

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:05:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006189.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_SRR1006189 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006189_1.fastq.gz SRR1006189_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:05:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006189.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,589,956
Mapped reads	6,443,589 / 84.9%
Unmapped reads	1,146,367 / 15.1%
Mapped paired reads	6,443,589 / 84.9%
Mapped reads, first in pair	3,245,233 / 42.76%
Mapped reads, second in pair	3,198,356 / 42.14%
Mapped reads, both in pair	5,975,700 / 78.73%
Mapped reads, singletons	467,889 / 6.16%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	216,659 / 2.85%
Duplication rate	2.79%
Clipped reads	370,342 / 4.88%

2.2. ACGT Content

Number/percentage of A's	67,686,015 / 27.14%
Number/percentage of C's	55,395,677 / 22.21%
Number/percentage of T's	69,059,146 / 27.69%
Number/percentage of G's	57,228,315 / 22.95%
Number/percentage of N's	29,810 / 0.01%
GC Percentage	45.16%

2.3. Coverage

Mean	0.0806
Standard Deviation	0.4487

2.4. Mapping Quality

Mean Mapping Quality	47.67
----------------------	-------

2.5. Insert size

Mean	50,250.12
Standard Deviation	2,125,720.75
P25/Median/P75	74 / 104 / 138

2.6. Mismatches and indels

General error rate	0.31%
Mismatches	777,008
Insertions	7,344
Mapped reads with at least one insertion	0.11%
Deletions	23,541
Mapped reads with at least one deletion	0.37%
Homopolymer indels	43.29%

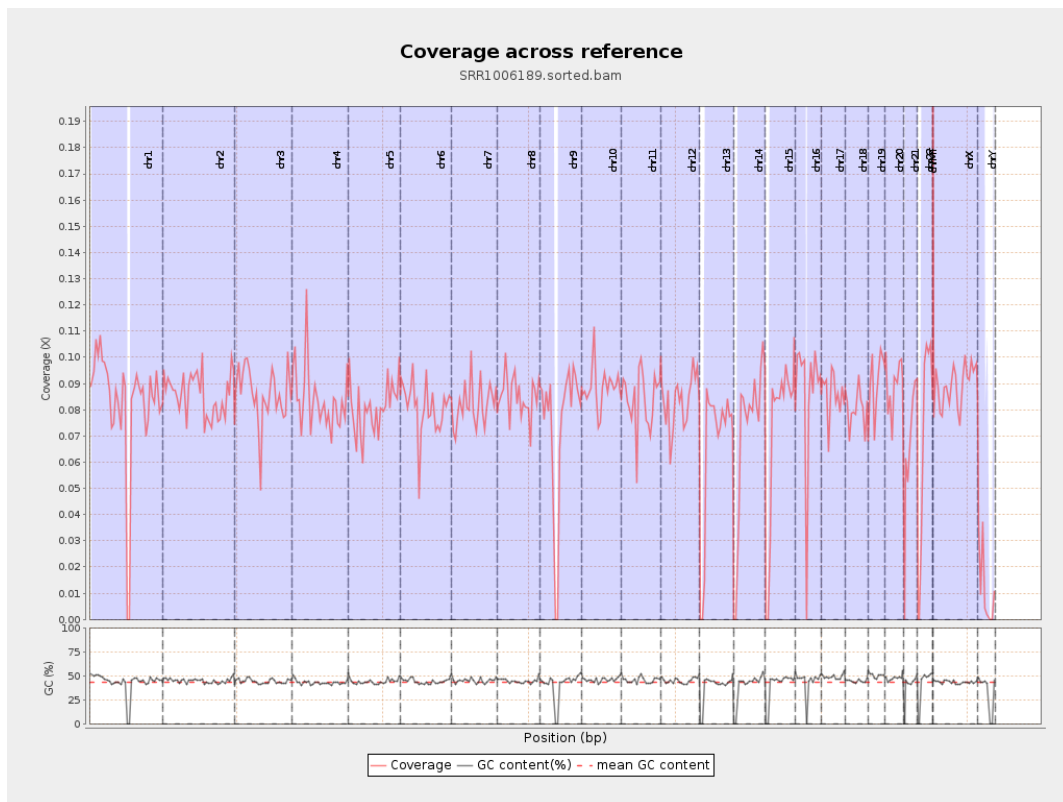
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

