Epigenetics Theoretical Limits of Synthetic Genomes : the cases of Artificials *Caulobacter* (*C. eth-2.0), Mycoplasma Mycoides (JCVI-Syn 1.0, JCVI-Syn 3.0 and JCVI_3A), E-coli and YEAST chr XII*

Suplementary Materials

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Results :

We analyse here, in one hand, Caulobacter crescentus NA1000 genome and synthetic genome Caulobacter ethensis-2.0 (C. eth-2.0), and, in other hand, Mycoplasma Mycoides JCVI-syn1.0, JCVI-syn3.0 and JCVI-syn3A.

Part I : Caulobacter crescentus NA1000 genome and synthetic genome Caulobacter ethensis-2.0 (C. eth-2.0).

The actual NA1000 genome being about 5 times longer than the synthetic genome C. eth-2.0, one might think that the comparison of these 2 genomes is skewed. However, in all the above results, we had already incorporated this difference by weighting the results by the length of the respective genomes.

TC/AG analysis :

Nota : All tables in this article are identical: each box contains 4 numerical values: 1 / The number "L" of Fibonacci or Lucas constituting the length of the sub-sequence analyzed. 2 / The cumulated volume of the corresponding resonances (n x L) in regular exploration (forward). 3 / The cumulative volume of the corresponding resonances (L x n) in reverse (backward) exploration. 4 / The ratio of the 2 values below regular / reverse.

Table 1 - TC/AG Fibonacci and Lucas analysis for real NA1000 genome and synthetic Caulobacter 2.0.

TC/AG Real genome NA1000		TC/AG Synthetic genome CAULOBACTER 2.0	
Fibonacci	Lucas	Fibonacci	Lucas
3 1580254 1582201 0.9987694357	3 1582201 1580254 1.00123208	**3** **290047** **293417** 0.9885146396	3 293417 290047 1.011618807
5 1346353 1346512 0.9998819171	4 993497 994619 0.9988719299	5 239292 242875 0.9852475553	4 194318 198624 0.9783208474
8 924521 926003 0.9983995732	7 1186993 1186953 1.0000337	8 168546 172325 0.9780705063	7 209444 211890 0.9884562745

13	650861 652564 0.9973902943	11	661049 662784 0.9973822542	13	120565 124586 0.9677251055	11	123932 128203 0.966685647
21	377329 378580 0.9966955465	18	489878 492487 0.9947023982	21	74278 77737 0.9555038141	18	92499 96693 0.9566256089
34	188645 190539 0.9900597778	29	232050 233697 0.9929524127	34	40816 44246 0.9224788681	29	48895 52692 0.9279397252
55	71250 72070 0.9886221729	47	104152 104668 0.9950701265	55	18131 20974 0.8644512253	47	24743 27988 0.8840574532
89	19694 19535 1.008139237	76	30804 31161 0.9885433715	89	6300 8172 0.7709251101	76	9026 11226 0.8040263674

Table 2 – TC/AG Fibonacci detailed data :

Real	Fibonacci	3	5	8	13	21	34	55	89
	Real	1580254	1346353	924521	650861	377329	188645	71250	19694
	reverse real	1582201	1346512	926003	652564	378580	190539	72070	19535
	ratiox1000000	998770	999882	998400	997391	996696	990060	988623	1008140
Synthetic	Fibonacci	3	5	8	13	21	34	55	89
	synthetic	290047	239292	168546	120565	74278	40816	18131	6300
	reverse synthe	293417	242875	172325	124586	77737	44246	20974	8172
	rariox1000000	988515	985248	978071	967726	955504	922479	864452	770926

Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
Real	998770	999882	998400	997391	996696	990060	988623	1008140
Synthetic	988515	985248	978071	967726	955504	922479	864452	770926

Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
Real distance	482	40	367	422	310	469	203	-39
synthetic dista	4289	4560	4810	5118	4403	4366	3619	2383

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example of weighting by the length of the genome computing here the case of synthetic caulobacterium genome (case of the first Fibonacci resonance of length = 3 nucleotides) :
regular - reverse distance = 290047-293417 = ¯3370
weighting by the genome length : ¯3370÷785750 = ¯0.004288895959
normalization multiply by 1000000 = 1000000×¯0.004288895959 = ¯4288.895959 = **-4289**

The average ratio of weighted distances by genome length between real genome and synthetic genome is 14.39 for TC / AG Fibonacci resonances.
Details :
real genome abs. Distances : 482 40 367 422 310 469 203 39
synthetic genome abs. Distances : 4289 4560 4810 5118 4403 4366 3619 2383
cumulating real genome abs. Distances :2332
cumulating synthetic genome abs. Distances : 33548
Ratio synthetic genome abs. Distances / real genome abs. Distances = 14.38593482
For information, the same ratio related to Lucas TC/AG is = **14.345484**

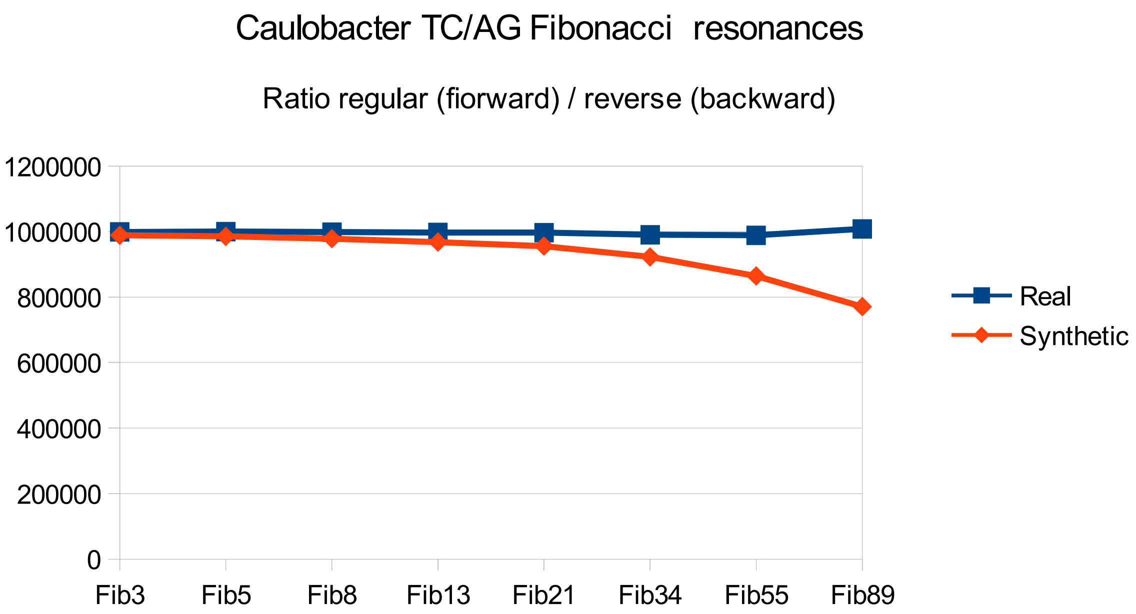


Figure 1 – Comparing TC/AG Fibonacci ratios in real and synthetic Caulobacter genomes.

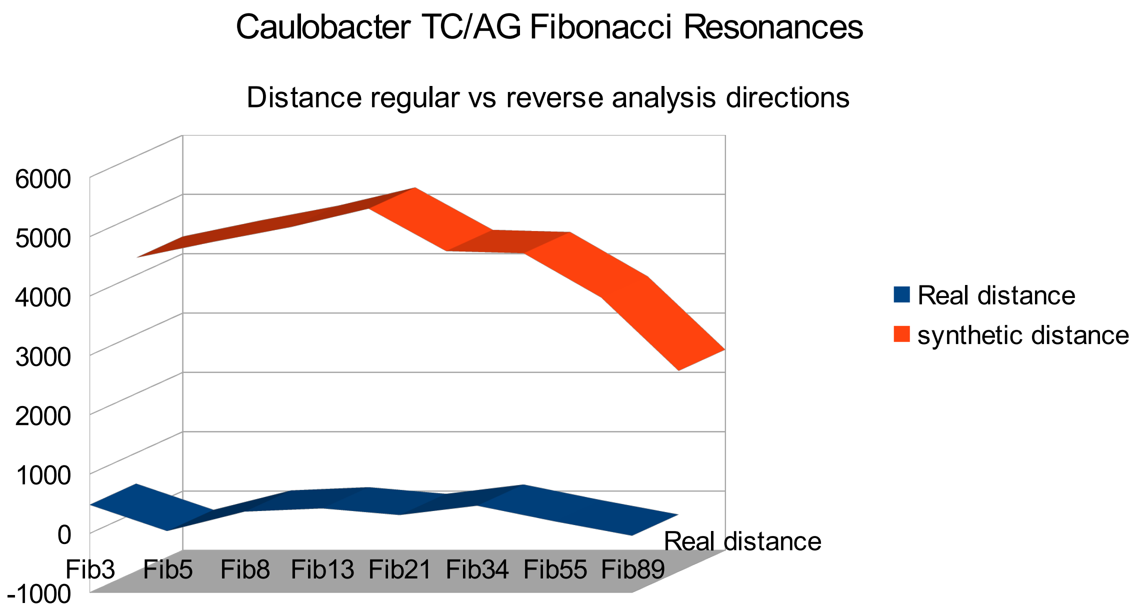


Figure 2 - Comparing TC/AG Fibonacci distances in real and synthetic Caulobacter genomes.

