

Table S1: Plasmid content of transposon mutants on Tables 1 and 2^a

Location	Locus	Insertion Site	Plasmids Missing In Arrayed STM Stock
chromosome	BB_0050	47204	cp9
chromosome	BB_0050	47284	cp32-6
chromosome	BB_0050	47348	cp32-6, cp9
chromosome	BB_0116	113343	Not Done
chromosome	BB_0157	158214	none
chromosome	BB_0157	158431	lp28-2
chromosome	BB_0163	163768	none
chromosome	BB_0224	228894	lp5
chromosome	BB_0224	228897	Not Done
chromosome	BB_0224	228901	lp5
chromosome	BB_0224	228925	lp5
chromosome	BB_0241	246612	Not Done
chromosome	BB_0241	247035	lp5
chromosome	BB_0241	247989	lp5
chromosome	BB_0243	248862	Complete
chromosome	BB_0243	249253	lp5, lp28-1
chromosome	BB_0243	249623	lp5
chromosome	BB_0243	249691	Complete
chromosome	BB_0408	420791	Not done
chromosome	BB_0408	421350	lp21, lp5
chromosome	BB_0420	431895	cp9
chromosome	BB_0420	431973	lp5
chromosome	BB_0420	432429	cp9, lp28-2
chromosome	BB_0420	432489	Complete
chromosome	BB_0420	434199	lp5
chromosome	BB_0420	434321	lp5
chromosome	BB_0420	434331	lp38, lp5
chromosome	BB_0420	434674	lp28-1, lp5
chromosome	BB_0629	659699	lp28-1, lp5
chromosome	BB_0629	659840	Complete
chromosome	BB_0629	660191	Complete
chromosome	BB_0629	661151	Not Done
chromosome	BB_0789	827550	Complete
chromosome	BB_0825	869189	cp9, lp5
plasmid_cp26	BB_B01	194	lp5
plasmid_cp26	BB_B04	2519	lp5, cp9
plasmid_cp26	BB_B04	2538	lp5
plasmid_cp26	BB_B04	2660	lp5, cp9
plasmid_cp26	BB_B04	2694	lp5, cp9
plasmid_cp26	BB_B04	2768	lp21, lp38
plasmid_cp26	BB_B04	2885	Complete

plasmid_cp26	BB_B04	2963	Not Done
plasmid_cp26	BB_B04	3039	Complete
plasmid_cp26	BB_B05	4228	lp5, cp9
plasmid_cp26	BB_B05	4354	Not Done
plasmid_cp26	BB_B06	4596	Complete
plasmid_cp26	BB_B16	12693	cp32-1
plasmid_cp26	BB_B16	12732	Not done
plasmid_cp26	BB_B16	12750	lp5
plasmid_cp26	BB_B16	13146	lp5
plasmid_cp26	BB_B16	13469	Not done
plasmid_cp26	BB_B29	24850	lp5
plasmid_cp26	BB_B29	25022	lp5
plasmid_cp26	BB_B29	25102	lp5
plasmid_cp26	BB_B29	25170	lp5
plasmid_cp26	BB_B29	25452	lp5
plasmid_cp26	BB_B29	25713	Complete
plasmid_cp26	BB_B29	25928	lp5
plasmid_cp26	BB_B29	25931	lp5
plasmid_cp26	BB_B29	25943	lp5
plasmid_cp26	BB_B29	26025	lp5
plasmid_cp26	BB_B29	26026	lp5
plasmid_lp25	BB_E22	15049	Complete
plasmid_lp25	BB_E22	15167	cp9
plasmid_lp54	BB_A04	2129	lp28-1
plasmid_lp54	BB_A04	2796	lp5

Table S2. Fitness values of all genes identified by the Tn-seq in the carbohydrate screen^a

Location	Locus	Gene	GlcNAc		Maltose		Mannose		Trehalose	
			Fitness Value ^b	p-value ^c	Fitness Value	p-value	Fitness Value	p-value	Fitness Value	p-value
chromosome	BB_0001		0.955 ± 0.405	0.718	1.351 ± 0.615	0.484	0.533 ± 0.200	0.158	0.727 ± 0.369	0.302
chromosome	BB_0002		1.151 ± 1.464	0.861	1.854 ± 2.673	0.000	0.978 ± 1.442	0.951	1.646 ± 2.241	0.538
chromosome	BB_0017		0.674 ± 0.259	0.153	0.624 ± 0.374	0.424	0.930 ± 0.397	0.464	0.984 ± 0.476	0.306
chromosome	BB_0021	<i>queA</i>	0.777 ± 0.290	0.269	1.135 ± 0.385	0.275	0.835 ± 0.314	0.319	0.945 ± 0.419	0.704
chromosome	BB_0022	<i>rvvB</i>	0.934 ± 0.172	0.085	1.127 ± 0.350	0.440	0.722 ± 0.082	0.052	0.991 ± 0.193	0.864
chromosome	BB_0023	<i>rvvA</i>	0.755 ± 0.424	0.248	0.999 ± 0.685	0.987	0.694 ± 0.374	0.199	0.838 ± 0.499	0.220
chromosome	BB_0024		0.861 ± 0.157	0.087	1.114 ± 0.627	0.737	0.699 ± 0.109	0.066	0.937 ± 0.144	0.576
chromosome	BB_0040	<i>cheR</i>	0.559 ± 0.223	0.175	0.334 ± 0.270	0.197	0.715 ± 0.352	0.136	0.821 ± 0.497	0.126
chromosome	BB_0043		1.268 ± 0.454	0.463	2.000 ± 1.636	0.439	0.942 ± 0.312	0.699	0.924 ± 0.329	0.059
chromosome	BB_0045		0.722 ± 0.349	0.502	0.901 ± 0.424	0.778	0.689 ± 0.430	0.257	1.022 ± 0.596	0.955
chromosome	BB_0046	<i>rnhB</i>	0.519 ± 0.356	0.265	0.663 ± 0.368	0.397	0.577 ± 0.153	0.041	0.981 ± 0.291	0.073
chromosome	BB_0050		0.220 ± 0.169	0.051	0.639 ± 0.610	0.148	0.817 ± 0.428	0.290	0.916 ± 0.466	0.543
chromosome	BB_0051		0.331 ± 0.207	0.067	0.671 ± 0.638	0.298	1.210 ± 0.663	0.126	1.007 ± 0.401	0.978
chromosome	BB_0053	<i>ung</i>	0.439 ± 0.222	0.028	0.975 ± 0.599	0.886	0.725 ± 0.288	0.115	1.024 ± 0.601	0.873
chromosome	BB_0071		1.005 ± 0.379	0.979	0.873 ± 0.521	0.708	0.551 ± 0.301	0.176	0.764 ± 0.264	0.251
chromosome	BB_0085		0.609 ± 0.208	0.097	0.473 ± 0.396	0.311	0.723 ± 0.284	0.089	0.864 ± 0.386	0.069
chromosome	BB_0086		0.419 ± 0.371	0.038	0.735 ± 0.731	0.066	0.739 ± 0.550	0.048	0.934 ± 0.690	0.494
chromosome	BB_0098		1.152 ± 0.672	0.387	1.626 ± 0.979	0.169	0.867 ± 0.434	0.064	1.093 ± 0.534	0.184
chromosome	BB_0102		0.751 ± 0.188	0.249	1.533 ± 0.542	0.179	0.783 ± 0.522	0.600	1.424 ± 0.368	0.171
chromosome	BB_0110		0.332 ± 0.119	0.085	0.583 ± 0.364	0.359	0.877 ± 0.416	0.068	1.059 ± 0.493	0.570
chromosome	BB_0116		0.785 ± 0.270	0.420	0.747 ± 0.507	0.605	0.814 ± 0.460	0.253	1.421 ± 0.920	0.328
chromosome	BB_0117		1.037 ± 0.405	0.904	1.429 ± 0.561	0.330	0.653 ± 0.252	0.294	1.116 ± 0.415	0.551
chromosome	BB_0134		0.634 ± 0.341	0.058	0.998 ± 1.287	0.998	0.422 ± 0.212	0.090	0.880 ± 0.434	0.734
chromosome	BB_0138		2.434 ± 2.082	0.070	2.185 ± 2.776	0.342	0.722 ± 0.647	0.327	1.596 ± 1.694	0.333
chromosome	BB_0140		1.003 ± 0.236	0.979	1.391 ± 0.566	0.295	0.717 ± 0.198	0.083	1.051 ± 0.246	0.713
chromosome	BB_0141		1.076 ± 0.160	0.592	1.250 ± 0.199	0.161	0.800 ± 0.272	0.417	1.095 ± 0.529	0.776
chromosome	BB_0142		1.121 ± 0.474	0.558	1.724 ± 1.319	0.394	0.694 ± 0.148	0.011	0.980 ± 0.271	0.774
chromosome	BB_0143		1.624 ± 2.134	0.587	1.364 ± 1.373	0.202	1.233 ± 1.727	0.811	1.265 ± 1.185	0.670
chromosome	BB_0155		0.393 ± 0.401	0.182	0.301 ± 0.274	0.180	0.662 ± 0.641	0.472	0.487 ± 0.341	0.324
chromosome	BB_0156		1.022 ± 0.532	0.723	1.126 ± 0.421	0.550	0.911 ± 0.318	0.718	1.149 ± 0.484	0.517
chromosome	BB_0157		0.315 ± 0.210	0.047	0.390 ± 0.197	0.137	0.439 ± 0.202	0.191	0.617 ± 0.346	0.090
chromosome	BB_0158		0.918 ± 0.186	0.143	1.600 ± 0.963	0.348	0.827 ± 0.180	0.254	1.066 ± 0.269	0.466
chromosome	BB_0159		0.797 ± 0.547	0.423	1.591 ± 1.725	0.579	0.622 ± 0.321	0.154	0.828 ± 0.509	0.401
chromosome	BB_0161		0.761 ± 0.367	0.034	1.086 ± 0.563	0.249	0.821 ± 0.375	0.158	1.061 ± 0.625	0.616
chromosome	BB_0163		2.437 ± 1.708	0.275	3.092 ± 2.326	0.258	0.941 ± 0.352	0.776	1.074 ± 0.625	0.852
chromosome	BB_0164		0.736 ± 0.390	0.409	1.260 ± 0.413	0.446	0.876 ± 0.258	0.208	1.206 ± 0.459	0.417
chromosome	BB_0165		0.809 ± 0.407	0.262	1.111 ± 0.785	0.762	0.598 ± 0.345	0.025	0.894 ± 0.482	0.253
chromosome	BB_0166	<i>malQ</i>	0.937 ± 0.458	0.556	1.991 ± 1.386	0.257	0.817 ± 0.326	0.074	1.328 ± 0.392	0.136
chromosome	BB_0167		1.147 ± 0.457	0.351	1.130 ± 0.418	0.612	0.854 ± 0.385	0.254	1.031 ± 0.453	0.694
chromosome	BB_0194		0.712 ± 0.416	0.108	1.035 ± 0.253	0.672	0.579 ± 0.194	0.154	1.069 ± 0.422	0.823
chromosome	BB_0202		0.514 ± 0.188	0.150	0.551 ± 0.466	0.426	0.843 ± 0.396	0.143	1.042 ± 0.545	0.242
chromosome	BB_0203	<i>hfIK</i>	0.870 ± 0.108	0.280	0.963 ± 0.219	0.715	0.749 ± 0.109	0.009	0.943 ± 0.207	0.569
chromosome	BB_0204	<i>hfIC</i>	0.781 ± 0.479	0.174	1.283 ± 0.639	0.197	0.721 ± 0.360	0.299	1.138 ± 0.579	0.463
chromosome	BB_0208		1.122 ± 0.340	0.012	2.039 ± 1.728	0.341	0.733 ± 0.191	0.089	1.049 ± 0.256	0.551
chromosome	BB_0211		1.250 ± 0.518	0.066	1.309 ± 0.902	0.397	0.883 ± 0.336	0.524	1.020 ± 0.328	0.905
chromosome	BB_0223		0.232 ± 0.112	0.060	0.442 ± 0.384	0.310	0.748 ± 0.340	0.252	0.832 ± 0.461	0.018
chromosome	BB_0224		0.267 ± 0.072	0.041	0.487 ± 0.402	0.281	0.782 ± 0.287	0.028	0.927 ± 0.368	0.407
chromosome	BB_0228		1.622 ± 0.540	0.130	1.582 ± 0.660	0.317	0.739 ± 0.226	0.248	1.251 ± 0.652	0.513
chromosome	BB_0235	<i>ychF</i>	1.293 ± 0.356	0.364	2.569 ± 2.446	0.375	1.229 ± 0.967	0.755	0.894 ± 0.519	0.580
chromosome	BB_0241	<i>glpK</i>	0.609 ± 0.346	0.160	0.803 ± 0.396	0.409	0.793 ± 0.536	0.244	0.996 ± 0.617	0.967
chromosome	BB_0242		0.596 ± 0.274	0.165	1.137 ± 0.659	0.050	0.645 ± 0.367	0.074	0.843 ± 0.510	0.222
chromosome	BB_0243		0.430 ± 0.420	0.186	0.928 ± 1.015	0.261	0.630 ± 0.703	0.121	0.837 ± 0.921	0.100
chromosome	BB_0247	<i>rdgB</i>	1.880 ± 2.287	0.606	1.845 ± 1.599	0.153	1.089 ± 0.905	0.874	0.668 ± 1.281	0.334
chromosome	BB_0252		0.950 ± 0.368	0.679	1.483 ± 1.110	0.457	0.684 ± 0.157	0.127	0.953 ± 0.236	0.424
chromosome	BB_0254	<i>recJ</i>	0.966 ± 0.671	0.771	1.383 ± 0.772	0.077	0.572 ± 0.512	0.419	0.791 ± 0.645	0.682
chromosome	BB_0255		1.177 ± 0.856	0.424	1.815 ± 1.436	0.232	0.799 ± 0.342	0.482	1.200 ± 0.703	0.089
chromosome	BB_0256	<i>rpsU</i>	0.860 ± 0.269	0.112	1.501 ± 1.179	0.500	0.714 ± 0.182	0.079	0.785 ± 0.181	0.102
chromosome	BB_0261		0.450 ± 0.375	0.120	1.133 ± 1.077	0.859	0.682 ± 0.824	0.626	0.731 ± 0.658	0.660
chromosome	BB_0262		1.185 ± 0.616	0.585	2.038 ± 1.056	0.193	0.661 ± 0.612	0.568	1.800 ± 0.943	0.124
chromosome	BB_0264		0.747 ± 0.330	0.014	1.202 ± 0.675	0.475	0.751 ± 0.278	0.100	0.768 ± 0.247	0.222

chromosome	BB_0266		1.147 ± 0.221	0.367		1.729 ± 0.509	0.121		0.801 ± 0.070	0.014		1.161 ± 0.237	0.371
chromosome	BB_0267		0.352 ± 0.386	0.018		2.011 ± 3.150	0.572		0.754 ± 0.537	0.522		2.911 ± 3.798	0.407
chromosome	BB_0295	<i>hsfU</i>	1.424 ± 0.730	0.394		1.341 ± 1.213	0.687		0.980 ± 0.448	0.923		0.878 ± 0.508	0.755
chromosome	BB_0296		0.722 ± 0.637	0.196		1.928 ± 2.379	0.586		0.811 ± 0.841	0.786		0.784 ± 0.773	0.784
chromosome	BB_0297		0.898 ± 0.231	0.622		1.312 ± 0.586	0.508		1.015 ± 0.275	0.926		1.137 ± 0.308	0.594
chromosome	BB_0315		1.250 ± 0.974	0.646		1.989 ± 1.786	0.422		1.030 ± 0.619	0.951		0.760 ± 0.367	0.259
chromosome	BB_0316		0.979 ± 1.249	0.982		0.663 ± 0.747	0.575		1.728 ± 1.009	0.233		0.705 ± 0.320	0.029
chromosome	BB_0322		0.480 ± 0.364	0.216		0.537 ± 0.353	0.368		0.674 ± 0.494	0.427		1.548 ± 1.454	0.275
chromosome	BB_0328		0.691 ± 0.541	0.348		0.996 ± 1.011	0.957		0.596 ± 0.484	0.251		0.885 ± 0.869	0.139
chromosome	BB_0329		0.675 ± 0.285	0.062		1.143 ± 0.730	0.573		0.646 ± 0.252	0.083		0.830 ± 0.523	0.262
chromosome	BB_0336		0.905 ± 0.274	0.395		1.161 ± 0.657	0.532		0.660 ± 0.195	0.080		0.912 ± 0.273	0.337
chromosome	BB_0344		0.926 ± 1.430	0.916		1.620 ± 1.801	0.493		0.625 ± 0.549	0.157		0.689 ± 0.467	0.255
chromosome	BB_0347		0.709 ± 0.097	0.031		1.306 ± 0.319	0.180		0.794 ± 0.102	0.102		1.190 ± 0.184	0.116
chromosome	BB_0359		1.646 ± 0.126	0.012		1.983 ± 1.939	0.473		0.597 ± 0.152	0.015		0.986 ± 0.625	0.972
chromosome	BB_0360		1.014 ± 0.172	0.850		1.180 ± 0.538	0.667		0.678 ± 0.233	0.031		0.996 ± 0.137	0.970
chromosome	BB_0361		0.813 ± 0.427	0.657		1.895 ± 1.613	0.404		0.841 ± 0.370	0.660		1.334 ± 0.659	0.030
chromosome	BB_0363		0.962 ± 0.303	0.057		1.548 ± 0.955	0.300		0.833 ± 0.218	0.111		1.076 ± 0.295	0.207
chromosome	BB_0365	<i>la7</i>	0.627 ± 0.296	0.108		0.586 ± 0.292	0.337		0.713 ± 0.301	0.229		0.912 ± 0.452	0.379
chromosome	BB_0368		1.117 ± 1.479	0.865		0.761 ± 0.506	0.654		0.277 ± 0.278	0.177		0.815 ± 0.688	0.630
chromosome	BB_0377	<i>luxS</i>	0.917 ± 0.443	0.243		1.622 ± 1.483	0.393		0.676 ± 0.300	0.114		0.887 ± 0.412	0.252
chromosome	BB_0378		0.922 ± 0.414	0.212		1.546 ± 1.473	0.473		0.648 ± 0.288	0.053		0.916 ± 0.470	0.338
chromosome	BB_0384	<i>bmpC</i>	0.766 ± 0.427	0.527		0.746 ± 0.408	0.533		0.773 ± 0.424	0.480		0.856 ± 0.519	0.627
chromosome	BB_0400		0.765 ± 0.233	0.258		1.055 ± 0.290	0.834		0.754 ± 0.296	0.029		0.946 ± 0.329	0.358
chromosome	BB_0404		0.796 ± 0.668	0.747		1.088 ± 0.744	0.757		0.796 ± 0.538	0.530		0.960 ± 0.670	0.872
chromosome	BB_0405		0.891 ± 0.481	0.778		1.292 ± 0.885	0.652		0.615 ± 0.123	0.099		0.864 ± 0.232	0.464
chromosome	BB_0406		0.857 ± 0.273	0.253		1.530 ± 1.016	0.382		0.773 ± 0.350	0.140		0.835 ± 0.504	0.478
chromosome	BB_0407		1.853 ± 0.994	0.257		1.874 ± 0.434	0.069		0.002 ± 0.004	0.001		2.003 ± 0.320	0.038
chromosome	BB_0408		1.282 ± 0.486	0.085		1.150 ± 0.738	0.494		0.022 ± 0.015	0.041		0.769 ± 0.305	0.467
chromosome	BB_0411		0.730 ± 0.197	0.019		1.190 ± 0.264	0.437		0.688 ± 0.243	0.039		0.901 ± 0.239	0.283
chromosome	BB_0412		0.824 ± 0.289	0.122		1.374 ± 0.952	0.425		0.773 ± 0.244	0.183		1.008 ± 0.359	0.940
chromosome	BB_0414		1.042 ± 0.945	0.959		1.230 ± 1.076	0.545		0.338 ± 0.476	0.423		0.703 ± 0.725	0.252
chromosome	BB_0415		1.091 ± 0.293	0.283		1.205 ± 0.646	0.686		0.895 ± 0.234	0.147		0.915 ± 0.152	0.313
chromosome	BB_0419		0.000^a ± x	0.149		0.094 ± 0.178	0.129		0.399 ± 0.426	0.259		0.913 ± 1.159	0.568
chromosome	BB_0420	<i>rrp1</i>	0.195 ± 0.190	0.037		0.592 ± 0.577	0.020		1.071 ± 0.571	0.540		0.924 ± 0.504	0.573
chromosome	BB_0421		1.005 ± 0.545	0.990		0.863 ± 0.434	0.656		1.057 ± 0.758	0.926		1.024 ± 0.693	0.970
chromosome	BB_0422		0.910 ± 0.400	0.241		1.493 ± 1.081	0.365		0.593 ± 0.182	0.059		0.911 ± 0.248	0.631
chromosome	BB_0429		0.890 ± 0.202	0.485		1.373 ± 0.973	0.475		0.650 ± 0.151	0.100		0.852 ± 0.200	0.378
chromosome	BB_0431		0.883 ± 0.496	0.734		1.968 ± 0.851	0.166		0.502 ± 0.328	0.105		1.095 ± 0.180	0.536
chromosome	BB_0450	<i>rpoN</i>	0.779 ± 0.408	0.166		0.926 ± 0.535	0.656		0.498 ± 0.145	0.107		0.773 ± 0.277	0.251
chromosome	BB_0453		0.757 ± 0.235	0.349		1.125 ± 0.884	0.739		0.523 ± 0.260	0.008		0.822 ± 0.333	0.109
chromosome	BB_0457		0.181 ± 0.224	0.219		1.636 ± 1.735	0.072		0.563 ± 0.679	0.486		1.154 ± 1.468	0.379
chromosome	BB_0459		0.952 ± 0.955	0.836		1.043 ± 1.233	0.901		0.770 ± 0.572	0.628		0.742 ± 0.762	0.392
chromosome	BB_0460		0.571 ± 0.326	0.106		0.872 ± 0.327	0.591		1.023 ± 0.358	0.920		0.950 ± 0.631	0.875
chromosome	BB_0475		0.961 ± 0.520	0.912		1.226 ± 1.190	0.715		0.703 ± 0.397	0.250		0.768 ± 0.463	0.563
chromosome	BB_0505		0.507 ± 0.266	0.040		0.727 ± 0.684	0.235		1.023 ± 0.618	0.794		0.921 ± 0.505	0.133
chromosome	BB_0506		0.655 ± 0.616	0.434		0.576 ± 0.670	0.439		0.803 ± 0.528	0.279		0.523 ± 0.434	0.134
chromosome	BB_0516		1.053 ± 1.569	0.819		1.361 ± 1.287	0.570		0.412 ± 0.498	0.256		1.567 ± 1.700	0.373
chromosome	BB_0524		2.251 ± 1.089	0.028		2.154 ± 2.271	0.388		1.327 ± 0.732	0.547		1.664 ± 1.033	0.160
chromosome	BB_0525		1.205 ± 0.356	0.433		1.744 ± 1.032	0.391		1.083 ± 0.370	0.778		1.033 ± 0.461	0.818
chromosome	BB_0528		0.757 ± 0.067	0.033		0.993 ± 0.159	0.939		0.804 ± 0.187	0.198		0.840 ± 0.211	0.307
chromosome	BB_0530		0.691 ± 0.304	0.050		1.231 ± 0.648	0.480		0.894 ± 0.372	0.544		1.155 ± 0.337	0.081
chromosome	BB_0531		0.736 ± 0.703	0.656		0.810 ± 0.779	0.715		0.769 ± 0.769	0.494		1.267 ± 0.765	0.647
chromosome	BB_0532		1.010 ± 0.429	0.974		1.039 ± 0.461	0.898		0.829 ± 0.432	0.624		0.974 ± 0.746	0.879
chromosome	BB_0536		1.109 ± 0.844	0.683		1.711 ± 1.728	0.182		0.718 ± 0.631	0.279		0.930 ± 0.873	0.446
chromosome	BB_0537		0.865 ± 0.239	0.423		1.116 ± 0.463	0.416		0.556 ± 0.180	0.063		0.856 ± 0.266	0.330
chromosome	BB_0542		0.948 ± 0.521	0.602		1.122 ± 0.787	0.528		0.756 ± 0.523	0.157		0.861 ± 0.853	0.645
chromosome	BB_0553		1.053 ± 0.370	0.642		1.441 ± 0.857	0.368		0.750 ± 0.138	0.155		0.975 ± 0.214	0.736
chromosome	BB_0554		0.818 ± 0.234	0.262		0.975 ± 0.433	0.814		0.659 ± 0.193	0.063		0.898 ± 0.287	0.109
chromosome	BB_0555		0.690 ± 0.136	0.066		1.295 ± 0.684	0.556		0.795 ± 0.304	0.430		0.783 ± 0.157	0.115
chromosome	BB_0556		0.869 ± 0.238	0.420		1.042 ± 0.621	0.856		0.624 ± 0.158	0.134		0.804 ± 0.275	0.010
chromosome	BB_0563		1.173 ± 0.622	0.140		1.418 ± 1.138	0.414		0.714 ± 0.365	0.049		1.082 ± 0.781	0.811
chromosome	BB_0565		1.031 ± 0.119	0.532		1.368 ± 0.656	0.448		0.717 ± 0.156	0.064		0.994 ± 0.313	0.977
chromosome	BB_0566		1.095 ± 0.608	0.488		2.075 ± 1.736	0.210		0.675 ± 0.467	0.071		1.470 ± 1.114	0.181
chromosome	BB_0567		0.791 ± 0.166	0.151		1.229 ± 0.638	0.430		0.656 ± 0.138	0.068		0.949 ± 0.258	0.147

chromosome	BB_0568		0.844 ± 0.195	0.073		1.322 ± 0.870	0.539		0.683 ± 0.103	0.024		0.926 ± 0.139	0.564
chromosome	BB_0569		0.918 ± 0.428	0.499		1.549 ± 1.131	0.383		0.853 ± 0.437	0.161		1.045 ± 0.333	0.787
chromosome	BB_0570		1.116 ± 0.449	0.728		1.477 ± 0.772	0.394		0.784 ± 0.308	0.304		1.145 ± 0.466	0.391
chromosome	BB_0576		1.154 ± 0.398	0.339		1.569 ± 1.174	0.321		0.788 ± 0.404	0.195		1.102 ± 0.472	0.663
chromosome	BB_0577		0.887 ± 0.308	0.058		1.505 ± 1.192	0.448		0.866 ± 0.256	0.502		0.923 ± 0.241	0.467
chromosome	BB_0578		0.943 ± 0.284	0.284		1.397 ± 0.752	0.291		0.719 ± 0.210	0.101		1.124 ± 0.347	0.231
chromosome	BB_0580		0.496 ± 0.425	0.199		0.399 ± 0.393	0.396		0.716 ± 0.662	0.201		0.923 ± 0.923	0.065
chromosome	BB_0581	<i>recG</i>	0.849 ± 0.214	0.379		1.384 ± 1.022	0.613		0.590 ± 0.188	0.166		0.947 ± 0.458	0.797
chromosome	BB_0582		0.868 ± 0.221	0.517		0.949 ± 0.547	0.878		0.599 ± 0.153	0.006		1.035 ± 0.278	0.815
chromosome	BB_0584		1.099 ± 0.653	0.654		1.500 ± 1.332	0.594		0.798 ± 0.828	0.446		1.260 ± 0.548	0.484
chromosome	BB_0588	<i>bgp</i>	0.775 ± 0.166	0.086		0.774 ± 0.369	0.317		0.626 ± 0.083	0.004		0.820 ± 0.129	0.169
chromosome	BB_0591		1.096 ± 0.342	0.540		1.636 ± 0.967	0.316		0.652 ± 0.192	0.046		0.870 ± 0.353	0.337
chromosome	BB_0597		1.107 ± 0.939	0.692		1.357 ± 0.789	0.136		1.246 ± 0.713	0.442		1.226 ± 0.845	0.138
chromosome	BB_0605		1.131 ± 0.945	0.773		1.556 ± 1.622	0.528		0.645 ± 0.501	0.193		0.998 ± 0.698	0.994
chromosome	BB_0607	<i>pcrA</i>	0.910 ± 0.677	0.862		2.133 ± 2.080	0.151		0.850 ± 0.703	0.429		1.041 ± 0.878	0.840
chromosome	BB_0608		1.202 ± 0.775	0.060		1.202 ± 0.888	0.721		0.542 ± 0.259	0.201		1.064 ± 0.520	0.815
chromosome	BB_0616		1.415 ± 0.831	0.536		1.651 ± 1.103	0.440		0.855 ± 0.507	0.766		1.262 ± 1.027	0.724
chromosome	BB_0617		0.792 ± 0.344	0.493		1.354 ± 1.289	0.648		0.359 ± 0.130	0.027		0.372 ± 0.086	0.044
chromosome	BB_0618	<i>cdd</i>	1.911 ± 1.401	0.082		1.670 ± 1.163	0.208		1.555 ± 1.222	0.224		0.928 ± 0.541	0.747
chromosome	BB_0619		0.283 ± 0.157	0.150		0.543 ± 0.298	0.299		0.570 ± 0.370	0.207		0.743 ± 0.434	0.359
chromosome	BB_0620		0.827 ± 0.352	0.148		1.517 ± 0.919	0.290		0.739 ± 0.286	0.202		1.037 ± 0.353	0.535
chromosome	BB_0623	<i>mfd</i>	1.280 ± 0.959	0.244		1.440 ± 1.617	0.461		0.817 ± 0.519	0.521		1.369 ± 0.844	0.410
chromosome	BB_0626	<i>rnmV</i>	0.845 ± 0.713	0.814		0.937 ± 1.404	0.890		0.570 ± 0.589	0.158		0.718 ± 0.658	0.338
chromosome	BB_0629		0.965 ± 0.178	0.815		1.382 ± 0.834	0.511		0.602 ± 0.118	0.061		0.888 ± 0.101	0.263
chromosome	BB_0630	<i>pfkB</i>	1.389 ± 1.842	0.577		2.700 ± 3.386	0.270		0.509 ± 0.798	0.163		1.887 ± 1.964	0.167
chromosome	BB_0631		1.357 ± 1.348	0.658		0.711 ± 0.537	0.344		0.711 ± 0.723	0.004		1.321 ± 0.952	0.291
chromosome	BB_0637		1.077 ± 0.178	0.377		2.060 ± 1.391	0.303		0.789 ± 0.316	0.454		0.979 ± 0.333	0.937
chromosome	BB_0638		0.853 ± 0.233	0.172		1.266 ± 0.389	0.449		0.777 ± 0.208	0.028		0.857 ± 0.178	0.209
chromosome	BB_0645		1.166 ± 0.810	0.794		1.189 ± 1.055	0.822		1.050 ± 0.703	0.372		0.781 ± 0.691	0.685
chromosome	BB_0656		0.784 ± 0.962	0.110		1.575 ± 1.215	0.311		0.730 ± 0.619	0.362		0.944 ± 0.851	0.922
chromosome	BB_0666		1.088 ± 0.955	0.737		1.603 ± 1.250	0.402		0.619 ± 0.495	0.516		0.604 ± 0.489	0.479
chromosome	BB_0670		0.729 ± 0.635	0.563		1.161 ± 1.000	0.825		0.361 ± 0.395	0.193		0.820 ± 0.952	0.184
chromosome	BB_0671		0.709 ± 0.283	0.047		1.056 ± 0.704	0.838		0.703 ± 0.297	0.039		0.824 ± 0.430	0.364
chromosome	BB_0674		0.923 ± 0.427	0.773		1.400 ± 0.714	0.450		0.495 ± 0.225	0.086		0.871 ± 0.233	0.216
chromosome	BB_0675		0.846 ± 0.376	0.374		2.072 ± 2.531	0.509		0.626 ± 0.278	0.053		1.023 ± 0.591	0.935
chromosome	BB_0680		1.047 ± 0.820	0.598		1.742 ± 1.846	0.359		0.659 ± 0.419	0.209		0.889 ± 0.593	0.376
chromosome	BB_0681		0.747 ± 0.192	0.008		1.140 ± 0.403	0.369		0.712 ± 0.222	0.021		0.961 ± 0.261	0.300
chromosome	BB_0707		0.760 ± 0.054	0.007		1.354 ± 0.480	0.322		0.474 ± 0.205	0.029		0.887 ± 0.462	0.690
chromosome	BB_0722		1.193 ± 0.233	0.173		1.745 ± 1.198	0.373		0.866 ± 0.277	0.356		1.102 ± 0.151	0.081
chromosome	BB_0723		0.716 ± 0.155	0.089		0.762 ± 0.677	0.516		1.022 ± 0.371	0.821		1.143 ± 0.281	0.044
chromosome	BB_0726		2.424 ± 3.150	0.504		9.225 ± 13.320	0.382		2.320 ± 2.230	0.444		3.209 ± 2.033	0.088
chromosome	BB_0739		1.426 ± 1.092	0.055		1.249 ± 1.303	0.566		0.434 ± 0.326	0.287		1.108 ± 0.738	0.701
chromosome	BB_0740		0.842 ± 0.388	0.167		1.361 ± 1.020	0.589		0.698 ± 0.280	0.355		0.991 ± 0.383	0.902
chromosome	BB_0743		0.645 ± 0.146	0.139		0.407 ± 0.317	0.119		0.472 ± 0.078	0.032		0.833 ± 0.249	0.359
chromosome	BB_0744	<i>p83/100</i>	0.790 ± 0.565	0.539		1.316 ± 0.952	0.602		0.817 ± 0.248	0.411		1.742 ± 0.617	0.138
chromosome	BB_0745		0.953 ± 0.371	0.571		1.335 ± 0.496	0.129		0.814 ± 0.179	0.142		0.911 ± 0.316	0.108
chromosome	BB_0756		0.707 ± 0.298	0.367		1.253 ± 0.983	0.714		0.323 ± 0.152	0.058		0.957 ± 0.551	0.887
chromosome	BB_0761		1.609 ± 2.096	0.508		0.990 ± 0.920	0.987		0.334 ± 0.206	0.178		0.408 ± 0.324	0.129
chromosome	BB_0767	<i>murG</i>	1.627 ± 1.140	0.413		1.807 ± 0.791	0.126		1.120 ± 0.423	0.365		1.743 ± 0.827	0.198
chromosome	BB_0771	<i>rpoS</i>	1.077 ± 0.974	0.385		1.624 ± 1.743	0.315		0.706 ± 0.549	0.228		1.024 ± 0.848	0.699
chromosome	BB_0772		1.147 ± 0.358	0.194		1.688 ± 1.175	0.342		0.721 ± 0.212	0.035		0.986 ± 0.265	0.820
chromosome	BB_0773		1.097 ± 1.031	0.236		2.058 ± 2.584	0.353		0.665 ± 0.494	0.338		1.031 ± 0.833	0.848
chromosome	BB_0789		0.829 ± 0.757	0.810		0.978 ± 1.057	0.960		0.096 ± 0.122	0.229		0.409 ± 0.755	0.059
chromosome	BB_0797	<i>mutS</i>	1.005 ± 0.361	0.956		1.281 ± 0.709	0.245		0.751 ± 0.360	0.016		1.063 ± 0.507	0.477
chromosome	BB_0803	<i>truB</i>	0.925 ± 0.355	0.759		0.893 ± 0.704	0.811		0.988 ± 0.299	0.946		1.527 ± 0.413	0.202
chromosome	BB_0811		1.594 ± 1.143	0.265		1.613 ± 1.101	0.061		0.744 ± 0.541	0.208		1.316 ± 1.214	0.440
chromosome	BB_0814	<i>panF</i>	1.527 ± 0.873	0.020		1.759 ± 1.241	0.382		1.141 ± 0.684	0.162		1.085 ± 0.774	0.474
chromosome	BB_0815		1.089 ± 0.351	0.506		1.617 ± 1.249	0.388		0.940 ± 0.248	0.708		1.062 ± 0.512	0.740
chromosome	BB_0823		0.860 ± 1.100	0.685		1.564 ± 1.359	0.594		0.894 ± 0.581	0.825		1.140 ± 1.443	0.857
chromosome	BB_0824		0.891 ± 0.676	0.684		0.842 ± 0.346	0.543		0.780 ± 0.465	0.137		0.493 ± 0.355	0.038
chromosome	BB_0825		0.449 ± 0.440	0.138		0.674 ± 0.735	0.243		0.280 ± 0.379	0.307		0.523 ± 0.390	0.310
chromosome	BB_0826		0.884 ± 1.010	0.826		1.207 ± 1.429	0.794		0.440 ± 0.635	0.563		1.065 ± 1.290	0.952
chromosome	BB_0829		0.667 ± 0.154	0.063		0.868 ± 0.292	0.645		0.717 ± 0.165	0.073		1.040 ± 0.364	0.546
chromosome	BB_0830		0.746 ± 0.510	0.203		1.203 ± 1.279	0.605		0.486 ± 0.323	0.131		0.803 ± 0.746	0.180

chromosome	BB_0831		0.691 ± 0.452	0.509	0.971 ± 0.398	0.937	0.965 ± 0.347	0.107	1.275 ± 0.549	0.130
chromosome	BB_0836	<i>uvrB</i>	0.284 ± 0.215	0.230	0.480 ± 0.430	0.337	0.548 ± 0.506	0.501	1.451 ± 0.956	0.306
chromosome	BB_0838		1.101 ± 0.605	0.620	1.987 ± 1.696	0.266	0.858 ± 0.489	0.393	1.441 ± 0.913	0.466
chromosome	BB_0844		1.142 ± 0.685	0.673	1.557 ± 1.071	0.404	0.966 ± 0.729	0.930	1.142 ± 0.882	0.783
chromosome	BB_0845a		1.245 ± 0.902	0.184	1.734 ± 1.691	0.335	0.807 ± 0.456	0.316	1.084 ± 0.671	0.395
chromosome	BB_0845b		0.895 ± 0.777	0.500	1.765 ± 1.591	0.302	0.684 ± 0.544	0.086	0.748 ± 0.717	0.200
chromosome	BB_0848a		0.853 ± 0.541	0.370	0.703 ± 0.528	0.573	1.153 ± 0.693	0.782	0.327 ± 0.317	0.118
chromosome	BB_0849b		1.153 ± 0.922	0.745	1.359 ± 1.317	0.631	0.789 ± 0.419	0.197	1.176 ± 0.621	0.523
chromosome	BB_0852		1.117 ± 0.405	0.397	1.134 ± 0.430	0.345	0.737 ± 0.320	0.454	1.090 ± 0.260	0.549
chromosome	BB_0853		0.896 ± 0.747	0.690	1.624 ± 1.330	0.228	0.982 ± 0.653	0.945	0.994 ± 0.746	0.949
chromosome	BB_r01	<i>5S_rrlA</i>	0.027 ± 0.027	0.027	0.257 ± 0.424	0.188	0.587 ± 0.193	0.189	0.374 ± 0.165	0.062
chromosome	BB_r02	<i>23S_rrlA</i>	0.572 ± 0.192	0.043	0.717 ± 0.180	0.170	0.621 ± 0.238	0.003	0.779 ± 0.320	0.055
chromosome	BB_r03	<i>5S_rrlB</i>	0.030 ± 0.025	0.042	0.278 ± 0.444	0.219	0.556 ± 0.238	0.240	0.388 ± 0.155	0.069
chromosome	BB_r04	<i>23S_rrlB</i>	0.568 ± 0.191	0.027	0.733 ± 0.177	0.135	0.622 ± 0.236	0.002	0.774 ± 0.311	0.061
plasmid_cp26	BB_B01		0.324 ± 0.343	0.021	0.459 ± 0.446	0.010	0.890 ± 0.556	0.119	0.949 ± 0.677	0.548
plasmid_cp26	BB_B02		1.653 ± 0.275	0.006	1.123 ± 0.164	0.129	0.928 ± 0.146	0.362	1.106 ± 0.213	0.320
plasmid_cp26	BB_B04		0.742 ± 0.540	0.394	0.741 ± 0.252	0.059	0.715 ± 0.103	0.026	0.950 ± 0.125	0.491
plasmid_cp26	BB_B05		0.954 ± 0.697	0.852	0.925 ± 0.293	0.743	0.921 ± 0.307	0.639	1.194 ± 0.374	0.253
plasmid_cp26	BB_B06		0.643 ± 0.610	0.544	0.748 ± 0.689	0.687	1.030 ± 0.374	0.861	1.121 ± 0.450	0.046
plasmid_cp26	BB_B07		1.557 ± 0.210	0.041	1.567 ± 0.829	0.358	0.853 ± 0.068	0.008	1.038 ± 0.067	0.020
plasmid_cp26	BB_B09		1.214 ± 0.339	0.023	0.920 ± 0.317	0.297	0.750 ± 0.247	0.001	0.907 ± 0.212	0.196
plasmid_cp26	BB_B12		1.139 ± 0.879	0.741	0.614 ± 0.495	0.530	0.630 ± 0.511	0.542	1.034 ± 0.882	0.951
plasmid_cp26	BB_B14		1.525 ± 0.588	0.200	1.316 ± 0.610	0.396	0.889 ± 0.113	0.102	1.060 ± 0.219	0.452
plasmid_cp26	BB_B16		0.142 ± 0.118	0.042	0.371 ± 0.366	0.021	0.961 ± 0.450	0.617	0.840 ± 0.351	0.469
plasmid_cp26	BB_B17		2.139 ± 0.550	0.063	1.494 ± 0.660	0.386	0.863 ± 0.342	0.209	1.145 ± 0.243	0.351
plasmid_cp26	BB_B18	<i>guAA</i>	1.996 ± 0.371	0.037	1.593 ± 0.892	0.406	0.850 ± 0.192	0.006	1.019 ± 0.160	0.646
plasmid_cp26	BB_B22		1.849 ± 0.524	0.106	1.238 ± 0.446	0.514	0.886 ± 0.249	0.023	1.022 ± 0.241	0.662
plasmid_cp26	BB_B23		0.830 ± 0.259	0.019	0.482 ± 0.318	0.216	0.803 ± 0.282	0.055	0.927 ± 0.290	0.154
plasmid_cp26	BB_B24		1.454 ± 0.106	0.023	1.132 ± 0.298	0.556	0.800 ± 0.097	0.076	1.007 ± 0.184	0.963
plasmid_cp26	BB_B25		1.367 ± 0.857	0.057	1.068 ± 0.567	0.689	0.818 ± 0.493	0.324	1.081 ± 0.685	0.480
plasmid_cp26	BB_B27		1.723 ± 0.660	0.007	1.079 ± 0.441	0.341	0.913 ± 0.341	0.462	1.389 ± 0.557	0.164
plasmid_cp26	BB_B28		1.465 ± 0.185	0.027	0.815 ± 0.392	0.449	0.847 ± 0.066	0.006	1.157 ± 0.171	0.200
plasmid_cp26	BB_B29		0.067 ± 0.079	0.124	0.321 ± 0.447	0.063	3.089 ± 2.711	0.064	0.097 ± 0.085	0.136
plasmid_cp32-1	BB_P01		2.055 ± 0.665	0.052	1.487 ± 1.018	0.424	0.983 ± 0.224	0.247	1.073 ± 0.303	0.393
plasmid_cp32-1	BB_P02		1.837 ± 0.524	0.028	1.085 ± 0.409	0.556	1.042 ± 0.238	0.532	1.010 ± 0.236	0.936
plasmid_cp32-1	BB_P03		1.962 ± 0.597	0.104	1.548 ± 0.738	0.325	1.036 ± 0.359	0.885	1.021 ± 0.137	0.864
plasmid_cp32-1	BB_P04		1.459 ± 0.782	0.013	1.103 ± 0.593	0.243	1.048 ± 0.519	0.629	1.293 ± 0.736	0.051
plasmid_cp32-1	BB_P05		2.443 ± 0.833	0.040	2.116 ± 1.774	0.337	1.067 ± 0.413	0.530	1.371 ± 0.430	0.041
plasmid_cp32-1	BB_P06		2.249 ± 1.137	0.147	1.670 ± 1.491	0.469	0.799 ± 0.278	0.112	1.045 ± 0.275	0.696
plasmid_cp32-1	BB_P07		1.516 ± 0.590	0.287	1.641 ± 1.591	0.555	0.814 ± 0.308	0.501	0.915 ± 0.395	0.810
plasmid_cp32-1	BB_P08		0.562 ± 0.175	0.142	0.489 ± 0.302	0.205	1.149 ± 0.400	0.043	1.063 ± 0.434	0.457
plasmid_cp32-1	BB_P09		2.759 ± 1.191	0.062	1.624 ± 1.133	0.338	0.967 ± 0.288	0.246	1.247 ± 0.420	0.064
plasmid_cp32-1	BB_P10		1.306 ± 0.230	0.052	0.817 ± 0.163	0.189	0.864 ± 0.169	0.066	1.037 ± 0.128	0.273
plasmid_cp32-1	BB_P11		1.974 ± 0.874	0.159	1.572 ± 1.127	0.428	1.088 ± 0.302	0.396	1.144 ± 0.232	0.181
plasmid_cp32-1	BB_P12		2.153 ± 0.806	0.092	1.986 ± 1.862	0.425	0.993 ± 0.260	0.960	1.021 ± 0.270	0.741
plasmid_cp32-1	BB_P13		2.432 ± 0.802	0.042	1.528 ± 0.995	0.355	1.152 ± 0.562	0.512	1.343 ± 0.487	0.291
plasmid_cp32-1	BB_P14		1.858 ± 0.543	0.004	1.703 ± 1.173	0.272	1.221 ± 0.397	0.459	1.096 ± 0.428	0.107
plasmid_cp32-1	BB_P15		2.023 ± 0.675	0.023	1.499 ± 1.171	0.437	0.891 ± 0.286	0.335	0.953 ± 0.311	0.001
plasmid_cp32-1	BB_P16		1.785 ± 0.631	0.090	1.593 ± 1.299	0.461	0.914 ± 0.238	0.440	1.085 ± 0.314	0.590
plasmid_cp32-1	BB_P17		1.972 ± 1.130	0.053	0.651 ± 0.304	0.374	0.955 ± 0.459	0.760	1.038 ± 0.544	0.562
plasmid_cp32-1	BB_P18		2.176 ± 0.542	0.026	1.908 ± 1.501	0.369	1.048 ± 0.165	0.547	1.258 ± 0.168	0.081
plasmid_cp32-1	BB_P19		3.577 ± 1.213	0.056	1.672 ± 1.459	0.500	0.998 ± 0.143	0.986	1.184 ± 0.330	0.411
plasmid_cp32-1	BB_P20		1.495 ± 0.262	0.016	1.029 ± 0.277	0.791	0.914 ± 0.112	0.279	1.107 ± 0.130	0.133
plasmid_cp32-1	BB_P21		1.993 ± 0.921	0.018	0.839 ± 0.442	0.279	0.875 ± 0.398	0.248	1.011 ± 0.475	0.951
plasmid_cp32-1	BB_P22		1.708 ± 0.787	0.038	1.203 ± 0.866	0.521	0.914 ± 0.425	0.439	1.037 ± 0.452	0.719
plasmid_cp32-1	BB_P23	<i>blyA</i>	1.100 ± 0.436	0.275	0.478 ± 0.346	0.292	0.915 ± 0.356	0.446	0.989 ± 0.422	0.819
plasmid_cp32-1	BB_P24	<i>blyB</i>	2.668 ± 1.384	0.109	1.547 ± 0.965	0.459	0.977 ± 0.653	0.925	0.780 ± 0.280	0.448
plasmid_cp32-1	BB_P25		2.174 ± 1.115	0.092	1.745 ± 1.470	0.365	1.015 ± 0.440	0.897	1.081 ± 0.413	0.425
plasmid_cp32-1	BB_P26		2.010 ± 1.637	0.329	1.389 ± 0.957	0.481	0.757 ± 0.320	0.061	0.743 ± 0.523	0.370
plasmid_cp32-1	BB_P27	<i>revA</i>	1.706 ± 0.707	0.200	1.311 ± 0.884	0.430	0.836 ± 0.359	0.498	0.852 ± 0.319	0.624
plasmid_cp32-1	BB_P28	<i>mlpA</i>	1.438 ± 1.435	0.659	1.173 ± 1.183	0.790	0.491 ± 0.433	0.336	1.007 ± 0.911	0.992
plasmid_cp32-1	BB_P29		2.774 ± 1.618	0.095	1.960 ± 1.719	0.321	1.064 ± 0.449	0.280	1.180 ± 0.509	0.080
plasmid_cp32-1	BB_P35	<i>bppA</i>	2.522 ± 1.378	0.090	1.863 ± 1.576	0.330	0.941 ± 0.355	0.489	1.044 ± 0.398	0.383
plasmid_cp32-1	BB_P36	<i>bppB</i>	2.416 ± 2.206	0.169	1.761 ± 1.954	0.359	0.978 ± 0.711	0.831	1.094 ± 0.877	0.172

plasmid_cp32-1	BB_P37	<i>bppC</i>	2.556 ± 1.582	0.118	0.906 ± 0.448	0.804	0.680 ± 0.346	0.452	1.259 ± 0.726	0.056
plasmid_cp32-1	BB_P38	<i>erpA</i>	2.916 ± 1.169	0.085	1.894 ± 1.259	0.309	1.005 ± 0.172	0.948	1.081 ± 0.157	0.053
plasmid_cp32-1	BB_P39	<i>erpB</i>	2.056 ± 0.212	0.002	1.693 ± 0.861	0.266	1.153 ± 0.192	0.338	1.265 ± 0.296	0.321
plasmid_cp32-1	BB_P40		2.578 ± 1.437	0.165	2.036 ± 1.874	0.406	0.908 ± 0.340	0.693	1.490 ± 0.614	0.197
plasmid_cp32-1	BB_P41		2.831 ± 2.663	0.164	2.253 ± 3.038	0.416	0.873 ± 0.699	0.350	0.950 ± 0.746	0.509
plasmid_cp32-1	BB_P42		2.335 ± 0.735	0.029	1.674 ± 1.202	0.351	0.911 ± 0.206	0.479	1.032 ± 0.292	0.721
plasmid_cp32-3	BB_S01		2.178 ± 0.623	0.051	1.501 ± 0.987	0.426	1.085 ± 0.197	0.144	1.104 ± 0.242	0.269
plasmid_cp32-3	BB_S02		1.793 ± 0.442	0.071	1.037 ± 0.245	0.773	1.020 ± 0.113	0.670	1.006 ± 0.121	0.930
plasmid_cp32-3	BB_S03		1.987 ± 0.646	0.110	1.481 ± 0.783	0.395	1.026 ± 0.390	0.928	0.982 ± 0.155	0.902
plasmid_cp32-3	BB_S04		1.656 ± 0.735	0.091	1.556 ± 1.074	0.332	1.013 ± 0.340	0.534	1.278 ± 0.365	0.066
plasmid_cp32-3	BB_S05		2.336 ± 0.710	0.027	1.743 ± 1.379	0.387	1.053 ± 0.345	0.698	1.212 ± 0.344	0.392
plasmid_cp32-3	BB_S06		2.320 ± 1.162	0.142	1.669 ± 1.481	0.469	0.826 ± 0.286	0.222	1.051 ± 0.303	0.701
plasmid_cp32-3	BB_S07		1.413 ± 0.561	0.353	1.551 ± 1.613	0.588	0.717 ± 0.366	0.470	0.918 ± 0.480	0.844
plasmid_cp32-3	BB_S08		0.573 ± 0.177	0.148	0.501 ± 0.309	0.212	1.166 ± 0.389	0.043	1.075 ± 0.437	0.441
plasmid_cp32-3	BB_S09		2.707 ± 0.904	0.054	1.513 ± 0.910	0.382	0.968 ± 0.259	0.778	1.151 ± 0.319	0.354
plasmid_cp32-3	BB_S10		2.416 ± 0.908	0.049	1.366 ± 0.874	0.420	0.882 ± 0.279	0.240	1.073 ± 0.334	0.241
plasmid_cp32-3	BB_S11		2.190 ± 0.964	0.157	1.679 ± 1.112	0.384	1.133 ± 0.289	0.410	1.245 ± 0.145	0.013
plasmid_cp32-3	BB_S12		2.075 ± 0.680	0.085	1.953 ± 1.762	0.425	0.983 ± 0.236	0.910	0.987 ± 0.246	0.866
plasmid_cp32-3	BB_S13		2.389 ± 0.823	0.077	1.438 ± 0.879	0.437	1.081 ± 0.477	0.606	1.305 ± 0.408	0.142
plasmid_cp32-3	BB_S14		1.926 ± 0.632	0.008	1.672 ± 1.192	0.278	1.257 ± 0.462	0.419	1.114 ± 0.451	0.004
plasmid_cp32-3	BB_S15		2.537 ± 0.704	0.020	1.626 ± 1.146	0.367	1.015 ± 0.232	0.875	1.191 ± 0.280	0.005
plasmid_cp32-3	BB_S16		1.792 ± 0.843	0.081	1.602 ± 1.493	0.462	0.929 ± 0.325	0.561	0.991 ± 0.404	0.911
plasmid_cp32-3	BB_S17		1.999 ± 1.127	0.057	0.630 ± 0.291	0.350	0.984 ± 0.465	0.909	1.048 ± 0.539	0.426
plasmid_cp32-3	BB_S18		2.258 ± 0.644	0.029	1.968 ± 1.675	0.378	1.077 ± 0.232	0.630	1.240 ± 0.199	0.138
plasmid_cp32-3	BB_S19		2.875 ± 1.135	0.080	1.333 ± 1.141	0.641	0.771 ± 0.117	0.122	1.009 ± 0.244	0.945
plasmid_cp32-3	BB_S20		1.491 ± 0.258	0.021	1.016 ± 0.257	0.869	0.895 ± 0.111	0.241	1.098 ± 0.119	0.124
plasmid_cp32-3	BB_S21		2.031 ± 1.011	0.013	0.853 ± 0.454	0.397	0.914 ± 0.453	0.426	1.018 ± 0.537	0.935
plasmid_cp32-3	BB_S22		1.799 ± 0.724	0.019	1.361 ± 0.969	0.395	0.973 ± 0.421	0.757	1.130 ± 0.487	0.292
plasmid_cp32-3	BB_S23	<i>blyA</i>	1.121 ± 0.458	0.180	0.479 ± 0.344	0.289	0.918 ± 0.363	0.419	1.005 ± 0.441	0.881
plasmid_cp32-3	BB_S24	<i>blyB</i>	2.624 ± 1.435	0.121	1.556 ± 0.784	0.354	0.988 ± 0.614	0.958	0.872 ± 0.365	0.693
plasmid_cp32-3	BB_S25		2.139 ± 1.231	0.107	1.773 ± 1.557	0.352	0.940 ± 0.425	0.659	1.029 ± 0.431	0.685
plasmid_cp32-3	BB_S26		1.546 ± 0.521	0.257	1.087 ± 0.411	0.798	1.035 ± 0.291	0.837	1.186 ± 0.277	0.044
plasmid_cp32-3	BB_S27		0.880 ± 0.794	0.811	0.923 ± 0.776	0.792	0.619 ± 0.531	0.266	0.882 ± 0.947	0.867
plasmid_cp32-3	BB_S29	<i>bdrF</i>	2.222 ± 0.955	0.047	2.091 ± 1.492	0.201	1.101 ± 0.426	0.256	1.379 ± 0.627	0.208
plasmid_cp32-3	BB_S30	<i>mlpC</i>	1.976 ± 1.661	0.076	1.940 ± 1.939	0.178	1.233 ± 0.839	0.504	1.139 ± 0.809	0.660
plasmid_cp32-3	BB_S31		2.509 ± 0.980	0.040	1.646 ± 1.203	0.340	0.991 ± 0.300	0.920	1.139 ± 0.348	0.233
plasmid_cp32-3	BB_S38	<i>bppA</i>	2.439 ± 1.368	0.117	1.725 ± 1.399	0.356	0.941 ± 0.295	0.584	1.047 ± 0.383	0.036
plasmid_cp32-3	BB_S39	<i>bppB</i>	2.956 ± 1.752	0.191	2.625 ± 2.489	0.380	1.130 ± 0.655	0.773	1.223 ± 0.510	0.530
plasmid_cp32-3	BB_S40	<i>bppC</i>	3.393 ± 2.159	0.107	2.168 ± 2.277	0.381	0.933 ± 0.477	0.225	1.105 ± 0.483	0.268
plasmid_cp32-3	BB_S41	<i>erpG</i>	0.849 ± 0.632	0.319	0.804 ± 0.574	0.348	1.013 ± 0.793	0.783	1.029 ± 0.827	0.632
plasmid_cp32-3	BB_S44		1.246 ± 0.724	0.170	0.636 ± 0.368	0.434	1.159 ± 0.700	0.131	1.263 ± 0.892	0.076
plasmid_cp32-3	BB_S45		1.432 ± 0.475	0.107	1.027 ± 0.425	0.867	0.845 ± 0.230	0.094	0.938 ± 0.217	0.221
plasmid_cp32-4	BB_R01		2.099 ± 0.708	0.063	1.510 ± 1.005	0.405	1.025 ± 0.219	0.245	1.121 ± 0.301	0.233
plasmid_cp32-4	BB_R02		3.761 ± 2.327	0.047	2.510 ± 2.414	0.245	1.092 ± 0.754	0.822	1.200 ± 0.671	0.206
plasmid_cp32-4	BB_R03		1.222 ± 0.602	0.057	0.560 ± 0.417	0.405	1.061 ± 0.570	0.406	1.251 ± 0.662	0.046
plasmid_cp32-4	BB_R04		3.762 ± 2.600	0.157	0.880 ± 0.281	0.291	1.066 ± 0.428	0.318	1.196 ± 0.526	0.145
plasmid_cp32-4	BB_R05		3.627 ± 2.181	0.172	0.872 ± 1.013	0.786	2.359 ± 1.332	0.167	1.895 ± 1.521	0.346
plasmid_cp32-4	BB_R06		2.334 ± 0.462	0.016	1.306 ± 0.368	0.364	0.994 ± 0.308	0.955	1.020 ± 0.261	0.733
plasmid_cp32-4	BB_R07		1.617 ± 0.522	0.138	1.036 ± 0.666	0.900	0.565 ± 0.208	0.161	0.590 ± 0.206	0.113
plasmid_cp32-4	BB_R08		2.022 ± 0.560	0.037	1.152 ± 0.657	0.677	0.848 ± 0.213	0.066	1.043 ± 0.338	0.575
plasmid_cp32-4	BB_R09		2.734 ± 1.195	0.062	1.635 ± 1.127	0.321	0.967 ± 0.301	0.195	1.242 ± 0.411	0.041
plasmid_cp32-4	BB_R10		3.460 ± 0.716	0.029	1.874 ± 1.015	0.284	0.957 ± 0.072	0.358	1.091 ± 0.110	0.352
plasmid_cp32-4	BB_R11		3.009 ± 1.223	0.024	1.508 ± 1.348	0.464	1.076 ± 0.361	0.479	1.191 ± 0.418	0.157
plasmid_cp32-4	BB_R12		2.127 ± 0.642	0.072	1.961 ± 1.784	0.433	0.995 ± 0.167	0.966	0.950 ± 0.199	0.526
plasmid_cp32-4	BB_R13		3.107 ± 0.799	0.044	2.025 ± 1.176	0.249	1.402 ± 0.795	0.437	1.253 ± 0.300	0.185
plasmid_cp32-4	BB_R14		1.928 ± 0.590	0.005	1.670 ± 1.193	0.306	1.269 ± 0.436	0.347	1.134 ± 0.415	0.097
plasmid_cp32-4	BB_R15		2.017 ± 0.655	0.014	1.496 ± 1.185	0.438	0.892 ± 0.309	0.433	0.973 ± 0.335	0.055
plasmid_cp32-4	BB_R16		2.999 ± 1.075	0.021	1.631 ± 1.354	0.401	0.886 ± 0.292	0.222	1.095 ± 0.359	0.133
plasmid_cp32-4	BB_R17		2.099 ± 1.191	0.052	0.774 ± 0.346	0.270	0.923 ± 0.465	0.508	1.045 ± 0.544	0.273
plasmid_cp32-4	BB_R18		2.298 ± 0.730	0.024	2.019 ± 1.719	0.356	1.031 ± 0.270	0.786	1.216 ± 0.257	0.125
plasmid_cp32-4	BB_R19		2.257 ± 0.294	0.021	1.543 ± 0.505	0.229	1.056 ± 0.245	0.678	1.640 ± 0.511	0.149
plasmid_cp32-4	BB_R20		2.369 ± 1.153	0.060	0.900 ± 0.294	0.513	1.028 ± 0.463	0.805	1.061 ± 0.361	0.759
plasmid_cp32-4	BB_R21		2.465 ± 1.290	0.066	1.776 ± 1.679	0.395	0.869 ± 0.371	0.119	0.990 ± 0.413	0.906
plasmid_cp32-4	BB_R22		2.860 ± 0.664	0.034	1.449 ± 0.489	0.282	1.146 ± 0.184	0.148	1.102 ± 0.299	0.385

plasmid_cp32-4	BB_R23	<i>blyA</i>	1.113 ± 0.439	0.288	0.466 ± 0.343	0.284	0.917 ± 0.383	0.422	0.993 ± 0.449	0.876
plasmid_cp32-4	BB_R24	<i>blyB</i>	2.679 ± 1.470	0.065	1.576 ± 1.000	0.406	0.991 ± 0.711	0.955	0.941 ± 0.455	0.884
plasmid_cp32-4	BB_R25		2.284 ± 1.132	0.083	1.629 ± 1.412	0.416	0.932 ± 0.388	0.587	1.043 ± 0.400	0.523
plasmid_cp32-4	BB_R26		1.023 ± 0.350	0.878	0.652 ± 0.422	0.262	1.027 ± 0.554	0.912	1.088 ± 0.399	0.003
plasmid_cp32-4	BB_R28	<i>mlpD</i>	2.920 ± 2.167	0.137	1.941 ± 2.087	0.391	0.957 ± 0.665	0.855	0.980 ± 0.680	0.805
plasmid_cp32-4	BB_R29		3.472 ± 1.171	0.027	1.807 ± 1.272	0.383	1.020 ± 0.251	0.893	1.134 ± 0.319	0.621
plasmid_cp32-4	BB_R32		2.056 ± 0.713	0.100	1.101 ± 0.301	0.430	0.885 ± 0.260	0.192	1.108 ± 0.323	0.350
plasmid_cp32-4	BB_R35	<i>brdG</i>	3.371 ± 0.544	0.014	1.641 ± 0.932	0.333	0.972 ± 0.098	0.164	1.209 ± 0.190	0.218
plasmid_cp32-4	BB_R36	<i>bppA</i>	1.800 ± 0.659	0.024	1.028 ± 0.536	0.903	0.705 ± 0.230	0.052	0.923 ± 0.267	0.575
plasmid_cp32-4	BB_R37	<i>bppB</i>	1.090 ± 0.262	0.372	0.935 ± 0.281	0.716	1.001 ± 0.248	0.993	1.129 ± 0.269	0.348
plasmid_cp32-4	BB_R38	<i>bppC</i>	3.378 ± 2.260	0.105	2.088 ± 2.246	0.384	0.991 ± 0.540	0.824	1.106 ± 0.528	0.351
plasmid_cp32-4	BB_R41		2.446 ± 1.107	0.039	1.105 ± 0.587	0.274	1.031 ± 0.484	0.254	0.997 ± 0.419	0.960
plasmid_cp32-4	BB_R42	<i>erpY</i>	2.939 ± 1.387	0.079	1.445 ± 0.964	0.353	0.847 ± 0.313	0.023	1.036 ± 0.546	0.811
plasmid_cp32-4	BB_R43		3.547 ± 0.460	0.003	1.733 ± 0.963	0.320	0.794 ± 0.560	0.641	1.360 ± 0.230	0.156
plasmid_cp32-4	BB_R44		2.895 ± 1.149	0.032	1.561 ± 1.068	0.311	0.891 ± 0.287	0.631	1.117 ± 0.472	0.258
plasmid_cp32-4	BB_R45		1.462 ± 0.555	0.062	0.822 ± 0.239	0.112	0.866 ± 0.296	0.077	0.982 ± 0.326	0.677
plasmid_cp32-6	BB_M01		2.067 ± 0.701	0.049	1.517 ± 1.076	0.411	0.998 ± 0.259	0.971	1.102 ± 0.324	0.208
plasmid_cp32-6	BB_M02		1.600 ± 0.444	0.106	1.166 ± 0.658	0.671	0.976 ± 0.114	0.166	0.938 ± 0.133	0.579
plasmid_cp32-6	BB_M03		1.380 ± 0.862	0.305	0.915 ± 0.301	0.484	0.792 ± 0.368	0.199	1.029 ± 0.316	0.798
plasmid_cp32-6	BB_M04		3.094 ± 0.725	0.023	1.635 ± 0.875	0.284	0.949 ± 0.433	0.878	1.056 ± 0.180	0.639
plasmid_cp32-6	BB_M05		1.306 ± 0.306	0.243	0.849 ± 0.572	0.718	1.537 ± 0.621	0.335	1.438 ± 0.769	0.452
plasmid_cp32-6	BB_M06		2.347 ± 0.510	0.015	1.299 ± 0.382	0.379	0.985 ± 0.333	0.865	1.006 ± 0.283	0.855
plasmid_cp32-6	BB_M07		1.718 ± 1.018	0.124	1.390 ± 1.428	0.562	0.899 ± 0.373	0.649	0.840 ± 0.349	0.419
plasmid_cp32-6	BB_M08		1.417 ± 0.445	0.121	1.171 ± 0.546	0.523	0.813 ± 0.155	0.068	0.970 ± 0.157	0.696
plasmid_cp32-6	BB_M10		1.218 ± 0.408	0.261	0.695 ± 0.491	0.269	0.975 ± 0.320	0.862	1.032 ± 0.263	0.608
plasmid_cp32-6	BB_M11		2.052 ± 0.880	0.104	1.902 ± 1.665	0.410	0.983 ± 0.224	0.830	1.157 ± 0.324	0.180
plasmid_cp32-6	BB_M12		2.097 ± 0.740	0.095	1.944 ± 1.765	0.428	0.992 ± 0.221	0.950	0.972 ± 0.231	0.700
plasmid_cp32-6	BB_M13		2.389 ± 0.863	0.059	1.465 ± 0.949	0.368	1.085 ± 0.543	0.703	1.288 ± 0.468	0.259
plasmid_cp32-6	BB_M14		2.532 ± 1.771	0.253	2.433 ± 2.678	0.477	1.924 ± 2.303	0.440	2.183 ± 1.826	0.361
plasmid_cp32-6	BB_M15		1.956 ± 0.623	0.019	1.477 ± 1.140	0.443	0.879 ± 0.299	0.225	0.977 ± 0.337	0.519
plasmid_cp32-6	BB_M16		1.759 ± 0.705	0.111	1.540 ± 1.285	0.483	0.929 ± 0.303	0.633	1.041 ± 0.333	0.769
plasmid_cp32-6	BB_M17		1.919 ± 1.166	0.044	0.695 ± 0.328	0.402	0.972 ± 0.524	0.847	1.053 ± 0.589	0.555
plasmid_cp32-6	BB_M18		2.278 ± 0.632	0.023	2.075 ± 1.636	0.327	1.157 ± 0.280	0.404	1.275 ± 0.227	0.082
plasmid_cp32-6	BB_M19		2.440 ± 0.554	0.026	1.710 ± 0.681	0.158	1.257 ± 0.535	0.557	1.665 ± 0.592	0.214
plasmid_cp32-6	BB_M20		1.964 ± 1.249	0.076	0.831 ± 0.365	0.556	1.098 ± 0.660	0.037	1.083 ± 0.619	0.048
plasmid_cp32-6	BB_M21		1.934 ± 0.957	0.023	0.723 ± 0.335	0.187	0.853 ± 0.414	0.214	0.986 ± 0.521	0.937
plasmid_cp32-6	BB_M22		1.801 ± 0.715	0.024	1.543 ± 1.205	0.380	0.969 ± 0.371	0.665	1.039 ± 0.453	0.507
plasmid_cp32-6	BB_M23	<i>blyA</i>	1.105 ± 0.433	0.208	0.473 ± 0.343	0.282	0.919 ± 0.359	0.411	0.993 ± 0.427	0.841
plasmid_cp32-6	BB_M24	<i>blyB</i>	1.730 ± 0.513	0.044	1.815 ± 1.293	0.341	0.738 ± 0.431	0.047	0.912 ± 0.290	0.733
plasmid_cp32-6	BB_M25		2.271 ± 1.185	0.095	1.684 ± 1.494	0.407	0.967 ± 0.400	0.764	1.070 ± 0.418	0.406
plasmid_cp32-6	BB_M26		1.680 ± 0.786	0.268	0.885 ± 0.255	0.324	0.782 ± 0.242	0.067	0.845 ± 0.245	0.491
plasmid_cp32-6	BB_M27	<i>revA</i>	1.520 ± 0.409	0.168	1.162 ± 0.522	0.618	0.736 ± 0.189	0.228	0.925 ± 0.227	0.736
plasmid_cp32-6	BB_M28	<i>mlpF</i>	1.457 ± 1.486	0.658	1.258 ± 1.249	0.697	0.537 ± 0.507	0.349	0.989 ± 0.914	0.988
plasmid_cp32-6	BB_M29		1.586 ± 0.792	0.110	1.297 ± 0.838	0.393	0.944 ± 0.315	0.695	1.084 ± 0.402	0.092
plasmid_cp32-6	BB_M34	<i>bdrK</i>	1.848 ± 1.465	0.261	1.569 ± 1.622	0.487	0.901 ± 0.431	0.721	1.046 ± 0.397	0.834
plasmid_cp32-6	BB_M35	<i>bppA</i>	1.780 ± 0.927	0.053	1.254 ± 0.831	0.348	1.023 ± 0.479	0.556	1.039 ± 0.551	0.331
plasmid_cp32-6	BB_M36	<i>bppB</i>	1.040 ± 0.286	0.707	0.921 ± 0.227	0.564	0.964 ± 0.253	0.675	1.093 ± 0.280	0.413
plasmid_cp32-6	BB_M37	<i>bppC</i>	1.900 ± 0.832	0.043	1.524 ± 1.197	0.392	0.840 ± 0.311	0.497	1.083 ± 0.431	0.578
plasmid_cp32-6	BB_M38	<i>erpK</i>	1.634 ± 0.580	0.092	1.542 ± 1.192	0.383	0.880 ± 0.259	0.621	1.093 ± 0.630	0.704
plasmid_cp32-6	BB_M39		1.745 ± 0.594	0.132	1.554 ± 1.687	0.588	0.684 ± 0.173	0.018	0.902 ± 0.397	0.717
plasmid_cp32-6	BB_M41		1.329 ± 0.776	0.054	0.748 ± 0.368	0.404	1.069 ± 0.596	0.454	1.168 ± 0.763	0.084
plasmid_cp32-6	BB_M42		1.641 ± 0.636	0.059	1.250 ± 0.666	0.359	1.028 ± 0.325	0.591	0.995 ± 0.382	0.912
plasmid_cp32-7	BB_O01		1.828 ± 0.456	0.052	1.360 ± 0.775	0.455	0.993 ± 0.180	0.867	1.068 ± 0.222	0.397
plasmid_cp32-7	BB_O02		1.796 ± 0.435	0.037	1.083 ± 0.286	0.437	1.015 ± 0.150	0.860	1.046 ± 0.162	0.649
plasmid_cp32-7	BB_O03		1.964 ± 0.631	0.106	1.513 ± 0.766	0.355	1.011 ± 0.370	0.967	0.973 ± 0.110	0.790
plasmid_cp32-7	BB_O04		1.856 ± 0.827	0.058	1.666 ± 1.364	0.371	1.024 ± 0.426	0.645	1.377 ± 0.430	0.055
plasmid_cp32-7	BB_O05		2.369 ± 0.950	0.039	2.027 ± 1.870	0.379	0.999 ± 0.438	0.996	1.255 ± 0.459	0.267
plasmid_cp32-7	BB_O06		2.273 ± 0.996	0.097	1.747 ± 2.120	0.325	0.828 ± 0.200	0.015	1.123 ± 0.410	0.562
plasmid_cp32-7	BB_O07		1.334 ± 0.560	0.467	1.337 ± 1.326	0.717	0.659 ± 0.401	0.471	0.791 ± 0.376	0.608
plasmid_cp32-7	BB_O08		1.392 ± 0.429	0.140	1.100 ± 0.485	0.665	0.785 ± 0.135	0.051	0.933 ± 0.140	0.404
plasmid_cp32-7	BB_O10		2.224 ± 0.621	0.007	1.847 ± 1.110	0.364	1.105 ± 0.521	0.711	1.124 ± 0.660	0.718
plasmid_cp32-7	BB_O11		2.002 ± 0.959	0.111	1.837 ± 1.701	0.426	0.963 ± 0.257	0.527	1.119 ± 0.425	0.316
plasmid_cp32-7	BB_O12		2.099 ± 0.459	0.039	2.051 ± 1.593	0.357	0.880 ± 0.153	0.316	0.927 ± 0.062	0.271
plasmid_cp32-7	BB_O13		1.913 ± 0.620	0.042	0.486 ± 0.423	0.172	0.451 ± 0.581	0.157	0.924 ± 0.995	0.922

plasmid_cp32-9	BB_N05	1.291 ± 0.267	0.256	0.695 ± 0.457	0.356	1.518 ± 0.341	0.123	1.149 ± 0.792	0.767	
plasmid_cp32-9	BB_N06	2.362 ± 0.518	0.016	1.343 ± 0.401	0.336	0.990 ± 0.313	0.901	1.033 ± 0.290	0.369	
plasmid_cp32-9	BB_N07	0.615 ± 0.413	0.418	0.822 ± 0.515	0.573	0.854 ± 0.481	0.707	0.922 ± 0.542	0.875	
plasmid_cp32-9	BB_N08	1.753 ± 0.592	0.056	1.127 ± 0.688	0.709	0.885 ± 0.301	0.006	1.138 ± 0.463	0.298	
plasmid_cp32-9	BB_N09	2.037 ± 1.019	0.211	1.219 ± 0.935	0.713	0.574 ± 0.120	0.010	0.900 ± 0.355	0.635	
plasmid_cp32-9	BB_N10	2.955 ± 1.137	0.047	1.789 ± 1.417	0.362	0.867 ± 0.257	0.275	1.062 ± 0.312	0.071	
plasmid_cp32-9	BB_N11	2.185 ± 1.049	0.005	1.172 ± 0.953	0.532	0.920 ± 0.464	0.596	1.102 ± 0.493	0.552	
plasmid_cp32-9	BB_N12	2.050 ± 0.690	0.082	1.997 ± 1.818	0.415	0.953 ± 0.203	0.654	0.965 ± 0.266	0.654	
plasmid_cp32-9	BB_N13	2.945 ± 0.931	0.065	2.021 ± 1.279	0.301	1.469 ± 0.599	0.323	1.210 ± 0.345	0.412	
plasmid_cp32-9	BB_N14	1.870 ± 0.501	0.003	1.724 ± 1.176	0.276	1.293 ± 0.472	0.399	1.125 ± 0.374	0.007	
plasmid_cp32-9	BB_N15	1.812 ± 0.532	0.018	1.425 ± 1.031	0.452	0.887 ± 0.208	0.286	0.984 ± 0.306	0.588	
plasmid_cp32-9	BB_N16	3.061 ± 1.776	0.088	1.595 ± 1.316	0.364	0.861 ± 0.515	0.192	1.054 ± 0.445	0.310	
plasmid_cp32-9	BB_N17	1.879 ± 1.106	0.034	0.579 ± 0.298	0.337	0.979 ± 0.525	0.882	1.026 ± 0.579	0.686	
plasmid_cp32-9	BB_N18	2.670 ± 2.667	0.113	2.613 ± 3.519	0.333	1.156 ± 0.987	0.387	1.141 ± 0.978	0.474	
plasmid_cp32-9	BB_N19	1.842 ± 0.056	0.001	1.455 ± 0.485	0.251	1.031 ± 0.315	0.885	1.604 ± 0.678	0.267	
plasmid_cp32-9	BB_N20	1.706 ± 0.570	0.005	0.787 ± 0.233	0.410	0.943 ± 0.406	0.318	1.014 ± 0.320	0.847	
plasmid_cp32-9	BB_N21	1.874 ± 1.129	0.023	0.726 ± 0.388	0.317	0.818 ± 0.463	0.324	0.913 ± 0.559	0.698	
plasmid_cp32-9	BB_N23	1.727 ± 1.107	0.039	1.634 ± 1.595	0.328	1.011 ± 0.604	0.959	1.176 ± 0.795	0.129	
plasmid_cp32-9	BB_N24	2.359 ± 1.447	0.098	1.476 ± 0.951	0.480	0.936 ± 0.586	0.519	0.845 ± 0.392	0.693	
plasmid_cp32-9	BB_N25	2.141 ± 1.160	0.100	1.701 ± 1.511	0.394	0.951 ± 0.413	0.710	1.069 ± 0.447	0.466	
plasmid_cp32-9	BB_N26	1.308 ± 0.489	0.206	0.793 ± 0.329	0.426	0.946 ± 0.306	0.836	0.838 ± 0.250	0.401	
plasmid_cp32-9	BB_N29	2.149 ± 0.740	0.073	1.761 ± 1.302	0.374	1.004 ± 0.309	0.970	1.059 ± 0.239	0.384	
plasmid_cp32-9	BB_N34	bdrQ	1.692 ± 1.330	0.322	1.089 ± 0.590	0.515	0.844 ± 0.565	0.288	0.748 ± 0.542	0.214
plasmid_cp32-9	BB_N35	bppA	1.367 ± 0.583	0.015	1.031 ± 0.581	0.810	0.942 ± 0.365	0.636	1.134 ± 0.490	0.035
plasmid_cp32-9	BB_N36	bppB	1.107 ± 0.313	0.399	0.828 ± 0.302	0.489	1.051 ± 0.306	0.383	1.117 ± 0.353	0.241
plasmid_cp32-9	BB_N38	erpP	2.648 ± 2.321	0.092	2.280 ± 2.879	0.354	1.185 ± 1.001	0.355	1.213 ± 0.921	0.260
plasmid_cp32-9	BB_N39	erpQ	2.935 ± 1.200	0.116	3.241 ± 2.294	0.228	1.730 ± 0.965	0.304	2.023 ± 1.006	0.196
plasmid_cp32-9	BB_N41		1.900 ± 0.990	0.028	1.896 ± 1.561	0.262	0.893 ± 0.404	0.469	0.809 ± 0.320	0.436
plasmid_cp32-9	BB_N42		1.979 ± 1.184	0.037	1.524 ± 1.442	0.267	0.624 ± 0.386	0.349	1.006 ± 0.693	0.984
plasmid_cp32-9	BB_N43		1.420 ± 0.523	0.084	0.988 ± 0.452	0.924	0.851 ± 0.243	0.086	0.942 ± 0.260	0.179
plasmid_cp9	BBC02		1.803 ± 1.272	0.168	0.888 ± 0.695	0.158	1.700 ± 1.092	0.155	1.579 ± 0.861	0.140
plasmid_cp9	BBC03		0.729 ± 0.203	0.228	0.412 ± 0.353	0.155	0.961 ± 0.179	0.811	1.026 ± 0.224	0.785
plasmid_cp9	BBC05		0.936 ± 0.502	0.204	0.737 ± 0.500	0.019	0.922 ± 0.517	0.047	1.053 ± 0.480	0.538
plasmid_cp9	BBC06		1.729 ± 0.913	0.032	1.095 ± 0.676	0.618	0.920 ± 0.586	0.642	0.685 ± 0.399	0.215
plasmid_cp9	BBC07		0.981 ± 0.751	0.942	0.862 ± 0.749	0.614	1.239 ± 0.627	0.227	1.192 ± 0.611	0.525
plasmid_cp9	BBC08		1.622 ± 0.552	0.069	0.922 ± 0.248	0.184	0.951 ± 0.205	0.673	1.150 ± 0.420	0.425
plasmid_cp9	BBC10		1.568 ± 0.613	0.003	0.839 ± 0.362	0.267	0.999 ± 0.424	0.986	1.271 ± 0.463	0.187
plasmid_cp9	BBC11		1.432 ± 0.454	0.097	0.727 ± 0.292	0.041	0.889 ± 0.391	0.109	1.123 ± 0.590	0.597
plasmid_cp9	BBC12		0.879 ± 0.239	0.363	0.524 ± 0.418	0.175	0.933 ± 0.182	0.580	0.999 ± 0.152	0.980
plasmid_lp17	BB_D0027		1.216 ± 0.973	0.197	1.101 ± 0.835	0.640	0.739 ± 0.544	0.353	0.846 ± 0.675	0.318
plasmid_lp17	BB_D0031		2.038 ± 2.005	0.310	2.601 ± 3.010	0.353	0.892 ± 0.462	0.563	0.978 ± 0.568	0.790
plasmid_lp17	BB_D01		2.269 ± 1.041	0.178	2.397 ± 2.173	0.390	0.964 ± 0.289	0.880	1.114 ± 0.368	0.630
plasmid_lp17	BB_D03		1.852 ± 0.410	0.052	1.363 ± 0.280	0.133	1.059 ± 0.237	0.774	1.391 ± 0.152	0.041
plasmid_lp17	BB_D04		2.490 ± 2.446	0.298	1.766 ± 1.968	0.440	1.049 ± 0.687	0.919	0.971 ± 0.569	0.935
plasmid_lp17	BB_D05a		1.589 ± 0.608	0.017	1.583 ± 0.902	0.180	1.056 ± 0.352	0.513	0.984 ± 0.355	0.758
plasmid_lp17	BB_D09		1.253 ± 0.844	0.118	0.630 ± 0.433	0.498	0.993 ± 0.551	0.968	1.031 ± 0.693	0.451
plasmid_lp17	BB_D10		1.739 ± 1.102	0.175	1.357 ± 1.014	0.659	0.792 ± 0.285	0.413	1.002 ± 0.702	0.998
plasmid_lp17	BB_D15		1.767 ± 0.706	0.113	1.692 ± 0.964	0.268	1.028 ± 0.399	0.922	1.203 ± 0.501	0.381
plasmid_lp17	BB_D20		1.220 ± 0.653	0.240	1.003 ± 0.437	0.983	0.916 ± 0.380	0.652	1.204 ± 0.633	0.074
plasmid_lp17	BB_D23		1.178 ± 0.952	0.333	0.695 ± 0.407	0.535	0.905 ± 0.626	0.499	0.945 ± 0.668	0.760
plasmid_lp17	BB_D24		2.124 ± 1.771	0.062	1.572 ± 2.080	0.506	1.075 ± 0.887	0.858	1.105 ± 0.812	0.553
plasmid_lp21	BB_U01		1.899 ± 1.686	0.131	1.906 ± 2.602	0.438	0.813 ± 0.641	0.450	1.084 ± 1.043	0.540
plasmid_lp21	BB_U02		2.280 ± 0.950	0.086	1.245 ± 0.565	0.346	1.169 ± 0.248	0.132	1.073 ± 0.264	0.024
plasmid_lp21	BB_U05		2.281 ± 1.921	0.086	2.096 ± 2.193	0.239	1.457 ± 1.171	0.014	0.996 ± 0.815	0.989
plasmid_lp21	BB_U06		3.861 ± 3.551	0.219	1.537 ± 1.961	0.729	1.011 ± 0.904	0.988	1.892 ± 2.214	0.318
plasmid_lp21	BB_U08		3.364 ± 2.497	0.088	1.534 ± 1.454	0.324	1.100 ± 0.755	0.692	1.330 ± 1.363	0.480
plasmid_lp21	BB_U09		2.430 ± 1.011	0.137	1.933 ± 1.257	0.366	1.332 ± 0.565	0.169	0.863 ± 0.345	0.682
plasmid_lp21	BB_U10		3.415 ± 3.047	0.162	1.721 ± 1.001	0.008	1.134 ± 0.761	0.314	1.438 ± 0.849	0.062
plasmid_lp21	BB_U11		3.354 ± 1.357	0.075	1.509 ± 0.739	0.399	1.075 ± 0.347	0.771	1.039 ± 0.360	0.886
plasmid_lp21	BB_U12		1.601 ± 0.300	0.096	1.330 ± 0.368	0.265	1.034 ± 0.285	0.859	0.943 ± 0.168	0.703
plasmid_lp25	BB_E02		2.672 ± 1.235	0.018	2.284 ± 1.503	0.138	0.957 ± 0.388	0.771	1.052 ± 0.490	0.435
plasmid_lp25	BB_E05		2.272 ± 2.006	0.052	1.436 ± 1.245	0.491	0.694 ± 0.686	0.438	0.791 ± 0.750	0.769
plasmid_lp25	BB_E09		2.179 ± 1.064	0.162	2.159 ± 1.580	0.304	1.060 ± 0.230	0.185	1.167 ± 0.309	0.290
plasmid_lp25	BB_E16		3.003 ± 0.810	0.030	2.210 ± 1.484	0.275	1.030 ± 0.196	0.763	1.330 ± 0.518	0.247

plasmid_lp25	BB_E17	0.566 ± 0.902	0.098	1.106 ± 1.812	0.930	1.167 ± 1.000	0.667	0.178 ± 0.246	0.214
plasmid_lp25	BB_E18	2.223 ± 1.725	0.027	0.899 ± 0.611	0.781	0.913 ± 0.827	0.443	1.182 ± 1.098	0.106
plasmid_lp25	BB_E22	3.626 ± 1.230	0.056	1.857 ± 1.214	0.307	1.278 ± 0.395	0.432	1.114 ± 0.299	0.428
plasmid_lp25	BB_E29	1.210 ± 0.807	0.356	0.684 ± 0.590	0.648	1.052 ± 0.868	0.225	1.243 ± 1.160	0.246
plasmid_lp25	BB_E29a	1.082 ± 0.483	0.841	0.891 ± 0.464	0.807	1.081 ± 0.429	0.766	0.942 ± 0.496	0.897
plasmid_lp28-1	BB_F001	1.494 ± 0.417	0.003	2.026 ± 0.902	0.139	0.997 ± 0.360	0.958	1.379 ± 0.458	0.022
plasmid_lp28-1	BB_F0034	1.577 ± 0.916	0.326	2.766 ± 3.313	0.436	1.075 ± 0.404	0.647	1.136 ± 0.660	0.698
plasmid_lp28-1	BB_F02	2.479 ± 0.749	0.035	2.024 ± 1.536	0.302	1.266 ± 0.461	0.483	1.616 ± 0.625	0.168
plasmid_lp28-1	BB_F03	1.408 ± 1.111	0.436	1.093 ± 0.458	0.799	1.141 ± 0.596	0.316	1.262 ± 0.947	0.508
plasmid_lp28-1	BB_F05	1.030 ± 0.684	0.664	2.583 ± 1.977	0.153	1.099 ± 0.478	0.690	1.231 ± 0.801	0.263
plasmid_lp28-1	BB_F08	1.115 ± 0.624	0.677	2.095 ± 1.670	0.321	0.932 ± 0.377	0.541	1.208 ± 0.296	0.005
plasmid_lp28-1	BB_F10	1.234 ± 0.566	0.113	1.666 ± 1.381	0.367	0.815 ± 0.272	0.212	1.006 ± 0.344	0.967
plasmid_lp28-1	BB_F12	0.952 ± 1.577	0.808	2.088 ± 3.214	0.220	0.940 ± 1.220	0.939	1.208 ± 1.574	0.593
plasmid_lp28-1	BB_F13	1.371 ± 0.572	0.019	1.764 ± 1.197	0.189	0.980 ± 0.431	0.909	1.240 ± 0.741	0.252
plasmid_lp28-1	BB_F14	2.241 ± 1.254	0.028	7.008 ± 4.389	0.062	1.122 ± 1.166	0.895	2.822 ± 1.491	0.030
plasmid_lp28-1	BB_F16	1.333 ± 0.334	0.248	1.697 ± 1.408	0.487	0.917 ± 0.127	0.496	1.216 ± 0.428	0.519
plasmid_lp28-1	BB_F17	1.155 ± 0.440	0.119	1.794 ± 1.174	0.248	0.881 ± 0.242	0.261	1.100 ± 0.425	0.206
plasmid_lp28-1	BB_F18	1.510 ± 1.023	0.260	2.202 ± 2.049	0.318	1.005 ± 0.583	0.959	0.985 ± 0.493	0.909
plasmid_lp28-1	BB_F19	1.252 ± 0.668	0.208	1.837 ± 1.517	0.307	1.050 ± 0.407	0.586	1.303 ± 0.644	0.077
plasmid_lp28-1	BB_F19a	1.100 ± 0.513	0.765	1.425 ± 0.672	0.335	0.930 ± 0.531	0.621	1.127 ± 0.428	0.684
plasmid_lp28-1	BB_F20	0.977 ± 0.251	0.897	1.314 ± 1.180	0.618	1.046 ± 0.406	0.804	0.715 ± 0.417	0.148
plasmid_lp28-1	BB_F26a	0.070 ± 0.091	0.192	0.043 ± 0.071	0.176	0.224 ± 0.388	0.087	0.389 ± 0.562	0.434
plasmid_lp28-1	BB_F30	1.015 ± 0.358	0.951	2.568 ± 0.926	0.009	0.780 ± 0.330	0.529	1.435 ± 0.506	0.255
plasmid_lp28-1	BB_F32	0.791 ± 0.379	0.197	0.899 ± 0.351	0.718	0.939 ± 0.431	0.563	1.139 ± 0.599	0.435
plasmid_lp28-2	BB_G01	1.792 ± 1.316	0.113	2.039 ± 1.835	0.240	0.881 ± 0.456	0.675	1.211 ± 0.657	0.401
plasmid_lp28-2	BB_G02	1.700 ± 0.849	0.013	0.819 ± 0.427	0.686	1.102 ± 0.586	0.260	1.249 ± 0.826	0.169
plasmid_lp28-2	BB_G03	2.230 ± 1.788	0.239	1.917 ± 2.081	0.412	0.679 ± 0.463	0.159	0.916 ± 0.642	0.782
plasmid_lp28-2	BB_G05	2.792 ± 1.045	0.040	2.027 ± 1.587	0.308	0.921 ± 0.232	0.356	1.065 ± 0.354	0.401
plasmid_lp28-2	BB_G10	1.966 ± 0.716	0.026	1.683 ± 0.971	0.192	0.736 ± 0.199	0.153	1.033 ± 0.328	0.547
plasmid_lp28-2	BB_G12	1.044 ± 1.235	0.950	1.160 ± 1.084	0.585	0.596 ± 0.674	0.611	1.010 ± 1.001	0.989
plasmid_lp28-2	BB_G13	2.241 ± 1.331	0.103	1.449 ± 0.878	0.269	1.045 ± 0.690	0.916	1.265 ± 0.791	0.480
plasmid_lp28-2	BB_G14	2.180 ± 1.876	0.111	2.268 ± 2.336	0.214	0.807 ± 0.518	0.691	1.244 ± 0.849	0.428
plasmid_lp28-2	BB_G15	2.090 ± 0.436	0.004	1.527 ± 1.145	0.427	0.868 ± 0.260	0.428	0.960 ± 0.392	0.810
plasmid_lp28-2	BB_G16	1.899 ± 0.510	0.072	1.328 ± 0.715	0.324	0.821 ± 0.424	0.364	0.959 ± 0.335	0.893
plasmid_lp28-2	BB_G17	1.746 ± 0.618	0.151	1.846 ± 1.440	0.405	0.658 ± 0.596	0.399	0.590 ± 0.614	0.353
plasmid_lp28-2	BB_G18	2.213 ± 1.564	0.032	1.423 ± 1.353	0.293	0.956 ± 0.727	0.831	0.918 ± 0.899	0.457
plasmid_lp28-2	BB_G20	1.961 ± 1.428	0.029	2.209 ± 2.235	0.239	0.782 ± 0.510	0.478	1.029 ± 0.678	0.863
plasmid_lp28-2	BB_G21	1.942 ± 1.434	0.187	2.044 ± 1.944	0.324	0.748 ± 0.311	0.456	0.802 ± 0.637	0.356
plasmid_lp28-2	BB_G22	2.657 ± 1.216	0.026	1.550 ± 0.943	0.166	0.873 ± 0.300	0.560	1.047 ± 0.448	0.345
plasmid_lp28-2	BB_G23	1.725 ± 0.808	0.014	1.375 ± 1.082	0.391	0.669 ± 0.346	0.134	0.841 ± 0.434	0.221
plasmid_lp28-2	BB_G24	0.848 ± 0.272	0.503	0.706 ± 0.275	0.357	0.914 ± 0.480	0.181	1.031 ± 0.528	0.693
plasmid_lp28-2	BB_G25	1.876 ± 0.735	0.044	1.253 ± 0.589	0.135	0.838 ± 0.377	0.670	1.092 ± 0.430	0.180
plasmid_lp28-2	BB_G27	2.430 ± 0.963	0.042	1.538 ± 1.173	0.319	1.070 ± 0.415	0.548	1.152 ± 0.498	0.394
plasmid_lp28-2	BB_G28	3.000 ± 3.746	0.238	2.202 ± 1.972	0.009	1.210 ± 1.529	0.397	1.621 ± 2.322	0.424
plasmid_lp28-2	BB_G29	2.380 ± 0.623	0.062	1.749 ± 0.967	0.310	0.999 ± 0.049	0.989	1.079 ± 0.151	0.483
plasmid_lp28-2	BB_G30	2.446 ± 2.105	0.202	3.776 ± 5.402	0.384	1.183 ± 1.507	0.711	1.412 ± 1.161	0.341
plasmid_lp28-2	BB_G31	2.199 ± 2.318	0.219	2.112 ± 2.789	0.135	0.713 ± 0.785	0.630	1.612 ± 1.745	0.411
plasmid_lp28-2	BB_G32	1.529 ± 0.924	0.071	0.804 ± 0.407	0.652	0.861 ± 0.378	0.548	1.024 ± 0.806	0.900
plasmid_lp28-2	BB_G34	2.715 ± 1.610	0.060	2.311 ± 2.046	0.223	0.936 ± 0.641	0.061	1.540 ± 0.918	0.101
plasmid_lp28-3	BB_H02	2.212 ± 1.115	0.198	2.359 ± 1.983	0.358	1.022 ± 0.315	0.931	1.069 ± 0.357	0.700
plasmid_lp28-3	BB_H04	2.001 ± 0.869	0.174	1.578 ± 0.741	0.120	1.642 ± 0.562	0.213	1.514 ± 0.902	0.324
plasmid_lp28-3	BB_H05	2.210 ± 1.363	0.150	1.651 ± 1.111	0.288	0.850 ± 0.278	0.346	1.112 ± 0.672	0.817
plasmid_lp28-3	BB_H06	1.650 ± 1.224	0.123	1.547 ± 1.271	0.240	0.990 ± 0.584	0.959	1.215 ± 0.782	0.214
plasmid_lp28-3	BB_H07	1.245 ± 0.116	0.019	2.062 ± 1.107	0.245	0.965 ± 0.313	0.864	0.946 ± 0.104	0.569
plasmid_lp28-3	BB_H09	1.128 ± 0.405	0.473	1.145 ± 0.539	0.584	0.940 ± 0.217	0.496	1.080 ± 0.361	0.521
plasmid_lp28-3	BB_H09a	1.426 ± 0.493	0.293	1.909 ± 1.435	0.370	0.838 ± 0.283	0.551	1.449 ± 0.586	0.312
plasmid_lp28-3	BB_H13	2.171 ± 0.923	0.099	2.866 ± 1.792	0.177	0.806 ± 0.351	0.549	1.400 ± 0.730	0.364
plasmid_lp28-3	BB_H17	2.525 ± 1.934	0.208	1.636 ± 1.265	0.156	1.153 ± 0.896	0.359	0.854 ± 0.546	0.594
plasmid_lp28-3	BB_H18	0.867 ± 0.324	0.290	1.136 ± 0.418	0.247	0.946 ± 0.283	0.648	1.042 ± 0.404	0.522
plasmid_lp28-3	BB_H20	1.441 ± 0.607	0.112	1.715 ± 1.229	0.300	1.061 ± 0.370	0.774	1.292 ± 0.509	0.037
plasmid_lp28-3	BB_H30	1.000 ± 0.700	0.998	0.741 ± 0.420	0.519	0.926 ± 0.656	0.546	1.143 ± 0.903	0.144
plasmid_lp28-3	BB_H32	1.088 ± 0.617	0.864	3.019 ± 2.431	0.286	1.392 ± 0.624	0.302	1.360 ± 0.678	0.526
plasmid_lp28-3	BB_H33	1.221 ± 0.724	0.328	1.945 ± 1.854	0.369	1.171 ± 0.515	0.591	1.026 ± 0.481	0.790
plasmid_lp28-3	BB_H37	1.096 ± 0.558	0.790	1.695 ± 1.363	0.429	0.666 ± 0.388	0.171	1.036 ± 0.527	0.827

