Supplementary Information

Microfluidic screening system based on boron-doped diamond electrodes and dielectrophoretic sorting for directed evolution of NAD(P)-dependent oxidoreductases

Haruna Goto,^a Yuki Kanai,^a Arisa Yotsui,^a Shota Shimokihara,^a Shunya Shitara,^a Ryo Oyobiki,^a Kei Fujiwara,^a Takeshi Watanabe,^b Yasuaki Einaga,^c Yoshinori Matsumoto,^d Norihisa Miki^e and Nobuhide Doi^{*a}

^a Department of Biosciences and Informatics, Keio University, Japan

- ^b Department of Electrical Engineering and Electronics, Aoyama Gakuin University, Sagamihara 252-5258, Japan
- ^c Department of Chemistry, Keio University, Japan
- ^d Department of Applied Physics and Physico-Informatics, Keio University, Japan

^e Department of Mechanical Engineering, Keio University, Japan

Contents

Supplementary Table S1	The oligonucleotide sequences used in this study
Supplementary Table S2	The data corresponding to Figure 3 for peak currents of plugs at various
	concentrations (0, 1, 10, 20 and 50 μ M) of NADH
Supplementary Table S3	The data corresponding to Figure 4 for peak currents of plugs containing microbeads on which the wild-type ADH (WT) or randomly mutated ADH (Mn^{2+} concentration: 0.1, 0.3 or 0.5 mM) was immobilized
Supplementary Table S4	The data corresponding to Figure 6 for relative peak currents of plugs containing microbeads on which the wild-type IDH (WT) or randomly mutated IDH library before (Mut) and after the first or second round of screening (1st and 2nd) was immobilized
Supplementary Figure S1	The DNA and amino acid sequences of dehydrogenases used in this study
Supplementary Figure S2	Masks for the fabrication of the encapsulating device
Supplementary Figure S3	Masks for the fabrication of the droplets-sorting device
Supplementary Figure S4	Fabrication method of the droplets-sorting device
Supplementary Figure S5	Fabrication of the data acquisition and control system
Supplementary Figure S6	Relationship between the plug size and flow rates in the encapsulating device
Supplementary Figure S7	Activity measurement of IDH clones by observing NADH absorbance

Primer	Sequence
T7-F	5'-TAATACGACTCACTATAGGG-3'
T7-R	5'-GCTAGTTATTGCTCAGCGG-3'
T7-F2	5'-TAATACGACTCAACTATAGGGAGACCACAAC-3'
T7-R2	5'-GCTAGTTATTGCTCAGCGGTGGC-3'
Insert-F	5'-ACCGCGAACAGATTGGAGGTGCGGAAAAAGTGTCGTTTGA-3'
Insert-R	5'-AGCAGCCGGATCCTCGAGTCACTCGAGGGCGGCCGGAGCGT-3'
Vector-F	5'-ACCTCCAATCTGTTCGCGGTG-3'
Vector-R	5'-TGACTCGAGGATCCGGCTGCT-3'

Supplementary Table S1 The oligonucleotide sequences used in this study

Supplementary Table S2 The data corresponding to Figure 3 for peak currents of plugs at various concentrations $(0, 1, 10, 20 \text{ and } 50 \,\mu\text{M})$ of NADH.

	0 µM	1 µM	10 µM	20 µM	50 µM
Mean	4.13	7.17	22.9	51.5	98.3
SD	2.08	3.38	4.75	3.71	12.0
Number of samples	1036	652	606	490	383

Supplementary Table S3 The data corresponding to Figure 4 for peak currents of plugs containing microbeads on which the wild-type ADH (WT) or randomly mutated ADH (Mn^{2+} concentration: 0.1, 0.3 or 0.5 mM) was immobilized.

	WT	0.1 mM	0.3 mM	0.5 mM	
Mean	68.0	48.4	56.8	52.9	
SD	16.0	10.8	9.9	36.8	
Number of samples	208	182	327	141	

Supplementary Table S4 The data corresponding to Figure 6 for relative peak currents of plugs containing microbeads on which the wild-type IDH (WT) or randomly mutated IDH library before (Mut) and after the first or second round of screening (1st and 2nd) was immobilized.

