

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:52:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173874.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_SRR10173874 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173874_1.fastq.gz SRR10173874_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:52:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173874.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,694,584
Mapped reads	2,623,346 / 97.36%
Unmapped reads	71,238 / 2.64%
Mapped paired reads	2,623,346 / 97.36%
Mapped reads, first in pair	1,312,890 / 48.72%
Mapped reads, second in pair	1,310,456 / 48.63%
Mapped reads, both in pair	2,575,398 / 95.58%
Mapped reads, singletons	47,948 / 1.78%
Secondary alignments	0
Supplementary alignments	253,744 / 9.42%
Read min/max/mean length	30 / 133 / 127.89
Duplicated reads (estimated)	1,958,775 / 72.69%
Duplication rate	63.69%
Clipped reads	1,047,445 / 38.87%

2.2. ACGT Content

Number/percentage of A's	93,025,985 / 30.04%
Number/percentage of C's	60,781,465 / 19.63%
Number/percentage of T's	92,894,552 / 30%
Number/percentage of G's	62,980,309 / 20.34%
Number/percentage of N's	3,940 / 0%

GC Percentage	39.96%
---------------	--------

2.3. Coverage

Mean	0.1001
Standard Deviation	1.5928

2.4. Mapping Quality

Mean Mapping Quality	52.65
----------------------	-------

2.5. Insert size

Mean	875,572.99
Standard Deviation	8,627,120.32
P25/Median/P75	145 / 205 / 296

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	3,174,625
Insertions	31,673
Mapped reads with at least one insertion	1.17%
Deletions	68,905
Mapped reads with at least one deletion	2.56%
Homopolymer indels	42.81%

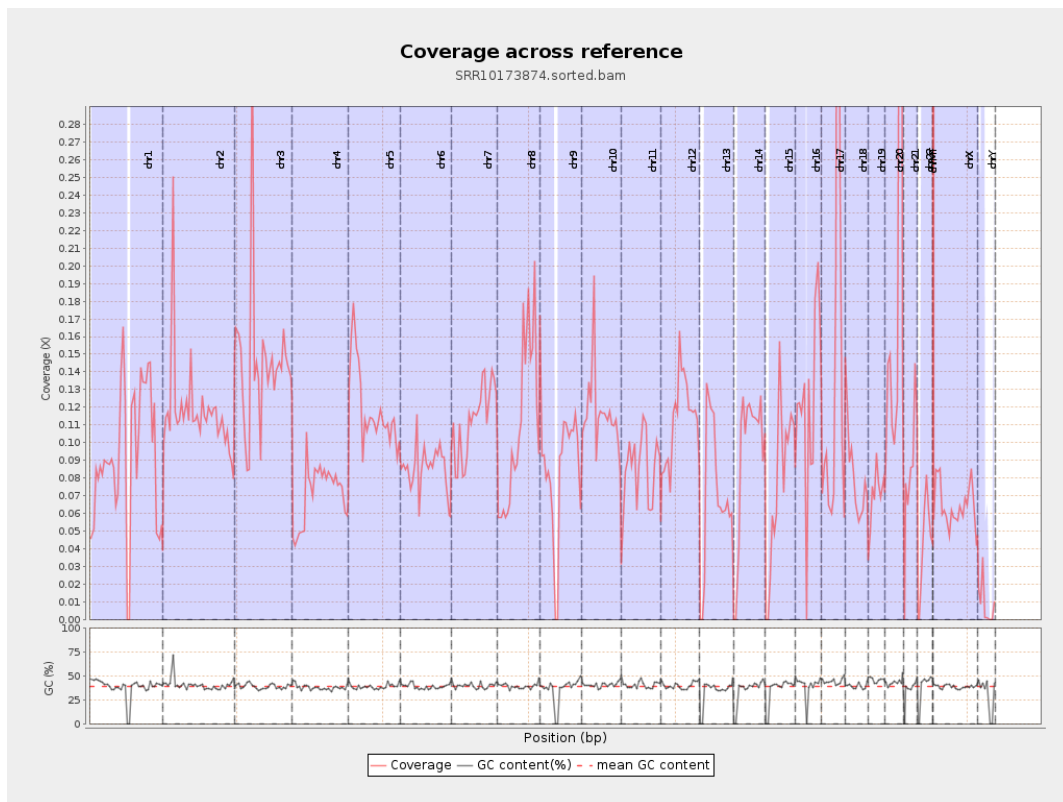
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

