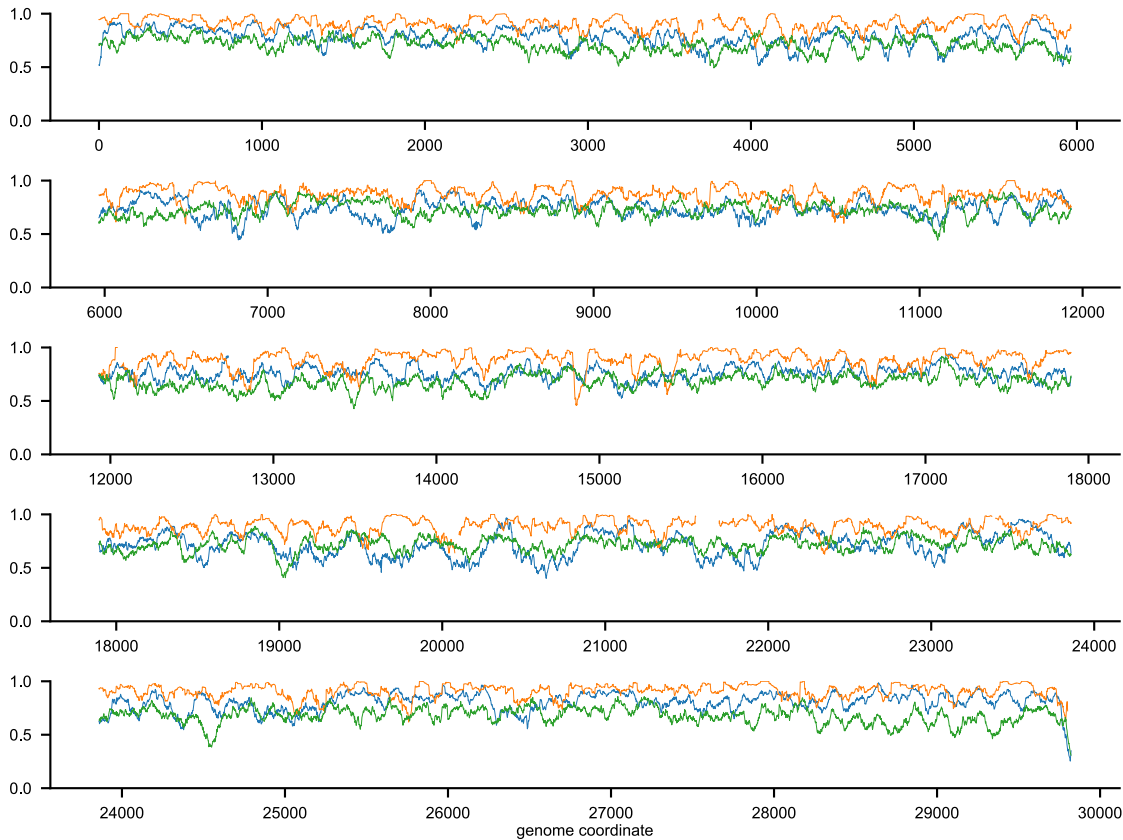
