

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 04:05:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174066.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_SRR10174066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174066_1.fastq.gz SRR10174066_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 04:05:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,910,206
Mapped reads	5,779,124 / 97.78%
Unmapped reads	131,082 / 2.22%
Mapped paired reads	5,779,124 / 97.78%
Mapped reads, first in pair	2,889,504 / 48.89%
Mapped reads, second in pair	2,889,620 / 48.89%
Mapped reads, both in pair	5,693,440 / 96.33%
Mapped reads, singletons	85,684 / 1.45%
Secondary alignments	0
Supplementary alignments	517,792 / 8.76%
Read min/max/mean length	30 / 133 / 127.44
Duplicated reads (estimated)	4,487,936 / 75.94%
Duplication rate	66.28%
Clipped reads	2,151,874 / 36.41%

2.2. ACGT Content

Number/percentage of A's	205,752,406 / 30.08%
Number/percentage of C's	134,510,887 / 19.67%
Number/percentage of T's	205,288,383 / 30.01%
Number/percentage of G's	138,424,335 / 20.24%
Number/percentage of N's	8,383 / 0%

GC Percentage	39.9%
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2.3. Coverage

Mean	0.2211
Standard Deviation	3.0561

2.4. Mapping Quality

Mean Mapping Quality	52.94
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2.5. Insert size

Mean	735,498.47
Standard Deviation	8,062,066.76
P25/Median/P75	143 / 196 / 276

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	6,529,140
Insertions	67,954
Mapped reads with at least one insertion	1.14%
Deletions	138,184
Mapped reads with at least one deletion	2.33%
Homopolymer indels	44.24%