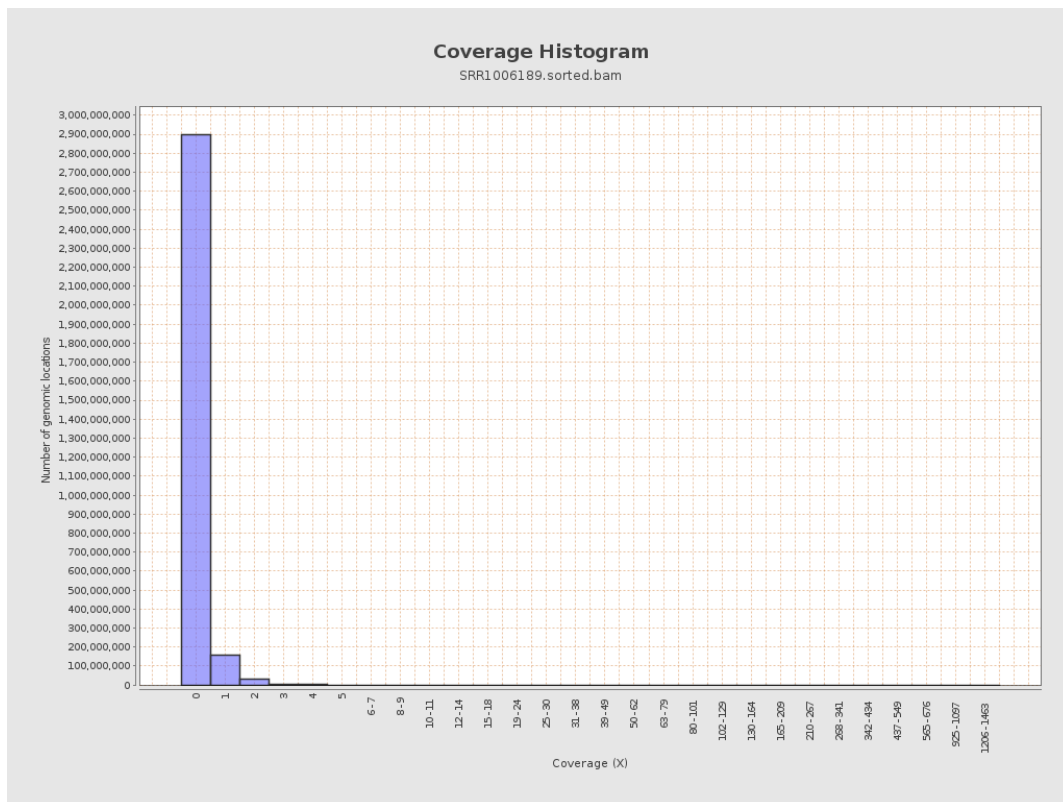
chr1	249250621	20604571	0.0827	0.5283
chr2	243199373	20889109	0.0859	0.4297
chr3	198022430	16979729	0.0857	0.3521
chr4	191154276	16056031	0.084	0.4124
chr5	180915260	14646581	0.081	0.3422
chr6	171115067	13830199	0.0808	0.3691
chr7	159138663	13059486	0.0821	0.4606
chr8	146364022	12445402	0.085	0.7976
chr9	141213431	10491342	0.0743	0.3697
chr10	135534747	11951919	0.0882	0.4977
chr11	135006516	11311681	0.0838	0.4065
chr12	133851895	11220000	0.0838	0.3506
chr13	115169878	7586836	0.0659	0.3102
chr14	107349540	7655004	0.0713	0.7212
chr15	102531392	7333957	0.0715	0.3252
chr16	90354753	7782428	0.0861	0.4094
chr17	81195210	7003095	0.0863	0.3693
chr18	78077248	6239874	0.0799	0.5226
chr19	59128983	5356036	0.0906	0.4714
chr20	63025520	5613378	0.0891	0.3851
chr21	48129895	3253314	0.0676	0.391
chr22	51304566	3574474	0.0697	0.348
chrMT	16571	4111	0.2481	0.6963
chrX	155270560	13857457	0.0892	0.3786

