

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 04:29:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124913.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_SRR3124913 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124913_1.fastq.gz SRR3124913_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 04:29:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124913.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,411,482
Mapped reads	4,372,984 / 99.13%
Unmapped reads	38,498 / 0.87%
Mapped paired reads	4,372,984 / 99.13%
Mapped reads, first in pair	2,188,107 / 49.6%
Mapped reads, second in pair	2,184,877 / 49.53%
Mapped reads, both in pair	4,358,772 / 98.81%
Mapped reads, singletons	14,212 / 0.32%
Secondary alignments	0
Supplementary alignments	17,398 / 0.39%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	201,778 / 4.57%
Duplication rate	2.53%
Clipped reads	2,596,148 / 58.85%

2.2. ACGT Content

Number/percentage of A's	115,485,075 / 28.89%
Number/percentage of C's	79,337,723 / 19.84%
Number/percentage of T's	118,127,761 / 29.55%
Number/percentage of G's	86,594,012 / 21.66%
Number/percentage of N's	261,956 / 0.07%

GC Percentage	41.5%
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2.3. Coverage

Mean	0.1292
Standard Deviation	1.3204

2.4. Mapping Quality

Mean Mapping Quality	52.57
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2.5. Insert size

Mean	67,955.93
Standard Deviation	2,521,869.12
P25/Median/P75	136 / 168 / 214

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	3,291,800
Insertions	60,180
Mapped reads with at least one insertion	1.35%
Deletions	117,780
Mapped reads with at least one deletion	2.64%
Homopolymer indels	45.98%

