

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 16:07:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472629.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_SRR3472629 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472629_1.fastq.gz SRR3472629_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 16:07:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472629.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,346,632
Mapped reads	16,236,459 / 99.33%
Unmapped reads	110,173 / 0.67%
Mapped paired reads	16,236,459 / 99.33%
Mapped reads, first in pair	8,136,087 / 49.77%
Mapped reads, second in pair	8,100,372 / 49.55%
Mapped reads, both in pair	16,165,964 / 98.89%
Mapped reads, singletons	70,495 / 0.43%
Secondary alignments	0
Supplementary alignments	70,438 / 0.43%
Read min/max/mean length	30 / 101 / 99.69
Duplicated reads (estimated)	10,940,381 / 66.93%
Duplication rate	50.15%
Clipped reads	1,096,653 / 6.71%

2.2. ACGT Content

Number/percentage of A's	424,564,745 / 26.58%
Number/percentage of C's	375,489,953 / 23.51%
Number/percentage of T's	425,979,612 / 26.67%
Number/percentage of G's	371,154,941 / 23.23%
Number/percentage of N's	296,795 / 0.02%

GC Percentage	46.74%
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2.3. Coverage

Mean	0.5161
Standard Deviation	20.0203

2.4. Mapping Quality

Mean Mapping Quality	54.8
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2.5. Insert size

Mean	20,974.07
Standard Deviation	1,445,650.07
P25/Median/P75	151 / 205 / 272

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	9,269,634
Insertions	91,807
Mapped reads with at least one insertion	0.56%
Deletions	86,343
Mapped reads with at least one deletion	0.52%
Homopolymer indels	47.37%

