

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 04:54:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124916.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_SRR3124916 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124916_1.fastq.gz SRR3124916_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 04:54:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,232,704
Mapped reads	2,214,777 / 99.2%
Unmapped reads	17,927 / 0.8%
Mapped paired reads	2,214,777 / 99.2%
Mapped reads, first in pair	1,108,579 / 49.65%
Mapped reads, second in pair	1,106,198 / 49.55%
Mapped reads, both in pair	2,207,548 / 98.87%
Mapped reads, singletons	7,229 / 0.32%
Secondary alignments	0
Supplementary alignments	608,810 / 27.27%
Read min/max/mean length	30 / 151 / 165.41
Duplicated reads (estimated)	799,433 / 35.81%
Duplication rate	24.81%
Clipped reads	2,476,910 / 110.94%

2.2. ACGT Content

Number/percentage of A's	86,232,842 / 28.9%
Number/percentage of C's	62,516,035 / 20.95%
Number/percentage of T's	86,085,172 / 28.85%
Number/percentage of G's	63,560,826 / 21.3%
Number/percentage of N's	18,219 / 0.01%

GC Percentage	42.25%
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2.3. Coverage

Mean	0.0965
Standard Deviation	5.0868

2.4. Mapping Quality

Mean Mapping Quality	47.1
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2.5. Insert size

Mean	1,189,901.84
Standard Deviation	10,335,033.71
P25/Median/P75	110 / 143 / 183

2.6. Mismatches and indels

General error rate	1.82%
Mismatches	5,110,085
Insertions	106,201
Mapped reads with at least one insertion	4.47%
Deletions	182,669
Mapped reads with at least one deletion	7.82%
Homopolymer indels	42.9%

