

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 13:32:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006017.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_SRR1006017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006017_1.fastq.gz SRR1006017_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 13:32:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,982,520
Mapped reads	12,211,815 / 71.91%
Unmapped reads	4,770,705 / 28.09%
Mapped paired reads	12,211,815 / 71.91%
Mapped reads, first in pair	6,155,461 / 36.25%
Mapped reads, second in pair	6,056,354 / 35.66%
Mapped reads, both in pair	10,805,582 / 63.63%
Mapped reads, singletons	1,406,233 / 8.28%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	702,310 / 4.14%
Duplication rate	5.13%
Clipped reads	999,390 / 5.88%

2.2. ACGT Content

Number/percentage of A's	134,865,192 / 28.59%
Number/percentage of C's	99,243,316 / 21.04%
Number/percentage of T's	135,189,456 / 28.66%
Number/percentage of G's	102,093,217 / 21.64%
Number/percentage of N's	363,368 / 0.08%
GC Percentage	42.68%

2.3. Coverage

Mean	0.1524
Standard Deviation	0.6876

2.4. Mapping Quality

Mean Mapping Quality	47.35
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2.5. Insert size

Mean	62,748.47
Standard Deviation	2,426,919.43
P25/Median/P75	72 / 107 / 159

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	3,139,406
Insertions	13,707
Mapped reads with at least one insertion	0.11%
Deletions	39,673
Mapped reads with at least one deletion	0.32%
Homopolymer indels	44.74%

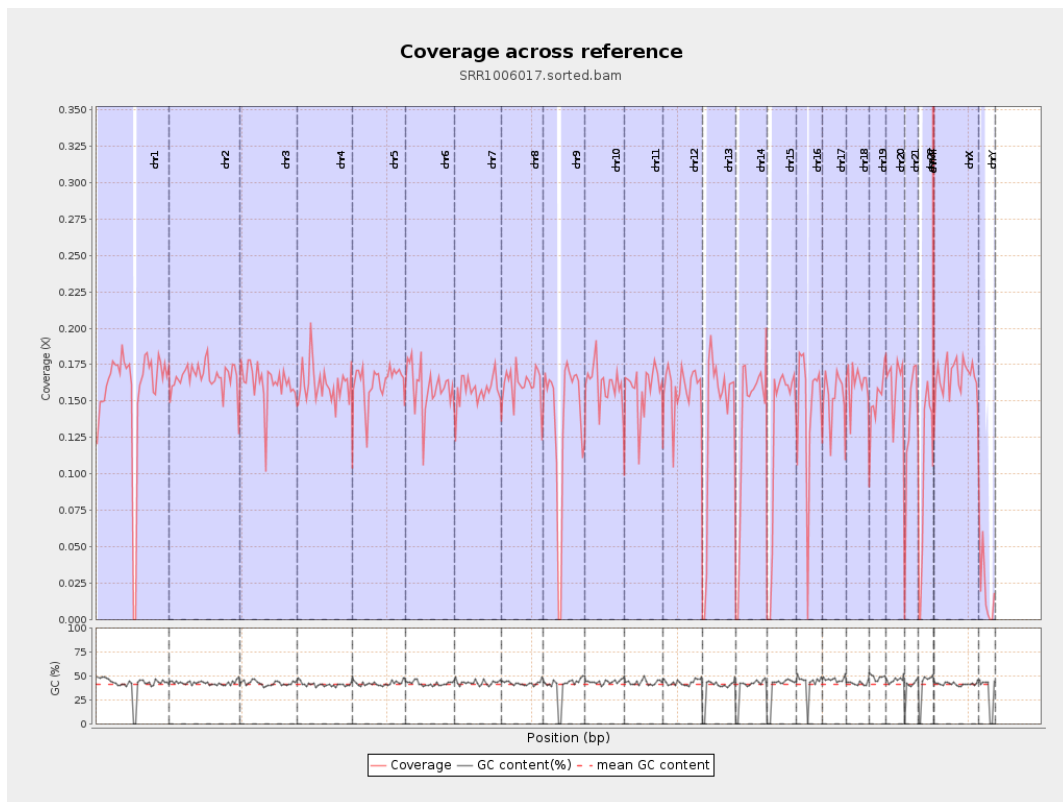
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

