

Polycomb repressive complex : DNA Repair

Yy1	0.58	0.385	0.752	1.25	1
Ep300	0.612	-0.305	-0.189	1.09	0.951
Crebbp	0.62	-0.394	0.239	0.97	0.675
Ube2d3	0.415	0.263	0.367	0.756	0.642
Kdm2a	0.206	-0.43	0.0344	1.03	0.261
Usp45	0.106	-0.209	-0.338	0.736	0.71
Phf1	0.661	1.28	0.756	0.384	0.347
Usp7	-0.197	-0.611	-0.699	0.22	0.191
Cbx8	0.0682	0.379	0.496	0.195	-0.124
Cbx3	-0.027	0.211	0.393	-0.272	-0.39
Usp16	-0.502	0.246	-0.0922	-0.568	-0.284
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Ras signaling pathway : APP Metabolism

Igf1r	0.632	-0.39	-0.0307	1.2	1.1
Grin2a	0.0457	-0.613	-0.335	0.666	0.594
Insr	0.36	-0.53	-0.246	0.747	0.685
Grin2b	-0.0287	-0.723	-0.397	0.553	0.334
Ntrk2	0.201	-0.54	-0.232	0.883	0.497
Grin1	0.599	-0.121	0.213	0.994	0.893
Ngfr	-0.171	-0.18	0.0867	0.286	0.405
Pla2g3	0.314	-0.102	0.201	0.257	-0.0379
Rab5a	-0.0208	0.36	-0.171	-0.0661	0.134
Igf1	0.793	0.704	0.628	1.29	0.22
Rela	0.38	0.951	0.346	0.923	0.172
Efna1	0.448	0.637	0.41	-0.0483	0.044
Efna3	-0.301	0.794	0.59	0.0582	-0.338
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Rap1 signaling pathway : APP Metabolism

Igf1r	0.632	-0.39	-0.0307	1.2	1.1
Insr	0.36	-0.53	-0.246	0.747	0.685
Grin2a	0.0457	-0.613	-0.335	0.666	0.594
Grin2b	-0.0287	-0.723	-0.397	0.553	0.334
Grin1	0.599	-0.121	0.213	0.994	0.893
Itgam	0.0483	-0.606	-0.373	0.557	-0.158
Ngfr	-0.171	-0.18	0.0867	0.286	0.405
Igf1	0.793	0.704	0.628	1.29	0.22
Itgb2	-0.142	0.145	-0.0708	-0.304	0.387
Efna1	0.448	0.637	0.41	-0.0483	0.044
Efna3	-0.301	0.794	0.59	0.0582	-0.338
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

cAMP signaling pathway : APP Metabolism

Gria3	-0.288	-0.82	-0.551	0.437	0.162
Gria2	-0.325	-0.743	-0.438	0.353	0.112
Grin2b	-0.0287	-0.723	-0.397	0.553	0.334
Gria1	-0.209	-0.247	-0.179	0.0202	0.0568
Rock2	0.0582	-0.472	-0.542	0.555	0.67
Grin2a	0.0457	-0.613	-0.335	0.666	0.594
Gria4	0.299	-0.232	-0.195	0.143	0.748
Rock1	0.205	0.00968	0.0123	0.464	0.255
Adrb2	0.0686	0.239	0.485	-0.206	0.00525
Grin1	0.599	-0.121	0.213	0.994	0.893
Atp1a3	0.535	0.0998	-0.201	1.23	1.01
Rela	0.38	0.951	0.346	0.923	0.172
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

PI3K–Akt signaling pathway : APP Metabolism

Il4	−0.744	−0.588	−0.248	−0.602	−1.01
Mdm2	0.0903	−0.185	0.261	−0.389	−0.295
Efna3	−0.301	0.794	0.59	0.0582	−0.338
Tlr2	0.348	−0.00945	0.34	0.0146	−0.246
Efna1	0.448	0.637	0.41	−0.0483	0.044
Ngfr	−0.171	−0.18	0.0867	0.286	0.405
Itga2	0.592	−0.149	0.262	0.175	0.3
Itga4	−0.158	−0.882	−0.584	0.33	0.471
Tlr4	0.096	0.00151	−0.0328	0.526	0.581
Rela	0.38	0.951	0.346	0.923	0.172
Ntrk2	0.201	−0.54	−0.232	0.883	0.497
Insr	0.36	−0.53	−0.246	0.747	0.685
Igf1	0.793	0.704	0.628	1.29	0.22
Gsk3b	0.27	−0.665	−0.288	0.995	0.614
Igf1r	0.632	−0.39	−0.0307	1.2	1.1
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

ECM–receptor interaction : Apoptosis

Col4a3	0.388	0.15	0.913	0.16	0.455
Comp	0.189	0.0868	−0.194	−0.342	0.329
Cd36	−0.0754	−0.31	0.164	0.103	0.0109
Col2a1	0.433	0.062	−0.27	−0.114	−0.246
Itgav	0.193	−0.185	−0.263	0.942	0.717
Thbs1	0.176	−0.32	−0.255	0.501	0.014
Itga1	0.051	−0.592	−0.17	0.453	0.301
Itgb3	0.0445	−0.315	−0.508	0.303	0.166
Itga6	0.251	−0.418	−0.466	0.656	0.364
Cd44	−0.00788	0.0873	−0.797	0.0946	−0.196
Cd47	−0.328	−0.884	−0.429	−0.00524	0.205
Itgb1	0.0996	−0.413	−0.804	0.278	−0.065
Itga4	−0.158	−0.882	−0.584	0.33	0.471
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

