

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 09:44:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472690.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_SRR3472690 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472690_1.fastq.gz SRR3472690_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 09:44:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472690.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,589,248
Mapped reads	23,372,046 / 99.08%
Unmapped reads	217,202 / 0.92%
Mapped paired reads	23,372,046 / 99.08%
Mapped reads, first in pair	11,710,717 / 49.64%
Mapped reads, second in pair	11,661,329 / 49.43%
Mapped reads, both in pair	23,239,760 / 98.52%
Mapped reads, singletons	132,286 / 0.56%
Secondary alignments	0
Supplementary alignments	152,130 / 0.64%
Read min/max/mean length	30 / 101 / 99.89
Duplicated reads (estimated)	18,178,989 / 77.06%
Duplication rate	48.48%
Clipped reads	1,717,300 / 7.28%

2.2. ACGT Content

Number/percentage of A's	619,316,341 / 26.91%
Number/percentage of C's	532,427,642 / 23.13%
Number/percentage of T's	618,563,741 / 26.88%
Number/percentage of G's	530,682,679 / 23.06%
Number/percentage of N's	457,915 / 0.02%

GC Percentage	46.19%
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2.3. Coverage

Mean	0.7435
Standard Deviation	71.2529

2.4. Mapping Quality

Mean Mapping Quality	54.38
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2.5. Insert size

Mean	21,839.09
Standard Deviation	1,492,935.39
P25/Median/P75	159 / 215 / 286

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	14,090,051
Insertions	136,652
Mapped reads with at least one insertion	0.58%
Deletions	108,318
Mapped reads with at least one deletion	0.46%
Homopolymer indels	45.76%