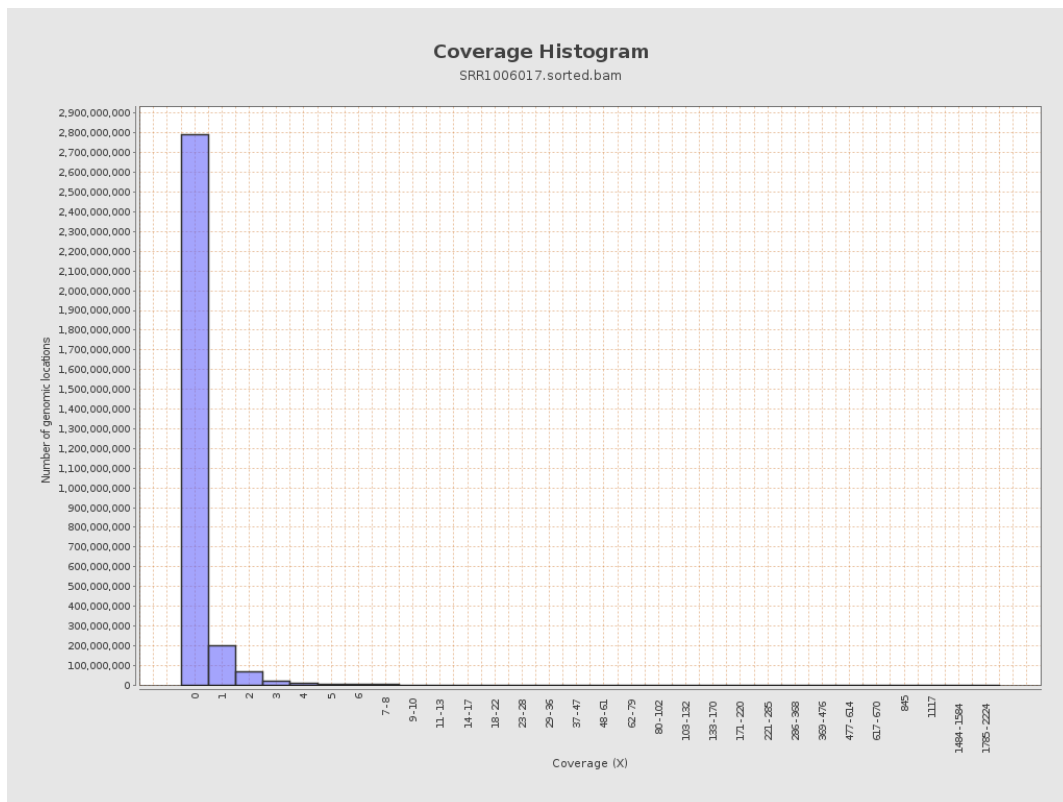
chr1	249250621	39030921	0.1566	0.7814
chr2	243199373	40564353	0.1668	0.7089
chr3	198022430	32163442	0.1624	0.5741
chr4	191154276	30900890	0.1617	0.6408
chr5	180915260	29475144	0.1629	0.5776
chr6	171115067	27288758	0.1595	0.6957
chr7	159138663	25139573	0.158	0.7207
chr8	146364022	23666007	0.1617	1.2343
chr9	141213431	19436390	0.1376	0.6082
chr10	135534747	21995887	0.1623	0.7404
chr11	135006516	21352364	0.1582	0.624
chr12	133851895	21230396	0.1586	0.5779
chr13	115169878	15738717	0.1367	0.5368
chr14	107349540	14405626	0.1342	0.5429
chr15	102531392	13290678	0.1296	0.5128
chr16	90354753	13278335	0.147	0.6093
chr17	81195210	12284829	0.1513	0.5744
chr18	78077248	12694980	0.1626	0.8401
chr19	59128983	9000356	0.1522	0.8457
chr20	63025520	10124017	0.1606	0.6075
chr21	48129895	6371975	0.1324	0.5853
chr22	51304566	5207127	0.1015	0.491
chrMT	16571	123531	7.4546	6.3282
chrX	155270560	25878865	0.1667	0.618

