

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 10:40:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173946.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_SRR10173946 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173946_1.fastq.gz SRR10173946_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 10:40:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,803,066
Mapped reads	13,447,796 / 97.43%
Unmapped reads	355,270 / 2.57%
Mapped paired reads	13,447,796 / 97.43%
Mapped reads, first in pair	6,731,710 / 48.77%
Mapped reads, second in pair	6,716,086 / 48.66%
Mapped reads, both in pair	13,217,412 / 95.76%
Mapped reads, singletons	230,384 / 1.67%
Secondary alignments	0
Supplementary alignments	1,890,845 / 13.7%
Read min/max/mean length	30 / 133 / 126.15
Duplicated reads (estimated)	11,045,313 / 80.02%
Duplication rate	65.89%
Clipped reads	7,054,323 / 51.11%

2.2. ACGT Content

Number/percentage of A's	453,999,740 / 29.76%
Number/percentage of C's	304,185,008 / 19.94%
Number/percentage of T's	449,964,849 / 29.5%
Number/percentage of G's	317,364,153 / 20.8%
Number/percentage of N's	11,323 / 0%

GC Percentage	40.74%
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2.3. Coverage

Mean	0.4931
Standard Deviation	8.9152

2.4. Mapping Quality

Mean Mapping Quality	52.36
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2.5. Insert size

Mean	1,162,584.93
Standard Deviation	9,924,425.49
P25/Median/P75	107 / 160 / 255

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	13,879,351
Insertions	177,907
Mapped reads with at least one insertion	1.27%
Deletions	458,639
Mapped reads with at least one deletion	3.32%
Homopolymer indels	40.71%

