

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 15:04:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354866.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_SRR22354866 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354866_1.fastq.gz SRR22354866_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 15:04:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354866.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,775,892
Mapped reads	17,505,977 / 98.48%
Unmapped reads	269,915 / 1.52%
Mapped paired reads	17,505,977 / 98.48%
Mapped reads, first in pair	8,760,206 / 49.28%
Mapped reads, second in pair	8,745,771 / 49.2%
Mapped reads, both in pair	17,472,148 / 98.29%
Mapped reads, singletons	33,829 / 0.19%
Secondary alignments	0
Supplementary alignments	609,666 / 3.43%
Read min/max/mean length	30 / 150 / 151.25
Duplicated reads (estimated)	9,113,065 / 51.27%
Duplication rate	52.12%
Clipped reads	7,499,776 / 42.19%

2.2. ACGT Content

Number/percentage of A's	637,244,153 / 28.13%
Number/percentage of C's	478,606,048 / 21.13%
Number/percentage of T's	647,941,619 / 28.6%
Number/percentage of G's	501,499,156 / 22.14%
Number/percentage of N's	35,562 / 0%

GC Percentage	43.27%
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2.3. Coverage

Mean	0.7321
Standard Deviation	28.5246

2.4. Mapping Quality

Mean Mapping Quality	53.84
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2.5. Insert size

Mean	301,280.09
Standard Deviation	6,266,653.93
P25/Median/P75	116 / 189 / 283

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	13,532,655
Insertions	381,557
Mapped reads with at least one insertion	2.04%
Deletions	406,521
Mapped reads with at least one deletion	2.22%
Homopolymer indels	45.2%

