

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 07:15:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173920.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_SRR10173920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173920_1.fastq.gz SRR10173920_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 07:15:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,922,194
Mapped reads	5,773,274 / 97.49%
Unmapped reads	148,920 / 2.51%
Mapped paired reads	5,773,274 / 97.49%
Mapped reads, first in pair	2,890,313 / 48.8%
Mapped reads, second in pair	2,882,961 / 48.68%
Mapped reads, both in pair	5,672,254 / 95.78%
Mapped reads, singletons	101,020 / 1.71%
Secondary alignments	0
Supplementary alignments	602,057 / 10.17%
Read min/max/mean length	30 / 133 / 128.47
Duplicated reads (estimated)	4,579,372 / 77.33%
Duplication rate	65.99%
Clipped reads	2,298,441 / 38.81%

2.2. ACGT Content

Number/percentage of A's	206,148,403 / 30.1%
Number/percentage of C's	133,495,565 / 19.5%
Number/percentage of T's	206,174,213 / 30.11%
Number/percentage of G's	138,939,246 / 20.29%
Number/percentage of N's	8,075 / 0%

GC Percentage	39.79%
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2.3. Coverage

Mean	0.2213
Standard Deviation	3.1503

2.4. Mapping Quality

Mean Mapping Quality	52.76
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2.5. Insert size

Mean	893,027.46
Standard Deviation	8,587,754.24
P25/Median/P75	145 / 200 / 284

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	6,943,103
Insertions	70,015
Mapped reads with at least one insertion	1.17%
Deletions	186,177
Mapped reads with at least one deletion	3.15%
Homopolymer indels	42.18%

