

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:27:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472537.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_SRR3472537 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472537_1.fastq.gz SRR3472537_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:27:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472537.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,075,938
Mapped reads	17,742,293 / 98.15%
Unmapped reads	333,645 / 1.85%
Mapped paired reads	17,742,293 / 98.15%
Mapped reads, first in pair	8,922,360 / 49.36%
Mapped reads, second in pair	8,819,933 / 48.79%
Mapped reads, both in pair	17,573,700 / 97.22%
Mapped reads, singletons	168,593 / 0.93%
Secondary alignments	0
Supplementary alignments	61,199 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,218,407 / 62.06%
Duplication rate	46.53%
Clipped reads	1,397,626 / 7.73%

2.2. ACGT Content

Number/percentage of A's	487,276,404 / 27.92%
Number/percentage of C's	387,749,078 / 22.22%
Number/percentage of T's	483,647,020 / 27.72%
Number/percentage of G's	386,059,807 / 22.12%
Number/percentage of N's	269,749 / 0.02%

GC Percentage	44.34%
---------------	--------

2.3. Coverage

Mean	0.5638
Standard Deviation	19.3133

2.4. Mapping Quality

Mean Mapping Quality	54.89
----------------------	-------

2.5. Insert size

Mean	27,558.57
Standard Deviation	1,626,439.6
P25/Median/P75	175 / 241 / 323

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	10,873,154
Insertions	99,362
Mapped reads with at least one insertion	0.55%
Deletions	100,935
Mapped reads with at least one deletion	0.56%
Homopolymer indels	45.09%

