

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 12:04:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173953.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_SRR10173953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173953_1.fastq.gz SRR10173953_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 12:04:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,210,678
Mapped reads	17,746,711 / 97.45%
Unmapped reads	463,967 / 2.55%
Mapped paired reads	17,746,711 / 97.45%
Mapped reads, first in pair	8,895,692 / 48.85%
Mapped reads, second in pair	8,851,019 / 48.6%
Mapped reads, both in pair	17,437,772 / 95.76%
Mapped reads, singletons	308,939 / 1.7%
Secondary alignments	0
Supplementary alignments	2,404,712 / 13.2%
Read min/max/mean length	30 / 133 / 126.16
Duplicated reads (estimated)	14,298,114 / 78.52%
Duplication rate	65.67%
Clipped reads	9,867,331 / 54.18%

2.2. ACGT Content

Number/percentage of A's	592,322,978 / 29.58%
Number/percentage of C's	401,952,488 / 20.08%
Number/percentage of T's	588,046,494 / 29.37%
Number/percentage of G's	419,865,974 / 20.97%
Number/percentage of N's	14,862 / 0%

GC Percentage	41.05%
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2.3. Coverage

Mean	0.6472
Standard Deviation	11.9826

2.4. Mapping Quality

Mean Mapping Quality	52.46
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2.5. Insert size

Mean	1,199,853.02
Standard Deviation	10,248,883.2
P25/Median/P75	107 / 159 / 249

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	17,495,686
Insertions	216,988
Mapped reads with at least one insertion	1.18%
Deletions	616,688
Mapped reads with at least one deletion	3.39%
Homopolymer indels	40.61%

