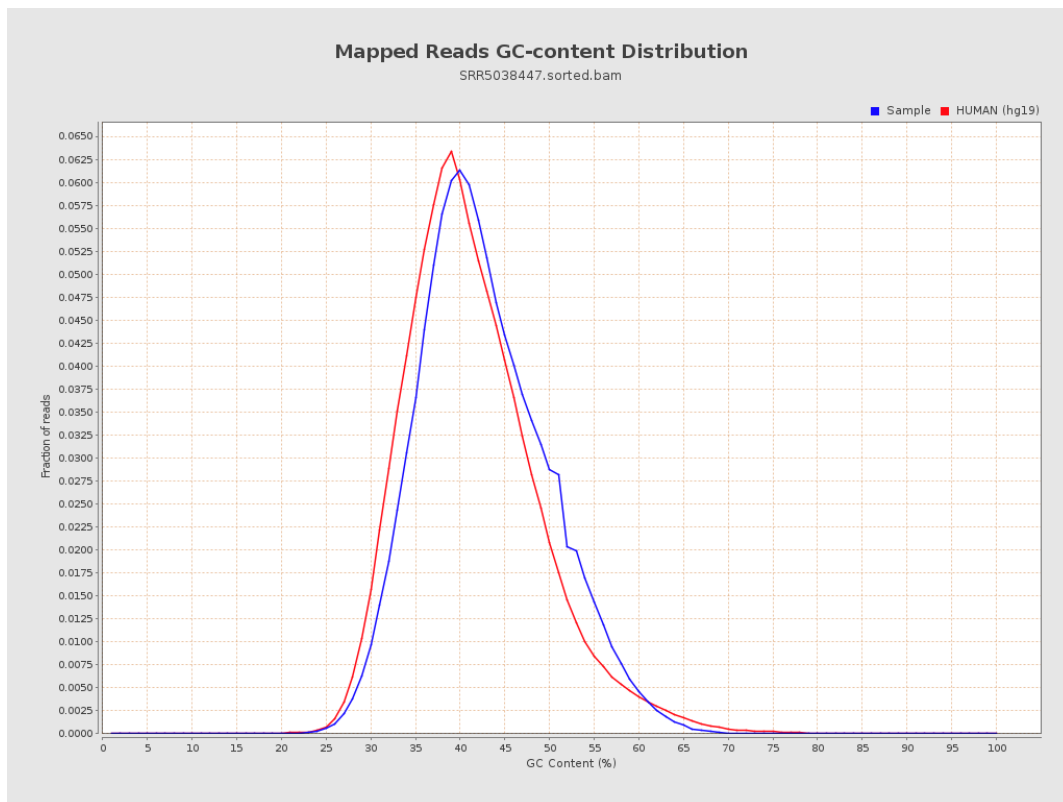
7. Results : Duplication Rate Histogram



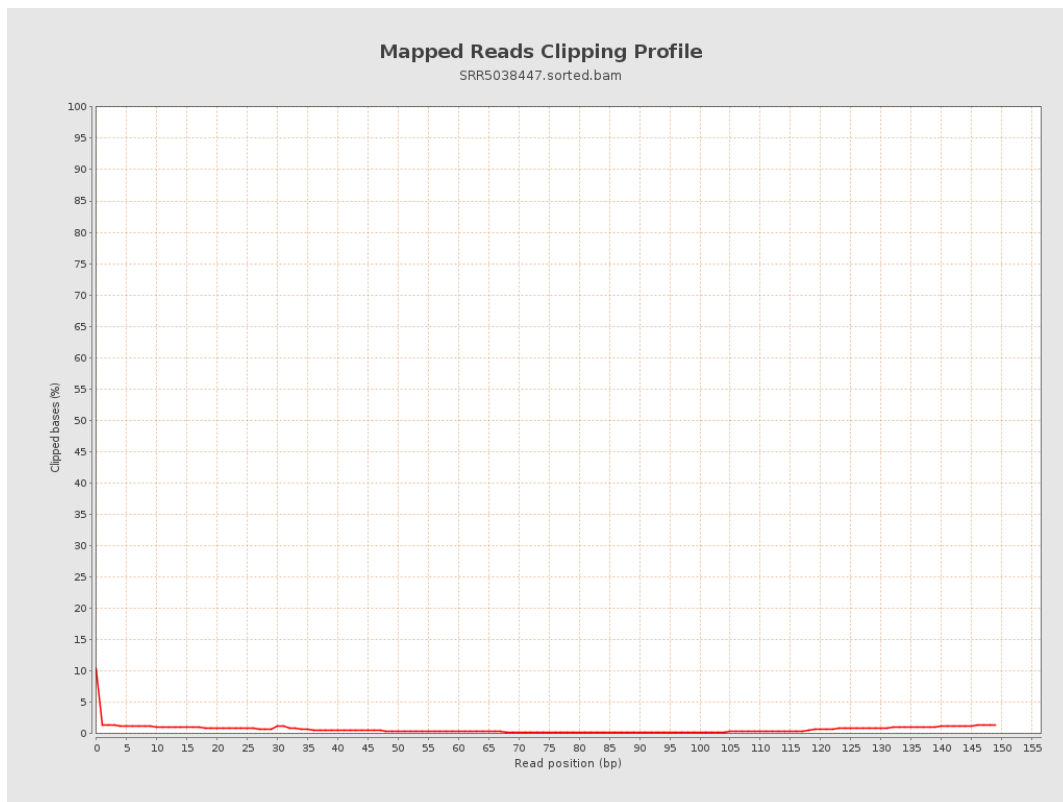
8. Results : Mapped