

Table S4. Functional enrichment of DRAL switch-resistant genes in WAT.

GO.ID	GO Term	Annotated ge	Significant ge	Enrichment	PValue	Ensembl ID
GO:0032981	mitochondria	41	11	1.9	1.60E-06	ENSMUSG000
GO:0055114	oxidation-red	584	62	27.01	2.60E-06	ENSMUSG000
GO:0042775	mitochondria	47	10	2.17	4.50E-05	ENSMUSG000
GO:0006911	phagocytosis,	30	7	1.39	0.00035	ENSMUSG000
GO:0044281	small molecu	1067	91	49.36	0.00053	ENSMUSG000
GO:0045762	positive regul	10	4	0.46	0.00076	ENSMUSG000
GO:1902624	positive regul	17	5	0.79	0.00081	ENSMUSG000
GO:0044243	multicellular r	17	5	0.79	0.00081	ENSMUSG000
GO:0022904	respiratory el	65	15	3.01	0.00098	ENSMUSG000
GO:0002691	regulation of	18	5	0.83	0.00107	ENSMUSG000
GO:0007610	behavior	249	23	11.52	0.00119	ENSMUSG000
GO:0072593	reactive oxyg	162	17	7.49	0.0013	ENSMUSG000
GO:0007188	adenylate cyc	37	7	1.71	0.00133	ENSMUSG000
GO:0016052	carbohydrate	73	10	3.38	0.00183	ENSMUSG000
GO:0006650	glycerophosp	127	14	5.87	0.00215	ENSMUSG000
GO:0006796	phosphate-cc	1666	117	77.06	0.00251	ENSMUSG000
GO:0045471	response to e	31	6	1.43	0.00259	ENSMUSG000
GO:0006839	mitochondria	173	17	8	0.00265	ENSMUSG000
GO:0015986	ATP synthesis	22	5	1.02	0.00283	ENSMUSG000
GO:0006665	sphingolipid r	65	9	3.01	0.00284	ENSMUSG000
GO:0090151	establishmen	14	4	0.65	0.00312	ENSMUSG000
GO:0030316	osteoclast dif	54	8	2.5	0.00314	ENSMUSG000
GO:0042391	regulation of	147	15	6.8	0.00323	ENSMUSG000
GO:0046173	polyol biosyn	33	6	1.53	0.00361	ENSMUSG000
GO:0055082	cellular chem	355	28	16.42	0.00392	ENSMUSG000
GO:1905517	macrophage i	24	5	1.11	0.00423	ENSMUSG000
GO:0030335	positive regul	296	28	13.69	0.00447	ENSMUSG000
GO:0046503	glycerolipid c	25	5	1.16	0.0051	ENSMUSG000
GO:0090407	organophosp	268	29	12.4	0.00525	ENSMUSG000
GO:0002446	neutrophil m	16	4	0.74	0.00527	ENSMUSG000
GO:0032370	positive regul	36	6	1.67	0.00565	ENSMUSG000
GO:0006954	inflammatory	299	24	13.83	0.00591	ENSMUSG000
GO:0032496	response to li	143	14	6.61	0.00631	ENSMUSG000
GO:0015711	organic anion	154	17	7.12	0.00636	ENSMUSG000
GO:0032655	regulation of	27	5	1.25	0.00718	ENSMUSG000
GO:0045453	bone resorpti	38	6	1.76	0.00741	ENSMUSG000
GO:0043299	leukocyte deę	38	6	1.76	0.00741	ENSMUSG000
GO:0051384	response to g	38	6	1.76	0.00741	ENSMUSG000
GO:0030593	neutrophil ch	38	6	1.76	0.00741	ENSMUSG000
GO:0002274	myeloid leuk	99	13	4.58	0.00747	ENSMUSG000
GO:0006929	substrate-deę	18	4	0.83	0.00823	ENSMUSG000
GO:0007618	mating	18	4	0.83	0.00823	ENSMUSG000
GO:0006766	vitamin meta	28	5	1.3	0.00841	ENSMUSG000
GO:0030301	cholesterol tr	39	6	1.8	0.00842	ENSMUSG000