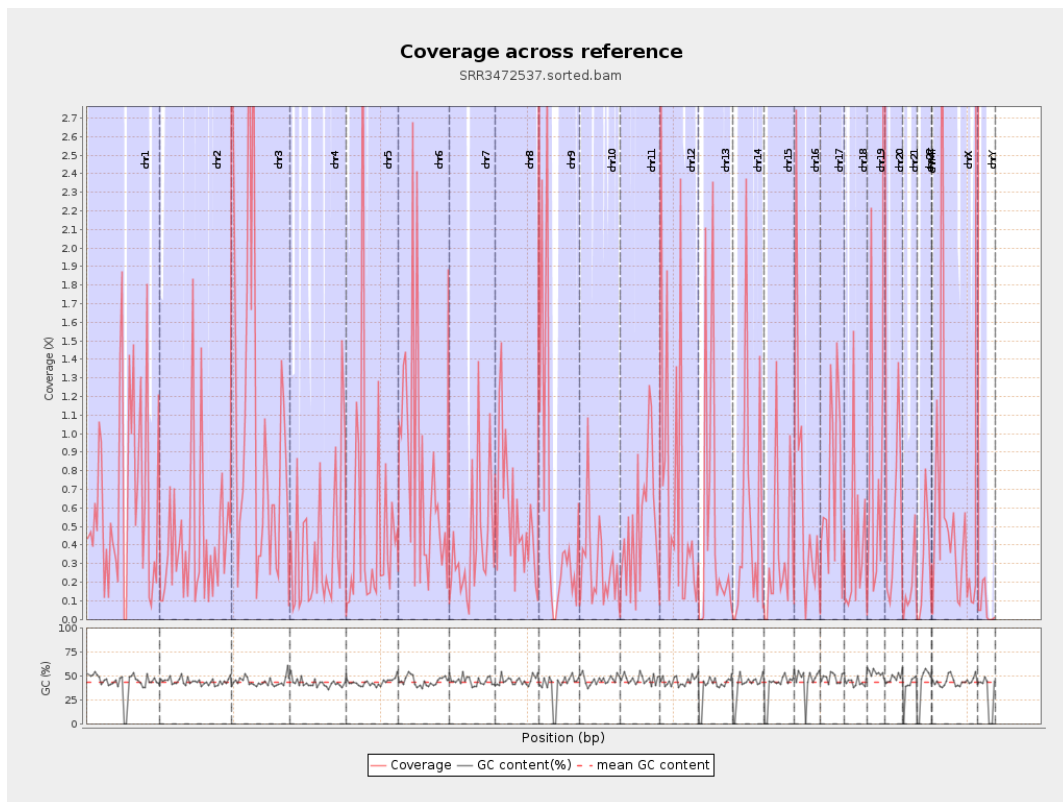
2.7. Chromosome stats

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

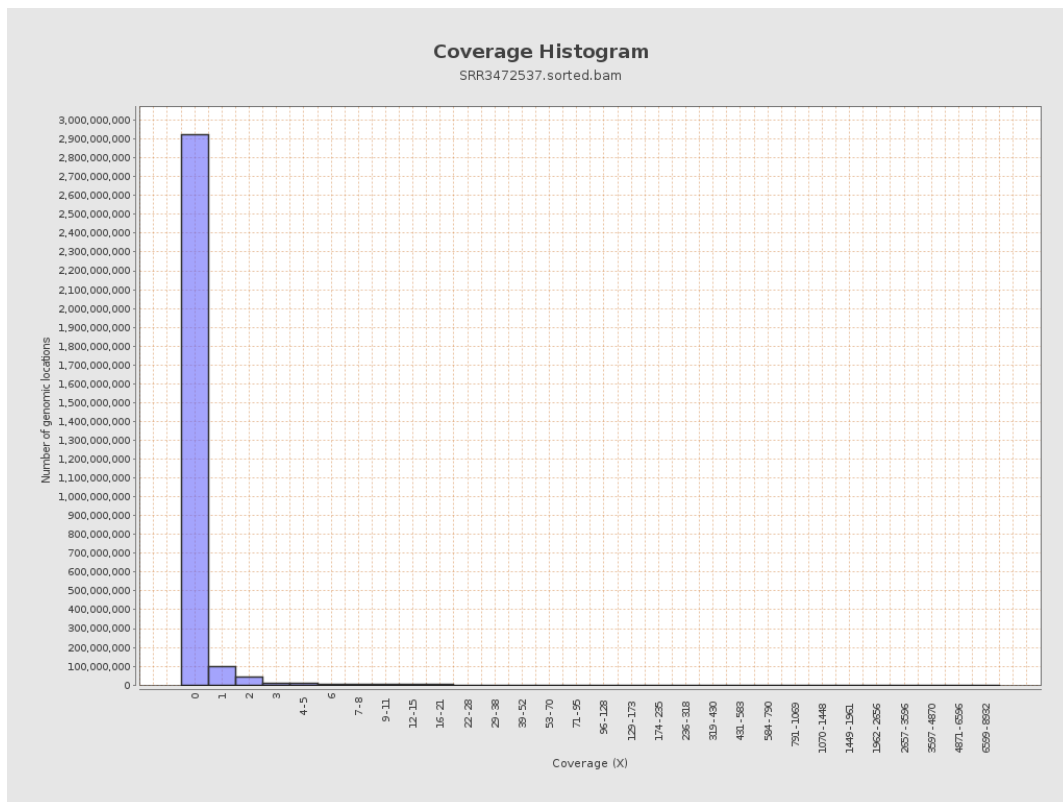
		bases	coverage	deviation
chr1	249250621	162361199	0.6514	19.5338
chr2	243199373	100835887	0.4146	15.2447
chr3	198022430	212613147	1.0737	25.406
chr4	191154276	74277084	0.3886	14.0597
chr5	180915260	96070295	0.531	18.6635
chr6	171115067	138724015	0.8107	25.092
chr7	159138663	64191714	0.4034	11.6732
chr8	146364022	81401281	0.5562	16.6503
chr9	141213431	83303175	0.5899	13.9295
chr10	135534747	40123778	0.296	13.6717
chr11	135006516	68834239	0.5099	17.9237
chr12	133851895	101370065	0.7573	22.395
chr13	115169878	55238888	0.4796	25.1064
chr14	107349540	55582858	0.5178	19.9488
chr15	102531392	36797512	0.3589	10.9052
chr16	90354753	53034070	0.587	19.8479
chr17	81195210	57337787	0.7062	17.2483
chr18	78077248	30426603	0.3897	17.5193
chr19	59128983	55749502	0.9428	32.7491
chr20	63025520	38555834	0.6117	20.5829
chr21	48129895	8677751	0.1803	6.8881
chr22	51304566	14417164	0.281	8.1238
chrMT	16571	4978	0.3004	0.8479
chrX	155270560	111182259	0.7161	29.3311

chrY	59373566	4131647	0.0696	2.8617
------	----------	---------	--------	--------