	WT	Mut (R0)	1st (R1)	2nd (R2)	
Mean	1.0	0.92	0.98	1.0	
SD	0.038	0.019	0.038	0.019	
Number of samples	493	534	837	439	

	TGA Vi I	10 AAGC/ K A	AGCC A	2 GTG(V	20 GTA(V	GAA E	CAG Q	30 TTT F	AAA K	GAG E	4 GCCG P	0 CTG L	AAA K	ATC I	50 CAA/ K	AGAA E	GT(V	60 GGAG E	AAA K	ICCG P	70 ACG T) ATC I	TCG S	3 TAT(Y	30 GGC G	GAAG E	90 TTTTA V L
GTGCO V F	GCA R	100 TCAAA I K	IGCA ⁻ A	11 GGC0 C	IO GGTO G	GTA [.] V	TGC C	120 CAT H	ACC T	GAT D	13 CTT L	0 CAC H	GCA A	1 GCT A	40 CAT H	GGG G	GA1 D	150 TGG W	CCG P	GTG V	160 AAA0 K	D CCA P	AAA K	17 Ctg(L	70 CCG ⁻ P	TTAA L	180 TTCCA I P
GGAC/ G I	ACG/ H I	190 AAGGT E G	GTGO	20 GGC/ G	00 ATCO I	GTG(V	GAA E	210 GAA E	GTT V	GGT G	22 CCT P	0 GGG G	GTT. V	2 ACG T	30 ICAC H	CTG L	AAA K	240 GTT V	GGC G	GAT D	250 CGC0 R	D GTC V	GGT. G	20 Atto I	60 CCT P	TGGC W	270 TGTAT L Y
TCAGO S		280 GTGGC C G	CAT H	29 ГGC0 С	90 Gaci D	TAT Y	TGC C	300 CTG L	TCT S	GGT G	31 CAG Q	0 GAA E	ACG T	3 TTA L	20 TGC C	GAA E	CAC H	330 CAG Q	AAG K	AAT N	340 GCA A) GGC G	TAT Y	35 TCCC S	50 GTG(V	GATG D	360 GTGGT G G
TATGO Y	CCG/ A I	370 AGTAC E Y	TGT(C	38 CGT (R	30 GCT (A	GCG(A	GCA A	390 GAC D	TAC Y	GTG V	40 GTT V	0 AAG K	ATT I	4 CCG P	10 GAC D	AAC N	TTC L	420 STCG S	TTT F	GAA E	430 GAA E	D GCT A	GCC A	44 CCGA P	40 ATT I	TTCT F	450 GTGCT C A
GGCG ⁻ G	TCA	460 CAACC T T	TAC/ Y	47 \AAC K	70 GCGC A	CTG/ L	AAA K	480 GTT V	ACC T	GGT G	49 GCT A	0 AAA K	CCA P	5 GGC G	00 GAA E	TGG W	GTT V	510 GCG A	ATT I	TAT Y	520 GGC/ G	D ATC I	GGT G	53 GGC1 G	30 FTA(L	GGTC G	540 ATGTT H V
GCGG ⁻ A	TGC/	550 AATAC Q Y	GCG/ A	56 \AAC K	60 GCCA A	ATG(M	GGC G	570 CTG L	AAT N	GTC V	58 GTG V	0 GCC A	GTG V	5 GAC D	90 ATT I	GGT G	GAC D	600 GAG E	AAG K	CTG L	610 GAA E	D CTC L	GCC. A	62 AAAQ K	20 GAA E	CTCG L	630 GTGCA G A
GATC ⁻ D I	TGG	640 TGGTC V V	AAT(N	65 CCGC P	50 CTG/ L	AAG K	GAA E	660 GAT D	GCC A	GCG A	67 AAA K	0 TTC F	ATG. M	6 AAA K	80 GAC E	iaaa K	GTC V	690 GGA G	GGG G	GTG V	700 CATO H) GCG A	GCT A	71 GTCC V	10 GTA V	ACTG T	720 CGGTA A V
AGTA/ S ł	AGC(K I	730 CGGCC P A	FTT	74 CAGA Q	40 AGC(S	GCG [.] A	TAC Y	750 AAC N	AGC S	ATT I	76 CGG R	0 CGT R	GGA G	7 GGC G	70 GCC A	TGT C	GTC V	780 GCTG L	GTT V	GGG G	790 CTT(L) CCG P	CCT P	80 GAAC E	DO GAG/ E	ATGC M	810 CCATT P I
CCGA P	TTT I I	820 TCGAC F D	ACTO T	83 GTGC V	30 CTGA L	AAC(N	GGG G	840 ATC I	AAA K	ATT I	85 ATC	0 GGA G	AGC S	8 ATT I	60 GTA V	lggc g	ACC T	870 CGC R	AAA K	GAT D	880 CTG L	D CAG Q	GAA E	89 GCGC A	90 CTC(L	CAAT Q	900 TTGCC F A
GCGG/ A I	AAG E (910 GCAAA G K	GTC/ V	92 \AG# K	20 ACCA T	ATC/ I	ATT I	930 GAA E	GTT V	CAA Q	94 CCC P	0 CTT L	GAG E	9 AAG K	50 ATC I	AAC N	GAA E	960 GTC V	TTT F	GAT D	970 CGC/ R	D ATG M	TTG. L	98 AAA0 K	30 GGC(G	CAGA Q	990 TTAAT I N
GGCCC G I	10 GTG R V	000 TCGTA V V	CTG/ L	101 ACA1 T	IO ITGO L	GAG E	1 GAT D	020 AAA K	<u>GGA</u> G	TCC S	103 GCG A	0 GCC A	GTT V	10 TAC Y	40 CC/ P	ATAC Y	1 GA D	050 IGTT V	CCT P	GAC D	1060 TAT Y) GCG A	GGC G	107 TAT(Y	70 CCC P	TATG Y	1080 ACGTC D V
CCGG/ P [10 ACT/ D	090 Atgca Y A	GGG ⁻ G	110 [CC] S	00 ГАТ(<u>Y</u>	CCC. P	1 TAT Y	110 GAC D	GTT V	CCA P	112 GAT D	0 TAC Y	GCT A	11 CCG P	30 IGCC A	GCC A	1 CT(L	140 2 <u>GAG</u> E									

