

Additional file 3: (a) Densities of TRs in repeat classes of all twelve genomes

unit-size	Dappu v1.1	DroMel-5.5	ApiMel-4.0	CaeEle-WS160	HomSap-36.2	MusMus-36.1	GalGal-2.1	AraTha-6.0	ThaPse-3.0	OstLuc-2.0	NeuCra-7.0	SacCer-2.1	min	max
	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp	bp/Mbp
1	1747.05	1638.96	4166.41	653.35	3889.59	2107.50	2617.82	1468.67	13.04	5.00	1971.02	1157.74	5.00	4166.41
2	1884.78	1961.64	7860.77	727.27	2267.41	8913.75	625.82	1264.85	235.75	3075.53	535.49	646.68	235.75	8913.75
3	2661.97	1543.72	3181.89	480.56	658.69	1877.24	450.07	1052.81	1457.03	3980.72	2752.73	900.43	450.07	3980.72
4	632.86	939.20	1742.14	224.94	2248.99	5360.09	1137.97	158.94	187.96	553.66	1095.23	118.55	118.55	5360.09
5	534.78	3253.74	1313.43	120.24	1032.11	1994.93	964.77	253.66	66.35	1160.18	619.32	133.38	66.35	3253.74
6	418.03	1538.05	1008.61	1372.97	511.48	1517.09	330.23	350.00	385.34	2223.80	1250.61	639.14	330.23	2223.80
7	246.38	1291.02	914.68	516.49	336.14	525.14	183.56	628.74	68.04	1602.74	277.98	81.10	68.04	1602.74
8	245.32	846.53	1003.27	646.63	304.20	823.71	428.91	118.92	243.15	898.30	306.26	84.75	84.75	1003.27
9	380.14	577.69	1054.88	801.62	236.09	336.77	154.76	112.27	74.69	1966.24	629.19	322.84	74.69	1966.24
10	572.33	473.75	1351.75	614.65	269.68	516.09	197.02	117.73	40.06	832.80	216.08	95.02	40.06	1351.75
11	234.00	6268.95	997.53	1172.56	176.97	220.16	171.08	109.34	36.00	818.79	202.36	125.43	36.00	6268.95
12	404.86	2272.43	1120.55	437.84	292.88	528.97	213.17	177.88	147.32	2077.34	536.20	371.89	147.32	2272.43
13	174.72	112.97	595.97	171.77	156.95	191.59	106.89	83.41	29.46	518.75	188.34	75.55	29.46	595.97
14	109.67	147.28	384.99	123.30	173.36	284.12	85.97	58.15	130.68	377.13	73.56	36.70	36.70	384.99
15	249.76	161.12	299.43	721.62	157.36	275.05	77.65	85.31	130.87	653.92	258.56	170.74	77.65	721.62
16	76.86	62.24	181.20	323.04	182.25	262.95	75.83	67.89	25.38	209.77	64.30	5.80	5.80	323.04
17	650.40	34.06	121.91	271.35	143.61	188.04	52.76	74.10	46.99	119.73	46.58	16.15	16.15	650.40
18	196.10	88.47	147.11	312.89	177.03	223.17	50.23	100.43	77.48	377.81	142.29	117.22	50.23	377.81
19	106.09	43.01	77.65	575.95	117.56	154.57	33.42	47.71	14.68	79.89	25.62	16.82	14.68	575.95
20	83.21	54.09	109.49	1048.63	167.71	231.89	44.99	66.69	56.70	88.45	29.55	36.04	29.55	1048.63
