***Supplementary Table 1**: Phage integrases and their predicted recognition sites*

Table 1: Phage integrases and their predicted recognition sites

Name[a]	NCBI No.	Organism	attB sequence[b]	attP sequence[b]
Int1	YP_353073	*Rhodobacter Sphaeroides* 2.4.1	ggaactccgccgggcccatctggtcgaagaagatgaaggggcccaccatctgcctccgggcc	atggggtcacaataccaatcatgttcaagaatgtgaagggtattttacccttgtcgtttcag
Int2	CBG73463	*Streptomyces scabiei* 87.22	ggacggcgcagaaggggagtagctcttcgccggaccgtcgacatactgctcagctcgtc	gctcatgtatgtgtctacgcgagattctcgcccgagaacttctgcaaggcactgctcttggct
Int3#	NP_268897	*Streptococcus pyogenes* M1 GAS [1]	gtttgtaaaggagactgataatggcatgtacaactatactcgtcggtaaaaaggcatcttat	atggataaaaaaatacagcgtttttcatgtacaactatactagttgtagtgcctaaataatgctt
Int4	YP_002747001	*Streptococcus equi* subsp. equi 4047	ttccaaagagcgcccaacgcgacctgaaatttgaataagactgctgcttgtgtaaaggcgatgatt	caaaaattacaaagttttcaacccttgatttgaattagcggtcaaataatttgtaattcgttt
Int5#	BAF03598	*Streptomyces* phage PhiK38-1[2]	gagcgccggatcagggagtggacggcctgggagcgctacacgctgtggctgcggtcggtgc	ccctaatacgcaagtcgataactctcctgggagcgttgacaacttgcgcaccctgatctg
Int6*	BAG46462	*Burkholderia multivorans* ATCC 17616	gatacggatgttcgtcgccggcacgctggtcacgctcggcaatcccaagatcatgctgttct	agttgtctgataatatattttcggacacgctcggcaacccgaacgagagtcaaaatacattt
Int7	YP_003251752	*Geobacillus sp.* Y412MC61	agacgagaaacgttccgtccgtctgggtcagttgggcaaagttgatgaccgggtcgtccgtt	gtgttataaacctgtgtgagagttaagtttacatgcctaaccttaacttttacgcaggttcagctt
Int8*	BAE05705	*Staphylococcus haemolyticus* JCSC1435	caatcatcagataactatggcggcacgtgcattaaccacggttgtatcccgtctaaagtactcgt	ttaataaactatggaagtatgtacagtcttgcaatgttgagtgaacaaacttccataataaaat
Int9	BAF67264	*Staphylococcus aureus* str. Newman	tttatattgcgaaaaataattggcgaacgaggtaactggatacctcatccgccaattaaaatttg	gtggttgtttttgttggaagtgtgtatcaggtatctgcatagttattccgaacttccaatta
Int10	YP_003880342	*Streptococcus pneumoniae* 670-6B	agcacgctgataatcagcaagaccaccaacatttccaccaatgtaaaagctttaaccttagc	ggaaaatataaataattttagtaacctacatctcaatcaaggatagtaaaactctcactctt
Int11*	YP_001886479	*Clostridium botulinum* B str. Eklund 17B	atggattttgcagattcccagatgcccctacagaaagaggtacaaaacatttattggaattaatt	gtttatatgtttactaataagacgctctcaacccataaagtcttattagtaaacatatttcaact
Int12*	YP_005759947	*Staphylococcus lugdunensis* N920143	gttcgtggtaactatgggtggtacaggtgccacattagttgtaccatttatgtttatgtggttaac	tttttgtatgttagttgtgtcactgggtagacctaaatagtgacacaactgctattaaatttaa
Int13	YP_001376196	*Bacillus cytotoxicus* NVH 391-98	cgcatacattgttgttgtttttccagatccagttggtcctgtaaatataagcaatccatgtgagt	caataacggttgtatttgtagaacttgaccagttgttttagtaacataaatacaactccgaata
Int14	NP_470568	*Listeria innocua* Clip11262	ttattgcaagaaaaatgggttataagtacacatcaggttatagtaatatcgaaaaaggaagc	ttatataaaatagtgtttttgtaaagtacacatcaccatatttgacaaaaaacctataaata
Int15	YP_006685721	*Listeria monocytogenes* SLCC2372	ctgtaacttttttcggatcaagctatgagggacgcaaagagggaactaaacacttaattggtg	ttgtttagtccctcgttttctctcgttggacggagacgaatcgagaaactaaaattataaat
Int16	YP_006538656	*Enterococcus faecalis* D32	ttctggaccatgatgcgccacttccgaaatttcaaaaagatcagtggtcaaacggctcatta	gtatcttgatgtacaacattactctttattttcaaatacagaataatgttgcatataatatt
Int17	YP_189066	*Staphylococcus epidermidis* RP62A	acttccaattaacccttcaccagccctataccaagttcctgtcgcgcatcctccagctaat	ttatatttcgacttaattaagtacagttccacctagagatagactaaataaagtattatta
Int18	YP_002736920	*Streptococcus pneumoniae* JJA	tctggtgtagacgttaaacgtccaatcaagataactttattatacatattttcttcctccta	tatttctgtattttagtcaaagtaattaagataagttagagttagtaacagtattttaactt
Int19#	FM864213	*Streptococcus* phage phi-m46.1[3]	gtagatttgtttccccagacgcacacgtggagtgtgtaagtttacttgagaaacggagttaa	tattagtatagaagaaagctctcagcacacgtggagtgtgttgctctctgctcgtaaagcct
Int20	YP_006082695	*Streptococcus* suis D12	cttccagcacatcacccacatggtctgtgtcggtgtgcgtcagcactagactatcaatccta	ggtattgtatcaatttcagaactcacacttcggtatgcgtactcaatttgatacaattacaa
Int21*	YP_003445547	*Streptococcus* mitis B6	taggaggaaaaaatatgtataataaagttatcatgattgggcgtttgacgtctacaccagaat	gttaataatatgtatttaagtctaacttatcatgacaaatttgactaaaatacaaaaaggc
Int22	YP_004586821	*Geobacillus thermoglucosidasius* C56-YS93	caagaaacgttccgtctgtttgtgtcagctgcgcgaaattaatgaccggatcgtttgttcc	ttataaacctgttttaaagttaactttacatgcctaacattaactcttatacaggttaaggt
Int23	YP_001089468	*Clostridium difficile* 630	tattctaagtaatgtagttttaccacatccactaggtccgagtaaacatagaaattcccct	tatataattatttggactaacatatagtatccacttggctattattagttagtccaaataaata
Int24	YP_005679179	*Clostridium botulinum* H04402 065	actacttaatatatccataagagaaatttcatttccttctttgtctaccccctataggatctt	gttaggtgtatatcatacctaacgcaattcattacatcacatatgttatacacctactttaa
Int25	YP_001384783	*Clostridium botulinum* A str. ATCC 19397	tattcaattatgtgtcgtaatttttatctattgcgacgaaaaaacaccataaaattctaac	tatatacttatagatactaaatatttttgtattgcgtaacttcttctacacctgtaatatct
Int26*	YP_001392519	*Clostridium botulinum* F str. Langeland	agaaatagacctttcaactggacaaggtgctgataaaactatgcagcaagtcttaagtaaa	aaatataacctgtgtattgaaacaaggtgctgataaaaccctttcataaacacaagtaaata
Int27	YP_005869510	*Lactococcus lactis* subsp. lactis CV56	aatactaataatagctagtacaattaacatctctatcaaagtaaaagcttttagctctttct	cgcttaattgcgagtttttatttcgcttatctcaattaaggtaactaaaaaactcctttt
Int28*	YP_001271396	*Lactobacillus reuteri* DSM 20016	aagtgtccaagctggcccccgatcccagtttcaatagtttggggaatctttgtaagtggtaa	tataatttcgtatattagatataaccggtttcaattggaaatacctaatatacgaaaaaagg
Int29	YP_001646422	*Bacillus weihenstephanensis* KBAB4	tttgtagccattaggcgcattaggttgacgccattaagccctaaagcatcattcgtcgaaac	cgtcaccttgttggcgtaattagatttactccaacagggtgatgacaaagctaatgaatttt
Int30	YP_002336631	*Bacillus cereus* AH187	gtaatatgtttggatatggggaagtgaatcagtacaaccgccacagtaccctcatgtcagcc	ataatagtgtatatggtagagaattaaaccagtttaatactccaccatgtacacgcagtgag
Int31*	YP_005549228	*Bacillus amyloliquefaciens* XH7	ttttttccgcctgtcgtaaccggatctgttgtaacgattatcggaatgaccttgatgccgg	ctttttgttgtacttaaacaataatgcttgtaagaattattgattgagtacgacataaacc
Int32	YP_706485	*Rhodococcus jostii* RHA1	atcgcgcagaacggtgcggtgatcagtgagtacgcaccgggcacgacaccggcgaagcatcg	ctatgtggtggtaatagcgagtaggggactactcgctccaggtacattaacaccatgga
Int33	YP_002804732	*Clostridium botulinum* A2 str. Kyoto	acgaaataaaagattgtatagatgctggtaggaaacatgcccttgtcatttagctgaaacag	aaaagaatccaaattatcgtactttaacatagtgaatactgtccatcatgtataaaagtacg
Int34	YP_003472505	*Staphylococcus lugdunensis* HKU09-01	aatctgcaaacatgtatggcggtacatgtatcaacattggttgtattcctacaaagacactcat	atttttgtacggaagtagatactatctttcaatatccatgttacttagtgccatacaaaaa

