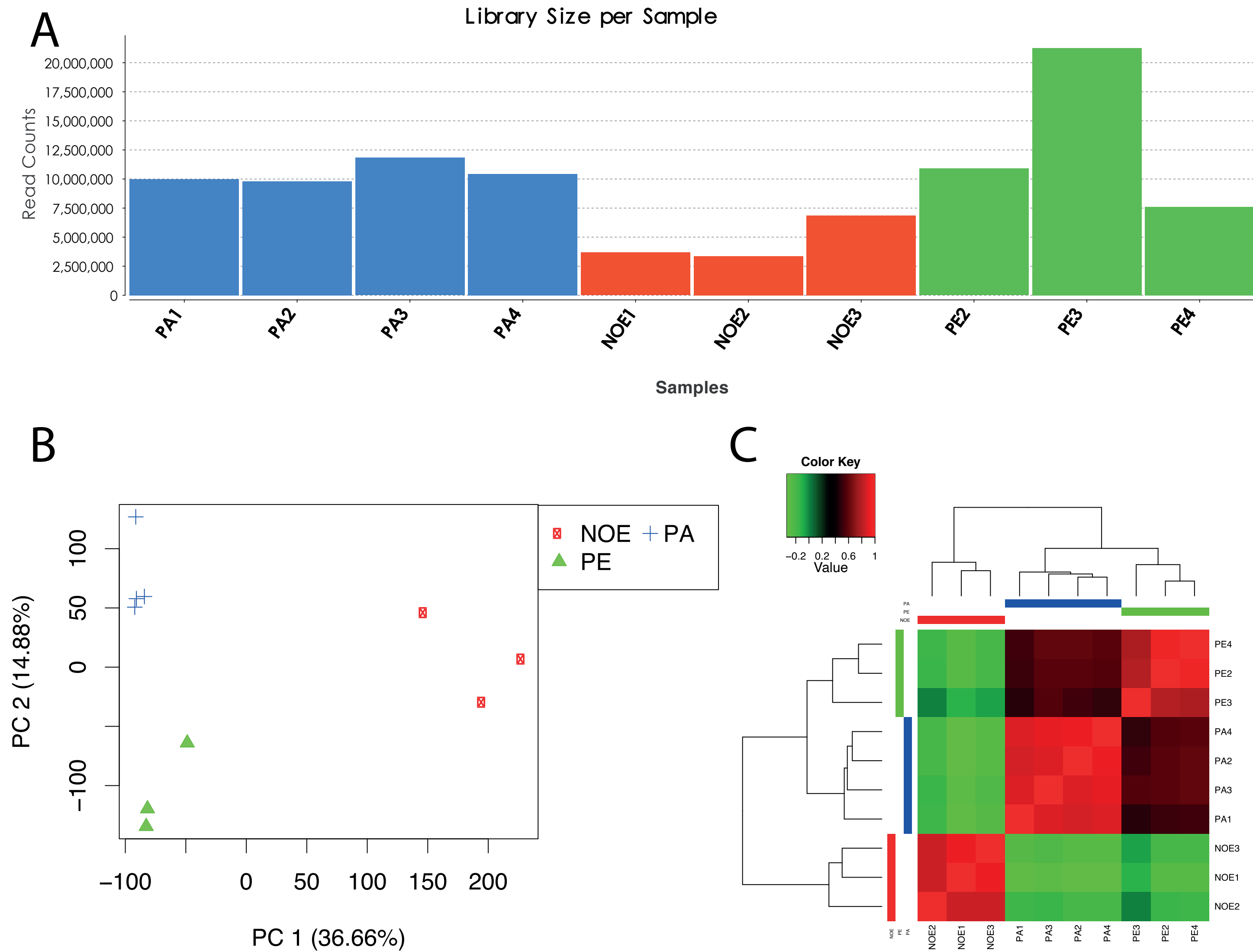
