Supplementary Information Weyn-Vanhentenryck et al.

Precise temporal regulation of alternative splicing during neural development

Supplementary Discussion

Validation of developing cortex RNA-seq data quality and AS quantification.

To assess the quality of the mouse cortex RNA-seq data we generated, we initially examined expression of all annotated genes and splicing of all annotated cassette exons. Overall, biological replicates of the same age are highly correlated (Pearson correlation r \geq 0.996 for expression; r \geq 0.991 for splicing). In contrast, we observed dramatic changes in expression and alternative splicing between time points, particularly in the embryonic and neonatal cortices.

To further validate the results of splicing quantification, we performed semi-quantitative RT-PCR for 10 exons that were previously reported to have developmental splicing changes (Supplementary Dataset 3). Selection of these exons was independent of the RNA-seq data. Instead, the developmental splicing pattern of these exons reported in the literature was used to determine the time points we should include for RNA-seq profiling. One example of these exons is *Mapt* exon 10. This exon is almost completely skipped in the embryonic cortex, shows intermediate inclusion between P4 and P7, and reaches almost complete inclusion after P30 (Supplementary Fig. 1c). The observed pattern is consistent with previous observations¹. Quantification of the exon based on the RNA-seq data and semi-quantitative RT-PCR gave very similar results (R^2 =0.99; Supplementary Fig. 1d). High correlation between RNA-seq and PCR validation was also observed in the other tested exons (overall R^2 =0.96; Supplementary Fig. 1e). These results confirm the reliability of the RNA-seq data and our quantification of exon inclusion levels.

Developmental splicing changes reflect pan-neuronal changes instead of changes in cell composition.

A recent study used RNA-seq to profile gene expression in all major cell types in the mouse cortex, including neurons, different types of glial cells and endothelial cells^{12,13}. In a comparison of the splicing profiles of these cell types, we found that neurons show the most distinct splicing profiles and are the most similar to the whole cortex tissue. In addition, we did not observe global developmental splicing switches during the differentiation and maturation of oligodendrocytes that would explain the modules we identified (Supplementary Fig. 4a). Cortical neurons are broadly classified as either pyramidal neurons or interneurons, which differ in their abundance and developmental origins. To assess whether the different representation of pyramidal neurons and interneurons can bias the developmental splicing profiles we observed in cortex tissues, we compared splicing profiles of 19 glutamatergic neuronal subtypes and 23 GABAergic neuronal subtypes defined by single-cell RNA-seq of the primary visual cortex of the adult mice². We observed no global differences between the two broad categories of neurons that are correlated with the modules we identified (Supplementary Fig. 4b).

Developmental origins of sensory receptor cells and sensory neurons.

The non-neuronal sensory receptor cells (enterochromaffin cells and sweet/bitter taste receptor cells) examined in this study derive from epithelial cells of non-neurogenic origin. OSNs and the somatic (from DRG and trigeminal ganglia) and visceral (from jugular and nodose ganglia) sensory ganglion neurons we analyzed arise from either the pre-placodal region or neural crest, which were derived from a zone of the ectoderm that borders the neural plate, or neural border³. For example, OSNs in the olfactory epithelium originate from cranial olfactory placode region developing from the neural plate border⁴, the DRG sensory neurons develop from neural crest, and the trigeminal ganglion is thought to differentiate either from neural crest and the trigeminal placodes^{5,6}. Importantly, the pre-placodal region and neural crest remain in close proximity to the neural plate and are subsequently coordinated throughout the development⁷. This common embryonic origin could provide one explanation for the distinct splicing program in the sensory neuron and ganglion neuron populations, as compared to CNS neurons, which derive from the neural plate. The rod and cone photoreceptors are derived from the optic vesicles that originate from the "outgrowth" of the developing brain and it interacts with the lens placode in close proximity, which could induce morphological and molecular changes in both tissues during retina development^{8,9}.



Supplementary Figure 1: Validation of developing cortex RNA-seq data and AS quantification. a, Pairwise correlation of gene expression in mouse cortices between different developmental stages. Duplicates were analyzed at each time point. b, Similar to (a), but pairwise correlation estimated from inclusion level of $\sim 16,000$ known cassette exons. c, *Mapt* exon 10 as an example of developmentally regulated exons. d, Semi-quantitative RT-PCR validation of splicing for *Mapt* exon 10 in the cortex and cerebellum. e, A summary of splicing quantification of 10 exons at different developmental stages using RT-PCR and RNA-seq.



Supplementary Figure 2: Robustness of the modular organization of developmentally regulated alternative exons in an independent dataset. a, Related to Fig. 1d in the main text, WGCNA initially identified five modules. Modules 4 and 5, together composed of 353 of 2,883 exons, both capture non-monotonic splicing changes with similar temporal patterns and were merged manually into a final module M4 presented in the paper. b, Comparison of splicing in an independent dataset derived from mouse frontal cortices at different developmental stages from E11 to adult. Exons are shown in the same order as in the right panel in (a). Exons in three of the four modules (M1, M2, and M4) show very similar developmental switches. Since P0 was not included in this second dataset, the reproducibility of the distinct splicing pattern of exons in module M3 could not be evaluated here (however, this module is reproducible in other datasets that include P0 or P1, see e.g., Fig. 2a in the main text). Note that the denser sampling of time points before P15 in our cortex RNA-seq dataset allows us to capture more dynamics.



Supplementary Figure 3: Functional enrichment of genes with splicing switches with specific timing. Related to Fig. 1e in the main text, exons were ranked based on the timing of splicing switches. Exons in each sliding window (with a window size of 300 exons) were compared to all casette exons with sufficient read coverage in the cortex to evaluate enrichment of genes with specific functional annotations (see Methods).



Supplementary Figure 4: The splicing profile of different cell types in the cortex. Related to Fig. 2 in the main text, splicing profiles of module exons are shown for different cell types isolated from the cortex. In each panel, exons are shown in the same order as in the cortex refence on the left. **a**, In the Zhang et al. dataset, oligodendrocyte progenitor cells (OPCs), newly formed oligodendrocyte (NFO) and myelinated oligodendrocytes (MO) were purified from P17 mice, while the remaining samples were purified from P7 mice. **b**, The Tasic et al. dataset are single-cell RNA-seq profiles from the primary visual cortex of adult mice. In this dataset, splicing profiles were quantified by pulling reads from cells that are core members of each cell type. Specific subtypes were ordered based on the broad categories (GABAergic interneurons, glutamatergic pyramidal neurons, and non-neuronal cell types).



Supplementary Figure 5: Different subpopulations of cells in germininal zones of embryonic cortex show different stages of maturation. a, Related to **Fig. 2b** in the main text, but samples from different germinal zones or different cell populations purified from embryonic cortex are labeled. VZ: ventricular zone; SVZ: subventricular zone; CP: cortical plate; aRG: apical radial glial cells; bRG: basal radial glial cells; bIP: basal intermediate progenitor cells; N: neurons. Note that while the correct stage (stage 1) was assigned to samples from the VZ or SVZ-IZ, which are enriched in progenitor cells, a more mature stage (stage 2) was assigned to CP samples enriched in post-mitotic neurons, which is consistent with the pattern of neuron migration and maturation during cortical development; similar classification inaccuracies were made for late-stage radial glial cells and neurons FACS-purified from the embryonic cortex. **b**, Splicing profiles of module exons are shown for samples labelled in panel (a).