ECM–receptor interaction : Synapse

Col4a1	1.08	0.845	0.963	0.988	0.682
Lama5	0.673	0.354	0.915	0.646	0.376
Lamb2	0.973	0.088	0.56	0.671	0.881
Col4a5	0.986	0.14	0.509	0.655	0.827
Itga3	0.742	0.159	0.203	0.472	0.884
Itgb4	0.472	0.565	0.164	0.489	0.31
Sv2c	0.683	0.0902	-0.056	0.936	0.734
Itgb5	0.311	0.61	0.189	0.0425	0.407
Dag1	0.45	-0.125	-0.184	0.99	0.897
Itga2	0.592	-0.149	0.262	0.175	0.3
Lama3	0.0846	0.288	0.258	0.299	-0.0817
Itgb8	0.39	-0.126	-0.352	1.08	0.679
Itga5	-0.178	0.215	0.615	-0.143	-0.0199
Itgav	0.193	-0.185	-0.263	0.942	0.717
Tnn	0.406	0.253	-0.409	0.25	0.393
Thbs2	0.34	-0.0435	0.0781	0.171	0.0822
Agrn	0.118	-0.0721	0.4	0.118	-0.3
Fn1	0.416	-0.421	-0.0188	0.503	0.406
Itgb7	0.295	-0.0191	0.123	-0.177	0.0914
Lama1	0.387	0.00454	-0.302	0.0508	0.558
Sv2a	0.517	-0.497	-0.253	0.761	0.324
Spp1	0.326	0.209	-0.329	-0.12	0.165
Reln	0.288	-0.655	-0.275	0.45	0.872
Cd36	-0.0754	-0.31	0.164	0.103	0.0109
Tnxb	0.108	-0.247	0.0139	-0.165	0.055
Itga6	0.251	-0.418	-0.466	0.656	0.364
Itga1	0.051	-0.592	-0.17	0.453	0.301
Tnr	0.148	-0.72	-0.351	0.71	0.501
Itgb3	0.0445	-0.315	-0.508	0.303	0.166
Lama2	0.18	-0.58	-0.69	0.432	0.459
Itga8	-0.282	-0.235	-0.382	0.0125	-0.0849
Itgb6	-0.0247	-0.574	-0.268	-0.328	0.139
Tnc	0.172	-0.519	-0.908	0.506	0.127
Itgb1	0.0996	-0.413	-0.804	0.278	-0.065
Itga4	-0.158	-0.882	-0.584	0.33	0.471
Sv2b	-0.476	-0.707	-0.81	0.366	0.287
Lamb1	-0.241	-0.986	-0.669	-0.405	-0.135
Lama4	-0.513	-1.04	-0.763	0.0132	0.246

WT/WT

WT/VS

VS/VS

WT/FC

FC/FC

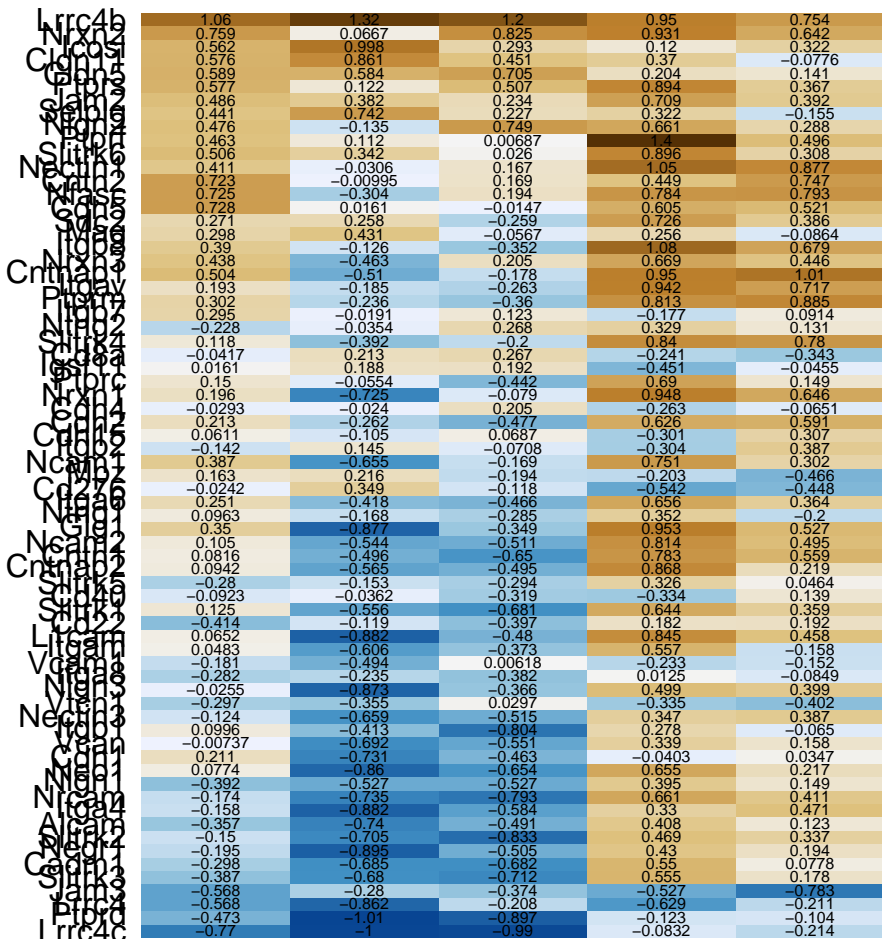
Cell adhesion molecules : Metal Binding and Homeostasis

