

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 16:43:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038405.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_SRR5038405 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038405_1.fastq.gz SRR5038405_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 16:43:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038405.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,099,464
Mapped reads	12,739,628 / 97.25%
Unmapped reads	359,836 / 2.75%
Mapped paired reads	12,739,628 / 97.25%
Mapped reads, first in pair	6,444,328 / 49.2%
Mapped reads, second in pair	6,295,300 / 48.06%
Mapped reads, both in pair	12,575,320 / 96%
Mapped reads, singletons	164,308 / 1.25%
Secondary alignments	0
Supplementary alignments	223,390 / 1.71%
Read min/max/mean length	30 / 150 / 150.88
Duplicated reads (estimated)	1,697,703 / 12.96%
Duplication rate	8.18%
Clipped reads	2,985,342 / 22.79%

2.2. ACGT Content

Number/percentage of A's	532,237,005 / 29.2%
Number/percentage of C's	370,879,313 / 20.35%
Number/percentage of T's	533,514,700 / 29.27%
Number/percentage of G's	386,261,445 / 21.19%
Number/percentage of N's	38,640 / 0%

GC Percentage	41.53%
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2.3. Coverage

Mean	0.5893
Standard Deviation	8.0814

2.4. Mapping Quality

Mean Mapping Quality	53.85
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2.5. Insert size

Mean	89,658.79
Standard Deviation	2,816,345.88
P25/Median/P75	226 / 266 / 317

2.6. Mismatches and indels

General error rate	1.4%
Mismatches	24,753,856
Insertions	305,394
Mapped reads with at least one insertion	2.26%
Deletions	611,864
Mapped reads with at least one deletion	4.62%
Homopolymer indels	47.3%