plasmid_lp28-3	BB_H41		1.459 ± 1.210	0.589	0.571 ± 0.744	0.215	0.946 ± 1.261	0.948	1.201 ± 1.724	0.885
plasmid_lp28-4	BB_I01	x	1.559 ± 1.500	0.218	0.436 ± 0.360	0.372	0.986 ± 0.768	0.925	1.030 ± 0.944	0.674
plasmid_lp28-4	BB_I02	x	2.290 ± 0.941	0.089	1.253 ± 0.561	0.356	1.174 ± 0.240	0.133	1.081 ± 0.257	0.051
plasmid_lp28-4	BB_I39	x	0.957 ± 0.461	0.763	1.031 ± 0.325	0.641	0.984 ± 0.374	0.890	1.251 ± 0.474	0.082
plasmid_lp28-4	BB_I42	x	0.816 ± 0.605	0.482	1.012 ± 0.708	0.804	0.438 ± 0.246	0.106	0.733 ± 0.412	0.508
plasmid_lp28-4	BB_I43	x	0.695 ± 0.485	0.511	1.165 ± 0.784	0.765	0.367 ± 0.178	0.164	0.417 ± 0.383	0.021
plasmid_lp36	BB_K0058		1.222 ± 0.860	0.605	1.603 ± 1.859	0.503	1.244 ± 1.590	0.779	0.867 ± 0.533	0.767
plasmid_lp36	BB_K01		1.208 ± 1.151	0.270	1.611 ± 1.787	0.339	0.747 ± 0.679	0.107	0.988 ± 0.939	0.834
plasmid_lp36	BB_K02a		0.617 ± 0.361	0.079	0.760 ± 0.297	0.124	0.753 ± 0.198	0.001	0.917 ± 0.161	0.205
plasmid_lp36	BB_K07		0.923 ± 0.441	0.437	1.170 ± 0.608	0.503	0.726 ± 0.199	0.192	0.955 ± 0.371	0.558
plasmid_lp36	BB_K12		1.117 ± 0.699	0.313	1.766 ± 1.818	0.412	0.771 ± 0.389	0.194	1.001 ± 0.567	0.955
plasmid_lp36	BB_K13		0.957 ± 0.379	0.637	1.006 ± 0.525	0.971	0.832 ± 0.213	0.423	0.927 ± 0.246	0.332
plasmid_lp36	BB_K15		1.101 ± 0.352	0.182	1.475 ± 0.838	0.230	0.760 ± 0.219	0.175	0.979 ± 0.340	0.716
plasmid_lp36	BB_K17		1.073 ± 0.517	0.117	1.623 ± 1.406	0.372	0.751 ± 0.308	0.183	1.144 ± 0.570	0.099
plasmid_lp36	BB_K19		1.011 ± 0.145	0.860	1.551 ± 0.948	0.403	0.695 ± 0.081	0.005	0.943 ± 0.074	0.327
plasmid_lp36	BB_K32		1.088 ± 0.387	0.281	1.442 ± 0.887	0.343	0.830 ± 0.237	0.151	1.082 ± 0.284	0.460
plasmid_lp36	BB_K34		1.524 ± 0.287	0.114	1.772 ± 1.270	0.420	0.950 ± 0.126	0.382	1.304 ± 0.269	0.250
plasmid_lp36	BB_K35		1.271 ± 0.481	0.182	1.829 ± 1.183	0.269	0.889 ± 0.200	0.186	1.125 ± 0.378	0.253
plasmid_lp36	BB_K37		1.390 ± 1.048	0.482	1.645 ± 0.897	0.202	0.739 ± 0.575	0.320	1.631 ± 0.514	0.066
plasmid_lp36	BB_K39		1.100 ± 0.206	0.593	0.923 ± 0.167	0.297	0.674 ± 0.170	0.088	0.839 ± 0.188	0.056
plasmid_lp36	BB_K40		1.095 ± 0.554	0.330	1.298 ± 0.960	0.430	0.664 ± 0.267	0.180	0.837 ± 0.337	0.342
plasmid_lp36	BB_K41		1.139 ± 0.671	0.364	1.579 ± 1.210	0.117	0.776 ± 0.434	0.405	1.108 ± 0.606	0.665
plasmid_lp36	BB_K42a		1.124 ± 0.523	0.046	1.919 ± 1.600	0.284	0.880 ± 0.392	0.302	1.223 ± 0.696	0.233
plasmid_lp36	BB_K45		0.978 ± 0.760	0.826	1.543 ± 1.569	0.383	0.730 ± 0.471	0.188	0.934 ± 0.583	0.630
plasmid_lp36	BB_K46		1.191 ± 0.379	0.212	1.495 ± 0.990	0.418	0.800 ± 0.197	0.358	0.941 ± 0.200	0.553
plasmid_lp36	BB_K47		1.274 ± 0.418	0.097	1.598 ± 1.201	0.403	0.783 ± 0.193	0.043	1.136 ± 0.399	0.253
plasmid_lp36	BB_K48		1.222 ± 0.465	0.285	1.316 ± 0.648	0.296	0.848 ± 0.234	0.037	1.251 ± 0.408	0.139
plasmid_lp36	BB_K49		1.105 ± 0.380	0.048	1.569 ± 1.107	0.334	0.817 ± 0.271	0.061	1.067 ± 0.433	0.316
plasmid_lp36	BB_K50		1.264 ± 0.333	0.184	1.225 ± 0.316	0.063	0.821 ± 0.189	0.313	1.118 ± 0.243	0.237
plasmid_lp36	BB_K52		1.240 ± 0.479	0.231	1.653 ± 1.014	0.204	0.957 ± 0.345	0.814	1.246 ± 0.529	0.152
plasmid_lp36	BB_K53		0.873 ± 0.427	0.502	1.016 ± 0.632	0.914	0.497 ± 0.243	0.028	0.728 ± 0.317	0.406
plasmid_lp36	BB_K55		1.144 ± 0.862	0.699	1.491 ± 1.349	0.071	0.743 ± 0.609	0.549	1.265 ± 0.999	0.469
plasmid_lp38	BB_J0056		1.526 ± 1.066	0.500	1.742 ± 0.737	0.041	1.277 ± 1.004	0.716	2.009 ± 1.365	0.199
plasmid_lp38	BB_J02a		0.795 ± 0.289	0.363	0.955 ± 0.407	0.856	0.867 ± 0.185	0.293	1.153 ± 0.155	0.201
plasmid_lp38	BB_J05		0.839 ± 0.638	0.008	0.970 ± 0.901	0.877	0.991 ± 0.668	0.760	1.077 ± 0.666	0.223
plasmid_lp38	BB_J08		0.837 ± 0.657	0.424	1.897 ± 1.958	0.303	0.703 ± 0.459	0.365	1.007 ± 0.647	0.962
plasmid_lp38	BB_J09		0.836 ± 0.168	0.216	1.368 ± 0.364	0.148	0.932 ± 0.425	0.668	1.361 ± 0.702	0.328
plasmid_lp38	BB_J11		0.524 ± 0.206	0.050	0.631 ± 0.466	0.243	0.543 ± 0.303	0.087	0.454 ± 0.335	0.136
plasmid_lp38	BB_J13		1.155 ± 0.979	0.611	2.022 ± 2.261	0.217	0.497 ± 0.434	0.267	0.898 ± 0.877	0.645
plasmid_lp38	BB_J15a		1.160 ± 0.193	0.141	1.500 ± 0.381	0.108	0.800 ± 0.076	0.103	1.260 ± 0.276	0.154
plasmid_lp38	BB_J20		0.822 ± 0.523	0.742	1.814 ± 1.477	0.259	0.708 ± 0.554	0.023	1.602 ± 0.817	0.157
plasmid_lp38	BB_J21a		1.534 ± 1.130	0.226	1.563 ± 1.413	0.248	0.797 ± 0.614	0.099	1.065 ± 0.740	0.842
plasmid_lp38	BB_J23		2.090 ± 1.905	0.069	0.904 ± 0.791	0.874	0.919 ± 0.979	0.694	0.875 ± 1.047	0.633
plasmid_lp38	BB_J24		0.768 ± 0.321	0.116	1.108 ± 0.596	0.330	0.687 ± 0.277	0.126	0.879 ± 0.350	0.499
plasmid_lp38	BB_J27		0.939 ± 0.376	0.675	1.302 ± 0.844	0.525	0.764 ± 0.170	0.010	0.891 ± 0.256	0.303
plasmid_lp38	BB_J28		1.117 ± 0.668	0.274	2.193 ± 1.747	0.214	0.964 ± 0.614	0.867	1.140 ± 0.643	0.555
plasmid_lp38	BB_J29		0.642 ± 0.560	0.050	0.891 ± 0.756	0.404	0.839 ± 0.573	0.109	0.987 ± 0.628	0.899
plasmid_lp38	BB_J31		1.049 ± 0.462	0.384	1.123 ± 0.553	0.245	0.922 ± 0.349	0.380	0.990 ± 0.457	0.769
plasmid_lp38	BB_J34		1.184 ± 0.426	0.161	1.588 ± 1.199	0.400	0.799 ± 0.183	0.212	1.018 ± 0.342	0.841
plasmid_lp38	BB_J36		1.296 ± 0.664	0.470	1.719 ± 1.852	0.567	0.906 ± 0.416	0.740	1.063 ± 0.358	0.775
plasmid_lp38	BB_J37		1.031 ± 0.150	0.698	1.451 ± 0.613	0.378	0.824 ± 0.111	0.009	1.070 ± 0.182	0.545
plasmid_lp38	BB_J41		0.938 ± 0.446	0.613	0.895 ± 0.224	0.546	0.964 ± 0.347	0.612	1.273 ± 0.506	0.083
plasmid_lp38	BB_J43		0.636 ± 0.582	0.047	0.872 ± 0.786	0.375	0.844 ± 0.600	0.096	0.991 ± 0.660	0.927
plasmid_lp38	BB_J45		1.041 ± 0.420	0.117	1.324 ± 0.741	0.236	0.924 ± 0.330	0.381	1.121 ± 0.509	0.241
plasmid_lp38	BB_J46		1.603 ± 0.569	0.081	1.367 ± 0.728	0.199	0.903 ± 0.350	0.596	1.188 ± 0.465	0.541
plasmid_lp38	BB_J47		2.213 ± 1.806	0.189	1.100 ± 0.705	0.870	1.203 ± 0.746	0.122	1.853 ± 1.268	0.265
plasmid_lp38	BB_J48		1.409 ± 1.409	0.487	2.280 ± 2.738	0.395	1.092 ± 0.913	0.820	1.246 ± 1.015	0.714
plasmid_lp38	BB_J50		1.692 ± 1.247	0.334	2.096 ± 2.050	0.403	1.336 ± 0.811	0.383	1.264 ± 0.718	0.402
plasmid_lp38	BB_J51		0.714 ± 0.119	0.116	0.815 ± 0.164	0.045	0.880 ± 0.266	0.357	0.976 ± 0.297	0.786
plasmid_lp5	BB_T01		2.315 ± 2.018	0.300	1.837 ± 1.266	0.237	0.966 ± 0.358	0.724	1.045 ± 0.516	0.861
plasmid_lp5	BB_T02		2.694 ± 2.386	0.209	0.898 ± 1.241	0.828	0.787 ± 0.452	0.417	0.737 ± 0.594	0.178
plasmid_lp5	BB_T03		3.084 ± 1.781	0.036	1.765 ± 1.429	0.208	1.085 ± 0.530	0.762	1.050 ± 0.948	0.876
plasmid_lp5	BB_T04		3.586 ± 3.242	0.169	1.811 ± 1.028	0.014	1.171 ± 0.763	0.241	1.449 ± 0.890	0.059
plasmid_lp5	BB_T06		3.318 ± 1.303	0.073	1.509 ± 0.705	0.379	1.075 ± 0.333	0.759	1.022 ± 0.345	0.934

plasmid_lp5	BB_T07		1.593 ± 0.266	0.080	1.302 ± 0.328	0.286	1.048 ± 0.301	0.803	0.955 ± 0.167	0.751
plasmid_lp54	BB_A0078		0.683 ± 0.842	0.480	1.488 ± 1.097	0.343	0.718 ± 0.471	0.046	1.154 ± 1.298	0.821
plasmid_lp54	BB_A01		1.283 ± 0.484	0.278	1.753 ± 0.689	0.037	1.681 ± 0.697	0.236	1.877 ± 1.069	0.141
plasmid_lp54	BB_A03		0.724 ± 1.079	0.724	1.035 ± 1.772	0.976	0.194 ± 0.286	0.012	0.264 ± 0.164	0.039
plasmid_lp54	BB_A04		1.147 ± 0.369	0.562	3.180 ± 4.129	0.423	0.977 ± 0.429	0.842	1.596 ± 0.904	0.162
plasmid_lp54	BB_A09		0.971 ± 0.505	0.857	1.605 ± 1.289	0.234	0.760 ± 0.384	0.333	1.139 ± 0.663	0.102
plasmid_lp54	BB_A10		1.046 ± 0.414	0.870	1.320 ± 0.559	0.417	0.737 ± 0.122	0.117	0.940 ± 0.427	0.836
plasmid_lp54	BB_A11		0.892 ± 0.370	0.274	1.391 ± 0.991	0.351	0.866 ± 0.377	0.097	1.050 ± 0.518	0.331
plasmid_lp54	BB_A13		0.951 ± 0.761	0.894	2.251 ± 1.099	0.120	0.832 ± 0.468	0.429	0.757 ± 0.495	0.300
plasmid_lp54	BB_A14		0.650 ± 0.234	0.138	0.739 ± 0.404	0.528	1.142 ± 0.354	0.557	1.110 ± 0.442	0.765
plasmid_lp54	BB_A23		0.762 ± 0.258	0.416	1.042 ± 0.381	0.898	0.603 ± 0.153	0.047	1.041 ± 0.262	0.839
plasmid_lp54	BB_A24	<i>dbpA</i>	0.564 ± 0.283	0.143	1.281 ± 0.694	0.486	1.043 ± 0.446	0.836	1.288 ± 0.797	0.193
plasmid_lp54	BB_A25	<i>dbpB</i>	0.919 ± 0.366	0.756	1.709 ± 1.217	0.436	0.623 ± 0.519	0.466	1.038 ± 0.333	0.758
plasmid_lp54	BB_A30		0.941 ± 0.404	0.215	1.527 ± 1.371	0.452	0.825 ± 0.288	0.428	1.215 ± 0.720	0.557
plasmid_lp54	BB_A31		0.854 ± 0.214	0.266	1.408 ± 0.563	0.118	0.789 ± 0.231	0.208	1.161 ± 0.314	0.378
plasmid_lp54	BB_A33		1.068 ± 0.776	0.909	2.397 ± 1.670	0.181	1.161 ± 0.558	0.313	2.011 ± 1.043	0.074
plasmid_lp54	BB_A34		0.616 ± 0.302	0.182	0.461 ± 0.377	0.341	0.795 ± 0.518	0.045	0.965 ± 0.627	0.334
plasmid_lp54	BB_A36		0.714 ± 0.350	0.019	1.423 ± 1.243	0.527	0.524 ± 0.256	0.039	0.885 ± 0.492	0.503
plasmid_lp54	BB_A38		1.447 ± 0.501	0.300	0.946 ± 0.416	0.866	0.490 ± 0.211	0.134	1.426 ± 0.508	0.039
plasmid_lp54	BB_A39		0.585 ± 0.190	0.106	1.218 ± 0.821	0.516	0.655 ± 0.248	0.028	0.844 ± 0.275	0.259
plasmid_lp54	BB_A40		0.347 ± 0.260	0.224	1.025 ± 0.750	0.969	0.569 ± 0.417	0.332	1.081 ± 0.923	0.738
plasmid_lp54	BB_A41		0.720 ± 0.125	0.110	1.271 ± 0.518	0.298	0.722 ± 0.126	0.090	1.088 ± 0.263	0.488
plasmid_lp54	BB_A42		0.760 ± 0.442	0.071	1.117 ± 0.516	0.657	0.984 ± 0.549	0.909	0.811 ± 0.572	0.545
plasmid_lp54	BB_A43		0.715 ± 0.431	0.184	1.195 ± 0.516	0.546	0.962 ± 0.507	0.827	0.888 ± 0.235	0.303
plasmid_lp54	BB_A44		1.111 ± 0.531	0.718	1.303 ± 1.133	0.660	0.842 ± 0.206	0.376	1.251 ± 0.251	0.017
plasmid_lp54	BB_A45		1.096 ± 0.465	0.435	1.681 ± 1.271	0.346	0.869 ± 0.232	0.257	1.001 ± 0.268	0.994
plasmid_lp54	BB_A46		0.714 ± 0.422	0.215	1.478 ± 1.138	0.161	0.718 ± 0.429	0.207	0.847 ± 0.549	0.302
plasmid_lp54	BB_A49		0.612 ± 0.296	0.157	1.173 ± 0.523	0.079	0.871 ± 0.273	0.513	0.935 ± 0.340	0.691
plasmid_lp54	BB_A50		0.893 ± 0.433	0.466	1.637 ± 1.483	0.353	0.755 ± 0.444	0.075	1.043 ± 0.659	0.503
plasmid_lp54	BB_A53		0.749 ± 0.237	0.307	1.019 ± 0.698	0.974	0.494 ± 0.296	0.065	0.681 ± 0.359	0.421
plasmid_lp54	BB_A55		0.768 ± 1.125	0.767	1.698 ± 1.674	0.464	0.731 ± 1.050	0.775	2.588 ± 2.945	0.067
plasmid_lp54	BB_A56		0.882 ± 0.640	0.584	1.634 ± 1.517	0.354	0.722 ± 0.500	0.271	1.082 ± 0.511	0.674
plasmid_lp54	BB_A57		0.799 ± 0.557	0.098	1.729 ± 1.597	0.374	0.789 ± 0.507	0.067	0.883 ± 0.539	0.524
plasmid_lp54	BB_A59		0.760 ± 0.158	0.180	0.636 ± 0.586	0.394	1.113 ± 0.422	0.463	0.936 ± 0.229	0.721
plasmid_lp54	BB_A60		0.949 ± 0.251	0.275	1.643 ± 1.398	0.448	0.813 ± 0.237	0.474	1.068 ± 0.260	0.444
plasmid_lp54	BB_A61		0.788 ± 0.164	0.073	1.251 ± 0.231	0.172	0.639 ± 0.340	0.106	0.925 ± 0.190	0.326
plasmid_lp54	BB_A64		0.901 ± 0.570	0.142	1.557 ± 1.392	0.421	0.815 ± 0.353	0.316	1.273 ± 0.693	0.092
plasmid_lp54	BB_A65		0.869 ± 0.347	0.434	1.485 ± 0.978	0.211	0.818 ± 0.332	0.292	1.054 ± 0.417	0.691
plasmid_lp54	BB_A66		0.665 ± 0.208	0.183	1.345 ± 0.997	0.531	0.795 ± 0.261	0.458	0.837 ± 0.250	0.532
plasmid_lp54	BB_A68	<i>cspA</i>	1.017 ± 0.479	0.952	1.359 ± 0.593	0.380	0.806 ± 0.161	0.079	1.049 ± 0.129	0.653
plasmid_lp54	BB_A69		1.692 ± 0.578	0.184	2.971 ± 2.254	0.213	1.447 ± 1.005	0.459	0.781 ± 0.362	0.450
plasmid_lp54	BB_A70		0.392 ± 0.183	0.166	0.591 ± 0.402	0.428	0.876 ± 0.393	0.417	0.931 ± 0.494	0.516
plasmid_lp54	BB_A71		0.992 ± 0.396	0.973	1.135 ± 0.272	0.061	0.779 ± 0.235	0.350	0.771 ± 0.224	0.376
plasmid_lp54	BB_A73		1.027 ± 0.404	0.803	1.083 ± 0.625	0.625	0.764 ± 0.344	0.536	0.863 ± 0.383	0.196
plasmid_lp54	BB_A74	<i>osm28</i>	1.146 ± 0.417	0.176	1.827 ± 1.366	0.322	0.825 ± 0.246	0.021	1.111 ± 0.408	0.242
plasmid_lp54	BB_A76	<i>thyX</i>	1.240 ± 1.170	0.201	0.310 ± 0.384	0.367	0.041 ± 0.077	0.147	0.191 ± 0.231	0.275
plasmid_lp56	BB_Q0091		4.684 ± 3.528	0.045	0.772 ± 0.666	0.363	1.870 ± 1.995	0.531	0.793 ± 0.497	0.597
plasmid_lp56	BB_Q01		1.268 ± 1.085	0.588	1.768 ± 1.279	0.276	0.739 ± 0.805	0.516	0.727 ± 0.347	0.475
plasmid_lp56	BB_Q03		0.812 ± 0.767	0.659	1.250 ± 1.361	0.274	0.572 ± 0.519	0.437	0.724 ± 0.699	0.629
plasmid_lp56	BB_Q12		1.393 ± 0.372	0.174	0.885 ± 0.653	0.812	1.581 ± 0.638	0.310	1.470 ± 0.736	0.406
plasmid_lp56	BB_Q13		2.325 ± 0.543	0.018	1.294 ± 0.400	0.392	0.973 ± 0.335	0.728	1.008 ± 0.314	0.720
plasmid_lp56	BB_Q14		0.752 ± 0.408	0.532	0.835 ± 0.586	0.638	0.758 ± 0.395	0.539	0.846 ± 0.475	0.737
plasmid_lp56	BB_Q15		1.807 ± 0.528	0.046	1.166 ± 0.699	0.658	0.907 ± 0.245	0.183	1.168 ± 0.429	0.267
plasmid_lp56	BB_Q16		2.335 ± 1.152	0.107	1.127 ± 0.951	0.781	0.874 ± 0.260	0.068	0.918 ± 0.234	0.379
plasmid_lp56	BB_Q17		1.350 ± 0.448	0.132	0.894 ± 0.198	0.394	0.829 ± 0.242	0.116	0.996 ± 0.274	0.928
plasmid_lp56	BB_Q18		2.186 ± 1.195	0.053	2.007 ± 1.890	0.325	1.135 ± 0.511	0.195	1.058 ± 0.432	0.702
plasmid_lp56	BB_Q19		2.120 ± 0.567	0.067	1.902 ± 1.732	0.453	0.973 ± 0.118	0.737	0.971 ± 0.157	0.660
plasmid_lp56	BB_Q20		4.448 ± 1.597	0.066	2.670 ± 0.718	0.055	1.776 ± 0.663	0.169	1.768 ± 0.145	0.015
plasmid_lp56	BB_Q21		1.898 ± 0.632	0.007	1.638 ± 1.269	0.334	1.270 ± 0.470	0.413	1.109 ± 0.407	0.163
plasmid_lp56	BB_Q22		2.587 ± 0.817	0.016	1.713 ± 1.229	0.320	1.059 ± 0.296	0.660	1.224 ± 0.319	0.028
plasmid_lp56	BB_Q23		1.879 ± 0.815	0.177	1.757 ± 1.014	0.321	0.577 ± 0.247	0.148	0.711 ± 0.312	0.242
plasmid_lp56	BB_Q24		1.890 ± 1.118	0.035	0.513 ± 0.356	0.359	0.975 ± 0.520	0.871	1.048 ± 0.587	0.590
plasmid_lp56	BB_Q25		2.230 ± 0.641	0.024	1.966 ± 1.640	0.370	1.062 ± 0.259	0.582	1.186 ± 0.218	0.260
plasmid_lp56	BB_Q26		2.537 ± 0.616	0.043	1.756 ± 0.623	0.131	1.369 ± 0.592	0.434	1.753 ± 0.588	0.173

plasmid_lp56	BB_Q27		1.847 ± 1.216	0.088	0.810 ± 0.365	0.533	1.031 ± 0.608	0.426	1.046 ± 0.603	0.497
plasmid_lp56	BB_Q28		1.945 ± 0.944	0.020	0.756 ± 0.364	0.194	0.846 ± 0.405	0.228	1.010 ± 0.520	0.957
plasmid_lp56	BB_Q29		2.268 ± 0.409	0.007	1.337 ± 0.563	0.320	0.989 ± 0.180	0.354	1.032 ± 0.292	0.723
plasmid_lp56	BB_Q30	<i>blyA</i>	1.126 ± 0.469	0.178	0.487 ± 0.361	0.309	0.923 ± 0.381	0.474	0.993 ± 0.445	0.881
plasmid_lp56	BB_Q31	<i>blyB</i>	2.432 ± 1.365	0.107	1.368 ± 0.788	0.530	0.966 ± 0.674	0.876	0.768 ± 0.259	0.419
plasmid_lp56	BB_Q32		2.304 ± 1.104	0.073	1.706 ± 1.449	0.383	0.961 ± 0.400	0.749	1.057 ± 0.398	0.459
plasmid_lp56	BB_Q33		1.141 ± 0.459	0.385	0.635 ± 0.504	0.241	1.009 ± 0.640	0.970	1.161 ± 0.547	0.089
plasmid_lp56	BB_Q34	<i>bdrW</i>	1.885 ± 1.295	0.310	1.122 ± 0.692	0.610	0.982 ± 0.627	0.971	1.230 ± 0.715	0.674
plasmid_lp56	BB_Q37		1.091 ± 0.547	0.056	1.015 ± 0.402	0.962	1.228 ± 0.441	0.453	1.109 ± 0.407	0.641
plasmid_lp56	BB_Q39		2.589 ± 1.319	0.126	1.998 ± 1.175	0.239	1.359 ± 0.981	0.567	0.982 ± 1.087	0.982
plasmid_lp56	BB_Q43	<i>bppA</i>	1.430 ± 0.584	0.028	1.120 ± 0.611	0.498	0.921 ± 0.326	0.496	1.122 ± 0.416	0.026
plasmid_lp56	BB_Q44	<i>bppB</i>	1.800 ± 0.755	0.198	1.467 ± 1.222	0.572	0.828 ± 0.383	0.528	1.162 ± 0.383	0.543
plasmid_lp56	BB_Q45	<i>bppC</i>	3.391 ± 2.290	0.114	2.151 ± 2.415	0.407	0.687 ± 0.272	0.196	0.945 ± 0.359	0.838
plasmid_lp56	BB_Q48		3.521 ± 1.109	0.039	2.532 ± 2.899	0.437	0.974 ± 0.303	0.836	1.955 ± 0.916	0.166
plasmid_lp56	BB_Q49		1.188 ± 0.549	0.269	0.485 ± 0.282	0.206	0.877 ± 0.279	0.125	0.949 ± 0.362	0.055
plasmid_lp56	BB_Q50		1.915 ± 1.131	0.001	0.958 ± 0.568	0.797	0.826 ± 0.459	0.509	0.949 ± 0.524	0.806
plasmid_lp56	BB_Q51		1.893 ± 0.689	0.164	1.449 ± 0.874	0.481	1.030 ± 0.189	0.799	1.168 ± 0.235	0.380
plasmid_lp56	BB_Q52		1.609 ± 0.519	0.130	1.198 ± 0.730	0.647	0.976 ± 0.162	0.556	0.981 ± 0.110	0.830
plasmid_lp56	BB_Q53		1.641 ± 1.130	0.199	1.309 ± 0.658	0.022	0.833 ± 0.354	0.397	1.022 ± 0.510	0.929
plasmid_lp56	BB_Q54		2.872 ± 0.475	0.007	1.675 ± 0.988	0.333	0.978 ± 0.482	0.952	0.981 ± 0.167	0.898
plasmid_lp56	BB_Q55		2.554 ± 1.297	0.060	1.660 ± 1.742	0.523	0.632 ± 0.213	0.174	0.729 ± 0.327	0.355
plasmid_lp56	BB_Q85		1.412 ± 1.207	0.145	1.077 ± 0.956	0.461	0.842 ± 0.699	0.751	0.856 ± 0.744	0.675
plasmid_lp56	BB_Q88		1.637 ± 1.301	0.419	2.724 ± 2.654	0.344	0.906 ± 0.303	0.400	1.101 ± 0.452	0.570

^aSamples with >10 sequences in all 3 glucose cultures

^b% of total reads following growth in specified carbohydrate/% total reads following growth in glucose

^cp-value was obtained using a Ttest

^dA fitness value of 0 indicates that insertions in this gene were not present in the population following growth in GlcNAc

Table S3. Fitness values of all transposon insertions identified in the carbohydrate Tn-seq screen^a

Location	Position	Locus	Gene	GlcNAc		Maltose		Mannose		Trehalose		Sequence obtained in the Tn-seq
				Fitness Value ^b	p-value ^c	Fitness Value	p-value	Fitness Value	p-value	Fitness Value	p-value	
chromosome	604	BB_0001		0.903 ± 0.386	0.481	1.320 ± 0.620	0.524	0.539 ± 0.204	0.164	0.715 ± 0.355	0.284	GTATTTACTATAAATTATCGACTCTTTAAAGAATTATCCTTTAGATC
chromosome	1084	BB_0002		1.100 ± 1.390	0.910	1.790 ± 2.529	0.006	1.002 ± 1.467	0.996	1.642 ± 2.222	0.544	GTTGTTCCCCTAATCCAGGAAAATGTTGATTGCCAAAAACTCCATTAA
chromosome	15805	IG 1		1.069 ± 0.605	0.649	0.972 ± 0.662	0.962	1.023 ± 0.453	0.848	1.236 ± 0.677	0.319	AATTACTAGCTTGAGCTTAAAGTGGCTCAACATTAAGATGAAAAGAA
chromosome	15914	IG 2		0.441 ± 0.210	0.174	0.685 ± 0.499	0.432	0.832 ± 0.538	0.368	1.077 ± 0.601	0.512	ATAAAAAAATTAAAGACTATAACTAAAATCTAAATTATTTGATAGC
chromosome	15930	IG 3		0.598 ± 0.344	0.202	0.447 ± 0.263	0.265	0.957 ± 0.758	0.723	0.975 ± 0.764	0.724	GTCTTAATTTTTATTAGTATTAGTAATAATAGTTGAGTTTTTTTA
chromosome	15935	IG 4		0.922 ± 1.574	0.951	0.797 ± 1.200	0.859	1.880 ± 2.194	0.326	2.331 ± 2.859	0.438	ACTAAAATCTAAATTATTTGATAGCACAAATACAATACTTTAGGA
chromosome	15939	IG 5		0.176 ± 0.207	0.214	0.243 ± 0.445	0.248	0.668 ± 0.623	0.462	0.281 ± 0.214	0.170	AAAATCTAAATTATTTGATAGCACAAATACAATACTTTAGGATCTG
chromosome	16023	BB_0017		0.681 ± 0.384	0.226	0.616 ± 0.374	0.446	0.913 ± 0.602	0.383	0.984 ± 0.619	0.884	TTCCCTCATGGACTCTTAGTGGGAAATGGGGCATTCTATTAGCTAC
chromosome	16167	BB_0017		0.724 ± 0.223	0.066	0.595 ± 0.382	0.163	0.905 ± 0.347	0.778	1.072 ± 0.412	0.822	TAATTCAAAGTGGATTCAATGGGATTATATTCTATTATCATAAACACT
chromosome	16198	BB_0017		0.671 ± 0.528	0.050	0.198 ± 0.204	0.154	0.867 ± 0.711	0.810	0.653 ± 0.454	0.537	TTCTATTATCATAAACCCTCCAGTTTACA AAAATACATCTAA
chromosome	16241	BB_0017		0.857 ± 1.186	0.857	0.354 ± 0.371	0.167	0.804 ± 0.982	0.764	0.621 ± 0.372	0.326	CATCTTAATGATATGCTTGATCAACTAGCTGGACTTTCTGGGA
chromosome	16245	BB_0017		1.937 ± 1.329	0.092	1.292 ± 0.856	0.403	1.278 ± 1.302	0.534	2.191 ± 1.766	0.206	AGATGTATTATTGTAAGAAAAGGGAGTGGTTTATGATAATAGAATAT
chromosome	16265	BB_0017		0.444 ± 0.548	0.528	0.189 ± 0.339	0.403	0.481 ± 0.804	0.272	0.813 ± 1.024	0.716	TCAACTACTGGACTTCTGGACTTGGGCTTGGGCTAATATTAAAG
chromosome	16271	BB_0017		0.658 ± 0.281	0.276	0.726 ± 0.597	0.578	0.863 ± 0.268	0.567	0.839 ± 0.354	0.031	CTAGCTGGACTTCTGGACTTGGGCTTGGGCTAATATTAAAGGC
chromosome	16341	BB_0017		0.800 ± 0.422	0.594	0.692 ± 0.383	0.444	1.209 ± 0.363	0.341	1.213 ± 1.016	0.690	TCTGATCCCCGTAAGATCCTTGGCCCTTAAATTAGCCAAGCCCAGT
chromosome	16350	BB_0017		1.481 ± 1.584	0.350	0.243 ± 0.484	0.173	0.763 ± 1.035	0.778	1.240 ± 1.821	0.835	GCAATTATATCTGATCCCCCTGAAGATCCTTGGCCCTTAAATTAGCCA
chromosome	16359	BB_0017		1.252 ± 0.826	0.599	0.234 ± 0.297	0.113	1.150 ± 1.144	0.869	1.202 ± 0.787	0.554	ATGATCATGACCAATTATATCTGATCCCCCTGAAGATCCTTGGCCCTTAAAT
chromosome	16407	BB_0017		0.721 ± 0.161	0.062	0.892 ± 1.177	0.891	0.604 ± 0.652	0.414	1.097 ± 1.055	0.885	ATCTGTGTTAATACATGGCAACCTTCTTTCTTAATATTGAAATCGCTC
chromosome	16469	BB_0017		1.183 ± 1.475	0.874	0.278 ± 0.386	0.444	2.379 ± 2.980	0.307	0.938 ± 1.350	0.653	ATAGCATTTGTAAACATCATGACAGATAAAACAAGTACTGGATT
chromosome	16610	BB_0017		0.000 ± 0.000 ^d	0.038	0.694 ± 0.424	0.236	0.997 ± 0.198	0.248	0.831 ± 0.296	0.716	ATAGCGAAAAGGTGCTTGGCAGGAAAGAAAAACTATAGTTTATA
chromosome	16610	BB_0017		0.668 ± 0.230	0.145	0.299 ± 0.528	0.419	0.317 ± 0.530	0.982	1.164 ± 0.952	0.171	TTAATGTAGCGGCTAATTTCATTGTTGTAAGAAGATAAGCAATTCTT
chromosome	16655	BB_0017		0.384 ± 0.270	0.075	0.595 ± 0.295	0.265	0.843 ± 0.609	0.570	0.670 ± 0.531	0.148	TTTATAGTAGTCCAATAATGCGTTTATCAAGAATTAAATATATACACAA
chromosome	16659	BB_0017		0.695 ± 0.264	0.190	0.630 ± 0.487	0.476	1.043 ± 0.474	0.490	1.015 ± 0.410	0.814	TAGTAGTCCAATAATGCGTTTATCAAGAATTAAATATATACACAAAAG
chromosome	16661	BB_0017		0.396 ± 0.152	0.088	0.570 ± 0.513	0.405	0.953 ± 0.294	0.857	0.969 ± 0.265	0.846	CTATAAACTATAGTTTCTGTTCTGCCAGCACCTTCTGCTA
chromosome	16661	BB_0017		0.676 ± 0.469	0.103	0.783 ± 0.499	0.679	1.046 ± 0.701	0.595	1.281 ± 0.954	0.159	GTAGTCCAATAATGCGTTTATCAAGAATTAAATATATACACAAAAGTT
chromosome	16689	BB_0017		0.299 ± 0.505	0.008	0.160 ± 0.271	0.008	0.627 ± 0.498	0.020	0.774 ± 0.951	0.535	ATTCTGTGAAACCGCATTATTGGAACTACTATAAATACTATAGTTTCT
chromosome	20058	BB_0021	queA	0.598 ± 0.322	0.012	0.734 ± 0.306	0.227	0.955 ± 0.475	0.693	0.979 ± 0.569	0.941	TTATTAGAATAACATAGCATCACCAGAAAGAAAAATTATAACCTTAA
chromosome	20314	BB_0021	queA	0.973 ± 0.897	0.972	2.559 ± 1.893	0.258	0.797 ± 0.716	0.743	0.803 ± 0.763	0.713	GAGTCATTTGTAAACCTTAAGAAATTAAAACAGGTCAGCAAAGT
chromosome	20888	BB_0021	queA	0.829 ± 0.568	0.548	1.764 ± 1.114	0.055	1.150 ± 1.045	0.790	1.364 ± 0.882	0.546	TTCTGATTTCAGTTGAGTTTAAAGAAATTACTATTATATT
chromosome	20933	BB_0021	queA	0.613 ± 0.578	0.460	0.523 ± 0.536	0.398	0.534 ± 0.273	0.195	0.928 ± 0.311	0.810	TATATTTAAATATTGTTACAGAATTTCATGTAATTTTGCAATT
chromosome	21111	BB_0022	rvuB	0.996 ± 0.929	0.969	2.040 ± 1.832	0.330	1.231 ± 1.502	0.786	1.227 ± 1.609	0.767	AACTTAGAGATGAAAGAGGGATGGCTTAATGAAAACCAAAGTTCT
chromosome	21547	BB_0022	rvuB	1.131 ± 0.429	0.622	0.745 ± 0.529	0.541	0.922 ± 0.272	0.685	1.190 ± 0.253	0.172	AAGTCAAACTTGTCACTTAAACGGCCCTTGGGCTACTCCGTTACTCA
chromosome	22001	BB_0022	rvuB	0.858 ± 0.318	0.042	1.329 ± 0.803	0.374	0.679 ± 0.172	0.136	0.887 ± 0.304	0.168	AAGGTAGGTTAATGTTAAGAAGAACCCATTAGTTTATAAGGCTTA
chromosome	22025	BB_0022	rvuB	0.676 ± 0.597	0.084	0.587 ± 0.528	0.053	0.666 ± 0.362	0.099	1.046 ± 0.521	0.830	GGCTAAAGTTTGAAGATTTAAAGGTCAAGGTTAATGTTAAGAACCC
chromosome	22466	BB_0023	rvuA	0.462 ± 0.393	0.281	0.197 ± 0.217	0.267	0.605 ± 0.590	0.231	0.721 ± 0.688	0.290	TATGGATAACACTTAAAGCGGCCCTGGGCTACTCCGTTACTCCAA
chromosome	22468	BB_0023	rvuA	0.842 ± 0.382	0.293	1.346 ± 0.880	0.229	0.810 ± 0.332	0.371	0.894 ± 0.430	0.313	TTGGATAACACTTAAAGCGGCCCTGGGCTACTCCGTTACTCCAA
chromosome	22600	BB_0023	rvuA	0.783 ± 0.313	0.127	1.200 ± 0.773	0.546	0.669 ± 0.215	0.036	0.851 ± 0.307	0.095	AATAACTCAATTGTCTGACAAATTAAATAGCAAGGCAAATGACTA
chromosome	22797	IG 6		0.734 ± 0.270	0.296	1.111 ± 0.618	0.803	0.532 ± 0.097	0.034	0.598 ± 0.094	0.041	AGGTTTGTCTTAAATTGTTGAATGTTCTGTGAATATAATTATAATT
chromosome	22856	BB_0024		0.656 ± 0.207	0.217	0.539 ± 0.431	0.288	0.692 ± 0.231	0.127	0.848 ± 0.595	0.688	ATTAATTGAAAATAGCTATTAAAATTGATTTCTATTAGTGTCTTT
chromosome	23008	BB_0024		1.134 ± 0.221	0.390	1.406 ± 0.348	0.206	0.610 ± 0.353	0.294	0.918 ± 0.802	0.848	TTCATAGGATCTGGAAAGCAGCTTGTCACTTGTAAACAAAAACAGAAA
chromosome	23099	BB_0024		2.057 ± 2.091	0.082	1.823 ± 2.397	0.429	1.121 ± 1.379	0.843	1.535 ± 1.562	0.472	TTGATTATGGGATAATAACACTACATATCTGTGATAAAAATATG
chromosome	23185	BB_0024		0.618 ± 0.428	0.264	1.985 ± 1.397	0.270	1.156 ± 0.710	0.781	0.989 ± 0.671	0.982	TGCTTTATTATTCCTTCTTACATTAAACTACATATTTTATCGA
chromosome	23630	BB_0024		0.800 ± 0.095	0.062	1.046 ± 0.521	0.874	0.740 ± 0.087	0.058	0.878 ± 0.120	0.326	TTTACGAACTCCCGCACATGTAGCTCCACTTGGAAACACTTTACCGGG
chromosome	23700	BB_0024		1.435 ± 1.069	0.249	2.309 ± 2.780	0.320	0.870 ± 0.638	0.744	1.341 ± 1.017	0.283	TTCTTTGGAAAGTTATTCCTGGTAAAGTGTATTCCAAGTGGAGCTAC
chromosome	23719	BB_0024		0.477 ± 0.442	0.352	0.410 ± 0.385	0.305	0.485 ± 0.571	0.443	1.140 ± 1.309	0.777	TGAATAATTATTTATGTATTCTTGGAAAGTTATTCCTGGTAAAGT

chromosome	23934	BB_0024		0.337 ± 0.371	0.422	0.733 ± 1.316	0.271	0.187 ± 0.247	0.227	0.301 ± 0.323	0.327	CAGAGTTTACTACGAAAAGATTAAATAAAAACCTTAATTCTTGGGA
chromosome	40220	BB_0040	<i>cheR</i>	0.528 ± 0.202	0.157	0.331 ± 0.269	0.190	0.727 ± 0.349	0.126	0.808 ± 0.469	0.111	TAAGGCTCTTACCACTTGAAACGCCAGCTGACCATATTCTAATTCTGAG
chromosome	41593	BB_0043		1.263 ± 0.571	0.544	1.790 ± 1.200	0.421	0.804 ± 0.316	0.456	0.942 ± 0.573	0.245	TTTGTGAAAACCTTATGAGTCTGAGAGCAAGCATAAAAGATTTTAAAG
chromosome	42362	BB_0043		1.056 ± 0.907	0.695	1.910 ± 3.262	0.637	1.241 ± 1.344	0.829	0.866 ± 0.632	0.626	TCTACCTCCACTACTAAATCAAGCTCATACGAATCGTCTGACTTATA
chromosome	43859	BB_0045		0.754 ± 0.471	0.608	0.849 ± 0.485	0.712	0.767 ± 0.549	0.403	0.860 ± 0.522	0.759	CCATCTATAAGTTAATTTCATCCAATTAAACTTAGAAAGCTCTATA
chromosome	45429	IG 7		0.973 ± 0.580	0.875	1.436 ± 1.066	0.385	0.735 ± 0.504	0.066	1.086 ± 0.630	0.677	AAATATTTTATTATAATGAAATTGTAGATTATCAGTAATTGGT
chromosome	45613	BB_0046	<i>rnhB</i>	0.297 ± 0.174	0.049	0.703 ± 0.197	0.201	0.591 ± 0.585	0.407	1.391 ± 1.028	0.531	TGAGTTTCAAGTATTAAATGAGGATAGGTACTCTTTCTTTTTAG
chromosome	45660	BB_0046	<i>rnhB</i>	0.457 ± 0.389	0.243	0.580 ± 0.503	0.400	0.588 ± 0.139	0.041	0.943 ± 0.234	0.272	TTTATTTTCTATTGTTATTGAAATTTCAGCAAATGCATAATATGAG
chromosome	45737	BB_0046	<i>rnhB</i>	0.974 ± 0.368	0.887	1.483 ± 1.358	0.477	0.532 ± 0.413	0.040	0.996 ± 0.914	0.991	GATGCAAATTGTACCCAAAATAACAGCAAAATGTTAACAGAATAATT
chromosome	47204	BB_0050		0.047 ± 0.056	0.229	0.611 ± 0.808	0.371	0.370 ± 0.420	0.344	0.870 ± 1.241	0.203	CCACTTACATTGATTGATCCATTTTTAAAAAAACCGGAT
chromosome	47284	BB_0050		0.186 ± 0.202	0.072	0.660 ± 0.667	0.203	0.881 ± 0.636	0.320	0.882 ± 0.614	0.237	TAATAATTGCTACTGCACCCATGCAAATAATCCGTTTTTTAAAAAA
chromosome	47302	BB_0050		0.326 ± 0.410	0.170	0.683 ± 0.759	0.057	1.088 ± 0.869	0.891	0.916 ± 0.681	0.821	AAACTGGAATGTTGCTATAATAATTGCTACTGCACCCATGCAAATACT
chromosome	47348	BB_0050		0.229 ± 0.250	0.028	0.658 ± 0.592	0.481	0.846 ± 0.281	0.133	0.973 ± 0.364	0.937	ATGTTGCCAATGTCATTAATTCCAAATATTGAAATTGTTTAAACAT
chromosome	47956	BB_0051		0.308 ± 0.380	0.025	0.613 ± 0.718	0.121	0.583 ± 0.371	0.161	0.897 ± 0.664	0.862	TAATAGAAAATCTGTCCACAAAGCTTAAATCAAACATATCCTTATTCA
chromosome	47957	BB_0051		0.605 ± 0.596	0.600	0.985 ± 1.255	0.988	1.722 ± 2.083	0.624	1.920 ± 1.684	0.302	TATATACAGCATGGGAATTCTTACCGATTTTTGGAAAATCTGGCTT
chromosome	48047	BB_0051		0.498 ± 0.471	0.059	0.551 ± 0.588	0.005	0.814 ± 0.807	0.400	0.522 ± 0.447	0.084	TAATATTAAGAAAATTAAAAATATTGGAATGTCCTTAAATTATCAGGCA
chromosome	48216	BB_0051		0.192 ± 0.193	0.124	1.597 ± 1.832	0.637	4.066 ± 3.010	0.194	1.818 ± 1.855	0.419	AAGCATAATTGAAAGTTATGTTAGCAAAGACTCAATACCACGGATT
chromosome	48544	BB_0051		0.160 ± 0.232	0.010	0.268 ± 0.376	0.001	1.416 ± 0.605	0.116	1.066 ± 0.493	0.877	ATTGCAATGCAACCATTTCACCTATTATAAAATTCTGGAAAAAAATA
chromosome	49326	IG 8		0.972 ± 0.359	0.748	1.188 ± 0.424	0.469	0.823 ± 0.328	0.148	0.902 ± 0.407	0.448	AGAAATAGTTGCAATTGAAATATAATTAAAGGACTGATTGTTATTGGT
chromosome	49717	BB_0053	<i>ung</i>	0.439 ± 0.197	0.028	0.923 ± 0.532	0.566	0.777 ± 0.300	0.089	1.094 ± 0.632	0.674	CAATTAAACAGTCGAAGAAGGCAAACCTCTTCTCACAAAGCTATTGGGT
chromosome	50110	IG 9		1.622 ± 2.645	0.725	1.087 ± 1.484	0.928	1.792 ± 2.033	0.489	1.696 ± 2.608	0.440	AATTATTTCTTCTTCAATTGTTCTTAAATTCTATTAAATTAGCATCT
chromosome	65791	BB_0071		0.796 ± 0.509	0.663	1.150 ± 1.206	0.847	0.810 ± 0.760	0.670	1.055 ± 0.876	0.621	TAAAAACCTAAAACAGCACCATTATTTCCTATGCTAAATAGCA
chromosome	66472	BB_0071		0.508 ± 0.579	0.350	0.227 ± 0.166	0.042	0.097 ± 0.107	0.079	0.176 ± 0.306	0.024	TAGAGCTGTAATGAAATAAAATAGTAATGTTTATTGTCATTAG
chromosome	66781	BB_0071		1.282 ± 0.438	0.411	0.987 ± 0.837	0.982	0.575 ± 0.244	0.110	0.619 ± 0.202	0.187	CTTGGATTATTAAATCTAATAACATTATAATGCTGGATACAACAA
chromosome	81398	BB_0085		0.576 ± 0.184	0.089	0.471 ± 0.395	0.304	0.733 ± 0.280	0.080	0.852 ± 0.360	0.073	GTTCTCTTAAAGGCTTATAGCTTCCAAACTATCTTAAATGATTGTTAT
chromosome	81970	BB_0086		0.588 ± 0.564	0.088	0.879 ± 0.840	0.653	0.796 ± 0.522	0.182	1.223 ± 0.885	0.410	ATATAATCTTTCAATTATTGATTGGGTTTGTATTGTTCTGGGGGG
chromosome	81973	BB_0086		0.400 ± 0.357	0.042	0.730 ± 0.728	0.055	0.745 ± 0.558	0.052	0.926 ± 0.696	0.453	TAGATTATGACTTAAACATAAAGGACACAAAGAGCAAAAGAGCAA
chromosome	84019	IG 10		0.420 ± 0.566	0.379	0.142 ± 0.152	0.093	0.365 ± 0.305	0.191	0.441 ± 0.464	0.149	CCTTAAATTTAAACAAATTAAATTATCATGGATTAGACCGCAA
chromosome	95635	BB_0098		0.441 ± 0.501	0.472	0.833 ± 1.341	0.342	0.693 ± 1.076	0.221	0.553 ± 0.616	0.545	ATTCTTATGTTAAATCACTTATTCAATTGCTTAAATATTGCTAT
chromosome	96334	BB_0098		1.177 ± 0.677	0.351	1.581 ± 0.842	0.112	0.889 ± 0.423	0.242	1.084 ± 0.568	0.466	GACTTAAGGCAAGGTTATTTGCTTAAACAAACAAAATTAGAA
chromosome	96794	BB_0098		0.883 ± 0.304	0.667	1.717 ± 0.841	0.308	0.856 ± 0.304	0.613	1.393 ± 0.651	0.452	AGTCTGATTGAAATGCTTTTGGAAAGTTGCAAGGATATCCTTAACTT
chromosome	100456	BB_0102		0.314 ± 0.324	0.293	0.739 ± 0.840	0.231	0.287 ± 0.295	0.285	1.110 ± 1.200	0.901	TATTGGAATTATTATTTTCGCTGTTGATCTTTAAATTGATT
chromosome	100459	BB_0102		0.802 ± 0.861	0.070	3.422 ± 3.417	0.287	0.808 ± 0.725	0.700	1.250 ± 1.011	0.274	TACATACAAAAATCAAAAAAAATTACCCCAACAGAAATTAGCAAT
chromosome	100508	BB_0102		1.176 ± 0.282	0.425	1.698 ± 0.874	0.221	1.066 ± 1.223	0.941	1.238 ± 0.321	0.383	TTGCCCTAAATTCTGTTGGGTAATTATTTTTGATTTGTTATGTT
chromosome	100723	BB_0102		0.076 ± 0.115	0.171	1.635 ± 2.625	0.699	1.830 ± 1.577	0.284	6.197 ± 6.815	0.212	TTAAAGTGTATCCCTTGTGTTTAGCATTTAAATTATTCTTAGATT
chromosome	108273	IG 11		1.584 ± 1.622	0.343	1.892 ± 2.045	0.348	2.445 ± 2.309	0.168	2.189 ± 1.844	0.266	TTAATAACAAAGCTAAATGTTATAATTAAAATGCGTTAAAAAAAT
chromosome	108498	BB_0110		1.132 ± 0.555	0.561	2.065 ± 1.479	0.250	0.831 ± 0.378	0.412	1.401 ± 0.459	0.091	TGTTCAAAACATAATTATAATGAAAGCACACATGTTAACCTA
chromosome	108588	BB_0110		0.872 ± 1.069	0.677	0.921 ± 1.342	0.900	0.023 ± 0.029	0.085	0.318 ± 0.330	0.049	ATTTCTAAATTAAATTCATGTAAGGTAATTAGAGCAAGCTTAA
chromosome	109402	BB_0110		0.271 ± 0.115	0.080	0.507 ± 0.422	0.335	0.890 ± 0.420	0.057	1.027 ± 0.468	0.792	ATTCGGGGTATTTCGCTATACTCAAACAAACATAAGGATACCAAGC
chromosome	109566	BB_0110		2.215 ± 1.599	0.034	3.619 ± 3.286	0.233	1.584 ± 1.140	0.328	1.894 ± 1.554	0.424	TCACAAAGGTTACTATTCTCATAGCTTAACTTAGATGAAAAAAATT
chromosome	109591	BB_0110		2.076 ± 1.541	0.164	1.925 ± 2.300	0.595	1.008 ± 0.954	0.985	1.548 ± 1.057	0.295	GCTTATAACTTAGATGAAAAAAATTAGAAAACATTCTATTAACTTAA
chromosome	113343	BB_0116		0.811 ± 0.211	0.374	0.718 ± 0.630	0.477	0.938 ± 0.409	0.837	1.591 ± 0.900	0.395	TCTGAAAATCAAAGTATCTAATAAGCCAACAGAAATTAAAGAG
chromosome	114678	IG 12		1.032 ± 0.829	0.901	1.396 ± 1.038	0.464	0.423 ± 0.375	0.179	0.843 ± 0.773	0.764	AGTAAAGTTTTTGCAAAAAAGCTTATAAAATAGTGTGTTCTG
chromosome	114972	BB_0117		0.980 ± 1.049	0.979	1.817 ± 2.090	0.588	0.925 ± 1.175	0.926	0.708 ± 1.141	0.698	AATCTTTCTTAAAGAGTAGATATTGTAACAAGAATTGTTGTTCAATGA
chromosome	115017	BB_0117		0.963 ± 0.427	0.912	1.307 ± 0.592	0.479	0.642 ± 0.268	0.281	1.113 ± 0.505	0.578	ATAGGGTCATTGAAAATCGTAAATCAAGAATACAACATGTTAAATCT
chromosome	120706	IG 13		0.734 ± 0.498	0.599	1.671 ± 1.192	0.448	0.576 ± 0.368	0.387	0.912 ± 0.559	0.853	TTTTAAATGAGGTGGACTTAAATTGGATTGTTATTATCTTAA
chromosome	131253	IG 14		0.246 ± 0.158	0.069	0.505 ± 0.482	0.420	0.579 ± 0.308	0.201	0.766 ± 0.400	0.163	TATTATAATTAAGAAAAGAAATTGTGGAGTCAAATTCTAGCTATGGA
chromosome	132171	BB_0134		0.309 ± 0.332	0.081	0.754 ± 1.020	0.712	0.178 ± 0.197	0.195	0.218 ± 0.401	0.220	TTGATGGATCTTTAAATATCTTTAGGTTAGTGTCAATAGCTAA
chromosome	132234	BB_0134		1.266 ± 1.021	0.638	1.441 ± 2.043	0.755	0.921 ± 0.755	0.756	2.252 ± 1.986	0.196	TGTTATCTTCTGATATTACTACCTCCCATTACATACATA

chromosome	137924	BB_0138	2.286 ± 1.902	0.067	2.076 ± 2.562	0.336	0.735 ± 0.651	0.335	1.566 ± 1.629	0.340	AAATTTTTAACTTGTGTTAGTTTTATTAAATTGATC	
chromosome	139215	BB_0140	2.297 ± 2.104	0.260	5.910 ± 4.893	0.147	1.662 ± 1.366	0.512	1.918 ± 1.379	0.386	CATTTCTGCAGGAGAAAAGCTTTCTATTGGCTCAATTGAATCTT	
chromosome	139328	BB_0140	1.018 ± 0.330	0.761	1.229 ± 0.542	0.457	0.728 ± 0.261	0.073	1.056 ± 0.287	0.757	TGATGGCTATTGGCTTGGTATTATGGCTTCATTGAATCTT	
chromosome	139335	BB_0140	0.782 ± 0.345	0.404	1.567 ± 0.685	0.077	0.653 ± 0.294	0.264	1.006 ± 0.455	0.935	ATCATTATGATGGCTATTGGCTTGGTATTATGGCTTCATT	
chromosome	139375	BB_0140	1.818 ± 2.185	0.261	1.312 ± 1.800	0.812	1.147 ± 1.416	0.887	0.664 ± 0.801	0.704	TTCTCCCTAACCTTAAGAGTTATGCCCTTATGGGCACCTTATT	
chromosome	139421	BB_0140	0.562 ± 0.530	0.196	0.852 ± 0.808	0.814	1.095 ± 0.751	0.812	0.638 ± 0.428	0.081	TTATAAATAAACTACAACCTTGGGGTACTGGGTTAAATTATCATCT	
chromosome	140094	BB_0140	1.183 ± 1.074	0.706	1.899 ± 1.553	0.245	0.826 ± 0.701	0.723	1.523 ± 1.273	0.505	TTCTATCAGCACGCAAAGTAGACAATAACTTTATACCTTAGCCCTCAC	
chromosome	140120	BB_0140	1.278 ± 1.890	0.842	2.000 ± 2.716	0.346	1.301 ± 1.667	0.573	0.588 ± 0.838	0.580	ATACTTTATATCCTTAGCCTACTTTACAATTCTAAAATCTTATA	
chromosome	141502	BB_0140	0.212 ± 0.357	0.362	1.534 ± 2.475	0.492	0.498 ± 0.788	0.537	1.009 ± 1.898	0.995	TCTTTAAGCTAGAAACTGGCCTTACAGAATTAAACAATTCCATTAC	
chromosome	141724	BB_0140	0.669 ± 0.330	0.279	0.608 ± 0.553	0.446	0.644 ± 0.218	0.202	0.943 ± 0.293	0.781	TATATTTTAAATTCTTACCGAACTCAAGCCACTCTCAAGGACTCTAGA	
chromosome	142878	BB_0141	0.705 ± 0.804	0.623	0.343 ± 0.474	0.142	0.449 ± 0.606	0.308	0.782 ± 1.003	0.835	TTCTTAGTTAGTGTGTTGGTATAACAAGCTAGATGACAAAAAAAT	
chromosome	142908	BB_0141	1.215 ± 0.558	0.550	1.710 ± 0.761	0.131	1.010 ± 0.521	0.970	1.269 ± 0.701	0.192	AATAATATAAAATCAAATTCACTAAAATACCTTCTAGTCTAATGAATT	
chromosome	143234	BB_0142	1.243 ± 1.093	0.511	1.315 ± 1.462	0.695	0.733 ± 0.441	0.482	0.308 ± 0.391	0.180	CAAAACATGTTAGGTTAAAGGTTAAATCAGGAAATTAAATCTAGTATTGTC	
chromosome	143828	BB_0142	1.039 ± 0.410	0.823	1.649 ± 1.183	0.398	0.703 ± 0.136	0.008	0.969 ± 0.241	0.648	GCTTGATATTGACAGCAGCTCCCTTCTATTGGCTTCATATT	
chromosome	143861	BB_0142	2.514 ± 3.015	0.038	1.931 ± 2.232	0.008	0.685 ± 1.114	0.098	2.089 ± 2.625	0.448	TTTTGCGCTTCATATTCAACATAACAAGTTGCTTCTTTAAACAG	
chromosome	144506	BB_0143	1.641 ± 2.176	0.585	1.414 ± 1.446	0.130	1.309 ± 1.857	0.766	1.321 ± 1.250	0.613	ACGCATTATTCAAAGGGGAAAGCATTACTCTAAATACAAACCCATT	
chromosome	150942	IG 15	0.001 ± 0.001	0.031	0.379 ± 0.365	0.067	0.526 ± 0.337	0.018	0.467 ± 0.181	0.123	GTAAAATAAAATAAAAGAAAATAAAATGCCAATTGCTTAT	
chromosome	157593	BB_0155	0.375 ± 0.385	0.177	0.293 ± 0.270	0.175	0.668 ± 0.647	0.477	0.479 ± 0.338	0.316	ATTTAATAATGCTTAAATTCCACAGTAAACACTAACACCAGTTT	
chromosome	157950	BB_0156	1.110 ± 0.727	0.595	1.160 ± 0.559	0.557	1.002 ± 0.476	0.995	1.157 ± 0.716	0.512	TGTTGAAAGTTTGTGCTTATAAAAGCAAATTGCTTCATTAAATT	
chromosome	157960	BB_0156	0.434 ± 0.447	0.282	0.929 ± 0.977	0.915	0.648 ± 0.473	0.256	1.004 ± 0.690	0.989	TATTAGCATATGTTGAAAGTTTGTGCTTATAAAAGCAAATTGCTT	
chromosome	157993	BB_0156	0.903 ± 0.324	0.600	1.196 ± 0.276	0.368	0.867 ± 0.223	0.556	1.150 ± 0.477	0.674	TTACTTAAATAAACTTCATTGATAGATTATATTGATATGTTGAA	
chromosome	157996	BB_0156	0.665 ± 0.613	0.336	0.514 ± 0.426	0.243	0.701 ± 0.676	0.232	1.138 ± 1.110	0.786	TTAAAGAGATAATGCAATAATAATGCTTTAGTAAAGAATAAAACCT	
chromosome	158214	BB_0157	0.310 ± 0.238	0.079	0.305 ± 0.173	0.106	0.280 ± 0.173	0.147	0.407 ± 0.242	0.122	ATCCAAAATGCTTTACCTTTATTATCGTTTAAATTACATTAAAC	
chromosome	158431	BB_0157	0.260 ± 0.314	0.056	0.636 ± 0.629	0.470	0.836 ± 0.680	0.752	1.247 ± 0.684	0.504	TAGGATAATTCACTTTAGCAGCAGAAACCTTTATTGTAAGATATT	
chromosome	158548	IG 16	1.175 ± 0.729	0.574	1.687 ± 1.070	0.269	0.934 ± 0.446	0.570	1.257 ± 0.596	0.317	GAATGCTAATGCTAAAGTCAGTCGCTTGGTTATTAAATGCTT	
chromosome	158769	BB_0158	0.563 ± 0.893	0.674	1.239 ± 1.890	0.584	0.207 ± 0.403	0.396	0.562 ± 0.594	0.568	ATATCAGGCAAATTCAAAATAAAATGCCAATCATAAATAGTAATCAT	
chromosome	159201	BB_0158	0.909 ± 0.165	0.311	1.602 ± 0.840	0.330	0.867 ± 0.171	0.146	1.117 ± 0.268	0.409	ACTGTCAAAATAAACTACTCAAGAAACTAAATTATAAAATTCTT	
chromosome	159465	BB_0159	0.804 ± 0.701	0.543	1.230 ± 1.429	0.773	0.240 ± 0.255	0.069	0.713 ± 0.488	0.045	TAATTTCGTTTCAAGATATTTCGTTTCAAGAAACCTTT	
chromosome	159613	BB_0159	0.667 ± 0.588	0.389	0.771 ± 0.629	0.576	0.185 ± 0.323	0.083	0.190 ± 0.049	0.014	TTCAATTAAATGTTTCAAAATGGATCTCTGCTTATTTCATT	
chromosome	159762	BB_0159	0.670 ± 0.378	0.176	1.751 ± 1.944	0.556	0.760 ± 0.330	0.413	0.918 ± 0.544	0.732	CTAGTGGAAAACAGCAATCAAAAGAGCTGCAAAGACGCTACTCAT	
chromosome	160086	IG 17	1.087 ± 0.744	0.576	1.560 ± 1.551	0.415	0.847 ± 0.472	0.306	1.008 ± 0.682	0.915	GCTCTCTTCTAGAGATAAACTTCTATTAAATTGTTAGTTATT	
chromosome	161965	BB_0161	0.732 ± 0.664	0.465	0.498 ± 0.613	0.221	0.801 ± 1.392	0.809	0.124 ± 0.194	0.039	TTACAAGGAATAATTACGACAATAATAATTTAACATCAGTC	
chromosome	162049	BB_0161	0.524 ± 0.630	0.279	0.307 ± 0.462	0.093	0.021 ± 0.037	0.004	0.519 ± 0.767	0.355	TGATATTAAACAACCTGACTCTGATGAAATAATGTCAGCAATTATCG	
chromosome	162108	BB_0161	0.723 ± 0.335	0.036	1.049 ± 0.550	0.535	0.828 ± 0.399	0.069	1.046 ± 0.617	0.727	CAGAAAATGGATTGAAACAGCATAAGCCGATTATCAAGATATTCTT	
chromosome	162161	BB_0161	0.322 ± 0.146	0.071	0.724 ± 0.422	0.328	0.579 ± 0.475	0.248	0.612 ± 0.837	0.327	TTAAAGAGGAATACTTGTATAATCGGTTATGCTGTTCAATCCATT	
chromosome	162247	BB_0161	0.289 ± 0.284	0.085	1.031 ± 0.622	0.952	0.997 ± 0.490	0.995	0.812 ± 0.204	0.403	CAAAACGTTTAAACAAATTGGTATGATCGTAGCTGATTTGAAATA	
chromosome	163768	BB_0163	2.425 ± 1.579	0.260	3.166 ± 2.335	0.246	1.015 ± 0.351	0.950	0.646 ± 0.315	0.194	CAAGCCTTTGATATGAGTTTTAGAAGAATATGAAAGAGTTTGAA	
chromosome	164876	IG 18	0.669 ± 1.122	0.710	1.292 ± 1.184	0.727	0.741 ± 0.482	0.201	0.466 ± 0.299	0.173	ACAAGTCAAATAAGATCAAATACTCAATAAAAGTTAAACATTAAAT	
chromosome	164996	BB_0164	0.701 ± 0.381	0.349	1.225 ± 0.395	0.505	0.888 ± 0.259	0.242	1.187 ± 0.431	0.439	GTGGTTAAATTTAAGGGTTTGGTAGGGCATTCTTAAATTGTTT	
chromosome	166288	BB_0165	0.667 ± 1.028	0.337	0.790 ± 1.051	0.844	0.511 ± 0.663	0.504	0.840 ± 1.184	0.615	TTAGTAGGAAACAGCCATTGACCCATAATCAACAGAAATAGGA	
chromosome	167086	BB_0165	1.692 ± 0.777	0.241	2.184 ± 2.025	0.312	0.625 ± 0.517	0.479	0.860 ± 0.808	0.811	GATAAGTCTAAATAACGCTTATTGCTTTGAAAGGAAAAGATTTT	
chromosome	167250	BB_0165	0.780 ± 0.384	0.297	1.140 ± 0.946	0.681	0.617 ± 0.389	0.148	0.891 ± 0.513	0.447	ATATCCTGCACCTAATAATCTCGGAACTAACGATTAAATTCTTAA	
chromosome	167772	IG 19	0.996 ± 0.423	0.973	1.921 ± 1.919	0.424	0.749 ± 0.407	0.109	0.973 ± 0.468	0.841	CTTGCACATTAAAGAAACCTTATTGCAACATTAG	
chromosome	168894	BB_0166	<i>malQ</i>	0.985 ± 0.389	0.931	2.279 ± 1.425	0.230	0.886 ± 0.406	0.472	1.266 ± 0.500	0.372	AAAGCATTCTTGACTCTTAAAGGAAACCTTAAACGCAACAAACTT
chromosome	169313	BB_0166	<i>malQ</i>	0.803 ± 0.714	0.293	1.088 ± 1.094	0.781	0.603 ± 0.453	0.513	1.164 ± 0.911	0.812	TGGCATTGGAGTTAGGGAAAGAGCTTATAAATTAGTATTGTTT
chromosome	169316	BB_0166	<i>malQ</i>	0.773 ± 0.255	0.350	2.162 ± 0.987	0.052	1.348 ± 0.806	0.584	2.694 ± 2.083	0.243	TTTAGATGTTAAAGAGCTTATGTTAGAAGCAAATACCACTTTTAA
chromosome	169456	IG 20	1.153 ± 1.275	0.796	0.992 ± 0.993	0.993	0.831 ± 1.180	0.879	1.510 ± 1.395	0.634	ATAAAATATCAGTCAGAACATATAAGCAATTAAAGGAAATA	
chromosome	170029	BB_0167	1.004 ± 0.866	0.967	0.911 ± 0.832	0.703	0.878 ± 0.830	0.248	0.953 ± 0.950	0.511	ACTACGAATATAAGGCAAAGAGCACAATGGCAAGCATTACACAA	
chromosome	170293	BB_0167	1.496 ± 0.964	0.452	1.226 ± 0.920	0.544	0.775 ± 0.495	0.575	1.283 ± 0.927	0.699	AGATTATCATTGGAAGGCTAATTGAAAGACTTCTGCAAGAGTTCCA	

chromosome	170487	BB_0167	1.240 ± 0.936	0.267	1.623 ± 0.993	0.317	1.209 ± 0.043	0.596	0.702 ± 0.673	0.499	CTAATAGAAGGCACATACTGAGCAATTGGATTGGAAGAAAGAGATGCACGAG
chromosome	170538	BB_0167	1.933 ± 0.687	0.025	1.433 ± 0.523	0.261	1.247 ± 0.550	0.378	1.357 ± 0.666	0.063	GCTCGTGCATCTCTTCCAATCCAAATTCAGTATGCTCTTCTATTAA
chromosome	170614	BB_0167	0.619 ± 0.450	0.154	1.185 ± 0.869	0.690	0.593 ± 0.299	0.052	0.945 ± 0.485	0.786	AATAGTATTGGTCTTGTCTTTACTTCATTTCATTAAATAATTCCA
chromosome	191551	BB_0194	0.544 ± 0.120	0.011	1.097 ± 0.326	0.692	0.657 ± 0.227	0.118	1.000 ± 0.330	0.999	TAATAGCTTAAAGATCTTTATTGCTGCATTAATTTATTAAATTAT
chromosome	192220	BB_0194	0.674 ± 0.568	0.152	0.881 ± 0.301	0.618	0.486 ± 0.155	0.105	0.938 ± 0.357	0.746	CATTATAATGATTTAAAACGGCTTCTTATTGATGTTGG
chromosome	202795	IG 21	1.125 ± 0.738	0.485	1.436 ± 0.780	0.365	0.507 ± 0.294	0.273	1.151 ± 0.972	0.420	CTTAAGGCACATACTTAAAGCATTTTATTAAAGATAAAATTAATAC
chromosome	202799	IG 22	0.436 ± 0.316	0.141	1.357 ± 0.637	0.180	0.428 ± 0.308	0.252	1.248 ± 0.711	0.680	AGGCACATACTTAAAGCATTTTATTAAAGATAAAATTAATACAT
chromosome	202829	IG 23	0.702 ± 0.595	0.494	0.650 ± 0.561	0.412	1.534 ± 0.320	0.107	1.700 ± 0.342	0.054	TCTTTAATAAAAATGCTTAAAGTATGCTCCTTAAAGTATAAAATTTTG
chromosome	202846	IG 24	0.587 ± 0.443	0.480	0.665 ± 0.668	0.645	0.796 ± 0.459	0.391	0.961 ± 0.517	0.862	TGTATTATTTAATTATCTTTAATAAAATGCTTAAAGTATGCTTAA
chromosome	202849	IG 25	0.075 ± 0.134	0.065	0.059 ± 0.060	0.071	0.300 ± 0.287	0.153	0.488 ± 0.430	0.004	TATGCTAGAATTAATCATAACTACTATTATAATATTCTGCTATT
chromosome	202851	BB_0202	0.442 ± 0.290	0.118	0.554 ± 0.469	0.291	0.846 ± 0.243	0.204	1.023 ± 0.320	0.851	TGCTAGAATTAATCATAACTACTATTATAATATTCTGCTATT
chromosome	202865	BB_0202	0.404 ± 0.734	0.470	0.000 ± 0.000	0.088	0.374 ± 0.679	0.429	0.846 ± 1.426	0.780	TGATTAATCTAGCATATATGTTATTATTATTCTTTAATAAAATG
chromosome	202871	BB_0202	1.014 ± 0.483	0.967	0.741 ± 0.631	0.564	1.054 ± 0.147	0.451	1.242 ± 0.270	0.223	CTACTTATATAATTATCTGCTATTCTCAGCATCTGAAACAGCTT
chromosome	202874	BB_0202	0.481 ± 0.172	0.117	0.690 ± 0.587	0.553	0.898 ± 0.203	0.352	1.071 ± 0.276	0.035	CTATTATAATATTCTGCTATTCTCAGCATCTGAAACAGCTT
chromosome	202896	BB_0202	0.480 ± 0.409	0.069	0.952 ± 0.930	0.849	1.185 ± 0.921	0.564	1.387 ± 0.855	0.233	TTTCTCAGCATCTGAAACAGCTTACTCTTACCATAGATAATT
chromosome	202921	BB_0202	0.397 ± 0.225	0.132	0.365 ± 0.305	0.206	0.696 ± 0.300	0.051	0.754 ± 0.361	0.020	TACTTCATTAAGCATAATTCAAGACATAAGAAAAAGGGGAAATC
chromosome	202955	BB_0202	0.461 ± 0.346	0.196	0.449 ± 0.439	0.406	0.772 ± 0.566	0.373	0.932 ± 0.726	0.594	AGAAAAAAAGGGGAAATCGGAAATATCCGTACAATTGTTCAATCTC
chromosome	202976	BB_0202	0.448 ± 0.219	0.211	0.483 ± 0.464	0.408	0.775 ± 0.381	0.361	0.907 ± 0.455	0.600	TTCCCGATTCCCCCTTTCTTATGTCTTGTATCTGAATTATGCTTA
chromosome	203025	BB_0202	0.471 ± 0.212	0.189	0.483 ± 0.430	0.389	0.857 ± 0.557	0.038	1.048 ± 0.679	0.589	TTCTTATCGCAACAAATATCAAACATTGAGCAAGCACACTAACAA
chromosome	203057	BB_0202	0.220 ± 0.144	0.033	0.682 ± 0.630	0.503	0.548 ± 0.355	0.295	0.981 ± 0.288	0.705	GCAAGCACACTTACAACAAAATTGACTTGTGAAAATACGGAACAGCG
chromosome	203067	BB_0202	0.594 ± 0.188	0.185	0.589 ± 0.514	0.460	0.894 ± 0.315	0.324	1.007 ± 0.473	0.951	AGTGTGCTGCTCATCATGTTGATATTGTCGCGATAAGAATAGTAG
chromosome	203255	BB_0202	0.577 ± 0.201	0.082	0.660 ± 0.419	0.422	0.915 ± 0.218	0.200	0.841 ± 0.311	0.316	TTAGTGGAGATAATATAAAATATTGCTTAAAGGAAAGTAGATAG
chromosome	203260	BB_0202	0.544 ± 0.194	0.120	0.607 ± 0.528	0.496	0.661 ± 0.318	0.045	0.978 ± 0.646	0.920	TATAATAACAAAATCATAAAAAAATATTAAATCTTAAAGTTAGAC
chromosome	203310	BB_0202	0.389 ± 0.158	0.129	0.486 ± 0.436	0.374	0.907 ± 0.554	0.172	1.020 ± 0.708	0.914	GTCTTAACCTTAAAGAGATTAAATTTTTATGATTTGTTATTATA
chromosome	203426	BB_0202	0.412 ± 0.212	0.204	0.559 ± 0.584	0.484	0.920 ± 0.521	0.663	0.594 ± 0.266	0.280	CTTGATCTATCTAACATTCTTGCATAATATTCTAGACTT
chromosome	203501	BB_0202	0.296 ± 0.393	0.328	0.816 ± 1.278	0.851	1.279 ± 1.495	0.797	0.822 ± 0.862	0.800	ATCAAATTGATCAAAGAAGAGGAACTCTAGAATTCTTATACAAAGG
chromosome	203538	BB_0202	0.420 ± 0.296	0.207	0.653 ± 0.623	0.595	0.749 ± 0.359	0.291	0.798 ± 0.468	0.283	GGAAATTCTAGAGTATCCTTCTTGTCAATTGATTACATCTT
chromosome	203545	BB_0202	0.441 ± 0.212	0.130	0.480 ± 0.445	0.394	0.904 ± 0.523	0.286	1.057 ± 0.599	0.343	CAAAGGACAAAGCGAGAAACAGATAATTGGGATTAAATGCCAAAGAC
chromosome	203690	BB_0202	0.477 ± 0.156	0.102	0.388 ± 0.344	0.236	0.822 ± 0.304	0.182	1.246 ± 0.559	0.060	CTAGATATTAGAGGAAAAACAAAAAATATGGCAATCGTAATCGATG
chromosome	203697	BB_0202	0.525 ± 0.180	0.132	0.510 ± 0.459	0.327	0.913 ± 0.483	0.741	1.104 ± 0.761	0.835	TTATGAGGAAAAACAAAAAATATGGCAATCGTAATCGATGTTG
chromosome	203768	BB_0202	0.566 ± 0.658	0.479	1.180 ± 1.681	0.887	1.080 ± 1.198	0.703	1.805 ± 1.508	0.068	TTGTAAGTATCCTGAAACACCATATTCTGATTACATGCGATT
chromosome	203771	BB_0202	0.562 ± 0.462	0.206	0.719 ± 0.663	0.494	0.969 ± 0.151	0.786	1.347 ± 0.453	0.324	GAAGAGATAGAGAAAAATTGGAGCAATATCTGACGAAATCGAC
chromosome	203801	BB_0202	0.500 ± 0.196	0.143	0.596 ± 0.540	0.497	0.994 ± 0.513	0.584	1.047 ± 0.486	0.361	TTGCTCCAAAATTCTACTATGTCATTGTAAGTATCCCTGAA
chromosome	203804	BB_0202	0.817 ± 0.647	0.567	0.806 ± 0.735	0.442	1.053 ± 0.606	0.839	1.485 ± 1.239	0.624	TCTGACGAATACGACATTAAGAGGAAAAGCCTCTGATTACTCAAC
chromosome	203823	BB_0202	0.489 ± 0.225	0.135	0.550 ± 0.453	0.439	0.785 ± 0.447	0.115	1.020 ± 0.626	0.818	AAGAGGAAAAGCCTCTGATTACTCAACATCGACAACTACTCAAC
chromosome	203844	BB_0202	0.464 ± 0.149	0.097	0.550 ± 0.445	0.395	0.865 ± 0.399	0.031	1.011 ± 0.475	0.562	CTCAAATCAACGACAATACTACTCAACACTGGAGAAACTACTT
chromosome	203859	BB_0202	0.280 ± 0.133	0.060	0.170 ± 0.299	0.130	0.875 ± 0.660	0.551	1.208 ± 0.585	0.359	TTGTCGTTGATTGAGTAATCAGAGGCTTCTTAAATGCTT
chromosome	203863	BB_0202	0.469 ± 0.196	0.183	0.532 ± 0.489	0.433	0.909 ± 0.450	0.387	1.065 ± 0.591	0.063	AGTATGTCGTTGATTGAGTAATCAGAGGCTTCTTAAATGCTG
chromosome	203866	BB_0202	0.161 ± 0.114	0.042	0.279 ± 0.294	0.008	0.637 ± 0.631	0.536	1.181 ± 1.570	0.880	CTCAACTATGGAGAAACTCTTGCAGGATTTGAGGCAATTGGG
chromosome	203963	BB_0202	0.421 ± 0.261	0.170	0.247 ± 0.220	0.098	1.043 ± 0.603	0.828	1.097 ± 1.124	0.867	ATAGATCTGCTGACAAATACCAACAAAAACGAAACCGTAAACAAAT
chromosome	203966	BB_0202	0.418 ± 0.169	0.135	0.697 ± 0.619	0.631	0.813 ± 0.347	0.553	1.110 ± 0.499	0.294	GATCTGCTGACAAATACCAACAAAAACGAAACCGTAAACAAATG
chromosome	204236	BB_0203	1.022 ± 0.718	0.951	0.806 ± 0.141	0.246	0.573 ± 0.213	0.110	0.310 ± 0.200	0.078	TGAATATGTTGCAATACTATTGATATTAGTACAGGGTAATAA
chromosome	204383	BB_0203	0.966 ± 0.149	0.041	1.003 ± 0.369	0.986	0.781 ± 0.216	0.121	1.033 ± 0.293	0.812	GAAATCCAAATTAAATTCTGGACTATTTCAGGTACGATAAAATT
chromosome	204788	BB_0203	0.733 ± 0.368	0.115	0.656 ± 0.368	0.424	0.495 ± 0.358	0.069	0.599 ± 0.543	0.033	TGTATTTATCTGCTTGAATTGCAATGTTACATCTCAAAGCT
chromosome	204791	BB_0203	0.447 ± 0.432	0.125	0.823 ± 0.725	0.674	0.714 ± 0.311	0.140	0.827 ± 0.165	0.217	AACGAAGGGAGAAAAGAATTAAACAAATGTTCCAAAATCAAGGT
chromosome	204855	BB_0203	0.864 ± 0.811	0.791	0.979 ± 0.833	0.974	0.785 ± 0.649	0.715	0.245 ± 0.263	0.247	TTGAAGAAGCTAGAGGATAAAAGAAAGCAGAATAACACATG
chromosome	205530	BB_0204	0.714 ± 0.420	0.221	1.255 ± 0.644	0.325	0.734 ± 0.398	0.309	1.155 ± 0.615	0.435	TCACACGTTGCTAATGGAAACTCACCCACAAAGAAACAAATTAC
chromosome	206092	IG 26	1.277 ± 1.348	0.749	2.109 ± 1.404	0.195	1.046 ± 0.706	0.897	1.367 ± 1.646	0.707	ATATATTTACAGGTATTAAAGAAAAATTATACTAATAACCTTC
chromosome	206103	IG 27	0.997 ± 1.157	0.998	1.344 ± 0.752	0.480	0.622 ± 0.241	0.110	0.861 ± 0.373	0.708	ATAGATTAATAATATATTACAGGTATTAAAGAAAAATTATACTA

chromosome	209624	BB_0208	1.366 ± 0.660	0.440	1.447 ± 0.700	0.446	0.557 ± 0.595	0.370	0.852 ± 0.260	0.398	TAGCATTCTCCAGCTTACAAATTAGAAAAACCTGAAATAATTGAAC	
chromosome	210000	BB_0208	0.970 ± 0.347	0.670	1.821 ± 1.424	0.307	0.756 ± 0.253	0.171	0.977 ± 0.305	0.894	TTGTTTGTCTAGGCTGTAATGTTAATTGGCTGGAAAATTAAATATAA	
chromosome	210003	BB_0208	1.784 ± 1.413	0.465	1.615 ± 0.305	0.064	0.782 ± 0.573	0.452	1.026 ± 0.939	0.959	GATATTCTGGTAGCTGTAAGAACAGAAAATAAAATTAAATATAAAT	
chromosome	210347	BB_0208	1.116 ± 0.253	0.065	2.044 ± 1.674	0.350	0.738 ± 0.140	0.051	1.059 ± 0.186	0.312	ATAAAGCTAATTTTACTCGAACCTTATAAAAATTTCATTAAGACT	
chromosome	210754	BB_0208	1.075 ± 0.785	0.737	1.655 ± 1.785	0.355	0.661 ± 0.700	0.441	1.802 ± 1.699	0.317	ATAAGGATAAAAAAATTGGTCAACGCATGAAAATTTCAAATCTA	
chromosome	210886	BB_0208	0.666 ± 0.421	0.221	1.540 ± 1.475	0.351	0.730 ± 0.579	0.038	1.512 ± 0.835	0.240	TATCAGACATACTACTCTACCTTGACGAAAATAAAATTACAACCTAA	
chromosome	210897	BB_0208	0.600 ± 0.630	0.223	0.316 ± 0.453	0.070	0.999 ± 0.775	0.998	0.451 ± 0.357	0.231	GTATGTCGATATAAATTGAAATGCTTATATTCAATATTGGGAAAAAG	
chromosome	215548	BB_0211	1.056 ± 0.592	0.806	0.722 ± 0.447	0.574	1.355 ± 0.801	0.279	0.894 ± 0.554	0.641	CTAAATTGAGGTTTCTTGAAGAAGGGGAACTCAAATCTAAATAA	
chromosome	215595	BB_0211	0.616 ± 0.330	0.344	0.985 ± 0.548	0.966	0.407 ± 0.191	0.077	0.626 ± 0.329	0.160	TTAAGATTTTGAATTCCCCCTCTCAAGAAAACCTCAATTAGTAG	
chromosome	215802	BB_0211	1.477 ± 0.260	0.016	1.608 ± 1.273	0.462	0.804 ± 0.184	0.338	1.141 ± 0.226	0.499	GAAAATGAAATTGAAAAATGCTTAAAAAACACCGGCCATAACGGAACA	
chromosome	216112	BB_0211	1.350 ± 1.189	0.164	1.959 ± 2.185	0.319	0.889 ± 0.636	0.716	1.218 ± 0.935	0.760	TTGTCATGTTCTTTAAGACCTTAAATTATTCTATTACATT	
chromosome	216163	BB_0211	0.781 ± 0.812	0.308	1.323 ± 1.458	0.501	0.171 ± 0.129	0.096	0.915 ± 0.620	0.857	AAAGACATATAAAACATTGTCACAGAACCTATCGATCAAAGATC	
chromosome	228894	BB_0224	0.217 ± 0.105	0.058	0.444 ± 0.384	0.305	0.756 ± 0.337	0.252	0.814 ± 0.441	0.016	TGTATATTGCTTAATTACCAATACATTGATATTGAAAAAATGAAAAG	
chromosome	228897	BB_0224	0.545 ± 0.498	0.432	0.324 ± 0.549	0.410	0.946 ± 1.211	0.956	1.206 ± 1.213	0.537	CATATTAATAAAAAGCTTAACTCTAGATAAAATTAAATTGGCTT	
chromosome	228901	BB_0224	0.029 ± 0.051	0.069	0.749 ± 1.335	0.820	0.921 ± 0.836	0.918	1.022 ± 1.295	0.965	TTAATAAAAAGCTTAACTCTAGATAAAATTAAATTGGCTTAATG	
chromosome	228925	BB_0224	0.271 ± 0.150	0.082	0.605 ± 0.591	0.011	0.610 ± 0.401	0.090	0.812 ± 0.481	0.354	GATAAATTAAATTATTGCTTAAATGCCGTATTAATCGAATCACTATT	
chromosome	229045	BB_0224	0.267 ± 0.090	0.057	0.491 ± 0.410	0.294	0.839 ± 0.376	0.025	0.975 ± 0.418	0.845	ATACAATTGCCATTTTAATGACAATTCTTACTCTGCAAGAAATTATA	
chromosome	229152	IG 28	0.326 ± 0.231	0.050	0.338 ± 0.400	0.227	0.478 ± 0.291	0.188	0.140 ± 0.124	0.062	ACAATTCTCTAAAAAGATAAAATAATTGTTAAATCAGCTCGTTATT	
chromosome	233085	BB_0228	2.145 ± 0.950	0.108	1.808 ± 1.198	0.407	0.870 ± 0.474	0.655	1.376 ± 0.848	0.507	TGTTAATTGACATTGCTTTCTTTATAAGGCCATTATTGTATT	
chromosome	233934	BB_0228	0.525 ± 0.279	0.039	1.588 ± 2.128	0.519	0.481 ± 0.698	0.408	1.262 ± 0.503	0.008	AAAGAGCTAATCTACATTCTTTAAGTTAAAGAGTAACAAATTCTTCA	
chromosome	240121	BB_0235	<i>ychF</i>	1.107 ± 0.295	0.677	2.272 ± 2.083	0.401	1.260 ± 0.966	0.718	0.834 ± 0.596	0.515	GTAGAGATCCCAGTAAAGGCTTAAATTCTCAGAGTGCATTATTCCA
chromosome	246612	BB_0241	<i>glpK</i>	0.588 ± 0.301	0.131	0.912 ± 0.417	0.638	0.778 ± 0.467	0.316	1.037 ± 0.639	0.828	TCTATTGATCAAGGTACTACTAGCTGAGAGCAATGGTATTGATAAAAT
chromosome	247035	BB_0241	<i>glpK</i>	0.520 ± 0.380	0.141	0.449 ± 0.267	0.125	0.533 ± 0.344	0.255	0.868 ± 0.507	0.772	GAAGTGCACAGACAAAGAGGCCAAAATGGCGAATTATGCTTGGAAACAATA
chromosome	247090	BB_0241	<i>glpK</i>	0.537 ± 0.335	0.359	0.427 ± 0.506	0.432	0.865 ± 0.687	0.670	0.996 ± 0.673	0.982	CATGGATATTGCGAACCTGACTCAAAAAAGAACATCAACCGATTACT
chromosome	247989	BB_0241	<i>glpK</i>	0.582 ± 0.579	0.192	0.752 ± 0.720	0.310	0.820 ± 0.761	0.657	0.721 ± 0.611	0.572	GACAAGATATTGAACTCTAACATGCCAAAAAATCAAAAGAAAAGCTTCTT
chromosome	248193	BB_0242	0.562 ± 0.242	0.155	1.077 ± 0.565	0.286	0.655 ± 0.360	0.066	0.849 ± 0.504	0.250	TGTTGTTTAGTTCAAAATCAAATAATTATGCATAATTGTTACCA	
chromosome	248355	BB_0242	0.016 ± 0.034	0.290	1.242 ± 1.936	0.834	0.548 ± 0.859	0.624	0.349 ± 0.583	0.328	TTAATCATTTTTGTATTGCTTAACTGAATTTCACCTTCAAAAGGTTA	
chromosome	248358	BB_0242	0.848 ± 0.178	0.231	1.618 ± 1.158	0.437	0.575 ± 0.380	0.289	0.622 ± 0.125	0.073	TTATAATCATTTTTGTATTGCTTAACTGAATTTCACCTTCAAAAGGT	
chromosome	248421	BB_0242	0.406 ± 0.617	0.122	1.190 ± 1.331	0.681	0.716 ± 0.872	0.286	0.714 ± 0.687	0.561	GTGCTATTCAATAAAATTAAACAAATGGTCTTTGCAATTCTTCAACT	
chromosome	248862	BB_0243	0.783 ± 0.991	0.664	0.258 ± 0.300	0.240	0.420 ± 0.470	0.287	1.271 ± 1.303	0.526	ATAAGTGTATTCTTAAACATTAAATAGGGCGTGTAAAGTCACATTGCTT	
chromosome	249253	BB_0243	0.377 ± 0.295	0.203	0.782 ± 0.676	0.438	0.616 ± 0.616	0.130	0.691 ± 0.546	0.364	AACATCATTAAACCTTCCCAAGGTGCGTAAAGTCAAAGACAA	
chromosome	249494	BB_0243	0.616 ± 0.643	0.254	1.708 ± 1.392	0.334	0.582 ± 0.712	0.321	0.601 ± 0.458	0.293	AAATAGAAAATCAGATGTAAGAGTGTATAACCGGAATAAGGCCATTAA	
chromosome	249623	BB_0243	0.405 ± 0.406	0.183	0.907 ± 0.109	0.093	0.653 ± 0.749	0.111	0.850 ± 0.989	0.021	ATAAGATTGAACTGTGATATAATTGTTCTTGTGAGATTGTTGAA	
chromosome	249691	BB_0243	0.364 ± 0.286	0.120	0.764 ± 0.572	0.174	0.521 ± 0.403	0.101	0.730 ± 0.570	0.113	GAACAAAATTAACTACGTCACCAACTACAGAACGATTAAAGTTG	
chromosome	249968	BB_0243	0.335 ± 0.297	0.004	0.846 ± 0.525	0.326	0.504 ± 0.464	0.035	0.972 ± 1.005	0.951	GCTTGAGGTTAAAGGTTAGTGTATTGTTCTTGTCTAAACATCTCA	
chromosome	259040	BB_0252	0.837 ± 0.580	0.650	3.642 ± 3.196	0.169	1.294 ± 1.155	0.682	1.985 ± 1.929	0.248	TATTGACAATATTCTAATTACTATTGTTAGGTTTTTGGAAAAA	
chromosome	259588	BB_0252	2.835 ± 1.630	0.176	3.257 ± 2.883	0.257	0.627 ± 0.745	0.415	0.927 ± 1.500	0.939	AGATTGTTCTCTACTATTAAACCCCGTAAGACAACTTAAATCTG	
chromosome	259793	BB_0252	0.111 ± 0.081	0.167	0.319 ± 0.492	0.300	0.501 ± 0.439	0.334	0.714 ± 1.173	0.804	AGTAAACAACTTGAATTGTTCTGGCACTGTAATAGGGATTGACAAGC	
chromosome	260736	BB_0252	0.931 ± 0.896	0.813	1.051 ± 1.199	0.880	0.502 ± 0.515	0.038	0.661 ± 0.479	0.366	TCATTCTCAGGTGTTATGATAAGGTTAAATAGCTAAACATGGTAA	
chromosome	260771	BB_0252	0.071 ± 0.068	0.074	0.690 ± 0.618	0.436	0.104 ± 0.153	0.103	0.217 ± 0.233	0.137	GCTTAAATACCTTATCATAACACCTGAGAAAATGATATTGTTTCTC	
chromosome	260797	BB_0252	0.453 ± 0.280	0.037	0.735 ± 0.666	0.348	0.617 ± 0.448	0.275	0.679 ± 0.423	0.193	TAACCTGTTCTTACATTGTTAGCTATTACCTTACATAACAC	
chromosome	261085	BB_0252	1.734 ± 0.558	0.077	2.747 ± 2.377	0.324	1.540 ± 0.674	0.335	1.399 ± 0.829	0.406	TTAATGGAAATTGCAATTCTATTGTTGGAAATAGGATTTTAATC	
chromosome	261262	BB_0252	1.114 ± 1.377	0.868	1.428 ± 1.745	0.651	0.715 ± 0.990	0.653	1.432 ± 1.325	0.679	AAGCTAGCTCAAACAAACATTAAAAACAAATAATTAAATGAC	
chromosome	261265	BB_0252	0.937 ± 0.268	0.771	1.533 ± 0.980	0.451	0.706 ± 0.118	0.105	0.990 ± 0.270	0.962	GCTTACTCTAGGTTAAATAAAATTAAATAGGAAGAGTAGTGT	
chromosome	266112	BB_0254	<i>recJ</i>	0.955 ± 0.546	0.742	1.382 ± 0.563	0.106	0.631 ± 0.535	0.429	0.764 ± 0.562	0.620	TAGAATACAAAAGCCACTTAACTACTGTGTATTCTAGGAATACAGT
chromosome	266183	BB_0255	1.140 ± 0.853	0.549	1.853 ± 1.584	0.278	0.812 ± 0.421	0.358	1.266 ± 0.760	0.268	GTATTGTTATTCTGTAATTATTTCTATTCTAGAATACAGTATA	
chromosome	267275	BB_0256	<i>rpsU</i>	0.767 ± 0.208	0.011	1.418 ± 1.070	0.533	0.723 ± 0.181	0.093	0.736 ± 0.148	0.046	GATGCGACAGAGATGTTCAAATGGATATCTCTTATTAAACAC
chromosome	273890	BB_0261	0.463 ± 0.411	0.205	1.026 ± 1.176	0.974	0.625 ± 0.860	0.566	0.766 ± 0.744	0.745	CTGTCATGAAGAGATTACTATAATAGTGACAACACTGTTCTCCTA	
chromosome	275622	BB_0262	1.110 ± 0.559	0.711	1.959 ± 0.948	0.179	0.669 ± 0.622	0.583	1.776 ± 0.941	0.125	AAAGTCTCCCTAAACCTCTTTAAAAATCTGGCAATCTCCCCCA	

