Supplementary Data

Table S1: Stoichiometric model for the ^{13}C flux measurements in OpenFLUX based on the model published by Baumann *et al*. 2010 BMC Syst Biol 4:141

RxnID	Reaction Equation	Carbon transition	Openflux Reaction type
R1	GLC_EX + ATP = G6P + ADP	abcdef + X = abcdef + X	F
R2	G6P = F6P	abcdef = abcdef	F
R3	F6P + ATP = FBP + ADP	abcdef + X = abcdef + X	F
R4	FBP = F6P + Pi	abcdef = abcdef + X	F
R5	FBP = G3P + G3P	abcdef = abc + def	F
R6	G3P + ADP + NAD = PG3 + ATP + NADH	abc + X + X = abc + X + X	F
R7	PG3 = PEP	abc = abc	F
R8	PEP + ADP = PYR + ATP	abc + X = abc + X	F
R9	PYR + NAD = ACCoA + CO2 + NADH	abc + X = bc + a + X	F
R10	PYR + CO2 + ADP = OAA + ATP	abc + d + X = abcd + X	F
R11	PYR = AcO + CO2	abc = bc + a	F
R12	G6P + NADP = RUL5P + CO2 + NADPH	abcdef + X = bcdef + a + X	F
R13	RUL5P = XYL5P	abcde = abcde	F
R14	XYL5P + ADP = XYL + ATP	abcde + X = abcde + X	F
R15	XYL + NADH = AROL + NAD	abcde + X = abcde + X	F
R16	RUL5P = RIB5P	abcde = abcde	F
R17	XYL5P + RIB5P = SED7P + G3P	abcde + fghij = fgabcde + hij	FR
R18	SED7P + G3P = XYL5P + RIB5P	abcdefg + hij = cdefg + abhij	R
R19	SED7P + G3P = E4P + F6P	abcdefg + hij = defg + abchij	FR
R20	E4P + F6P = SED7P + G3P	abcd + efghij = efgabcd + hij	R
R21	XYL5P + E4P = F6P + G3P	abcde + fghi = abfghi + cde	FR
R22	F6P + G3P =XYL5P + E4P	abcdef + ghi = abghi + cdef	R
R23	ACCoA + OAA = CIT	ab + cdef = fedbac	F
R24	CIT = ICIT	abcdef = abcdef	F
R25	ICIT + NAD = AKG + CO2 + NADH	abcdef + X = abcde + f + X	F
R26	AKG + NAD + ADP + FAD = 0.5 SUCC + 0.5 SUCC + CO2 + NADH + FADH2 + ATP	abcde + X + X + X = 0.5 bcde + 0.5 edcb + a + X + X + X	F
R27	SUCC + NAD = FUM + NADH	abcd + X = abcd + X	F
R28	FUM + H2O = MAL	abcd + X = abcd	F
R29	MAL + NAD = OAA + NADH	abcd + X = abcd + X	FR
R30	OAA + NADH = MAL + NAD	abcd + X = abcd + X	R
R31	ICIT = GLYOXY + 0.5 SUCC + 0.5 SUCC	abcdef = ab + 0.5 fcde + 0.5 edcf	F
R32	ACCoA + GLYOXY = MAL	ab + cd = cdba	F
R33	AcO + NADH = ETOH + NAD	ab + X = ab + X	F
R34	AcO + ATP = Ac + ADP	ab + X = ab + X	F
R35	AcO + NADP + CoA + ATP = ACCoA + NADPH + Pi + AMP	ab + X + X + X = ab + X + X + X	F
R36	G3P + NADH + ATP = GLYO + Pi + ADP + NAD	abc + X + X = abc + X + X + X	FR
R37	GLYO + Pi + ADP + NAD = G3P + ATP + NADH	abc + X + X + X = abc + X + X	R
R38	GLYO = GLYOex		B
R39	PYR = PYRex		B
R40	CIT = CITex		B

