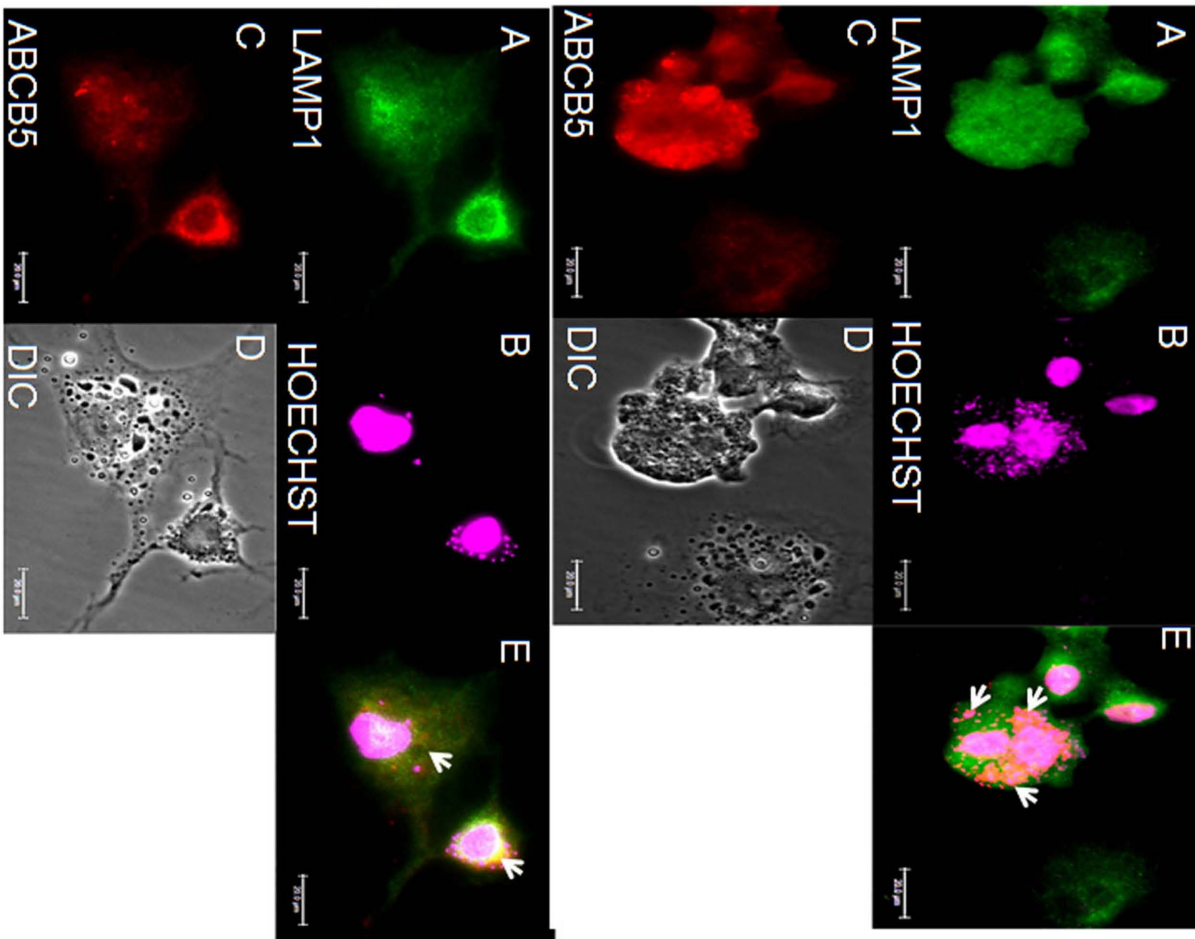


Fig. S1

Human M $\phi$   
infected

Human M $\phi$  infected  
and treated



**Supplementary FIG. S1. Immunolocalization of ABCB5 by confocal laser microscopy in human macrophages.** Human MDMs infected with *Leishmania braziliensis* (Upper panel); human MDMs infected with *L. braziliensis* and treated with Glucantime (Bottom panel); A. LAMP1, marker for lysosomes and late endosomes. B. Nuclei of macrophages and parasites were stained with Hoechst (violet). C. Subcellular localization of ABCB5 drug transporter, D. DIC: differential interference contrast images of human macrophages cells, E. Merged Hoechst and Lamp1 and ABCB5 images. White arrow indicates the subcellular localization of ABCB5 in phagolysosomal structures.