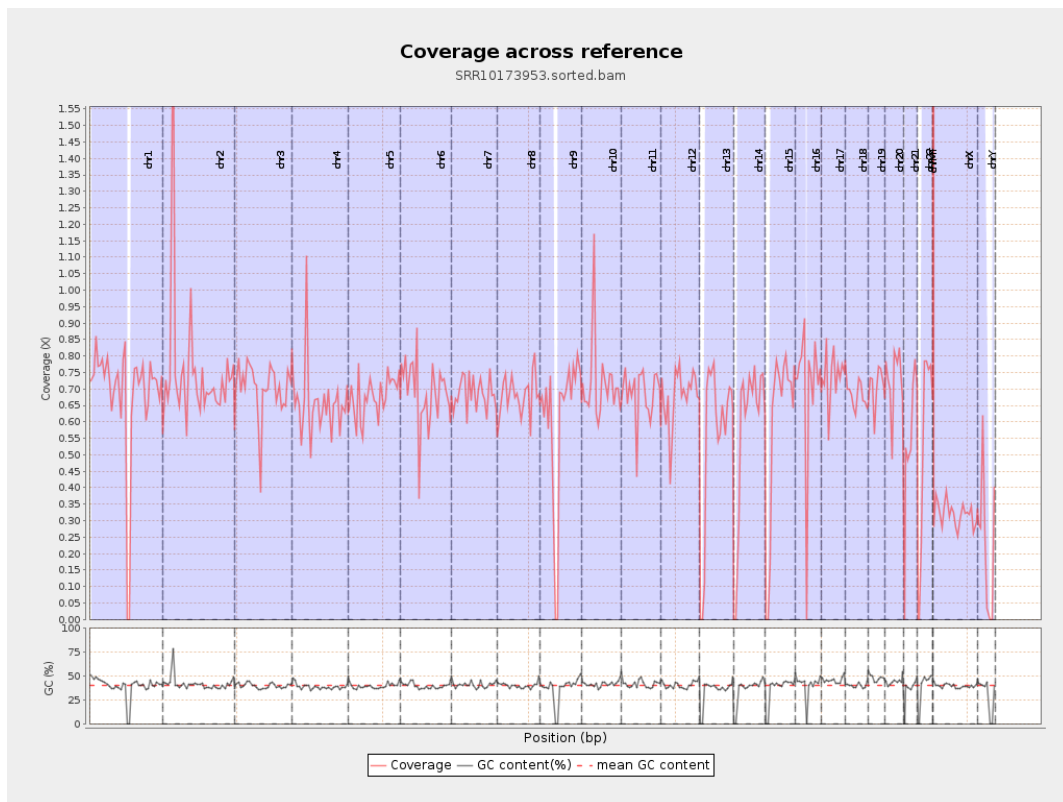
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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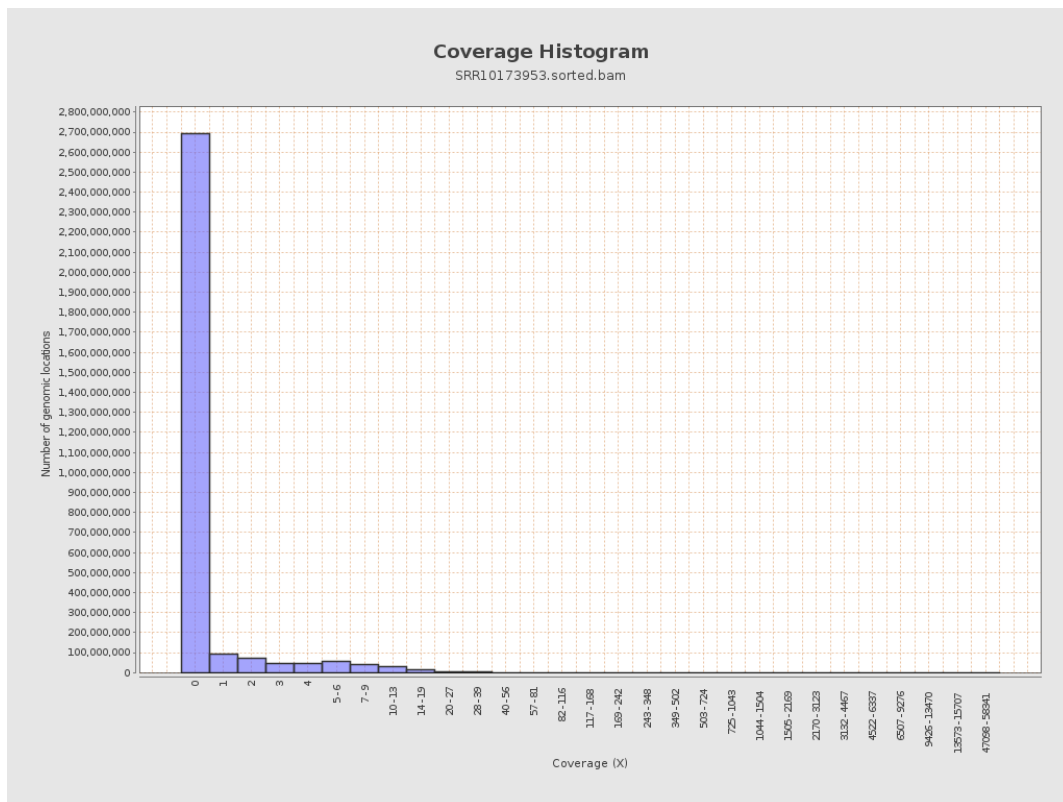
		bases	coverage	deviation
chr1	249250621	171069418	0.6863	4.9388
chr2	243199373	182195080	0.7492	40.7034
chr3	198022430	138591588	0.6999	2.5252
chr4	191154276	125591145	0.657	4.4573
chr5	180915260	122651678	0.678	2.4772
chr6	171115067	117774394	0.6883	3.448
chr7	159138663	108954814	0.6847	4.4695
chr8	146364022	99839897	0.6821	5.2792
chr9	141213431	86366806	0.6116	4.6545
chr10	135534747	96661404	0.7132	5.4948
chr11	135006516	92419374	0.6846	2.7404
chr12	133851895	91385474	0.6827	2.7357
chr13	115169878	63942942	0.5552	2.2539
chr14	107349540	62249978	0.5799	2.4267
chr15	102531392	59500782	0.5803	2.5032
chr16	90354753	63590314	0.7038	3.5759
chr17	81195210	60175270	0.7411	3.1636
chr18	78077248	53350019	0.6833	6.0023
chr19	59128983	41666175	0.7047	3.8465
chr20	63025520	45658633	0.7244	2.9116
chr21	48129895	26901300	0.5589	3.5813
chr22	51304566	27118039	0.5286	2.906
chrMT	16571	2353359	142.0167	98.1417
chrX	155270560	49732830	0.3203	1.7749