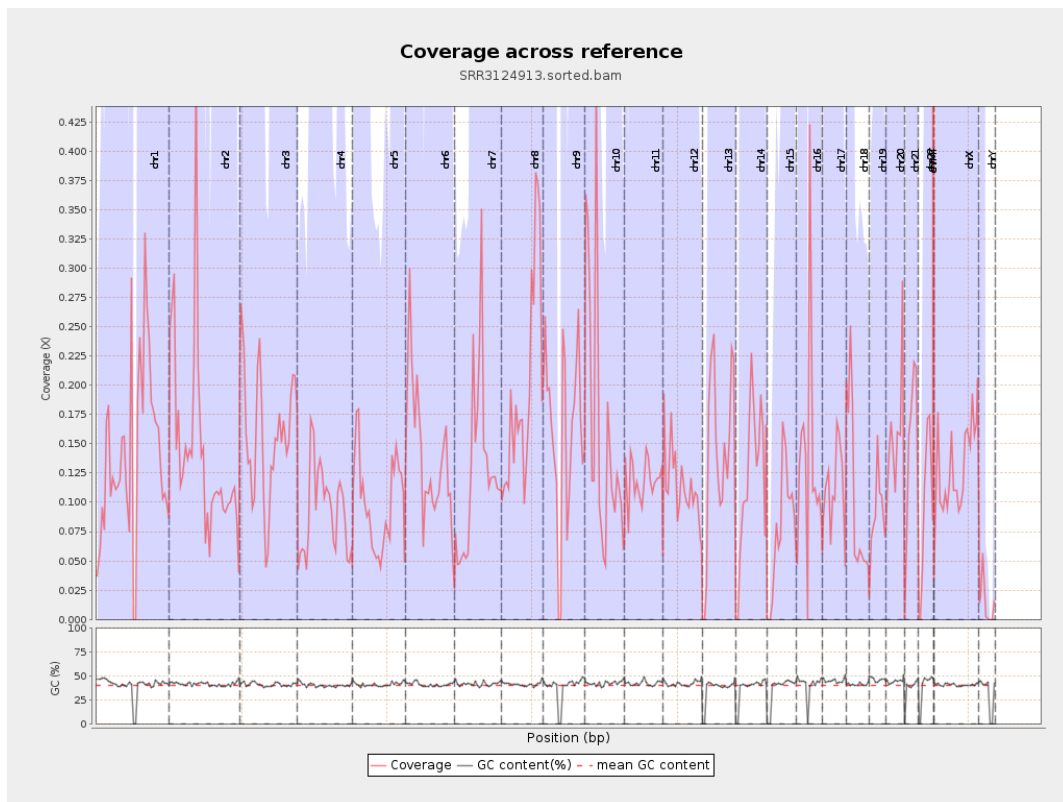
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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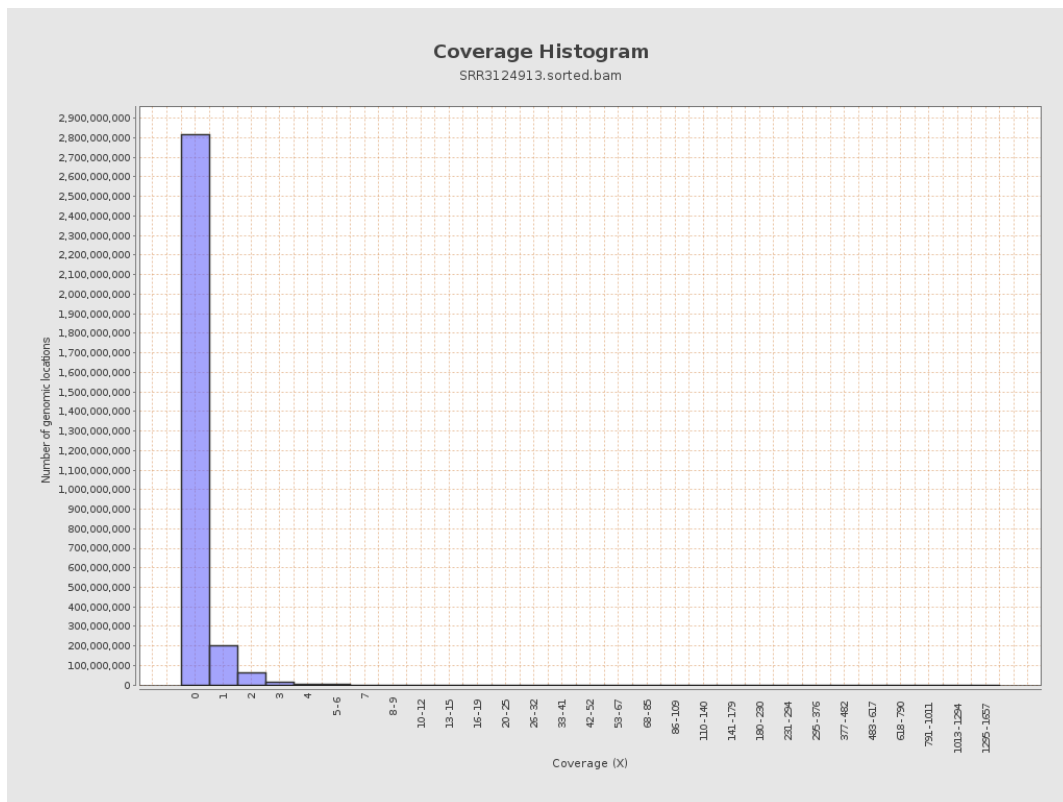
		bases	coverage	deviation
chr1	249250621	35428012	0.1421	1.4712
chr2	243199373	35223702	0.1448	1.7549
chr3	198022430	31385698	0.1585	0.5236
chr4	191154276	17443664	0.0913	0.86
chr5	180915260	17956543	0.0993	0.4003
chr6	171115067	23609309	0.138	0.7487
chr7	159138663	20315630	0.1277	2.2277
chr8	146364022	28812219	0.1969	0.7933
chr9	141213431	22544831	0.1597	2.259
chr10	135534747	21799059	0.1608	2.7862
chr11	135006516	15971594	0.1183	0.6716
chr12	133851895	15389752	0.115	0.4317
chr13	115169878	15990309	0.1388	0.4743
chr14	107349540	12924986	0.1204	0.5127
chr15	102531392	7872638	0.0768	0.3465
chr16	90354753	12139866	0.1344	1.938
chr17	81195210	8981264	0.1106	0.8317
chr18	78077248	8161509	0.1045	2.2366
chr19	59128983	5486288	0.0928	0.8917
chr20	63025520	9975432	0.1583	0.556
chr21	48129895	6916239	0.1437	0.5978
chr22	51304566	4934905	0.0962	0.3981
chrMT	16571	135302	8.165	5.0745
chrX	155270560	19793192	0.1275	0.6043

