

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 21:58:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038414.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_SRR5038414 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038414_1.fastq.gz SRR5038414_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 21:58:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038414.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,019,392
Mapped reads	13,678,119 / 97.57%
Unmapped reads	341,273 / 2.43%
Mapped paired reads	13,678,119 / 97.57%
Mapped reads, first in pair	6,902,139 / 49.23%
Mapped reads, second in pair	6,775,980 / 48.33%
Mapped reads, both in pair	13,534,984 / 96.54%
Mapped reads, singletons	143,135 / 1.02%
Secondary alignments	0
Supplementary alignments	150,672 / 1.07%
Read min/max/mean length	30 / 150 / 150.55
Duplicated reads (estimated)	1,486,915 / 10.61%
Duplication rate	7.87%
Clipped reads	1,558,756 / 11.12%

2.2. ACGT Content

Number/percentage of A's	580,016,337 / 28.89%
Number/percentage of C's	427,637,406 / 21.3%
Number/percentage of T's	573,921,752 / 28.58%
Number/percentage of G's	426,305,597 / 21.23%
Number/percentage of N's	45,613 / 0%

GC Percentage	42.53%
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2.3. Coverage

Mean	0.6489
Standard Deviation	6.9843

2.4. Mapping Quality

Mean Mapping Quality	54.37
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2.5. Insert size

Mean	91,234.12
Standard Deviation	2,996,924.48
P25/Median/P75	216 / 263 / 327

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	21,280,113
Insertions	265,894
Mapped reads with at least one insertion	1.82%
Deletions	272,344
Mapped reads with at least one deletion	1.9%
Homopolymer indels	44.04%

