

SUPPLEMENTARY MATERIAL

Supplementary Materials and Methods

Assessment of viral infection-To determine purity of the monocyte preparations and progeny virion production, 1×10^6 cells were stained with APC-conjugated anti-CD14 mAb in 5 % BSA, 0.1% sodium azide in 1X PBS for 30 min at room temperature. Cells were washed with 1X PBS by three subsequent centrifugations at $500 \times g$ for 2 min and fixed in the dark with 4% PFA pH 7.4 for 15 min at room temperature (RT). Cells were washed and permeabilized with 1% Triton X-100 in 1X PBS. Incubation was with FITC-conjugated IgG2a mouse anti-HIV-1 p24 followed for 45 min at RT. Data acquisition was performed on FACSCalibur flow cytometer (Becton Dickinson) using CellQuest software (Becton Dickinson). Live cells were gated by forward and side scatter using FCS Express V3 software (De Novo Software, Los Angeles, CA). Data are shown as density plots of HIV-treated and control monocytes at day 7 after viral exposure. RT activity was determined in culture supernatant fluids as previously described [76].

Quantification of HIV-1 cDNA and 2-LTR circles- Monocytes (10×10^6 cells) 7 d after exposure to HIV-1_{ADA} were counted by trypan blue exclusion, washed with PBS and pelleted by centrifugation at $800 \times g$ for 5 min. Total DNA was isolated by DNAzol[®] Genomic DNA Isolation Reagent (MP Biomedicals, Inc. Solon, OH) according to manufacturer's instructions and was analyzed by Real-Time PCR. The TaqMan method with primers and probes specific for late reverse transcripts and 2-LTR circle forms was performed. Products were amplified from 10 (late) or 20 (2-LTR) μ l of DNA in 50 μ l reactions containing 2X TaqMan Universal PCR Master Mix, 300 nM primers and 100 nM probe. Late products were amplified with primers: For LATE (5'-TGTGTGCCCGTCTGTTGTGT-3'), REV-LATE (5'-GAGTCCTGCGTCGAGA GAGC-3') and the probe (5'-/56-FAM/CAGTGGCGCC CGAACAGG GA/36-TAMTph/-3'); 2-LTR circle products: 2-LTR-FOR (5'-TAGACCA GATCTGAGCCTGGGA-3'), 2-LTR-REV (5'-GTAGTTCTGCCAA TCAGGGAGG-3') and the probe (5'-56-/FAM/AG CCTCAATAAAGCTTGCCCTTGAGTGC/36-TAMSp/-3'). Thermal Cycling Conditions were maintained as follows: incubation at 50°C -2 min; at 95°C -10 min; 45 cycles of 95°C - 15 s, 60°C -1 min; 72°C -20

s; assay reading; incubation at 72°C -5 min; assay reading; incubation at 4°C. DyNAmo SYBR Green qPCR Kit (New England Biolabs, Ipswich, MA) was used with primers for specific detection of early reverse transcripts. Products were amplified from 8 µl of DNA in 50 µl reaction containing 2X Master Mix and 0.3 µM primers M667 (5'-GGCTAACTAGGGAACCCACTG-3') and AA55 (5'-CTGCTAGAGATTTTCCACACTGA C-3') specific for the negative-strand "strong-stop" DNA. Thermal Cycling conditions were: 50°C for 2 min; 95°C for 10 min; 45 cycles of 94°C -12 s, 62°C -25 s, 72°C - 25 s; assay reading; incubate at 72°C for 5 min; assay reading; melting curve: temperature 65-95°C, reading every 0.5°C, hold 0.1 s, 72°C - 5 min, incubation at 4°C. Real-time PCR was performed in triplicate and fluorescence was measured on CFD 3200 Opticon System (Bio-Rad, Hercules, CA). Serial dilutions of DNA from 8E5 cells were used as the quantitative standards.

Supplementary Figure Legends

Figure S1. Oxidative stress and viability in latently infected cells. (A) Increased hROS in HIV-1-exposed monocytes. Levels of hROS in HIV-1-treated and non treated monocytes at day 7 after exposure were measured after 30 min of incubation with APF. Fluorescence levels were acquired on a plate reader and tabulated as MFI units. Data show significantly augmented levels of hROS in latently infected monocytes ($P = 0.008$; error bars= \pm SEM; $n=3$). **(B) PMA-induced hROS production.** Concentration of PMA inducing similar levels of hROS to those found in HIV-1-treated cells was determined by performing dose response experiments in non-treated monocytes. Fluorescence readings of APF activation were used as a read out method. Incubation of 1×10^6 cells for 1 h with 10 ng/ml of PMA induced similar hROS levels as their latently infected counterparts. **(C) HIV-1-treated and non-treated and (D) PMA-exposed (1 h) monocytes** were stained with PI (top panels) and PI and Annexin V (bottom panels), and analyzed by flow cytometry. Analysis shows exposure to HIV-1 does not affect cell viability ($M1 < 2\%$ for HIV-exposed monocytes compared to controls), similar levels of hROS in PMA-induced cells generate very similar cell death activity (5% of all cells).