R41	CO2 = CO2ex		B
R42	AcO = AcOex		B
R43	Ac = Acex		B
R44	ETOH = ETOHex		B
R45	AROL = AROLex		B
R46	0.136 PYR + 0.006 RIB5P + 0.013 E4P + 0.040 OAA + 0.075 AKG + 0.027 ACCoA = Protein + 0.002 G3P + 0.058 CO2		B
R47	0.113 G6P + 0.053 F6P + 0.167 ATP = Carbohydrate + 0.167 ADP		B
R48	0.002 G6P + 0.0055 PYR + 0.011 G3P + 0.006 CO2 + 0.039 ACCoA + 0.441 ACCoA + 0.07 NADH + 0.599 NADPH + 0.42 ATP + 0.065 O2 = Lipid + 0.07 NAD + 0.599 NADP + 0.42 ADP + 0.42 Pi		B
R49	0.056 PYR + 0.1136 CO2 + 0.105 RIB5P + 0.104 NAD + 0.075 NADPH + 1.1 ATP + 0.0479 OAA = RNA + 1.1 Pi + 1.1 ADP + 0.075 NADP + 0.104 NADH		B
R50	0.051 PYR + 0.132 CO2 + 0.102 RIB5P + 0.102 NAD + 0.273 NADPH + 1.146 ATP + 0.051 OAA = DNA + 1.146 Pi + 1.146 ADP + 0.273 NADP + 0.102 NADH		B
R51 SOD	0.416 Protein + 0.055 RNA + 0.001 DNA + 0.110 Lipid + 0.418 Carbohydrate + ATP = Biomass + ADP + Pi		B
R51 X-33	0.455 Protein + 0.055 RNA + 0.001 DNA + 0.106 Lipid + 0.383 Carbohydrate + ATP = Biomass + ADP + Pi		B
R52	PYR = ALA	abc = abc	S
R53	OAA = ASP	abcd = abcd	S
R54	OAA = ASN	abcd = abcd	S
R55	AKG = GLU	abcde = abcde	S
R56	AKG = GLN	abcde = abcde	S
R57	G3P = 3PG	abc = abc	S
R58	3PG = SER	abc = abc	S
R59	SER = GLY + MTHF	abc = ab + c	S
R60	OAA = THR	abcd = abcd	S
R61	THR = GLY + ACETAL	abcd = ab + cd	S
R62	PYR + PYR = VAL + CO2	abc + def = abefc + d	S
R63	E4P + PYR = SHKM	abcd + efg = efgabcd	S
R64	SHKM + PYR = CHRM	abcdefg + hij = abcdefghij	S
R65	CHRM = PHE + CO2	abcdefghij = hijbcdefg + a	S
R66	CHRM = TYR + CO2	abcdefghij = hijbcdefg + a	S
R67	CHRM = ANTHR + PYR	abcdefghij = abcdefg + hij	S
R68	ANTHR + RIB5P = CPADRIB5P	abcdefg + hijkl = abcdefghijkl	S
R69	CPADRIB5P = INDG + CO2	abcdefghijkl = abcdfghijkl + e	S
R70	INDG = IND + G3P	abcdefghijk = abcdefgh + ijk	S
R71	IND + 3PG = TRP	abcdefgh + ijk = abcdefghkji	S
R72	PYR + OAA = ILE + CO2	abc + defg = debfgc + a	S
R73	PYR + PYR = ISV + CO2	abc + def = abefc + d	S
R74	ISV + ACCoA = LEU + CO2	abcde + fg = fgbcde + a	S
R75	AKG + CO2 = ARG	abcde + f = abcdef	S
R76	3PG = CYS	abc = abc	S
R77	OAA + MTHF = MET	abcd + e = abcde	S
R78	AKG = PRO	abcde = abcde	S
R79	AKG + ACCoA = LYS + CO2	abcde + fg = fgbcde + a	S
R80	RIB5P + MTHF = HIS	abcde + f = edcbaf	S

excludedMetabolites
GLC_EX
MeOH_EX
ADP
ATP
NAD
NADH
NADP
NADPH
GLYOex
CO2ex
ETOHex
CITex
PYRex
FAD
O2
FADH2
AMP
Biomass
CoA
H2O
Pi
AROLex
Acex
AcOex

simulatedMDVs
ALA#111
ALA#011
ASP#1111
ASP#0111
ASP#1100
GLU#11111
GLU#01111
GLY#11
GLY#01
HIS#111111
HIS#011111
ILE#011111
LYS#111111
LYS#011111
MET#11111
MET#01111
PHE#111111111
PHE#011111111
PHE#110000000
PRO#11111
PRO#01111
PRO#01111
SER#111
SER#111
SER#011
SER#011
SER#110
THR#1111
THR#1111
THR#0111
TYR#111111111
TYR#011111111
VAL#11111
VAL#11111
VAL#01111
VAL#01111
VAL#11000

Table S2: Mass distribution values (MDV) of strain hSOD and X-33 cultivated on a mixture of 17 % ^{13}C uniformly labelled glucose and 83 % naturally labelled glucose and the respective deviations of 3 biological replicates. hSOD sim and X-33 sim are the respective MDVs of the OpenFLUX fitting yielding the lowest residual error.

