

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 05:57:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038480.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_SRR5038480 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038480_1.fastq.gz SRR5038480_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 05:57:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038480.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,627,970
Mapped reads	16,452,679 / 93.33%
Unmapped reads	1,175,291 / 6.67%
Mapped paired reads	16,452,679 / 93.33%
Mapped reads, first in pair	8,344,842 / 47.34%
Mapped reads, second in pair	8,107,837 / 45.99%
Mapped reads, both in pair	16,172,278 / 91.74%
Mapped reads, singletons	280,401 / 1.59%
Secondary alignments	0
Supplementary alignments	240,125 / 1.36%
Read min/max/mean length	30 / 150 / 150.68
Duplicated reads (estimated)	3,274,057 / 18.57%
Duplication rate	14.1%
Clipped reads	7,756,612 / 44%

2.2. ACGT Content

Number/percentage of A's	634,922,568 / 28.63%
Number/percentage of C's	437,883,853 / 19.74%
Number/percentage of T's	647,450,002 / 29.19%
Number/percentage of G's	497,546,774 / 22.43%
Number/percentage of N's	176,807 / 0.01%

GC Percentage	42.17%
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2.3. Coverage

Mean	0.717
Standard Deviation	8.8138

2.4. Mapping Quality

Mean Mapping Quality	53.38
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2.5. Insert size

Mean	75,615.91
Standard Deviation	2,655,520.41
P25/Median/P75	205 / 256 / 323

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	27,698,889
Insertions	396,798
Mapped reads with at least one insertion	2.29%
Deletions	797,562
Mapped reads with at least one deletion	4.68%
Homopolymer indels	48.08%