a. A * indicates the attB/P sites were from prophages within a conserved gene. A # indicates those that were identified from the literature (citations). The rest of the library was identified using the genome comparison approach.

b. Sequences in green are the core sequence of the *att* sites.

<u>Supplementary Table 2:</u> The optimal RBS sequence for each integrase

Table 2: The optimal RBS sequence for each integrase

Name	Optimal RBS sequence	Translation Initiation rate[a]
Int2	aacatagcgaatcgtaaggagttaaaag**atg**	7965
Int3	tcacacaggaagaaggctcg**atg**	15
Int4	agtaatttcaacacaataactaggattcga**atg**	2363
Int5	cagaggaaggaggctcg**atg**	529
Int7	agtaatttcaacaaaataactaggattcga**atg**	472
Int8	aaaacaataactaggattcga**atg**	4
Int9	tcacacaggatgaagcctag**atg**	13
Int10	tcaaacaggaagaaggctag**atg**	308
Int11	tcaaacaggacggaggctag**atg**	221
Int12	acacaggaagaaggctcg**atg**	40
Int13	agtaatttcaacaaaataacgagcattcga**atg**	1473

a. Calculated using the RBS calculator v1.1 (au)[4].

Supplementary Table 3: Recombinases and recognition sites used to build memory switches

Table 3. Recombinases and recognition sites used to build memory switches

Name	NCBI No.	attB sequence[a,b]	attP sequence[a,b]
Int2	CBG73463	ggacggcgcagaaggggagtagctcttcgccggaccgtcgacatactgctcagctcgtc	gctcatgtatgtgtctacgcgagattctcgcccgagaacttctgcaaggcactgctcttggct
Int3	NP_268897[1]	gtttgtaaaggagactgataatggcatgtacaactatactcgtcggtaaaaaggcatcttat	atggataaaaaaatacagcgtttttcatgtacaactatactagttgtagtgcctaaataatgctt
Int4	YP_002747001	ttccaaagagcgcccaacgcgacctgaaatttgaataagactgctgcttgtgtaaaggcgatgatt	aaaaattacaaagttttcaacccttgatttgaattagcggtcaaataatttgtaattcgttt
Int5	BAF03598	gagcgccggatcagggagtggacggcctgggagcgctacacgctgtggctgcggtcggtgc	ccctaatacgcaagtcgataactctcctgggagcgttgacaacttgcgcaccctgatctg
Int7	YP_003251752	agacgagaaacgttccgtccgtctgggtcagttgggcaaagttgatgaccgggtcgtccgtt	gtgttataaacctgtgtgagagttaagtttacatgcctaaccttaacttttacgcaggttcagctt
Int8	BAE05705	caatcatcagataactatggcggcacgtgcattaaccacggttgtatcccgtctaaagtactcgt	ttaataaactatggaagtatgtacagtcttgcaatgttgagtgaacaaacttccataataaaat
Int9	BAF67264	tttatattgcgaaaaataattggcgaacgaggtaactggatacctcatccgccaattaaaatttg	gtggttgtttttgttggaagtgtgtatcaggtatctgcatagttattccgaacttccaatta
Int10	YP_003880342	agcacgctgataatcagcaagaccaccaacatttccaccaatgtaaaagctttaaccttagc	ggaaaatataaataattttagtaacctacatctcaatcaaggatagtaaaactctcactctt
Int11	YP_001886479	atggattttgcagattcccagatgcccctacagaaagaggtacaaaacatttattggaattaatt	gtttatatgtttactaataagacgctctcaacccataaagtcttattagtaaacatatttcaact
Int12	YP_005759947	gttcgtggtaactatgggtggtacaggtgccacattagttgtaccatttatgtttatgtggttaac	tttttgtatgttagttgtgtcactgggtagacctaaatagtgacacaactgctattaaaatttaa
Int13	YP_001376196	gcatacattgttgttgtttttccagatccagttggtcctgtaaatataagcaatccatgtgagt	caataacggttgtatttgtagaacttgaccagttgttttagtaacataaatacaactccgaata
		IRL sequence	IRR sequence
HbiF	ABB83955[5]	aatacaagacaattggggccaaactgtccatatcat	ctctatgagtcaaaatggccccaaatgtttcatcttttg
FimE	CAA27561[6]	aatacaagacaattggggccattttgactcatagag	atgatatggacagtttggccccaaatgtttcatcttttg

a. The core sequence is shown in green.

b. The recognition sites of Int3, 5, HbiF and FimE are from literatures.