Figure S1

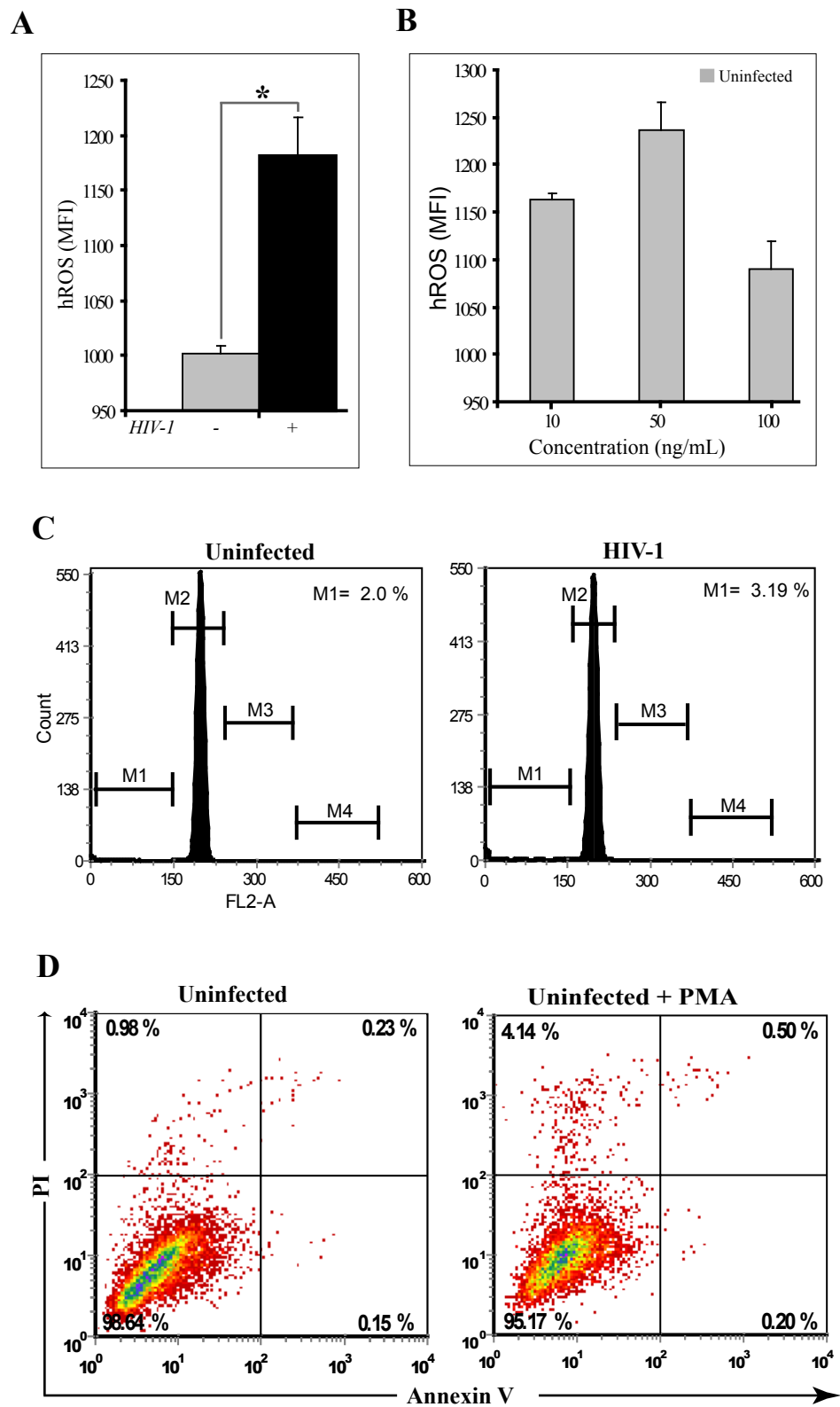


Table S1. PM differentially expressed proteins

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
Inward rectifier potassium channel 13	-2.62	2	3271	O60928	PMi (multipass)
Calcium-independent alpha-latrotoxin receptor 1 (GPCR)	-2.37	3	162717	O94910	PMi (multipass)
Probable N-acetyltransferase 8	-2.92	3	25596	Q9UHE5	PMi (multipass)
MHC class II HLA-DR-beta cell surface glycoprotein (fragment)	-2.0	2	7921	Q29830	PMi (multipass)
Integrin alpha v (CD51)	-2.67	2	6739	P06756	PMi (singlepass TI)
HLA class II histocompatibility antigen, DX beta chain [Precursor]	-4.18	3	10551	P05538	PMi (singlepass TI)
IgG Fc gamma receptor IIA (CD32)	2.0	2	1085	P12318	PMi (singlepass TI)
Leukocyte immunoglobulin-like receptor 6 (CD85i)	-2.0	2	55096	O75019	PMi (singlepass TI)
Pro-neuregulin-1, membrane-bound isoform [Precursor]	-3.81	7	36974	Q02297	PMi (singlepass TI)
Tumor necrosis factor ligand (CD40)	-2.0	2	25644	P01375	PMi (singlepass TII)
Glutamate receptor C [Fragment]	-4.18	2	6814	Q9UHA9	PMi
Voltage-gated potassium channel accessory subunit 5	1.9	3	14984	Q5JWV7	PMi
Leucocyte antigen DRB5	-2.62	3	10723	Q9MY54	PMi
Major histocompatibility class II antigen (HLA-DRB5) (fragment)	-2.0	3	10139	Q30199	PMi
Leucocyte antigen (HLA-DRBI*1303)	-2.0	2	8978	Q29919	PMi
Amyloid beta A4 precursor protein-binding family B member 1	-4.04; -2.76	3	73183	Q7Z5R6	PM
Endomembrane proton pump 58 kDa subunit	2.12	6	56465	BC003100	PM
LIM and SH3 protein 1 (LASP-1)	-2.69	3	29717	Q14847	PM
Annexin I	7.05	12	35040	P04083	PM
Chloride intracellular channel protein 1	5.67	2	23543	O00299	PM
Vasodilator-stimulated phosphoprotein (VASP)	2.75; 3.36	2	39764	BC026019	PM
Band 4.1-like protein 3	4.72	20	123704	Q9Y2J2	PM
Annexin V	2.17; 3.96	6	35804	P08758	PM
Protein phosphatase (PP2A)	-2.25	19	65136	P30153	PM
HSP90 protein 1 beta	-4.56; -4.44;	11	83264	Q29092	PM
Chaperonin containing TCP1, subunit 8	-2.5	2	59659	Q53HU0	PM
TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR (CD120b)	-2.18	3	66005	P20333	PM
Ras GTPase activating protein (p195)	-3.7	21	189134	A54854	PM
