

Table S2. QPCR data of early mesoderm and endoderm genes

	<i>FocA</i>	<i>SoxB1</i>	<i>Blimp1</i>	<i>Wnt8</i>	<i>Delta</i>	<i>Eve</i>	<i>Hox11/13</i>	<i>Gcm</i>
WNT6 morpholinos at hatched blastula	NS	1.86	NS	-1.47	NS	-2.95	-2.37	-1.56
	NS		-1.13	-3.2	NS	-4.89	-1.29	NS
	-1.82		NS	NS	NS		-2.06	1.03
			-1.09	-1.6				
			1.07					
			1.56					

QPCR data for effects of Wnt6 morpholinos on transcripts at hatched blastula (16.5 hpf).

All numbers represent the $\Delta\Delta C_t$, with ubiquitin as the reference standard and control levels of each RNA at 16.5 hpf as the reference level.

RNA was collected from control and Wnt morpholino-treated *S. purpuratus* embryos at 16.5 hours (300 μ M). Each of the genes in the table was examined by QPCR with ubiquitin as a control and the $\Delta\Delta C_t$ determined. Differences of greater than 1.5 (threefold) were considered significant. Each number represents an average of three samples per time point and the experiment was repeated at least three times for each gene.