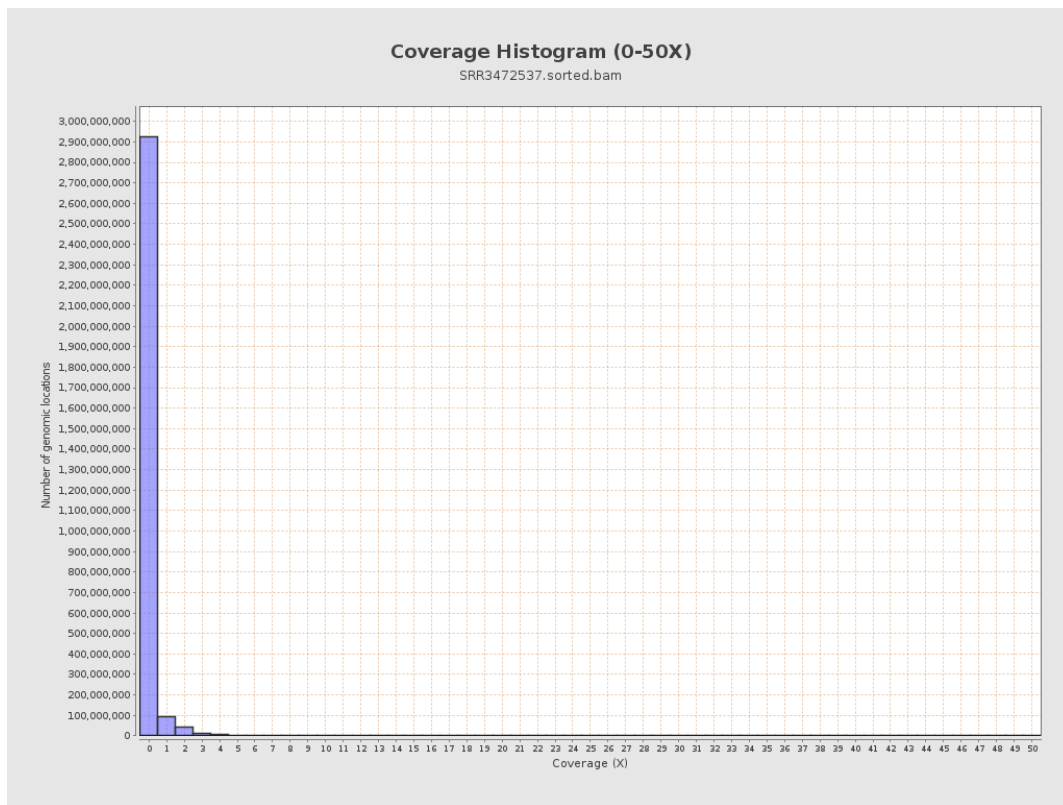
3. Results : Coverage across reference



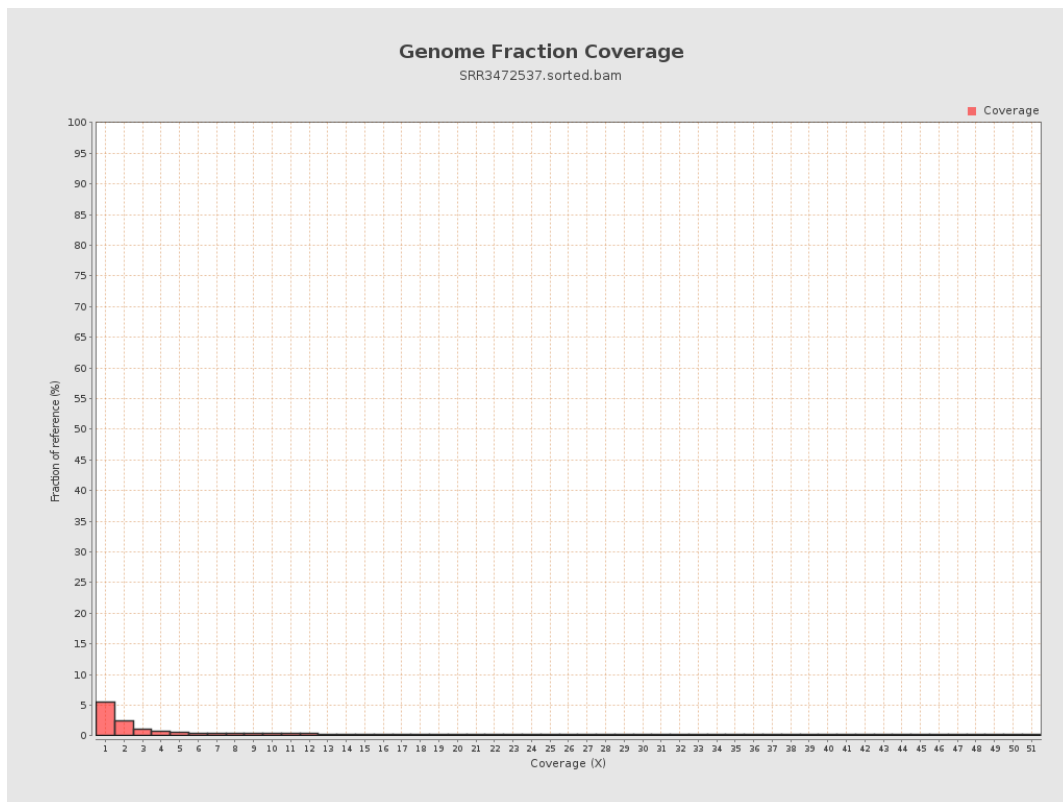
