

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 19:29:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046487.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_SRR2046487 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046487_1.fastq.gz SRR2046487_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 19:29:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046487.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,513,252
Mapped reads	8,469,064 / 99.48%
Unmapped reads	44,188 / 0.52%
Mapped paired reads	8,469,064 / 99.48%
Mapped reads, first in pair	4,246,888 / 49.89%
Mapped reads, second in pair	4,222,176 / 49.6%
Mapped reads, both in pair	8,435,478 / 99.09%
Mapped reads, singletons	33,586 / 0.39%
Secondary alignments	0
Supplementary alignments	77,893 / 0.91%
Read min/max/mean length	30 / 100 / 100.37
Duplicated reads (estimated)	6,793,954 / 79.8%
Duplication rate	26.46%
Clipped reads	1,491,176 / 17.52%

2.2. ACGT Content

Number/percentage of A's	220,460,947 / 26.81%
Number/percentage of C's	191,373,886 / 23.27%
Number/percentage of T's	216,698,483 / 26.35%
Number/percentage of G's	193,687,462 / 23.55%
Number/percentage of N's	65,647 / 0.01%

GC Percentage	46.83%
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2.3. Coverage

Mean	0.2657
Standard Deviation	57.8972

2.4. Mapping Quality

Mean Mapping Quality	51.45
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2.5. Insert size

Mean	63,576.46
Standard Deviation	2,669,158.69
P25/Median/P75	114 / 144 / 180

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	3,438,152
Insertions	56,900
Mapped reads with at least one insertion	0.66%
Deletions	64,421
Mapped reads with at least one deletion	0.74%
Homopolymer indels	49.58%