Fragment	hSOD MDV		hSOD dev.	hSOD sim	X-33 MDV		X-33 dev.	X-33 sim
ALA-57	0.744	±	0.004	0.798	0.752	±	0.001	0.798
	0.092	±	0.003	0.042	0.079	±	0.001	0.043
	0.029	±	0.000	0.017	0.030	±	0.001	0.018
	0.134	±	0.001	0.142	0.140	±	0.001	0.141
ALA-85	0.804	±	0.001	0.809	0.800	±	0.001	0.808
	0.042	±	0.000	0.048	0.039	±	0.000	0.048
	0.154	±	0.001	0.144	0.161	±	0.001	0.143
ASP-57	0.651	±	0.003	0.605	0.637	±	0.005	0.620
	0.164	±	0.002	0.202	0.177	±	0.003	0.184
	0.079	±	0.001	0.125	0.060	±	0.001	0.117
	0.090	±	0.001	0.056	0.106	±	0.000	0.064
	0.016	±	0.000	0.012	0.020	±	0.001	0.015
ASP-85	0.707	±	0.003	0.647	0.687	±	0.005	0.654
	0.147	±	0.002	0.223	0.154	±	0.004	0.210
	0.117	±	0.001	0.111	0.127	±	0.001	0.116
	0.029	±	0.001	0.019	0.031	±	0.001	0.020
ASPf302	0.786	±	0.001	0.779	0.781	±	0.001	0.790
	0.092	±	0.001	0.106	0.086	±	0.000	0.086
	0.123	±	0.001	0.114	0.134	±	0.001	0.124
GLU-57	0.561	±	0.002	0.523	0.559	±	0.016	0.529
	0.160	±	0.001	0.211	0.161	±	0.004	0.202
	0.196	±	0.001	0.194	0.194	±	0.005	0.197
	0.059	±	0.000	0.052	0.062	±	0.005	0.052
	0.018	±	0.000	0.017	0.018	±	0.002	0.018
	0.006	±	0.000	0.003	0.006	±	0.001	0.003
GLU-159	0.607	±	0.002	0.584	0.609	±	0.013	0.595
	0.160	±	0.001	0.213	0.158	±	0.003	0.193
	0.191	±	0.001	0.160	0.193	±	0.005	0.171
	0.027	±	0.000	0.034	0.026	±	0.002	0.031
	0.014	±	0.000	0.008	0.014	±	0.001	0.010
GLY-57	0.799	±	0.001	0.800	0.790	±	0.001	0.805
	0.064	±	0.000	0.065	0.069	±	0.001	0.055
	0.138	±	0.001	0.135	0.141	±	0.000	0.140
GLY-85	0.833	±	0.001	0.833	0.826	±	0.002	0.833
	0.167	±	0.001	0.167	0.174	±	0.002	0.167
HIS-57	0.585	±	0.005	0.605	0.568	±	0.007	0.610
	0.164	±	0.003	0.164	0.185	±	0.004	0.164
	0.069	±	0.001	0.064	0.069	±	0.001	0.060
	0.067	±	0.001	0.061	0.064	±	0.001	0.056
	0.023	±	0.001	0.016	0.025	±	0.001	0.015

