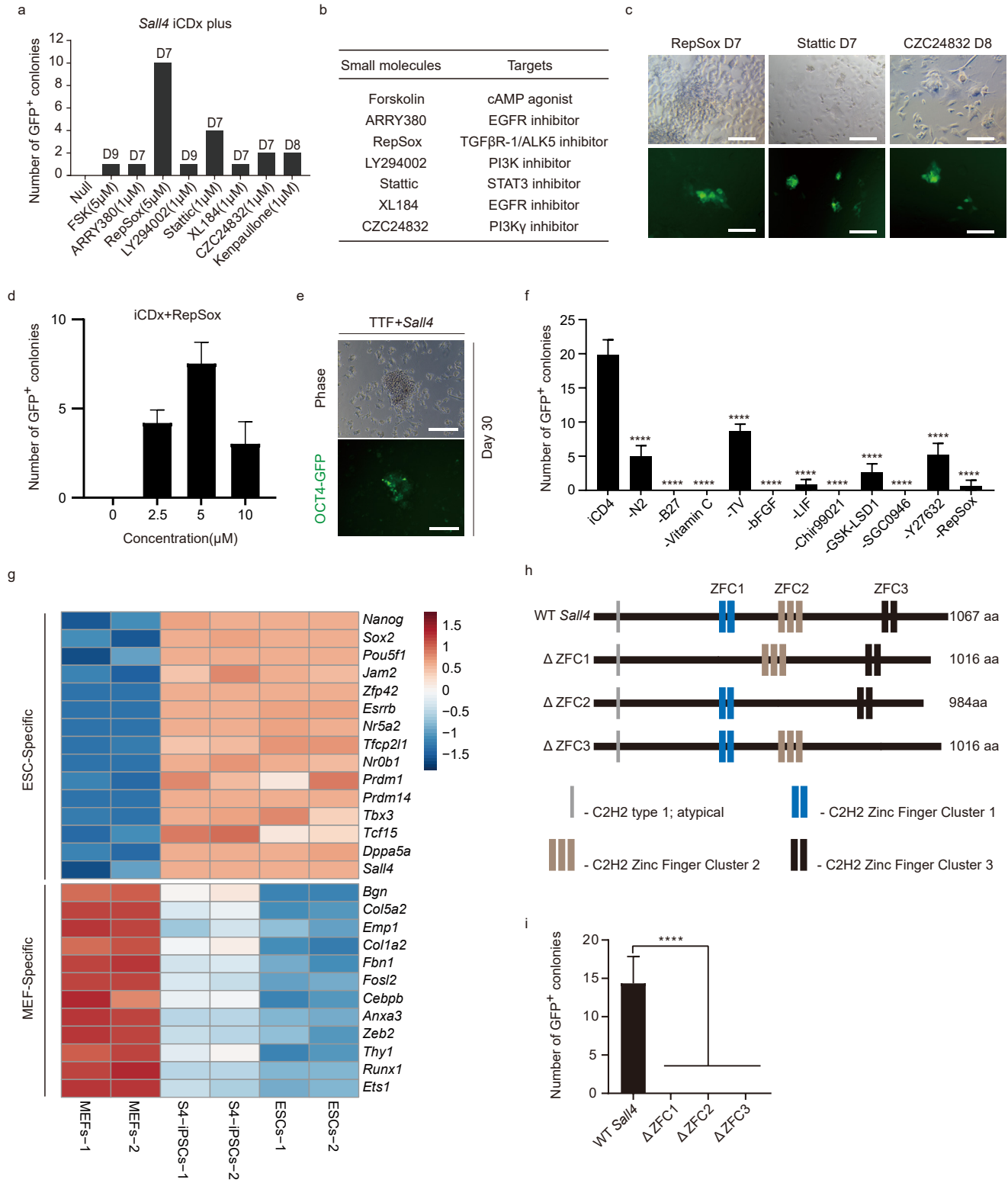


Extended Fig.1



Extended Fig.2

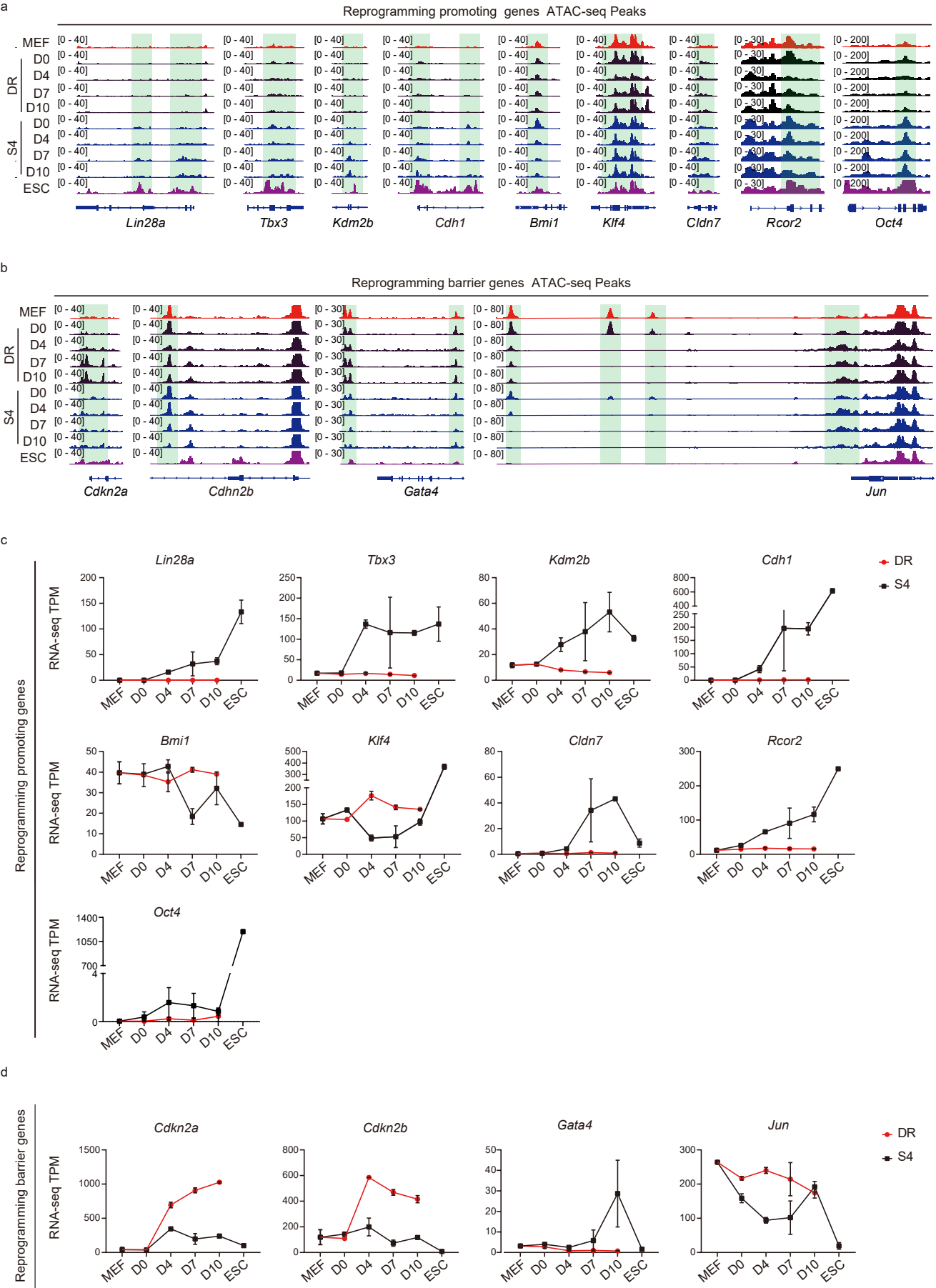
a

| Cluster                   | GO biological process and count                                                   | -Log P-value | Cluster                   | GO biological process and count                         | -Log P-value |
|---------------------------|-----------------------------------------------------------------------------------|--------------|---------------------------|---------------------------------------------------------|--------------|
| SALL4 Specific up<br>(C2) | <b>cell cycle(79)</b>                                                             | 19.524       | SALL4 Specific up<br>(C3) | multicellular organism development(92)                  | 18.959       |
|                           | cell division(56)                                                                 | 16.582       |                           | cell differentiation(67)                                | 8.777        |
|                           | positive regulation of chromosome segregation(7)                                  | 5.227        |                           | intermediate filament organization(16)                  | 8.776        |
|                           | mitotic spindle midzone assembly(6)                                               | 5.113        |                           | positive regulation of gene expression(47)              | 8.770        |
|                           | G2/M transition of mitotic cell cycle(11)                                         | 4.989        |                           | cartilage development(18)                               | 8.680        |
|                           | mitotic sister chromatid segregation(9)                                           | 4.678        |                           | skeletal system development(19)                         | 7.826        |
|                           | G1/S transition of mitotic cell cycle(12)                                         | 4.362        |                           | embryonic limb morphogenesis(14)                        | 7.469        |
|                           | mitotic spindle organization(10)                                                  | 4.238        |                           | chondrocyte differentiation(14)                         | 7.138        |
|                           | glycolytic process(9)                                                             | 4.034        |                           | cell-cell signaling(15)                                 | 7.130        |