Table 3 – TC/AG Lucas detailed data ;

Real	Lucas	3	4	7	11	18	29	47	76
	Real	1582201	993497	1186993	661049	489878	232050	104152	30804
	reverse real	1580254	994619	1186953	662784	492487	233697	104668	31161
	ratiox1000000	1001233	998872	1000034	997383	994703	992953	995071	988544
Synthetic	Lucas	3	4	7	11	18	29	47	76
	synthetic	293417	194318	209444	123932	92499	48895	24743	9026
	reverse synthe	290047	198624	211890	128203	96693	52692	27988	11226
	ratiox1000000	1011619	978321	988457	966686	956626	927940	884058	804027

Lucas	L3	L4	L7	L11	L18	L29	L47	L76
Real	1001233	998872	1000034	997383	994703	992953	995071	988544
synthetic	1011619	978321	988457	966686	956626	927940	884058	804027

Lucas	L3	L4	L7	L11	L18	L29	L47	L76
Real distance	-481	278	-9	430	646	408	128	89
synthetic dista	-4288	5481	3113	5436	5338	4833	4130	2800

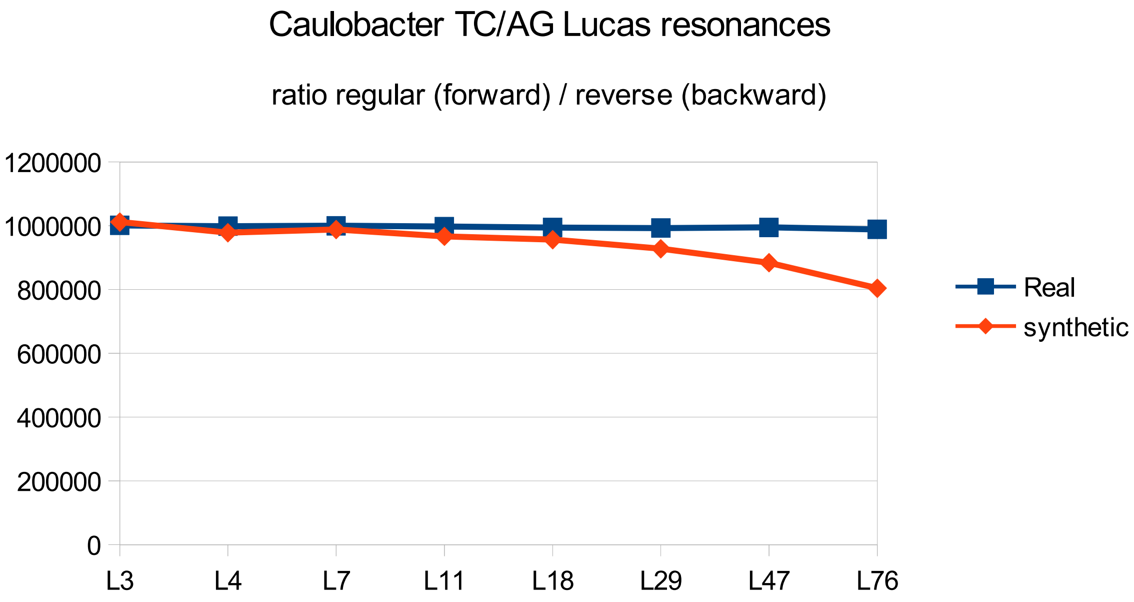


Figure 3 - Comparing TC/AG Lucas ratios in real and synthetic Caulobacter genomes.

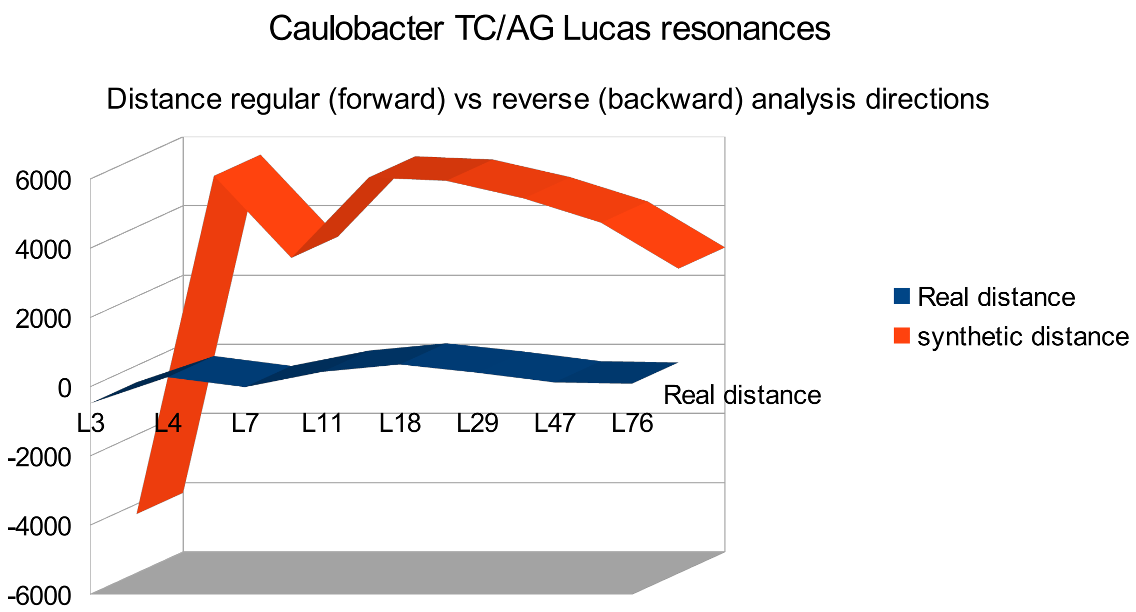


Figure 4 - Comparing TC/AG Lucas distances in real and synthetic Caulobacter genomes.

TG/AC analysis :

Table 4 - TG/AC Fibonacci and Lucas analysis for real NA1000 genome and synthetic Caulobacter 2.0.

TG/CA Real genome NA1000		TG/CA Synthetic genome CAULOBACTER 2.0	
Fibonacci	Lucas	Fibonacci	Lucas
3 1607779 1614874 0.9956064684	3 1614874 1607779 1.00441292	3 296256 299993 0.9875430427	3 299993 296256 1.012614091
5 1349192 1358378 0.993237523	4 1011587 1022025 0.9897869426	5 244860 248873 0.9838753099	4 195156 199978 0.9758873476
8 915781 925976 0.9889899954	7 1174192 1180896 0.9943229548	8 169216 174299 0.9708374689	7 213326 216126 0.9870445944
13 642769 652548 0.9850141292	11 654997 665831 0.9837286038	13 120130 125243 959176	11 123819 128731 0.9618429127
21 384426 392873 0.9784994133	18 489376 497649 0.9833758332	21 73909 78870 0.9370990237	18 92670 96745 0.9578789602
34 209433 218299 0.9593859798	29 251102 259033 0.9693822795	34 42458 46179 0.9194222482	29 50145 53889 0.9305238546
55 91756 97158 0.9443998436	47 127067 133142	55 20641 22427 0.9203638471	47 27305 29582 0.9230275167

	0.9543720239		
89 31478 34303 0.917645687	76 45537 49636 0.9174188089	89 8188 9531 0.859091386	76 11334 12669 0.8946246744

Table 5 – TG/AC Fibonacci detailed data :

Real	Fibonacci	3	5	8	13	21	34	55	89
	Real	1607779	1349192	915781	642769	384426	209433	91756	31478
	reverse real	1614874	1358378	925976	652548	392873	218299	97158	34303
	ratiox1000000	995607	993238	988990	985015	978500	959386	944400	917646
Synthetic	Fibonacci	3	5	8	13	21	34	55	89
	synthetic	296256	244860	169216	120130	73909	42458	20641	8188
	reverse synthe	299993	248873	174299	125243	78870	46179	22427	9531
	rariox1000000	987544	983876	970838	959176	937100	919423	920364	859092

Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
Real	995607	993238	988990	985015	978500	959386	944400	917646
synthetic	987544	983876	970838	959176	937100	919423	920364	859092

Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
Real distance	1755	2273	2522	2419	2090	2193	1337	699
synthetic dista	4756	5108	6469	6508	6314	4736	2273	1710

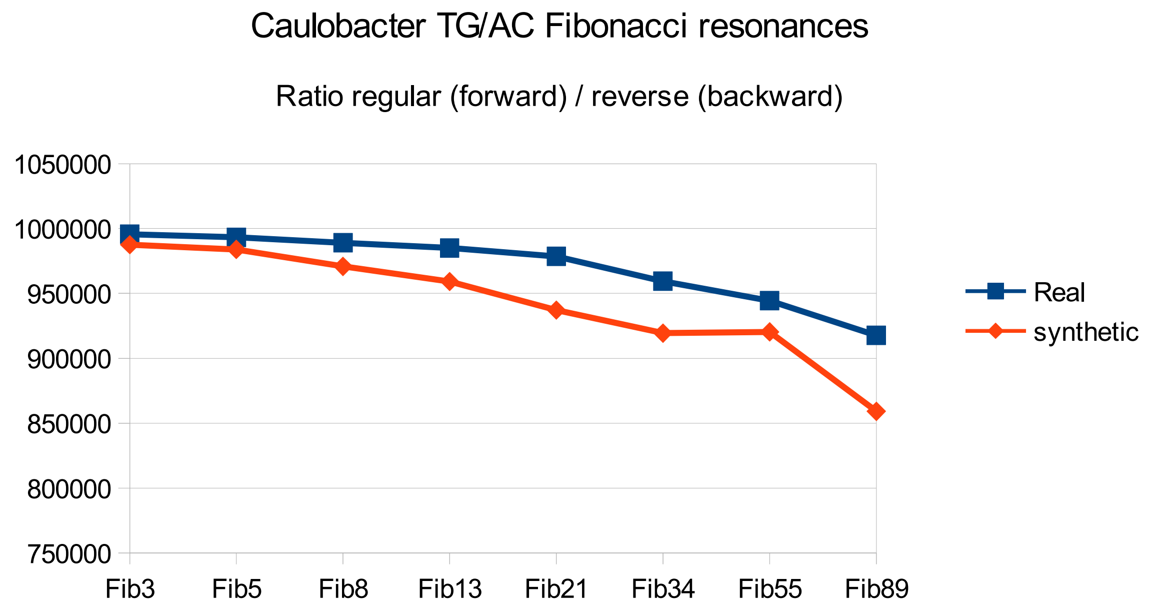


Figure 5 - Comparing TG/AC Fibonacci ratios in real and synthetic Caulobacter genomes.