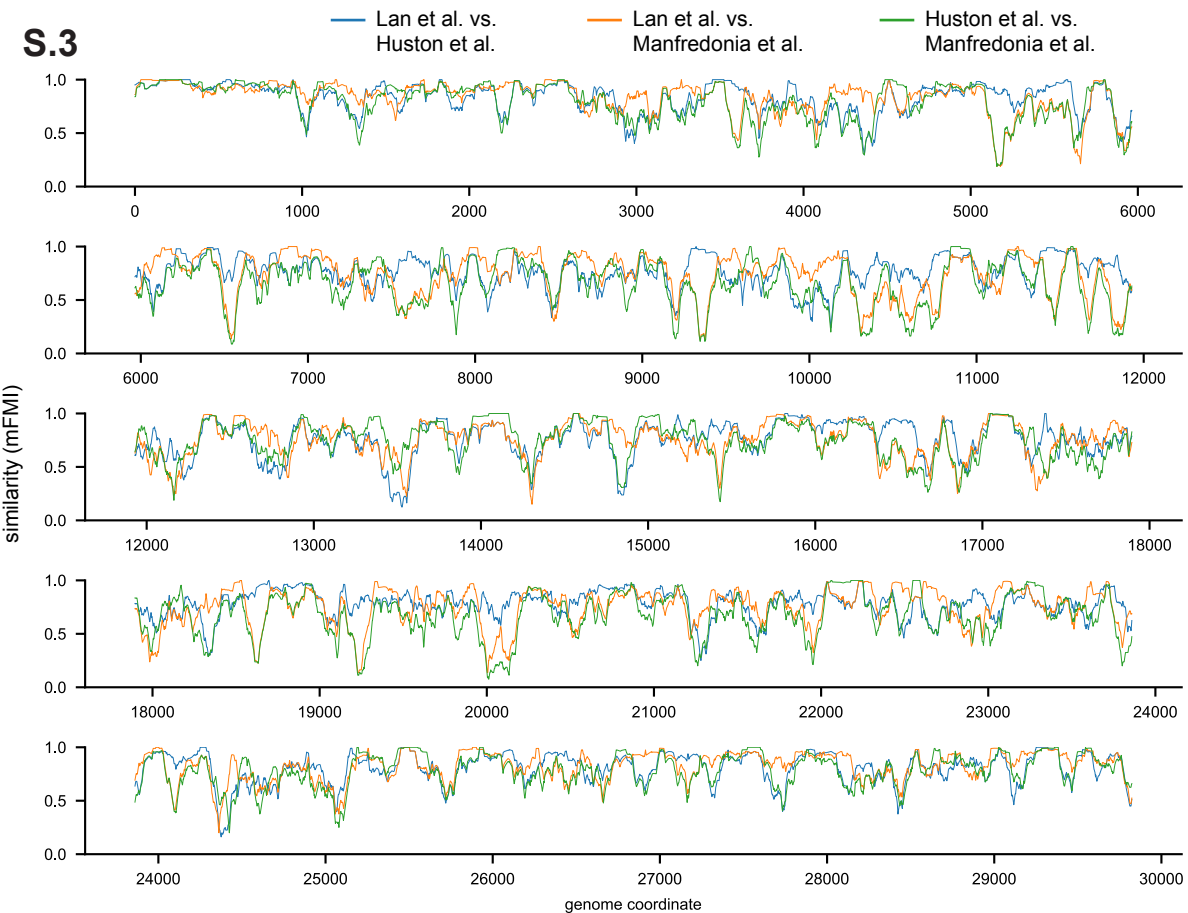