21	162.30	111.73	75.21	654.99	119.19	156.64	32.60	120.39	64.10	232.94	55.61	58.98	32.60	654.99
22	40.72	122.84	47.25	182.24	115.55	176.17	22.85	56.70	6.63	39.46	12.72	0.00	0.00	182.24
23	47.33	553.69	55.51	89.15	109.82	115.84	16.81	46.80	34.74	21.43	5.18	17.40	5.18	553.69
24	336.99	88.41	93.40	50.91	179.23	177.82	16.00	111.08	55.10	247.26	31.13	84.83	16.00	336.99
25	22.59	31.14	47.62	623.15	102.89	107.47	13.86	42.47	10.44	27.49	5.79	17.56	5.79	623.15
26	37.39	34.65	200.86	639.95	137.71	127.14	9.21	138.36	31.83	57.48	6.58	0.00	0.00	639.95
27	86.97	46.73	58.80	342.08	114.22	134.80	11.65	263.77	30.10	98.90	12.75	30.74	11.65	342.08
28	22.39	38.00	75.73	53.78	151.47	127.21	20.88	308.45	9.20	25.98	11.96	0.00	0.00	308.45
29	15.56	14.11	40.00	130.12	116.61	127.68	10.27	70.85	1.89	6.66	27.61	0.00	0.00	130.12
30	110.51	80.52	87.47	230.31	146.99	161.34	13.59	124.61	34.71	96.25	24.65	40.68	13.59	230.31
31	56.62	181.65	31.80	391.56	115.02	158.31	9.19	96.56	24.87	22.72	0.00	0.00	0.00	391.56
32	39.92	67.85	35.94	746.33	143.44	136.35	9.71	157.45	2.05	5.45	3.72	0.00	0.00	746.33
33	80.85	315.82	43.61	278.12	103.98	101.06	6.96	65.59	15.26	129.88	12.62	15.57	6.96	315.82
34	80.81	139.60	53.91	807.92	137.61	104.60	4.82	20.56	2.57	0.00	0.00	12.34	0.00	807.92
35	82.93	130.77	57.16	1913.16	108.22	79.51	8.74	49.66	2.92	24.38	8.21	0.00	0.00	1913.16
36	79.28	85.31	285.87	267.25	127.17	106.47	7.52	66.76	27.60	101.93	30.34	728.69	7.52	728.69
37	24.70	19.44	44.96	149.58	158.69	89.06	4.10	29.67	8.98	21.43	0.00	0.00	0.00	158.69
38	39.08	23.37	27.96	155.51	125.10	112.93	6.90	38.54	3.72	35.21	2.19	0.00	0.00	155.51
39	37.79	153.51	37.98	282.65	124.77	103.95	9.83	37.01	10.25	82.32	5.79	25.68	5.79	282.65
40	9.30	19.86	47.00	847.74	176.08	86.76	12.72	17.46	10.87	74.29	8.41	0.00	0.00	847.74
41	20.68	4.57	26.31	346.74	92.43	66.53	13.69	12.92	16.02	6.36	0.00	118.30	0.00	346.74
42	61.60	30.42	25.78	218.70	87.56	106.76	9.71	44.67	32.15	200.61	0.00	118.22	0.00	218.70
43	31.36	22.45	17.42	366.26	62.58	52.03	13.78	34.21	0.00	15.68	2.80	0.00	0.00	366.26
44	11.54	22.55	29.55	98.18	68.17	61.98	8.58	22.33	0.00	0.00	0.00	0.00	0.00	98.18
45	73.75	80.73	43.16	228.68	57.89	50.01	5.61	49.20	6.28	28.63	8.92	0.00	0.00	228.68
46	25.23	152.10	31.15	24.00	60.84	64.81	1.53	15.35	3.01	50.89	0.00	0.00	0.00	152.10
47	23.71	36.03	20.18	44.01	87.18	43.57	2.81	10.57	3.72	0.00	0.00	30.07	0.00	87.18