|                           | centrosome cycle(9)                                                               | 3.877        |                           | mesenchymal cell apoptotic process(7)                   | 6.933        |
|                           | chromatin organization(28)                                                        | 3.835        |                           | keratinization(15)                                      | 6.469        |
|                           | mitotic cell cycle phase transition(7)                                            | 3.713        |                           | embryonic hindlimb morphogenesis(10)                    | 6.275        |
|                           | canonical glycolysis(6)                                                           | 3.530        |                           | canonical Wnt signaling pathway(16)                     | 6.228        |
|                           | negative regulation of double-strand break repair via homologous recombination(6) | 3.402        |                           | outflow tract morphogenesis(12)                         | 6.094        |
|                           | positive regulation of protein phosphorylation(23)                                | 3.315        |                           | embryonic forelimb morphogenesis(10)                    | 6.051        |
|                           | DNA repair(29)                                                                    | 3.176        |                           | branching involved in ureteric bud morphogenesis(11)    | 5.731        |
|                           | mitotic cell cycle(15)                                                            | 3.144        |                           | <b>positive regulation of BMP signaling pathway(10)</b> | 5.647        |
|                           | positive regulation of mitotic cell cycle                                         |              |                           | anterior/posterior pattern specification(16)            | 5.326        |
|                           | spindle assembly checkpoint(5)                                                    | 3.135        |                           | cell fate commitment(13)                                | 5.287        |
|                           |                                                                                   |              |                           | ventricular septum morphogenesis(10)                    | 5.206        |

