Supplementary Material

Table S1: NCBI genome access date (mm/dd/yyyy) and assembly version numbers.

	S. cerevisiae	*H. sapiens*	*A. thaliana*	*C. elegans*	*D. melanogaster*
Access Date	04/30/2022	05/30/2022	06/09/2022	06/09/2022	06/10/2022
Assembly Version	GCF_000146045.2	GCF_000001405.40	GCF_000001735.4	GCF_000002985.6	GCF_000001215.4

Table S2: Alternate `Seg` parameters used to identify LCRs from protein sequences in the five model organisms. Correlation coefficients and number of LCR data points are given for each parameter set.

parameters			S. cerevisiae				H. sapiens				A. thaliana				C. elegans				D. melanogaster			
W	K1	K2	r	n	95% CI		r	n	95% CI		r	n	95% CI		r	n	95% CI		r	n	95% CI	
		1.7	0.420	1182	0.367	0.471	0.341	5812	0.315	0.366	0.454	5601	0.431	0.477	0.291	3588	0.257	0.324	0.350	4222	0.320	0.379
	1.7	2	0.474	1182	0.423	0.522	0.361	5812	0.336	0.386	0.475	5601	0.452	0.497	0.325	3588	0.292	0.357	0.382	4222	0.353	0.410
		2.7	0.591	1182	0.548	0.630	0.478	5812	0.456	0.500	0.596	5601	0.577	0.615	0.477	3588	0.448	0.505	0.535	4222	0.511	0.559
		1.9	0.404	2078	0.363	0.443	0.347	9944	0.328	0.366	0.452	10314	0.435	0.469	0.288	6456	0.263	0.313	0.358	6200	0.334	0.382
12	1.9	2.2	0.443	2078	0.403	0.480	0.340	9944	0.320	0.359	0.468	10314	0.451	0.485	0.341	6456	0.317	0.365	0.394	6200	0.370	0.417
		2.9	0.545	2078	0.510	0.578	0.481	9944	0.464	0.498	0.595	10314	0.581	0.609	0.496	6456	0.475	0.516	0.560	6200	0.541	0.579
		2.1	0.416	3359	0.384	0.446	0.296	14282	0.279	0.313	0.427	16318	0.413	0.441	0.296	10530	0.276	0.315	0.369	8669	0.349	0.389
	2.1	2.4	0.443	3359	0.412	0.473	0.308	14282	0.291	0.324	0.457	16318	0.443	0.470	0.326	10530	0.307	0.345	0.406	8669	0.386	0.425
		3.1	0.550	3359	0.523	0.575	0.556	14282	0.543	0.569	0.650	16318	0.640	0.660	0.580	10530	0.566	0.594	0.631	8669	0.617	0.645
		1.7	0.425	654	0.352	0.492	0.347	3167	0.312	0.381	0.483	2712	0.450	0.515	0.276	1976	0.230	0.321	0.336	2880	0.299	0.372
	1.7	2	0.466	654	0.396	0.530	0.361	3167	0.327	0.394	0.510	2712	0.478	0.540	0.303	1976	0.258	0.347	0.394	2880	0.359	0.428
		2.7	0.581	654	0.521	0.634	0.480	3167	0.450	0.509	0.613	2712	0.586	0.639	0.447	1976	0.407	0.485	0.537	2880	0.507	0.565
		1.9	0.458	1034	0.402	0.510	0.357	5005	0.330	0.384	0.482	4470	0.457	0.507	0.314	3074	0.278	0.349	0.371	3859	0.340	0.401
15	1.9	2.2	0.488	1034	0.435	0.538	0.374	5005	0.347	0.400	0.510	4470	0.485	0.534	0.353	3074	0.318	0.387	0.407	3859	0.377	0.436
		2.9	0.582	1034	0.535	0.625	0.502	5005	0.479	0.525	0.614	4470	0.593	0.634	0.470	3074	0.439	0.500	0.562	3859	0.537	0.586
		2.1	0.463	1661	0.420	0.504	0.345	8326	0.324	0.366	0.465	7889	0.445	0.484	0.315	5149	0.287	0.342	0.389	5349	0.363	0.414
	2.1	2.4	0.505	1661	0.464	0.544	0.356	8326	0.335	0.377	0.502	7889	0.483	0.520	0.360	5149	0.333	0.386	0.401	5349	0.376	0.426
		3.1	0.587	1661	0.551	0.621	0.504	8326	0.486	0.522	0.616	7889	0.601	0.631	0.511	5149	0.488	0.533	0.575	5349	0.555	0.595
		1.7	0.412	320	0.306	0.509	0.349	1428	0.297	0.399	0.420	1010	0.362	0.475	0.191	892	0.120	0.261	0.378	1710	0.332	0.422
	1.7	2	0.445	320	0.341	0.538	0.390	1428	0.340	0.438	0.473	1010	0.418	0.525	0.228	892	0.157	0.296	0.432	1710	0.388	0.474
		2.7	0.604	320	0.520	0.676	0.527	1428	0.484	0.568	0.561	1010	0.512	0.606	0.369	892	0.304	0.431	0.550	1710	0.512	0.586
		1.9	0.454	437	0.367	0.534	0.349	2163	0.307	0.390	0.478	1601	0.435	0.519	0.248	1388	0.192	0.302	0.357	2261	0.316	0.396
20	1.9	2.2	0.524	437	0.443	0.595	0.387	2163	0.346	0.426	0.509	1601	0.467	0.548	0.259	1388	0.203	0.313	0.385	2261	0.345	0.423
		2.9	0.629	437	0.561	0.688	0.520	2163	0.485	0.553	0.597	1601	0.561	0.631	0.417	1388	0.367	0.464	0.542	2261	0.509	0.574
		2.1	0.515	699	0.451	0.573	0.363	3564	0.331	0.394	0.499	2752	0.467	0.530	0.285	2242	0.242	0.327	0.365	3052	0.330	0.399
	2.1	2.4	0.538	699	0.477	0.594	0.391	3564	0.360	0.422	0.525	2752	0.494	0.555	0.324	2242	0.282	0.365	0.395	3052	0.361	0.428
		3.1	0.607	699	0.552	0.657	0.536	3564	0.509	0.562	0.624	2752	0.598	0.649	0.468	2242	0.431	0.503	0.585	3052	0.558	0.610

Table S3: Alternate `Seg` parameters used to identify LCRs from DNA sequences in the five model organisms. Correlation coefficients and number of LCR data points are given for each parameter set.

W	K1	K2	S. cerevisiae r	n	95% CI		H. sapiens r	n	95% CI		A. thaliana r	n	95% CI		C. elegans r	n	95% CI		D. melanogaster r	n	95% CI	
		1	0.279	565	0.192	0.362	0.207	3663	0.172	0.241	0.220	3013	0.182	0.258	0.263	1205	0.203	0.321	0.184	620	0.098	0.267
	1	1.2	0.269	565	0.182	0.352	0.257	3663	0.223	0.290	0.238	3013	0.200	0.275	0.331	1205	0.274	0.386	0.113	620	0.026	0.199
		1.3	0.387	565	0.306	0.462	0.405	3663	0.374	0.435	0.414	3013	0.380	0.446	0.423	1205	0.370	0.473	0.230	620	0.145	0.311
		1.3	0.509	3175	0.480	0.537	0.478	12142	0.463	0.493	0.461	12706	0.446	0.476	0.469	8163	0.450	0.488	0.307	3844	0.275	0.339
21	1.3	1.5	0.572	3175	0.545	0.598	0.557	12142	0.543	0.571	0.541	12706	0.527	0.555	0.521	8163	0.503	0.538	0.371	3844	0.340	0.401
		1.6	0.626	3175	0.602	0.649	0.622	12142	0.610	0.634	0.621	12706	0.609	0.633	0.588	8163	0.572	0.604	0.430	3844	0.401	0.458
		1.7	0.626	5982	0.609	0.643	0.606	19868	0.596	0.616	0.606	27407	0.598	0.614	0.578	19847	0.568	0.588	0.555	13806	0.542	0.568
	1.7	1.9	0.631	5982	0.614	0.648	0.602	19868	0.592	0.612	0.634	27407	0.626	0.642	0.614	19847	0.604	0.624	0.591	13806	0.579	0.603
		2	0.773	5982	0.761	0.784	0.740	19868	0.733	0.747	0.814	27407	0.809	0.818	0.773	19847	0.767	0.779	0.807	13806	0.800	0.813
		1	0.101	23	-0.369	0.530	-0.190	144	-0.360	-0.008	0.354	53	0.061	0.591	0.336	28	-0.087	0.656	0.669	12	0.081	0.912
	1	1.2	0.094	23	-0.375	0.525	0.111	144	-0.072	0.287	0.439	53	0.161	0.653	0.683	28	0.378	0.854	0.526	12	-0.143	0.865
		1.3	0.294	23	-0.183	0.659	0.305	144	0.130	0.461	0.460	53	0.186	0.668	0.796	28	0.572	0.909	0.512	12	-0.161	0.860
		1.3	0.379	171	0.226	0.513	0.433	1571	0.387	0.477	0.459	676	0.390	0.523	0.526	314	0.431	0.610	0.232	182	0.073	0.380
45	1.3	1.5	0.428	171	0.281	0.555	0.579	1571	0.541	0.615	0.571	676	0.512	0.625	0.526	314	0.431	0.610	0.281	182	0.125	0.424
		1.7	0.528	171	0.396	0.639	0.649	1571	0.616	0.680	0.622	676	0.568	0.671	0.590	314	0.503	0.665	0.365	182	0.216	0.497
		1.7	0.623	4362	0.602	0.643	0.606	16102	0.595	0.617	0.617	18815	0.607	0.627	0.541	12953	0.527	0.554	0.443	6721	0.421	0.464
	1.7	1.9	0.740	4362	0.725	0.755	0.736	16102	0.728	0.744	0.748	18815	0.741	0.755	0.700	12953	0.690	0.710	0.612	6721	0.595	0.628
		2	0.850	4362	0.841	0.859	0.877	16102	0.873	0.881	0.902	18815	0.899	0.905	0.858	12953	0.853	0.863	0.859	6721	0.852	0.866
		1	0.214	10	-0.543	0.779	-0.156	46	-0.455	0.174	0.788	15	0.410	0.935	0.732	8	-0.044	0.957	0.620	6	-0.490	0.963
	1	1.2	0.204	10	-0.550	0.775	0.298	46	-0.026	0.565	0.594	15	0.053	0.865	0.596	8	-0.282	0.931	0.625	6	-0.484	0.964
		1.3	0.381	10	-0.401	0.842	0.242	46	-0.086	0.523	0.707	15	0.245	0.907	0.297	8	-0.586	0.857	0.746	6	-0.289	0.977
		1.3	0.364	55	0.078	0.594	0.352	607	0.272	0.427	0.531	195	0.409	0.635	0.490	108	0.312	0.635	0.363	38	0.011	0.635
60	1.3	1.5	0.434	55	0.160	0.646	0.573	607	0.510	0.630	0.584	195	0.471	0.678	0.607	108	0.455	0.725	0.227	38	-0.137	0.537
		1.7	0.570	55	0.332	0.740	0.673	607	0.621	0.719	0.655	195	0.556	0.736	0.529	108	0.359	0.665	0.316	38	-0.042	0.602
		1.7	0.634	2711	0.608	0.658	0.631	11069	0.618	0.643	0.628	10319	0.615	0.641	0.508	6909	0.488	0.527	0.420	3493	0.389	0.450
	1.7	1.9	0.759	2711	0.741	0.776	0.759	11069	0.750	0.768	0.761	10319	0.752	0.770	0.687	6909	0.673	0.701	0.601	3493	0.577	0.624
		2	0.852	2711	0.840	0.863	0.882	11069	0.877	0.887	0.901	10319	0.897	0.905	0.851	6909	0.844	0.858	0.853	3493	0.843	0.863