	0.067	±	0.001	0.075	0.070	±	0.000	0.079
	0.025	±	0.001	0.015	0.018	±	0.000	0.016
HIS-159	0.546	±	0.007	0.616	0.543	±	0.009	0.620
	0.156	±	0.004	0.157	0.170	±	0.003	0.157
	0.120	±	0.006	0.108	0.114	±	0.002	0.101
	0.060	±	0.004	0.027	0.063	±	0.002	0.025
	0.077	±	0.002	0.077	0.079	±	0.001	0.081
	0.040	±	0.003	0.015	0.032	±	0.004	0.016
ILE-159	0.586	±	0.004	0.523	0.552	±	0.005	0.529
	0.141	±	0.002	0.211	0.150	±	0.003	0.202
	0.201	±	0.002	0.194	0.219	±	0.000	0.197
	0.048	±	0.001	0.052	0.052	±	0.002	0.052
	0.019	±	0.001	0.017	0.022	±	0.000	0.018
	0.005	±	0.000	0.003	0.005	±	0.000	0.003
LYS-57	0.585	±	0.005	0.473	0.558	±	0.007	0.481
	0.084	±	0.000	0.200	0.080	±	0.000	0.185
	0.261	±	0.004	0.224	0.283	±	0.005	0.233
	0.025	±	0.000	0.066	0.025	±	0.001	0.061
	0.040	±	0.001	0.031	0.049	±	0.001	0.034
	0.002	±	0.000	0.005	0.002	±	0.000	0.005
	0.002	±	0.000	0.001	0.003	±	0.000	0.001
LYS-159	0.568	±	0.004	0.486	0.542	±	0.006	0.495
	0.136	±	0.002	0.275	0.149	±	0.004	0.260
	0.227	±	0.002	0.169	0.232	±	0.000	0.175
	0.043	±	0.001	0.055	0.050	±	0.002	0.055
	0.024	±	0.000	0.013	0.024	±	0.000	0.014
	0.003	±	0.000	0.001	0.004	±	0.000	0.002
MET-57	0.559	±	0.009	0.503	0.549	±	0.004	0.516
	0.219	±	0.004	0.269	0.241	±	0.004	0.257
	0.079	±	0.002	0.138	0.068	±	0.001	0.128
	0.083	±	0.003	0.068	0.093	±	0.001	0.073
	0.045	±	0.003	0.020	0.043	±	0.001	0.023
	0.015	±	0.003	0.002	0.007	±	0.001	0.003
MET-159	0.609	±	0.007	0.538	0.586	±	0.005	0.544
	0.215	±	0.004	0.294	0.232	±	0.003	0.284
	0.105	±	0.002	0.130	0.116	±	0.001	0.132
	0.060	±	0.002	0.034	0.057	±	0.001	0.036
	0.012	±	0.002	0.003	0.008	±	0.000	0.003
PHE-57	0.469	±	0.004	0.480	0.452	±	0.002	0.484
	0.116	±	0.001	0.114	0.118	±	0.000	0.111
	0.114	±	0.002	0.110	0.121	±	0.001	0.110
	0.148	±	0.000	0.140	0.151	±	0.001	0.136
	0.076	±	0.001	0.086	0.082	±	0.001	0.089
	0.033	±	0.000	0.032	0.034	±	0.000	0.031
	0.025	±	0.001	0.021	0.025	±	0.000	0.021
	0.012	±	0.000	0.013	0.013	±	0.000	0.013
	0.004	±	0.000	0.002	0.003	±	0.000	0.002