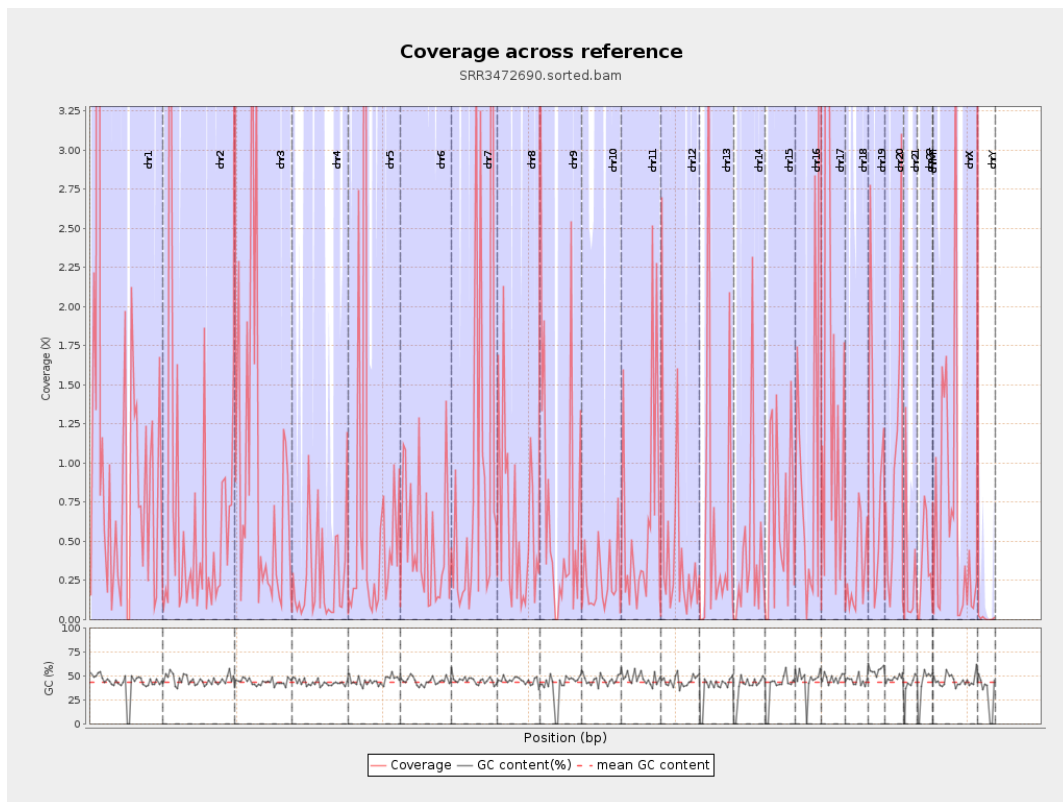
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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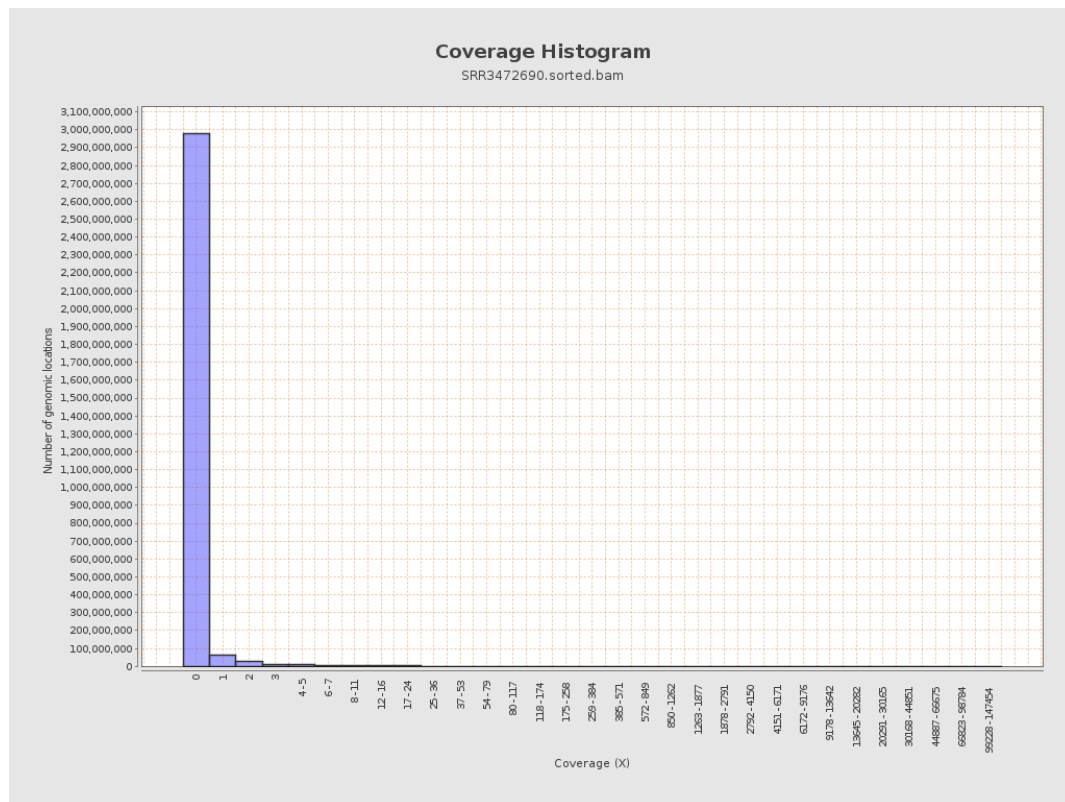
		bases	coverage	deviation
chr1	249250621	322632529	1.2944	107.8057
chr2	243199373	152231257	0.626	37.8228
chr3	198022430	198893428	1.0044	32.9495
chr4	191154276	55353601	0.2896	15.3347
chr5	180915260	137716538	0.7612	147.2309
chr6	171115067	84004844	0.4909	19.3008
chr7	159138663	167495691	1.0525	147.4444
chr8	146364022	89301649	0.6101	24.8867
chr9	141213431	90626957	0.6418	33.8785
chr10	135534747	34057527	0.2513	13.8423
chr11	135006516	84042495	0.6225	26.9858
chr12	133851895	62678615	0.4683	21.414
chr13	115169878	75009107	0.6513	45.2737
chr14	107349540	43300823	0.4034	18.2863
chr15	102531392	67469227	0.658	47.0609
chr16	90354753	187567552	2.0759	164.9851
chr17	81195210	157279099	1.937	88.9978
chr18	78077248	23268842	0.298	21.0196
chr19	59128983	56715878	0.9592	37.7276
chr20	63025520	63918997	1.0142	51.0562
chr21	48129895	15636805	0.3249	33.032
chr22	51304566	18210446	0.3549	12.2848
chrMT	16571	12433	0.7503	1.1223
chrX	155270560	113837089	0.7332	49.6794

