

# 1 Additional file 6

Sections and responses	GOBP	Proximal significant genes	Middle significant genes	Distal significant genes
Prox – Mid – Dist (all linear)	GO:0006953: acute-phase response	<b>UP:</b> <i>Saa3, Serpina1b</i> <b>DOWN:</b> <i>Reg3b, Reg3g, Stat3</i>	<b>UP:</b> <i>Serpina1b</i> <b>DOWN:</b> <i>Reg3b, Reg3g, Saa2, Stat3, SigIRR</i>	<b>UP:</b> <i>Serpina1b</i> <b>DOWN:</b> <i>Saa1, Saa2</i>
Prox – Mid (all linear)	GO:0006629: lipid metabolic process	<b>UP:</b> <i>Acadl, Acadvl, Acads, Apoc2, Cpt2, Crat, Ldlr, Acer1, Acot2, Acot4, Acaa1b, Slc27a2, Acot1, Plxld1, Ech1, Acaa2, Gde1, Hacl1, Pnpla8, Abhd5, Adipor2, Arv1, Crot, Acsl3, Echs1, Hadha</i>  <b>DOWN:</b> <i>Plcb3, Daglb, Scap, Npc1l1, Apob, Asah2, Serinc1</i>	<b>UP:</b> <i>Tecr, Hdlbp, Acadl, Acadvl, Acox1, Cpt1a, Cpt2, Crat, Fdxr, Gpx1, Hsd17b4, Lipa, Acer1, Acot4, Mttp, Pck1, Soat2, Acaa1b, Slc27a2, Slc27a4, Acot1, Hsd17b6, Acsl5, Ech1, Echdc2, Acaa2, Gde1, Hacl1, Lpin2, Lpin3, Pnpla8, Adipor2, Acot12, Gpcpd1, Acsl3, Acox2, Echs1, Hadha</i>  <b>DOWN:</b> <i>Pafah1b2, Ppard, Daglb, Gdpd5, Napefd, Asah2, Plb1, Plce1</i>	
	GO:0006631: fatty acid metabolic process	<b>UP:</b> <i>Acadl, Acadvl, Acads, Apoa2, Cd36, Cpt2, Crat, Prkar2b, Acaa1b, Slc27a2, Ech1, Acaa2, Pnpla8, Abhd5, Adipor2, Crot, Acsl3, Echs1, Hadha</i>  <b>DOWN:</b>	<b>UP:</b> <i>Acadl, Acadvl, Acox1, Cd36, Cpt1a, Cpt2, Crat, Faah, Fabp2, Hsd17b4, Lipa, Acaa1b, Slc27a2, Slc27a4, Mecr, Acsl5, Ech1, Echdc2, Acaa2, Lpin2, Lpin3, Pnpla8, Adipor2, Acot12, Acsl3, Acox2, Echs1, Hadha</i>  <b>DOWN:</b>	
	GO:0006635: fatty acid beta-oxidation	<b>UP:</b> <i>Acadvl, Eci1, Slc25a17, Eci2, Acaa2, Decr1, Bdh2, Echs1, Hadha</i>  <b>DOWN:</b>	<b>UP:</b> <i>Acadvl, Acox1, Hsd17b4, Pex5, Slc25a17, Eci2, Acaa2, Bdh2, Acox2, Echs1, Hadha</i>  <b>DOWN:</b>	
	GO:0006637: acyl-CoA metabolic process	<b>UP:</b> <i>Hmgcl, Acot8, Acot2, Acot4, Acot1, Oxsm</i>  <b>DOWN:</b> <i>Ces1d</i>	<b>UP:</b> <i>Hmgcl, Acot8, Acot4, Acot1, Oxsm, Acot12</i>  <b>DOWN:</b>	
	GO:0007040: lysosome organization	<b>UP:</b> <i>Cln8</i>  <b>DOWN:</b> <i>Abca1, Tpp1, Hexa, Cln6</i>	<b>UP:</b> <i>Acp2, Fam160a2</i>  <b>DOWN:</b> <i>Tpp1, Hexa, Hexb, Ppt1</i>	