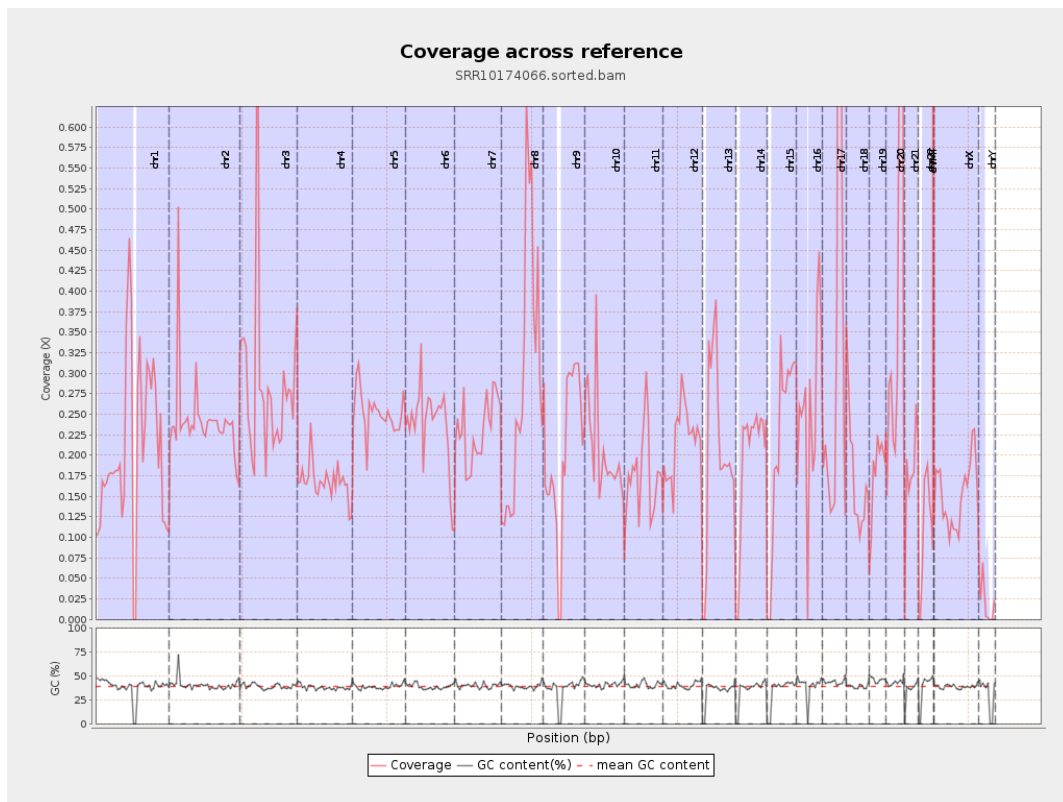
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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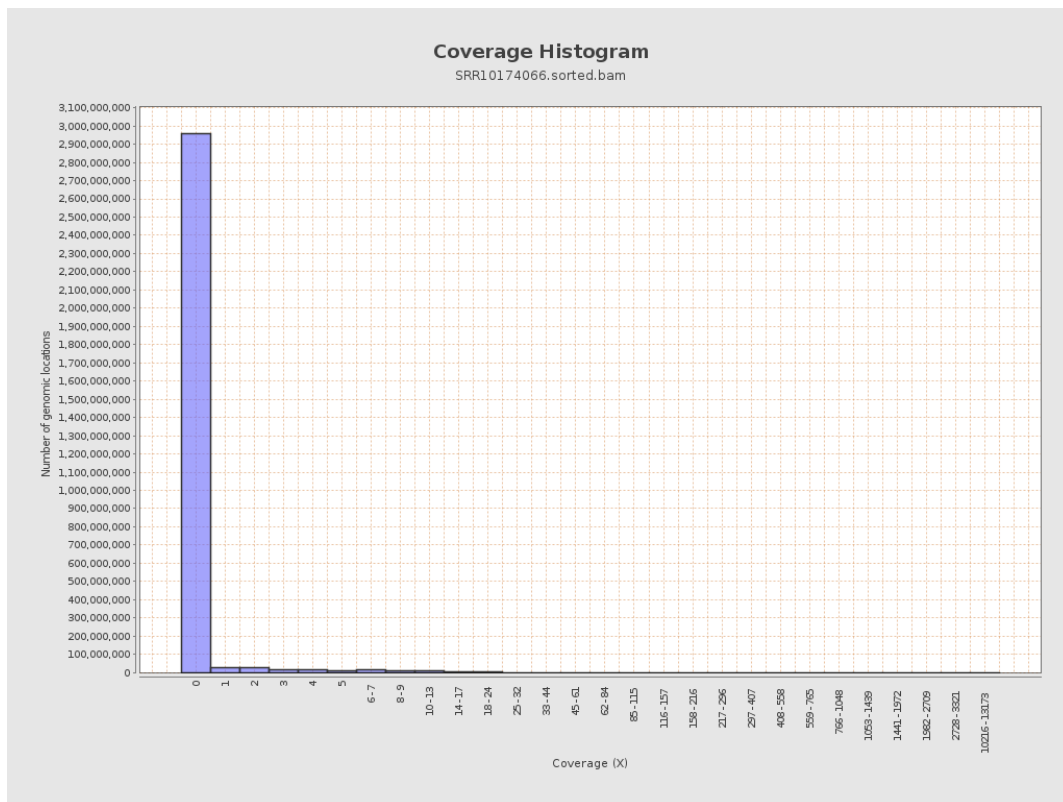
		bases	coverage	deviation
chr1	249250621	51480519	0.2065	2.0977
chr2	243199373	58836435	0.2419	9.2568
chr3	198022430	55840009	0.282	1.5711
chr4	191154276	32027912	0.1676	1.366
chr5	180915260	45607218	0.2521	1.4531
chr6	171115067	40489573	0.2366	1.669
chr7	159138663	36825902	0.2314	1.8485
chr8	146364022	42086958	0.2875	2.0416
chr9	141213431	28346896	0.2007	1.5922
chr10	135534747	27928077	0.2061	2.5586
chr11	135006516	23882890	0.1769	1.2327
chr12	133851895	29193917	0.2181	1.3564
chr13	115169878	23362676	0.2029	1.3223
chr14	107349540	20620381	0.1921	1.2706
chr15	102531392	22202220	0.2165	1.3493
chr16	90354753	23555897	0.2607	1.8421
chr17	81195210	27743549	0.3417	1.8659
chr18	78077248	13531764	0.1733	2.0313
chr19	59128983	10720254	0.1813	1.5858
chr20	63025520	30151759	0.4784	2.2171
chr21	48129895	8536844	0.1774	1.2828
chr22	51304566	5439959	0.106	0.93
chrMT	16571	1078804	65.1019	60.4384
chrX	155270560	23718432	0.1528	1.1247

