

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 03:08:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174060.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_SRR10174060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174060_1.fastq.gz SRR10174060_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 03:08:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,353,814
Mapped reads	2,291,453 / 97.35%
Unmapped reads	62,361 / 2.65%
Mapped paired reads	2,291,453 / 97.35%
Mapped reads, first in pair	1,145,632 / 48.67%
Mapped reads, second in pair	1,145,821 / 48.68%
Mapped reads, both in pair	2,248,998 / 95.55%
Mapped reads, singletons	42,455 / 1.8%
Secondary alignments	0
Supplementary alignments	235,495 / 10%
Read min/max/mean length	30 / 133 / 128.51
Duplicated reads (estimated)	1,815,818 / 77.14%
Duplication rate	64.61%
Clipped reads	933,298 / 39.65%

2.2. ACGT Content

Number/percentage of A's	81,495,730 / 30.03%
Number/percentage of C's	53,340,875 / 19.66%
Number/percentage of T's	81,244,502 / 29.94%
Number/percentage of G's	55,298,265 / 20.38%
Number/percentage of N's	3,021 / 0%

GC Percentage	40.03%
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2.3. Coverage

Mean	0.0877
Standard Deviation	1.4794

2.4. Mapping Quality

Mean Mapping Quality	52.7
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2.5. Insert size

Mean	1,212,179.14
Standard Deviation	10,398,609.82
P25/Median/P75	147 / 204 / 286

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	2,793,517
Insertions	28,760
Mapped reads with at least one insertion	1.22%
Deletions	61,329
Mapped reads with at least one deletion	2.61%
Homopolymer indels	43%