chrY	59373566	684304	0.0115	0.2837
------	----------	--------	--------	--------

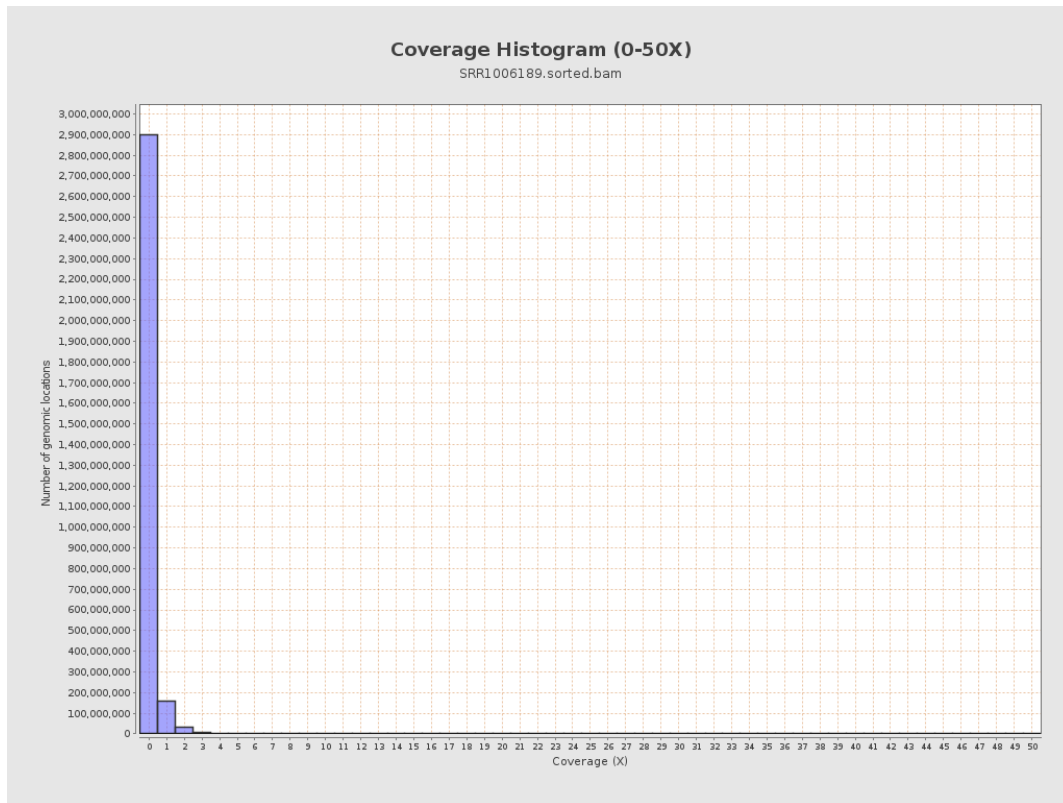
3. Results : Coverage across reference



