

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 03:10:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472669.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_SRR3472669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472669_1.fastq.gz SRR3472669_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 03:10:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,413,320
Mapped reads	15,306,892 / 99.31%
Unmapped reads	106,428 / 0.69%
Mapped paired reads	15,306,892 / 99.31%
Mapped reads, first in pair	7,669,174 / 49.76%
Mapped reads, second in pair	7,637,718 / 49.55%
Mapped reads, both in pair	15,233,062 / 98.83%
Mapped reads, singletons	73,830 / 0.48%
Secondary alignments	0
Supplementary alignments	83,883 / 0.54%
Read min/max/mean length	30 / 101 / 99.59
Duplicated reads (estimated)	10,324,034 / 66.98%
Duplication rate	49.01%
Clipped reads	1,242,824 / 8.06%

2.2. ACGT Content

Number/percentage of A's	409,651,130 / 27.31%
Number/percentage of C's	342,642,906 / 22.84%
Number/percentage of T's	409,626,503 / 27.31%
Number/percentage of G's	337,959,667 / 22.53%
Number/percentage of N's	285,864 / 0.02%

GC Percentage	45.37%
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2.3. Coverage

Mean	0.4847
Standard Deviation	20.0562

2.4. Mapping Quality

Mean Mapping Quality	54.62
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2.5. Insert size

Mean	20,862.29
Standard Deviation	1,413,465.3
P25/Median/P75	143 / 200 / 272

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	8,779,756
Insertions	92,242
Mapped reads with at least one insertion	0.6%
Deletions	79,671
Mapped reads with at least one deletion	0.51%
Homopolymer indels	46.65%

