

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 06:38:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038482.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_SRR5038482 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038482_1.fastq.gz SRR5038482_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 06:38:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038482.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,033,856
Mapped reads	14,652,728 / 97.46%
Unmapped reads	381,128 / 2.54%
Mapped paired reads	14,652,728 / 97.46%
Mapped reads, first in pair	7,400,673 / 49.23%
Mapped reads, second in pair	7,252,055 / 48.24%
Mapped reads, both in pair	14,483,340 / 96.34%
Mapped reads, singletons	169,388 / 1.13%
Secondary alignments	0
Supplementary alignments	265,237 / 1.76%
Read min/max/mean length	30 / 150 / 150.9
Duplicated reads (estimated)	2,473,872 / 16.46%
Duplication rate	10.11%
Clipped reads	3,218,837 / 21.41%

2.2. ACGT Content

Number/percentage of A's	625,000,191 / 29.71%
Number/percentage of C's	421,222,038 / 20.02%
Number/percentage of T's	624,626,683 / 29.69%
Number/percentage of G's	432,634,340 / 20.57%
Number/percentage of N's	45,191 / 0%

GC Percentage	40.59%
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2.3. Coverage

Mean	0.68
Standard Deviation	10.8227

2.4. Mapping Quality

Mean Mapping Quality	53.65
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2.5. Insert size

Mean	80,427.29
Standard Deviation	2,657,624.62
P25/Median/P75	208 / 254 / 313

2.6. Mismatches and indels

General error rate	1.51%
Mismatches	30,530,106
Insertions	433,255
Mapped reads with at least one insertion	2.74%
Deletions	798,689
Mapped reads with at least one deletion	5.21%
Homopolymer indels	46.37%