chrY	59373566	1162025	0.0196	0.3841
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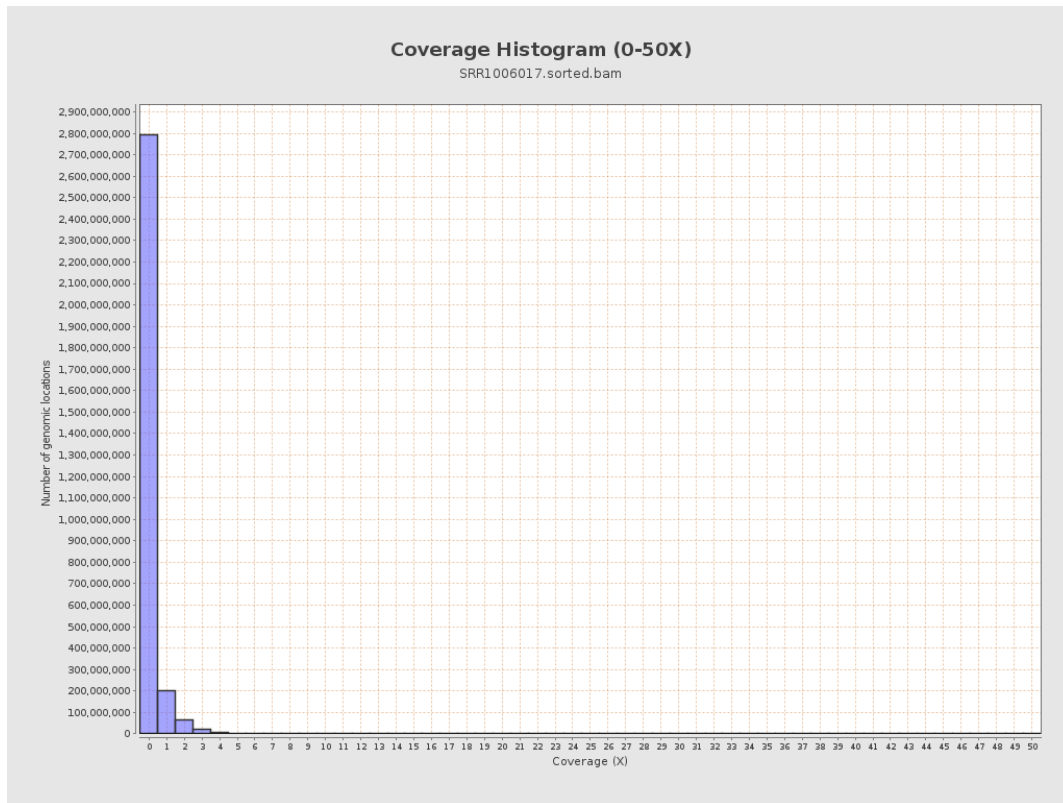
3. Results : Coverage across reference



