

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.0.1

2015/01/29 13:57:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam  
/home/harrir/groups/harrisonlab/project_files/rootstock_genetics/m9/analysis/  
m9.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/home/harrir/groups/harrisonlab/project_files/rootstock_genetics/m9/analysis/m9.sorted.bam
Program:	bowtie2 (2.0.5)
Command line:	
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu Jan 29 13:54:52 GMT 2015
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	578,875,605
Number of reads	365,617,104
Mapped reads	169,789,112 / 46.44%
Unmapped reads	195,827,992 / 53.56%
Paired reads	169,789,112 / 46.44%
Mapped reads, only first in pair	133,443,537 / 36.5%
Mapped reads, only second in pair	36,345,575 / 9.94%
Mapped reads, both in pair	72,109,134 / 19.72%
Mapped reads, singletons	97,679,978 / 26.72%
Read min/max/mean length	101 / 101 / 101
Clipped reads	0 / 0%
Duplication rate	33.63%

2.2. ACGT Content

Number/percentage of A's	5,326,552,362 / 31.13%
Number/percentage of C's	3,228,691,285 / 18.87%
Number/percentage of T's	5,331,119,649 / 31.15%
Number/percentage of G's	3,226,150,204 / 18.85%
Number/percentage of N's	0 / 0%
GC Percentage	37.72%

2.3. Coverage

Mean	29.61
Standard Deviation	151.82

2.4. Mapping Quality

Mean Mapping Quality	16.17
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2.5. Insert size

Mean	1,860.53
Standard Deviation	183,023.88
P25/Median/P75	0 / 0 / 0

2.6. Mismatches and indels

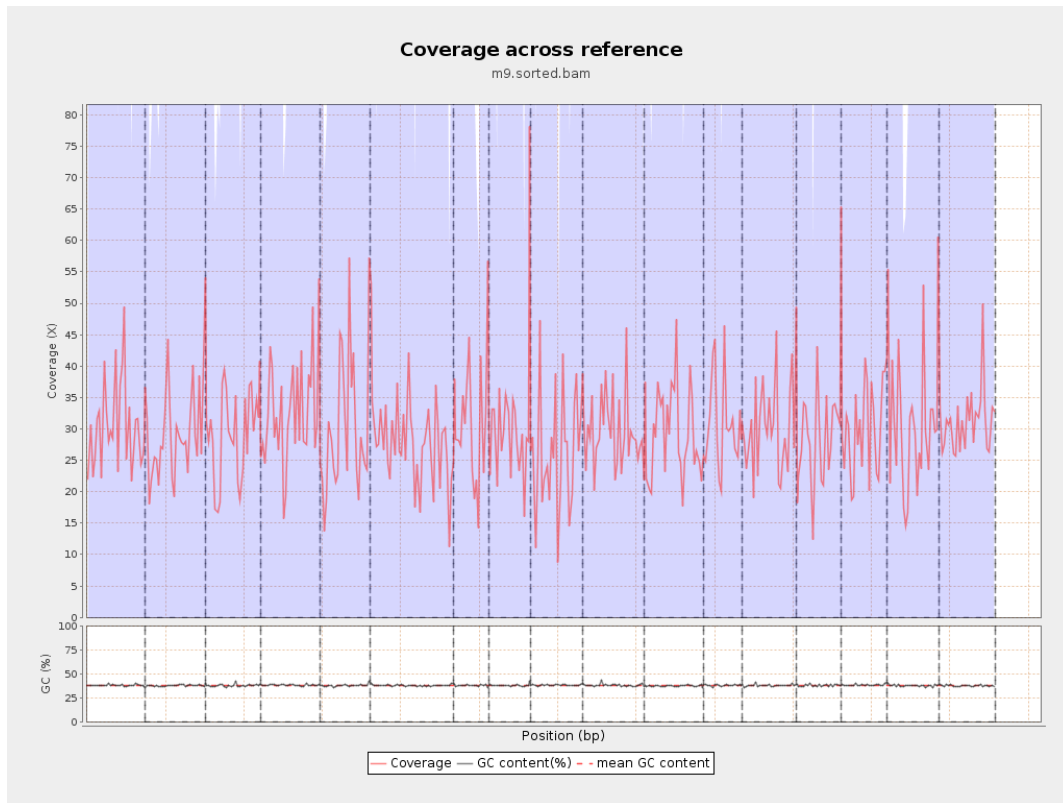
General error rate	3.51%
Mismatches	493,954,748
Insertions	17,077,469
Deletions	14,885,849
Homopolymer indels	53.14%

