Modifying the control of gene expression behavior by the deletion of connectrons and by the design and addition of synthetic connectrons in prokaryotic, archea and eukaryotic genomes

Reference to Related Application

The present application includes the subject of Provisional Application Serial No. 60/393,558 filed July 5, 2002

The present application is a continuation in part of US Patent Application Serial Number 09/866,925 filed May 30, 2001 entitled ALGORITHMIC DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES

The present application is also related to US Patent Application Serial Number 10/339,666 filed January 10, 2003 entitled SIMULATION OF GENE EXPRESSION CONTROL USING CONNECTRONS, INTERFERENCE RNAS (IRNAS) AND SMALL TEMPORAL RNAS (STRNAS) IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES

The present application is also related to US Patent Application Serial Number 10/364,516 filed February 12, 2003 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE ESCHERICHIA COLI K-12 MG1655 COMPLETE GENOME

The present application is also related to US Patent Application Serial Number 10/364,412 filed February 12, 2003 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE SACCHAROMYCES CEREVISIAE COMPLETE GENOME

The present application is also related to US Patent Application Serial Number 10/299,056 filed November 19, 2002 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE HALOBACTERIUM SP. NRC-1 COMPLETE GENOME

The present application is also related to US Patent Application Serial Number 10/367,832 filed February 19, 2003 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE PSEUDOMONAS AERUGINOSA PA01, COMPLETE GENOME

The present application is also related to US Patent Application Serial Number 10/287,818 filed November 5, 2002 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE VIBRIO CHOLERAE CHROMOSOME I, COMPLETE CHROMOSOME

The present application is also related to US Patent Application Serial Number 10/305,275 filed November 27, 2002 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE AEROPYRUM PERNIX K1 COMPLETE GENOME

Introduction

The connectron structure of a genome determines sets of four DNA sequences of minimum length of 15-bases (C1 and C2 which are in the 3'UTR of a gene, T1 which is on the 5'-side and T2 which is on the 3'-side of a set of genes). The connectrons in a genome control the expression of sets of genes. Each native genome has a particular set of connectrons that control the expression of sets of genes in many different ways. The gene expression behavior can be changed by deleting existing connectrons and by adding new connectrons that have been designed to achieve specific new gene expression patterns. This patent application describes the invention of methods for deleting connectrons as well as the invention of four classes of synthetic and designed connectrons that can be used to modify the connectron behavior of a genome. In addition this application describes the invention of four methods that implement synthetic connectrons with differing proportions of novelty.

Definitions

Double stranded DNA - Watson and Crick showed in 1953 that DNA naturally forms a double-stranded helix. A typical double stranded sequence is

5'-TAGAGGAGTACCAC-3'
3'-ATCTCCTCATGGTG-5'

Hydrogen Bond - The force between a hydrogen atom and another heavier atom such as Oxygen (O), Nitrogen (N), Phosphorus (P), or Sulfur (S).

Positive strand - The positive strand is normally represented 5′ to 3′ running left to right as in

5′-TAGAGGAGTACCAC-3′

Negative strand - The negative strand is normally represented 5′ to 3′ running right to left as in

3′-ATCTCCTCATGGTG-5′

Single stranded RNA - Either the positive or the negative strand of the double-stranded DNA can be transcribed by the polymerase. In RNA U replaces T.

RNA of positive strand sequence	5′-UAGAGGAGUACCAC-3′
RNA of negative strand sequence	5′-GUGGUACUCCUCUA-3′

Antisense RNA - The antisense strand of any RNA sequence is the complement sequence

RNA sequence	5′-UAGAGGAGUACCAC-3′
Antisense RNA sequence	3′-AUCUCCUCAUGGUG-5′

Triple Strand Helix - The RNA sequence of a RNA/DNA triple-strand complex is the same as the positive strand of the DNA

DNA positive strand	5′-TAGAGGAGTACCAC-3′
DNA negative strand	3′-ATCTCCTCATGGTG-5′

RNA strand 5'-UAGAGGAGUACCAC-3'

Promoter - Any region of DNA, that binds proteins which engage the polymerase transcription mechanism.

TATA Box - A region near the 3' end of a promoter with the sequence TATA.

mRNA - The RNA produced from the DNA by the polymerase as a result of transcription

Start of transcription - The 3' end of a promoter where the polymerase mechanism begins to transcribe DNA into mRNA.

Exon - Any region of mRNA which is used to code for proteins

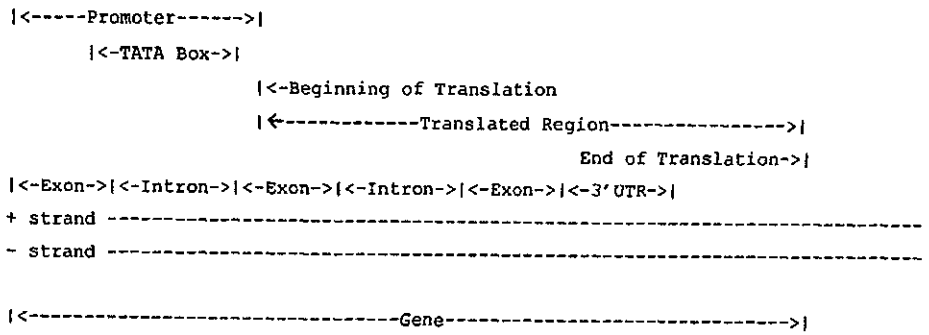
Intron - Any region of mRNA lying between two exons which is not used to code for proteins. The introns are edited out of the initial RNA transcript to form the mature mRNA.

3' UTR - The untranslated 3' end of an mRNA is beyond the end of the last exon. A stop codon in the mRNA causes the ribosome to stop the translation of mRNA into protein.

End of translation - The 3' end of the 3'-most exon.

Translated region - Any collection of exons and introns.

Gene - Any DNA region that codes for a protein. Introns do not occur in prokaryotic genes and they sometime fail to occur in eukaryotic genes. A typical model of a gene is



Positive strand gene - Any gene in which the features run 5′ to 3′ on the positive strand

Negative strand gene - Any gene in which the features run 5′ to 3′ on the negative strand

C1 sequence - Any positive or negative strand DNA sequence of 15 bases or more. The C2 sequence must occur in the same chromosome as the C1 sequence.

C2 sequence - Any positive or negative strand DNA sequence of 15 bases or more. The C1 sequence must occur in the same chromosome as the C2 sequence.

C1/C2 - Any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence

T1 sequence - Any positive or negative strand DNA sequence of 15 bases or more that is on the same chromosome as the T2 sequence. The T1 and T2 sequences must be between about 1kb and 105kb apart.

T2 sequence - Any positive or negative strand DNA sequence of 15 bases or more that is on the same chromosome as the T1 sequence. The T2 and T1 sequences must be between about 1kb and 105kb apart.

Last exon gap or **Gap-Distance** - The number of bases between the end of transcription and the beginning of the C1/C2 sequence. In prokaryotes and single-celled eukaryotes this gap can range from no bases to 500 bases. In multi-celled eukaryotes the gap can be as large as 10,000 bases.

Poly-adenylation signal - A number of Adenosine (A) bases are added to the mRNA at the end of the 3'UTR.

Possible Connectron - Any set of T1, T2 and C1/C2 sequences such that the C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence. The promoter of some gene causes the mRNA of the gene to be expressed. The mRNA is edited to eliminate the introns. The whole mRNA including the 3'UTR can move about in the cell or the nucleus of the cell. The C1/C2 RNA that is part of the 3'UTR moves to the T1 and T2 DNA sequences. A triple-stranded complex of the DNA and the RNA forms such that the C1 sequence forms hydrogen bonds with the T1 sequence and the C2 sequence forms hydrogen bonds with the T2 sequence. Because the C1 sequence is adjacent to the C2 sequence, the T1 sequence is brought physically close to the T2 sequence. This produces a loop of between about 1kb and 105kb in the DNA. Histone proteins reduce the length of the DNA by binding 200 bases. Histone/DNA complexes form six-fold symmetry chromatin assemblies. The diameter of the chromatin assemblies is approximately 30nm.

Real Connectron - Any Possible Connectron which is within the Gap-Distance of some gene

Homologous connectron - The T1 sequence and the T2 sequence are on the same chromosome as the C1/C2 sequence

Heterologous connectron - The T1 sequence and the T2 sequence are on a chromosome different from chromosome of the C1/C2 sequence

Permanent connectron - Any C1/C2 sequence, which is 3′ UTR to some gene that is not surrounded by any T1 and T2 sequence pairs

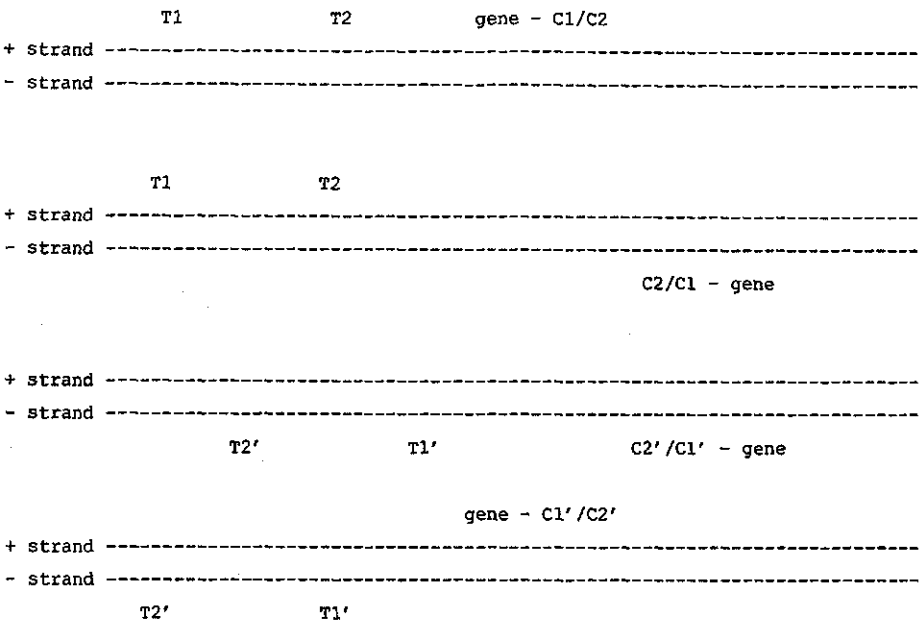
Transient connectron - Any C1/C2 sequence, which is 3′ UTR to some gene that is surrounded by one or more T1 and T2 sequence pairs

One-shot or Self-limiting connectron - Any C1/C2 sequence which is 3′UTR to some gene that is surrounded by the T1 and T2 sequences such that C1=T1 and C2=T2

Geneless connectron - Any C1/C2 sequence that is not 3′UTR to some gene but is surrounded by some T1 and T2. A promoter may lie 5′ to the C1/C2 sequence.

Bi-directionality of Connectron Excitation - A C1/C2 short loop on one strand selects a T1-T2 long loop pair on the same or the opposite strand. The C1/C2 short loop has a complementary C1′/C2′ sequence on the opposite strand. Similarly the T1-T2 long loop pair has a complementary long loop pair T1′-T2′. Wherever a C1/C2, T1-T2 tetrad exists there is a complementary C1′/C2′, T1′-T2′ tetrad. The C1/C2 short loop can be

transcribed as a 3'UTR to a gene on the same strand. The C1'/C2' short loop which is on the strand opposite to the C1/C2 short loop can also can be transcribed as a 3'UTR to a gene on the same strand. There are four possible models of action



Of course, the short loops and the long loops do not have to be on the same chromosome.

Hierarchy of connectron action - When a C1/C2 is expressed it forms a T1-T2 loop by forming a connectron. The C1/C2 sequence does not have to be on the same chromosome as the T1 and T2 sequences. This provides a way of causing interaction between chromosomes. When the T1-T2 loop forms, any genes in that loop region which had been expressing C1/C2 sequences in their 3'UTRs, now cease expressing the C1/C2 sequences. The connectrons formed by these C1/C2 sequences will cease to exist after some time thus opening up the genes inside the respective T1-T2 loops to expression. The hierarchy of connectron action

is alternates between repression and expression. The connectron hierarchies can be of any depth.

One-to-Many connectron action - One C1/C2 sequence can form connectrons in many different places on many different chromosomes. The only requirement is that C1=T1 and C2=T2. This makes it possible for one expression event to control the expression of many genes on different chromosomes.

Many-to-One connectron action - C1/C2s that come from many different places on many different chromosomes can form a connectron for a specific T1-T2 sequence pair. The only requirement is that C1=T1 and C2=T2. This makes it possible for many different expression events to control the expression of one set of genes on a particular chromosome.

Many-to-Many connectron action - The arrangement of C1/C2s and T1-T2s across chromosomes can form a complex web of gene expression control relationships.

Percentage of the Genome Regulated by Connectrons - Since the connectrons for a sequenced genome can be calculated, the percentage of the genome that is open to connectron regulation can be known.

Emergent Property - The network of connectrons in any genome emerges from a knowledge of the complete DNA sequence of the genome. Because both the C1/C2 sequences and the T1-T2 sequences can be any place in the genome, the whole genomic sequence must be known before all the connectrons can be determined.

Paradigm Shift - For the past fifty years since the discovery by Watson and Crick of the double-helical nature of DNA, the reigning paradigm for scientific discovery has been the study of one gene and its effects on the behavior of a cell. The advent of genomic sequencing and this invention of connectrons that emerge from the whole genome will produce a shift in the way scientists view biological systems and the way they formulate and execute experiments. The many-to-many relationships between the connectrons mean that there are many ways in which the expression of a set of genes can be modulated. The multiplicity of control pathways produces a system stability that makes it possible for biological systems to be stable for long periods of evolutionary time. The thinking that goes into formulating scientific experiments will have to change to accommodate the changes in understanding that will be induced by the application and extension of this patent application.

Sequence Element - The double-stranded sequence of either a C1, a C2, a T1 or a T2 of some connectron.

Native Sequence Element - Any sequence element of a connectron which is a constitutive part of the native genome.

Native Connectron - Any connectron in which all four (i.e. the C1, C2, T1 and T2 sequence) sequence elements are constitutive parts of the native genome.

Synthetic Sequence Element - Any sequence element that has been added into a genome at some particular place. The actual sequence of bases may occur in one or more places in the genome.

The synthetic aspect is that an instance has been placed into the genome at a specific place by design.

Copied Sequence Element - Any sequence element that has been copied from one place in a genome to another place in that genome.

Unique Sequence Element - Any double-stranded DNA sequence element for which there is only one pair of instances. Such a pair of instances can be used to implement the C1 and T1 synthetic sequence elements of a connectron or the C2 and T2 synthetic sequence elements of a connectron.

Extracted Sequence - Any sequence element that is moved from one place in a genome to another place in the same genome. The moved sequence element can be unique or non-unique.

Synthetic Connectron - Any connectron in which one or more of the sequence elements in a native connectron are substituted by synthetic sequence elements.

Designed Connectron - Any connectron that does not exist in the native genome.

RNA-Based Connectron - Any connectron in which the C1 and C2 elements are generated as RNA in the 3'UTR of some gene.

DBP - A multi-domain zinc-finger DNA Binding Protein that binds to a specific DNA double-stranded sequence.

Protein-Based Synthetic Connectron - Any synthetic connectron in which the C1 and C2 elements are generated by a DBP.

PNA - A Peptide Nucleic Acid is a molecular construct patented and supplied by Boehringer-Mannheim. The A, T, G, C base portions of are the same as an RNA but the ribose ring has been replaced by a peptide-like configuration of atoms.

PNA-Based Synthetic Connectron - Any synthetic connectron in which the C1 and C2 elements are generated by a sequence of Peptide Nucleic Acid (PNA) bases.

Generalized Synthetic Connectron - Any synthetic connectron in which the C1 and C2 elements are generated by two linked double-strand DNA binding elements.

Individual Connectron State - A binary representation of whether the C1-C2 elements are bound to the cognate T1 and T2 elements. A **0** means that the connectron is not formed. A **1** means that the connectron is formed and hence the expression of the genes between the T1 and T2 elements are turned off.

Genomic Connectron State - The collection of all the individual native and synthetic connectron states in a genome. The individual connectron states are ordered along each chromosome and plasmid by the position of the T1 element.

Connectron Simulation - The temporal transitions of the genomic connectron states as the individual connectron states interact with each other.

Content of the CD

The Sequence Listing Part is incorporated herein by reference. The material contained on this compact disc attached hereto was created on 6/30/03,

synthetic.sequences has 13,770 bytes

Brief Description of the Objects of the Invention

The basic methods patent application provides the methods for determining the structure of the native connectrons in a variety of genomes. Since the original conceptualization of connectrons followed from the work that we did on the design of zinc-finger DNA Binding Proteins (DBPs), US Patent 6,205,404, it has always been the applicant's intention to use these designed proteins to modify genomic connectron behavior.

An object of this invention is to provide a method for utilizing the genomic simulation of connectron behavior to facilitate the optimization of design decisions related to deleting connectrons from a genome or adding connectrons to a genome.

An object of this invention is to provide a method for utilizing the genomic simulation by computer of connectron behavior to facilitate the optimization by computer of design decisions related to deleting connectrons from a genome or adding connectrons to a genome.

An object of this invention is to provide a method for modifying the connectron behavior of a genome by deleting and adding connectrons.

An object of the invention is to provide a method for creating new connectrons in a genome by copying one or more double-stranded DNA sequence elements from one place in the genome to another place in the genome or by extracting a double-stranded DNA sequence element from one place in the genome and moving it

to another place in the genome or by introducing a new unique pair of double-stranded DNA sequence elements into the genome at specific places.

An object of the invention if to provide a method for creating new connectrons in a genome by copying, extracting or adding unique DNA elements in addition to using either DBPs, PNAs or a linked pair of generalized DNA binding elements to implement the C1 and C2 elements of the new connectron.

Description of the Tables

Table 1 - The 10 possible ways of deleting a connectron

Table 2 - The 15 possible synthetic connectrons defined by combinations of native and synthetic elements

Table 3 - The 4 possible synthetic connectrons defined by combinations of native and synthetic DNA elements and synthetic DBP elements

Table 4 - The 4 possible synthetic connectrons defined by combinations of native and synthetic DNA elements and synthetic PNA elements

Table 5 - The 4 possible synthetic connectrons defined by combinations of native and synthetic DNA elements and a pair of linked double-strand DNA binding elements

Table 6 - The 2 possible ways of implementing a single synthetic element in a synthetic connectron

Table 7 - The 14 possible ways of implementing a pair of synthetic elements in a synthetic connectron

Table 8 - The 41 possible ways of implementing three synthetic elements in a synthetic connectron

Table 9 - The 25 possible ways of implementing four synthetic elements in a synthetic connectron

Description of the Invention

The simulation of the connectron behavior of a genome provides a powerful way of understanding how individual connectrons interact with each other. From the more than 100 genomes whose connectron structure we have determined, it is clear that a given C1-C2 may generate many different connectrons - the one-to-many conectron action mode. Similarly it is clear that a given connectron may be generated by the expression of many different instances of the C1-C2 signal - the many-to-one connectron action mode. The temporal interaction of these one-to-many and many-to-one modes of connectron control of gene expression can best be understood by doing a genomic connectron simulation and looking at the results. This is especially important when determining when and where to delete connectrons from a native genome or add new connectrons to a native genome. Genomic connectron simulation is the subject of a related patent application.

Although there are instances in different genomes of a C1-C2 generating only one connectron, much more frequently a given C1-C2 will generate several connectrons. When only one connectron is generated by a given C1-C2, a decision to delete the connectron or to add another connectron using the same or different C1 or C2 elements will have no side effects as long as the T1 and T2 elements are only used by this connectron. This is the relative infrequent example of one-to-one. Much more frequently, deleting or changing a given C1 or C2 may have multiple consequences and serious behavioral side effects. Modification of genomic connectron control of gene expression will inevitably involve compromises, design decisions, and -

worst of all - patch-ups. Consider an example in which a given C1-C2 generates two connectrons. For some reason we desire to delete one of the two connectrons. A patch-up can be achieved by finding some other way to generate the second connectron. This could be achieved by adding one or more synthetic connectron elements to generate the second connectron as a synthetic connectron.

If there are no side effects of a design decision then that is the optimum. If there are side effects, the genomic simulation of connectron behavior makes it possible to evaluate the genomic behavioral consequences of the design and implementation decisions.

The deletion of a connectron as shown in table 1 can occur in 10 different ways ranging from deleting or modifying just one sequence element to deleting or modifying all four sequence elements. Anything that destroys the sequence recognition of the T1 by the C1 or the T2 by the C2 will have the effect of deleting the connectron.