GO:0070228	regulation of	39	6	1.8	0.00842	ENSMUSG000
GO:0015698	inorganic anic	39	6	1.8	0.00842	ENSMUSG000
GO:1901655	cellular respo	39	6	1.8	0.00842	ENSMUSG000
GO:0010821	regulation of	133	13	6.15	0.00845	ENSMUSG000
GO:0042493	response to c	119	12	5.5	0.00881	ENSMUSG000
GO:0034104	negative regu	10	3	0.46	0.00924	ENSMUSG000
GO:0002283	neutrophil ac	10	3	0.46	0.00924	ENSMUSG000
GO:1902932	positive regul	10	3	0.46	0.00924	ENSMUSG000
GO:0043090	amino acid in	10	3	0.46	0.00924	ENSMUSG000
GO:0045087	innate immur	345	26	15.96	0.00951	ENSMUSG000
GO:0007160	cell-matrix ad	121	12	5.6	0.01001	ENSMUSG000
GO:0090077	foam cell diff	19	4	0.88	0.01005	ENSMUSG000
GO:0097164	ammonium ic	80	9	3.7	0.01123	ENSMUSG000
GO:0033002	muscle cell pr	124	12	5.74	0.01204	ENSMUSG000
GO:0032715	negative regu	20	4	0.93	0.01212	ENSMUSG000
GO:1902895	positive regul	20	4	0.93	0.01212	ENSMUSG000
GO:0033622	integrin activ	11	3	0.51	0.01228	ENSMUSG000
GO:0046475	glycerophosp	11	3	0.51	0.01228	ENSMUSG000
GO:0032695	negative regu	11	3	0.51	0.01228	ENSMUSG000
GO:0006122	mitochondria	11	3	0.51	0.01228	ENSMUSG000
GO:0006123	mitochondria	11	3	0.51	0.01228	ENSMUSG000
GO:0042133	neurotransmi	11	3	0.51	0.01228	ENSMUSG000
GO:0043436	oxoacid meta	548	37	25.35	0.01259	ENSMUSG000
GO:0055067	monovalent i	68	8	3.15	0.01273	ENSMUSG000
GO:0033627	cell adhesion	31	5	1.43	0.01299	ENSMUSG000
GO:0043647	inositol phosp	31	5	1.43	0.01299	ENSMUSG000
GO:0070374	positive regul	96	10	4.44	0.013	ENSMUSG000
GO:0006082	organic acid r	552	37	25.53	0.014	ENSMUSG000
GO:0031623	receptor inte	56	7	2.59	0.0141	ENSMUSG000
GO:0007612	learning	56	7	2.59	0.0141	ENSMUSG000
GO:0006692	prostanoid m	21	4	0.97	0.01444	ENSMUSG000
GO:0006693	prostaglandir	21	4	0.97	0.01444	ENSMUSG000
GO:0007200	phospholipas	21	4	0.97	0.01444	ENSMUSG000
GO:0005996	monosacchar	174	15	8.05	0.01478	ENSMUSG000
GO:0015914	phospholipid	32	5	1.48	0.01482	ENSMUSG000
GO:0061045	negative regu	32	5	1.48	0.01482	ENSMUSG000
GO:0006672	ceramide me	44	6	2.04	0.01502	ENSMUSG000
GO:0015748	organophosp	44	6	2.04	0.01502	ENSMUSG000
GO:0034220	ion transmem	315	27	14.57	0.01529	ENSMUSG000
GO:0009185	ribonucleosid	57	7	2.64	0.01545	ENSMUSG000
GO:0070230	positive regul	12	3	0.56	0.01582	ENSMUSG000
GO:0007617	mating behav	12	3	0.56	0.01582	ENSMUSG000
GO:1990542	mitochondria	12	3	0.56	0.01582	ENSMUSG000
GO:0001952	regulation of	71	8	3.28	0.01626	ENSMUSG000
GO:0045806	negative regu	33	5	1.53	0.01683	ENSMUSG000
GO:2000108	positive regul	22	4	1.02	0.01701	ENSMUSG000