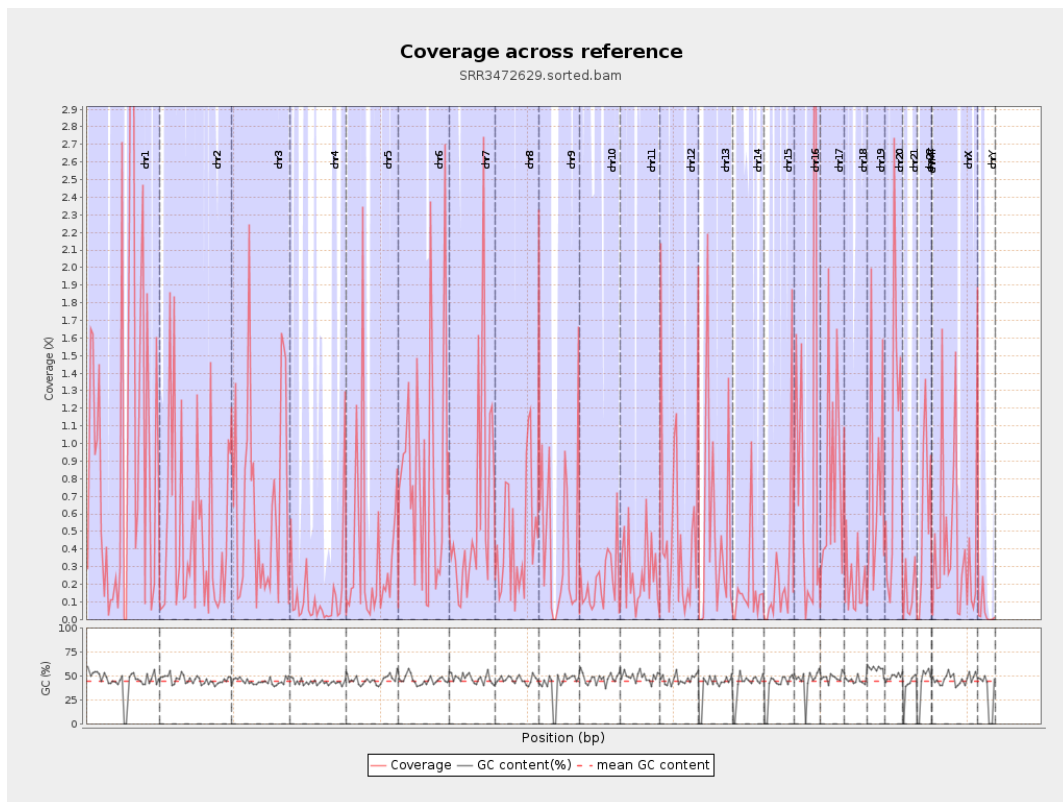
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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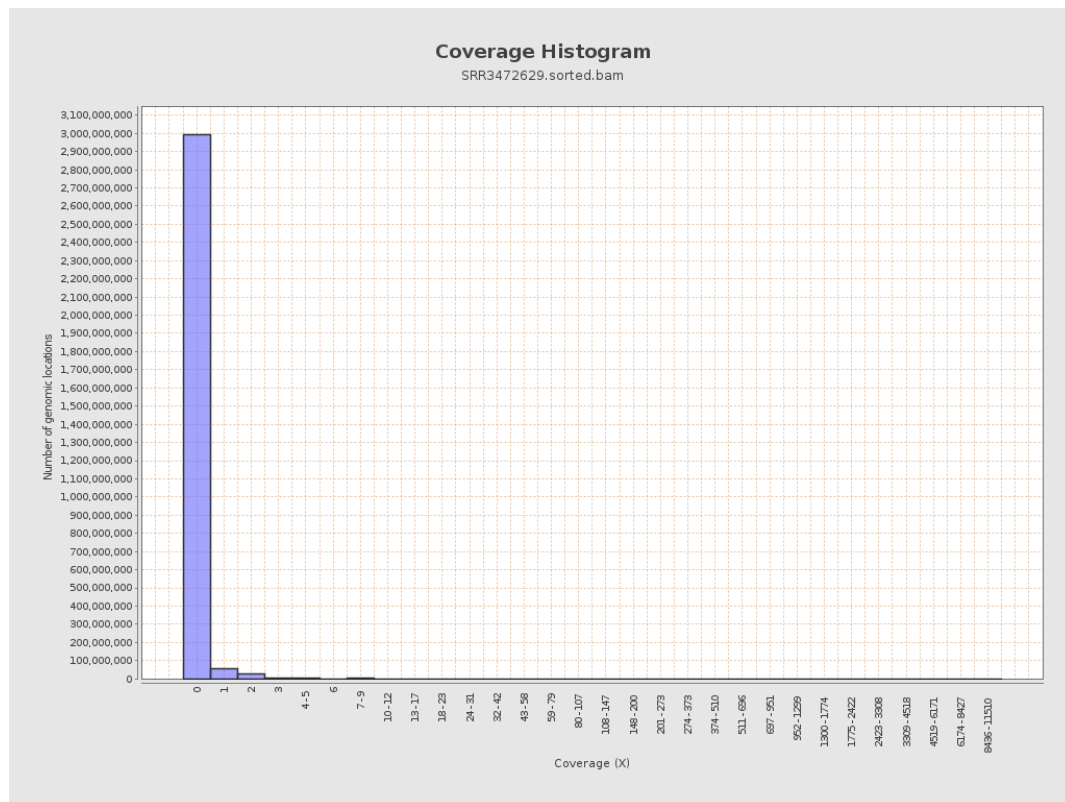
		bases	coverage	deviation
chr1	249250621	252398449	1.0126	32.4479
chr2	243199373	122866528	0.5052	23.487
chr3	198022430	134439453	0.6789	18.1368
chr4	191154276	26221224	0.1372	7.0434
chr5	180915260	67074788	0.3708	15.2276
chr6	171115067	138022814	0.8066	23.3655
chr7	159138663	96394875	0.6057	31.4421
chr8	146364022	68424903	0.4675	14.3472
chr9	141213431	62658077	0.4437	15.3644
chr10	135534747	29215458	0.2156	8.6199
chr11	135006516	36025229	0.2668	12.8717
chr12	133851895	68281657	0.5101	13.4822
chr13	115169878	59664495	0.5181	20.5665
chr14	107349540	17785482	0.1657	7.0499
chr15	102531392	28666174	0.2796	16.9579
chr16	90354753	86503359	0.9574	32.0945
chr17	81195210	66082336	0.8139	23.8186
chr18	78077248	16936226	0.2169	7.777
chr19	59128983	50393651	0.8523	24.3762
chr20	63025520	62777058	0.9961	25.9278
chr21	48129895	7487138	0.1556	6.6576
chr22	51304566	31065935	0.6055	17.0011
chrMT	16571	1206	0.0728	0.2882
chrX	155270560	65746734	0.4234	14.8126

