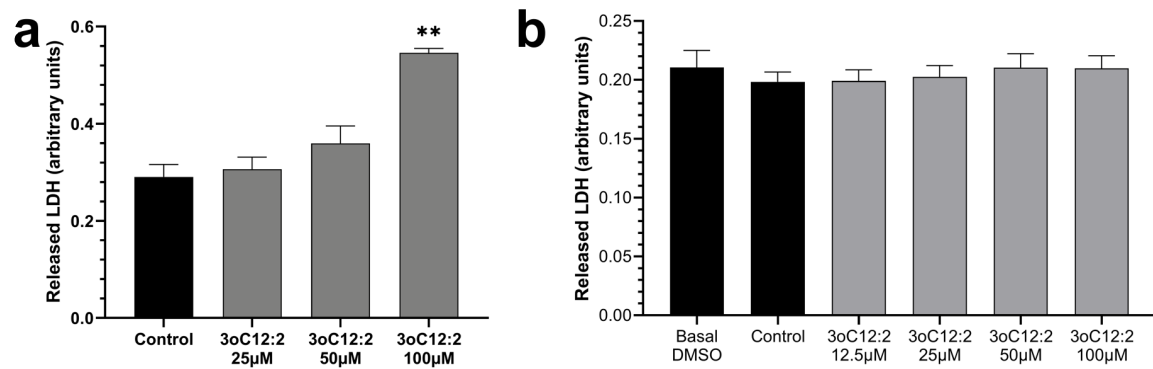


3-oxo-C12:2-HSL, Quorum Sensing molecule from human intestinal microbiota, inhibits pro-inflammatory pathways in immune cells *via* bitter taste receptors

Garance Coquant^{1,2}, Doriane Aguanno^{1,2,3}, Loïc Brot^{1,2}, Christine Belloir⁴, Julie Delugeard^{1,2}, Nathalie Roger^{1,2}, Hang-Phuong Pham⁵, Loïc Briand⁴, Marielle Moreau⁶, Luisa De Sordi^{1,2}, Véronique Carrière^{1,2}, Jean-Pierre Grill^{1,2}, Sophie Thenet^{1,2,3}, Philippe Seksik^{1,2,7*}