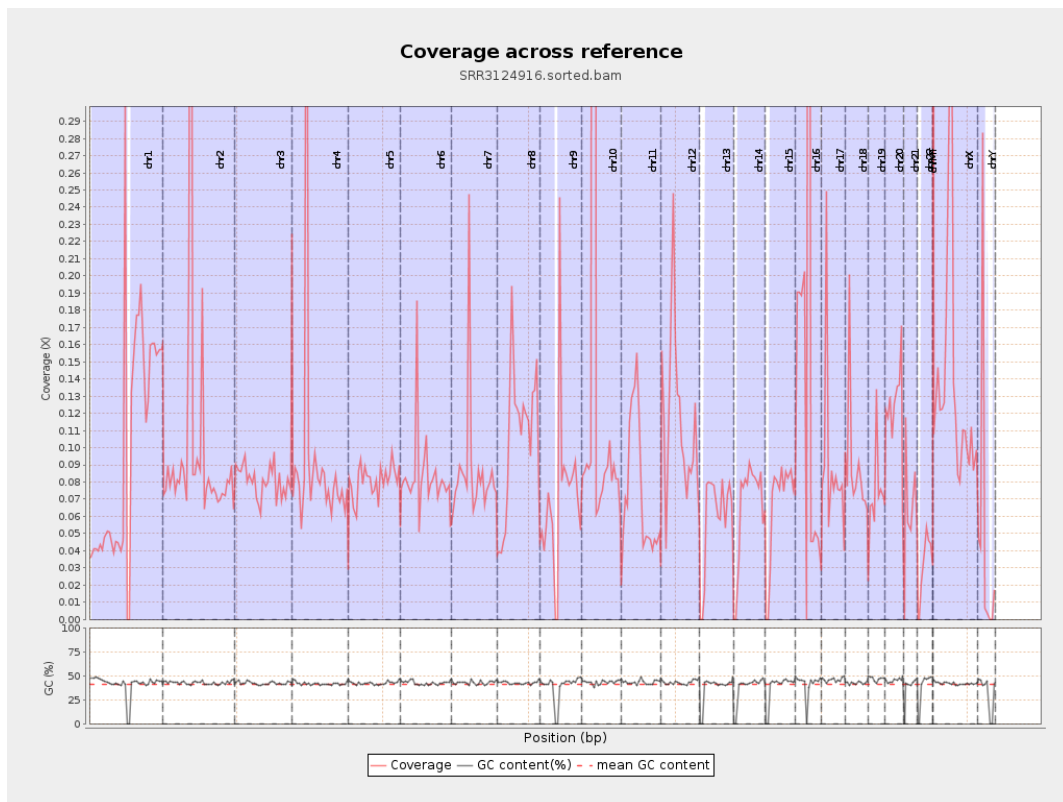
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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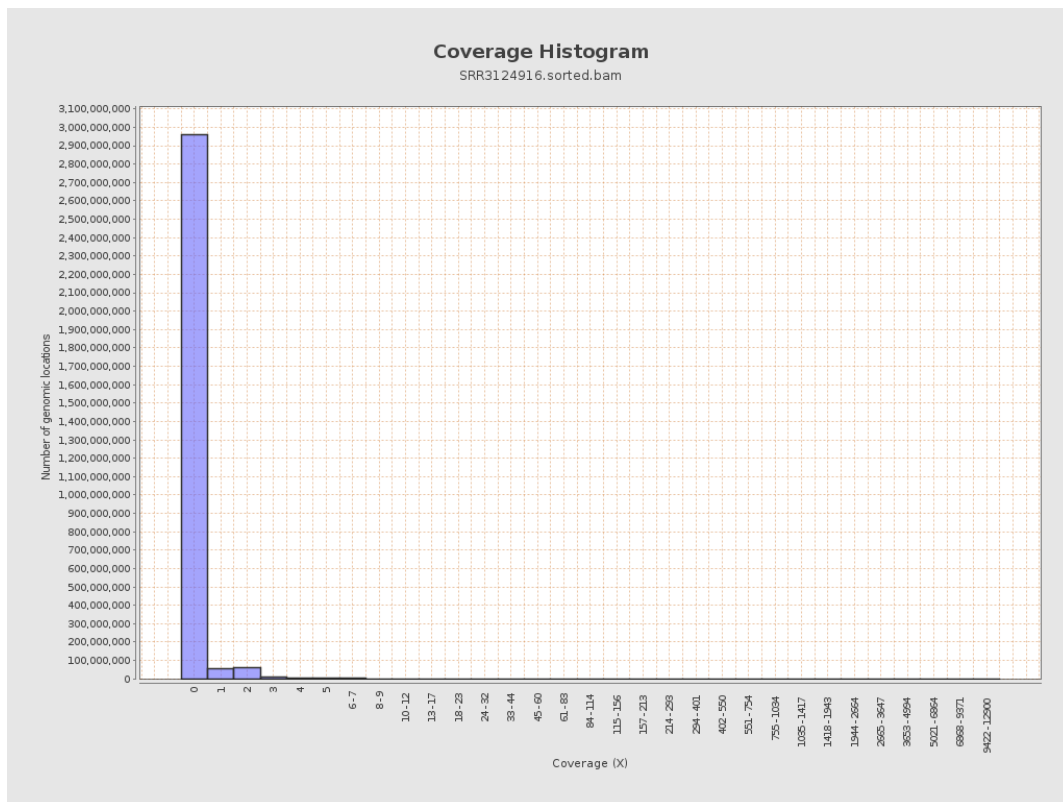
		bases	coverage	deviation
chr1	249250621	24617198	0.0988	2.6012
chr2	243199373	25046376	0.103	3.0665
chr3	198022430	16201854	0.0818	1.6153
chr4	191154276	18149330	0.0949	2.4084
chr5	180915260	14590508	0.0806	0.4668
chr6	171115067	14289062	0.0835	1.2428
chr7	159138663	13696390	0.0861	2.2887
chr8	146364022	15420182	0.1054	0.9373
chr9	141213431	10174066	0.072	3.108
chr10	135534747	28807487	0.2125	21.9771
chr11	135006516	10084257	0.0747	1.1117
chr12	133851895	15388625	0.115	0.5732
chr13	115169878	6861061	0.0596	0.3744
chr14	107349540	7112958	0.0663	0.4643
chr15	102531392	6725177	0.0656	0.3914
chr16	90354753	15638855	0.1731	5.652
chr17	81195210	7446425	0.0917	3.0823
chr18	78077248	7025332	0.09	2.5914
chr19	59128983	4394744	0.0743	1.4771
chr20	63025520	8019338	0.1272	0.9506
chr21	48129895	3201344	0.0665	1.507
chr22	51304566	1646179	0.0321	0.3441
chrMT	16571	34561	2.0856	2.5364
chrX	155270560	21250708	0.1369	1.2601