Pleckstrin homology domain containing, family A member 1	5.10	2	45553	Q9HB21	PM
Prolactin receptor intermediate isoform (fragment)	-2.12	2	5269	Q16264	PM
Copine-2	-3.01	2	61151	AF492484	PM
Ezrin	-4.02	6	69398	P15311	PM
Dynamin 1-like protein isoform 1	-2.0	2	81891	O00429	PM
Shootin-1	-2.89	2	51473	A0MZ66	PM
HSP70	1.9	6	73680	Q1HB43	PM/S
Annexin A2 isoform 2	5.12	8	38604	P07355	PM/S

Table S1. PM differentially expressed proteins (continued)

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
Calreticulin precursor	-2.48	8	48141	P27797	PM/S
LPS-associated protein 1	-2.0	5	53517	A4D110	PM/S
Enolase 1	-6.35; -3.55 ;	2	47169	P06733	PM/S
Interleukin 16	2.0	2	66646	A8MU65	PM/S
Protein disulfide-isomerase precursor	2.1	20	57081	P07237	PM/S
Clathrin, Light peptide chain isoform B	2.1	3	25190	Q53Y37	PMa
Phosphoinositide-3-kinase	-2.0	2	81624	A0JP11	PMa
Neuritin-like protein precursor	-2.0	5	17774	Q496H8	PMa
Migration inhibitory factor-related protein 8	-2.0	2	10938	P05109	PMa
Calreticulin	2.0	2	24338	Q9UDG2	PMa
Rab geranyl-geranyl transferase	-3.44	2	65001	Q6FHF7	PMa
Protein phosphatase 2, isoform b (PP2B)	-2.25	5	73538	Q8NHV8	PMa
Autophagy-related protein 16-1	-3.32	6	47656	Q676U5	PMa
Disintegrin and metalloprotease domain 33	-2.0	2	5266	Q8N6B9	PMa
Regulator of G-protein signaling 6	-2.0	2	2938	P49758	PMa
Phospholipase C-gamma 1	-2.87	2	1051	Q6LC80	PMa
Plastin 2	-2.18; -2.15	18	70114	P13796	PMa
Coronin 1A	-5.37	3	51026	P31146	PMa
Talin 1	-6.35; -2.43	2	269764	Q9Y490	PMa
Early endosome antigen	3.3	2	162464	Q15075	PMa
Transforming growth factor alpha precursor	-2.13	3	9303	Q9UQ91	PMa
Synphilin-1g protein	-3.06	3	6883	Q6L980	PMa
Valosin-containing protein (ATP-ase)	-3.0; 2.63	6	89321	Q0V924	PMa
Syntaxin-binding protein 1-like 2	3.81	11	72203	Q8WVM8	PM/G
Mannose-6-phosphate receptor-binding protein 1	5.25	4	47018	O60664	PM/G
Vacuolar ATP synthase (VATA)	-1.9	5	68165	P31400	PM/L
Vacuolar proton pump subunit alpha	-2.0	18	68232	AF113129	PM/L
Prolyl 4-hydroxylase precursor	-2.7	12	57116	P13674	PM/ER
HSP90 (gp96)	-4.56	2	79810	P14625	PM/ER
Glucosidase II	-6.35; -2.3	16	106899	Q14697	PM/ER
Protein disulfide isomerase-associated 4	2.0	2	72932	P13667	PM/ER