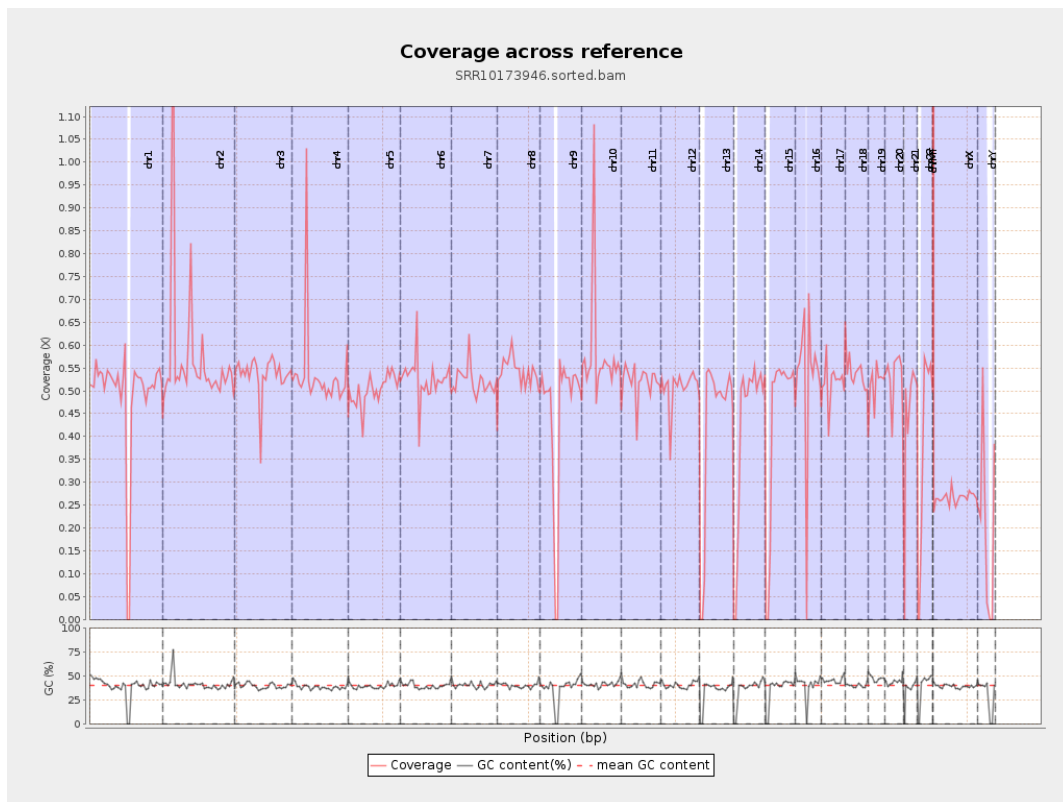
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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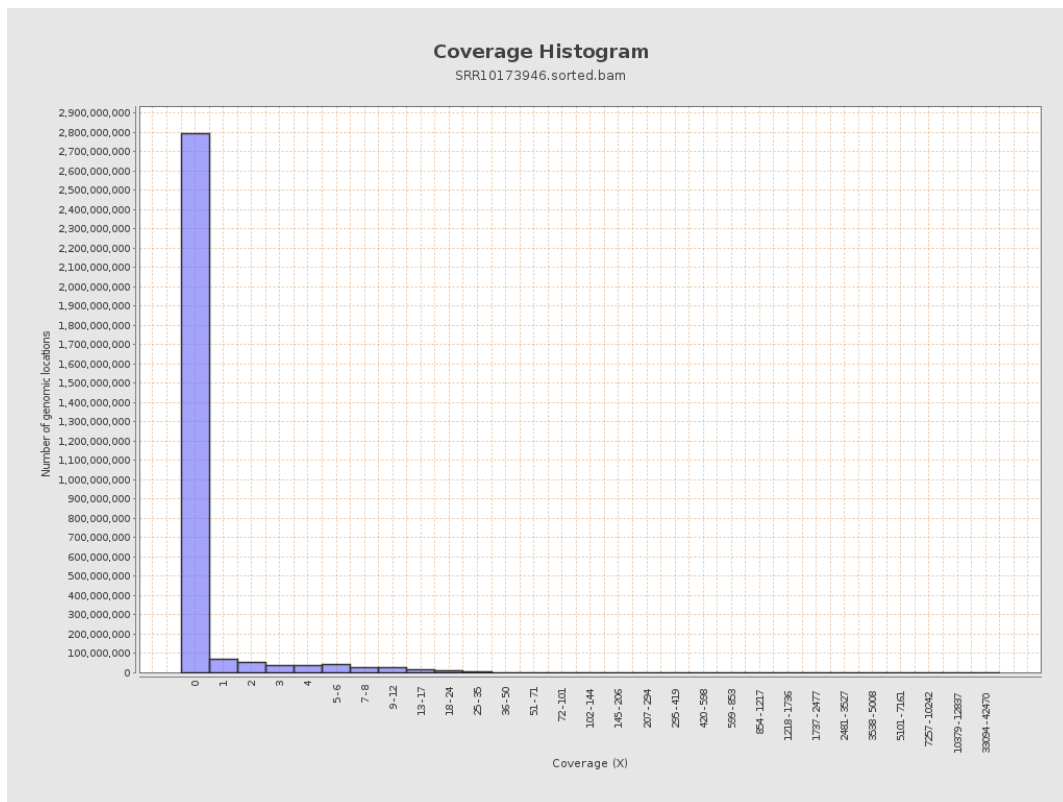
		bases	coverage	deviation
chr1	249250621	122270137	0.4906	4.152
chr2	243199373	138599208	0.5699	29.5401
chr3	198022430	106081942	0.5357	2.2673
chr4	191154276	102632134	0.5369	4.3384
chr5	180915260	90900461	0.5024	2.1858
chr6	171115067	90080820	0.5264	2.9697
chr7	159138663	82994111	0.5215	3.9767
chr8	146364022	79526454	0.5433	5.0785
chr9	141213431	64202600	0.4546	3.7011
chr10	135534747	78077272	0.5761	5.2621
chr11	135006516	70225838	0.5202	2.4535
chr12	133851895	68178645	0.5094	2.3979
chr13	115169878	49161694	0.4269	2.0126
chr14	107349540	46382152	0.4321	2.0986
chr15	102531392	43983927	0.429	2.1565
chr16	90354753	47540551	0.5262	3.4277
chr17	81195210	42232127	0.5201	2.6896
chr18	78077248	42201259	0.5405	5.6551
chr19	59128983	30500398	0.5158	3.1853
chr20	63025520	33521277	0.5319	2.6136
chr21	48129895	21832146	0.4536	3.374
chr22	51304566	19728843	0.3845	2.3913
chrMT	16571	1964087	118.5256	90.3153
chrX	155270560	41283137	0.2659	1.646