Supplementary Fig. S1 The DNA and amino acid sequences of dehydrogenases used in this study. (a) Alcohol dehydrogenase (ADH) from *Geobacillus stearothermophilus*. (b) Isocitrate dehydrogenase (IDH) from *Streptococcus mutans*. The codon usage is optimized for expression in *Escherichia coli*. NdeI, BamHI and XhoI recognition sites are indicated in the boxes. Underline indicates 3xHA-tag.

а

b

CAT	ATC M	1 GCG A	0 Igaa E	AAA K	GTO V	20 GTC(S	GTTI F	GAA E	30 IGAG E	GGT G	AAA K	4(CTT L	0 CAA Q	GTG V	CCG P	50 IGA1 D	TAAA K	CCC P	60 GGTT V	ATA I	ICCG P	70 TAC <i>i</i> Y) ATT I	GAA E	8 GGT(G	BO GAT D	GGAC G	90 TTGGT V G
CAC Q	igac D	10 ATT I	0 TGG W	AAG. K	1 AAT N	10 GCC A	AACAA Q	ATC I	120 GTC V	TTC F	GAC. D	130 AAA0 K	0 GCC A	ATT I	1 GCC A	40 AAG K	igtg V	TAT Y	150 GGG G	GGT G	CAC/ H	160 AAA0 K) CAG Q	GTG/ V	17 Atct I	20 GG(W	CGTG R	180 AAGTT E V
CTT L	GCA A	19 GGC G	0 AAA K	AAG K	2 GCC A	00 TA1 Y	TAAC N	GAA E	210 ACG T	GGC G	AAC [®] N	220 TGG W	0 CTG L	CCG P	2 AAT N	30 GAG E	ACG T	CTG L	240 igaa E	ATC I	ATC/ I	250 AAAA K) ACC T	CAC1 H	26 ITAC L	60 CTG(L	GCGA A	270 TAAAA I K
GGG G	icca P	28 CTG L	0 GAA E	ACT T	2 CCG P	90 GT1 V	GGT G	GGG G	300 GGC G	ATT I	CGT R	310 TCA S	0 CTG L	AAC N	3 GTA V	20 GCG A	itta L	CGT R	330 CAA Q	GAA E	CTG L	340 Gaco D) CTG L	TTTC F	35 GCCT A	50 GC(C	GTTC V	360 GACCA R P
GTA V	CGC R	37 TAC Y	0 TTC F	AAG K	3 GGT G	80 GT <i>A</i> V	ACCC P	TCT S	390 CCT P	CTG L	AAA K	400 CATO H	0 CCG P	GAA E	4 AAA K	10 ACG T	GCT A	ATT I	420 ACG T	ATT I	TTC(F	430 CGG0 R) GAA E	AAC <i>i</i> N	44 ACCO T	10 Gago E	GACA D	450 TTTAT I Y
GCT A	GGC G	46 ATT I	0 GAA E	TGG. W	4 AAT N	70 GCC A	GGGT G	ACT T	480 GCG A	GAA E	GTG V	49(CAG/ Q	0 AAA K	GTG. V	5 ATC I	00 AAC N	TTT F	TTG L	510 ICAG Q	GAT D	GAT/ D	520 Atgo M) CAG Q	GTAA V	53 AAGA K	80 (AG/ K	ATCC I	540 GCTTT R F
