

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:39:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173909.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_SRR10173909 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173909_1.fastq.gz SRR10173909_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:38:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173909.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,887,734
Mapped reads	4,764,523 / 97.48%
Unmapped reads	123,211 / 2.52%
Mapped paired reads	4,764,523 / 97.48%
Mapped reads, first in pair	2,387,401 / 48.84%
Mapped reads, second in pair	2,377,122 / 48.63%
Mapped reads, both in pair	4,682,050 / 95.79%
Mapped reads, singletons	82,473 / 1.69%
Secondary alignments	0
Supplementary alignments	466,295 / 9.54%
Read min/max/mean length	30 / 133 / 127.94
Duplicated reads (estimated)	3,538,863 / 72.4%
Duplication rate	62.83%
Clipped reads	1,959,173 / 40.08%

2.2. ACGT Content

Number/percentage of A's	170,698,999 / 30.39%
Number/percentage of C's	108,577,946 / 19.33%
Number/percentage of T's	170,314,501 / 30.32%
Number/percentage of G's	112,036,558 / 19.95%
Number/percentage of N's	6,786 / 0%

GC Percentage	39.28%
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2.3. Coverage

Mean	0.1815
Standard Deviation	2.648

2.4. Mapping Quality

Mean Mapping Quality	52.79
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2.5. Insert size

Mean	717,033.89
Standard Deviation	7,603,590.45
P25/Median/P75	140 / 192 / 271

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	5,585,115
Insertions	57,781
Mapped reads with at least one insertion	1.17%
Deletions	123,682
Mapped reads with at least one deletion	2.53%
Homopolymer indels	43.55%