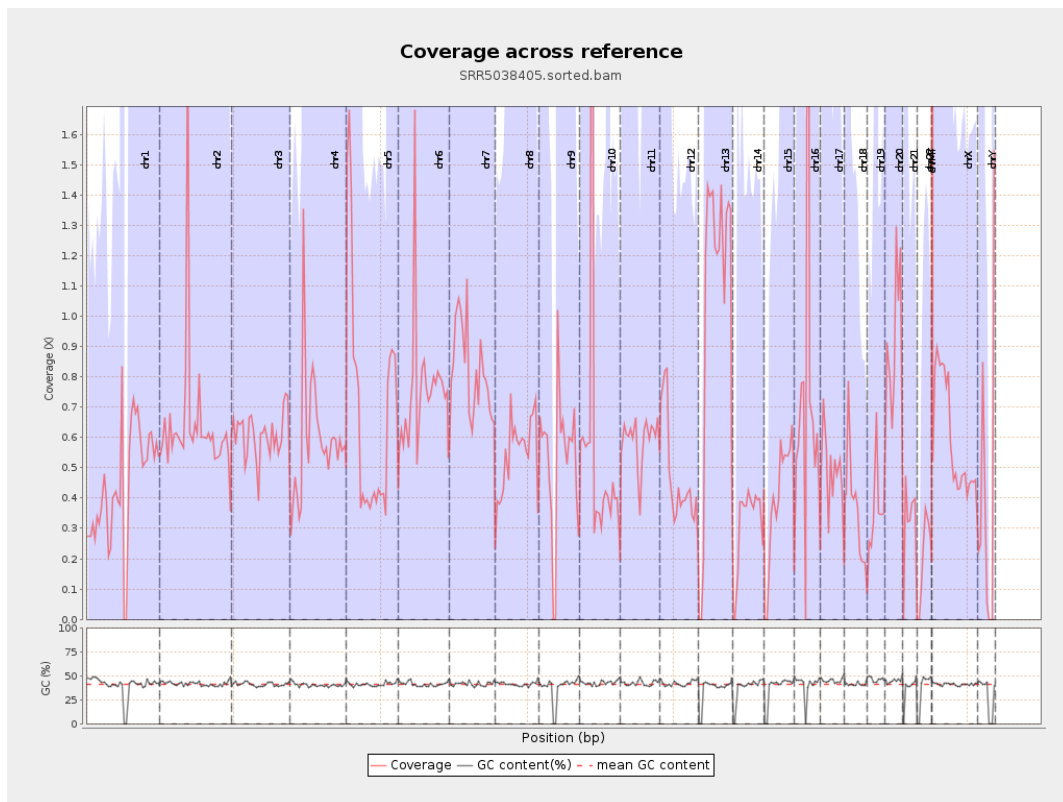
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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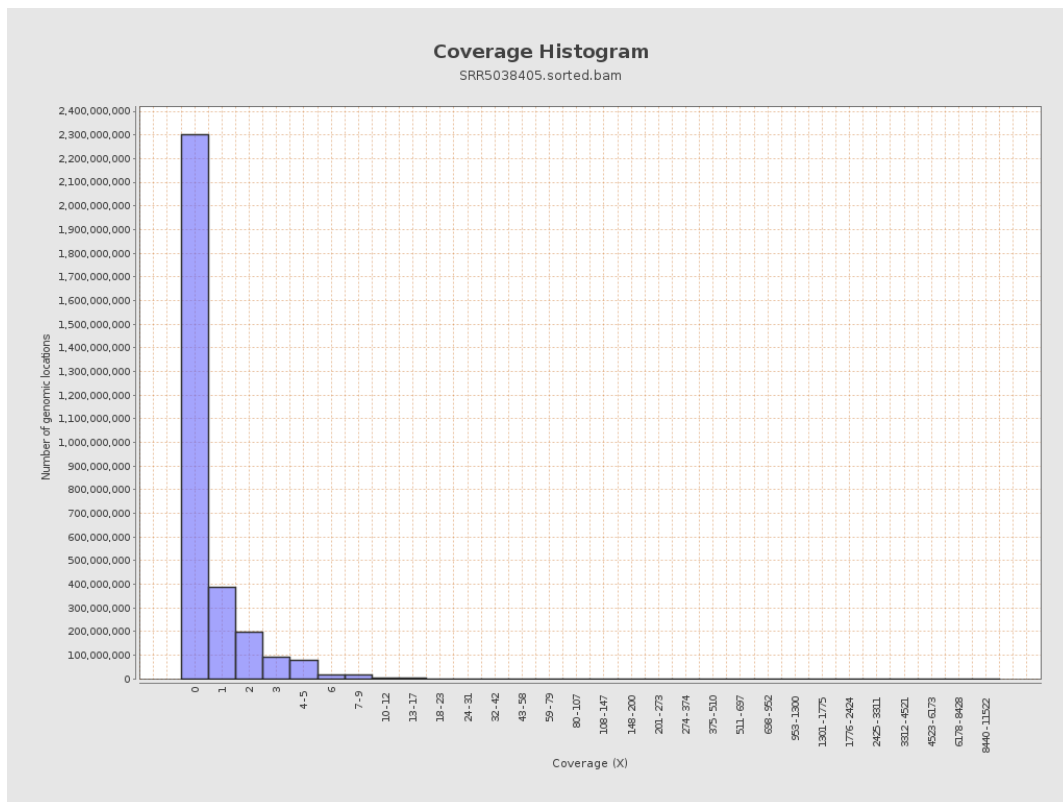
		bases	coverage	deviation
chr1	249250621	111055206	0.4456	7.1824
chr2	243199373	156406512	0.6431	8.007
chr3	198022430	120786602	0.61	1.3891
chr4	191154276	112157314	0.5867	6.2916
chr5	180915260	124227356	0.6867	1.58
chr6	171115067	130391928	0.762	9.82
chr7	159138663	129812618	0.8157	8.7861
chr8	146364022	80749666	0.5517	2.049
chr9	141213431	72507485	0.5135	10.7437
chr10	135534747	79766374	0.5885	22.635
chr11	135006516	78649677	0.5826	3.5397
chr12	133851895	63888953	0.4773	1.2003
chr13	115169878	123521101	1.0725	2.035
chr14	107349540	33689750	0.3138	1.0133
chr15	102531392	40727359	0.3972	1.0478
chr16	90354753	69728342	0.7717	16.7221
chr17	81195210	39057452	0.481	4.2136
chr18	78077248	28420014	0.364	8.9842
chr19	59128983	20634371	0.349	4.0548
chr20	63025520	57102668	0.906	2.4942
chr21	48129895	15651772	0.3252	3.069
chr22	51304566	10447869	0.2036	0.8178
chrMT	16571	7452993	449.7612	197.1772
chrX	155270560	91957002	0.5922	1.6437

