

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 03:10:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504672.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_SRR504672 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504672_1.fastq.gz SRR504672_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 03:10:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504672.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	91,259,870
Mapped reads	90,772,576 / 99.47%
Unmapped reads	487,294 / 0.53%
Mapped paired reads	90,772,576 / 99.47%
Mapped reads, first in pair	45,474,241 / 49.83%
Mapped reads, second in pair	45,298,335 / 49.64%
Mapped reads, both in pair	90,551,326 / 99.22%
Mapped reads, singletons	221,250 / 0.24%
Secondary alignments	0
Supplementary alignments	1,108,427 / 1.21%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	40,992,721 / 44.92%
Duplication rate	25.73%
Clipped reads	28,925,317 / 31.7%

2.2. ACGT Content

Number/percentage of A's	2,544,311,389 / 30.17%
Number/percentage of C's	1,667,210,343 / 19.77%
Number/percentage of T's	2,571,874,727 / 30.5%
Number/percentage of G's	1,643,866,341 / 19.5%
Number/percentage of N's	4,692,219 / 0.06%

GC Percentage	39.27%
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2.3. Coverage

Mean	2.726
Standard Deviation	344.4743

2.4. Mapping Quality

Mean Mapping Quality	53.06
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2.5. Insert size

Mean	30,838.5
Standard Deviation	1,641,719.82
P25/Median/P75	97 / 148 / 221

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	83,763,640
Insertions	2,648,558
Mapped reads with at least one insertion	2.85%
Deletions	2,814,240
Mapped reads with at least one deletion	3.02%
Homopolymer indels	37.93%

