

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 06:08:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038433.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_SRR5038433 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038433_1.fastq.gz SRR5038433_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 06:08:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038433.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,440,166
Mapped reads	15,576,850 / 94.75%
Unmapped reads	863,316 / 5.25%
Mapped paired reads	15,576,850 / 94.75%
Mapped reads, first in pair	7,911,956 / 48.13%
Mapped reads, second in pair	7,664,894 / 46.62%
Mapped reads, both in pair	15,283,158 / 92.96%
Mapped reads, singletons	293,692 / 1.79%
Secondary alignments	0
Supplementary alignments	240,782 / 1.46%
Read min/max/mean length	30 / 150 / 150.73
Duplicated reads (estimated)	2,657,166 / 16.16%
Duplication rate	11.77%
Clipped reads	7,257,894 / 44.15%

2.2. ACGT Content

Number/percentage of A's	601,348,825 / 28.59%
Number/percentage of C's	417,101,132 / 19.83%
Number/percentage of T's	614,110,021 / 29.2%
Number/percentage of G's	470,519,417 / 22.37%
Number/percentage of N's	164,696 / 0.01%

GC Percentage	42.2%
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2.3. Coverage

Mean	0.6799
Standard Deviation	9.5644

2.4. Mapping Quality

Mean Mapping Quality	53.39
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2.5. Insert size

Mean	92,491.89
Standard Deviation	2,964,302.51
P25/Median/P75	207 / 259 / 327

2.6. Mismatches and indels

General error rate	1.36%
Mismatches	27,711,837
Insertions	364,846
Mapped reads with at least one insertion	2.22%
Deletions	746,092
Mapped reads with at least one deletion	4.61%
Homopolymer indels	47.42%

