Description of Medicago R108 genome assembly data

Medicago HapMap project  
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R108 SOURCE MATERIAL
Seeds were obtained from Pascal Ratet derived from M. truncatula R108-1 C3 in July 2012. This is the stock propagated in Gif from the original regenerable line and used by the community for transformation (i.e., to produce also the Tnt1 line originally). The same seeds were distributed to all the labs who wanted to have R108 plants or produce transgenics.

R108 ASSEMBLY VERSION 0.9
An initial draft assembly was created using ALLPATHS (Gnerre et al., 2011) in February 2013 using default parameters. The following are the assembly statistics obtained:

Assembly Statistics:
- num_scaffolds = 6,118
- num_contigs = 32,949
- total genome length incl. gaps = 369,383,725
- total genome length w/o gaps = 334,415,625
- Contig N50 = 22,849
- Scaffold N50 = 351,578
- Max scaffold size = 2,244,698
- Min scaffold size = 920

INPUT DATA
- 166,118,124 (~60 X) SIPE reads, 2 x 100 bp from the HiSeq 2000, insert size 142 bp
- 82,323,745 (~30 X) LIPE (i.e. mate pair) reads, 2 x 100 bp from the HiSeq 2000 with insert size 6500 bp

LIST OF FILES
Medicago_R108_HM340_v0.9_assembly.fasta.gz (102 MB)

REFERENCES