chrY	59373566	2971964	0.0501	4.877
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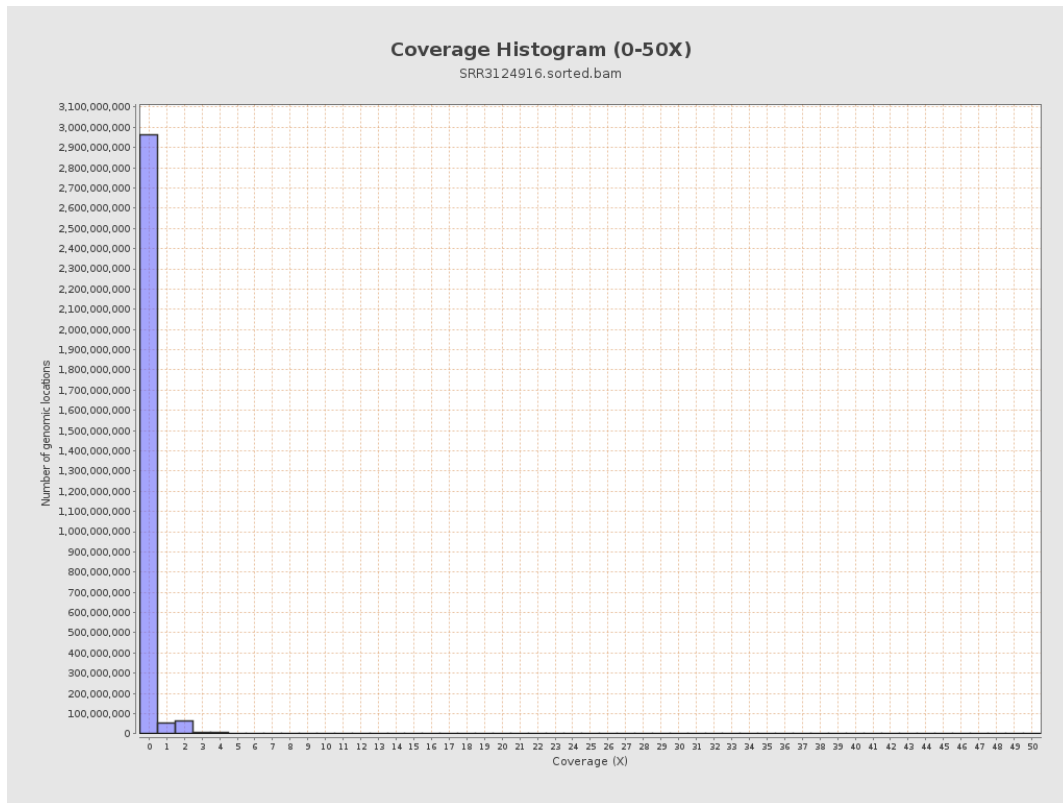
3. Results : Coverage across reference