Table S1. PM differentially expressed proteins (continued)

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
Voltage-dependent anion channel 1 (VDAC1)	2.17	7	30772	P21796	PM/M
Hsp60 isoform C	-2.0	2	61587	Q9VMN5	PM/M
Caldesmon-LSP1 protein	2.14	11	37169	Q6FHM3	PM/CSK
Membrane-organizing extension spike protein (moesin)	-4.02	20	67820	P26038	PM/CSK
IQ motif containing GTPase activating protein 1	-4.24; -3.67;	2	189250	A4QPB0	PM/CSK
ELMO domain-containing protein 3	-2.25	5	43003	Q96FG2	PM/CSK
Fascin (Singed-like protein)	5.7	2	54365	Q16658	PM/CSK
HSP 86	-4.44; -3.67	5	35760	P07900	PM/C
Phosphodiesterase 10A7 (PDE10A7)	2.86	2	965	Q9HCQ0	PM/C
Cytotoxic granule-associated RNA-binding protein p40-TIA-1	-4.46; -3.06	2	1256	P31483	PM/C
Cyclophilin A	2.0	10	17881	P62937	PM/C
Glyceraldehyde-3-phosphate dehydrogenase	3.97	3	36053	P04406	PM/C
Annexin VI	-3.74	7	75873	P08133	PM/C
Plastin 1	12.95	6	70278	Q8NEG6	PM/C
Immunoglobulin lambda light chain variable region	2.1	3	11594	Q96SB0	S
Ig heavy chain V-III region VH26	-3.63; -2.88	2	12582	P01764	S
Cystatin B	2.0	3	11140	P04080	S
Prolidase	-2.0	2	54582	P12955	S
Vitamin D-Binding Protein	-4.3	2	41816	P02774	S
Endothelin-1 [Precursor]	2.57	3	24425	P05305	S
Ferritin H subunit	-4.18	2	21226	P02794	S
Neurotrophic Factor Artemin	2.0	4	23601	Q5T4W7	S
Chordin	-2.87	3	102032	Q9H2X0	S
Apolipoprotein C-II precursor	-2.62	2	11284	P02655	S
Apolipoprotein C-I [Precursor]	-2.62	2	9332	P02654	S
Protein NOV homolog [Precursor]	2.6	5	39162	P48745	S
Defensin, alpha 1 preproprotein	-3.9	3	10201	Q6EZF6	S
Hepcidin [Precursor]	-1.9	4	9402	P81172	S
Beta-1B-glycoprotein	2.0	3	51676	P02790	S
Complement Component C3c precursor	3.4	2	39488	P01024	S
HSP60	-2.0	11	61054	P10809	S
Leukotriene A-4 hydrolase	2.0	16	69110	P09960	S
L-Lactate Dehydrogenase	2.30	16	69285	P00338	S

Table S1. PM differentially expressed proteins (continued)

