

Supplemental data 1: Accession numbers for PPAR proteins

Table S1: All PPAR protein Accession numbers used for Protein alignment using Praline and Phylogentic tree (Geneious)

PPAR	Species	Accession numbers
PPARA	Mouse	<i>Mus musculus</i> NP_001106889.1
	Rat	<i>Rattus norvegicus</i> NP_037328.1
	Human	<i>Homo sapiens</i> CAG33716.1
	Crab-eating macaque	<i>Macaca fascicularis</i> XP_005567059.1
	Rhesus macaque	<i>Macaca mulatta</i> NP_001028201.1
	Chicken	<i>Gallus gallus</i> NP_001001464.1
	African clawed frog	<i>Xenopus laevis</i> AAH79684.1
	Japanese medaka	<i>Oryzias latipes</i> BAH58103.1
	Cow	<i>Bos taurus</i> NP_001029208.1
	Salmon	<i>Salmo salar</i> NP_001117032.1
	Dog	<i>Canis lupus familiaris</i> NP_001003093.1
	Wild boar	<i>Sus scrofa</i> NP_001037991.1
	Rainbow trout	<i>Oncorhynchus mykiss</i> ADN92684.1
	Zebrafish a	<i>Danio rerio</i> NP_001154805.1
	Zebrafish b	NP_001096037.1
PPARD	Mouse	<i>Mus musculus</i> NP_035275.1
	Rat	<i>Rattus norvegicus</i> NP_037273.2
	Human	<i>Homo sapiens</i> NP_001165289.1
	Crab-eating macaque	<i>Macaca fascicularis</i> XP_005553282.1
	Rhesus macaque	<i>Macaca mulatta</i> AFI33297.1
	Chicken	<i>Gallus gallus</i> NP_990059.1
	African clawed frog	<i>Xenopus laevis</i> NP_001081310.1
	Japanese medaka	<i>Oryzias latipes</i> BAH58104.1
	Cow	<i>Bos taurus</i> NP_001077105.1
	Salmon	<i>Salmo salar</i> AAK76399.1
	Dog	<i>Canis lupus familiaris</i> NP_001041567.1
	Wild boar	<i>Sus scrofa</i> NP_999317.2
	Rainbow trout	<i>Oncorhynchus mykiss</i> ADN92685.1
	Zebrafish a	<i>Danio rerio</i> XP_005168343.1
	Zebrafish b	NP_571543.1
PPARG	Mouse 1	<i>Mus musculus</i> NP_001120802.1
	Mouse 2	NP_035276.2
	Rat 1	<i>Rattus norvegicus</i> NP_037256.1
	Rat 2	NP_001138838.1
	Human 1	<i>Homo sapiens</i> NP_005028.4
	Human 2	NP_056953.2
	Crab-eating macaque	<i>Macaca fascicularis</i> NP_001270028.1
	Rhesus macaque	<i>Macaca mulatta</i> NP_001028032.1
	Chicken	<i>Gallus gallus</i> NP_001001460.1
	African clawed frog	<i>Xenopus laevis</i> NP_001081312.1
	Japanese medaka	<i>Oryzias latipes</i> NP_001158348.1
	Cow 1	<i>Bos taurus</i> AAI16099.1
	Cow 2	NP_851367.1
	Salmon	<i>Salmo salar</i> CAC95231.1
	Dog	<i>Canis lupus familiaris</i> NP_001019803.1
	Wild boar	<i>Sus scrofa</i> NP_999544.1
	Rabbit	<i>Oryctolagus cuniculus</i> NP_001075617.1
	Rainbow trout	<i>Oncorhynchus mykiss</i> ADN92686.1
	Zebrafish	<i>Danio rerio</i> NP_571542.1

Supplemental data 2A: Protein alignment PPARA

		10	20	30	40	50
mmPPARA	----	MVDTES	PICPLSPLEA	DDLESPLSEE	FLQEMGNIQE	ISQSIGEESS
rnPPARA	----	MVDTES	PICPLSPLEA	DDLESPLSEE	FLQEMGNIQE	ISQSLGEESS
btPPARA	----	MEMVDTES	PIGFLSPLEA	DDLESPLSAD	FLQEMGTIQE	ISQSIGEDSS
clPPARA	----	MVDTES	PICPLSPLEA	DDLESPLSEE	FLQEMGNIQE	ISQSIGEDSS
ssPPARA	----	MVDTES	PICPLSPLEA	DDLESPLSEE	FLQEMGTIQE	ISQSIGEDSS
hsPPARA	----	MVDTES	PLCPLSPLEA	GDLESPLSEE	FLQEMGNIQE	ISQSIGEDSS
ggPPARA	----	MVDTEN	QLYPLTPLEE	DDIGSPLSGE	FLQDMENIQD	ISQSLGDDSS
xlPPARA	----	MSTIMVDTNS	ELCILTPLDE	DDLESPLSGE	FLQDIVDIQD	ITQTIGDDGS
macfPPARA	----	MVDTES	PLCPLSPLEA	GDLESPLSEE	FLQEMGNIQE	ISQSIGEDSS
macmPPARA	----	MVDTES	PLCPLSPLEA	GDLESPLSEE	FLQEMGNIQE	ISQSIGEDSS
drPPARAa	----	MVDMPS	LYSPSSPLGD	PIMYSPLSGE	LIGDMQVLED	ISQSLSDDTF
olPPARA	----	M---AAE	LYSPSSPLGD	SLLDSPLCGD	LIEDL---RK	ISASIG--DNS
drPPARAb	----	MVDMEN	RYRPPSPLEA	SVLDS---	ALFVRGMEELRD	ISQSMDEDAL
omPPARA	----	M---AR	XYPSPSPLED	SVLGSPVCGD	FLGGMEELQD	IPQSIDGDTL
salsPPARA	----	M---AS	HYRPPSPLED	SVLGSPVCGD	FLGGMEELQD	ISQSIDGDAL
Consistency	0000	*66567	464858**75	5595*87657	8866944787	*899875976
		60	70	80	90	100
mmPPARA	GSFGFADYQY	LGSCPGSEGS	V---ITDTLS	PASSPSSVSC	PVIPASTDES	
rnPPARA	GSFSFADYQY	LGSCPGSEGS	V---ITDTLS	PASSPSSVSC	PAVPTSTDES	
btPPARA	GSFSFTEYQY	LGSGPGSDGS	V---ITDTLS	PASSPSSVSY	PAVPGSAEES	
clPPARA	GSFSFTEYQY	LGSGPGSDGS	V---ITDTLS	PAPSPSSVTH	PAAPGGAEEP	
ssPPARA	GSFSFTDYQY	LGSGPGSDGS	V---ITDTLS	PASSPSSVTY	PVAPAGADES	
hsPPARA	GSFGFTEYQY	LGSCPGSDGS	V---ITDTLS	PASSPSSVTY	PVVPGSVDES	
ggPPARA	GALSLTEFQS	LGNGPGSDGS	V---ITDTLS	PASSPSSINF	ATAPGSIDES	
xlPPARA	TPFGASEHQF	FGNSPGSIGS	VSTDLTDTLS	PASSPASITF	PAASGSAEDA	
macfPPARA	GSFGFTEYQY	LGSCPGSDGS	V---ITDTLS	PASSPSSVTY	PVVPGSVDES	
macmPPARA	GSFSFTEYQY	LGSCPGSDGS	V---ITDTLS	PASSPSSVTY	PVVPGSVDES	
drPPARAa	NSFHMLDYQN	CDTAVDNSS-	---ILDVLT	PASSPSSEVF	-SASTGQDEN	
olPPARA	LEFDFPECQR	ND--SGAKSS	V---MPDPLT	PASSPSPEVC	GAAPA--AED	
drPPARAb	SSFEMTENQS	-GLSGSESS	T---ELDALT	PASSPSSGVY	G-CPVGQDEF	
omPPARA	SSLDVPEYLS	QSS--NGSEGS	T---VLDALT	PASSPSSGGY	G-AAAGLEEF	
salsPPARA	SSLDVPEYQS	QSS--NGSEGS	T---VLDALT	PASSPSSGGY	G-AAAGLEEF	
Consistency	5785658685	4762598688	700076*6*8	*9*99555	5467564795	
		110	120	130	140	150
mmPPARA	PGSALNIECR	ICGDKASGYH	YGVHACEGCK	GFFRRTIRLK	LVYDKCDRSC	
rnPPARA	PGNALNIECR	ICGDKASGYH	YGVHACEGCK	GFFRRTIRLK	LAYDKCDRSC	
btPPARA	SSIALNIECR	ICGDKASGYH	YGVHACEGCK	GFFRRTIRLK	LVYDKCDRSC	
clPPARA	SSVALNIECR	ICGDRASGYH	YGVHACEGCK	GFFRRTIRLK	LAYDKCDRSC	
ssPPARA	PSVALNIECR	ICGDKASGYH	YGVHACEGCK	GFFRRTIRLK	LVYDKCDRSC	
hsPPARA	PSGALNIECR	ICGDKASGYH	YGVHACEGCK	GFFRRTIRLK	LVYDKCDRSC	
ggPPARA	PSGAENIECR	ICGDKASGYH	YGVHACEGCK	GFFRRTIRLK	LIYDKCDRNC	
xlPPARA	ACKSLNLECR	VCSDKASGFH	YGVHACEGCK	GFFRRTIRLK	LVYDRCCERM	
macfPPARA	PSGALNIECR	ICGDKASGYH	YGVHACEGCK	GFFRRTIRLK	LVYDKCDRSC	
macmPPARA	PSGALNIECR	ICGDKASGYH	YGVHACEGCK	GFFRRTIRLK	LVYDKCDRSC	
drPPARAa	SSGSLTLECR	VCADRASGFH	YGVHACEGCK	GFFRRTIRLK	LEYDKCERNC	
olPPARA	SVGPLSLLECR	VCSDRASGFH	YGVHACEGCK	GFFRRTIRLK	LEYNKCERNC	
drPPARAb	TSTSLNLECR	VCSDRASGYH	YGVHACEGCK	GFFRRTIRLK	LEYDKCERRC	
omPPARA	SSTSLNLECR	VCADRASGYH	YGVHACEGCK	GFFRRTIRLK	LEYDKCERRC	
salsPPARA	SSTSLNLECR	VCADRASGYH	YGVHACEGCK	GFFRRTIRLK	LEYDKCERRC	
Consistency	5647888**	9*6*8***8*	*****	*****	*5*99*8*5*	
		160	170	180	190	200
mmPPARA	KIQKKNRNKC	QYCRFHKCLS	VGMSHNAIRF	GRMPRSEKAK	LKAEILTCEH	
rnPPARA	KIQKKNRNKC	QYCRFHKCLS	VGMSHNAIRF	GRMPRSEKAK	LKAEILTCEH	
btPPARA	KIQKKNRNKC	QYCRFHKCLS	VGMSHNAIRF	GRMPRSEKAK	LKAEILTCEH	
clPPARA	KIQKKNRNKC	QYCRFHKCLS	VGMSHNAIRF	GRMPRSEKAK	LKAEILTCEQ	
ssPPARA	KIQKKNRNKC	QYCRFHKCLS	AGMSHNAIRF	GRMPRSEKAK	LKAEILTCEH	
hsPPARA	KIQKKNRNKC	QYCRFHKCLS	VGMSHNAIRF	GRMPRSEKAK	LKAEILTCEH	
ggPPARA	KIQKKNRNKC	QYCRFQKCLS	VGMSHNAIRF	GRMPRSEKAK	LKAEILTGEN	
xlPPARA	KIQKKNRNKC	QYCRFEKCLN	VGMSHNAIRF	GRMPRSEKAK	LKAEVLMCDQ	
macfPPARA	KIQKKNRNKC	QYCRFHKCLS	VGMSHNAIRF	GRMPRSEKAK	LKAEILTCEH	
macmPPARA	KIQKKNRNKC	QYCRFHKCLS	VGMSHNAIRF	GRMPRSEKAK	LKAEILTCEH	
drPPARAa	KIQKKNRNKC	QYCRFNKCM	VGMSHNAIRF	GRMPQSEKQR	LKAEQDVSGK	
olPPARA	KIQKKNRNKC	QYCRFNKCM	VGMSHNAIRF	GRMPHAEKLL	LKEESKVAEK	
drPPARAb	KIQKKNRNKC	QYCRFQKCLS	VGMSHNAIRF	GRMPQSEKLR	LKAEILTGER	
omPPARA	KIQKKNRNKC	QYCRFQKCLS	VGMSHNAIRF	GRMPQSEKLL	LKAEILTGDR	
salsPPARA	KIQKKNRNKC	QYCRFQKCLS	VGMSHNAIRF	GRMPQSEKLL	LKAEILTGDR	
Consistency	*****	*****6*97	9*****	*9*79*69	*9*777575	