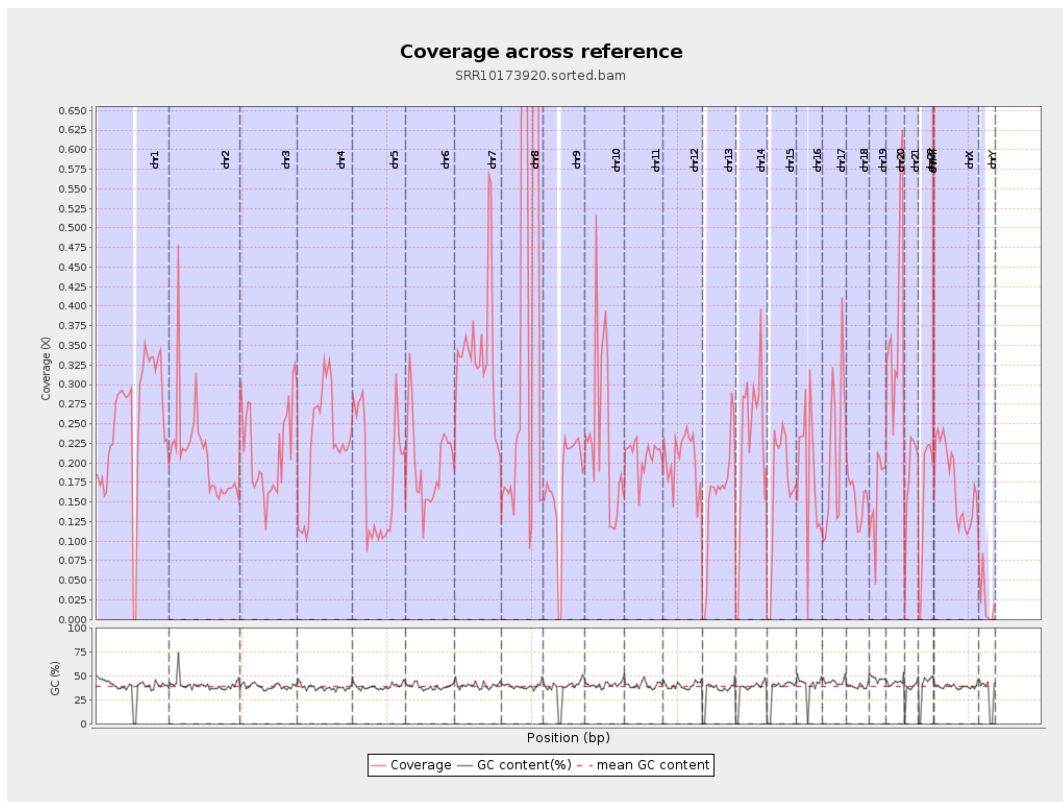
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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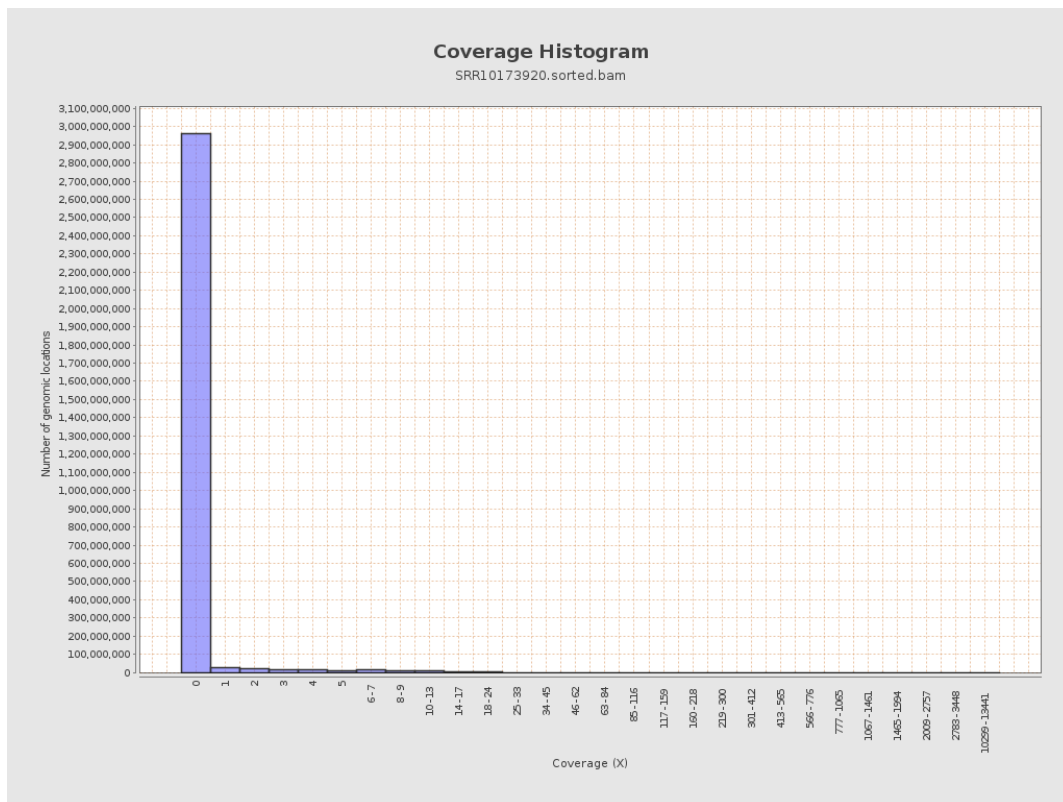
		bases	coverage	deviation
chr1	249250621	62704759	0.2516	1.8155
chr2	243199373	50856681	0.2091	9.4143
chr3	198022430	42942911	0.2169	1.3899
chr4	191154276	42518519	0.2224	1.6139
chr5	180915260	32771059	0.1811	1.2553
chr6	171115067	33826781	0.1977	1.4071
chr7	159138663	54269546	0.341	2.9517
chr8	146364022	68674247	0.4692	2.413
chr9	141213431	24468643	0.1733	1.4804
chr10	135534747	32101962	0.2369	3.6239
chr11	135006516	28203197	0.2089	1.367
chr12	133851895	27486249	0.2053	1.3311
chr13	115169878	18221543	0.1582	1.1816
chr14	107349540	24117583	0.2247	1.4107
chr15	102531392	17072247	0.1665	1.1844
chr16	90354753	16670341	0.1845	1.7344
chr17	81195210	17763088	0.2188	1.5206
chr18	78077248	12110321	0.1551	1.875
chr19	59128983	9371208	0.1585	1.3943
chr20	63025520	24099957	0.3824	1.8369
chr21	48129895	8779797	0.1824	1.3286
chr22	51304566	7815466	0.1523	1.0981
chrMT	16571	245377	14.8076	15.253
chrX	155270560	26837552	0.1728	1.226

