Coordinated mRNA/microRNA Changes in Fibroblasts of Patients with Major Depression

Supplemental Information

Table S1. Subject information

Group	ID	Age	Avg Age	Sex	Race	BMI	Group	ID	Age	Avg Age	Sex	Race	BMI
CNTR1	C1	34	37.5	M	AA	23.1	MDD1	D1	38	36.5	M	AA	31.6
	C2	38		M	W	20.5		D2	33		M	W	41.9
	C3	48		M	W	N/A		D3	46		M	W	31
	C4	30		M	W	N/A		D4	29		M	W	19
CNTR2	C5	35	32.25	F	W	27.1	MDD2	D5	34	31	F	W	N/A
	C6	40		F	W	21.2		D6	37		F	W	N/A
	C7	27		F	W	21.8		D7	27		F	W	46.2
	C8	27		F	AA	34.7		D8	26		F	AA	31.4
CNTR3	C9	51	49	F	AA	26	MDD3	D9	51	49.75	F	AA	28.9
	C10	49		F	W	26.2		D10	52		F	W	24
	C11	52		F	W	26.3		D11	53		F	W	28
	C12	44		F	W	25.1		D12	43		F	W	50.7
CNTR4	C13	20	21.8	F	W	24	MDD4	D13	22	22.4	F	W	49.8
	C14	22		F	W	26.8		D14	22		F	W	22.5
	C15	22		F	W	22		D15	23		F	W	30.1
	C16	25		F	AA	30.5		D16	23		F	AA	18.4

AA, African-American; Avg, average; BMI, body mass index; CNTR, controls; F, female; M, male; MDD, major depressive disorder; W, white.