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
S100 calcium-binding protein A8	-5.42	2	10938	P05109	S/L
S100 calcium-binding protein A9	-6.32	3	13242	P06702	S/L
Actin, gamma	3.42	2	41607	Q9UVW9	S/CSK
Gelsolin precursor	-3.74	6	85644	A03011	S/CSK
Vimentin	3.42; 5.39;	82	53488	P08670	S/CSK
Sorting nexin-18	2.0	10	68880	Q96RF0	G
Coated vesicle-associated kinase	-3.6	2	82023	Q6P3W7	E
Ubiquitin-activating enzyme E1	-3.0; -2.51	8	117848	P22314	E
Sorting nexin 2 (fragment)	2.25	7	58409	Q53GG3	E
De-ubiquitinase	-3.40	6	95744	P45974	L
Beta-N-acetylhexosaminidase	5.39	8	60650	P06865	L
ATPase, H ⁺ transporting, lysosomal 70kDa, V1 subunit A	-3.27	18	68260	Q53YD9	L
ATPase, H ⁺ transporting, lysosomal 56/58kD, V1 subunit B,	2.12	3	56797	Q6P4H6	L
HSP 90 alpha 2	-2.25	16	98052	Q5CAQ7	L
Cathepsin D pre-protein	-2.9	2	44552	P07339	L
Nadh- Ubiquinone Oxidoreductase Complex I	-6.44	4	11171	O15239	M (membrane)
Ferredoxin 1 precursor	2.0	2	19393	P10109	M
Neurolysin	2.0	2	80651	Q9BYT8	M
Dihydrolipoamide dehydrogenase	5.7	7	54116	A92622	M
Glutamate dehydrogenase	5.7	4	61359	P00367	M
ATP synthase, H ⁺ transporting	2.61	2	18491	Q53FE1	M
Pyruvate kinase 3 isoform 1	5.48	5	57937	Q15118	M
Pyruvate carboxylase precursor	-1.9	3	129633	Q16822	M
Isocitrate dehydrogenase 1 (NADP+)	3.42	3	46659	Q567U4	M
Putative NF-kappa-B-activating protein 107	-2.0	2	44840	Q8WVQ1	ER (membrane)
Ribosome-binding protein 1	2.0	20	87433	Q9P2E9	ER (membrane)

Table S1. PM differentially expressed proteins (continued)

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
Fatty aldehyde dehydrogenase	-1.9	4	54848	P51648	ER (membrane)
Calcium ATPase, fast twitch 1 isoform 1	7.3	2	110252	O14983	ER (membrane)
Calcium ATPase, slow twitch 2 isoform 1	3.7	3	114756	P16615	ER (membrane)
Microsomal glutathione S-transferase 2	-2.2	3	23356	Q99735	ER (membrane)
Procollagen-proline dioxygenase	-3.01	3	60929	P13674	ER
Glycosyltransferase 25	-2.0	2	71636	Q8IYK4	ER
6-phosphogluconolactonase	2.0	2	27547	O95336	ER
Monocyte/macrophage serine esterase	-4.02	17	62358	Q549X7	ER
Transitional endoplasmic reticulum ATPase	-3.1	20	89135	P55072	ER
Glutathione peroxidase 1	-3.3	4	21899	P07203	C
Biliverdin reductase B	1.9	2	22119	P30043	C
Rho GDP dissociation inhibitor (GDI) beta	2.6	6	22988	P52566	C
Protein kinase C and casein kinase substrate in neurons protein 2	-2.25	9	55704	Q6FIA3	C
Phosphoglucomutase 1	-2.43	3	61449	P36871	C
Phosphogluconate dehydrogenase	2.60	3	53140	P52209	C
Pyruvate kinase 3	-8.2	17	57937	P14618	C
Nicotinamide phosphoribosyltransferase	3.40	4	55487	A55927	C
Malic enzyme	2.12	3	64150	P48163	C
Calmodulin	-8.38	6	17163	P62158	C
Major vault protein	-6.35	7	99326	Q14764	C
Visfatin	2.0	7	55521	P43490	C
Proteasome assembling chaperone-3	-2.0	3	13096	A4D216	C
Proteasome 26S ATPase subunit 2	-2.6	4	48634	A4D0Q1	C
Tumor protein, translationally-controlled 1	-8.50	3	15587	Q8TBK7	C

Table S1. PM differentially expressed proteins (continued)

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
Thyroid receptor-interacting protein 14	2.02	9	59189	Q15646	C
Glycylpeptide N-tetradecanoyltransferase (fragment)	-3.32	3	7122	Q9BS83	C
Histidine-tRNA ligase	2.12	2	57374	I37559	C
glycyl-tRNA synthetase	2.0	40	77530	P41250	C
Type I AF10 protein [Fragment]	-4.46	3	8954	Q71UR7	C
HSP90AA1	-3.01	3	68329	Q2VPJ6	C
HSP 84	-1.9	3	83264	P08238	C
Ras-GTPase-activating protein SH3-domain-binding protein	-2.0	3	52132	Q5U0Q1	C
Lamin-B1	-2.15	44	66367	BC012295	N (membrane)
Lamin-B2	-2.15	8	67647	BC006551	N (membrane)
Lamin-A/C	2.76	7	79397	P02545	N (membrane)
Monocyte protein 5	2.49	2	72200	Q9Y3Z3	N
Rhabdomyosarcoma antigen MU-RMS-40.12.	2.0	4	55605	Q3BDU5	N
Heterogeneous nuclear ribonucleoprotein H	-2.0	3	49067	P31943	N
Histone h2a variant	4.3	2	14714	Q59FH0	N
splicing factor proline/glutamine rich	-3.94	3	76149	P23246	N
Protein Mago-nashi homolog 2	-2.72	6	17265	Q96A72	N
Major NOS-binding protein	-3.81	2	1387	Q9UDJ7	N
MYF-5	1.9	2	28381	P13349	N
CMP-NeuNAc synthetase	-8.5	4	48379	Q8NFW8	N
Tubulin alpha 1	2.74; 2.87;	41	50120	P68363	CSK
Tubulin alpha 3	2.74	39	50126	Q71U36	CSK
Tubulin alpha 6	2.12	41	49791	Q53GA7	CSK
Tubulin beta	5.39	2	47736	Q5JP53	CSK
Actinin alpha 1	-3.95; -2.89	2	103057	P12814	CSK
Actinin alpha 4	-3.29; -4.56	6	102268	O43707	CSK
Desmin	2.74	8	53372	Q8TD99	CSK
Kappa-actin	-2.6	14	41989	Q9BYX7	CSK