	210	220	230	240	250	
mmPPARA	DLKDS	ETADL	KSLGKRIHEA	YLNENNMNKV	KARVILAGKT	SNNPPFVIHD
rnPPARA	DLKDS	ETADL	KSLAKRIHEA	YLNENNMNKV	KARVILAGKT	SNNPPFVIHD
btPPARA	DLEDSE	ETADL	KSLAKRIYEA	YLNENNMNKI	KARVILAGKT	NNNPPFVIHD
clPPARA	DPEDA	ETADL	KSLAKRIYEA	YLNENNMNKV	KARVILAGKA	SNNPPFVIHD
ssPPARA	DLEDA	ETADL	KSLAKRIYEA	YLNENNMNKV	KARVILAGKA	SNNPPFVIHD
hsPPARA	DIEDSE	ETADL	KSLAKRIYEA	YLNENNMNKV	KARVILSGKA	SNNPPFVIHD
ggPPARA	YVEDSE	ETADL	KSLAKRIHDA	YLNENNMNKV	KARVILAGKT	NNNPPFVIHD
xlPPARA	DVKDTQ	ETADL	LSLARLIYDA	YLNENNMNKV	KARAILTGKA	SN-PPFVIHD
macfPPARA	DIEDSE	ETADL	KSLAKRIYEA	YLNENNMNKV	KARVILSGKA	SNNPPFVIHD
macmPPARA	DIEDSE	ETADL	KSLAKRIYEA	YLNENNMNKV	KARVILSGKA	SNNPPFVIHD
drPPARAa	EEHKCQ	QPPDM	RSLARQMHEA	YLNENNMNKA	KARVFLTGKT	S-T-PPFVIHD
olPPARA	EVESE	MEGEGD	KTLLVRQIHDA	YMKSFMTMKA	KARLILTGKT	S-E-PPFVIHD
drPPARAb	DVED---	---DQ	KTLLAKQIYEA	YVKNENNMNKS	KARTILTGKT	S-T-PPFVIHD
omPPARA	EVEDPQ	QADQ	KTLLARHIYEA	YLNENNMNKA	KARTILTGKT	S-T-PPFVIHD
salsPPARA	EVEDPQ	QADQ	KTLLARHIYEA	YLNENNMNKA	KARTILTGKT	S-T-PPFVIHD
Consistency	76784	657*6	88*886978*	*9*8*8***7	***79*6**7	845***9***

	260	270	280	290	300
mmPPARA	METLCMAEKT	LVAKMVAN	---	---	GVEDKEAE
rnPPARA	METLCMAEKT	LVAKMVAN	---	---	GVENKEAE
btPPARA	METLCMAEKT	LVAKLVAN	---	---	GIQNKAEAE
clPPARA	METLCMAEKT	LVAKLVAN	---	---	GIQNKAEAE
ssPPARA	METLCMAEKT	LVAKLVAN	---	---	GIQNKAEAE
hsPPARA	METLCMAEKT	LVAKLVAN	---	---	GIQNKAEAE
ggPPARA	MDTLCMAEKT	LVAKLVAN	---	---	GIQNKAEAE
xlPPARA	METLCMAEKT	LVAKLVAN	---	---	GIQNKAEAE
macfPPARA	METLCMAEKT	LVAKLVAN	---	---	GIQNKAEAE
macmPPARA	METLCMAEKT	LVAKLVAN	---	---	GIQNKAEAE
drPPARAa	MDTLQHA	EKK LVTQLLGN	---	---	VASGD ISTLQEREVE
olPPARA	MDTFQLA	EERT FVAKMMGMS	---	---	CGGLLNKDP
drPPARAb	METLQLAEQT	LVAKMVG	---	---	A GGHLEKEAE
omPPARA	METLQLAEQT	LVAKMVG	---	---	A GGHLEKEAE
salsPPARA	METLQLAEQT	LVAKMVG	---	---	A GSHLEKEAE
Consistency	*8*957*	*89 99988867	00 0000000000	0000000000	006867998*

	310	320	330	340	350
mmPPARA	VRFFHCCQCM	SVETVTELTE	FAKAIPGFAN	LDLNDQVTLL	KYGVYEAIIFT
rnPPARA	VRFFHCCQCM	SVETVTELTE	FAKAIPGFAN	LDLNDQVTLL	KYGVYEAIIFT
btPPARA	VRIFHCCQCT	SVETVTELTE	FAKSIPGFAN	LDLNDQVTLL	KYGVYEAIIFA
clPPARA	VRIFHCCQCT	SVETVTELTE	FAKSIPGFAN	LDLNDQVTLL	KYGVYEAIIFA
ssPPARA	VRIFHCCQCT	SVETVTELTE	FAKSIPGFAS	LDLNDQVTLL	KYGVYEAIIFA
hsPPARA	VRIFHCCQCT	SVETVTELTE	FAKAIPGFAN	LDLNDQVTLL	KYGVYEAIIFA
ggPPARA	VRIFHCCQCT	SVETVTELTE	FAKSIPGFAN	LDLNDQVTLL	KYGVYEAIIFA
xlPPARA	VRIFHCCQCT	SVETVTELTE	FAKSIPGFTE	LDLNDQVTLL	KYGVYEAMFA
macfPPARA	VRIFHCCQCT	SVETVTELTE	FAKAIPGFAN	LDLNDQVTLL	KYGVYEAIIFA
macmPPARA	VRIFHCCQCT	SVETVTELTE	FAKAIPGFAN	LDLNDQVTLL	KYGVYEAIIFA
drPPARAa	ARLFLFCQYA	SVATVTELTE	YAKAVPGFAD	LDLNDQVTLL	KYGVYEALFT
olPPARA	ARLFLHCCQST	SVETVTELTE	FAKAMPDFKT	LDLNDQVTLL	KYAVHEALFT
drPPARAb	VRIFHCCQCT	SVETVTELTE	FAKSVPGFAN	LDLNDQVTLL	KYGVHEALFA
omPPARA	VRIFHCCQCT	SVETVTELTE	FAKSVPGFSS	LDLNDQVTLL	KYGVYEALFA
salsPPARA	VRIFHCCQCT	SVETVTELTE	FAKSVPGFSS	LDLNDQVTLL	KYGVYEALFA
Consistency	8*8*88*	*87 **9*****	9**88*9*76	*****	**9*8*8*7

	360	370	380	390	400
mmPPARA	MLSSLMNKDG	MLIAYGNGFI	TREFLKNLRK	PFCDIMEPKF	DFAMKFNAL
rnPPARA	MLSSLMNKDG	MLIAYGNGFI	TREFLKNLRK	PFCDIMEPKF	DFAMKFNAL
btPPARA	MLSSVMNKDG	MLVAYGNGFI	TREFLKSLRK	PFCDIMEPKF	DFAMKFNAL
clPPARA	MLSSVMNKDG	MLVAYGNGFI	TREFLKSLRK	PFCDIMEPKF	DFAMKFNAL
ssPPARA	MLSSVMNKDG	MLVAYGNGFI	TREFLKSLRK	PFCDIMEPKF	DFAMKFNAL
hsPPARA	MLSSVMNKDG	MLVAYGNGFI	TREFLKSLRK	PFCDIMEPKF	DFAMKFNAL
ggPPARA	MLASVMNKDG	MLVAYGNGFI	TREFLKSLRK	PFCDIMEPKF	DFAMKFNAL
xlPPARA	MLASVMNKDG	MLVAYGNGFI	TREFLKSLRK	PIGDMMEPKF	EFAMKFNAL
macfPPARA	MLSSVMNKDG	MLVAYGNGFI	TREFLKSLRK	PFCDIMEPKF	DFAMKFNAL
macmPPARA	MLSSVMNKDG	MLVAYGNGFI	TREFLKSLRK	PFCDIMEPKF	DFAMKFNAL
drPPARAa	LLASCMNKDG	LLVAQGGGFI	TREFLKSLRK	PFSDMMEPKF	QFAMKFNAL
olPPARA	LLASCMNKDG	LLVARGGFI	TREFLKSLRR	PFSDMMEPKF	QFATRFNSMD
drPPARAb	LLASCMNKDG	LLVAYGSGFI	TREFLKSLRR	PFSDMMEPKF	QFAMKFNSLE
omPPARA	LLASCMNKDG	LLVAYGSGFI	TREFLKSLRR	PFSDMMEPKF	QFAMKFNGL
salsPPARA	LLASCMNKDG	LLVAYGSGFI	TREFLKSLRR	PFSDMMEPKF	QFAMKFNGL
Consistency	8*8*6*****	8*9*8*7***	*****8**8	*95*7*****	7**99**799