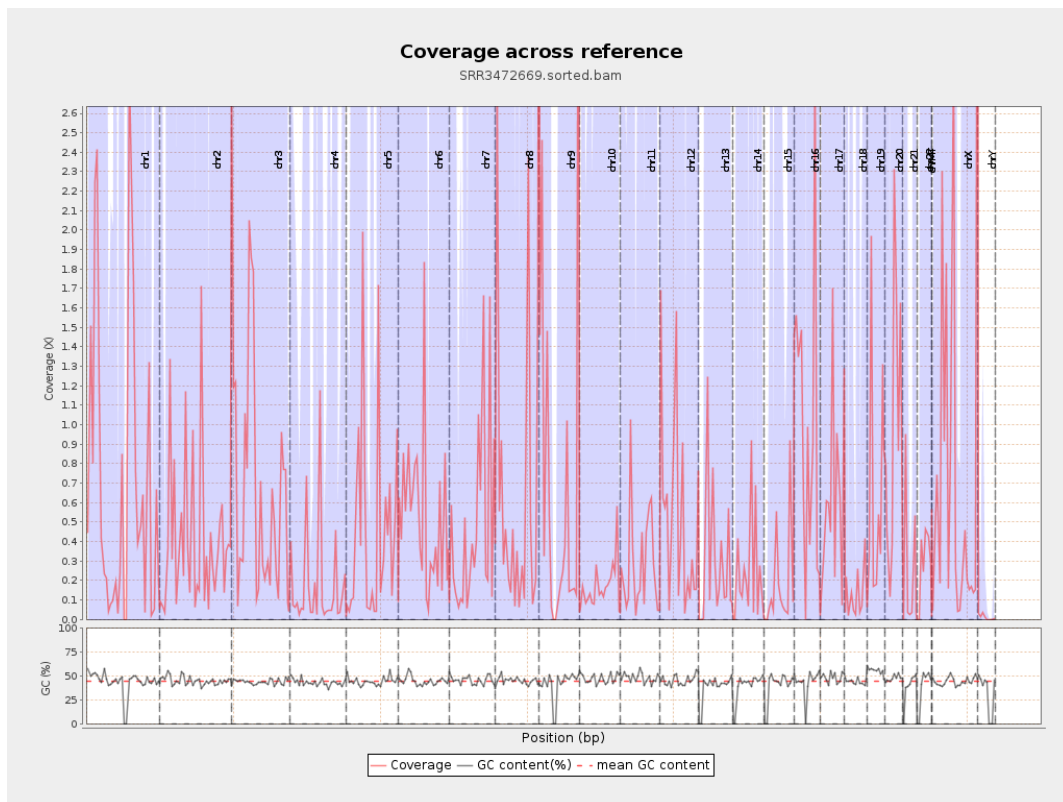
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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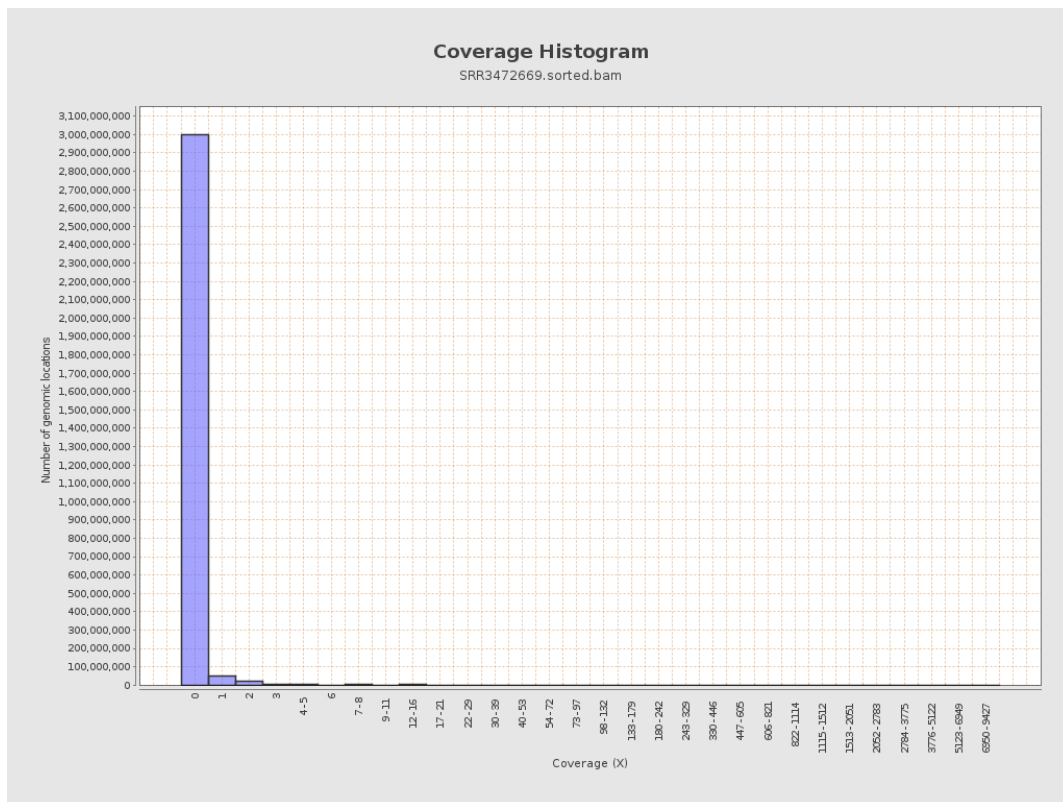
		bases	coverage	deviation
chr1	249250621	179224081	0.7191	26.2797
chr2	243199373	99452919	0.4089	18.098
chr3	198022430	137113917	0.6924	19.8497
chr4	191154276	32670940	0.1709	10.1888
chr5	180915260	84818349	0.4688	21.89
chr6	171115067	90979497	0.5317	15.229
chr7	159138663	73776712	0.4636	19.8787
chr8	146364022	96425537	0.6588	28.7708
chr9	141213431	107323517	0.76	31.9358
chr10	135534747	23840410	0.1759	7.8289
chr11	135006516	38651206	0.2863	14.1525
chr12	133851895	70974646	0.5302	17.2023
chr13	115169878	35094962	0.3047	12.7633
chr14	107349540	24920118	0.2321	12.4171
chr15	102531392	18842072	0.1838	9.1135
chr16	90354753	89732455	0.9931	37.5918
chr17	81195210	49160200	0.6055	16.2787
chr18	78077248	10720126	0.1373	7.1845
chr19	59128983	39376595	0.6659	18.827
chr20	63025520	63585198	1.0089	26.159
chr21	48129895	12413469	0.2579	18.5112
chr22	51304566	14283791	0.2784	10.1143
chrMT	16571	9403	0.5674	1.0337
chrX	155270560	106273593	0.6844	23.1355