2.7. Chromosome stats

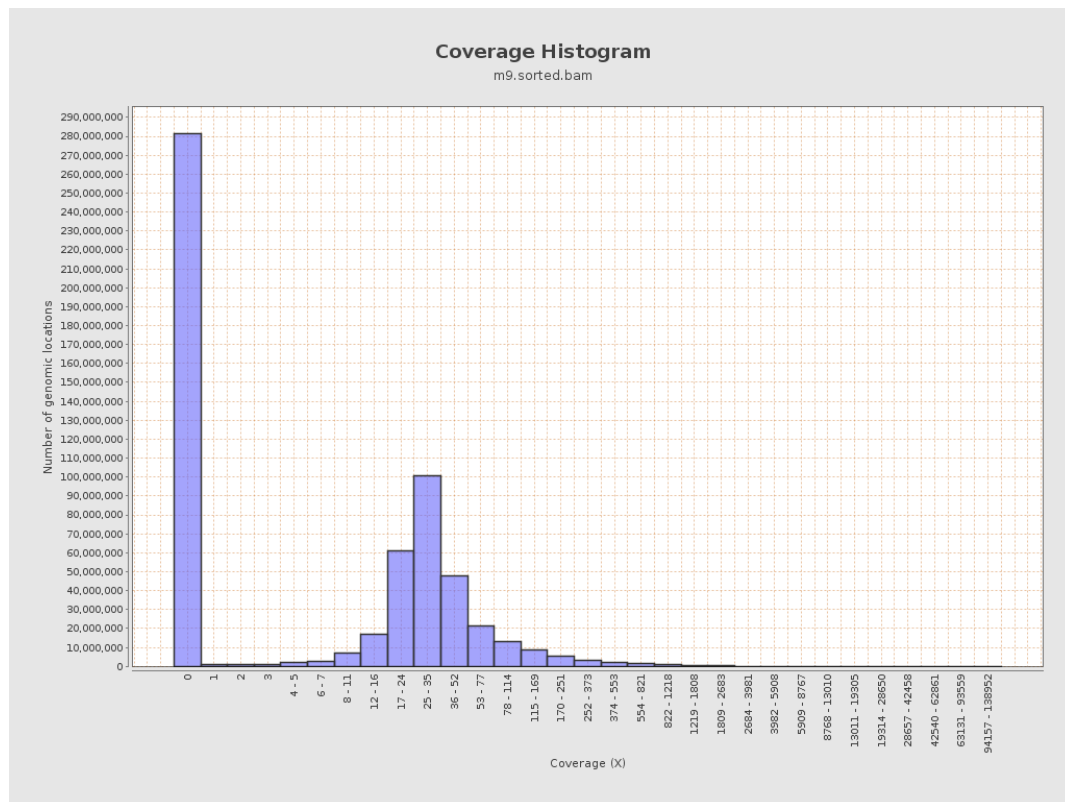
Name	Length	Mapped bases	Mean coverage	Standard deviation
LG10_pht	36966320	1119293439	30.28	137.15
LG11_pht	38535128	1123215176	29.15	120.12
LG12_pht	34924356	1023609718	29.31	254.97
LG13_pht	37956969	1232955768	32.48	140.73

LG14_pht	32305939	964958215	29.87	257.16
LG15_pht	53078040	1467976319	27.66	120.57
LG16_pht	22123682	683480469	30.89	165.87
LG17_pht	26512479	765469736	28.87	93.48
LG1_pht	33466746	889888494	26.59	112.29
LG2_pht	39136869	1161300577	29.67	119.39
LG3_pht	37898467	1110737031	29.31	150.27
LG4_pht	24311090	747726259	30.76	123.12
LG5_pht	34832717	1047399389	30.07	128.14
LG6_pht	28552943	813798476	28.5	138.25
LG7_pht	29555396	889010295	30.08	150.06
LG8_pht	32612457	970183492	29.75	140.5
LG9_pht	36106007	1129470835	31.28	138.04