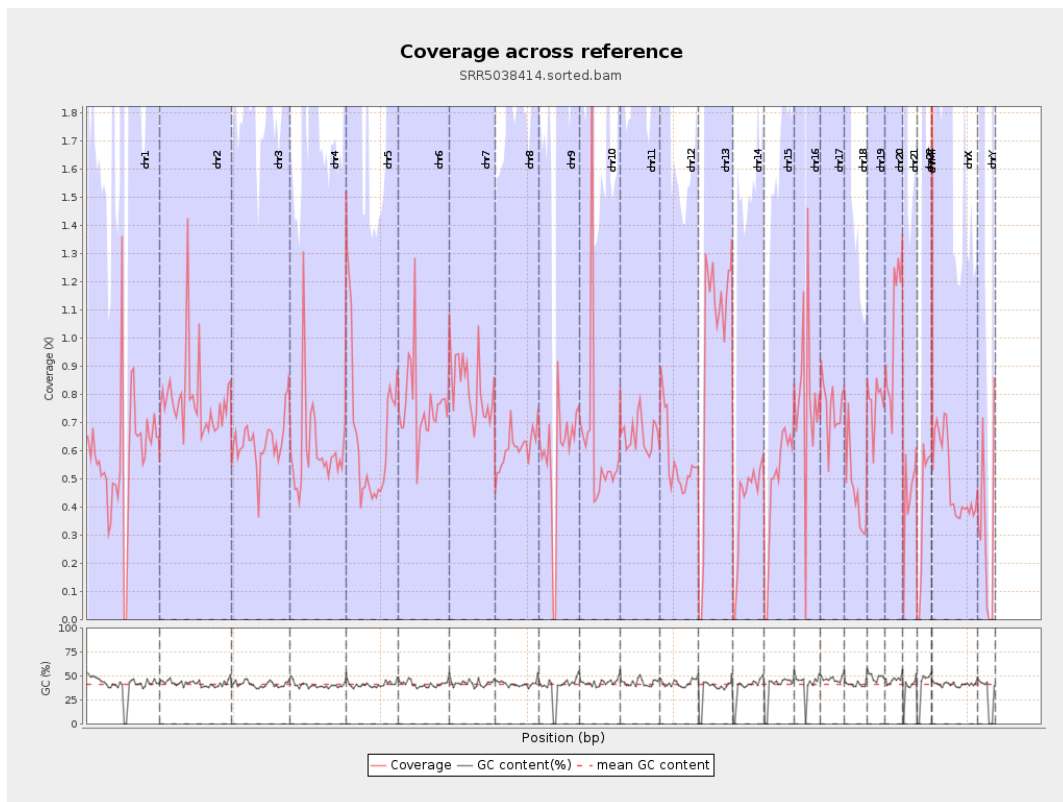
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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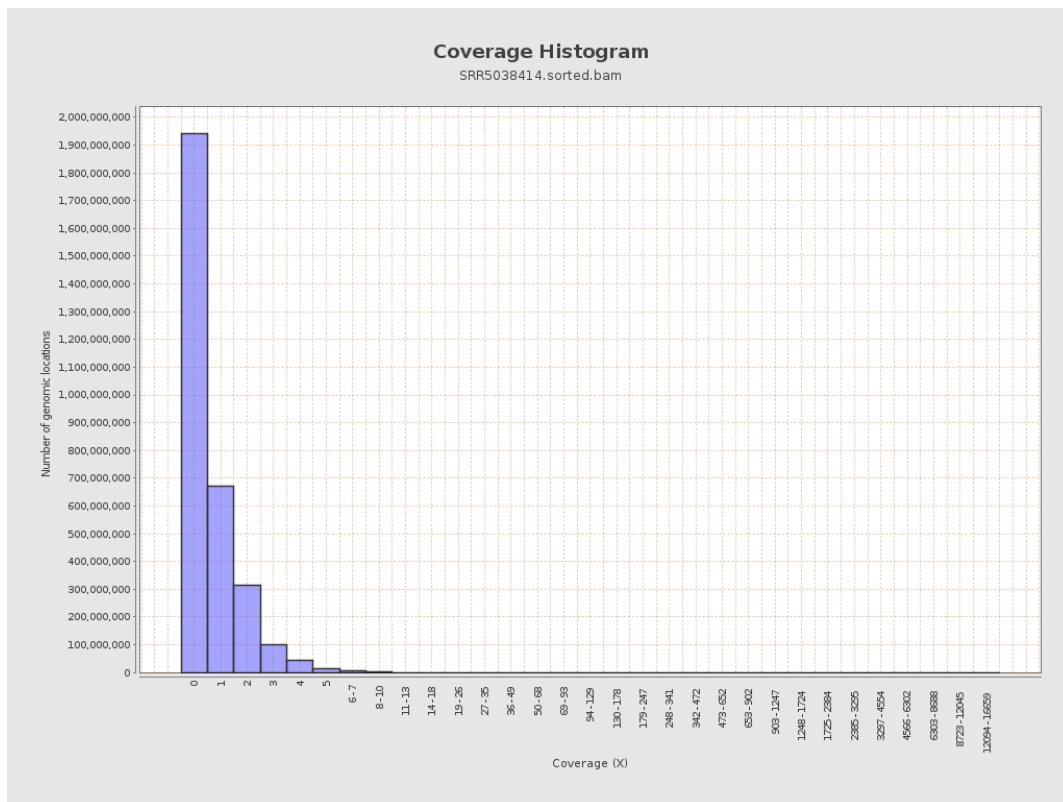
		bases	coverage	deviation
chr1	249250621	144556655	0.58	17.202
chr2	243199373	190063861	0.7815	5.4058
chr3	198022430	125097718	0.6317	1.0483
chr4	191154276	114920481	0.6012	6.3825
chr5	180915260	120909310	0.6683	1.1675
chr6	171115067	130614393	0.7633	5.8505
chr7	159138663	131319669	0.8252	4.9293
chr8	146364022	89845924	0.6139	3.8367
chr9	141213431	82183985	0.582	7.3943
chr10	135534747	86465035	0.638	13.0886
chr11	135006516	89248556	0.6611	3.1836
chr12	133851895	77111145	0.5761	1.0292
chr13	115169878	112601631	0.9777	1.3363
chr14	107349540	44041226	0.4103	0.9392
chr15	102531392	49357461	0.4814	0.9041
chr16	90354753	71216058	0.7882	5.5827
chr17	81195210	61397781	0.7562	3.2334
chr18	78077248	35560952	0.4555	7.3589
chr19	59128983	45664185	0.7723	7.8933
chr20	63025520	65183828	1.0342	2.3892
chr21	48129895	21566196	0.4481	3.3266
chr22	51304566	20520009	0.4	1.7629
chrMT	16571	3327752	200.8178	24.5336
chrX	155270560	76652421	0.4937	1.2499