Neo1	0.0774	-0.86	-0.654	0.655	0.217
Itga4	-0.158	-0.882	-0.584	0.33	0.471
Itgb1	0.0996	-0.413	-0.804	0.278	-0.065
Cdh1	0.211	-0.731	-0.463	-0.0403	0.0347
Itgam	0.0483	-0.606	-0.373	0.557	-0.158
Itga8	-0.282	-0.235	-0.382	0.0125	-0.0849
Vcam1	-0.181	-0.494	0.00618	-0.233	-0.152
Itga6	0.251	-0.418	-0.466	0.656	0.364
Itga9	-0.125	-0.223	-0.356	0.211	0.317
Cdh2	0.213	-0.262	-0.477	0.626	0.591
Itgal	-0.126	-0.322	-0.119	-0.0365	0.425
Nrxn1	0.196	-0.725	-0.079	0.948	0.646
Cd4	-0.0773	-0.263	0.0962	-0.418	-0.133
Itgav	0.193	-0.185	-0.263	0.942	0.717
Itgb2	-0.142	0.145	-0.0708	-0.304	0.387
Cdh15	0.0611	-0.105	0.0687	-0.301	0.307
Cdh4	-0.0293	-0.024	0.205	-0.263	-0.0651
Nrxn3	0.438	-0.463	0.205	0.669	0.446
Itgb7	0.295	-0.0191	0.123	-0.177	0.0914
Cdh5	0.728	0.0161	-0.0147	0.605	0.521
Nectin1	0.411	-0.0306	0.167	1.05	0.877
Selp	0.319	0.445	0.416	0.226	0.319
Cldn3	0.234	0.391	0.813	-0.0321	0.0295
Nrxn2	0.759	0.0667	0.825	0.931	0.642
Cdh3	0.53	0.519	0.882	0.148	0.791
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Cell adhesion molecules : Myelination

Ptp ^{prf}	0.463	0.112	0.00687	1.4	0.496
Cntnap1	0.504	-0.51	-0.178	0.95	1.01
Nfasc	0.725	-0.304	0.194	0.784	0.793
Ptp ^{rs}	0.577	0.122	0.507	0.894	0.367
Cntn2	0.723	-0.00995	0.169	0.449	0.747
Jam2	0.486	0.382	0.234	0.709	0.392
Cdh2	0.213	-0.262	-0.477	0.626	0.591
Cldn5	0.589	0.584	0.705	0.204	0.141
Cntn1	0.0816	-0.496	-0.65	0.783	0.559
Cldn11	0.576	0.861	0.451	0.37	-0.0776
Neo1	0.0774	-0.86	-0.654	0.655	0.217
Mag	0.298	0.431	-0.0567	0.256	-0.0864
Itgb1	0.0996	-0.413	-0.804	0.278	-0.065
Mpz	0.163	0.216	-0.194	-0.203	-0.466
Jam3	-0.568	-0.28	-0.374	-0.527	-0.783
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Cell adhesion molecules : Synapse



WT/WT

WT/VS

VS/VS

WT/FC

FC/FC

Adherens junction : Lipid Metabolism

Rhoa	-0.405	0.517	-0.214	-0.718	-0.658
Fyn	-0.367	0.546	-0.0637	-0.508	-0.428
Rac1	-0.531	0.399	-0.0148	-0.479	-0.353
Mapk3	0.151	1.19	0.511	0.0282	0.2
Rap1b	-0.158	0.517	0.134	0.449	-0.149
Smurf1	0.269	0.648	0.371	0.422	0.365
Fgfr1	0.864	0.733	0.563	0.0956	0.558
Snai1	0.28	0.187	0.153	0.0389	0.356
ErbB2	0.154	-0.519	-0.0179	0.0914	-0.167
Mapk1	-0.499	-0.631	-0.692	0.191	-0.168
Snai2	0.306	0.267	-0.263	0.344	0.243
Cdh1	0.211	-0.731	-0.463	-0.0403	0.0347
Ctnnb1	-0.0459	0.0455	-0.246	0.723	0.169
Src	0.373	0.436	0.381	0.906	0.474
Fer	-0.233	-0.89	-0.75	0.204	0.0705
Iqgap1	0.5	-0.271	0.127	0.312	0.602
Yes1	0.171	0.0257	-0.208	0.733	0.51
Wsf2	0.842	0.171	0.149	0.672	0.427
Pard3	0.66	0.237	-0.133	0.858	0.302
Egfr	0.134	-0.623	-0.32	0.44	0.303
Tgfr1	0.0833	-0.622	-0.787	0.697	-0.119
Cdh5	0.728	0.0161	-0.0147	0.605	0.521
Heg1	0.345	-0.263	-0.176	0.568	0.643
Krit1	0.299	-0.0984	-0.255	0.764	0.642
Smurf2	0.226	-0.477	-0.744	0.559	0.46
Rock2	0.0582	-0.472	-0.542	0.555	0.67
Ptpri	0.181	-0.552	-0.352	0.608	0.554
Vcl	0.484	0.109	0.124	1.14	0.538
Tgfr2	0.494	-0.326	0.182	0.692	0.825
Sorbs1	0.0959	-0.586	-0.502	0.769	0.65
Insr	0.36	-0.53	-0.246	0.747	0.685
Tjp1	0.475	-0.271	-0.4	1.1	0.622
Igf1r	0.632	-0.39	-0.0307	1.2	1.1