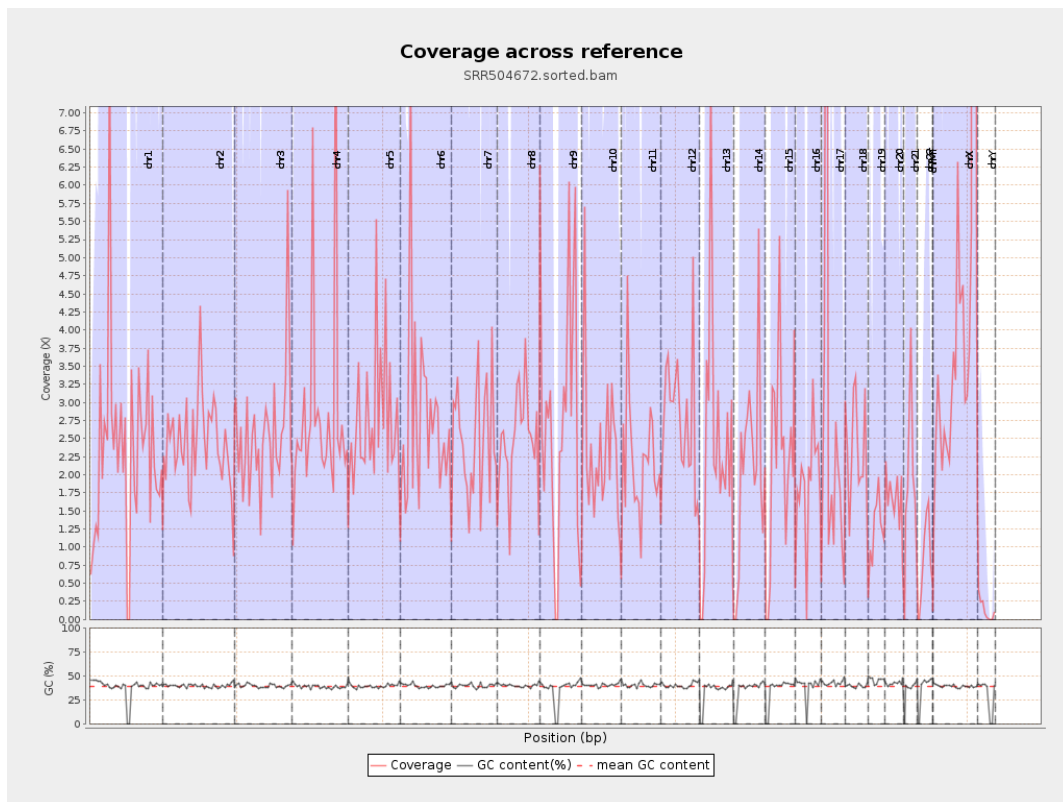
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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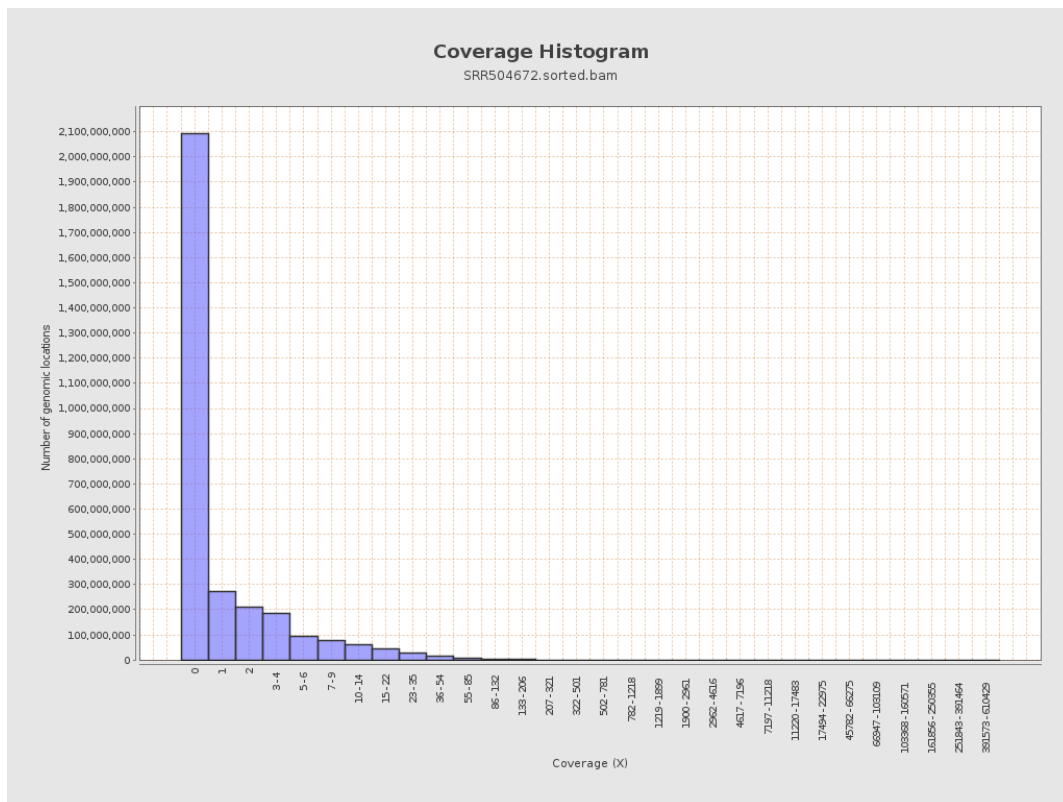
		bases	coverage	deviation
chr1	249250621	581396552	2.3326	34.0508
chr2	243199373	591826319	2.4335	14.015
chr3	198022430	505099998	2.5507	24.8
chr4	191154276	540762211	2.8289	46.5298
chr5	180915260	492201760	2.7206	16.4455
chr6	171115067	468419413	2.7375	28.1073
chr7	159138663	392980939	2.4694	13.8141
chr8	146364022	363401196	2.4829	8.9759
chr9	141213431	370296988	2.6223	32.976
chr10	135534747	318302517	2.3485	36.2287
chr11	135006516	298573859	2.2116	12.9928
chr12	133851895	369543286	2.7608	30.1424
chr13	115169878	274210419	2.3809	42.8768
chr14	107349540	222767117	2.0752	14.1104
chr15	102531392	218307185	2.1292	15.7485
chr16	90354753	165678362	1.8336	9.1173
chr17	81195210	242137061	2.9822	129.3209
chr18	78077248	181471474	2.3243	11.7795
chr19	59128983	74740287	1.264	6.3812
chr20	63025520	106299121	1.6866	6.6879
chr21	48129895	87671719	1.8216	10.9892
chr22	51304566	42881857	0.8358	3.2643
chrMT	16571	1949	0.1176	0.7467
chrX	155270560	1522397617	9.8048	1,531.3464