4. Results : Coverage Histogram



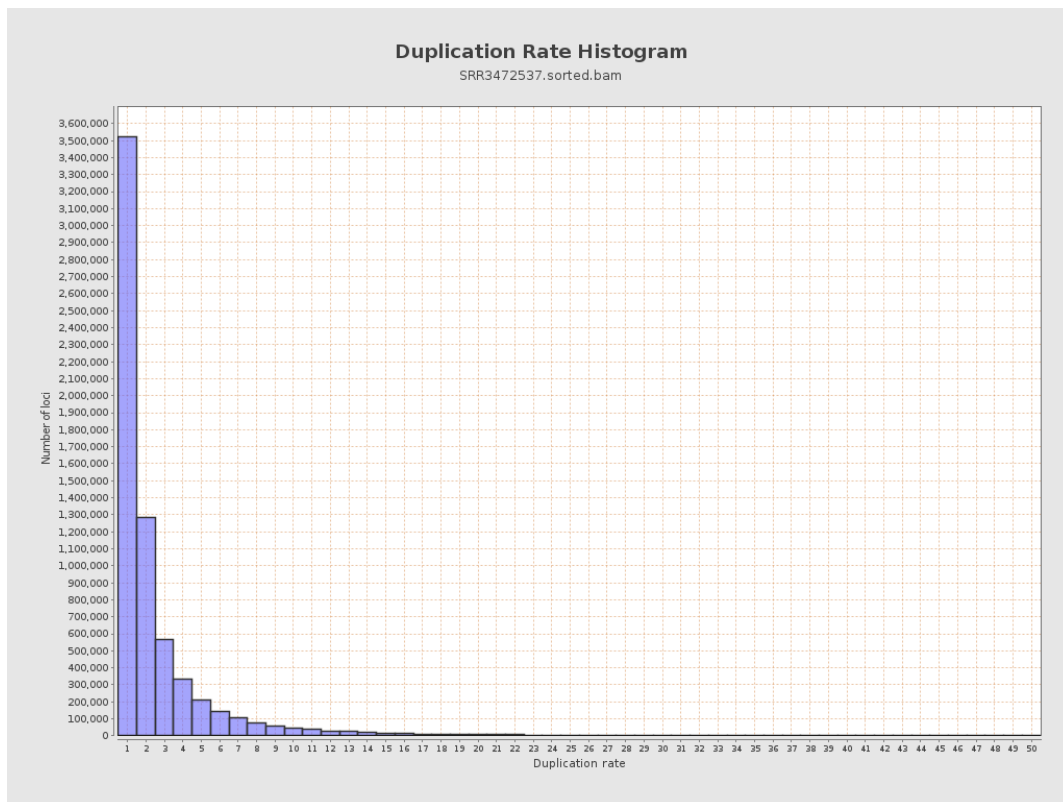
5. Results : Coverage Histogram (0-50X)