Table S1. PM differentially expressed proteins (continued)

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
EML4 protein	-4.46	3	7492	Q96HE3	CSK
Katanin p60 subunit A-like protein 2	-3.1	2	52775	Q8IYT4	CSK
Dynein	-2.43	8	71456	AB002323	CSK
Tau-tubulin kinase	3.27	2	182353	Q8IWI7	CSK
Actin related protein 2/3 complex subunit 2	9.60	3	34333	O15144	Ubiquitous
Profilin	5.77	5	14852	P07737	Ubiquitous
Annexin I	2.08	2	35040	P04083	Ubiquitous
Huntington disease gene regulatory region-binding protein 1	-2.67	3	41267	Q9NR83	Ubiquitous
Fatty acid binding protein 4, adipocyte	2.26	3	14719	P15090	Ubiquitous
26S proteasome ATPase subunit	-3.1	2	47337	AAC26843	Ubiquitous
cAMP-dependent protein kinase catalytic subunit alpha	-2.8	2	40589	Q32P54	Ubiquitous
leucine rich repeat containing 20	-2.25	3	14878	Q8TCA0	Not Classified
TTL/TEL fusion protein TTL-B2	-2.13	3	2688	Q8NEU1	Not Classified
CDNA: FLJ21555 fis, clone COL06351	-4.46	3	14668	Q9H716	Not Classified
cDNA FLJ76349	2.02	8	29432	A8K262	Not Classified
Putative uncharacterized protein PRO0628	-4.79	3	6383	Q9UI54	Not Classified
IQGAP1 protein	-3.7	21	107472	Q6PIN4	Not Classified
U62317.15 protein	2.41	5	49924	U62317	Not Classified
NSFL1 (P97) cofactor	5.25	3	40791	Q5JXA5	Not Classified
Putative uncharacterized protein GPD2	2.25	2	77204	Q53T76	Not Classified
Sequence 1216 from Patent EP1033401	2.74	8	8733	AX885353	Not Classified
Sequence 2661 from Patent EP1104808	-2.6	10	7636	AX971858	Not Classified
Sequence 15632 from Patent EP1074617	2.11	3	72155	AX880727	Not Classified
Sequence 3 from Patent WO0068693	-3.7; -2.18	28	84621	CAC18967	Not Classified
Sequence 5 from Patent WO03083117	-3.7	4	84593	AX925926	Not Classified

^a Protein ID

^b Protein fold changes in HIV-1 infected monocytes. Negative DIGE Index indicates protein downregulation in infected monocytes. Presence of several values for fold changes indicate multiple modified/degraded protein forms.

^c Number of unique peptides identified for each protein

^dTheoretical molecular mass for the primary translation product calculated from DNA sequences protein.

^e Accession numbers for Swiss-Prot (accessible at <http://ca.expasy.org/sprot/>).

^f Postulated subcellular localization (accessible at <http://locate.imb.uq.edu.au>) as follows: Plasma membrane integral proteins (PMi) type I (T1) and II (T2), single and multipass; plasma membrane associated (PMa) secreted (S); endoplasmatic reticulum (ER); cytoskeleton (CSK); cytosol (C); mitochondria (M); endosomes (E); lysosomes (L); Golgi (G); ubiquitous (U); unknown (proteins with no postulated localization).