chrY	59373566	1123990	0.0189	0.6867
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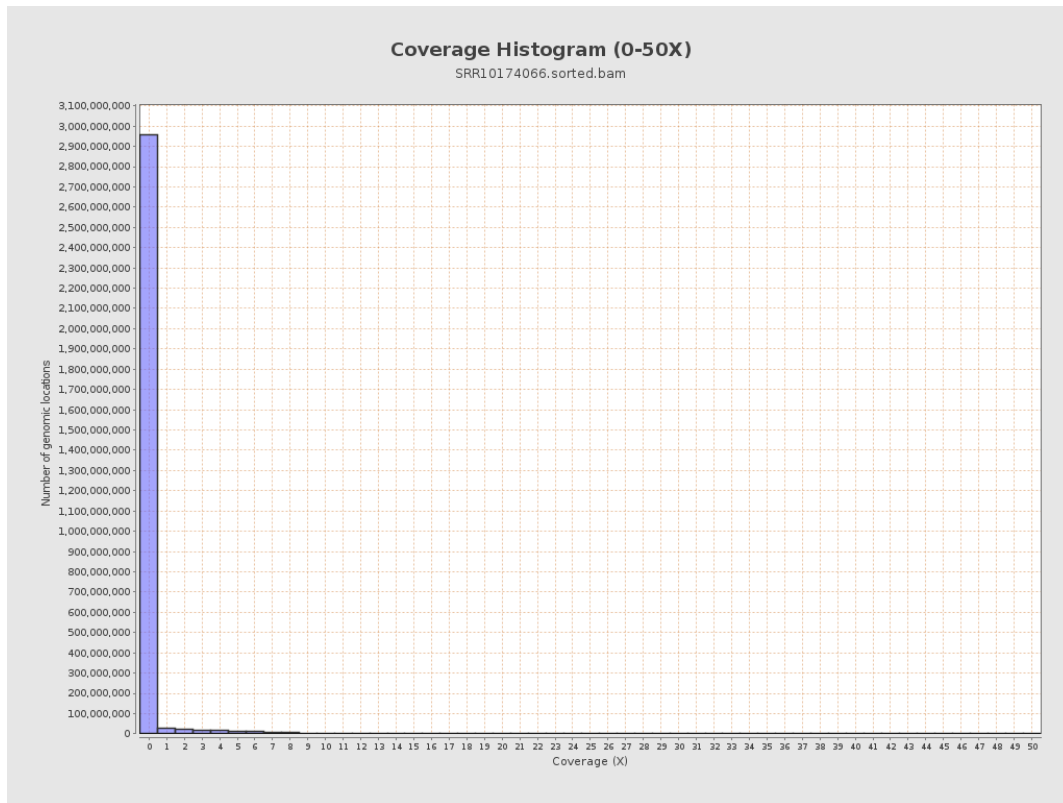
3. Results : Coverage across reference