chrY	59373566	12519736	0.2109	3.5326
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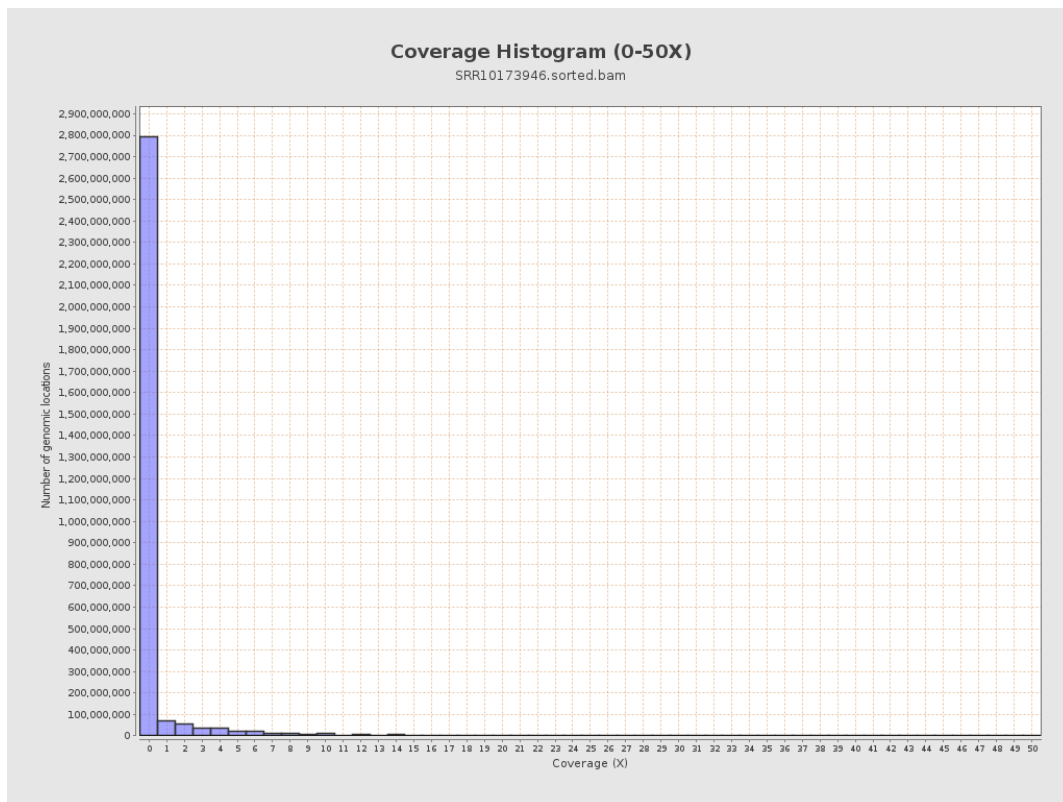
3. Results : Coverage across reference



