

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 14:56:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472625.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_SRR3472625 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472625_1.fastq.gz SRR3472625_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 14:56:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472625.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,676,580
Mapped reads	18,532,119 / 99.23%
Unmapped reads	144,461 / 0.77%
Mapped paired reads	18,532,119 / 99.23%
Mapped reads, first in pair	9,285,605 / 49.72%
Mapped reads, second in pair	9,246,514 / 49.51%
Mapped reads, both in pair	18,438,708 / 98.73%
Mapped reads, singletons	93,411 / 0.5%
Secondary alignments	0
Supplementary alignments	86,443 / 0.46%
Read min/max/mean length	30 / 101 / 99.59
Duplicated reads (estimated)	13,168,000 / 70.51%
Duplication rate	50.64%
Clipped reads	1,304,560 / 6.99%

2.2. ACGT Content

Number/percentage of A's	480,750,836 / 26.41%
Number/percentage of C's	431,756,074 / 23.72%
Number/percentage of T's	482,723,608 / 26.51%
Number/percentage of G's	425,029,375 / 23.35%
Number/percentage of N's	329,355 / 0.02%

GC Percentage	47.06%
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2.3. Coverage

Mean	0.5882
Standard Deviation	25.9385

2.4. Mapping Quality

Mean Mapping Quality	54.76
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2.5. Insert size

Mean	19,839.21
Standard Deviation	1,427,565.29
P25/Median/P75	146 / 200 / 266

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	10,611,883
Insertions	96,362
Mapped reads with at least one insertion	0.52%
Deletions	86,909
Mapped reads with at least one deletion	0.46%
Homopolymer indels	45.14%