	410.....	420.....	430.....	440.....	450
mmPPARA	LDDSDISLFV	AAIICCGDRP	GLLNIGYIEK	LQEGIVHVLK	LHLQSNHPDD	
rnPPARA	LDDSDISLFV	AAIICCGDRP	GLLNIGYIEK	LQEGIVHVLK	LHLQSNHPDD	
btPPARA	LDDSDISLFV	AAIICCGDRP	GLLNVGHIEK	MQEGIVHVLK	LHLQNNHPDD	
clPPARA	LDDSDISLFV	AAIICCGDRP	GLLNVGHIEK	MQEGIVHVLK	LHLQTNHPDN	
ssPPARA	LDDSDISLFV	AAIICCGDRP	GLLNVGHIEK	MQEGIVHVLK	LHLQTNHPDD	
hsPPARA	LDDSDISLFV	AAIICCGDRP	GLLNVGHIEK	MQEGIVHVLK	LHLQSNHPDD	
ggPPARA	LDDSDISLFV	AAIICCGDRP	GLLNVGHIEK	MQEGIVHVLK	LHLQTNHPDD	
xlPPARA	LDDSDISLFV	AAIICCGDRP	GLVNIPISEK	MQESIVHVLK	LHLQSNHPDD	
macfPPARA	LDDSDISLFV	AAIICCGDRP	GLLNVGHIEK	MQEGIVHVLK	LHLQSNHPDD	
macmPPARA	LDDSDISLFV	AAIICCGDRP	GLLNVGHIEK	MQEGIVHVLK	LHLQSNHPDD	
drPPARAa	LDDSDALFV	AAIICCGDRP	GLSNVPQIER	IQESVIHSLR	LHLTSNHPDN	
olPPARA	LDDSDALFV	AAIICCGDRP	GLVDIPVVER	LQESI IQALR	HHLLANHPDD	
drPPARAb	LDDSDALFV	AAIICCGDRP	GLVNVPHIER	MQESIVNVLIH	LHLKSNHPDH	
omPPARA	LDDSDALFV	AAIICCGDRP	GLVNVTHIEC	MQENIVQVLQ	LHLLANHPDD	
salsPPARA	LDDSDALFV	AAIICCGDRP	GLVNVTHIEC	MQENIVQVLQ	LHLLANHPDD	
Consistency	*****88***	**9*8*****	**799569*6	8**69978*6	8**67****7	

	460.....	470.....	480.....	490.....	
mmPPARA	TFLFPKLLQK	MVDLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
rnPPARA	TFLFPKLLQK	MVDLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
btPPARA	VFLFPKLLQK	MADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
clPPARA	IFLFPKLLQK	MADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
ssPPARA	VFLFPKLLQK	LADLRQLVTE	HAQLVQVIKK	TEADAALHPL	LQEIYRDMY	
hsPPARA	IFLFPKLLQK	MADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
ggPPARA	IFLFPKLLQK	MADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
xlPPARA	SFLFPKLLQK	MADLRQLVTE	HAQLVQVIKK	TETDAALHPL	LQEIYRDMY	
macfPPARA	IFLFPKLLQK	MADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
macmPPARA	IFLFPKLLQK	MADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
drPPARAa	SLFLFPKLLQK	LADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
olPPARA	TFLFPKLLQK	LADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
drPPARAb	GFLFPKLLQK	LADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
omPPARA	TFLFPKLLQK	LADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
salsPPARA	TFLFPKLLQK	LADLRQLVTE	HAQLVQVIKK	TESDAALHPL	LQEIYRDMY	
Consistency	59***8****	88***9****	**9*9*5*9*6	9*3*77****	*****9***	



Supplemental data 2B: Protein alignment PPARD

Unconserved 0 1 2 3 4 5 6 7 8 9 10 Conserved

 10	20	30	40	50
mmPPARD	-----	-----	-----	-----	-----
rnPPARD	-----	-----	-----	-----	-----
ggPPARD	-----	-----	-----	-----	-----
hsPPARD	-----	-----	-----	-----	-----
macfPPARD	-----	-----	-----	-----	-----
macmPPARD	-----	-----	-----	-----	-----
btPPARD	-----	-----	-----	-----	-----
ssPPARD	-----	-----	-----	-----	-----
clPPARD	-----	-----	-----	-----	-----
omPPARD	-----	-----	-----	-----	-----
olPPARD	MDGFQHSAAK	QF--EGVNGY	FEP-ASPQDT	ADVRWKHPEG	-E
drPPARDb	MEQVEEPTSE	MKCDGQVDGV	MKS-QSSLQT	ELSSVPILRD	-AAWLGAQEG
drPPARDa	-----	MSV	CEMDRRHVLA	LRSRLPRNLG	SVGGVYM-DP
xlPPARD	-----	-----	-----	-----	-----
salsPPARD	-----	-----	-----	-----	-----
Consistency	0000000000	0000000000	0000000000	0000000000	0000000000
 60	70	80	90	100
mmPPARD	-----	MEQPQE	ETPEARREEEK	E	EVAM GDG
rnPPARD	-----	MEQPQE	ETPEARREEEK	E	EVAT GDG
ggPPARD	-----	MEQLQEEVP	EVREEEEEEE	E	AVTV PSG
hsPPARD	-----	MEQPQE	APEVREEEEK	E	EVAE AEG
macfPPARD	-----	MEQPQE	APEVREEEEK	E	EVAE AEG
macmPPARD	-----	MEQPQE	APEVREEEEK	E	EVAE AEG
btPPARD	-----	MEQPPE	APEARPEEEK	E	EAAG AEG
ssPPARD	-----	MEQPPE	APEVREEEEK	K	EVAE AEG
clPPARD	-----	MEQPPGE	AAEVREEEEK	K	EVAE AEG
omPPARD	-----	M-KSSDE	--EVVQEQE	D	QQEK GSS
olPPARD	-SAGSDSCG	-ETSGFELTD	VQELKTRES	DEEGKEEAPP	SKSPKRDPKK
drPPARDb	ESASSDCGGT	SDLQEPSSVS	GEEVEGSETS	DITGLEASPG	SKGSWGGNQO
drPPARDa	GDSSPCSSQG	EGPDDQRLQD	VLCELGEAG	LNLELESEGG	VA-----L
xlPPARD	-----	-----	-----	-----	-----
salsPPARD	-----	-----	-----	-----	-----
Consistency	0000000000	0445335300	3244335644	4000005443	4450000000
 110	120	130	140	150
mmPPARD	-----	APELN	GGPEHTLPSS	SCADLSQNSS	PSS--LLDQLQ
rnPPARD	-----	APELN	GGPEHTLPSS	SCTDLSQNSS	PSS--LLDQLQ
ggPPARD	-----	ASDPS	AGPDSSLPSS	SYTDLSQSSS	P--S--LSDQLQ
hsPPARD	-----	APELN	GGPQHALPSS	SYTDLSRSSS	PPS--LLDQLQ
macfPPARD	-----	APELN	GGPQHALPSS	SYTDLSRSSS	PPS--LLDQLQ
macmPPARD	-----	APELN	GGPQHALPSS	SYTDLSRSSS	PPS--LLDQLQ
btPPARD	-----	APELN	GGPEHSLPSS	SYTDLSQSCS	PLS--LLDQLQ
ssPPARD	-----	GPELN	GGPEHSLPSS	SCTDLSQSCS	PPA--LLDQLQ
clPPARD	-----	APELN	GGPEHSLPSS	SYTDLSRSSS	PPS--LLDQLQ
omPPARD	-----	NSHST	SNMDSPALSS	SCTDLSQTSS	P--S--LSDQLL
olPPARD	REGECQDQEN	NQNKQNNNAS	SSYTDLSHTS	SPS--LSEQLR	LGREDNAGSG
drPPARDb	NGDRTPQESP	PPNSETPVTA	GAFSDPLQVP	SLS--LSDQLR	LGREDPNKLG
drPPARDa	QGEELSWETS	RQEEQSNTSS	TSPDRSSAST	DLS--TALSEQ	LLRGREEVSG
xlPPARD	-----	-----	MKEEIP	PRSP--ILDEQP	STPLEHQETS
salsPPARD	-----	-----	-----	-----	-----
Consistency	0000043535	4444444467	6346565556	6280757766	6635445355
 160	170	180	190	200
mmPPARD	LNMECRVCGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	KCDRICKIQK
rnPPARD	LNMECRVCGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	KCDRICKIQK
ggPPARD	LNVECRVCGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	KCERSCKIQK
hsPPARD	LNMECRVCGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	KCERSCKIQK
macfPPARD	LNMECRVCGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	KCERSCKIQK
macmPPARD	LNMECRVCGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	KCERSCKIQK
btPPARD	LNMECRVCGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	KCERICKIQK
ssPPARD	LSMECRVCGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	KCERICKIQK
clPPARD	LNMECRVCGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	KCERICKIQK
omPPARD	LNVECRICGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLDYE	RCERSCKIQK
olPPARD	ISVECKVCGD	KASGFHYGVH	ACEGCKGFFR	RTVRMKLEYE	RCERSCKIQK
drPPARDb	LNVECRICGD	KASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	RCERACKVQK
drPPARDa	LNMECRICGD	RASGFHYGVH	ACEGCKGFFR	RTIRMKLEYE	RCERSCKIQK
xlPPARD	QSVCKICGD	RASGFHYGVH	ACEGCKGFFR	RTIRMLQYE	HCDRNCKIQK
salsPPARD	-----	-----	-----	-----	-CERRCKIQK
Consistency	6768878888	7888888888	8888888888	8888888788	6*8*5**9**