Table S2. PM Proteins with similar expression

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
Transmembrane protein 77	1.14	2	15718	Q6UX65	PMi (multipass)
potassium channel tetramerisation domain containing 12	1.45	3	35701	A4D2M4	PMi (multipass)
Myelin peripheral protein	-1.23	6	27537	P25189	PMi (singlepass TI)
IgG Fc gamma receptor IIA (CD32)	-1.05	2	1085	P12318	PMi (singlepass TI)
Ldl Receptor Ligand-Binding Module 5, Calcium-Coordinating	-1.29	3	4062	Q92673	PMi (singlepass TI)
ErbB-3 Tyrosine Kinase Receptor	1.07	2	5726	Q9NNX3	PMi (singlepass TI)
Myeloid plasma membrane glycoprotein (CD13)	-1.27	3	109540	P15144	PMi (singlepass TII)
CD14 antigen	1.37	3	40051	P08571	PM
H ⁺ -transporting two-sector ATPase	1.11	16	56525	A33370	PM
Amyloid beta A4 precursor protein-binding family B member 1	-1.43	3	73183	Q7Z5R6	PM
Immunoglobulin heavy chain variant	1.03	2	44758	Q9NPP6	PM
rf-an igmLAMBDA fab, chain L	1.03	1	22534	1ADQL	PM
Adenylyl cyclase-associated protein 1 (CAP 1)	1.03	12	51510	Q01518	PM
HSP90 protein 1 beta	1.03	11	83264	Q29092	PM
Ezrin	1.13	6	69398	P15311	PM
Annexin A2 isoform 2	1.01; 1.47	8	38604	P07355	PM/S
Epilysin (MMP28)	1.3	2	1439	Q96PI0	PM/S
HSP60 isoform	-1.35	3	61587	Q0VDF9	PM/S
Enolase 1	-1.06; 1.48	2	47169	P06733	PM/S
Protein disulfide-isomerase precursor	1.11	20	57081	P07237	PM/S
Neuritin-like protein [Precursor]	-1.22;	5	17774	Q496H8	PMa
TNF receptor-associated factor 2	1.24	4	55859	Q12933	PMa
Toll-interacting protein	-1.03	4	22798	Q9H0E2	PMa
Leupaxin	1.03	3	43307	Q6FI07	PMa
Reptin 52	1.09	2	50994	Q9Y230	Pma
Coronin 1A	-1.27	3	51026	P31146	PMa
Talin 1	1.09;	2	269764	Q9Y490	PMa
Transforming growth factor alpha precursor	-1.34; -1.22	3	9303	Q9UQ91	PMa
Phospholipase C-gamma 1	-2.87; 1.24	2	1051	Q6LC80	PMa

Table S2. PM Proteins with similar expression (cont)

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
Plastin 2	-1.33	18	70114	P13796	PMa
Dystrophin	1.07;	2	1299	Q16427	PM/ER
Glucosidase II	1.54	16	106899	Q14697	PM/ER
Protein disulfide isomerase-associated 4	-1.30	2	72932	P13667	PM/ER
Tumor rejection antigen (Gp96)	-1.46	15	92282	Q5CAQ5	PM/ER
Membrane-organizing extension spike protein (moesin)	1.09	20	67820	P26038	PM/CSK
Zyxin	1.13	7	61277	Q15942	PM/CSK
PKA C-alpha	-1.44	2	3470	P17612	PM/C
PKA C-beta	-1.44	2	40623	P22694	PM/C
Cyclophilin A	1.09	10	17881	P62937	PM/C
Tumor necrosis factor type 1 receptor assoc. protein (HSP75)	1.09	2	75342	Q12931	PM/C
Enolase beta	1.04	2	46826	P13929	PM/C
Enolase gama	1.04	2	47108	P09104	PM/C
Fermitin family homolog 3	-1.33	1	75437	AK093719	PM/C
Ig heavy chain V-III region VH26	1.07; 1.14	2	12582	P01764	S
Defensin, alpha 3	-1.29	3	10245	P59666	S
Glia-activating factor [Precursor]	-1.46	4	23426	P31371	S
Galactosidase, beta 1 variant	-1.46	2	76021	Q53G40	S
Gelsolin precursor	-1.43 -1.3	6	85644	A03011	S
Vimentin	1.11	82	53488	P08670	S
HSP60	-1.35	11	61054	P10809	S
GRIP1-associated protein 1	-1.65	5	95258	Q4V328	E
Ubiquitin-activating enzyme E1	-1.24	8	117848	P22314	E
Sorting nexin 2 (fragment)	1.08	7	58409	Q53GG3	E
Sorting nexin 1 isoform A	1.08	2	59069	Q53HL9	E
H ⁺ -transporting two-sector ATPase	1.11	16	56525	A33370	L
ATPase, H ⁺ transporting, lysosomal 70kDa, V1 subunit A	-1.22	18	68260	Q53YD9	L
VDAC2	1.3	3	30412	P45880	M (membrane)
Nadh- Ubiquinone Oxidoreductase Complex I	-1.11	4	11171	O15239	M (membrane)
Prohibitin	-1.37	7	29804	P35232	M (membrane)
Complex I-75kD	1.4	10	79417	BC022368	M (membrane)
Flavoprotein-ubiquinone oxidoreductase	1	2	68464	Q16134	M (membrane)
Ubiquinol-cytochrome-c reductase	1.03	8	52585	A48043	M (membrane)