Table S4: Alternate `Seg` parameters used to identify LCRs from (a) protein sequences and (b) DNA sequences in the Null simulated proteomes. Correlation coefficients, number of LCR data points, and 95% confidence intervals are given for each parameter set.

(a)

W	K1	K2	r	n	95% CI	
				Null		
	1.7	1.7	0.162	203	0.009	0.308
	1.7	2	0.222	203	0.071	0.363
		2.7	0.485	203	0.358	0.594
12	1.9	1.9	0.319	1587	0.269	0.367
		2.2	0.351	1587	0.302	0.398
		2.9	0.533	1587	0.493	0.571
	2.1	2.1	0.318	7303	0.295	0.341
		2.4	0.369	7303	0.347	0.391
		3.1	0.597	7303	0.580	0.613
	1.7	1.7	0.652	18	0.211	0.872
		2	0.658	18	0.221	0.875
		2.7	0.188	18	-0.357	0.638
15	1.9	1.9	0.217	70	-0.046	0.452
		2.2	0.126	70	-0.139	0.374
		2.9	0.323	70	0.068	0.538
	2.1	2.1	0.211	638	0.127	0.292
		2.4	0.255	638	0.172	0.334
		3.1	0.447	638	0.375	0.514
	1.7	1.7	NA	0	NA	NA
		2	NA	0	NA	NA
		2.7	NA	0	NA	NA
20	1.9	1.9	-1.000	2	NaN	NaN
		2.2	-1.000	2	NaN	NaN
		2.9	1.000	2	NaN	NaN
	2.1	2.1	0.047	17	-0.491	0.559
		2.4	0.048	17	-0.490	0.559
		3.1	0.294	17	-0.274	0.710

(b)

W	K1	K2	r	n	95% CI	
				Null		
	1	1	0.200	64	-0.077	0.448
		1.2	0.308	64	0.039	0.536
		1.3	0.473	64	0.230	0.660
21	1.3	1.3	0.606	2211	0.576	0.635
		1.5	0.675	2211	0.649	0.700
		1.6	0.704	2211	0.680	0.727
	1.7	1.7	0.649	92462	0.645	0.653
		1.9	0.728	92462	0.725	0.731
		2	0.868	92462	0.866	0.870
	1	1	NA	0	NA	NA
		1.2	NA	0	NA	NA
		1.3	NA	0	NA	NA
45	1.3	1.3	NA	1	NA	NA
		1.5	NA	1	NA	NA
		1.6	NA	1	NA	NA
	1.7	1.7	0.645	2853	0.620	0.668
		1.9	0.733	2853	0.713	0.751
		2	0.825	2853	0.811	0.838
	1	1	NA	0	NA	NA
		1.2	NA	0	NA	NA
		1.3	NA	0	NA	NA
60	1.3	1.3	NA	0	NA	NA
		1.5	NA	0	NA	NA
		1.6	NA	0	NA	NA
	1.7	1.7	0.660	159	0.550	0.748
		1.9	0.666	159	0.557	0.752
		2	0.735	159	0.644	0.806

Table S5: Alternate `Seg` parameters used to identify LCRs from species specific Slip simulated protein sequences. Correlation coefficients, number of LCR data points, and 95% confidence intervals are given for each parameter set.

parameters			S. cerevisiae		95% CI		H. sapiens		95% CI		A. thaliana		95% CI		C. elegans		95% CI		D. melanogaster		95% CI	
W	K1	K2	r	n			r	n			r	n			r	n			r	n		
		1.7	0.543	24346	0.533	0.553	0.639	7042	0.623	0.654	0.578	14052	0.566	0.590	0.536	15094	0.523	0.549	0.582	18911	0.571	0.592
	1.7	2	0.574	24346	0.565	0.583	0.658	7042	0.643	0.673	0.605	14052	0.593	0.617	0.562	15094	0.550	0.574	0.610	18911	0.600	0.620
		2.7	0.629	24346	0.620	0.637	0.690	7042	0.676	0.703	0.650	14052	0.639	0.661	0.608	15094	0.597	0.619	0.652	18911	0.643	0.661
		1.9	0.661	37295	0.655	0.667	0.726	17604	0.718	0.734	0.691	24174	0.684	0.698	0.655	24552	0.647	0.663	0.688	30851	0.681	0.694
12	1.9	2.2	0.680	37295	0.674	0.686	0.738	17604	0.730	0.745	0.708	24174	0.701	0.715	0.673	24552	0.665	0.681	0.706	30851	0.700	0.712
		2.9	0.728	37295	0.723	0.733	0.759	17604	0.752	0.766	0.742	24174	0.736	0.748	0.712	24552	0.705	0.719	0.743	30851	0.737	0.749
		2.1	0.743	57393	0.739	0.747	0.749	41835	0.744	0.754	0.763	43014	0.759	0.767	0.743	40865	0.738	0.748	0.765	50823	0.761	0.769
	2.1	2.4	0.756	57393	0.752	0.760	0.756	41835	0.751	0.761	0.774	43014	0.770	0.778	0.755	40865	0.750	0.760	0.778	50823	0.774	0.782
		3.1	0.800	57393	0.797	0.803	0.769	41835	0.765	0.773	0.800	43014	0.796	0.804	0.787	40865	0.783	0.791	0.807	50823	0.804	0.810
		1.7	0.459	12507	0.443	0.474	0.535	2062	0.500	0.568	0.484	6281	0.463	0.505	0.450	7002	0.429	0.471	0.498	8847	0.480	0.515
	1.7	2	0.484	12507	0.469	0.499	0.552	2062	0.518	0.585	0.504	6281	0.483	0.524	0.472	7002	0.451	0.492	0.518	8847	0.501	0.535
		2.7	0.530	12507	0.516	0.544	0.600	2062	0.568	0.630	0.548	6281	0.528	0.567	0.514	7002	0.495	0.533	0.560	8847	0.544	0.576
		1.9	0.539	17239	0.527	0.551	0.638	3765	0.616	0.659	0.569	9274	0.553	0.584	0.520	10087	0.504	0.536	0.570	12577	0.557	0.583
15	1.9	2.2	0.566	17239	0.555	0.577	0.658	3765	0.637	0.678	0.594	9274	0.579	0.608	0.547	10087	0.532	0.562	0.596	12577	0.583	0.608
		2.9	0.618	17239	0.608	0.628	0.689	3765	0.670	0.707	0.638	9274	0.624	0.651	0.594	10087	0.580	0.608	0.637	12577	0.625	0.648
		2.1	0.654	24896	0.646	0.662	0.739	8510	0.728	0.750	0.688	14729	0.678	0.697	0.639	15109	0.628	0.649	0.678	19109	0.669	0.686
	2.1	2.4	0.674	24896	0.666	0.681	0.752	8510	0.742	0.762	0.704	14729	0.695	0.713	0.657	15109	0.647	0.667	0.696	19109	0.688	0.704
		3.1	0.720	24896	0.713	0.727	0.769	8510	0.759	0.779	0.737	14729	0.729	0.745	0.697	15109	0.688	0.706	0.733	19109	0.726	0.740
		1.7	0.343	4821	0.315	0.370	0.393	369	0.292	0.485	0.365	2100	0.323	0.406	0.342	2424	0.302	0.381	0.377	2988	0.342	0.411
	1.7	2	0.363	4821	0.335	0.390	0.417	369	0.318	0.507	0.379	2100	0.337	0.419	0.357	2424	0.318	0.395	0.397	2988	0.363	0.430
		2.7	0.397	4821	0.370	0.423	0.461	369	0.367	0.546	0.412	2100	0.372	0.451	0.383	2424	0.344	0.420	0.425	2988	0.392	0.457
		1.9	0.413	6253	0.390	0.436	0.474	600	0.402	0.540	0.429	2773	0.395	0.462	0.408	3212	0.375	0.440	0.437	4030	0.409	0.464
20	1.9	2.2	0.435	6253	0.412	0.457	0.488	600	0.417	0.553	0.449	2773	0.415	0.482	0.426	3212	0.394	0.457	0.454	4030	0.426	0.481
		2.9	0.472	6253	0.450	0.493	0.531	600	0.464	0.592	0.485	2773	0.453	0.516	0.449	3212	0.418	0.479	0.491	4030	0.464	0.517
		2.1	0.496	8816	0.478	0.513	0.592	1131	0.548	0.633	0.525	4191	0.500	0.549	0.488	4649	0.463	0.512	0.532	5869	0.511	0.552
	2.1	2.4	0.523	8816	0.506	0.540	0.609	1131	0.566	0.648	0.548	4191	0.524	0.571	0.504	4649	0.480	0.528	0.554	5869	0.534	0.573
		3.1	0.568	8816	0.552	0.584	0.643	1131	0.603	0.680	0.588	4191	0.565	0.610	0.541	4649	0.518	0.563	0.589	5869	0.570	0.607

