

Supplemental Table 2

Key Pathways	
<i>Pathway name</i>	<i>p-value</i>
Pathways associated with genes selectively regulated in Sox9-EGFP^{Low} cells in uninjured intestine by IGF1	
Digestive System Development and Function	3.83E-03
Mouse Embryonic Stem Cell Pluripotency	5.22E-04
p53 signaling	1.61E-02
Pathways associated with genes selectively regulated in Sox9-EGFP^{High} cells in uninjured intestine by IGF1	
Cell Death	6.53E-06
Cellular Growth and Proliferation	1.60E-06
Oxidative Phosphorylation	6.73E-03
Cytochrome P450 Panel	4.59E-03
Pathways associated with genes selectively regulated in Sox9-EGFP^{Low} cells in regenerating intestine by IGF1	
DNA Replication, Recombination and Repair	1.44E-03
Role of BRCA1 in DNA Damage Response	1.04E-02
Assembly of RNA Polymerase I Complex	1.59E-02
Cleavage and Polyadenylation of Pre-mRNA	2.78E-02
Anti-Apoptosis	2.34E-02
Pathways associated with genes selectively regulated in Sox9-EGFP^{High} cells in regenerating intestine by IGF1	
Tissue Development	2.55E-03
Oxidative Phosphorylation	4.86E-02

Supplemental Table 2: Key pathways associated with genes regulated by IGF1 exclusively in Sox9-EGFP^{Low} or Sox9-EGFP^{High} cell populations in uninjured or regenerating intestines. Selected pathways identified by Ingenuity Pathway Analysis (IPA) as significantly associated with genes regulated by IGF1 in Sox9-EGFP^{Low} or Sox9-EGFP^{High} cell population isolated from uninjured small intestine or at day 5 post-radiation.