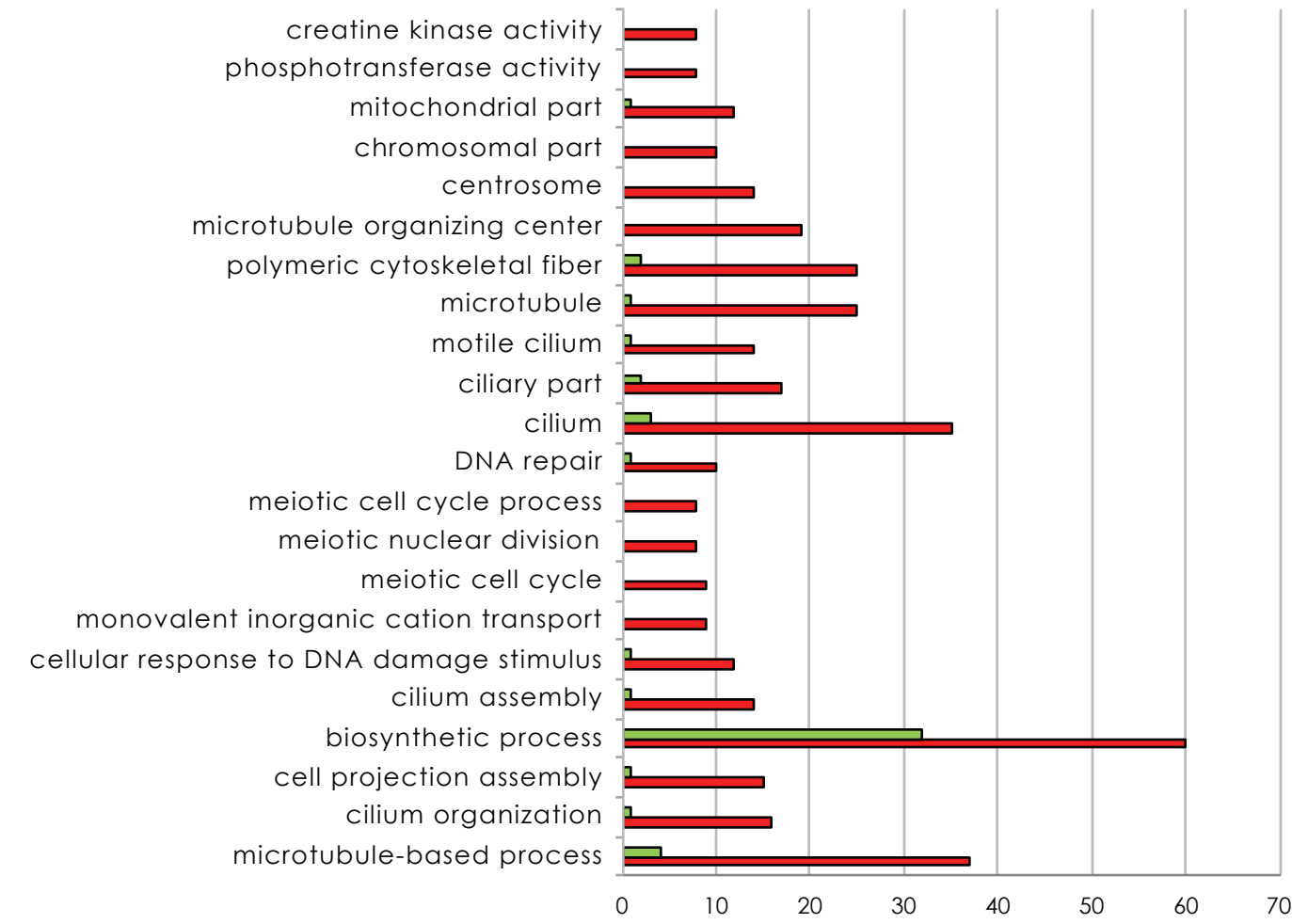