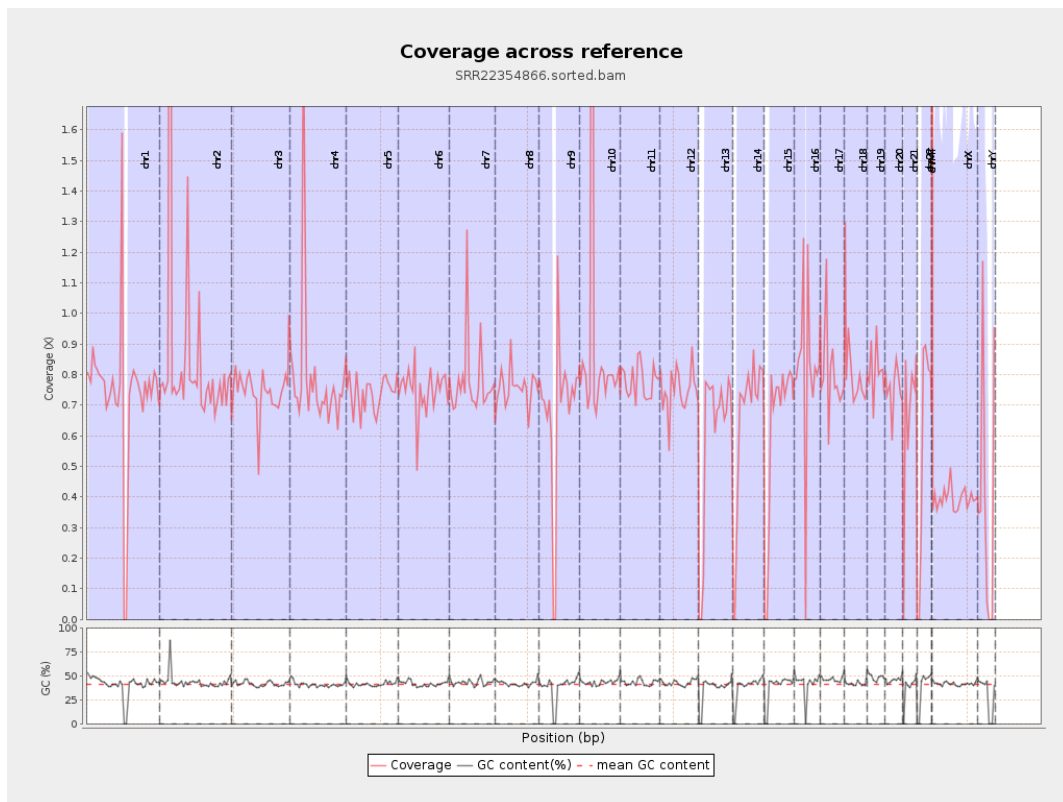
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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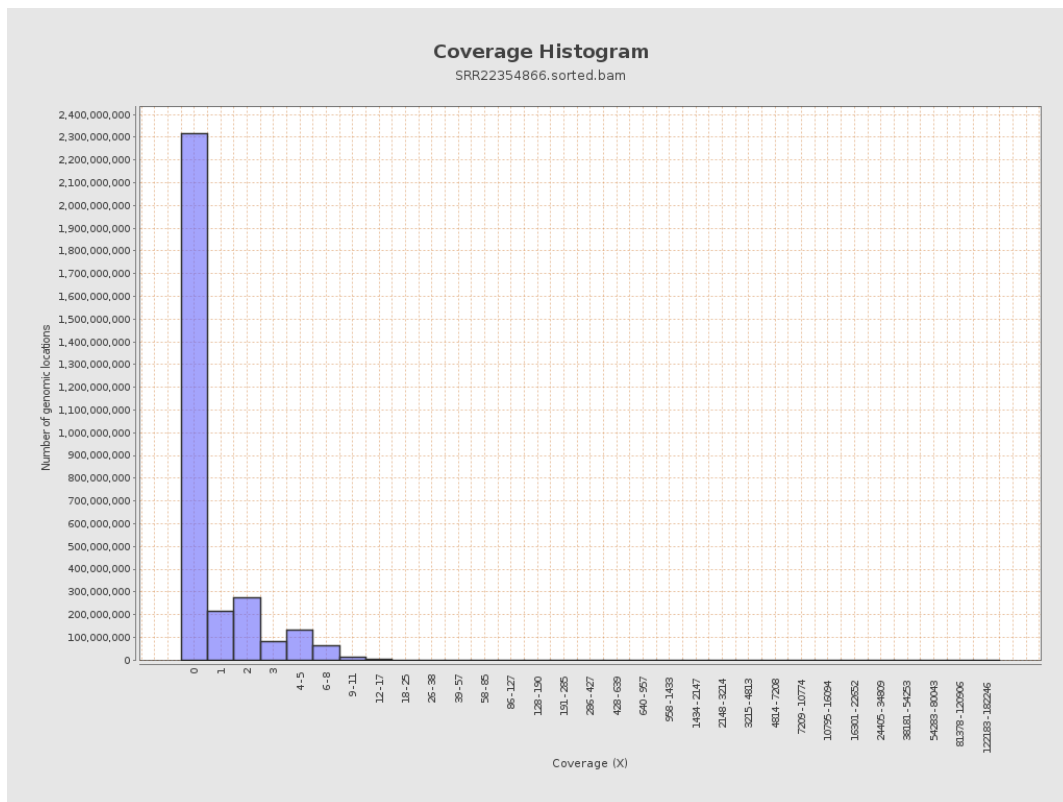
		bases	coverage	deviation
chr1	249250621	185553949	0.7444	19.086
chr2	243199373	211630755	0.8702	95.2634
chr3	198022430	147282197	0.7438	1.9054
chr4	191154276	150040955	0.7849	9.1614
chr5	180915260	133616393	0.7386	1.6512
chr6	171115067	128182947	0.7491	2.9703
chr7	159138663	123506422	0.7761	22.8935
chr8	146364022	111125809	0.7592	5.6695
chr9	141213431	95601526	0.677	11.0065
chr10	135534747	124727343	0.9203	22.3026
chr11	135006516	105088807	0.7784	3.6534
chr12	133851895	100267765	0.7491	1.6677
chr13	115169878	69436573	0.6029	1.4733
chr14	107349540	69273480	0.6453	2.5704
chr15	102531392	63563346	0.6199	1.4967
chr16	90354753	73953882	0.8185	4.5117
chr17	81195210	64637171	0.7961	4.5798
chr18	78077248	62366888	0.7988	8.8781
chr19	59128983	48265713	0.8163	9.8754
chr20	63025520	47508795	0.7538	3.3857
chr21	48129895	32459951	0.6744	5.009
chr22	51304566	30028469	0.5853	2.6162
chrMT	16571	2673398	161.3299	33.644
chrX	155270560	61123902	0.3937	1.6723