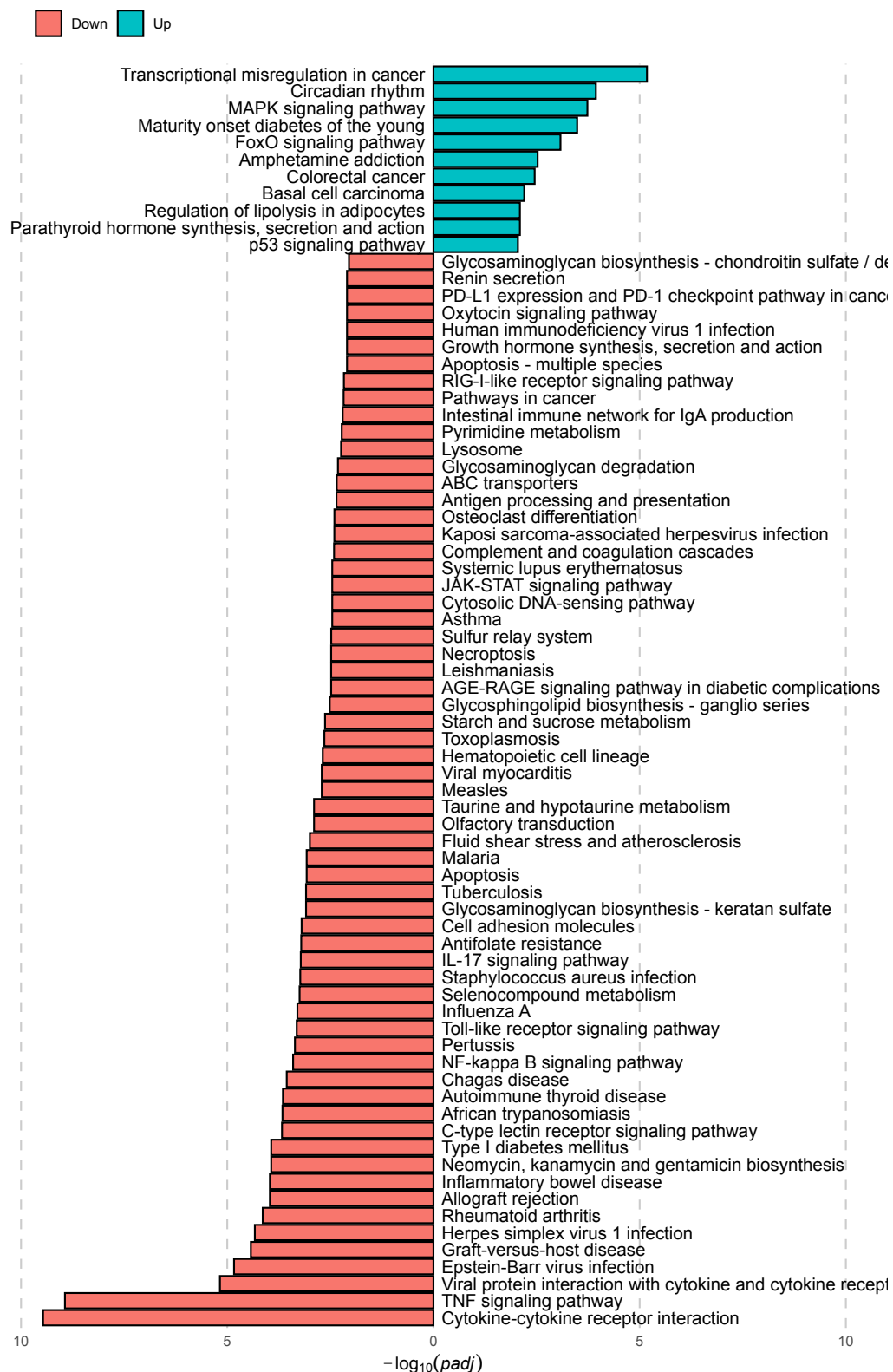
¹Sorbonne Université, INSERM, Centre de Recherche Saint-Antoine, CRSA, F-75012 Paris, France ² Paris Center for Microbiome Medicine (PaCeMM) FHU, APHP, Paris, Ile-de-France, France ³EPHE, PSL University, Paris, France, ⁴Centre des Sciences du Goût et de l'Alimentation, UMR 1324 INRAE, UMR 6265 CNRS, University of Bourgogne Franche-Comté, F-21000 Dijon, France, ⁵Parean Biotechnologies, Saint Malo, France, ⁶LVMH Recherche. Life Science Department, 185 Avenue de Verdun, 45800. Saint Jean de Braye. France ⁷Sorbonne Université, Département de Gastroentérologie et Nutrition, APHP Hôpital Saint-Antoine, F-75012 Paris, France