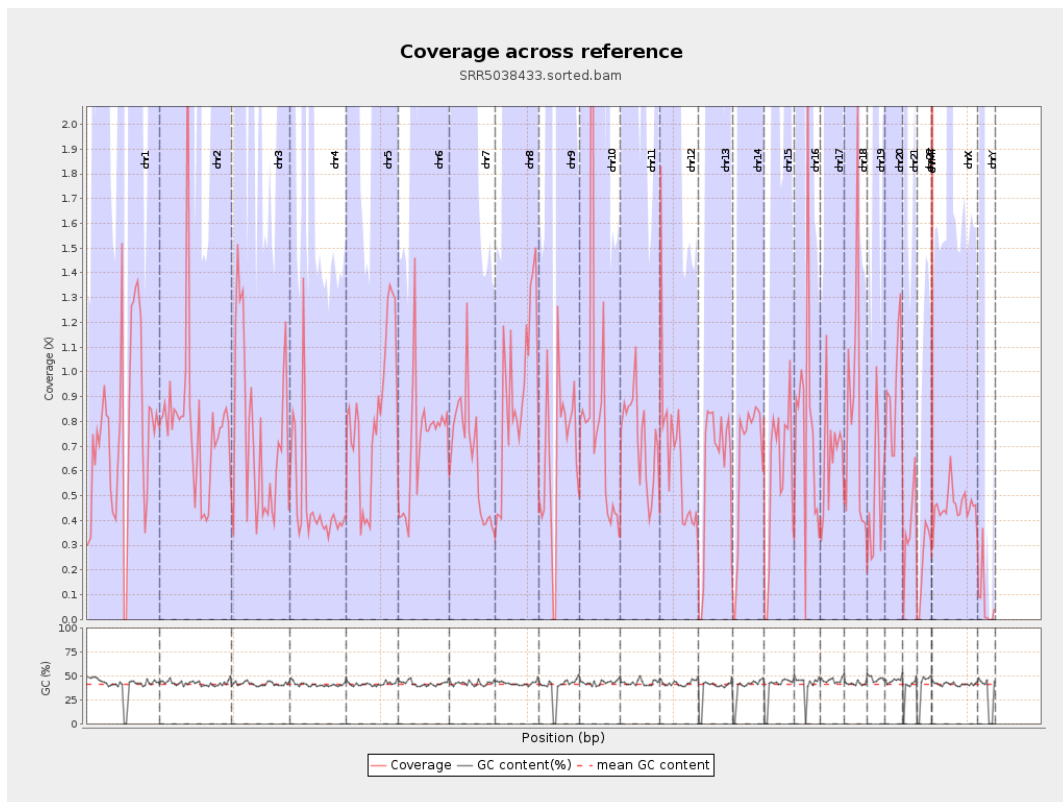
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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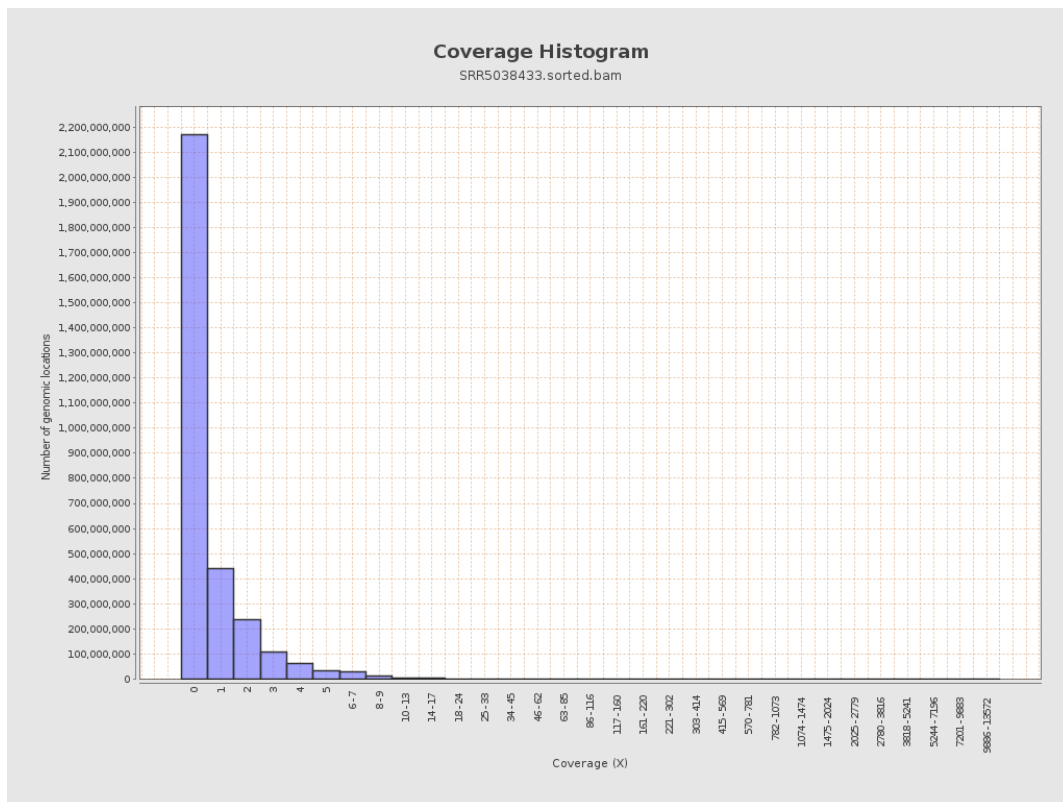
		bases	coverage	deviation
chr1	249250621	187853773	0.7537	13.4925
chr2	243199373	192446639	0.7913	10.3162
chr3	198022430	146874837	0.7417	1.5855
chr4	191154276	90570670	0.4738	8.0804
chr5	180915260	147450508	0.815	1.5566
chr6	171115067	123885060	0.724	7.5389
chr7	159138663	103648436	0.6513	10.1663
chr8	146364022	136242582	0.9308	3.6475
chr9	141213431	91469592	0.6477	15.3275
chr10	135534747	116930457	0.8627	25.8877
chr11	135006516	98019009	0.726	7.6847
chr12	133851895	87844225	0.6563	1.5295
chr13	115169878	71333433	0.6194	1.3049
chr14	107349540	69863421	0.6508	1.4383
chr15	102531392	58601862	0.5716	1.2759
chr16	90354753	69569977	0.77	10.2668
chr17	81195210	53227644	0.6556	11.6124
chr18	78077248	63638375	0.8151	10.5404
chr19	59128983	28791544	0.4869	5.5927
chr20	63025520	57642731	0.9146	2.9357
chr21	48129895	18019413	0.3744	3.7917
chr22	51304566	12031931	0.2345	0.8141
chrMT	16571	3195404	192.8311	97.9647
chrX	155270560	71111097	0.458	2.1139