Reads Nucleotide Content



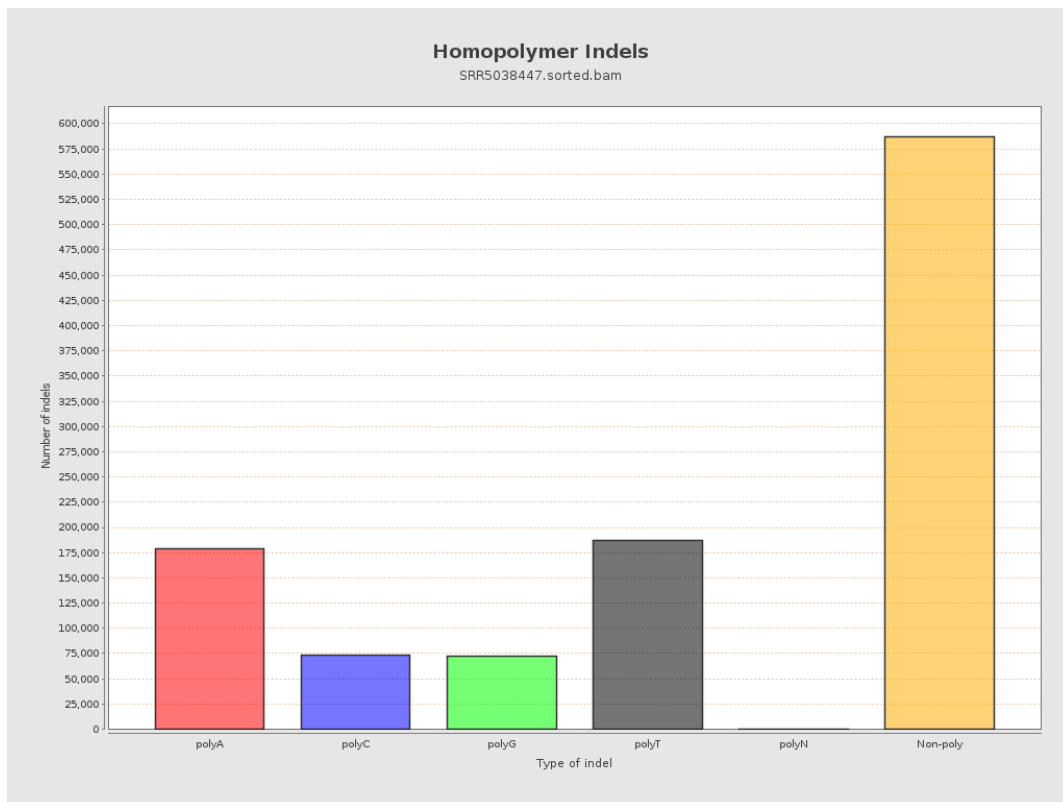
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



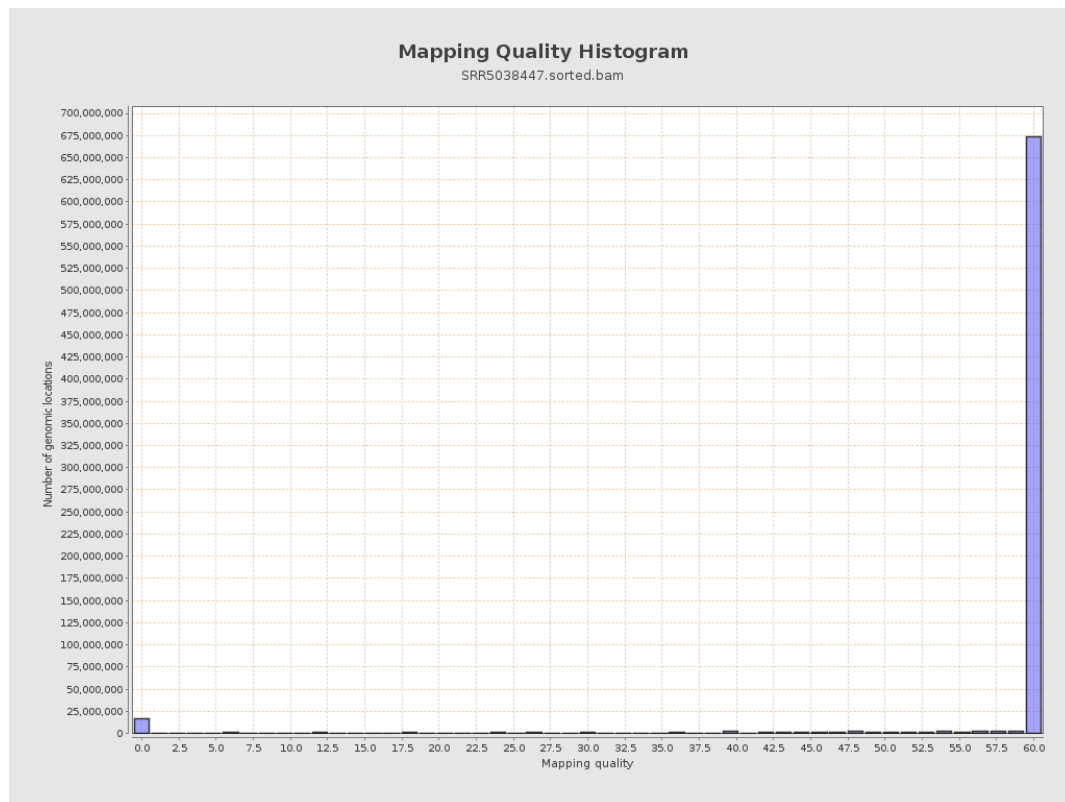
