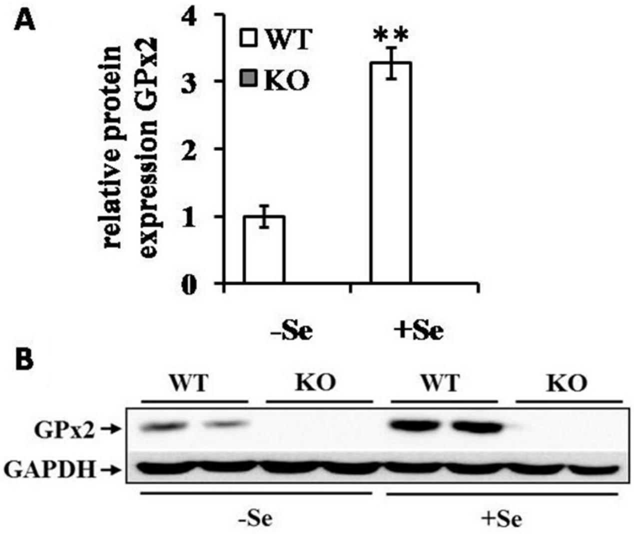
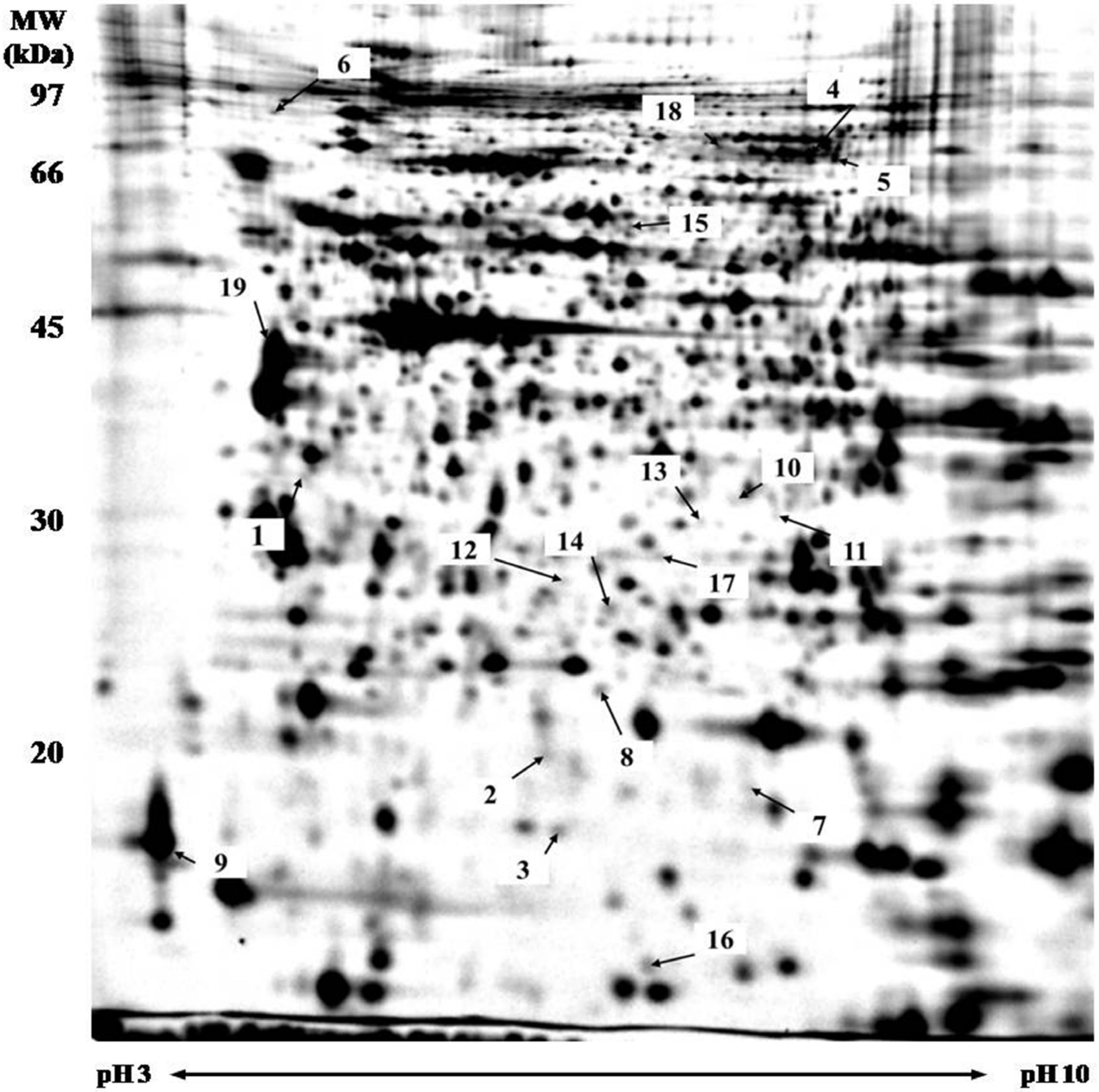
# Loss of epithelium-specific GPx2 results in aberrant cell fate decisions during intestinal differentiation