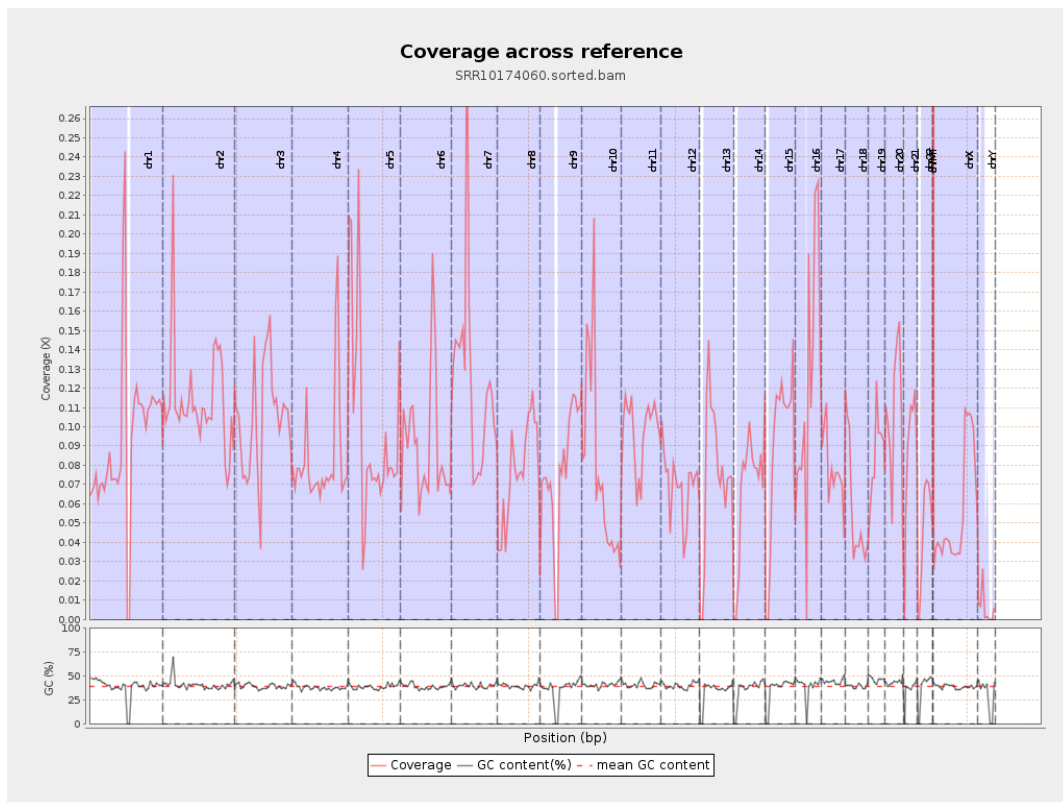
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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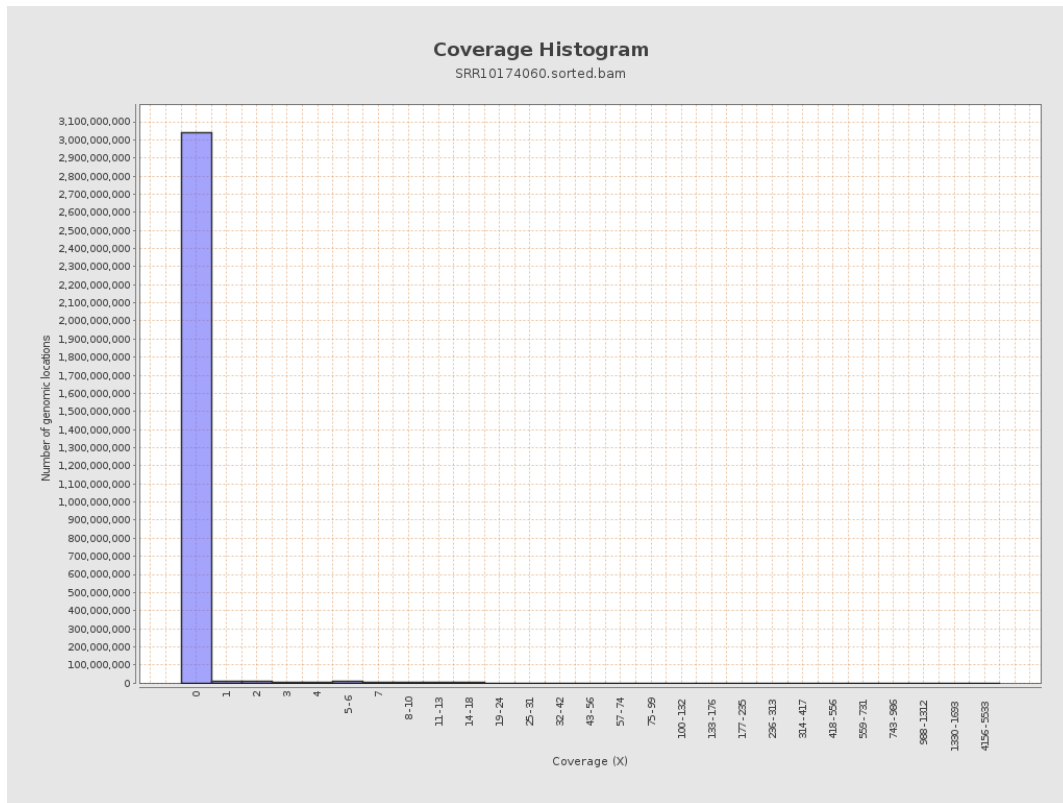
		bases	coverage	deviation
chr1	249250621	23417920	0.094	1.2581
chr2	243199373	27601645	0.1135	3.9541
chr3	198022430	20544345	0.1037	0.9525
chr4	191154276	16002745	0.0837	0.9664
chr5	180915260	18350070	0.1014	0.9469
chr6	171115067	15451350	0.0903	0.9073
chr7	159138663	19624674	0.1233	1.3849
chr8	146364022	11294818	0.0772	0.905
chr9	141213431	10978021	0.0777	0.8877
chr10	135534747	10472633	0.0773	1.2718
chr11	135006516	13150672	0.0974	0.9376
chr12	133851895	9445998	0.0706	0.7816
chr13	115169878	8645615	0.0751	0.8097
chr14	107349540	7166895	0.0668	0.7665
chr15	102531392	9148829	0.0892	0.8695
chr16	90354753	10809648	0.1196	1.1476
chr17	81195210	6410137	0.0789	0.9073
chr18	78077248	4376247	0.0561	1.1889
chr19	59128983	5032957	0.0851	1.2619
chr20	63025520	6782369	0.1076	0.9785
chr21	48129895	4125660	0.0857	0.8836
chr22	51304566	2384108	0.0465	0.5922
chrMT	16571	1286618	77.6427	59.0929
chrX	155270560	8667865	0.0558	0.6897

