

Table S1 Genes Enriched in the Rodent DA by Three or More Microarrays (Fold Change (FC); DA vs Ao)

Gene Symbol ^{1,2}	Gene Name	Entrez ID	Study #	Jin FC	Hseih FC	Shelton FC	Bokenkamp SMC FC	Bokenkamp Endo FC
<i>Abcc9</i>	ATP binding cassette subfamily C member 9	25560	4	5.6	2.6	2.8	1.7	1.5
<i>Actg2</i>	actin, gamma 2, smooth muscle, enteric	25365	4	2.8	2.3	7.8	2.2	2.0
<i>Dpep1</i>	dipeptidase 1 (renal)	94199	4	6.1	3.7	1.5	3.0	
<i>Ecn1</i>	endothelin 1	24323	4	1.4	1.6	1.5		1.7
<i>Fhl2</i>	four and a half LIM domains 2	63839	4	4.9	2.7	1.8	3.0	2.8
<i>Lrba</i>	LPS responsive beige-like anchor protein	361975	4	9.2	2.9	2.0	1.9	1.7
<i>Ncam1</i>	neural cell adhesion molecule 1	24586	4	2.0	1.4	2.3	1.5	
<i>Nr4a1</i>	nuclear receptor subfamily4, group A, member1	79240	4	1.7	1.5	1.5	1.5	
<i>Pcsk5</i>	proprotein convertase subtilisin/kexin type 5	116548	4	4.8	2.5	1.6	3.0	-1.2
<i>Penk</i>	proenkephalin	29237	4	1.8	1.3	2.4	2.2	2.3
<i>Ppp1r12a</i>	protein phosphatase 1, regulatory subunit 12A	116670	4	2.3	1.4	2.4	1.8	
<i>Ptger4</i>	prostaglandin E receptor 4	84023	4	2.6	2.4	3.8	3.8	-1.3
<i>Tnfrsf11b</i>	TNF receptor superfamily member 11B	25341	4	4.8	2.7	3.8	2.8	3.5
<i>Adamts1</i>	ADAM metalloproteinase with thrombospondin type 1 motif, 1	79252	3		3.1	1.8	2.4	
<i>Adamts9</i>	ADAM metalloproteinase with thrombospondin type 1 motif, 9	312566	3		3.9	3.1	2.7	2.7
<i>Adamts12</i>	ADAMTS-like 2	311827	3		4.0	3.1	2.0	
<i>Adgrl3</i>	adhesion G protein-coupled receptor L3	170641	3	3.9	1.3	1.4		-1.4
<i>Agtr1a</i>	angiotensin II receptor, type 1a	24180	3	1.4	1.5	-1.8	1.5	4.3
<i>Akap5</i>	A-kinase anchoring protein 5	171026	3		2.1	8.4	1.9	2.1
<i>Atp1b1</i>	ATPase Na ⁺ /K ⁺ transporting subunit beta 1	25650	3	2.8	1.5	-1.7	2.6	
<i>Barx1</i>	BARX homeobox 1	364680	3		1.3	1.3	1.2	
<i>Bmp2</i>	bone morphogenetic protein 2	29373	3		1.3	1.5		1.9
<i>Bmp4</i>	bone morphogenetic protein 4	25296	3	2.6	1.5			1.8
<i>Cacna1c</i>	calcium voltage-gated channel subunit alpha1C	24239	3	2.1		1.5	1.2	
<i>Cd55</i>	CD55 molecule, decay accelerating factor for complement	64036	3	6.4		1.5		1.5
<i>Cdk17</i>	cyclin-dependent kinase 17	314743	3	1.4		1.4	1.5	
<i>Celsr2</i>	cadherin, EGF LAG seven-pass G-type receptor 2	83465	3	1.6	1.4	1.5		
<i>Cnn1</i>	calponin 1	65204	3	1.4	1.4	2.7		
<i>Cntn3</i>	contactin 3	54279	3		1.9	3.6		1.3
<i>Cyr61</i>	cysteine-rich, angiogenic inducer, 61	83476	3	2.2	1.4	4.0		
<i>Dab2</i>	DAB2, clathrin adaptor protein	79128	3		1.4	2.3		1.9
<i>Des</i>	desmin	64362	3	6.1	2.6	5.0		
<i>Egr1</i>	early growth response 1	24330	3	-1.2	1.4	1.3	2.0	1.9
<i>Enpp3</i>	ectonucleotide pyrophosphatase/phosphodiesterase 3	54410	3	2.0	2.9	-1.9	1.9	
<i>Fat4</i>	FAT atypical cadherin 4	310341	3		1.4	2.1		1.5
<i>Fgfr2</i>	fibroblast growth factor receptor 2	25022	3	5.8	2.0	3.1		-1.2
<i>Ghr</i>	growth hormone receptor	25235	3	9.5	1.8		2.0	
<i>Gpm6b</i>	glycoprotein m6b	192179	3		6.3	2.8	2.6	
<i>Greml1</i>	gremlin 1, DAN family BMP antagonist	50566	3		1.6	12.3	2.9	
<i>Grm3</i>	glutamate metabotropic receptor 3	24416	3	3.6	1.6	1.4		
<i>Higd1a</i>	HIG1 hypoxia inducible domain family, member 1A	140937	3	7.5	1.5		2.1	1.6
<i>Hoxa4</i>	homeo box A4	100912525	3		1.4	2.8	1.5	
<i>Hspa1a</i>	heat shock 70kD protein 1A	24472	3	18.5	3.3		5.2	
<i>Hspb1</i>	heat shock protein family B (small) member 1	24471	3	2.1	3.0		2.2	
<i>Hspb8</i>	heat shock protein family B (small) member 8	113906	3		1.5	1.3	2.7	
<i>Il15</i>	interleukin 15	25670	3	6.1	1.6	2.5		
<i>Inhba</i>	inhibin beta A subunit	29200	3		3.5	2.2	2.6	2.4
<i>Kcnj8</i>	potassium voltage-gated channel subfamily J member 8	25472	3	2.8	1.8	9.0		
<i>Kcnk3</i>	potassium two pore domain channel subfamily K member 3	29553	3	5.8		2.4	1.8	
<i>Kctd1</i>	potassium channel tetramerization domain containing 1	291772	3		2.3	1.7	2.9	2.5
<i>Lama1</i>	laminin subunit alpha 1	316758	3		2.1	2.2	2.1	2.0
<i>Lrrn3</i>	leucine rich repeat neuronal 3	81514	3		1.4	2.4	1.7	
<i>Ltbp1</i>	latent transforming growth factor beta binding protein 1	59107	3	2.7	1.5	2.3		
<i>Mab21l2</i>	mab-21 like 2	680102	3		7.2		3.7	1.7
<i>Marc2</i>	mitochondrial amidoxime reducing component 2	171451	3	3.1	2.9			1.8
<i>Meis1</i>	Meis homeobox 1	686117	3		1.7	2.2	1.5	1.4
<i>Mfsd2a</i>	major facilitator superfamily domain containing 2A	298504	3		2.0	1.5	1.2	
<i>Mgll</i>	monoglyceride lipase	29254	3	3.2	1.5	1.3		
<i>Nalcn</i>	sodium leak channel, non-selective	266760	3	6.2	1.4	1.7	-2.3	
<i>Nr4a3</i>	nuclear receptor subfamily 4, group A, member 3	58853	3		1.2	3.5	2.4	3.2
<i>Olfml2b</i>	olfactomedin-like 2B	304960	3		1.4	1.8	1.7	
<i>Parm1</i>	prostate androgen-regulated mucin-like protein 1	286894	3		1.8	1.8	1.7	
<i>Pde4b</i>	phosphodiesterase 4B	24626	3	2.1		2.0	2.4	1.6

Table S1 (cont.) Genes Enriched in the Rodent DA by Three or More Microarrays (Fold Change (FC); DA vs Ao)

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<i>Prkar2b</i>	protein kinase cAMP-dependent type 2 regulatory subunit beta	24679	3	1.4	1.4		2.0	1.6
<i>Ptbp1</i>	polypyrimidine tract binding protein 1	29497	3	1.4		1.2		1.5
<i>Ptn</i>	pleiotrophin	24924	3	1.7	3.2	1.5		
<i>Rdh10</i>	retinol dehydrogenase 10	353252	3		1.8	1.5	1.7	1.8
<i>Rgs5</i>	regulator of G-protein signaling 5	54294	3		1.5	4.4	3.1	3.3
<i>Runx1</i>	runt-related transcription factor 1	50662	3		1.6	2.9	2.8	2.0
<i>Ryr3</i>	ryanodine receptor 3	170546	3		1.4	1.8	2.5	
<i>Scx</i>	scleraxis bHLH transcription factor	680712	3		1.6	2.3	2.9	
<i>Serinc3</i>	serine incorporator 3	296350	3	1.9		1.4	1.2	
<i>Sfrp1</i>	secreted frizzled-related protein 1	84402	3		2.4	2.3	2.5	2.1
<i>Sfrp2</i>	secreted frizzled-related protein 2	310552	3		1.9	1.4	1.8	
<i>Skap2</i>	src kinase associated phosphoprotein 2	155183	3		1.2	1.6		1.8
<i>Slc2a4</i>	solute carrier family 2 member 4	25139	3	2.7	1.8	2.3		
<i>Slit2</i>	slit guidance ligand 2	360272	3		2.5	3.4	2.3	4.0
<i>Snd1</i>	staphylococcal nuclease and tudor domain containing 1	64635	3	1.2	-1.3	1.3		1.3
<i>Sox9</i>	SRY box 9	140586	3		1.6	3.8	1.3	
<i>Tagln</i>	transgelin	25123	3	1.9	1.4	1.4		
<i>Tfap2a</i>	transcription factor AP-2 alpha	306862	3		1.9	1.5	1.4	
<i>Tfap2b</i>	transcription factor AP-2 beta	301285	3		13.5	33.1	13.9	9.0
<i>Tgfb1</i>	transforming growth factor, beta induced	116487	3		4.3	3.3	2.6	2.4
<i>Tmem150c</i>	transmembrane protein 150C	360916	3		14.1	1.3	21.1	12.4
<i>Tmem26</i>	transmembrane protein 26	309724	3		1.4	1.5		1.9
<i>Tnn</i>	tenascin N	304913	3		5.0	3.4	11.5	3.3
<i>Tom11l</i>	target of myb1 like 1 membrane trafficking protein	287622	3		1.4	1.3	1.5	