chrY	59373566	1276559	0.0215	0.8129
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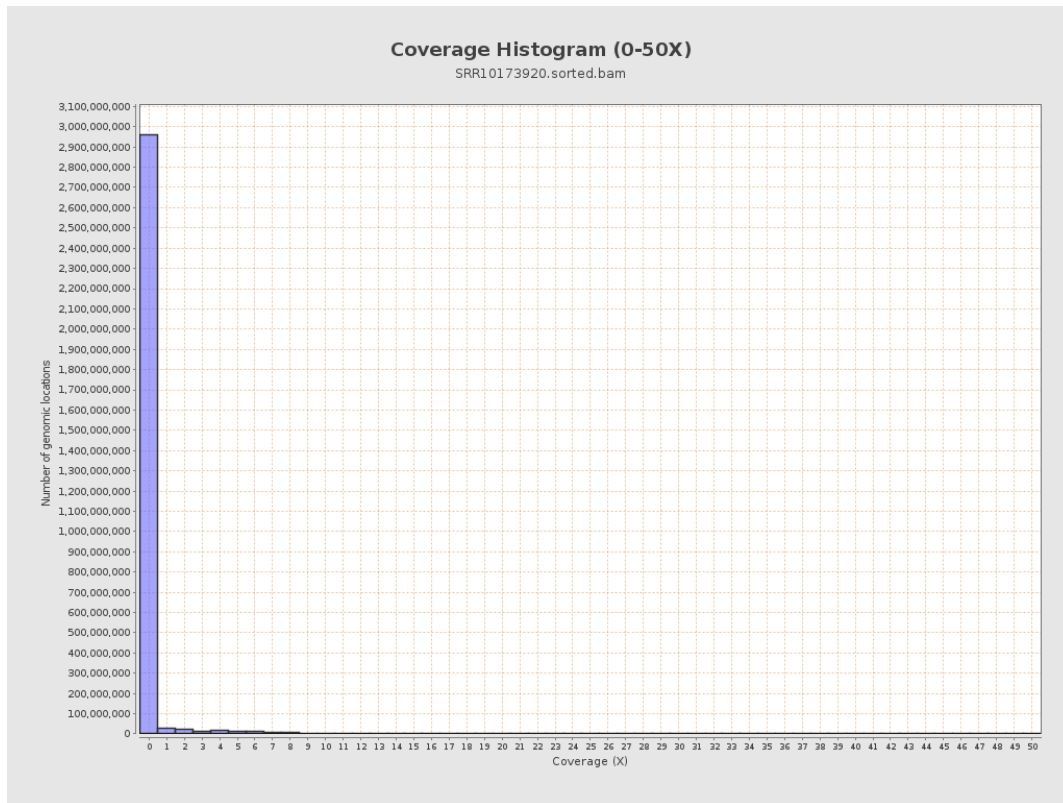
3. Results : Coverage across reference