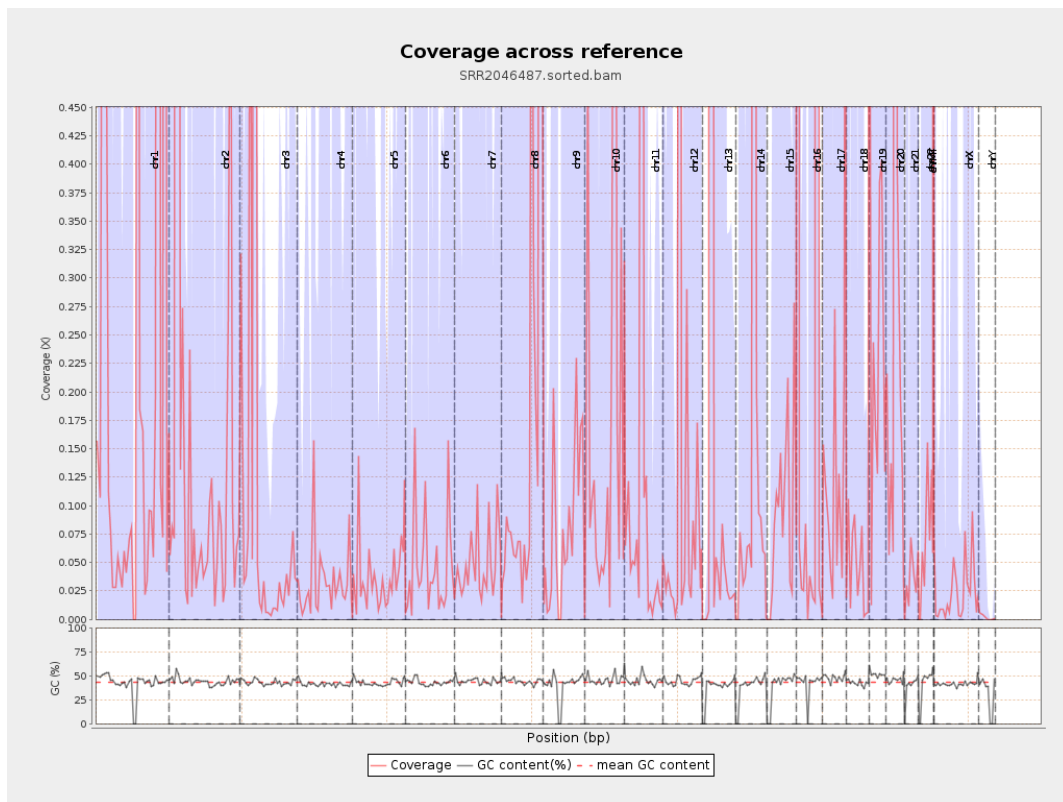
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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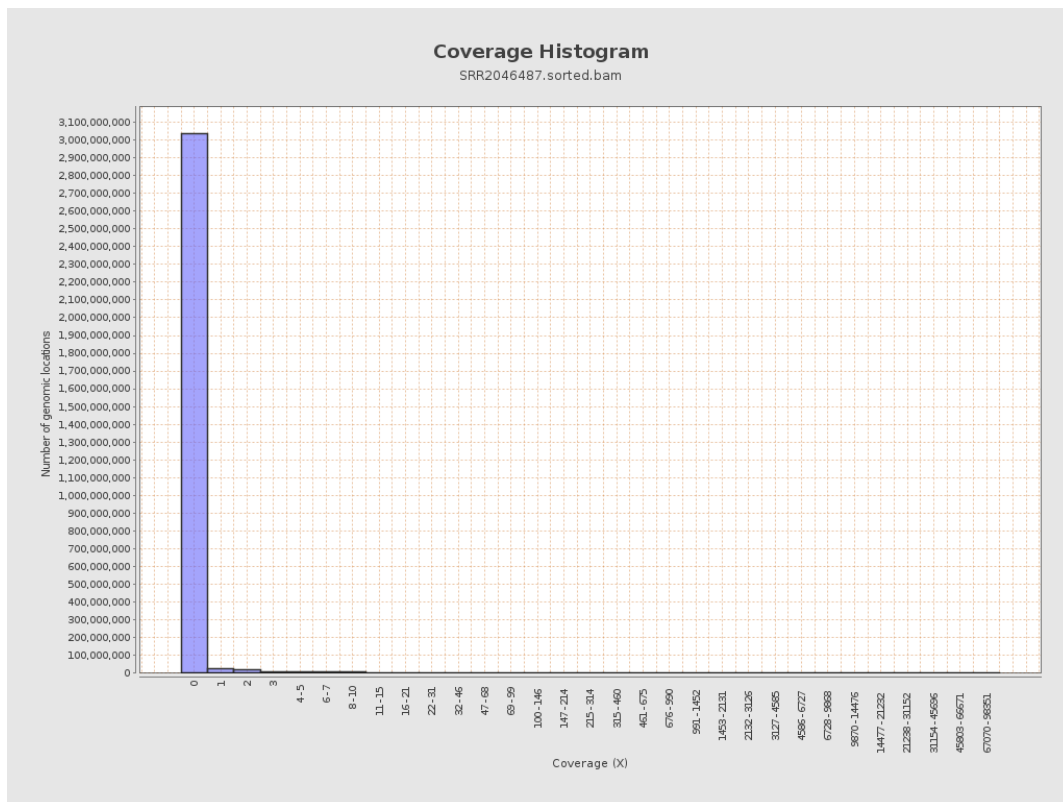
		bases	coverage	deviation
chr1	249250621	92411014	0.3708	40.2862
chr2	243199373	50327328	0.2069	21.2622
chr3	198022430	27263488	0.1377	14.985
chr4	191154276	6274715	0.0328	1.4468
chr5	180915260	6795875	0.0376	1.77
chr6	171115067	8024453	0.0469	1.7821
chr7	159138663	7792951	0.049	2.7087
chr8	146364022	34236026	0.2339	23.8618
chr9	141213431	11623206	0.0823	4.1461
chr10	135534747	25864507	0.1908	14.067
chr11	135006516	21253190	0.1574	25.6877
chr12	133851895	29430505	0.2199	24.2216
chr13	115169878	76215015	0.6618	128.3231
chr14	107349540	20504322	0.191	25.8237
chr15	102531392	9747529	0.0951	7.1898
chr16	90354753	329140313	3.6428	286.8874
chr17	81195210	11800132	0.1453	6.6792
chr18	78077248	3498501	0.0448	1.9634
chr19	59128983	14582145	0.2466	11.7588
chr20	63025520	26195342	0.4156	42.0916
chr21	48129895	1649456	0.0343	1.2305
chr22	51304566	3570469	0.0696	0.8575
chrMT	16571	259670	15.6701	6.6717
chrX	155270560	3911985	0.0252	1.2824