chrY	59373566	4439781	0.0748	7.895
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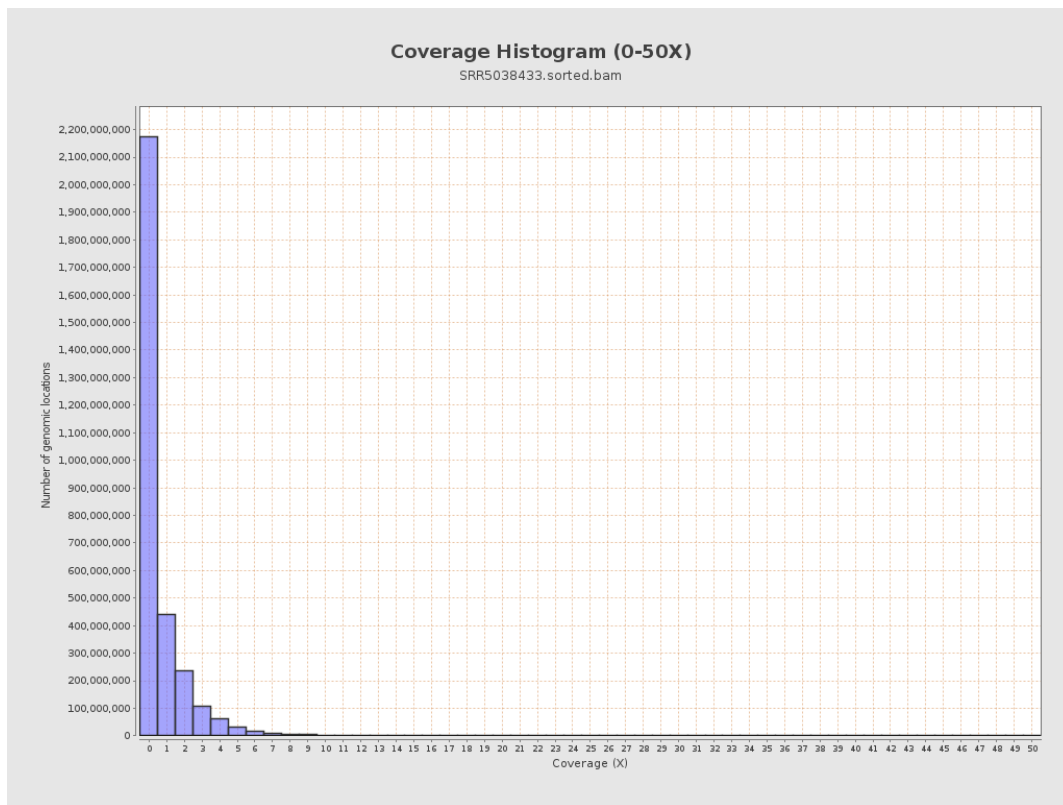
3. Results : Coverage across reference