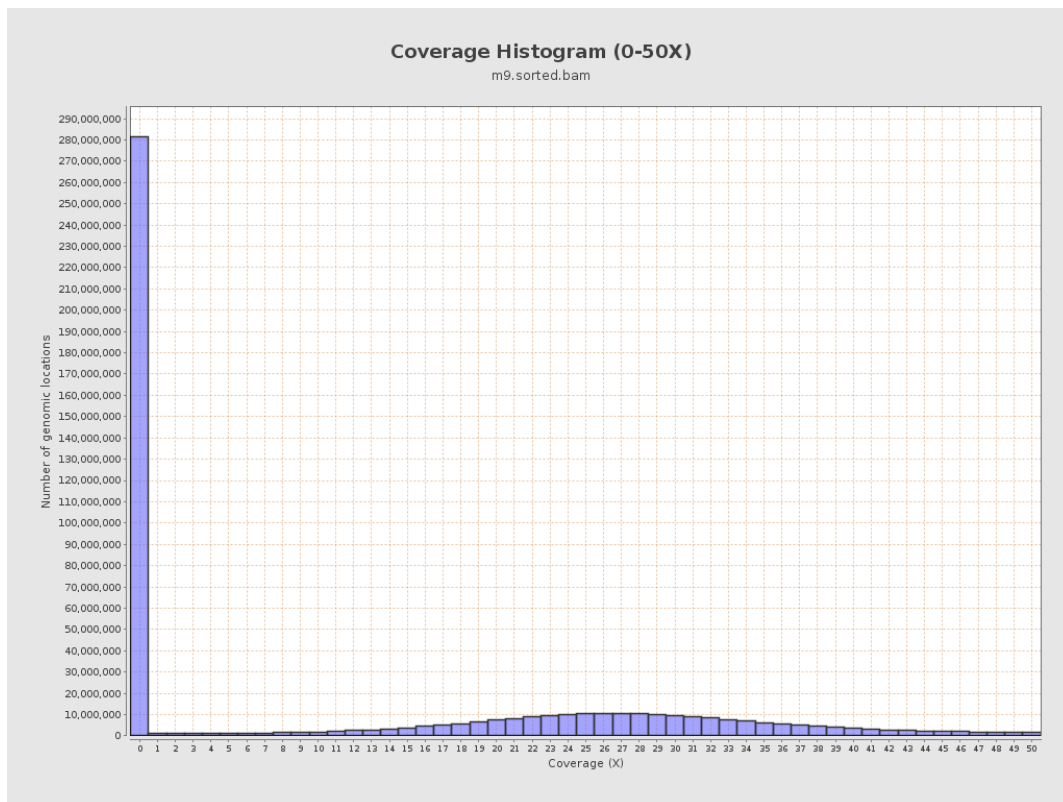
3. Results : Coverage across reference



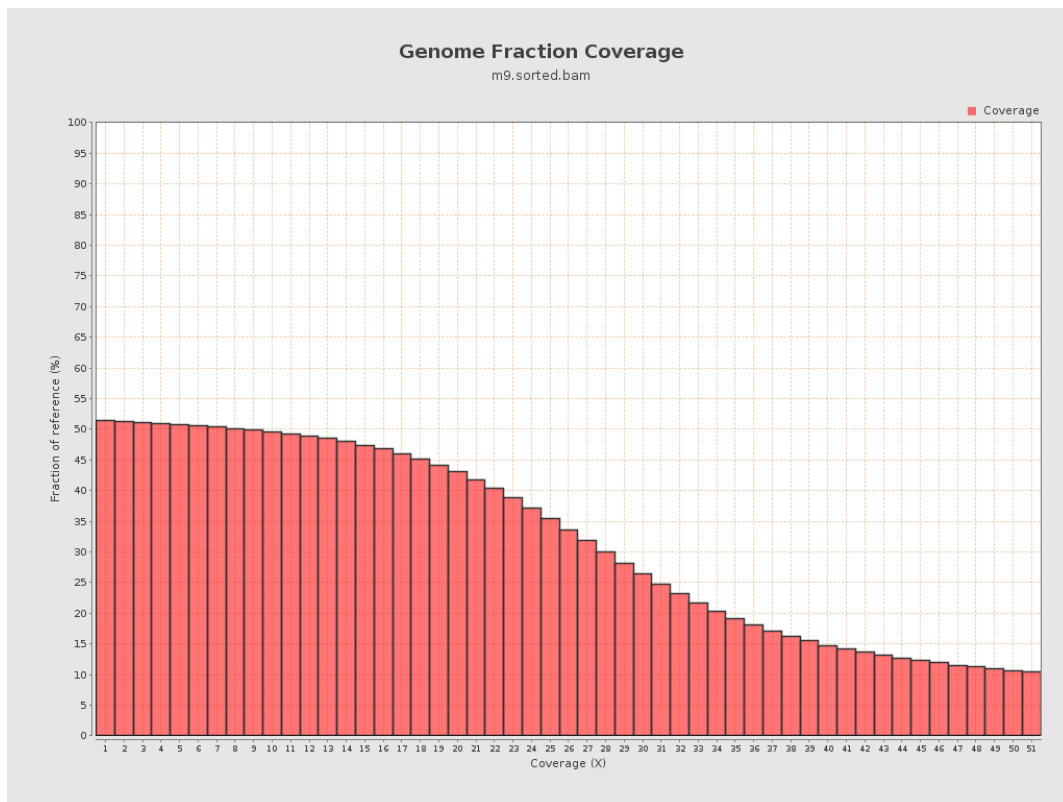