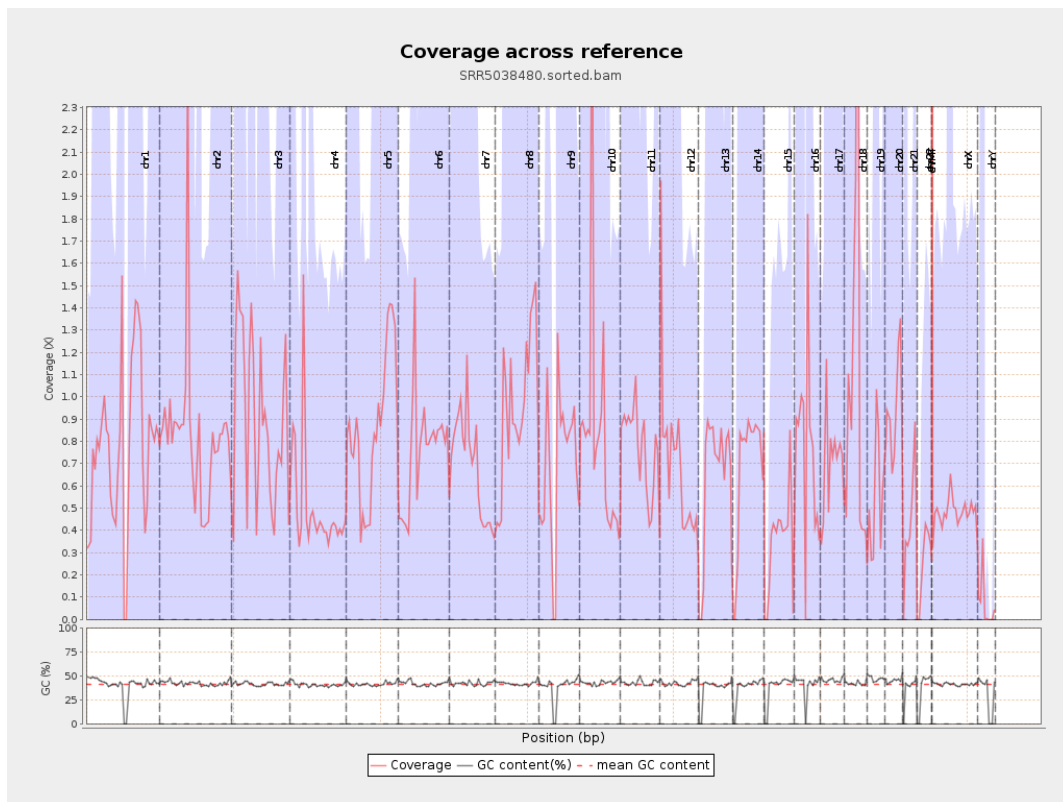
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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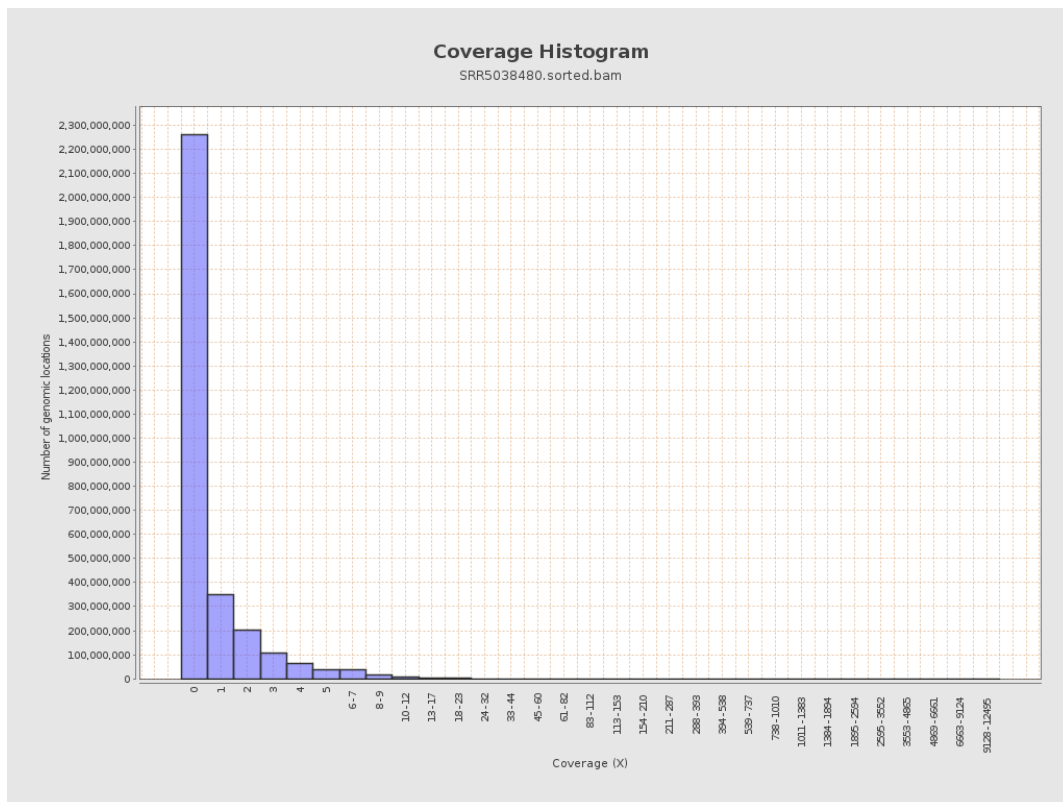
		bases	coverage	deviation
chr1	249250621	194520995	0.7804	12.6918
chr2	243199373	201296112	0.8277	10.4889
chr3	198022430	177873115	0.8982	1.9244
chr4	191154276	95959772	0.502	9.2497
chr5	180915260	155226687	0.858	1.8083
chr6	171115067	131569151	0.7689	7.5783
chr7	159138663	108487659	0.6817	9.0734
chr8	146364022	141293822	0.9654	3.7082
chr9	141213431	95457734	0.676	15.4386
chr10	135534747	116108505	0.8567	19.9195
chr11	135006516	103795873	0.7688	7.2471
chr12	133851895	92759497	0.693	1.7379
chr13	115169878	74425649	0.6462	1.5153
chr14	107349540	72926574	0.6793	1.6526
chr15	102531392	36473378	0.3557	1.0964
chr16	90354753	67377564	0.7457	7.8305
chr17	81195210	56371905	0.6943	11.5585
chr18	78077248	88865804	1.1382	10.5346
chr19	59128983	31773846	0.5374	5.3819
chr20	63025520	59151928	0.9385	3.3082
chr21	48129895	21726160	0.4514	4.1687
chr22	51304566	13059250	0.2545	0.95
chrMT	16571	4076090	245.9773	149.3021
chrX	155270560	74618020	0.4806	2.0618