chrY	59373566	678336	0.0114	0.5457
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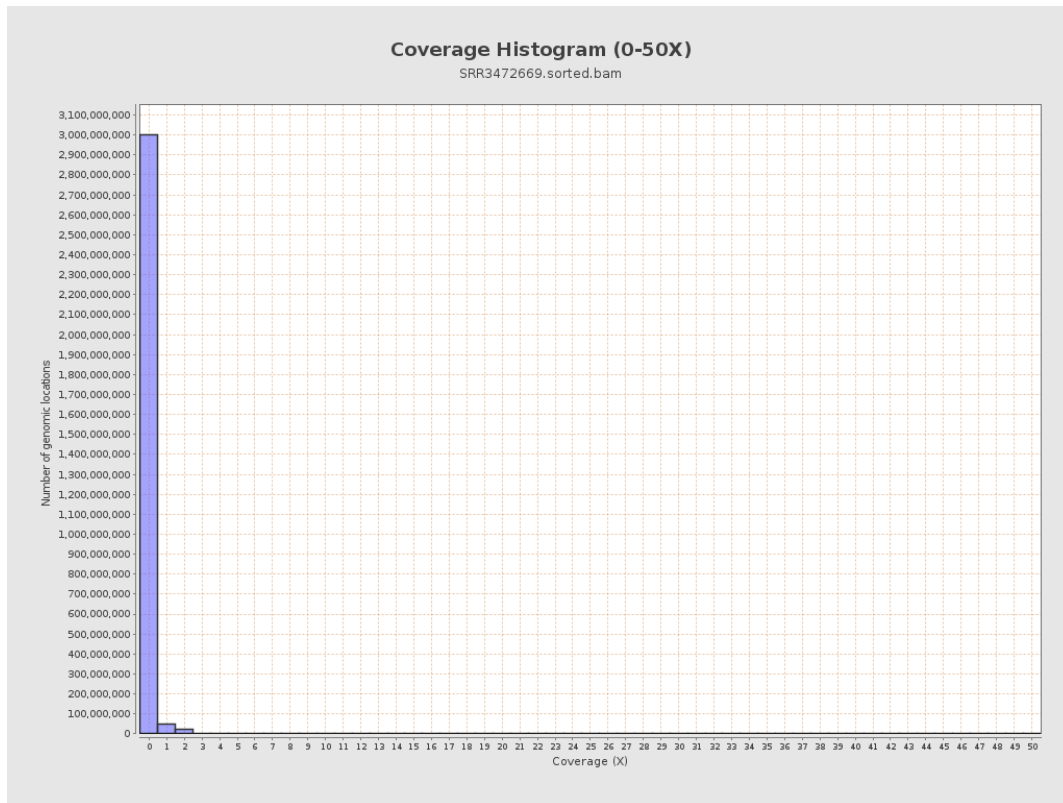
3. Results : Coverage across reference