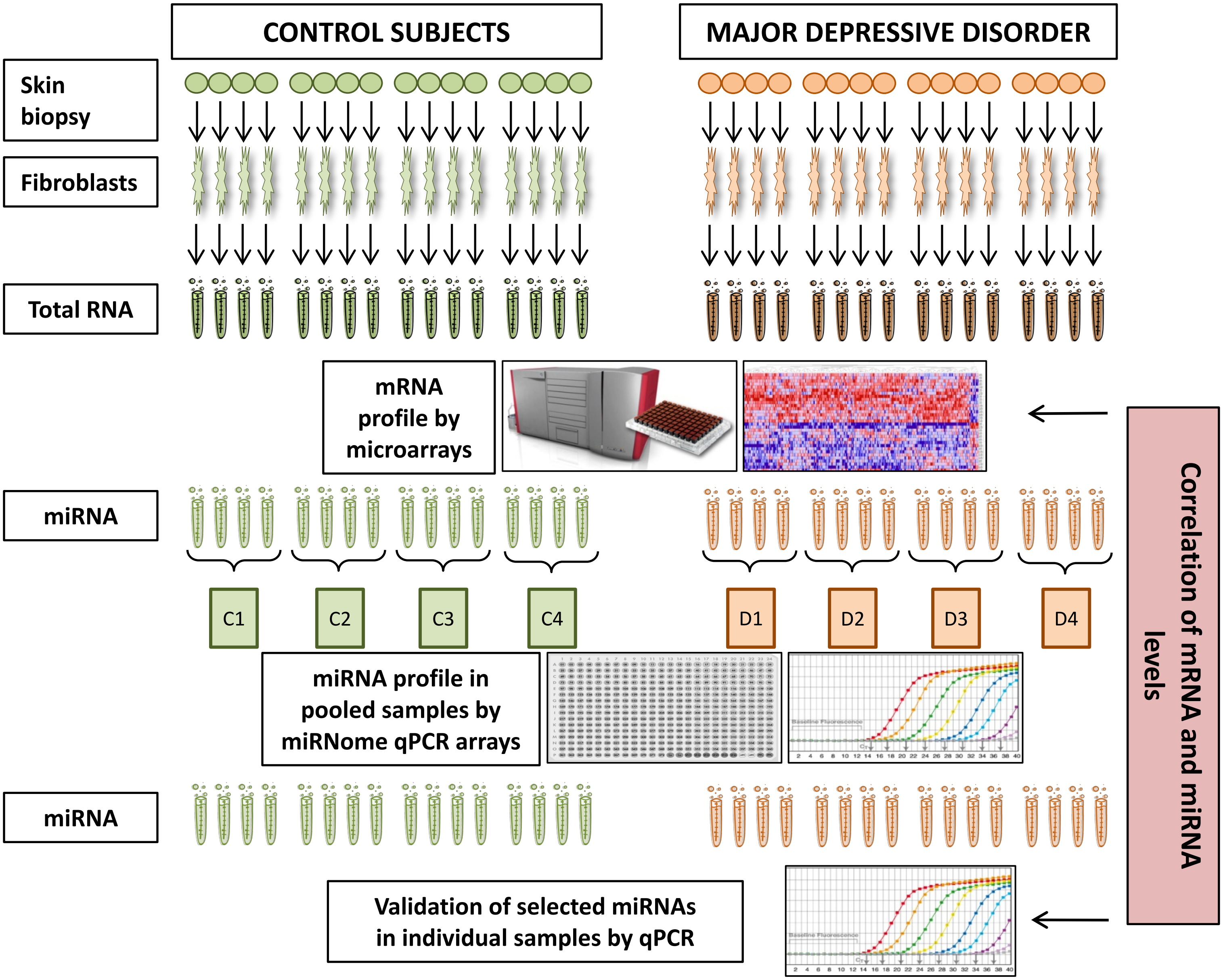

Figure S1. Experimental design. Skin biopsies were obtained using tissue punches from 16 major depressive disorder patients and 16 matched control subjects. Fibroblasts were propagated in tissue cultures with matching patient/control pairs cultured simultaneously under same conditions. This was followed by isolation on mRNA and miRNA. Individual mRNA expression profile was determined using GeneChip HT HG-U133+ PM Array Plate (Affymetrix Inc, Santa Clara, CA, USA). Initial miRNA profiling was performed using miRNome miRNA PCR Arrays (Qiagen, Valencia, CA, USA). The individual sample cDNAs were pooled in equal proportions into four groups based on gender and age (Table S1). The most robustly changed miRNAs were validated using quantitative polymerase chain reaction (qPCR) on individual samples. To better understand the relationship between the mRNA and miRNA changes, we correlated the two datasets based on the predicted miRNA targets.

Table S2. mRNA expression changes between fibroblasts originating from major depressive disorder (MDD) patients and matched healthy controls (CNTR). CNTR and MDD columns denote average log2 expression levels for the two diagnostic classes, ALR column represents magnitude of differential expression (positive values denote higher expression in MDD, negative values correspond to higher expression in controls). Paired *t*-test – pairwise comparison *p*-value; Group *t*-test – groupwise comparison *p*-value. Note that the downregulated genes in MDD fibroblasts greatly outnumber the upregulated ones.

Probe Set ID	Public ID	Gene Symbol	Gene Name	CNTR	MDD	ALR (MDD-CNTR)	Paired *t*-test	Group *t*-test
208894_PM_at	M60334	HLA-DRA	major histocompatibility complex, class II, DR alpha	5.31	7.17	1.86	0.02893	0.04768
229479_PM_at	AI739132	---	---	7.11	8.87	1.76	0.01735	0.01206
215193_PM_x_at	AJ297586	HLA-DRB	major histocompatibility complex, class II, DR beta	5.30	7.00	1.70	0.02389	0.04638
210982_PM_s_at	M60333	HLA-DRA	major histocompatibility complex, class II, DR alpha	5.74	7.40	1.66	0.02374	0.04891
209619_PM_at	K01144	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	5.88	7.39	1.51	0.02547	0.04955
215047_PM_at	AL080170	TRIM58	tripartite motif-containing 58	4.64	5.99	1.34	0.01396	0.01728
204035_PM_at	NM_003469	SCG2	secretogranin II	6.80	8.07	1.27	0.00706	0.01554
201137_PM_s_at	NM_002121	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	6.85	7.99	1.15	0.02463	0.03573
1558882_PM_at	BI868572	LOC401233	cofactor required for Tat activation of HIV-1 transcription	5.60	6.56	0.96	0.00437	0.02345
229802_PM_at	AA147884	---	---	10.46	11.28	0.81	0.03227	0.03040
1555963_PM_x_at	CA503291	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	4.21	5.02	0.81	0.02155	0.02074
213831_PM_at	X00452	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	4.03	4.83	0.80	0.03874	0.04060
1555962_PM_at	CA503291	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	4.25	5.04	0.79	0.01367	0.02526
215014_PM_at	AL512727	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	6.94	7.69	0.75	0.00954	0.00514
221854_PM_at	AI378979	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	4.22	4.96	0.74	0.03414	0.04686
211836_PM_s_at	U18800	MOG	myelin oligodendrocyte glycoprotein	4.03	4.73	0.70	0.00588	0.03425
207145_PM_at	NM_005259	MSTN	myostatin	4.62	5.31	0.69	0.04953	0.03888
221558_PM_s_at	AF288571	LEF1	lymphoid enhancer-binding factor 1	4.57	5.25	0.68	0.01958	0.03653
1569942_PM_at	BC037802	---	---	4.11	4.77	0.66	0.01611	0.02984
233337_PM_s_at	AF131749	SEZ6L2	seizure related 6 homolog (mouse)-like 2	6.18	6.83	0.65	0.01618	0.04045
201250_PM_s_at	NM_006516	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	7.06	7.71	0.64	0.01076	0.02150
206560_PM_s_at	NM_006533	MIA	melanoma inhibitory activity	4.88	5.51	0.63	0.00887	0.03750
1554133_PM_at	BC041092	RUFY2	RUN and FYVE domain containing 2	5.33	5.95	0.62	0.02043	0.02962
1560031_PM_at	R19413	FRMD4A	FERM domain containing 4A	5.61	6.21	0.60	0.03118	0.03774
219497_PM_s_at	NM_022893	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	6.66	7.25	0.59	0.04756	0.02429
230574_PM_at	AW139393	LOC100130938	hypothetical LOC100130938	4.98	5.57	0.59	0.00697	0.00790
231361_PM_at	AI912122	NLGN1	neuroligin 1	7.28	6.70	-0.59	0.03680	0.04543