S.2

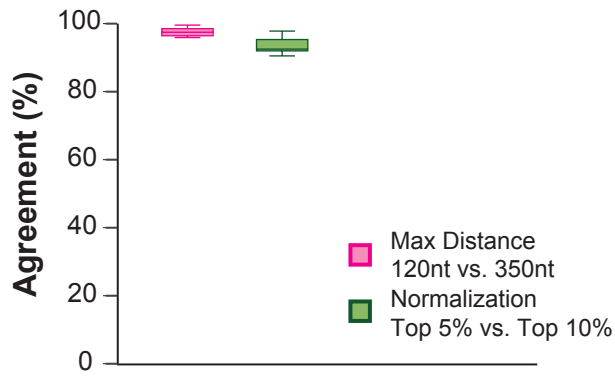
— Lan et al. — Huston et al. — Manfredonia et al.

DSCI

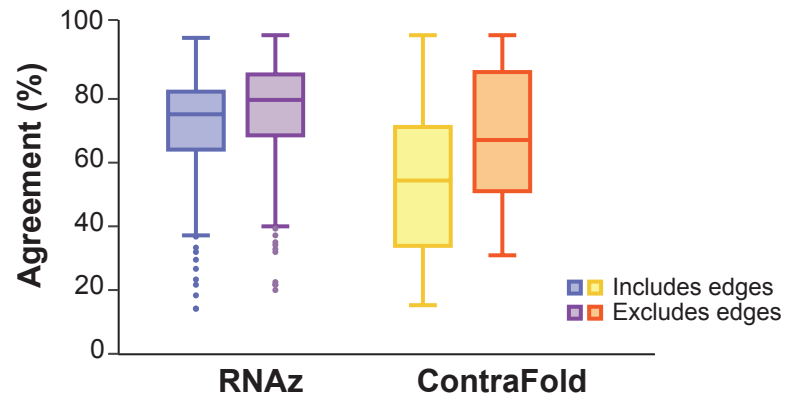


S.3

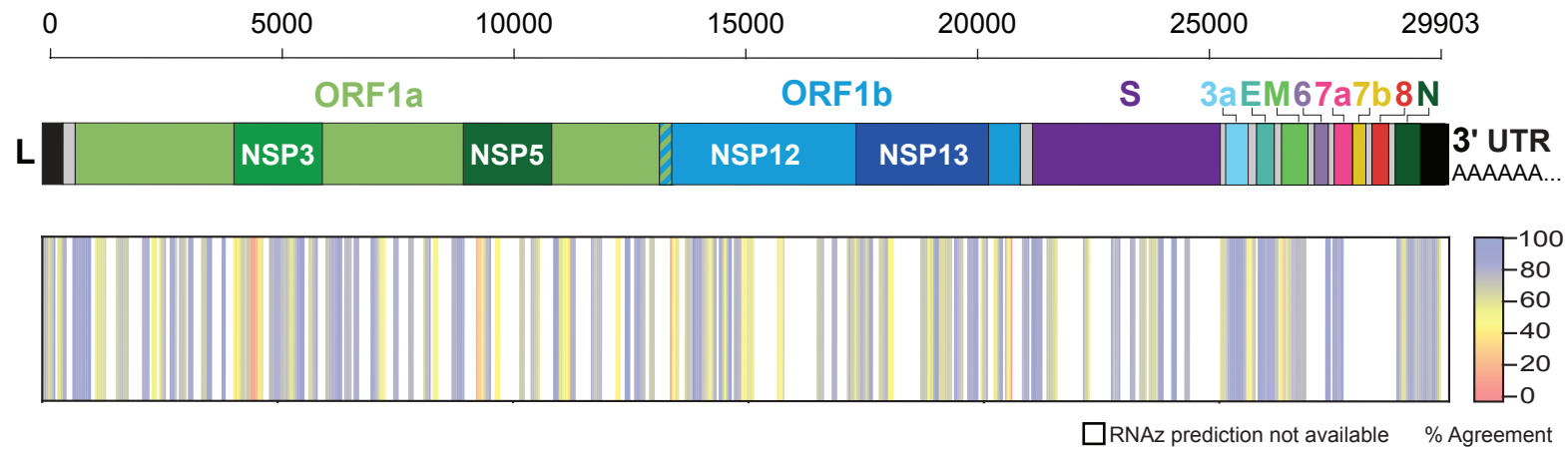
S.4A In-cell model consistency



B Comparison to purely computational models

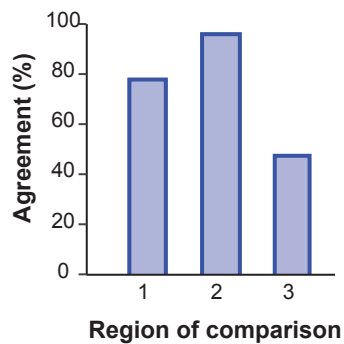


