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This 40kb region was chosen as it is overlapped by 2 phase 3 BACs, and the positions map identically to Mt 4.0 (offset by 1011538 bases).

The regions for both assemblies are:

Mt3.5: Mt5:33541735..33581735

Mt4.0: chr5:34553273..34593273

Fig 1. SNPs called in both Mt 3.5 and Mt 4.0. 95% of calls remain unchanged, either matching the reference or making the same SNP call. An additional 3% were undetermined (called N) in the previous release and now have an identified genotype (either matching the 4.0 reference assembly or are now SNP). Fewer than 0.1% of calls that were formerly reference are now SNPs. Additionally, fewer than 0.1% of calls that were SNPs are now reference calls. Note that heterozygous calls were not made in Mt 3.5 but were only called in Mt 4.0 if 1 in 10,000 likelihood difference from the reference call. These heterozygous calls represent 0.3% of calls in this region.

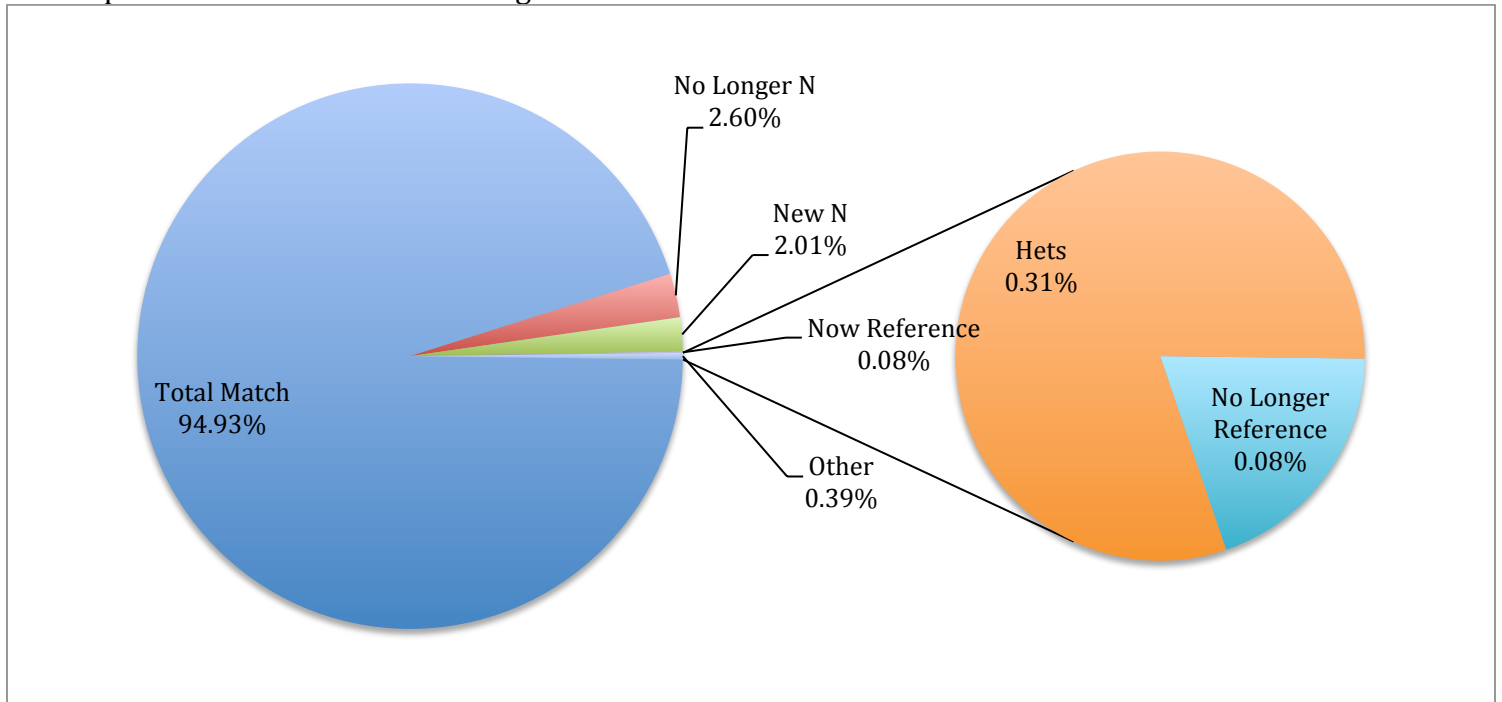


Fig 2. Stacked bar chart showing the relative distribution of SNP status changes for the first 100 positions in this region. There does not appear to be any significant clustering of status changes in this region, which might be indicative of local artifacts. Position 33563015 stands out for having 75 heterozygous calls. This may be a problematic site given that in Mt 3.5 an additional 71 lines were called N (presumably due to some filter), but are called in Mt 4.0.

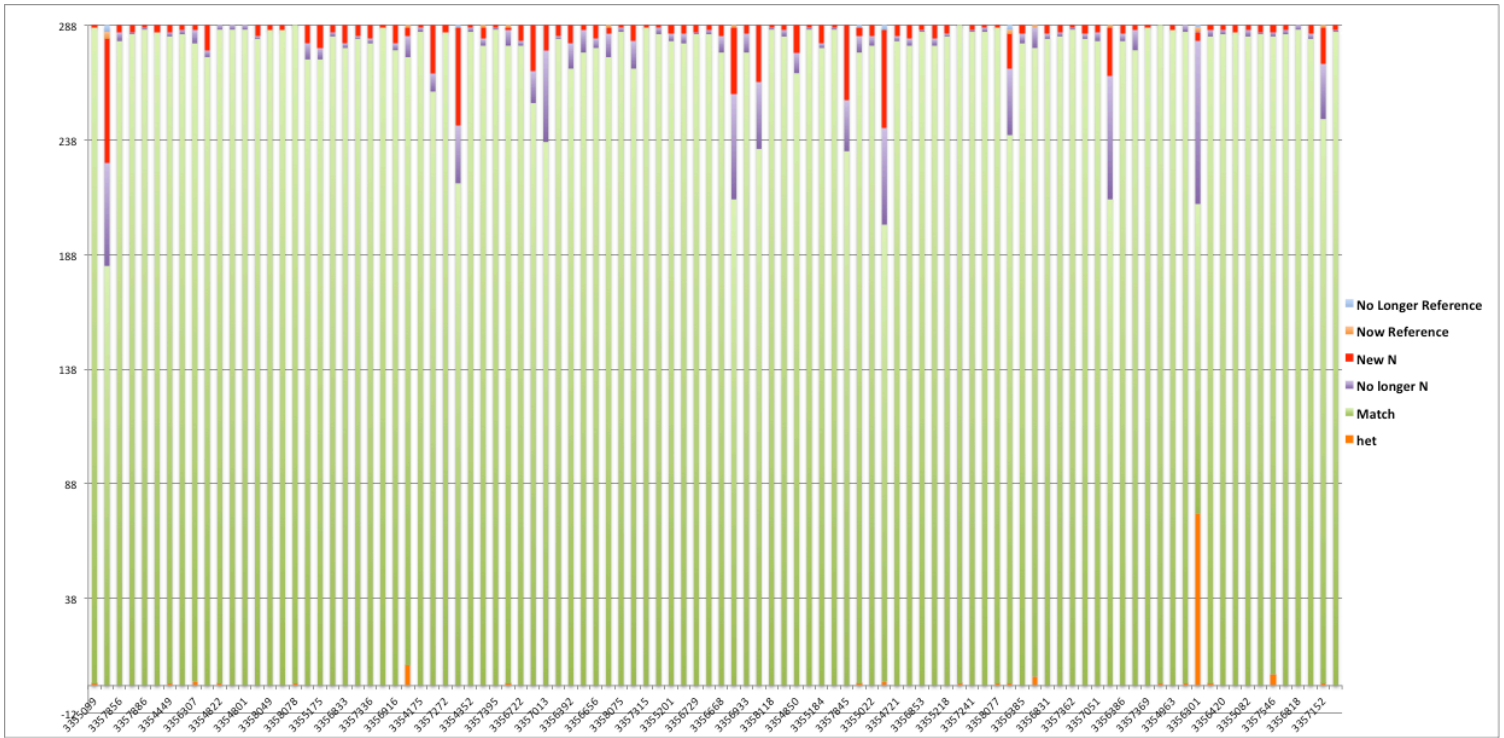


Fig 3. New SNPs in 4.0 relative to 3.5 calls. In this region, Mt 4.0 1,556 new SNP positions are called relative to Mt 3.5. The majority (82%) of accession calls match the *M. truncatula* 4.0 reference at these sites. Nearly all of the remaining accession calls (18%) are undetermined at these positions.

