Supplemental Digital Content 1. Differential proteases and protease inhibitors in the lumbar dorsal horn during complete Freud's adjuvant (CFA)-induced chronic pain by microarray analysis in rats.

Gene symbol	Accession number	Gene name	Fold change*	*p* values**				
				Unadjusted[†]	BONF	HOLM	FDR_BH	FDR_BY
CTSG	NM_001106041	Cathepsin G	6.17	0.036	1.000	1.000	0.046	0.257
Ace2	NM_001012006	Angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	1.77	0.017	1.000	1.000	0.039	0.219
Prss21	NM_181477	Protease, serine, 21	1.55	0.008	1.000	0.992	0.032	0.182
Adamts6	NM_001108544	ADAM metallopeptidase with thrombospondin type 1 motif, 6	-1.85	0.034	1.000	1.000	0.045	0.257
Usp18	NM_001014058	Ubiquitin specific peptidase 18	-1.74	0.001	1.000	0.149	0.012	0.070
CTSQ	BC107913	Cathepsin Q	-1.51	0.010	1.000	1.000	0.032	0.182
Serpine1	NM_012620	Serine (or cysteine) peptidase inhibitor, clade E, member 1	-2.65	0.012	1.000	1.000	0.033	0.187
Spint2	NM_199087	Serine peptidase inhibitor, Kunitz type, 2 (Spint2), transcript variant 2	2.00	0.016	1.000	1.000	0.039	0.219
Serpina5	NM_022957	Serine (or cysteine) peptidase inhibitor, clade A, member 5	1.63	0.026	1.000	1.000	0.043	0.247

*Fold change indicates the expression level of genes in CFA group versus saline group.
[†]*p* value was determined using unpaired *t* test (unadjusted).
**Multiple testing was corrected using 4 techniques. BONF = Bonferroni single-step adjustment; HOLM = Holm-Bonferroni method; FDR_BH = False Discovery Rate Benjamini-Hochberg method; FDR_BY = False Discovery Rate Benjamini-Hochberg Yekutieli method. Statistical analysis was performed using R version 2.12.0 (The R Foundation for Statistical Computing, Vienna, Austria)