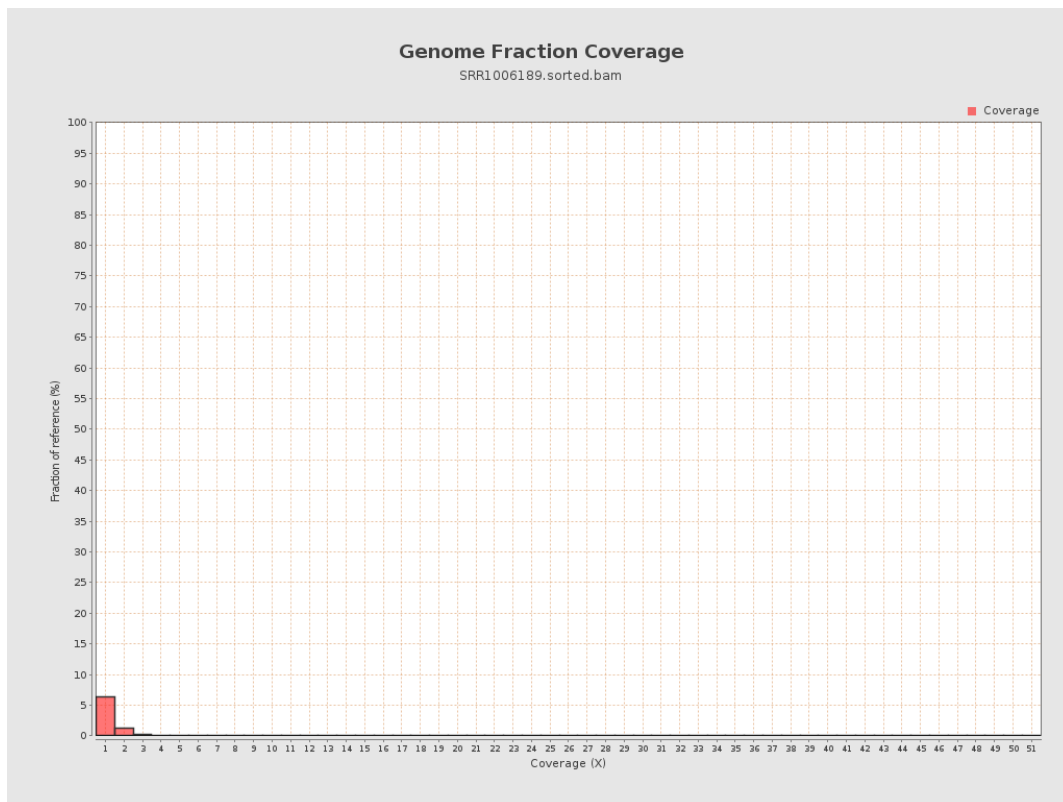
4. Results : Coverage Histogram



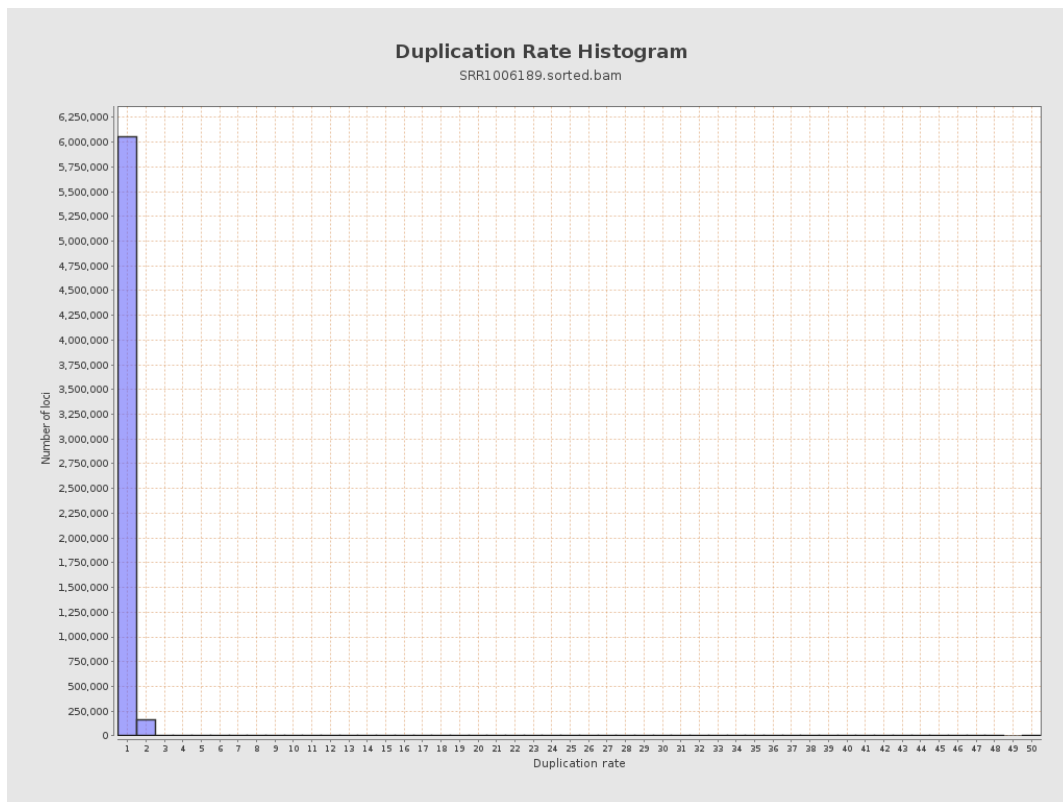
5. Results : Coverage Histogram (0-50X)



