Supplementary Table 1. Gene sets for OXPHOS, PPAR and podocyte genes in the GSEA

HSA00190_OXIDATIVE_PHOSPHORYLAT Enriched in backcross mice with FVB/FVB genotype on chromosome 8

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
row_0	COX7A1	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	263	0.146417409	0.00594456	Yes
row_1	ATP12A	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	284	0.14450869	0.027140278	Yes
row_2	ATP6V1G3	ATP6V1G3	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G3	330	0.139583111	0.045970332	Yes
row_3	ATP4A	ATP4A	ATPase, H+/K+ exchanging, alpha polypeptide	380	0.134138197	0.06369761	Yes
row_4	ATP6V0A4	ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a4	449	0.12729311	0.07914458	Yes
row_5	ATP6V1C2	ATP6V1C2	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2	538	0.121352933	0.092388004	Yes
row_6	ATP6V1B1	ATP6V1B1	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1 (Renal tubular acidosis with deafness)	590	0.117458925	0.10739319	Yes
row_7	COX5A	COX5A	cytochrome c oxidase subunit Va	985	0.097940154	0.097416244	Yes
row_8	ATP5I	ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	1045	0.095254622	0.10845613	Yes
row_9	NDUFB10	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	1175	0.090574965	0.114289336	Yes
row_10	UQCR	UQCR	ubiquinol-cytochrome c reductase, 6.4kDa subunit	1178	0.090515725	0.12823926	Yes
row_11	COX6B2	COX6B2	cytochrome c oxidase subunit VIb polypeptide 2 (testis)	1187	0.090246782	0.14176343	Yes
row_12	ATP6V1A	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	1288	0.087566487	0.14898427	Yes
row_13	COX8A	COX8A	cytochrome c oxidase subunit 8A (ubiquitous)	1308	0.087181441	0.16132788	Yes
row_14	COX6A1	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	1339	0.086401209	0.17284632	Yes
row_15	NDUFB8	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	1443	0.083423562	0.17923085	Yes
row_16	UCRC	UCRC	-	1468	0.082824782	0.19057696	Yes
row_17	NDUFB2	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	1508	0.081944257	0.20082636	Yes
row_18	COX6A2	COX6A2	cytochrome c oxidase subunit VIa polypeptide 2	1558	0.080838859	0.210264	Yes
row_19	NDUFB6	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	1638	0.078940123	0.21748683	Yes
row_20	ATP6V1C1	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	1774	0.075742625	0.22062927	Yes
row_21	NDUFA2	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	1865	0.073461987	0.22629626	Yes
row_22	ATP6V0E1	ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	1935	0.072087929	0.2330932	Yes
row_23	ATP6V0C	ATP6V0C	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	1936	0.072084904	0.24430455	Yes
row_24	NDUFC2	NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	1969	0.071603522	0.25339353	Yes
row_25	NDUFA1	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	2012	0.070787638	0.2617158	Yes
row_26	PPA2	PPA2	pyrophosphatase (inorganic) 2	2165	0.068122745	0.2625854	Yes
row_27	NDUFA13	NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	2180	0.067848481	0.2722421	Yes
row_28	ATP6V1G1	ATP6V1G1	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	2199	0.06754224	0.2815952	Yes
row_29	UQCRFS1	UQCRFS1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	2214	0.067259751	0.29116032	Yes
row_30	ATP5G3	ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	2360	0.065211818	0.2920251	Yes
row_31	ATP5L	ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	2381	0.064975306	0.300851	Yes
row_32	NDUFS8	NDUFS8	NADH dehydrogenase (ubiquinone)	2544	0.062724061	0.3002411	Yes