chrY	59373566	116312	0.002	0.092
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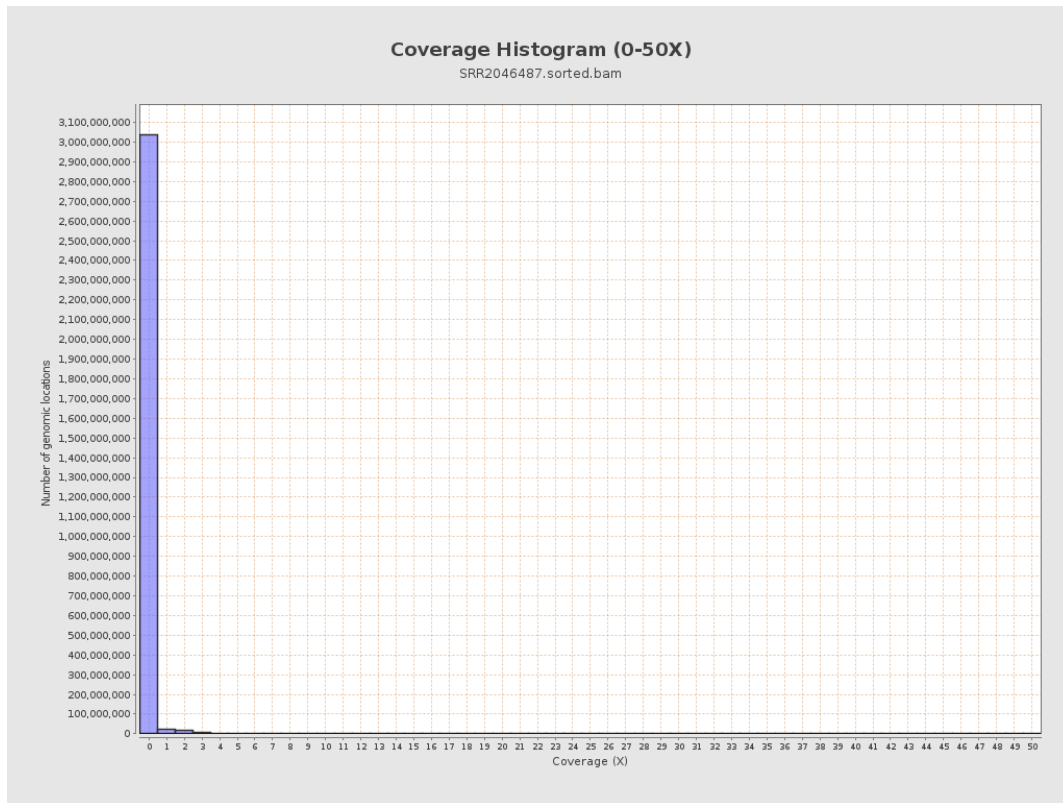
3. Results : Coverage across reference