chrY	59373566	7452708	0.1255	1.7077
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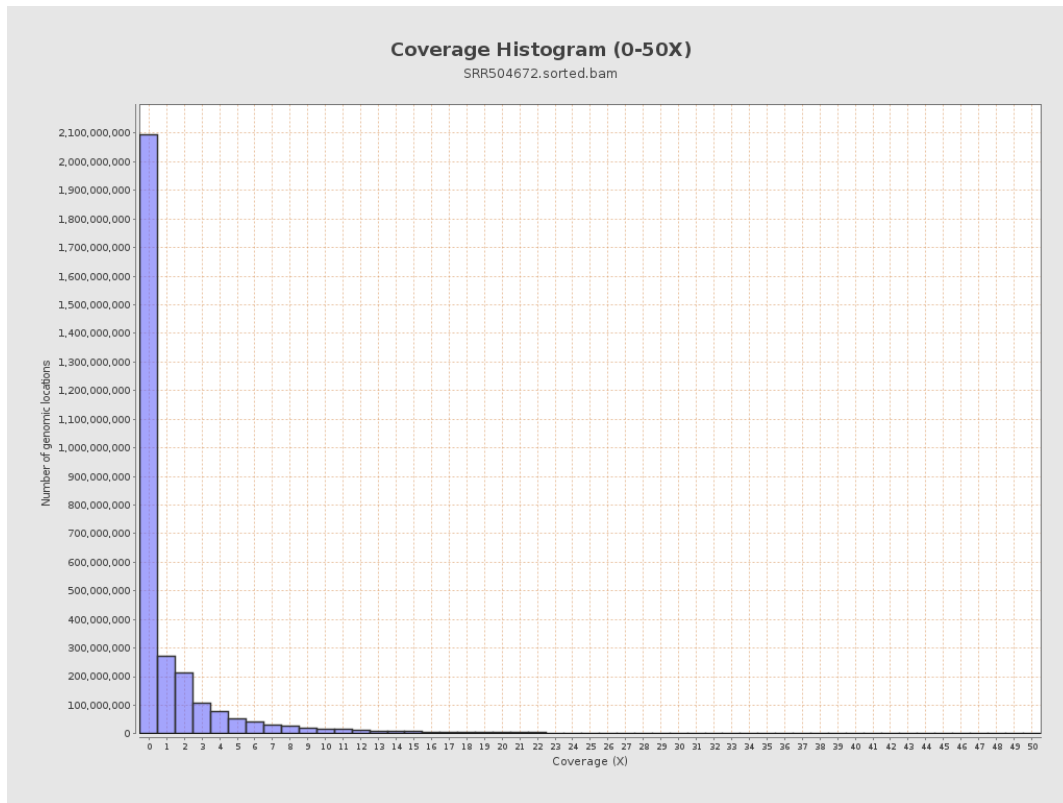
3. Results : Coverage across reference