chrY	59373566	24550901	0.4135	11.2623
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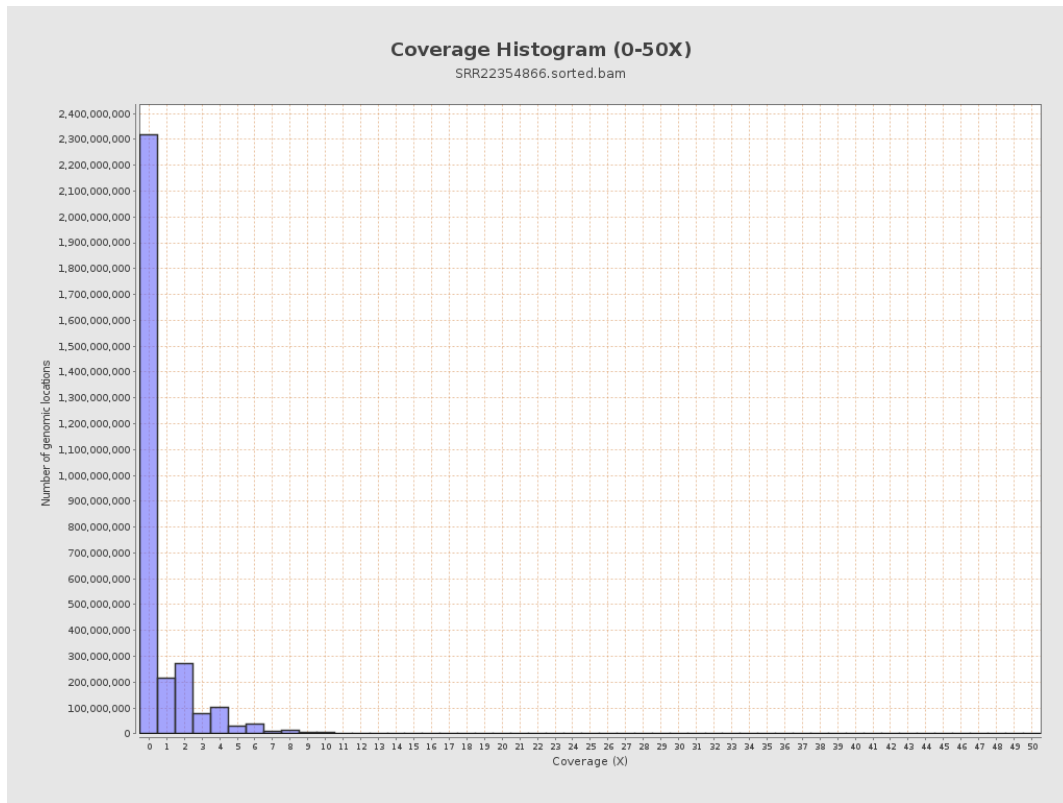
3. Results : Coverage across reference



