

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 01:20:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038471.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_SRR5038471 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038471_1.fastq.gz SRR5038471_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 01:20:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038471.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,299,416
Mapped reads	19,704,497 / 97.07%
Unmapped reads	594,919 / 2.93%
Mapped paired reads	19,704,497 / 97.07%
Mapped reads, first in pair	9,911,080 / 48.82%
Mapped reads, second in pair	9,793,417 / 48.24%
Mapped reads, both in pair	19,564,164 / 96.38%
Mapped reads, singletons	140,333 / 0.69%
Secondary alignments	0
Supplementary alignments	211,020 / 1.04%
Read min/max/mean length	30 / 150 / 150.54
Duplicated reads (estimated)	2,183,760 / 10.76%
Duplication rate	8.67%
Clipped reads	1,974,914 / 9.73%

2.2. ACGT Content

Number/percentage of A's	832,493,417 / 28.69%
Number/percentage of C's	620,812,162 / 21.4%
Number/percentage of T's	826,704,947 / 28.49%
Number/percentage of G's	620,974,525 / 21.4%
Number/percentage of N's	267,991 / 0.01%

GC Percentage	42.8%
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2.3. Coverage

Mean	0.9375
Standard Deviation	9.1458

2.4. Mapping Quality

Mean Mapping Quality	54.35
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2.5. Insert size

Mean	109,083.28
Standard Deviation	3,310,403.24
P25/Median/P75	231 / 282 / 349

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	25,144,120
Insertions	337,382
Mapped reads with at least one insertion	1.62%
Deletions	366,471
Mapped reads with at least one deletion	1.78%
Homopolymer indels	44.6%

