

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.0.1

2015/01/30 08:12:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam  
/home/harrir/groups/harrisonlab/project_files/rootstock_genetics/mm106/anal  
ysis/mm106.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/home/harrir/groups/harrisonlab/proje ct_files/rootstock_genetics/mm106/an alysis/mm106.sorted.bam
Program:	bowtie2 (2.0.5)
Command line:	
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Fri Jan 30 01:11:55 GMT 2015
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	578,875,605
Number of reads	409,177,920
Mapped reads	295,687,318 / 72.26%
Unmapped reads	113,490,602 / 27.74%
Paired reads	295,687,318 / 72.26%
Mapped reads, only first in pair	151,081,010 / 36.92%
Mapped reads, only second in pair	144,606,308 / 35.34%
Mapped reads, both in pair	272,350,162 / 66.56%
Mapped reads, singletons	23,337,156 / 5.7%
Read min/max/mean length	101 / 101 / 101
Clipped reads	0 / 0%
Duplication rate	38.85%

2.2. ACGT Content

Number/percentage of A's	9,177,889,060 / 30.79%
Number/percentage of C's	5,719,745,938 / 19.19%
Number/percentage of T's	9,189,640,443 / 30.83%
Number/percentage of G's	5,720,175,746 / 19.19%
Number/percentage of N's	0 / 0%
GC Percentage	38.38%

2.3. Coverage

Mean	51.57
Standard Deviation	356.95

2.4. Mapping Quality

Mean Mapping Quality	21.37
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2.5. Insert size

Mean	5,966.02
Standard Deviation	318,818.42
P25/Median/P75	140 / 366 / 393

2.6. Mismatches and indels

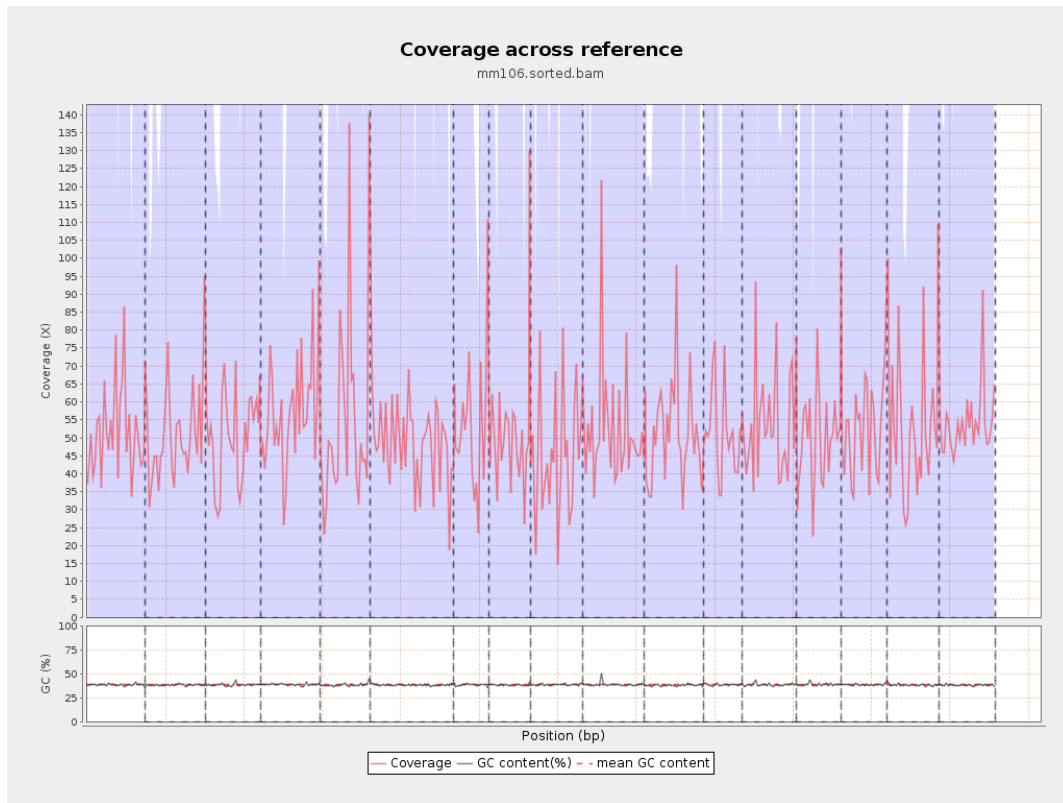
General error rate	3.41%
Mismatches	813,183,306
Insertions	25,072,877
Deletions	21,727,984
Homopolymer indels	53.61%