chrY	59373566	4324015	0.0728	9.0529
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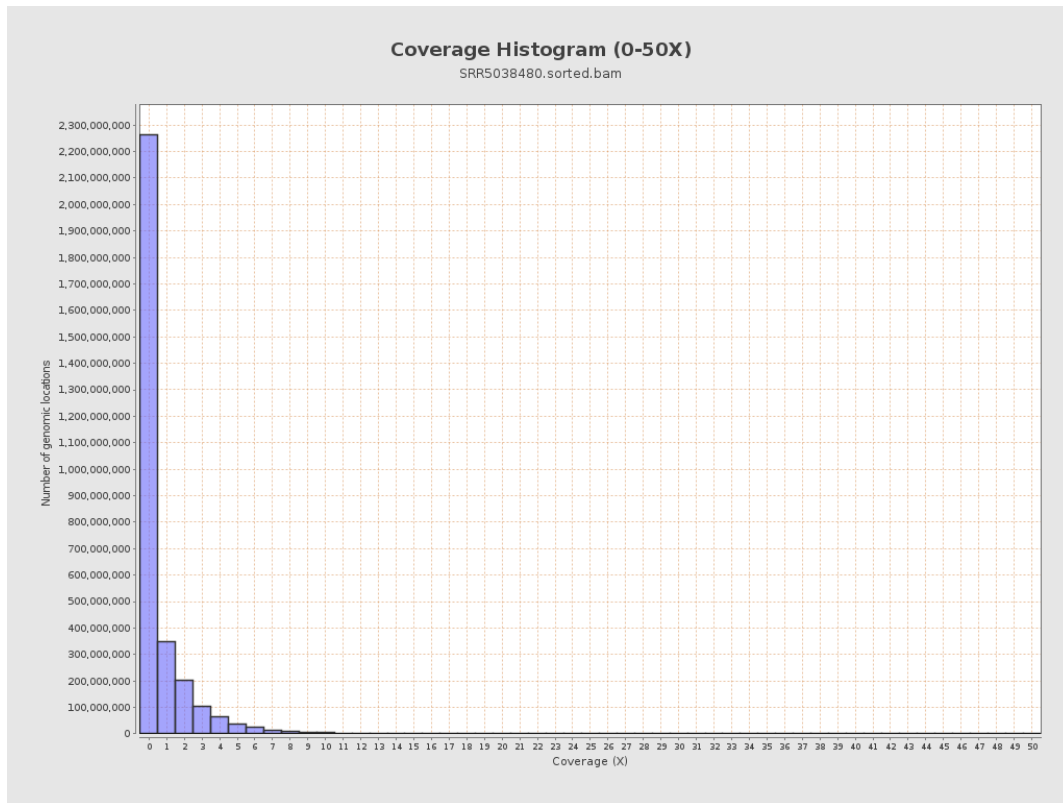
3. Results : Coverage across reference



