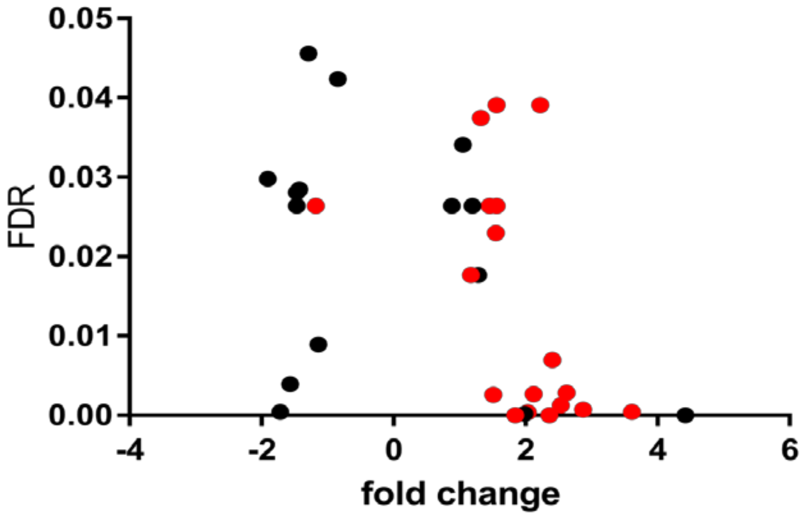
Supplementary File 2 eIF2BεArg191His–regulated shifts in mouse forebrain polysome association

	Probe on microarray chip	Gene	Transcript	FDR	logFC	Regulated by ATF4[1]
1.	A_52_P532982	Gdf15	NM_011819	0,00000006130	4.42	-
2.	A_51_P331570	Trib3	NM_175093	0,00042700000	3.61	+
3.	A_51_P519251	Nupr1	NM_019738	0,00074300000	2.87	+
4.	A_51_P453475	Slc1a5	NM_009201	0,00284000000	2.62	+
5.	A_51_P269216	Atf5	NM_030693	0,00126000000	2.53	+
6.	A_52_P374960	Ostn	NM_198112	0,00699000000	2.40	+
7.	A_51_P263965	Hmox1	NM_010442	0,00003840000	2.36	+
8.	A_51_P129502	Slc7a11	NM_011990	0,03910000000	2.22	+
9.	A_51_P283473	Fibin	NM_026271	0,00267000000	2.12	+
10.	A_51_P493987	Moxd1	NM_021509	0,00039900000	2.03	+
11.	A_51_P421140	Tubb6	NM_026473	0,00017300000	1.98	-
12.	A_51_P273639	Slc7a5	NM_011404	0,00000975000	1.84	+
13.	A_52_P245648	Slc3a2	NM_008577	0,03910000000	1.56	+
14.	A_51_P275016	Slc7a3	NM_007515	0,02640000000	1.56	+
15.	A_51_P268697	Slc1a3	NM_148938	0,02300000000	1.55	-
16.	A_52_P533146	Ddit3	NM_007837	0,00261000000	1.51	+
17.	A_52_P21659	Pck2	NM_028994	0,02640000000	1.45	+
18.	A_51_P319460	Osmr	NM_011019	0,03750000000	1.32	+[2]
19.	A_51_P489153	Crot	NM_023733	0,01770000000	1.28	-
20.	A_51_P427674	Cpt1a	NM_013495	0,02640000000	1.19	-
21.	A_51_P317427	Psat1	NM_177420	0,01770000000	1.17	+
22.	A_51_P427674	Cpt1a	NM_013495	0,03410000000	1.05	-
23.	A_51_P136303	Cyp4f15	NM_134127	0,02640000000	0.88	-
24.	A_52_P57013	Nxn	NM_008750	0,04240000000	-0.85	-
25.	A_51_P436269	Grin2c	NM_010350	0,00892000000	-1.14	-
26.	A_51_P209327	Apln	NM_013912	0,02640000000	-1.18	+
27.	A_52_P266686	Ntsr2	NM_008747	0,04560000000	-1.29	-
28.	A_51_P362066	Chi3l1	NM_007695	0,02850000000	-1.43	-
29.	A_52_P467930	BC158068	BC158068	0,02810000000	-1.47	-
30.	A_51_P194099	Thrsp	NM_009381	0,02640000000	-1.47	-
31.	A_51_P456465	Cldn10	NM_021386	0,00393000000	-1.57	-
32.	A_51_P244540	Ntsr2	NM_008747	0,00041900000	-1.72	-
33.	A_51_P443819	2610034M16Rik	NM_027001	0,02980000000	-1.91	-

[1]) reported in Han et al. 2013

[2]) downregulation by ATF4 reported (Han et al. 2013)



Visualization of the 33 probes representing eIF2BεArg191His–regulated shifts in mouse forebrain polysome association. All data points have a false discovery rate (FDR) < 0.05 and are considered significantly different from WT mouse brain. The fold change (FC) Δ(Δ(B2b5ho,A2b5ho) is plotted, with B indicating abundance in polysomes and A indicating abundance in monosomes (signals obtained from normalized microarray data). Red dots indicate ATF4-regulated mRNAs.