chrY	59373566	361383	0.0061	0.3217
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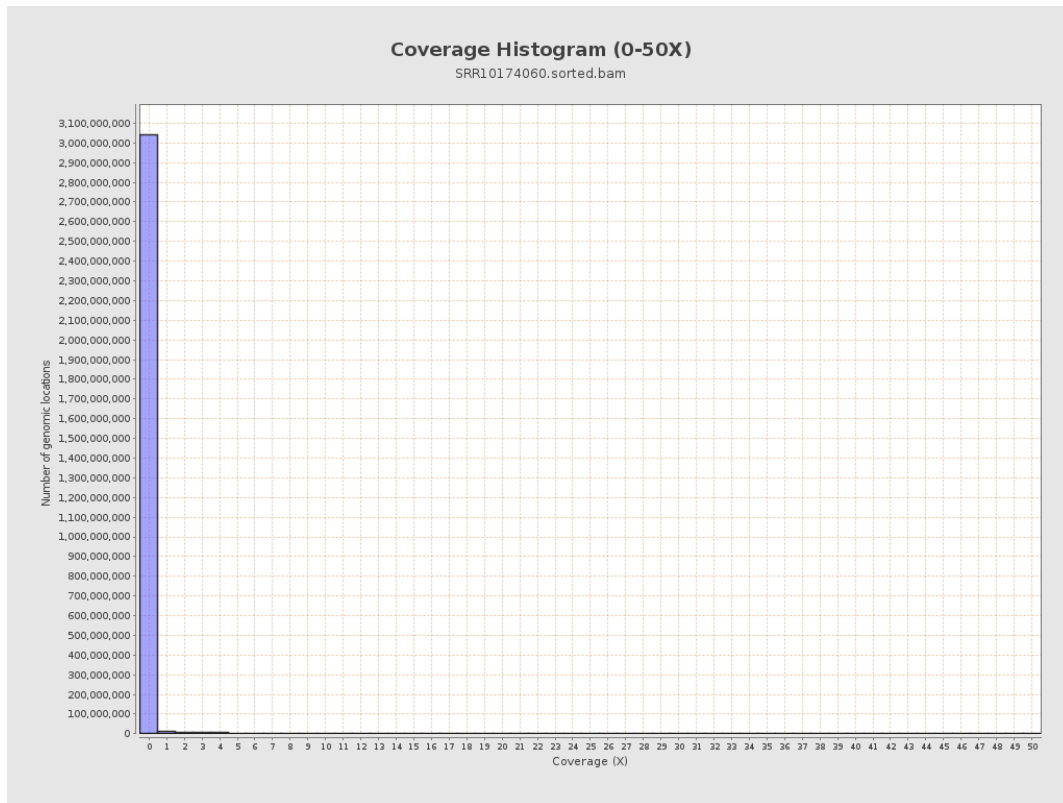
3. Results : Coverage across reference