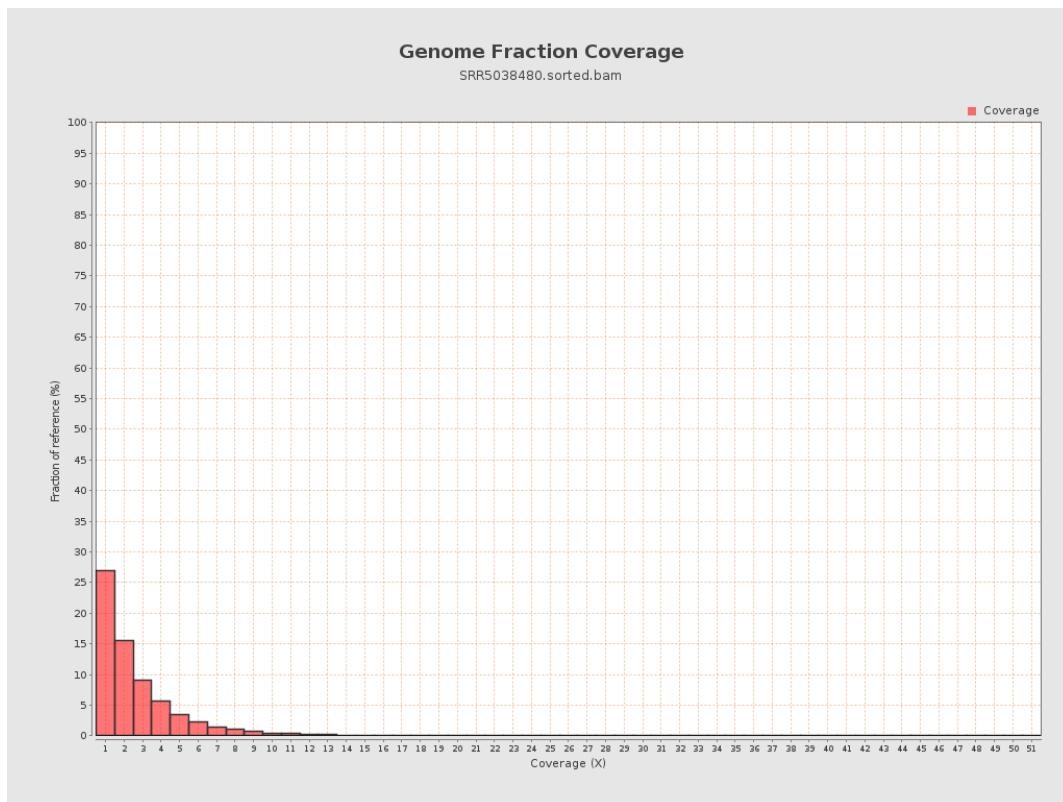
4. Results : Coverage Histogram



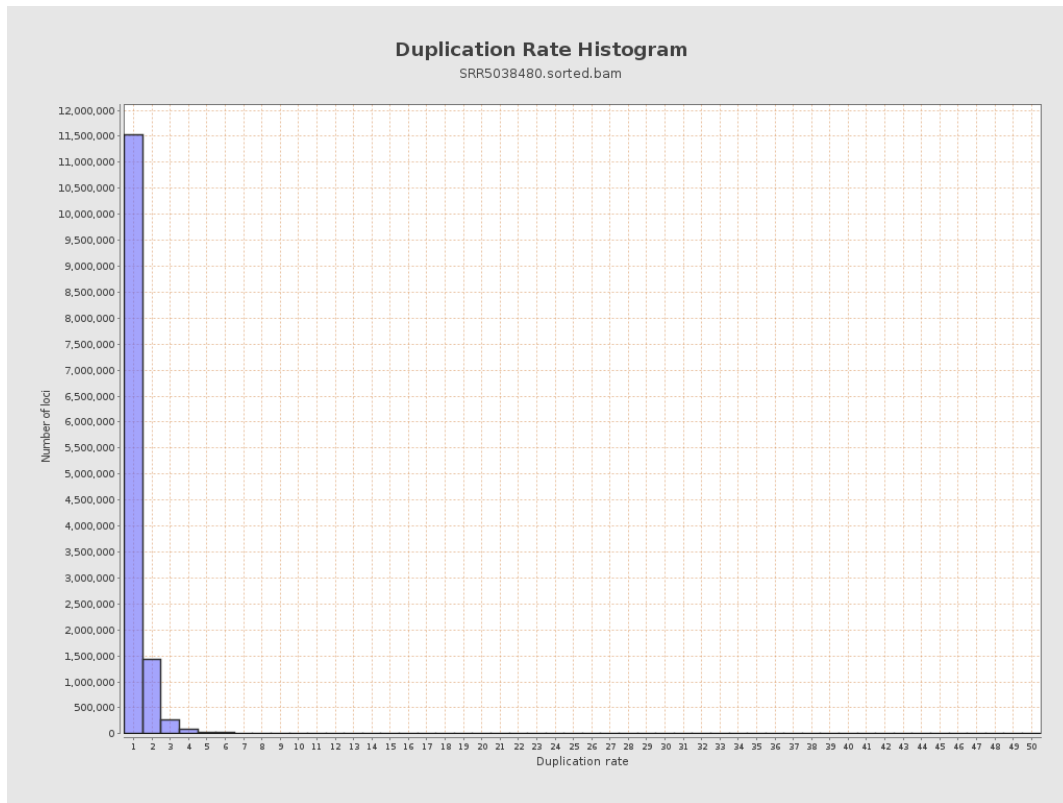
5. Results : Coverage Histogram (0-50X)