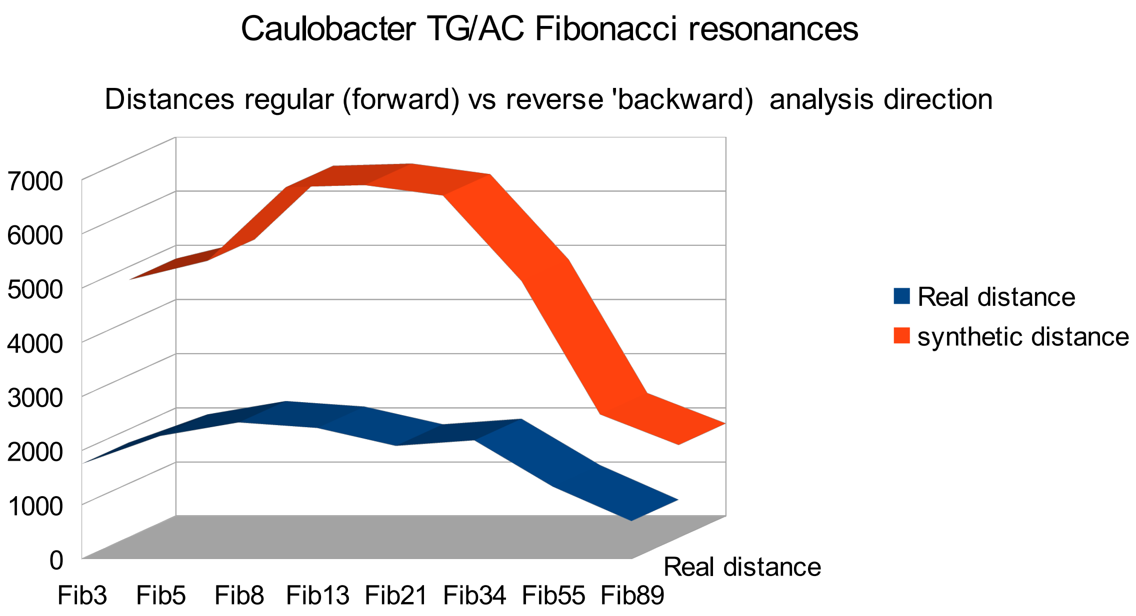


Figure 6 - Comparing TG/AC Fibonacci distances in real and synthetic Caulobacter genomes.

Table 6 – TG/AC Lucas detailed data :

	Real	1614874	1011587	1174192	654997	489376	251102	127067	45537
	reverse real	1607779	1022025	1180896	665831	497649	259033	133142	49636
	ratiox1000000	1004413	989787	994323	983729	983376	969383	954373	917419
Synthetic	Lucas	3	4	7	11	18	29	47	76
	synthetic	299993	195156	213326	123819	92670	50145	27305	11334
	reverse synthe	296256	199978	216126	128731	96745	53889	29582	12669
	ratiox1000000	1012615	975888	987045	961843	957879	930524	923028	894625

Lucas	L3	L4	L7	L11	L18	L29	L47	L76
Real	1004413	989787	994323	983729	983376	969383	954373	917419
synthetic	1012615	975888	987045	961843	957879	930524	923028	894625

Lucas	L3	L4	L7	L11	L18	L29	L47	L76
Real distance	-1754	2582	1659	2680	2047	1962	1503	1014
synthetic dista	-4755	6137	3564	6252	5187	4765	2898	1700

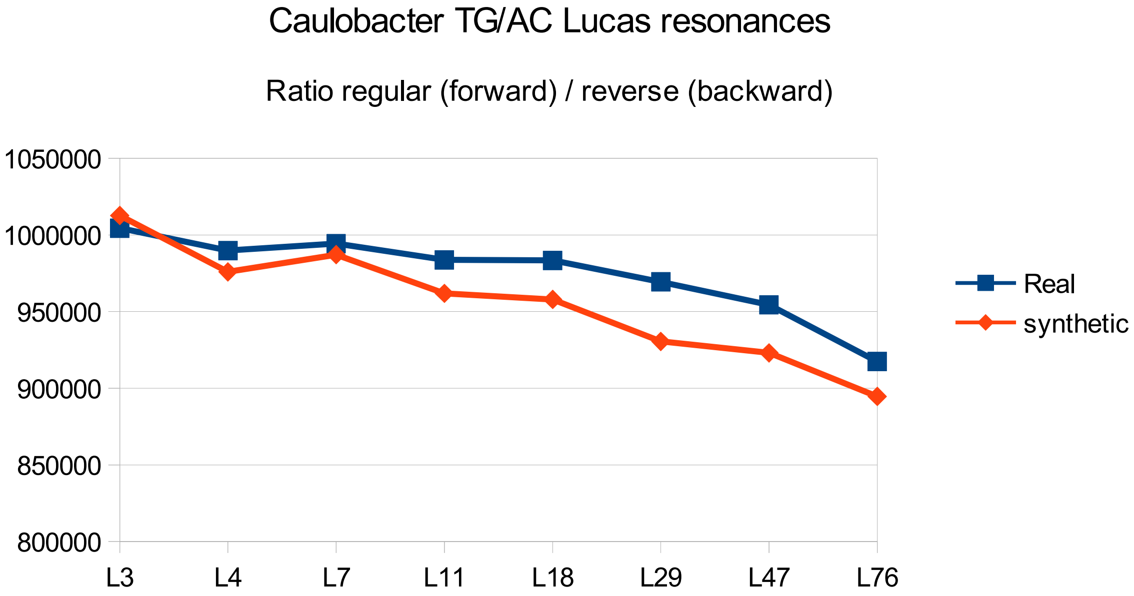


Figure 7 - Comparing TG/AC Lucas ratios in real and synthetic Caulobacter genomes.

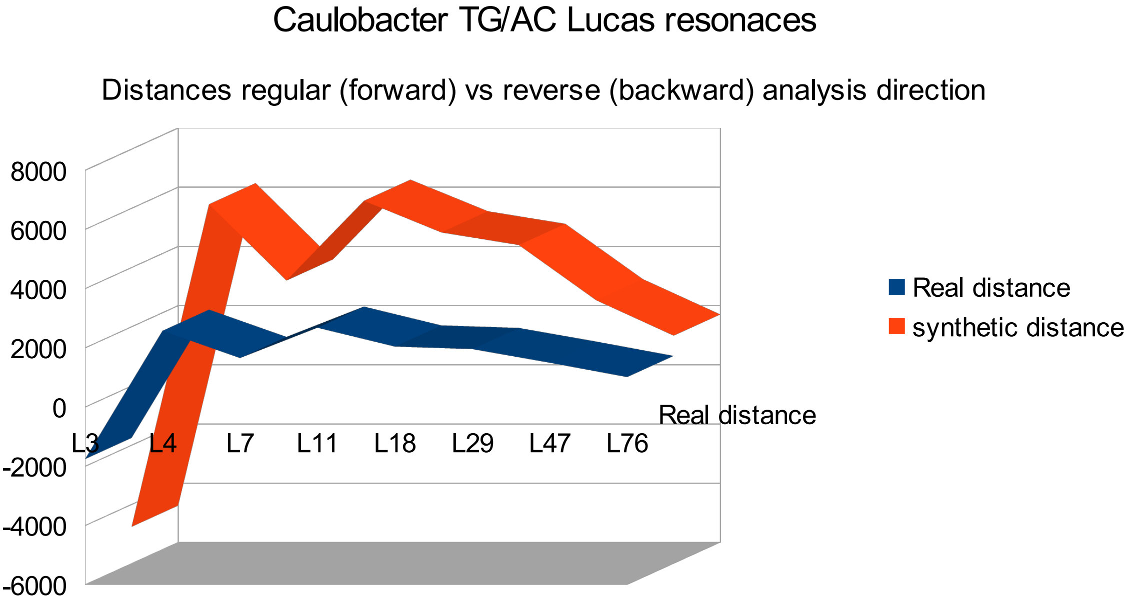


Figure 8 - Comparing TG/AC Lucas distances in real and synthetic Caulobacter genomes.

