

Table S1. Related to Figure 3

gene symbol	reference
MGP	Gilbert and Rannels, 2004
SPAC	Strandjord et al., 1995
ANGPT1	Hato et al., 2009
LIMCH1	Costello et al., 2008
CHI3L1	Ober et al., 2008
KDR	Clerch et al., 2004
PECAM	DeLisser et al., 2006
ANXA3	Abdul-Salam et al.
SLC39A8	He et al., 2009
ERRFI1	Jin et al., 2009
PDPN	Rishi et al., 1995
TSPAN8	Cardoso and Lu, 2006

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Table S2. Related to Figure 7

## Pathways enriched in Cluster A (515 genes ) by GO with p&lt; 0.02

Cluster A			
Pathways	% of cluster A	% of whole genome	P value
Fructose galactose metabolism	0.66	0.05	0.00203
Glutamine glutamate conversion	0.44	0.02	0.0036
PI3 kinase pathway	1.31	0.42	0.0138
Axon guidance mediated by netrin	0.66	0.11	0.0149
Insulin/IGF pathway-protein kinase B signaling cascade	1.09	0.32	0.0162
Flavin biosynthesis	0.22	0.00	0.0173

## Pathways enriched in Cluster B (281 genes ) by GO with p&lt; 0.02

Cluster B			
Pathways	% of cluster B	% of whole genome	P value
5-Hydroxytryptamine degradation	1.91	0.09	0.0000429
Phenylethylamine degradation	1.53	0.05	0.000014
Alzheimer disease-presenilin pathway	3.05	0.47	0.0000431
Endothelin signaling pathway	2.29	0.34	0.000312
Angiogenesis	3.05	0.74	0.000827
Cadherin signaling pathway	2.67	0.64	0.00163
Hedgehog signaling pathway	1.15	0.10	0.00214
Wnt signaling pathway	3.44	1.33	0.00908
GABA-B_receptor_II_signaling	1.15	0.16	0.00957
EGF receptor signaling pathway	1.91	0.53	0.0132
Beta2 adrenergic receptor signaling pathway	1.15	0.19	0.0136
Beta1 adrenergic receptor signaling pathway	1.15	0.19	0.0136
Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway	1.91	0.53	0.0136
TCA cycle	0.76	0.07	0.0144
Nicotinic acetylcholine receptor signaling pathway	1.53	0.37	0.0176
Metabotropic glutamate receptor group II pathway	1.15	0.21	0.0184
Succinate to propionate conversion	0.38	0.01	0.0198

## Pathways enriched in Cluster C (600 genes ) by GO with p&lt; 0.02

Cluster C			
Pathways	% of cluster C	% of whole genome	P value
Integrin signalling pathway	4.08	0.71	4.06E-11
Angiogenesis	3.72	0.74	2.92E-09
Nicotinic acetylcholine receptor signaling pathway	2.13	0.37	0.0000217
Alzheimer disease-presenilin pathway	2.13	0.47	0.0000222
Axon guidance mediated by semaphorins	1.24	0.17	0.0000582
VEGF signaling pathway	1.24	0.29	0.00149
Inflammation mediated by chemokine and cytokine signaling pathway	2.66	1.14	0.00247
PDGF signaling pathway	1.60	0.62	0.00946
Axon guidance mediated by Slit/Robo	0.53	0.08	0.011
B cell activation	1.06	0.33	0.0123

## Pathways enriched in Cluster D (809 genes ) by GO with p&lt; 0.02

Cluster D			
Pathways	% of cluster D	% of whole genome	P value
Inflammation mediated by chemokine and cytokine signaling pathway	4.40	1.14	2.11E-10
T cell activation	3.02	0.54	2.2E-10
B cell activation	2.34	0.33	8.35E-10
Toll receptor signaling pathway	1.37	0.24	0.0000169
DNA replication	0.69	0.10	0.000754
PDGF signaling pathway	1.79	0.62	0.000775
Integrin signalling pathway	1.79	0.71	0.00246
JAK/STAT signaling pathway	0.55	0.08	0.00255
p53 pathway feedback loops 2	0.82	0.19	0.00336
EGF receptor signaling pathway	1.37	0.53	0.00604
Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway	1.37	0.53	0.00633
Apoptosis signaling pathway	1.37	0.54	0.00696
Axon guidance mediated by netrin	0.55	0.11	0.00927
FGF signaling pathway	1.24	0.48	0.00929
Interferon-gamma signaling pathway	0.55	0.11	0.0104
Thyrotropin-releasing hormone receptor signaling pathway	0.82	0.27	0.0155