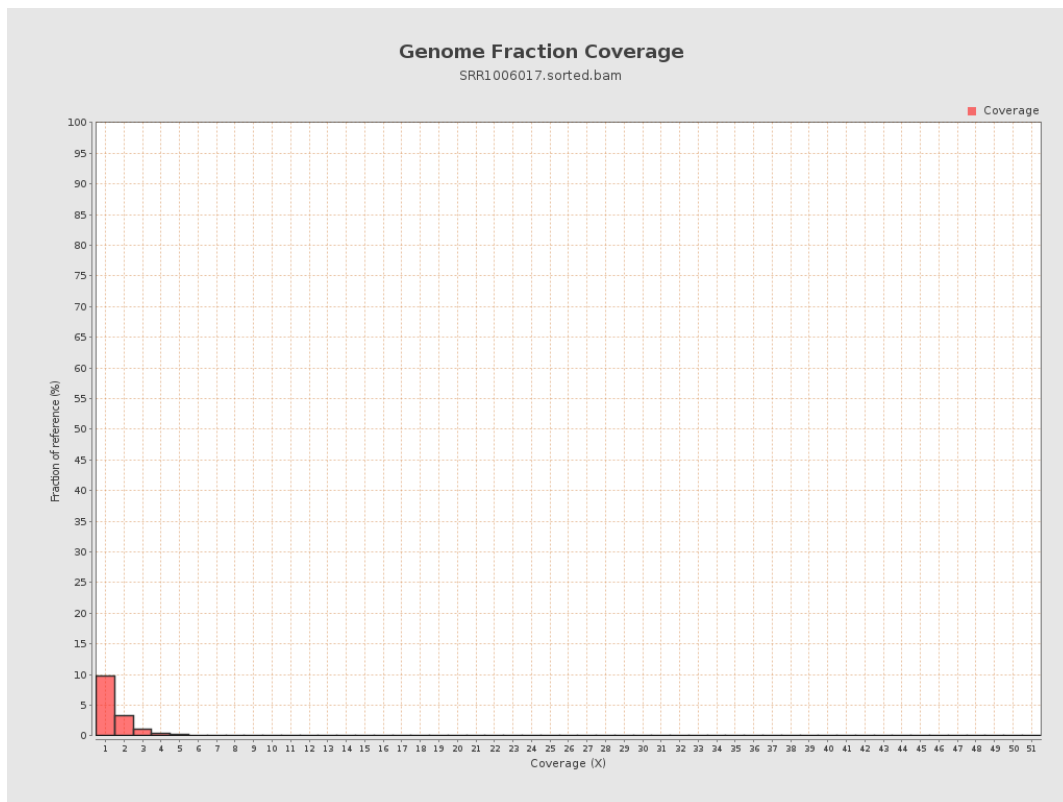
4. Results : Coverage Histogram



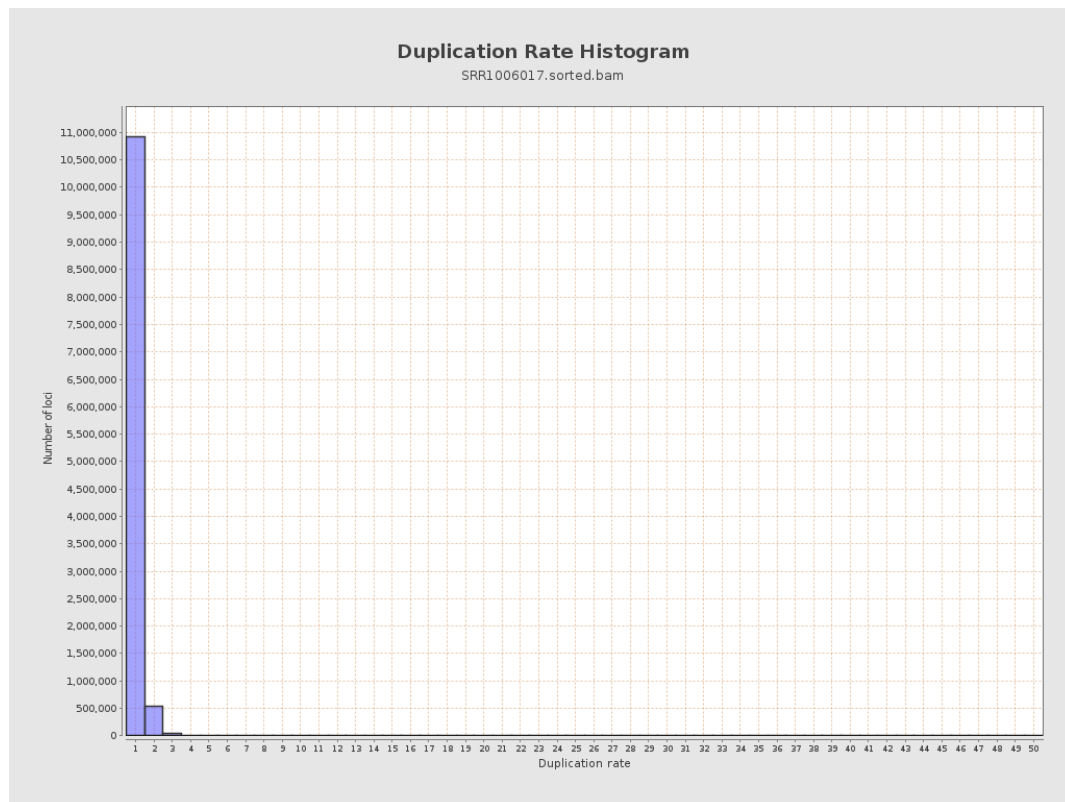
5. Results : Coverage Histogram (0-50X)