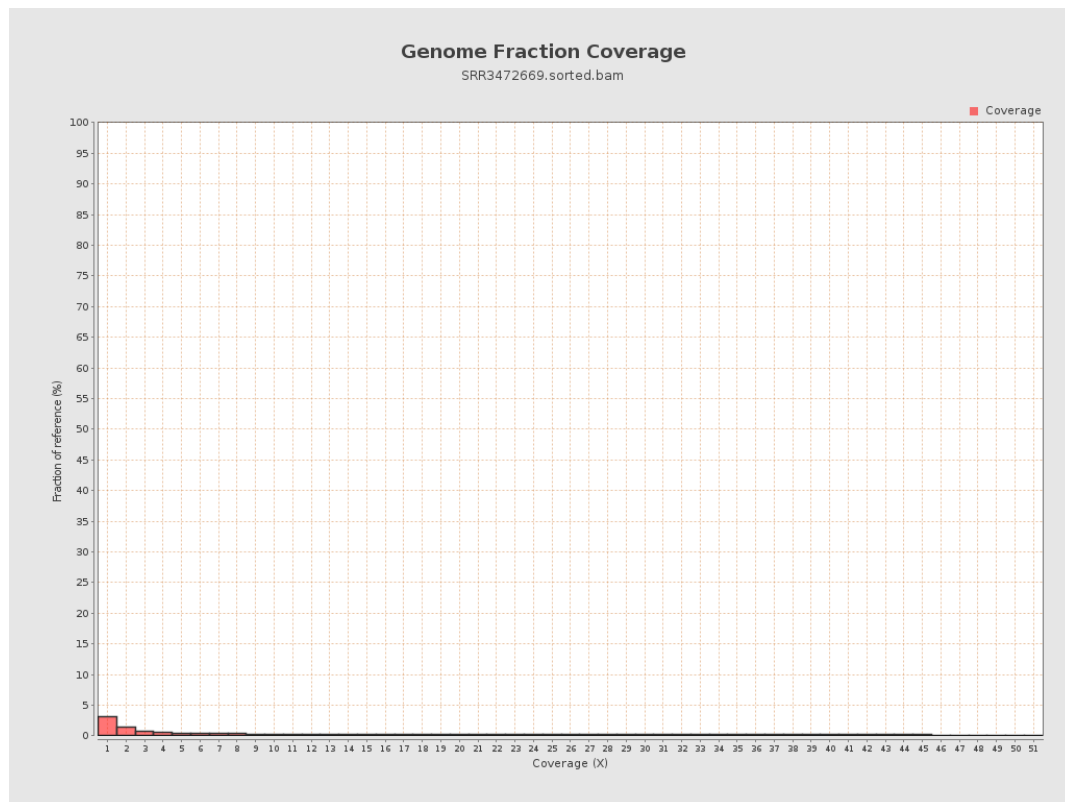
4. Results : Coverage Histogram



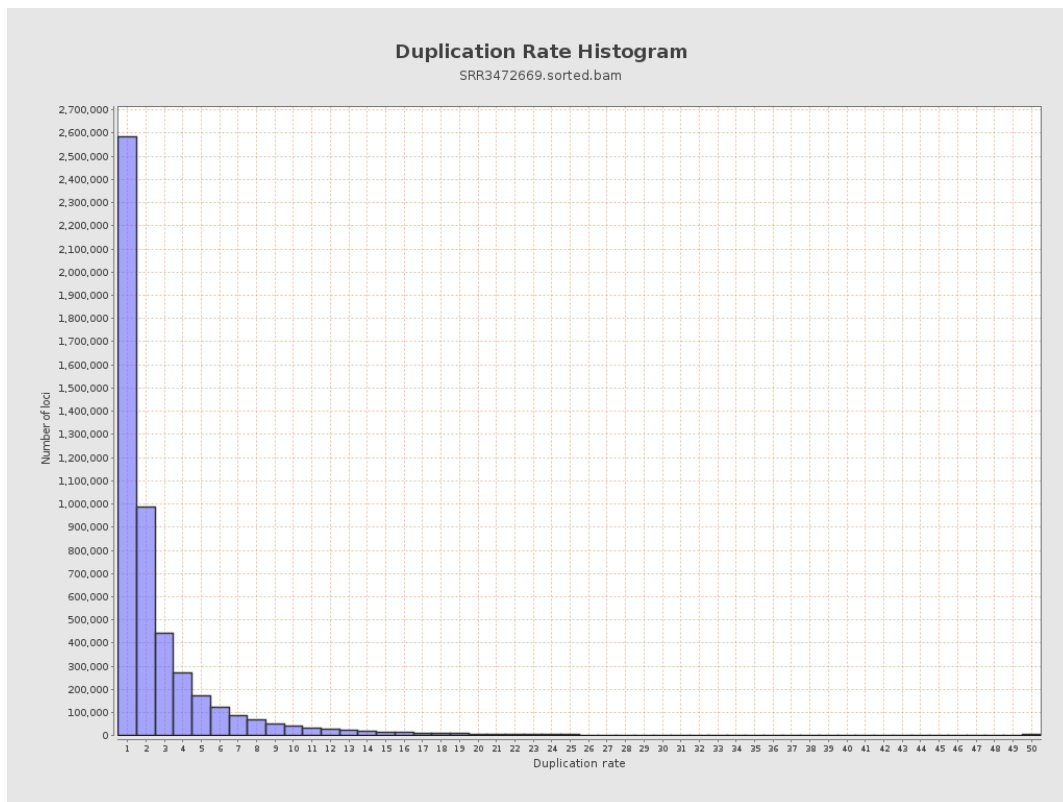
5. Results : Coverage Histogram (0-50X)