¹Genes in blue have previously been identified as important for DA function in the literature

²Bokenkamp *et al.* is divided by SMC and EC in accordance with this study's experimental design

Table S2 Genes Enriched in the Rodent Aorta by Three or More Microarrays (Fold Change (FC); DA vs Ao)

Gene Symbol ^{1,2}	Gene Name	Entrez ID	Study #	Jin FC	Hseih FC	Shelton FC	Bokenkamp SMC FC	Bokenkamp Endo FC
<i>Add3</i>	adducin 3	25230	4	-1.8	-1.9	-1.5	-2.2	
<i>Akap1</i>	A-kinase anchoring protein 1	114124	4	-1.5	-1.3	-1.3		-1.2
<i>Cpq</i>	carboxypeptidase Q	58952	4	-1.8	-1.6	-1.3	-1.8	-1.8
<i>Golgb1</i>	golgin B1	192243	4	-1.2	-1.4	-1.2	-1.7	
<i>Igfbp6</i>	insulin-like growth factor binding protein 6	25641	4	-1.7	-2.1	-2.9	-1.6	
<i>Itga7</i>	integrin subunit alpha 7	81008	4	-1.4	-2.3	-2.3	-1.5	-1.3
<i>Pdgfra</i>	platelet derived growth factor receptor alpha	25267	4	-1.9	-2.2	-1.7	-3.6	
<i>Rrad</i>	RRAD, Ras related glycolysis inhibitor and calcium channel regulator	83521	4	-1.4	-2.0	-2.0		-1.8
<i>Slc6a9</i>	solute carrier family 6 member 9	116509	4	-3.4	-2.1	-1.3		-1.4
<i>Syt7</i>	synaptotagmin 7	59267	4	-1.4	-1.7	-1.5		-1.3
<i>Abhd14a</i>	abhydrolase domain containing 14A	300982	3		-1.2	-1.3	-1.3	-1.3
<i>Acsf5</i>	acyl-CoA synthetase long-chain family member 5	94340	3	-1.7	-1.5	-1.2		
<i>Adam33</i>	ADAM metallopeptidase domain 33	311425	3		-1.6	-1.3		-1.8
<i>Adamts15</i>	ADAMTS-like 5	314626	3		-1.2	-1.9		-1.5
<i>Adcy4</i>	adenylate cyclase 4	54223	3	-1.4		-1.4	-1.9	
<i>Adcy9</i>	adenylate cyclase 9	302950	3		-1.3	-1.3		-1.6
<i>Adgrd1</i>	adhesion G protein-coupled receptor D1	689257	3		-1.9	-1.8		-1.5
<i>Agap1</i>	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	316611	3		-1.3	-1.7		-1.4
<i>Agtr2</i>	angiotensin II receptor, type 2	24182	3	-1.3	-1.6	1.7	-3.8	
<i>Aig1</i>	androgen-induced 1	292486	3		-1.9	-1.8	-1.6	
<i>Akap6</i>	A-kinase anchoring protein 6	64553	3		-1.8	-3.9		-1.3
<i>Alcam</i>	activated leukocyte cell adhesion molecule	79559	3		-1.9	-2.2	-1.7	
<i>Alx1</i>	ALX homeobox 1	25401	3	-1.2		-3.3		-1.3
<i>Amigo2</i>	adhesion molecule with Ig like domain 2	300186	3		-1.2	-3.2		-1.6
<i>Ampd2</i>	adenosine monophosphate deaminase 2	362015	3		-1.4	-1.4	-1.3	
<i>Ank2</i>	ankyrin 2	362036	3		-2.1	-1.3	-2.4	-2.2
<i>Arhgap44</i>	Rho GTPase activating protein 44	303222	3		-1.8	-1.4	-1.6	
<i>B4galt2</i>	beta-1,4-galactosyltransferase 2	313536	3		-1.3	-1.2	-1.3	
<i>Bcar3</i>	breast cancer anti-estrogen resistance 3	310838	3		-1.5	-3.3	-2.1	
<i>Bche</i>	butyrylcholinesterase	65036	3		-2.4	-2.0	-2.0	
<i>Bdkrb2</i>	bradykinin receptor B2	25245	3	-3.4	-1.5			-1.3
<i>C2cd2</i>	C2 calcium-dependent domain containing 2	304055	3		-1.5	-1.6		-1.5
<i>Calml4</i>	calmodulin-like 4	691455	3	-2.1	-2.9			-2.1
<i>Casq2</i>	calsequestrin 2	29209	3	-2.4	-3.5		-2.1	-2.1
<i>Cdh13</i>	cadherin 13	192248	3		-3.0	-3.3	-1.9	-2.5
<i>Cdh6</i>	cadherin 6	25409	3		-2.3	-3.4		-1.4
<i>Cdk6</i>	cyclin-dependent kinase 6	114483	3		-1.3	-1.9		-1.3
<i>Cnm2</i>	cyclin and CBS domain divalent metal cation transport mediator 2	294014	3		-1.8	-1.5		-1.7
<i>Col11a1</i>	collagen type XI alpha 1 chain	25654	3	-1.7	-2.1	4.1	-3.8	
<i>Col3a1</i>	collagen type III alpha 1 chain	84032	3		-1.6	-1.3	-2.0	
<i>Col5a2</i>	collagen type V alpha 2 chain	85250	3		-1.9	-1.3	-1.3	
<i>Col6a3</i>	collagen type VI alpha 3 chain	367313	3		-1.9	-1.4	-2.5	
<i>Corin</i>	corin, serine peptidase	289596	3		-4.2	-5.1		-2.3
<i>Cpd</i>	carboxypeptidase D	25306	3	-1.8	-1.6	-1.3		
<i>Cped1</i>	cadherin-like and PC-esterase domain containing 1	500046	3		-2.0	-2.6	-1.7	
<i>Cplx2</i>	complexin 2	116657	3	-1.4		-1.3		-1.4
<i>Csf1</i>	colony stimulating factor 1	78965	3		-2.0	-1.9	-1.4	-1.3
<i>Cxcl13</i>	C-X-C motif chemokine ligand 13	498335	3	-5.4	-1.6		-2.7	
<i>Cyth3</i>	cytohesin 3	116693	3		-2.3	-1.4	-1.7	-1.3
<i>Dcn</i>	decorin	29139	3	-1.9		-1.3	-4.1	2.4
<i>Dhtkd1</i>	dehydrogenase E1 and transketolase domain containing 1	361272	3		-1.4	-1.3	-1.7	
<i>Dpysl3</i>	dihydropyrimidinase-like 3	25418	3	-14.2	-1.4	1.7		-1.3
<i>Ebf1</i>	early B-cell factor 1	116543	3		-1.4	-1.5	-2.0	-1.5
<i>Fam13a</i>	family with sequence similarity 13, member A	362378	3		-1.9	-1.4	-1.5	
<i>Fam20c</i>	FAM20C, golgi associated secretory pathway kinase	304334	3		-2.0	-1.4	-1.4	-1.6
<i>Fchsd2</i>	FCH and double SH3 domains 2	308864	3		-1.6	-1.3		-1.3
<i>Fgf2</i>	fibroblast growth factor 2	54250	3		-1.4	-1.5		-1.3
<i>Fmo2</i>	flavin containing monooxygenase 2	246245	3		-2.9	-3.0		-1.8
<i>Foxc1</i>	forkhead box C1	364706	3		-1.4	-1.5		-1.3
<i>Frm4b</i>	FERM domain containing 4B	252858	3	-2.0	-1.7	-1.9		
<i>Frm6</i>	FERM domain containing 6	257646	3		-1.7	-1.5	-1.4	
<i>Galm</i>	galactose mutarotase	313843	3		-1.2	-1.5		-1.4
<i>Galt</i>	galactose-1-phosphate uridylyltransferase	298003	3		-1.3	-1.2	-1.3	
<i>Gas7</i>	growth arrest specific 7	85246	3		-2.6	-1.9	-1.8	
<i>Gdf10</i>	growth differentiation factor 10	79216	3	-1.9	-1.4		-1.8	
<i>Gfra2</i>	GDNF family receptor alpha 2	25136	3	-2.0	-3.7	-1.4		
<i>Glis2</i>	GLIS family zinc finger 2	302946	3		-1.3	-1.5	-1.4	-1.2