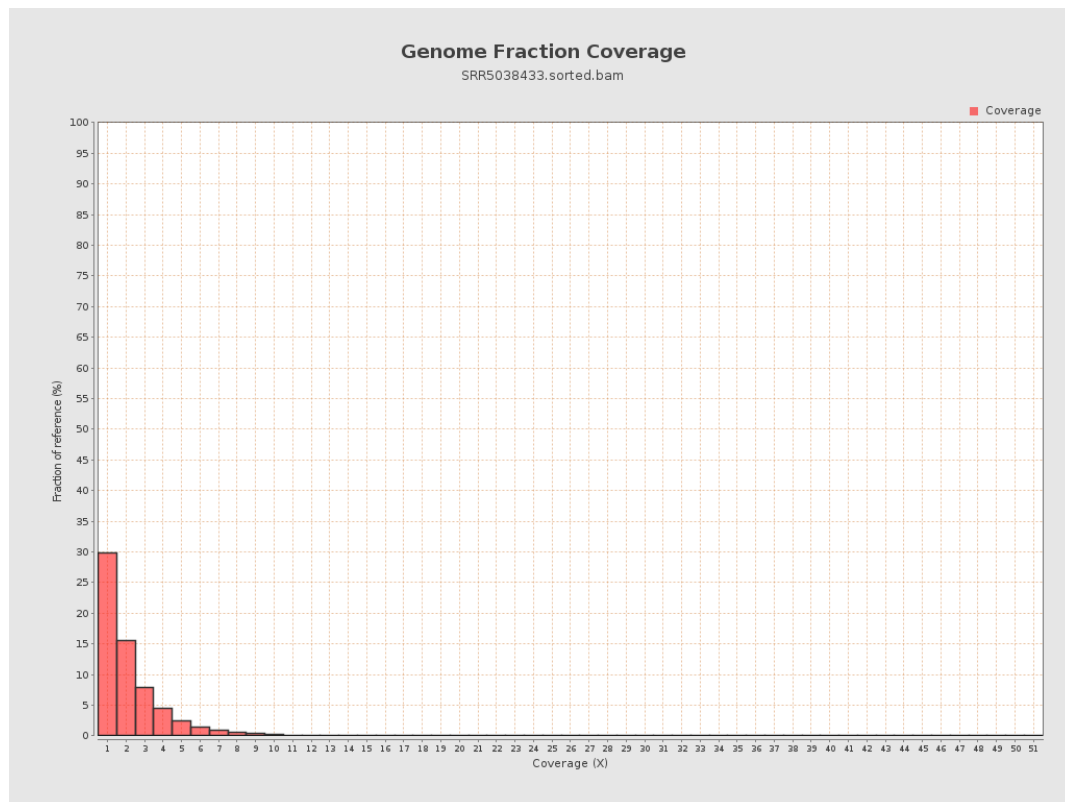
4. Results : Coverage Histogram



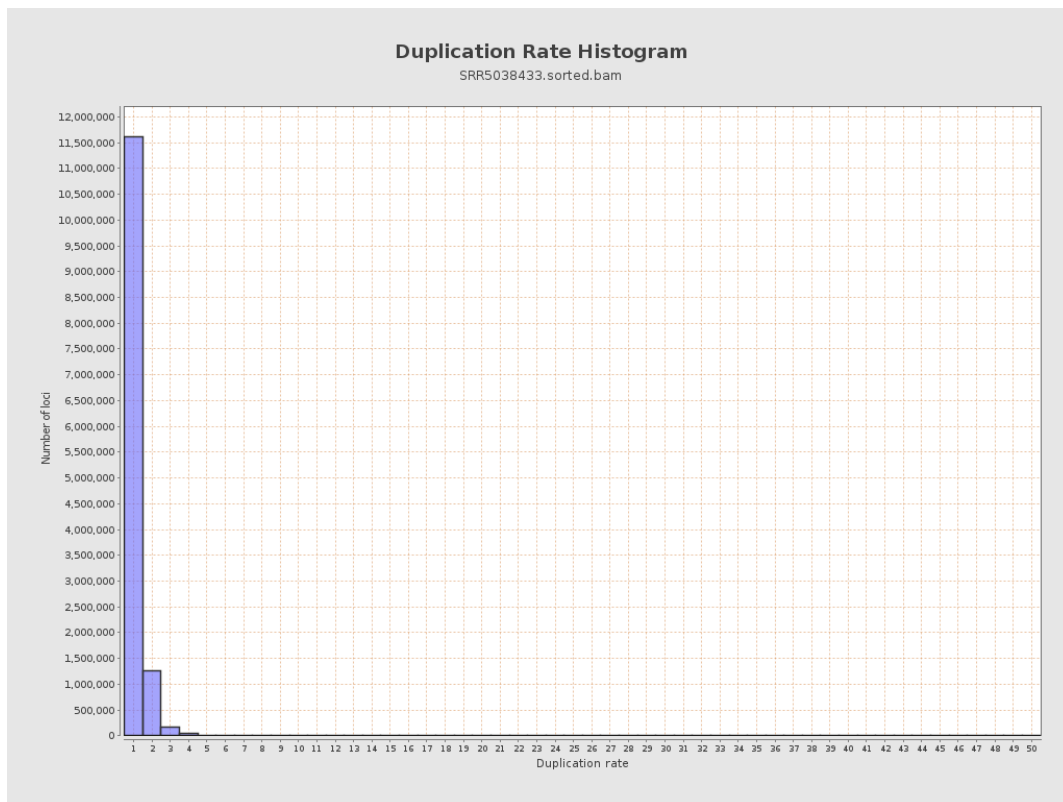
5. Results : Coverage Histogram (0-50X)