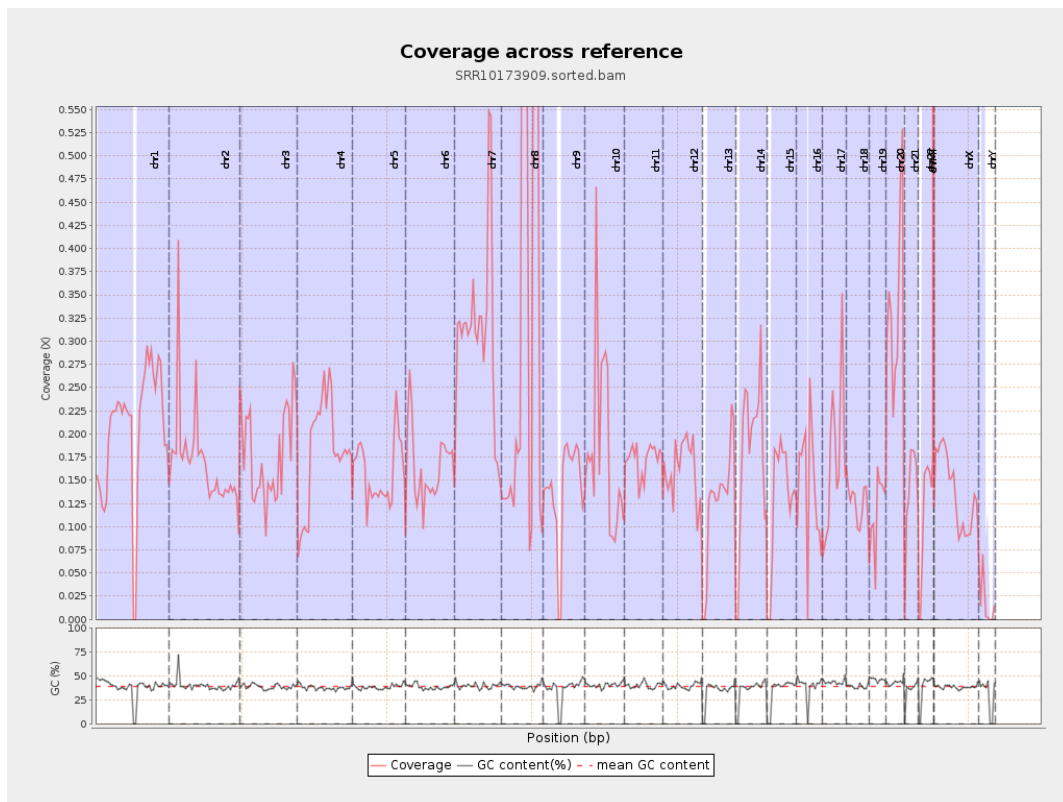
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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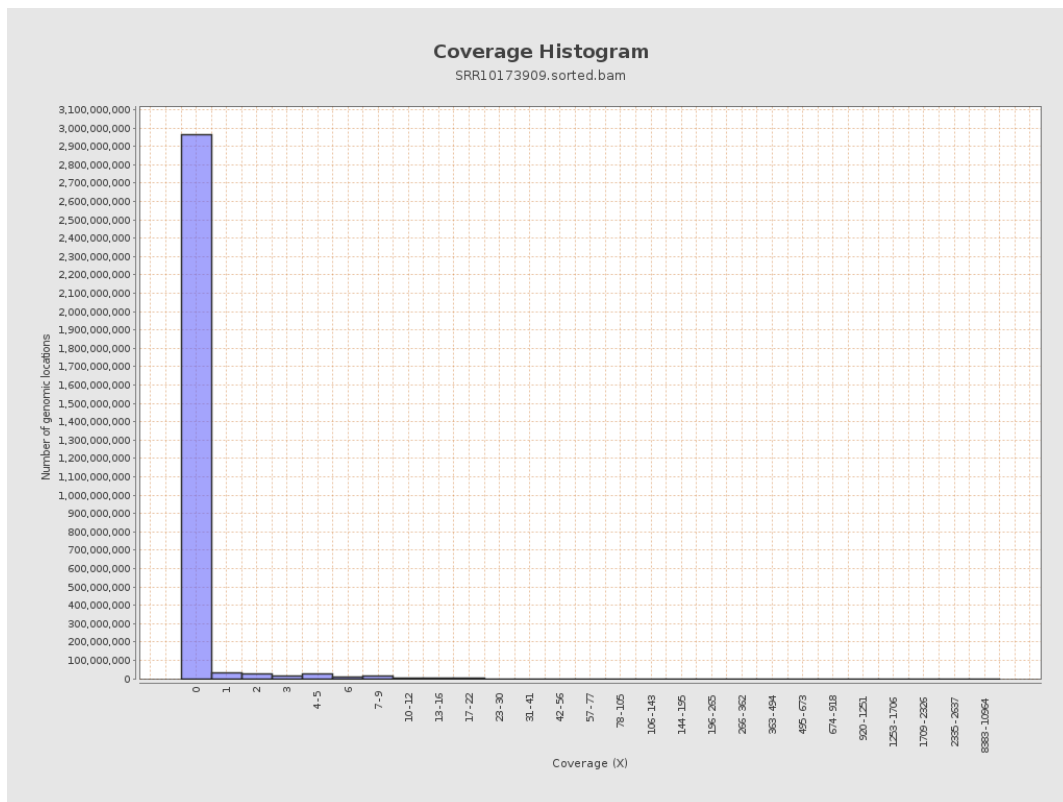
		bases	coverage	deviation
chr1	249250621	50962303	0.2045	1.5444
chr2	243199373	41160907	0.1692	7.6763
chr3	198022430	35323180	0.1784	1.1736
chr4	191154276	34466114	0.1803	1.4372
chr5	180915260	28652282	0.1584	1.0889
chr6	171115067	27746071	0.1621	1.1496
chr7	159138663	49578165	0.3115	2.8635
chr8	146364022	55728087	0.3807	2.0639
chr9	141213431	19748340	0.1398	1.3083
chr10	135534747	25108637	0.1853	3.3278
chr11	135006516	23278480	0.1724	1.1751
chr12	133851895	21700175	0.1621	1.1224
chr13	115169878	14698029	0.1276	0.9909
chr14	107349540	19148362	0.1784	1.178
chr15	102531392	13444568	0.1311	0.9994
chr16	90354753	12819350	0.1419	1.478
chr17	81195210	14222986	0.1752	1.2444
chr18	78077248	9854411	0.1262	1.5067
chr19	59128983	6904055	0.1168	1.1114
chr20	63025520	21233424	0.3369	1.6286
chr21	48129895	6602416	0.1372	1.099
chr22	51304566	5722533	0.1115	0.8777
chrMT	16571	1586932	95.7656	70.3176
chrX	155270560	21244820	0.1368	1.0288