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<i>Glt8d2</i>	glycosyltransferase 8 domain containing 2	366859	3		-1.5	-2.0	-1.2	
<i>Grasp</i>	general receptor for phosphoinositides 1 associated scaffold protein	192254	3		-1.5	-1.9		-1.3
<i>Grb14</i>	growth factor receptor bound protein 14	58844	3		-1.6	-2.3	-1.8	-1.7
<i>Grip2</i>	glutamate receptor interacting protein 2	171571	3	-1.8	-1.7	-2.7		
<i>Gstk1</i>	glutathione S-transferase kappa 1	297029	3		-1.5	-1.8	-1.5	-1.3
<i>Hapln1</i>	hyaluronan and proteoglycan link protein 1	29331	3		-1.4	-2.0		-1.5
<i>Herc3</i>	HECT and RLD domain containing E3 ubiquitin protein ligase 3	362377	3		-1.3	-1.3	-2.0	
<i>Heyl</i>	hes-related family bHLH transcription factor with YRPW motif-like	313575	3		-2.0	-1.9		-1.7
<i>Hmgcs2</i>	3-hydroxy-3-methylglutaryl-CoA synthase 2	24450	3	-10.4	-2.2			-1.3
<i>Hpcal4</i>	hippocalcin-like 4	50872	3	-2.3	-2.4		-2.2	-1.3
<i>Igf1r</i>	insulin-like growth factor 1 receptor	25718	3	-1.5	-1.3		-1.7	-1.4
<i>Igf2bp2</i>	insulin-like growth factor 2 mRNA binding protein 2	303824	3		-1.3	-1.2	-1.3	
<i>Igfbp2</i>	insulin-like growth factor binding protein 2	25662	3	-3.7	-2.6	6.2	-1.9	
<i>Igsf3</i>	immunoglobulin superfamily, member 3	295325	3		-1.7	-1.3	-2.0	
<i>Inpp5k</i>	inositol polyphosphate-5-phosphatase K	287533	3		-1.3	-1.4		-1.2
<i>Kcnma1</i>	potassium calcium-activated channel subfamily M alpha 1	83731	3	-5.9	-2.4	2.1	-2.5	-4.2
<i>Kcnq1</i>	potassium voltage-gated channel subfamily Q member 1	84020	3	-1.8	-2.2			-1.7
<i>Kif3a</i>	kinesin family member 3a	84392	3		-1.2	-1.5	-1.3	
<i>Klf15</i>	Kruppel-like factor 15	85497	3		-1.6	-2.2	-1.7	-1.8
<i>Krt8</i>	keratin 8	25626	3	-2.0	-3.6	-1.8		
<i>Lama4</i>	laminin subunit alpha 4	309816	3		-1.6	-1.5	-1.3	
<i>Lamb1</i>	laminin subunit beta 1	298941	3		-2.0	-2.0	-1.8	
<i>Laptm4b</i>	lysosomal protein transmembrane 4 beta	315047	3		-1.3	-1.7	-1.3	
<i>Lbh</i>	limb bud and heart development	683626	3		-1.3	-2.2	-1.5	
<i>Ldhb</i>	lactate dehydrogenase B	24534	3	-1.4	-1.6		-1.7	
<i>Lhfp2</i>	lipoma HMGIC fusion partner-like 2	294643	3		-1.6	-1.7	-1.7	
<i>Lifr</i>	leukemia inhibitory factor receptor alpha	81680	3		-1.8	-1.3		-1.3
<i>Limd1</i>	LIM domains containing 1	316101	3		-1.6	-1.6		-1.2
<i>Lingo1</i>	leucine rich repeat and Ig domain containing 1	315691	3		-1.6	-1.7	-1.5	-2.2
<i>Lox</i>	lysyl oxidase	24914	3	-1.8	-1.4		-1.5	
<i>Lox1</i>	lysyl oxidase-like 1	315714	3	-1.3	-2.0		-2.0	
<i>Lrrfp1</i>	LRR binding FLII interacting protein 1	367314	3		-1.4	-1.3	-1.4	-1.4
<i>Lrtm2</i>	leucine-rich repeats and transmembrane domains 2	680883	3		-1.2	-1.3	-1.4	
<i>Ltbp2</i>	latent transforming growth factor beta binding protein 2	59106	3	-1.9	-2.1	1.7	-1.7	
<i>Map2</i>	microtubule-associated protein 2	25595	3	-3.6	-4.8		-3.7	
<i>Matn2</i>	matrilin 2	299996	3		-2.0	-1.3	-1.7	-1.8
<i>Meis2</i>	Meis homeobox 2	311311	3		-1.5	-1.7	-1.5	
<i>Mfhas1</i>	malignant fibrous histiocytoma amplified sequence1	306508	3		-1.3	-1.7	-1.4	
<i>Mobp</i>	myelin-associated oligodendrocyte basic protein	25037	3	-2.2	-1.6		-1.6	-1.6
<i>Mtdh</i>	metadherin	170910	3	-1.6	-1.4		-1.3	1.2
<i>Mtus1</i>	microtubule associated tumor suppressor 1	306487	3		-2.5	-1.9	-2.4	
<i>Mtus2</i>	microtubule associated tumor suppressor candidate2	498136	3		-2.4	-3.5	-1.9	-3.4
<i>Mycbp2</i>	MYC binding protein 2, E3 ubiquitin protein ligase	290447	3		-1.3	-1.3	-1.3	
<i>Myh10</i>	myosin heavy chain 10	79433	3	-7.5	-1.2	-1.3		
<i>Myo1d</i>	myosin ID	25485	3		-2.2	-1.5	-1.6	
<i>Ndrp2</i>	NDRG family member 2	171114	3		-1.7	-1.5		-1.8
<i>Nf2</i>	neurofibromin 2	25744	3		-1.3	-1.6		-1.2
<i>Nid1</i>	nidogen 1	25494	3		-1.5	-1.8	-1.6	
<i>Nid2</i>	nidogen 2	302248	3		-2.0	-2.3	-2.2	-1.7
<i>Nrarp</i>	Notch-regulated ankyrin repeat protein	499745	3		-1.8	-1.6		-1.4
<i>Ntrk2</i>	neurotrophic receptor tyrosine kinase 2	25054	3		-2.1	-1.2	-4.3	
<i>Ntrk3</i>	neurotrophic receptor tyrosine kinase 3	29613	3	1.4	-1.3	-2.9	-1.9	-1.8
<i>P4ha2</i>	prolyl 4-hydroxylase subunit alpha 2	360526	3		-1.5	-1.3	-1.5	-1.3
<i>Pck2</i>	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	361042	3		-1.5	-1.4	-1.8	-1.6
<i>Pde1c</i>	phosphodiesterase 1C	81742	3	-2.4	-1.3	-2.9		
<i>Pdlim5</i>	PDZ and LIM domain 5	64353	3	-2.3	-1.3	-1.4		
<i>Phkg1</i>	phosphorylase kinase, gamma 1	29353	3	-4.2		-3.4		-1.2
<i>Pld1</i>	phospholipase D1	25096	3		-1.5	-1.7		-1.7
<i>Plpp3</i>	phospholipid phosphatase 3	192270	3	-1.6	-1.7		-2.0	
<i>Polg</i>	DNA polymerase gamma, catalytic subunit	85472	3		-1.3	-1.2		-1.3
<i>Postn</i>	periostin	361945	3	-2.5	-3.8		-2.7	
<i>Ppp1r9a</i>	protein phosphatase 1, regulatory subunit 9A	84685	3		-1.5	-1.7		-2.1
<i>Prrc1</i>	proline-rich coiled-coil 1	291444	3		-1.3	-1.5	-1.3	
<i>Ptger3</i>	prostaglandin E receptor 3	24929	3	-3.5	-1.9		-2.4	-1.3

Table S2 Genes Enriched in the Rodent Aorta by Three or More Microarrays (Fold Change (FC); DA vs Ao)
(cont.)