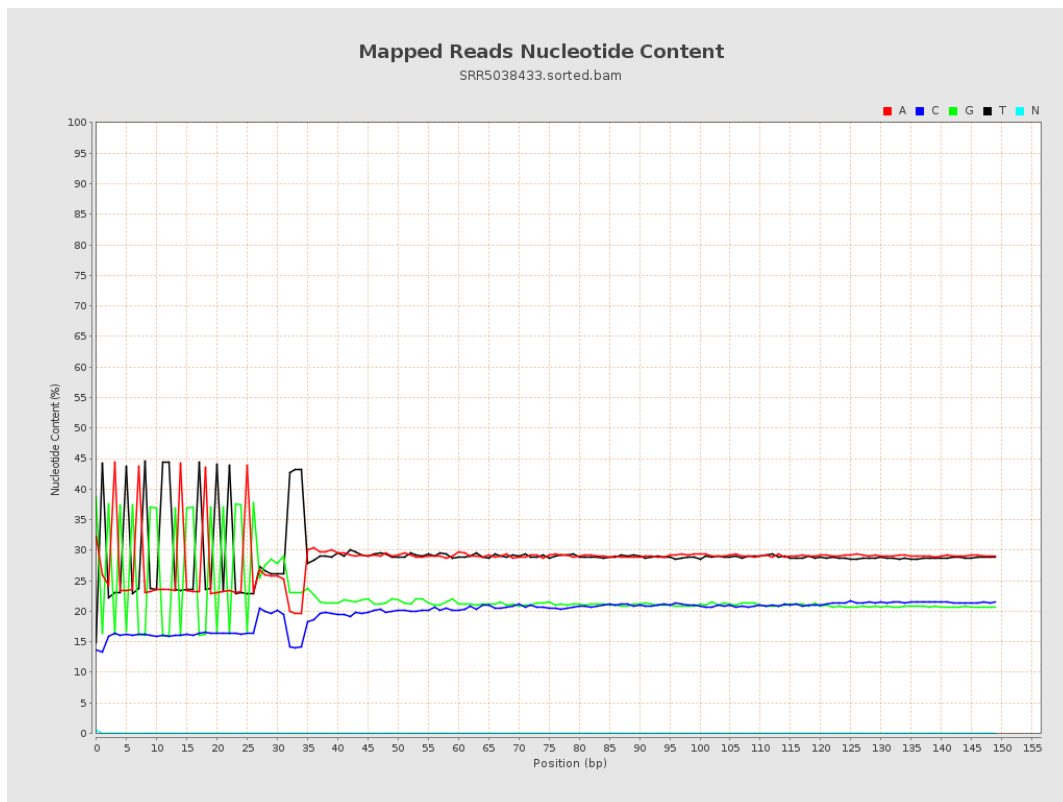
6. Results : Genome Fraction Coverage



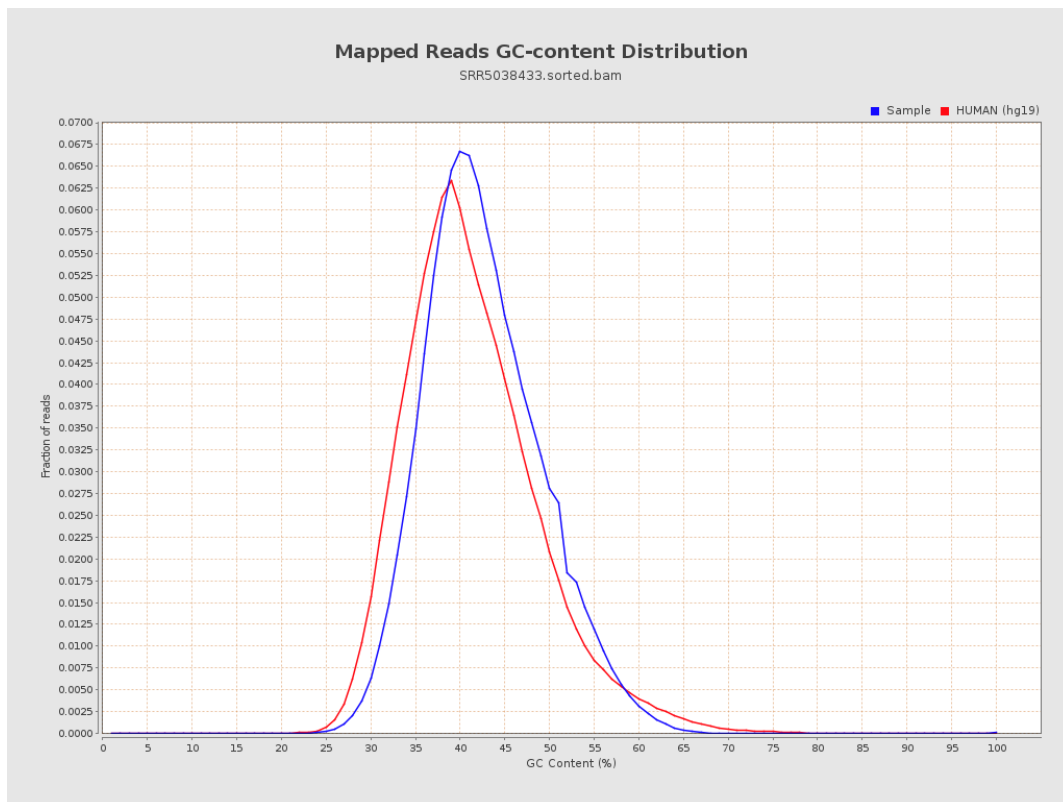