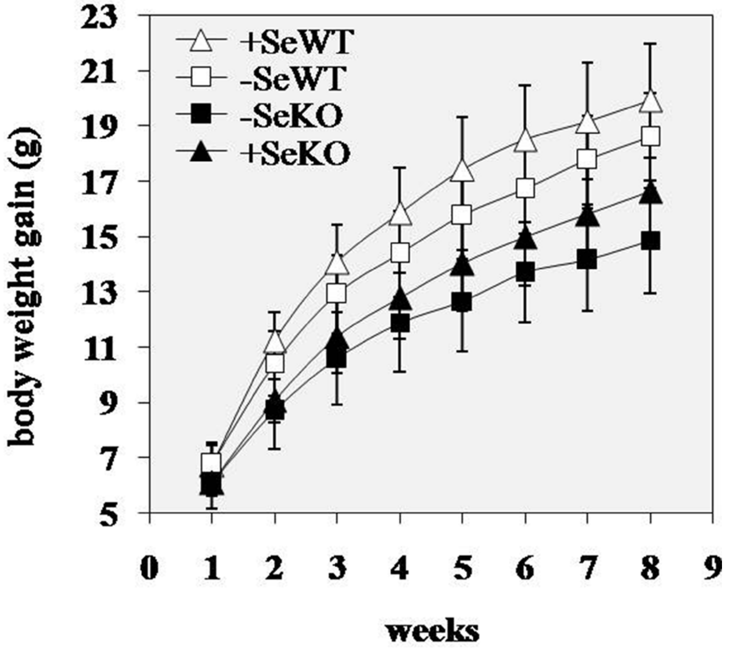
## SUPPLEMENTARY MATERIALS



**Supplementary Figure 1: Confirmation of the GPx2 KO by western blot analysis.** (**A**) Colon tissue lysates of four mice/group were analyzed for GPx2 protein abundance by Western blot, quantified by densitometry, normalized to the expression of GAPDH and expressed in relation to the -SeWT group. $^{**}p < 0.01$, student´s *t*-test. (**B**) Representative Western blots of two animals/group.



**Supplementary Figure 2: GPx2 KO influenced the protein expression pattern of murine colon tissues.** Representative proteome profile of colon tissues (sample + Se WT) generated as described in the Materials and Methods section. Significant differentially expressed and identified proteins are indicated with numbers ($p < 0.05$; see also Table 1).



**Supplementary Figure 3: GPx2 knockout mice exhibit decreased weight gain.** Weights of the mice were recorded weekly and the cumulative weight gain (g) was calculated across the eight-week feeding period.