UI3 (200 nt)

DI5 (200 nt)

#	word	fg	fg+bg	log2FC	pval	FDR	RBP
1	CTCTCT	104	2828	0.74	1.05E-06	4.29E-03	Ptbp
2	CCTTCT	74	1898	0.83	4.92E-06	1.01E-02	Ptbp
3	CCTTTC	72	1849	0.83	6.79E-06	9.28E-03	Ptbp
4	тстстс	93	2597	0.70	1.03E-05	1.05E-02	Ptbp
5	CCCTCT	66	1702	0.82	1 79E-05	1 47E-02	Pthp
6	TTCTCT	107	3103	0.60	3.62E-05	2.47E-02	Pthp
7	TOCOTO	60	1612	0.00	4.02E-05	2.47 -02	Dthp
		02	1013	0.01	4.02E-05	2.35E-02	Pibp
8	GICICI	59	1513	0.83	4.10E-05	2.10E-02	
9	ICICIG	83	2376	0.67	6.65E-05	3.03E-02	
10	GITTCI	71	1958	0.72	7.16E-05	2.93E-02	
11	CCTCCT	68	1858	0.74	7.66E-05	2.85E-02	
12	TTCCCT	74	2075	0.70	8.53E-05	2.91E-02	
13	TCCCCT	58	1528	0.79	9.62E-05	3.03E-02	
14	CCTCCC	69	1913	0.71	1.04E-04	3.05E-02	
15	TCCCTT	67	1880	0.70	1.80E-04	4.92E-02	
16	TGTCTC	64	1782	0.71	2.01E-04	5.15E-02	
17	CTTCCT	85	2553	0.60	2.55E-04	6.15E-02	
18	TCTCTT	90	2738	0.58	2.60E-04	5.93E-02	
19	CTCCCT	68	1958	0.66	3.27E-04	7.06E-02	
20	TOTGOO	54	1469	0.74	3 48E-04	7 13E-02	
20	101000	57	1405	0.14	5.402-04	7.102-02	
1	CGCAIG	12	170	2.38	7.91E-06	3.24E-02	Rbtox
2	CUTGCT	4/	1618	1.03	8.50E-06	1.74E-02	Mbnl
3	TOOGT	15	272	2.00	1.25E-05	1./1E-02	INIDNI
4	TCGCTG	15	278	1.97	1.62E-05	1.66E-02	Mbnl
5	CGCTGC	16	347	1.73	5./4E-05	4./1E-02	Mbnl
6	CCGCAT	9	128	2.37	1.08E-04	7.40E-02	
7	GCACGC	10	158	2.21	1.10E-04	6.45E-02	
8	ATTAAC	21	576	1.37	1.32E-04	6.74E-02	
9	CCCACC	37	1347	0.95	2.12E-04	9.65E-02	
10	CTGTGC	40	1537	0.87	3.55E-04	1.45E-01	
11	GIGIGI	51	2116	0.76	3.72E-04	1.39E-01	
12	TCCCGC	13	292	1.67	3.81E-04	1.30E-01	
13	TGTGTG	61	2716	0.65	6.41E-04	2.02E-01	
14	CCGCCT	12	273	1.65	7.03E-04	2.06E-01	
15	CCGCGG	8	135	2.11	8.09E-04	2.21E-01	
16	GTGCAT	22	714	1.12	8.94E-04	2.29E-01	
17	GCTCCC	25	881	1.00	1.32E-03	3.18E-01	
18	CTGCTG	44	1868	0.72	1.38E-03	3.13E-01	
19	TCCTAA	24	836	1.02	1.40E-03	3.01E-01	
20	CTGCTC	20	1604	0 77			
	010010	00	1004	0.77	1.43E-03	2.93E-01	
	010010	00	1004	0.77	1.43E-03	2.93E-01	
1	TTCTCT	145	3193	1.04	1.43E-03	4.55E-11	Ptbp
1	ттстст	145 132	3193 2828	1.04 1.09	1.43E-03 1.11E-14 2.34E-14	4.55E-11 4.79E-11	Ptbp Ptbp
1 2 3		145 132 128	3193 2828 2738	1.04 1.09 1.09	1.11E-14 2.34E-14 5.08E-14	4.55E-11 4.79E-11 6.94E-11	Ptbp Ptbp Ptbp
1 2 3 4	TTCTCT CTCTCT TCTCTT TCTCTC	145 132 128 120	3193 2828 2738 2597	1.04 1.09 1.09 1.07	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13	4.55E-11 4.79E-11 6.94E-11 6.57E-10	Ptbp Ptbp Ptbp Ptbp
1 2 3 4 5	TTCTCT CTCTCT TCTCTT TCTCTC TCTTTC	145 132 128 120 111	3193 2828 2738 2597 2534	1.04 1.09 1.09 1.07 0.99	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08	Ptbp Ptbp Ptbp Ptbp Ptbp
1 2 3 4 5 6	TTCTCT CTCTCT TCTCTT TCTCTC TCTTTC TTTCTC	145 132 128 120 111 122	3193 2828 2738 2597 2534 2882	1.04 1.09 1.09 1.07 0.99 0.94	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp
1 2 3 4 5 6 7	TTCTCT CTCTCT TCTCTT TCTCTC TCTTTC TTTCTC CTTTCT	145 132 128 120 111 122 128	3193 2828 2738 2597 2534 2882 3080	1.04 1.09 1.09 1.07 0.99 0.94 0.91	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp
1 2 3 4 5 6 7 8	TTCTCT CTCTCT TCTCTT TCTCTC TCTTC TTTCTC CTTTCT CTCTGC	145 132 128 120 111 122 128 84	3193 2828 2738 2597 2534 2882 3080 1845	1.04 1.09 1.09 1.07 0.99 0.94 0.91 1.05	1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp nSR100
1 2 3 4 5 6 7 8 9	TTCTCT CTCTCT TCTCTT TCTCTC TCTTTC TTTCTC CTTTCT CTCTGC TTTCCT	145 132 128 120 111 122 128 84 118	3193 2828 2738 2597 2534 2882 3080 1845 3034	1.04 1.09 1.09 1.07 0.99 0.94 0.91 1.05 0.81	1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06 1.01E-05	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp nSR100 Ptbp
1 2 3 4 5 6 7 8 9 10	TTCTCT CTCTCT TCTCTT TCTCTC TCTTTC TTTCTC CTCTGC TTTCCT TCTCCT	145 132 128 120 111 122 128 84 118 91	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171	1.04 1.09 1.09 1.07 0.99 0.94 0.91 1.05 0.81 0.92	1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 3.31E-08	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06 1.01E-05 1.36E-05	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp nSR100 Ptbp
1 2 3 4 5 6 7 8 9 10 11	TICICI CTCTCT TCTCTC TCTTCT TCTTCC TTTCT CTCTGC TTTCCT CTCCCT CTGCCT	145 132 128 120 111 122 128 84 118 91 83	3193 2828 2738 2534 2882 3080 1845 3034 2171 1950	1.04 1.09 1.09 1.07 0.99 0.94 0.91 1.05 0.81 0.92 0.95	1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 3.31E-08 6.77E-08	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.01E-05 1.36E-05 2.52E-05	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp nSR100 Ptbp Mbnl/nSR100
1 2 3 4 5 6 7 8 9 10 11 12	TTCTCT CTCTCT TCTCTT TCTCTC TTTTCTC CTTTCT CTCTGC TTTCCT CTGCCT TCCTTT	145 132 128 120 111 122 128 84 118 91 83 97	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408	1.04 1.09 1.09 1.07 0.99 0.94 0.91 1.05 0.81 0.92 0.95 0.86	1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 3.31E-08 6.77E-08 7.63E-08	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06 1.01E-05 1.36E-05 2.52E-05 2.60E-05	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp nSR100 Ptbp Mbnl/nSR100 Ptbp
1 2 3 4 5 6 7 8 9 10 11 12 13	TTCTCT CTCTT TCTCTT TCTCTC TCTTTC CTTTCC CTCTGC TTTCCT TCCTTT TCCTTT TCCTCT	145 132 128 120 111 122 128 84 118 91 83 97 81	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408 1894	1.04 1.09 1.09 1.07 0.99 0.94 0.91 1.05 0.81 0.92 0.95 0.86 0.95	1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.16E-10 3.07E-09 2.21E-08 3.31E-08 6.77E-08 7.63E-08 7.63E-08 7.94E-08	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06 1.01E-05 1.36E-05 2.52E-05 2.60E-05 2.50E-05	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp nSR100 Ptbp Mbnl/nSR100 Ptbp Ptbp
1 2 3 4 5 6 7 8 9 10 11 12 13 14	TICICI CTCTCT TCTCTT TCTCTC TCTTC CTCTCC CTTCCC TTCCCT TCCCT TCCCT TCCCT TCCCT TCCCT	145 132 128 120 111 122 128 84 118 91 83 97 81 107	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408 1894 2758	1.04 1.09 1.09 1.07 0.99 0.94 0.91 1.05 0.81 0.92 0.95 0.86 0.95 0.81	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 3.31E-08 7.94E-08 7.94E-08 1.07E-07	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06 1.01E-05 2.62E-05 2.62E-05 2.60E-05 2.50E-05	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp NSR100 Ptbp Mbnl/nSR100 Ptbp Ptbp
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	TTCTCT CTCTCT TCTCTC TCTTCC TCTTCC CTTTCT CTCTCC CTCTCC CTGCCT TCCTTT TTCCCT TCCCTT CTCCTT	145 132 128 120 111 122 128 84 118 91 83 97 81 107 94	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408 1894 2758 2372	1.04 1.09 1.09 1.07 0.94 0.91 1.05 0.81 0.92 0.95 0.86 0.95 0.81 0.84	1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 3.31E-08 6.77E-08 7.63E-08 7.63E-08 1.07E-07 2.43E-07	4.55E-111 4.79E-111 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06 1.01E-05 2.52E-05 2.50E-05 2.50E-05 3.14E-05 6.64E-05	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp NSR100 Ptbp Mbnl/nSR100 Ptbp Ptbp Ptbp Ptbp