chrY	59373566	1004030	0.0169	0.7461
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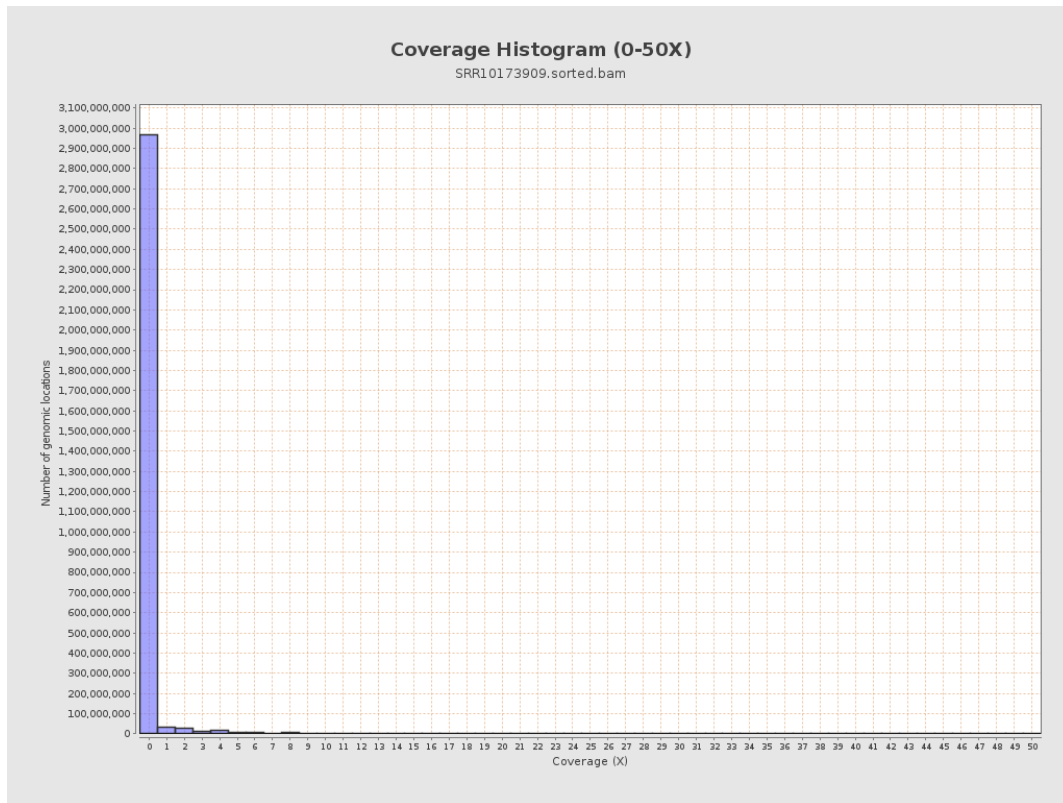
3. Results : Coverage across reference