***Supplementary Table 4:* Sequences of genetic parts used in this work**

Table 4. Sequences of genetic parts used in this work

Part name	Type	DNA sequence
BBa_J23119	promoter	ttgacagctagctcagtcctaggtataatgctagc
BBa_J23101	promoter	tttacagctagctcagtcctaggtattatgctagc
P_{Bad}	promoter[7]	gaaaccaattgtccatattgcatcagacattgccgtcactgcgtcttttactggctcttctcgctaaccaaaccggtaacccgcttattaaaagcattctgtaacaaagcgggaccaaagccatgacaaaaacgcgtaacaaaagtgtctataatcacggcagaaaagtccacattgattatttgcacggcgtcacactttgctatgccatagcatttttatccataagattagcggatcctacctg
P_{Tac}	promoter[8]	tgttgacaattaatcatcggctcgtataatgtgtggaattgtgagcgctcacaatt
P_{Tet}	promoter[8]	tactccaccgttggctttttccctatcagtgatagagattgacatccctatcagtgatagagataatgagcac
P_{SrpR}	promoter[8]	tctatgattggtccagattcgttaccaattgacagctagctcagtcctaggtatatacatacatgcttgtttgtttgtaaac
P_{BM3R1}	promoter[8]	aatccgcgtgataggtctgattcgttaccaattgacggaatgaacgttcattccgataatgctagc
P_{PhlF}	promoter[8]	cgacgtacggtggaatctgattcgttaccaattgacatgatacgaaacgtaccgtatcgttaaggt
RiboJ	insulator[9]	agctgtcaccggatgtgctttccggtctgatgagtccgtgaggacgaaacagcctctacaaataattttgtttaa
SarJ	insulator[9]	agactgtcgccggatgtgtatccgacctgacgatggcccaaaagggccgaaacagtcctctacaaataattttgtttaa
SccJ	insulator[9]	agatgctgtagtgggatgtgtgtctcacctgaagagtacaaaagtccgaaacggtatcctctacaaataattttgtttaa
LtsvJ	insulator[9]	agtacgtctgagcgtgatacccgctcactgaagatggcccggtagggccgaaacgtacctctacaaataattttgtttaa
D/E20	spacer[10]	agttcgatgagagcgataac
Sequence of the reporter for characterization of the integrases (with the example of Int2)[a]	sequence	ttgacagctagctcagtcctaggtataatgctagcagttcgatgagagcgataacggacggcgcagaaggggagtagctcttcgccggaccgtcgacatactgctcagctcgtcttaagcgtagttttcgtcgtttgctgcaggccttttgtatagttcatccatgccatgtgtaatcccagcagctgttacaaactcaagaaggaccatgtggtctctcttttcgttgggatctttcgaaagggcagattgtgtggacaggtaatggttgtctggtaaaaggacagggccatcgccaattggagtattttgttgataatggtctgctagttgaacgcttccatcttcaatgttgtgtctaattttgaagttaactttgattccattcttttgtttgtctgccatgatgtatacattgtgtgagttatagttgtattccaacttgtgtccaagaatgtttccatcttctttaaaatcaataccttttaactcgattctattaacaagtgtatcaccttcaaacttgacttcagcacgtgtcttatagttcccgtcatctttgaaaaatatagttctttcctgtacataaccttcgggcatggcactcttgaaaaagtcatgccgtttcatatgatctgggtatcttgaaaagcattgaacaccataagtcaaagtagtgacaagtgttggccatggaacaggtagttttccagtagtgcaaataaatttaagggtaagttttccgtatgctgcatcaccttcaccctctccactgacagaaaatttgtgcccattaacattaccatctaattcaacaagaattgggacaactccagtgaaaagttcttctcctttactcatctagtatttctcctctttctctagattaaacaaaattatttgtagaggctgtttcgtcctcacggactcatcagaccggaaagcacatccggtgacagctagccaagagcagtgccttgcagaagttctcgggcgagaatctcgcgtagacacatacatgagc
gfpmut3	gene[11]	atgagtaaaggagaagaacttttcactggagttgtcccaattcttgttgaattagatggtaatgttaatgggcacaaattttctgtcagtggagagggtgaaggtgatgcagcatacggaaaacttacccttaaatttatttgcactactggaaaactacctgttccatggccaacacttgtcactactttgacttatggtgttcaatgcttttcaagatacccagatcatatgaaacggcatgactttttcaagagtgccatgcccgaaggttatgtacaggaaagaactatatttttcaaagatgacgggaactataagacacgtgctgaagtcaagtttgaaggtgatacacttgttaatagaatcgagttaaaaggtattgattttaaagaagatggaaacattcttggacacaagttggaatacaactataactcacacaatgtatacatcatggcagacaaacaaaagaatggaatcaaagttaacttcaaaattagacacaacattgaagatggaagcgttcaactagcagaccattatcaacaaaatactccaattggcgatggccctgtccttttaccagacaaccattacctgtccacacaatctgccctttcgaaagatcccaacgaaaagagagaccacatggtccttcttgagtttgtaacagctgctgggattacacatggcatggatgaactatacaaaggcctgcagcaaacgacgaaaactacgcttaa
yfp	gene[11]	atggtgagcaagggcgaggagctgttcaccggggtggtgcccatcctggtcgagctggacggcgacgtaaacggccacaagttcagcgtgtccggcgagggcgagggcgatgccacctacggcaagctgaccctgaagttcatctgcaccaccggcaagctgcccgtgccctggcccaccctcgtgaccaccttcggctacggcctgcaatgcttcgcccgctaccccgaccacatgaagctgcacgacttcttcaagtccgccatgcccgaaggctacgtccaggagcgcaccatcttcttcaaggacgacggcaactacaagacccgcgccgaggtgaagttcgagggcgacaccctggtgaaccgcatcgagctgaagggcatcgacttcaaggaggacggcaacatcctggggcacaagctggagtacaactacaacagccacaacgtctatatcatggccgacaagcagaagaacggcatcaaggtgaacttcaagatccgccacaacatcgaggacggcagcgtgcagctcgccgaccactaccagcagaacacccccatcggcgacggccccgtgctgctgcccgacaaccactacctgagctaccagtccgccctgagcaaagaccccaacgagaagcgcgatcacatggtcctgctggagttcgtgaccgccgccgggatcactctcggcatggacgagctgtacaagtaa
mrfp1	gene[12]	atggcttcctccgaagacgttatcaaagagttcatgcgtttcaaagttcgtatggaaggttccgttaacggtcacgagttcgaaatcgaaggtgaaggtgaaggtcgtccgtacgaaggtacccagaccgctaaactgaaagttaccaaaggtggtccgctgccgttcgcttgggacatcctgtccccgcagttccagtacggttccaaagcttacgttaaacacccggctgacatcccggactacctgaaactgtccttcccggaaggtttcaaatgggaacgtgttatgaacttcgaagacggtggtgttgttaccgttacccaggactcctccctgcaagacggtgagttcatctacaaagttaaactgcgtggtaccaacttcccgtccgacggtccggttatgcagaaaaaaaccatgggttgggaagcttccaccgaacgtatgtacccggaagacggtgctctgaaaggtgaaatcaaaatgcgtctgaaactgaaagacggtggtcactacgacgctgaagttaaaaccacctacatggctaaaaaaccggttcagctgccgggtgcttacaaaaccgacatcaaactggacatcacctcccacaacgaagactacaccatcgttgaacagtacgaacgtgctgaaggtcgtcactccaccggtgcttaataa
araC	gene[7]	atggctgaagcgcaaaatgatcccctgctgccgggatactcgtttaatgcccatctggtggcgggtttaacgccgattgaggccaacggttatctcgatttttttatcgaccgaccgctgggaatgaaaggttatattctcaatctcaccattcgcggtcagggggtggtgaaaaatcagggacgagaatttgtttgccgaccgggtgatattttgctgttcccgccaggagagattcatcactacggtcgtcatccggaggctcgcgaatggtatcaccagtgggtttactttcgtccgcgcgcctactggcatgaatggcttaactggccgtcaatatttgccaatacggggttctttcgcccggatgaagcgcaccagccgcatttcagcgacctgtttgggcaaatcattaacgccgggcaaggggaagggcgctattcggagctgctggcgataaatctgcttgagcaattgttactgcggcgcatg