chrY	59373566	2559945	0.0431	2.9086
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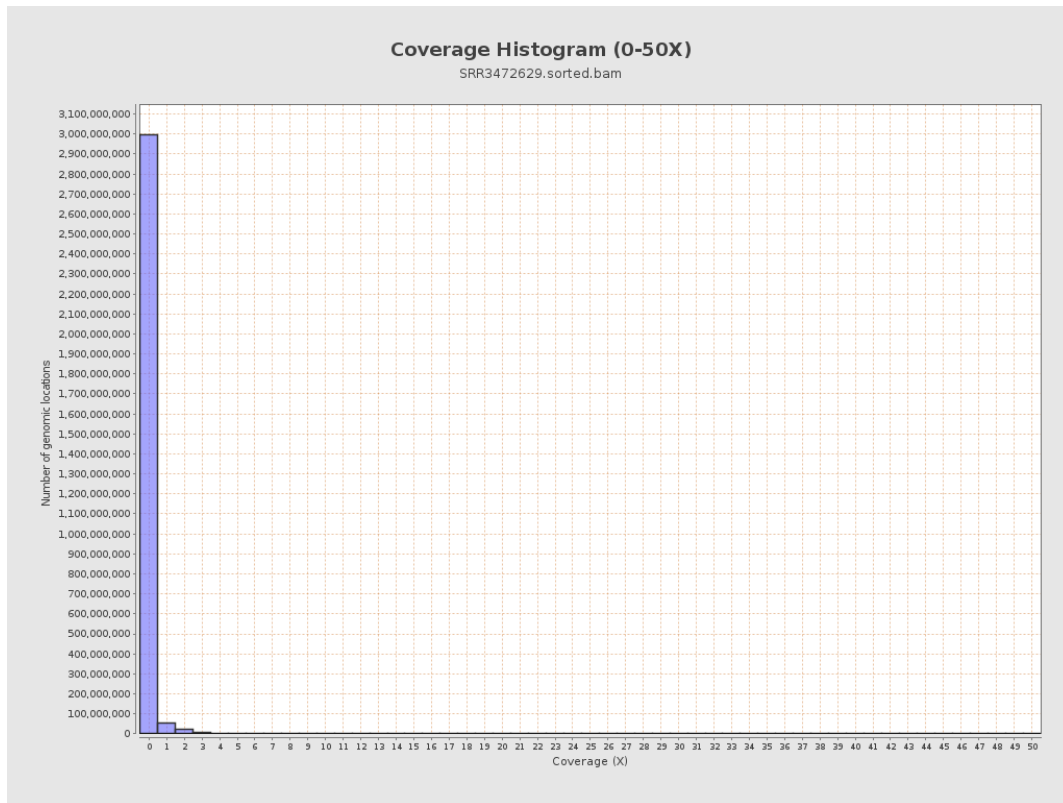
3. Results : Coverage across reference



