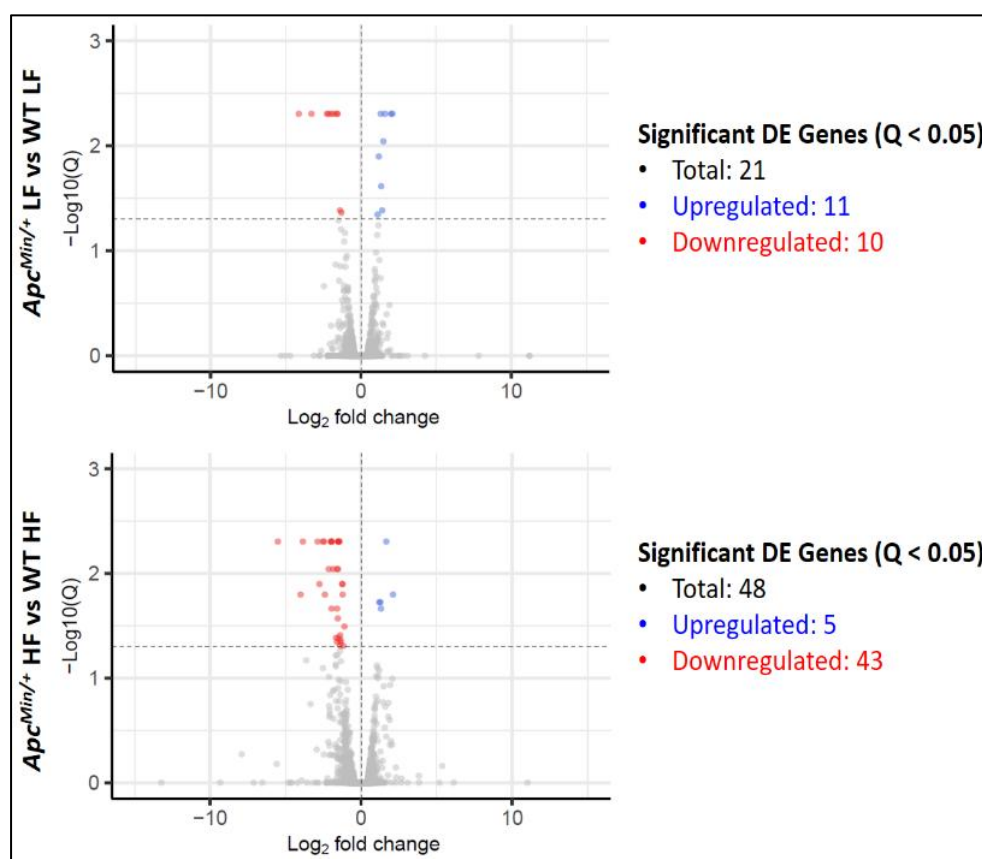


Sample ID	Concentration (ng/uL)	RNA Quality Number (RQN)
WT LF 1	63.6	8.5
WT LF 2	56.5	10
WT HF 1	43.5	9
WT HF 2	63.5	9.1
Apc Min/+ LF 1	58.3	9.6
Apc Min/+ LF 2	62.6	9.5
Apc Min/+ HF 1	54.3	9.9
Apc Min/+ HF 2	53.7	10

**Supplementary Figure 1.** RNA sample isolated from intestinal epithelia used for RNA-SEQ.



**Supplementary Figure 2.** Total number of DEGs identified in comparison between WT and *Apc<sup>Min/+</sup>* genotypes (FDR  $Q$ -value  $< 0.05$ )