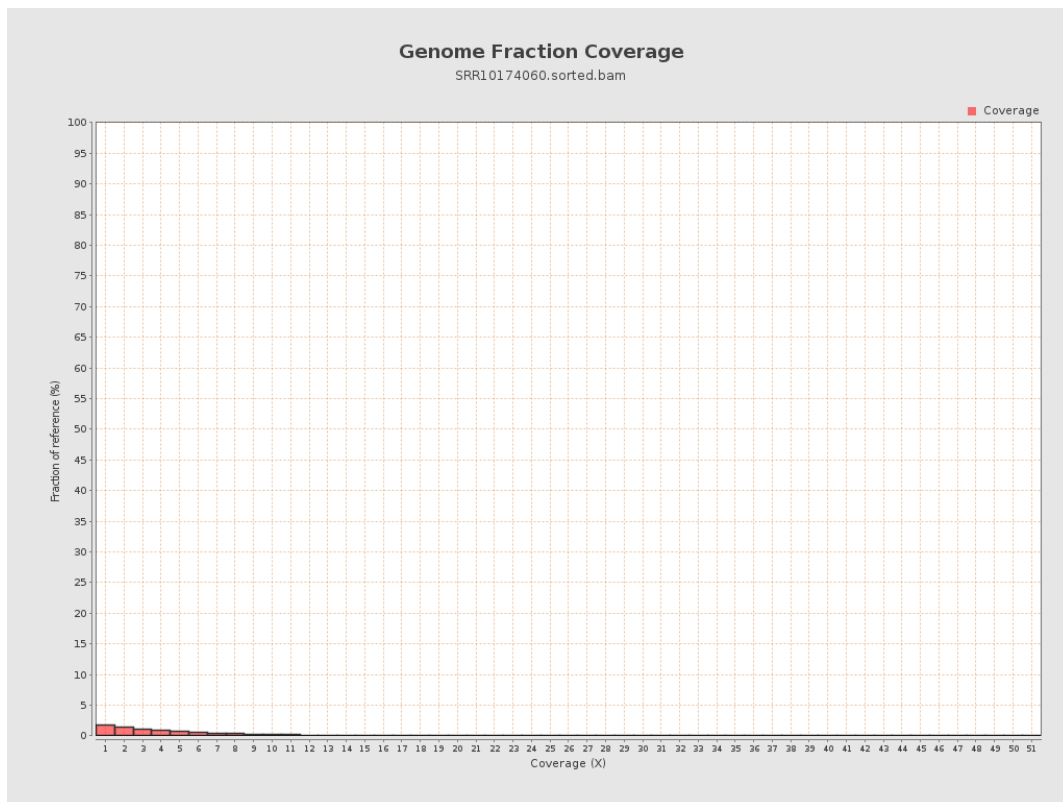
4. Results : Coverage Histogram



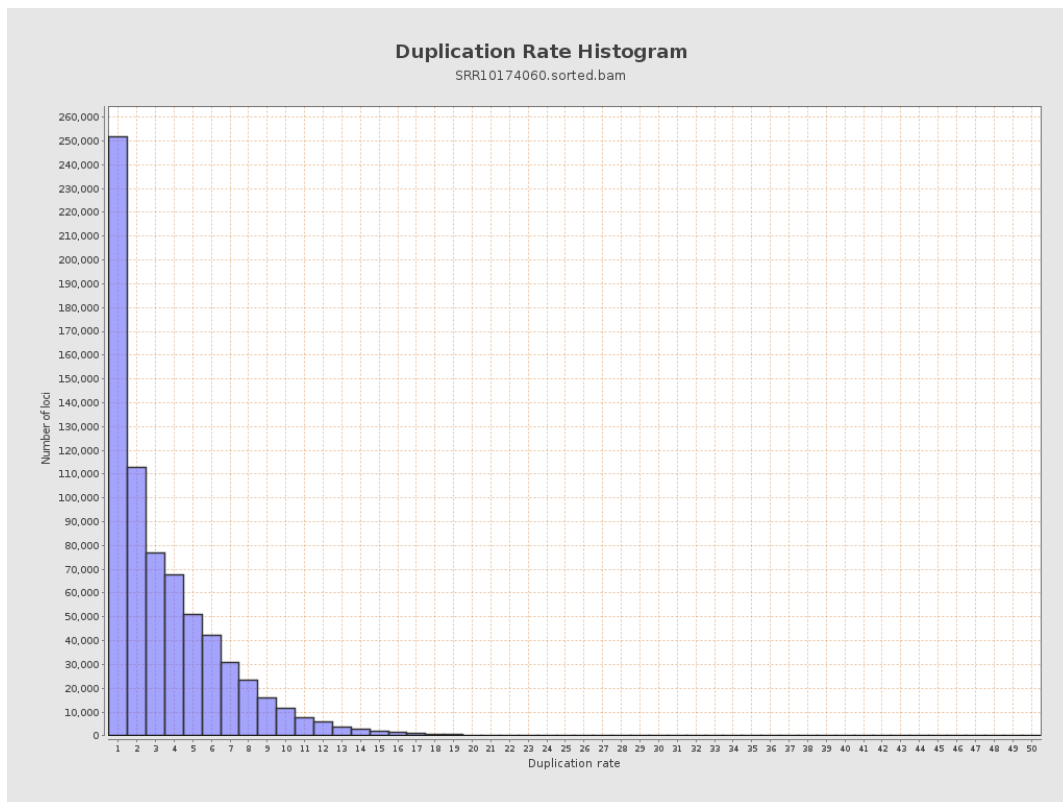
5. Results : Coverage Histogram (0-50X)



