

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.0.1

2015/01/29 22:36:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam  
/home/harrir/groups/harrisonlab/project_files/rootstock_genetics/m27/analys  
is/m27.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/home/harrir/groups/harrisonlab/proje ct_files/rootstock_genetics/m27/analy sis/m27.sorted.bam
Program:	bowtie2 (2.0.5)
Command line:	
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu Jan 29 20:21:02 GMT 2015
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	578,875,605
Number of reads	441,364,670
Mapped reads	317,827,798 / 72.01%
Unmapped reads	123,536,872 / 27.99%
Paired reads	317,827,798 / 72.01%
Mapped reads, only first in pair	162,127,120 / 36.73%
Mapped reads, only second in pair	155,700,678 / 35.28%
Mapped reads, both in pair	293,532,478 / 66.51%
Mapped reads, singletons	24,295,320 / 5.5%
Read min/max/mean length	101 / 101 / 101
Clipped reads	0 / 0%
Duplication rate	41.01%

2.2. ACGT Content

Number/percentage of A's	9,957,626,344 / 31.08%
Number/percentage of C's	6,051,509,889 / 18.89%
Number/percentage of T's	9,971,753,497 / 31.13%
Number/percentage of G's	6,054,100,266 / 18.9%
Number/percentage of N's	0 / 0%
GC Percentage	37.79%

2.3. Coverage

Mean	55.43
Standard Deviation	314.18

2.4. Mapping Quality

Mean Mapping Quality	21.64
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2.5. Insert size

Mean	6,323.09
Standard Deviation	328,152.5
P25/Median/P75	164 / 315 / 345

2.6. Mismatches and indels

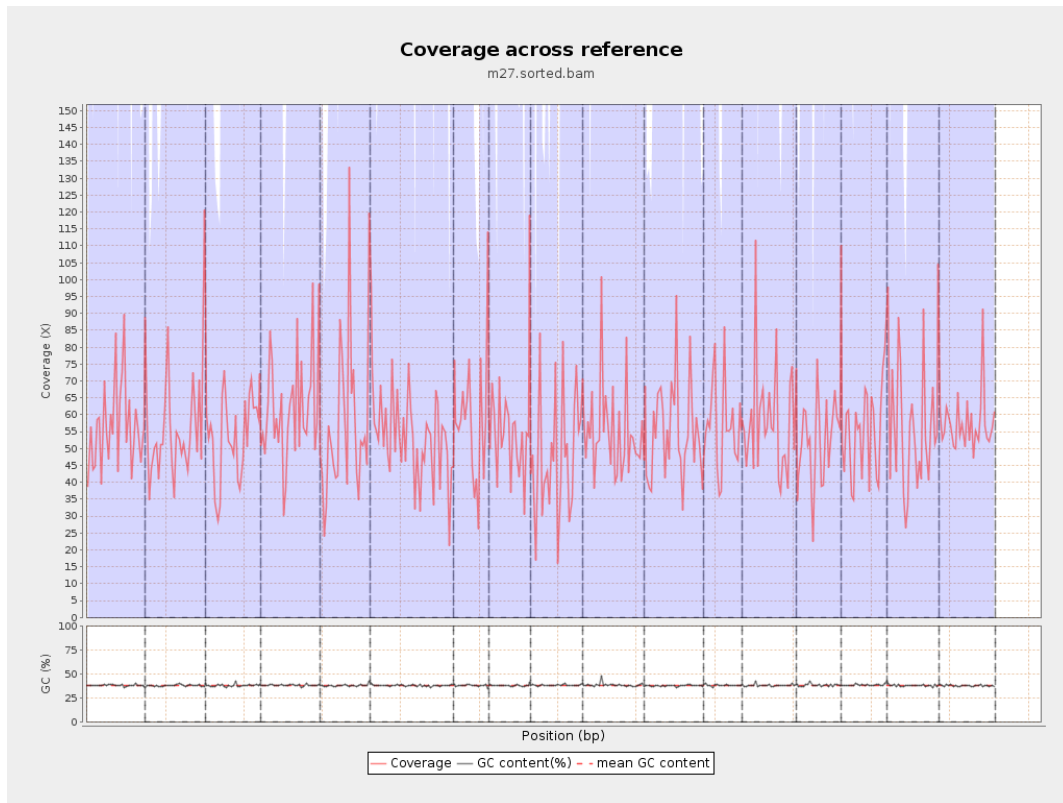
General error rate	3.33%
Mismatches	843,177,128
Insertions	28,608,317
Deletions	24,840,878
Homopolymer indels	54.21%