chrY	59373566	25380247	0.4275	11.781
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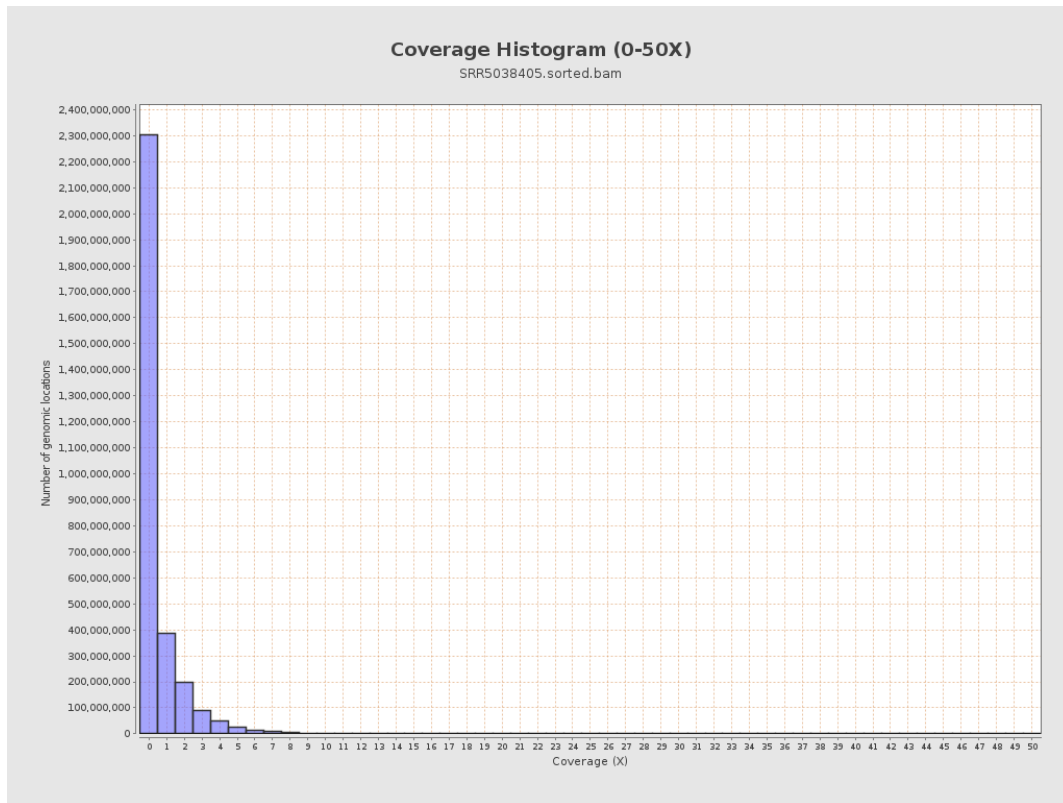
3. Results : Coverage across reference