Any or all of the four elements (C1, C2, T1 and T2) of a native connectron can be replaced with synthetic elements to form a synthetic connectron. Table 2 gives the 15 possible types of synthetic connectrons. A designed connectron can be introduced into a genome to either (1) control the expression of a set of genes already controlled by other native connectrons, or (2) control the expression of a newly selected set of genes. Using DNA sequences, a designed connectron be made from any of the 15 combinations of native and synthetic elements in Table 2. If the C1 and C2 elements of a connectron are generated by a zinc-finger DBP then the 4 combinations of synthetic and designed

connectrons in table 3 are possible. If the C1 and C2 elements of a connectron are generated by a PNA then the 4 combinations of synthetic and designed connectrons in table 4 are possible. If the C1 and C2 elements of a connectron are generated by a linked pair of DNA binding elements then the 4 combinations of synthetic and designed connectrons in table 5 are possible. The DNA binding elements G1 and G2 can be proteins or any other molecular material that recognizes the DNA sequences of the T1 and T2 elements.

The implementation of the synthetic elements of a designed connectron can be achieved in several different ways. In table 2 from one to four of the sequence elements of a connectron can be substituted by a synthetic sequence element. There are three different ways of creating a synthetic sequence element. An existing sequence element somewhere in the genome can be copied into a new location. An existing sequence element can be extracted from one location in the genome and placed in another position in the genome. A new pair of sequence elements not otherwise present in the genome can be created. One instance of this new, unique sequence element must be a C1 or a C2. If the first instance is a C1 then the second instance of this new, unique sequence element must be a T1. Similarly, if the first instance is a C2 then the second instance of this new, unique sequence element must be a T2. Table 6 shows that there are only two ways of generating a synthetic connectron when only one synthetic sequence element is used. Implementing a new, unique sequence element is not possible because these sequence elements must come in pairs. Table 7 shows that there are 14 ways of implementing a pair of synthetic sequence elements to form a synthetic connectron. Table 8 shows that there are 41 ways of implementing three synthetic sequence elements to form a

synthetic connectron. Table 9 shows that there are 25 ways of implementing four synthetic sequence elements to form a synthetic connectron.

Examples

Tables 1 thru 9 provide a large combinatorial number of ways of deleting connectrons from a genome and of adding connectrons to a genome. We give one example of deleting one connectron from a single genome and five examples of a connectron to four different genomes. It is clear that many other variations would be obvious to someone skilled in the art.

Deletion of a Transient Connectron from one chromosome to itself

Connectron 13 is an example of a transient connectron in the *S. cerevisiae* genome. As per table 1, this connectron can be deleted by either deleting or modifying any one or all four of the connectron elements. The C1 and the C2 identifiers are 36 while the T1 identifier is 39 and the T2 identifier is 111. When this connectron is deleted, all the properties stated below disappear.

The original connectron 13 is described as

		C1/C2			T1-T2		
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
13	1	36	36	1	39	111	transient

The C1/C2 source of the transient connectron 13 is represented in table 1 as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
CPT	36	1	1	12.572	12.788	.217	OS->	!!!!!!!!!!!!!!!!!!

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB).

The T1-T2 target of the transient connectron 13 as shown in table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TP	39	1	1	12.572	12.807	.236		*-+++++++++++++++++++*
TN	40	8	1	12.908	12.964	.057		*-+++++++++++++++++++++*
CNT	41	1	1	12.908	12.964	.057	-->	|||||||||||||||||||
CPT	42	1	1	12.908	12.964	.057	-->	|||||||||||||||||||
TP	43	1	1	12.922	12.964	.043		*-++++++++++++++++++++*
CNT	44	1	1	12.966	12.986	.021	-->	||||||||||||||||||||
CPT	45	8	1	12.966	12.986	.021	-->	||||||||||||||||||||
TP	46	1	1	12.966	12.986	.021		*-++++++++++++++++++++*
TN	47	1	1	13.027	13.159	.133		*-++++++++++++++++++++++*
CNT	48	1	1	13.028	13.099	.072	OS->	|||||||||||||||||||||
TP	49	1	1	13.028	13.099	.072		*-++++++++++++++++++++++*
CPT	50	1	1	13.053	13.124	.072	OS->	||||||||||||||||||||||
TP	51	1	1	13.102	13.159	.058		*-++++++++++++++++++++++*
CNT	52	1	1	13.105	13.246	.142	-->	||||||||||||||||||||||
CPT	53	1	1	13.130	13.246	.117	-->	||||||||||||||||||||||
TN	54	1	1	13.176	13.194	.019		*-++++++++++++++++++++++*
TN	55	1	1	13.196	13.231	.036		*-++++++++++++++++++++++++**
TP	56	1	1	13.211	13.246	.036		*-++++++++++++++++++++++++
CPT	57	1	1	13.253	13.290	.038	-->	|||||||||||||||||||||||
TN	58	1	1	13.253	13.290	.038		*-++++++++++++++++++++++++
TP	59	1	1	13.255	13.285	.031		*-++++++++++++++++++++++++
CNT	60	1	1	13.255	13.290	.036	-->	|||||||||||||||||||||||
CPT	61	8	1	13.295	13.315	.021	-->	|||||||||||||||||||||||
TN	62	8	1	13.295	13.317	.023		*-++++++++++++++++++++++++
CNT	63	8	1	13.340	13.379	.040	-->	|||||||||||||||||||||||
CPT	64	8	1	13.341	13.380	.040	-->	|||||||||||||||||||||||

	GG	65	1	1	13.364	13.744	.381	Group0004
	CPT	66	1	1	13.387	13.405	.019	-->
	TN	67	8	1	13.387	13.413	.027	
	TP	68	1	1	13.444	13.460	.017	
5	CPT	69	8	1	13.566	13.582	.017	-->
	TN	70	8	1	13.574	13.591	.018	
	CPT	71	8	1	13.585	13.599	.016	-->
	TN	72	1	1	13.656	13.681	.026	
	TP	73	1	1	13.656	13.706	.051	
10	TN	74	9	1	13.704	13.726	.023	
	CPT	75	1	1	13.709	13.726	.018	-->
	TN	76	1	1	13.734	13.750	.017	
	CPT	77	1	1	13.734	13.782	.049	-->
	TP	78	1	1	13.734	13.782	.049	
15	TN	79	1	1	13.768	13.782	.015	
	CPT	80	1	1	13.815	13.858	.044	-->
	TN	81	1	1	13.840	13.858	.019	
	CPT	82	1	1	14.422	14.460	.039	-->
	CPT	83	1	1	14.941	14.962	.022	-->
20	CPT	84	1	1	14.966	14.993	.028	-->
	CPT	85	1	1	14.997	15.018	.022	-->
	TP	86	1	1	15.795	15.816	.022	
	TP	87	1	1	15.996	16.020	.025	
	TP	88	1	1	16.874	16.898	.025	
25	CNT	89	1	1	20.136	20.151	.016	-->
	CNT	90	1	1	20.157	20.176	.020	-->
	GG	91	1	1	21.526	21.852	.327	Group0005
	CPT	92	1	1	22.257	22.304	.048	-->
	CNT	93	1	1	22.275	22.304	.030	-->
30	CNT	94	1	1	22.307	22.322	.016	-->
	CPT	95	1	1	22.307	22.322	.016	-->
	CNT	96	1	1	22.324	22.338	.015	-->
	CNT	97	1	1	22.351	22.367	.017	-->
	CPT	98	8	1	22.351	22.367	.017	-->
35	CNT	99	1	1	22.376	22.392	.017	-->
	CPT	100	8	1	22.376	22.392	.017	-->
	TN	101	1	1	23.300	23.324	.025	
	CPT	102	8	1	23.683	23.716	.034	-->
	GG	103	1	1	24.001	27.969	3.969	Group0006
40	TN	104	1	1	24.119	24.431	.313	
	CPT	105	1	1	24.283	24.352	.070	OS->
	TP	106	1	1	24.287	24.431	.145	
	TN	107	1	1	24.433	24.514	.082	
	TN	108	1	1	24.516	24.603	.088	
45	TN	109	8	1	24.605	24.703	.099	
	TN	110	1	1	24.743	24.854	.112	
	TP	111	1	1	24.863	25.001	.039	

The "Type" descriptor of the T1 (Id number 39) is "TP" showing that is T1 target is on the positive strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 111) also has the type descriptor "TP".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
TP	xx	1	1	278.452	278.892	.441	*---*

Group0004 (Id number 65) has the type descriptor "GG". The same is true for Group0006 (Id number 103).

Group0004 through Group0006 are described in table 2 as

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
YAL064C-A	-	1	negative	13.364	13.744	.381

Group0005

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
YAL064W	-	1	positive	21.526	21.852	.327

Group0006

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length

```
FLO9        -                    1  negative    24.001    27.969     3.969
 ---------------------------------------------------------------------
```

All of the data for the transient connectron 13 are pulled together in the following table that is the "terse" description of the connectron.

```
 ---------------------------------------------------------------------
Connectron Relationships - Global_Id  Type
                                13  transient

Control Sequences - Direction  Chromosome  C1/C2_Id      Start      Stop  Length
                    positive           1        36     12.572    12.788    .217

Trigger Gene - Name      COG_Id      Start      Stop  Length
               YAL064W-B -          12.047    12.427    .381

Target Sequences  - Direction  Chromosome     T1_Id      Start      Stop  Length
                    positive           1        39     12.572    12.807    .236

                                          T2_Id      Start      Stop  Length
                                           111     24.863    25.001    .020

Controlled Genes
Local_Id  Chromosome  Group      Name       COG_Id  Direction     Start      Stop    Length
       1           1  Group0004  YAL064C-A  -       positive     13.364    13.744      .381
       2           1  Group0005  YAL064W    -       positive     21.526    21.852      .327
       3           1  Group0006  FLO9       -       positive     24.001    27.969     3.969

Controlled Connectrons
Local_Id  Chromosome    C1/C2_Id  Direction     Start      Stop    Length
       1           1          41  negative     12.964    12.908      .057
       2           1          42  positive     12.908    12.964      .057
       3           1          44  negative     12.986    12.966      .021
       4           1          45  positive     12.966    12.986      .021
       5           1          48  negative     13.099    13.028      .072
       6           1          50  positive     13.053    13.124      .072
       7           1          52  negative     13.246    13.105      .142
       8           1          53  positive     13.130    13.246      .117
       9           1          57  positive     13.253    13.290      .038
      10           1          60  negative     13.290    13.255      .036
      11           1          61  positive     13.295    13.315      .021
      12           1          63  negative     13.379    13.340      .040
      13           1          64  positive     13.341    13.380      .040
      14           1          66  positive     13.387    13.405      .019
      15           1          69  positive     13.566    13.582      .017
```

16	1	71	positive	13.585	13.599	.016
17	1	75	positive	13.709	13.726	.018
18	1	77	positive	13.734	13.782	.049
19	1	80	positive	13.815	13.858	.044
20	1	82	positive	14.422	14.460	.039
21	1	83	positive	14.941	14.962	.022
22	1	84	positive	14.966	14.993	.028
23	1	85	positive	14.997	15.018	.022
24	1	89	negative	20.151	20.136	.016
25	1	90	negative	20.176	20.157	.020
26	1	92	positive	22.257	22.304	.048
27	1	93	negative	22.304	22.275	.030
28	1	94	negative	22.322	22.307	.016
29	1	95	positive	22.307	22.322	.016
30	1	96	negative	22.338	22.324	.015
31	1	97	negative	22.367	22.351	.017
32	1	98	positive	22.351	22.367	.017
33	1	99	negative	22.392	22.376	.017
34	1	100	positive	22.376	22.392	.017
35	1	102	positive	23.683	23.716	.034
36	1	105	positive	24.283	24.352	.070

Addition of a Synthetic Connectron of Type 2 from Table 2

A synthetic connectron of type 2 in which the C1 and C2 are synthetic elements, the T1 is a synthetic element and the T2 is a natural element can be introduced into the *E. coli* genome by modifying the DNA double-strand sequences at 4626.130kb through 4626.166kb for a length of 0.036kb and by modifying the DNA double-strand sequence at 705.150kb through 705.203kb for a length of 0.054kb.

Connectron 62521 is an example of a synthetic transient connectron. It is described as

		C1/C2			T1-T2		
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
62521	1	4651a	4651a	1	811a	975	transient

The C1/C2 source of the transient connectron 62521 is represented in Table 1 as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
CPT	4651a	1	1	4626.130	4626.166	.037		||| ||	|||| ||	||

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB).

The T1-T2 target of the transient connectron 62521 as shown in Table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TN	811a	1	1	705.150	705.203	.054		*-*
TP	812	1	1	705.122	705.141	.020		*-+
GG	813	1	1	705.316	706.980	1.665	Group0150	|
TN	814	1	1	707.013	707.028	.016		*-+
TP	815	1	1	707.014	707.028	.015		*-+
CPT	816	1	1	707.055	707.109	.055	-->	|
TN	817	1	1	707.055	707.109	.055		*-+
TP	818	1	1	707.055	707.109	.055		*-+
CPT	819	1	1	707.112	707.162	.051	OS->	|
TN	820	1	1	707.112	707.162	.051		*-+
TP	821	1	1	707.112	707.162	.051		*-+
GG	822	1	1	707.557	710.688	3.131	Group0151	|
CNT	823	1	1	710.633	710.647	.015	OS->	|
TN	824	1	1	710.633	710.647	.015		*-+

CNT	825	1	1	710.652	710.666	.015	-->	|
GG	826	1	1	710.828	712.755	1.927	Group0152	|
TN	827	1	1	712.281	712.296	.016	*-+	
GG	828	1	1	712.781	714.421	1.641	Group0153	|
TN	829	1	1	714.481	714.518	.038	*-+	
CPT	830	1	1	714.481	714.519	.039	OS->	|
TP	831	1	1	714.482	714.519	.038	*-+	
CPT	832	1	1	714.524	714.540	.017	-->	|
TN	833	1	1	714.524	714.540	.017	*-+	
TP	834	1	1	714.524	714.540	.017	*-+	
CNT	835	1	1	714.543	714.593	.051	OS->	|
TN	836	1	1	714.543	714.593	.051	*-+	
TP	837	1	1	714.543	714.593	.051	*-+	
CPT	838	1	1	714.544	714.606	.063	OS->	|
GG	839	1	1	714.635	715.928	1.293	Group0154	|
GN	840	1	1	715.170	715.532	.363	ybfg	|
TN	841	1	1	716.085	716.103	.019	*-+	
TP	842	1	1	716.085	716.103	.019	*-+	
GG	843	1	1	716.169	724.202	8.033	Group0155	|
CNT	844	1	1	720.278	720.296	.019	-->	|
GN	845	1	1	720.279	724.202	3.924	kdpe	|
TP	846	1	1	721.769	721.783	.015	*-+	
TN	847	1	1	721.812	721.827	.016	*-+	
GG	848	1	1	724.211	727.955	3.744	Group0156	|
TP	849	1	1	726.665	726.679	.015	*-+	
GG	850	1	1	728.357	733.325	4.968	Group0157	|
GP	851	1	1	728.806	733.325	4.520	rhsc	|
CPT	852	1	1	729.408	729.446	.039	-->	|
TP	853	1	1	730.270	730.284	.015	*-+	
CPT	854	1	1	730.443	730.457	.015	-->	|
CPT	855	1	1	730.468	730.482	.015	-->	|
CPT	856	1	1	730.484	730.507	.024	-->	|
CPT	857	1	1	731.251	731.290	.040	-->	|
TP	858	1	1	731.475	731.508	.034	*-+	
TP	859	1	1	731.512	731.562	.051	*-+	
TP	860	1	1	731.564	731.693	.130	*-+	
TP	861	1	1	731.698	731.755	.058	*-+	
TP	862	1	1	731.757	731.819	.063	*-+	
TP	863	1	1	731.821	731.903	.083	*-+	
TP	864	1	1	731.906	732.033	.128	*-+	
CPT	865	1	1	731.994	732.016	.023	-->	|
CPT	866	1	1	732.019	732.034	.016	-->	|
TP	867	1	1	732.035	732.050	.016	*-+	
TP	868	1	1	732.052	732.179	.128	*-+	
CPT	869	1	1	732.065	732.179	.115	OS->	|
CPT	870	1	1	732.198	732.212	.015	-->	|
TP	871	1	1	732.198	732.212	.015	*-|	
CPT	872	1	1	732.214	732.233	.020	-->	|

	TP	873	1	1	732.214	732.233	.020	*-+
	CPT	874	1	1	732.235	732.283	.049	--> |
	TP	875	1	1	732.235	732.283	.049	*-+
	CPT	876	1	1	732.306	732.326	.021	--> |
5	TP	877	1	1	732.306	732.326	.021	*-+
	CPT	878	1	1	732.328	732.452	.125	--> |
	TP	879	1	1	732.328	732.482	.155	*-+
	CPT	880	1	1	732.454	732.482	.029	--> |
	CPT	881	1	1	732.488	732.519	.032	--> |
10	TN	882	1	1	733.330	733.344	.015	*-+
	TP	883	1	1	733.330	733.344	.015	*-+
	TP	884	1	1	733.371	733.513	.143	*-+
	GG	885	1	1	733.443	735.442	2.000 Group0158	|
	TP	886	1	1	733.515	733.564	.050	*-+
15	TP	887	1	1	733.569	733.626	.058	*-+
	TP	888	1	1	733.628	733.645	.018	*-+
	TP	889	1	1	733.647	733.696	.050	*-+
	TP	890	1	1	733.698	733.774	.077	*-+
	TP	891	1	1	733.776	733.904	.129	*-+
20	CPT	892	1	1	733.865	733.887	.023	OS-> |
	CPT	893	1	1	733.890	733.905	.016	--> |
	TP	894	1	1	733.906	734.050	.145	*-+
	CPT	895	1	1	733.936	734.050	.115	--> |
	TP	896	1	1	734.052	734.075	.024	*-+
25	CPT	897	1	1	734.052	734.139	.088	--> |
	TP	898	1	1	734.084	734.139	.056	*-+
	TP	899	1	1	734.149	734.179	.031	*-+
	CPT	900	1	1	734.164	734.321	.158	--> |
	TP	901	1	1	734.192	734.321	.130	*-+
30	TP	902	1	1	734.323	734.378	.056	*-+
	CPT	903	1	1	734.323	734.381	.059	--> |
	CPT	904	1	1	735.525	735.569	.045	--> |
	TP	905	1	1	735.525	735.569	.045	*-+
	CPT	906	1	1	735.606	735.703	.098	--> |
35	TP	907	1	1	735.606	735.703	.098	*-+
	TP	908	1	1	735.707	735.721	.015	*-+
	CPT	909	1	1	735.707	735.728	.022	--> |
	TP	910	1	1	735.749	735.803	.055	*-+
	CPT	911	1	1	735.807	735.964	.158	OS-> |
40	TP	912	1	1	735.814	735.895	.082	*-+
	TP	913	1	1	735.905	735.934	.030	*-+
	TP	914	1	1	735.938	736.083	.146	*-+
	CPT	915	1	1	735.986	736.083	.098	OS-> |
	TP	916	1	1	736.152	736.173	.022	*-+
45	TP	917	1	1	736.187	736.217	.031	*-+
	TP	918	1	1	736.219	736.265	.047	*-+
	TP	919	1	1	736.288	736.334	.047	*-+
	GG	920	1	1	736.327	737.184	.858 Group0159	|

