

**Table ST1 - GO enrichment.**

	bacterial challenge vs. placebo		
ErmineJ category	Stationary-placebo	dead-placebo	mid-log-placebo
cellular component	<ul style="list-style-type: none"> <li>intrinsic to organelle membrane</li> <li>peroxisome</li> <li>endosome</li> <li>synaptic vesicle</li> <li>intrinsic to Golgi membrane</li> <li>ER membrane</li> <li>nuclear-ER network</li> <li>perinuclear region</li> <li>synaptic membrane</li> </ul>	<ul style="list-style-type: none"> <li>chromosomal pericentric activity</li> <li>external side of plasma membrane</li> <li>receptor and MHC protein complex</li> <li>peroxisomes</li> <li>vesicles</li> <li>nuclear envelope and immunological synapse</li> </ul>	<ul style="list-style-type: none"> <li>voltage-gated K-channel complex</li> <li>chromosome pericentric region</li> <li>cytoskeleton</li> <li>spliceosome complex</li> <li>spindle</li> <li>nuclear envelope</li> <li>mitochondrial lumen</li> <li>receptor complex</li> </ul>
Molecular function	<ul style="list-style-type: none"> <li>transcription corepressor activity</li> <li>vitamin binding</li> <li>redox activity</li> <li>G-protein-coupled receptor binding</li> <li>chemokine receptor binding</li> <li>symporter activity</li> <li>peptide receptor activity</li> </ul>	<ul style="list-style-type: none"> <li>transcription corepressor activity</li> <li>vitamin binding</li> <li>redox activity</li> <li>receptor binding and activity</li> <li>pattern binding</li> <li>cytokine and chemokine binding</li> <li>kinase regulator activity</li> </ul>	<ul style="list-style-type: none"> <li>K ion binding</li> <li>voltage-gated K channel activity</li> <li>peptide receptor and K-channel activity</li> <li>neurotransmitter binding</li> <li>endonuclease activity</li> <li>unfolded protein binding</li> <li>neuropeptide hormone and transferase activity</li> </ul>
Biological process	<ul style="list-style-type: none"> <li>Fe and Na ion transport</li> <li>steroid biosynthesis</li> <li>protein import</li> <li>positive regulation of organismal physiology</li> <li>sensory perception of chemical stimulus</li> <li>response to bacterium</li> <li>branching morphogenesis tube</li> </ul>	<ul style="list-style-type: none"> <li>antimicrobial humoral response</li> <li>T cell activation</li> <li>regulation of immune system process</li> <li>lymphocyte proliferation</li> <li>acute inflammatory response and cytokine production</li> <li>antigen processing and presentation</li> </ul>	<ul style="list-style-type: none"> <li>rRNA processing</li> <li>cytoplasm organisation and biogenesis</li> <li>tRNA and rRNA metabolism</li> <li>cyclic nucleotide-mediated signaling</li> <li>ribosome biogenesis and assembly</li> <li>G-protein and cAMP-mediated signalling</li> </ul>

Global transcriptional profiles represented based on Gene Ontology (GO) annotation as determined in ErmineJ analysis after consumption of bacteria or placebo control. CC: cellular components; MF: molecular functions, BP: biological processes. For general GO info, please refer to: [www.geneontology.org](http://www.geneontology.org)