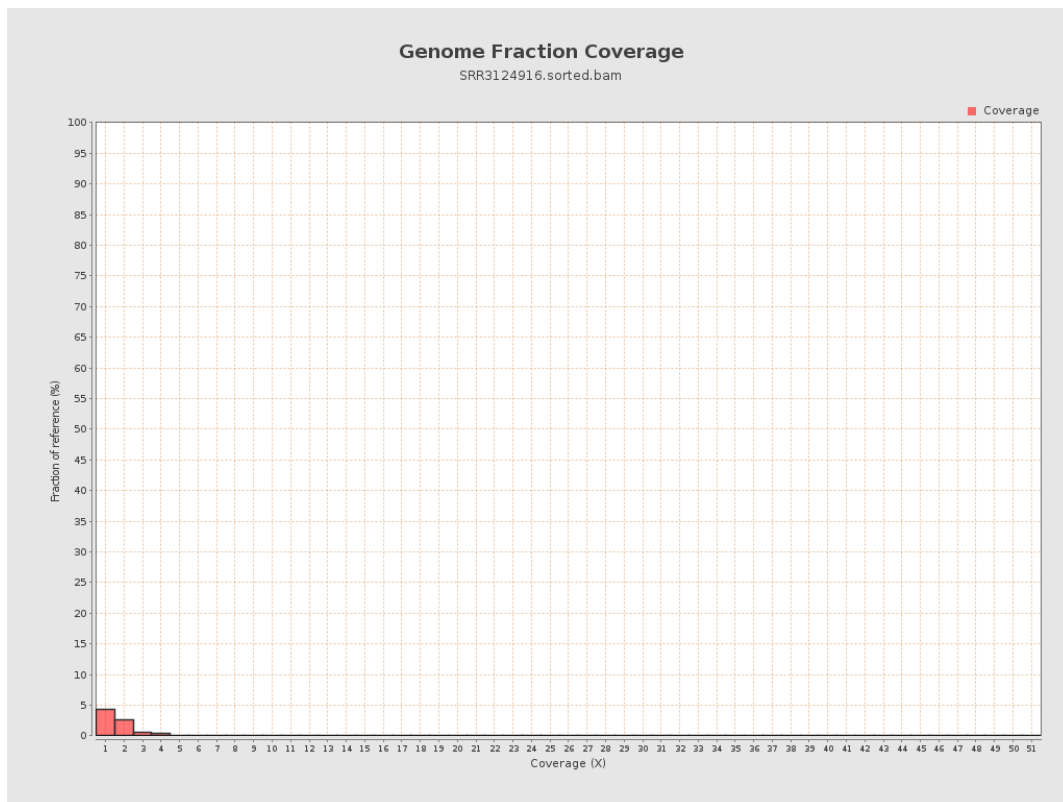
4. Results : Coverage Histogram



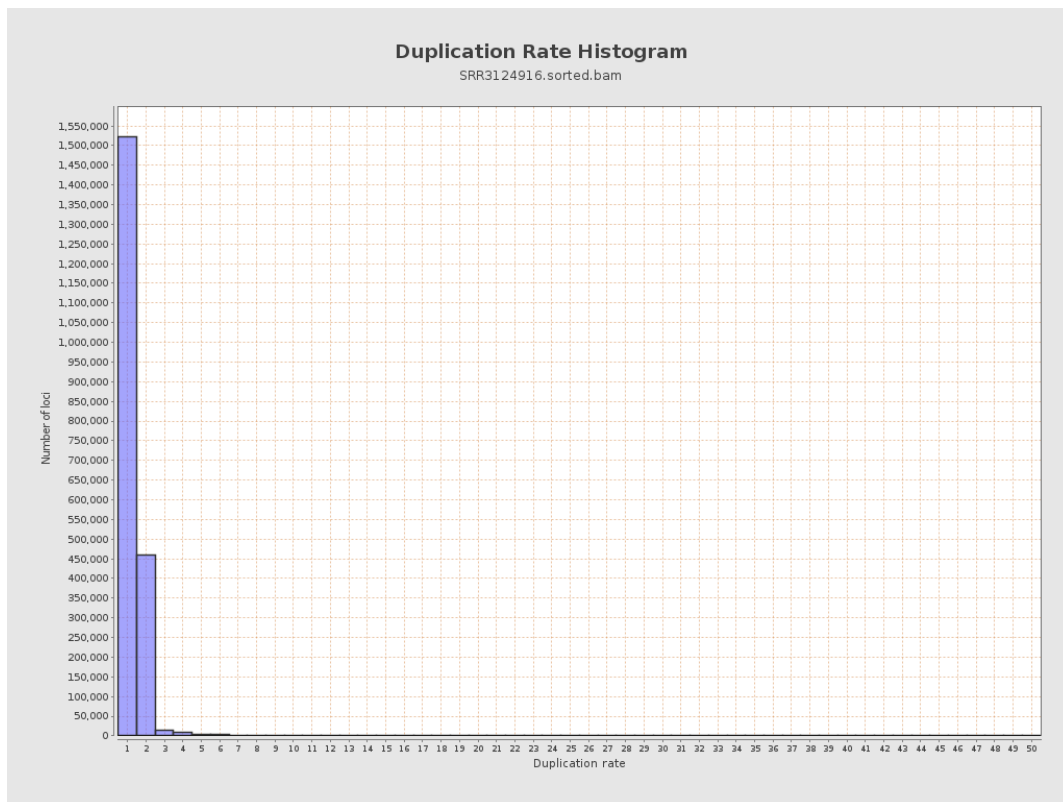
5. Results : Coverage Histogram (0-50X)