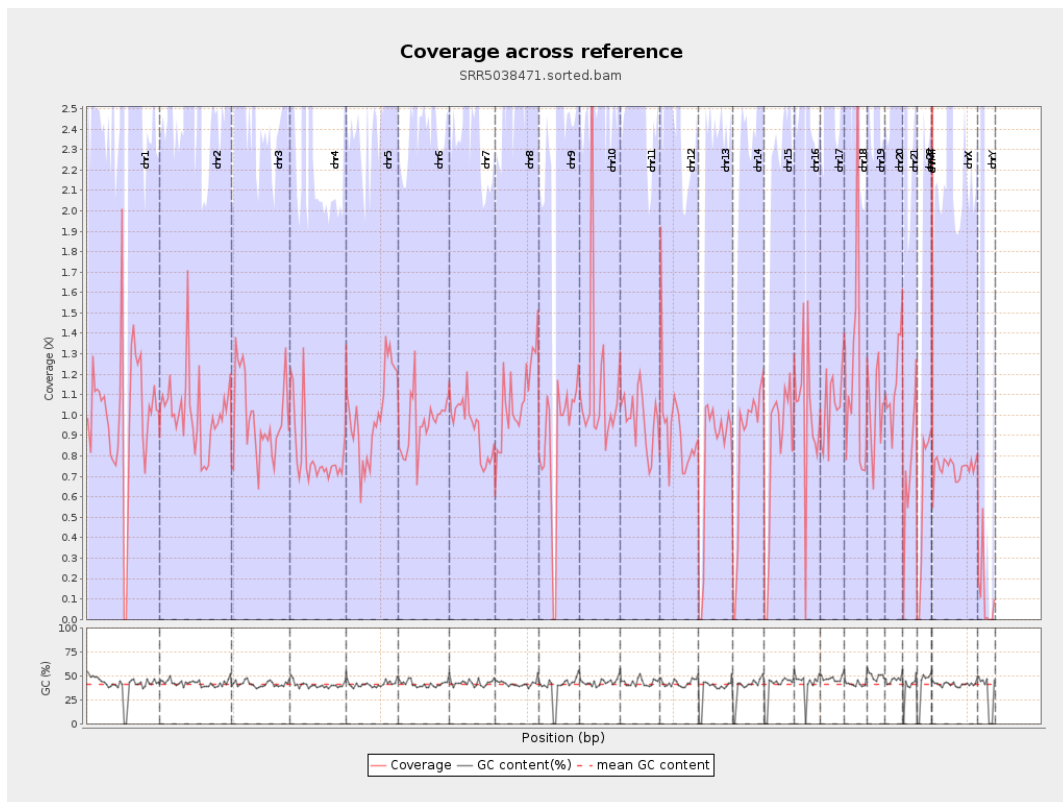
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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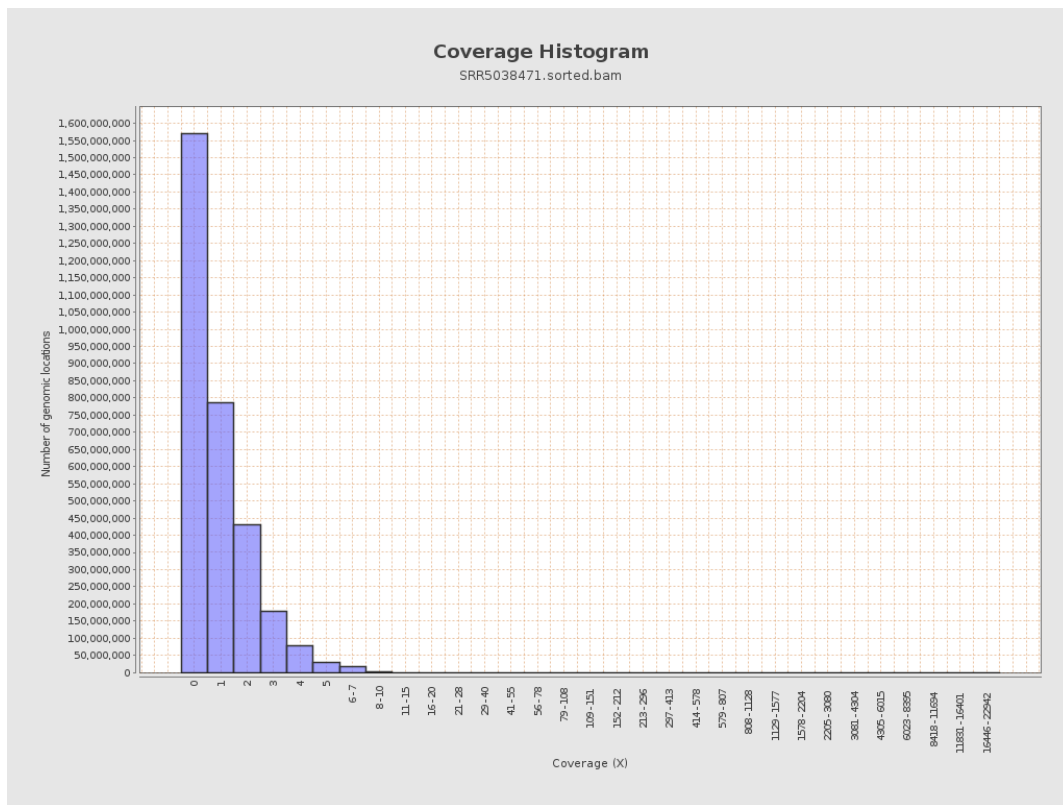
		bases	coverage	deviation
chr1	249250621	250138558	1.0036	23.1588
chr2	243199373	245398108	1.009	7.3792
chr3	198022430	194884856	0.9842	1.3456
chr4	191154276	154092622	0.8061	5.6724
chr5	180915260	181576986	1.0037	1.3159
chr6	171115067	164513760	0.9614	4.182
chr7	159138663	149581731	0.9399	7.3225
chr8	146364022	159053225	1.0867	5.9546
chr9	141213431	123400868	0.8739	10.0279
chr10	135534747	155022871	1.1438	19.2574
chr11	135006516	133847965	0.9914	4.0613
chr12	133851895	125588280	0.9383	1.5235
chr13	115169878	92444192	0.8027	1.1751
chr14	107349540	91131985	0.8489	1.26
chr15	102531392	83237301	0.8118	1.2014
chr16	90354753	91721954	1.0151	5.2414
chr17	81195210	85765562	1.0563	5.1505
chr18	78077248	92507301	1.1848	8.4369
chr19	59128983	60487855	1.023	9.4715
chr20	63025520	73013126	1.1585	2.2701
chr21	48129895	36452803	0.7574	3.0926
chr22	51304566	31195918	0.6081	1.0755
chrMT	16571	5585639	337.0731	37.987
chrX	155270560	114765294	0.7391	1.9475