Table S2. PM Proteins with similar expression (cont)

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
Peroxiredoxin 3 isoform a precursor	-1.43	4	27692	P30048	M
Fumarate hydratase	1.04	6	54602	P07954	M
Succinate dehydrogenase complex, flavoprotein variant	1.11	8	73130	Q59GW8	M
Flavoprotein subunit of complex II	1.11	8	72645	P31040	M
Citrate synthase precursor, isoform A	-1.27	2	51712	O75390	M
3-hydroxyisobutyryl-coenzyme A hydrolase	1.01	3	42907	Q6NVY1	M
Aconitase 2 precursor	1.40	5	85425	Q99798	M
ATP synthase, H ⁺ transporting	1.22	2	18491	Q53FE1	M
Pyruvate kinase 3 isoform 1	1.37	5	57937	Q15118	M
Malate dehydrogenase, mitochondrial precursor	1.8	4	35531	P40926	M
Cyclophilin B	-1.18	3	22742	P23284	ER
Glucosidase 2 subunit beta [Precursor]	-1.44	4	59296	P14314	ER
Cep192	1.09	2	189536	Q8TEP8	C
Phosphoglycerate kinase 1	-1.30	2	44614	P00558	C
Aspartate aminotransferase	1.07	1	46087	P17174	C
NADPH oxidase activator 2	1.45	4	59695	P19878	C
Major vault protein	1.40	7	99326	Q14764	C
Neutrophil cytosol factor 2	1.45	4	67545	Q59F14	C
Cell growth-inhibiting gene 33 protein	1.14	2	2438	P18077	C
HSP90AA1	-1.46	3	68329	Q2VPJ6	C
Lamin-B1	-1.22; 1.08	44	66367	BC012295	N (membrane)
Scaffold-attachment factor A2	-1.35	2	72422	Q1KMD3	N
Poly(ADP-ribose) polymerase	1.14	4	64175	P09874	N
C-Rel proto-oncogene protein	-1.18	4	12037	Q04864	N
p53-binding protein Mdm2	-1.05	2	995	Q00987	N
Nucleosome assembly protein 1-like 5	-1.23	5	19581	Q96NT1	N
Tubulin alpha 3	1.1	39	50126	Q71U36	CSK
Tubulin alpha 6	1.2	41	49791	Q53GA7	CSK
Tubulin alpha 8	1.3	14	50062	Q2M3N4	CSK
Actinin alpha 1	1.07;	2	103057	P12814	CSK
Actinin alpha 4	1.07	6	102268	O43707	CSK
Desmin	1.2	8	53372	Q8TD99	CSK
Kappa-actin	-1.12	14	41989	Q9BYX7	CSK

Table S2. PM Proteins with similar expression (cont)

Reference ^a	DIGE Index ^b	Pept. # ^c	MW ^d	SwissProt ^e	Location ^f
F-actin capping protein subunit alpha	1.08	5	32923	P52907	CSK
Dynein	-1.14, 1.16	8	71456	AB002323	CSK
Annexin I	1.01; 1.47	2	35040	P04083	Ubiquitous
Annexin A11	1.03	3	54302	P50995	Ubiquitous
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	-1.25	4	73243	A2AB15	Unknown
Tumor protein D52-like 2	1.07	5	22503	Q5JWU5	Unknown
PNAS-122	1.75	2	11768	Q9BZS5	Unknown
cDNA FLJ44090 fis, clone TESTI4041903	-1.23	5	13964	Q6ZU00	Unknown
LOC389906 protein [Fragment]	-1.4	4	21228	Q6PJD4	Unknown
Sequence 769 from Patent EP1104808	-1.33	2	17459	AX969966	Unknown
Sequence 1290 from Patent EP1033401	1.03	2	9254	AX885427	Unknown
Sequence 2892 from Patent EP1104808	-1.33	2	12413	AX972089	Unknown

^a Protein ID

^b Protein fold changes in HIV-1 infected monocytes. Negative DIGE Index indicates protein downregulation in infected monocytes. Presence of several values for fold changes indicate multiple modified/degraded protein.

^c Number of unique peptides identified for each protein

^d Theoretical molecular mass for the primary translation product calculated from DNA sequences protein.

^e Accession numbers for Swiss-Prot (accessible at <http://ca.expasy.org/sprot/>).

^f Postulated subcellular localization (accessible at <http://locate.imb.uq.edu.au>) as follows: Plasma membrane integral proteins (PMi) type I (T1) and II (T2), single and multipass; plasma membrane associated (PMa) secreted (S); endoplasmatic reticulum (ER); cytoskeleton (CSK); cytosol (C); mitochondria (M); endosomes (E); lysosomes (L); Golgi (G); ubiquitous (U); unknown (proteins with no postulated localization).