chrY	59373566	19279301	0.3247	7.754
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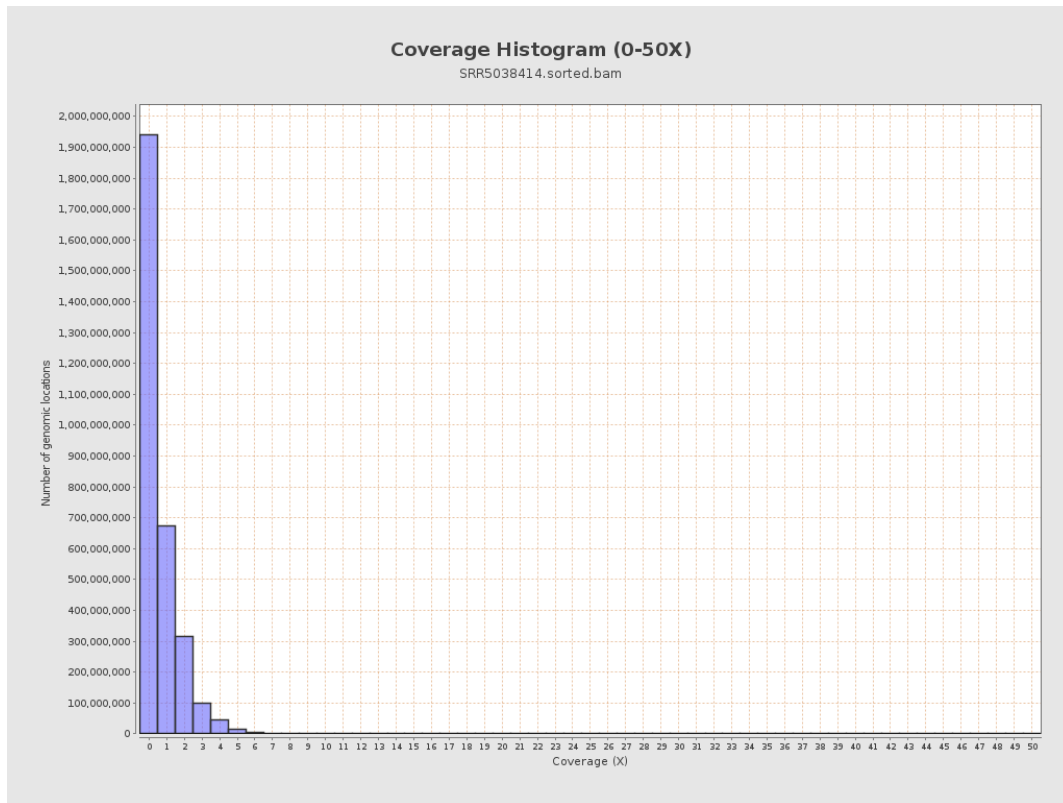
3. Results : Coverage across reference