	TP	921	1	1	736.349	736.469	.121	*-+
	TP	922	1	1	736.516	736.628	.113	*-+
	TP	923	1	1	736.630	736.645	.016	*-+
	TP	924	1	1	736.654	736.792	.139	*-+
5	TN	925	1	1	736.654	736.809	.156	*-+
	TN	926	1	1	736.816	736.832	.017	*-+
	CPT	927	1	1	737.017	737.032	.016	--> |
	CPT	928	1	1	737.035	737.057	.023	--> |
	TN	929	1	1	737.168	737.188	.021	*-++
10	TP	930	1	1	737.196	737.290	.095	*-+
	CPT	931	1	1	737.261	737.275	.015	--> |
	CPT	932	1	1	737.278	737.292	.015	--> |
	TP	933	1	1	737.292	737.393	.102	*-+
	GG	934	1	1	737.315	738.076	.762 Group0160	|
15	TP	935	1	1	737.411	737.475	.065	*-+
	TP	936	1	1	737.479	737.557	.079	*-+
	TP	937	1	1	737.580	737.597	.018	*-+
	TP	938	1	1	737.605	737.626	.022	*-+
	TP	939	1	1	737.633	737.648	.016	*-+
20	TP	940	1	1	737.653	737.679	.027	*-+
	TP	941	1	1	737.683	737.752	.070	*-+
	TP	942	1	1	737.798	737.822	.025	*-+
	TP	943	1	1	737.828	737.895	.068	*-+
	TP	944	1	1	737.897	737.931	.035	*-+
25	CPT	945	1	1	737.930	737.967	.038	--> |
	TP	946	1	1	737.936	737.967	.032	*-+
	TP	947	1	1	737.970	737.988	.019	*-+
	TN	948	1	1	737.990	738.015	.026	*-+
	TP	949	1	1	737.990	738.015	.026	*-+
30	TN	950	1	1	738.019	738.051	.033	*-+
	TP	951	1	1	738.019	738.051	.033	*-++
	TP	952	1	1	738.053	738.074	.022	*-+
	TN	953	1	1	738.058	738.074	.017	*-+
	TN	954	1	1	738.107	738.126	.020	*-+
35	GG	955	1	1	738.224	740.148	1.925 Group0161	|
	TN	956	1	1	740.172	740.213	.042	*-+
	CNT	957	1	1	740.172	740.290	.119 OS->	|
	CPT	958	1	1	740.172	740.290	.119 OS->	|
	TP	959	1	1	740.173	740.213	.041	*-+
40	TP	960	1	1	740.216	740.241	.026	*-+
	TN	961	1	1	740.216	740.288	.073	*-+
	TP	962	1	1	740.244	740.288	.045	*-+
	GG	963	1	1	740.298	757.628	17.330 Group0162	|
	GP	964	1	1	742.816	745.122	2.307 ybgj	|
45	CPT	965	1	1	744.643	744.657	.015 -->	|
	CPT	966	1	1	744.664	744.678	.015 -->	|
	GP	967	1	1	754.400	756.896	2.497 sdhc	|
	CPT	968	1	1	755.680	755.714	.035 -->	|

```
GP      969    1  1   756.912   757.628     .717 sdhb        |
TN      970    1  1   757.626   757.712     .087           *-+
CPT     971    1  1   757.628   757.712     .085       OS-> |
TP      972    1  1   757.629   757.712     .084           *-+
GG      973    1  1   757.687   760.730    3.044 Group0163  |
CPT     974    1  1   757.717   757.736     .020        --> |
TN      975    1  1   757.718   757.753     .036           *-*
```

The "Type" descriptor of the T1 (Id number 811a) is "TN" showing that is T1 target is on the negative strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 975) also has the type descriptor "TN".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

```
Type     Num Jobno  Chr   Start      Stop    Length GeneName
TN        xx     1  1   278.386   279.148     .763          *---*
XX        xx     1  1   278.387   278.416     .030          *   @
XX        xx     1  1   278.421   278.450     .030          *   @
TP        xx     1  1   278.452   278.892     .441          *---*
```

Group0150 through Group0163 are described in Table 2 as

```
-------------------------------------------------------------------------
Group0150

Gene_Name  COG_Id        Chromosome  Direction    Start      Stop     Length
glns       COG0008    b           1  positive   705.316   706.980     1.665
-------------------------------------------------------------------------
Group0151
```

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybfm	-	b	1	positive	707.557	708.963	1.407
ybfn	-	b	1	positive	709.013	709.339	.327
fur	COG0735	b	1	negative	709.423	709.869	.447
flda	COG0716	b	1	negative	710.158	710.688	.531

Group0152

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybfe	-	b	1	negative	710.828	711.190	.363
ybff	COG0596	b	1	negative	711.261	712.025	.765
seqa	COG3057	b	1	positive	712.210	712.755	.546

Group0153

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
pgm	COG0033	b	1	positive	712.781	714.421	1.641

Group0154

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybfp	-	b	1	positive	714.635	715.129	.495
ybfg	-	b	1	negative	715.170	715.532	.363
ybfh	-	b	1	negative	715.611	715.928	.318

Group0155

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
pote	COG0531	b	1	negative	716.169	719.683	3.515
kdpe	COG0745	b	1	negative	720.279	724.202	3.924

Group0156

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
kdpb	COG2216	b	1	negative	724.211	726.259	2.049
kdpa	COG2060	b	1	negative	726.282	727.955	1.674

Group0157

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybfa	-	b	1	positive	728.357	728.563	.207
rhsc	-	b	1	positive	728.806	733.325	4.520

Group0158

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
b0703	COG3209	b	1	positive	733.443	735.442	2.000

Group0159

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybfI	-	b	1	positive	736.327	737.184	.858

Group0160

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybfd	-	b	1	positive	737.315	738.076	.762

Group0161

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybga	COG3272	b	1	positive	738.224	740.148	1.925

Group0162

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybgh	COG3104	b	1	negative	740.298	741.779	1.482
ybgi	COG0327	b	1	positive	742.050	742.793	.744
ybgj	COG2049	b	1	positive	742.816	745.122	2.307
nei	COG0266	b	1	positive	745.158	745.949	.792
abrb	-	b	1	negative	745.946	747.037	1.092
ybgo	-	b	1	negative	747.144	748.930	1.787
ybgq	-	b	1	negative	748.945	751.401	2.457
ybgd	-	b	1	negative	751.452	752.018	.567
glta	COG0372	b	1	negative	752.408	753.691	1.284
sdhc	COG2009	b	1	positive	754.400	756.896	2.497
sdhb	COG0479	b	1	positive	756.912	757.628	.717

Group0163

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
b0725	-	b	1	positive	757.687	760.730	3.044

All of the data for the transient connectron 62521 are pulled together in the following table that is the "terse" description of the connectron.

Connectron Relationships - Global_Id	Type
62521	transient

Control Sequences - Direction	Chromosome	C1/C2_Id	Start	Stop	Length

positive	1	4651a	4626.130	4626.166	.036

Trigger Gene - Name	COG_Id	Start	Stop	Length
sms		4623.481	4626.116	2.636

Target Sequences - Direction	Chromosome	T1_Id	Start	Stop	Length
negative	1	811a	705.150	705.203	.054

T2_Id	Start	Stop	Length
975	757.753	757.718	.036

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0150	glns	COG0008	positive	705.316	706.980	1.665
2	1	Group0151	ybfm	-	positive	707.557	710.688	3.131
3	1	Group0151	ybfn	-	positive	709.013	709.339	.327
4	1	Group0151	fur	COG0735	negative	709.869	709.423	.447
5	1	Group0151	flda	COG0716	negative	710.688	710.158	.531
6	1	Group0152	ybfe	-	positive	710.828	712.755	1.927
7	1	Group0152	ybff	COG0596	negative	712.025	711.261	.765
8	1	Group0152	seqa	COG3057	positive	712.210	712.755	.546
9	1	Group0153	pgm	COG0033	positive	712.781	714.421	1.641
10	1	Group0154	ybfp	-	positive	714.635	715.928	1.293
11	1	Group0154	ybfg	-	negative	715.532	715.170	.363
12	1	Group0154	ybfh	-	negative	715.928	715.611	.318
13	1	Group0155	pote	COG0531	positive	716.169	724.202	8.033
14	1	Group0155	kdpe	COG0745	negative	724.202	720.279	3.924
15	1	Group0156	kdpb	COG2216	positive	724.211	727.955	3.744
16	1	Group0156	kdpa	COG2060	negative	727.955	726.282	1.674
17	1	Group0157	ybfa	-	positive	728.357	733.325	4.968
18	1	Group0157	rhsc	-	positive	728.806	733.325	4.520
19	1	Group0158	b0703	COG3209	positive	733.443	735.442	2.000
20	1	Group0159	ybfl	-	positive	736.327	737.184	.858
21	1	Group0160	ybfd	-	positive	737.315	738.076	.762
22	1	Group0161	ybga	COG3272	positive	738.224	740.148	1.925
23	1	Group0162	ybgh	COG3104	positive	740.298	757.628	17.330
24	1	Group0162	ybgi	COG0327	positive	742.050	742.793	.744
25	1	Group0162	ybgj	COG2049	positive	742.816	745.122	2.307
26	1	Group0162	nei	COG0266	positive	745.158	745.949	.792
27	1	Group0162	abrb	-	negative	747.037	745.946	1.092
28	1	Group0162	ybgo	-	negative	748.930	747.144	1.787
29	1	Group0162	ybgq	-	negative	751.401	748.945	2.457
30	1	Group0162	ybgd	-	negative	752.018	751.452	.567
31	1	Group0162	glta	COG0372	negative	753.691	752.408	1.284
32	1	Group0162	sdhc	COG2009	positive	754.400	756.896	2.497
33	1	Group0162	sdhb	COG0479	positive	756.912	757.628	.717
34	1	Group0163	b0725	-	positive	757.687	760.730	3.044

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	816	positive	707.055	707.109	.055
2	1	819	positive	707.112	707.162	.051
3	1	823	negative	710.647	710.633	.015
4	1	825	negative	710.666	710.652	.015
5	1	830	positive	714.481	714.519	.039
6	1	832	positive	714.524	714.540	.017
7	1	835	negative	714.593	714.543	.051
8	1	838	positive	714.544	714.606	.063
9	1	844	negative	720.296	720.278	.019
10	1	852	positive	729.408	729.446	.039
11	1	854	positive	730.443	730.457	.015
12	1	855	positive	730.468	730.482	.015
13	1	856	positive	730.484	730.507	.024
14	1	857	positive	731.251	731.290	.040
15	1	865	positive	731.994	732.016	.023
16	1	866	positive	732.019	732.034	.016
17	1	869	positive	732.065	732.179	.115
18	1	870	positive	732.198	732.212	.015
19	1	872	positive	732.214	732.233	.020
20	1	874	positive	732.235	732.283	.049
21	1	876	positive	732.306	732.326	.021
22	1	878	positive	732.328	732.452	.125
23	1	880	positive	732.454	732.482	.029
24	1	881	positive	732.488	732.519	.032
25	1	892	positive	733.865	733.887	.023
26	1	893	positive	733.890	733.905	.016
27	1	895	positive	733.936	734.050	.115
28	1	897	positive	734.052	734.139	.088
29	1	900	positive	734.164	734.321	.158
30	1	903	positive	734.323	734.381	.059
31	1	904	positive	735.525	735.569	.045
32	1	906	positive	735.606	735.703	.098
33	1	909	positive	735.707	735.728	.022
34	1	911	positive	735.807	735.964	.158
35	1	915	positive	735.986	736.083	.098
36	1	927	positive	737.017	737.032	.016
37	1	928	positive	737.035	737.057	.023
38	1	931	positive	737.261	737.275	.015
39	1	932	positive	737.278	737.292	.015
40	1	945	positive	737.930	737.967	.038
41	1	957	negative	740.290	740.172	.119
42	1	958	positive	740.172	740.290	.119
43	1	965	positive	744.643	744.657	.015
44	1	966	positive	744.664	744.678	.015
45	1	968	positive	755.680	755.714	.035
46	1	971	positive	757.628	757.712	.085

47	1	974	positive	757.717	757.736	.020

Addition of a Synthetic Connectron of Type 4 from Table 2

A synthetic connectron of type 4 in which the C1 and C2 are synthetic elements and the T1 and T2 are natural elements can be introduced into the *E. coli* genome by modifying the DNA double-strand sequences at 4626.130kb through 4626.166kb for a length of 0.036kb.

Connectron 62520 is an example of a synthetic transient connectron. It is described as

		C1/C2			T1-T2		
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
62520	1	4651a	4651a	1	809	975	transient

The C1/C2 source of the transient connectron 62520 is represented in Table 1 as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
CPT	4651a	1	1	4626.130	4626.166	.036		||| ||	|||| ||	||

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The

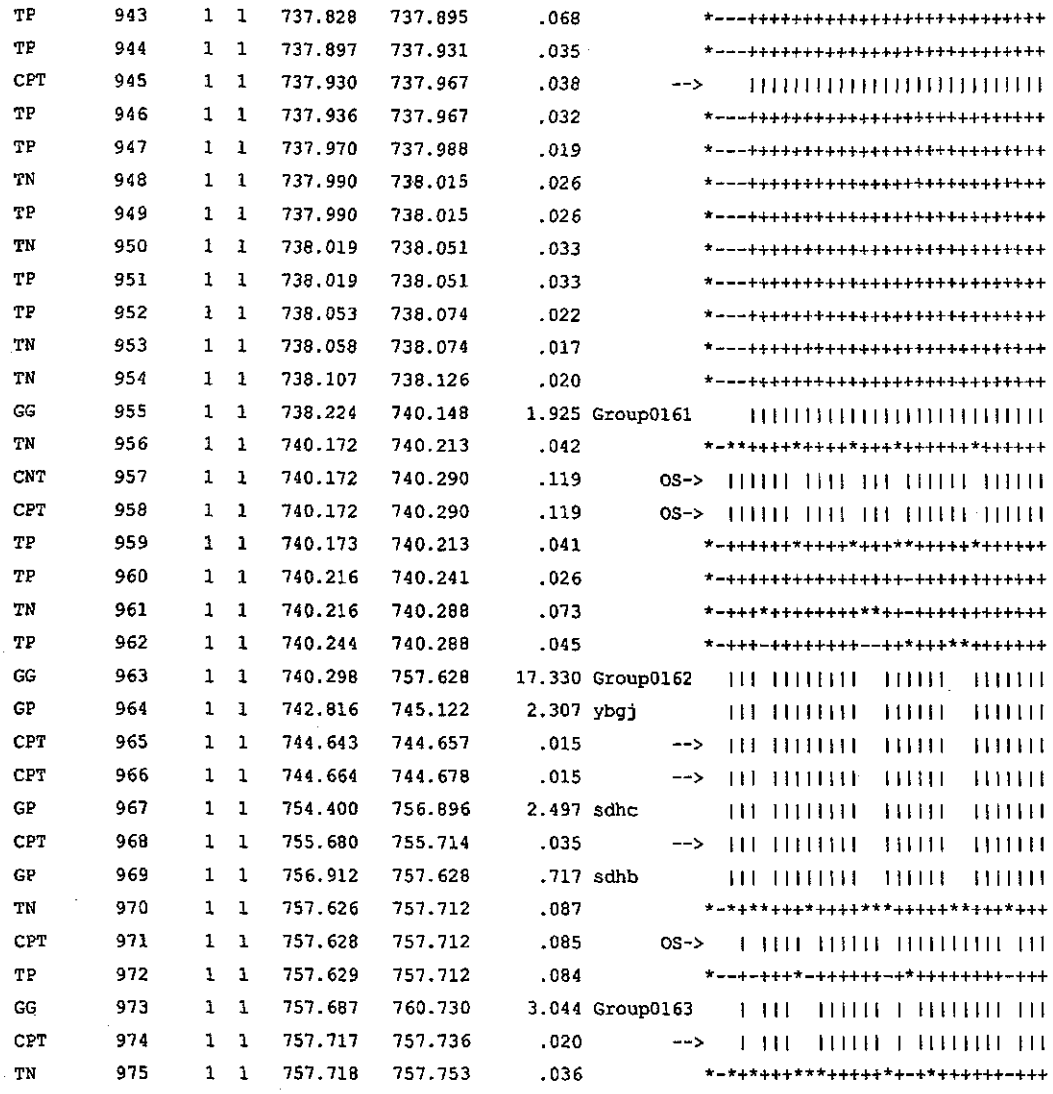
"Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB).

The T1-T2 target of the transient connectron 62520 as shown in Table 1 is represented as

```
Type   Num Jobno Chr  Start    Stop    Length GeneName
TN     809   1   1   698.713  698.766   .054            *-+++*+++**++*+++++-++++++++++
GG     810   1   1   698.797  705.113  6.316 Group0149  ||||||||||| ||||| ||||||||||
TN     811   1   1   705.121  705.141   .021            *-++*++++++++**++++*+++++*+++++
TP     812   1   1   705.122  705.141   .020            *-++-+++++++++-+++++++++-+++++
GG     813   1   1   705.316  706.980  1.665 Group0150  || ||||||||| ||||||||| |||||
TN     814   1   1   707.013  707.028   .016            *-++*++++++++++*++++++++++*++++*
TP     815   1   1   707.014  707.028   .015            *-++++++++++++++++++++++++++++-
CPT    816   1   1   707.055  707.109   .055       -->  |||||||||||||||||||||||||||
TN     817   1   1   707.055  707.109   .055            *-+++++++++*+*++++++++*+*+++++*
TP     818   1   1   707.055  707.109   .055            *-+++++++++-+-++++++++-+-++++++
CPT    819   1   1   707.112  707.162   .051      OS->  ||||||||| | |||||||| | ||||||
TN     820   1   1   707.112  707.162   .051            *-++++*++++*+*+++++*+**+*+*+*++
TP     821   1   1   707.112  707.162   .051            *-++++-+++++++++++-+-++++-+-++
GG     822   1   1   707.557  710.688  3.131 Group0151  |||| ||||||||||| | |||| | ||
CNT    823   1   1   710.633  710.647   .015      OS->  |||| ||||||||||| | |||| | ||
TN     824   1   1   710.633  710.647   .015            *-++++-*|||||||||| | |||| | ||
CNT    825   1   1   710.652  710.666   .015       -->  ||||  |||||||||| | |||| | ||
GG     826   1   1   710.828  712.755  1.927 Group0152  ||||  |||||||||| | |||| | ||
TN     827   1   1   712.281  712.296   .016            *-++++--+++++++++++-+-++++-+-++
GG     828   1   1   712.781  714.421  1.641 Group0153  ||||  |||||||||| | |||| | ||
TN     829   1   1   714.481  714.518   .038            *-++++**+++*+++++++*+*++++*+***
CPT    830   1   1   714.481  714.519   .039      OS->  ||||||||| ||||||||||||||||
TP     831   1   1   714.482  714.519   .038            *-+++++++++-++++++++++++++++--
CPT    832   1   1   714.524  714.540   .017       -->  ||||||||| ||||||||||||||||
TN     833   1   1   714.524  714.540   .017            *-+++++++++*+*++++++++++++++**
TP     834   1   1   714.524  714.540   .017            *-+++++++++++-+++++++++++++++++
CNT    835   1   1   714.543  714.593   .051      OS->  ||||||||||| ||||||||||||||||
TN     836   1   1   714.543  714.593   .051            *-++*+++++++**++++++++*++++++++
TP     837   1   1   714.543  714.593   .051            *-++-+++++++-+++++++++-++++++++
CPT    838   1   1   714.544  714.606   .063      OS->  || ||||||| ||||||||| ||||||||
GG     839   1   1   714.635  715.928  1.293 Group0154  || ||||||| ||||||||| ||||||||
GN     840   1   1   715.170  715.532   .363 ybfg       || ||||||| ||||||||| ||||||||
TN     841   1   1   716.085  716.103   .019            *-++*+++++++*||||||||| ||||||||
TP     842   1   1   716.085  716.103   .019            *-+++++++++++++++++++++*++++++++
GG     843   1   1   716.169  724.202  8.033 Group0155  |||||||||||||||||||||||||||||
CNT    844   1   1   720.278  720.296   .019       -->  |||||||||||||||||||||||||||||
GN     845   1   1   720.279  724.202  3.924 kdpe       |||||||||||||||||||||||||||||
TP     846   1   1   721.769  721.783   .015            *-+++++++++++++++++++++++++++++
```

