Table 2. Summary of cDNA array data analysis. (Supplementary)

	p-value	Fold decrease (vs WT)	Gene Symbol	Gene Assignment
Genes down-regulated in KO mice	**0.001**	**4.51**	**Prkg2**	**protein kinase, cGMP-dependent, type II**
	0.010	**2.14**	**Slc15a2**	**solute carrier family 15 (H+/peptide transporter), membe**
	0.039	**2.04**	**Cldn4**	**claudin 4, tight juncion**
	0.000	1.63	Sprr2j	small proline-rich protein 2J
	0.040	**1.58**	**Olfr1310**	**olfactory receptor 1310**
	0.007	1.58	EG382156	predicted gene, EG382156
	0.007	1.56	Trim13	tripartite motif-containing 13
	0.005	**1.55**	**Dusp10**	**dual specificity phosphatase 10**
	0.035	1.55	Mt2	metallothionein 2
	0.043	**1.55**	**Myef2**	**myelin basic protein expression factor 2, brain muscle differentiation**
	0.049	1.54	Ppm1j	protein phosphatase 1J
	0.033	**1.52**	**Efna3**	**ephrin A3**
	0.018	**1.50**	**Ifrd1**	**interferon-related developmental regulator 1, differentiation in muscle**
	0.007	1.50	Il1rl2	interleukin 1 receptor-like 2
	0.040	**1.48**	**Adh6b**	**alcohol dehydrogenase 6B (class V)**
	0.014	1.44	Xirp2	xin actin-binding repeat containing 2
	0.025	1.43	Tacstd2	tumor-associated calcium signal transducer 2
	0.032	1.41	Arl4a	ADP-ribosylation factor-like 4A
	0.027	**1.41**	**Ddc**	**dopa decarboxylase, serotonin synthesis**
	0.036	**1.41**	**Olfr24**	**olfactory receptor 24**
	0.004	**1.40**	**Ddi1**	**DNA-damage inducible 1, homolog 1 (S. cerevisiae)**
	0.013	**1.39**	**Olfr958**	**olfactory receptor 958**
	0.048	**1.38**	**Best2**	**bestrophin 2, calcium activated cloride channel**
	0.014	**1.36**	**Olfr521**	**olfactory receptor 521**

	p-value	Fold increase (vs WT)	Gene Symbol	Gene Assignment
Genes up-regulated in KO mice	**0.031**	**1.75**	**Nap1l2**	**nucleosome assembly protein 1-like 2**
	0.016	1.72	Pgk1	phosphoglycerate kinase 1
	0.005	1.72	Cma2	chymase 2, mast cell
	0.048	1.58	Gng3	G protein, gamma 3
	0.024	**1.55**	**Hist1h2ab**	**histone cluster 1, H2ab**
	0.037	1.51	Clca4	chloride channel calcium activated 4
	0.045	**1.51**	**Nusap1**	**nucleolar and spindle associated protein 1**
	0.014	**1.50**	**Rab18**	**RAB18, member RAS oncogene family**
	0.037	**1.49**	**Ccna2**	**cyclin A2**
	0.021	1.47	Kprp	keratinocyte expressed, proline-rich
	0.009	1.45	Mak16	MAK16 homolog (S. cerevisiae), mutation casue G1 arrest
	0.039	**1.43**	**Kdelr3**	**KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein rete**
	0.017	1.43	Ccl28	chemokine (C-C motif) ligand 28
	0.040	1.42	Ly9	lymphocyte antigen 9
	0.022	**1.42**	**Zfp804a**	**zinc finger protein 804A, activated by HOXC8**
	0.043	**1.41**	**Rab3c**	**RAB3C, member RAS oncogene family**
	0.022	**1.40**	**Rps6ka6**	**ribosomal protein S6 kinase polypeptide 6**
	0.024	**1.38**	**Kif11**	**kinesin family member 11, mitosis**
	0.046	1.38	Lcp2	lymphocyte cytosolic protein 2
	0.036	1.38	Prune2	prune homolog 2 (Drosophila)
	0.014	1.37	Khdc1a	KH domain containing 1A
	0.040	1.37	434166	predicted gene, 434166
	0.021	1.37	Scgn	secretagogin, EF-hand calcium binding protein
	0.030	**1.37**	**Ccnb1**	**cyclin B1**
	0.011	1.36	Mirhg1	microRNA host gene 1

Total RNA was extracted from the proximal colon mucosa from three *Prkg2*$^{-/-}$ and three *Prkg2*$^{+/+}$ mice. Labeling, hybridization to Affimetrix GeneChip Mouse Genome Array, quantitation and statistical analysis of gene expression were all performed by the Genomics Core facility at the Georgia Regents University Cancer Center. Genes marked by bold-face were related to differentiation (downregulated) or proliferation (upregulated) using Panther Analysis Software (http://www.pantherdb.org).

Supplementary Table 2