chrY	59373566	6841180	0.1152	5.9356
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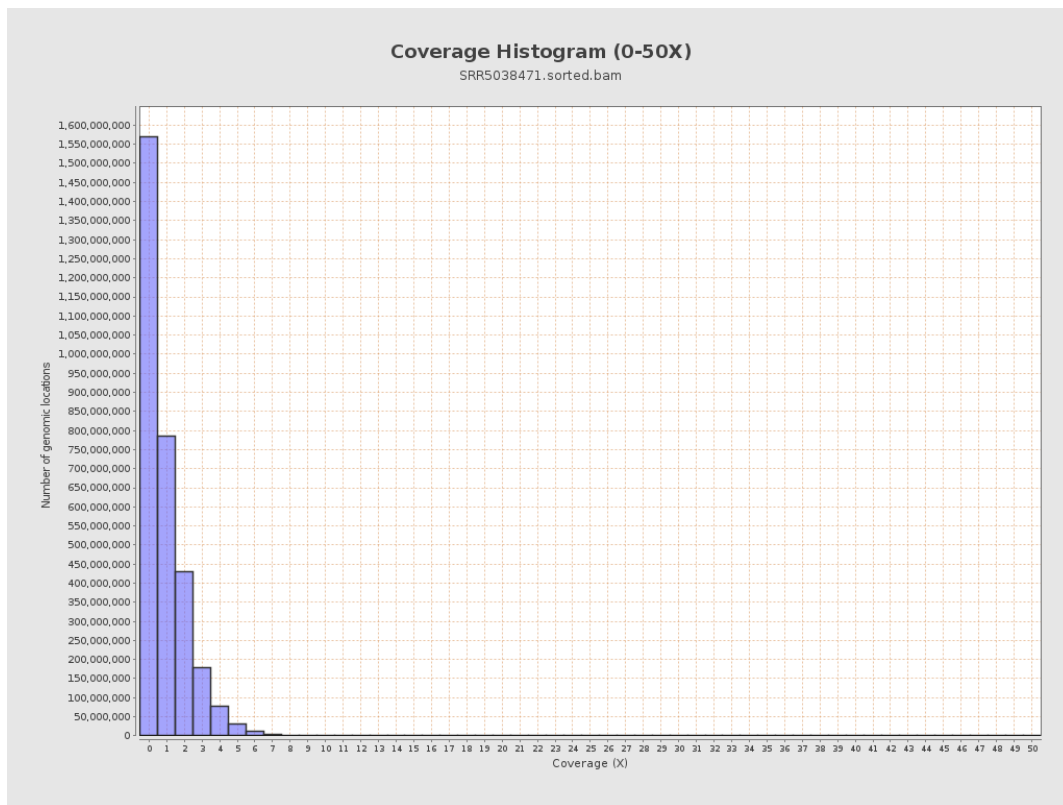
3. Results : Coverage across reference