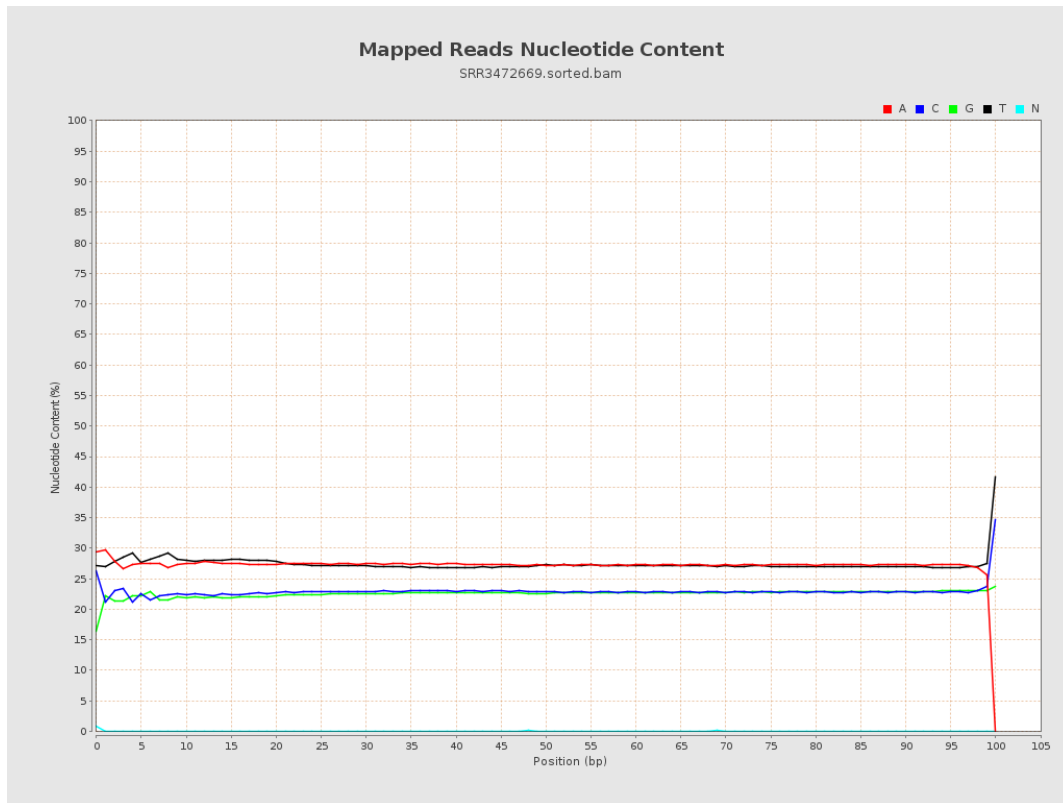
6. Results : Genome Fraction Coverage



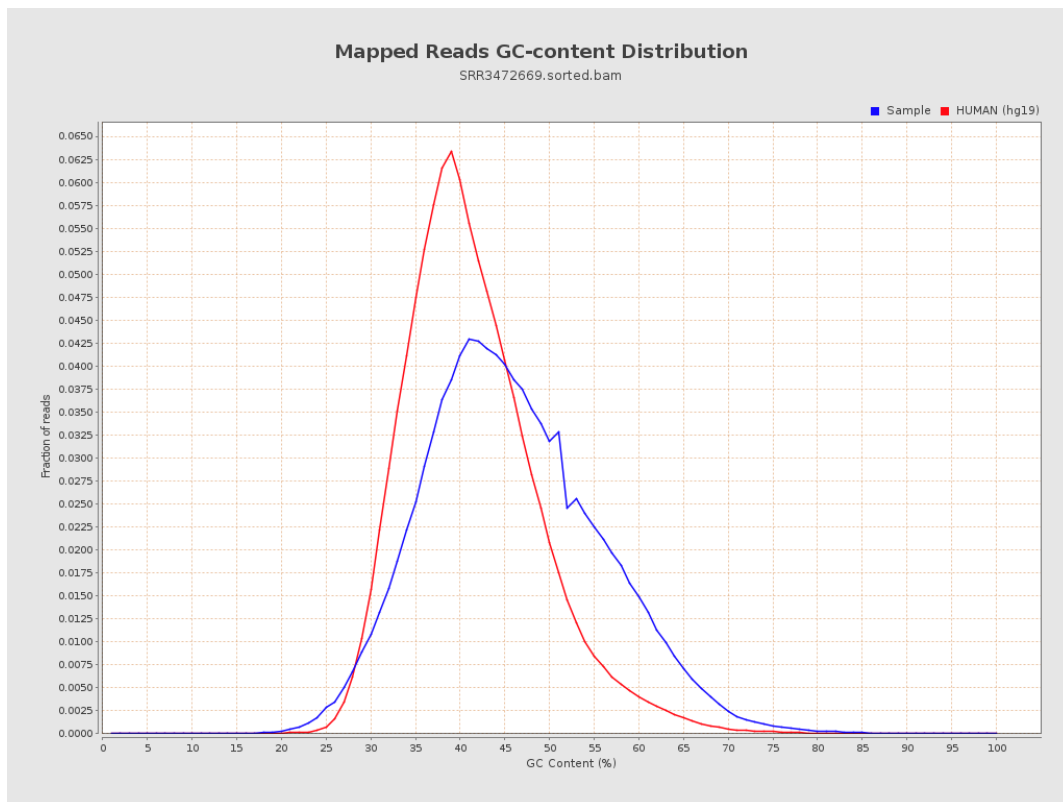