		gaagcgattaacgagtcgctccatccaccgatggataatcgggtacgcgaggcttgtcagtacatcagcgatcacctggcag acagcaattttgatatcgccagcgtcgcacagcatgtttgcttgtcgccgtcgcgtctgtcacatcttttccgccagcagtt agggattagcgtcttaagctggcgcgaggaccaacgtatcagccaggcgaagctgcttttgagcaccacccggatgcctatc gccaccgtcggtcgcaatgttggttttgacgatcaactctatttctcgcgggtatttaaaaaatgcaccggggccagcccga gcgagttccgtgccggttgtgaagaaaaagtgaatgatgtagccgtcaagttgtcataa
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int11	gene	atgctgcgttgtgcaatctatattcgtgttagcaccgaagaacaggcaatgcatggtctgagcatggatgcacagaaagcag atctgaccgattatgccaaaaaacacaactatgagattattgattattatgtggacagcggtaaaaccgcacgtaaacgtct gagcaaacgtaaagatctgcagcgtatgattgaagatgtgaagctgaacaaaattgatattatcatttttaccaaactggat cgctggtttcgtaatgtgcgtgattattacaaaatccaagaggtgctggaagatcataacgttgattggaaaaccatctttg agaactatgataccagcaccgcaaatggtcgtctgcatattaacattatgctgagcgttgcacaggatgaagcagatcgtac cagcgaacgtattaaacgtgtgtttgaaaacaaactgaagaacaatgaaccgaccagcggtagcctgccgattggctataaa atcaaagaaaaaagcattattatcgatgaagaaaaagcaccgatcgccaaagatgtgttcgatttctattattaccatcaga gccagaccaaggtgtttaaagaaatcctgaacaaatacaacctgagcctgtgcgaaaaaaccattcgtcgtatgctggaaaa caagctgtatattggtatctatcgcgagcacgaaaacttttgtccgcctctgattgacaaaaacaaatttgatgaagtgcag ctgattctgaaacgtcgcaacattaaatacattccgaccaaacgcatctttctgtttaccagcctgctgatttgtaaagaat gccgtcataaaatgattggcaatgcccagattcgtaataccaaagccggtaaaattgagtatattctgtatcgctgcaatca gagctatgcacgtcatacctgtaatcatcgtaaagtgatctacgaaaacaaaatcgaaacctatctgctgaacaacatcgaa agcgaactgaaaaaattcatttatgattatgaactggaagatattccgaaagtgaaaaacaaagtgaataaaaccaatatca aacgcaaactggaaaaactgaaagaactgtacatcaacgatctgatcgacattgacatgtataaagaagattataagaaata taccgaaattctgaacaccaaagaagaaaaaattgagcagcgtaatctgcagccgctgaaagattttctgaatagcgatttc aaaagcctgtatagcagcattagtcgcgaagaaaaacgtctgctgtggcgtggtattattagcgaaattcagattgattgca ataatgatatcaccatcatcccgcatccgtaa
int12	gene	atgaaagtggccatttatacccgtgttagcagcgcagaacaggcaaatgaaggttatagcattcacgagcagaagaagaaac tgatcagctattgcgaaatccacgattggaacgagtataaagtttttaccgatgcaggtattagcggtggtagcatgaaacg tccggcactgcaaaaactgatgaaacatctgagttcatttgatctggtgctggtgtataaactggatcgtctgacccgtaat gttcgtgatctgctggatatgctggaagaatttgaacagtataacgtgagctttaaaagcgccaccgaagtttttgatacca ccagtgcaattggcaaactgtttattaccatggttggtgcaatggcagaatgggaacgtgaaaccattcgtgaacgtagcct gtttggtagccgtgcagcagttcgtgaaggtaactatattcgtgaagcaccgttttgctatgataacattgaaggtaaactg cacccgaacgaatatgccaaagttattgatctgattgtgagcatgttcaaaaaaggcattagcgccaatgaaattgcacgtc gtctgaatagcagcaaagttcatgttccgaacaaaaaaagctggaatcgtaatagcctgattcgtctgatgcgtagtccggt tctgcgtggtcataccaaatatggtgatatgctgattgaaaacacccatgaaccggtgctgagcgaacatgattataatgca attaacaacgccatcagcagcaaaacccataaaagcaaagttaaacaccatgccattttcgtggtgcactggtttgtccgc agtgtaatcgtcgtctgcatctgtatgcaggcaccgttaaagatcgtaaaggctataaatacgatgtgcgtcgctataaatg tgaaacctgcagcaaaaacaaagatgtgaagaatgtgagcttcaacgaaagcgaagtggaaaacaaattcgtcaatctgctg aaaagctacgagctgaacaaatttcatatccgtaaagtggaaccggtgaaaaaaatcgagtatgacatcgataagattaaca aacagaaaattaactatacccgcagttggagcctgggctatattgaagatgatgaatatttcgagctgatggaagaaatcaa cgccaccaaaaaaatgatcgaagaacagaccaccgagaataaacagagcgttagcaaagagcagattcagagcattaacaac tttatcctgaaaggctgggaagaactgaccatcaaagataaagaggaactgattctgagcaccgtggataaaatcgaattta acttcatcccgaaagataaaaaacataaaaccaataccctggatattaacaatattcactttaaattctaa
int13	gene	atggccgtgggtatctatattcgtgttagcacccaagaacaggcaagcgaaggtcatagcattgaaagccagaaaaaaaagc tggcgagctattgtgaaattcagggttggatgattatcgcttctatattgaagaaggcatcagcggcaaaaataccaatcg tccgaaactgaaactgctgatggaacatatcgaaaagggcaaaattaacatcctgctggtttatcgtctggatcgtctgacc cgtagcgttattgatctgcataagctgctgaattttctgcaagaacatggttgtgcatttaaaagcgcaaccgaaacctatg ataccaccaccgcaaatggtcgtatgagcatgggtattgttagcctgctggcacagtgggaaaccgaaaatatgagcgaacg tattaaactgaacctggaacacaaagttctggttgaaggtgaacgtgttggtgcaattccgtatggttttgatctgtccgat gatgagaaactggtgaaaaatgaaaaaagcgccattctgctggatatggttgaacgtgtggaaaatggttggagcgttaatc gcattgtgaattatctgaatctgaccaacaatgaccgtaattggagcccgaatggtgttctgcgtctgctgcgtaatccggc actgtatggtgcaacccgttggaatgataaaattgccgaaaatacgcacgaaggcattattagcaaagaacgttttaatcgc ctgcagcagattctggcagatcgtagcattcatcatcgtcgtgatgttaaaggcacctatatctttcagggtgtgctgcgtt gtccggtttgtgatcagaccctgagcgtgaatcgttttatcaaaaaacgtaaagatggcaccgaatattgtggtgtgctgta tcgttgtcagccgtgtattaaacagaataaatacaatctggccattggcgaagcacgttttctgaaagcactgaatgaatat