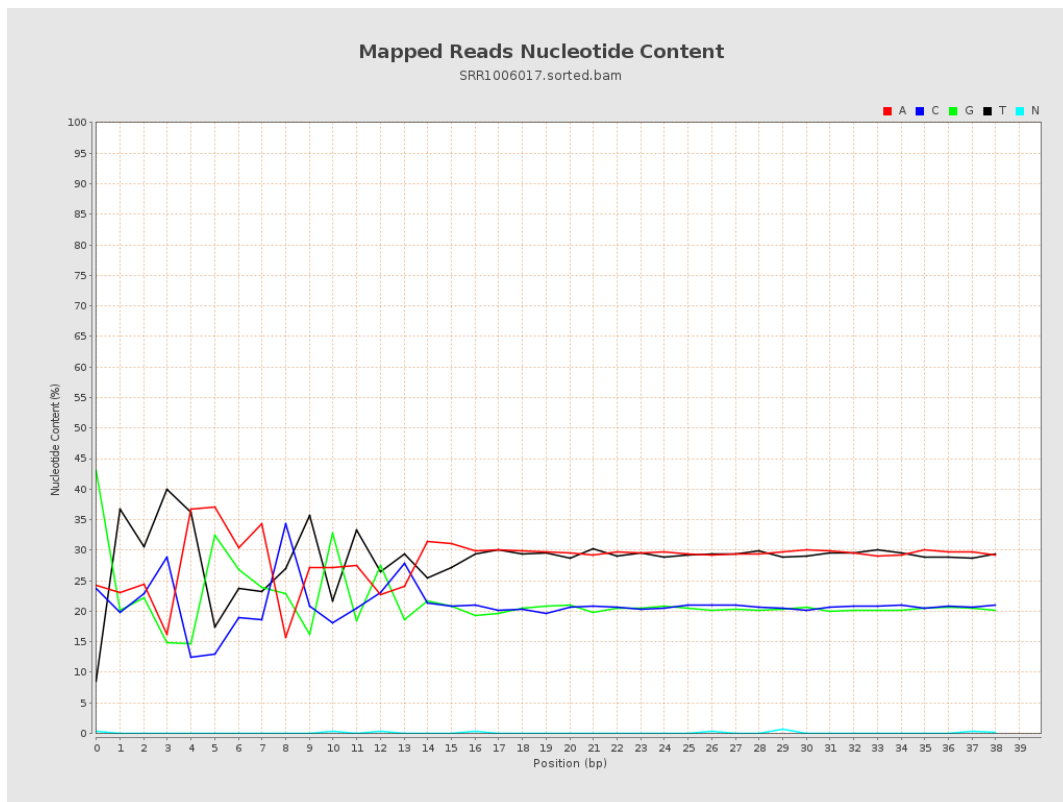
6. Results : Genome Fraction Coverage



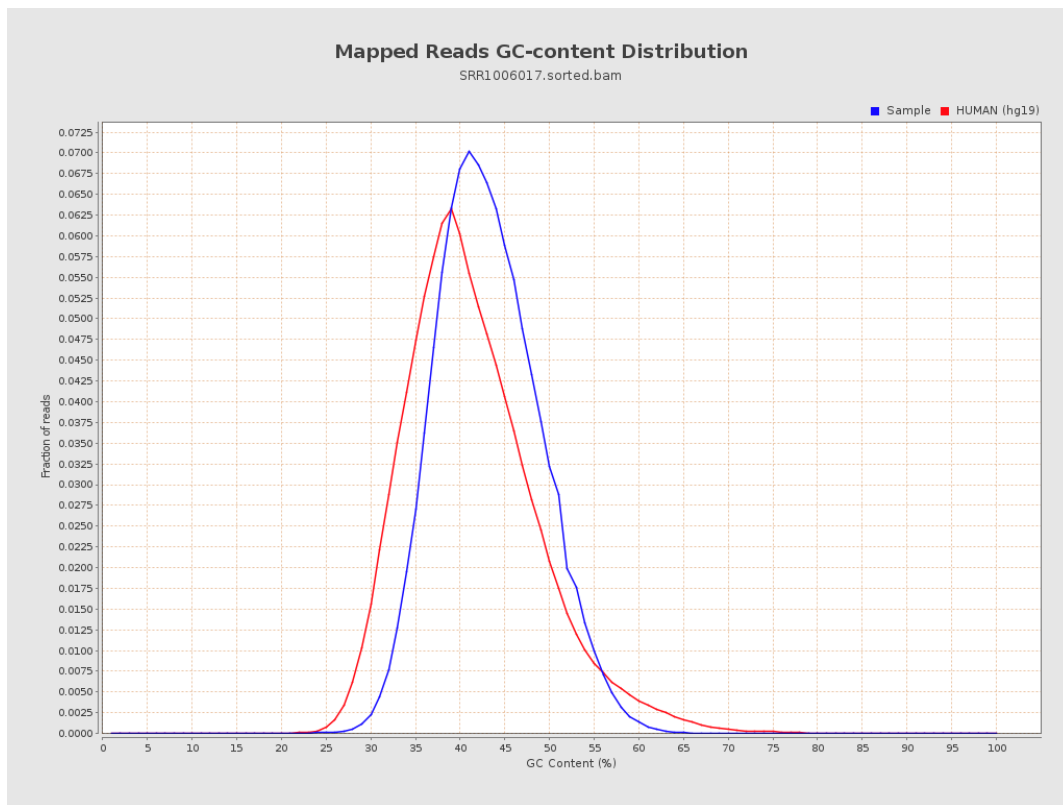