chrY	59373566	811166	0.0137	0.8447
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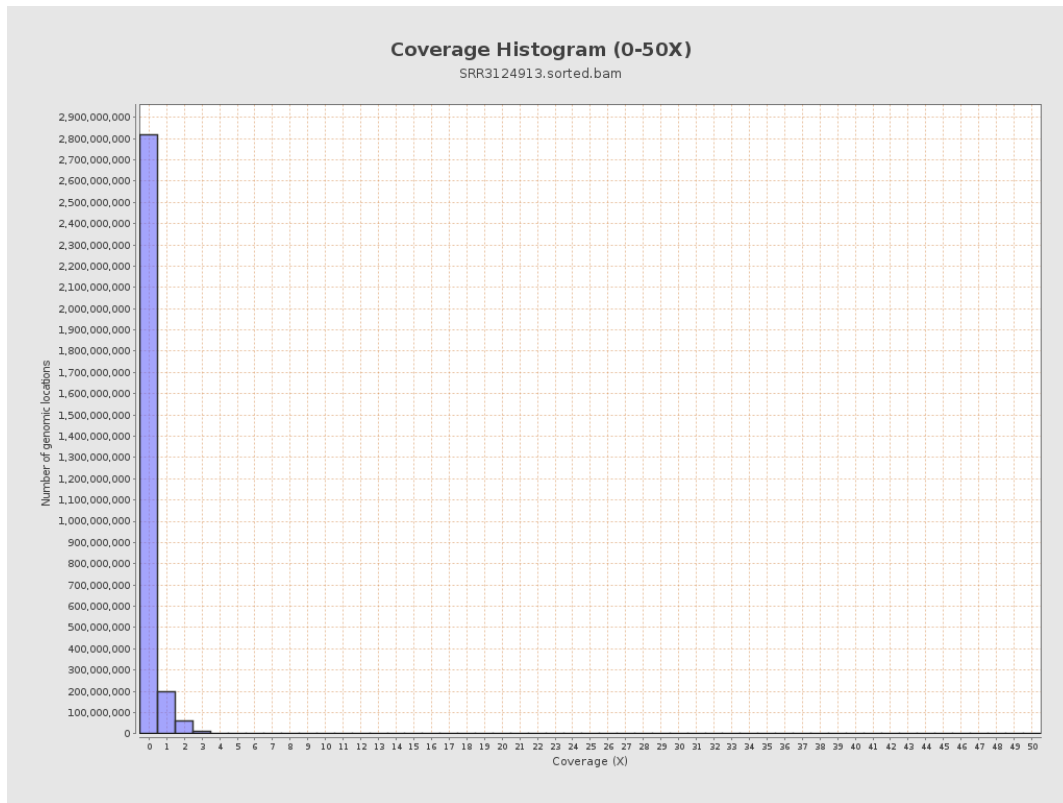
3. Results : Coverage across reference