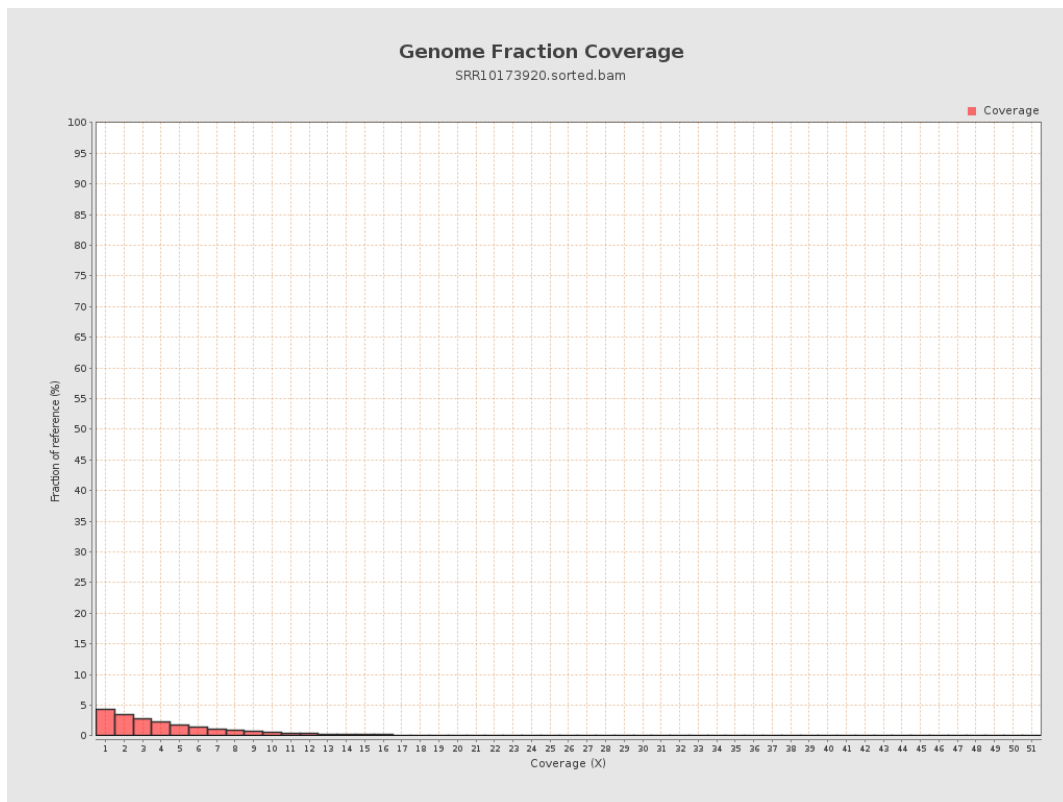
4. Results : Coverage Histogram



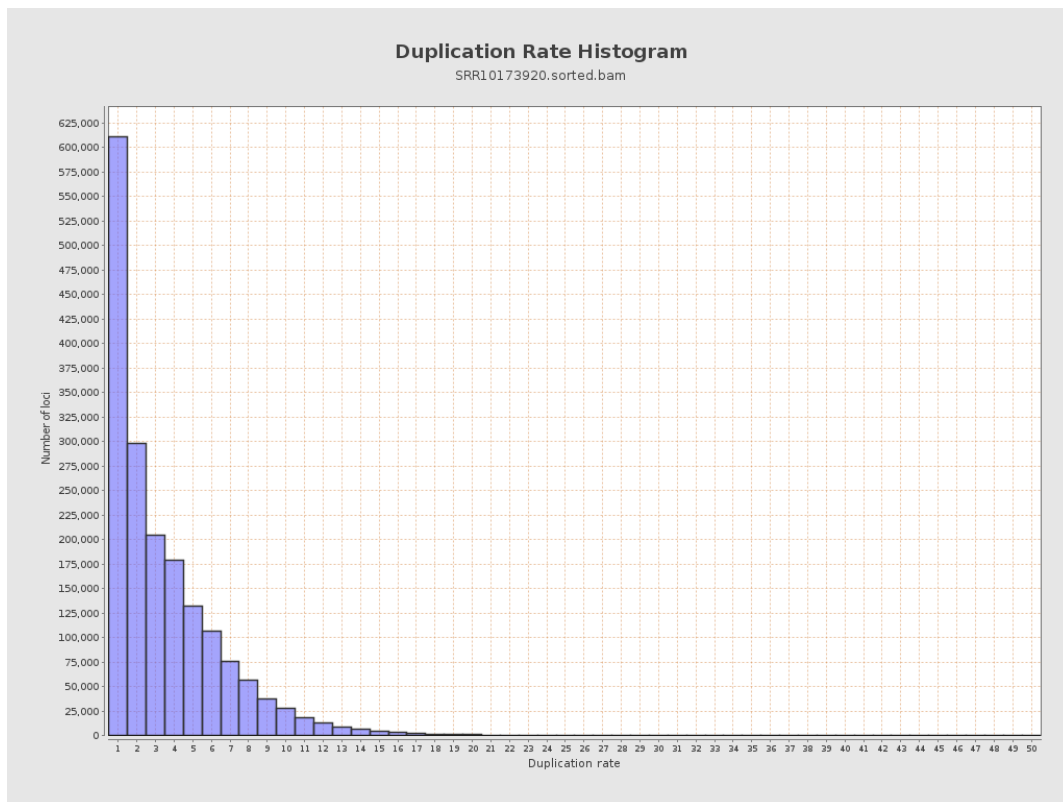
5. Results : Coverage Histogram (0-50X)