2.7. Chromosome stats

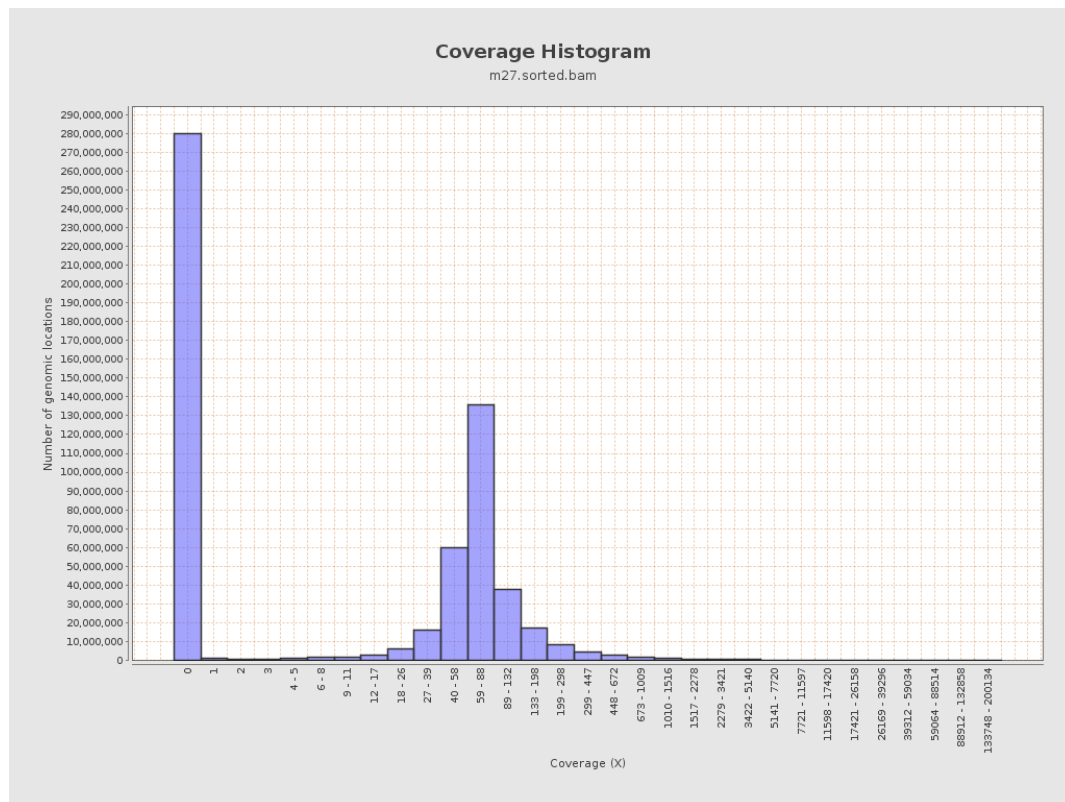
Name	Length	Mapped bases	Mean coverage	Standard deviation
LG10_pht	36966320	2079730841	56.26	255.91
LG11_pht	38535128	2162491580	56.12	266.73
LG12_pht	34924356	1884751613	53.97	394.92
LG13_pht	37956969	2335664495	61.53	310.03

LG14_pht	32305939	1842418176	57.03	588.79
LG15_pht	53078040	2809261748	52.93	269.2
LG16_pht	22123682	1288915259	58.26	391.9
LG17_pht	26512479	1418125246	53.49	154.05
LG1_pht	33466746	1623994212	48.53	211.35
LG2_pht	39136869	2150134173	54.94	309.3
LG3_pht	37898467	2081385714	54.92	340.9
LG4_pht	24311090	1380262439	56.78	229.39
LG5_pht	34832717	2010208395	57.71	310.75
LG6_pht	28552943	1501782848	52.6	266.89
LG7_pht	29555396	1645168506	55.66	279.83
LG8_pht	32612457	1792391163	54.96	267.47
LG9_pht	36106007	2078897824	57.58	280.29

