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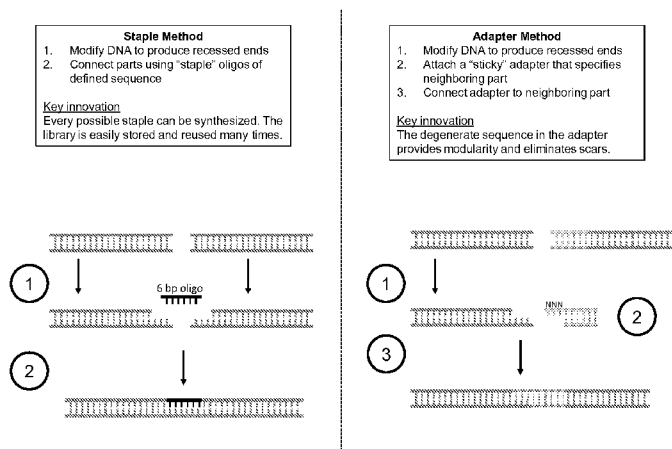
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(54) Title: METHODS FOR MULTIPART, MODULAR AND SCARLESS ASSEMBLY OF DNA MOLECULES

Figure 1

MMS Assembly

Multipart, Modular and Scarless Assembly



(57) Abstract: The present invention consists of methods for joining DNA molecules (parts) together to form larger DNA molecules (assemblies) of specified sequence and organization. The invention exhibits three necessary characteristics. Firstly, the invention enables 2 or more parts to be joined in a single reaction. Secondly, the seam between joined parts is scarless, producing no residual sequence dependencies like restriction enzyme recognition sites. Thirdly, parts are modular and can easily be reused in novel assemblies without modification. Prior technologies have exhibited no more than two of the three necessary characteristics, limiting their utility in synthesizing and editing DNA molecules of arbitrary sequence.

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## **METHODS FOR MULTIPART, MODULAR AND SCARLESS ASSEMBLY OF DNA MOLECULES**

### **PRIORITY**

**[001]** The present application claims priority to, and the benefit of, US Provisional Application No. 61/670,061 filed July 10, 2012, and US Provisional Application No. 61/789,032 filed March 15, 2013, each of which is hereby incorporated by reference in its entirety.

### **FIELD OF THE INVENTION**

**[002]** The present invention relates to methods for multipart, modular and scarless assembly of nucleic acids, including for high-throughput, automated, and/or large scale engineering of biological systems.

### **BACKGROUND**

**[003]** A key concept within synthetic biology is that biological DNA parts can be standardized, abstracted, and combined to produce complex, engineered systems. Parts are routinely generated via cloning from the DNA of organisms or using DNA synthesis. However, assembling parts into complex systems remains a key bottleneck in the synthetic biology workflow.

**[004]** Numerous technologies have been developed to facilitate DNA assembly, yet none provide a robust solution. (See, e.g., U.S. Patent Application No. 2010/0035768, U.S. Patent Application No. US 2012/0040870; Engler C. et al., *A One Pot, One Step, Precision Cloning Method with High Throughput Capability*, PLoS ONE 3(11):e3647 (2008), doi:10.1371/journal.pone.0003647; Weber E., et al., *A Modular Cloning System for Standardized Assembly of Multigene Constructs*. PLoS ONE 6(2):e16765 (2011), doi:10.1371/journal.pone.0016765; and Ellis, T., et al. *DNA assembly for synthetic biology: from parts to pathways and beyond*, Integr. Biol., 3:109-118 (2011), DOI: 10.1039/C0IB00070A 2; and information found on the World Wide Web at [j5.jbei.org/j5manual/pages/1.html](http://j5.jbei.org/j5manual/pages/1.html); all of which are incorporated by reference herein in their entireties.)

**[005]** There remains a need in the synthetic biology field by which biological DNA parts can be routinely combined, and at high-throughput, to produce complex, engineered systems. The present invention meets these objectives.

### **SUMMARY OF THE INVENTION**

**[006]** The present invention provides for multipart, modular and scarless nucleic acid assembly in vitro. In some embodiments, the DNA assembly reactions, which can proceed in parallel and series, are designed computationally based on a desired sequence. For example, the nucleic acid assembly may involve a plurality of reactions in parallel and/or in series that are designed in silico for accurate, cost-effective engineering of biological systems. In some embodiments the methods and kits described herein can be employed with high-throughput, automated processing systems.

**[007]** In some embodiments, the invention provides a method for constructing a scarless nucleic acid molecule comprising a plurality of heterologous parts. Nucleases and nucleic acid staples or adaptors are selected, as described herein, to assemble the heterologous parts into a scarless nucleic acid molecule. Nuclease and ligation reactions can take place in parallel and/or in series, as needed for optimum control of the process. The process can be controlled computationally by user inputs, with reaction assembly and processing taking place by automation.

**[008]** In some embodiments, the method comprises generating a first nucleic acid molecule having a single stranded terminus, generating a second nucleic acid molecule having a single stranded terminus, and then ligating the first and second nucleic acid molecules with the aid of an intervening linker molecule such that the ligation product corresponds to the combined sequence of the first and second nucleic acid molecules. In some embodiments, the nucleic acid molecule is a DNA molecule. An algorithm can be employed to computationally determine, identify and/or optimize any of the parts, enzymes and/or other reagents to be employed with the present methods.

**[009]** Scarless nucleic acid assembly according to the methods of the present invention requires two classes of enzymes. The first enzyme catalyzes the formation of short (about 1 bp to 8 bp), single stranded 5'-overhangs on a nucleic acid. The second enzyme catalyzes the formation of short (about 1 bp to 8 bp), single stranded

3'-overhangs on a nucleic acid. Each of these enzymes and overhang size can be independently selected, and can be a Type II restriction enzyme in some embodiments.

**[0010]** In some embodiments, the linker is a staple. A staple may be single stranded and can be DNA or RNA. In some embodiments, the staple is a defined sequence capable of binding with perfect complementarity to the single stranded DNA termini generated on the first and second DNA molecules. In some embodiments, the staple binds to a single stranded DNA terminus with a 3'-overhang on a first DNA molecule and a single stranded DNA terminus with a 5'-overhang on a second DNA molecule. In some embodiments, the staple binds to a single stranded DNA terminus with a 5'-overhang on a first DNA molecule and a single stranded DNA terminus with a 3'-overhang on a second DNA molecule.

**[0011]** In some aspects, the present invention provides a plurality of reaction mixtures for performing one and/or a series of reaction mixtures for scarless nucleic acid assembly.

### **BRIEF DESCRIPTION OF THE DRAWINGS**

**[0012]** **Figure 1:** Schematic diagram showing Staple Implementation and Adapter Implementation for multipart, modular and scarless assembly (MMS).

**[0013]** **Figure 2: Assembly of two DNA parts using a “staple” linker.** Two input DNA parts each with a size of 250bp and 400bp are ligated together to form a 650bp product. Lane 1: 100 bp NEB DNA ladder. Lane 2: Input DNA only. Lane 3: Input DNA (without oligonucleotide “staple”) after ligation reaction. Lane 4: Input DNA + oligonucleotide staple after ligation reaction.

**[0014]** **Figure 3: Assembly of two DNA parts using an “adapter” linker.** Lane 1: 1kb NEB ladder. Lane 2: Two input DNA parts of sizes 1800 bp and 300 bp are assembled to form a 2100 bp product. Lane 3: Two input DNA parts of sizes 700 bp and 1800 bp are assembled to form a 2500 bp product.

**[0015]** **Figure 4: Isothermal Scarless Subcloning.** Reaction mixture containing T4 ligase buffer, T7 DNA ligase, BsaI and BsaXI, and DNA parts. Isothermal reaction was performed at 37°C for 1hr. Colony PCRs and sequencing show 11 of 12 clones assembled correctly.

**[0016]**            **Figure 5: Scarless Assembly of Multiple Parts.** Reaction mixture containing T4 ligase buffer, T7 DNA ligase, Bsal and BstXI, and DNA parts. Isothermal reaction was performed at 37°C for 8hr. Colony PCRs and sequencing show 6 of 12 clones assembled correctly.

**[0017]**            **Figure 6: Multiplex Assembly in One Tube.** Reaction mixture containing T4 ligase buffer, T7 DNA ligase, Bsal and BstXI, and DNA parts. Isothermal reaction was performed at 37°C for 8hr. Colony PCRs and sequencing show 23 of 24 clones assembled correctly.

### **DETAILED DESCRIPTION OF THE INVENTION**

**[0018]**            The present invention provides for multipart, modular and scarless nucleic acid assembly in vitro. In some embodiments, the DNA assembly reactions, which can proceed in parallel and series, are designed computationally based on a desired sequence. For example, the nucleic acid assembly may involve a plurality of reactions in parallel and/or in series that are designed in silico for accurate, cost-effective engineering of biological systems. In some embodiments the methods and kits described herein can be employed with high-throughput, automated processing systems.