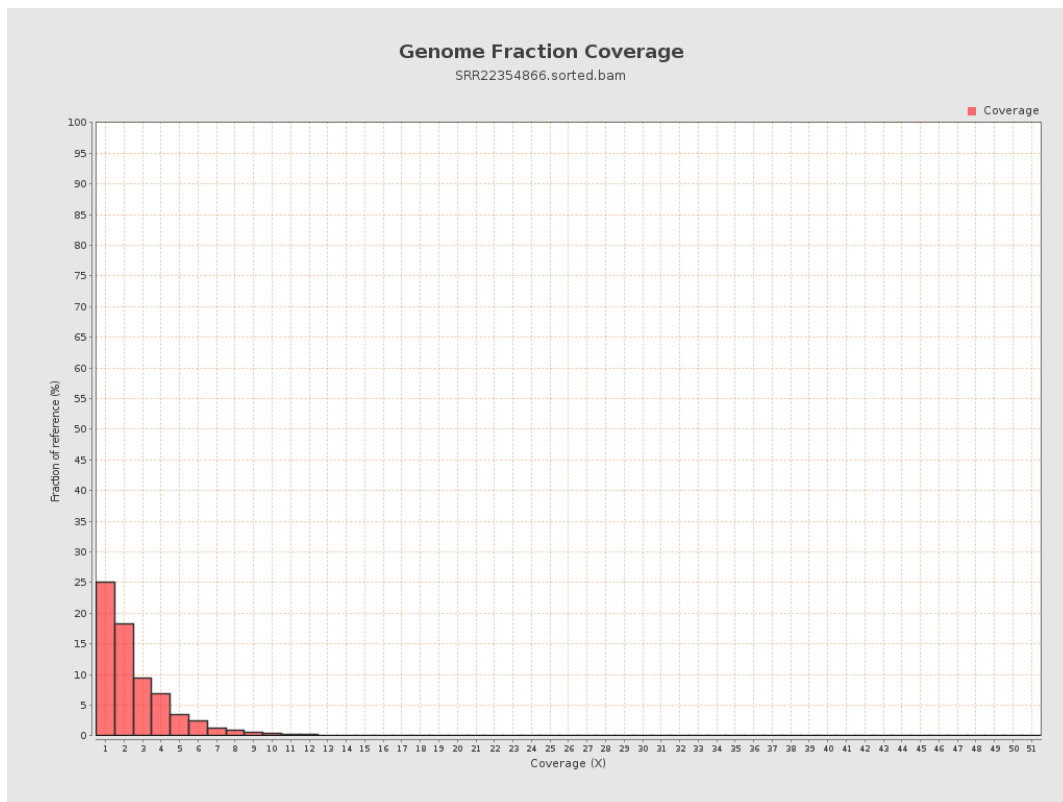
4. Results : Coverage Histogram



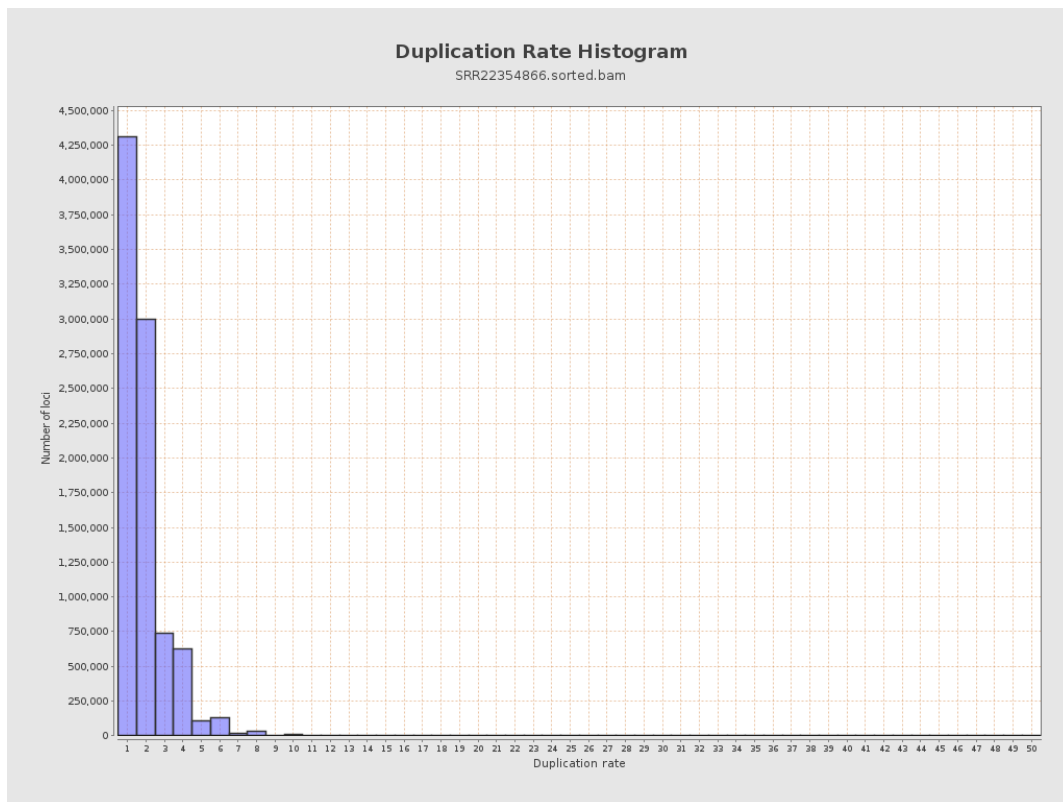
5. Results : Coverage Histogram (0-50X)