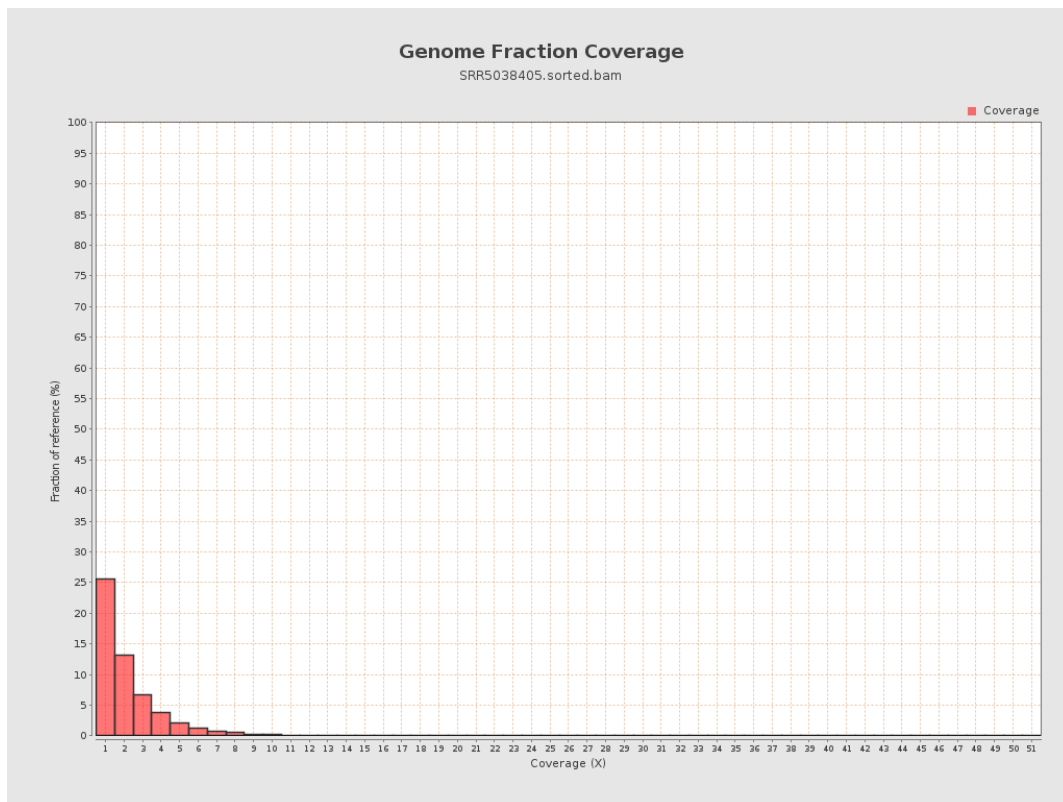
4. Results : Coverage Histogram



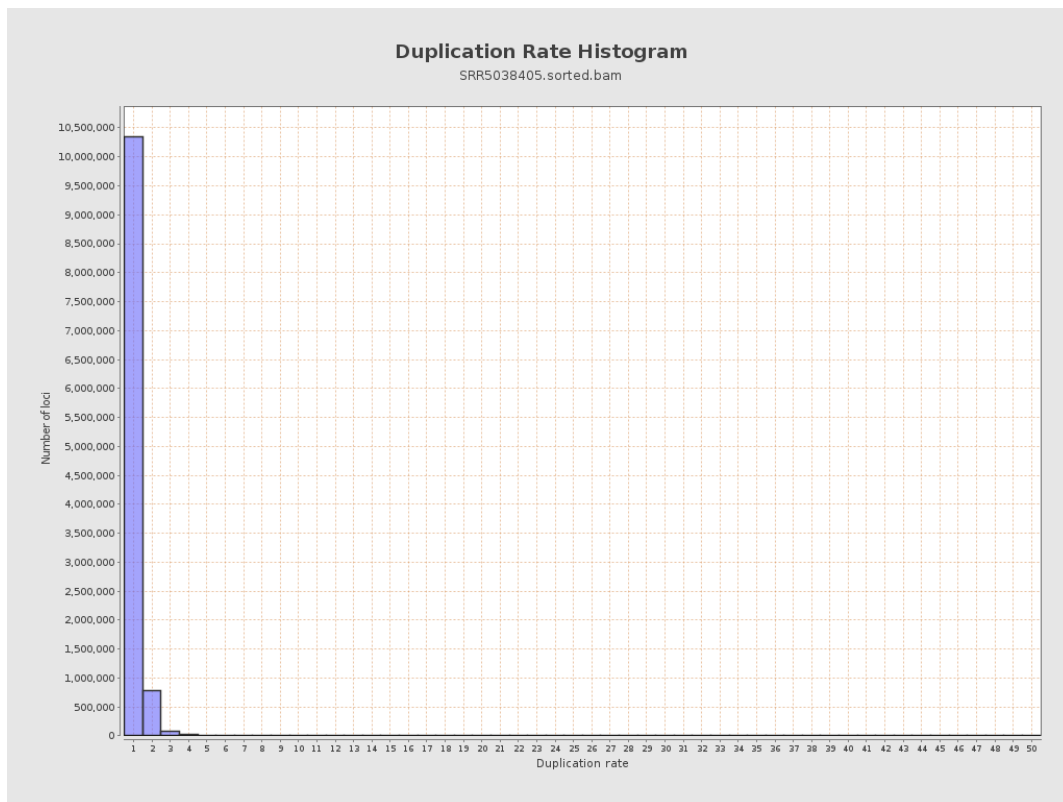
5. Results : Coverage Histogram (0-50X)



