

## Supporting Information

### ***De novo design of the ArsR regulated P<sub>ars</sub> promoter enables a highly sensitive whole-cell biosensor for arsenic contamination***

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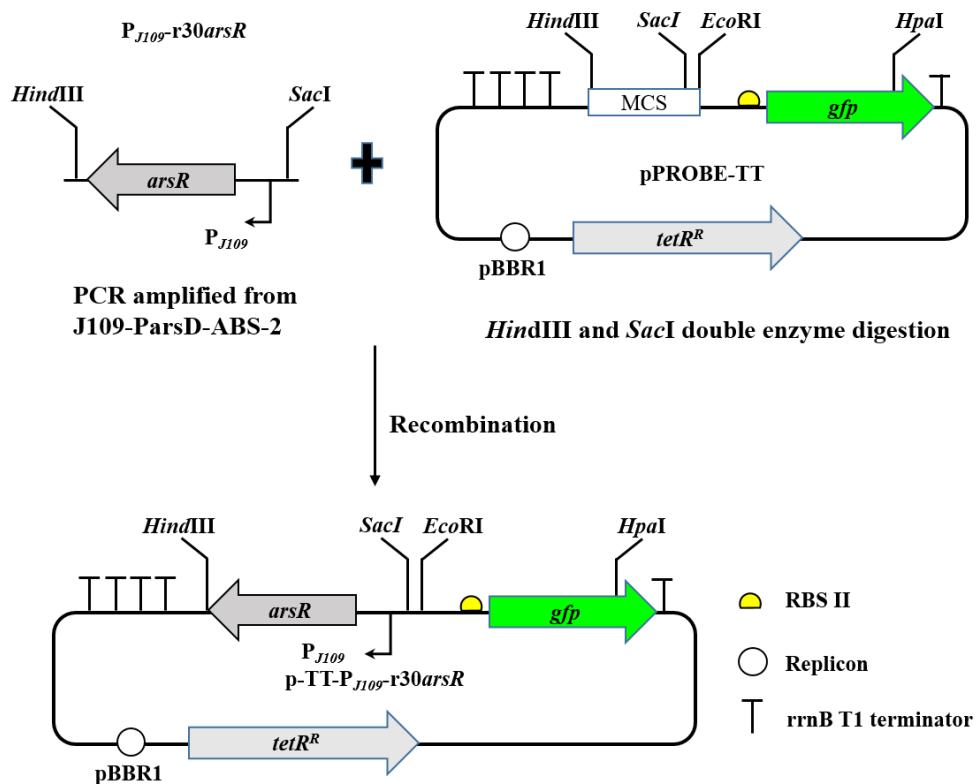
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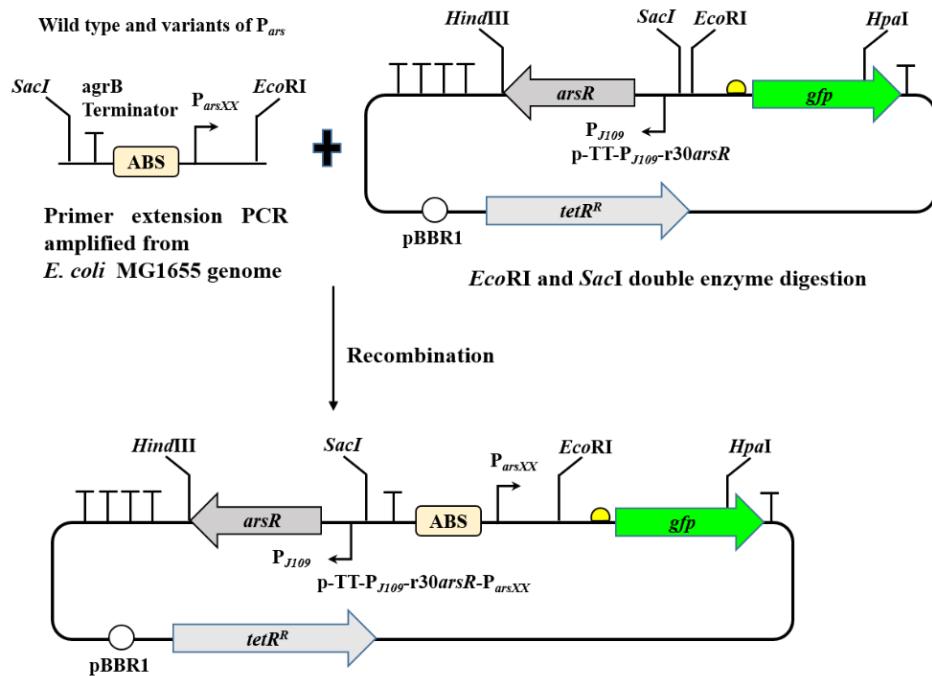
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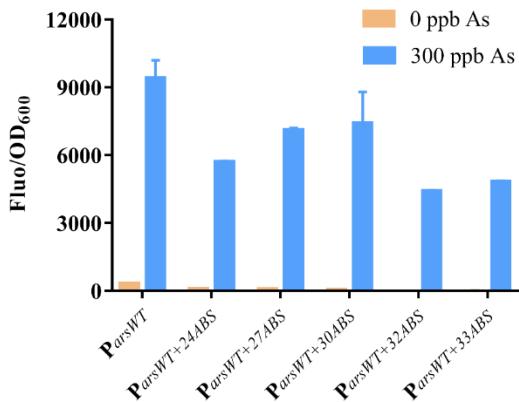
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**Figure S1. Schematic diagram of the p-TT-P<sub>J109</sub>-r30arsR plasmid construct.**