A

WT HF vs LF				Apc Min/+ HF vs LF			
Gene	VEL Count	log2(AVG VEL FC)	log2(RNA FC)	Gene	VEL Count	log2(AVG VEL FC)	log2(RNA FC)
Cyp4a31	1	1.8251	inf	Scd1	7	3.1892	8.9463
Glyat	1	1.4384	inf	Cyp4a10	5	1.8109	5.2691
Scd1	6	2.6448	8.8338	Synn	4	1.6929	4.7891
Cyp4a10	4	2.3222	5.7195	Acot1	4	1.6440	4.6354
Cyp1a1	2	1.2781	4.7616	Acacb	1	2.0985	4.6244
Acot1	4	2.0103	4.1881	Tcf23	1	1.4165	4.5879
Me1	2	2.8414	4.0958	H2-Q10	1	2.0132	4.2186
H2-Q10	1	2.2635	3.8523	Me1	2	2.2074	4.1061
Tubb2a	2	0.9836	3.6851	Akr1b8	1	1.1532	4.0611
Slc6a3	1	1.5936	3.4256	Slc22a3	3	1.6563	3.8486
Mfsd7c	6	1.4547	3.3338	Mfsd7c	5	1.3018	3.4020
Acacb	2	1.5494	3.2807	Hmgcs2	9	1.7167	3.3538
Synn	2	1.6349	3.2671	Acot2	1	0.9961	3.1785
Cntnap1	1	2.6771	3.1936	Slc6a3	2	1.8274	3.0833
Tm4sf4	6	1.4684	3.0891	Acot3	1	1.1385	3.0752
Tcf23	1	1.3154	3.0231	Etv4	1	1.9068	3.0669
Lamb3	6	1.5426	3.0060	Lamb3	5	1.3871	3.0498
Hmgcs2	9	1.9713	2.9736	Rab30	1	1.2208	3.0112
Rab30	1	1.1868	2.9706	Cntnap1	1	2.3542	2.9849
Slc22a3	2	1.5280	2.9217	Kmo	1	1.0714	2.9828
Pmm1	1	0.9180	2.7500	Thsd4	1	0.9197	2.9568
Matn2	1	1.5967	2.5532	Spy4	1	1.6754	2.9426
Dgkh	2	1.1636	2.5289	Aldh1a1	2	1.6686	2.9278
Acaa1b	1	1.3021	2.4822	Tm4sf4	6	1.6357	2.9060
Insig1	1	1.3899	2.3838	Bbox1	1	0.8254	2.8582
Scd2	3	1.2276	2.3784	Akr1c19	1	1.2405	2.8180
Pdgfrb	1	1.1956	2.3503	Acaa1b	2	1.0928	2.8121
Paqr7	1	1.2031	2.1900	Matn2	1	1.7235	2.7874
Aqp3	1	1.0151	2.1856	Aqp3	2	1.1285	2.6315
Gsta3	1	0.9468	2.1819	Papln	1	0.8785	2.6271
Acot2	1	2.0147	2.1155	Tubb2a	2	1.0132	2.4580
Acsf3	3	1.1496	2.1145	Plscr4	6	1.7182	2.4540
Utp14b	1	0.8552	2.0892	Acadl	1	1.0463	2.2102
Slc28a1	1	0.9674	2.0281	Adh7	2	1.0112	2.1293
Akr1c19	1	0.9547	2.0114	Slit2	3	1.4245	2.0662
Plscr4	7	1.4981	2.0007	Rusc2	2	1.6612	2.0556
Ugt2b5	1	1.0938	1.9639	Mgst1	1	0.9525	2.0370
Hsd1b3	2	1.1464	1.9482	Pmm1	1	0.7843	2.0050
1190002N15Rik	3	1.4178	1.9481	Rpn	2	1.6999	1.9992
Mfsd2a	3	1.2612	1.9435	Por	3	1.6582	1.9845
Marc1	1	0.7392	1.9036	Dgkh	4	1.1095	1.9753
Ltc4s	1	0.7311	1.7846	Mgl1	4	1.8665	1.9239
Slc16a12	1	2.5955	1.7815	Retsat	2	1.3454	1.9165