WT/WT

WT/VS

VS/VS

WT/FC

FC/FC

Adipocytokine signaling pathway : Autophagy

Akt1	0.513	1.49	0.819	0.167	0.446
Stk11	0.462	1.03	0.857	0.0923	0.05
Stat3	0.402	0.188	0.0846	0.303	-0.0215
Lepr	0.336	-0.364	0.112	-0.13	0.471
Cd36	-0.0754	-0.31	0.164	0.103	0.0109
Mapk8	0.0348	-0.378	-0.405	0.714	0.486
Mtor	0.344	-0.423	-0.445	1.03	0.506
Ikbkg	-0.0314	-0.375	-0.821	0.414	0.195
Camkk2	-0.0513	-0.854	-0.27	0.189	0.545
Appl1	0.0584	-0.568	-0.464	0.832	0.517
Prkaa1	-0.0883	-0.55	-0.678	0.403	0.188
Prkaa2	-0.0612	-0.51	-0.642	0.656	0.482
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Adipocytokine signaling pathway : Oxidative Stress

Camkk2	-0.0513	-0.854	-0.27	0.189	0.545
Prkaa1	-0.0883	-0.55	-0.678	0.403	0.188
Prkaa2	-0.0612	-0.51	-0.642	0.656	0.482
Mapk8	0.0348	-0.378	-0.405	0.714	0.486
Ppargc1a	0.102	-0.451	-0.27	0.731	0.313
Mapk9	0.0872	-0.153	-0.701	0.538	0.599
Cd36	-0.0754	-0.31	0.164	0.103	0.0109
Ppara	0.217	0.132	-0.0486	1.06	0.473
Chuk	0.386	-0.0647	0.515	0.045	-0.102
Jak2	0.474	0.72	0.0364	0.874	0.501
Rela	0.38	0.951	0.346	0.923	0.172
Akt1	0.513	1.49	0.819	0.167	0.446
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Aldosterone-regulated sodium reabsorption : Apoptosis

Prkcb	-0.266	-1.09	-0.484	0.1	0.181
Mapk1	-0.499	-0.631	-0.692	0.191	-0.168
Prkcg	-0.549	-0.236	-0.268	-0.429	-0.0164
Prkca	-0.19	-0.447	-0.466	0.452	0.131
Pik3cb	-0.117	-0.22	-0.833	0.676	0.429
Nr3c2	-0.201	-0.213	-0.407	0.595	0.0852
Pdpk1	0.174	-0.456	-0.445	0.915	0.736
Pik3ca	0.298	-0.502	-0.363	0.542	0.75
Pik3r1	0.349	-0.439	-0.303	0.842	0.756
Kras	0.556	0.142	0.308	0.804	0.915
Sgk1	0.356	0.641	0.267	0.408	-0.236
Mapk3	0.151	1.19	0.511	0.0282	0.2
Sfn	0.553	0.927	0.532	0.123	0.914
Igf1	0.793	0.704	0.628	1.29	0.22
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Aldosterone-regulated sodium reabsorption : Vasculature

Igf1	0.793	0.704	0.628	1.29	0.22
Pik3cd	0.41	0.816	0.883	0.542	0.438
Sgk1	0.356	0.641	0.267	0.408	-0.236
Atp1b2	0.513	0.298	0.0032	0.242	0.715
Atp1a3	0.535	0.0998	-0.201	1.23	1.01
Scnn1a	0.248	0.0675	0.171	0.336	0.205
Scnn1g	-0.0351	-0.0155	0.437	0.129	0.671
Scnn1b	0.0467	0.26	0.16	-0.143	0.134
Atp1a2	0.433	-0.253	0.229	0.335	0.345
Nedd4l	0.153	-0.384	0.0473	0.449	0.426
Insr	0.36	-0.53	-0.246	0.747	0.685
Pik3r3	0.284	-0.283	-0.284	0.14	0.75
Pdpk1	0.174	-0.456	-0.445	0.915	0.736
Pik3ca	0.298	-0.502	-0.363	0.542	0.75
Atp1a4	-0.331	-0.223	-0.145	0.345	-0.133
Atp1b1	-0.313	0.033	-0.382	0.0252	-0.181
Atp1a1	0.12	-0.658	-0.22	0.317	0.744
Pik3cb	-0.117	-0.22	-0.833	0.676	0.429
Prkca	-0.19	-0.447	-0.466	0.452	0.131
Mapk1	-0.499	-0.631	-0.692	0.191	-0.168
Prkcb	-0.266	-1.09	-0.484	0.1	0.181
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Dopaminergic synapse : APP Metabolism

Gria3	-0.288	-0.82	-0.551	0.437	0.162
Cacna1b	0.00354	-0.952	-0.359	0.698	0.372
Gria2	-0.325	-0.743	-0.438	0.353	0.112
Grin2b	-0.0287	-0.723	-0.397	0.553	0.334
Gsk3b	0.27	-0.665	-0.288	0.995	0.614
Grin2a	0.0457	-0.613	-0.335	0.666	0.594
Gria1	-0.209	-0.247	-0.179	0.0202	0.0568
Cacna1a	0.427	-0.497	-0.123	0.456	1.1
Gria4	0.299	-0.232	-0.195	0.143	0.748
Gsk3a	0.53	1.21	0.892	0.221	0.412
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Longevity regulating pathway : Endolysosome