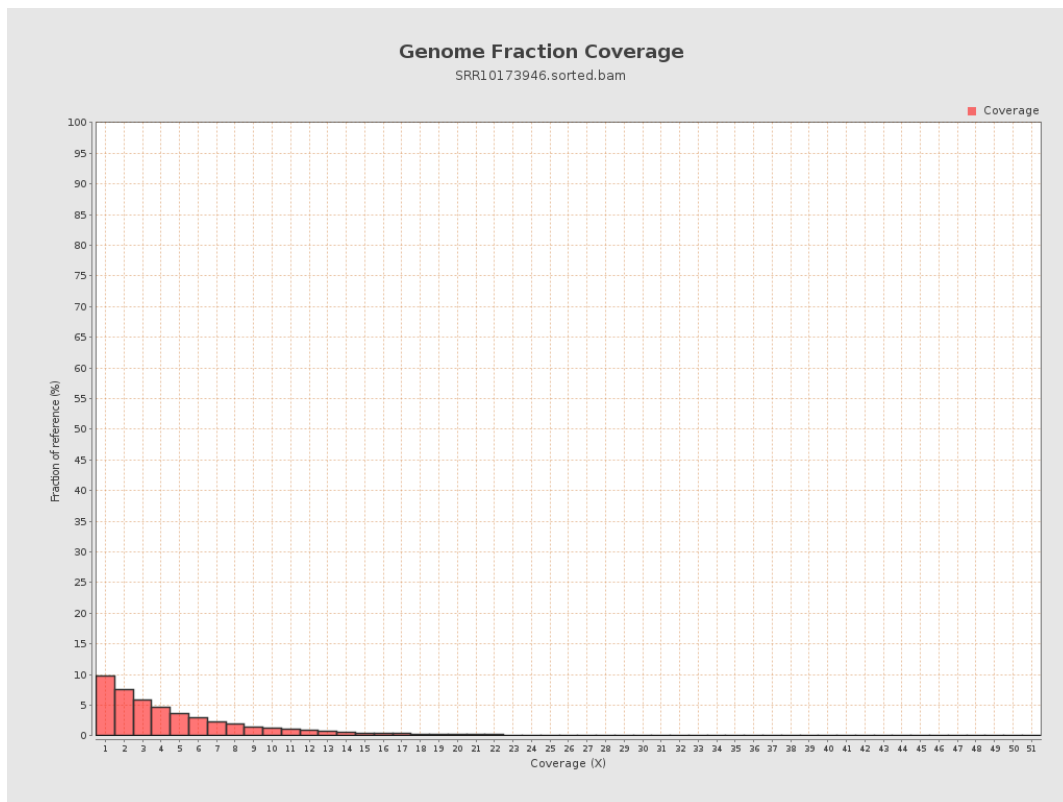
4. Results : Coverage Histogram



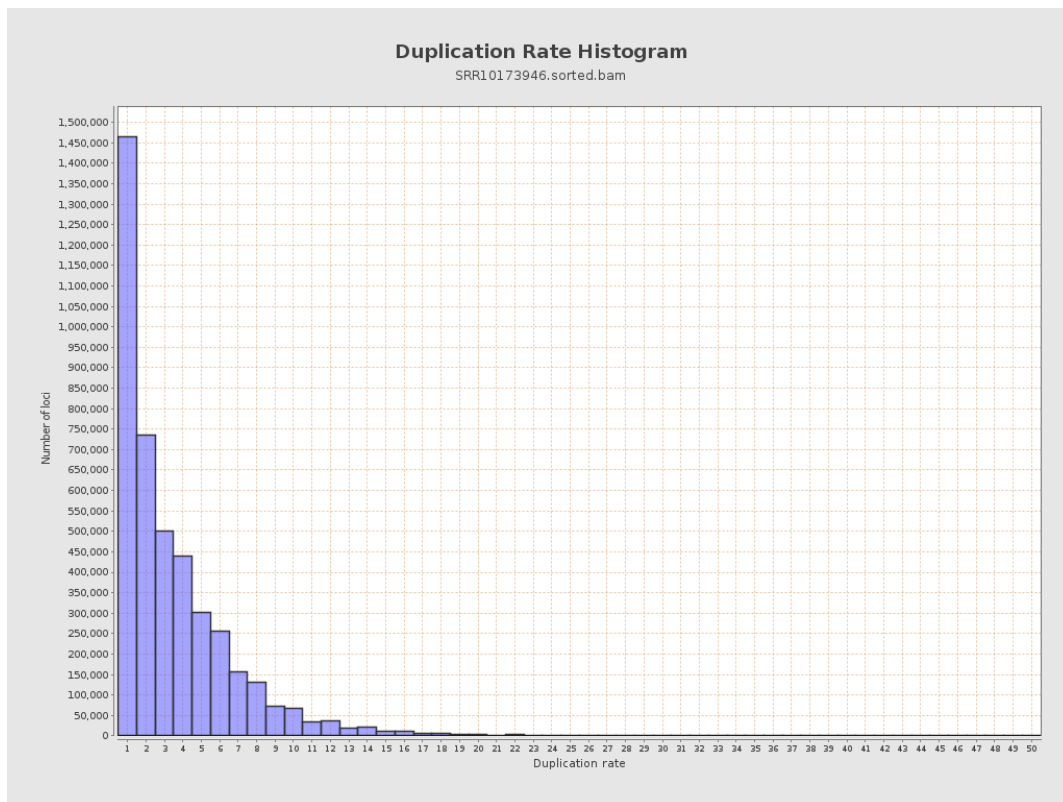
5. Results : Coverage Histogram (0-50X)