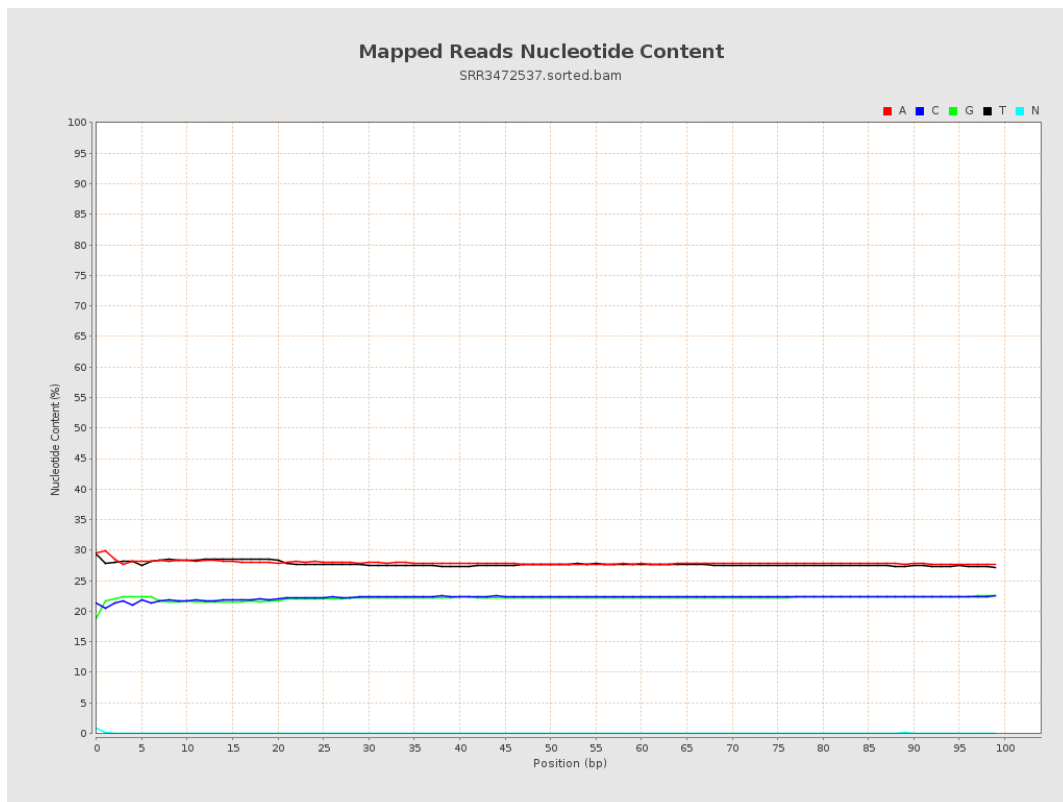
6. Results : Genome Fraction Coverage



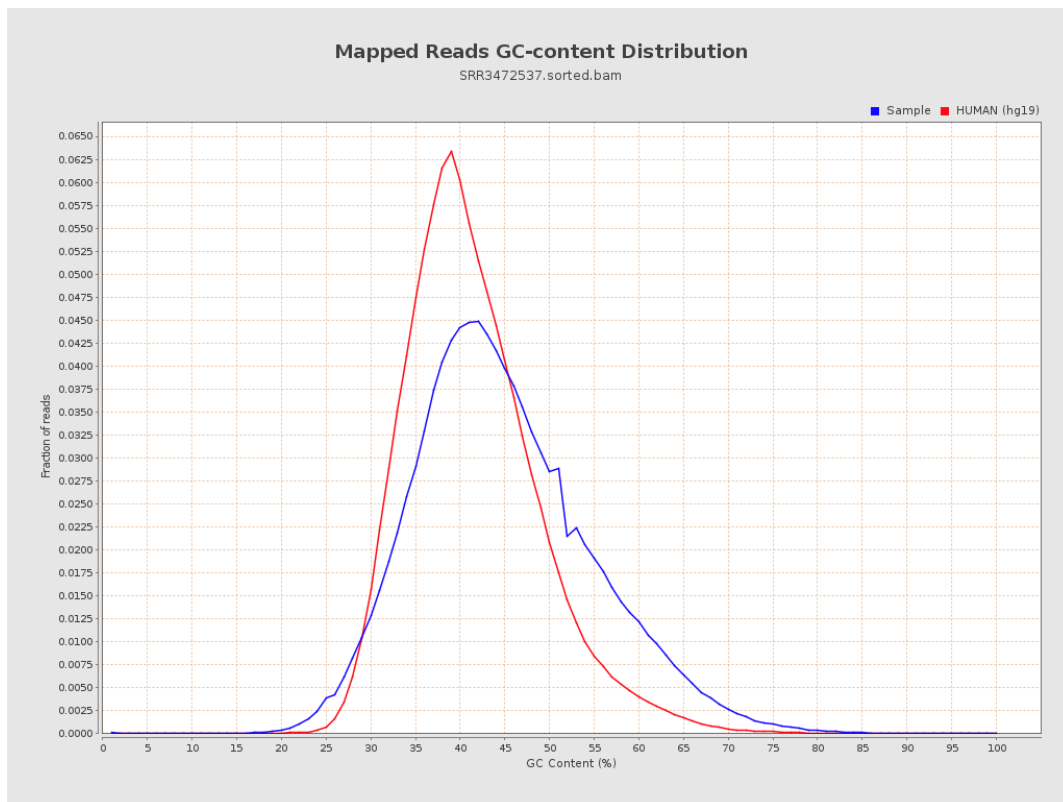