Hras	-0.767	0.182	0.0103	-0.776	-1.02
Rheb	0.0942	0.949	0.427	-0.513	-0.317
Akt2	0.35	0.604	0.702	-0.172	0.912
Pik3cb	-0.117	-0.22	-0.833	0.676	0.429
Appl1	0.0584	-0.568	-0.464	0.832	0.517
Rb1cc1	0.0443	-0.42	-0.392	0.724	0.674
Tsc2	0.286	0.253	0.119	0.824	0.632
Insr	0.36	-0.53	-0.246	0.747	0.685
Adcy8	0.541	0.033	-0.166	0.856	0.525
Mtor	0.344	-0.423	-0.445	1.03	0.506
Igf1	0.793	0.704	0.628	1.29	0.22
Atg13	0.567	0.708	0.464	1.06	0.887
Ulk1	0.844	0.574	0.399	0.936	1.23
Rptor	0.985	0.216	0.132	1.26	1.44
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Transcriptional misregulation in cancer : APP Metabolism

Fus	-0.37	-1.24	-0.185	-0.31	-0.419
Hdac1	-0.436	0.193	-0.17	-0.631	-0.447
Gria3	-0.288	-0.82	-0.551	0.437	0.162
Mdm2	0.0903	-0.185	0.261	-0.389	-0.295
Itgam	0.0483	-0.606	-0.373	0.557	-0.158
Ngfr	-0.171	-0.18	0.0867	0.286	0.405
Sp1	0.446	-0.233	-0.461	0.907	0.835
Igf1r	0.632	-0.39	-0.0307	1.2	1.1
Rela	0.38	0.951	0.346	0.923	0.172
Mmp9	0.652	0.814	0.391	0.599	0.67
Igf1	0.793	0.704	0.628	1.29	0.22
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Proteoglycans in cancer : APP Metabolism

Hspg2	0.897	0.19	0.627	1.01	0.82
Igf1	0.793	0.704	0.628	1.29	0.22
Igf1r	0.632	-0.39	-0.0307	1.2	1.1
Mmp9	0.652	0.814	0.391	0.599	0.67
Tlr4	0.096	0.00151	-0.0328	0.526	0.581
Fzd5	0.0975	-0.075	-0.28	0.724	0.187
Rock2	0.0582	-0.472	-0.542	0.555	0.67
Rock1	0.205	0.00968	0.0123	0.464	0.255
Itga2	0.592	-0.149	0.262	0.175	0.3
Stat3	0.402	0.188	0.0846	0.303	-0.0215
Timp3	0.334	-0.00522	0.203	0.216	0.196
Fzd4	0.52	-0.323	-0.255	0.25	0.039
Tlr2	0.348	-0.00945	0.34	0.0146	-0.246
Tgfb2	-0.233	-0.148	-0.173	0.0194	0.0122
Mmp2	-0.177	0.062	-0.131	0.0973	-0.422
Mdm2	0.0903	-0.185	0.261	-0.389	-0.295
Casp3	-0.691	-0.615	0.105	-1.06	-0.897
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Bacterial invasion of epithelial cells : Lipid Metabolism

Rhoa	-0.405	0.517	-0.214	-0.718	-0.658
Rac1	-0.531	0.399	-0.0148	-0.479	-0.353
Itga5	-0.178	0.215	0.615	-0.143	-0.0199
Shc1	0.233	0.451	0.252	0.227	-0.478
Pik3r2	0.36	0.803	0.813	0.201	0.213
Cav1	0.228	0.192	0.165	0.228	-0.281
Pik3cd	0.41	0.816	0.883	0.542	0.438
Cdh1	0.211	-0.731	-0.463	-0.0403	0.0347
Itgb1	0.0996	-0.413	-0.804	0.278	-0.065
Ctnnb1	-0.0459	0.0455	-0.246	0.723	0.169
Src	0.373	0.436	0.381	0.906	0.474
Wasf2	0.842	0.171	0.149	0.672	0.427
Pik3r3	0.284	-0.283	-0.284	0.14	0.75
Pik3cb	-0.117	-0.22	-0.833	0.676	0.429
Crk	0.434	0.357	-0.0213	0.881	0.835
Cltc	-0.17	-0.556	-0.851	0.607	0.293
Cav2	0.45	0.137	-0.213	0.852	0.662
Vcl	0.484	0.109	0.124	1.14	0.538
Crkl	0.439	0.00316	-0.232	0.974	0.582
Pik3ca	0.298	-0.502	-0.363	0.542	0.75
Pik3r1	0.349	-0.439	-0.303	0.842	0.756
Cbl	0.421	-0.435	-0.196	1.09	0.6
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Spinocerebellar ataxia : Vasculature