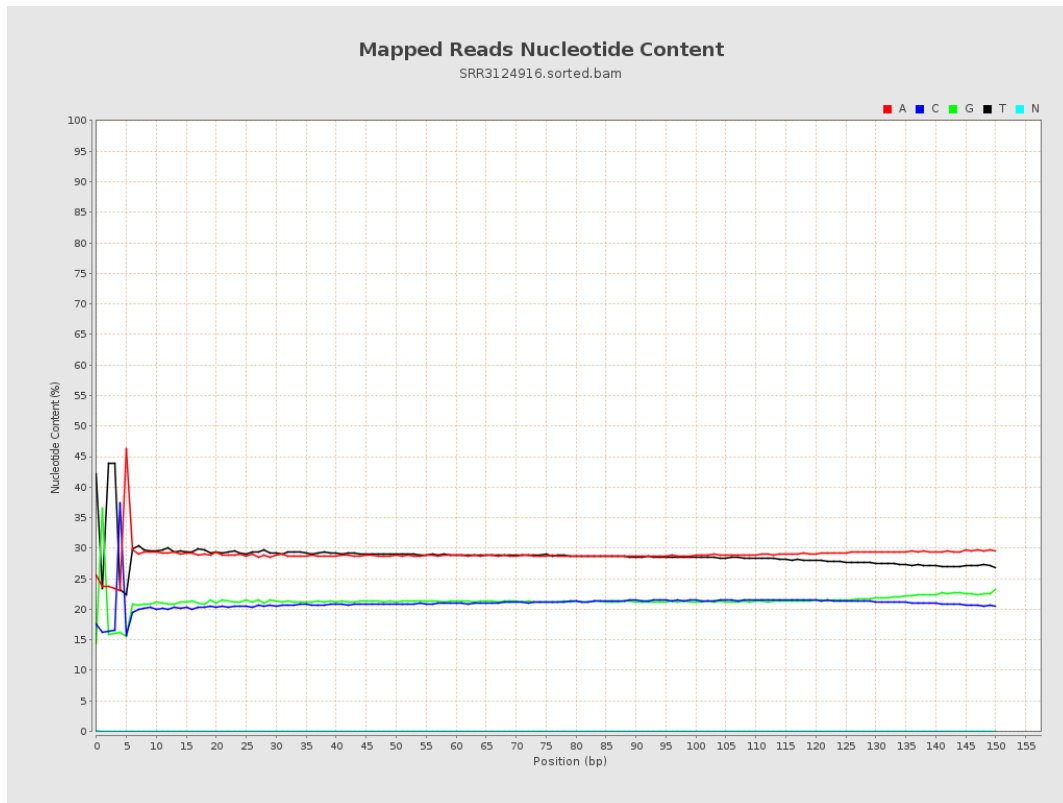
6. Results : Genome Fraction Coverage



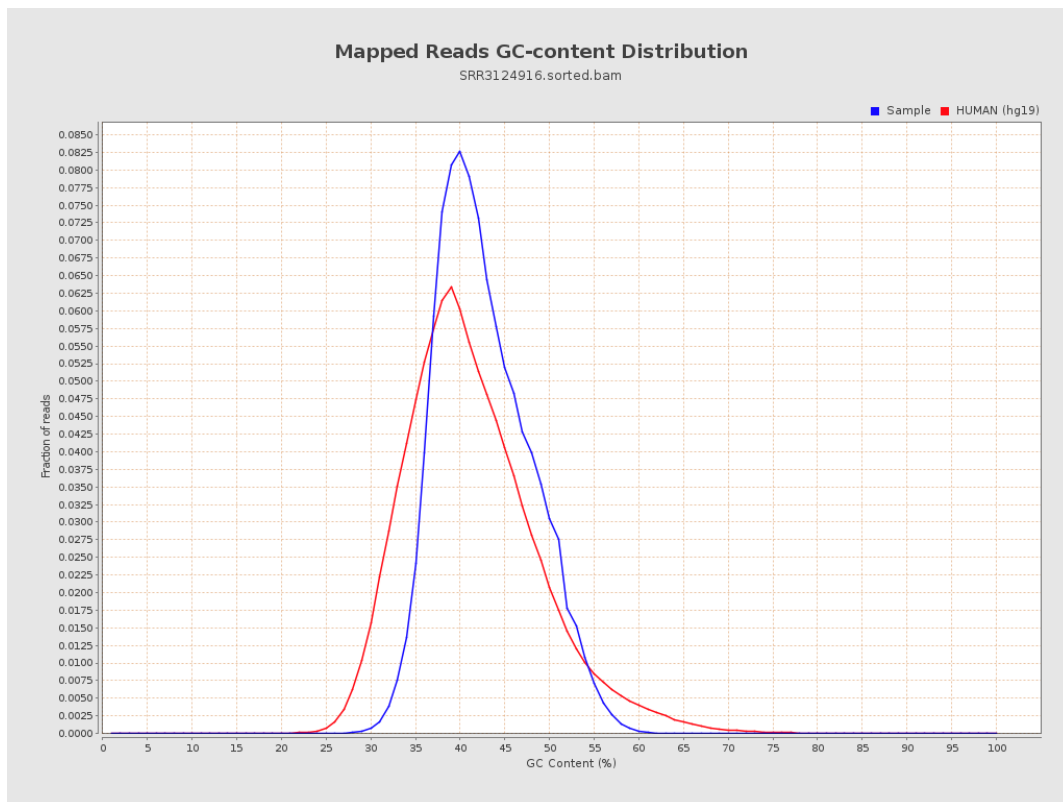