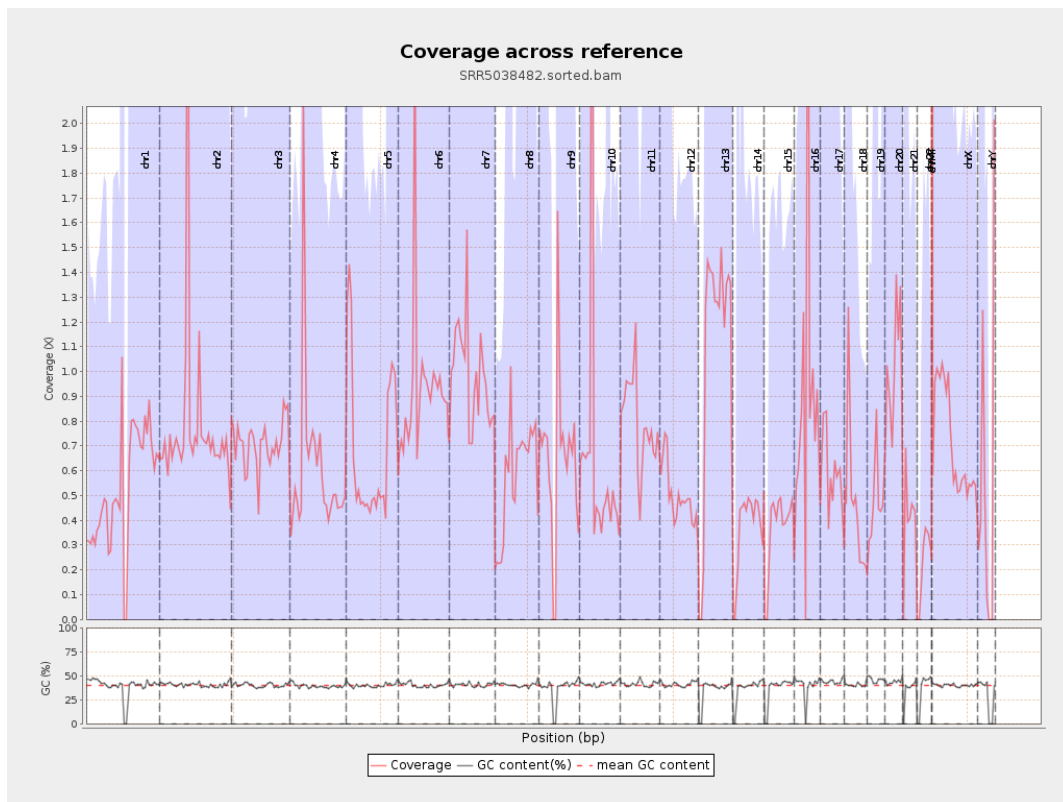
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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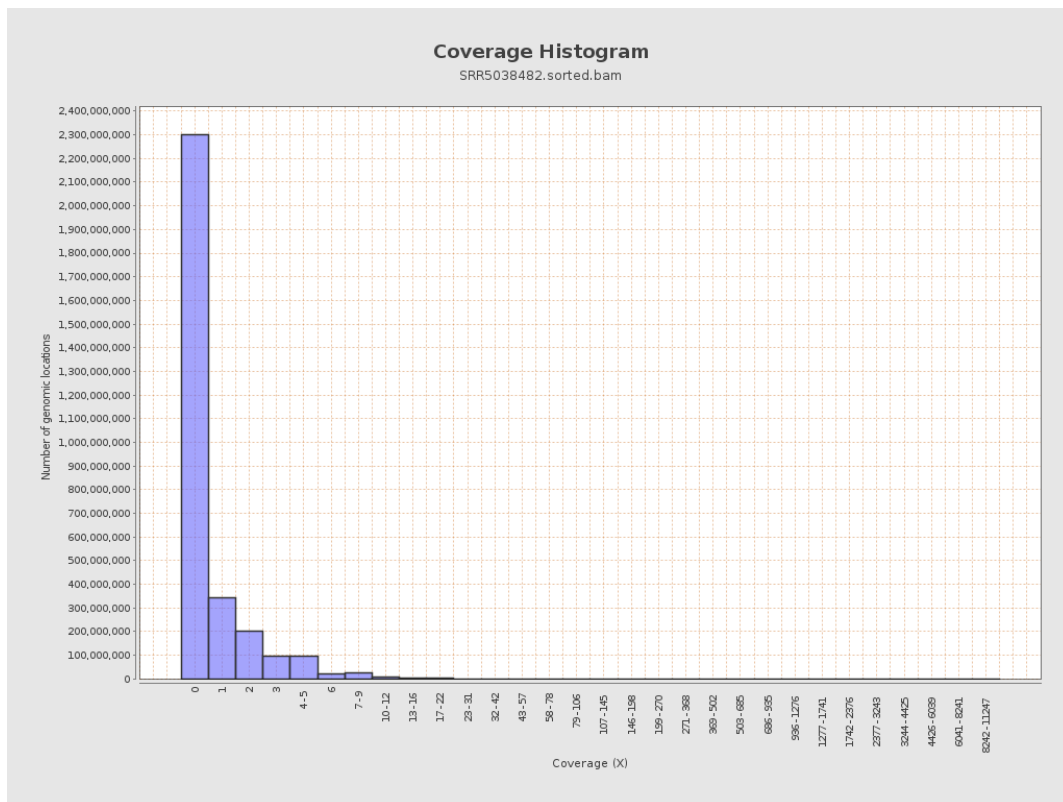
		bases	coverage	deviation
chr1	249250621	133910693	0.5373	9.7239
chr2	243199373	191963205	0.7893	14.0861
chr3	198022430	140281760	0.7084	1.6661
chr4	191154276	114383845	0.5984	10.4126
chr5	180915260	125226951	0.6922	1.7856
chr6	171115067	161054271	0.9412	15.902
chr7	159138663	156343236	0.9824	11.9805
chr8	146364022	85740716	0.5858	3.0991
chr9	141213431	89096931	0.6309	18.3563
chr10	135534747	91158932	0.6726	22.4956
chr11	135006516	105463681	0.7812	7.3857
chr12	133851895	66925191	0.5	1.4211
chr13	115169878	127767724	1.1094	2.1983
chr14	107349540	39504760	0.368	1.4189
chr15	102531392	37214454	0.363	1.0895
chr16	90354753	85122979	0.9421	17.7227
chr17	81195210	47101911	0.5801	6.744
chr18	78077248	35708316	0.4573	15.7002
chr19	59128983	27364187	0.4628	5.8661
chr20	63025520	63617464	1.0094	3.5721
chr21	48129895	19854592	0.4125	5.1387
chr22	51304566	11592049	0.2259	1.121
chrMT	16571	4619113	278.7468	174.1992
chrX	155270560	109940376	0.7081	2.4818