11. Results : Homopolymer Indels



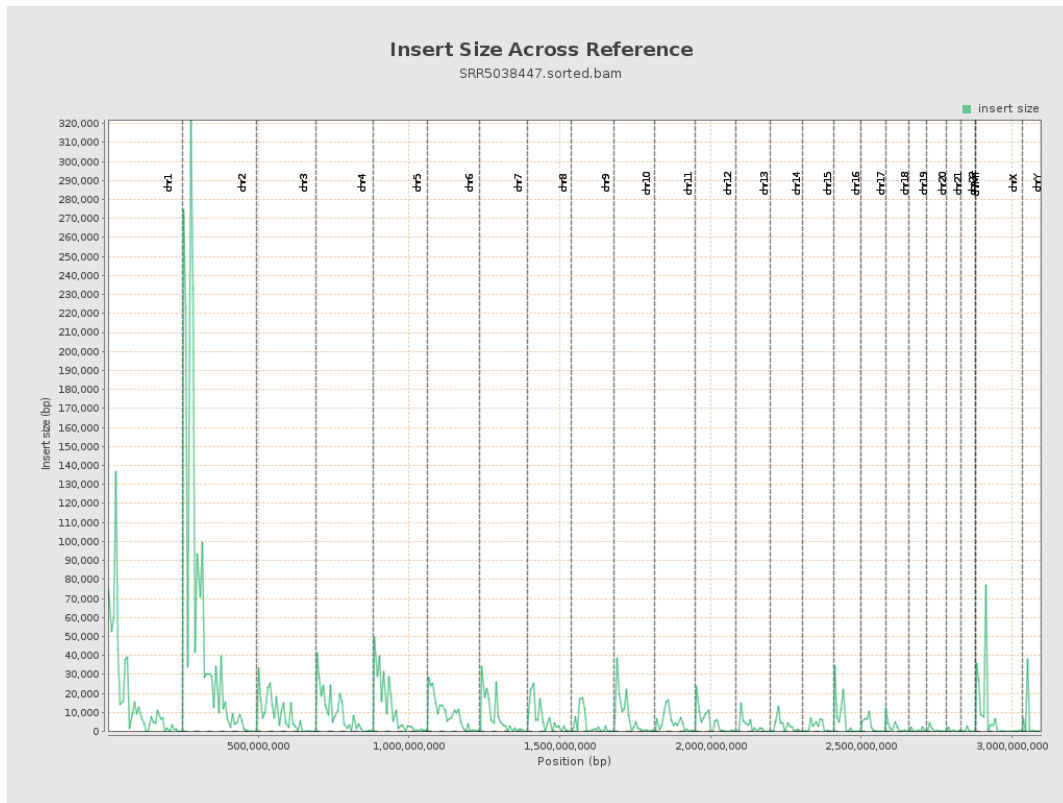
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