	GO:0015031: protein transport	<b>UP:</b> <i>Kdelr3, Bet1, Nacad, Rab1, Rab6, Mcfd2, Sec22b, Sec23a, Timm17b, Vps45, Atg4d, Rabep1, Rab9, Vps29, Apba3, Cope, Xpo7, Sar1b, Gpr89, Yif1a, Golt1a, Snx4, Pex13, Senp2, Snx7</i>  <b>DOWN:</b> <i>Sft2d2, Gdi1, Cog1, Myo1c, Rab12, Vps33b, Rab8b, Scamp2, Gga3, Agap1, Copg2, Nup210, Sec61a2, Rab37, Rab32, Kdelr1, Ap2b1, Gga2, Chmp4b, Rrbp1</i>	<b>UP:</b> <i>Chmp7, Kdelr3, Sec13, Vps4a, Ap1m1, Arf4, Bet1, Pex5, Sec22b, Sec23a, Stam, Arcn1, Timm17a, Timm17b, Cox18, Bcap31, Eif5a, Serp1, Timm13, Ipo8, Uevld, Copg, Pex14, Copz1, Gosr2, Apba3, Rab2a, Cope, Tomm6, Sar1b, Kdelr2, Derl1, Yif1a, Golt1a, Sec62, Dopey2, Tmem48, Fam160a2, Senp2, Sil1</i>  <b>DOWN:</b> <i>Arrb1, Ap3d1, Gdi1, Mtm1, Ppt1, Rab17, Rab19, Rab33b, Rab3ip, Rufy1, Vps33b, Rab8b, Sec61a2, Rab37, Tomm40l, Duoxa2, Rab32, Rab27b, Rrbp1, Cog8</i>	
	GO:0022900: electron	<b>UP:</b> <i>Ndufb11, Etfb, Etfa,</i>	<b>UP:</b> <i>Etfb, Etfa, Fdxr,</i>	

	transport chain	<i>Ndufa4, Ndufs8, Ndufs6, Cyb561d2, Ndufa7, Cyb5b, Uqcrfs1, Etfdh</i>  <b>DOWN:</b> <i>Cmah, Cyb561, Cyba</i>	<i>Ndufs8, Ndufs2, Ndufb6, Ndufs6, Cyb561d2, Ndufs5, Ndufa9, Cyb5b, Uqcrfs1, Etfdh, Ndufa5</i>  <b>DOWN:</b> <i>Cyb561, Frrs1, Enox2, Cyb561d1</i>	
	GO:0055085: transmembrane transport	<b>UP:</b> <i>Slc30a9, Aqp7, Aqp8, Cacna1d, Slc6a3, Sfxn1, Slc22a1, Slc23a1, Slc25a17, Slc6a2, Mfsd6l, Timm17b, Slc6a20b, Slc4a11, Gpr172b, Xpo7, Slc16a13, Abcb6, Senp2, Mfsd2a</i>  <b>DOWN:</b> <i>Abca1, Atp8a1, Slc7a1, Itpr3, Myo1c, Slc12a7, Slc19a1, Slc2a2, Mfsd4, Slc36a1, Slc7a9, Atp2a3, Slc4a4, Nup210, Abcb10, Sec61a2, Cacna1h, Slc30a7, Slc39a8, Slc29a3, Hvcn1, Rrbp1</i>	<b>UP:</b> <i>Slc25a45, Slc30a9, Slc35b1, Sec13, Aqp3, Aqp7, Abcc2, Slc6a3, Slc26a3, Sfxn1, Slc1a3, Slc22a1, Slc23a1, Slc25a17, Slc7a7, Mfsd7c, Timm17a, Timm17b, Catsper1, Slc6a20b, Slc16a12, Mfsd7a, Eif5a, Serp1, Timm13, Gpr172b, Pex14, Slc47a1, Sec62, Slc16a13, Slc39a11, Slc39a5, Tmem48, Abcb6, Abcb8, Senp2, Sil1</i>  <b>DOWN:</b> <i>Slc26a2, Kcnu1, Slc24a6, Slc1a1, Slc2a2, Slc5a1, Spns2, Trpm6, Slc5a9, Slc17a5, Slc7a9, Atp9b, Sec61a2, Tomm40l, Hiatl1, Mfsd1, Spns1, Hvcn1, Rrbp1, Slc4a10</i>	