**[0019]**            The term “scarless” refers to the fact that no changes or undesired sequences are introduced into assembled DNA by the reactions. The combined sequence will correspond to the exact sequence desired with no changes being introduced by the restriction enzyme/ligation procedure. The combined sequence can correspond exactly to a natural sequence, an engineered sequence, a synthetic sequence or any other desired reference sequence.

**[0020]**            The term “modular” refers to the fact that prepared nucleic acid parts can be ligated with any other prepared nucleic acid parts without dependencies on the nucleic acid sequence of the two parts.

**[0021]**            The term “multipart” refers to the fact that two or more nucleic acid parts can be ligated in a single in vitro reaction.

**[0022]**            The term “reagent” can include any component of a reaction described herein. Reagents can include but are not limited to buffers, enzymes (e.g., nucleases, ligases) and nucleic acids (e.g., parts, linkers, staples). Nucleic acid reagents

can include one or more chemically modified bases, including for example but not limited to phosphorothioates, locked nucleic acids (LNAs), peptide nucleic acids (PNAs), 2'-OMe nucleotides, methylphosphonates or morpholinos, as well as any other modifications known in the art and that one of skill would find useful for the present methods.

**[0023]** Perfect or near perfect complementarity occurs when two nucleic acids regions of interest share about 100%, about 99%, about 98%, about 97%, about 96%, about 95%, about 94%, about 93%, about 92%, about 91%, about 90%, about 89%, about 88%, about 85%, about 80%, about 75%, or about 70% sequence identity, homology or complementarity to one another.

**[0024]** In some embodiments, the method provides for assembly of any desired nucleic acid molecule, including DNA or RNA, as well as modified DNA and RNA molecules (e.g., nucleic acids containing chemically modified bases, such as but not limited to phosphorothioates, locked nucleic acids (LNAs), peptide nucleic acids (PNAs), 2'-OMe nucleotides, methylphosphonates or morpholinos). In some embodiments, assembly is via high-throughput methods and in some embodiments, said high-throughput methods are automated. The resulting DNA molecules can be at least 1 kb in length, at least 10 kb in length, at least 100 kb in length, or over 500 kb in length, or over 1000 kb in length.

**[0025]** In some embodiments, the invention involves computational selection of the desired DNA parts, and/or desired reagents, as well as design of optimal parallel and/or series reactions for generating the desired DNA product.

**[0026]** In some embodiments, the invention provides a method for constructing a scarless nucleic acid molecule comprising 2 or more heterologous parts, such as 5 or more, 10 or more, 15 or more, 20 or more, 30 or more, 40 or more, 50 or more, or 100 or more heterologous parts. Nucleases and nucleic acid staples and/or adaptors are selected, as described herein, to assemble the heterologous parts into a scarless nucleic acid molecule by ligation. The restriction and ligation reactions can take place in parallel and/or in series, as needed for optimum control of the process. The process can be controlled computationally by user inputs, with reaction assembly and processing taking place by automation.

**[0027]** In some embodiments, the method comprises generating a first nucleic acid molecule having a single stranded terminus, generating a second nucleic

acid molecule having a single stranded terminus, and then ligating the first and second nucleic acid molecules with the aid of an intervening linker molecule such that the ligation product corresponds to the combined sequence of the first and second nucleic acid molecules. In some embodiments, the nucleic acid molecule is a DNA molecule. In some embodiments, an algorithm can be employed to computationally determine, identify and/or optimize any of the parts, enzymes and/or other reagents to be employed with the present methods. Ligation methods are well known in the art and any of these known ligation methods can be employed with the present invention.

**[0028]** In some embodiments, the first nucleic acid molecule or the second nucleic acid molecule have single stranded termini generated with a restriction enzyme. In some embodiments, the nucleic acid molecule is a DNA molecule.

**[0029]** Scarless nucleic acid assembly according to the methods of the present invention requires two classes of enzymes. The first enzyme catalyzes the formation of short (about 1 bp to 8 bp), single stranded 5'-overhangs on a nucleic acid. The second enzyme catalyzes the formation of short (about 1 bp to 8 bp), single stranded 3'-overhangs on a nucleic acid. Each of these enzymes and overhang size can be independently selected. In some embodiments, such restriction enzymes are selected from Type IIs, Type IIb, or Type IIp family enzymes. In some embodiments, in part in order to bypass constraints on nucleic acid sequences, the enzymes are selected from types that cleave the nucleic acid sequence at a position distal (about 1bp to 25bp) to the recognition site.

**[0030]** In some embodiments, the single stranded termini can include 5'-overhangs, 3'-overhangs which are independently selected. In some embodiments, the overhangs are independently selected from the following ranges: about 1 bp to 8 bp, about 2 bp to 8 bp, about 2 bp to 6 bp, about 3 bp to 6 bp, about 3 bp to 5 bp, about 2 bp to 6 bp, about 2 bp to 5 bp, about 1 bp to 5 bp, about 2 bp to 4 bp, about 1 bp to about 4 bp, about 1 bp to 3 bp or about 1 bp to 2 bp. In some embodiments, the overhangs are about 1 bp, 2 bp, 3 bp, 4 bp, 5 bp, 6 bp, 7 bp, or 8 bp or more in length.

**[0031]** In some embodiments, the restriction enzyme is a Type IIs restriction enzyme. The Type II restriction enzymes that find use with the methods of the present invention can generate a single stranded nucleic acid terminus with a 3'-overhang or a 5'-overhang. Enzyme properties can also be found on the World Wide Web at [rebase.neb.com](http://rebase.neb.com).

**Table 1: Type II restriction enzymes producing 5'-overhangs**

Length	Overhang	Enzymes	Recognition Sequence
1	N	BccI	CCATC (4/5)
1	N	BceFI	ACGGC (12/13)
1	N	BinI	GGATC (4/5)
1	N	EcoNI	CCTNN↓NNNAGG
1	N	Fnu4HI	GC↓NGC
1	N	PleI	GAGTC (4/5)
1	N	ScrFI	CC↓NGG
1	N	Tth111I	GACN↓NNGTC
1	S	CauI	CC↓SGG
1	W	BstNI	CC↓WGG
2	AT	Asi256I	G↓ATC
2	AT	CviAII	C↓ATG
2	CG	AccI	CCGC (-3/-1)
2	CG	AccI	AA↓CGTT
2	CG	AccI	GR↓CGYC
2	CG	AsuII	TT↓CGAA
2	CG	ClaI	AT↓CGAT
2	CG	HinP1I	G↓CGC
2	CG	HpaII	C↓CGG
2	CG	MaeII	A↓CGT
2	CG	NarI	GG↓CGCC
2	CG	TaqI	T↓CGA
2	MK	AccI	GT↓MKAC
2	NN	BceAI	ACGGC (12/14)
2	NN	BscAI	GCATC (4/6)
2	NN	BspD6I	GA CTC (4/6)
2	NN	FauI	CCCGC (4/6)
2	NN	Hpy178III	TC↓NNGA
2	TA	CviQI	G↓TAC
2	TA	MaeI	C↓TAG
2	TA	MseI	T↓TAA
2	TA	NdeI	CA↓TATG
2	TA	VspI	AT↓TAAT
3	ANT	HinFI	G↓ANTC
3	AWT	TfiI	G↓AWTC
3	CWG	PasI	CC↓CWGGG
3	CWG	TseI	G↓CWGC
3	GNC	AsuI	G↓GNCC
3	GNC	DraII	RG↓GNCCY
3	GTC	SimI	GGGTC (-3/0)
3	GWC	Avall	G↓GWCC
3	GWC	PpuMI	RG↓GWCCY
3	GWC	RsrII	CG↓GWCCG