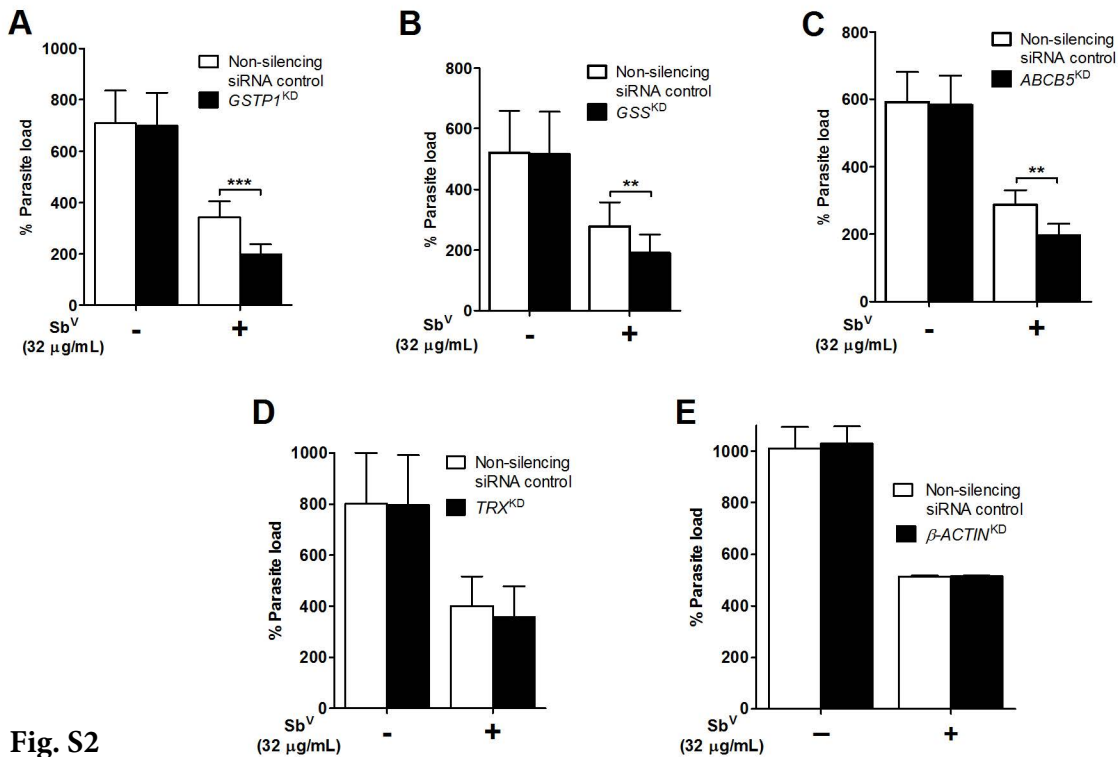
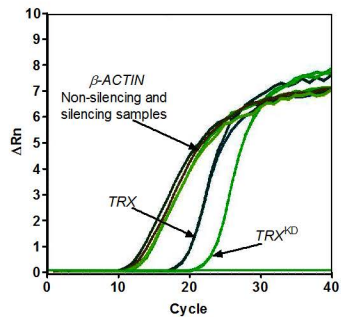
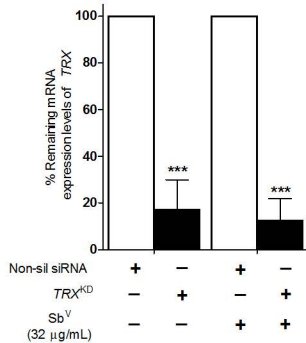
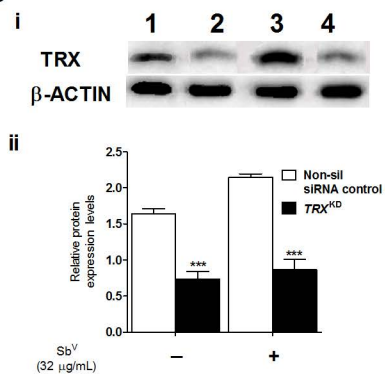
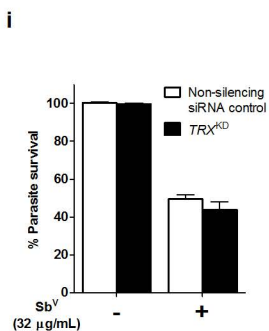
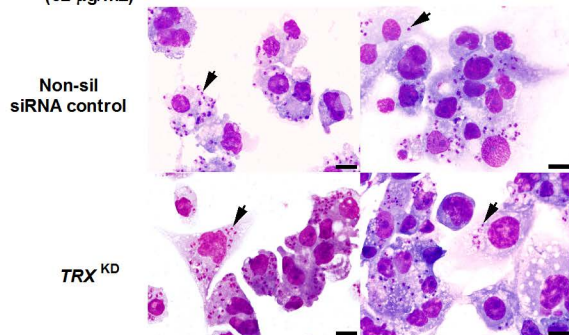
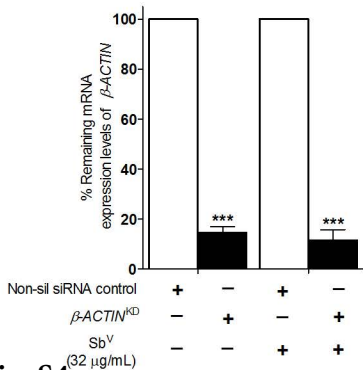
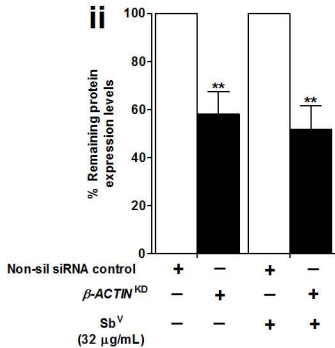
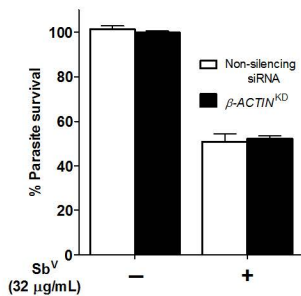


Fig. S2

**Supplementary FIG. S2. Silencing effect of *GSTP1*, *GSS*, *ABCB5*, *TRX* and  $\beta$ -*ACTIN* genes on intracellular *L. braziliensis* amastigote parasitic load in THP1 M $\Phi$  cells silenced and not silenced.** A = *GSTP1*, B = *GSS*, C = *ABCB5*, D = *TRX* and E =  $\beta$ -*ACTIN*. THP-1 M $\Phi$  cells were treated with Sb<sup>V</sup> (32  $\mu$ g/mL); THP-1 M $\Phi$  cells infected and not treated were used as controls. The results represent the average of 2-3 independent experiments  $\pm$  SE. Significant differences were determined by two-way ANOVA, followed by multiple comparison test of Bonferroni, \*\*  $P < 0.01$  and \*\*\*  $P < 0.001$ .