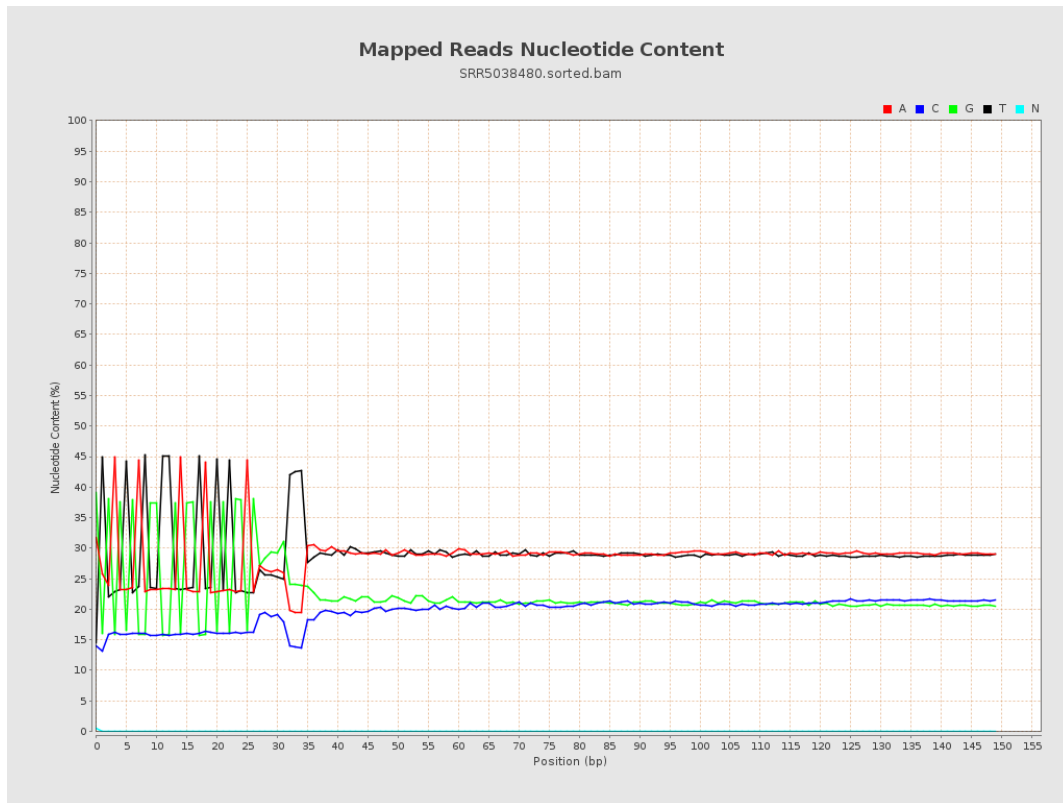
6. Results : Genome Fraction Coverage



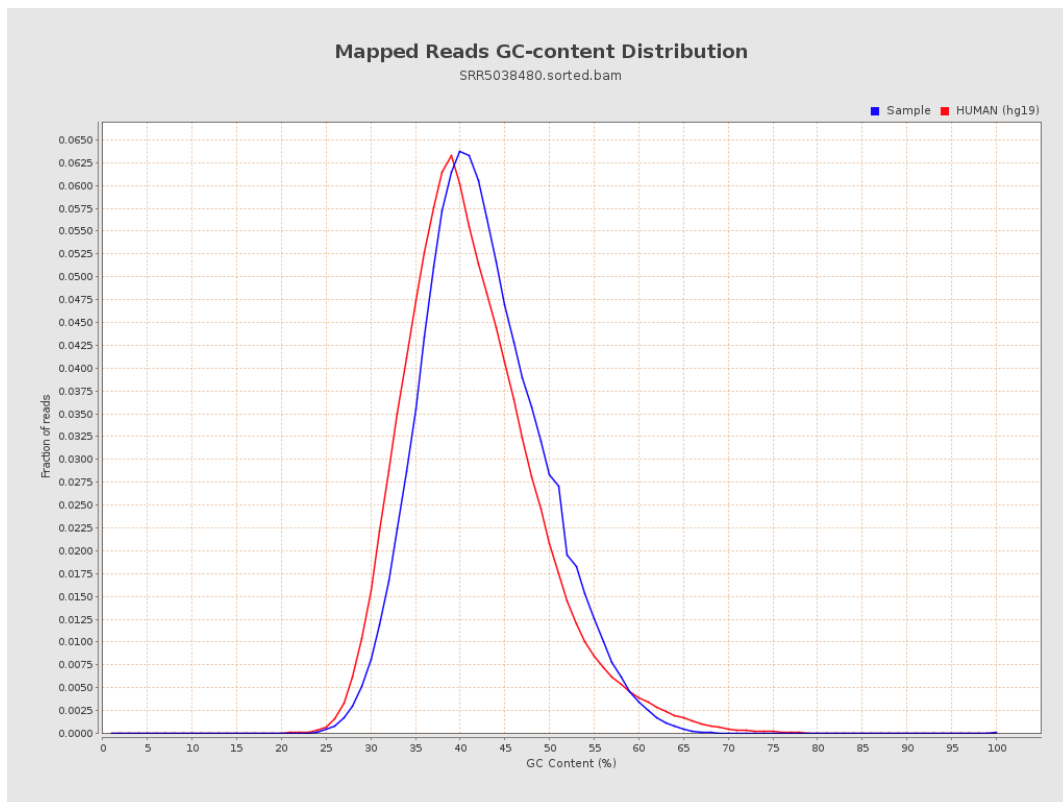