Prox – Mid (linear - logarithmic)	GO:0042632: cholesterol homeostasis	<b>UP:</b> <i>Apoa2, Ldlr, Nr1h3, Pla2g10, Npc2</i>  <b>DOWN:</b> <i>Abca1, Npc1, Npc1l1, Apob, Abcg5, Abcg8</i>	<b>UP:</b> <i>Apoa4, Cav1, Pla2g10</i>  <b>DOWN:</b> <i>Cyp7a1</i>	
Prox – Mid (linear - exponential)	GO:0030301: cholesterol transport	<b>UP:</b> <i>Apoa2, Cd36, Ldlr, Npc2</i>  <b>DOWN:</b> <i>Abca1, Npc1l1, Apob</i>	<b>UP:</b>  <b>DOWN:</b> <i>Abca1, Abcg1, Scarb1, Stard3</i>	
Mid – Dist (all linear)	GO:0006520: cellular amino acid metabolic process		<b>UP:</b> <i>Cth, Acy1, Ddc, Got1</i>  <b>DOWN:</b> <i>Ccbl2</i>	<b>UP:</b> <i>Cth</i>  <b>DOWN:</b> <i>Tat</i>
	GO:0016042: lipid catabolic process		<b>UP:</b> <i>Lipa, Pla2g2c, Nceh1, Pnpla8, Ddhd2</i>  <b>DOWN:</b> <i>Ddhd1, Pafah1b2, Pla2g2a, Pld2, Ppt1, Daglb, Plb1, Plbd1, Plce1</i>	<b>UP:</b> <i>Apoc2</i>  <b>DOWN:</b> <i>Pla2g2a, Daglb, Pla2g2f, Plce1</i>
	GO:0051262: protein tetramerization		<b>UP:</b> <i>Me1, Pex5, Txrnd1</i>  <b>DOWN:</b> <i>Igf1r, Sbf2</i>	<b>UP:</b> <i>Me1</i>  <b>DOWN:</b> <i>Sbf2</i>
Mid – Dist (linear - exponential)	GO:0043154: negative regulation of caspase activity		<b>UP:</b> <i>Prdx3, Birc5, Gpx1, Igf1, Por</i>  <b>DOWN:</b> <i>Arrb1, Bcl2l1, Naip1, Igbp1, Usp47</i>	<b>UP:</b> <i>Birc5</i>  <b>DOWN:</b> <i>Igbp1</i>
Mid – Dist (logarithmic - linear)	GO:0006644: phospholipid metabolic process		<b>UP:</b> <i>Pla2g2d, Pla2g10, Pla2g12a, Ppap2b</i>  <b>DOWN:</b>	<b>UP:</b>  <b>DOWN:</b> <i>Pla2g2a, Pla2g2f</i>
	GO:0006749: glutathione metabolic process		<b>UP:</b> <i>Gpx3, Gstm1, Gstm3, Gstk1</i>  <b>DOWN:</b>	<b>UP:</b> <i>Cth, Hagh</i>  <b>DOWN:</b>
	GO:0045859: regulation of protein kinase activity		<b>UP:</b> <i>Prkar2b, Mtor</i>  <b>DOWN:</b> <i>Tsc1, Akap13</i>	<b>UP:</b> <i>Ect2</i>  <b>DOWN:</b> <i>Plce1</i>

3      **Table A6: Over-represented Gene Ontology Biological Process (GOBP) terms that can be found in various intestinal sections.** For  
4      each GOBP term we specify up- and down-regulated genes (adjusted p-value < 0.1; however, most of the results of gene set  
5      enrichment analysis are well below this threshold - see Additional file 5).