**A****ii****B****C****ii**  $Sb^V$  (32  $\mu$ g/mL)**Fig. S3**

**Supplementary FIG. S3. Silencing of the human *TRX* gene increased the intracellular susceptibility of *L. braziliensis* amastigotes to Sb<sup>V</sup> treatment in THP1 human MΦ cells.** **A.** Efficacy of *TRX* gene silencing was determined at the mRNA expression level by real-time PCR analyses. (i) Representative amplification plot of *TRX* and  $\beta$ -*ACTIN* genes showing the  $\Delta R_n$  vs the cycles observed in the THP-1 MΦ cells infected with *L. braziliensis* and treated with Sb<sup>V</sup>. (ii) Percentage of the remaining levels of mRNA expression in the THP-1 MΦ infected and infected and treated groups (non-silencing siRNA negative control and silenced samples). **Bi.** Protein expression analyses by western blotting; equivalent protein loading was assessed by immunodetection of  $\beta$ -*ACTIN*. Line 1: THP-1 MΦ cells transfected with non-silencing siRNA negative control and infected. Line 2: THP-1 MΦ cells transfected with *TRX* siRNA (*TRX*<sup>KD</sup>) and infected. Line 3: THP-1 MΦ cells transfected with non-silencing siRNA, infected and treated with Sb<sup>V</sup> (32  $\mu$ g/mL). Line 4: THP-1 MΦ cells transfected with *TRX* siRNA (*TRX*<sup>KD</sup>), infected and treated with Sb<sup>V</sup>. **Bii.** Densitometric analysis of signals shown in panel Bi was carried out with ImageJ software. **Ci.** Percentage of intracellular survival of *L. braziliensis* amastigotes infecting THP-1 MΦ cells transfected with non-silencing siRNA or *TRX* siRNA (*TRX*<sup>KD</sup>) and treated with Sb<sup>V</sup> (32  $\mu$ g/mL); infected and untreated THP-1 MΦ were used as controls. **Cii.** Photomicrographs of human THP-1 MΦ cells containing amastigotes (arrow) transfected with non-silencing or *TRX*<sup>KD</sup> and treated or not with 32  $\mu$ g/mL of Sb<sup>V</sup>. (Giemsa stain; scale bar = 20  $\mu$ m). The results represent the average of two to three independent experiments + SEM. Significant differences were determined by two-way ANOVA, followed by Bonferroni's Multiple Comparison Test, \*\*\*  $P < 0.01$ .

**A****B i****ii****C****Fig. S4**

**Supplementary FIG. S4. Silencing of the human  $\beta$ -ACTIN gene did not increase the intracellular susceptibility of *L. braziliensis* amastigotes to Sb<sup>V</sup> treatment in THP1 human M $\Phi$  cells.** Efficacy of  $\beta$ -ACTIN gene silencing was determined at the mRNA and protein expression levels by real-time PCR and western blotting analyses, respectively. A. Percentage of the remaining levels of mRNA expression in the THP-1 M $\Phi$  infected and infected and treated groups (non-silencing siRNA negative control and silenced samples). Bi = Remaining levels of protein expression. Line 1 = THP-1 M $\Phi$  transfected with non-silencing siRNA and infected with *L. braziliensis* (negative control). Line 2 = THP-1 M $\Phi$  cells transfected with  $\beta$ -ACTIN siRNA ( $\beta$ -ACTIN<sup>KD</sup>) and infected. Line 3 = THP-1 M $\Phi$  cells transfected with non-silencing siRNA, infected and treated with Sb<sup>V</sup> (32  $\mu$ g/mL). Line 4 = THP-1 M $\Phi$  cells transfected with  $\beta$ -ACTIN siRNA ( $\beta$ -ACTIN<sup>KD</sup>), infected and treated with Sb<sup>V</sup>. Bii = Densitometric analysis of the signals shown in panel Bi using the software ImageJ. C = Percentage of intracellular survival of *L. braziliensis* amastigotes infecting THP-1 M $\Phi$  cells transfected with non-silencing siRNA or  $\beta$ -ACTIN<sup>KD</sup> and treated with Sb<sup>V</sup> (32  $\mu$ g/mL); infected and untreated THP-1 M $\Phi$  cells were used as controls. The results represent the average of two to three independent experiments + SEM. Significant differences were determined by two-way ANOVA, followed by Bonferroni's Multiple Comparison Test, \*\*  $P < 0.01$  and \*\*\*  $P < 0.01$ .



Supplementary Table S1. Sequences of siRNA genes involved in the antioxidant defense used for the gene-inhibition assays.

siRNA name	Gene	Gene symbol	5'-3' target sequence	5'-3' sense strand	5'-3' antisense strand
HsACTB6	NM_001101	<i>ACTB</i>	CGCCGCGCTCGTCGTCGACAA	CCGCGCUCGUCGUCGACAATT	UUGUCGACGACGAGCGCGGCG
HsTRX_1	NM_003329	<i>TRX</i>	CACCATTAATGAATTAGTCTA	CCAUUAUGAAUUAGUCUATT	UAGACUAAUUCAUUAAUGGTG
HsTRX_2	NM_003329	<i>TRX</i>	AACCAGCCATTGGCTATTTAA	CCAGCCAUUGGCUAUUUAAATT	UUAAAUAGCCAAUGGCUGGTT
HsTRX_3	NM_003329	<i>TRX</i>	TGCCATCTGCGTGACAATAAA	CCAUCUGCGUGACAAUAAATT	UUUAAUUGUCACGCAGAUGGCA
HsGSTP1_1	NM_000852	<i>GSTP1</i>	AAGGATGACTATGTGAAGGCA	GGAUGACUAUGUGAAGGCATT	UGCCUUCACAUAGUCAUCCTT
HsGSTP1_2	NM_000852	<i>GSTP1</i>	CCAGATCTCCTTCGCTGACTA	AGAUCUCCUUCGCUGACUATT	UAGUCAGCGAAGGAGAUCUGG
HsGSTP1_7	NM_000852	<i>GSTP1</i>	CCCATCAATGGCAACGGGAAA	CAUCA AUGGCAACGGGAAATT	UUUCCCGUUGCCAUUGAUGGG
HsGSS_1	NM_000178	<i>GSS</i>	TCCGACGAACATTTGAAGATA	CGACGAACA UUGAAGAUATT	UAUCUUCAAAUGUUCGUCGGA
HsGSS_2	NM_000178	<i>GSS</i>	CTGGTGCTACTGATTGCTCAA	GGUGCUACUGAUUGCUCUATT	UUGAGCAAUCAGUAGCACCAG
HsGSS_8	NM_000178	<i>GSS</i>	TTGGGATAGGACTGAGTGGTA	GGGAUAGGACUGAGUGGUATT	UACCACUCAGUCCUAUCCCAA
HsABCB5_9	NM_178559	<i>ABCB5</i>	TTTGATGTTCTGTGTAATGCAA	UGAUGUUCGUGUAAUGCAATT	UUGCAUUAACACGAACAUCAAA
HsABCB5_12	NM_178559	<i>ABCB5</i>	GAGAATGACATCAGAGCTTTA	GAAUGACAUCAGAGCUUUATT	UAAAGCUCUGAUGUCAUUCTC
HsABCB5_14	NM_178559	<i>ABCB5</i>	CAGAGGTTATATGATCCGGAT	GAGGUUAUAUGAACCGGAUTT	AUCCGGAUCAUUAACCUCTG
Allstars AF 488 Negative control	Not apply	DSsiRNA control sequence	Not apply	QIAGEN Property	QIAGEN Property