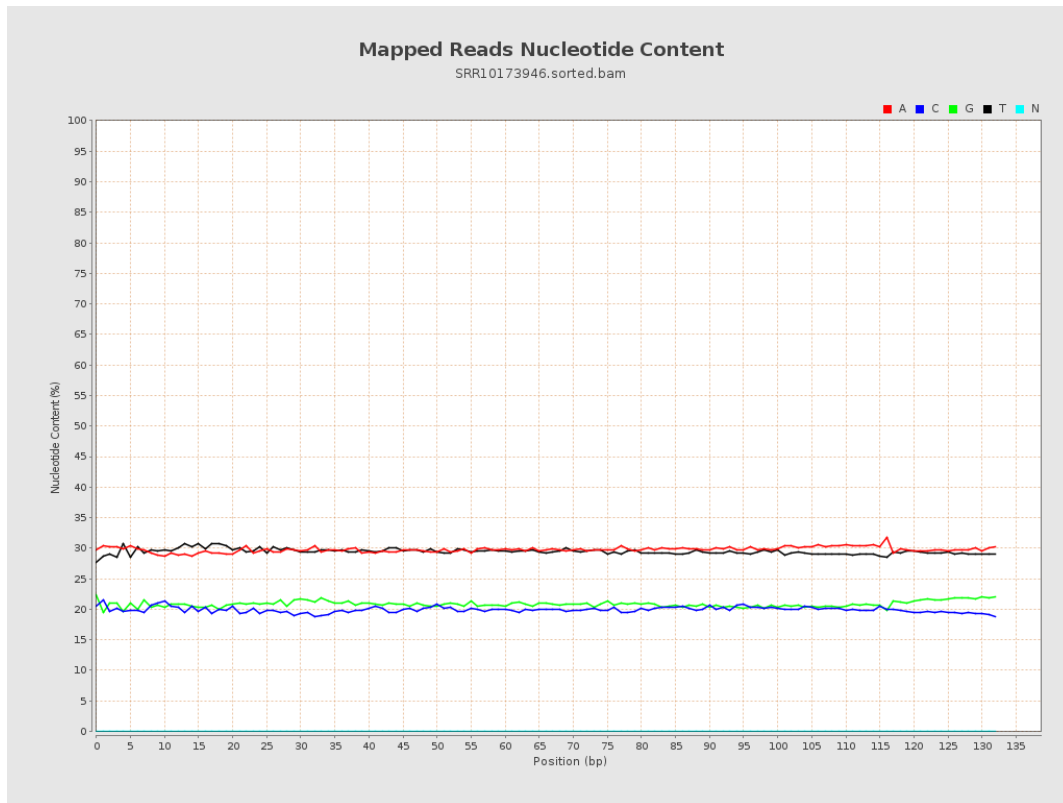
6. Results : Genome Fraction Coverage



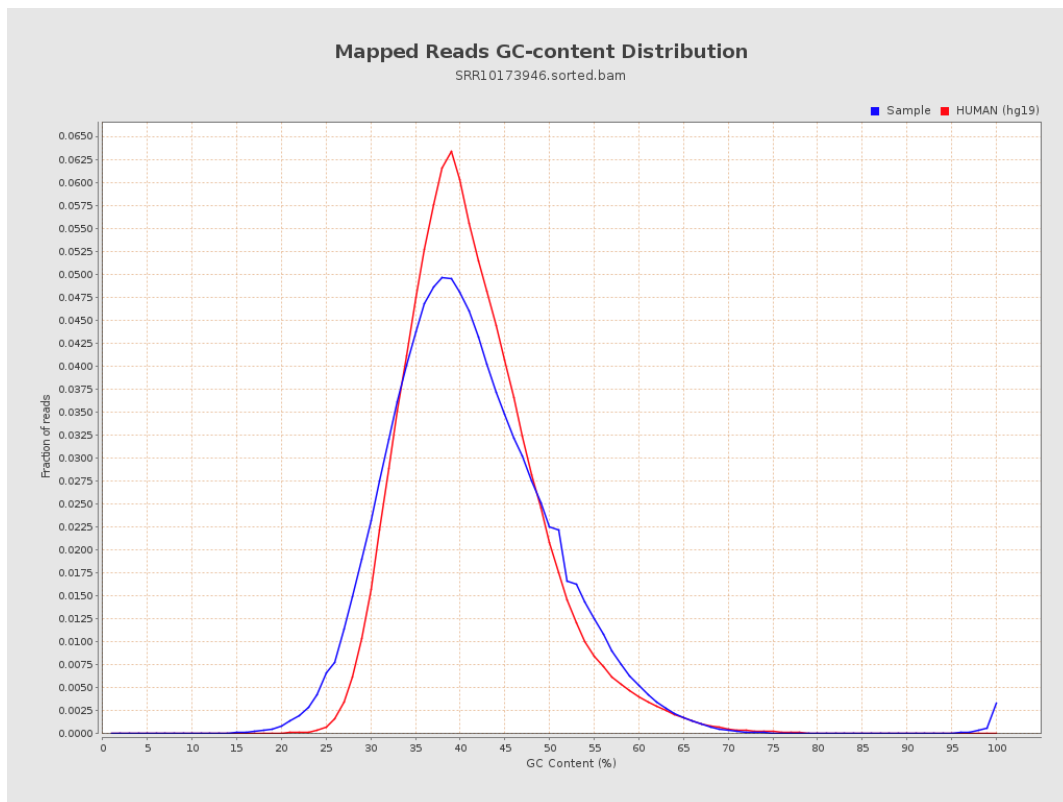
