

Supplementary Table 3. Biogroups showing significant overlap with both postmortem schizophrenia brain tissue and the PFC in Shn-2 KO mice.

Rank	Biogroup name	Source	BA10 in schizophrenia				PFC in Shn-2 KO					
			Common genes	Direction	P value	common genes (opposite direction)	P value	Common genes	Direction	P value	Common genes (opposite direction)	P value
1	response to stress	GO	125	up	5.4E-44	78	1.0E-04	36	up	1.9E-03	18	8.3E-01
2	immune response	GO	76	up	3.9E-37	17	3.8E-01	24	up	4.3E-07	5	8.9E-01
3	response to wounding	GO	65	up	3.5E-34	22	1.1E-01	22	up	4.8E-08	7	4.4E-01
4	inflammatory response	GO	49	up	6.8E-33	12	1.2E-01	19	up	7.4E-10	4	1.3E-01
5	synaptic transmission	GO	57	down	5E-32	10	1.5E-01	11	down	2.5E-02	7	5.5E-01
6	transmission of nerve impulse	GO	59	down	3.2E-29	12	1.4E-01	12	down	4.1E-02	9	4.7E-01
7	cell-cell signaling	GO	74	down	5.5E-28	26	5.0E-03	18	down	5.9E-03	16	6.5E-02
8	immune effector process	GO	33	up	4.7E-24	5	6.5E-01	14	up	4.6E-06	2	7.2E-01
9	regulation of response to stimulus	GO	46	up	7.7E-24	21	1.7E-01	23	up	2.5E-07	6	5.1E-01
10	regulation of immune system process	GO	41	up	1.3E-21	12	6.6E-01	18	up	2.9E-06	6	4.2E-01
11	leukocyte mediated immunity	GO	25	up	2.5E-20	4	3.2E-01	14	up	1.1E-07	1	6.1E-01
12	Neutrophil Pathway	Broad MSigDB - Canonical Pathways	6	up	2.8E-20	0		0			0	
13	neuron projection	GO	51	down	8.3E-20	8	9.1E-01	22	up	3.3E-06	15	1.6E-02
14	positive regulation of immune system process	GO	33	up	1.1E-19	5	1.7E-01	15	up	8.9E-07	4	6.2E-01
15	regulation of immune response	GO	31	up	5.2E-19	7	6.9E-01	14	up	7.7E-06	1	7.3E-01
16	transport	GO	170	down	9.9E-19	91	3.1E-06	61	up	2.1E-02	45	1.6E-01
17	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	GO	20	up	1.9E-18	3	8.4E-01	11	up	9.6E-08	1	5.2E-01
18	response to other organism	GO	33	up	3.3E-18	10	2.2E-01	5	up	2.2E-01	2	5.8E-01
19	positive regulation of signal transduction	GO	31	up	3.3E-18	8	4.1E-01	8	up	3.8E-06	6	1.3E-01
20	adaptive immune response	GO	20	up	3.8E-18	3	8.6E-01	11	up	9.6E-08	1	5.2E-01
21	response to organic substance	GO	57	up	5.6E-18	52	3.3E-05	27	up	1.5E-05	10	5.5E-01
22	Metallothionein superfamily, eukaryotic	InterPro	6	up	6E-18	0		0			0	
23	Metallothionein, vertebrate	InterPro	6	up	6E-18	0		0			0	
24	Monocyte Pathway	Broad MSigDB - Canonical Pathways	6	up	2.1E-17	0		1	down	1.7E-01		
25	E12 binding site geneset 2	Broad MSigDB - Regulatory Motifs	150	down	7.6E-17	80	6.4E-06	62	up	3.0E-04	57	1.3E-03
26	cell death	GO	68	up	8.3E-17	61	1.0E-04	30	up	8.1E-05	16	7.9E-01
27	death	GO	68	up	1E-16	61	1.0E-04	30	up	9.1E-05	16	8.0E-01
28	lymphocyte mediated immunity	GO	19	up	1.2E-16	3	8.3E-01	11	up	1.7E-07	1	5.3E-01
29	acute inflammatory response	GO	17	up	1.3E-16	3	1.4E-01	11	up	4.9E-09	2	2.3E-01
30	cell proliferation	GO	68	up	1.6E-16	47	2.5E-02	35	up	4.8E-08	17	1.8E-01
31	synapse	GO	44	down	2.3E-16	5	8.6E-01	14	down	1.5E-03	17	3.1E-03
32	Lymphocyte Pathway	Broad MSigDB - Canonical Pathways	5	up	2.9E-16	0		1	down	1.4E-01	0	
33	Hematopoietic Cell Lineage	Broad MSigDB - Canonical Pathways	16	up	3.7E-16	1	9.0E-01	5	up	2.7E-05	1	6.4E-01
34	response to external stimulus	GO	40	up	1.8E-15	29	9.7E-02	17	up	4.0E-05	5	8.1E-02
35	cytokine binding	GO	18	up	2E-15	0		0			0	