chrY	59373566	415316	0.007	0.5694
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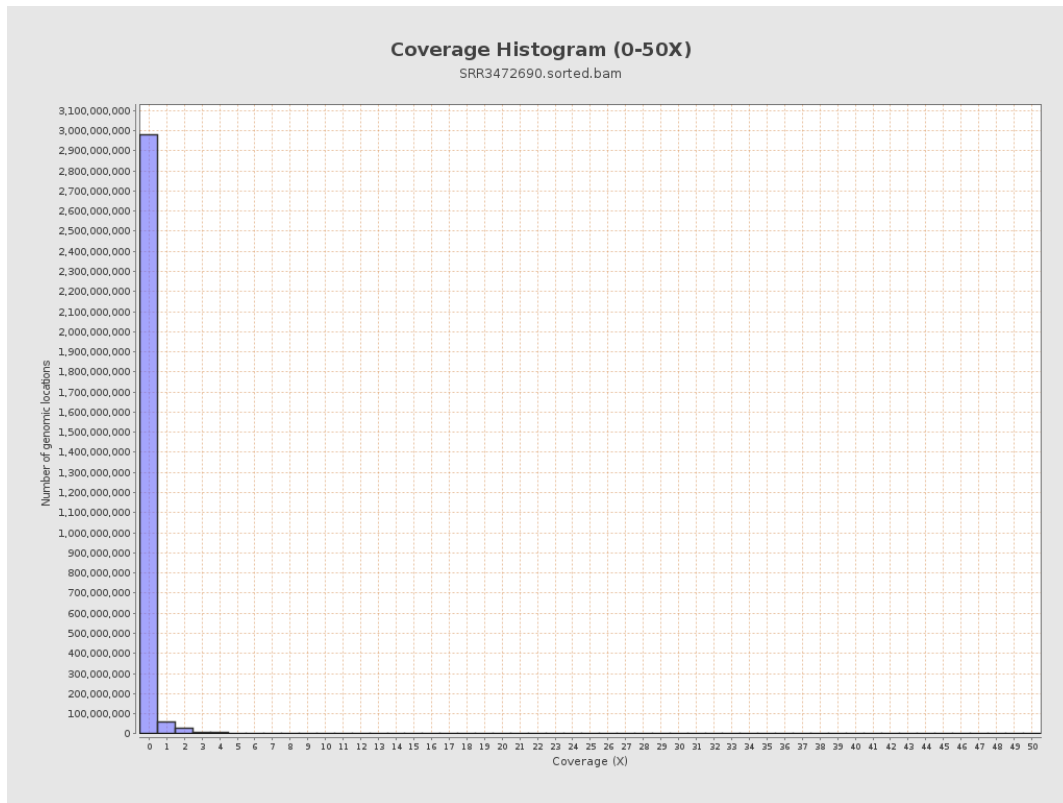
3. Results : Coverage across reference