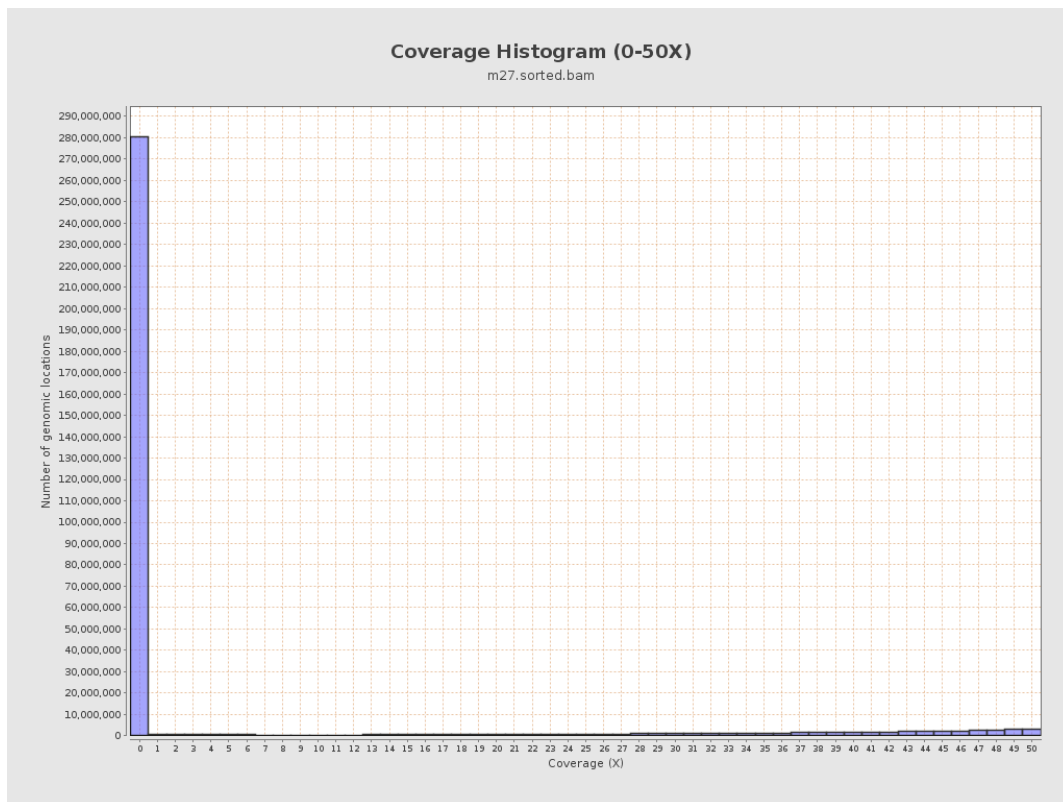
3. Results : Coverage across reference



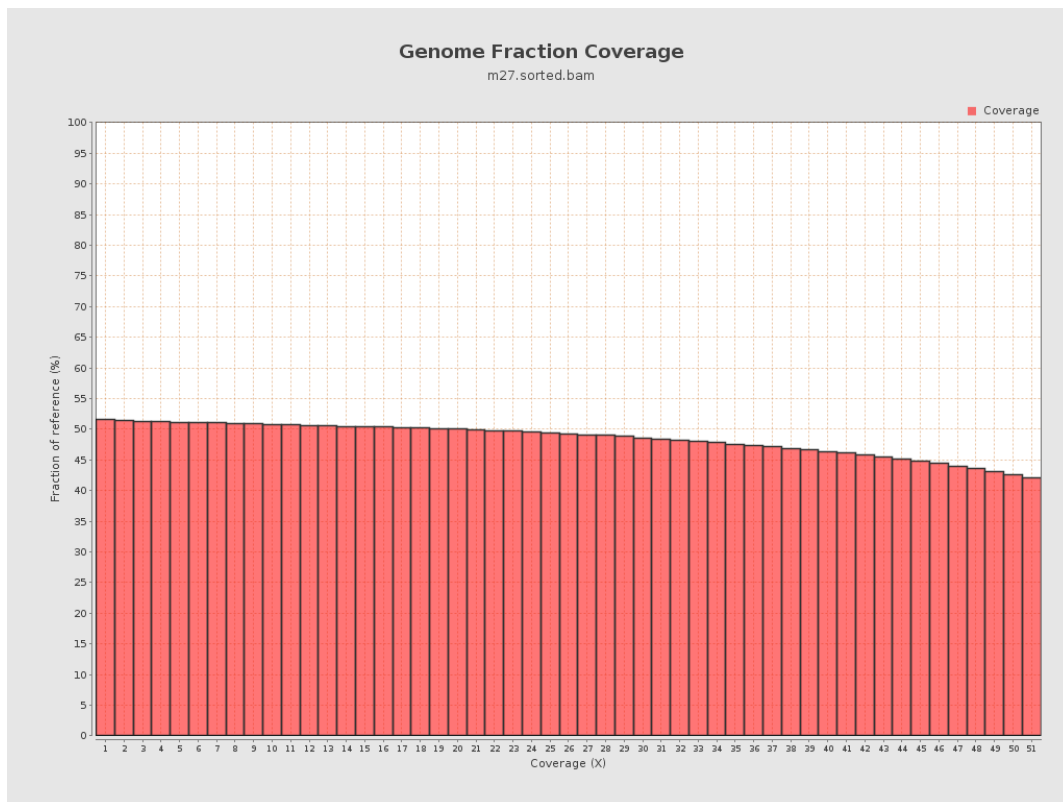