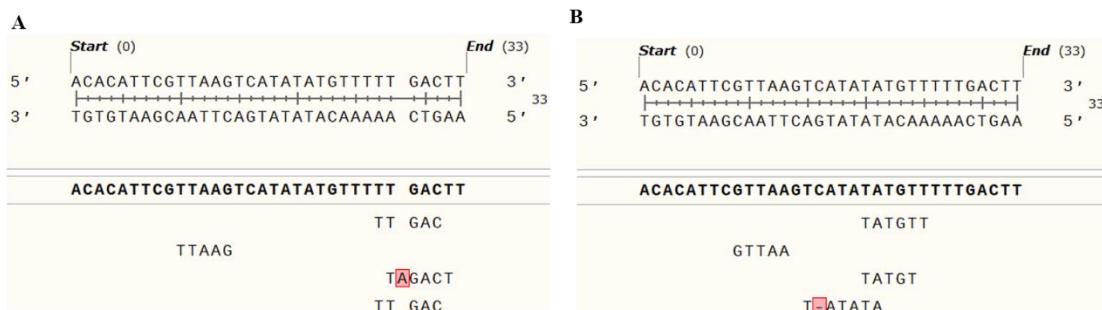


**Figure S2. Schematic diagram of the p-TT-P<sub>J109</sub>-r30arsR-P<sub>arsXX</sub> (named as P<sub>J109</sub>-P<sub>arsXX</sub>) plasmid construct.**



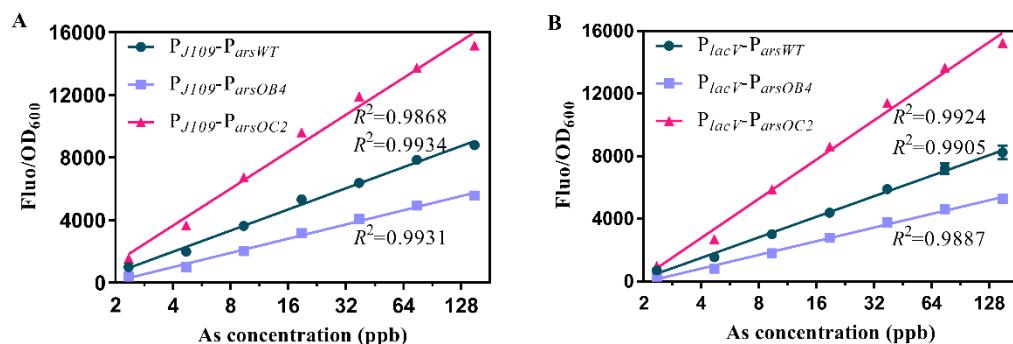
**Figure S3. Validation of the effective length of the ArsR binding site.**

The ABS of different lengths were added downstream of the wild-type promoter to test the leakage level of the sensor.



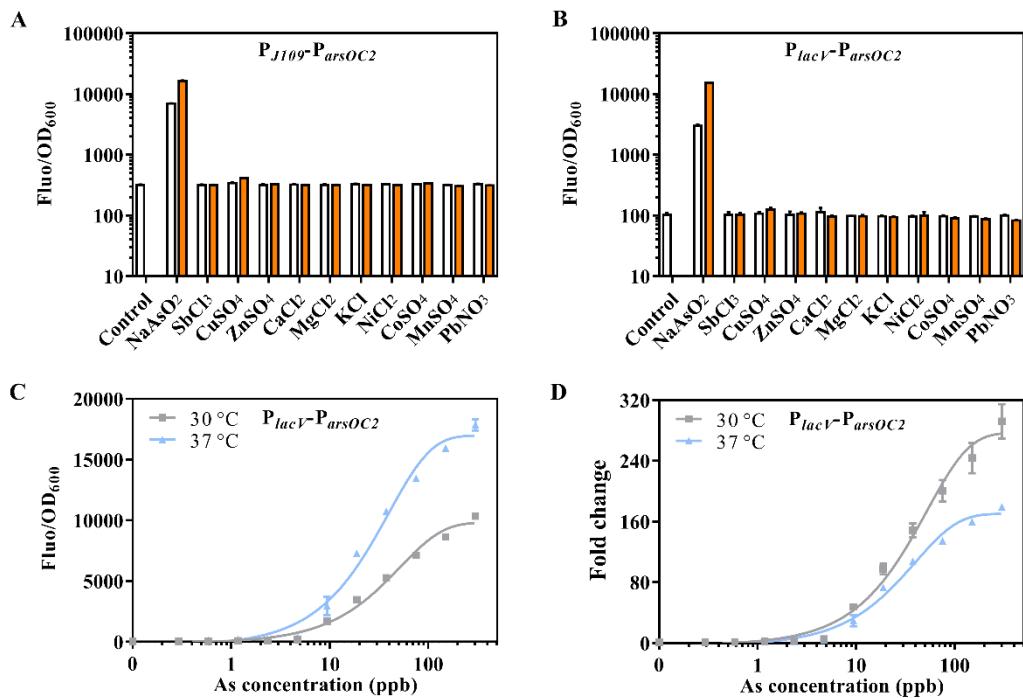
**Figure S4. Results showing ABS sequence alignment with the RNA polymerase binding site.**

- (A) Alignment with the  $-35$  sites library allows the ABS sequence to generate new  $-35$  sites.  
(B) Alignment with the  $-10$  sites library allows the ABS sequence to generate new  $-10$  sites.