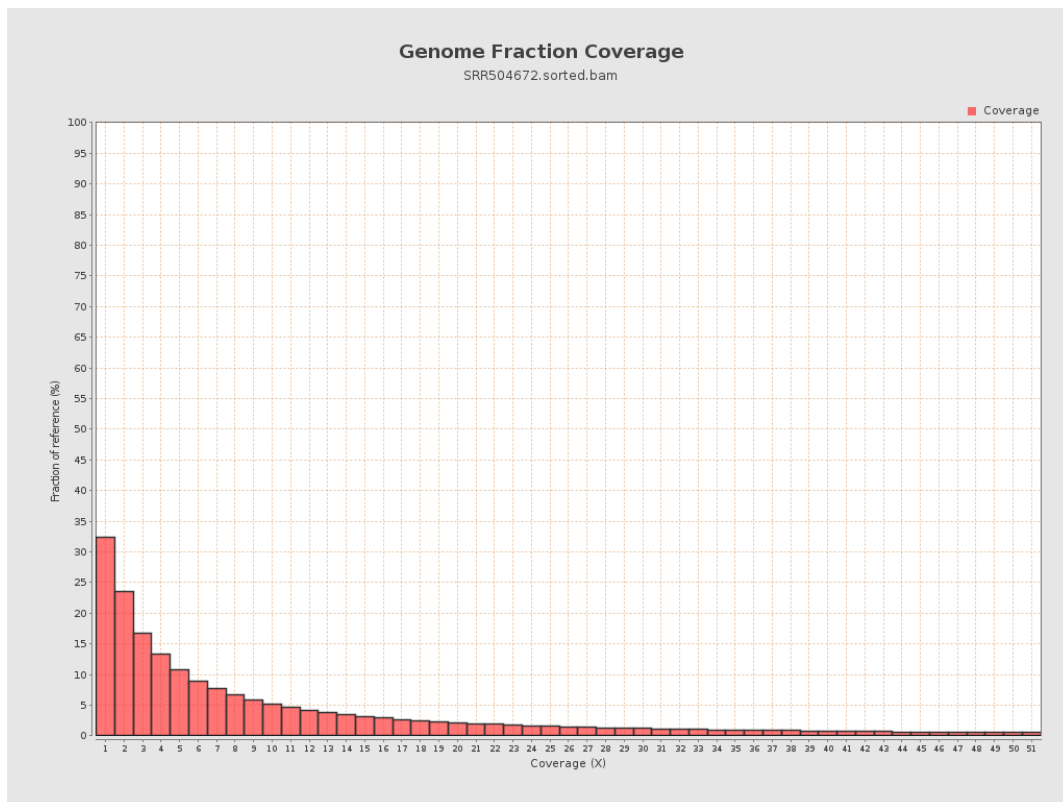
4. Results : Coverage Histogram



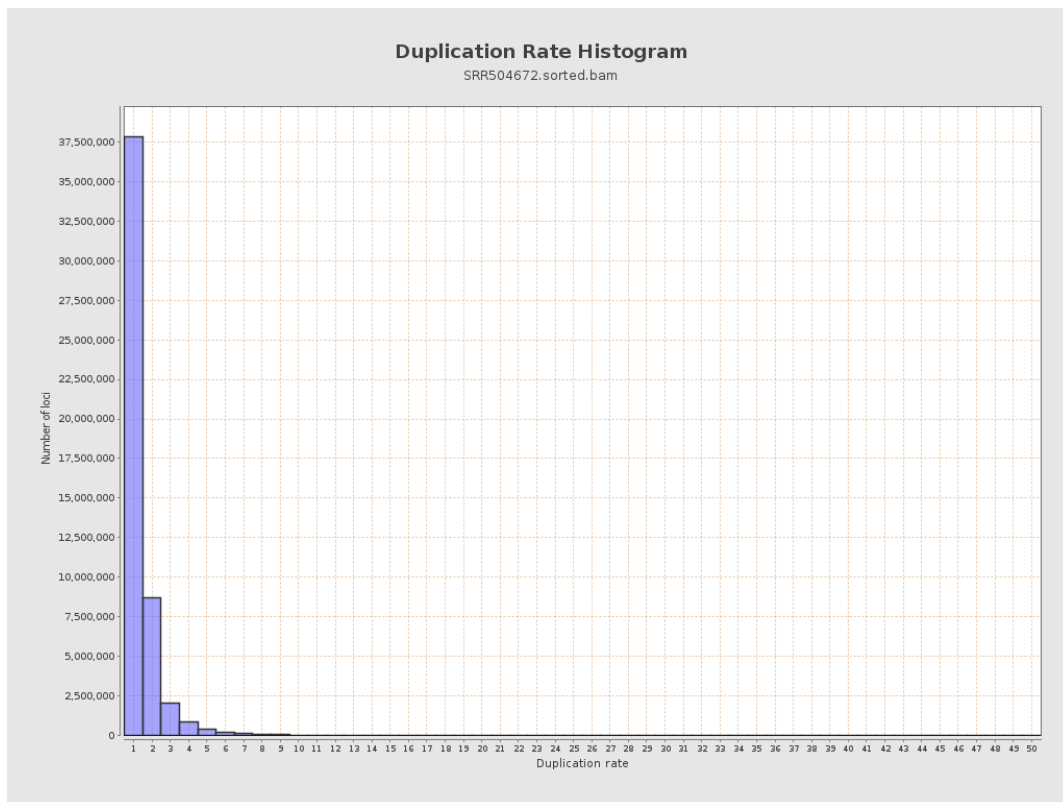
5. Results : Coverage Histogram (0-50X)