Probe Set ID	Public ID	Gene Symbol	Gene Name	CNTR	MDD	ALR (MDD-CNTR)	Paired *t*-test	Group *t*-test
204864_PM_s_at	NM_002184	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	8.18	7.59	-0.59	0.00121	0.00032
211839_PM_s_at	U22386	CSF1	colony stimulating factor 1 (macrophage)	5.78	5.19	-0.59	0.00756	0.00604
219247_PM_s_at	NM_024630	ZDHHC14	zinc finger, DHHC-type containing 14	6.79	6.20	-0.59	0.00009	0.00116
213309_PM_at	AL117515	PLCL2	phospholipase C-like 2	6.93	6.34	-0.59	0.02215	0.01868
212992_PM_at	AI935123	AHNAK2	AHNAK nucleoprotein 2	10.27	9.68	-0.60	0.01680	0.03502
211572_PM_s_at	AF092511	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	6.41	5.80	-0.60	0.00002	0.00001
212240_PM_s_at	AI679268	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	9.38	8.78	-0.60	0.01641	0.00986
220945_PM_x_at	NM_018050	MANSC1	MANSC domain containing 1	6.50	5.90	-0.60	0.02106	0.02263
239002_PM_at	AA748494	ASPM	asp (abnormal spindle) homolog, microcephaly associated	6.01	5.40	-0.60	0.01244	0.00882
1560020_PM_at	BC043583	DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	7.09	6.48	-0.61	0.00051	0.00006
236557_PM_at	AW085625	ZBTB38	zinc finger and BTB domain containing 38	7.78	7.17	-0.61	0.00011	0.00001
214537_PM_at	NM_005320	HIST1H1D	histone cluster 1, H1d	5.73	5.12	-0.61	0.00393	0.00330
215324_PM_at	AA343027	SEMA3D	semaphorin 3D	5.77	5.16	-0.61	0.02033	0.01689
216493_PM_s_at	AL023775	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	6.09	5.48	-0.61	0.03735	0.01742
220580_PM_at	NM_025044	BICC1	bicaudal C homolog 1 (Drosophila)	6.83	6.22	-0.61	0.00263	0.00790
205543_PM_at	NM_014278	HSPA4L	heat shock 70kDa protein 4-like	6.52	5.91	-0.61	0.00142	0.01122
203619_PM_s_at	NM_012306	FAIM2	Fas apoptotic inhibitory molecule 2	5.58	4.97	-0.62	0.04341	0.04587
216218_PM_s_at	AK023546	PLCL2	phospholipase C-like 2	5.81	5.19	-0.62	0.00770	0.00090
241495_PM_at	AI675298	CCNL1	cyclin L1	6.08	5.45	-0.62	0.02390	0.01103
242665_PM_at	AL042120	FMNL2	formin-like 2	6.21	5.58	-0.62	0.00541	0.00058
229244_PM_at	AI400057	LSAMP	limbic system-associated membrane protein	5.97	5.34	-0.63	0.01310	0.01848
202434_PM_s_at	N21019	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	9.77	9.14	-0.63	0.03448	0.01964
227463_PM_at	AW057540	ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	5.66	5.03	-0.63	0.01802	0.04951
219779_PM_at	NM_024721	ZFHX4	zinc finger homeobox 4	8.39	7.76	-0.63	0.04016	0.02516
235201_PM_at	AW167727	FOXP2	forkhead box P2	8.02	7.39	-0.64	0.04573	0.04479
242458_PM_at	AA721230	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	6.92	6.28	-0.64	0.00774	0.00541
232940_PM_s_at	AK025911	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	7.22	6.58	-0.64	0.00082	0.00015
210990_PM_s_at	U77706	LAMA4	laminin, alpha 4	10.44	9.80	-0.64	0.00040	0.00051
220154_PM_at	NM_020388	DST	dystonin	6.21	5.57	-0.64	0.00117	0.00010
1555131_PM_a_at	BC026102	PER3	period homolog 3 (Drosophila)	5.57	4.93	-0.64	0.00102	0.00049
213844_PM_at	NM_019102	HOXA5	homeobox A5	6.19	5.55	-0.64	0.02158	0.01117
207419_PM_s_at	NM_002872	RAC2	ras-related C3 botulinum toxin substrate 2	6.44	5.79	-0.65	0.02733	0.02948
1556329_PM_a_at	BC042378	---	---	4.49	3.85	-0.65	0.04453	0.02951
207099_PM_s_at	NM_000390	CHM	choroideremia (Rab escort protein 1)	7.35	6.71	-0.65	0.00014	0.00000
232238_PM_at	AK001380	ASPM	asp (abnormal spindle) homolog, microcephaly associated	6.63	5.98	-0.65	0.00474	0.00401