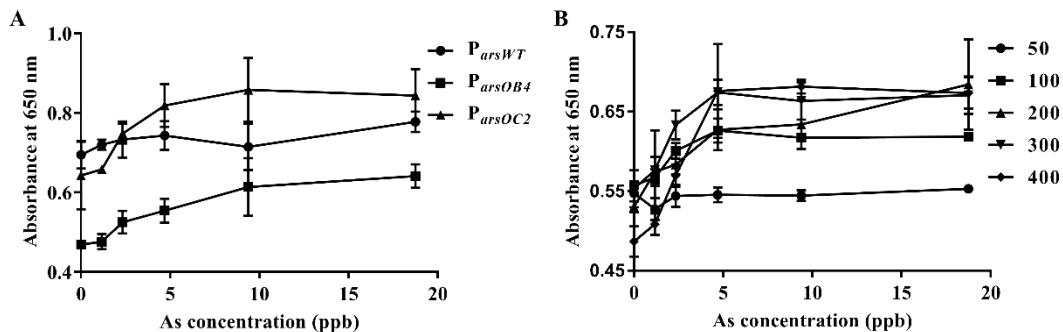
**Figure S5. Different fluorescent sensors showing linear response to arsenic.**

- (A) Best-fit parameters for the P<sub>J109</sub>-P<sub>arsWT</sub>, P<sub>J109</sub>-P<sub>arsOB4</sub>, and P<sub>J109</sub>-P<sub>arsOC2</sub> biosensors in the 2.34 to 150 ppb arsenic concentration. (B) Best-fit parameters for the P<sub>lacV</sub>-P<sub>arsWT</sub>, P<sub>lacV</sub>-P<sub>arsOB4</sub>, and P<sub>lacV</sub>-P<sub>arsOC2</sub> biosensors in the 2.34 to 150 ppb arsenic concentration. The data from Figure 3.A and C, the error bars are smaller than the data symbols ( $n = 3$ ).



**Figure S6. Sensor specificity and temperature effect on sensor performance.**

**(A-B)** Characterization of the specificity of the  $P_{J109}\text{-}P_{arsOC2}$  and  $P_{lacV}\text{-}P_{arsOC2}$  sensor, for arsenic and antimony, the induced final concentrations were 0.1  $\mu\text{M}$  (7.5 ppb for As) and 1  $\mu\text{M}$  (75 ppb for As); for all other compounds, the induced concentrations were 10  $\mu\text{M}$  and 100  $\mu\text{M}$ . **(C-D)** The dose-response and fold change of the  $P_{lacV}\text{-}P_{arsOC2}$  sensor to different concentrations of arsenic at 30 °C and 37 °C. Error bars show the standard deviation ( $n = 3$ ).



**Figure S7. Absorbance of diverse colorimetric sensors at 650 nm was monitored across various arsenic concentrations.**

**(A)** OD<sub>650</sub> of cell cultures with different colorimetric sensors at various concentrations of arsenic (X-gal = 200  $\mu\text{g}/\text{mL}$ ). **(B)** OD<sub>650</sub> of the  $P_{lacV}\text{-}P_{arsOB4}\text{-}lacZ$  sensor at different X-gal substrate concentrations. Error bars show the standard deviation ( $n = 3$ ).

**Table S1. Primers used in this study**

Primer name	Sequence
HR-EcoRI-Pars-R	gttagttaggaataagcc <u>gaattc</u> TTGTTGCAGGTAGTGTCTCTTCG
arsO-R1	AGGAAGGTAATAGGTGTGAATTGG
arsO-R3	gggataagcc <u>gaattc</u> TTCGAAGCGGATAAGTCAAAAACATATATGACTAACGAATGT
arsOA1-R2	AAAACATATATGACTAACGAATGTGTAAATGCAGAGGAAGGTAATAGGTG TGAATTGG
arsOB1-R2	AAAACATATATGACTAACGAATGTGTAAAGCAGAGGAAGGTAATAGGTG TGAATTGG
arsOB2-R2	AAAACATATATGACTAACGAATGTGTAAAGCAGAGGAAGGTAATAGGTG TGAATTGG
arsOB3-R2	AAAACATATATGACTAACGAATGTGTAAAGCAGAGGAAGGTAATAGGTG TGAATTGG
arsOB4-R2	AAAACATATATGACTAACGAATGTGTACAAGCAGAGGAAGGTAATAGGTG TGAATTGG
arsOB5-R2	AAAACATATATGACTAACGAATGTGTAAAGCAGAGGAAGGTAATAGGTG TGAATTGG
arsOC1-R2	AAAACATATATGACTAACGAATGTGTAAACAGAGGAAGGTAATAGGTG TGAATTGG
arsOC2-R2	AAAACATATATGACTAACGAATGTGTCAACAGAGGAAGGTAATAGGTG TGAATTGG
arsOC3-R2	AAAACATATATGACTAACGAATGTGAGTCAACAGAGGAAGGTAATAGGTG TGAATTGG
arsOD1-R2	AAAACATATATGACTAACGAATGTGTGTAAAGAGGAAGGTAATAGGTG TGAATTGG
arsOE1-R2	AAAACATATATGACTAACGAATGTGTATGTAAAGAGGAAGGTAATAGGTGT GAATTGG
arsOE2-R2	AAAACATATATGACTAACGAATGTGTATGTCAAGAGGAAGGTAATAGGTGT GAATTGG
arsOF1-R2	AAAACATATATGACTAACGAATGTGTAAATGTAAAAGGAAGGTAATAGGTGT GAATTGG
arsOG1-R2	AAAACATATATGACTAACGAATGTGTAAAGTGTAAAGGAAGGTAATAGGTG TGAATTGG
arsOH1-R2	AAAACATATATGACTAACGAATGTGTAAAGTGTAAAGGAAGGTAATAGGTGT GAATTGG
ParsWT24arsO-R	<u>CGAATT</u> CGCGGAAAGTC AAAAACATATATGACTAACGTTATTGTCAGGTAGTGT CTCTCTTC
ParsWT27arsO-R	<u>CGAATT</u> CGCGGAAAGTC AAAAACATATATGACTAACGATTGTTGCAGGT GTGTCTCTTC
ParsWT30arsO-R	<u>CGAATT</u> CGCGGAAAGTC AAAAACATATATGACTAACGAATGTTGTTGCAG GTAGTGTCTCTTC