7. Results : Duplication Rate Histogram



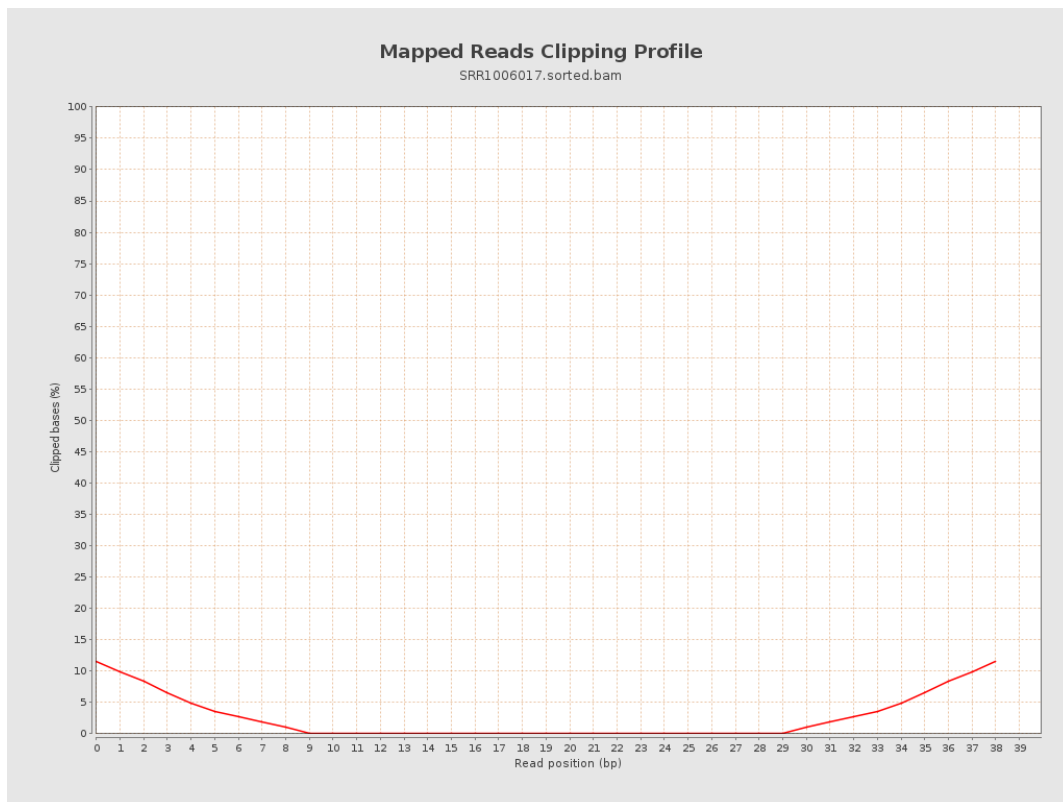
8. Results : Mapped Reads Nucleotide Content