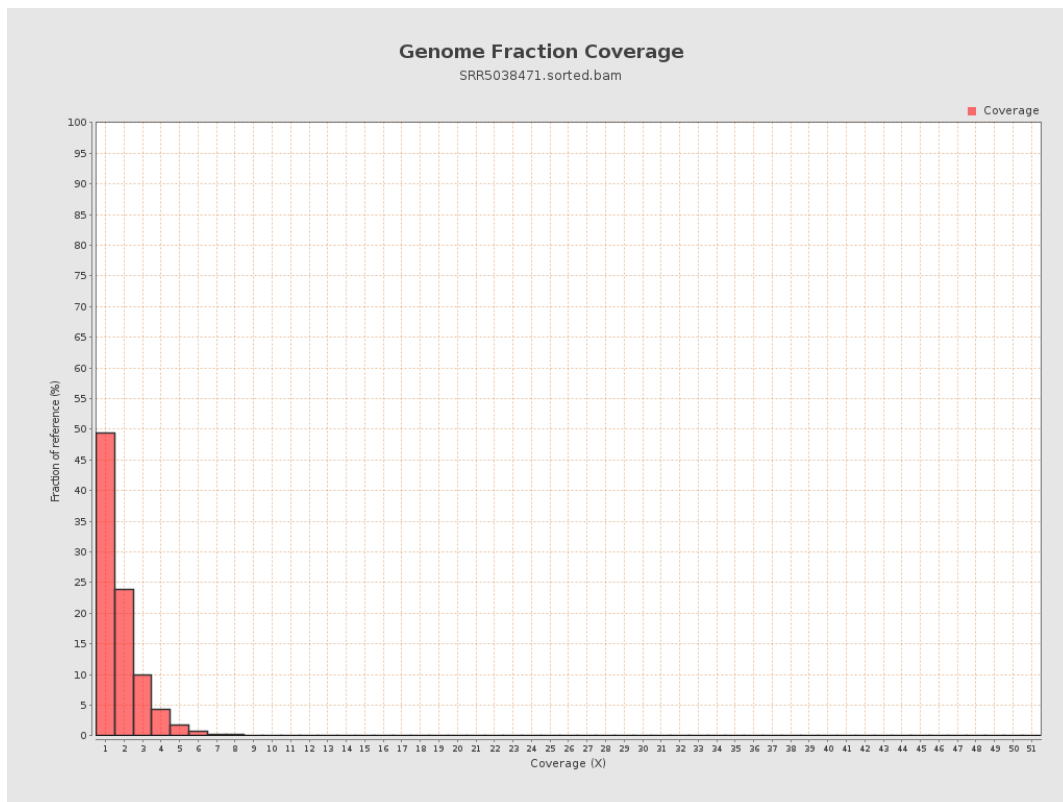
4. Results : Coverage Histogram



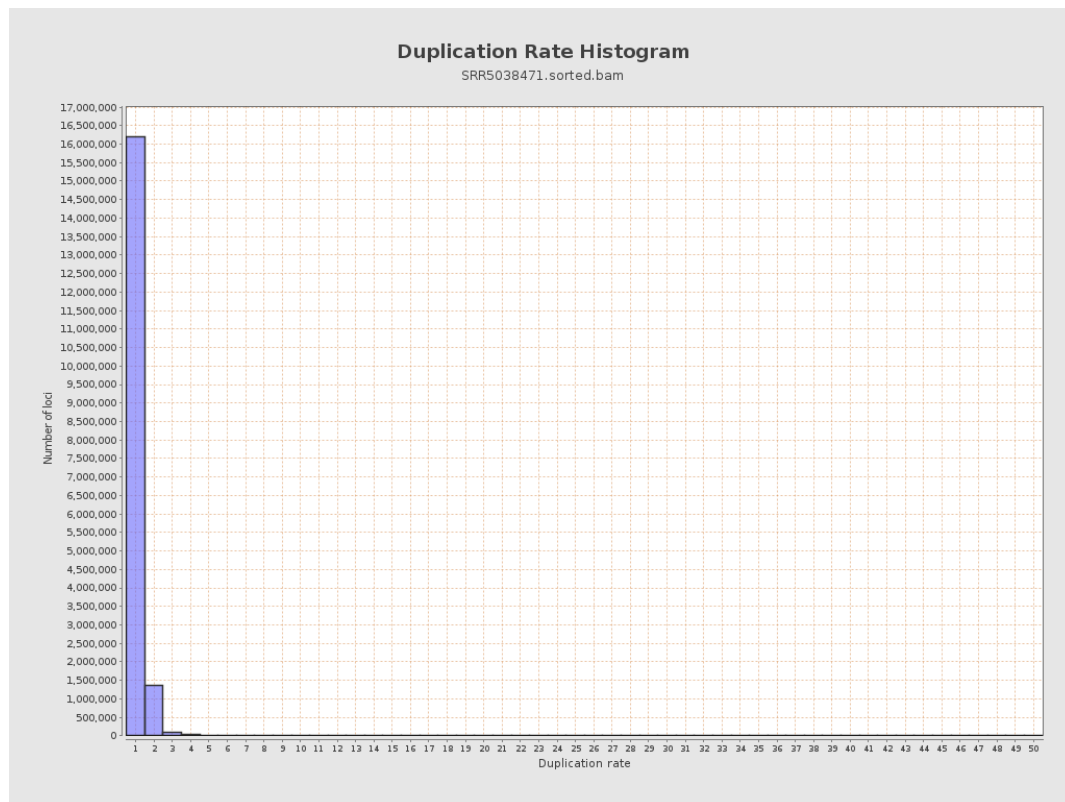
5. Results : Coverage Histogram (0-50X)