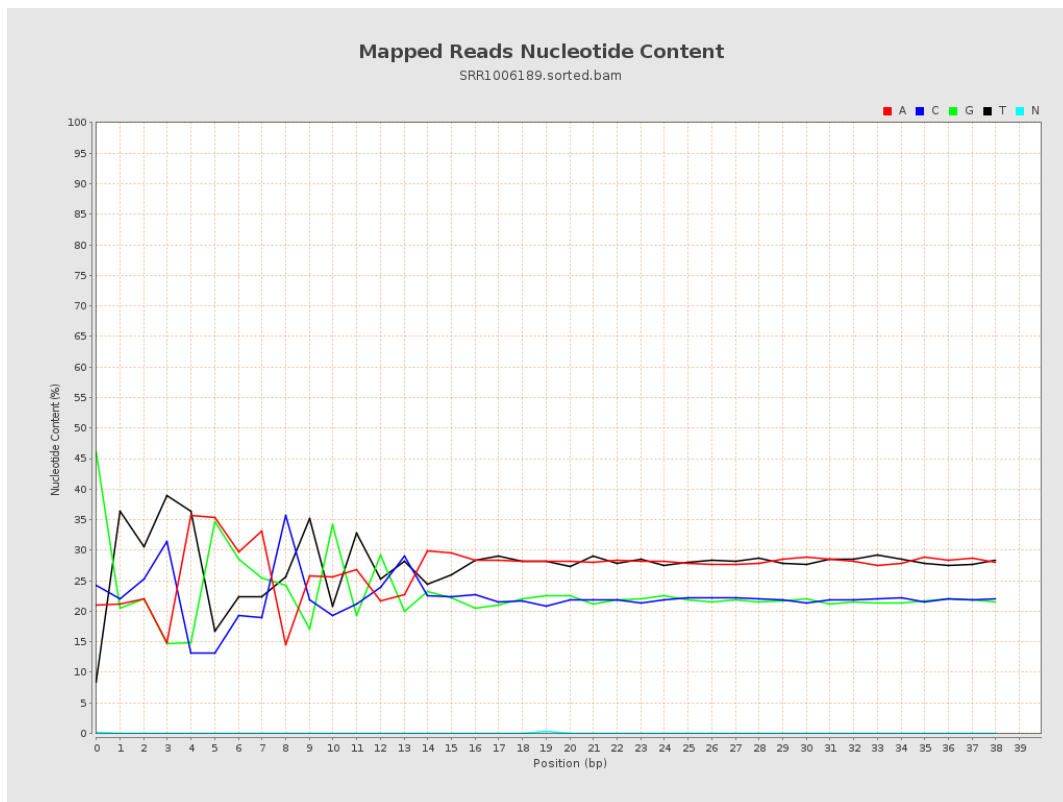
6. Results : Genome Fraction Coverage



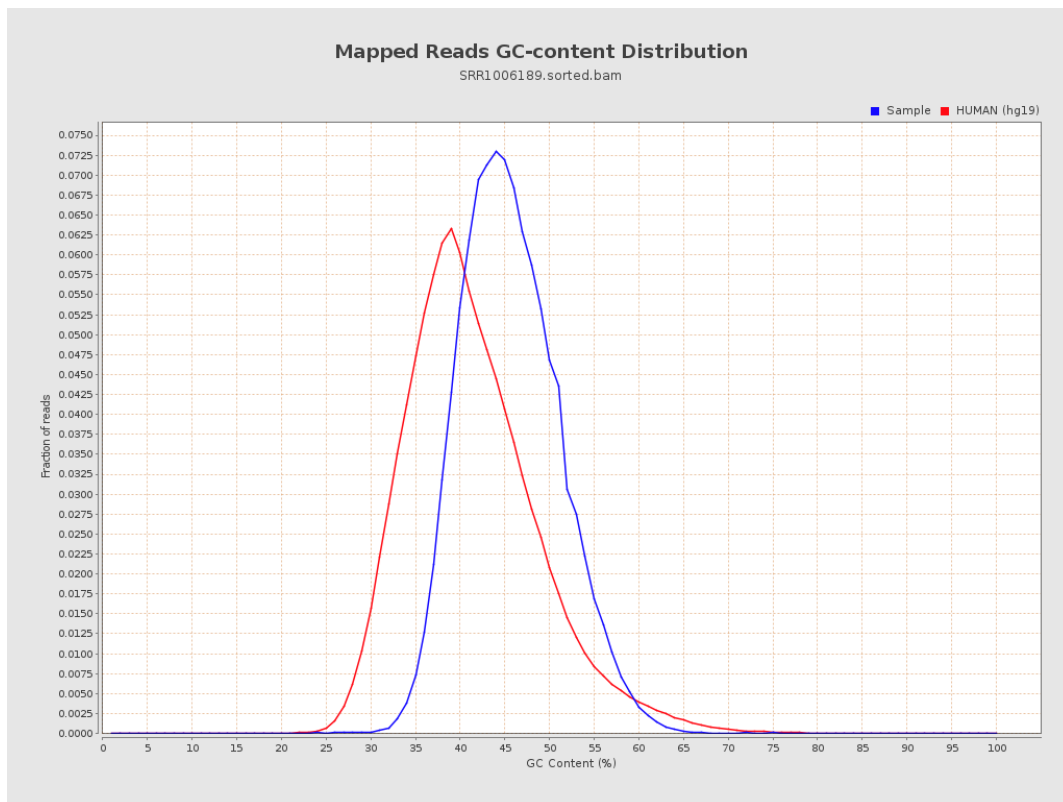