CCG P	iaaa K	55 AGT S	0 TCC S	AGC. S	5 ATT I	60 GGC G	CATT I	AAA K	570 CCG P	ATA I	AGC. S	580 ATCO I	0 GAA E	GGG G	5 TCG S	90 CAA Q	ICGC R	CTC L	600 ATT I	AGA R	GCC(A	610 GCA <i>A</i> A) ATT I	GAG1 E	62 Fato Y	20 GCA(A	CTGG L	630 CCAAT A N
AAC N	CTG L	64 ACC T	0 AAA K	GTG. V	6 ACC T	50 CTC L	GTC V	CAT H	660 AAA K	GGA G	AAC N	670 ATCO I	0 CAG Q	AAG K	6 TTC F	80 ACC T	GAA E	GGA G	690 (GGC G	TTT F	CGC/ R	700 4441 K) FGG W	GGG1 G	71 ГАТС Ү	0 GAG1 E	TTGG L	720 CTAAA A K
CGC R	GAG E	73 itat Y	0 GCT A	GCC A	7 GAA E	40 CT1 L	GCG A	AGT S	750 GGC G	CAG Q	TTA L	760 GTG0 V	0 GTT V	GAC D	7 GAC D	70 ATT I	ATT I	GCG A	780 GAT D	AAC N	TTC(F	790 CTCC L) CAG Q	CAG/ Q	80 ATTC I)0 CTG(L	CTGA L	810 AACCT K P
GAG E	icgt R	82 TTT F	0 GAT D	GTG V	8 GTG V	30 GCA A	ACTG L	ACC T	840 AAC N	CTT L	AAC N	850 GGC0 G	0 GAT D	TAC Y	8 GCC A	60 AGT S	GAT D	GCG A	870 Itta	GCT A	GCA A	880 CAAC Q) GTT V	GGCC G	89 GTA G	00 ATC(I	GGCA G	900 TTTCA I S
CCA P	GGT G	91 GCG A	0 AAT N	ATC. I	9 AAT N	20 TAC Y	CAG Q	ACT T	930 GGC G	CAT H	GCC/ A	94(ATT I	0 TTC F	GAA E	9 GCG A	50 ACA T	CAC H	GGA G	960 ACC T	GCA A	CCC(P	970 GAT <i>A</i> D) Atc I	GCA0 A	98 GGTC G	30 CAA(Q	GATC D	990 TCGCG L A
AAT N	CCT P	100 AGC S	0 TCC S	GTC V	10 TTG L	10 CTC L	ATCG S	GGT G	020 TGT C	ATG M	CTC L	1030 TTT(F	0 GAC D	TAT. Y	10 ATC I	40 GGC G	TGG W	1 TCT S	050 AAA K	GTT V	AGC(S	1060 GATO D) CTG. L	ATC# I	107 Atga M	70 (AA(K	GCTG A	1080 TCGAG V E
AAA K	IGCA A	109 ATT I	0 GCG A	AAT N	11 GGC G	00 CAC Q	GTG V	ACA T	110 ATC I	GAT D	TTT F	1120 GCC/ A	0 AAA K	GAA E	11 CTA L	30 GGC G	GTC V	1 GAA E	140 GCG A	TTG L	ACC/ T	1150 ACAC T) CGT R	CAG1 Q	116 FTTA F	60 NGC(S	GAAG E	1170 TCCTG V L
CTO L	ACG T	118 itac Y	0 TTA L	GGA G	11 TCC S	90 GC(A	GGCC A	1 GTT V	200 TAC Y	CCA P	TAC Y	121) GAT D	0 GTT V	CCT P	12 GAC D	20 TA1 Y	GCG A	1 GGC G	230 CTAT Y	CCC P	TAT Y	1240 GAC(D) GTC V	CCG P	125 GAC1 D	50 FAT(Y	GCAG A	1260 GGTCC <u>G S</u>
TAT Y	CCC P	127 TAT Y	0 GAC D	GTT	12 CCA P	280 GAT D	TAC Y	GCT A	290 CCG P	GCC A	GCC A	1300 <u>CTC</u> L	0 GAG E															