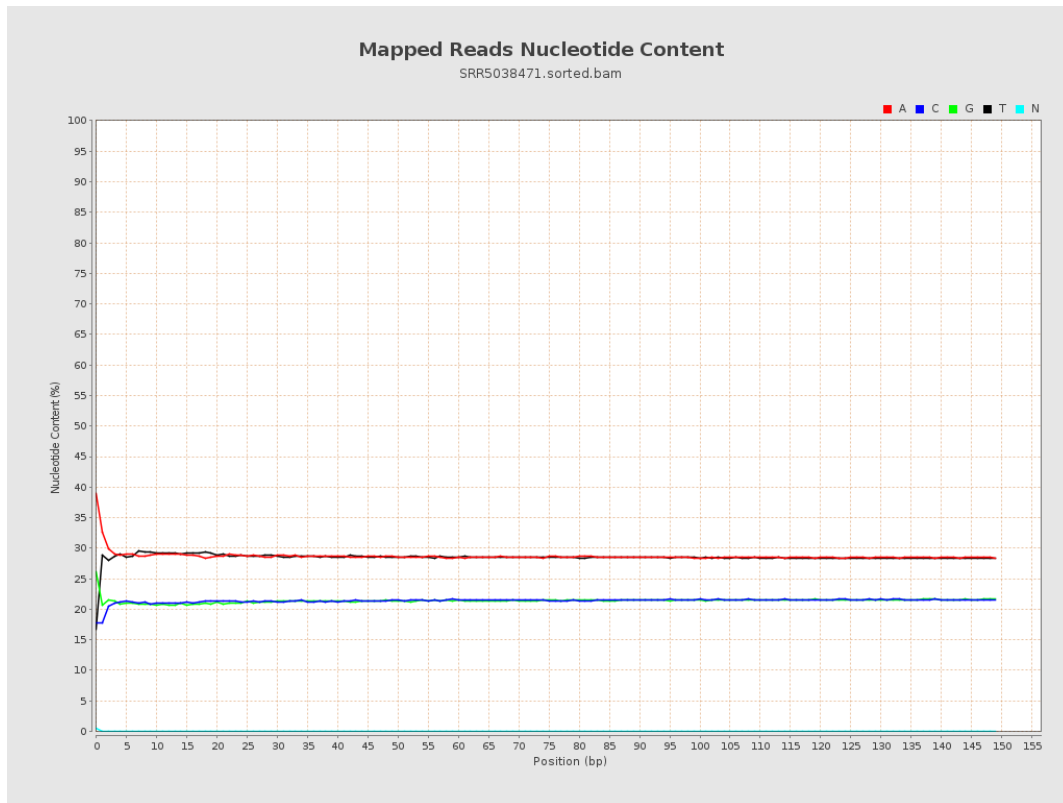
6. Results : Genome Fraction Coverage



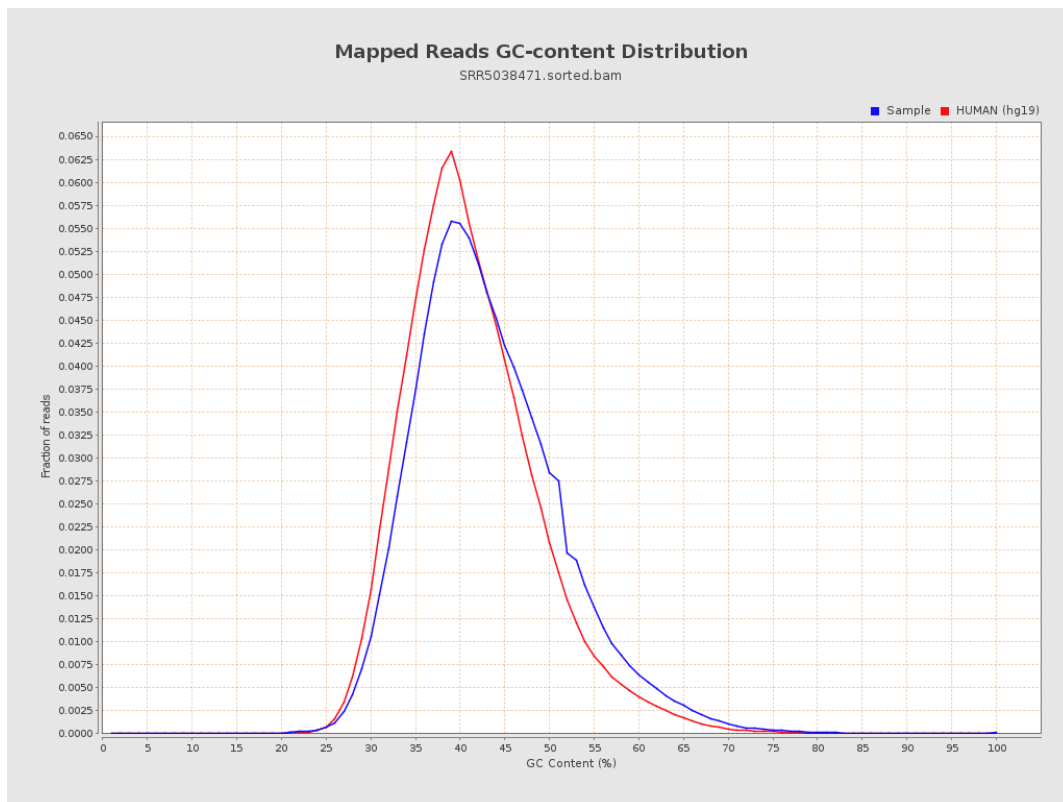