3	GWC	SanDI	GG↓GWCCC
3	GWC	Sse8647I	AG↓GWCCT
3	NNN	Ksp632I	CTCTTC (1/4)
3	NNN	SapI	GCTCTTC (1/4)
3	TCA	BbvCI	CCTCAGC (-5/-2)
3	TNA	Bpu10I	CCTNAGC (-5/-2)
3	TNA	DdeI	C↓TNAG
3	TNA	EspI	GC↓TNAGC
3	TNA	SauI	CC↓TNAGG
4	AATT	ApoI	R↓AATTY
4	AATT	EcoRI	G↓AATTC
4	AATT	MfeI	C↓AATTG
4	AATT	TspEI	↓AATT
4	ACGA	BsiI	CACGAG (-5/-1)
4	AGCT	HindIII	A↓AGCTT
4	CATG	BspHI	T↓CATGA
4	CATG	BspLU11I	A↓CATGT
4	CATG	FatI	↓CATG
4	CATG	NcoI	C↓CATGG
4	CCAG	BseYI	CCCAGC (-5/-1)
4	CCGG	AgeI	A↓CCGGT
4	CCGG	BclI	W↓CCGGW
4	CCGG	BspMII	T↓CCGGA
4	CCGG	Cfr10I	R↓CCGGY
4	CCGG	Eco56I	G↓CCGGC
4	CCGG	SgrAI	CR↓CCGGYG
4	CCGG	Sse232I	CG↓CCGGCG
4	CCGG	XmaI	C↓CCGGG
4	CGCG	AscI	GG↓CGCGCC
4	CGCG	BsePI	G↓CGCGC
4	CGCG	MauBI	CG↓CGCGCG
4	CGCG	MluI	A↓CGCGT
4	CGCG	SelI	↓CGCG
4	CNNG	SecI	C↓CNNGG
4	CRYG	AflIII	A↓CRYGT
4	CRYG	DsaI	C↓CRYGG
4	CTAG	AvrII	C↓CTAGG
4	CTAG	NheI	G↓CTAGC
4	CTAG	SpeI	A↓CTAGT
4	CTAG	XbaI	T↓CTAGA
4	CWWG	StyI	C↓CWWGG
4	GATC	BamHI	G↓GATCC
4	GATC	BclI	T↓GATCA
4	GATC	BglII	A↓GATCT
4	GATC	MboI	↓GATC
4	GATC	XhoI	R↓GATCY

4	GCGC	KasI	G↓GCGCC
4	GGCC	Bsp120I	G↓GGCCC
4	GGCC	CfrI	Y↓GGCCR
4	GGCC	GdIII	CGGCCR (-5/-1)
4	GGCC	NotI	GC↓GGCCGC
4	GGCC	XmaIII	C↓GGCCG
4	GTAC	Asp718I	G↓GTACC
4	GTAC	Bsp1407I	T↓GTACA
4	GTAC	SplI	C↓GTACG
4	GTAC	TatI	W↓GTACW
4	GYRC	HgiCI	G↓GYRCC
4	NNNN	AarI	CACCTGC (4/8)
4	NNNN	AclII	CAGCTC (7/11)
4	NNNN	Bbr7I	GAAGAC (7/11)
4	NNNN	BbvI	GCAGC (8/12)
4	NNNN	BbvII	GAAGAC (2/6)
4	NNNN	BsmAI	GTCTC (1/5)
4	NNNN	BsmFI	GGGAC (10/14)
4	NNNN	BspMI	ACCTGC (4/8)
4	NNNN	BtgZI	GCGATG (10/14)
4	NNNN	Eco31I	GGTCTC (1/5)
4	NNNN	Esp3I	CGTCTC (1/5)
4	NNNN	FokI	GGATG (9/13)
4	NNNN	SfaNI	GCATC (5/9)
4	NNNN	Sth132I	CCCG (4/8)
4	NNNN	StsI	GGATG (10/14)
4	TCGA	AbsI	CC↓TCGAGG
4	TCGA	PspXI	VC↓TCGAGB
4	TCGA	SalI	G↓TCGAC
4	TCGA	SgrDI	CG↓TCGACG
4	TCGA	XhoI	C↓TCGAG
4	TGCA	ApaLI	G↓TGCAC
4	TGCA	Ppu10I	A↓TGCAT
4	TRYA	SfeI	C↓TRYAG
4	TTAA	AflII	C↓TTAAG
4	TYRA	SmlI	C↓TYRAG
4	YCGR	AvaI	C↓YCGRG
5	CCNGG	PfoI	T↓CCNGGA
5	CCNGG	SsoII	↓CCNGG
5	CCSGG	EcoHI	↓CCSGG
5	CCWGG	EcoRII	↓CCWGG
5	CCWGG	SexAI	A↓CCWGGT
5	GGNCC	UnbI	↓GGNCC
5	GGWCC	VpaK11AI	↓GGWCC
5	GTNAC	BstEII	G↓GTNACC
5	GTNAC	MaellI	↓GTNAC

5	GTSAC	Tsp45I	↓GTSAC
5	NNNNN	HgaI	GACGC (5/10)

**Table 2: Type II restriction enzymes producing 3'-overhangs**

Length	Overhang	Enzymes	Recognition Sequence
1	N	BciVI	GTATCC (6/5)
1	N	BfiI	ACTGGG (5/4)
1	N	Eam1105I	GACNNN↓NNGTC
1	N	Hin4II	CCTTC (6/5)
1	N	HphI	GGTGA (8/7)
1	N	Hpy188I	TCN↓GA
1	N	MbolI	GAAGA (8/7)
1	N	MnlI	CCTC (7/6)
1	N	Tsp4CI	ACN↓GT
1	N	XcmI	CCANNNNN↓NNNNTGG
1	S	AgeI	TTS↓AA
2	AT	BspKT6I	GAT↓C
2	AT	PacI	TTAAT↓TAA
2	AT	PvuI	CGAT↓CG
2	AT	SgfI	GCGAT↓CGC
2	CG	HhaI	GCG↓C
2	CN	BsmI	GAATGC (1/-1)
2	GC	McaTI	GCGC↓GC
2	GC	SacII	CCGC↓GG
2	GN	BsrI	ACTGG (1/-1)
2	NN	ApyPI	ATCGAC (20/18)
2	NN	AquII	GCCGNAC (20/18)
2	NN	AquIII	GAGGAG (20/18)
2	NN	AquIV	GRGGAAG (19/17)
2	NN	Bce83I	CTTGAG (16/14)
2	NN	BsbI	CAACAC (21/19)
2	NN	BseMII	CTCAG (10/8)
2	NN	BseRI	GAGGAG (10/8)
2	NN	BsgI	GTGCAG (16/14)
2	NN	BspCNI	CTCAG (9/7)
2	NN	BsrDI	GCAATG (2/0)
2	NN	BstF5I	GGATG (2/0)
2	NN	BtsI	GCAGTG (2/0)
2	NN	BtsIMutI	CAGTG (2/0)
2	NN	CchII	GGARGA (11/9)
2	NN	CchIII	CCCAAG (20/18)
2	NN	Cdpl	GCGGAG (20/18)
2	NN	CjeNI	GKAAYG (19/17)
2	NN	CstMI	AAGGAG (20/18)

2	NN	DraRI	CAAGNAC (20/18)
2	NN	DrdI	GACNNNN↓NNGTC
2	NN	Ecil	GGCGGA (11/9)
2	NN	Eco57I	CTGAAG (16/14)
2	NN	Eco57MI	CTGRAG (16/14)
2	NN	Gsul	CTGGAG (16/14)
2	NN	HauI	TGGCCANNNNNNNNNN↓
2	NN	MaqI	CRTTGAC (21/19)
2	NN	MmeI	TCCRAC (20/18)
2	NN	NlaCI	CATCAC (19/17)
2	NN	NmeAIII	GCCGAG (21/19)
2	NN	PlaDI	CATCAG (21/19)
2	NN	PspOMII	CGCCCAR (20/18)
2	NN	PspPRI	CCYCAG (15/13)
2	NN	RceI	CATCGAC (20/18)
2	NN	RdeGBII	ACCCAG (20/18)
2	NN	RpaI	GTYGGAG (11/9)
2	NN	RpaBI	CCCGCAG (20/18)
2	NN	RpaB5I	CGRGGAC (20/18)
2	NN	SdeAI	CAGRAG (21/19)
2	NN	SstE37I	CGAAGAC (20/18)
2	NN	TaqII	GACCGA (11/9)
2	NN	TsoI	TARCCA (11/9)
2	NN	TspDTI	ATGAA (11/9)
2	NN	TspGWI	ACGGA (11/9)
2	NN	Tth111II	CAARCA (11/9)
2	NN	WviI	CACRAG (21/19)
2	RY	McrI	CGRY↓CG
2	TA	PabI	GTA↓C
3	CNG	BthCI	GCNG↓C
3	CSG	TauI	GCSG↓C
3	GNC	FmuI	GGNC↓C
3	GNC	PssI	RGGNC↓CY
3	GWC	Psp03I	GGWC↓C
3	NNN	AlwNI	CAGNNN↓CTG
3	NNN	BglI	GCCNNNN↓NGGC
3	NNN	BsiYI	CCNNNNN↓NNGG
3	NNN	BstAPI	GCANNNN↓NTGC
3	NNN	DraIII	CACNNN↓GTG
3	NNN	MwoI	GCNNNNN↓NNGC
3	NNN	PfiMI	CCANNNN↓NTGG
3	NNN	RleAI	CCCACA (12/9)
3	NNN	SfiI	GGCCNNNN↓NGGCC
4	ACGT	AatII	GACGT↓C
4	ACGT	TaiI	ACGT↓
4	AGCT	SacI	GAGCT↓C