Supplementary Table S2. Modulation of Oxidative Stress gene expression levels in human MDMs cells by *L. braziliensis* infection and Glucantime® (Sb<sup>V</sup>) treatment<sup>a</sup>.

Refseq	Symbol	Description Oxidative Stress	Fold change gene expression					
			<i>L. braziliensis</i>	<i>p value</i>	Sb <sup>V</sup>	<i>p value</i>	<i>L. braziliensis</i> and Sb <sup>V</sup>	<i>p value</i>
NM_000477	<i>ALB</i>	Albumin	1.4773	0.47	1.695	0.48	2.4182	0.25
NM_000697	<i>ALOX12</i>	Arachidonate 12-lipoxygenase	2.081	0.25	-1.0475	0.88	<b>3.6403</b>	0.24
NM_001159	<i>AOX1</i>	Aldehyde oxidase 1	-1.0513	0.61	1.0163	0.47	1.1979	0.31
NM_000041	<i>APOE</i>	Apolipoprotein E	2.7876	0.80	<b>6.461</b>	0.21	<b>5.816</b>	0.32
NM_004045	<i>ATOX1</i>	ATX1 antioxidant protein 1 homolog (yeast)	<b>3.6225</b>	0.23	<b>4.4184</b>	0.05	<b>4.1014</b>	0.29
NM_004052	<i>BNIP3</i>	BCL2/adenovirus E1B 19kDa interacting protein 3	<b>4.5989</b>	0.09	<b>6.6093</b>	<b>0.004</b>	<b>4.987</b>	0.33
NM_001752	<i>CAT</i>	Catalase	<b>3.3574</b>	0.12	<b>8.0953</b>	<b>&lt;0.001</b>	<b>5.0263</b>	0.28
NM_002985	<i>CCL5</i>	Chemokine (C-C motif) ligand 5	1.529	0.26	1.7075	0.24	1.3582	0.26
NM_005125	<i>CCS</i>	Copper chaperone for superoxide dismutase	1.9522	0.42	<b>3.5493</b>	0.093	2.0695	0.30
NM_000397	<i>CYBB</i>	Cytochrome b-245, beta polypeptide	2.863	<b>0.047</b>	<b>3.3381</b>	0.084	1.3859	0.24
NM_134268	<i>CYGB</i>	Cytoglobin	<b>3.1808</b>	0.96	<b>6.3211</b>	0.29	<b>5.1408</b>	0.35
NM_014762	<i>DHCR24</i>	24-dehydrocholesterol reductase	1.2843	0.83	1.3273	0.52	1.2039	0.33
NM_175940	<i>DUOX1</i>	Dual oxidase 1	-1.3039	0.83	-1.588	0.21	1.5295	0.32
NM_014080	<i>DUOX2</i>	Dual oxidase 2	-2.4566	0.26	-1.346	0.33	-1.7661	0.69
NM_004417	<i>DUSP1</i>	Dual specificity phosphatase 1	2.1864	0.49	1.7915	0.91	2.503	0.33
NM_001979	<i>EPHX2</i>	Epoxide hydrolase 2, cytoplasmic	-1.0266	0.55	1.7351	0.72	-1.1448	0.85
NM_000502	<i>EPX</i>	Eosinophil peroxidase	1.2326	0.81	2.9288	0.13	2.456	0.32
NM_021953	<i>FOXM1</i>	Forkhead box M1	2.1408	0.44	<b>3.5217</b>	0.12	2.4957	0.33
NM_002032	<i>FTH1</i>	Ferritin, heavy polypeptide 1	<b>5.9163</b>	0.13	<b>8.4497</b>	0.03	<b>4.3093</b>	0.20
NM_001498	<i>GCLC</i>	Glutamate-cysteine ligase, catalytic subunit	1.3661	0.46	1.8373	0.15	-1.3118	0.67
NM_002061	<i>GCLM</i>	Glutamate-cysteine ligase, modifier subunit	2.3032	0.26	<b>9.737</b>	<b>&lt;0.001</b>	2.0801	0.18
NM_000581	<i>GPX1</i>	Glutathione peroxidase 1	1.6099	0.12	1.5006	0.20	1.4147	0.34
NM_002083	<i>GPX2</i>	Glutathione peroxidase 2 (gastrointestinal)	<b>3.2323</b>	0.22	<b>3.0554</b>	0.22	<b>5.5774</b>	<b>&lt;0.05</b>
NM_002084	<i>GPX3</i>	Glutathione peroxidase 3 (plasma)	1.7614	<b>0.036</b>	1.3925	0.29	<b>3.0632</b>	0.26
NM_002085	<i>GPX4</i>	Glutathione peroxidase 4 (phospholipid hydroperoxidase)	2.2846	0.55	2.5378	0.47	<b>5.5142</b>	0.31
NM_001509	<i>GPX5</i>	Glutathione peroxidase 5 (epididymal androgen-related protein)	-2.849	<b>0.013</b>	<b>-3.0026</b>	0.011	-2.5977	0.50
NM_182701	<i>GPX6</i>	Glutathione peroxidase 6 (olfactory)	-2.8681	0.084	-2.8257	0.085	-2.7885	0.34
NM_015696	<i>GPX7</i>	Glutathione peroxidase 7	2.0799	0.45	2.8148	0.11	2.5332	0.32
NM_000637	<i>GSR</i>	Glutathione reductase	1.8274	0.57	<b>5.5407</b>	<b>&lt;0.05</b>	<b>6.3131</b>	<b>&lt;0.01</b>
NM_000178	<i>GSS</i>	Glutathione synthetase	1.4432	0.55	2.9867	<b>0.03</b>	<b>3.3843</b>	0.32
NM_000852	<i>GSTP1</i>	Glutathione S-transferase pi 1	<b>3.4622</b>	0.46	<b>8.6994</b>	<b>&lt;0.001</b>	<b>15.9838</b>	<b>&lt;0.001</b>
NM_001513	<i>GSTZ1</i>	Glutathione transferase zeta 1	1.1629	0.62	2.9844	<b>0.05</b>	2.2111	0.34