4. Results : Coverage Histogram



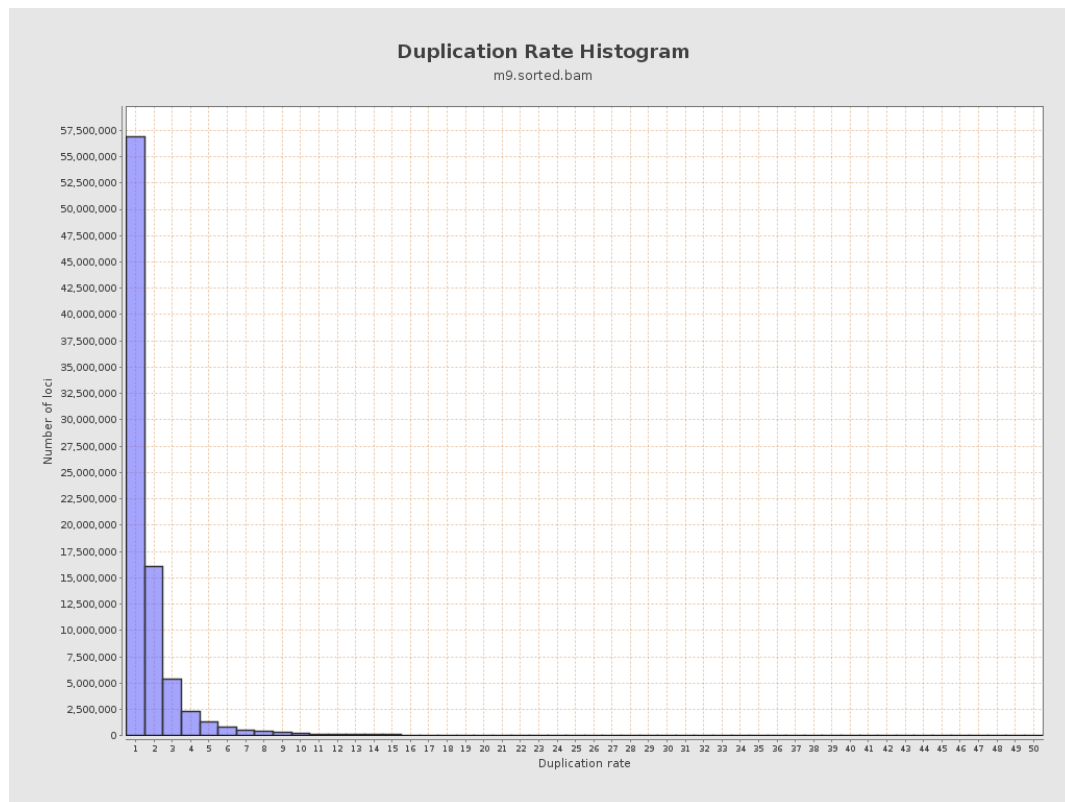
5. Results : Coverage Histogram (0-50X)