4	ASST	SetI	ASST↓
4	CATG	NlaIII	CATG↓
4	CATG	NspI	RCATG↓Y
4	CATG	SphI	GCATG↓C
4	CCAG	GsaI	CCCAGC (-1/-5)
4	CCGG	FseI	GGCCGG↓CC
4	CTAG	AclI	GCTAG↓C
4	DGCH	SduI	GDGCH↓C
4	GATC	Chai	GATC↓
4	GCGC	BbeI	GGCGC↓C
4	GCGC	HaeIII	RGCGC↓Y
4	GGCC	ApaI	GGGCC↓C
4	GTAC	KpnI	GGTAC↓C
4	KGCM	BseSI	GKGCM↓C
4	NNNN	BstXI	CCANNNNN↓NTGG
4	RGCY	HgiIII	GRGCY↓C
4	TGCA	EcoT22I	ATGCA↓T
4	TGCA	PstI	CTGCA↓G
4	TGCA	Sse8387I	CCTGCA↓GG
4	WGCW	HgiAI	GWGCW↓C
4	YCGR	Nli3877I	CYCGR↓G
5	CGWCG	Hpy99I	CGWCG↓
5	NNNNN	ApaBI	GCANNNNN↓TGC
9	NNCASTGNN	TspRI	CASTGNN↓

**[0032]** The standard IUPAC nucleic acid codes are shown in Table 3 below:

**Table 3: IUPAC nucleic acid codes**

IUPAC nucleotide code	Base
A	Adenine
C	Cytosine
G	Guanine
T (or U)	Thymine (or Uracil)
R	A or G
Y	C or T
S	G or C
W	A or T
K	G or T
M	A or C
B	C or G or T
D	A or G or T
H	A or C or T

V	A or C or G
N	any base

**[0033]** In some embodiments, the restriction enzymes do not have a specific recognition sequence.

**[0034]** In some embodiments, the Type II restriction enzyme that generates a single stranded DNA with a 3'-overhang can include but is not limited to BsaXI (Type IIb), BstXI (Type IIp), R1eAI (Type IIs) or TstI (Type IIb).

**[0035]** In some embodiments, the Type IIs restriction enzyme that generates a single stranded DNA with a 3'-overhang can include but is not limited to R1eAI.

**[0036]** In some embodiments, the Type IIb restriction enzyme that generates a single stranded DNA with a 3'-overhang can include but is not limited to BsaXI.

**[0037]** In some embodiments, the Type IIp restriction enzyme that generates a single stranded DNA with a 3'-overhang can include but is not limited to BstXI.

**[0038]** In some embodiments, the Type IIs restriction enzyme that generates a single stranded DNA with a 5'-overhang can include but is not limited to EarI, BspMI, BsaI, BbsI, or BsmBI.

**[0039]** In some embodiments, the first DNA molecule or the second DNA molecule have single stranded termini generated with an exonuclease.

**[0040]** In some embodiments, the exonuclease that generates single stranded DNA with a 3'-overhang can include but is not limited to T7 exonuclease, T5 exonuclease, or Lambda exonuclease.

**[0041]** In some embodiments, the exonuclease acts on DNA parts that were created via PCR with primers containing phosphorothioate bonds. Primers can also contain other chemically modified bases, such as but not limited to phosphorothioates, locked nucleic acids (LNAs), peptide nucleic acids (PNAs), 2'-OMe nucleotides, methylphosphonates or morpholinos.

**[0042]** In some embodiments, the first DNA molecule or the second DNA molecule have single stranded termini generated with an endonuclease and a second enzyme.

**[0043]** In some embodiments, the endonuclease that generates single stranded DNA with a 3'-overhang can include but is not limited to DNA glycosylase-lyase endonuclease VIII. In some embodiments, the second enzyme used in concert with DNA glycosylase-lyase endonuclease VIII to generate single stranded termini can include but is not limited to uracil DNA glycosylase (UDG).

**[0044]** In some embodiments, the single stranded terminus on one DNA molecule is a 3'-overhang and the single stranded terminus on the other DNA molecule is a 5'-overhang. In some embodiments, the first and second DNA molecules can be ligated using a single stranded DNA (ssDNA) linker (staple).

**[0045]** In some embodiments, the linker is a staple. A staple may be single stranded and can be DNA or RNA. In some embodiments, the staple is a defined sequence capable of binding with perfect complementarity to the single stranded DNA termini generated on the first and second DNA molecules. In some embodiments, the staple binds to a single stranded DNA terminus with a 3'-overhang on a first DNA molecule and a single stranded DNA terminus with a 5'-overhang on a second DNA molecule. In some embodiments, the staple binds to a single stranded DNA terminus with a 5'-overhang on a first DNA molecule and a single stranded DNA terminus with a 3'-overhang on a second DNA molecule.

**[0046]** In some embodiments, the staple is an oligonucleotide between about 4 and about 20 nucleotides in length, and in some embodiments between about 4 nucleotides and about 16 nucleotides, in some embodiments between about 4 nucleotides and about 12 nucleotides, and in some embodiments about 4 nucleotides to about 10 nucleotides in length. In some embodiments, the staple is single stranded DNA or RNA.

**[0047]** In some embodiments, the present invention provides a plurality of reaction mixtures. The reaction mixtures include 1) a first reaction mixture comprising DNA molecules and a restriction enzyme capable of generating a 5' single stranded DNA terminus for use with the methods of the present invention, 2) a second reaction mixture comprising DNA molecules and a restriction enzyme capable of generating a 3' single

stranded DNA terminus for use with the methods of the present invention, and 3) a third reaction in which the products of the first two reactions are pooled together with a staple linker and ligated. In some embodiments, the first reaction mixture generates a single stranded DNA terminus that is the opposite orientation of the single stranded terminus generated by the second reaction mixture (*i.e.*, one reaction generates a terminus with a 3'-overhang and one reaction generates a terminus with a 5'-overhang). In some embodiments, the single stranded termini generated by both the first and second reaction mixtures are complementary to the staple. In some embodiments, the staple in the reaction mixture contains a defined sequence capable of binding with perfect complementarity to the single stranded terminus generated by the first and second reaction mixtures. In some embodiments, the reaction mixture can contain a staple that is an oligonucleotide between 4 and 10 nucleotides in length, between 4 and 8 nucleotides, or between 6 and 10 nucleotides.

**[0048]** In some embodiments, the first DNA molecule has a single stranded terminus and the second DNA molecule has a single stranded terminus that are each ligated to an intervening double stranded DNA (dsDNA) linker (adapter).

**[0049]** In some embodiments, the linker is an adapter. An adapter is double stranded and can be DNA or RNA. In some embodiments, the adapter contains at least one single stranded terminus containing a degenerate sequence. In some embodiments, the adapter is comprised of oligonucleotides between at least about 5 bp and about 500 bp in length or more, in some embodiments between about 5 bp and about 300 bp, in some embodiments between about 5 bp and about 200 bp and in some embodiments between about 5 bp and 100 bp.

**[0050]** In some embodiments, the single stranded terminus of the adapter is ligated to a 3' or 5'-overhang of one DNA molecule. In some embodiments, a second single stranded terminus of the adapter is ligated to the 3' or 5'-overhang of a second DNA molecule. The second single stranded terminus of the adapter can be generated prior to or after ligation of the adapter to the first DNA molecule.

**[0051]** In some embodiments, the present invention provides a plurality of reaction mixtures. The reaction mixtures include 1) a first reaction mixture comprising DNA molecules and enzyme(s) capable of generating a 3' or 5' single stranded DNA terminus for use with the methods of the present invention, 2) a second reaction mixture of the same nature as the first reaction but comprising different DNA molecules for use

with the methods of the present invention, 3) a third reaction mixture in which the product of the first reaction is ligated to an adapter that contains a degenerate single stranded terminus, 4) a fourth reaction in which the product of the third reaction is pooled with the product of the second reaction and ligated. In some embodiments, the second reaction mixture generates a single stranded DNA terminus that is complementary to the single stranded terminus of the adapter. In some embodiments, the single stranded termini generated by the first reaction mixtures are complementary to the adapter. In some embodiments, the reaction mixture can contain an adapter with a single stranded terminus that contains a degenerate sequence capable of binding to a single stranded DNA terminus complementary to the single stranded DNA terminus generated by the first reaction mixture. In some embodiments, the reaction mixture can contain an adapter that is between 5 and 100 bp in length.

**[0052]** The methods of the present invention can be repeated as tandem steps to assemble final ligation products that contain at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 30, 40, 50, 70, 100 or more starting molecules, such as DNA or RNA molecules.