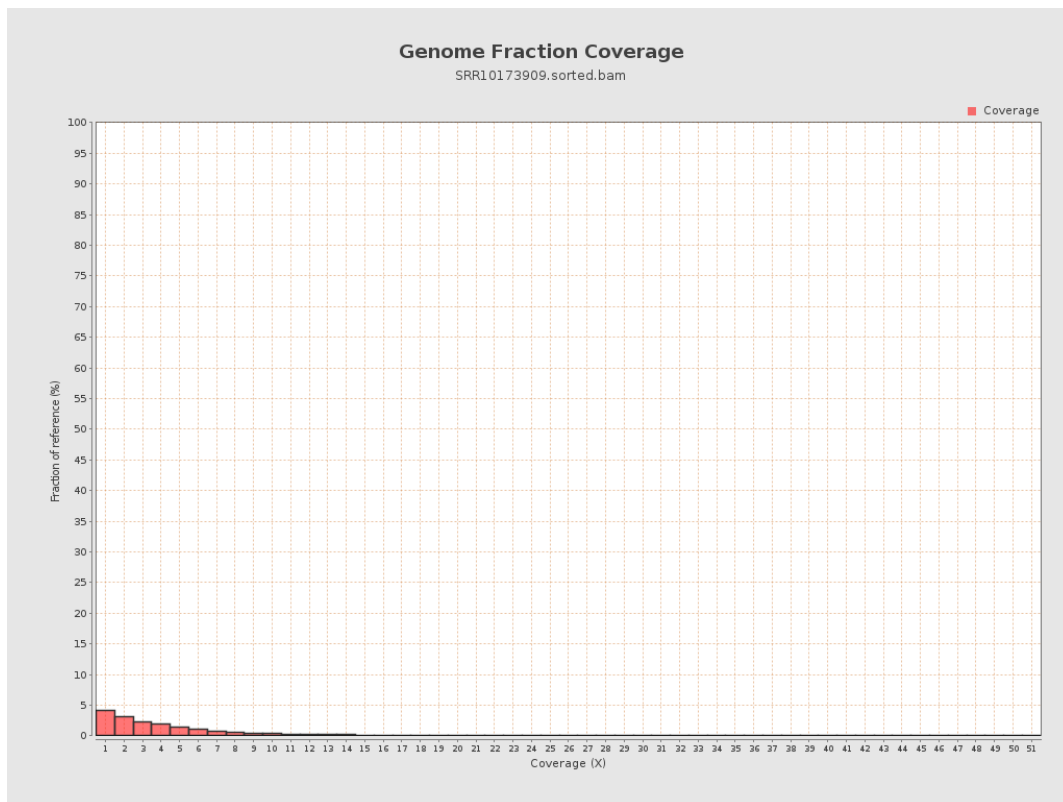
4. Results : Coverage Histogram



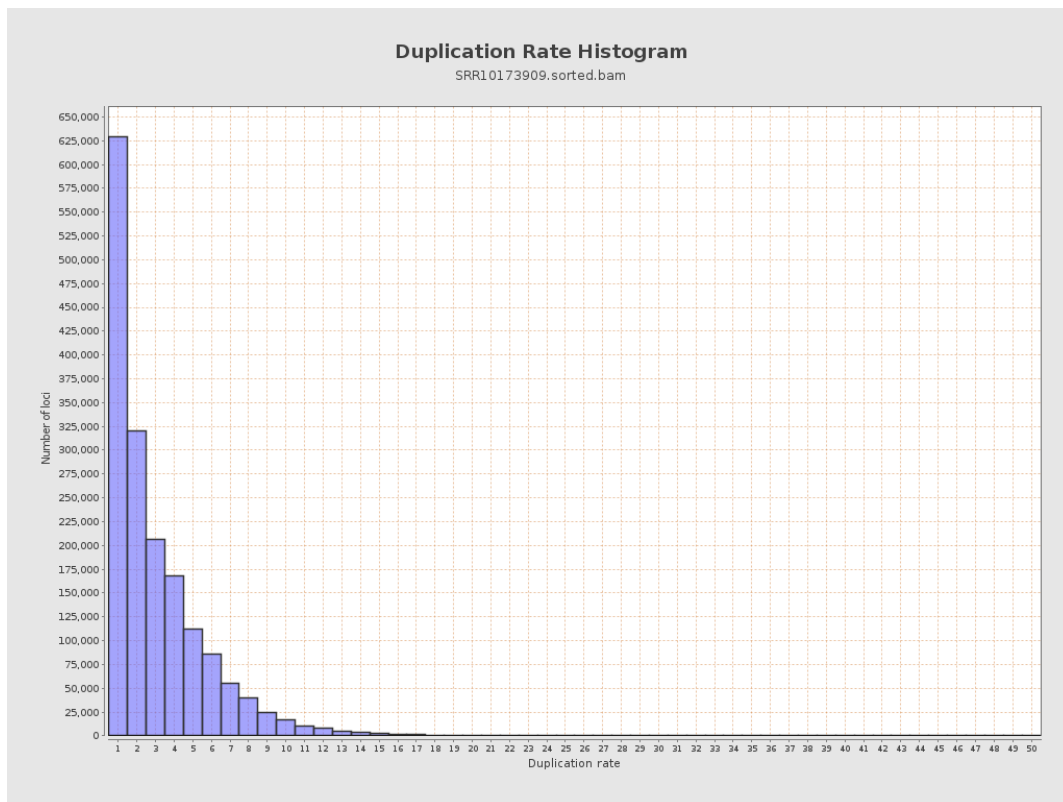
5. Results : Coverage Histogram (0-50X)