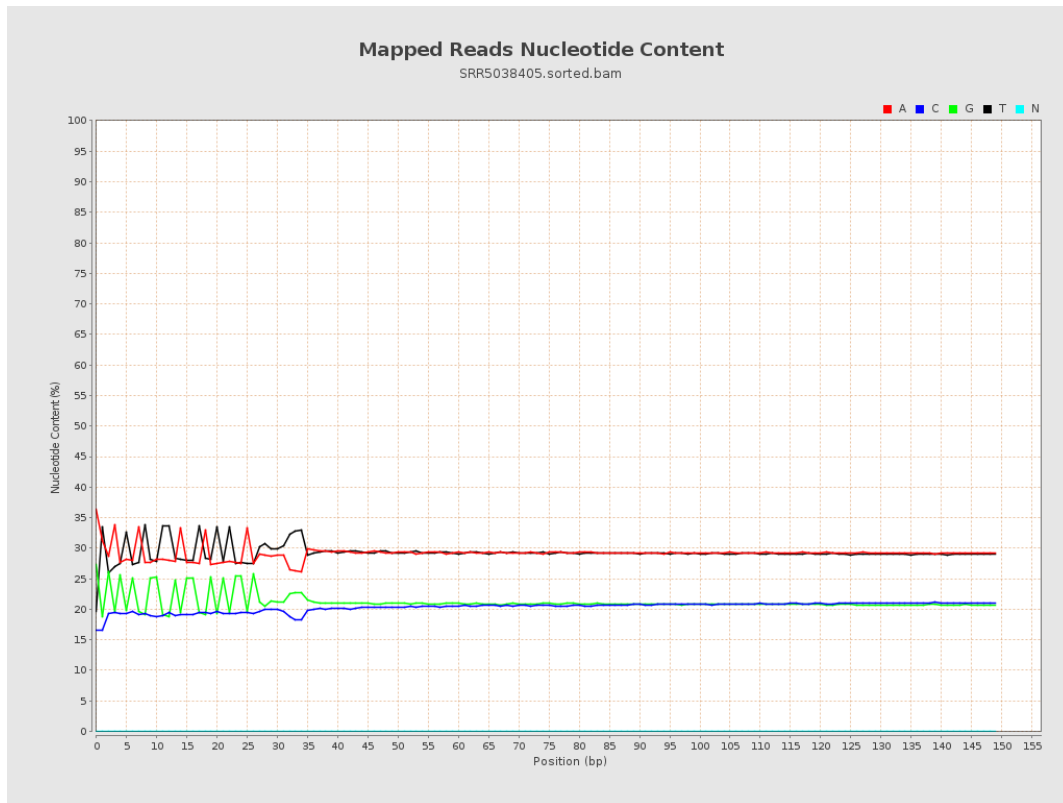
6. Results : Genome Fraction Coverage



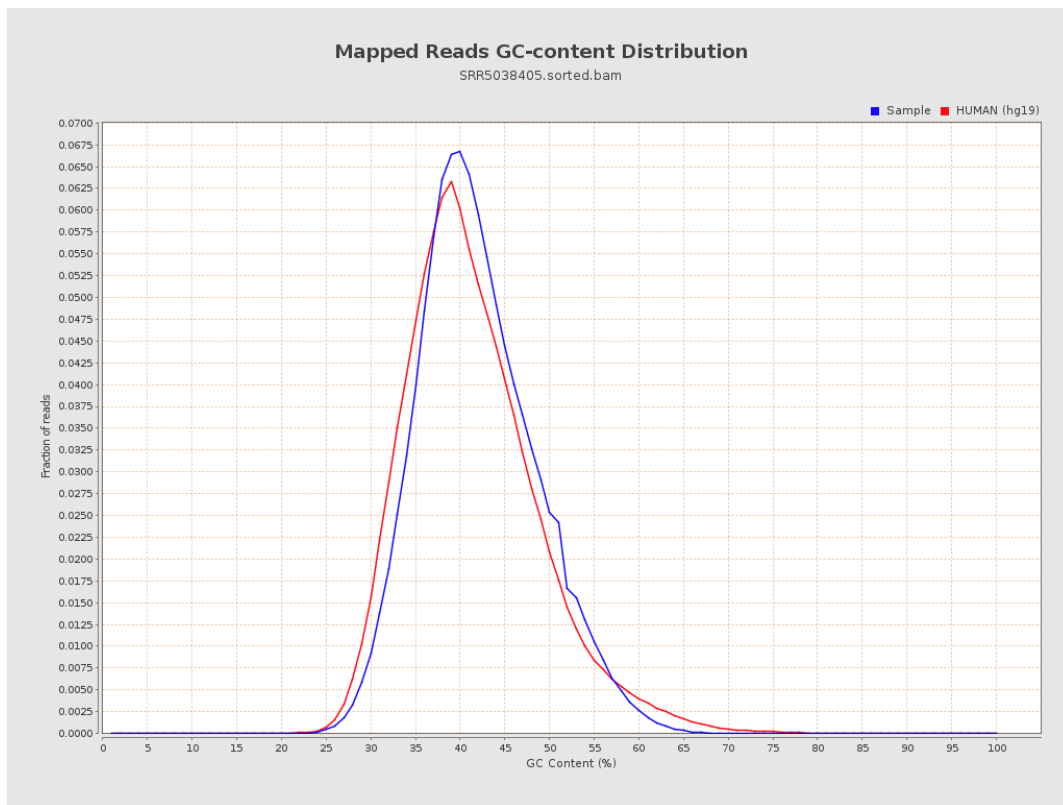