48	82.42	83.25	20.82	220.51	144.03	51.66	6.01	60.49	10.35	15.07	3.26	29.33	3.26	220.51
49	20.65	20.42	30.60	26.28	148.67	38.60	2.03	25.66	0.00	10.53	4.82	0.00	0.00	148.67
50	40.13	15.12	43.63	83.08	85.79	51.12	3.38	34.67	4.04	0.00	0.00	0.00	0.00	85.79

Additional file 3: (b) Mean lengths of TRs in repeat classes of all twelve genomes

	Dappu v1.1	DroMel-5.5	ApiMel-4.0	CaeEle-WS160	HomSap-36.2	MusMus-36.1	GalGal-2.1	AraTha-6.0	ThaPse-3.0	OstLuc-2.0	NeuCra-7.0	SacCer-2.1	min	max
unit-size	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]
1	16.15	16.95	17.79	15.96	18.79	18.78	18.05	16.66	14.03	13.20	24.04	17.25	13.20	24.04
2	18.57	21.95	26.31	24.28	28.93	40.42	22.29	23.26	21.40	19.80	22.97	23.31	18.57	40.42
3	19.69	26.08	26.29	18.75	24.29	37.74	20.47	20.83	20.49	23.82	24.11	26.47	18.75	37.74
4	21.71	32.06	24.09	24.34	32.24	39.21	28.75	19.26	24.74	25.67	24.04	21.36	19.26	39.21
5	24.45	89.30	26.45	20.72	28.25	36.60	39.54	19.60	20.50	25.17	24.35	22.69	19.60	89.30
6	27.84	30.55	26.96	56.81	26.49	41.64	35.04	22.73	59.51	26.21	26.13	30.19	22.73	59.51
7	23.49	41.27	27.10	33.07	27.48	34.66	28.37	47.64	24.98	40.18	25.06	23.88	23.49	47.64
8	24.47	43.37	27.03	34.26	30.82	41.18	28.42	24.44	101.01	27.11	30.38	24.36	24.36	101.01
9	27.39	39.58	28.53	32.53	37.63	40.66	29.58	25.21	26.48	28.85	28.33	31.50	25.21	40.66
10	45.20	50.17	32.68	34.35	35.06	40.46	30.75	28.07	28.41	29.35	30.76	26.67	26.67	50.17
11	27.78	369.57	29.26	47.85	35.05	36.81	29.66	28.66	28.07	30.98	31.55	32.91	27.78	369.57
12	35.74	161.36	31.18	35.54	37.92	42.21	31.02	31.25	31.92	32.43	33.61	37.41	31.02	161.36
13	35.26	34.61	34.42	35.66	44.13	46.74	33.25	35.45	35.35	34.08	44.31	43.43	33.25	46.74
14	37.90	57.12	37.35	44.86	46.67	55.46	37.63	37.77	69.10	36.89	37.96	55.38	36.89	69.10
15	50.92	63.52	48.80	125.09	58.58	60.81	43.91	42.40	54.30	40.49	50.54	49.19	40.49	125.09
16	68.93	56.45	49.17	149.96	65.12	70.29	52.69	50.81	41.68	40.14	51.71	35.00	35.00	149.96
17	270.15	60.12	50.62	89.48	71.98	84.94	51.29	46.16	61.08	40.54	50.75	48.75	40.54	270.15
18	85.90	67.99	67.14	92.36	80.08	87.92	55.39	54.63	71.09	48.91	64.45	64.77	48.91	92.36
19	59.36	63.48	58.06	195.15	83.52	109.38	54.35	52.56	45.80	45.87	50.25	50.75	45.80	195.15
20	85.16	98.66	90.70	334.67	99.10	102.55	69.68	59.01	61.00	61.47	55.19	108.75	55.19	334.67
21	70.93	204.72	78.65	227.28	100.28	124.66	72.55	62.60	58.82	59.15	64.15	72.60	58.82	227.28