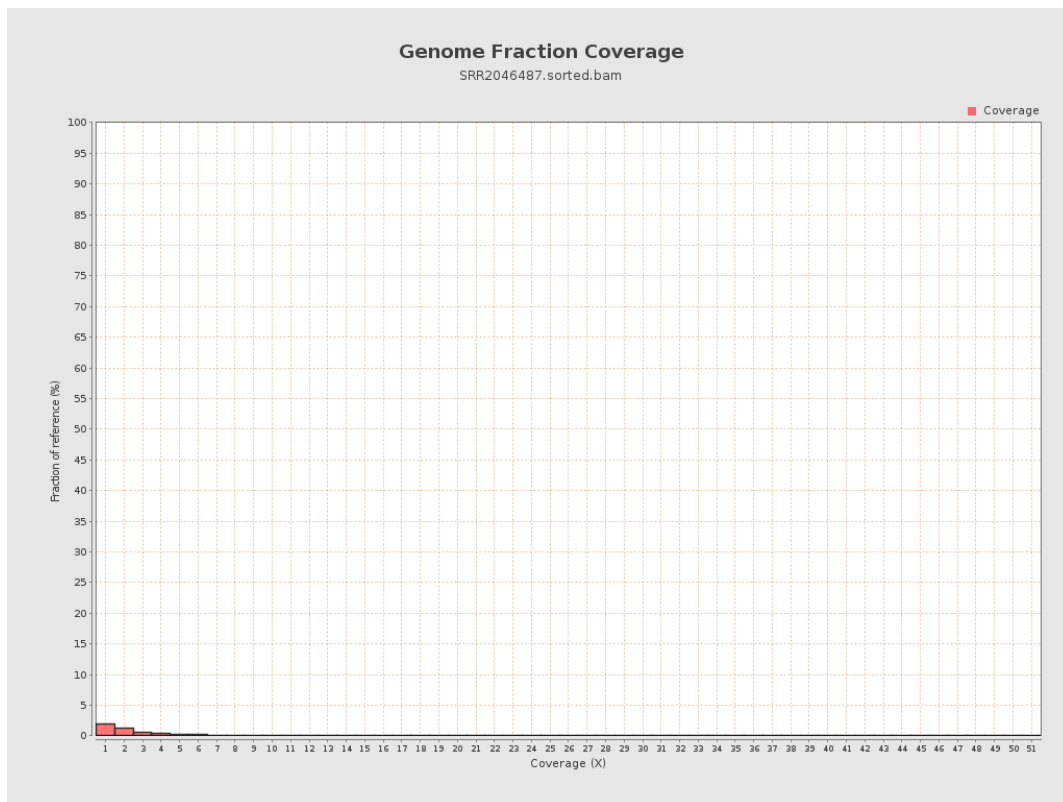
4. Results : Coverage Histogram



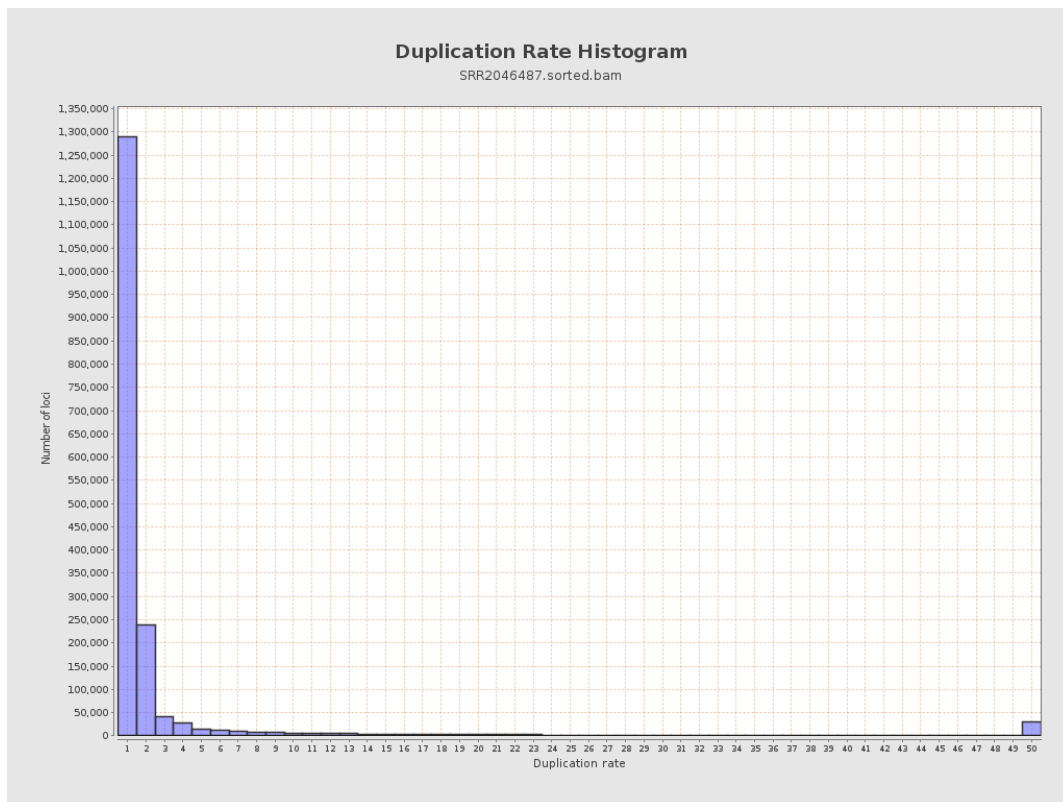
5. Results : Coverage Histogram (0-50X)