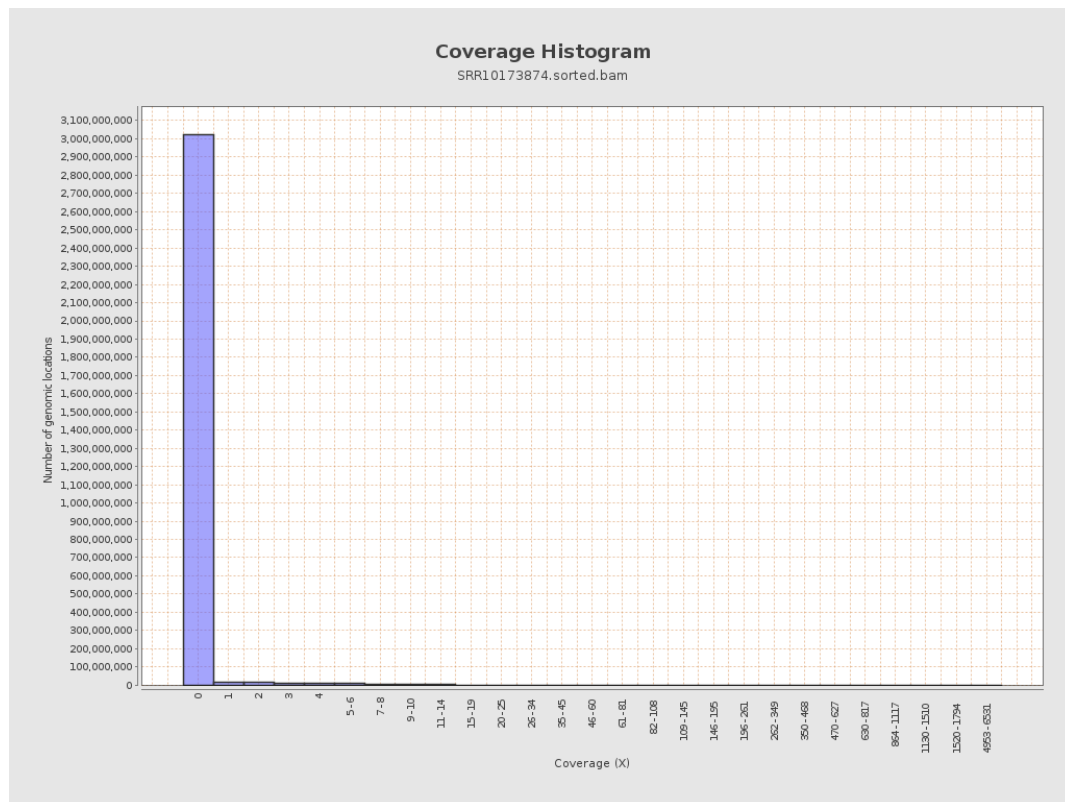
		bases	coverage	deviation
chr1	249250621	22861310	0.0917	1.0582
chr2	243199373	28458226	0.117	4.6123
chr3	198022430	28513541	0.144	1.0394
chr4	191154276	13701773	0.0717	0.799
chr5	180915260	21448644	0.1186	0.9303
chr6	171115067	14670958	0.0857	0.8532
chr7	159138663	17950396	0.1128	1.1388
chr8	146364022	15961338	0.1091	1.091
chr9	141213431	11804852	0.0836	0.9128
chr10	135534747	15785226	0.1165	1.3122
chr11	135006516	11428545	0.0847	0.7885
chr12	133851895	15199963	0.1136	0.9103
chr13	115169878	8104918	0.0704	0.7207
chr14	107349540	10132376	0.0944	0.8276
chr15	102531392	7794038	0.076	0.7453
chr16	90354753	10947577	0.1212	1.0811
chr17	81195210	13173619	0.1622	1.1428
chr18	78077248	6371099	0.0816	1.0891
chr19	59128983	4211417	0.0712	0.8703
chr20	63025520	13530349	0.2147	1.3193
chr21	48129895	4112051	0.0854	0.7986
chr22	51304566	2238071	0.0436	0.5377
chrMT	16571	882532	53.2576	44.8376
chrX	155270560	10041397	0.0647	0.6794