	TN	847	1	1	721.812	721.827	.016	*-+++++++++++++++++++++++++++++++
	GG	848	1	1	724.211	727.955	3.744 Group0156	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	TP	849	1	1	726.665	726.679	.015	*-+++++++++++++++++++++++++++++++
	GG	850	1	1	728.357	733.325	4.968 Group0157	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
5	GP	851	1	1	728.806	733.325	4.520 rhsc	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	CPT	852	1	1	729.408	729.446	.039 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	TP	853	1	1	730.270	730.284	.015	*-+++++++++++++++++++++++++++++++
	CPT	854	1	1	730.443	730.457	.015 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	CPT	855	1	1	730.468	730.482	.015 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
10	CPT	856	1	1	730.484	730.507	.024 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	CPT	857	1	1	731.251	731.290	.040 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	TP	858	1	1	731.475	731.508	.034	*-+++++++++++++++++++++++++++++++
	TP	859	1	1	731.512	731.562	.051	*-+++++++++++++++++++++++++++++++
	TP	860	1	1	731.564	731.693	.130	*-+++++++++++++++++++++++++++++++
15	TP	861	1	1	731.698	731.755	.058	*-+++++++++++++++++++++++++++++++
	TP	862	1	1	731.757	731.819	.063	*-+++++++++++++++++++++++++++++++
	TP	863	1	1	731.821	731.903	.083	*-+++++++++++++++++++++++++++++++
	TP	864	1	1	731.906	732.033	.128	*-+++++++++++++++++++++++++++++++
	CPT	865	1	1	731.994	732.016	.023 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
20	CPT	866	1	1	732.019	732.034	.016 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	TP	867	1	1	732.035	732.050	.016	*-+++++++++++++++++++++++++++++++
	TP	868	1	1	732.052	732.179	.128	*-*+++++++++++++++++++++++++++++
	CPT	869	1	1	732.065	732.179	.115 OS->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	CPT	870	1	1	732.198	732.212	.015 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
25	TP	871	1	1	732.198	732.212	.015	*-*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	CPT	872	1	1	732.214	732.233	.020 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	TP	873	1	1	732.214	732.233	.020	*-+++++++++++++++++++++++++++++++
	CPT	874	1	1	732.235	732.283	.049 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	TP	875	1	1	732.235	732.283	.049	*-+++++++++++++++++++++++++++++++
30	CPT	876	1	1	732.306	732.326	.021 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	TP	877	1	1	732.306	732.326	.021	*-+++++++++++++++++++++++++++++++
	CPT	878	1	1	732.328	732.452	.125 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	TP	879	1	1	732.328	732.482	.155	*-+++++++++++++++++++++++++++++++
	CPT	880	1	1	732.454	732.482	.029 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
35	CPT	881	1	1	732.488	732.519	.032 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	TN	882	1	1	733.330	733.344	.015	*-+++++++++++++++++++++++++++++++
	TP	883	1	1	733.330	733.344	.015	*-+++++++++++++++++++++++++++++++
	TP	884	1	1	733.371	733.513	.143	*-+++++++++++++++++++++++++++++++
	GG	885	1	1	733.443	735.442	2.000 Group0158	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
40	TP	886	1	1	733.515	733.564	.050	*-+++++++++++++++++++++++++++++++
	TP	887	1	1	733.569	733.626	.058	*-+++++++++++++++++++++++++++++++
	TP	888	1	1	733.628	733.645	.018	*-+++++++++++++++++++++++++++++++
	TP	889	1	1	733.647	733.696	.050	*-+++++++++++++++++++++++++++++++
	TP	890	1	1	733.698	733.774	.077	*-+++++++++++++++++++++++++++++++
45	TP	891	1	1	733.776	733.904	.129	*-+++++++++++++++++++++++++++++++
	CPT	892	1	1	733.865	733.887	.023 OS->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	CPT	893	1	1	733.890	733.905	.016 -->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
	TP	894	1	1	733.906	734.050	.145	*-+*++++++++++++++++++++++++++++++

	CPT	895	1	1	733.936	734.050	.115	-->
	TP	896	1	1	734.052	734.075	.024	
	CPT	897	1	1	734.052	734.139	.088	-->
	TP	898	1	1	734.084	734.139	.056	
5	TP	899	1	1	734.149	734.179	.031	
	CPT	900	1	1	734.164	734.321	.158	-->
	TP	901	1	1	734.192	734.321	.130	
	TP	902	1	1	734.323	734.378	.056	
	CPT	903	1	1	734.323	734.381	.059	-->
10	CPT	904	1	1	735.525	735.569	.045	-->
	TP	905	1	1	735.525	735.569	.045	
	CPT	906	1	1	735.606	735.703	.098	-->
	TP	907	1	1	735.606	735.703	.098	
	TP	908	1	1	735.707	735.721	.015	
15	CPT	909	1	1	735.707	735.728	.022	-->
	TP	910	1	1	735.749	735.803	.055	
	CPT	911	1	1	735.807	735.964	.158	OS->
	TP	912	1	1	735.814	735.895	.082	
	TP	913	1	1	735.905	735.934	.030	
20	TP	914	1	1	735.938	736.083	.146	
	CPT	915	1	1	735.986	736.083	.098	OS->
	TP	916	1	1	736.152	736.173	.022	
	TP	917	1	1	736.187	736.217	.031	
	TP	918	1	1	736.219	736.265	.047	
25	TP	919	1	1	736.288	736.334	.047	
	GG	920	1	1	736.327	737.184	.858	Group0159
	TP	921	1	1	736.349	736.469	.121	
	TP	922	1	1	736.516	736.628	.113	
	TP	923	1	1	736.630	736.645	.016	
30	TP	924	1	1	736.654	736.792	.139	
	TN	925	1	1	736.654	736.809	.156	
	TN	926	1	1	736.816	736.832	.017	
	CPT	927	1	1	737.017	737.032	.016	-->
	CPT	928	1	1	737.035	737.057	.023	-->
35	TN	929	1	1	737.168	737.188	.021	
	TP	930	1	1	737.196	737.290	.095	
	CPT	931	1	1	737.261	737.275	.015	-->
	CPT	932	1	1	737.278	737.292	.015	-->
	TP	933	1	1	737.292	737.393	.102	
40	GG	934	1	1	737.315	738.076	.762	Group0160
	TP	935	1	1	737.411	737.475	.065	
	TP	936	1	1	737.479	737.557	.079	
	TP	937	1	1	737.580	737.597	.018	
	TP	938	1	1	737.605	737.626	.022	
45	TP	939	1	1	737.633	737.648	.016	
	TP	940	1	1	737.653	737.679	.027	
	TP	941	1	1	737.683	737.752	.070	
	TP	942	1	1	737.798	737.822	.025	



The "Type" descriptor of the T1 (Id number 809) is "TN" showing that is T1 target is on the negative strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 975) also has the type descriptor "TN".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing

a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
TP	xx	1	1	278.452	278.892	.441	*---*

Group0149 through Group0163 are described in Table 2 as

Group0149

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
nagd	COG0647	b 1	negative	698.797	699.549	.753
nagc	COG1940	b 1	negative	699.597	700.817	1.221
naga	COG1820	b 1	negative	700.826	701.974	1.149
nagb	COG0363	b 1	negative	702.034	702.834	.801
nage	COG1264	b 1	positive	703.167	705.113	1.947

Group0150

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
glns	COG0008	b 1	positive	705.316	706.980	1.665

Group0151

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
ybfm	-	b 1	positive	707.557	708.963	1.407
ybfn	-	b 1	positive	709.013	709.339	.327
fur	COG0735	b 1	negative	709.423	709.869	.447
flda	COG0716	b 1	negative	710.158	710.688	.531

Group0152

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
ybfe	-	b 1	negative	710.828	711.190	.363
ybff	COG0596	b 1	negative	711.261	712.025	.765
seqa	COG3057	b 1	positive	712.210	712.755	.546

Group0153

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
pgm	COG0033	b	1	positive	712.781	714.421	1.641

Group0154

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybfp	-	b	1	positive	714.635	715.129	.495
ybfq	-	b	1	negative	715.170	715.532	.363
ybfh	-	b	1	negative	715.611	715.928	.318

Group0155

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
pote	COG0531	b	1	negative	716.169	719.683	3.515
kdpe	COG0745	b	1	negative	720.279	724.202	3.924

Group0156

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
kdpb	COG2216	b	1	negative	724.211	726.259	2.049
kdpa	COG2060	b	1	negative	726.282	727.955	1.674

Group0157

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybfa	-	b	1	positive	728.357	728.563	.207
rhsc	-	b	1	positive	728.806	733.325	4.520

Group0158

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
b0703	COG3209	b	1	positive	733.443	735.442	2.000

Group0159

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybfl	-	b	1	positive	736.327	737.184	.858

Group0160

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
ybfd	-	b	1	positive	737.315	738.076	.762

Group0161

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length

ybga	COG3272	b	1	positive	738.224	740.148	1.925

Group0162

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
ybgh	COG3104	b 1	negative	740.298	741.779	1.482
ybgi	COG0327	b 1	positive	742.050	742.793	.744
ybgj	COG2049	b 1	positive	742.816	745.122	2.307
nei	COG0266	b 1	positive	745.158	745.949	.792
abrb	-	b 1	negative	745.946	747.037	1.092
ybgo	-	b 1	negative	747.144	748.930	1.787
ybgq	-	b 1	negative	748.945	751.401	2.457
ybgd	-	b 1	negative	751.452	752.018	.567
glta	COG0372	b 1	negative	752.408	753.691	1.284
sdhc	COG2009	b 1	positive	754.400	756.896	2.497
sdhb	COG0479	b 1	positive	756.912	757.628	.717

Group0163

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
b0725	-	b 1	positive	757.687	760.730	3.044

All of the data for the transient connectron 62520 are pulled together in the following table that is the "terse" description of the connectron.

Connectron Relationships - Global_Id Type

62520 transient

Control Sequences - Direction	Chromosome	C1/C2_Id	Start	Stop	Length
positive	1	4651a	4626.130	4626.166	.036

Trigger Gene - Name COG_Id Start Stop Length

sms 4623.481 4626.116 2.636

Target Sequences - Direction	Chromosome	T1_Id	Start	Stop	Length
negative	1	809	698.766	698.713	.054

T2_Id	Start	Stop	Length
975	757.753	757.718	.036

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length

1	1	Group0149	nagd	COG0647	positive	698.797	705.113	6.316
2	1	Group0149	nagc	COG1940	negative	700.817	699.597	1.221
3	1	Group0149	naga	COG1820	negative	701.974	700.826	1.149
4	1	Group0149	nagb	COG0363	negative	702.834	702.034	.801
5	1	Group0149	nage	COG1264	positive	703.167	705.113	1.947
6	1	Group0150	glns	COG0008	positive	705.316	706.980	1.665
7	1	Group0151	ybfm	-	positive	707.557	710.688	3.131
8	1	Group0151	ybfn	-	positive	709.013	709.339	.327
9	1	Group0151	fur	COG0735	negative	709.869	709.423	.447
10	1	Group0151	flda	COG0716	negative	710.688	710.158	.531
11	1	Group0152	ybfe	-	positive	710.828	712.755	1.927
12	1	Group0152	ybff	COG0596	negative	712.025	711.261	.765
13	1	Group0152	seqa	COG3057	positive	712.210	712.755	.546
14	1	Group0153	pgm	COG0033	positive	712.781	714.421	1.641
15	1	Group0154	ybfp	-	positive	714.635	715.928	1.293
16	1	Group0154	ybfg	-	negative	715.532	715.170	.363
17	1	Group0154	ybfh	-	negative	715.928	715.611	.318
18	1	Group0155	pote	COG0531	positive	716.169	724.202	8.033
19	1	Group0155	kdpe	COG0745	negative	724.202	720.279	3.924
20	1	Group0156	kdpb	COG2216	positive	724.211	727.955	3.744
21	1	Group0156	kdpa	COG2060	negative	727.955	726.282	1.674
22	1	Group0157	ybfa	-	positive	728.357	733.325	4.968
23	1	Group0157	rhsc	-	positive	728.806	733.325	4.520
24	1	Group0158	b0703	COG3209	positive	733.443	735.442	2.000
25	1	Group0159	ybfl	-	positive	736.327	737.184	.858
26	1	Group0160	ybfd	-	positive	737.315	738.076	.762
27	1	Group0161	ybga	COG3272	positive	738.224	740.148	1.925
28	1	Group0162	ybgh	COG3104	positive	740.298	757.628	17.330
29	1	Group0162	ybgi	COG0327	positive	742.050	742.793	.744
30	1	Group0162	ybgj	COG2049	positive	742.816	745.122	2.307
31	1	Group0162	nei	COG0266	positive	745.158	745.949	.792
32	1	Group0162	abrb	-	negative	747.037	745.946	1.092
33	1	Group0162	ybgo	-	negative	748.930	747.144	1.787
34	1	Group0162	ybgq	-	negative	751.401	748.945	2.457
35	1	Group0162	ybgd	-	negative	752.018	751.452	.567
36	1	Group0162	glta	COG0372	negative	753.691	752.408	1.284
37	1	Group0162	sdhc	COG2009	positive	754.400	756.896	2.497
38	1	Group0162	sdhb	COG0479	positive	756.912	757.628	.717
39	1	Group0163	b0725	-	positive	757.687	760.730	3.044

40

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	816	positive	707.055	707.109	.055
2	1	819	positive	707.112	707.162	.051
3	1	823	negative	710.647	710.633	.015
4	1	825	negative	710.666	710.652	.015
5	1	830	positive	714.481	714.519	.039
6	1	832	positive	714.524	714.540	.017

7	1	835	negative	714.593	714.543	.051
8	1	838	positive	714.544	714.606	.063
9	1	844	negative	720.296	720.278	.019
10	1	852	positive	729.408	729.446	.039
11	1	854	positive	730.443	730.457	.015
12	1	855	positive	730.468	730.482	.015
13	1	856	positive	730.484	730.507	.024
14	1	857	positive	731.251	731.290	.040
15	1	865	positive	731.994	732.016	.023
16	1	866	positive	732.019	732.034	.016
17	1	869	positive	732.065	732.179	.115
18	1	870	positive	732.198	732.212	.015
19	1	872	positive	732.214	732.233	.020
20	1	874	positive	732.235	732.283	.049
21	1	876	positive	732.306	732.326	.021
22	1	878	positive	732.328	732.452	.125
23	1	880	positive	732.454	732.482	.029
24	1	881	positive	732.488	732.519	.032
25	1	892	positive	733.865	733.887	.023
26	1	893	positive	733.890	733.905	.016
27	1	895	positive	733.936	734.050	.115
28	1	897	positive	734.052	734.139	.088
29	1	900	positive	734.164	734.321	.158
30	1	903	positive	734.323	734.381	.059
31	1	904	positive	735.525	735.569	.045
32	1	906	positive	735.606	735.703	.098
33	1	909	positive	735.707	735.728	.022
34	1	911	positive	735.807	735.964	.158
35	1	915	positive	735.986	736.083	.098
36	1	927	positive	737.017	737.032	.016
37	1	928	positive	737.035	737.057	.023
38	1	931	positive	737.261	737.275	.015
39	1	932	positive	737.278	737.292	.015
40	1	945	positive	737.930	737.967	.038
41	1	957	negative	740.290	740.172	.119
42	1	958	positive	740.172	740.290	.119
43	1	965	positive	744.643	744.657	.015
44	1	966	positive	744.664	744.678	.015
45	1	968	positive	755.680	755.714	.035
46	1	971	positive	757.628	757.712	.085
47	1	974	positive	757.717	757.736	.020

Addition of a Synthetic Transient Connectron between chromosomes - Type 7 from Table 2

A synthetic virtual connectron of type 7 in which the C1 is a synthetic element and C2 is a natural element, the T1 is a natural element and the T2 is a synthetic element can be introduced into the *S. cerevisiae* genome by modifying the DNA double-strand sequence at 221.330kb through 221.345kb on chromosome 2 for a length of 0.016kb and by modifying the DNA double-strand sequence at 488.140kb through 488.297 on chromosome 5 for a length of 0.158kb.

To create this example of a synthetic connectron of type 7 the T2 sequence for natural connectron 3558 (old position 497.581kb through 498.091kb) was copied into the new position stated above.

Connectron 75273 is an example of a transient connectron. It is described as

		C1/C2			T1-T2		
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
75273	2	792a	793	5	4749	4824a	transient

The C1/C2 source of the transient connectron 75273 is represented in table 1 as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
CPT	792a	22	2	221.330	221.345	.016	-->
CPT	793	22	2	221.346	221.361	.016	-->

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA

of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB). The symbol OS-> occurs because there is another connectron formed by this C1/C2 that happens to be a one-shot connectron.

The T1-T2 target of the transient connectron 75273 as shown in table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TN	4749	59	5	448.454	448.992	.539		*-*
TP	4750	68	5	448.454	448.992	.539		*-+
CNT	4751	64	5	448.454	448.992	.539	-->	|
TP	4752	63	5	449.003	449.315	.313		*-+
TN	4753	65	5	449.003	449.315	.313		*-+
CNT	4754	60	5	449.003	449.315	.313	OS->	|
CNT	4755	5	5	449.317	449.482	.166	OS->	|
TN	4756	5	5	449.317	449.482	.166		*-+
TP	4757	64	5	449.317	449.482	.148		*-+
GG	4758	59	5	449.470	449.574	.105	Group0615	|
CPT	4759	70	5	449.490	449.563	.074	-->	|
TN	4760	70	5	449.490	449.563	.074		*-+
TP	4761	67	5	449.490	449.558	.069		*-+
CNT	4762	70	5	449.490	449.563	.074	-->	|
TN	4763	59	5	449.575	449.603	.029		*-+
TP	4764	59	5	449.575	449.603	.029		*-+
GG	4765	59	5	450.558	453.230	2.672	Group0616	|
TP	4766	59	5	452.176	452.190	.015		*-+
GG	4767	59	5	453.454	454.914	1.461	Group0617	|
CNT	4768	20	5	453.909	453.923	.015	-->	|
CNT	4769	20	5	453.928	453.942	.015	-->	|
TP	4770	59	5	454.644	454.658	.015		*-+
GG	4771	59	5	455.141	457.600	2.460	Group0618	|
TN	4772	66	5	456.316	456.331	.016		*-+
GG	4773	59	5	457.801	460.218	2.418	Group0619	|
TN	4774	66	5	460.340	460.355	.016		*-+
GG	4775	59	5	460.521	466.020	5.500	Group0620	|
GP	4776	59	5	462.580	462.861	.282	LSM5	|

	TN	4777	59	5	463.743	463.758	.016	*-+
	TP	4778	59	5	463.743	463.758	.016	*-+
	CPT	4779	61	5	463.990	464.004	.015	--> |
	CPT	4780	61	5	464.010	464.024	.015	--> |
5	TP	4781	59	5	465.739	465.754	.016	*-|
	GG	4782	59	5	466.203	468.811	2.609 Group0621	|
	GP	4783	59	5	468.365	468.811	.447 SPI1	|
	TP	4784	69	5	469.451	469.518	.059	*-+
	CNT	4785	67	5	469.451	469.530	.080 OS->	|
10	GG	4786	59	5	469.452	469.525	.074 Group0622	|
	TN	4787	59	5	469.452	469.532	.081	*-+
	CPT	4788	67	5	469.452	469.531	.080 -->	|
	GG	4789	59	5	469.681	472.419	2.739 Group0623	|
	TN	4790	20	5	471.772	471.786	.015	*-+
15	TP	4791	20	5	471.772	471.786	.015	*-+
	GG	4792	59	5	472.652	482.843	10.192 Group0624	|
	GP	4793	59	5	475.015	476.223	1.209 OXA1	|
	TP	4794	63	5	476.803	476.817	.015	*-+
	CPT	4795	60	5	478.412	478.426	.015 -->	|
20	CPT	4796	60	5	478.436	478.450	.015 -->	|
	CNT	4797	47	5	481.782	481.812	.031 -->	|
	TN	4798	20	5	482.192	482.206	.015	*-+
	CNT	4799	67	5	482.676	482.690	.015 -->	|
	CNT	4800	67	5	482.701	482.715	.015 -->	|
25	GG	4801	59	5	483.320	487.188	3.869 Group0625	|
	GP	4802	59	5	484.783	487.188	2.406 SEC34	|
	CNT	4803	61	5	485.099	485.113	.015 -->	|
	CNT	4804	61	5	485.119	485.134	.016 -->	|
	TN	4805	64	5	487.041	487.056	.016	*-+
30	GG	4806	59	5	487.326	487.397	.072 Group0626	|
	CPT	4807	61	5	487.375	487.397	.023 -->	|
	CPT	4808	61	5	487.400	487.415	.016 -->	|
	CNT	4809	34	5	487.830	487.848	.019 OS->	|
	CPT	4810	62	5	487.830	487.848	.019 OS->	|
35	TP	4811	60	5	487.830	487.848	.019	*-+
	TN	4812	59	5	487.830	487.848	.019	*-+
	CNT	4813	34	5	487.850	488.016	.167 OS->	|
	CPT	4814	5	5	487.850	488.016	.167 OS->	|
	TP	4815	5	5	487.850	488.016	.167	*-+
40	TN	4816	64	5	487.850	488.016	.167	*-+
	CNT	4817	47	5	488.024	488.137	.114 OS->	|
	CPT	4818	47	5	488.024	488.068	.045 -->	|
	TN	4819	34	5	488.024	488.067	.044	*-+
	TP	4820	34	5	488.024	488.067	.044	*-+
45	CPT	4821	69	5	488.069	488.137	.069 OS->	|
	TN	4822	67	5	488.069	488.122	.054	*-+
	TP	4823	59	5	488.069	488.085	.017	*-+
	TP	4824	5	5	488.094	488.137	.044	*-+

TN	4824a	5	5	468.140	468.297	.158	*-*

The "Type" descriptor of the T1 (Id number 4749) is "TN" showing that is T1 target is on the negative strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 4824a) also has the type descriptor "TN".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
TP	xx	1	1	278.452	278.892	.441	*---*

Group0615 (Id number 4758) has the type descriptor "GG". The same is true for Group0626 (Id number 4806).