	210.	220.	230.	240.	250
mmPPARD	KNRNKCQYCR	FQKCLALGMS	HNAIRFGRMP	EAEKRRLVAG	LTASE-GCQH
rnPPARD	KNRNKCQYCR	FQKCLALGMS	HNAIRFGRMP	EAEKRRLVAG	LTASE-GCQQ
ggPPARD	KNRNKCQYCR	FQKCLSLGMS	HNAIRFGRMP	EAEKRRLVAG	LTASE-ISCQ
hsPPARD	KNRNKCQYCR	FQKCLALGMS	HNAIRFGRMP	EAEKRRLVAG	LTANE-GSQY
macfPPARD	KNRNKCQYCR	FQKCLALGMS	HNAIRFGRMP	EAEKRRLVAG	LTANE-GSQY
macmPPARD	KNRNKCQYCR	FQKCLALGMS	HNAIRFGRMP	EAEKRRLVAG	LTANE-GSQY
btPPARD	KNRNKCQYCR	FQKCLALGMS	HNAIRFGRMP	EAEKRRLVAG	LTANE-GSQH
ssPPARD	KNRNKCQYCR	FQKCLALGMS	HNAIRFGRMP	EAEKRRLVAG	LTANE-GSQH
clPPARD	KNRNKCQYCR	FQKCVLALGMS	HNAIRFGRMP	EAEKRRLVAG	LTANE-GTQH
omPPARD	KSRNKCQYCR	FQKCLLLGMS	HDAIRYGRMP	EAEKRRLVAG	LLAGEKAPT
olPPARD	KNRNKCQYCR	FQKCLSLGMS	HDAIRYGRMP	EAEKRRLVAG	LLAEE-MNLS
drPPARDb	KSRNKCQYCR	FQKCLALGMS	HDAIRYGRMP	EAEKRRLVAG	LLAGE--NPQ
drPPARDa	KSRNKCQYCR	FQKCLMLGMS	HDAIRYGRMP	EAEKRRLVAG	LLAGE-RGSQ
xlPPARD	KNRNKCQYCR	FNKCLSLGMS	HNAIRFGRMP	EAEKRRLVQA	PVSDS--AAP
salsPPARD	KSRNKCQYCR	FQKCLLLGMS	HDAIRYGRMP	EAEKRRLVAG	LLAGDTAPT
Consistency	*8*****9**	*9**96****	*7***8****	*9*99***99	8695803454

	260.	270.	280.	290.	300
mmPPARD	NPQLADLKAF	SKHIYNAYLK	NFNMTKKKAR	SILTGKSSHN	A-----PFVI
rnPPARD	NPQLADLKAF	SKHIYNAYLK	NFNMTKKKAR	SILTGKSSHN	A-----PFII
ggPPARD	NPQVADLKAF	SKHIYNAYLK	NFNMTKKKAR	GILTGKASST	P-----PFVI
hsPPARD	NPQVADLKAF	SKHIYNAYLK	NFNMTKKKAR	SILTGKASHT	A-----PFVI
macfPPARD	NPQVADLKAF	SKHIYNAYLK	NFNMTKKKAR	SILTGKASHT	A-----PFVI
macmPPARD	NPQVADLKAF	SKHIYNAYLK	NFNMTKKKAR	SILTGKASHT	A-----PFVI
btPPARD	NPQVADLKAF	SKHIYSAYLK	NFNMTKKKAR	GILTGKASHT	A-----PFVI
ssPPARD	NPQVADLKAF	SKHLYSAYLK	NFNMTKKKAR	AILTGKASHT	A-----PFVI
clPPARD	NPQVADLKAF	SKHIYNAYLK	NFNMTKKKAR	GILTGKASHT	A-----PFVI
omPPARD	NPNSSDLKSL	AKRVNNAYLK	NLNMTKKKAR	SILTGKTSST	PVAYPYPFVI
olPPARD	KPGGSDLKTL	AKQVNTAYQK	NLSMTKKKAR	SILTGKTSST	S-----PFVI
drPPARDb	SSSGADLKTL	AKHVNTAYLR	NLNMTKKKAR	SILTGKTSCT	A-----PFVI
drPPARDa	NSNESDLKTL	AKRVNNAYLK	NLNMTKKKAR	NILTGKTSAS	T-----PFVI
xlPPARD	DSPVSDLDVL	SQLIHSSYMN	TFTMTKKRAR	DILTGGRNIS	-----PFVI
salsPPARD	NPNGSDLKSL	AKRVNNAYLK	NLNMTKKKAR	SILTGKNSSS	PVAYPYPFVI
Consistency	87648**877	8969579*88	978*****9**	6*****96*57	500000**9*

	310.	320.	330.	340.	350
mmPPARD	HDIETLWQAE	KGLVWKQLVN	GLPPYNEISV	HVFYRCQSTT	VETVRELTEF
rnPPARD	HDIETLWQAE	KGLVWKQLVN	GPPPYNEISV	HVFYRCQSTT	VETVRELTEF
ggPPARD	HDMDTLWQAE	KGLVWKQLVN	GIPPYKEIGV	HVFYRCQCTT	VETVRELTEF
hsPPARD	HDIETLWQAE	KGLVWKQLVN	GLPPYKEISV	HVFYRCQCTT	VETVRELTEF
macfPPARD	HDIETLWQAE	KGLVWKQLVN	GLPPYKEISV	HVFYRCQCTT	VETVRELIEF
macmPPARD	HDIETLWQAE	KGLVWKQLVN	GLPPYKEISV	HVFYRCQCTT	VETVRELIEF
btPPARD	HDIETLWQAE	KGLVWKQLVN	SLPPYKEISV	HVFYRCQCTT	VETVRELTEF
ssPPARD	HDIETLWQAE	KGLVWKQLVN	GLPPYKEISV	HVFYRCQCTT	VETVRELTEF
clPPARD	HDIETLWQAE	KGLVWKQLVN	GLPPYKEISV	HVFYRCQCTT	VETVRELTEF
omPPARD	HDMDSLQAE	NGLVWKQLIN	GTTPNKEIGV	HVFYRCQCTT	VETVRELTEF
olPPARD	YDVETLWKAE	SGLVWSQLVP	GAPLTKEIGV	HVFYRCQCTT	VETVRELTEF
drPPARDb	HDMDSLQAE	NGLVWNQLNG	A-PLNKEIGV	HVFYRCQCTT	VETVRELTEF
drPPARDa	HDMDSLQAE	NGLVWNQVIH	GAPPNKEIGV	HVFYRCQCTT	VETVRELTEF
xlPPARD	HDMDTLWQAE	QGTVWEQLPT	QNLTGTEIGV	HVFYRCQCTS	VETVRALTDF
salsPPARD	HDMDSLQAE	NGLVWNQLIN	GTTPNKEIGV	HVFYRCQCTT	VETVRELTEF
Consistency	9*788**69**	6*9**7*976	747757**7*	*****8*9	*****9*89*

	360.	370.	380.	390.	400
mmPPARD	AKNIPNFSLL	FLNDQVTLLK	YGVHEAIFAM	LASIVNKDGL	LVANGSGFVT
rnPPARD	AKNIPNFSLL	FLNDQVTLLK	YGVHEAIFAM	LASIVNKDGL	LVANGSGFVT
ggPPARD	AKSIPSFIDL	YLNDQVTLLK	YGVHEAIFAM	LASIMNKDGL	LVANGNGFVT
hsPPARD	AKSIPSFSSLL	FLNDQVTLLK	YGVHEAIFAM	LASIVNKDGL	LVANGSGFVT
macfPPARD	AKSIPSFSSLL	FLNDQVTLLK	YGVHEAIFAM	LASIVNKDGL	LVANGSGFVT
macmPPARD	AKSIPSFSSLL	FLNDQVTLLK	YGVHEAIFAM	LASIVNKDGL	LVANGSGFVT
btPPARD	AKSIPSFIDL	FLNDQVTLLK	YGVHEAIFAM	LASIVNKDGL	LVANGTGFVT
ssPPARD	AKSIPSFIDL	FLNDQVTLLK	YGVHEAIFAM	LASIVNKDGL	LVANGTGFVT
clPPARD	AKSIPSFSSLL	FLNDQVTLLK	YGVHEAIFAM	LASIVNKDGL	LVANGTGFVT
omPPARD	AKSIPSGFVLD	FLNDQVTLLK	YGVHEAIFAM	LPSLMNKDGL	LVANGKGFVT
olPPARD	AKCIPGFDL	YLNDQVTLLK	YGVHGAIFAM	LPSLMNKDGL	LVANGKGFVT
drPPARDb	AKNIPGFDL	FLNDQVTLLK	YGVHEAIFAM	LPSLMNKDGL	LVANGKGFVT
drPPARDa	AKSIPGFDL	FLNDQVTLLK	YGVHEAIFAM	LPSLMNKDGL	LVANGRGFVT
xlPPARD	AKRIPGFDL	FLNDQVTLLK	YGVHEAIFCM	LASLMNKDGL	LVAGGRGFVT
salsPPARD	AKSIPGFDL	FLNDQVTLLK	YGVHEAIFAM	LPSLMNKDGL	LVANGKGFVT
Consistency	9*6**6*45*	8*****	****8***9*	*6*87*****	***9*5****

	410.	420.	430.	440.	450
mmPPARD	HEFLRSLRKP	FSDIIEPKFE	FAVKFNALEL	DDSDLALFIA	AIILCGDRPG					
rnPPARD	HEFLRSLRKP	FSDIIEPKFE	FAVKFNALEL	DDSDLALFIA	AIILCGDRPG					
ggPPARD	REFLRTLRLKP	FNEIMEPKFE	FAVKFNALEL	DDSDLALFVA	AIILCGDRPG					
hsPPARD	REFLRLSLRKP	FSDIIEPKFE	FAVKFNALEL	DDSDLALFIA	AIILCGDRPG					
macfPPARD	REFLRLSLRKP	FSDIIEPKFE	FAVKFNALEL	DDSDLALFIA	AIILCGDRPG					
macmPPARD	REFLRLSLRKP	FSDIIEPKFE	FAVKFNALEL	DDSDLALFIA	AIILCGDRPG					
btPPARD	REFLRLSLRKP	FSDIIEPKFE	FAVKFNALEL	DDSDLALFIA	AIILCGDRPG					
ssPPARD	REFLRLSLRKP	FSDIIEPKFE	FAVKFNALEL	DDSDLALFIA	AIILCGDRPG					
clPPARD	REFLRLSLRKP	FSDIIEPKFE	FAVKFNALEL	DDSDLALFIA	AIILCGDRPG					
omPPARD	REFLRLSLRRP	FSEIMEPKLE	FAVKFNALEL	DDSDLALFVA	AIILCGDRPG					
olPPARD	REFLRLSLRKP	FSEIMEPKFE	FAVKFNALEL	DDSDLALFVA	AIILCGDRPG					
drPPARDb	REFLRLSLRKP	FSEIMEPKFE	FAVKFNALEL	DDSDLALFVA	AIILCGDRPG					
drPPARDa	REFLRLSLRKP	FSEIMEPKFE	FAVKFNALEL	DDSDLALFVA	AIILCGDRPG					
xlPPARD	REFLRLSLRQP	FCHIMEPKFH	FASKFNALEL	NDSDLALFVA	SIILCGDRPG					
salsPPARD	REFLRLSLRRP	FSEIMEPKFE	FAVKFNALEL	DDSDLALFVA	AIILCGDRPG					
Consistency	8****99*8*	*87*7****99	**9*****	9****9**9*	9*****7					