chrY	59373566	34213375	0.5762	17.5823
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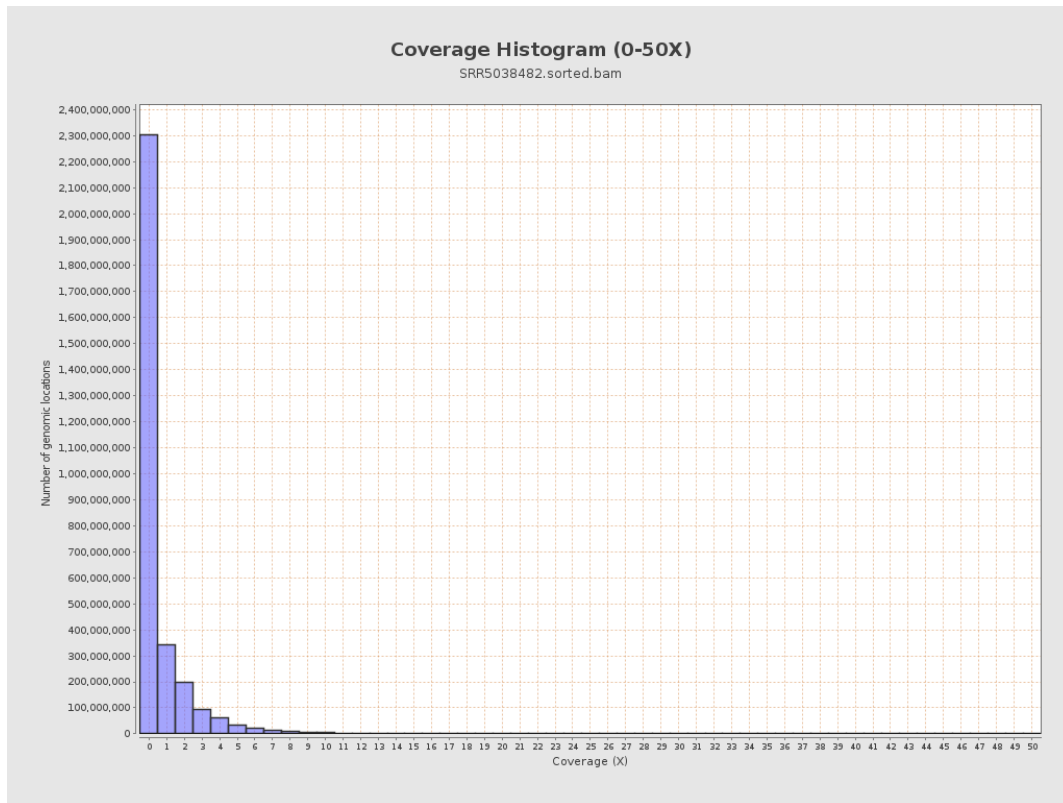
3. Results : Coverage across reference