Supplementary Figure 1. A. Library size (in number of reads) per sample. **B.** PCA of the final samples used in the differential expression analysis. **C.** Correlation matrix of the final samples used in the differential expression analysis. **D.** Enrichment analysis of the Gene Ontology (GO) terms per condition. **E.** Treemaps showing the GO categories associated to the differentially expressed genes in each condition (NOE and PE) obtained in REVIGO. **F.** Treemaps showing the GO categories associated to the differentially expressed genes in each condition (PA and PE) obtained in REVIGO. **G–J.** Gene networks showing the connections between the differentially expressed genes in each condition.

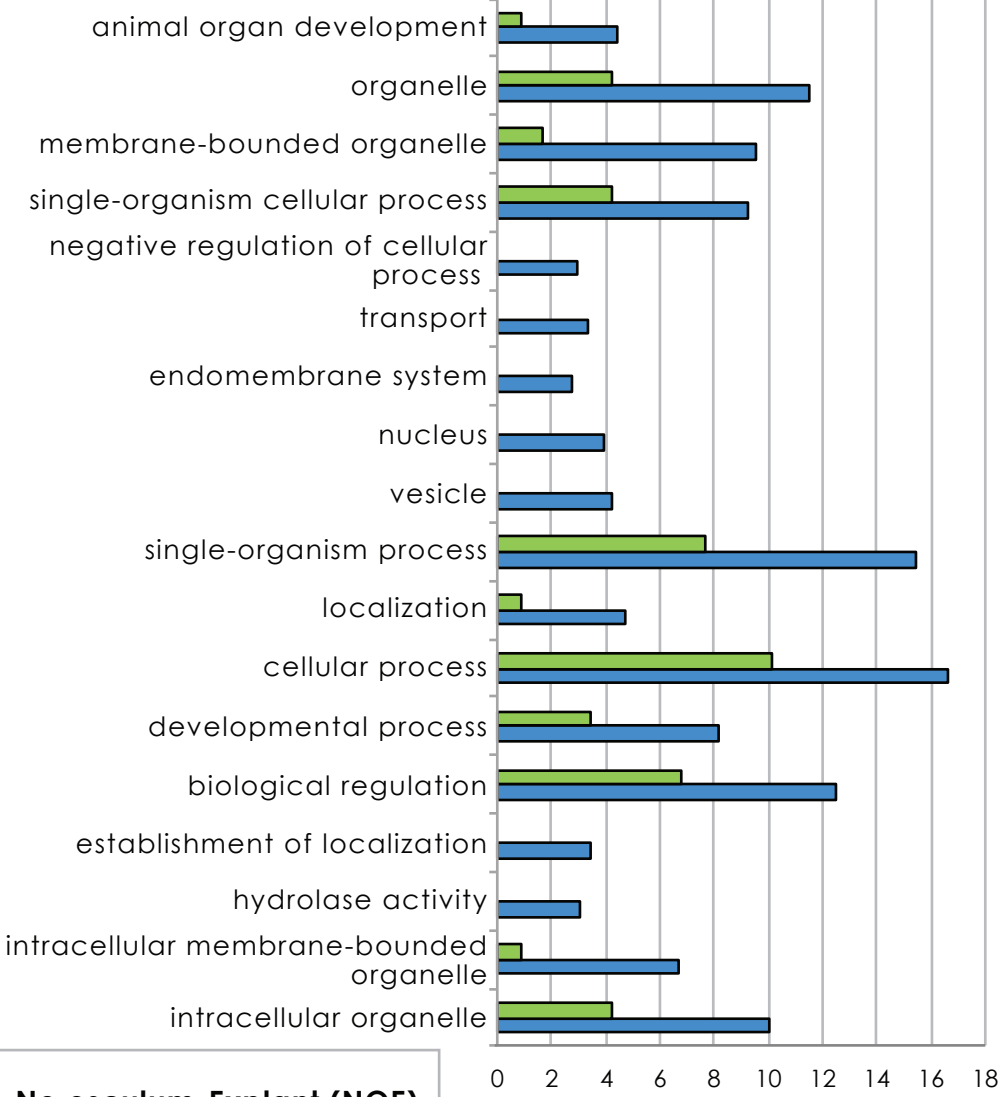


D

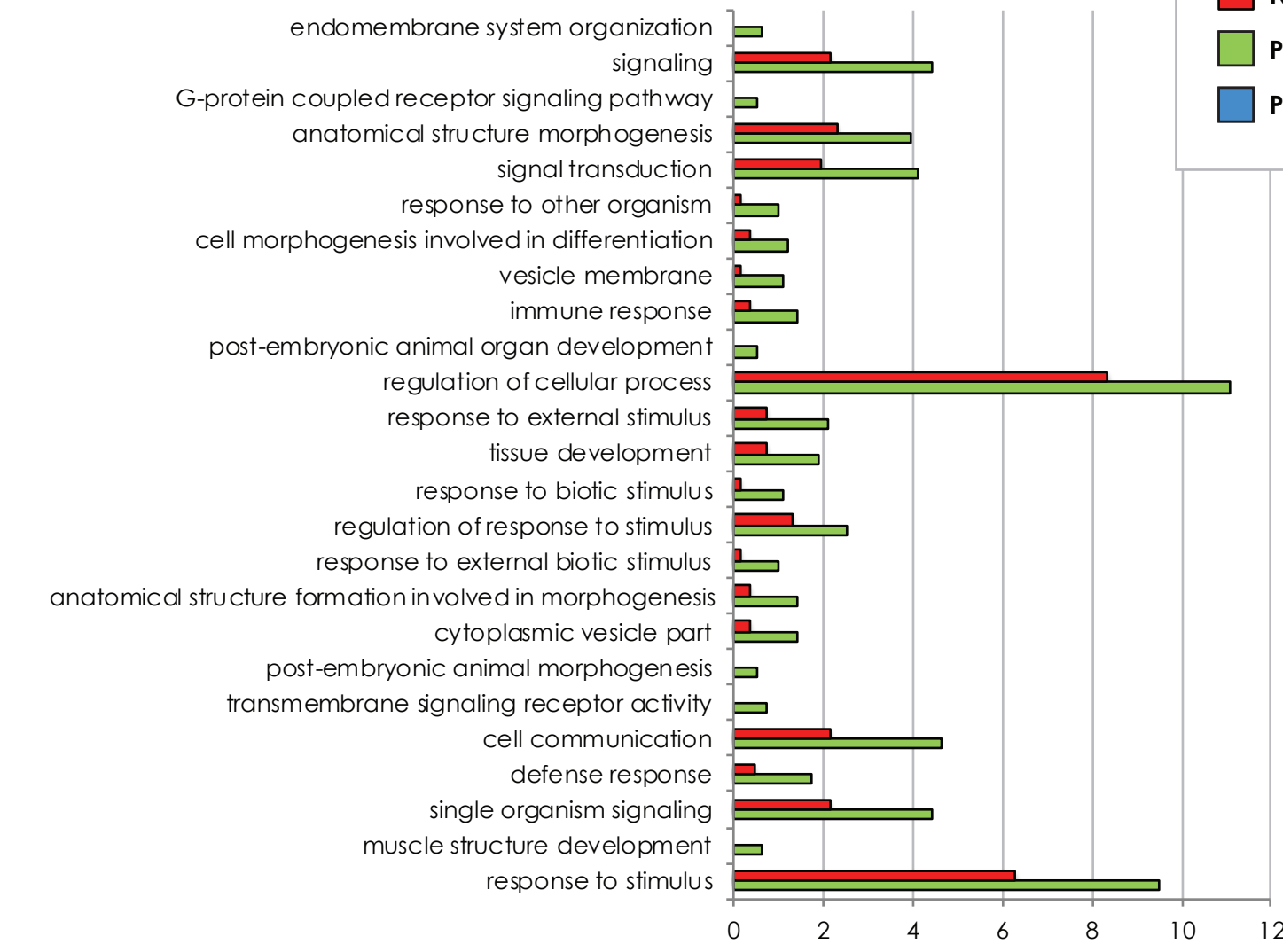
Enrichment in NOE (NOE vs. PE)