7. Results : Duplication Rate Histogram



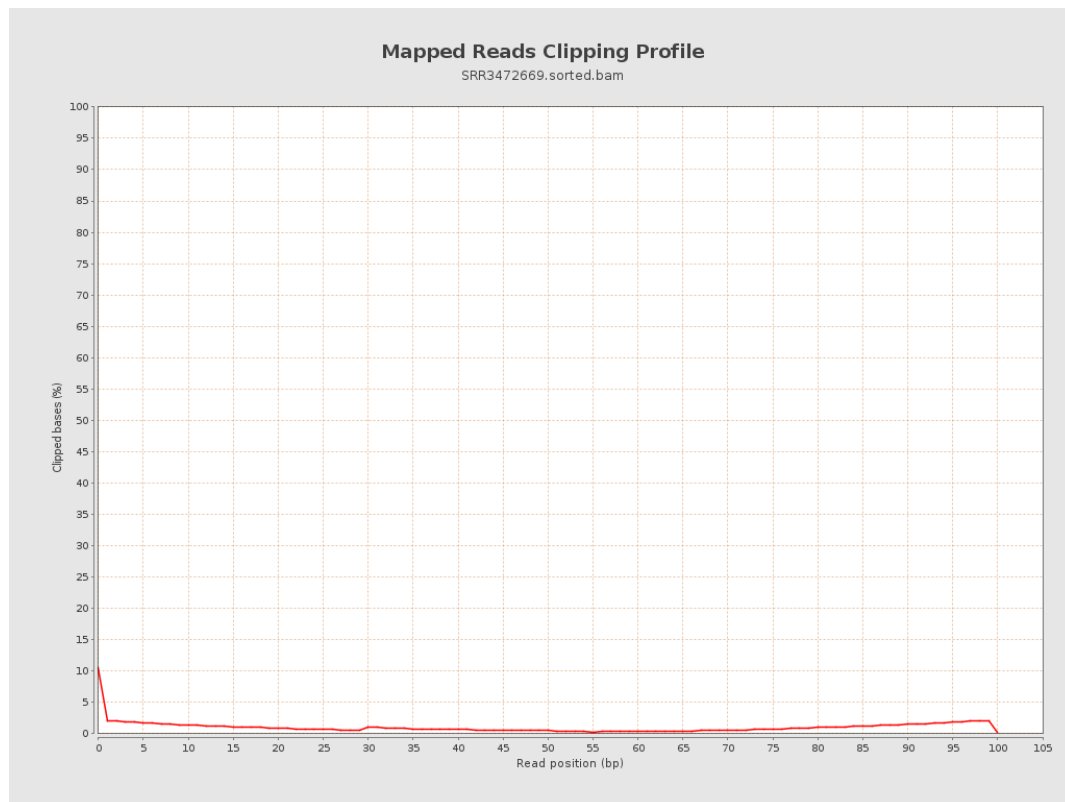
8. Results : Mapped Reads Nucleotide Content