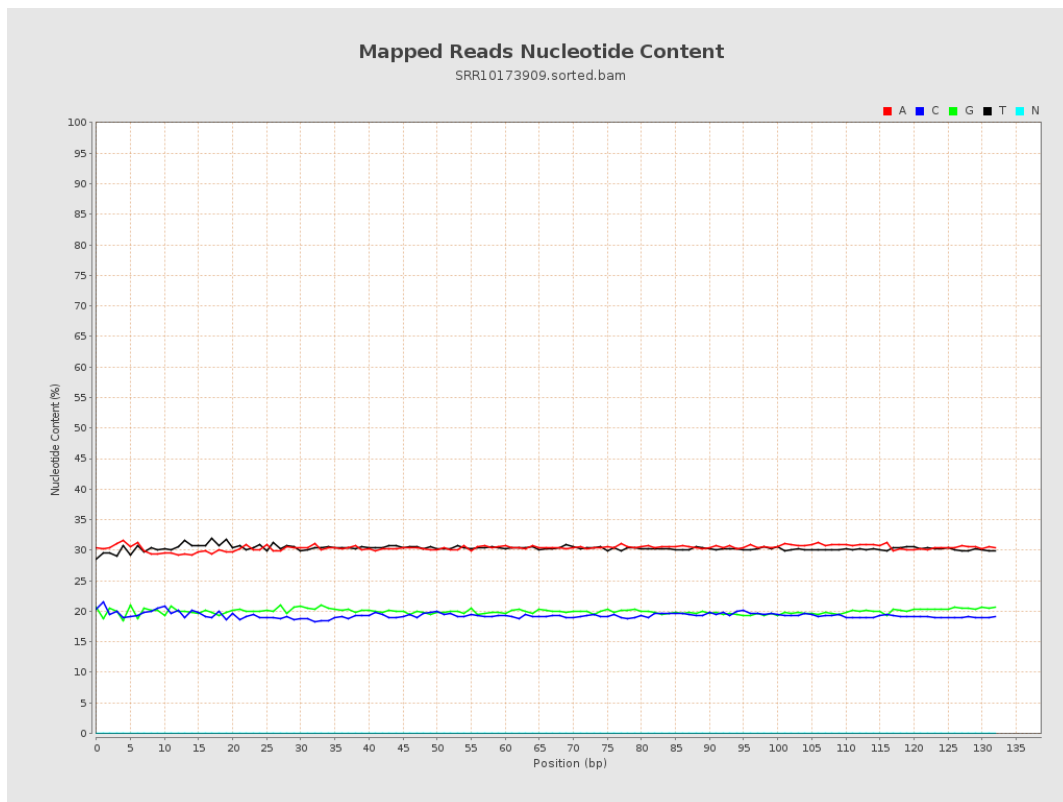
6. Results : Genome Fraction Coverage



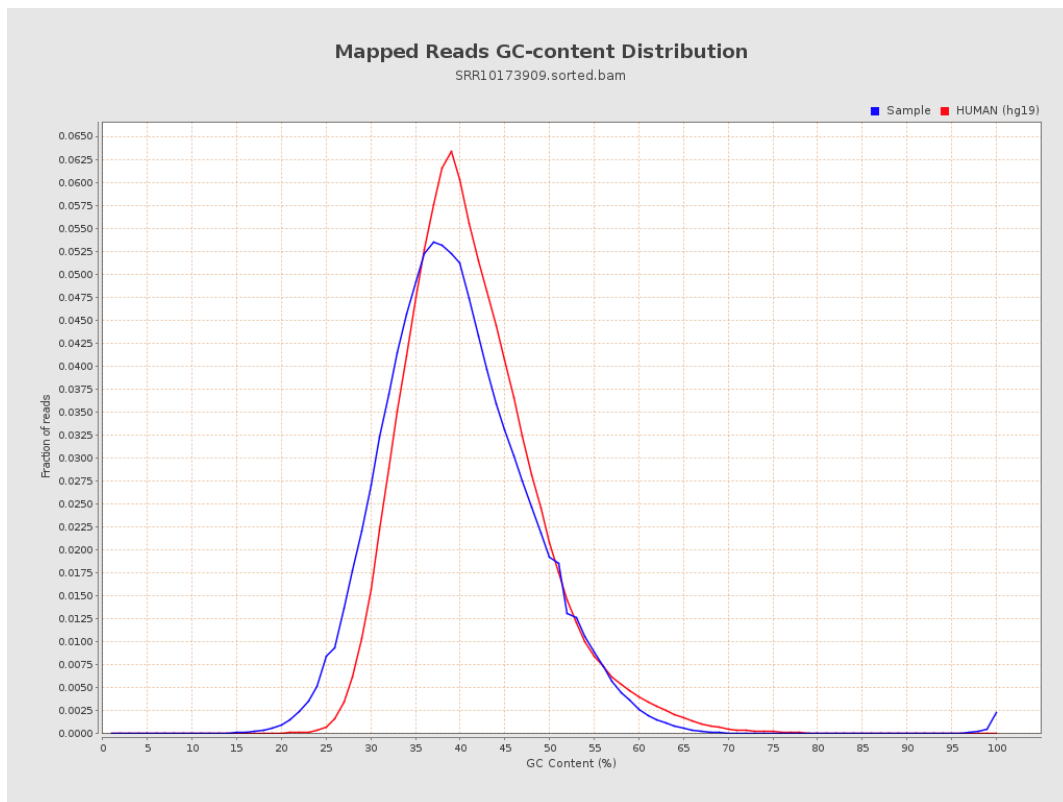