chrY	59373566	13902774	0.2342	3.5313
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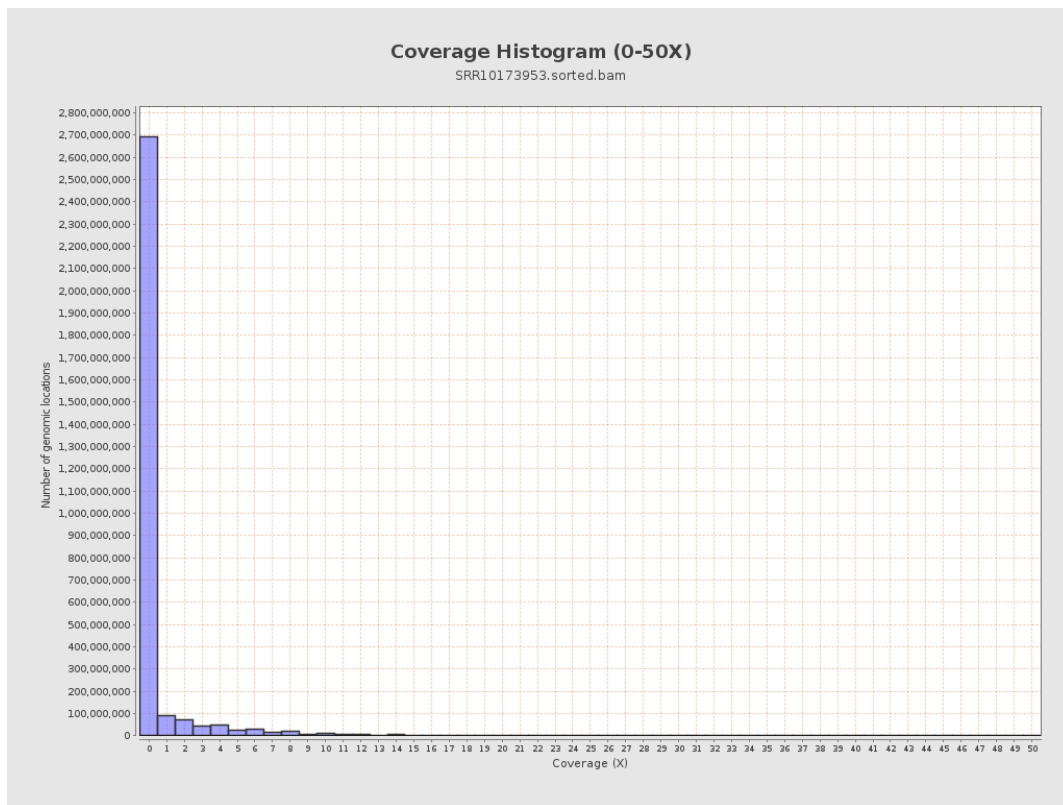
3. Results : Coverage across reference