chromosome	277304	BB_0264	0.966 ± 1.165	0.952	1.778 ± 2.562	0.566	0.865 ± 0.833	0.192	0.492 ± 0.579	0.132	TAGGTAGGTTTCTTGGCAATTCAAAAAGCTTAAAGGAATTCCA	
chromosome	277777	BB_0264	0.526 ± 0.677	0.297	1.182 ± 1.381	0.741	0.605 ± 0.632	0.533	0.528 ± 0.638	0.342	ATTCAAATGCTTGCCATCAAGAAAAAGCAAAAGTAATGTCGACCTCTTCCAT	
chromosome	278129	BB_0264	1.039 ± 0.428	0.746	0.761 ± 0.424	0.084	0.598 ± 0.275	0.110	0.767 ± 0.578	0.321	ATGAACCAACCGCAGCTGCTATTGCTTATGCCCTTGAAGACAGATTGATG	
chromosome	278206	BB_0264	0.711 ± 0.291	0.119	1.448 ± 0.879	0.401	0.986 ± 0.478	0.931	0.913 ± 0.423	0.499	GGCAGGGACTGTTATTACAGCATTTCATACTCTCATCTAAAATTTTC	
chromosome	278432	BB_0264	0.471 ± 0.311	0.116	0.621 ± 0.366	0.045	0.468 ± 0.158	0.114	0.401 ± 0.149	0.113	TCTGAGAAAACAATAGAAGGGTTATTGCTCACCCCTTCATTAAAT	
chromosome	278481	BB_0264	0.761 ± 1.045	0.824	1.083 ± 1.667	0.952	1.433 ± 1.471	0.667	2.792 ± 2.767	0.001	ATATTATCTTAGAACTAACATCAAATACGATGCAACAGTATTGTGGTTC	
chromosome	279215	BB_0266	1.088 ± 0.230	0.568	1.672 ± 0.416	0.102	0.813 ± 0.068	0.024	1.147 ± 0.222	0.392	GTTAATAAAGTAGGGATAATTATTCGTTCTGCAGTTAAAAAAAT	
chromosome	279477	BB_0267	0.526 ± 0.582	0.123	1.277 ± 1.616	0.699	0.996 ± 1.024	0.996	3.763 ± 4.488	0.315	ACAAACGTTACTTTAGAGGATGATAATTATAAAGTTATGACCTATA	
chromosome	303742	IG 29	0.292 ± 0.135	0.021	0.402 ± 0.161	0.022	2.149 ± 0.763	0.047	0.388 ± 0.168	0.019	TTGAAACCTCCCTCATTTAAATTGCTTTAACTAAATTATAATAATT	
chromosome	303902	BB_0295	<i>hsfU</i>	1.310 ± 0.643	0.464	1.248 ± 1.150	0.762	0.859 ± 0.425	0.547	0.674 ± 0.420	0.446	TTTCATACACCGTGAAGTCTCTGCACCAAGATTTCACTCTCAAGAT
chromosome	305051	BB_0295	<i>hsfU</i>	0.090 ± 0.124	0.195	0.499 ± 0.485	0.390	0.469 ± 0.716	0.520	1.220 ± 1.317	0.840	GGTAAAGACGAAGCTAAAAATTAGTATCAATTGCTCTGTTAATAGATAT
chromosome	305483	BB_0296	0.668 ± 0.613	0.152	1.778 ± 2.117	0.613	0.801 ± 0.819	0.771	0.767 ± 0.749	0.766	CTCTTTGAAAAATTGAGAAGAAAAAACTAAAGCAAAAGGTGATGGCTTGA	
chromosome	305705	BB_0297	0.100 ± 0.197	0.276	0.292 ± 0.420	0.388	0.361 ± 0.536	0.398	0.817 ± 0.995	0.725	AGAACATCAGATACATTTCACAACTACACTTTAGAATCATCTTC	
chromosome	305884	BB_0297	0.908 ± 0.510	0.694	1.321 ± 1.117	0.729	0.734 ± 0.420	0.341	0.925 ± 0.600	0.867	AACATCAAGCTCTAAGTCAGACCAAGCTAGCTGAATTAAAGCTCTGA	
chromosome	305947	BB_0297	1.814 ± 1.404	0.029	3.968 ± 4.993	0.390	1.959 ± 1.815	0.446	2.658 ± 2.815	0.265	TGCACCTTGAATCAGGAGCTTAATTACAGCTGAGCTTGTCTGACTT	
chromosome	306377	BB_0297	0.845 ± 0.365	0.089	0.964 ± 0.692	0.950	1.230 ± 0.717	0.663	1.388 ± 0.892	0.586	GGATAAGACTTAGACCCTAGAATAGCAACTTGGCTTGGCCTTGAATA	
chromosome	306539	BB_0297	0.720 ± 0.544	0.586	0.841 ± 0.584	0.614	1.136 ± 0.619	0.798	0.706 ± 0.407	0.529	AAATCAAATTATTAAAAGTTAATTTCCTGCCTTTAAAATTC	
chromosome	321686	BB_0315	1.203 ± 1.627	0.790	1.219 ± 1.564	0.643	1.000 ± 1.531	1.000	0.144 ± 0.271	0.210	TCTCTGGCATACTTTAATAGGAGAAGTTAAAATTCAATGGACTATA	
chromosome	321865	BB_0315	1.072 ± 0.977	0.915	1.437 ± 1.021	0.550	0.859 ± 0.321	0.566	0.921 ± 0.369	0.774	TCTTCAACGTTCAATTAGCACTCAATGACGACACATTGTTATAATT	
chromosome	322438	BB_0316	0.935 ± 1.196	0.942	0.659 ± 0.742	0.567	1.748 ± 1.023	0.223	0.698 ± 0.328	0.028	TAACATAAACAGTAATAAATAAAAAAATGAACAAAAACAGCAATAAAAACAA	
chromosome	326309	IG 30	0.427 ± 0.544	0.423	0.249 ± 0.308	0.134	1.054 ± 0.826	0.919	1.540 ± 1.959	0.409	ATAAAAGGATGTTTATTATTTAGTGTAAAGGGTTTTAAAGGGTTT	
chromosome	327693	BB_0322	0.405 ± 0.418	0.095	0.421 ± 0.379	0.310	0.649 ± 0.496	0.439	1.120 ± 1.033	0.443	GTGTTGTTAGAAATACATTCGGTTAAGTTAGATTAGATGACGAAATT	
chromosome	327715	BB_0322	0.644 ± 1.045	0.703	0.479 ± 0.542	0.505	0.856 ± 0.712	0.747	3.224 ± 3.623	0.222	AAAGAATAGAAGGTAGAGTTAGTGTGTTAGAAATACATTCCCGTTAAG	
chromosome	334910	IG 31	0.877 ± 0.723	0.719	1.002 ± 0.679	0.997	0.631 ± 0.392	0.182	1.345 ± 0.826	0.591	TATAAAATTGAAAAAGGAAATCCCATGAAATATATAAAAATAGCCTTA	
chromosome	335200	BB_0328	0.835 ± 0.841	0.727	1.167 ± 1.586	0.284	0.714 ± 0.842	0.426	1.023 ± 1.219	0.892	CACATTAACCTAAGAGAAGATAGTTGGAGCGATGGAGTTGCCATTAC	
chromosome	335210	BB_0328	0.555 ± 0.367	0.142	0.721 ± 0.503	0.222	0.542 ± 0.361	0.142	0.788 ± 0.645	0.021	GGTTAAATGTGAAATAATTCCATCTCAGAAATATTCAACATTTCGCAA	
chromosome	335333	BB_0328	0.619 ± 0.313	0.211	1.361 ± 0.498	0.297	0.844 ± 0.408	0.473	1.022 ± 0.419	0.948	TTGTAGATTTTAATTAATTAGCATACATTGAGCTGTTTTTTTTTTTA	
chromosome	335795	BB_0328	0.597 ± 0.536	0.385	0.889 ± 0.872	0.626	0.498 ± 0.401	0.334	0.686 ± 0.806	0.067	GCATTCATACAAACATAAAACCACTAGACAAATTAAAAGTTAGACAAGCC	
chromosome	335960	BB_0328	0.768 ± 0.654	0.670	1.182 ± 1.433	0.507	0.616 ± 0.685	0.184	1.046 ± 1.168	0.798	TTAAATTTCCATAAGAAATACATCAAAATTGGAGTTAGATTCTTG	
chromosome	336408	BB_0328	0.707 ± 1.012	0.468	1.701 ± 2.921	0.353	0.505 ± 0.657	0.473	0.668 ± 1.084	0.306	TACCCAAATCTCATTCATTCAGAAATGATAAATGGACGGGGTGTAC	
chromosome	336523	IG 32	0.842 ± 0.708	0.476	1.153 ± 0.698	0.799	0.904 ± 0.721	0.840	0.724 ± 0.467	0.419	TTTACTTAATTATTATTTTGTAGTTAAATCTCATATAAAATAGCT	
chromosome	337151	BB_0329	1.026 ± 0.536	0.888	1.195 ± 0.776	0.349	0.686 ± 0.325	0.391	0.880 ± 0.746	0.584	ACATATCAATAAAATAAGGTTTGGTAGTTCCAGTGTATTCTAATGTTT	
chromosome	337852	BB_0329	0.414 ± 0.183	0.032	1.033 ± 0.719	0.902	0.685 ± 0.329	0.020	0.731 ± 0.407	0.056	TGTGTCATTCTCGTTCAAGTTCCACATCAATTAAAAATTTTTTT	
chromosome	337856	BB_0329	1.198 ± 1.109	0.825	1.263 ± 1.541	0.748	0.309 ± 0.477	0.261	1.559 ± 1.370	0.413	AGTATGTTGCCATTCTCGTTCAAGTCCACATCAATTAAAAATT	
chromosome	338107	BB_0329	0.590 ± 0.386	0.366	0.761 ± 0.528	0.537	0.292 ± 0.178	0.074	0.702 ± 0.502	0.550	TATTGGTGTCTTGGAAATCTTTCAATAATTATCTCTGTTGCT	
chromosome	340285	IG 33	0.605 ± 0.789	0.284	0.801 ± 1.335	0.416	0.367 ± 0.371	0.375	0.986 ± 1.088	0.968	TATGATATAATTGACTAATACGTAAGTTATCAATATCTTACAAAGGAG	
chromosome	344196	BB_0336	0.867 ± 0.241	0.107	1.208 ± 0.654	0.478	0.684 ± 0.172	0.077	0.899 ± 0.227	0.239	AGTAAGCTTTAATTATTCTGTTCATCTCATCAAAAGGTATTAGT	
chromosome	344355	BB_0336	0.745 ± 0.748	0.720	0.286 ± 0.328	0.292	0.552 ± 0.392	0.184	0.951 ± 0.674	0.831	GTATAATTCCCTTATTGTCCTCTTCATAAGCCTTAAAAAGGA	
chromosome	352512	BB_0344	0.902 ± 1.421	0.886	1.599 ± 1.800	0.474	0.670 ± 0.635	0.283	0.713 ± 0.541	0.386	ATAAAAGGATGAAATTGTTAGTTTCAAGACCTCAGATGAAGCT	
chromosome	355454	IG 34	0.918 ± 0.800	0.417	1.950 ± 2.514	0.418	1.005 ± 0.755	0.977	0.898 ± 0.729	0.756	GATAAACACCTTGAAGAAATAGGTTGATAAAAATGTTGAATTA	
chromosome	355857	BB_0347	0.866 ± 0.281	0.354	1.927 ± 0.831	0.083	0.902 ± 0.388	0.301	1.311 ± 0.462	0.151	TATGGGGCGAGGATGGCCACAATTAAATAAGATAATCATATT	
chromosome	355864	BB_0347	0.450 ± 0.383	0.156	0.779 ± 0.693	0.662	1.025 ± 0.411	0.932	0.991 ± 0.200	0.955	GCTATTATGGGGCGAGGATGGCCACAATTAAATAAGATAATCATA	
chromosome	356641	BB_0347	0.538 ± 0.349	0.251	0.796 ± 0.818	0.096	0.611 ± 0.371	0.266	1.116 ± 0.783	0.317	CAAGAGATTACCTGGAGCTTATGTTTATTAAAAAATCAAAAAT	
chromosome	366967	BB_0359	1.559 ± 0.115	0.014	1.885 ± 1.768	0.480	0.606 ± 0.153	0.018	0.968 ± 0.595	0.933	ATTACCTAATTAGACAATACTCACAGCTGTTTTAAACTTGTCT	
chromosome	368613	BB_0360	0.574 ± 0.478	0.480	0.785 ± 0.732	0.714	1.670 ± 1.442	0.221	1.626 ± 1.741	0.514	AATGTTAACATAAACTTATGGAGTAAATTAAATGAAAATT	
chromosome	368735	BB_0360	0.981 ± 0.176	0.665	1.014 ± 0.362	0.963	0.638 ± 0.238	0.028	0.906 ± 0.137	0.482	ATGTTAACATTATTGGAAATATTAGTTACTATAATGCTGTGAAGAA	
chromosome	368760	BB_0360	0.860 ± 0.964	0.652	3.228 ± 4.507	0.353	0.715 ± 0.981	0.375	0.687 ± 0.991	0.143	TTTTAAATACAGTCTACAAACCTCTAGCCATAATTAGGAATT	
chromosome	369224	BB_0361	0.612 ± 0.351	0.391	1.302 ± 0.694	0.599	0.770 ± 0.857	0.713	1.327 ± 0.662	0.064	AGTAATCATTTAAAGATTAAATTAGGATTTATGATTTTTGGG	
chromosome	369552	BB_0361	1.054 ± 0.681	0.883	1.863 ± 2.022	0.396	0.715 ± 0.720	0.374	1.160 ± 0.775	0.491	ATATGCTCAAAGCTCCAAAAGACATTGAAAAACCGAAAAATAAAAAT	

chromosome	369706	BB_0361	0.150 ± 0.144	0.011	1.313 ± 1.435	0.705	0.458 ± 0.425	0.221	0.955 ± 0.454	0.795	CAAACCTACAAGCTCAACTCTAAAAGTATAAAAAAATTGCAAAAAAATT	
chromosome	371284	BB_0363	0.540 ± 0.480	0.422	2.875 ± 4.052	0.303	0.665 ± 0.777	0.246	0.578 ± 0.663	0.382	GAATGGATTGTTGCATTTTTAATTGCTTGCAATGTTATTGAAAAAA	
chromosome	371287	BB_0363	1.193 ± 0.670	0.711	1.764 ± 1.026	0.324	1.200 ± 0.592	0.585	1.398 ± 0.605	0.351	TCATAATTAGCAAAGAAAAATTGATGAGGAATATTAAAACCTGATCACA	
chromosome	371367	BB_0363	0.761 ± 0.460	0.603	0.735 ± 0.646	0.663	0.017 ± 0.029	0.052	0.402 ± 0.603	0.131	GAATATAAGCAAAGCTTAATACATCAAAAAAAATTATTTGCGACAATAAA	
chromosome	371416	BB_0363	0.742 ± 0.665	0.548	1.771 ± 2.822	0.640	0.478 ± 0.551	0.247	0.640 ± 0.750	0.374	AAAACACAACCTGGATTCTTTAAATTATCAGAACTCATAAAAGAAA	
chromosome	371577	BB_0363	0.808 ± 0.402	0.170	0.761 ± 0.412	0.601	0.905 ± 0.433	0.467	1.081 ± 0.584	0.111	TGTGGTTACTTGATTATTTCCAGAGGTTTCATTGGAAGATTAAGAT	
chromosome	371580	BB_0363	1.835 ± 1.759	0.502	0.313 ± 0.227	0.246	1.004 ± 0.938	0.972	0.378 ± 0.384	0.224	GATATCAGAGATGGGAAAAGCTAGAAAAAAATAATTAGTTACACACA	
chromosome	371865	BB_0363	1.415 ± 1.101	0.576	1.161 ± 0.858	0.804	0.404 ± 0.391	0.338	0.838 ± 0.723	0.503	GTAAACCATATGGATATTACAAAAAAAAGCATATTTACTTAATT	
chromosome	372009	BB_0363	0.949 ± 0.538	0.661	2.126 ± 2.463	0.451	0.734 ± 0.350	0.021	1.020 ± 0.516	0.837	ATGACATTATTTGAATACATTATTTAAGTATTGATTAAGTTTT	
chromosome	372271	BB_0363	0.974 ± 0.123	0.580	1.779 ± 0.756	0.239	0.866 ± 0.178	0.126	1.092 ± 0.333	0.625	GTGGATTAGATTCTTGATTCCGATGATTTTGAGCCATCATTAAT	
chromosome	372273	BB_0363	0.673 ± 0.741	0.674	4.224 ± 7.109	0.447	1.279 ± 2.334	0.791	2.320 ± 3.836	0.521	TAGTGGGATTAGATTCTTGATTCCGATGATTTGAGCCATCATTA	
chromosome	373080	IG 35	1.264 ± 0.446	0.494	2.263 ± 0.625	0.014	1.321 ± 0.785	0.613	1.530 ± 0.487	0.229	TGCCAAATTATTAATTAACTTCAACAAAATTATTTACATTGAAAAGGA	
chromosome	373580	BB_0365	<i>la7</i>	1.170 ± 0.388	0.143	1.550 ± 1.102	0.434	0.728 ± 0.273	0.015	1.032 ± 0.302	0.800	TGTTAACGAATTATTTATATTGATTTATAGGCTTAATCTAAATT
chromosome	374015	BB_0365	<i>la7</i>	0.513 ± 0.247	0.103	0.445 ± 0.405	0.341	0.723 ± 0.321	0.258	0.882 ± 0.449	0.343	GAATCATCAGGCTTAGAAGAGTCTCGCCTTCTGCTCCTCAACATATT
chromosome	387433	BB_0377	<i>luxS</i>	0.719 ± 0.315	0.063	1.375 ± 1.084	0.465	0.714 ± 0.254	0.157	0.828 ± 0.397	0.151	TTGTAGAAATTACATTTCAAAGGTATTTCTGAGACATATATGC
chromosome	387491	BB_0377	<i>luxS</i>	1.034 ± 0.646	0.696	1.818 ± 1.961	0.367	0.635 ± 0.443	0.091	0.950 ± 0.512	0.832	TGTATTGCTGCTTCAATTATTGGTCGATGTTGGGAGCTTGTCTA
chromosome	387744	BB_0377	<i>luxS</i>	0.838 ± 0.431	0.293	1.185 ± 0.291	0.269	0.785 ± 0.286	0.012	0.755 ± 0.187	0.266	TGAATCTCTAAATACTTACAAATATTAAACAATATTAAAGAAGAAAATT
chromosome	388124	BB_0378	0.912 ± 0.517	0.818	1.396 ± 1.001	0.147	0.704 ± 0.469	0.219	1.877 ± 1.486	0.131	ATTACCATACATTCTCAGTGAACATGAAACATTTTATTATGAAATAATT	
chromosome	388213	BB_0378	1.566 ± 1.582	0.451	1.635 ± 1.551	0.496	1.742 ± 1.612	0.271	1.666 ± 1.162	0.339	TTTATGTTGGATGATCAAGCATATTGAAGCATTCTCAAATTATTTCATA	
chromosome	388229	BB_0378	0.854 ± 0.429	0.275	1.477 ± 1.513	0.503	0.631 ± 0.356	0.062	0.839 ± 0.537	0.171	TACCAATGAGATTATTTATGTTGGATGATCAAGCATATTGAAGCATT	
chromosome	388328	BB_0378	0.854 ± 0.555	0.746	1.278 ± 1.008	0.728	0.827 ± 1.238	0.738	0.393 ± 0.337	0.334	TCAATTITTCAGTGGAGTGGTGTAAATGTTCTCAAATTAGCATTGG	
chromosome	391873	IG 36	1.204 ± 0.310	0.153	1.008 ± 0.525	0.978	0.436 ± 0.202	0.117	1.049 ± 0.762	0.937	AATAACACATAATTAAAAAAATTAAAAAACTGAGAAAATTAAACATTTCTATT	
chromosome	394232	BB_0384	<i>bmpC</i>	1.412 ± 0.881	0.505	1.863 ± 0.796	0.038	0.595 ± 0.491	0.802	1.159 ± 0.509	0.396	AGGATCCCGATGTTTAAACAAATAGGTTGGTGTGAAGTTATTGATCTAG
chromosome	394997	BB_0384	<i>bmpC</i>	0.450 ± 0.464	0.361	0.481 ± 0.495	0.511	0.668 ± 0.678	0.539	0.479 ± 0.527	0.421	GGGATAATTGGAATAAGCTTATAACTAAATCTTAAAGCCTTATCCTA
chromosome	410663	IG 37		0.768 ± 0.303	0.298	1.079 ± 0.314	0.602	0.791 ± 0.251	0.297	0.871 ± 0.245	0.563	TGACCACAAAAACGTTGAAAAAAATCTTATAATGACCTATAATAATGTT
chromosome	411699	BB_0400		0.813 ± 0.849	0.776	0.676 ± 0.839	0.538	0.406 ± 0.591	0.477	0.819 ± 0.898	0.603	ATATTGGCCTGTAATTCTGTTCCATCCACCTAAAGAAGCTGCTCTT
chromosome	411730	BB_0400		0.393 ± 0.399	0.074	0.665 ± 0.712	0.065	0.897 ± 0.841	0.617	1.212 ± 1.150	0.344	GGTGGATGAAACAGGAATTACAGGCCAATATTACGATTATTGTTAAAT
chromosome	411815	BB_0400		1.254 ± 1.851	0.559	1.079 ± 1.341	0.931	0.218 ± 0.367	0.301	0.891 ± 1.092	0.827	TAGGTATTAAATTACCCCTACCATTTGCTGTTTAAACATCAATTG
chromosome	411817	BB_0400		1.000 ± 0.252	0.998	1.101 ± 0.196	0.520	0.686 ± 0.124	0.118	0.818 ± 0.215	0.408	GGTATTAAATTACCCCTACCATTTGCTGTTTAAACATCAATTGAT
chromosome	412681	BB_0400		0.915 ± 0.497	0.269	1.574 ± 1.373	0.412	0.717 ± 0.279	0.119	0.680 ± 0.322	0.020	GATTGCGCACTTCCATCCAAATGCACTGGATCTGAAATTAGCTATTAA
chromosome	416911	BB_0404		0.757 ± 0.635	0.700	1.059 ± 0.702	0.847	0.809 ± 0.537	0.542	0.949 ± 0.642	0.841	TTTACACTGACTGTATATTGATTTAATCTGTTGTTGAAAGGAT
chromosome	417114	BB_0405		0.719 ± 0.534	0.539	0.786 ± 0.348	0.510	0.567 ± 0.294	0.063	0.694 ± 0.238	0.029	ATAGCATCTTCAATTGAAATTCTCTTTTATTTCATAATTGAAATTAT
chromosome	417567	BB_0405		0.697 ± 0.290	0.160	1.186 ± 0.986	0.758	0.556 ± 0.365	0.202	0.982 ± 0.482	0.935	ATAGAGTACAGCTTCTTAAATTGATGTTGGATTGAAAGCTGTTGCT
chromosome	417570	BB_0405		0.949 ± 0.719	0.938	0.982 ± 0.407	0.953	0.641 ± 0.431	0.140	0.503 ± 0.364	0.281	GAGTACAGCTTCTTAAATTGATGTTGGATTAAAGCTGTTGCTACT
chromosome	417879	BB_0406		0.378 ± 0.736	0.448	0.017 ± 0.027	0.196	0.039 ± 0.070	0.202	0.009 ± 0.008	0.191	ATTTTCTTTCTTTATTCTTAAAGCTTGTGATACAGGTTGGTTGAATC
chromosome	418056	BB_0406		0.789 ± 0.220	0.239	1.480 ± 0.870	0.294	0.799 ± 0.265	0.011	0.913 ± 0.521	0.654	TTGTCCTTAAATTGCTTAAATTGATGTTGGATTGAAAGCTGTTGCT
chromosome	419412	BB_0407	<i>manA</i>	1.735 ± 0.879	0.269	1.821 ± 0.407	0.074	0.002 ± 0.004	0.000	1.982 ± 0.338	0.043	AGATTGATGAAAGCCAAAGGCTGAAATGTCGGCTTGAGGACACAAAGCAT
chromosome	420551	BB_0408		1.773 ± 1.688	0.272	0.777 ± 0.795	0.544	0.094 ± 0.071	0.171	0.838 ± 0.710	0.708	AAGCTTCGGTTGCAACAGGCAAAGGTAGTTTATAATTTAATGAGTG
chromosome	420791	BB_0408		0.814 ± 0.548	0.541	0.945 ± 0.903	0.648	0.002 ± 0.002	0.110	0.722 ± 0.479	0.571	ATGCTATAACCTGCTTCTGCTTCAATTCTTAACTTCTAGCTGAATA
chromosome	421350	BB_0408		1.346 ± 0.380	0.083	1.559 ± 0.605	0.300	0.002 ± 0.003	0.023	0.864 ± 0.260	0.550	CAAGATCTTAAATTAAAAACATAACTGTCGGTCTCTAGTAAT
chromosome	421406	IG 38		0.960 ± 1.099	0.946	1.351 ± 1.763	0.215	0.342 ± 0.398	0.402	0.516 ± 0.816	0.266	TGTTTAATTAGGAGACCACAGTTATTTAAATTGAAAGCTGTTGAA
chromosome	422726	BB_0411		0.453 ± 0.186	0.072	1.163 ± 1.081	0.756	0.689 ± 0.350	0.314	1.250 ± 0.637	0.547	ATTTTCAAGTTTAGCCAATTCCAGAATTAACTCGCTTTTGAGGTG
chromosome	422757	BB_0411		0.767 ± 0.306	0.001	1.193 ± 0.336	0.367	0.738 ± 0.311	0.009	0.821 ± 0.351	0.043	TATCCTTTGAGATTGCCATTCTCTACTAATTTCAGTTCAGGCAA
chromosome	422885	BB_0411		0.417 ± 0.196	0.090	0.834 ± 0.591	0.265	0.386 ± 0.259	0.176	0.998 ± 0.745	0.998	ATCTCTTTATTCTCCAATGAAAAAGCAAAGACTTGGATTGGAAAAT
chromosome	423338	BB_0412		0.761 ± 0.820	0.758	0.668 ± 0.518	0.516	0.619 ± 0.679	0.142	0.615 ± 0.359	0.411	CATTAGACCTTAAATTCTCTGAAGATTTTTAAACAAATCTAA
chromosome	423470	BB_0412		0.427 ± 0.424	0.343	1.117 ± 1.644	0.695	0.547 ± 0.499	0.423	0.584 ± 0.592	0.361	TATAAACTGAGAAAAAATAATTAAATGAAAAAGTGTACAAAAAGG
chromosome	423472	BB_0412		0.839 ± 0.524	0.286	1.043 ± 0.612	0.911	0.759 ± 0.251	0.204	1.015 ± 0.408	0.959	TATATAAACTGAGAAAAAATAATTAAATGAAAAAGTGTACAAAAAGG
chromosome	423539	BB_0412		1.171 ± 0.732	0.032	1.822 ± 0.981	0.242	0.523 ± 0.425	0.041	1.764 ± 1.055	0.010	TATATGCAGGCAAAGTCAAATAATGTAATTGATATTGATTT
chromosome	423554	BB_0412		0.608 ± 0.692	0.078	1.122 ± 1.034	0.818	0.433 ± 0.599	0.316	1.056 ± 0.825	0.932	GGCATTGTAACATATATGCGAGCAAAGTCAAATAATGTAATTGTA

chromosome	423619	BB_0412	0.780 ± 0.533	0.128	1.463 ± 1.488	0.414	0.732 ± 0.425	0.306	1.029 ± 0.733	0.556	TGTAAAATTTGATTTCTATTTAAGAATTCCGTGGTTGGCTATTT	
chromosome	423622	BB_0412	0.800 ± 0.222	0.063	1.346 ± 0.747	0.385	0.854 ± 0.213	0.255	1.013 ± 0.262	0.892	GATGCATTCCTGCTACTTATTAAACAAACTTATAGTAGCCTTTAAAGA	
chromosome	424558	IG 39	0.423 ± 0.135	0.067	0.416 ± 0.382	0.265	0.780 ± 0.436	0.051	0.901 ± 0.497	0.422	TAAACCTATGCTTATAATAAAATTACTTATTAAATTAAACATTTTT	
chromosome	425060	BB_0414	0.470 ± 0.596	0.566	1.056 ± 1.302	0.955	0.216 ± 0.324	0.359	0.848 ± 1.075	0.646	GCATTTGTAECTCAAATCAAAGCTTCCAAAAGAAAATAGATTTGTTATTATT	
chromosome	425806	BB_0415	1.300 ± 0.580	0.077	1.774 ± 1.760	0.567	1.351 ± 0.926	0.531	1.342 ± 0.559	0.050	AACTTTTTCTCCAAAATAGAACATCTTAATATTGTTCTTCTA	
chromosome	425888	BB_0415	1.174 ± 0.672	0.553	1.149 ± 0.578	0.748	0.822 ± 0.369	0.148	0.882 ± 0.469	0.704	AGATCATCGCGGCCCTTGAAGCAGCAATTTATTAGGTTTGATTGAA	
chromosome	426473	BB_0415	0.729 ± 0.303	0.410	0.800 ± 0.275	0.406	0.905 ± 0.301	0.656	0.673 ± 0.242	0.233	GATTGAAATAATACCCAATAGATGGTTGACCATTATGTTACCA	
chromosome	426647	BB_0415	1.050 ± 0.956	0.905	0.903 ± 1.069	0.645	0.203 ± 0.180	0.145	0.510 ± 0.577	0.124	TAGACTATAGTTCCACTAAGCCATATGGTAAATTAAAGCTATAC	
chromosome	431895	BB_0420	<i>hk1</i>	0.066 ± 0.106	0.032	0.094 ± 0.165	0.072	1.736 ± 1.055	0.274	1.002 ± 0.909	0.997	TAATGAAATAACGATAATTCAAGAGGGTATTGACTTGCACAAATAA
chromosome	431973	BB_0420	<i>hk1</i>	0.048 ± 0.080	0.092	0.168 ± 0.194	0.153	1.404 ± 0.888	0.567	0.816 ± 1.028	0.826	GAAGAGCATCCAATAAAATCGAACAGTGTCAAAATTAAAGATTT
chromosome	432429	BB_0420	<i>hk1</i>	0.033 ± 0.057	0.008	0.512 ± 0.503	0.196	0.779 ± 0.211	0.378	0.566 ± 0.516	0.142	AAAGCATTTCTTAAATTAAACTGTTAATTAAACATCA
chromosome	432489	BB_0420	<i>hk1</i>	0.045 ± 0.039	0.007	0.476 ± 0.422	0.100	1.421 ± 0.428	0.166	0.856 ± 0.316	0.536	TAATTAAATAAGTATTAGAATAAGGAAATAATCAATATTCTTCTT
chromosome	434199	BB_0420	<i>hk1</i>	0.172 ± 0.186	0.098	0.717 ± 0.797	0.057	0.773 ± 0.618	0.271	0.919 ± 0.683	0.702	ATATCCTTGGAAAATCCCTAAAATAGGTTAAAGATATGTTGCTT
chromosome	434321	BB_0420	<i>hk1</i>	0.284 ± 0.327	0.136	0.587 ± 0.654	0.082	0.884 ± 0.785	0.787	0.880 ± 0.728	0.563	TCTCCTTTAAAGTTTATTAACTCACAGGGAAAATTGTCGCATTAGT
chromosome	434331	BB_0420	<i>hk1</i>	0.797 ± 1.063	0.679	1.565 ± 2.217	0.609	3.156 ± 4.817	0.466	2.737 ± 3.082	0.270	TATAAACCAACATCAACAAACCTCCCTAGCATGCTATCTAAAAAGAA
chromosome	434333	BB_0420	<i>hk1</i>	0.075 ± 0.138	0.120	0.012 ± 0.023	0.097	0.309 ± 0.371	0.134	0.254 ± 0.338	0.224	TAACCAACATCAACAAACCTCCCTAGCATGCTATCTAAAAAGAAA
chromosome	434643	BB_0420	<i>hk1</i>	0.158 ± 0.216	0.052	0.209 ± 0.205	0.085	1.100 ± 1.310	0.807	0.670 ± 0.569	0.289	ACACCATTTTTGGCTGATAATTCTCAAGAGTTAGTATTGCCCTAAAAA
chromosome	434674	BB_0420	<i>hk1</i>	0.321 ± 0.575	0.092	0.365 ± 0.375	0.010	0.780 ± 0.349	0.469	1.189 ± 0.738	0.350	TATGAAGATATCTAAGGTTAAAAACGTTAACACCATTGGCTGAT
chromosome	435277	BB_r01	<i>5S_rrlA</i>	0.026 ± 0.026	0.025	0.258 ± 0.425	0.184	0.596 ± 0.188	0.186	0.370 ± 0.159	0.060	TCATTCGAACACAGAAGTTAAGCTTATTGCTGATGGTACTGCGAGTT
chromosome	436105	BB_r02	<i>23S_rrlA</i>	0.521 ± 0.180	0.057	0.605 ± 0.147	0.108	0.641 ± 0.291	0.089	0.775 ± 0.358	0.285	TGTGTTAGGATAGGTGGGAGACTTGAAGCTATCTGTCAGGGTAGTGGAG
chromosome	436476	BB_r02	<i>23S_rrlA</i>	0.132 ± 0.231	0.059	0.358 ± 0.401	0.130	0.952 ± 1.600	0.957	0.223 ± 0.203	0.026	GGTCGTAATTCCCGAAGTACGTCAGTATTGAGCTTCTAACGT
chromosome	436798	BB_r02	<i>23S_rrlA</i>	0.101 ± 0.178	0.075	0.061 ± 0.107	0.017	0.413 ± 0.526	0.034	0.039 ± 0.069	0.046	TAAACCGTGGGATCCATCGACTACACTTCACTGGCTTAGGGGCAGAC
chromosome	437188	BB_r02	<i>23S_rrlA</i>	0.411 ± 0.435	0.427	1.094 ± 1.095	0.842	0.452 ± 0.614	0.387	0.889 ± 1.611	0.835	AGGTCCTAAAAATGTGTTAGTGGAAAAGGAGGTTAGGTACGAAACAGC
chromosome	437543	BB_r02	<i>23S_rrlA</i>	0.656 ± 0.335	0.105	0.938 ± 0.406	0.758	0.614 ± 0.250	0.234	0.807 ± 0.427	0.535	AAAGGGCGATTAGTTAGTATGTTAGGTGGTAGACCCGAAGCCGAGTGATCTTTA
chromosome	438349	IG 40	1.137 ± 1.111	0.882	1.355 ± 1.182	0.469	1.268 ± 1.286	0.288	1.854 ± 1.838	0.415	TATTTTATTTTATGTTATTAAACAACACATTAAAAACACCAATATT	
chromosome	438522	BB_r03	<i>5S_rrlB</i>	0.029 ± 0.025	0.041	0.280 ± 0.447	0.220	0.568 ± 0.240	0.247	0.385 ± 0.148	0.069	TCATTCGAACACAGAAGTTAAGCTTATTGCTGATGGTACTGCGAGTT
chromosome	439350	BB_r04	<i>23S_rrlB</i>	0.511 ± 0.172	0.045	0.615 ± 0.150	0.101	0.643 ± 0.296	0.084	0.773 ± 0.348	0.256	TGTGTTAGGATAGGTGGGAGACTTGAAGCTATCTGTCAGGGTAGTGGAG
chromosome	439721	BB_r04	<i>23S_rrlB</i>	0.166 ± 0.289	0.042	0.409 ± 0.357	0.060	0.975 ± 1.510	0.979	0.212 ± 0.203	0.019	GGTCGTAATTCCCGAAGTACGTCAGTATTGAGCTTCTAACGT
chromosome	440043	BB_r04	<i>23S_rrlB</i>	0.248 ± 0.448	0.241	0.072 ± 0.129	0.057	0.519 ± 0.677	0.080	0.115 ± 0.209	0.135	TTAACCGGTTCCCATCGACTACACTTCACTGGCTTAGGGGCCAG
chromosome	440433	BB_r04	<i>23S_rrlB</i>	0.337 ± 0.346	0.295	1.053 ± 0.993	0.917	0.456 ± 0.687	0.373	0.834 ± 1.419	0.758	AGGTCTAAAAATGTGTTAGTGGAAAAGGAGGTTAGGTACGAAACAGC
chromosome	440788	BB_r04	<i>23S_rrlB</i>	0.660 ± 0.339	0.083	0.951 ± 0.397	0.773	0.603 ± 0.238	0.228	0.784 ± 0.399	0.476	AAAGGGCGATTAGTTAGTATGTTAGGCTAGACCCGAAGCCGAGTGATCTTTA
chromosome	442346	BB_0421	0.555 ± 0.700	0.629	0.651 ± 0.879	0.712	0.595 ± 0.733	0.665	0.990 ± 0.961	0.991	ATTTCATTAACATAATTCTTAAATTGGCTCTTATTTAACTTC	
chromosome	442356	BB_0421	1.011 ± 0.697	0.983	0.864 ± 0.521	0.638	1.141 ± 0.984	0.861	1.011 ± 0.824	0.988	TTAATGAAAATTATCTGTAACGGCGAATGGGGCTGAAGTGTGTCAG	
chromosome	442646	IG 41	0.879 ± 0.199	0.337	1.273 ± 0.886	0.554	0.655 ± 0.221	0.006	0.977 ± 0.459	0.905	TATTTTAAACAAATTAAACAAACATCAACGGCTTCTTGGCTTAGGGGCCAG	
chromosome	443012	BB_0422	0.817 ± 0.214	0.152	1.829 ± 1.178	0.269	0.772 ± 0.236	0.085	0.876 ± 0.338	0.662	ATGCATACCATATTATACACATAAGAACATCTCTTCTATCAT	
chromosome	443028	BB_0422	0.871 ± 0.794	0.767	1.653 ± 0.894	0.025	0.390 ± 0.236	0.160	1.380 ± 0.977	0.380	TAATATGTTAGTACATTATGTTAACGTTGTACTGCAGATAAAATA	
chromosome	443190	BB_0422	1.081 ± 0.671	0.661	1.253 ± 1.449	0.713	0.719 ± 0.309	0.191	1.051 ± 0.390	0.835	ATTGTTGATCAGAAAGTCGACAAAGGAGGAATAGTACGAGATTGTTG	
chromosome	443217	BB_0422	0.687 ± 0.512	0.063	0.941 ± 0.600	0.699	0.258 ± 0.232	0.076	0.680 ± 0.360	0.341	CTACCGTGTGCAAAGTATTGCTTGTAAATTGTTGATCAGAAAGTCGACA	
chromosome	444299	IG 42	1.157 ± 0.760	0.643	1.861 ± 1.331	0.420	1.888 ± 1.286	0.310	1.666 ± 0.867	0.208	AAAACATACATTAAACATTAGGGCATAAGCCAAATGGAGGTTAGGG	
chromosome	448245	BB_0429	0.843 ± 0.189	0.360	1.314 ± 0.870	0.493	0.659 ± 0.146	0.095	0.844 ± 0.197	0.363	TAACACCTCTGGGATTCTAACGTTCAACAGCTTCTGCCCCGTC	
chromosome	450091	BB_0431	0.762 ± 0.736	0.704	1.748 ± 0.670	0.037	0.581 ± 0.423	0.108	1.171 ± 0.393	0.561	TATGAATATGACAAGGAAAGGCAATGCTGCAAAAGATTAGGCTCTCA	
chromosome	450978	IG 43	1.196 ± 0.856	0.752	1.430 ± 0.650	0.435	0.342 ± 0.140	0.109	1.333 ± 1.316	0.707	TTTGTAGTTAAATTAAAAGTAAAAAATATTTAAAAAATGACAATA	
chromosome	470334	BB_0450	<i>rpoN</i>	0.505 ± 0.279	0.112	0.667 ± 0.335	0.281	0.462 ± 0.170	0.068	0.800 ± 0.228	0.356	CATTGCAAAAAGAATTCTAAGAAGAGGATTTAAAGCTTAAAGCCAATGA
chromosome	470340	BB_0450	<i>rpoN</i>	0.926 ± 0.963	0.589	1.262 ± 1.815	0.691	0.658 ± 0.620	0.399	0.760 ± 0.584	0.614	TATATACATTGCAAAAAGAATTCTAAGAAGAGGATTTAAAGCTTAAAGGC
chromosome	470344	BB_0450	<i>rpoN</i>	0.387 ± 0.382	0.169	0.946 ± 1.423	0.957	0.507 ± 0.224	0.004	0.424 ± 0.262	0.133	GCTATATACATTGCAAAAAGAATTCTAAGAAGAGGATTTAAAGCTTAA
chromosome	470961	BB_0450	<i>rpoN</i>	1.244 ± 1.932	0.571	0.760 ± 1.454	0.043	0.169 ± 0.355	0.248	0.838 ± 1.524	0.221	CTTCTTAAAGAACACCTTTACTGCAATTAGAACAGAATAATG
chromosome	470986	BB_0450	<i>rpoN</i>	0.820 ± 0.322	0.491	1.387 ± 0.467	0.200	0.689 ± 0.130	0.142	0.873 ± 0.480	0.637	GCTCTGAAAAACACAAACAAACTCTTTAAAAGAACACCTTTACTG
chromosome	473038	BB_0453	0.718 ± 0.219	0.294	1.077 ± 0.802	0.816	0.523 ± 0.264	0.004	0.812 ± 0.307	0.104	ACAAAGAAATTAAACACAGTAAGCTTACATCCAATTGGTTG	
chromosome	480445	BB_0459	1.193 ± 0.991	0.724	1.485 ± 1.425	0.454	0.807 ± 0.346	0.574	0.454 ± 0.213	0.106	AAGCTTAAATTCTCTAATTTACAGTCACATATGCAATTG	

chromosome	481500	BB_0460	0.815 ± 0.885	0.832	3.126 ± 3.824	0.384	0.642 ± 1.129	0.632	0.989 ± 0.961	0.990	TCTTGGAAAGATTGTTGAATTTCCTTCAATTCTTTGACTGTGTTT
chromosome	481558	BB_0460	0.897 ± 1.063	0.884	1.200 ± 1.206	0.835	0.534 ± 0.432	0.397	1.110 ± 1.137	0.856	ACATAAAAAACTTTAATTCTACTATTAGCTGTTCTTTAACGTTTATT
chromosome	481910	BB_0460	0.461 ± 0.345	0.166	0.652 ± 0.669	0.538	1.150 ± 0.701	0.705	0.912 ± 0.797	0.808	TATGGAGAAATATTATTGTTTGAGTATTTCATTTCTTGATATTTTAG
chromosome	485312	IG 44	0.904 ± 0.559	0.740	2.753 ± 2.126	0.276	0.839 ± 0.376	0.666	1.432 ± 0.716	0.372	AGGGTAATTACAACCTATTCTTTAAGAGAGATAGACTTATAAAAATTAAC
chromosome	492227	IG 45	0.821 ± 0.601	0.421	0.629 ± 0.423	0.295	0.399 ± 0.435	0.275	0.501 ± 0.524	0.056	AAAATAAAAATCAGAAACCTCTCGCAAATTTCATCAATCT
chromosome	494403	BB_0475	0.858 ± 0.522	0.681	1.233 ± 1.202	0.704	0.675 ± 0.414	0.178	0.731 ± 0.483	0.530	GCACTATAAAAATCAACAAAAAGTAGAAAATGAAACTACAAATCCGACA
chromosome	494479	BB_0475	1.147 ± 1.135	0.838	0.306 ± 0.255	0.026	1.130 ± 0.941	0.805	1.047 ± 0.411	0.810	ATTGTTTTATGTCATGAAAACAAGCACAATAAACTAAAAGAAAAT
chromosome	494783	IG 46	0.671 ± 0.380	0.192	1.098 ± 0.601	0.821	0.789 ± 0.441	0.509	0.759 ± 0.343	0.492	TATGTGAGTGAATTGAGTTAAAGAGTTAAGCTATTAGTACTATATTG
chromosome	511099	BB_0505	0.176 ± 0.176	0.149	0.551 ± 0.610	0.207	0.386 ± 0.588	0.351	0.599 ± 0.517	0.379	TGTTGCTTATTAGTAATCATTTTTGCAATTAGAATACACATGATT
chromosome	511102	BB_0505	0.176 ± 0.183	0.269	0.478 ± 0.924	0.609	0.875 ± 0.867	0.839	0.489 ± 0.733	0.590	TATCTAAAGCCAATAATTTCAGATTGTTAGATGGCATGGTATTG
chromosome	511104	BB_0505	0.323 ± 0.300	0.213	0.680 ± 0.691	0.501	0.940 ± 0.448	0.885	0.467 ± 0.357	0.060	TCTTAAAGGCCAATAATTTCAGATTGTTAGATGGCATGGTATTG
chromosome	511389	BB_0505	0.506 ± 0.392	0.189	0.746 ± 0.808	0.078	1.031 ± 0.884	0.832	1.059 ± 0.954	0.142	TGACTCAAGATGAGAAGAATATTGTCAAAGGGGACAGCCTATATTAGTG
chromosome	511426	BB_0505	0.459 ± 0.327	0.044	0.792 ± 0.869	0.687	2.016 ± 1.817	0.282	1.188 ± 0.761	0.148	GGCTGCCCCCTTGACAATATTCTTCATCTGAGTCATAACATGGATG
chromosome	511429	BB_0505	0.594 ± 0.268	0.012	0.762 ± 0.682	0.531	0.901 ± 0.199	0.513	0.846 ± 0.191	0.279	TATTAGTGATATTGGGATGACAGGTGGATTAAATTCTGAATAGGATTAA
chromosome	511431	BB_0505	0.489 ± 0.263	0.045	0.719 ± 0.674	0.216	1.040 ± 0.650	0.730	0.933 ± 0.517	0.206	TTAGTGATATTGGGATGACAGGTGGATTAAATTCTGAATAGGATTAA
chromosome	511578	BB_0505	0.351 ± 0.322	0.078	0.727 ± 0.793	0.150	0.914 ± 0.821	0.346	0.758 ± 0.647	0.256	ATTTAAAGACAGGCCGCCTTAAATTGAAAGGATTGAGAAATAATT
chromosome	527312	IG 47	1.302 ± 1.502	0.713	5.557 ± 6.761	0.350	0.491 ± 0.706	0.349	2.387 ± 3.590	0.501	ATAAAAAACTATTTAAAAAAATTCTCAACTCAACAGATGCAATAACCCCCT
chromosome	527735	BB_0516	0.990 ± 1.458	0.954	1.346 ± 1.278	0.605	0.423 ± 0.513	0.260	1.562 ± 1.689	0.382	GATCTGTAATTACTACTCAAAACGCGCAGAGACAATTCAACAGTT
chromosome	531910	IG 48	0.885 ± 0.575	0.073	1.490 ± 1.345	0.378	0.673 ± 0.338	0.156	1.050 ± 0.563	0.456	TAAGAATATTGGTATCATTTTGATTGTTGTTAGTCTTTAGTGTTT
chromosome	533659	IG 49	0.686 ± 0.891	0.609	1.176 ± 1.606	0.836	0.929 ± 1.086	0.816	1.810 ± 2.064	0.417	TTAATAATATTGGTGGAAAAATTGAAAGAAATGCTTTAGTAAAAA
chromosome	533745	IG 50	1.496 ± 1.401	0.632	1.306 ± 0.980	0.656	1.025 ± 0.609	0.963	2.124 ± 1.308	0.237	TGTCTTATTAAACAGATTAAAGGTTAAAGGTTAACTTTAATTCTAA
chromosome	533790	IG 51	1.166 ± 0.579	0.705	1.125 ± 0.809	0.854	0.679 ± 0.404	0.361	1.175 ± 0.790	0.608	TTAATATTATTAAATTTTATGTTGACAGCTTAAATAACACAAGTCCTT
chromosome	533824	IG 52	0.362 ± 0.297	0.220	0.591 ± 0.472	0.510	0.235 ± 0.200	0.167	0.923 ± 0.771	0.898	AATAACACAACTTTTAAGTGTAAATCATGTCATAATTATTATTG
chromosome	534361	BB_0524	2.852 ± 1.778	0.007	2.855 ± 2.793	0.217	1.542 ± 1.549	0.652	2.602 ± 1.906	0.039	AGTGGTTGCTAAATTAAATTAGATTAAATCTGATGGGTCTATTGTA
chromosome	534851	BB_0524	1.406 ± 1.927	0.611	0.102 ± 0.187	0.076	0.951 ± 1.010	0.886	0.758 ± 1.390	0.675	TGAGAAGAAATATCAAGATTAACCTTATAATAGACCTGAAACTGCA
chromosome	535234	BB_0525	1.136 ± 0.346	0.568	1.664 ± 0.925	0.398	1.094 ± 0.382	0.755	1.021 ± 0.474	0.884	GCTTGTGAGGTCAGCTGAAATTATTGTAAGCATTAAATGGAT
chromosome	538411	BB_0528	0.698 ± 0.085	0.045	0.959 ± 0.150	0.524	0.801 ± 0.180	0.141	0.809 ± 0.229	0.249	CTTTATCATTAATTCTGCTTAAATGTAATTACGTTGATTCTACATAAT
chromosome	539372	BB_0530	1.533 ± 1.687	0.555	0.830 ± 0.981	0.855	0.373 ± 0.551	0.450	0.496 ± 0.614	0.372	GTTTGTTAATTATTGGCAATTTCCTTAAATTCTTAAATCTTATTCT
chromosome	539539	BB_0530	0.547 ± 0.247	0.133	1.150 ± 0.625	0.748	0.885 ± 0.470	0.544	1.043 ± 0.481	0.863	AATAGTTTGAAGCAATGCTTGTATGAGTATCATTGGCACTATAAGC
chromosome	539787	BB_0530	0.393 ± 0.187	0.067	0.582 ± 0.372	0.113	0.641 ± 0.625	0.335	0.607 ± 0.547	0.420	TTATAAAAACCAAGATTAACTACTGATGAGTAAATTAAAGCATAT
chromosome	540125	BB_0530	0.717 ± 0.367	0.057	1.247 ± 0.734	0.428	0.938 ± 0.514	0.794	1.253 ± 0.317	0.127	TCCTAAACATTAACAAAAAAATTATCATCTGATCCTTGAATTCT
chromosome	540183	BB_0531	0.784 ± 0.744	0.717	0.272 ± 0.317	0.042	0.816 ± 0.737	0.711	1.384 ± 0.969	0.546	TTCTAATAGTTCTAATATTTTAAAGTTTTGTCGAAAGTTGTC
chromosome	541213	BB_0532	0.719 ± 0.444	0.558	0.844 ± 0.663	0.026	0.658 ± 0.410	0.502	0.769 ± 0.542	0.242	GATGCAATATCAGCTTTCTATTAAGGATATTGGCAGGCTCAATTAAATAG
chromosome	541438	BB_0532	1.427 ± 1.013	0.589	1.423 ± 1.229	0.661	1.200 ± 0.917	0.779	1.379 ± 2.128	0.552	AGTAAAACAGAAATCATATAGTTTGGTATTGCTAATAAGGGTTTTA
chromosome	544951	BB_0536	0.979 ± 0.679	0.951	1.239 ± 1.271	0.525	0.622 ± 0.616	0.024	0.842 ± 0.837	0.221	ATAAGTGAATCAAACACTAGTAGCAGCATTATGTCAGCACCAATTGCA
chromosome	545430	BB_0536	0.518 ± 0.680	0.620	0.284 ± 0.575	0.473	0.492 ± 0.585	0.444	1.386 ± 1.482	0.603	GGCTCTTCAACTCCAAATCTCTAAAGTAAACAAATTCTTAAAGCT
chromosome	547074	BB_0536	1.176 ± 1.161	0.692	2.295 ± 2.779	0.137	0.834 ± 0.869	0.655	0.891 ± 0.998	0.690	CTACCGAGCTAAGGAGCTGGACATGCTTAAATTCTTAAATCGCTATA
chromosome	548301	BB_0537	0.818 ± 0.224	0.324	1.077 ± 0.406	0.491	0.564 ± 0.179	0.058	0.845 ± 0.248	0.307	TTGTCCTAGCATCTAAGTTACTAGGATTAGTCGAATTCTCTAAGCT
chromosome	553011	BB_0542	0.892 ± 0.471	0.358	1.080 ± 0.713	0.594	0.768 ± 0.526	0.166	0.845 ± 0.825	0.600	AGAGTTAATTTTAAGTTTTGTTACTTTGCTTGTGAAATTCTTAA
chromosome	562118	IG 53	0.992 ± 1.098	0.989	0.528 ± 0.532	0.407	0.600 ± 0.389	0.171	1.246 ± 0.923	0.714	GTAAAGTCGGTTTTGCTTGTGAAATTGTTGATAAAAATATAAGAATA
chromosome	562121	IG 54	0.536 ± 0.232	0.029	0.512 ± 0.421	0.343	0.736 ± 0.278	0.100	0.936 ± 0.422	0.049	AGTCGGTTTTGCTTGTGAAATTGTTGATAAAAATATAAGAATGTT
chromosome	564192	BB_0553	0.843 ± 0.851	0.817	1.136 ± 1.186	0.828	0.151 ± 0.082	0.079	0.101 ± 0.180	0.125	AATAAAAATAACACTTTATCCAACATACTAAGTAACTTTTATGCTT
chromosome	564240	BB_0553	1.262 ± 1.450	0.314	1.500 ± 1.640	0.175	0.680 ± 0.672	0.409	0.918 ± 0.848	0.838	ATTCTCTAGTCGGATATTTCAGCTTAAAGTTCTAAACAAATTCT
chromosome	564404	BB_0553	1.095 ± 0.174	0.520	1.212 ± 0.521	0.586	0.911 ± 0.280	0.524	0.983 ± 0.237	0.923	CTATATTGAAATAGATCCCACTAACATTAAATGAGGCTTAAAAATCA
chromosome	564472	BB_0553	0.986 ± 0.409	0.887	1.442 ± 0.704	0.445	0.750 ± 0.176	0.217	0.987 ± 0.320	0.867	TGTCAGGGTAGATTGAAAATCTGCTGTTTTATCATAGTTGTTTGGGG
chromosome	564832	BB_0553	0.634 ± 0.222	0.090	1.352 ± 0.236	0.121	0.512 ± 0.435	0.179	0.796 ± 0.456	0.545	AAAAGAAAAATCAGCGCAATGAAGCAATAACAAAGAAAATCAAAAAAA
chromosome	565683	IG 55	0.771 ± 0.157	0.106	1.025 ± 0.500	0.952	0.320 ± 0.108	0.008	0.667 ± 0.161	0.027	AGGTCTTGTGTTTCAAGAAAACATCTATAATTATAATGTTAGCATA
chromosome	565712	IG 56	1.527 ± 0.618	0.332	1.389 ± 0.730	0.483	0.812 ± 0.204	0.281	1.065 ± 0.337	0.267	TAGATGTTTCTGAATAAAAACAGGACCTTATGAATAACAAACAAAATCG
chromosome	565713	IG 57	0.964 ± 0.874	0.826	1.117 ± 0.947	0.753	0.976 ± 0.489	0.941	0.867 ± 0.680	0.581	TAATTATAATGTTAGCATAATTGTCCTATTATGTCACAAAGAGATAAAATA

chromosome	566271	BB_0554	1.710 ± 1.947	0.536	1.722 ± 2.066	0.194	1.523 ± 1.434	0.519	1.247 ± 1.531	0.168	GTTATTCTCTGGATTACAAGAAAGACTGGAACCTGCAATGTTTGA
chromosome	566514	BB_0554	0.288 ± 0.325	0.140	1.197 ± 1.567	0.879	0.846 ± 1.405	0.898	0.225 ± 0.270	0.127	GACCACTAATTACAAGAGAAATTATTTTATTGTCTTACTTACACCA
chromosome	567281	BB_0554	0.266 ± 0.338	0.397	0.948 ± 1.141	0.852	0.541 ± 1.071	0.705	0.923 ± 1.062	0.939	ATACACTCTCGCTTACAAAAAATTACACTGCTATAAGGCAAGCCCCAGTG
chromosome	567598	BB_0554	0.749 ± 0.419	0.167	0.914 ± 0.547	0.451	0.638 ± 0.452	0.028	0.929 ± 0.540	0.383	ATCAACCGCTAACCAAATATTGTGCGAATTCTCTGTATTAACTTAAAG
chromosome	567801	BB_0554	0.718 ± 0.263	0.239	0.871 ± 0.368	0.557	0.635 ± 0.272	0.130	0.773 ± 0.291	0.188	CTCCAACTATTAAAATTCTCAAATCAAGGGCGTTTGCTTCATTA
chromosome	567987	BB_0555	0.759 ± 0.207	0.132	1.639 ± 1.254	0.490	1.099 ± 0.723	0.846	0.827 ± 0.203	0.392	AATCAGAATAAACAAAGTTGAATCCAATAAAATTAAAAAAATCTGTTAT
chromosome	568020	BB_0555	0.602 ± 0.108	0.022	0.965 ± 0.187	0.710	0.625 ± 0.102	0.041	0.778 ± 0.211	0.033	CATTCCGACCATTAAAATAAAAGCGGGAATTAAATCAGAATAAACAGTT
chromosome	568210	BB_0555	0.346 ± 0.209	0.101	0.777 ± 0.221	0.195	0.226 ± 0.150	0.038	0.288 ± 0.113	0.043	CAATTACATTTAATGACTTTCTATAGCTTAAATATCTGATTGCTTACA
chromosome	568222	BB_0555	0.436 ± 0.218	0.096	0.898 ± 0.792	0.815	0.526 ± 0.376	0.110	0.807 ± 0.386	0.285	ATACTTTTATCTTTATTGAAAGCTGAAGAATTGTATAGAAAAAAATG
chromosome	568582	BB_0556	0.434 ± 0.135	0.052	0.265 ± 0.341	0.168	0.461 ± 0.133	0.054	0.908 ± 0.306	0.740	AATATATTATCATTAATTTGAAATAATTCAAAAACAACCTGGAA
chromosome	568718	BB_0556	0.785 ± 0.269	0.393	0.695 ± 0.234	0.097	0.658 ± 0.105	0.076	0.651 ± 0.188	0.112	TAAGCACTAAAAACATAAGTTTTGGTAAACATTAAACTCAATT
chromosome	568739	BB_0556	1.227 ± 1.067	0.779	2.758 ± 1.016	0.020	0.448 ± 0.316	0.272	0.579 ± 0.780	0.417	TATTCACTCTATTAAATTATAAGCACTAAAAACATAAGTTTTGGTT
chromosome	568772	BB_0556	0.969 ± 0.299	0.764	1.390 ± 1.031	0.445	0.710 ± 0.197	0.247	0.819 ± 0.365	0.027	AATTAAATTCTCAATGATGATTATTGAAACAGAAGCTTTTATCATAAA
chromosome	575962	IG 58	0.915 ± 0.349	0.714	1.129 ± 0.566	0.051	0.693 ± 0.269	0.254	0.847 ± 0.327	0.496	AAAAGTTTAAAAAGAACAAATTGTTGAAAATCAAACCGAGCTCCAAAA
chromosome	576237	BB_0563	1.042 ± 1.316	0.886	1.561 ± 2.387	0.302	0.797 ± 0.927	0.785	1.177 ± 1.535	0.650	ATATTGGATTTCAGTTGGCGCAGGGGATATGGAACATATGGTTT
chromosome	576257	BB_0563	1.789 ± 1.096	0.086	0.724 ± 0.494	0.148	1.368 ± 0.725	0.260	1.729 ± 1.799	0.393	CACATCCCAGGAGCTGCTAATATTGGATTTCAGTGGCGCAGGGGG
chromosome	576318	BB_0563	0.959 ± 0.691	0.908	1.390 ± 1.177	0.673	0.339 ± 0.562	0.420	0.607 ± 0.490	0.399	TTTACTCCGCTGTAAGACCAATGTCAGATCAAAGTTCCTATATTAAATC
chromosome	576468	BB_0563	0.012 ± 0.021	0.095	1.627 ± 1.062	0.162	0.443 ± 0.608	0.402	0.585 ± 0.581	0.292	TTATTTATTAGCCCCAATCTCAGGATTCTAATTCAAAGAATCTGCAA
chromosome	576510	IG 59	0.730 ± 0.201	0.120	1.260 ± 0.399	0.295	0.913 ± 0.270	0.643	1.345 ± 0.452	0.399	TCTCCTAAAGTAGCATTCTAGCCTTAAAGAATTAGTCCAATATT
chromosome	576571	IG 60	1.582 ± 0.590	0.223	1.971 ± 1.091	0.247	1.135 ± 0.628	0.793	1.389 ± 0.524	0.080	AAAAGTAAACATATCTTAAAGAGAGCCTTTATCCAAATAGAAAAGTTA
chromosome	577481	BB_0565	0.886 ± 0.467	0.793	1.792 ± 1.652	0.475	0.359 ± 0.261	0.135	1.387 ± 0.726	0.399	TGTTGTTGAGGTTTAAAGATATAAGATATCAAACATCCAGGACTCC
chromosome	577911	BB_0565	0.964 ± 0.129	0.471	1.284 ± 0.531	0.477	0.738 ± 0.159	0.083	0.965 ± 0.325	0.864	TATGATCTGAAATATCAGCAGCAATAGGAGTTTGTATGTTAGG
chromosome	577944	IG 61	1.254 ± 0.368	0.311	0.882 ± 0.604	0.732	0.889 ± 0.659	0.816	0.549 ± 0.467	0.289	AAAACCTCTATTGCTGCTGATATTCCAGGATCATATTTGTTGATTCTAA
chromosome	578116	BB_0566	0.887 ± 0.352	0.744	2.590 ± 1.964	0.235	0.788 ± 0.329	0.204	1.668 ± 0.963	0.217	TTAGATGCATACAAAATTGTTATAAAAGTAATATCTATTTCACATT
chromosome	579080	BB_0567	0.718 ± 0.534	0.546	1.068 ± 0.569	0.853	0.618 ± 0.418	0.128	0.802 ± 0.315	0.550	TTAGAGGCAAATGAAGGTGATAATGTAGAGTCTAAAATTTCATTGTT
chromosome	579274	BB_0567	0.895 ± 0.166	0.332	1.396 ± 0.748	0.331	0.718 ± 0.136	0.112	0.962 ± 0.261	0.166	ATACTAGCAATATTAACTCTGCTCTAGCAGTATCATCTGAATTAGAT
chromosome	579331	BB_0567	0.350 ± 0.143	0.064	0.529 ± 0.183	0.140	0.535 ± 0.167	0.033	0.810 ± 0.261	0.509	CAATACAATCAAACCTTCAAAAGAAGCTGAAATAGGAATAGTAATTT
chromosome	580054	BB_0567	0.127 ± 0.167	0.133	0.644 ± 0.631	0.601	0.459 ± 0.320	0.285	0.653 ± 0.328	0.254	AAATGCTCATCTTACTCTAACAAAGCCAACCTCAATAATAGCCAAAGTC
chromosome	580495	BB_0568	0.969 ± 0.664	0.941	1.680 ± 2.031	0.599	0.845 ± 0.651	0.747	1.008 ± 0.653	0.986	TTAGTAATTGATATTCAAGGCTTATAAGCAGGTTTGTAGAGCTTT
chromosome	580783	BB_0568	0.749 ± 0.391	0.037	1.257 ± 1.124	0.609	0.566 ± 0.296	0.025	0.728 ± 0.316	0.039	ATTAACCTTCTTCTGCTTCAAGACATCCAAAATTGGTAACATT
chromosome	581300	BB_0568	0.767 ± 0.660	0.513	1.050 ± 0.744	0.926	0.718 ± 0.578	0.350	0.929 ± 0.817	0.917	GCAATTATCAAAAGCTGGAGCAAGATGTCTCATCTCAGCTTCTTA
chromosome	581359	BB_0568	0.872 ± 0.475	0.685	1.318 ± 0.571	0.468	1.021 ± 0.607	0.921	1.513 ± 0.963	0.173	ATAGTTTACAAAATAATTCCGCTACTATATTTCACAAATGATAAC
chromosome	581378	BB_0568	0.832 ± 0.765	0.792	0.970 ± 0.642	0.904	0.605 ± 0.687	0.183	0.519 ± 0.340	0.308	GTAGACATAAGCCTCTGTAATGACTTTAGGCTGCTGCAATGTATG
chromosome	582416	BB_0569	0.692 ± 0.281	0.212	1.279 ± 0.517	0.410	0.772 ± 0.325	0.038	1.059 ± 0.455	0.863	AATATTATGTTCTAATATTGATGTTTAAATTAGAGATATAAGTGAG
chromosome	583086	BB_0569	0.789 ± 0.869	0.229	1.798 ± 1.731	0.379	0.627 ± 0.604	0.620	0.508 ± 0.589	0.108	TTGATAATATTGCTTATGAGTTTTCAATTGAATTATGGAAATAT
chromosome	583193	BB_0569	0.743 ± 0.320	0.398	0.996 ± 0.927	0.993	0.671 ± 0.468	0.150	1.167 ± 0.589	0.638	GATATAGATAACTTTTAAAGCAATATGGAAGCAAATAATTCAATCTT
chromosome	583308	BB_0569	1.235 ± 0.992	0.010	1.730 ± 1.952	0.372	1.148 ± 1.194	0.533	0.819 ± 0.573	0.712	GAATTGCTATCTGTTTACATTGTTCATAAAAAAACACTTATTATCT
chromosome	583406	BB_0569	1.000 ± 0.758	1.000	2.044 ± 1.944	0.357	0.995 ± 0.690	0.990	1.255 ± 0.602	0.590	ATTTGTTTAAATTCTAATATTGATGTTTAAATTAGAGATATAAGTGAG
chromosome	583497	BB_0570	0.853 ± 0.533	0.702	1.187 ± 0.989	0.793	0.494 ± 0.320	0.347	0.847 ± 0.499	0.646	TTGCCCTATTGTCATCAAACCAAATTCTTCTCATCTAATTCTC
chromosome	583575	BB_0570	1.084 ± 0.785	0.877	1.059 ± 0.478	0.890	0.573 ± 0.434	0.377	0.854 ± 0.316	0.466	AAACCCCTTCTAAACCATCTTGTCTGAGACTCCAAAACCGTTTGT
chromosome	583677	BB_0570	1.140 ± 0.503	0.510	1.708 ± 0.743	0.151	1.051 ± 0.486	0.729	1.404 ± 0.604	0.040	TCTGCTTAAACCCCAATGCCGCTAAATTAGGCATGTTGATCTGAA
chromosome	589848	BB_0576	1.328 ± 1.017	0.671	3.086 ± 2.384	0.279	1.125 ± 0.588	0.769	1.614 ± 0.901	0.345	TATCGTTTAAATTGCTGAGCTAAAGGCAAGGCCAGTTGCTAGATA
chromosome	589892	BB_0576	1.447 ± 0.958	0.524	1.202 ± 0.598	0.432	0.790 ± 0.320	0.228	1.033 ± 0.584	0.932	GCATAACTTGGCTTGCCTTAGCTTACCCAAAGTAATAACAGCATATACT
chromosome	589958	BB_0576	0.412 ± 0.325	0.082	0.421 ± 0.383	0.333	0.191 ± 0.228	0.048	0.685 ± 0.782	0.336	GTAAGAGTTATTAGATGTTGAATAATTGATAAGGAGCATTATTTAAA
chromosome	590202	BB_0576	0.910 ± 0.433	0.508	1.293 ± 1.061	0.445	0.828 ± 0.503	0.348	1.001 ± 0.485	0.994	ATCAAATTCTGCTCAATATTAAATTAAATTAGTCAGCATGACT
chromosome	590247	IG 62	0.560 ± 0.278	0.123	0.281 ± 0.255	0.133	0.933 ± 0.393	0.813	0.732 ± 0.374	0.109	ATTATAATTAAATTCTGCGAAATGAAAGGGAAAATTATGTTAATCAA
chromosome	590480	BB_0577	0.861 ± 0.270	0.034	1.436 ± 1.079	0.473	0.936 ± 0.258	0.744	0.930 ± 0.223	0.414	CTTCTCAATCTTGTGAAATTGCAAAATCTCCTTTAATAAGCAATAT
chromosome	590768	BB_0577	0.670 ± 0.267	0.135	1.449 ± 1.129	0.432	0.500 ± 0.209	0.087	0.791 ± 0.394	0.520	CTGTAATAATTATCATCTGCTGAGGATAACTTTTGGGTTGCCAAA
chromosome	590975	IG 63	1.026 ± 0.779	0.924	0.886 ± 0.350	0.739	0.674 ± 0.326	0.078	0.819 ± 0.419	0.615	ATTAAATTAAATTAAATTAAACTTAATTAAATTAAATTACTCTTCTT

chromosome	591289	BB_0578	0.890 ± 0.265	0.114	1.351 ± 0.687	0.303	0.731 ± 0.205	0.096	1.109 ± 0.335	0.286	TAAGGCTCTGTTAAGGAATGCTAAAGGGATTATCATACCAAGCTC	
chromosome	591897	BB_0578	1.052 ± 1.124	0.944	0.233 ± 0.403	0.094	0.500 ± 0.411	0.169	0.603 ± 0.566	0.359	ATATGGCTTATTATTCAAGAACCTGTGATTCTTGATTGGCTGTGACTT	
chromosome	592427	IG 64	0.689 ± 0.802	0.683	0.986 ± 1.095	0.983	0.219 ± 0.320	0.188	1.107 ± 0.826	0.789	AAAATTAAAAAGTCATAATAATTTTAAATCTCTAATTAAATTATTGCA	
chromosome	596069	BB_0580	1.276 ± 1.533	0.582	1.001 ± 1.293	0.995	1.170 ± 1.287	0.227	1.200 ± 1.905	0.660	CATGTTGTCACAGAACCATTTTATCTTTTAGAAAAAATTCCCTTTT	
chromosome	596205	BB_0580	0.463 ± 0.383	0.191	0.395 ± 0.393	0.392	0.726 ± 0.663	0.191	0.906 ± 0.881	0.106	AGCTTTCTACATTATTATTTATTCACTGTTGAAGTTGGGAGATATT	
chromosome	597029	BB_0581	<i>recG</i>	1.204 ± 0.497	0.559	1.822 ± 1.322	0.424	0.453 ± 0.299	0.193	0.863 ± 0.557	0.026	ATGAAATTCTTGGACGTTAACCTCTGTCAAAGAAATAAACCGGAAGAA
chromosome	597792	BB_0581	<i>recG</i>	0.833 ± 0.449	0.213	1.644 ± 2.139	0.598	0.920 ± 0.636	0.595	0.732 ± 0.935	0.543	TTCTCTAGAAGTTGCTTAACACTTTGGTGTCTGAAGTTTCGTTA
chromosome	598014	BB_0581	<i>recG</i>	0.424 ± 0.404	0.052	0.471 ± 0.659	0.041	0.520 ± 0.338	0.347	1.128 ± 0.973	0.572	TTATTAACATCTTTAATTCAAATTCTGAAGATGAAATTATGGATAA
chromosome	598564	BB_0581	<i>recG</i>	0.819 ± 0.721	0.590	2.004 ± 2.214	0.299	0.445 ± 0.628	0.395	0.987 ± 1.646	0.980	AGAACAAAAAGATTGTCAGTAAATCAATCAAGCTTACGTAGCAGA
chromosome	598845	BB_0582		0.862 ± 0.276	0.499	0.958 ± 0.573	0.868	0.699 ± 0.219	0.121	1.219 ± 0.476	0.294	GATGATAATTACTAACACAAAAGAAGGAAATGCCATTGAAAACCTCT
chromosome	598848	BB_0582		0.604 ± 0.531	0.452	0.623 ± 1.060	0.693	0.313 ± 0.472	0.321	0.681 ± 0.566	0.534	TATTATTAATTAATCTATTGCTGTTCCCATTGATGTTGAGAATGCCCTGAA
chromosome	599352	BB_0582		1.156 ± 0.401	0.618	1.369 ± 0.401	0.274	0.697 ± 0.429	0.213	0.711 ± 0.313	0.129	TTTCTATTATTAATTCTTTGCTAACACAATTCAAAAAGAG
chromosome	600890	IG 65		0.819 ± 0.567	0.578	0.957 ± 0.792	0.954	1.037 ± 0.785	0.700	1.309 ± 1.090	0.247	ATCTGGTGGATCTAGAATTCTCTGATTATACTAATTGAAAGCAATT
chromosome	601548	BB_0584		0.792 ± 0.737	0.588	2.415 ± 2.763	0.438	0.832 ± 0.800	0.754	1.619 ± 0.747	0.170	ATTATTTTATTTGTTTATCATGGGAGTAGTTGGAGCTGTTAT
chromosome	607171	BB_0588	<i>bgp</i>	0.627 ± 0.146	0.048	0.576 ± 0.497	0.189	0.684 ± 0.152	0.086	0.962 ± 0.189	0.807	AAAAAATAAAAAACTTTATTAAACAATTATTCTACAAAACACTCTTAT
chromosome	607225	BB_0588	<i>bgp</i>	0.807 ± 0.586	0.724	1.074 ± 0.604	0.762	0.438 ± 0.240	0.188	0.892 ± 0.576	0.826	TTAAACATGACATTTTAGAAAAGCACATAACTGTTGAAAAAAACTA
chromosome	607302	BB_0588	<i>bgp</i>	0.851 ± 0.231	0.425	1.101 ± 0.308	0.268	0.434 ± 0.339	0.083	0.281 ± 0.193	0.066	CTCTTAAGAACATTCTCTCTTATTAGACATAAGCTTATTCTGATC
chromosome	607476	BB_0588	<i>bgp</i>	1.006 ± 0.951	0.988	0.994 ± 1.128	0.995	0.763 ± 0.662	0.441	0.713 ± 0.535	0.114	TTTAGCACTAACACGCCACCAGCAACGCCAGAATTATGACATGACTT
chromosome	609981	BB_0591		0.845 ± 0.234	0.304	1.380 ± 0.793	0.409	0.595 ± 0.202	0.029	0.753 ± 0.262	0.085	ACTTACATTATTATAATAACGAAACTAAAAAATTAAATAATTCTTAT
chromosome	610468	BB_0591		1.395 ± 0.466	0.318	2.133 ± 1.199	0.254	0.758 ± 0.214	0.319	0.948 ± 0.362	0.814	CAAACTAATTACGGCAAATTAAATAAGCTGCACACTTATTAGTT
chromosome	610916	BB_0591		1.096 ± 0.996	0.628	0.539 ± 0.641	0.566	0.970 ± 0.660	0.927	1.666 ± 2.410	0.542	TTTGATTATTGTCATTACTCTCAATGTTGTTGAATCTTTTAA
chromosome	619647	BB_0597		0.936 ± 1.023	0.890	1.674 ± 1.105	0.239	1.147 ± 0.983	0.794	0.963 ± 1.100	0.938	GCTTATGCTAAAAGATTCTCTAGTCTCAGTACACTTAAATTGAA
chromosome	619652	BB_0597		0.202 ± 0.343	0.277	0.121 ± 0.231	0.231	1.766 ± 1.422	0.191	1.516 ± 1.974	0.429	TGCTAAAAAAAGATTCTAGCTCTAGTACACTTTAAATTGAAAGAGA
chromosome	630776	IG 66		0.843 ± 0.982	0.779	0.515 ± 0.611	0.271	0.494 ± 0.521	0.317	0.587 ± 0.604	0.464	CTATTATGTTGAATATTAATTATATTATTGATTGTTAATTA
chromosome	630917	BB_0605		1.135 ± 1.188	0.829	1.636 ± 1.967	0.555	0.710 ± 0.688	0.429	1.118 ± 0.830	0.608	GTATCAAATCTATTAAACTATTGACTTGCATACTGTATAATTATA
chromosome	631804	BB_0605		1.008 ± 1.171	0.986	1.544 ± 1.792	0.317	0.297 ± 0.387	0.328	0.728 ± 0.674	0.719	AGTTATGTTGATAAATTGTTGCTCCTAGTGGGGATATGCCTGTT
chromosome	633080	BB_0607	<i>pcrA</i>	0.537 ± 0.535	0.516	0.987 ± 1.162	0.954	0.466 ± 0.614	0.276	0.662 ± 0.693	0.491	TTAGAAATAATATTCTAAAGATATAATATGTTTGATTGAGGTTTC
chromosome	633083	BB_0607	<i>pcrA</i>	0.413 ± 0.632	0.371	0.935 ± 1.231	0.941	0.910 ± 0.457	0.600	0.588 ± 0.488	0.163	GAAATAATATTCTAAAGATATAATATGTTTGATTGAGGAGTTCAAG
chromosome	633563	BB_0607	<i>pcrA</i>	1.438 ± 0.798	0.332	3.969 ± 2.993	0.074	1.729 ± 1.197	0.247	1.587 ± 1.749	0.400	GAAGACAAGGCATAAAATAAAGTTCAGGGGGAAACATCTTTTCCAGA
chromosome	634505	IG 67		1.873 ± 1.966	0.294	2.646 ± 1.689	0.000	1.468 ± 0.881	0.307	1.724 ± 1.282	0.251	AATAATCTTAAATTCTTCAATAATTCAATAATTGGTTAAGCTT
chromosome	634516	IG 68		0.941 ± 0.141	0.619	1.368 ± 0.271	0.196	0.727 ± 0.193	0.158	1.168 ± 0.182	0.339	TATTATTAATTATAATTAACTCAAGTATAATTATGGTTAATTAA
chromosome	634547	IG 69		0.935 ± 0.216	0.661	1.516 ± 0.769	0.420	0.631 ± 0.168	0.040	0.951 ± 0.215	0.787	TTATGGTTAATTATACTAACAGGAAAGTTATTGAGTATTGTAATTG
chromosome	634720	BB_0608		1.104 ± 0.812	0.517	1.131 ± 0.775	0.794	0.601 ± 0.279	0.219	1.000 ± 0.462	0.999	TTGAGTGCAGATAAACTAACAAATAATATTGATATGCATCTTATT
chromosome	642261	IG 70		0.928 ± 0.338	0.676	0.872 ± 0.520	0.788	1.013 ± 0.697	0.963	0.885 ± 0.900	0.840	TTAAATTTATTTAGGAGTAGATCTATGAAAGATGGAGTTAGAAC
chromosome	643328	BB_0616		1.236 ± 0.649	0.588	2.590 ± 1.520	0.176	1.458 ± 0.658	0.200	1.678 ± 0.576	0.191	AAAGAAATAATGATATAATTGTTAGTCTAATTAAATAATAAAC
chromosome	643353	BB_0616		1.498 ± 1.061	0.449	3.038 ± 1.777	0.030	0.614 ± 0.503	0.412	1.779 ± 0.881	0.042	TTAAAAAAATCTAAACAAAGAAATATAAGAAATAATGATATAATT
chromosome	643748	BB_0616		1.817 ± 1.949	0.477	1.659 ± 1.325	0.240	1.137 ± 0.947	0.786	2.161 ± 3.707	0.608	TTTGACAAAATTCAACATAGGAAAAAGATAAACAACTCTCTAGC
chromosome	644034	BB_0616		0.932 ± 1.201	0.947	0.880 ± 1.259	0.920	0.477 ± 0.635	0.601	0.410 ± 0.508	0.502	TGACAGGAGTTACACTTCTTAACTACACCGGATTAAATAATTCTA
chromosome	644947	BB_0617		0.598 ± 0.379	0.182	1.067 ± 1.736	0.943	0.433 ± 0.147	0.046	0.303 ± 0.093	0.063	ATAGTTTATACAGCTTATGAAAAATTGTTCCAATTATAATT
chromosome	645073	BB_0617		1.040 ± 0.534	0.919	1.724 ± 1.955	0.611	0.232 ± 0.175	0.066	0.494 ± 0.130	0.038	TGAGCAGATAAACTACATGTTTCTCATCAGAATT
chromosome	645402	BB_0618	<i>cdd</i>	1.953 ± 1.418	0.084	1.752 ± 1.210	0.228	1.672 ± 1.292	0.168	0.978 ± 0.554	0.920	TTAAAATCGCACTTCTTCTGCACACAAAGTGTCTCAAAGCTGCATT
chromosome	646668	BB_0619		0.270 ± 0.150	0.146	0.510 ± 0.298	0.280	0.580 ± 0.400	0.171	0.708 ± 0.439	0.288	TTATCCTTAATGTTGCTAGCATCTTGATTTACATCTAGAGAAC
chromosome	646770	BB_0620		1.144 ± 0.848	0.311	1.933 ± 1.481	0.146	0.943 ± 0.555	0.689	1.583 ± 1.054	0.152	AATAATTACTATGTTTATCAATTAAATTGTTGAGGAGT
chromosome	647823	BB_0620		0.857 ± 0.333	0.194	1.572 ± 0.958	0.302	0.794 ± 0.272	0.264	1.026 ± 0.326	0.402	TATATCTACTATGGCGCAAGTTAGTTATTCAAGTGTCTTAGCT
chromosome	647883	BB_0620		0.742 ± 0.271	0.104	1.737 ± 0.244	0.010	0.594 ± 0.328	0.239	1.286 ± 0.534	0.508	CATAGCACAAGGAGCTAAGCAACTTGAATACTCAAACCTTGCGCCAT
chromosome	648354	IG 71		0.657 ± 0.136	0.001	0.190 ± 0.173	0.039	0.617 ± 0.500	0.220	0.823 ± 0.500	0.493	AATTAGCATTTTATTTATGTTAAATGAAAAGAAATTTTATCTCAT
chromosome	649134	IG 72		1.296 ± 0.535	0.486	1.442 ± 0.793	0.378	0.888 ± 0.433	0.626	1.008 ± 0.699	0.983	TTATAATCATTAAATGAGTTTATTAACCTTGCAAAGCAAAGTTGC
chromosome	652140	BB_0623	<i>mfd</i>	0.634 ± 0.639	0.214	1.438 ± 1.789	0.532	0.921 ± 0.942	0.926	0.721 ± 0.586	0.600	TTAATTGTCGAATCTCTGATTCTTGTGCGTTGTTTT
chromosome	652591	BB_0623	<i>mfd</i>	1.824 ± 1.529	0.097	1.614 ± 2.002	0.391	0.721 ± 0.868	0.052	1.751 ± 1.408	0.071	TATTTCAAAGAATTGCCAAAAGTCAATTGAGGTTAAATATCTAG

chromosome	657295	BB_0626	<i>rnmV</i>	0.571 ± 0.467	0.408	0.995 ± 1.527	0.992	0.513 ± 0.688	0.119	0.696 ± 0.751	0.452	TCTTAACTAAAGACACTGAGGTTGAATCAGTAAATAAACAGAAAATAAT
chromosome	659699	BB_0629		1.335 ± 0.839	0.022	1.998 ± 1.432	0.168	0.742 ± 0.401	0.563	1.185 ± 0.952	0.738	TAACAGCTTTTAATAGGAATCCTTAAAAAAGAATACAAGAAATATAAACG
chromosome	659840	BB_0629		0.836 ± 0.586	0.677	0.061 ± 0.106	0.007	0.025 ± 0.044	0.009	0.159 ± 0.276	0.020	CATGCGGGTATTACCCCTTAAAGGATCTGCTGCAAATGGAAATTACTCCT
chromosome	660191	BB_0629		0.862 ± 0.198	0.369	1.285 ± 0.723	0.584	0.602 ± 0.145	0.079	0.851 ± 0.083	0.160	ATGAATCAATAACAAATATGCTAACTAGCGGTACTAATATGGCAA
chromosome	661151	BB_0629		1.190 ± 1.142	0.826	1.090 ± 1.294	0.926	0.691 ± 0.690	0.596	1.667 ± 1.421	0.504	ATACTTTAGCAACACCTTAAAGACATGAACCTTATGAGCACAATAATG
chromosome	661332	BB_0629		0.970 ± 1.046	0.926	1.463 ± 1.385	0.014	0.438 ± 0.432	0.217	0.726 ± 0.702	0.672	GCTATGCCCATGCACAAAGGCAATTCTATTAAAAAACACGGAATTGCTATT
chromosome	661527	IG 73		0.797 ± 0.770	0.653	1.596 ± 1.505	0.471	0.345 ± 0.300	0.222	0.258 ± 0.256	0.262	AAGGTGATTATTATGCACAAAATTATTTCACAAAAACTTGATTGTTTAAAT
chromosome	661543	IG 74		1.370 ± 0.719	0.494	1.788 ± 1.324	0.245	1.282 ± 0.748	0.253	1.605 ± 1.406	0.353	CACTATAATATATAAAGGTGATTATTATGCACAAAATTATTCAAAAAA
chromosome	662588	IG 75		1.026 ± 0.134	0.586	1.133 ± 0.261	0.358	0.897 ± 0.136	0.420	0.925 ± 0.248	0.537	CAGTATTAGTTGCTTAATTTTAAATTGATTATATAATTCTTTT
chromosome	662622	BB_0631		1.278 ± 1.265	0.721	0.691 ± 0.515	0.339	0.712 ± 0.728	0.013	1.302 ± 0.909	0.313	AATAAAATTAAAATTAAAGCAAACAAACTAAACTGTAGCTTTAAAAGCTA
chromosome	675102	BB_0637		0.961 ± 0.143	0.720	1.863 ± 0.817	0.227	0.762 ± 0.460	0.458	0.913 ± 0.465	0.802	TTATCTTATTAGGACACGGGATTATTGGAGTTATTGGTAGAAATGG
chromosome	676104	BB_0637		1.287 ± 0.904	0.507	0.716 ± 0.700	0.452	0.486 ± 0.295	0.055	1.136 ± 0.843	0.757	AGTATGGCAATTGTTATTAGCAGAAAACATCAACTATTGAAACAAA
chromosome	676107	BB_0637		1.085 ± 0.442	0.040	2.339 ± 2.474	0.376	0.904 ± 0.322	0.658	1.067 ± 0.337	0.779	TTGCGGCAAAAGTAGCAAAAGATAGCTTTGAAAATACATCAGTGTTC
chromosome	676847	BB_0638		0.584 ± 0.353	0.056	0.630 ± 0.514	0.069	0.638 ± 0.279	0.045	0.637 ± 0.220	0.150	CTATTAATTCATGGAACATATTAAAGACCAATTACTACAGCATCAA
chromosome	677556	BB_0638		0.917 ± 0.206	0.567	1.630 ± 0.741	0.315	0.896 ± 0.254	0.005	0.951 ± 0.198	0.465	TTTAATGAGTGGCTGTGTAGAACATACAGGAAATAATTAA
chromosome	677783	BB_0638		0.955 ± 0.866	0.952	1.521 ± 1.565	0.477	0.625 ± 0.674	0.275	1.142 ± 0.966	0.801	TAGACAAAGCAATCAAAAGATCAAAACCTTGTATAATTAAATGGAA
chromosome	684881	BB_0645		0.242 ± 0.245	0.145	0.158 ± 0.114	0.129	0.888 ± 0.998	0.550	0.399 ± 0.528	0.369	ATTATTAAAGGCAATGGGGTCAGGTAGTTACGGACCAGGTTAGTGT
chromosome	684980	IG 76		0.590 ± 0.352	0.321	0.735 ± 0.624	0.631	0.451 ± 0.337	0.098	0.396 ± 0.300	0.053	CTTATTAAAAAAATCAAGCCTCTAGCAATTCTTATTCTATTCTAAGAA
chromosome	684983	IG 77		0.925 ± 0.537	0.691	1.128 ± 0.606	0.791	0.699 ± 0.507	0.200	1.351 ± 0.745	0.361	TTACTTATTAAAAAAATCAAGCCTCTAGCAATTCTTATTCTATTCTAA
chromosome	688393	IG 78		0.972 ± 0.333	0.709	2.305 ± 1.093	0.197	1.292 ± 1.153	0.649	0.761 ± 0.232	0.045	GAAGTAAATCGCTACTATAGCGAACATTGTTAACATTCTTATAT
chromosome	695782	BB_0656		0.000 ± 0.000	0.150	0.000 ± 0.000	0.150	1.351 ± 2.556	0.840	0.439 ± 0.508	0.474	ATGTAAGTGTATTGTTAAATTGGATGACCGAACGATTAAACGATCTT
chromosome	696474	BB_0656		0.817 ± 1.109	0.303	1.317 ± 1.242	0.518	0.624 ± 0.509	0.477	1.005 ± 0.959	0.993	GTAACGTTGAATTGTTAGAGGATTGGGATTTTGTTATCATTTTATT
chromosome	704543	BB_0666		1.029 ± 0.895	0.911	1.567 ± 1.213	0.440	0.630 ± 0.499	0.525	0.601 ± 0.486	0.476	TAGATAAAATATAACATTGGGAAATTGGCTTATTGCATTGGCAA
chromosome	710277	BB_0670		1.764 ± 1.009	0.248	2.373 ± 1.295	0.070	0.788 ± 0.684	0.310	1.667 ± 1.799	0.487	AGTIGACGCCATTGATAATGATTCAAAAGTTGTTGAAACTCTAGGT
chromosome	710423	BB_0670		0.303 ± 0.444	0.230	0.658 ± 0.761	0.682	0.116 ± 0.154	0.239	0.528 ± 0.705	0.332	GGATTCTGACTTAAATTATAAACTCCGGACTTGTCAAAGAATTCC
chromosome	710857	BB_0671		0.347 ± 0.337	0.167	0.501 ± 0.242	0.112	0.624 ± 0.330	0.186	0.718 ± 0.353	0.430	ATTATTGATATGGACATAGAAACAGCTTTTGTGTCTAAATTAAAT
chromosome	710872	BB_0671		0.975 ± 0.896	0.874	1.741 ± 1.732	0.263	0.890 ± 0.647	0.536	0.979 ± 0.931	0.881	TGTCCATATCAATAATTACTGCCCCAACCTCAGTGGAGTTGAGCT
chromosome	711002	BB_0671		0.220 ± 0.239	0.068	1.203 ± 0.659	0.709	0.567 ± 0.534	0.372	0.469 ± 0.161	0.087	ACAAATTTCCAGCAATAATTGCCAACCTCAGTGGAGCTAGCAACC
chromosome	711079	BB_0671		1.005 ± 0.737	0.978	0.734 ± 0.452	0.579	0.581 ± 0.319	0.204	0.795 ± 0.418	0.602	AGTAATAAGGTTCTGAGGCTTAAATTGTTCTTTCTGCTGATGTT
chromosome	713133	BB_0674		0.840 ± 0.412	0.530	1.307 ± 0.583	0.477	0.483 ± 0.208	0.071	0.858 ± 0.249	0.206	TTAGTGCACATGTTATTGTTAGGGTAAAGGAAATTATTGAGGTTCTT
chromosome	713908	BB_0675		0.971 ± 1.096	0.948	3.902 ± 7.076	0.398	1.012 ± 1.204	0.970	1.354 ± 1.766	0.009	TCTGTTTATCTGTGACGTATTGTTAGGTTATTCTGATTCTGATTT
chromosome	713936	BB_0675		0.774 ± 0.382	0.386	1.656 ± 1.783	0.588	0.565 ± 0.272	0.126	0.954 ± 0.522	0.888	GGTCTTTATCTGTGATTCAAATCATTTTGATAATTGAGCTTGTGTT
chromosome	718797	IG 79		0.605 ± 0.309	0.265	0.920 ± 0.613	0.610	0.800 ± 0.606	0.305	0.602 ± 0.211	0.147	TTAATCAAATAACTCAAGACCAAAAGGGTATCAAATTTTACAGCA
chromosome	718825	IG 80		0.577 ± 0.639	0.470	0.804 ± 1.068	0.455	0.422 ± 0.470	0.464	0.872 ± 1.188	0.561	ATAAACTACCTCACAAATCACCTACTATTAACTCAAATAACTCAAGACC
chromosome	718943	BB_0680		0.338 ± 0.388	0.278	0.871 ± 1.403	0.845	0.327 ± 0.538	0.036	0.402 ± 0.700	0.101	TTATAAGCAGCTTACAAGGGCGCAAGTAAGAAGAGCAGCTTTCTTGCA
chromosome	719180	BB_0680		1.030 ± 0.372	0.905	1.538 ± 0.505	0.180	0.795 ± 0.064	0.013	0.688 ± 0.148	0.093	TTGTCGATATTCTGTGCTCACCTTACAGAGCTAATAACAAATTGGGATT
chromosome	719551	BB_0680		1.009 ± 0.940	0.970	1.325 ± 1.438	0.250	0.641 ± 0.591	0.331	0.983 ± 1.083	0.855	AATCTATCAAATACTCTGCCAACATATCATTAGCAATACTGGGCAAAT
chromosome	719748	BB_0680		1.000 ± 0.917	0.997	1.943 ± 2.328	0.338	0.583 ± 0.430	0.264	0.851 ± 0.631	0.609	CTTTGTCGAAATGGGAGAAGATTGTTATTGCAATGTTGCCATAAGT
chromosome	719919	BB_0680		0.513 ± 0.448	0.447	0.186 ± 0.358	0.113	0.377 ± 0.342	0.357	0.159 ± 0.237	0.156	ATGCTATAATGCTTAAAGCTTAATGAAATTTAAACTCTGAACTTAGCTAG
chromosome	720015	BB_0680		0.962 ± 0.763	0.771	1.631 ± 1.587	0.375	0.711 ± 0.467	0.042	0.914 ± 0.545	0.228	GATAAGATTATGCTTGTGATGATGAAAATACTCTGTGAGTCTGG
chromosome	720235	BB_0680		0.897 ± 0.503	0.773	0.966 ± 0.338	0.846	0.828 ± 0.146	0.295	0.926 ± 0.193	0.553	GCTGACATTCTCAAGGAGCAGATGCTGTTGCAATGCACTAGAGCTAA
chromosome	720330	BB_0680		1.867 ± 1.430	0.263	1.277 ± 0.951	0.551	2.301 ± 3.714	0.524	1.119 ± 1.271	0.588	TCTGAGAATTTCATCGCTTTAAAGCTATTGTTGTTGATGAACT
chromosome	720364	BB_0680		0.813 ± 0.816	0.781	1.264 ± 1.529	0.610	0.823 ± 1.119	0.877	1.289 ± 1.271	0.716	GCAAAACAGATTCTCAACGGCCCTACCACTATGAGAATTCTTCATTC
chromosome	720760	BB_0680		1.397 ± 1.061	0.634	1.946 ± 1.634	0.329	1.019 ± 0.451	0.694	0.755 ± 0.706	0.395	CTAGAAAGCTGCTACTGCTGAGCTGAAGATTGAAACACTCTCCAACC
chromosome	721174	BB_0681		0.675 ± 0.203	0.002	0.591 ± 0.436	0.347	0.719 ± 0.207	0.043	1.031 ± 0.336	0.751	TATCAATTGTTTTGTTGGAATGCTTAAATAGTAATTGGTGG
chromosome	721162	BB_0681		0.357 ± 0.362	0.074	1.526 ± 1.882	0.680	0.080 ± 0.144	0.096	1.016 ± 1.006	0.985	TTAATATGTAAGGAATCTGACCTTTTATTGTTTATCTGGAAATATCTT
chromosome	721740	BB_0681		0.831 ± 0.260	0.500	1.143 ± 1.083	0.813	1.073 ± 0.325	0.468	0.761 ± 0.446	0.508	TATAGGTCTTTAGAGGGATAATTGGAAACTCTGAGCGTCGTGCG
chromosome	721742	BB_0681		1.169 ± 0.720	0.158	0.878 ± 0.413	0.699	0.458 ± 0.241	0.206	0.976 ± 0.598	0.927	TAGGTCTTTAGAGGGATAATTGGAAACTCTGAGCGTCGTGCG
chromosome	722079	BB_0681		0.740 ± 0.379	0.299	1.371 ± 1.264	0.569	0.477 ± 0.477	0.138	1.122 ± 0.439	0.358	ATCTTAGCAATTAGTTGTTACATTACTGCTGATTGCAACT