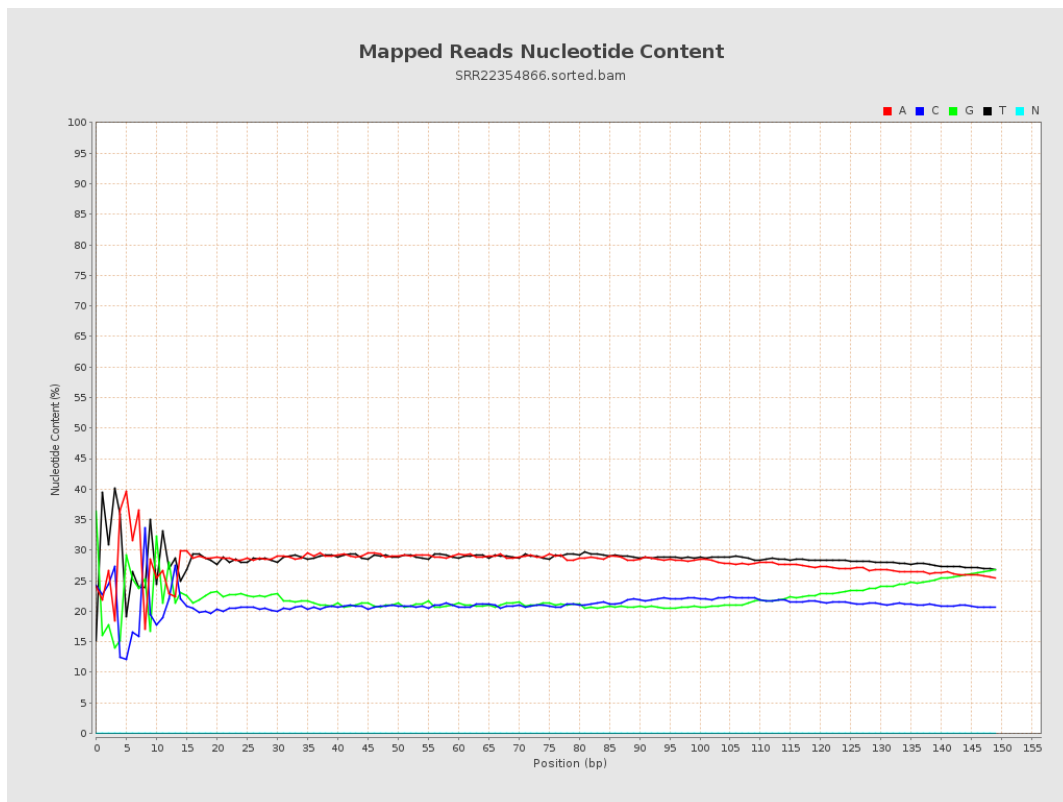
6. Results : Genome Fraction Coverage



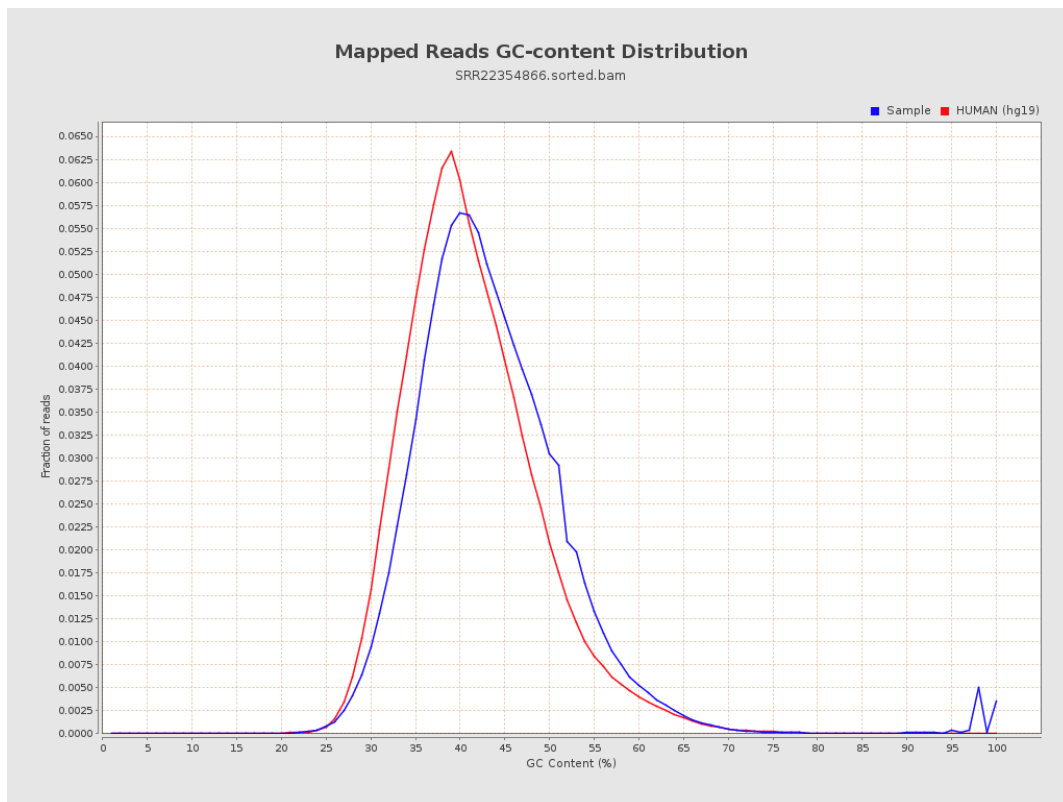