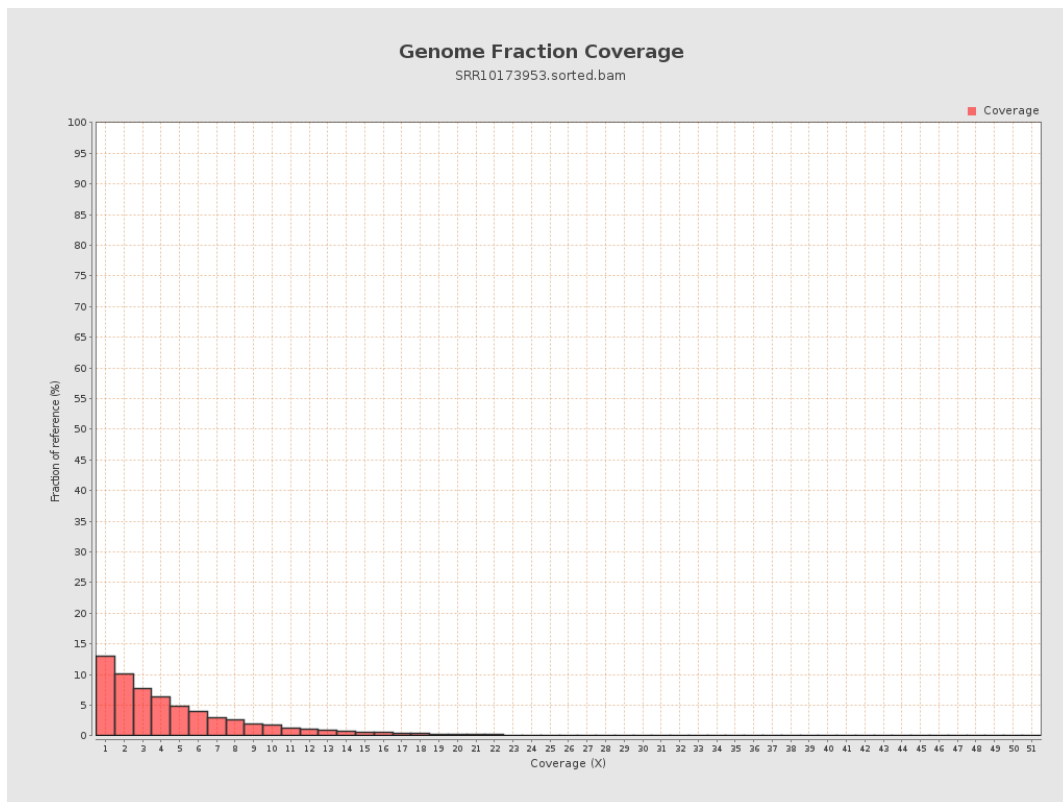
4. Results : Coverage Histogram



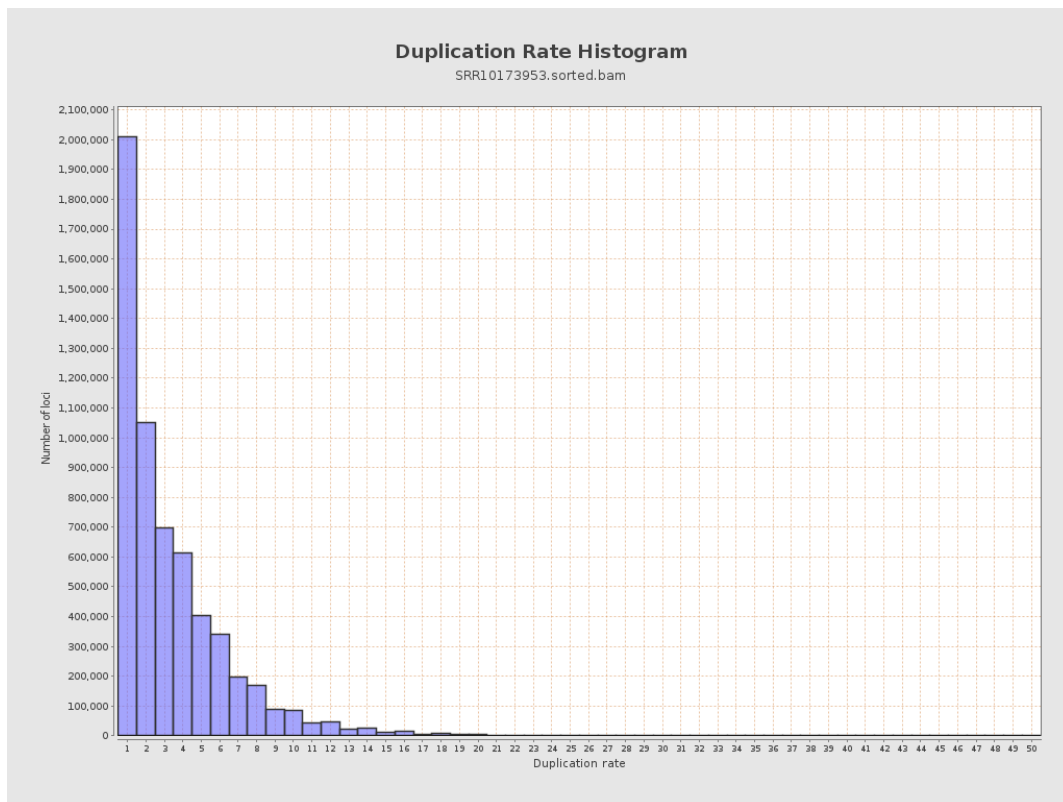
5. Results : Coverage Histogram (0-50X)