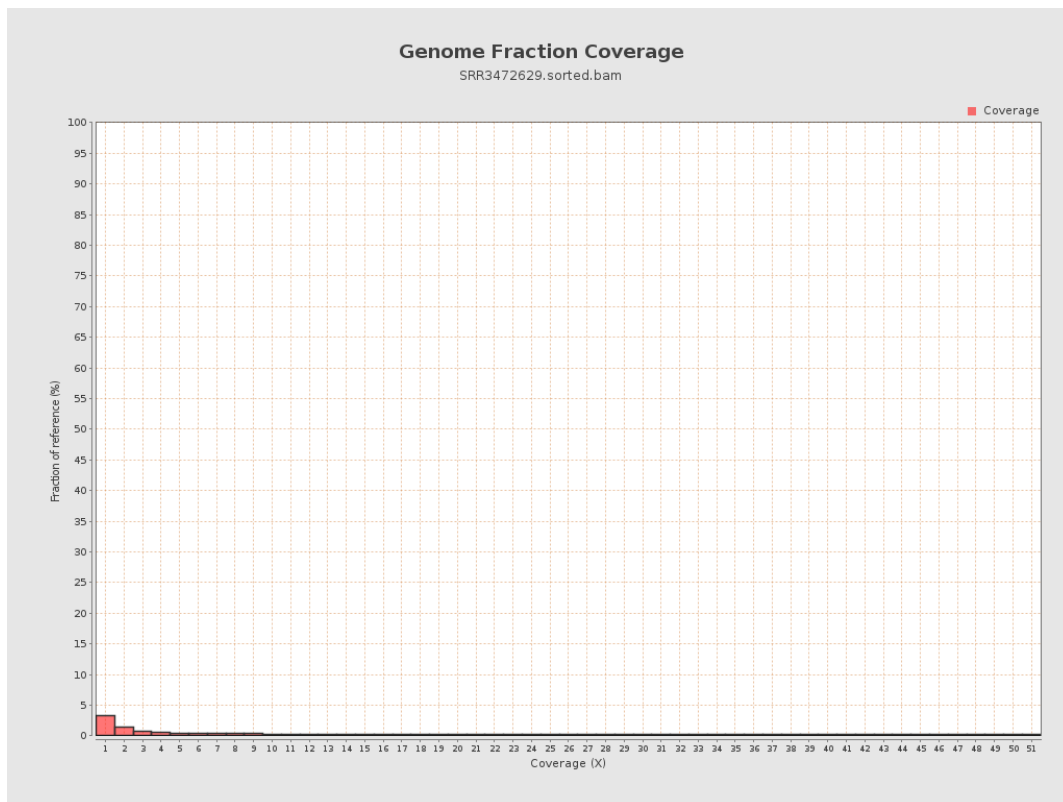
4. Results : Coverage Histogram



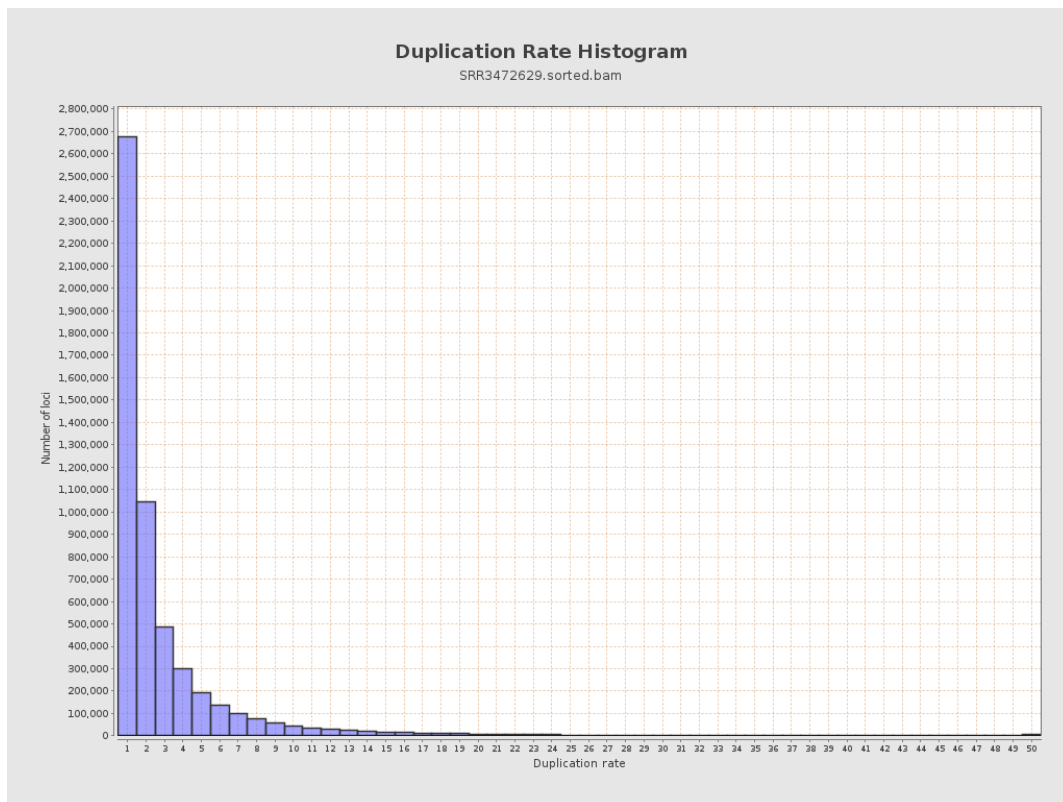
5. Results : Coverage Histogram (0-50X)