7. Results : Duplication Rate Histogram



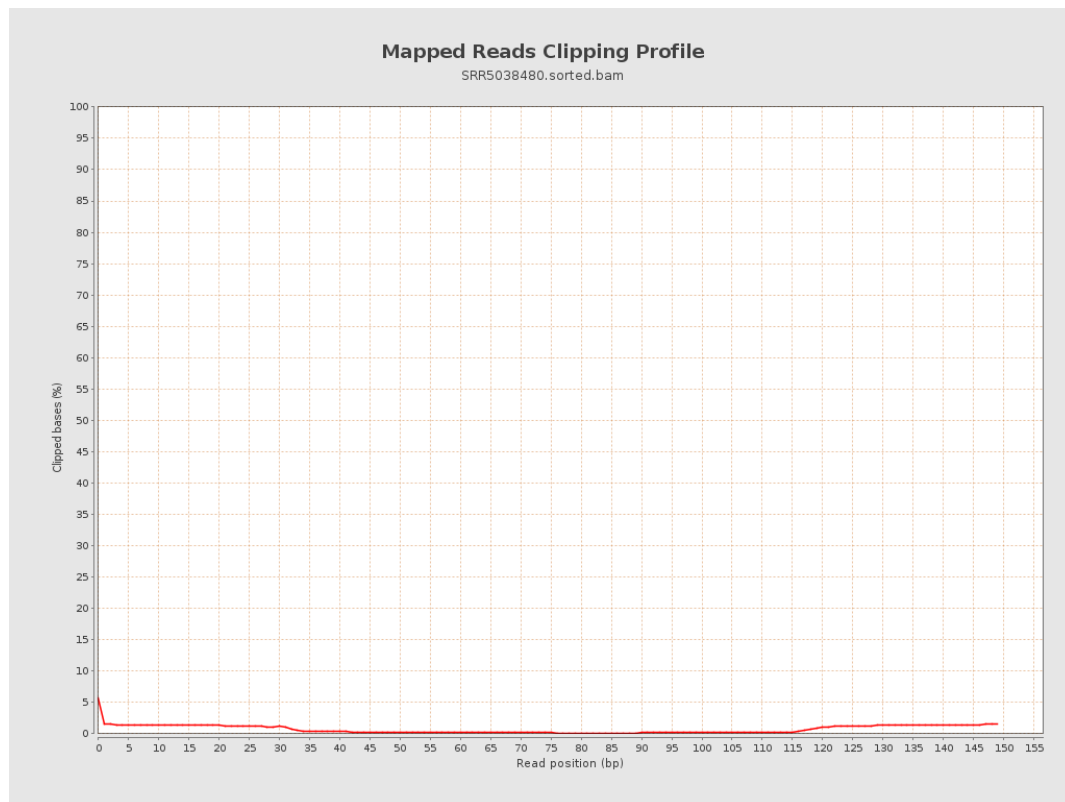
8. Results : Mapped Reads Nucleotide Content