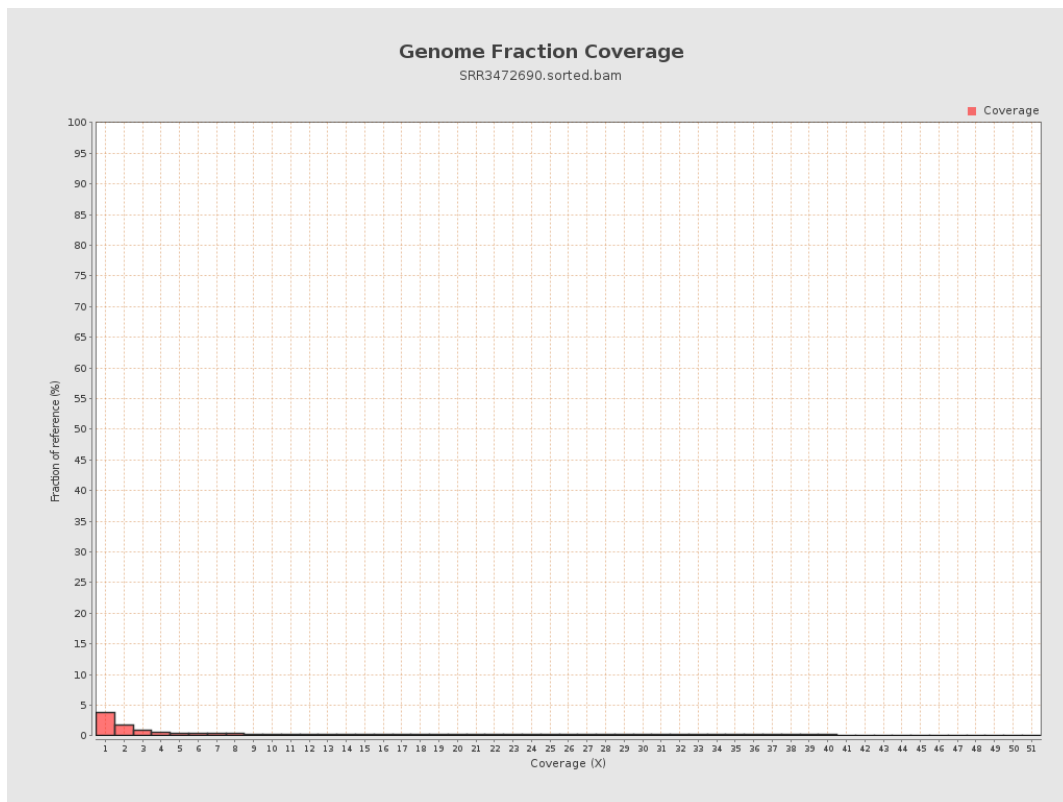
4. Results : Coverage Histogram



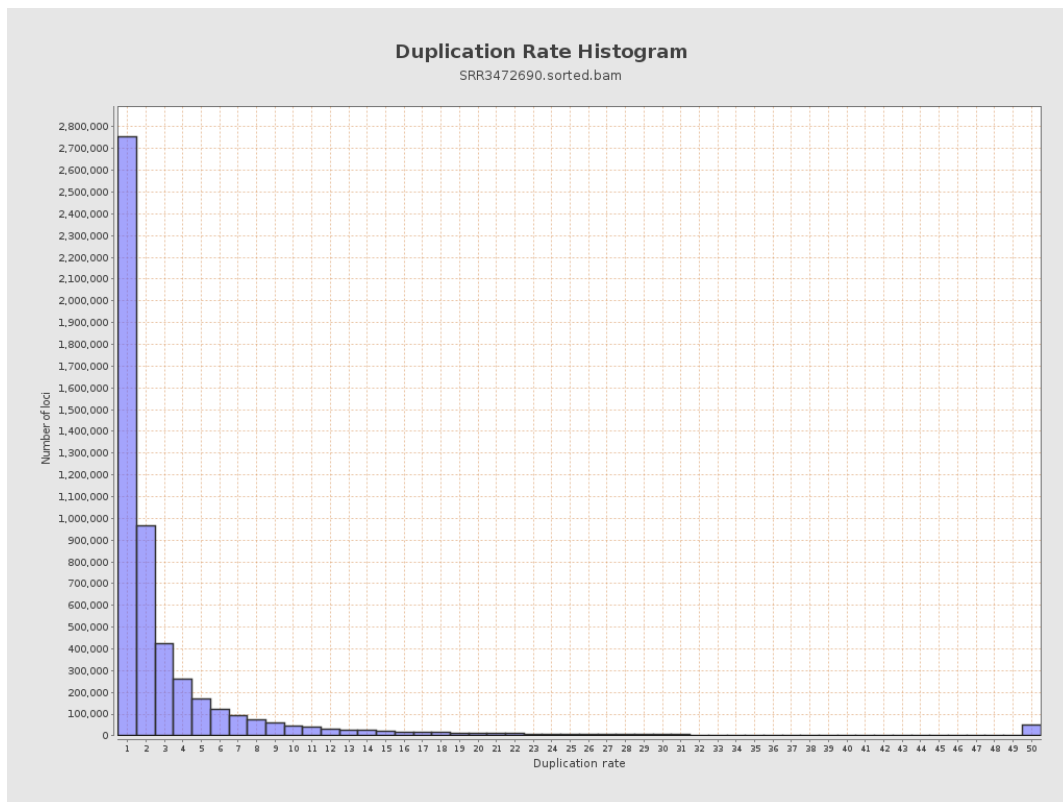
5. Results : Coverage Histogram (0-50X)