7. Results : Duplication Rate Histogram



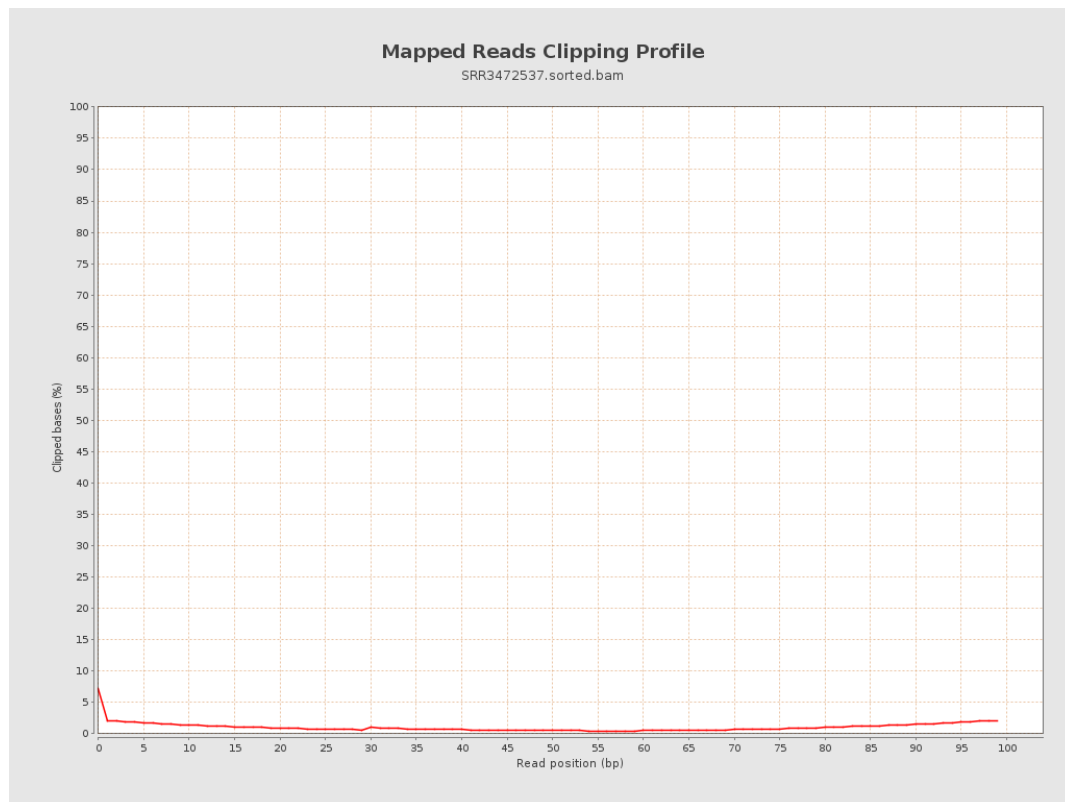
8. Results : Mapped Reads Nucleotide Content



