

Library information

See Tsuritani_etal_SupTable1.xls

A

	#Total cDNAs	#Mapped cDNAs	#Possible truncated cDNAs	#Total cDNAs allocated to Entrez genes
Human	1,780,295	1,548,357	181,237	1,359,000
Mouse	580,209	457,007	28,081	364,487

B

	#covered RefSeq genes	#different TSS positions	#PPRs (mutually separated by >500)	#total allocated cDNAs
Human	14,628	269,774	30,964	1,171,916
Mouse	13,704	129,135	19,023	330,819

C

	#covered RefSeq genes	#different TSS positions	#PPRs (mutually separated by >500)	#total allocated cDNAs
Human	5,463	156,951	17,245	708,657
Mouse	5,463	63,262	8,622	165,818

Information of PPRs belonging to each category

See Tsuritani_etal_SupTable3.xls

Promoter activities of the PPRs belonging to each category observed in HEK293 cells

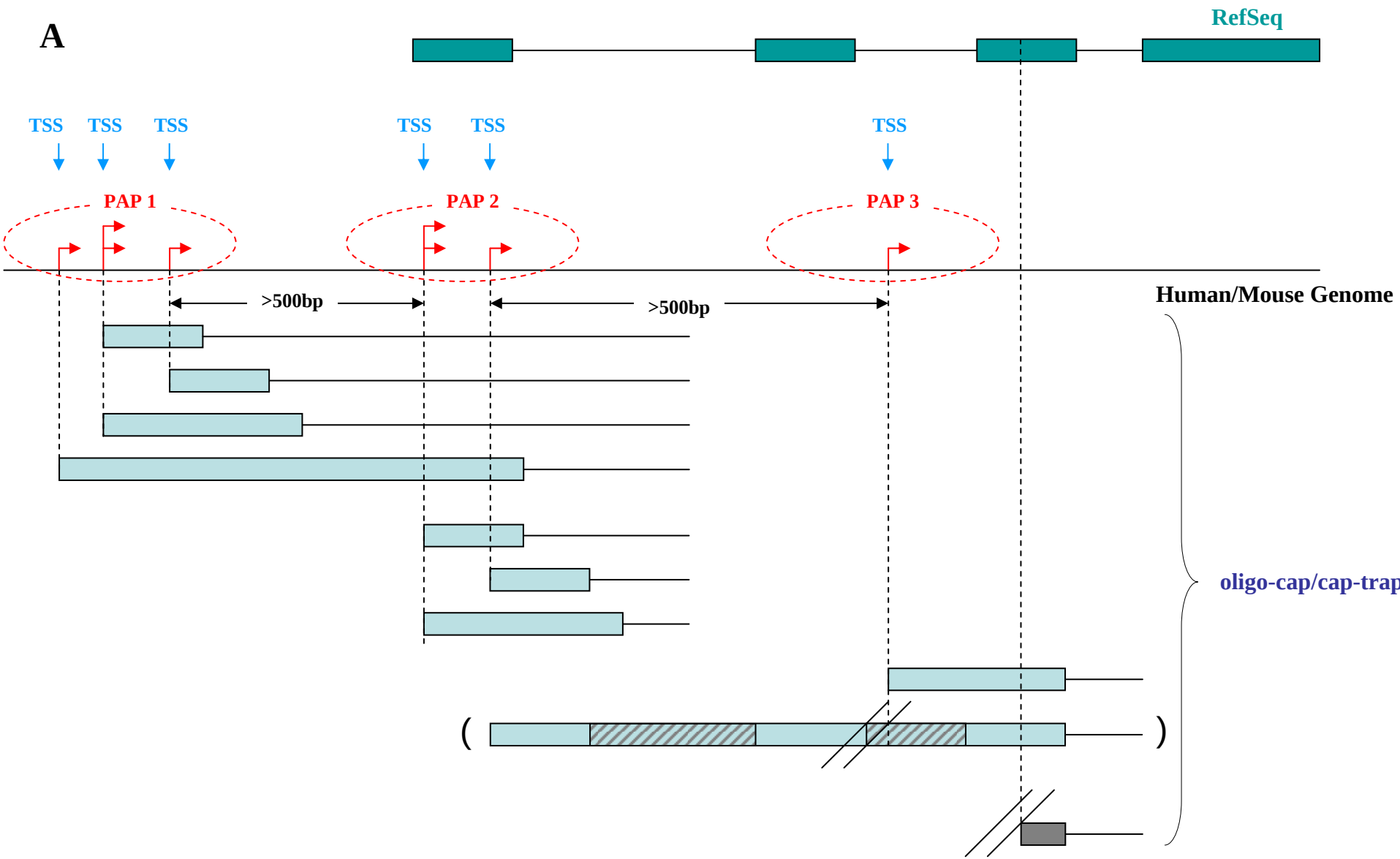
See Tsuritani_etal_SupTable4.xls

GO_id	GO_term	# of locus related to GO and AP	# of locus related to GO	P value
GO:0003700	transcription factor activity	65	682	2.8E-07
GO:0007165	signal transduction	65	747	6.8E-06
GO:0004713	protein-tyrosine kinase activity	24	196	2.1E-05
GO:0006468	protein amino acid phosphorylation	47	508	2.4E-05
GO:0007242	intracellular signaling cascade	32	310	4.8E-05
GO:0003779	actin binding	23	199	7.5E-05
GO:0004674	protein serine/threonine kinase activity	33	359	3.6E-04
GO:0005515	protein binding	81	1,120	4.4E-04
GO:0016301	kinase activity	17	155	9.1E-04
GO:0005737	cytoplasm	55	730	1.3E-03
GO:0007517	muscle development	13	112	1.6E-03
GO:0007399	neurogenesis	20	207	2.0E-03
GO:0005856	cytoskeleton	22	245	3.5E-03
GO:0005096	GTPase activator activity	12	117	6.5E-03
GO:0005634	nucleus	163	2,725	7.9E-03

Primers used for semi-quantitative RT-PCR assays of putative “ncRNAs”