C Genome-wide comparison with RNAz



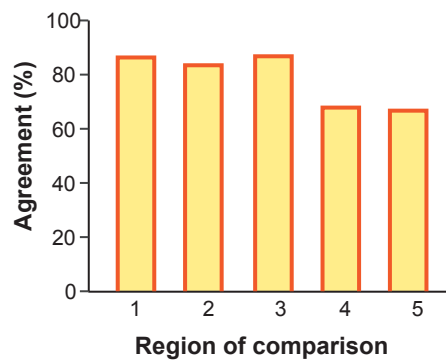
D

Comparison with high P-value RNAz



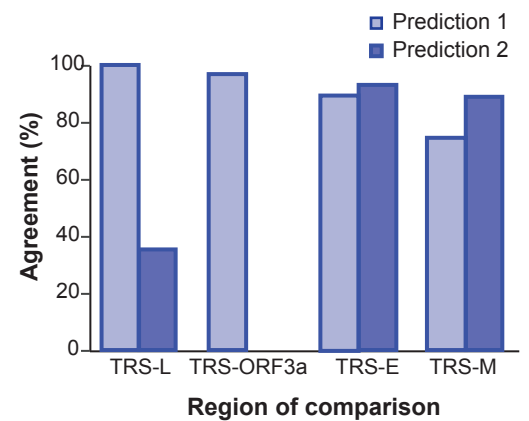
E

Comparison with high confidence ContraFold



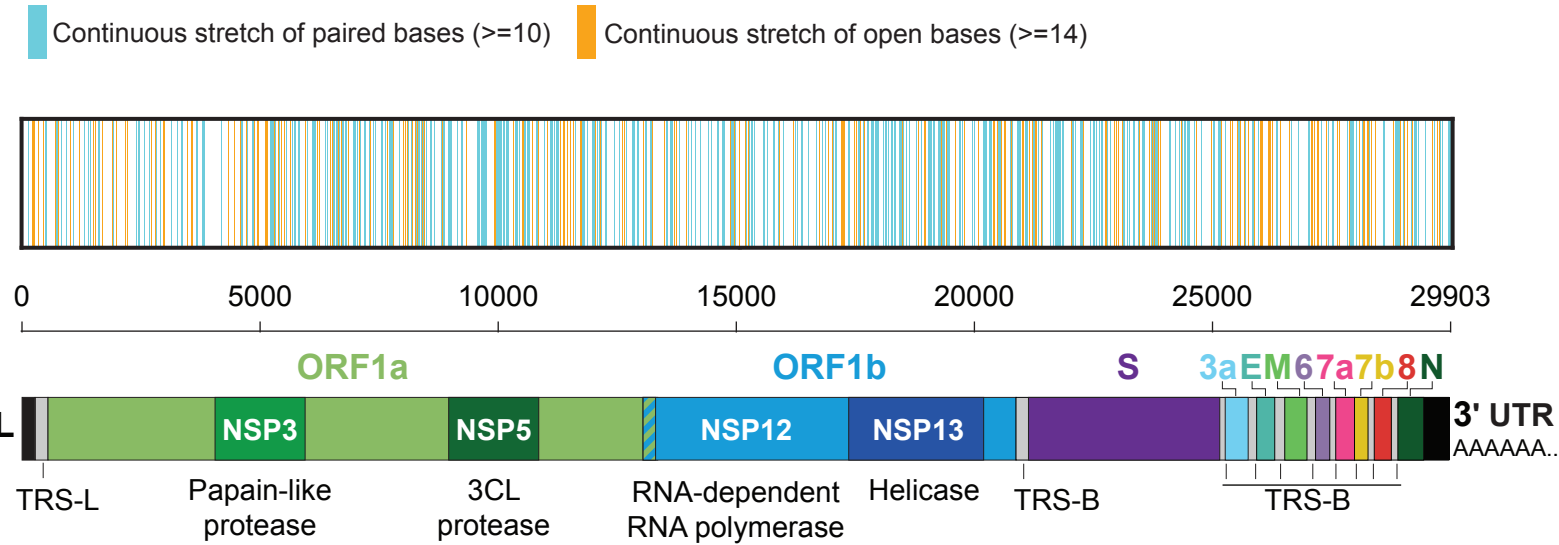
F

Comparison of TRS structures (RNAz)

