Supplemental Table Legends

Supplementary Table 1 Expressed genes common to iT_{reg} (n=5 independent replicates) and Freshly isolated nT_{reg} (n=4) cell preparations as compared to $CD4^{+}EGFP^{-}$ T_{conv} cells (n=3) of *Foxp3*^{EGFP} mice. Common genes were selected at 2 fold change cut-off. Results represent means $\pm$ S.E.M., with each replicate derived from pooled cells from several mice (4-10). Probe comparisons were analyzed by the Student unpaired two-tailed T test with p values <0.05 considered significant.

Supplementary Table 2 Expressed genes common to iT_{reg} (n=5 independent replicates) and nT_{reg} cells that have been activated *in vitro* with anti-CD3 mAb + IL-2 (A-nT_{reg} cells; n=3) as compared to in vitro activated $CD4^{+}EGFP^{-}$ T_{conv} (A-T_{conv}) cells, all originally derived from *Foxp3*^{EGFP} mice (n=4). Common genes were selected at 2 fold change cut-off. Results represent means of independent replicates (n=5 for iT_{reg} and 4 for nT_{reg}) $\pm$ S.E.M., with $p<0.05$ by Student unpaired two tailed T test.

Supplementary Table 3 Differential gene expression between iT_{reg} and freshly isolated nT_{reg} cell preparations (n=5 and 4, respectively). Results were analyzed at a 2 fold change cut off, and represent means ($\pm$ S.E.M) that scored at $p<0.05$ by Student's unpaired two-tailed T test.

Supplementary Table 4 Differential gene expression between iT_{reg} and activated nT_{reg} cell preparations (n=5 and 3, respectively). Results were analyzed at a 2 fold change cut off, and represent means ($\pm$ S.E.M) that scored at $p<0.05$ by Student's unpaired two-tailed T test.

Supplementary Table 5 Differential gene expression between successfully derived iT_{reg} cells and $CD4^{+}EGFP^{-}$ cells from the same cultures that failed to convert into iT_{reg} cells following anti-CD3 mAb+TGF-β treatment (n=5 and 3, respectively). Results were analyzed at a 2 fold change

cut off, and represent means (± S.E.M) that scored at $p<0.05$ by Student's unpaired two-tailed T test.

Supplementary Table 6 Differential gene expression between iT_{reg} and ΔiT_{reg} cell preparations (n=5 and 3, respectively). Results were analyzed at a 2 fold change cut off, and represent means (± S.E.M) that scored at $p<0.05$ by Student's unpaired two-tailed T test. 2 genes were found selectively enriched in each population: *Ddx3y* and *Jarid1d* in iT_{reg} cells and *2310047K21Rik* and *Foxp3* in ΔiT_{reg} cells. Both *Ddx3y* and *Jarid1d* are found on the Y chromosome. Their enrichment in iT_{reg} cells reflects a sex bias in the origin of the analyzed samples in that a majority of the iT_{reg} cell populations (3/5) were from $Foxp3^{EGFP}$ males (3/5) whereas all the ΔiT_{reg} cells were from heterozygous $Foxp3^{\Delta EGFP+/}$ females. The latter choice was necessitated by the need to avoid the problem of intense T cell activation at baseline associated with sick $Foxp3^{\Delta EGFP}$ males, which interferes with the derivation of ΔiT_{reg} cells. The identification of *Foxp3* as the more enriched of the 2 genes found overexpressed in ΔiT_{reg} cells reflects a technical anomaly, namely that the gene array probe for *Foxp3* lies distal to the poly-A start site introduced as part of the bicistronic EGFP cassette in the $Foxp3^{EGFP}$ allele. This results in a false negative signal for *Foxp3* in $Foxp3^{EGFP}$ T cells.

Supplementary Table 7 Differential gene expression between iT_{reg} and ΔiT_{reg} cells that have been rested in culture for 7 days with IL-2 (n=5 and 3, respectively). Results were analyzed at a 2 fold change cut off, and represent means (± S.E.M) that scored at $p<0.05$ by Student's unpaired two-tailed T test.