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215303_PM_at	BE046461	DCLK1	doublecortin-like kinase 1	5.11	4.46	-0.65	0.01074	0.03212
1563947_PM_a_at	AK097177	ERC1	ELKS/RAB6-interacting/CAST family member 1	6.89	6.24	-0.65	0.00000	0.00013
216361_PM_s_at	AJ251844	MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	5.37	4.72	-0.65	0.00007	0.00001
220266_PM_s_at	NM_004235	KLF4	Kruppel-like factor 4 (gut)	8.40	7.74	-0.65	0.01748	0.00618
1555675_PM_at	AF303179	BLID	BH3-like motif containing, cell death inducer	6.01	5.35	-0.66	0.00665	0.00840
205197_PM_s_at	BE567813	ATP7A	ATPase, Cu++ transporting, alpha polypeptide	7.01	6.35	-0.66	0.00119	0.00159
223842_PM_s_at	AB007830	SCARA3	scavenger receptor class A, member 3	7.49	6.83	-0.66	0.01892	0.03511
242019_PM_at	BG257755	LASS6	LAG1 homolog, ceramide synthase 6	5.47	4.80	-0.66	0.00009	0.00010
223551_PM_at	AF225513	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	4.51	3.84	-0.66	0.02345	0.03252
215992_PM_s_at	AL117397	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	6.48	5.81	-0.67	0.00009	0.00001
242349_PM_at	AW275658	HECTD1	HECT domain containing 1	7.77	7.11	-0.67	0.00000	0.00000
1568598_PM_at	BF434771	KAZALD1	Kazal-type serine peptidase inhibitor domain 1	6.29	5.62	-0.67	0.02721	0.01036
231382_PM_at	AI798863	FGF18	fibroblast growth factor 18	5.40	4.73	-0.67	0.04928	0.03708
224909_PM_s_at	BF308645	PREX1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	5.51	4.84	-0.68	0.00030	0.00016
1553191_PM_at	NM_020388	DST	dystonin	8.06	7.38	-0.68	0.00211	0.00037
205290_PM_s_at	NM_001200	BMP2	bone morphogenetic protein 2	5.25	4.57	-0.68	0.00271	0.00959
212650_PM_at	BF116032	EHBP1	EH domain binding protein 1	10.65	9.97	-0.69	0.00004	0.00004
204322_PM_at	BF002254	GOLIM4	golgi integral membrane protein 4	6.91	6.21	-0.70	0.00001	0.00006
230285_PM_at	BF447829	SVIP	small VCP/p97-interacting protein	5.19	4.49	-0.70	0.00232	0.00231
243844_PM_at	AI816790	---	---	5.51	4.81	-0.70	0.02986	0.03983
203788_PM_s_at	AI962897	SEMA3C	semaphorin 3C	9.95	9.24	-0.70	0.03050	0.01035
232166_PM_at	AL045516	KIAA1377	KIAA1377	7.23	6.52	-0.71	0.00042	0.00105
1554310_PM_a_at	BC030578	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	7.41	6.70	-0.71	0.00000	0.00000
206638_PM_at	NM_000867	HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	4.52	3.80	-0.72	0.03023	0.02146
217504_PM_at	AA099357	ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	7.31	6.59	-0.72	0.01175	0.03929
235281_PM_x_at	AA523289	AHNAK	AHNAK nucleoprotein	7.79	7.07	-0.73	0.00000	0.00000
241955_PM_at	BE243270	HECTD1	HECT domain containing 1	8.87	8.15	-0.73	0.00000	0.00001
217053_PM_x_at	X87175	ETV1	ets variant 1	5.80	5.07	-0.73	0.03184	0.00638
215561_PM_s_at	AK026803	IL1R1	interleukin 1 receptor, type I	7.34	6.61	-0.73	0.00837	0.01801
207992_PM_s_at	NM_000480	AMPD3	adenosine monophosphate deaminase 3	7.97	7.23	-0.73	0.01784	0.01575
238356_PM_at	AW968823	DOCK11	dedicator of cytokinesis 11	6.90	6.17	-0.73	0.00793	0.00332
235996_PM_at	BF979984	RASSF8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	7.43	6.70	-0.73	0.00147	0.00054
213033_PM_s_at	AI186739	NFIB	nuclear factor I/B	7.26	6.52	-0.74	0.03147	0.02905
210461_PM_s_at	BC002448	ABLIM1	actin binding LIM protein 1	5.96	5.21	-0.75	0.00285	0.00265
236207_PM_at	BE083088	SSFA2	sperm specific antigen 2	6.32	5.57	-0.75	0.00002	0.00000

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238332_PM_at	AI307802	ANKRD29	ankyrin repeat domain 29	7.37	6.61	-0.76	0.00697	0.00792
1555097_PM_a_at	BC035694	PTGFR	prostaglandin F receptor (FP)	9.00	8.24	-0.76	0.02465	0.04005
203634_PM_s_at	NM_001876	CPT1A	carnitine palmitoyltransferase 1A (liver)	5.90	5.14	-0.76	0.00000	0.00000
229010_PM_at	AI807026	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	7.67	6.91	-0.76	0.00002	0.00009
231666_PM_at	AA194168	PAX3	paired box 3	6.82	6.06	-0.76	0.04452	0.02876
228057_PM_at	AA528140	DDIT4L	DNA-damage-inducible transcript 4-like	6.20	5.44	-0.76	0.00680	0.01095
238865_PM_at	AI822134	PABPC4L	poly(A) binding protein, cytoplasmic 4-like	6.06	5.30	-0.76	0.03726	0.02234
224543_PM_at	AF308289	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	7.39	6.62	-0.77	0.02379	0.03056
224950_PM_at	BF476250	PTGFRN	prostaglandin F2 receptor negative regulator	8.10	7.33	-0.77	0.00887	0.03698
1553141_PM_at	BC035749	C13orf31	chromosome 13 open reading frame 31	7.53	6.76	-0.77	0.03820	0.02437
227910_PM_at	AI635379	XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	6.75	5.97	-0.77	0.00924	0.02987
223997_PM_at	BC001956	FNIP1	folliculin interacting protein 1	6.47	5.69	-0.78	0.00001	0.00003
219552_PM_at	NM_024500	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	7.86	7.08	-0.78	0.01237	0.02400
226305_PM_at	AV696976	LYNX1	Ly6/neurotoxin 1	7.12	6.34	-0.78	0.02177	0.03345
204160_PM_s_at	AW194947	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	7.39	6.60	-0.78	0.00893	0.02243
227492_PM_at	AI829721	OCLN	occludin	6.10	5.30	-0.79	0.04518	0.03142
241683_PM_at	AW207734	HECTD1	HECT domain containing 1	6.19	5.39	-0.80	0.00000	0.00000
242762_PM_s_at	AA372349	FAM171B	family with sequence similarity 171, member B	6.24	5.44	-0.80	0.00028	0.00018
213488_PM_at	N73970	SNED1	sushi, nidogen and EGF-like domains 1	8.90	8.10	-0.80	0.01682	0.02093
222816_PM_s_at	BE676543	ZCCHC2	zinc finger, CCHC domain containing 2	6.94	6.13	-0.81	0.00769	0.00401
235301_PM_at	AI797353	KIAA1324L	KIAA1324-like	8.08	7.26	-0.81	0.04383	0.04483
231213_PM_at	AU146305	PDE1A	phosphodiesterase 1A, calmodulin-dependent	5.08	4.27	-0.81	0.00826	0.03124
244317_PM_at	BF035563	KIAA1324L	KIAA1324-like	7.33	6.51	-0.82	0.02203	0.02105
214012_PM_at	BE551138	ERAP1	endoplasmic reticulum aminopeptidase 1	6.16	5.34	-0.82	0.01352	0.02543
213749_PM_at	AV686235	MASP1	mannan-binding lectin serine peptidase 1	7.07	6.23	-0.84	0.01552	0.01738
223827_PM_at	AF246998	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	6.54	5.70	-0.84	0.04530	0.01480
203819_PM_s_at	AU160004	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	7.61	6.77	-0.85	0.03655	0.02416
240815_PM_at	R62588	---	---	6.69	5.84	-0.85	0.01266	0.00622
207754_PM_at	NM_007211	RASSF8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	7.58	6.72	-0.85	0.00008	0.00001
203571_PM_s_at	NM_006829	C10orf116	chromosome 10 open reading frame 116	9.01	8.15	-0.86	0.01469	0.04169
207388_PM_s_at	NM_004878	PTGES	prostaglandin E synthase	7.85	6.99	-0.86	0.03371	0.00913
227243_PM_s_at	AL354950	EBF3	early B-cell factor 3	6.81	5.93	-0.88	0.00248	0.00701

