S3 Fig. Distribution of pairwise estimated relatedness for individuals with expected relationships: Full-sib (a), Half-sib (b), and Unrelated (c). From left to right estimates obtained using G matrices constructed from subsets of randomly selected of 500 (05K), 1,000 (1K), 3,000 (3K), 5,000 (5K), 10,000 (10K), 20,000 (20K), 30,000 (30K) and all 33K SNP markers, and 500 (05K), 1,000 (1K), 3,000 (3K), 5,000 (5K), 10,000 (10K), 20,000 (20K) and all 24K DArT-seq markers and using only the 10,501 (10.5K) DArT-seq markers mapped to the eleven *Eucalyptus* chromosome scaffolds.