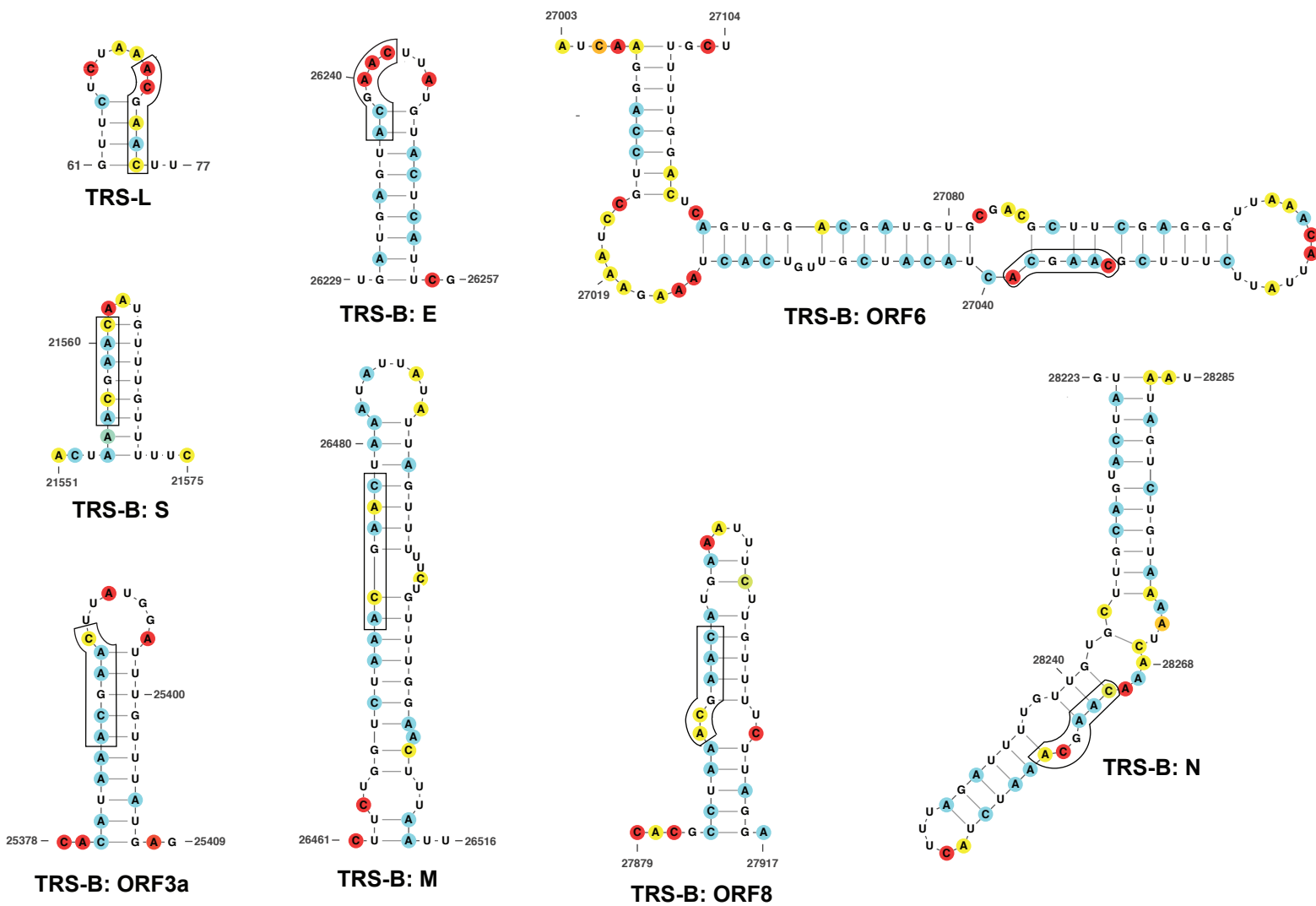


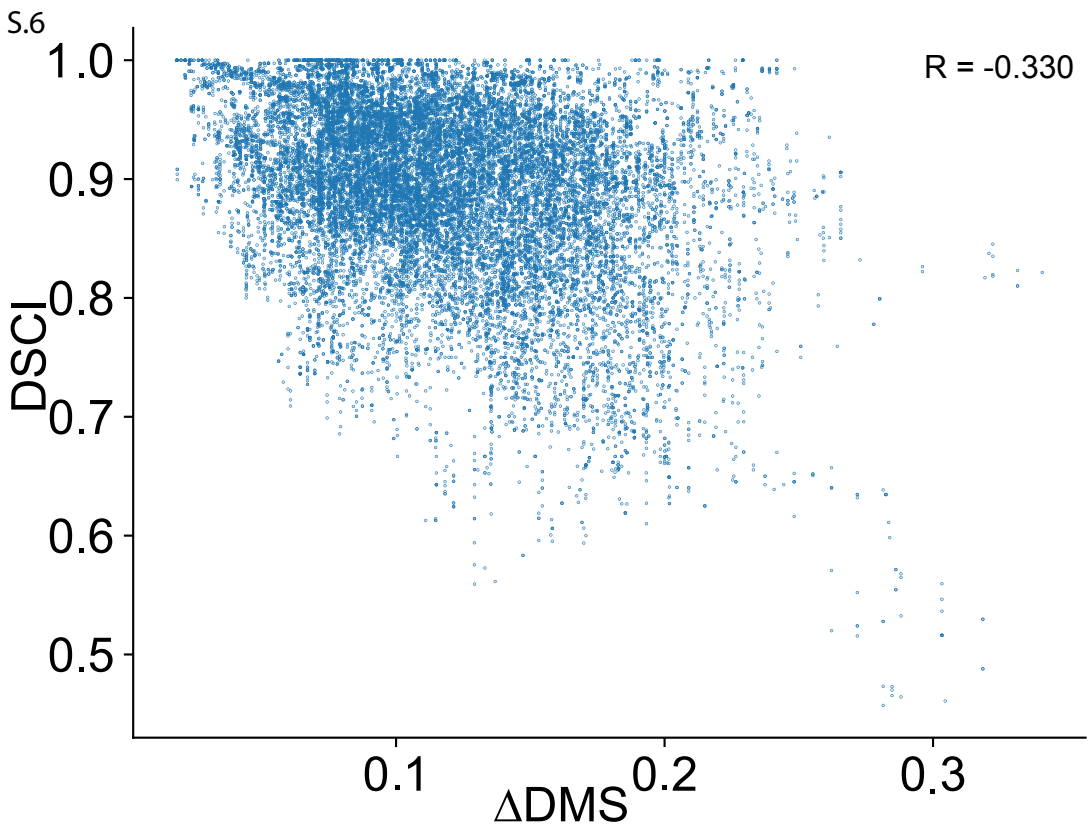
S.5A

Structured regions and accessible regions across the genome



B Structures at the TRS-L and TRS-B





S. Table 1`

index	start	end	length	
1	128	149	22	
2	505	528	24	
3	726	756	31	
4	823	837	15	
5	926	939	14	
6	1071	1089	19	
7	1304	1321	18	
8	1330	1359	30	
9	1377	1399	23	
10	1421	1438	18	
11	1573	1598	26	
12	1610	1636	27	
13	1919	1939	21	
14	2385	2398	14	
15	2435	2458	24	
16	2550	2568	19	
17	2667	2682	16	
18	2801	2819	19	
19	2901	2918	18	
20	3116	3129	14	
21	3258	3273	16	
22	3349	3371	23	
23	3647	3662	16	
24	3668	3683	16	
25	3733	3818	86	
26	3863	3883	21	
27	4101	4122	22	
28	4264	4307	44	
29	4580	4608	29	
30	4619	4645	27	
31	4702	4715	14	
32	4826	4846	21	
33	4877	4897	21	
34	5020	5036	17	
35	5297	5311	15	
36	5382	5399	18	
37	5522	5535	14	
38	5647	5662	16	
39	5688	5715	28	
40	5773	5795	23	
41	5933	5949	17	
42	5955	5969	15	

43	6058	6090	33
44	6103	6145	43
45	6307	6325	19
46	6346	6362	17
47	6390	6403	14
48	6505	6532	28
49	6538	6554	17
50	6567	6589	23
51	6622	6640	19
52	6697	6736	40
53	6771	6785	15
54	6925	6973	49
55	7010	7025	16
56	7073	7092	20
57	7146	7193	48
58	7214	7229	16
59	7260	7280	21
60	7391	7404	14
61	7511	7536	26
62	7547	7567	21
63	7590	7603	14
64	7690	7716	27
65	7725	7743	19
66	8075	8095	21
67	8128	8143	16
68	8290	8327	38
69	8336	8349	14
70	8379	8392	14
71	8459	8472	14
72	8523	8537	15
73	8556	8576	21
74	8621	8647	27
75	8669	8690	22
76	8766	8779	14
77	8800	8822	23
78	8906	8942	37
79	8957	8992	36
80	9096	9117	22
81	9131	9158	28
82	9187	9224	38
83	9281	9294	14
84	9527	9546	20
85	9555	9569	15