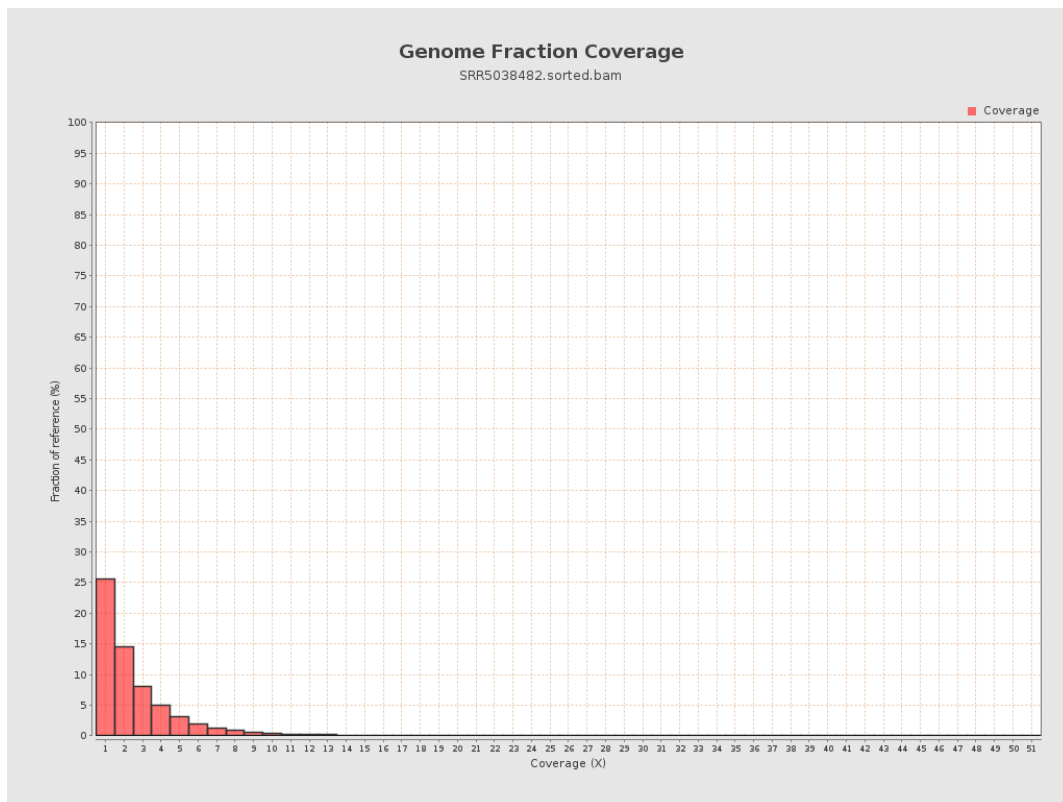
4. Results : Coverage Histogram



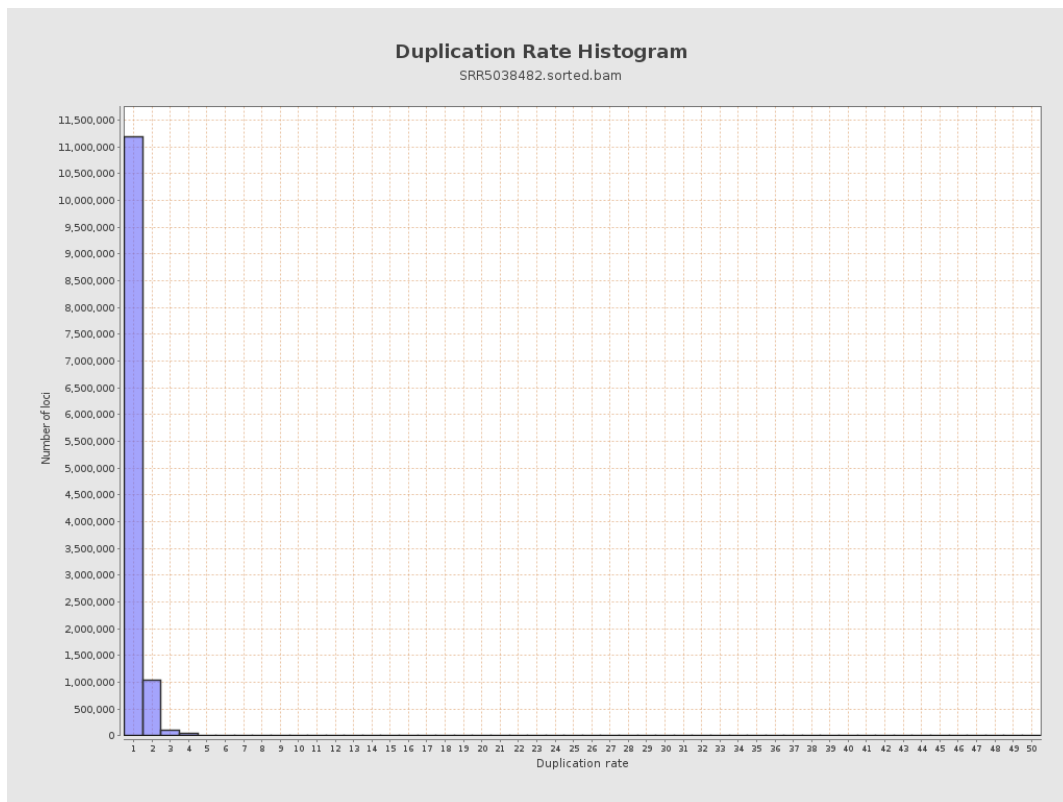
5. Results : Coverage Histogram (0-50X)