36	Predicted Gene Targets for miR-30	TargetScan miRNA targets DB	70	down	3.3E-15	22	4.7E-02	23	down	4.6E-03	24	8.0E-03
37	response to hypoxia	GO	19	up	8.5E-15	7	2.9E-01	4	down	1.4E-02	3	1.6E-02
38	Predicted Gene Targets for miR-381	TargetScan miRNA targets DB	55	down	8.5E-15	15	1.8E-01	15	down	1.9E-01	7	9.5E-01
39	Complement and Coagulation Cascades	Broad MSigDB - Canonical Pathways	11	up	1.3E-14	0		6	up	6.9E-06	1	3.7E-01
40	cell differentiation	GO	84	up	1.5E-14	87	1.7E-06	55	up	3.9E-06	51	2.0E-04
41	vasculature development	GO	30	up	3.6E-14	13	6.9E-01	20	up	2.9E-07	11	3.8E-02
42	Cell Adhesion Molecules (CAMs)	Broad MSigDB - Canonical Pathways	21	up	4.2E-14	5	3.0E-01	5	down	5.2E-02	4	1.9E-01
43	Calcium Regulation In Cardiac Cells	Broad MSigDB - Canonical Pathways	25	down	4.2E-14	4	7.3E-01	6	down	1.7E-03	4	3.3E-01
44	Cytokine Cytokine Receptor Interaction	Broad MSigDB - Canonical Pathways	25	up	4.6E-14	4	9.3E-01	9	up	9.2E-03	4	8.2E-02
45	cellular component movement	GO	40	up	4.7E-14	41	8.6E-05	21	up	2.0E-04	16	8.6E-02
46	MMP Cytokine Connection	Broad MSigDB - Canonical Pathways	7	up	9.1E-14	0		0			0	
47	MAZ binding site geneset 2	Broad MSigDB - Regulatory Motifs	130	down	9.8E-14	73	9.5E-05	62	up	1.9E-06	48	6.9E-02
48	ATF3 binding site geneset 3	Broad MSigDB - Regulatory Motifs	47	down	1.2E-13	14	2.1E-01	14	up	2.4E-02	10	1.2E-01
49	CREBP1 binding site geneset 2	Broad MSigDB - Regulatory Motifs	30	down	2.7E-13	8	3.2E-01	8	down	3.8E-03	4	4.1E-01
50	positive regulation of response to stimulus	GO	29	up	2.7E-13	11	5.3E-02	15	up	1.4E-07	5	2.8E-01
51	AP1 binding site geneset 9	Broad MSigDB - Regulatory Motifs	69	down	3.1E-13	41	3.4E-05	35	up	2.0E-04	26	5.1E-03
52	innate immune response	GO	25	up	4.1E-13	3	5.0E-01	7	up	1.0E-04	1	6.5E-01
53	ATF1 binding site geneset 1	Broad MSigDB - Regulatory Motifs	25	down	4.5E-13	6	6.8E-01	7	down	9.0E-02	2	8.6E-01
54	ion transport	GO	60	down	5.2E-13	20	1.1E-01	8	up	1.0E-04	21	3.0E-04
55	LEF1 binding site geneset 4	Broad MSigDB - Regulatory Motifs	128	down	5.6E-13	62	2.0E-04	44	down	2.3E-02	43	5.1E-01
56	Immunoglobulin-like fold	InterPro	41	up	5.7E-13	12	8.2E-01	20	up	2.0E-06	7	5.4E-01
57	negative regulation of response to stimulus	GO	12	up	6E-13	7	1.8E-01	8	up	1.7E-03	1	2.1E-02
58	response to endogenous stimulus	GO	34	up	7.5E-13	37	8.8E-05	12	up	5.6E-03	6	2.4E-01
59	immune system development	GO	30	up	8.9E-13	9	4.3E-01	18	up	3.2E-05	6	2.3E-01
60	regulation of anatomical structure morphogenesis	GO	28	up	1E-12	15	8.5E-02	19	up	1.7E-05	12	2.6E-03
61	SP1 binding site geneset 6	Broad MSigDB - Regulatory Motifs	156	down	1.2E-12	65	6.0E-01	56	down	5.7E-02	58	2.8E-01
62	AP4 binding site geneset 5	Broad MSigDB - Regulatory Motifs	92	down	1.4E-12	49	1.7E-03	49	up	1.8E-05	36	1.3E-03
63	Calcium Signaling Pathway	Broad MSigDB - Canonical Pathways	24	down	2.3E-12	4	8.2E-01	5	up	1.6E-01	5	2.5E-01
64	leukocyte migration	GO	15	up	2.7E-12	3	4.5E-01	0			0	
65	production of molecular mediator of immune response	GO	11	up	2.8E-12	3	4.8E-01	0			0	
66	growth	GO	27	up	3.5E-12	20	4.6E-01	18	up	1.7E-02	8	7.5E-01
67	CREB binding site geneset 1	Broad MSigDB - Regulatory Motifs	28	down	3.6E-12	7	5.0E-01	7	down	2.8E-02	0	
68	response to hormone stimulus	GO	32	up	4.1E-12	31	1.4E-03	12	up	2.0E-03	6	1.6E-01