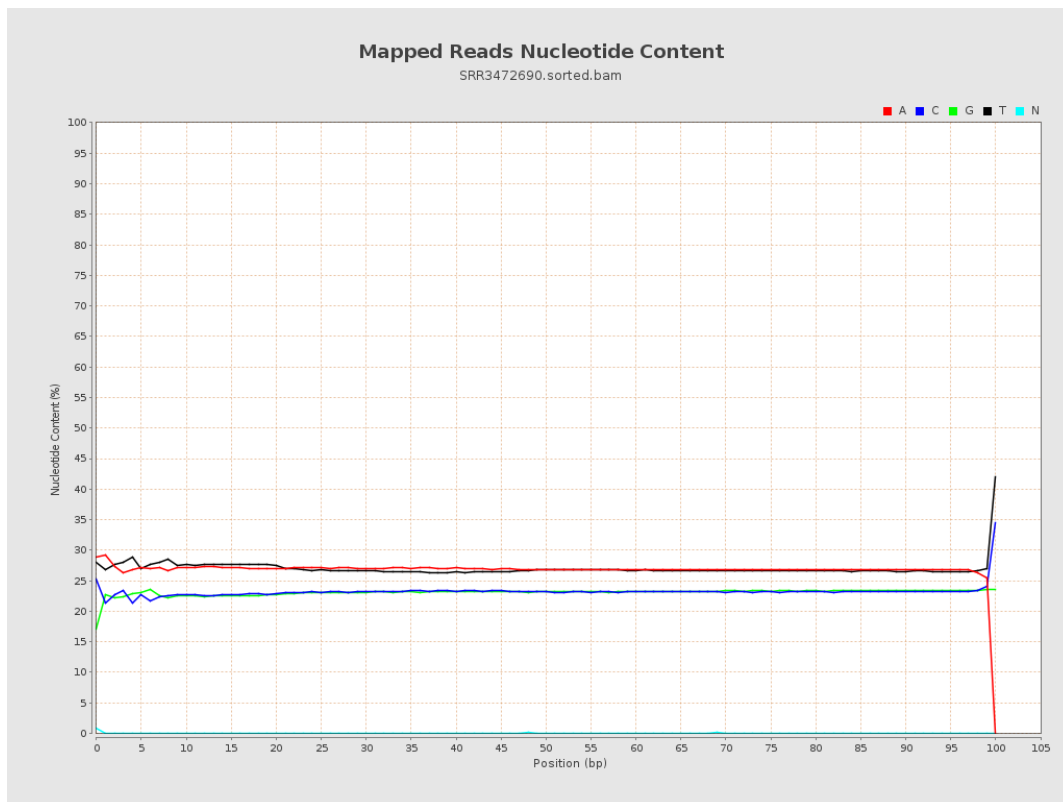
6. Results : Genome Fraction Coverage



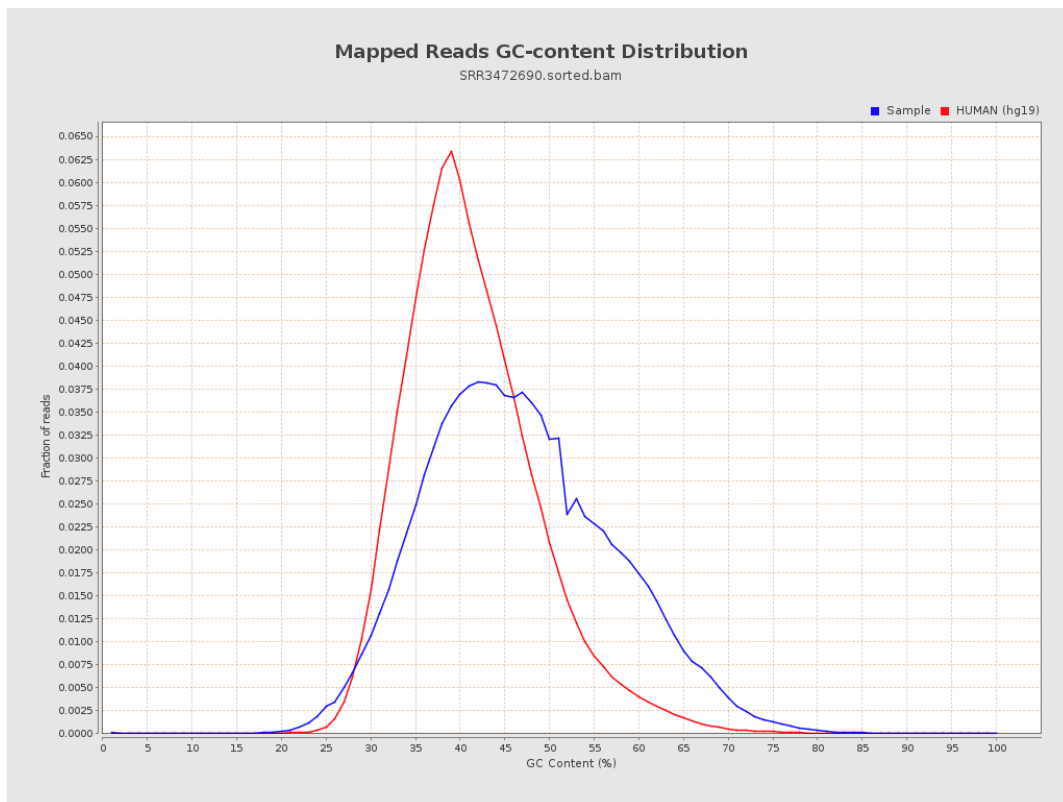