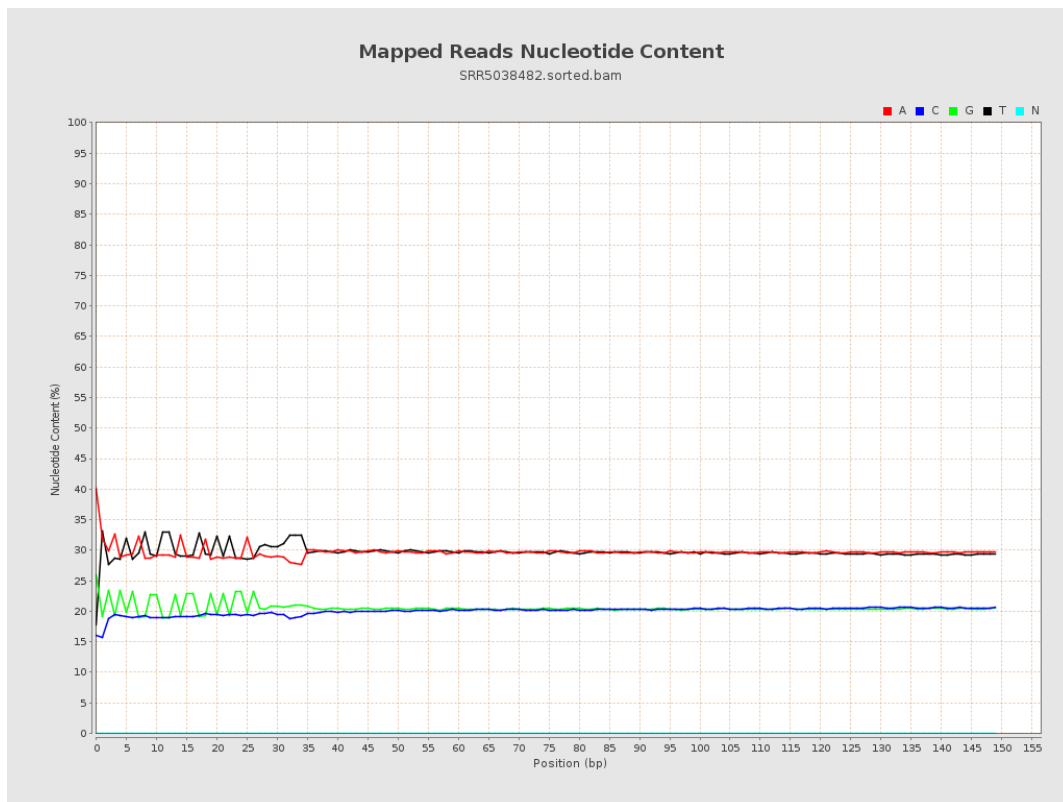
6. Results : Genome Fraction Coverage



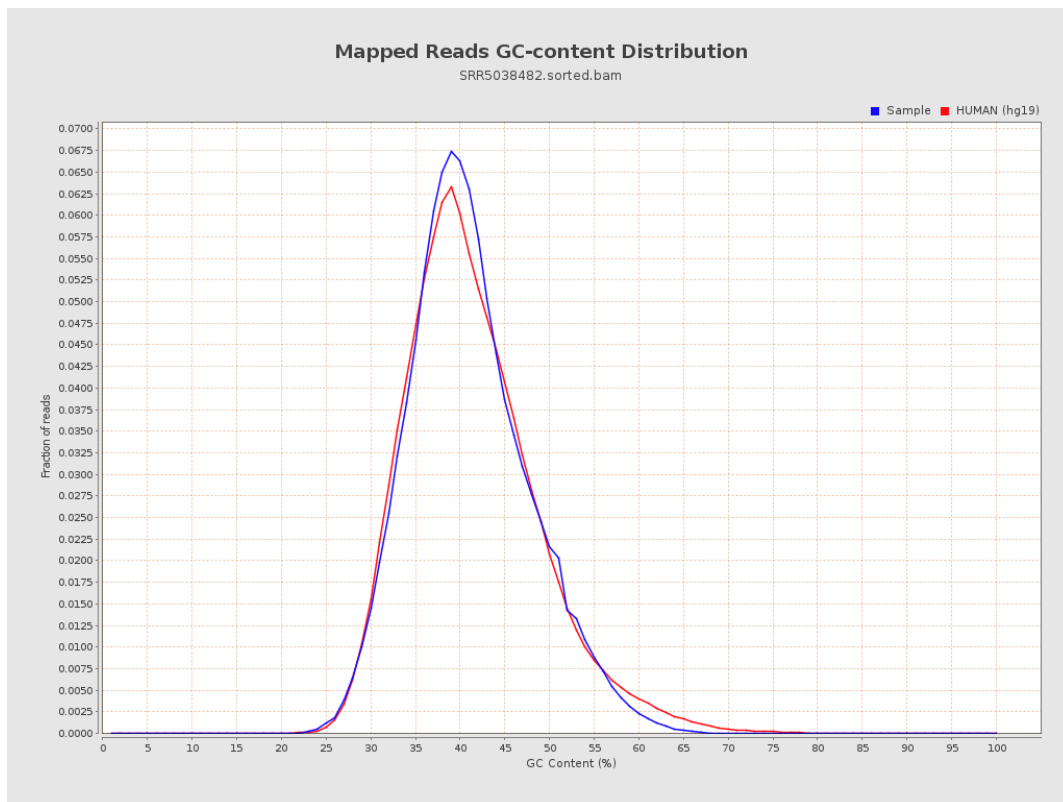