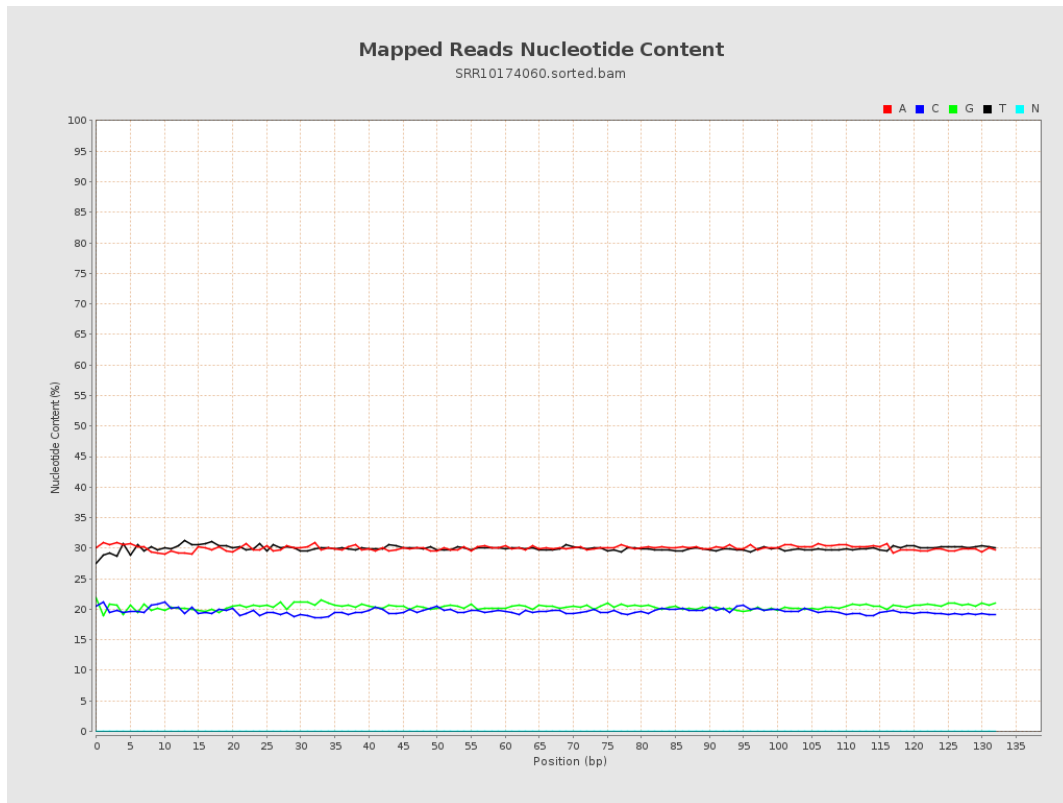
6. Results : Genome Fraction Coverage



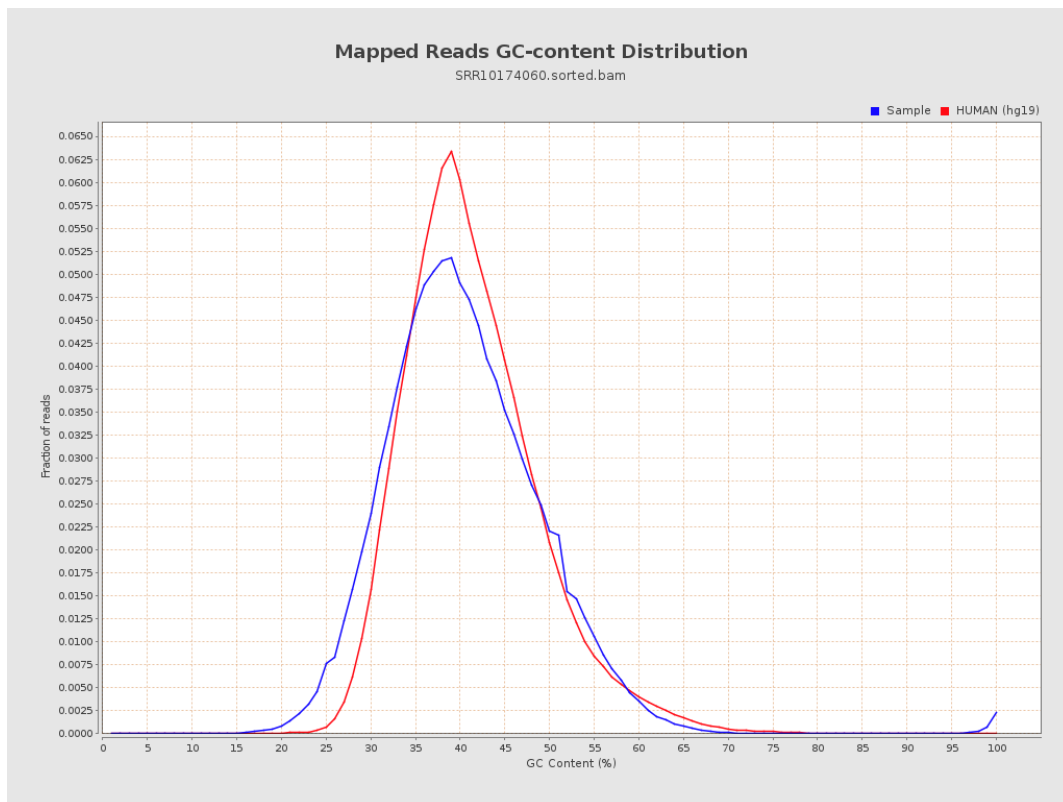