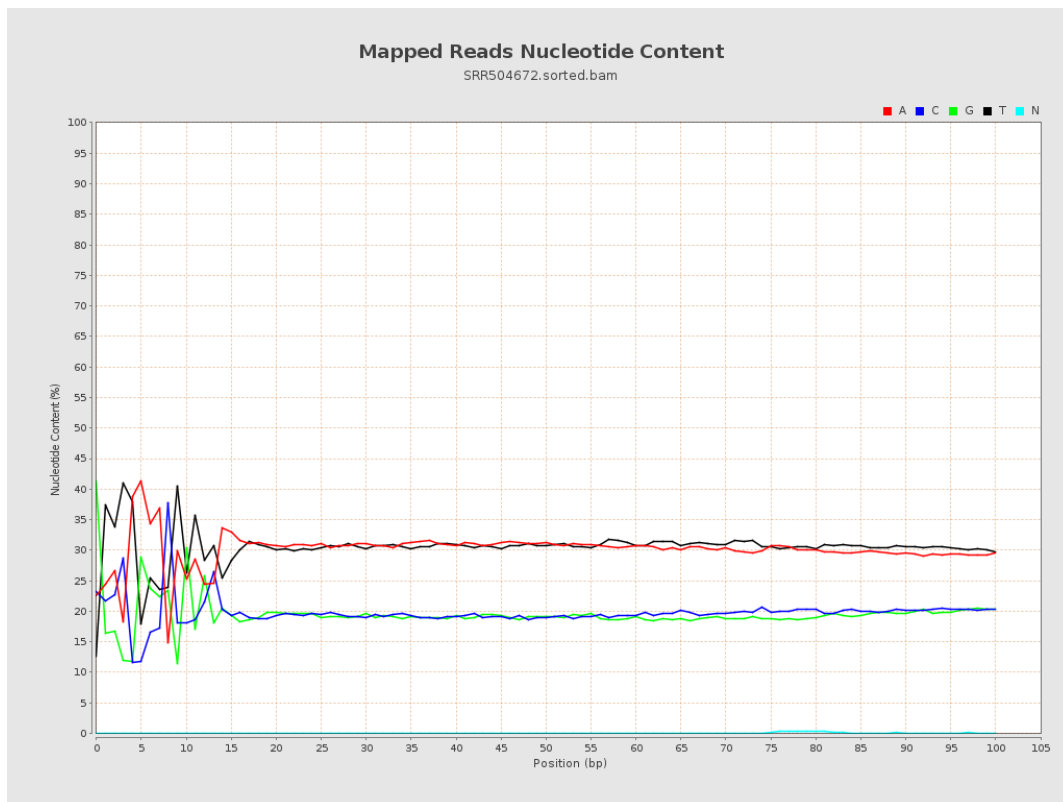
6. Results : Genome Fraction Coverage



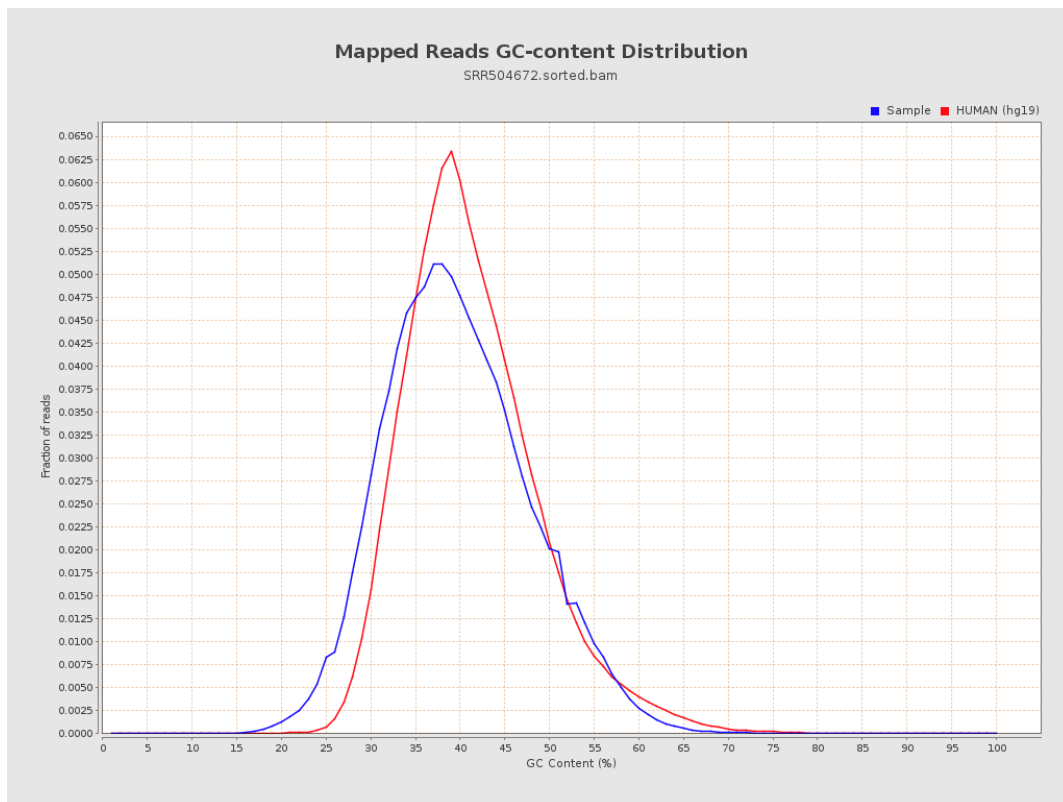