ParsWT32arsO-R	<u>CGAATT</u> CGCGGAAAGTCAAAAACATATATGACTTAACGAATGTGTTGTTGC AGGTAGTGTCTCTCTTC
ParsWT33arsO-R	<u>CGAATT</u> CGCGGAAAGTCAAAAACATATATGACTTAACGAATGTGTTGTTGC AGGTAGTGTCTCTCTTC
(pTTsacI)J109-R	gaataagcc <u>gaattcgagctc</u> TTTACAGCTAGCTCAGTCCTAGGGAC
(J109)Pars-F	ctaggactgagctagctgtaa <u>agagctc</u> AGCCACTGGCTAATAGTAT
(pTTsacI)PlacV-R	gaataagcc <u>gaattcgagctc</u> GCGCCCAATACGCAAACCG
(lacVsacI)Pars-F	ggtttgcgtattggg <u>cgagctc</u> AGCCACTGGCTAATAGTATTGAGCTG
(pTTRBS)lacZ-F	CTAACTAAAGATTAACTTATAAGGAGGAAAAACATATGACCATGATTACGG ATTCACTG
(Parswt)pTTRBS-F	tacctcaaca <u>agaatc</u> GGCTTATTCCCTAACTAACAAAGATTAACTTATAAGGAG G
(arsO)pTTRBS-F	atccgc <u>ttcgagaatc</u> GGCTTATTCCCTAACTAACAAAGATTAACTTATAAGGAG G
(HRhapI)lacZ-R	tttgtctaattt <u>gaagttaac</u> TTATTATTTTGACACCAGACCAACTG
pPROBE-TT-F	GGAATTGGGGATCGGAAGCTT (sequencing primer)
pPROBE-TT-R	GCATCACCTTCACCCCTCTCCAC (sequencing primer)

Note: The DNA sequence (lowercase) indicates the homologous recombination sequence on the plasmid. The underlined sequences are restriction endonuclease sites.

**Table S2. Sequences of the genetic constructs used in this study**

Gene name	Sequence and characteristic
P <sub>J109</sub> -RBS30	(SacI)TTTACAGCTAGCTCAGTCCTAGGGACTGTGCTAGCTACTAGAGATTAAGAGGAG AAATACTAG( <i>arsR</i> ) RBS30: ATTAAAGAGGAGAAATACTAG
P <sub>lacV</sub> -RBS <sub>arsR</sub>	(SacI)ACGCAAACCGCCTCTCCCGCGTTGCCGATTCAATGCAGCTGGCACGAC AGGTTCCCGACTGGAAAGCGGGCAGTGAGCGAACGCAATTATGTGAGTTAGCTCA CTCATTAGGCACCCAGGCTTACGTTGAGCGCTCACAAATTATAGTGTGGAATCA ATCAGGAGCGCAAT ( <i>arsR</i> ) RBS <sub>arsR</sub> : CAATCAGGAGCGCAAT
<i>arsR</i>	(P <sub>J109</sub> -RBS30 or P <sub>lacV</sub> -RBS <sub>arsR</sub> ) <b>ATGTCATTCTGTTACCCATCCAATTGTTCAAAATTCTGCTGATGAAACCGTCTGGC</b> ATCGTTTACTGCTCAGCGAACCTGGGAGAGTTATGCGTCTGCGATCTGCACTGCTCT CGACCAGTCGCAAGCCAAAGATCTCCGCCACCTGGCATTGCTGCGTGAAGCGGGCTA TTGCTGGACCGCAAGCAAGGTAAGTGGGTCATTACCGCTTATCACCGCATATTCCAGC ATGGGCGGGAAAATTATTGATGAGGCCTGGCGATGTGAACAGGAAAAGGTTCAGGCG ATTGTCCGCAACCTGGCTCGACAAAATGTTCCGGGGACAGTAAGAACATTGCAGT <b>T</b> <b>AA(HindIII)</b>