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	TICICI CICICI TCTCTC TCTTC TCTTC CTTTC CTTCC CTTCC CTCCC CTCCCT TCCCTT TCCTC TCCCTT TCCCTT CTCCTTT CTGCCT	145 132 128 120 111 122 128 84 118 84 118 83 97 81 107 94 93	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408 1894 2758 2372 2356	1.04 1.09 1.09 1.07 0.99 0.94 0.91 1.05 0.81 0.95 0.86 0.95 0.86 0.95 0.81 0.95 0.86 0.95	1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 3.31E-08 7.63E-08 7.63E-08 7.94E-08 1.07E-07 2.43E-07 3.31E-07	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06 1.01E-05 1.36E-05 2.50E-05 2.50E-05 3.14E-05 6.64E-05	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp nSR100 Ptbp Mbnl/nSR100 Ptbp Ptbp Ptbp Ptbp Ptbp
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1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	TICICI CTCTCT TCTCTT TCTCTC CTTTCT CTTTCT CTTCCCT TCTCCT TCTCCT TCCTTT CTGCTT CTGTTT CCTGCT TCTGCT	145 132 128 120 111 122 128 84 118 91 83 97 81 107 94 93 77 76	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408 1894 2758 2372 2356 1849 1829	1.04 1.09 1.09 1.07 0.94 0.91 1.05 0.81 0.92 0.95 0.86 0.95 0.81 0.84 0.93 0.91 0.91	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 3.31E-08 6.77E-08 7.94E-08 7.94E-08 1.07E-07 2.43E-07 3.31E-07 4.47E-07 5.72E-07	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 1.57E-06 1.37E-06 1.36E-05 2.52E-05 2.52E-05 2.52E-05 2.52E-05 2.52E-05 3.14E-05 8.47E-05 1.08E-04 1.30E-04	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp NSR100 Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Mbnl/nSR100
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19	TICICI CTCTCT TCTCTC TCTTC TCTCTC CTTTCT CTCTCC TTTCCT CTGCCT TCCTCT CTGCTT CTGTCT CTGTCT CCTTTC TCTCCT	145 132 128 120 111 122 128 84 118 83 97 81 107 94 93 77 76 83	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408 1894 2758 2372 2356 1849 1829 2089	1.04 1.09 1.09 1.07 0.94 0.91 1.05 0.81 0.92 0.95 0.86 0.95 0.81 0.84 0.83 0.91 0.91 0.84	1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 7.63E-08 7.63E-08 7.63E-08 7.63E-08 7.63E-07 3.31E-07 4.47E-07 5.72E-07 1.05E-06	4.55E-111 4.79E-111 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06 1.01E-05 2.52E-05 2.50E-05 2.50E-05 3.14E-05 8.47E-05 1.08E-04 1.30E-04 1.30E-04	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp NSR100 Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	TICICT CTCTCT TCTCTC TCTTCT CTTTCT CTCTGC CTTCT CTCCCT CTGCCT TCCTTT CTGCTT CTGTCT CCTTTC TCTGCT TCCTCT TCCTCT TCCTCT	145 132 128 120 111 122 128 84 118 83 91 83 97 81 107 94 93 77 76 83 69	3193 2828 2738 2597 2534 2882 3080 1845 3034 2408 1894 2408 1894 2758 2372 2356 1849 1829 2089 1662	1.04 1.09 1.09 1.07 0.99 0.94 0.91 1.05 0.81 0.92 0.95 0.86 0.95 0.86 0.95 0.86 0.95 0.81 0.84 0.91	1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.03E-10 3.07E-09 2.21E-08 3.31E-08 6.77E-08 7.63E-08 7.63E-08 7.63E-08 7.94E-08 1.07E-07 5.72E-07 5.72E-07 5.72E-06 1.87E-06	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.700E-08 1.57E-06 1.01E-05 2.60E-05 2.60E-05 2.60E-05 2.60E-05 3.14E-05 6.64E-05 8.47E-05 1.08E-04 1.30E-04 2.27E-04	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp nSR100 Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp
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$\begin{array}{c} 1\\ 2\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ \end{array}$	TICICT CTCTCT TCTCT TCTCT CTCTC CTTTCT CTCTGC TTTCT CTCTGCT TCCCT TCCTT TCCTT CTGCT CCCTT CTGCT CCCTT CCTTT CTGTT CCTTT TCCTC TCTGCT TCTGT TCCTCT TCTGT TCCCT TTTGT TCCATCA TTTGTT TCCATCA TTTGCTT TCCATCA	145 132 128 120 111 122 128 84 118 91 83 97 81 107 94 93 77 76 83 97 81 107 94 93 77 76 83 83 28 83 28 83 28 78 134 24 65 25 50 76 43 24 45 27 20 20 20 20 20 20 20 20 20 20 20 20 20	3193 2828 2738 2597 2534 2828 3080 1845 3034 2171 1950 2408 1894 2758 2372 2356 1849 1829 2089 1662 3489 704 3839 7685 720 3212 852 2345 4148 2020 909 2196 1118	1.04 1.09 1.09 1.07 0.94 0.91 1.05 0.81 0.92 0.95 0.86 0.95 0.86 0.95 0.81 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.91 0.84 0.91 1.08 1.84 0.83 0.91 0.91 0.84 0.91 1.08 1.84 0.91 0.91 0.84 0.91 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.83 0.84 0.91 0.84 0.83 0.84 0.91 0.84 0.83 0.84 0.91 0.84 0.84 0.92 0.95 0.86 0.91 0.84 0.91 0.84 0.92 0.95 0.86 0.91 0.84 0.91 0.84 0.92 0.95 0.86 0.91 0.84 0.91 0.84 0.91 0.84 0.92 0.95 0.86 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.92 0.86 0.95 0.86 0.95 0.86 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.92 0.86 0.92 0.86 0.91 0.84 0.91 0.84 0.91 0.84 0.83 0.84 0.83 0.84 0.83 0.84 0.84 0.83 0.84 0.84 0.84 0.84 0.84 0.84 0.84 0.84	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 7.94E-08 7.94E-08 7.94E-08 7.94E-08 7.94E-08 7.94E-07 3.31E-07 4.47E-07 3.31E-07 4.47E-07 5.72E-07 1.05E-06 1.87E-06 1.87E-06 1.28E-05 2.60E-05 2.60E-05 2.60E-05 2.60E-05 1.66E-04 1.82E-04 1.82E-04 3.08E-	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.700E-08 6.76E-08 1.57E-06 1.01E-05 1.36E-05 2.52E-05 2.52E-05 2.50E-05 2.50E-05 2.50E-05 3.14E-05 6.64E-05 8.47E-05 1.30E-04 4.383E-04 4.56E-06 4.383E-04 4.56E-03 3.92E-03	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp NSR100 Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp
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$\begin{array}{c} 1\\ 2\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 2\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 5\\ 10\\ 10\\ 10\\ 10\\ 10\\ 10\\ 10\\ 10\\ 10\\ 10$		145 132 128 120 121 128 120 121 122 128 111 122 128 91 83 97 81 107 94 93 77 76 83 69 83 84 134 24 25 50 76 43 24 45 27 23 18	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408 2872 2356 1894 2758 2372 2356 1849 2689 1662 3489 704 3839 704 3839 704 3839 704 3839 704 3839 704 3839 704 3835 720 3212 852 2345 4148 2020 909 2196 1118 888 615	1.04 1.09 1.09 1.09 1.09 0.94 0.91 1.05 0.81 0.82 0.95 0.86 0.95 0.86 0.95 0.86 0.95 0.81 0.84 0.91 0.84 0.91 1.08 1.84 0.85 0.62 1.58 0.84 1.39 0.92 0.91 1.23 0.84 0.91 1.23 0.84 1.23 0.85 1.20	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.03E-10 1.03E-10 3.07E-09 2.21E-08 3.31E-08 6.77E-08 7.63E-08 7.63E-08 7.63E-08 7.63E-08 7.63E-07 3.31E-07 4.47E-07 5.72E-07 1.05E-06 1.87E-06 1.28E-05 3.32E-04 3.36E-04 3.08E-	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06 1.01E-05 1.36E-05 2.50E-05 2.50E-05 2.50E-05 2.50E-05 3.14E-05 8.47E-05 1.08E-04 4.36E-06 4.83E-05 2.27E-04 4.36E-06 4.83E-05 2.26E-03 2.27E-04 4.56E-06 4.83E-05 2.26E-03 3.871E-03 3.871E-03 3.82E-02 1.70E-02 3.03E-02 4.74E-02 6.78E-02 6.78E-02 9.70E-02 9.34E-02 9.34E-02 9.34E-02 9.34E-02 9.34E-02	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp NSR100 Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp
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$\begin{array}{c} 1\\ 2\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ \end{array}$	TICICT CTCTCT TCTCT CTCTTC TTTCTC CTCTGC TTTCT CTCTGCT TCTCCT TCCCT TCCCT TCCTT TCCCT TCCTT TCCTT CTGCT CCGTT CCTTTC TCTGCT TCCCT TCTGCT TCCCT TCTGCT TCCCCT TCCCT	145 132 128 120 121 122 128 84 118 91 83 97 81 107 94 93 77 76 83 28 78 134 24 65 25 50 76 43 24 45 27 23 18 20 28	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408 1894 2758 2372 2356 1849 1829 2089 1662 3489 704 3839 7685 720 3212 852 2345 4148 2020 909 2196 1118 888 615 728 1202	1.04 1.09 1.09 1.07 0.99 0.94 0.91 1.05 0.81 0.92 0.95 0.86 0.95 0.86 0.95 0.81 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 1.08 1.84 0.91 1.08 1.84 0.91 1.08 1.84 0.91 1.08 1.84 0.91 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.91 0.84 0.92 0.85 0.86 0.95 0.86 0.91 0.84 0.91 0.84 0.91 0.84 0.92 0.85 0.84 0.91 0.84 0.92 0.85 0.84 0.91 0.84 0.92 0.84 0.91 0.84 0.91 0.84 0.92 0.84 0.91 0.84 0.91 0.84 0.92 0.84 0.92 0.84 0.91 0.84 0.92 0.84 0.92 0.85 0.84 0.91 0.84 0.92 0.85 0.84 0.92 0.85 0.84 0.92 0.92 0.92 0.85 0.84 0.92 0.92 0.92 0.92 0.92 0.92 0.92 0.92	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 3.07E-09 2.21E-08 7.94E-08 7.94E-08 7.94E-08 7.94E-08 7.94E-08 7.94E-08 7.94E-08 7.94E-08 7.94E-07 3.31E-07 4.47E-07 3.31E-07 4.47E-07 5.72E-07 1.05E-06 1.87E-06 1.28E-05 2.60E-05 2.32E-05 6.66E-05 1.16E-04 1.82E-04 3.36E-	4.55E-111 4.79E-111 6.94E-111 6.97E-10 8.26E-08 7.700E-08 6.76E-08 1.57E-06 1.01E-05 2.52E-05 2.52E-05 2.50E-05 2.50E-05 2.50E-05 2.50E-05 3.14E-05 6.64E-05 8.47E-05 1.03E-04 4.227E-04 3.34E-05 2.26E-03 2.27E-04 3.392E-03 3.92E-03 3.92E-03 3.92E-03 3.92E-02 3.03E-02 9.34E-02	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp NSR100 Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Mbnl/nSR100 Ptbp Ptbp Ptbp Elavl Nova Elavl Nova Elavl Nova Elavl Nova Elavl Nova
$\begin{array}{c} 1\\ 2\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 13\\ 14\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 2\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 6\\ 17\\ 18\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 6\\ 17\\ 18\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 18\\ 19\\ 20\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 19\\ 20\\ 10\\ 10\\ 10\\ 10\\ 10\\ 10\\ 10\\ 10\\ 10\\ 1$	TICICT CTCTCT TCTCTT CTCTC CTCTTC CTCTCC CTTCCT CTCCCT CTCCCT CTCCCT CTCCCT CTCCCT CTCCCT CTCCTT CTCTTC CTCTTC CTCTCT CCTTTC TCCCTT CCTTC TCCCT TCCCT TCCCT TCCCT TCCCT TCCCCT TCCCCT TCCCT TCCCCCT TCCCCCT TCCCCCT TCCCCCC	145 132 128 120 111 122 128 84 91 83 97 81 107 94 93 77 76 83 28 78 134 25 50 76 45 27 23 18 20 28 42	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408 1894 2758 2372 2356 1849 1829 2089 1662 3489 704 3839 704 3839 704 3839 704 3839 704 3839 704 3839 704 3839 704 3822 2345 4148 2020 909 2196 1118 888 615 728 1202 2096	1.04 1.09 1.09 1.09 1.07 0.99 0.94 0.91 1.05 0.81 0.92 0.95 0.86 0.95 0.81 0.84 0.91 0.91 0.84 0.91 0.91 0.91 0.84 0.91 1.08 1.84 0.91 0.91 0.91 0.91 0.84 0.91 0.91 0.92 0.86 0.95 0.81 0.91 0.84 0.91 0.91 0.92 0.86 0.95 0.81 0.91 0.84 0.91 0.91 0.84 0.91 0.91 0.84 0.91 0.91 0.84 0.91 0.84 0.91 0.91 0.84 0.92 0.86 0.95 0.84 0.91 0.84 0.91 0.84 0.92 0.86 0.91 0.84 0.92 0.86 0.91 0.84 0.91 0.84 0.85 0.84 0.92 0.86 0.92 0.84 0.91 0.84 0.85 0.84 0.92 0.69 0.91 0.86 0.92 0.86 0.91 0.86 0.91 0.86 0.91 0.86 0.85 0.86 0.91 0.86 0.85 0.86 0.91 0.86 0.85 0.86 0.86 0.85 0.86 0.86 0.85 0.86 0.85 0.86 0.86 0.85 0.86 0.86 0.85 0.86 0.85 0.86 0.86 0.85 0.86 0.85 0.86 0.85 0.86 0.85 0.86 0.85 0.86 0.85 0.86 0.85 0.86 0.85 0.86 0.85 0	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 7.64E-08 7.64E-08 7.64E-08 7.64E-08 7.64E-08 7.64E-08 7.94E-08 7.64E-08 7.94E-08 7.94E-08 7.94E-08 7.94E-08 1.07E-07 2.43E-07 3.31E-07 4.47E-07 1.05E-06 1.87E-06 1.28E-05 3.32E-04 3.66E-04 4.66E-04 4.66E-04 4.66E-04 4.66E-04 4.66E-04 4.66E-04 4.66E-04 4.66E-04 4.66E-04 4.66E-04 4.66E-04 4.66E-05 5.66E-	4.55E-111 4.79E-111 6.94E-111 6.7E-10 8.26E-08 7.700E-08 6.76E-08 1.57E-06 1.01E-05 2.52E-05 2.52E-05 2.50E-05 3.14E-05 8.47E-05 1.08E-06 4.83E-05 2.27E-04 3.83E-04 4.56E-06 4.83E-05 2.27E-04 3.83E-04 4.56E-03 3.17E-03 3.87E-03	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp NSR100 Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Mbnl/nSR100 Ptbp Ptbp Ptbp Elavl Nova Elavl Nova Elavl Nova Elavl Nova Elavl Nova
$\begin{array}{c} 1\\ 2\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 12\\ 13\\ 14\\ 15\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 2\\ 3\\ 4\\ 5\\ 6\\ 7\\ 8\\ 9\\ 10\\ 11\\ 2\\ 13\\ 14\\ 15\\ 16\\ 17\\ 18\\ 9\\ 20\\ \end{array}$		145 132 128 120 121 128 120 121 122 128 111 122 128 91 83 97 83 69 83 134 24 65 25 50 76 43 24 45 27 23 18 20 28 42 36 36	3193 2828 2738 2597 2534 2882 3080 1845 3034 2171 1950 2408 1894 2758 2372 2356 1849 1829 2089 1662 3489 704 3839 7685 720 3212 852 2345 4148 2020 909 2196 1118 888 615 728 1202 2096 11714	1.04 1.09 1.09 1.09 1.09 1.09 0.94 0.91 1.05 0.81 0.82 0.95 0.86 0.95 0.86 0.95 0.86 0.95 0.81 0.84 0.91 1.08 1.09 1.08 1.08 1.23 0.89 1.23 0.83 0.91 1.23 0.83 0.95 1.05 0.83 0.95 1.05 0.83 0.95 1.05 0.83 0.95 1.05 0.83 0.95 1.05 0.83 0.95 1.05 0.83 0.95 1.05 0.83 0.95 0.83 0.95 0.95 0.83 0.95 0.83 0.95 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.83 0.95 0.95 0.95 0.95 0.83 0.95 0	1.43E-03 1.11E-14 2.34E-14 5.08E-14 6.41E-13 1.01E-10 1.03E-10 1.03E-10 1.16E-10 3.07E-09 2.21E-08 7.63E-08 7.63E-08 7.63E-08 7.63E-08 7.63E-08 7.63E-07 3.31E-07 4.47E-07 5.72E-07 5.72E-07 1.05E-06 1.87E-06 1.28E-05 2.60E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-05 3.32E-04 3.66E-04 1.82E-04 3.65E-	4.55E-11 4.79E-11 6.94E-11 6.57E-10 8.26E-08 7.00E-08 6.76E-08 1.57E-06 1.01E-05 2.50E-05 2.50E-05 2.50E-05 2.50E-05 2.50E-05 3.14E-05 8.47E-05 1.08E-04 4.36E-06 4.83E-05 2.27E-04 4.56E-06 4.83E-05 2.26E-03 2.27E-04 4.56E-06 4.83E-05 2.26E-03 3.82E-03 3.82E-03 3.82E-03 3.82E-03 3.82E-03 3.82E-03 3.82E-03 3.82E-02 3.82E-02 4.15E-02 9.34E-02 9.3	Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp NSR100 Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp Ptbp

