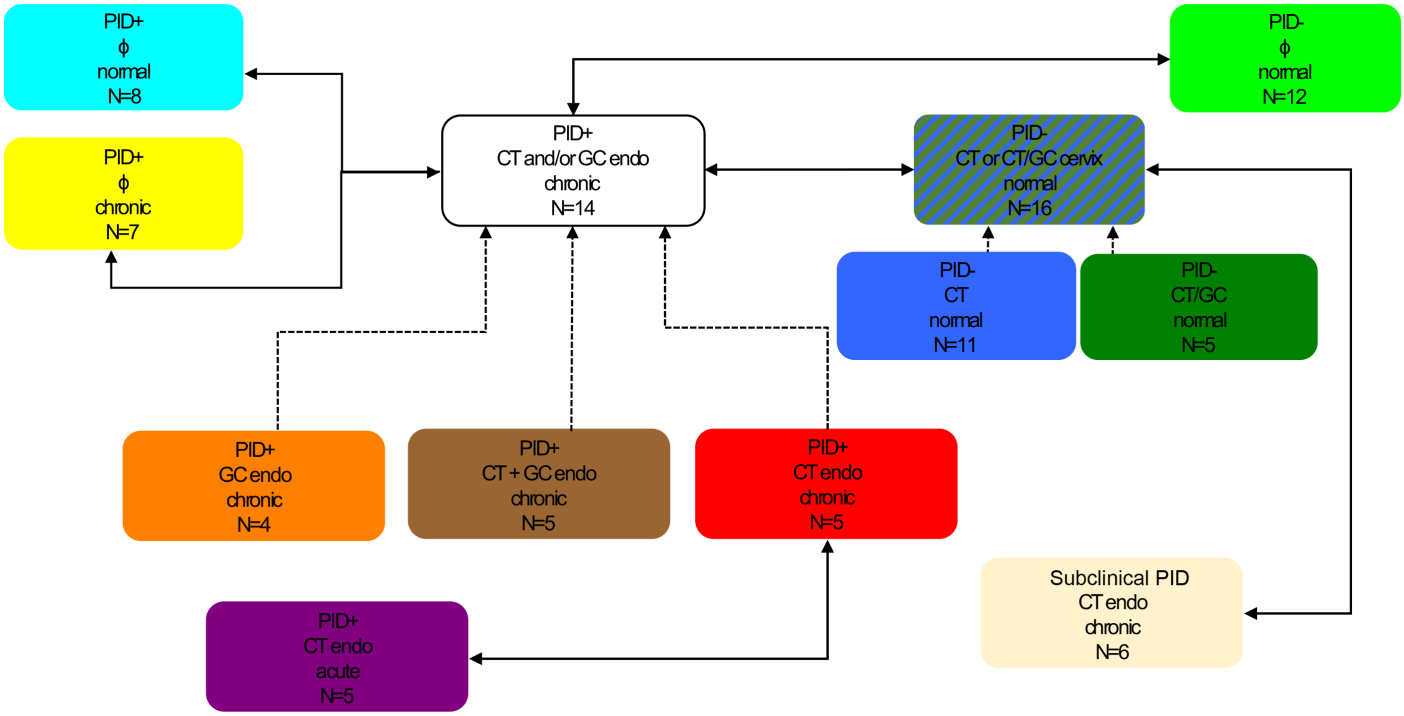
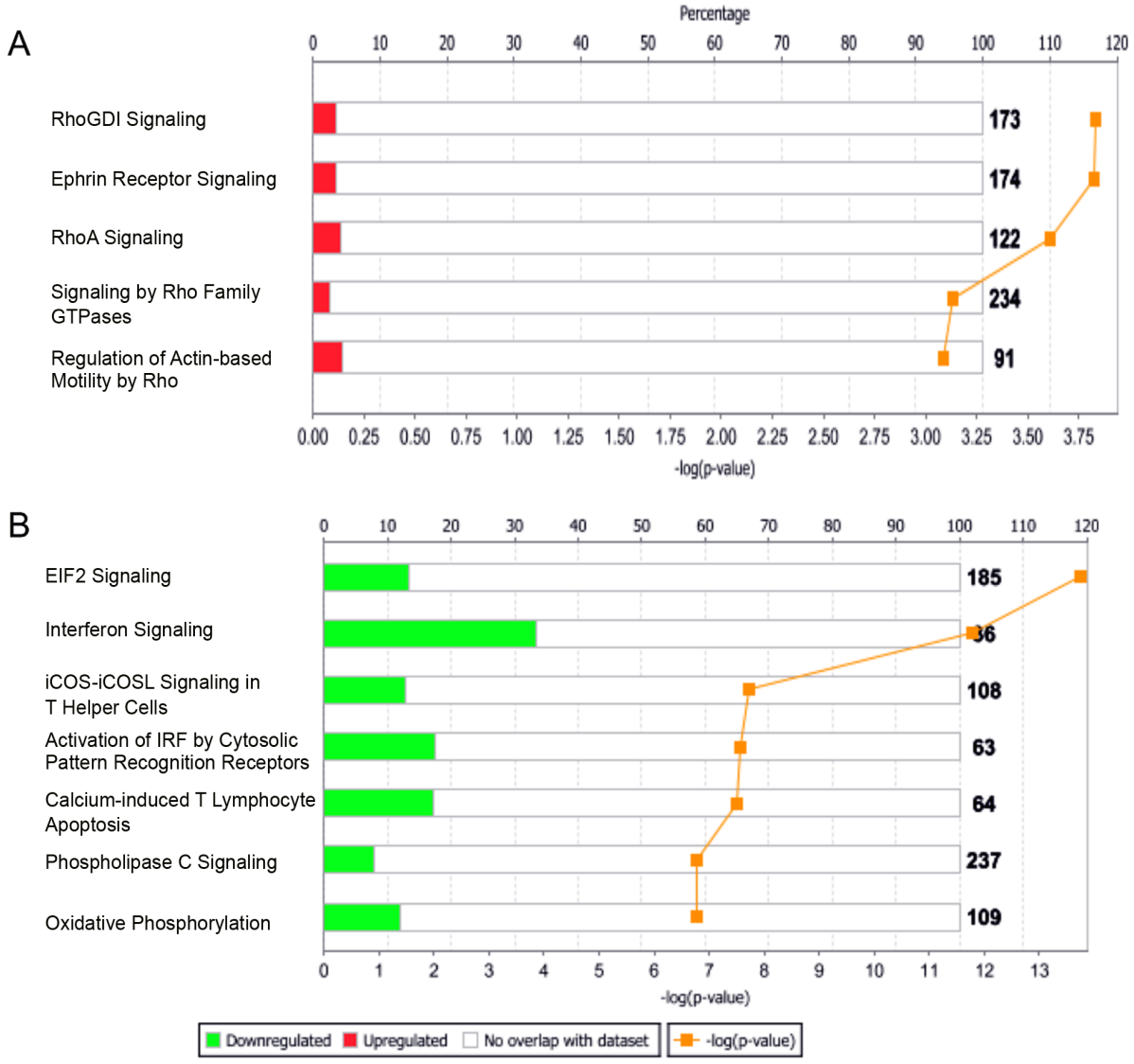
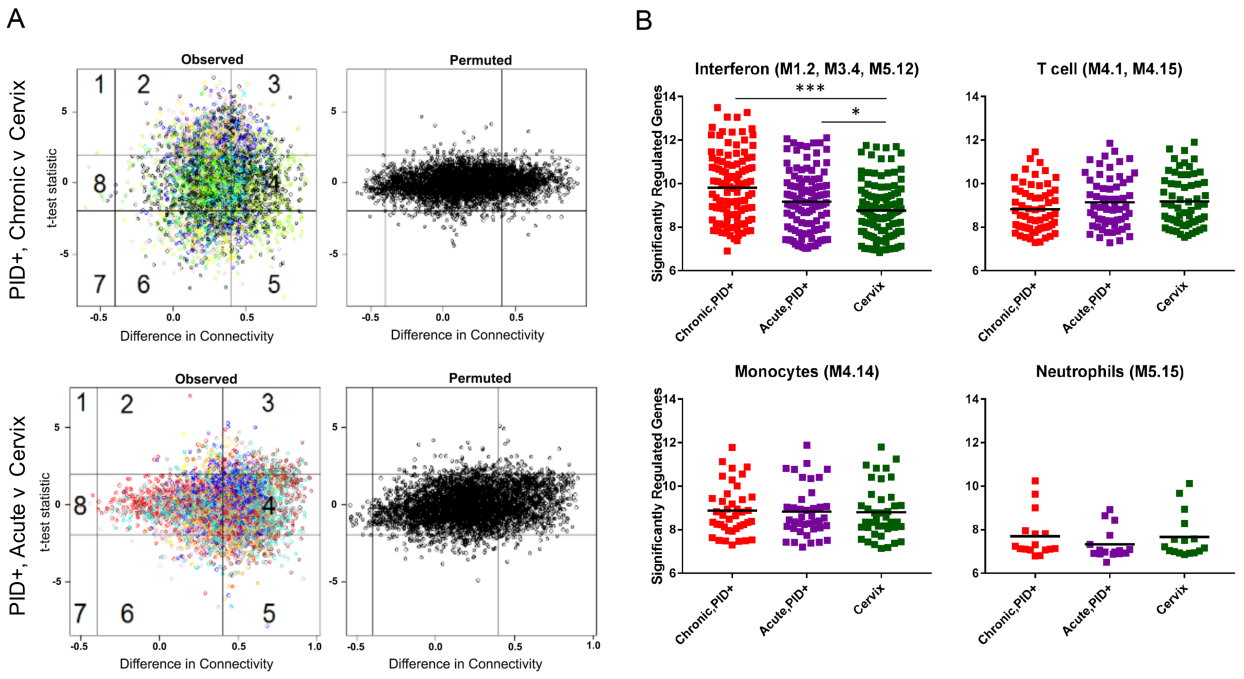


Supplementary Fig. 1. Stratification of patient samples according to clinical, microbiological, and histologic diagnoses. For each subset of patient samples, the *first line of text* indicates presence (+) or absence (+) of a clinical diagnosis of pelvic inflammatory disease (PID). The *second line of text* indicates PCR detection results for CT and GC in cervical swabs and endometrial biopsy samples. “Cervix” indicates PCR detection only in cervical swabs, “Endo” indicates PCR detection in cervical swabs and endometrial biopsies; null sign (ϕ) indicates PCR tests for CT and GC were negative in both cervical swabs and endometrial biopsies. The *third line of text* indicates endometrial histology; no significant finding (normal); chronic endometritis (chronic): presence of ≥1 plasma cell per 120X field in the endometrial stroma; acute endometritis (acute): presence of ≥1 plasma cell per 120X field in the endometrial stroma and ≥5 neutrophils per 400X field in the