Gene Symbol ^{1,2}	Gene Name	Entrez ID	Study #	Jin FC	Hseih FC	Shelton FC	Bokenkamp SMC FC	Bokenkamp Endo FC
<i>Ptprd</i>	protein tyrosine phosphatase, receptor type, D	313278	3		-1.7	-1.6	-2.0	-1.7
<i>Qpct</i>	glutaminy-peptide cyclotransferase	313837	3	-1.6	-1.3	1.3	-2.4	
<i>Rab3ip</i>	RAB3A interacting protein	29885	3		-3.6	-1.3	-3.6	-3.1
<i>Rab7b</i>	Rab7b, member RAS oncogene family	501854	3		-2.3	-2.8	-1.5	-1.7
<i>Ramp1</i>	receptor activity modifying protein 1	58965	3		-1.7	-3.0	-1.4	
<i>Rarb</i>	retinoic acid receptor, beta	24706	3		-1.3	-1.5	-2.0	
<i>Rarres2</i>	retinoic acid receptor responder 2	297073	3		-1.8	-2.5	-1.7	-1.5
<i>Rasd2</i>	RASD family, member 2	171099	3		-1.3	-2.6		-1.3
<i>Rassf9</i>	Ras association domain family member 9	65053	3	-2.6	-2.4	-1.8		
<i>Rbm6</i>	RNA binding motif protein 6	315997	3		-1.3	-1.2	-1.3	
<i>Rhoj</i>	ras homolog family member J	299145	3		-1.4	-1.2		-1.3
<i>Rif1</i>	replication timing regulatory factor 1	295602	3		-1.5	-1.3	-1.5	
<i>Ryr2</i>	ryanodine receptor 2	689560	3		-1.3	-1.7		-2.5
<i>Sash1</i>	SAM and SH3 domain containing 1	365037	3		-2.1	-1.7	-2.5	
<i>Scarf1</i>	scavenger receptor class F, member 1	303313	3		-1.4	-1.3		-1.3
<i>Scube3</i>	signal peptide, CUB domain and EGF like domain containing 3	294297	3		-2.1	-1.5		-2.3
<i>Sema5a</i>	semaphorin 5A	310207	3		-1.5	-2.0	-1.4	
<i>Sema6d</i>	semaphorin 6D	311384	3		-2.2	-1.4	-1.9	
<i>Sept8</i>	septin 8	303135	3		-1.3		-2.1	-1.3
<i>Sh3pxd2a</i>	SH3 and PX domains 2A	309460	3		-1.6	-1.2	-1.9	-1.9
<i>Sipa1l2</i>	signal-induced proliferation-associated 1 like 2	361442	3		-1.6	-1.3		-1.5
<i>Slc1a4</i>	solute carrier family 1 member 4	305540	3		-1.9	-1.6		-1.6
<i>Slc24a3</i>	solute carrier family 24 member 3	85267	3		-1.5	-2.0	-2.1	-1.8
<i>Slc44a1</i>	solute carrier family 44 member 1	85254	3		-1.5	-1.2	-1.4	
<i>Slc7a3</i>	solute carrier family 7 member 3	29485	3	-2.5	-6.3		-4.1	-2.9
<i>Slc9a3r2</i>	SLC9A3 regulator 2	116501	3		-1.4	-1.8		-1.2
<i>Slx4ip</i>	SLX4 interacting protein	499895	3		-1.4	-1.4	-1.3	
<i>Smarca2</i>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	361745	3		-1.7	-1.3		-1.6
<i>Smpd3</i>	sphingomyelin phosphodiesterase 3	94338	3		-2.0	-1.9	-1.7	
<i>Snta1</i>	syntrophin, alpha 1	362242	3		-1.8	-1.9	-1.5	
<i>Sod2</i>	superoxide dismutase 2	24787	3	-1.8	-1.3	-1.3		
<i>Sorbs3</i>	sorbin and SH3 domain containing 3	282843	3		-1.4	-1.4		-1.4
<i>Specc1</i>	sperm antigen with calponin homology and coiled-coil domains 1	303208	3		-2.1	-1.5	-2.3	-1.5
<i>Sphkap</i>	SPHK1 interactor, AKAP domain containing	316561	3		-2.7	-3.8		-2.0
<i>Spock2</i>	SPARC/osteonectin, cwcv and kazal like domains proteoglycan 2	361840	3	-2.8	-1.3	-2.0		
<i>Spon1</i>	spondin 1	64456	3	-1.6	-1.9	-4.2		
<i>St3gal3</i>	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	64445	3	-1.5	-1.2		-1.4	
<i>Stc1</i>	stanniocalcin 1	81801	3		-2.9	-3.9	-2.3	-1.9
<i>Stmn4</i>	stathmin 4	79423	3	-1.6	-3.0			-2.1
<i>Stx1a</i>	syntaxin 1A	116470	3		-1.6	-2.0	-1.7	-1.4
<i>Stx3</i>	syntaxin 3	81802	3		-1.4	-2.1		-1.3
<i>Sult1a1</i>	sulfotransferase family 1A member 1	83783	3	-3.1	-2.6		-2.0	
<i>Tbx18</i>	T-box18	315870	3		-1.2	-1.9	-2.4	
<i>Tet1</i>	tet methylcytosine dioxygenase 1	309902	3		-1.3	-1.6	-1.9	
<i>Tgfb2</i>	transforming growth factor, beta receptor 2	81810	3		-2.1	-1.6		-1.2
<i>Thbs2</i>	thrombospondin 2	292406	3		-1.7	-1.8	-2.0	
<i>Timp4</i>	tissue inhibitor of metalloproteinase 4	680130	3		-2.8	-5.0	-1.5	-1.7
<i>Tmem117</i>	transmembrane protein 117	500921	3		-1.7	-2.3	-1.6	
<i>Tmx4</i>	thioredoxin-related transmembrane protein 4	296182	3		-1.9	-1.4		-1.4
<i>Traf3</i>	Tnf receptor-associated factor 3	362788	3		-1.5	-1.2	-1.4	
<i>Trim47</i>	tripartite motif-containing 47	690374	3		-1.4	-1.8		-1.3
<i>Tspan5</i>	tetraspanin 5	362048	3		-1.7	-2.3	-1.3	
<i>Tub</i>	tubby bipartite transcription factor	25609	3	-3.3		-1.5	-1.5	
<i>Usp54</i>	ubiquitin specific peptidase 54	408223	3		-1.6	-1.3	-1.6	
<i>Vasn</i>	vasorin	679921	3		-1.5	-1.6	-1.4	
<i>Vstm4</i>	V-set and transmembrane domain containing 4	361112	3		-1.4	-1.6	-2.3	
<i>Xirp1</i>	xin actin-binding repeat containing 1	100910104	3		-2.3	-2.3		-1.7
<i>Zmiz1</i>	zinc finger, MIZ-type containing 1	361103	3	-4.8	-1.2		-1.3	

¹Genes in blue have previously been identified as important for DA function in the literature

²Bokenkamp *et al.* is divided by SMC and EC in accordance with this study's experimental design

Table S3 Summary of Transcript¹ Reads

Sample	Vessel	Transcript Reads	Exonic Reads	Intronic Reads	Intergenic Reads
122	Ao	26761371	48.28%	35.60%	6.85%
122	DA	28415074	43.54%	28.42%	18.13%
134	Ao	49240999	58.16%	24.76%	6.51%
134	DA	44456169	49.42%	33.93%	7.36%
162	Ao	65157040	30.93%	52.77%	8.91%
162	DA	56289111	32.26%	51.34%	8.43%
208	Ao	73200814	29.42%	54.20%	8.28%
208	DA	75899608	32.84%	50.83%	8.16%
Mean		52427523	40.61%	41.48%	9.08%

¹ Transcriptome reads aligned to RefSeq Transcripts 83

Table S4

Genes Enriched in the Human DA by RNA-seq (Fold Change; DA vs Ao)