22	72.34	443.20	72.78	112.31	97.58	139.71	70.18	61.90	51.75	52.10	62.38			443.20
23	97.68	553.91	108.69	144.18	112.99	140.26	69.56	60.53	120.44	56.60	50.75	70.00	50.75	553.91
24	152.93	110.67	127.69	82.34	114.76	132.86	76.87	80.28	71.62	85.92	67.83	128.00	67.83	152.93
25	83.35	248.39	130.96	833.13	132.53	145.47	82.22	78.97	54.33	60.50	56.75	70.67	54.33	833.13
26	95.66	125.00	226.09	588.72	154.88	154.17	93.47	144.06	141.86	75.90	64.50			588.72
27	107.90	93.86	138.61	357.31	175.01	173.82	98.09	180.35	67.07	72.56	83.33	74.20	67.07	357.31
28	84.60	134.13	166.98	158.62	182.47	168.43	139.47	239.90	57.40	68.60	93.80			239.90
29	85.07	163.71	144.42	383.74	201.32	194.41	121.87	136.15	59.00	88.00	216.60			383.74
30	152.46	146.89	150.72	231.93	201.45	204.20	125.76	116.59	72.20	84.73	107.44	98.20	72.20	231.93
31	94.55	581.38	166.95	265.81	212.87	290.37	113.11	117.26	86.22	75.00				581.38
32	93.14	196.71	148.27	409.41	220.27	207.84	127.91	127.46	64.00	72.00	73.00			409.41
33	152.21	457.87	146.36	224.93	234.99	205.23	114.20	111.50	79.33	131.92	123.75	94.00	79.33	457.87
34	210.16	444.41	161.77	248.70	279.41	218.59	113.02	84.48	80.00			149.00		444.41
35	139.95	849.28	164.52	307.70	273.98	194.97	141.13	109.43	91.00	80.50	107.33			849.28
36	155.41	231.07	183.84	282.08	253.09	224.59	145.24	120.53	107.62	149.56	170.00	233.95	107.62	282.08
37	156.68	150.29	173.13	306.08	307.11	245.91	118.62	130.74	93.33	94.33				307.11
38	112.73	189.75	137.45	577.52	321.32	242.69	161.81	131.03	116.00	232.50	86.00			577.52
39	153.69	361.48	162.48	480.64	313.20	216.46	153.75	137.62	106.67	155.29	227.00	155.00	106.67	480.64
40	105.36	322.40	231.02	438.28	239.64	233.48	181.59	138.53	113.00	327.00	165.00			438.28
41	105.84	247.67	160.32	643.85	251.65	224.82	312.79	109.79	100.00	84.00		1428.00		1428.00
42	139.90	189.92	186.12	203.05	294.32	196.07	180.47	136.31	250.75	132.45		475.67		475.67
43	130.92	364.40	236.71	270.19	319.97	229.13	226.90	145.43		207.00	110.00			364.40
44	183.00	915.25	200.76	298.33	294.39	236.93	176.02	115.52						915.25
45	208.91	409.59	243.29	546.19	334.30	245.28	221.33	130.09	98.00	189.00	175.00			546.19
46	363.91	2057.92	179.95	240.60	325.94	314.81	137.09	130.50	94.00	336.00				2057.92
47	313.50	619.58	233.10	1103.25	455.45	248.09	162.47	157.12	116.00			363.00		1103.25