Group0615 through Group0626 are described in table 2 as

Group0615

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
YER138W-A	-	5	positive	449.470	449.574	.105

Group0616

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length

YER139C	-		5	negative	450.558	451.238	.681
YER140W	-		5	positive	451.560	453.230	1.671

Group0617

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
COX15	COG1612 O	5	positive	453.454	454.914	1.461

Group0618

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
MAG1	COG0122 L	5	negative	455.141	456.031	.891
DDI1	-	5	positive	456.314	457.600	1.287

Group0619

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
UBP5	-	5	negative	457.801	460.218	2.418

Group0620

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
FTR1	COG0672 P	5	negative	460.521	461.735	1.215
LSM5	COG1958 K	5	positive	462.580	462.861	.282
YER147C	-	5	negative	462.963	464.837	1.875
SPT15	COG2101 K	5	positive	465.298	466.020	.723

Group0621

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
PEA2	-	5	negative	466.203	467.465	1.263
SPI1	-	5	positive	468.365	468.811	.447

Group0622

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
		5	positive	469.452	469.525	.074

Group0623

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
UBP3	-	5	negative	469.681	472.419	2.739

Group0624

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
YER152C	COG1167 K	5	negative	472.652	473.983	1.332
PET122	-	5	negative	474.036	474.800	.765

OXA1	COG0706	N	5	positive	475.015	476.223	1.209
BEM2	-		5	negative	476.340	482.843	6.504

Group0625

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
YER156C	-	5	negative	483.320	484.336	1.017
SEC34	-	5	positive	484.783	487.188	2.406

Group0626

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
		5	positive	487.326	487.397	.072

All of the data for the transient connectron 75273 are pulled together in the following table that is the "terse" description of the connectron.

Connectron Relationships - Global_Id Type

75273 transient

Control Sequences - Direction	Chromosome	C1/C2_Id	Start	Stop	Length
positive	2	792a	221.330	221.345	.016
positive	2	793	221.346	221.361	.016

Trigger Gene - Name	COG_Id	Start	Stop	Length
YBL005W-B	-	221.293	226.561	5.269

Target Sequences - Direction	Chromosome	T1_Id	Start	Stop	Length
negative	5	4749	448.992	448.454	.539

T2_Id	Start	Stop	Length
4824a	488.140	488.297	.158

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	5	Group0615	YER138W-A	-	positive	449.470	449.574	.105
2	5	Group0616	YER139C	-	positive	450.558	453.230	2.673
3	5	Group0616	YER140W	-	positive	451.560	453.230	1.671
4	5	Group0617	COX15	COG1612	positive	453.454	454.914	1.461
5	5	Group0618	MAG1	COG0122	positive	455.141	457.600	2.459
6	5	Group0618	DDI1	-	positive	456.314	457.600	1.287
7	5	Group0619	UBP5	-	positive	457.801	460.218	2.418

8	5	Group0620	FTR1	COG0672	positive	460.521	466.020	5.499
9	5	Group0620	LSM5	COG1958	positive	462.580	462.861	.282
10	5	Group0620	YER147C	-	negative	464.837	462.963	1.875
11	5	Group0620	SPT15	COG2101	positive	465.298	466.020	.723
12	5	Group0621	PEA2	-	positive	466.203	468.811	2.608
13	5	Group0621	SPI1	-	positive	468.365	468.811	.447
14	5	Group0622			positive	469.452	469.525	.074
15	5	Group0623	UBP3	-	positive	469.681	472.419	2.739
16	5	Group0624	YER152C	COG1167	positive	472.652	482.843	10.191
17	5	Group0624	PET122	-	negative	474.800	474.036	.765
18	5	Group0624	OXA1	COG0706	positive	475.015	476.223	1.209
19	5	Group0624	BEM2	-	negative	482.843	476.340	6.504
20	5	Group0625	YER156C	-	positive	483.320	487.188	3.868
21	5	Group0625	SEC34	-	positive	484.783	487.188	2.406
22	5	Group0626			positive	487.326	487.397	.072

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	5	4751	negative	448.992	448.454	.539
2	5	4754	negative	449.315	449.003	.313
3	5	4755	negative	449.482	449.317	.166
4	5	4759	positive	449.490	449.563	.074
5	5	4762	negative	449.563	449.490	.074
6	5	4768	negative	453.923	453.909	.015
7	5	4769	negative	453.942	453.928	.015
8	5	4779	positive	463.990	464.004	.015
9	5	4780	positive	464.010	464.024	.015
10	5	4785	negative	469.530	469.451	.080
11	5	4788	positive	469.452	469.531	.080
12	5	4795	positive	478.412	478.426	.015
13	5	4796	positive	478.436	478.450	.015
14	5	4797	negative	481.812	481.782	.031
15	5	4799	negative	482.690	482.676	.015
16	5	4800	negative	482.715	482.701	.015
17	5	4803	negative	485.113	485.099	.015
18	5	4804	negative	485.134	485.119	.016
19	5	4807	positive	487.375	487.397	.023
20	5	4808	positive	487.400	487.415	.016
21	5	4809	negative	487.848	487.830	.019
22	5	4810	positive	487.830	487.848	.019
23	5	4813	negative	488.016	487.850	.167
24	5	4814	positive	487.850	488.016	.167
25	5	4817	negative	488.137	488.024	.114
26	5	4818	positive	488.024	488.068	.045
27	5	4821	positive	488.069	488.137	.069

Addition of a Synthetic Connectron of Type 14 from Table 2

A synthetic virtual connectron of type 14 in which the C1 and C2 are natural elements, the T1 is a synthetic element and the T2 is a natual element can be introduced into the *Halobacterium sp.* genome by modifying the DNA double-strand sequences at 734.750kb through 734.942kb for a length of 0.193kb.

To create this example of a synthetic connectron of type 15 the T1 sequence for natural connectron 6627 (old position 733.018kb through 733.210kb) was copied into the new position stated above.

Connectron 7341 is an example of a transient connectron. It is described as

		C1/C2			T1-T2		
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
2587	1	6612	6612	1	6627	6852	transient

The C1/C2 source of the transient connectron 7341 is represented in Table 1 as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
CPT	6612	1	1	732.401	732.534	.134	OS->	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient"

connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB). The symbol OS-> occurs because there is another connectron formed by this C1/C2 that happens to be a one-shot connectron.

The T1-T2 target of the transient connectron 7341 as shown in Table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TP	6644a	1	1	734.750	734.942	.193		*-*
GG	6646	1	1	735.009	735.881	.873	Group0493	|
CNT	6647	1	1	735.364	735.378	.015	OS->	|
TN	6648	1	1	735.364	735.378	.015		*-+
CNT	6649	1	1	735.389	735.403	.015	-->	|
CNT	6650	1	1	735.753	735.767	.015	-->	|
CNT	6651	1	1	735.775	735.789	.015	-->	|
GG	6652	1	1	735.910	737.544	1.634	Group0494	|
TN	6653	1	1	735.969	735.984	.016		*-+
TN	6654	1	1	736.126	736.140	.015		*-+
CPT	6655	1	1	736.325	736.339	.015	-->	|
TN	6656	1	1	736.327	736.342	.016		*-+
CPT	6657	1	1	736.345	736.359	.015	-->	|
TP	6658	1	1	736.903	736.917	.015		*-+
TN	6659	1	1	737.233	737.247	.015		*-+
TP	6660	1	1	737.271	737.285	.015		*-+
TN	6661	1	1	737.331	737.346	.016		*-+
GG	6662	1	1	737.643	737.972	.330	Group0495	|
TN	6663	1	1	737.752	737.766	.015		*-+
CNT	6664	1	1	737.752	737.782	.031	-->	|
TP	6665	1	1	737.761	737.775	.015		*-+
TN	6666	1	1	738.049	738.063	.015		*-+
GG	6667	1	1	738.107	739.835	1.728	Group0496	|
TN	6668	1	1	738.122	738.136	.015		*-+
TP	6669	1	1	738.122	738.136	.015		*-+
TP	6670	1	1	738.425	738.439	.015		*-+
TP	6671	1	1	738.503	738.517	.015		*-+
CNT	6672	1	1	738.517	738.562	.046	-->	|
TN	6673	1	1	738.544	738.559	.016		*-+
TN	6674	1	1	738.862	738.878	.017		*-+
TP	6675	1	1	738.862	738.878	.017		*-+
CNT	6676	1	1	738.975	738.989	.015	-->	|

	CNT	6677	1	1	738.992	739.007	.016	--> |
	TN	6678	1	1	739.107	739.122	.016	*-+
	GN	6679	1	1	739.248	739.835	.588 cheC1	|
	TP	6680	1	1	739.435	739.449	.015	*-+
5	TN	6681	1	1	739.685	739.707	.023	*-+
	TN	6682	1	1	739.761	739.775	.015	*-+
	GG	6683	1	1	739.838	741.844	2.007 Group0497	|
	TN	6684	1	1	739.849	739.863	.015	*-+
	TP	6685	1	1	740.345	740.360	.016	*-+
10	TN	6686	1	1	740.362	740.376	.015	*-+
	TP	6687	1	1	740.611	740.625	.015	*-+
	TN	6688	1	1	741.100	741.116	.017	*-+
	TP	6689	1	1	741.101	741.132	.032	*-+
	TN	6690	1	1	741.218	741.232	.015	*-+
15	CNT	6691	1	1	741.352	741.368	.017	--> |
	TP	6692	1	1	741.354	741.376	.023	*-+
	TN	6693	1	1	741.354	741.380	.027	*-+
	CNT	6694	1	1	741.374	741.388	.015	--> |
	TN	6695	1	1	741.401	741.417	.017	*-+
20	CNT	6696	1	1	741.519	741.533	.015	--> |
	CNT	6697	1	1	741.538	741.552	.015	--> |
	TN	6698	1	1	741.538	741.552	.015	*-+
	TN	6699	1	1	741.561	741.575	.015	*-+
	GG	6700	1	1	741.846	743.248	1.403 Group0498	|
25	TN	6701	1	1	741.924	741.942	.019	*-+
	TN	6702	1	1	742.194	742.208	.015	*-+
	TP	6703	1	1	742.618	742.632	.015	*-+
	TN	6704	1	1	742.943	742.957	.015	*-+
	GG	6705	1	1	743.295	743.831	.537 Group0499	|
30	TP	6706	1	1	743.730	743.748	.019	*-+
	GG	6707	1	1	743.896	744.489	.594 Group0500	|
	TN	6708	1	1	743.916	743.930	.015	*-+
	GG	6709	1	1	744.606	745.511	.906 Group0501	|
	TN	6710	1	1	744.950	744.964	.015	*-+
35	TN	6711	1	1	745.047	745.061	.015	*-+
	GG	6712	1	1	745.648	746.763	1.116 Group0502	|
	CPT	6713	1	1	745.865	745.879	.015	--> |
	TN	6714	1	1	745.865	745.879	.015	*-+
	CPT	6715	1	1	745.888	745.902	.015	--> |
40	CPT	6716	1	1	746.140	746.155	.016	--> |
	TN	6717	1	1	746.153	746.175	.023	*-+
	TP	6718	1	1	746.157	746.175	.019	*-+
	CPT	6719	1	1	746.162	746.176	.015	--> |
	TN	6720	1	1	746.229	746.243	.015	*-+
45	CNT	6721	1	1	746.229	746.259	.031	--> |
	TN	6722	1	1	746.271	746.285	.015	*-+
	TP	6723	1	1	746.356	746.380	.025	*-+
	TN	6724	1	1	746.361	746.380	.020	*-+

	TN	6725	1	1	746.386	746.400	.015	*-+
	CPT	6726	1	1	746.453	746.467	.015	--> |
	TN	6727	1	1	746.453	746.472	.020	*-+
	TP	6728	1	1	746.457	746.475	.019	*-+
5	CPT	6729	1	1	746.469	746.483	.015	--> |
	TP	6730	1	1	746.528	746.545	.018	*-+
	TN	6731	1	1	746.532	746.556	.025	*-+
	GG	6732	1	1	746.843	748.851	2.008 Group0503	|
	CNT	6733	1	1	746.905	746.919	.015	--> |
10	CNT	6734	1	1	746.927	746.941	.015	--> |
	GN	6735	1	1	747.151	748.605	1.455 VNG0983C	|
	TN	6736	1	1	747.260	747.274	.015	*-+
	TP	6737	1	1	747.475	747.489	.015	*-+
	TN	6738	1	1	747.547	747.571	.025	*-+
15	TN	6739	1	1	747.934	747.948	.015	*-+
	TP	6740	1	1	747.936	747.950	.015	*-+
	TN	6741	1	1	748.130	748.144	.015	*-+
	TP	6742	1	1	749.157	749.172	.016	*-+
	TN	6743	1	1	749.375	749.389	.015	*-+
20	GG	6744	1	1	749.392	759.277	9.885 Group0504	|
	CNT	6745	1	1	759.509	759.552	.044	--> |
	TP	6746	1	1	759.509	760.014	.506	*-+
	TN	6747	1	1	759.528	760.031	.504	*-+
	GG	6748	1	1	759.667	762.487	2.820 Group0505	|
25	GP	6749	1	1	760.682	762.487	1.806 boa4	|
	CPT	6750	1	1	760.774	760.789	.016	--> |
	CPT	6751	1	1	760.798	760.814	.017	--> |
	TN	6752	1	1	760.875	760.889	.015	*-+
	CPT	6753	1	1	760.878	760.892	.015	--> |
30	CPT	6754	1	1	760.897	760.912	.016	--> |
	CPT	6755	1	1	761.496	761.510	.015	--> |
	CPT	6756	1	1	761.516	761.533	.018	--> |
	CPT	6757	1	1	761.542	761.557	.016	--> |
	TN	6758	1	1	761.542	761.557	.016	*-+
35	CPT	6759	1	1	761.576	761.597	.022	--> |
	CPT	6760	1	1	761.601	761.617	.017	--> |
	TN	6761	1	1	761.754	761.768	.015	*-+
	CPT	6762	1	1	761.933	761.950	.018	--> |
	TP	6763	1	1	761.933	761.950	.018	*-+
40	CPT	6764	1	1	761.953	761.968	.016	--> |
	TN	6765	1	1	762.423	762.437	.015	*-+
	GG	6766	1	1	762.609	764.612	2.004 Group0506	|
	TN	6767	1	1	762.874	762.900	.027	*-+
	TN	6768	1	1	762.946	762.960	.015	*-+
45	TN	6769	1	1	763.108	763.122	.015	*-+
	TN	6770	1	1	763.273	763.304	.032	*-+
	CPT	6771	1	1	763.283	763.304	.022	--> |
	TN	6772	1	1	763.306	763.320	.015	*-+

	CPT	6773	1	1	763.306	763.321	.016	--> |
	CPT	6774	1	1	763.346	763.360	.015	--> |
	TN	6775	1	1	763.351	763.365	.015	*-+
	TP	6776	1	1	763.351	763.365	.015	*-+
5	CPT	6777	1	1	763.362	763.376	.015	--> |
	TP	6778	1	1	763.391	763.407	.017	*-+
	TN	6779	1	1	763.843	763.857	.015	*-+
	TP	6780	1	1	763.843	763.857	.015	*-+
	CNT	6781	1	1	763.965	763.986	.022	--> |
10	CPT	6782	1	1	763.965	763.995	.031	--> |
	CNT	6783	1	1	763.990	764.011	.022	--> |
	CPT	6784	1	1	764.000	764.015	.016	--> |
	CNT	6785	1	1	764.075	764.089	.015	--> |
	CNT	6786	1	1	764.093	764.108	.016	--> |
15	CPT	6787	1	1	764.156	764.171	.016	--> |
	CNT	6788	1	1	764.156	764.177	.022	OS-> |
	TN	6789	1	1	764.156	764.177	.022	*-+
	CNT	6790	1	1	764.181	764.195	.015	--> |
	TP	6791	1	1	764.181	764.201	.021	*-+
20	CPT	6792	1	1	764.181	764.204	.024	--> |
	CPT	6793	1	1	764.213	764.227	.015	--> |
	TP	6794	1	1	764.309	764.328	.020	*-+
	TN	6795	1	1	764.312	764.326	.015	*-+
	TN	6796	1	1	764.383	764.397	.015	*-+
25	TP	6797	1	1	764.530	764.545	.016	*-+
	TN	6798	1	1	764.530	764.548	.019	*-+
	GG	6799	1	1	764.619	765.629	1.011 Group0507	|
	CPT	6800	1	1	764.791	764.808	.018	--> |
	CNT	6801	1	1	764.794	764.813	.020	OS-> |
30	TN	6802	1	1	764.794	764.832	.039	*-+
	CPT	6803	1	1	764.810	764.826	.017	--> |
	CNT	6804	1	1	764.818	764.832	.015	--> |
	CPT	6805	1	1	764.831	764.853	.023	--> |
	CPT	6806	1	1	764.856	764.870	.015	--> |
35	CNT	6807	1	1	764.984	764.998	.015	OS-> |
	TN	6808	1	1	764.984	765.014	.031	*-+
	CNT	6809	1	1	765.000	765.014	.015	--> |
	TN	6810	1	1	765.075	765.089	.015	*-+
	CNT	6811	1	1	765.431	765.446	.016	--> |
40	CNT	6812	1	1	765.456	765.473	.018	--> |
	CNT	6813	1	1	765.479	765.494	.016	--> |
	TN	6814	1	1	765.508	765.523	.016	*-+
	TP	6815	1	1	765.573	765.587	.015	*-+
	GG	6816	1	1	765.775	766.044	.270 Group0508	|
45	TN	6817	1	1	765.822	765.837	.016	*-+
	TP	6818	1	1	766.162	766.176	.015	*-+
	TN	6819	1	1	766.432	766.447	.016	*-+
	GG	6820	1	1	766.603	766.812	.210 Group0509	|

CNT	6821	1	1	766.635	766.653	.019	OS->	|
TN	6822	1	1	766.635	766.653	.019		*-+
CNT	6823	1	1	766.655	766.675	.021	-->	|
TN	6824	1	1	766.863	766.878	.016		*-+
GG	6825	1	1	766.955	768.538	1.584	Group0510	|
TN	6826	1	1	767.682	767.700	.019		*-+
TP	6827	1	1	767.831	767.845	.015		*-+
TN	6828	1	1	768.028	768.048	.021		*-+
TP	6829	1	1	768.033	768.049	.017		*-+
TN	6830	1	1	768.377	768.391	.015		*-+
GG	6831	1	1	768.965	769.882	.918	Group0511	|
TN	6832	1	1	769.502	769.516	.015		*-+
TN	6833	1	1	769.541	769.555	.015		*-+
TP	6834	1	1	769.559	769.573	.015		*-+
GG	6835	1	1	769.965	770.189	.225	Group0512	|
TN	6836	1	1	770.120	770.134	.015		*-+
GG	6837	1	1	770.194	770.406	.213	Group0513	|
CPT	6838	1	1	770.226	770.240	.015	-->	|
CPT	6839	1	1	770.251	770.265	.015	-->	|
TP	6840	1	1	770.251	770.268	.018		*-+
CPT	6841	1	1	770.347	770.363	.017	-->	|
CPT	6842	1	1	770.365	770.379	.015	-->	|
GG	6843	1	1	770.516	771.546	1.030	Group0514	|
TN	6844	1	1	771.564	772.071	.508		*-+
CNT	6845	1	1	771.564	772.086	.523	-->	|
TP	6846	1	1	771.583	772.084	.502		*-+
GG	6847	1	1	771.722	771.925	.204	Group0515	|
TN	6848	1	1	772.963	772.977	.015		*-+
TP	6849	1	1	773.358	773.387	.030		*-+
GG	6850	1	1	773.360	773.950	.591	Group0516	|
CPT	6851	1	1	773.399	773.483	.085	OS->	|
TP	6852	1	1	773.399	773.483	.085		*-*

The "Type" descriptor of the T1 (Id number 6644a) is "TP" showing that is T1 target is on the negative strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 6852) also has the type descriptor "TP".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines

(indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
TP	xx	1	1	278.452	278.892	.441	*---*

Group0493 (Id number 6646) has the type descriptor "GG". The same is true for the group headers through to Group0516 (Id number 6847).