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
			Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)				
row_33	NDUFA5	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	2648	0.061466325	0.30321062	Yes
row_34	ATP5O	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	2688	0.060708564	0.31015724	Yes
row_35	COX4I1	COX4I1	cytochrome c oxidase subunit IV isoform 1	2745	0.059883062	0.31588775	Yes
row_36	NDUFA3	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	2778	0.059420981	0.323082	Yes
row_37	COX6B1	COX6B1	cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)	2793	0.059255853	0.33140227	Yes
row_38	ATP6V0B	ATP6V0B	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	2798	0.05913388	0.34034342	Yes
row_39	NDUFB3	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	2809	0.059039596	0.34888598	Yes
row_40	ATP6V1H	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	2860	0.058267698	0.35474917	Yes
row_41	COX17	COX17	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	2947	0.057131935	0.3581323	Yes
row_42	NDUFAB1	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	2980	0.056749132	0.364911	Yes
row_43	NDUFS7	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	3094	0.055093866	0.36624956	Yes
row_44	COX7A2	COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	3100	0.055025637	0.37448776	Yes
row_45	NDUFB7	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	3106	0.054933064	0.3827116	Yes
row_46	SDHD	SDHD	succinate dehydrogenase complex, subunit D, integral membrane protein	3114	0.054735865	0.39077675	Yes
row_47	COX6C	COX6C	cytochrome c oxidase subunit VIc	3135	0.054513697	0.39797556	Yes
row_48	SDHB	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	3169	0.054155197	0.40428686	Yes
row_49	NDUFA9	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	3223	0.053435154	0.40920648	Yes
row_50	ATP5J2	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	3320	0.052301317	0.41119844	Yes
row_51	ATP5G1	ATP5G1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	3358	0.05187875	0.41689974	Yes
row_52	ATP6V1D	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	3392	0.051405035	0.4227833	Yes
row_53	NDUFA11	NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	3398	0.051321279	0.43044534	Yes
row_54	ATP5G2	ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	3414	0.051111236	0.4374349	Yes
row_55	NDUFB11	NDUFB11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa	3482	0.050515436	0.44100466	Yes
row_56	NDUFB5	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	3495	0.050409045	0.44807696	Yes
row_57	ATP6V1F	ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	3530	0.050050516	0.45368585	Yes
row_58	COX10	COX10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	3653	0.048669662	0.45344943	Yes
row_59	NDUFC1	NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	3655	0.048664346	0.4609542	Yes
row_60	NDUFB9	NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	3657	0.048647691	0.4684564	Yes
row_61	NDUFS6	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	3826	0.046677671	0.4649669	Yes
row_62	ATP6V1E1	ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1	3863	0.046266485	0.4698593	Yes
row_63	ATP5D	ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	3934	0.045618113	0.4724754	Yes
row_64	ATP6V1B2	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	4001	0.045052744	0.47525954	Yes

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
row_65	UQCRQ	UQCRQ	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	4049	0.044544566	0.4791803	Yes
row_66	ATP5F1	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	4114	0.043945294	0.48192015	Yes
row_67	COX7C	COX7C	cytochrome c oxidase subunit VIIc	4174	0.043163523	0.48485833	Yes
row_68	CYC1	CYC1	cytochrome c-1	4195	0.042933811	0.49025613	Yes
row_69	NDUFV3	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	4318	0.041829336	0.48895583	Yes
row_70	COX15	COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	4379	0.041227683	0.49152896	Yes
row_71	NDUFS2	NDUFS2	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	4519	0.040029161	0.48886093	No
row_72	NDUFS3	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	4883	0.036457434	0.4713051	No
row_73	ATP6V0D1	ATP6V0D1	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	4896	0.036312252	0.47618493	No
row_74	UQCRC1	UQCRC1	ubiquinol-cytochrome c reductase core protein I	5073	0.034766909	0.4703311	No
row_75	ATP5B	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	5088	0.034618415	0.4748195	No
row_76	NDUFV1	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	5105	0.034508523	0.47916287	No
row_77	ATP6AP1	ATP6AP1	ATPase, H+ transporting, lysosomal accessory protein 1	5220	0.033605803	0.47709545	No
row_78	COX7B	COX7B	cytochrome c oxidase subunit VIIb	5485	0.031109437	0.4650422	No
row_79	NDUFA6	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	5504	0.031013148	0.46871397	No
row_80	NDUFA7	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	5626	0.029982839	0.46563518	No
row_81	UQCRC2	UQCRC2	ubiquinol-cytochrome c reductase core protein II	5746	0.029003846	0.46253207	No
row_82	ATP5A1	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	5756	0.028952152	0.46645916	No
row_83	NDUFS5	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)	5797	0.028591825	0.4683467	No
row_84	COX5B	COX5B	cytochrome c oxidase subunit Vb	5828	0.028301094	0.47082883	No
row_85	ATP5J	ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	6040	0.026580039	0.4614623	No
row_86	NDUFS1	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	6068	0.0263699	0.463836	No
row_87	NDUFA4	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	6077	0.026281144	0.46741164	No
row_88	COX4I2	COX4I2	cytochrome c oxidase subunit IV isoform 2 (lung)	6258	0.024969779	0.45977813	No
row_89	SDHC	SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	6384	0.023978684	0.45550957	No
row_90	ATP5C1	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	6472	0.023214167	0.4535535	No
row_91	SDHA	SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	6557	0.022620434	0.45169702	No
row_92	NDUFA8	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	6776	0.020870605	0.4409946	No
row_93	ATP6V0D2	ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	6862	0.020299235	0.43871313	No
row_94	ATP6V0A2	ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit a2	6882	0.020076033	0.44061986	No
row_95	NDUFS4	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	6916	0.01980632	0.44158888	No
row_96	NDUFV2	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	6932	0.019679364	0.44368982	No
row_97	ATP4B	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	6992	0.019276714	0.4429129	No
row_98	NDUFA10	NDUFA10	NADH dehydrogenase (ubiquinone) 1	7088	0.01862363	0.43973097	No