chromosome	722249	BB_0681	0.659 ± 0.159	0.039	1.490 ± 0.656	0.286	0.776 ± 0.223	0.182	0.891 ± 0.231	0.411	AAGCTCTACAGTATCCATTGCCAAAATTAAATATCAGCAGTAAATTAC	
chromosome	742717	IG 81	0.672 ± 0.465	0.282	1.194 ± 1.152	0.797	0.643 ± 0.220	0.070	0.947 ± 0.206	0.492	TTTTTTAAATGGTTTATTGGGTTTATGAGTGTAAATAACAAATAGCGTA	
chromosome	742960	BB_0707	0.640 ± 0.176	0.052	1.245 ± 0.213	0.248	0.468 ± 0.252	0.070	0.791 ± 0.268	0.425	ACTATTITAATTTTTCAGAAAGATAAAAGCAAAGAAGATAATATAAA	
chromosome	743654	BB_0707	0.639 ± 0.840	0.657	1.231 ± 1.715	0.850	0.267 ± 0.210	0.212	1.086 ± 1.009	0.841	ATTCAAGAGATAATTCAAGAGAAGATCATATATCTCGGGTAGAATATGT	
chromosome	743700	BB_0707	1.173 ± 1.711	0.888	1.309 ± 0.935	0.543	0.574 ± 0.438	0.458	0.868 ± 0.772	0.853	TGTATTTAAATGTTTATCTATTGTATCTAACGATTGTTGGCTTCGAG	
chromosome	760507	BB_0722	1.463 ± 1.468	0.349	2.237 ± 2.548	0.325	1.585 ± 1.500	0.389	1.379 ± 0.919	0.427	TGTTGGACTAAAAATGAAACATAAACGTTTCGCTTACAGATTAGATT	
chromosome	760800	BB_0722	0.960 ± 0.605	0.537	1.881 ± 2.329	0.504	0.774 ± 0.532	0.465	0.842 ± 0.565	0.506	TTCTATTAAACAGATGAATCAAGATTAAACCAACATCTCAATAAAAT	
chromosome	760938	BB_0722	0.902 ± 0.605	0.372	1.327 ± 1.215	0.465	0.620 ± 0.443	0.107	1.028 ± 0.487	0.879	ATATCAATCCTTTCTACTATTAAATTCTTAACTATAAGCTCGTGC	
chromosome	761348	BB_0722	0.918 ± 1.217	0.850	0.784 ± 0.694	0.738	0.768 ± 0.598	0.716	0.477 ± 0.402	0.175	CAATAGGTCTATTTCAGAACAAACTCATATAATTGATTAAATTAG	
chromosome	761544	BB_0722	1.226 ± 0.382	0.181	1.752 ± 0.829	0.302	0.896 ± 0.259	0.623	1.163 ± 0.407	0.417	ATGTTAAAGCCCTCAGATTGAATTGCAATCAAGGGCTGTAACTCT	
chromosome	762145	BB_0723	0.665 ± 0.129	0.049	0.756 ± 0.671	0.509	1.035 ± 0.358	0.774	1.131 ± 0.255	0.012	TTTCAAACATATAAAATGTAATTGATAATTCTCAATGTTAA	
chromosome	765080	BB_0726	0.325 ± 0.159	0.089	5.046 ± 7.969	0.469	0.204 ± 0.306	0.084	3.541 ± 2.487	0.200	TGTGTGAAATTGATGTTGTTAGAATAATTAAATTACCAATAG	
chromosome	774543	IG 82	0.215 ± 0.076	0.004	0.779 ± 0.728	0.612	2.127 ± 0.921	0.161	1.789 ± 1.372	0.393	GATTATTGATTTCGGCTAACAGCTTGTATTAGCTTAATTGTTAAACT	
chromosome	781573	BB_0739	1.258 ± 1.072	0.214	1.184 ± 1.244	0.642	0.455 ± 0.349	0.299	1.105 ± 0.727	0.687	AATTGATGAAAGCTTTCTTGATCAAAATTGAAATTGAAATCAAGAAT	
chromosome	782351	BB_0740	0.758 ± 0.395	0.010	0.829 ± 0.419	0.660	0.475 ± 0.230	0.153	0.960 ± 0.383	0.809	ATCCCCAAAATCTGAAATGTGGAGCAATGAAATTATTAAATT	
chromosome	782729	BB_0740	0.809 ± 1.333	0.846	1.972 ± 1.976	0.229	0.066 ± 0.094	0.090	0.655 ± 0.699	0.417	AATGTATAAAAATCTCTCAATTCCCTGCTTGGATTGTAATAGATGTCA	
chromosome	782794	BB_0740	0.767 ± 0.501	0.234	1.551 ± 1.400	0.502	0.908 ± 0.383	0.804	0.996 ± 0.447	0.907	TTCAAGCAAATTCTGATGACATCTATTACAATCCAAGCAGGAAATTGAAAGA	
chromosome	786520	BB_0743	0.616 ± 0.116	0.086	0.424 ± 0.336	0.147	0.487 ± 0.071	0.020	0.858 ± 0.226	0.287	ATTGTATATAATACAATCTGCCATAATAACTTCAAAATTGAAATAGT	
chromosome	787898	BB_0744	p83/100	0.418 ± 0.459	0.318	1.528 ± 1.354	0.483	0.349 ± 0.205	0.029	1.298 ± 0.507	0.434	AGTTCTCAAAGTTGATAAGCAACTACAATAAAAGAGAGCTGGAAAGAT
chromosome	788466	BB_0744	p83/100	0.641 ± 0.780	0.275	0.818 ± 0.833	0.831	1.520 ± 1.387	0.369	1.639 ± 1.276	0.360	TGCTATAGATTCCAGTAGTCTCTGATTAGGTTATTGATCCAATT
chromosome	788959	BB_0744	p83/100	0.707 ± 0.741	0.447	1.100 ± 0.878	0.842	0.929 ± 0.681	0.537	1.532 ± 2.285	0.641	CTTAACTTCTTAAAGTATTACATCTAAATAACTAGACTTTAAACTC
chromosome	789272	IG 83	0.349 ± 0.619	0.473	0.775 ± 0.617	0.644	0.406 ± 0.523	0.298	0.608 ± 0.689	0.301	CAAAGAAAGGTATCTAGACTTATTGACAAGGATTTCAAATGATA	
chromosome	789649	BB_0745	0.688 ± 0.585	0.603	1.278 ± 0.479	0.279	0.611 ± 0.257	0.160	0.698 ± 0.690	0.652	ATAAGATCAAATAATTATTGGATAAACACATTAAATTCTTAA	
chromosome	789850	BB_0745	0.004 ± 0.007	0.021	1.331 ± 0.684	0.361	0.851 ± 0.324	0.612	0.997 ± 0.414	0.060	ATAGCCATGAAAATCTATACTGCTTACAGGCTTATTCTCTTTAGA	
chromosome	789850	BB_0745	1.015 ± 0.437	0.883	0.826 ± 0.545	0.075	0.579 ± 1.014	0.474	0.292 ± 0.511	0.981	TTAATAAGCATGCAAGGAAAATTGACTCTAGAAATGTAATTGTGATA	
chromosome	793817	IG 84	0.203 ± 0.225	0.158	0.404 ± 0.438	0.310	0.469 ± 0.261	0.252	0.449 ± 0.555	0.430	AAAGAAAAACATATAAAATAATATAATTAAATACCATGACAAGAC	
chromosome	793836	IG 85	1.040 ± 1.146	0.953	1.401 ± 0.607	0.061	1.271 ± 0.503	0.474	2.240 ± 0.811	0.046	GCAAGATTAACTGCTGATTGGTGTGATGTCATGATCTCTGATTATC	
chromosome	799420	BB_0756	0.543 ± 0.266	0.131	0.953 ± 0.744	0.937	0.257 ± 0.134	0.050	0.634 ± 0.421	0.193	AGGCCCTCAACTCTGATAGAGAACCTTCTGGGAGAACATCCTAAGCAT	
chromosome	800345	IG 86	1.357 ± 1.033	0.645	1.785 ± 1.478	0.441	0.835 ± 0.763	0.519	1.652 ± 1.382	0.237	ATCAAGCTCTTAAAGTTAAATAACTCTAAATTACAAATTAAATGAA	
chromosome	803429	BB_0761	1.959 ± 2.787	0.386	1.889 ± 1.691	0.044	0.776 ± 0.750	0.715	0.857 ± 0.836	0.713	TGTTGTTTTTGTATTCTTAAAGTTAAAGTCAGAAAAAAACAC	
chromosome	803630	BB_0761	0.797 ± 0.779	0.776	0.790 ± 0.980	0.801	0.862 ± 0.923	0.789	0.592 ± 0.575	0.533	ATTGCTTGTAGCAACAGGATCTGCTAAAGCTGAAAAGGTTAAATT	
chromosome	803878	BB_0761	1.753 ± 3.145	0.560	0.901 ± 1.147	0.911	0.108 ± 0.166	0.245	0.293 ± 0.377	0.175	GATCTGAGCTCAATGAATGCTGAAGTGTATTCTCTCTGAAATA	
chromosome	808493	BB_0767	<i>murG</i>	1.547 ± 1.106	0.452	1.768 ± 0.821	0.143	1.133 ± 0.436	0.349	1.723 ± 0.843	0.205	ATAAAAGATATAAAGGAGACAAATCTAAATGATAATAAACGATCCTGTA
chromosome	812771	BB_0771	<i>rpoS</i>	1.086 ± 0.687	0.354	1.440 ± 1.163	0.287	0.853 ± 0.496	0.408	1.091 ± 0.645	0.480	TACTGTGAGCAGGAGATAGGTTGAATCTTCTATTCTTTGG
chromosome	813176	BB_0771	<i>rpoS</i>	0.768 ± 0.672	0.682	1.322 ± 1.359	0.289	0.385 ± 0.354	0.329	0.577 ± 0.552	0.574	ATTACTCAGAAAGAAATCAAACCTGCGAGCACAAACAAAGAGGCAAT
chromosome	813209	BB_0771	<i>rpoS</i>	1.013 ± 0.904	0.836	1.556 ± 1.629	0.315	0.721 ± 0.559	0.216	1.014 ± 0.832	0.783	TGTTTAAATCCTCATTACTAAATATGTTCATGTTTATTATCTCCCC
chromosome	813292	IG 87	1.184 ± 0.405	0.541	1.251 ± 0.798	0.660	0.739 ± 0.215	0.232	1.191 ± 0.151	0.084	AGTAGTAAAACCTTAACTCACAAATTCAAGAAAGGGGAGAAAATAAAT	
chromosome	813787	BB_0772	0.537 ± 0.414	0.352	1.673 ± 1.361	0.074	0.598 ± 0.558	0.554	0.245 ± 0.224	0.262	GCAATAAAGAATTAACCAATAATTCAAGCTGCGCAAATAATTAAAT	
chromosome	814172	BB_0772	1.080 ± 0.307	0.330	1.622 ± 1.061	0.343	0.728 ± 0.208	0.028	0.970 ± 0.235	0.632	ATAAAATGAGAAATCAAATTAACCACAGTATAATATAATTCTTAA	
chromosome	814175	BB_0772	1.240 ± 0.513	0.023	1.648 ± 1.095	0.320	0.799 ± 0.284	0.422	0.879 ± 0.369	0.426	TTACACTATCATGATATCTCAGATCTTAAATTATGGGCTGTG	
chromosome	814184	BB_0772	1.190 ± 0.179	0.264	1.616 ± 0.539	0.211	0.732 ± 0.129	0.107	1.440 ± 0.676	0.427	GATAGTGAATAATATGAGAATCAAATTAACACAGTTAAATATA	
chromosome	814187	BB_0772	1.082 ± 0.570	0.858	0.907 ± 0.500	0.845	1.070 ± 0.673	0.517	1.220 ± 0.811	0.081	TAGTATATCCAGATCTTAAATTATGGGCTGTGATTCTCTGATG	
chromosome	814729	IG 88	0.991 ± 0.478	0.951	1.433 ± 0.937	0.200	0.753 ± 0.416	0.133	1.154 ± 0.576	0.295	TCTATTATTTATATCAATTGCAATTATGAAACTTTCTCGTAAAT	
chromosome	814997	BB_0773	0.974 ± 1.044	0.793	2.120 ± 2.699	0.350	0.720 ± 0.552	0.390	1.044 ± 0.881	0.704	TTTAAAGTATGTATTGACTCTAAGGATTCTTCTTTAGATTT	
chromosome	815081	BB_0773	1.461 ± 0.883	0.513	0.702 ± 0.425	0.492	0.337 ± 0.175	0.168	0.822 ± 0.910	0.799	CATTGATGAATCGAGCCAATTGATTGCAAAAGAAAATCTAAAAA	
chromosome	823107	IG 89	0.123 ± 0.200	0.227	0.078 ± 0.149	0.141	0.008 ± 0.016	0.162	0.222 ± 0.262	0.249	ATTGTTGACAAAGCTCGTTATCTGTATGCTTCAATTGTAAGT	
chromosome	827550	BB_0789	0.790 ± 0.718	0.768	0.949 ± 0.109	0.911	0.098 ± 0.124	0.226	0.398 ± 0.730	0.060	AGGTAGTAACTGATTCTCATGAGACTACAAAGAAGTAAAGG	
chromosome	839113	IG 90	1.845 ± 0.643	0.110	1.040 ± 0.499	0.914	0.510 ± 0.255	0.085	1.157 ± 1.054	0.763	TTAAAAGCCTAATGTTAAATTAAACTTAAAGGGTTTATTGTC	
chromosome	839794	BB_0797	<i>mutS</i>	0.120 ± 0.156	0.347	0.176 ± 0.379	0.423	1.026 ± 1.657	0.986	1.072 ± 1.990	0.962	ATCTTAGTGTATTAACTAACAGAGTCTTCTGATCTTGTAAAGG

chromosome	840000	BB_0797	<i>mutS</i>	1.059 ± 0.369	0.309	1.427 ± 0.983	0.364	0.825 ± 0.396	0.092	1.028 ± 0.326	0.707	GATATCAATAATGATTCTCGTACATGTTCTGATGACGTAACACTAAGTT
chromosome	840049	BB_0797	<i>mutS</i>	2.136 ± 1.379	0.320	0.763 ± 1.113	0.787	2.008 ± 3.451	0.680	0.999 ± 1.594	0.999	ACTTGAGTACGTACAGAAACATGTACGAAGAACATTATTGATATCT
chromosome	840052	BB_0797	<i>mutS</i>	0.689 ± 0.340	0.278	0.587 ± 0.447	0.466	0.781 ± 0.561	0.107	1.211 ± 1.084	0.586	ATCTTGAACCTGTAAAAAATAATAATGATTCTCTTCAATATTCTTAT
chromosome	840598	BB_0797	<i>mutS</i>	0.936 ± 0.893	0.939	0.298 ± 0.488	0.405	0.859 ± 0.857	0.772	0.612 ± 1.043	0.726	ATCTTGCATAAGCAATCTCTGATTCAAGATATTGATCAATATATTAT
chromosome	840847	BB_0797	<i>mutS</i>	1.105 ± 0.962	0.826	2.150 ± 2.443	0.127	0.959 ± 0.846	0.952	0.724 ± 0.950	0.750	AAAAGGTTGCAGAATTTTTCATATTTGATTAGTTAACCTGGTT
chromosome	841046	BB_0797	<i>mutS</i>	1.308 ± 0.793	0.290	3.188 ± 3.501	0.341	0.938 ± 0.458	0.838	1.291 ± 0.794	0.344	CTTTCTTATTAAATTCTTACAAAATTTCAGTAAAGATTCTAGTATT
chromosome	841131	BB_0797	<i>mutS</i>	0.525 ± 0.427	0.182	0.277 ± 0.099	0.005	0.409 ± 0.549	0.196	0.148 ± 0.217	0.019	TATGCGCCATTAAAGTAATTAAAGGCCCTGACGCAAATAGGGTATTAC
chromosome	841588	BB_0797	<i>mutS</i>	1.094 ± 0.536	0.290	1.316 ± 0.650	0.517	0.484 ± 0.165	0.092	0.954 ± 0.641	0.763	ATGTTATTCTAGAAAGTTGGTGGCCGAGAGGGCACTCTTAGAGT
chromosome	847871	BB_0803	<i>truB</i>	1.129 ± 0.578	0.741	0.856 ± 0.497	0.766	0.631 ± 0.395	0.472	1.047 ± 0.663	0.909	GGCTCTGCCATCAATATGAACAGAAGAAAATCTAGGGGACTTGT
chromosome	848239	BB_0803	<i>truB</i>	0.420 ± 0.272	0.030	0.447 ± 0.350	0.074	0.692 ± 0.154	0.152	0.939 ± 0.322	0.753	TTGATTTCATTAAACACCATTTAACAAAGATTCTTATT
chromosome	848320	BB_0803	<i>truB</i>	1.015 ± 0.399	0.956	1.071 ± 0.956	0.908	1.206 ± 0.488	0.491	1.827 ± 0.748	0.229	AATATGTCATTATTTAATTATAATATATTGACATTAAATTTTAT
chromosome	858686	BB_0811		1.792 ± 1.000	0.137	1.995 ± 1.189	0.213	0.804 ± 0.776	0.538	1.132 ± 0.855	0.683	TTAATAGACCTCATAATGTTAAGGGCGCTGCTCAATGTTGCTGGTA
chromosome	861758	BB_0814	<i>panF</i>	1.446 ± 0.842	0.040	1.711 ± 1.195	0.383	1.159 ± 0.708	0.120	1.058 ± 0.767	0.554	TTTTTTTACAAAAAAAATTAACACTAAAAAATGTAATATGAAACAAA
chromosome	861841	BB_0815		1.463 ± 1.320	0.670	3.651 ± 6.234	0.550	0.165 ± 0.275	0.104	1.080 ± 1.477	0.946	GTCGCTTCGCTTACATTAGCAAGCACTTCTAAAAAATATTATCTCA
chromosome	862301	BB_0815		0.956 ± 0.344	0.841	1.405 ± 1.071	0.477	0.934 ± 0.328	0.820	1.128 ± 0.544	0.669	GATCCCCACCAAAATGCCTACTAGCTTCTGCAGTATTATTTTT
chromosome	862513	BB_0815		1.217 ± 0.575	0.220	1.811 ± 1.209	0.211	1.084 ± 0.553	0.781	0.789 ± 0.546	0.560	TTTGTGGTAAAGCCTGTTCAATAACAATCTGACAAGAGTAGCTCTT
chromosome	867777	BB_0823		0.819 ± 1.056	0.581	1.489 ± 1.260	0.620	0.792 ± 0.531	0.595	1.051 ± 1.297	0.940	TAGTCACAAATTAAATAATTGATCATTCTAAATAGCTTACTACATAACCG
chromosome	868626	BB_0824		0.959 ± 0.649	0.857	0.927 ± 0.517	0.848	0.846 ± 0.571	0.409	0.542 ± 0.344	0.062	TATTAGGCCATTGTTATGCTTCTATTCTCATTCTAATTATAAAA
chromosome	868703	BB_0824		0.298 ± 0.501	0.076	0.348 ± 0.586	0.254	0.557 ± 0.315	0.206	0.231 ± 0.344	0.021	TGCTGGATTAAATCGTTGGAGATTTCATTAGGAAGTTTATTCC
chromosome	869189	BB_0825		0.493 ± 0.569	0.359	0.953 ± 1.174	0.882	0.357 ± 0.498	0.449	0.377 ± 0.553	0.213	TAATAAAAGATTTCACAAACAAATAACTACGGAGAGATTGAAT
chromosome	869195	BB_0825		1.174 ± 1.619	0.878	1.498 ± 2.309	0.770	0.056 ± 0.105	0.127	1.900 ± 2.341	0.330	CATATATAAAAGATTTCACAAACAAATAACTACGGAGAGAT
chromosome	869564	BB_0826		1.235 ± 1.039	0.464	1.538 ± 1.749	0.648	0.754 ± 0.742	0.709	1.505 ± 1.488	0.625	ATACTAACAAACTATCCAAAAGCATTATTCTTATAAAAAGAAAT
chromosome	870075	IG 91		1.046 ± 0.288	0.644	1.546 ± 0.679	0.220	0.726 ± 0.411	0.380	1.141 ± 0.437	0.608	TATTATATTATAACAGCTTCAAGGTTAGTTTAAAAAAAGTAAT
chromosome	870079	IG 92		0.600 ± 0.670	0.552	0.835 ± 0.672	0.724	0.305 ± 0.152	0.100	0.059 ± 0.047	0.055	AAATATAATAATCAAATATTACAAAGTTAACAGCAATGAAGTTATAAT
chromosome	875775	BB_0829		0.549 ± 0.116	0.063	0.747 ± 0.570	0.570	0.775 ± 0.084	0.058	1.074 ± 0.316	0.594	AGATATTAATGGCGCATTCTTTGGCAGCAGTAAAAGATTGACACCT
chromosome	876183	BB_0829		0.933 ± 0.571	0.890	2.416 ± 2.200	0.389	0.173 ± 0.183	0.099	1.022 ± 1.564	0.968	TTTATGATTAGCAAGGCTTAAATTGTAATTAGTTCTATTCTTCTATT
chromosome	876441	BB_0829		0.883 ± 0.770	0.071	1.092 ± 0.986	0.393	0.596 ± 0.485	0.145	0.847 ± 0.576	0.523	TCCTCATATTACCCAAATATCGCTTAGCTAAACCTCGTAAAAGAGAA
chromosome	876672	BB_0830		1.103 ± 1.357	0.868	1.843 ± 2.515	0.649	0.748 ± 0.850	0.786	1.675 ± 1.565	0.524	ATTTAACATAAGCGCTAGTCGCTTTGATAATATCTACAATTTTTT
chromosome	876817	BB_0830		0.695 ± 0.521	0.237	1.100 ± 1.100	0.654	0.485 ± 0.351	0.156	0.758 ± 0.763	0.071	AAAGTCTTGTGATTAGCTTAACTTACCAACTGTAATTCTTAC
chromosome	879352	BB_0831		0.502 ± 0.618	0.347	1.396 ± 1.615	0.664	1.818 ± 1.577	0.358	2.117 ± 2.137	0.399	GTACCAAATATTGCTTCAAGGCTTCAAGCGGTTTGTATAAAAGAT
chromosome	879784	BB_0831		0.644 ± 0.526	0.486	1.014 ± 0.442	0.971	1.039 ± 0.343	0.141	1.311 ± 0.529	0.148	AATACAACTTCGGACATAAAAAGATTCTCTAAAGCTTGCCTT
chromosome	880234	BB_0831		0.740 ± 0.330	0.329	0.635 ± 0.293	0.338	0.605 ± 0.306	0.079	0.917 ± 0.363	0.619	TTTTGATTTCAGGTTAAATTAATGAAACAAAGCTTCAATTACCATGAGAT
chromosome	888240	IG 93		0.281 ± 0.049	0.010	0.802 ± 0.203	0.127	0.529 ± 0.094	0.000	0.751 ± 0.430	0.374	ATTCAATTAAATCAATATAATTAAATTCATTGTTAATAAAATAAAA
chromosome	896550	BB_0838		1.037 ± 0.544	0.851	1.899 ± 1.544	0.252	0.870 ± 0.491	0.405	1.417 ± 0.881	0.484	ATAGAAAACAAAAAAATAATAATGATTTCATTAGTAATATAATT
chromosome	903759	IG 94		1.072 ± 0.857	0.285	2.026 ± 2.004	0.257	0.573 ± 0.330	0.241	0.869 ± 0.601	0.373	AAAGAATTTCATATTAAAAAATTATAGATAAACATAATCTAAAC
chromosome	904267	BB_0844		1.041 ± 0.715	0.930	1.340 ± 1.277	0.630	1.177 ± 1.611	0.871	0.833 ± 0.978	0.834	AATAGTGGACTAGCGAGAGAGCATCTGCAAATACCTTTGAGAAAGCC
chromosome	904270	BB_0844		1.371 ± 1.643	0.461	1.897 ± 1.914	0.175	1.344 ± 1.320	0.131	1.972 ± 1.733	0.195	ATTGAGTATGAGATTTCATATTGCTCTTTCTAATACTGATG
chromosome	904861	BB_0844		0.727 ± 0.878	0.727	0.421 ± 0.532	0.527	0.547 ± 0.620	0.521	0.635 ± 0.919	0.649	TTAGCATTATCATGTAATTGATAAATTCTTCTATATTCTCTCC
chromosome	905027	BB_0845a		1.179 ± 0.833	0.246	1.698 ± 1.580	0.325	0.834 ± 0.458	0.325	1.079 ± 0.640	0.375	CATAGCTAAATATTAAAAAATTAAACAAAAAATTACGATATGGAAAAA
chromosome	905094	BB_0845a		0.759 ± 0.965	0.816	0.194 ± 0.193	0.275	0.356 ± 0.328	0.363	0.742 ± 0.659	0.708	ATTACAACTAAATAAAAAATTGATTATAAGAATTATTAGTAACCTT
chromosome	905412	IG 95		0.892 ± 0.429	0.377	1.253 ± 0.420	0.225	0.694 ± 0.245	0.145	0.988 ± 0.415	0.922	TGGTGTATAGCTTGTCTTTTAAATATTAAATCTAAGTCTTGA
chromosome	905666	BB_0845b		0.856 ± 0.709	0.360	1.705 ± 1.451	0.306	0.710 ± 0.550	0.113	0.725 ± 0.658	0.169	TCTTGTACATTTCATTTAGTACTAGCCATATGCTCAATAATTGATAG
chromosome	906234	BB_0848a		0.871 ± 0.554	0.619	0.623 ± 0.755	0.582	1.321 ± 0.931	0.666	0.352 ± 0.345	0.213	CTTGGCTTAATTAAGATTTTTATTCTTCTATAATACTCTCTAT
chromosome	906896	IG 96		1.158 ± 0.770	0.788	3.436 ± 2.744	0.103	1.097 ± 0.806	0.864	2.070 ± 2.000	0.289	TACTTAAGATTGGAATTCTCATGAAAATATACTCGTACCCATGTA
chromosome	906899	IG 97		0.670 ± 0.130	0.092	0.694 ± 0.464	0.480	0.683 ± 0.172	0.019	0.855 ± 0.280	0.080	GAGCATTAAGCGTCCCTATAAAGGACTTCCATATTACAAAACAAT
chromosome	906983	IG 98		0.938 ± 0.798	0.323	1.364 ± 1.359	0.441	0.628 ± 0.453	0.114	0.871 ± 0.822	0.256	GAGATGTAATAAAATTATCTTATAATTATAAGATCTGCTTAA
chromosome	906988	IG 99		1.274 ± 0.279	0.211	1.815 ± 1.273	0.386	0.755 ± 0.204	0.187	1.082 ± 0.194	0.456	CATCTATTAATAGAAGATGCAAATATGATCAAATTGTTATT
chromosome	907088	IG 100		1.064 ± 0.268	0.712	1.617 ± 0.573	0.232	0.655 ± 0.164	0.138	0.728 ± 0.230	0.148	AGGTTGCTATAACACCAACAGATTTAATTCTTTAAACCCATTATCA
chromosome	907788	BB_0849b		1.160 ± 0.956	0.821	1.275 ± 1.282	0.766	0.734 ± 0.471	0.513	1.158 ± 0.567	0.723	TTTTATAGAAACACAATAATAATTCTTATTGAGATAAGTCTAATCATGGT

chromosome	908223	BB_0849b	0.919 ± 0.726	0.212	1.268 ± 1.333	0.535	0.858 ± 0.607	0.651	1.177 ± 0.828	0.005	AATACTAAAATTTAGTATAAATAAGGTAAGGAAAAATAATAAAATTAA
chromosome	908782	BB_0852	1.076 ± 0.412	0.572	0.838 ± 0.876	0.783	1.129 ± 1.140	0.810	1.478 ± 1.228	0.464	ATATACCAAATCAACTCTTGTGAGAACGAATATTTCAAATAAG
chromosome	909197	BB_0852	1.080 ± 0.827	0.793	1.020 ± 0.702	0.958	0.489 ± 0.316	0.307	0.847 ± 0.820	0.386	TTATCTTTATACCAGAACATCTGTGTCATCTCTATGTCACTTTCTTGCTG
chromosome	909453	BB_0852	0.907 ± 0.141	0.516	1.239 ± 0.429	0.455	0.779 ± 0.364	0.447	1.156 ± 0.264	0.493	TCTAGAAAACCCCTTTAAATTATTGTGATCTAGAGCACAGTAATAGT
chromosome	910040	BB_0853	0.843 ± 0.681	0.560	1.576 ± 1.265	0.260	0.998 ± 0.652	0.993	0.981 ± 0.715	0.855	AGAAAATATTGCAATAATAAAAGGATTGAAATATCTTATTAGAAAAGAAT
plasmid_cp26	194	BB_B01	0.307 ± 0.326	0.034	0.455 ± 0.451	0.014	0.891 ± 0.582	0.247	0.939 ± 0.694	0.440	GTATTTAAAGAAAGCTACAATTCTACCCCTTCATCGTTGAGATTTTACA
plasmid_cp26	346	BB_B02	1.682 ± 0.228	0.017	1.166 ± 0.179	0.111	0.968 ± 0.107	0.572	1.168 ± 0.208	0.212	CTTGTAAACGAGGGCAAGGCCATAATAAAATTAAATCATTAAATT
plasmid_cp26	383	BB_B02	1.117 ± 0.369	0.652	0.672 ± 0.312	0.293	0.531 ± 0.257	0.118	0.637 ± 0.086	0.033	TGTGCACAAATTAAACAAAAAATAAGGTTAAGGTTAAGGAAACGAGA
plasmid_cp26	404	BB_B02	1.435 ± 0.686	0.068	0.777 ± 0.357	0.422	0.886 ± 0.415	0.751	0.730 ± 0.320	0.332	GCAAGACACACTAGTTCTAAAAAAATGTTGACTTTAAATTCAAAACTC
plasmid_cp26	552	BB_B02	1.105 ± 0.977	0.846	1.553 ± 1.092	0.196	1.095 ± 0.908	0.867	1.786 ± 1.426	0.343	TTTCGTGAGTTTTAAACAAAGTGTAAATTGGGGCTGATATTAAAT
plasmid_cp26	757	IG_101	1.600 ± 0.552	0.022	1.274 ± 0.393	0.388	0.808 ± 0.276	0.099	1.086 ± 0.421	0.495	ATTITGATGAAAATAGGTCTCATTTTTTTAAAAAATTAAATTTAATCT
plasmid_cp26	760	IG_102	1.666 ± 0.317	0.046	1.130 ± 0.259	0.369	0.847 ± 0.190	0.184	1.090 ± 0.299	0.628	TATAATCTTATTAAATAAAATTTCTCATATTTCCTAAATATTGAT
plasmid_cp26	801	IG_103	1.653 ± 0.336	0.024	1.234 ± 0.710	0.565	0.804 ± 0.111	0.192	1.095 ± 0.256	0.639	TTTGGAAATTAGGAAATATTGATAATTAAAGATATTATAATTGTA
plasmid_cp26	2258	IG_104	1.067 ± 0.392	0.579	0.842 ± 0.306	0.616	0.696 ± 0.368	0.165	0.955 ± 0.382	0.796	TAAGCATATTTTAAATCAGAAATTTTACTAGCTAAAGATTAA
plasmid_cp26	2276	IG_105	1.397 ± 0.565	0.221	1.232 ± 0.739	0.562	0.784 ± 0.259	0.049	1.076 ± 0.509	0.809	TATAATATGTAATTAGGATGATAATAACCAAAGAAATTCTATTACAC
plasmid_cp26	2280	IG_106	1.585 ± 1.471	0.459	1.722 ± 1.129	0.426	0.751 ± 0.294	0.315	0.975 ± 0.654	0.832	ATATGTAATTAGGATGCAATAAAACCAAAGAAATTCTATTACACCGAT
plasmid_cp26	2290	IG_107	1.680 ± 0.380	0.073	1.016 ± 0.254	0.848	0.802 ± 0.490	0.575	0.868 ± 0.664	0.767	GGATGCATAATAACCAAAGAAATTCTATTACACCGATAAACTTTT
plasmid_cp26	2350	IG_108	1.885 ± 0.424	0.081	1.560 ± 0.824	0.386	0.992 ± 0.348	0.972	1.369 ± 0.277	0.186	AATCATAAAATAATAAACTCGAATTAAATAATTCTTTATCCTCAA
plasmid_cp26	2419	IG_109	1.525 ± 0.492	0.086	0.917 ± 0.207	0.021	0.844 ± 0.319	0.198	1.024 ± 0.241	0.531	TTTATAAAATAGCTTTTTGGGAGATAAAAGAATTATTAAATTCGAA
plasmid_cp26	2519	BB_B04	0.879 ± 0.466	0.624	1.560 ± 1.783	0.544	0.737 ± 0.499	0.207	1.357 ± 0.783	0.068	ATAAAAGGTAAATACATAAAACTGAAATAATATAAAACTAGA
plasmid_cp26	2538	BB_B04	0.765 ± 0.645	0.702	0.725 ± 0.310	0.335	0.818 ± 0.417	0.183	1.026 ± 0.459	0.887	TTTATGTTATCCCTTATTAAAGCGTATGATAAGGCTCTATTGCG
plasmid_cp26	2660	BB_B04	0.705 ± 0.570	0.456	0.688 ± 0.470	0.353	0.723 ± 0.085	0.053	1.031 ± 0.133	0.782	ATTCCAAAATTAGTAAGAGTATATGCAACAAATTATAATTAGGGATA
plasmid_cp26	2694	BB_B04	0.531 ± 0.373	0.272	0.850 ± 0.507	0.729	0.864 ± 0.205	0.118	1.252 ± 0.269	0.219	TATTTAAATAGGGATAAGAAAAAGGAATTGCTAATATAGGTTAAAA
plasmid_cp26	2768	BB_B04	0.701 ± 0.578	0.238	0.684 ± 0.379	0.056	0.699 ± 0.225	0.066	0.871 ± 0.285	0.354	GGTTCATTAATTTAAAGACCAGCGCAGAATGCTACCTATAGCC
plasmid_cp26	2885	BB_B04	0.389 ± 0.628	0.299	0.343 ± 0.386	0.132	0.292 ± 0.322	0.002	0.198 ± 0.136	0.053	TTGGTGGTGTGGCGAACCCTAGGGCTTCTATTGCTATGCTTAGTA
plasmid_cp26	2963	BB_B04	0.863 ± 1.251	0.882	1.773 ± 2.442	0.424	1.543 ± 1.454	0.581	1.274 ± 1.275	0.671	GAATCAAGATTGACAAAATTATAGGATAAGAGGCAATAAACATTG
plasmid_cp26	3039	BB_B04	0.645 ± 0.720	0.196	0.027 ± 0.030	0.129	0.481 ± 0.702	0.108	0.184 ± 0.160	0.207	TTATGGTTTGTGGTCTCATGGTACCAATTATTGCTCTTAAAT
plasmid_cp26	3861	IG_110	0.180 ± 0.191	0.077	1.060 ± 0.680	0.909	0.668 ± 0.921	0.481	0.875 ± 0.614	0.796	TAATATAATTATCTCAATAAAACTAATTAAAGTTATAATTGAC
plasmid_cp26	4228	BB_B05	0.856 ± 0.707	0.612	0.877 ± 0.377	0.011	1.026 ± 0.344	0.903	1.214 ± 0.443	0.375	TAGTAAGCTGCTTGTCAATTCTTGTGTTGGCATATTCAAAGCTT
plasmid_cp26	4354	BB_B05	0.757 ± 0.711	0.481	0.260 ± 0.304	0.164	0.408 ± 0.357	0.009	0.795 ± 0.588	0.624	ATGTCGAACTTCAGAATTAAAGCTATTGCAAGAATTACATGTTAC
plasmid_cp26	4596	BB_B06	0.618 ± 0.583	0.504	0.747 ± 0.685	0.682	1.046 ± 0.369	0.785	1.103 ± 0.418	0.092	CTTCGACCACTGCAAGATTAAATAAAAAGACTGAGAACATCAAA
plasmid_cp26	4956	BB_B07	0.830 ± 0.325	0.462	1.143 ± 0.874	0.830	0.669 ± 0.451	0.471	0.901 ± 0.408	0.766	ATAGTTTCATCCGTTTTATTGCAATGCTAAGTAATTCTTGAATATG
plasmid_cp26	5144	BB_B07	1.373 ± 1.283	0.593	1.141 ± 1.177	0.464	0.856 ± 0.892	0.808	1.037 ± 1.009	0.901	AGCAATATAAAACATATTGATAACAATAATGTTAGCTTAATA
plasmid_cp26	5163	BB_B07	1.312 ± 0.630	0.340	0.684 ± 0.545	0.514	0.863 ± 0.144	0.280	0.967 ± 0.205	0.832	TTGATACAAATGTATTITAAGCCTAATATAAAAATTACTGGGTGTC
plasmid_cp26	5217	BB_B07	0.841 ± 0.336	0.394	1.430 ± 0.850	0.490	0.741 ± 0.249	0.348	0.833 ± 0.298	0.515	ATTTTATCCTACAAATATAACGGACTTCAAGAAATTCTTAAAGAAA
plasmid_cp26	5233	BB_B07	2.338 ± 2.036	0.236	1.157 ± 1.188	0.850	0.961 ± 0.805	0.847	0.926 ± 0.593	0.892	TTTGTGAGGATAAAAATTATGACACCCAAGTAAATTCTTATAGGCTT
plasmid_cp26	5696	BB_B07	1.534 ± 0.126	0.015	1.642 ± 0.897	0.348	0.886 ± 0.078	0.010	1.046 ± 0.065	0.027	GGATGTCTTCTTTAATTGCAATTGCTAAGTAATTCTTGAATATG
plasmid_cp26	5809	BB_B07	0.831 ± 0.367	0.616	0.925 ± 0.678	0.862	0.548 ± 0.245	0.140	0.992 ± 0.478	0.977	TATTTCATCATGATTATTTCACACTACGTTACAAGCATTATTG
plasmid_cp26	5816	BB_B07	2.844 ± 1.048	0.034	0.924 ± 0.615	0.867	1.016 ± 0.694	0.978	0.822 ± 0.269	0.318	CTTGAAAAAAATAGAACCTGGGAAATTCAAAATAATAGAAAATAA
plasmid_cp26	5863	BB_B07	3.253 ± 2.363	0.212	2.655 ± 1.888	0.199	0.942 ± 0.547	0.718	1.439 ± 1.026	0.587	TTTATTTCTATTATTGTAATTTCACCAAGGTTTATTTCAAGTAG
plasmid_cp26	5872	IG_111	1.528 ± 1.484	0.285	1.883 ± 2.089	0.332	0.835 ± 0.783	0.252	0.961 ± 0.875	0.610	GTGCAATTATTTATTATTGTAATTATTGTAATTTCAGGTTCTATT
plasmid_cp26	6559	IG_112	3.213 ± 3.440	0.253	1.229 ± 1.123	0.21912	0.818 ± 0.6245	0.36591	0.365 ± 0.2297	0.21704	AAGAAAAGCTGCAAAAAAGTATAACAAATTCTTATAATTAAATCAA
plasmid_cp26	6572	IG_113	1.417 ± 0.4524	0.306451	1.488 ± 0.6699	0.37893	0.853 ± 0.1287	0.07354	1.059 ± 0.2809	0.76287	TGCAAGCTTCTTAAATATAATATTTAGTATTTAATGAGAAATT
plasmid_cp26	6806	BB_B09	0.729 ± 0.1033	0.079702	0.243 ± 0.2166	0.03327	0.739 ± 0.2406	0.1929	0.794 ± 0.2981	0.40387	TTATCGAGTCTCTGTGAAATTCTGCTTCAATTATGTTGTTATCGT
plasmid_cp26	6845	BB_B09	1.410 ± 0.4818	0.078106	1.12 ± 0.4323	0.18586	0.785 ± 0.3071	0.05399	0.95 ± 0.3174	0.66923	CTCCCACAACTGGATAATTATCATATACTTGTGCTTATTATGAGTCTT
plasmid_cp26	6848	BB_B09	1.465 ± 0.2079	0.006451	1.177 ± 0.2254	0.35769	0.817 ± 0.1376	0.09211	1.014 ± 0.253	0.92958	TACAACCTTAAACGAAAAAGAAAATTAAAGTCATAATTCTCATCAA
plasmid_cp26	6967	BB_B09	0.579 ± 0.6509	0.053423	0.682 ± 0.7512	0.10495	0.617 ± 0.5871	0.16853	0.633 ± 0.5936	0.15054	TAAAGCAGAACTCAAAGTAAATCTAGCTTAATAAGCATTATCAGT
plasmid_cp26	7043	BB_B09	2.183 ± 1.4065	0.28316	1.031 ± 0.5856	0.95198	0.921 ± 0.4571	0.73738	1.112 ± 0.7466	0.78666	ATAGATCTCTGAAATTAGTTAGTGTGAAATACTGATAATTGCTTTATAAAGC
plasmid_cp26	7150	BB_B09	1.067 ± 0.5494	0.711468	0.905 ± 0.6131	0.67958	0.867 ± 0.3346	0.68499	0.432 ± 0.335	0.07553	TGCTAAAATACTCCTTAAATTTACTGTGCGATACTGTTCCAATT

plasmid_cp26	7279	BB_B09	4.760 \pm 5.703	0.065273	1.144 \pm 1.531	0.68366	3.034 \pm 3.7036	0.18341	1.753 \pm 2.6176	0.13119	CATCTACAGTATGAAAATTCCAAAATTATTGAAAAATCAGACGCTCCCTC
plasmid_cp26	7363	BB_B09	2.298 \pm 2.241	0.199864	0.837 \pm 0.7642	0.57926	1.22 \pm 1.07	0.79053	0.668 \pm 0.7286	0.58608	TTACCCCTGTAAAAATTAAATAACTGTTTGAATTAAAGCTTATACTC
plasmid_cp26	7406	BB_B09	0.708 \pm 0.805	0.670064	1.621 \pm 1.3569	0.01862	0.568 \pm 0.6295	0.12368	1.45 \pm 1.2268	0.14915	AGCTTAAATTCAAAAACAGTATATTAAATTTCACAGGGTAATAATTG
plasmid_cp26	7520	BB_B09	0.978 \pm 0.6089	0.962995	0.249 \pm 0.2435	0.22995	0.661 \pm 0.48	0.41394	1.237 \pm 0.8741	0.06283	ATGTTCTTTATTGTTTGAATTCTTAAAGGCTTCACAGGAGGCTCCA
plasmid_cp26	7634	BB_B09	0.362 \pm 0.6471	0.394478	1.558 \pm 1.8703	0.58348	1.321 \pm 1.4326	0.62225	1.704 \pm 1.0791	0.39094	TATAAACCACTCTTTAAATTCTAAAAGAAGTAGATCATTCGATAAAA
plasmid_cp26	9420	BB_B12	1.003 \pm 0.8028	0.97494	0.798 \pm 0.5801	0.72537	0.317 \pm 0.4307	0.09941	0.905 \pm 1.0296	0.85483	GTACAAGTTTATTAATATTAAGAAAAAAACCTTAGTCAAAAG
plasmid_cp26	10843	IG_114	1.825 \pm 0.7275	0.137791	1.839 \pm 1.6613	0.38557	1.119 \pm 0.554	0.65552	1.128 \pm 0.8298	0.72045	ATATAGCCTATATCACTTCTATTGCAATAAAAATTATTAACTG
plasmid_cp26	10964	BB_B14	1.936 \pm 0.8772	0.114463	1.429 \pm 0.733	0.27504	0.925 \pm 0.2778	0.6206	1.083 \pm 0.2807	0.44239	GAAAGTCCAAAATTATTTCAAGCTTAAATCTTAATCCAATTC
plasmid_cp26	11059	BB_B14	1.683 \pm 1.0738	0.260652	1.648 \pm 1.2908	0.37076	0.913 \pm 0.3603	0.58706	1.203 \pm 0.5943	0.33727	ATCATCTTCCAATAAGATTGGTCAAACAAATGATGAATAATTATC
plasmid_cp26	11145	BB_B14	2.064 \pm 1.3812	0.312532	1.569 \pm 0.7471	0.29021	1.209 \pm 0.5144	0.39558	1.151 \pm 0.4116	0.37256	GCTTACTTTCCCTCAATTAGTCCATCCAGCAGCAATAAGGATTCTG
plasmid_cp26	11183	BB_B14	0.922 \pm 1.1658	0.942647	0.751 \pm 0.7499	0.74014	0.314 \pm 0.3918	0.24488	0.754 \pm 0.9042	0.07705	TTGCTGCTGGATGGAACCTAAATTGAGGAAAAGTAAGCTACAAAGAGAT
plasmid_cp26	11203	BB_B14	1.372 \pm 0.4028	0.218904	1.167 \pm 0.453	0.5568	0.913 \pm 0.0537	0.09599	0.985 \pm 0.1551	0.84897	TAACAGAACAGAACCTTTATTGCTGCTGGATGGAACCTAAATTGAGGGA
plasmid_cp26	11234	BB_B14	1.325 \pm 0.6328	0.521635	1.327 \pm 0.6425	0.49773	0.936 \pm 0.3759	0.83436	0.868 \pm 0.2988	0.62433	CTATTAGTTATTCTGTTTATAATTAAAATACCTTAAAGTCTGCAT
plasmid_cp26	11239	BB_B14	1.611 \pm 0.4511	0.058488	1.062 \pm 0.3462	0.75488	1.02 \pm 0.2047	0.85353	0.763 \pm 0.1939	0.1315	AAATAGTATTACACAGGTTAGAACCATAGTATAACAGAACAGAACAT
plasmid_cp26	11266	BB_B14	1.067 \pm 0.2158	0.686256	1.126 \pm 0.1154	0.28797	0.844 \pm 0.1354	0.05586	1.024 \pm 0.132	0.82598	TTTTAATTAAACACAGGATAACTAAATAGTATTACACAGGTTTA
plasmid_cp26	11304	BB_B14	1.584 \pm 0.574	0.20789	1.626 \pm 0.841	0.35566	1.332 \pm 0.2135	0.06795	1.052 \pm 0.3541	0.86171	TATTCTAAATGTTTCCAAATTGATCGTGTCAACGTTAAGGAAGTGCA
plasmid_cp26	11306	BB_B14	1.626 \pm 0.7113	0.111719	1.3 \pm 0.8594	0.30288	0.838 \pm 0.3346	0.31817	1.002 \pm 0.3835	0.99445	TTCTAAATGTTTCCAAATTGATCGTGTCAACGTTAAGGAAGTGCAAG
plasmid_cp26	11360	BB_B14	1.542 \pm 1.562	0.110069	0.508 \pm 0.6077	0.09121	0.702 \pm 0.5883	0.55106	0.91 \pm 0.8915	0.79869	ATATCTGCACTTCTTAAACCTGAGCACGATCAATTGAAAAACATT
plasmid_cp26	11409	BB_B14	1.163 \pm 0.1349	0.053551	0.898 \pm 0.1539	0.3942	0.85 \pm 0.0498	0.02003	0.999 \pm 0.15	0.994	TAATATCATATCCCTCTCTTGTATAAAAATTATAACTAGTGAACATA
plasmid_cp26	11414	BB_B14	2.601 \pm 2.8257	0.08203	0.522 \pm 0.928	0.60583	1.59 \pm 1.722	0.45278	1.746 \pm 1.7924	0.44365	TCATATTCTCTCTTGTATAAAAATTATAAACTAGTGAACATAATAAT
plasmid_cp26	11457	IG_115	1.213 \pm 0.2473	0.345106	1.17 \pm 0.554	0.67082	0.678 \pm 0.2644	0.12656	0.901 \pm 0.1776	0.54101	TGTTCACTGTTTAAATTTTTTATTCAAAGGAGAGGAATATGATATTATA
plasmid_cp26	11475	IG_116	0.246 \pm 0.3442	0.348513	0.19 \pm 0.2166	0.27199	0.209 \pm 0.321	0.34964	0.561 \pm 0.7672	0.32466	ATAAAAAAATATTATTATATTGTTCACTAGTTATAATTTTTATCAAAGGA
plasmid_cp26	11640	IG_117	1.522 \pm 0.5196	0.016736	1.523 \pm 0.645	0.06961	0.932 \pm 0.2984	0.64701	1.039 \pm 0.3015	0.68726	TACAGAACCTTCTGCTTTAAAACACCTTTAAAGAGTTAAAACATT
plasmid_cp26	11837	IG_118	1.617 \pm 0.7518	0.138914	1.389 \pm 0.8833	0.56518	1.028 \pm 0.5312	0.53591	1.36 \pm 0.7223	0.28841	TTGTTGCTCTCAAATGGTATTACATATAAAAATAATTAAATT
plasmid_cp26	12069	BB_B16	0.216 \pm 0.2361	0.157382	0.412 \pm 0.4873	0.20586	0.523 \pm 0.5011	0.25253	1.242 \pm 1.4417	0.57666	AGTAAAATTAAATTGAGAAATAACAACTTTAATTCTTCAATT
plasmid_cp26	12693	BB_B16	0.116 \pm 0.0999	0.09858	0.35 \pm 0.3844	0.09011	0.968 \pm 0.6456	0.82457	0.791 \pm 0.4741	0.65144	TTATTCTTCAAGAACACCTTTCAATTAAACTCTAGATTAAATT
plasmid_cp26	12732	BB_B16	0.054 \pm 0.083	0.033415	0.221 \pm 0.2213	0.09388	0.64 \pm 0.3671	0.21346	0.517 \pm 0.3474	0.28168	TTATATTCTTGTACAGATAATAGCATTACAGCTTATAATGTATTAA
plasmid_cp26	12750	BB_B16	0.018 \pm 0.0339	0.160576	0.008 \pm 0.0162	0.16326	1.213 \pm 0.9853	0.6626	1.155 \pm 1.8519	0.77978	TCTGTGACAAAAAATATAACTGTCAAGAACACATTTGAAATTATA
plasmid_cp26	13146	BB_B16	0.528 \pm 0.5726	0.18674	0.839 \pm 0.8579	0.39444	1.426 \pm 1.4966	0.50924	1.728 \pm 1.1135	0.11437	TTGTAATTCTTAAATAAGGAAAATTACCATGGGATATCTGCA
plasmid_cp26	13469	BB_B16	0.134 \pm 0.1336	0.006824	0.417 \pm 0.376	0.02301	1.131 \pm 0.3278	0.54606	0.935 \pm 0.382	0.31234	TTATTGCTCTGCTTTTTGAAATTCTGTCTTTAAAATCTCT
plasmid_cp26	13728	IG_119	0.239 \pm 0.2639	0.130732	0.102 \pm 0.1919	0.21807	1.575 \pm 1.4913	0.60587	0.651 \pm 0.8179	0.57962	TTAAAAAAATATAATTCTAAAATTAAGGTTAAAGGAAATGTTAA
plasmid_cp26	13867	IG_120	1.350 \pm 0.6817	0.476099	0.329 \pm 0.3789	0.09622	0.521 \pm 0.2437	0.03812	1.171 \pm 0.6577	0.69137	TTAAATTGATAAATGTTTATTTTATGTTATGCTAAACATCGTGA
plasmid_cp26	13879	IG_121	1.635 \pm 0.2901	0.006737	1.519 \pm 0.5636	0.16748	0.706 \pm 0.0934	0.02872	0.989 \pm 0.1425	0.8516	AATGTTTTATTTTATGTTATGCTAAACACATCGTGAGGATGGGATTCT
plasmid_cp26	13931	BB_B17	2.445 \pm 0.6658	0.057584	1.652 \pm 0.3941	0.11706	0.866 \pm 0.1601	0.44074	1.363 \pm 0.3585	0.2882	AAAGAACATCCCTCACGATGTTTTAGCATACATAAAAACACAA
plasmid_cp26	13949	BB_B17	2.076 \pm 1.4808	0.002679	2.357 \pm 3.2373	0.49366	1.215 \pm 0.9174	0.28841	1.611 \pm 1.1227	0.16547	TTTTACAAACTTAAATTATTCATGAGTATTGTTGCTCTTA
plasmid_cp26	14428	BB_B17	1.871 \pm 0.6895	0.139297	1.389 \pm 0.7713	0.54745	0.873 \pm 0.3947	0.13714	1.141 \pm 0.3877	0.57673	CTACCCGGACCTATTCTACTTTAACACATCTGCTTACACTTAA
plasmid_cp26	14471	BB_B17	1.904 \pm 0.9755	0.145187	1.775 \pm 1.1758	0.39527	1.059 \pm 0.9212	0.85954	0.876 \pm 0.5009	0.55436	AGTGTAGGAGCAGATTGTTAAAAGTAGGAATAGGCCGGTAGTATG
plasmid_cp26	14518	BB_B17	2.817 \pm 2.665	0.375221	1.525 \pm 1.55	0.64616	1.083 \pm 1.1538	0.90816	1.213 \pm 2.1142	0.87142	AGGCTTAAGTTGGGACTTGTGTTTAAATTCTGTTAAGCTTATAATT
plasmid_cp26	14606	BB_B17	1.854 \pm 1.3138	0.321181	0.815 \pm 0.656	0.70519	0.661 \pm 0.5084	0.56815	1.04 \pm 0.6837	0.93856	TATCTACATGCTTAAACTGCTCAACTCGTTCTATGGTATCAATT
plasmid_cp26	15059	BB_B17	2.100 \pm 0.7335	0.086909	0.652 \pm 0.6861	0.44835	0.729 \pm 0.3609	0.25955	1.116 \pm 0.4759	0.50131	AAGACACATCATAAACTGTTTAAAGGCTTCTTTGTATCTTGGCATAA
plasmid_cp26	15095	BB_B17	1.088 \pm 1.1895	0.87935	0.983 \pm 0.9769	0.97436	0.705 \pm 0.989	0.75579	1.043 \pm 1.5786	0.97121	TCTTATTGGCATATAATTCTCTTTATTGTTCTTATTACCTCTA
plasmid_cp26	15172	BB_B18	2.022 \pm 0.606	0.035135	1.341 \pm 0.6173	0.46973	0.936 \pm 0.309	0.57692	1.174 \pm 0.3803	0.45474	TCATAACAAACTCTATTACACCCGAACCTTAAATTCTGAAGAA
plasmid_cp26	15205	BB_B18	1.249 \pm 1.6597	0.517966	1.331 \pm 1.2696	0.24141	0.596 \pm 0.5397	0.31752	0.514 \pm 0.8016	0.04405	ATGAAGTCCGGGGTATAAATAGAGTTGTTATGATATCTCTAAC
plasmid_cp26	15212	BB_B18	1.667 \pm 0.9065	0.229071	1.623 \pm 0.9575	0.31872	1.029 \pm 0.4991	0.27318	1.006 \pm 0.4255	0.98809	TTCTGAGAAAATTCTTTAAAACACTGTAAGGAAGTTCAGTCATTCTG
plasmid_cp26	15296	BB_B18	1.908 \pm 0.4541	0.004581	1.454 \pm 0.5043	0.31133	0.903 \pm 0.3343	0.31426	1.006 \pm 0.3093	0.97468	ATTAGATGTGAAATACCAAGACTCATGACTGCAGAATGGACTGA
plasmid_cp26	15304	BB_B18	1.560 \pm 0.7462	0.246289	1.455 \pm 1.6721	0.71809	0.471 \pm 0.2427	0.08789	0.68 \pm 0.4658	0.09758	CAGCTGTAATTAGATGTGAAATACCAAGACTCATGACTGCAGAATGG
plasmid_cp26	15484	BB_B18	1.331 \pm 0.8149	0.338171	0.825 \pm 0.6416	0.76247	0.838 \pm 0.5642	0.243	0.682 \pm 0.2752	0.07975	GCTAGCTCCTGGGGAAATGGATGCTGAAAGAGATTCTTTAATA
plasmid_cp26	15849	BB_B18	1.969 \pm 0.4477	0.075503	1.845 \pm 1.121	0.34591	0.847 \pm 0.0866	0.07483	1.031 \pm 0.1431	0.71597	TTTTATTTAAATCATATTGATGCTTAAATTCTAGTATTCTCTC
plasmid_cp26	15853	BB_B18	1.717 \pm 0.3232	0.023979	1.337 \pm 0.5219	0.4336	0.883 \pm 0.2771	0.04499</td			

plasmid_cp26	16007	BB_B18	guoA	1.858 ± 2.0196 0.510563	0.508 ± 0.3529 0.3873	0.522 ± 0.5639 0.10375	1.078 ± 1.1199 0.73091	GGACTTCTGGTGCACAGACTCTTAGTTGCGCATTGCTTATAA
plasmid_cp26	16204	BB_B18	guoA	1.879 ± 0.1793 0.014129	1.275 ± 0.7232 0.60203	0.802 ± 0.1833 0.09471	1.068 ± 0.257 0.65775	GAAGCAATACAATTTTGTAAAGCTAATTGTTGAAATTACAGGAATT
plasmid_cp26	16409	BB_B18	guoA	1.895 ± 0.774 0.019208	1.1 ± 0.4114 0.71404	0.831 ± 0.3629 0.29175	0.863 ± 0.3909 0.25073	TTTCATTCATAACATATAACCCAAAATAGGTATTCAAATTAAA
plasmid_cp26	16424	BB_B18	guoA	0.993 ± 0.5786 0.966784	0.896 ± 0.4334 0.77815	0.597 ± 0.3229 0.05714	0.649 ± 0.2365 0.04907	TGTTATGGAATGCAAATAATTGTTAAATTGGGGCTAGTATCTAAA
plasmid_cp26	16427	BB_B18	guoA	1.764 ± 0.5208 0.156594	1.459 ± 0.6685 0.40694	0.794 ± 0.3408 0.29659	0.955 ± 0.3863 0.8676	TACCCAAATAGGTATTCAAATTAAAATTCCATATTCAAGGTAGGAG
plasmid_cp26	16616	BB_B18	guoA	2.070 ± 1.2608 0.202533	1.638 ± 1.3479 0.53308	0.98 ± 0.6202 0.93176	1.1 ± 0.7695 0.8256	GTTGCCATTGGGATCCAAAATCTAACAGTATTGCTGAGTATTCA
plasmid_cp26	16621	BB_B18	guoA	1.918 ± 1.1204 0.304784	1.073 ± 0.8972 0.92328	1.178 ± 0.576 0.4931	1.433 ± 0.6621 0.17652	GCCAACATTGCAAGAAGAATTAGAGAAATTGGCGTTTACAAAAGTA
plasmid_cp26	16674	IG_122		2.070 ± 0.6853 0.058566	1.35 ± 0.4901 0.398	0.86 ± 0.2622 0.46737	1.138 ± 0.5132 0.66894	AGTCCTTAATAATTAAAACCTTTTATTAAAGTATCTCATTTAATT
plasmid_cp26	17685	IG_123		1.515 ± 0.2945 0.086846	1.29 ± 0.4819 0.44359	0.852 ± 0.1031 0.05279	1.075 ± 0.1884 0.34908	AAGAATAAAAACCTATTACAAAAGCGTAAATAATTGAATTAGCATTT
plasmid_cp26	18064	BB_B22		1.960 ± 1.0475 0.217333	1.384 ± 0.6817 0.33941	1.014 ± 0.2754 0.76073	1.221 ± 0.4184 0.27306	TGTTTATTAACATAAAATTATTCCAATCTTATCCCCAAGAGATAT
plasmid_cp26	18156	BB_B22		0.473 ± 0.4226 0.100485	0.973 ± 1.6839 0.98111	0.036 ± 0.0618 0.01516	0.137 ± 0.1676 0.03596	TTCCAGTTTTAATACTTTCTAATCCCCTAACATACAATATCTT
plasmid_cp26	18223	BB_B22		1.476 ± 0.2822 0.135854	0.953 ± 0.2244 0.60204	0.812 ± 0.2439 0.29244	0.907 ± 0.2154 0.38213	TTAGTGTGAGCAGCTGGTACAGCAGGAACTGCAATAAAATATGGTAA
plasmid_cp26	18310	BB_B22		1.432 ± 0.8872 0.51407	0.512 ± 0.393 0.32081	0.599 ± 0.2326 0.15826	0.638 ± 0.3048 0.02092	TGTTGTAAGTCGGTTTACACCTTCTCTTCTGTGCAACTTCAA
plasmid_cp26	18532	BB_B22		2.347 ± 1.8026 0.146823	0.67 ± 0.3488 0.25394	0.69 ± 0.5677 0.29426	1.086 ± 0.8284 0.56203	TGCTGTTAACGATTATTGATACTTGGCACTTTAATGCACTGGCA
plasmid_cp26	18574	BB_B22		0.695 ± 1.3358 0.616894	1.226 ± 2.2522 0.73141	0.326 ± 0.7657 0.60563	0.489 ± 0.7963 0.5973	TAAAGCAACATTTGGAGCTTATTACAATTGTATTGGTATTGCTGTT
plasmid_cp26	18577	BB_B22		1.628 ± 0.7103 0.062228	1.267 ± 0.4337 0.41413	0.885 ± 0.5736 0.5835	0.915 ± 0.42 0.68629	TGAGGAAAAATCTAATTGTTAAATTGGCCAATAGATTGCAATTCTTA
plasmid_cp26	18597	BB_B22		1.953 ± 0.3502 0.008611	1.745 ± 0.9646 0.347	1.188 ± 0.4393 0.46418	1.434 ± 0.2317 0.00657	ACCAATTGATTTCTACATATTAAAGCAAACATTGGAGCTTATTAA
plasmid_cp26	18700	BB_B22		1.195 ± 0.5097 0.658971	0.837 ± 0.5146 0.39875	0.995 ± 0.2355 0.96676	1.341 ± 0.6873 0.5235	TGGCAGTGAATGAGCAAATTGCCAAAGTATACCTCCCTTATTTAAATT
plasmid_cp26	18727	BB_B22		3.958 ± 1.5165 0.045243	4.563 ± 5.276 0.36485	1.902 ± 1.001 0.16225	2.9 ± 1.5913 0.09477	CTTGGGCAATTGCTCAGTCACTGCCATAGCTGGATATGCAATTCTT
plasmid_cp26	18744	BB_B22		1.604 ± 0.6236 0.10442	1.132 ± 0.464 0.7154	0.77 ± 0.4051 0.3536	1.191 ± 0.513 0.04772	TTTAATTGTTCAAAATTACAATAAAATACTCTAAAATGTAAATAAA
plasmid_cp26	18906	BB_B22		1.852 ± 1.1199 0.313243	0.874 ± 0.469 0.4451	0.87 ± 0.4453 0.41313	0.805 ± 0.4895 0.39284	ATAGAGTATTAAATTACCGGTATGGAATTGCAATTCTCCAGT
plasmid_cp26	18996	BB_B22		0.965 ± 0.4122 0.817698	0.517 ± 0.4221 0.28072	0.986 ± 0.4204 0.94245	1.087 ± 0.2228 0.39698	AAAACAGCAGCTAGTGCACATTGCAAGGAATTCTTCAATTACACA
plasmid_cp26	19098	BB_B22		1.251 ± 0.7575 0.688995	1.852 ± 1.2961 0.25552	0.973 ± 0.6908 0.95868	0.807 ± 0.2834 0.53153	CCCTATATCACTAGCACAGGTATGGGCTTAATGATTTGCTATT
plasmid_cp26	19106	BB_B22		1.042 ± 0.7636 0.933144	1.131 ± 1.2123 0.89014	0.751 ± 0.3788 0.32658	0.496 ± 0.3048 0.31371	TACTAATACCCTATATCACTAGCACAGGTATGGGCTTAATGCAATT
plasmid_cp26	19123	BB_B22		1.083 ± 0.5212 0.856562	0.926 ± 0.6165 0.88654	0.62 ± 0.2439 0.26076	0.691 ± 0.2678 0.17957	TACTAGAAAATGCTGATTTAGCAAGTGTGAGTAACATGCGCAATTG
plasmid_cp26	19162	BB_B22		2.287 ± 1.344 0.235486	0.964 ± 0.5645 0.9219	0.735 ± 0.4811 0.23174	1.013 ± 0.6998 0.93435	ATGCGCCAATTGCGATACCTGTGCTAGATAATTGCGGATTACAGCTA
plasmid_cp26	19210	BB_B22		2.407 ± 2.8533 0.245253	1.098 ± 1.3078 0.87429	0.516 ± 0.6341 0.52575	1.504 ± 1.7684 0.48475	GCTGTTAACCGCAATATTAGTACAGCAGGTATGCCATTGCGCATTA
plasmid_cp26	19582	BB_B23		2.339 ± 2.8903 0.316941	0.32 ± 0.4793 0.07559	0.423 ± 0.786 0.52959	0.599 ± 0.706 0.58496	TAAGCTAAAGGAATCAAATAAAATATTAAAAGCTGAAATTCTCTA
plasmid_cp26	19682	BB_B23		0.935 ± 0.2252 0.635287	0.898 ± 0.2775 0.37643	1.095 ± 0.2301 0.2713	1.001 ± 0.1372 0.96131	CATATATTAGTGCAGCTGGCTAGCAGGAACCGCAATAACAACTG
plasmid_cp26	19831	BB_B23		1.164 ± 1.2654 0.557417	2.958 ± 4.2438 0.26329	0.769 ± 0.8368 0.60916	2.374 ± 2.3914 0.25051	CTTATATTGAAAGTTTACAGGAATTGCTGAGGGTGGAAAACGGCTTA
plasmid_cp26	20002	BB_B23		2.404 ± 1.6262 0.030121	2.091 ± 1.4197 0.02875	1.762 ± 1.3348 0.1943	1.407 ± 1.179 0.42997	AAAATATTGATATAAAAGCTTCAATTGCTTAAACATAAGAAAAAA
plasmid_cp26	20165	BB_B23		1.663 ± 0.2219 0.028141	1.012 ± 0.3562 0.95969	0.857 ± 0.2259 0.376	1.246 ± 0.2414 0.12551	TGGCAGTGAATGAGCAAATTGCCAAAGTATACCTCCCTTACATTAAATT
plasmid_cp26	20192	BB_B23		3.689 ± 0.9231 0.034335	4.189 ± 4.6243 0.36023	1.841 ± 0.8239 0.19028	2.628 ± 1.3108 0.13534	CTTGGGCAATTGCTCAGTCACTGCCATAGCTGGATATGCAATTCTT
plasmid_cp26	20209	BB_B23		1.702 ± 0.6406 0.069924	1.135 ± 0.4339 0.69659	0.783 ± 0.4709 0.48668	1.239 ± 0.5629 0.03996	TTAATTGTTCAAAATTACAATAAAATACTCTAAAATGTAAATAAA
plasmid_cp26	20299	BB_B23		2.153 ± 1.8076 0.254488	1.748 ± 1.9543 0.41273	0.624 ± 0.313 0.35264	1.218 ± 1.001 0.40112	GCATCATTTAATGATAATTCCCCGCTGACAAAGCAATAAAAGCAATA
plasmid_cp26	20458	BB_B23		0.962 ± 0.6097 0.873127	0.451 ± 0.4024 0.25349	0.64 ± 0.4706 0.35663	0.64 ± 0.2314 0.02955	TTGAAGGACTAATTCTTCAATTCTTATCTTTTAAGAGTAAGGGAGCAA
plasmid_cp26	20461	BB_B23		0.749 ± 0.2235 0.023288	0.434 ± 0.362 0.21827	0.803 ± 0.2916 0.05004	0.903 ± 0.2753 0.12435	AAAACAGCAGCTAATGCAACTGCCAAGGTATTCATCCAAATTACAC
plasmid_cp26	20462	BB_B23		1.540 ± 0.6576 0.302863	0.5 ± 0.4005 0.14027	0.926 ± 0.1762 0.59556	1.317 ± 0.5024 0.3972	AAACAGCAGCTAATGCAACTGCCAAGGTATTCATCCAAATTACAC
plasmid_cp26	20489	BB_B23		1.288 ± 0.6314 0.40105	1.24 ± 0.1032 0.68827	0.827 ± 0.2167 0.29286	0.856 ± 0.2008 0.07776	CCTTGGCAATTGCTGATTAGCTGCTGTTTATTGAGGACTAATTCTT
plasmid_cp26	20555	BB_B23		1.592 ± 1.5753 0.331633	1.043 ± 1.0066 0.93549	1.246 ± 1.2942 0.80031	1.077 ± 1.1066 0.9245	GCATGGCTTCTGGATAGGCTTGAATGCGCTTGTGATTTGCTAGTA
plasmid_cp26	20728	BB_B23		1.271 ± 2.0547 0.688917	0.736 ± 1.5584 0.24936	0.684 ± 1.023 0.77568	2.07 ± 3.043 0.37257	AAAAGGAAATTCTGGCGGGCATTACTCTTTGAGTATGCTATATTA
plasmid_cp26	20737	BB_B23		0.708 ± 0.7641 0.25421	0.869 ± 1.0153 0.51462	0.454 ± 0.4648 0.08947	1.04 ± 1.1717 0.88412	ATATCACTGTTTAAATTGAAAAAATAACCTTTACACTTACCCATA
plasmid_cp26	20775	BB_B23		0.570 ± 0.9132 0.02694	1.759 ± 1.9601 0.58447	1.034 ± 1.2924 0.96336	1.067 ± 1.3116 0.80512	TGAAAAGGTTTATTGCAATTAAAACAGTGTATTAACATATAAAA
plasmid_cp26	20996	BB_B24		1.200 ± 0.8731 0.719768	2.184 ± 1.16 0.18104	0.802 ± 0.2424 0.01289	1.305 ± 0.584 0.31334	AGCTTTAAAGAAATGCTTCAACGCTAAAAGGTTGAAGTATT
plasmid_cp26	21044	BB_B24		1.594 ± 0.8964 0.202822	1.429 ± 0.6609 0.26752	0.863 ± 0.4813 0.76727	1.511 ± 0.8641 0.38529	TTTATTATCAATTAGCTTATGCCGATTAATAGAAATAAGGCATTAT
plasmid_cp26	21058	BB_B24		1.074 ± 1.2769 0.938142	1.449 ± 2.0906 0.19674	0.844 ± 0.9981 0.85273	0.917 ± 1.0712 0.93038	GCTTATGCCGATTAATAGAAATAAGGCATTATCATCCAACTTTA
plasmid_cp26	21198	BB_B24		1.345 ± 0.2097 0.056725	1.001 ± 0.2265 0.99423	0.797 ± 0.138 0.06992	0.961 ± 0.2151 0.79604	AATTAATTCAAGAGAATAATAAAATTCTTAAAGCATTATTACTT
plasmid_cp26	21325	BB_B24		1.506 ± 1.6338 0.010171	1.419 ± 1.6119 0.24113	0.71 ± 0.4799 0.95515	0.674 ± 0.3626 0.91407	ATATGTAAGTTTAAATTGTTAAATGCATATTCTAAAGTA
plasmid_cp26	21325	BB_B24		1.210 ± 0.7568 0.621395	0.846 ± 1.0486 0.66778	0.964 ± 0.8631 0.4638	0.911 ± 1.0035 0.07631	TTATGGACTTCTGAAAATTTTAAATTACTTTTATTG

plasmid_cp26	21328	BB_B24	1.484 ± 0.1259 0.01144	1.244 ± 0.205 0.24366	0.83 ± 0.1082 0.01807	1.028 ± 0.1612 0.8153	TGTAAGTTTTTATAAAATTGTTTTAAATGCATATTCTAAAGTATT
plasmid_cp26	21420	BB_B25	1.299 ± 0.847 0.081476	1.057 ± 0.5726 0.6942	0.836 ± 0.5022 0.33037	1.08 ± 0.6857 0.49506	TTGAAGGTATCCTTAGTCCAAACCTGAAAAGAACTCTCATTAATAAAAA
plasmid_cp26	23099	BB_B27	1.844 ± 1.4327 0.052779	1.133 ± 0.8485 0.70428	0.914 ± 0.8492 0.67502	0.774 ± 0.7403 0.25032	TATCTTGGTAAAATACCGAAAAAGATAAAATAAATTAACTGTTTAT
plasmid_cp26	23100	BB_B27	1.562 ± 0.4181 0.085936	0.955 ± 0.3257 0.44454	0.863 ± 0.2345 0.57679	1.626 ± 0.3866 0.09107	TAGTTGAACAACCATAAAACAATAAAAATAACGGATATTAAAACCTCT
plasmid_cp26	23194	IG_124	0.832 ± 0.9301 0.468929	0.495 ± 0.8257 0.54668	0.566 ± 0.7293 0.24471	1.302 ± 1.4244 0.58886	CTTTACTTTTACTAAAGCATACAATTAGGCATTAATGAAGAAGTT
plasmid_cp26	23240	IG_125	2.121 ± 1.2788 0.103098	1.302 ± 0.9034 0.54658	0.887 ± 0.5231 0.69981	1.269 ± 1.1337 0.72324	AAGTTTATTTTAAATTATCAAATAATTCTATATTTTATTACTTTA
plasmid_cp26	23253	IG_126	2.589 ± 2.1444 0.299333	2.112 ± 2.111 0.49371	1.443 ± 1.2136 0.3282	1.706 ± 1.2195 0.17968	AAATGAGTTATTATGTGCTAACGAAATATTCTATATTCTGGTACCTTG
plasmid_cp26	23266	BB_B28	1.785 ± 0.6797 0.063707	1.247 ± 1.7995 0.82693	1.139 ± 0.8024 0.83022	0.869 ± 0.2873 0.06933	TGTGCTAACGAAATATTCTATATTCTGGTACCTTGTATTGGATTTT
plasmid_cp26	23270	BB_B28	1.636 ± 0.6236 0.054952	0.87 ± 0.5813 0.56405	0.866 ± 0.3299 0.05916	1.024 ± 0.5234 0.91718	GCACATAATAACTCATTTACATCCTTTAACGTTTAAAGTTTAAATTAT
plasmid_cp26	23342	BB_B28	2.107 ± 0.8396 0.007659	1.05 ± 0.6228 0.70924	0.88 ± 0.4536 0.01994	1.29 ± 0.6775 0.15521	AATTTTATTGAAAATTGTAAGATAAAATCCAATAACAGGTACCCAG
plasmid_cp26	23421	BB_B28	1.419 ± 0.4609 0.017404	0.822 ± 0.35 0.02301	0.729 ± 0.3239 0.03145	0.905 ± 0.2608 0.51519	GTCAAATTATCTTACTTCACCGAAAAGCAATTAGAAGGATT
plasmid_cp26	23437	BB_B28	1.548 ± 0.5847 0.006443	1.192 ± 0.5191 0.07214	0.673 ± 0.2252 0.26884	1.089 ± 0.4978 0.44467	ATAAGATAAAATTGAACTATAAATAAAAGAGTAAAAAAAGTTAAATAA
plasmid_cp26	23590	BB_B28	1.057 ± 1.2391 0.942622	0.2 ± 0.1689 0.05697	1.738 ± 2.071 0.58317	1.115 ± 0.9397 0.86685	TAGTGGATCAAATTGACATCACTTCTATTGGTACTGGAAAATT
plasmid_cp26	23593	BB_B28	1.836 ± 0.1537 0.010038	1.09 ± 0.1576 0.41149	0.903 ± 0.0965 0.21531	1.179 ± 0.2528 0.34083	TACAGTGTAAATGCTAGTTGAGAAAATATGCTAAAACATTGGAAAAG
plasmid_cp26	23682	BB_B28	1.035 ± 0.2028 0.738283	0.634 ± 0.5475 0.44677	0.899 ± 0.3433 0.51256	1.381 ± 0.2747 0.13716	GGACAACAAATTAGCAGAAATTAAAGAAAATAGAACAAATAAGAAAATA
plasmid_cp26	23733	BB_B28	0.968 ± 0.1723 0.79112	0.585 ± 0.5194 0.32992	0.851 ± 0.0716 0.02147	1.131 ± 0.1568 0.17992	ATATTTCTTTATTGTTCTAGTTTCTTAAATTCTGAATTGTTGTC
plasmid_cp26	23755	BB_B28	0.998 ± 0.821 0.995802	0.493 ± 0.6777 0.56724	1.116 ± 0.9602 0.72811	1.631 ± 1.6922 0.09124	AAATTACCTATTCTAAATGGAGAAAATACAGAAATAAGTATTGATGAGAA
plasmid_cp26	23793	BB_B28	1.787 ± 0.5514 0.035659	1.07 ± 0.4341 0.47897	0.84 ± 0.2587 0.1863	1.202 ± 0.4916 0.36913	CTTATTCTGTATTCTCCATTAGAATAGGTAATTATATTATTATAA
plasmid_cp26	23913	BB_B28	1.877 ± 0.5852 0.074192	1.137 ± 0.2976 0.27988	0.82 ± 0.1249 0.12021	1.182 ± 0.1405 0.11568	AAGTAGATTGATCTAACCCAGAAAATAAACATAACCAAAGAAC
plasmid_cp26	23977	BB_B28	1.247 ± 0.1066 0.038809	0.84 ± 0.0553 0.02344	0.633 ± 0.2571 0.12635	0.704 ± 0.2808 0.23817	GTAACGTTTATTAGTCTTGAAGTTATGTTTATTCTGGATTAG
plasmid_cp26	24046	BB_B28	1.883 ± 1.3899 0.165126	0.535 ± 0.3921 0.16719	1.126 ± 1.0139 0.81382	0.938 ± 0.8866 0.71961	ATAAGGGCTCATGCTATATTCTTATAATTCTATGGGAGTAA
plasmid_cp26	24116	BB_B28	1.861 ± 0.7812 0.198887	1.494 ± 0.763 0.07181	1.127 ± 0.5238 0.38679	0.87 ± 0.3447 0.50363	TACATTGAGAAAATAAGCAACTACAAAATTAACTGAAATGATAA
plasmid_cp26	24216	BB_B28	1.517 ± 1.1336 0.436246	0.58 ± 0.4947 0.48843	0.332 ± 0.2864 0.17134	0.632 ± 0.5212 0.53181	TTTGTGAAAATATTATTATTATAAATAAAATTCTTAAATCATCA
plasmid_cp26	24266	BB_B28	1.849 ± 1.0489 0.151922	0.883 ± 0.4721 0.78476	0.756 ± 0.5613 0.6761	1.158 ± 0.6337 0.5187	AAAGCAAAAGTATTATAAATTATAAACAAAAGAATTATAAAT
plasmid_cp26	24608	IG_127	0.838 ± 0.7094 0.592613	0.923 ± 0.9141 0.8209	1.535 ± 0.9492 0.4984	1.401 ± 0.1116 0.41975	TAAGCAATGCTTATAACAAATGCCATGAAATTAAAGGGAAAACATCT
plasmid_cp26	24850	BB_B29	0.094 ± 0.1173 0.03747	0.327 ± 0.3856 0.12484	1.796 ± 1.3016 0.21371	0.336 ± 0.4504 0.10139	GATATAGATGCTGATGATGTTGACATAATTCCCCTTTATTAGTGC
plasmid_cp26	25022	BB_B29	0.109 ± 0.1358 0.167427	0.303 ± 0.4026 0.25666	2.47 ± 2.1534 0.13268	0.139 ± 0.2034 0.16892	AAGTATTGAGTTGACAAAGTCTTCCATTCAAGGACTTCTTAATCCATA
plasmid_cp26	25102	BB_B29	0.142 ± 0.0685 0.010599	0.349 ± 0.1941 0.01444	2.494 ± 0.9087 0.08454	0.246 ± 0.0681 0.00715	GCAAGTCCGATTGGAATTGGCGCTGCAAACATTAAAGGGAGATTAGC
plasmid_cp26	25170	BB_B29	0.168 ± 0.2756 0.229554	0.924 ± 1.686 0.72611	2.485 ± 3.691 0.23778	0.169 ± 0.291 0.22329	AATGGGATTGTCACATACAGGAATCACACAGAAAAGCCAGCTTAA
plasmid_cp26	25233	BB_B29	0.066 ± 0.0651 0.058903	0.275 ± 0.3517 0.01269	3.125 ± 1.9325 0.044	0.09 ± 0.0553 0.06758	ATTCCAAATGCTGATGTTTAAAGCTGCGTTCTGGTGTATTGCTTGT
plasmid_cp26	25452	BB_B29	0.138 ± 0.0809 0.10892	0.441 ± 0.5891 0.12083	2.442 ± 1.5172 0.17766	0.161 ± 0.0448 0.02048	CCACAAACATTGCCATTGTTACATTGGCACAAATCTTGTGCCCCAA
plasmid_cp26	25464	BB_B29	0.002 ± 0.004 0.093547	0.028 ± 0.0507 0.09195	0.195 ± 0.2032 0.07433	0 ± 0 0.09374	AAAATATTCTTACCAACAAACATTGCCATTGTTAGTTACATTGGCACAAATC
plasmid_cp26	25710	BB_B29	0.169 ± 0.1767 0.118183	0.37 ± 0.3309 0.16111	8.593 ± 7.1636 0.08328	0.088 ± 0.1076 0.11143	CAGTATTGGATCTGCAAGTTGTTGAAAATATTGTTGCTCTGAGA
plasmid_cp26	25713	BB_B29	0.058 ± 0.0707 0.13663	0.291 ± 0.3996 0.089	3.187 ± 2.9396 0.07109	0.091 ± 0.0817 0.14797	CACTTGAAGTTGCAAAAGGAACAGATTTTAGCGGGGAAATTGTTGTT
plasmid_cp26	25928	BB_B29	0.053 ± 0.039 0.102985	0.272 ± 0.3451 0.26042	1.763 ± 1.1553 0.26948	0.166 ± 0.125 0.13631	AAGTGTGGTCTGCAAAAGGAACATGCAAATTCAAGGGCTCTGTAATTCC
plasmid_cp26	25931	BB_B29	0.104 ± 0.0577 0.02486	0.386 ± 0.3862 0.03066	2.64 ± 1.0173 0.02771	0.145 ± 0.0943 0.01584	ATAAAGTGTGGTCTGCAAAAGGAATGCAAATTCAAGGGCTCTGTAAT
plasmid_cp26	25940	BB_B29	0.121 ± 0.1943 0.136654	0.445 ± 0.4386 0.43409	2.497 ± 2.4325 0.14073	0.082 ± 0.0981 0.20552	TATAAGTAATAAAGTGTGGTCTGCAAAAGGAATGCAAATTCAAGG
plasmid_cp26	25943	BB_B29	0.108 ± 0.1242 0.091359	0.718 ± 1.032 0.27705	3.017 ± 2.1193 0.02018	0.217 ± 0.168 0.1136	TGTTCTTCTTGGACTAGCATATTCTTAAACACCTTTAAACGTAG
plasmid_cp26	25959	BB_B29	0.274 ± 0.4673 0.149827	0.306 ± 0.5301 0.14589	1.148 ± 0.9207 0.79091	0.057 ± 0.059 0.00163	GTCCAAAAGAGGAGACATATTAAAGTATAAGTGTGGTCTGCAAAA
plasmid_cp26	25992	BB_B29	0.008 ± 0.0137 0.079907	0.179 ± 0.3243 0.11659	3.288 ± 3.3998 0.2404	0.099 ± 0.1691 0.0894	GGAGTGGACTAACATTGTTGGCGATTATAGATGTTCCATTGGA
plasmid_cp26	26025	BB_B29	0.065 ± 0.0906 0.172219	0.525 ± 0.8814 0.00873	2.104 ± 2.4275 0.14793	0.145 ± 0.1758 0.18493	GATATGTTCTTGGAAATCTCAGGAAAATAGCAAAACATTGGATA
plasmid_cp26	26026	BB_B29	0.047 ± 0.0438 0.10615	0.364 ± 0.472 0.30276	2.629 ± 1.8578 0.17115	0.136 ± 0.1295 0.11	TCTATAATCCGCCAGAAAATGTTAGTCAACTCTACGTTAAAGGTGT
plasmid_cp26	26099	BB_B29	0.000 ± 0 0.0302	1.391 ± 1.5674 0.66566	5.269 ± 3.3401 0.10539	0.267 ± 0.3341 0.10914	GAAGATCCCAGAGAATAGGAATTGCTATCCAATTGTTGCTATTCCCTG
plasmid_cp26	26464	IG_128	0.389 ± 0.5822 0.476658	0.055 ± 0.0834 0.15428	1.012 ± 1.6049 0.98387	0.432 ± 0.4941 0.38868	TTTTAAAATTTACATAAGCTGTCGATTCCATTATATTCGAC
plasmid_cp32-1	96	BB_P01	2.280 ± 1.0036 0.047613	1.536 ± 1.2742 0.4247	1.016 ± 0.3476 0.79076	1.071 ± 0.4785 0.49702	GATAAAATAAGTCACTAGAACTATAACAAACTCAATTGTTTAAAGAAT
plasmid_cp32-1	274	BB_P01	1.030 ± 0.8162 0.919729	0.826 ± 0.9591 0.83058	1.591 ± 1.3985 0.54105	0.87 ± 0.8061 0.76931	ATACAATTAGCAGAGCATTTAAAGCTGACCTTAACTAGCTCAAGGTCA
plasmid_cp32-1	279	BB_P01	1.713 ± 0.5685 0.105948	1.629 ± 1.2968 0.44654	0.82 ± 0.2575 0.11005	1.103 ± 0.3494 0.50466	AGCTACCGTTTCATGGGATGGCTATGTTTAGTAAAACCAAGGATACC
plasmid_cp32-1	333	BB_P01	2.978 ± 1.5031 0.082068	1.151 ± 1.045 0.83713	0.592 ± 0.5186 0.51499	0.71 ± 0.601 0.6271	ATAGATCTGCAACACCCTTAATAGAATTACCTATTGGTTTGAATAC
plasmid_cp32-1	395	BB_P01	1.782 ± 0.2913 0.004012	1.406 ± 0.7207 0.41429	1.071 ± 0.1627 0.17033	0.959 ± 0.1696 0.60805	TTCATAACTCAAGGTATTCAAACCAATAGGTAATTCTATATTACACGGGTTG

plasmid_cp32-1	398	BB_P01	1.526 ± 0.4147 0.05796	1.313 ± 0.6857 0.44545	0.596 ± 0.2163 0.00216	0.818 ± 0.1893 0.23134	TGTAAGAGATTTGGGAGTTGATTTGATCATATAACCTATAAAAGTAAAATC
plasmid_cp32-1	399	BB_P01	1.238 ± 0.359 0.408874	0.585 ± 0.4386 0.16135	1.091 ± 0.2928 0.66889	1.177 ± 0.3496 0.48854	CATATTCAATCAAGGTATTCAAACCAATAGGTAATTCTATTAAACGG
plasmid_cp32-1	444	BB_P01	1.517 ± 1 0.523457	1.365 ± 0.3748 0.22168	1.09 ± 0.5114 0.82492	0.775 ± 0.2457 0.39059	AAATCCAACAATAAGAACAACTTCTTAGACGCAGTTAAACATAAAAAGT
plasmid_cp32-1	478	BB_P01	1.495 ± 1.2194 0.417015	0.999 ± 0.9196 0.99941	0.597 ± 0.357 0.31678	1.219 ± 0.5412 0.48404	ACTCGCTCTAAAGAATTGTTCTATTGTTGGATTTTACTTTAGGTTATA
plasmid_cp32-1	490	BB_P01	2.403 ± 0.8146 0.104048	1.647 ± 2.3284 0.68214	0.366 ± 0.3279 0.11693	1.106 ± 0.6609 0.84142	AAAGTCGACTTATCATATATGAAAACTTGATTATATCTAAAAAGATATG
plasmid_cp32-1	504	BB_P01	0.445 ± 0.3457 0.188967	0.277 ± 0.2506 0.12525	0.716 ± 0.5081 0.44098	0.412 ± 0.4138 0.33019	TGATAAGTCGACTTTATGTATTAACTGCGTCAAAGAATTGTTCTTAT
plasmid_cp32-1	506	BB_P01	3.577 ± 2.4429 0.016664	2.251 ± 2.7763 0.36116	1.056 ± 0.6522 0.90794	1.314 ± 0.10436 0.01826	TATGATAAGTCGACTTTATGTATTAACTGCGTCAAAGAATTGTTCTT
plasmid_cp32-1	507	BB_P01	1.659 ± 1.3457 0.229008	1.33 ± 1.2077 0.24226	1.215 ± 0.9585 0.54762	1.36 ± 0.2115 0.46203	TATGAAAACCTTGATTATATCTAAAAGATATGTTCCGTGTTAACCGAA
plasmid_cp32-1	521	BB_P01	2.113 ± 0.8427 0.048969	1.214 ± 0.6985 0.71823	1.001 ± 0.4037 0.99531	1.196 ± 0.5158 0.53981	ATCAAAGTTTCATATATGATAAGTCGACTTTATGTATTAACTGCGTC
plasmid_cp32-1	524	BB_P01	1.957 ± 0.5097 0.027066	1.041 ± 0.7545 0.92281	1.14 ± 0.2148 0.31921	1.548 ± 0.1029 0.44309	TATCTAAAAGATATGTTCCGTGTTAACCGAAAGCTTTACTAGATATG
plasmid_cp32-1	526	BB_P01	1.058 ± 0.7696 0.764083	0.096 ± 0.1041 0.16641	0.743 ± 1.2024 0.43473	1.626 ± 1.5848 0.30218	TCTTTAAAAGATATGTTCCGTGTTAACCGAAAGCTTTACTAGATATT
plasmid_cp32-1	578	BB_P01	2.146 ± 1.4406 0.186939	2.394 ± 2.1106 0.29176	0.86 ± 0.4398 0.60232	1.4 ± 0.6696 0.28969	TTTATTGGAAGAAGATATACGTAGAAATAGAAAAGACGTATTGAAAACCAA
plasmid_cp32-1	744	BB_P01	1.860 ± 0.7445 0.168438	1.979 ± 1.5429 0.37461	0.979 ± 0.1539 0.86885	1.054 ± 0.1305 0.2138	TCTCTTTTTGAGAAAACAAAATTCAACATCATAGTAAAGATATTCT
plasmid_cp32-1	1039	BB_P01	1.097 ± 0.6946 0.793925	1.092 ± 0.6683 0.85886	0.319 ± 0.2202 0.16236	0.389 ± 0.4203 0.24513	TCACCTTACCATCTTCTAGTCTTAGCTGCTCATAAAACCTCTG
plasmid_cp32-1	1042	BB_P01	3.679 ± 2.2079 0.038148	2.525 ± 3.6892 0.45691	1.072 ± 0.5944 0.82227	0.932 ± 0.6191 0.88805	GGAGTAATTATTACGATTTCTAAAGGTGTCAGAACAGTTGAGAACT
plasmid_cp32-1	1214	BB_P01	1.808 ± 1.3941 0.116166	1.998 ± 2.5137 0.33369	1.166 ± 1.171 0.18317	1.065 ± 1.1122 0.75102	TAACACGCTTACAAAGTAGCTCATTTATAATGAGGAGCTAGCGATGTT
plasmid_cp32-1	1626	BB_P02	2.309 ± 1.5952 0.304761	1.039 ± 0.687 0.89964	0.613 ± 0.2268 0.24071	0.868 ± 1.2903 0.89712	TCCTTTGCAAGTAGCACCTTGTAAATGATTGCTAACATGTTGCTTT
plasmid_cp32-1	1631	BB_P02	0.998 ± 1.2008 0.999189	0.997 ± 1.0413 0.99174	1.029 ± 0.9905 0.91786	1.047 ± 0.9052 0.48162	CATAAAAGACATTATGCAAGCACACGTAGAGAACATTGACGAAAGTTCG
plasmid_cp32-1	1747	BB_P02	1.257 ± 0.5877 0.292939	0.296 ± 0.2226 0.10262	0.843 ± 0.683 0.61	1.059 ± 0.5219 0.78167	TTAGAGCAACTTGTCTTAGAAAAGTGAATTAAATTAAAGAAAAAAAT
plasmid_cp32-1	1928	BB_P02	1.344 ± 0.6553 0.46496	1.296 ± 0.2656 0.17421	0.752 ± 0.3421 0.38505	0.657 ± 0.4883 0.43764	TTACTTATCGCTTGACAAATTCTGTGAAATTAAATAGGTACAAAATTAGAA
plasmid_cp32-1	1931	BB_P02	2.538 ± 1.7838 0.060833	1.621 ± 1.4582 0.22343	1.428 ± 0.8359 0.13292	1.06 ± 0.6865 0.6872	CATACAAGAACAGCAATTCAATTAACTTATGAAAATCTAAAAGACATAAAA
plasmid_cp32-1	2216	BB_P03	1.713 ± 0.9633 0.28183	1.165 ± 0.8508 0.77659	0.843 ± 0.5357 0.61491	0.857 ± 0.499 0.48262	TACGGATACCTTGTAGCAGGTTAATTCTCTATTGTCTTACTGCTAGTG
plasmid_cp32-1	2231	BB_P03	1.700 ± 2.1548 0.307871	1.886 ± 2.005 0.20887	1.427 ± 0.9376 0.42509	1.373 ± 0.4671 0.29505	AGCTTAGTTGGAGATGGAACACCGAACTAGAAGTTGAGGCTGGTGGT
plasmid_cp32-1	2341	BB_P03	1.972 ± 0.8316 0.1902	1.41 ± 0.8776 0.51964	0.94 ± 0.4884 0.85649	0.913 ± 0.2061 0.53406	TAACAGTGGCATACCGCTAAACTCATATATCGAACACACTCATATA
plasmid_cp32-1	2698	BB_P04	0.365 ± 0.3425 0.27761	0.316 ± 0.5496 0.3361	0.635 ± 0.375 0.12358	0.418 ± 0.4649 0.09502	CGTCCTCAGCTTGTCTGCTTGCCTTAGCTCTAGGAGCAGCGGAAACCT
plasmid_cp32-1	2993	BB_P04	0.982 ± 0.6553 0.935165	0.734 ± 0.6667 0.70331	1.227 ± 0.8127 0.31245	1.336 ± 0.1052 0.04237	TCAGTATCAGCTCAACTTCAACATATATAGAGTTCTTTGAAACAGT
plasmid_cp32-1	3004	BB_P04	2.468 ± 1.4539 0.109376	1.374 ± 1.4693 0.64434	0.746 ± 0.447 0.14365	1.026 ± 0.7426 0.96198	TCCCACATATCAGTATCAGCTCAACTTCAACATATATAGAGTTCTT
plasmid_cp32-1	3124	BB_P04	0.062 ± 0.0884 0.158757	0.308 ± 0.5173 0.14059	1.414 ± 1.4419 0.57193	0.241 ± 0.2909 0.16205	AATAATAACGGTGTATTATCAAGGCCAGGTGGCCACCAACCGCAATT
plasmid_cp32-1	3203	BB_P04	1.863 ± 0.7859 0.042691	1.757 ± 1.2708 0.28274	1.002 ± 0.4646 0.9856	1.435 ± 0.47 0.07818	CAATCAATTGCAACCGGAAGATGGAACATCAAGATCAAATAGATATCTA
plasmid_cp32-1	3249	BB_P04	0.132 ± 0.2143 0.191155	0.342 ± 0.5405 0.33251	0.179 ± 0.1905 0.20708	0.411 ± 0.5974 0.41797	TCCTAGGCAAGTAGTTCTATTAAATTGAAAAAGTTGCAATTGGAACAA
plasmid_cp32-1	3376	BB_P05	3.449 ± 2.3648 0.054092	2.037 ± 1.7995 0.19953	1.146 ± 0.861 0.42411	1.138 ± 0.8326 0.51796	TCTCCATTATTACCTCTTTTATTGCCCCAAAGTTAACCCACCATG
plasmid_cp32-1	3393	BB_P05	2.624 ± 2.4954 0.358798	2.291 ± 2.6994 0.35442	1.689 ± 0.9845 0.1162	1.741 ± 1.2449 0.38865	AAAGAGTATCAAGAGAAAAGAAGTAAACTGAAAAGTTATGAAAATC
plasmid_cp32-1	3668	BB_P05	1.996 ± 1.9308 0.358105	1.772 ± 2.3338 0.52477	0.737 ± 0.4721 0.59403	1.275 ± 0.8162 0.66196	TGGAATATGCATTGACATAGATGAGTTAGTAAACAGCTACTATTGTGCC
plasmid_cp32-1	3694	BB_P05	2.062 ± 0.6931 0.105575	2.249 ± 1.9007 0.35902	1.052 ± 0.3335 0.66848	1.457 ± 0.6698 0.13253	AACTCATCTATGCAATGCATATTCCATATAAGTCTTACCTCCACCAGCC
plasmid_cp32-1	3727	BB_P05	2.266 ± 1.2985 0.210641	1.586 ± 1.3554 0.58415	1.2 ± 0.9847 0.8075	1.192 ± 0.5802 0.43585	TTGGTAATTGGCACAATAGTAGCTGTTTACTAAACTCATCTATGCAATG
plasmid_cp32-1	3796	BB_P05	1.586 ± 0.9333 0.144643	1.804 ± 1.4676 0.14477	0.944 ± 0.6347 0.82814	1.387 ± 0.1046 0.23281	AAGACGGTGTCTTGTAAAAGGGTACTGGAGCACCAATAAGCAACTTATA
plasmid_cp32-1	4067	BB_P06	1.604 ± 0.7149 0.20649	0.901 ± 0.2527 0.31777	0.784 ± 0.1548 0.20858	0.894 ± 0.139 0.42489	AGATGTTGATCTACAAATGGGATATCAAACACCGTAAAATGGACGCGTT
plasmid_cp32-1	4222	BB_P06	2.510 ± 1.3467 0.127714	2.37 ± 1.543 0.34611	0.83 ± 0.4248 0.31537	1.09 ± 0.5750 0.60426	AATTCAAGCATTTAAACGAGACTTCTGAGAAAATTTACTTCAGATT
plasmid_cp32-1	4489	BB_P06	2.184 ± 1.7254 0.213156	1.841 ± 2.3711 0.51663	0.734 ± 0.5448 0.1453	1.088 ± 0.528 0.57479	AAATGGATAAAATCTTGTGAAAGGATGAGGCTGGACTTTCAAAGTTAGAC
plasmid_cp32-1	4678	BB_P06	1.973 ± 1.4602 0.178762	0.348 ± 0.2792 0.19596	0.35 ± 0.2098 0.10774	0.833 ± 0.6643 0.0713	AGGCTTAAATATAGAGAAGATGTTACATTGAAACACTTCAAAGCTGTA
plasmid_cp32-1	4789	BB_P06	2.161 ± 0.8913 0.126112	1.268 ± 0.7014 0.61265	0.915 ± 0.3866 0.81054	0.985 ± 0.3889 0.92663	TACTGCTAGGTTAAATTATAAGTTCAGAATTAGTTAGGATAATGAGT
plasmid_cp32-1	5093	BB_P07	1.440 ± 0.3179 0.163951	1.375 ± 1.6638 0.74041	0.898 ± 0.5507 0.79338	0.869 ± 0.3613 0.6106	GCTTGAAGTAAGGATAATGAAGTAGAGAAAATTTCGCTCTAGTGC
plasmid_cp32-1	5259	BB_P07	1.370 ± 0.9894 0.603427	1.806 ± 1.5328 0.33807	0.698 ± 0.3871 0.45124	0.952 ± 0.6738 0.94017	TTATCCTAGTAGCAGTGGAGGGCGAAGAAGCGCGGAGGGGAGTTGGC
plasmid_cp32-1	5566	BB_P08	1.647 ± 0.6918 0.085502	1.634 ± 1.642 0.50049	0.798 ± 0.2566 0.16205	1.095 ± 0.5414 0.60156	TTATGACATAAGGCCACAAGAACACTGCAATTCTTATGATTCTGATATG
plasmid_cp32-1	5633	BB_P08	0.430 ± 0.198 0.118765	0.424 ± 0.3851 0.22071	1.184 ± 0.4085 0.05578	1.043 ± 0.3976 0.51287	TTCCAAACTTACACATATCAAGACCTTAACATGAACCAAAGACCGAAT
plasmid_cp32-1	5648	BB_P08	3.692 ± 2.2784 0.105271	0.762 ± 0.5292 0.30066	1.065 ± 0.5731 0.72684	1.192 ± 0.7544 0.71266	TGTGAAAAGTTGGAATATCCTTGAATATCAGACATATCAGAACATAAAG
plasmid_cp32-1	5917	BB_P09	2.650 ± 0.8984 0.044053	1.404 ± 0.7464 0.4008	0.98 ± 0.2619 0.83855	1.106 ± 0.2647 0.47206	TATCAATAATAGCTATATAAGTCAAGTTAATCTTGACCTAAATCGGG
plasmid_cp32-1	5928	BB_P09	2.463 ± 2.0326 0.199416	1.986 ± 2.115 0.37913	1.084 ± 0.6761 0.69229	2.174 ± 1.4272 0.18354	GCTATATAAACTCTAAGTTAATCTTGACCTAAATCGGGATGGAGGCTA
plasmid_cp32-1	6014	BB_P09	2.603 ± 1.2648 0.062078	1.668 ± 1.1689 0.27608	0.994 ± 0.3353 0.94769	1.291 ± 0.5233 0.15445	GATAATTTCATAGTATCTTAAAGAGCTTGTCCAATGCGCTTACCCG