$P_{arsWT}$ promoter	( <i>SacI</i> )AGCCACTGGCTAATAGTATTGAGCTGTAGATAAGAACTCTCACTCCAGGCCAG AGCCACCAACTCAGGGCTGGAAAGTAAAAAACGACGCAAAGTCGGTTTTTACG <b>TCTGATT</b> CAGACCTCTTCAAATGAATAGCCA <b>ACTCAAAATT</b> CACACCTATTACCT CCTCTGCACTT <u>ACACATTGTTAAGTCATATATGTTTTGACTT</u> ATCCGCTTCGAAGAG <b>AGACACTAC</b> CTGCAACAA ( <i>EcoRI</i> ) agrB Terminator: <b>AAAAAACCGACGCAAAGTCGGTTTTTACGTCCTGA</b> <sup>1</sup> ArsR Binding site: <u>ACACATTGTTAAGTCATATATGTTTTGACTT</u> <sup>2</sup> -35 site: <b>TTGACT</b> -10 site: <b>GACACT</b>
<i>gfp</i> gene (pPROBE-TT carrying a <i>gfp</i> )	( <i>EcoRI</i> )ggcttattccctaactaactaaagattaactttataaggaggaaaaacat <b>ATG</b> AGTAAAGGAGAAGAACTTT CACTGGAGTTGTCCAATTCTTGTGAATTAGATGGTGATGTTAATGGGCACAAATTTC TGTCACTGGAGAGGGTGAAGGTGATGCAACATAACGGAAA <b>ACTTACCCCTAAATT</b> TATT GCACTACTGGAAA <b>ACTACCTGTCCATGGCAACACTTGTCACTACTTGTACTTATGGT</b> GTTCAATGCTTTCAAGATA <b>ACCCAGATCATATGAAACGGCATGACTTTCAAGAGTGC</b> CATGCCGAAGGTTATGTACAGGAAAGAA <b>ACTATTTCAAAAGATGACGGAACTACA</b> AGACACGTGCTGAAGTCAAGTTGAAGGTGATACCCTGTTAATAGAATCGAGTTAAA GGTATTGATTAAAGAAGATGGAA <b>ACATTCTGGACACAAATTGGAATACAAC</b> ATAA CTCACACAATGTATA <b>CATGGCAGACAAACAAAAGAATGGAATCAAAGTTA</b> ACTTCA AAATTAGACACA <b>ACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC</b> AAA TACTCCAATTGGCGATGGCCCTGTCCTTACCA <b>GACACACCATTACCTGTCCACACA</b> ATC TGCCCTTCGAAAGATCCCACGAAAAGAGAGACCACATGGCCTTCTGAGTTGTA ACAGCTGCTGGATTACACATGGCATGGATGAACTATAAA <b>TAG</b>
<i>lacZ</i> gene (Amplified from <i>E. coli</i> MG1655 by PCR)	( <i>EcoRI</i> )ggcttattccctaactaactaaagattaactttataaggaggaaaaacat <b>ATG</b> ACCATGATTACGGATTCACTG GCCGTGTTTACAACGTCGTGACTGGGAAA <b>ACCCCTGGCGTTACCCAACTTA</b> ATCGCCT TGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCGACCGATCGC CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCTTGGCCTGGTTCCGGCACC AGAACGGTGCCGGAAAGCTGGCTGGAGTGCGATCTCCTGAGGCCGATACTGTCGTC GTCCCCCTCAA <b>ACTGGCAGATGCACGGTTACGATGCGCCCATCTACACCAACGTGACCTA</b> TCCCATTACGGTCAATCCGCCGTTGTTCCCACGGAGAATCCGACGGGTTGTTACTCGC TCACATTAA <b>ATGTTGATGAAAGCTGGCTACAGGAAGGCCAGACCGA</b> ATTATTTTGAT GGCGTTAACTCGCGTTCATCTGTTGCAACGGCGCTGGCGTTACGGCCAGG ACAGTCGTTGCGCTGAATTGACCTGAGCGCATTTCACGCCCGGAGAAA <b>ACCG</b> CCTCGCGGTGATGGTGTGCGCTGGAGTGACGGCAGTTATCTGGAAGATCAGGATATGT GGCGGATGAGCGGCATTTCCTGACGTCTCGTGTGCAAA <b>ACCGACTACACAA</b> ATC AGCGATTCCATGTTGCCACTCGCTTAATGATGATTTCAGCCCGCTGTACTGGAGGCT GAAGTTCAGATGTGGCGAGTTGCGTGA <b>CTACCCGTAACAGTTCTTATGGCA</b> GGGTGAAACGCAAGTCGCCAGCGGACCGCGCTTCGGCGGTGAA <b>ATTATCGATGAG</b> CGTGGTGGTTATGCCATCGCGTACACTACGTCTGAACGTCGAA <b>ACCCGAAACTGT</b> GGAGCGCCGAAATCCGAATCTATCGTGGCGTGGTGA <b>ACTGCACACCGCCACGG</b> CACGCTGATTGAAGCAGAAGCCTGCGATGTCGGTTCCCGAGGTGCGGATTGAAAAT GGTCTGCTGCTGAACGGCAAGCGTTGCTGATTGAGGCGTTAACCGTCACGAGC ATCATCCTCTGCATGGTCAGGTATGGATGAGCAGACGATGGCAGGATATCCTGCTG ATGAAGCAGAACAACTTAACGCCGTGCGCTGTCGATTATCGAACCATCCGCTGTG GTACACGCTGTGCGACCGCTACGGCCTGTATGTGGTGGATGAAGCCAATATTGAAACCC