7. Results : Duplication Rate Histogram



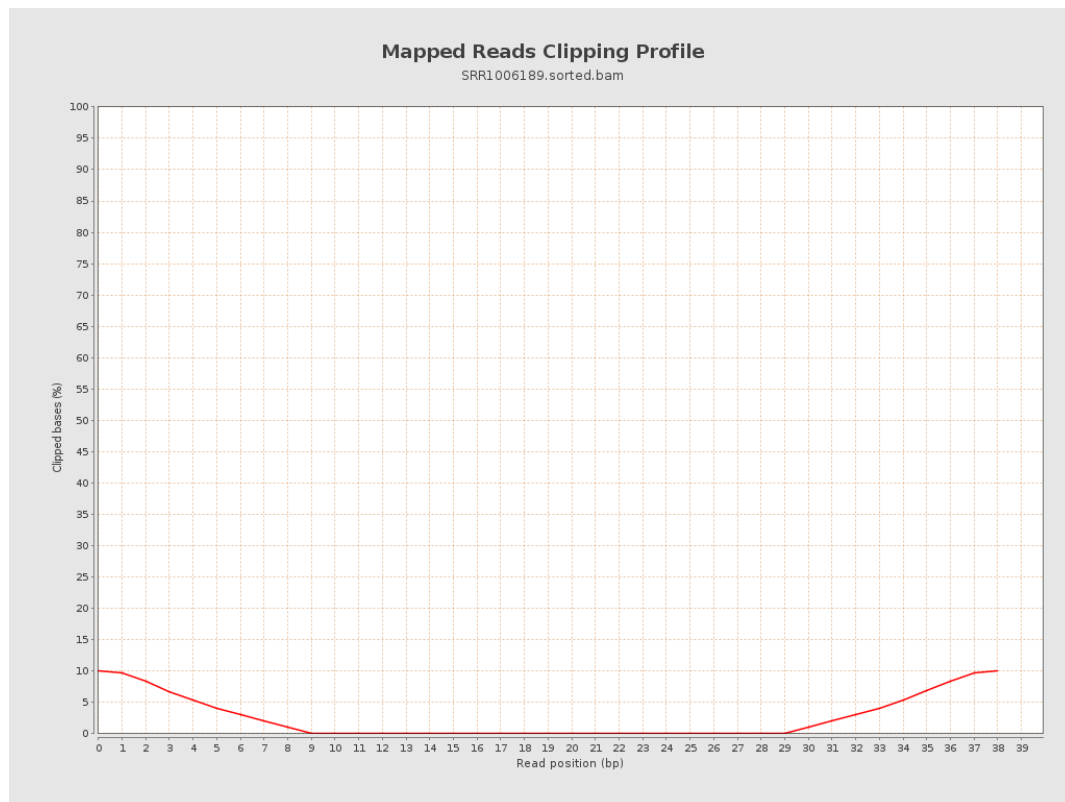
8. Results : Mapped Reads Nucleotide Content