7. Results : Duplication Rate Histogram



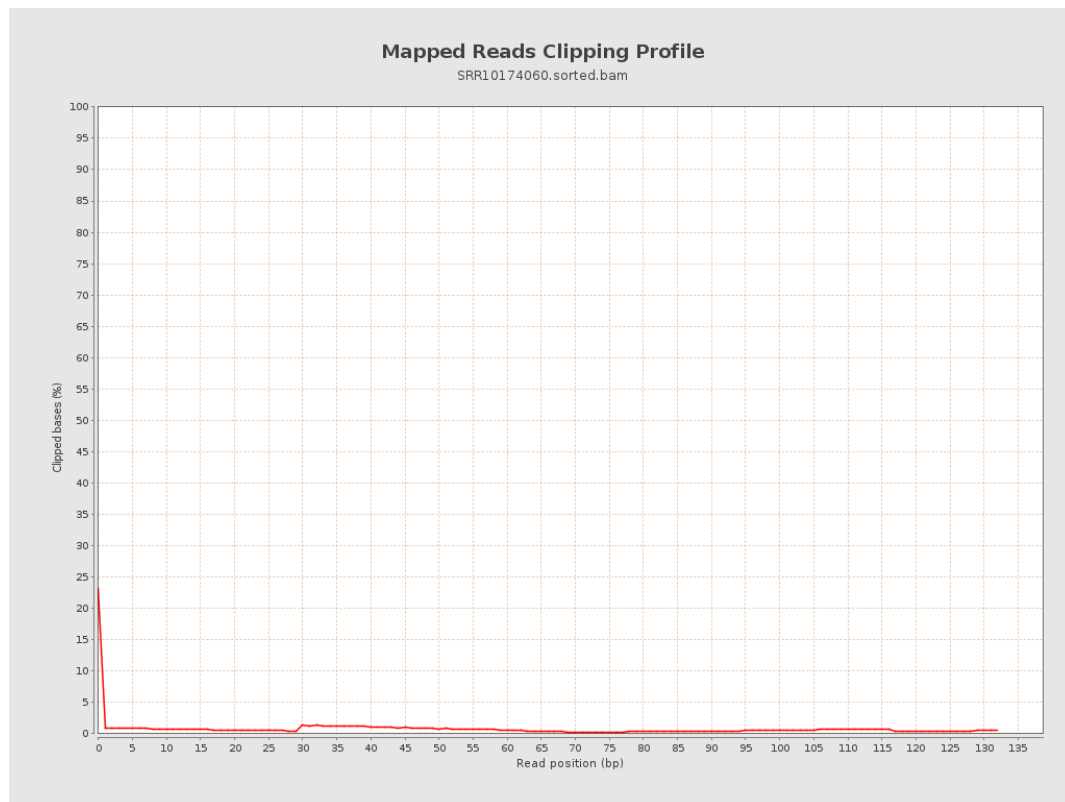
8. Results : Mapped Reads Nucleotide Content