	ACGGCATGGTCCAATGAATCGTCTGACCGATGATCCGCCTGGCTACCGGCATGAGC GAACCGTAACCGAATGGTCAGCGCATCGAATCACCGAGTGTATCATCTGGTC GCTGGGAATGAATCAGGCCACGGCGCTAACGACGCGCTGTATCGCTGGATCAAAT CTGTCGATCCTCCGCCGGTGCAGTATGAAGGCGCGGAGCCGACACCACGGCAC CGATATTATTGCCCAGTGTACCGCGCTGGATGAAGACCAGCCCTCCGGCTGTGC CGAAATGGTCCATCAAAAATGGCTTCGCTACCTGGAGAGACCGCCGCTGATCCT TGCAGAACGCCCCACCGATGGTAACAGTCTTGGCGGTTCGCTGGACTGGTGATCAGTC TGATTAAATATGATAACGGCAACCGTGGCTGGCTACGGCGGTGATTTGGCGAT ACGCCGAACGATGCCAGTTCTGTATGAACGGTCTGGCTTGCGACCGCACGCC ATCCAGCGTACGGAAGCAAACACCAGCAGCAGTTTCCAGTCCGTTATCCGG GCAAACCATCGAAGTGACCAGCGAATACCTGTTCCGTATAGCGATAACGAGCTCCTGC ACTGGATGGTGGCGCTGGATGGTAAGCCGCTGGCAAGCGGTGAAGTGCCTCTGGATGT CGCTCCACAAGGTAAACAGTTGATTGAACTGCCTGAACCTACCGCAGCCGAGAGCGCC GGCAACTCTGGCTCACAGTACCGTAGTGCACCGAACGCGACCGCATGGTCAGAA GCCGGGCACATCAGGCCCTGGCAGCAGTGGCTGGCGAAAACCTCAGTGTGACG CTCCCCGCCGTCCCACGCCATCCGCATCTGACCACCAGCGAAATGGATTTGCAT CGAGCTGGTAATAAGCGTGGCAATTAAACGCCAGTCAGGCTTCTTCACAGATGT GGATTGGCGATAAAAAACAACTGCTGACGCCGCTGCGCATCGTACCTGGCACC GCTGGATAACGACATTGGCGTAAGTGAAGCGACCCGATTGACCCCTAACGCC GAACGCTGGAAGGCGCGGCCATTACCGAGCGAACGCGTTGCAGTCAC GCAGATACACTTGCTGATGCGGTGCTGATTACGACCGCTCACCGTGGCAGCATCAGG GGAAAACCTTATTIATCAGCGGAAAACCTACCGGATTGATGGTAGTGGCAAATGGCG ATTACCGTTGATGTTGAAAGTGGCGAGCGATACACCGCATCCGGCGGGATTGGCCTGAA CTGCCAGCTGGCGCAGGTAGCAGAGCGGGTAAACTGGCTGGATTAGGGCGCAAGA AAACTATCCCACCGCCTACTGCCGCTGTTGACCGCTGGGATCTGCCATTGTCAG ACATGTATACCCGTACGTCTCCGAGCGAAAACGGTCTGCGCTGGGACGCC ATTGAATTATGGCCCACCCAGTGGCGCGGACTTCCAGTCAACATCAGCC GTCAACAGCAACTGATGGAAACCAGCCATGCCATCTGCTGCACGCC CATGGCTGAATATCGACGGTTCCATGGGATTGGCGACGACTCCTGGAGCCCG TCAGTATCGCGGAATTCCAGCTGAGCGCCGTCGCTACCATTACCA TCAAAAA <b>TAA</b> ( <i>Hpa</i> I)
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Note: The parentheses before and after the gene indicate the gene or restriction endonuclease site directly connected to it; for the promoter, its characteristic sequence is indicated. The start and stop codons of the gene are marked in red.

**Table S3. Plasmid constructs used in this study**

Plasmid	Sequence differences of different arsenite-regulated promoters.
P <sub>J109</sub> -P <sub>arsWT</sub>	: CCTCTGCACTT <u>ACACATTGTTAAGTCATA</u> TATGTT <u>TTGACT</u> TATCCGCTTCGAA-GAGAGACACTACCTGCAACAA <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsWT+24ABS</sub>	: CCTCTGCACTT <u>ACACATTGTTAAGTCATA</u> TATGTT <u>TTGACT</u> TATCCGCTTCGAA-GAGAGACACTACCTGCAACAA <u>TTAAGTCATA</u> TATGTT <u>TTGACT</u> TCCGC <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsWT+27ABS</sub>	: CCTCTGCACTT <u>ACACATTGTTAAGTCATA</u> TATGTT <u>TTGACT</u> TATCCGCTTCGAA-GAGAGACACTACCTGCAACAA <u>TCGTTAAGTCATA</u> TATGTT <u>TTGACT</u> TCCGC <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsWT+30ABS</sub>	: CCTCTGCACTT <u>ACACATTGTTAAGTCATA</u> TATGTT <u>TTGACT</u> TATCCGCTTCGAA-GAGAGACACTACCTGCAACAA <u>CATTGTTAAGTCATA</u> TATGTT <u>TTGACT</u> TCCGC <b>GAA</b> <b>TTC</b>
P <sub>J109</sub> -P <sub>arsWT+32ABS</sub>	: CCTCTGCACTT <u>ACACATTGTTAAGTCATA</u> TATGTT <u>TTGACT</u> TATCCGCTTCGAA-GAGAGACACTACCTGCAACAA <u>CACATTGTTAAGTCATA</u> TATGTT <u>TTGACT</u> TCCGC <b>G</b> <b>AATT</b> C
P <sub>J109</sub> -P <sub>arsWT+33ABS</sub>	: CCTCTGCACTT <u>ACACATTGTTAAGTCATA</u> TATGTT <u>TTGACT</u> TATCCGCTTCGAA-GAGAGACACTACCTGCAACAA <u>ACACATTGTTAAGTCATA</u> TATGTT <u>TTGACT</u> TCCGC <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsO</sub>	: CCTCTGCACTT <u>ACACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOA1</sub>	: CCTCTGCA <b>TTTACACATTGTTAAGTCATA</b> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOB1</sub>	: CCTCTG <b>TTTACA</b> <u>ACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOB2</sub>	: CCTCTG <b>TTTACC</b> <u>ACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOB3</sub>	: CCTCTG <b>TTTAAC</b> <u>ACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOB4</sub>	: CCTCTG <b>TTGTAC</b> <u>ACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOB5</sub>	: CCTCTG <b>TTTTACACATTGTTAAGTCATA</b> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOC1</sub>	: CCTCTG <b>TTTACA</b> <u>ACACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOC2</sub>	: CCTCTG <b>TTGACA</b> <u>ACACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOC3</sub>	: CCTCTG <b>TTGACT</b> <u>ACACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOD1</sub>	: CCTCT <b>TTTACA</b> <u>ACACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOE1</sub>	: CCTCT <b>TTTACAT</b> <u>ACACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C
P <sub>J109</sub> -P <sub>arsOE2</sub>	: CCTCT <b>TTGACAT</b> <u>ACACATTGTTAAGTCATA</u> <b>TATGTT</b> <u>TTGACT</u> TATCCGCTTCGAA- <b>GAATT</b> C