7. Results : Duplication Rate Histogram



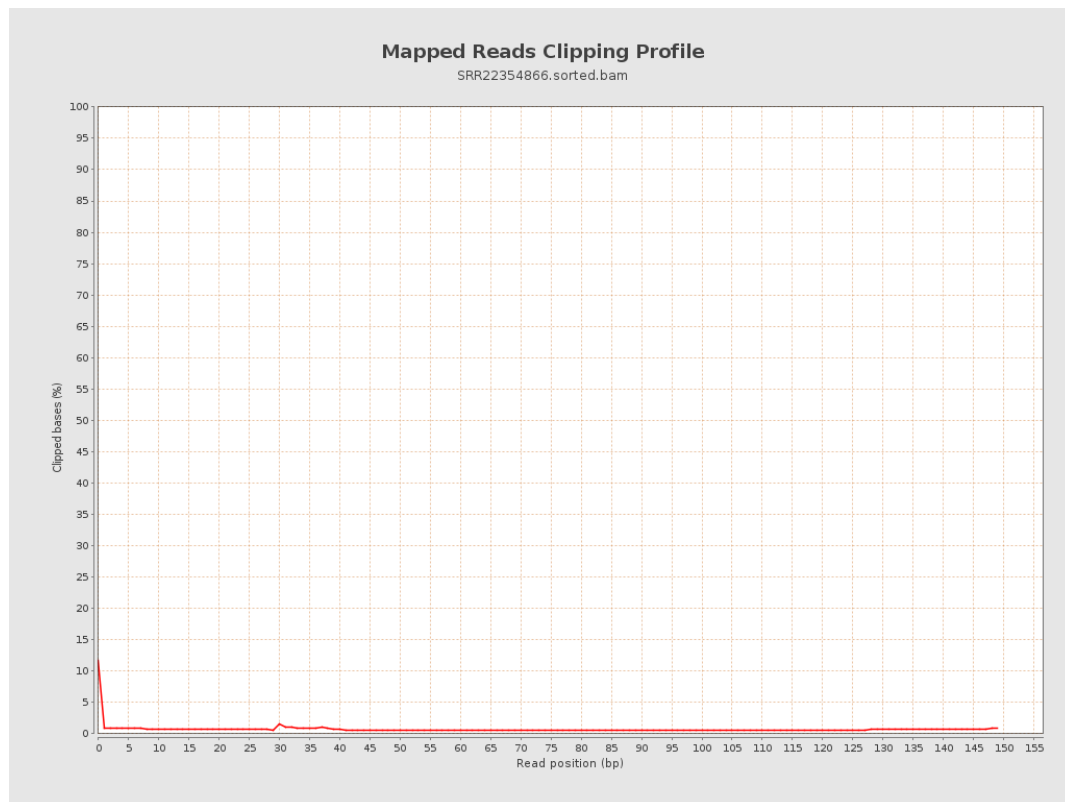
8. Results : Mapped Reads Nucleotide Content