. #	word	fg	fg+bg	log2FC	pval	FDR	RBP
1	TGCATG	80	1395	1.34	8.41E-13	3.45E-09	Rbfox
2	GTGTGC	67	1182	1.33	8.99E-11	1.84E-07	Celf/nSR100
3	GCATGC	52	826	1 4 9	3 05E-10	4 16E-07	Rhfox
4	GTGCTT	65	1201	1.26	1 06E-09	1.09E-06	Mbnl
5	TGTGCT	8/	17/1	1.08	1 14E-00	0.38E-07	Mbnl
6	CCTGCC	77	1612	1.00	9.21E.00	5.61E.06	Mbnl
7	TOOTTO	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	1012	1.07	0.21E-09	0.01E-00	Man
/	IGUIIC	68	1364	1.13	1.16E-08	6.79E-06	INDNI
8	CIGGCI	74	1538	1.08	1.18E-08	6.02E-06	
9	GCTTCT	69	1420	1.09	2.44E-08	1.11E-05	
10	TGCTTG	65	1322	1.11	3.95E-08	1.62E-05	Mbnl
11	CCCCCC	57	1103	1.19	5.08E-08	1.89E-05	
12	TGGCTG	73	1585	1.01	8.05E-08	2.75E-05	
13	TGCTGC	66	1396	1.05	1.29E-07	4.06E-05	Mbnl
14	CTGCCT	82	1923	0.89	3.23E-07	9.45E-05	Mbnl
15	GCTTGC	45	834	1.25	3.74E-07	1.02E-04	
16	CTGCTT	74	1684	0.94	3.90E-07	9.97E-05	Mbnl
17	CCATCC	46	916	1.14	1.95E-06	4.71E-04	Nova
18	TGCCTG	70	1639	0.90	2 08E-06	4 74F-04	Mbnl
19	GCATGG	45	905	1 13	3 23E-06	6 95E-04	Rhfox
20	TGTGTG	107	2869	0.69	3 30E-06	6 75E-04	Celf/nSR100
20	101010	107	2005	0.00	0.00E-00	0.702-04	001/11011100
1		37	1103	1.28	2.29E-06	9.39E-03	
2	CAICGT	11	171	2.26	3.75E-05	7.68E-02	
3	ACAGGT	23	655	1.34	0.73E-05	1.19E-01	
4	ACCCCT	25	775	1.22	1.65E-04	1.69E-01	
5	IGATIG	24	/60	1.19	2.98E-04	2.44E-01	
6	CATGTT	28	979	1.04	4.82E-04	3.29E-01	
7	GCTTGC	25	834	1.11	4.83E-04	2.83E-01	
8	TCATCG	8	132	2.17	6.23E-04	3.19E-01	
9	IGITIG	46	1933	0.77	6.26E-04	2.85E-01	
10	CICGCT	11	243	1.73	7.88E-04	3.23E-01	
11	IGIGIC	36	1434	0.84	9.24E-04	3.44E-01	
12	CGGTCG	4	31	3.37	9.27E-04	3.16E-01	
13	GCATCG	(110	2.24	1.01E-03	3.18E-01	
14	AGACGC	8	144	2.04	1.10E-03	3.21E-01	
15	CACCCC	28	1037	0.95	1.14E-03	3.11E-01	
16	GICIGI	36	1452	0.83	1.14E-03	2.93E-01	
17	CGCTCA	9	185	1.83	1.40E-03	3.37E-01	
18	CICAII	27	1012	0.93	1.63E-03	3.70E-01	
19	CIGCAC	22	767	1.04	1.75E-03	3.77E-01	
20	TIACIG	25	919	0.96	1.83E-03	3.74E-01	
1	TGCATG	88	1395	1.53	6.62E-17	2.71E-13	Rbfox
1 2	TGCATG GCATGC	88 51	1395 826	1.53 1.50	6.62E-17 3.69E-10	2.71E-13 7.55E-07	Rbfox Rbfox
1 2 3	TGCATG GCATGC GCATGT	88 51 47	1395 826 945	1.53 1.50 1.17	6.62E-17 3.69E-10 1.00E-06	2.71E-13 7.55E-07 1.37E-03	Rbfox Rbfox Rbfox
1 2 3 4	TGCATG GCATGC GCATGT TGCTCC	88 51 47 48	1395 826 945 1017	1.53 1.50 1.17 1.09	6.62E-17 3.69E-10 1.00E-06 3.21E-06	2.71E-13 7.55E-07 1.37E-03 3.29E-03	Rbfox Rbfox Rbfox Mbnl
1 2 3 4 5	TGCATG GCATGC GCATGT TGCTCC TCCATC	88 51 47 48 41	1395 826 945 1017 819	1.53 1.50 1.17 1.09 1.18	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03	Rbfox Rbfox Rbfox Mbnl Nova
1 2 3 4 5 6	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC	88 51 47 48 41 60	1395 826 945 1017 819 1396	1.53 1.50 1.17 1.09 1.18 0.94	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03	Rbfox Rbfox Rbfox Mbnl Nova
1 2 3 4 5 6 7	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT	88 51 47 48 41 60 46	1395 826 945 1017 819 1396 987	1.53 1.50 1.17 1.09 1.18 0.94 1.07	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03	Rbfox Rbfox Rbfox Mbnl Nova Nova
1 2 3 4 5 6 7 8	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA	88 51 47 48 41 60 46 34	1395 826 945 1017 819 1396 987 662	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC	88 51 47 48 41 60 46 34 39	1395 826 945 1017 819 1396 987 662 829	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10	TGCATG GCATGC GCATGT TGCTCC TGCTGC CTCCAT GCATGA CATGGC GCTCCT	88 51 47 48 41 60 46 34 39 48	1395 826 945 1017 819 1396 987 662 829 1115	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02 1.37E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10 11	TGCATG GCATGC GCATGT TGCTCC TCCATC TCCATC CTCCAT GCATGA CATGGC GCTCCT CCTGTT	88 51 47 48 41 60 46 34 39 48 48	1395 826 945 1017 819 1396 987 662 829 1115 1145	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 6.32E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02 1.37E-02 2.35E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10 11 12	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTCCC	88 51 47 48 41 60 46 34 39 48 48 61	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 6.32E-05 7.59E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02 1.37E-02 2.35E-02 2.59E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10 11 12 13	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTCCC CCCACC	88 51 47 48 41 60 46 34 39 48 48 61 50	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.87	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 6.32E-05 7.59E-05 7.84E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02 1.37E-02 2.35E-02 2.59E-02 2.47E-02	Rbfox Rbfox Mbnl Nova Rbfox Rbfox
1 2 3 4 5 6 7 8 9 10 11 12 13 14	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTCCC CCCACC CTGCTT	88 51 47 48 41 60 46 34 39 48 48 61 50 64	1395 826 945 1017 819 1396 987 662 829 1115 1580 1220 1684	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.87 0.76	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.10E-06 4.10E-06 0.97E-06 1.50E-05 2.68E-05 3.34E-05 6.32E-05 7.59E-05 7.84E-05 8.04E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02 1.37E-02 2.35E-02 2.47E-02 2.35E-02 2.35E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	TGCATG GCATGC GCATGT TGCTCC TCCATC TCCATC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTCCC CCCACC CTGCTT CATGCC	88 51 47 48 41 60 46 34 39 48 48 61 50 64 34	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.87 0.76 1.08	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 6.32E-05 7.84E-05 8.04E-05 8.68E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02 1.37E-02 2.35E-02 2.47E-02 2.35E-02 2.37E-02 2.37E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTCCC CTGCTT CATGCC CTTGTC	88 51 47 48 41 60 46 34 39 48 48 61 50 64 34 41	