7. Results : Duplication Rate Histogram



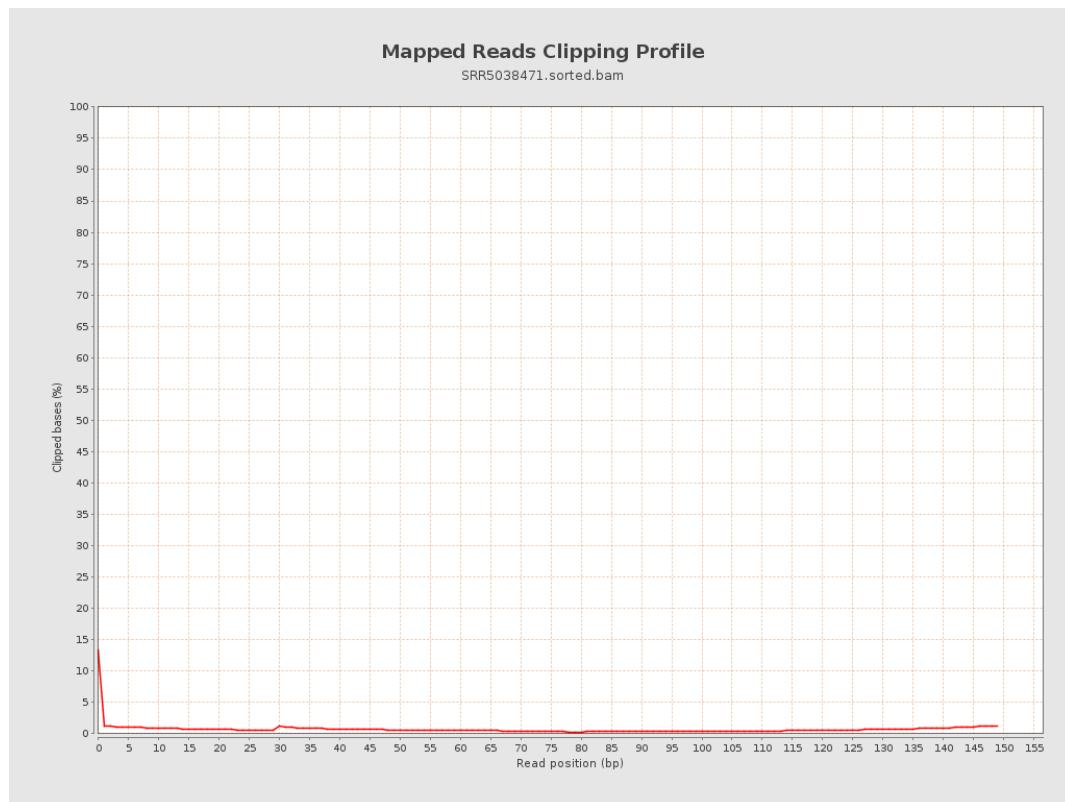
8. Results : Mapped Reads Nucleotide Content