86	9624	9680	57
87	9913	9931	19
88	10006	10030	25
89	10067	10096	30
90	10157	10174	18
91	10440	10456	17
92	10500	10536	37
93	10551	10614	64
94	10754	10781	28
95	10912	10927	16
96	11040	11082	43
97	11118	11131	14
98	11165	11230	66
99	11560	11577	18
100	11728	11742	15
101	11755	11772	18
102	11814	11830	17
103	11910	11928	19
104	11957	11970	14
105	12014	12027	14
106	12055	12129	75
107	12173	12220	48
108	12281	12309	29
109	12314	12330	17
110	12484	12498	15
111	12619	12635	17
112	12665	12696	32
113	12741	12766	26
114	12775	12791	17
115	12881	12928	48
116	12967	12988	22
117	13052	13065	14
118	13327	13347	21
119	13723	13736	14
120	13912	13957	46
121	13990	14005	16
122	14056	14070	15
123	14170	14185	16
124	14405	14418	14
125	14642	14690	49
126	14819	14841	23
127	14861	14889	29
128	14900	14915	16

129	14926	14942	17
130	15139	15156	18
131	15196	15213	18
132	15236	15272	37
133	15459	15472	14
134	15498	15514	17
135	15560	15573	14
136	15695	15720	26
137	15801	15818	18
138	15902	15918	17
139	16199	16213	15
140	16297	16312	16
141	16419	16434	16
142	16592	16607	16
143	16712	16737	26
144	16761	16775	15
145	16787	16805	19
146	16938	16954	17
147	16990	17026	37
148	17273	17294	22
149	17491	17504	14
150	17515	17538	24
151	17561	17593	33
152	17651	17667	17
153	17739	17796	58
154	17822	17853	32
155	17875	17898	24
156	18008	18052	45
157	18102	18115	14
158	18151	18180	30
159	18219	18260	42
160	18321	18360	40
161	18371	18384	14
162	18415	18436	22
163	18471	18486	16
164	18531	18546	16
165	18789	18802	14
166	18918	18937	20
167	18965	18991	27
168	19003	19018	16
169	19046	19065	20
170	19249	19271	23
171	19569	19593	25

172	19601	19615	15
173	19623	19664	42
174	19861	19876	16
175	19883	19899	17
176	20003	20023	21
177	20092	20161	70
178	20198	20213	16
179	20230	20253	24
180	20403	20443	41
181	20652	20667	16
182	20693	20708	16
183	20794	20835	42
184	20947	21008	62
185	21123	21147	25
186	21235	21248	14
187	21304	21317	14
188	21478	21501	24
189	21573	21752	180
190	21855	21868	14
191	21949	21974	26
192	22115	22137	23
193	22153	22170	18
194	22390	22405	16
195	22442	22459	18
196	22547	22573	27
197	22611	22624	14
198	22736	22750	15
199	23010	23047	38
200	23079	23135	57
201	23155	23168	14
202	23306	23324	19
203	23395	23409	15
204	23414	23460	47
205	23590	23607	18
206	23626	23641	16
207	23655	23695	41
208	23705	23725	21
209	23910	23934	25
210	23960	23973	14
211	23984	23999	16
212	24095	24108	14
213	24165	24184	20
214	24235	24250	16

215	24270	24304	35
216	24337	24353	17
217	24361	24384	24
218	24490	24503	14
219	24633	24647	15
220	24888	24911	24
221	24985	25008	24
222	25015	25032	18
223	25133	25148	16
224	25408	25439	32
225	25546	25563	18
226	25579	25592	14
227	25703	25719	17
228	25798	25816	19
229	25823	25836	14
230	26198	26224	27
231	26508	26531	24
232	26722	26742	21
233	26862	26886	25
234	26902	26919	18
235	27128	27148	21
236	27289	27302	14
237	27363	27408	46
238	27546	27560	15
239	27669	27692	24
240	27751	27777	27
241	27800	27828	29
242	27869	27882	14
243	27997	28012	16
244	28142	28163	22
245	28333	28346	14
246	28431	28455	25
247	28688	28711	24
248	28721	28754	34
249	28767	28781	15
250	29004	29025	22
251	29074	29089	16
252	29110	29133	24
253	29155	29178	24
254	29307	29320	14
255	29488	29502	15
256	29614	29628	15
257	29658	29673	16

258	29786	29800	15
259	29824	29844	21