2.7. Chromosome stats

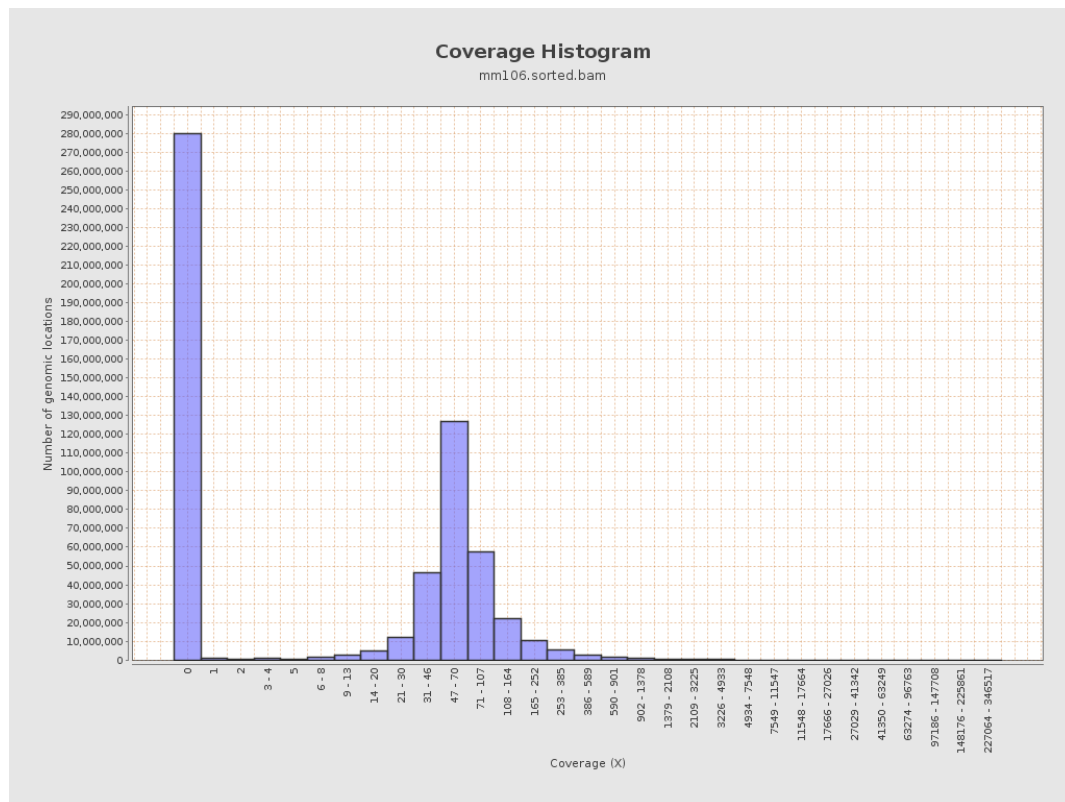
Name	Length	Mapped bases	Mean coverage	Standard deviation
LG10_pht	36966320	1900840816	51.42	248.1
LG11_pht	38535128	1963178788	50.95	234.03
LG12_pht	34924356	1764155753	50.51	564.59
LG13_pht	37956969	2153668466	56.74	279.99

LG14_pht	32305939	1761607792	54.53	818.37
LG15_pht	53078040	2579539927	48.6	234.57
LG16_pht	22123682	1177858345	53.24	377.53
LG17_pht	26512479	1284526163	48.45	147.28
LG1_pht	33466746	1528431411	45.67	206.36
LG2_pht	39136869	2051656459	52.42	411.26
LG3_pht	37898467	1939604805	51.18	338.45
LG4_pht	24311090	1255223907	51.63	224.5
LG5_pht	34832717	1855952637	53.28	271.99
LG6_pht	28552943	1425439396	49.92	319.54
LG7_pht	29555396	1569187405	53.09	282.83
LG8_pht	32612457	1679741561	51.51	283.9
LG9_pht	36106007	1960874687	54.31	282.37