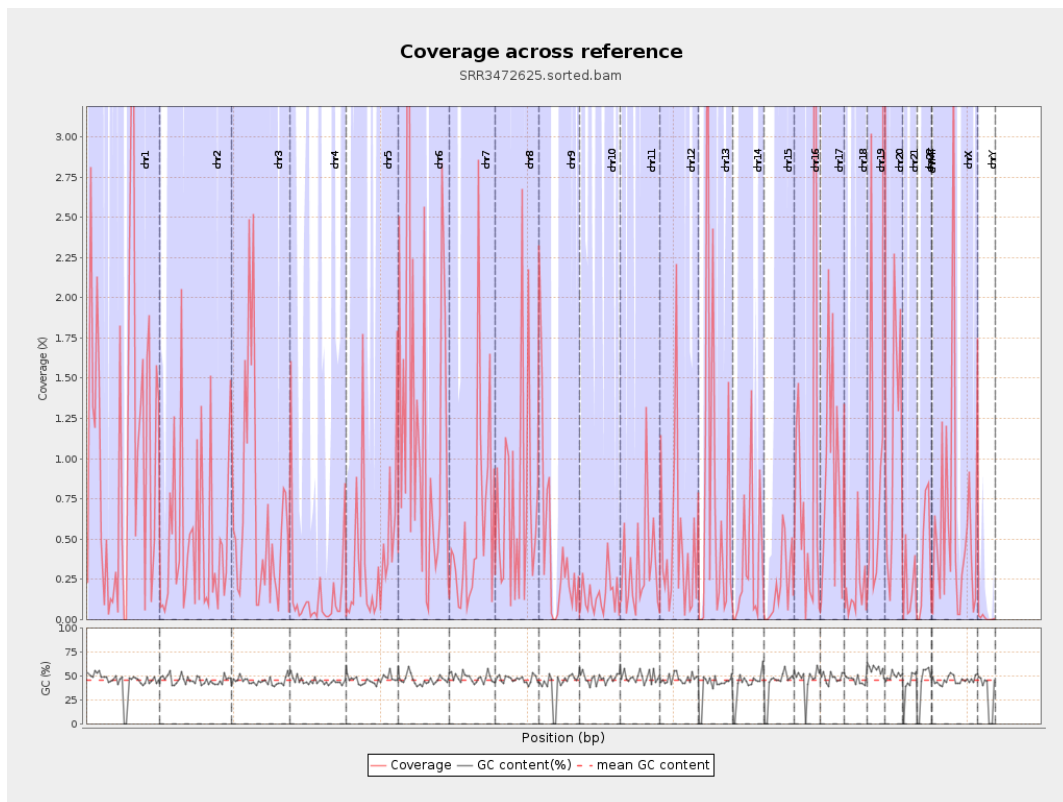
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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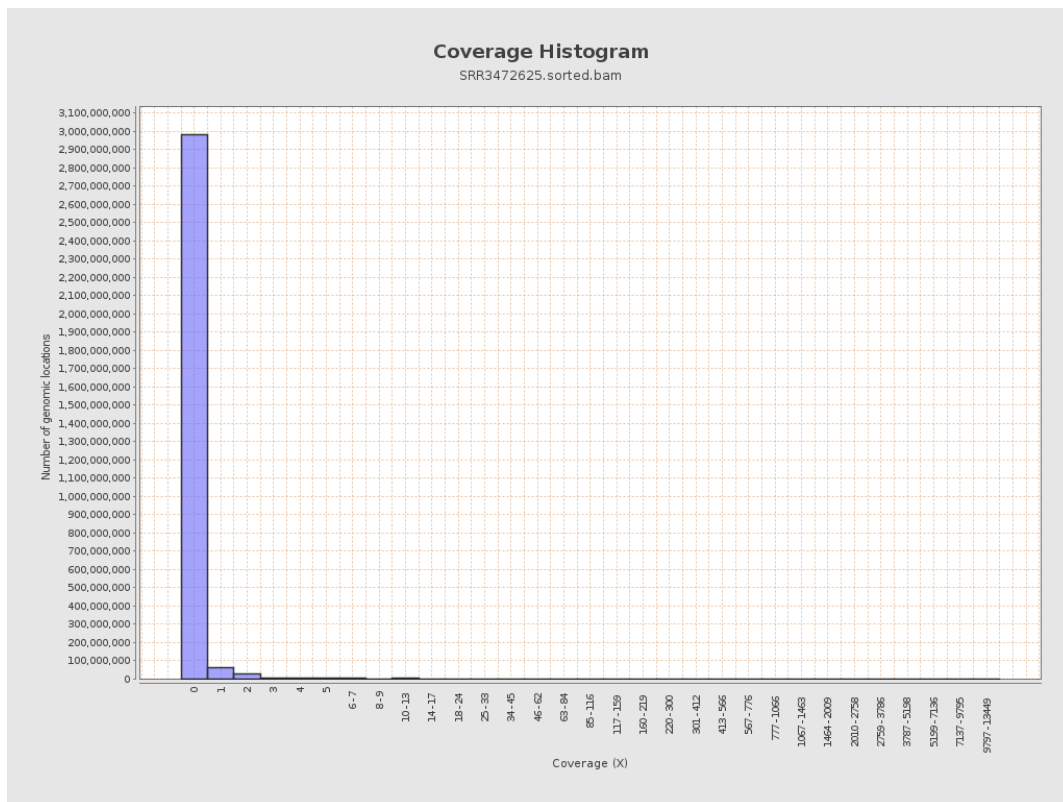
		bases	coverage	deviation
chr1	249250621	264675414	1.0619	33.967
chr2	243199373	121091715	0.4979	22.3553
chr3	198022430	133521086	0.6743	18.7318
chr4	191154276	29441747	0.154	12.9023
chr5	180915260	74094978	0.4096	17.4297
chr6	171115067	212473952	1.2417	45.8402
chr7	159138663	94079268	0.5912	23.9156
chr8	146364022	106405994	0.727	35.1307
chr9	141213431	63551144	0.45	16.1293
chr10	135534747	20153393	0.1487	5.9376
chr11	135006516	43748077	0.324	15.3576
chr12	133851895	63769897	0.4764	19.9033
chr13	115169878	93364290	0.8107	38.3125
chr14	107349540	34570404	0.322	13.7917
chr15	102531392	21861605	0.2132	13.7052
chr16	90354753	89846115	0.9944	45.0156
chr17	81195210	75322521	0.9277	33.6357
chr18	78077248	15661432	0.2006	9.0542
chr19	59128983	70830246	1.1979	46.5572
chr20	63025520	70161471	1.1132	31.3847
chr21	48129895	9424041	0.1958	10.7596
chr22	51304566	19219075	0.3746	13.0953
chrMT	16571	4051	0.2445	0.621
chrX	155270560	92886613	0.5982	20.4219