Gene Symbol	Gene Name	Fold Change	P-value	FDR	FPKM DA	FPK M Ao	Entrez ID
<i>GRM1</i>	glutamate metabotropic receptor 1	57.9	1.26E-06	3.98E-03	0.97	0.02	2911
<i>FENDRR</i>	FOXF1 adjacent non-coding developmental regulatory RNA	45.1	1.21E-07	1.60E-03	2.47	0.05	400550
<i>WFDC1</i>	WAP four-disulfide core domain 1	40.2	1.64E-05	1.51E-02	0.89	0.02	58189
<i>FSTL5</i>	folliculin like 5	39.4	6.78E-05	3.14E-02	2.74	0.07	56884
<i>TFAP2B</i>	transcription factor AP-2 beta	37.9	1.94E-07	1.73E-03	3.49	0.09	7021
<i>ADAP1</i>	ArfGAP with dual PH domains 1	36.7	9.70E-06	1.24E-02	0.72	0.02	11033
<i>PCDH11Y</i>	protocadherin 11 Y-linked	33.6	1.14E-04	4.04E-02	0.48	0.01	83259
<i>PDE1C</i>	phosphodiesterase 1C	33.2	3.97E-06	7.85E-03	0.43	0.01	5137
<i>NRXN3</i>	neurexin 3	32.7	3.66E-04	7.57E-02	0.58	0.02	9369
<i>VTCN1</i>	V-set domain containing T-cell activation inhibitor 1	31.9	2.63E-04	6.08E-02	0.18	0.01	79679
<i>ASIC2</i>	acid sensing ion channel subunit 2	31.5	3.48E-05	2.24E-02	1.72	0.05	40
<i>GALNT14</i>	polypeptide N-acetylgalactosaminyltransferase 14	29.9	4.76E-04	8.77E-02	0.08	0.00	79623
<i>CLEC3A</i>	C-type lectin domain family 3 member A	29.9	5.92E-05	2.92E-02	1.08	0.04	10143
<i>FOXF1</i>	forkhead box F1	29.4	4.37E-07	2.17E-03	2.74	0.09	2294
<i>SCUBE1</i>	signal peptide, CUB domain and EGF like domain containing1	28.7	1.03E-05	1.28E-02	0.62	0.02	80274
<i>VIT</i>	vitrin	28.5	5.35E-04	9.42E-02	0.63	0.02	5212
<i>IRS4</i>	insulin receptor substrate 4	26.2	1.30E-06	3.98E-03	1.88	0.07	8471
<i>MAB21L2</i>	mab-21 like 2	25.3	2.08E-06	5.51E-03	16.77	0.66	10586
<i>ROBO2</i>	roundabout guidance receptor 2	24.6	1.50E-06	4.26E-03	5.37	0.22	6092
<i>KRT17</i>	keratin 17	24.6	5.31E-05	2.74E-02	10.97	0.45	3872
<i>HECW1</i>	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	23.2	1.72E-04	4.76E-02	1.39	0.06	23072
<i>FLJ30901</i>	uncharacterized protein FLJ30901	22.0	6.62E-05	3.14E-02	0.31	0.01	150378
<i>GLP1R</i>	glucagon like peptide 1 receptor	21.9	4.65E-04	8.65E-02	0.85	0.04	2740
<i>FAM19A1</i>	family with sequence similarity 19 member A1, C-C motif chemokine like	20.6	7.37E-06	1.05E-02	8.08	0.39	407738
<i>PTGER4</i>	prostaglandin E receptor 4	20.5	9.38E-08	1.60E-03	21.27	1.04	5734
<i>SYTL2</i>	synaptotagmin like 2	20.4	2.84E-04	6.36E-02	0.48	0.02	54843
<i>TNMD</i>	tenomodulin	19.9	3.43E-07	1.95E-03	2.28	0.11	64102
<i>RBP3</i>	retinol binding protein 3	19.7	4.56E-05	2.57E-02	0.53	0.03	5949
<i>LINC-PINT</i>	long intergenic non-protein coding RNA, p53 induced transcript	19.1	2.67E-05	2.00E-02	0.55	0.03	378805
<i>CD48</i>	CD48 molecule	17.8	2.55E-04	5.96E-02	0.21	0.01	962
<i>ANKRD1</i>	ankyrin repeat domain 1	16.5	1.67E-05	1.51E-02	2.08	0.13	27063
<i>UBL7</i>	ubiquitin like 7	16.2	3.27E-05	2.24E-02	0.36	0.02	84993
<i>ICAM4</i>	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	16.1	2.21E-04	5.58E-02	0.12	0.01	3386
<i>ALKAL1</i>	ALK And LTK Ligand 1	16.1	2.22E-04	5.58E-02	0.43	0.03	389658
<i>SCTR</i>	secretin receptor	15.1	1.05E-04	3.90E-02	0.14	0.01	6344
<i>CDH3</i>	cadherin 3	14.0	3.93E-04	7.86E-02	0.33	0.02	1001
<i>C16orf89</i>	chromosome 16 open reading frame 89	14.0	1.23E-04	4.21E-02	2.43	0.17	146556
<i>ICAM3</i>	intercellular adhesion molecule 3	13.8	1.93E-04	5.10E-02	0.10	0.01	3385
<i>LOC349160</i>	uncharacterized LOC349160	13.8	1.62E-05	1.51E-02	1.63	0.12	349160
<i>PCSK2</i>	proprotein convertase subtilisin/kexin type 2	13.6	6.61E-06	1.05E-02	3.24	0.24	5126
<i>GRIN2A</i>	glutamate ionotropic receptor NMDA type subunit 2A	13.3	1.40E-04	4.38E-02	1.41	0.11	2903
<i>PCDH11X</i>	protocadherin 11 X-linked	13.0	2.29E-04	5.67E-02	0.81	0.06	27328
<i>S1PR5</i>	sphingosine-1-phosphate receptor 5	12.9	7.68E-06	1.05E-02	2.15	0.17	53637
<i>COL9A1</i>	collagen type IX alpha 1 chain	12.6	1.61E-04	4.71E-02	2.33	0.18	1297
<i>TNC</i>	tenascin C	12.1	7.76E-08	1.60E-03	99.27	8.22	3371
<i>DGKA</i>	diacylglycerol kinase alpha	12.1	2.49E-04	5.90E-02	0.07	0.01	1606
<i>COL8A2</i>	collagen type VIII alpha 2 chain	11.8	4.14E-06	7.85E-03	2.49	0.21	1296
<i>ICAM5</i>	intercellular adhesion molecule 5	11.8	1.68E-04	4.71E-02	0.62	0.05	7087
<i>DLX1</i>	distal-less homeobox 1	11.5	1.69E-04	4.71E-02	0.63	0.05	1745
<i>DNAH11</i>	dynein axonemal heavy chain 11	9.9	1.15E-04	4.06E-02	0.88	0.09	8701
<i>RHBDL2</i>	rhomboid like 2	9.9	1.33E-04	4.26E-02	0.76	0.08	54933
<i>LOC101927069</i>	uncharacterized LOC101927069	9.6	8.80E-05	3.54E-02	1.07	0.11	101927069
<i>C1QTNF3</i>	C1q and tumor necrosis factor related protein 3	9.5	1.21E-05	1.42E-02	20.52	2.16	114899
<i>CHD5</i>	chromodomain helicase DNA binding protein 5	9.5	3.57E-06	7.75E-03	2.48	0.26	26038
<i>DIO2</i>	iodothyronine deiodinase 2	9.5	1.43E-05	1.47E-02	2.41	0.25	1734
<i>MAPK10</i>	mitogen-activated protein kinase 10	9.4	7.00E-05	3.16E-02	0.80	0.09	5602
<i>KCTD16</i>	potassium channel tetramerization domain containing 16	9.1	5.78E-05	2.91E-02	1.81	0.20	57528
<i>CHRM2</i>	cholinergic receptor muscarinic 2	8.8	3.06E-05	2.17E-02	3.60	0.41	1129
<i>FOXD1</i>	forkhead box D1	8.7	4.48E-05	2.57E-02	0.73	0.08	2297
<i>COL19A1</i>	collagen type XIX alpha 1 chain	8.7	3.70E-05	2.27E-02	2.50	0.29	1310
<i>CSGALNACT1</i>	chondroitin sulfate N-acetylgalactosaminyltransferase 1	8.5	5.09E-04	9.12E-02	0.55	0.06	55790
<i>LINC00643</i>	long intergenic non-protein coding RNA 643	8.2	5.92E-04	9.98E-02	1.06	0.13	646113
<i>PKHD1</i>	polycystic kidney and hepatic disease 1 (autosomal recessive)	8.2	1.62E-04	4.71E-02	0.45	0.06	5314
<i>FOXP1</i>	forkhead box G1	8.1	3.08E-04	6.76E-02	0.18	0.02	2290

<i>MEIS1-AS3</i>	MEIS1 antisense RNA 3	7.9	1.78E-04	4.85E-02	0.35	0.04	730198
<i>NEXMIF</i>	Neurite Extension And Migration Factor	7.8	7.96E-07	3.52E-03	11.00	1.40	340533
<i>DLX2</i>	distal-less homeobox 2	7.4	2.61E-05	2.00E-02	14.15	1.90	1746

**Table S4
(Cont.)**

Genes Enriched in the Human DA by RNA-seq (Fold Change; DA vs Ao)