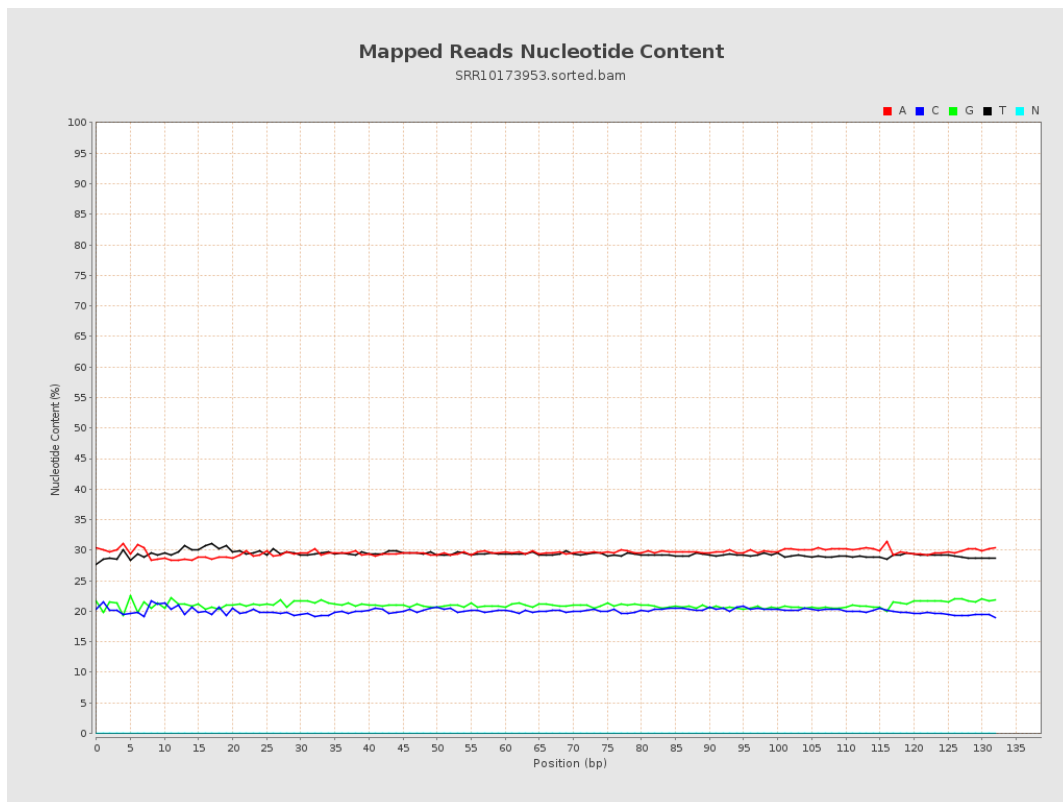
6. Results : Genome Fraction Coverage



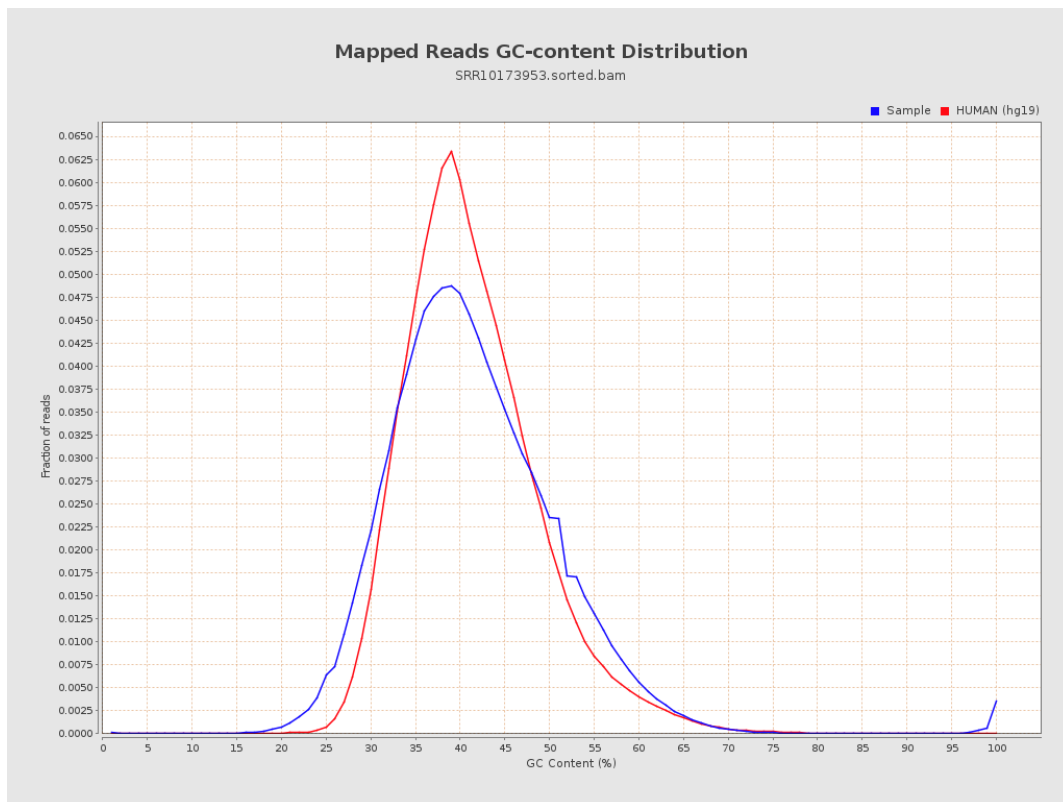