chrY	59373566	633087	0.0107	0.3987
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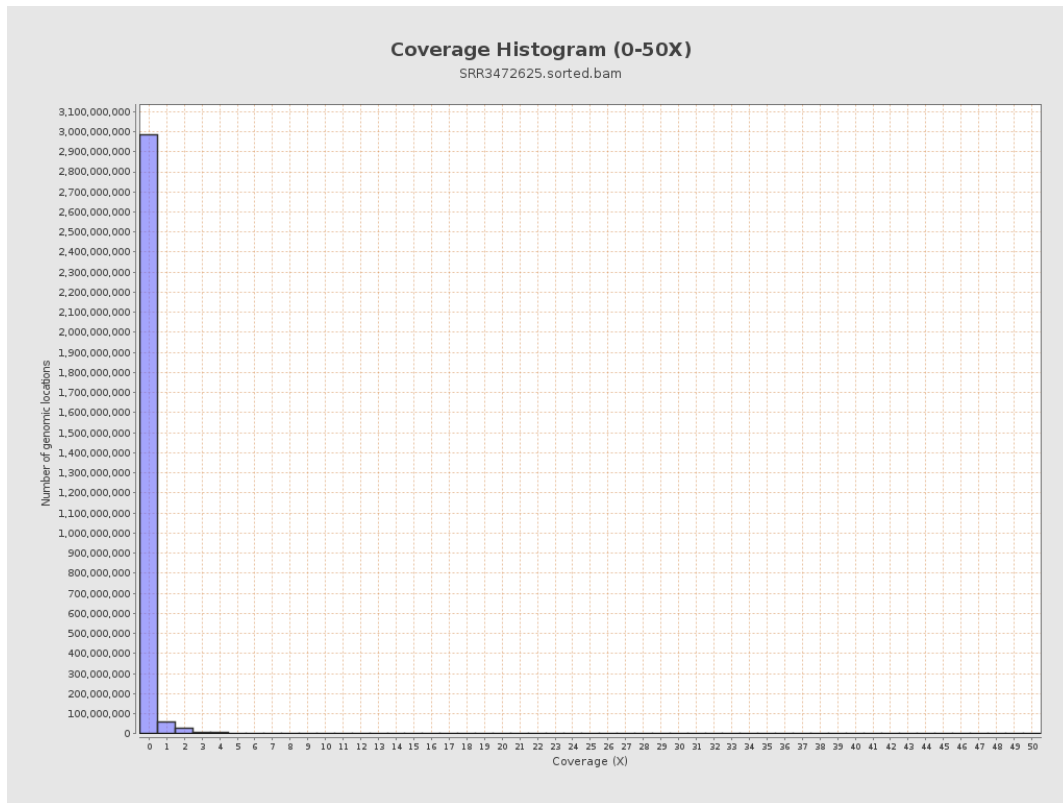
3. Results : Coverage across reference