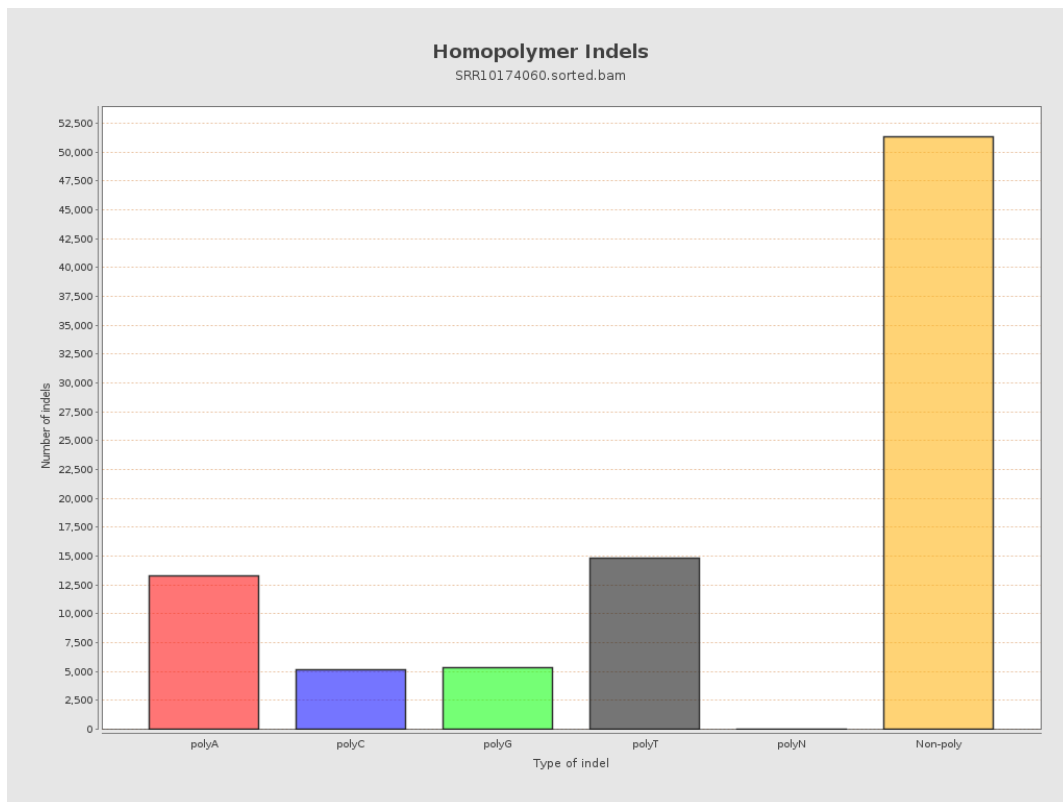
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