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
			alpha subcomplex, 10, 42kDa				
row_99	ATP6V1G2	ATP6V1G2	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2	7178	0.017916573	0.436823	No
row_100	UQCRB	UQCRB	ubiquinol-cytochrome c reductase binding protein	7418	0.016037006	0.42402515	No
row_101	NDUFA12	NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	7914	0.012351546	0.3942743	No
row_102	ATP6V1E2	ATP6V1E2	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E2	7930	0.012237792	0.39521787	No
row_103	ND1	ND1	mitochondrially encoded NADH dehydrogenase 1	8584	0.007557465	0.35461196	No
row_104	CYTB	CYTB	mitochondrially encoded cytochrome b	9138	0.003745858	0.3198116	No
row_105	ND3	ND3	mitochondrially encoded NADH dehydrogenase 3	9219	0.003203547	0.31519118	No
row_106	ATP6	ATP6	mitochondrially encoded ATP synthase 6	9233	0.003114851	0.31484386	No
row_107	ND5	ND5	mitochondrially encoded NADH dehydrogenase 5	9280	0.002705407	0.31232136	No
row_108	COX2	COX2	mitochondrially encoded cytochrome c oxidase II	9394	0.001940248	0.30539298	No
row_109	COX1	COX1	mitochondrially encoded cytochrome c oxidase I	9797	-0.001130274	0.27984735	No
row_110	ND4L	ND4L	mitochondrially encoded NADH 4L	11005	-0.011678575	0.2044355	No
row_111	ATP6V0A1	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	11309	-0.014455482	0.18729672	No
row_112	NDUFA4L2	NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	12097	-0.023736797	0.14063339	No
row_113	TCIRG1	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3	14523	-0.092372634	-1.60E-04	No
row_114	PPA1	PPA1	pyrophosphatase (inorganic) 1	15145	-0.176813647	-0.01239427	No
row_115	LHPP	LHPP	-	15466	-0.325703025	0.017787462	No

HSA03320_PPAR_SIGNALING_PATHWAY Enriched in backcross mice with FVB/B6 genotype on chromosome 8