Pdk4	3	1.5091	1.7584	Ltc4s	1	0.8796	1.9060
Retsat	2	1.4744	1.7530	Acot2	1	1.7317	1.9012
Aldh1a1	4	1.2756	1.7076	Mfsd2a	2	1.1770	1.8828
Srebf1	2	0.9573	1.6952	44256	1	0.9332	1.8817
Por	4	1.2158	1.6419	Slc20a1	1	1.0020	1.8744
Susd2	1	1.0966	1.6325	Dus2	1	0.9354	1.8160
Cd36	4	2.3184	1.6211	N4bp2l1	1	1.4722	1.8033
Rgn	2	1.3124	1.6108	Plscr1	3	1.7581	1.7734
Angptl4	1	1.1914	1.5998	Cd36	3	2.0604	1.7717
Csf1r	4	1.2424	1.5699	Mcm2	1	1.7004	1.7503
Mgst1	1	0.9078	1.5297	Nkain1	2	0.9954	1.7489
Mgl1	4	1.7453	1.5204	Aldh3a2	1	2.3561	1.7254
Celf5	1	0.8286	1.4881	Usp	2	1.8640	1.7158
Ces1f	4	1.1727	1.4596	Paqr7	1	1.0397	1.6979
Plin2	3	1.1343	1.4377	Acsf3	2	1.2405	1.6947
Ahcy	3	1.5493	1.4121	Hsd17b4	3	1.5514	1.6913
Acot4	2	2.0505	1.3997	Slc16a12	1	2.2866	1.6465
Nceh1	4	1.4832	1.3834	Ddah1	2	1.3409	1.6337
Aadac	1	1.1431	1.3805	Plekho2	1	1.0131	1.6150
Hsd17b4	2	1.6749	1.3494	Slc25a33	2	1.2735	1.5628
Hsd1	1	1.9612	1.3243	Acta1	1	1.0500	1.5582
Slc27a2	1	0.9780	1.3239	Slc5a3	1	1.3764	1.5551
Gpm	1	1.6149	1.2958	Hsd12	1	1.9266	1.5539
Ccdc114	1	0.9502	1.2766	Aadac	1	0.9440	1.5441
Acaa2	3	1.3198	1.2438	Acot4	2	1.6020	1.5346
Ces2b	5	1.4227	1.2275	Adh1	2	1.0112	1.4979
Mcm2	1	1.8104	1.2104	Ahcy	2	1.6064	1.4937
Mfge8	2	1.0856	1.1879	Gramd4	1	1.7378	1.4933
Gramd4	2	1.2645	1.1395	Scd2	1	1.1045	1.4859
Pik1	2	1.4513	1.1133	Plin2	2	1.1396	1.4856
Aqp7	1	1.0151	1.1093	Suco	4	1.3605	1.4449
Vkorc1l1	4	1.9078	1.0824	Nceh1	3	1.6517	1.4305
Scarb2	1	1.2717	1.0617	Ccdc114	1	1.1182	1.4294
				Hsd17b13	1	0.9545	1.4267
				Banp	1	0.9880	1.3810
				Phlda1	3	0.9948	1.3583
				Ppara	1	1.1587	1.3421
				Insig1	1	1.4053	1.3358
				Acac2	3	0.1923	1.3218
				Celf5	1	0.7290	1.3193
				Shmt2	1	1.4400	1.3031
				Fasn	2	1.2183	1.2994
				Eci2	2	1.3273	1.2898
				Bri3bp	2	1.0297	1.2647
				Pdk4	1	1.8697	1.2341
				1700037H94Rik	1	1.2749	1.2323
				Ephb2	1	1.8145	1.2008
				Slco2b1	1	1.0760	1.1950
				Vkorc1l1	4	1.5983	1.1628
				Pik1	1	1.0095	1.1495
				Thns12	3	1.7797	1.1372
				Slc25a20	1	0.9735	1.1282
				Rhbdd2	3	1.6582	1.1276
				Cotl1	2	1.0701	1.1230
				Gusb	4	1.5983	1.0839
				Def8	2	1.1370	1.0761