		atgagcaccgttgaatttcagaccgttgaagatgaagtgatcccgaaaaaaagcgaacgtgaaatgctggaaagccagctgcagcaaattgcacgtaaacgtgaaaaatatcagaaagcatgggcaagcgatctgatgagcgacgatgaatttgaaaaactgatggttgaaacccgtgaaacctacgatgaatgtaaacagaaactggaaagctgtgaggatccgatcaaaatcgatgaaacctatctgaaagaaattgtgtatatgtttcaccagacctttaacgatctggaaagcgaaaaacagaaagaatttatcagcaagttcattcgcaccattcgctataccgttaaagaacagcagccgattcgtccggataaaagcaaaaccggtaaaggcaaacagaaggtgattattaccgaggtggaattctaccagtaa
hbiF	gene[5]	atgacgagaaaatatctcacacaggatgaagtctacaggctgatggatgcagcccagagcatgtcctttcctgaaagaaatcgctgtctgattatgatggctttcattcacggttttagggccagtgaacttcttgatttacgtttatccgatattgatgcatctggaaaacaacttaatattcggcgtattaaaaatggtttctcgacaacacatcctcttcttcctgatgaatataatttgatcaagttgtggcttaagcagaggaagttaattgaaaacggagttgaaggagactggctttttctctcccggaaacgccgccctatcagcagacaacatttttttttctatcattcgtgaggctggaaaacgtgcaggattagctgtaaaagcacatcctcatatgttacgtcatgcctgtggttttgctctggctgacaatggtgtcgatacccgactacttcaggattacctgggtcatcgaaatattcagcatactgtcagatacacagccagtaatgctgctcgttttaaagggtgtggaaaaaaaagcctcgttaa
fimE	gene[7]	atgatgcaggcggtttgttacggggcaacgggagccagagattattgtcttattctgttggcatatcggcatgggatgcgtattagtgaactgcttgatctgcattatcaggaccttgaccttaatgaaggtagaataaatattcgccgactgaagaacggatttctaccgttcacccgttacgttttgatgagcgtgaagccgtggaacgctggacccaggaacgtgctaactggaaaggcgctgaccggactgacgctatatttatttctcgccgcgggagtcggctttctcgccagcaggcctatcgcattattcgcgatgccggtattgaagctggaaccgtaacgcagactcatcctcatatgttaaggcatgcttgcggttatgaattggcggagcgtggtgcagatactcgtttaattcaggattatctcgggcatcgaaatattcgccatactgtgcgttataccgccagtaatgctgctcgttttgccggattatgggaaagaaataatctcataaacgaaaaattaaaaagagaagaggtttga

a. color code of the sequence: brown, promoter J23119; blue, spacer D/E20; green, gfp mut3; magenta, RBS; black, att B/P sites ;purple, RiboJ.

<u>Supplementary Table 5:</u> Orthogonality matrix (% ON)

Table 5: Orthogonality matrix (% ON)