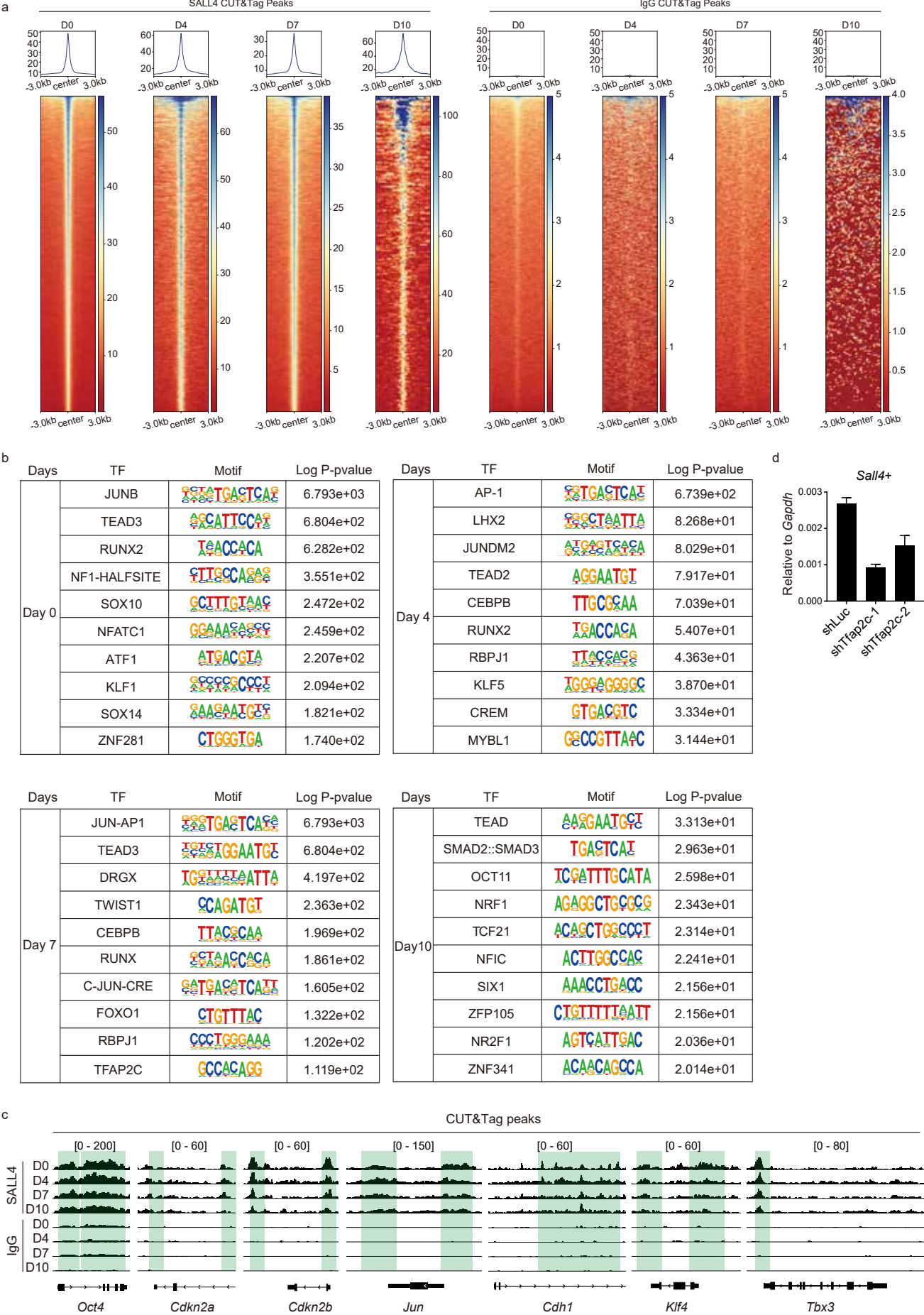
b

| Cluster                     | GO biological process and count                                       | -Log P-value | Cluster                     | GO biological process and count                                     | -Log P-value |
|-----------------------------|-----------------------------------------------------------------------|--------------|-----------------------------|---------------------------------------------------------------------|--------------|
| SALL4 Specific down<br>(C4) | lipid metabolic process(38)                                           | 5.723        | SALL4 Specific down<br>(C5) | lipid metabolic process(70)                                         | 11.934       |
|                             | defense response to virus(20)                                         | 5.631        |                             | <b>immune system process(42)</b>                                    | 4.977        |
|                             | <b>immune system process(31)</b>                                      | 5.617        |                             | transmembrane transport(37)                                         | 4.644        |
|                             | cellular response to interferon-beta(10)                              | 5.000        |                             | positive regulation of reactive oxygen species metabolic process(9) | 4.452        |
|                             | cellular detoxification of nitrogen compound(5)                       | 4.831        |                             | response to interferon-gamma(8)                                     | 3.573        |
|                             | innate immune response(34)                                            | 4.604        |                             | fatty acid beta-oxidation(9)                                        | 3.309        |
|                             | response to bacterium(18)                                             | 3.607        |                             | synaptic vesicle clustering(5)                                      | 3.285        |
|                             | negative regulation of viral genome replication(8)                    | 3.582        |                             | negative regulation of neuron projection development(12)            | 3.280        |