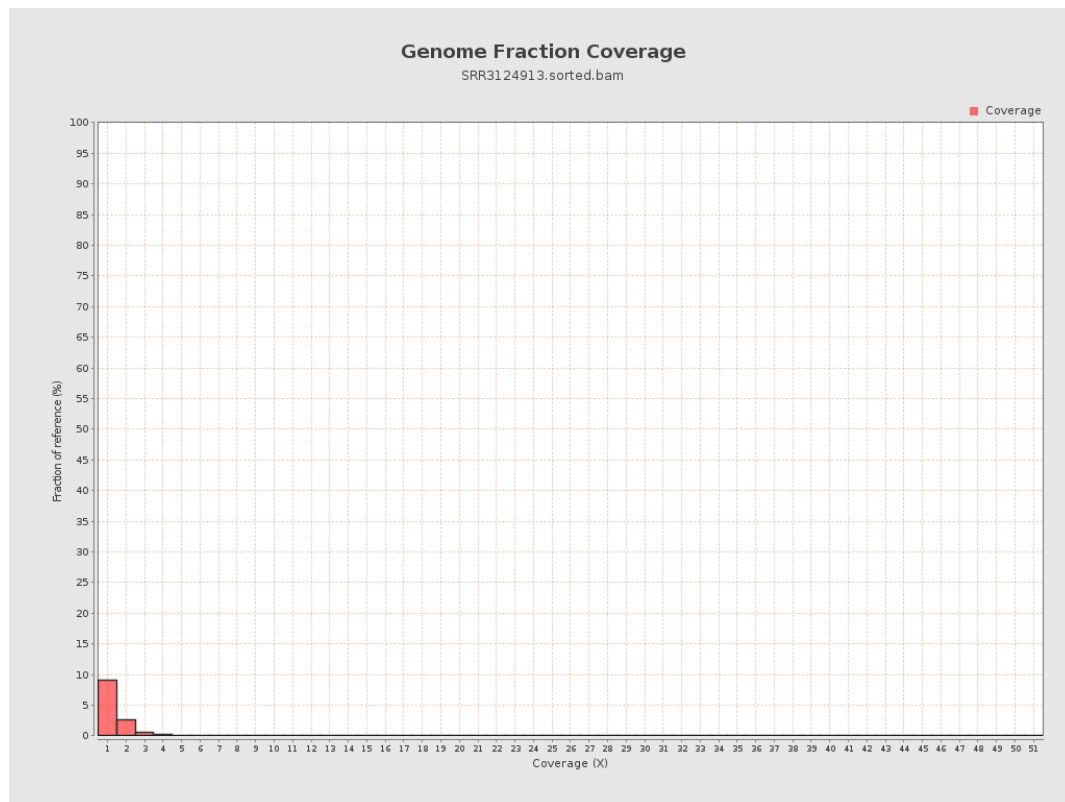
4. Results : Coverage Histogram



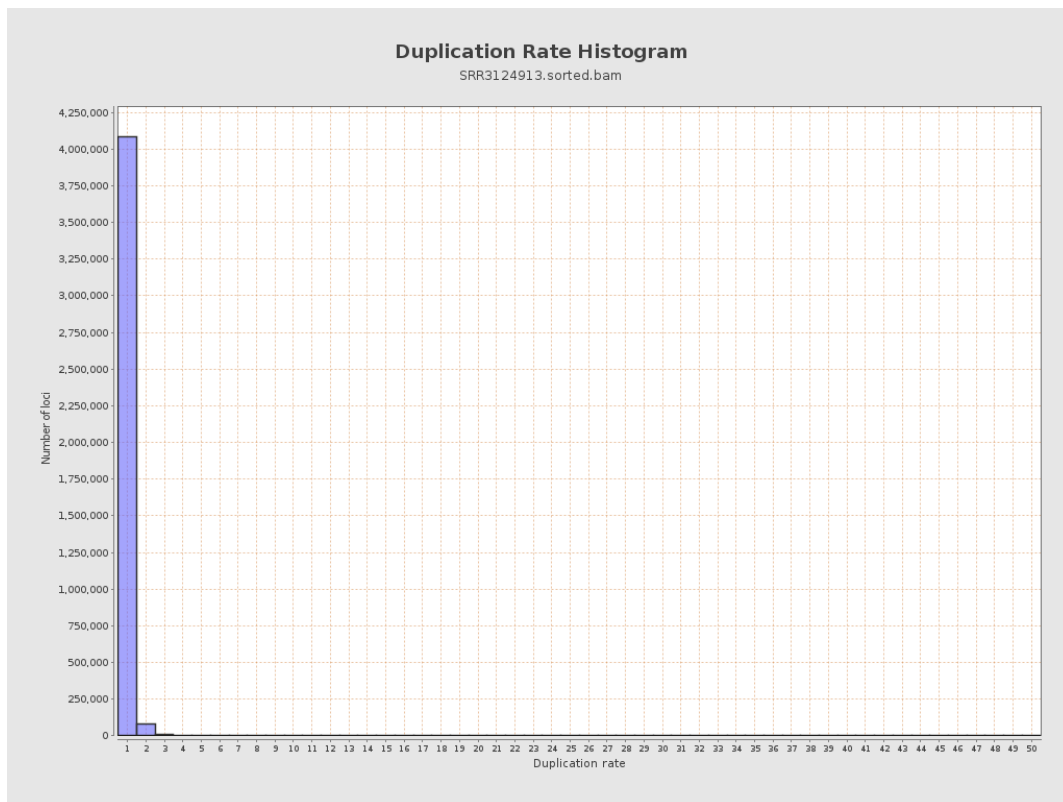
5. Results : Coverage Histogram (0-50X)