NM_001518	<i>GTF2I</i>	General transcription factor Iii	1.0334	0.97	<b>3.2754</b>	<b>0.032</b>	2.3125	0.31
NM_002133	<i>HMOX1</i>	Heme oxygenase (decycling) 1	1.4678	0.31	<b>9.9907</b>	0.072	<b>6.3742</b>	<b>0.05</b>
NM_005345	<i>HSPA1A</i>	Heat shock 70kDa protein 1A	1.3499	0.43	<b>4.4116</b>	<b>0.034</b>	2.10	0.12
NM_006121	<i>KRT1</i>	Keratin 1	1.6194	0.47	1.5952	0.44	2.023	0.36
NM_006151	<i>LPO</i>	Lactoperoxidase	1.1563	0.92	2.6097	0.12	2.7078	0.33
NM_005368	<i>MB</i>	Myoglobin	<b>-4.2296</b>	<b>0.026</b>	<b>-3.9552</b>	<b>0.025</b>	-1.379	0.62
NM_000242	<i>MBL2</i>	Mannose-binding lectin (protein C) 2, soluble	<b>-3.3322</b>	0.34	-2.3832	0.34	-2.9091	0.35
NM_004528	<i>MGST3</i>	Microsomal glutathione S-transferase 3	1.5336	0.94	1.4235	0.96	2.6939	0.34
NM_000250	<i>MPO</i>	Myeloperoxidase	-1.0571	0.98	1.1371	0.65	2.2895	0.32
NM_002437	<i>MPV17</i>	MpV17 mitochondrial inner membrane protein	1.1726	0.67	1.2307	0.55	1.5951	0.37
NM_012331	<i>MSRA</i>	Methionine sulfoxide reductase A	-1.259	0.81	1.1616	0.76	1.0718	0.40
NM_005954	<i>MT3</i>	Metallothionein 3	1.6406	0.38	-1.8118	0.74	-1.4194	0.28
NM_000265	<i>NCF1</i>	Neutrophil cytosolic factor 1	1.2888	0.58	1.3073	0.33	1.2646	0.47
NM_000433	<i>NCF2</i>	Neutrophil cytosolic factor 2	1.1849	0.41	<b>3.159</b>	<b>0.007</b>	2.8046	0.27
NM_000625	<i>NOS2</i>	Nitric oxide synthase 2, inducible	1.1484	0.97	-1.7605	0.24	1.4365	0.41
NM_016931	<i>NOX4</i>	NADPH oxidase 4	1.003	0.99	1.4251	0.30	1.245	0.44
NM_024505	<i>NOX5</i>	NADPH oxidase, EF-hand calcium binding domain 5	-1.6054	0.12	-1.2794	0.27	-1.0048	0.41
NM_000903	<i>NQO1</i>	NAD(P)H dehydrogenase, quinone 1	<b>-3.3659</b>	0.078	1.3748	0.57	<b>3.2951</b>	0.28
NM_002452	<i>NUDT1</i>	Nudix (nucleoside diphosphate linked moiety X)-type motif 1	1.175	0.79	1.285	0.95	1.3635	0.63
NM_181354	<i>OXR1</i>	Oxidation resistance 1	1.4948	0.40	1.5869	0.28	2.3281	0.32
NM_005109	<i>OXS1</i>	Oxidative-stress responsive 1	-1.0414	0.61	1.1977	0.61	2.0056	0.34
NM_020992	<i>PDLIM1</i>	PDZ and LIM domain 1	-1.2736	0.65	1.1662	0.67	1.5183	0.40
NM_007254	<i>PNKP</i>	Polynucleotide kinase 3'-phosphatase	-1.0926	0.64	1.6981	0.13	1.5312	0.34
NM_002574	<i>PRDX1</i>	Peroxiredoxin 1	1.0676	0.87	1.5026	0.30	1.8425	0.28
NM_005809	<i>PRDX2</i>	Peroxiredoxin 2	1.4165	0.26	2.3535	0.04	1.9024	0.17
NM_006793	<i>PRDX3</i>	Peroxiredoxin 3	1.1347	0.73	2.266	0.13	1.6317	0.38
NM_006406	<i>PRDX4</i>	Peroxiredoxin 4	1.3988	0.15	2.5332	<b>0.0006</b>	1.8357	0.08
NM_181652	<i>PRDX5</i>	Peroxiredoxin 5	1.3844	0.25	2.5919	<b>0.0019</b>	2.2753	0.07
NM_004905	<i>PRDX6</i>	Peroxiredoxin 6	1.0327	0.84	1.7842	0.43	2.4915	0.32
NM_020820	<i>PREX1</i>	Phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	-1.0496	0.48	1.0177	0.66	1.4496	0.62
NM_183079	<i>PRNP</i>	Prion protein	-1.4223	0.35	-1.2756	0.49	-1.0444	0.49
NM_000962	<i>PTGS1</i>	Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	-1.4678	0.085	-1.1121	0.99	1.105	0.49
NM_000963	<i>PTGS2</i>	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	<b>-3.1546</b>	<b>0.043</b>	-1.657	0.18	-1.9232	0.23
NM_012293	<i>PXDN</i>	Peroxidasin homolog (Drosophila)	1.2474	0.80	-1.3226	0.82	-1.3178	0.60
NM_014245	<i>RNF7</i>	Ring finger protein 7	-1.2722	0.34	1.3455	0.37	-1.1987	0.66
NM_182826	<i>SCARA3</i>	Scavenger receptor class A, member 3	2.1652	0.36	2.4605	0.30	1.2269	0.52
NM_203472	<i>SELS</i>	Selenoprotein S	1.1293	0.62	2.4311	<b>0.018</b>	1.2551	0.38
NM_005410	<i>SEPP1</i>	Selenoprotein P, plasma, 1	-1.3672	0.54	<b>-3.7941</b>	0.42	-1.3966	0.69
NM_003019	<i>SFTPD</i>	Surfactant protein D	-1.1039	0.95	-2.1389	0.80	2.4943	0.31
NM_012237	<i>SIRT2</i>	Sirtuin 2	1.6318	0.16	2.5347	0.11	2.684	0.12
NM_000454	<i>SOD1</i>	Superoxide dismutase 1, soluble	1.344	0.49	1.9183	0.11	1.9282	0.27
NM_000636	<i>SOD2</i>	Superoxide dismutase 2, mitochondrial	-1.3283	0.32	-1.3185	0.43	1.0679	0.87
NM_003102	<i>SOD3</i>	Superoxide dismutase 3, extracellular	<b>-5.6173</b>	<b>&lt; 0.001</b>	-1.3981	0.87	-2.5788	0.59
NM_003900	<i>SQSTM1</i>	Sequestosome 1	-2.3728	<b>0.043</b>	1.371	0.38	<b>4.6373</b>	0.26