7. Results : Duplication Rate Histogram



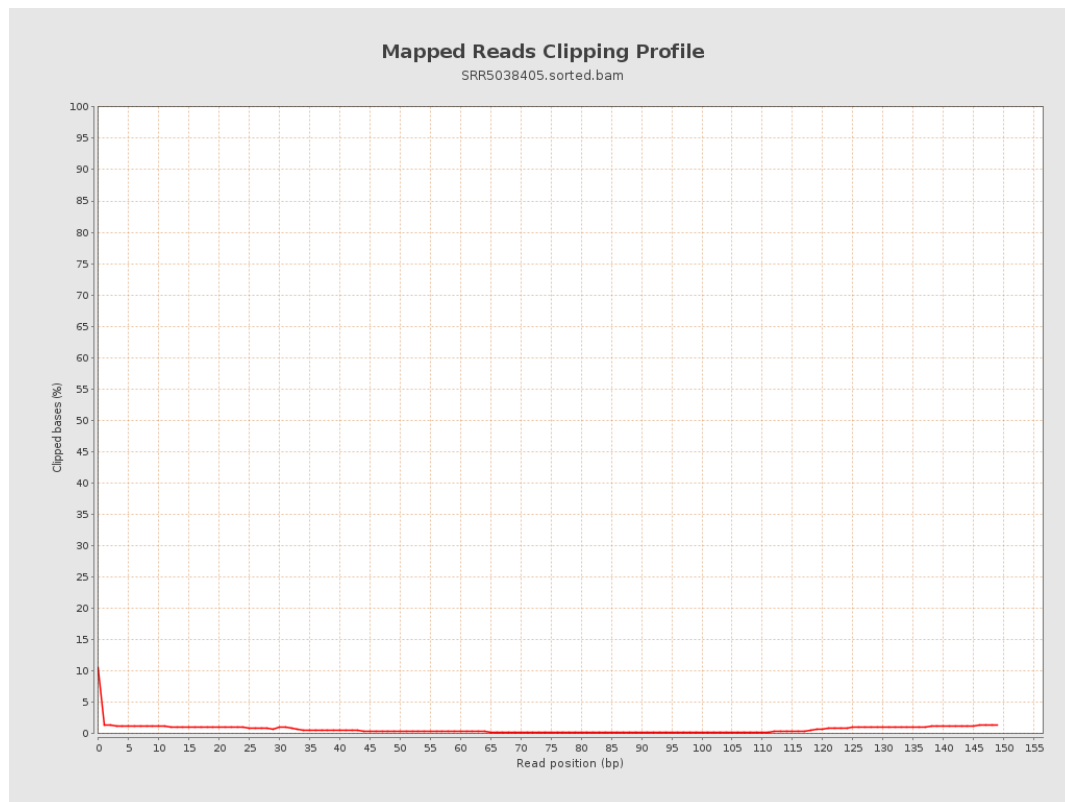
8. Results : Mapped Reads Nucleotide Content