4. Results : Coverage Histogram



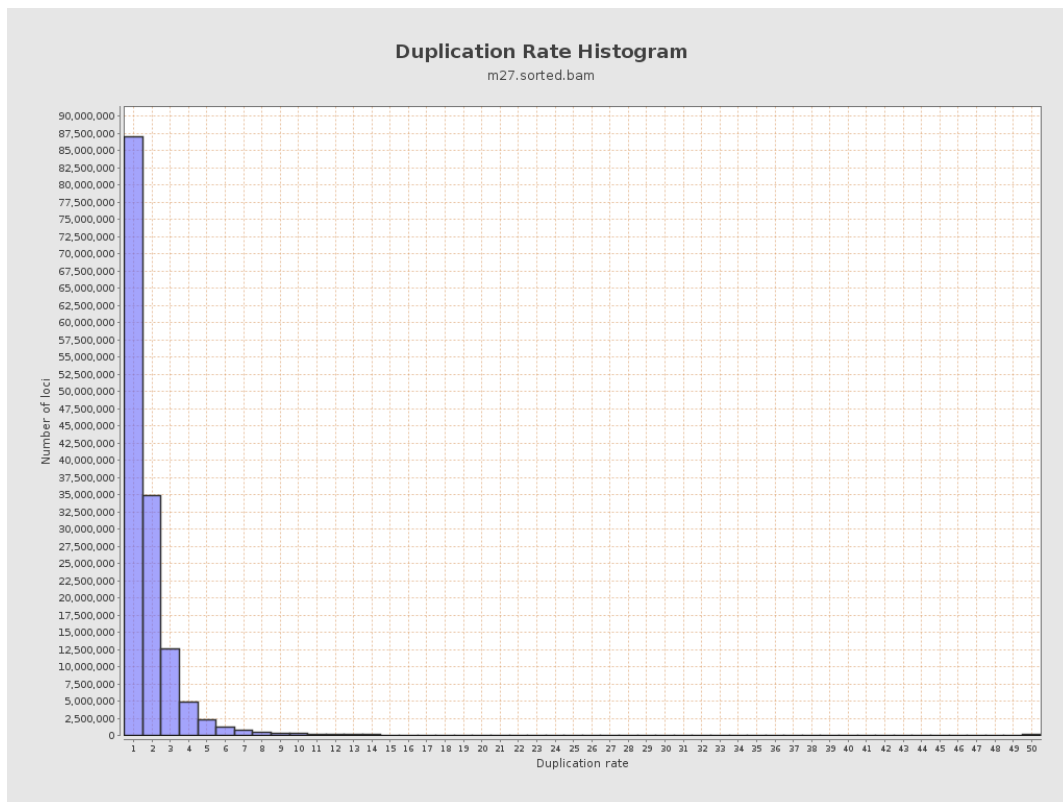
5. Results : Coverage Histogram (0-50X)