Group0493

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VNG0964C	COG2469	S	1	positive	735.009	735.881	.873

Group0494

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VNG0965C	COG2469	S	1	negative	735.910	736.773	.864
cheR	COG1352	N	1	negative	736.840	737.544	.705

Group0495

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
cheD	COG1871	N	1	negative	737.643	737.972	.330

Group0496

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VNG0969H	COG1776	N	1	negative	738.107	739.246	1.140
cheC1	COG1776	N	1	negative	739.248	739.835	.588

Group0497

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
cheA	COG0643	N	1	negative	739.838	741.844	2.007

Group0498

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
cheB	COG2201	N	1	negative	741.846	743.248	1.403

Group0499

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
cheW1	COG0835	N	1	negative	743.295	743.831	.537

Group0500

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VNG0978H			1	negative	743.896	744.489	.594

Group0501

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VNG0979H			1	positive	744.606	745.511	.906

Group0502

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VNG0981C	COG0436	E	1	positive	745.648	746.763	1.116

Group0503

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VNG0982C	COG1873	S	1	positive	746.843	747.133	.291
VNG0983C	COG0618	R	1	negative	747.151	748.605	1.455
tRNA-Lys			1	positive	748.778	748.851	.074

Group0504

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VNG0985H			1	positive	749.392	751.398	2.007
VNG0986H			1	positive	752.276	752.803	.528
VNG0987H			1	positive	753.131	753.547	.417
VNG0988H			1	positive	754.149	754.391	.243
VNG0989C	COG0582	L	1	negative	754.459	755.481	1.023
VNG0990H			1	positive	756.010	756.183	.174
VNG0991H			1	negative	756.675	757.016	.342
VNG0992H			1	negative	757.409	758.119	.711
VNG0993H			1	positive	758.465	759.277	.813

Group0505

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length

VNG0994H			1	negative	759.667	759.870	.204
VNG0995H			1	positive	760.365	760.553	.189
boa4	COG3413	R	1	positive	760.682	762.487	1.806

Group0506

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
acs2	COG0365	I 1	positive	762.609	764.612	2.004

Group0507

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
yajO2	COG0667	C 1	negative	764.619	765.629	1.011

Group0508

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG0999H		1	negative	765.775	766.044	.270

Group0509

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG1000H	COG3205	S 1	positive	766.603	766.812	.210

Group0510

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
guaB	COG0516	F 1	negative	766.955	768.538	1.584

Group0511

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG1002H		1	positive	768.965	769.882	.918

Group0512

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG1003H		1	positive	769.965	770.189	.225

Group0513

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG1005H		1	negative	770.194	770.406	.213

Group0514

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
tRNA-Trp		1	positive	770.516	770.691	.176

```
VNG1006H                          1  positive   770.827   771.546      .720
-------------------------------------------------------------------------
Group0515

Gene_Name  COG_Id        Chromosome  Direction    Start      Stop    Length
VNG1007H                          1  negative   771.722   771.925      .204
-------------------------------------------------------------------------
Group0516

Gene_Name  COG_Id        Chromosome  Direction    Start      Stop    Length
flaA1a     COG1681    N           1  positive   773.360   773.950      .591
-------------------------------------------------------------------------
```

All of the data for the transient connectron 7341 are pulled together in the following table that is the "terse" description of the connectron.

```
-------------------------------------------------------------------------

Connectron Relationships - Global_Id  Type
                              7341  transient

Control Sequences - Direction  Chromosome  C1/C2_Id      Start      Stop  Length
                    positive           1      6612    732.401   732.534    .134

Trigger Gene - Name      COG_Id      Start      Stop  Length
               flaB1     COG1681   731.799   732.380    .582

Target Sequences  - Direction  Chromosome     T1_Id      Start      Stop  Length
                    positive           1      6644a   734.750   734.942    .193

                                          T2_Id      Start      Stop  Length
                                           6852    773.399   773.483    .085

Controlled Genes
Local_Id  Chromosome  Group      Name       COG_Id    Direction     Start      Stop    Length
       1           1  Group0493  VNG0964C   COG2469   positive    735.009   735.881      .873
       2           1  Group0494  VNG0965C   COG2469   positive    735.910   737.544     1.634
       3           1  Group0494  cheR       COG1352   negative    737.544   736.840      .705
       4           1  Group0495  cheD       COG1871   positive    737.643   737.972      .330
       5           1  Group0496  VNG0969H   COG1776   positive    738.107   739.835     1.728
       6           1  Group0496  cheC1      COG1776   negative    739.835   739.248      .588
       7           1  Group0497  cheA       COG0643   positive    739.838   741.844     2.007
       8           1  Group0498  cheB       COG2201   positive    741.846   743.248     1.403
       9           1  Group0499  cheW1      COG0835   positive    743.295   743.831      .537
      10           1  Group0500  VNG0978H              positive    743.896   744.489      .594
```

11	1	Group0501	VNG0979H		positive	744.606	745.511	.906
12	1	Group0502	VNG0981C	COG0436	positive	745.648	746.763	1.116
13	1	Group0503	VNG0982C	COG1873	positive	746.843	748.851	2.008
14	1	Group0503	VNG0983C	COG0618	negative	748.605	747.151	1.455
15	1	Group0504	VNG0985H		positive	749.392	759.277	9.885
16	1	Group0504	VNG0986H		positive	752.276	752.803	.528
17	1	Group0504	VNG0987H		positive	753.131	753.547	.417
18	1	Group0504	VNG0988H		positive	754.149	754.391	.243
19	1	Group0504	VNG0989C	COG0582	negative	755.481	754.459	1.023
20	1	Group0504	VNG0990H		positive	756.010	756.183	.174
21	1	Group0504	VNG0991H		negative	757.016	756.675	.342
22	1	Group0504	VNG0992H		negative	758.119	757.409	.711
23	1	Group0504	VNG0993H		positive	758.465	759.277	.813
24	1	Group0505	VNG0994H		positive	759.667	762.487	2.820
25	1	Group0505	VNG0995H		positive	760.365	760.553	.189
26	1	Group0505	boa4	COG3413	positive	760.682	762.487	1.806
27	1	Group0506	acs2	COG0365	positive	762.609	764.612	2.004
28	1	Group0507	yajO2	COG0667	positive	764.619	765.629	1.011
29	1	Group0508	VNG0999H		positive	765.775	766.044	.270
30	1	Group0509	VNG1000H	COG3205	positive	766.603	766.812	.210
31	1	Group0510	guaB	COG0516	positive	766.955	768.538	1.584
32	1	Group0511	VNG1002H		positive	768.965	769.882	.918
33	1	Group0512	VNG1003H		positive	769.965	770.189	.225
34	1	Group0513	VNG1005H		positive	770.194	770.406	.213
35	1	Group0514	tRNA-Trp		positive	770.516	771.546	1.030
36	1	Group0514	VNG1006H		positive	770.827	771.546	.720
37	1	Group0515	VNG1007H		positive	771.722	771.925	.204
38	1	Group0516	flaA1a	COG1681	positive	773.360	773.950	.591

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	6644	positive	734.735	734.749	.015
2	1	6647	negative	735.378	735.364	.015
3	1	6649	negative	735.403	735.389	.015
4	1	6650	negative	735.767	735.753	.015
5	1	6651	negative	735.789	735.775	.015
6	1	6655	positive	736.325	736.339	.015
7	1	6657	positive	736.345	736.359	.015
8	1	6664	negative	737.782	737.752	.031
9	1	6672	negative	738.562	738.517	.046
10	1	6676	negative	738.989	738.975	.015
11	1	6677	negative	739.007	738.992	.016
12	1	6691	negative	741.368	741.352	.017
13	1	6694	negative	741.388	741.374	.015
14	1	6696	negative	741.533	741.519	.015
15	1	6697	negative	741.552	741.538	.015
16	1	6713	positive	745.865	745.879	.015
17	1	6715	positive	745.888	745.902	.015

18	1	6716	positive	746.140	746.155	.016
19	1	6719	positive	746.162	746.176	.015
20	1	6721	negative	746.259	746.229	.031
21	1	6726	positive	746.453	746.467	.015
22	1	6729	positive	746.469	746.483	.015
23	1	6733	negative	746.919	746.905	.015
24	1	6734	negative	746.941	746.927	.015
25	1	6745	negative	759.552	759.509	.044
26	1	6750	positive	760.774	760.789	.016
27	1	6751	positive	760.798	760.814	.017
28	1	6753	positive	760.878	760.892	.015
29	1	6754	positive	760.897	760.912	.016
30	1	6755	positive	761.496	761.510	.015
31	1	6756	positive	761.516	761.533	.018
32	1	6757	positive	761.542	761.557	.016
33	1	6759	positive	761.576	761.597	.022
34	1	6760	positive	761.601	761.617	.017
35	1	6762	positive	761.933	761.950	.018
36	1	6764	positive	761.953	761.968	.016
37	1	6771	positive	763.283	763.304	.022
38	1	6773	positive	763.306	763.321	.016
39	1	6774	positive	763.346	763.360	.015
40	1	6777	positive	763.362	763.376	.015
41	1	6781	negative	763.986	763.965	.022
42	1	6782	positive	763.965	763.995	.031
43	1	6783	negative	764.011	763.990	.022
44	1	6784	positive	764.000	764.015	.016
45	1	6785	negative	764.089	764.075	.015
46	1	6786	negative	764.108	764.093	.016
47	1	6787	positive	764.156	764.171	.016
48	1	6788	negative	764.177	764.156	.022
49	1	6790	negative	764.195	764.181	.015
50	1	6792	positive	764.181	764.204	.024
51	1	6793	positive	764.213	764.227	.015
52	1	6800	positive	764.791	764.808	.018
53	1	6801	negative	764.813	764.794	.020
54	1	6803	positive	764.810	764.826	.017
55	1	6804	negative	764.832	764.818	.015
56	1	6805	positive	764.831	764.853	.023
57	1	6806	positive	764.856	764.870	.015
58	1	6807	negative	764.998	764.984	.015
59	1	6809	negative	765.014	765.000	.015
60	1	6811	negative	765.446	765.431	.016
61	1	6812	negative	765.473	765.456	.018
62	1	6813	negative	765.494	765.479	.016
63	1	6821	negative	766.653	766.635	.019
64	1	6823	negative	766.675	766.655	.021
65	1	6838	positive	770.226	770.240	.015

66	1	6839	positive	770.251	770.265	.015
67	1	6841	positive	770.347	770.363	.017
68	1	6842	positive	770.365	770.379	.015
69	1	6845	negative	772.086	771.564	.523
70	1	6851	positive	773.399	773.483	.085

Addition of a Synthetic Virtual Connectron of Type 15 from Table 2

A synthetic virtual connectron of type 15 in which the C1 and C2 are natural elements, the T1 is a natural element and the T2 is a synthetic element can be introduced into the *P. aeruginosa* genome by modifying the DNA double-strand sequences at 4838.155kb through 4838.323kb for a length of 0.169kb.

To create this example of a synthetic connectron of type 14 the T2 sequence for natural connectron 23295 (old position 4848.679kb through 4939.847kb) was copied into the new position stated above.

Connectron 28739 is an example of a synthetic transient connectron. It is described as

		C1/C2			T1-T2		
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
28739	1	53464	53464	1	53531	53569	transient

The C1/C2 source of the transient connectron 28739 is represented in table 1 as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
CPT	53464	1	1	4832.718	4832.838	.121	-->																											

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB).

The T1-T2 target of the transient connectron 28739 as shown in table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TP	53531	1	1	4836.528	4836.721	.194	*-*
CPT	53532	1	1	4836.728	4836.746	.019	OS-> |
TP	53533	1	1	4836.728	4836.746	.019	*-+
TN	53534	1	1	4836.728	4836.779	.052	*-+
CPT	53535	1	1	4836.748	4836.779	.032	OS-> |
TP	53536	1	1	4836.748	4836.779	.032	*-+
CPT	53537	1	1	4836.781	4836.821	.041	OS-> |
TP	53538	1	1	4836.781	4836.821	.041	*-+
TN	53539	1	1	4836.781	4836.918	.138	*-+
TP	53540	1	1	4836.840	4836.855	.016	*-+
CPT	53541	1	1	4836.877	4836.918	.042	OS-> |
TP	53542	1	1	4836.877	4836.918	.042	*-+
TP	53543	1	1	4836.940	4836.957	.018	*-+
CPT	53544	1	1	4836.940	4836.982	.043	OS-> |
CPT	53545	1	1	4836.990	4837.123	.134	OS-> |
TP	53546	1	1	4836.990	4837.123	.134	*-+
TN	53547	1	1	4836.990	4837.153	.164	*-+
CPT	53548	1	1	4837.126	4837.148	.023	--> |
TP	53549	1	1	4837.129	4837.153	.025	*-+
TP	53549a	1	1	4838.155	4838.323	.169	*-*

The "Type" descriptor of the T1 (Id number 53531) is "TP" showing that is T1 target is on the positive strand of the

double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 53549a) also has the type descriptor "TP".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TN	xx	1	1	278.386	279.148	.763		*---*
XX	xx	1	1	278.387	278.416	.030		* @
XX	xx	1	1	278.421	278.450	.030		* @
TP	xx	1	1	278.452	278.892	.441		*---*

Since this synthetic connectron is a virtual connectron there are no gene groups that are controlled by the existence of this connectron. Instead the expression of the C1/C2 sources of six one-shot connectrons (type designator "CPT" for Id numbers 53532, 53535, 53537, 53541, 53544, and 53544) and one transient connectron (type designator "CPT" for Id numbers 53548) are controlled by this connectron.

All of the data for the transient connectron 28739 are pulled together in the following table that is the "terse" description of the connectron.

Connectron Relationships - Global_Id	Type
28739	transient

Control Sequences - Direction	Chromosome	C1/C2_Id	Start	Stop	Length
positive	1	53464	4832.718	4832.838	.121

Trigger Gene - Name	COG_Id	Start	Stop	Length
pctC	COG0840	4831.371	4833.269	1.899

Target Sequences - Direction	Chromosome	T1_Id	Start	Stop	Length
positive	1	53531	4836.528	4836.721	.194

T2_Id	Start	Stop	Length
53549a	4838.155	4838.323	.169

Controlled Genes

none

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	53532	positive	4836.728	4836.746	.019
2	1	53535	positive	4836.748	4836.779	.032
3	1	53537	positive	4836.781	4836.821	.041
4	1	53541	positive	4836.877	4836.918	.042
5	1	53544	positive	4836.940	4836.982	.043
6	1	53545	positive	4836.990	4837.123	.134
7	1	53548	positive	4837.126	4837.148	.023
8	1	53551	positive	4837.419	4837.448	.030
9	1	53552	positive	4837.572	4837.622	.051
10	1	53554	positive	4837.962	4837.999	.038
11	1	53557	positive	4838.217	4838.258	.042
12	1	53559	positive	4838.295	4838.362	.068
13	1	53563	positive	4838.457	4838.476	.020
14	1	53564	positive	4838.478	4838.645	.168
15	1	53567	positive	4838.654	4838.847	.194

Synthetic Connectron formed by a DBP

A synthetic connectron can be introduced into the *V. cholerae* genome by introducing a 12-domain zinc-finger protein that recognizes the sequence

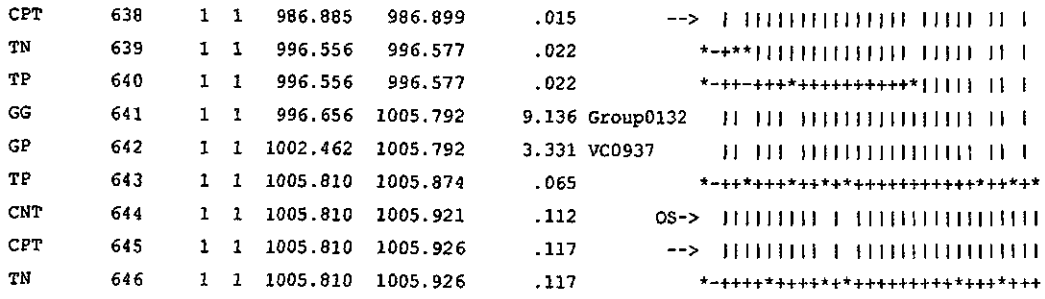
tccccatgag catagatatg caggtaggcg gcaagt

Connectron 7580 is an example of a synthetic transient connectron.

		C1/C2			T1-T2		
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
7580	1	Synthetic	DBP	1	607	646	synthetic

The T1-T2 target of the transient connectron 7580 as shown in Table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TN	607	1	1	952.642	952.777	.136		*-++++*+++*++++++++*+*++++*++++
TP	608	1	1	952.648	952.777	.130		*-++++-+++-*+++*+*-++*++++-++++
GG	609	1	1	952.846	954.393	1.548	Group0127	|||| ||| ||| | || ||| |||
TN	610	1	1	954.486	954.587	.102		*-++++*+++*-+++-+-*+*-++*+**+++
TP	611	1	1	954.486	954.587	.102		*-++++++++++*++*+*++-**+-++-+*+
CNT	612	1	1	954.497	954.589	.093	OS->	||||||||| |||||| | | || | |
CPT	613	1	1	954.503	954.520	.018	-->	||||||||| |||||| | | || | |
CPT	614	1	1	954.522	954.588	.067	-->	||||||||| |||||| | | || | |
TP	615	1	1	954.601	954.658	.058		*-++++++++++*++++++*+*+*++-+-*
TN	616	1	1	954.602	954.658	.057		*-++++++++++++++++++*++++++*+***-
CNT	617	1	1	954.616	954.658	.043	-->	||||||||||||||||| |||| || |
CPT	618	1	1	954.624	954.639	.016	-->	||||||||||||||||| |||| || |
CPT	619	1	1	954.641	954.658	.018	-->	||||||||||||||||| |||| || |
GG	620	1	1	954.684	958.635	3.951	Group0128	||||||||||||||||| |||| || |
GP	621	1	1	955.956	956.342	.387	VC0897	||||||||||||||||| |||| || |
CPT	622	1	1	956.873	956.887	.015	-->	||||||||||||||||| |||| || |
CPT	623	1	1	956.896	956.910	.015	-->	||||||||||||||||| |||| || |
TN	624	1	1	958.089	958.103	.015		*-+*||||||||||||||||| |||| || |
GG	625	1	1	958.840	972.992	14.152	Group0129	| ||||||||||||||||| |||| || |
GP	626	1	1	971.304	972.992	1.689	VC0911	| ||||||||||||||||| |||| || |
TP	627	1	1	973.170	973.250	.081		*-+*||||||||||||||||| |||| || |
GG	628	1	1	973.171	973.763	.592	Group0130	||||||||||||||||| |||| || |
CPT	629	1	1	973.339	973.434	.096	OS->	||||||||||||||||| |||| || |
CPT	630	1	1	973.508	973.603	.096	OS->	||||||||||||||||| |||| || |
TP	631	1	1	973.693	973.773	.081		*-+*||||||||||||||||| |||| || |
GG	632	1	1	973.767	996.501	22.734	Group0131	| ||||||||||||||||| |||| || |
GP	633	1	1	974.049	978.217	4.169	VC0913	| ||||||||||||||||| |||| || |
CPT	634	1	1	977.711	977.725	.015	-->	| ||||||||||||||||| |||| || |
CPT	635	1	1	977.732	977.746	.015	-->	| ||||||||||||||||| |||| || |
GP	636	1	1	986.166	990.921	4.756	VC0923	| ||||||||||||||||| |||| || |
CPT	637	1	1	986.862	986.877	.016	-->	| ||||||||||||||||| |||| || |



Group0127 through Group0132 are described in Table 2 as

Group0127

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0894	COG0607	P	1	positive	952.846	954.393	1.548

Group0128

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0895			1	negative	954.684	954.860	.177
VC0896	COG0583	K	1	positive	955.014	955.934	.921
VC0897	COG2363	S	1	positive	955.956	956.342	.387
VC0898	COG0258	L	1	negative	956.372	957.223	.852
VC0899	COG1611	R	1	negative	957.262	958.635	1.374

Group0129

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0900	COG2199	T	1	negative	958.840	960.414	1.575
VC0901	COG0457	R	1	negative	960.516	962.777	2.262
VC0902	COG0780	R	1	negative	962.792	963.655	.864
VC0903			1	positive	963.686	964.282	.597
VC0904			1	positive	964.284	965.060	.777
VC0905	COG1464	M	1	negative	965.193	966.020	.828
VC0906	COG2011	R	1	negative	966.039	967.740	1.702
VC0908	COG0241	E	1	positive	967.976	968.536	.561
VC0909	COG1609	K	1	positive	968.601	969.551	.951
VC0910	COG1263	G	1	positive	969.788	971.224	1.437
VC0911	COG0366	G	1	positive	971.304	972.992	1.689

Group0130

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
tRNA-Tyr-2			1	positive	973.171	973.255	.085
tRNA-Tyr-3			1	positive	973.340	973.424	.085

tRNA-Tyr-4		1	positive	973.509	973.593	.085
tRNA-Tyr-5		1	positive	973.679	973.763	.085

Group0131

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0912			1	positive	973.767	973.862	.096
VC0913	COG0845	Q	1	positive	974.049	978.217	4.169
VC0915			1	positive	978.272	978.382	.111
VC0916	COG0394	T	1	positive	978.644	979.144	.501
VC0917	COG0381	M	1	positive	979.457	980.575	1.119
VC0918	COG0677	M	1	positive	980.595	986.155	5.561
VC0923	COG1045	E	1	positive	986.166	990.921	4.756
VC0928			1	positive	991.117	991.932	.816
VC0929			1	negative	992.138	993.364	1.227
VC0930			1	positive	993.628	996.501	2.874

Group0132

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0931	COG3307	M	1	negative	996.656	997.972	1.317
VC0932			1	negative	998.148	998.752	.605
VC0934	COG2148	M	1	positive	999.242	1000.639	1.398
VC0935			1	positive	1000.710	1001.906	1.197
VC0936	COG1596	M	1	positive	1001.910	1002.437	.528
VC0937	COG3206	N	1	positive	1002.462	1005.792	3.331

All of the data for the transient connectron 7580 are pulled together in the following table that is the "terse" description of the connectron.