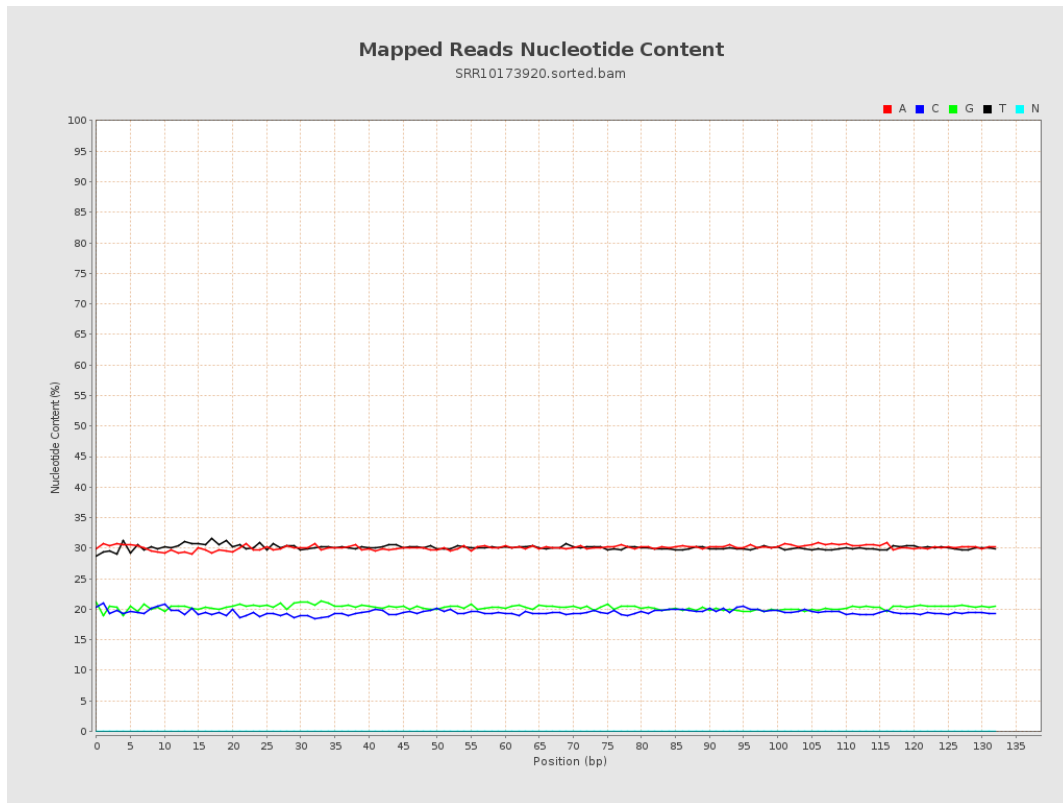
6. Results : Genome Fraction Coverage



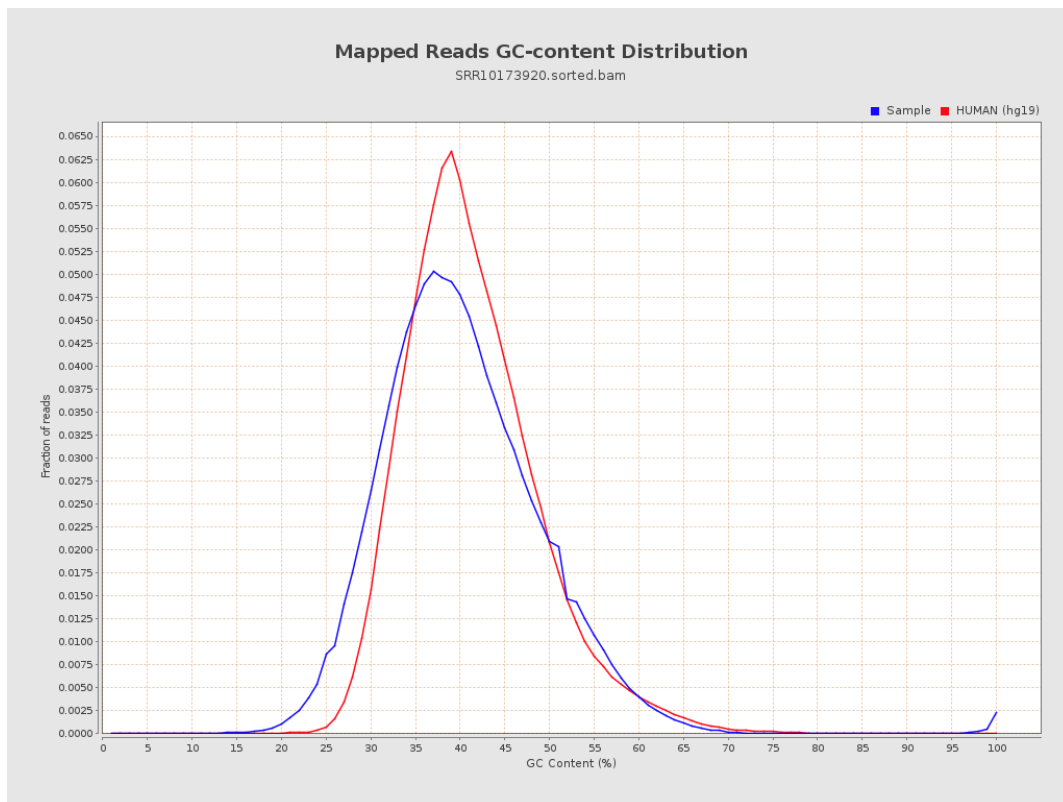