GO:0055085	transmembra	460	35	21.28	0.01737	ENSMUSG000
GO:0097191	extrinsic apo	146	13	6.75	0.01755	ENSMUSG000
GO:0006638	neutral lipid r	72	8	3.33	0.01758	ENSMUSG000
GO:0006639	acylglycerol n	72	8	3.33	0.01758	ENSMUSG000
GO:2000379	positive regul	59	7	2.73	0.01844	ENSMUSG000
GO:0003014	renal system	46	6	2.13	0.01846	ENSMUSG000
GO:0001678	cellular gluco	73	8	3.38	0.01897	ENSMUSG000
GO:0097006	regulation of	34	5	1.57	0.019	ENSMUSG000
GO:0045670	regulation of	34	5	1.57	0.019	ENSMUSG000
GO:0031589	cell-substrate	196	16	9.07	0.01935	ENSMUSG000
GO:0048246	macrophage	23	4	1.06	0.01986	ENSMUSG000
GO:0070232	regulation of	23	4	1.06	0.01986	ENSMUSG000
GO:0044030	regulation of	13	3	0.6	0.01987	ENSMUSG000
GO:1905523	positive regul	13	3	0.6	0.01987	ENSMUSG000
GO:0071624	positive regul	13	3	0.6	0.01987	ENSMUSG000
GO:0090023	positive regul	13	3	0.6	0.01987	ENSMUSG000
GO:0034390	smooth musc	13	3	0.6	0.01987	ENSMUSG000
GO:0034391	regulation of	13	3	0.6	0.01987	ENSMUSG000
GO:0030168	platelet activa	60	7	2.78	0.02007	ENSMUSG000
GO:0071804	cellular potas	47	6	2.17	0.02036	ENSMUSG000
GO:0071805	potassium ion	47	6	2.17	0.02036	ENSMUSG000
GO:0019752	carboxylic aci	513	34	23.73	0.02105	ENSMUSG000
GO:0002224	toll-like recep	61	7	2.82	0.02181	ENSMUSG000
GO:0046434	organophosp	61	7	2.82	0.02181	ENSMUSG000
GO:0006873	cellular ion ho	284	21	13.14	0.02256	ENSMUSG000
GO:0043410	positive regul	250	19	11.56	0.02271	ENSMUSG000
GO:0048660	regulation of	90	9	4.16	0.0229	ENSMUSG000
GO:0072595	maintenance	24	4	1.11	0.02299	ENSMUSG000
GO:0007007	inner mitoch	24	4	1.11	0.02299	ENSMUSG000
GO:0007611	learning or m	105	10	4.86	0.02311	ENSMUSG000
GO:0050801	ion homeosta	355	25	16.42	0.02345	ENSMUSG000
GO:0046488	phosphatidyl	76	8	3.52	0.02363	ENSMUSG000
GO:0050805	negative regu	36	5	1.67	0.02389	ENSMUSG000
GO:0042116	macrophage	36	5	1.67	0.02389	ENSMUSG000
GO:0006812	cation transp	454	34	21	0.02436	ENSMUSG000
GO:0002755	MyD88-depen	14	3	0.65	0.02444	ENSMUSG000
GO:0045579	positive regul	14	3	0.65	0.02444	ENSMUSG000
GO:0002693	positive regul	14	3	0.65	0.02444	ENSMUSG000
GO:0002675	positive regul	14	3	0.65	0.02444	ENSMUSG000
GO:0006629	lipid metabol	661	53	30.58	0.02557	ENSMUSG000
GO:0006821	chloride trans	25	4	1.16	0.0264	ENSMUSG000
GO:0001953	negative regu	25	4	1.16	0.0264	ENSMUSG000
GO:0051453	regulation of	37	5	1.71	0.0266	ENSMUSG000
GO:0098771	inorganic ion	324	23	14.99	0.02675	ENSMUSG000
GO:0050764	regulation of	50	6	2.31	0.02686	ENSMUSG000
GO:2001057	reactive nitro	50	6	2.31	0.02686	ENSMUSG000