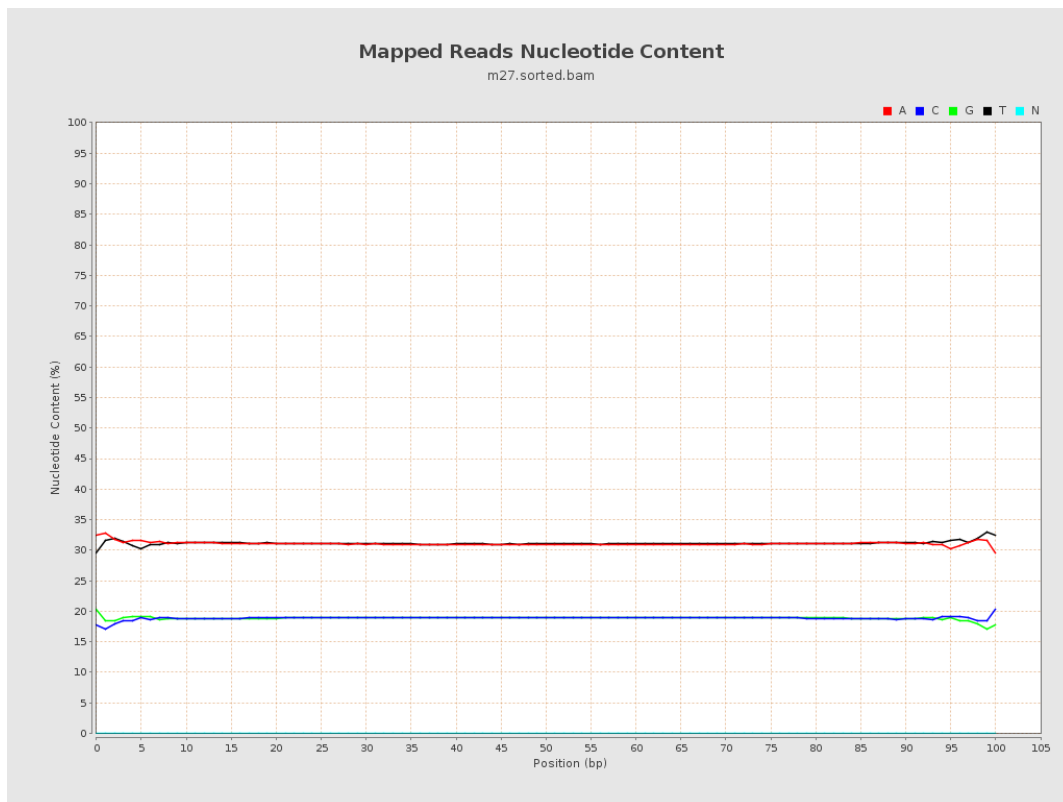
6. Results : Genome Fraction Coverage



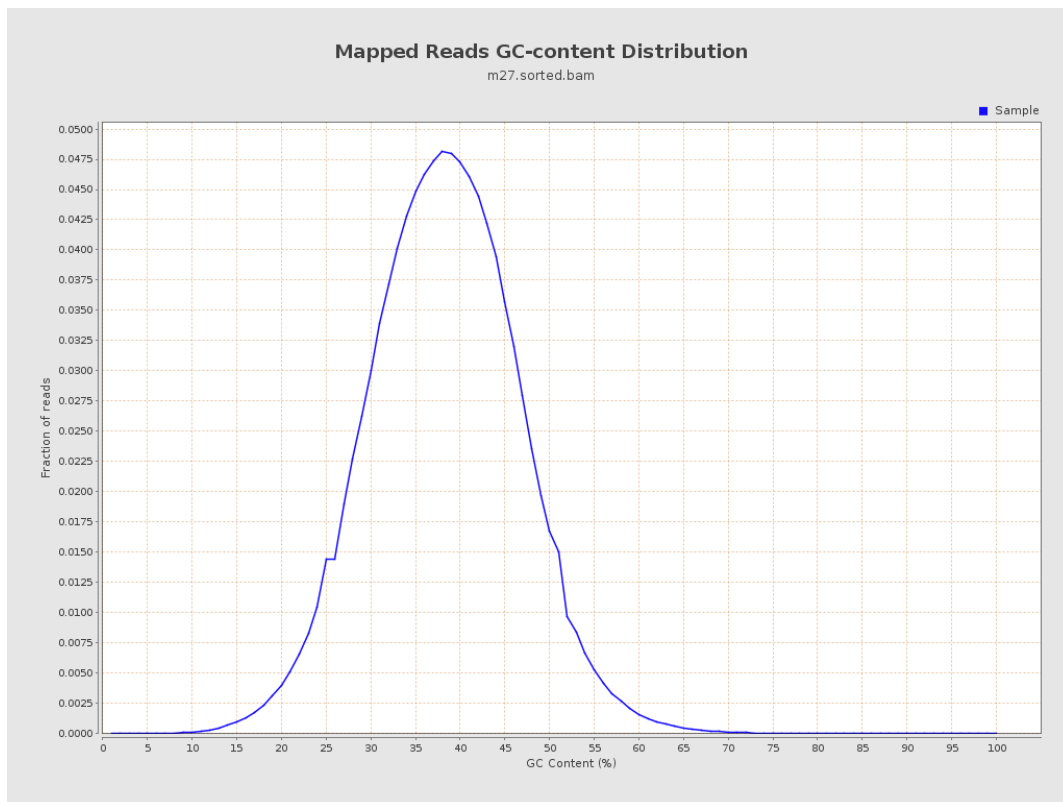
