



Supplementary Fig. 2: *rest/nrsf* mRNA levels are not regulated by wild-type and mutant huntingtin. (a) upper panel, RNase protection assay showing REST/NRSF full length mRNA levels in huntingtin overexpressing cells. P are parental ST14A cells while FLwt and FLmu are wild-type and mutant huntingtin overexpressing cells, respectively. (b) upper panel, *rest4* (dominant negative form) mRNA levels were detected by radioactive semiquantitative RT-PCR in huntingtin overexpressing cells. (c) upper panel, *rest/nrsf* full length mRNA was detected by radioactive semiquantitative RT-PCR performed in knock-in cells (7/7, 109/7 and 109/109 are littermate, heterozygous and homozygous mutant huntingtin cells, respectively). (d) upper panel, *rest/nrsf* full length mRNA was detected by radioactive semiquantitative RT-PCR performed on RNA from YAC HD mice. L is the littermate while YAC18 and YAC72 are mice expressing human wild-type and mutant huntingtin, respectively. Lower panels, quantitative evaluation by densitometric analyses of *rest/nrsf* full length and *rest/nrsf 4* mRNA levels compared to β -actin (a,b,c) or SNAP-25 (d) signal. Values represent % of a.u. (arbitrary units) calculated versus P, 7/7 and L to which 100 % value was assigned. Shown are the calculated mean values + SD of three independent experiments.