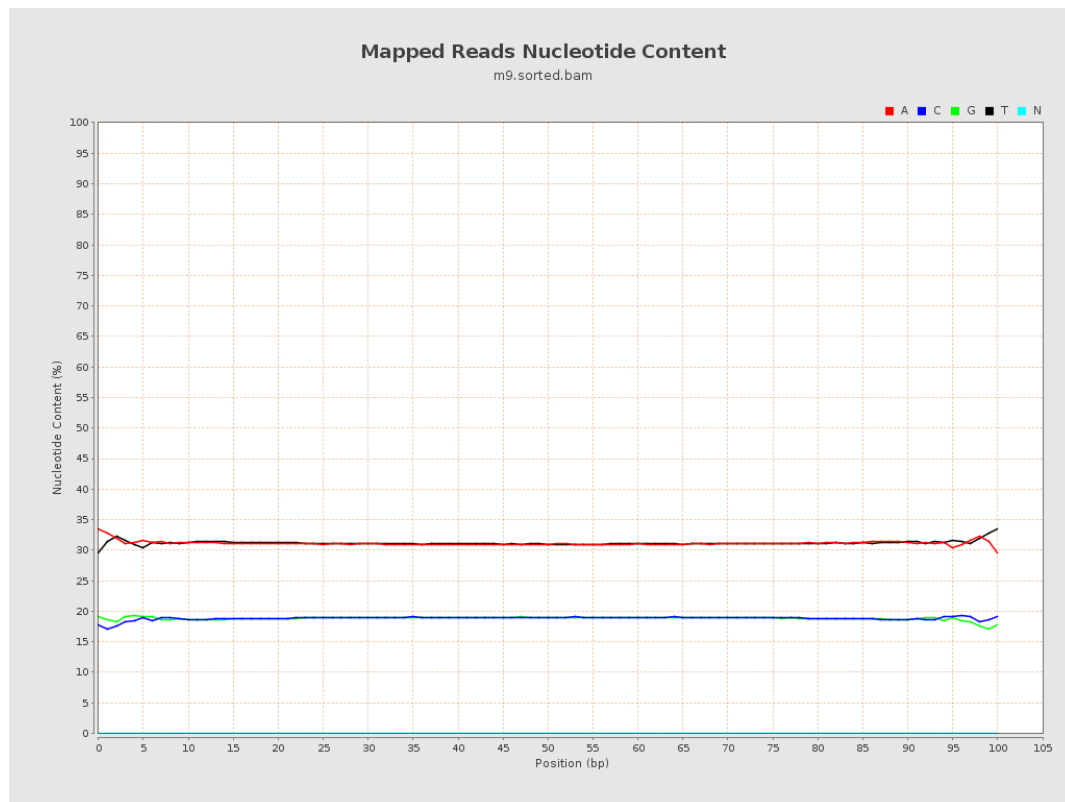
6. Results : Genome Fraction Coverage



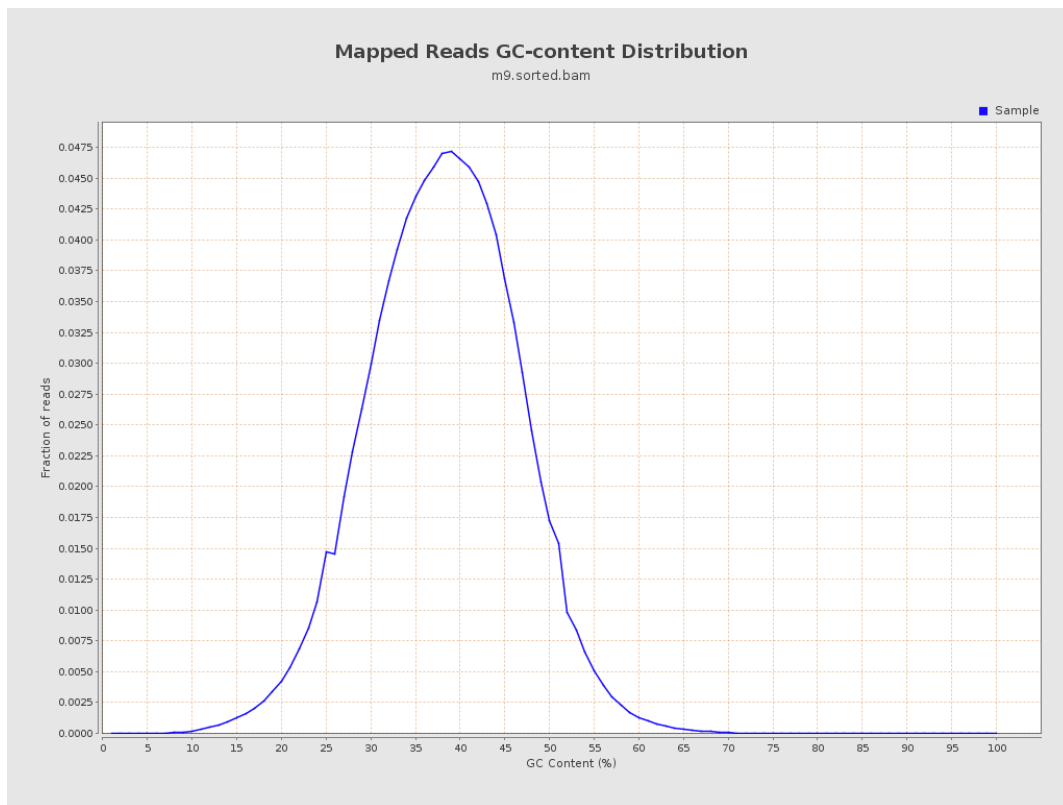