endometrial surface epithelium. Subclinical PID, indicates asymptomatic women with endometrial infection and chronic endometritis. N = number of subjects in each sample set. Solid lines with bidirectional arrows indicate comparison groups, dashed lines with single arrows indicate subgroups contributing to analyses.



Supplementary Fig.2. Top differentially expressed canonical pathways in women with PID and chronic endometritis due to GC/CT co-infection compared to women with PID and chronic endometritis due to CT alone. IPA showed **(A)** monocyte and neutrophil signaling pathways were up-regulated, while pathways associated with **(B)** Interferon and T cell signaling, and mitochondrial respiration and protein synthesis were down-regulated.



Supplementary Fig.3. Up-regulation of IFN signaling pathway genes are observed in women with CT-induced PID and acute endometritis. (A). Scatterplot of differences in connectivity, *DiffK* vs. expression level, *t statistic*, for transcriptional responses between women with PID, CT endometrial infection, and chronic or acute endometritis versus women without PID, CT infection limited to the cervix, and no endometritis. Colored plots are observed data and black plots are permuted data. Horizontal lines depict sector boundaries based on t-statistic values, and vertical lines depict boundaries based on DiffK. Numbers mark eight sectors; colors represent individual modules. For Chronic PID versus Cervix, P < 0.005 for sectors 2, 3, 5, and 6. Sectors 1, 4, 7, and 8 were NS. For Acute PID versus Cervix, P < 0.005 for sectors 3, 4, and 5. All other sectors were not significant. P value derived after 1000 permutations **(B).** Median expression values of genes within interferon, T cell, monocyte and neutrophil modules in women with CT-PID and chronic endometritis, CT-PID and acute endometritis, and asymptomatic women with CT cervical infection only. Dots represent the median expression value for each individual transcript (log2 transformed expression). ANOVA p< 0.05 after Bonferroni correction for interferon module. Pairwise comparisons after ANOVA in interferon module were conducted via Student's t-Test. *p< 0.05, *** p < 0.005.