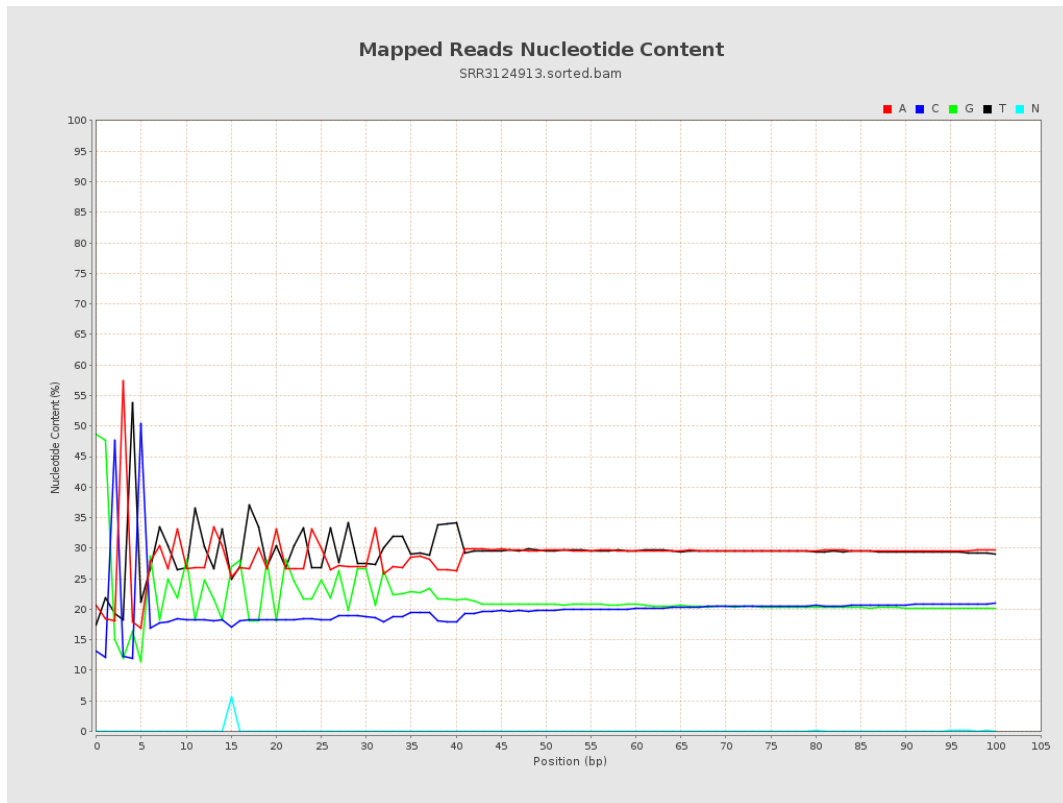
6. Results : Genome Fraction Coverage



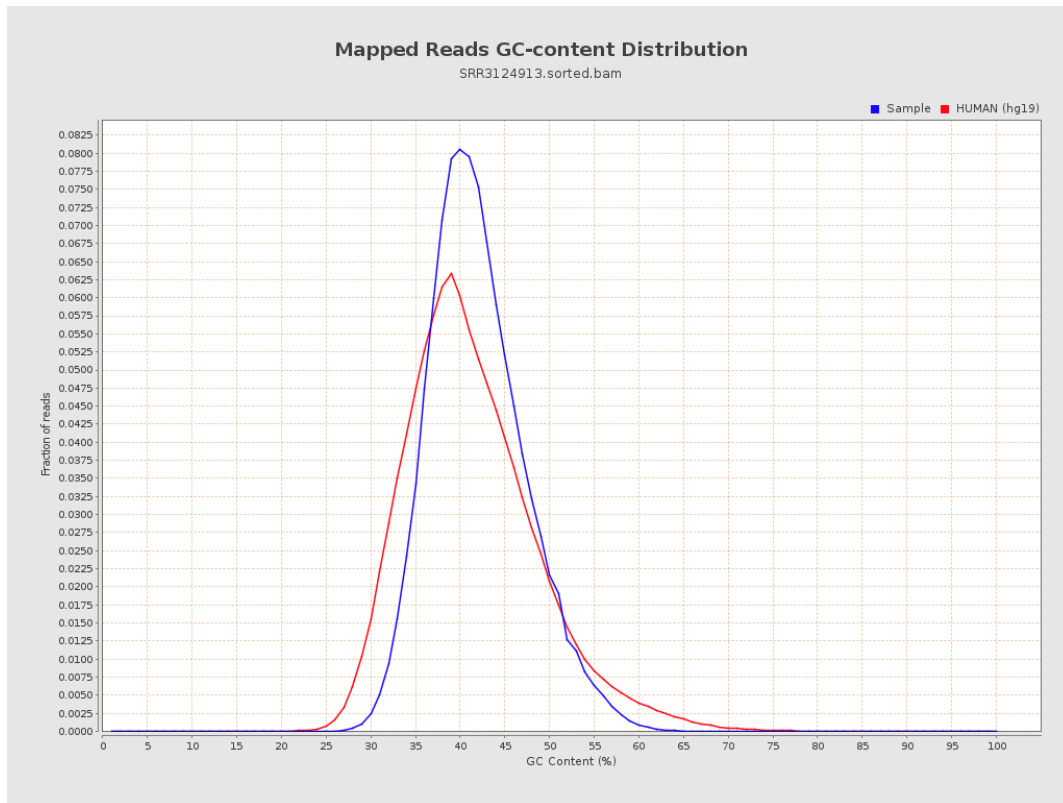