7. Results : Duplication Rate Histogram



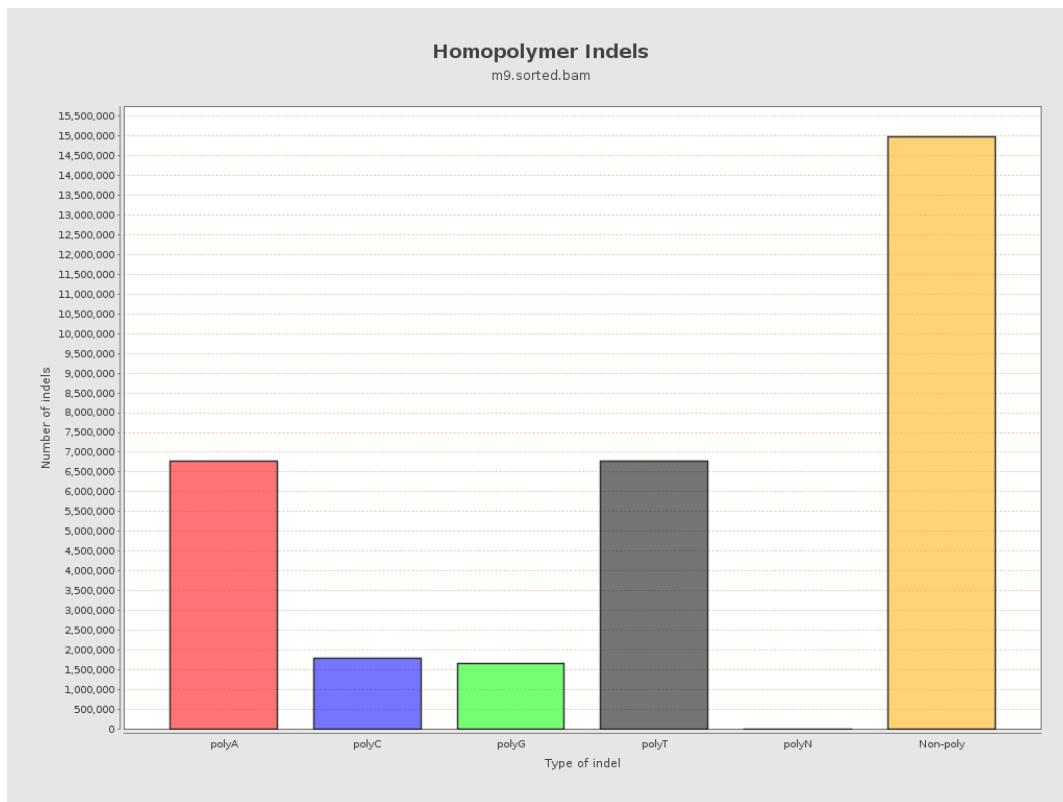
8. Results : Mapped Reads Nucleotide Content