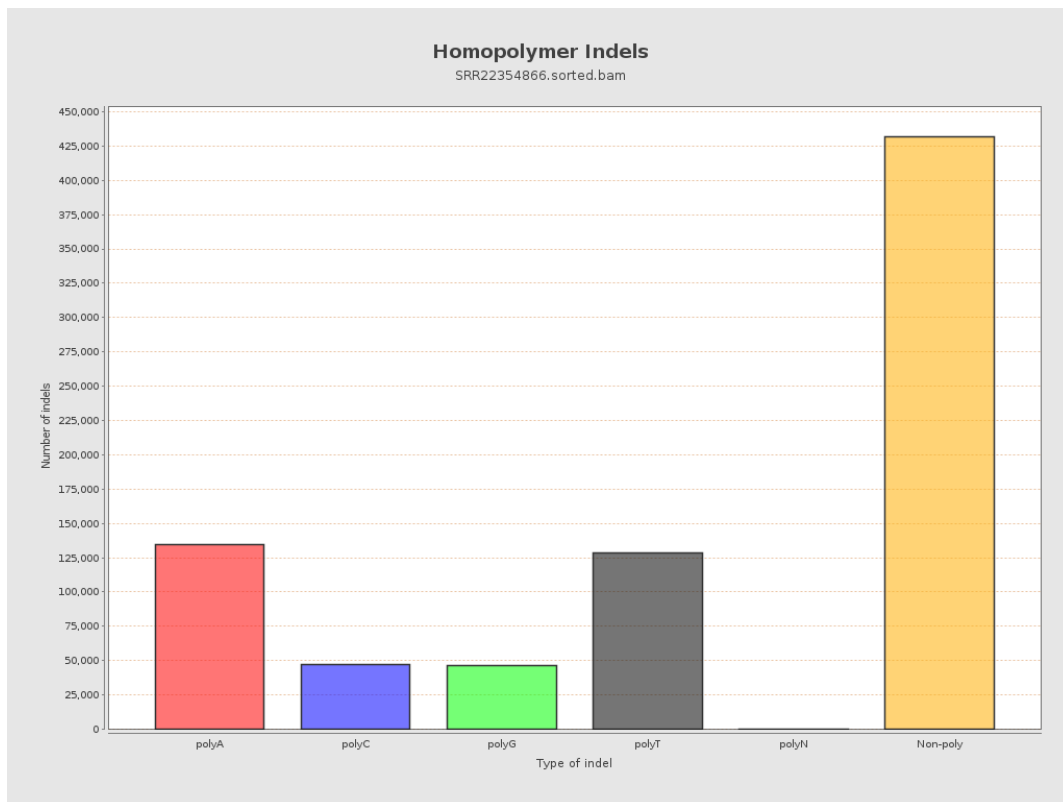
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