Supplementary figure 1



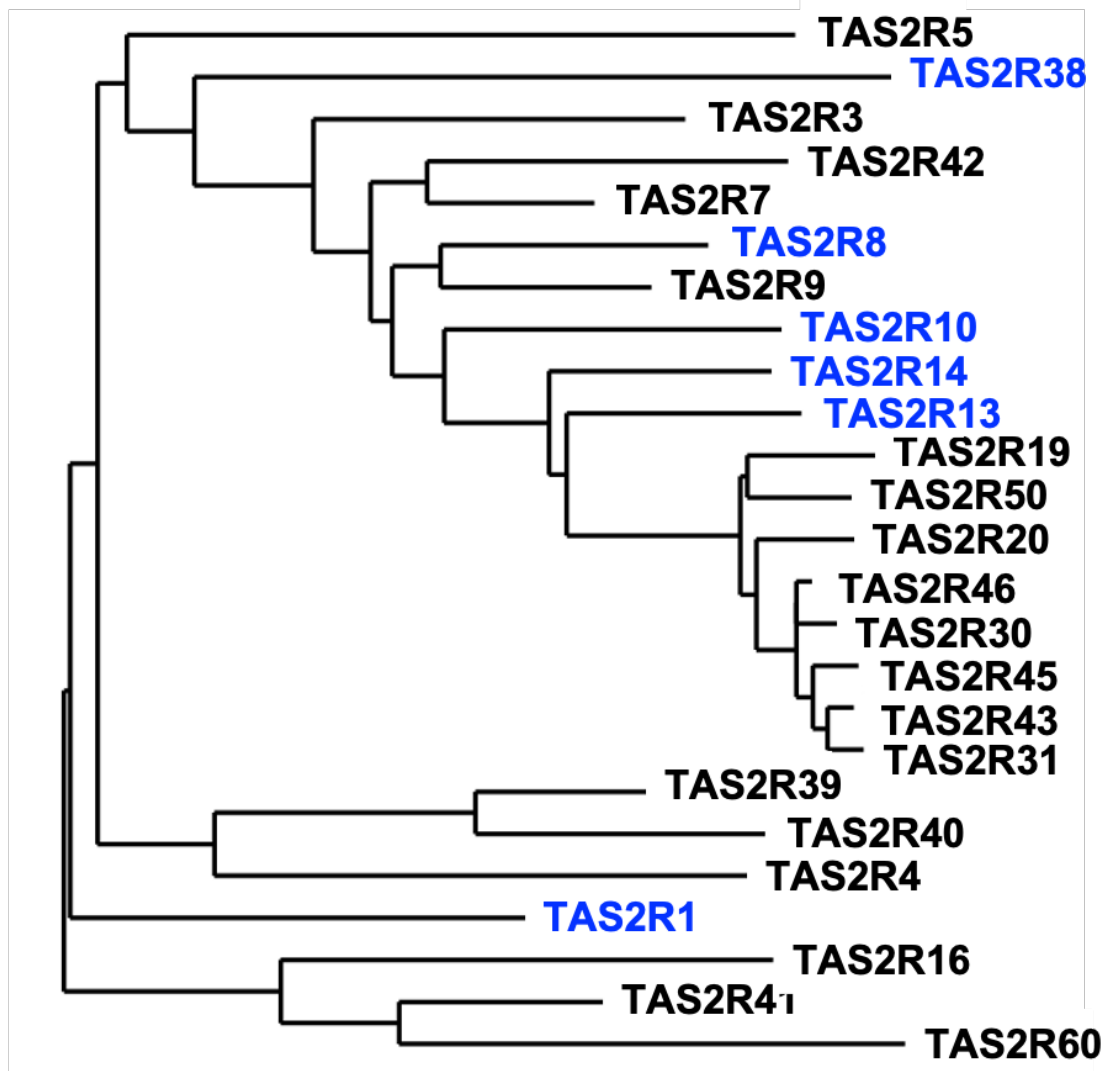
Supplementary Figure 1: LDH release by (a) RAW264.7 murine macrophages and (b) human peripheral blood mononuclear cell exposed to a range of concentration of 3-oxo-C12:2-HSL

Supplementary figure 2



Supplementary Figure 2: Significant KEGG pathways involved in the inflammation process and differentially modulated by 3-oxo-C12:2-HSL were identified by EGSA method (p value <0.01). Red and green bars represent down-regulated and up-regulated pathways respectively.

Supplementary Figure 3:



Supplementary Figure 3: Phylogenetic tree based on alignment of amino acid sequences of TAS2Rs. The neighbor-joining tree was constructed after a multiple sequence alignment of the TAS2Rs. The 6 TAS2R receptors responding to 3-oxo-C12:2-HSL are indicated in blue.