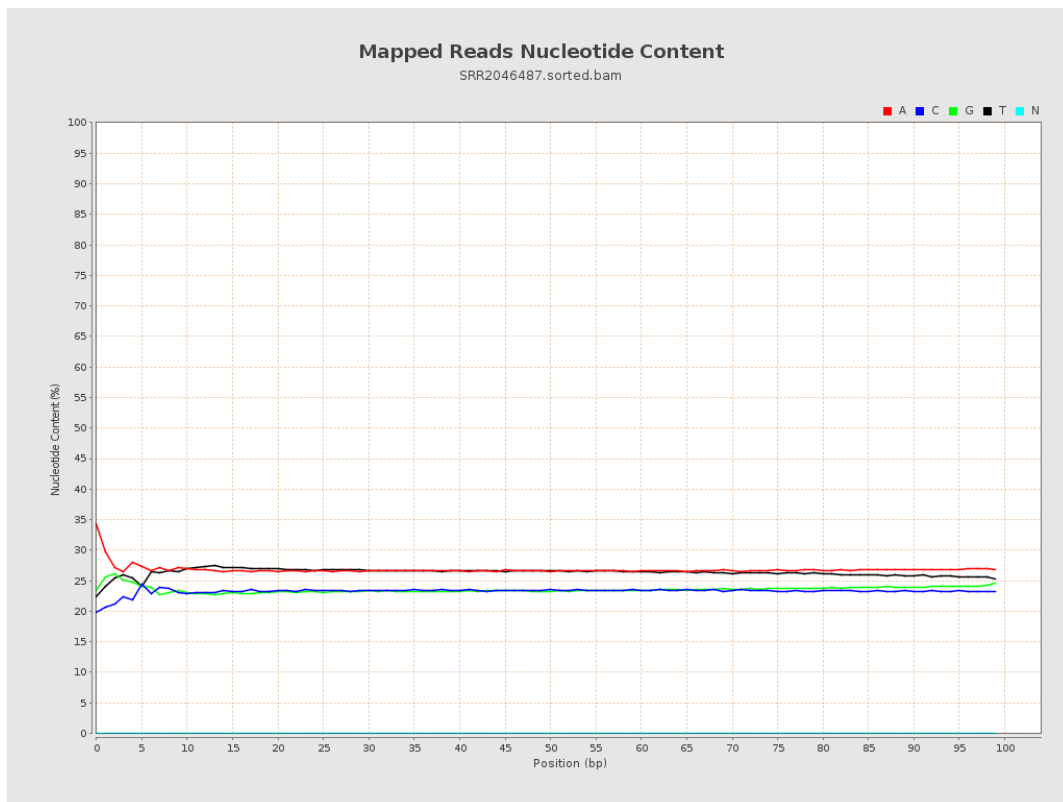
6. Results : Genome Fraction Coverage



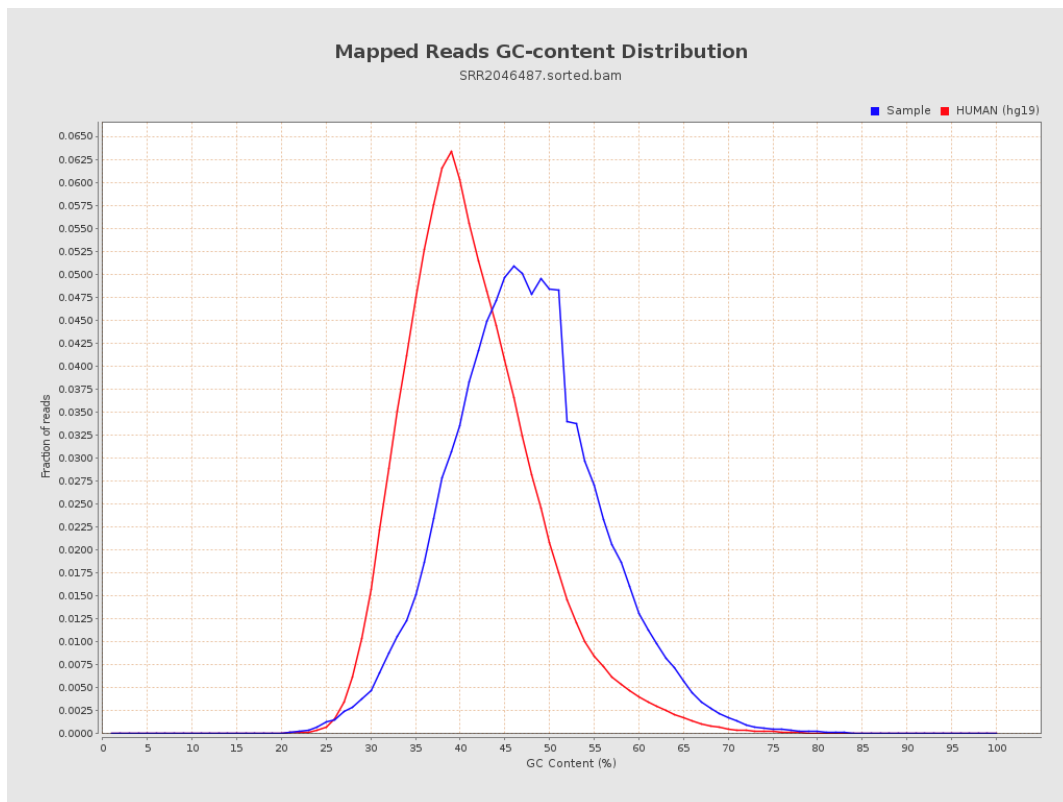