Part II : *Mycoplasma Mycoides* JCVI-syn1.0 (2010), JCVI-syn3.0 (2016) and JCVI-syn3A (2019)

In 2010, a 1079-kb genome based on the genome of *Mycoplasma mycoides* (JCV-syn1.0) was chemically synthesized and supported cell growth when transplanted into cytoplasm. (Gibson, 2010). In 2016, (Hutchinson 2016), Hutchinson et al design, build, and test cycle to reduce this *Mycoplasma mycoides* genome to 531 kb (473 genes). JCV-syn3.0 retains genes involved in key processes such as transcription and translation, but also contains 149 genes of unknown function. In the following section, we compare 6 (six) genomes : two reference real strain mycoplasma genomes including CAPRI strain, one transgenic building strain and the 3 strong JCV Labs ; synthetic genomes.

Table 7 – Comparing TC/AG Fibonacci analysis for 6 real or synthetic Mycoplasm genomes.

Mycoplasm REF real genomes			Synthetic Mycoplasm genomes		
Natural reference genomes		Transgenic genome	Synthetic genomes		
Reference real strain	Reference real strain CAPRI	Transgenic CAPRI strain	JCVI-Syn1.0	JCVI-Syn3.0	JCVI-Syn3A
3 425653 418009 1.018286688	3 431863 424453 1.017457763	3 389604 383147 1.01685254	3 386328 380244 1.016000252	3 191148 188330 1.014963097	3 195794 192178 1.018815889
5 349081 342772 1.018405821	5 353999 348030 1.01715082	5 322151 314644 1.02385871	5 319643 312321 1.023443829	5 158678 155189 1.022482264	5 162644 158262 1.027688264
8 249100 241395 1.03191864	8 252787 244971 1.031905817	8 228917 220387 1.038704642	8 227112 218687 1.038525381	8 112973 108400 1.042186347	8 116120 110250 1.05324263
13 182285 173428 1.051070185	13 184673 175894 1.049910742	13 167319 158110 1.05824426	13 166119 156734 1.05987852	13 83100 77329 1.074629182	13 85559 78424 1.090979802
21 122345 114349 1.069926278	21 123850 116312 1.064808446	21 111834 103016 1.085598354	21 110910 101748 1.090045996	21 55296 50364 1.097927091	21 57103 50837 1.123256683
34 80074 73025 1.096528586	34 81099 74515 1.088358049	34 72890 66214 1.100824599	34 72247 65356 1.105437909	34 36064 31989 1.127387539	34 37460 32353 1.15785244
55 49907 44879 1.112034582	55 50665 46176 1.097215003	55 45287 40085 1.12977423	55 44848 39272 1.141984111	55 22000 19301 1.139837314	55 22992 19368 1.187112763
89 30152 26319 1.145636232	89 30708 27108 1.132802125	89 27153 22722 1.195009242	89 26742 22243 1.202265881	89 13030 10741 1.213108649	89 13749 10743 1.279810109

Table 8 – TC/AG Fibonacci detailed data :

Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
real mycoplasr	1018287	1018406	1031919	1051071	1069927	1096529	1112035	1145637
real capri strai	1017458	1017151	1031906	1049911	1064809	1088359	1097216	1132803
transgenic cap	1016853	1023859	1038705	1058245	1085599	1100825	1129775	1195010
synthetic SYN	1016001	1023444	1038526	1059879	1090046	1105438	1141985	1202266
synthetic Syn3	1014964	1022483	1042187	1074630	1097928	1127388	1139838	1213109
synthetic Syn3	1018816	1027689	1053243	1090980	1123257	1157853	1139838	1279811

Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
real mycoplasr	18287	18406	31919	51071	69927	96529	112035	145637
real capri strai	17458	17151	31906	49911	64809	88359	97216	132803
transgenic cap	16853	23859	38705	58245	85599	100825	129775	195010
synthetic SYN	16001	23444	38526	59879	90046	105438	141985	202266
synthetic Syn3	14964	22483	42187	74630	97928	127388	139838	213109
synthetic Syn3	18816	27689	53243	90980	123257	157853	139838	279811

Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
distance real n	-6410	-5290	-6461	-7427	-6705	-5911	-4216	-3214
distance real c	-6115	-4926	-6450	-7245	-6220	-5433	-3704	-2971
distance trans	-5928	-6892	-7831	-8454	-8095	-6129	-4775	-4068
distance SYN1	-5639	-6787	-7809	-8699	-8492	-6387	-5168	-4170
distance syn3.	-5302	-6564	-8604	-10858	-9279	-7667	-5078	-4306
distance syn3	-6654	-8064	-10802	-13130	-11531	-9398	-4967	-5532

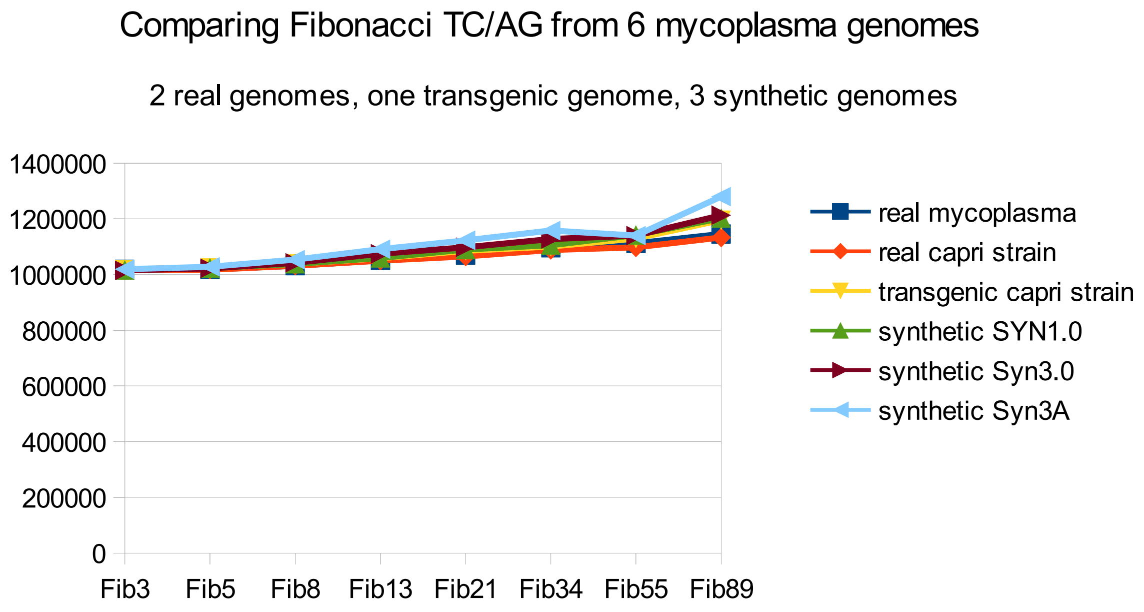


Figure 9 - Comparing TC/AG Fibonacci ratios from 6 mycoplasma genomes.

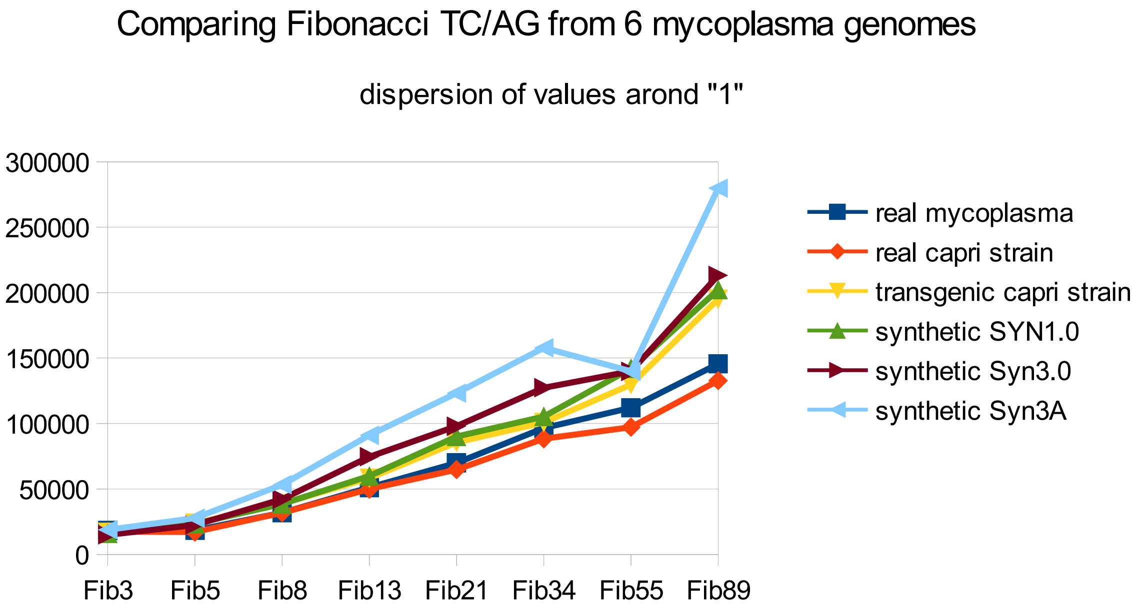


Figure 10 - Comparing TC/AG Fibonacci ratios from 6 mycoplasma genomes (relative values around 1).