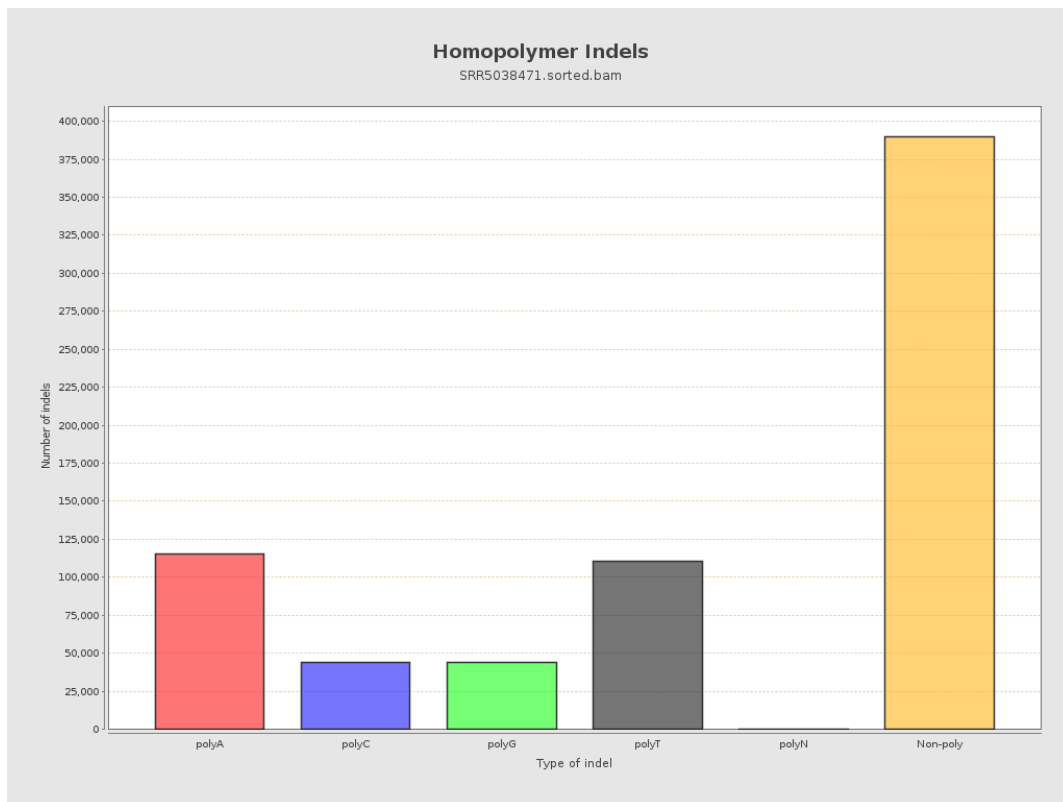
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