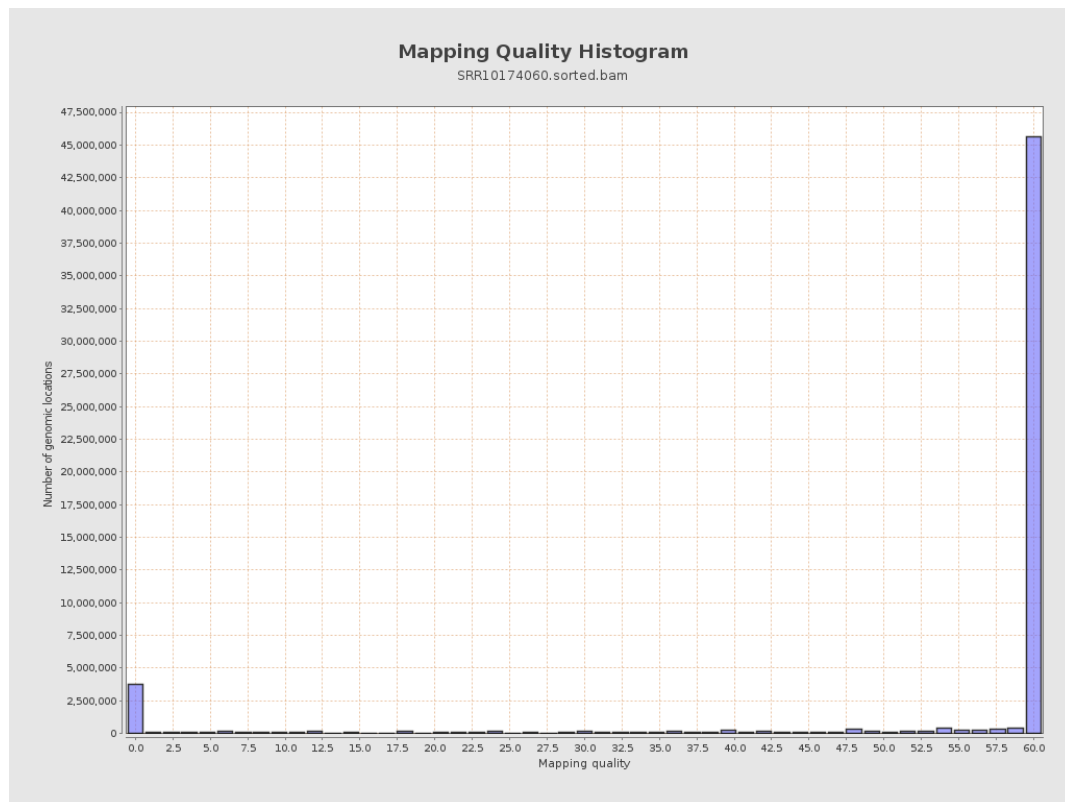
11. Results : Homopolymer Indels



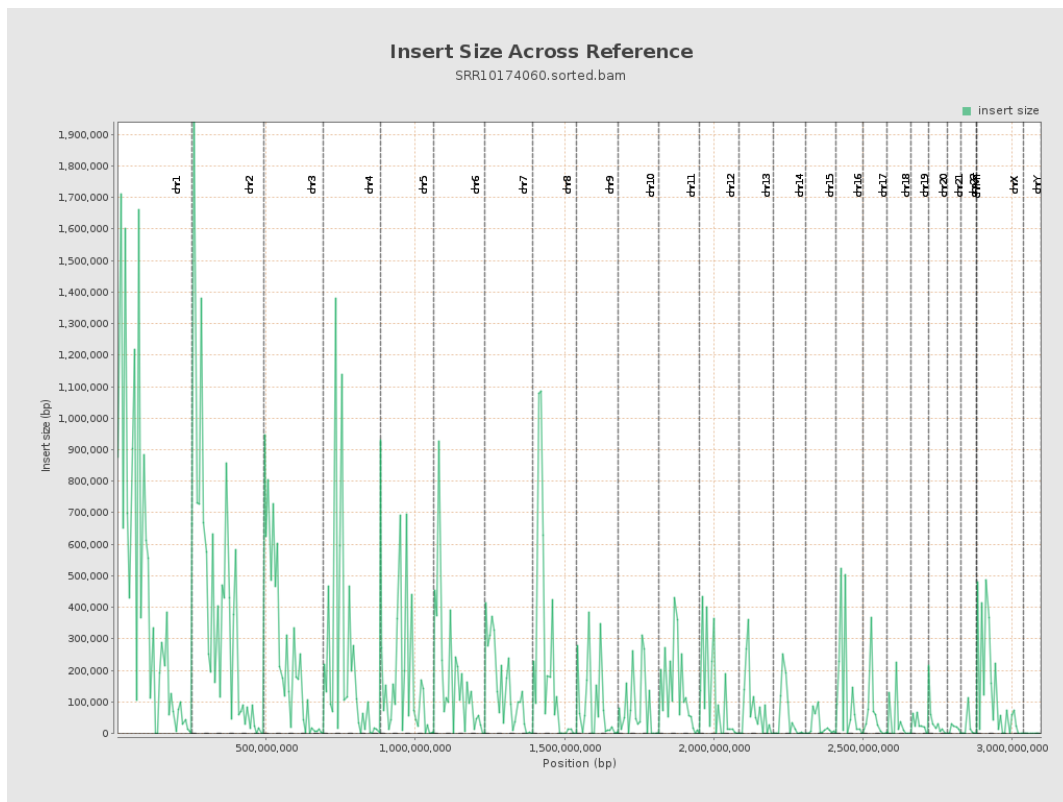
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

