

Table S5. False discovery rate analysis

	Nodal	Cripto	Control
Nodal	463±361	573±295	1648±820
Cripto		506±375	2627±512

To estimate the rate of false discoveries, we computed the number of differentially expressed genes when comparing different replicates of Cripto treatment to each other, and different replicates of Nodal treatment to each other. Since we performed five replicates per treatment, we computed the number of differentially expressed genes from the 15 possible combinations of the five replicates taken by pairs. These results constitute a measure of the false discoveries. The table shows the mean \pm s.d. for the number of differentially expressed genes at $P < 0.01$ for 15 permutations of Nodal versus Nodal, Cripto versus Cripto, Nodal versus Cripto, Cripto versus control samples and Nodal versus control samples. The number of differentially expressed genes between Cripto and Nodal was not different as the Nodal versus Nodal ($P=0.36$) and Cripto versus Cripto ($P=0.59$). However, the number of genes responding to Nodal treatment was higher than Nodal versus Nodal comparison ($P < 5.7E-5$), and the number of genes responding to Cripto treatment was higher than Cripto versus Cripto comparison ($P < 1E-12$).