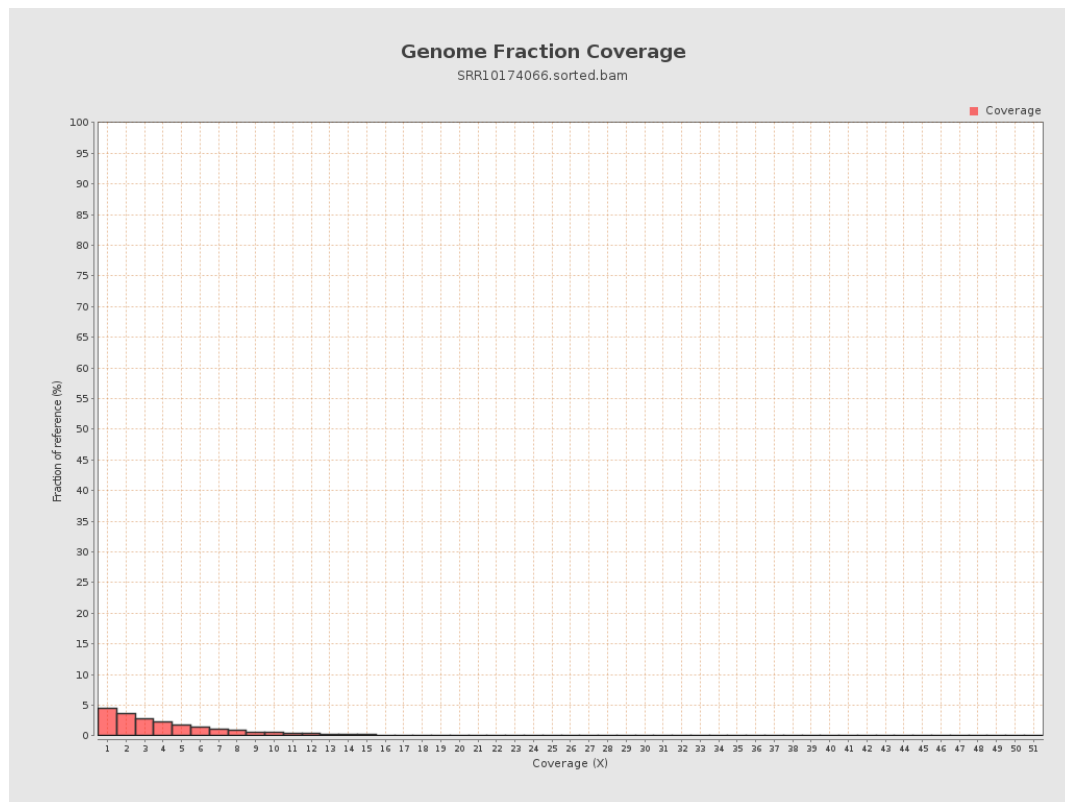
4. Results : Coverage Histogram



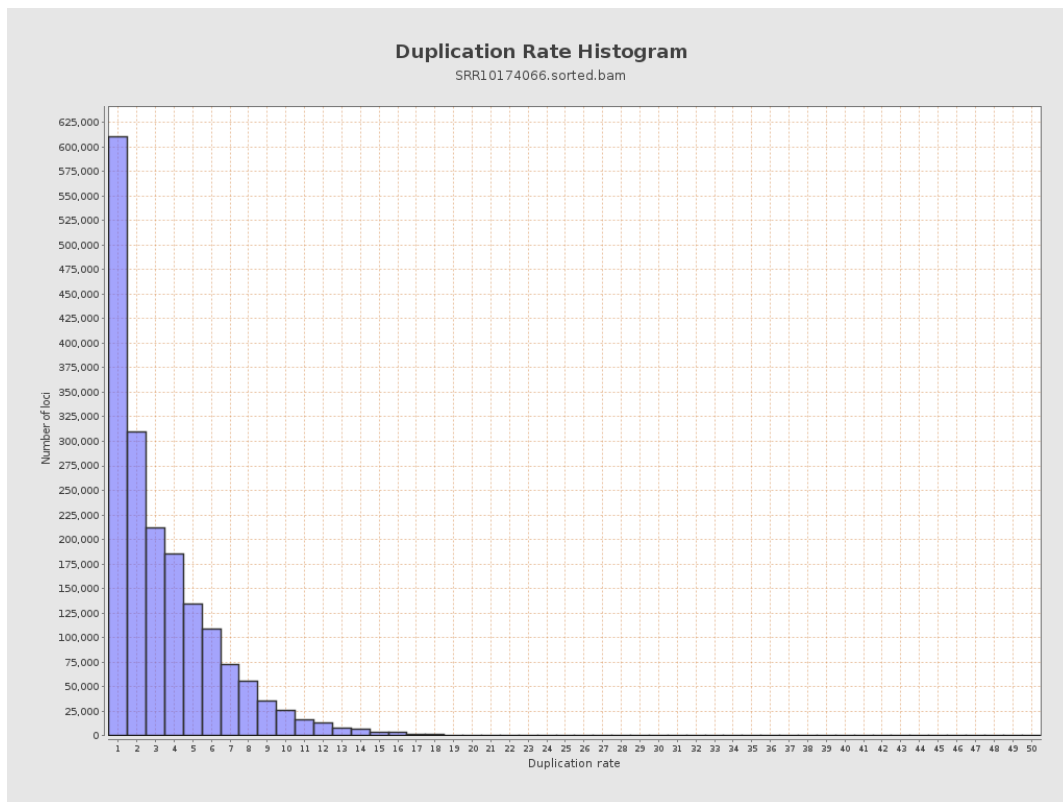
5. Results : Coverage Histogram (0-50X)