P <sub>J109</sub> -P <sub>arsOF1</sub>	: CCT <b>TTTACA</b> TT <u>ACACATT</u> CGTAAGTCATA <b>TATGTT</b> <u>TTTGACTT</u> ATCCGCTTCGAA- <b>GAATTC</b>
P <sub>J109</sub> -P <sub>arsOG1</sub>	: CCT <b>TTTACA</b> CTT <u>ACACATT</u> CGTAAGTCATA <b>TATGTT</b> <u>TTTGACTT</u> ATCCGCTTCGAA- <b>GAATTC</b>
P <sub>J109</sub> -P <sub>arsOH1</sub>	: C <b>TTTACA</b> ACTT <u>ACACATT</u> CGTAAGTCATA <b>TATGTT</b> <u>TTTGACTT</u> ATCCGCTTCGAA- <b>GAATTC</b>
Plasmid	Description
P <sub>lacV</sub> -P <sub>arsWT</sub>	pPROBE-TT carrying P <sub>lacV</sub> -RBS <sub>arsR</sub> -arsR-P <sub>arsWT</sub> in between HindIII and EcoRI sites
P <sub>lacV</sub> -P <sub>arsOB4</sub>	pPROBE-TT carrying P <sub>lacV</sub> -RBS <sub>arsR</sub> -arsR-P <sub>arsOB4</sub> in between HindIII and EcoRI sites
P <sub>lacV</sub> -P <sub>arsOC2</sub>	pPROBE-TT carrying P <sub>lacV</sub> -RBS <sub>arsR</sub> -arsR-P <sub>arsOC2</sub> in between HindIII and EcoRI sites
P <sub>lacV</sub> -P <sub>arsWT-lacZ</sub>	pPROBE-TT carrying P <sub>lacV</sub> -RBS <sub>arsR</sub> -arsR-P <sub>arsWT-lacZ</sub> in between HindIII and HpaI sites
P <sub>lacV</sub> -P <sub>arsOB4-lacZ</sub>	pPROBE-TT carrying P <sub>lacV</sub> -RBS <sub>arsR</sub> -arsR-P <sub>arsOB4-lacZ</sub> in between HindIII and HpaI sites
P <sub>lacV</sub> -P <sub>arsOC2-lacZ</sub>	pPROBE-TT carrying P <sub>lacV</sub> -RBS <sub>arsR</sub> -arsR-P <sub>arsOC2-lacZ</sub> in between HindIII and HpaI sites

Note: P<sub>J109</sub>-P<sub>arsXX</sub> (XX means a different name) is the abbreviation of p-TT-P<sub>J109</sub>-r30arsR-P<sub>arsXX</sub>. The plasmids shown in sequence illustrate that their arsenic-regulated promoter sequences are different. The bolded sequence represents the original -10 and -35 positions of the wild-type promoter, and the bolded and italicized sequence represents the restriction endonuclease site EcoRI. The ArsR binding site is shown in underlined blue font, and the potential -10 site and the reconstructed -35 site are shown in bold red.

**Table S4. RNAP binding site library contains eighteen -35 sites and thirty-six -10 sites**

	-35 site		-10 site			
1	TTGACA <sup>3</sup>	CTTAGA <sup>4</sup>	TATAAT <sup>3, 4</sup>	GATAAC <sup>4</sup>	TACAAT*	ACAATG <sup>5</sup>
2	TAGACA <sup>3</sup>	ATCTGA <sup>6</sup>	TATAGT <sup>3</sup>	GTAAA <sup>4</sup>	GACTAT*	TAGGAT <sup>5</sup>
3	TTTACA <sup>3, 4</sup>	TAGACT <sup>6</sup>	GATAAT <sup>3</sup>	GTGTA <sup>4</sup>	TAGGCT <sup>5</sup>	GTATGT <sup>7</sup>
4	TTGTGA <sup>3</sup>	TTTATA*	GATACT <sup>3</sup>	ATATTA <sup>6</sup>	TAATAT <sup>5</sup>	TATATA <sup>7</sup>
5	CTGACA <sup>3</sup>	TTTACG*	TAAATT <sup>3</sup>	TACAGT*	TATGAT <sup>5</sup>	TATCGT <sup>7</sup>
6	TTTACC <sup>4</sup>	GCGGTG <sup>5</sup>	TACTGT <sup>3</sup>	TATTAT*	GTATCT <sup>5</sup>	AGGTG <sup>7</sup>
7	ATTACA <sup>4</sup>	TTGATG <sup>5</sup>	TATGTT <sup>3, 4</sup>	GATTAT*	GAGGAT <sup>5</sup>	TAGGTT <sup>7</sup>
8	TTAAGA <sup>4</sup>	TTGCAA	AATAAT <sup>4</sup>	TATTGT*	GATGAT <sup>5</sup>	TTTAAT <sup>7</sup>
9	CTCAGA <sup>4</sup>	TTGACG <sup>7</sup>	GACACT <sup>8</sup>	TACTAT*	TAAAAT <sup>5</sup>	TTAGTA <sup>7</sup>