See Tsuritani_etal_SupTable6.xls

Enriched in "conserved" PPRs							
MatrixID	TFname	NMID	#hit in "conserved"	#hit in "non-conserved"	chisq- pvalue	cutoff	consensus
V\$E2F_Q2	E2F	NM_005225	514	76	<1E-100	1	GGCGSG
V\$CHCH_01	CHURC1	NM_145165	416	74	2.0E-76	1	CGGGNN
V\$SP1_01	SP1	NM_138473	311	47	4.7E-62	0.95	GGGGCGGGGT
V\$USF2_Q6	USF2	NM_003367	377	85	9.2E-60	1	CASGYG
V\$ZF5_01	ZF5	NM_003409	264	31	1.3E-58	0.93	GSGCGCGR
V\$SP1_Q6_01	SP1	NM_138473	256	29	1.5E-57	0.97	GGGGCGGGGC
V\$MAZ_Q6	MAZ	NM_002383	225	36	1.4E-43	1	GGGGAGGG
Enriched in "non-conserved" PPRs							
MatrixID	TFname	NMID	hit in "conserved"	hit in "non-conserved"	chisq- pvalue	cutoff	consensus
V\$HNF1_Q6	HNF1	NM_000545	491	1469	7.5E-90	0.85	WRGTTAATNATTAACNNN
V\$PAX4_02	PAX4	NM_006193	311	1030	1.8E-70	0.95	NAAWAATTANS
V\$CDXA_01	CDXA	NM_204676	330	1029	2.2E-64	0.98	MTTTATR
V\$CEBP_01	CEBP	NM_004364	692	1591	7.8E-59	0.96	NNTKTGGWNANNN
V\$CDXA_02	CDXA	NM_204676	225	784	2.6E-56	1	AWTWMTR
V\$CDX_Q5	CDX	NM_001804	235	749	1.4E-47	0.88	NAYNRHNAKTHATAAA
V\$CRX_Q4	CRX	NM_000554	115	494	1.0E-44	0.97	YNNNTAATCYSMN
V\$AML1_01	AML1	NM_001754	687	1450	3.7E-42	1	TGTGGT
V\$AML1_Q6	AML1	NM_001754	687	1450	3.7E-42	1	TGTGGT
V\$TST1_01	POU3F1	NM_002699	410	1007	6.6E-41	0.89	NNKGAATTAVAVTDN
V\$HNF3_Q6_01	HNF3	NM_004496	192	625	1.0E-40	0.96	NNNNNTRTTTRYTYWNKN



Alternative Promoters in the Homo sapiens nucleoporin 93kDa (NUP93; NM_014669)

B



Class

“Conserved”

“Non-conserved”

“Non-conserved”

“Marginal”

“Conserved”

AP1 (Human)

APA (Mouse)

LALIGN score: 8e-198

AP4 (Human)

UCSC BLASTZ

AP5 (Human)

APB (Mouse)

LALIGN score: 3e-63

Alternative Promoters in the Calmodulin-dependent phosphodiesterase 1A gene (PDE1A; NM_005019)