	Sites[a]												
	2	**3**	**4**	**5**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**FimE**	**HbiF**
Int2	**97.4**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**2.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
	0.7	0.0	0.0	0.0	0.0	0.0	0.0	1.7	0.0	0.0	0.0	0.0	0.0
Int3	**0.0**	**97.3**	**0.0**	**0.0**	**0.0**	**0.0**	**0.1**	**0.7**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
	0.0	0.6	0.0	0.0	0.0	0.0	0.2	0.5	0.0	0.0	0.0	0.0	0.0
Int4	**0.0**	**0.1**	**94.7**	**0.0**	**0.0**	**0.0**	**0.0**	**1.9**	**0.0**	**0.1**	**0.0**	**0.0**	**0.0**
	0.0	0.0	1.7	0.0	0.0	0.0	0.0	1.7	0.0	0.1	0.0	0.0	0.0
Int5	**0.0**	**0.1**	**0.0**	**93.8**	**0.0**	**0.0**	**0.0**	**1.2**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
	0.0	0.1	0.0	3.4	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0
Int7	**0.0**	**0.0**	**0.0**	**0.0**	**94.1**	**1.3**	**0.0**	**32.5**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
	0.0	0.0	0.0	0.0	0.5	1.4	0.0	5.3	0.0	0.0	0.0	0.0	0.0
Int8	**0.0**	**0.1**	**0.0**	**0.0**	**0.0**	**98.5**	**0.4**	**9.5**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
	0.0	0.1	0.0	0.0	0.0	0.3	0.2	5.9	0.0	0.0	0.0	0.0	0.0
Int9	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.8**	**69.6**	**24.6**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
	0.0	0.0	0.0	0.0	0.0	0.7	5.0	9.7	0.0	0.1	0.0	0.0	0.0
Int10	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**92.6**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.4	0.0	0.0	0.0	0.0	0.0
Int11	**0.0**	**0.3**	**0.0**	**0.0**	**0.0**	**0.6**	**0.0**	**8.7**	**81.1**	**0.0**	**0.0**	**0.0**	**0.0**
	0.0	0.2	0.0	0.0	0.0	0.5	0.0	3.2	1.8	0.0	0.0	0.0	0.0
Int12	**0.0**	**0.3**	**0.0**	**0.0**	**0.0**	**1.5**	**0.0**	**9.6**	**0.0**	**96.0**	**0.0**	**0.0**	**0.0**
	0.0	0.5	0.0	0.0	0.0	1.7	0.0	3.4	0.0	0.5	0.0	0.0	0.0
Int13	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.2**	**0.0**	**0.1**	**90.6**	**0.0**	**0.0**
	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.1	0.5	0.0	0.0
FimE	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.5**	**0.0**	**0.0**	**0.0**	**97.9**	**0.4**
	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.2	0.2
HbiF	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.2**	**0.0**	**0.0**	**0.0**	**29.0**	**90.1**
	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	3.3	2.1

a. The average (upper row, bold) and standard deviation (lower row) of three independent triplicates are shown.

Supplementary Table 6: ***Orthogonality matrix in average fluorescence***

Table 6: Orthogonality matrix (average fluorescence)

	Sites[a]											
	2	**3**	**4**	**5**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**FimE**	**HbiF**
Int2	**1181**	**9.4**	**7.5**	**7.2**	**8.6**	**13.3**	**7.7**	**25.7**	**7.5**	**7.8**	**7.3**	**7.2**	**6.9**
	73.5	0.9	0.7	0.9	0.3	3.7	1.0	5.5	0.5	0.4	0.3	0.2	0.2
Int3	**7.3**	**1190**	**7.1**	**7.5**	**8.3**	**10.4**	**9.4**	**22.6**	**7.6**	**7.4**	**7.6**	**7.2**	**7.2**
	0.1	141.0	0.5	0.5	0.4	1.9	3.2	2.7	0.4	0.4	0.0	0.2	0.1
Int4	**7.4**	**8.1**	**661.5**	**8.0**	**7.8**	**11.1**	**7.7**	**21.1**	**7.4**	**7.5**	**7.8**	**7.3**	**7.1**
	0.3	0.3	188.5	1.0	0.2	1.1	0.4	4.2	0.1	0.1	0.3	0.1	0.4
Int5	**8.0**	**14.8**	**8.3**	**241.9**	**8.7**	**13.6**	**8.5**	**22.2**	**7.9**	**8.7**	**8.1**	**7.6**	**7.6**
	0.5	3.2	0.7	38.3	0.4	2.9	0.8	0.6	0.4	0.7	0.1	0.2	0.2
Int7	**7.1**	**9.5**	**7.3**	**7.0**	**1292**	**17.8**	**7.3**	**57.9**	**7.1**	**7.2**	**7.2**	**7.3**	**6.8**
	0.2	0.9	0.2	0.4	117.9	5.7	0.3	6.1	0.3	0.2	0.1	0.1	0.3
Int8	**7.6**	**10.4**	**7.2**	**7.1**	**8.0**	**2669**	**7.6**	**41.0**	**7.2**	**7.5**	**7.3**	**7.0**	**6.6**
	0.6	1.7	0.6	0.7	0.3	286	0.7	4.7	0.3	0.5	0.2	0.3	0.2
Int9	**6.9**	**8.1**	**7.0**	**6.8**	**7.8**	**20.4**	**251.7**	**50.1**	**6.9**	**7.3**	**7.1**	**6.6**	**6.7**
	0.2	0.3	0.3	0.2	0.6	4.9	50.7	16.0	0.3	0.2	0.4	0.2	0.2
Int10	**6.9**	**8.4**	**7.2**	**7.1**	**7.8**	**11.5**	**7.3**	**943.7**	**7.3**	**7.4**	**7.5**	**7.0**	**7.2**
	0.3	0.3	0.3	0.3	0.3	1.0	0.2	405.4	0.5	0.3	0.3	0.1	0.2
Int11	**6.9**	**9.4**	**7.2**	**7.1**	**7.7**	**12.1**	**7.3**	**28.4**	**346.9**	**7.1**	**7.4**	**7.1**	**7.4**
	0.2	0.5	0.0	0.0	0.3	1.8	0.1	2.4	18.4	0.2	0.2	0.0	0.3
Int12	**6.9**	**14.4**	**7.4**	**7.2**	**8.8**	**22.5**	**7.8**	**38.9**	**7.6**	**794.4**	**7.6**	**7.1**	**7.1**
	0.5	4.0	0.5	0.4	0.8	6.5	0.7	6.7	0.4	129.2	0.2	0.2	0.2
Int13	**7.1**	**9.5**	**7.3**	**7.2**	**7.9**	**11.0**	**7.5**	**17.2**	**7.6**	**8.4**	**390**	**7.6**	**7.7**
	0.3	2.6	0.3	0.4	0.5	1.4	0.4	1.1	0.4	0.8	28.4	0.2	0.3
FimE	**7.6**	**5.7**	**7.6**	**7.4**	**8.0**	**11.6**	**7.6**	**21.7**	**7.3**	**7.5**	**7.3**	**885.7**	**10.0**
	0.6	4.9	0.1	0.0	0.1	0.0	0.2	2.5	0.0	0.1	0.1	10.8	0.1
HbiF	**7.3**	**8.8**	**7.5**	**7.6**	**7.6**	**8.7**	**7.6**	**13.8**	**7.3**	**7.4**	**7.5**	**43.5**	**225.7**
	0.1	0.1	0.1	0.2	0.2	0.2	0.2	0.5	0.0	0.1	0.2	4.2	5.0

a. The average (upper row, bold) and standard deviation (lower row) of three independent triplicates are shown.