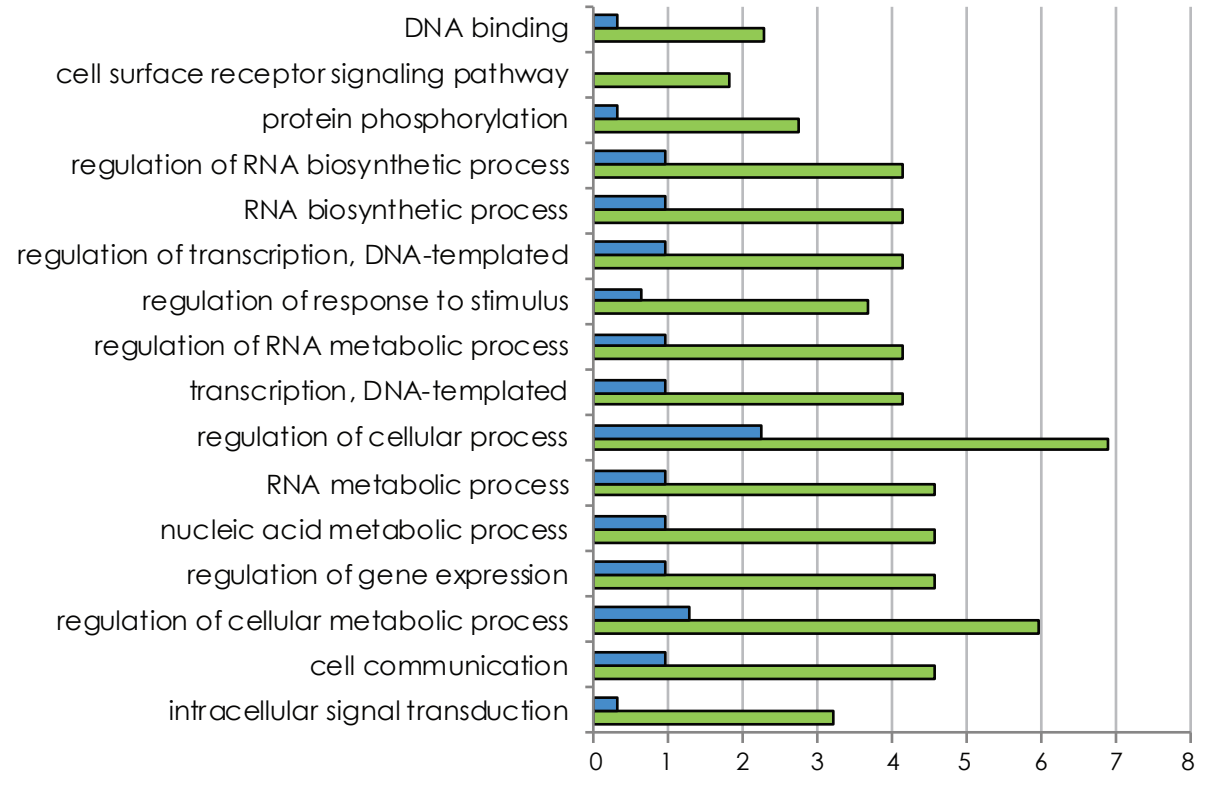
Enrichment in PA (PA vs. PE)



Enrichment in PE (NOE vs. PE)



Enrichment in PE (PA vs. PE)