Table S6: Alternate `Seg` parameters used to identify LCRs from species specific Slip simulated DNA sequences. Correlation coefficients, number of LCR data points, and 95% confidence intervals are given for each parameter set.

parameters			*S. cerevisiae*				*H. sapiens*				*A. thaliana*				*C. elegans*				*D. melanogaster*			
W	K1	K2	r	n	95% CI		r	n	95% CI		r	n	95% CI		r	n	95% CI		r	n	95% CI	
	1	1	0.311	30077	0.300	0.322	0.392	8091	0.371	0.412	0.286	15254	0.270	0.302	0.286	17855	0.271	0.301	0.195	15938	0.178	0.212
		1.2	0.375	30077	0.364	0.386	0.428	8091	0.408	0.448	0.329	15254	0.313	0.345	0.340	17855	0.325	0.354	0.244	15938	0.228	0.260
		1.3	0.454	30077	0.444	0.464	0.488	8091	0.469	0.506	0.400	15254	0.385	0.415	0.414	17855	0.400	0.427	0.337	15938	0.322	0.352
		1.3	0.685	71346	0.681	0.689	0.709	35126	0.703	0.715	0.662	42112	0.656	0.668	0.671	47726	0.665	0.676	0.605	36893	0.598	0.612
21	1.3	1.5	0.748	71346	0.744	0.752	0.759	35126	0.754	0.764	0.721	42112	0.716	0.726	0.728	47726	0.723	0.733	0.684	36893	0.678	0.690
		1.6	0.781	71346	0.778	0.784	0.783	35126	0.778	0.787	0.750	42112	0.745	0.755	0.758	47726	0.754	0.762	0.720	36893	0.714	0.725
		1.7	0.748	100000	0.745	0.751	0.638	100000	0.634	0.642	0.719	100000	0.716	0.722	0.734	100000	0.731	0.737	0.732	100000	0.729	0.735
	1.7	1.9	0.743	100000	0.740	0.746	0.602	100000	0.598	0.606	0.709	100000	0.706	0.712	0.724	100000	0.721	0.727	0.731	100000	0.728	0.734
		2	0.289	100000	0.283	0.295	0.630	100000	0.626	0.634	0.519	100000	0.514	0.524	0.436	100000	0.430	0.442	0.595	100000	0.591	0.599
	1	1	0.193	3187	0.155	0.230	0.313	154	0.145	0.463	0.179	1092	0.114	0.242	0.205	1434	0.149	0.260	0.144	1352	0.085	0.202
		1.2	0.301	3187	0.265	0.336	0.351	154	0.187	0.496	0.271	1092	0.209	0.331	0.289	1434	0.235	0.341	0.237	1352	0.180	0.292
		1.3	0.342	3187	0.307	0.376	0.351	154	0.187	0.496	0.301	1092	0.240	0.360	0.312	1434	0.259	0.363	0.261	1352	0.205	0.316
		1.3	0.537	6615	0.518	0.556	0.533	488	0.458	0.600	0.453	2290	0.416	0.489	0.473	3034	0.442	0.503	0.395	2664	0.359	0.430
45	1.3	1.5	0.591	6615	0.573	0.608	0.573	488	0.503	0.636	0.492	2290	0.457	0.526	0.514	3034	0.484	0.543	0.427	2664	0.392	0.461
		1.6	0.610	6615	0.593	0.627	0.580	488	0.510	0.642	0.505	2290	0.470	0.538	0.529	3034	0.500	0.557	0.437	2664	0.402	0.471
		1.7	0.837	85352	0.835	0.839	0.868	37583	0.865	0.871	0.850	44526	0.847	0.853	0.855	52501	0.852	0.858	0.835	39088	0.832	0.838
	1.7	1.9	0.884	85352	0.882	0.886	0.889	37583	0.887	0.891	0.876	44526	0.874	0.878	0.883	52501	0.881	0.885	0.864	39088	0.861	0.867
		2	0.935	85352	0.934	0.936	0.945	37583	0.944	0.946	0.944	44526	0.943	0.945	0.946	52501	0.945	0.947	0.938	39088	0.937	0.939
	1	1	0.200	1419	0.144	0.255	0.352	35	-0.018	0.637	0.225	439	0.124	0.322	0.183	565	0.093	0.270	0.198	561	0.108	0.285
		1.2	0.288	1419	0.234	0.340	0.428	35	0.071	0.688	0.295	439	0.197	0.387	0.258	565	0.170	0.342	0.265	561	0.177	0.349
		1.3	0.315	1419	0.262	0.366	0.428	35	0.071	0.688	0.311	439	0.214	0.402	0.258	565	0.170	0.342	0.272	561	0.184	0.355
		1.3	0.456	2773	0.423	0.488	0.508	113	0.338	0.646	0.380	878	0.315	0.441	0.406	1135	0.350	0.459	0.331	1041	0.269	0.390
60	1.3	1.5	0.490	2773	0.458	0.521	0.531	113	0.366	0.664	0.391	878	0.327	0.452	0.430	1135	0.376	0.481	0.359	1041	0.299	0.417
		1.6	0.502	2773	0.470	0.532	0.531	113	0.366	0.664	0.402	878	0.338	0.462	0.444	1135	0.390	0.495	0.361	1041	0.301	0.418
		1.7	0.875	42378	0.872	0.877	0.887	5849	0.881	0.893	0.840	11511	0.834	0.846	0.856	16008	0.851	0.861	0.794	9491	0.786	0.802
	1.7	1.9	0.901	42378	0.899	0.903	0.899	5849	0.893	0.904	0.859	11511	0.854	0.864	0.875	16008	0.871	0.879	0.820	9491	0.813	0.827
		2	0.947	42378	0.946	0.948	0.935	5849	0.931	0.938	0.925	11511	0.922	0.928	0.939	16008	0.937	0.941	0.901	9491	0.897	0.905

Table S7: Alternate `Seg` parameters used to identify LCRs from species specific Slip+Syn simulated protein sequences. Correlation coefficients, number of LCR data points, and 95% confidence intervals are given for each parameter set.