48	335.33	1126.33	253.21	1228.39	464.36	260.71	197.30	206.17	161.50	99.50	128.00	354.00	99.50	1228.39
49	218.47	174.53	227.00	376.71	261.44	257.04	222.11	190.81		139.00	189.00			376.71
50	172.05	245.50	252.00	417.20	305.28	266.11	261.31	187.50	126.00					417.20

Additional file 3: (c) Numbers of TRs in repeat classes of all twelve genomes

unit-size	Dappu v1.1 #sat	DroMel-5.5 #sat	ApiMel-4.0 #sat	CaeEle-WS160 #sat	HomSap-36.2 #sat	MusMus-36.1 #sat	GalGal-2.1 #sat	AraTha-6.0 #sat	ThaPse-3.0 #sat	OstLuc-2.0 #sat	NeuCra-7.0 #sat	SacCer-2.1 #sat	min #sat	max #sat
1	17161	15701	54104	4104	591617	286206	142803	10492	29	5	3216	810	5	591617
2	16104	14511	69036	3004	224459	563483	27674	6471	344	2051	915	335	335	563483
3	21458	9622	28005	2570	77621	127365	21667	6017	2222	2208	4484	414	414	127365
4	4630	4770	16755	927	200797	351575	39190	982	237	285	1788	67	67	351575
5	3476	5984	11528	582	105107	140683	24240	1540	101	610	1000	71	71	140683
6	2382	8220	8673	2430	55324	93653	9382	1840	202	1124	1889	256	202	93653
7	1664	5133	7810	1567	35008	38803	6385	1577	85	527	435	41	41	38803
8	1591	3204	8585	1895	28276	51278	14888	579	76	438	417	42	42	51278
9	2213	2386	8557	2476	18011	21212	5159	530	88	902	876	127	88	21212
10	2041	1535	9572	1807	22085	32701	6358	499	44	375	276	43	43	32701
11	1336	2776	7884	2472	14492	15284	5685	454	40	350	252	46	40	15284
12	1814	2310	8313	1240	22202	32112	6778	678	144	846	629	120	120	32112
13	786	530	4001	483	10204	10500	3175	280	26	201	168	21	21	10500
14	459	419	2383	278	10654	13130	2253	185	59	135	76	8	8	13130
15	780	415	1421	581	7756	11604	1747	241	80	215	201	42	42	11604
16	177	179	852	219	8085	9568	1426	159	19	69	49	2	2	9568
17	389	92	558	313	5767	5700	1017	191	24	39	36	4	4	5767
18	366	212	509	340	6398	6519	895	219	34	102	87	22	22	6519
19	284	110	309	296	4115	3631	606	108	10	23	20	4	4	4115
20	155	89	279	338	4894	5825	4894	136	29	19	21	4	4	5825
21	363	89	221	298	3453	3239	444	230	34	52	34	10	10	3453
22	91	45	150	164	3428	3342	323	109	4	10	8	0	0	3428
23	77	175	118	62	2815	2116	241	92	9	5	4	3	3	2815
24	350	130	169	62	4497	3428	205	165	24	38	18	8	8	4497
25	43	23	84	75	2254	1893	166	64	6	6	4	3	3	2254
26	62	45	214	109	2579	2116	99	117	7	10	4	0	0	2579
27	128	85	98	96	1898	2021	117	182	14	18	6	5	5	2021
28	42	46	106	34	2399	1942	149	153	5	5	5	0	0	2399
29	29	14	64	34	1674	1706	83	66	1	1	5	0	0	1706
30	119	89	136	100	2122	2032	109	128	15	15	9	5	5	2122