**[0053]** The present invention can be employed to assemble, for example plasmids, cosmids, and genomes, of novel sequence. The utility of engineered and synthetic DNA can be found throughout life sciences. In some embodiments, the methods of the present invention generate nucleic acid molecules that are linear or circular. Molecules generated by the methods of the present invention can include but are not limited to plasmids, cosmids, operons, genes, synthetic genes, complete genes, partial genomes, complete genomes, partial synthetic genomes, and complete synthetic genomes. Molecules generated by the methods of the present invention can also include naturally occurring pathway components or synthetically derived pathway components.

**[0054]** In some embodiments, the assembly of the desired nucleic acid molecule can be performed in a single step. In some embodiments, the step is a single isothermal step. According to the present methods, the nucleic acid portions of the invention desired to be assembled are combined with appropriate staples and an assembly buffer to form a reaction mixture. The assembly buffer can include for example, the desired restriction and ligase enzymes necessary to assemble the nucleic acid. In some embodiments, the assembly buffer includes restriction enzymes (at least one 5'-overhang-generating enzyme and at least one 3'-overhang-generating enzyme) and DNA ligase (e.g., T7 DNA ligase). The reaction mixture can then be incubated at a single

temperature reaction (i.e., isothermal reaction) that allows for digestion, annealing and ligation steps. In some embodiments the temperature is about 30°C to about 50°C, about 30°C to about 40°C, about 37°C to about 42°C, about 37°C or about 42°C. In some embodiments, the reaction mixture is incubated at 37°C and all necessary digestion, annealing and ligation steps occur to assemble DNA and/or RNA molecules together. In some embodiments, at least about 2 to 100 or more DNA and/or RNA molecules are assembled in a isothermal reaction. In some embodiments at least about 2 to about 100, about 2 to 70, about 2 to 50, about 2 to 20, about 2 to about 12, about 2 to about 10, about 2 to about 8, about 2 to 6, about 2 to 4 or about 2 DNA and/or RNA molecules are assembled in an isothermal reaction. In some embodiments, at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 30, 40, 50, 70, 100 DNA and/or RNA molecules are assembled in an isothermal reaction.

**[0055]** The methods of the present invention further provide for the ability to multiplex different assemblies within the same reaction vessel. Multiple reactions can be carried out in the same buffer due to the specificity afforded by each staple. As a result, assembly reagents can be minimized while increasing the productivity of an assembly process.

**[0056]** In some embodiments, the DNA molecules generated by the present invention can be transformed or transfected into a variety of cells, including but not limited to bacteria, insect and mammal cells. The DNA molecules of the present invention can also be inserted into viruses or virus-like particles. Transfection and transformation methods are well known in the art and any standard methods can be employed with the present invention.

**[0057]** The selection of nucleic acid parts, restriction enzymes, and staples, as well as the individual reaction assemblies and/or reagents employed therein, can be determined computationally, taking into account a variety of parameters, including logistical, cost and biophysical parameters. For example, the reaction assemblies and assembly routes can be guided by limitations or parameters for enzymes or other reagents, as experimentally-derived or known from the literature, and/or guided by cost, availability, or compatibility of the various reagents.

**[0058]** Parameters can include logistical parameters. In some embodiments, logistical parameters for designing the assembly route include logistical considerations such as part availability or historical performance metrics. Part availability

can include availability of nucleic acid sequences, restriction enzymes, buffers, or any other reagent employed with the multipart, modular and scarless assembly described herein. Historical performance can include but is not limited to compatibility of reagents, efficiency of reagents, and/or specificity of reagents.

**[0059]** Parameters can include financial parameters. In some embodiments, financial parameters may address part cost, manipulation, reagents, and/or overhead. Consideration of financial parameters may determine that certain optimal parts should be synthesized by de novo nucleic acid synthesis (rather than scarless assembly).

**[0060]** Parameters can also include functional or biophysical parameters. Ligation conditions and/or enzymatic digestion conditions are exemplary functional parameters. In some embodiments, an algorithm selects nucleic acid parts based on desired functional properties of the desired sequence. For instance, the algorithm can select DNA parts that encode promoters, ribosome binding sites, terminators, or other regulatory elements to elicit designed levels of gene expression.

**[0061]** In some embodiments, the method utilizes an algorithm to determine and/or optimize the steps for assembling a complex nucleic acid molecule, i.e., for assembly of a multipart, modular and scarless nucleic acid sequence. In some embodiments, the algorithm selects reaction reagents to ensure sufficient reaction efficiency and fidelity during multiplex reactions and across multiple rounds of nucleic acid assembly. Reaction efficiency and fidelity can be predicted from empirical and biophysical data, and can include selecting the number and composition of nucleic acid parts in each reaction. For example, empirical data might suggest a maximum of 5 nucleic acid parts per reaction based on ligation efficiency. In some exemplary embodiments, the algorithm would determine that a 10 part nucleic acid assembly be split into 3 reactions spanning 2 iterative rounds of assembly to produce the final nucleic acid molecule.

**[0062]** In some embodiments, ssDNA overhangs generated during assembly must be specific to ensure correct assembly. In some embodiments, the algorithm identifies incompatible ssDNA overhangs and separates component parts into different reactions in order to ensure specificity of assembly.

**[0063]** In some embodiments, the algorithm considers specifications and limitations of automation hardware when determining the required and/or optimal

assembly steps. Such specifications and/or limitations can include, for example, but are not limited to volume tolerances of a liquid handling robot, speed of execution, and throughput of the system.

**[0064]** The present invention also provides for kits. Kits contemplated by the methods of the of the present invention can include 1) a single stranded staple or a double stranded terminus adapter, 2) enzymes capable of generating single stranded DNA termini and 3) an instruction for use. In some embodiments, the kit comprises a DNA ligase, a 5'-overhang-generating enzyme, and a 3'-overhang-generating enzyme. In some embodiments, the kit comprises the enzymes capable of generating single stranded DNA termini and an appropriate buffer for enzyme function. In some embodiments, the kit comprises a standard set of staples. In some embodiments, the staples are not part of the kit. In some embodiments, the kit comprise a plurality of reaction mixtures. In some embodiments, the kit comprises a plurality of adapters and enzymes for performing a plurality of reactions.

**[0065]** In some embodiments, the kit further comprises an implementation of an algorithm as described herein, i.e. software for use according to the present methods.

**[0066]** In some embodiments, the enzyme in the kit for generating the 5'-overhang is selected from Type IIs, Type IIb or Type IIp restriction enzymes or combinations thereof, including those listed in Table 1. In some embodiments, the enzymes in the kit for generating the 5'-overhang is selected from Earl, BspMI, Bsal, BbsI, and BsmBI, or combinations thereof. In some embodiments, the enzyme in the kit for generating the 3'-overhang is selected from Type IIs, Type IIb or Type IIp restriction enzymes or combinations thereof, including those listed in Table 2. In some embodiments, the enzymes in the kit for generating the 3'-overhang is selected from BsaXI, RleAI, and TstI and combinations thereof.

## EXAMPLES

### **Example 1: Staple Method**

**[0067]** One example of the methods is the “Staple Method.” DNA parts are prepared by digestion with Type IIs restriction enzymes to generate termini with 5' and 3' single stranded DNA overhangs. Most Type IIs enzymes create short single stranded DNA overhangs (about 2 bp to 6bp). This results in a relatively small “gap” at the junction between two DNA parts. This “gap” can be filled by a defined oligonucleotide (*i.e.*, staple linker) that is perfectly complementary to the generated single stranded DNA overhangs. The oligonucleotide spans the junction and anneals to both the 5' single stranded DNA overhang of one part and the 3' single stranded DNA overhang of the other part. More than two DNA parts can be simultaneously joined together, and the order of assembly will be dictated by the sequence of the oligonucleotides provided in the reaction. See, for example, Figures 1 and 2.

**[0068]** The staple method can also be employed in performing isothermal scarless subcloning. For isothermal scarless subcloning, the reaction mixture contained T4 ligase buffer, T7 DNA ligase, BsaI and BsaXI, and DNA parts. The isothermal reaction was performed at 37°C for 1 hr. Colony PCRs and sequencing show that 11 of 12 clones assembled correctly. See, for example, Figure 4.

**[0069]** In another example, the reaction mixture contained T4 ligase buffer, T7 DNA ligase, BsaI and BstXI, and DNA parts. The isothermal reaction was performed at 37°C for 8 hr. Colony PCRs and sequencing show that 6 of 12 clones assembled correctly.

**[0070]** In a further example, performing the multiplex assembly in one tube, the reaction mixture contained T4 ligase buffer, T7 DNA ligase, BsaI and BstXI, and DNA parts. The isothermal reaction was performed at 37°C for 8 hr. Colony PCRs and sequencing show that 23 of 24 clones assembled correctly.

