Supplementary Table 2. Computed Values of Module Parameters

This table shows the computed values of various parameters for the individual modules. Recall that in five cases, no evidence of modularity was found (based on the footprinting methodology). Values are for three-species alignments.

Key: **Symb** = Gene symbol; **Loc** = Site location relative to the most relevant transcription start point; **Trunc** = Module truncated at transcription start or not; **MmRn** = Percent ID, mouse and rat; **MmHs** = Percent ID, mouse and man; **HsRn** = Percent ID, rat and man; **ID** = Percent ID for all three species; **GCx** = G/C content for species x; **Disp** = Measure of dispersal (see text); **Blks** = Number of blocks of length ≥ 5 with identical nucleotides in all three species; **Cent** = Measure of centrality (see text); **SiteLoc** = Relative position of the 5´-most nucleotide in the site[*]; **Rep** = Whether the module contains any repeats; **Clsr** = Which species is closer to Hs (assuming a difference of more than 1% in the two measures) 'S' indicates that the difference is less than 1%, so the two rodents are about equally close to Hs; **Len** = Module length; **μ Blk** = Mean block size based only on blocks of identity ≥ 5 nucleotides; **In.Blk** = proportion nucleotides that are in blocks of length ≥ 1.

[*] Surprisingly, this does not appear to be normally distributed, even among non-truncated blocks.

Symb	Loc	Trunc	MmRn	MmHs	HsRn	ID	GCm	GCh	GCr	Disp	Blks	Cent	Site Loc	Rep	Clsr	Len	μ Blk	In.Blk
Abcc2	-413	0	0.823	0.573	0.544	0.510	0.314	0.303	0.297	1.276	7	0.383	0.816	1	M	196	5.6	0.51
ACADM	-336	0	0.802	0.435	0.470	0.400	0.468	0.529	0.470	1.070	4	0.546	0.639	0	R	230	8.0	0.40
Adrb1	-41	1	0.827	0.635	0.631	0.582	0.724	0.722	0.758	2.884	25	0.570	0.950	0	S	661	10.1	0.58
Afp	-6327	0	0.882	0.559	0.580	0.525	0.452	0.467	0.391	1.539	12	0.559	0.512	0	R	295	6.8	0.53
Afp	-139	1	0.882	0.559	0.580	0.525	0.452	0.467	0.391	1.539	12	0.559	0.512	0	R	295	6.8	0.64
Aldh1a1	-91	1	0.843	0.676	0.659	0.615	0.455	0.471	0.404	2.184	20	0.555	0.850	0	M	548	8.4	0.61
Apoa1	-210	1	0.946	0.764	0.767	0.740	0.603	0.591	0.620	3.717	14	0.492	0.213	0	S	258	9.5	0.74
Apoa1	-132	1	0.946	0.764	0.767	0.740	0.603	0.591	0.620	3.717	14	0.492	0.512	0	S	258	9.5	0.74
APOA2	-733	0	0.873	0.522	0.536	0.500	0.517	0.488	0.518	2.025	9	0.538	0.525	0	R	276	8.9	0.50
Apoc3	-732	0	0.778	0.677	0.590	0.559	0.585	0.597	0.676	1.712	6	0.471	0.221	0	M	222	7.7	0.56
Apoc3	-83	1	0.764	0.479	0.495	0.439	0.583	0.567	0.613	1.446	18	0.697	0.861	0	R	547	7.1	0.44
Bmp2	-2373	1	0.916	0.682	0.688	0.657	0.676	0.677	0.701	3.065	62	0.508	0.210	0	S	1364	8.7	0.66
Cdx1	-511	1	0.823	0.557	0.551	0.504	0.563	0.570	0.553	2.618	39	0.592	0.422	0	S	1237	9.9	0.50
Crabp1	-1008	0	0.849	0.514	0.500	0.469	0.479	0.481	0.416	1.850	8	0.577	0.510	0	M	294	8.8	0.47
Crabp2	-1090	0	0.875	0.486	0.473	0.443	0.596	0.602	0.609	1.333	5	0.481	0.492	0	M	183	7.4	0.44
Crabp2	-586	0	0.938	0.675	0.637	0.634	0.595	0.589	0.650	3.576	10	0.532	0.447	1	M	295	10.8	0.63
Cryab	-132	0	0.888	0.711	0.714	0.672	0.546	0.536	0.583	3.896	47	0.579	0.885	0	S	1076	10.9	0.67
Cryab	-69	0	0.888	0.711	0.714	0.672	0.546	0.536	0.583	3.896	47	0.579	0.942	0	S	1076	10.9	0.67
CYP1A1	-468	0	0.812	0.575	0.546	0.502	0.561	0.538	0.725	1.783	10	0.375	0.512	0	M	295	8.6	0.50
CYP24A1	-291	1	0.871	0.574	0.567	0.534	0.596	0.586	0.619	2.141	30	0.554	0.553	0	S	861	8.3	0.53
CYP24A1	-269	1	0.871	0.574	0.567	0.534	0.596	0.586	0.619	2.141	30	0.554	0.707	0	S	861	8.3	0.53
Cyp7a1	-139	1	0.861	0.687	0.693	0.628	0.413	0.439	0.368	2.181	13	0.446	0.517	0	S	298	7.7	0.63
DIO1	-105	1	0.667	0.646	0.555	0.485	0.477	0.476	0.426	1.509	11	0.537	0.677	0	M	328	7.5	0.48
Drd2	-66	1	0.873	0.540	0.505	0.479	0.703	0.662	0.721	1.484	7	0.545	0.704	0	M	213	7.3	0.48