7. Results : Duplication Rate Histogram



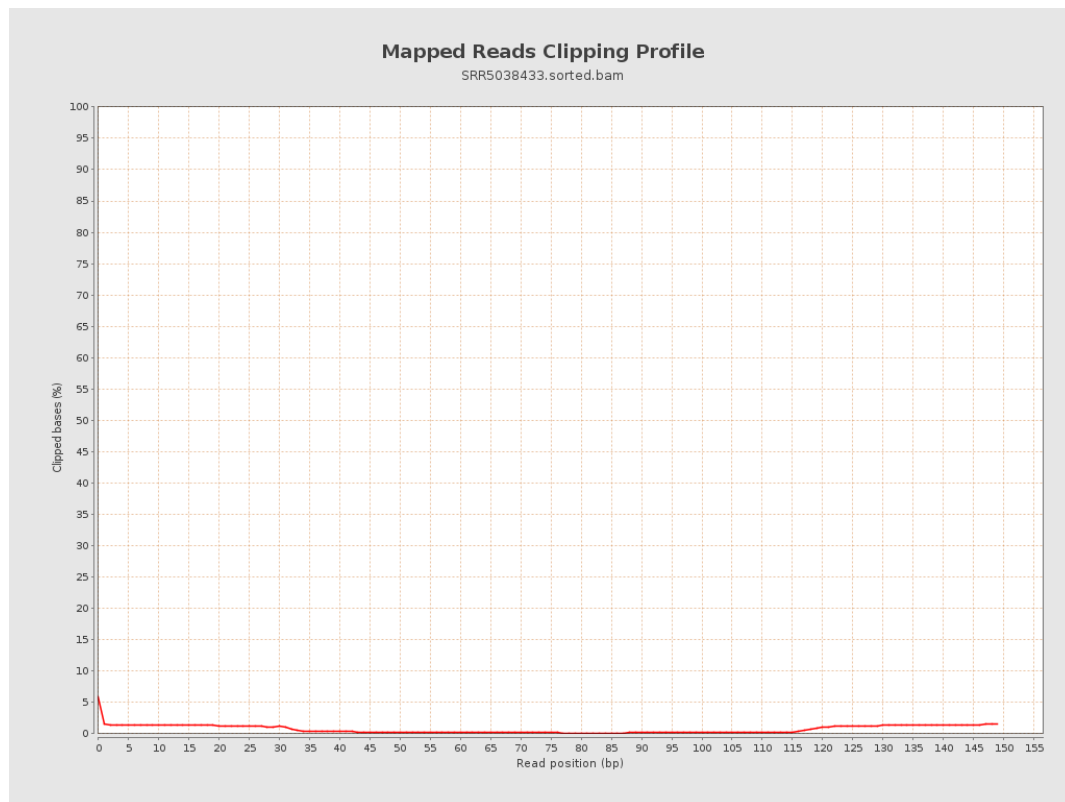
8. Results : Mapped Reads Nucleotide Content