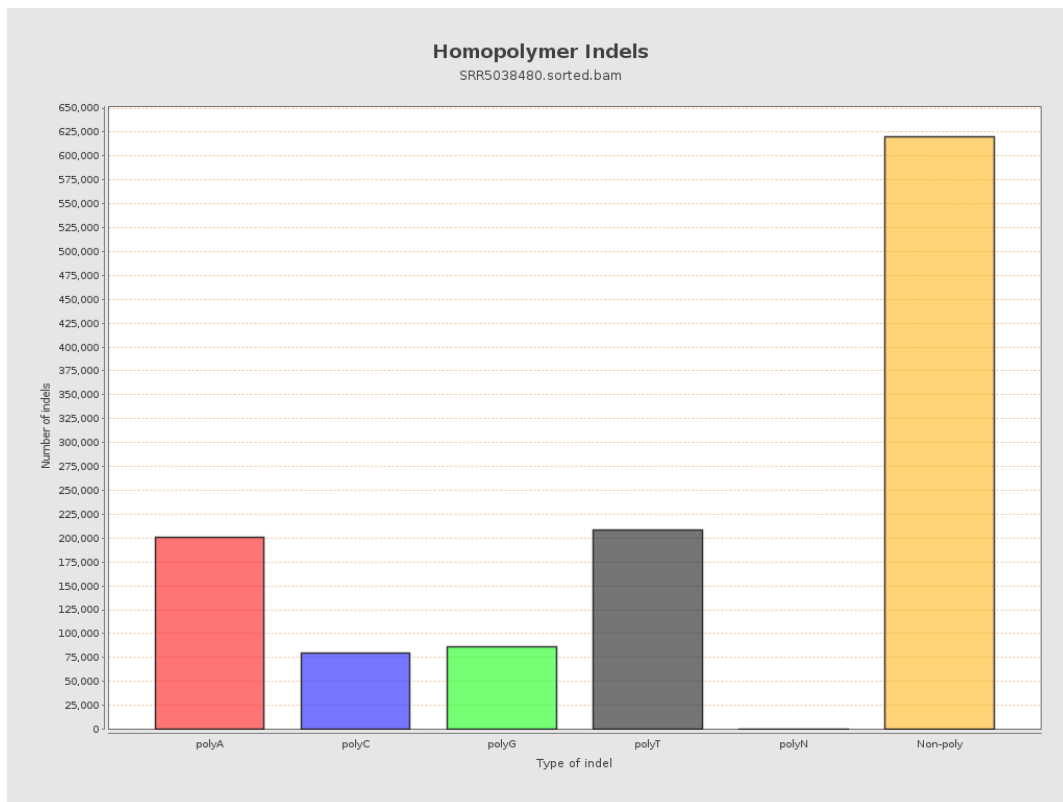
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