B

WT HF vs LF				Apc Min/+ HF vs LF			
Gene	VEL Count	log2(AVG VEL FC)	log2(RNA FC)	Gene	VEL Count	log2(AVG VEL FC)	log2(RNA FC)
Pml	1	-1.0372	-1.0671	Trim12c	1	-1.0005	-1.1353
Gprn3	1	-1.0630	-1.0817	Dio1	2	-0.9621	-1.2214
Fzd7	2	-1.4557	-1.1269	Slc52a3	1	-1.2808	-1.2678
Trim36	1	-1.1265	-1.1296	Camk2n1	1	-1.1773	-1.2690
Elmo1	1	-1.1089	-1.1430	Akr1b7	1	-1.0261	-1.2758
Slc52a3	1	-0.9582	-1.1479	Slc9a3	1	-0.8392	-1.3062
4930402H24Rik	3	-0.9335	-1.2438	Aplp1	1	-0.9051	-1.3438
Pparg1a	1	-0.8366	-1.2632	Foxq1	1	-1.2632	-1.4454
Ifit1	1	-0.9511	-1.3006	Ifit2	1	-1.4658	-1.5382
Rnf186	2	-1.5875	-1.3061	Cpne2	1	-1.0225	-1.6347
Aplp1	1	-1.0261	-1.3517	Setbp1	1	-0.8823	-1.6502
Psmb8	1	-0.8169	-1.4555	Spats2l	2	-1.1516	-1.6772
Citla	1	-1.6888	-1.4635	Arntl	1	-1.0672	-1.7292
Trim30a	1	-1.0093	-1.4665	Apol9b	1	-1.0097	-1.7670
Smpd13b	1	-1.0960	-1.6654	Trim12a	1	-1.0005	-1.8376
Mtus2	1	-1.0355	-1.6786	Dock3	1	-1.0091	-1.8429
Cpne2	2	-1.5168	-1.6947	Upp1	3	-1.2993	-1.8682
Syde1	1	-0.8098	-1.6958	Lama3	1	-0.8955	-1.8807
Neur1b	1	-0.8511	-1.7081	Pdx1	2	-1.6288	-1.9527
Ifit1b1	2	-0.9552	-1.7130	Tnfrsf13b	2	-1.1127	-1.9999
Oas3	1	-1.1605	-1.7143	Mtus2	1	-1.1643	-2.0845
Bmf	1	-1.0047	-1.7477	Fgf15	1	-1.1306	-2.3203
Ifit2	2	-1.4320	-1.7672	Ifit47	1	-1.1530	-2.3206
Upp1	3	-1.1952	-1.7674	Trim30a	1	-0.9541	-2.3402
Sifn5	1	-1.5570	-1.8966	Ifit1	1	-1.3156	-2.4215
Socs3	1	-1.5218	-1.9714	Igtp	1	-1.0078	-2.4431
Casp4	1	-1.0714	-2.0342	Fbxo32	1	-1.1646	-2.4660
Herc6	1	-0.9801	-2.0394	Car2	1	-1.7294	-2.4669
Tifa	1	-1.2468	-2.1397	Apol10a	1	-1.3385	-2.4933
Npl	2	-1.1851	-2.3182	Fam189a2	1	-1.2998	-2.5927
Alpk1	1	-1.4762	-2.3828	Herc6	1	-1.0173	-2.8083
B3galt5	2	-1.5709	-2.4540	AA467197	1	-1.4844	-2.8981
Aldh4a1	2	-1.3513	-2.4660	Sifn5	1	-1.7473	-2.9005
Gm5431	2	-1.1705	-2.6197	Slc40a1	2	-1.3528	-3.0115
Bco1	2	-1.5132	-2.7558	Sl00g	1	-1.2686	-3.1431
Sifn2	1	-1.0332	-3.0138	Akp3	1	-0.9669	-3.1750
Barrx2	4	-1.6059	-3.4121	Gm5431	2	-1.5081	-3.2775
Nos2	1	-1.9492	-3.7120	Trpv6	2	-1.6601	-3.5628
Ubd	1	-2.1216	-4.3912	Ifit1b1	2	-1.3009	-3.6906
				Bco1	2	-1.2991	-4.4173

**Supplementary Figure 3.** (A) Upregulated genes predicted to be associated with gained H3K27ac and (B) downregulated genes predicted to be associated with lost H3K27ac were identified when comparing HFD and LFD for both genotypes.