7. Results : Duplication Rate Histogram



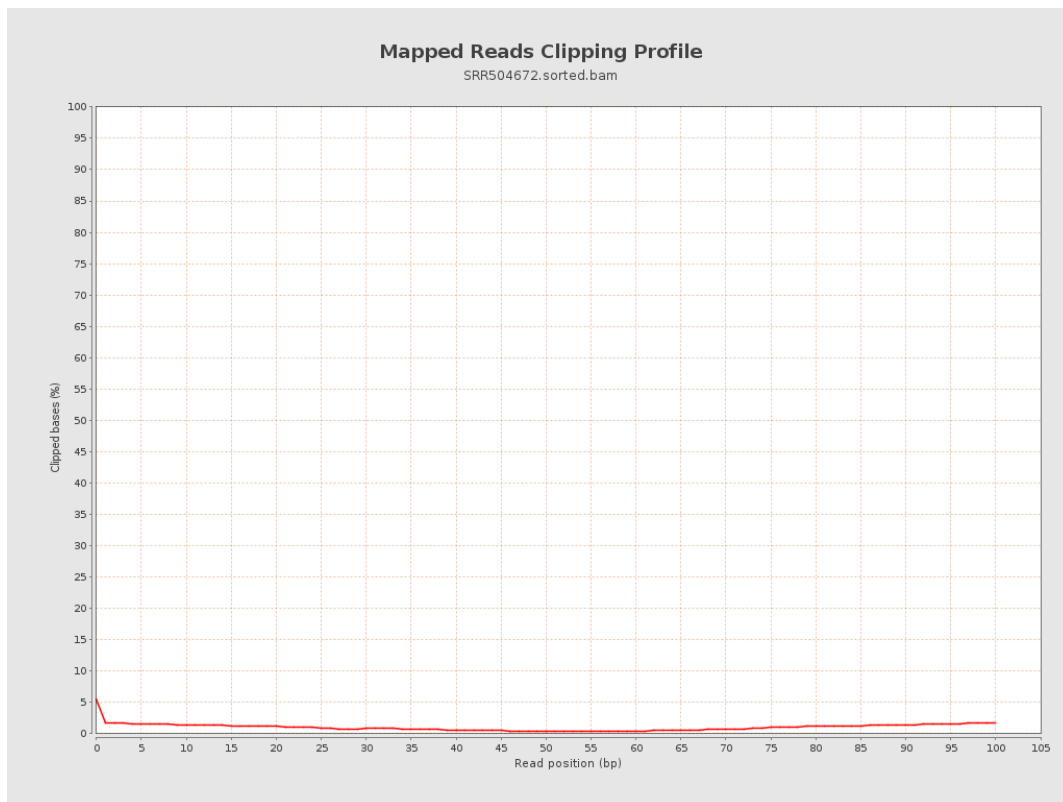
8. Results : Mapped Reads Nucleotide Content