Probe Set ID	**Public ID**	**Gene Symbol**	**Gene Name**	**CNTR**	**MDD**	**ALR (MDD-CNTR)**	**Paired *t*-test**	**Group *t*-test**
205352_PM_at	NM_005025	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	6.37	5.48	-0.89	0.00626	0.01004
215451_PM_s_at	BF575588	AFF1	AF4/FMR2 family, member 1	6.86	5.95	-0.91	0.00000	0.00000
213032_PM_at	AI186739	NFIB	nuclear factor I/B	8.36	7.43	-0.93	0.04215	0.03556
217767_PM_at	NM_000064	C3	complement component 3	8.05	7.10	-0.95	0.00357	0.01306
201641_PM_at	NM_004335	BST2	bone marrow stromal cell antigen 2	5.22	4.26	-0.96	0.02141	0.00839
235743_PM_at	AA808178	---	---	7.61	6.64	-0.97	0.00972	0.01408
212865_PM_s_at	BF449063	COL14A1	collagen, type XIV, alpha 1	7.88	6.91	-0.97	0.02833	0.03163
206765_PM_at	AF153820	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	6.70	5.72	-0.98	0.02105	0.03535
233547_PM_x_at	N53248	PDE1A	phosphodiesterase 1A, calmodulin-dependent	6.66	5.67	-0.98	0.01056	0.03217
205830_PM_at	NM_004362	CLGN	calmegin	5.70	4.71	-0.99	0.01615	0.01278
224090_PM_s_at	AB040434	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	6.69	5.69	-1.00	0.02977	0.00854
206108_PM_s_at	NM_006275	SFRS6	splicing factor, arginine/serine-rich 6	9.23	8.22	-1.00	0.02418	0.03451
235182_PM_at	AI816793	ISM1	isthmin 1 homolog (zebrafish)	5.54	4.53	-1.00	0.00852	0.01052
208719_PM_s_at	U59321	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	9.03	8.02	-1.01	0.01500	0.01539
208151_PM_x_at	NM_030881	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	9.38	8.37	-1.01	0.01152	0.01259
205399_PM_at	NM_004734	DCLK1	doublecortin-like kinase 1	7.70	6.67	-1.03	0.03105	0.02870
218730_PM_s_at	NM_014057	OGN	osteoglycin	5.44	4.35	-1.09	0.03972	0.01478
206172_PM_at	NM_000640	IL13RA2	interleukin 13 receptor, alpha 2	7.16	6.02	-1.14	0.03670	0.03408
206176_PM_at	NM_001718	BMP6	bone morphogenetic protein 6	7.10	5.97	-1.14	0.03339	0.01775
1558378_PM_a_at	BC004283	AHNAK2	AHNAK nucleoprotein 2	9.61	8.47	-1.15	0.00009	0.00009
208396_PM_s_at	NM_005019	PDE1A	phosphodiesterase 1A, calmodulin-dependent	7.81	6.66	-1.16	0.01221	0.02972
222722_PM_at	AV700059	OGN	osteoglycin	6.17	5.00	-1.17	0.03798	0.02058
210367_PM_s_at	AF010316	PTGES	prostaglandin E synthase	9.10	7.93	-1.17	0.03073	0.00715
213816_PM_s_at	AA005141	MET	met proto-oncogene (hepatocyte growth factor receptor)	7.68	6.48	-1.21	0.00474	0.00128
208609_PM_s_at	NM_019105	TNXB	tenascin XB	7.67	6.38	-1.30	0.04043	0.02516
216333_PM_x_at	M25813	TNXB	tenascin XB	8.50	7.19	-1.30	0.04545	0.02515
1558680_PM_s_at	BQ894022	PDE1A	phosphodiesterase 1A, calmodulin-dependent	8.07	6.76	-1.31	0.00904	0.02333
203407_PM_at	NM_002705	PPL	periplakin	8.59	7.25	-1.34	0.00556	0.02714
227242_PM_s_at	BF592034	EBF3	early B-cell factor 3	6.91	5.57	-1.34	0.00506	0.00510
206093_PM_x_at	NM_007116	TNXA /// TNXB	tenascin XA pseudogene /// tenascin XB	8.29	6.85	-1.44	0.02777	0.01369
213451_PM_x_at	BE044614	TNXA /// TNXB	tenascin XA pseudogene /// tenascin XB	8.74	7.29	-1.46	0.03398	0.01774
203815_PM_at	NM_000853	GSTT1	glutathione S-transferase theta 1	8.48	6.96	-1.51	0.01804	0.01345
228635_PM_at	AI640307	PCDH10	protocadherin 10	5.86	4.13	-1.73	0.00154	0.00057