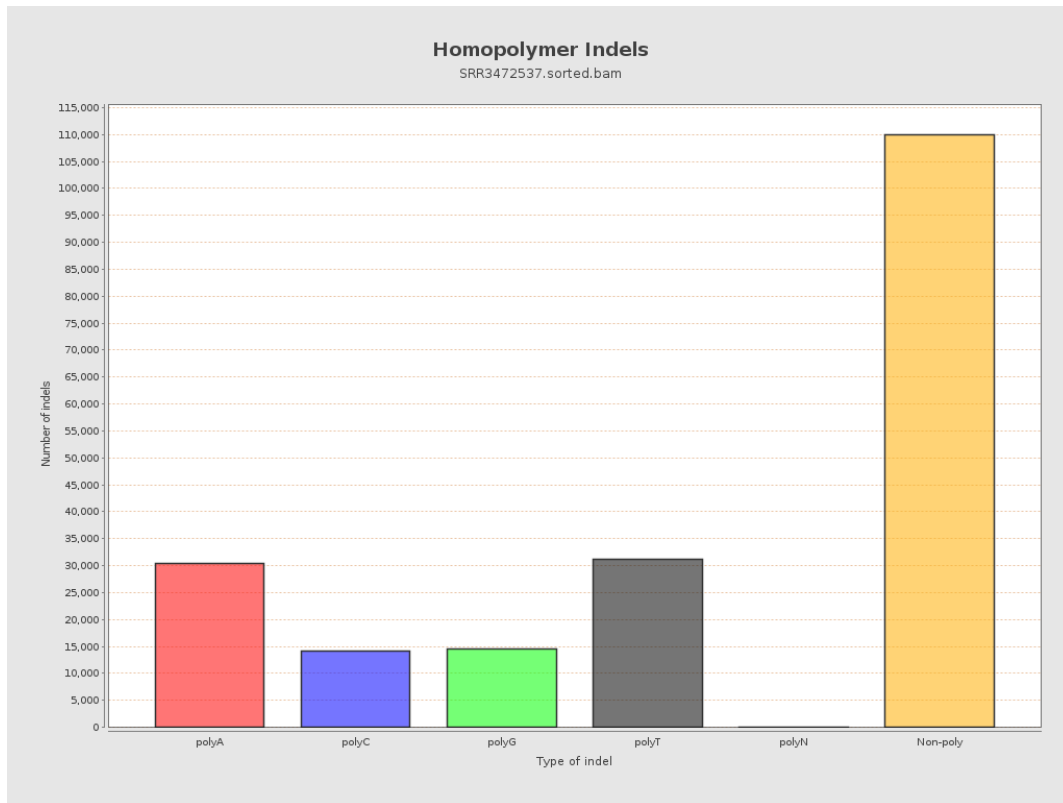
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