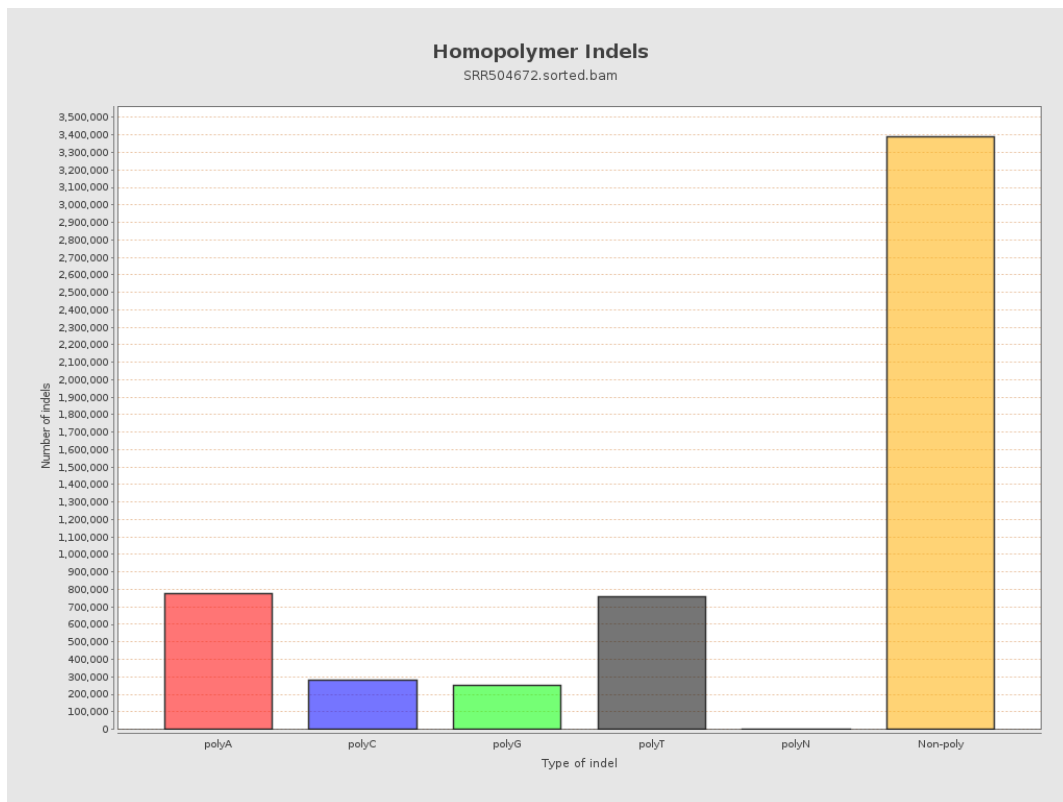
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