7. Results : Duplication Rate Histogram



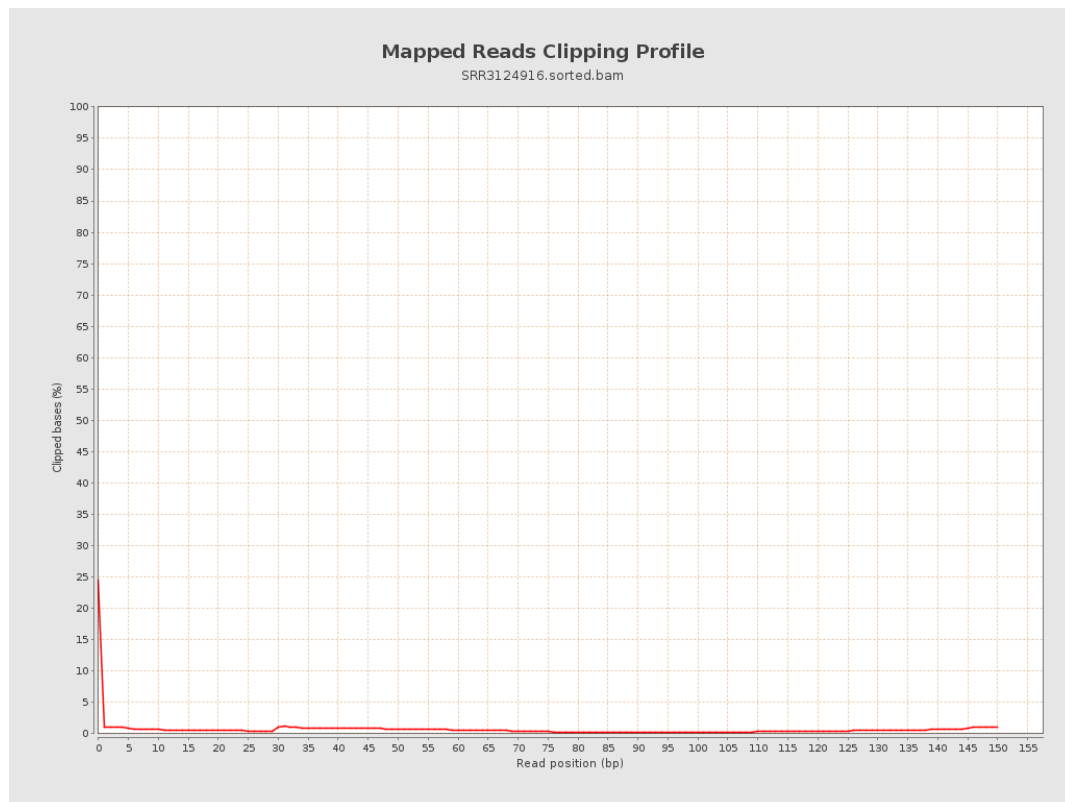
8. Results : Mapped Reads Nucleotide Content