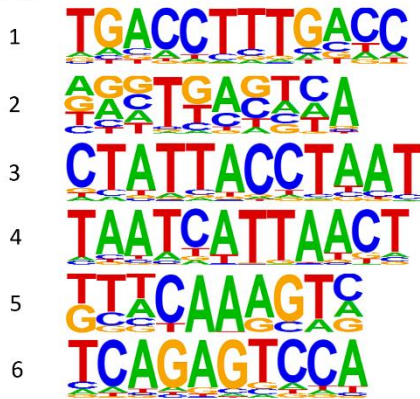
WT HF vs LF			Apc Min HF vs LF		
Gene	Chromosome	Log2(FC)	Gene	Chromosome	Log2(FC)
AF366264	8	0.957246	AF366264	8	1.130094
Axin2	11	1.262206	Axin2	11	1.973693
Camk2g	14	1.27222	Camk2b	11	0.993982
Ccnd1	7	0.962548	Camk2g	14	1.64773
Ctbp2	7	0.897299	Ctbp2	7	2.200558
		1.951858	Ctbp3	7	1.541006
Dkk4	8	1.224642	Ctbp4	7	0.788489
Fzd2	11	1.549727	Ctnnb1	9	1.378863
Jun	4	1.438616	Dkk4	8	1.440516
Lrp5	19	1.183137	Fzd2	11	1.557902
Lrp6	6	1.092265	Jul	4	1.224063
Myc	15	1.281227	Jun	4	1.540921
Nfatc1	18	1.381062	Lrp5	19	0.900883
Nfatc2	2	1.374678	Myc	15	1.229607
Nfatc3	8	0.870843	Nfatc1	18	1.212435
Plcb1	2	1.808879	Nfatc1	18	1.424671
Plcb4	2	1.808879	Nfatc2	2	1.230217
Rbx1	15	1.926345	Nfatc3	8	0.935368
Ror2	13	1.20083	Plcb1	2	2.586879
		1.091875	Plcb2	2	1.14806
		1.032132	Plcb4	2	2.586879
Rspo1	4	1.216613	Ror1	4	1.413505
Ryk	9	1.191162	Ror2	13	1.426124
Siah1a	8	0.731683			0.984884
		0.730792	Rspo1	4	1.835295
		0.681032			1.376297
Tbl1xr1	3	1.549353	Siah1a	8	0.876798
		1.341887	Tbl1xr1	3	1.344234
		0.949417	Tbl1xr2	3	1.071013
Wnt3	11	1.121668	Tcf7l2	19	0.83646
Wnt8b	19	3.367555	Wif1	10	0.911754
		2.365746	Wnt3	11	0.913675
		2.329874	Wnt7b	15	1.158716
		2.319161	Wnt8b	19	3.945001
Camk2a	18	-1.43404			2.581491
Cul1	6	-1.06219			2.897042
Fzd1	5	-1.30584			3.471081
Fzd7	1	-1.09343	Wnt9b	11	0.913675
		-1.94061	Crebbp	16	-0.94913
Mapk10	5	-1.0089	Fzd7	1	-1.21369
Ruvbl1	6	-1.05596	Map3k7	4	-1.40045
			Ppard	17	-0.82339
			Tbl1xr3	3	-1.29325

**Supplementary Figure 4.** Identified VELs predicted to be associated with genes involved in the KEGG Pathway “Wnt Signaling Pathway”



### WT HF vs LF Gained VELs

Rank



Rank	P-value	% of Targets	% of Backgrounds	Best Match/Details
1	1.00E-89	59.69%	32.43%	Nr2f6/MA0677.1/Jaspar(0.971)
2	1.00E-18	29.27%	18.91%	Fos(bZIP)/TSC-Fos-ChIP-Seq(GSE110950)/Homer(0.877)
3	1.00E-16	10.57%	4.89%	TEF/MA0843.1/Jaspar(0.746)
4	1.00E-15	15.25%	8.48%	HNF1b(Homeobox)/PDAC-HNF1B-ChIP-Seq(GSE64557)/Homer(0.893)
5	1.00E-13	34.41%	25.23%	HNF4G/MA0484.2/Jaspar(0.791)
6	1.00E-12	33.87%	24.99%	HNF4G/MA0484.2/Jaspar(0.827)

### *Apc*<sup>Min/+</sup> HF vs LF Gained VELs

Rank



Rank	P-value	% of Targets	% of Backgrounds	Best Match/Details
1	1.00E-97	36.78%	11.71%	PPARa(NR).DR1/Liver-Ppara-ChIP-Seq(GSE47954)/Homer(0.953)
2	1.00E-17	9.76%	3.75%	HNF1b(Homeobox)/PDAC-HNF1B-ChIP-Seq(GSE64557)/Homer(0.820)
3	1.00E-14	1.71%	0.12%	HOXA13/MA0650.2/Jaspar(0.773)
4	1.00E-14	36.11%	25.41%	JunB(bZIP)/Dendritic Cells-Junb-ChIP-Seq(GSE36099)/Homer(0.957)
5	1.00E-12	6.82%	2.65%	HOXD3/MA0912.2/Jaspar(0.769)