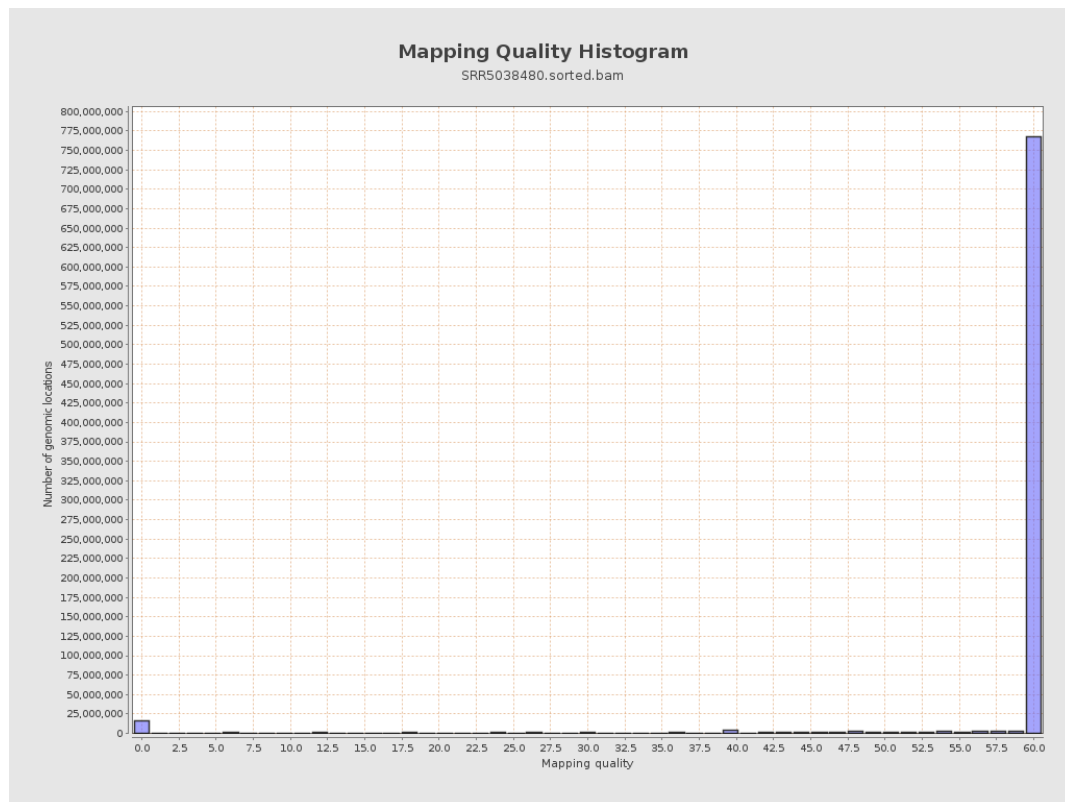
11. Results : Homopolymer Indels



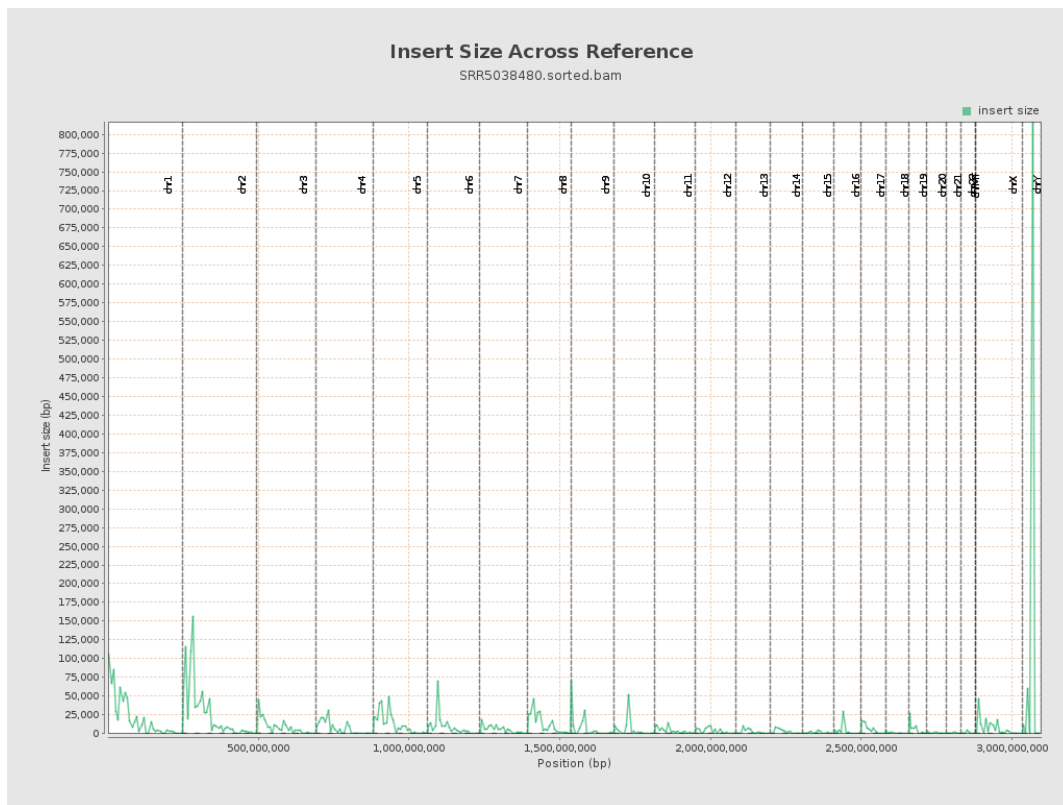
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