69	wound healing	GO	18	up	4.5E-12	5	8.2E-01	0		0		
70	Predicted Gene Targets for miR-330	TargetScan miRNA targets DB	37	down	5.6E-12	9	6.3E-01	9	down	1.5E-01	5	9.4E-01
71	cell projection part	GO	37	down	5.8E-12	6	9.1E-01	10	down	2.5E-02	7	1.8E-01
72	Immunoglobulin-like	InterPro	36	up	6E-12	14	5.5E-01	20	up	5.9E-06	7	3.9E-01
73	regulation of cell size	GO	18	up	7.9E-12	12	2.6E-01	8	up	6.4E-02	3	7.2E-01
74	cell growth	GO	17	up	8.7E-12	12	1.9E-01	8	up	4.2E-02	3	6.6E-01
75	positive regulation of programmed cell death	GO	33	up	1E-11	23	3.1E-02	17	up	4.8E-08	6	6.3E-01
76	cell junction	GO	48	down	1.1E-11	21	5.0E-04	22	up	1.2E-05	10	9.5E-02
77	CREBP1CJUN binding site geneset 1	Broad MSigDB - Regulatory Motifs	27	down	1.4E-11	6	5.0E-01	6	down	7.2E-02		0
78	hemopoiesis	GO	26	up	1.9E-11	9	3.8E-01	14	up	4.0E-04	5	3.0E-01
79	learning or memory	GO	18	down	1.9E-11	1	6.6E-01	6	down	2.8E-03	5	4.7E-02
80	Predicted Gene Targets for miR-181	TargetScan miRNA targets DB	49	down	2E-11	20	5.3E-02	14	down	1.1E-01	12	6.4E-01
81	Predicted Gene Targets for miR-539	TargetScan miRNA targets DB	33	down	2E-11	10	2.7E-01	12	down	2.8E-03	5	4.6E-01
82	cell activation	GO	31	up	2.1E-11	17	3.0E-03	17	up	5.0E-04	9	2.7E-01
83	activation of immune response	GO	18	up	2.2E-11	3	3.2E-01	0				0
84	cell migration	GO	31	up	2.2E-11	29	1.1E-03	16	up	1.2E-03	11	1.9E-01
85	hemopoietic or lymphoid organ development	GO	27	up	2.2E-11	9	4.0E-01	16	up	2.0E-04	6	1.9E-01
86	Complement Pathway	Broad MSigDB - Canonical Pathways	6	up	2.4E-11	0		0				0
87	NRSF binding site geneset 1	Broad MSigDB - Regulatory Motifs	16	down	2.4E-11	0		3	up	2.2E-01	1	5.8E-01
88	regulation of neurological system process	GO	20	down	3E-11	4	5.7E-01	4	down	1.2E-01	5	3.9E-01
89	regulation of angiogenesis	GO	13	up	3E-11	3	4.6E-01	0				0
90	ATF binding site geneset 2	Broad MSigDB - Regulatory Motifs	23	down	3.3E-11	4	7.0E-01	4	down	1.4E-01		0
91	Smooth Muscle Contraction	Broad MSigDB - Canonical Pathways	22	down	3.4E-11	6	1.5E-01	5	down	2.7E-03	7	3.4E-02
92	membrane raft	GO	18	up	3.5E-11	9	1.1E-01	5	up	5.3E-02	4	2.9E-01
93	vesicle	GO	62	down	3.8E-11	29	4.0E-04	19	up	3.0E-04	13	2.6E-01
94	positive regulation of immune response	GO	21	up	4E-11	3	5.5E-01	11	up	1.3E-05	1	6.0E-01
95	behavior	GO	41	down	4.1E-11	22	4.0E-04	16	down	9.5E-03	14	1.6E-02
96	cellular response to stimulus	GO	50	up	4.3E-11	47	8.6E-03	21	up	2.8E-02	9	9.7E-01
97	MYOD binding site geneset 4	Broad MSigDB - Regulatory Motifs	64	down	4.6E-11	32	2.2E-02	23	down	1.1E-03	28	2.4E-03
98	Predicted Gene Targets for miR-25	TargetScan miRNA targets DB	42	down	5.4E-11	13	6.7E-01	19	up	8.3E-05	11	4.2E-02
99	Gamma-aminobutyric acid A receptor	InterPro	6	down	5.6E-11	0		1	down	3.5E-03		0
100	immunoglobulin production	GO	8	up	5.9E-11	3	3.1E-01	0				0
101	transporter activity	GO	71	down	7.1E-11	29	1.3E-01	19	down	2.0E-02	20	2.9E-01
102	regulation of neurotransmitter levels	GO	14	down	8.1E-11	0		4	down	5.3E-02	3	2.0E-01
103	regulation of transmission of nerve impulse	GO	19	down	8.4E-11	4	5.3E-01	4	down	9.1E-02	4	4.1E-01
104	cytoplasmic vesicle	GO	60	down	1.1E-10	28	4.0E-04	17	up	1.3E-03	13	1.8E-01
105	regulation of peptidyl-tyrosine phosphorylation	GO	8	up	1.1E-10	2	1.8E-01	4	up	5.4E-02	1	4.5E-01
106	calmodulin binding	GO	18	down	1.2E-10	5	5.5E-01	6	up	8.0E-04	4	3.8E-03