|                             | response to drug(19)                                                  | 3.534        |                             | lipid catabolic process(14)                                         | 3.153        |
|                             | response to virus(10)                                                 | 3.493        |                             | negative regulation of cell cycle(9)                                | 3.078        |
|                             | nitrobenzene metabolic process(4)                                     | 3.467        |                             | carbohydrate metabolic process(19)                                  | 2.999        |
|                             | negative regulation of NF-kappaB transcription factor activity(9)     | 3.444        |                             | negative regulation of axon regeneration(5)                         | 2.975        |
|                             | glutathione metabolic process(8)                                      | 3.400        |                             | phosphatidic acid biosynthetic process(6)                           | 2.952        |
|                             | activation of innate immune response(7)                               | 3.326        |                             | response to virus(12)                                               | 2.930        |
|                             | inflammatory response(21)                                             | 3.325        |                             | neurotransmitter secretion(7)                                       | 2.903        |
|                             | response to organic cyclic compound(9)                                | 3.300        |                             | positive regulation of protein phosphorylation(22)                  | 2.885        |
|                             | hemopoiesis(9)                                                        | 2.975        |                             | regulation of synaptic vesicle exocytosis(11)                       | 2.863        |
|                             | negative regulation of chemokine (C-X-C motif) ligand 2 production(4) | 2.954        |                             | NADP metabolic process(5)                                           | 2.842        |