### **Example 2: Adapter Method**

**[0071]** A second example of the methods is the “Adapter Method.” A dsDNA adapter (*i.e.*, single stranded terminus adapter) is created for each part (linker paired part or LPP) such that it contains a single stranded DNA termini comprising degenerate bases, *e.g.* NNNN. The dsDNA sequence in the adapter can either duplicate the terminal sequence of the LPP, or it can serve as a replacement for the terminal sequence of the LPP. In the latter case, the LPP would be reconstructed to be a smaller size. In the

“Adapter Method,” DNA parts are modified with restriction enzymes to generate single stranded DNA termini. The adapter corresponding to the desired neighboring part is then ligated to the single stranded DNA termini. Finally, the adapter is joined to its LPP. In the accompanying example, we utilized the second class of assembly (exonuclease based) to ligate the adapter to its LPP. See, for example, Figures 1 and 3.

**[0072]** It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. It is understood that the disclosed invention is not limited to the particular methodology, protocols and materials described as these can vary. It is also understood that the terminology used herein is for the purposes of describing particular embodiments only and is not intended to limit the scope of the present invention which will be limited only by the appended claims. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the appended claims.

**[0073]** All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

**CLAIMS:**

1. A method for scarless assembly of two or more DNA molecules, said method comprising:  
generating a first DNA molecule having a single stranded terminus,  
generating a second DNA molecule having a single stranded terminus,  
ligating the first and second DNA molecules such that the ligation product corresponds to the combined sequence of the first and second DNA molecules.
2. The method of claim 1, wherein the following reactions are performed:
  - a. generating a first DNA molecule having a 5' single stranded overhang;
  - b. generating a second DNA molecule having a 3' single stranded overhang;
  - c. providing a short oligonucleotide staple linker containing perfect or near perfect complementarity to the 5' and 3'-overhangs; and
  - d. ligating the first DNA molecule, the second DNA molecule, and the staple linker.
3. The method of any of the preceding claims, wherein the 5' or 3' single stranded overhangs are generated with a restriction enzyme.
4. The method of any of the preceding claims, wherein a Type IIs restriction enzyme generates DNA with 3' single stranded overhangs.
5. The method of any of the preceding claims, wherein a Type IIb restriction enzyme generates DNA with 3' single stranded overhangs.
6. The method of any of the preceding claims, wherein a Type IIp restriction enzyme generates DNA with 3' single stranded overhangs.
7. The method of any of the preceding claims, wherein a Type IIs restriction enzyme generates DNA with 3' single stranded overhangs, and the Type IIs restriction enzyme is optionally RleAI.
8. The method of any of the preceding claims, wherein a Type IIb restriction enzyme generates DNA with 3' single stranded overhangs, and the Type IIb restriction enzyme is optionally BsaXI.

9. The method of any of the preceding claims, wherein a Type IIp restriction enzyme generates DNA with 3' single stranded overhangs, and the Type IIp restriction enzyme is optionally BstXI.
10. The method of any of the preceding claims, wherein the Type IIs restriction enzyme generates DNA with 5' single stranded overhangs.
11. The method of any of the preceding claims, wherein the Type IIs restriction enzyme generates DNA with 5' single stranded overhangs, and the Type IIs restriction enzyme is optionally selected from Earl, BspMI, Bsal, BbsI, or BsmBI.
12. The method of any of the preceding claims, wherein the single stranded DNA terminus with a 3' overhang is generated through the action of an exonuclease.
13. The method of any of the preceding claims, wherein the exonuclease digests DNA that was produced by PCR using oligos containing phosphorothioate bonds.
14. The method of any of the preceding claims, wherein the exonuclease is selected from T7 exonuclease, T5 exonuclease, or Lambda exonuclease.
15. The method of any of the preceding claims, wherein the single stranded DNA terminus with a 3'-overhang is generated through the action of uracil DNA glycosylase (UDG) and DNA glycosylase-lyase endonuclease VIII.
16. The method of any of the preceding claims, wherein the staple linker contains a defined sequence capable of binding with perfect or near perfect complementarity to the single stranded DNA termini of the first and second DNA molecules.
17. The method of any of the preceding claims, wherein the staple linker binds to both a single stranded terminus with a 3'-overhang and a single stranded terminus with a 5'-overhang.
18. The method of any of the preceding claims, wherein the single stranded terminus with a 3'-overhang and the single stranded terminus with a 5'-overhang are ligated together with the staple linker by a DNA ligase, and the DNA ligase enzyme is optionally selected from T4 DNA ligase, T7 DNA ligase, and Taq DNA ligase.

19. The method of any of the preceding claims, wherein the staple linker is an oligonucleotide of DNA, RNA, or modified DNA and RNA molecules between 4 and 20 nucleotides in length.
20. The method of any of the preceding claims, wherein the staple linker contains single stranded DNA, double stranded DNA, or combination thereof.
21. The method of any of the preceding claims, wherein the ligating step involves a single stranded terminus adapter containing a degenerate sequence or a defined sequence.
22. The method of any of the preceding claims, wherein the single stranded terminus adapter contains dsDNA.
23. The method of any of the preceding claims, wherein the single stranded terminus adapter is between 5 and 100 nucleotides in length.
24. The method of any of the preceding claims, wherein the single stranded terminus adapter duplicates the terminal sequence of the second DNA molecule.
25. The method of any of the preceding claims, wherein the single stranded terminus adapter includes a single stranded DNA terminus of defined sequence.
26. The method of any of the preceding claims, wherein the single stranded terminus adapter and/or the second DNA molecule are modified via the action of an exonuclease.
27. The method of any of the preceding claims, wherein the single stranded terminus adapter contains a degenerate sequence capable of binding to a single stranded DNA terminus complementary to the single stranded DNA terminus.
28. The method of any of the preceding claims, wherein the single stranded terminus adapter is between 5 and 100 nucleotides in length.
29. The method of any of the preceding claims, wherein the single stranded DNA terminus of the single stranded terminus adapter and second DNA molecule are annealed and ligated.
30. A reaction mixture capable of generating a 3' single stranded DNA terminus overhang according to the method of any of the preceding claims.

31. A reaction mixture capable of generating a 5' single stranded DNA terminus overhang according to the method of any of the preceding claims.
32. A reaction mixture comprising enzymes capable of generating 3', 5', and/or combination of 3' and 5' single stranded DNA terminus overhang in a single reaction, according to the method of any of the preceding claims.
33. The reaction mixture of any of the preceding claims, wherein the restriction enzyme is a Type IIs, Type IIb or Type IIp restriction enzyme.
34. The reaction mixture of any of the preceding claims, wherein the Type IIs, Type IIb or Type IIp restriction enzyme is selected from BsaXI, RleAI, and TstI and the restriction enzyme generates single stranded terminus with a 3'-overhang.
35. The reaction mixture of any of the preceding claims, wherein the Type IIs restriction enzyme is selected from EarI, BspMI, BsaI, BbsI, and BsmBI and the restriction enzyme generates single stranded terminus with a 5'-overhang.
36. A reaction mixture for performing the method of any of the preceding claims.
37. The method of any of the preceding claims, in which the product of scarless assembly method is circular DNA.
38. The method any of the preceding claims, in which the product of scarless assembly method can be transformed or transfected into cells.
39. The method or reaction mixture of any of the preceding claims, wherein more than two DNA molecules are simultaneously ligated together.