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
row_0	FABP3	FABP3	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	184	0.156955391	0.006339061	No
row_1	FABP7	FABP7	fatty acid binding protein 7, brain	260	0.146765053	0.018457001	No
row_2	AQP7	AQP7	aquaporin 7	356	0.137024879	0.028177576	No
row_3	ACOX3	ACOX3	acyl-Coenzyme A oxidase 3, pristanoyl	1518	0.081703998	-0.03646607	No
row_4	GK	GK	glycerol kinase	2060	0.069891594	-0.062924184	No
row_5	CPT1B	CPT1B	carnitine palmitoyltransferase 1B (muscle)	2117	0.068694092	-0.05858514	No
row_6	FABP6	FABP6	fatty acid binding protein 6, ileal (gastrotropin)	3582	0.049399152	-0.14627552	No
row_7	ACSL6	ACSL6	acyl-CoA synthetase long-chain family member 6	4096	0.044154759	-0.17391159	No
row_8	RXRB	RXRB	retinoid X receptor, beta	4580	0.039380409	-0.20018397	No
row_9	CPT1C	CPT1C	carnitine palmitoyltransferase 1C	5186	0.033813104	-0.2348791	No
row_10	DBI	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	5779	0.028722875	-0.26933125	No
row_11	MMP1	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	6171	0.025530715	-0.2913305	No
row_12	UCP1	UCP1	uncoupling protein 1 (mitochondrial, proton carrier)	6657	0.021833958	-0.31975114	No
row_13	PDPK1	PDPK1	3-phosphoinositide dependent protein kinase-1	7400	0.016148843	-0.36521888	No
row_14	CPT2	CPT2	carnitine palmitoyltransferase II	7810	0.013249605	-0.38978052	No
row_15	GK2	GK2	glycerol kinase 2	7901	0.012510447	-0.39408034	No
row_16	SLC27A2	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	7924	0.012266201	-0.39407098	No
row_17	ILK	ILK	integrin-linked kinase	8025	0.01165052	-0.39910766	No
row_18	ME1	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	8169	0.010475153	-0.4070224	No
row_19	ACADL	ACADL	acyl-Coenzyme A dehydrogenase, long chain	8260	0.00986198	-0.41162717	No
row_20	CD36	CD36	CD36 molecule (thrombospondin receptor)	8523	0.007935122	-0.42742467	No
row_21	UBC	UBC	ubiquitin C	8530	0.007886427	-0.42689916	No
row_22	ACADM	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	8796	0.006091108	-0.44310036	No
row_23	SLC27A6	SLC27A6	solute carrier family 27 (fatty acid transporter), member 6	9049	0.004355448	-0.45867226	No
row_24	EHHADH	EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	9172	0.003494015	-0.4660515	No
row_25	SORBS1	SORBS1	sorbin and SH3 domain containing 1	9179	0.003430893	-0.4660391	No
row_26	PPARD	PPARD	peroxisome proliferative activated receptor, delta	9272	0.002763955	-0.47158888	No
row_27	CPT1A	CPT1A	carnitine palmitoyltransferase 1A (liver)	9601	4.44E-04	-0.49245882	No
row_28	ACSL4	ACSL4	acyl-CoA synthetase long-chain family member 4	9715	-5.65E-04	-0.4996013	No
row_29	OLR1	OLR1	oxidised low density lipoprotein (lectin-like) receptor 1	9982	-0.002729255	-0.5162535	No
row_30	SLC27A4	SLC27A4	solute carrier family 27 (fatty acid transporter), member 4	10457	-0.006595494	-0.5457274	No
row_31	PCK2	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	11012	-0.011719294	-0.5797139	No
row_32	SLC27A1	SLC27A1	solute carrier family 27 (fatty acid transporter), member 1	11536	-0.016875587	-0.6111293	No
row_33	PCK1	PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	11849	-0.020470466	-0.6286724	No
row_34	ACSL3	ACSL3	acyl-CoA synthetase long-chain family member 3	12156	-0.024375826	-0.645383	No
row_35	LPL	LPL	lipoprotein lipase	12163	-	-0.64294946	No