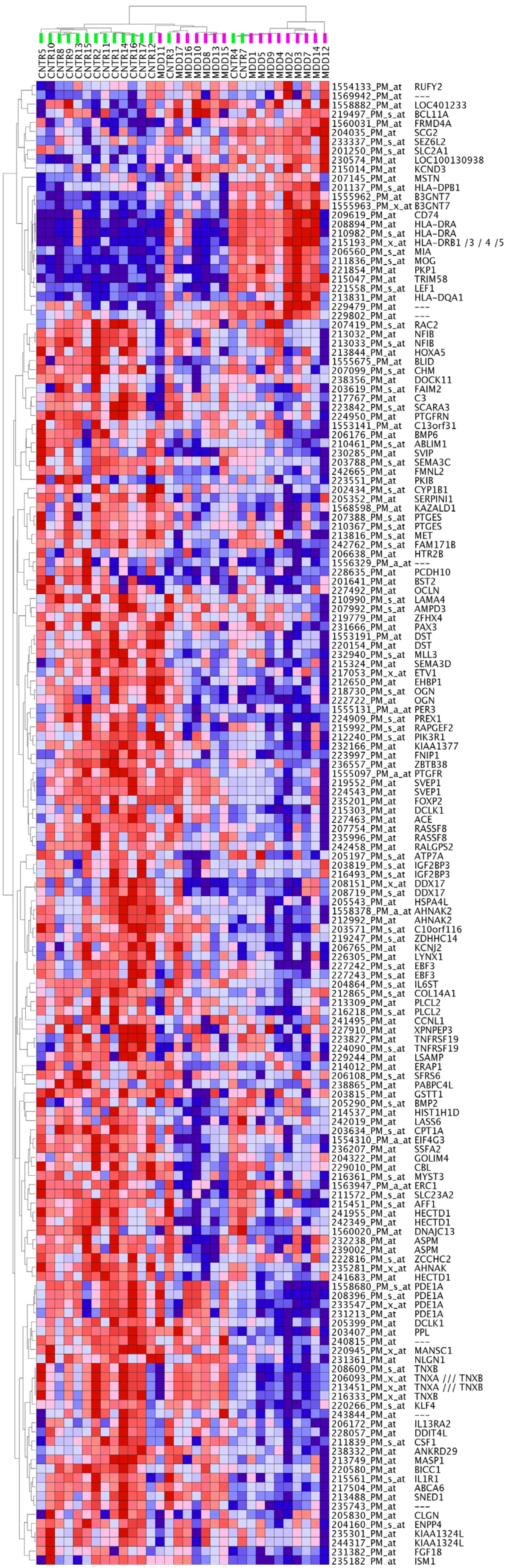

Figure S2. mRNA expression profile differences between fibroblasts from major depressive disorder (MDD) and control (CNTR) subjects. Two-way unsupervised hierarchical clustering was performed on the Log 2 expression levels of 162 differentially expressed mRNAs. Samples were clustered vertically, mRNAs were clustered horizontally. Each colored square represents a normalized gene expression level, color coded for increase (red) or decrease (blue) from the mean. Color intensity is proportional to magnitude of change. Alpha-numerical entries to the right of the column denote microarray probe sets and gene symbols. The clustering resulted in a separation of the majority of samples that was related to the diagnostic condition (vertical dendrogram: green - CNTR samples, purple – MDD samples). For more detail, see Table S2.

Figure S3. Microarray data validation by quantitative polymerase chain reaction (qPCR). qPCR analyses were used to independently test the expression level of 14 mRNAs. The Ct values for each of them was normalized to the GAPDH Ct value and the difference between controls (CNTR) and major depressive disorder (MDD) patients was measured by ΔΔCt ($\Delta\Delta Ct = \Delta Ct_{CNTR} - \Delta Ct_{MDD}$). Microarray expression differences measured by average logarithmic ratio (ALR) (y-axis) were correlated to the qPCR differences measured by ΔΔCt (x-axis).