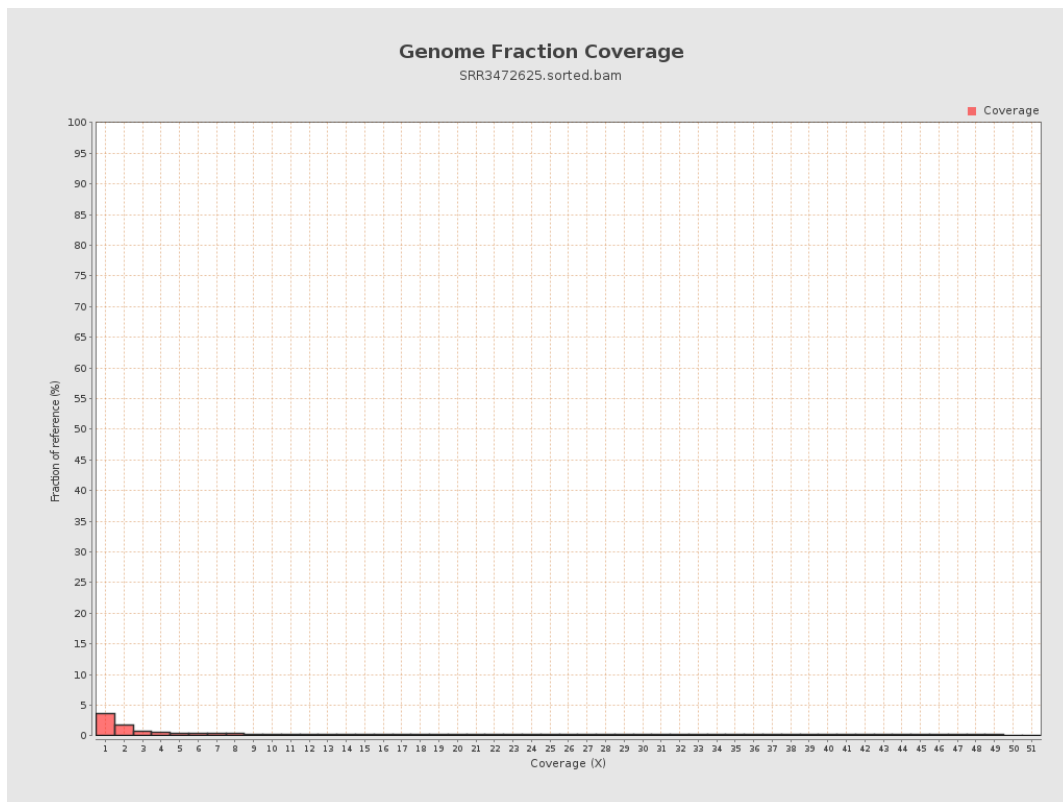
4. Results : Coverage Histogram



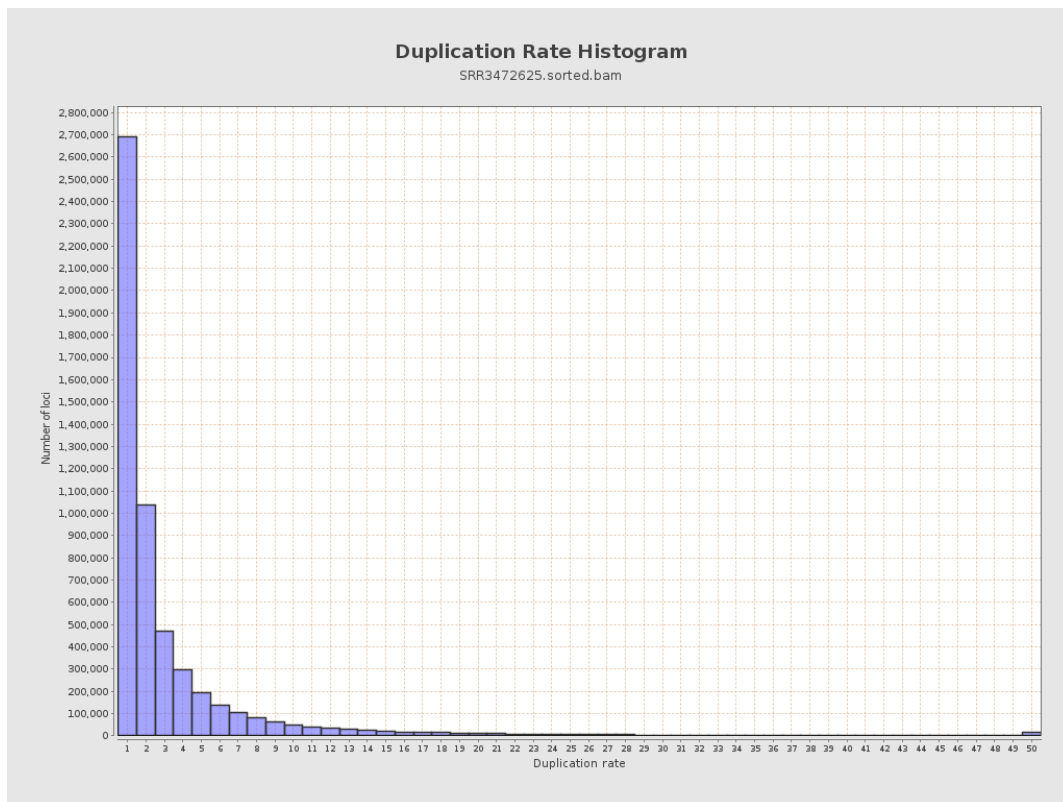
5. Results : Coverage Histogram (0-50X)