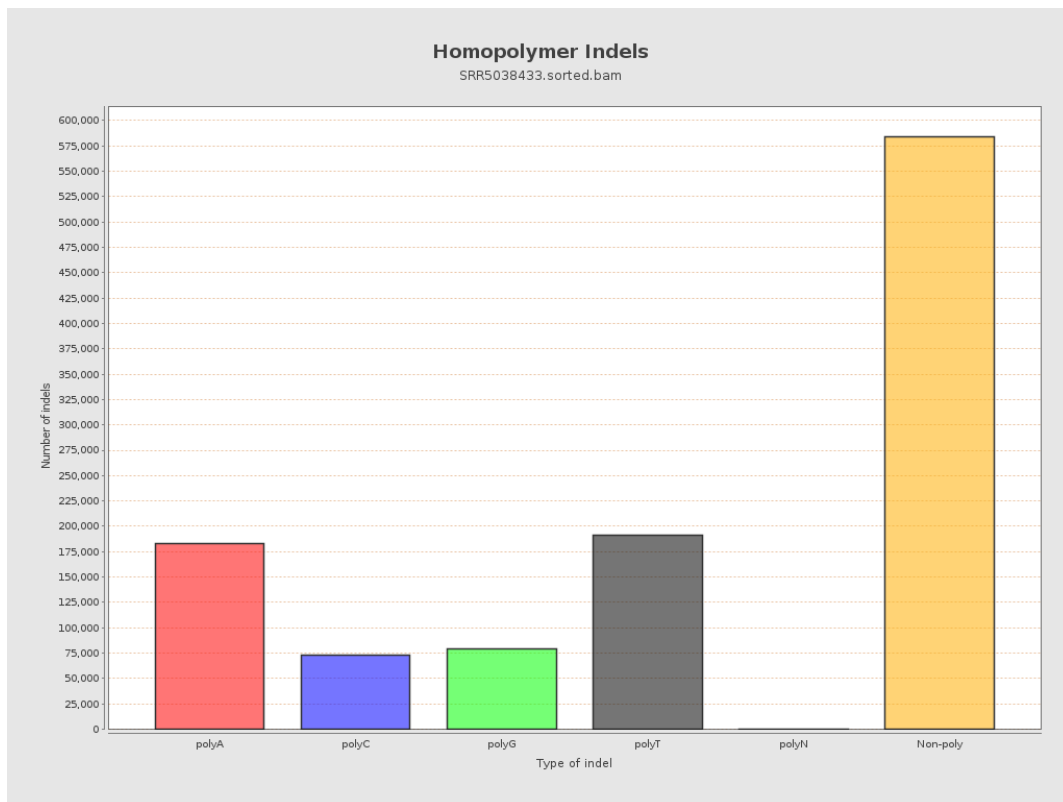
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