plasmid_cp32-1	6081	BB_P09	2.515 ± 1.4508 0.016206	0.915 ± 0.7981 0.45571	1.44 ± 1.288 0.33882	0.997 ± 0.6447 0.99599	CTACCCCTTTAAACTTACTTTGATTGATTAGCCTTAAGGCTGGAGTG
plasmid_cp32-1	6139	BB_P09	2.087 ± 1.5695 0.327364	1.369 ± 1.325 0.68081	0.535 ± 0.2103 0.14009	0.889 ± 0.3042 0.65134	TAAGGTAACACTTGAATGATTTCACITTAGATATGGTATAAATCATTTA
plasmid_cp32-1	6178	BB_P10	1.083 ± 0.4458 0.27756	0.466 ± 0.4127 0.29266	0.935 ± 0.4764 0.01299	1.051 ± 0.4689 0.41061	TAAATCATTAACCCAATATTAAAGGGTTAAGGCATATGCAACTGAA
plasmid_cp32-1	6254	BB_P10	1.632 ± 1.9814 0.602998	2.779 ± 1.2174 0.09858	1.398 ± 1.3653 0.70509	2.12 ± 1.0328 0.20236	TTATGATATCGCAGTCAAATTATTTCAAGTCATATGCCCTAACCCCT
plasmid_cp32-1	6307	BB_P10	1.995 ± 0.4346 0.052843	1.082 ± 0.2716 0.73325	0.83 ± 0.2523 0.45457	0.896 ± 0.1523 0.39828	TTATTTGAGTAGCAGCTGTAGTTTGAAGAGATATGGATGATTGAGG
plasmid_cp32-1	6372	BB_P10	2.139 ± 1.1599 0.028682	2.051 ± 2.2611 0.33754	0.911 ± 0.4955 0.82278	1.079 ± 0.7299 0.86757	TGAAAATGCTTGGAAATTAGTATAAATTTCAATATATATTGCAAT
plasmid_cp32-1	6473	BB_P10	1.987 ± 1.8735 0.199636	3.072 ± 2.8304 0.17004	0.629 ± 0.76 0.60546	0.77 ± 0.9973 0.78462	TAAAGCATTAAACATCGCTGAATTAGCGCTCAAAGCTTGGCGTTAACACT
plasmid_cp32-1	6496	BB_P10	0.673 ± 0.6114 0.211213	0.584 ± 0.519 0.07215	0.81 ± 0.2842 0.14598	0.99 ± 0.4843 0.8866	CACAATAAAAGCTCATAAAGTATAATTGCCAGTCTACAAACCGACTATATT
plasmid_cp32-1	6545	BB_P10	2.010 ± 1.521 0.113415	1.827 ± 1.6912 0.26351	0.867 ± 0.5061 0.45505	1.13 ± 0.5852 0.5771	TTAATAAAAATTAACTTCTACATTACCAACATCTAATATGCAAACAGTTG
plasmid_cp32-1	6822	BB_P11	1.084 ± 0.904 0.767608	0.473 ± 0.6666 0.40355	1.099 ± 0.672 0.6834	1.658 ± 1.3566 0.28671	GCAGCATCTTAACTTGTAGTTAGCTGTGTTGAAACCAAAAGTGGAA
plasmid_cp32-1	7364	BB_P11	2.696 ± 1.3097 0.102444	2.117 ± 1.8298 0.34674	1.133 ± 0.3929 0.33217	1.24 ± 0.3206 0.38759	ATTGAAAAGTGGCAACTGCAAATAACTTACTTCACTTCAATGAA
plasmid_cp32-1	7728	BB_P11	1.997 ± 0.7451 0.060887	2.039 ± 1.2502 0.3132	1.138 ± 0.4469 0.61787	1.066 ± 0.5098 0.09659	ATATTACGGCTAATGCTTAAGTGTGGCGTAGGAGAAAGAGTAAGC
plasmid_cp32-1	7737	BB_P11	1.183 ± 1.7267 0.848713	0.087 ± 0.1334 0.10869	1.003 ± 0.6485 0.98769	1.286 ± 0.1017 0.6462	ACTTTAGCATTAATGCTGTTGCTTAGAATTACTACTCAAGATAGTTG
plasmid_cp32-1	7969	BB_P12	1.987 ± 0.9769 0.113446	1.946 ± 1.9107 0.41032	1.044 ± 0.4739 0.83203	1.044 ± 0.4757 0.59676	AGAGATCCAAAACAATAACTTATGTTCAACATTGAAGTGACACTAGGT
plasmid_cp32-1	8141	BB_P12	2.974 ± 1.415 0.035931	1.798 ± 2.0554 0.48686	1.382 ± 0.7197 0.45906	1.207 ± 0.5296 0.06412	GAAAATTTGGTAGCAATTCTATCATTGAATGCTAAATCAAGCATTTA
plasmid_cp32-1	8219	BB_P12	1.918 ± 0.5309 0.082332	1.872 ± 1.5724 0.42552	0.964 ± 0.1453 0.70307	0.975 ± 0.1416 0.58989	GCCCTAATTCAAAGAGATACTTTCGGCCCTAGCAGAAATACTCTTGAA
plasmid_cp32-1	8270	IG_129	1.862 ± 1.3967 0.365823	0.565 ± 0.689 0.46488	1.29 ± 0.9759 0.7043	0.503 ± 0.1998 0.01766	ATAAGAATTCCTTTAAGAGTTGGTTGTTAGATTTTGGCAATTATA
plasmid_cp32-1	8434	BB_P13	1.639 ± 0.6784 0.194323	1.663 ± 1.5004 0.57593	1.453 ± 0.9607 0.55662	0.717 ± 0.5242 0.59632	AGCTGTGATTCTCTTAAGTATTAAACCTCATTAAGCTTAAACAGCGT
plasmid_cp32-1	8575	BB_P13	2.753 ± 1.6251 0.215585	1.143 ± 0.5681 0.72473	1.49 ± 0.775 0.14878	1.284 ± 0.4591 0.17542	AAAAAGCCCTTTAGTATTTGAGTAGTGAAGATAATGTTGGTGT
plasmid_cp32-1	8645	BB_P13	2.134 ± 0.8313 0.057738	1.314 ± 0.9261 0.52734	1.077 ± 0.5972 0.76436	1.416 ± 0.7364 0.41308	TAAATGAAAATTGATTGAAAGAGTACCTTCACTTCAATCAAGTA
plasmid_cp32-1	8746	BB_P14	1.753 ± 0.5253 0.013163	1.637 ± 1.09 0.25616	1.23 ± 0.4612 0.47539	1.082 ± 0.4026 0.17825	TGATAAAAGCTTCAAGTCTGATGAGACTAGAAAAAAATATTAACT
plasmid_cp32-1	8839	BB_P14	2.523 ± 1.4666 0.18437	2.876 ± 2.6049 0.31792	1.557 ± 1.8238 0.6365	1.793 ± 2.1938 0.5816	ATTCTGAAAATAGTATTATCCTGTTAATCTCGTAAGCAAGTAAAAA
plasmid_cp32-1	8934	BB_P14	1.378 ± 0.10249 0.634466	0.819 ± 0.4208 0.50035	0.77 ± 0.8764 0.49913	0.656 ± 0.5387 0.502	TTGTATGAATTAATTAAAGCAAGTGGAGACTAGTGAGCGACAAATT
plasmid_cp32-1	8965	IG_130	2.511 ± 0.4907 0.011118	1.524 ± 0.7571 0.27639	1.189 ± 0.7259 0.71751	1.121 ± 0.946 0.8533	AGTCCTACTGCTAAATTATCATACAATTCTTCTAATTAAATC
plasmid_cp32-1	8968	BB_P15	2.253 ± 0.8345 0.064396	1.708 ± 0.8499 0.26874	1.228 ± 0.3112 0.29427	1.085 ± 0.2914 0.63361	GTGAGCGACAAATTCCACCATTAATTAAAGGTATTCTGTATGCTGCA
plasmid_cp32-1	9140	BB_P15	2.330 ± 1.7174 0.314083	1.777 ± 1.8487 0.53771	0.374 ± 0.3038 0.08779	0.743 ± 0.2628 0.36884	AGTTCTTTCTGTCGACAAATTATTTTACAATATCTTGTGCTA
plasmid_cp32-1	9665	BB_P15	2.145 ± 0.7972 0.007991	1.209 ± 0.9051 0.55894	0.777 ± 0.2857 0.2857	0.947 ± 0.4326 0.24265	ATTGAAAAACGCGAGTAAATTGAGCTATGCTTAATCCAGTGGTGCTA
plasmid_cp32-1	9746	BB_P15	2.447 ± 0.5224 0.036451	1.765 ± 1.2539 0.3942	1.257 ± 0.2943 0.27099	1.198 ± 0.1273 0.12782	TTACAGCCTTACTGCATCTCGCTCATAGCACCACTGGATTAAAGC
plasmid_cp32-1	9784	BB_P15	2.337 ± 0.5151 0.046286	1.413 ± 0.9683 0.543	0.83 ± 0.2426 0.39571	1.029 ± 0.2863 0.8822	GATCAAAAGCTACTCCATCACCCCAAGAACACTATTAAACGCCCTTA
plasmid_cp32-1	10121	BB_P15	1.401 ± 0.615 0.031987	1.316 ± 1.1215 0.48826	0.769 ± 0.3678 0.1926	0.791 ± 0.3832 0.14918	ATTATTCCTGCAAATTAAACCTGATGCTACCTGGATGGGGCGGAG
plasmid_cp32-1	10650	BB_P16	1.385 ± 0.9896 0.378165	1.862 ± 1.5037 0.30603	0.721 ± 0.5456 0.12637	0.771 ± 0.7475 0.42942	TGTTCCAGGTCTTACCGGATTGCTGATCATATTCCGTTTCTAT
plasmid_cp32-1	10687	BB_P16	0.862 ± 0.9027 0.220699	0.871 ± 0.9716 0.68632	0.425 ± 0.3321 0.12877	1.872 ± 1.8742 0.32191	TAAGGATATGATTCTTACTAAAGTACTGTTTTGGCAATCATATGCT
plasmid_cp32-1	10807	BB_P16	1.167 ± 0.567 0.102866	1.089 ± 0.8398 0.71292	0.678 ± 0.4238 0.3969	0.778 ± 0.4168 0.14254	TATACTAAAAGGACTTGTGCTGTATCTATTGGCTAGTTGTTCTTAC
plasmid_cp32-1	10810	BB_P16	2.534 ± 1.6303 0.01583	0.899 ± 0.9424 0.89654	0.706 ± 0.6719 0.67751	0.52 ± 0.3407 0.37574	TAGTCCAACCTTGGCTTAAAGAATTAGCTGTAATTACAAGTCTTCGTT
plasmid_cp32-1	10812	BB_P16	1.985 ± 0.8386 0.12951	1.898 ± 1.8161 0.45196	1.217 ± 0.2512 0.05059	1.145 ± 0.4073 0.5079	GTCCAACCTTGGCTTAAAGAATTAGCTGTAATTACAAGTCTTCGTTA
plasmid_cp32-1	10977	BB_P17	1.676 ± 0.6061 0.119803	1.412 ± 0.8889 0.33545	0.914 ± 0.3504 0.79354	1.319 ± 0.7848 0.3958	AAATTGAGTCTACAAATGTAAGTACATCAAAAAAATCACCTGATGAAATT
plasmid_cp32-1	10997	BB_P17	1.801 ± 1.1973 0.060641	1.565 ± 1.2436 0.21228	0.817 ± 0.4595 0.32851	1.097 ± 0.6453 0.35501	GATACATCAAAAAAATCACCTGATGGAATTCTTCGCCGAAGAAATTCT
plasmid_cp32-1	10998	BB_P17	1.753 ± 1.0161 0.02245	0.473 ± 0.3808 0.35425	0.992 ± 0.5291 0.95829	1.011 ± 0.5626 0.09069	TCTACATTGAGACTCAATTAAACATATTGAGTAACAGCATTTT
plasmid_cp32-1	11001	BB_P17	1.946 ± 1.1146 0.312544	1.14 ± 0.6645 0.76105	0.73 ± 0.2329 0.13635	0.677 ± 0.2256 0.08363	CATCAAAATTAAACCTGATGGAATTCTTCGCCGAAGAAATTCTCAAA
plasmid_cp32-1	11204	BB_P17	1.854 ± 1.5734 0.480651	1.629 ± 1.9967 0.65523	0.459 ± 0.2068 0.18324	0.743 ± 0.6304 0.23501	AAAATATATTAAAGAATTGCTCATGAAAAAAATTGATTCTCATAT
plasmid_cp32-1	11212	BB_P17	2.343 ± 0.8261 0.079093	1.604 ± 0.8255 0.27119	1.01 ± 0.1943 0.92869	1.271 ± 0.3301 0.19247	ATATATTCTTACTATCTCAAATTAAATGTCGCGTGAAGTCTAAGGG
plasmid_cp32-1	11533	BB_P17	3.038 ± 1.4205 0.139058	0.766 ± 0.3898 0.31377	1.053 ± 0.2813 0.75583	1.031 ± 0.2252 0.86518	TGTTCCCTTAATTGGTCAATAAAACTCTTGGTGTGGCATAAATATC
plasmid_cp32-1	11536	BB_P17	1.226 ± 0.3908 0.489249	0.468 ± 0.1901 0.01303	0.737 ± 0.2903 0.43083	0.869 ± 0.2712 0.63371	TGTTCATACAGTAATAGCCGATATTGGTACTGGTTACGGGGATATGAATG
plasmid_cp32-1	12122	BB_P18	1.686 ± 0.6117 0.148762	1.525 ± 1.5109 0.60672	0.707 ± 0.2749 7.3E-05	1.49 ± 0.6751 0.16079	GAGATATTGGTGTGAAATTCTCAAATTCCGGGTATTGTAACA
plasmid_cp32-1	12235	BB_P18	3.331 ± 1.6935 0.033131	3.17 ± 3.1113 0.31432	2.219 ± 1.7557 0.37676	1.102 ± 0.8006 0.66213	CTTAGTGCACATTAGCCAAAGACTTAACTCAATCTGATACTGTTAAA
plasmid_cp32-1	12236	BB_P18	1.133 ± 0.4517 0.714109	1.413 ± 0.7653 0.3378	1.25 ± 0.5662 0.54405	1.214 ± 0.8605 0.75559	AGTATATAAAAATGATGTTGTCAGTGAATATCGTTATTGTTATCAAA
plasmid_cp32-1	12239	BB_P18	2.225 ± 0.7483 0.019877	1.848 ± 1.2877 0.28887	1.055 ± 0.2616 0.71401	1.14 ± 0.3519 0.14139	GTGCAATTAGCCAAAGACTTAACTCAATCTGATACTGTTAAAATT
plasmid_cp32-1	12334	BB_P18	1.352 ± 1.1318 0.579757	1.187 ± 1.2406 0.76527	0.694 ± 0.2607 0.20724	1.761 ± 0.10878 0.4007	AAAAAAATTCTAGATAATATTGTTAGTGTCTAATGGTATAAAATTATA
plasmid_cp32-1	12535	BB_P19	2.141 ± 1.3248 0.213033	1.113 ± 0.8916 0.86995	0.865 ± 0.5577 0.5993	0.766 ± 0.5222 0.61365	TTAAATCCAATTCAAATTGCTCATTAATCTAAATCCATACTAGTAATT

plasmid_cp32-1	12735	BB_P19	1.379 ± 1.7062 0.685502	1.542 ± 1.8164 0.60576	0.35 ± 0.2764 0.08564	0.735 ± 0.5402 0.4742	AATCTAAGTTAACGCTTTAGATATTCATGAAAATAATTACAGCGT
plasmid_cp32-1	12775	BB_P19	3.200 ± 0.7598 0.005198	1.41 ± 1.2499 0.5831	0.895 ± 0.2907 0.00029	1.005 ± 0.5261 0.98351	TGTGCTTGTGCTGTAGTAGTTGAAATATTAAATCTAAGTTA
plasmid_cp32-1	13065	BB_P20	2.114 ± 1.5843 0.30625	1.724 ± 1.4005 0.05423	0.786 ± 0.6324 0.7251	1.265 ± 0.9572 0.73019	TGTTCTCAATAGCAGCCCCAATAAGTACCCACGGGTTCATTTAGAAAAA
plasmid_cp32-1	13169	BB_P20	1.769 ± 0.519 0.00812	1.46 ± 0.8457 0.34196	0.924 ± 0.5683 0.75775	1.428 ± 0.5263 0.11859	TGTTGGCTTACCAAGCTGCACTTTAATATTAGTGTACTCACTCCATCAA
plasmid_cp32-1	13172	BB_P20	1.069 ± 0.5944 0.609287	0.528 ± 0.4605 0.04986	1.031 ± 0.372 0.79742	1.095 ± 0.3648 0.44169	TATCTAATTCTAAAGGAAACTTACTAGACACTAGTAAATCTAATATTAAAT
plasmid_cp32-1	13206	BB_P20	1.407 ± 0.3439 0.019487	1.049 ± 0.3295 0.49562	0.9 ± 0.1685 0.35954	1.075 ± 0.1942 0.48226	GTAAATCTAATATTAAATAGTCTGAATTAAAGCAAACCTTGGGAAACAT
plasmid_cp32-1	13256	BB_P20	1.753 ± 0.7173 0.120739	1.359 ± 1.5181 0.71537	0.325 ± 0.1464 0.06141	0.9 ± 0.6031 0.7237	ATGTTCCCAAAGTTTGCTTAAATTCAAGGACTATTAAATTAGATTAC
plasmid_cp32-1	13408	BB_P20	2.700 ± 1.7775 0.019042	1.122 ± 1.1436 0.89742	1.397 ± 1.3003 0.2868	0.98 ± 0.6428 0.97133	GTTTTAAGGTCAGTTATACTTTACTTCATGAAACATATTCTTT
plasmid_cp32-1	13467	BB_P20	1.769 ± 0.5043 0.019421	1.244 ± 0.4818 0.45717	0.819 ± 0.2131 0.42511	1.086 ± 0.2375 0.36771	TTTGAATAATCCTAGAATAATGCTCTAATTGAGAGTCTATGTTAAG
plasmid_cp32-1	13533	BB_P20	0.998 ± 0.7253 0.997754	0.747 ± 0.8188 0.67449	1.2 ± 0.3692 0.11808	0.599 ± 0.5244 0.45399	AAGGAATTAAGTTATGGAAATAAGTGTGTATTAAAGATAACAGACACTG
plasmid_cp32-1	13838	BB_P21	2.444 ± 1.4436 0.051907	1.492 ± 1.2947 0.35391	0.812 ± 0.4126 0.39896	0.876 ± 0.4179 0.62845	GAAAATATAAACTAACAGATATTGCAATATGGATATCTCAAGTTTATCT
plasmid_cp32-1	14088	BB_P21	1.798 ± 1.2126 0.389322	1.803 ± 1.79 0.5158	0.984 ± 0.2955 0.94811	1.142 ± 0.4153 0.63767	CTACATTATTCGCTAGCACTAAAGGAAAAGCACTAAAAAAAGATAA
plasmid_cp32-1	14186	BB_P21	4.634 ± 3.6797 0.216867	4.899 ± 6.1198 0.38128	2.907 ± 2.7694 0.36595	2.013 ± 0.55 0.09452	GTATTCACTCACTCCCTAAGGGCTATGATCATTCATTATGCTTTATT
plasmid_cp32-1	14224	BB_P21	3.324 ± 0.8287 0.020712	2.283 ± 1.4283 0.254	1.591 ± 0.4604 0.18261	1.367 ± 0.7347 0.41128	AATTGAATGATCATAGCCTCTAGGAAGTGTGAATACTAAAGCCTTT
plasmid_cp32-1	14280	BB_P21	1.624 ± 0.8428 0.004903	0.349 ± 0.2715 0.23051	0.82 ± 0.471 0.25913	0.966 ± 0.5779 0.85582	CAGATGGTAACAATTATAACTTTAACACAATAGGAGGTTTATGGCTG
plasmid_cp32-1	14289	BB_P21	1.725 ± 0.1379 0.003234	1.217 ± 0.3554 0.45887	0.957 ± 0.1164 0.54636	1.19 ± 0.7453 0.70806	ACAATTATAACTTTAACACAATAGGAGGTTTATGGCTGATGATCAAG
plasmid_cp32-1	14420	BB_P22	1.026 ± 0.63 0.94333	0.512 ± 0.5634 0.49845	1.031 ± 0.7695 0.91636	1.094 ± 0.7575 0.64826	AAAGATCAGTATCGTAACCGGCGTAAACCTTATTAAATCTTTATTGAA
plasmid_cp32-1	14448	BB_P22	0.798 ± 0.9673 0.834103	0.765 ± 0.9044 0.78436	0.191 ± 0.3605 0.26701	1.81 ± 2.3049 0.57832	CTGCTTCAGCCTCCATCATCAAGCAGTAAAGATCAGTATGTTAACGGTC
plasmid_cp32-1	14523	BB_P22	1.939 ± 1.5231 0.098113	1.395 ± 1.0791 0.0962	0.611 ± 0.3863 0.44012	1.037 ± 0.7023 0.91472	AAATAGTCTAATCCCCTCCCTTAAATTATTGTCTTTAGAAGCATCTAA
plasmid_cp32-1	14616	BB_P22	1.977 ± 1.12 0.082325	1.659 ± 1.6024 0.4221	0.901 ± 0.4625 0.27868	1 ± 0.4777 0.98934	ATTAATTGTGCGTTATTAGCATAAATTCTACAAAATCTTATCA
plasmid_cp32-1	14676	BB_P22	1.319 ± 1.0669 0.674024	1.069 ± 1.4537 0.89286	0.661 ± 0.6616 0.04754	1.095 ± 0.715 0.42319	TCTGTAAGGCGTGTATTAACTTAAAGGTTGAAATATTAGTAGAA
plasmid_cp32-1	14684	BB_P22	0.913 ± 0.7744 0.881823	1.184 ± 0.1054 0.60553	0.184 ± 0.1802 0.10169	0.331 ± 0.3333 0.2735	TCATCAGCCACTTATCAGAATGATCATTTGATAATGCCCTCATCA
plasmid_cp32-1	14736	BB_P22	2.666 ± 1.2227 0.645282	0.362 ± 0.1575 0.04787	0.647 ± 0.3657 0.04773	0.582 ± 0.2807 0.09291	TCTGATGAAAGCATTATCAAAGATGATCATCTGATAAAGTGGCTGAT
plasmid_cp32-1	14768	BB_P22	1.770 ± 0.8487 0.101672	0.978 ± 0.5465 0.95314	1.217 ± 0.497 0.133	0.909 ± 0.4392 0.60322	TATGTTAGGAACGGGTTTTGAAATAGTATCTGATGAGGCAATTATCA
plasmid_cp32-1	14872	BB_P22	1.618 ± 0.3584 0.077503	1.517 ± 0.7989 0.28561	1.064 ± 0.22 0.55589	0.993 ± 0.3207 0.97224	CAATGATGATGTAACCTTTCTAAAGTTACGATAATTCTCCCGT
plasmid_cp32-1	14961	BB_P22	1.621 ± 0.7537 0.059734	2.678 ± 1.1576 0.0353	0.856 ± 0.6426 0.79487	0.95 ± 0.4592 0.80003	TTATCATTGATTCTTACTGAAATTCAATATCAAGATAAACGGGAGAATT
plasmid_cp32-1	15050	BB_P22	1.302 ± 0.4021 0.239637	0.347 ± 0.2839 0.1748	1.249 ± 0.7882 0.53703	1.419 ± 0.7231 0.40495	TCACCAGAACTCCCATTTAAAGGATGGTATGTCAAAAAAAGAGCCTCC
plasmid_cp32-1	15067	BB_P22	2.070 ± 0.7703 0.047751	1.669 ± 1.485 0.48089	0.829 ± 0.3619 0.09526	0.993 ± 0.9156 0.99079	AATGGAATTCTGGTAATAGTCCGGGGGGCGCAATTCTAAACCCCT
plasmid_cp32-1	15170	IG_131	1.841 ± 1.3374 0.193233	2.133 ± 1.255 0.34643	0.941 ± 0.5745 0.83327	1.123 ± 0.6402 0.28329	TATACCAAACTATAATTCTGCTAAAGTTACAGTTTAAAGATCTG
plasmid_cp32-1	15178	IG_132	2.825 ± 0.3301 0.010091	1.786 ± 0.9755 0.29816	1.035 ± 0.0852 0.45814	1.238 ± 0.0852 0.01887	CGTATAAAAATAAAATTAATGAGGATTTAAAGGTTGAAATATTAGTAA
plasmid_cp32-1	15335	BB_P23	2.510 ± 1.1294 0.85639	1.814 ± 0.81 0.1305	0.942 ± 0.6553 0.85369	0.755 ± 0.6473 0.43904	AAAGACATATTGACTATTGTAATAGGCAAGATTTTAAGAATGTTAGGT
plasmid_cp32-1	15353	BB_P23	1.008 ± 0.378 0.937856	0.448 ± 0.3659 0.28329	0.921 ± 0.3508 0.44206	0.97 ± 0.3907 0.64219	CAATAGTCAATATGTTAGTAAAGGCTGAGAAGAATTAACTCTTA
plasmid_cp32-1	15356	BB_P23	2.930 ± 2.0463 0.228939	2.01 ± 1.5983 0.21641	1.74 ± 0.8345 0.24332	1.904 ± 1.0797 0.05868	ATAGGCAAGATTTTAAGAATGGAATGGCAAAAATCACATTTAA
plasmid_cp32-1	15441	BB_P24	1.935 ± 1.5754 0.315569	2.95 ± 3.2666 0.42955	0.767 ± 0.9571 0.69055	0.564 ± 0.2363 0.19141	ATGTTGAGCTGGTACCTACGCTTTATCACCCCTATTGATATTTCTA
plasmid_cp32-1	15702	BB_P24	2.095 ± 1.3045 0.033469	2.086 ± 1.5543 0.1732	1.123 ± 0.6496 0.27203	0.891 ± 0.4764 0.80035	GATATTGAGATTCTTACATCAGAATTAAGTCAATGCTATTGATTG
plasmid_cp32-1	15744	BB_P24	3.184 ± 2.3342 0.22788	0.783 ± 0.252 0.12696	0.98 ± 0.8864 0.96746	0.729 ± 0.3342 0.32458	AGGAAAGAACAAATAATGCAAATAACACTATTGGTTAGGACTTAATT
plasmid_cp32-1	15787	BB_P25	3.776 ± 1.9062 0.059775	1.535 ± 0.8957 0.46922	0.536 ± 0.2896 0.23211	0.802 ± 0.7506 0.6833	AGTCTAACCAATAGTGTATTGCTTATTGCTTCTTCTTATAGAT
plasmid_cp32-1	15808	BB_P25	0.945 ± 0.8631 0.850707	0.942 ± 0.7849 0.80904	0.67 ± 0.3484 0.21358	0.41 ± 0.2063 0.19564	GTTAACGCTGAGTAAAGTCTAAACCAATAGTGTATTGCTT
plasmid_cp32-1	15892	BB_P25	1.895 ± 1.5809 0.133048	1.713 ± 1.9123 0.38103	0.78 ± 0.5158 0.39891	1.118 ± 0.8208 0.2114	TATGTTTGTAGAAAAAAATCTTACTACTAAAGTTAAAGTAA
plasmid_cp32-1	15894	BB_P25	1.970 ± 0.8624 0.047465	1.477 ± 0.8688 0.19569	0.805 ± 0.3187 0.24995	1.6 ± 0.8817 0.13344	TATATGTTTGTAGAAAAAAATCTTACTACTAAAGTTAAAGTAA
plasmid_cp32-1	15895	BB_P25	2.617 ± 1.1461 0.106931	1.382 ± 0.8688 0.49623	0.591 ± 0.2011 0.1982	1.38 ± 0.6905 0.51131	TAAGCACACTAAATCTAGGAAACAGCTGAGTCAACTAAATATTGAG
plasmid_cp32-1	15897	BB_P25	2.083 ± 0.9746 0.076969	1.752 ± 1.4796 0.37395	1.099 ± 0.4798 0.52659	1.08 ± 0.4032 0.39172	AGCACACTAAATCTATGAAACAGCTGAGTCAACTAAATATTGAGAA
plasmid_cp32-1	15998	BB_P25	2.113 ± 1.2083 0.275877	0.9 ± 0.6376 0.83887	0.929 ± 0.643 0.886	0.68 ± 0.2253 0.23549	TGACAAAAATAAAATATCACTTAAAGCAAAACGCACAAAT
plasmid_cp32-1	16139	BB_P26	2.044 ± 3.2411 0.553482	2.937 ± 2.8593 0.17508	1.058 ± 1.1357 0.94761	1.236 ± 1.555 0.65562	GTGGTGCACATAACAAACAAATTAGTAAACATGCAATTTAAGC
plasmid_cp32-1	16336	BB_P26	2.114 ± 1.2094 0.257426	2.232 ± 1.0092 0.14783	0.882 ± 0.5516 0.65102	0.993 ± 0.28 0.97301	TAGAGTGTGCTTGTAGTGTGATAAGTCTGGATAAGGATATTCTGGAT
plasmid_cp32-1	16413	BB_P26	1.801 ± 1.0366 0.204671	0.107 ± 0.1518 0.04537	0.435 ± 0.4203 0.27739	0.188 ± 0.217 0.03959	TCATCAATTCTGAACTTAAAGTAAATACAAAGGTTTCTTGCA
plasmid_cp32-1	16574	IG_133	0.577 ± 0.4636 0.000567	0.609 ± 0.5991 0.04735	1.068 ± 0.6882 0.50961	1.026 ± 0.6421 0.64361	CTAATTAAATTAGTGCCTCTCGAGGAACTTAACTTTGTCTATCTGTT
plasmid_cp32-1	16718	BB_P27	2.005 ± 0.9638 0.104652	1.409 ± 1.1067 0.39435	0.87 ± 0.511 0.70852	0.763 ± 0.3711 0.53023	TTTTCTTTGAAATATCTGATCTGTAGTAATGTTCAATGGTAT
plasmid_cp32-1	16753	BB_P27	1.339 ± 0.8183 0.609845	1.168 ± 0.6101 0.37558	0.827 ± 0.2808 0.3793	0.919 ± 0.3542 0.8133	ATGTTTCAATGGTATTAGTGTGCTTAAACGCTGCTAATTGGCCGCT

plasmid_cp32-1	17274	BB_P28	<i>mlpA</i>	1.748 ± 1.66	0.475018	1.257 ± 0.7745	0.21238	0.656 ± 0.3232	0.32174	1.476 ± 0.9515	0.51259	GTAGTAGTAAAAATAAACAAAATAATGTTGATGATTTCATGGTTATT
plasmid_cp32-1	17768	BB_P29		2.487 ± 2.4944	0.264042	3.319 ± 3.8162	0.23765	1.227 ± 1.2013	0.70765	1.302 ± 1.2918	0.72476	TCCTTTAGTATCTAAAGAACGAAACGGTTGATGAGATATTGAGCA
plasmid_cp32-1	17845	BB_P29		3.217 ± 2.828	0.160907	2.26 ± 2.6481	0.35815	1.253 ± 0.9142	0.114	1.402 ± 0.9368	0.07038	TTATTTTCTGAAATAGTTTTATAATCTCGGCCAATAGTTATGCTT
plasmid_cp32-1	17953	BB_P29		2.064 ± 0.6303	0.069977	2.475 ± 1.3153	0.15213	1.115 ± 0.4791	0.66843	1.025 ± 0.5165	0.81315	TCATCAAATTATTGGGGTCTATATTCTGAATAAGCTTATTGAAATA
plasmid_cp32-1	17975	BB_P29		1.885 ± 0.8471	0.058079	2.048 ± 1.1499	0.07844	0.724 ± 0.2851	0.20731	1.136 ± 0.5368	0.16534	TATTCGATAAAAGCTTATTGAGATAATTGAGTTTATATTCTTTG
plasmid_cp32-1	18013	BB_P29		2.432 ± 0.6852	0.07397	2.457 ± 2.7149	0.46451	1.395 ± 0.554	0.40058	1.606 ± 0.337	0.07949	TAAACTCAATTATTCAAAAATAAGCTTATTGAGATAAGCCCCATA
plasmid_cp32-1	18331	BB_P29		1.882 ± 0.5392	0.029356	1.289 ± 0.934	0.56512	0.754 ± 0.214	0.18363	0.854 ± 0.192	0.35549	CTTATGTCAAAGAGTATGCTTAGTTGCAGCCTCTGGTATAGAAAGTGAA
plasmid_cp32-1	18364	BB_P29		2.058 ± 1.6242	0.111554	1.682 ± 1.6018	0.25416	1.197 ± 0.8166	0.71026	1.227 ± 0.9774	0.48655	TTTGTAACTTAGACCATTTCATTGTCATTGTAATTCTGTAGGA
plasmid_cp32-1	18456	BB_P29		1.459 ± 0.817	0.422769	2.466 ± 3.2475	0.50573	1.125 ± 0.4896	0.67438	1.655 ± 0.9829	0.24848	CAGTACAAGTACTGGATATGAATTTCATACGCGAATTCTACAGA
plasmid_cp32-1	18485	BB_P29		1.599 ± 0.8128	0.021099	1.473 ± 0.1073	0.23884	0.914 ± 0.4484	0.72507	0.677 ± 0.352	0.23868	TGCCATATTGACCCCTATAGAAATTGGATATTGCTCAATACAGCTCCA
plasmid_cp32-1	18503	BB_P29		2.927 ± 1.4604	0.145014	1.579 ± 1.3615	0.52823	0.91 ± 0.4791	0.75926	1.047 ± 0.476	0.87384	TAGAAATTGGATATTGCTCAATATCAAGCTCAAATTGTCCTTTAATAA
plasmid_cp32-1	18526	BB_P29		2.743 ± 1.3085	0.060615	1.633 ± 1.184	0.30913	1.05 ± 0.3817	0.46384	1.107 ± 0.3673	0.36603	TCAAGCTCCAAATTGCTTTAATAACATTTTAATTCTCTAACTATT
plasmid_cp32-1	18685	BB_P29		2.246 ± 0.4805	0.031951	1.674 ± 0.9827	0.36746	0.588 ± 0.2143	0.09493	0.965 ± 0.0716	0.30441	TTCAAGCAAAATAAGCTTGGAAAAGATGAAAACCCCTAAAATGAATT
plasmid_cp32-1	18768	IG_134		0.989 ± 0.3062	0.966569	0.61 ± 0.4892	0.34634	0.887 ± 0.2589	0.62116	0.896 ± 0.4063	0.54112	GCAAAAACATTTTGCCAATTTCACAAAAATTAA
plasmid_cp32-1	23054	IG_135		1.350 ± 1.0537	0.244051	0.833 ± 0.728	0.81241	0.783 ± 0.5776	0.36813	0.906 ± 0.5572	0.84335	CATATACATATGTATAACAAAACATTTCAGGCTTTACAGAAAT
plasmid_cp32-1	23056	IG_136		3.180 ± 2.7666	0.197659	3.476 ± 4.3669	0.35509	0.93 ± 0.5681	0.34715	1.986 ± 1.69	0.26245	TACATATACATATGTATAACAAAACATTTCAGGCTTTACAGAA
plasmid_cp32-1	23059	IG_137		0.857 ± 0.3886	0.643177	0.439 ± 0.3668	0.32685	0.975 ± 0.7338	0.9246	1.192 ± 0.8676	0.43703	GCTAAAAAAATATTGCTATCAAAAAAATCAATTAGTTGGTTAGCT
plasmid_cp32-1	23191	IG_138		0.994 ± 0.3086	0.980184	0.603 ± 0.5181	0.34139	1.07 ± 0.2795	0.72459	1.009 ± 0.3769	0.96996	GCAAAAACATTTCAGGCAACTTTTACAAAAAAATTACAAAAAATAG
plasmid_cp32-1	23220	IG_139		1.852 ± 0.9084	0.124272	1.66 ± 1.8519	0.53851	1.138 ± 0.4786	0.4511	1.077 ± 0.4394	0.62202	GGAGAAAAAGATGAAAATCTTCACAAATAATCCACAAAGAAAATA
plasmid_cp32-1	23769	BB_P35	<i>bppA</i>	2.156 ± 2.3257	0.346096	1.054 ± 0.9443	0.88746	0.821 ± 0.7241	0.73977	1.039 ± 0.6264	0.93813	TTAATAACAGCCATCAATTGAGCCACTAAAGTTCTGAACGCTCC
plasmid_cp32-1	23957	BB_P35	<i>bppA</i>	3.588 ± 2.4561	0.090648	2.324 ± 2.6334	0.37433	1.075 ± 0.5948	0.31904	1.245 ± 0.7649	0.25638	GATGCTGCACCAATTACTGTAAGTAAAGAGATGAGGCCTTAATATCA
plasmid_cp32-1	24002	BB_P35	<i>bppA</i>	2.043 ± 1.2807	0.329291	2.696 ± 1.8836	0.27602	1.609 ± 1.4447	0.58868	0.898 ± 0.3786	0.75785	ATATCAAAGTGTGATTGTAATTGTAATTAGAAATTATAAAT
plasmid_cp32-1	24072	BB_P35	<i>bppA</i>	1.777 ± 0.6373	0.146619	1.082 ± 0.427	0.79831	0.987 ± 0.4836	0.86039	0.921 ± 0.3963	0.17755	GTAACTATAGAGAGGAACATCTAACGACATAATTAAACGAGGATACGT
plasmid_cp32-1	24075	BB_P35	<i>bppA</i>	1.976 ± 1.4987	0.091425	1.825 ± 1.8834	0.32841	0.971 ± 0.591	0.89904	1.033 ± 0.6537	0.86898	ACTATAGAGAGGAACATCTAACGACATAATTAAACGAGGATACGTTA
plasmid_cp32-1	24206	BB_P35	<i>bppA</i>	0.973 ± 0.2756	0.90945	2.077 ± 1.4637	0.26824	0.776 ± 0.7373	0.55932	0.585 ± 0.2827	0.001	GAATATGTTGATTGTCAGACCTTGAATTAGGATAATCAATCTGCTAA
plasmid_cp32-1	24305	BB_P35	<i>bppA</i>	2.064 ± 1.1417	0.075498	1.905 ± 1.0774	0.00122	0.769 ± 0.7081	0.21665	0.911 ± 0.6405	0.88309	AATAAGATCAAACAGGAAAATAAAAGAGAGAAAGCCATTAAAGATAG
plasmid_cp32-1	24378	BB_P35	<i>bppA</i>	2.420 ± 1.4921	0.049991	1.579 ± 1.5201	0.38815	0.913 ± 0.4808	0.55711	0.818 ± 0.532	0.12987	ATATTGAAATTAGCATCTAACCTATCTTAATGGCTTTCTT
plasmid_cp32-1	24388	BB_P35	<i>bppA</i>	2.049 ± 1.6129	0.302298	1.959 ± 0.9631	0.11947	0.943 ± 0.4137	0.84669	1.691 ± 0.6287	0.10347	TGTTTTGTAATATTGTAATTAGCATCTAACCTATCTTAATGGGCTT
plasmid_cp32-1	24596	IG_140		1.853 ± 0.8039	0.24507	1.994 ± 0.6035	0.01901	0.803 ± 0.8383	0.67494	1.849 ± 0.6153	0.13424	GGAGGATTAATTAACTGTTTAATAAAACAAAGATAATGAAACTT
plasmid_cp32-1	24936	BB_P36	<i>bppB</i>	2.269 ± 2.0011	0.160681	1.679 ± 1.7958	0.35622	0.995 ± 0.7135	0.95796	1.079 ± 0.8367	0.17696	GCAACAAAGATAAAAGAAAATTATGATTGATTTAAAGCCACGT
plasmid_cp32-1	25143	BB_P37	<i>bppC</i>	2.551 ± 1.408	0.106643	0.899 ± 0.5299	0.7987	0.67 ± 0.3602	0.45281	1.102 ± 0.9518	0.61547	AGTTCTTAATTGGAAAAGATAATTACCATTAGATTAAATATGAAATA
plasmid_cp32-1	25881	IG_141		3.512 ± 2.0002	0.111841	1.769 ± 1.7406	0.50485	1.375 ± 1.1534	0.63158	1.864 ± 0.7081	0.20596	CTATTTCATTCTATTTCATTCTTAATTAAAGTAACACCTTC
plasmid_cp32-1	26314	BB_P38	<i>erpA</i>	2.431 ± 0.799	0.067878	1.538 ± 1.6514	0.61295	1.13 ± 0.5716	0.71125	0.805 ± 0.3038	0.23233	TGAATCTTCAAGCACCTATAAGTATAAAACAGCACAATAAACATT
plasmid_cp32-1	26569	BB_P38	<i>erpA</i>	1.919 ± 0.7793	0.071768	0.998 ± 0.9654	0.99672	0.914 ± 0.8557	0.9026	0.868 ± 0.4418	0.71612	GTTTTAAATGATCCACCTTCAGTCATTGCTTTATAAAGTTATTAAATTCT
plasmid_cp32-1	26623	BB_P38	<i>erpA</i>	2.865 ± 1.522	0.11172	2.124 ± 1.4102	0.22342	1.036 ± 0.3191	0.82286	1.205 ± 0.2714	0.23405	TTCTTAATGACATTTCATCTTCCTGCTATTATCCATAATACAAA
plasmid_cp32-1	26668	BB_P38	<i>erpA</i>	2.462 ± 0.7659	0.063541	1.168 ± 0.4466	0.6625	0.981 ± 0.4331	0.84185	0.892 ± 0.2527	0.37636	TATTTCAGTATCTTAATTTCATTCTTGTCTTTATCTCTTATTCTTA
plasmid_cp32-1	26669	BB_P38	<i>erpA</i>	2.792 ± 0.9255	0.06033	1.695 ± 0.8182	0.39817	0.964 ± 0.1733	0.7565	0.971 ± 0.2993	0.91344	TATTACATTAGGAGATAAAATAACAGTGGGGGGAGACAAAAT
plasmid_cp32-1	26970	BB_P39	<i>erpB</i>	2.209 ± 1.9961	0.406171	1.513 ± 0.9799	0.43502	1.059 ± 0.6213	0.89633	1.005 ± 0.9092	0.99198	ATTCTCATTTGAACTCTGTAATTGTTCTGGATCC
plasmid_cp32-1	27009	BB_P39	<i>erpB</i>	1.179 ± 1.1984	0.722693	0.952 ± 1.1197	0.93196	1.095 ± 0.8566	0.7449	1.233 ± 0.7477	0.09973	CACCTTTATTTATCTCTGTAATTCTGCTTAATTCTCATCTACTT
plasmid_cp32-1	27565	BB_P39	<i>erpB</i>	2.271 ± 1.3113	0.249191	1.792 ± 0.9347	0.29618	0.757 ± 0.4997	0.64424	0.779 ± 0.4083	0.56318	ACACCTGTGGCCCCACACTGTTGCTCTTTAACATCAATTCTCTA
plasmid_cp32-1	27591	BB_P39	<i>erpB</i>	2.325 ± 1.2013	0.024995	2.009 ± 1.753	0.25652	1.281 ± 0.6449	0.1439	1.356 ± 0.5836	0.36763	TATGATGTTTACTGATGGGATAAAAGCTATACAAAACGGGGGGAT
plasmid_cp32-1	27754	BB_P39	<i>erpB</i>	2.828 ± 1.8027	0.117973	1.287 ± 0.7051	0.56585	1.284 ± 0.9367	0.3558	1.566 ± 1.7003	0.54518	GTATCAATAATATGCTTATTACCCCTATTAATTGGTTCTAAATT
plasmid_cp32-1	27910	BB_P39	<i>erpB</i>	1.858 ± 1.4824	0.358379	2.206 ± 2.3882	0.22268	0.842 ± 0.815	0.84798	0.605 ± 0.452	0.44075	TCCTCACTTACAGCAACGTATTCTTAAATTCTCTAAATTATCTTAT
plasmid_cp32-1	28206	BB_P40		2.994 ± 1.1373	0.036996	2.271 ± 2.6236	0.44715	0.879 ± 0.3271	0.33386	1.843 ± 1.2133	0.23749	ACTAGCCAAATAACTCTAAAGCAAAAGACAAATATCAGTGGTGG
plasmid_cp32-1	28271	BB_P40		2.620 ± 1.8698	0.263845	1.801 ± 1.8122	0.51423	0.856 ± 0.4008	0.68194	1.364 ± 1.2233	0.67418	CGTAATAAAACCGGAAAAGTGTGTTAGAATCGGAAAAGAATTG
plasmid_cp32-1	28559	BB_P40		1.948 ± 1.1817	0.278309	1.806 ± 1.2082	0.32214	0.944 ± 0.3342	0.8266	1.259 ± 0.4867	0.23259	GTGTATACTCAAAATAATCTCTAAATTCTTAAATCGCATCTATTG
plasmid_cp32-1	28895	BB_P41		2.714 ± 2.5758	0.178312	2.239 ± 3.1032	0.43859	0.915 ± 0.747	0.39286	0.908 ± 0.7148	0.25361	AGTGATGTAAGAAATGCGAAGAAAAGTGTGTTAGAATGTTG
plasmid_cp32-1	29160	BB_P41		1.728 ± 1.658	0.566387	2.183 ± 2.9282	0.44426	0.555 ± 1.0078	0.61289	1.002 ± 0.5724	0.9989	GTATGCATACTAAATAGAAAATTAGAGCGAAATTGACGCTTAAATA
plasmid_cp32-1	29163	BB_P41		2.378 ± 1.5043	0.019948	1.291 ± 0.977	0.19533	0.864 ± 0.5299	0.44064	0.961 ± 0.8003	0.70473	TGCATACTAAATAGAAAATTAGAGCGGAAATTGACGCTTAAATAAG

plasmid_cp32-1	29288	BB_P41	2.141 ± 1.8381 0.220562	1.377 ± 1.1771 0.6443	0.579 ± 0.3725 0.24969	0.992 ± 0.5599 0.97827	AAAGAGTGTCAATAAGAGAAATGGAGCTTACTATGAATGTATGAAAAAA
plasmid_cp32-1	29407	BB_P42	1.890 ± 0.6167 0.052187	2.038 ± 1.3722 0.26059	0.861 ± 0.232 0.27302	1.098 ± 0.3434 0.43727	TATCAAACAAAACCTTTTACAACACTACAAAAGGAATACAAAATAAATAT
plasmid_cp32-1	29482	BB_P42	1.744 ± 0.9326 0.124901	1.125 ± 1.041 0.61768	0.645 ± 0.5656 0.52853	1.076 ± 0.7161 0.53257	AAGCTAACAAATTCTCAATTAAATTGATAAGTTGAAGAAGAACAGTTA
plasmid_cp32-1	29539	BB_P42	2.416 ± 1.8201 0.076524	1.938 ± 2.505 0.4385	1.062 ± 0.7172 0.8961	1.021 ± 0.605 0.95458	AAACAAAAAAATGTGATAAAAAGCATTAAGAATAATGAAAAGAAGATT
plasmid_cp32-1	29573	BB_P42	0.694 ± 0.8072 0.174829	1.502 ± 0.962 0.35678	0.529 ± 0.443 0.09664	0.278 ± 0.3277 0.05719	TTCTTTTAATGCTTTTACATTTTTGTTAAAGTTAATGTTCT
plasmid_cp32-1	29590	BB_P42	2.000 ± 0.9853 0.151959	0.907 ± 1.0395 0.9106	1.198 ± 1.1651 0.7074	1.197 ± 0.9984 0.64098	TAATCTCTTTCATATTCTTTAATGCTTTTACATTTTTGTT
plasmid_cp32-1	29687	BB_P42	1.443 ± 0.9322 0.566051	0.591 ± 0.3741 0.26892	0.376 ± 0.293 0.08921	0.432 ± 0.2087 0.10297	CTAAATAATTCTTACAGGGAAATTCAACGTTAGTTGAAGTTAATGTTT
plasmid_cp32-1	29792	BB_P42	1.997 ± 0.581 0.096686	1.488 ± 0.6873 0.38872	0.989 ± 0.2306 0.92759	1.07 ± 0.5107 0.86905	TGCTTGGAAATAAGGAATTAAAGAAGTTACAGCTTCAAATTGC
plasmid_cp32-1	29882	BB_P42	0.906 ± 0.4205 0.083265	0.519 ± 0.4337 0.36196	1.017 ± 0.6938 0.92148	0.921 ± 0.4077 0.28871	CTTCCCCTAAATCTTCAAAATCACTTGCTTATCCTCCATATAGATT
plasmid_cp32-1	30027	BB_P42	3.104 ± 1.2235 0.061367	1.557 ± 0.5387 0.09934	0.761 ± 0.2381 0.03596	0.974 ± 0.3326 0.92174	ATCGTTTAAATAGTGTCTGGATGTCAGGATTAGTACAAAATAAAT
plasmid_cp32-1	30209	BB_P42	3.830 ± 2.2636 0.026181	1.836 ± 2.004 0.39289	1.359 ± 0.872 0.52104	0.98 ± 0.6255 0.96515	ATATTTATTGTGAAAAATTGAATCAGTGTGCTTACACTCACCTAAC
plasmid_cp32-1	30221	BB_P42	1.694 ± 0.2963 0.044333	1.53 ± 1.3251 0.55253	0.776 ± 0.1578 0.25054	0.809 ± 0.5555 0.61967	TAATCATCAGTAATTATTGTGAAAAATTGAATCAGTGTGCTTAC
plasmid_cp32-1	30289	BB_P42	3.544 ± 2.3139 0.194546	1.897 ± 1.2324 0.3326	1.928 ± 0.1359 0.00623	2.808 ± 1.4619 0.15534	TGTTTATGGAGCGAGTTGATGATAAGTATTATGCTTTGATTCAAGAC
plasmid_cp32-1	30363	BB_P42	2.794 ± 1.1913 0.034041	1.536 ± 1.4821 0.48774	0.915 ± 0.2844 0.6739	0.733 ± 0.2414 0.30803	TATTATGAATATGGTAAAGACTGTTATAGAAAATTCAATGTCATACT
plasmid_cp32-1	30417	BB_P42	2.310 ± 1.977 0.3468	3.197 ± 4.2177 0.44612	1.099 ± 0.8358 0.59611	1.687 ± 1.9856 0.61634	TTTAGAGGATAGAGATAATACAAAAGGTGTGGTGGATTGACCGTGAATA
plasmid_cp32-3	96	BB_S01	2.360 ± 1.1572 0.041204	1.631 ± 1.3959 0.37179	1.038 ± 0.4109 0.71532	1.124 ± 0.5075 0.33501	GATAAAATAAGTCACTAGAACTATACAAACTCAATATTTTAGAAAT
plasmid_cp32-3	274	BB_S01	1.004 ± 1.0572 0.988962	0.864 ± 0.1057 0.87294	1.962 ± 1.8625 0.45427	0.942 ± 0.936 0.9136	ATACAATTAAAGCAGAGCATCTTAAGCTGTACCTTAAACCTAGAAGTTCA
plasmid_cp32-3	279	BB_S01	1.892 ± 0.7575 0.110658	1.837 ± 1.5653 0.38842	0.923 ± 0.2832 0.05946	1.212 ± 0.4228 0.26052	AGCTACC GTTTCATGGGATGGCTATGTTAGTAAACCAAGAATACC
plasmid_cp32-3	333	BB_S01	3.461 ± 1.4654 0.024179	1.187 ± 0.6704 0.69274	0.486 ± 0.5781 0.41691	0.463 ± 0.3717 0.29835	ATAGATCTCGAACACCCGTTAATATAGAATTACCTATTGTTTGAATAC
plasmid_cp32-3	395	BB_S01	1.755 ± 0.352 0.012161	1.385 ± 0.7996 0.47339	1.073 ± 0.2015 0.20594	0.95 ± 0.2167 0.57872	TTCATATACTCAAGGTATTCAAACAACTAGGTAACTTATTAACGGGTTG
plasmid_cp32-3	398	BB_S01	1.833 ± 0.3939 0.017104	1.594 ± 0.9031 0.29224	0.677 ± 0.2276 0.11803	1.043 ± 0.2146 0.38008	TGTAAGAGATTGGGAGTTGATTGTATATAACCTATAAAAGTAAAC
plasmid_cp32-3	399	BB_S01	1.179 ± 0.3457 0.476907	0.524 ± 0.347 0.07344	1.046 ± 0.2662 0.79155	1.09 ± 0.2924 0.66365	CATATTCTAAATCAAGGTATTCAAACCAATAGGTAACTTATTAACCG
plasmid_cp32-3	432	BB_S01	2.489 ± 0.8756 0.056686	1.864 ± 1.6198 0.42602	1.633 ± 1.2195 0.36132	0.925 ± 0.5867 0.88138	ACCTATAAGAAAATCCAACAAATAAGAACAACTTCTTAGATGCGATTAA
plasmid_cp32-3	490	BB_S01	3.703 ± 1.4605 0.050095	2.146 ± 2.8599 0.54277	0.671 ± 0.3817 0.14297	1.332 ± 0.8742 0.47229	AAAGTCGACTTATCATATATGAAACATTGATTATCTAAAAGATATG
plasmid_cp32-3	578	BB_S01	2.460 ± 1.8644 0.239054	2.673 ± 2.5912 0.32906	0.959 ± 0.4898 0.89964	1.446 ± 0.7424 0.22105	TTTATTGAAAAGATATACGTAGAAATAGAAAAGACGTATTGAAAACCAA
plasmid_cp32-3	744	BB_S01	2.090 ± 0.8061 0.131012	2.006 ± 1.4641 0.3477	1.078 ± 0.2507 0.7137	1.178 ± 0.1502 0.00908	TCTTCTTTTGTGAGAAAACAAAATTCAAACATCATAGTAAAGATATTCT
plasmid_cp32-3	1042	BB_S01	4.307 ± 3.5556 0.058917	3.187 ± 4.6717 0.36647	1.204 ± 0.9084 0.69193	0.971 ± 0.7976 0.96765	GGAGTAATTATTACGATTTCAAAGGTGTAAGAACAAAGTGTGAGACT
plasmid_cp32-3	1214	BB_S01	1.702 ± 1.1478 0.17882	1.858 ± 2.2698 0.39234	1.144 ± 1.1222 0.50549	1.048 ± 0.1089 0.84898	TAACCAGCTTACACAAAGTAGCTCATTAATATGAGGAGGCTAGCGATGTT
plasmid_cp32-3	1224	BB_S01	2.622 ± 1.3152 0.033361	1.045 ± 0.555 0.89341	1.39 ± 0.8018 0.04707	1.133 ± 0.6455 0.7381	TAAGCTGGTTATTTACTGTAAAGCTCAATTAGCTTATATCTCTTCA
plasmid_cp32-3	1410	BB_S02	1.352 ± 0.9095 0.562345	1.073 ± 0.8031 0.36351	0.795 ± 0.6163 0.56973	1.161 ± 0.7347 0.29821	CATGCGTTTAAAGAGCAGGCCAATAGTAAATCTAAAGAGAACAGTCGAGA
plasmid_cp32-3	1626	BB_S02	2.105 ± 1.478 0.342604	0.826 ± 0.5059 0.45812	0.586 ± 0.2963 0.14797	0.843 ± 0.2961 0.87769	TCTTTGCAAGTAGCACCTTGTAAAATGATTGCTAAGATGTCGTT
plasmid_cp32-3	1631	BB_S02	1.035 ± 1.2185 0.914361	0.918 ± 1.0315 0.71313	1.109 ± 1.0065 0.59652	0.986 ± 0.8923 0.81559	CATAAAAGACATTATGCAAGCACACGTAGAGAACATTGACGCAAGTTCG
plasmid_cp32-3	1636	BB_S02	2.911 ± 2.1487 0.12877	2.271 ± 2.8301 0.46211	0.81 ± 0.7107 0.69923	1.07 ± 0.716 0.76249	AAAGACATTATGCAAGCACACGTAGAGAACATTGACGCAAGTTCGTTCCA
plasmid_cp32-3	1747	BB_S02	1.378 ± 0.8344 0.283003	0.272 ± 0.1982 0.11996	0.88 ± 0.7201 0.63147	1.066 ± 0.692 0.81386	TTAGAGCAACTTGTCTTAGCAAAGATTAATTAAATAGAAAAGAAAAT
plasmid_cp32-3	1928	BB_S02	1.698 ± 0.7635 0.242917	1.34 ± 0.297 0.17338	0.922 ± 0.3758 0.72743	0.648 ± 0.5574 0.31415	TTACTTATCGCTTGTACAAATTCTGTGAAATTATAGGTACAAAATTAGAA
plasmid_cp32-3	1931	BB_S02	2.293 ± 1.4564 0.081622	1.402 ± 1.1993 0.34095	1.335 ± 0.6771 0.17808	0.961 ± 0.5468 0.80477	CATACAAGCAAAGCGAACCTTAATTTTGAAAATCTAAAAGACATAAAA
plasmid_cp32-3	2216	BB_S03	1.676 ± 0.957 0.301533	0.988 ± 0.6965 0.98096	0.751 ± 0.5295 0.51246	0.839 ± 0.543 0.52875	TACGGATACCTTACGAGGTTAATTCTCTATTGTTACTGCTAGTGT
plasmid_cp32-3	2231	BB_S03	1.707 ± 1.2821 0.282464	1.763 ± 1.3384 0.31254	1.488 ± 1.1789 0.49268	1.361 ± 0.5971 0.39325	AGCTTAGTTGGAGATGGAACACCGAACCTAGAAGTTGAGGCTGGTGTG
plasmid_cp32-3	2341	BB_S03	2.054 ± 0.9121 0.184824	1.448 ± 0.9147 0.49339	0.919 ± 0.4127 0.76285	0.83 ± 0.1519 0.15249	TAACAGTTGGCATACCGCTAACACTCATATCGGAACACACTCCATATA
plasmid_cp32-3	3042	BB_S04	1.267 ± 1.5341 0.784636	0.917 ± 1.5221 0.93017	1.282 ± 0.816 0.51788	0.738 ± 0.5 0.31714	TGTTTGCAAGTAACTAACATAACATTGAAAGGGTACCTGTCAAGGAATCC
plasmid_cp32-3	3180	BB_S04	0.181 ± 0.2178 0.108803	0.637 ± 0.2123 0.24745	0.541 ± 0.2538 0.22788	1.09 ± 0.6773 0.66754	TATGTTAAATTACGGTTGGTGGGCCACCTCCAGCTTGTATAATAACACCGTT
plasmid_cp32-3	3203	BB_S04	1.848 ± 0.7076 0.039166	1.7 ± 1.2622 0.30812	1.031 ± 0.432 0.66029	1.42 ± 0.4855 0.09049	CAATCAATTGCAACCGGAAGATGGAACATACAGATCAAATAGATATCTA
plasmid_cp32-3	3249	BB_S04	0.079 ± 0.1395 0.065656	0.308 ± 0.4671 0.12979	0.201 ± 0.2433 0.07677	0.406 ± 0.5054 0.23127	TCCTAGGCAAGAGTATTCTATTGAAAAGTTGCAATTGTTGGGAA
plasmid_cp32-3	3376	BB_S05	3.517 ± 2.4788 0.063243	2.261 ± 2.0025 0.19757	1.097 ± 0.7789 0.63663	1.312 ± 0.5078 0.29062	TCTCCATTATTACCTCCTTTATTGCCAAAAGTTAACCCACCATGAG
plasmid_cp32-3	3393	BB_S05	2.744 ± 2.3961 0.33245	2.161 ± 2.7386 0.42292	1.806 ± 1.038 0.09797	2.153 ± 1.5261 0.29484	AAAGAGTATCAAGGAAAAGAGTAACTGGAAAAGTTATGAAAATCCTCC
plasmid_cp32-3	3668	BB_S05	1.748 ± 1.7723 0.298131	1.313 ± 1.6543 0.6211	0.64 ± 0.4175 0.40356	0.996 ± 0.7803 0.99574	TGGAATATGCACTAGATGAGTTAGTAAACAGCTACTATTGTCGCC
plasmid_cp32-3	3694	BB_S05	1.765 ± 0.6129 0.061794	1.868 ± 1.6572 0.38067	0.916 ± 0.2675 0.40753	1.274 ± 0.5037 0.23277	AACTCATCTATGCAATTCATATACTGCAATTGCAACCTCCACCGAGC
plasmid_cp32-3	3712	BB_S05	1.992 ± 1.1535 0.169723	1.794 ± 1.6955 0.47637	0.877 ± 0.6066 0.75364	0.863 ± 0.3611 0.49591	TTGTGCAATTACCAATAATTGAGGGATAATTGAGTGGCAAAGAGATTCTA
plasmid_cp32-3	3727	BB_S05	2.153 ± 1.2768 0.230603	1.409 ± 1.1874 0.67456	1.188 ± 0.9666 0.79167	1.074 ± 0.6281 0.84115	TTGGTAATTGGCACAATAGTAGTGTCTTACTAAACTCATCTATGCAATG

plasmid_cp32-3	3796	BB_S05	1.852 ± 1.0859 0.020218	2.118 ± 1.614 0.12747	1.057 ± 0.6187 0.76902	1.946 ± 1.5894 0.21616	AAGACGGTGTCTGAAAAGGTGACTGGAGCACCAATAAAGCAACTATTA
plasmid_cp32-3	3919	BB_S05	2.643 ± 3.0231 0.420073	0.807 ± 0.7183 0.74857	1.524 ± 1.2916 0.0735	1.259 ± 1.2669 0.76659	TTCCCAAATACAGCTACTTTACTAAATAACCTCATTGCTAATTGTTTC
plasmid_cp32-3	4067	BB_S06	1.634 ± 0.6681 0.168463	0.898 ± 0.2207 0.22978	0.777 ± 0.1231 0.11755	0.942 ± 0.1387 0.44433	AGATGTTGATCTACAAATGGGATATCAAAACCGTAAAATGGGACCGT
plasmid_cp32-3	4222	BB_S06	2.477 ± 1.3756 0.153512	2.401 ± 2.1379 0.34346	0.881 ± 0.42 0.50916	1.103 ± 0.615 0.62445	AATTAGACATTTAACGAGACTTCTGAGAAAATTTTACTTCAGATTCT
plasmid_cp32-3	4489	BB_S06	2.381 ± 1.8984 0.197332	1.933 ± 2.5274 0.5015	0.823 ± 0.6436 0.38741	1.102 ± 0.5739 0.36604	AAATGGATAAAATCTTGAAGAAGATTGAGGCTGGACTTCAAAGTTAGAAC
plasmid_cp32-3	4678	BB_S06	1.749 ± 1.1679 0.111112	0.326 ± 0.2392 0.18689	0.279 ± 0.1668 0.11816	0.683 ± 0.5152 0.03465	AGGCTTAAATAATAGAGAAGATGTTACATTGAAACTTGTCTGA
plasmid_cp32-3	4789	BB_S06	2.098 ± 0.8575 0.1175	1.108 ± 0.588 0.81117	0.872 ± 0.3999 0.72783	0.925 ± 0.3603 0.70228	TACTGCTAGGTTAATTATAAGTTCAGAAATTAGTGGATAATGAGT
plasmid_cp32-3	5093	BB_S07	1.413 ± 0.312 0.177738	1.321 ± 1.6287 0.7675	0.817 ± 0.4763 0.64876	0.909 ± 0.4925 0.8049	GCTTGAAGTAAGGATAATGAAGTAGAAAATTTCGCTGCTTAGTGC
plasmid_cp32-3	5259	BB_S07	1.160 ± 0.7807 0.78803	1.689 ± 1.4834 0.342	0.587 ± 0.3425 0.39935	0.913 ± 0.7279 0.90136	TTATCCTAGTAGCAGTGGAGGCGAAGAAGGCCGAGGGGAGTTG
plasmid_cp32-3	5566	BB_S08	1.673 ± 0.72 0.065	1.744 ± 1.7429 0.45534	0.852 ± 0.3186 0.13832	1.192 ± 0.6037 0.30569	TTATTGACATAAGGCCACAAGAACCTGCAATTCTTATGATTCTGATATG
plasmid_cp32-3	5633	BB_S08	0.439 ± 0.2004 0.120455	0.432 ± 0.3947 0.22741	1.2 ± 0.3941 0.05595	1.049 ± 0.3979 0.52171	TTCCCAAATTACACATATCAAGACCTTAACATGAACCAAAGACCGAAT
plasmid_cp32-3	5648	BB_S08	3.885 ± 2.5294 0.099834	0.76 ± 0.5695 0.32622	1.126 ± 0.6659 0.56144	1.25 ± 0.8158 0.62365	TGTGAACTGTTGGAAATCTCTTGAATATCAGACATATCAGAATCATAAAG
plasmid_cp32-3	5917	BB_S09	2.592 ± 0.8463 0.045167	1.404 ± 0.6765 0.36109	0.965 ± 0.2571 0.79949	1.084 ± 0.309 0.68334	TATCAATAATAGCTATAAACTTAACTAGTTAATCTGACCTTAATCAGG
plasmid_cp32-3	5928	BB_S09	2.603 ± 1.8998 0.183821	2.231 ± 2.1229 0.35359	1.322 ± 0.7296 0.08487	2.454 ± 1.7161 0.25007	GCTATAAAATTCTAACGTTAACCTGACCTTAAATCGGGAAATGGAGGCTA
plasmid_cp32-3	6014	BB_S09	3.561 ± 1.8623 0.050418	2.229 ± 1.8025 0.23893	1.156 ± 0.5674 0.09611	1.566 ± 0.8773 0.11305	GATAATTTCATAGTACCTTATAAAAGCTTGTCAAATGCCTCCATTCCC
plasmid_cp32-3	6081	BB_S09	2.426 ± 1.3334 0.088811	1.049 ± 0.7413 0.68249	1.625 ± 1.1657 0.25444	0.877 ± 0.623 0.83872	CTACCCCTTTAAACTTACTTTGATTGATTAGCCTTAAGGCTGGAGT
plasmid_cp32-3	6139	BB_S09	1.913 ± 1.3518 0.294649	1.415 ± 1.4424 0.65713	0.562 ± 0.2958 0.27249	0.778 ± 0.2452 0.19474	TAAGGTAACACTGAAATGATTTCACCTTAGATATGGTATAATCATT
plasmid_cp32-3	6178	BB_S10	1.101 ± 0.3997 0.104004	0.463 ± 0.3857 0.26087	0.915 ± 0.4122 0.04263	1.067 ± 0.4337 0.35245	TTAAATCATTAAACCCAATTTAAAGGGTTAACGGCATATGCAACTGAA
plasmid_cp32-3	6254	BB_S10	1.448 ± 1.829 0.684715	2.629 ± 0.9198 0.0869	1.464 ± 1.3622 0.65441	2.068 ± 1.0631 0.24676	TTTATGATATCGCACTCAAATTATTTCAGTTGCATATGCCAACCC
plasmid_cp32-3	6307	BB_S10	2.014 ± 0.5346 0.070116	1.069 ± 0.3972 0.83566	0.783 ± 0.291 0.41881	0.888 ± 0.2047 0.50102	TTATATTGAGCTAGCAGCTGTGATTGAAAGATATGGATGTTAGG
plasmid_cp32-3	6473	BB_S10	2.030 ± 1.8749 0.31233	3.116 ± 2.8317 0.19698	0.876 ± 0.953 0.8498	0.87 ± 1.0428 0.83169	TAAAGCATTAAACATCGCTGAATTAGCGCTCAAAGTCTTGGCGTTAAC
plasmid_cp32-3	6529	BB_S10	3.191 ± 1.1711 0.050018	1.813 ± 1.4328 0.37478	0.909 ± 0.2677 0.40988	1.068 ± 0.3119 0.43941	GACTGGCCTAACAGTACTATTAGCTTATTGTAGAAAGTCAAGCA
plasmid_cp32-3	6545	BB_S10	2.031 ± 1.6829 0.10199	1.781 ± 1.7494 0.25092	0.844 ± 0.6449 0.29652	1.123 ± 0.669 0.67255	TTAATAAAATTCTACATTACCCACATTAATATGCAAACAGGT
plasmid_cp32-3	6822	BB_S11	1.274 ± 1.1557 0.630873	0.597 ± 0.8101 0.49029	1.29 ± 0.6318 0.29624	1.874 ± 1.3302 0.23135	GCAGCATTTTATTAACTTGTAGTTAGCTGTTGAAACCAAAAGTGG
plasmid_cp32-3	7364	BB_S11	2.947 ± 1.3966 0.093751	2.177 ± 1.9249 0.35439	1.076 ± 0.3742 0.46267	1.259 ± 0.4074 0.47751	ATTGGAAAGTTGCGAACTGCAAAACAACTTACTTCACTCTTAATGAA
plasmid_cp32-3	7728	BB_S11	2.210 ± 1.0652 0.10016	2.125 ± 1.3526 0.28317	1.255 ± 0.5973 0.46484	1.064 ± 0.6856 0.34111	ATATTCACTGCTAAAGTCTAAATTAAAGTTGTCAGGCTAGAACG
plasmid_cp32-3	7737	BB_S11	1.224 ± 1.9547 0.85478	0.131 ± 0.2203 0.21443	0.663 ± 0.4583 0.47455	1.76 ± 1.45 0.4504	ACTTTAGCATTAATGCTTGTCTTGTAGTAAATTACTCAAGATATGTT
plasmid_cp32-3	7969	BB_S12	1.985 ± 0.9426 0.107116	1.999 ± 1.8792 0.38259	1.091 ± 0.5209 0.69805	1.045 ± 0.4987 0.66397	AGAGATCCAAAACAACTTACATTGTTTCAACATTGAAGTGAACACTG
plasmid_cp32-3	8141	BB_S12	2.777 ± 1.0795 0.030294	1.654 ± 1.7801 0.53913	1.375 ± 0.5601 0.41857	1.313 ± 0.458 0.02792	GAAATAATTGGTAGCAATTCTACTTGAATGCTAACTCAGCATTTA
plasmid_cp32-3	8219	BB_S12	1.818 ± 0.4279 0.081824	1.822 ± 1.4708 0.43485	0.932 ± 0.1331 0.53905	0.905 ± 0.1311 0.26544	GCCCTTAATTCTAAAGAGATACTTTTCGGCCTCAGCAGATAACTCTGAA
plasmid_cp32-3	8270	IG 142	1.839 ± 1.5213 0.476696	0.569 ± 0.7203 0.51947	1.055 ± 0.6731 0.91418	0.489 ± 0.1916 0.02793	ATAAGAATCTCTTAAAGGTTGTTGTTAGATTGGCAATTATA
plasmid_cp32-3	8434	BB_S13	2.012 ± 1.1719 0.280933	1.98 ± 1.9084 0.49921	1.454 ± 1.0233 0.5819	0.91 ± 0.4542 0.83612	AGCTTGTGATTCTCTTAAAGTATTAAACCTCATTAAGCTTAAACAGCG
plasmid_cp32-3	8575	BB_S13	3.108 ± 2.4473 0.246991	1.152 ± 0.5969 0.76296	1.611 ± 0.9139 0.15657	1.306 ± 0.6748 0.22238	AAAAAGCCCGTTAGTATTTAGTGTAGGATGAAACAAATTGTTG
plasmid_cp32-3	8645	BB_S13	1.974 ± 0.7386 0.094973	1.215 ± 0.7149 0.60559	0.959 ± 0.5125 0.83947	1.264 ± 0.5976 0.45268	TTAATGAAAATTGATTATGAAAAAGTAGGCCACTTCACTTCATCAAGTA
plasmid_cp32-3	8746	BB_S14	1.824 ± 0.6073 0.017963	1.609 ± 1.1011 0.25721	1.275 ± 0.5247 0.42801	1.103 ± 0.4359 0.05942	TTGATAAAGCTATTGCAAGTCTGTGAGACAGTAGAAAAAAATTTTA
plasmid_cp32-3	8934	BB_S14	1.521 ± 0.8869 0.466157	0.762 ± 0.4673 0.43418	0.793 ± 0.4826 0.54832	0.982 ± 0.8016 0.96705	TTGTATGAAATTAAATTAAAGCAAGTGGAGACTAGTGGCGACAAATT
plasmid_cp32-3	8965	IG 143	2.774 ± 1.4185 0.006526	1.418 ± 1.0124 0.42293	1.011 ± 0.523 0.97972	1.257 ± 0.9237 0.73549	AGTCTCTACTGCTAAATTCTACATACATTCTTCTAATT
plasmid_cp32-3	8968	BB_S15	2.382 ± 0.9733 0.074609	1.83 ± 0.9264 0.25515	1.195 ± 0.3508 0.47859	1.134 ± 0.371 0.42009	GTGAGCGACAAATTCCACCATTAATTAAAGGTATTCTGATCATGCTG
plasmid_cp32-3	9140	BB_S15	2.834 ± 2.3443 0.29456	2.066 ± 2.286 0.48605	0.277 ± 0.2987 0.06825	0.736 ± 0.4423 0.52383	AGTTCTTCTTCTGTCGACAAATTATTTCACATCTTGTGCTA
plasmid_cp32-3	9665	BB_S15	2.108 ± 0.767 0.010408	1.217 ± 0.8614 0.51027	0.78 ± 0.3134 0.34602	0.972 ± 0.4622 0.67195	ATTGAAAAAACCGCAGTAGATAATTGCTGAGCTATGCTTAAATCC
plasmid_cp32-3	9746	BB_S15	2.510 ± 0.4656 0.025459	1.814 ± 1.2724 0.37437	1.299 ± 0.2399 0.16162	1.231 ± 0.16 0.10412	TTAACAGCCTTACTGCATTCCTGCTGCTCATAGCACCTGGATTAAAGC
plasmid_cp32-3	9784	BB_S15	2.303 ± 0.5936 0.045031	1.349 ± 0.9095 0.54392	0.852 ± 0.2852 0.40081	1.093 ± 0.2883 0.51338	GATCAAAAGCTCACTCCATCACCCCCAAGAACACTTAAACAGCCTT
plasmid_cp32-3	9813	BB_S15	2.343 ± 2.7181 0.512601	1.284 ± 1.0775 0.62943	1.354 ± 1.0014 0.28438	0.581 ± 0.2957 0.18909	TTGTCTCAAACACCTGACTCTTAAATAGATCAAAAGCTCACTTC
plasmid_cp32-3	10025	BB_S15	2.564 ± 1.7545 0.00932	1.455 ± 1.3912 0.23386	1.021 ± 0.6818 0.96543	1.768 ± 1.1431 0.21436	TCATTAAGCTGATCCAGCCTAAATTAAAGGTTACCAAAAGATA
plasmid_cp32-3	10259	IG 144	1.522 ± 1.2045 0.003094	1.801 ± 2.0111 0.29824	0.994 ± 0.7676 0.97769	1.015 ± 0.8587 0.82947	ATTACCTTTACCAAAATTATGGAGTTGTTAGCATTTGCTGATTCT
plasmid_cp32-3	10650	BB_S16	1.631 ± 1.048 0.089563	1.913 ± 1.8687 0.34008	0.711 ± 0.5233 0.14733	0.85 ± 0.9072 0.57582	TGTCACCAAGTCATTACCGGATTGAGCTACATTCGGCTTTCTATCA
plasmid_cp32-3	10807	BB_S16	1.195 ± 0.6188 0.155983	1.021 ± 0.7397 0.90441	0.681 ± 0.4424 0.43348	0.838 ± 0.4493 0.30394	TATACTAAAGGGACTTGTGCTTGTATTCTATGGCTAGTTGTTTAC
plasmid_cp32-3	10810	BB_S16	2.521 ± 1.3403 0.007313	1.211 ± 1.3529 0.82723	0.827 ± 0.7063 0.78582	0.612 ± 0.3344 0.37549	AGTCACCAACTTTGGCCTTAAAGAATTAGCTGAAATTACAAGTCTTC
plasmid_cp32-3	10812	BB_S16	1.802 ± 0.8846 0.127685	1.809 ± 1.7975 0.45309	1.143 ± 0.3289 0.02717	1.071 ± 0.4451 0.68331	GTCCAACCTTGGCCTTAAAGAATTAGCTGAAATTACAAGTCTTC

plasmid_cp32-3	10997	BB_S17	2.163 ± 1.4128 0.1126	1.806 ± 1.5379 0.28493	1.165 ± 0.7965 0.56165	1.507 ± 1.0519 0.30074	GATACATCAAAAAAATCCCTGATGGAATTCCCGAAGAAATTCTT	
plasmid_cp32-3	10998	BB_S17	1.760 ± 1.0175 0.023083	0.478 ± 0.3836 0.35806	1.002 ± 0.5292 0.98888	1.021 ± 0.5680 0.80988	TCTACATTGTAGAACCTCAATTAAAATCATATTGTAGTAACAGCATT	
plasmid_cp32-3	11001	BB_S17	2.083 ± 1.0962 0.108664	1.907 ± 1.8202 0.38842	0.939 ± 0.376 0.73612	1.092 ± 0.5585 0.43093	CATCAAAAAAAATCCCTGATGGAATTCCCTGCCGAAGAAATTCTCAA	
plasmid_cp32-3	11204	BB_S17	1.924 ± 1.109 0.311218	1.173 ± 1.5155 0.86894	0.336 ± 0.1834 0.07208	0.608 ± 0.3984 0.11772	AAAATATTTATAAGAAATTGCTCATGAAAAAAATTGATTCTATAG	
plasmid_cp32-3	11212	BB_S17	2.264 ± 0.8795 0.106947	1.531 ± 0.7571 0.31015	0.984 ± 0.1473 0.84333	1.185 ± 0.3097 0.41492	ATATATTTACTATCTCAAATTATGTGTCGGTGAAGTCTAAGGG	
plasmid_cp32-3	11533	BB_S17	3.058 ± 1.4407 0.140193	0.799 ± 0.4227 0.40399	1.059 ± 0.2427 0.71796	1.088 ± 0.2165 0.6008	TGTTCCCTTAATTGTCATAAACTCTTTGTGTTGCGATAATATC	
plasmid_cp32-3	11536	BB_S17	1.357 ± 0.4876 0.408066	0.521 ± 0.1973 0.00179	0.86 ± 0.2621 0.58732	0.992 ± 0.2339 0.97207	TGTTCATAACGTAATAGCGATATTGGTACTGGTTACGGGGATATGA	
plasmid_cp32-3	12122	BB_S18	1.785 ± 0.6873 0.166101	1.755 ± 1.5612 0.47578	0.84 ± 0.3765 0.34909	1.694 ± 0.7232 0.15149	GAGATTTTGTTGTAATTCTAAATCTCAAATTGGGTATTGTAACA	
plasmid_cp32-3	12235	BB_S18	2.956 ± 1.461 0.036382	2.786 ± 2.8233 0.38607	1.974 ± 1.2262 0.31914	0.976 ± 0.6463 0.6853	CTTAGTGCATTAGGCCAAGACTTAAATCTAATCTGACTGTAAA	
plasmid_cp32-3	12236	BB_S18	1.141 ± 0.2615 0.498593	1.332 ± 0.5946 0.2538	1.128 ± 0.4578 0.70847	1.222 ± 0.8442 0.73736	AGTATATAAAAATGATGTTGTCAAAGTGAATATCGTTTTTATCAA	
plasmid_cp32-3	12239	BB_S18	2.305 ± 0.8476 0.027311	1.862 ± 1.518 0.34521	1.064 ± 0.2692 0.68181	1.101 ± 0.3102 0.25969	GTGAAATTAGCCAAAGACTTAAATCTAATCTGATACTGTAAAATT	
plasmid_cp32-3	12334	BB_S18	1.479 ± 1.4247 0.572512	1.32 ± 1.638 0.66521	0.765 ± 0.4292 0.61967	1.289 ± 0.8628 0.68633	AAAAAAATCTAGATAATATTGTTAGTGTCTATCAATGGTATAAAAATTATA	
plasmid_cp32-3	12535	BB_S19	1.961 ± 1.2914 0.2517	0.947 ± 0.8597 0.94145	0.673 ± 0.4655 0.3	0.811 ± 0.5605 0.68197	TTAAATACCAATTCAAATTATGCTTAATCTAAATCCATAGTAATT	
plasmid_cp32-3	12735	BB_S19	2.125 ± 1.0453 0.655132	1.419 ± 1.7695 0.67684	0.289 ± 0.1928 0.09136	0.548 ± 0.4215 0.24162	AATCTAAGTAACTCTTAGATATTCTAGAAAATAATTTTACAGCGT	
plasmid_cp32-3	12775	BB_S19	2.338 ± 0.6278 0.004003	1.066 ± 0.8255 0.8858	0.637 ± 0.1715 0.0735	0.711 ± 0.42 0.29122	TGTGTTTGTGTTGATAGTAGTTGAAATTATTAAATCTAAGTTA	
plasmid_cp32-3	13065	BB_S20	2.246 ± 1.2722 0.193492	1.744 ± 1.2141 0.09329	0.781 ± 0.5646 0.69807	1.287 ± 0.7286 0.6241	TGTTCTCAATAGCAGCCAAATAAGTACCAACCAGGTTCATTTAGAAAAA	
plasmid_cp32-3	13169	BB_S20	1.664 ± 0.5309 0.074661	1.342 ± 0.7959 0.4481	0.793 ± 0.5563 0.27101	1.398 ± 0.5656 0.0984	TGTTGGTTTACAGCTGCACCTTAAATTAGTGTACTCAATCCCATCAA	
plasmid_cp32-3	13172	BB_S20	1.065 ± 0.6304 0.717065	0.577 ± 0.5022 0.0964	1.028 ± 0.3446 0.78657	1.125 ± 0.356 0.30711	TATCTAATTCTAAAGGAAACTTAACTAGACACTAGTAAATCTAATTAA	
plasmid_cp32-3	13206	BB_S20	1.387 ± 0.3277 0.038726	1.019 ± 0.3026 0.81118	0.882 ± 0.1384 0.28527	1.049 ± 0.1607 0.56527	GTAAATCTAATTAAATAGTCTGATTTAAAGCAAACCTTGGGAAACAT	
plasmid_cp32-3	13256	BB_S20	1.669 ± 0.6731 0.224721	1.204 ± 1.4727 0.83259	0.301 ± 0.1278 0.0115	0.791 ± 0.6516 0.63243	ATGTTCCCAAAGTTGCTTAAATTGAGACTTAAATATTAGATTAC	
plasmid_cp32-3	13408	BB_S20	2.349 ± 0.9715 0.058691	1.119 ± 0.8586 0.86097	1.39 ± 0.8035 0.33414	0.856 ± 0.2991 0.59115	GTTTTAAGGTCAGTTACTTACTTCTGTAACACATATTCTTTTT	
plasmid_cp32-3	13467	BB_S20	1.861 ± 0.3928 0.038844	1.232 ± 0.3509 0.25976	0.841 ± 0.1657 0.35523	1.114 ± 0.159 0.05764	TTGAAATACTCTAGAATAATTGCTTAATTGAGAGTCTATGTTAAG	
plasmid_cp32-3	13533	BB_S20	1.139 ± 0.8805 0.850871	1.034 ± 0.9857 0.96138	0.978 ± 0.588 0.89942	0.67 ± 0.4662 0.50644	AAGGAATTAAGTTATGGAATAAGTCTGTATTAAAGATAACAGAC	
plasmid_cp32-3	13838	BB_S21	2.726 ± 1.6177 0.05683	1.707 ± 1.45 0.28916	0.899 ± 0.4314 0.6579	0.93 ± 0.4327 0.80694	GAAAATATAAAAATCAAGATATTGCAATATGGATATCTAAGTTTATCT	
plasmid_cp32-3	14186	BB_S21	2.672 ± 2.3876 0.367651	3.162 ± 4.1027 0.46455	2.113 ± 2.0987 0.45001	1.356 ± 0.4411 0.13851	GTATTCAACTCACTCTAAAGGGCTATGATCATTAATTATGCTTTATT	
plasmid_cp32-3	14224	BB_S21	2.998 ± 0.742 0.042638	2.101 ± 1.4346 0.31623	1.453 ± 0.339 0.14768	1.1 ± 0.6086 0.79978	AATTGAATGATCATAGCCTTAGGAAGTGTGATTGAATACTAAAGC	
plasmid_cp32-3	14280	BB_S21	1.657 ± 0.9273 0.005359	0.38 ± 0.2995 0.2766	0.863 ± 0.5332 0.34436	0.989 ± 0.6542 0.95874	CAGATGGTAAACAATTATAACTTTAACAACTAAGGAGGTTTATGGCTG	
plasmid_cp32-3	14289	BB_S21	1.496 ± 0.1087 0.022234	1.309 ± 0.4157 0.33457	0.973 ± 0.1303 0.79671	1.224 ± 0.8032 0.66328	ACAATTATAACTTTAACAACTAAGGAGGTTTATGGCTGATGATCAAG	
plasmid_cp32-3	14420	BB_S22	0.991 ± 0.6103 0.981089	0.555 ± 0.581 0.52851	0.992 ± 0.7536 0.97118	1.073 ± 0.7679 0.73427	AAAGATGCTAGTCTGTAACGGCTGTAACCTTATTAAATCTTTATTGAA	
plasmid_cp32-3	14523	BB_S22	1.962 ± 1.4305 0.078335	1.653 ± 1.3327 0.1576	0.621 ± 0.3447 0.39956	1.389 ± 0.9921 0.55718	AAATAGTCTAATCCCTCTCTTAAATTGTTGCTTTAGAGCATCTAA	
plasmid_cp32-3	14616	BB_S22	1.969 ± 1.0752 0.06851	1.672 ± 1.6026 0.41287	0.914 ± 0.4329 0.33753	1.018 ± 0.5407 0.71305	TTAATTGTCCTGTTATTGATCATTAATTCTTACAAAATCTTATCA	
plasmid_cp32-3	14676	BB_S22	1.073 ± 0.783 0.912298	0.904 ± 1.1349 0.86089	0.554 ± 0.3355 0.00993	0.902 ± 0.5647 0.6213	TCTGTAAGGGTGTATTAAATTACTAAAGGTTGAAATATTAGTGAAGA	
plasmid_cp32-3	14768	BB_S22	2.188 ± 0.6299 0.014892	1.088 ± 0.5947 0.82142	1.298 ± 0.47 0.03676	1.053 ± 0.3909 0.81052	TATGTTAGGAACGGGTGTTTTGAATAGTATCTGATGAAGGCATTATCA	
plasmid_cp32-3	14771	BB_S22	2.514 ± 2.7604 0.372444	2.292 ± 2.7719 0.38197	0.965 ± 1.2052 0.91582	0.844 ± 1.1053 0.70923	CTTGGAGTACCATCAAATTGCTTATGGCAGAACTAGAAGTACTACACTT	
plasmid_cp32-3	14862	BB_S22	1.084 ± 0.5407 0.802003	1.091 ± 0.7904 0.66312	1.069 ± 0.6994 0.88182	0.607 ± 0.5893 0.55051	TGGAATACAATGATGATGTAACCTTATTCTTAAAGTTACGATAATT	
plasmid_cp32-3	14869	BB_S22	1.548 ± 0.3608 0.013152	1.426 ± 0.8585 0.36929	1.025 ± 0.2201 0.82512	0.95 ± 0.3413 0.85741	CAATGATGATGTAACCTTATTCTTAAAGTTACGATAATTCTCCCGT	
plasmid_cp32-3	14958	BB_S22	1.953 ± 0.8481 0.086783	3.006 ± 1.2536 0.02096	1.084 ± 0.6156 0.84208	1.208 ± 0.5879 0.55755	TTATCATTGATTCTTAATTCTGATTAAGTCTAAAGATAAAACGGGAGAATT	
plasmid_cp32-3	15047	BB_S22	1.411 ± 0.4605 0.086744	0.415 ± 0.3241 0.21545	1.221 ± 0.8463 0.59433	1.571 ± 0.8995 0.35872	TTCACCGAAATCCCATTTAAAGAGGATGTTATGTCAAAAAAGAGCCTCC	
plasmid_cp32-3	15064	BB_S22	2.269 ± 1.1744 0.103221	1.61 ± 1.6462 0.56614	0.851 ± 0.417 0.36452	0.968 ± 0.7698 0.95111	AATGGGAATCTGGTAATAGTCCGGGGGGCCGAATTCTAAACCCCT	
plasmid_cp32-3	15167	IG 145	2.027 ± 1.6941 0.226497	2.412 ± 2.505 0.32346	0.932 ± 0.5385 0.7495	1.309 ± 0.6795 0.0813	TATACAAAATCATTAATTCTTCAAAAGTTACGTTTAAAGATCTG	
plasmid_cp32-3	15175	IG 146	2.872 ± 0.3556 0.009966	1.834 ± 0.9847 0.27538	1.063 ± 0.0852 0.15958	1.269 ± 0.0943 0.01248	CGTATAAAAATAAAATTAAGAAGGTTAAAAAATGGATACTTTAA	
plasmid_cp32-3	15332	BB_S23	2.508 ± 1.4197 0.151355	1.585 ± 0.7776 0.20458	0.855 ± 0.5337 0.63181	0.7 ± 0.6266 0.38108	AAAGACATATTGACTATTGTAATAGGCAAGATTTAAGAATGGTAATGGT	
plasmid_cp32-3	15350	BB_S23	1.023 ± 0.3991 0.812654	0.449 ± 0.3652 0.28188	0.924 ± 0.3594 0.40927	0.987 ± 0.4105 0.77143	CAATAGTCAATATGTCATTAGTAAAGGCTTGAAGAAGAATTAACTCCTA	
plasmid_cp32-3	15353	BB_S23	blyA	2.951 ± 2.0688 0.215219	1.939 ± 1.495 0.15674	1.792 ± 0.987 0.24636	1.78 ± 0.1017 0.00781	ATAGGCAAGATTCTTAAAGAATGGTAATGGCAAAAATCACATTAA
plasmid_cp32-3	15699	BB_S24	blyB	2.019 ± 1.1682 0.008114	2.111 ± 1.4305 0.08701	1.105 ± 0.7347 0.6427	0.94 ± 0.5399 0.90377	GATATTTGAGATTCTTACAGAAATCAAGTCATGCTTATTGATTG
plasmid_cp32-3	15741	BB_S24	blyB	3.017 ± 2.6165 0.252344	0.79 ± 0.4981 0.12153	1 ± 0.9801 0.99933	0.795 ± 0.5424 0.64892	AGGAAAGACAACAAATAATGCAAACAACTATTGGTTAGGACTTAA
plasmid_cp32-3	15784	BB_S25		5.142 ± 2.948 0.064436	1.565 ± 1.169 0.55193	0.54 ± 0.497 0.45521	0.801 ± 0.7568 0.62795	AGTCCTAAACCAATAGTGTATTGTCATTGTTCTTCTTATAGAT
plasmid_cp32-3	15805	BB_S25		0.961 ± 0.8957 0.905632	0.911 ± 0.5669 0.43188	0.639 ± 0.2329 0.20697	0.562 ± 0.3123 0.27707	GTTAAGCTGGATAGTAAATTAGTCCTAAACCAATAGTGTATTGTCATT
plasmid_cp32-3	15889	BB_S25		2.092 ± 1.8364 0.160799	1.713 ± 1.8855 0.36368	0.801 ± 0.4992 0.47149	1.175 ± 0.949 0.19137	TATGTTTGTAGAAAAATCTTACTTAAAGTATTAGTGAATTA