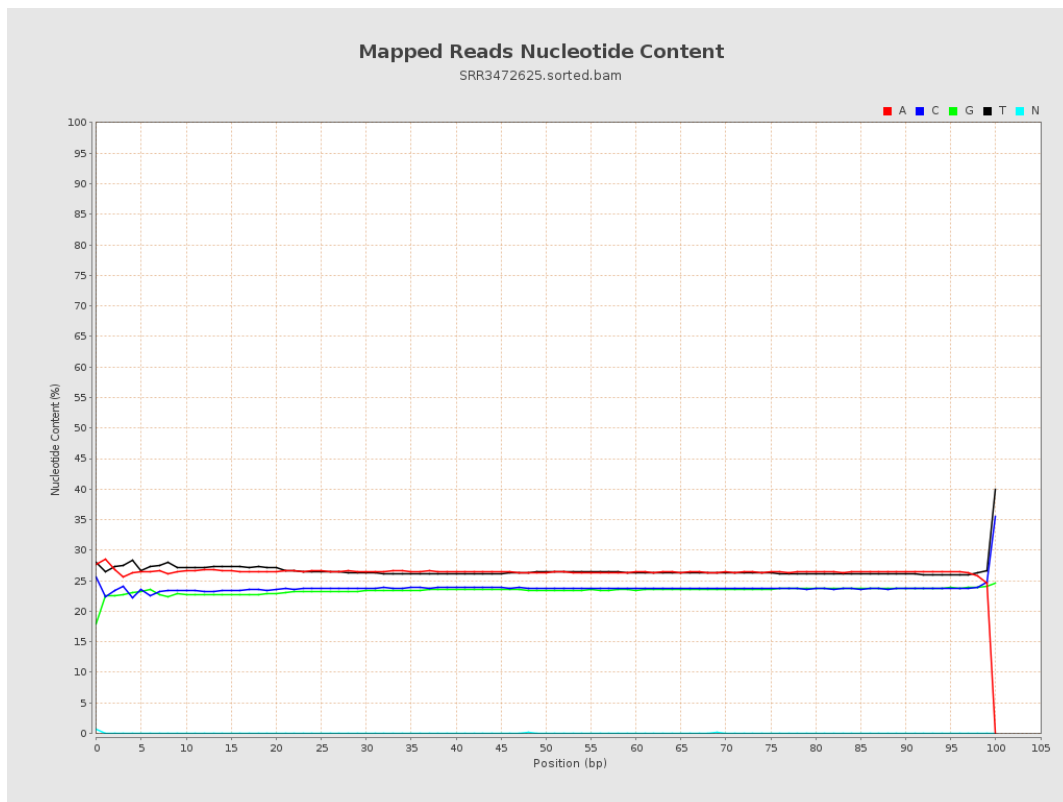
6. Results : Genome Fraction Coverage



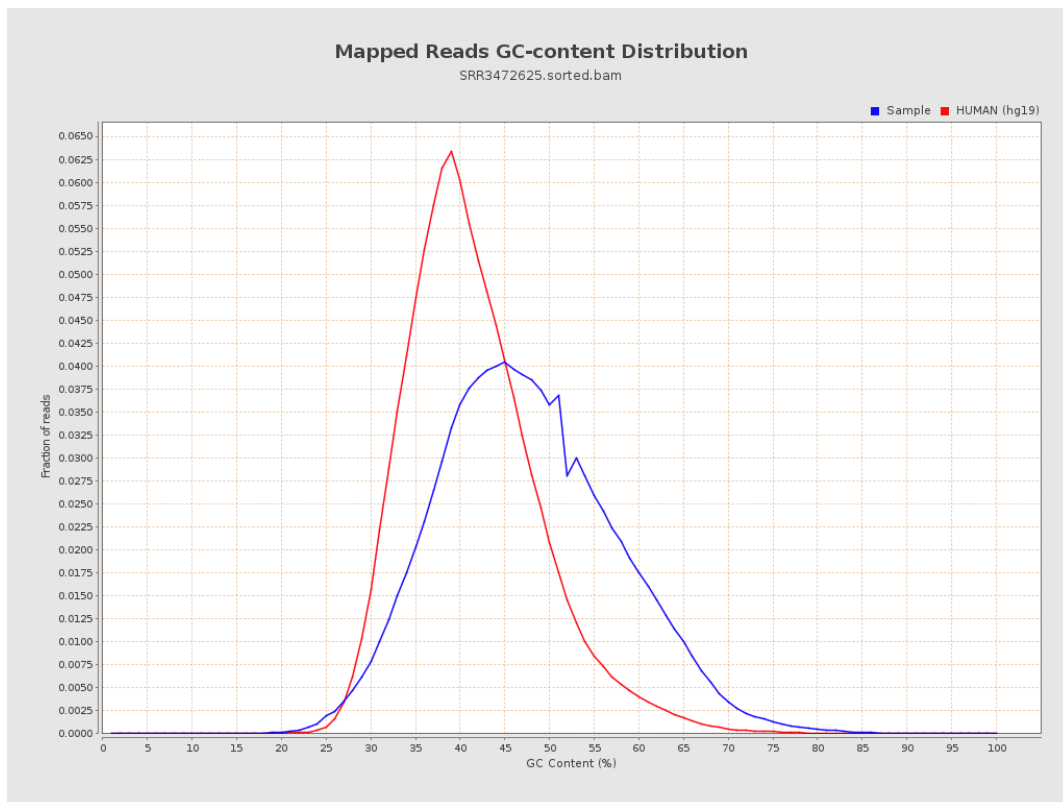