chrY	59373566	529316	0.0089	0.3719
------	----------	--------	--------	--------

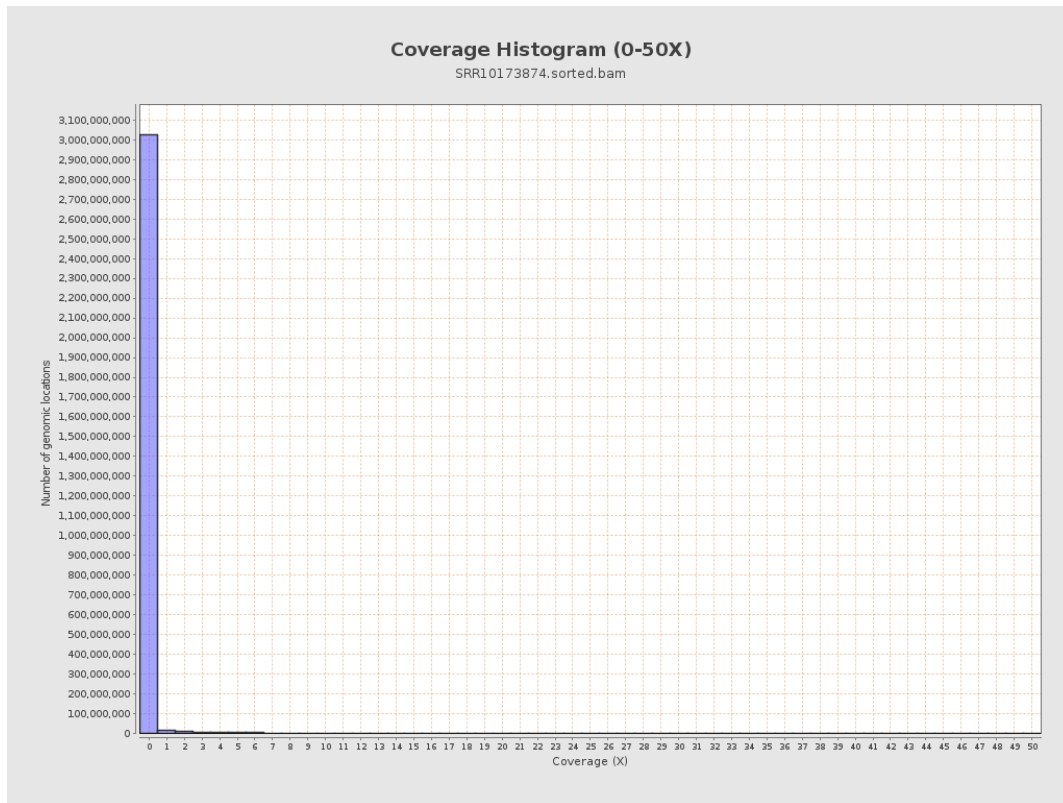
3. Results : Coverage across reference



