Inference of master regulators Normalized expression **Raw Count Matrix FPKM** 48 samples **DEGs Co-Expression** 3 tissues x 4 time points x 4 reps. T4 vs T1 per tissue | PT1-T4 OT1-T4 LT1-T4 113 pituitary TFs 4x4 4x4 3 RIF analyses key regulators gene1 68 ovary TFs gene2 298 TFs 124 liver TFs gene3 **Transcription factors** T4 vs T1 per tissue gene37,253 pituitary(P); ovary(O); liver(L) Gene selection for gene regulatory network (GRN) construction PCIT input matrix gene attributes DEG 8.625 PCIT output get PCIT FPKM expression DMG 2,315 DE DMG DAC DMP TS SNP TF gene1-gene2 0.97294 POS PT1-T4 OT1-T4 LT1-T4 **DAC 859** #subcategory 3 genes FPKM gene1-gene3 0.96860 POS

gene1,858

gene1-gene1,858