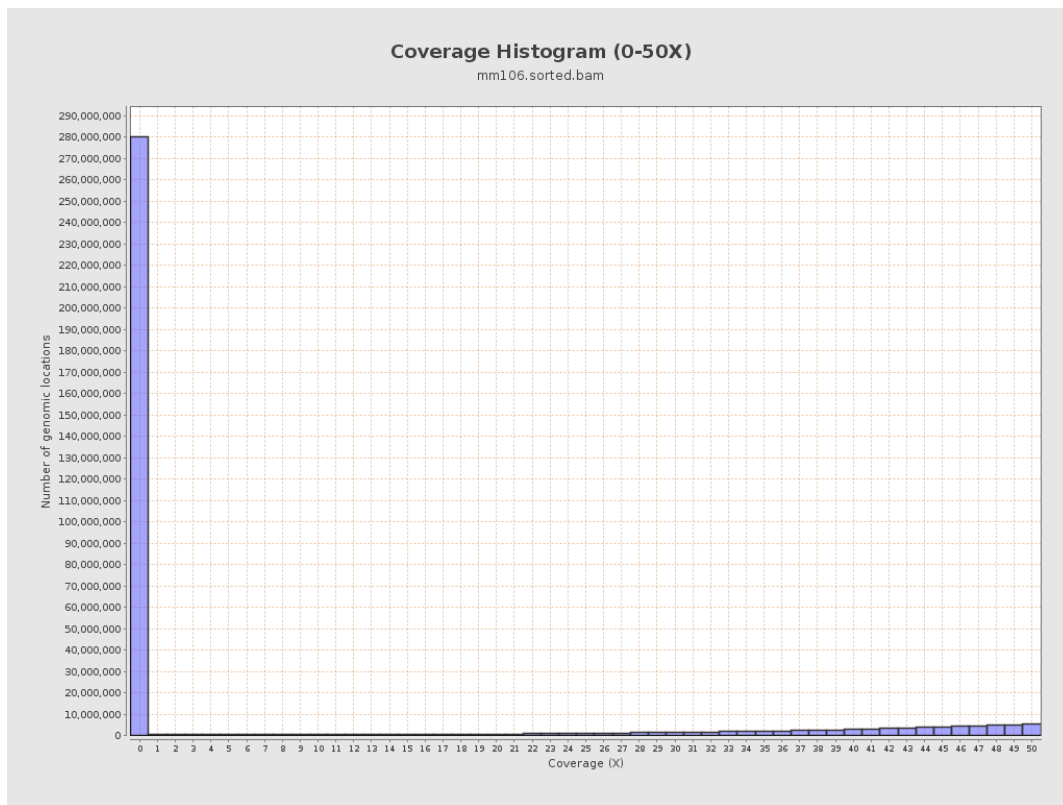
3. Results : Coverage across reference



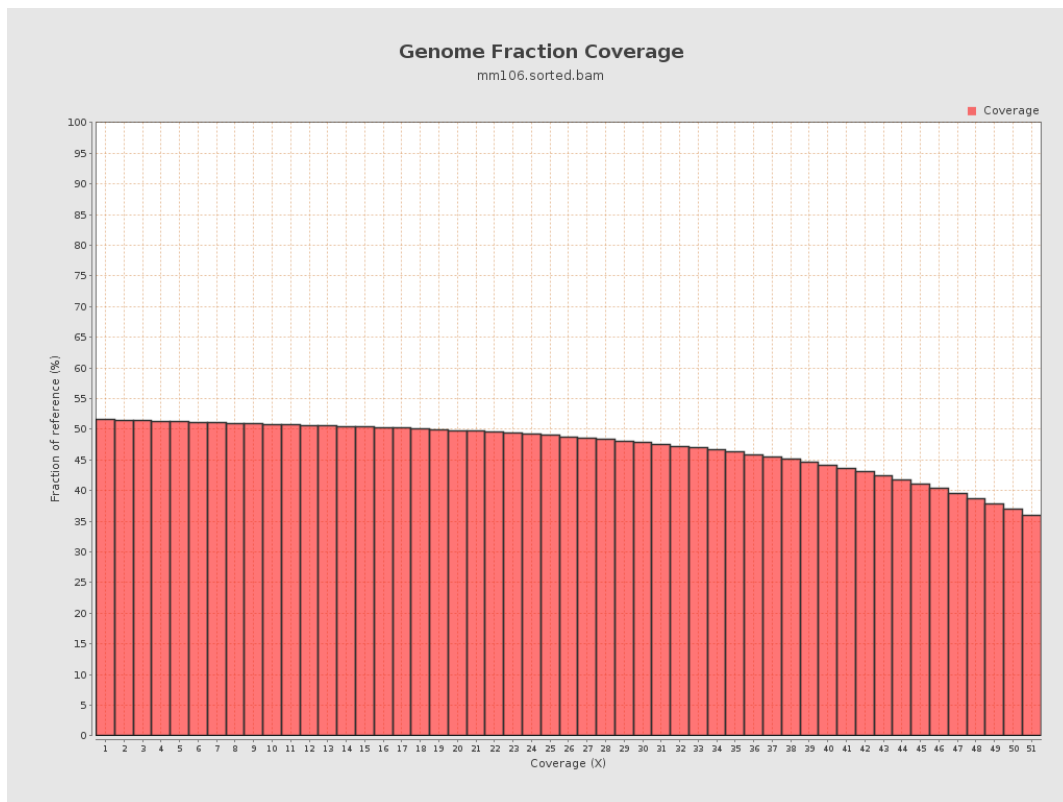