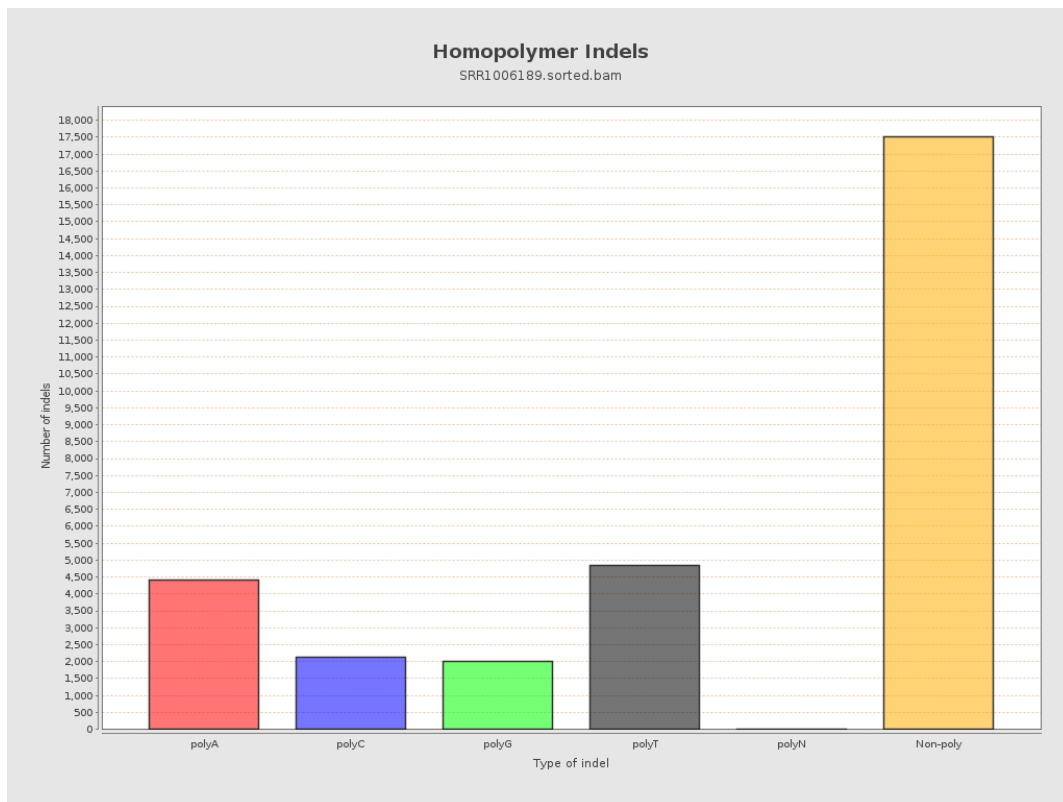
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