7. Results : Duplication Rate Histogram



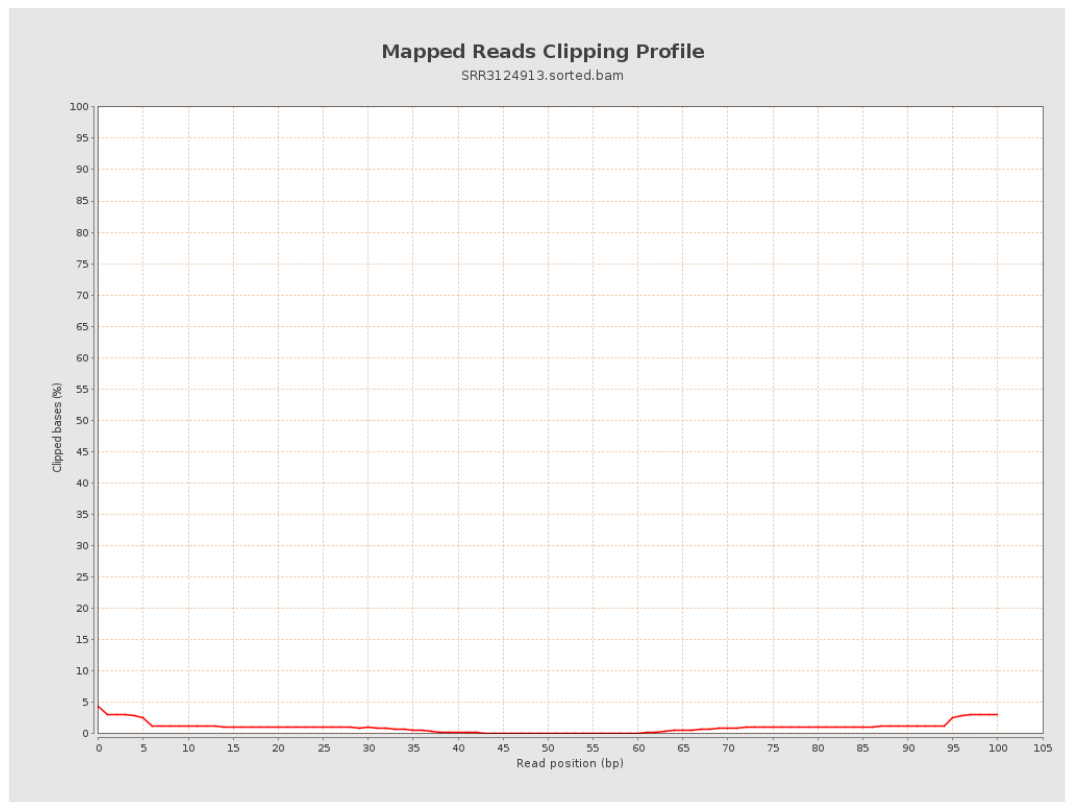
8. Results : Mapped Reads Nucleotide Content