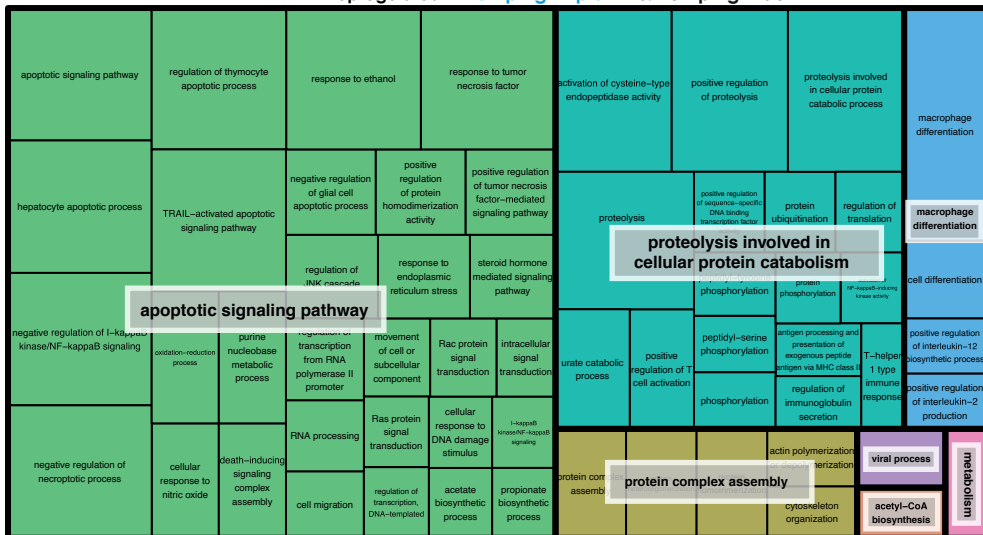
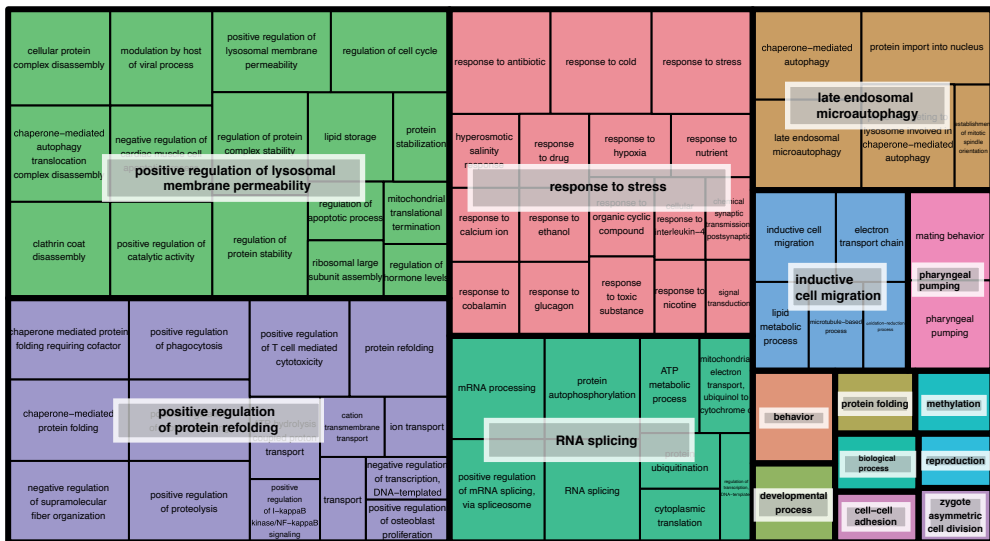
Upregulated in No Osculum-Explant vs. Pumping-Explant

hematopoietic progenitor cell differentiation	negative regulation of peptidase activity	male gonad development	defense response to Gram-negative bacterium	response to organic cyclic compound	epidermis development	hair follicle development	extracellular matrix organization	creatine metabolic process	centrosome organization	epithelial structure maintenance	establishment of organelle localization	protein localization to organelle			
negative regulation of T cell mediated cytotoxicity directed against tumor cell target	lymphocyte homeostasis	long term synaptic depression	substantia nigra development	cellular response to cGMP	positive regulation of heart contraction	oocyte development	response to gravity	platelet degranulation	potassium ion import across plasma membrane	L-cysteine catabolic process to pyruvate, using cysteine dioxygenase	sulfur amino acid biosynthetic process	taurine biosynthetic process	phosphocreatine biosynthetic process		
regulation of receptor activity	nail development	amacrine cell differentiation	embryonic organ development	cellular response to mechanical stimulus	negative regulation of striated muscle contraction	regulation of respiratory gaseous exchange by neurological system process	relaxation of cardiac muscle	response to glycoside	lymphoid lineage cell migration into thymus	attachment of spindle microtubules to kinetochore	cilium or flagellum-dependent cell motility	ATP hydrolysis coupled proton transport	cellular sodium ion homeostasis	negative regulation of calcium ion transmembrane transport	
	positive regulation of epithelial cell differentiation	atrioventricular canal development	meiosis I	negative regulation of epidermal growth factor receptor signaling pathway	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	NIK/NF-kappaB signaling	Notch signaling pathway	nucleotide-excision repair, DNA damage recognition	cellular calcium ion homeostasis	regulation of cytokinesis	DNA replication	lateral element assembly	sodium ion export from cell	regulation of necrotic cell death	negative regulation of NFAT protein import into nucleus
blood vessel maturation	T cell commitment	ventral spinal cord development	DNA damage response, detection of	nucleotide-excision repair, DNA incision	nucleotide-excision repair, prevention of	positive regulation of I-kappaB transcription factor activity	positive regulation of NF-kappaB transcription factor activity	positive regulation of protein monoubiquitination	cellular chloride ion homeostasis	regulation of glycogen catabolic process	regulation of protein localization	endosomal transport	regulation of neuron death	regulation of NFAT protein import into nucleus	negative regulation of NFAT protein import into nucleus
embryo implantation	thymus epithelium morphogenesis	inorganic substance	I-kappaB kinase/NF-kappaB signaling	nucleotide-excision repair, DNA incision	signal transduction by p53 class mediator	receptor signaling pathway	regulation of protein kinase A signaling	DNA-dependent DNA replication	peptidyl-tyrosine phosphorylation	rRNA methylation	glyceroldehyde-3-phosphate metabolic process	cyclic nucleotide biosynthetic process	neural precursor cell proliferation	cell-matrix adhesion	
negative regulation of metalloendopeptidase activity	learning	activation of protein kinase activity	MAPK cascade	nucleotide-excision repair, DNA incision, 5'-to-3'	regulation of type I interferon production	Wnt signaling pathway	double-strand break repair via homologous recombination	response to heat	protein autophosphorylation	fructose 6-phosphate metabolic process	ATP metabolic process	polyubiquitination	nucleic acid phosphodiester bond hydrolysis	locomotion	macroautophagy