GO:0048659	smooth musc	93	9	4.3	0.02767	ENSMUSG000
GO:0030036	actin cytoskel	361	25	16.7	0.02806	ENSMUSG000
GO:0030029	actin filament	398	27	18.41	0.02899	ENSMUSG000
GO:0030004	cellular monoc	51	6	2.36	0.0293	ENSMUSG000
GO:0010822	positive regul	94	9	4.35	0.0294	ENSMUSG000
GO:2000191	regulation of	15	3	0.69	0.02953	ENSMUSG000
GO:0090022	regulation of	15	3	0.69	0.02953	ENSMUSG000
GO:0007628	adult walking	15	3	0.69	0.02953	ENSMUSG000
GO:0030574	collagen catal	15	3	0.69	0.02953	ENSMUSG000
GO:0034389	lipid particle c	15	3	0.69	0.02953	ENSMUSG000
GO:0032958	inositol phosph	15	3	0.69	0.02953	ENSMUSG000
GO:0009132	nucleoside di	65	7	3.01	0.02977	ENSMUSG000
GO:0019882	antigen proce	65	7	3.01	0.02977	ENSMUSG000
GO:1901135	carbohydrate	624	52	28.86	0.02996	ENSMUSG000
GO:1902893	regulation of	26	4	1.2	0.03009	ENSMUSG000
GO:0015980	energy deriva	178	25	8.23	0.03017	ENSMUSG000
GO:0009161	ribonucleosid	180	24	8.33	0.03067	ENSMUSG000
GO:0009123	nucleoside m	180	24	8.33	0.03067	ENSMUSG000
GO:0005975	carbohydrate	336	29	15.54	0.03092	ENSMUSG000
GO:0008654	phospholipid	95	9	4.39	0.0312	ENSMUSG000
GO:0007162	negative regu	142	12	6.57	0.03146	ENSMUSG000
GO:0032787	monocarboxy	312	22	14.43	0.03185	ENSMUSG000
GO:0016310	phosphorylat	1215	76	56.2	0.03195	ENSMUSG000
GO:0002757	immune resp	175	14	8.1	0.03205	ENSMUSG000
GO:0035556	intracellular s	1344	76	62.17	0.03234	ENSMUSG000
GO:1903035	negative regu	39	5	1.8	0.03261	ENSMUSG000
GO:0010038	response to n	127	11	5.87	0.03294	ENSMUSG000
GO:0030003	cellular cation	278	20	12.86	0.033	ENSMUSG000
GO:0050776	regulation of	367	25	16.98	0.03332	ENSMUSG000
GO:0098655	cation transp	251	22	11.61	0.0337	ENSMUSG000
GO:0000266	mitochondria	27	4	1.25	0.03408	ENSMUSG000
GO:0071675	regulation of	27	4	1.25	0.03408	ENSMUSG000
GO:0006091	generation of	230	28	10.64	0.03429	ENSMUSG000
GO:0032675	regulation of	67	7	3.1	0.03441	ENSMUSG000
GO:0008202	steroid metal	128	11	5.92	0.03461	ENSMUSG000
GO:0090200	positive regul	16	3	0.74	0.03512	ENSMUSG000
GO:0071827	plasma lipopr	16	3	0.74	0.03512	ENSMUSG000
GO:0007215	glutamate rec	16	3	0.74	0.03512	ENSMUSG000
GO:0090659	walking beha	16	3	0.74	0.03512	ENSMUSG000
GO:0046461	neutral lipid c	16	3	0.74	0.03512	ENSMUSG000
GO:0046464	acylglycerol c	16	3	0.74	0.03512	ENSMUSG000
GO:0006953	acute-phase r	16	3	0.74	0.03512	ENSMUSG000
GO:2000114	regulation of	16	3	0.74	0.03512	ENSMUSG000
GO:0097242	amyloid-beta	16	3	0.74	0.03512	ENSMUSG000
GO:1903306	negative regu	16	3	0.74	0.03512	ENSMUSG000
GO:0001934	positive regul	497	32	22.99	0.03521	ENSMUSG000