Supplementary Fig. S1 (continued)



Supplementary Fig. S2 Masks for the fabrication of the encapsulating device.



Supplementary Fig. S3 Masks for the fabrication of the droplets-sorting device.(a) Forty patterns of devices with different channel widths [inlet, center, outlet (collect) and outlet (waste)] and with (right) or without (left) a shunt structure. (b) Nine patterns of devices. Box, optimized device.



















Supplementary Fig. S3 (continued)



Supplementary Fig. S4 Fabrication method of the droplet-sorting device. (1) PDMS structured by using standard soft lithography. (2) Punched holes as the low-melting-temperature solder wire inlets and outlets. (3) The structured PDMS was sealed by oxygen plasma to a flat surface to enclose the channels. (4) The conducting wire was set at the outlet holes and the low-melting-temperature solder wire at the inlet hole on the 200°C hot plate. (5) After the solder wire melted, it was removed from the hot plate to harden.



Supplementary Fig. S5 Fabrication of data acquisition and control system. (a) A flow chart of our detection and sorting system. First, the continuous analog signals detected by the NAD(P)H-measuring device were converted to digital signals *via* a DAQ device. Then, each signal was compared with a threshold value and divided into high and low signals to the function generator by the LabVIEW program (b) on a PC. When only high signals were sent, the function generator output AC signal using burst oscillation. Then, signals were amplified by voltage amplifier. The amplified signals to the dielectrophoretic electrode controlled switching and duration. Finally, on the droplet-sorting device, droplets containing enzymes with higher activity were collected *via* the "collect channel." (b) A block diagram of the LabVIEW program.



Supplementary Fig. S6 Relationship between the plug size and flow rates in the encapsulating device. Dimensionless droplet length (L/w) was plotted as a function of ratios of the rates of flow of the dispersed and continuous phases (Q_{in}/Q_{out}) for the reference geometry $(h = 65 \ \mu m, w = 400 \ \mu m)$.



Supplementary Fig. S7 Activity measurement of IDH clones by observing NADH absorbance. Each seven clones were randomly picked from the library after two rounds of screening (top) and the initial library (bottom), respectively. These clones were translated by the PURE system and the activities of the products were measured by absorbance of NADH at 340 nm. Mean ± SD. N = 3. WT; wild-type. Mutants; R2-1 (V358A), R2-2 (I304V), R2-3 (P300L), R2-4 (R197C, Y420C), R2-5 (K12E, A36Q), R2-6 (K17R), R2-7 (M1T, S286G), R0-1 (frameshift), R0-2 (Q162H, V275M, K360N), R0-3 (A2E, Q13R, N104D, K131R), R0-4 (E24G, E153G, G157D), R0-5 (L251F, D254G, K268R, E270G, D343G, T368A, A431P), R0-6 (nonsense), R0-7 (frameshift).