107 localization of cell	GO	31	up	1.3E-10	30	1.6E-03	16	up	2.5E-03	12	1.6E-01
108 Interferon-induced transmembrane protein	InterPro	3	up	1.5E-10	0		0			0	
109 membrane-bounded vesicle	GO	57	down	1.5E-10	29	9.1E-05	10	up	3.0E-02	10	1.5E-01
110 locomotion	GO	37	up	1.7E-10	35	4.0E-04	17	up	6.2E-03	12	3.1E-01
111 cytokine production	GO	21	up	1.9E-10	5	7.4E-01	11	up	2.0E-04	4	9.1E-03
112 receptor binding	GO	63	down	2.4E-10	46	5.3E-09	18	up	1.2E-03	20	3.9E-03
113 complement activation	GO	10	up	2.5E-10	0		0			0	
114 Predicted Gene Targets for miR-26	TargetScan miRNA targets DB	47	down	2.6E-10	17	1.7E-01	0			0	
115 response to bacterium	GO	20	up	2.7E-10	6	3.1E-01	4	up	1.5E-01	1	4.9E-01
116 cytoplasmic membrane-bounded vesicle	GO	56	down	3E-10	28	1.0E-04	10	down	1.1E-01	8	1.2E-01
117 regulation of immune effector process	GO	13	up	3E-10	2	9.4E-01	5	up	5.9E-02	1	4.7E-01
118 NFAT binding site geneset 3	Broad MSigDB – Regulatory Motifs	110	down	4.3E-10	64	1.7E-05	48	down	2.0E-04	44	3.0E-02
119 FOXO4 binding site geneset 3	Broad MSigDB – Regulatory Motifs	121	down	4.4E-10	75	1.6E-06	50	down	1.2E-03	34	5.7E-01
120 regulation of cellular component movement	GO	22	up	4.9E-10	17	1.4E-02	0			0	
121 response to steroid hormone stimulus	GO	21	up	5.2E-10	13	1.0E-01	4	down	2.7E-02	4	1.3E-01
122 ATF binding site geneset 1	Broad MSigDB – Regulatory Motifs	26	down	5.2E-10	4	7.7E-01	5	down	5.4E-03	3	5.7E-01
123 site of polarized growth	GO	12	down	5.3E-10	1	7.9E-01	4	up	8.0E-04	2	5.1E-01
124 axon	GO	25	down	5.4E-10	4	8.1E-01	8	down	7.6E-02	4	8.4E-01
125 positive regulation of developmental process	GO	28	up	5.8E-10	12	6.8E-01	22	up	5.7E-09	16	1.0E-04
126 axon part	GO	17	down	5.9E-10	8	6.1E-10	5	down	3.6E-02	0	
127 positive regulation of cellular component movement	GO	16	up	7.3E-10	10	3.1E-02	5	up	7.9E-02	3	1.0E-01
128 morphogenesis of a branching structure	GO	13	up	7.3E-10	2	9.9E-01	8	up	3.0E-04	5	4.7E-02
129 leukocyte activation	GO	27	up	7.7E-10	14	2.8E-03	16	up	5.0E-04	8	3.2E-01
130 MAPK Signaling Pathway	Broad MSigDB – Canonical Pathways	26	down	8.2E-10	16	2.4E-03	16	up	3.1E-06	5	6.5E-01
131 negative regulation of developmental process	GO	22	up	9.1E-10	14	1.9E-01	14	down	7.0E-04	12	3.2E-02
132 ATF3 binding site geneset 2	Broad MSigDB – Regulatory Motifs	24	down	9.6E-10	4	7.8E-01	6	down	3.0E-02	0	
133 myeloid cell differentiation	GO	16	up	9.7E-10	4	7.9E-01	11	up	4.3E-06	2	1.2E-01
134 neuronal cell body	GO	24	down	9.9E-10	4	7.9E-01	19	up	9.0E-10	9	2.6E-02
135 response to organic cyclic substance	GO	13	up	9.9E-10	9	2.6E-02	0			0	
136 Predicted Gene Targets for miR-1	TargetScan miRNA targets DB	40	down	9.9E-10	10	7.0E-01	11	down	6.5E-02	6	2.8E-01
137 cell surface	GO	23	up	1.0E-09	13	5.3E-01	15	up	1.1E-07	9	7.3E-02
138 CD44 antigen	InterPro	1	up	1.1E-09	0		0			0	
139 CREB binding site geneset 4	Broad MSigDB – Regulatory Motifs	28	down	1.1E-09	7	5.2E-01	5	up	3.1E-02	8	8.2E-02
140 generation of a signal involved in cell-cell signaling	GO	18	down	1.2E-09	4	7.0E-01	11	down	2.1E-03	10	6.0E-03

