**S10 Table.** Clusters of IAE genes, associated types of crosstalk and functional annotations (DAVIDA, *p*<0.1).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Cluster** | **Numbers of *ERG*s** |  | **IAE-I** | **Transcription** **factor (n)** | **Biological process (n)** | **Subcellular** **compartment (n)** |
| **total** | **FC > 2** |  | **n**B | **Type of crosstalk (n)** |
| **1** | 62(*down*C) | 3 |  | 46 | Synergy (34)Counteraction I (9)Neg. Redundancy (3) | PPARG (49) | Organic acid biosynthetic process (5)Carboxylic acid biosynthetic process (5)Icosanoid metabolic process (3) | Plasma membrane part (16)Endoplasmic reticulum (9) |
| **2** | 46(*down*) | 8 |  | 11 | Synergy (1)Counteraction I (2)Counteraction II (7)Redundancy (1) | BACH2 (25)NRF2 (19)MYB (25) | Regulation of cellular component size (5)Response to vitamin (3)Regulation of cell growth (4) | Actin cytoskeleton (4)Extracellular space (5) |
| **3** | 23(*up*C) | 23 |  | 12 | Counteraction I (8)Synergy (4) | NFKB (15)NFKAPPAB (12)NKX25 (15) | Regulation of smooth muscle cell proliferation (4)Regulation of cytokine biosynthetic process (4)Positive regulation of immune system process (5) | Extracellular space (8) |
| **4** | 48(*up*) | 43 |  | 18 | Synergy (10)Counteraction I (8) | FOXO1 (20)STAT5B (16)IRF1 (13) | Response to cytokine stimulus (4)Response to progesterone stimulus (3)Response to organic substance (8) | Cell surface (6)Membrane raft (3) |
| **5** | 68(*up*) | 7 |  | 20 | Synergy (9)Counteraction I (9)Counteraction III (1)Redundancy (1) | AP1 (46)MEF2 (51)CEBPB (41) | Membrane protein proteolysis (3)Response to lipopolysaccharide (4)Negative regulation of multicellular organismal process (5) | Integral to plasma membrane (11)Basolateral plasma membrane (5) |
| **6** | 4(*up*) | 1 |  | 3 | Synergy (1)Counteraction I (3) | *n.s.*D | *n.s.* | *n.s.* |

A According to DAVID Bioinformatics Resources 6.7 (http://david.abcc.ncifcrf.gov:8080/)

B n, number of IAE-I genes or of IAE genes associated with gene annotations (transcription factor binding sites, biological process, subcellular compartment)

C *U*p- or down-regulation in response to *E. coli*

D *n.s.*, no significant hit