7. Results : Duplication Rate Histogram



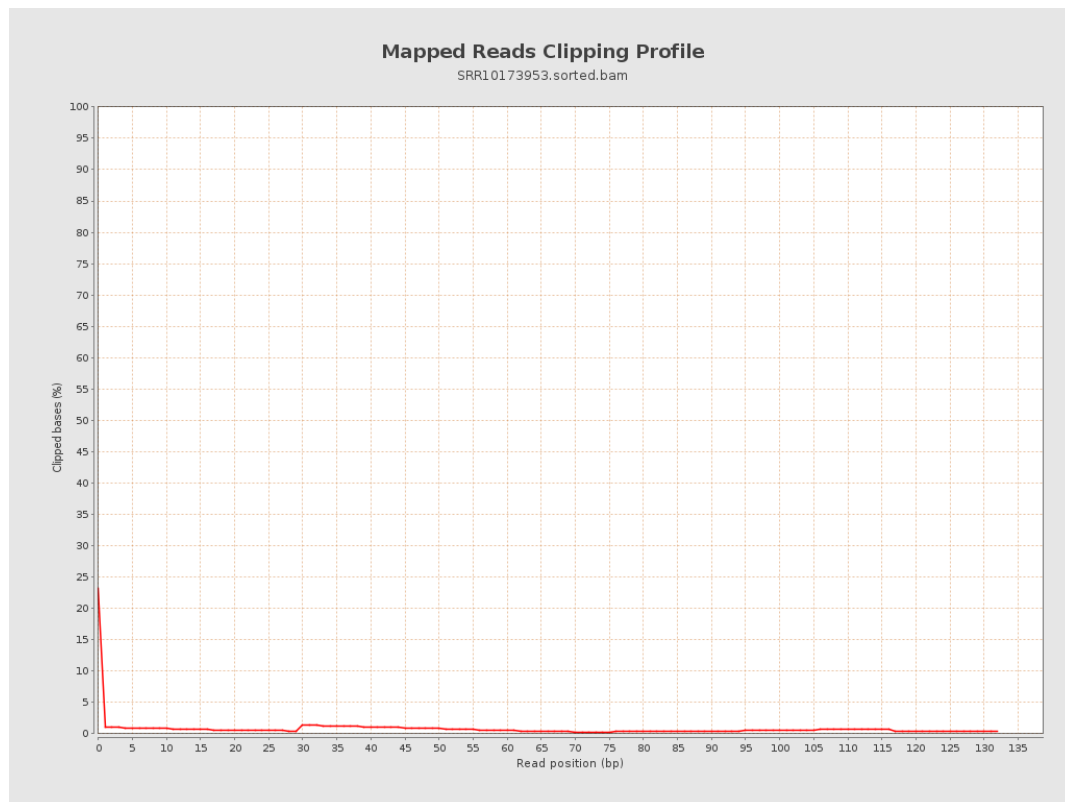
8. Results : Mapped Reads Nucleotide Content