parameters			S. cerevisiae				H. sapiens				A. thaliana				C. elegans				D. melanogaster			
W	K1	K2	r	n	95% CI		r	n	95% CI		r	n	95% CI		r	n	95% CI		r	n	95% CI	
12	1.7	1.7	0.431	24346	0.42	0.442	0.548	7042	0.53	0.566	0.452	14052	0.437	0.467	0.438	15094	0.424	0.452	0.462	18911	0.449	0.474
		2	0.465	24346	0.454	0.476	0.571	7042	0.553	0.588	0.483	14052	0.469	0.497	0.467	15094	0.453	0.481	0.492	18911	0.48	0.504
		2.7	0.531	24346	0.521	0.541	0.618	7042	0.602	0.634	0.54	14052	0.527	0.553	0.522	15094	0.509	0.535	0.544	18911	0.533	0.555
	1.9	1.9	0.555	37295	0.547	0.563	0.65	17604	0.64	0.659	0.573	24174	0.563	0.582	0.562	24552	0.552	0.571	0.579	30851	0.571	0.587
		2.2	0.58	37295	0.572	0.587	0.667	17604	0.658	0.676	0.595	24174	0.586	0.604	0.584	24552	0.575	0.593	0.6	30851	0.592	0.608
		2.9	0.647	37295	0.64	0.654	0.706	17604	0.698	0.714	0.652	24174	0.644	0.66	0.639	24552	0.631	0.647	0.656	30851	0.649	0.663
	2.1	2.1	0.653	57393	0.648	0.658	0.683	41835	0.677	0.689	0.665	43014	0.659	0.671	0.661	40865	0.655	0.667	0.67	50823	0.665	0.675
		2.4	0.673	57393	0.668	0.678	0.698	41835	0.692	0.703	0.683	43014	0.677	0.689	0.68	40865	0.674	0.686	0.69	50823	0.685	0.695
		3.1	0.749	57393	0.745	0.753	0.742	41835	0.737	0.747	0.744	43014	0.739	0.749	0.742	40865	0.737	0.747	0.75	50823	0.746	0.754
15	1.7	1.7	0.357	12507	0.34	0.374	0.462	2062	0.423	0.499	0.369	6281	0.345	0.393	0.358	7002	0.335	0.381	0.38	8847	0.36	0.4
		2	0.381	12507	0.364	0.398	0.48	2062	0.442	0.516	0.388	6281	0.364	0.411	0.381	7002	0.358	0.403	0.399	8847	0.379	0.418
		2.7	0.43	12507	0.414	0.446	0.536	2062	0.501	0.569	0.435	6281	0.412	0.457	0.422	7002	0.4	0.443	0.445	8847	0.426	0.463
	1.9	1.9	0.431	17239	0.417	0.444	0.557	3765	0.532	0.581	0.448	9274	0.43	0.466	0.427	10087	0.409	0.445	0.451	12577	0.435	0.466
		2.2	0.459	17239	0.446	0.472	0.585	3765	0.561	0.608	0.475	9274	0.457	0.492	0.457	10087	0.44	0.474	0.48	12577	0.465	0.495
		2.9	0.519	17239	0.507	0.531	0.628	3765	0.606	0.649	0.528	9274	0.511	0.544	0.507	10087	0.491	0.523	0.529	12577	0.515	0.543
	2.1	2.1	0.548	24896	0.538	0.558	0.667	8510	0.654	0.68	0.568	14729	0.556	0.58	0.545	15109	0.532	0.557	0.567	19109	0.556	0.578
		2.4	0.572	24896	0.563	0.581	0.685	8510	0.672	0.697	0.591	14729	0.579	0.603	0.566	15109	0.554	0.578	0.588	19109	0.578	0.598
		3.1	0.635	24896	0.627	0.643	0.719	8510	0.707	0.73	0.641	14729	0.63	0.651	0.619	15109	0.608	0.63	0.64	19109	0.631	0.649
20	1.7	1.7	0.26	4821	0.23	0.289	0.301	369	0.194	0.401	0.27	2100	0.225	0.314	0.259	2424	0.217	0.3	0.283	2988	0.246	0.319
		2	0.277	4821	0.248	0.306	0.326	369	0.22	0.424	0.284	2100	0.24	0.327	0.272	2424	0.23	0.313	0.303	2988	0.266	0.339
		2.7	0.31	4821	0.281	0.338	0.374	369	0.272	0.468	0.314	2100	0.27	0.356	0.298	2424	0.257	0.338	0.328	2988	0.292	0.363
	1.9	1.9	0.323	6253	0.298	0.348	0.393	600	0.315	0.466	0.327	2773	0.289	0.364	0.321	3212	0.286	0.355	0.335	4030	0.304	0.365
		2.2	0.343	6253	0.318	0.367	0.408	600	0.331	0.48	0.347	2773	0.31	0.383	0.337	3212	0.302	0.371	0.355	4030	0.325	0.385
		2.9	0.38	6253	0.356	0.403	0.453	600	0.379	0.521	0.38	2773	0.344	0.415	0.362	3212	0.328	0.395	0.388	4030	0.358	0.417
	2.1	2.1	0.393	8816	0.373	0.412	0.523	1131	0.474	0.569	0.411	4191	0.383	0.439	0.397	4649	0.37	0.424	0.416	5869	0.392	0.439
		2.4	0.421	8816	0.402	0.44	0.542	1131	0.494	0.586	0.436	4191	0.408	0.463	0.413	4649	0.386	0.439	0.44	5869	0.417	0.463
		3.1	0.469	8816	0.451	0.487	0.583	1131	0.538	0.624	0.478	4191	0.452	0.504	0.454	4649	0.428	0.479	0.479	5869	0.457	0.501

Table S8: Alternate `Seg` parameters used to identify LCRs from species specific Slip+Syn simulated DNA sequences. Correlation coefficients, number of LCR data points, and 95% confidence intervals are given for each parameter set.

parameters			S. cerevisiae		95% CI		H. sapiens		95% CI		A. thaliana		95% CI		C. elegans		95% CI		D. melanogaster		95% CI	
W	K1	K2	r	n			r	n			r	n			r	n			r	n		
		1	0.351	15258	0.335	0.366	0.371	4586	0.343	0.399	0.336	8132	0.314	0.357	0.317	9039	0.296	0.338	0.279	9185	0.258	0.300
	1	1.2	0.398	15258	0.383	0.413	0.399	4586	0.371	0.426	0.369	8132	0.348	0.390	0.350	9039	0.330	0.370	0.309	9185	0.288	0.329
		1.3	0.473	15258	0.459	0.487	0.487	4586	0.462	0.512	0.454	8132	0.435	0.473	0.435	9039	0.416	0.453	0.410	9185	0.391	0.429
		1.3	0.602	51110	0.596	0.608	0.651	29814	0.644	0.658	0.617	31451	0.609	0.625	0.602	34230	0.594	0.609	0.578	34035	0.570	0.586
21	1.3	1.5	0.664	51110	0.659	0.669	0.707	29814	0.700	0.713	0.672	31451	0.665	0.679	0.657	34230	0.650	0.664	0.638	34035	0.631	0.645
		1.6	0.704	51110	0.699	0.709	0.740	29814	0.734	0.745	0.707	31451	0.701	0.713	0.693	34230	0.687	0.699	0.677	34035	0.671	0.683
		1.7	0.713	100000	0.710	0.716	0.609	100000	0.604	0.613	0.675	100000	0.671	0.679	0.695	100000	0.691	0.699	0.677	100000	0.673	0.681
	1.7	1.9	0.722	100000	0.719	0.725	0.578	100000	0.573	0.583	0.675	100000	0.671	0.679	0.705	100000	0.702	0.708	0.676	100000	0.672	0.680
		2	0.596	100000	0.592	0.600	0.580	100000	0.575	0.584	0.669	100000	0.665	0.673	0.695	100000	0.691	0.699	0.619	100000	0.615	0.623
		1	0.245	1338	0.188	0.300	0.303	73	0.052	0.518	0.200	497	0.104	0.292	0.197	610	0.110	0.281	0.135	624	0.048	0.220
	1	1.2	0.340	1338	0.286	0.392	0.365	73	0.121	0.567	0.293	497	0.201	0.380	0.330	610	0.249	0.407	0.261	624	0.178	0.341
		1.3	0.391	1338	0.339	0.440	0.446	73	0.215	0.630	0.352	497	0.263	0.435	0.371	610	0.292	0.445	0.352	624	0.273	0.426
		1.3	0.419	3315	0.387	0.450	0.496	260	0.387	0.592	0.428	1255	0.376	0.477	0.368	1564	0.319	0.415	0.388	1553	0.340	0.434
45	1.3	1.5	0.517	3315	0.489	0.544	0.588	260	0.492	0.670	0.513	1255	0.466	0.557	0.445	1564	0.400	0.488	0.475	1553	0.431	0.517
		1.6	0.558	3315	0.531	0.584	0.605	260	0.511	0.684	0.549	1255	0.504	0.591	0.474	1564	0.430	0.516	0.512	1553	0.470	0.552
		1.7	0.812	58431	0.809	0.815	0.834	33600	0.830	0.837	0.824	31815	0.820	0.828	0.824	35489	0.820	0.828	0.800	36624	0.796	0.804
	1.7	1.9	0.857	58431	0.855	0.859	0.870	33600	0.867	0.873	0.856	31815	0.853	0.859	0.858	35489	0.855	0.861	0.841	36624	0.838	0.844
		2	0.948	58431	0.947	0.949	0.951	33600	0.950	0.952	0.933	31815	0.931	0.935	0.939	35489	0.938	0.940	0.935	36624	0.934	0.936
		1	0.176	602	0.088	0.261	0.125	17	-0.428	0.611	0.161	204	0.008	0.306	0.158	262	0.024	0.287	0.129	260	-0.007	0.260
	1	1.2	0.274	602	0.190	0.354	0.405	17	-0.153	0.767	0.214	204	0.063	0.355	0.317	262	0.190	0.433	0.280	260	0.150	0.400
		1.3	0.303	602	0.220	0.382	0.405	17	-0.153	0.767	0.211	204	0.060	0.353	0.347	262	0.222	0.460	0.312	260	0.184	0.429
		1.3	0.351	1355	0.298	0.402	0.491	57	0.236	0.683	0.305	480	0.212	0.393	0.305	615	0.223	0.383	0.328	600	0.246	0.405
60	1.3	1.5	0.455	1355	0.407	0.501	0.582	57	0.352	0.746	0.421	480	0.335	0.500	0.400	615	0.323	0.471	0.421	600	0.345	0.492
		1.6	0.471	1355	0.423	0.516	0.582	57	0.352	0.746	0.432	480	0.347	0.510	0.416	615	0.340	0.486	0.446	600	0.372	0.515
		1.7	0.833	18986	0.828	0.838	0.878	4791	0.871	0.885	0.823	6952	0.814	0.831	0.814	8280	0.806	0.822	0.793	8096	0.784	0.802
	1.7	1.9	0.863	18986	0.859	0.867	0.897	4791	0.891	0.903	0.848	6952	0.840	0.855	0.842	8280	0.835	0.849	0.823	8096	0.815	0.831
		2	0.944	18986	0.942	0.946	0.942	4791	0.939	0.946	0.902	6952	0.897	0.907	0.906	8280	0.902	0.910	0.900	8096	0.895	0.905

Table S9: Alternate minimum repeat lengths for protein LCRs containing periodic amino acid repeats. Correlation coefficients, number of LCR data points, and 95% confidence intervals are given for each parameter set.

