

GPS-15-0054, "Genomic predictors of remission in geriatric depression using genome-wide expression analyses: a pilot study"

Supplement 1: Microarray genomic regulation differences between non-remitter and early remitter groups at baseline

Probe ID	Fold Change (abs)	Regulation	Symbol	p-value
6370315	11.29394	Down	HLA-DRB5	0.005371
1230376	2.878403	Down	ALAS2	0.040313
7550292	2.587224	Down	SELENBP1	0.019046
2190139	2.538225	Down	CA1	0.02866
2350274	2.511729	Down	AHSP	0.010137
10681	2.421306	Down	LOC100131164	0.023538
2120152	2.399837	Down	SLC4A1	0.017559
5690187	2.360582	Down	EPB42	0.007224
4150563	2.320725	Down	C16orf35	0.017368
6860347	2.301184	Down	FAM46C	0.025754
1450358	2.297963	Down	HBD	0.00744
1510612	2.236673	Down	MYL4	0.034842
5960564	2.180386	Down	SNCA	0.03586
7610615	2.164032	Down	SLC6A10P	0.024972
4180768	2.156951	Down	ALAS2	0.00684
3140750	2.079619	Down	RBM38	0.008701
3840400	2.036645	Down	GMPR	0.043985
3420372	2.005976	Down	RBM38	0.025779

Supplement 2: Gene ontology outputs from DAVID analysis for biologically significant functions relevant early remitters

Gene ontology details	P-value	Genes
002002; hemoglobin metabolic process	3.23E-05	ALAS2, EPB42, AHSP
0050801; ion homeostasis	0.004924	ALAS2, EPB42, SNCA, SLC4A1
0005938; cell cortex	0.005491	EPB42, SNCA, SLC4A1
0048878; chemical homeostasis	0.009184	ALAS2, EPB42, SNCA, SLC4A1
0005833; hemoglobin complex	0.009352	AHSP, HBD
0005829; cytosol	0.014651	AHSP, SNCA, RBM38, SELENBP1, HBD
0030097; hemopoiesis	0.017825	ALAS2, EPB42, AHSP
0048534; hemopoietic or lymphoid organ development	0.021389	ALAS2, EPB42, AHSP
0002520; immune system development	0.023919	ALAS2, EPB42, AHSP
0050821; protein stabilization	0.024566	AHSP, RBM38
0042592; homeostatic process	0.025726	ALAS2, EPB42, SNCA, SLC4A1
0055072; iron ion homeostasis	0.031483	ALAS2, EPB42
0031647; regulation of protein stability	0.036641	AHSP, RBM38
0030218; erythrocyte differentiation	0.037498	ALAS2, EPB42
0030863; cortical cytoskeleton	0.037694	EPB42, SLC4A1
0006873; cellular ion homeostasis	0.041895	ALAS2, SNCA, SLC4A1
0034101; erythrocyte homeostasis	0.042627	ALAS2, EPB42
0055082; cellular chemical homeostasis	0.043125	ALAS2, SNCA, SLC4A1
0019725; cellular homeostasis	0.062202	ALAS2, SNCA, SLC4A1
0044448; cell cortex part	0.063092	EPB42, SLC4A1
0008092; cytoskeletal protein binding	0.065602	MYL4, SNCA, SLC4A1
0030017; sarcomere	0.074104	MYL4, SLC4A1
0030099; myeloid cell differentiation	0.079478	ALAS2, EPB42
0030016; myofibril	0.083553	MYL4, SLC4A1
0005856; cytoskeleton	0.084634	MYL4, EPB42, SNCA, SLC4A1
0044449; contractile fiber part	0.084999	MYL4, SLC4A1
0048872; homeostasis of number of cells	0.085219	ALAS2, EPB42
0043292; contractile fiber	0.090763	MYL4, SLC4A1