31	95	55	44	153	1554	1428	80	98	9	4	0	0	0	1554
32	70	56	56	187	1904	1690	76	147	1	1	2	0	0	1904
33	85	112	69	124	1271	1261	60	70	6	13	4	2	2	1271
34	61	51	77	330	1416	1221	42	29	1	0	0	1	0	1416
35	94	25	81	632	1138	1041	61	54	1	4	3	0	0	1138
36	81	61	360	95	1454	1217	51	66	8	9	7	41	7	1454
37	25	21	60	49	1506	927	34	27	3	3	0	0	0	1506
38	55	20	47	27	1117	1188	42	35	1	2	1	0	0	1188
39	39	69	54	59	1150	1237	63	32	3	7	1	2	1	1237
40	14	10	47	195	2106	951	69	15	3	3	2	0	0	2106
41	31	3	38	54	1051	757	48	14	5	1	0	1	0	1051
42	70	26	32	108	867	1389	53	39	4	20	0	3	0	1389
43	38	10	17	140	559	579	62	28	0	1	1	0	0	579
44	10	4	34	33	662	669	48	23	0	0	0	0	0	669
45	56	32	41	42	509	520	27	45	2	2	2	0	0	520
46	11	12	40	10	534	525	11	14	1	2	0	0	0	534
47	12	12	20	4	560	448	17	8	1	0	0	1	0	560
48	39	12	19	18	908	507	30	35	2	2	1	1	1	908
49	15	19	32	7	1629	383	9	16	0	1	1	0	0	1629
50	37	10	40	20	809	490	13	22	1	0	0	0	0	809

Additional file 3: (d) Mean percentage perfection of TRs in repeat classes of all twelve genomes

unit-size	Dappu v1.1 [%]	DroMel-5.5 [%]	ApiMel-4.0 [%]	CaeEle-WS160 [%]	HomSap-36.2 [%]	MusMus-36.1 [%]	GalGal-2.1 [%]	AraTha-6.0 [%]	ThaPse-3.0 [%]	OstLuc-2.0 [%]	NeuCra-7.0 [%]	SacCer-2.1 [%]	min [%]	max [%]
1	99.5	99.4	99.1	99.4	99.6	99.5	99.4	99.6	99.8	100.0	99.2	99.4	99.1	100.0
2	99.4	98.6	98.7	99.4	98.4	98.6	98.8	99.4	99.3	97.7	99.1	98.8	97.7	99.4
3	99.4	98.1	98.5	99.3	98.9	98.4	99.2	99.1	99.4	98.7	99.0	98.3	98.1	99.4
4	99.1	98.6	98.7	99.0	98.1	98.3	98.8	99.5	98.7	98.9	99.2	99.1	98.1	99.5
5	98.9	98.2	98.2	99.3	98.3	98.4	98.6	99.5	99.8	98.4	99.0	98.6	98.2	99.8
6	98.6	98.3	98.1	95.7	98.2	97.6	97.7	99.0	99.3	98.8	98.7	98.2	95.7	99.3
7	98.7	98.2	97.8	98.3	97.8	97.1	97.7	96.1	99.0	97.4	98.8	98.7	96.1	99.0
8	99.1	98.3	98.1	98.7	97.5	96.7	98.4	99.1	97.6	98.6	98.9	99.4	96.7	99.4
9	98.5	98.0	98.2	98.5	97.4	96.9	98.2	98.9	99.2	98.6	98.6	98.5	96.9	99.2
10	98.2	98.1	98.3	97.9	97.5	96.9	98.5	98.5	98.8	98.4	98.5	99.6	96.9	99.6
11	99.0	95.6	98.6	97.1	97.9	97.7	98.7	98.7	99.6	98.2	98.7	98.4	95.6	99.6
12	98.6	96.6	98.5	98.4	97.7	97.4	98.8	98.8	99.1	98.8	98.5	98.2	96.6	99.1
13	98.6	98.5	98.4	98.8	97.7	97.6	98.8	98.2	99.0	98.4	96.9	98.3	96.9	99.0
14	98.3	97.9	98.1	98.0	97.6	96.9	98.6	97.9	98.5	98.0	98.2	97.5	96.9	98.6
15	97.3	97.0	97.8	96.6	97.2	97.2	98.4	98.0	98.8	98.7	97.5	98.3	96.6	98.8