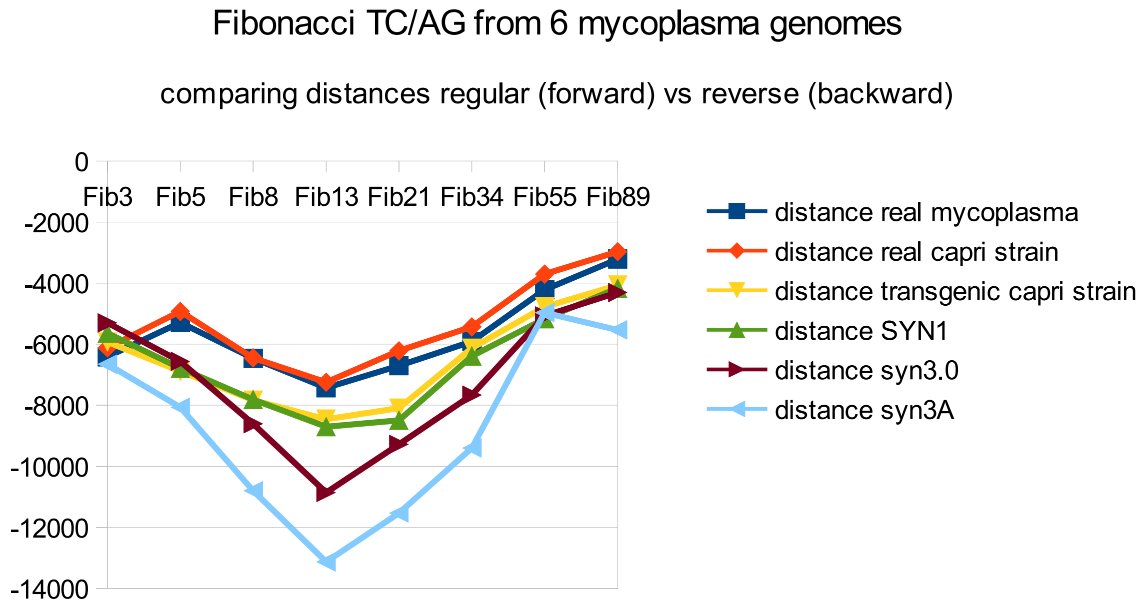


Figure 11 - Comparing TC/AG Fibonacci distances from 6 mycoplasma genomes.

In summary of this double analysis it seems obvious that synthetic genomes disturb and destroy a characteristic dimension of real genomes. This property could concern the mathematical topology of the genome (Rapoport 2018) and probably its fractal, dynamic, Evolution, and three-dimensional structures.

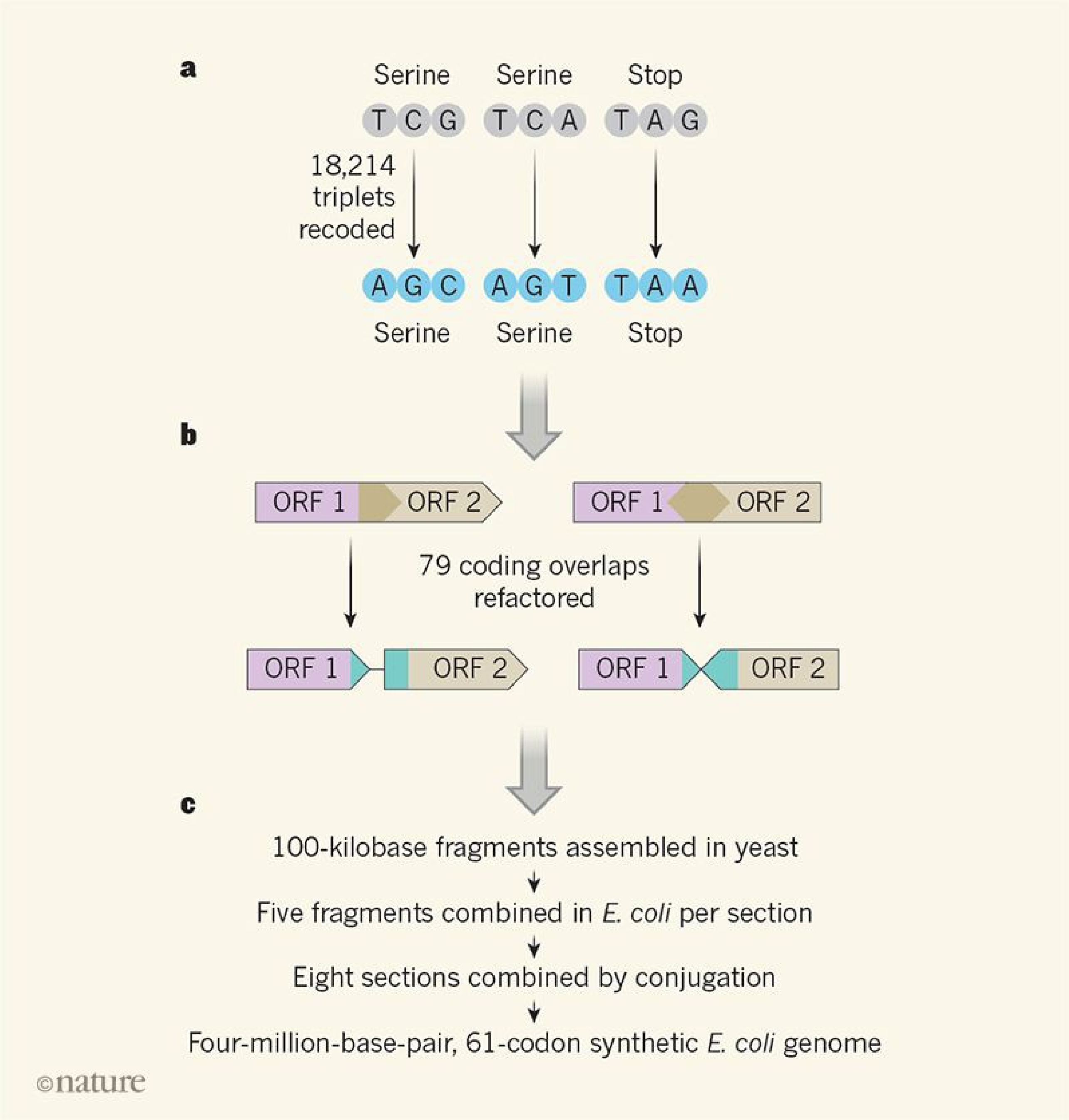
Discussion :

Comparing real E COLI Genome and synthetic changing TAG by TAA stop codons :

In (Fredens 2019), researchers published a synthetic genome of E COLI changing systematically genetic code equivalent codons. They replaced every occurrence of the serine codon TCG with AGC, every TCA (also serine) with AGT, and every TAG (stop) with TAA, for a total of 18,214 replacements. Here we run a sample comparison of TG Fibonacci resonances changing stop codons TAG in TAA, then 7725 changes considering only TAG of the first codons reading frame.

In (Fredens 2019), the sequences and genome design details used in this study are available in the Supplementary Data. Supplementary Data 1 provides the GenBank file of the *E. coli* MDS42 genome (NCBI accession number AP012306.1);

Fredens's team systematically replaced every occurrence of the serine codon TCG with AGC, every TCA (also serine) with AGT, and every TAG (stop) with TAA, for a total of 18,214 replacements



from (Blount 2019) https://www.nature.com/articles/d41586-019-01584-x

Figure 12 | Design and construction of a recoded genome. **a**, Fredens *et al*.3 recoded three base triplets (codons) — TCG and TCA, which encode the amino acid serine, and TAG, a stop codon that marks the end of a protein-coding sequence — to alternatives that have the same functions (AGC, AGT and TAA respectively) in the genome of the bacterium *Escherichia coli*. **b**, In some genomic locations, open reading frames (ORFs; protein-coding regions) overlap, and a change in the codons of one ORF might produce an unwanted change in the overlapping region. Fredens *et al.*'refactored' these ORFs to separate them, as illustrated for ORF1 and ORF2 (the two ORFs on the left are 'read' in the same direction; the two on the right are read in opposite directions). **c**, Redesigned DNA was synthesized and assembled into 100-kilobase fragments in the yeast*Saccharomyces cerevisiae*; fragments were then combined into sections and integrated into the *E. coli* genome. The sections were brought together to generate the complete functional synthetic genome.

Not having access to the modified sequence of the synthetic genome yet, we simply changed all TAG codons to TAA codons, that is, 7,725 altered codons. We have limited this change to only the first reading frame codons.