Symb	Loc	Trunc	MmRn	MmHs	HsRn	ID	GCm	GCh	GCr	Disp	Blks	Cent	Site Loc	Rep	Clsr	Len	μ Blk	In.Blk
Ebaf	-70	1	0.840	0.733	0.721	0.665	0.585	0.601	0.658	4.132	8	0.467	0.533	0	M	167	10.5	0.66
Egr1	-469	1	0.915	0.708	0.710	0.678	0.636	0.640	0.675	3.820	79	0.554	0.714	0	S	1742	9.7	0.68
ETS1	-432	0	0.842	0.589	0.574	0.535	0.663	0.669	0.687	3.090	19	0.405	0.355	0	M	592	10.3	0.54
Fgf8	-4542	0	0.849	0.652	0.652	0.606	0.542	0.528	0.586	4.417	41	0.479	0.846	0	S	1009	10.3	0.61
Foxa1	-1094	1	0.862	0.653	0.665	0.613	0.507	0.511	0.515	4.417	109	0.563	0.604	0	R	2734	10.4	0.61
Gh1	-190	1	0.913	0.621	0.617	0.587	0.543	0.521	0.537	2.911	9	0.548	0.342	0	S	269	9.9	0.59
Gnrh1	-1490	0	0.807	0.595	0.620	0.558	0.359	0.358	0.310	1.884	36	0.524	0.908	0	R	960	7.5	0.56
H1f0	-531	1	0.907	0.763	0.762	0.733	0.680	0.679	0.699	5.848	41	0.546	0.442	0	S	961	11.9	0.73
Hnf4a	-295	1	0.751	0.600	0.576	0.519	0.540	0.513	0.553	2.256	25	0.636	0.581	0	M	724	9.0	0.52
Hoxa4	-3054	0	0.859	0.780	0.773	0.723	0.421	0.436	0.404	7.609	80	0.498	0.356	0	S	1750	12.0	0.72
Hoxa7	-238	1	0.921	0.795	0.759	0.751	0.506	0.513	0.564	4.599	20	0.516	0.603	0	M	317	9.6	0.75
Hoxa7	-175	1	0.921	0.795	0.759	0.751	0.506	0.513	0.564	4.599	20	0.516	0.804	0	M	317	9.6	0.75
Hoxb1	-1623	1	0.880	0.733	0.733	0.692	0.488	0.495	0.502	5.504	88	0.543	0.089	0	S	1787	10.8	0.69
Hoxd4	-2551	1	0.857	0.668	0.668	0.626	0.500	0.498	0.516	4.966	68	0.525	0.178	0	S	1763	10.9	0.63
Icam1	-225	0	0.814	0.643	0.626	0.588	0.651	0.649	0.670	2.259	10	0.593	0.605	0	M	243	8.5	0.59
Igfbp6	-27	1	0.788	0.558	0.585	0.507	0.516	0.557	0.574	1.977	17	0.635	0.972	0	R	471	7.9	0.51
Lamb1-1	-467	1	0.753	0.656	0.567	0.537	0.564	0.572	0.624	2.384	32	0.494	0.300	0	M	773	8.1	0.54
Mdk	-971	0	0.831	0.580	0.589	0.537	0.577	0.570	0.671	2.166	30	0.475	0.445	1	S	894	8.3	0.54
Mmp11	-385	0	0.788	0.512	0.504	0.451	0.523	0.534	0.542	1.187	7	0.537	0.155	1	S	284	6.6	0.45
Mmp11	-367	0	0.788	0.512	0.504	0.451	0.523	0.534	0.542	1.187	7	0.537	0.613	1	S	284	6.6	0.45
Mycn	-186	1	0.929	0.831	0.854	0.814	0.565	0.570	0.596	7.505	14	0.542	0.424	1	R	295	13.8	0.81
Oxt	-162	1	0.844	0.589	0.580	0.533	0.533	0.529	0.627	1.402	9	0.545	0.524	0	S	353	6.9	0.53
Oxt	-103	1	0.844	0.589	0.580	0.533	0.533	0.529	0.627	1.402	9	0.545	0.728	0	S	353	6.9	0.53