Connectron Relationships - Global_Id Type
7580 synthetic

Control Sequences - Synthetic DNA Binding Protein that recognizes the sequence
tccccatgag catagatatg caggtaggcg gcaagt

Target Sequences -	Direction	Chromosome	T1_Id	Start	Stop	Length
	negative	1	607	952.777	952.642	.136
			T2_Id	Start	Stop	Length
			646	1005.926	1005.810	.117

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0127	VC0894	COG0607	positive	952.846	954.393	1.548
2	1	Group0128	VC0895		positive	954.684	958.635	3.951
3	1	Group0128	VC0896	COG0583	positive	955.014	955.934	.921
4	1	Group0128	VC0897	COG2363	positive	955.956	956.342	.387
5	1	Group0128	VC0898	COG0258	negative	957.223	956.372	.852
6	1	Group0128	VC0899	COG1611	negative	958.635	957.262	1.374
7	1	Group0129	VC0900	COG2199	positive	958.840	972.992	14.152
8	1	Group0129	VC0901	COG0457	negative	962.777	960.516	2.262
9	1	Group0129	VC0902	COG0780	negative	963.655	962.792	.864
10	1	Group0129	VC0903		positive	963.686	964.282	.597
11	1	Group0129	VC0904		positive	964.284	965.060	.777
12	1	Group0129	VC0905	COG1464	negative	966.020	965.193	.828
13	1	Group0129	VC0906	COG2011	negative	967.740	966.039	1.702
14	1	Group0129	VC0908	COG0241	positive	967.976	968.536	.561
15	1	Group0129	VC0909	COG1609	positive	968.601	969.551	.951
16	1	Group0129	VC0910	COG1263	positive	969.788	971.224	1.437
17	1	Group0129	VC0911	COG0366	positive	971.304	972.992	1.689
18	1	Group0130	tRNA-Tyr-		positive	973.171	973.763	.592
19	1	Group0131	VC0912		positive	973.767	996.501	22.734
20	1	Group0131	VC0913	COG0845	positive	974.049	978.217	4.169
21	1	Group0131	VC0915		positive	978.272	978.382	.111
22	1	Group0131	VC0916	COG0394	positive	978.644	979.144	.501
23	1	Group0131	VC0917	COG0381	positive	979.457	980.575	1.119
24	1	Group0131	VC0918	COG0677	positive	980.595	986.155	5.561
25	1	Group0131	VC0923	COG1045	positive	986.166	990.921	4.756
26	1	Group0131	VC0928		positive	991.117	991.932	.816
27	1	Group0131	VC0929		negative	993.364	992.138	1.227
28	1	Group0131	VC0930		positive	993.628	996.501	2.874
29	1	Group0132	VC0931	COG3307	positive	996.656	1005.792	9.136
30	1	Group0132	VC0932		negative	998.752	998.148	.605
31	1	Group0132	VC0934	COG2148	positive	999.242	1000.639	1.398
32	1	Group0132	VC0935		positive	1000.710	1001.906	1.197
33	1	Group0132	VC0936	COG1596	positive	1001.910	1002.437	.528
34	1	Group0132	VC0937	COG3206	positive	1002.462	1005.792	3.331

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	612	negative	954.589	954.497	.093
2	1	613	positive	954.503	954.520	.018
3	1	614	positive	954.522	954.588	.067
4	1	617	negative	954.658	954.616	.043
5	1	618	positive	954.624	954.639	.016
6	1	619	positive	954.641	954.658	.018
7	1	622	positive	956.873	956.887	.015
8	1	623	positive	956.896	956.910	.015
9	1	629	positive	973.339	973.434	.096

10	1	630	positive	973.508	973.603	.096
11	1	634	positive	977.711	977.725	.015
12	1	635	positive	977.732	977.746	.015
13	1	637	positive	986.862	986.877	.016
14	1	638	positive	986.885	986.899	.015
15	1	644	negative	1005.921	1005.810	.112
16	1	645	positive	1005.810	1005.926	.117

Synthetic Connectron formed by a PNA

A synthetic connectron can be introduced into the *V. cholerae* genome by introducing a PNA that recognizes the sequence

tccccatgag catagatatg caggtaggcg gcaagt

Connectron 7581 is an example of a synthetic transient connectron.

		C1/C2			T1-T2		
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
7581	1	Synthetic	PNA	1	607	646	synthetic

The T1-T2 target of the transient connectron 7581 as shown in Table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TN	607	1	1	952.642	952.777	.136		*-++++*+++*++++++++*+*++++++*++++
TP	608	1	1	952.648	952.777	.130		*-++++-+++-*+++*+*-++*++++-++++
GG	609	1	1	952.846	954.393	1.548	Group0127	|||| ||| ||| | || |||| ||||
TN	610	1	1	954.486	954.587	.102		*-++++*+++*-+++-+-*+*-++*+*+*+++
TP	611	1	1	954.486	954.587	.102		*-++++++++++*+++*+*++-**+-++-+*+
CNT	612	1	1	954.497	954.589	.093	OS->	||||||||| |||||| | | || | |
CPT	613	1	1	954.503	954.520	.018	-->	||||||||| |||||| | | || | |
CPT	614	1	1	954.522	954.588	.067	-->	||||||||| |||||| | | || | |
TP	615	1	1	954.601	954.658	.058		*-++++++++++*++++++++*+*+*++-+-*
TN	616	1	1	954.602	954.658	.057		*-++++++++++++++++++*+++++*+***-
CNT	617	1	1	954.616	954.658	.043	-->	|||||||||||||||| ||||| || |

CPT	618	1	1	954.624	954.639	.016	-->	
CPT	619	1	1	954.641	954.658	.018	-->	
GG	620	1	1	954.684	958.635	3.951	Group0128	
GP	621	1	1	955.956	956.342	.387	VC0897	
CPT	622	1	1	956.873	956.887	.015	-->	
CPT	623	1	1	956.896	956.910	.015	-->	
TN	624	1	1	958.089	958.103	.015		
GG	625	1	1	958.840	972.992	14.152	Group0129	
GP	626	1	1	971.304	972.992	1.689	VC0911	
TP	627	1	1	973.170	973.250	.081		
GG	628	1	1	973.171	973.763	.592	Group0130	
CPT	629	1	1	973.339	973.434	.096	OS->	
CPT	630	1	1	973.508	973.603	.096	OS->	
TP	631	1	1	973.693	973.773	.081		
GG	632	1	1	973.767	996.501	22.734	Group0131	
GP	633	1	1	974.049	978.217	4.169	VC0913	
CPT	634	1	1	977.711	977.725	.015	-->	
CPT	635	1	1	977.732	977.746	.015	-->	
GP	636	1	1	986.166	990.921	4.756	VC0923	
CPT	637	1	1	986.862	986.877	.016	-->	
CPT	638	1	1	986.885	986.899	.015	-->	
TN	639	1	1	996.556	996.577	.022		
TP	640	1	1	996.556	996.577	.022		
GG	641	1	1	996.656	1005.792	9.136	Group0132	
GP	642	1	1	1002.462	1005.792	3.331	VC0937	
TP	643	1	1	1005.810	1005.874	.065		
CNT	644	1	1	1005.810	1005.921	.112	OS->	
CPT	645	1	1	1005.810	1005.926	.117	-->	
TN	646	1	1	1005.810	1005.926	.117		

Group0127 through Group0132 are described in Table 2 as

Group0127

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0894	COG0607	P	1	positive	952.846	954.393	1.548

Group0128

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0895			1	negative	954.684	954.860	.177
VC0896	COG0583	K	1	positive	955.014	955.934	.921
VC0897	COG2363	S	1	positive	955.956	956.342	.387
VC0898	COG0258	L	1	negative	956.372	957.223	.852
VC0899	COG1611	R	1	negative	957.262	958.635	1.374

Group0129

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0900	COG2199	T	1	negative	958.840	960.414	1.575
VC0901	COG0457	R	1	negative	960.516	962.777	2.262
VC0902	COG0780	R	1	negative	962.792	963.655	.864
VC0903			1	positive	963.686	964.282	.597
VC0904			1	positive	964.284	965.060	.777
VC0905	COG1464	M	1	negative	965.193	966.020	.828
VC0906	COG2011	R	1	negative	966.039	967.740	1.702
VC0908	COG0241	E	1	positive	967.976	968.536	.561
VC0909	COG1609	K	1	positive	968.601	969.551	.951
VC0910	COG1263	G	1	positive	969.788	971.224	1.437
VC0911	COG0366	G	1	positive	971.304	972.992	1.689

Group0130

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
tRNA-Tyr-2		1	positive	973.171	973.255	.085
tRNA-Tyr-3		1	positive	973.340	973.424	.085
tRNA-Tyr-4		1	positive	973.509	973.593	.085
tRNA-Tyr-5		1	positive	973.679	973.763	.085

Group0131

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0912			1	positive	973.767	973.862	.096
VC0913	COG0845	Q	1	positive	974.049	978.217	4.169
VC0915			1	positive	978.272	978.382	.111
VC0916	COG0394	T	1	positive	978.644	979.144	.501
VC0917	COG0381	M	1	positive	979.457	980.575	1.119
VC0918	COG0677	M	1	positive	980.595	986.155	5.561
VC0923	COG1045	E	1	positive	986.166	990.921	4.756
VC0928			1	positive	991.117	991.932	.816
VC0929			1	negative	992.138	993.364	1.227
VC0930			1	positive	993.628	996.501	2.874

Group0132

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0931	COG3307	M	1	negative	996.656	997.972	1.317
VC0932			1	negative	998.148	998.752	.605
VC0934	COG2148	M	1	positive	999.242	1000.639	1.398
VC0935			1	positive	1000.710	1001.906	1.197
VC0936	COG1596	M	1	positive	1001.910	1002.437	.528
VC0937	COG3206	N	1	positive	1002.462	1005.792	3.331

All of the data for the transient connectron 7581 are pulled together in the following table that is the "terse" description of the connectron.

Connectron Relationships - Global_Id Type
7581 synthetic

Control Sequences - Synthetic PNA that recognizes the sequence
tccccatgag catagatatg caggtaggcg gcaagt

Target Sequences - Direction	Chromosome	T1_Id	Start	Stop	Length
negative	1	607	952.777	952.642	.136

T2_Id	Start	Stop	Length
646	1005.926	1005.810	.117

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0127	VC0894	COG0607	positive	952.846	954.393	1.548
2	1	Group0128	VC0895		positive	954.684	958.635	3.951
3	1	Group0128	VC0896	COG0583	positive	955.014	955.934	.921
4	1	Group0128	VC0897	COG2363	positive	955.956	956.342	.387
5	1	Group0128	VC0898	COG0258	negative	957.223	956.372	.852
6	1	Group0128	VC0899	COG1611	negative	958.635	957.262	1.374
7	1	Group0129	VC0900	COG2199	positive	958.840	972.992	14.152
8	1	Group0129	VC0901	COG0457	negative	962.777	960.516	2.262
9	1	Group0129	VC0902	COG0780	negative	963.655	962.792	.864
10	1	Group0129	VC0903		positive	963.686	964.282	.597
11	1	Group0129	VC0904		positive	964.284	965.060	.777
12	1	Group0129	VC0905	COG1464	negative	966.020	965.193	.828
13	1	Group0129	VC0906	COG2011	negative	967.740	966.039	1.702
14	1	Group0129	VC0908	COG0241	positive	967.976	968.536	.561
15	1	Group0129	VC0909	COG1609	positive	968.601	969.551	.951
16	1	Group0129	VC0910	COG1263	positive	969.788	971.224	1.437
17	1	Group0129	VC0911	COG0366	positive	971.304	972.992	1.689
18	1	Group0130	tRNA-Tyr-		positive	973.171	973.763	.592
19	1	Group0131	VC0912		positive	973.767	996.501	22.734
20	1	Group0131	VC0913	COG0845	positive	974.049	978.217	4.169
21	1	Group0131	VC0915		positive	978.272	978.382	.111
22	1	Group0131	VC0916	COG0394	positive	978.644	979.144	.501
23	1	Group0131	VC0917	COG0381	positive	979.457	980.575	1.119
24	1	Group0131	VC0918	COG0677	positive	980.595	986.155	5.561
25	1	Group0131	VC0923	COG1045	positive	986.166	990.921	4.756
26	1	Group0131	VC0928		positive	991.117	991.932	.816

27	1	Group0131	VC0929		negative	993.364	992.138	1.227
28	1	Group0131	VC0930		positive	993.628	996.501	2.874
29	1	Group0132	VC0931	COG3307	positive	996.656	1005.792	9.136
30	1	Group0132	VC0932		negative	998.752	998.148	.605
31	1	Group0132	VC0934	COG2148	positive	999.242	1000.639	1.398
32	1	Group0132	VC0935		positive	1000.710	1001.906	1.197
33	1	Group0132	VC0936	COG1596	positive	1001.910	1002.437	.528
34	1	Group0132	VC0937	COG3206	positive	1002.462	1005.792	3.331

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	612	negative	954.589	954.497	.093
2	1	613	positive	954.503	954.520	.018
3	1	614	positive	954.522	954.588	.067
4	1	617	negative	954.658	954.616	.043
5	1	618	positive	954.624	954.639	.016
6	1	619	positive	954.641	954.658	.018
7	1	622	positive	956.873	956.887	.015
8	1	623	positive	956.896	956.910	.015
9	1	629	positive	973.339	973.434	.096
10	1	630	positive	973.508	973.603	.096
11	1	634	positive	977.711	977.725	.015
12	1	635	positive	977.732	977.746	.015
13	1	637	positive	986.862	986.877	.016
14	1	638	positive	986.885	986.899	.015
15	1	644	negative	1005.921	1005.810	.112
16	1	645	positive	1005.810	1005.926	.117

Synthetic Connectron formed by a Pair of Linked DNA Binding Objects

A synthetic connectron can be introduced into the *A. pernix* genome by introducing a pair of linked DNA binding objects that recognize the sequences

G1 cccgacacaacctgc

and

G2 cccggggttcccgag

Connectron 917 is an example of a synthetic transient connectron.

			C1/C2			T1-T2		
Global_Id	Chromosome		C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
917		1	G1	G2	1	218	295	synthetic

The T1-T2 target of the transient connectron 917 as shown in Table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TN	218	1	1	284.008	284.071	.064		*-+*+-+++*|||| ||| |
TP	219	1	1	284.008	284.071	.064		*-+++*|| |||| ||| |
CPT	220	1	1	284.009	284.071	.063	-->	|||||| |||| ||| |
CNT	221	1	1	284.073	284.144	.072	-->	|||||| |||| ||| |
CPT	222	1	1	284.073	284.145	.073	-->	|||||| |||| ||| |
TP	223	1	1	284.073	284.160	.088		*-+++++++++++*||| |
TN	224	1	1	284.073	284.251	.179		*-+++++++++++++++++**+*
CNT	225	1	1	284.158	284.251	.094	-->	||||||||||||||||||
CPT	226	1	1	284.158	284.251	.094	-->	||||||||||||||||||
TP	227	1	1	284.162	284.251	.090		*-++++++++++++++++++++**
CPT	228	1	1	284.253	284.280	.028	-->	|||||||||||||||||||
TN	229	1	1	284.253	284.305	.053		*-++++++++++++++++++++++*
TP	230	1	1	284.253	284.316	.064		*-++++++++++++++++++++++**
CPT	231	1	1	284.283	284.305	.023	-->	||||||||||||||||||||
GG	232	1	1	284.391	287.510	3.120	Group0053	||||||||||||||||||||
TN	233	1	1	286.094	286.108	.015		*-++++++++++++++++++++++*
GG	234	1	1	287.521	291.639	4.118	Group0054	||||||||||||||||||||
TP	235	1	1	288.611	288.625	.015		*-++++++*|||||||||||||||
GG	236	1	1	291.643	295.139	3.496	Group0055	||||| ||||||||||||||
TP	237	1	1	295.230	295.259	.030		*-++++++*|||||||||||||||
GG	238	1	1	295.231	295.529	.298	Group0056	||||||||||||||||||||
GP	239	1	1	295.342	295.518	.177	APES013	||||||||||||||||||||
CPT	240	1	1	295.415	295.444	.030	-->	||||||||||||||||||||
TP	241	1	1	295.417	295.444	.028		*-++++++++++*++++++++++++++++*
GG	242	1	1	295.572	296.676	1.104	Group0057	||||||||| ||||||||||||
TN	243	1	1	296.080	296.095	.016		*-++++++++++*||||||||||||||
TN	244	1	1	296.913	296.927	.015		*-++++++++++++++++++++++++++*
GG	245	1	1	297.071	298.857	1.786	Group0058	||||||||||||||||||||||||
TP	246	1	1	298.617	298.631	.015		*-++++++++++++++++++++++++++*
GG	247	1	1	298.856	305.941	7.085	Group0059	||||||||||||||||||||||||
CNT	248	1	1	300.742	300.757	.016	-->	||||||||||||||||||||||||
CNT	249	1	1	300.767	300.781	.015	-->	||||||||||||||||||||||||
GN	250	1	1	301.243	303.153	1.911	APE0428	||||||||||||||||||||||||
TN	251	1	1	301.733	301.748	.016		*-++++++++++++*++++++++++++++++*
GP	252	1	1	305.005	305.611	.607	APE0434	|||||||||||| |||||||||||||

	CPT	253	1	1	305.334	305.348	.015	-->
	CPT	254	1	1	305.358	305.372	.015	-->
	CNT	255	1	1	305.552	305.566	.015	-->
	TN	256	1	1	305.562	305.576	.015	
5	CNT	257	1	1	305.568	305.582	.015	-->
	GG	258	1	1	306.121	308.859	2.738	Group0060
	TP	259	1	1	307.532	307.547	.016	
	TN	260	1	1	307.814	307.828	.015	
	TN	261	1	1	308.559	308.573	.015	
10	GG	262	1	1	308.989	312.190	3.201	Group0061
	TN	263	1	1	311.735	311.750	.016	
	GG	264	1	1	312.215	313.258	1.043	Group0062
	TP	265	1	1	312.894	312.909	.016	
	GG	266	1	1	313.378	315.728	2.350	Group0063
15	TN	267	1	1	314.051	314.065	.015	
	TN	268	1	1	314.826	314.840	.015	
	TN	269	1	1	315.511	315.525	.015	
	TP	270	1	1	315.747	315.761	.015	
	GG	271	1	1	315.792	318.996	3.204	Group0064
20	GP	272	1	1	317.638	318.996	1.359	APE0457
	CNT	273	1	1	317.668	317.682	.015	-->
	TP	274	1	1	317.689	317.703	.015	
	CNT	275	1	1	317.690	317.704	.015	-->
	GG	276	1	1	318.432	318.914	.483	Group0065
25	CPT	277	1	1	319.097	319.127	.031	-->
	TN	278	1	1	319.122	319.137	.016	
	GG	279	1	1	319.335	319.673	.339	Group0066
	TN	280	1	1	319.515	319.529	.015	
	TP	281	1	1	319.572	319.586	.015	
30	GG	282	1	1	319.733	324.526	4.793	Group0067
	CNT	283	1	1	320.484	320.513	.030	-->
	GN	284	1	1	320.700	322.241	1.542	APE0462
	TN	285	1	1	323.674	323.688	.015	
	GG	286	1	1	324.030	324.335	.306	Group0068
35	TN	287	1	1	324.137	324.151	.015	
	GG	288	1	1	324.606	325.575	.969	Group0069
	GP	289	1	1	325.141	325.575	.435	APE0469
	CNT	290	1	1	325.950	325.979	.030	-->
	CPT	291	1	1	325.950	325.979	.030	-->
40	TN	292	1	1	325.959	325.975	.017	
	GG	293	1	1	325.980	326.717	.738	Group0070
	CNT	294	1	1	326.716	326.878	.163	OS->
	TN	295	1	1	326.716	326.878	.163	

45 The "Type" descriptor of the T1 (Id number 218) is "TN" showing that is T1 target is on the negative strand of the double-

stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 295) also has the type descriptor "TN".

