Table 1. Hypothalamus and pituitary library construction.

	hypothalamic library			pituitary library		
# total clones (1)	448			558		
total unusable clones (2)	114 (25.4%)			78 (14.0%)		
total analyzed clones (3)	334 (74.6%)			480 (86.0%)		
total identified sequences (4)	348			492		
	# sequences (5)	# unique genes or genomic sequences (6)	% of total (7)	# sequences (5)	# unique genes or genomic sequences (6)	% of total (7)
➢ mitochondrial sequences	21	5	6.0%	3	2	0.6%
➢ ribosomal sequences	4	2	1.1%	7	6	1.4%
➢ known genes	199	22	57.2%	438	54	89.0%
➢ ESTs and new genes	83	17	23.9%	34	23	6.9%
➢ genomic DNA sequences	41	12	11.8%	10	8	2.0%

(1) Represents the number of clones isolated after subtraction and stored as glycerol stocks. (2) From these clones, some did not survive, did not contain an insert, or were resistant to sequencing because of their base composition. The remaining clones were analyzed by sequencing. Some clones contained more than one insert. Therefore, the total number of identified sequences in row (4) is larger than the number of analyzed clones in row (3). Identified sequences were grouped into categories: mitochondrial sequences, ribosomal sequences, sequences of known genes, published ESTs, predicted genes or genomic DNA sequences. In each category, column (5) lists the number of sequences found, (6) indicates the number of unique genes or unique genomic sequences represented and in (7) the percentage of sequences is listed compared to the total number of identified sequences in column (4).