7. Results : Duplication Rate Histogram



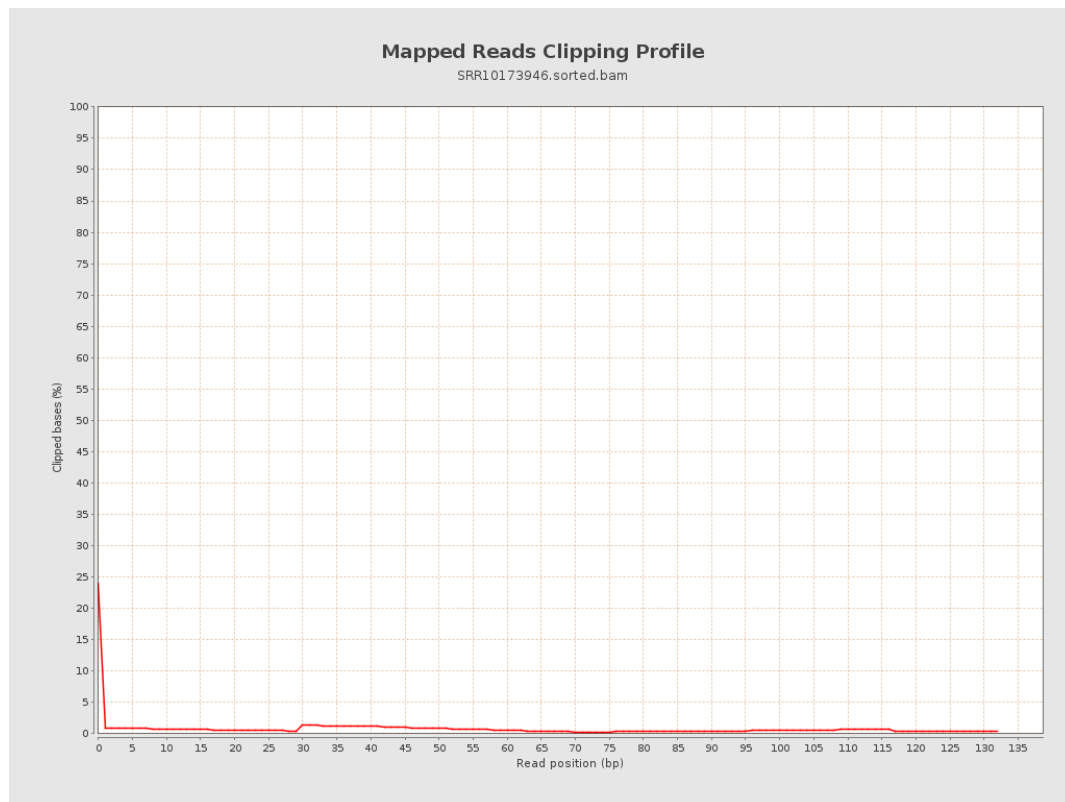
8. Results : Mapped Reads Nucleotide Content