4. Results : Coverage Histogram



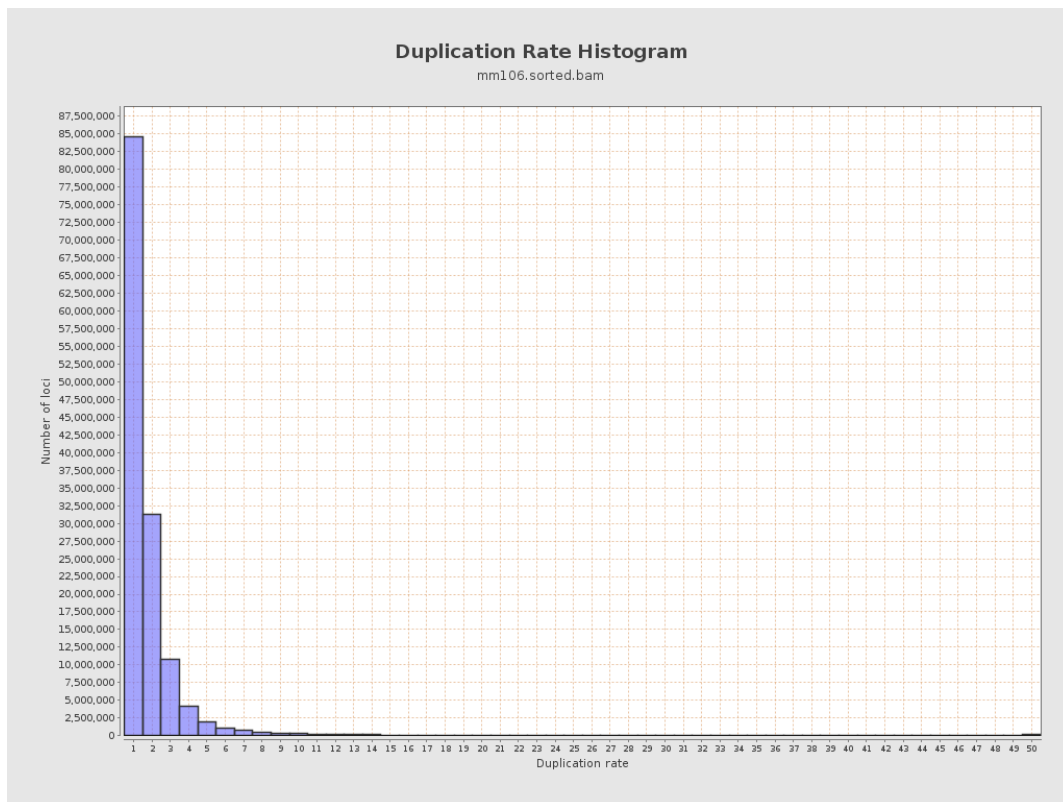
5. Results : Coverage Histogram (0-50X)