Gene Symbol	Gene Name	Fold Change	P-value	FDR	FPKM DA	FPK M Ao	Entrez ID
<i>MME</i>	membrane metalloendopeptidase	7.3	7.41E-05	3.17E-02	0.89	0.12	4311
<i>WIF1</i>	WNT inhibitory factor 1	7.2	1.11E-04	3.99E-02	0.94	0.13	11197
<i>LOC100130238</i>	uncharacterized LOC100130238	7.1	5.66E-05	2.89E-02	0.84	0.12	100130238
<i>CCDC129</i>	coiled-coil domain containing 129	7.0	3.81E-05	2.29E-02	0.96	0.14	223075
<i>SHISA2</i>	shisa family member 2	6.9	3.70E-06	7.75E-03	6.29	0.91	387914
<i>INMT</i>	indolethylamine N-methyltransferase	6.8	7.89E-05	3.23E-02	23.55	3.47	11185
<i>JAKMIP2</i>	janus kinase and microtubule interacting protein 2	6.7	2.06E-05	1.75E-02	2.20	0.33	9832
<i>HOXC4</i>	homeobox C4	6.7	1.37E-05	1.47E-02	2.72	0.41	3221
<i>MTCL1</i>	microtubule crosslinking factor 1	6.6	7.29E-06	1.05E-02	2.24	0.34	23255
<i>GLP2R</i>	glucagon like peptide 2 receptor	6.6	3.84E-04	7.77E-02	0.37	0.06	9340
<i>HOXA5</i>	homeobox A5	6.5	1.69E-04	4.71E-02	1.65	0.25	3202
<i>FAM84A</i>	family with sequence similarity 84 member A	6.5	7.32E-05	3.17E-02	0.67	0.10	151354
<i>SYT4</i>	synaptotagmin 4	6.2	5.70E-04	9.69E-02	0.50	0.08	6860
<i>GIRK1</i>	glutamate ionotropic receptor kainate type subunit 1	6.2	3.71E-04	7.61E-02	2.88	0.46	2897
<i>LIMK2</i>	LIM domain kinase 2	6.2	2.93E-06	6.85E-03	4.64	0.75	3985
<i>TNNC1</i>	troponin C1, slow skeletal and cardiac type	6.0	4.35E-04	8.33E-02	1.22	0.20	7134
<i>ARHGEF3</i>	Rho guanine nucleotide exchange factor 3	5.9	5.17E-04	9.18E-02	1.72	0.29	50650
<i>EPB42</i>	erythrocyte membrane protein band 4.2	5.9	1.11E-04	3.99E-02	1.46	0.25	2038
<i>ADAMTS9</i>	ADAM metallopeptidase with thrombospondin type 1 motif 9	5.8	1.09E-06	3.98E-03	68.53	11.83	56999
<i>THBS1</i>	thrombospondin 1	5.4	5.19E-06	9.38E-03	60.97	11.20	7057
<i>FREM3</i>	FRAS1 related extracellular matrix 3	5.4	5.21E-04	9.21E-02	1.04	0.19	166752
<i>FRZB</i>	frizzled-related protein	5.3	4.85E-05	2.62E-02	113.2	21.47	2487
<i>PIP5K1B</i>	phosphatidylinositol-4-phosphate 5-kinase type 1 beta	5.2	2.08E-04	5.37E-02	2.84	0.54	8395
<i>ISM1</i>	isthmin 1	5.0	5.45E-04	9.53E-02	0.80	0.16	140862
<i>SERPINB6</i>	serpin family B member 6	5.0	4.34E-04	8.33E-02	0.55	0.11	5269
<i>COL8A1</i>	collagen type VIII alpha 1 chain	4.8	3.72E-05	2.27E-02	5.21	1.09	1295
<i>MAMDC2</i>	MAM domain containing 2	4.8	2.79E-05	2.06E-02	20.56	4.30	256691
<i>CBLN2</i>	cerebellin 2 precursor	4.7	5.94E-05	2.92E-02	31.68	6.68	147381
<i>CD82</i>	CD82 molecule	4.4	4.87E-05	2.62E-02	5.01	1.13	3732
<i>PAMR1</i>	peptidase domain containing associated with muscle regeneration 1	4.3	1.98E-04	5.19E-02	2.37	0.54	25891
<i>DCLK2</i>	doublecortin like kinase 2	4.3	2.83E-06	6.85E-03	158.6	36.98	166614
<i>LINC00672</i>	long intergenic non-protein coding RNA 672	4.2	3.93E-04	7.86E-02	3.51	0.84	100505576
<i>GCNT2</i>	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	4.2	1.66E-04	4.71E-02	1.13	0.27	2651
<i>APCDD1L</i>	APC down-regulated 1 like	4.1	4.84E-04	8.88E-02	1.42	0.35	164284
<i>ENTPD1</i>	ectonucleoside triphosphate diphosphohydrolase 1	3.9	4.59E-05	2.57E-02	6.62	1.71	953
<i>ABCC9</i>	ATP binding cassette subfamily C member 9	3.8	2.36E-05	1.88E-02	12.06	3.17	10060
<i>HOXB4</i>	homeobox B4	3.8	3.61E-04	7.57E-02	1.12	0.30	3214
<i>CADM1</i>	cell adhesion molecule 1	3.7	3.97E-04	7.90E-02	3.86	1.05	23705
<i>HOXB3</i>	homeobox B3	3.5	6.07E-05	2.94E-02	16.72	4.79	3213
<i>SAMD11</i>	sterile alpha motif domain containing 11	3.5	4.69E-04	8.68E-02	82.12	23.69	148398
<i>DNAH14</i>	dynein axonemal heavy chain 14	3.3	2.80E-04	6.36E-02	5.58	1.67	127602
<i>LINC00607</i>	long intergenic non-protein coding RNA 607	3.3	4.54E-04	8.58E-02	2.71	0.83	646324
<i>HMGA2</i>	high mobility group AT-hook 2	3.2	4.57E-04	8.58E-02	5.04	1.59	8091
<i>LINC00623</i>	long intergenic non-protein coding RNA 623	3.2	2.62E-04	6.08E-02	21.25	6.72	728855
<i>RAI14</i>	retinoic acid induced 14	3.1	9.78E-05	3.79E-02	7.81	2.56	26064
<i>DOK6</i>	docking protein 6	3.0	2.03E-04	5.28E-02	7.04	2.32	220164
<i>HOMER1</i>	homer scaffolding protein 1	3.0	9.81E-05	3.79E-02	5.58	1.85	9456
<i>TENM3</i>	teneurin transmembrane protein 3	2.7	4.97E-04	8.99E-02	19.90	7.41	55714
<i>CAMK1D</i>	calcium/calmodulin dependent protein kinase ID	2.5	2.85E-04	6.36E-02	4.94	1.95	57118
<i>STIM2</i>	stromal interaction molecule 2	2.5	3.31E-04	7.12E-02	5.34	2.16	57620
<i>PRICKLE2</i>	prickle planar cell polarity protein 2	2.3	5.55E-04	9.56E-02	10.20	4.35	166336

Table S5

Genes Enriched in the Human Ao by RNA-seq (Fold Change; DA vs Ao)

Gene Symbol	Gene Name	Fold Change	P-value	FDR	FPKM DA	FPKM Ao	Entrez ID
<i>RIMS2</i>	regulating synaptic membrane exocytosis 2	-67.9	2.07E-05	1.75E-02	0.01	0.53	9699
<i>HPSE2</i>	heparanase 2 (inactive)	-24.6	1.21E-04	4.20E-02	0.01	0.17	60495
<i>DCSTAMP</i>	dendrocyte expressed seven transmembrane protein	-20.3	3.26E-05	2.24E-02	0.03	0.68	81501
<i>PPFIBP1</i>	PPFIA binding protein 1	-19.8	5.48E-04	9.53E-02	0.01	0.22	8496
<i>TM6SF1</i>	transmembrane 6 superfamily member 1	-17.8	6.76E-05	3.14E-02	0.01	0.22	53346
<i>MGAT4C</i>	MGAT4 family member C	-16.3	1.30E-04	4.26E-02	0.02	0.34	25834
<i>RAPSN</i>	receptor associated protein of the synapse	-15.7	1.04E-04	3.89E-02	0.03	0.46	5913
<i>TBX20</i>	T-box 20	-14.8	3.34E-04	7.13E-02	0.06	0.88	57057
<i>SPATA6L</i>	spermatogenesis associated 6 like	-14.6	1.27E-04	4.26E-02	0.01	0.15	55064
<i>ANXA8L1</i>	annexin A8-like 1	-14.2	1.58E-05	1.51E-02	0.16	2.30	728113
<i>STAC2</i>	SH3 and cysteine rich domain 2	-13.6	7.47E-05	3.17E-02	0.02	0.27	342667
<i>GAS2</i>	growth arrest specific 2	-13.4	3.66E-04	7.57E-02	0.01	0.07	2620
<i>BRINP2</i>	BMP/retinoic acid inducible neural specific 2	-12.3	1.46E-04	4.44E-02	0.03	0.37	57795
<i>NEIL1</i>	nei like DNA glycosylase 1	-11.4	5.04E-04	9.07E-02	0.00	0.05	79661
<i>RSPO2</i>	R-spondin 2	-11.2	4.25E-04	8.32E-02	0.06	0.69	340419
<i>RBFA</i>	ribosome binding factor A (putative)	-11.1	2.25E-04	5.59E-02	0.01	0.08	79863
<i>SLC26A6</i>	solute carrier family 26 member 6	-9.9	5.70E-04	9.69E-02	0.01	0.08	65010
<i>FCGR3A</i>	Fc fragment of IgG receptor IIIa	-9.9	4.28E-04	8.33E-02	0.01	0.07	2214
<i>MSLN</i>	mesothelin	-9.4	2.18E-04	5.55E-02	0.03	0.25	10232
<i>TFPI2</i>	tissue factor pathway inhibitor 2	-9.2	5.12E-05	2.68E-02	0.74	6.78	7980
<i>A4GALT</i>	alpha 1,4-galactosyltransferase	-8.9	1.48E-04	4.44E-02	0.04	0.38	53947
<i>GABRB2</i>	gamma-aminobutyric acid type A receptor beta2 subunit	-6.7	2.97E-05	2.15E-02	0.40	2.72	2561
<i>LDB3</i>	LIM domain binding 3	-6.6	1.20E-04	4.19E-02	0.14	0.89	11155
<i>LRP1B</i>	LDL receptor related protein 1B	-5.9	1.37E-05	1.47E-02	1.43	8.48	53353
<i>PKHD1L1</i>	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	-5.5	7.52E-05	3.17E-02	2.31	12.81	93035
<i>KALRN</i>	kalirin, RhoGEF kinase	-5.3	1.24E-04	4.21E-02	2.36	12.63	8997
<i>RBM20</i>	RNA binding motif protein 20	-5.1	6.84E-06	1.05E-02	1.72	8.76	282996
<i>RIPK4</i>	receptor interacting serine/threonine kinase 4	-5.1	3.27E-04	7.07E-02	0.09	0.44	54101
<i>MTUS2</i>	microtubule associated tumor suppressor candidate 2	-5.0	1.75E-05	1.55E-02	7.97	39.45	23281
<i>HAND2</i>	heart and neural crest derivatives expressed 2	-4.8	5.10E-05	2.68E-02	1.17	5.61	9464
<i>TACC2</i>	transforming acidic coiled-coil containing protein 2	-4.7	1.45E-05	1.47E-02	1.11	5.17	10579
<i>PLD5</i>	phospholipase D family member 5	-4.6	1.82E-04	4.85E-02	0.35	1.64	200150
<i>LINC01099</i>	long intergenic non-protein coding RNA 1099	-4.3	7.38E-05	3.17E-02	0.29	1.23	101928656
<i>CDH13</i>	cadherin 13	-4.2	1.43E-04	4.44E-02	3.69	15.67	1012
<i>MFAP3L</i>	microfibrillar associated protein 3 like	-4.2	2.42E-04	5.86E-02	0.34	1.44	9848
<i>PDE10A</i>	phosphodiesterase 10A	-4.0	1.33E-04	4.26E-02	1.22	4.89	10846
<i>KDEL1C1</i>	KDEL motif containing 1	-3.8	2.23E-04	5.59E-02	3.06	11.78	79070
<i>PHACTR1</i>	phosphatase and actin regulator 1	-3.7	4.03E-04	7.97E-02	0.70	2.61	221692
<i>PAPPA2</i>	pappalysin 2	-3.7	2.49E-04	5.90E-02	0.69	2.56	60676
<i>RYR2</i>	ryanodine receptor 2	-3.7	1.35E-04	4.28E-02	7.41	27.15	6262
<i>MAP3K7CL</i>	MAP3K7 C-terminal like	-3.7	3.54E-05	2.24E-02	2.64	9.66	56911
<i>SDK1</i>	sidekick cell adhesion molecule 1	-3.6	4.02E-05	2.39E-02	2.89	10.40	221935
<i>FAM19A2</i>	family with sequence similarity 19 member A2, C-C motif chemokine like	-3.6	2.49E-04	5.90E-02	1.54	5.51	338811
<i>KCNMA1</i>	potassium calcium-activated channel subfamily M alpha 1	-3.5	2.74E-04	6.27E-02	0.49	1.69	3778
<i>DUSP27</i>	dual specificity phosphatase 27 (putative)	-3.5	1.25E-04	4.21E-02	1.17	4.05	92235
<i>ASTN1</i>	astrotactin 1	-3.4	9.73E-05	3.79E-02	0.83	2.77	460
<i>KANK4</i>	KN motif and ankyrin repeat domains 4	-3.3	4.31E-04	8.33E-02	2.30	7.62	163782
<i>TMTC1</i>	transmembrane and tetratricopeptide repeat containing 1	-3.3	9.52E-05	3.79E-02	1.64	5.37	83857
<i>POSTN</i>	periostin	-3.2	1.45E-04	4.44E-02	49.83	161.49	10631
<i>FIGN</i>	fidgetin, microtubule severing factor	-3.2	3.12E-04	6.79E-02	2.64	8.54	55137
<i>RGS17</i>	regulator of G-protein signaling 17	-3.2	4.92E-04	8.97E-02	0.95	3.02	26575
<i>PAPPA</i>	pappalysin 1	-3.1	1.83E-04	4.85E-02	2.57	8.03	5069
<i>DSEL</i>	dermatan sulfate epimerase-like	-3.1	2.38E-04	5.84E-02	33.23	103.24	92126
<i>NOV</i>	nephroblastoma overexpressed	-3.0	3.40E-04	7.23E-02	10.92	32.35	4856
<i>CYFIP2</i>	cytoplasmic FMR1 interacting protein 2	-2.9	1.09E-04	3.99E-02	1.76	5.15	26999
<i>WWP2</i>	WW domain containing E3 ubiquitin protein ligase 2	-2.9	1.62E-04	4.71E-02	1.69	4.90	11060
<i>ADAM22</i>	ADAM metalloproteinase domain 22	-2.9	2.92E-04	6.49E-02	0.72	2.10	53616
<i>ZBTB16</i>	zinc finger and BTB domain containing 16	-2.8	5.48E-04	9.53E-02	0.64	1.80	7704
<i>PAPPA-AS1</i>	PAPPA antisense RNA 1	-2.7	1.48E-04	4.44E-02	5.10	13.89	493913
<i>RNF144A</i>	ring finger protein 144A	-2.7	5.55E-04	9.56E-02	3.67	9.98	9781
<i>FOXCUT</i>	FOXC1 upstream transcript (non-protein coding)	-2.7	5.62E-04	9.64E-02	0.65	1.74	101927703
<i>ERBB4</i>	erb-b2 receptor tyrosine kinase 4	-2.7	1.33E-04	4.26E-02	13.50	35.88	2066
<i>BVES</i>	blood vessel epicardial substance	-2.6	1.67E-04	4.71E-02	3.96	10.32	11149
<i>ADAMTS8</i>	ADAM metalloproteinase with thrombospondin type 1 motif 8	-2.6	6.86E-05	3.14E-02	6.12	15.95	11095
<i>PRELP</i>	proline and arginine rich end leucine rich repeat protein	-2.5	4.60E-04	8.59E-02	1.11	2.75	5549
<i>NPR1</i>	natriuretic peptide receptor 1	-2.5	3.79E-04	7.74E-02	17.33	42.88	4881
<i>ENPP1</i>	ectonucleotide pyrophosphatase/phosphodiesterase 1	-2.3	2.55E-04	5.96E-02	28.96	67.73	5167