## Supplementary Table 1: Real-time PCR primer pairs applied in this study

| gene | primer sequence (5′→3′) | | gene bank accession No. | product size (bp) |
|---|---|---|---|---|
| Atoh1 | forward | AGAAGCTGTCCAAATATGAGACCC | NM_007500.4 | 141 |
| | reverse | GTGCGAAGGTGATGGTGGTC | | |
| Cbfa2t3 | forward | TCTGAGGAGGGGAAGAAGGG | NM_177289.1 | 356 |
| | reverse | CAGTTCCAGCAGCTCTCGC | | |
| Chga | forward | TACCCAATCACCAACCAGCC | NM_007693.2 | 249 |
| | reverse | GAGTCCGACTGACCATCATCT | | |
| Clca1 | forward | GATAACGGAGCAGGTGCCG | NM_017474.2 | 486 |
| | reverse | TGAGGTGTTGAAGTGGTCCC | | |
| Clca2 | forward | GTCACCAGGTGTTCATCTGAC | NM_178697.5 | 257 |
| | reverse | ACGTCCCAAGTGCTTCTGAG | | |
| Clca3a1 | forward | GACCCCGAGGCAGAGTCTTT | NM_009899.4 | 150 |
| | reverse | CCACATTGGTGCCAGTGATCC | | |
| Clca4a | forward | CAACAAGGTGCTCCACAGG | NM_207208.3 | 343 |
| | reverse | GAGAAGAAGGGTGGAGAGGG | | |
| Ghrl | forward | CCAGAGGACAGAGGACAAGC | NM_021488.5 | 170 |
| | reverse | GCTGGCGCCTCTTTGACC | | |
| Glp-1 | forward | TGTCTACACCTGTTCGCAGC | NM_008100.4 | 151 |
| | reverse | AAGCTGGGAATGATCTGGGG | | |
| Hes1 | forward | AACACGACACCGGACAAACCA | NM_008233.2 | 150 |
| | reverse | GCCGGGAGCTATCTTTCTTAAGTG | | |
| Lgr5 | forward | AAGTTCAAGATGAGCGGGACCT | NM_010195.2 | 142 |
| | reverse | GATTCGGATCAGCCAGCTACCA | | |
| Lysozym | forward | TTCGAGCATGGGTGGCATGG | NM_013590.3 | 100 |
| | reverse | GGCTGCAGTAGAAGCACACC | | |
| Muc2 | forward | ACTGTTTTGGGTCCTGTGGG | NM_023566.3 | 241 |
| | reverse | AGAAAACGGGGGCTAGAACG | | |
| Pax4 | forward | CTGCTCCTGAGTGAAGGCTC | NM_011038.2 | 277 |
| | reverse | TCACACTGCTGAGTCCGTCC | | |
| Rapgef3 | forward | CTGCTGCTCAAAGACGTGACC | NM_001177810.1 | 393 |
| | reverse | CCTCTGGACCTCTTGGTTGC | | |
| Spdef | forward | ACATCTGGAAGTCAGCGGC | NM_013891.4 | 319 |
| | reverse | TAATACTGGCGGATGGAGCG | | |
| Sst | forward | TGCCACCGGGAAACAGGAAC | NM_009215.1 | 322 |
| | reverse | GTCAAGTTGAGCATCGGGGG | | |
| Tph1 | forward | TACACTCCAGAGCCAGACACC | NM_009414.3 | 415 |
| | reverse | TGTACTTCAGTCCAAACGGGC | | |
| beta-actin | forward | ACTGTCGAGTCGCGTCC | NM_007393.5 | 487 |
| | reverse | ATGGCTACGTACATGGCTGG | | |
| Gapdh | forward | TTGTGCAGTGCCAGCCTCGT | NM_008084.3 | 214 |
| | reverse | TCGGCCTTGACTGTGCCGTT | | |
| Rpl13a | forward | GACCTCCTCCTTTCCCAGG | NM_009438.5 | 148 |
| | reverse | TTCACAGCGTACGACCACC | | |