Xbp1	0.971	1.61	1.1	0.453	0.572
Akt1	0.513	1.49	0.819	0.167	0.446
Pik3cd	0.41	0.816	0.883	0.542	0.438
Psmc5	-0.0519	0.876	0.312	-0.653	-0.474
Plcb3	0.566	0.000967	0.0396	-0.062	0.582
Atp2a3	0.173	-0.158	0.029	-0.252	0.59
Ern1	0.364	-0.252	0.00251	0.93	0.775
Pik3r3	0.284	-0.283	-0.284	0.14	0.75
Atp2a1	-0.0194	-0.174	-0.332	0.611	-0.173
Sp1	0.446	-0.233	-0.461	0.907	0.835
Kcnd3	0.108	-0.3	-0.39	0.875	0.416
Rora	0.413	-0.57	-0.225	0.672	0.844
Pik3ca	0.298	-0.502	-0.363	0.542	0.75
Mtor	0.344	-0.423	-0.445	1.03	0.506
Prkca	-0.19	-0.447	-0.466	0.452	0.131
Pik3cb	-0.117	-0.22	-0.833	0.676	0.429
Rbpj	0.249	-0.601	-0.49	0.77	0.485
Map3k5	-0.4	-0.799	-0.293	0.114	0.303
Atp2a2	0.186	-0.645	-0.571	0.681	0.894
Akt3	0.0491	-0.603	-0.638	0.735	0.652
Prkcb	-0.266	-1.09	-0.484	0.1	0.181
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Hypertrophic cardiomyopathy : Mitochondrial Metabolism

Prkaa1	-0.0883	-0.55	-0.678	0.403	0.188
Prkaa2	-0.0612	-0.51	-0.642	0.656	0.482
Atp2a2	0.186	-0.645	-0.571	0.681	0.894
Ryr2	0.137	-0.794	-0.305	0.748	0.601
Dmd	0.219	-0.588	-0.436	0.796	0.588
Prkag2	-0.475	-0.293	-0.0981	-0.781	-0.585
Itgb3	0.0445	-0.315	-0.508	0.303	0.166
Atp2a1	-0.0194	-0.174	-0.332	0.611	-0.173
Prkag3	-0.23	0.0962	-0.374	0.046	0.303
Nos1	0.419	-0.423	-0.216	0.671	0.697
Edn1	0.0693	0.147	-0.221	-0.223	0.559
Slc8a3	0.941	0.142	0.393	0.712	0.191
Tgfb1	0.709	0.605	0.289	0.361	0.546
Igf1	0.793	0.704	0.628	1.29	0.22
Lmna	0.638	1.36	1.24	0.306	0.258
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Dilated cardiomyopathy : Mitochondrial Metabolism

Lmna	0.638	1.36	1.24	0.306	0.258
Igf1	0.793	0.704	0.628	1.29	0.22
Tgfb1	0.709	0.605	0.289	0.361	0.546
Slc8a3	0.941	0.142	0.393	0.712	0.191
Nos1	0.419	-0.423	-0.216	0.671	0.697
Atp2a1	-0.0194	-0.174	-0.332	0.611	-0.173
Prkaca	-0.344	0.0402	-0.435	-0.431	-1.2
Itgb3	0.0445	-0.315	-0.508	0.303	0.166
Dmd	0.219	-0.588	-0.436	0.796	0.588
Pln	0.0809	-0.625	-0.192	0.167	-0.154
Ryr2	0.137	-0.794	-0.305	0.748	0.601
Atp2a2	0.186	-0.645	-0.571	0.681	0.894
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Diabetic cardiomyopathy : Epigenetic

Mapk10	-0.33	-0.987	-0.595	0.272	0.253
Prkcb	-0.266	-1.09	-0.484	0.1	0.181
Smad2	-0.0279	-0.407	-0.903	0.669	0.217
Prkca	-0.19	-0.447	-0.466	0.452	0.131
Mapk8	0.0348	-0.378	-0.405	0.714	0.486
Pik3ca	0.298	-0.502	-0.363	0.542	0.75
Mapk9	0.0872	-0.153	-0.701	0.538	0.599
Pik3r1	0.349	-0.439	-0.303	0.842	0.756
Sp1	0.446	-0.233	-0.461	0.907	0.835
Cd36	-0.0754	-0.31	0.164	0.103	0.0109
Mapk14	0.114	-0.0246	-0.00571	-0.00349	0.359
Ppara	0.217	0.132	-0.0486	1.06	0.473
Smad3	0.292	-0.109	0.203	0.0195	0.515
Nfkb1	0.542	0.118	0.408	0.703	0.314
Parp1	0.214	0.483	0.306	0.327	0.672
Tgfb1	0.709	0.605	0.289	0.361	0.546
Rela	0.38	0.951	0.346	0.923	0.172
Pik3r2	0.36	0.803	0.813	0.201	0.213
Tgfb3	0.647	0.874	0.752	0.185	0.385
Akt1	0.513	1.49	0.819	0.167	0.446
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Type II diabetes mellitus : Synapse

Cacna1b	0.00354	-0.952	-0.359	0.698	0.372
Mapk1	-0.499	-0.631	-0.692	0.191	-0.168
Cacna1e	0.102	-0.617	-0.312	0.69	0.554
Mtor	0.344	-0.423	-0.445	1.03	0.506
Mapk8	0.0348	-0.378	-0.405	0.714	0.486
Insr	0.36	-0.53	-0.246	0.747	0.685
Mapk9	0.0872	-0.153	-0.701	0.538	0.599
Cacna1c	0.386	-0.336	-0.059	1.08	0.664
Cacna1a	0.427	-0.497	-0.123	0.456	1.1
Prkce	-0.173	-0.254	0.109	-0.0314	0.0983
Cacna1d	0.26	-0.244	0.229	0.717	0.318
Abcc8	0.388	-0.377	-0.00177	0.0433	0.494
Slc2a4	0.383	0.268	0.0807	0.0559	0.0937
Kcnj11	0.512	0.236	0.498	0.184	0.903
Cacna1g	1.08	0.448	0.589	0.917	1.18
Prkcz	0.187	0.773	0.286	-0.127	0.615
Mapk3	0.151	1.19	0.511	0.0282	0.2
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Nicotine addiction : APP Metabolism