7. Results : Duplication Rate Histogram



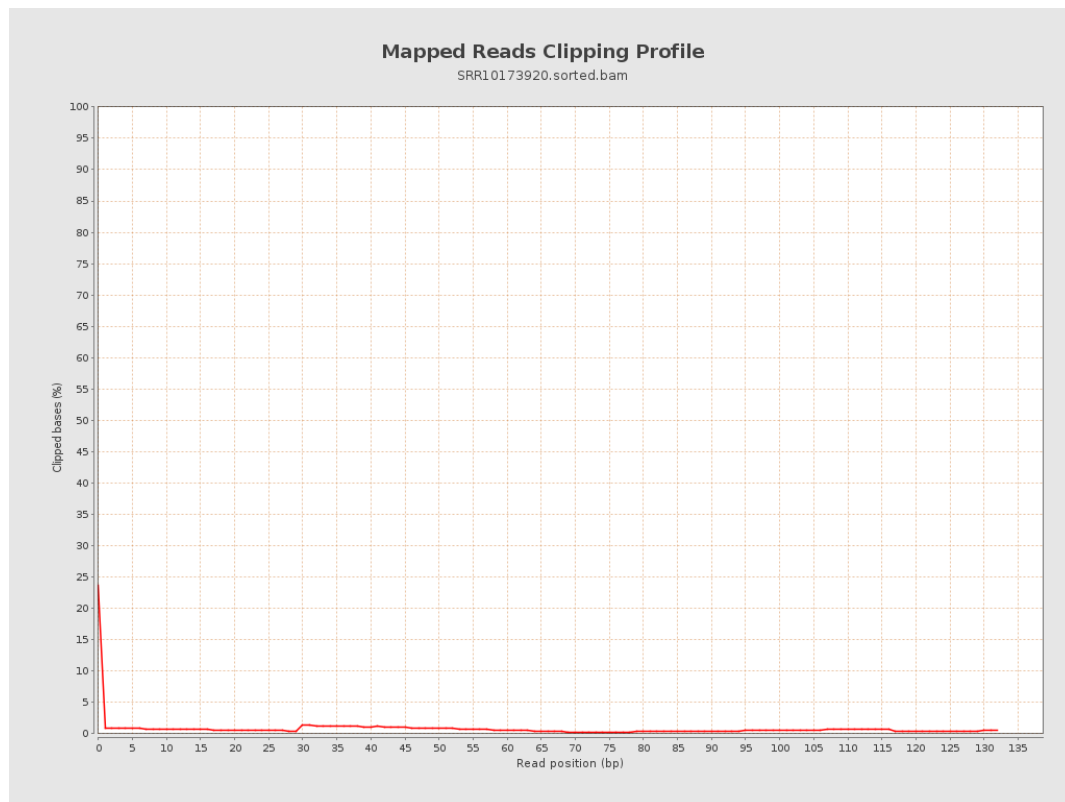
8. Results : Mapped Reads Nucleotide Content