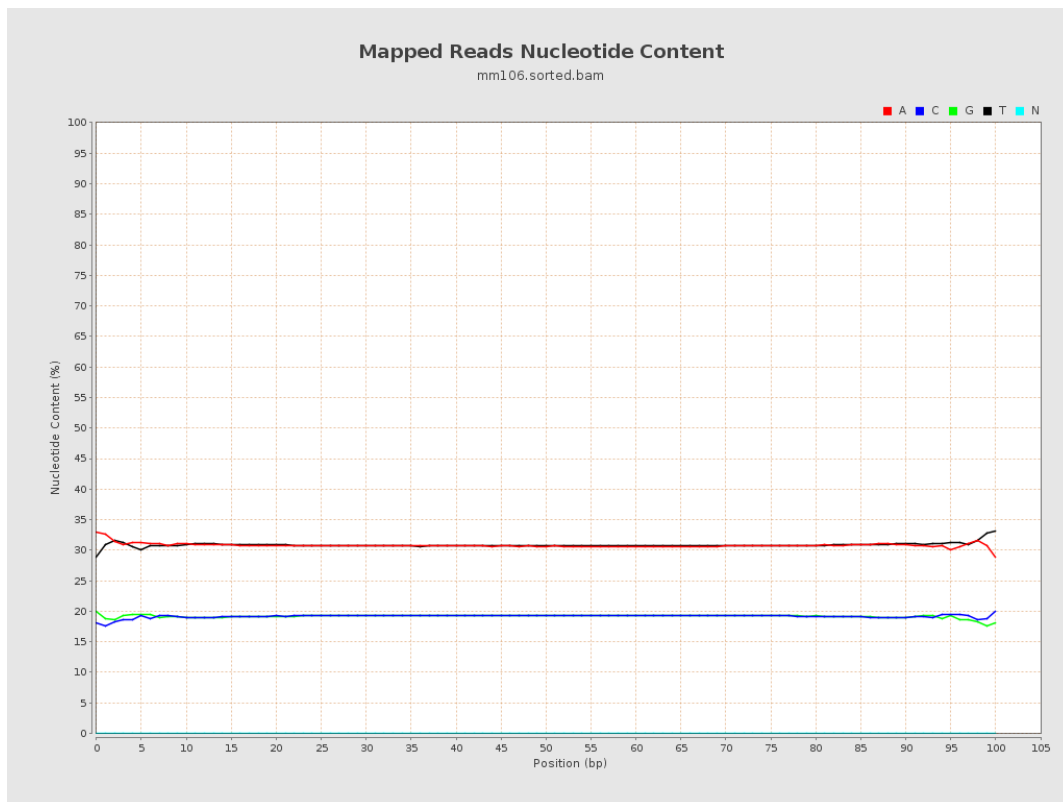
6. Results : Genome Fraction Coverage



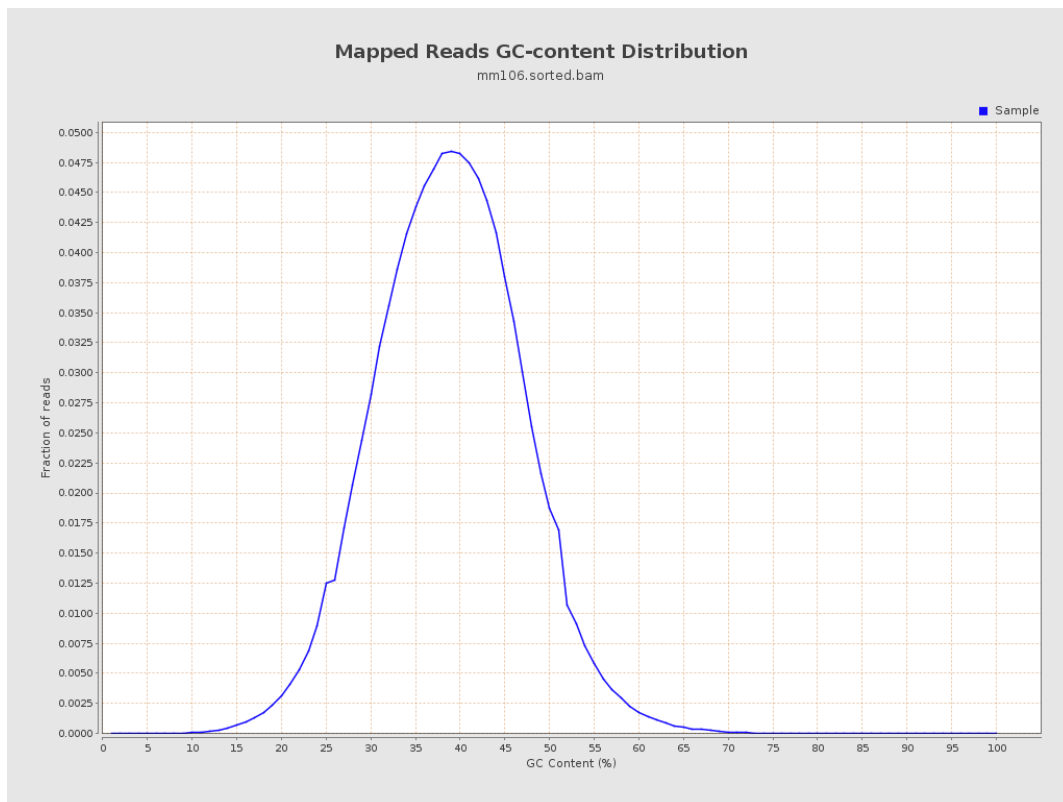