7. Results : Duplication Rate Histogram



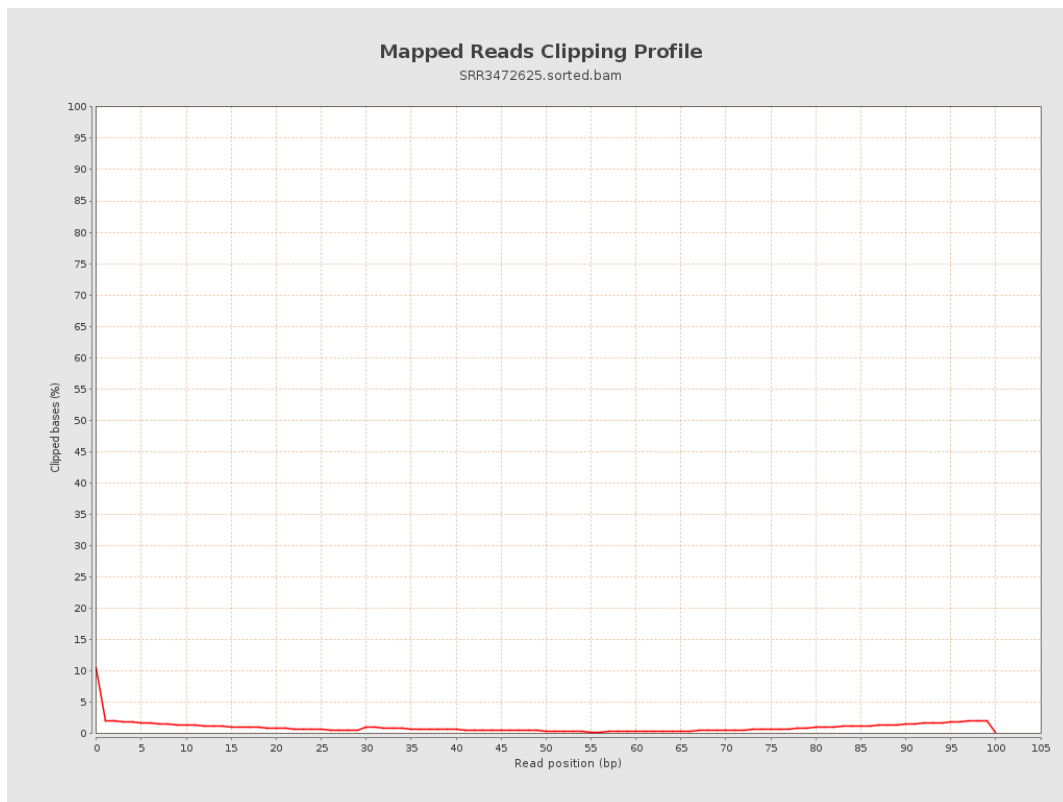
8. Results : Mapped Reads Nucleotide Content