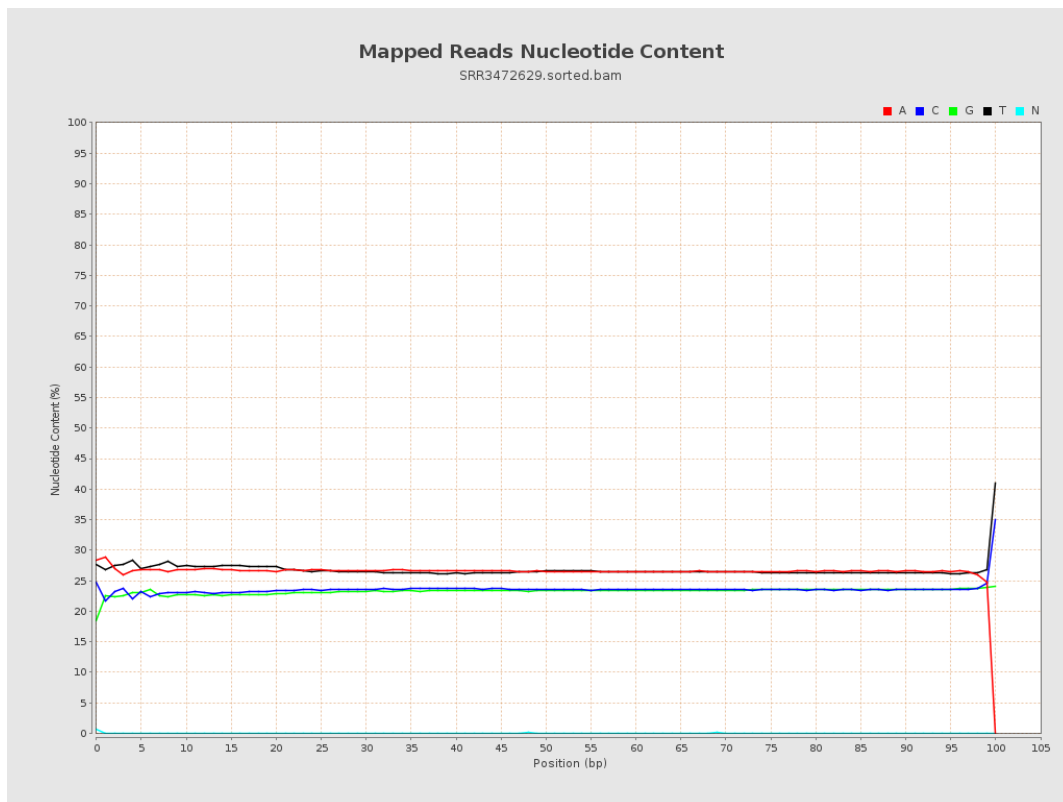
6. Results : Genome Fraction Coverage



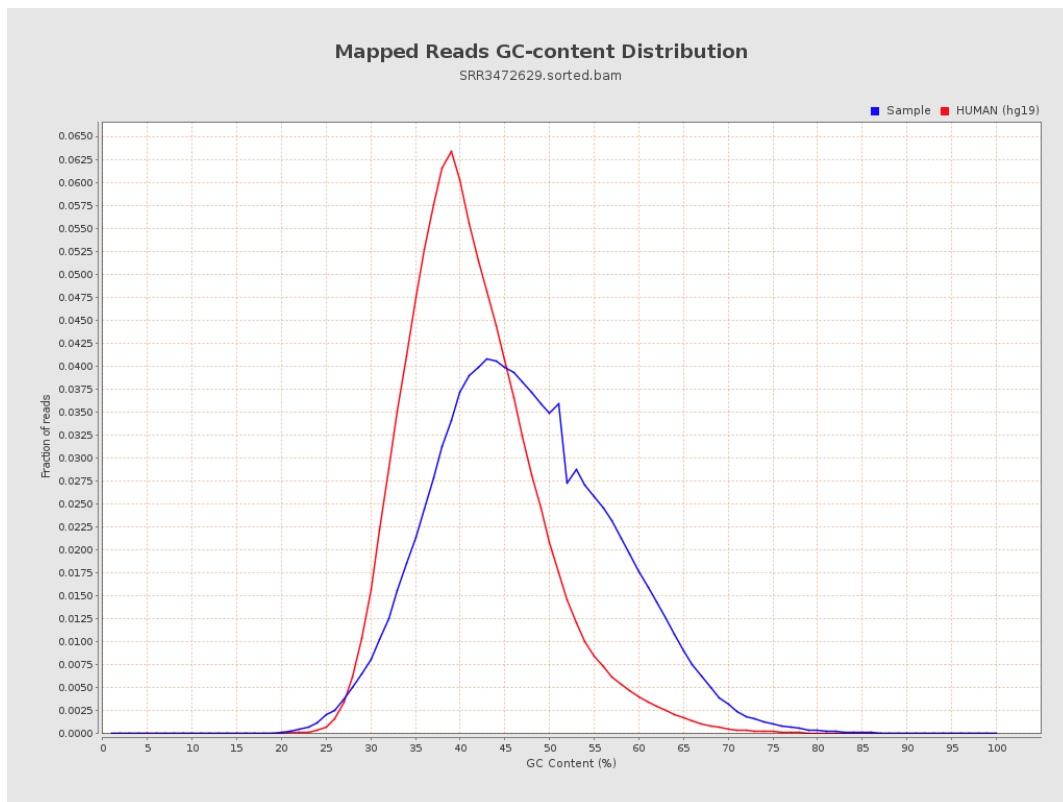