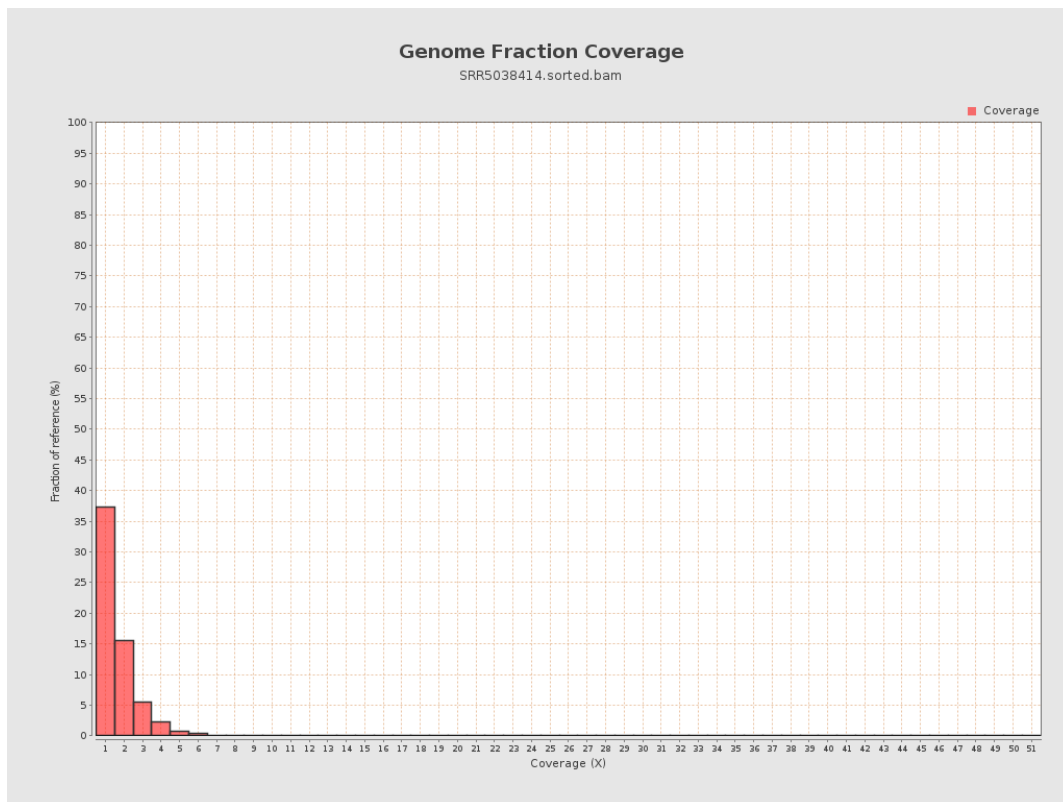
4. Results : Coverage Histogram



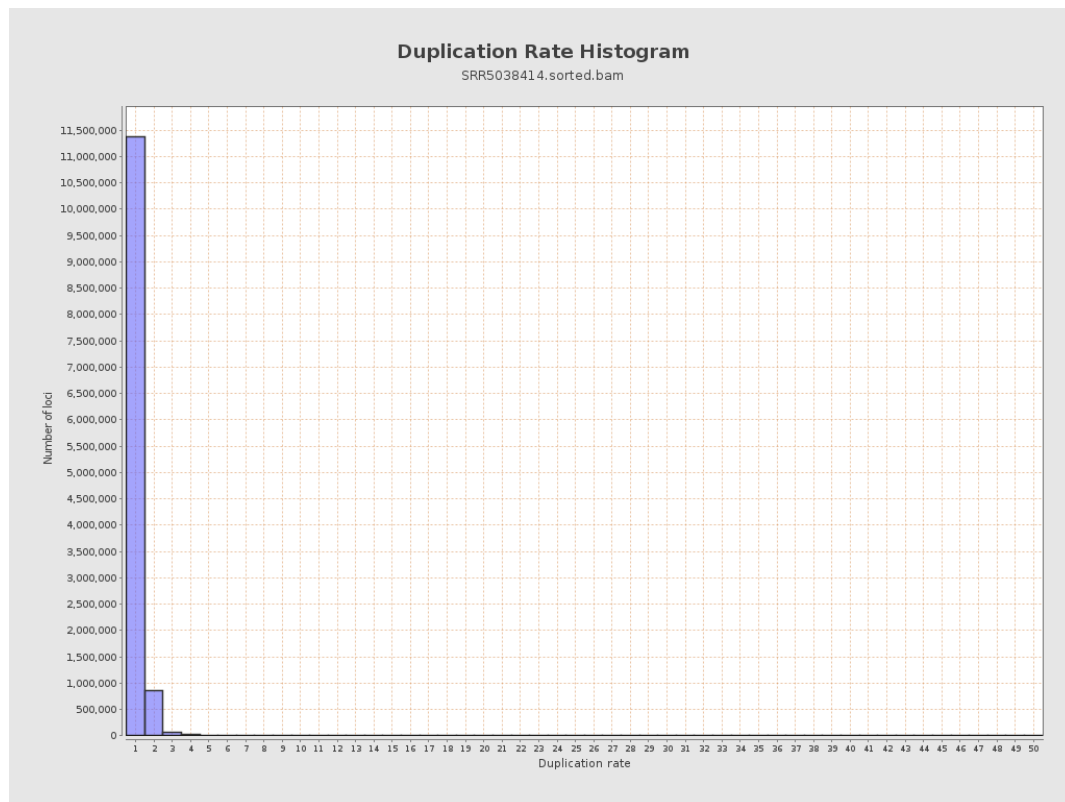
5. Results : Coverage Histogram (0-50X)