GO:0051899	membrane de	40	5	1.85	0.03591	ENSMUSG000
GO:0045428	regulation of	40	5	1.85	0.03591	ENSMUSG000
GO:0001836	release of cyt	40	5	1.85	0.03591	ENSMUSG000
GO:0071674	mononuclear	40	5	1.85	0.03591	ENSMUSG000
GO:0048002	antigen proce	40	5	1.85	0.03591	ENSMUSG000
GO:1901136	carbohydrate	68	7	3.15	0.0369	ENSMUSG000
GO:0055080	cation homec	317	22	14.66	0.03705	ENSMUSG000
GO:0009179	purine ribonu	54	6	2.5	0.03747	ENSMUSG000
GO:0009135	purine nuclec	54	6	2.5	0.03747	ENSMUSG000
GO:0051592	response to c	54	6	2.5	0.03747	ENSMUSG000
GO:0010660	regulation of	54	6	2.5	0.03747	ENSMUSG000
GO:0070585	protein locali	113	13	5.23	0.03749	ENSMUSG000
GO:2000377	regulation of	114	10	5.27	0.03795	ENSMUSG000
GO:0031399	regulation of	979	57	45.29	0.03819	ENSMUSG000
GO:0044282	small molecu	163	13	7.54	0.03876	ENSMUSG000
GO:0032504	multicellular	301	21	13.92	0.03907	ENSMUSG000
GO:0006626	protein targe	99	9	4.58	0.0392	ENSMUSG000
GO:0002764	immune resp	180	14	8.33	0.03929	ENSMUSG000
GO:0005747	mitochondria	43	14	1.98	3.60E-09	ENSMUSG000
GO:0016021	integral comp	1986	141	91.6	2.10E-07	ENSMUSG000
GO:0005764	lysosome	351	32	16.19	0.00017	ENSMUSG000
GO:0098800	inner mitoch	113	27	5.21	0.00041	ENSMUSG000
GO:0005741	mitochondria	121	15	5.58	0.00043	ENSMUSG000
GO:0005886	plasma meml	1916	123	88.37	0.0005	ENSMUSG000
GO:0070062	extracellular	1736	107	80.07	0.00055	ENSMUSG000
GO:0005758	mitochondria	57	8	2.63	0.00434	ENSMUSG000
GO:0045177	apical part of	173	16	7.98	0.00614	ENSMUSG000
GO:0005887	integral comp	368	28	16.97	0.00617	ENSMUSG000
GO:0015078	hydrogen ion	68	13	3.14	1.10E-05	ENSMUSG000
GO:0008137	NADH dehydr	26	7	1.2	0.00013	ENSMUSG000
GO:0009055	electron tran	57	10	2.63	0.00024	ENSMUSG000
GO:0005178	integrin bindi	69	11	3.19	0.00029	ENSMUSG000
GO:0008374	O-acyltransfe	24	6	1.11	0.00062	ENSMUSG000
GO:0004553	hydrolase act	60	9	2.77	0.0016	ENSMUSG000
GO:0033218	amide bindin	184	18	8.5	0.00208	ENSMUSG000
GO:0016298	lipase activity	53	8	2.45	0.00276	ENSMUSG000
GO:0004930	G-protein cou	79	10	3.65	0.00329	ENSMUSG000
GO:0030246	carbohydrate	135	14	6.24	0.00374	ENSMUSG000

Functional enrichment of DRAL switch-resistant genes in WAT. Corresponding to Supplementar enrichment of DRAL switch-resistant genes in WAT. Indicated are GO term associated genes in ta p-values using two-sided Fisher's exact test and used ontology class. Biologically independent an n=3 (AL, DR, ALDR, AL 5m) n=5 (ALDR, DRAL).