Repeat Lengths			S. cerevisiae		95% CI		H. sapiens		95% CI		A. thaliana		95% CI		C. elegans		95% CI		D. melanogaster		95% CI	
mono	di	tri	r	n			r	n			r	n			r	n			r	n		
		3	0.524	485	0.448	0.592	0.422	2396	0.385	0.458	0.566	2457	0.535	0.595	0.476	1363	0.429	0.521	0.485	2171	0.448	0.520
	3	4	0.534	470	0.458	0.602	0.421	2364	0.383	0.457	0.569	2436	0.538	0.598	0.480	1283	0.432	0.526	0.486	2136	0.449	0.521
		5	0.534	466	0.458	0.603	0.422	2349	0.384	0.458	0.569	2435	0.538	0.598	0.481	1269	0.432	0.527	0.487	2116	0.450	0.522
		3	0.539	437	0.460	0.609	0.425	2214	0.386	0.462	0.570	2302	0.538	0.600	0.494	1267	0.446	0.539	0.492	2007	0.454	0.528
5	4	4	0.550	421	0.471	0.620	0.423	2180	0.384	0.461	0.573	2280	0.541	0.603	0.499	1186	0.450	0.545	0.493	1970	0.455	0.529
		5	0.551	417	0.472	0.621	0.424	2165	0.385	0.462	0.573	2279	0.541	0.603	0.501	1171	0.452	0.547	0.494	1949	0.456	0.531
		3	0.549	423	0.470	0.619	0.426	2140	0.387	0.464	0.570	2250	0.538	0.600	0.505	1230	0.457	0.550	0.499	1945	0.461	0.535
	5	4	0.561	407	0.482	0.631	0.424	2105	0.384	0.462	0.573	2228	0.541	0.603	0.511	1148	0.462	0.557	0.499	1908	0.460	0.536
		5	0.562	403	0.483	0.632	0.425	2090	0.385	0.463	0.573	2227	0.541	0.603	0.514	1133	0.465	0.560	0.501	1887	0.462	0.538
		3	0.532	379	0.446	0.608	0.445	1847	0.403	0.485	0.595	1842	0.561	0.627	0.520	991	0.467	0.569	0.505	1715	0.465	0.543
	3	4	0.545	364	0.459	0.621	0.443	1813	0.401	0.483	0.600	1817	0.566	0.632	0.530	906	0.476	0.580	0.506	1678	0.465	0.545
		5	0.546	360	0.460	0.622	0.444	1798	0.402	0.484	0.599	1815	0.565	0.631	0.531	891	0.476	0.582	0.508	1658	0.467	0.547
		3	0.544	327	0.453	0.624	0.451	1641	0.407	0.493	0.599	1659	0.563	0.632	0.547	877	0.493	0.597	0.517	1526	0.475	0.557
6	4	4	0.560	311	0.469	0.639	0.448	1604	0.403	0.491	0.604	1633	0.569	0.637	0.559	791	0.503	0.610	0.517	1487	0.474	0.557
		5	0.561	307	0.469	0.641	0.449	1589	0.404	0.492	0.603	1631	0.567	0.636	0.562	775	0.506	0.613	0.520	1466	0.477	0.560
		3	0.556	313	0.464	0.636	0.451	1562	0.406	0.494	0.598	1600	0.562	0.632	0.566	837	0.512	0.615	0.525	1453	0.482	0.565
	5	4	0.573	297	0.481	0.652	0.448	1524	0.402	0.492	0.603	1574	0.567	0.637	0.579	750	0.523	0.630	0.525	1413	0.482	0.566
		5	0.574	293	0.482	0.654	0.449	1509	0.403	0.493	0.603	1572	0.567	0.637	0.584	734	0.528	0.635	0.527	1392	0.483	0.568
		3	0.532	379	0.446	0.608	0.445	1847	0.403	0.485	0.595	1842	0.561	0.627	0.520	991	0.467	0.569	0.505	1715	0.465	0.543
	3	4	0.545	364	0.459	0.621	0.443	1813	0.401	0.483	0.600	1817	0.566	0.632	0.530	906	0.476	0.580	0.506	1678	0.465	0.545
		5	0.546	360	0.460	0.622	0.444	1798	0.402	0.484	0.599	1815	0.565	0.631	0.531	891	0.476	0.582	0.508	1658	0.467	0.547
		3	0.539	265	0.436	0.628	0.468	1209	0.417	0.516	0.626	1129	0.585	0.664	0.566	627	0.504	0.623	0.556	1186	0.511	0.598
7	4	4	0.557	248	0.453	0.646	0.464	1168	0.412	0.513	0.632	1100	0.591	0.670	0.584	540	0.518	0.643	0.560	1139	0.514	0.603
		5	0.558	244	0.454	0.647	0.465	1153	0.413	0.514	0.632	1098	0.591	0.670	0.588	523	0.522	0.647	0.563	1118	0.517	0.606
		3	0.550	250	0.446	0.640	0.467	1128	0.415	0.516	0.626	1068	0.584	0.665	0.592	581	0.530	0.648	0.566	1105	0.520	0.609
	5	4	0.568	233	0.463	0.658	0.463	1085	0.409	0.514	0.632	1039	0.589	0.671	0.612	493	0.547	0.670	0.570	1057	0.523	0.614
		5	0.570	229	0.464	0.660	0.464	1070	0.410	0.515	0.632	1037	0.589	0.671	0.618	476	0.552	0.676	0.573	1036	0.526	0.617
		3	0.532	379	0.446	0.608	0.445	1847	0.403	0.485	0.595	1842	0.561	0.627	0.520	991	0.467	0.569	0.505	1715	0.465	0.543
	3	4	0.545	364	0.459	0.621	0.443	1813	0.401	0.483	0.600	1817	0.566	0.632	0.530	906	0.476	0.580	0.506	1678	0.465	0.545
		5	0.546	360	0.460	0.622	0.444	1798	0.402	0.484	0.599	1815	0.565	0.631	0.531	891	0.476	0.582	0.508	1658	0.467	0.547
		3	0.519	214	0.401	0.620	0.452	884	0.392	0.509	0.646	771	0.598	0.690	0.566	474	0.494	0.631	0.562	918	0.511	0.609
10	4	4	0.539	197	0.419	0.641	0.445	841	0.382	0.503	0.654	742	0.606	0.698	0.589	385	0.511	0.657	0.568	868	0.516	0.616
		5	0.541	193	0.419	0.643	0.447	826	0.384	0.506	0.653	740	0.604	0.697	0.593	367	0.514	0.662	0.572	845	0.519	0.620
		3	0.504	161	0.363	0.622	0.486	594	0.414	0.552	0.646	454	0.582	0.702	0.543	315	0.450	0.624	0.549	637	0.486	0.607
	5	4	0.518	120	0.355	0.650	0.463	420	0.375	0.543	0.678	298	0.603	0.741	0.580	164	0.454	0.683	0.564	447	0.489	0.631
		5	0.521	116	0.356	0.655	0.464	405	0.374	0.545	0.676	296	0.601	0.739	0.594	146	0.463	0.700	0.572	423	0.496	0.639

Table S10: Alternate repeat lengths for cryptic repeat protein LCRs defined as LCRs which do not contain sequences with the minimal periodic amino acid repeat length. Correlation coefficients, number of LCR data points, and 95% confidence intervals are given for each parameter set.

