

**Table 1** : Genes that are regulated by chronic morphine in rat hippocampus based on microarray analysis. Data are the mean of 6 hybridizations.

Clone ID	Fold change	Gene	Accession N°	Function
M 1247	1.34	Sip30	NM_147138	Vesicle mediated transport
M 24	1.30			
M 44	1.26			
M 6	1.34			
M 482	1.27	3 $\beta$ HSD type II.2	NM_017265	Hormon metabolism
M 15	1.42			
M 81	1.35			
M 19	1.38	Mss4	X70496	Intracellular transport
M 38	1.52			
M 41	1.48			
M 982	1.24	unknown	n.a.	unknown
M 46	1.24	Hsp90 $\beta$	XM_217339	Heat shock protein activity
M 1532	1.27	Gapdh	NM_017008	Oxydoreductase activity
73++	0.79	unknown	n.a.	unknown
S71	0.77	Flt1	NM_019306	growth factor receptor binding
S52	0.63	Similar to Sfx4	XM_342072	Iron ion transport
S66	0.70	Similar to Protocadherin9	XM_224429	extracellular matrix constituent
S113	0.78	Got1	NM_012571	Transaminase activity
S82	0.79	Synphilin-1	XM_225768	Vesicle mediated transport
S94	0.8	Flna	XM_238167	Cytoskeletal protein binding

Columns represent the clone ID in the two libraries, fold change values (morphine-treated/controls), gene symbols and GenBank Accession Numbers. Molecular function of the genes according to the Gene Ontology database are also indicated. (n.a. = not applicable).