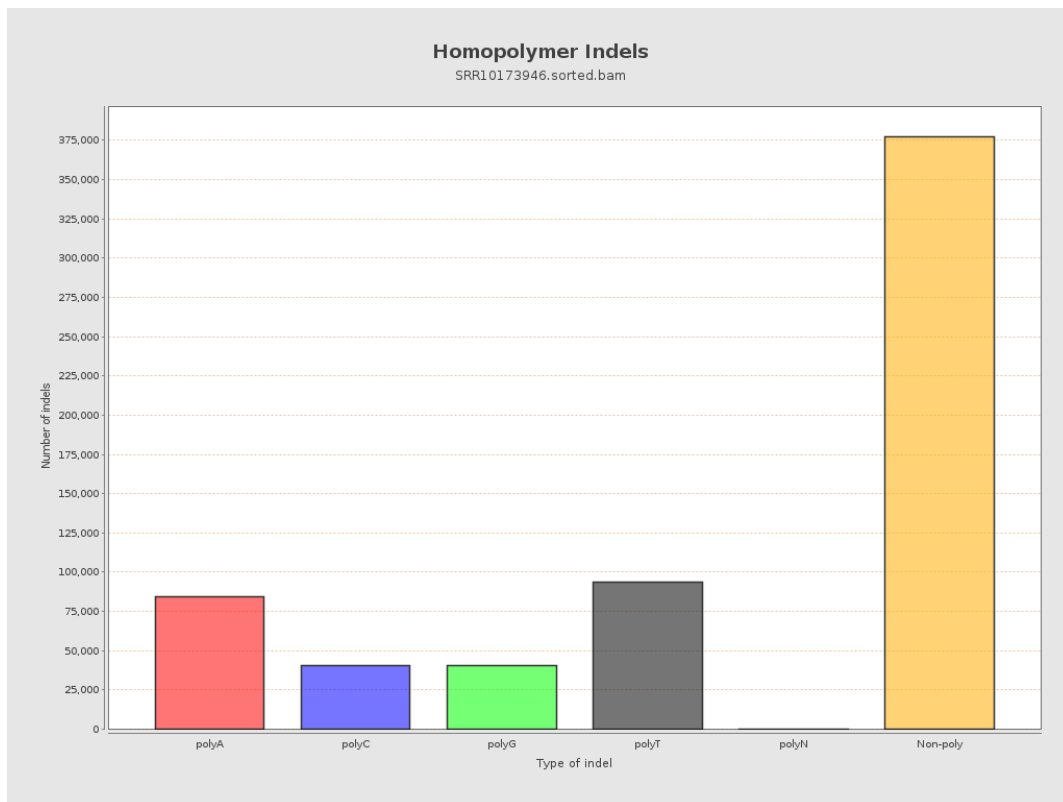
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