Gene Symbol Ontology.Source
Ndufa2, Nduf Biological process
Akt2, Ndufs3, Biological process
Cox7c, Ndufa Biological process
Itgb2, Nckap1 Biological process
Comt, Hk2, Tc Biological process
Adcy3, Adrb3 Biological process
Nckap1l, Ada Biological process
Mmp14, Ctsk Biological process
Cox7c, Ndufa Biological process
Abr, Adam8, I Biological process
Comt, Man2b Biological process
Itgb2, Hk2, Ak Biological process
Psap, Adcy3, I Biological process
Hk2, Dhhd, P Biological process
Pten, Lpcat1, Biological process
Itgb2, Hk2, Ck Biological process
Pten, Hpgd, A Biological process
Hk2, Timm23 Biological process
Tcirg1, Atp5o Biological process
Psap, Hexb, C Biological process
Timm13, Mtc Biological process
Fos, Fam213a Biological process
Akt2, Pten, M Biological process
Scp2, Pts, Pth Biological process
Hk2, Ckb, Tcir Biological process
Mmp14, Myo Biological process
Mmp14, Akt2 Biological process
Pla2g15, Abh Biological process
Tcirg1, Adcy3 Biological process
Itgb2, Abr, M Biological process
Retn, Pltp, Ab Biological process
Itgb2, Cd163, Biological process
Mgst1, Abr, C Biological process
Akt2, Psap, Sl Biological process
Nfkb1, Unc93 Biological process
Adam8, Inpp Biological process
Itgb2, Abr, M Biological process
Rps6kb1, Bch Biological process
Itgb2, Nckap1 Biological process
Itgb2, Spi1, Al Biological process
Tnfrsf12a, Ad Biological process
Pten, Hexb, G Biological process
Pltp, Rfk, Slc2 Biological process
Pltp, Stard3, / Biological process

Pten, Adam8, Biological process
Slc11a1, Slc37, Biological process
Rps6kb1, Adc Biological process
Hk2, Hnmt, C Biological process
Dnmt1, Mgst, Biological process
Abr, Inpp5d, I Biological process
Itgb2, Abr, M Biological process
Abcg1, Scp2, Biological process
Slc3a2, Slc11a, Biological process
Cxcl16, Trem, Biological process
Itgb2, Mmp14 Biological process
Abcg1, Msr1, Biological process
Comt, Lpcat1, Biological process
Comt, Tgfbr1, Biological process
Nckap1l, Inpp Biological process
Spi1, Tgfbr1, I Biological process
Fermt3, Tln1, Biological process
Pla2g15, Abh Biological process
Nfkb1, Tlr8, A Biological process
Uqcrq, Uqcr1 Biological process
Cox7c, Cox5b Biological process
Comt, Hnmt, Biological process
Comt, Hk2, A Biological process
Comt, Tcirg1, Biological process
Plau, Nckap1l Biological process
Pten, Scp2, P Biological process
Pten, Trem2, Biological process
Comt, Hk2, A Biological process
Itgb2, Lrpap1, Biological process
Comt, Adcy3, Biological process
Hpgds, Hpgd, Biological process
Hpgds, Hpgd, Biological process
Pth1r, Ptger3 Biological process
Hk2, Akt2, M Biological process
Pltp, Abcg1, S Biological process
Pten, Plau, Cc Biological process
Hexb, Cln8, P Biological process
Pltp, Abcg1, S Biological process
Tcirg1, Akt2, I Biological process
Hk2, Entpd2, Biological process
Adam8, Siglec Biological process
Pten, Hexb, G Biological process
Timm13, Mpc Biological process
Mmp14, Pten Biological process
Pten, Lrpap1, Biological process
Adam8, Siglec Biological process

Tcirg1, Akt2, I Biological process
Tgfbr1, Pten, Biological process
Cpt1a, Cat, G Biological process
Cpt1a, Cat, G Biological process
Itgb2, Akt2, P Biological process
Comt, Lgmn, Biological process
Hk2, Ppp2ca, Biological process
Pltp, Abcg1, Biological process
Fos, Fam213a Biological process
Itgb2, Mmp14 Biological process
Myo9b, C3ar1 Biological process
Adam8, Siglec Biological process
Spi1, Dnmt1, Biological process
Mmp14, C3ar Biological process
Nckap1l, C3ar Biological process
Nckap1l, C3ar Biological process
Apopt1, Pde1 Biological process
Apopt1, Pde1 Biological process
Entpd2, Evi, F Biological process
Pten, Slc9a9, Biological process
Pten, Slc9a9, Biological process
Comt, Hk2, A Biological process
Pik3ap1, Tlr1 Biological process
Pten, Entpd2, Biological process
Ckb, Tcirg1, H Biological process
Map3k11, Ps Biological process
Comt, Retn, R Biological process
Hk2, Skp1a, T Biological process
Timm13, Apo Biological process
Comt, Man2b Biological process
Comt, Ckb, Tc Biological process
Pten, Inpp5d, Biological process
Pten, Bche, S Biological process
Slc11a1, Cd1c Biological process
Tcirg1, Akt2, Biological process
Tlr13, Cd300e Biological process
Mmp14, Nck Biological process
Adam8, Icam Biological process
Adam8, Tnfrs Biological process
Comt, Pld3, A Biological process
Slc26a2, Ttyh Biological process
Mmp14, Pten Biological process
Tcirg1, Slc11a Biological process
Comt, Ckb, Tc Biological process
Pten, Abr, Ncl Biological process
Itgb2, Akt2, G Biological process