7. Results : Duplication Rate Histogram



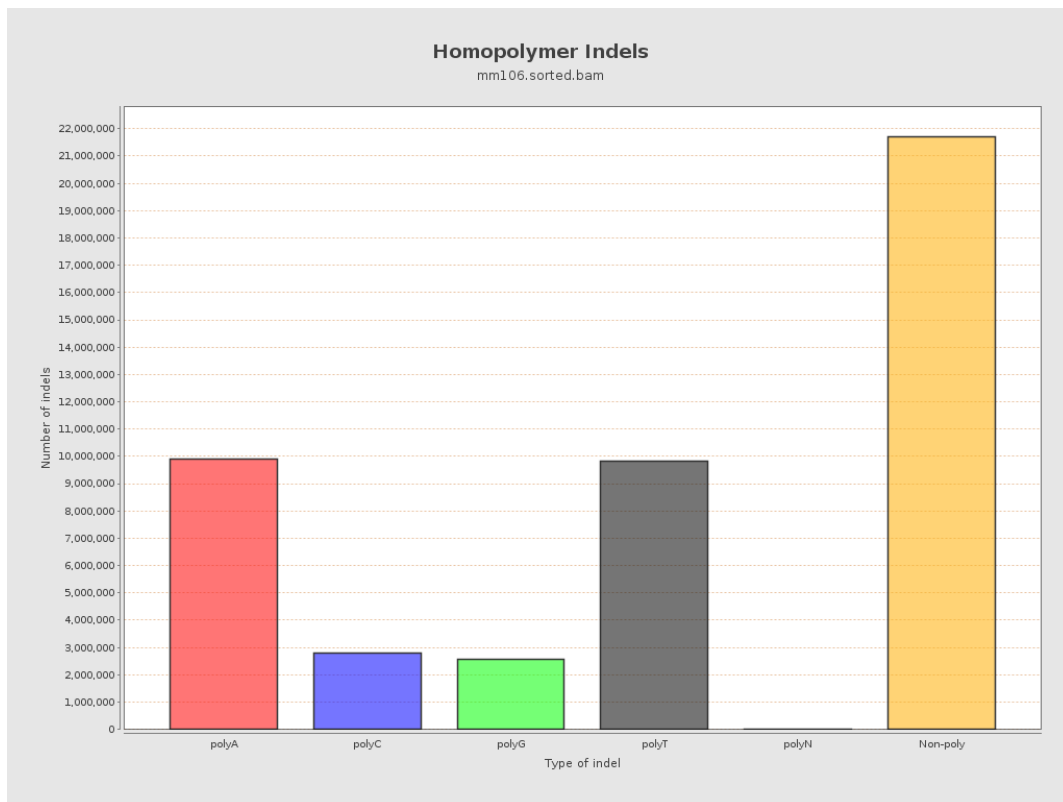
8. Results : Mapped Reads Nucleotide Content