plasmid_cp32-3	15891	BB_S25	1.697 ± 0.7194 0.103516	1.536 ± 0.779 0.16391	0.886 ± 0.4916 0.57441	1.396 ± 0.7911 0.27497	TATATGTTTGTAGAAAAAACTATTACTTAAAGTATTAAATGTAAT	
plasmid_cp32-3	15892	BB_S25	2.545 ± 1.3427 0.096588	1.22 ± 0.8252 0.62027	0.639 ± 0.295 0.26423	1.204 ± 0.6468 0.71288	TAAGCACACTAAAATCTATGAAACAGCTAGTCAGTCAACTAAAATATTGAAAG	
plasmid_cp32-3	15894	BB_S25	2.028 ± 0.0151 0.086396	1.672 ± 1.452 0.39517	1.068 ± 0.4522 0.50974	1.059 ± 0.428 0.50875	AGCACACTAAAATCTATGAAACAGCTAGTCAGTCAACTAAAATATTGAAAG	
plasmid_cp32-3	15978	BB_S25	2.770 ± 0.9221 0.07283	1.202 ± 1.0109 0.74906	0.722 ± 0.1219 0.1309	0.825 ± 0.1007 0.16817	TTATCTCAATGTTGATTTTAAATGTCTGTATTCTCAAATATTCTTAG	
plasmid_cp32-3	16055	BB_S25	1.701 ± 1.2614 0.203189	2.019 ± 1.7483 0.25088	0.929 ± 0.53 0.73838	0.964 ± 0.4734 0.76559	TTCTTCATGATTTGTTACGTGTTGATTAGTGAAGTGATAATTCTTT	
plasmid_cp32-3	16333	BB_S26	1.938 ± 1.1669 0.210301	1.746 ± 1.3038 0.3368	0.792 ± 0.4969 0.28443	1.089 ± 0.3199 0.65287	TGGAGTGTGCTCTTTAGTGTGATAAATCTGGATAAGGATATTCTGGAT	
plasmid_cp32-3	16409	BB_S26	1.005 ± 0.4891 0.982231	0.594 ± 0.6078 0.31122	1.098 ± 0.8041 0.78115	1.114 ± 0.6451 0.04684	TAGACTTTCCGCTATTGGTTGTTTTAAATGTACTCTAAATATATG	
plasmid_cp32-3	16880	BB_S27	0.540 ± 0.6458 0.403958	0.534 ± 0.7485 0.30762	0.514 ± 0.6309 0.15559	0.495 ± 0.6309 0.34843	GTATACAAAAGAAAAAGAAAAGTAATCTAAGAGTTTGCAACTGTGTTT	
plasmid_cp32-3	17027	IG 147	1.671 ± 0.9449 0.347311	1.233 ± 1.4476 0.80909	0.493 ± 0.2811 0.05582	0.535 ± 0.2626 0.11935	AAAAATCTCTAAAGCCAATTAACTCTAAATAGTATATAATGACCATAA	
plasmid_cp32-3	17459	BB_S29	<i>bdrF</i>	2.217 ± 1.8205 0.002693	2.48 ± 2.816 0.21755	1.17 ± 1.0134 0.55858	1.318 ± 1.0654 0.23332	TCAATCTTAGTATCTAAATTAGATATCTTTGAAATTCTCTCTACA
plasmid_cp32-3	17513	BB_S29	<i>bdrF</i>	2.413 ± 1.7673 0.008101	2.608 ± 2.7918 0.22857	1.319 ± 1.0026 0.26756	1.592 ± 1.2038 0.05174	TCAATCTTAGTATCTAAATTAGATATCTTTGAAATTCTCTCTACA
plasmid_cp32-3	17694	BB_S29	<i>bdrF</i>	1.716 ± 1.3121 0.417149	1.182 ± 0.7924 0.56849	0.994 ± 0.692 0.99114	1.263 ± 0.7599 0.61243	TTTAGAAATGAAAGCAATTAGGCCGGCTATCATTGTGATAGACATTGC
plasmid_cp32-3	18119	BB_S30	<i>mlpC</i>	1.861 ± 1.5161 0.075091	1.86 ± 1.783 0.15628	1.256 ± 0.8388 0.45865	1.124 ± 0.7758 0.70441	TCAAGTTGAGTTTATGATCAAGTGCTGATTATTATCATCA
plasmid_cp32-3	18547	BB_S31		0.969 ± 0.4197 0.877972	0.922 ± 0.5434 0.71297	0.888 ± 0.3849 0.75765	1.49 ± 0.9943 0.54545	TATTATTTTCTTCACCTCTATTACCAATTTTTATTAACACAGTG
plasmid_cp32-3	18834	BB_S31		1.759 ± 0.5607 0.03272	1.313 ± 0.9443 0.54023	0.716 ± 0.1912 0.13569	0.8 ± 0.1894 0.26836	CTTATGTCAAAAGGTATGCTTGTGAGCTCTGGTAGAAAGTGAAA
plasmid_cp32-3	18867	BB_S31		1.938 ± 1.8352 0.17698	1.731 ± 1.7768 0.23249	1.208 ± 0.9563 0.69485	1.294 ± 0.9854 0.35604	TTTGTAACTTAGACCCATTCTATTGTTCCATTGTAATTTCTGTAGGA
plasmid_cp32-3	18959	BB_S31		1.275 ± 0.641 0.530743	2.498 ± 3.1868 0.49601	1.073 ± 0.416 0.78975	1.84 ± 0.8418 0.17185	CAGTACAAGTACTGGATATGAATTCTTTGATACCGCAATTCTACAGA
plasmid_cp32-3	18988	BB_S31		1.726 ± 0.7154 0.030149	1.578 ± 1.2433 0.34148	1.039 ± 0.4405 0.88595	0.736 ± 0.3402 0.15083	TGCCATATTGACCCCTATAGAAATTGGATTGCTCAATATCAAGCTCA
plasmid_cp32-3	19006	BB_S31		2.651 ± 1.4123 0.11202	1.518 ± 1.2621 0.46827	0.795 ± 0.5234 0.42563	1.004 ± 0.4801 0.97899	TAGAAATTGGATTGCTCAATATCAAGCTCAAATTGTGCTTTTAAATAA
plasmid_cp32-3	19029	BB_S31		2.831 ± 1.2991 0.053567	1.669 ± 1.1932 0.29551	1.094 ± 0.3884 0.19169	1.147 ± 0.3684 0.30011	TCAAGCTCAAATTGTGCTTTAATAACATTTTAATTCTCTAACTATT
plasmid_cp32-3	19078	BB_S31		1.341 ± 1.2377 0.71687	0.781 ± 0.7244 0.51707	0.176 ± 0.2541 0.09761	0.305 ± 0.2586 0.15422	TTTCATTGAAATTGTGATATTATCCATATCCTTTAAGACTTTGTCAA
plasmid_cp32-3	19188	BB_S31		2.667 ± 0.9468 0.037905	1.541 ± 0.4689 0.15476	1.088 ± 0.3972 0.20615	1.204 ± 0.2965 0.27867	TTCAAGCAAAATAAGCTCAGAAAAGATGAAAACCTTAAAGAATT
plasmid_cp32-3	19239	IG 148		1.896 ± 0.6269 0.121276	2.097 ± 2.4128 0.52602	1.29 ± 0.9746 0.66716	1.005 ± 0.3968 0.98089	GGAGAAAAAAAGATGAAAATTCTTCAACAAATAATCCACAAAGAAAATA
plasmid_cp32-3	19267	IG 149		0.965 ± 0.3555 0.81916	0.637 ± 0.4909 0.47954	0.854 ± 0.303 0.59396	0.931 ± 0.4328 0.85405	GCAAAAACATTTTGCCAACCTTTTACAAACAA
plasmid_cp32-3	19325	IG 150		0.844 ± 0.3744 0.406866	1.335 ± 0.8764 0.61327	0.636 ± 0.2484 0.15809	0.546 ± 0.3117 0.16767	GCTACGTTCTGTGTTAAAGAACCTAGCTAAGCCCATATCTTTCTTG
plasmid_cp32-3	23229	IG 151		1.522 ± 0.8591 0.396507	0.598 ± 0.1077 0.02529	0.581 ± 0.2596 0.0997	0.716 ± 0.2061 0.14993	TTGATGAAGAGTATTATTAACACTTAATTITGCTTTTCAAAATT
plasmid_cp32-3	23652	IG 152		1.449 ± 0.6234 0.104482	0.581 ± 0.6012 0.29409	1.15 ± 0.3373 0.56498	1.075 ± 0.7917 0.82388	GCAAAAACATTTTGCCAACCTTTTACAA
plasmid_cp32-3	24049	BB_S38	<i>bppA</i>	1.764 ± 1.3805 0.324526	0.802 ± 0.6094 0.27937	0.837 ± 0.893 0.63492	0.7 ± 0.4875 0.43765	TGCTCAAGGCCAAGAGTTAGAGAATTAGGATTAGAGA
plasmid_cp32-3	24154	BB_S38	<i>bppA</i>	0.209 ± 0.2068 0.139145	0.771 ± 0.7338 0.73139	1.865 ± 1.412 0.29968	0.78 ± 0.4394 0.39512	TCAACACCGTTGCGATATTATATAAAATATCAATTATCACCG
plasmid_cp32-3	24229	BB_S38	<i>bppA</i>	1.943 ± 1.8136 0.347218	1.068 ± 0.9622 0.89794	0.734 ± 0.6896 0.68776	0.785 ± 0.4483 0.63453	TTAACAAACAGGCCATATTGTTGAGGCCACTAAAGTTCTGAACTGCC
plasmid_cp32-3	24283	BB_S38	<i>bppA</i>	2.809 ± 0.614 0.009655	1.811 ± 0.6638 0.05012	0.713 ± 0.641 0.54282	0.74 ± 0.6437 0.44292	TGAGTAGTGTATTGCTGAGTACAATAAAATGGCAATTTTAAAGTAGTA
plasmid_cp32-3	24417	BB_S38	<i>bppA</i>	3.226 ± 2.2596 0.092877	2.13 ± 2.3631 0.37222	0.968 ± 0.5488 0.80684	1.157 ± 0.7125 0.2807	GATGCTGCAACCAATTAACTGTAAGATTAAAAGAGATGAGGCTTAATATCA
plasmid_cp32-3	24462	BB_S38	<i>bppA</i>	1.464 ± 0.9476 0.554615	1.442 ± 1.5475 0.71922	1.023 ± 0.6376 0.96817	0.428 ± 0.1881 0.1665	ATATCAAAAGTGTGTTAATAATGTGAATTGAGAATTATAAAT
plasmid_cp32-3	24532	BB_S38	<i>bppA</i>	1.626 ± 0.5673 0.150422	0.923 ± 0.3744 0.78707	0.83 ± 0.4531 0.38386	0.886 ± 0.3224 0.3502	GTAACATAGAGAGGAATCTTAATGGCACATAATTAAACGAGGATACGT
plasmid_cp32-3	24535	BB_S38	<i>bppA</i>	2.211 ± 1.6681 0.149532	2.128 ± 1.9317 0.25642	1.223 ± 0.6389 0.19999	1.214 ± 0.592 0.32712	ACTATAGAGAGGAATCTTAATGGCACATAATTAAACGAGGATACGTTA
plasmid_cp32-3	24765	BB_S38	<i>bppA</i>	2.078 ± 1.4935 0.052712	2.237 ± 1.5316 0.15428	0.857 ± 0.8366 0.62937	0.985 ± 0.7247 0.98156	AATAAGATCAAAACGAAATAAAAAAGAGAAAAGCCATTAAAGATAG
plasmid_cp32-3	24838	BB_S38	<i>bppA</i>	2.668 ± 1.7772 0.070926	1.609 ± 1.6418 0.41451	0.984 ± 0.5515 0.88375	0.757 ± 0.4865 0.10967	ATATGTAATTAGCATCTCAACCTATCTTATGGCTTTCTTTTT
plasmid_cp32-3	24848	BB_S38	<i>bppA</i>	2.025 ± 1.9635 0.293735	1.875 ± 1.3093 0.09384	1.008 ± 0.6475 0.98756	1.573 ± 0.8099 0.03059	TGTTTGTGTTAATTGTAATTAGCATCTCAACCTATCTTATGGCTTT
plasmid_cp32-3	25155	BB_S39	<i>bppB</i>	2.927 ± 1.7496 0.208415	2.662 ± 2.4855 0.3788	1.223 ± 0.7201 0.67931	1.246 ± 0.5652 0.57794	TTTACAAAGCTTATTAAAGCAACGTGAATTATGTCATGAAATAATAC
plasmid_cp32-3	25834	BB_S40	<i>bppC</i>	3.150 ± 1.8333 0.089807	1.988 ± 1.9627 0.38048	0.877 ± 0.4259 0.1085	1.053 ± 0.4094 0.64484	TGTTGCTTTGGATACGCTCAGACTCTGTAGTTGATGACAATTTCCTCA
plasmid_cp32-3	25927	BB_S40	<i>bppC</i>	4.278 ± 3.0285 0.157488	2.612 ± 3.0134 0.40975	1.389 ± 0.7284 0.16594	1.486 ± 0.8289 0.18894	GTATATAAAGTTTTCCGGTTGCTTAAAGTTGAAATATCTTCGATT
plasmid_cp32-3	25932	BB_S40	<i>bppC</i>	1.966 ± 1.6668 0.132588	2.237 ± 2.5832 0.32205	1.103 ± 0.8934 0.06936	0.704 ± 0.4266 0.41933	AAAGTTTTCCGGTTGCTTAAAGTTGAAATATCTTCGATT
plasmid_cp32-3	26109	BB_S40	<i>bppC</i>	2.620 ± 1.5989 0.024135	1.643 ± 1.4665 0.33472	1.461 ± 0.9009 0.41015	1.491 ± 0.8975 0.15436	TTAACCCCTAAAGTATTAAATTCTAAAGTGC
plasmid_cp32-3	26686	IG 153		1.900 ± 1.2247 0.359262	1.878 ± 1.811 0.52016	1.262 ± 0.7069 0.66363	0.972 ± 0.7633 0.96502	TTAGTACTTTATGGAGTAATTGAAATAAGAAAATTAATTAT
plasmid_cp32-3	26888	BB_S41	<i>erpG</i>	1.679 ± 1.1981 0.464543	1.917 ± 1.7589 0.50226	1.47 ± 0.7758 0.46996	1.04 ± 0.3517 0.89603	CTGGTGGTGGATTAAACAGACTGTTATTAGGATGTCACCTGCAATTAACT
plasmid_cp32-3	27039	BB_S41	<i>erpG</i>	1.189 ± 0.9559 0.749085	1.211 ± 1.0795 0.68369	0.333 ± 0.2994 0.12689	0.242 ± 0.3184 0.1407	GCCTCTCTAAATTCTTTCTTTATCTTATCCTTAACTCTGA
plasmid_cp32-3	27096	BB_S41	<i>erpG</i>	0.686 ± 0.693 0.1369	0.681 ± 0.7533 0.11174	1.05 ± 0.9696 0.37289	1.051 ± 0.9979 0.55881	CTGAGAAAAGTAAAAACAGGAAATATTGGACAAAAGCTTAAAGT
plasmid_cp32-3	27224	BB_S41	<i>erpG</i>	1.650 ± 0.5238 0.13495	1.183 ± 0.9015 0.71994	0.61 ± 0.2036 0.13996	0.838 ± 0.2798 0.33689	GATGATGCTTAAAGTATTGAGGAAGAACTTGAAAGACTGAGCAGGCT
plasmid_cp32-3	28340	BB_S44		2.397 ± 2.3852 0.128378	2.28 ± 3.0199 0.35163	0.891 ± 0.6624 0.76425	1.351 ± 0.9725 0.38969	TGTTGCAATTAGGAGGATTGTTAGATGATAGGGAAATAGCGGATAA

plasmid_cp32-3	28407	BB_S44	1.104 ± 0.5772 0.59945	0.525 ± 0.4284 0.41193	1.194 ± 0.6878 0.04244	1.23 ± 0.8479 0.13054	CCCTAGAAACCCCCAATTATCCGCTATTCCTATCATCTAACATCCTT
plasmid_cp32-3	28858	BB_S44	1.346 ± 0.6735 0.508759	0.558 ± 0.3247 0.07786	1.143 ± 0.2582 0.53473	1.364 ± 0.1946 0.06385	CTATTTTGATGTGCTTACTTCAGCTTCAAGTCAGTTGAAGTTTT
plasmid_cp32-3	28880	BB_S45	1.834 ± 0.6752 0.070023	2.078 ± 1.3525 0.23415	0.932 ± 0.296 0.58841	1.09 ± 0.3373 0.41829	TATCAAACAAAACTTTTACAACACTACAAAAGGAATACAAAAATAATAT
plasmid_cp32-3	28955	BB_S45	1.709 ± 0.6233 0.131215	1.512 ± 0.9636 0.39439	1.085 ± 0.3548 0.60464	0.991 ± 0.3922 0.9581	AAGCTAACAAATTCTCAATTAAATTGATAAGTTGAAGAAAAACAGTTA
plasmid_cp32-3	28977	BB_S45	1.307 ± 0.4748 0.423413	1.515 ± 0.8256 0.3759	1.062 ± 0.4419 0.82913	0.891 ± 0.241 0.11279	ATTTGATAAGTTGAAGAAAAACAGTTAACCTAAACAAAAAATGTGA
plasmid_cp32-3	29355	BB_S45	1.045 ± 0.4809 0.629501	0.49 ± 0.3743 0.27465	0.967 ± 0.4251 0.57572	1.028 ± 0.3855 0.1841	CTTCCCCTAAATCTTCAAATCACTTGCTTATCTCACCATATAGATTA
plasmid_cp32-3	29500	BB_S45	3.151 ± 1.2245 0.057739	1.572 ± 0.4823 0.10804	0.806 ± 0.2326 0.06703	0.948 ± 0.2884 0.8312	ATCGGTTTAAATAGTGTCTGGATGTCAGGATTAGTATCAAATAAT
plasmid_cp32-3	29614	BB_S45	1.738 ± 1.1736 0.108127	0.818 ± 0.5635 0.13508	0.743 ± 0.4714 0.13619	0.903 ± 0.5994 0.20047	TGATGGTATATCTTATAGAGTTTCTGTGTTCGATAAACCTTTACT
plasmid_cp32-3	29616	BB_S45	2.086 ± 1.6988 0.054205	1.14 ± 0.9298 0.18786	0.747 ± 0.5326 0.39675	0.899 ± 0.5929 0.73501	TATGATGGTATATCTTATAGAGTTTCTGTGTTCGATAAACCTTTA
plasmid_cp32-3	29694	BB_S45	1.589 ± 0.2761 0.06704	1.475 ± 0.10989 0.51471	0.72 ± 0.2207 0.23478	0.83 ± 0.4896 0.58593	TAATCATCAGTAATTTTGTGAAAAATTGAATCAGTGCTTGCATC
plasmid_cp32-3	29759	BB_S45	1.388 ± 0.5546 0.340019	1.747 ± 1.62 0.50661	0.571 ± 0.3639 0.13998	0.758 ± 0.1476 0.09515	ATCAGTGTATCTCTCCAACACTAAATGCTGGCTAAATATGCTATTG
plasmid_cp32-3	29762	BB_S45	4.201 ± 2.7607 0.184299	2.214 ± 1.1129 0.20708	2.092 ± 0.2907 0.02587	3.218 ± 1.6849 0.14857	TGTGTTAGGAGCGAGTGTGATAGTAAAGTATTGCTTTGTTCAAGAC
plasmid_cp32-3	29787	BB_S45	2.347 ± 1.122 0.140894	1.313 ± 0.9443 0.64367	0.879 ± 0.4698 0.76985	0.754 ± 0.2556 0.24127	AGTATTGTTGTTGATTTCAAGACCAACGCCAGCCAATGATCCTTATA
plasmid_cp32-3	29833	BB_S45	0.509 ± 0.3995 0.089537	0.477 ± 0.3959 0.06799	0.759 ± 0.3005 0.00517	0.862 ± 0.3035 0.45928	AGGATCATTGGCTGGCTGGCTTGTGAAATACAAAAGCATATACTTATC
plasmid_cp32-3	30075	BB_S45	0.384 ± 0.532 0.15188	0.602 ± 0.6822 0.36369	2.457 ± 1.023 0.06223	0.212 ± 0.1426 0.01474	GTTCTCTGTTAATGATATTCTCGTATAAGGGGGATAGCAAAACCC
plasmid_cp32-3	30180	BB_S45	6.312 ± 2.8882 0.070814	0.564 ± 0.5814 0.19083	0.901 ± 1.5312 0.92658	1.433 ± 1.2541 0.5387	TATCCTAAAGACAACATCAAATATGCTGCAGACATTGCATCAAGAGCATCA
plasmid_cp32-4	96	BB_R01	2.278 ± 1.028 0.048352	1.622 ± 1.3403 0.38383	1.012 ± 0.3748 0.7817	1.091 ± 0.4887 0.43513	GATAAAATAAGTCACTAGAACTATACAAATACTCAATTTTTAGAAAT
plasmid_cp32-4	274	BB_R01	1.018 ± 0.9244 0.977042	0.791 ± 0.8697 0.75661	2.087 ± 1.5781 0.34369	0.75 ± 0.5472 0.45556	ATACAATTAAAGCAGAGCATCTTAAGCTGACCTTAACCTAGCAAGTTCA
plasmid_cp32-4	279	BB_R01	1.866 ± 0.8587 0.075154	1.865 ± 1.5981 0.34221	0.927 ± 0.3438 0.40011	1.2 ± 0.5594 0.1697	AGCTACCCTTTCATGGGATTGGCTATGTTTAGTAAAAACCAAAGATACC
plasmid_cp32-4	333	BB_R01	3.002 ± 1.4305 0.036258	1.328 ± 1.1982 0.67817	0.575 ± 0.7409 0.56806	0.61 ± 0.5199 0.49507	ATAGATCTCGAACACCCGTTAATAGAAATTACCTATTGTTGAATAC
plasmid_cp32-4	395	BB_R01	1.785 ± 0.3012 0.008631	1.459 ± 0.7463 0.3815	1.092 ± 0.1751 0.02645	1.021 ± 0.2137 0.75811	TTCAATCAAGGTATTCAAACCAATAGGTAATTCTATATAACGGGTTG
plasmid_cp32-4	398	BB_R01	1.637 ± 0.3724 0.047274	1.266 ± 0.6213 0.44297	0.616 ± 0.1417 0.02338	0.793 ± 0.1192 0.05219	TGTAAGAGATTTGGAGTTGATTTGATCATATAACCTATAAAAGTAAATC
plasmid_cp32-4	399	BB_R01	1.255 ± 0.4151 0.399386	0.548 ± 0.388 0.13397	1.173 ± 0.2509 0.36694	1.148 ± 0.2733 0.44745	CATTCTATAATCAAGGTATTCAAACCAATAGGTAACTCTATATAACGG
plasmid_cp32-4	427	BB_R01	3.326 ± 4.5447 0.453774	1.157 ± 1.7266 0.8968	1.534 ± 0.7519 0.29132	2.043 ± 2.1551 0.49118	TGATCAAATCAACTCCAAATCTCATATCTCATATCAATCAAGGTATTCA
plasmid_cp32-4	432	BB_R01	1.751 ± 1.934 0.468547	1.999 ± 1.5724 0.27808	0.581 ± 0.3074 0.18856	0.715 ± 0.8784 0.52586	ACCTATAAAGTAAACCAACAATAAGAACACAATTCTTAGCAGCAGTTAA
plasmid_cp32-4	444	BB_R01	2.107 ± 1.1749 0.258686	1.39 ± 0.2681 0.01562	1.314 ± 0.4241 0.35936	0.825 ± 0.2667 0.51881	AAATCCAACAAATAAGAACACAATTCTTAGCAGCAGTTAAACATAAAAGT
plasmid_cp32-4	478	BB_R01	1.829 ± 1.3118 0.288412	1.288 ± 1.1767 0.75554	0.611 ± 0.3253 0.29095	1.266 ± 0.5304 0.31747	ACTCGCTCTAAAGAATTGTTCTATTGTTGGATTTTACTTTAGGTTATA
plasmid_cp32-4	490	BB_R01	2.636 ± 0.9097 0.090208	1.281 ± 1.6475 0.81028	0.52 ± 0.2086 0.13079	1.11 ± 0.5172 0.75336	AAAGTCGACTTATCATATATGAAACATTGTTGATTATCTAAAAAGATATG
plasmid_cp32-4	506	BB_R01	3.382 ± 2.3015 0.01087	2.169 ± 2.6571 0.35718	1.013 ± 0.6313 0.97759	1.198 ± 0.8709 0.18611	TATGATAAGTCGACTTTGATTTACTGCTCTAAAGAATTGTTCTT
plasmid_cp32-4	507	BB_R01	1.256 ± 1.1004 0.541439	1.286 ± 1.2096 0.38168	1.135 ± 0.9517 0.58181	1.433 ± 1.1962 0.22813	TATGAAAATCTTGATTATCTTAAACCAATAGGTTATTCTGGTTATACCGAA
plasmid_cp32-4	521	BB_R01	2.267 ± 1.0141 0.044785	1.205 ± 0.6987 0.72787	1.074 ± 0.4754 0.77493	1.343 ± 0.6074 0.2387	ATCAAAGTTCTATATGATAAGTCGACTTTGATTTAACTGCGCTT
plasmid_cp32-4	524	BB_R01	2.031 ± 0.5587 5.26E-05	1.288 ± 0.8774 0.48393	1.453 ± 0.3832 0.13245	1.85 ± 0.3912 0.40821	TATCTAAAAGATATGTCCTGTTATACCGAAAGCTTTACTAGATAT
plasmid_cp32-4	526	BB_R01	0.892 ± 0.538 0.250274	0.123 ± 0.1284 0.11691	0.602 ± 0.8562 0.23565	1.394 ± 0.9853 0.37994	TCTTTAAAAGATATGTCCTGTTATACCGAAAGCTTTACTAGATATT
plasmid_cp32-4	578	BB_R01	2.543 ± 1.6552 0.122255	2.833 ± 2.2887 0.20836	0.909 ± 0.5229 0.79867	1.56 ± 0.9858 0.28439	TTTATTTGAAAAGATATACGTAGAAATAGAAAAGACGTGAAACCCACAA
plasmid_cp32-4	744	BB_R01	1.976 ± 0.8579 0.182943	1.856 ± 1.3905 0.39415	0.992 ± 0.2688 0.96819	1.126 ± 0.1415 0.09025	TCTTCTTTTGTGAGAAAACAAACATCATAGTAAAGATATTCT
plasmid_cp32-4	1471	BB_R02	3.645 ± 1.0052 0.03956	3.05 ± 1.2454 0.10068	2.29 ± 2.7707 0.48492	0.993 ± 0.654 0.98452	TAUTCATCACGCCCTACCTCTTAGGGGTTACATTGCTTGTCTT
plasmid_cp32-4	1568	BB_R02	3.350 ± 2.7535 0.071277	2.45 ± 2.7401 0.25888	0.771 ± 0.5307 0.4992	1.214 ± 0.8466 0.35746	TCAATTCTATAATTCGCTCAGCCTCTAGTAACATTGCTTCAACACGC
plasmid_cp32-4	2222	BB_R03	1.148 ± 0.5293 0.132285	0.545 ± 0.4273 0.39525	1.083 ± 0.5727 0.33041	1.237 ± 0.6255 0.03837	CAAGCGTGGAGTCAGCTTGTGAGTACTACAGAGCTAGA
plasmid_cp32-4	2434	BB_R03	1.440 ± 0.9383 0.200843	1.207 ± 0.6083 0.04314	0.754 ± 0.307 0.26716	0.981 ± 0.4685 0.94403	ATGCACAAGGAGAGCTTGAAGAAAAGATGGGGAAATGATACTGTTAATG
plasmid_cp32-4	2668	BB_R04	3.574 ± 2.5461 0.16496	0.805 ± 0.2745 0.31105	1.086 ± 0.4841 0.41593	1.172 ± 0.5326 0.16415	GGAGCAACTGGATTCTGTGATCAAACCTTAATTGTTGATTATCATCAAC
plasmid_cp32-4	2900	BB_R04	3.464 ± 1.3564 0.000233	1.465 ± 0.5701 0.26248	1.23 ± 0.8535 0.59168	1.203 ± 0.5641 0.56655	TTCTCTATTGTCCTGAAACTGTTGAAATAGTAAAGATAACGATTAAC
plasmid_cp32-4	3126	BB_R04	2.507 ± 1.3124 0.041309	1.708 ± 1.7974 0.48151	0.727 ± 0.2845 0.37726	0.771 ± 0.4043 0.48357	TATCCAATTTCTCCATTCTACTCGGATTCTGTAACAGATAC
plasmid_cp32-4	4019	BB_R06	1.439 ± 0.5328 0.357582	1.708 ± 0.8883 0.23584	0.915 ± 0.4556 0.75124	1.085 ± 0.6273 0.80212	TTATAGGGGAAGTTAAAGATCTATAATGTTATAATGGTTGCGCTGATC
plasmid_cp32-4	4043	BB_R06	4.074 ± 3.3974 0.174359	1.787 ± 1.3842 0.24268	2.058 ± 0.9403 0.1125	1.326 ± 0.744 0.40254	TAATGTATAATGGTTGCTGATCAAATGAAAGATGTTGATCTTCAGA
plasmid_cp32-4	4215	BB_R06	4.545 ± 3.645 0.049092	1.885 ± 1.8177 0.07728	1.363 ± 1.8358 0.58655	1.153 ± 1.1266 0.00493	CTTAAATTACAGTACAAATTAGGCACTTAAAGCAGCGCTGAAAAATT
plasmid_cp32-4	4243	BB_R06	2.607 ± 0.5646 0.026377	1.231 ± 0.7219 0.6232	0.831 ± 0.1313 0.21338	1.025 ± 0.171 0.86611	AGTGCTAAATTGACTGTAATTAAAGTAATTAAGCTTACCACTTCAG
plasmid_cp32-4	4355	BB_R06	2.011 ± 0.6866 0.011389	1.21 ± 0.3841 0.32654	1.046 ± 0.4646 0.66642	0.986 ± 0.4057 0.56496	AACTTATTAATCAGTTGACTAACAGGCAGTGTCAATTCAAAAGATG
plasmid_cp32-4	4807	BB_R06	1.099 ± 1.4271 0.870074	1.255 ± 1.5831 0.70069	0.463 ± 0.4662 0.03326	0.881 ± 0.6944 0.13665	CCTACACCAATGAACAGTGGATAAGATCAACTGATATTGCTCATCA
plasmid_cp32-4	5096	BB_R07	0.947 ± 0.7105 0.799385	1.197 ± 1.227 0.73637	0.261 ± 0.1283 0.07212	0.331 ± 0.4676 0.03874	CTTCAAGCTTGTAGTAACAGCTGGGATTGATGCTAGCTTACATAT

plasmid_cp32-4	5277	BB_R07	0.538 ± 0.3298 0.32213	0.529 ± 0.4889 0.38801	0.929 ± 0.598 0.90049	0.781 ± 0.5885 0.71872	GTAGCAGTGGAGGCGAAGAAGGTGGCGAGGGGGGGTTGGCTCAAACAAGA
plasmid_cp32-4	5407	BB_R08	2.595 ± 0.6667 0.031707	1.127 ± 0.6982 0.78004	0.637 ± 0.2025 0.22784	0.662 ± 0.1644 0.17408	ATGAATGGTGTAGAAAAAGACTTTCTGATATGTCATTCTGATGATAAC
plasmid_cp32-4	5552	BB_R08	3.656 ± 3.123 0.033976	1.045 ± 1.0432 0.83701	0.447 ± 0.4332 0.40329	1.424 ± 1.6937 0.47643	AGTACACTGAATTCTGCAGGAGTTATTGACATAAAAGCCACAAGAACCTG
plasmid_cp32-4	5576	BB_R08	1.614 ± 0.7945 0.1199	1.606 ± 1.5366 0.46503	0.79 ± 0.3145 0.12119	1.148 ± 0.5841 0.35196	TTATTGACATAAAAGCCACAAGAACCTGCAATTCTTATGATTCTGATATGT
plasmid_cp32-4	5643	BB_R08	0.471 ± 0.2757 0.101936	0.472 ± 0.4201 0.22877	1.178 ± 0.3856 0.26935	1.163 ± 0.4 0.29324	TTCCAAACTTACACATATCAAGACCTTAACATGAACACTAAAAGACCGAAT
plasmid_cp32-4	5658	BB_R08	3.703 ± 2.3609 0.108858	0.798 ± 0.502 0.47264	1.025 ± 0.5725 0.89855	1.259 ± 0.787 0.60835	TGTGAAAGTTGGAATATCTTGAATATCAGACATATCAGAACTATAAAG
plasmid_cp32-4	5927	BB_R09	2.521 ± 0.7771 0.049119	1.363 ± 0.6166 0.3853	0.956 ± 0.2727 0.77434	1.085 ± 0.281 0.65259	TATCAATAATAGCTATATAAATTCTAAGTTAATCTTGACCCTAAATCGGG
plasmid_cp32-4	5938	BB_R09	2.872 ± 2.0122 0.134799	2.598 ± 2.4638 0.2777	1.147 ± 1.0459 0.70957	2.44 ± 1.6048 0.18768	GCTATATAAATTCTAAGTTAATCTTGACCCTAAATCGGGAAATGGAGGCTA
plasmid_cp32-4	6024	BB_R09	2.651 ± 1.3945 0.057632	1.702 ± 1.2577 0.25738	1.01 ± 0.3813 0.94363	1.315 ± 0.5655 0.14739	GATAATTTCATAGTATCTTATAAAAGCTTGTCCAATAGCCTCATTCCCG
plasmid_cp32-4	6091	BB_R09	2.670 ± 1.8785 0.098687	1.036 ± 0.8768 0.87154	1.465 ± 1.163 0.4485	0.943 ± 0.7189 0.93302	CTACCCCCTTAAACTTACTTTGATTGATTAGCCTTAAGGCTGGAGTG
plasmid_cp32-4	6149	BB_R09	1.726 ± 1.1499 0.358361	1.257 ± 1.3472 0.78062	0.514 ± 0.2058 0.14291	0.669 ± 0.2874 0.15726	TAAGGTAACACTTGAATGATTTCAGTTAGATATGGTATTAATCATTTA
plasmid_cp32-4	6317	BB_R10	1.972 ± 0.4821 0.071099	1.064 ± 0.3283 0.82052	0.769 ± 0.2913 0.42076	0.863 ± 0.1716 0.304	TTATATTGGACTAGCAGCTGTGATTGTTGAAAGATATGGATGATTGAGG
plasmid_cp32-4	6426	BB_R10	4.748 ± 2.7775 0.105034	2.243 ± 1.3626 0.13362	1.139 ± 0.7199 0.42827	1.046 ± 0.6488 0.90088	TTGCAATAGTGTAAACGCCAAAGCTTGTGCTAATTCA CGCATGTAA
plasmid_cp32-4	6539	BB_R10	3.140 ± 1.1376 0.049796	1.764 ± 1.4059 0.39108	0.888 ± 0.2623 0.39221	1.036 ± 0.3043 0.61818	GACTGGC CAAAGTACTTATGAGCTTATTGTTGAGAAAAGTCACTAAG
plasmid_cp32-4	6555	BB_R10	1.953 ± 1.4691 0.114163	1.774 ± 1.7136 0.30484	0.841 ± 0.5443 0.24122	1.109 ± 0.5721 0.63365	TTAATAAAAATTAACTTCTACATTACCCAACTCATTAATATGCAAACAGTTG
plasmid_cp32-4	6591	BB_R10	2.674 ± 2.4721 0.280916	3.343 ± 4.0659 0.35171	0.95 ± 0.8849 0.95259	1.343 ± 1.2554 0.67745	TTAGATGTTGGTAAATGAGTTAAGTTAATTTAATATCTGGGTTGT
plasmid_cp32-4	7133	BB_R11	2.689 ± 0.6632 0.010416	1.218 ± 0.8454 0.63063	0.782 ± 0.1729 0.06145	1.075 ± 0.2818 0.64349	TAATAAACTCAAATGCCCTCAACTTTTGTATTCTCGACTAAAGAAC
plasmid_cp32-4	7197	BB_R11	0.385 ± 0.3439 0.308704	0.414 ± 0.5122 0.49321	1.201 ± 1.0761 0.62542	1.189 ± 1.0962 0.73643	GTTCTTTTATTCTTGTCTTGTGAGAAATACAAAAAAAGTTGAAGGCA
plasmid_cp32-4	7374	BB_R11	2.832 ± 1.0729 0.093104	2.274 ± 2.1323 0.4035	1.001 ± 0.3695 0.9964	1.274 ± 0.1709 0.14344	ATTGAAAAGTGGCAACTGCAAAAATCAACTTTTACTCTTAATGAA
plasmid_cp32-4	7702	BB_R11	4.772 ± 2.0321 0.029307	2.178 ± 2.3379 0.41985	1.467 ± 0.4916 0.1593	1.307 ± 0.5203 0.33582	GGAGAAAAGAGTAAGACTTAAATTCTATTACGCTCTATCC
plasmid_cp32-4	7747	BB_R11	1.283 ± 1.973 0.823251	0.141 ± 0.1472 0.16001	0.875 ± 0.7264 0.83538	1.767 ± 1.5918 0.50904	ACTTTAGCAATTAGCTGTGCTTGTAGTAATACTACTCAAGATATAGTTG
plasmid_cp32-4	8151	BB_R12	2.987 ± 1.1745 0.037533	1.71 ± 1.8339 0.54104	1.357 ± 0.5858 0.4774	1.093 ± 0.4134 0.56609	GAAATAATTGGTAGCAATTCTATCGTAATGCTAATACAGCATTTA
plasmid_cp32-4	8229	BB_R12	1.880 ± 0.4557 0.064362	1.899 ± 1.6006 0.42187	0.973 ± 0.1084 0.66233	0.929 ± 0.1417 0.26701	GCCCATAATTCAAAGATACTTTTCCGCGCTCAGCAGAAATACTCTTGA
plasmid_cp32-4	8444	BB_R13	2.171 ± 0.7727 0.125646	2.016 ± 1.545 0.39375	1.776 ± 0.7951 0.26015	0.765 ± 0.3113 0.42124	AGCTGTGATTCTTCTTAAGTATTAACCTCATTAAGCTTAAACAGCGT
plasmid_cp32-4	8585	BB_R13	2.986 ± 1.9519 0.18452	1.129 ± 0.4799 0.75931	1.516 ± 1.0088 0.44332	1.252 ± 0.5911 0.44585	AAAAAGCCCGTTAGTATATTGAGTGTAGTGAAGAAATAATGTTGTGAT
plasmid_cp32-4	8756	BB_R14	1.835 ± 0.5597 0.008769	1.642 ± 1.1319 0.28087	1.287 ± 0.4996 0.354	1.132 ± 0.423 0.14988	TTGATAAAGCTATTGCAAGTCTGTGAGACTAGAAAAAAATTTTAAC
plasmid_cp32-4	8944	BB_R14	1.455 ± 1.1907 0.63715	0.568 ± 0.3147 0.24726	0.797 ± 1.0512 0.57934	0.765 ± 0.5631 0.61222	TTGTATGAAATTATTTAACGCAAGTGGAGCTAGTGTGAGCGACAAATTAC
plasmid_cp32-4	8975	IG 154	2.161 ± 1.1092 0.001369	1.598 ± 1.1466 0.28828	1.293 ± 0.7267 0.59561	1.152 ± 0.7822 0.81409	AGTCTCTACTGCTTAAATTACATACAACTCTTCTAATTGAA
plasmid_cp32-4	8978	BB_R15	2.316 ± 0.9376 0.054155	1.764 ± 0.9135 0.24649	1.18 ± 0.4404 0.61652	1.18 ± 0.4516 0.51049	GTGAGCGACAAATTCCACCATTAATTAAAGGTATTCTGATCATGCTGCA
plasmid_cp32-4	9150	BB_R15	2.833 ± 2.1507 0.268942	2.514 ± 3.2492 0.48985	0.482 ± 0.2836 0.13971	0.764 ± 0.3372 0.46439	AGTTCTTTTCTCTGCGCACAAATTATTTACAAATATCTTGTGCTA
plasmid_cp32-4	9696	BB_R15	2.130 ± 0.765 0.008521	1.185 ± 0.8057 0.54505	0.769 ± 0.2933 0.2948	0.929 ± 0.4441 0.30688	ATTGAAAAAACGCGTAGAATTGTCAGCTATGCTTAAATCCAGTGGCTA
plasmid_cp32-4	9777	BB_R15	2.453 ± 0.4758 0.016207	1.782 ± 1.2529 0.36168	1.288 ± 0.3346 0.21551	1.243 ± 0.1943 0.0689	TTAACAGCCTTTACTGCATTCCTCGCTCATAGCACCACTGGATTAAAGC
plasmid_cp32-4	9815	BB_R15	2.255 ± 0.4894 0.028879	1.363 ± 0.997 0.5721	0.864 ± 0.3009 0.50363	1.004 ± 0.3418 0.97998	GATCAAAAAGCTACTTCCATCACCCCCCAAGAACACTATTACAGCCTTAA
plasmid_cp32-4	10152	BB_R15	1.401 ± 0.5774 0.030107	1.297 ± 1.127 0.53829	0.747 ± 0.3401 0.17739	0.794 ± 0.3633 0.09526	ATTATTCTTGTCAAATTAAACGATCTGGATGGATGGCGGGAG
plasmid_cp32-4	10290	IG 155	1.055 ± 1.0992 0.82445	1.896 ± 2.8412 0.38774	0.912 ± 1.0353 0.67522	0.773 ± 0.7986 0.57433	ATTACCTTTACCAAAATTATGGAGTGTGTTAGCATGTCTGATTTTGA
plasmid_cp32-4	10426	BB_R16	0.727 ± 0.9761 0.638436	0.327 ± 0.4576 0.47202	0.51 ± 0.8265 0.16094	1.906 ± 2.5481 0.14836	GAATGGATCAAAGGTGGATGTTCTCAATTGTTTTATAAAAC
plasmid_cp32-4	10510	BB_R16	3.508 ± 1.0447 0.002927	2.31 ± 2.2632 0.38725	0.757 ± 0.4706 0.39277	1.179 ± 0.5336 0.16761	GTATTGTAAGTGGTGTGAGTCGGTTTTGGTTATAAAACAAAT
plasmid_cp32-4	10596	BB_R16	6.031 ± 2.9706 0.083895	1.432 ± 1.2446 0.59786	0.926 ± 0.5967 0.89028	1.779 ± 0.6202 0.08301	TATGTTCACCGTCAATTACCGGATTGAGTCGACATATTCCGTTTCTAT
plasmid_cp32-4	10597	BB_R16	2.916 ± 1.5148 0.065464	1.522 ± 1.1696 0.35568	0.902 ± 0.5067 0.29462	1.009 ± 0.3681 0.91597	TATCATTAAACGGTGAATACATCCTTATATAAGGATATGCTTCTT
plasmid_cp32-4	10630	BB_R16	2.300 ± 0.7251 0.087591	1.115 ± 0.2807 0.58901	1.091 ± 0.459 0.76551	0.989 ± 0.1842 0.93379	TATAAGGATGTGTTAGTACCTCAGCTTGTATGTTCAACAGCTATT
plasmid_cp32-4	10751	BB_R16	1.081 ± 0.6269 0.532034	1.015 ± 0.8496 0.94246	0.616 ± 0.3879 0.34158	0.739 ± 0.428 0.21588	TATACAAAAGGGACTGTGCTGTATTCTATGGCTAGTTGTTCTTAC
plasmid_cp32-4	10754	BB_R16	2.199 ± 1.3614 0.077849	0.931 ± 0.8403 0.91749	0.843 ± 0.6752 0.8102	0.376 ± 0.24 0.1721	TAGTCCAACCTTGGCCTTAAAGAAATTAGCTGTAATTACAGCTTCTGTT
plasmid_cp32-4	10756	BB_R16	2.024 ± 0.9774 0.148402	1.886 ± 1.8141 0.44807	1.167 ± 0.2512 0.04558	1.149 ± 0.4009 0.37656	GTCCAACCTTGGCCTTAAAGAAATTAGCTGTAATTACAGCTTCTGTTA
plasmid_cp32-4	10921	BB_R17	1.609 ± 0.5967 0.114024	1.35 ± 0.9107 0.42408	0.846 ± 0.3017 0.61378	1.294 ± 0.7099 0.33077	AAATTGAGTCTACATGTAGATACATCAAAACATCCTGATGAACTTC
plasmid_cp32-4	10941	BB_R17	1.875 ± 1.1551 0.059772	1.61 ± 1.2587 0.2337	0.829 ± 0.4404 0.28148	1.146 ± 0.6191 0.26202	GATACATCAAAACATCCTGATGGAATTCTTCGCCAGAAACTTCT
plasmid_cp32-4	10942	BB_R17	1.748 ± 1.0302 0.02095	0.473 ± 0.3791 0.35514	0.982 ± 0.5434 0.90216	1.006 ± 0.575 0.94335	TCTACATTGTAAGCTCAATTAAACATATGTAGTAACAGCATT
plasmid_cp32-4	10945	BB_R17	2.116 ± 1.4266 0.334113	1.082 ± 0.7706 0.89545	0.857 ± 0.3864 0.24841	0.742 ± 0.3436 0.05935	CATCAAAAATCACCTGATGGAATTCTTCGCCAGAAACTTCT
plasmid_cp32-4	11148	BB_R17	2.009 ± 1.1812 0.225794	1.313 ± 1.0854 0.70445	0.42 ± 0.111 0.06473	0.615 ± 0.3446 0.25581	AAAATATATTATAAGAAATTGTCATGAAAAAAATTGATTTCATAATG
plasmid_cp32-4	11156	BB_R17	2.253 ± 0.9425 0.081843	1.521 ± 0.8233 0.26338	0.965 ± 0.2118 0.73503	1.166 ± 0.3771 0.39256	ATATATTCTCCTAAATTGTCGTCGGTAAAGCTAAAGG

plasmid_cp32-4	11480	BB_R17	1.155 ± 0.6166 0.594832	0.283 ± 0.2979 0.17516	1.038 ± 0.4045 0.87848	0.51 ± 0.3084 0.04062	TGTTCTATAACGTAATAGCCGATATTGGTACTGGGTACGGGGATATGAATGCTATCTGA
plasmid_cp32-4	11488	BB_R17	2.866 ± 1.2196 0.075396	1.3 ± 1.1521 0.65847	0.83 ± 0.3496 0.19425	1.056 ± 0.3719 0.79391	ACGTAATAGCCGATATTGGTACTGGGTACGGGGATATGAATGCTATCTGA
plasmid_cp32-4	12066	BB_R18	1.569 ± 0.5153 0.107424	1.643 ± 1.5015 0.51171	0.597 ± 0.1603 0.01131	1.549 ± 0.5435 0.07471	GAGATATTGGTGTGAATTCTAAATCTCAAATTGGGTATTGTAACA
plasmid_cp32-4	12179	BB_R18	3.359 ± 1.6956 0.023435	3.268 ± 3.3524 0.31486	2.382 ± 1.7189 0.3051	1.267 ± 0.876 0.47704	CTTAGTGCAATTAGCCCAAAGACTTAAATCTAATCTGTGATACTGTTAAA
plasmid_cp32-4	12183	BB_R18	2.235 ± 0.8084 0.016432	1.865 ± 1.4636 0.3179	1.034 ± 0.2844 0.84363	1.074 ± 0.3468 0.58606	GTGCAATTAGCCCAAAGACTTAAATCTAATCTGTGATACTGTTAAAATTA
plasmid_cp32-4	12488	BB_R19	2.173 ± 1.4356 0.237101	1.032 ± 0.8968 0.96649	0.721 ± 0.4909 0.31579	0.704 ± 0.4765 0.57948	TTAAATACCAATTCAAATTATTGCCATACTTAAATCCATAGTAAATT
plasmid_cp32-4	12712	BB_R19	4.306 ± 4.1841 0.191261	1.823 ± 1.4376 0.28154	2.241 ± 1.5424 0.023	2.17 ± 0.2031 0.19757	CAAGACAACAAAGCACACATATCCTTTTCTCAGGCATGTTGAAT
plasmid_cp32-4	12728	BB_R19	2.621 ± 0.7543 0.007602	1.291 ± 1.2961 0.7161	0.777 ± 0.206 0.26912	1.074 ± 0.7591 0.8784	TGTGCTTGTGTCTGTATAGTAGTTGAAATTATTAAATCTAAGTTA
plasmid_cp32-4	12731	BB_R19	1.785 ± 0.3304 0.010216	1.543 ± 0.3029 0.12005	1.056 ± 0.4257 0.78779	1.799 ± 0.9051 0.22443	TATCCTTTCTCAGGCCATGTTGAATATGGAGTTAATTATGAG
plasmid_cp32-4	12995	BB_R20	1.395 ± 0.2966 0.196853	1.045 ± 0.3201 0.82564	1.11 ± 0.4353 0.73266	1.531 ± 0.2307 0.02598	AGTGCACCCGGTTCATTTAGAAAAAAAGAGATTAAGCTCATTAATTAT
plasmid_cp32-4	13122	BB_R20	1.302 ± 0.7502 0.539951	1.016 ± 0.5215 0.96508	0.595 ± 0.5426 0.30803	0.741 ± 0.4330 0.37256	TGTTGGCTTACAGCTGCACTTAAATTAGTAGTACTCAACCCCATCAA
plasmid_cp32-4	13131	BB_R20	1.574 ± 1.1236 0.495468	0.319 ± 0.2005 0.17536	0.892 ± 0.9474 0.71384	0.284 ± 0.33 0.0542	ATTTAAAGGAAACTTACTAGACGATAGTAAATCTAACATTAAGTCCT
plasmid_cp32-4	13159	BB_R20	1.874 ± 0.4457 0.092148	1.118 ± 0.5409 0.76217	1.104 ± 0.1333 0.41312	1.029 ± 0.217 0.85657	GTAAATCTAACATTAATAGTCTGAATTAAAGCAAAACTTGGGAAACAT
plasmid_cp32-4	13361	BB_R20	1.723 ± 0.9517 0.017351	0.572 ± 0.492 0.47986	1.017 ± 0.6176 0.64855	0.916 ± 0.463 0.5775	GTTTTAAAGGTCAGGTTACTTTACTTCATATAAACATATTCTTT
plasmid_cp32-4	13396	BB_R20	5.735 ± 3.6029 0.150525	2.58 ± 1.9262 0.29499	1.187 ± 0.6078 0.67475	2.145 ± 0.6711 0.11486	TCCCTAATTGAGAGTCATATTAAAGTAGAGGTAGTTTAAGGTCAAGT
plasmid_cp32-4	13486	BB_R20	1.429 ± 1.1895 0.606115	1.1 ± 1.2414 0.90269	1.161 ± 0.2158 0.31542	0.652 ± 0.4938 0.38807	AAGGAATTAAAGTTATGGAAATAAGTGTGTTATTAAAGATACAGACACTG
plasmid_cp32-4	13791	BB_R21	2.540 ± 1.4506 0.041022	1.503 ± 1.2157 0.29155	0.861 ± 0.4427 0.41383	0.938 ± 0.4515 0.82579	GAAAATATAAAATCAAGATATATTGCAATATGGATATCTCAAGTTTATCT
plasmid_cp32-4	14041	BB_R21	1.468 ± 1.1176 0.535763	1.709 ± 1.884 0.56895	0.813 ± 0.1957 0.28099	0.887 ± 0.3674 0.63896	CTACATTATTCGCCTAGCACAAGAAAGGAAACGACTAAAAAGATAA
plasmid_cp32-4	14484	BB_R22	2.644 ± 0.8781 0.084823	1.229 ± 0.626 0.55047	1.741 ± 0.2427 0.02416	1.519 ± 0.5082 0.18554	TCTCTTAAATAGCTAGCTTCCGCCTTAAATGTTGGTGTATTAACCG
plasmid_cp32-4	14494	BB_R22	5.900 ± 3.6315 0.078824	2.687 ± 1.3582 0.08413	1.197 ± 1.1506 0.6148	0.896 ± 0.8034 0.58743	GATTAAATTCTCTTAAATAGCCTAGCTTCCGCCTTAAATGTTGG
plasmid_cp32-4	14634	BB_R22	5.005 ± 4.507 0.236815	3.742 ± 3.7803 0.33725	2.32 ± 0.3082 0.54563	0.618 ± 0.3903 0.43194	TGCTATCTGTAAGGCGCAGTTGATTACTAAAAGATTTGAAAGTTTAC
plasmid_cp32-4	14721	BB_R22	1.735 ± 0.6924 0.058535	1.021 ± 0.5821 0.95862	1.131 ± 0.5503 0.35564	1.017 ± 0.4451 0.95816	TATGTTAGGAACGGGTTGTTGAATAGTATCTGATGAAGGCATTATCA
plasmid_cp32-4	14733	BB_R22	1.981 ± 0.7925 0.032429	0.976 ± 0.6221 0.89078	0.918 ± 0.377 0.15899	1.002 ± 0.6198 0.99128	CCTACATTAACTTACTTATGGCAGCATAACTAGAAGTACTACCTTATCCT
plasmid_cp32-4	14780	BB_R22	3.260 ± 1.4815 0.038173	1.789 ± 1.491 0.37936	1.237 ± 0.4799 0.07912	1.161 ± 0.4788 0.03805	TCCCTCTGACTATGAGAATAAAGCGATATCTTAAATATGGAAGACATGA
plasmid_cp32-4	15035	BB_R22	2.624 ± 1.7267 0.086157	1.334 ± 1.4348 0.57499	0.708 ± 0.7302 0.48704	0.698 ± 0.4023 0.31325	TATCCAAAAAAGAGCCTCTGTATGGAGATTAGTCCAGTCCCAGATCTTTAA
plasmid_cp32-4	15122	IG 156	1.655 ± 0.6009 0.04225	0.552 ± 0.1394 0.10275	0.99 ± 0.4551 0.95546	0.839 ± 0.4461 0.63192	TATCAAAATCGTAATTCTGCTAAAAAAAGCTTACAGTTTAAAGATCTGG
plasmid_cp32-4	15287	BB_R23	blyA 2.599 ± 1.3167 0.074497	1.621 ± 0.7888 0.1181	0.897 ± 0.7535 0.72693	0.712 ± 0.6672 0.2894	AAAGACATATTGACTATTGTAATAGGCAAGATTTTAAGAATGGTAATGGT
plasmid_cp32-4	15305	BB_R23	blyA 1.020 ± 0.3806 0.859086	0.438 ± 0.359 0.27499	0.927 ± 0.378 0.43741	0.975 ± 0.4142 0.6766	CAATGTCATATTGCTTAAAGGCTGAGAAGAATTAACTCTTA
plasmid_cp32-4	15308	BB_R23	blyA 2.228 ± 1.6541 0.301115	1.586 ± 1.3622 0.22959	1.352 ± 0.7845 0.5215	1.639 ± 1.13 0.10067	ATAGGCAAGATTTTAAGAATGGTAATGGTAAAGCATAACATTAA
plasmid_cp32-4	15654	BB_R24	blyB 2.002 ± 1.5178 0.078986	2.09 ± 1.6888 0.1451	1.177 ± 0.8147 0.50863	1.032 ± 0.7265 0.95833	GATATTGGAGATTTTTCATCAGAAATTAACTAAGTCATGCTGATTG
plasmid_cp32-4	15696	BB_R24	blyB 3.053 ± 2.2475 0.188319	0.809 ± 0.3207 0.30283	0.937 ± 0.9424 0.8695	0.831 ± 0.4899 0.63672	AGGAAAGAACAAATAATGCAAAATAACACTATTGGTTAGGACTTAA
plasmid_cp32-4	15739	BB_R25	5.537 ± 3.3858 0.058473	1.548 ± 0.9714 0.44191	0.341 ± 0.234 0.20386	0.811 ± 0.688 0.65235	AGTCTAACAAATAGTTGTTATTGCTATTGTTCTCTTATAGAT
plasmid_cp32-4	15760	BB_R25	0.791 ± 0.8031 0.523713	0.876 ± 0.6693 0.57063	0.613 ± 0.2118 0.11473	0.516 ± 0.2302 0.15669	GTAAAGCTGGATAGTAAATTAGTCTAAACCAATAGTTGTTATTGCTT
plasmid_cp32-4	15844	BB_R25	2.032 ± 1.5236 0.106501	1.823 ± 2.003 0.38292	0.8 ± 0.5296 0.16925	1.271 ± 0.9518 0.24635	TATGTTGTAGAAAAAATCTTACTAAAGTATTAAATGTAATT
plasmid_cp32-4	15846	BB_R25	1.619 ± 0.7027 0.09766	1.418 ± 0.8762 0.30164	0.869 ± 0.382 0.56031	1.281 ± 0.6998 0.29063	TATATGTTGTAGAAAAAATCTTACTAAAGTATTAAATGTAATT
plasmid_cp32-4	15847	BB_R25	2.771 ± 1.4776 0.111996	1.298 ± 0.7519 0.49252	0.611 ± 0.2549 0.1992	1.258 ± 0.569 0.59512	TAAGCACACTAAATCTATGGAAACAGCTGAGTCACAAATATTGAG
plasmid_cp32-4	15849	BB_R25	2.069 ± 1.003 0.083373	1.66 ± 1.4229 0.40172	1.054 ± 0.4705 0.7206	1.044 ± 0.4148 0.56372	AGCACACAAATCTATGGAAACAGCTGAGTCACAAATATTGAGAA
plasmid_cp32-4	15933	BB_R25	3.044 ± 0.8513 0.054761	1.31 ± 1.0031 0.6453	0.773 ± 0.0901 0.09657	0.871 ± 0.0787 0.16045	TTATCTCAATGTTGTTATTAAATGTTCTGTATTCTCAAATATTAG
plasmid_cp32-4	16318	BB_R26	1.379 ± 1.161 0.648915	0.621 ± 0.1019 0.31626	0.745 ± 1.0875 0.51366	0.981 ± 0.9485 0.94433	TATTAGAGTACATTAAAAAAACCAATAGCGGAAAAGTCTATAAT
plasmid_cp32-4	16364	BB_R26	1.017 ± 0.4924 0.92315	0.595 ± 0.5674 0.23436	1.04 ± 0.7493 0.89831	1.106 ± 0.6193 0.17789	TAGACTTTCCGCTATTGGTTTGTATTAAATGTAACATATTG
plasmid_cp32-4	16428	IG 157	1.412 ± 0.7328 0.044485	1.447 ± 1.3969 0.537	0.959 ± 0.5021 0.85459	1.232 ± 0.5966 0.50922	AAATGAAATTCTGCAAGAAAAACCTTTGTAATTACATTAAATTG
plasmid_cp32-4	16431	IG 158	5.239 ± 3.049 0.054787	4.093 ± 3.3586 0.16605	1.337 ± 0.7915 0.60739	1.939 ± 1.3716 0.3348	CATATAAAATCTCAAAGCCAATTAACTCTAAATAGTGTATAATGACC
plasmid_cp32-4	16435	IG 159	2.745 ± 1.8457 0.079215	1.412 ± 1.35 0.4459	0.794 ± 0.5015 0.32027	0.87 ± 0.3991 0.69262	AAAAATCTCAAAGCCAATTAACTCTAAATAGTGTATAATGACCATAA
plasmid_cp32-4	17440	BB_R28	2.745 ± 1.964 0.129763	1.85 ± 1.9204 0.39009	0.977 ± 0.6733 0.92196	0.948 ± 0.6223 0.34864	CCTTCAAGCAGGTCGTTAGGAGGCCCTTAAAGGGGGCATAGCGCTT
plasmid_cp32-4	17557	IG 160	2.392 ± 1.7678 0.122704	1.298 ± 1.2029 0.5182	1.028 ± 0.6261 0.78659	0.638 ± 0.3171 0.22957	CCATGTAAGAATTCTGCTATGCTGAAATATCTCATCAAACCGTTAT
plasmid_cp32-4	17564	IG 161	1.901 ± 1.3435 0.015609	2.246 ± 2.5546 0.32776	1.62 ± 0.9961 0.19462	1.055 ± 0.6279 0.87582	AGAATCTGCTATGCTGAAATATCTCATCAAACCGTTAT
plasmid_cp32-4	17695	BB_R29	3.193 ± 1.3825 0.039961	1.631 ± 1.1094 0.4231	0.974 ± 0.3258 0.90878	1.113 ± 0.4795 0.78857	AAGGATTACAAGATTGAAAGACTTTGTTAGGACTCT
plasmid_cp32-4	17703	BB_R29	2.480 ± 2.3036 0.170182	2.126 ± 2.62 0.37201	0.834 ± 0.7579 0.09458	0.795 ± 0.6243 0.33421	TTATTTCTGAAATAGTTTATAATCTCCGCCAATAGTTTACTC
plasmid_cp32-4	17833	BB_R29	3.996 ± 0.8908 0.024087	1.781 ± 1.42 0.42222	1.253 ± 0.2745 0.32119	1.145 ± 0.3856 0.50526	TATCTGCAATAAGCTTATTGTTGAATAATTGAGTTTATTTCTTAA

plasmid_cp32-4	17871	BB_R29	2.914 ± 1.33 0.13629	3.224 ± 3.4817 0.38641	1.785 ± 1.0801 0.34482	1.813 ± 0.1896 0.01919	TAAACTCAATTATTCAAAAAATAAGCTTATTCAAATAGACCCAATA	
plasmid_cp32-4	17973	BB_R29	1.558 ± 0.6711 0.328658	0.93 ± 0.4096 0.72468	0.362 ± 0.2212 0.16219	0.535 ± 0.2453 0.04763	AGCAAGAACAAAAAAAGATAGGTTTATTACGGTTTTAAAGAAG	
plasmid_cp32-4	18381	BB_R29	1.922 ± 1.7674 0.400747	1.449 ± 1.605 0.57037	0.802 ± 0.8264 0.77462	0.548 ± 0.2681 0.09145	AAAAAAAGATCCAATTATGCTTATCAATAACAC	
plasmid_cp32-4	18502	BB_R29	4.676 ± 2.4326 0.015829	3.166 ± 2.2004 0.18293	1.813 ± 1.2785 0.38836	1.635 ± 1.3852 0.30466	ATCAGAAACTTGCCCGTATTGACAAAAGCTTAAAGGGTATGGGTATAAG	
plasmid_cp32-4	18594	IG_162	1.573 ± 0.7101 0.175655	1.733 ± 2.0152 0.56083	1.052 ± 0.5551 0.82522	1 ± 0.4392 0.99962	GGAGGAAAAGATGAAAATCTTCAAACAAATAATCCACAAGAAAATA	
plasmid_cp32-4	18620	IG_163	1.098 ± 0.2855 0.702226	0.664 ± 0.5485 0.42773	0.92 ± 0.1851 0.63872	0.971 ± 0.3982 0.88364	GCAAAAACATTTCGCCAATTTCACAAAAAAATTTCACAA	
plasmid_cp32-4	18862	IG_164	2.741 ± 3.1677 0.22098	1.715 ± 2.5547 0.19388	1.129 ± 1.527 0.5362	0.952 ± 1.2255 0.9001	TTAATCTTATTAAATTAAACACTTTGTAATTGGTAAAAAGATTATT	
plasmid_cp32-4	20242	BB_R32	1.947 ± 0.7148 0.116317	1.074 ± 0.316 0.53724	0.895 ± 0.2672 0.19347	1.098 ± 0.3412 0.40461	GATTATCATGGGGCCTTATTAAATGGGAAAGGATTGTTGAAGAACCTC	
plasmid_cp32-4	22145	BB_R35	<i>brdG</i>	1.808 ± 1.6843 0.236883	0.834 ± 0.6624 0.77584	0.383 ± 0.2797 0.20887	0.733 ± 0.6745 0.71323	GAAAAGATTTCAAAAAGATAGATAGTGTAAACTAAATAGATAGT
plasmid_cp32-4	22166	BB_R35	<i>brdG</i>	3.268 ± 0.3734 0.009274	1.509 ± 0.5635 0.26866	0.954 ± 0.024 0.05024	1.225 ± 0.1891 0.19446	TATCTTTGAAAATTCTTCTACATTAATTATTGTTGTTCAAAGAAAT
plasmid_cp32-4	22224	BB_R35	<i>brdG</i>	2.904 ± 0.8305 0.037363	2.195 ± 1.9143 0.42049	1.034 ± 0.3445 0.91084	1.098 ± 0.2423 0.41249	GATATATCTTTGCACAAAGTTTCTACACTATCTATTAGTATTACAA
plasmid_cp32-4	22248	BB_R35	<i>brdG</i>	3.168 ± 1.7546 0.094201	1.826 ± 1.9706 0.47046	1.219 ± 0.5988 0.30107	1.181 ± 0.3751 0.23983	TTTAAAAAAGACTTAATGCAAGCAATAAGAACATAACAGTAATTCTAA
plasmid_cp32-4	22385	IG_165	2.891 ± 2.0521 0.135041	2.108 ± 1.168 0.06686	1.927 ± 1.3787 0.07011	2.353 ± 1.2843 0.12175	ATAAGTTAGTATAGCTCTAAAGTAGAACCTTATTGAAATTTTAACAG	
plasmid_cp32-4	22654	IG_166	2.705 ± 4.0805 0.515013	1.049 ± 1.7881 0.97142	1.879 ± 1.9505 0.46347	0.456 ± 0.5494 0.52928	CATACATATGTATAACTAAACACTATTGGCTAGGCTTTACAGAAAT	
plasmid_cp32-4	22794	IG_167	1.159 ± 0.34 0.599018	0.757 ± 0.6092 0.6118	1.172 ± 0.2753 0.47595	1.143 ± 0.6551 0.71998	GCAAAAACATTTCGCCAATTTCACAAAAAAATTTCACAAAAAA	
plasmid_cp32-4	23070	BB_R36	<i>bppA</i>	3.121 ± 1.3927 0.011884	1.736 ± 1.088 0.11935	0.895 ± 0.3722 0.54759	1.229 ± 0.5309 0.16997	TTTATCTAATTGTTCTTGAAGACTAAATCAATTTGATTAAACT
plasmid_cp32-4	23090	BB_R36	<i>bppA</i>	1.155 ± 1.7024 0.4085	1.028 ± 1.3208 0.93986	0.207 ± 0.3119 0.23213	1.094 ± 1.2382 0.89145	CCTACTTCACTAGCACCGTATTCTAATTGTTCTTGAAGACTAAAA
plasmid_cp32-4	23189	BB_R36	<i>bppA</i>	1.694 ± 1.5916 0.518543	0.472 ± 0.5834 0.11932	0.772 ± 1.062 0.13919	0.621 ± 0.4916 0.50663	TGCTCAAGGGCAAAGAGTTAGAGAATTAGGATTAGAGAATTGTTAAAG
plasmid_cp32-4	23307	BB_R36	<i>bppA</i>	0.961 ± 0.5218 0.295447	0.547 ± 0.2641 0.06312	0.615 ± 0.3171 0.05581	0.759 ± 0.4042 0.32422	TTTCAAAAAATGGTAGTTCACAAACTTAGGGCTCAACATTGATGG
plasmid_cp32-4	23423	BB_R36	<i>bppA</i>	2.519 ± 1.0608 0.007506	1.295 ± 1.1149 0.46615	0.865 ± 0.3852 0.71457	1.09 ± 0.5774 0.68706	TGAGTAGTGTATTGCTGAGTACAATAAAATGGCAATTAAAGCAGTA
plasmid_cp32-4	23557	BB_R36	<i>bppA</i>	3.171 ± 2.4859 0.076464	2.125 ± 2.501 0.35315	0.953 ± 0.6147 0.82779	1.146 ± 0.8257 0.42962	GATGCTGCAACCAATTACTGTAAGGAAAGAGATGAGGCTTAACTATCA
plasmid_cp32-4	23602	BB_R36	<i>bppA</i>	1.989 ± 1.2252 0.337497	2.159 ± 1.9603 0.45006	1.071 ± 0.773 0.91432	0.404 ± 0.2531 0.11759	ATATCAAAGTGTATTGTAATTAAATGTGAATTAGAAATTATAAAT
plasmid_cp32-4	23905	BB_R36	<i>bppA</i>	2.483 ± 1.3235 0.067013	2.253 ± 1.0596 0.02979	0.927 ± 0.7895 0.76466	1.283 ± 0.603 0.52787	AATAAGATCAAAAGCAAATAAAAGAGAAAAGCCCATTAAAGATAGG
plasmid_cp32-4	23978	BB_R36	<i>bppA</i>	2.465 ± 1.6028 0.095744	1.581 ± 1.5195 0.41599	0.914 ± 0.446 0.49452	0.776 ± 0.4443 0.07375	ATATTGTAATTAGCATCTTCAACCTATCTTAAATTGGCTTTCTTTT
plasmid_cp32-4	23981	BB_R36	<i>bppA</i>	1.821 ± 1.2163 0.384761	2.553 ± 2.1501 0.2699	0.605 ± 0.3392 0.22131	1.069 ± 0.4718 0.46125	CGAATACATATCCACTAATTGAGCAGTTAAATTATAATTGGAGAGTTG
plasmid_cp32-4	24356	BB_R37	<i>bppB</i>	1.962 ± 1.1556 0.227772	1.478 ± 1.4089 0.61055	0.693 ± 0.5089 0.47443	1.049 ± 0.331 0.87046	TAGATTATAGGACTGGATATTAAAGAGCAATTGTTTATTATAAATCC
plasmid_cp32-4	24409	BB_R37	<i>bppB</i>	0.813 ± 0.4812 0.627181	1.052 ± 0.3838 0.86272	0.801 ± 0.2981 0.31658	1.141 ± 0.5442 0.44151	CATGGATTATAATAAAACATTGCTCTTAATATCCAAGTCTATAAAT
plasmid_cp32-4	24534	BB_R37	<i>bppB</i>	2.361 ± 0.7675 0.027904	1.315 ± 0.7193 0.58697	1.305 ± 0.459 0.2384	1.26 ± 0.4209 0.37137	TAAAGTGTATTCCATTACCTTACCTATGCTTTACTTCGCTTATTCAAATT
plasmid_cp32-4	24535	BB_R37	<i>bppB</i>	2.778 ± 3.4517 0.432404	0.025 ± 0.043 0.02352	1.659 ± 2.3786 0.64166	1.689 ± 1.4022 0.47265	TAGCAACAAAAAAATAAGAAATTATATTGATTCACTGACTGAAACCTC
plasmid_cp32-4	24537	BB_R37	<i>bppB</i>	0.725 ± 0.3143 0.328125	0.631 ± 0.5624 0.47126	1.043 ± 0.31 0.72869	1.057 ± 0.3843 0.59798	CGAACAAAAAAATAAGAAATTATATTGATTCACTGACTGAAACCTCGT
plasmid_cp32-4	24822	BB_R38	<i>bppC</i>	0.000 ± 0 0.159512	0.34 ± 0.6468 0.4481	0.836 ± 1.2754 0.88178	1.776 ± 0.2372 0.62578	AATCTCTCATCTATGTCGAATTATTATTTCAAATTGAAATCTAACG
plasmid_cp32-4	24929	BB_R38	<i>bppC</i>	2.798 ± 2.7875 0.076079	1.481 ± 1.7641 0.25675	1.398 ± 1.2802 0.04844	1.2 ± 0.1016 0.52524	TCTTTTCAAAAGAACAAACATAAGTTAAAGATAACCAAATTGATATTGT
plasmid_cp32-4	24975	BB_R38	<i>bppC</i>	3.214 ± 1.8564 0.088102	1.987 ± 2.001 0.39166	0.885 ± 0.4372 0.08998	1.047 ± 0.4068 0.67002	TGTGCTGTTGGATAGCTCGAATTCTCTGAGTTGATGACAATTCTCTA
plasmid_cp32-4	25068	BB_R38	<i>bppC</i>	4.297 ± 3.1763 0.164064	2.674 ± 3.0092 0.38709	1.443 ± 0.8518 0.17817	1.492 ± 0.9375 0.22788	GTATATAAAGTTTCCGGTTGCTTAAAGGTTGAAATATCTGCTT
plasmid_cp32-4	25073	BB_R38	<i>bppC</i>	2.011 ± 1.8123 0.12257	2.319 ± 2.7459 0.30425	1.121 ± 0.8806 0.27757	0.757 ± 0.5101 0.53461	AAAGTTTTCCGGTTGCTTAAAGGTTGAAATATCTGCTTATTTCAC
plasmid_cp32-4	25284	BB_R38	<i>bppC</i>	1.423 ± 1.0203 0.493052	0.419 ± 0.5605 0.20355	0.963 ± 1.2706 0.93977	0.483 ± 0.6558 0.33527	AGAAAAAAATTCAAACCAACTCTAAGTTTATTGACCCTAAAGTA
plasmid_cp32-4	25734	IG_168		4.574 ± 3.8543 0.220731	1.252 ± 1.204 0.7432	1.049 ± 0.7892 0.94196	0.974 ± 0.9458 0.96379	TGAGTTGATTTAACATTACATTAGTTGTAACAATGTAATTGCAAATG
plasmid_cp32-4	25826	IG_169		1.544 ± 0.7138 0.358376	1.273 ± 1.1324 0.6657	0.865 ± 0.4985 0.71855	1.444 ± 0.5007 0.14897	ATAATGCAATTTCACATTCACATTAAATGTTACATTGCTTACATTG
plasmid_cp32-4	25959	IG_170		3.151 ± 2.3913 0.100162	1.31 ± 1.579 0.62124	0.957 ± 0.6284 0.56998	1.006 ± 0.6097 0.97912	CTTGCTCATCATATAAGATAAAAGATTATTATTCACAGAAATTCTCAAA
plasmid_cp32-4	25966	IG_171		3.223 ± 3.251 0.011284	2.752 ± 3.3351 0.13658	1.189 ± 1.1387 0.65256	1.641 ± 1.8559 0.07502	GCCAATACTTGCTCATCATATAAGATAAAAGTTTACAGAAATTCTCAAA
plasmid_cp32-4	25970	IG_172		0.841 ± 0.6501 0.792464	0.964 ± 0.8549 0.9638	0.519 ± 0.4482 0.46504	0.239 ± 0.248 0.177	CCTGACCATTTGCTCATCATATAAGATAAAAGTTTACAGAAATTCTCAAA
plasmid_cp32-4	26138	BB_R41		3.037 ± 1.6115 0.136307	1.481 ± 0.5908 0.15943	0.813 ± 0.3082 0.53665	1.041 ± 0.4255 0.88366	ATTATCGAAGTTAGATGACATAGTTGAGAAAATTAAACGTTTATTGATA
plasmid_cp32-4	26209	BB_R41		3.885 ± 2.049 0.091892	1.612 ± 1.4352 0.58666	1.113 ± 0.4711 0.69756	1.142 ± 0.6189 0.18712	AAAAAAAGATCCAATTATGCTTATCAATAACGTTTAAATTCTCAACTA
plasmid_cp32-4	26210	BB_R41		3.377 ± 1.1662 0.067887	1.545 ± 1.0264 0.49955	1.169 ± 0.1957 0.23254	1.23 ± 0.3622 0.11316	AAAAAAAGATCCAATTATGCTTATCAATAACGTTTAAATTCTCAACT
plasmid_cp32-4	26248	BB_R41		1.235 ± 0.8499 0.048935	0.5 ± 0.4343 0.41909	1.176 ± 0.9138 0.24342	0.905 ± 0.6566 0.12876	TGCCATATTGCCCTCTACAGAAATTGGATCTGGTAAAGAAAAGATCCA
plasmid_cp32-4	26261	BB_R41		2.934 ± 2.1701 0.025852	1.481 ± 1.5663 0.28251	1.028 ± 0.7696 0.9568	1.034 ± 0.6823 0.94345	ATATAATCAACTATGCCATTGCCCCCTACAGAAATTGGATCTGGTAA
plasmid_cp32-4	26593	BB_R41		3.158 ± 0.7153 0.024325	1.453 ± 0.9512 0.48092	0.877 ± 0.2241 0.26596	0.985 ± 0.1553 0.9101	TTTCAGTAAAGAGTCAGAAATTACAACTTGTAAATTCAATGATTAGA
plasmid_cp32-4	26747	BB_R41		3.233 ± 2.0998 0.201859	1.136 ± 1.2353 0.83387	0.727 ± 0.3192 0.35921	0.876 ± 0.3841 0.74043	TTACATTTTAGGAAGAGATAATACATATGCAATTATTAGAGGAATT
plasmid_cp32-4	27394	BB_R42	<i>erpY</i>	2.759 ± 1.2595 0.079471	1.371 ± 0.8312 0.34198	0.857 ± 0.3179 0.02934	1.021 ± 0.5102 0.87197	GTTGGGGTTAAAATATGACTAGTGGTAATAACTAGCGATATGACCA

plasmid_cp32-4	27963	BB_R43	3.910 ± 0.8838 0.03014	1.843 ± 0.8498 0.25399	0.775 ± 0.1039 0.75089	1.502 ± 0.2161 0.07431	TAAGAAAGGAATGCTAGAAAAATGTTGAAAAAATGGGAGAGAAAATATTG
plasmid_cp32-4	28712	BB_R44	2.724 ± 0.9999 0.02558	1.496 ± 0.9514 0.30433	0.905 ± 0.2832 0.66481	1.098 ± 0.4356 0.27502	TGCATACTAAATAAGAAAATTGATGCTTAAATAAG
plasmid_cp32-4	28956	BB_R45	1.956 ± 0.7615 0.057894	2.122 ± 1.4328 0.22838	0.94 ± 0.3421 0.63787	1.109 ± 0.371 0.24225	TATCAAACAAAATTCTTACAACACTACAAAAGGAATACAAAATAAAAT
plasmid_cp32-4	29031	BB_R45	1.942 ± 0.9468 0.006709	0.92 ± 0.9406 0.79507	0.97 ± 0.5686 0.92466	1.163 ± 0.6388 0.26217	AAGCTAACAAATTCTCAATTAAATTGATAAGTTGAAAAAGAACAGTTA
plasmid_cp32-4	29307	BB_R45	1.501 ± 0.7126 0.401954	1.503 ± 1.0015 0.51499	0.659 ± 0.2181 0.19398	0.889 ± 0.2079 0.40548	TGTAAACTCTTAAATTCTTATATCCAAGACATACAAATAATTCATAT
plasmid_cp32-4	29320	BB_R45	1.165 ± 1.6546 0.703046	3.938 ± 5.9468 0.36112	0.937 ± 1.4041 0.84462	1.115 ± 1.3447 0.76637	AAATTCTTATATCCAAGACATACAAATAATTCATATATTAAATTGATT
plasmid_cp32-4	29576	BB_R45	3.254 ± 1.3838 0.057514	1.717 ± 0.6555 0.0833	0.773 ± 0.2557 0.08722	1.005 ± 0.3784 0.98848	ATCGGTTTAAATAGTGTCTGGATGTCAGGATTAGTACAAAATAAT
plasmid_cp32-4	29634	BB_R45	1.390 ± 0.7926 0.040676	0.492 ± 0.4144 0.36507	1.029 ± 0.6233 0.33345	1.092 ± 0.7482 0.49317	GCACATTATCATAAGTTGAAAATTATGCTTAAATGCGCTATATT
plasmid_cp32-4	29690	BB_R45	1.727 ± 1.0953 0.099244	0.848 ± 0.5486 0.13691	0.758 ± 0.4674 0.0711	0.896 ± 0.5399 0.0952	TGATGGTATATCTTATAGAGTTTCTGTGTTCGATAAACCTTACT
plasmid_cp32-4	29692	BB_R45	2.069 ± 1.7478 0.063017	1.163 ± 0.9676 0.07498	0.759 ± 0.5335 0.50798	0.828 ± 0.5669 0.59232	TATGATGGTATATCTTATAGAGTTTCTGTGTTCGATAAACCTTAA
plasmid_cp32-4	29782	BB_R45	2.548 ± 1.0199 0.12602	2.251 ± 2.3715 0.47646	1.102 ± 0.874 0.83627	1.559 ± 0.6049 0.30359	GCCCCGATAGCATATTAGACCCAGCATTTAGTGTGGAGGGGATAACCTG
plasmid_cp32-4	29838	BB_R45	3.447 ± 2.2135 0.202973	1.998 ± 1.2242 0.30939	1.902 ± 0.2433 0.01873	2.55 ± 1.2614 0.17972	TGTGTTAGGGAGCGAGTGTGATGAAAGTATTATGCTTTGATTCAGAC
plasmid_cp32-4	29863	BB_R45	2.361 ± 1.014 0.105135	1.384 ± 0.9363 0.58099	0.921 ± 0.4013 0.82489	0.76 ± 0.2394 0.24295	AGTATTATGCTTTGATTCAGACCAACGACCAGCCAATGATCTTATA
plasmid_cp32-4	29909	BB_R45	0.507 ± 0.3987 0.097934	0.468 ± 0.3842 0.06137	0.732 ± 0.2881 0.01115	0.87 ± 0.302 0.42235	AGGATCATTGGCTGGCTGGCTTGTGAAATACAAAAGCATATACTTATC
plasmid_cp32-4	30151	BB_R45	0.319 ± 0.4695 0.085684	0.608 ± 0.7216 0.32989	2.322 ± 1.2501 0.07583	0.164 ± 0.1188 0.02968	GTTCTCTGTATTTAATGATATTATTCTGTATAAGGGGGATAGCAAAACCC
plasmid_cp32-4	30256	BB_R45	4.782 ± 2.0939 0.081841	0.376 ± 0.4017 0.0466	0.566 ± 0.9487 0.55342	1.168 ± 0.8281 0.70409	TATCCTAAAGACAACATCAAATATGCTGCAGACATTGCATCAAGAGCATCA
plasmid_cp32-6	96	BB_M01	2.324 ± 1.0453 0.043531	1.638 ± 1.3692 0.38165	0.989 ± 0.3846 0.80012	1.104 ± 0.502 0.37018	GATAAAATAAGTCACTAGAACTATACAAATACTCAATTTTTAGAAAT
plasmid_cp32-6	274	BB_M01	0.987 ± 1.0846 0.985607	0.745 ± 0.8232 0.69365	1.473 ± 1.3859 0.58339	0.746 ± 0.5798 0.41491	ATACAATTAAAGCAGAGCATCTTAAGCTGACCTTAACTTAGCTAAGTTCA
plasmid_cp32-6	279	BB_M01	1.857 ± 0.8236 0.077203	1.851 ± 1.7183 0.38488	0.885 ± 0.329 0.20437	1.304 ± 0.5949 0.19006	AGCTACCCTTTCATGGGATTGGCTATGTTTAGTAAAAACCAAAGATACC
plasmid_cp32-6	333	BB_M01	3.004 ± 1.1264 0.04328	0.926 ± 0.8339 0.9121	0.519 ± 0.423 0.35055	0.576 ± 0.4512 0.37083	ATAGATCTCGAACACCCGTTAATAGAAATTACCTATTGTTGAATAC
plasmid_cp32-6	395	BB_M01	1.732 ± 0.2397 0.011129	1.405 ± 0.7406 0.42236	1.081 ± 0.11 0.00875	0.956 ± 0.1446 0.61666	TTCAATCAAGGTTTACCAAGGATTCAACAGGATTCTTAACTGGGTTG
plasmid_cp32-6	398	BB_M01	1.682 ± 0.1936 0.019204	1.369 ± 0.6441 0.37722	0.72 ± 0.1609 0.09168	0.984 ± 0.1949 0.8556	TGTAAGAGATTTGGAGTTGATTGATCATATAACCTATAAAAGTAAAATC
plasmid_cp32-6	399	BB_M01	1.191 ± 0.3756 0.499722	0.558 ± 0.3854 0.1016	1.109 ± 0.2817 0.59203	1.13 ± 0.307 0.52348	CATTATCATAATCAAGGTTTACAAACCAATAGGTAATTCTATTAACCGG
plasmid_cp32-6	444	BB_M01	1.976 ± 1.1853 0.291953	1.852 ± 0.7574 0.0156	1.29 ± 0.6263 0.57016	0.855 ± 0.3909 0.68899	AAATCCAACAAATAAGAACAAATTCTTAGACCGAGTAAATACATAAAAGT
plasmid_cp32-6	478	BB_M01	1.921 ± 1.4906 0.354671	1.195 ± 1.0572 0.80933	0.714 ± 0.303 0.28139	1.191 ± 0.3388 0.1868	ACTGCGTCTAAAGAATTGTTCTATTGTTGATTTTACTTATAGGTTATA
plasmid_cp32-6	490	BB_M01	2.808 ± 1.0933 0.042682	1.408 ± 0.2021 0.7804	0.32 ± 0.1992 0.08907	1.003 ± 0.6394 0.99237	AAAGTCGACTTATCATATATGAAACATTGATTATCTAAAAAGATATG
plasmid_cp32-6	506	BB_M01	3.491 ± 2.4497 0.012494	2.117 ± 2.6599 0.37143	1.051 ± 0.6997 0.92706	1.239 ± 0.9126 0.14071	TATGATAAGTCGACTTTATGTTTACTGCGCTAAAGAATTGTTCTT
plasmid_cp32-6	507	BB_M01	1.226 ± 1.1015 0.6669	1.166 ± 1.1837 0.6499	1.12 ± 0.939 0.76578	1.306 ± 1.1582 0.28856	TATGAAAATTGATTATCTTAAAGATATGTTCCGTGTTTACCGGAA
plasmid_cp32-6	521	BB_M01	2.146 ± 1.0583 0.143053	1.128 ± 0.7609 0.84706	0.987 ± 0.4617 0.96201	1.101 ± 0.507 0.72072	ATCAAGATTTCATATGATAAGTCGACTTTATGTTTACTGCGTC
plasmid_cp32-6	524	BB_M01	1.876 ± 0.8147 0.06672	1.203 ± 0.9568 0.63694	1.134 ± 0.5399 0.14858	1.864 ± 1.3205 0.32051	TATCTAAAGAATGTTCCGTGTTTACCGGAAAGCTTTACTAGATAT
plasmid_cp32-6	526	BB_M01	1.116 ± 0.8665 0.709818	0.185 ± 0.2143 0.25154	0.836 ± 1.2777 0.57562	1.607 ± 1.5436 0.16319	TCTTAAAGAATGTTCCGTGTTTACCGGAAAGCTTTACTAGATATT
plasmid_cp32-6	578	BB_M01	2.194 ± 1.5738 0.145944	2.55 ± 2.5459 0.28741	0.878 ± 0.5476 0.69486	1.39 ± 0.9524 0.17835	TTTATTGAAAAGATATCGTAGAAATAGAACAGCTTGAACACCAACAA
plasmid_cp32-6	744	BB_M01	1.898 ± 0.789 0.128788	1.956 ± 1.5247 0.35209	1.028 ± 0.2696 0.88338	1.087 ± 0.1858 0.34913	TCTTCTTTTGAGAAAACAAATTCAAACATAGTAAAGATATTCT
plasmid_cp32-6	1214	BB_M01	1.705 ± 1.1113 0.135911	1.861 ± 2.3428 0.40626	1.149 ± 1.0702 0.43148	1.08 ± 1.0651 0.69167	TAACCAGCTTACAAAGTAGCTCATTAATAATGAGGGAGCTCGATGTT
plasmid_cp32-6	1410	BB_M02	1.467 ± 0.9439 0.51485	1.126 ± 0.8744 0.37568	1.021 ± 0.8166 0.95686	1.256 ± 0.7976 0.2016	CATGCGTTTAAAGAGCAGGCCAATAGTAAATCTAAAGAGAACAGTCGAGA
plasmid_cp32-6	1626	BB_M02	2.109 ± 1.5058 0.322479	0.883 ± 0.6097 0.65903	0.62 ± 0.3149 0.15029	0.631 ± 0.9927 0.68502	TCCCTTTCAGTACAGTAGCACCTTGTAAATGATTGCTAAGATGTTCTT
plasmid_cp32-6	1631	BB_M02	0.917 ± 1.0601 0.748214	0.852 ± 0.9171 0.25926	1.063 ± 1.0383 0.78034	0.956 ± 0.9024 0.56596	CATTAACAAAGACATTATGCAAGCACAACGCTAGAGAACCTTACGCAAGTCG
plasmid_cp32-6	1747	BB_M02	1.231 ± 0.6386 0.295935	0.24 ± 0.185 0.09586	0.76 ± 0.6162 0.34044	1.014 ± 0.5514 0.93883	TTAGGAGCAACTGTTCTTAGCAAAGTGAATTAAATTAAAGAAAAAT
plasmid_cp32-6	1826	BB_M02	1.691 ± 0.7531 0.156892	1.437 ± 1.3983 0.59243	1.109 ± 0.3 0.52956	0.9 ± 0.1869 0.56503	GAGTCACAGAGAAGAATTGCTACTCGCATTCTTCTTAATTATTC
plasmid_cp32-6	1915	BB_M02	1.301 ± 1.3135 0.743619	1.865 ± 1.3521 0.35574	0.992 ± 1.2895 0.99191	0.151 ± 0.2422 0.04417	CAAGCGATAAGTAATTCTGAAACAGAACGAAATTCATTATGATTT
plasmid_cp32-6	1928	BB_M02	1.324 ± 0.6124 0.464909	1.075 ± 0.2796 0.69304	0.706 ± 0.3186 0.28597	0.606 ± 0.4675 0.36327	TTACTTACGCGTGTACAAATTCTGAAATTATAGGTACAAACATTAGGAA
plasmid_cp32-6	2219	BB_M03	1.022 ± 0.6664 0.919546	0.395 ± 0.2598 0.18044	0.747 ± 0.4708 0.15911	1.072 ± 0.3711 0.77795	CAAGCGTGGAGTCAGCTAGTTAGTCAGATGGTACAACAGAACACTAGA
plasmid_cp32-6	2431	BB_M03	1.525 ± 0.9214 0.227986	1.334 ± 0.5699 0.04982	0.826 ± 0.2945 0.2734	0.975 ± 0.4048 0.91164	ATGCACAAGGAGAGCTGAAAAGAATGGGGAAATGATAATCTGTTAATG
plasmid_cp32-6	2665	BB_M04	4.968 ± 3.3071 0.16346	1.222 ± 0.3291 0.2883	1.256 ± 0.6459 0.52082	1.555 ± 0.6089 0.1936	GGAGCAACTGGAATTCTGATTCTGCCATTGTTGAGTATCATCAACA
plasmid_cp32-6	2897	BB_M04	3.633 ± 1.2712 0.002802	1.518 ± 0.5105 0.14921	1.236 ± 0.8383 0.58474	1.29 ± 0.5679 0.34445	TTCTCTTGTGCAAAGCTGAACTTGTGAAATTAGGTACAAACATTAGGAA
plasmid_cp32-6	3031	BB_M04	0.163 ± 0.309 0.354217	0 ± 0 0.23619	0.089 ± 0.1797 0.29144	0.156 ± 0.3146 0.34957	GTAGTACTGCGTATTAACCAATTAGGAATACTTGAAGGGTATCTG
plasmid_cp32-6	3082	BB_M04	1.709 ± 1.4294 0.415744	2.415 ± 2.3799 0.33452	0.747 ± 0.7106 0.52411	0.764 ± 0.3471 0.516	ACAAGGATCCCTCAAAGTTTCTGAAATTACATACGCGAGTACTA
plasmid_cp32-6	3123	BB_M04	2.604 ± 1.2137 0.03899	1.822 ± 1.8174 0.45562	0.695 ± 0.2722 0.1026	0.785 ± 0.3246 0.41393	TATCCAATATTCTCCCATTTTACTCGGATTCTGTAAACAGATACC
plasmid_cp32-6	3748	BB_M05	1.654 ± 0.796 0.09432	1.172 ± 1.1488 0.85223	1.967 ± 1.5784 0.44178	2.027 ± 1.4505 0.37306	AATAACCCCTCAAATTATTGTAATCGGAACAAATAGTGGCTTTGCTAA