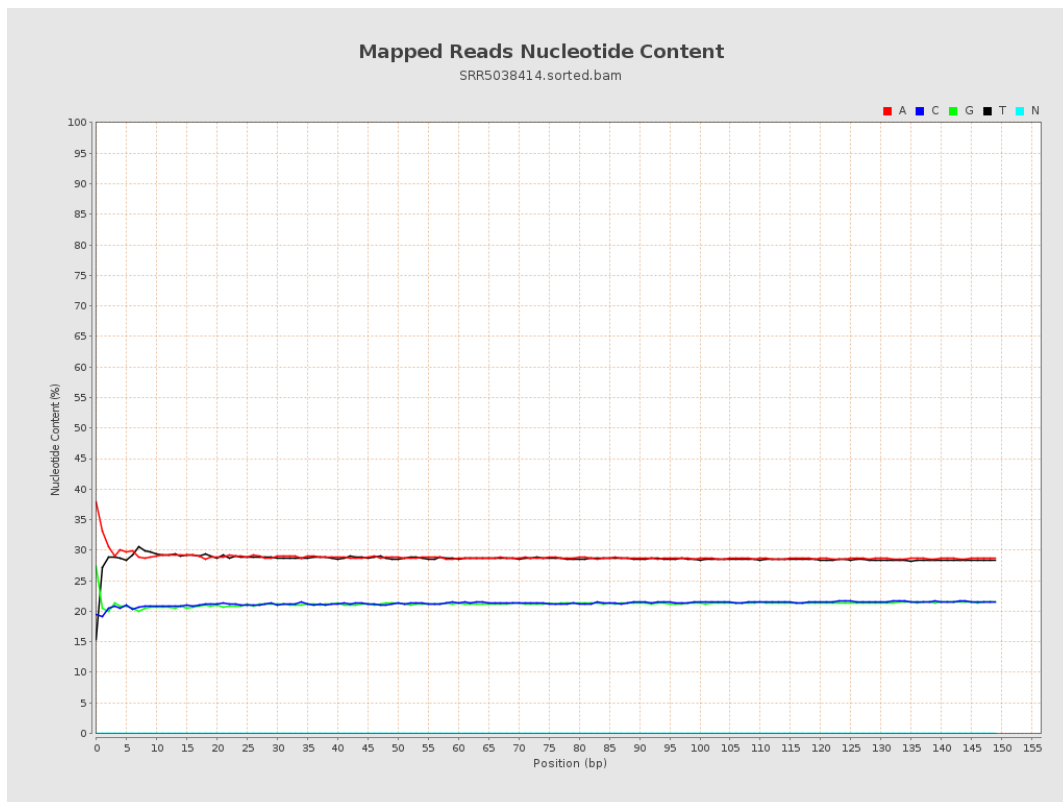
6. Results : Genome Fraction Coverage



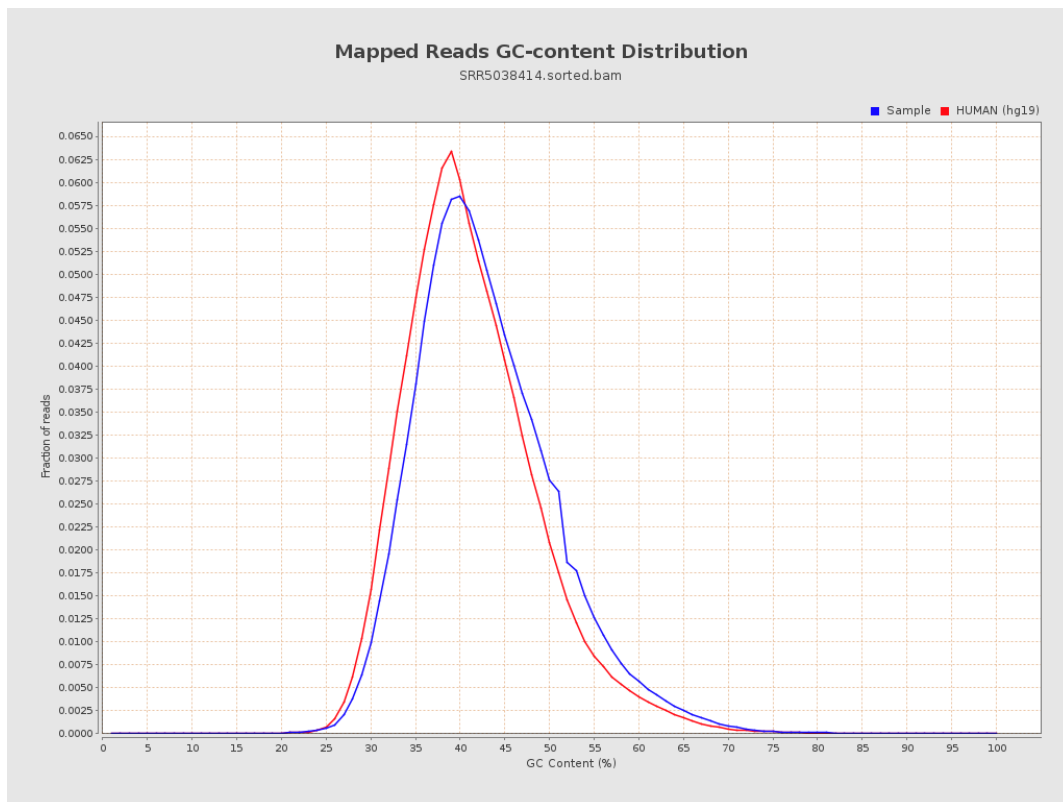