16	97.7	96.8	97.6	97.0	97.1	96.8	98.3	97.8	99.7	97.8	98.3	100.0	96.8	100.0
17	95.0	97.3	97.7	96.1	97.5	97.0	98.4	97.6	97.5	99.2	97.8	98.9	95.0	99.2
18	97.1	97.6	96.8	96.2	97.0	96.6	98.2	97.8	97.7	98.8	97.3	96.7	96.2	98.8
19	97.9	98.4	97.0	95.5	97.4	96.8	98.3	98.2	98.9	98.8	98.5	99.0	95.5	99.0
20	96.4	97.6	97.0	94.9	96.8	96.4	97.7	97.8	97.5	97.6	97.0	95.7	94.9	97.8
21	97.0	95.1	96.8	95.7	97.0	96.5	97.9	97.4	98.2	98.5	97.7	97.6	95.1	98.5
22	97.8	93.6	97.2	95.9	97.1	96.5	98.3	98.3	98.3	98.5	98.4			98.5
23	97.0	92.4	96.6	97.2	96.7	96.8	98.4	98.0	96.1	98.8	99.6	94.0	92.4	99.6
24	97.4	96.0	95.8	97.2	96.5	96.6	98.1	97.7	97.7	98.2	98.3	94.9	94.9	98.3
25	97.9	92.9	96.5	97.0	96.7	96.8	98.2	98.2	99.1	98.7	98.7	98.5	92.9	99.1
26	97.0	95.7	95.2	96.9	96.1	96.6	98.1	95.6	97.9	97.6	100.0			100.0
27	97.0	96.8	95.8	96.7	96.5	96.7	97.7	94.4	99.2	98.5	97.1	98.4	94.4	99.2
28	97.9	96.2	97.0	95.4	96.4	96.6	96.7	94.8	100.0	98.4	97.7			100.0
29	97.8	95.9	95.7	93.9	96.4	96.7	97.5	96.7	100.0	95.4	96.5			100.0
30	95.8	95.4	96.4	95.3	96.3	96.3	97.5	96.5	98.7	98.5	96.7	97.5	95.3	98.7
31	97.0	89.8	96.4	94.4	96.2	96.5	97.7	95.5	98.8	97.9				98.8
32	97.6	96.3	96.2	94.1	96.3	96.4	97.5	95.4	100.0	100.0	98.8			100.0
33	96.0	97.2	96.6	94.5	96.1	96.7	97.6	96.8	98.7	98.5	98.2	96.3	94.5	98.7
34	94.7	94.7	96.4	93.3	96.0	96.5	97.6	98.5	97.5			93.5		98.5
35	95.2	91.1	95.1	93.8	96.0	97.0	96.8	97.0	96.7	99.3	96.4			99.3
36	97.2	94.8	95.1	93.7	95.9	96.5	96.6	96.5	98.9	98.8	96.1	94.8	93.7	98.9
37	97.5	94.6	95.4	95.3	93.9	96.8	97.3	96.2	99.0	100.0				100.0
38	97.6	95.3	97.0	94.6	95.6	96.1	96.7	97.3	96.6	96.9	100.0			100.0
39	96.4	96.4	96.6	93.8	95.0	97.4	97.0	97.5	97.2	98.8	99.1	97.8	93.8	99.1
40	97.8	93.6	95.2	94.8	95.1	96.9	96.3	97.8	95.5	97.4	93.8			97.8
41	98.3	93.7	97.4	95.1	95.8	96.9	95.0	97.5	97.6	100.0		87.1		100.0
42	97.3	97.7	96.3	94.6	95.7	97.4	96.1	97.3	97.1	98.4		96.3		98.4
43	97.6	94.5	97.1	94.0	95.7	97.2	95.7	97.9		95.7	96.4			97.9
44	95.4	92.6	96.0	93.9	96.1	96.5	96.6	97.8						97.8
45	96.7	95.5	95.8	94.3	95.9	97.0	96.6	97.6	100.0	99.1	94.2			100.0
46	95.6	88.9	96.7	95.2	95.8	96.6	98.4	98.5	100.0	92.3				100.0
47	93.1	90.8	95.9	92.3	95.3	97.2	96.5	96.6	97.4			90.8		97.4
48	94.8	93.9	94.6	95.6	95.1	96.9	96.4	96.4	98.7	100.0	96.1	95.2	93.9	100.0
49	94.9	96.7	96.5	95.8	95.8	97.4	94.4	96.1		95.8	93.8			97.4
50	96.8	94.2	95.8	95.3	95.6	96.4	94.6	96.2	96.8					96.8