Gria2	-0.325	-0.743	-0.438	0.353	0.112
Gria3	-0.288	-0.82	-0.551	0.437	0.162
Gria1	-0.209	-0.247	-0.179	0.0202	0.0568
Grin2b	-0.0287	-0.723	-0.397	0.553	0.334
Cacna1b	0.00354	-0.952	-0.359	0.698	0.372
Chrna7	-0.0199	-0.506	-0.59	0.968	0.338
Grin2a	0.0457	-0.613	-0.335	0.666	0.594
Gria4	0.299	-0.232	-0.195	0.143	0.748
Cacna1a	0.427	-0.497	-0.123	0.456	1.1
Grin1	0.599	-0.121	0.213	0.994	0.893
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Inositol phosphate metabolism : Autophagy

Mtmr14	-0.447	0.199	-0.612	-0.405	-0.257
Pik3c3	-0.258	0.0159	-0.82	0.129	0.266
Pip5k1a	-0.393	-0.332	0.236	-0.182	-0.171
Pik3cb	-0.117	-0.22	-0.833	0.676	0.429
Pip4k2b	-0.118	-0.683	-0.401	0.774	0.211
Inpp5b	-0.00492	-0.296	0.0857	-0.551	0.624
Pikfyve	0.094	-0.576	-0.367	0.746	0.856
Mtm1	0.336	-0.255	-0.00127	0.24	0.121
Pik3ca	0.298	-0.502	-0.363	0.542	0.75
Ocrl	0.269	0.0438	-0.443	0.551	0.258
Pik3c2a	0.464	-0.192	-0.357	0.758	0.652
Plcg2	0.0794	0.592	0.219	0.423	0.0207
Mtmr3	0.569	-0.137	-0.191	0.668	0.796
Pip4k2c	0.0757	0.303	0.508	0.339	0.499
Pip4k2a	0.376	0.971	-0.229	0.428	0.396
Pik3c2b	0.699	-0.00713	0.17	0.621	0.117
Mtmr4	0.839	0.251	0.127	1.17	0.392
Pip5k1c	0.71	0.691	0.995	0.62	0.948
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Inositol phosphate metabolism : Endolysosome

Pik3cg	-0.258	-0.501	-0.686	-0.00379	-0.0387
Synj1	-0.117	-0.722	-0.803	0.76	0.307
Fig4	-0.175	-0.348	-0.651	-0.32	0.125
Mtmr6	-0.2	-0.411	-0.781	0.496	0.265
Pik3c3	-0.258	0.0159	-0.82	0.129	0.266
Pik3cb	-0.117	-0.22	-0.833	0.676	0.429
Pi4kb	-0.531	0.0507	-0.507	0.211	-0.0754
Synj2	0.129	-0.383	-0.515	0.717	0.403
Pikfyve	0.094	-0.576	-0.367	0.746	0.856
Inpp5f	-0.082	0.153	-0.214	-0.234	-0.25
Pi4k2b	0.055	0.0351	-0.378	-0.13	0.367
Inpp4a	0.327	-0.488	-0.435	0.863	0.832
Inpp5b	-0.00492	-0.296	0.0857	-0.551	0.624
Ocrl	0.269	0.0438	-0.443	0.551	0.258
Mtm1	0.336	-0.255	-0.00127	0.24	0.121
Pik3c2a	0.464	-0.192	-0.357	0.758	0.652
Mtmr2	0.129	0.636	-0.445	0.536	0.436
Inpp1	0.366	-0.323	0.471	0.145	0.782
Pik3c2b	0.699	-0.00713	0.17	0.621	0.117
Pip4k2a	0.376	0.971	-0.229	0.428	0.396
Mtmr4	0.839	0.251	0.127	1.17	0.392
Pi4k2a	0.504	1.25	0.74	0.247	0.69
Pip5k1c	0.71	0.691	0.995	0.62	0.948
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Lysine degradation : Epigenetic