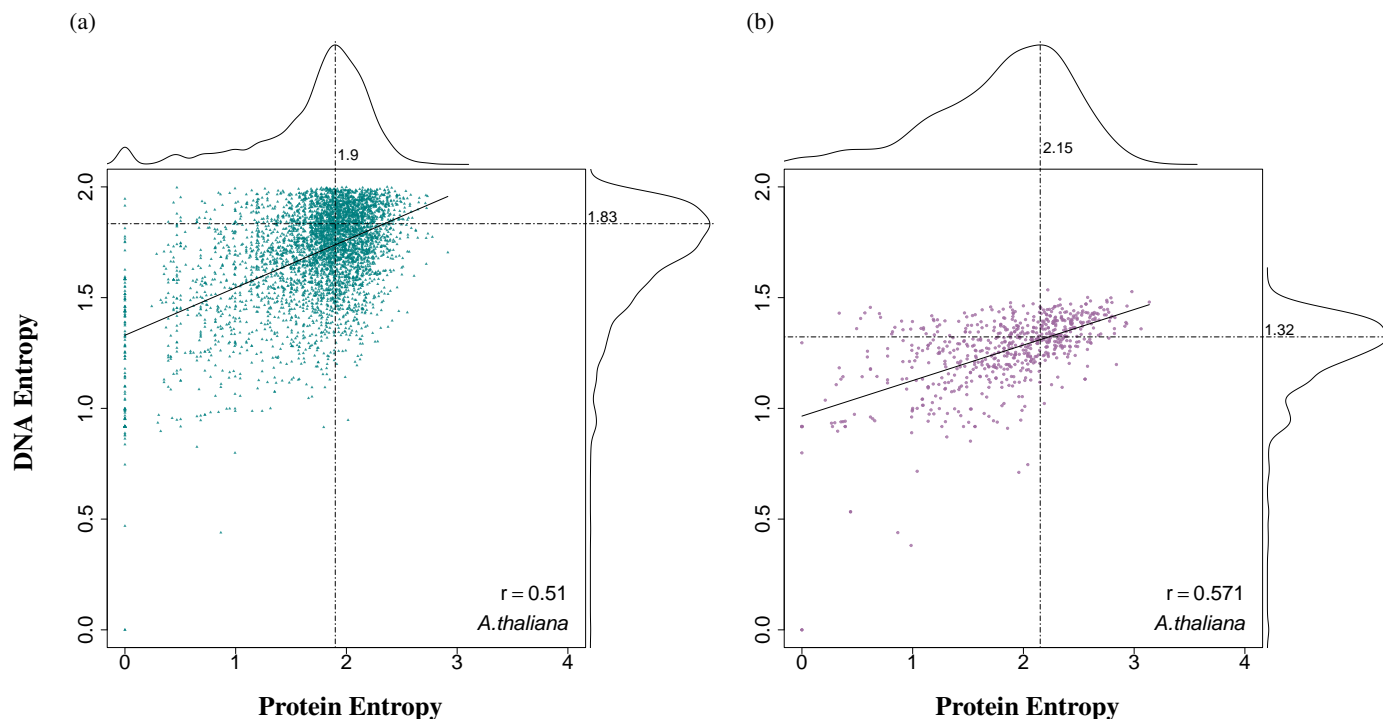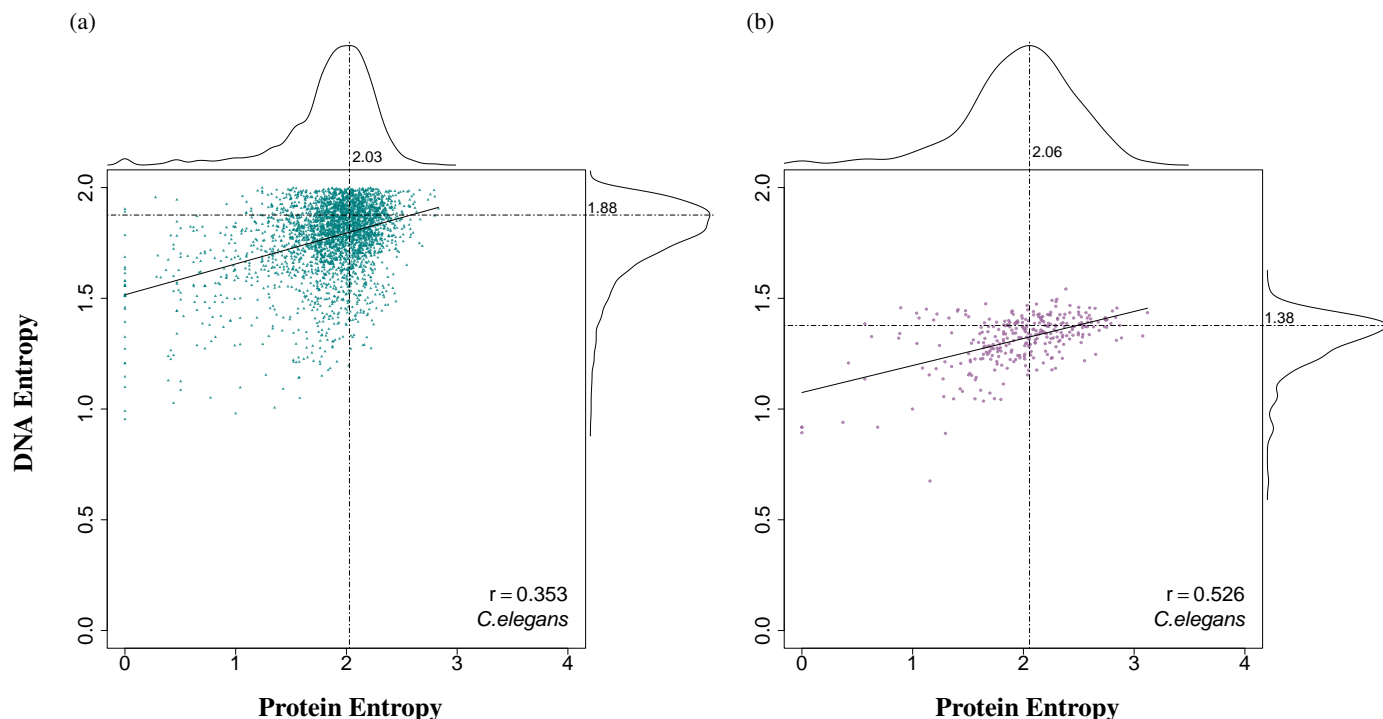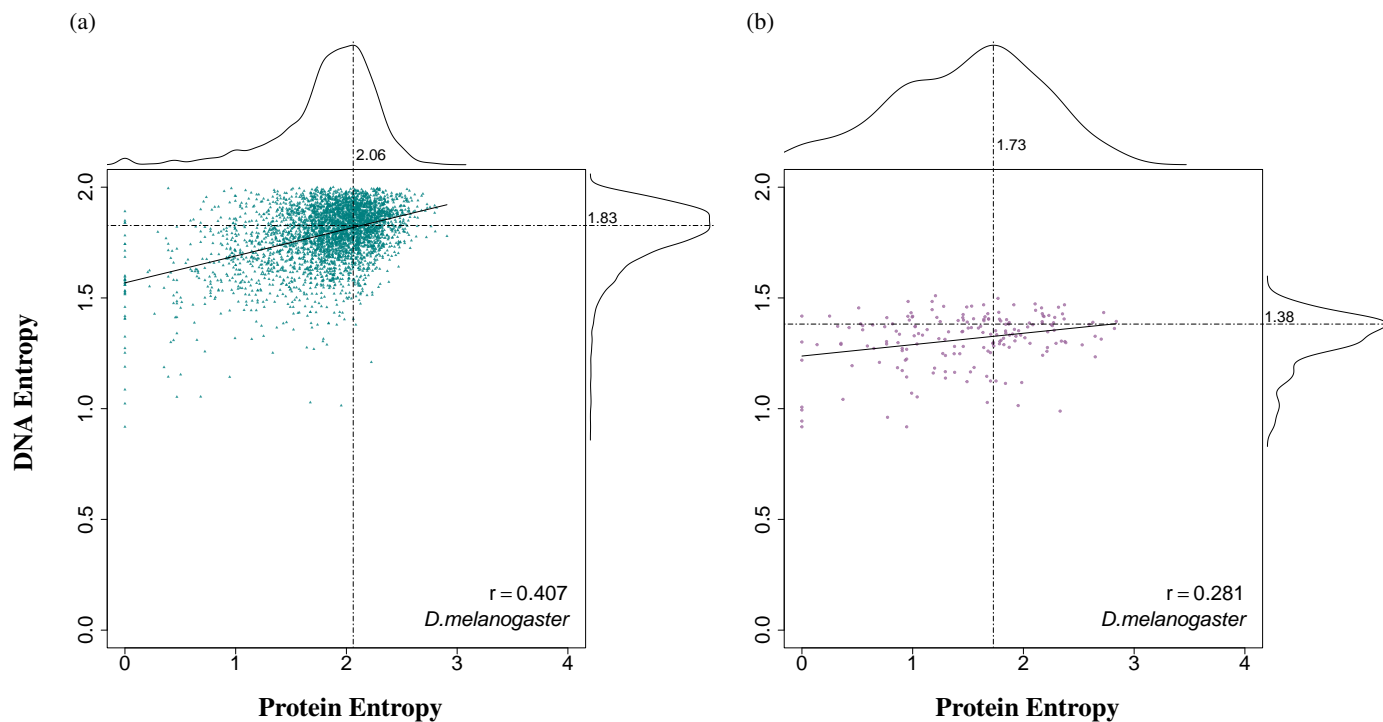| Repeat Lengths			S. cerevisiae				H. sapiens				A. thaliana				C. elegans				D. melanogaster			
mono	di	tri	r	n	95% CI		r	n	95% CI		r	n	95% CI		r	n	95% CI		r	n	95% CI	
	3	3	0.325	549	0.239	0.406	0.233	2609	0.192	0.273	0.272	2013	0.226	0.316	0.210	1711	0.159	0.260	0.224	1688	0.173	0.274
		4	0.328	564	0.243	0.408	0.235	2641	0.194	0.275	0.266	2034	0.220	0.310	0.212	1791	0.162	0.261	0.234	1723	0.184	0.283
		5	0.332	568	0.248	0.411	0.233	2656	0.193	0.273	0.266	2035	0.220	0.310	0.213	1805	0.163	0.262	0.231	1743	0.181	0.280
5	4	3	0.314	597	0.231	0.392	0.239	2791	0.200	0.278	0.273	2168	0.229	0.316	0.205	1807	0.155	0.254	0.232	1852	0.183	0.279
		4	0.316	613	0.234	0.393	0.242	2825	0.203	0.280	0.267	2190	0.223	0.310	0.207	1888	0.158	0.255	0.241	1889	0.193	0.288
		5	0.320	617	0.239	0.397	0.240	2840	0.201	0.278	0.267	2191	0.223	0.310	0.207	1903	0.159	0.254	0.239	1910	0.191	0.286
	5	3	0.302	611	0.219	0.380	0.238	2865	0.199	0.276	0.285	2220	0.242	0.327	0.201	1844	0.152	0.249	0.224	1914	0.176	0.271
		4	0.304	627	0.223	0.381	0.241	2900	0.202	0.279	0.279	2242	0.236	0.321	0.203	1926	0.155	0.250	0.233	1951	0.186	0.279
		5	0.309	631	0.228	0.386	0.239	2915	0.200	0.277	0.279	2243	0.236	0.321	0.203	1941	0.155	0.250	0.231	1972	0.184	0.277
	3	3	0.339	655	0.261	0.412	0.233	3158	0.196	0.269	0.299	2628	0.260	0.337	0.219	2083	0.173	0.264	0.267	2144	0.223	0.310
		4	0.340	670	0.263	0.413	0.237	3192	0.200	0.273	0.294	2653	0.255	0.332	0.219	2168	0.174	0.263	0.274	2181	0.230	0.317
		5	0.344	674	0.268	0.416	0.235	3207	0.198	0.271	0.294	2655	0.255	0.332	0.221	2183	0.176	0.265	0.272	2201	0.228	0.315
6	4	3	0.331	707	0.256	0.402	0.240	3364	0.204	0.275	0.298	2811	0.260	0.335	0.215	2197	0.170	0.259	0.270	2333	0.228	0.311
		4	0.332	723	0.258	0.402	0.243	3401	0.207	0.278	0.293	2837	0.255	0.330	0.215	2283	0.171	0.258	0.276	2372	0.234	0.317
		5	0.335	727	0.261	0.405	0.242	3416	0.206	0.277	0.294	2839	0.256	0.331	0.215	2299	0.171	0.258	0.275	2393	0.233	0.316
	5	3	0.321	721	0.246	0.392	0.239	3443	0.204	0.274	0.307	2870	0.270	0.343	0.211	2237	0.166	0.255	0.264	2406	0.222	0.305
		4	0.322	737	0.248	0.392	0.242	3481	0.207	0.277	0.302	2896	0.265	0.338	0.211	2324	0.167	0.254	0.271	2446	0.230	0.311
		5	0.325	741	0.251	0.395	0.241	3496	0.206	0.275	0.303	2898	0.266	0.339	0.211	2340	0.167	0.254	0.269	2467	0.228	0.309
	3	3	0.339	655	0.261	0.412	0.233	3158	0.196	0.269	0.299	2628	0.260	0.337	0.219	2083	0.173	0.264	0.267	2144	0.223	0.310
		4	0.340	670	0.263	0.413	0.237	3192	0.200	0.273	0.294	2653	0.255	0.332	0.219	2168	0.174	0.263	0.274	2181	0.230	0.317
		5	0.344	674	0.268	0.416	0.235	3207	0.198	0.271	0.294	2655	0.255	0.332	0.221	2183	0.176	0.265	0.272	2201	0.228	0.315
7	4	3	0.347	769	0.276	0.414	0.260	3796	0.227	0.293	0.336	3341	0.302	0.369	0.258	2447	0.216	0.299	0.283	2673	0.244	0.321
		4	0.351	786	0.281	0.417	0.264	3837	0.231	0.297	0.332	3370	0.298	0.365	0.257	2534	0.216	0.297	0.287	2720	0.248	0.325
		5	0.353	790	0.283	0.419	0.262	3852	0.229	0.294	0.332	3372	0.298	0.365	0.257	2551	0.216	0.297	0.285	2741	0.246	0.323
	5	3	0.338	784	0.267	0.405	0.259	3877	0.226	0.291	0.342	3402	0.308	0.375	0.254	2493	0.213	0.294	0.279	2754	0.240	0.317
		4	0.342	801	0.272	0.408	0.262	3920	0.229	0.294	0.338	3431	0.305	0.371	0.253	2581	0.212	0.293	0.284	2802	0.246	0.322
		5	0.344	805	0.274	0.410	0.261	3935	0.228	0.293	0.339	3433	0.306	0.372	0.253	2598	0.212	0.293	0.282	2823	0.244	0.319
	3	3	0.339	655	0.261	0.412	0.233	3158	0.196	0.269	0.299	2628	0.260	0.337	0.219	2083	0.173	0.264	0.267	2144	0.223	0.310
		4	0.340	670	0.263	0.413	0.237	3192	0.200	0.273	0.294	2653	0.255	0.332	0.219	2168	0.174	0.263	0.274	2181	0.230	0.317
		5	0.344	674	0.268	0.416	0.235	3207	0.198	0.271	0.294	2655	0.255	0.332	0.221	2183	0.176	0.265	0.272	2201	0.228	0.315
10	4	3	0.376	820	0.309	0.440	0.312	4121	0.281	0.342	0.368	3699	0.337	0.399	0.285	2600	0.245	0.324	0.328	2941	0.292	0.363
		4	0.377	837	0.310	0.440	0.314	4164	0.283	0.344	0.364	3728	0.333	0.395	0.283	2689	0.244	0.321	0.330	2991	0.294	0.365
		5	0.379	841	0.313	0.442	0.313	4179	0.282	0.343	0.364	3730	0.333	0.395	0.283	2707	0.244	0.321	0.329	3014	0.293	0.364
	5	3	0.399	873	0.335	0.459	0.321	4411	0.291	0.350	0.437	4016	0.409	0.464	0.322	2759	0.284	0.359	0.366	3222	0.332	0.399
		4	0.427	914	0.366	0.484	0.342	4585	0.313	0.370	0.455	4172	0.428	0.481	0.333	2910	0.297	0.369	0.377	3412	0.344	0.409
		5	0.428	918	0.367	0.485	0.341	4600	0.312	0.369	0.455	4174	0.428	0.481	0.333	2928	0.297	0.368	0.376	3436	0.344	0.408