Upregulated in Pumping-Explant vs. No-Osculum Explant

apoptotic signaling pathway	hepatocyte apoptotic process	negative regulation of I-kappaB kinase/NF-kappaB signaling	negative regulation of necroptotic process	heart development	actin filament organization	ectoderm development	embryonic hemopoiesis	formation of a compartment boundary	germ-line stem cell population maintenance	hemocyte proliferation	receptor-mediated endocytosis
regulation of thymocyte apoptotic process	response to ethanol	response to tumor necrosis factor	negative regulation of cell cycle G1/S phase transition	macrophage differentiation	anesthesia-resistant memory	imaginal disc pattern formation	neuroblast fate determination	neurological system process	oogenesis	open tracheal system development	endosomal transport
negative regulation of translational initiation	negative regulation of cell-cell adhesion mediated by cadherin	negative regulation of gene expression	positive regulation of Notch signaling pathway	neural tube formation	chaeta development	lateral inhibition	peripheral nervous system development	regulation of filopodium assembly	regulation of R8 cell apoptosis in compound eye	stem cell differentiation	transmembrane transport
response to topologically incorrect protein	defense response to bacterium	I-kappaB kinase/NF-kappaB signaling	interstrand cross-link repair	immune response	crystal cell differentiation	Malpighian tubule tip cell differentiation	regulation of cardioblast cell fate specification	body morphogenesis	positive regulation of interleukin-4 production	positive regulation of T-helper 17 cell differentiation	mitochondrion transport along microtubule
response to unfolded protein	transcription factor activity	factor receptor signaling pathway	gap filling	negative regulation of vulval development	dorsal/ventral lineage restriction, imaginal disc	morphogenesis of follicular epithelium	regulation of cell differentiation	interleukin-1 secretion	positive regulation of interleukin-5 production	regulation of cardiac conduction	reproduction
asymmetric cell division	DNA damage response, detection of DNA damage	NIK/NF-kappaB signaling	positive regulation of protein monoubiquitination	activation of cysteine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process	peptidyl-serine phosphorylation	germ-line stem-cell niche homeostasis	cell redox homeostasis	protein deglutathionylation	cellular protein metabolic process	metabolic metabolism process
defense response to insect	global genome nucleotide-excision repair	nucleotide-excision repair, DNA duplex unwinding	regulation of signal transduction by p53 class mediator	positive regulation of proteolysis	peptidyl-threonine phosphorylation	positive regulation of multicellular organism growth	regulation of translation	regulation of glycolytic process	peptidyl-proline hydroxylation to 4-hydroxy-L-proline	regulation of mitochondrial membrane potential	macroautophagy

F

Upregulated in **Pumping-Explant** vs. Pumping-AdultUpregulated in **Pumping-Adult** vs. Pumping-Explant

nuclear division



voltage-gated ion channel activity



Up in PA



Up in PE