	460.	470.	480.	490.	500
mmPPARD	LMNVQVEAI	QDTILRALEF	HLQVNHPDSQ	YLFPKLLQKM	ADLRQLVTEH					
rnPPARD	LMNVQVEAI	QDTILQALEF	HLQVNHPDSQ	YLFPKLLQKM	ADLRQLVTEH					
ggPPARD	LMNVKQVEEI	QDNILRALEF	HLQSNHPDAQ	YLFPKLLQKM	ADLRQLVTEH					
hsPPARD	LMNVPRVEAI	QDTILRALEF	HLQANHPDAQ	YLFPKLLQKM	ADLRQLVTEH					
macfPPARD	LMNVQVEAI	QDTILRALEF	HLQANHPDAQ	YLFPKLLQKM	ADLRQLVTEH					
macmPPARD	LMNVQVEAI	QDTILRALEF	HLQANHPDAQ	YLFPKLLQKM	ADLRQLVTEH					
btPPARD	LMNVQVEAI	QDTILRALEF	HLQANHPDAQ	YLFPKLLQKM	ADLRQLVTEH					
ssPPARD	LMNVQVEAI	QDTILRALEF	HLQANHPDAQ	YLFPKLLQKM	ADLRQLVTEH					
clPPARD	LINVPQVEAI	QDTILRALEF	HLQANHPYAQ	YLFPKLLQKM	ADLRQLVTEH					
omPPARD	LMNIKQVEEI	QDSILQALDQ	HLLANHTDSK	YLFPKLLNKM	ADLRQLVTEN					
olPPARD	LMNVKQVEQS	QDNILQALDL	HLQANHSDSL	YLFPKLLQKM	ADLRQLVTEN					
drPPARDb	LMNVKQVEQI	QDGILQALDQ	HLQVHHPDSS	HLFPKLLQKM	ADLRQLVTEN					
drPPARDa	LMNVHQVEKI	QDSILQALNQ	HLQLNHPDGR	FIFPRLQLKL	ADLRQLVTEN					
xlPPARD	LINPSQVEDI	QEGILGALRR	HLKASHTDAP	FLFPKLLHKM	ADLRQLVTEH					
salsPPARD	LMNIKQVEEI	QDSILQALDQ	HLLGNHADSH	YLFPKLLNKM	ADLRQLVTEN					
Consistency	*8*859**59	*96**6**75	**768*6875	89**9**7*9	*****7					

	510.	520.
mmPPARD	AQMMQWLKKT	ESETLLHPLL	QEIIYKDMY		
rnPPARD	AQMMQWLKKT	ESETLLHPLL	QEIIYKDMY		
ggPPARD	AQLVQKIKKT	ETETSLHPLL	QEIIYKDMY		
hsPPARD	AQMMQRIKKT	ETETSLHPLL	QEIIYKDMY		
macfPPARD	AQMMQRIKKT	ETETSLHPLL	QEIIYKDMY		
macmPPARD	AQMMQRIKKT	ETETSLHPLL	QEIIYKDMY		
btPPARD	AQMMQRIKKT	ETETSLHPLL	QEIIYKDMY		
ssPPARD	AQMMQRIKKT	ETETSLHPLL	QEIIYKDMY		
clPPARD	AQMMQRIKKT	ETETSLHPLL	QEIIYKDMY		
omPPARD	AMLVQKIKKT	ESETSLHPLL	QEIIYRDMY		
olPPARD	AQLVQKIKKT	ESETSLHPLL	QEIIYKDMY		
drPPARDb	AQLVQMIKKT	ESETSLHPLL	QEIIYKDMY		
drPPARDa	AQLVQKIKKT	ESETSLHPLL	QEIIYRDMY		
xlPPARD	AELVQSIKRT	ESSAALHPLL	QEIIYRDMY		
salsPPARD	AMLVQKIKKT	ESETSLHPLL	QEIIYRDI		
Consistency	*887*59*9*	*7997*****	****8*99		