Figure S1: Entropy comparisons of LCRs and corresponding sequences in the *A. thaliana* genome. Distributions of sequence entropies can be found along the vertical and horizontal axes with values indicating the mode. (a) 4470 LCRs were identified from 48 265 protein sequences and their entropies were plotted against entropies of the corresponding DNA sequences ($r = 0.510$). (b) 676 LCRs were identified from 48 265 coding sequences and their entropies were plotted against the entropies of the corresponding protein sequences ($r = 0.571$).

Figure S2: Entropy comparisons of LCRs and corresponding sequences in the *C. elegans* genome. Distributions of sequence entropies can be found along the vertical and horizontal axes with values indicating the mode. (a) 3074 LCRs were identified from 30 502 protein sequences and their entropies were plotted against the entropies of the corresponding DNA sequences ($r = 0.353$). (b) 314 LCRs were identified from 30 502 coding sequences and their entropies were plotted against the entropies of the corresponding protein sequences ($r = 0.526$).

Figure S3: Entropy comparisons of LCRs and corresponding sequences in the *D. melanogaster* genome. Distributions of sequence entropies can be found along the vertical and horizontal axes with values indicating the mode. (a) 3859 LCRs were identified from 30 726 protein sequences and their entropies were plotted against the entropies of the corresponding DNA sequences ($r = 0.407$). (b) 182 LCRs were identified from 30 726 coding sequences and their entropies were plotted against the entropies of the corresponding protein sequences ($r = 0.281$).

Table S11: Summary of correlation coefficients and 95% confidence intervals for the main parameters: $W = 15$, $K1 = 1.9$, $K2 = 2.2$ (protein LCRs), $W = 45$, $K1 = 1.3$, $K2 = 1.5$ (DNA LCRs), LCRs with amino acid repeats of minimal length 6, 5, and 4 for mono-, di- and tri- repeats, respectively (periodic LCRs). LCRs without repeats of minimal length 6, 5, and 4 for mono-, di-, and tri- repeats, respectively (cryptic LCRs). Results for the main parameters are given for the five model organisms (bio), the periodic repeat and cryptic LCRs, as well as the four species specific slippage and substitution models. Information for the Null simulation which is not species specific is given at the bottom.

