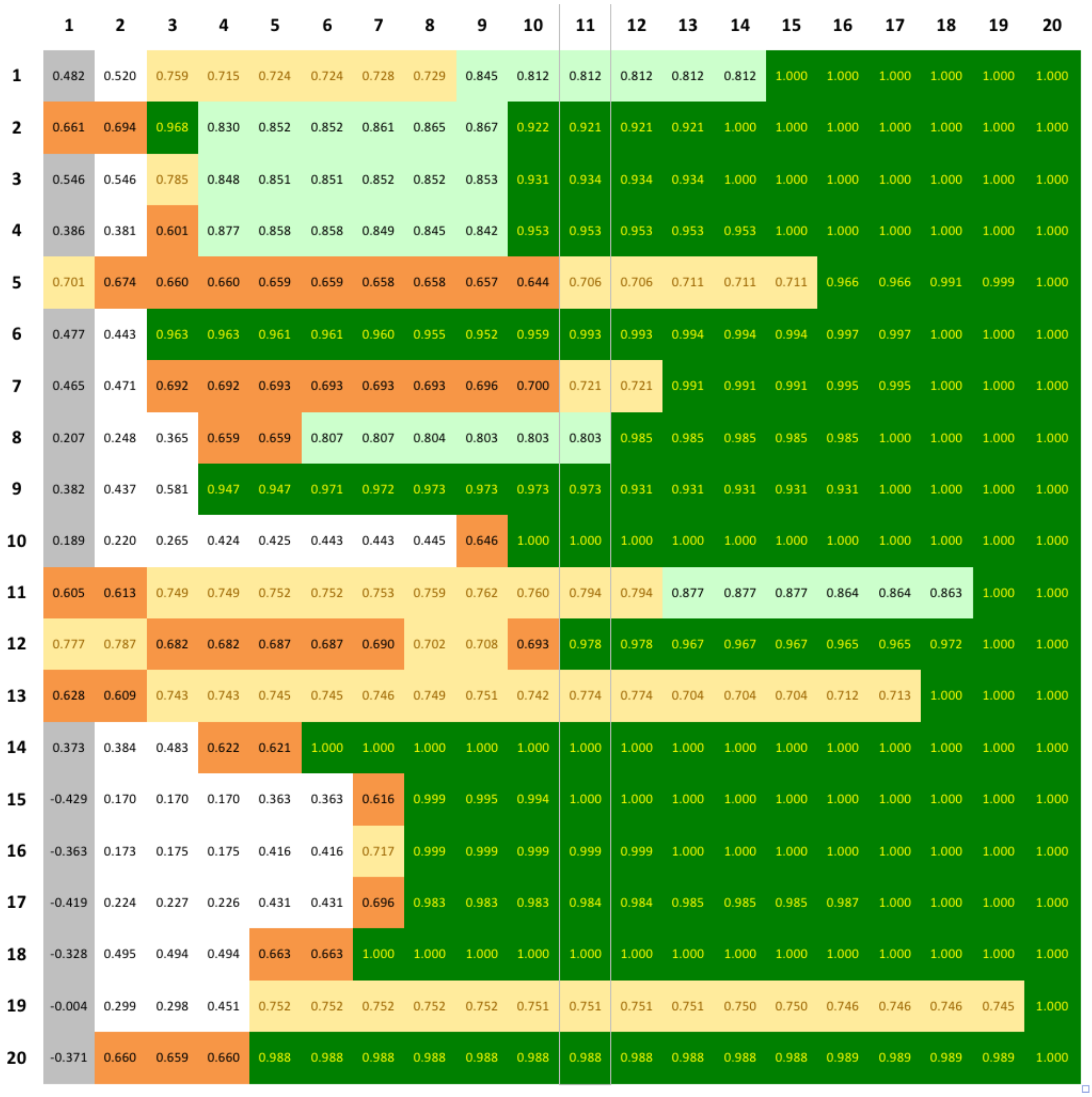

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	0.482	0.520	0.759	0.715	0.724	0.724	0.728	0.729	0.845	0.812	0.812	0.812	0.812	0.812	1.000	1.000	1.000	1.000	1.000	1.000
2	0.661	0.694	0.968	0.830	0.852	0.852	0.861	0.865	0.867	0.922	0.921	0.921	0.921	1.000	1.000	1.000	1.000	1.000	1.000	1.000
3	0.546	0.546	0.785	0.848	0.851	0.851	0.852	0.852	0.853	0.931	0.934	0.934	0.934	1.000	1.000	1.000	1.000	1.000	1.000	1.000
4	0.386	0.381	0.601	0.877	0.858	0.858	0.849	0.845	0.842	0.953	0.953	0.953	0.953	0.953	1.000	1.000	1.000	1.000	1.000	1.000
5	0.701	0.674	0.660	0.660	0.659	0.659	0.658	0.658	0.657	0.644	0.706	0.706	0.711	0.711	0.711	0.966	0.966	0.991	0.999	1.000
6	0.477	0.443	0.963	0.963	0.961	0.961	0.960	0.955	0.952	0.959	0.993	0.993	0.994	0.994	0.994	0.997	0.997	1.000	1.000	1.000
7	0.465	0.471	0.692	0.692	0.693	0.693	0.693	0.693	0.696	0.700	0.721	0.721	0.991	0.991	0.991	0.995	0.995	1.000	1.000	1.000
8	0.207	0.248	0.365	0.659	0.659	0.807	0.807	0.804	0.803	0.803	0.803	0.985	0.985	0.985	0.985	0.985	1.000	1.000	1.000	1.000
9	0.382	0.437	0.581	0.947	0.947	0.971	0.972	0.973	0.973	0.973	0.973	0.931	0.931	0.931	0.931	0.931	1.000	1.000	1.000	1.000
10	0.189	0.220	0.265	0.424	0.425	0.443	0.443	0.445	0.646	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
11	0.605	0.613	0.749	0.749	0.752	0.752	0.753	0.759	0.762	0.760	0.794	0.794	0.877	0.877	0.877	0.864	0.864	0.863	1.000	1.000
12	0.777	0.787	0.682	0.682	0.687	0.687	0.690	0.702	0.708	0.693	0.978	0.978	0.967	0.967	0.967	0.965	0.965	0.972	1.000	1.000