7. Results : Duplication Rate Histogram



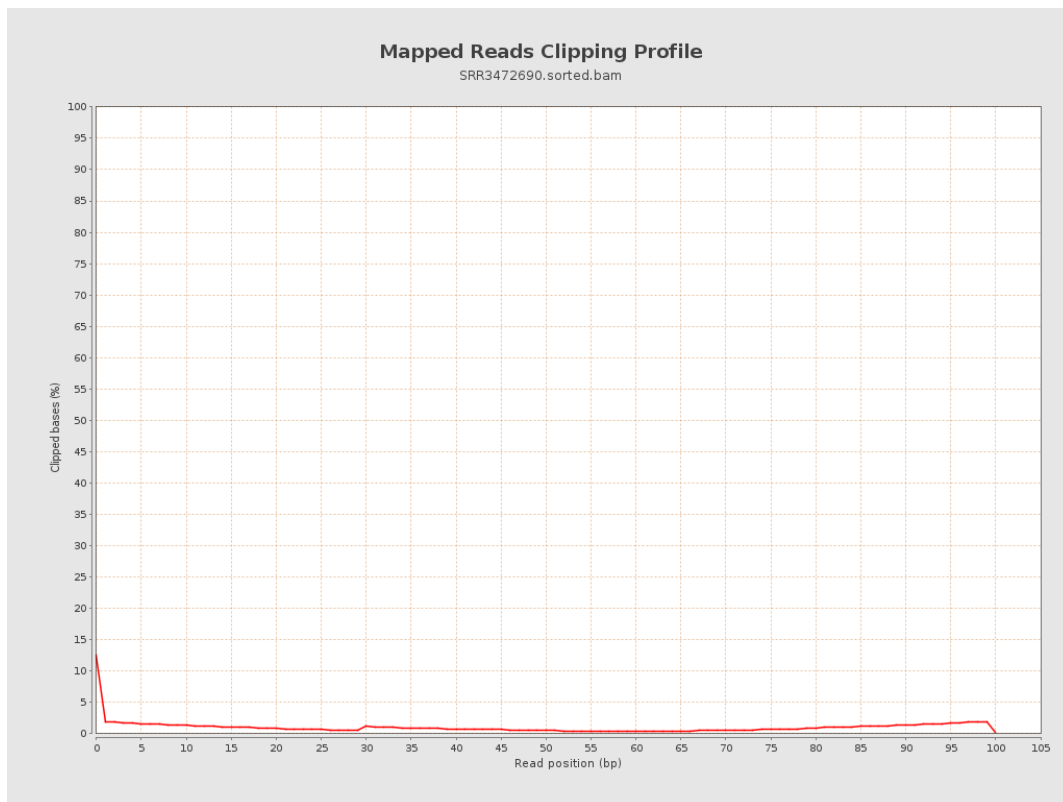
8. Results : Mapped Reads Nucleotide Content