Gene symbol	qPCR ddCT	*qPCR pVal*	MA ALR	*MA pVal*
CD74	2.29	*0.012*	1.51	*0.049*
HLA-DRA	1.61	*0.017*	1.86	*0.048*
HLA-DQB1	1.31	*0.018*	0.76	*0.043*
IL11	1.13	*0.017*	0.83	*0.019*
DPA1	1.08	*0.011*	0.96	*0.037*
S100B	1.05	*0.031*	1.14	*0.037*
BEGF	1.00	*0.010*	0.83	*0.031*
HLA-DPB1	0.43	*0.156*	1.15	*0.036*
HLA-DQA1	0.29	*0.285*	0.80	*0.041*
MET	-0.42	*0.043*	-1.21	*0.001*
PCDH10	-0.91	*0.036*	-1.73	*0.002*
TNF19	-1.11	*0.007*	-0.84	*0.015*
GSTT1	-3.77	*0.007*	-1.51	*0.013*

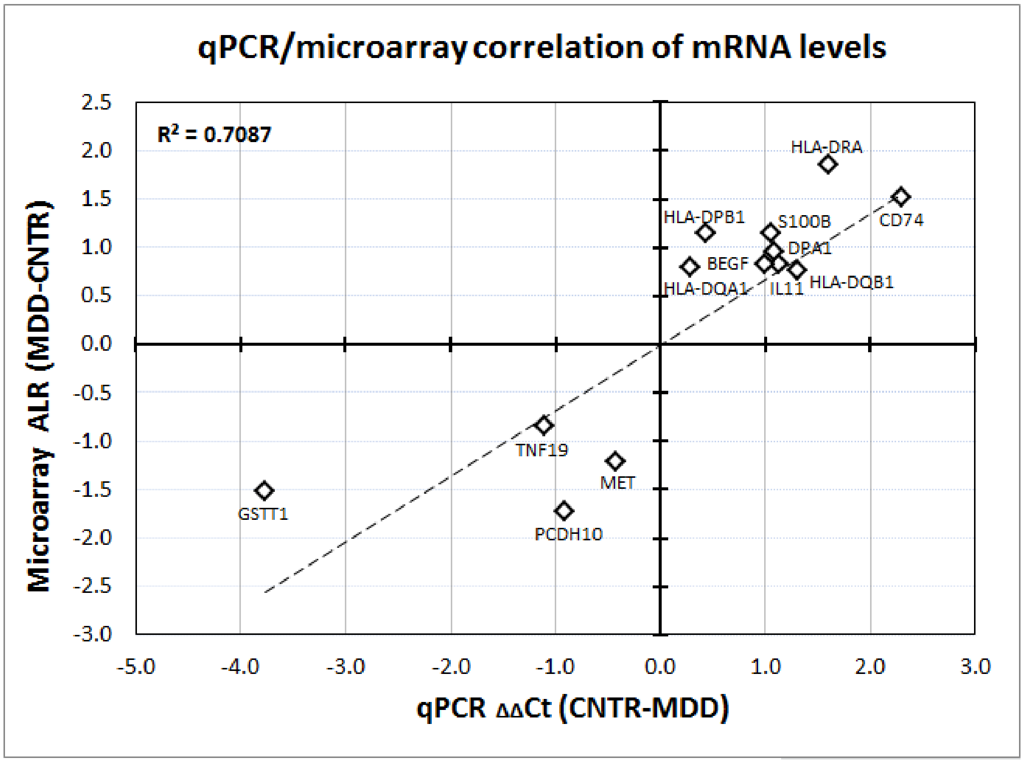

Table S3. miRNA changes between fibroblasts originating from major depressive disorder (MDD) patients and healthy controls. Positive ΔΔCt values denote miRNA downregulation in MDD fibroblasts (17 miRNAs), negative values correspond to the magnitude of upregulation (21 miRNAs).

miRNA ID	**ddCt D-C**	***p*-value**
hsa-miR-122	2.17	0.00004
hsa-miR-32	2.01	0.02137
hsa-miR-196b*	1.96	0.02807
hsa-miR-377	1.62	0.01040
hsa-miR-193a-3p	1.52	0.01756
hsa-miR-337-5p	1.52	0.00428
hsa-miR-675*	1.46	0.00648
hsa-miR-3176	1.39	0.01719
hsa-miR-21*	0.91	0.03960
hsa-miR-22	0.76	0.04233
hsa-miR-425*	0.71	0.02273
hsa-miR-185	0.60	0.00380
hsa-miR-296-5p	0.56	0.01870
hsa-miR-103a	0.55	0.01982
hsa-miR-107	0.53	0.03574
hsa-miR-186	0.53	0.03432
hsa-miR-887	0.45	0.02768
hsa-miR-132	-0.42	0.00278
hsa-miR-421	-0.43	0.00129
hsa-miR-542-3p	-0.44	0.00783
hsa-miR-450a	-0.50	0.02326
hsa-miR-16-2*	-0.54	0.03806
hsa-miR-424	-0.69	0.03091
hsa-miR-628-3p	-0.72	0.01009
hsa-miR-629	-0.76	0.02441
hsa-miR-4293	-0.77	0.00858
hsa-miR-661	-0.80	0.00724
hsa-miR-3909	-0.80	0.02860
hsa-miR-33a*	-0.80	0.01558
hsa-miR-135b	-0.84	0.02895
hsa-miR-7	-0.96	0.03198
hsa-miR-4267	-0.97	0.03604
hsa-miR-548aa	-1.05	0.00520
hsa-miR-548d-3p	-1.25	0.01201
hsa-miR-613	-1.53	0.00250
hsa-miR-3714	-1.58	0.02024
hsa-miR-1294	-1.78	0.03714
hsa-miR-429	-2.00	0.01091

Table S4. Differentially expressed miRNAs in major depressive disorder (MDD) fibroblasts and their predicted mRNA targets (TargetScan).