Supplemental data 2C: Protein alignment PPARG

Unconserved 0 1 2 3 4 5 6 7 8 9 10 Conserved

	10	20	30	40	50
mmPPARGi1	-----	-----	-----	MVDTEMPF-W	PTNFGISSV
rnPPARGi2	-----	-----	-----	MVDTEMPF-W	PTNFGISSV
macfPPARG	-----	-----	-----	MVDTEMPF-W	PTNFGISSV
ggPPARG	-----	-----	-----	MVDTEMPF-W	PVNFGISPV
ocPPARG	-----	-----	-----	MVDTEMPF-W	PTNFGIGSV
mmPPARGi2	MGETLGDSPV	DPEHGAFADA	LPMSTSQEIT	MVDTEMPF-W	PTNFGISSV
rnPPARGi1	MGETLGDPFV	DPEHGAFADA	LPMSTSQEIT	MVDTEMPF-W	PTNFGISSV
btPPARGi2	MGETLGDAI	DPESEPFVAVT	VSARTSQEIT	MVDTEMPF-W	PTNFGISSV
clPPARG	MGETLGDSL	DPESDSFADT	LSASTSQETT	MVDTEMPF-W	PTNFGISSV
ssPPARG	MGETLGDSL	DPESDAF-DT	LSANISQEV	MVDTEMPF-W	PTNFGISSV
hsPPARGi2	MGETLGDSPI	DPESDSFDT	LSANISQEMT	MVDTEMPF-W	PTNFGISSV
macmPPARG	MGETLGDSPI	DPESDSFDT	LSANISQEIT	MVDTEMPF-W	PTNFGISSV
drPPARG	-----	-MLHRRFS-	-VQKASLSAD	MVDTQTFG-W	PVGFGLSAL
hsPPARGi1	-----	-----	-MT	MVDTEMPF-W	PTNFGISSV
btPPARGi1	-----	-----	-----	MVDTEMPF-W	PTNFGISSV
xlPPARG	-----	-----	-----	MVDTEMPF-W	SNLNFGMNSM
olPPARG	-----	-----	-----	MVDTQQLLAW	P-VGFSLSSTV
salsPPARG	-----	-----	-----	MVDTRRAA-W	SLLSFGLGTL
omPPARG	-----	-----	-----	MVDTRRAA-W	SLLSFGLGTL
Consistency	1111111001	1111001000	1010011111	****87670*	0678*98878
	60	70	80	90	100
mmPPARGi1	DLSVMEDHSH	SFDIKPFTTV	DFSSISAPHY	E	-----
rnPPARGi2	DLSVMDDHSH	SFDIKPFTTV	DFSSISAPHY	E	-----
macfPPARG	DLSVMDDHSH	SFDIKPFTTV	DFSSISAPHY	E	-----
ggPPARG	DLSAMDDHMH	SFDIKPFTTV	DFSSISSPHY	E	-----
ocPPARG	DLSVMDDHSH	SFDIKPFTTV	DFSSISAPHY	E	-----
mmPPARGi2	DLSVMEDHSH	SFDIKPFTTV	DFSSISAPHY	E	-----
rnPPARGi1	DLSVMDDHSH	SFDIKPFTTV	DFSSISAPHY	E	-----
btPPARGi2	DLSMDDHSH	AFDIKPFTTV	DFSSISTPHY	E	-----
clPPARG	DLSVMDDHSH	SFDIKPFTTV	DFSSISTPHY	E	-----
ssPPARG	DLSVMDDHSH	SFDIKPFTTV	DFSSISTPHY	E	-----
hsPPARGi2	DLSVMEDHSH	SFDIKPFTTV	DFSSISTPHY	E	-----
macmPPARG	DLSVMDDHSH	SFDIKPFTTV	DFSSISAPHY	E	-----
drPPARG	ELEELEDTH	SLDIKPFSTL	DYSSISGIDY	E	-----
hsPPARGi1	DLSVMEDHSH	SFDIKPFTTV	DFSSISTPHY	E	-----
btPPARGi1	DLSMDDHSH	AFDIKPFTTV	DFSSISTPHY	E	-----
xlPPARG	DMSALEDHQC	PYDIKPFTTV	DFSSIN-SHY	D	-----
olPPARG	DLPEFNDSSH	CLDMKHLSTS	DYASISSSSI	P	-----
salsPPARG	DLVEMDNKMN	SFDMKTLSTL	DYPYLPSSLEY	SHNS	-----
omPPARG	DLAEMDNKMN	SFDMETLSTL	DYPYLPSSLEY	SHNSPHHHSP	DRSHSFNHSP
Consistency	9976879778	78*89788*8	*888985679	7000000000	0000000000
	110	120	130	140	150
mmPPARGi1	DIP	FT	RADP	-----	MVADYKYD
rnPPARGi2	DIP	FT	RADP	-----	MVADYKYD
macfPPARG	DIP	FT	RTDP	-----	MVADYKYD
ggPPARG	DIP	LG	RADQ	-----	TSIDYKYD
ocPPARG	DLP	FA	RADP	-----	MVADYKYD
mmPPARGi2	DIP	FT	RADP	-----	MVADYKYD
rnPPARGi1	DIP	FT	RADP	-----	MVADYKYD
btPPARGi2	DIP	FP	RADP	-----	MVADYKYD
clPPARG	DIP	FS	RADP	-----	MVADYKYD
ssPPARG	DIP	FP	RADP	-----	MVADYKYD
hsPPARGi2	DIP	FT	RTDP	-----	VVADYKYD
macmPPARG	DIP	FT	RTDP	-----	MVADYKYD
drPPARG	NNP	T	QNDPT	-----	P-HMMDLTHMYS
hsPPARGi1	DIP	FT	RTDP	-----	VVADYKYD
btPPARGi1	DIP	FP	RADP	-----	MVADYKYD
xlPPARG	DILDEKTEFLC	RNDQ	-----	-----	SPIDYKYD
olPPARG	-----	SS	LSPP	-----	LVSSMSSTGM
salsPPARG	PHHHHSP	DRSHSCNHSP	DRSHS	-----	FNHSP
omPPARG	DRSQSFNHSP	DRNHSINHSP	DRSYSYNHRS	DRSHSFNHSP	DRSHSFNHSP
Consistency	0000000000	8660000065	7587000000	0000000000	0065777777


```
..... 160. .... 170. .... 180. .... 190. .... 200
mmPPARGi1 LKLQ EY-----QSAIKVE PASPPYYSEK
rnPPARGi2 LKLQ EY-----QSAIKVE PASPPYYSEK
macfPPARG LKLQ EY-----QSAIKVE PASPPYYSEK
ggPPARG IKLQDC-----QSAIKME PPSPPYFSEK
ocPPARG LKLQ EY-----QSAIKVE PASPPYYSEK
mmPPARGi2 LKLQ EY-----QSAIKVE PASPPYYSEK
rnPPARGi1 LKLQ EY-----QSAIKVE PASPPYYSEK
btPPARGi2 LKLQ EY-----QSAIKVE PVSPPYYSEK
clPPARG LKLQ EY-----QSAIKVE PASPPYYSEK
ssPPARG LKLQDY-----QSAIKVE PVSPPYYSEK
hsPPARGi2 LKLQ EY-----QSAIKVE PASPPYYSEK
macmPPARG LKLQ EY-----QSAIKVE PASPPYYSEK
drPPARG YRTQENYRTH EPIYRPEHSS YSPEENTYRA QQI QNSIKLE PESPPQFAEN
hsPPARGi1 LKLQ EY-----QSAIKVE PASPPYYSEK
btPPARGi1 LKLQ EY-----QSAIKVE PVSPPYYSEK
xlPPARG LKLQEC-----QSSIKLE PPSPPYFSDK
olPPARG AYDPSS PQSE DHLTNMDY--TNLHSYRTE LDT HSSVKLE PDSPPQYSDS
salsPPARG DRNHSFNHSP DRSHSFNHSP DRSHSYNDTY SVY QGSVNDK PLSPSQSSDC
omPPARG DRSSQSFNHSP DRNHSFNHSP DRSHSYNHRS DRSHSFNHSP DRSHSFNHSP
Consistency 6868760000 0000000000 0000000000 0008878878 95*9877887
```

```
..... 210. .... 220. .... 230. .... 240. .... 250
mmPPARGi1 TQLYNRP-----HEEPSNSLM AIECRVCGDK
rnPPARGi2 TQLYNRP-----HEEPSNSLM AIECRVCGDK
macfPPARG TQLYNKP-----HEEPSNSLM AIECRVCGDK
ggPPARG VQLYNKP-----HEEPSNSLM AIECRVCGDK
ocPPARG TQLYNKT-----HEEPSNSLM AIECRVCGDK
mmPPARGi2 TQLYNRP-----HEEPSNSLM AIECRVCGDK
rnPPARGi1 TQLYNRP-----HEEPSNSLM AIECRVCGDK
btPPARGi2 TQLYSKP-----HEEPSNSLM AIECRVCGDK
clPPARG TQLYNKP-----HEEPSNSLM AIECRVCGDK
ssPPARG TQLYNKP-----HEEPSNSLM AIECRVCGDK
hsPPARGi2 TQLYNKP-----HEEPSNSLM AIECRVCGDK
macmPPARG TQLYNKP-----HEEPSNSLM AIECRVCGDK
drPPARG SVSFSKT-----PEDPSSSSL NIECRVCGDK
hsPPARGi1 TQLYNKP-----HEEPSNSLM AIECRVCGDK
btPPARGi1 TQLYSKP-----HEEPSNSLM AIECRVCGDK
xlPPARG PQCSKA-----FEDTPNSFI AIECRVCGDK
olPPARG PVFSKLP-----EDTPSSSL NIECRVCGDK
salsPPARG SIVSLSR FRP HSNP-----FTYTDASSLL NIDCRVCGDK
omPPARG DRSHSFNHSP DRSHSFNHSP DKSHSYNYTY SGNQNASPL NIDCRVCGDK
Consistency 6776766000 0000000000 0000000000 0688678*78 7*9*****
```

```
..... 260. .... 270. .... 280. .... 290. .... 300
mmPPARGi1 ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
rnPPARGi2 ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
macfPPARG ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
ggPPARG ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
ocPPARG ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
mmPPARGi2 ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
rnPPARGi1 ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
btPPARGi2 ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
clPPARG ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
ssPPARG ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
hsPPARGi2 ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
macmPPARG ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
drPPARG ASGFHYGVHA CEGCKGFFRR TIRLKL VYDH CDLHCR IHKK SRNKCQYCRF
hsPPARGi1 ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
btPPARGi1 ASGFHYGVHA CEGCKGFFRR TIRLKL IYDR CDLNCRIHKK SRNKCQYCRF
xlPPARG ASGFHYGVHA CEGCKGFFRR TIRLKL IYER CDLNCRIHKK SRNKCQFCRF
olPPARG ASGFHYGVHA CEGCKGFFRR TIRLKL VYDH CDLHCR IHKK SRNKCQYCRF
salsPPARG ASGFHYGVHV CEGCKGFFRR TVRLKL VYDH CDLHCR IHKK SRNKCQYCRF
omPPARG ASGFHYGVHA CEGCKGFFRR TVRLKL VYDH CELHCR IHKK SRNKCQYCRF
Consistency *****9 *****9 99*****9*97 *9*8***** *****9***
```

```
..... 310. .... 320. .... 330. .... 340. .... 350
mmPPARGi1 QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
rnPPARGi2 QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
macfPPARG QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
ggPPARG QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
ocPPARG QKCLAVGMSH NAIRFGRMPG AEKEKLLAEI SSDIDQLNPE SADLRALAKH
mmPPARGi2 QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
rnPPARGi1 QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
btPPARGi2 QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
clPPARG QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
ssPPARG QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
hsPPARGi2 QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
macmPPARG QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
drPPARG QKCLMVGMSH NAIRFGRMPQ AEKEKLLAEF SSDVNHMHP E SADLRALARH
hsPPARGi1 QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
btPPARGi1 QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADLRALAKH
xlPPARG QKCLAVGMSH NAIRFGRMPQ AEKEKLLAEI SSDIDQLNPE SADQRLAKH
olPPARG QKCLNVGMSH NAIRFGRMPQ AEKEKLLAEF SSDMEHMHP E AADLRALARH
salsPPARG QKCLLVGMSH DAIRFGRMPQ VEREKLLQAE FMDVEPRNPE SADLRALSRQ
omPPARG QKCLLVGMSH DAIRFGRMPQ VEREKLLQAEF MDVDPNPE SAE LRALSRQ
Consistency ***7***** 9*****9 9*9***9997 8889878** 9*99*9*988
```

	360	370	380	390	400
mmPPARGi1	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
rnPPARGi2	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
macfPPARG	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
ggPPARG	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLRM	GEDQIKCKHA
ocPPARG	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
mmPPARGi2	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
rnPPARGi1	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
btPPARGi2	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
clPPARG	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
ssPPARG	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
hsPPARGi2	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
macmPPARG	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
drPPARG	LYESYLKYFP	LTKAKARAIL	SGKTSNAPF	VIHDMKSLVE	GEQM INCRYM
hsPPARGi1	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
btPPARGi1	LYDSYIKSFP	LTKAKARAIL	TGKTDDKSPF	VIYDMNSLMM	GEDKIKFKHI
xlPPARG	LYDSYVKSFP	LTKAKARAIL	TGRATDKTPV	VIHDMNSLMM	GEDQIKGQCV
olPPARG	LYEAYLKYFP	LTKAKARAIL	SGKSGDNVFP	VIHDIKSLME	GKQLINNGQT
salsPPARG	LCLSYHRHFP	LTKSKAKAIL	SGKTHGNSPF	VIHDMKSLTA	GQYFINCRQL
omPPARG	LCLSYHRHFP	LTKSKAKAIL	SGKTHGNSPF	VIHDMKSLTA	GQYFINCRQL
Consistency	*879*797**	***9**9***	8*997878*9	**8*97**77	*876*75777

	410	420	430	440	450
mmPPARGi1	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
rnPPARGi2	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
macfPPARG	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
ggPPARG	-----	-----	-----	---SPLQEQN	KEVAIRIFQR
ocPPARG	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
mmPPARGi2	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
rnPPARGi1	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
btPPARGi2	-----	-----	-----	---SPLQEFS	KEVAIRIFQG
clPPARG	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
ssPPARG	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
hsPPARGi2	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
macmPPARG	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
drPPARG	PLHEHR	-----	-----	---RSDLGIM	HEVELRFFHS
hsPPARGi1	-----	-----	-----	---TPLQEQS	KEVAIRIFQG
btPPARGi1	-----	-----	-----	---SPLQEFS	KEVAIRIFQG
xlPPARG	-----	-----	-----	---TPEQN	KEVAIRIFQR
olPPARG	SFQEQQIATA	GHGVSGIAGA	LSGPDCNVFG	MASNIGSEPP	DGVELRFFYS
salsPPARG	PVLERQRSV	-----	-----	---LPPEEPA	EELLSVFRR
omPPARG	PVLERQRSV	-----	-----	---LPPEEPA	EELLSVFRR
Consistency	0000000000	0000000000	0000000000	0005757967	7997988*76