Table 9 – Comparing Fibonacci TG/AC from E-COLI real genome and E-Coli synthetic where all TAG codons are removed in TAA codons (1st codons reading frame only) :

ECOLI reference wild type genome	ECOLI syn61 like where 7725 TAG ==> TAA
3 1471002 1476399 0.9963444841	3 1458201 1484100 0.9825490196
5 1211718 1215554 0.9968442373	5 1204279 1221598 0.9858226683
8 852126 857586 0.9936332916	8 844110 865264 0.9755519703
13 612152 618151 0.9902952515	13 604631 625851 0.9660941662
21 385231 390203 0.9872579145	21 378106 397617 0.9509301665
34 222919 227478 0.9799585015	34 216935 233775 0.9279649235
55 107343 110152 0.9744988743	55 102252 114831 0.8904564099
89 43863 45199 0.9704418239	89 41531 47929 0.8665108807

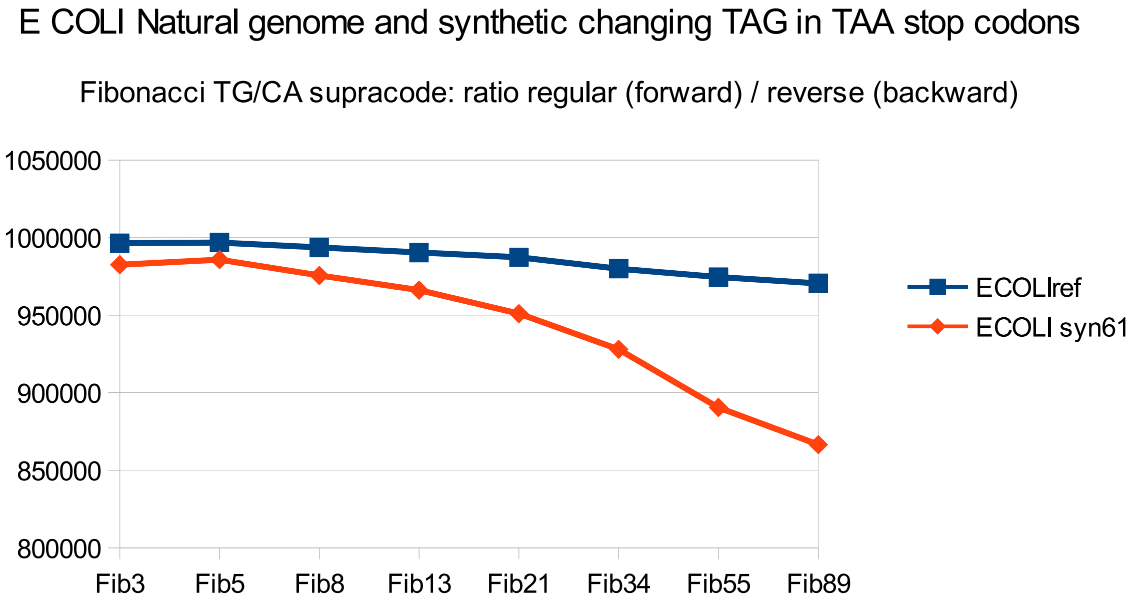
Note, the TAG ==> TAA mutations (where G is mutated to A) does not affect the TC / AG structures, we have here to analyze the TG / AC structures.

Table 10 – TG/AC Fibonacci detailed data :

real	Fibonacci	3	5	8	13	21	34	55	89
	ECOLIref	1471002	1211718	852126	612152	385231	222919	107343	43863
	reverse	1476399	1215554	857586	618151	390203	227478	110152	45199
	ratiox1000000	996345	996845	993634	990296	987258	979959	974499	970442
trans	Fibonacci	3	5	8	13	21	34	55	89
	ECOLI syn61	1458201	1204279	844110	604631	378106	216935	102252	41531
	reverse	1484100	1221598	865264	625851	397617	233775	114831	47929
	ratiox1000000	982550	985823	975552	966095	950931	927965	890457	866511

			7					
Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
ECOLIref	996345	996845	993634	990296	987258	979959	974499	970442
ECOLI syn61	982550	985823	975552	966095	950931	927965	890457	866511

Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
distance ECOI	1358	965	1374	1509	1251	1147	707	336
distance ECOI	6514	4356	5321	5337	4907	4236	3164	1610


E COLI Natural genome and synthetic changing TAG in TAA stop codons

Fibonacci TG/CA supracode: ratio regular (forward) / reverse (backward)

Figure 13 - Comparing TG/AC Fibonacci ratios in real and synthetic E-Coli genomes.

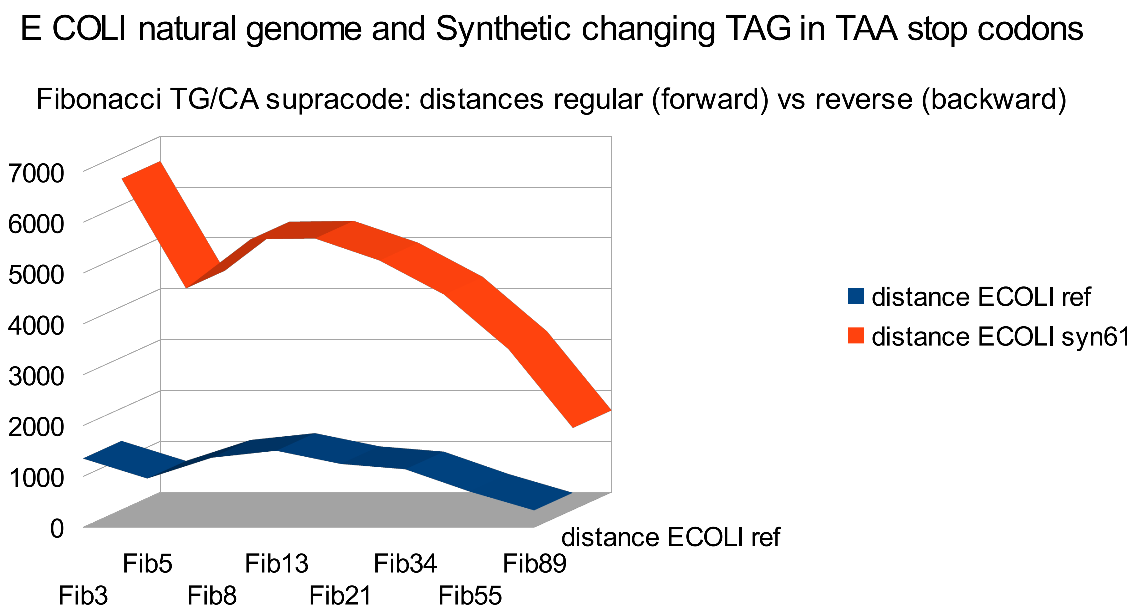


Figure 14 - Comparing TG/AC Fibonacci distances in real and synthetic E-Coli genomes.

YEAST SYNTHETIC GENOME, the case of the longer chromosome XII :

Since 2012 the Synthetic Yeast Genome Project (Sc2.0 **http://syntheticyeast.org/sc2-0/**) results from a worlwide partnership, « Sc2.0 International Consortium team », members spanning 4 continents to provide remote mentorship and solve challenges associated with synthetic individual chromosomes design features and assembly (Jee Loon Foo 2018).

Sources :
synthetic yeast project
http://syntheticyeast.org/

7 chromosomes now synthetised
http://syntheticyeast.org/sc2-0-data/

Sc2.0 Data

Consorsium has successfully synthesized seven chromosomes. Check the following links to learn about details related of each finished chromosomes:

- synII
- synIII
- synV
- synVI
- synIXR
- synX
- synXII

In (Weiming Zhang et al 2017) process building the whole synthetic chromosome XII.

Having not yet obtained the synthetic genome from the authors, we have limited here our study to the concatenation of all wild type PCRTags on the one hand and synthetic ones on the other hand. example:
Forward wild type PCRTag : TGCTTGAACTGCAAATACAGGCCCACTC
Forward synthetic PCRTag : AGCTTGGACAGCGAAAACTGGACCTGAT

They published particularly all the wild type and synthetic PCTTags.
The full PCRTags are available online :
http://syntheticyeast.org/wp-content/uploads/2016/10/synXII_PCRtag.txt

Details : PCRTags

« PCRTags are alterations incorporated into most open reading frames (ORFs) (on average one per ORF, as some ORFs are too small and others contain multiple PCRTags). These are made by recoding a ~20bp segments of the coding region of an ORF to a different DNA sequence encoding the same amino acid sequence. PCR primer pairs can then be designed that will selectively amplify only the synthetic or wild type sequences. In this way, transformants that have incorporated a synthetic segment can be quickly scanned to ascertain that a complete substitution of the segment has occurred. PCRTags can also be used to monitor for the deletion of non-essential segments post-SCRaMbLE induction. » (from http://syntheticyeast.org/designs/alterations/pcrtags/).

We analysed 681 PCRTags of each 28 bp from wild YEAST XII and artificial SYN XII chromosomes. Then only resonances < 28 bp are to be considered in the following analysis.