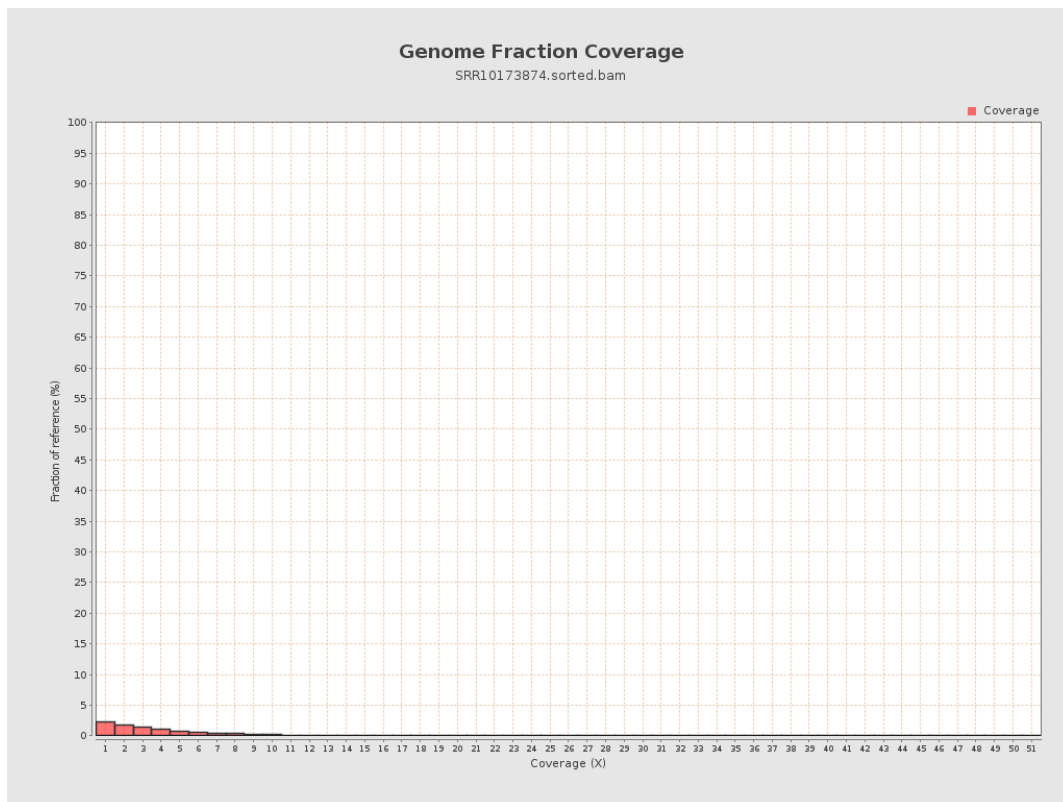
4. Results : Coverage Histogram



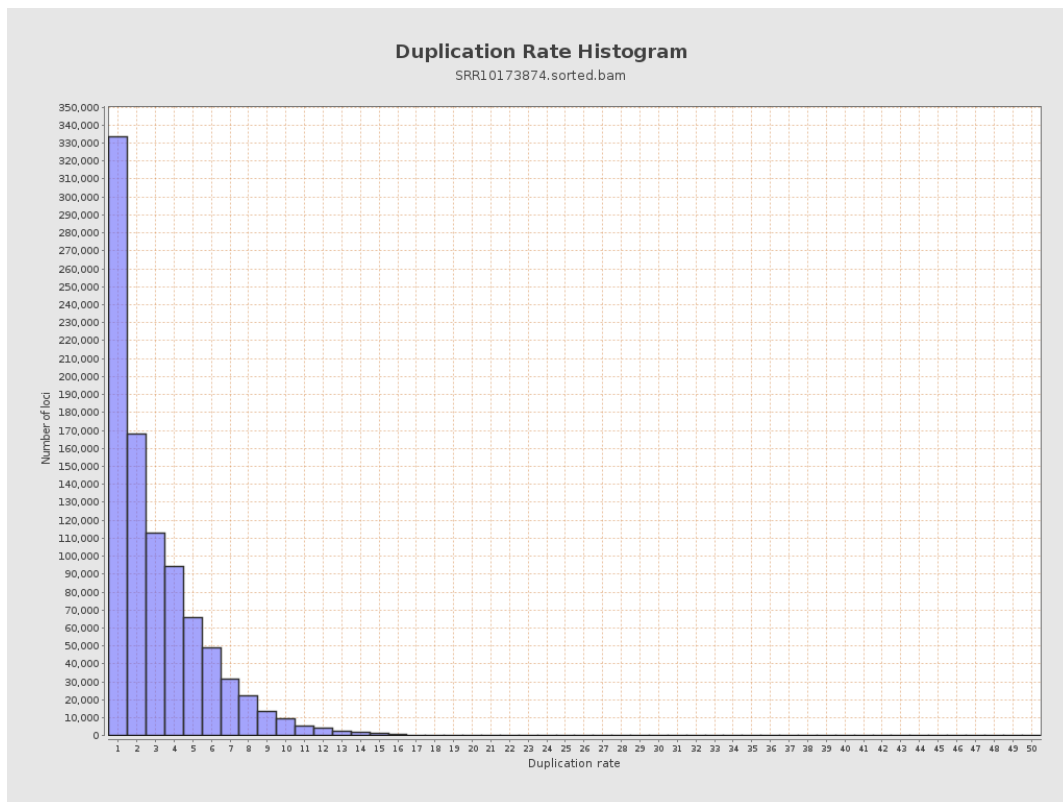
5. Results : Coverage Histogram (0-50X)