\*Promoters/Catalog/Anderson - parts.igem.org

**Table S5. Best fits for the characterized responses of the arsenic sensors with diverse promoters**

Expression of ArsR	Promoter	Leaky <sup>a</sup>	$k^b$ (Fluo/OD <sub>600</sub> )	$Km^c$ /LOD <sup>d</sup> (ppb)	$R^2$	Fold change at various conc. (ppb)				
						0.29	1.17	9.38	75	300
P <sub>J109</sub>	P <sub>arsWT</sub>	387.71	9798.30	17.46/0.18	0.9837	1.12	1.59	9.39	20.24	25.27
	P <sub>arsOB4</sub>	84.75	6184.69	18.48/0.27	0.9836	1.20	2.28	24.16	58.43	73.21
	P <sub>arsOC2</sub>	319.66	16133.81	14.23/0.21	0.9899	1.25	2.38	21.12	43.04	50.54
P <sub>lacV</sub>	P <sub>arsWT</sub>	221.11	9065.22	21.84/0.21	0.9868	1.08	1.79	13.66	32.67	41.04
	P <sub>arsOB4</sub>	40.13	5889.15	22.10/0.31	0.9870	1.09	3.04	45.11	116.04	148.11
	P <sub>arsOC2</sub>	92.39	16942.84	18.40/0.24	0.9884	1.25	3.90	63.80	147.93	183.52

<sup>a</sup> Leaky: Basal expression in the absence of inducers.

<sup>b</sup>  $k$ : Maximum expression level in 300 ppb arsenic.

<sup>c</sup>  $Km$ : Inducer concentration achieving half-maximal activation.

<sup>d</sup> LOD: LOD stands for limit of detection and is the lowest analyte concentration that can probably be reliably distinguished from the basal signal.

**Table S6. Accuracy and reliability of the constructed biosensors for real samples**

Sample	AFS (ppb)	Final As (ppb)	255 – R <sup>a</sup> (Dilution factor)	Estimated (ppb)	Recover
G-Sample 1	20.7	20.7	129 (6)	17.82	86.08%
G-Sample 2		50.7	148 (10)	45.88	90.49%
G-Sample 2		80.7	137.33 (20)	76.07	94.26%

<sup>a</sup>Mean 255 – R value (n = 3).

**Table S7. Comparison of previously reported arsenic sensors with this study**

Microbial chassis Biosensor	LOD (ppb) <sup>a</sup>	Linear or input range (ppb) <sup>b</sup>	Description, reference
<b>gfp reporter</b>			
E. coli DH5α	0.24	2.34-150	This study
P <sub>lacV</sub> -P <sub>arsOC2</sub>			
E. coli DH5α	7.5	7.5-75	Gray value analysis, <i>ars</i> operon from R773 plasmid of <i>E. coli</i> . <sup>9</sup>
pPR-arsR-ABS			
E. coli DH5α	7.5	37.5-450	Non-specificity, high background noise, <i>ars</i> operon from pI258 plasmid of <i>S. aureus</i> . <sup>10</sup>
pVLAS1			
E. coli DH5α	0.75	1-50	Flow cytometry analysis, directed evolution <i>ars</i> operon, <i>ars</i> operon from pPR-arsR-ABS. <sup>11</sup>
pUC18-ep3ars-gfp			
E. coli K-12	5	5-140	With a T7 RNAP amplifier, <i>ars</i> operon from <i>E.</i>

POLA				
<i>E. coli</i> TOP10	0.75	2.3-7.5		<i>coli</i> genome. <sup>12</sup>
pAsS				Low fold changes, narrow response range. <i>ars</i> operon from <i>G. sulfurreducens</i> genome. <sup>13</sup>
Cell-free	3.65	4-50		Cell-free expression, fast response, <i>ars</i> operon from pUC18-ep3ars-gfp. <sup>14</sup>
ep3-gfp				
<b><i>lacZ</i> reporter</b>				
<i>E. coli</i> DH5α	0.39	1-5		This study
<i>PlacV-ParsOC2-lacZ</i>				
<i>E. coli</i>	8	8-78		Semi-quantitative analysis, <i>ars</i> operon from R773 plasmid of <i>E. coli</i> . <sup>9</sup>
pMV-arsR-ABS				
<i>E. coli</i> JM109	5	5-20		Output pH change, <i>ars</i> operon from <i>E. coli</i> genome. <sup>15</sup>
Pars/arsR-lacZ				
<i>B. subtilis</i>	7.5	7.5-7500		Coupled enzyme reaction for luminescence, <i>ars</i> operon from <i>B. subtilis</i> . <sup>16</sup>
ars-23				
<i>E. coli</i> DH5α	0.8	3.75-30		Electrochemical read-out, contain pPR-arsR-ABS-RBS-lacZ, with RBS optimal. <sup>17</sup>
strain 2245				
<i>E. coli</i> DH5α	10	10-500		High background, <i>E. coli</i> DH5α, <i>ars</i> operon from pI258 plasmid of <i>S. aureus</i> . <sup>18</sup>
pAs-lacZ				

<sup>a</sup> The LOD indicated in the paper, or the lowest concentration actually used.

<sup>b</sup> The linear range concentration indicated in the paper, or the actual concentration range used.

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