Supplementary Table 7: ***Sequence of the memory array***

Table 7. Sequence of the memory array[a]

Memory array	ggacggcgcagaaggggagtagctcttcgccggaccgtcgacatactgctcagctcgtcgtcgccaaatggatccgagcgttgatccgg taaaaccggattcggggaatagccaagagcagtgccttgcagaagttctcgggcgagaatctcgcgtagacacatacatgagcgtttgt aaaggagactgataatggcatgtacaactatactcgtcggtaaaaaggcatcttatcggtagtcccggtcgcctctctcgacgaaccgc ttacatgcctagccgataagcattatttaggcactacaactagtatagttgtacatgaaaaacgctgtatttttttatccatttccaaa gagcgcccaacgcgacctgaaatttgaataagactgctgcttgtgtaaaggcgatgattgttgtgaacattagaggtcgtatcctatcg cgataattccatatcgtacaaaacgaattacaaattatttgaccgctaattcaaatcaagggttgaaaactttgtaatttttggagcgc cggatcagggagtggacggcctgggagcgctacacgctgtggctgcggtcggtgcaaaaagatttgatgcccgctgcgcacatctagtt aatgtccgcaagactccagatcagggtgcgcaagttgtcaacgctcccaggagagttatcgacttgcgtattagggagacgagaaacgt tccgtccgtctgggtcagttgggcaaagttgatgaccgggtcgtccgttccttatcggtgtaggtcgattttggacagaaatatatggg gccagtaagcttacaagctgaacctgcgtaaaagttaaggttaggcatgtaaacttaactctcacacaggtttataacacccaatcatc agataactatggcggcacgtgcattaaccacggttgtatcccgtctaaagtactcgtgcgttggtatacttcagtcttaaccaatgcac cggtttgtgcggatgcctattttattatggaagtttgttcactcaacattgcaagactgtacatacttccatagtttattaatttatat tgcgaaaaataattggcgaacgaggtaactggatacctcatccgccaattaaaatttgagcaccattgccttggcgatcagcatgaggc tgcctgagatcctctagaataattggaagttcggaataactatgcagatacctgatacacacttccaacaaaaacaaccacaagcacgc tgataatcagcaagaccaccaacatttccaccaatgtaaaagctttaaccttagcttatacacaaatctaattttccatgtaggctgca cgaccccgtccaatagtcaaaagagtgagagttttactatccttgattgagatgtaggttactaaaattatttatattttccaaatgga ttttgcagattcccagatgcccctacagaaagaggtacaaaacatttattggaattaattagttcgtgttttggattgttacacgttct ctagcttatgatctgagcgtaagttgaaatatgtttactaataagactttatgggttgagagcgtcttattagtaaacatataaacgtt cgtggtaactatgggtggtacaggtgccacattagttgtaccatttatgtttatgtggttaacccagaggaacactccgtcggtcgcgc actaggaagaattccgaaggtcccttaaattttaatagcagttgtgtcactatttaggtctacccagtgacacaactaacatacaaaac aataacggttgtatttgtagaacttgaccagttgttttagtaacataaatacaactccgaatactcatagccccccgattcgccaggta cttacgaggaattacttatatccgactcacatggattgcttatatttacaggaccaactggatctggaaaaacaacaacaatgtatgcg
Sequence after Int2/5/7/8 Induction	ggacggcgcagaaggggagtagctcttcgcccgagaacttctgcaaggcactgctcttggctattccccgaatccggttttaccggatc aacgctcggatccatttggcgacgacgagctgagcagtatgtcgacggtccggcgagaatctcgcgtagacacatacatgagcgtttgt aaaggagactgataatggcatgtacaactatactcgtcggtaaaaaggcatcttatcggtagtcccggtcgcctctctcgacgaaccgc ttacatgcctagccgataagcattatttaggcactacaactagtatagttgtacatgaaaaacgctgtatttttttatccatttccaaa gagcgcccaacgcgacctgaaatttgaataagactgctgcttgtgtaaaggcgatgattgttgtgaacattagaggtcgtatcctatcg cgataattccatatcgtacaaaacgaattacaaattatttgaccgctaattcaaatcaagggttgaaaactttgtaatttttggagcgc cggatcagggagtggacggcctgggagcgttgacaacttgcgcaccctgatctggagtcttgcggacattaactagatgtgcgcagcgg gcatcaaatctttttgcaccgaccgcagccacagcgtgtagcgctcccaggagagttatcgacttgcgtattagggagacgagaaacgt tccgtccgtctgggtcagttgcctaaccttaacttttacgcaggttcagcttgtaagcttactggccccatatatttctgtccaaaatc gacctacaccgataaggaacggacgacccggtcatcaactttgcccatgtaaacttaactctcacacaggtttataacacccaatcatc agataactatggcggcacgtgcattaatgttgagtgaacaaacttccataataaaataggcatccgcacaaaccggtgcattggttaag actgaagtataccaacgcacgagtactttagacgggatacaaccgtggttgcaagactgtacatacttccatagtttattaatttatat tgcgaaaaataattggcgaacgaggtaactggatacctcatccgccaattaaaatttgagcaccattgccttggcgatcagcatgaggc tgcctgagatcctctagaataattggaagttcggaataactatgcagatacctgatacacacttccaacaaaaacaaccacaagcacgc tgataatcagcaagaccaccaacatttccaccaatgtaaaagctttaaccttagcttatacacaaatctaattttccatgtaggctgca cgaccccgtccaatagtcaaaagagtgagagttttactatccttgattgagatgtaggttactaaaattatttatattttccaaatgga ttttgcagattcccagatgcccctacagaaagaggtacaaaacatttattggaattaattagttcgtgttttggattgttacacgttct ctagcttatgatctgagcgtaagttgaaatatgtttactaataagactttatgggttgagagcgtcttattagtaaacatataaacgtt cgtggtaactatgggtggtacaggtgccacattagttgtaccatttatgtttatgtggttaacccagaggaacactccgtcggtcgcgc actaggaagaattccgaaggtcccttaaattttaatagcagttgtgtcactatttaggtctacccagtgacacaactaacatacaaaac aataacggttgtatttgtagaacttgaccagttgttttagtaacataaatacaactccgaatactcatagccccccgattcgccaggta cttacgaggaattacttatatccgactcacatggattgcttatatttacaggaccaactggatctggaaaaacaacaacaatgtatgcg

a. The colors of the att sequences correspond to **Figure 3a**. The 50bp spacer sequences flanked by att sites are shown in grey.