We run 3 analysis :
Fibonacci sequence= 1 2 3 5 8 13 21 34 55 89
Lucas sequence= 1 3 4 7 11 18 29 47 76
FibLuc sequence= 5 7 12 19 31 50 81 131

Table 11 – Comparing real and synthetic YEAST chromosome XII PCRTags with Fibonacci, Lucas and FibLuc resonances :

YEAST XII real genome (681 wild type PCRTags)			Synthetic genome SYNXII (681 synthetic PCRTags)		
Fibonacci	Lucas	FibLuc	Fibonacci	Lucas	FibLuc
3 6906 7073 0.9763890853	3 7073 6906 1.024181871	5 5726 5649 1.013630731	3 7133 7436 0.9592522862	3 7436 7133 1.04247862	5 6195 5982 1.03560682
5 5649 5726 0.9865525672	4 4760 4886 0.9742120344	7 3094 3237 0.9558232932	5 5982 6195 0.9656174334	4 4611 4948 0.9318916734	7 3024 3330 0.9081081081
8 4012 4124 0.9728419011	7 4894 5032 0.9725755167	12 3518 3552 0.9904279279	8 4142 4396 0.9422202002	7 5272 5456 0.9662756598	12 3636 3918 0.9280245023
13 2942 3009	11 2993 3058	19 1769 1924	13 2877 3272	11 2950 3383	19 1678 2038

0.9777334663	0.9787442773	0.9194386694	0.8792787286	0.8720070943	0.8233562316
21 1785 1864 0.9576180258	18 2232 2317 0.963314631	31 1236 1272 0.9716981132	21 1749 2055 0.8510948905	18 2193 2511 0.8733572282	31 1057 1362 0.7760646109
34 1038 1121 0.9259589652	29 1261 1264 0.9976265823	50 607 623 0.974317817	34 853 1121 0.7609277431	29 1101 1298 0.8482280431	50 419 566 0.7402826855
55 538 507 1.061143984	47 719 697 1.031563845	81 221 212 1.04245283	55 358 438 0.8173515982	47 491 710 0.6915492958	81 172 177 0.9717514124
89 195 179 1.089385475	76 265 237 1.11814346	131 37 38 0.9736842105	89 105 122 0.8606557377	76 188 212 0.8867924528	131 17 19 0.8947368421

Table 12 – TC/AG Fibonacci detailed data :

fibonacci	TC								
				7					12
Real	Fibonacci	3	5	8	13	21	34	55	89
	Real SynIII	6906	5649	4012	2942	1785	1038	538	195
	reverse real	7073	5726	4124	3009	1864	1121	507	179
	ratiox1000000	976390	986553	972842	977734	957619	925959	1061144	1089386
Synthetic	Fibonacci	3	5	8	13	21	34	55	89
	synthetic Syn1	7133	5982	4142	2877	1749	853	358	105
	reverse synthe	7436	6195	4396	3272	2055	1121	438	122
	ratiox1000000	959253	965618	942221	879279	851095	760928	817352	860656

			7					
Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
Real ChrIII	976390	986553	972842	977734	957619	925959	1061144	1089386
synthetic Syn1	959253	965618	942221	879279	851095	760928	817352	860656

Fibonacci	Fib3	Fib5	Fib8	Fib13	Fib21	Fib34	Fib55	Fib89
Real distance	8810	4063	5909	3535	4168	4379	-1635	-844
synthetic dista	15987	11238	13401	20840	16145	14140	4221	897

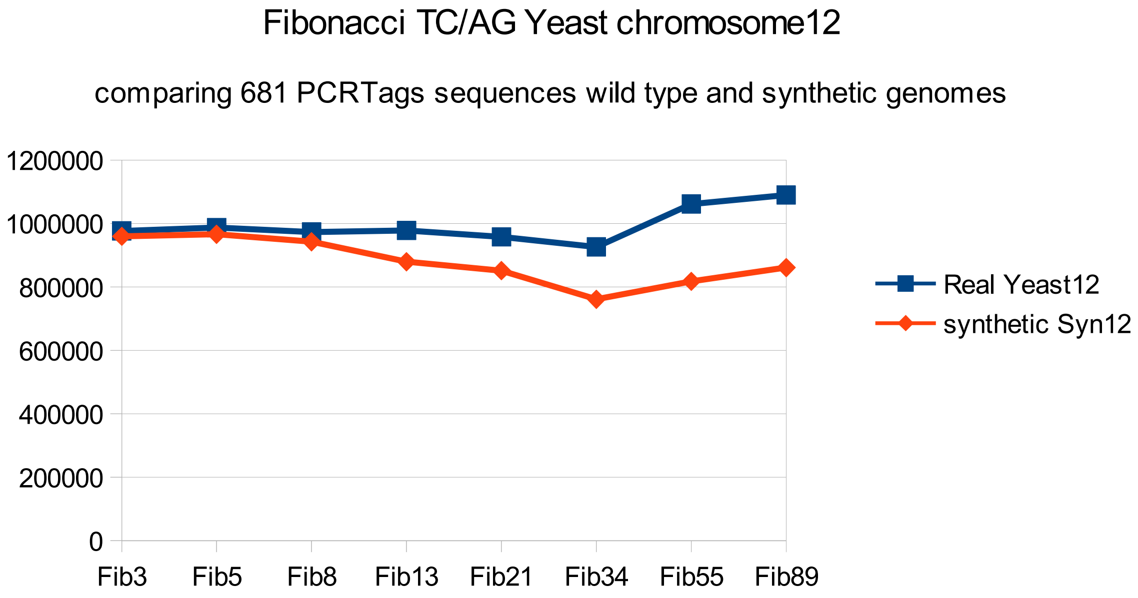


Figure 15 - Comparing TC/AG Fibonacci ratios in real and synthetic YEAST Chromosome XII PCRTags.

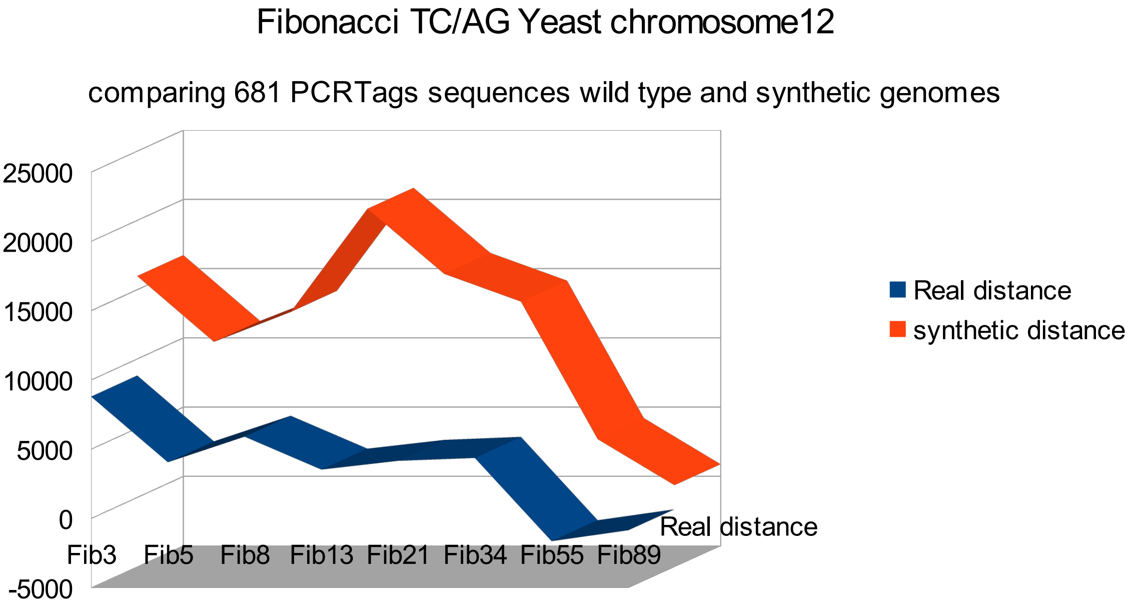


Figure 16 - Comparing TC/AG Fibonacci distances in real and synthetic YEAST Chromosome XII PCRTags.

Table 13 – TC/AG Lucas detailed data :

Lucas	TC								
				7					
Real	Lucas	3	4	7	11	18	29	47	76
	Real Yeast12	7073	4760	4894	2993	2232	1261	719	265
	reverse real	6906	4886	5032	3058	2317	1264	697	237
	ratiox1000000	1024182	974213	972576	978745	963315	997627	1031564	1118144
Synthetic	Lucas	3	4	7	11	18	29	47	76
	synthetic Syn1	7436	4611	5272	2950	2193	1101	491	188
	reverse synthe	7133	4948	5456	3383	2511	1298	710	212
	rariox1000000	1042479	931892	966276	872008	873358	848229	691550	886793

Lucas	L3	L4	L7	L11	L18	L29	L47	L76
Real Yeast12	1024182	974213	972576	978745	963315	997627	1031564	1118144
synthetic Syn1	1042479	931892	966276	872008	873358	848229	691550	886793

Lucas	L3	L4	L7	L11	L18	L29	L47	L76
Real distance	-8809	6647	7281	3429	4485	159	-1160	-1477
synthetic dista	-15986	17780	9708	22845	16778	10394	11555	1267

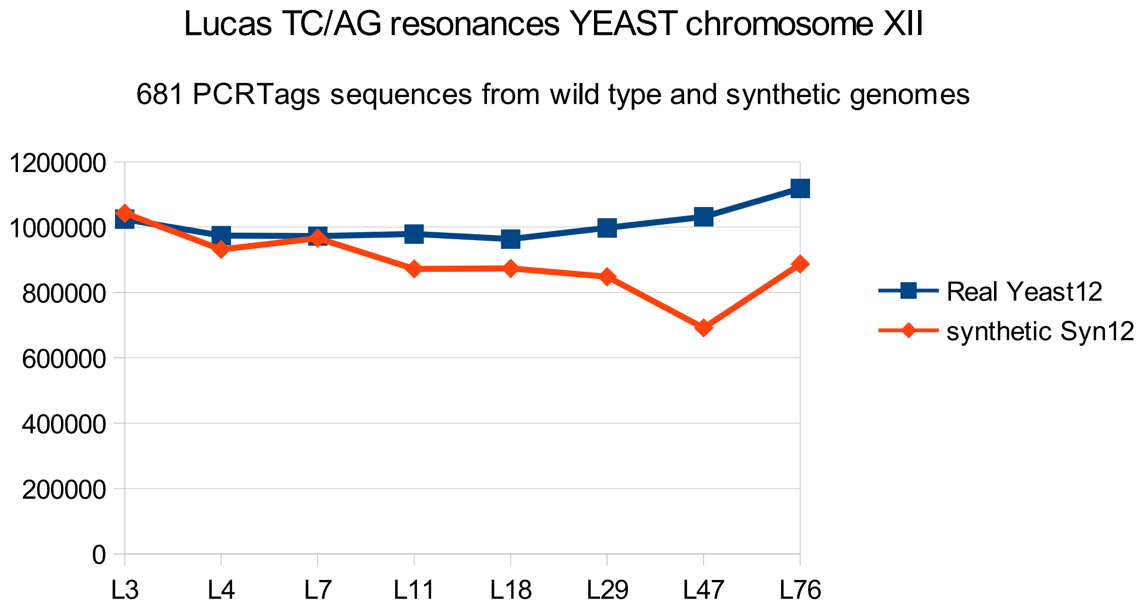


Figure 17- Comparing TC/AG Lucas ratios in real and synthetic YEAST Chromosome XII PCRTags.