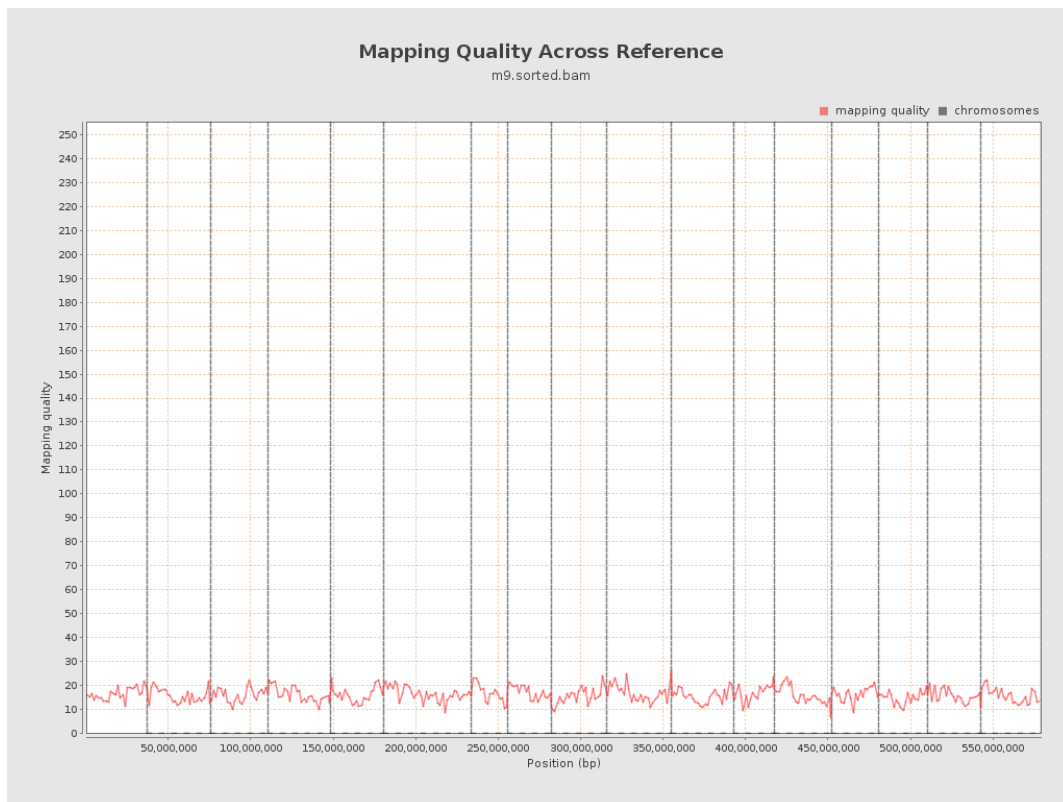
9. Results : Mapped Reads GC-content Distribution