7. Results : Duplication Rate Histogram



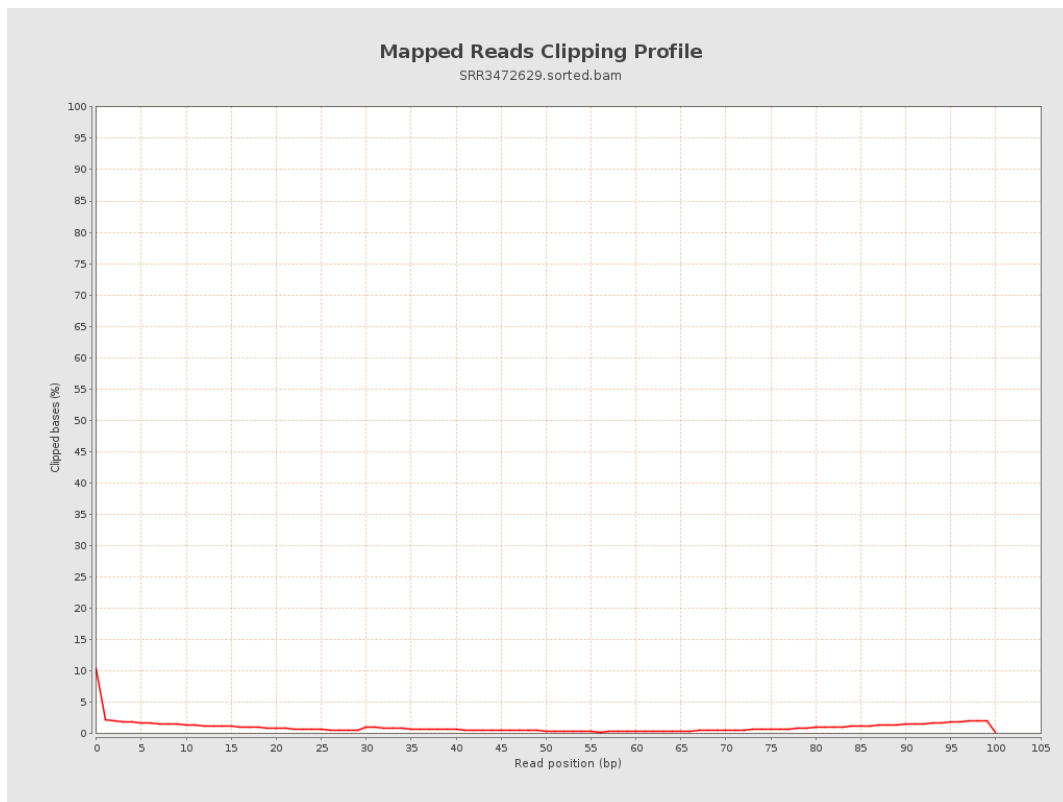
8. Results : Mapped Reads Nucleotide Content