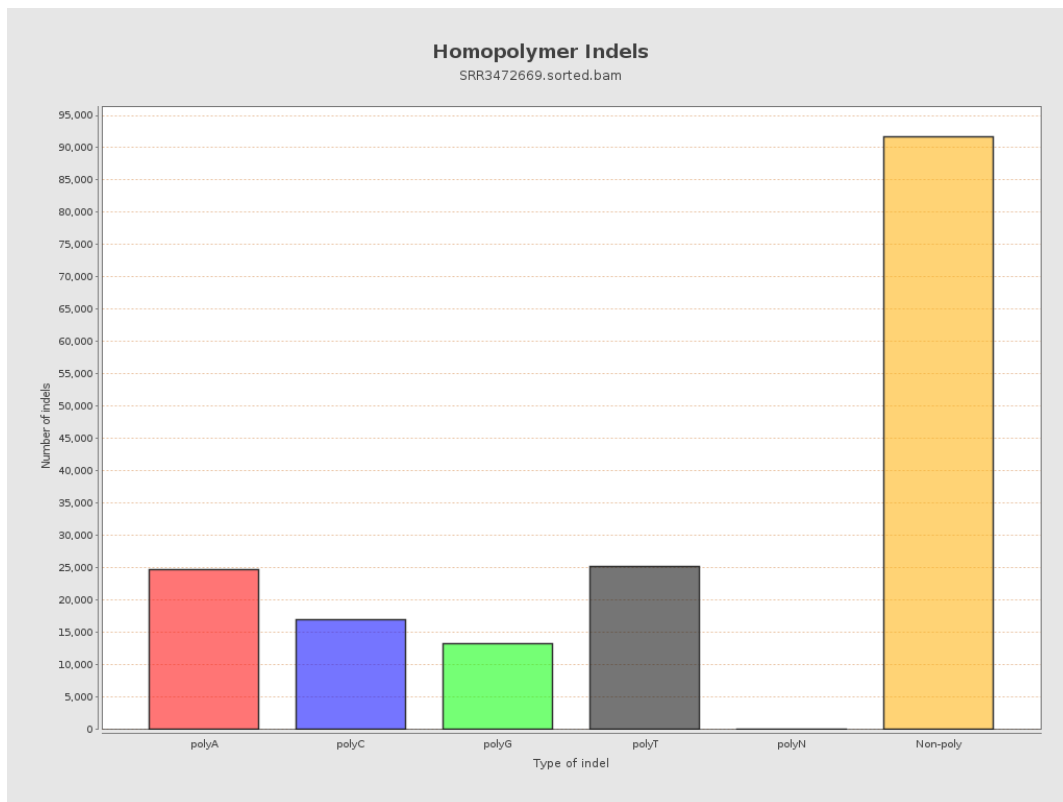
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