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.76 1.08 0.96	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 3.34E-05 6.32E-05 7.59E-05 7.59E-05 8.04E-05 8.68E-05 9.38E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 3.280E-03 4.08E-03 7.66E-03 1.22E-02 1.37E-02 2.35E-02 2.45E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.37E-02 2.37E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTGCT CATGCC CTGCTC CTGCT CTGCC	88 51 47 48 41 60 46 34 39 48 48 61 50 64 34 41 41	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.87 0.76 1.08 0.96 0.96 0.92	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.10E-06 6.97E-06 1.50E-05 3.34E-05 3.34E-05 7.59E-05 7.59E-05 7.84E-05 8.68E-05 9.38E-05 9.38E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02 1.37E-02 2.35E-02 2.35E-02 2.35E-02 2.37E-02 2.37E-02 2.37E-02 2.37E-02 2.37E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	TGCATG GCATGT GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTCCC CCCACC CTGCTT CATGCC CTGCTT CTGCAT TGCACG	88 51 47 48 41 60 46 34 39 48 48 61 50 64 34 41 44 14	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.76 1.08 0.87 0.76 1.08 0.92 1.82	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 1.50E-05 3.34E-05 6.32E-05 7.59E-05 7.59E-05 7.84E-05 8.04E-05 8.68E-05 9.67E-05 9.67E-05	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 4.08E-03 7.66E-03 1.22E-02 2.35E-02 2.59E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTGCT CCCACC CTGCTT CATGCC CTGCAT TGCACG GTGCAT	88 51 47 48 41 60 46 34 48 48 48 61 50 64 34 41 41 41 37	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.76 1.08 0.92 1.82 1.01	6.62E-17 3.69E-10 1.00E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 6.32E-05 7.84E-05 8.04E-05 8.04E-05 9.68E-05 9.68E-05 9.68E-05 1.13E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 3.280E-03 4.08E-03 1.22E-02 2.59E-02 2.35E-02 2.35E-02 2.47E-02 2.47E-02 2.47E-02 2.42E-02 2.33E-02 2.33E-02 2.20E-02 2.45E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTGCT CCCACC CTGCTT CATGCC CTGCAT TGCACG GTGCAT TTCTGC	88 51 47 48 41 60 46 34 48 48 48 61 50 64 34 41 41 41 37 49	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826 1207	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.76 1.08 0.96 0.92 1.82 1.01 0.86	6.62E-17 3.69E-10 1.00E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 6.32E-05 7.59E-05 7.84E-05 8.04E-05 9.38E-05 9.68E-05 9.68E-05 9.68E-05 1.13E-04 1.14E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 4.08E-03 4.08E-03 1.22E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.37E-02 2.37E-02 2.37E-02 2.37E-02 2.33E-02 2.20E-02 2.20E-02 2.245E-02 2.34E-02	Rbfox Rbfox Mbnl Nova Nova Rbfox
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTCCC CTGCTT CATGCC CTGCTT CATGCC CTGCAT TGCACG GTGCAT TTCTGC	88 51 47 48 41 60 46 34 48 61 50 64 34 41 44 41 44 14 37 49	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826 1207	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.76 0.76 0.92 1.82 0.92 1.01 0.86	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 8.04E-05 8.68E-05 9.38E-05 9.38E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 1.13E-04 1.14E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28DE-03 4.08E-03 7.66E-03 1.22E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.45E-02 2.45E-02 2.45E-02	Rbfox Rbfox Mbni Nova Nova Rbfox Nova
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 7 18 19 20	TGCATG GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTGCT CTGCTT CTGCC CTGCTT CTGCAT TGCACG GTGCAT TGCACG	88 51 47 48 41 60 46 34 39 48 48 48 61 50 64 34 41 44 14 37 49	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826 1207 511 530	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.87 0.76 1.08 0.92 1.82 1.01 0.82 1.02 1.82 1.01 0.86	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 1.50E-05 2.68E-05 3.34E-05 8.04E-05 8.04E-05 9.38E-05 9.67E-05 9.68E-05 1.13E-04 1.14E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 4.08E-03 7.66E-03 1.22E-02 1.37E-02 2.35E-02 2.47E-02 2.35E-02 2.47E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.34E-02 1.74E-01 4.23E-01	Rbfox Rbfox Mbnl Nova Rbfox Nova
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 1 2 3	TGCATG GCATGT GCATGC TGCTCC TCCATC TGCTGC CTCCAT GCATGA GCATGAC GCTCCT CCTGCT CCTGCT CCTGCT CTGCC CTGCTT CATGCC CTGCAT TGCACG GTGCAT TTCTGC ACATCC GAGCGT	88 51 47 48 41 60 46 34 39 48 48 61 50 64 34 41 44 14 37 49 18 17 8	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826 1207 511 530 141	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.76 1.08 0.95 0.91 0.76 1.08 0.92 1.82 1.01 0.86 1.64 1.64	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 3.34E-05 8.32E-05 7.59E-05 9.38E-05 9.38E-05 9.67E-05 9.68E-05 1.13E-04 1.14E-04 4.24E-05 2.66E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02 2.35E-02 2.35E-02 2.47E-02 2.35E-02 2.35E-02 2.34E-02 2.34E-02 2.34E-02 1.72E-01 4.23E-01 4.23E-01	Rbfox Rbfox Mbnl Nova Rbfox Nova
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 1 2 3 4	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTGCT CCCACC CTGCTT CATGCC CTGCAT TGCACG GTGCAT TCCGC	88 51 47 48 41 60 46 34 39 48 48 61 50 64 34 41 41 37 49 18 17 8 18	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826 1207 511 530 141 619	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.76 1.08 0.92 1.82 1.01 0.86 1.64 1.53	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 8.04E-05 8.04E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 1.13E-04 1.14E-04 4.24E-05 2.66E-04 2.64E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 3.280E-03 4.08E-03 7.66E-03 1.22E-02 2.35E-02 2.35E-02 2.35E-02 2.47E-02 2.35E-02 2.47E-02 2.32E-02 2.32E-02 2.34E-02 2.34E-02 1.74E-01 4.23E-01 3.61E-01	Rbfox Rbfox Mbnl Nova Nova Rbfox Nova