13	0.628	0.609	0.743	0.743	0.745	0.745	0.746	0.749	0.751	0.742	0.774	0.774	0.704	0.704	0.704	0.712	0.713	1.000	1.000	1.000
14	0.373	0.384	0.483	0.622	0.621	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
15	-0.429	0.170	0.170	0.170	0.363	0.363	0.616	0.999	0.995	0.994	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
16	-0.363	0.173	0.175	0.175	0.416	0.416	0.717	0.999	0.999	0.999	0.999	0.999	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
17	-0.419	0.224	0.227	0.226	0.431	0.431	0.696	0.983	0.983	0.983	0.984	0.984	0.985	0.985	0.985	0.987	1.000	1.000	1.000	1.000
18	-0.328	0.495	0.494	0.494	0.663	0.663	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
19	-0.004	0.299	0.298	0.451	0.752	0.752	0.752	0.752	0.752	0.751	0.751	0.751	0.751	0.750	0.750	0.746	0.746	0.746	0.745	1.000
20	-0.371	0.660	0.659	0.660	0.988	0.988	0.988	0.988	0.988	0.988	0.988	0.988	0.988	0.988	0.988	0.989	0.989	0.989	0.989	1.000

Figure S2: Performance characteristics of different chromatin state models: Each column represents a state model for a state number between 1 and 20. Each cell represents the performance of the corresponding state model *versus* the 20-state model. Performance values are colour-coded. The optimum state model combines a minimal number of states and a maximal set of performance values. The vertical grey lines highlight the 11-state model used in this study (comprising 10 states with modified histone occupancies and 1 zero-modification state).