7. Results : Duplication Rate Histogram



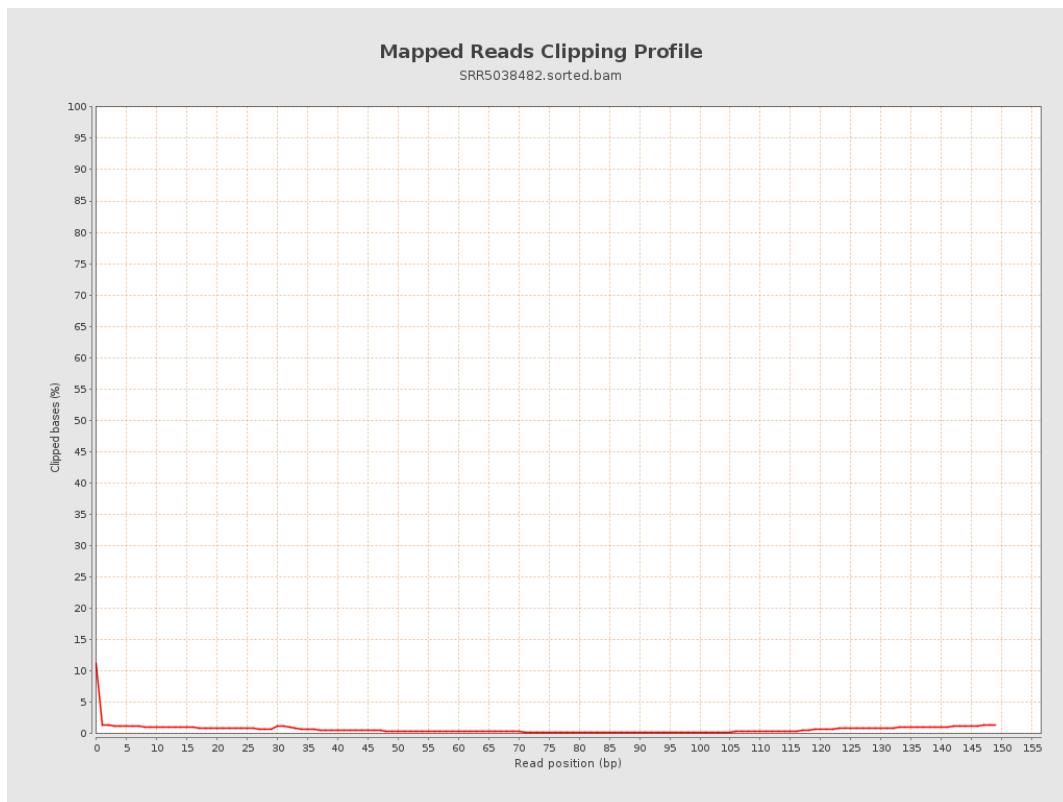
8. Results : Mapped Reads Nucleotide Content