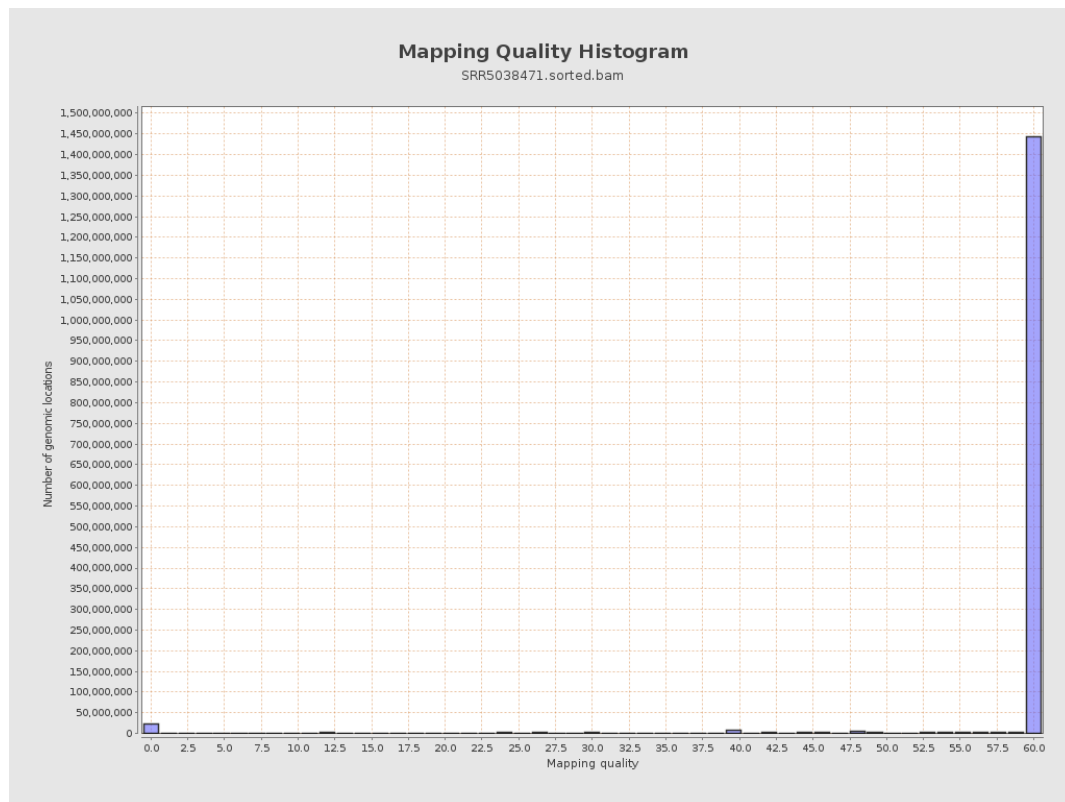
11. Results : Homopolymer Indels



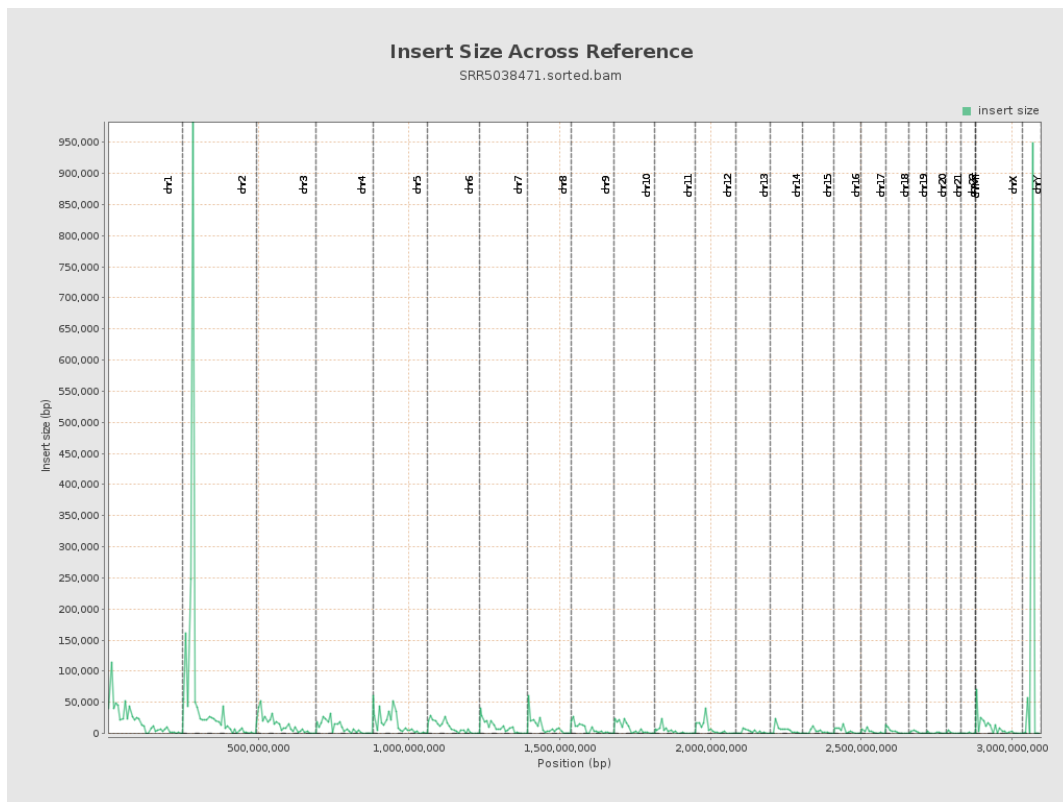
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