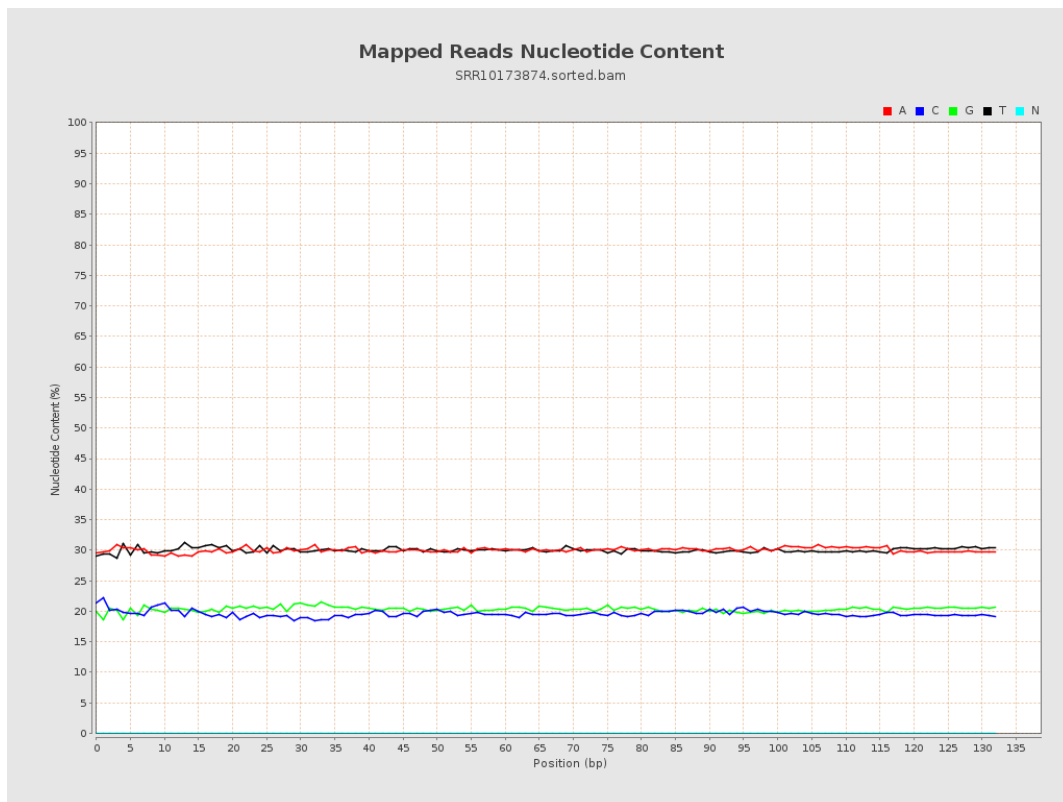
6. Results : Genome Fraction Coverage



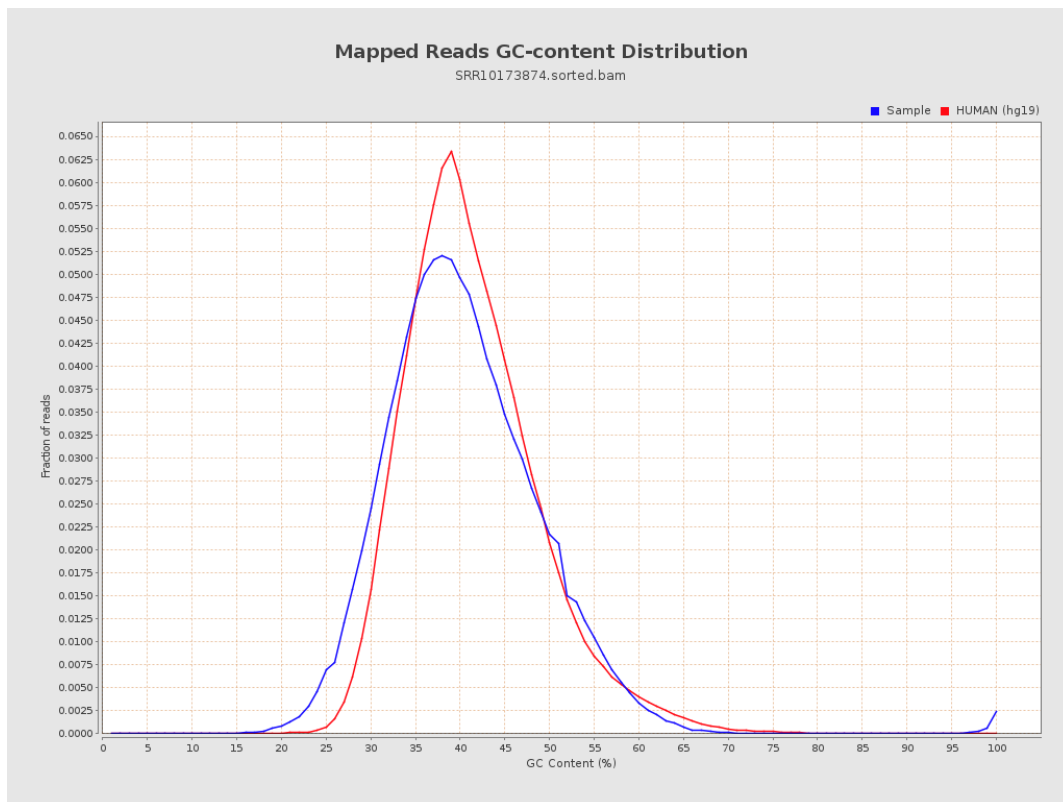