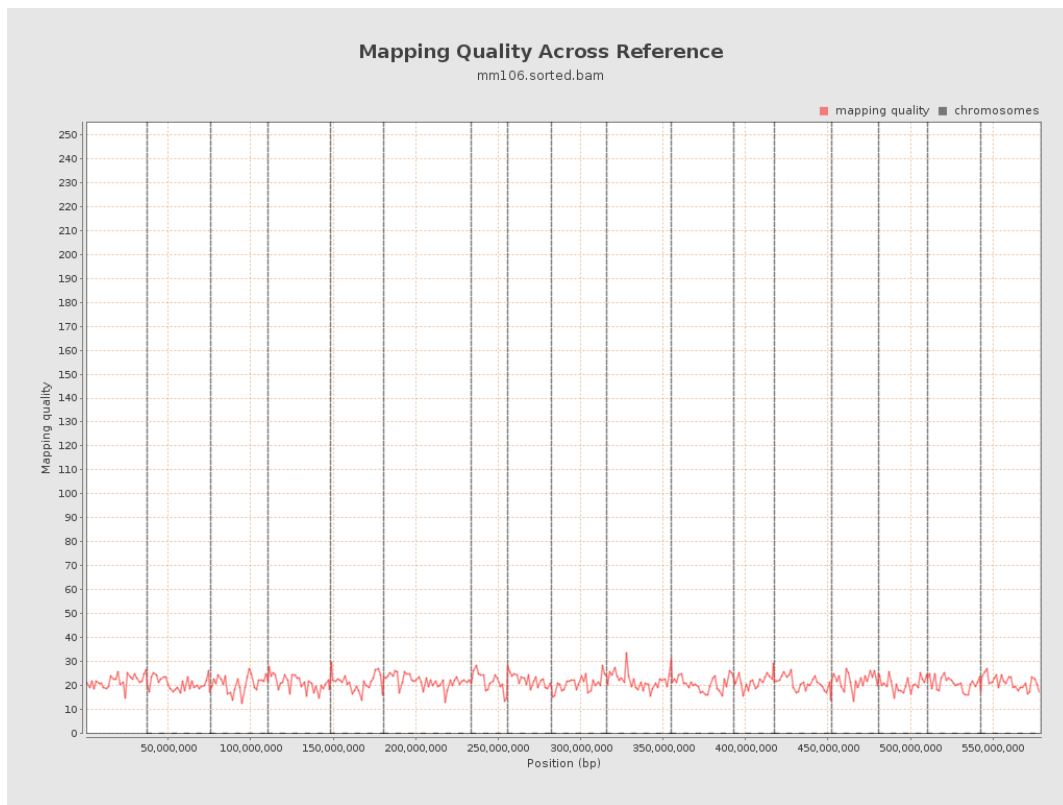
9. Results : Mapped Reads GC-content Distribution