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					0.024454838		
row_36	CYP4A11	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	12164	-0.02445963	-0.64013267	No
row_37	ACOX1	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	12298	-0.026169602	-0.64560217	No
row_38	FADS2	FADS2	fatty acid desaturase 2	12917	-0.036361918	-0.6808329	No
row_39	CYP4A22	CYP4A22	cytochrome P450, family 4, subfamily A, polypeptide 22	13336	-0.044825472	-0.7023323	No
row_40	RXRG	RXRG	retinoid X receptor, gamma	13398	-0.046121597	-0.7009117	No
row_41	ACAA1	ACAA1	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	13620	-0.051785085	-0.7090442	No
row_42	FABP4	FABP4	fatty acid binding protein 4, adipocyte	13981	-0.063642614	-0.72467715	Yes
row_43	PLIN	PLIN	perilipin	14061	-0.066581093	-0.72204846	Yes
row_44	ACOX2	ACOX2	acyl-Coenzyme A oxidase 2, branched chain	14063	-0.066680446	-0.7144332	Yes
row_45	NR1H3	NR1H3	nuclear receptor subfamily 1, group H, member 3	14233	-0.074696057	-0.7166105	Yes
row_46	ADIPOQ	ADIPOQ	adiponectin, C1Q and collagen domain containing	14247	-0.075301267	-0.7087679	Yes
row_47	ACSL1	ACSL1	acyl-CoA synthetase long-chain family member 1	14355	-0.081421435	-0.7062161	Yes
row_48	CYP27A1	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	14441	-0.086327061	-0.7016961	Yes
row_49	RXRA	RXRA	retinoid X receptor, alpha	14477	-0.088543884	-0.69373167	Yes
row_50	ACSL5	ACSL5	acyl-CoA synthetase long-chain family member 5	14782	-0.117919549	-0.6995421	Yes
row_51	PPARA	PPARA	peroxisome proliferative activated receptor, alpha	14812	-0.122051336	-0.6873362	Yes
row_52	PLTP	PLTP	phospholipid transfer protein	14971	-0.14311789	-0.6809323	Yes
row_53	ANGPTL4	ANGPTL4	angiopoietin-like 4	15070	-0.158049285	-0.66898185	Yes
row_54	SCP2	SCP2	sterol carrier protein 2	15095	-0.162264138	-0.6518261	Yes
row_55	PPARG	PPARG	peroxisome proliferative activated receptor, gamma	15258	-0.207940832	-0.6382122	Yes
row_56	HMGCS2	HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	15421	-0.289545238	-0.61520064	Yes
row_57	SCD	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	15560	-0.418036878	-0.5758609	Yes
row_58	CYP8B1	CYP8B1	cytochrome P450, family 8, subfamily B, polypeptide 1	15576	-0.433613658	-0.526882	Yes
row_59	APOA5	APOA5	apolipoprotein A-V	15603	-0.468184412	-0.47462344	Yes
row_60	FABP2	FABP2	fatty acid binding protein 2, intestinal	15616	-0.482269734	-0.4198498	Yes
row_61	APOC3	APOC3	apolipoprotein C-III	15631	-0.499563843	-0.36321217	Yes
row_62	CYP7A1	CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	15676	-0.565514505	-0.300893	Yes
row_63	APOA2	APOA2	apolipoprotein A-II	15682	-0.569992483	-0.23557062	Yes
row_64	SLC27A5	SLC27A5	solute carrier family 27 (fatty acid transporter), member 5	15690	-0.5886603	-0.16822597	Yes
row_65	APOA1	APOA1	apolipoprotein A-I	15724	-0.695596039	-0.0902248	Yes
row_66	FABP1	FABP1	fatty acid binding protein 1, liver	15741	-0.793983042	1.91E-04	Yes

Hand curated gene set of podocyte expressed genes

Symbol	Description	Location
Col4a4	collagen, type IV, alpha 4	1 C5
Usp40	ubiquitin specific peptidase 40	1 D
Itgb5	integrin beta 5	16 B3
Scyl3	SCY1-like 3 (S. cerevisiae)	1 H2.2
Tcf21	transcription factor 21	10 A3|10 16.0 cM
Wt1	Wilms tumor homolog	2 E|2 58.0 cM
Timp3	tissue inhibitor of metalloproteinase 3	10 C1-D1|10 47.0 cM
Adcy1	adenylate cyclase 1	11 A2
Podnl1	podocan-like 1	8 C3
Mapt	microtubule-associated protein tau	11 E1|11 64.0 cM
Sdk2	sidekick homolog 2 (chicken)	11 E2
C1qtnf1	C1q and tumor necrosis factor related protein 1	11 E2
2310051M13Rik	RIKEN cDNA 2310051M13 gene	13 B2
Synpo2l	synaptopodin 2-like	14 A3
Podxl2	podocalyxin-like 2	6 D1
Bmp4	bone morphogenetic protein 4	14 C1|14 15.0 cM
Galnt10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10	11 B1.3
Fyb	FYN binding protein	15 A1
Clic3	chloride intracellular channel 3	2 A3
Myh9	myosin, heavy polypeptide 9, non-muscle	15 E1|15 43.3 cM
Rtn4r	reticulon 4 receptor	---
Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome	16 A3|16 11.18 cM
Rab3b	RAB3B, member RAS oncogene family	4 C7
Plat	plasminogen activator, tissue	8 A2|8 9.0 cM
Cd2ap	CD2-associated protein	17 B3
Vegfa	vascular endothelial growth factor A	17 C|17 24.2 cM
Ehd3	EH-domain containing 3	17 43.25 cM
Plekhh2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	17 E4
Sncaip	synuclein, alpha interacting protein (synphilin)	18 D1
Synpo	synaptopodin	18 D3
Plce1	phospholipase C, epsilon 1	19 D1
Vim	vimentin	2 A2|2 7.0 cM
Nrp1	neuropilin 1	8 E|8 73.0 cM
Ralgps1	Ral GEF with PH domain and SH3 binding motif 1	2 B
Angptl2	angiopoietin-like 2	2 B
Lmx1b	LIM homeobox transcription factor 1 beta	2 B|2 21.0 cM
Lrp2	low density lipoprotein receptor-related protein 2	2 C2|2 40.0 cM
Cd59a	CD59a antigen	2 55.0 cM
Nrp1	neuropilin 1	8 E|8 73.0 cM
Ptpro	protein tyrosine phosphatase, receptor type, O	6 G1
Trpc3	transient receptor potential cation channel, subfamily C, member 3	3 B|3 18.2 cM