Table S6 **Differentially Expressed Genes Most Highly Expressed in the Human DA by RNA-seq (Fold Change; DA vs Ao)**

Gene ID	Gene Name	Fold change	P-value	FDR	FPKM DA	FPKM Ao	Entrez Gene
<i>DCLK2</i>	doublecortin like kinase 2	4.3	2.83E-06	6.85E-03	158.67	36.98	166614
<i>FRZB</i>	frizzled-related protein	5.3	4.85E-05	2.62E-02	113.24	21.47	2487
<i>TNC</i>	tenascin C	12.1	7.76E-08	1.60E-03	99.27	8.22	3371
<i>SAMD11</i>	sterile alpha motif domain containing 11	3.5	4.69E-04	8.68E-02	82.12	23.69	148398
<i>ADAMTS9</i>	ADAM metalloproteinase with thrombospondin type 1 motif 9	5.8	1.09E-06	3.98E-03	68.53	11.83	56999
<i>THBS1</i>	thrombospondin 1	5.4	5.19E-06	9.38E-03	60.97	11.20	7057
<i>CBLN2</i>	cerebellin 2 precursor	4.7	5.94E-05	2.92E-02	31.68	6.68	147381
<i>INMT</i>	indoletylamine N-methyltransferase	6.8	7.89E-05	3.23E-02	23.55	3.47	11185
<i>PTGER4</i>	prostaglandin E receptor 4	20.5	9.38E-08	1.60E-03	21.27	1.04	5734
<i>LINC00623</i>	long intergenic non-protein coding RNA 623	3.2	2.62E-04	6.08E-02	21.25	6.72	728855
<i>MAMDC2</i>	MAM domain containing 2	4.8	2.79E-05	2.06E-02	20.56	4.30	256691
<i>C1QTNF3</i>	C1q and tumor necrosis factor related protein 3	9.5	1.21E-05	1.42E-02	20.52	2.16	114899
<i>TENM3</i>	teneurin transmembrane protein 3	2.7	4.97E-04	8.99E-02	19.90	7.41	55714
<i>MAB21L2</i>	mab-21 like 2	25.3	2.08E-06	5.51E-03	16.77	0.66	10586
<i>HOXB3</i>	homeobox B3	3.5	6.07E-05	2.94E-02	16.72	4.79	3213
<i>DLX2</i>	distal-less homeobox 2	7.4	2.61E-05	2.00E-02	14.15	1.90	1746
<i>ABCC9</i>	ATP binding cassette subfamily C member 9	3.8	2.36E-05	1.88E-02	12.06	3.17	10060
<i>NEXMIF</i>	Neurite Extension And Migration Factor	7.8	7.96E-07	3.52E-03	11.00	1.40	340533
<i>KRT17</i>	keratin 17	24.6	5.31E-05	2.74E-02	10.97	0.45	3872
<i>PRICKLE2</i>	prickle planar cell polarity protein 2	2.3	5.55E-04	9.56E-02	10.20	4.35	166336

Table S7 GO, KEGG, and UP Keywords Common in Human RNA-seq and Rodent Microarrays