Group0053 through Group0070 are described in Table 2 as

Group0053

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0413	COG0553	K	1	negative	284.391	287.510	3.120

Group0054

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0414			1	negative	287.521	288.066	.546
APE0415	COG1483	R	1	negative	288.073	291.639	3.567

Group0055

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0416	COG1743	L	1	negative	291.643	294.666	3.024
APE0417			1	positive	292.319	292.636	.318
APE0418			1	positive	294.690	295.139	.450

Group0056

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
tRNA-Thr			1	positive	295.231	295.325	.095
APES013			1	positive	295.342	295.518	.177
tRNA-Met			1	positive	295.405	295.529	.125

Group0057

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APES014			1	negative	295.572	295.754	.183
APE0419			1	negative	295.891	296.676	.786

Group0058

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0420			1	positive	297.071	298.113	1.043
APE0422			1	negative	297.448	297.993	.546
APE0423	COG0084	L	1	negative	298.099	298.857	.759

Group0059

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0424			1	positive	298.856	299.269	.414
APE0425			1	negative	298.973	299.332	.360
APE0426	COG2246	S	1	positive	299.481	300.602	1.122
APE0427	COG1573	L	1	positive	300.649	301.296	.648
APE0428	COG1750	R	1	negative	301.243	303.153	1.911
APE0429			1	positive	303.244	303.786	.543
APE0430			1	negative	303.403	303.720	.318
APE0431			1	positive	303.833	304.911	1.079
APE0432			1	negative	304.284	304.688	.405
APE0434			1	positive	305.005	305.611	.607
APE0436	COG1093	J	1	negative	305.192	305.941	.750

Group0060

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APES015	COG2051	J	1	negative	306.121	306.342	.222
APES016	COG1631	J	1	negative	306.359	306.550	.192
APE0437			1	negative	306.674	308.859	2.186
APE0439			1	positive	307.209	307.841	.633

Group0061

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APES017			1	negative	308.989	309.186	.198
APE0442	COG1594	K	1	negative	309.201	309.515	.315
APES018			1	negative	309.642	309.842	.201
APE0443	COG1761	K	1	negative	309.915	310.223	.309
APE0444	COG3286	S	1	negative	310.227	310.832	.606
APE0445	COG1096	J	1	negative	310.912	312.190	1.279

Group0062

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0447	COG1736	J	1	negative	312.215	313.237	1.023
APE0448			1	positive	312.650	313.258	.609

Group0063

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0449	COG0197	J	1	negative	313.378	313.902	.525
APE0450	COG0303	H	1	positive	313.995	315.728	1.734
APE0451			1	negative	314.028	314.714	.687

Group0064

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APES019			1	negative	315.792	315.986	.195
APE0452			1	negative	316.237	316.791	.555
APE0453			1	positive	316.247	317.576	1.330
APE0454	COG1489	G	1	negative	316.820	317.542	.723
APE0456			1	negative	317.632	318.099	.468
APE0457	COG0160	E	1	positive	317.638	318.996	1.359

Group0065

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0458			1	negative	318.432	318.914	.483

Group0066

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0459			1	negative	319.335	319.673	.339

Group0067

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0460			1	positive	319.733	320.038	.306
APE0461	COG1591	L	1	positive	320.272	320.703	.432
APE0462	COG1855	R	1	negative	320.700	322.241	1.542
APE0463			1	positive	321.610	322.074	.465
APE0464			1	positive	322.317	323.228	.912
APE0465	COG0301	H	1	negative	323.288	324.526	1.239

Group0068

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0466			1	positive	324.030	324.335	.306

Group0069

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0468			1	positive	324.606	325.049	.444
APE0469	COG1318	K	1	positive	325.141	325.575	.435

Group0070

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0470	COG1277	R	1	negative	325.980	326.717	.738

All of the data for the transient connectron 917 are pulled together in the following table that is the "terse" description of the connectron.

Connectron Relationships - Global_Id Type
917 synthetic

Control Sequences - Synthetic Pair of Linked DNA Binding Objects that recognize the sequences G1 = cccgacacaacctgc and G2 = cccggggttcccgag

Target Sequences	Direction	Chromosome	T1_Id	Start	Stop	Length
	negative	1	218	284.071	284.008	.064
			T2_Id	Start	Stop	Length
			295	326.878	326.716	.163

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0053	APE0413	COG0553	positive	284.391	287.510	3.120
2	1	Group0054	APE0414		positive	287.521	291.639	4.118
3	1	Group0054	APE0415	COG1483	negative	291.639	288.073	3.567
4	1	Group0055	APE0416	COG1743	positive	291.643	295.139	3.496
5	1	Group0055	APE0417		positive	292.319	292.636	.318
6	1	Group0055	APE0418		positive	294.690	295.139	.450
7	1	Group0056	tRNA-Thr		positive	295.231	295.529	.298
8	1	Group0056	APES013		positive	295.342	295.518	.177
9	1	Group0057	APES014		positive	295.572	296.676	1.104
10	1	Group0057	APE0419		negative	296.676	295.891	.786
11	1	Group0058	APE0420		positive	297.071	298.857	1.786
12	1	Group0058	APE0422		negative	297.993	297.448	.546
13	1	Group0058	APE0423	COG0084	negative	298.857	298.099	.759
14	1	Group0059	APE0424		positive	298.856	305.941	7.085
15	1	Group0059	APE0425		negative	299.332	298.973	.360
16	1	Group0059	APE0426	COG2246	positive	299.481	300.602	1.122
17	1	Group0059	APE0427	COG1573	positive	300.649	301.296	.648
18	1	Group0059	APE0428	COG1750	negative	303.153	301.243	1.911
19	1	Group0059	APE0429		positive	303.244	303.786	.543
20	1	Group0059	APE0430		negative	303.720	303.403	.318
21	1	Group0059	APE0431		positive	303.833	304.911	1.079
22	1	Group0059	APE0432		negative	304.688	304.284	.405
23	1	Group0059	APE0434		positive	305.005	305.611	.607
24	1	Group0059	APE0436	COG1093	negative	305.941	305.192	.750
25	1	Group0060	APES015	COG2051	positive	306.121	308.859	2.738
26	1	Group0060	APES016	COG1631	negative	306.550	306.359	.192

27	1	Group0060	APE0437		negative	308.859	306.674	2.186
28	1	Group0060	APE0439		positive	307.209	307.841	.633
29	1	Group0061	APES017		positive	308.989	312.190	3.201
30	1	Group0061	APE0442	COG1594	negative	309.515	309.201	.315
31	1	Group0061	APES018		negative	309.842	309.642	.201
32	1	Group0061	APE0443	COG1761	negative	310.223	309.915	.309
33	1	Group0061	APE0444	COG3286	negative	310.832	310.227	.606
34	1	Group0061	APE0445	COG1096	negative	312.190	310.912	1.279
35	1	Group0062	APE0447	COG1736	positive	312.215	313.258	1.043
36	1	Group0062	APE0448		positive	312.650	313.258	.609
37	1	Group0063	APE0449	COG0197	positive	313.378	315.728	2.350
38	1	Group0063	APE0450	COG0303	positive	313.995	315.728	1.734
39	1	Group0063	APE0451		negative	314.714	314.028	.687
40	1	Group0064	APES019		positive	315.792	318.996	3.204
41	1	Group0064	APE0452		negative	316.791	316.237	.555
42	1	Group0064	APE0453		positive	316.247	317.576	1.330
43	1	Group0064	APE0454	COG1489	negative	317.542	316.820	.723
44	1	Group0064	APE0456		negative	318.099	317.632	.468
45	1	Group0064	APE0457	COG0160	positive	317.638	318.996	1.359
46	1	Group0065	APE0458		positive	318.432	318.914	.483
47	1	Group0066	APE0459		positive	319.335	319.673	.339
48	1	Group0067	APE0460		positive	319.733	324.526	4.793
49	1	Group0067	APE0461	COG1591	positive	320.272	320.703	.432
50	1	Group0067	APE0462	COG1855	negative	322.241	320.700	1.542
51	1	Group0067	APE0463		positive	321.610	322.074	.465
52	1	Group0067	APE0464		positive	322.317	323.228	.912
53	1	Group0067	APE0465	COG0301	negative	324.526	323.288	1.239
54	1	Group0068	APE0466		positive	324.030	324.335	.306
55	1	Group0069	APE0468		positive	324.606	325.575	.969
56	1	Group0069	APE0469	COG1318	positive	325.141	325.575	.435
57	1	Group0070	APE0470	COG1277	positive	325.980	326.717	.738

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	220	positive	284.009	284.071	.063
2	1	221	negative	284.144	284.073	.072
3	1	222	positive	284.073	284.145	.073
4	1	225	negative	284.251	284.158	.094
5	1	226	positive	284.158	284.251	.094
6	1	228	positive	284.253	284.280	.028
7	1	231	positive	284.283	284.305	.023
8	1	240	positive	295.415	295.444	.030
9	1	248	negative	300.757	300.742	.016
10	1	249	negative	300.781	300.767	.015
11	1	253	positive	305.334	305.348	.015
12	1	254	positive	305.358	305.372	.015
13	1	255	negative	305.566	305.552	.015
14	1	257	negative	305.582	305.568	.015

15	1	273	negative	317.682	317.668	.015
16	1	275	negative	317.704	317.690	.015
17	1	277	positive	319.097	319.127	.031
18	1	283	negative	320.513	320.484	.030
19	1	290	negative	325.979	325.950	.030
20	1	291	positive	325.950	325.979	.030
21	1	294	negative	326.878	326.716	.163

Tables

Table 1

Type	C1	C2	T1	T2
1	D			
2		D		
3			D	
4				D
5	D	D		
6	D		D	
7	D			D
8	D	D	D	
9	D	D		D
10	D	D	D	D

Where D is a connectron element to be deleted or modified.

Table 2

Type	C1	C2	T1	T2
1	S	S	S	S
2	S	S	S	N
3	S	S	N	S
4	S	S	N	N
5	S	N	S	S
6	S	N	S	N
7	S	N	N	S
8	S	N	N	N
9	N	S	S	S
10	N	S	S	N
11	N	S	N	S
12	N	S	N	N
13	N	N	S	S
14	N	N	S	N
15	N	N	N	S

Where N is native DNA sequence and S is a synthetic DNA sequence

Table 3

Type	C1	C2	T1	T2
1	D	D	S	S
2	D	D	S	N
3	D	D	N	S
4	D	D	N	N

Where N is native DNA sequence, S is a synthetic DNA sequence and D is a synthetic DBP

Table 4

Type	C1	C2	T1	T2
1	P	P	S	S
2	P	P	S	N
3	P	P	N	S
4	P	P	N	N

Where N is native DNA sequence, S is a synthetic DNA sequence and P is a synthetic PNA.

Table 5

Type	C1	C2	T1	T2
1	G1	G2	S	S
2	G1	G2	S	N
3	G1	G2	N	S
4	G1	G2	N	N

Where N is native DNA sequence, S is a synthetic DNA sequence and where G1 and G2 are a linked pair of DNA binding elements.

Table 6

Type	Element-1-Style
1	C
2	E

Where C is a copied sequence element and E is an extracted sequence element.

Table 7

	Element-1		Element-2	
Type	Type	Style	Type	Style
1	C1	C	C2	C
2	C1	C	C2	E
3	C1	E	C2	E
4	C1	C	T1	C
5	C1	C	T1	E
6	C1	U	T1	U
7	C1	E	T2	E
8	C2	C	T2	C
9	C2	C	T2	E
10	C2	U	T2	U
11	C2	E	T2	E
12	T1	C	T2	C
13	T1	C	T2	E
14	T1	E	T2	E

Where C is a copied sequence element, U is a unique sequence element and E is an extracted sequence element.

Table 8

	Element-1		Element-2		Element-3	
Type	Type	Style	Type	Style	Type	Style
1	C1	C	C2	C	T1	C
2	C1	C	C2	C	T1	E
3	C1	C	C2	E	T1	C
4	C1	C	C2	E	T1	E
5	C1	U	C2	C	T1	U
6	C1	U	C2	U	T1	E
7	C1	U	C2	E	T1	U
8	C1	E	C2	C	T1	C
9	C1	E	C2	C	T1	E
10	C1	E	C2	E	T1	C
11	C1	E	C2	E	T1	E
12	C1	C	C2	C	T2	C
13	C1	C	C2	C	T2	E
14	C1	C	C2	U	T2	U
15	C1	C	C2	E	T2	C
16	C1	C	C2	E	T2	E
17	C1	E	C2	C	T2	C
18	C1	E	C2	C	T2	E
19	C1	E	C2	U	T2	U
20	C1	E	C2	E	T2	C
21	C1	E	C2	E	T2	E
22	C1	C	T1	C	T2	C
23	C1	C	T1	C	T2	E
24	C1	C	T1	E	T2	C
25	C1	C	T1	E	T2	E
26	C1	U	T1	U	T2	C
27	C1	U	T1	U	T2	E
28	C1					C

29	C1	E	T1	C	T2	E
30	C1	E	T1	E	T2	C
31	C1	E	T1	E	T2	E
32	C2	C	T1	C	T2	C
33	C2	C	T1	C	T2	E
34	C2	C	T1	E	T2	C
35	C2	C	T1	E	T2	E
36	C2	U	T1	C	T2	U
37	C2	U	T1	E	T2	U
38	C2	E	T1	C	T2	C
39	C2	E	T1	C	T2	E
40	C2	E	T1	E	T2	C
41	C2	E	T1	E	T2	E

Where C is a copied sequence element, U is a unique sequence element and E is an extracted sequence element.

Table 9

Type	C1 Style	C2 Style	T1 Style	T2 Style
1	C	C	C	C
2	C	C	C	E
3	C	C	E	C
4	C	C	E	E
5	C	U	C	U
6	C	U	E	U
7	C	E	C	C
8	C	E	C	E
9	C	E	E	C
10	C	E	E	E
11	U	C	U	C
12	U	C	U	E
13	U	U	U	U
14	U	E	U	C
15	U	E	U	E
16	E	C	C	C
17	E	C	C	E
18	E	C	E	C
19	E	C	E	E
20	E	U	C	U
21	E	U	E	U
22	E	E	C	C
23	E	E	C	E
24	E	E	E	C
25	E	E	E	E

Where C is a copied sequence element, U is a unique sequence element and E nt.

I claim:

1. The method of modifying genomic behavior comprising the selective deletion and/or addition of connectrons.

2. The method of simulating connectron behavior of a genome for the purpose of modifying, by computer, genomic behavior comprising the selective deletion and/or addition of connectrons.

3. A genome having a connectron comprised of the DNA elements C1, C2, T1 and T2, wherein at least one of said DNA elements has been deleted according to the following table

Type	C1	C2	T1	T2
1	D			
2		D		
3			D	
4				D
5	D	D		
6	D		D	
7	D			D
8	D	D	D	
9	D	D		D
10	D	D	D	D

where D is a connectron element to be deleted or modified.

4. A genome having a connectron comprised of the DNA elements C1, C2, T1 and T2, wherein at least one of said DNA elements has been replaced with a synthetic DNA element.

5. A genome having a connectron comprised of the native DNA elements C1, C2, T1 and T2, wherein at least one of said DNA elements has been replaced with a synthetic DNA element according to the following table

Type	C1	C2	T1	T2
1	S	S	S	S
2	S	S	S	N
3	S	S	N	S
4	S	S	N	N
5	S	N	S	S
6	S	N	S	N
7	S	N	N	S
8	S	N	N	N
9	N	S	S	S
10	N	S	S	N
11	N	S	N	S
12	N	S	N	N
13	N	N	S	S
14	N	N	S	N
15	N	N	N	S

where N is native DNA sequence and S is a synthetic DNA sequence.

6. A genome having a connectron comprised of the native DNA elements T1 and T2, wherein none, one or both of said DNA elements have been replaced with a synthetic DNA element

according to the following table and where the C1 and C2 sequences are generated by the binding of a synthetic DBP according to the following table

Type	C1	C2	T1	T2
1	D	D	S	S
2	D	D	S	N
3	D	D	N	S
4	D	D	N	N

where N is native DNA sequence, S is a synthetic DNA sequence and D is a synthetic DBP.

7. A genome having a connectron comprised of the native DNA elements T1 and T2, wherein none, one or both of said DNA elements have been replaced with a synthetic DNA element according to the following table and where the C1 and C2 sequences are generated by the binding of a synthetic PNA according to the following table

Type	C1	C2	T1	T2
1	P	P	S	S
2	P	P	S	N
3	P	P	N	S
4	P	P	N	N

where N is native DNA sequence, S is a synthetic DNA sequence and P is a synthetic PNA.

8. A genome having a connectron comprised of the native DNA elements T1 and T2, wherein none, one or both of said DNA elements has been replaced with a synthetic DNA element according to the following table and where the C1 and C2 sequences are generated by the binding a linked pair of DNA binding elements G1 and G2 according to the following table

Type	C1	C2	T1	T2
1	G1	G2	S	S
2	G1	G2	S	N
3	G1	G2	N	S
4	G1	G2	N	N

where N is native DNA sequence, S is a synthetic DNA sequence and where G1 and G2 are a linked pair of double-strand DNA binding elements.

9. A genome having a connectron comprised of the native DNA elements C1, C2, T1 and T2, wherein one of said DNA elements has been replaced with a synthetic DNA element according to the following table

Type	Element-1-Style
1	C
2	E

where C is a copied sequence element, E is an extracted sequence element.

10. A genome having a connectron comprised of the native DNA elements C1, C2, T1 and T2, wherein two of said DNA elements have been replaced with a synthetic DNA element according to the following table

	Element-1		Element-2	
Type	Type	Style	Type	Style
1	C1	C	C2	C
2	C1	C	C2	E
3	C1	E	C2	E
4	C1	C	T1	C
5	C1	C	T1	E
6	C1	U	T1	U
7	C1	E	T2	E
8	C2	C	T2	C
9	C2	C	T2	E
10	C2	U	T2	U
11	C2	E	T2	E
12	T1	C	T2	C
13	T1	C	T2	E
14	T1	E	T2	E

where C is a copied sequence element, U is a unique sequence element and E is an extracted sequence element.

11. A genome having a connectron comprised of the native DNA elements C1, C2, T1 and T2, wherein three of said DNA elements have been replaced with a synthetic DNA element according to the following table

	Element-1		Element-2		Element-3	
Type	Type	Style	Type	Style	Type	Style
1	C1	C	C2	C	T1	C
2	C1	C	C2	C	T1	E
3	C1	C	C2	E	T1	C
4	C1	C	C2	E	T1	E
5	C1	U	C2	C	T1	U
6	C1	U	C2	U	T1	E
7	C1	U	C2	E	T1	U
8	C1	E	C2	C	T1	C
9	C1	E	C2	C	T1	E
10	C1	E	C2	E	T1	C
11	C1	E	C2	E	T1	E
12	C1	C	C2	C	T2	C
13	C1	C	C2	C	T2	E
14	C1	C	C2	U	T2	U
15	C1	C	C2	E	T2	C
16	C1	C	C2	E	T2	E
17	C1	E	C2	C	T2	C
18	C1	E	C2	C	T2	E
19	C1	E	C2	U	T2	U
20	C1	E	C2	E	T2	C
21	C1	E	C2	E	T2	E
22	C1	C	T1	C	T2	C
23	C1	C	T1	C	T2	E
24	C1	C	T1	E	T2	C
25	C1					E

26	C1	U	T1	U	T2	C
27	C1	U	T1	U	T2	E
28	C1	E	T1	C	T2	C
29	C1	E	T1	C	T2	E
30	C1	E	T1	E	T2	C
31	C1	E	T1	E	T2	E
32	C2	C	T1	C	T2	C
33	C2	C	T1	C	T2	E
34	C2	C	T1	E	T2	C
35	C2	C	T1	E	T2	E
36	C2	U	T1	C	T2	U
37	C2	U	T1	E	T2	U
38	C2	E	T1	C	T2	C
39	C2	E	T1	C	T2	E
40	C2	E	T1	E	T2	C
41	C2	E	T1	E	T2	E

where C is a copied sequence element, U is a unique sequence element and E is an extracted sequence element.

12. A genome having a connectron comprised of the native DNA elements C1, C2, T1 and T2, wherein four of said DNA elements have been replaced with a synthetic DNA element according to the following table

	C1	C2	T1	T2
Type	Style	Style	Style	Style
1	C	C	C	C
2	C	C	C	E
3	C	C	E	C
4	C	C	E	E
5	C	U	C	U
6	C	U	E	U
7	C	E	C	C
8	C	E	C	E
9	C	E	E	C
10	C	E	E	E
11	U	C	U	C
12	U	C	U	E
13	U	U	U	U
14	U	E	U	C
15	U	E	U	E
16	E	C	C	C
17	E	C	C	E
18	E	C	E	C
19	E	C	E	E
20	E	U	C	U
21	E	U	E	U
22	E	E	C	C
23	E	E	C	E
24	E	E	E	C
25	E			

where C is a copied sequence element, U is a unique sequence element and E is an extracted sequence element.