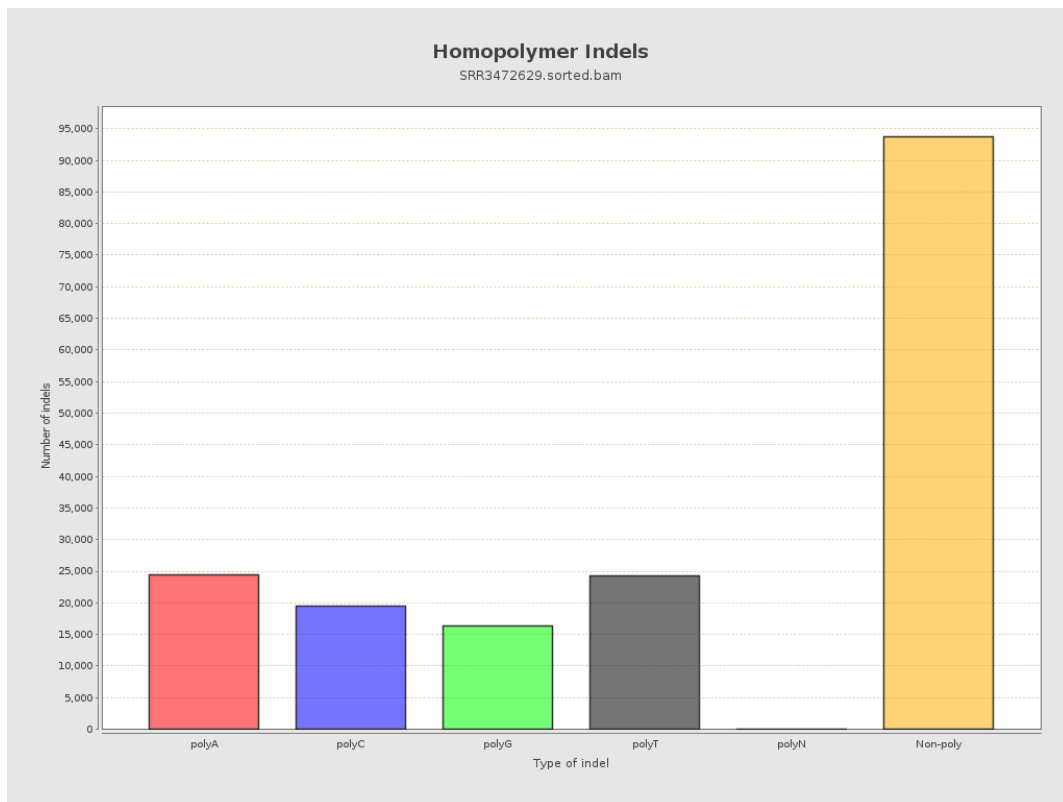
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