A. Downregulated miRNAs in MDD and their putative mRNA expression targets (TargetScan)

miRNA ID	ddCt D-C	*p*-value	# of mRNA targets	mRNA up in MDD	mRNA down in MDD	# mRNAs up	# mRNAs down
hsa-miR-122	2.17	0.0000	172	---	FOXP2, CBL, OCLN, MASP1	0	4
hsa-miR-32	2.01	0.0214	306	BCL11A	IL6ST, SSFA2, PAX3, PCDH10	1	4
hsa-miR-196b*	1.96	0.0281	38	---	---	0	0
hsa-miR-377	1.62	0.0104	566	---	SEMA3D, LSAMP, RALGPS2, DCLK1, ERC1, RASSF8, NFIB, CBL, PCDH10	0	9
hsa-miR-193a-3p	1.52	0.0176	207	---	SLC23A2, FAIM2, ETV1,	0	3
hsa-miR-337-5p	1.52	0.0043	14	---	---	0	0
hsa-miR-675*	1.46	0.0065	4	---	---	0	0
hsa-miR-3176	1.39	0.0172	179	---	SLC23A2, KCNJ2	0	2
hsa-miR-21	0.91	0.0396	164	BCL11A	PIK3R1, RALGPS2	1	2
hsa-miR-22	0.76	0.0423	508	SLC2A1	FMNL2, ETV1,NFIB, CBL, OGN	1	5
hsa-miR-425*	0.71	0.0227	212	---	ZFHX4, CBL, XPNPEP3	0	3
hsa-miR-185	0.60	0.0038	188	---	NFIB	0	1
hsa-miR-296-5p	0.56	0.0187	172	---	---	0	0
hsa-miR-103a	0.55	0.0198	636	FRMD4A , BCL11A	PIK3R1, PER3, DCLK1, KLF4, FGF18, RASSF8, NFIB, SVEP1, ZCCHC2	2	9
hsa-miR-107	0.53	0.0357	14	---	---	1	3
hsa-miR-186	0.53	0.0343	849	FRMD4A	SLC23A2, FOXP2, KIAA1324L, NFIB, OCLN, AFF1	1	6
hsa-miR-887	0.45	0.0277	10	---	---	0	0

Red lettering - upregulated mRNAs in MDD; Green lettering - downregulated mRNAs in MDD.

B. Upregulated miRNAs in MDD and their putative mRNA expression targets (TargetScan)

miRNA ID	ddCt D-C	*p*-value	# of mRNA targets	mRNA up in MDD	mRNA down in MDD	# mRNAs up	# mRNAs down
hsa-mir-132	-0.42	0.0028	261	SLC2A1	ETV1, ANKRD29	1	2
hsa-mir-421	-0.43	0.0013	426	---	RAPGEF2, NFIB, CBL, DDX17	0	4
hsa-mir-542	-0.44	0.0078	286	---	LSAMP, ZFHX4, CBL	0	3
hsa-mir-450a	-0.50	0.0233	9	---	---	0	0
hsa-mir-16	-0.54	0.0381	387	---	SEMA3D, HECTD1, ATP7A, RASSF8, SVEP1, ZCCHC2	0	6
hsa-mir-424	-0.69	0.0309	175	---	ZFHX4	0	1
hsa-mir-628-3p	-0.72	0.0101	112	---	DCLK1, AMPD3	0	1
hsa-mir-629-5p	-0.76	0.0244	196	---	ERAP1	0	1
hsa-mir-4293	-0.77	0.0086	189	SLC2A1	XPNPEP3	1	1
hsa-mir-661	-0.80	0.0072	319	---	IGF2BP3, NFIB, CBL,	1	3
hsa-mir-3909	-0.80	0.0286	186	---	CHM, CBL, PTGFRN	1	3
hsa-mir-33a	-0.80	0.0156	417	---	ZFHX4, DST, DCLK1, ERC1, RASSF8, CPT1A, PTGFRN, PCDH10	0	8
hsa-mir-135b	-0.84	0.0289	69	BCL11A	MASP1	1	1
hsa-mir-7	-0.96	0.0320	444	---	ZBTB38, KLF4, NFIB, KCNJ2	0	4
hsa-mir-4267	-0.97	0.0360	442	---	ZFHX4, DST, DCLK1, ERC1, RAPGEF2, RALGPS2, AFF1	0	7
hsa-mir-548a-3p	-1.05	0.0052	706	SCG2, B3GNT7, SLC2A1, FRMD4A, BCL11A	SLC23A2, PIK3R1, LSAMP, ZFHX4, FOXP2, RAPGEF2, IL1R1, NFIB, ERAP1	5	9
hsa-mir-548d-3p	-1.25	0.0120	145	---	FOXP2, PCDH10	0	2
hsa-mir-613	-1.53	0.0025	240	---	CHM, DDX17	0	2
hsa-mir-3714	-1.58	0.0202	1276	FRMD4A	DNAJC13, RALGPS2, PER3, ERC1, KLF4, ATP7A, RAPGEF2, ETV1, AMPD3, RASSF8, EBF3, KIAA1324L, NFIB, CPT1A, CBL, ENPP4, AFF1, KCNJ2, BMP6	1	19
hsa-mir-1294	-1.78	0.0371	298	RUFY2, FRMD4A	SEMA3D, NFIB, CBL	2	3
hsa-mir-429	-2.00	0.0109	237	FRMD4A	RAPGEF2, RASSF8, CBL, OCLN	2	7

Red lettering - upregulated mRNAs in MDD; Green lettering - downregulated mRNAs in MDD.