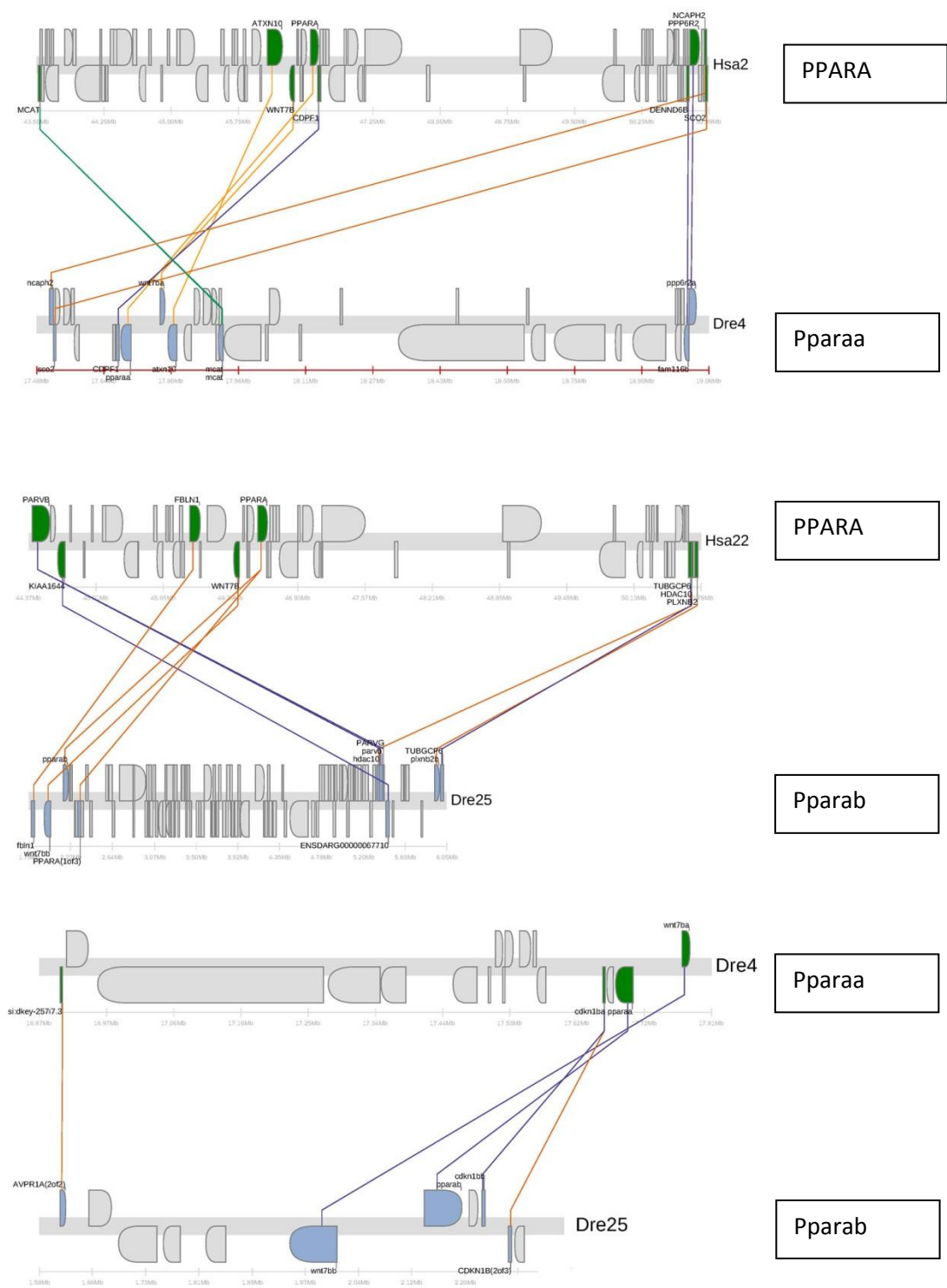
	460	470	480	490	500
mmPPARGi1	CQFRSVEAVQ	EITEYAKNIP	GFINLDLNDQ	VTLLKYGVHE	IIYTMLASLM
rnPPARGi2	CQFRSVEAVQ	EITEYAKNIP	GFINLDLNDQ	VTLLKYGVHE	IIYTMLASLM
macfPPARG	CQFRSVEAVQ	EITEYAKSIP	GFVNLDLNDQ	VTLLKYGVHE	IIYTMLASLM
ggPPARG	CQFRSVEAVQ	EITEFAKNIP	GFVNLDLNDQ	VTLLKYGVHE	IIYTMLASLM
ocPPARG	CQFRSVEAVQ	EITEYAKNIP	GFVSLDLNDQ	VTLLKYGVHE	IIYTMLASLM
mmPPARGi2	CQFRSVEAVQ	EITEYAKNIP	GFINLDLNDQ	VTLLKYGVHE	IIYTMLASLM
rnPPARGi1	CQFRSVEAVQ	EITEYAKNIP	GFINLDLNDQ	VTLLKYGVHE	IIYTMLASLM
btPPARGi2	CQFRSVEAVQ	EITEYAKNIP	GFVNLDLNDQ	VTLLKYGVHE	IIYTMLASLM
clPPARG	CQFRSVEAVQ	EITEYAKSIP	GFVNLDLNDQ	VTLLKYGVHE	IIYTMLASLM
ssPPARG	CQFRSVEAVQ	EITEYAKNIP	GFVNLDLNDQ	VTLLKYGVHE	IIYTMLASLM
hsPPARGi2	CQFRSVEAVQ	EITEYAKSIP	GFVNLDLNDQ	VTLLKYGVHE	IIYTMLASLM
macmPPARG	CQFRSVEAVQ	EITEYAKSIP	GFVNLDLNDQ	VTLLKYGVHE	IIYTMLASLM
drPPARG	YQSRSAEAI	EVTEFAKSIP	GFINLDLNDQ	VTLLKYGVIE	VMIIMISPLM
hsPPARGi1	CQFRSVEAVQ	EITEYAKSIP	GFVNLDLNDQ	VTLLKYGVHE	IIYTMLASLM
btPPARGi1	CQFRSVEAVQ	EITEYAKNIP	GFVNLDLNDQ	VTLLKYGVHE	IIYTMLASLM
xlPPARG	CQSRSAEAVR	EITEFAKNIP	GFVSLDLNDQ	VTLLKYGVHE	IIYTMLASLM
olPPARG	CQSRSAEAVR	EVTEFAKSIP	GFVNLDLNDQ	VTLLKYGVIE	VLIIMMSPLM
salsPPARG	IQFRSAEAVQ	EVTEFTKSIP	GFTELDMNDQ	VILLKYGVIE	VMTTMLAPLM
omPPARG	IQFRSAEAVQ	EVTEFAKSIP	GFTELDMNDQ	VILLKYGVIE	VMTTMLAPLM
Consistency	7*7**7**98	*9**89*7**	**88**9***	*8*****6*	98689997**

	510.	520.	530.	540.	550				
mmPPARGi1	NKDGVLI	SEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
rnPPARGi2	NKDGVLI	SEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
macfPPARG	NKDGVI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
ggPPARG	NKDGVLI	SDG	QG	FMTREF	LK	SLRKP	F	CDFM	EPKFE	FAVKF	NALEL	DDSD	L	
ocPPARG	NKDGVLI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
mmPPARGi2	NKDGVLI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
rnPPARGi1	NKDGVLI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
btPPARGi2	NKDGVLI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
clPPARG	NKDGVI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
ssPPARG	NKDGVI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
hsPPARGi2	NKDGVI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
macmPPARG	NKDGVI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
drPPARG	NKDGTL	ISYG	QI	FMTREF	LK	SLRKP	F	CEMM	EPKFE	FSIKF	NMLEL	DDCD	M	
hsPPARGi1	NKDGVI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
btPPARGi1	NKDGVI	ISEG	QG	FMTREF	LK	SLRKP	F	GDFM	EPKFE	FAVKF	NALEL	DDSD	L	
xlPPARG	NKDGVL	VAEG	QG	FMTREF	LK	SLRKP	F	SDFM	EPKFE	FAIRF	NSLEL	DDSD	L	
olPPARG	NKDGTL	ISYG	QI	FMTREF	LK	SLRKP	F	CQML	EPKF	DFS	SVKF	NTLEL	DDSD	M
salsPPARG	NKDGTL	FAYG	QI	FMTREF	LK	SLRKP	F	CEMM	EPKFE	FAAKF	NLLEL	DDSD	M	
omPPARG	NKDGTL	FAYG	QI	FMTREF	LK	SLRKP	F	CEMM	EPKFE	FAVKF	NVLEL	DDSD	M	
Consistency	***8	9886	*	*6	*****	*****	5879	*****	9*999*	*7	*****	9*8		