7. Results : Duplication Rate Histogram



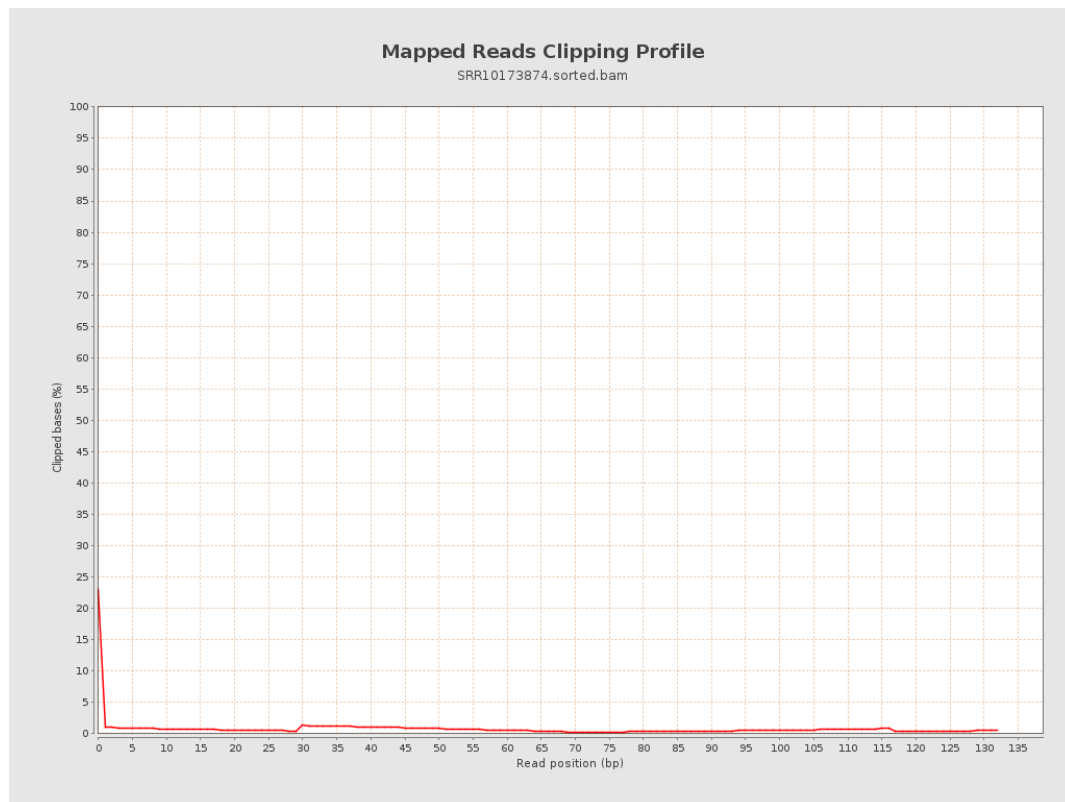
8. Results : Mapped Reads Nucleotide Content



