

Supplementary tables

Table S1. High score pathways in the LOAD vs. HC discrimination using the list of most frequently sampled genes with sampling frequency higher than 0.2 (93 identified genes).

Score	Path Name	# Total Genes	# Matched Genes
46.96	Viral mRNA translation	549	22
27.89	Influenza viral RNA transcription and replication	158	10
27.34	Respiratory electron transport, ATP synthesis	556	16
24.50	Gene expression	1842	27
21.45	Mitochondrial translation	95	7
20.96	rRNA processing in the nucleus and cytosol	203	9
20.38	Metabolism	2547	30
17.92	Metabolism of proteins	1630	22
17.79	Organelle biogenesis and maintenance	341	10
16.54	HIV life cycle	866	15
15.27	Antigen processing-Cross presentation	123	6
15.20	TCR signaling (REACTOME)	124	6

Table S2. High score pathways in the MCI vs. HC discrimination using the list of most frequently sampled genes with sampling frequency higher than 0.2 (161 identified genes).

Score	Path Name	# Total Genes	# Matched Genes
49.83	Viral mRNA translation	549	29
33.20	Gene expression	1842	43
26.93	Influenza viral RNA transcription and replication	158	12
23.81	Metabolism of proteins	1630	35
23.03	rRNA processing in the nucleus and cytosol	203	12
20.30	Ubiquitin-proteasome dependent proteolysis	122	9
20.20	Antigen processing-Cross presentation	123	9
19.98	Cell cycle checkpoints	204	11
19.01	HIV life cycle	866	22
18.56	Mitotic metaphase and anaphase	182	10
18.28	Mitotic G1-G1/S phases	145	9
18.12	CLEC7A (Dectin-1) signaling	147	9
17.76	Cellular senescence	454	15
16.84	TCR signaling (REACTOME)	124	8
16.15	Regulation of degradation of DeltaF508 CFTR	63	6
15.77	Activation of the mRNA	66	6
15.52	Signaling by hedgehog	141	8

Table S3. High score pathways in the MCI vs. LOAD discrimination using the list of most frequently sampled genes with sampling frequency higher than 0.5 (116 identified genes).

Score	Path Name	# Total Genes	# Matched Genes
14.25	Regulation of activated PAK-2p34 by proteasome mediated degradation	884	16
12.28	G-protein signaling regulation of P38 and JNK Signaling mediated by G-proteins	91	5
10.99	Plasma membrana estroben receptor signaling	26	3
10.04	Translation regulation by alpha-1 adrenergic receptors	74	4

Table S4. High score pathways in the LOAD+MCI vs. HC discrimination using the list of most frequently sampled genes with sampling frequency higher than 0.2 (154 genes).

Score	Path Name	# Total Genes	# Matched Genes
51.42	Viral mRNA translation	549	29
31.19	Influenza viral RNA transcription and replication	158	13
29.78	Gene expression	1842	40
29.16	Metabolism of proteins	1630	37
22.92	Metabolism	2547	44
22.08	HIV life cycle	866	23
20.83	Ubiquitin-proteasome dependent proteolysis	122	9
20.74	Antigen processing-Cross presentation	123	9
20.68	rRNA processing in the nucleus and cytosol	203	11
19.32	Respiratory electron transport, ATP synthesis	556	17
19.14	Mitotic metaphase and anaphase	182	10
18.81	Mitotic G1-G1/S phases	145	9
18.65	CLEC7A (Dectin-1) signaling	147	9
17.70	Cell cycle checkpoints	204	10
17.31	TCR signaling (REACTOME)	124	8
17.16	Regulation of PLK1 activity at G2/M transition	213	10
16.53	Chks in checkpoint regulation	224	10
16.14	Activation of the mRNA	66	6
15.99	Signaling by hedgehog	141	8
14.68	P53 signaling	117	7
14.45	RNA polymerase II transcription initiation	213	9
14.38	SMAD signaling network	121	7
14.19	Cellular senescence	454	13
13.78	Signaling By Wnt	340	11