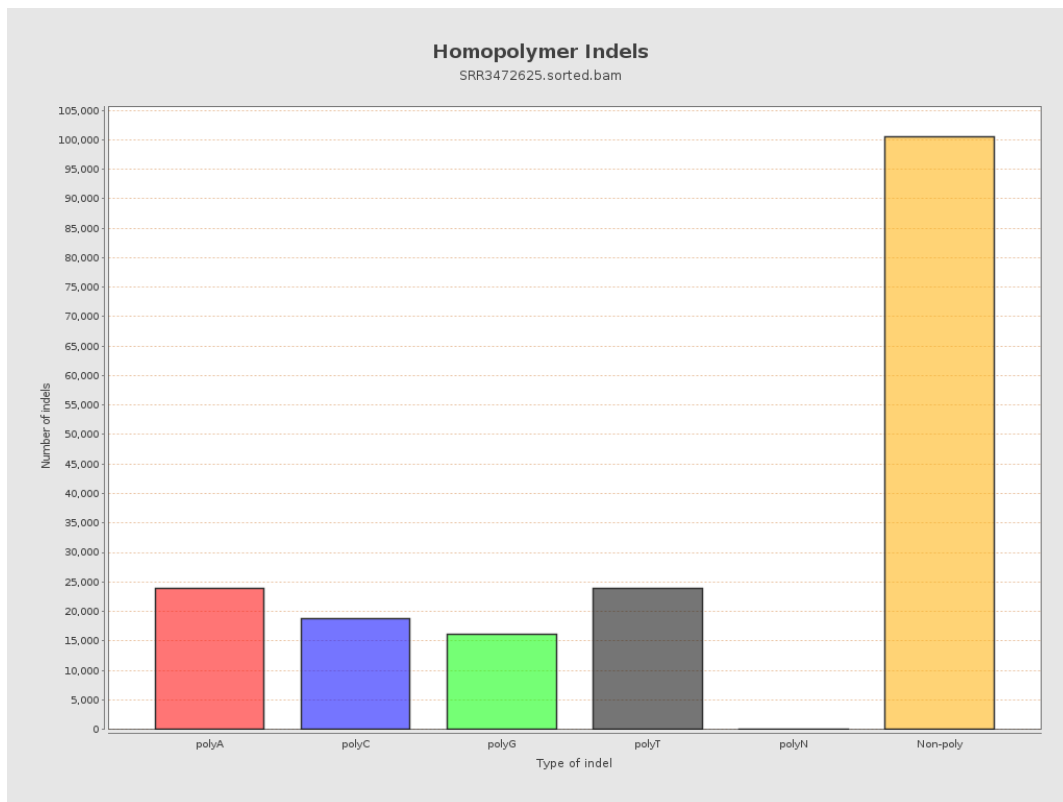
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