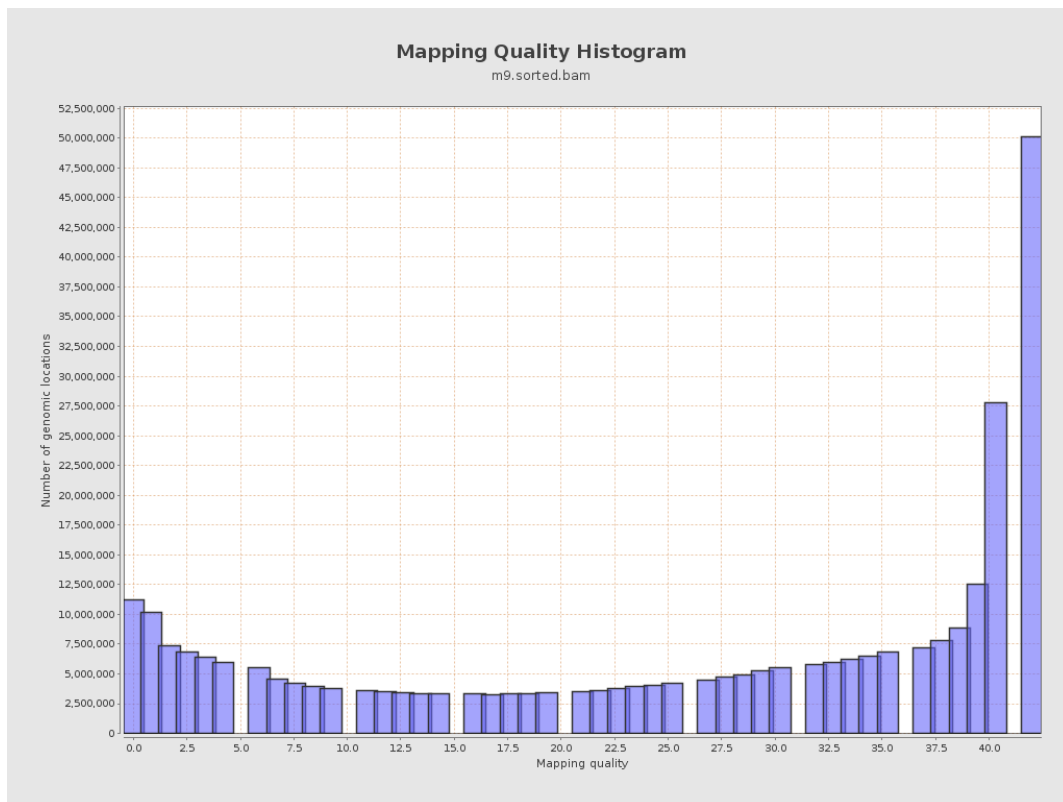
10. Results : Homopolymer Indels



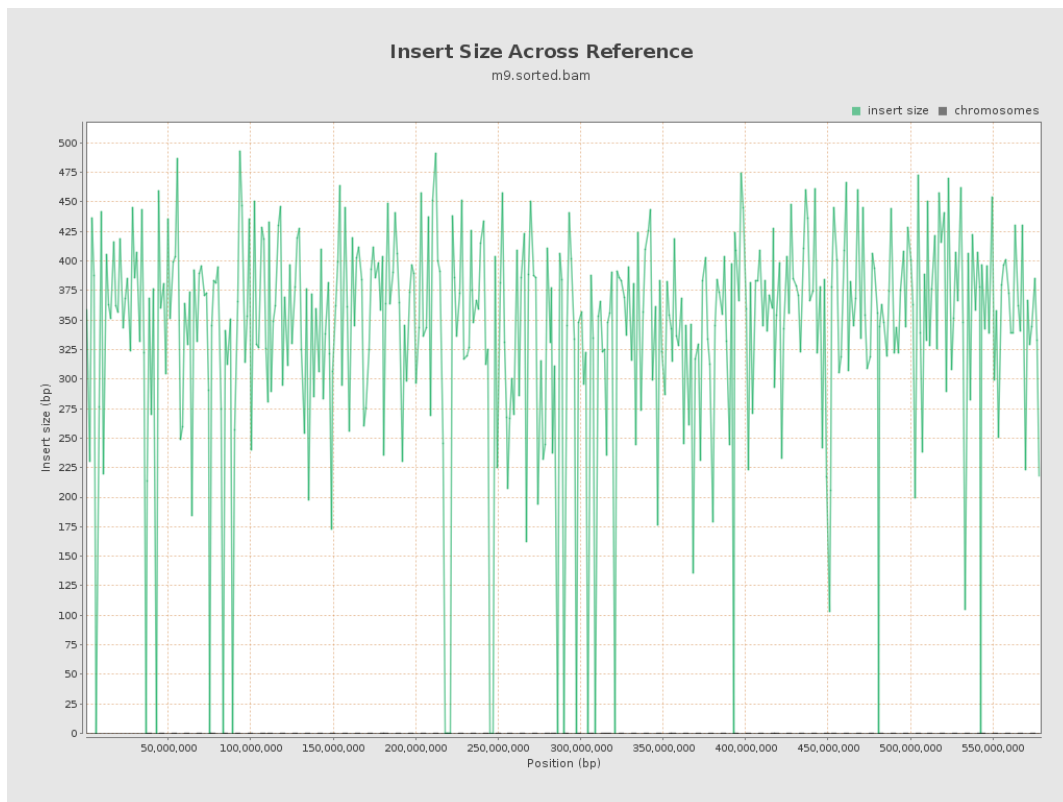
11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram



13. Results : Insert Size Across Reference



14. Results : Insert Size Histogram