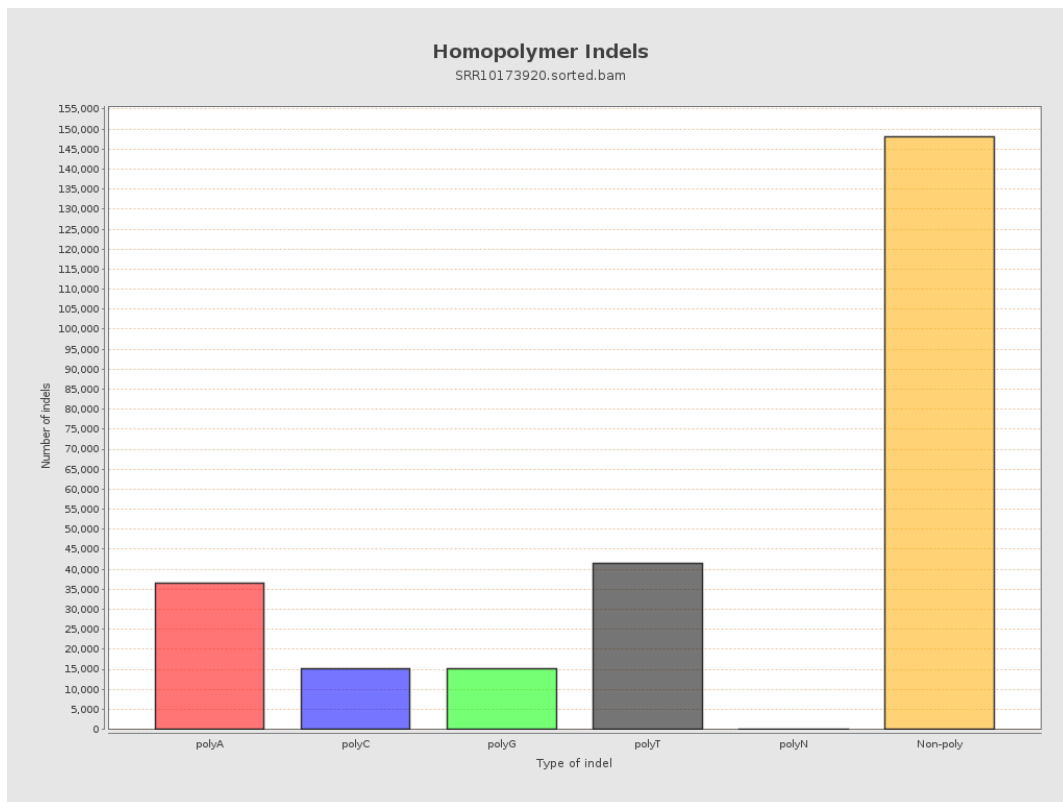
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