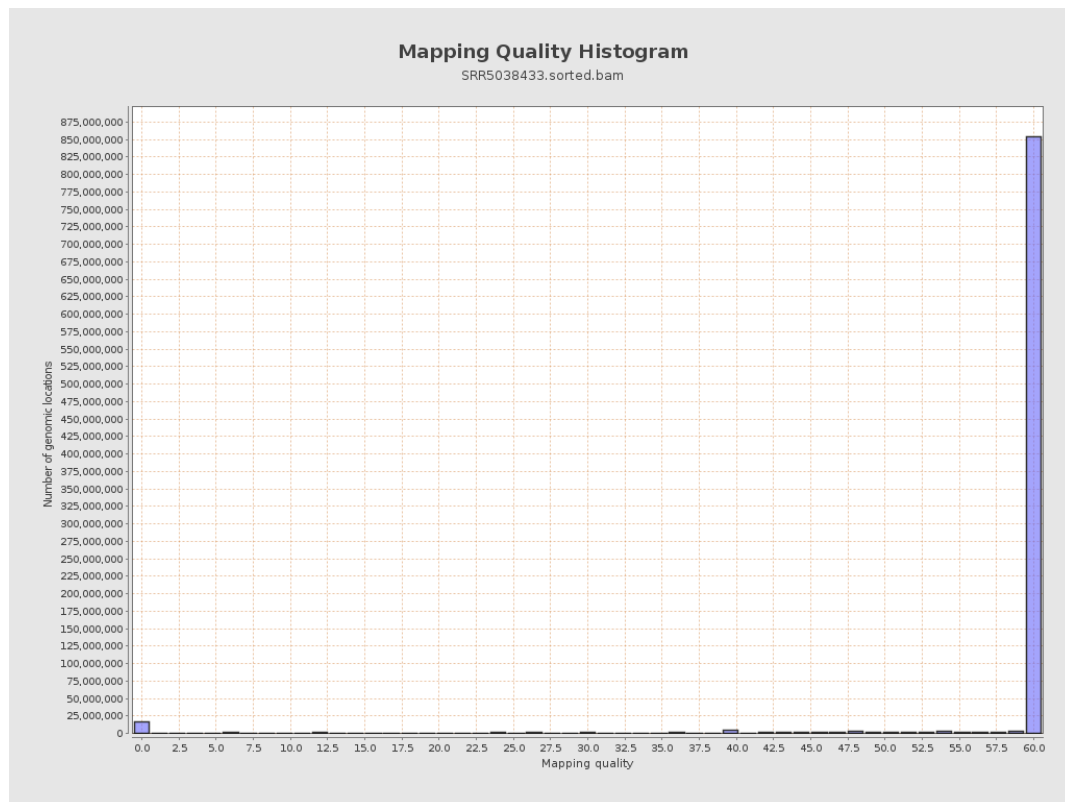
11. Results : Homopolymer Indels



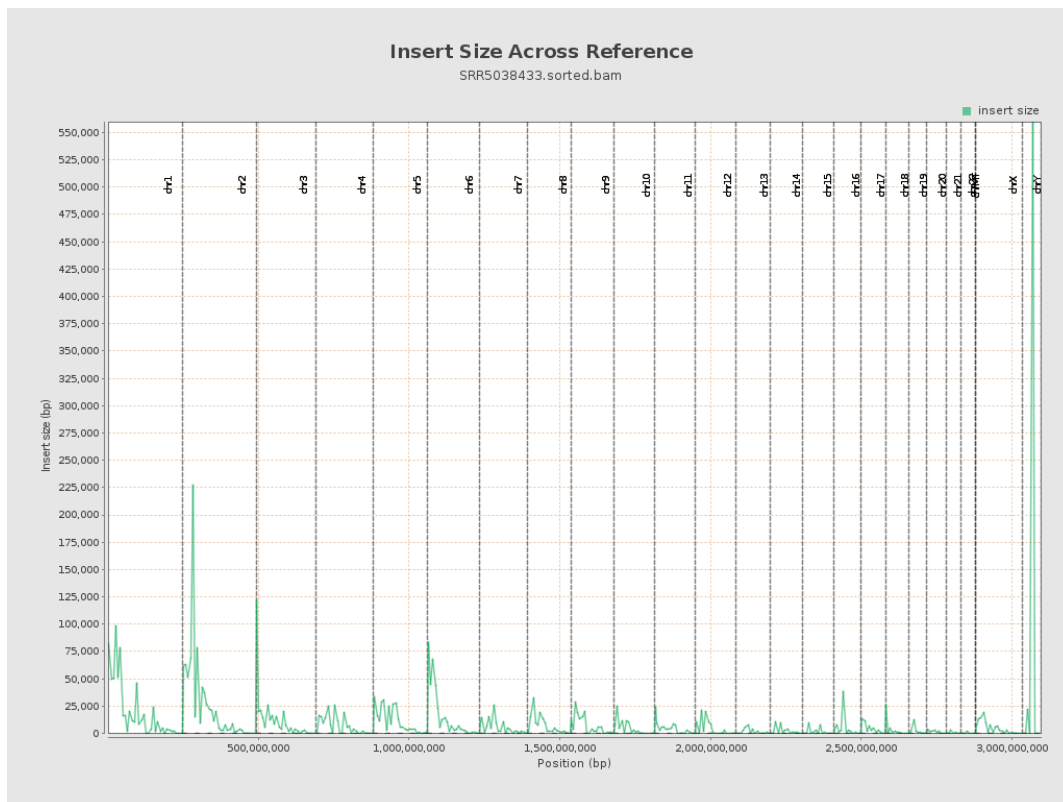
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