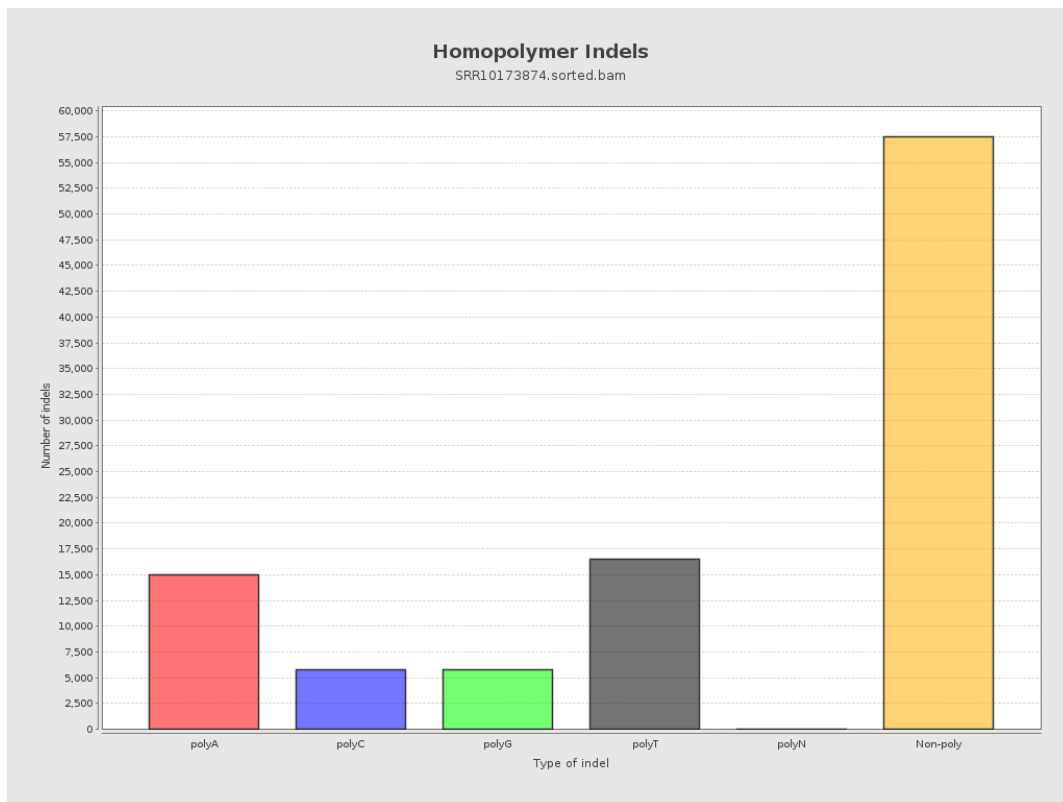
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



