**Supplementary Figure Legends**.

C:\Users\roshankulkarni.524\Desktop\Histograms\10017.wmfC:\Users\roshankulkarni.524\Desktop\Histograms\10602.wmfC:\Users\roshankulkarni.524\Desktop\Histograms\30076.wmfC:\Users\roshankulkarni.524\Desktop\Histograms\TxAg-6.wmfC:\Users\roshankulkarni.524\Desktop\Histograms\UF439.wmfC:\Users\roshankulkarni.524\Desktop\Histograms\9484.wmf

**Figure S1.** Histograms showing the distribution of reported heterozygotes. Based on these results, it was estimated that a range between 25% to 75% reference allele denoted true heterozygotes. Minor allele frequencies less than 20% were deemed to result from a combination of presence of paralogous sequences containing the target region sequence (Bar represents the region of putative heterozygous SNPs).

C:\Roshan\Rplot01.tiff

**Figure S2.** PCA plot clustering tetraploids based on botanical type (Green- *hypogaea*, Red- *fastigiata*, Black- Others (TxAG-6, 308-TAN, 60-02-03-03, 43-09-03-02). Note: 60-02-03-03 and 43-09-03-02 are BC3 tetraploids from a TxAG-6 x UF439-16-10-3-2 cross.