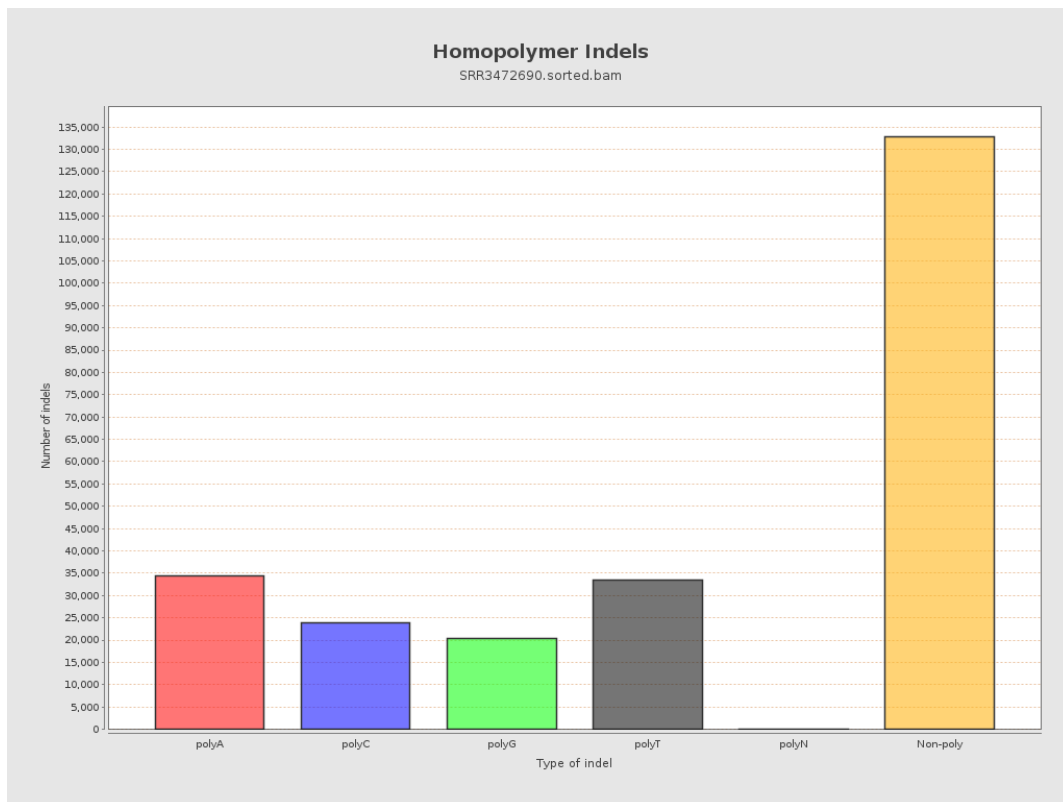
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