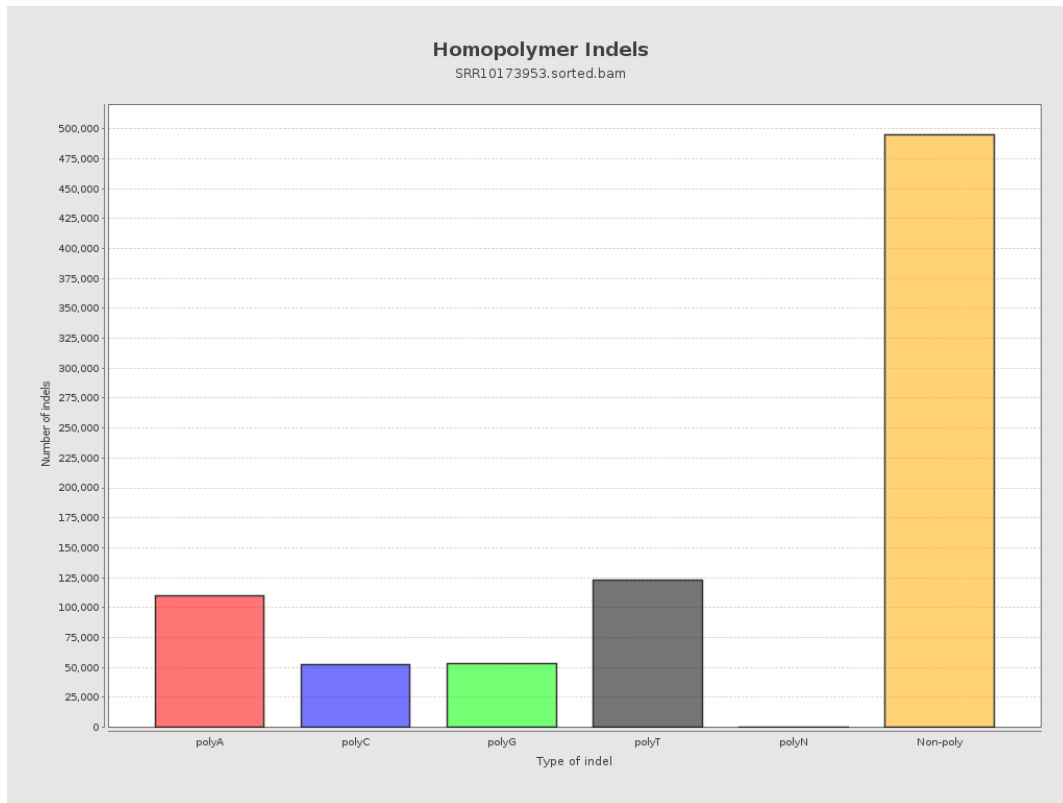
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