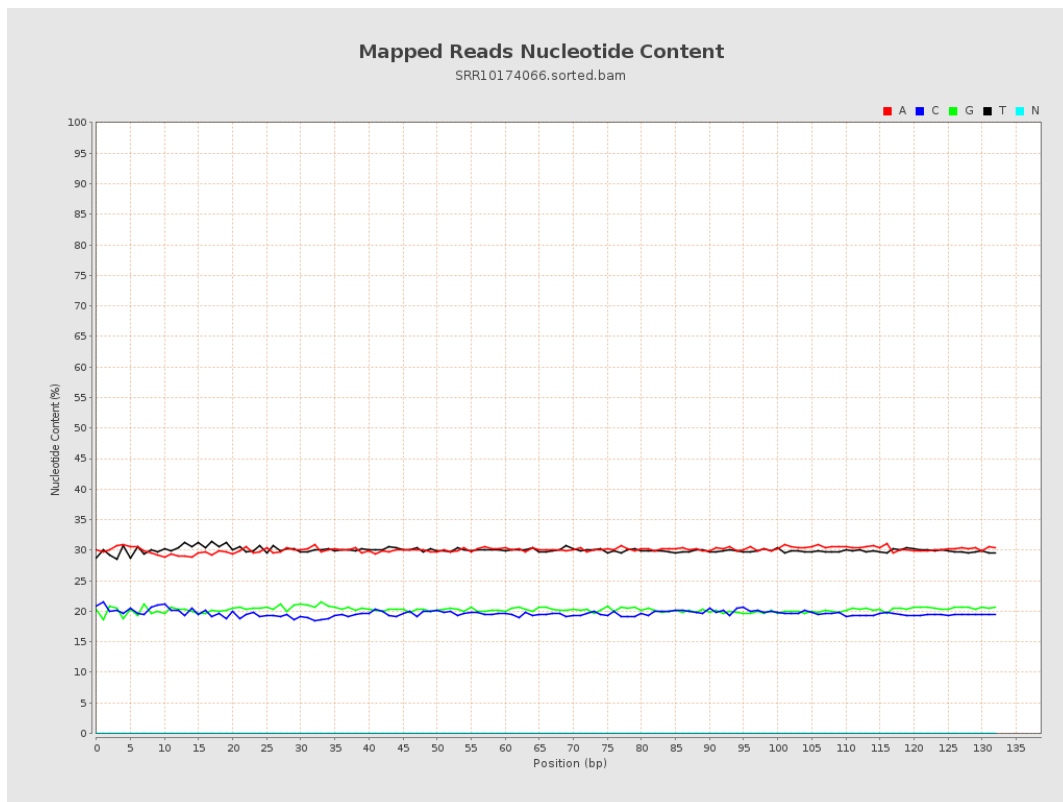
6. Results : Genome Fraction Coverage



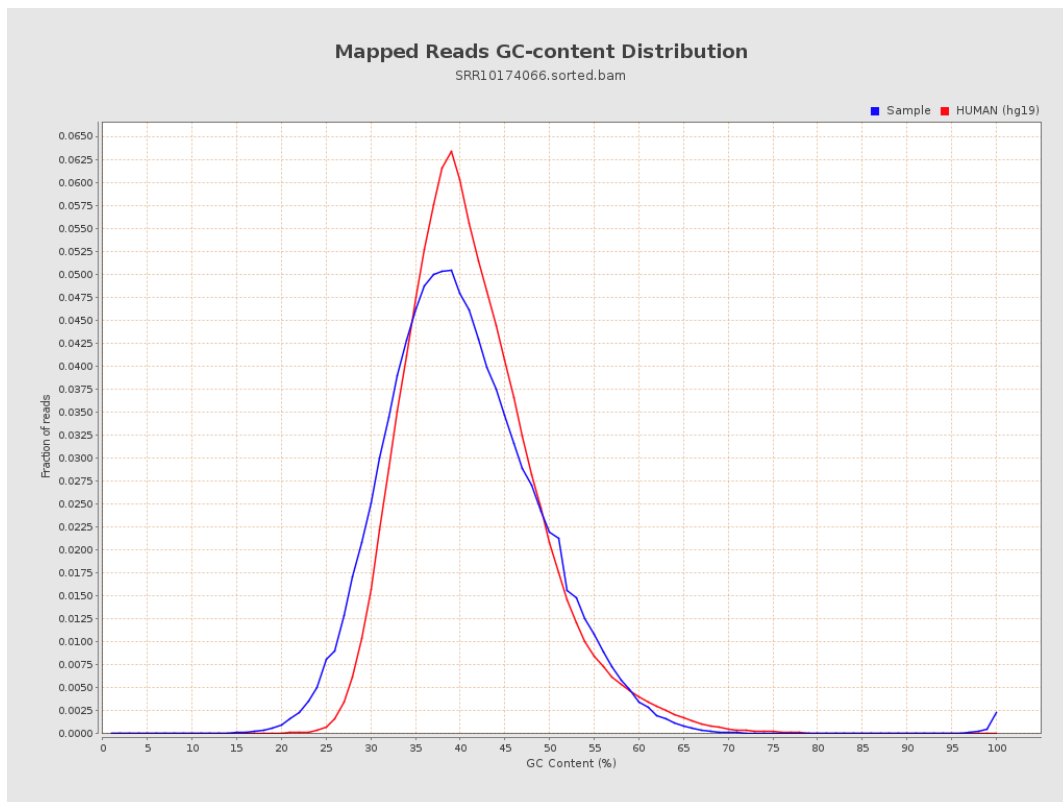