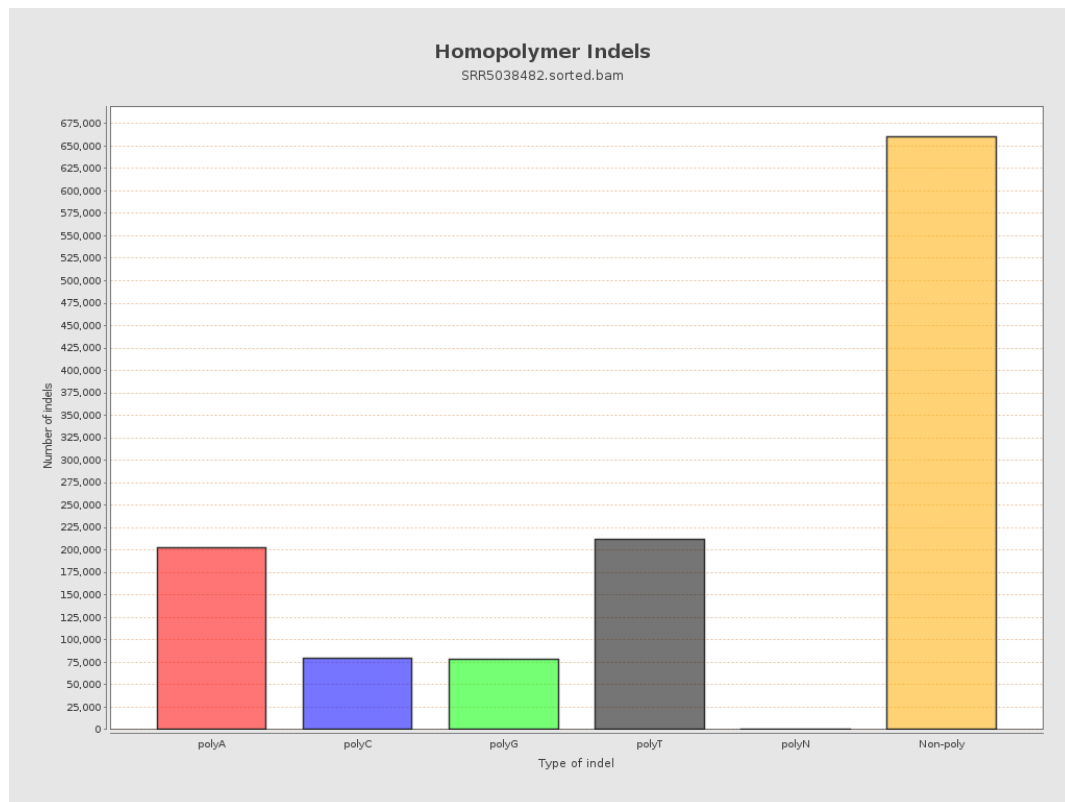
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



