AZ/LiCl treatments + Genome wide expression array
(~24,000 gene models)

Selection of 104 transcription factors and signaling molecules affected by AZ/LiCl treatments (Table 2)

Selection of 51 previously published “endomesodermal” genes (Table S2) that include 23 of the 104 selected AZ/LiCl genes

Temporal and Spatial expression analysis (and re-analysis) of 131 unique genes:

51 potential components of the cnidarian endomesodermal GRN (Fig. 7)

18 previously undescribed (Fig. 3), 33 updated spatial expression patterns (Fig. 4) as well as 69 high density qPCR gene expression profiles (Fig. 8, Fig. 6,S5,S6)

Input of cWnt signaling into provisional cnidarian endomesodermal GRN (Fig. 11)

Gene-specific (NvTcf) functional analysis including temporal and spatial expression analysis (Fig. 8,9,10)