Pck1	-451	0	0.905	0.653	0.631	0.613	0.515	0.529	0.484	2.434	37	0.512	0.116	0	M	708	7.9	0.61
Pck1	-337	0	0.905	0.653	0.631	0.613	0.515	0.529	0.484	2.434	37	0.512	0.297	0	M	708	7.9	0.65
Pit1	-10145	0	0.859	0.700	0.688	0.647	0.316	0.302	0.282	2.710	31	0.503	0.510	0	M	731	8.7	0.65
Pit1	-9999	0	0.859	0.700	0.688	0.647	0.316	0.302	0.282	2.710	31	0.503	0.718	0	M	731	8.7	0.65
PLAT	-7319	0	0.762	0.618	0.619	0.545	0.525	0.523	0.538	2.218	3	0.595	0.500	0	S	110	8.3	0.55
Pou5f1	-45	1	0.928	0.865	0.883	0.856	0.667	0.613	0.654	7.640	6	0.559	0.676	0	R	111	12.8	0.86
Prkca	-93	1	0.902	0.663	0.655	0.627	0.453	0.466	0.439	2.657	23	0.408	0.807	0	S	461	8.3	0.63
PTAFR	-66	1	0.816	0.632	0.619	0.564	0.560	0.532	0.647	2.439	11	0.537	0.801	0	M	296	8.0	0.56
Ptgds	-586	0	0.899	0.589	0.557	0.539	0.536	0.518	0.608	1.500	10	0.589	0.300	0	M	280	6.5	0.54
Pthr1	-2714	0	0.840	0.634	0.636	0.580	0.549	0.548	0.590	2.148	55	0.539	0.657	0	S	1400	7.7	0.58
Rara	-55	1	0.906	0.656	0.645	0.620	0.582	0.577	0.629	3.209	37	0.532	0.948	0	M	764	9.6	0.62
Rarb	-53	1	0.959	0.684	0.706	0.684	0.578	0.583	0.486	9.375	8	0.650	0.864	0	R	323	21.8	0.68
Rarg	-393	1	0.931	0.699	0.720	0.686	0.626	0.620	0.645	3.542	39	0.532	0.537	0	R	876	10.0	0.69
Rbp1	-1011	0	0.826	0.458	0.480	0.426	0.434	0.391	0.389	1.213	5	0.468	0.317	0	R	202	6.2	0.43
Rbp2	-125	1	0.916	0.680	0.687	0.658	0.482	0.479	0.486	2.429	15	0.513	0.611	0	S	319	8.1	0.66
Rbp2	-74	1	0.916	0.680	0.687	0.658	0.482	0.479	0.486	2.429	15	0.513	0.771	0	S	319	8.1	0.66
Rbp4	-194	1	0.914	0.627	0.614	0.593	0.536	0.538	0.553	2.631	43	0.482	0.839	0	M	915	8.1	0.59
Ren1	-2674	0	0.875	0.721	0.694	0.656	0.527	0.554	0.543	2.477	12	0.555	0.960	0	M	302	9.0	0.66
Rxrg	-98	1	0.920	0.772	0.782	0.746	0.496	0.481	0.461	3.758	14	0.558	0.744	0	R	355	10.0	0.75
SFTPB	-458	1	0.791	0.567	0.572	0.503	0.567	0.568	0.589	1.561	21	0.523	0.479	0	S	749	7.8	0.50
Slc10a1	-53	1	0.817	0.471	0.455	0.421	0.459	0.461	0.530	1.479	3	0.380	0.355	0	M	121	7.0	0.42
Stat1	-467	0	0.803	0.507	0.539	0.471	0.350	0.358	0.394	1.141	9	0.586	0.454	1	R	361	6.2	0.47
Tcf1	-68	1	0.895	0.705	0.702	0.659	0.615	0.598	0.598	4.816	16	0.615	0.849	0	S	370	8.8	0.66
Tlx2	-1163	0	0.906	0.729	0.715	0.688	0.622	0.622	0.620	3.584	33	0.527	0.879	0	M	770	10.5	0.69
Ucp3	-71	1	0.892	0.648	0.648	0.615	0.529	0.515	0.516	3.061	15	0.557	0.821	0	S	358	9.5	0.61