### WT HF vs LF Lost VELs

Rank



Rank	P-value	% of Targets	% of Backgrounds	Best Match/Details
1	1.00E-13	48.70%	25.82%	ELF3(ETS)/PDAC-ELF3-ChIP-Seq(GSE64557)/Homer(0.958)

### *Apc*<sup>Min/+</sup> HF vs LF Gained VELs

Rank



Rank	P-value	% of Targets	% of Backgrounds	Best Match/Details
1	1.00E-28	17.03%	2.92%	ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer(0.960)
2	1.00E-25	36.76%	14.55%	ELF3(ETS)/PDAC-ELF3-ChIP-Seq(GSE64557)/Homer(0.960)

**Supplementary Figure 5.** Notable *de novo* motifs were identified from the VELs using HOMER analysis. The percentage of target sequences as well as the percentage of background sequences containing the motif was noted. Known motif that most closely matches the *de novo* motifs are also noted.

WT VELs				
Locus	Log2(Fold-Change)	Q-value	-Log(Q)	Genes
chr9: 86593210-086594683	3.446945748	4.50E-21	20.35	Me1 (-4000)
chr19: 44489642-44492211	3.367555271	1.70E-23	22.77	Wnt8b (-77035), Scd1 (-8728)
chr19: 44480332-44483612	3.340702254	5.72E-29	28.24	Scd1 (+227)
chr4: 115176360-115178539	2.909126154	1.55E-11	10.81	Cyp4a10 (-13419), Cyp4a14 (-8703)
chr5: 17382694-17383654	2.776266782	5.27E-11	10.28	Gnat3 (-85265), Cd36 (-27564)
chr5: 17385604-17387914	2.645476921	1.25E-13	12.90	Gnat3 (-81680), Cd36 (-31149)
chr19: 44501866-44503173	2.365745908	1.72E-05	4.76	Wnt8b (-65442), Scd1 (-20321)
chr4: 115185859-115188695	2.263902491	5.01E-17	16.30	Cyp4a10 (-3592)
chr5: 17315839-17317427	2.073964175	0.00014189	3.85	Cd36 (+38977), Sema3c (+236534)
chr4: 115190229-115192416	2.051807598	3.35E-09	8.48	Cyp4a10 (+454)
chr5: 114592757-114596921	1.999563769	7.38E-19	18.13	Acacb (-1705)
chr4: 94733979-94736057	1.438615901	7.63E-06	5.12	Fggy (-489180), Jun (-16105)
chr19: 44367741-44370983	1.306706028	0.000665067	3.18	Scd4 (-38220), Scd2 (+1196)
chr15: 61728278-61730622	1.281227212	0.008045716	2.09	A1bg (-976625), Myc (-87496)
chr11: 108816516-108818471	1.262205576	0.019059714	1.72	Axin2 (+35831), E030025P04Rik (+188189)
Apc Min/+ VELs				
Locus	Log2(Fold-Change)	Q-value	-Log(Q)	Genes
chr19: 44480332-44483612	4.136092828	1.68E-41	40.78	Scd1 (+227)
chr19: 44489642-44492211	3.945001263	1.21E-31	30.92	Wnt8b (-77035), Scd1 (-8728)
chr19: 44504425-44506311	3.471080966	4.20E-15	14.38	Wnt8b (-62594), Scd1 (-23169)
chr19: 44501866-44503173	2.897042095	3.93E-08	7.41	Wnt8b (-65442), Scd1 (-20321)
chr9: 86593210-86594683	2.549166354	4.34E-12	11.36	Me1 (-4000)
chr5: 17382694-17383654	2.309785836	1.10E-07	6.96	Gnat3 (-85265), Cd36 (-27564)
chr4: 115225498-115225939	2.266004995	0.003806215	2.42	Cyp4a31 (-10584), Cyp4a10 (+34850)
chr5: 114592757-114596921	2.098515026	1.28E-20	19.89	Acacb (-1705)
chr11: 108816516-108818471	1.973692953	1.42E-05	4.85	Axin2 (+35831), E030025P04Rik (+188189)
chr4: 115185859-115188695	1.79929721	1.85E-10	9.73	Cyp4a10 (-3592)
chr4: 94733979-94736057	1.540920907	1.12E-06	5.95	Fggy (-489180), Jun (-16105)
chr11: 120691508-120696082	1.261634714	0.001850552	2.73	Fasn (-8303), Ccdc57 (+100391)
chr15: 61728278-61730622	1.229606782	0.014500981	1.84	A1bg (-976625), Myc (-87496)
chr4: 94742053-94743449	1.224062698	0.029967415	1.52	Fggy (-481447), Jun (-23838)
chr19: 44340446-44342794	1.104469296	0.004176435	2.38	Scd2 (-26546), Scd3 (+63858)