plasmid_cp32-6	3934	BB_M05	1.066 ± 0.2572 0.71318	0.72 ± 0.5427 0.4806	1.443 ± 0.3217 0.12316	1.13 ± 0.7333 0.77881	CAGCTTATTCCAATACTGCTACTTTTATTAAATAAACATCGTTACTAA
plasmid_cp32-6	4040	BB_M06	3.386 ± 2.8896 0.122269	1.482 ± 1.0934 0.0301	1.547 ± 0.9407 0.35522	1.041 ± 0.8028 0.87335	TAATGTATAATGGTTCCCTGATCAAATTGAAGATGTTGATCTTCAGA
plasmid_cp32-6	4240	BB_M06	2.739 ± 0.5359 0.022708	1.289 ± 0.7525 0.54693	0.887 ± 0.1164 0.15805	1.047 ± 0.1229 0.579	AGTCGCTAAATTGTAACCTTACACTGTTCAATTCAACAGGCACTGTTCAATTCAAAAAGATG
plasmid_cp32-6	4352	BB_M06	2.019 ± 0.7081 0.0074	1.208 ± 0.3989 0.35097	1.035 ± 0.476 0.74875	0.98 ± 0.406 0.57854	AACCTTAAATACCTTGACTAACAGGCAGTGTTCATTCAACACCATTCA
plasmid_cp32-6	4430	BB_M06	2.794 ± 3.6687 0.41786	2.092 ± 1.3356 0.16586	0.618 ± 0.7494 0.38611	0.635 ± 0.8868 0.68938	TTGGGAAGTAGACGTTTGATTTTCCATTTTGAAATTGAAACAGTG
plasmid_cp32-6	4804	BB_M06	1.174 ± 1.4617 0.7921	1.359 ± 1.8191 0.67241	0.536 ± 0.5786 0.00451	0.845 ± 0.651 0.06667	CCTCACACCAATGAACAAGTGGATAAAGATTCAACTGATATTGCTCATCA
plasmid_cp32-6	5175	BB_M07	0.752 ± 0.6018 0.263937	1.318 ± 1.7074 0.73956	0.839 ± 0.5858 0.33533	1.091 ± 0.8808 0.65528	TGGGTTGTCATTAAGAAAACAGGGAGTTGTCGAGAATTGAAATTGATA
plasmid_cp32-6	5277	BB_M07	1.645 ± 0.9376 0.127966	1.316 ± 1.2904 0.59024	0.907 ± 0.3632 0.67259	0.814 ± 0.3253 0.37887	GCAGTGGAGGCCAGAAGGCCGGCAGGGGGTTGGCTCAACAAAGAATT
plasmid_cp32-6	5455	BB_M08	1.822 ± 0.9521 0.010902	2.026 ± 1.6623 0.25798	0.813 ± 0.4691 0.45533	1.022 ± 0.4471 0.94745	CGTTGATCATGCGGAAAGACATATCTGAAAGTCTTCAACACCATTCA
plasmid_cp32-6	5546	BB_M08	0.887 ± 0.3841 0.507692	0.672 ± 0.5196 0.11967	0.737 ± 0.34 0.00458	0.949 ± 0.4758 0.67617	TTTTATCAAAAACCTCTGATAAGAAGAATCGTTCAAGTTAACACA
plasmid_cp32-6	5618	BB_M08	1.525 ± 0.6749 0.350529	1.124 ± 0.7729 0.82719	0.665 ± 0.2058 0.23691	0.844 ± 0.272 0.55581	TCAGAGTCATAAACGACTGCAAGTTGGCCCTATGTCATAAATAC
plasmid_cp32-6	5640	BB_M08	0.503 ± 0.2898 0.1479	0.473 ± 0.4186 0.26005	1.108 ± 0.3484 0.38733	1.105 ± 0.3653 0.39788	TTCCAACTTACATACATCAAGACCTTAACATGAACTAAAAGACCGCAT
plasmid_cp32-6	5652	BB_M08	3.403 ± 4.665 0.452541	1.006 ± 1.6838 0.99573	1.513 ± 0.9843 0.39681	1.023 ± 0.3845 0.9262	CACATCAAGACCTTAACATGAACTAAAAGACCGCATATCAATTTCGA
plasmid_cp32-6	5655	BB_M08	2.632 ± 2.0099 0.148373	0.589 ± 0.5148 0.43835	0.792 ± 0.3799 0.59583	1.18 ± 0.5845 0.70286	TGTGAAAGTTGGAATATCTTGAATATCAGACATATCAGAGTCATAAAG
plasmid_cp32-6	6520	BB_M10	1.156 ± 0.4133 0.373731	0.687 ± 0.5014 0.2608	0.989 ± 0.3307 0.93925	1.023 ± 0.2808 0.71744	CTTATGGCTTATTGTGTAGAAAATTGCTAAGCATAACCATAAACGATTA
plasmid_cp32-6	7167	BB_M11	1.816 ± 0.6101 0.10664	1.823 ± 1.563 0.46236	0.676 ± 0.0974 0.01614	0.84 ± 0.4402 0.6008	TTCTCAACTAAAGAACAGAAAATAAGAATTGAAAGATAAGGCAAT
plasmid_cp32-6	7255	BB_M11	2.445 ± 1.0189 0.004922	3.511 ± 3.3392 0.2533	2.113 ± 0.819 0.10212	2.264 ± 1.1262 0.17878	ATAAAGACAATTACACCTCAAATTATAAGTCATAATTACATCAAGCTA
plasmid_cp32-6	7498	BB_M11	1.863 ± 1.972 0.256528	1.116 ± 1.3755 0.77112	1.039 ± 1.1067 0.92575	1.267 ± 0.836 0.53206	CATACCACATATAAAAAATGAAGCGATTATTGAGCTTATTGAGAATTGGA
plasmid_cp32-6	7738	BB_M11	2.356 ± 0.653 0.049517	2.538 ± 1.1637 0.15653	1.287 ± 0.4098 0.30981	1.247 ± 0.6089 0.36323	ATATTCACTAAAGTCTAATTAAAGTTGTCAGGAGAAAGAGTAAGC
plasmid_cp32-6	7747	BB_M11	1.560 ± 2.043 0.647841	0.104 ± 0.1591 0.08904	0.816 ± 0.2974 0.32035	1.595 ± 0.9596 0.3874	ACTTTAGCAATTACTGTTGCTTAGTAATTACTACTCAAGATATAGTTG
plasmid_cp32-6	7979	BB_M12	1.960 ± 0.9746 0.129873	2.003 ± 1.9024 0.39426	1.1 ± 0.5051 0.61682	1.049 ± 0.4399 0.59726	AGAGATCCAAAACAATAACTTGTTCACATTGAAGTGACACTAGGT
plasmid_cp32-6	8151	BB_M12	2.914 ± 1.0327 0.028335	1.616 ± 1.7162 0.54503	1.399 ± 0.5423 0.38369	1.109 ± 0.3257 0.54773	GAAATAATTGGTAGCAATTCTATCATTGAATGCTAAATCAGCATTTA
plasmid_cp32-6	8229	BB_M12	1.841 ± 0.5055 0.093624	1.829 ± 1.4944 0.43095	0.94 ± 0.1114 0.44078	0.909 ± 0.1556 0.33183	GCCCTAATTCAAAGATACTTTCCGCCCTCAGCAGAATACTCTGAA
plasmid_cp32-6	8280	IG_173	1.733 ± 1.4581 0.512444	0.556 ± 0.8512 0.59875	0.98 ± 0.9603 0.97977	0.603 ± 0.2707 0.28617	ATAAGAATCTCTTTAAGAGTTGGTTAGATTGGCAATTATA
plasmid_cp32-6	8444	BB_M13	1.872 ± 0.5809 0.148858	1.757 ± 1.2318 0.40639	1.619 ± 0.6386 0.19304	0.811 ± 0.5037 0.58545	AGCTTGTGATTCTTCAAGTATTAAACCTCTTAAAGCTTAAACAGCGT
plasmid_cp32-6	8585	BB_M13	2.870 ± 1.6848 0.194005	1.248 ± 0.3009 0.24949	1.571 ± 0.4961 0.19695	1.285 ± 0.3916 0.35315	AAAAAGCCGCTTAGTATATTGAGTGAAGATAATGTTGGTGT
plasmid_cp32-6	8655	BB_M13	2.096 ± 0.8803 0.077899	1.232 ± 0.8744 0.615	0.966 ± 0.5906 0.89049	1.316 ± 0.6759 0.43683	TTAATGAAAATTGATTATGAAAAAGTAGGCCACTTCACTTCATCAAGTA
plasmid_cp32-6	8756	BB_M14	1.841 ± 0.4044 0.029949	1.909 ± 1.6956 0.40388	1.273 ± 0.5169 0.50187	1.078 ± 0.2585 0.03615	TTGATAAAAGCTTGCAGTCTAATGAGACTAGAAAAAAATTTTAACT
plasmid_cp32-6	8835	BB_M14	2.675 ± 2.9455 0.365827	2.515 ± 3.4157 0.52969	2.357 ± 4.1416 0.49903	2.811 ± 3.4684 0.38048	ATATTGCTGTTCTTAACTCGTCAAGCACTTAAATTGTTCTAGT
plasmid_cp32-6	8978	BB_M15	2.046 ± 1.0923 0.186471	1.908 ± 0.8549 0.13543	0.926 ± 0.2307 0.73164	0.921 ± 0.3083 0.71967	GTGAGCGCAAAATTCCACCTAAATTAAAGGGATTCTGTATCGTGC
plasmid_cp32-6	9111	BB_M15	1.302 ± 0.1289 0.046792	1.418 ± 0.1011 0.56745	0.622 ± 0.369 0.22059	1.081 ± 0.3693 0.74256	TCTTAGTGTCTCCCAAACCTGGAGTTCTGGGTTAAGATATTCTTCA
plasmid_cp32-6	9675	BB_M15	2.277 ± 0.8114 0.005887	1.172 ± 0.8256 0.57784	0.827 ± 0.2946 0.45927	0.97 ± 0.44 0.41307	ATTGGAAAACCGAGTAGAATTGAGCTATGCTTAACTCAGTGGTCTA
plasmid_cp32-6	9756	BB_M15	2.513 ± 0.4877 0.023592	1.838 ± 1.2181 0.33735	1.315 ± 0.3222 0.20348	1.238 ± 0.1544 0.06078	TTAACAGCCTTACTGCATCTCGCTGCTCATAGCACCCTGGATTAA
plasmid_cp32-6	9794	BB_M15	2.354 ± 0.503 0.029753	1.455 ± 0.9691 0.47096	0.842 ± 0.256 0.26154	1.081 ± 0.3838 0.70023	GATCAAAAAGCTCACTTCCATCACCCTTAAAGAACACTATTAAACGCTT
plasmid_cp32-6	10131	BB_M15	1.401 ± 0.6073 0.009241	1.295 ± 1.0878 0.51131	0.79 ± 0.3646 0.17927	0.802 ± 0.358 0.18001	ATTATTCTTGTCAAATTAAACGATGCTACCTGGATGGATGGCGGAG
plasmid_cp32-6	10660	BB_M16	1.228 ± 0.8778 0.508983	1.94 ± 1.5203 0.27592	0.719 ± 0.6321 0.21698	0.719 ± 0.6404 0.18855	TGTTCACCAAGTCTTCCGGATTGTAGCTTACATTCCGTTTCTATCA
plasmid_cp32-6	10696	BB_M16	1.710 ± 0.7615 0.237158	0.945 ± 0.9193 0.92656	0.957 ± 0.8242 0.93596	0.82 ± 0.6012 0.64965	TATAAGGATGTTAGTATCCCCCTTAAAGAGATATGTTCAACCACTGATT
plasmid_cp32-6	10697	BB_M16	0.883 ± 0.9271 0.454693	1.032 ± 0.996 0.904	0.448 ± 0.3184 0.14745	1.992 ± 1.7768 0.26484	TAAGGATATGATTCTTACTCAAATTAGCTGTTGGCAATTACTGCT
plasmid_cp32-6	10817	BB_M16	1.143 ± 0.619 0.131527	0.982 ± 0.858 0.93427	0.67 ± 0.4435 0.43302	0.77 ± 0.4049 0.31818	TATACTAAAGGGACTGTGCTGTATTCTGGCTAGTTGTTCTTAC
plasmid_cp32-6	10820	BB_M16	2.546 ± 1.1758 0.081967	1.106 ± 0.9937 0.87905	0.814 ± 0.9182 0.79377	0.608 ± 0.2072 0.16231	TAGTCCAACTTGGCTTAAAGAATTAGCTGTAATTAAAGCTTCTCGTT
plasmid_cp32-6	10822	BB_M16	2.010 ± 0.9285 0.148569	1.977 ± 1.8269 0.41915	1.235 ± 0.2426 0.1125	1.13 ± 0.4067 0.5493	GTCCAACTTGGCTTAAAGAATTAGCTGTAATTAAAGCTTCTCGTTA
plasmid_cp32-6	10987	BB_M17	1.603 ± 0.6691 0.181038	1.349 ± 0.8806 0.32341	0.973 ± 0.4089 0.94022	1.513 ± 0.8962 0.21009	AAATTGAGTTCTACAAATGAGATACATCAAAACACCTGTGATGAA
plasmid_cp32-6	11007	BB_M17	1.907 ± 1.1885 0.057226	1.608 ± 1.2902 0.24589	0.865 ± 0.4694 0.34704	1.156 ± 0.6508 0.22096	GATACATCAAAAATCACCTGTGATGGAATTCTTCGCCGAAGAAATTCC
plasmid_cp32-6	11008	BB_M17	1.753 ± 1.0146 0.017813	0.473 ± 0.3787 0.35403	0.986 ± 0.5325 0.92692	1.004 ± 0.5684 0.96442	TCTACATTGTAGAACTCAATTAAACATATTGAGTAAACAGCATT
plasmid_cp32-6	11011	BB_M17	2.049 ± 1.4752 0.376369	1.334 ± 0.8259 0.58185	0.922 ± 0.285 0.4472	0.815 ± 0.3222 0.46569	CATCAAAACACCTGTGATGGAATTCTTCGCCGAAGAAATTCTCAA
plasmid_cp32-6	11214	BB_M17	1.648 ± 0.8635 0.359461	1.137 ± 1.2192 0.84982	0.471 ± 0.2022 0.12457	0.694 ± 0.2663 0.09179	AAAATATATTATAAGAATTGCTCATGAAAAAAATTGTTACATGAA
plasmid_cp32-6	11222	BB_M17	2.196 ± 0.8399 0.089212	1.469 ± 0.8874 0.3855	0.927 ± 0.2459 0.56773	1.138 ± 0.2828 0.48205	ATATATTCTTACTCAAATTAAAGCTGCGTGAAGTCTAAGGG
plasmid_cp32-6	11284	BB_M17	0.759 ± 0.9701 0.691328	0.42 ± 0.7451 0.29598	0.285 ± 0.1993 0.05387	0.912 ± 0.7337 0.74538	GGAGGTCTCAAAGTCTGCCATTATGAAATCAAATTCTCATGAGCA
plasmid_cp32-6	11546	BB_M17	3.011 ± 3.146 0.334373	3.247 ± 2.8361 0.26239	2.054 ± 1.946 0.41253	1.667 ± 0.7514 0.24815	TGTCATACATAATGAGCGATATTGGTACTGGTTACGGGGATGAA

plasmid_cp32-6	12132	BB_M18	1.603 ± 0.6365 0.242918	1.484 ± 1.3342 0.60877	0.747 ± 0.3675 0.13387	1.303 ± 0.4094 0.11198	GAGATTTTGTGAATTCTAAATCTCAAATTGGGTATTGTAACA	
plasmid_cp32-6	12245	BB_M18	3.289 ± 1.2286 0.006266	3.191 ± 2.855 0.28899	2.397 ± 1.5516 0.28141	1.214 ± 0.7752 0.50067	CTTAGTGCATTAGCCAAAGACTTAAATCTAATCTGTACTGTTAAA	
plasmid_cp32-6	12246	BB_M18	1.185 ± 0.5081 0.597206	1.408 ± 0.635 0.23226	1.311 ± 0.7803 0.54083	1.298 ± 0.8297 0.64994	AGTATATAAAAATGATGTTGCAAGTGAAATATCGTTATTITATCAAAA	
plasmid_cp32-6	12249	BB_M18	2.332 ± 0.9117 0.014217	2.066 ± 1.6053 0.26094	1.14 ± 0.3512 0.529	1.239 ± 0.4252 0.10206	GTGCAATTAGCCAAAGACTTAAATCTAATCTGTACTGTTAAAATTA	
plasmid_cp32-6	12547	BB_M19	2.933 ± 3.0541 0.171582	1.226 ± 1.5187 0.22212	2.065 ± 3.067 0.5729	0.752 ± 0.9747 0.46174	CCAATTGCAAATTATGCTTAATCTAAATCCACTAGTAATTACCAT	
plasmid_cp32-6	12794	BB_M19	2.713 ± 0.7391 0.015493	1.509 ± 1.2633 0.51139	0.831 ± 0.2589 0.39216	1.006 ± 0.7484 0.98989	TGTGCTTGTGCTGTATAGTAGTTGAAATATTATTAATCTAAGTTA	
plasmid_cp32-6	12797	BB_M19	1.809 ± 0.3752 0.033195	1.628 ± 0.43 0.13632	1.068 ± 0.4378 0.81338	1.87 ± 0.9579 0.2458	TATCCTTTCTCAGCGATGTTGAATATGGAGTTAATTATGAG	
plasmid_cp32-6	13061	BB_M20	1.305 ± 0.1929 0.133478	1.133 ± 0.4306 0.69011	1.112 ± 0.5264 0.73739	1.333 ± 0.2088 0.00585	AGTGCACCCGGTTCTTTAGAAAAAAAGAGATTAAGCTCATTAATTAT	
plasmid_cp32-6	13128	BB_M20	1.163 ± 1.1436 0.467358	1.412 ± 1.5971 0.34078	0.722 ± 0.6728 0.55375	1.043 ± 0.9274 0.91975	AAGCAGTGCACCGCGCTGTAAGTTGCTTTAGAAGAAATGTTCT	
plasmid_cp32-6	13225	BB_M20	1.165 ± 0.4031 0.530216	0.831 ± 0.281 0.51765	0.643 ± 0.3646 0.16737	0.787 ± 0.119 0.12877	GTAAATCTAATTTAAATAGTCCTAAATTAAAGCAAACCTTGGAGACAT	
plasmid_cp32-6	13427	BB_M20	1.855 ± 1.0617 0.017967	0.607 ± 0.5359 0.53354	1.084 ± 0.7211 0.36403	0.931 ± 0.4914 0.63938	GTTTTAAAGGTCAGTTACTTACATATAAACATATTTCTTT	
plasmid_cp32-6	13462	BB_M20	5.445 ± 3.6686 0.155181	2.488 ± 2.0218 0.30343	1.082 ± 0.6439 0.7998	2.26 ± 0.8682 0.08169	TCCCTTAATTGAGAGTCATTTAGAGGTTAGTTAAGGTCAAGT	
plasmid_cp32-6	13469	BB_M20	1.104 ± 0.6961 0.511493	0.318 ± 0.2613 0.20152	1.211 ± 0.7046 0.23543	0.949 ± 0.1249 0.88436	TTCTAGGATTATTCAAAATAATTCTGATATGGGAATCAGCTTGAATA	
plasmid_cp32-6	13552	BB_M20	2.216 ± 1.0072 0.741863	0.933 ± 0.8376 0.90322	0.892 ± 0.1065 0.24482	0.608 ± 0.5205 0.32833	AAGGAATTAAGTTATGGAAATAAGTGTCTGTATTAAAGATAACAGACACTG	
plasmid_cp32-6	13696	BB_M20	1.616 ± 0.8634 0.030825	1.754 ± 2.015 0.46958	1.04 ± 0.4861 0.81484	1.212 ± 0.851 0.67637	GATTGCTTATTGATATTGGATAGTTAACAAATATGAAAATACCAATCTT	
plasmid_cp32-6	13857	BB_M21	2.778 ± 1.5368 0.058389	1.604 ± 1.2927 0.31298	0.841 ± 0.3929 0.27319	0.918 ± 0.389 0.71849	GAAAATATAAAAATCAAGATATATTGCAATATGGATATCTCAAGTTTATCT	
plasmid_cp32-6	14107	BB_M21	1.643 ± 1.196 0.468706	1.606 ± 1.5554 0.58406	0.877 ± 0.129 0.35658	1.045 ± 0.3814 0.87819	CTACATTATTTCGCTAGCACTAAGAAAGAAAACGACTAAAAAAAGATAAA	
plasmid_cp32-6	14299	BB_M21	1.639 ± 0.854 0.002648	0.358 ± 0.2751 0.23388	0.85 ± 0.4848 0.32362	0.958 ± 0.5979 0.82823	CAGATGGTAAACAATATTATAACTTTAACAACTAAGGAGGTTTATGGCTG	
plasmid_cp32-6	14308	BB_M21	1.681 ± 0.167 0.015907	1.206 ± 0.3884 0.38912	1.029 ± 0.1917 0.8548	1.189 ± 0.7101 0.66665	ACAATTATAACTTTAACAACTAAGGAGGTTTATGGCTGATGATCAAG	
plasmid_cp32-6	14439	BB_M22	0.866 ± 0.4503 0.709604	0.447 ± 0.5106 0.41795	0.906 ± 0.6723 0.75624	1.033 ± 0.6609 0.89011	AAAGATCAGTACGTTAACGGTCTGTAACCTTATTAAATCTTTATTGAA	
plasmid_cp32-6	14467	BB_M22	0.944 ± 1.0243 0.943232	0.65 ± 0.6364 0.59095	0.193 ± 0.2907 0.22149	1.629 ± 2.0531 0.6476	CTGCTTGCAGCTTCCATCATCAGTCAGTAAAGATCAGTATGTTAACGGTC	
plasmid_cp32-6	14635	BB_M22	2.004 ± 1.1816 0.085073	1.655 ± 1.6066 0.41522	0.932 ± 0.4626 0.28769	0.986 ± 0.5023 0.62425	ATTAATTGTCGGTTATTAGCATAAATTTTTACAAAATCTTATTCATA	
plasmid_cp32-6	14695	BB_M22	2.217 ± 0.6506 0.617315	0.879 ± 1.1862 0.8187	0.706 ± 0.4453 0.16787	1.069 ± 0.6221 0.59598	TCTGTAAGGGTGTATTAACTTAAAGGTTGAAATATTAGTAAAG	
plasmid_cp32-6	14787	BB_M22	1.989 ± 0.7059 0.045142	1.048 ± 0.514 0.90226	1.159 ± 0.4304 0.08843	0.894 ± 0.442 0.78272	TATGTTAGGAACGGGTGTTTTGAATAGTATCTGATGAGGCAATTATCA	
plasmid_cp32-6	14790	BB_M22	2.840 ± 2.7785 0.278782	2.628 ± 2.9003 0.32561	1.217 ± 1.4288 0.64296	0.753 ± 0.8667 0.65066	CTTGGAGTACATCAAATTGCTTATGGCAGAACTAGAAGTACTACACTT	
plasmid_cp32-6	14881	BB_M22	0.981 ± 0.5103 0.957026	1.184 ± 1.0291 0.49875	0.917 ± 0.589 0.83926	0.525 ± 0.6328 0.48382	TGGAATACAATGATGATGTAACCTTATTCTAAAGTTACGATAATT	
plasmid_cp32-6	14888	BB_M22	1.614 ± 0.2355 0.004848	1.585 ± 0.8942 0.30312	1.157 ± 0.2325 0.18124	1.014 ± 0.3637 0.95782	CAATGATGATGTAACCTTATTCTAAAGTTACGATAATTCTCCG	
plasmid_cp32-6	14977	BB_M22	2.129 ± 0.9476 0.073009	2.627 ± 1.3086 0.04302	1.072 ± 0.6759 0.90223	1.044 ± 0.4458 0.81583	TTATCATTGATTCTGAATTCAATATCAAGATAAACGGGAGAATT	
plasmid_cp32-6	15066	BB_M22	1.075 ± 0.8782 0.566284	0.259 ± 0.2826 0.27553	1.216 ± 1.2468 0.47616	1.071 ± 0.695 0.83989	TTCACCGAACTCCATTATAAAGGATGTTATGTCAAAAAAAGACTCTCC	
plasmid_cp32-6	15083	BB_M22	2.243 ± 1.0966 0.063299	1.654 ± 1.6344 0.50109	0.918 ± 0.4261 0.70667	0.938 ± 0.8837 0.90058	AATGGGAATTCTGGTAATGTCGGCCGGGGCCGCAATTCTAAACCCCT	
plasmid_cp32-6	15186	IG_174	1.951 ± 1.5527 0.233288	2.227 ± 2.4025 0.37261	0.948 ± 0.5355 0.79971	1.168 ± 0.6036 0.29813	TATACAAAATCATAAATTCTGCTAAAGTTACGTTAAAGATCTG	
plasmid_cp32-6	15194	IG_175	2.837 ± 0.3192 0.009485	1.813 ± 0.9819 0.28866	1.06 ± 0.0753 0.22873	1.268 ± 0.6094 0.01096	CGTATACAAAATAAAAATTAAAGAAGGTTAAAAAATGGATACTTTAA	
plasmid_cp32-6	15351	BB_M23	blyA	2.307 ± 1.3339 0.086939	1.527 ± 0.8461 0.0616	0.855 ± 0.6516 0.31323	0.718 ± 0.7524 0.31206	AAAGACATATTGACTATTGTAATAGGCAAGATTTTAAGAATGGTAATGGT
plasmid_cp32-6	15369	BB_M23	blyA	1.014 ± 0.3743 0.878378	0.444 ± 0.3661 0.27385	0.925 ± 0.35 0.38456	0.975 ± 0.3907 0.61864	CAATAGTCATATTGCTTATTAGGCTGAGAAGAATTAACTCTC
plasmid_cp32-6	15372	BB_M23	blyA	2.482 ± 1.8853 0.280535	1.786 ± 1.6155 0.24947	1.607 ± 0.9953 0.36082	1.748 ± 1.153 0.05037	ATAGGCAAGATTTTAAGAATGTAATGGCAAAATCACATTAA
plasmid_cp32-6	15457	BB_M24	blyB	2.564 ± 1.7513 0.269575	3.397 ± 3.4579 0.34886	0.818 ± 1.0216 0.78583	0.81 ± 0.4769 0.52848	ATGTTGAGCTTGCACCTGGCTTTACACCCATTGATATTTCTA
plasmid_cp32-6	15718	BB_M24	blyB	1.715 ± 1.1157 0.088693	1.847 ± 1.3371 0.15197	0.897 ± 0.6484 0.74945	1.02 ± 0.6774 0.97228	GATATTGGAGATTCTGATCAGAACTAAGTCATGATTGATTT
plasmid_cp32-6	15824	BB_M25		0.836 ± 0.6493 0.479892	1.049 ± 1.7413 0.85917	0.724 ± 0.2254 0.17466	0.561 ± 0.2346 0.1843	GTTAACGTCAGTAAAGTCTAAACCAATAGTGTATTGCTT
plasmid_cp32-6	15908	BB_M25		2.113 ± 1.7968 0.104636	1.947 ± 2.198 0.32287	0.708 ± 0.4438 0.39873	1.242 ± 1.0319 0.15968	TATGTTTGTAGAAAAAATCTTACTCTAAAGTTAAATGTAATT
plasmid_cp32-6	15910	BB_M25		1.798 ± 0.7695 0.045327	1.51 ± 0.9555 0.24974	0.849 ± 0.4406 0.48695	1.538 ± 0.8659 0.17863	TATATGTTTGTAGAAAAAATCTTACTCTAAAGTTAAATGTAATT
plasmid_cp32-6	15911	BB_M25		2.813 ± 1.4349 0.092413	1.279 ± 0.7758 0.50239	0.657 ± 0.231 0.21305	1.424 ± 0.7315 0.49572	TAAGCACACTAAATCTGGAAACAGCTGAGTCACCTAAATTTGAAG
plasmid_cp32-6	15913	BB_M25		2.055 ± 1.0391 0.093995	1.715 ± 1.4998 0.3933	1.102 ± 0.5028 0.50519	1.065 ± 0.4237 0.38833	AGCACACTAAATCTGGAAACAGCTGAGTCACCTAAATTTGAAGAA
plasmid_cp32-6	15997	BB_M25		2.796 ± 0.9309 0.07001	1.218 ± 1.0254 0.73641	0.739 ± 0.1144 0.12063	0.769 ± 0.1336 0.18381	TTATCTCAATGTTGATTAAAGTCTGTATTCTCAAATATTCTAG
plasmid_cp32-6	16164	BB_M26		2.009 ± 1.7089 0.248057	1.105 ± 0.5849 0.77325	0.524 ± 0.3548 0.16464	0.628 ± 0.3468 0.4059	ACCTACCAGAAGAGCCAAAACGCCATTCTAAACACTAAATTTG
plasmid_cp32-6	16428	BB_M26		1.099 ± 0.6099 0.736932	0.592 ± 0.5987 0.29296	1.152 ± 0.9377 0.72427	1.16 ± 0.7554 0.1808	TAGACTTTCCGCTATTGGTTTGTATTGTAATGTAATTTATG
plasmid_cp32-6	16490	IG_176		1.839 ± 0.5022 0.040547	1.454 ± 0.8798 0.38939	0.994 ± 0.2684 0.91872	1.201 ± 0.3809 0.23837	CTTATAATTAAATTGGCTTACACAGAAAGAAAATCTGATTTAAATT
plasmid_cp32-6	16589	IG_177		0.572 ± 0.458 0.00138	0.613 ± 0.6059 0.0517	1.07 ± 0.6889 0.47635	1.03 ± 0.6464 0.58399	CTAATTAAATTGTCGCCCTCTGAGGAAACTTAACTTGTCTATGTT
plasmid_cp32-6	16733	BB_M27	<i>revA</i>	1.829 ± 0.8656 0.142129	1.411 ± 1.0098 0.38732	0.795 ± 0.4961 0.58272	0.83 ± 0.414 0.67845	TTTTCTTTGAAATCTGATCTGTAGTAATGTTCAATGGTAT
plasmid_cp32-6	16768	BB_M27	<i>revA</i>	1.227 ± 0.7736 0.711697	0.988 ± 0.5483 0.93023	0.745 ± 0.26 0.26838	0.882 ± 0.3439 0.73089	ATGTTTCAATGGTATTGGCTGCTTAAACGCTGCTAATTGGCCGCT

plasmid_cp32-6	17006	BB_M27	<i>revA</i>	1.293 ± 1.0182 0.404052	0.955 ± 0.6821 0.88836	0.661 ± 0.4957 0.33046	1.113 ± 0.7975 0.80795	CATATGCTTACAAGCCATTACAAATAACATTGATGCAAAAATAATTAA
plasmid_cp32-6	17289	BB_M28	<i>mlpF</i>	1.840 ± 1.7804 0.481276	1.43 ± 0.859 0.16039	0.72 ± 0.4078 0.37389	1.494 ± 0.9408 0.5159	GTAGTAGTAAAAATAAACAAAATAATATGTTGATGATTTCATGTTATT
plasmid_cp32-6	17806	BB_M29		1.698 ± 0.7309 0.074435	1.324 ± 0.7962 0.40399	0.726 ± 0.3951 0.14842	1.018 ± 0.5521 0.93843	TAAACGTCTGATTATCAGACATAAAACTTAAGCTTATTAGATCATCA
plasmid_cp32-6	17993	BB_M29		0.997 ± 0.4498 0.986386	0.875 ± 0.486 0.62291	0.883 ± 0.3941 0.74929	1.477 ± 0.10531 0.57653	TATTATTTTTCTTCACCTTCATTACCCAATTTTATATTAAACAGTG
plasmid_cp32-6	18286	BB_M29		1.041 ± 0.5602 0.706544	1.021 ± 0.4878 0.962	1.411 ± 0.4737 0.19378	1.011 ± 0.3821 0.94075	GCTGCACCAACAAAGTTGGCATTGTATTCAAATTAGACCCATTTC
plasmid_cp32-6	18593	BB_M29		1.788 ± 1.3136 0.203624	1.464 ± 1.608 0.56621	0.907 ± 0.4538 0.80282	1.089 ± 0.4888 0.62202	AGAATGAACCTGCCACGTATTGACAAAAGCTTAAAGGATACGGATATAAG
plasmid_cp32-6	22252	BB_M34	<i>bdrK</i>	0.988 ± 1.7351 0.960386	2.726 ± 4.5857 0.19626	1.493 ± 0.2029 0.65352	1.953 ± 2.6291 0.16046	GAGAAGAAATTGCAAAAAGACATATCTAATTAGATGCCAAATAGACAAT
plasmid_cp32-6	22277	BB_M34	<i>bdrK</i>	1.882 ± 1.7827 0.338416	1.453 ± 1.4291 0.48863	1 ± 0.5867 0.99943	0.786 ± 0.3586 0.57741	GATATGTTTTGCAAATTCTCTATATCAATTATTTCTTTAAA
plasmid_cp32-6	22369	BB_M34	<i>bdrK</i>	1.072 ± 0.6396 0.696979	0.768 ± 0.8953 0.54387	0.423 ± 0.2598 0.25525	1.065 ± 0.8342 0.92435	AGCTCTTTCTACATTGTCTATTGATATTAAACCATATTTTAAAT
plasmid_cp32-6	22800	IG_178		1.625 ± 0.7551 0.203536	1.631 ± 0.8574 0.06729	0.969 ± 0.7728 0.92982	1.334 ± 0.6152 0.29678	ACTTATTACTTTATAAAATTAACTATTCTAATTAAAAAAACTTATT
plasmid_cp32-6	22896	IG_179		1.796 ± 0.7684 0.221947	1.548 ± 1.6258 0.61281	1.043 ± 0.418 0.87369	0.865 ± 0.3538 0.63295	GAATTTAAATTTTGTTAAAATAAAAGAACCTTAAATTC
plasmid_cp32-6	23064	IG_180		1.601 ± 1.5777 0.170363	0.624 ± 0.6001 0.57508	0.82 ± 0.6709 0.63936	0.906 ± 0.6682 0.87481	CATATACATATGTATAACAAAATTTGTCAGGCTTTACAGAAAT
plasmid_cp32-6	23066	IG_181		2.617 ± 2.127 0.261963	3.33 ± 3.4629 0.31636	0.716 ± 0.4217 0.08748	1.708 ± 1.1633 0.29561	TACATACATATGTATAACAAAATTTGTCAGGCTTTACAGAA
plasmid_cp32-6	23067	IG_182		0.555 ± 0.4395 0.383451	0.367 ± 0.6684 0.48115	0.549 ± 0.4737 0.42463	0.716 ± 0.6469 0.25231	TAGCTAAAAAAATATTGCTATCAAAAATCCAATTAGTTGGTTAG
plasmid_cp32-6	23069	IG_183		0.944 ± 0.4984 0.844812	0.53 ± 0.4476 0.43154	1.092 ± 0.8265 0.72633	1.376 ± 0.9287 0.14505	GCTAAAAAAATATTGCTATCAAAAATCCAATTAGTTGGTTAGCT
plasmid_cp32-6	23204	IG_184		1.077 ± 0.2404 0.498203	0.619 ± 0.3765 0.25387	0.959 ± 0.2203 0.83313	0.935 ± 0.4132 0.693	GCAAAAACATTTTGCCACCTTTACAAAATTTCACAAAAAA
plasmid_cp32-6	23595	BB_M35	<i>bppA</i>	0.060 ± 0.1058 0.008006	1.16 ± 1.0441 0.84471	0.371 ± 0.3694 0.16934	0.594 ± 0.6169 0.46681	TATATGCTAAGGGCAAAGAGTTAGAGAATTAGGATTAGAGA
plasmid_cp32-6	23599	BB_M35	<i>bppA</i>	1.005 ± 0.6916 0.980007	0.665 ± 0.6419 0.4269	0.73 ± 0.9543 0.63648	0.514 ± 0.3742 0.33091	TGCTCAAGGGCAAAGAGTTAGAGAATTAGGATTAGAGA
plasmid_cp32-6	23704	BB_M35	<i>bppA</i>	0.176 ± 0.1956 0.20606	0.679 ± 0.7443 0.70303	2.067 ± 1.9043 0.25205	0.585 ± 0.5003 0.19762	TCAACACCGTTGCATTTTATATAAAATATCAATTATCACCG
plasmid_cp32-6	23779	BB_M35	<i>bppA</i>	2.531 ± 2.5861 0.302635	1.197 ± 0.916 0.59571	1.021 ± 0.8831 0.97455	0.977 ± 0.5967 0.96067	TTAATAAACCGGCCATCAATTGAGCCACTAAAGTTCTGAACCTGCC
plasmid_cp32-6	23833	BB_M35	<i>bppA</i>	2.544 ± 1.0926 0.002176	1.206 ± 0.9275 0.46338	0.809 ± 0.3257 0.47406	1.076 ± 0.5635 0.63463	TGAGTAGTGTATTGCTGAGTACAATAAAATGGCAATTTTAACAGCAGTA
plasmid_cp32-6	23967	BB_M35	<i>bppA</i>	3.224 ± 2.4809 0.097321	2.158 ± 2.4502 0.35135	0.982 ± 0.6302 0.89235	1.18 ± 0.7719 0.30061	GATGCTGCACCAATACTGTAAGGATAAGAGATGAGGCTTAATATCA
plasmid_cp32-6	24012	BB_M35	<i>bppA</i>	1.586 ± 0.5968 0.261262	1.993 ± 1.6159 0.40808	0.948 ± 0.8881 0.93546	0.295 ± 0.1823 0.08515	ATACAAAAGTTGTAATTGTTAATAATGTGAATTAGAAATTATAAT
plasmid_cp32-6	24073	BB_M35	<i>bppA</i>	1.660 ± 0.4856 0.059062	1.659 ± 1.4801 0.50349	0.945 ± 0.2503 0.75476	1.051 ± 0.2748 0.67187	TCTTTTCAAAATTATAATTCTAATTACATTTATAACAAATTCAAAC
plasmid_cp32-6	24077	BB_M35	<i>bppA</i>	1.243 ± 0.9581 0.546977	0.618 ± 0.9202 0.67632	0.462 ± 0.5749 0.09027	0.663 ± 0.6965 0.66138	AATATCTTTTCAAAATTATAATTCTAATTACATTTATAACAAATT
plasmid_cp32-6	24082	BB_M35	<i>bppA</i>	1.673 ± 0.4922 0.108402	1.036 ± 0.3937 0.88859	0.9 ± 0.4828 0.37037	0.884 ± 0.3639 0.04339	GTAACTATAGAGAGGAATACTTAATGGCACATAATTAAACAGGAGTACGT
plasmid_cp32-6	24085	BB_M35	<i>bppA</i>	2.039 ± 1.4721 0.13511	2 ± 1.9726 0.31989	0.988 ± 0.5173 0.95358	1.073 ± 0.5511 0.72057	ACTATAGAGAGGAATACTTAATGGCACATAATTAAACAGGAGTACGTTA
plasmid_cp32-6	24216	BB_M35	<i>bppA</i>	1.262 ± 0.5547 0.201374	1.85 ± 1.6205 0.32429	0.902 ± 0.8059 0.69406	0.754 ± 0.4183 0.05745	GAATATGTTGATTGTCAGACCTGAAATTAGGATAATCAATCTGCTAA
plasmid_cp32-6	24388	BB_M35	<i>bppA</i>	2.652 ± 1.5918 0.049565	1.72 ± 1.7172 0.38547	0.943 ± 0.459 0.72067	0.757 ± 0.4428 0.1242	ATATTGTAATTAGCATCTTCAACCTATCTTATGGCTTTCTTTT
plasmid_cp32-6	24391	BB_M35	<i>bppA</i>	1.638 ± 1.0904 0.469863	2.319 ± 1.9802 0.32391	0.638 ± 0.4674 0.48582	1.071 ± 0.596 0.772	CGAATACATATCCAACTTGTGAGCTTAATTATAATTTGGAGAGTTG
plasmid_cp32-6	24550	BB_M35	<i>bppA</i>	0.942 ± 0.5435 0.530476	0.54 ± 0.4598 0.44032	1.125 ± 0.8177 0.35242	1.06 ± 0.8435 0.6951	ACATTATGCTAAATGCTATTTGCTAGGGAAAAAAACTGTACCTGTTG
plasmid_cp32-6	24606	IG_185		1.857 ± 0.3414 0.05139	2.275 ± 0.1258 0.00363	0.619 ± 0.4058 0.23637	1.644 ± 0.8594 0.33326	GGAGGTTAAATTAGCTTATAAATAAAACAAAGATAATAGAACTT
plasmid_cp32-6	24765	BB_M36	<i>bppB</i>	1.837 ± 1.1694 0.220161	1.418 ± 1.326 0.58026	0.686 ± 0.5062 0.40132	1.054 ± 0.425 0.88101	TAGTTTATAGGACTGGATATAAAGAGCAATTGTTTATTAAATCC
plasmid_cp32-6	24818	BB_M36	<i>bppB</i>	0.725 ± 0.4644 0.511922	1.067 ± 0.4229 0.84906	0.765 ± 0.3267 0.35213	1.069 ± 0.508 0.61843	CATGGATTATAATAAAACAAATTGCTCTTAAATATCAAGCTCTATAAAT
plasmid_cp32-6	24946	BB_M36	<i>bppB</i>	0.752 ± 0.3037 0.340251	0.621 ± 0.5439 0.45526	1.064 ± 0.3254 0.4128	1.061 ± 0.4214 0.45266	GCAACAAAAAAATAAGAAATTATATGATTCACTTGACTTGAACCTGCT
plasmid_cp32-6	25028	BB_M36	<i>bppB</i>	1.759 ± 1.3793 0.353434	1.634 ± 1.4647 0.56317	0.814 ± 0.5384 0.66366	0.93 ± 0.1042 0.83175	TATTTAGACTAAAGTAGTTTTAAAGTTAAGGTTATTCTGATT
plasmid_cp32-6	25113	BB_M37	<i>bppC</i>	1.849 ± 0.6913 0.001235	1.301 ± 0.8972 0.40386	0.964 ± 0.5063 0.92693	1.152 ± 0.4696 0.35095	TGGACTCTGCTGTAACAAAATTACGCTTATAATGCTGAAAAATAA
plasmid_cp32-6	25120	BB_M37	<i>bppC</i>	1.927 ± 0.5561 0.067499	1.457 ± 1.0677 0.42663	0.881 ± 0.3126 0.00665	1.213 ± 0.4072 0.33964	TTATCAATTGTTGAGTATTTCTAAAGTTCTTAACTGTTAATCTGGAAA
plasmid_cp32-6	25174	BB_M37	<i>bppC</i>	1.461 ± 0.7622 0.109608	1.25 ± 0.8683 0.49695	0.66 ± 0.2735 0.22755	0.85 ± 0.3468 0.53879	ACTCTTCCAGATTAAGAACTTGTAAACCAATGAAATGG
plasmid_cp32-6	25216	BB_M37	<i>bppC</i>	2.134 ± 0.6409 0.085396	2.641 ± 2.4082 0.35394	1.021 ± 0.9043 0.96951	1.764 ± 0.3485 0.06419	AATAATGAGAGGATTTAGCAGAAAGCTGATTTTAAGAAGAATT
plasmid_cp32-6	25217	BB_M37	<i>bppC</i>	2.005 ± 1.9001 0.359091	2.245 ± 2.6282 0.42474	0.884 ± 0.4372 0.51713	0.943 ± 0.5892 0.76131	TTTAGAAATTATTATAATTCAAAATTCTAATGGCTATACTCTTC
plasmid_cp32-6	25813	BB_M37	<i>bppC</i>	2.801 ± 1.1276 0.025591	2.322 ± 1.2645 0.16106	1.395 ± 0.9869 0.50862	1.497 ± 0.797 0.22111	ATTATTTAATTAAATAATTCAATATGGATTATGCTCAAACATTTC
plasmid_cp32-6	25822	IG_186		1.559 ± 0.8992 0.048967	1.832 ± 1.4149 0.18795	1.057 ± 0.4896 0.79177	1.328 ± 0.723 0.28659	TCTATAAAATCTCTCTAGAAGTGTACTTTAAATTAAGTAAAAGTAA
plasmid_cp32-6	26185	IG_187		1.527 ± 0.5883 0.14325	1.437 ± 1.8456 0.66044	0.94 ± 0.749 0.91753	0.746 ± 0.7113 0.33847	ATTTGTGATTCTAGCTATTACATTAACAAAACGCAAATATAATT
plasmid_cp32-6	26390	BB_M38	<i>erpK</i>	1.540 ± 0.6326 0.133237	1.454 ± 0.0277 0.32845	0.932 ± 0.309 0.79189	1.056 ± 0.6562 0.82102	CAAAAAAGAAGAGTTTTGGAGATTAAAAACCGAGAAGCAAAGTC
plasmid_cp32-6	27147	BB_M39		1.560 ± 0.5937 0.239997	1.727 ± 1.4856 0.47491	0.583 ± 0.2184 0.17504	0.858 ± 0.1902 0.33008	GTTAATTCTCAGGATCTTCACCTTCAGGAATTCAATTGTTATTGTTACG
plasmid_cp32-6	27288	BB_M39		2.403 ± 1.5646 0.031672	1.086 ± 1.4166 0.93005	1.267 ± 0.6675 0.51096	1.194 ± 1.0504 0.82712	TATGAATTATTCCAATTTCACACATAACTCTATTACAAATT
plasmid_cp32-6	27955	BB_M41		2.303 ± 2.282 0.155602	2.194 ± 2.8852 0.3727	0.851 ± 0.6048 0.66033	1.35 ± 0.9246 0.34343	TGTTGCATATTAGAGAAGGATTGTTAGATGATAGGAAATAGCGGATAA
plasmid_cp32-6	28022	BB_M41		1.117 ± 0.585 0.578348	0.529 ± 0.4325 0.41746	1.193 ± 0.6932 0.034	1.231 ± 0.8567 0.14562	CCCTAGAAACCCCAATTATCCGCTATTCCCTATCTAACAACTCCT

plasmid_cp32-6	28176	BB_M41	1.952 ± 1.7093 0.112403	1.9 ± 2.147 0.31761	0.937 ± 0.6828 0.7662	1.004 ± 0.7386 0.98089	TCTAATTCACTTAACTTCCTAGCGTTAACCTCTGATTTAAAGTTGT
plasmid_cp32-6	28473	BB_M41	1.103 ± 0.4328 0.249525	0.453 ± 0.3243 0.21434	0.868 ± 0.2538 0.16698	0.926 ± 0.3238 0.01723	CTATTTTGATGTGCTTTGCCTTCAGCCTATTAGCAGTTGAAGTTT
plasmid_cp32-6	28495	BB_M42	1.864 ± 0.6976 0.077961	2.016 ± 1.3443 0.2574	0.853 ± 0.2578 0.27071	1.063 ± 0.3247 0.52929	TATCAAACAAAACTTTTACAACACTACAAAAGGAATACAAAAAATAAT
plasmid_cp32-6	28570	BB_M42	1.772 ± 0.6731 0.087142	1.557 ± 1.0229 0.33998	1.079 ± 0.3664 0.6902	0.972 ± 0.3846 0.80718	AAGCTAACAAATTCTCAATTAAATTGATAAGTTGAAGAAAAACAGTTA
plasmid_cp32-6	28592	BB_M42	1.306 ± 0.5194 0.482163	1.362 ± 0.7228 0.43279	0.988 ± 0.4032 0.95499	0.894 ± 0.2298 0.40601	ATTTTGATAAGTTGAAGAAAAACAGTTAACCTTAAACAAAAAATGTGA
plasmid_cp32-6	28970	BB_M42	0.961 ± 0.441 0.156904	0.467 ± 0.3687 0.28242	0.928 ± 0.445 0.24832	0.96 ± 0.368 0.60221	CTTCCCCATAATCTTCAAATCACTTGCTTATCTCCACCATATAGATTA
plasmid_cp32-6	29115	BB_M42	3.502 ± 1.4909 0.071187	1.688 ± 0.3223 0.00113	0.774 ± 0.1854 0.32361	1.091 ± 0.1879 0.51547	ATCGGTTTAAATAGTGTCTGGATGATCGGGATTAGTATCAAATAAT
plasmid_cp32-6	29173	BB_M42	1.381 ± 0.6968 0.000219	0.852 ± 0.9132 0.84991	2.363 ± 1.9971 0.22714	1.447 ± 0.10262 0.20951	GCACATTATCATAAGTTGAAAATTATGTCTTAAAGGTGCTATATTAT
plasmid_cp32-6	29309	BB_M42	1.653 ± 0.3934 0.112946	1.473 ± 1.2661 0.55511	0.754 ± 0.2223 0.33707	0.761 ± 0.5366 0.47749	TAATCATCAGTAATATTATTGTGAAAATTGAATCAGTGCTGCTATC
plasmid_cp32-6	29377	BB_M42	3.394 ± 2.1474 0.186088	1.592 ± 0.9185 0.35346	1.769 ± 0.1714 0.01831	2.376 ± 1.1402 0.16885	TGTGTTAGGAGCGAGTTGATGATAAGTATTATGCTTTGTATTCAAGAC
plasmid_cp32-6	29451	BB_M42	2.998 ± 1.5462 0.011684	1.676 ± 1.6149 0.35625	1.005 ± 0.4537 0.9878	0.804 ± 0.3830 0.38915	TATTATGAATATGGTAAAGACTGTATAGAAAATTCAATGTGCATAACT
plasmid_cp32-6	29505	BB_M42	2.134 ± 2.207 0.467983	3.276 ± 4.4061 0.44681	1.015 ± 0.8612 0.9525	1.752 ± 1.9622 0.58961	TTTAGAGGATAGAGATAATACAAAAGGTGCTGGTGGATTGACCCGCTGAATA
plasmid_cp32-6	29690	BB_M42	0.355 ± 0.5251 0.085929	0.588 ± 0.7489 0.30855	2.247 ± 1.2135 0.09399	0.144 ± 0.0807 0.02706	GTTCTCTGTGTTAATGATTTATTCTGATAAGGGGGATAGCAAAACCC
plasmid_cp32-6	29795	BB_M42	4.789 ± 3.2742 0.121542	0.535 ± 0.7801 0.09766	0.658 ± 1.181 0.76263	1.084 ± 0.1066 0.77557	TATCCTAAAGACAACATCAAATAGTCTGCGACATTGATCAAGAGCATCA
plasmid_cp32-7	278	BB_O01	1.832 ± 0.7563 0.094368	1.818 ± 1.4893 0.35966	0.923 ± 0.2593 0.2505	1.184 ± 0.4593 0.24903	AGCTACCGTTTCATGGGATTGGCTATGTTTAGTAAAACCAAAGATACC
plasmid_cp32-7	394	BB_O01	1.717 ± 0.2639 0.009524	1.377 ± 0.7432 0.46512	1.051 ± 0.1634 0.02226	0.948 ± 0.1779 0.30527	TTCATAATCAAGGTATTCAAACCAATAGGTAATTCTATATAACGGGTTG
plasmid_cp32-7	397	BB_O01	1.781 ± 0.2737 0.036728	1.45 ± 0.7123 0.36222	0.68 ± 0.1328 0.02701	0.913 ± 0.1118 0.17162	TGTAAGAGATTGGGAGTTGATTTGATCATATAACCTATAAGTAAATC
plasmid_cp32-7	398	BB_O01	1.246 ± 0.379 0.446604	0.569 ± 0.4227 0.12222	1.064 ± 0.2459 0.74144	1.133 ± 0.2629 0.53142	CATATTCTATAATCAAGGTATTCAAACCAATAGGTAATTCTATATAACGG
plasmid_cp32-7	426	BB_O01	2.944 ± 3.8192 0.487399	1.167 ± 1.001 0.83387	1.537 ± 0.5156 0.24157	1.677 ± 1.854 0.62766	TGATCAAATCAACTCCAAATCTCTACATATTCTATAATCAAGGTATTCA
plasmid_cp32-7	443	BB_O01	2.070 ± 1.4168 0.299676	1.858 ± 0.7254 0.12735	1.36 ± 0.6026 0.43052	0.975 ± 0.3807 0.90013	AAATCCAACAAAGAACAACTTTAGCGAGTTAAAATACATAAAAAGT
plasmid_cp32-7	477	BB_O01	1.796 ± 1.1855 0.239196	1.018 ± 0.9397 0.97658	0.753 ± 0.3813 0.54658	1.212 ± 0.3558 0.19972	ACTGCGTCTAAAGATAATGTTCTTATTGTTGATTTTACTTTAGGTTATA
plasmid_cp32-7	489	BB_O01	2.713 ± 1.931 0.229639	1.833 ± 1.4296 0.70696	0.579 ± 0.4411 0.45317	0.995 ± 0.7127 0.99338	AAAGTCGACTTATGATATAGAAAATTGATTATATCTAAAAGATAGT
plasmid_cp32-7	505	BB_O01	3.360 ± 2.6271 0.024932	2.038 ± 2.5606 0.35878	1.153 ± 0.7881 0.77022	1.161 ± 0.9693 0.12267	TATGATAAGTCGACTTTATGTTATTAACTGCGCTAAAGAATTGTTCTT
plasmid_cp32-7	506	BB_O01	1.300 ± 1.1008 0.657356	1.217 ± 1.0815 0.24196	1.113 ± 0.9022 0.64538	1.389 ± 1.1395 0.12119	TATGAAAATTGATTATCTAAAAGATATGTCGTTATACCGAA
plasmid_cp32-7	520	BB_O01	2.221 ± 0.8948 0.054989	1.356 ± 0.8425 0.6133	1.071 ± 0.4412 0.7685	1.226 ± 0.5011 0.45433	ATCAAAGTTTCATATATGATAAGTCGACTTTATGTTTTACTGCGTC
plasmid_cp32-7	523	BB_O01	1.653 ± 0.4168 0.015952	1.085 ± 0.7282 0.80774	1.1 ± 0.216 0.3175	1.533 ± 0.10985 0.52222	TATCTAAAAGATATGTCGTTATACCGAAAGCTTTACTAGATAT
plasmid_cp32-7	525	BB_O01	1.013 ± 0.6697 0.694267	0.122 ± 0.1234 0.11061	0.58 ± 0.8114 0.15576	1.773 ± 1.3648 0.25025	TCTTTAAAGATATGTCGTTATACCGAAAGCTTTACTAGATATT
plasmid_cp32-7	577	BB_O01	2.586 ± 1.9396 0.145015	3.015 ± 2.949 0.25652	1.026 ± 0.6657 0.91892	1.533 ± 0.8823 0.08626	TTTATTTGAAAAGATATACCTGAGAAATAGAAAAGCGTATTGAAAACACAA
plasmid_cp32-7	941	BB_O01	1.291 ± 0.7555 0.526066	1.537 ± 2.4098 0.69498	0.941 ± 1.4471 0.93974	0.504 ± 0.6388 0.34093	GCATTAATTAAAGCaaaaATTGGTCAGATACAAAGAACCTTAACCTAGA
plasmid_cp32-7	1409	BB_O02	1.450 ± 0.9856 0.513162	1.201 ± 0.952 0.4273	0.83 ± 0.6581 0.52837	1.255 ± 0.8314 0.17474	CATCGCTTTAAAGAGCAGCAGAAATAGTAAATCTAAAGAGACAGTCGAGA
plasmid_cp32-7	1625	BB_O02	2.232 ± 1.728 0.363366	0.877 ± 0.6432 0.57021	0.479 ± 0.2505 0.13702	0.734 ± 1.2077 0.80312	TCCCTTGCAAGTAGCACCTTGTGTTAAATGATTGCTAAAGATGTTCTT
plasmid_cp32-7	1630	BB_O02	1.079 ± 1.2624 0.865484	1.047 ± 1.1033 0.87711	1.163 ± 1.0818 0.65011	1.053 ± 0.8705 0.42743	CATTTAAAGACATTATGCAAGCACACAGTAGAGAACTTGTACCGAAGTTCG
plasmid_cp32-7	1746	BB_O02	1.425 ± 0.8132 0.170567	0.318 ± 0.2544 0.17661	0.841 ± 0.7046 0.41755	1.205 ± 0.7358 0.50574	TTAGAGCAACTTGTCTTAGAAAAGATTAATTAAATTAGAAAAT
plasmid_cp32-7	1927	BB_O02	1.331 ± 0.7391 0.52949	0.95 ± 0.178 0.63602	0.83 ± 0.3109 0.47547	0.515 ± 0.3646 0.16537	TTACTTATCGCTGTACAAATTCTGTGAAATTAAATAGGTACAAAATTAGAA
plasmid_cp32-7	1930	BB_O02	2.360 ± 1.5945 0.047521	1.505 ± 1.4104 0.29823	1.364 ± 0.7842 0.27946	1.041 ± 0.6592 0.79582	CATACAAGCAAAGCGAATTCAATTCTATGAAAATCTAAAAGACATAAAA
plasmid_cp32-7	2215	BB_O03	1.753 ± 0.8235 0.224409	1.148 ± 0.8075 0.78996	0.777 ± 0.5065 0.52201	0.857 ± 0.5166 0.61584	TACGGATACCTTGTAGCAGGTTAACCTCTATTTGTCTTACTGCTAGTG
plasmid_cp32-7	2230	BB_O03	1.617 ± 1.2439 0.284793	1.628 ± 1.2355 0.30976	1.355 ± 0.906 0.47318	1.179 ± 0.4896 0.55418	AGCTTAGTTTGGAGATGGAACACCGAACAGTAAGTTGAGGCTGGTGGT
plasmid_cp32-7	2340	BB_O03	2.026 ± 0.9569 0.219236	1.506 ± 1.0032 0.49878	0.962 ± 0.5346 0.91995	0.909 ± 0.1156 0.39451	TAACAGTGTGCCATTACCGCTAACACTCATCTATCGAACACACTCCATATA
plasmid_cp32-7	3041	BB_O04	1.077 ± 1.3937 0.933798	0.993 ± 1.5852 0.99496	1.287 ± 0.9711 0.64584	0.708 ± 0.5759 0.30503	TGTATTGCAAAATTCTAACACATTGTTGAAAGGGTACCTTGTCAACAGGAATCC
plasmid_cp32-7	3202	BB_O04	1.866 ± 0.7788 0.043649	1.727 ± 1.2905 0.30957	1.005 ± 0.457 0.94832	1.477 ± 0.4761 0.04387	CAATCAATTGTCAGCCGAAGATGGAAATCAAGATCAAATAGATCTCTA
plasmid_cp32-7	3248	BB_O04	0.108 ± 0.1961 0.132565	0.296 ± 0.4842 0.32394	0.268 ± 0.2885 0.2563	0.504 ± 0.5369 0.48245	TCCTAGGCAAGAGTATTCTATAATTGATAAAAAGTTGCAATTGTTGGAAA
plasmid_cp32-7	3375	BB_O05	3.819 ± 2.5235 0.07431	2.133 ± 1.902 0.26331	1.151 ± 0.8054 0.63463	1.305 ± 0.9785 0.23254	TCTCCATTATTCACCTCTTTATCGCCAAAAGTTAACACCATCAG
plasmid_cp32-7	3392	BB_O05	2.567 ± 2.5587 0.36755	2.172 ± 3.0414 0.41423	1.803 ± 1.2934 0.12393	1.708 ± 1.4968 0.50841	AAAGAGTATCAAGGAAAAGAGTAACTGGAAAAGTTATGAAAATCC
plasmid_cp32-7	3667	BB_O05	1.538 ± 1.432 0.434543	1.273 ± 1.8436 0.72741	0.546 ± 0.4245 0.41358	0.881 ± 0.5652 0.82843	TGGAATATGCGATCATAGATGAGTTAGTAAACAGCTACTATTGTGCC
plasmid_cp32-7	3693	BB_O05	2.002 ± 0.5087 0.053898	2.05 ± 1.7118 0.36477	0.981 ± 0.2296 0.15089	1.34 ± 0.5081 0.1776	AACTCATCTATGCAATATCCATATAAGTCTTACCCAGCC
plasmid_cp32-7	3711	BB_O05	2.056 ± 1.0617 0.088361	1.861 ± 1.7932 0.46874	0.898 ± 0.5692 0.7921	0.941 ± 0.5206 0.84019	TTGTGCAATTACCAATAATTGAGGGATTTAGTGGCAAAGATTCTA
plasmid_cp32-7	3726	BB_O05	2.697 ± 1.6083 0.220167	2.118 ± 1.8522 0.43741	1.476 ± 1.0404 0.57525	1.597 ± 0.7885 0.09628	TTGGTAATTGGCACAATAGTAGCTTTACTAAACTCATCTATGCAATG
plasmid_cp32-7	3795	BB_O05	1.878 ± 1.1495 0.063371	2.017 ± 1.7182 0.15082	1.161 ± 0.7272 0.61231	1.773 ± 1.5254 0.29765	AAGACGGTGTCTGAAAAGGTGACTGGAGCACCAATAAGCAACTATTA
plasmid_cp32-7	4066	BB_O06	1.668 ± 0.7166 0.166219	0.862 ± 0.2545 0.11702	0.745 ± 0.1565 0.17226	0.942 ± 0.1385 0.58408	AGATGTTGATCTACAAATGGGATATCAAAAACCGTAAAATGGGACCGCTT

plasmid_cp32-7	4221	BB_O06	2.367 ± 1.2036 0.12557	2.292 ± 2.0886 0.35546	0.768 ± 0.4076 0.18575	1.134 ± 0.6009 0.54655	AATTAGACATTTAACGAGACTTCTGAGAAATTATACTTCAGATTCAT
plasmid_cp32-7	5092	BB_O07	1.495 ± 0.5074 0.221789	1.338 ± 1.6464 0.74614	0.912 ± 0.5332 0.81515	0.959 ± 0.4633 0.8904	GCTTGAAGTAAGGATAAATGAAGTAGAAAATTTCCTGCTTAGTGC
plasmid_cp32-7	5135	BB_O07	0.990 ± 0.7069 0.977382	0.71 ± 0.6767 0.69787	0.502 ± 0.8897 0.51435	0.519 ± 0.3676 0.34147	TGAACAAATATTTCCTACTTCTACCATATGGGCTGCCAATTAAAGAAA
plasmid_cp32-7	5258	BB_O07	1.159 ± 0.7528 0.78604	1.678 ± 1.5383 0.44672	0.517 ± 0.2701 0.26861	0.797 ± 0.598 0.74376	TTATCCTAGTAGCAGTGGAGGCGAAGAAGGCCGAGGGGAGTTGTGGCTC
plasmid_cp32-7	5447	BB_O08	1.740 ± 0.9016 0.008996	1.823 ± 1.4413 0.27329	0.77 ± 0.4479 0.41354	0.952 ± 0.4192 0.87913	CGTTGATCATCGGAAAGACATATCTGAAAGTCTTCAACACCATTCA
plasmid_cp32-7	5538	BB_O08	0.877 ± 0.4537 0.521557	0.672 ± 0.5151 0.06373	0.736 ± 0.4154 0.11235	0.993 ± 0.5544 0.95376	TTTTATCAAAAACCTCTGATAAGAAGAATCGTTCAAGTTAACACA
plasmid_cp32-7	5610	BB_O08	1.578 ± 0.7177 0.3568	1.099 ± 0.7254 0.86352	0.632 ± 0.1664 0.16874	0.789 ± 0.2141 0.37918	TCAGAGTCATAAAGCACTGCAAGTTCTGGCCTTATGTCATAATAACT
plasmid_cp32-7	5632	BB_O08	0.436 ± 0.2686 0.125057	0.428 ± 0.3894 0.23875	1.027 ± 0.4014 0.79588	1.038 ± 0.3819 0.27693	TTCCAAACTTACACATATCAAGACCTTAACATGAACTAAAGACCGCAT
plasmid_cp32-7	5644	BB_O08	3.963 ± 5.7405 0.446819	1.065 ± 1.8182 0.95163	1.927 ± 1.1152 0.25874	1.005 ± 0.3821 0.98628	CACATATCAAGACCTTAACATGAACTAAAGACCGCATATCAATTTCGGA
plasmid_cp32-7	5647	BB_O08	2.294 ± 1.8257 0.255479	0.607 ± 0.3584 0.42098	0.538 ± 0.3265 0.14769	0.932 ± 0.5028 0.84623	TGTGAAAGTTGAATATCCTGAAATCAGACATATCAGAGTCATAAAG
plasmid_cp32-7	6472	BB_O10	1.880 ± 1.7383 0.295838	2.793 ± 2.4253 0.18899	0.664 ± 0.7424 0.57893	0.818 ± 0.9351 0.81036	TAAAGCATTAAACATGCGTGAATTAGCGTCAAAGTCTTGGCCTTAAACACT
plasmid_cp32-7	6512	BB_O10	2.098 ± 1.3418 0.16383	0.91 ± 0.6395 0.42663	1.319 ± 0.7178 0.57292	1.084 ± 0.7267 0.85133	CTTATGGGCTTATTGTGAGAAAGTCATAAGCATACCAAAAGCATTAA
plasmid_cp32-7	6824	BB_O11	1.214 ± 1.146 0.625417	0.501 ± 0.7686 0.44976	1.058 ± 0.6163 0.76357	1.294 ± 0.1099 0.42833	GCAGCATCTTATTAACTTGTGATTAGCTGTTGTAAACCAAAAGTGG
plasmid_cp32-7	7159	BB_O11	1.854 ± 0.6761 0.139232	1.834 ± 1.5002 0.43891	0.679 ± 0.0791 0.00269	0.888 ± 0.4761 0.72924	TTCTCAACTAAAGAACAGAAAATAAGAAGATATTAAAGATAAAGGCAAT
plasmid_cp32-7	7247	BB_O11	2.301 ± 1.0413 0.016352	3.026 ± 3.0126 0.2914	1.968 ± 0.8461 0.17771	1.859 ± 0.9524 0.27694	ATAAAAGACAAATTACACCTAAATTATAAGTCATAATTACATCAAGCTA
plasmid_cp32-7	7490	BB_O11	1.846 ± 1.9821 0.224676	1.167 ± 1.4768 0.69732	1.049 ± 1.1992 0.91703	1.273 ± 0.9016 0.56722	CATACCACTATAAAAAATGAAGCGATTATTGAGCTTATTAGAATTGGGA
plasmid_cp32-7	7884	BB_O12	1.965 ± 0.5671 0.113552	2.182 ± 1.2235 0.19223	0.596 ± 0.3007 0.04255	0.841 ± 0.4409 0.55114	CATAGTGGAAACTAGAACCTACAAGCGAACCCACAACAAGAGCAGTGTATT
plasmid_cp32-7	8143	BB_O12	2.799 ± 1.1871 0.019927	1.712 ± 1.8275 0.50205	1.315 ± 0.6769 0.57128	1.07 ± 0.4438 0.60164	GAAATAATTGGTAGCAATTCTATCATGAAATGCTAATCAAGCATTTA
plasmid_cp32-7	8221	BB_O12	1.874 ± 0.4672 0.072587	1.884 ± 1.5817 0.42508	0.974 ± 0.1056 0.7036	0.929 ± 0.1259 0.18395	GCCCTAATTCAAAGAGATACTTTTCCGGCTCAGCAGAATACTCTTGAA
plasmid_cp32-7	8698	BB_O13	2.034 ± 0.7989 0.004543	0.483 ± 0.6422 0.4392	0.281 ± 0.4293 0.01562	0.933 ± 1.245 0.93495	CATCAAATTCCAATGAGCTGTTGCTAAATGATCAAAGAACATAGAGATAT
plasmid_cp32-7	9142	BB_O15	2.557 ± 2.0523 0.303872	1.929 ± 2.2669 0.53054	0.337 ± 0.2732 0.0928	0.727 ± 0.3031 0.43811	AGTTCTTTCTTGTGCGACAAATTATTTCACCATATCTTGTGCTA
plasmid_cp32-7	9520	BB_O15	1.835 ± 1.486 0.438526	1.936 ± 1.3773 0.27435	0.687 ± 0.8614 0.40213	1.632 ± 1.4811 0.47111	ATAAAAGTGTGTTACAGTGAAGAACGCTGAAAATATTGGGTGCTTATT
plasmid_cp32-7	10214	BB_O15	2.002 ± 1.9981 0.314991	0.748 ± 0.787 0.7693	1.252 ± 1.4961 0.75913	0.982 ± 1.3597 0.98622	AGTATTACCAACACATTACTAGCGGTTATTATAATGAGCTGCAATGTT
plasmid_cp32-7	10219	BB_O15	2.898 ± 3.6207 0.412517	3.169 ± 4.2549 0.42711	0.765 ± 0.3903 0.50178	1.5 ± 0.9056 0.47883	ACTTCGCGACTGTTGGATTATAATACGATTITGGAAAGAACAAACATA
plasmid_cp32-7	10568	BB_O16	2.784 ± 3.7458 0.319779	2.091 ± 1.8113 0.29167	0.592 ± 0.5808 0.40644	1.457 ± 1.3874 0.57058	AGTGCCTGCTATGAGTCGTTTTGGTTATAAAAACAATTGAGGAAC
plasmid_cp32-7	11080	BB_O17	1.430 ± 0.6489 0.370593	2.516 ± 2.2493 0.27498	0.965 ± 0.7601 0.92449	1.752 ± 0.999 0.26627	CACAAACATGGAATTCATATTGATATTACCATATCTAATGAGTTTCAAATT
plasmid_cp32-7	11181	BB_O17	1.772 ± 0.7557 0.252635	1.058 ± 0.8737 0.89404	0.951 ± 0.5248 0.72189	1.068 ± 0.4623 0.85751	AGGGCAAATTCCAAGTACAATTGGTCTGTTAGATTTCACAAATTAT
plasmid_cp32-7	11214	BB_O17	1.967 ± 1.1103 0.061669	1.728 ± 1.5834 0.35894	0.934 ± 0.4886 0.49944	1.069 ± 0.5456 0.38111	TATCTCTACTTCATGTGTTGGTAAAGTCTAAGGGCAATTCAAAGTA
plasmid_cp32-7	12048	BB_O18	1.802 ± 0.5999 0.07376	1.493 ± 0.9865 0.40561	1.043 ± 0.3566 0.87978	0.952 ± 0.3837 0.89313	AAGGAGTTAAACAAACAACTCAAGAGGCTATTGTTACAATACCGAAATT
plasmid_cp32-7	12130	BB_O18	1.550 ± 0.5624 0.17304	1.513 ± 1.2808 0.55048	0.782 ± 0.4377 0.13368	1.443 ± 0.5615 0.05506	GAGATATTGGTTGTGAAATTCTCAAATTGGTATTGTAACAA
plasmid_cp32-7	12247	BB_O18	2.828 ± 2.4085 0.174971	3.115 ± 4.2885 0.46174	1.407 ± 1.125 0.27652	1.39 ± 1.0123 0.23965	GTGCAATTAGGCCAAAGACTTAACTATTCTGATACTGTTAAATT
plasmid_cp32-7	12289	BB_O18	0.600 ± 0.6355 0.480527	2.793 ± 2.9223 0.15352	0.863 ± 0.8375 0.86084	0.978 ± 1.1041 0.97129	ACAGTATCAGAAATTAGATTAAAGTCTGGCTAATTGACTAAGTATA
plasmid_cp32-7	12429	BB_O18	2.012 ± 1.1785 0.024298	2.011 ± 1.6054 0.18921	0.852 ± 0.43 0.63592	1.107 ± 0.871 0.59785	GCAACATCTAGAATTAGCAATAATTAAAGTGTGTTAGTAATT
plasmid_cp32-7	12543	BB_O19	1.482 ± 1.2302 0.600855	0.789 ± 0.7484 0.78545	0.634 ± 0.4648 0.35096	0.6 ± 0.4998 0.41013	TTAAATACCAATTCAAATTATTGCTTAATCTAAATCCATACTGTAATT
plasmid_cp32-7	12743	BB_O19	1.344 ± 1.3776 0.662057	1.801 ± 2.3895 0.59744	0.376 ± 0.4139 0.22675	0.656 ± 0.4509 0.39303	AATCTAAGTTAACTCTTAACTATTCTGATACTTACAGCGT
plasmid_cp32-7	12783	BB_O19	2.406 ± 0.3306 0.004464	1.149 ± 0.9499 0.79422	0.696 ± 0.1472 0.02091	0.867 ± 0.48 0.62436	TGTGTTGGTCTGTATAGTAGTTGAAATATTAACTAAAGTTA
plasmid_cp32-7	13073	BB_O20	2.108 ± 1.3966 0.294924	1.573 ± 1.0819 0.06439	0.717 ± 0.5959 0.65436	1.349 ± 0.8582 0.60678	TGTTCTCAATAGCGCCAAATAAGTACCCACAGGTTTATTAGAAAAA
plasmid_cp32-7	13177	BB_O20	1.731 ± 0.2577 0.039045	1.528 ± 0.8933 0.41935	0.886 ± 0.1931 0.42239	0.913 ± 0.2488 0.64485	TGTTGGCTTACCAAGCGGCACTTTAAATATTAGTATACTCAACCCCTAA
plasmid_cp32-7	13182	BB_O20	0.881 ± 0.7662 0.834684	0.859 ± 0.993 0.80461	0.87 ± 0.3948 0.48633	1.157 ± 0.4296 0.6413	TCTAATTCTAAAGAACAACTTAGAGCCTAGTAATCTACTTAAATAG
plasmid_cp32-7	13416	BB_O20	1.778 ± 1.1032 0.014381	0.609 ± 0.5361 0.54543	1.023 ± 0.6631 0.81549	0.925 ± 0.5118 0.70197	GTTTTAAGGTCAGTTTATCTTCAATAAACATATTCTTT
plasmid_cp32-7	13458	BB_O20	0.341 ± 0.4549 0.000668	0.133 ± 0.1391 0.10727	0.868 ± 0.4763 0.45229	0.23 ± 0.2537 0.13804	TTCTAGGTTTATTCAAATACTATTCTGATACTGGAAATTAGCTTGAATA
plasmid_cp32-7	13845	BB_O21	2.717 ± 1.6476 0.039132	1.692 ± 1.552 0.30756	0.857 ± 0.439 0.49641	1 ± 0.524 0.9961	GAAAAATATAAAATCAAGATATATTGCAATATGGATACTCAAGTTTATCT
plasmid_cp32-7	14032	BB_O21	3.484 ± 5.0831 0.3647	2.876 ± 5.1218 0.52036	1.683 ± 2.234 0.40286	1.808 ± 2.2675 0.41804	ACTTCATACTGCCCACATTAAAGAGGCTTAAAATTAGTCTAAACGACTCA
plasmid_cp32-7	14095	BB_O21	1.486 ± 1.0982 0.508191	1.687 ± 1.933 0.58611	0.9 ± 0.2868 0.58715	1.034 ± 0.3822 0.86568	CTACATTATTCGCCTAGCACTAGAAAGAACGACTAAAAAGATAA
plasmid_cp32-7	14193	BB_O21	2.416 ± 1.7603 0.305859	2.283 ± 3.0699 0.53449	1.576 ± 1.3224 0.44904	1.218 ± 0.4937 0.17556	GTATTCAACTCCTCTAAGGGCTATGATCATTAATTGCTTTTATT
plasmid_cp32-7	14231	BB_O21	3.167 ± 0.7495 0.021087	2.236 ± 1.5189 0.26314	1.513 ± 0.5132 0.26008	1.376 ± 0.7562 0.49156	AATTGAATGATCATGCCCTAGGAAGTGAATTAACTAAAGCCTTTT
plasmid_cp32-7	14287	BB_O21	1.665 ± 0.8909 0.009108	0.361 ± 0.2676 0.23679	0.825 ± 0.4678 0.26678	0.99 ± 0.6082 0.95625	CAGATGGTAACAATTAACTAAACAACTAAGGAGGTTTATGGCTGATGATCAAG
plasmid_cp32-7	14296	BB_O21	1.666 ± 0.2574 0.05761	1.337 ± 0.4095 0.28862	1.077 ± 0.1616 0.57754	1.239 ± 0.7316 0.56957	ACAATATTATAACTTTAACAACTAAGGAGGTTTATGGCTGATGATCAAG
plasmid_cp32-7	14427	BB_O22	0.903 ± 0.6126 0.831406	0.514 ± 0.5931 0.5198	1.027 ± 0.8746 0.89396	1.142 ± 0.8513 0.62585	AAAGATCAGTATCGTTAACGGCTGTAACCTTATAATGTTTAACTT

plasmid_cp32-7	14455	BB_O22	0.968 ± 0.964 0.96819	0.686 ± 0.5311 0.57839	0.168 ± 0.3056 0.17359	1.318 ± 1.1747 0.65687	CTGCTTCAGCTCCATCATCAAGCAGTAAAGATCAGTACGTTAACGGTC	
plasmid_cp32-7	14530	BB_O22	1.939 ± 1.2521 0.126122	1.09 ± 0.8404 0.79962	0.69 ± 0.401 0.4734	1.006 ± 0.4822 0.98548	AAATAGTCTAATCCCCTCCTTTAAATATTGTCTTAGAAGCATCTAA	
plasmid_cp32-7	14623	BB_O22	1.910 ± 0.9657 0.057598	1.598 ± 1.5662 0.46181	0.893 ± 0.3966 0.25913	0.977 ± 0.4534 0.45344	ATTAATTGTCGGTTATTAGCATAAATTTCTACAAAATCTTATCA	
plasmid_cp32-7	14683	BB_O22	0.921 ± 0.4086 0.822052	0.786 ± 0.9469 0.65404	0.573 ± 0.2175 0.02993	0.796 ± 0.5269 0.40578	TCTGTAAGGCCTGATTAACTTAAAGGTTAGAAATATTAGTAGAA	
plasmid_cp32-7	14691	BB_O22	1.008 ± 1.0068 0.989906	1.385 ± 1.4336 0.33672	0.176 ± 0.2126 0.20698	0.261 ± 0.2853 0.27519	TTCATCAGCCACTTATCTAGAAGTGATCATTTGATAATGCCCTCATCA	
plasmid_cp32-7	14743	BB_O22	1.448 ± 1.3548 0.456767	0.351 ± 0.1685 0.08066	0.754 ± 0.5194 0.23004	0.577 ± 0.2955 0.15118	TCTGATGAAGGCATTATCAAAGATGATCACTCTAGATAAAGTGGCTGAT	
plasmid_cp32-7	14775	BB_O22	1.897 ± 0.7309 0.057797	1.173 ± 0.6306 0.6721	1.297 ± 0.6896 0.19318	0.994 ± 0.4379 0.97857	TATGTTAGGAACGGGTGTTTTGAATAGTATCTGATGAAGGCATTATCA	
plasmid_cp32-7	14879	BB_O22	1.808 ± 0.5179 0.02436	1.724 ± 0.9937 0.18646	1.128 ± 0.3302 0.21665	1.084 ± 0.4257 0.77695	CAATGATGATGTAACCTTATTCTAAAGTACGATAATTCTCCCGT	
plasmid_cp32-7	14968	BB_O22	1.713 ± 0.5946 0.016439	2.568 ± 1.5958 0.12584	0.721 ± 0.2979 0.43164	0.962 ± 0.4399 0.24417	TTATCATTGATTCTACTGAAATTCAATATCAAGATAAACGGGAGAATT	
plasmid_cp32-7	15057	BB_O22	1.216 ± 0.3941 0.062373	0.391 ± 0.2659 0.16236	1.151 ± 0.7936 0.65508	1.491 ± 0.8149 0.33433	TTACACCAGATTCCCATTTAAAGGATGGATGTCTCAAAGAGGCC	
plasmid_cp32-7	15074	BB_O22	2.239 ± 1.4605 0.094587	1.705 ± 1.7818 0.49349	0.963 ± 0.5274 0.90625	1.09 ± 1.0927 0.89094	AATGGAAATTCTGCTGAATAGTCGCCGGGCCAATTCTAAACCC	
plasmid_cp32-7	15177	IG_188	1.722 ± 1.4487 0.226464	2.143 ± 2.3397 0.34492	0.796 ± 0.5432 0.47046	1.056 ± 0.7768 0.6309	TATACCAAAATCATAATTCTGCTAAAGGTTACAGTTAAAGATCTG	
plasmid_cp32-7	15185	IG_189	2.829 ± 0.3436 0.10884	1.809 ± 0.9817 0.28984	1.061 ± 0.0896 0.27133	1.25 ± 0.0835 0.01755	CGTATAAAAAATAAAAATTAATGAAGGATAAAAATGGATACTTAA	
plasmid_cp32-7	15342	BB_O23	<i>blyA</i>	2.609 ± 1.2262 0.082676	1.827 ± 0.7254 0.07695	1.001 ± 0.5764 0.99528	0.819 ± 0.5968 0.47033	AAAGACATATTGACTATTGTAATAGGCAAGATTAAAGAATGGTAATGGT
plasmid_cp32-7	15360	BB_O23	<i>blyA</i>	1.015 ± 0.3783 0.895542	0.449 ± 0.368 0.28277	0.941 ± 0.35 0.54267	0.979 ± 0.4016 0.64266	CAATAGTCATAATGTCCTTAGTAAAGGCTTGGAGAAGATAATTACTCCTA
plasmid_cp32-7	15363	BB_O23	<i>blyA</i>	2.741 ± 2.3085 0.262588	2.005 ± 1.8584 0.16831	1.777 ± 1.199 0.31485	1.787 ± 1.2906 0.00871	ATAGGCAAGATTTTAAGAATGGTAATGGCAAAAATCACATTAA
plasmid_cp32-7	15448	BB_O24	<i>blyB</i>	2.986 ± 1.7786 0.198183	3.67 ± 4.2924 0.38946	0.744 ± 0.7481 0.59169	0.678 ± 0.2388 0.1037	ATGTTGAGCTTGGACTTACGCTTTACACCTTATTGATATTTCTA
plasmid_cp32-7	15841	BB_O25		1.348 ± 0.7545 0.192925	1.218 ± 1.2851 0.63453	0.636 ± 0.4593 0.28413	0.828 ± 0.4145 0.59405	TGTTGTATCAGTTTAGCTATGTTAGTAAGCTAGATGAAATTAAAGTC
plasmid_cp32-7	15904	BB_O25		2.420 ± 1.5037 0.238089	2.22 ± 0.20636 0.4092	1.063 ± 0.436 0.8156	1.195 ± 0.1804 0.17443	AGCACACTAAATCTATGAAACAGCTGAATCAACTAAATATTGAAAGAA
plasmid_cp32-7	16005	BB_O25		2.584 ± 1.5773 0.240218	1.056 ± 0.9319 0.93613	1.128 ± 0.8327 0.84318	0.935 ± 0.3891 0.851	TGACAAAAATAAAAATTACTCACTAAAGCAAACGCAACAAAAT
plasmid_cp32-7	16146	BB_O26		1.730 ± 2.663 0.615895	2.656 ± 2.7697 0.2215	0.726 ± 0.7095 0.7129	1.234 ± 1.5956 0.70756	GTGGTGCACATAACACAAACAAATTGTAACATGCAATTCTTAAGC
plasmid_cp32-7	16343	BB_O26		1.737 ± 1.1465 0.328599	1.698 ± 1.3613 0.41966	0.832 ± 0.4625 0.42597	1.086 ± 0.3117 0.59711	TGGAGTGTGCTTTAGTTAGGTGATAATCTGGATAAGGATATTCTGG
plasmid_cp32-7	16373	BB_O26		2.097 ± 0.9535 0.190608	0.721 ± 1.2584 0.57861	1.002 ± 1.6003 0.99698	0.787 ± 0.639 0.66269	TATTAGAGTACATTAAAAAAACACCAATAGCGGAAAAGTCTATAAT
plasmid_cp32-7	16419	BB_O26		1.065 ± 0.5132 0.768088	0.574 ± 0.5842 0.22682	1.007 ± 0.7445 0.98047	1.17 ± 0.6608 0.19537	TAGACTTTCCGCTATGGTTTGTGTTTTAATGTACTCTAAATATG
plasmid_cp32-7	16996	BB_O27	<i>bdrN</i>	1.979 ± 2.3101 0.271717	0.971 ± 1.1308 0.95839	0.9 ± 0.956 0.84452	0.861 ± 1.0579 0.7247	GAAAAGAATTAAACACTAAATAGACAATGTTGAAAGAATTAAATGTC
plasmid_cp32-7	17041	BB_O27	<i>bdrN</i>	2.529 ± 1.8011 0.245221	2.355 ± 2.8367 0.5073	0.581 ± 0.5838 0.31935	1.598 ± 1.3899 0.56585	ATGTCTTTCAGAAATGCTTAAATGGGTATTAGGAATCATGGAGCAATG
plasmid_cp32-7	17136	BB_O27	<i>bdrN</i>	1.776 ± 1.145 0.322482	1.077 ± 0.6426 0.78593	0.926 ± 0.5363 0.8666	1.248 ± 0.6421 0.59904	TTTAGAAATGAAAGCAAATATTAGCCGGTATATTGATAGACATTG
plasmid_cp32-7	17703	IG_190		1.855 ± 0.7363 0.04373	2.099 ± 2.2157 0.42248	1.039 ± 0.2954 0.74085	0.965 ± 0.2823 0.63598	AGAATCTGCTATGTCGAAATATCTCATCAACCCGTTGTTACCTTAA
plasmid_cp32-7	17765	BB_O29		2.384 ± 2.3486 0.248262	3.026 ± 3.3455 0.2306	1.263 ± 1.3364 0.74074	1.291 ± 1.2673 0.73070	TTCTTGTAGTCTAAAGAATACGAAACGGTTGATGAGATATTGAGCA
plasmid_cp32-7	17768	BB_O29		2.337 ± 1.0204 0.034578	1.876 ± 1.374 0.25851	1.111 ± 0.4563 0.44444	1.127 ± 0.4067 0.29236	TTAATGGACTAGGGCCTAAAGCAGTCTTAAACGACACAAACTTCAA
plasmid_cp32-7	17842	BB_O29		2.733 ± 2.3729 0.196552	1.885 ± 2.4442 0.49208	0.73 ± 0.6651 0.07192	0.882 ± 0.5111 0.60651	TTATTTCTTGTAAATGTTTATAATCTGGCCAATAGTTACACTC
plasmid_cp32-7	17972	BB_O29		1.719 ± 0.861 0.126124	1.96 ± 1.2106 0.12163	0.572 ± 0.39 0.15878	1.201 ± 0.5864 0.32703	TATTCTGAATAAGCTTTTGTAAATTGAGTTTATATTCTTTG
plasmid_cp32-7	18011	BB_O29		0.914 ± 0.691 0.57308	0.575 ± 0.9097 0.33938	0.606 ± 0.4728 0.04055	0.534 ± 0.3153 0.31279	TATTATTTGGTAGGGCTATTACCAACATTTTTATATTAGACAAAG
plasmid_cp32-7	18275	BB_O29		1.245 ± 1.0517 0.634491	1.445 ± 1.4761 0.57441	1.013 ± 0.5827 0.93467	1.136 ± 0.6701 0.52902	GATACTGATGCGACTCTATTACAATAATCACGAAAACGAAATTCTG
plasmid_cp32-7	18328	BB_O29		1.783 ± 0.5021 0.039676	1.335 ± 0.9306 0.51968	0.737 ± 0.1872 0.13897	0.799 ± 0.1784 0.28449	CTTATGTCAAAAGGTATGCTTGTAGTCAGCTCTGGTATAGAAAGT
plasmid_cp32-7	18361	BB_O29		2.085 ± 1.6135 0.118628	1.776 ± 1.6208 0.21984	1.284 ± 0.8834 0.58673	1.259 ± 0.8732 0.34143	TTGTAACTTAGACCCATTTCATTGTTCCATTGTAATTTCTGAGGA
plasmid_cp32-7	18453	BB_O29		1.333 ± 0.8802 0.593148	2.322 ± 0.30419 0.53046	1.072 ± 0.4679 0.82002	1.692 ± 0.7902 0.19962	CAGTACGACTGGATATGAATTCTTGTATACGCGAATTCTACAGA
plasmid_cp32-7	18482	BB_O29		1.902 ± 0.9786 0.014718	1.609 ± 1.2625 0.21053	1.039 ± 0.5423 0.89171	0.74 ± 0.4078 0.28594	TGCCATATTGACCCCTATAGAAATTGGATATTGCTAAATCAAGCT
plasmid_cp32-7	18500	BB_O29		2.544 ± 1.3023 0.118258	1.527 ± 1.268 0.48723	0.864 ± 0.5013 0.62734	0.899 ± 0.3631 0.50875	TAGAAATTGGATATTGCTCAATACAGCTCAAATTGTGTTTAA
plasmid_cp32-7	18523	BB_O29		2.732 ± 1.2502 0.061715	1.624 ± 1.3139 0.30646	1.055 ± 0.3677 0.45497	1.081 ± 0.315 0.51607	TCAAGCTCAAATTGTGTTTAAATACATTTTAATTCTCAACTATT
plasmid_cp32-7	18682	BB_O29		2.646 ± 0.9201 0.05642	1.454 ± 0.4297 0.10671	1.058 ± 0.3413 0.10042	1.182 ± 0.2955 0.27702	TCAAGCAAAATAAGCTTCAAGAAAAGATGAAAACCCAAAAATGA
plasmid_cp32-7	18767	BB_O29		1.030 ± 0.4473 0.091393	0.755 ± 0.6441 0.68071	0.85 ± 0.3805 0.66848	0.959 ± 0.491 0.9038	GCAAAAACATTTTGCCAACCTTTTACAAAATTGTAACAGAAAAG
plasmid_cp32-7	22158	BB_O34	<i>bdrM</i>	2.029 ± 0.9883 0.047874	1.195 ± 0.6955 0.64512	1.081 ± 0.5234 0.06964	0.829 ± 0.4163 0.67973	GTGAGGAGGCAATAGTTGTTTCTCATATGATAATTCAATTCTG
plasmid_cp32-7	22274	BB_O34	<i>bdrM</i>	1.245 ± 0.7606 0.564871	1.021 ± 0.6068 0.96709	0.546 ± 0.2604 0.0377	0.823 ± 0.2929 0.0356	TATCTAAATTAGATATCTTCTCAAATTCTTCTAAATCGATTATT
plasmid_cp32-7	22527	BB_O34	<i>bdrM</i>	1.782 ± 1.485 0.263144	2.028 ± 1.9986 0.37129	1.048 ± 1.1376 0.92018	0.94 ± 0.9361 0.91368	GTCTAGATAATAAAAGATGTTTAAATGAACTTAATGCAAGCAATA
plasmid_cp32-7	22953	IG_191		1.678 ± 1.069 0.068337	1.774 ± 0.26021 0.38719	0.997 ± 0.7036 0.98837	1.08 ± 0.7847 0.67961	TGTTGATAGCTAATAAGTATTTGCTATCAAAATACTCAATTAGT
plasmid_cp32-7	23096	BB_O36	<i>bppA</i>	1.038 ± 0.1651 0.688998	0.694 ± 0.5723 0.47359	0.942 ± 0.2654 0.70983	1.088 ± 0.5877 0.82717	GCAAAAACATTTTGCCAACCTTTTACAAAATTGTAACAGAAAAG
plasmid_cp32-7	23113	BB_O36	<i>bppA</i>	2.371 ± 1.0673 0.096309	1.458 ± 0.4986 0.00666	0.891 ± 0.4465 0.49093	1.191 ± 0.449 0.61844	ATAAAATATAAGTATAGCAAAACACTTTGCAAACCTTTTACAAA
plasmid_cp32-7	23124	BB_O36	<i>bppA</i>	1.706 ± 0.8222 0.220203	1.681 ± 1.8722 0.56183	1.1 ± 0.5413 0.74254	0.999 ± 0.3411 0.99109	GGAGTAAAAGATGGAAAATCTTCAAACAAATAATCCACAGAAAATA