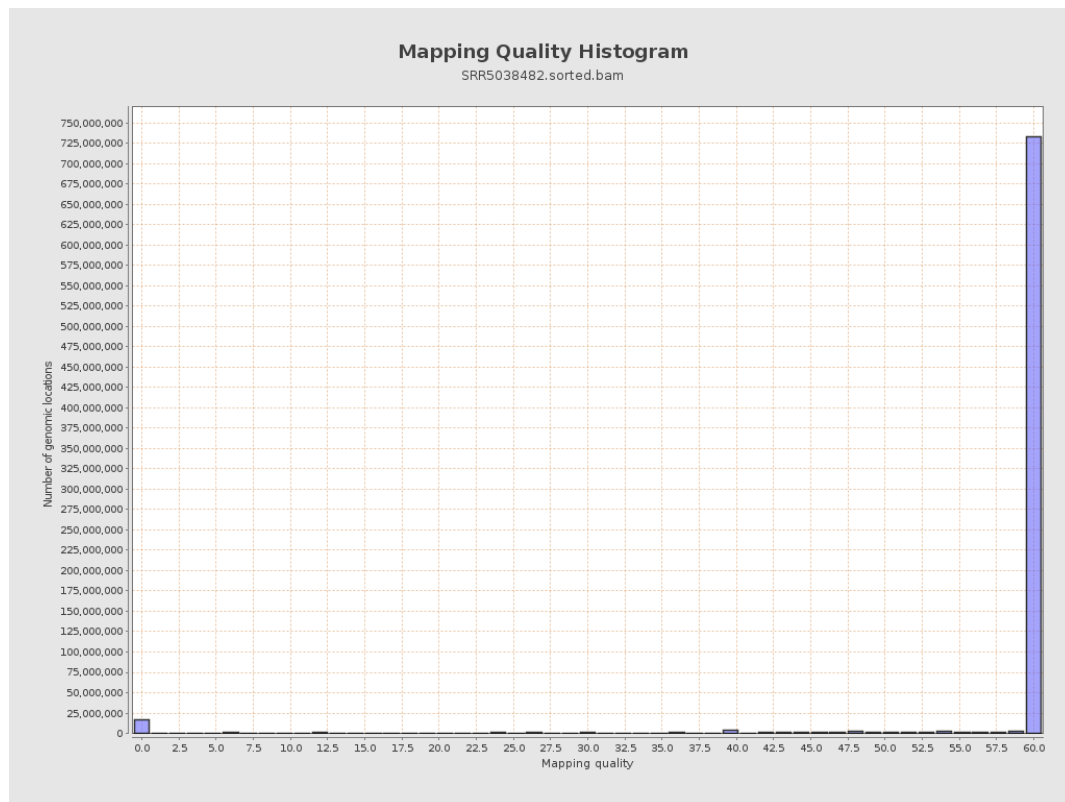
11. Results : Homopolymer Indels



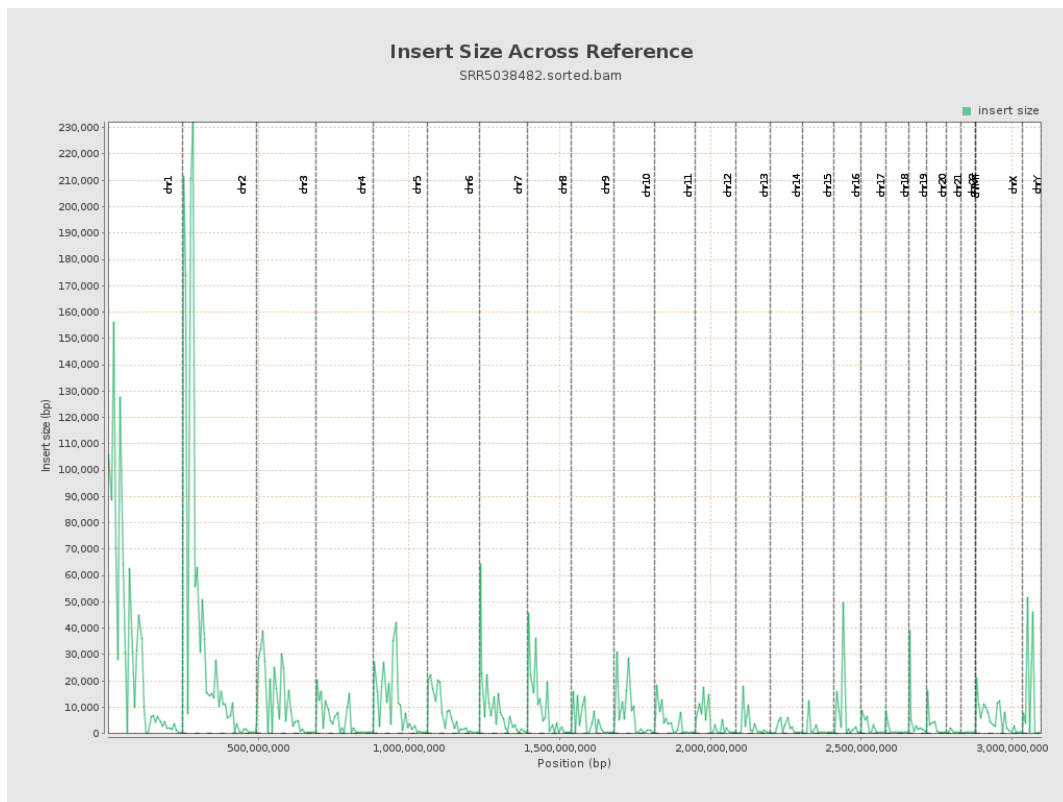
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