Figure 1

# MMS Assembly

Multipart, Modular and Scarless Assembly

<p><b>Staple Method</b></p> <ol style="list-style-type: none"><li>1. Modify DNA to produce recessed ends</li><li>2. Connect parts using "staple" oligos of defined sequence</li></ol> <p><u>Key innovation</u> Every possible staple can be synthesized. The library is easily stored and reused many times.</p>	<p><b>Adapter Method</b></p> <ol style="list-style-type: none"><li>1. Modify DNA to produce recessed ends</li><li>2. Attach a "sticky" adapter that specifies neighboring part</li><li>3. Connect adapter to neighboring part</li></ol> <p><u>Key innovation</u> The degenerate sequence in the adapter provides modularity and eliminates scars.</p>
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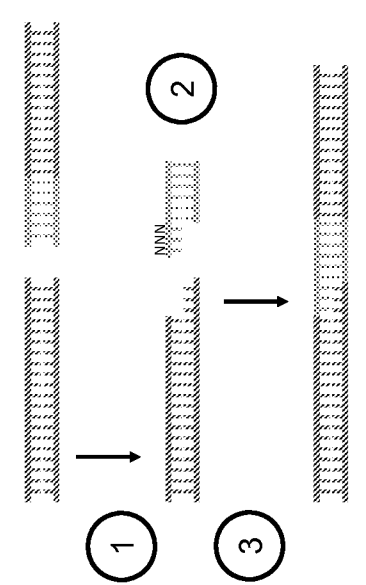
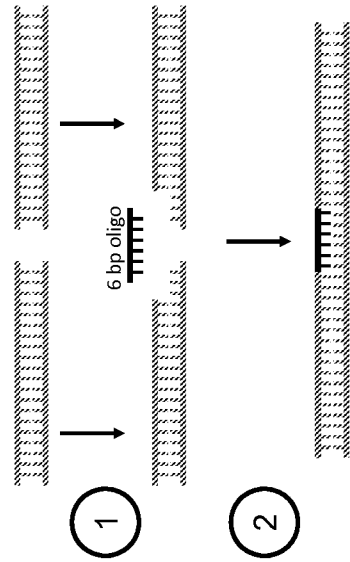
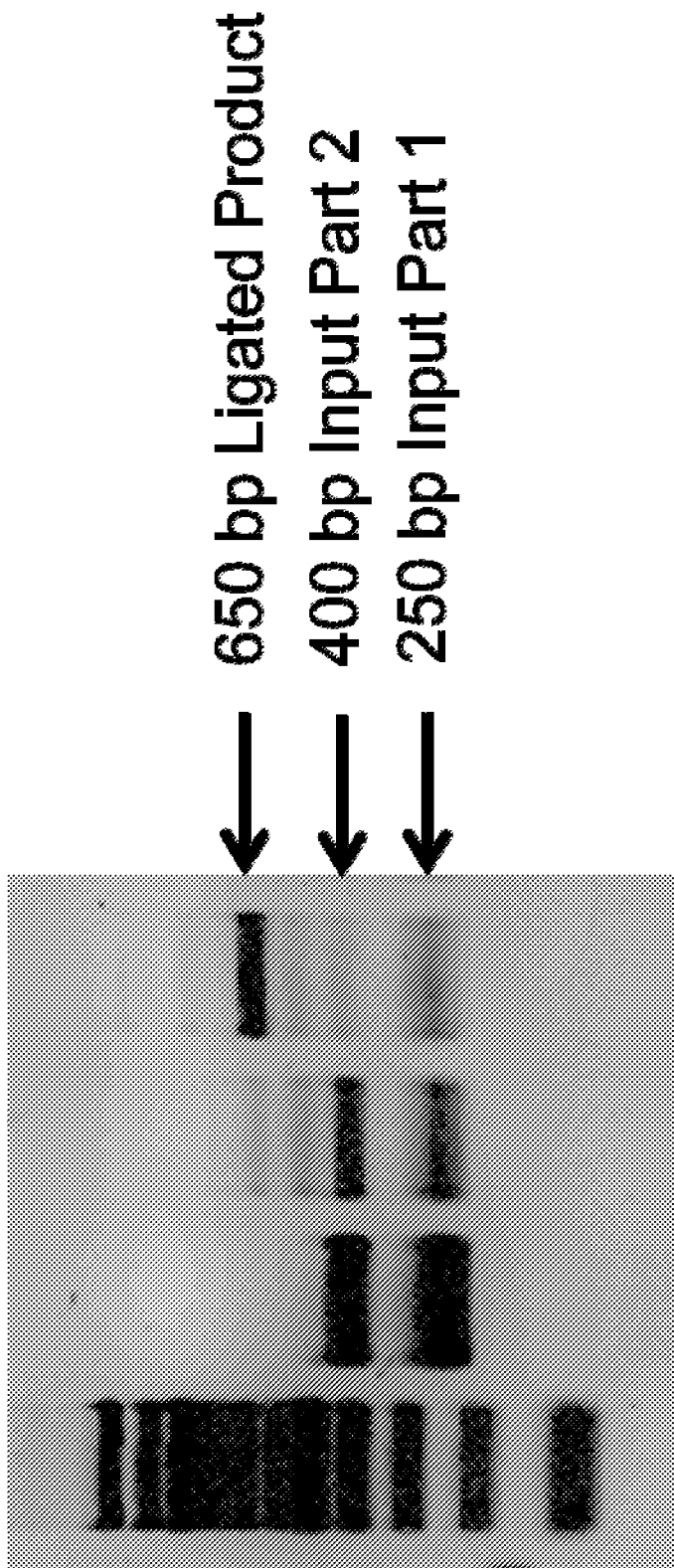