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 7 18 19 20 1 2 3 4 5	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTGCT CCCACC CTGCTT CATGCC CTGCAT TGCACG GTGCAT TTCTGC	88 51 47 48 41 60 46 34 48 48 61 50 64 34 41 41 41 37 49 18 17 8 8 18 9	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826 1207 511 530 141 619 195	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.96 0.92 1.82 1.01 0.86 1.50 2.36 1.35 2.04	6.62E-17 3.69E-10 1.00E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 6.32E-05 7.59E-05 7.84E-05 8.04E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 1.13E-04 4.24E-05 2.06E-04 2.64E-04 4.40E-04 4.40E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 3.280E-03 4.08E-03 7.66E-03 1.22E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.37E-02 2.35E-02 2.37E-02 2.35E-02 2.37E-02 2.35E-02 3.55E-02 3.	Rbfox Rbfox Mbnl Nova Rbfox Nova
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	TGCATG GCATGT GCATGC TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGCT CCTGCT CCTGCT CCTGCT CTGCAT TGCACG GTGCAT TGCACG GTGCAT TGCACG GTGCAT TCCGC	88 51 47 48 41 60 46 34 39 48 48 41 50 64 34 50 64 34 14 44 14 14 17 8 18 17 8 9 6	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826 1207 511 530 141 619 195 88	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.95 0.95 0.95 0.95 0.95 0.95 0.95 0.95	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 1.50E-05 2.68E-05 3.34E-05 8.04E-05 8.04E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 1.13E-04 4.24E-05 2.06E-04 2.64E-04 4.40E-04 5.85E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 3.28E-03 4.08E-03 7.66E-03 1.22E-02 1.37E-02 2.35E-02 2.47E-02 2.35E-02 2.47E-02 2.35E-02 2.47E-02 2.35E-02 2.40E-02 2.40E-02 2.43E-02 1.74E-01 4.23E-01 3.61E-01 4.20E-01 3.99E-01	Rbfox Rbfox Mbnl Nova Rbfox Nova
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 6 7 8 9 10 11 2 3 4 5 6 7 7	TGCATG GCATGT GCATGC TGCTCC TCCATC TGCTGC CTCCAT GCATGA GCATGA GCATGGC GCTCCT CCTGCT CCTGCT CCTGCT CTGCC CTGCTT CATGCC CTGCAT TGCACG GTGCAT TTCTGC ACATCC GAGCGT ACCATC TCCAGA TTCCAGA	88 51 47 48 41 60 46 34 39 48 48 61 50 64 34 41 44 14 37 49 18 18 17 8 18 9 6 22	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826 1207 511 511 530 141 619 195 88 88	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.76 1.08 0.95 0.91 0.76 1.08 0.92 1.82 1.01 0.86 1.64 1.64 1.55 2.04 2.36 1.35 2.04 2.64 1.17	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 3.34E-05 3.34E-05 8.04E-05 8.04E-05 9.38E-05 9.38E-05 9.67E-05 9.68E-05 1.13E-04 1.14E-04 4.24E-05 2.06E-04 4.40E-04 5.85E-04 5.85E-04 6.03E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02 2.35E-02 2.35E-02 2.35E-02 2.37E-02 2.35E-02 2.35E-02 2.35E-02 2.35E-02 2.34E-02 2.34E-02 1.74E-01 4.23E-01 4.50E-01 4.50E-01 3.53E-01	Rbfox Rbfox Mbnl Nova Rbfox Nova
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 6 7 8 9 10 11 2 3 4 5 6 7 8	TGCATG GCATGC GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGTT CCTGCT CCCACC CTGCTT CATGCC CTGCAT TGCACG GTGCAT TCCGC ACATCC GAGCGT ACCATT TCCGAG ACCGAA TTAGAG	88 51 47 48 41 60 46 34 39 48 48 61 50 64 34 41 41 37 49 18 17 8 18 17 8 18 9 6 22 20	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826 1207 511 530 141 619 195 88 858 760	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.76 1.08 0.95 0.91 0.76 1.08 0.92 1.82 1.01 0.86 1.64 1.50 2.04 2.64 1.20 2.64 1.20	6.62E-17 3.69E-10 1.00E-06 3.21E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 6.32E-05 7.84E-05 8.04E-05 8.68E-05 9.67E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 1.13E-04 2.64E-04 2.64E-04 2.64E-04 5.85E-04 6.03E-04 6.03E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.28E-03 2.80E-03 4.08E-03 7.66E-03 1.22E-02 2.35E-02 2.35E-02 2.35E-02 2.47E-02 2.35E-02 2.47E-02 2.37E-02 2.32E-02 2.32E-02 2.34E-02 2.34E-02 1.74E-01 4.23E-01 3.61E-01 4.50E-01 3.53E-01 3.63E-01	Rbfox Rbfox Mbnl Nova Nova Rbfox Nova
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 9 20 1 2 3 4 5 6 7 8 9 9	TGCATG GCATGT GCATGT TGCTCC TCCATC TGCTGC CTCCAT GCATGA CATGGC GCTCCT CCTGCT CCTGCT CCTGCT CTGCTC CTGCTT CATGCC CTGCTT CATGCC CTGCAT TGCACG GTGCAT TCCGCAT ACCATC ACCATC	88 51 47 48 41 60 46 34 39 48 48 61 50 64 41 44 14 44 14 14 17 8 18 17 8 18 17 8 18 17 8 18 17 8 18 17 8 17 8 17 8 17 17 18 17 17 18 17 17 18 17 18 17 18 19 19 19 19 19 19 19 19 19 19 19 19 19	1395 826 945 1017 819 1396 987 662 829 1115 1145 1580 1220 1684 724 942 1038 184 826 1207 511 530 141 619 195 88 858 760 492	1.53 1.50 1.17 1.09 1.18 0.94 1.07 1.21 1.08 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.95 0.91 0.78 0.96 0.92 1.08 0.95 0.91 0.78 0.95 0.91 0.78 0.96 0.92 1.08 0.95 0.91 0.78 0.96 0.92 1.08 0.95 0.91 0.78 0.96 0.92 1.08 0.95 0.91 0.78 0.96 0.92 1.08 0.95 0.91 0.78 0.96 0.92 1.08 0.95 0.91 0.76 1.08 0.95 0.92 1.02 1.08 0.95 0.92 1.08 0.95 0.92 1.08 0.95 0.92 1.08 0.95 0.92 1.08 0.95 0.92 1.08 0.96 0.92 1.08 0.96 0.92 1.08 0.96 0.92 1.08 0.96 0.92 1.08 0.96 0.92 1.01 0.86 1.01 0.86 1.01 0.86 1.01 0.86 1.01 0.86 1.02 1.01 0.86 1.02 1.01 0.26 1.02 1.01 0.86 1.02 1.02 1.02 1.02 1.02 1.02 1.02 1.02	6.62E-17 3.69E-10 1.00E-06 4.00E-06 4.10E-06 6.97E-06 1.50E-05 2.68E-05 3.34E-05 6.32E-05 7.59E-05 7.84E-05 8.04E-05 8.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 9.68E-05 1.13E-04 1.14E-04 4.24E-05 2.06E-04 2.64E-04 4.40E-04 4.40E-04 4.40E-04 7.58E-04 6.03E-04 7.90E-04 7.90E-04	2.71E-13 7.55E-07 1.37E-03 3.29E-03 3.29E-03 3.28E-03 7.66E-03 7.66E-03 7.66E-03 2.35E-02 2.35E-02 2.35E-02 2.47E-02 2.35E-02 2.47E-02 2.40E-02 2.40E-02 2.43E-02 1.74E-01 4.50E-01 3.69E-01 3.89E-01 3.80E-01	Rbfox Rbfox Mbni Nova Nova Rbfox Nova
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M2-