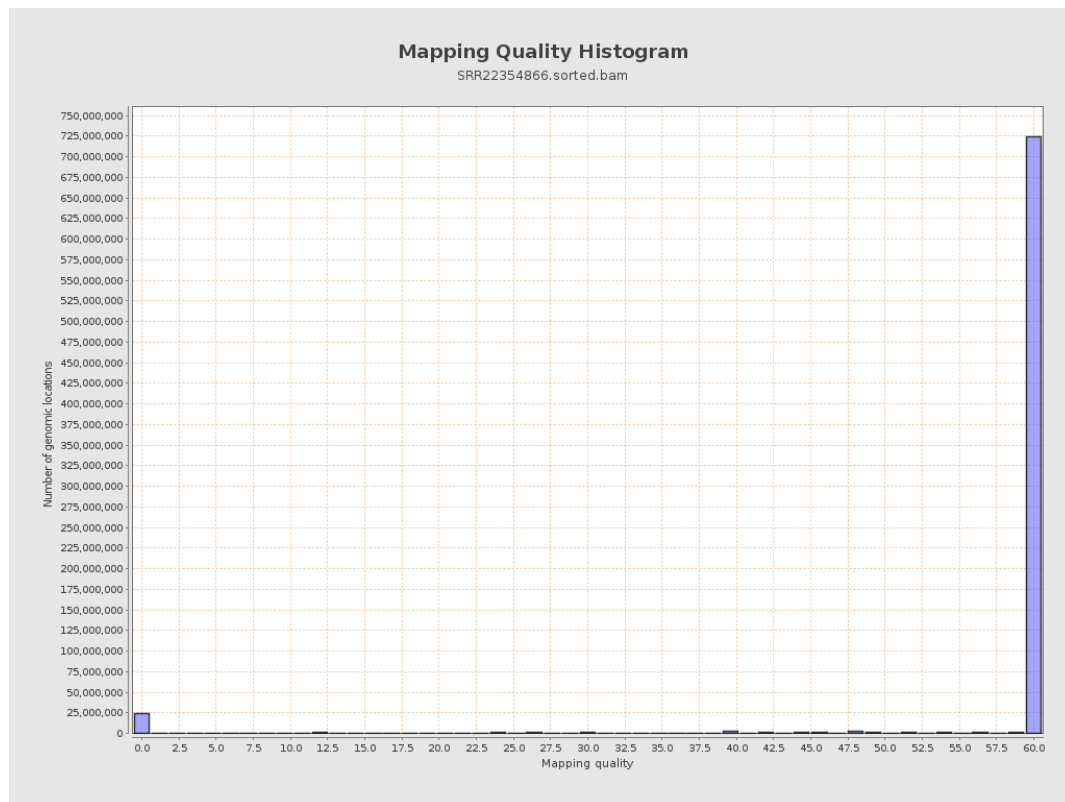
11. Results : Homopolymer Indels



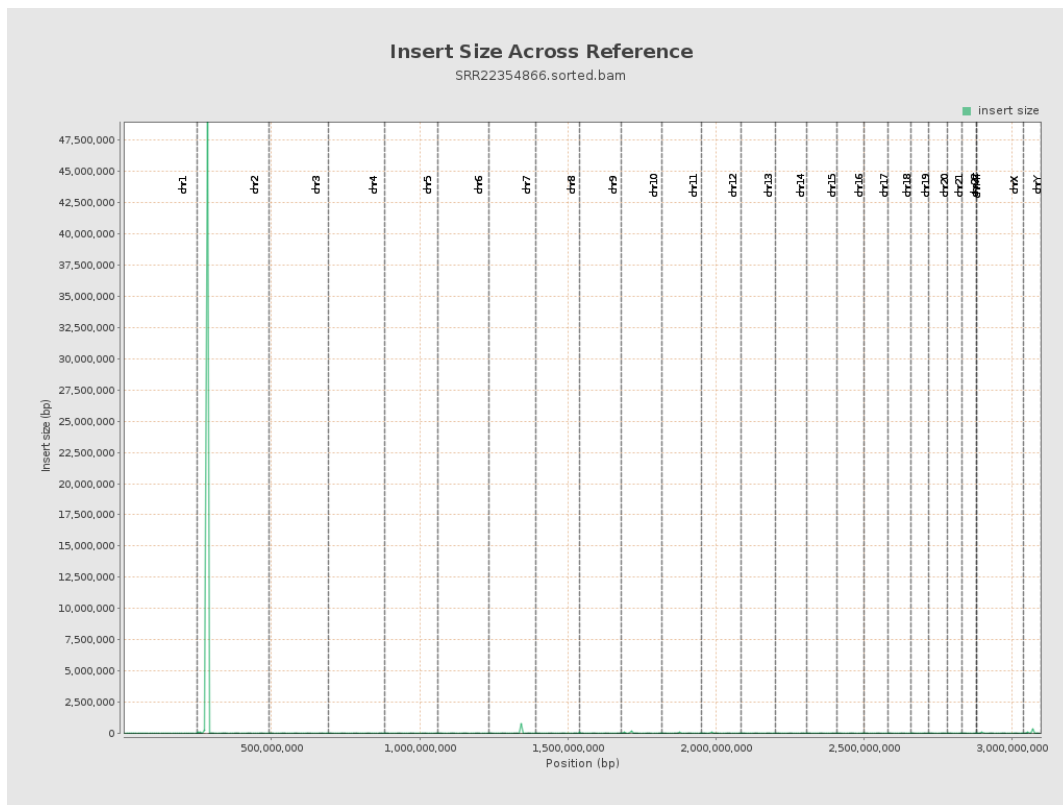
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