BA10, Brodmann Area 10; PFC, prefrontal cortex; GO, the Gene Ontology.

“Biogroup name”: A collection of genes that are associated with a specific biological function, pathway, or similar criteria.

“Source”: Data source from which the biogroups are derived as follows:

Gene Ontology (biological processes, cellular components, molecular functions)

MSigDB (canonical pathways, positional gene sets, regulatory motif gene sets)

InterPro (protein families)

TargetScan (predicted miRNA targets)

"Common genes": Number of overlapping genes in the bioset and the biogroup

"Direction": direction of expression for each gene in the biosets (up-regulated or down-regulated)

"p-value": Probability that such an overlap would occur by chance assuming that there is no biological link between the bioset and the biogroup

"Common genes (opposite direction)": Number of overlapping genes between the bioset and the biogroup, but the direction of the expression change was different from each other

Biogroups related to inflammation

- up up-regulated genes expressed in each bioset
- down down-regulated genes expressed in each bioset

Bioset vs Biogroups record downloaded from NextBio(2012/03/08 21:37:19)

Bioset: Brain BA10 from all schizophrenic samples _vs_ controls above control group mean pH6.5

Study: Post-mortem tissue from brain BA10 region of schizophrenic and control patients

Bioset vs Biogroups record downloaded from NextBio(2012/04/06 17:12:16)

Bioset: Prefrontal cortex from Shn2 KO mice _vs_ wildtype mice

Study: Shn2_PFC

<https://www.nextbio.com/b/search/bg/?type=bioset&id=101611>