7. Results : Duplication Rate Histogram



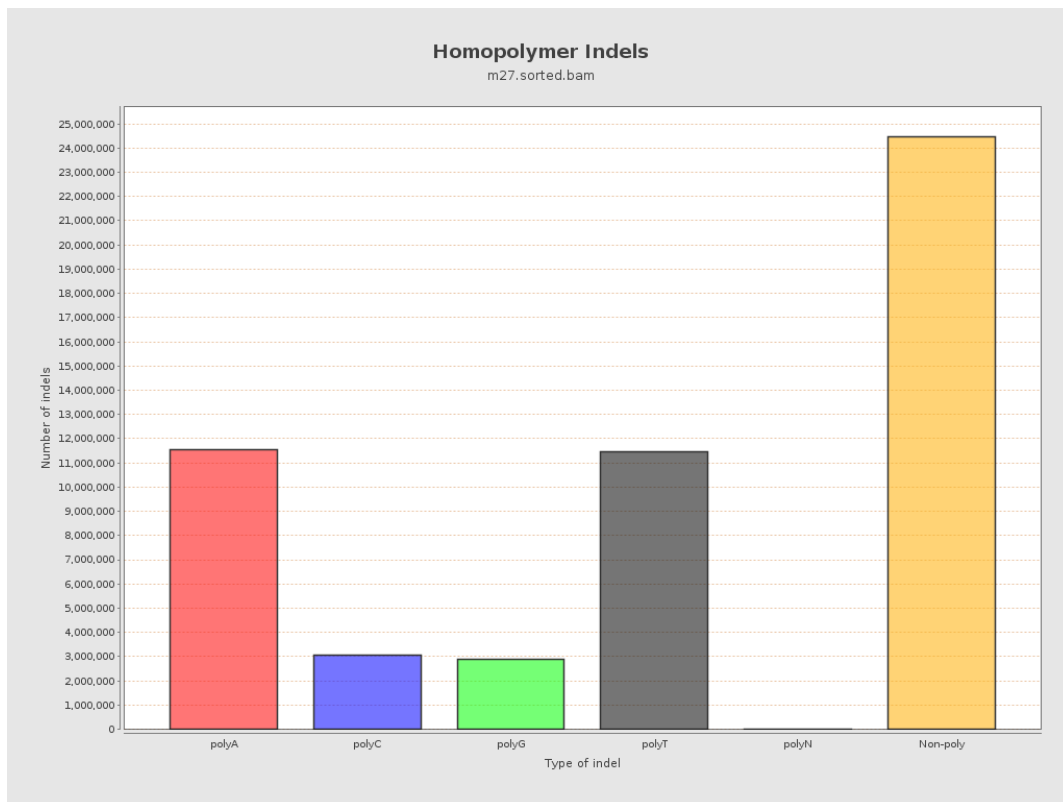
8. Results : Mapped Reads Nucleotide Content