7. Results : Duplication Rate Histogram



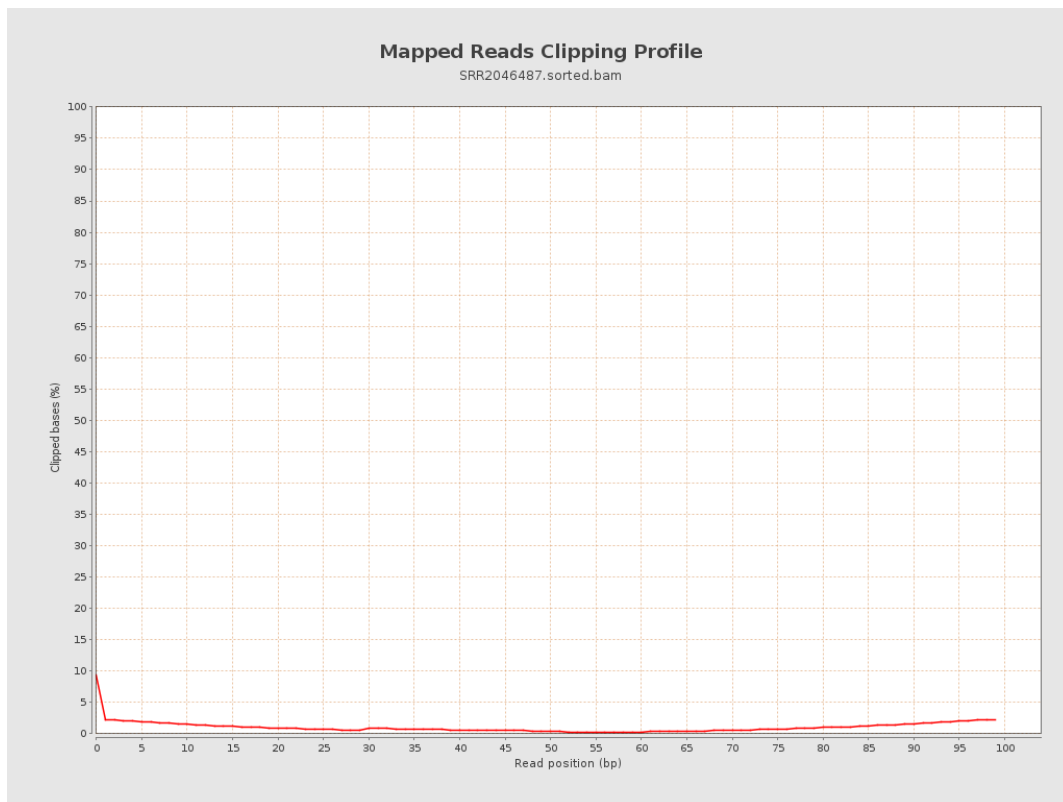
8. Results : Mapped Reads Nucleotide Content