7. Results : Duplication Rate Histogram



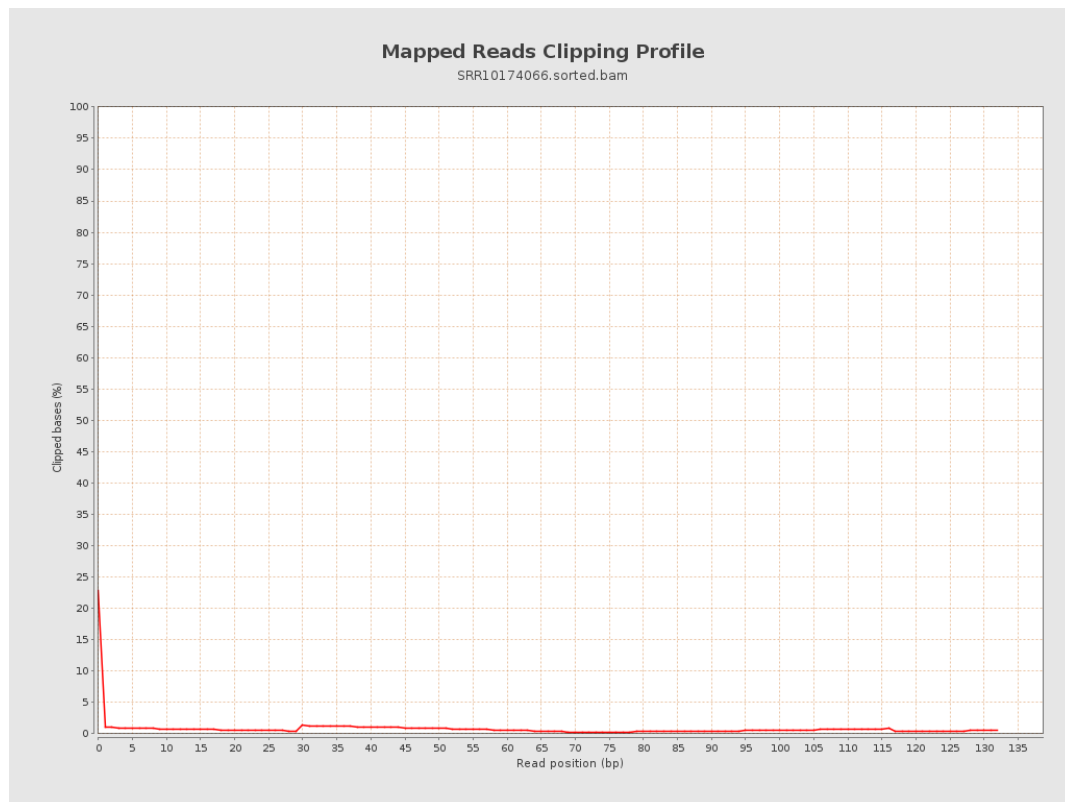
8. Results : Mapped Reads Nucleotide Content