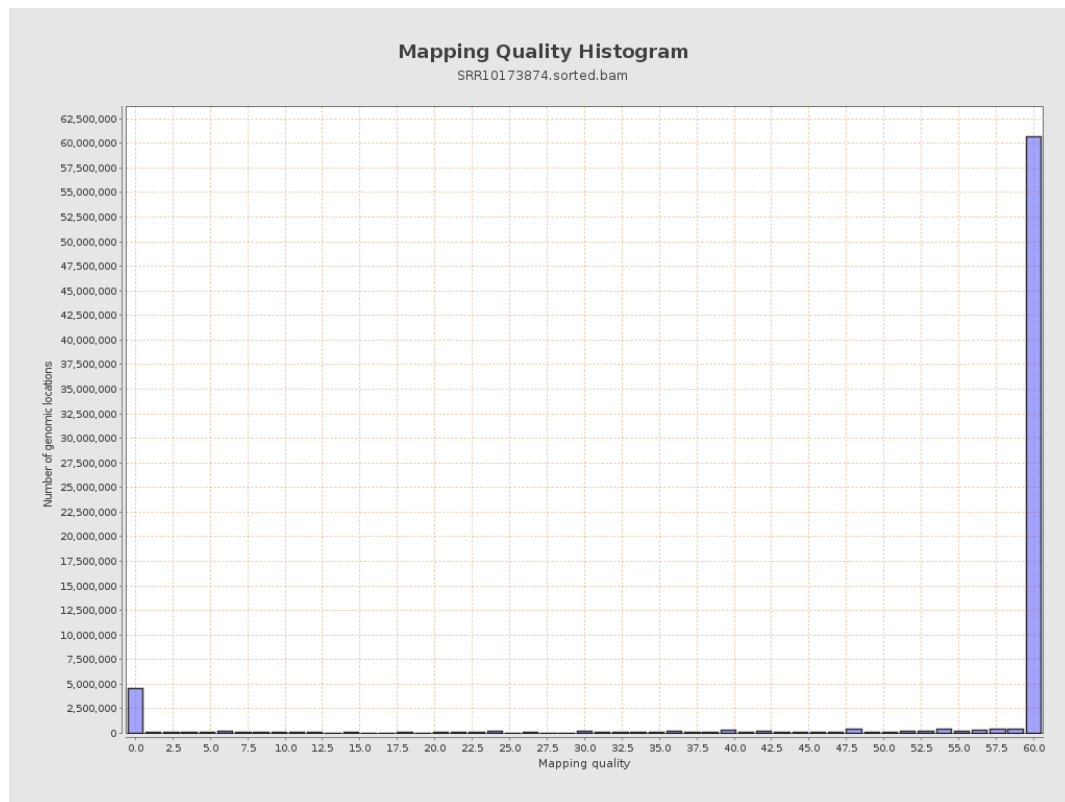
11. Results : Homopolymer Indels



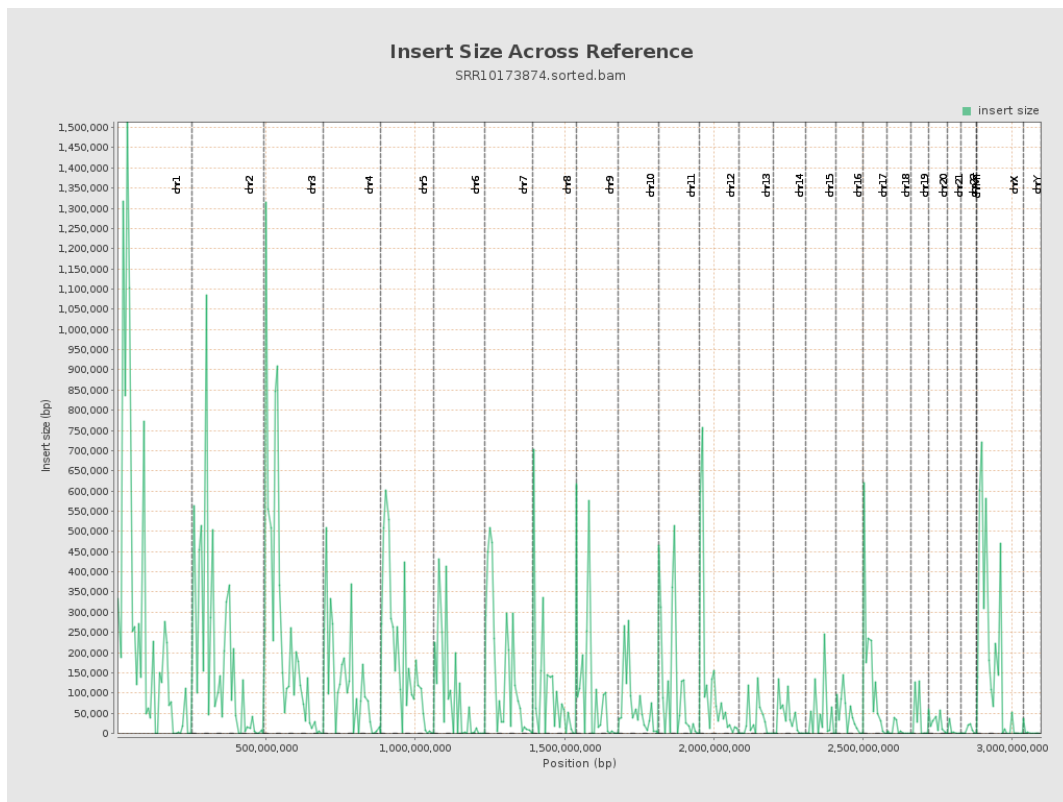
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