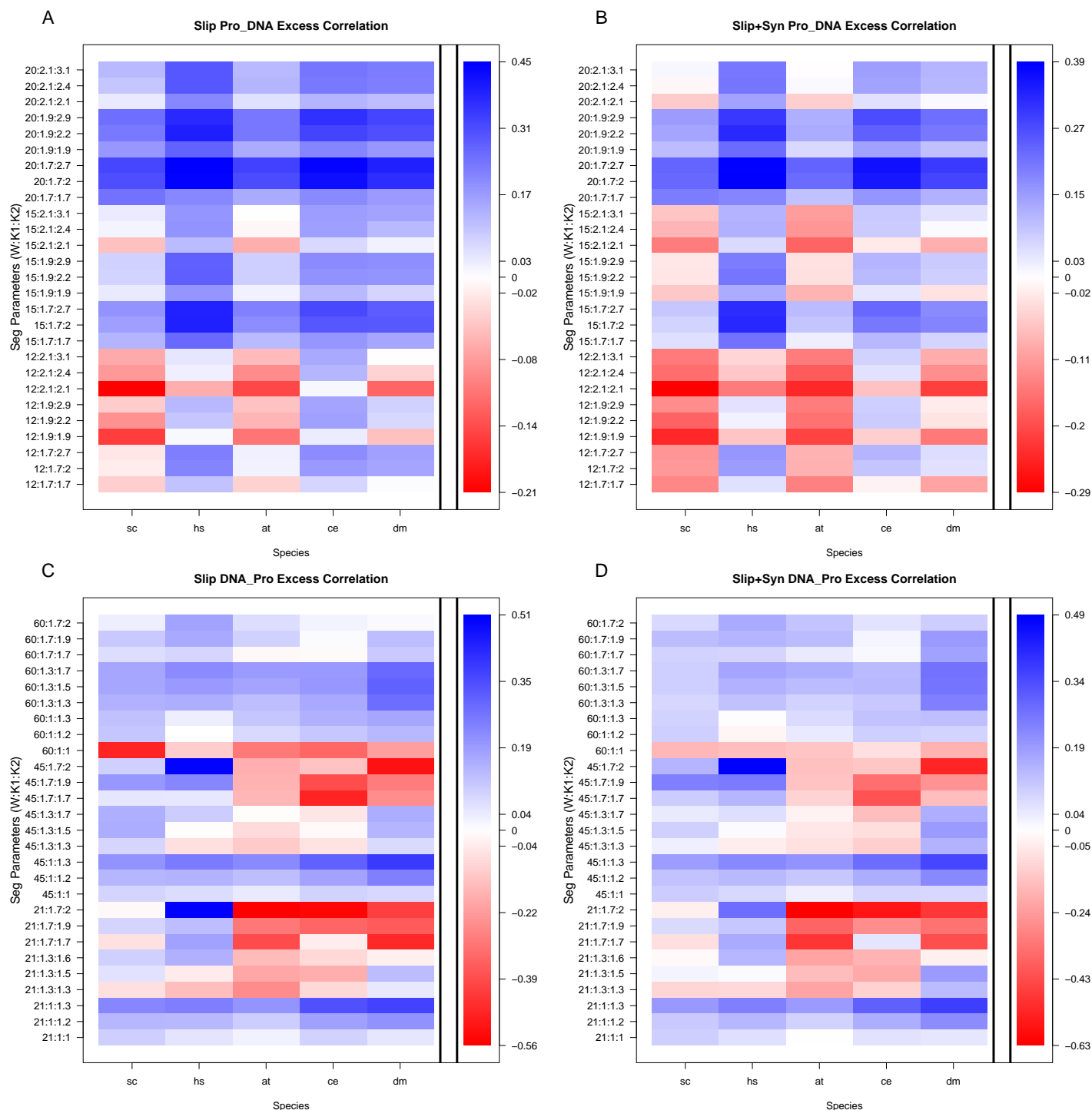|		*S. cerevisiae*		*H. sapiens*		*A. thaliana*		*C. elegans*		*D. melanogaster*	
Bio	**Protein LCRs**	0.488	(0.435-0.538)	0.374	(0.347-0.400)	0.510	(0.485-0.534)	0.353	(0.318-0.387)	0.407	(0.377-0.436)
	DNA LCRs	0.428	(0.281-0.555)	0.579	(0.541-0.614)	0.571	(0.512-0.625)	0.526	(0.431-0.610)	0.281	(0.125-0.424)
Slip	**Protein LCRs**	0.566	(0.555-0.577)	0.658	(0.637-0.678)	0.594	(0.579-0.608)	0.547	(0.532-0.562)	0.596	(0.583-0.608)
	DNA LCRs	0.591	(0.573-0.608)	0.573	(0.503-0.636)	0.492	(0.457-0.526)	0.514	(0.484-0.543)	0.427	(0.392-0.461)
Slip+Syn	**Protein LCRs**	0.459	(0.446-0.472)	0.585	(0.561-0.608)	0.475	(0.457-0.492)	0.457	(0.440-0.474)	0.480	(0.465-0.495)
	DNA LCRs	0.517	(0.489-0.544)	0.588	(0.492-0.670)	0.513	(0.466-0.557)	0.445	(0.400-0.488)	0.475	(0.431-0.517)
Slip+CC	**Protein LCRs**	0.699	(0.690-0.707)	0.808	(0.795-0.820)	0.757	(0.747-0.767)	0.718	(0.707-0.728)	0.671	(0.660-0.682)
	DNA LCRs	0.553	(0.534-0.572)	0.546	(0.479-0.607)	0.535	(0.503-0.565)	0.497	(0.467-0.526)	0.582	(0.554-0.608)
Slip+CC+Syn	**Protein LCRs**	0.490	(0.477-0.503)	0.620	(0.598-0.641)	0.518	(0.501-0.534)	0.504	(0.488-0.520)	0.486	(0.471-0.501)
	DNA LCRs	0.430	(0.397-0.462)	0.536	(0.446-0.615)	0.452	(0.403-0.498)	0.396	(0.348-0.442)	0.458	(0.415-0.499)
Protein LCRs	**Periodic**	0.573	(0.481-0.652)	0.448	(0.402-0.492)	0.603	(0.567-0.637)	0.579	(0.523-0.630)	0.525	(0.482-0.566)
	Cryptic	0.322	(0.248-0.392)	0.242	(0.207-0.277)	0.302	(0.265-0.338)	0.211	(0.167-0.254)	0.271	(0.230-0.311)
Null	**Protein LCRs**	0.126	(-0.139-0.374)								
	DNA LCRs	NA	NA								

Figure S4: Heat maps showing the excess correlation of the slippage and substitution models compared to the biological correlations in *S. cerevisiae* (sc), *H. sapiens* (hs), *A. thaliana* (at), *C. elegans* (ce), and *D. melanogaster* (dm). Blue indicates a higher correlation in the simulated sequences relative to the biological sequences while red indicates a lower correlation in the simulated sequences relative to the biological sequences. **A)** Excess correlation in protein LCRs and corresponding coding sequences in the Slip simulated sequences. **B)** Excess correlation in DNA LCRs and corresponding protein sequences in the Slip simulated sequences. **C)** Excess correlation in protein LCRs and corresponding coding sequences in the Slip+Syn simulated sequences. **D)** Excess correlation in DNA LCRs and corresponding protein sequences in the Slip+Syn simulated sequences.
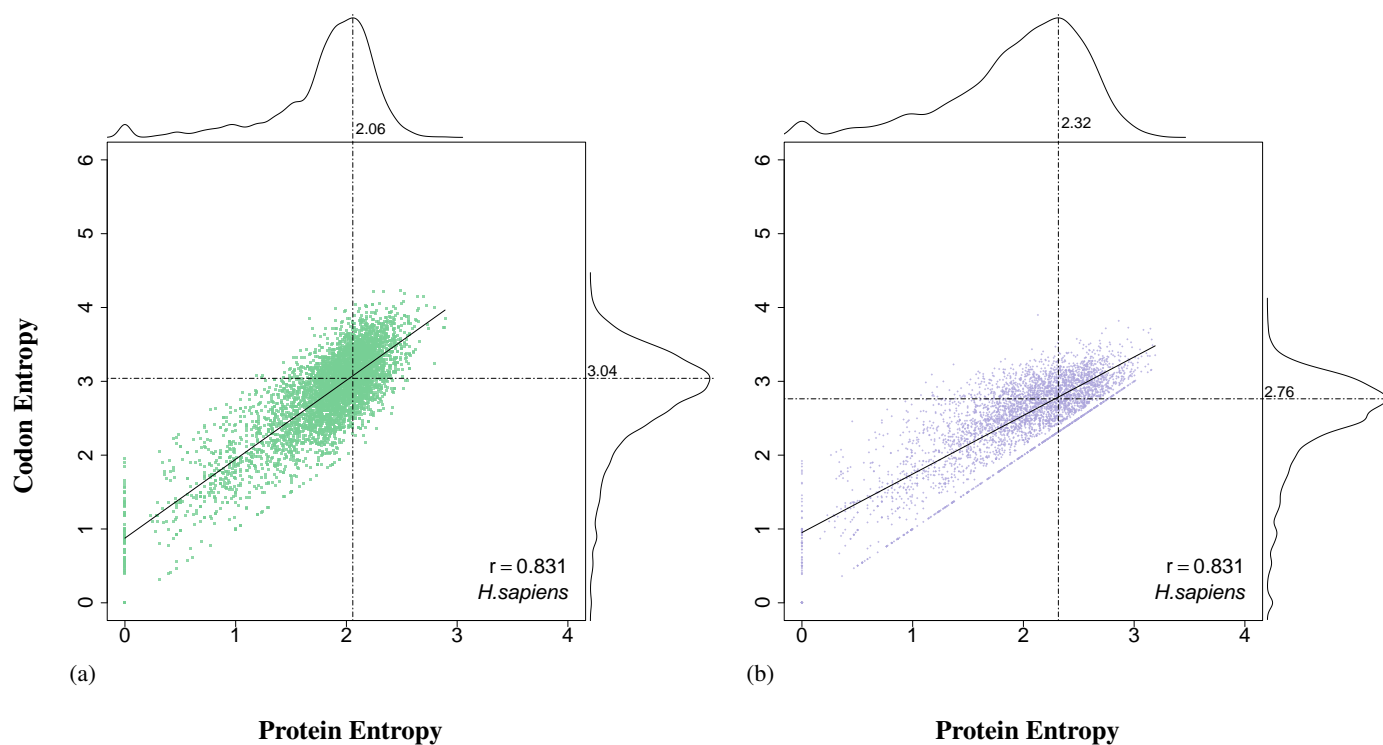
Figure S5: Entropy comparisons of LCRs and corresponding sequences in the *H. sapiens* genome. Distributions of sequence entropies can be found along the vertical and horizontal axes with values indicating the mode. (a) 5005 LCRs were identified from 133 689 protein sequences and their entropies were plotted against the codon entropies from the corresponding DNA sequences ($r = 0.831$). (b) 4493 LCRs were identified from the codons in 133 689 coding sequences and their entropies were plotted against the entropies of the corresponding protein sequences ($r = 0.831$).