	0.003	±	0.000	0.002	0.003	±	0.000	0.002
PHE-85	0.481	±	0.003	0.486	0.467	±	0.002	0.490
	0.108	±	0.001	0.118	0.111	±	0.000	0.116
	0.195	±	0.002	0.188	0.201	±	0.001	0.188
	0.082	±	0.001	0.070	0.080	±	0.001	0.065
	0.078	±	0.001	0.087	0.084	±	0.001	0.090
	0.025	±	0.000	0.023	0.026	±	0.000	0.022
	0.023	±	0.000	0.024	0.025	±	0.000	0.025
	0.004	±	0.000	0.002	0.004	±	0.000	0.002
	0.003	±	0.000	0.002	0.003	±	0.000	0.002
PHEf302	0.806	±	0.002	0.820	0.796	±	0.001	0.820
	0.054	±	0.001	0.025	0.062	±	0.001	0.024
	0.140	±	0.002	0.155	0.143	±	0.001	0.155
PRO-15	0.576	±	0.004	0.523	0.557	±	0.006	0.529
	0.158	±	0.002	0.211	0.162	±	0.001	0.202
	0.185	±	0.002	0.194	0.192	±	0.004	0.197
	0.060	±	0.001	0.052	0.065	±	0.001	0.052
	0.017	±	0.000	0.017	0.018	±	0.000	0.018
	0.005	±	0.000	0.003	0.007	±	0.000	0.003
PRO-85	0.621	±	0.003	0.584	0.605	±	0.003	0.595
	0.163	±	0.002	0.213	0.164	±	0.000	0.193
	0.179	±	0.002	0.160	0.190	±	0.003	0.171
	0.025	±	0.000	0.034	0.028	±	0.001	0.031
	0.012	±	0.000	0.008	0.013	±	0.000	0.010
PRO-159	0.620	±	0.003	0.584	0.602	±	0.004	0.595
	0.159	±	0.001	0.213	0.162	±	0.000	0.193
	0.182	±	0.001	0.160	0.193	±	0.003	0.171
	0.026	±	0.000	0.034	0.028	±	0.001	0.031
	0.013	±	0.000	0.008	0.015	±	0.000	0.010
SER-15	0.752	±	0.003	0.798	0.740	±	0.003	0.798
	0.086	±	0.002	0.042	0.098	±	0.003	0.043
	0.054	±	0.001	0.017	0.059	±	0.001	0.018
	0.108	±	0.002	0.142	0.103	±	0.001	0.141
SER-57	0.750	±	0.001	0.798	0.732	±	0.002	0.798
	0.089	±	0.001	0.042	0.102	±	0.002	0.043
	0.054	±	0.000	0.017	0.063	±	0.001	0.018
	0.106	±	0.001	0.142	0.103	±	0.000	0.141
SER-85	0.777	±	0.002	0.809	0.761	±	0.002	0.808
	0.104	±	0.000	0.048	0.123	±	0.002	0.048
	0.119	±	0.002	0.144	0.117	±	0.001	0.143
SER-159	0.775	±	0.001	0.809	0.761	±	0.003	0.808
	0.105	±	0.001	0.048	0.123	±	0.002	0.048
	0.119	±	0.002	0.144	0.116	±	0.001	0.143
SERf302	0.796	±	0.001	0.820	0.788	±	0.001	0.820
	0.058	±	0.001	0.025	0.066	±	0.000	0.024
	0.146	±	0.002	0.155	0.146	±	0.001	0.155
THR-15	0.674	±	0.003	0.605	0.661	±	0.003	0.620

	0.147	±	0.002	0.202	0.156	±	0.002	0.184
	0.070	±	0.002	0.125	0.057	±	0.001	0.117
	0.095	±	0.002	0.056	0.104	±	0.001	0.064
	0.014	±	0.001	0.012	0.022	±	0.001	0.015
THR-57	0.674	±	0.004	0.605	0.653	±	0.006	0.620
	0.142	±	0.002	0.202	0.160	±	0.005	0.184
	0.077	±	0.001	0.125	0.059	±	0.001	0.117
	0.092	±	0.001	0.056	0.109	±	0.001	0.064
	0.014	±	0.001	0.012	0.019	±	0.001	0.015
THR-85	0.709	±	0.004	0.647	0.686	±	0.005	0.654
	0.144	±	0.003	0.223	0.154	±	0.004	0.210
	0.120	±	0.002	0.111	0.132	±	0.001	0.116
	0.027	±	0.000	0.019	0.027	±	0.002	0.020
TYR-57	0.470	±	0.003	0.480	0.455	±	0.001	0.484
	0.114	±	0.001	0.114	0.114	±	0.001	0.111
	0.116	±	0.001	0.110	0.121	±	0.001	0.110
	0.147	±	0.001	0.140	0.150	±	0.002	0.136
	0.078	±	0.001	0.086	0.082	±	0.001	0.089
	0.033	±	0.000	0.032	0.034	±	0.000	0.031
	0.023	±	0.000	0.021	0.024	±	0.000	0.021
	0.012	±	0.000	0.013	0.013	±	0.001	0.013
	0.003	±	0.000	0.002	0.004	±	0.000	0.002
	0.003	±	0.000	0.002	0.004	±	0.000	0.002
TYR-159	0.474	±	0.004	0.486	0.461	±	0.003	0.490
	0.107	±	0.001	0.118	0.107	±	0.001	0.116
	0.195	±	0.002	0.188	0.202	±	0.001	0.188
	0.083	±	0.001	0.070	0.083	±	0.001	0.065
	0.080	±	0.001	0.087	0.087	±	0.001	0.090
	0.027	±	0.001	0.023	0.026	±	0.001	0.022
	0.024	±	0.000	0.024	0.025	±	0.001	0.025
	0.005	±	0.000	0.002	0.005	±	0.000	0.002
	0.005	±	0.000	0.002	0.005	±	0.000	0.002
VAL-15	0.640	±	0.005	0.646	0.626	±	0.004	0.645
	0.082	±	0.003	0.072	0.079	±	0.002	0.073
	0.140	±	0.002	0.131	0.147	±	0.002	0.131
	0.108	±	0.002	0.121	0.117	±	0.001	0.121
	0.011	±	0.001	0.009	0.011	±	0.001	0.009
	0.019	±	0.001	0.020	0.020	±	0.001	0.020
VAL-57	0.638	±	0.003	0.646	0.626	±	0.003	0.645
	0.079	±	0.001	0.072	0.077	±	0.001	0.073
	0.140	±	0.001	0.131	0.146	±	0.001	0.131
	0.116	±	0.001	0.121	0.121	±	0.001	0.121
	0.008	±	0.000	0.009	0.008	±	0.000	0.009
	0.020	±	0.001	0.020	0.021	±	0.000	0.020
VAL-85	0.653	±	0.002	0.654	0.646	±	0.002	0.654
	0.072	±	0.000	0.077	0.066	±	0.001	0.078
	0.241	±	0.003	0.235	0.251	±	0.002	0.234