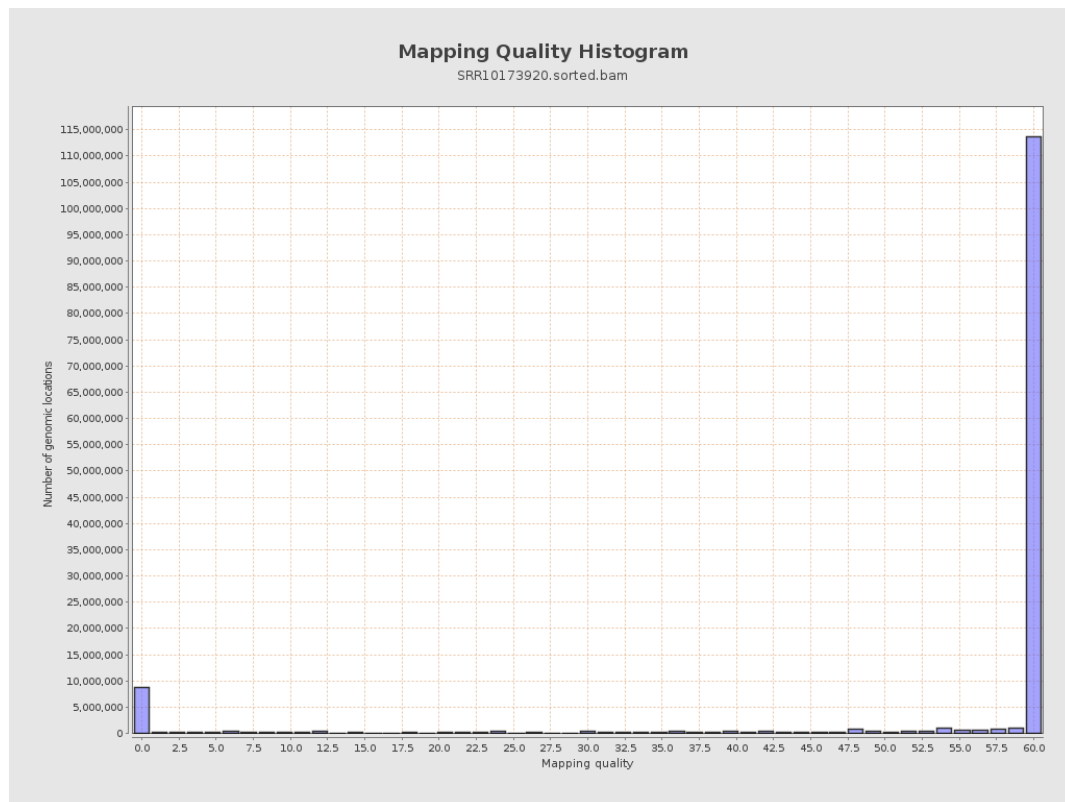
11. Results : Homopolymer Indels



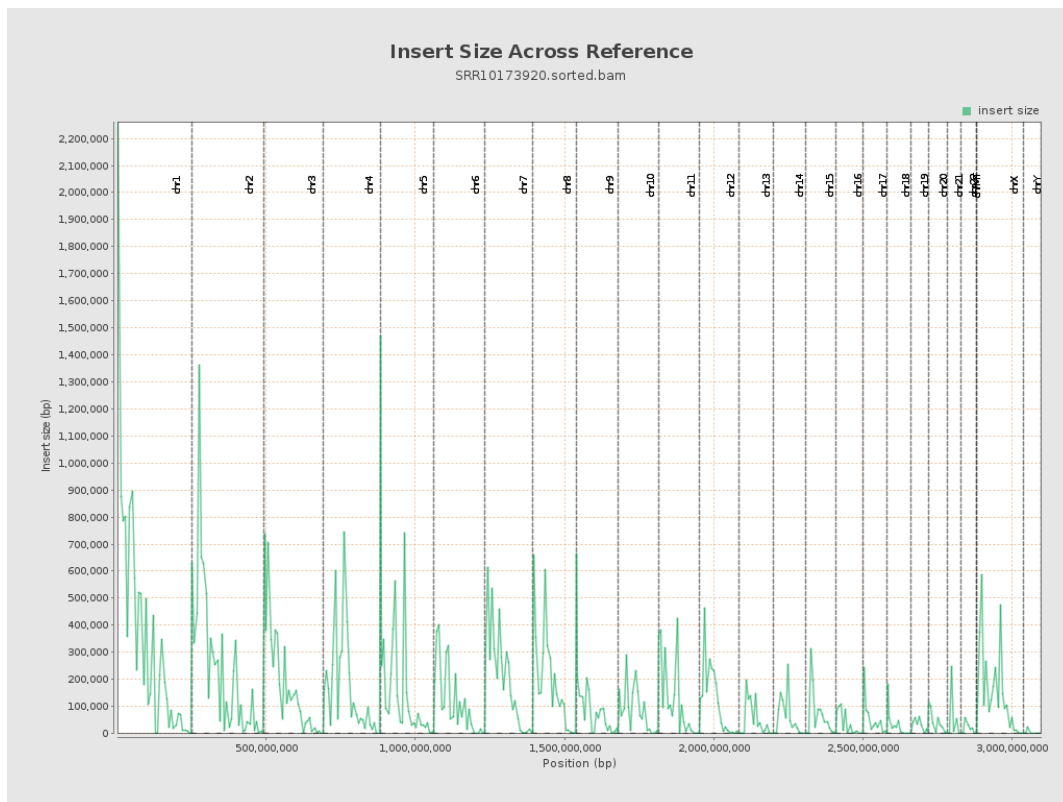
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