7. Results : Duplication Rate Histogram



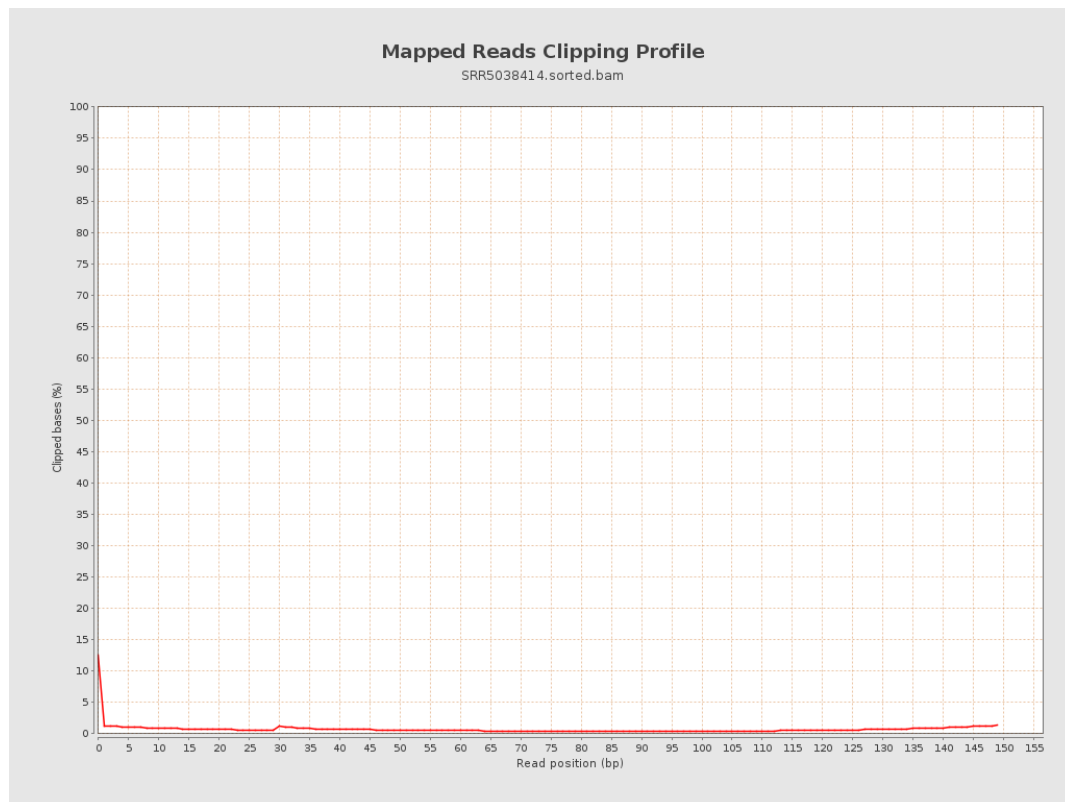
8. Results : Mapped Reads Nucleotide Content