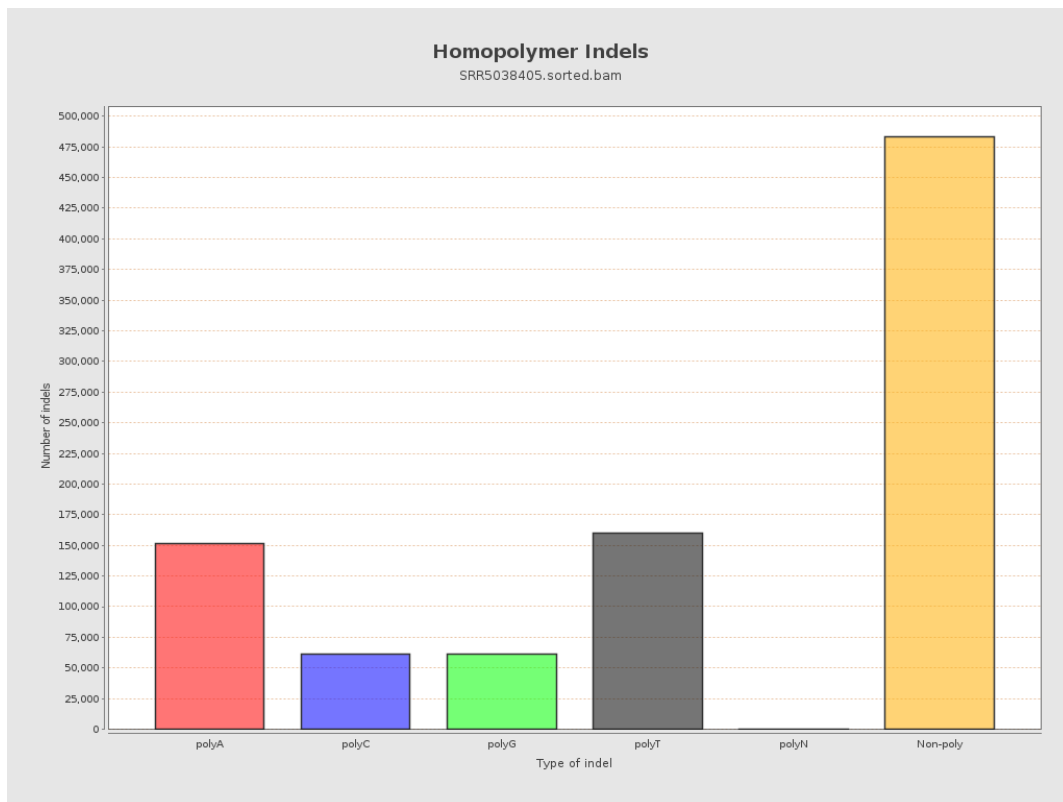
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