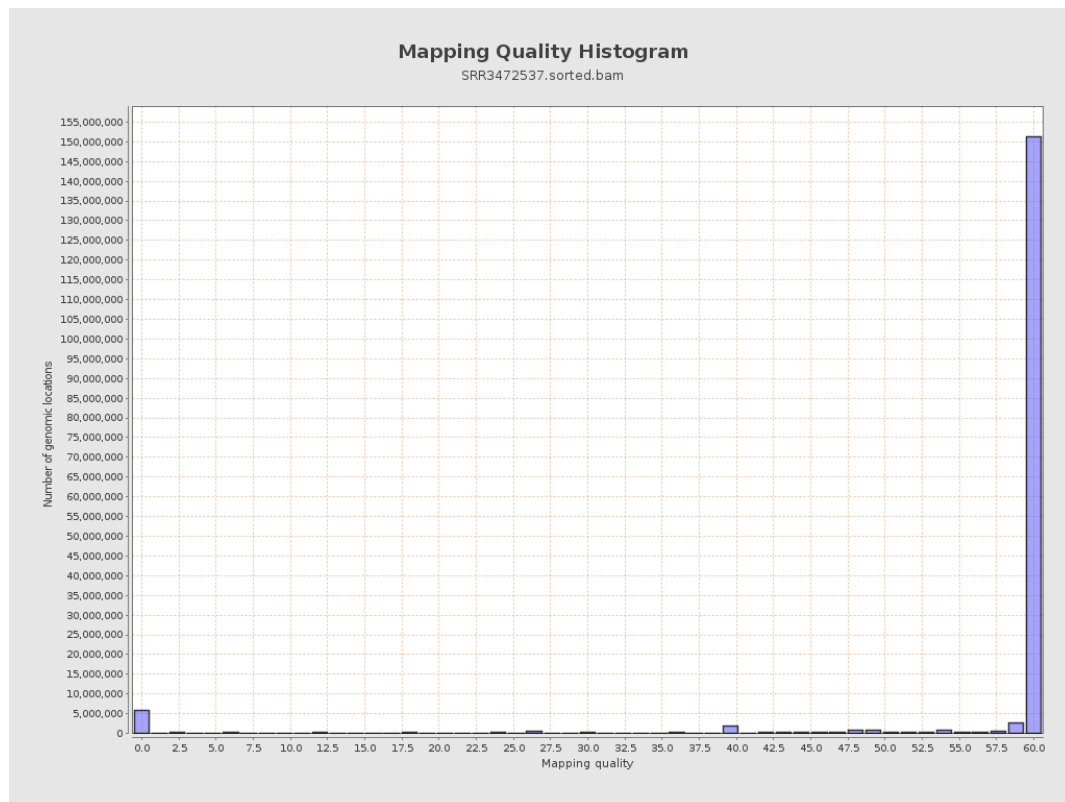
11. Results : Homopolymer Indels



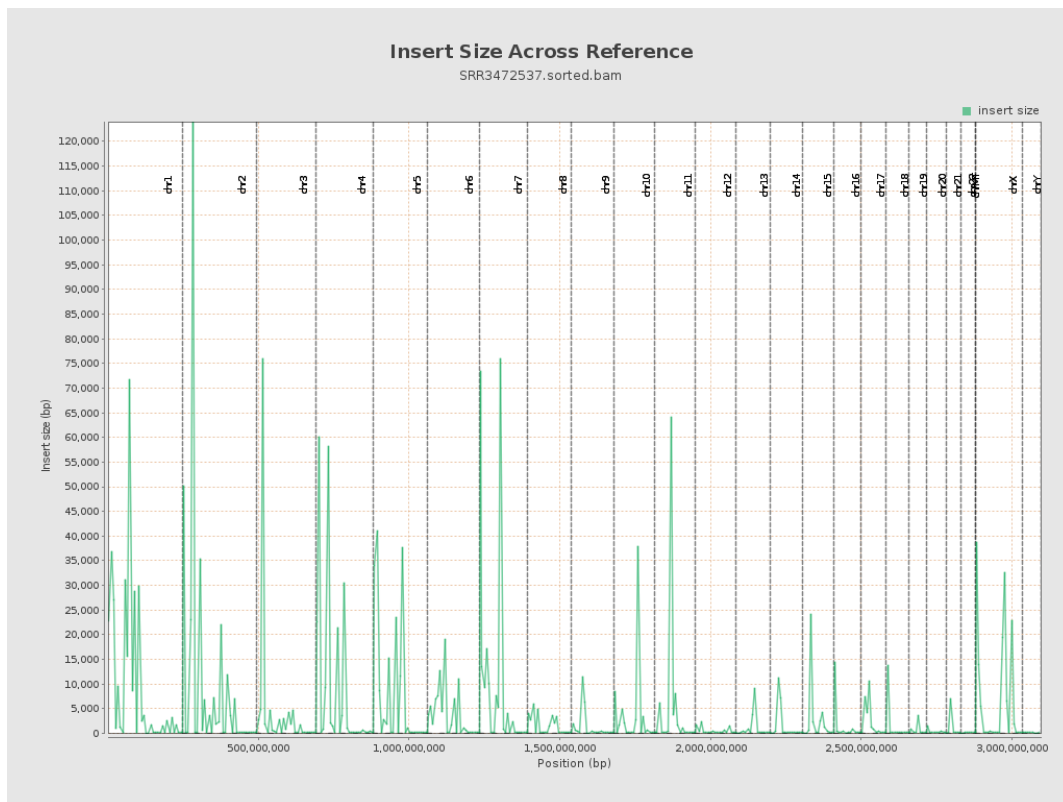
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