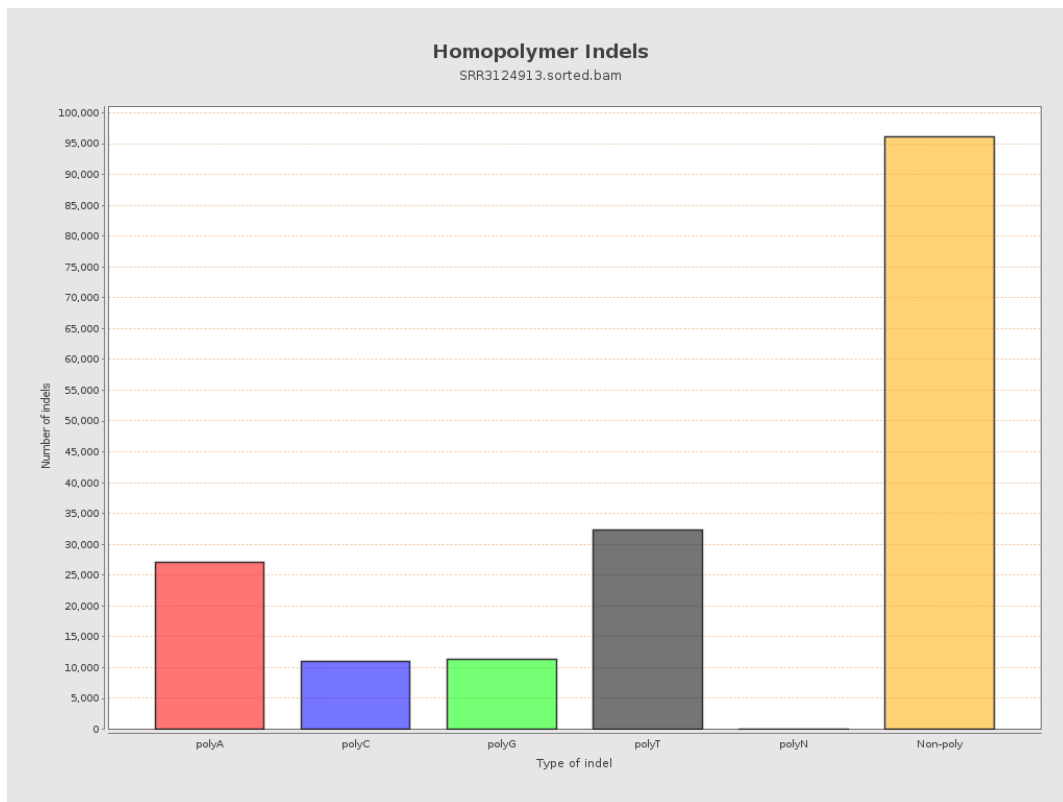
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