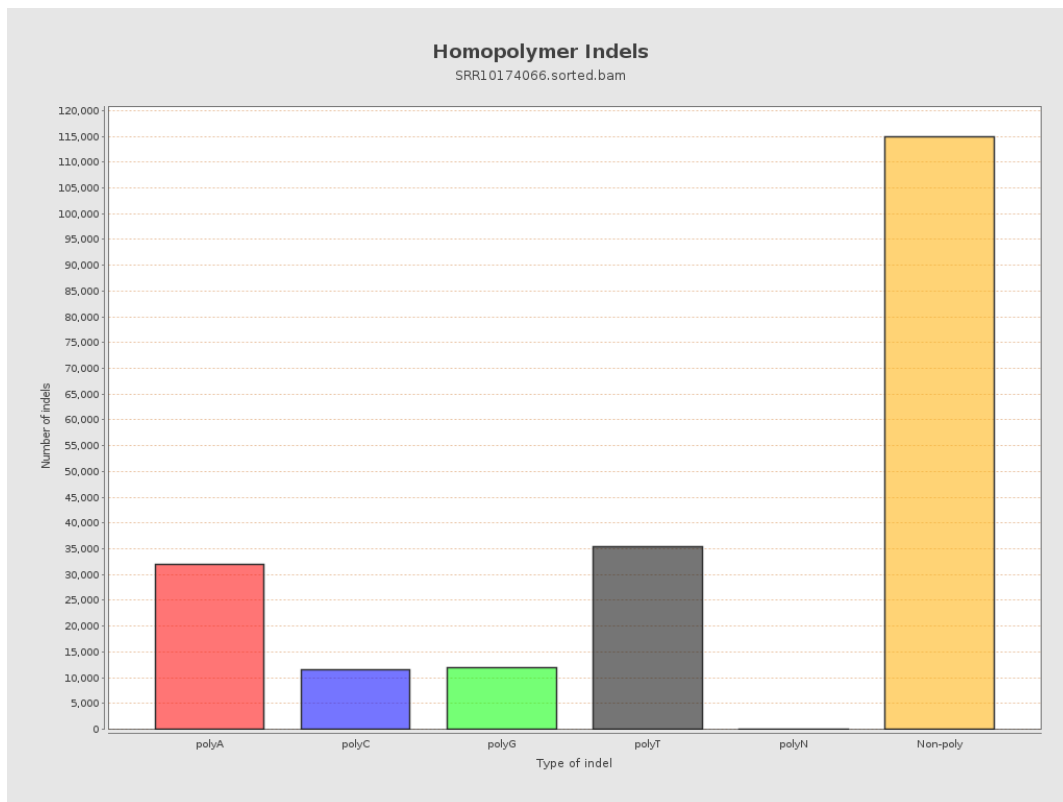
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