NM_080725	<i>SRXN1</i>	Sulfiredoxin 1	-1.8999	0.27	1.8687	0.47	2.2622	0.27
NM_006374	<i>STK25</i>	Serine/threonine kinase 25	-1.2861	0.32	2.2788	<b>0.029</b>	1.1259	0.79
NM_000547	<i>TPO</i>	Thyroid peroxidase	1.8106	0.35	2.3046	0.21	1.4283	0.35
NM_003319	<i>TTN</i>	Titin	1.388	0.88	2.1973	0.31	1.2805	0.98
NM_003329	<i>TXN</i>	Thioredoxin	-1.2295	0.49	<b>3.6591</b>	<b>&lt;0.001</b>	<b>6.6256</b>	0.23
NM_003330	<i>TXNRD1</i>	Thioredoxin reductase 1	-1.0954	0.53	<b>-11.085</b>	0.99	1.8225	0.61
NM_006440	<i>TXNRD2</i>	Thioredoxin reductase 2	1.6792	0.92	2.9196	0.56	2.7332	0.43
NM_003355	<i>UCP2</i>	Uncoupling protein 2 (mitochondrial, proton carrier)	2.4417	<b>0.038</b>	<b>6.6794</b>	<b>&lt;0.001</b>	<b>5.0742</b>	0.10

<sup>a</sup> Modulation of gene expression was measured after 3 days of incubation with 32 µg/mL of Sb<sup>v</sup> using the RT<sup>2</sup> Human Oxidative Stress PCR expression array analysis (QIAGEN). Data are represented as fold change and mean ± S:E:M

Supplementary Table S3. Modulation of drug transporters gene expression levels in human MDMs cells by *L. braziliensis* infection and Glucantime® (Sb<sup>V</sup>)<sup>a</sup> treatment.

Refseq	Symbol	Description Drug Transporters	Fold change gene expression					
			<i>L. braziliensis</i>	p value	Sb <sup>V</sup>	p value	<i>L. braziliensis</i> and Sb <sup>V</sup>	p value
NM_005502	<i>ABCA1</i>	ATP-binding cassette, sub-family A (ABC1), member 1	2.7882	0.38	-	0.51	6.0721	0.24
NM_173076	<i>ABCA12</i>	ATP-binding cassette, sub-family A (ABC1), member 12	1.2124	0.44	1.4417	0.37	1.5115	0.25
NM_152701	<i>ABCA13</i>	ATP-binding cassette, sub-family A (ABC1), member 13	1.6592	0.93	2.0333	0.41	2.5366	0.36
NM_001606	<i>ABCA2</i>	ATP-binding cassette, sub-family A (ABC1), member 2	1.2663	0.30	2.1881	0.71	4.9661	0.34
NM_001089	<i>ABCA3</i>	ATP-binding cassette, sub-family A (ABC1), member 3	1.2887	0.52	1.5093	0.89	2.3793	0.37
NM_000350	<i>ABCA4</i>	ATP-binding cassette, sub-family A (ABC1), member 4	1.2334	0.39	1.5156	0.36	2.2194	0.32
NM_018672	<i>ABCA5</i>	ATP-binding cassette, sub-family A (ABC1), member 5	1.5198	0.50	2.0152	0.89	1.3186	0.59
NM_080283	<i>ABCA9</i>	ATP-binding cassette, sub-family A (ABC1), member 9	1.7557	0.25	1.5586	0.39	2.5727	0.21
NM_000927	<i>ABCB1/PGP</i>	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.0709	0.42	-	0.75	1.3397	0.78
NM_003742	<i>ABCB11/BSEP</i>	ATP-binding cassette, sub-family B (MDR/TAP), member 11	1.8299	0.90	9.5751	<0,001	5.2472	0.25
NM_000443	<i>ABCB4</i>	ATP-binding cassette, sub-family B (MDR/TAP), member 4	1.752	0.55	1.4065	0.86	1.3751	0.54
NM_178559	<i>ABCB5</i>	ATP-binding cassette, sub-family B (MDR/TAP), member 5	17.0634	<0,001	8.8499	<0,001	13.8963	<0,001
NM_005689	<i>ABCB6</i>	ATP-binding cassette, sub-family B (MDR/TAP), member 6	3.3862	0.48	4.795	0.14	10.1194	<0,001
NM_004996	<i>ABCC1</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	1.0506	0.88	1.1613	0.95	2.1409	0.35
NM_033450	<i>ABCC10</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	-2.0837	0.22	1.4739	0.92	1.7027	0.43
NM_032583	<i>ABCC11</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 11	-2.6092	0.33	2.0677	0.84	3.1774	0.44
NM_033226	<i>ABCC12</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	1.6172	0.39	3.637	0.25	2.952	0.04
NM_000392	<i>ABCC2</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	1.0925	0.63	1.1162	0.67	2.3375	0.45
NM_003786	<i>ABCC3</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	1.1527	0.73	1.1234	0.71	1.8241	0.34
NM_005845	<i>ABCC4</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	-1.0153	0.59	1.0319	0.69	1.761	0.45
NM_005688	<i>ABCC5</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	1.4657	0.95	1.4338	0.60	2.9503	0.27
NM_000033	<i>ABCD1</i>	ATP-binding cassette, sub-family D (ALD), member 1	-1.0815	0.47	2.1793	0.31	1.7251	0.41
NM_002858	<i>ABCD3</i>	ATP-binding cassette, sub-family D (ALD), member 3	1.7856	0.33	1.734	0.52	1.9456	0.34