**Supplementary Figure 6.** Top fifteen significant VELs with the highest H3K27ac activity fold-change between HFD and LFD for WT and *Apc<sup>Min/+</sup>* mice. Genes located near the VELs were identified with their relative distance shown.

WT DEGs				
Gene	Locus	Log2(Fold-Change)	Q-value	-Log(Q)
Scd1	chr19: 44468939-44482199	8.8338	0.004937	2.306511
Cyp4a10	chr4: 115190891-115206254	5.7195	0.004937	2.306511
Me1	chr9: 86474969-86595286	4.09577	0.004937	2.306511
Acacb	chr5: 114615526-114700767	3.2807	0.004937	2.306511
Lamb3	chr1: 195128187-195170072	3.00596	0.004937	2.306511
Pdgfra	chr5: 75548315-75594229	2.51629	0.004937	2.306511
Pdgfrb	chr18: 61204803-61244721	2.35033	0.004937	2.306511
Gsta3	chr1: 21230665-21255656	2.18186	0.004937	2.306511
Col6a2	chr10: 76058500-76086149	1.99458	0.036739	1.43487
Cd36	chr5: 17287507-17394777	1.62109	0.004937	2.306511
Mgst1	chr6: 138089057-138105273	1.52966	0.004937	2.306511
H2-T23	chr17: 36131448-36175119	-1.21923	0.02162	1.665152
H2-DMa	chr17: 34259776-34276046	-2.18605	0.004937	2.306511
H2-Ab1	chr17: 34400171-34406363	-2.3784	0.004937	2.306511
H2-DMb1	chr17: 34290135-34297174	-2.82595	0.012603	1.899512
<i>Apc</i> <i>Min</i> /+ DEGs				
Gene	Locus	Log2(Fold-Change)	Q-value	-Log(Q)
Scd1	chr19:44468939-44482199	8.94627	0.004937	2.306511
Cyp4a10	chr4:115190891-115206254	5.26914	0.004937	2.306511
Acacb	chr5:114615526-114700767	4.62441	0.004937	2.306511
Me1	chr9:86474969-86595286	4.10613	0.004937	2.306511
Lamb3	chr1:195128187-195170072	3.04979	0.004937	2.306511
Col1a2	chr6:4455696-4491543	2.18197	0.004937	2.306511
Col1a1	chr11:94797583-94813170	2.08095	0.004937	2.306511
Mgst1	chr6:138089057-138105273	2.03698	0.004937	2.306511
Pdgfra	chr5:75548315-75594229	1.84919	0.04712	1.326797
Cd36	chr5:17287507-17394777	1.77168	0.004937	2.306511
Gstm3	chr3:107766613-107772092	1.60158	0.004937	2.306511
H2-DMa	chr17:34259776-34276046	-2.31638	0.004937	2.306511
H2-Aa	chr17:34419695-34424716	-3.04097	0.004937	2.306511
H2-Ab1	chr17:34400171-34406363	-3.32936	0.004937	2.306511
H2-DMb1	chr17:34290135-34297174	-4.14059	0.004937	2.306511

**Supplementary Figure 7.** Notable differentially expressed genes identified between HFD and LFD for WT and *Apc*<sup>Min/+</sup> mice.