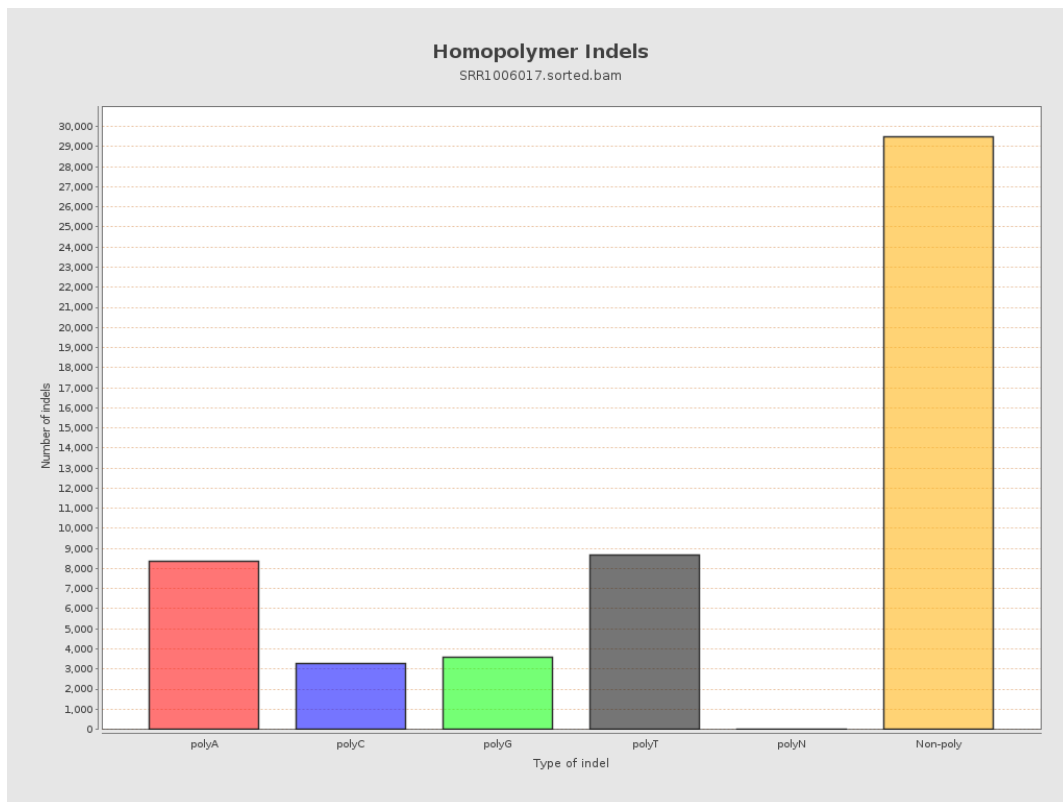
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