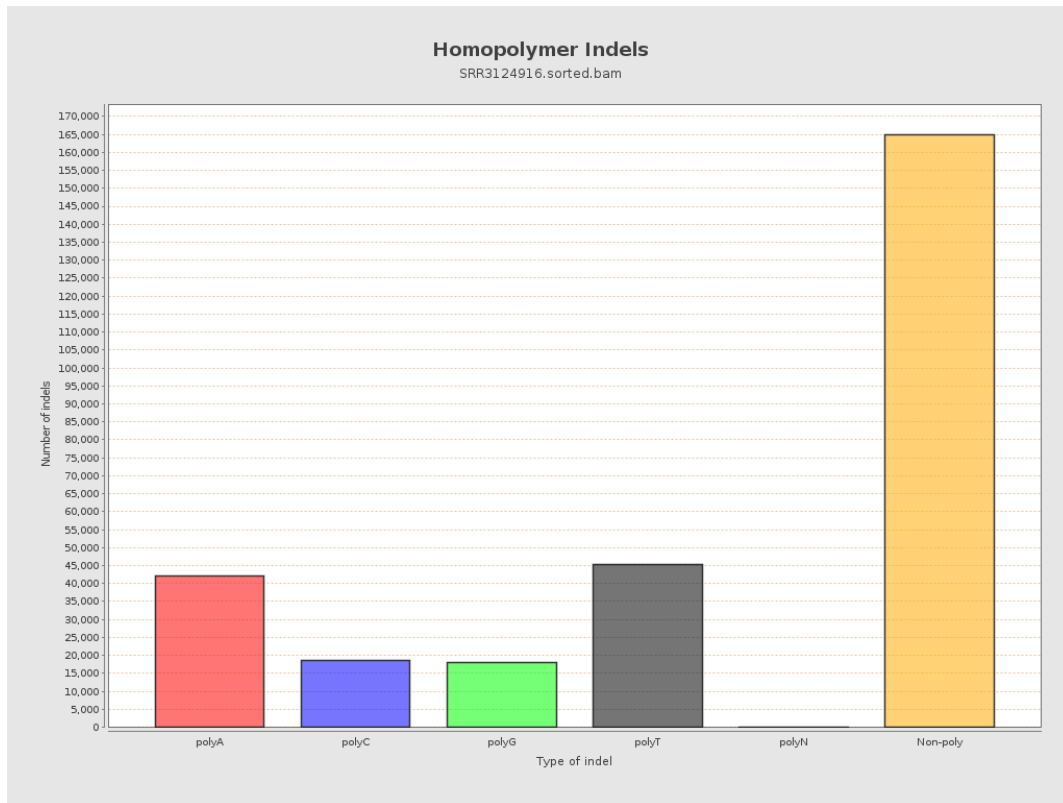
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