Comt, Retn, R Biological process
Tgfbr1, Actn1 Biological process
Myo9b, Tgfbr Biological process
Tcirg1, Slc11a Biological process
Hk2, Hnmt, Ci Biological process
Akt2, Tnfrsf1: Biological process
Nckap1l, C3ar Biological process
Cln8, Abhd12 Biological process
Mmp14, Ctsk Biological process
Cidec, Pnpla3 Biological process
Scp2, Pth1r, F Biological process
Hk2, Entpd2, Biological process
Trem2, Slc11a: Biological process
Hk2, Tcirg1, S Biological process
Spi1, Tgfbr1, I Biological process
Akt2, Ndufs3, Biological process
Hk2, Tcirg1, C Biological process
Hk2, Tcirg1, C Biological process
Hk2, Akt2, M: Biological process
Lpcat1, Hexb, Biological process
Mmp14, Pten Biological process
Hk2, Akt2, Eci Biological process
Itgb2, Hk2, Ck Biological process
Nckap1l, Pik3 Biological process
Map3k11, Aki Biological process
Pten, Plau, Cc Biological process
Rasa4, Fos, Sl Biological process
Tcirg1, Hexb, Biological process
Itgb2, Abr, Nc Biological process
Tcirg1, Pten, I Biological process
Slc25a46, Mtr Biological process
C3ar1, C5ar1, Biological process
Hk2, Akt2, Nd Biological process
Nckap1l, Inpp Biological process
Comt, Stard3, Biological process
Pdcd5, Apopt Biological process
Pltp, Abcg1, S Biological process
Mink1, Atp1a Biological process
Cln8, Abhd12 Biological process
Abhd12, Pnpl Biological process
Abhd12, Pnpl Biological process
Cd163, Tnfrsf Biological process
Rufy3, Shtn1, Biological process
Itgb2, Msr1, I Biological process
Abr, Cd300a, Biological process
Map3k11, Aki Biological process

P2rx7, Scn7a, Biological process
 Itgb2, Akt2, G Biological process
 Pdcd5, Apopt Biological process
 Myo9b, C3ar1 Biological process
 Trem2, Slc11a Biological process
 Sgsh, Fuca2, F Biological process
 Comt, Tcirg1, Biological process
 Hk2, Entpd2, Biological process
 Hk2, Entpd2, Biological process
 Rasa4, Fos, P Biological process
 Pten, Apopt1 Biological process
 Hk2, Timm23, Biological process
 Itgb2, Hk2, Ak Biological process
 Itgb2, Chordc Biological process
 Akt2, Dhdh, P Biological process
 Comt, Tgfbr1, Biological process
 Timm23, Timi Biological process
 Nckap1l, Pik3 Biological process
 Ndufs3, Nduf Cellular component
 Itgb2, Comt, I Cellular component
 Tcirg1, Dnase Cellular component
 Ndufs3, Timr Cellular component
 Hk2, Mgst1, F Cellular component
 Itgb2, Comt, I Cellular component
 Itgb2, Comt, (Cellular component
 Timm23, Timi Cellular component
 Tcirg1, Pard6 Cellular component
 Itgb2, Esyt2, / Cellular component
 Tcirg1, Cox7c, Molecular function
 Ndufs3, Nduf Molecular function
 Cox7c, Ndufa Molecular function
 Mmp14, Actn Molecular function
 Lpcat1, Cpt1a Molecular function
 Psap, Man2b Molecular function
 Itgb2, Psap, N Molecular function
 Pld3, Lipa, Pl Molecular function
 Adrb3, Hpgd, Molecular function
 Hk2, Man2b1 Molecular function

y Figure 6i. GO
 arget set and background,
 imals used for RNA-seq: