

ADDITIONAL DATA FILE 1

Supplemental Table 1. Tissues, cDNA libraries, genes, ESTs, and poly(A) sites used in this study.

Supplemental Table 2. Poly(A) site usage of type II genes.

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Supplemental Table 4. Usage of strong and weak poly(A) sites using 60% as cutoff.

Supplemental Table 5. Usage of strong and weak poly(A) sites using 75% as cutoff.

Supplemental Table 6. Usage of strong and weak poly(A) sites using 90% as cutoff.

Supplemental Figure 1. Schematic representation of three types of genes.

Supplemental Figure 2. Boxplots of mRNA expression levels of polyadenylation-related factors in brain tissues versus other tissues. (A) U95Av2 data. (B) U133A data. For each plot, values from brain tissues are on the left, and those from other tissues are on the right.

Supplemental Figure 3. Selection of hexamers in different poly(A) regions. (A) -100/-41, (B) -40/-1, (C) +1/+40, and (D) +41/+100. For each panel, a two-dimensional scatter-plot for z_{un} and z_{pc} is shown on the left, and clustering of hexamers is shown on the right. In each scatter-plot, x-axis is z_{un} , and y-axis is z_{pc} . Each dot represents a hexamer. Cutoffs of 2.5 were used for both z_{un} and z_{pc} , as indicated by vertical and horizontal lines, respectively. Hexamers in green are the ones with $z_{sw} > 2.5$. Hexamers in red are the selected ones for clustering. Sequence logos of *cis* elements are shown under corresponding hexamer groups.

Supplemental Figure 4. Multiple sequence alignments of PTB and nPTB (A), and CstfF-64 and τ CstF-64 (B). Only the isoform a of PTB (NP_002810) was used here. ClustalW was used to align protein sequences with default settings. Identical residues in the alignment are marked with asterisks “*”; strongly and weakly conserved residues are marked with colons “:” and periods “.”, respectively. The protein sequence accessions for nPTB, CstfF-64 and τ CstF-64 are NP_067013, NP_001316, and NP_056050, respectively.

Supplemental Table 1. Tissues, cDNA libraries, genes, ESTs, and poly(A) sites used in this study.

Tissue	# of lib	# of genes	# of ESTs	# of PA				
adipose	3	115	137	115				
adrenal cortex	2	269	321	273				
blood	28	747	1903	791				
bone	8	3944	11057	4454				
bone marrow	10	1337	3535	1410				
brain	48	2226	5717	2355				
cerebrum	13	251	321	253				
cervix	5	811	1372	833				
colon	50	1795	3039	1881				
ear	1	1213	2576	1283				
endocrine	5	569	875	580				
esophagus	1	302	356	304				
eye	14	3626	8896	3989				
genitourinary	6	382	446	390				
germ cell	4	415	522	421				
head and neck	34	726	1205	740				
heart	7	46	64	47				
kidney	14	1533	2692	1605				
liver	13	1380	3617	1460				
lung	31	2859	8012	3068				
lymph/lymph node	8	1299	2425	1343				
mammary gland	37	507	1721	513				
muscle	7	1302	2474	1354				
nervous	9	276	315	282				
ovary	25	2035	5596	2133				
pancreas	13	2541	5566	2718				
pancreatic islet	6	2509	9769	2759				
peripheral nervous system	6	984	1276	1007				
pineal gland	2	154	185	155				
pituitary gland	5	157	259	158				
placenta	28	3690	8539	4092				
prostate	32	2044	5505	2183				
retina	10	3117	5697	3367				
skin	17	2280	6753	2436				
soft tissue	5	537	681	545				
spleen	3	263	415	267				
stomach	34	2569	5284	2736				
testis	11	1168	1854	1218				
thymus	1	18	18	18				
thyroid	30	387	558	394				
uterus	16	4253	10844	4775				
vascular	7	356	548	363				

of lib: number of non-normalized libraries

of genes: number of genes studied

of ESTs: number of poly(A/T)-tailed ESTs from non-normalized libraries

of PA: number of poly(A) sites

Supplemental Table 2. Poly(A) site usage of type II genes.

Tissue	# of genes	# of ESTs	Vf	Vm	VI	Pf	Pm	PI	Df	Dm	DI	Pval
adipose	48	59	19	9	20	0.40	0.19	0.42	0.19	-0.07	-0.11	6.31E-01
adrenal cortex	108	123	29.5	25	53.5	0.27	0.23	0.50	-0.18	0.15	0.06	4.16E-01
blood	267	797	120.39	52.46	94.15	0.45	0.20	0.35	0.36	-0.03	-0.25	6.99E-05
bone	1476	4404	464.85	296.12	715.03	0.31	0.20	0.48	-0.05	-0.01	0.03	3.62E-01
bone marrow	554	1407	156	136.53	261.47	0.28	0.25	0.47	-0.15	0.22	0.01	7.77E-03
brain	794	1969	239.44	147.82	406.74	0.30	0.19	0.51	-0.09	-0.08	0.09	4.26E-02
cerebrum	96	116	21.5	19.5	55	0.22	0.20	0.57	-0.33	0.01	0.22	6.16E-02
cervix	317	498	109.47	73.58	133.95	0.35	0.23	0.42	0.04	0.15	-0.10	2.14E-01
colon	689	1122	233.52	120.2	335.28	0.34	0.17	0.49	0.02	-0.14	0.04	2.12E-01
ear	534	1272	129.33	134.22	270.45	0.24	0.25	0.51	-0.27	0.25	0.08	2.70E-05
endocrine	234	337	79.27	42.23	112.5	0.34	0.18	0.48	0.02	-0.11	0.02	7.31E-01
esophagus	91	110	28	24	39	0.31	0.26	0.43	-0.07	0.31	-0.09	3.31E-01
eye	1285	3207	444.93	264.81	575.26	0.35	0.21	0.45	0.04	0.02	-0.05	3.37E-01
genitourinary	159	188	50.83	41	67.17	0.32	0.26	0.42	-0.04	0.28	-0.10	1.93E-01
germ cell	144	188	55.45	24.75	63.8	0.39	0.17	0.44	0.16	-0.15	-0.06	3.55E-01
head and neck	276	451	94.75	52.33	128.92	0.34	0.19	0.47	0.03	-0.06	0.00	8.55E-01
heart	13	14	6	0	7	0.46	0.00	0.54	0.39	-1.00	0.15	1.82E-01
kidney	581	1003	181.81	112.83	286.36	0.31	0.19	0.49	-0.06	-0.04	0.05	4.73E-01
liver	510	1287	179.63	108.86	221.51	0.35	0.21	0.43	0.06	0.06	-0.07	3.18E-01
lung	995	2705	349.04	186.12	459.84	0.35	0.19	0.46	0.06	-0.07	-0.02	3.26E-01
lymph node	505	958	167.09	116.3	221.61	0.33	0.23	0.44	0.00	0.14	-0.07	2.20E-01
mammary gland	188	549	59.59	36	92.41	0.32	0.19	0.49	-0.05	-0.05	0.05	8.08E-01
muscle	484	877	155.1	98.34	230.57	0.32	0.20	0.48	-0.04	0.01	0.01	8.81E-01
nervous	116	137	23.67	30.33	62	0.20	0.26	0.53	-0.39	0.30	0.14	1.22E-02
ovary	754	1987	290.11	160.77	303.12	0.38	0.21	0.40	0.16	0.06	-0.14	8.83E-04
pancreas	950	2226	293.09	199.88	457.03	0.31	0.21	0.48	-0.07	0.04	0.02	3.31E-01
pancreatic islet	1003	3765	275.13	216.25	511.61	0.27	0.22	0.51	-0.17	0.07	0.09	6.87E-04
peripheral nervous system	353	444	112.33	67	173.67	0.32	0.19	0.49	-0.04	-0.06	0.05	6.56E-01
pineal gland	58	74	20.5	11.5	26	0.35	0.20	0.45	0.06	-0.02	-0.04	9.33E-01
pituitary gland	57	82	20	14	23	0.35	0.25	0.40	0.06	0.22	-0.14	5.69E-01
placenta	1428	3066	511.66	315.95	600.39	0.36	0.22	0.42	0.08	0.10	-0.10	1.59E-03
prostate	808	2069	267.26	167.68	373.06	0.33	0.21	0.46	0.00	0.03	-0.02	8.90E-01
retina	1106	2021	419.34	213.41	473.26	0.38	0.19	0.43	0.14	-0.04	-0.09	2.66E-03
skin	852	2396	286.6	166.91	398.49	0.34	0.20	0.47	0.01	-0.03	0.00	9.04E-01
soft tissue	206	258	55.6	38.4	112	0.27	0.19	0.54	-0.19	-0.08	0.16	7.93E-02
spleen	82	118	27.8	13.2	41	0.34	0.16	0.50	0.02	-0.20	0.07	6.52E-01
stomach	999	2137	325.36	195.85	477.78	0.33	0.20	0.48	-0.02	-0.03	0.02	7.95E-01
testis	436	686	160.61	94.33	181.06	0.37	0.22	0.42	0.11	0.07	-0.12	8.64E-02
thymus	6	6	2	1	3	0.33	0.17	0.50	0.00	-0.17	0.07	9.76E-01
thyroid	162	214	52	34	76	0.32	0.21	0.47	-0.03	0.04	0.00	9.46E-01
uterus	1607	4300	487.28	365.07	754.65	0.30	0.23	0.47	-0.09	0.13	0.00	1.04E-02
vascular	156	221	61.2	30.5	64.3	0.39	0.20	0.41	0.18	-0.03	-0.12	2.44E-01

of genes: number of genes studied

of ESTs: number of poly(A/T)-tailed ESTs from non-normalized libraries

Vf, Vm, and VI: votes for 2F, 2M, and 2L poly(A) sites, respectively

Pf, Pm, and PI: percent of usage of 2F, 2M, and 2L poly(A) sites, respectively

Df, Dm, and DI: distance to the median usage for 2F, 2M, and 2L poly(A) sites, respectively

Pval: p-value from Chi-squared test

Supplemental Table 3. Poly(A) site usage of type III genes.

Supplemental Table 3. Poly(A) site usage of type III genes.									
Tissue	# of genes	# of ESTs	Vu	Vd	Pu	Pd	Du	Dd	Pval
adipose	23	28	3	20	0.13	0.87	0.11	-0.02	8.41E-01
adrenal cortex	64	85	3	61	0.05	0.95	-0.60	0.08	8.09E-02
blood	172	380	37.22	134.78	0.22	0.78	0.85	-0.11	5.02E-05
bone	1085	3219	140.59	944.41	0.13	0.87	0.11	-0.01	1.98E-01
bone marrow	373	984	39.63	333.37	0.11	0.89	-0.09	0.01	5.17E-01
brain	516	1274	72.51	443.49	0.14	0.86	0.20	-0.03	9.67E-02
cerebrum	64	79	2	62	0.03	0.97	-0.73	0.10	3.28E-02
cervix	187	333	19	168	0.10	0.90	-0.13	0.02	5.12E-01
colon	423	761	48.67	374.33	0.12	0.88	-0.02	0.00	9.00E-01
ear	397	790	37.2	359.8	0.09	0.91	-0.20	0.03	1.48E-01
endocrine	121	201	9.06	111.94	0.07	0.93	-0.36	0.05	1.49E-01
esophagus	73	78	14	59	0.19	0.81	0.64	-0.08	4.69E-02
eye	955	2271	193.63	761.37	0.20	0.80	0.73	-0.10	1.69E-16
genitourinary	91	108	5	86	0.05	0.95	-0.53	0.07	6.55E-02
germ cell	108	140	8.5	99.5	0.08	0.92	-0.33	0.04	2.15E-01
head and neck	163	243	13.83	149.17	0.08	0.92	-0.27	0.04	2.01E-01
heart	15	27	2.5	12.5	0.17	0.83	0.42	-0.06	5.50E-01
kidney	378	658	46.93	331.07	0.12	0.88	0.06	-0.01	6.66E-01
liver	318	980	40.93	277.07	0.13	0.87	0.10	-0.01	5.17E-01
lung	676	1770	97.92	578.08	0.14	0.86	0.24	-0.03	2.44E-02
lymph node	329	587	37.65	291.35	0.11	0.89	-0.02	0.00	8.84E-01
mammary gland	101	214	12	89	0.12	0.88	0.02	0.00	9.55E-01
muscle	331	576	38.14	292.86	0.12	0.88	-0.02	0.00	9.19E-01
nervous	67	76	3.5	63.5	0.05	0.95	-0.55	0.07	9.90E-02
ovary	479	1079	66.35	412.65	0.14	0.86	0.18	-0.02	1.43E-01
pancreas	621	1207	56.05	564.95	0.09	0.91	-0.23	0.03	3.80E-02
pancreatic islet	615	1878	78.24	536.76	0.13	0.87	0.09	-0.01	4.31E-01
peripheral nervous system	256	360	25	231	0.10	0.90	-0.17	0.02	3.35E-01
pineal gland	29	38	1	28	0.03	0.97	-0.71	0.09	1.67E-01
pituitary gland	33	44	2	31	0.06	0.94	-0.48	0.06	3.13E-01
placenta	1008	2164	192.25	815.75	0.19	0.81	0.63	-0.08	3.34E-13
prostate	478	1269	70.76	407.24	0.15	0.85	0.27	-0.04	3.49E-02
retina	777	1391	167.6	609.4	0.22	0.78	0.84	-0.11	1.15E-17
skin	540	1485	99	441	0.18	0.82	0.57	-0.08	1.63E-06
soft tissue	152	202	9	143	0.06	0.94	-0.49	0.07	2.66E-02
spleen	57	82	8	49	0.14	0.86	0.20	-0.03	5.84E-01
stomach	645	1182	77.35	567.65	0.12	0.88	0.02	0.00	8.19E-01
testis	327	530	47.56	279.44	0.15	0.85	0.24	-0.03	1.10E-01
thymus	5	5	0	5	0.00	1.00	-1.00	0.13	4.16E-01
thyroid	93	138	6.05	86.95	0.07	0.93	-0.44	0.06	1.19E-01
uterus	1123	2833	137.08	985.92	0.12	0.88	0.04	-0.01	5.99E-01
vascular	79	132	6.5	72.5	0.08	0.92	-0.30	0.04	3.37E-01

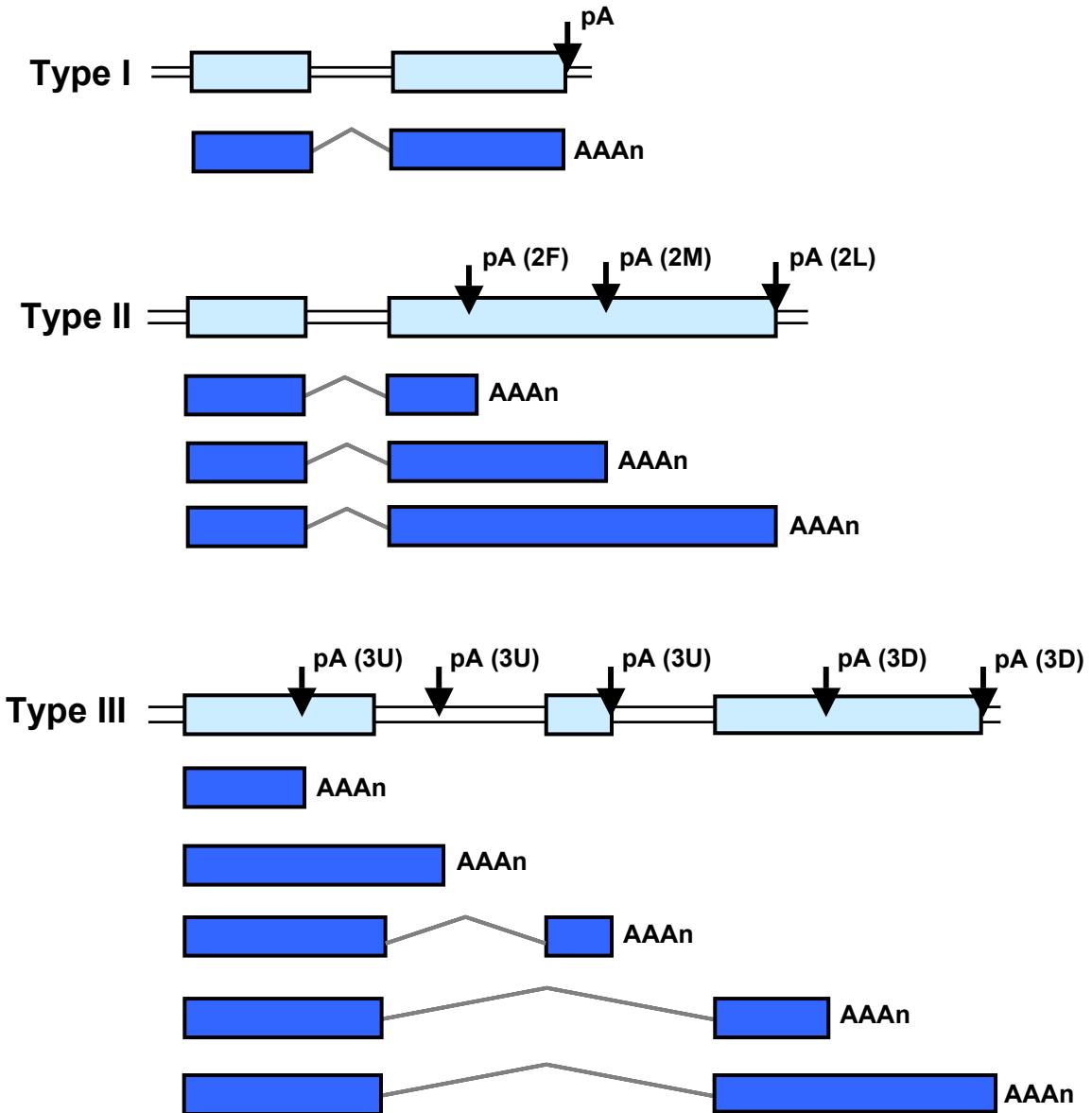
Supplemental Table 4. Usage of strong and weak poly(A) sites using 60% as cutoff

Supplemental Table 5. Usage of strong and weak poly(A) sites using 75% as cutoff

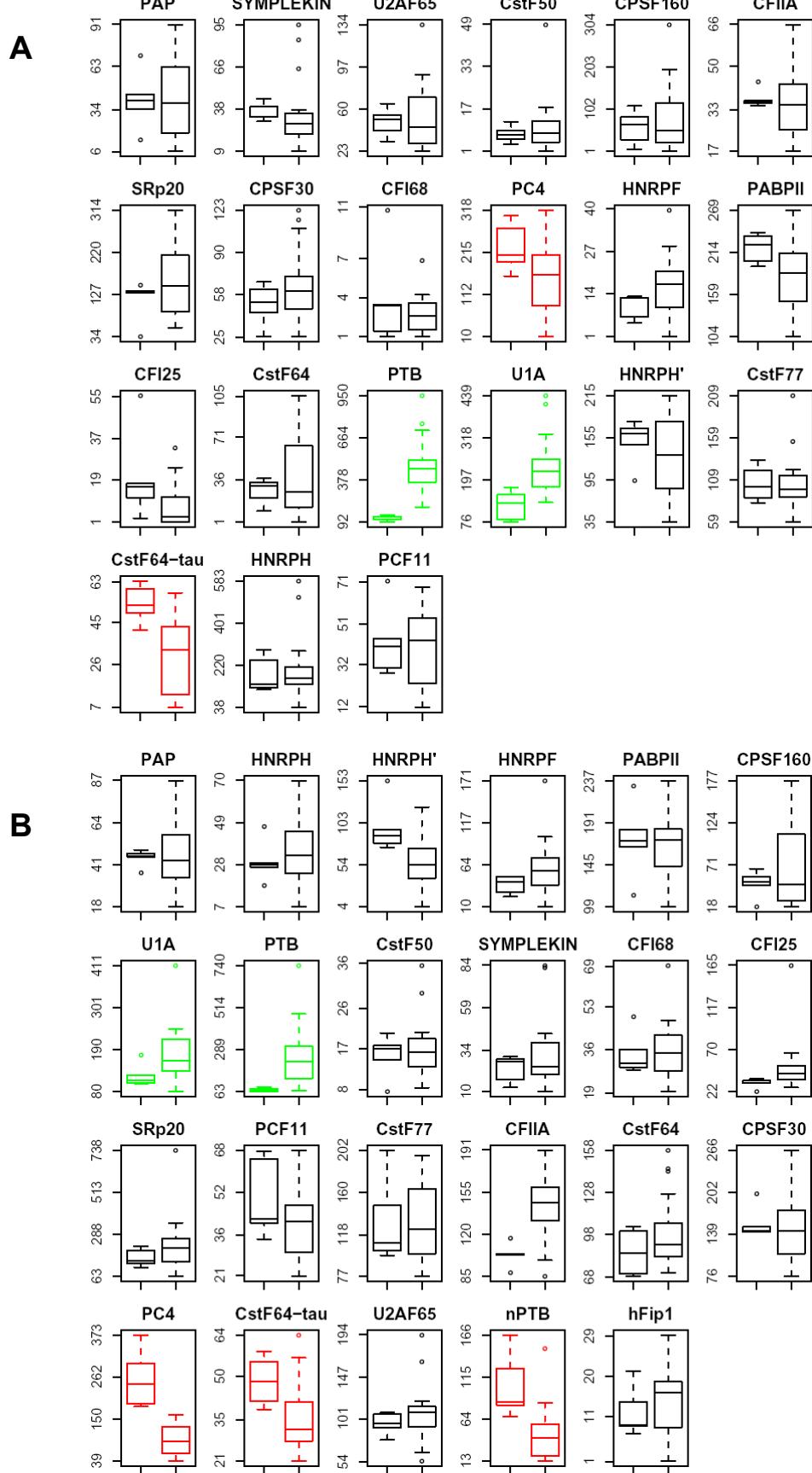
Supplemental Table 6. Usage of strong and weak poly(A) sites using 90% as cutoff