NM_005050	<i>ABCD4</i>	ATP-binding cassette, sub-family D (ALD), member 4	19.7497	0.35	3.5205	0.57	2.393	0.87	
NM_001090	<i>ABCF1</i>	ATP-binding cassette, sub-family F (GCN20), member 1	2.7232	0.44	-	1.0142	0.68	2.7466	0.40
NM_004827	<i>ABCG2/BCRP</i>	ATP-binding cassette, sub-family G (WHITE), member 2	-1.2278	0.30	1.3645	0.30	2.2644	<b>0.005</b>	
NM_022437	<i>ABCG8</i>	ATP-binding cassette, sub-family G (WHITE), member 8	-2.3154	0.14	-	1.5256	0.28	-1.3179	0.50
NM_198098	<i>AQP1</i>	Aquaporin 1 (Colton blood group)	1.997	0.39	3.7719	0.16	4.8047	0.12	
NM_001170	<i>AQP7</i>	Aquaporin 7	1.6601	0.37	2.6159	0.28	4.5497	0.20	
NM_020980	<i>AQP9</i>	Aquaporin 9	1.0335	0.75	1.4472	0.45	1.6963	0.40	
NM_001694	<i>ATP6V0C</i>	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	-1.0566	0.94	-	1.2204	0.84	1.3498	0.31
NM_000052	<i>ATP7A</i>	ATPase, Cu++ transporting, alpha polypeptide	-1.3336	0.51	-	1.1477	0.84	1.2083	0.46
NM_000053	<i>ATP7B</i>	ATPase, Cu++ transporting, beta polypeptide	-1.0339	0.83	2.2603	0.39	2.2512	0.35	
NM_017458	<i>MVP</i>	Major vault protein	-1.0625	0.66	1.6415	0.68	1.9275	0.35	
NM_003049	<i>SLC10A1</i>	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1	2.2255	0.18	1.1896	0.40	4.3593	<b>0.04</b>	
NM_000452	<i>SLC10A2</i>	Solute carrier family 10 (sodium/bile acid cotransporter family), member 2	1.0248	0.94	4.6554	0.17	3.3093	0.24	
NM_005073	<i>SLC15A1</i>	Solute carrier family 15 (oligopeptide transporter), member 1	-1.3637	0.29	2.4727	0.13	2.4577	0.17	
NM_021082	<i>SLC15A2</i>	Solute carrier family 15 (H+/peptide transporter), member 2	-1.4179	0.32	1.59	0.25	1.632	0.22	
NM_003051	<i>SLC16A1</i>	Solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	-1.3368	0.73	-1.059	0.95	1.3932	0.94	
NM_006517	<i>SLC16A2</i>	Solute carrier family 16, member 2 (monocarboxylic acid transporter 8)	1.1281	0.74	1.3588	0.47	1.814	0.42	
NM_004207	<i>SLC16A3</i>	Solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	-1.12	0.64	2.5082	<b>0.02</b>	3.2376	0.099	
NM_194255	<i>SLC19A1</i>	Solute carrier family 19 (folate transporter), member 1	-1.1381	0.88	1.2764	0.66	1.4809	0.39	
NM_006996	<i>SLC19A2</i>	Solute carrier family 19 (thiamine transporter), member 2	1.2952	0.38	2.9151	0.074	2.0503	0.06	
NM_025243	<i>SLC19A3</i>	Solute carrier family 19, member 3	1.0728	0.88	1.9823	0.26	1.7264	0.36	
NM_003057	<i>SLC22A1/OCT1</i>	Solute carrier family 22 (organic cation transporter), member 1	2.5649	0.09	1.5658	0.17	4.5953	0.16	
NM_003058	<i>SLC22A2/OCT2</i>	Solute carrier family 22 (organic cation transporter), member 2	-1.0497	0.58	-	1.0436	0.89	1.1259	0.49
NM_021977	<i>SLC22A3</i>	Solute carrier family 22 (extraneuronal monoamine transporter), member 3	1.1381	0.91	1.8145	0.29	1.8979	0.27	
NM_004790	<i>SLC22A6</i>	Solute carrier family 22 (organic anion transporter), member 6	1.4323	0.45	1.9293	0.32	3.0695	0.30	
NM_006672	<i>SLC22A7</i>	Solute carrier family 22 (organic anion transporter), member 7	-1.4221	0.27	-1.07	0.42	1.8342	0.45	
NM_004254	<i>SLC22A8</i>	Solute carrier family 22 (organic anion transporter), member 8	-1.2561	0.67	1.4076	0.46	2.6641	0.19	
NM_080866	<i>SLC22A9</i>	Solute carrier family 22 (organic anion transporter), member 9	1.1509	0.10	1.9423	0.21	2.489	0.07	
NM_014251	<i>SLC25A13</i>	Solute carrier family 25, member 13 (citrin)	1.0622	0.59	1.2905	0.16	1.5898	0.32	