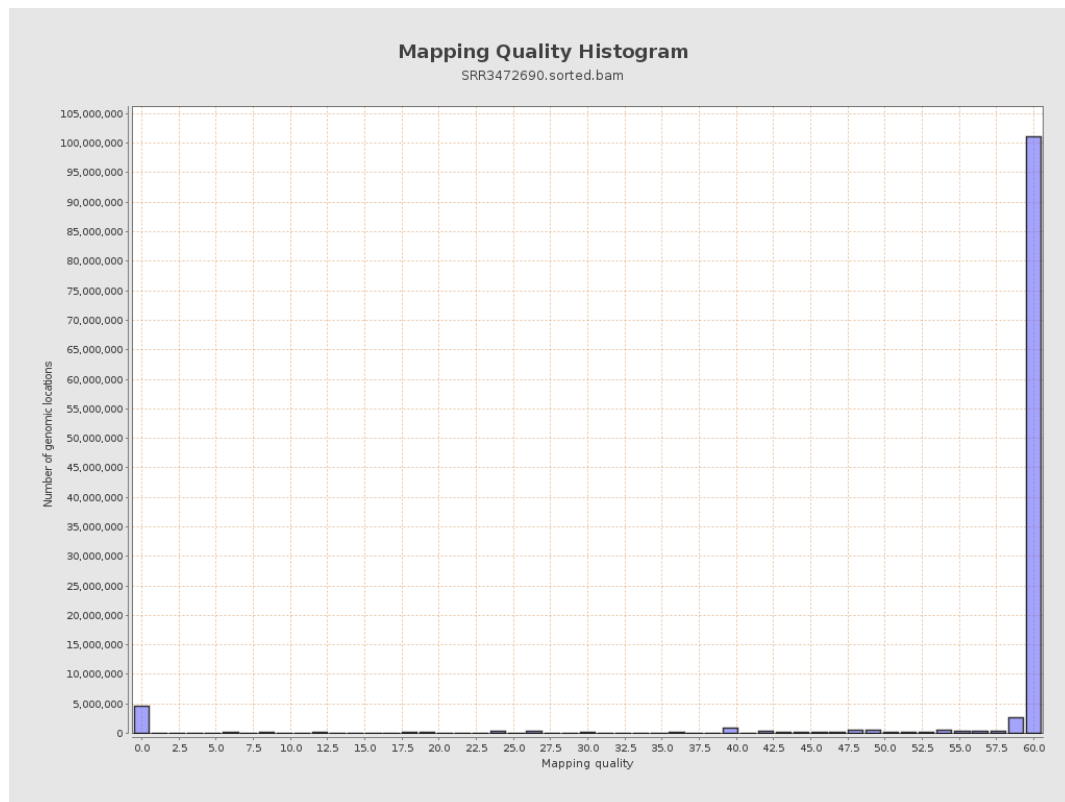
11. Results : Homopolymer Indels



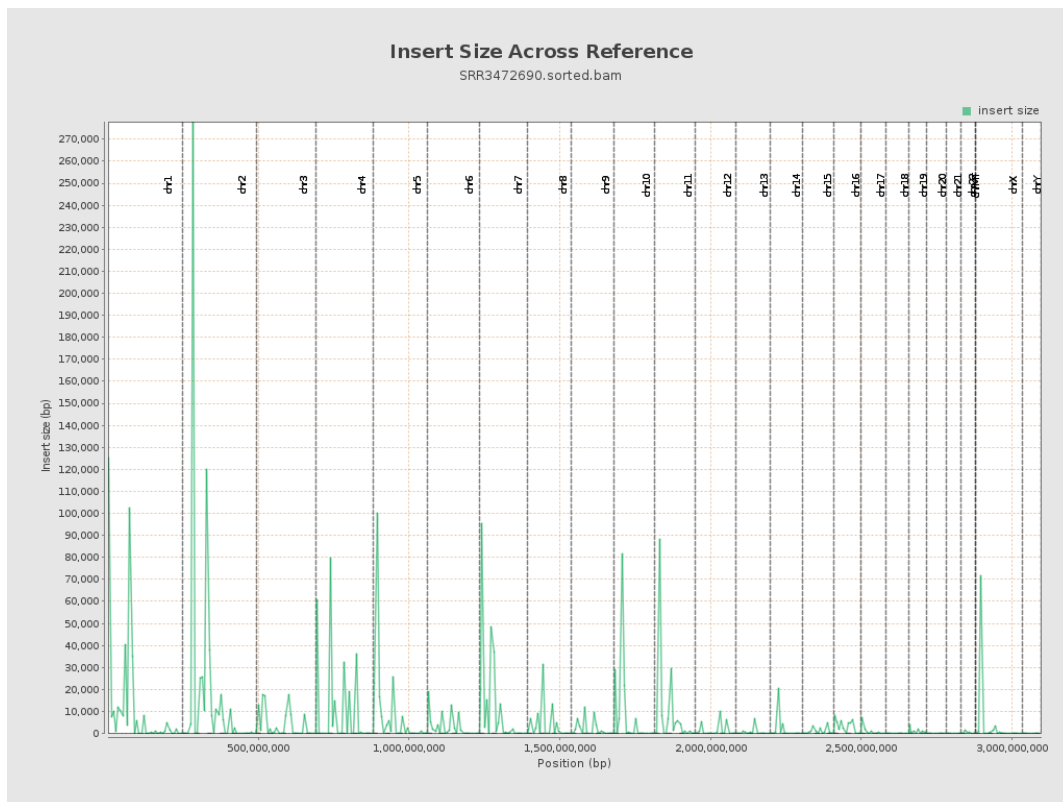
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