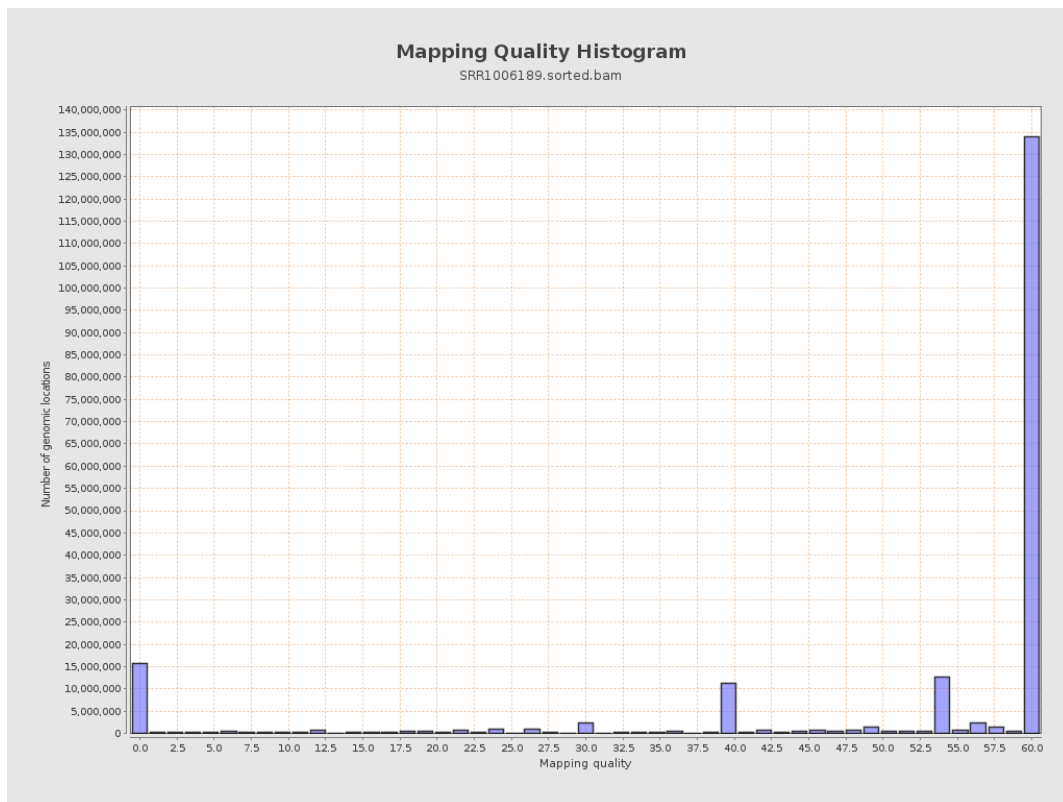
11. Results : Homopolymer Indels



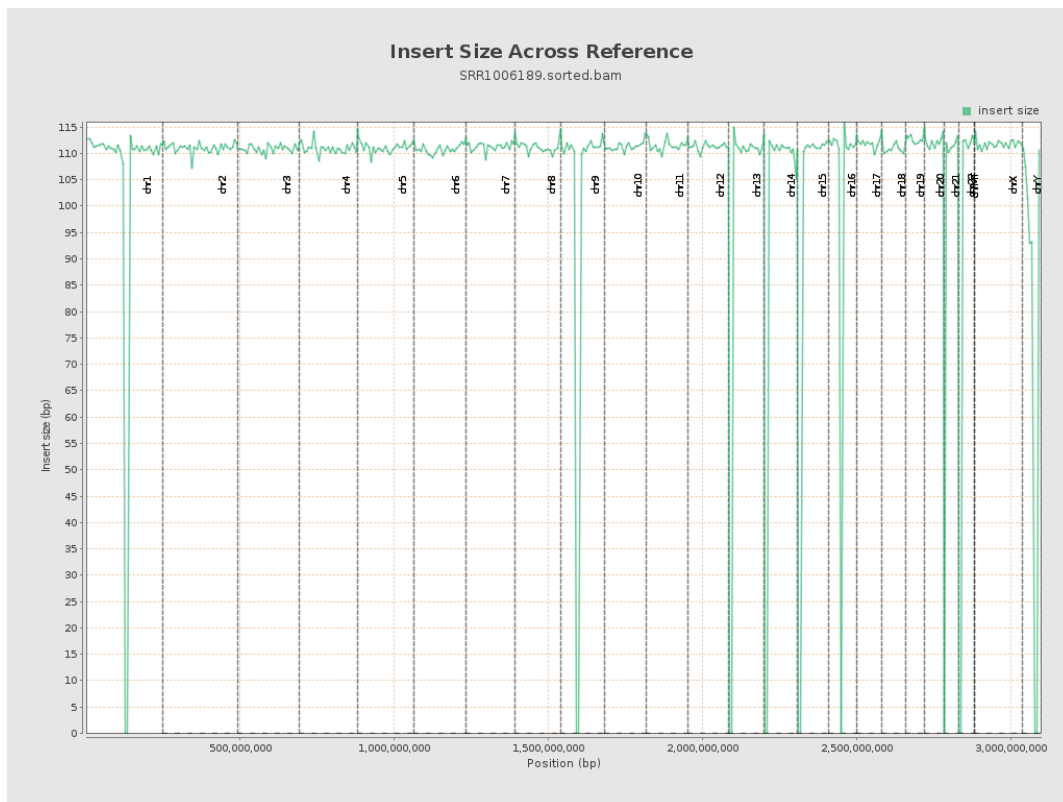
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