NM_004213	SLC28A1	Solute carrier family 28 (sodium-coupled nucleoside transporter), member 1	1.7294	0.87	1.9761	0.32	5.1152	0.189
NM_004212	SLC28A2	Solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	-1.639	0.65	1.2693	0.60	-1.1724	0.47
NM_022127	SLC28A3	Solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	-1.6493	0.67	1.1962	0.49	-1.3013	0.89
NM_004955	SLC29A1	Solute carrier family 29 (nucleoside transporters), member 1	1.1007	0.87	1.4824	0.45	1.8015	0.26
NM_001532	SLC29A2	Solute carrier family 29 (nucleoside transporters), member 2	1.0231	0.70	2.362	0.22	2.256	0.28
NM_006516	SLC2A1	Solute carrier family 2 (facilitated glucose transporter), member 1	1.9482	0.25	1.4985	0.62	2.2889	0.31
NM_000340	SLC2A2	Solute carrier family 2 (facilitated glucose transporter), member 2	-1.1387	0.49	1.5713	0.33	2.0765	0.14
NM_006931	SLC2A3	Solute carrier family 2 (facilitated glucose transporter), member 3	-1.1478	0.10	1.1963	0.59	1.5309	0.36
NM_001859	SLC31A1	Solute carrier family 31 (copper transporters), member 1	-1.4639	0.28	1.4811	0.50	1.689	0.41
NM_018976	SLC38A2	Solute carrier family 38, member 2	-1.3534	0.32	-1.005	0.10	-1.1358	0.90
NM_033518	SLC38A5	Solute carrier family 38, member 5	1.1475	0.92	1.2243	0.94	1.7964	0.33
NM_000341	SLC3A1	Solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1	-1.585	0.39	1.0462	0.81	1.0633	0.44
NM_002394	SLC3A2	Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	-1.0275	0.91	1.2543	0.33	2.0758	0.11
NM_000343	SLC5A1	Solute carrier family 5 (sodium/glucose cotransporter), member 1	-1.3023	0.51	1.5097	0.63	2.5716	0.75
NM_014227	SLC5A4	Solute carrier family 5 (low affinity glucose cotransporter), member 4	1.1371	0.99	1.8769	0.37	1.4851	0.54
NM_014331	SLC7A11	Solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	1.951	0.26	2.3558	0.14	5.3677	0.13
NM_003486	SLC7A5	Solute carrier family 7 (amino acid transporter light chain, L system), member 5	-1.1129	0.80	1.1322	0.65	1.5785	0.22
NM_003983	SLC7A6	Solute carrier family 7 (amino acid transporter light chain, y+L system), member 6	1.3	0.83	1.1632	0.89	1.4166	0.62
NM_003982	SLC7A7	Solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	1.4153	0.39	1.4727	0.32	1.6238	0.30
NM_182728	SLC7A8	Solute carrier family 7 (amino acid transporter light chain, L system), member 8	1.4066	0.70	3.0578	0.05	2.6496	0.22
NM_014270	SLC7A9	Solute carrier family 7 (glycoprotein-associated amino acid transporter light chain, bo,+ system), member 9	-1.1469	0.65	1.6963	0.89	1.731	0.76
NM_021094	SLCO1A2	Solute carrier organic anion transporter family, member 1A2	-1.0442	0.93	1.2662	0.99	2.8988	0.16
NM_006446	SLCO1B1/ OATP1B1	Solute carrier organic anion transporter family, member 1B1	-1.3877	0.30	1.1257	0.77	1.647	0.43
NM_019844	SLCO1B3/ OATP1B3	Solute carrier organic anion transporter family, member 1B3	1.3578	0.51	1.5161	0.45	1.8029	0.35
NM_005630	SLCO2A1	Solute carrier organic anion transporter family, member 2A1	1.5173	0.30	4.5364	0.10	2.5803	0.06

NM_007256	<i>SLCO2B1</i>	Solute carrier organic anion transporter family, member 2B1	-1.0372	0.66	1.2573	0.94	2.0468	0.26	
NM_013272	<i>SLCO3A1</i>	Solute carrier organic anion transporter family, member 3A1	-1.5625	0.22	-	1.2381	0.40	1.0574	0.96
NM_016354	<i>SLCO4A1</i>	Solute carrier organic anion transporter family, member 4A1	1.9763	0.24	2.4582	0.16	2.6362	0.26	
NM_000593	<i>TAP1</i>	Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	1.1781	0.99	1.1559	0.76	1.5873	0.93	
NM_000544	<i>TAP2</i>	Transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	1.1559	0.92	1.7514	0.23	2.4777	0.13	
NM_003374	<i>VDAC1</i>	Voltage-dependent anion channel 1	1.6296	0.45	2.2844	0.08	1.9606	0.28	
NM_003375	<i>VDAC2</i>	Voltage-dependent anion channel 2	1.2376	0.85	2.0892	0.19	2.2265	0.18	

<sup>a</sup> Modulation of gene expression was measured after 3 days of incubation with 32 µg/mL of Sb<sup>V</sup> using the RT<sup>2</sup> Human Drug Transporters PCR expression array analysis (QIAGEN). Data are represented as fold change and mean ± S:E:M