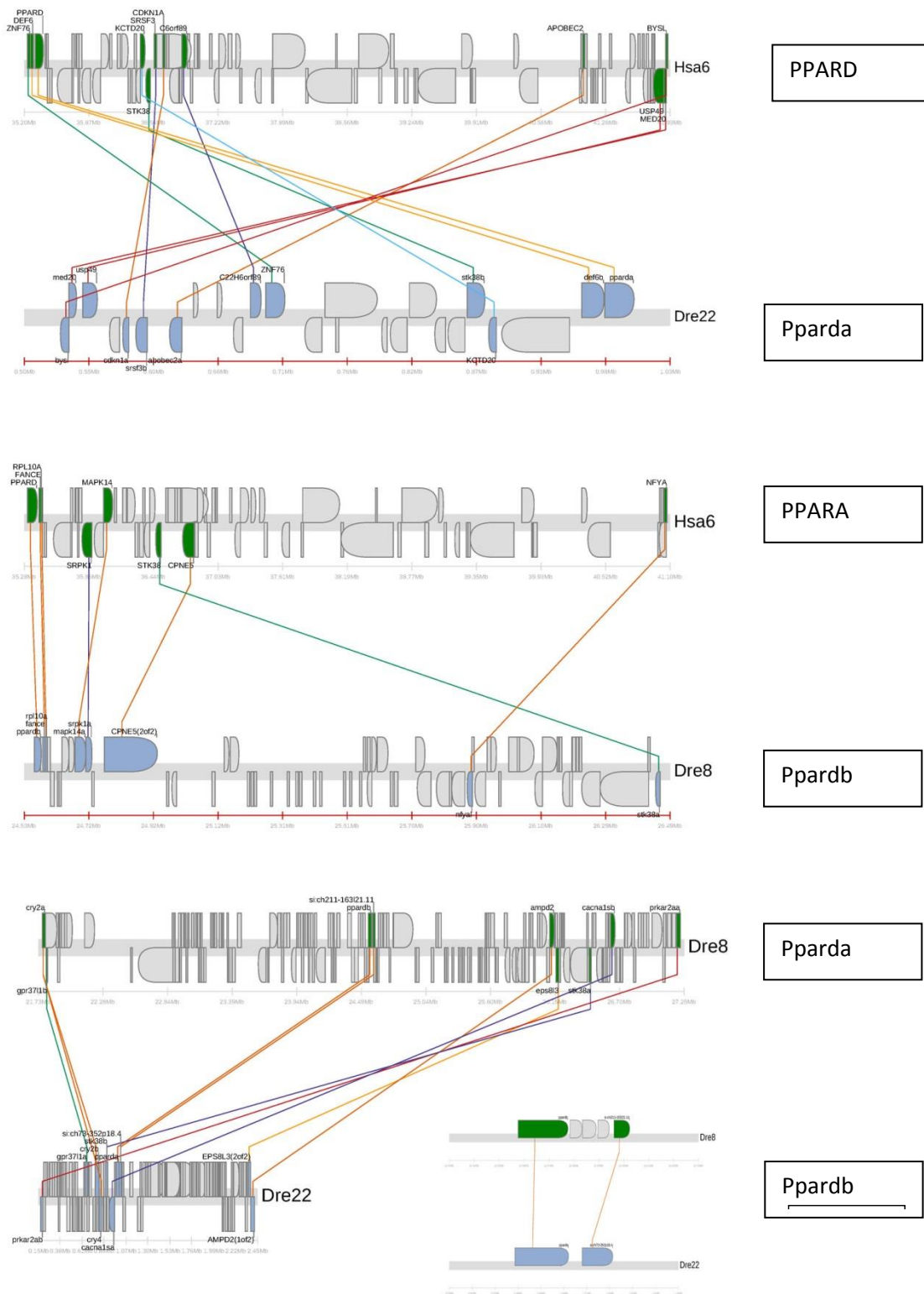
	560.	570.	580.	590.	600		
mmPPARGi1	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
rnPPARGi2	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
macfPPARG	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
ggPPARG	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
ocPPARG	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPEAS	QLFAK	
mmPPARGi2	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
rnPPARGi1	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
btPPARGi2	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
clPPARG	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
ssPPARG	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
hsPPARGi2	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
macmPPARG	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
drPPARG	ALFLAVI	IILS	GDRP	GLLDV	K	PIEDL	QETVL	HSLEL	QLKIN	HPDSL	QLFAK	
hsPPARGi1	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
btPPARGi1	AIFIAVI	IILS	GDRP	GLLNV	K	PIEDI	QDNLL	QALEL	QLKLN	HPESS	QLFAK	
xlPPARG	AIFVAVI	IILS	GDRP	GLLNV	K	PIEDI	QDSL	QALEL	QLKLN	HPDSA	QLFAK	
olPPARG	ALFLAVI	IILS	GDRP	GLLNV	K	PIEQL	QETVL	HSLEL	HLKIN	HPDSL	QLFAK	
salsPPARG	ALFFAVI	IILS	GDRP	GLVNV	K	PIEDL	QETVL	QALEL	QLKTI	HPDCP	QLFAK	
omPPARG	ALFFAVI	IILS	GDRP	GLVNV	K	PIEDL	QETVL	QALEL	QLKTI	HPDCP	QLFAK	
Consistency	*9*8	*****	*****	99**	***99	*878*	89***	9**88	**886	*****		

	610.	620.	630.	640.	...
mmPPARGi1	VLQKMTD	DLRQ	IVTEH	VQLLH	VIKKT	ETDMS	LHPLL	QEIIK	DLY
rnPPARGi2	VLQKMTD	DLRQ	IVTEH	VQLLH	VIKKT	ETDMS	LHPLL	QEIIK	DLY
macfPPARG	LLQKMTD	DLRQ	IVTEH	VQLLQ	VIKKT	ETDMS	LHPLL	QEIIK	DLY
ggPPARG	LLQKMTD	DLRQ	IVTEH	VQLLQ	VIKKT	ETDMS	LHPLL	QEIIK	DLY
ocPPARG	LLQKMTD	DLRQ	IVTEH	VQLLQ	VIKKT	ETDMS	LHPLL	QEIIK	DLY
mmPPARGi2	VLQKMTD	DLRQ	IVTEH	VQLLH	VIKKT	ETDMS	LHPLL	QEIIK	DLY
rnPPARGi1	VLQKMTD	DLRQ	IVTEH	VQLLH	VIKKT	ETDMS	LHPLL	QEIIK	DLY
btPPARGi2	LLQKMTD	DLRQ	IVTEH	VQLLQ	VIKKT	ETDMS	LHPLL	QEIIK	DLY
clPPARG	LLQKMTD	DLRQ	IVTEH	VQLLQ	VIKKT	ETDMS	LHPLL	QEIIK	DLY
ssPPARG	LLQKMTD	DLRQ	IVTEH	VQLLQ	VIKKT	ETDMS	LHPLL	QEIIK	DLY
hsPPARGi2	LLQKMTD	DLRQ	IVTEH	VQLLQ	VIKKT	ETDMS	LHPLL	QEIIK	DLY
macmPPARG	LLQKMTD	DLRQ	IVTEH	VQLLQ	VIKKT	ETDMS	LHPLL	QEIIK	DLY
drPPARG	VLQKMTD	DLRQ	LVTDH	VQLIQ	MMKETE	ADWS	LHPLL	QEIMR	DLY
hsPPARGi1	LLQKMTD	DLRQ	IVTEH	VQLLQ	VIKKT	ETDMS	LHPLL	QEIIK	DLY
btPPARGi1	LLQKMTD	DLRQ	IVTEH	VQLLQ	VIKKT	ETDMS	LHPLL	QEIIK	DLY
xlPPARG	LLQKMTD	DLRQ	VVTEH	VQLLQ	LIKKTE	ADMC	LHPLL	QEIIK	DLY
olPPARG	VLQKMTD	DLRQ	MVTDH	VQLIQ	LLKKTE	VDMF	LHPLL	QEIMK	DLY
salsPPARG	LLQKMTD	DLRQ	LVANH	VRLIH	LLKKQE	ELQMC	LHPLL	QEIMR	DLY
omPPARG	LLQKMTD	DLRQ	LVANH	VRLIH	LLKKQE	ELVC	LHPLL	QEIMR	DLY
Consistency	8*****		8*88	*9997	88*98	*7987	*****	*79	***

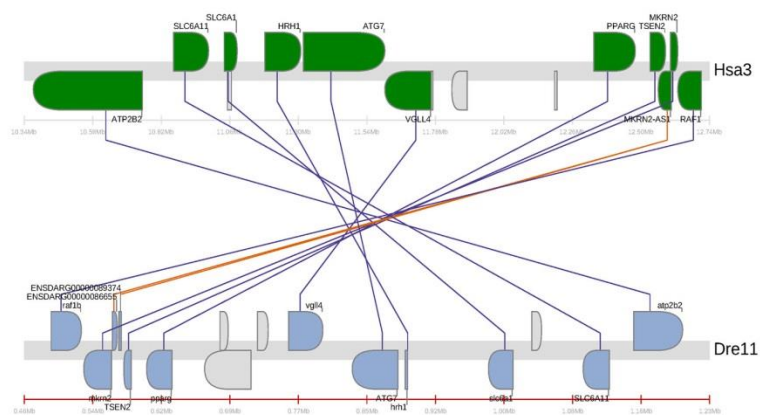
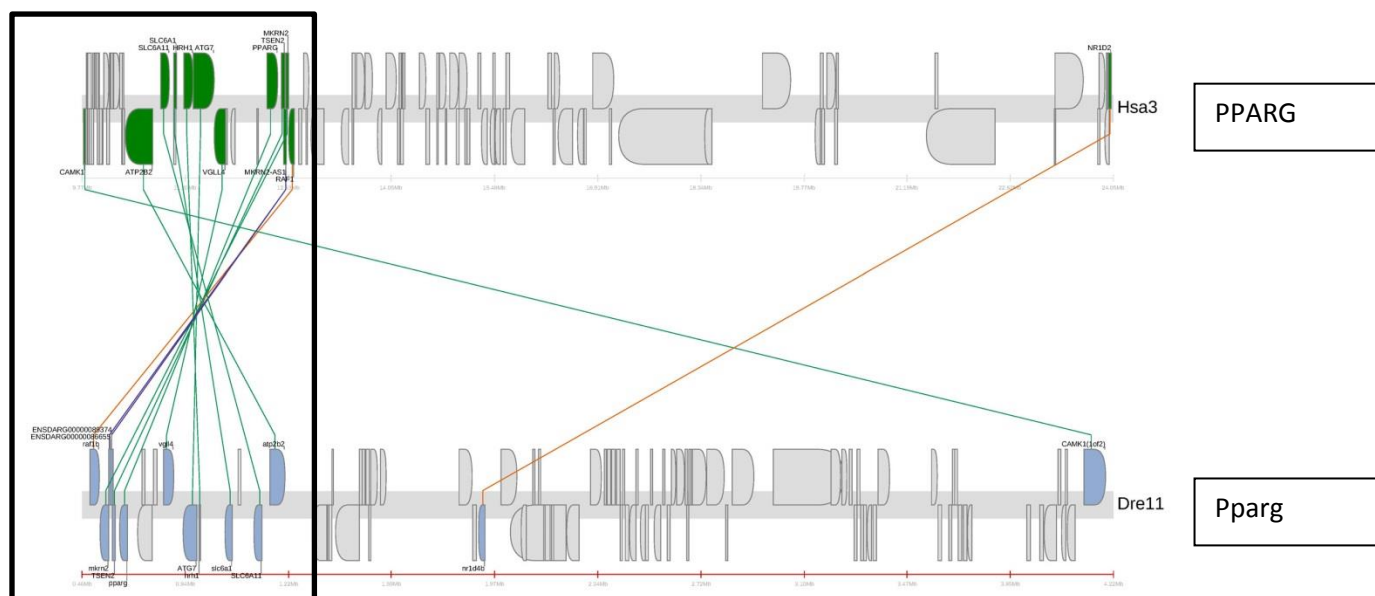
Supplemental data 3A: Synteny of zebrafish genomic regions of Pparaa and Pparab to human genomic region of PPARA



Supplemental data 3B: Synteny of zebrafish genomic regions of Pparda and Ppardb to human genomic region of PPARD



Supplemental data 3C: Synteny of zebrafish genomic regions of Pparg to human genomic region of PPARG



Zoom in at indicated region