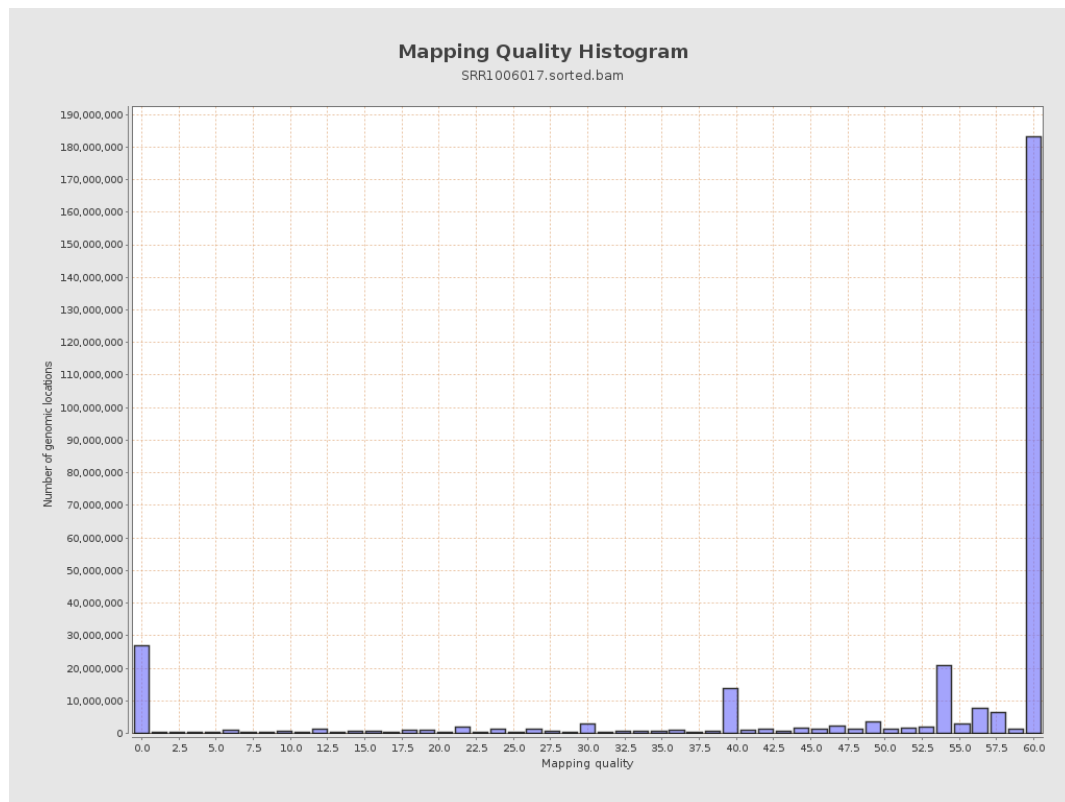
11. Results : Homopolymer Indels



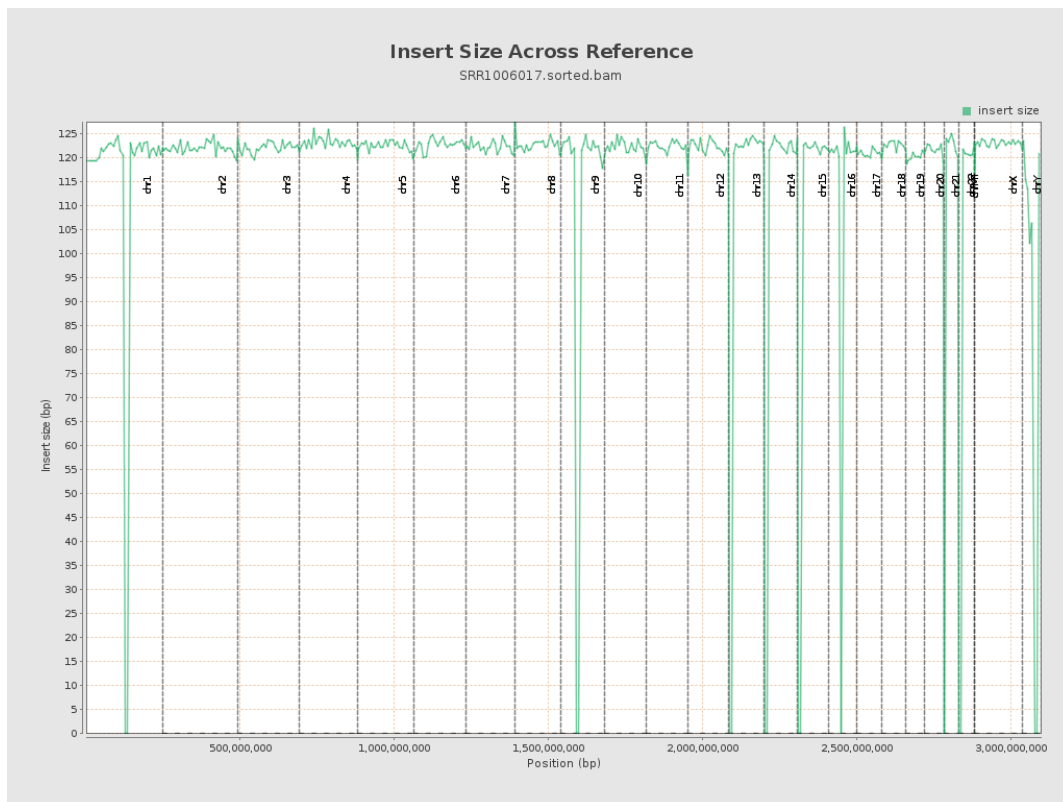
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