Tissue	# of genes	# of ESTs	Vs	Vw	Ps	Pw	Ds	Dw	Pval
adipose	19	27	19.00	0.00	1.00	0.00	0.04	-1.00	3.60E-01
adrenal cortex	36	49	34.50	1.50	0.96	0.04	0.00	-0.01	9.88E-01
blood	91	379	86.31	4.69	0.95	0.05	-0.01	0.22	6.56E-01
bone	225	2143	215.40	9.60	0.96	0.04	0.00	0.01	9.70E-01
bone marrow	135	914	130.98	4.02	0.97	0.03	0.01	-0.29	4.74E-01
brain	167	966	160.25	6.75	0.96	0.04	0.00	-0.04	9.11E-01
cerebrum	28	40	28.00	0.00	1.00	0.00	0.04	-1.00	2.67E-01
cervix	92	266	89.05	2.95	0.97	0.03	0.01	-0.24	6.30E-01
colon	142	445	136.88	5.12	0.96	0.04	0.01	-0.14	7.17E-01
ear	112	527	110.39	1.61	0.99	0.01	0.03	-0.66	1.43E-01
endocrine	88	148	84.00	4.00	0.95	0.05	0.00	0.08	8.78E-01
esophagus	28	39	25.00	3.00	0.89	0.11	-0.07	1.54	8.71E-02
eye	196	1118	176.39	19.61	0.90	0.10	-0.06	1.37	5.52E-05
genitourinary	43	63	40.50	2.50	0.94	0.06	-0.02	0.38	6.02E-01
germ cell	60	112	58.55	1.45	0.98	0.02	0.02	-0.43	4.88E-01
head and neck	103	261	99.42	3.58	0.97	0.03	0.01	-0.18	7.08E-01
heart	8	9	8.00	0.00	1.00	0.00	0.04	-1.00	5.53E-01
kidney	152	458	143.97	8.03	0.95	0.05	-0.01	0.25	5.13E-01
liver	139	815	131.03	7.97	0.94	0.06	-0.02	0.36	3.73E-01
lung	205	1435	194.64	10.36	0.95	0.05	-0.01	0.20	5.51E-01
lymph node	111	478	103.76	7.24	0.93	0.07	-0.02	0.55	2.27E-01
mammary gland	74	225	70.33	3.67	0.95	0.05	-0.01	0.18	7.51E-01
muscle	104	412	99.89	4.11	0.96	0.04	0.00	-0.06	8.93E-01
nervous	27	43	25.67	1.33	0.95	0.05	-0.01	0.17	8.54E-01
ovary	163	822	154.20	8.80	0.95	0.05	-0.01	0.28	4.53E-01
pancreas	185	1021	179.88	5.12	0.97	0.03	0.02	-0.34	3.27E-01
pancreatic islet	175	1835	165.67	9.33	0.95	0.05	-0.01	0.26	4.63E-01
peripheral nervous system	90	155	88.50	1.50	0.98	0.02	0.03	-0.60	2.29E-01
pineal gland	16	26	16.00	0.00	1.00	0.00	0.04	-1.00	4.01E-01
pituitary gland	26	40	24.00	2.00	0.92	0.08	-0.04	0.82	3.78E-01
placenta	197	725	182.42	14.58	0.93	0.07	-0.03	0.76	2.62E-02
prostate	176	1124	165.63	10.37	0.94	0.06	-0.02	0.40	2.69E-01
retina	128	322	111.19	16.81	0.87	0.13	-0.09	2.11	5.18E-07
skin	185	1411	177.40	7.60	0.96	0.04	0.00	-0.03	9.41E-01
soft tissue	69	105	65.67	3.33	0.95	0.05	-0.01	0.14	8.01E-01
spleen	40	75	38.80	1.20	0.97	0.03	0.01	-0.29	7.02E-01
stomach	174	824	167.85	6.15	0.96	0.04	0.01	-0.16	6.54E-01
testis	94	296	84.30	9.70	0.90	0.10	-0.06	1.45	3.24E-03
thymus	3	3	3.00	0.00	1.00	0.00	0.04	-1.00	7.16E-01
thyroid	57	94	55.50	1.50	0.97	0.03	0.02	-0.38	5.52E-01
uterus	227	1724	213.62	13.38	0.94	0.06	-0.02	0.40	2.09E-01
vascular	69	132	68.00	1.00	0.99	0.01	0.03	-0.66	2.53E-01

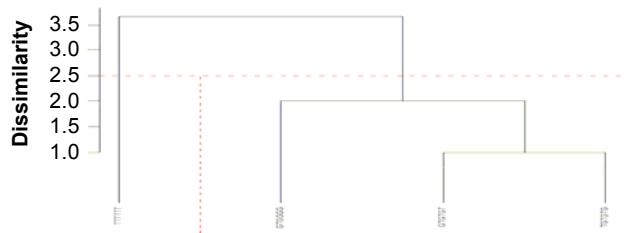
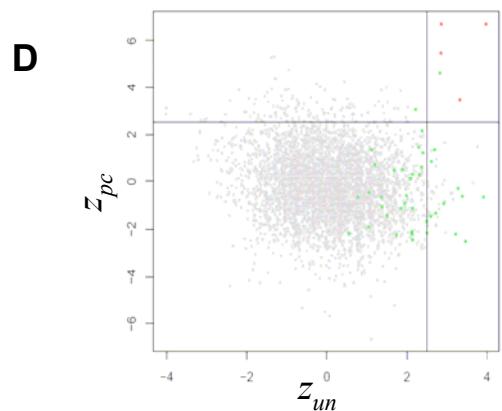
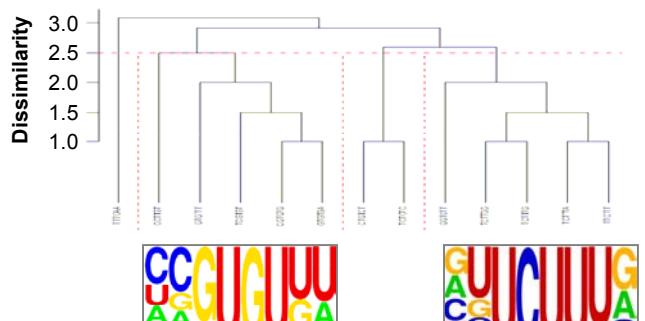
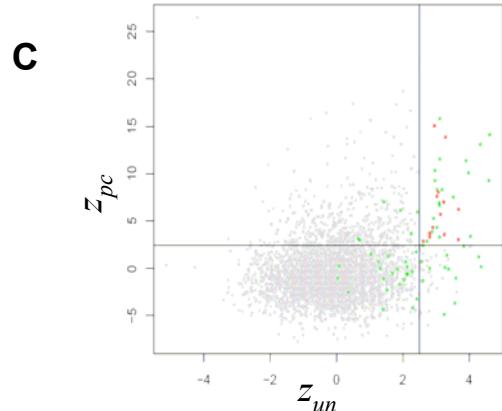
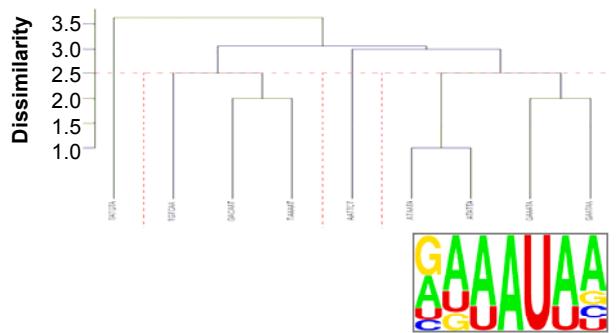
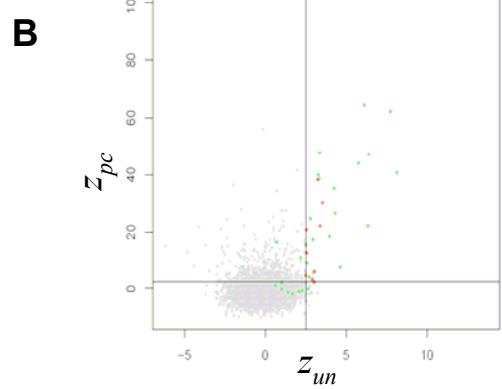
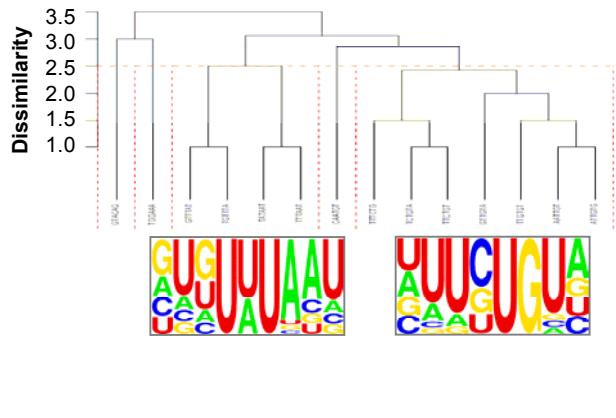
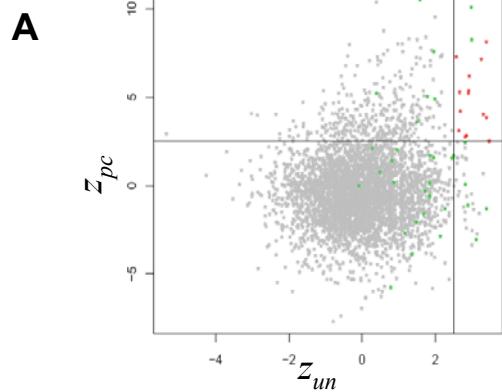
Supplemental Figure 1.



Supplemental Figure 2.



Supplemental Figure 3.



Supplemental Figure 4.