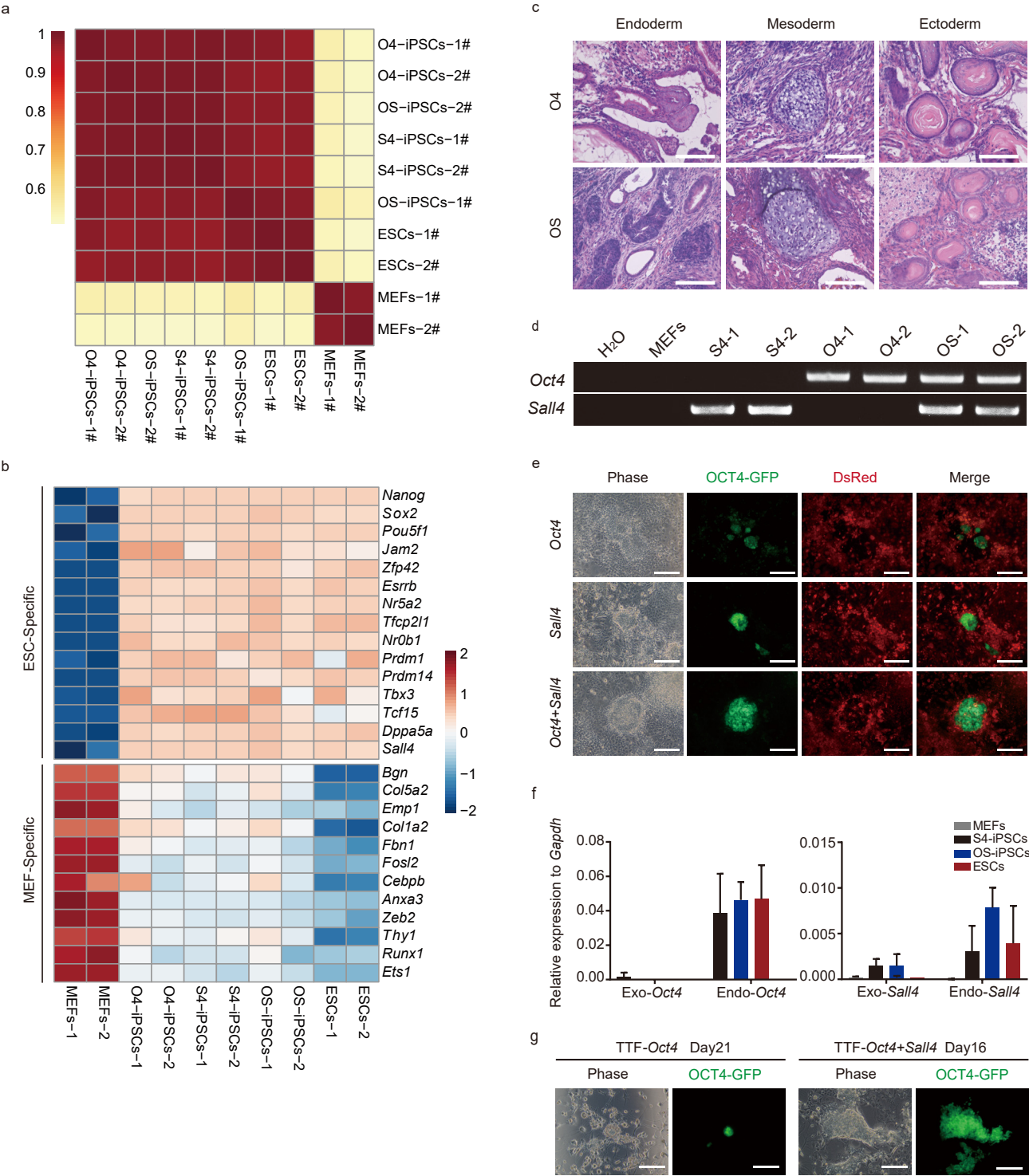
Extended Fig.3



Extended Fig.4



Extended Fig.5



Extended Fig.6