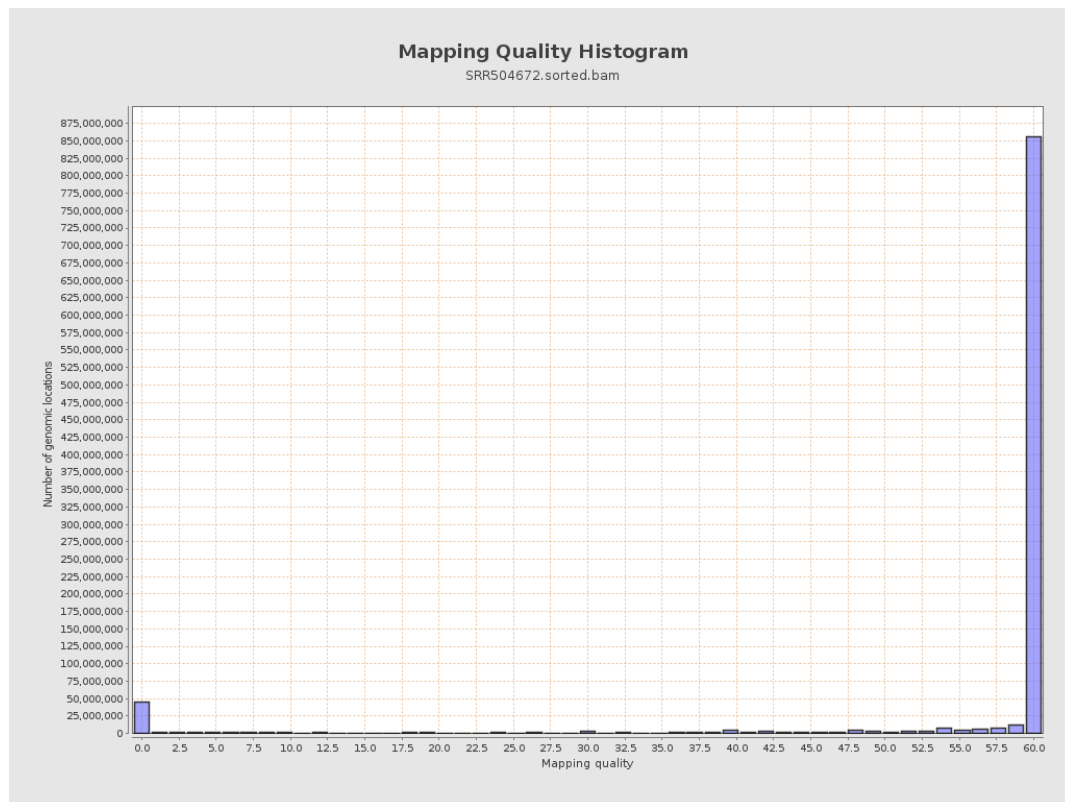
11. Results : Homopolymer Indels



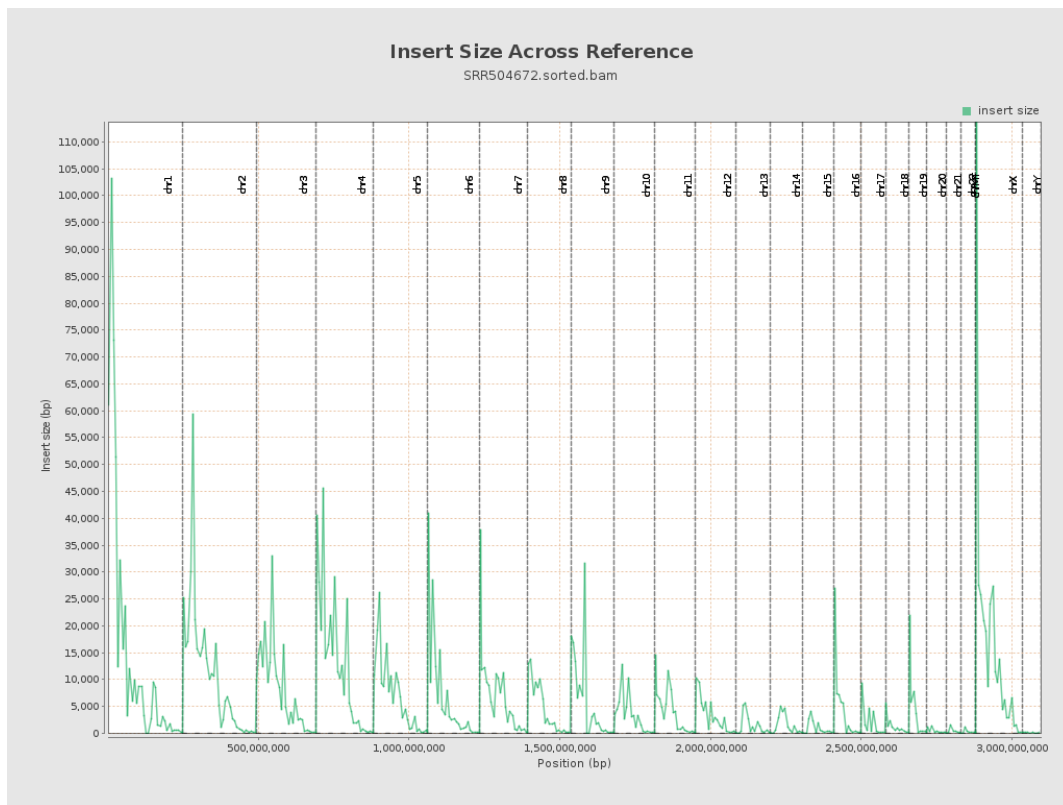
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