Smyd2	-0.486	0.326	-0.229	-0.726	-1.01
Prdm9	-0.274	-0.787	0.204	-0.561	-0.717
Smyd3	-0.0339	-0.911	-0.437	-0.37	-0.504
Ezh2	-0.0377	-0.186	-0.426	-0.702	-0.0981
Suv39h2	-0.516	-0.0566	-0.729	-0.0341	-0.164
Suv39h1	-0.117	0.613	0.0855	-0.198	-0.38
Smyd1	0.146	0.267	-0.363	0.0403	-0.169
Kmt2e	-0.0811	-0.998	-0.426	0.293	0.129
Setdb1	0.105	-0.246	0.349	-0.27	0.342
Setdb2	0.363	0.0161	-0.252	-0.0917	0.277
Kmt5c	0.468	0.531	0.584	-0.277	0.0431
Setd2	0.00558	-0.877	-0.83	0.408	0.623
Prdm6	-0.171	0.267	0.0918	0.12	0.603
Mecom	-0.0783	-0.0456	-0.218	0.783	0.0942
Aass	0.193	0.086	-0.0488	0.467	0.425
Ehmt1	0.437	-0.744	-0.106	0.283	0.582
Ehmt2	0.525	0.881	1.19	0.428	-0.123
Kmt5b	0.0316	-0.485	-0.0389	0.355	0.866
Nsd1	0.281	-0.609	-0.222	0.686	0.615
Ash1l	0.254	-0.577	-0.394	0.777	0.69
Nsd2	0.32	-0.571	-0.366	0.861	0.566
Ezh1	0.27	0.306	-0.364	0.506	1.04
Kmt5a	0.461	0.923	0.81	0.435	0.483
Dot1l	0.724	0.56	0.957	0.111	0.619
Prdm16	0.775	0.255	-0.0993	0.753	0.576
Kmt2c	0.525	-0.427	-0.192	0.823	0.881
Setd7	0.392	-0.529	-0.318	0.872	1.05
Kmt2a	0.778	-0.29	0.225	1.15	0.738
Nsd3	0.773	-0.154	0.0872	0.911	1.14
Kmt2d	0.873	-0.247	0.423	1.18	0.901
Setd1b	0.867	-0.207	0.414	1.15	1.11
Prdm2	0.862	0.289	0.634	0.966	1.26
Kmt2b	0.879	0.0145	0.69	1.36	0.982
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Mineral absorption : Vasculature

Atp1a3	0.535	0.0998	-0.201	1.23	1.01
Atp2b2	0.282	-0.724	-0.328	0.757	0.899
Slc8a1	0.2	-0.475	-0.416	0.931	0.712
Atp2b3	0.266	-0.851	-0.546	0.579	0.734
Atp7a	0.217	-0.4	-0.689	0.796	0.529
Atp1a1	0.12	-0.658	-0.22	0.317	0.744
Slc8a3	0.941	0.142	0.393	0.712	0.191
Atp1b2	0.513	0.298	0.0032	0.242	0.715
Atp1a2	0.433	-0.253	0.229	0.335	0.345
Atp2b4	-0.193	-0.626	-0.508	0.544	0.182
Slc5a1	0.237	0.00105	0.385	-0.0841	0.623
Atp2b1	-0.26	-0.657	-0.391	0.224	0.0711
Trf	0.262	0.431	-0.194	-0.0225	0.212
Atp1a4	-0.331	-0.223	-0.145	0.345	-0.133
Slc8a2	-0.386	-0.543	-0.112	-0.103	-0.028
Atp1b1	-0.313	0.033	-0.382	0.0252	-0.181
Slc31a1	-0.15	-0.0724	-0.485	-0.157	-0.304
Hmox1	-0.522	0.739	-0.0907	-0.306	0.0145
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Endocrine and other factor–regulated calcium reabsorption : Vascul

Prkaca	−0.344	0.0402	−0.435	−0.431	−1.2
Bdkrb2	−0.239	−0.225	−0.754	−0.371	−0.481
Atp1b1	−0.313	0.033	−0.382	0.0252	−0.181
Slc8a2	−0.386	−0.543	−0.112	−0.103	−0.028
Prkcb	−0.266	−1.09	−0.484	0.1	0.181
Atp1a4	−0.331	−0.223	−0.145	0.345	−0.133
Atp2b1	−0.26	−0.657	−0.391	0.224	0.0711
Prkca	−0.19	−0.447	−0.466	0.452	0.131
Atp2b4	−0.193	−0.626	−0.508	0.544	0.182
Kl	0.141	−0.0786	0.362	−0.0548	0.39
Ap2b1	−0.0872	−0.13	−0.395	0.596	0.442
Atp1a1	0.12	−0.658	−0.22	0.317	0.744
Plcb3	0.566	0.000967	0.0396	−0.062	0.582
Atp1a2	0.433	−0.253	0.229	0.335	0.345
Atp2b3	0.266	−0.851	−0.546	0.579	0.734
Atp1b2	0.513	0.298	0.0032	0.242	0.715
Slc8a1	0.2	−0.475	−0.416	0.931	0.712
Atp2b2	0.282	−0.724	−0.328	0.757	0.899
Slc8a3	0.941	0.142	0.393	0.712	0.191
Adcy6	0.539	−0.037	0.675	0.795	0.573
Atp1a3	0.535	0.0998	−0.201	1.23	1.01
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC

Carbohydrate digestion and absorption : Metal Binding and Homeo

Prkcb	-0.266	-1.09	-0.484	0.1	0.181
Plcb1	-0.287	-0.782	-0.447	0.306	0.147
Atp1a4	-0.331	-0.223	-0.145	0.345	-0.133
Plcb2	-0.25	-0.0262	-0.557	-0.347	0.281
Atp1a1	0.12	-0.658	-0.22	0.317	0.744
Plcb4	0.335	-0.427	-0.37	0.212	0.664
Cacna1d	0.26	-0.244	0.229	0.717	0.318
Atp1a2	0.433	-0.253	0.229	0.335	0.345
Atp1a3	0.535	0.0998	-0.201	1.23	1.01
Akt2	0.35	0.604	0.702	-0.172	0.912
	WT/WT	WT/VS	VS/VS	WT/FC	FC/FC