7. Results : Duplication Rate Histogram



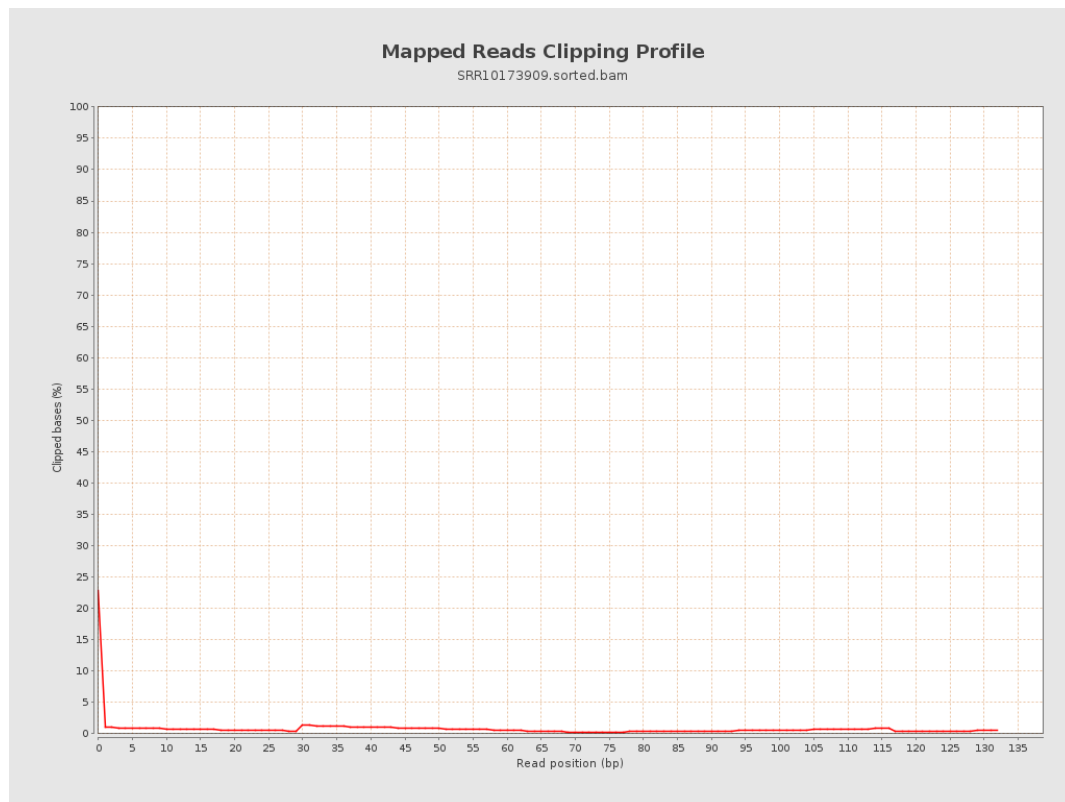
8. Results : Mapped Reads Nucleotide Content