708 Hets, 2108 SNPs, 79k N

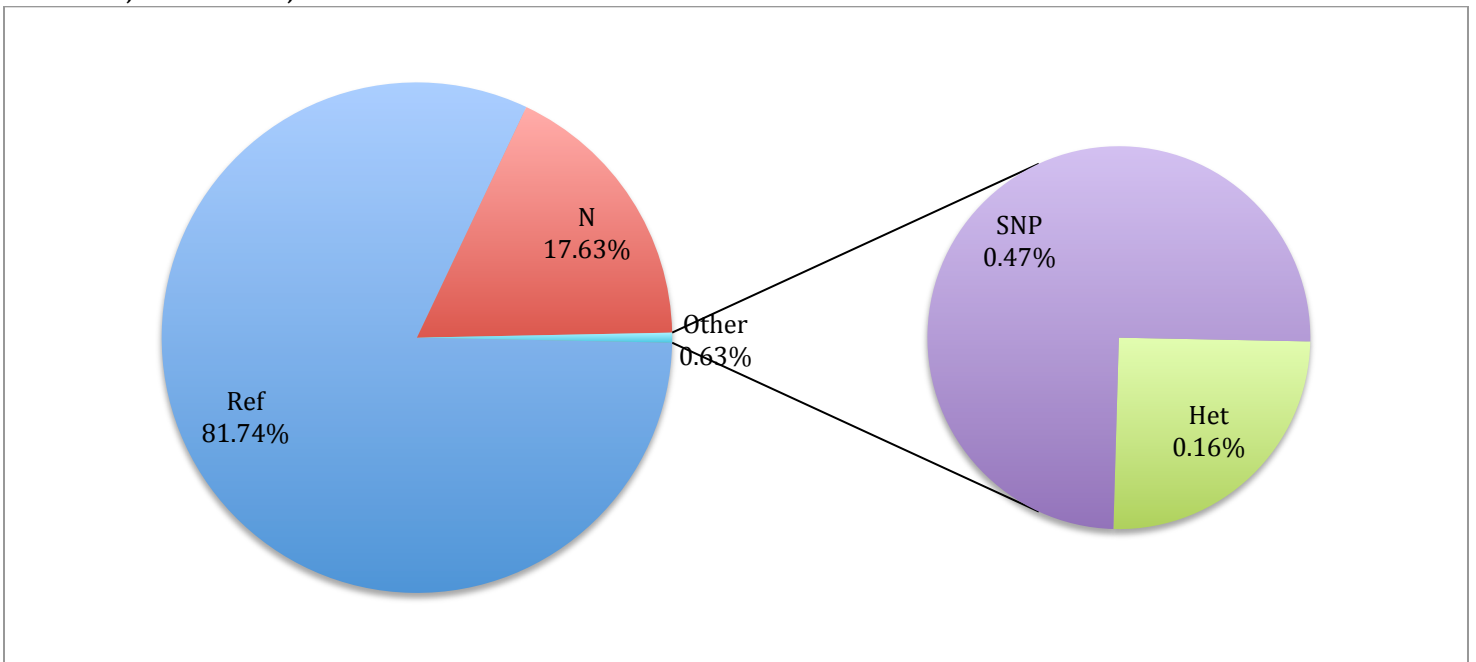


Fig 4. In this region 556 previously called positions from Mt 3.5 now match the reference. However, most of these accession calls at these sites already matched the reference in Mt 3.5 (or were undetermined). Only 4% of the accession calls in Mt 3.5 were actually called SNPs in the first place.

555 Removed from 3.5, 5846 SNPs, 47k N's