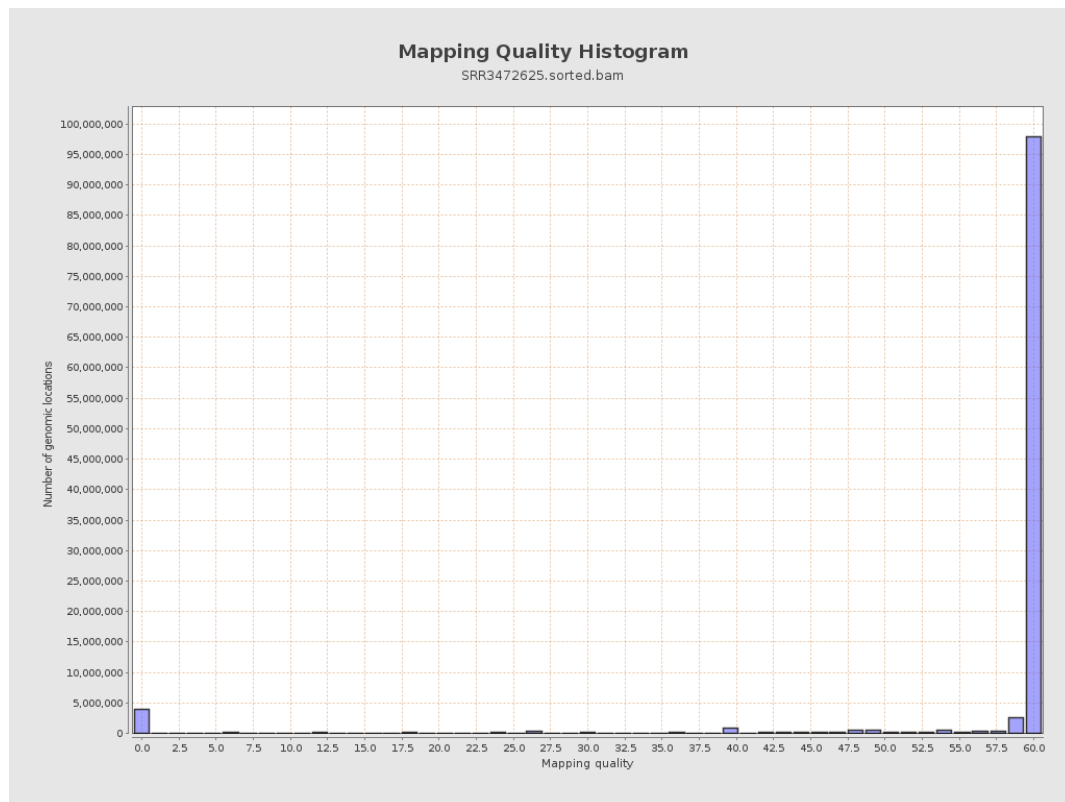
11. Results : Homopolymer Indels



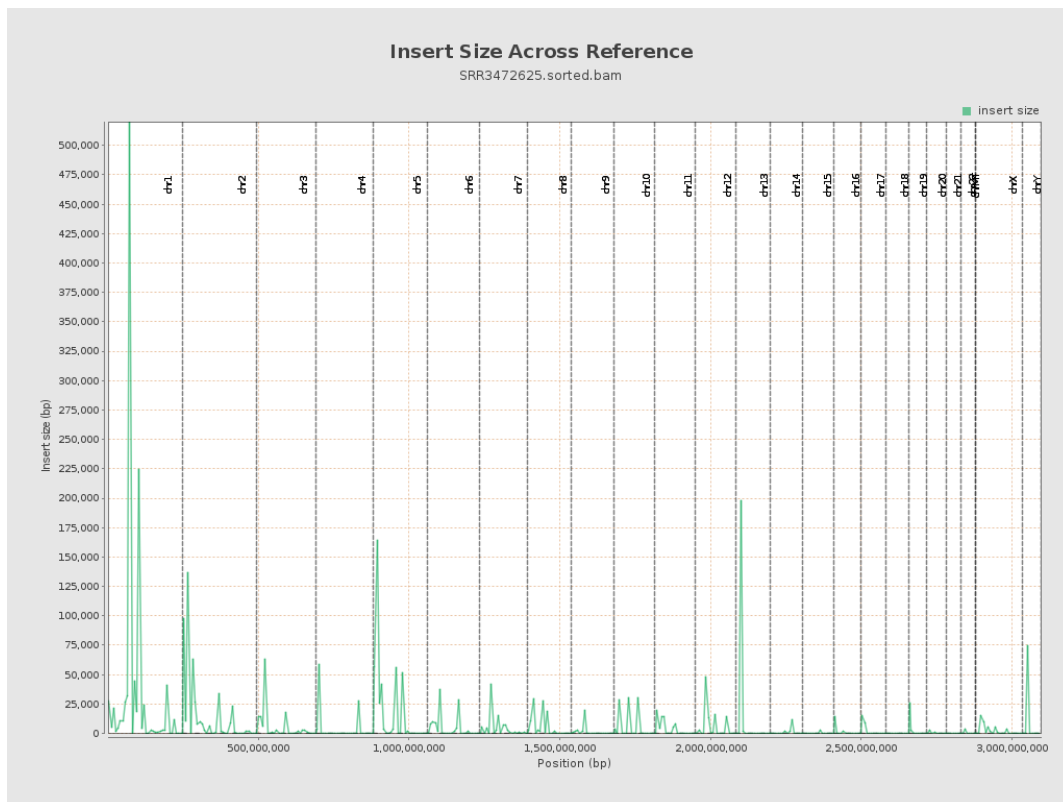
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