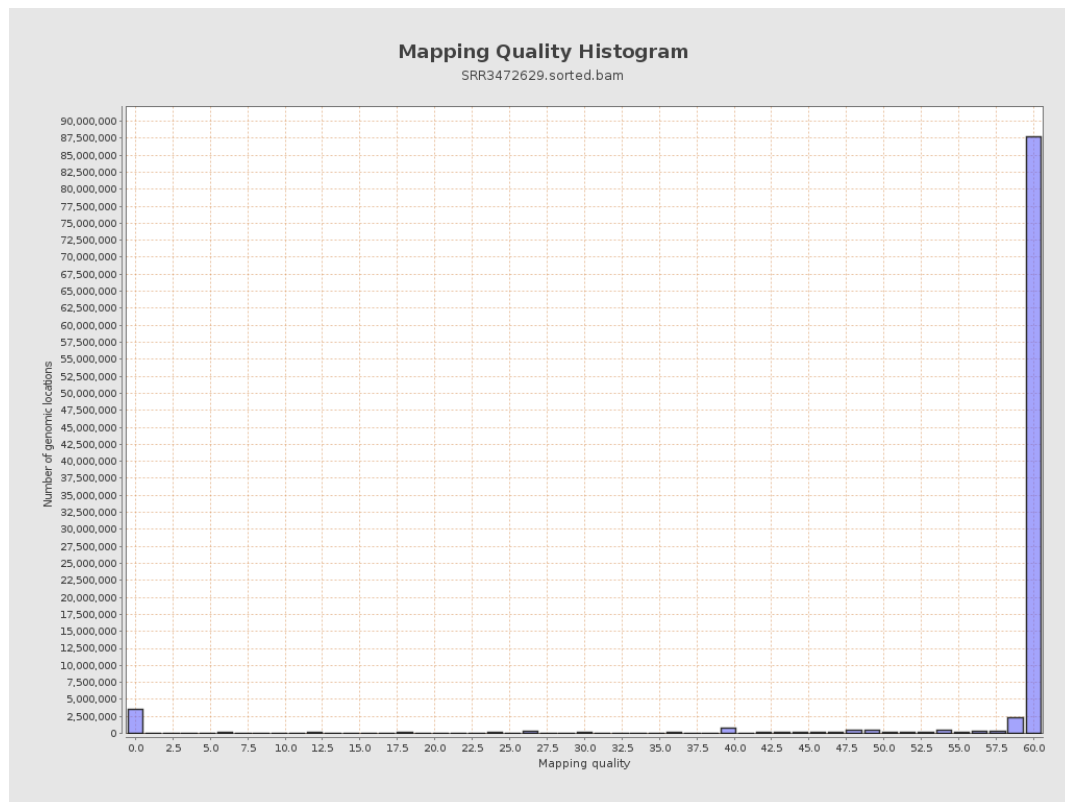
11. Results : Homopolymer Indels



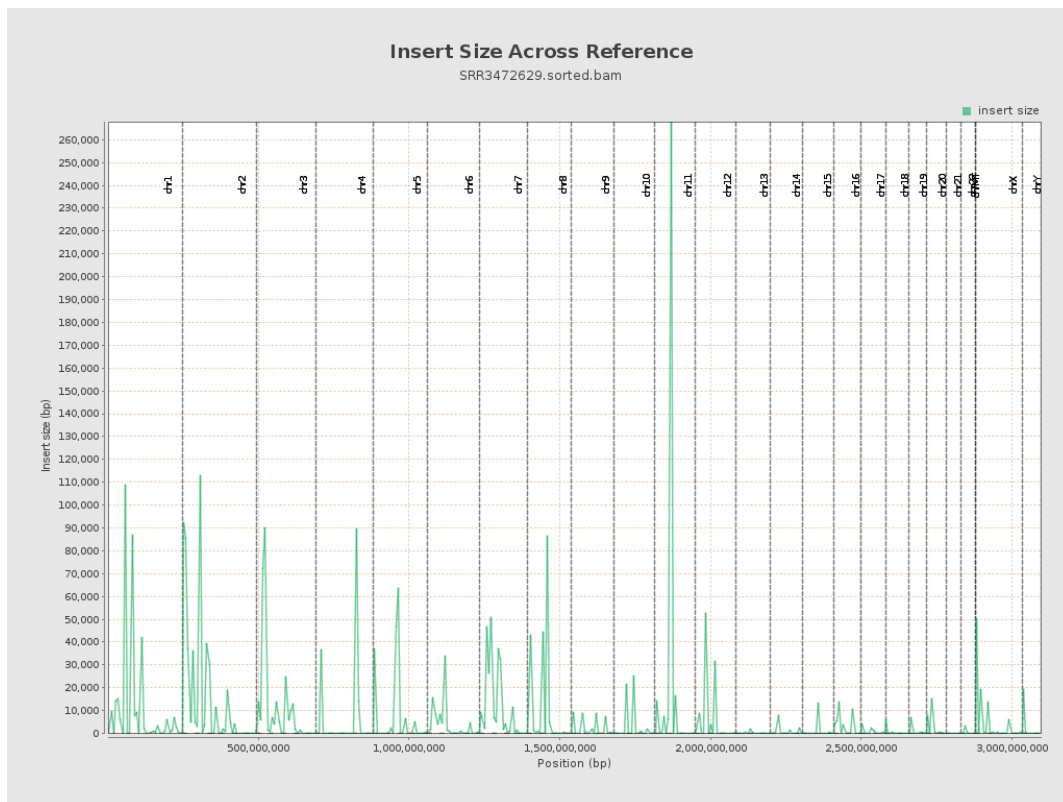
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