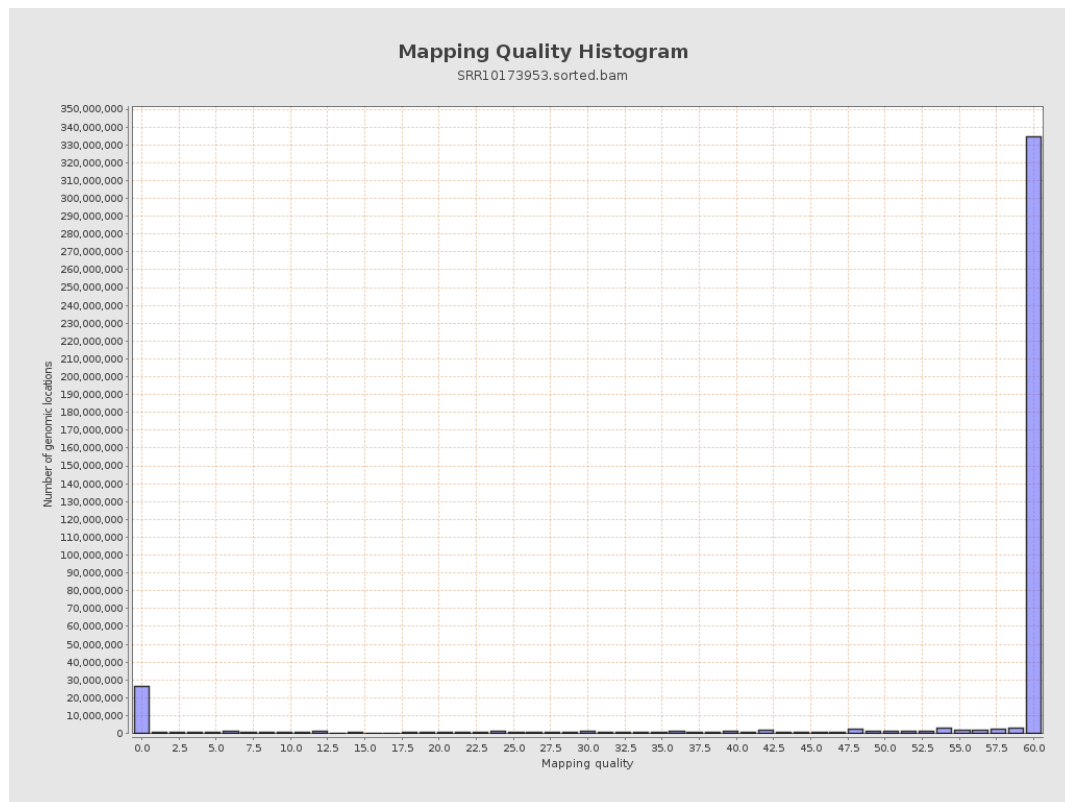
11. Results : Homopolymer Indels



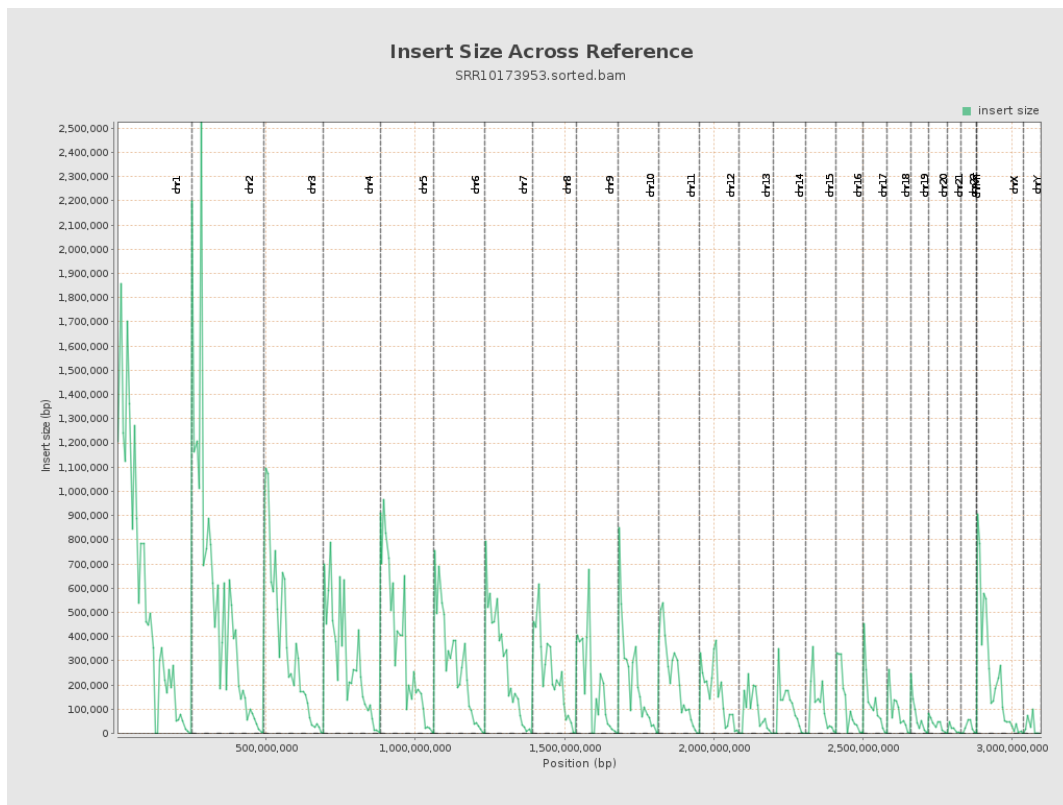
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