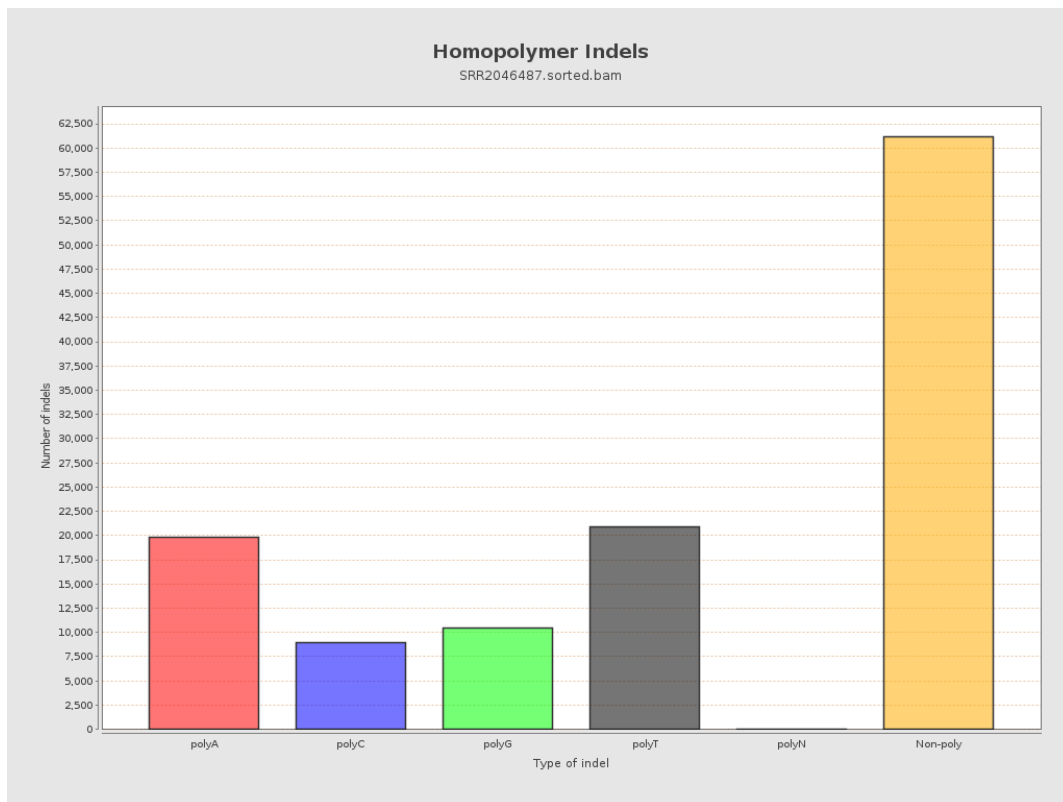
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