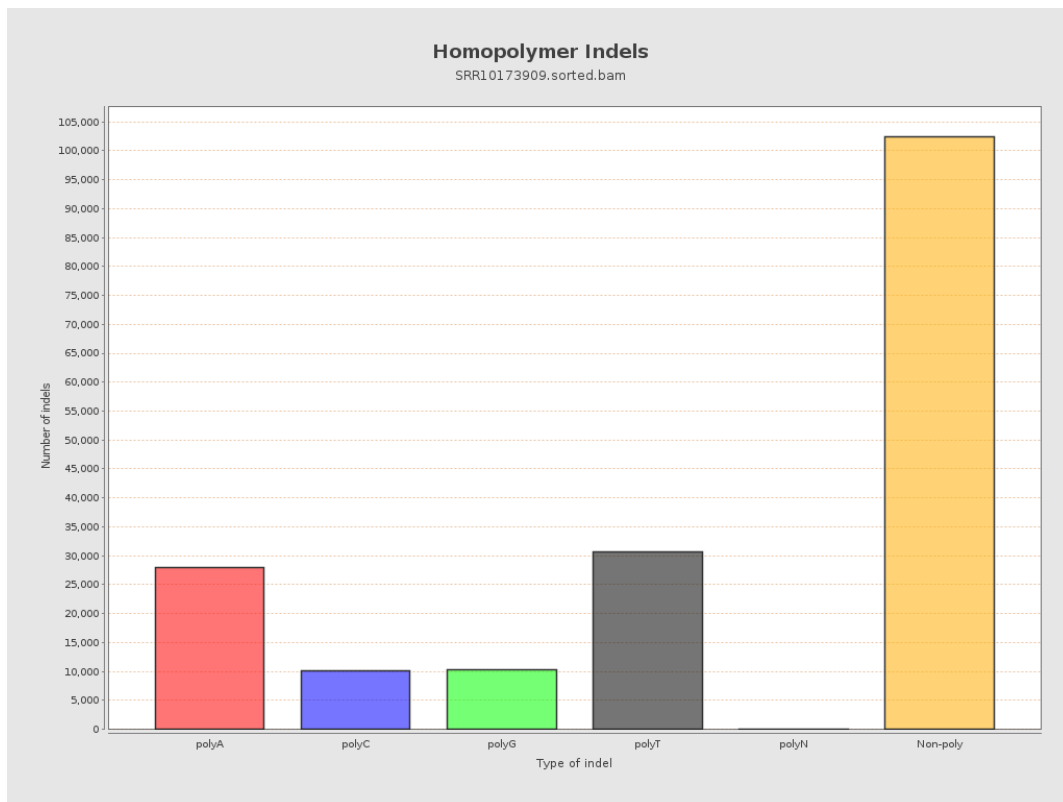
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