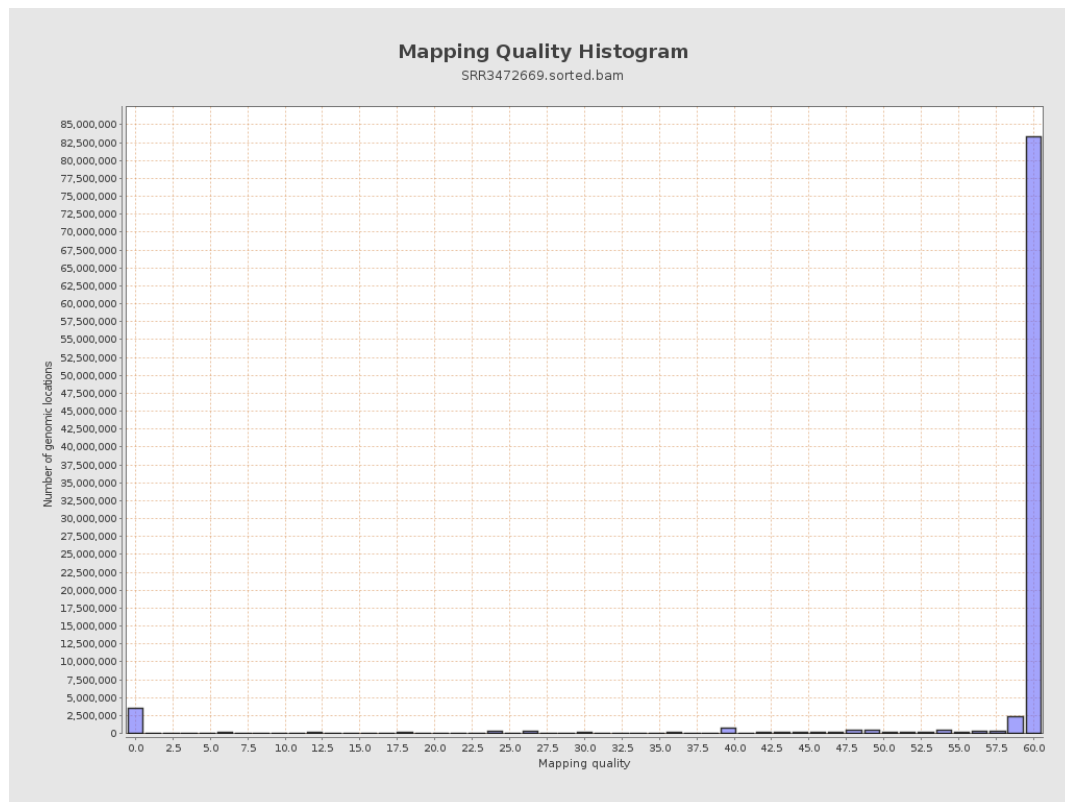
11. Results : Homopolymer Indels



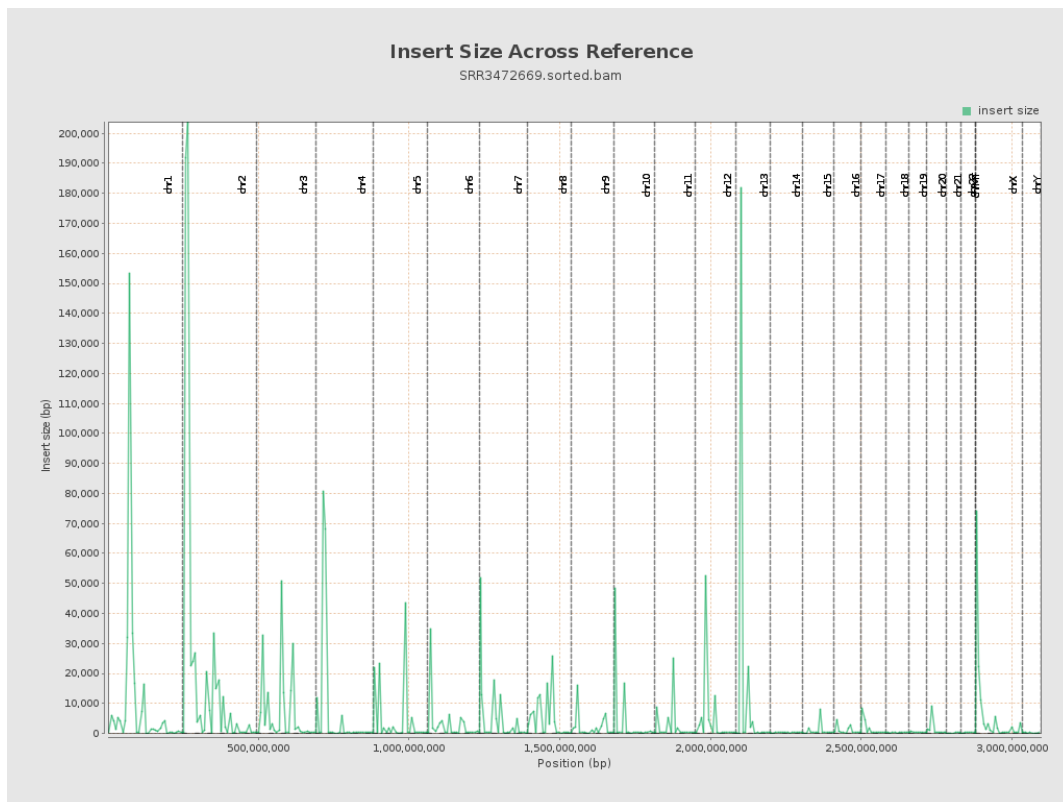
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