М1+

М1-

M2+

Supplementary Figure 6: *De novo* **motif analysis on WGCNA module exons.** Core exons in modules M1 and M2 in each direction were compared with all mouse cassette exons to evaluate the enrichment of each hexamer in the upstream and downstream intronic sequences (200 nt on each side). Only the top 20 words are shown and hexamers that resemble consensus binding sites of known RBPs are indicated. Motif enrichment in the alternative exon is also evaluated but no significant hexamers were found.

	UI3 (200 nt)				DI5 (200 nt)	DI5 (200 nt)		
<i>.</i>			I	۱.				

Motif	fg	log2FC	pval		fg	log2FC	pval
TCTY (Ptbp)	1219	0.30	7.40E-13		891	0.11	1.03E-02
YCAY (Nova)	1085	0.10	9.46E-03	M1+	1097	0.11	5.49E-03
TGCATG (Rbfox)	33	0.36	9.50E-02		80	1.34	8.41E-13
YGCY (Mbnl)	876	0.06	1.17E-01		1271	0.59	3.72E-42
TCTY (Ptbp)	689	0.11	2.70E-02		532	0.10	6.76E-02
YCAY (Nova)	704	0.11	2.08E-02	M1-	690	0.17	1.22E-03
TGCATG (Rbfox)	27	0.71	1.15E-02		31	0.66	1.08E-02
YGCY (Mbnl)	733	0.44	1.94E-15		587	0.19	1.09E-03
TCTY (Ptbp)	1392	0.48	1.64E-32		864	0.11	1.72E-02
YCAY (Nova)	1020	0.00	5.33E-01	M2+	1233	0.32	2.14E-14
TGCATG (Rbfox)	34	0.39	7.62E-02		88	1.53	6.62E-17
YGCY (Mbnl)	1079	0.35	1.13E-14		1069	0.37	8.21E-16
TCTY (Ptbp)	504	-0.01	5.67E-01		437	0.10	8.45E-02
YCAY (Nova)	664	0.37	1.63E-10	M2-	534	0.08	9.17E-02
TGCATG (Rbfox)	25	0.94	2.29E-03		17	0.07	4.52E-01
YGCY (Mbnl)	479	0.16	1.01E-02		453	0.10	7.98E-02

Supplementary Figure 7: Consensus motif analysis on WGCNA module exons. Core exons in modules M1 and M2 in each direction were compared with all mouse cassette exons to evaluate the enrichment of the consensus motif for Nova, Rbfox, Mbnl and Ptbp in the upstream and downstream intronic sequences (200 nt on each side).



Supplementary Figure 8: 10-fold cross validation of Bayesian network analysis to predict RBP target exons. a, Rbfox. b, Mbnl. c, Ptbp. In each panel, exons used for model training and cross validation are shown. Previously validated exons are highlighted in blue.



Supplementary Figure 9: Gene Set Enrichment Analysis (GSEA) of RBP targets in WGCNA module exons. GSEA was performed for exons in modules M1, M2 and M4 separately. Each gene set is defined by the group of target exons activated or repressed by specific RBPs.



Supplementary Figure 10: Performance of random forest in predicting module exons using different parameters. a, Performance vs. number of variables per tree in the forest (mtry). b, Performance vs. number of trees in the forest (ntree).



Supplementary Figure 11: Additional neuronal RBPs contributing to early splicing switches. a, Activation or repression of module exons by Elavl3/4 and nSR100. Elavl3/4-dependent exons were identified by comparison of WT and Elavl3/4 dKO mouse cortices using exon-junction microarrays (Ince-Dunn et al.; $|\Delta IRank| \ge 6.5$). nSR100 (SRRM4)-dependent exons were identified by comparison of WT and nSR100 KO mouse hippocampi using RNA-seq ($|\Delta \Psi| \ge 0.1$, Benjamini FDR ≤ 0.05). b, Similar to Fig. 4j in the main text. Prediction performance of exon module membership based on regulation by each RBP family. Activation or repression by each RBP as determined from exon-junction microarrays or RNA-seq was used to predict early and late splicing switches, as well as the direction of switches. The performance is measured by partial area under curve (pAUC) of the receiver operating characteristic (ROC) plot with a cutoff at false positive rate (FPR) ≤ 0.1 .



Supplementary Figure 12: Differential splicing analysis of peripheral and sensory neurons compared to mature CNS neurons. a, Heatmap showing exons with statistically significant inclusion (yellow) and exclusion (blue) in each type of peripheral and sensory cells (sensory receptors, sensory neurons and sensory ganglion neurons) compared to the mature CNS neurons. b, Overlap between core module exons and exons showing differential splicing in each type of peripheral sensory cells compared to mature CNS neurons. Exons with increased or decreased inclusion in each module and direction are shown separately.



Supplementary Figure 13: Only specific RBPs show distinct expression in peripheral and sensory neurons compared to mature CNS neurons. a, Expression of RBPs (log2 transformed, median centered RPKM values) across different tissue or neuronal samples was used in the analysis. This analysis included all RBPs compiled in The same list of 346 samples used to predict maturation stages RBPDB (http://rbpdb.ccbr.utoronto.ca). (Supplementary Dataset 1) was analyzed. Samples were ordered by the predicted maturation stage, and RBPs were ordered by the correlation of their expression with the predicted sample maturation stages. Sensory cell types are highlighted. The data matrix used to generate this heatmap is available in Supplementary Dataset 13. **b**, Differential expression analysis of RBPs in each cell type from the peripheral and sensory system compared to mature CNS neurons purified from adult mouse brains. The Benjamini FDR (in log2 scale) with sign indicating the direction of expression difference is shown. RBPs are shown in the same order as in (a). A subset of RBPs are highlighted. c, Noval (top) and Rbfox2 (bottom) expression in P4 mouse spinal cord using in situ hybridization. Data were obtained from Allen Brain Atlas (http://mousespinal.brain-map.org). In the spinal cord, gray matter and white matter are indicated due to neuron-specifix or enriched expression of Nova and Rbfox2. Probes for Nova2 and Rbfox1/3 are not available. SC, spinal cord; DRG, dorsal root ganglion; WM, white matter; GM, gray matter. Scale bar: 100 µm.

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