<u>Supplementary Table 8:</u> Spacer sequences used to construct the memory array

Table 8. Spacer sequences used to construct the memory array

Flanking att sites	sequences
Int2	`gtcgccaaatggatccgagcgttgatccggtaaaaccggattcggggaat`
Int3	`cggtagtcccggtcgcctctctcgacgaaccgcttacatgcctagccgat`
Int4	`gttgtgaacattagaggtcgtatcctatcgcgataattccatatcgtaca`
Int5	`aaaaagatttgatgcccgctgcgcacatctagttaatgtccgcaagactc`
Int7	`atcggtgtaggtcgattttggacagaaatatatggggccagtaagcttac`
Int8	`gcgttggtatacttcagtcttaaccaatgcaccggtttgtgcggatgcct`
Int9	`agcaccattgccttggcgatcagcatgaggctgcctgagatcctctagaa`
Int10	`atacacaaatctaattttccatgtaggctgcacgaccccgtccaatagtc`
Int11	`agttcgtgttttggattgttacacgttctctagcttatgatctgagcgta`
Int12	`ccagaggaacactccgtcggtcgcgcactaggaagaattccgaaggtccc`
Int13	`ctcatagccccccgattcgccaggtacttacgaggaattacttatatccg`

<u>Supplementary Table 9:</u> Primer sequences used to characterize the memory array

Table 9. Primer sequences used to characterize the memory array

Name	Sequences
Int2_fwd	caaaatgttctttacgatgccattggg
Int2_rev	tccgagcgttgatccggtaaaac
Int3_fwd	gcccgatcaactcgcgc
Int3_rev	tctctcgacgaaccgcttacatgc
Int4_fwd	gcgtagacacatacatgagcgtttgtaaagg
Int4_rev	cattagaggtcgtatcctatcgcgataattcc
Int5_fwd	ttttatccatttccaaagagcgccc
Int5_rev	atgcccgctgcgcacat
Int7_fwd	gtaatttttggagcgccggatcag
Int7_rev	cgattttggacagaaatatatggggcc
Int8_fwd	gggagacgagaaacgttccgtcc
Int8_rev	gtatacttcagtcttaaccaatgcaccggtttg
Int9_fwd	gtttataacacccaatcatcagataactatggcg
Int9_rev	gcatgaggctgcctgagatcctcta
Int10_fwd	atacttccatagtttattaatttatattgcgaaaaataattggcg
Int10_rev	ctaattttccatgtaggctgcacgacc
Int11_fwd	caacaaaaacaaccacaagcacgct
Int11_rev	gtgttttggattgttacacgttctctagcttatgatc
Int12_fwd	tatttatattttccaaatggattttgcagattccc
Int12_rev	cactccgtcggtcgcgc
Int13_fwd	gtaaacatataaacgttcgtggtaactatgggtggtac
Int13_rev	atagccccccgattcgcca

<u>Supplementary Note 1</u>: Discovery strategy when prophages occur within a conserved gene

Our method to identify the recognition sites of an LSTP integration is based on a genome comparisons of those regions that occur up- and downstream of the prophage. This requires a reference genome that lacks the prophage. We also developed a complimentary method that does not require a reference genome when the prophage occurs within a conserved gene. In these cases, the truncated gene fragments corresponding to the N- and C-terminal protein fragments can be identified up- and downstream of the prophage. The truncated protein fragments are compared against the NCBI protein database using a BLASTP search (default parameters). If a protein is found that is longer than the fragments, it can be used as the reference protein. The 5'- and 3'- gene fragments corresponding to the protein fragments are aligned with the gene for the reference protein (**Supplementary Fig.1**). This yields the 2-18bp core sequence that occurs where the protein coding sequence splits. The *attL* and *attR* sites were defined by taking about 60bp around the core sequence. The *attB* and *attP* sites were reconstructed using *attL* and *attR* sequences, as described in **Figure 1b**. Eight out of the 34 members of integrase-*attB/P* library was discovered using this strategy and they are demarcated in Table 1. For some integrases both strategies can be applied.

***Supplementary Note 2*: Weak promoter activity of the Int13 attP site**

When building all the memory switches, the first construct that was attempted by placing the *attP* site upstream of the *gfp* coding sequence. For the majority this was not a problem, but we found that the Int13 site generated a weak constitutive promoter (**Supplementary Fig.2**). This activity was sufficient to move the OFF cell population past the threshold that we used across the memory switches to determine the % of cells that turn on. Unintentional promoters appearing within parts or at part junctions have been observed previously[13]. We eliminated this problem by swapping the *att* sites so that *attP* occurs downstream of *gfp*. Note that after flipping, the resulting *attR* site is insulated by the spacer and RiboJ sequence.

***<u>Supplementary Note 3:</u>* Optimization of RBS sequence for each integrase**

Optimizing the dynamic range of each memory switch required tuning the ribosome binding site (RBS) controlling the expression of the integrase. If the expression is too high, then the switch turns on prior to the addition of inducer. If the expression is too low, then the switch cannot turn on or only a subpopulation of cells turns on.

The optimal level of expression depends on a number of factors and is not known *a priori*. Therefore, to identify the optimal RBS, degenerate RBS sequences consisting of 16-32 sequences were designed using the RBS Calculator for each integrase that encompassed translation initiation rates from 10^0 to 10^4 au[4]. The degenerate RBS sequences were synthesized in primers and inserted upstream of the coding sequence of each integrase gene using inverse PCR. In detail, the plasmid sequence was amplified using Phusion HF DNA polymerase (New England Biolabs), digested with DpnI restriction enzyme (New England Biolabs) and gel-recovered. The product was then phosphorylated by T4 Polynucleotide Kinase (New England Biolabs) and ligated by T4 ligase (Invitrogen) in a single reaction for 1 hour at room temperature. *E. coli* DH10b cells containing only the reporter plasmid were made electro-competent and transformed with the cognate controller plasmids with degenerate RBS by electroporation. For each integrase 32-64 colonies were picked and cultured in LB media plus 0.5% glucose, 34 μg/ml chloramphenicol and 50 μg/ml kanamycin for screening. The overnight (16 hour) cultures of transformants were washed twice and diluted 200 times in LB containing 0.5% glucose (control) or 1 mM arabinose (induction), and then grown for 6h before flow cytometry analysis. A clone was chosen to have an "optimal" RBS if it exhibited minimal leakage (<0.5% population expressing GFP) and maximal GFP expression when induced (**Supplementary Table 3**).

<u>Supplementary Note 4:</u> The impact on growth when single or multiple integrases were induced

In Figure 2G the impact on growth is measured when single integrases were induced. To investigate if the growth defect is additive when multiple integrases are used, cells containing 2-integrase cascade (**Supplementary Fig. 8**, Cas_2+5), 3-integrase cascade (**Figure 3f**, Cas_2+5+7) and 4-integrase operon (**Figure 3c**, Cis_2+7+8+5) were compared with strains containing single integrases (**Figure 2**, Int2, Int5, Int7 and Int8) after 12 hours induction with various concentrations of arabinose (**Supplementary Fig. 9**). The final OD (600mm) decreased slightly in cells containing single integrases at high concentration of arabinose for cells expressing single integrases. However the same effect was not observed in cells incorporating multiple integrases, suggesting that using multiple integrases in parallel is not constrained by growth defect.

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