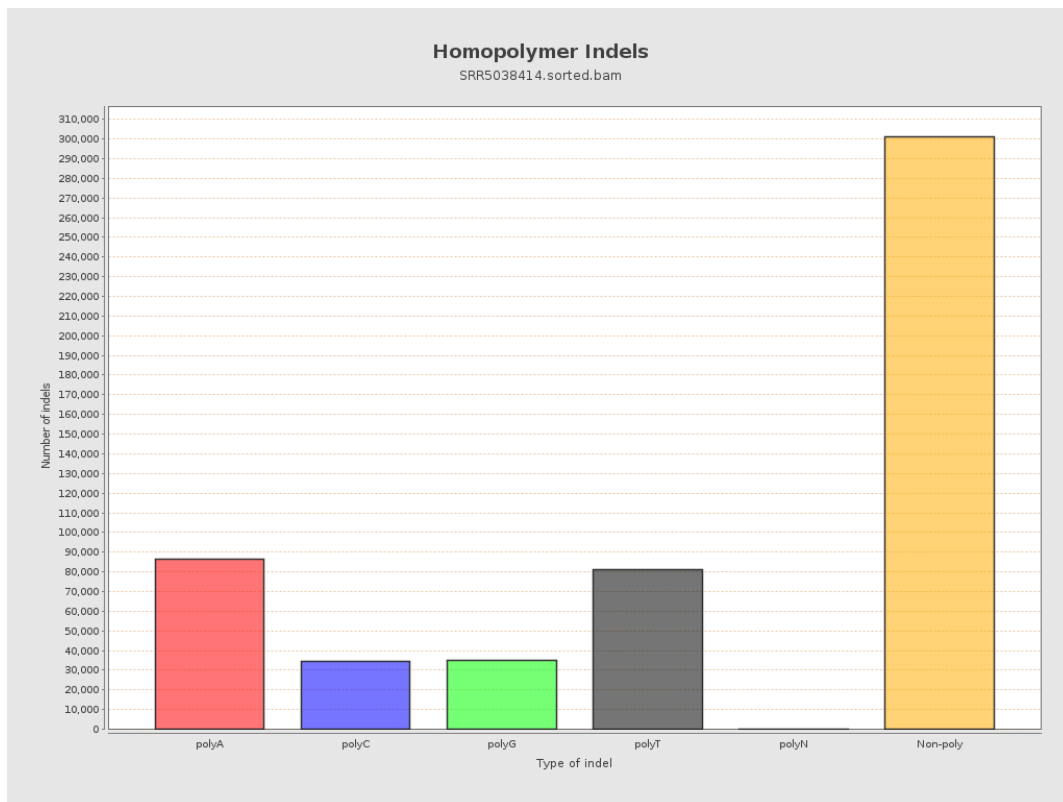
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