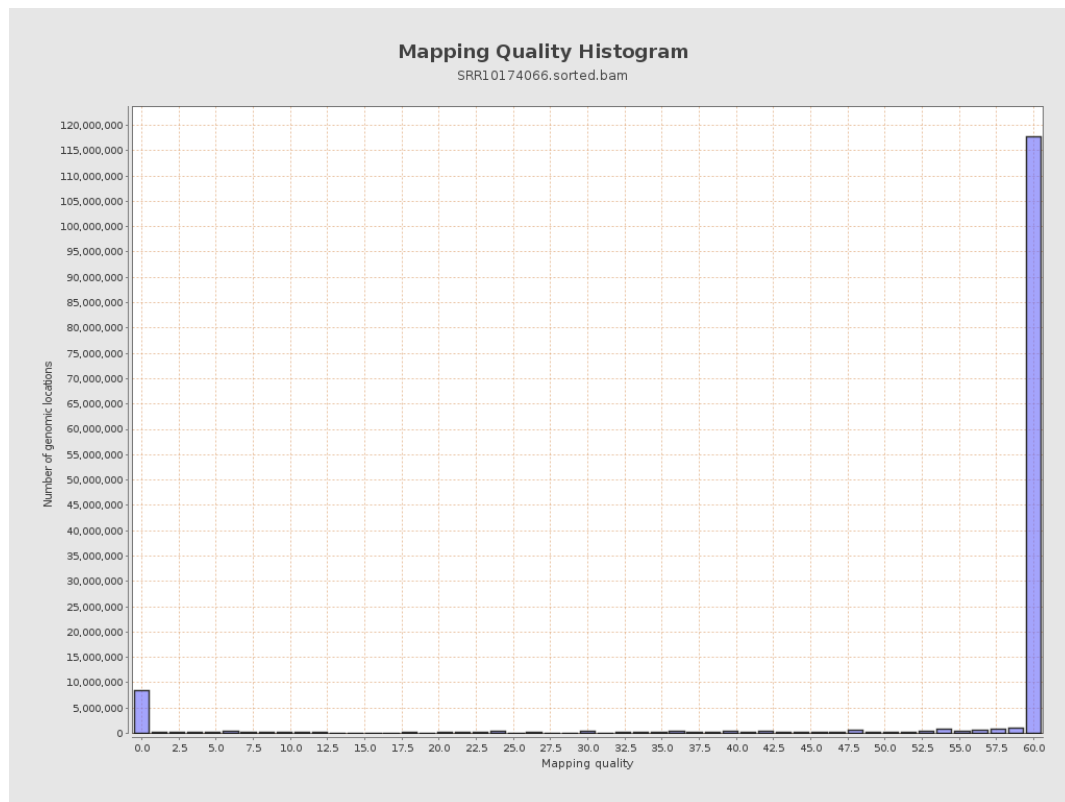
11. Results : Homopolymer Indels



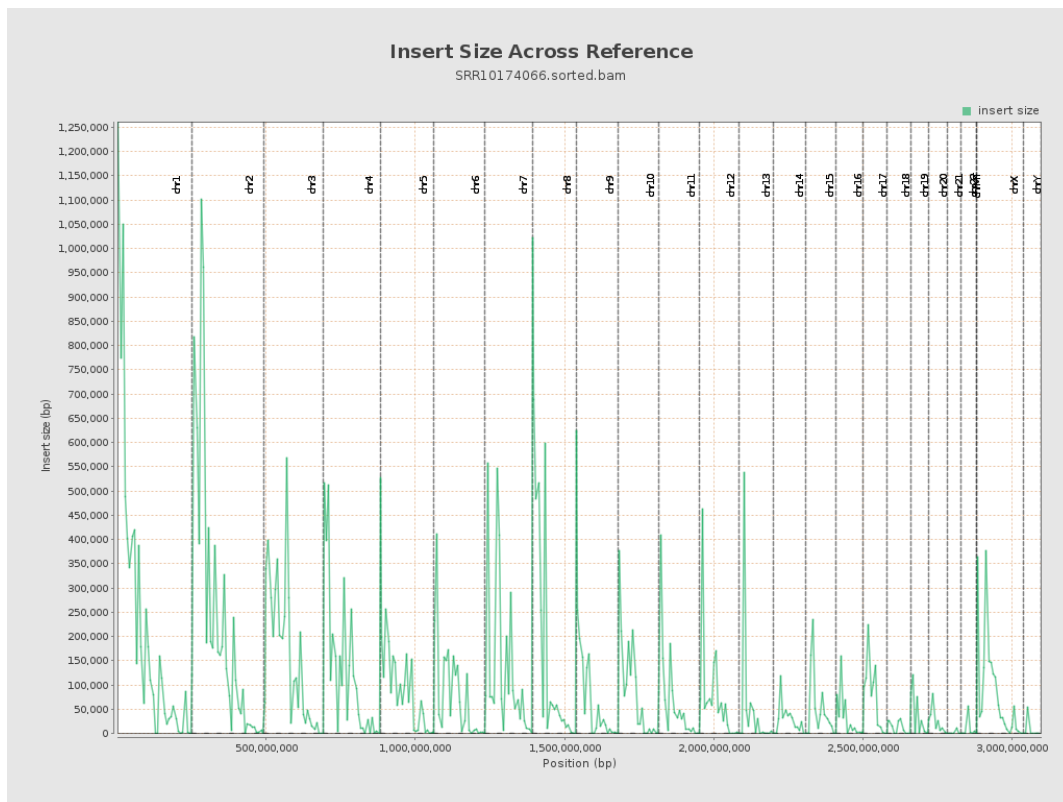
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