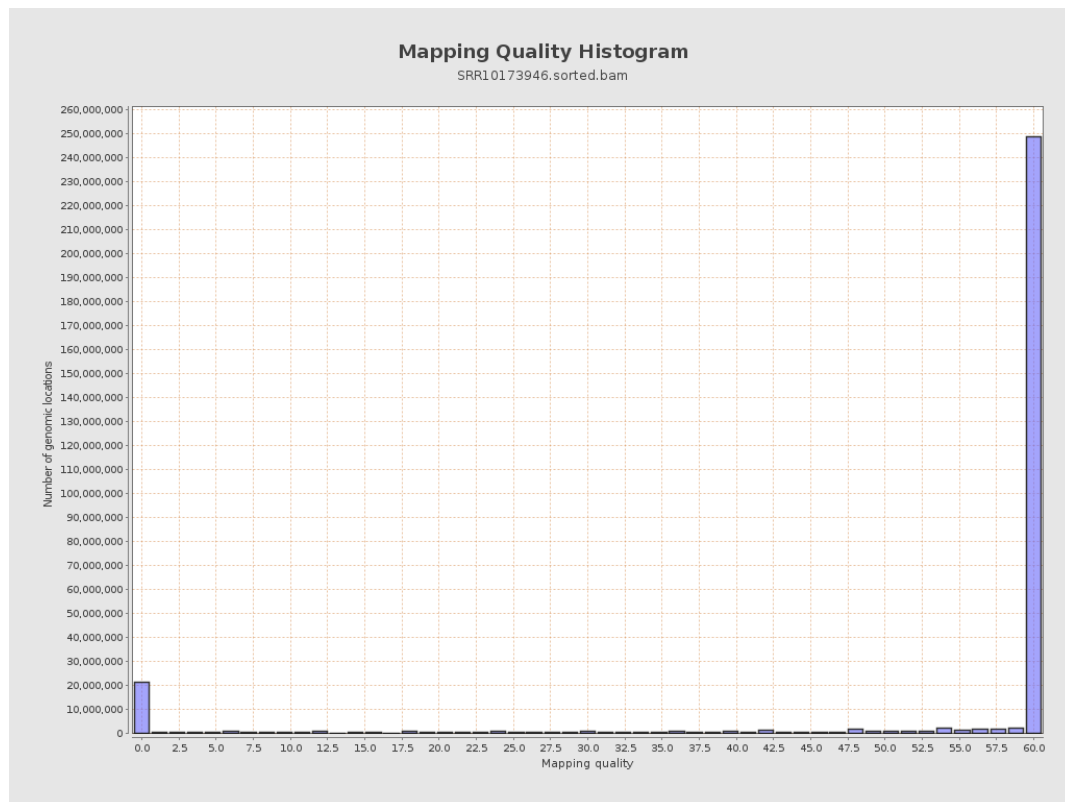
11. Results : Homopolymer Indels



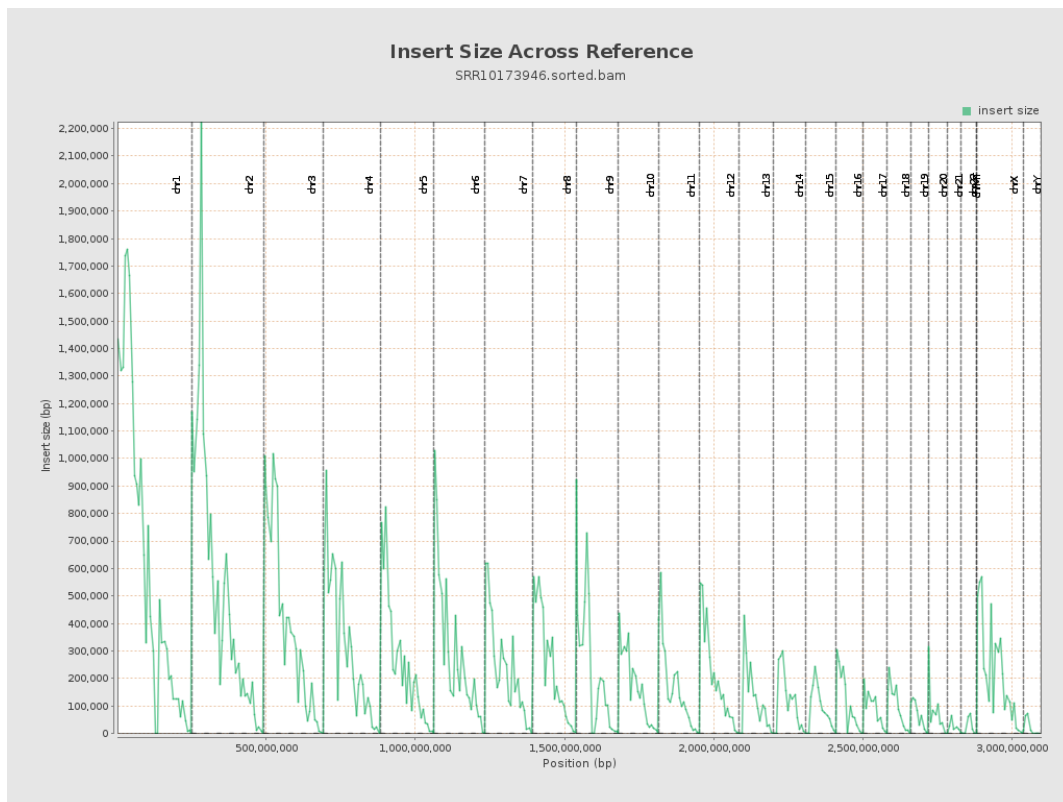
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