	0.013	±	0.000	0.014	0.013	±	0.001	0.014
	0.022	±	0.000	0.021	0.024	±	0.000	0.021
VAL-159	0.650	±	0.003	0.654	0.638	±	0.001	0.654
	0.067	±	0.000	0.077	0.063	±	0.000	0.078
	0.239	±	0.002	0.235	0.253	±	0.001	0.234
	0.022	±	0.000	0.014	0.022	±	0.000	0.014
	0.023	±	0.000	0.021	0.025	±	0.000	0.021
VAL-f302	0.791	±	0.001	0.820	0.780	±	0.003	0.820
	0.058	±	0.000	0.025	0.063	±	0.003	0.024
	0.151	±	0.001	0.155	0.157	±	0.002	0.155

Table S3: PCR primers used for gene cloning for overexpression and cloning of overlapping fragments for knockout.

Target sequence	Forward primer	Reverse primer
Overexpression		
ZWF1	ATGACCGATACGAAAGCCG	TTACATCTTGTGCAGCACATCG
SOL3	ATGGTACAAATCTATTCCTATGAACG	TCAGTATTTCGAAGTAGAAACGGA
GND2	ATGGTTGAAGCAACAGGAGA	TTAAGCATCGTAGGTACTGGC
RPE1	ATGGTCAAACCTGTTATTGCTC	TTAATCTAAAAGCCCTTTCTTTTTGAGA
MDH1	ATGTTGTCCACAATTGCCAAGCG	TTATGGGTTTTGCTTAACAAACTCTTGACC
GDH1	ATGGTCCAACCACAAGAACC	CTAAAACACATCACCTTGGGC
GPD2	ATGTACTTAACCAGCACAGTGAG	TTAGTCTTCCCAATGCTTAACGTC
Deletion		
5'ADH2	ACACCCCATGGCTGCTCTC	GGCACGAATTCGCACCCCG
3'ADH2	ATCGGTGACTACGCTGGTATC	CGTATCTACCGATGATGGCACC
5'ALD4	CAGACGTTAAGCAGATCCAC	GAAATCGAGGAGGTATCAAG
3'ALD4	TGGAGTTGGGTGGTAAATC	GACATAGTAAAGAGCGTGAG
5'GUT2	TATGGTTTACGAGAATGCGG	CCTGTTAGAACTGGATTGAG
3'GUT2	TTCCCTTGTGTACCATGATG	CAGATCACTTGGTACTTTG
5'PDC1	TGGCATTGTTTACTTCCGC	GGTCTATGTAGCCTCTGAG
3'PDC1	TGCTTCACCACACCCTCGG	AACGATACCGAAAGCAGAGG
Verification of deletion		
ADH2	AATGATTATGTAAGAAGAGG	CAGAGGCTAGTTGAATTGAG
ALD4	AGAAGCGACAATGGGATAAC	GAAGACGCACAATGACTAGG
GUT2	GAAACTCGAATCATTGCAGC	GTAGTTGGAAGCTAAATGAG
PDC1	TTTCCGGCTAGTCAATCTCG	CAGATACGTGGGTTGGGAAT