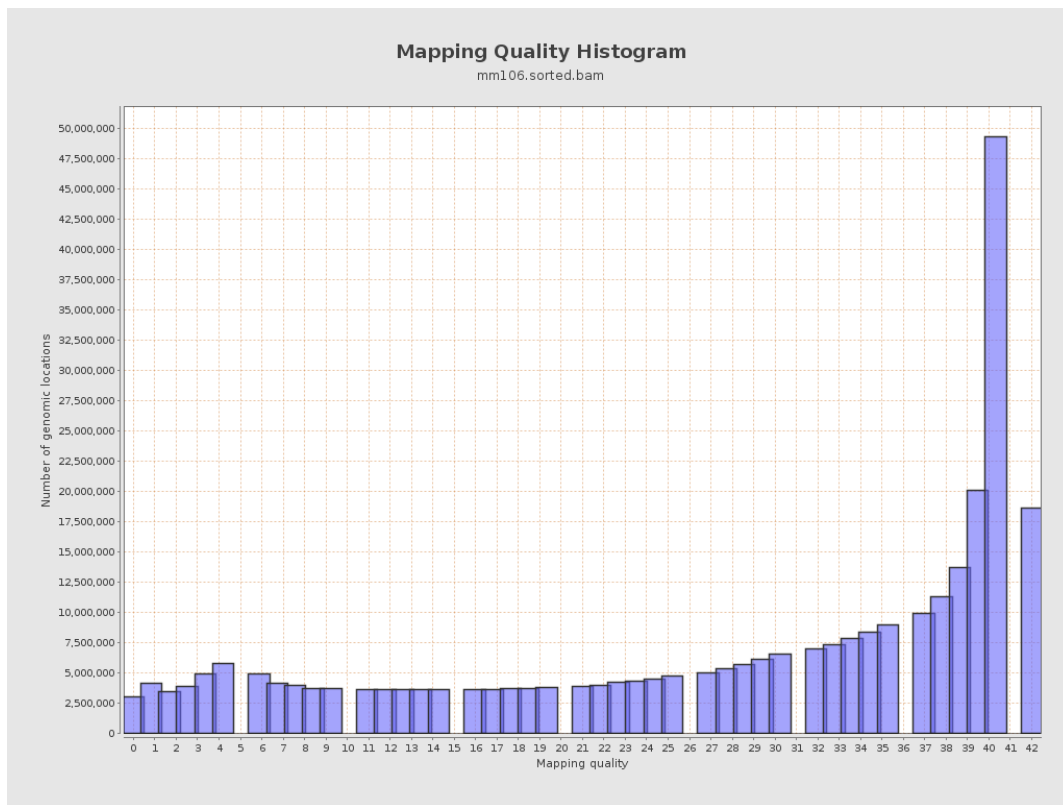
10. Results : Homopolymer Indels



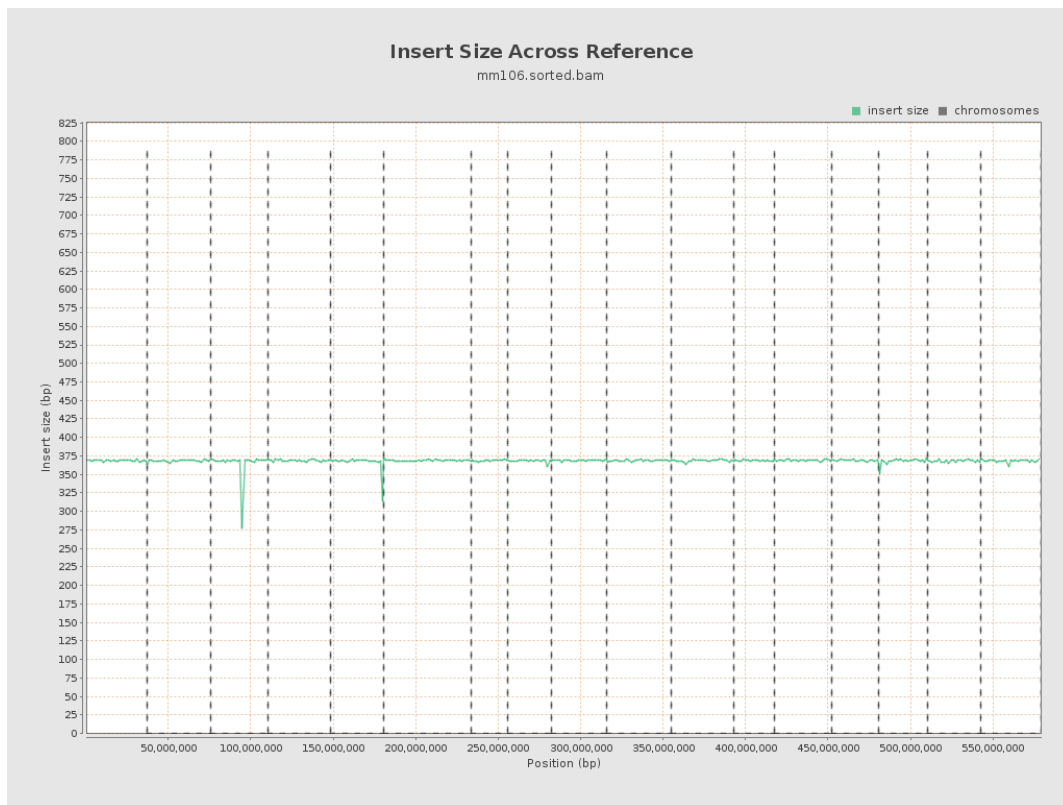
11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram



13. Results : Insert Size Across Reference



14. Results : Insert Size Histogram