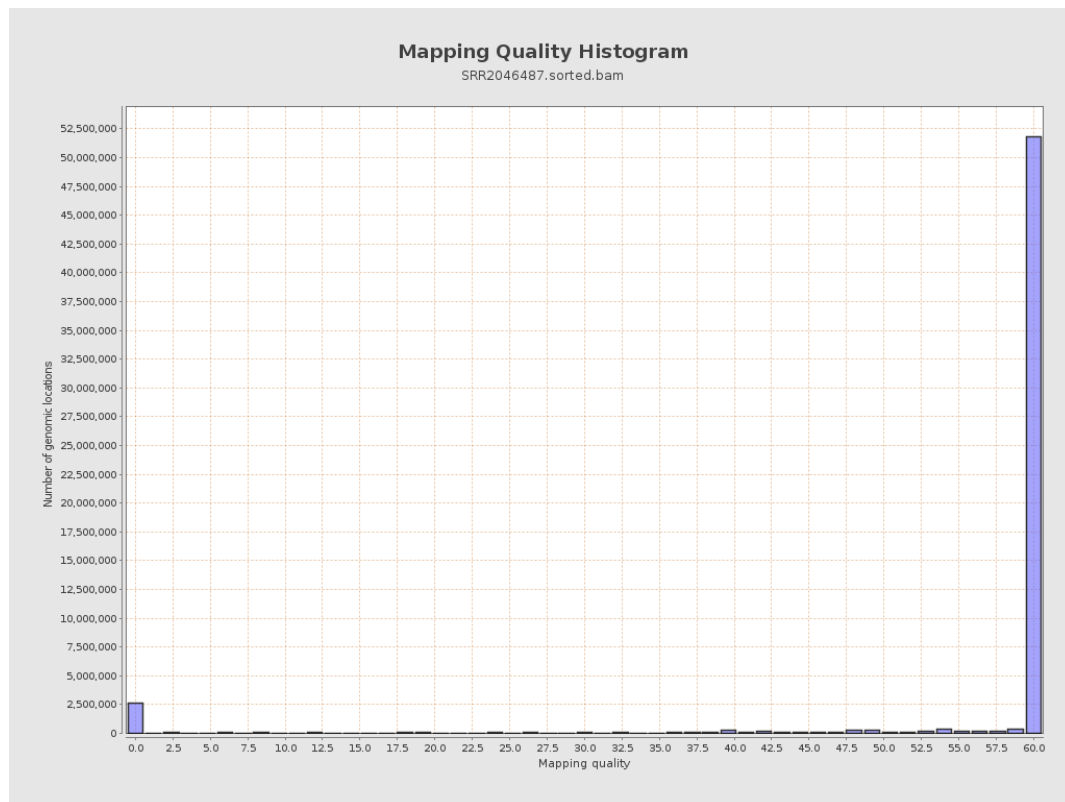
11. Results : Homopolymer Indels



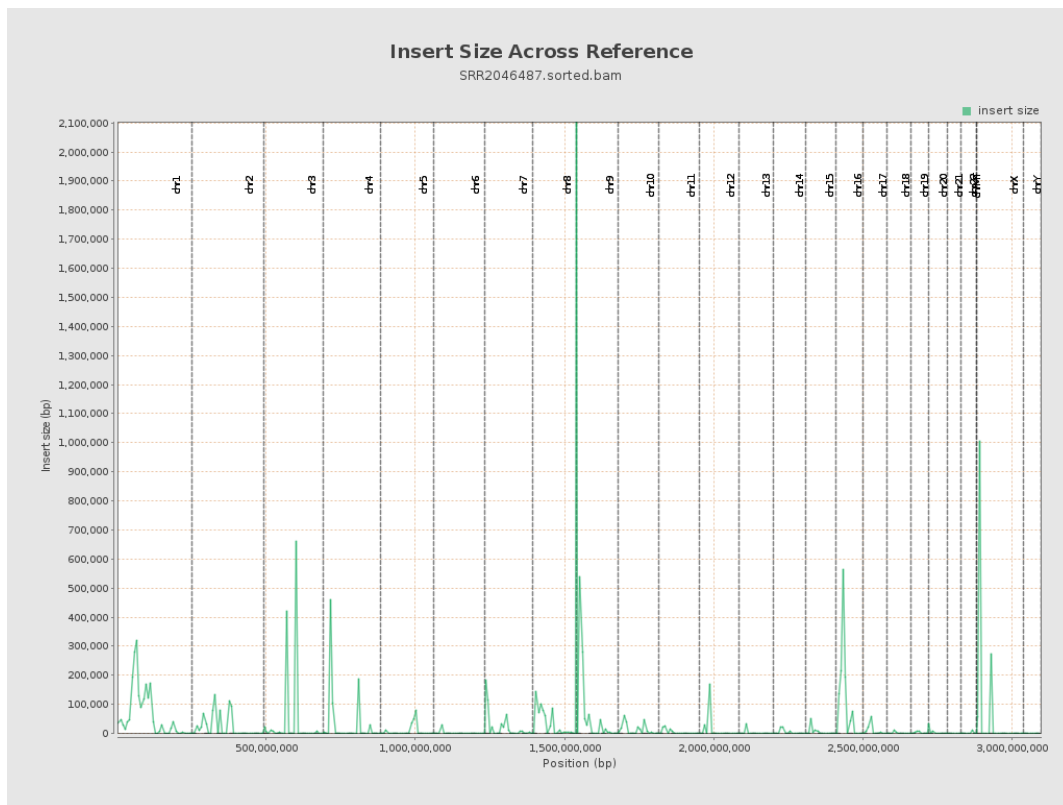
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