Symbol	Description	Location
Schip1	schwannomin interacting protein 1	3 E2
Schip1	schwannomin interacting protein 1	3 E2
Rhpn1	rhophilin, Rho GTPase binding protein 1	15 E1
Synpo2	synaptopodin 2	3 G3
Podn	podocan	4 C7
Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	1 D
Pdpn	podoplanin	4 E1
Mmp23	matrix metallopeptidase 23	4 E2
Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	5 A1
Arrb1	arrestin, beta 1	7 E2|7 50.0 cM
Ubc	ubiquitin C	5 G1.1|5 64.0 cM
Sdk1	sidekick homolog 1 (chicken)	5 G2
Glcci1	glucocorticoid induced transcript 1	6 A1
Podxl	podocalyxin-like	6 A3.3|6 10.0 cM
Col4a3	collagen, type IV, alpha 3	1 C5
Pax2	paired box gene 2	19 C3|19 43.0 cM
Robo2	roundabout homolog 2 (Drosophila)	16 C3.1
Kirrel2	kin of IRRE like 2 (Drosophila)	7 B1
Nphs1	nephrosis 1 homolog, nephrin (human)	---
Kirrel	kin of IRRE like (Drosophila)	3 F1
Ypel3	yippee-like 3 (Drosophila)	7 F3
Trib2	tribbles homolog 2 (Drosophila)	12 A1.1
Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	10 A2
Vegfc	vascular endothelial growth factor C	8 B3
Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	7 F5|7 69.49 cM
2310066E14Rik	RIKEN cDNA 2310066E14 gene	8 D3
Foxc2	forkhead box C2	8 E1|8 65.5 cM
Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	7 F5|7 69.49 cM
Trpc6	transient receptor potential cation channel, subfamily C, member 6	9 A1|9 1.0 cM
Kirrel3	kin of IRRE like 3 (Drosophila)	9 A4
Actn4	actinin alpha 4	7 A3
Efnb1	ephrin B1	X D|X 37.0 cM
Nphs2	nephrosis 2 homolog, podocin (human)	1 G3
Plaur	plasminogen activator, urokinase receptor	7 A3
Itga3	integrin alpha 3	11 D|11 56.0 cM
Itgb4	integrin beta 4	11 E2|11 76.0 cM
Khdrbs3	KH domain containing, RNA binding, signal transduction associated 3	15 D3|15 37.5 cM
Fat1	FAT tumor suppressor homolog 1 (Drosophila)	8 B1.1|8 25.0 cM
Plcb1	phospholipase C, beta 1	2 F3|2 76.7 cM
Plcg1	phospholipase C, gamma 1	2 H2|2 92.0 cM

Additional GSEA methods

We performed GSEA by comparing the arrays between mice with FVB/FVB or FVB/B6 genotypes across chromosome 8 (N=5 for each genotype). To detect empiric significance of enrichment results, we performed 10,000 permutation of gene labels in the arrays. As recommended, empiric p-values were corrected based on the Family-Wise Error rate (FWER), with FWER $p<0.05$ considered significant evidence of enrichment. To confirm enrichment for OXPHOS and PPAR signaling pathways, we re-analyzed the microarray data using three alternative MSD gene sets representing these pathways (MOOTHA_VOXPHOS, PPARA_PATHWAY, PPARG_PATHWAY). To calculate correlation of expression of positional candidates with the oxidative phosphorylation and PPAR signaling pathways, we identified the leading edge subset for each pathway, as determined by GSEA (supplementary table 3). The expression of each component of the leading edge subset was standardized to a mean of 0 + 1 and a mean value was calculated for the OXPHOS and PPAR signaling pathways. We next calculated the Spearman correlation coefficient between each positional candidate and the mean expression for the OXPHOS and PPAR signaling pathways.