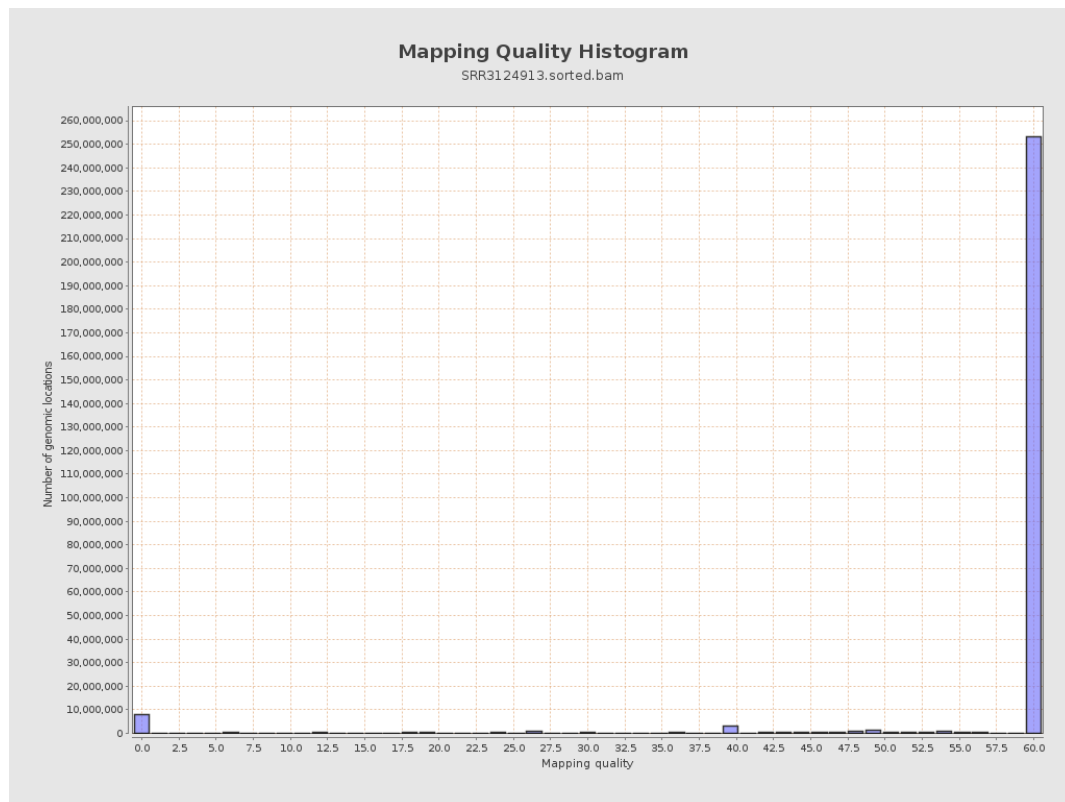
11. Results : Homopolymer Indels



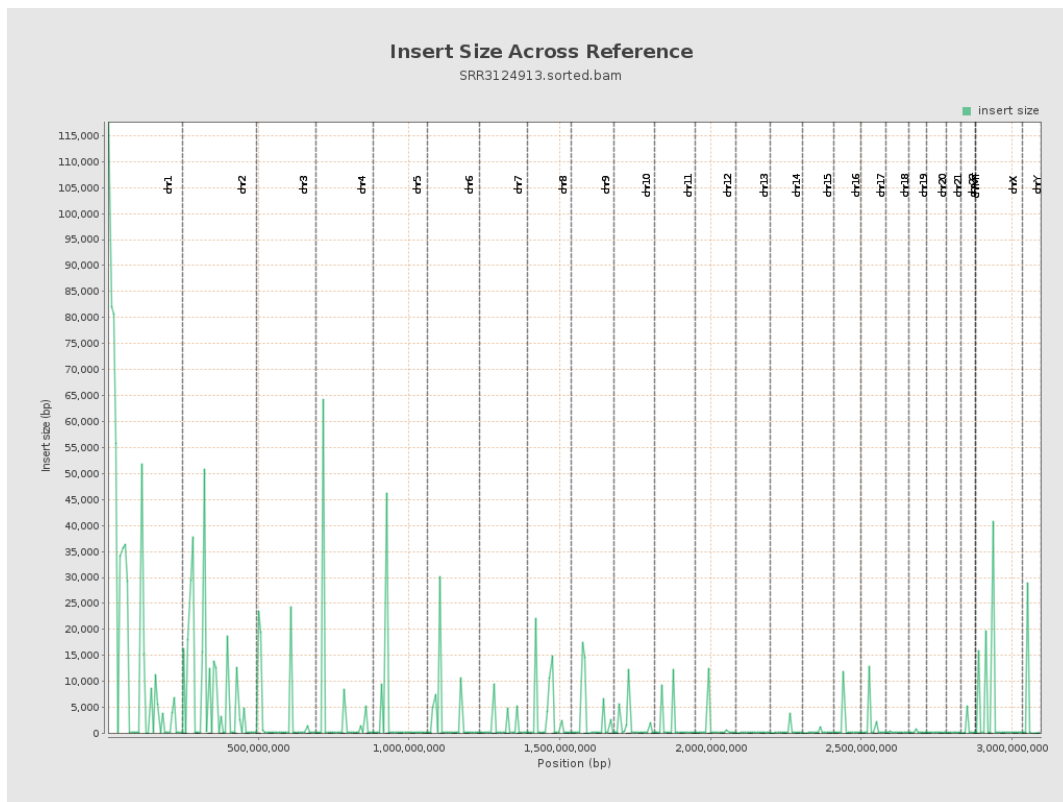
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