Figure 2



*Figure 3*

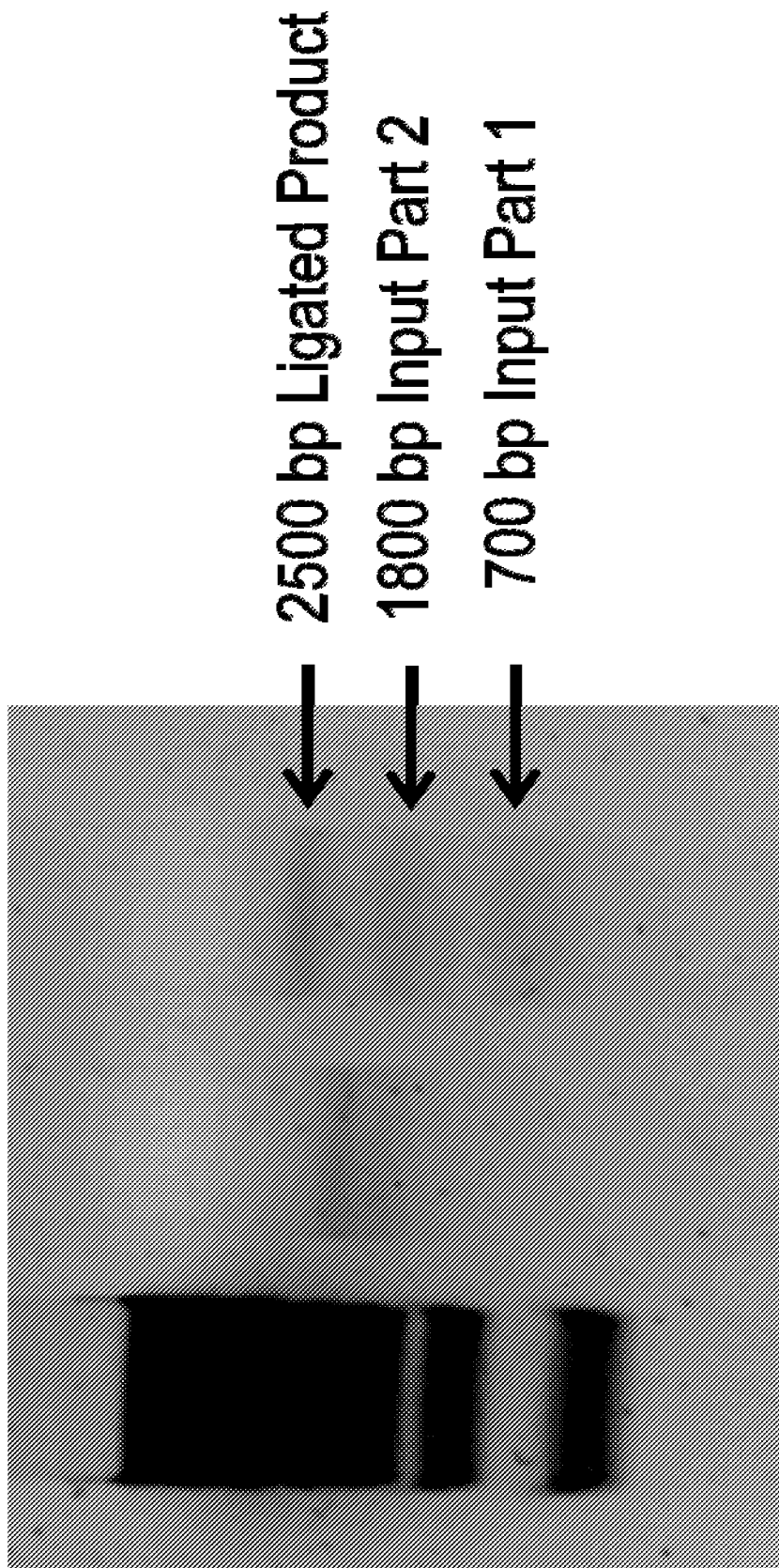


Figure 4

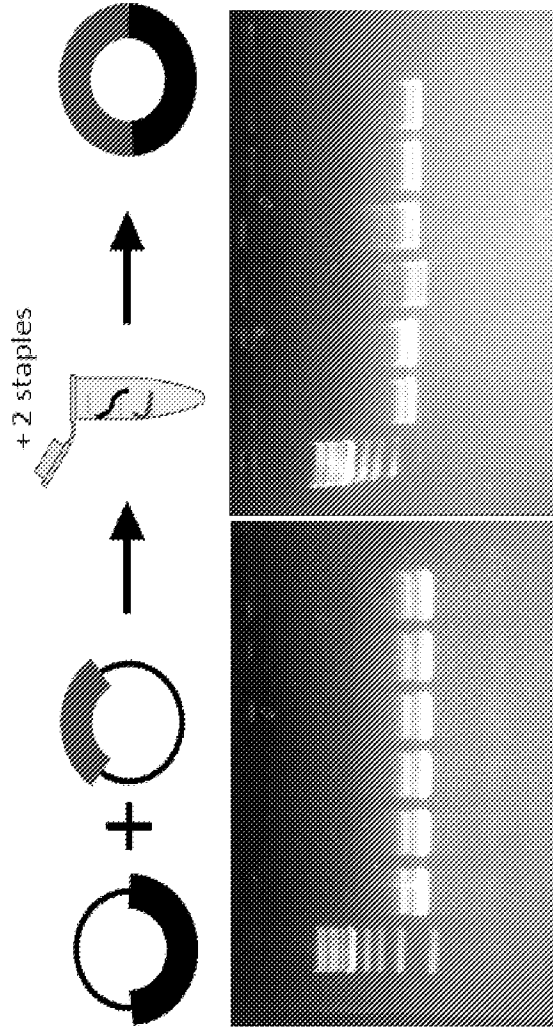


Figure 5

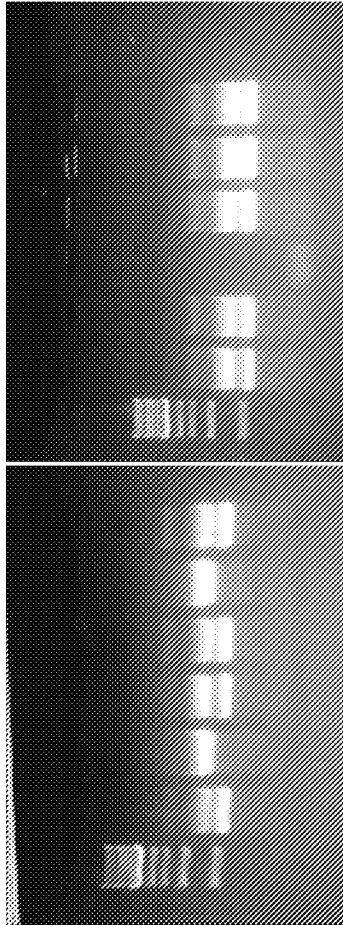
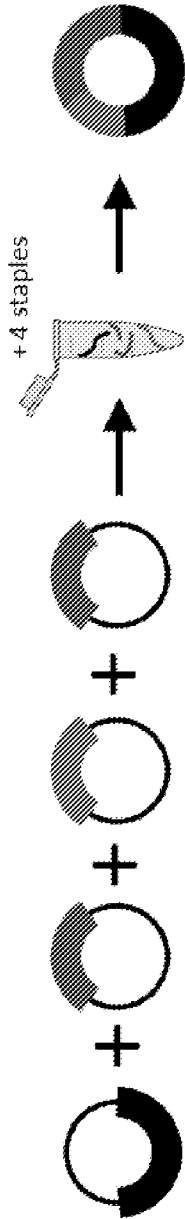
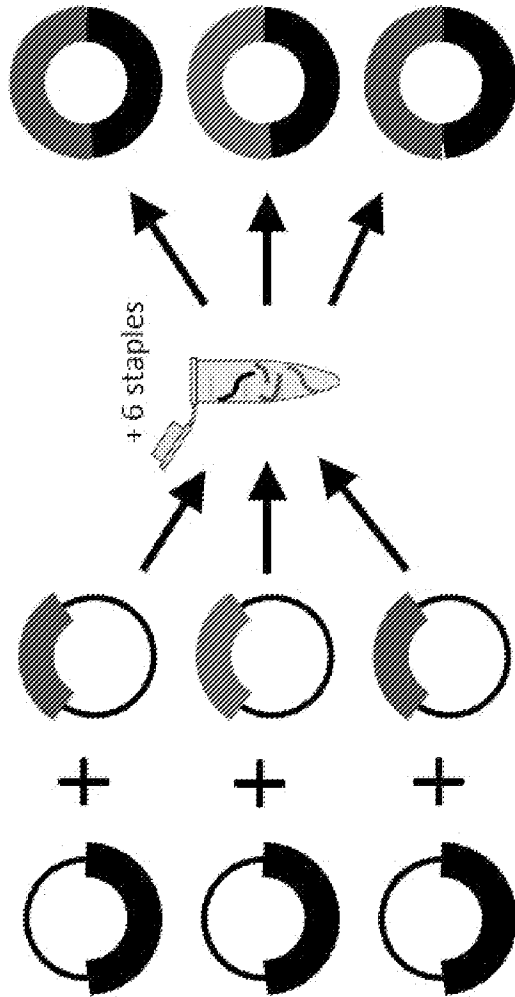


Figure 6



INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2013/049965

<p>A. CLASSIFICATION OF SUBJECT MATTER                  IPC(8) - C12N 15/66 (2013.01)                  USPC - 435/6.1                  According to International Patent Classification (IPC) or to both national classification and IPC</p>																	
<p>B. FIELDS SEARCHED</p> <p>Minimum documentation searched (classification system followed by classification symbols)                  IPC(8) - C07H 21/00; C12N 15/00, 15/09, 15/66; C12P 19/34 (2013.01)                  USPC - 435/6.1, 91.2, 91.52; 536/23.1, 24.2, 25.3</p> <p>Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched                  CPC - C12N 15/10, 15/66, 15/115, 2300/16; C12Q 1/6811 (2013.01)</p> <p>Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)                  PatBase, Google Patents, Google, PubMed</p>																	
<p>C. DOCUMENTS CONSIDERED TO BE RELEVANT</p> <table border="1"> <thead> <tr> <th>Category*</th> <th>Citation of document, with indication, where appropriate, of the relevant passages</th> <th>Relevant to claim No.</th> </tr> </thead> <tbody> <tr> <td>X</td> <td>ZENG et al., "Benchmarks: Ligation of 5' DNA Overhangs to 3' DNA Overhangs Using Short Single-Stranded Oligonucleotide Linkers," BioTechniques 23: 418-420. September 1997. entire document</td> <td>1-3</td> </tr> <tr> <td>A</td> <td>US 2012/0040870 A1 (CHE et al) 16 February 2012 (16.02.2012) entire document</td> <td>1-3</td> </tr> <tr> <td>A</td> <td>US 4,719,179 (BARANY) 12 January 1988 (12.01.1988) entire document</td> <td>1-3</td> </tr> <tr> <td>A</td> <td>US 2008/0044862 A1 (SCHATZ et al) 21 February 2008 (21.02.2008) entire document</td> <td>1-3</td> </tr> </tbody> </table>			Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.	X	ZENG et al., "Benchmarks: Ligation of 5' DNA Overhangs to 3' DNA Overhangs Using Short Single-Stranded Oligonucleotide Linkers," BioTechniques 23: 418-420. September 1997. entire document	1-3	A	US 2012/0040870 A1 (CHE et al) 16 February 2012 (16.02.2012) entire document	1-3	A	US 4,719,179 (BARANY) 12 January 1988 (12.01.1988) entire document	1-3	A	US 2008/0044862 A1 (SCHATZ et al) 21 February 2008 (21.02.2008) entire document	1-3
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<p><input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/></p>																	
<p>* Special categories of cited documents:</p> <table border="0"> <tr> <td>"A" document defining the general state of the art which is not considered to be of particular relevance</td> <td>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td> </tr> <tr> <td>"E" earlier application or patent but published on or after the international filing date</td> <td>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td> </tr> <tr> <td>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td> <td>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td> </tr> <tr> <td>"O" document referring to an oral disclosure, use, exhibition or other means</td> <td>"&amp;" document member of the same patent family</td> </tr> <tr> <td>"P" document published prior to the international filing date but later than the priority date claimed</td> <td></td> </tr> </table>			"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	"E" earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family	"P" document published prior to the international filing date but later than the priority date claimed						
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<p>Date of the actual completion of the international search                  13 November 2013</p>		<p>Date of mailing of the international search report  <b>26 NOV 2013</b></p>															
<p>Name and mailing address of the ISA/US                  Mail Stop PCT, Attn: ISA/US, Commissioner for Patents                  P.O. Box 1450, Alexandria, Virginia 22313-1450                  Facsimile No. 571-273-3201</p>		<p>Authorized officer:                  Blaine R. Copenheaver                  PCT Helpdesk: 571-272-4300                  PCT OSP: 571-272-7774</p>															

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2013/049965

**Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2.  Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3.  Claims Nos.: 4-39  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

1.  As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2.  As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3.  As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4.  No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

**Remark on Protest**

- The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- No protest accompanied the payment of additional search fees.