S2 Appendix - Reads behind Figure 3

The following fastq reads overlap with the region shown in Figure 3 (reads ID from fastq with SRA ID SRR931836).

SRR931836.531994, SRR931836.952533, SRR931836.1053622, SRR931836.1069887, SRR931836.1420071, SRR931836.1569407, SRR931836.2175300, SRR931836.2611801, SRR931836.2851952, SRR931836.3202289, SRR931836.3224927, SRR931836.4770490, SRR931836.5407974, SRR931836.6352336, SRR931836.7388866, SRR931836.7505309, SRR931836.7713938, SRR931836.7918128, SRR931836.8527838, SRR931836.8677342, SRR931836.9036755, SRR931836.9101957, SRR931836.9526182, SRR931836.9557079, SRR931836.9597616, SRR931836.10067214, SRR931836.11485357, SRR931836.11791390, SRR931836.11811808, SRR931836.12373570, SRR931836.14154848, SRR931836.14313085, SRR931836.14502580, SRR931836.16566511, SRR931836.16928475, SRR931836.17213611, SRR931836.17405600

These reads result in alignments with the following sequences when aligned to the A. *thaliana* reference graph (sequences are in same order as the read IDs above):

```
catctaccttgtttttctttgacggcgacatacaaaaaataaaacaaaac
ccttcttcttcatctaccttgtttttctttgacggcgacatacaaaaaat
catctaccttgtttttctttgacggcgacatacaaaaaataaaacaaaac
cttcttcttcatctaccttgtttttctttgacggcgacatacaaaaaat
aatccattttctcgttttcgatgtccttcttcttcatctaccttgttttt
gacatacaaaaaataaaacaaaacagaaccctagatgggtgtgatgggct
tctcgttttcgatgtccttcttcttcatctaccttgtttttctttgacgg
ttttctcgttttcgatgtccttcttcttcatctaccttgtttttctttg
gacggcgacatacaaaaaataaaacaaaacagaaccctagatgggtgtg
tcttcatctaccttgtttttctttgacggcgacatacaaaaaataaaa
ccattttctcgttttcgatgtccttcttcttcatctaccttgtttttct
gacggcgacatacaaaaaataaaacaaaacagaaccctagatgggtgtga
gttttcgatgtccttcttcttcatctaccttgtttttctttgacggcgac
gacggcgacatacaaaaaataaaacaaaacagaaccctagatgggtgtg
ttctcgttttcgatgtccttcttcttcatctaccttgtttttctttgacg
tctcgttttcgatgtccttcttcttcatctaccttgtttttctttgacgg
ctaccttgtttttctttgacggcgacatacaaaaaataaaacaaaac
gttttcgatgtccttcttcttcatctaccttgtttttctttgacggcgac
ctaccttgtttttctttgacggcgacatacaaaaaataaaacaaaac
cgatgtccttcttcttcatctaccttgtttttctttgacggcgacataca
cgttttcgatgtccttcttcttcatctaccttgtttttctttgacggcga
ccttcttcttcatctaccttgtttttctttgacggcgacatacaaaaaat
ccttgtttttctttgacggcgacatacaaaaaataaaacaaaacagaacc
tctcgttttcgatgtccttcttcttcatctaccttgtttttctttgacgg
ttttctttgacggcgacatacaaaaaataaaacaaaacagaaccct
gttttctttgacggcgacatacaaaaaataaaacaaaacagaaccctag
accttgtttttctttgacggcgacatacaaaaaataaaacaaaacagaac
catctaccttgtttttctttgacggcgacatacaaaaaataaaacaaaac
ttttctttgacggcgacatacaaaaaataaaacaaaacagaaccct
atgtccttcttcttcatctaccttgtttttctttgacggcgacatacaa
ttgacggcgacatacaaaaaataaaacaaaacagaaccctagatgggtg
gatgtccttcttcttcatctaccttgtttttctttgacggcgacatacaa
cacaaatccattttctcgttttcgatgtccttcttcttcatctaccttgt
atccattttctcgttttcgatgtccttcttcttcatctaccttgtttttc
tttgacggcgacatacaaaaaataaaacaaaacagaaccctagatgggtg
ttttctttgacggcgacatacaaaaaataaaacaaaacagaaccctaga
cgttttcgatgtccttcttcttcatctaccttgtttttctttgacggcga
```

This is the sequence on haplotype 628 from the 1001 genomes vcf (http://1001genomes.org/data/GMI-MPI/releases/v3.1/1001genomes_snp-short-indel_only_ACGTN.vcf.gz) used to build the graph:

CACAAATCCATTTTCTCGTTTTCGATGTCCTTCTTCTTCATCTACCTTGTTTTTCTTTGACGGCGACATACAAAAAATAAAACA
AAACAGAACCCTAGATGGGTGTGATGGGCT

All above sequences are found within this sequence, either direct or in reverse complement.