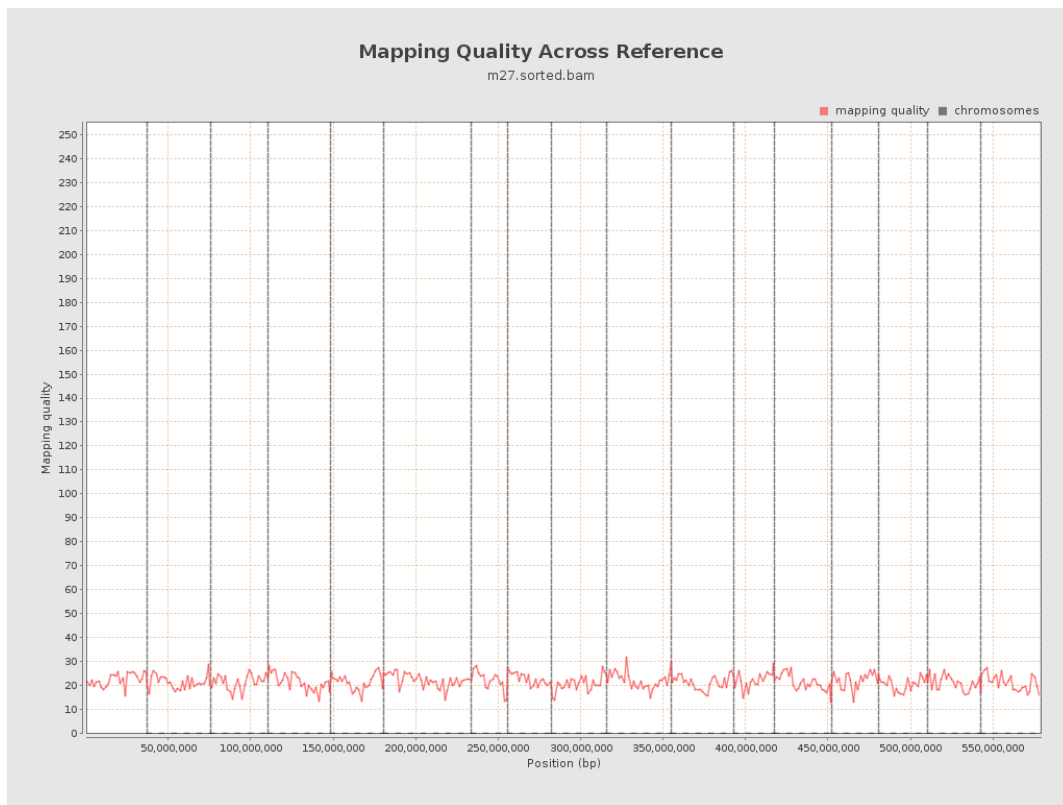
9. Results : Mapped Reads GC-content Distribution