A	PTB MDGIVPDIAGTGRGSDELFSTCVNGPFIMSSNSASAANGNDSKFKGDSRSAGVPSRVIIHRLPIDVTEGEVISLGL nPTB MDGIVTEAVGVKRGSDELLSGSVLSSPNMSSMVVTANGNDSKFKGEDKMDGAPSRLVHLIRKLPGEVTTETEVIALGL	80
	*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****: PTB PFGKVTNLMLKGKQNQAFIEMNTREAANTMVNYYTSVTPVLRGQPIYIQFSNHKELTDTSSPNQARAQALQAVNSVQSG nPTB PFGKVTNLMLKGKQNQAFIELATEEAAITMVNYYSAVTPLRNQPIYIQFSNHKELTDTNLN-QRAQAVLQAVTAVQTA	160 159
	* . *: :*: . . .*****:*****:*****:*****:*****:*****:*****:*****:*****:*****: PTB NLALAASAAAVIDAGMAMAGQSPVLRRIIVENLFYPVTLDVLHQIFPSKFGTVLKIIITFTKNNQFQALLQYADPVSAQHAKLS nPTB NTPLSG---TTVSESAVTPAQSPVLRRIIDNMYYPVTLVLHQIFPSKFGAVLKIIITFTKNNQFQALLQYGDVPNAQQAKLA	240 237
	*****:*****:*****:*****:*****:*****:*****:*****:*****:*****: PTB LDGQNIYNACCTLRIDFSKLTSLNVKYNNDKSRDYTRPDLPSPGDQSPLSDQTMAAAAGAPGIISASPYAGAGFPPTFAIP nPTB LDGQNIYNACCTLRIDFSKLVLNVKYNNDKSRYTRPDLPSPGDQGPALDPAIAAAFAK-----	320 296
	: : *: **: ***: ****: *****:*****:*****:*****:*****:*****:*****:*****:*****:*****: PTB QAAGLSVPNVHGALAPLAIP---SAAAAAAAAGRIAIPGLAGAGNSVLLVSNLNPVERVTPQSLFILFGVYGDVQRVKILFN nPTB ETSLLAIP---GALSPLAIPNAAAAAAAAGRVMGPGVSAGGNTVLLVSNLNEEMVTPQSLFTLFGVYGDVQRVKILYN	398 373
	: . *:**:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****: PTB KKENALVQMADGNQAQLAMSHLNHGKHLHGKPIRITLSKHNQVQLPREQGQEDGLTKDYGNSPNPLHRFKKPGSKNFQNIFFPP nPTB KKDSLQIOMADGNQSQLAMNHLNQKMYGKIRVTLQKPREGLDDQGLTKDFGNSPNPLHRFKKPGSKNFQNIFFPP	478 453
	*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****: PTB SATLHSNIPPSVSEEDLKVLFSSNGGVVKGFKFQKDRKMALIQMGSVEEAVQALIDLHNDLGENHHLRVSFSKSTI nPTB SATLHSNIPPSVAEEDLRTLFANTGGTVKAFFQ-DHKMALLQMATVEEAIQALIDLHNYNLGENHHLRVSFSKSTI	557 531
B	CstF64 MAGLTVRDPAVDRSLRSVFVGNIPYEATEEQLKIDFSEGVPSFRLVYDRETGPKGYGFCEYQDQETALSAMRNLN tCstF64 MSSLAVRDPAMDRLRSVFVGNIPYEATEEQLKIDFSEGVPSFRLVYDRETGPKGYGFCEYQDQETALSAMRNLN	80 80
	*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****: CstF64 EFSGRALRVDNAASEKNKEELSLGTGAPVIESPYGETISPEDAPESISKAVASLPPEQMFLMKQMKLCVQNSPQEARN tCstF64 EFSGRALRVDNAASEKNKEELSLGPAPIIDSPYGDPIPDEDAPESITRAVASLPPEQMFLMKQMKLCVQNSHQEARN	160 160
	*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****: CstF64 MLLQNPQLAYALLQAQVVMRIRDPEIALKILHRQTNIPTLIAGNPQPVGAGPGSGS-----NVSMNQNPQAPQAQ tCstF64 MLLQNPQLAYALLQAQVVMRIMDPEIALKILHRKIHTPLIGKQSOSVSVGPGPGPGLCPGPVNLLNQNPAPQPQ	232 240
	. *: . *:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****: CstF64 SLGGMHVNQAPPLMQASMQGGVPAPGQMPAAVTGPGPGLSIALPGGGMQAQVGMPGSGPVSMERQVPMQDPRAAMQRGSLP tCstF64 HLARRPVKDIPPLMQTPIQGGIPAPGPPIAAPVGAGPGSLTPGGAMQPQLGMPGVGPVLERGQVQMSDPRAPIPRGPV	312 320
	.. .*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****: CstF64 ANVPTPRGLGDAPNDPRGGTLLSVTGEVEPRGYLGPPHOGPPMHHVPGHESRGPPHELRGGLPPEPRPLMAEPRGPML tCstF64 PGGLPPRGLGDAPNDPRGGTLLSVTGEVEPRGYLGPPHOGPPMHHASGHDRGPSSHEMRGGPLGDPRLLIGEPRGPML	392 400
	**** *:*****:*****:*****:*****:*****:*****:*****:*****:*****: CstF64 DQRGPPLDGRGGDRPGIDARGMEBARAMEARGLDARGLEARAMEARAMEARAMEARAMEVGRMEARGMDTRGPV tCstF64 DQRGLPMGDRGGRD----SRAMETRAMET-----EVLETRVMERRGMETCAMETRGMEARGMDARGLEMGRGPV	472 465
	...***: . *:*****:*****:*****:*****: CstF64 GPRGPPISGMQGPSPINMGAAPP-QGSRQVP-----VMQGTGMQGASIQGG----- tCstF64 SSRGPMPTGGIQQGPGINIGAGGGPQGPQRPVPGISGVGNPGAGMGTGIIQGTGMQGAGIQQGGMQGAGIQQGVSIQGGGIQ	517 545
	* . .*****:*****:*****:*****:*****:*****:*****:*****: CstF64 -----SQPGGFSPGQNQVTPQDHKAALIMQVLQLTADQIAMLPEQRQSILILKEQIKQSTGAP tCstF64 GGIQGASKQGGSPSSFSFGQSOVTPQDQEKAALIMQVLQLTADQIAMLPEQRQSILILKEQIKQSTGAS	577 616