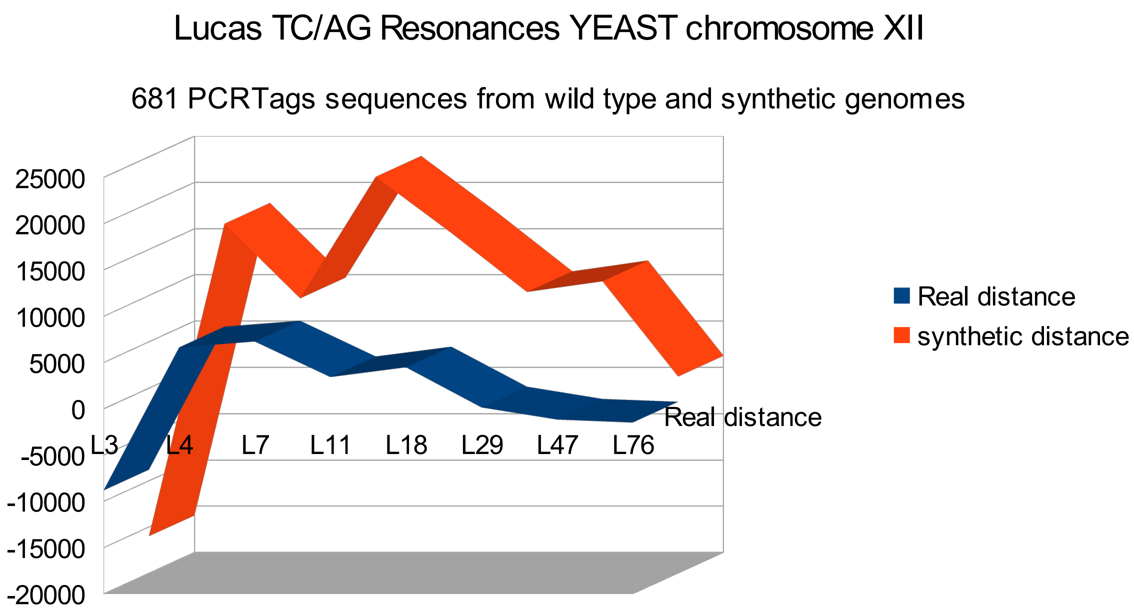


Figure 18 - Comparing TC/AG Lucas distances real and synthetic YEAST Chromosome XII PCRTags.

Table 14 – TC/AG FibLuc detailed data :

Real	FibLuc	5	7	12	19	31	50	81	131
	Real Yeast12	5726	3094	3518	1769	1236	607	221	37
	reverse real	5649	3237	3552	1924	1272	623	212	38
	ratiox1000000	1013631	955824	990428	919439	971699	974318	1042453	973685
Synthetic	FibLuc	5	7	12	19	31	50	81	131
	synthetic Syn1	6195	3024	3636	1678	1057	419	172	17
	reverse synthe	5982	3330	3918	2038	1362	566	177	19
	rariox1000000	1035607	908109	928025	823357	776065	740283	971752	894737

FibLuc	Eva5	Eva7	Eva12	Eva19	Eva31	Eva50	Eva81	Eva131
Real Yeast12	1013631	955824	990428	919439	971699	974318	1042453	973685
synthetic Syn1	1035607	908109	928025	823357	776065	740283	971752	894737

FibLuc	Eva5	Eva7	Eva12	Eva19	Eva31	Eva50	Eva81	Eva131
Real distance	-4062	7544	1794	8177	1900	845	-474	53
synthetic dista	-11237	16145	14879	18994	16092	7756	264	106

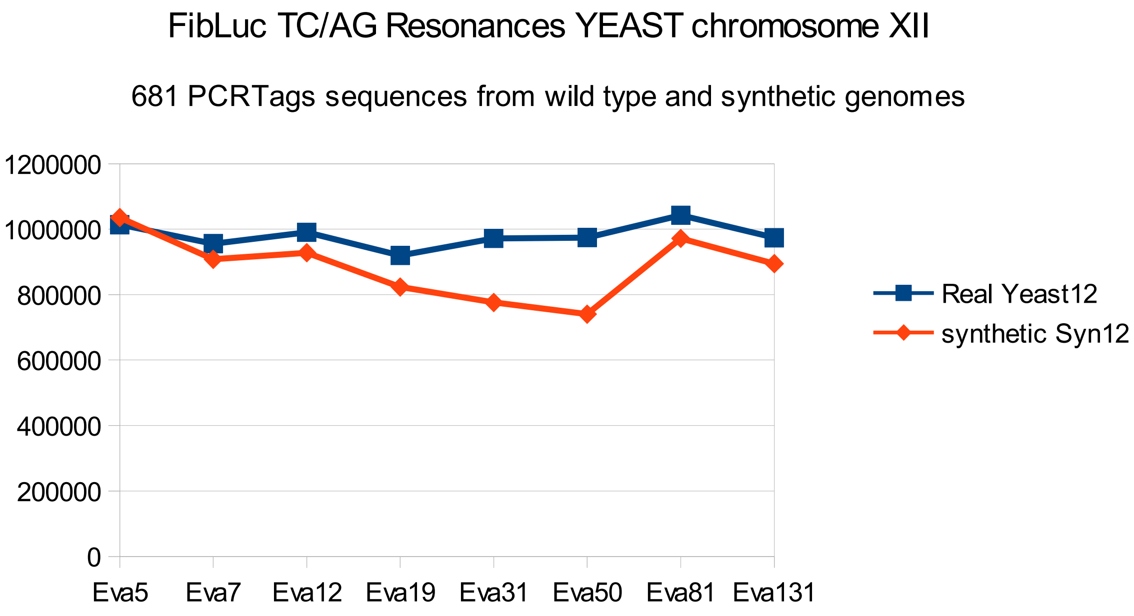


Figure 19 - Comparing TC/AG FibLuc ratios in real and synthetic YEAST Chromosome XII PCRTags.

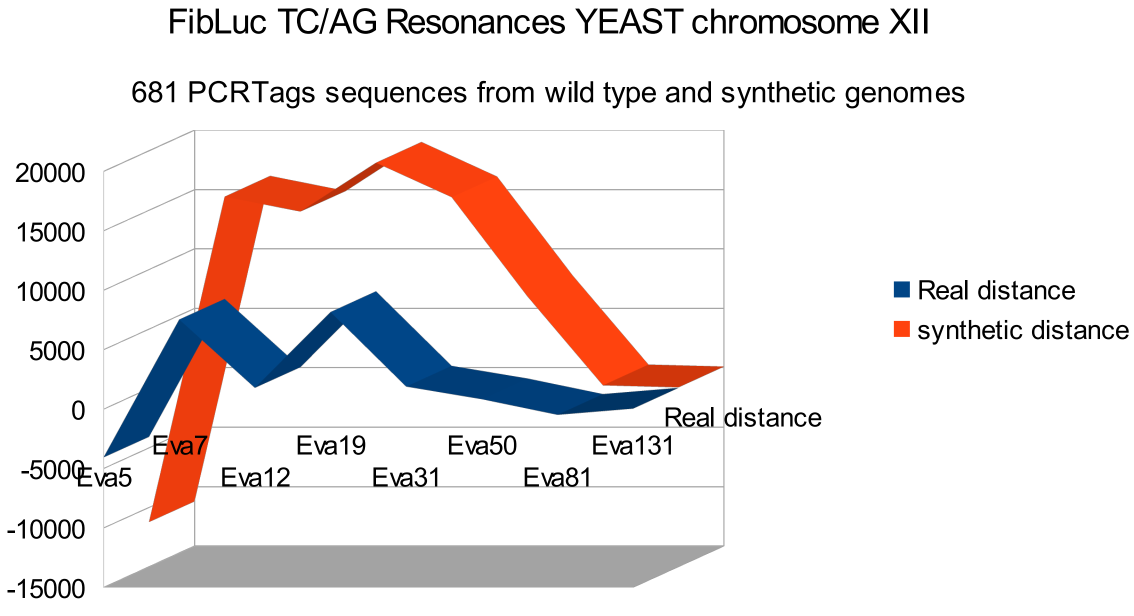


Figure 20 - Comparing TC/AG FibLuc distances in real and synthetic YEAST Chromosome XII PCRTags.

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