	RNA-seq Count	RNA-seq PValue	Microarray Count ¹	Microarray PValue
GO Biological Process – Overlap: 30/62 Common 48.4%				
GO:0001501–skeletal system development	6	7.53E-03	10	1.87E-05
GO:0001525–angiogenesis	6	4.88E-02	8	1.79E-02
GO:0001822–kidney development	4	4.11E-02	14	2.86E-07
GO:0006366–transcription from RNA polymerase II promoter	9	8.68E-02	15	2.10E-03
GO:0007155–cell adhesion	16	1.45E-05	16	6.55E-06
GO:0007166–cell surface receptor signaling pathway	6	9.73E-02	10	1.98E-03
GO:0007188–adenylate cyclase-modulating G-protein coupled receptor signaling pathway	3	4.25E-02	3	7.81E-02
GO:0007399–nervous system development	7	4.30E-02	10	2.52E-03
GO:0007420–brain development	5	8.88E-02	13	1.61E-03
GO:0007507–heart development	6	2.36E-02	19	2.22E-07
GO:0008284–positive regulation of cell proliferation	9	5.61E-02	23	4.38E-06
GO:0009612–response to mechanical stimulus	5	1.86E-03	10	2.02E-05
GO:0009952–anterior/posterior pattern specification	5	5.59E-03	7	6.59E-03
GO:0010628–positive regulation of gene expression	6	8.42E-02	19	8.36E-06
GO:0010811–positive regulation of cell-substrate adhesion	3	4.47E-02	4	2.73E-02
GO:0016337–single organismal cell-cell adhesion	9	3.20E-06	6	1.84E-02
GO:0016525–negative regulation of angiogenesis	4	1.77E-02	4	7.07E-02
GO:0021766–hippocampus development	3	8.83E-02	5	4.93E-02
GO:0030198–extracellular matrix organization	14	2.09E-08	10	1.15E-05
GO:0030308–negative regulation of cell growth	6	4.48E-03	9	4.04E-04
GO:0042475–odontogenesis of dentin-containing tooth	4	1.28E-02	5	1.46E-02
GO:0043065–positive regulation of apoptotic process	11	3.50E-04	11	2.57E-02
GO:0045600–positive regulation of fat cell differentiation	3	6.52E-02	4	3.40E-02
GO:0048704–embryonic skeletal system morphogenesis	3	4.68E-02	5	8.76E-03
GO:0050715–positive regulation of cytokine secretion	3	2.05E-02	3	7.81E-02
GO:0051216–cartilage development	5	1.86E-03	6	3.04E-03
GO:0060441–epithelial tube branching involved in lung morphogenesis	4	2.88E-04	4	4.85E-03
GO:0071356–cellular response to tumor necrosis factor	4	7.45E-02	7	1.30E-02
GO:0072210–metanephric nephron development	2	1.77E-02	2	5.67E-02
GO:0097070–ductus arteriosus closure	2	4.36E-02	2	8.38E-02
GO Cellular Component – Overlap: 12/19 Common, 63.2%	Count	PValue	Count	PValue
GO:0005576–extracellular region	22	5.39E-02	18	2.87E-02
GO:0005578–proteinaceous extracellular matrix	12	3.19E-05	31	3.83E-19
GO:0005615–extracellular space	21	1.85E-02	46	3.97E-08
GO:0005886–plasma membrane	52	7.34E-03	78	1.91E-03
GO:0005887–integral component of plasma membrane	23	8.29E-03	28	4.81E-04
GO:0009897–external side of plasma membrane	7	1.27E-02	8	8.98E-02
GO:0016020–membrane	31	1.29E-02	48	3.18E-03
GO:0030424–axon	6	5.05E-02	15	7.40E-04
GO:0030425–dendrite	7	8.26E-02	18	5.96E-04
GO:0031012–extracellular matrix	11	3.57E-04	23	1.62E-11
GO:0043005–neuron projection	6	6.34E-02	17	1.82E-04
GO:0045211–postsynaptic membrane	7	1.22E-02	8	2.35E-02
GO Molecular Function – Overlap: 9/19 Common, 47.4%	Count	PValue	Count	PValue
GO:0001077–transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	6	6.38E-02	11	4.61E-03
GO:0005178–integrin binding	7	3.87E-04	9	1.17E-04
GO:0005201–extracellular matrix structural constituent	4	2.29E-02	6	5.65E-04
GO:0005509–calcium ion binding	17	8.07E-04	23	6.72E-04
GO:0008201–heparin binding	6	1.53E-02	13	1.77E-06
GO:0042803–protein homodimerization activity	12	6.82E-02	29	2.36E-05
GO:0043565–sequence-specific DNA binding	9	9.93E-02	15	4.36E-02
GO:0044325–ion channel binding	4	8.33E-02	9	6.00E-04
GO:0050839–cell adhesion molecule binding	4	1.87E-02	4	8.78E-02
Kegg Pathway – Overlap: 5/9 Common, 55.6%	Count	PValue	Count	PValue
hsa04020–Calcium signaling pathway	8	1.13E-03	11	4.17E-04
hsa04024–cAMP signaling pathway	6	3.38E-02	10	2.45E-03
hsa04724–Glutamatergic synapse	4	8.53E-02	5	9.25E-02
hsa04911–Insulin secretion	4	4.21E-02	7	1.72E-03
hsa04924–Renin secretion	4	2.03E-02	5	1.75E-02
UP Keywords – Overlap: 22/37 Common, 59.5%	Count	PValue	Count	PValue
Alternative splicing	108	2.76E-03	41	4.73E-11
Calcium	21	4.63E-05	18	2.18E-03
cAMP	3	3.63E-02	3	4.54E-02
Cell adhesion	23	9.66E-11	12	1.52E-03
Cell junction	16	5.61E-04	11	8.95E-02
Cell membrane	43	1.35E-03	53	1.74E-02
Cleavage on pair of basic residues	7	3.74E-02	12	2.45E-05
Collagen	5	9.26E-03	4	5.19E-02

Developmental protein	19	1.02E-03	22	2.44E-06
Disulfide bond	56	5.71E-07	75	1.21E-14
EGF-like domain	10	1.82E-04	9	1.81E-03
Extracellular matrix	14	2.77E-07	11	1.06E-05
Glycoprotein	83	1.03E-13	72	6.87E-14
Heparin-binding	4	3.76E-02	7	4.75E-05
Hydroxylation	4	4.54E-02	6	5.90E-04
Immunoglobulin domain	12	6.32E-03	10	6.76E-03
Membrane	81	4.02E-03	112	2.91E-02
Metalloprotease	5	3.88E-02	5	4.29E-02
Secreted	36	1.31E-05	40	3.87E-09
Signal	73	7.28E-11	88	1.99E-10
Signal-anchor	9	3.78E-02	7	7.95E-02
Synapse	14	1.02E-05	8	9.50E-02

[†]Number of genes identified within each term

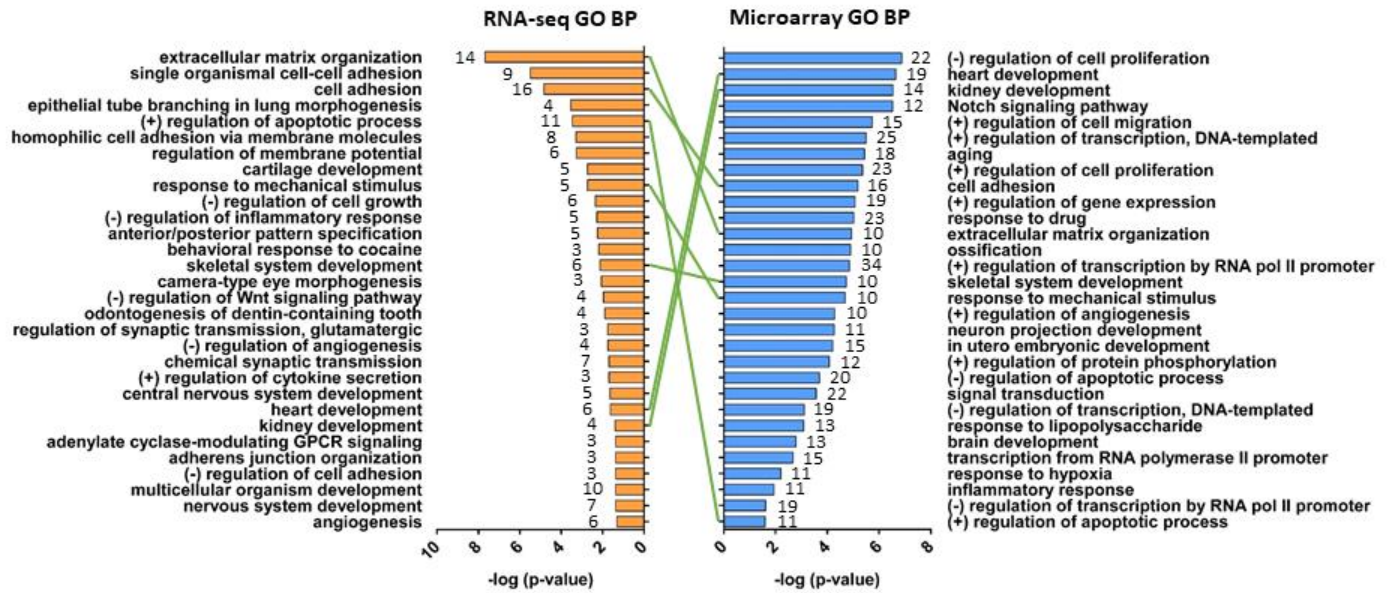


Figure S1. 'Tornadogram' showing top 30 GO Biological Process (BP) terms common between Microarray and RNAseq analyses. Genes differentially expressed in DA vs. Ao were categorized by functional annotation (DAVID), plotted by p-value, and compared across platforms. Number of genes represented in each category shown at the end of bars.

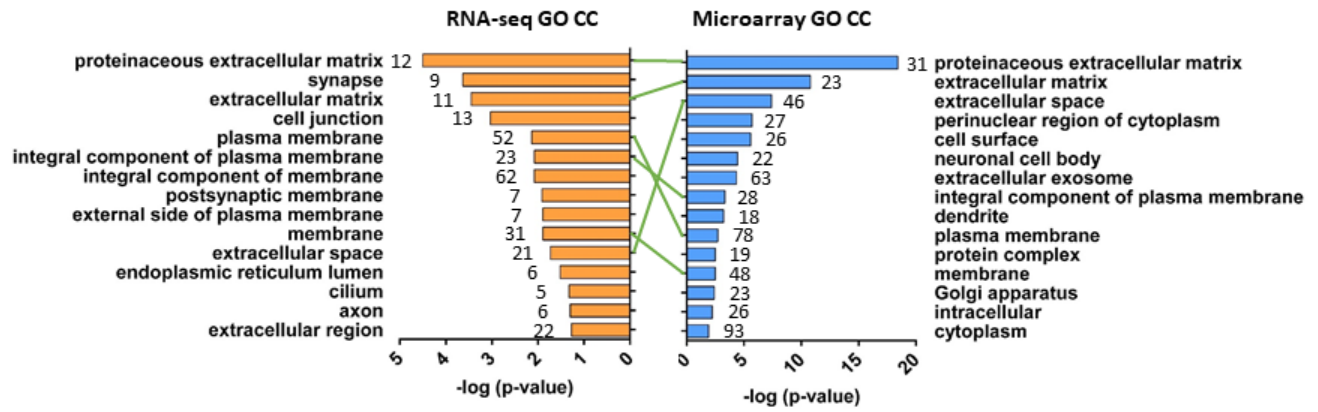


Figure S2. ‘Tornadogram’ showing top 30 GO Cellular Component (CC) terms common between Microarray and RNAseq analyses. Genes differentially expressed in DA vs. Ao were categorized by functional annotation (DAVID), plotted by p-value, and compared across platforms. Number of genes represented in each category shown at the end of bars.