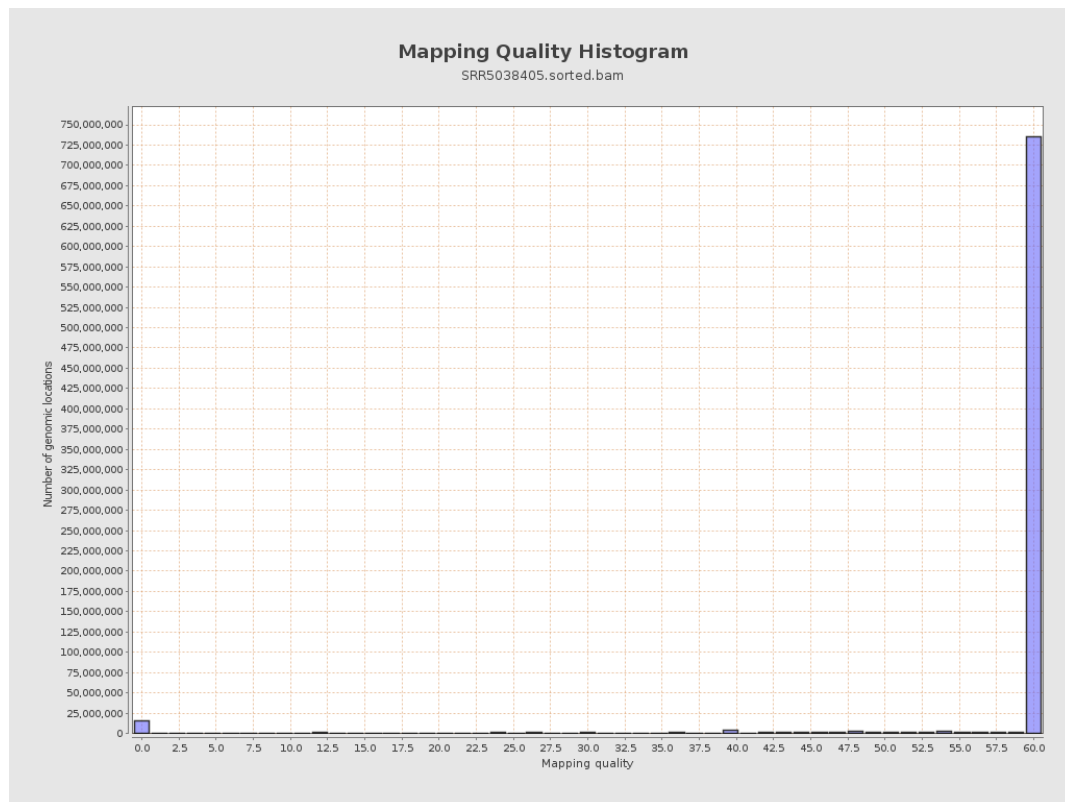
11. Results : Homopolymer Indels



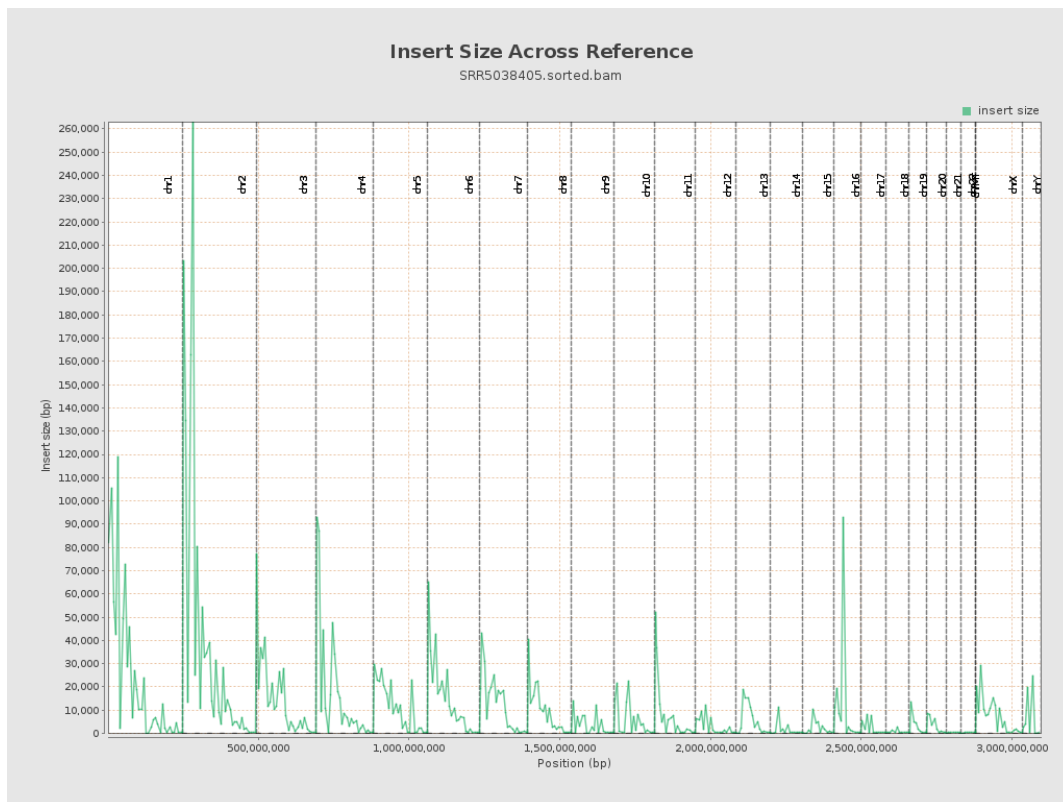
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