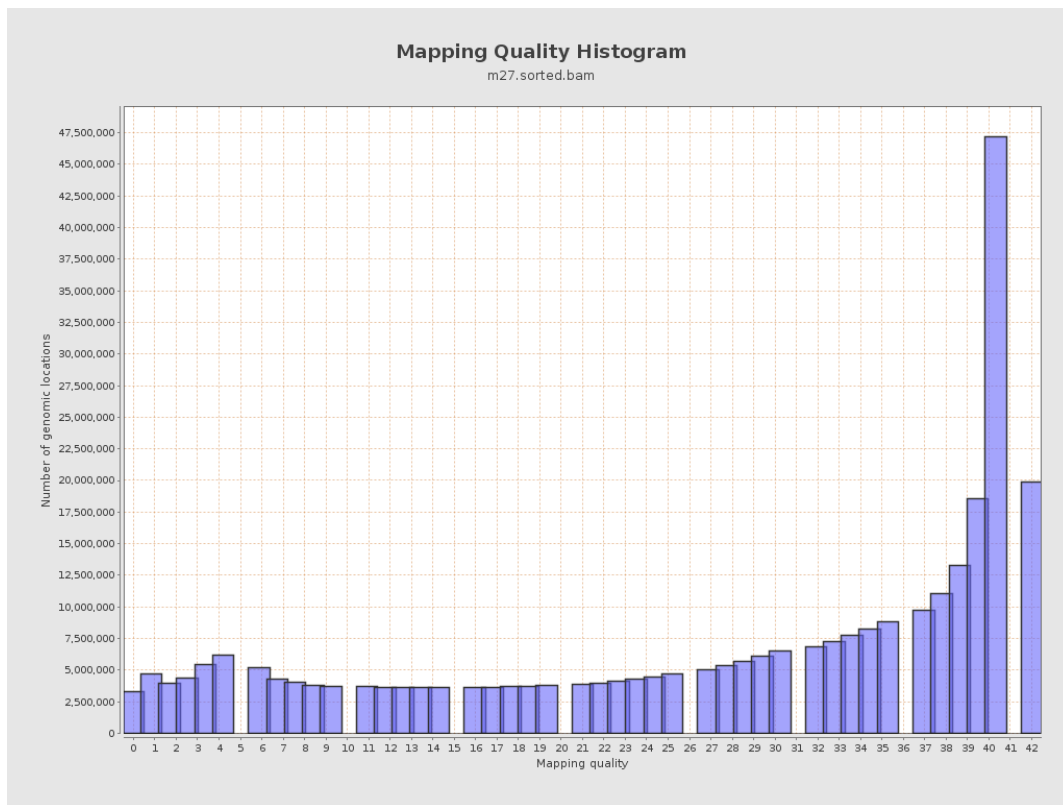
10. Results : Homopolymer Indels



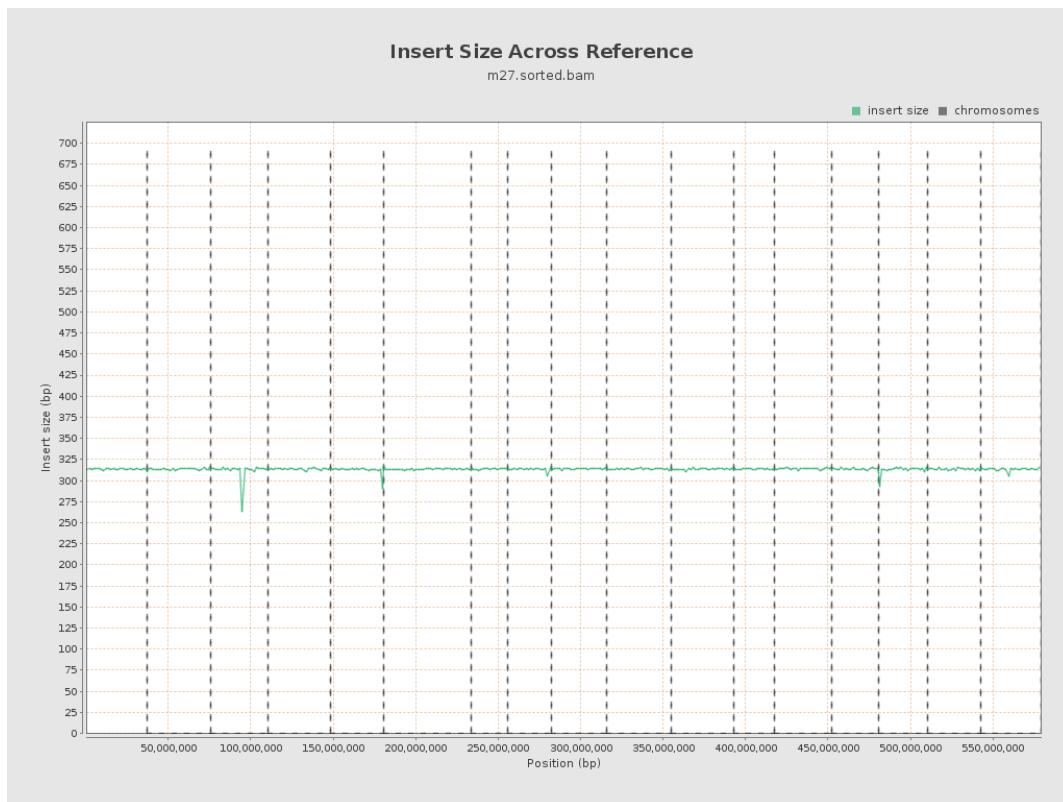
11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram



13. Results : Insert Size Across Reference



14. Results : Insert Size Histogram