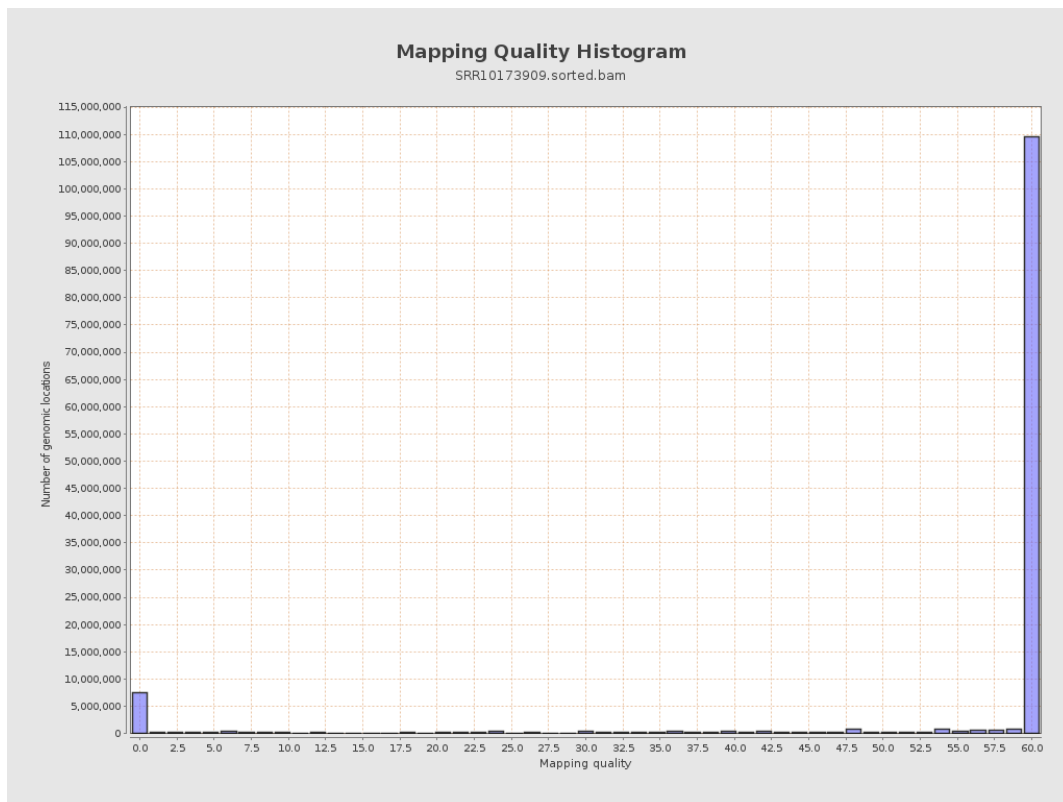
11. Results : Homopolymer Indels



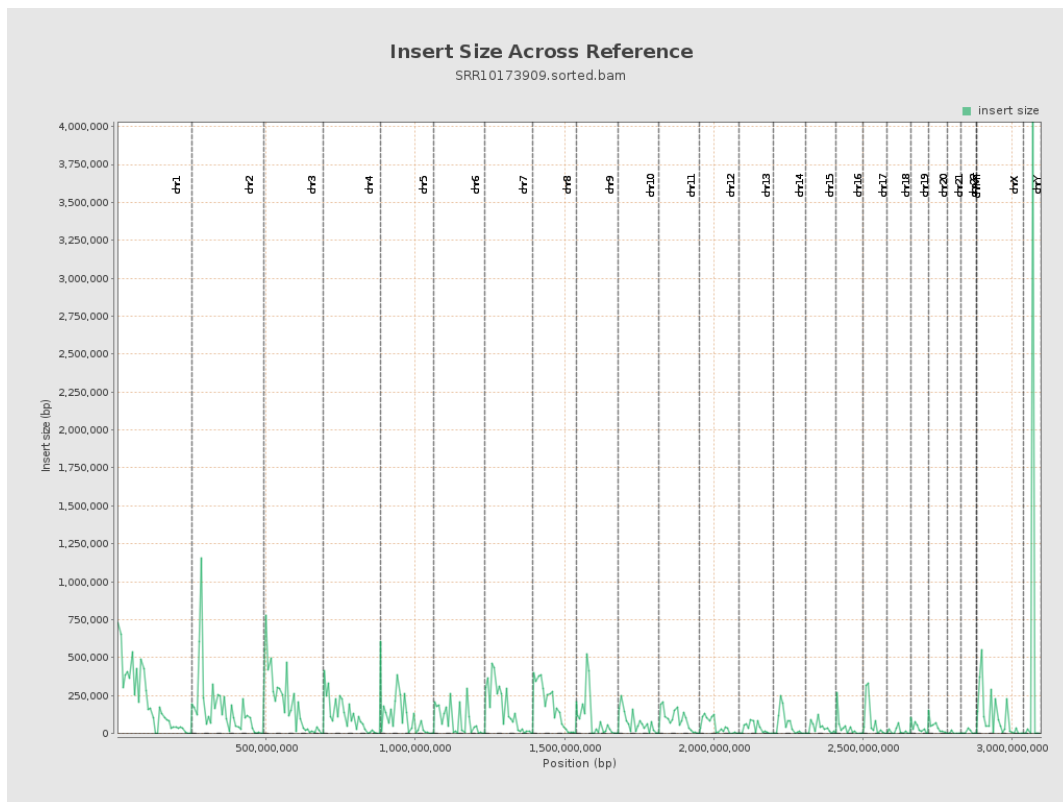
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