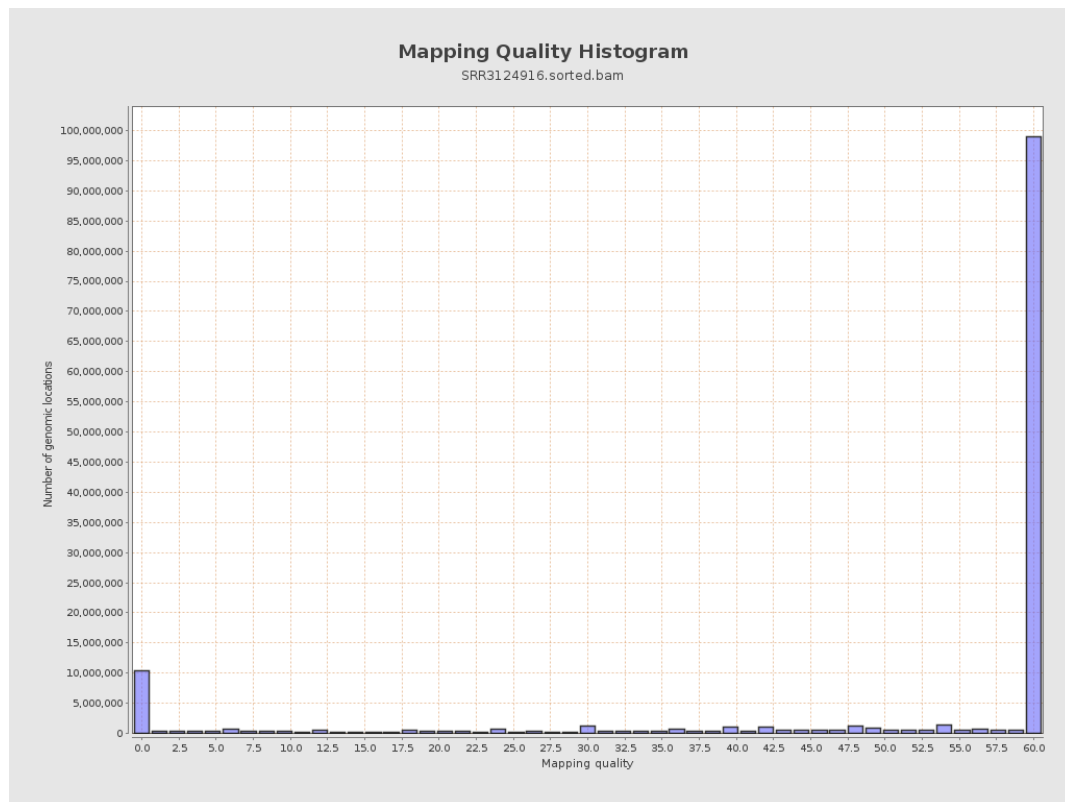
11. Results : Homopolymer Indels



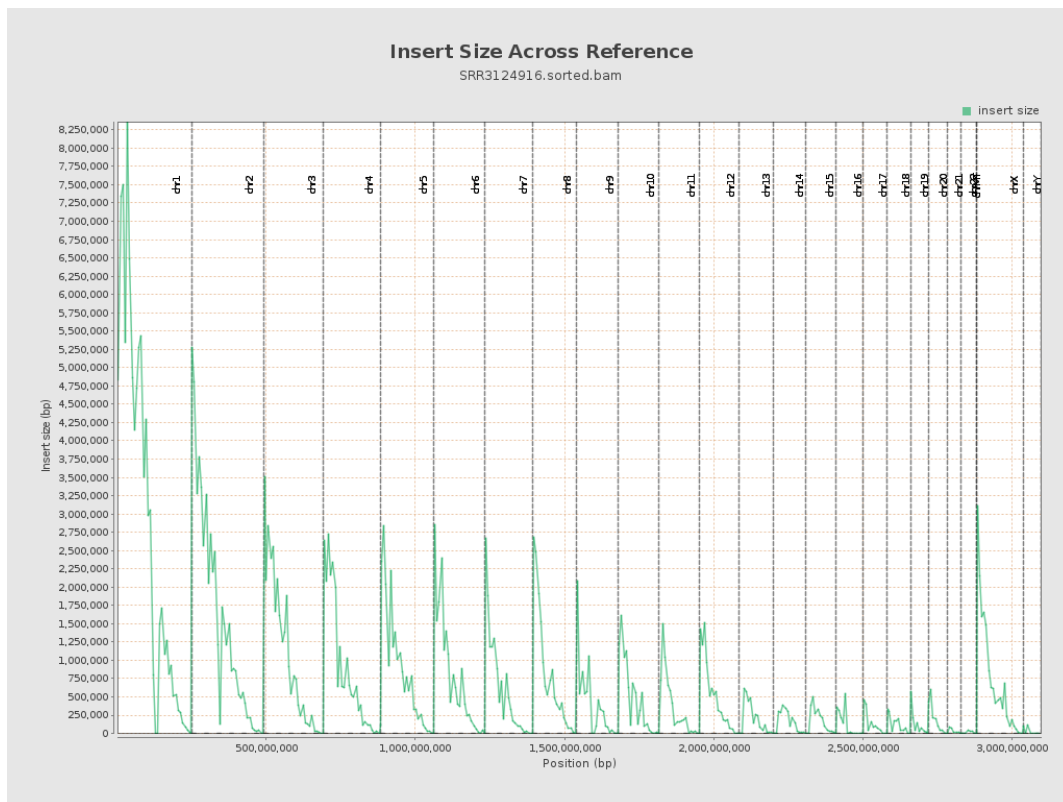
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