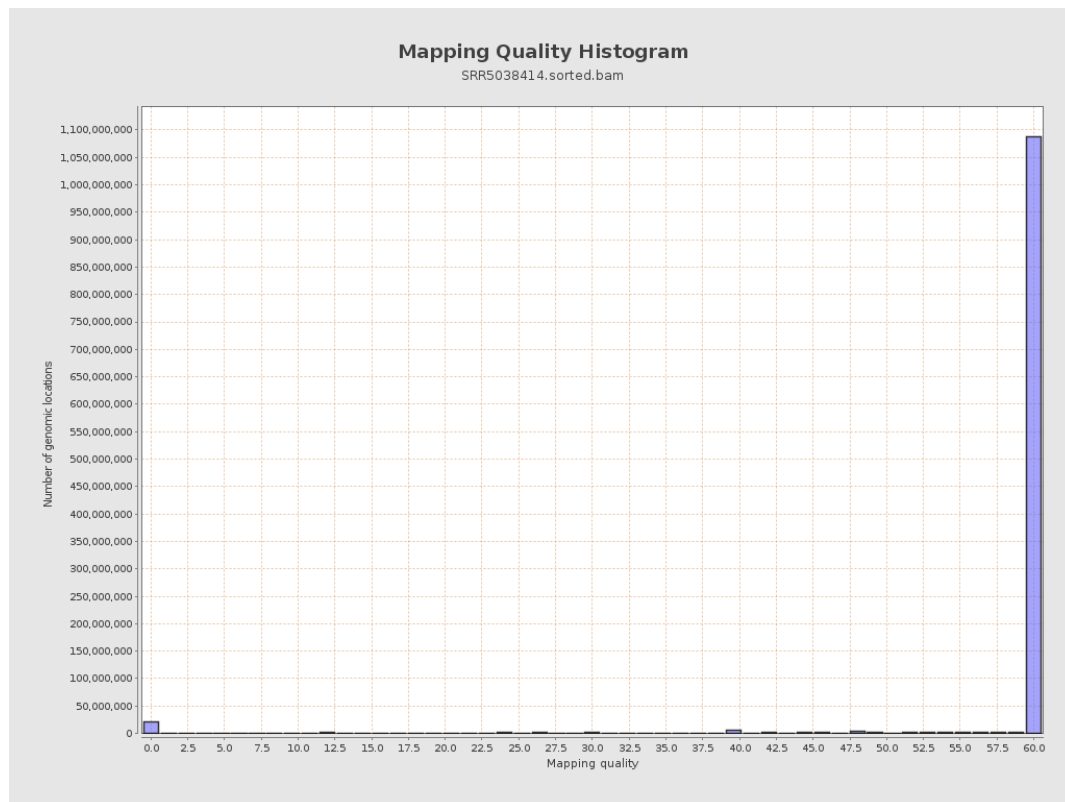
11. Results : Homopolymer Indels



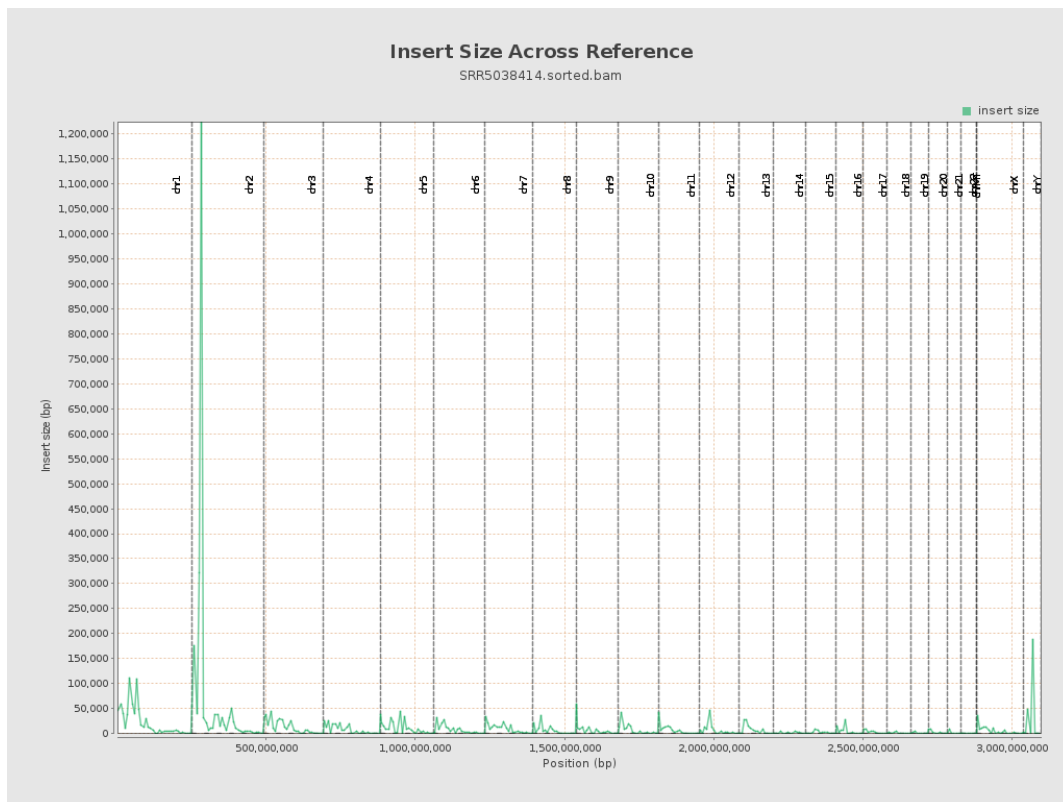
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