plasmid_cp32-7	23160	BB_O36	<i>bppA</i>	1.480 ± 1.6339 0.447649	0.848 ± 0.7668 0.84078	0.987 ± 0.552 0.97485	2.186 ± 1.3427 0.00604	ATCCACAAGAAAATATTCAAGGAGAGCTAAATGATAAGTATTAATCAAC
plasmid_cp32-7	23493	BB_O36	<i>bppA</i>	1.257 ± 1.2412 0.702766	0.513 ± 0.4387 0.281	0.552 ± 0.6619 0.15831	0.447 ± 0.3076 0.23759	TGCTCAAGGGCAAAGAGTTAGAGAATTAGGATTAGAGA
plasmid_cp32-7	23673	BB_O36	<i>bppA</i>	1.990 ± 1.8813 0.253735	1.006 ± 0.7681 0.96117	0.886 ± 0.7612 0.81406	0.953 ± 0.606 0.91317	TTAATAAACCGCCATCAATTGTTGAGGCCACTAAAGTTCTGAACTGCC
plasmid_cp32-7	23727	BB_O36	<i>bppA</i>	2.288 ± 0.9411 0.018957	1.086 ± 0.8276 0.7107	0.76 ± 0.3537 0.55009	1.018 ± 0.4947 0.89451	TGAGTAGTGTCTATTGCTGAGTACAATAAAAATGGCAATTNTAAAGCAGTA
plasmid_cp32-7	23861	BB_O36	<i>bppA</i>	3.333 ± 2.2928 0.079521	2.256 ± 2.5815 0.37276	0.971 ± 0.544 0.85981	1.157 ± 0.7995 0.47052	GATGCTGCACCAATTAACTGTAAAGATTAAGAGATGAGGCTTAATATCA
plasmid_cp32-7	23906	BB_O36	<i>bppA</i>	1.429 ± 0.9347 0.529947	1.923 ± 1.2369 0.32998	1.174 ± 0.8964 0.77113	0.623 ± 0.1745 0.13943	ATATCAAAGTGTGAATTGTTAATAATGTGAATTGAAATTATAAAT
plasmid_cp32-7	23967	BB_O36	<i>bppA</i>	1.720 ± 0.4141 0.048514	1.523 ± 1.3253 0.54252	0.941 ± 0.1353 0.50274	0.982 ± 0.3154 0.88144	TCTTTTTCAAAATTATAATTCTAATTCAACATTATAACAAATTCAAAC
plasmid_cp32-7	23971	BB_O36	<i>bppA</i>	1.478 ± 0.6648 0.293366	1.061 ± 1.5941 0.95621	0.397 ± 0.3448 0.027	0.522 ± 0.5531 0.38142	AATATCTTTTCAAAATTATAATTCTAATTCAACATTATAACAAATT
plasmid_cp32-7	23976	BB_O36	<i>bppA</i>	1.449 ± 0.4712 0.187614	0.919 ± 0.3545 0.76145	0.807 ± 0.4062 0.17865	0.798 ± 0.2827 0.1827	GTAACTATAGAGAGGAACTTAATGGCACATAATTAAACGAGGATACGT
plasmid_cp32-7	23979	BB_O36	<i>bppA</i>	2.074 ± 1.5138 0.103799	1.893 ± 1.8175 0.28935	1.055 ± 0.6055 0.70752	1.103 ± 0.6244 0.55274	ACTATAGAGAGGAACTTAATGGCACATAATTAAACGAGGATACGTTA
plasmid_cp32-7	24110	BB_O36	<i>bppA</i>	0.941 ± 0.3715 0.789062	1.787 ± 1.4374 0.3578	0.648 ± 0.6153 0.32511	0.721 ± 0.3845 0.09745	GAATATGTTGATTGTGAGACCTTGAAATTAAAGGATAATCAATCTGCTAA
plasmid_cp32-7	24209	BB_O36	<i>bppA</i>	2.661 ± 1.9228 0.083211	2.473 ± 1.4729 0.00901	0.937 ± 0.8851 0.58625	1.189 ± 0.9314 0.80986	AATAAGATCCAACGAAACGAAATAAAAAGAGAAAAGCCCATTAAAGATAGG
plasmid_cp32-7	24282	BB_O36	<i>bppA</i>	2.422 ± 1.6374 0.078447	1.57 ± 1.543 0.40265	0.932 ± 0.4836 0.70197	0.78 ± 0.4766 0.16613	ATATTGTAATTAGCATCTTCACCTATCTTAAATGGGTTCTCTTTT
plasmid_cp32-7	24292	BB_O36	<i>bppA</i>	1.913 ± 1.6573 0.325565	1.862 ± 1.3189 0.21468	1.035 ± 0.6849 0.94819	1.652 ± 0.8177 0.05228	TGTTTTGTAATTGTAAATTAGCATCTTCACCTATCTTAATGGGCTT
plasmid_cp32-7	24318	BB_O36	<i>bppA</i>	4.600 ± 5.1214 0.24928	3.96 ± 4.6518 0.30036	1.592 ± 2.6814 0.75835	3.225 ± 3.8108 0.329	TAATTAGCTCTCAATTAGTGGATATGTATTGTAATTTGAAATTAGC
plasmid_cp32-7	24386	BB_O36	<i>bppA</i>	2.784 ± 1.6738 0.170946	2.059 ± 1.4203 0.27518	0.954 ± 0.5989 0.87308	1 ± 0.1952 0.99983	GTCCCTTCAATCTATCTGATATTGCCCTTCTTAGGGTCAAGAGTAAACA
plasmid_cp32-7	24389	BB_O36	<i>bppA</i>	3.847 ± 4.8604 0.358124	3.443 ± 4.4642 0.36946	1.313 ± 1.3983 0.69414	1.324 ± 1.9769 0.78834	GTAGCCCTTCAATCTATCTGATATTGCCCTTCTTAGGGTCAAGAGTAA
plasmid_cp32-7	24500	IG_192		2.014 ± 0.6619 0.132723	2.082 ± 0.4066 0.00667	0.776 ± 0.8387 0.62936	1.758 ± 0.3478 0.0234	GGAGGATTAAATTATGCTTATAAATAAAAACAGATAATAGAACTTT
plasmid_cp32-7	24601	BB_O37	<i>bppB</i>	2.415 ± 0.965 0.075875	1.337 ± 0.9996 0.55205	1.297 ± 0.4987 0.34143	1.204 ± 0.4512 0.41892	TAATAATGTAGACACAAAAGTAACACCCCCATTTTGTACTCCGGCTT
plasmid_cp32-7	24840	BB_O37	<i>bppB</i>	0.842 ± 0.3324 0.434243	0.673 ± 0.5913 0.48966	1.065 ± 0.402 0.71279	1.032 ± 0.5958 0.92533	GCAACAAAAATAAAGAAATTATGATTCACTTACTTGAAGCCTCGT
plasmid_cp32-7	24922	BB_O37	<i>bppB</i>	1.809 ± 1.2968 0.267689	1.43 ± 1.3699 0.67883	1.013 ± 0.6716 0.97882	1.135 ± 1.1887 0.69305	TATTTAGACTAAAGTAGTTTTAAAGGTTAAAGGTTATTCTCATGCTT
plasmid_cp32-7	25007	BB_O38	<i>bppC</i>	1.739 ± 0.7472 0.014816	1.27 ± 0.9153 0.43223	0.94 ± 0.4997 0.87574	1.134 ± 0.4688 0.31165	TGGACTCTCTGCTGCAACAAATTACGCTTATAATGCTGAAAATAA
plasmid_cp32-7	25014	BB_O38	<i>bppC</i>	1.893 ± 0.5169 0.055262	1.483 ± 1.1082 0.43591	0.94 ± 0.2837 0.00319	1.215 ± 0.4225 0.30683	TTATCAATTCTGGTTGAATGATATTCTATAAAGTTCTTAATCTGGAAA
plasmid_cp32-7	25068	BB_O38	<i>bppC</i>	1.473 ± 0.7274 0.120693	1.238 ± 0.8577 0.53019	0.684 ± 0.2795 0.23017	0.88 ± 0.3404 0.6299	ACTTTCCAGATTAAAGAACCTATGAAATATCATTCAACCAATGAAATTG
plasmid_cp32-7	25110	BB_O38	<i>bppC</i>	2.270 ± 1.3117 0.05731	3.543 ± 4.1671 0.29983	1.463 ± 1.4883 0.50852	2.097 ± 1.1984 0.08878	AATAAAATGAAGAGATTATTAGCACGAAAGCCTGATTTTAAAGAAGAATT
plasmid_cp32-7	25111	BB_O38	<i>bppC</i>	2.009 ± 2.0554 0.395898	2.327 ± 2.8433 0.43078	0.98 ± 0.5845 0.93813	0.957 ± 0.7113 0.88217	TTTAGAAATTATTATTCTAAATTAACTTAATGGCTATACTCTTC
plasmid_cp32-7	25707	BB_O38	<i>bppC</i>	2.352 ± 1.132 0.03645	2.181 ± 1.4489 0.22564	1.48 ± 1.1839 0.4852	1.581 ± 1.0906 0.19013	ATTATTTAATTAAATAATTCAATATGGATTTTATGCTCAACTATTTC
plasmid_cp32-7	25713	BB_O38	<i>bppC</i>	1.927 ± 1.2198 0.005251	1.656 ± 1.6078 0.26587	0.88 ± 0.5852 0.57375	1.293 ± 0.8994 0.26323	ATATCCATAAACTCTCTTCTTGAAGTGTACTTTAAATTAGAAAG
plasmid_cp32-7	26862	IG_193		1.380 ± 1.0188 0.65608	2.288 ± 2.5294 0.46271	0.215 ± 0.2949 0.05503	0.512 ± 0.5462 0.44774	GAAATTCACAAACAAAGGAGAAAACAAAAGTATGAATAAAAATATTGAT
plasmid_cp32-7	27142	BB_O40	<i>erpM</i>	1.432 ± 0.3386 0.104952	1.344 ± 1.2675 0.7101	0.78 ± 0.3021 0.27027	0.676 ± 0.1736 0.20754	TTGCTCTGTTATTAGGATCATGCCCTGCTTAATTCTTCATCTT
plasmid_cp32-7	27664	BB_O40	<i>erpM</i>	1.661 ± 1.5516 0.238581	3.013 ± 3.2055 0.10604	1.011 ± 0.8348 0.98447	1.103 ± 1.3603 0.92543	TATGATGTTTACTGATGGGAAATAAGCTATACAAAACGGTGGGAGAT
plasmid_cp32-7	28011	BB_O41		1.944 ± 1.0337 0.092255	2.016 ± 1.4176 0.19656	0.814 ± 0.2985 0.36989	1.348 ± 0.5168 0.34977	AAATTAGTTGATATTAAAGGTTTATCAATATGAATTACTATCTCAAT
plasmid_cp32-7	28408	BB_O42		2.036 ± 0.7542 0.057901	1.825 ± 1.4438 0.36693	0.863 ± 0.5068 0.49548	1.123 ± 0.418 0.33034	AGCATATAATAGAAAAGTATAAAAATTCTACAAATAGGAAGTTGATTGA
plasmid_cp32-7	29138	BB_O43		1.961 ± 1.7271 0.105633	1.879 ± 2.1654 0.32639	0.918 ± 0.6795 0.7274	1.001 ± 0.7537 0.99327	TCTAATTCACTTAACTTCTAGCGTTAACCTCTGATTAAAGTTGTTG
plasmid_cp32-7	29435	BB_O43		1.093 ± 0.4407 0.381313	0.443 ± 0.3171 0.2012	0.863 ± 0.2552 0.09924	0.928 ± 0.3149 0.00354	CTATTCTTGTAGTGTCTTCTGCTTACGCTTATTAGCTGTTAAAGTTT
plasmid_cp32-7	29457	BB_O44		1.941 ± 0.7235 0.046253	2.121 ± 1.4284 0.22737	0.927 ± 0.3222 0.050857	1.074 ± 0.3716 0.38736	TATCAAACAAAATTCTTACACACTACAAAAGGAATACAAAATAAT
plasmid_cp32-7	29532	BB_O44		1.536 ± 0.8311 0.077451	0.766 ± 0.73 0.12161	0.559 ± 0.4012 0.36106	0.721 ± 0.4709 0.17399	AAGCTAACAAATTCTCAATTATTTGATAAGTTGAAGAAGACGCTA
plasmid_cp32-7	29589	BB_O44		2.436 ± 1.8543 0.071507	2.074 ± 2.6417 0.40973	1.047 ± 0.6984 0.91697	1.09 ± 0.6403 0.80387	AAACAAAAAAATGTGATAAAAAGCATTTAAAAGAATAATGAAAGAAGATT
plasmid_cp32-7	29623	BB_O44		1.741 ± 2.1129 0.372187	1.954 ± 2.6099 0.4149	0.528 ± 0.3996 0.2893	0.608 ± 0.6462 0.05321	TTCTTTTAATGCTTTTATCATTCTTAACTTCTTAAAGTTGCTGTTCT
plasmid_cp32-7	29640	BB_O44		1.950 ± 0.855 0.11551	0.906 ± 1.027 0.862	1.202 ± 1.1062 0.71896	1.11 ± 0.8994 0.76236	TAATCTCTTCTTCAATTCTTAAAGCTTATCACATTCTTGT
plasmid_cp32-7	29932	BB_O44		1.034 ± 0.455 0.421904	0.48 ± 0.3701 0.28398	0.953 ± 0.4189 0.4331	0.989 ± 0.37 0.82126	CTTCCCCAAATCTTCAAAACTCTGCTTATCTCCACCATATAGATTA
plasmid_cp32-7	30062	BB_O44		1.458 ± 2.0056 0.402521	1.386 ± 1.319 0.31887	0.753 ± 0.7025 0.5328	0.576 ± 0.5882 0.30111	GTGTCGGATGATGGGGTTAGTACAAAATAATAGTTCTGCCACA
plasmid_cp32-7	30283	BB_O44		2.201 ± 0.6594 0.102887	1.771 ± 1.9421 0.58273	1.063 ± 0.792 0.88391	1.404 ± 0.727 0.48897	GCCCAGATAGCATATTAGACCCAGCATTTAGTGTGGAGGGGATAACCTG
plasmid_cp32-7	30339	BB_O44		3.442 ± 2.3676 0.212121	1.786 ± 0.9971 0.28748	1.687 ± 0.166 0.00647	2.595 ± 0.3155 0.17076	TGTGTTAGGAGCGAGTGTGATGATAAGTATTGCTTTGTTACAGAC
plasmid_cp32-7	30673	BB_O44		0.332 ± 0.3408 0.250791	0.29 ± 0.2739 0.23311	0.55 ± 0.4271 0.271	0.348 ± 0.4679 0.17572	TTTATCGTATAAGGAGATAACAAAACCATGATGATGCTTGTGAA
plasmid_cp32-8	96	BB_L01		2.321 ± 1.0994 0.054683	1.575 ± 1.2925 0.38674	0.993 ± 0.3533 0.93772	1.11 ± 0.4837 0.23536	GATAAAATAAGTCACTAGAACTATACAAATACTCAATTTTTAGAAAT
plasmid_cp32-8	274	BB_L01		0.824 ± 0.7734 0.641957	0.867 ± 1.0196 0.86692	1.74 ± 1.4363 0.47675	0.623 ± 0.6437 0.4208	ATACAATTAGCAGAGCATTTAACGCTTACCTTAACCTAGCAAGTCA
plasmid_cp32-8	279	BB_L01		1.866 ± 0.8098 0.07712	1.869 ± 1.6323 0.34196	0.944 ± 0.3279 0.69611	1.135 ± 0.5438 0.31412	AGCTACCCTTCATGGGATGGCTATGTTAGAAAAACCAAGATACC
plasmid_cp32-8	333	BB_L01		2.979 ± 1.2954 0.008456	1.226 ± 0.9175 0.71119	0.461 ± 0.4529 0.3753	0.582 ± 0.5334 0.47078	ATAGATCTGAAACACCCGTTAATAGAATTACCTATTGGTTGAATAC

plasmid_cp32-8	395	BB_L01	1.731 ± 0.2909 0.015623	1.412 ± 0.7606 0.43504	1.053 ± 0.1634 0.03457	0.924 ± 0.171 0.21421	TTCATAATCAAGGTATTCAAAACCAATAGGTATTCTATTAACGGGTTG
plasmid_cp32-8	398	BB_L01	1.774 ± 0.5458 0.022984	1.495 ± 0.8404 0.34788	0.685 ± 0.2415 0.01611	0.989 ± 0.2571 0.93409	TGTAAGAGATTGGGAGTTGATTGATCATATAACCTATAAAGTAAAATC
plasmid_cp32-8	399	BB_L01	1.258 ± 0.369 0.336319	0.57 ± 0.4082 0.18297	1.09 ± 0.2371 0.55322	1.145 ± 0.339 0.51841	CATATTCTAAATCAAGGTATTCAAACCAATAGGTATTCTTATTAACCG
plasmid_cp32-8	427	BB_L01	3.354 ± 3.9966 0.401016	1.261 ± 1.346 0.77742	2.111 ± 0.7495 0.07795	2.063 ± 1.8242 0.41844	TGATCAAAATCACTCCCAAATCTCTTACATATTCTAAATCAAGGTATTCA
plasmid_cp32-8	432	BB_L01	1.243 ± 1.4319 0.611091	1.75 ± 1.5577 0.25749	0.402 ± 0.3193 0.08436	0.463 ± 0.6155 0.13435	ACCTATAAGTAAAATCCAACAATAAGAACAAATTCTTAGACGCAGTTAA
plasmid_cp32-8	444	BB_L01	2.009 ± 1.2408 0.290683	1.541 ± 0.6316 0.07078	1.193 ± 0.5201 0.52085	0.809 ± 0.3279 0.53202	AAATCCAACAATAAGAACAACTTCTTAGACGCAGTTAAATACATAAAAGT
plasmid_cp32-8	478	BB_L01	2.177 ± 1.7175 0.243426	1.266 ± 1.1539 0.74736	0.665 ± 0.2876 0.33484	1.461 ± 0.5527 0.08559	ACTCGCTCTAAAGAATTGTTCTATTGTTGATTACTTTAGGTTATA
plasmid_cp32-8	490	BB_L01	2.693 ± 1.2086 0.146663	1.54 ± 2.3436 0.73529	0.454 ± 0.251 0.15435	1.078 ± 0.4605 0.84628	AAAGTCGACTTATCATATATGAAAACATTGATTATCTAAAAAGATATG
plasmid_cp32-8	504	BB_L01	0.556 ± 0.3781 0.138187	0.327 ± 0.216 0.0395	0.764 ± 0.4867 0.40807	0.354 ± 0.3141 0.22148	TGATAAGTCGACTTTATGTATTAACTGCGCTAAAGAATTGTTCTAT
plasmid_cp32-8	506	BB_L01	3.459 ± 2.5074 0.034033	2.087 ± 2.4884 0.34816	1.134 ± 0.7023 0.7769	1.244 ± 0.8777 0.2233	TATGATAAGTCGACTTTATGTATTAACTGCGCTAAAGAATTGTTCTT
plasmid_cp32-8	507	BB_L01	1.444 ± 1.0689 0.30772	1.392 ± 1.25 0.41664	1.066 ± 0.818 0.83294	1.303 ± 1.0652 0.45856	TATGAAAACTTGATTATACTTTAAAAGATATGTTCCGTGTTACCGAA
plasmid_cp32-8	521	BB_L01	2.125 ± 0.8452 0.075966	1.192 ± 0.6524 0.73271	0.979 ± 0.4124 0.9157	1.132 ± 0.4489 0.67731	ATCAAAAGTTTCATATGATAGTCGACTTTATGTATTAACTGCGTC
plasmid_cp32-8	524	BB_L01	1.952 ± 0.3438 0.040761	1.254 ± 0.7914 0.63563	1.363 ± 0.2121 0.01232	1.855 ± 1.0007 0.22175	TATCTAAAAGATAGTTCCTGTTACCGAAAGCTTTACTAGATAT
plasmid_cp32-8	526	BB_L01	1.026 ± 0.7511 0.908095	0.131 ± 0.1434 0.07004	0.616 ± 0.9321 0.37572	1.466 ± 0.8075 0.39905	TCTTAAAAGATAGTTCCTGTTACCGAAAGCTTTACTAGATATT
plasmid_cp32-8	578	BB_L01	2.531 ± 1.3542 0.070257	2.52 ± 2.1761 0.25992	0.714 ± 0.3684 0.21953	1.375 ± 0.7421 0.1758	TTTATTGAAAAGATATACCTAGAAATAGAAAAGCGTATTGAAAACCACAA
plasmid_cp32-8	744	BB_L01	1.886 ± 0.7223 0.12099	1.983 ± 1.5906 0.36844	0.978 ± 0.2182 0.91123	1.121 ± 0.218 0.00087	TCTTCTTTTGAGAAAACAAATTCAAACATAGTAAAGATATTCT
plasmid_cp32-8	1039	BB_L01	0.874 ± 0.5228 0.670779	0.779 ± 0.4553 0.62981	0.269 ± 0.1794 0.11879	0.345 ± 0.3548 0.2382	TCACCTTACCATCATTCCTAGTCCTTAGCCTGCTCATAAACCTCTG
plasmid_cp32-8	1042	BB_L01	3.983 ± 3.1022 0.065092	2.941 ± 4.4439 0.40865	0.871 ± 0.6276 0.76688	1.021 ± 0.8598 0.97655	GGAGTAATTATTACGATTTCCTCAAAGGTGTAAGAACAACTGAGACT
plasmid_cp32-8	1214	BB_L01	1.529 ± 1.0012 0.192184	1.898 ± 2.3946 0.41608	1.061 ± 1.009 0.70159	0.963 ± 0.9029 0.82169	TAACAGCTTACACAAAGTAGCTATTAAATATGAGGAGCTAGCGATGTT
plasmid_cp32-8	1626	BB_L02	2.305 ± 1.306 0.241101	1.25 ± 1.1645 0.71307	0.571 ± 0.2889 0.07514	0.904 ± 1.3094 0.9242	TCCCTTGCAGTACGACCTCTTGTAAAATGATTGCTAAGATGTTCTT
plasmid_cp32-8	1631	BB_L02	0.995 ± 1.138 0.99211	0.985 ± 1.0603 0.96673	1.023 ± 0.8489 0.92537	0.999 ± 0.8531 0.99404	CATAAAAGACATTGCAAGCACACGTAGAGAACCTGTACGCAAGTTCG
plasmid_cp32-8	1636	BB_L02	2.449 ± 1.7397 0.173578	1.211 ± 2.6358 0.51335	0.791 ± 0.6103 0.7036	1.004 ± 0.7513 0.98954	AAAGACATTATGCAAGCACACGTAGAGAACCTGTACGCAAGTTCGTTCCA
plasmid_cp32-8	1747	BB_L02	1.498 ± 0.8228 0.127346	0.375 ± 0.2836 0.20461	0.929 ± 0.7317 0.75297	1.237 ± 0.7875 0.50313	TTAGAGCAACTGTTCTTAGCAAAGTAGAATATTAAATTAGAAAAGAAAAAT
plasmid_cp32-8	1928	BB_L02	1.498 ± 0.6306 0.29279	1.15 ± 0.2003 0.34661	0.669 ± 0.2495 0.127	0.546 ± 0.4492 0.21909	TTACTTATCGCTGTACAAATTCTGTGAAATTAACTGGTACAAAATTAGAA
plasmid_cp32-8	1931	BB_L02	2.224 ± 1.526 0.07095	1.451 ± 1.3456 0.34177	1.28 ± 0.6971 0.27242	0.945 ± 0.5339 0.78542	CATACAAGCAAAGCGAATTCAATTTTGAAAATCTAAAAGACATAAAA
plasmid_cp32-8	2216	BB_L03	1.639 ± 0.8869 0.257919	1.037 ± 0.7328 0.94208	0.676 ± 0.5043 0.39249	0.775 ± 0.4821 0.34387	TACGGATACCCCTTAGCAGGGTAATTCTCTATTGTCTTAGCTAGTG
plasmid_cp32-8	2231	BB_L03	1.609 ± 1.0994 0.210506	1.727 ± 1.2233 0.26648	1.333 ± 0.9368 0.5349	1.215 ± 0.5338 0.54219	AGCTTAGTTTGAGATGGAACAAACCGAACAGTAGAATTGAGGCTGGTGG
plasmid_cp32-8	2341	BB_L03	2.051 ± 1.0791 0.2103	1.468 ± 0.1012 0.48474	0.926 ± 0.4887 0.78411	0.858 ± 0.2155 0.20914	TAACAGTTCGCCATACCGCTAACACTCATATCGGAACACACTCCATATA
plasmid_cp32-8	2698	BB_L04	0.400 ± 0.3495 0.224086	0.349 ± 0.555 0.23756	0.74 ± 0.2943 0.38178	0.476 ± 0.377 0.00919	CGTCCTCAGCTTGTCTTGCCTGCTAGCTTAGGAGCAGCGGAAACTT
plasmid_cp32-8	2993	BB_L04	1.028 ± 0.692 0.914354	0.755 ± 0.7024 0.73351	1.29 ± 0.8928 0.19648	1.317 ± 1.0137 0.07769	TCAGTATGCTCCTAACATCATATAGAGTTCTTTGGAAACAGT
plasmid_cp32-8	3004	BB_L04	2.410 ± 1.2925 0.096309	1.414 ± 1.4532 0.62095	0.767 ± 0.3976 0.0542	1.067 ± 0.7405 0.90262	TCCCACATACATGCTAACATTAACATATAGAGTTCTT
plasmid_cp32-8	3203	BB_L04	1.827 ± 0.7526 0.040686	1.721 ± 1.2206 0.28307	1.081 ± 0.5251 0.51947	1.419 ± 0.4984 0.11882	CAATCAATTGGCACCCGAAGATGGAACATAGCTAAAGATAGATCTCA
plasmid_cp32-8	3249	BB_L04	0.102 ± 0.1794 0.074225	0.33 ± 0.5252 0.182	0.275 ± 0.3209 0.12329	0.347 ± 0.4222 0.17455	TCCTAGGCAAGAGTATTCTATTAAATTGATAAAAGTTGCAATTGTTGAAA
plasmid_cp32-8	3376	BB_L05	4.180 ± 2.8506 0.072454	2.451 ± 2.0423 0.17063	1.163 ± 0.7616 0.32117	1.353 ± 0.9844 0.35724	TCTCCCATTTTACCTCTTATTGCCCAAAGTTAACCCACATCG
plasmid_cp32-8	3393	BB_L05	2.510 ± 1.9165 0.315743	2.171 ± 2.5598 0.43195	1.404 ± 0.5821 0.07674	1.741 ± 1.0904 0.36728	AAAGAGTATCAAGAGAAAAGAGAACCTGGAAAAGTTGAAAATCCC
plasmid_cp32-8	3668	BB_L05	2.177 ± 2.1573 0.317354	1.882 ± 2.4068 0.45564	0.543 ± 0.4424 0.40579	1.12 ± 0.7906 0.85524	TGGAATATGCTTACATAGTGGATTTAGTGGAAAACAGCTACTTGTGCC
plasmid_cp32-8	3694	BB_L05	1.730 ± 0.5709 0.143306	1.88 ± 1.6022 0.41942	0.88 ± 0.2089 0.09013	1.153 ± 0.3921 0.26607	AACACTCATATGCTAACATTCATATAAGTCTTACCCATACCAGCC
plasmid_cp32-8	3727	BB_L05	2.862 ± 1.6353 0.164144	2.116 ± 1.8237 0.43693	1.61 ± 1.3411 0.55936	1.416 ± 0.749 0.02255	TTGGTAATTGGCACAAATAGTAGCTTACTAAACTCATCTGTAATG
plasmid_cp32-8	3796	BB_L05	1.726 ± 1.1742 0.138387	2.015 ± 1.7257 0.13835	1.037 ± 0.7269 0.91454	1.697 ± 1.382 0.18031	AAAGCGGTCTTGTGAAAGGGTACTGGAGCAGCAAAATAGCAATT
plasmid_cp32-8	4067	BB_L06	1.600 ± 0.5938 0.12024	0.876 ± 0.2676 0.13033	0.773 ± 0.1393 0.16263	0.988 ± 0.1675 0.88817	AGATGTTGATCTACAAATGGGATATCAAAACCGTAAATGGGACCGT
plasmid_cp32-8	4222	BB_L06	2.510 ± 1.5204 0.142759	2.481 ± 2.1822 0.30112	0.868 ± 0.4358 0.31854	1.113 ± 0.6472 0.56808	AATTAGCAGTAAAGCAGACTTGTGAGAAATTTTACTTCAGATTCT
plasmid_cp32-8	4489	BB_L06	2.297 ± 1.7884 0.212385	1.877 ± 2.4674 0.52393	0.82 ± 0.6401 0.46039	1.139 ± 0.5904 0.37318	AAATGGATAAAATCTTGAAGAGATTGAGGCTGGACTTCAAAGTAAAC
plasmid_cp32-8	4678	BB_L06	1.959 ± 1.149 0.111318	0.324 ± 0.1307 0.10012	0.433 ± 0.1807 0.11067	0.675 ± 0.4823 0.06387	AGGCTTAAATAATAGAGAACAGTAGTTACATTGAAACTTGTGCTGA
plasmid_cp32-8	4789	BB_L06	2.250 ± 1.0413 0.1203	1.224 ± 0.7348 0.69937	0.981 ± 0.5128 0.96256	1.059 ± 0.4697 0.78739	TACTTGCTAGGTTAAATTATAAGTTCAGAACATTAGTGGATAATGAGT
plasmid_cp32-8	5093	BB_L07	1.295 ± 0.4026 0.399042	1.324 ± 1.6053 0.76807	0.8 ± 0.4146 0.57973	0.772 ± 0.339 0.45252	GCTTGAAGTAAAGGATAATGAAGTAGAAAATTGCTGCTTAGTGC
plasmid_cp32-8	5259	BB_L07	1.108 ± 0.7718 0.849363	1.497 ± 1.1928 0.40219	0.501 ± 0.2902 0.26577	0.653 ± 0.4799 0.55955	TTATCCCTAGTAGGGAGGGAGAGAACGGCGGAGGGGAGTTGTTGCC
plasmid_cp32-8	5566	BB_L08	1.605 ± 0.6492 0.064241	1.593 ± 1.5768 0.50773	0.826 ± 0.2878 0.09832	1.132 ± 0.5279 0.39985	TTATTGACATAAGGCCACAAAGAACCTGCAATTCTTATGATTGATATG
plasmid_cp32-8	5633	BB_L08	0.433 ± 0.1944 0.118028	0.428 ± 0.3908 0.22418	1.184 ± 0.4044 0.06844	1.048 ± 0.3894 0.46924	TTCCAAACTTACACATATCAAGAACCTTAACATGAAACCAAAAGACCGAAT
plasmid_cp32-8	5648	BB_L08	4.295 ± 2.7306 0.110222	0.822 ± 0.5553 0.58807	1.214 ± 0.662 0.15603	1.323 ± 0.8142 0.48237	TGTGAAAGTTGGAATATCCTTGAATATCAGACATATCAGAACATAAAG

plasmid_cp32-8	5917	BB_L09	2.704 ± 0.836 0.041662	1.384 ± 0.7755 0.46957	0.985 ± 0.2302 0.90407	1.116 ± 0.2817 0.53976	TATCAATAATAGCTATATAATTCTAAGTTAACCTTACCGGAAATCGGG
plasmid_cp32-8	5928	BB_L09	2.936 ± 1.8381 0.109398	2.787 ± 2.5703 0.26985	1.337 ± 0.9727 0.41535	2.467 ± 1.5763 0.18607	GCTATATAAACTCTAAGTTAACCTTACGGGAATGGAGGGTA
plasmid_cp32-8	6014	BB_L09	2.661 ± 1.3368 0.058942	1.679 ± 1.2374 0.28644	1.032 ± 0.3704 0.78236	1.29 ± 0.5541 0.13273	GATAATTTCATAGTATCTTATAAAAGCTTGTCCAATAGCCTCCATTCCCG
plasmid_cp32-8	6081	BB_L09	2.408 ± 1.0752 0.074975	0.976 ± 0.6056 0.85633	1.372 ± 0.8804 0.41117	0.991 ± 0.5537 0.98588	CTACCCCTTTAAACTTACTTTGATTGATTAGCCTTAAGGCTGGAGTG
plasmid_cp32-8	6139	BB_L09	2.048 ± 1.5004 0.314838	1.191 ± 1.175 0.81289	0.56 ± 0.2348 0.17781	0.759 ± 0.2475 0.2442	TAAGGTAACACTGAATGATTTCACTTAGATATGGTATAAATCATTTA
plasmid_cp32-8	6178	BB_L10	1.044 ± 0.4566 0.549023	0.448 ± 0.3827 0.27929	0.893 ± 0.4488 0.06914	1.007 ± 0.4729 0.91376	TTAACATTTAACCCAAATATTAAAGGGTTAACGGCATATGCACTGAA
plasmid_cp32-8	6254	BB_L10	1.687 ± 2.2547 0.536598	2.622 ± 1.4171 0.03922	1.186 ± 1.1386 0.83946	1.976 ± 1.2019 0.24517	TTTATGATATCGCACTCAAATTATTTCAAGTTGCATATGCCCTAACCC
plasmid_cp32-8	6307	BB_L10	2.064 ± 0.4086 0.034524	1.148 ± 0.3377 0.59691	0.866 ± 0.275 0.59551	0.958 ± 0.1726 0.72488	TTATATTGAGCTAGCAGCTGTGATTGTTGAAAGATATGGATGATTGAGG
plasmid_cp32-8	6372	BB_L10	2.524 ± 1.5377 0.058623	2.071 ± 2.2711 0.31285	0.711 ± 0.4507 0.36774	1.037 ± 0.7682 0.91913	TGAAAATGCTTGGAAATTAGTATAAATTTCAAATATATTATTGCAAT
plasmid_cp32-8	6421	BB_L10	1.255 ± 0.5973 0.296807	1.693 ± 1.2048 0.3437	0.202 ± 0.2059 0.02253	0.423 ± 0.1476 0.0286	TTGCAATAATATATATTGAAAATTACTAAATTCCAAAGCATTTCAT
plasmid_cp32-8	6473	BB_L10	1.918 ± 1.5728 0.255361	2.914 ± 2.358 0.20299	0.55 ± 0.6524 0.49136	0.777 ± 1.0377 0.77766	TAAAGCATTAACATGCGTGAATTAGGCTAAAGTCTTGGCCTTAACACT
plasmid_cp32-8	6496	BB_L10	0.733 ± 0.6602 0.322922	0.619 ± 0.5394 0.10482	0.872 ± 0.3419 0.15469	1.051 ± 0.4961 0.54408	CACAATAAAAGCTCATAAGTATAATTGCCAGTCTCACACCCGACTATT
plasmid_cp32-8	6545	BB_L10	2.131 ± 1.6187 0.125182	1.882 ± 1.8164 0.29915	0.902 ± 0.6105 0.33825	1.223 ± 0.6154 0.36031	TAAATAAAAATTAACCTCTACATTACCAACATCTAATATGCAAACAGCTG
plasmid_cp32-8	6822	BB_L11	1.272 ± 1.0585 0.42923	0.453 ± 0.5186 0.33152	1.17 ± 0.8782 0.51502	1.649 ± 1.3235 0.23479	CGACGATCTTATTAACTTGTGTTTAGCTTGTAAACAAAAGTGG
plasmid_cp32-8	7364	BB_L11	2.724 ± 0.9683 0.053977	2.014 ± 1.7425 0.37937	1.11 ± 0.4551 0.66492	1.196 ± 0.3246 0.49724	ATTGAAAAGTTGCGAACTGCAAAATCAACTTATTCACTTCTTAATGAA
plasmid_cp32-8	7728	BB_L11	2.504 ± 0.9742 0.062492	2.502 ± 1.2692 0.18306	1.685 ± 0.7261 0.1697	1.084 ± 0.5143 0.4139	ATATTCA CGCTAAGTCTAATTAAAGTTGTCGGCTAGGAGAAAAGAGTAAGC
plasmid_cp32-8	7737	BB_L11	0.984 ± 1.4289 0.98491	0.105 ± 0.1376 0.15298	0.708 ± 0.5705 0.32407	1.254 ± 0.9986 0.71301	ACTTTAGCATTAATGCTGTTGCTTGTAAATTACTACTCAAGATATAGTTG
plasmid_cp32-8	7969	BB_L12	2.045 ± 0.9472 0.118907	2.007 ± 1.8747 0.39427	1.121 ± 0.5103 0.63866	1.075 ± 0.4353 0.49239	AGAGATCCAAAACAATAACCTATGTTCAACATTGAAGT GACACTAGGT
plasmid_cp32-8	8141	BB_L12	2.712 ± 0.9152 0.027022	1.643 ± 1.7338 0.53188	1.171 ± 0.4362 0.60913	1.096 ± 0.3246 0.31409	GAAATAATTGTTGAGCAATTCTATGGAATGCTAAATCAAGCATT
plasmid_cp32-8	8219	BB_L12	1.917 ± 0.4945 0.068491	1.914 ± 1.5753 0.40612	0.595 ± 0.1379 0.61863	0.96 ± 0.1972 0.58476	GCCCTAATTCAAAGATACTTCCGGCCTCAGCAGAATAACTCTTGAA
plasmid_cp32-8	8270	IG_194	2.244 ± 2.0402 0.425559	0.814 ± 1.1995 0.85655	1.278 ± 1.1118 0.57919	0.866 ± 0.4043 0.50761	ATAAGAATCTCCTTTAAGAGTTGTTGGTTAGATTGCAATTATA
plasmid_cp32-8	8434	BB_L13	1.681 ± 0.623 0.240125	1.898 ± 1.5047 0.44265	1.432 ± 0.8888 0.52698	0.652 ± 0.3042 0.30657	AGCTGTGATTCTCTTAAGTATTAACCTCATTAGCTTAAACAGCGT
plasmid_cp32-8	8575	BB_L13	3.058 ± 1.8407 0.202016	1.469 ± 0.6561 0.30956	1.542 ± 0.7541 0.17396	1.417 ± 0.6396 0.2472	AAAAGCCCTTTAGTATTTGAGTGAAGTATGAAAATAATGTTGTGAT
plasmid_cp32-8	8645	BB_L13	1.969 ± 0.5814 0.041463	1.178 ± 0.7338 0.64293	0.937 ± 0.502 0.80429	1.156 ± 0.4603 0.62291	TTAATGAAAATTGATTATGAAAAGTAGGCCACTTCACCTTCAAGTA
plasmid_cp32-8	8746	BB_L14	1.861 ± 0.6164 0.006025	1.715 ± 1.2193 0.2715	1.4 ± 0.5703 0.27799	1.224 ± 0.4426 0.02699	TTGATAAAAGCTATTGCAAGTCTGATGAGACTAGAAAAAAATTTTA
plasmid_cp32-8	8934	BB_L14	1.189 ± 0.6466 0.739752	0.551 ± 0.2795 0.12623	0.718 ± 0.636 0.32542	0.531 ± 0.5791 0.27654	TTGTATGAAATTAAATTGAAAGCACTGAGGACTTAGTGAGCGACAAATT
plasmid_cp32-8	8965	IG_195	2.687 ± 0.6394 0.024885	1.244 ± 0.5152 0.41395	1.53 ± 0.4958 0.15947	1.319 ± 0.9793 0.66526	AGTCCTCACTGCTTAAATTCAATTGATGCTTCTAATTAAATC
plasmid_cp32-8	8968	BB_L15	2.233 ± 0.7826 0.049005	1.684 ± 0.8626 0.2946	1.17 ± 0.2878 0.40243	1.121 ± 0.3407 0.59222	GTGAGCGACAAATTCCACCAATTAAAGGTATTGATCATGCTGCA
plasmid_cp32-8	9140	BB_L15	2.490 ± 1.9981 0.30603	1.841 ± 2.2078 0.55171	0.411 ± 0.4438 0.10778	0.781 ± 0.328 0.4906	AGTTCTTTCTGTGCGACAAATTATTGAAATTCTTGTGCTA
plasmid_cp32-8	9419	BB_L15	2.308 ± 1.9141 0.384553	2.207 ± 1.9114 0.34923	0.485 ± 0.5548 0.15778	0.158 ± 0.2743 0.03176	CGCTGCTAATGATATTCCCTAGGGCACTTACCTATAGCAATTGGCAAC
plasmid_cp32-8	9665	BB_L15	2.130 ± 0.7885 0.011609	1.188 ± 0.8431 0.5611	0.795 ± 0.3234 0.3776	0.951 ± 0.4105 0.39903	ATTGAAAACCGCAGTGAAGTTGAGCTATGCTTAAATCCAGTGGCTA
plasmid_cp32-8	9746	BB_L15	2.388 ± 0.4743 0.025761	1.698 ± 1.1526 0.38493	1.297 ± 0.2861 0.18303	1.172 ± 0.1351 0.10945	TTAACAGCCTTTACTGCATTCCTCGCTGCTCATAGCACCACTGGATTAA
plasmid_cp32-8	9784	BB_L15	2.222 ± 0.4958 0.040068	1.395 ± 0.9721 0.53467	0.823 ± 0.2189 0.19678	0.979 ± 0.2602 0.88307	GATCAAAAAGCTCACTTCATCACCCCCAAGAACACTATTACAGCCTT
plasmid_cp32-8	10121	BB_L15	1.392 ± 0.6233 0.024278	1.316 ± 1.1186 0.49828	0.775 ± 0.3759 0.17636	0.799 ± 0.3711 0.15515	ATTATTCTTGAAATTAAATCGATGCTACCTGGATGGATGGCGGAG
plasmid_cp32-8	10650	BB_L16	1.482 ± 0.8738 0.449742	2.137 ± 1.4818 0.31904	0.858 ± 0.6962 0.75397	0.865 ± 0.8395 0.80623	TGTTCACCACTGATTCCGGATTGTAGCTTACATATTGCGTTTCTATCA
plasmid_cp32-8	10687	BB_L16	0.756 ± 0.7722 0.082607	0.963 ± 0.1034 0.91158	0.428 ± 0.3324 0.09037	1.852 ± 1.7619 0.36966	TAAGGATATGATTCTTACTCAAATGACTGTTTTGGCAACTATGCT
plasmid_cp32-8	10807	BB_L16	1.147 ± 0.5274 0.080724	0.991 ± 0.7144 0.96535	0.63 ± 0.3615 0.32262	0.761 ± 0.4019 0.1356	TATACTAAAAGGACTTGTGCTTGTATCTTGGTAGTTGTTCTTAC
plasmid_cp32-8	10810	BB_L16	2.978 ± 1.5743 0.072651	1.024 ± 1.0426 0.97302	0.771 ± 0.7286 0.67797	0.622 ± 0.3672 0.33955	TAGTCCAATTGGCCTTAAAGAAATTAGCTGTAATTACAAGTCTTCTG
plasmid_cp32-8	10812	BB_L16	1.961 ± 0.9441 0.135155	1.908 ± 1.8164 0.42793	1.125 ± 0.2511 0.27279	1.115 ± 0.4263 0.58122	GTCCAATTGGCCTTAAAGAAATTAGCTGTAATTACAAGTCTTCTG
plasmid_cp32-8	10977	BB_L17	1.682 ± 0.599 0.065028	1.282 ± 0.7934 0.45388	0.877 ± 0.3258 0.69097	1.302 ± 0.6416 0.25485	AAATTGAGTTCTACATGTAGATACATCAA AAAAATCACCTGATGGAATT
plasmid_cp32-8	10997	BB_L17	1.889 ± 1.2409 0.053554	1.591 ± 1.2836 0.21447	0.845 ± 0.4989 0.309	1.09 ± 0.6204 0.53393	GATACATCAAAAATCACCTGATGGAATTCTCGCCGAAGAAACTATTACAGCCTT
plasmid_cp32-8	10998	BB_L17	1.743 ± 0.9998 0.024487	0.473 ± 0.3729 0.34641	0.994 ± 0.5311 0.96998	1.024 ± 0.5672 0.74843	TCTACATTGAGAACTCAATTAAAATCATATTGAGTAACAGCATT
plasmid_cp32-8	11001	BB_L17	1.585 ± 1.0258 0.481573	1.254 ± 0.7304 0.6251	0.762 ± 0.3537 0.30843	0.637 ± 0.196 0.14523	CATCAAAAATCACCTGATGGAATTCTCGCCGAAGAAATTCTCAA
plasmid_cp32-8	11204	BB_L17	1.350 ± 0.7337 0.508694	1.212 ± 1.2643 0.73366	0.386 ± 0.2083 0.05955	0.571 ± 0.2756 0.1613	AAAATATATTATAAGAAATTGCTCATGAAAAAAATTGATTCATAATG
plasmid_cp32-8	11212	BB_L17	2.262 ± 0.862 0.095947	1.538 ± 0.8309 0.32775	0.974 ± 0.2827 0.8483	1.18 ± 0.329 0.45154	ATATATTCTTACTATCTCAAATTATGTGCGTGGTGAAGTCTAAGGG
plasmid_cp32-8	11533	BB_L17	2.957 ± 1.4879 0.156774	0.799 ± 0.4441 0.32847	1.064 ± 0.2853 0.7019	1.029 ± 0.218 0.86252	TGTTCCATTGCAATTGACTCTTTGGTTGTTGGCATAAATATC
plasmid_cp32-8	11536	BB_L17	1.181 ± 0.3613 0.563096	0.444 ± 0.1996 0.00408	0.731 ± 0.1669 0.15872	0.861 ± 0.2007 0.43461	TGTTCATACGTAATAGCCGATATTGGTACTGGTTACGGGGATATGAATG
plasmid_cp32-8	12122	BB_L18	1.516 ± 0.4982 0.132783	1.363 ± 1.1283 0.60858	0.62 ± 0.3221 0.08214	1.424 ± 0.5353 0.11695	GAGATATTGTTGTTGAAATTCTCAAATTGGTATTGTAACA
plasmid_cp32-8	12235	BB_L18	3.600 ± 1.2004 0.016281	3.176 ± 3.1984 0.33688	2.271 ± 1.5329 0.31335	1.152 ± 0.6978 0.66959	CTTAGTGCAATTGCCCCAAGACTTAAATCATCTGATCTGTTAA

plasmid_cp32-8	12236	BB_L18	1.251 ± 0.7346 0.660639	1.144 ± 0.6682 0.656661	1.213 ± 0.7942 0.64257	1.133 ± 0.6778 0.80317	AGTATATAAAAATGATGTTGTCAAAGTGAATATCGTTATTTTATCAAA	
plasmid_cp32-8	12239	BB_L18	2.238 ± 0.8931 0.93002	1.935 ± 1.4865 0.29156	1.067 ± 0.3021 0.73833	1.162 ± 0.3602 0.19031	GTGCAATTAGCCCCAAGACTTTAACCTAACTCTGATACTGTAAAAATT	
plasmid_cp32-8	12334	BB_L18	1.219 ± 0.9912 0.674263	1.183 ± 1.3914 0.79459	0.788 ± 0.2832 0.37119	1.308 ± 0.7627 0.6316	AAAAAAATTCTAGATAATATTGTTAGTGCTCATGGTATAAAAATTATA	
plasmid_cp32-8	12535	BB_L19	1.983 ± 1.1464 0.263919	0.914 ± 0.5453 0.84194	0.678 ± 0.522 0.17016	0.694 ± 0.396 0.45042	TTAAATACCAATTCAAATTATTGCCTAATCTAAATCCATACTAGTAATT	
plasmid_cp32-8	12618	BB_L19	1.951 ± 3.1669 0.168233	0.17 ± 0.3738 0.43994	0.64 ± 1.0697 0.53371	0.83 ± 1.2504 0.81937	AGCTATGCTCCTCATGGGGATTGGACTATTCTGCTTTAAAGCTGTTA	
plasmid_cp32-8	12735	BB_L19	1.137 ± 1.2324 0.848132	1.092 ± 1.1587 0.90105	0.272 ± 0.2614 0.12515	0.67 ± 0.4745 0.45668	AATCTAAGTTAAGCTCTTAGATATTTCATGAAAATAATTTTTACAGCGT	
plasmid_cp32-8	12775	BB_L19	2.940 ± 0.8635 0.003942	1.339 ± 1.01 0.56035	0.843 ± 0.2518 0.31633	1.138 ± 0.6329 0.72166	TGTGCTTGTGCTGTAGTAGTTGAAATATTATTAACTAAGTTA	
plasmid_cp32-8	12780	BB_L19	2.562 ± 3.3418 0.123363	1.842 ± 2.4454 0.47743	0.893 ± 1.2658 0.92432	0.962 ± 1.2235 0.96669	TCCTTTTTCTCCGGCAGTGTGGAATATGGAGTTAATTATGAGCA	
plasmid_cp32-8	13169	BB_L20	1.684 ± 0.6493 0.084819	1.532 ± 0.9931 0.36346	0.932 ± 0.6052 0.70014	1.451 ± 0.7254 0.08386	TGTTGGCTTACAGCTGCACTTTAATATTAGTACTCAATCCCATCAA	
plasmid_cp32-8	13172	BB_L20	1.077 ± 0.5892 0.576301	0.543 ± 0.4666 0.07253	0.994 ± 0.3458 0.94999	1.111 ± 0.376 0.35713	TATCTAATTCTAAAGGAAACTTACTAGACACTAGTAAATCTAATTAAAT	
plasmid_cp32-8	13206	BB_L20	1.413 ± 0.3326 0.018206	1.037 ± 0.3161 0.62703	0.887 ± 0.149 0.32823	1.083 ± 0.1758 0.47446	GTAAATCTAATTAACTAGTCTGAATTAAAGCAAAACCTTGGGAAACAT	
plasmid_cp32-8	13256	BB_L20	1.627 ± 0.5893 0.202939	1.178 ± 1.3875 0.84816	0.323 ± 0.1217 0.00884	0.8 ± 0.5343 0.56825	ATGTTTCCCAGGGCTTTGCTTAAATTCAAGGACTTAAATTAGATTAC	
plasmid_cp32-8	13346	BB_L20	1.965 ± 1.8973 0.391704	1.585 ± 1.5346 0.44443	0.845 ± 0.6523 0.62523	1.082 ± 0.8013 0.88785	TTTATAGGATTTCGTTGTCAGTTGAATTGAGACCATCAATTCTATGT	
plasmid_cp32-8	13377	BB_L20	1.465 ± 2.0412 0.50895	1.294 ± 1.8708 0.09794	0.467 ± 0.6046 0.46364	0.667 ± 1.0733 0.30283	TGAAAGTAAAGTAAACCTTGACCTTAAACACTATCTACTTAAACATAG	
plasmid_cp32-8	13408	BB_L20	2.842 ± 1.2664 0.000619	1.071 ± 0.8589 0.92221	1.347 ± 1.0378 0.32359	1.255 ± 0.6072 0.49173	GTTTTAAAGGTCAAGTTATACTTACTTCATGTAACATATTCTTT	
plasmid_cp32-8	13467	BB_L20	1.763 ± 0.3456 0.023294	1.237 ± 0.342 0.37919	0.792 ± 0.2331 0.28574	1.07 ± 0.1408 0.11843	TTTGAATAATCCTAGAATAATGTCCTAATTGAGAGTCATGTTAAG	
plasmid_cp32-8	13533	BB_L20	0.904 ± 0.6879 0.860386	0.607 ± 0.6671 0.48626	0.741 ± 0.16 0.033	0.423 ± 0.3142 0.16815	AAGGAATTAAAGTTATGGAATAAGTGTGTTAATTAGACACTG	
plasmid_cp32-8	13838	BB_L21	2.698 ± 1.5884 0.062121	1.7 ± 1.4015 0.28243	0.886 ± 0.4746 0.45867	0.982 ± 0.4491 0.94207	GAAAATATAAAATCAAGATATATTGCAATATGGATATCTCAAGTTTATCT	
plasmid_cp32-8	14088	BB_L21	1.742 ± 1.3551 0.410557	1.855 ± 1.9183 0.4918	1.064 ± 0.2833 0.75273	1.059 ± 0.4193 0.74681	CTACATTATTCGCTAGCACTAAGAAGGAAACGACTAAAAAGATAA	
plasmid_cp32-8	14186	BB_L21	2.506 ± 1.6311 0.26324	2.78 ± 3.771 0.51125	1.299 ± 0.9126 0.65189	1.191 ± 0.2203 0.10507	GTATTCAACTACTCTAAGGGCTATGATCATTCAATTATGCTTTATT	
plasmid_cp32-8	14224	BB_L21	3.239 ± 1.0681 0.038804	2.202 ± 1.4577 0.25657	1.572 ± 0.4346 0.19382	1.286 ± 0.7312 0.5471	AATTGAATGATCATGCCCTTAGGAAAGTGAATACTAAAGCCTTTT	
plasmid_cp32-8	14280	BB_L21	1.612 ± 0.8491 0.009872	0.362 ± 0.2725 0.24018	0.852 ± 0.4722 0.32943	0.977 ± 0.6102 0.09081	CAGATGTTAACATATTAAACTTAAACAACAGGGTTTATGGCTG	
plasmid_cp32-8	14289	BB_L21	1.923 ± 0.1762 0.006793	1.275 ± 0.4119 0.40716	1.137 ± 0.0721 0.00154	1.308 ± 0.8443 0.59921	ACATATTATAACCTTAAACAACAGGGTTTATGGCTGATGATCAAG	
plasmid_cp32-8	14420	BB_L22	0.969 ± 0.5717 0.922447	0.511 ± 0.5565 0.48715	1.065 ± 0.8024 0.71487	1.173 ± 0.7745 0.41625	AAAGATCAGTATGTTAACCGTGTAACTTATTAACTTAACTTAA	
plasmid_cp32-8	14448	BB_L22	0.891 ± 0.901 0.89658	0.931 ± 1.058 0.93871	0.241 ± 0.4114 0.28359	1.685 ± 1.827 0.57405	CTGCTGCGAGCTCATCATCAAGCAGTAAAGATCAGTATGTTAACGGTC	
plasmid_cp32-8	14523	BB_L22	1.618 ± 0.8943 0.017166	1.209 ± 1.0133 0.54413	0.606 ± 0.3454 0.39592	0.993 ± 0.5825 0.97555	AAATAGTCTAATCCCTCCCTTAAATATTGGCTTTAGAGCATCTAA	
plasmid_cp32-8	14616	BB_L22	1.907 ± 0.968 0.062992	1.635 ± 1.5864 0.44639	0.907 ± 0.4178 0.11481	0.976 ± 0.4586 0.51382	TTAATTGTCGTTATTAGCATAATTTCACAAATCTTATCA	
plasmid_cp32-8	14676	BB_L22	0.895 ± 0.5455 0.778223	0.835 ± 1.1018 0.77362	0.497 ± 0.3435 0.05593	0.782 ± 0.342 0.21156	TCTGTAAGGCGTGTATTAACTTAACTAAAGGTTAGAAATATTAGTAGAA	
plasmid_cp32-8	14684	BB_L22	1.123 ± 1.1834 0.873956	1.462 ± 1.4094 0.38021	0.298 ± 0.2867 0.1984	0.452 ± 0.4837 0.41164	TCATCAGCCACTTATCTAGAAGTGTATCATTGATAATGCCCTCATCA	
plasmid_cp32-8	14736	BB_L22	1.423 ± 1.501 0.498641	0.405 ± 0.2427 0.10381	0.776 ± 0.5513 0.17186	0.578 ± 0.3265 0.16244	TCTGATGAAGGCATTATCAAAGATGATCATTCTAGATAAGTGGCTGAT	
plasmid_cp32-8	14768	BB_L22	1.992 ± 0.737 0.079082	1.046 ± 0.5868 0.90917	1.218 ± 0.5233 0.23891	0.897 ± 0.2776 0.55665	TATGTTAGGAACGGGTGTTTGAATAGTATCTGATGAAGGCATTATCA	
plasmid_cp32-8	14872	BB_L22	1.762 ± 0.3139 0.015732	1.496 ± 0.8885 0.35365	1.168 ± 0.225 0.09255	1.049 ± 0.405 0.84687	CAATGATGATGTAACCTTATTTCACAAAGTACGATAATTCCCGT	
plasmid_cp32-8	14961	BB_L22	2.148 ± 0.814 0.006147	2.455 ± 1.207 0.08668	1.385 ± 0.7748 0.45504	1.335 ± 0.485 0.11446	TTATCATTGATTTCCTACTGAAATTCAATATCAAGATAAACGGGAGAATT	
plasmid_cp32-8	15050	BB_L22	1.291 ± 0.4946 0.170419	0.394 ± 0.3172 0.21673	1.178 ± 0.7633 0.57669	1.417 ± 0.8033 0.40336	TTCACCAGAATTCCCATTTAAAGGATGGTATGTCAAAAAGAGCCTCC	
plasmid_cp32-8	15067	BB_L22	2.295 ± 1.1308 0.125691	1.685 ± 1.7832 0.54381	0.863 ± 0.3852 0.47142	0.968 ± 0.756 0.94558	AATGGAAATTCTGGTAATGTCGGGGGGCCGCAATTCTAAACACCT	
plasmid_cp32-8	15170	IG 196	1.729 ± 1.2861 0.255811	2.037 ± 2.0872 0.39405	0.879 ± 0.4635 0.62743	1.106 ± 0.5256 0.0538	TATACCAAATCATATTTCACAAAGTACGATAATTCCCGT	
plasmid_cp32-8	15178	IG 197	2.832 ± 0.3486 0.010717	1.809 ± 0.9785 0.28561	1.051 ± 0.0858 0.29333	1.265 ± 0.1045 0.02585	CGTATAAAATAAAATTAATTAAGAAGGATTAAAAATGGATACATTAA	
plasmid_cp32-8	15335	BB_L23	blyA	2.455 ± 1.534 0.130888	1.663 ± 0.9394 0.13158	0.937 ± 0.6768 0.76703	0.756 ± 0.6081 0.22219	AAAGACATATTGACTATTGTAATAGGCAAGATTTTAAGAATGGTATGG
plasmid_cp32-8	15353	BB_L23	blyA	1.033 ± 0.4046 0.748773	0.446 ± 0.3721 0.28595	0.913 ± 0.3595 0.38314	0.965 ± 0.4093 0.50841	CAATAGTCAATGTCCTTGTAGAAGGCTGAGAAGATAATTACTCTA
plasmid_cp32-8	15356	BB_L23	blyA	2.840 ± 2.4081 0.269927	2.061 ± 2.114 0.27239	1.726 ± 1.1599 0.33256	1.829 ± 1.3282 0.03281	ATAGGCAAGATTTTAAGAATGGTAATGGCAAAAATCACATTAAA
plasmid_cp32-8	15702	BB_L24	blyB	1.715 ± 1.096 0.10573	2.016 ± 1.5046 0.13284	1.043 ± 0.7966 0.86828	0.999 ± 0.6371 0.99902	GATATTGGAGTTTTCATCAGAAATTAACTAAGTCATGATTGATTG
plasmid_cp32-8	15744	BB_L24	blyB	3.091 ± 2.4777 0.243775	0.838 ± 0.3577 0.37788	0.96 ± 0.8283 0.92166	0.816 ± 0.4132 0.5538	AGGAAAGAACAAATAATGCAAATAACACTATTGGTTAGGACTTAATT
plasmid_cp32-8	15787	BB_L25		5.161 ± 2.4189 0.026253	1.82 ± 0.9358 0.28187	0.59 ± 0.4629 0.46312	1.14 ± 1.1983 0.83296	AGTCCTAACCAATAGTGTATTGTCATTGTTCTTCTTATAGAT
plasmid_cp32-8	15808	BB_L25		0.798 ± 0.7066 0.297884	0.933 ± 0.7303 0.68357	0.583 ± 0.2985 0.19653	0.521 ± 0.3102 0.25957	GTTAAGCTGGATAGTAAATTAGTCTAACCAATAGTGTATTGTCATT
plasmid_cp32-8	15892	BB_L25		2.067 ± 1.6372 0.13526	1.935 ± 2.0566 0.33608	0.83 ± 0.4956 0.38229	1.184 ± 0.95 0.29752	TATGTTTGTAGAAAAATCTTACTAACTTAAAGTATTAGTAATT
plasmid_cp32-8	15894	BB_L25		1.836 ± 0.7979 0.031233	1.619 ± 0.9158 0.1536	0.948 ± 0.4566 0.56432	1.571 ± 0.8494 0.13148	TATATGTTTGTAGAAAAATCTTACTAACTTAAAGTATTAGTAATT
plasmid_cp32-8	15895	BB_L25		2.815 ± 1.4197 0.101952	1.323 ± 0.8241 0.54851	0.607 ± 0.2562 0.29364	1.471 ± 0.7713 0.45833	TAAGCACACTAAATCTGAAACAGCTGAGTCAACTAAATTTGAAG
plasmid_cp32-8	15897	BB_L25		2.076 ± 1.0383 0.092648	1.675 ± 1.474 0.41045	1.063 ± 0.473 0.64325	1.027 ± 0.4049 0.76135	AGCACACTAAATCTGAAACAGCTGAGTCAACTAAATTTGAAGAA
plasmid_cp32-8	15981	BB_L25		2.843 ± 0.9722 0.074034	1.324 ± 0.1034 0.63122	0.692 ± 0.1315 0.14168	0.798 ± 0.1416 0.20115	TTATCTCAATGTTGATTAAATGTCATTGTTCAATATT

plasmid_cp32-8	15984	BB_L25	2.567 ± 1.8208 0.076878	1.683 ± 1.3226 0.15429	1.18 ± 0.8113 0.5834	0.89 ± 0.4625 0.65499	GAGGCTATCTACTGACAAAAGCAAAGAAATTACTTCACTTAAAGCA	
plasmid_cp32-8	16336	BB_L26	1.961 ± 1.1038 0.234425	1.875 ± 1.3749 0.35575	0.939 ± 0.5498 0.83898	1.201 ± 0.261 0.34286	TGGAGTGTTCGTCCTTTAGTGTGATAAATCTGGATAAGGATATTCTGGAT	
plasmid_cp32-8	16412	BB_L26	1.078 ± 0.5645 0.745912	0.579 ± 0.5673 0.22662	1.029 ± 0.7915 0.92809	1.178 ± 0.6688 0.16677	TAGACTTTTCCGCTATTGGTTTGTGTTTTAATGTACTCTAAATATG	
plasmid_cp32-8	16483	IG_198	2.257 ± 1.1104 0.082702	1.358 ± 1.0408 0.47451	1.016 ± 0.5337 0.91164	1.093 ± 0.4757 0.43513	TAAAATCTCAAAGCCAATTAAATCTAAAATAGTGATAATATGACTATAA	
plasmid_cp32-8	17162	IG_199	0.952 ± 0.5343 0.871533	0.744 ± 0.7289 0.67993	0.627 ± 0.5856 0.58226	1.272 ± 0.9445 0.67605	TTAATACTAAATATTGGATAAACAAATTATTGGATAATTGATATGTTTAA	
plasmid_cp32-8	17669	IG_200	1.159 ± 0.9429 0.679049	1.522 ± 2.581 0.72637	0.812 ± 0.6701 0.46069	1.086 ± 0.9759 0.86795	TTGGGGGCTTAATCTGCTATGCTGCAAATATCTCATCAAACCGTTCGT	
plasmid_cp32-8	17741	BB_L29	2.441 ± 2.5363 0.262808	2.936 ± 3.4901 0.2638	1.206 ± 1.3404 0.7565	1.141 ± 1.1964 0.87154	TTCTTTAGTATCTAAAAGAACATCGAACGGTTGATGAGATATTGCAGCA	
plasmid_cp32-8	17818	BB_L29	3.098 ± 2.7682 0.172533	2.258 ± 2.6195 0.35369	1.266 ± 0.9537 0.13332	1.404 ± 0.9619 0.06938	TTATTTTCTGAAATAGTTTTATAATCTGGCCAATAGTTATGCTT	
plasmid_cp32-8	17926	BB_L29	1.875 ± 0.6757 0.067015	2.255 ± 1.226 0.17922	1.008 ± 0.4454 0.97747	1.016 ± 0.5324 0.70218	TCATCAAATTATTGGGTCTATATTCTGAATAAAAGCTTATTGGATA	
plasmid_cp32-8	17948	BB_L29	1.498 ± 0.7466 0.154448	2.065 ± 1.3533 0.13088	0.527 ± 0.3022 0.15059	1.065 ± 0.5137 0.53129	TATTCGATAAAGCTTATTGGATAATTGAGTTTATATTCTT	
plasmid_cp32-8	17986	BB_L29	3.120 ± 2.1203 0.099077	3.19 ± 3.4084 0.39301	1.606 ± 0.7768 0.35486	1.637 ± 0.3326 0.08208	TAAACTAATTCTAAAAGAACATAGAACGTTTACAGAATATAGACCCAAATA	
plasmid_cp32-8	18281	BB_L29	1.715 ± 1.9866 0.632623	2.366 ± 1.1637 0.16365	0.346 ± 0.3422 0.18737	0.731 ± 0.5507 0.58109	GTTGCAGCTTGGTATAGAAAGTGAAATAGATACTGATGAGCTCTT	
plasmid_cp32-8	18304	BB_L29	1.821 ± 0.5356 0.023421	1.262 ± 0.8754 0.56063	0.767 ± 0.185 0.16762	0.843 ± 0.2122 0.41083	CTTATGTCAAAGGATGCTTGTAGTTGAGCTTGGTAGAGAAGTGA	
plasmid_cp32-8	18337	BB_L29	2.170 ± 1.6256 0.086751	1.953 ± 1.7946 0.21395	1.379 ± 0.8967 0.47695	1.237 ± 0.8592 0.32133	TTTGTAACTTAGACGCCATTTCATTGTCATTGAAATTCTGAGGA	
plasmid_cp32-8	18429	BB_L29	1.266 ± 0.7272 0.604614	2.129 ± 2.5705 0.5264	1.121 ± 0.4434 0.69177	1.595 ± 0.6858 0.20729	CAGTACAAGTACTGGATATGAATTCTTTGATACGCGATTCTCAGA	
plasmid_cp32-8	18458	BB_L29	1.881 ± 1.0492 0.013963	1.651 ± 1.2735 0.17318	1.032 ± 0.5613 0.9192	0.735 ± 0.4137 0.33292	TGCCATTGACCCCTATAGAAATTGGATTGCTCAATATCAAGCTCCA	
plasmid_cp32-8	18476	BB_L29	2.611 ± 1.3275 0.123419	1.465 ± 1.1274 0.48012	0.904 ± 0.5183 0.68076	0.971 ± 0.5044 0.89095	TAGAAATTGGATTGCTCAATATCAAGCTCAAATTGTGCTTTAATAA	
plasmid_cp32-8	18499	BB_L29	2.795 ± 1.2715 0.053641	1.672 ± 1.1937 0.29696	1.067 ± 0.371 0.38715	1.126 ± 0.3546 0.35976	TCAAGCTCAAATTGTGCTTTAATAACATTAAATTCTAACTATT	
plasmid_cp32-8	18658	BB_L29	2.718 ± 0.8771 0.046273	1.555 ± 0.4136 0.12333	1.067 ± 0.3381 0.33351	1.116 ± 0.2209 0.38844	TCAAGCAAAATAAGCTTAGAAAAGATATGAAAACCTTAAAGAATT	
plasmid_cp32-8	18722	IG_201	1.081 ± 0.7626 0.880926	0.655 ± 0.6124 0.55614	0.267 ± 0.2361 0.13942	0.386 ± 0.2672 0.13997	TTAATAAAATATAAGTATATGACAAAAACTATTGGCAACTTTTACAA	
plasmid_cp32-8	18742	IG_202	0.968 ± 0.4209 0.886467	0.62 ± 0.5182 0.50321	0.777 ± 0.3608 0.56368	0.855 ± 0.4047 0.67461	GCAAAACTATTGGCAACTTTTACAAAATTTTACAAAAAAATA	
plasmid_cp32-8	22341	BB_L35	3.126 ± 1.1001 0.06751	0.921 ± 0.8885 0.86531	1.579 ± 1.1365 0.51989	1.203 ± 0.8542 0.76072	GATAGTGTAGAGAAGAATTACACAGATATATGTTAGATATCAA	
plasmid_cp32-8	22688	BB_L35	2.782 ± 2.1625 0.200018	2.138 ± 2.0768 0.35083	0.651 ± 0.4802 0.0271	1.104 ± 0.3931 0.44465	TTTGTATGTTGAAATACCTCATAAATAGGGCATTAAATTGGACCTAG	
plasmid_cp32-8	22816	IG_203	2.861 ± 2.2911 0.054408	2.37 ± 2.5459 0.23971	1.254 ± 1.0927 0.19809	1.306 ± 1.0233 0.00463	ACTTAAATAAGTCTTTATTGAAACAAATACAAATTGATTAACTTCAA	
plasmid_cp32-8	22912	IG_204	1.034 ± 0.6464 0.83829	0.825 ± 0.832 0.59299	0.961 ± 0.4001 0.75743	1.19 ± 0.5032 0.19808	TTAAAATAATTAAAAGCTTCAATAATTGAGTATAGTCAATTAGA	
plasmid_cp32-8	23172	IG_205	2.335 ± 1.4994 0.19616	2.097 ± 1.5438 0.30127	1.004 ± 0.9256 0.99483	1.231 ± 0.5971 0.4751	TATAACAAAAACTATTGGCAACTTTTACAAATTTTATAAAAAAA	
plasmid_cp32-8	23325	IG_206	1.284 ± 0.2541 0.217163	0.876 ± 0.707 0.82832	0.884 ± 0.1878 0.49854	1.34 ± 0.642 0.51133	GCAAAACTATTGGCAACTTTTACAAAATCTTACAA	
plasmid_cp32-8	23342	IG_207	2.215 ± 0.8818 0.030704	1.436 ± 0.841 0.2946	1.033 ± 0.423 0.01412	1.466 ± 0.6241 0.38793	ATAAATATAAGTATATAGCAAAACTATTGGCAACTTTTACAAAAA	
plasmid_cp32-8	23345	IG_208	1.384 ± 1.086 0.61643	0.849 ± 0.9255 0.84983	0.217 ± 0.229 0.09802	0.441 ± 0.4709 0.03818	TTAATAAAATATAAGTATATGACAAAAACTATTGGCAACTTTTACAA	
plasmid_cp32-8	23391	BB_L36	bppA	1.632 ± 1.8151 0.430216	0.846 ± 0.7391 0.82663	1.085 ± 0.6576 0.86484	2.031 ± 1.1975 0.01985	ATCCACAAAGAAAATTCAAGGAGGCTCAAATGATAAGTATTAAAC
plasmid_cp32-8	23720	BB_L36	bppA	0.066 ± 0.1195 0.056031	0.571 ± 0.5723 0.52267	0.237 ± 0.2899 0.19777	0.277 ± 0.2798 0.21093	TATATGCTCAAGGGCAAAGAGTTAGAGATTAGGTTAGAGA
plasmid_cp32-8	23724	BB_L36	bppA	1.238 ± 1.1864 0.586252	0.545 ± 0.4772 0.37488	0.764 ± 0.9003 0.6753	0.664 ± 0.4295 0.45255	TGCTCAAGGGCAAAGAGTTAGAGAATTAGGGTTAGAGA
plasmid_cp32-8	23904	BB_L36	bppA	2.959 ± 2.8599 0.266166	1.316 ± 0.9479 0.44411	0.989 ± 0.832 0.98703	1.148 ± 0.5788 0.72472	TTAATAACACGCCATATTGTCAGGCCACTAAAGTCTGAACTGCC
plasmid_cp32-8	23958	BB_L36	bppA	2.547 ± 1.1783 0.022324	1.254 ± 0.9028 0.31207	0.81 ± 0.3925 0.60935	1.075 ± 0.5986 0.77482	TGAGTAGTGTCTATTGTCAGTACAATAAAAGGCAATTGGCTTAAAGCAGTA
plasmid_cp32-8	24092	BB_L36	bppA	3.313 ± 2.5859 0.076361	2.248 ± 2.6736 0.34949	1.07 ± 0.7126 0.68615	1.189 ± 0.8452 0.2204	GATGCTGCACCAATTACTGTAAGATTAAAAGAGATGAGGCCATTATCA
plasmid_cp32-8	24137	BB_L36	bppA	2.491 ± 1.4431 0.228467	2.165 ± 2.1304 0.45987	1.64 ± 1.3449 0.52548	0.656 ± 0.3592 0.41745	ATATCAAAGTGTGTTAATTGTTAATAATGTGAATTAGAAATTATAAAT
plasmid_cp32-8	24198	BB_L36	bppA	1.797 ± 0.3896 0.033776	1.671 ± 1.5504 0.51287	0.958 ± 0.1492 0.74095	1.068 ± 0.2761 0.46477	TCTTTTCAAAATTATAATTCTAACATTATTAAACAAATTCAAAC
plasmid_cp32-8	24202	BB_L36	bppA	1.108 ± 0.8197 0.819869	0.555 ± 0.10266 0.6128	0.366 ± 0.337 0.1377	0.426 ± 0.4369 0.3843	AATATCTTTCAAAATTATAATTCTAACATTATTAAACAAATTCT
plasmid_cp32-8	24207	BB_L36	bppA	1.575 ± 0.4638 0.132882	1.008 ± 0.3586 0.9766	0.841 ± 0.3486 0.04646	0.867 ± 0.2936 0.03214	GTAATAGTGTAGAGGAAATTACTATGGCACAATATTAAAGGAGGATACG
plasmid_cp32-8	24210	BB_L36	bppA	1.793 ± 1.4017 0.13359	1.892 ± 1.8842 0.28798	1.003 ± 0.6033 0.9899	1.051 ± 0.625 0.82521	ACTATAGAGAGGAATTCTATGGCACAATATTAAACGAGGATACGTTA
plasmid_cp32-8	24440	BB_L36	bppA	2.230 ± 1.2601 0.061519	2.068 ± 1.0236 0.05524	0.93 ± 0.8236 0.76287	1.089 ± 0.8121 0.89712	AATAAGATCCAAACAAAGAAAATAAAAAGAGAAAAGCCATTAAAGATAG
plasmid_cp32-8	24513	BB_L36	bppA	2.403 ± 1.6696 0.074383	1.523 ± 1.4828 0.37688	0.884 ± 0.4974 0.5037	0.727 ± 0.514 0.0667	ATATTGTAATTAGCATCTTCAACCTATCTTAACTGGCTTCTTTT
plasmid_cp32-8	24523	BB_L36	bppA	2.353 ± 1.9491 0.259097	1.902 ± 1.0452 0.10469	1.215 ± 0.7031 0.67707	1.583 ± 0.5138 0.04081	TGTATTGTAATTGTAATTAGCATCTTCAACCTATCTTAACTGGCTT
plasmid_cp32-8	24617	BB_L36	bppA	2.980 ± 1.8556 0.19649	2.246 ± 1.4951 0.27321	1.015 ± 0.5367 0.96422	1.219 ± 0.7033 0.03172	GTCCCTTCATCTGATATTGCCCTTTCTAGGGTCAAGAGTAAACA
plasmid_cp32-8	24620	BB_L36	bppA	3.518 ± 4.6248 0.344108	3.294 ± 4.4888 0.35948	1.249 ± 1.5656 0.72905	1.274 ± 1.9343 0.78739	GTAGCCCTTCATCTGATATTGCCCTTTCTAGGGTCAAGAGTAA
plasmid_cp32-8	24731	IG_209	2.074 ± 1.0114 0.189402	2.016 ± 0.9185 0.04141	0.889 ± 0.7942 0.65449	2.065 ± 1.1112 0.10178	GGAGGATTAATTAGCTTAAATAAAACAAAGATAATAGAACACTT	
plasmid_cp32-8	24832	BB_L37	bppB	2.284 ± 0.9281 0.083831	1.323 ± 0.9746 0.55655	1.271 ± 0.4795 0.38195	1.16 ± 0.4894 0.54681	TAATAATGTAACACAAAAGTAACACCCATTGGCTTCTCCGGCTT
plasmid_cp32-8	25071	BB_L37	bppB	0.963 ± 0.4085 0.891997	0.765 ± 0.6164 0.61935	1.014 ± 0.2662 0.91293	1.044 ± 0.4491 0.85485	GCAACAAAAATAAGGAAATTATGATTCATGACTTGAAGGCCCTG
plasmid_cp32-8	25153	BB_L37	bppB	1.773 ± 1.234 0.228729	1.41 ± 1.4789 0.72679	0.734 ± 0.5439 0.59319	0.978 ± 1.2129 0.95612	TATTTAGACTAAAGTAGTTTAAAGTTAAGGTTATTCTCATG

plasmid_cp32-8	25278	BB_L38	<i>bppC</i>	2.183 ± 1.5207 0.159239	0.927 ± 0.5794 0.86456	0.697 ± 0.3943 0.45182	0.973 ± 0.8527 0.85924	AGTTCTTAATTGGAAAGAATTATAACCATTAGATTAAATATGAAATA
plasmid_cp32-8	26016	IG_210	<i>erpN</i>	3.290 ± 2.6301 0.165957	1.499 ± 1.6348 0.60073	1.398 ± 1.3392 0.63797	1.575 ± 1.208 0.35002	CTATTTTACTATTTTATACCTTAACTAACTAAAGTAACACCTTC
plasmid_cp32-8	26449	BB_L39	<i>erpN</i>	2.373 ± 0.9352 0.073475	1.515 ± 1.7359 0.626	1.121 ± 0.5754 0.71282	0.846 ± 0.2897 0.14674	TGAATCTGCAAGCACCTATAAGTATAAAAACAGCACAATAAAACATT
plasmid_cp32-8	26704	BB_L39	<i>erpN</i>	1.820 ± 0.9578 0.140915	0.922 ± 0.9273 0.89894	1.178 ± 1.1431 0.84099	0.851 ± 0.5306 0.76244	GTTTTAAATGATCCACCTTCAGTCATTGCTTTATAAGTTATAATTCT
plasmid_cp32-8	26758	BB_L39	<i>erpN</i>	2.877 ± 1.4994 0.102097	2.136 ± 1.3948 0.20829	1.021 ± 0.3645 0.90024	1.213 ± 0.2878 0.29497	TTCTTAATGACATTTTATCATTCTCGTCAATTATCCATAATACAAA
plasmid_cp32-8	26803	BB_L39	<i>erpN</i>	2.203 ± 0.7296 0.092202	1.134 ± 0.4539 0.72855	1.001 ± 0.4704 0.99625	0.904 ± 0.2517 0.50397	TATTACAGTATCATTAATTTTCTATCTTGTCTTCTTCTTCTTCTA
plasmid_cp32-8	26804	BB_L39	<i>erpN</i>	2.683 ± 0.8619 0.07001	1.692 ± 0.1055 0.3698	0.97 ± 0.1039 0.65018	0.934 ± 0.2919 0.78638	TATTACATTAGGAGATAAAATTAAACAGTGCGGGGGGAGACAAAAT
plasmid_cp32-8	27105	BB_L40	<i>erpO</i>	1.934 ± 1.8532 0.502659	1.701 ± 0.968 0.26066	1.095 ± 0.6184 0.84735	1.112 ± 0.1061 0.81912	ATTCATCTACTTTGAACTACTTGAAGTAATTATCTTGTGGATCCA
plasmid_cp32-8	27144	BB_L40	<i>erpO</i>	1.172 ± 1.2525 0.736409	0.946 ± 0.1071 0.91454	1.096 ± 0.8706 0.72089	1.253 ± 0.8116 0.14824	CACCTTATTCTCTCTGTAAATTCTGTAAATTCACTACTT
plasmid_cp32-8	27700	BB_L40	<i>erpO</i>	2.331 ± 0.8357 0.119262	2.244 ± 1.1311 0.22122	0.799 ± 0.5409 0.67942	0.901 ± 0.354 0.73584	ACACCTTGCCCCACACTAGTTGCTCTTATAACATCAATTTCTA
plasmid_cp32-8	27726	BB_L40	<i>erpO</i>	2.231 ± 1.113 0.30745	1.925 ± 1.6963 0.27492	1.209 ± 0.6133 0.14893	1.235 ± 0.5249 0.49172	TATGATGATTACTGATGGAAAGCTATACAAAACCTGGGGGGAT
plasmid_cp32-8	27889	BB_L40	<i>erpO</i>	2.969 ± 2.0895 0.091027	1.302 ± 0.9466 0.67376	1.343 ± 1.0778 0.13723	1.62 ± 1.5581 0.40595	GTATCAATAATATGCTTATTACCCCTCATTAATTGGTTCTAAATT
plasmid_cp32-8	28045	BB_L40	<i>erpO</i>	1.860 ± 1.3119 0.319422	2.291 ± 2.3641 0.21572	0.79 ± 0.7277 0.78209	0.574 ± 0.3991 0.42308	TCCTCACTACAGCAACGTATTCTCAAATTATCTTCTAAATTATCT
plasmid_cp32-8	28341	BB_L41		3.153 ± 0.9349 0.205274	2.228 ± 2.5688 0.4665	0.846 ± 0.2328 0.340008	1.816 ± 0.9193 0.20351	ACTAGCAAAATAACTAAAGCAGAAAAAGACAAATACAGTGTGTTGAA
plasmid_cp32-8	28406	BB_L41		2.689 ± 2.1759 0.300444	1.842 ± 1.6245 0.45068	0.774 ± 0.4484 0.62752	1.417 ± 1.5512 0.7116	CGTAATAAAACGGAAAAAGTGTAGGAGATCGGAAAGAATTGTG
plasmid_cp32-8	28694	BB_L41		2.005 ± 1.0703 0.21801	1.857 ± 1.1983 0.30213	1.003 ± 0.4507 0.9932	1.234 ± 0.4092 0.26715	GTGTATACTAAAAATAATCTCTAAATTCTTAAATCGCATCTATTG
plasmid_cp32-8	29030	BB_L42		2.706 ± 2.641 0.175918	2.209 ± 3.095 0.43606	0.846 ± 0.7289 0.23506	0.895 ± 0.7526 0.29169	AGTGTGTAAGAAATAGCGAAGAAATTAGGAGTTCTAAAGTAAATGTG
plasmid_cp32-8	29298	BB_L42		2.598 ± 1.4181 0.034887	1.524 ± 1.1075 0.30911	0.749 ± 0.4765 0.03414	1.095 ± 0.6494 0.33162	TGCATACTAAATAGAAAATTAGAGCCAAATTGACGCTTAAATAAG
plasmid_cp32-8	29423	BB_L42		2.648 ± 2.3575 0.247292	1.832 ± 1.5148 0.41073	0.558 ± 0.4383 0.22	1.176 ± 0.7575 0.38021	AAAGAGTGTCAATAAGGAAATTGGAGCTTACTATGAATGTGAAAAAA
plasmid_cp32-8	29542	BB_L43		1.772 ± 0.63 0.087421	1.986 ± 1.3297 0.2738	0.857 ± 0.327 0.40056	1.074 ± 0.3418 0.53831	TATCAAACAAAACCTTTAACACACTACAAAGGAATACAAAATAAT
plasmid_cp32-8	29617	BB_L43		1.758 ± 0.9236 0.059193	1.022 ± 0.9771 0.93917	0.599 ± 0.4015 0.3344	0.745 ± 0.5409 0.08103	AAGCTAAACAAATTCTCAATTATTGTGATAAGTTGAGAAGAACAGT
plasmid_cp32-8	29674	BB_L43		2.207 ± 1.523 0.084286	1.889 ± 2.4277 0.47691	1.016 ± 0.5555 0.96888	0.997 ± 0.4934 0.99203	AAACAAAAAAATGTGATAAAAGCATTAAAAGAATAATGAAAGAATT
plasmid_cp32-8	29725	BB_L43		1.797 ± 0.8317 0.248271	0.992 ± 1.0818 0.99257	1.079 ± 0.9809 0.86625	1.018 ± 0.827 0.96231	TAATCTTCTTATTCTTAAATGCTTATTACACATTGTTGTT
plasmid_cp32-8	29822	BB_L43		1.463 ± 0.9985 0.076031	0.668 ± 0.4538 0.3514	0.329 ± 0.2158 0.08704	0.424 ± 0.1838 0.11345	CTAATAATTCTTATTAGGAAATTACAACGTTAGTGAAGTTATGTT
plasmid_cp32-8	29927	BB_L43		2.077 ± 0.5557 0.07523	1.596 ± 0.7113 0.33141	1.092 ± 0.2441 0.30101	1.211 ± 0.5924 0.65788	TGTCTTGGAAATATAAGGAATTAAAGAAGTTACAGTCTTCAAATTG
plasmid_cp32-8	30017	BB_L43		0.991 ± 0.428 0.854977	0.522 ± 0.4824 0.36821	1.045 ± 0.5479 0.70069	0.929 ± 0.4002 0.0846	CTTCCCCTAAATCTTCAAATACACTGCTTATCTCCTCATATAGAT
plasmid_cp32-8	30162	BB_L43		3.036 ± 1.1696 0.04798	1.581 ± 0.6088 0.11679	0.798 ± 0.2705 0.05046	1.068 ± 0.3818 0.81947	ATCGTTTTAAATAGTGTGTTGATCAGGATTAGTACAAATAAT
plasmid_cp32-8	30344	BB_L43		4.103 ± 2.9965 0.023809	2.094 ± 2.5141 0.3348	1.345 ± 1.0951 0.59675	1.108 ± 0.9624 0.86357	ATATTATTGTGAAAAATTGAAATCACTGTTGCTATCCACTCAC
plasmid_cp32-8	30356	BB_L43		1.598 ± 0.3679 0.115471	1.516 ± 1.2485 0.51989	0.677 ± 0.2176 0.24261	0.807 ± 0.531 0.56079	TAATCATCGATAATTATTGTGAAAAATTGAAATCACTGTTGCTATC
plasmid_cp32-8	30368	BB_L43		2.017 ± 0.7325 0.146135	1.835 ± 1.9885 0.56065	0.836 ± 0.5537 0.60586	1.422 ± 0.5731 0.39751	GCCCCATAGCATATTAGACCAGCATTTAGTTGAGGAGGGATAACACT
plasmid_cp32-8	30424	BB_L43		4.272 ± 2.7232 0.162458	1.934 ± 2.1805 0.30272	1.92 ± 0.224 0.01151	2.707 ± 1.2722 0.14391	TGTGTTATGGAGCAGTGTGATGATAAGTATTGTTGATTTCAAGAC
plasmid_cp32-8	30498	BB_L43		2.706 ± 1.3024 0.027289	1.567 ± 1.5529 0.45258	0.959 ± 0.3719 0.86968	0.775 ± 0.3079 0.47939	TATTATGAATATGGTAAAGACTGTTATAGAAAATTTCATGTGACACT
plasmid_cp32-8	30552	BB_L43		1.924 ± 1.5844 0.43432	3.536 ± 4.3291 0.39975	0.952 ± 0.7592 0.57111	1.759 ± 1.8784 0.56914	TTTAGAGGATAGAGATAATACAAAAGGTGTTGATTGACCGTGAATA
plasmid_cp32-9	96	BB_N01		2.270 ± 0.9651 0.059878	1.56 ± 1.3037 0.44174	0.991 ± 0.3097 0.80274	1.078 ± 0.4717 0.59215	GATAAAATAAGTCACTAGAAACTATACAAATACTCAATTCTTAAAG
plasmid_cp32-9	274	BB_N01		0.879 ± 0.7816 0.74986	0.703 ± 0.7456 0.6588	1.542 ± 1.183 0.50513	0.755 ± 0.5583 0.48664	ATACAATTAAAGCAGAGCATCTTAACTGCTACCTTAGCAAGTTCA
plasmid_cp32-9	279	BB_N01		1.547 ± 1.5302 0.00911	1.315 ± 1.4498 0.21876	0.431 ± 0.3858 0.33752	1.093 ± 1.0368 0.845	AGCTACCGTTTACGGGATGGCTATGTTAGTAAACCAAGAAACT
plasmid_cp32-9	395	BB_N01		2.318 ± 1.0755 0.052119	1.814 ± 1.3039 0.39016	1.209 ± 0.592 0.29572	1.396 ± 0.9658 0.16576	TTCATACAAAGGTATTCTTAAACCAATGGTAAATTCTTAAACGGTT
plasmid_cp32-9	398	BB_N01		1.646 ± 0.4392 0.063027	1.355 ± 0.7577 0.47808	0.713 ± 0.1366 0.04121	0.919 ± 0.1403 0.36353	TGTAGAGGATTTGGGAGTTGTTGATCATATAACCTTAAAGTAAATC
plasmid_cp32-9	399	BB_N01		1.467 ± 0.6107 0.353066	0.613 ± 0.4596 0.07023	1.085 ± 0.575 0.8551	1.014 ± 0.3735 0.96395	CATATTCAATACAGGTTAAACCAATGGTAAATTCTTAAACGG
plasmid_cp32-9	432	BB_N01		1.348 ± 1.4753 0.484482	1.958 ± 1.8173 0.18734	0.613 ± 0.3692 0.39759	0.581 ± 0.885 0.15428	ACCTATAAGGAAACCAATAACAGAACAATTCTTAGCAGCAGTAA
plasmid_cp32-9	444	BB_N01		1.889 ± 1.264 0.378882	1.432 ± 0.5116 0.17256	1.185 ± 0.4736 0.62557	0.673 ± 0.2845 0.26982	AAATCCAACAAAGAACAACTTCTTAGCAGCAGTAAATACATAAG
plasmid_cp32-9	478	BB_N01		1.856 ± 1.3718 0.301062	1.19 ± 0.3931 0.80986	0.605 ± 0.3003 0.22873	1.338 ± 0.4195 0.29784	ACTCGTCTAAAGAATTGTTCTATTGTTGATTCTTACTAGTTA
plasmid_cp32-9	490	BB_N01		3.107 ± 1.1052 0.055753	2.034 ± 2.8804 0.61077	0.518 ± 0.1603 0.07765	1.04 ± 0.4462 0.86575	AAAGTCGACTTATCATATGAAACCTTGTATTATCTTAAAGATATG
plasmid_cp32-9	504	BB_N01		0.761 ± 0.486 0.334701	0.385 ± 0.4372 0.12855	0.802 ± 0.5047 0.60902	0.493 ± 0.3939 0.3667	TGATAAGTCGACTTTATGTTACTGCTCAAAGAATTGTTCTT
plasmid_cp32-9	506	BB_N01		3.900 ± 2.4136 0.01555	2.396 ± 2.9116 0.36334	1.269 ± 0.7001 0.56003	1.321 ± 0.8583 0.116	TATGATAAGTCGACTTTATGTTACTGCTCAAAGAATTGTTCT
plasmid_cp32-9	507	BB_N01		1.325 ± 1.2519 0.543972	1.045 ± 1.1378 0.88375	1.107 ± 1.0503 0.75855	1.209 ± 1.1631 0.64029	TATGAAAATTGTTGATTATCTTAAAGATATGTTCCGTGTTACCGA
plasmid_cp32-9	521	BB_N01		2.053 ± 0.6561 0.076656	1.111 ± 0.5241 0.80279	1.055 ± 0.31 0.76799	1.133 ± 0.3292 0.53556	ATCAAAGTTCATATGATAAGTCGACTTTATGTTACTGCGTC
plasmid_cp32-9	524	BB_N01		2.133 ± 0.2238 0.014581	1.022 ± 0.6553 0.96097	1.105 ± 0.1396 0.24315	1.845 ± 0.9664 0.26134	TATCTAAAAGATATGTTCCGTGTTACCGAAAGCTTTACTAGATA
plasmid_cp32-9	526	BB_N01		1.115 ± 0.696 0.325768	0.126 ± 0.1378 0.12265	0.59 ± 0.7656 0.14878	1.673 ± 1.2925 0.35401	TCTTAAAAGATATGTTCCGTGTTACCGAAAGCTTTACTAGATA

plasmid_cp32-9	578	BB_N01	2.366 ± 1.6756 0.107355	2.605 ± 2.6367 0.28554	0.753 ± 0.4463 0.43603	1.209 ± 0.8954 0.40114	TTTATTGAAAAGATACGTAGAAATAGAAAGACGTATTGAAAACCACAA
plasmid_cp32-9	747	BB_N01	1.841 ± 0.7605 0.179958	1.923 ± 1.4368 0.37546	0.983 ± 0.2378 0.93436	1.058 ± 0.2472 0.48697	TCTTCCTTTTGAGAAAACAATTCAAACATCATAGTAAGATATTCT
plasmid_cp32-9	1055	BB_N01	1.331 ± 0.6052 0.376505	1.506 ± 0.7768 0.42609	1.136 ± 0.4187 0.45572	1.099 ± 0.5742 0.75752	TTACGATTTCTCAAGGGTGTGCAAGAACAAATTGAGAACACTTGTAAATT
plasmid_cp32-9	1555	BB_N02	0.856 ± 0.3032 0.41796	0.109 ± 0.1924 0.03266	0.401 ± 0.6432 0.19974	0 ± 0 0.03306	TGCCTCAGCCTCTAGCAATAATTGCTTTAATACGCTCCCTCTTC
plasmid_cp32-9	1706	BB_N02	2.045 ± 0.8897 0.201324	1.667 ± 0.5679 0.0493	1.178 ± 1.2665 0.81009	1.404 ± 0.4849 0.12245	GCTTTAATTGCTCAATTGAAAGAACACTGCGCACAAAGTTCTACGTGT
plasmid_cp32-9	1750	BB_N02	0.797 ± 0.6292 0.578014	0.164 ± 0.2586 0.21414	0.853 ± 1.0183 0.76366	0.799 ± 0.5493 0.33659	TTAGAGCAACTGTTCTTAGAAAAGTGAATATTAAATTAGAAAAACT
plasmid_cp32-9	1918	BB_N02	1.048 ± 1.3553 0.952862	1.578 ± 1.087 0.44755	0.662 ± 0.8924 0.56248	0.121 ± 0.1598 0.01298	CAAGCGATAAGTAACCTACAAGAACGAATTCAATTATGAAAAT
plasmid_cp32-9	1931	BB_N02	1.504 ± 0.5629 0.283386	1.177 ± 0.1922 0.1828	0.843 ± 0.3421 0.54326	0.547 ± 0.3972 0.22505	TTACTTATCGCTGTACAATTCTGTGAAATTAAAGGTACAAAATTAGAA
plasmid_cp32-9	2222	BB_N03	0.964 ± 0.6611 0.879282	0.456 ± 0.3086 0.24096	0.795 ± 0.49 0.1432	1.163 ± 0.4255 0.63294	CAAGCGTGGAGTCAGCTAGTTAGTGCAGATGGTACACAGAACTAGA
plasmid_cp32-9	2437	BB_N03	1.533 ± 0.9798 0.125505	1.29 ± 0.6808 0.00901	0.822 ± 0.3711 0.37601	0.992 ± 0.4901 0.97737	ATGCACAAAGGAGAGCTTGAAGAATGGGGAAATGATAATCTGTTAATG
plasmid_cp32-9	2671	BB_N04	2.768 ± 2.1034 0.276696	0.713 ± 0.1429 0.0723	0.961 ± 0.4401 0.90219	0.821 ± 0.211 0.04534	GGAGCAACTGGAATTCTGATTCTAACCTATAATTGGGATTATCATGAAC
plasmid_cp32-9	3005	BB_N04	2.671 ± 3.3891 0.393949	2.28 ± 2.1925 0.27903	1.783 ± 1.8715 0.37757	1.209 ± 0.9856 0.52986	CATATCAGTATCAGCACCACCTAACATATAGAATTCTTTGGAAAC
plasmid_cp32-9	3088	BB_N04	1.619 ± 1.2533 0.457547	2.371 ± 2.2937 0.36687	0.699 ± 0.6206 0.30254	0.675 ± 0.3239 0.41391	ACAAGATACCCCTTCAAATTCTGTAAATTGGAATACATACGCGACTA
plasmid_cp32-9	3129	BB_N04	2.594 ± 1.2726 0.027383	1.616 ± 1.7355 0.52782	0.639 ± 0.239 0.22327	0.668 ± 0.3169 0.33812	TATCCATATTCTCCCATTTTACTCGGATTCTTGTAAACAGATACC
plasmid_cp32-9	3939	BB_N05	1.177 ± 0.2498 0.44934	0.704 ± 0.4835 0.37526	1.557 ± 0.3794 0.12302	1.111 ± 0.6984 0.79927	CAGCTTATTCCAATACTGCTACTTTATTAAATAACATCGTTACTAA
plasmid_cp32-9	4021	BB_N06	1.559 ± 0.4526 0.201068	1.766 ± 1.0553 0.26933	0.928 ± 0.439 0.76955	1.136 ± 0.5065 0.56209	TTATAGGGAGTTAAAGATCTATAATGTATAATGGTTTCGCCTGATC
plasmid_cp32-9	4045	BB_N06	3.642 ± 3.0637 0.182334	1.567 ± 1.1523 0.23683	1.845 ± 0.9026 0.20703	0.991 ± 0.583 0.97932	TAATGTATAATGGTTTCGCCTGATCAAATTGAAGATGTTGATCTTCAGA
plasmid_cp32-9	4245	BB_N06	2.696 ± 0.4894 0.025656	1.312 ± 0.77 0.5533	0.892 ± 0.11 0.25028	1.069 ± 0.1275 0.49062	AGTGCTTAATTGTACTGTAATTAAAGTAATTAGCTTACCACTTCAG
plasmid_cp32-9	4357	BB_N06	2.023 ± 0.702 0.00542	1.233 ± 0.4207 0.30789	1.027 ± 0.4659 0.77439	0.995 ± 0.4183 0.85313	AACTTATAACTCTTGTACTAACAGGCACTGTTCAATTCAAAAGATG
plasmid_cp32-9	4435	BB_N06	3.877 ± 4.7375 0.311735	2.559 ± 1.4987 0.074	0.918 ± 0.8942 0.58448	1.089 ± 1.5318 0.94186	TTGGGAAGTAGACGTTTGATTTTCCACTTTGAATTGAAACAGTG
plasmid_cp32-9	4813	BB_N06	1.173 ± 1.3864 0.814003	1.067 ± 1.4237 0.92283	0.491 ± 0.5724 0.9044	0.666 ± 0.458 0.11441	CCTCACACCAAAGAACAACTGGTAAAGATCAACTGATATTGCTCATTCA
plasmid_cp32-9	5184	BB_N07	0.765 ± 0.6145 0.438402	1.368 ± 1.7797 0.72915	0.859 ± 0.728 0.6277	1.011 ± 0.7591 0.9559	TGGGGTGTCAATTAAAGAACAAAGGGAGTTGTCGAGAATTGATTGATA
plasmid_cp32-9	5283	BB_N07	0.532 ± 0.3593 0.336187	0.538 ± 0.5123 0.41739	0.913 ± 0.5735 0.87371	0.831 ± 0.6814 0.80568	GTAGCAGTGGAGGCGAAAGAGGTGGCGAGGGGGTTGGCTCAAACAAAGA
plasmid_cp32-9	5558	BB_N08	3.211 ± 2.4621 0.050072	0.91 ± 0.6234 0.81786	0.3 ± 0.2516 0.22642	1.135 ± 1.3446 0.80098	AGTACACTGAATTGCGAGGAGTTATTGACATAAAAGCCAACAAGACTG
plasmid_cp32-9	5582	BB_N08	1.661 ± 0.7408 0.090473	1.638 ± 1.6377 0.48829	0.757 ± 0.2879 0.06624	1.103 ± 0.5905 0.50902	TTATTGACATAAAGGCCAACAGAACACTGCAATTCTTATGATTCTGATATGT
plasmid_cp32-9	5649	BB_N08	0.427 ± 0.2673 0.108635	0.434 ± 0.3972 0.23419	1.032 ± 0.3961 0.62034	1.083 ± 0.4333 0.44581	TTCCAAACTTACACATATCAAGACCTTAACATGAACAAAGACCGAAT
plasmid_cp32-9	5664	BB_N08	4.354 ± 2.9138 0.104431	0.805 ± 0.5402 0.61641	1.211 ± 0.7213 0.23837	1.339 ± 0.8329 0.47552	TGTGAAAGTTGGATATCCTGAAATATCAGACATATCAGAACATCAAAG
plasmid_cp32-9	5933	BB_N09	1.837 ± 0.9682 0.174242	0.987 ± 0.415 0.90413	0.807 ± 0.3096 0.50431	1.163 ± 0.7952 0.71381	TATCAATAATAGCTATAAACTTCAAGTTAACCTTGCACCTAAATCAGG
plasmid_cp32-9	6155	BB_N09	1.926 ± 1.3547 0.315356	1.255 ± 1.4084 0.78214	0.482 ± 0.2414 0.15438	0.712 ± 0.2466 0.07911	TAAGGTAACACTGATTTCACTTTAGATATGGTATAATCATTAA
plasmid_cp32-9	6323	BB_N10	1.959 ± 0.3921 0.056497	1.048 ± 0.2836 0.84184	0.774 ± 0.2084 0.32118	0.891 ± 0.13 0.29507	TTATATTGAGCTAGCAGCTGATTTTGAAAGATATGGTATTGAG
plasmid_cp32-9	6426	BB_N10	0.440 ± 0.5573 0.444137	0.742 ± 0.9739 0.78386	0.334 ± 0.2249 0.18171	0.529 ± 0.5946 0.48869	TATATTGAAATTACTAAATTCTGAAATTTCAATAAAACACCG
plasmid_cp32-9	6489	BB_N10	2.035 ± 1.7397 0.308821	3.638 ± 2.6927 0.12494	0.822 ± 1.0114 0.7769	0.988 ± 1.2823 0.98801	TAAAGCATTAACATGCGTAATTAGCGTCAAAGTCTTGGCTTAAACACT
plasmid_cp32-9	6545	BB_N10	3.135 ± 1.2072 0.045943	1.809 ± 1.4816 0.37581	0.898 ± 0.2771 0.36946	1.055 ± 0.3195 0.2708	GACTGGGCAAAGTACATTGAGCTTATTGAGTAAAGTCACAAAGCA
plasmid_cp32-9	6561	BB_N10	2.041 ± 1.4467 0.119592	1.866 ± 1.6774 0.27755	0.844 ± 0.5145 0.10325	1.133 ± 0.5392 0.45773	TTAATAAAATTAACTCTACATTACCAACATCTAAATGCAAACAGTTG
plasmid_cp32-9	7139	BB_N11	2.688 ± 0.7418 0.00636	1.207 ± 0.9017 0.63337	0.817 ± 0.2327 0.07558	1.045 ± 0.2834 0.69669	TAATAAATTCAAATGCCTTCAACTTTTGTATTCTGACTAAAGAAC
plasmid_cp32-9	7203	BB_N11	0.347 ± 0.3233 0.316611	0.332 ± 0.4185 0.43716	1.145 ± 1.0973 0.76159	1.18 ± 1.1426 0.72291	GTTCTTTATTCTGTTCTTAGTCGAGAATACAAAAAAGTTGAAGGCA
plasmid_cp32-9	7380	BB_N11	2.729 ± 1.3295 0.082367	2.137 ± 1.9425 0.35248	1.006 ± 0.453 0.97197	1.162 ± 0.3136 0.54009	ATTGGAAAGTTGCGAACCTGCAAACATCACTTTTACTCTTAATGAA
plasmid_cp32-9	7986	BB_N12	1.947 ± 1.0176 0.10812	1.903 ± 1.8929 0.40543	1.006 ± 0.4958 0.97895	1.013 ± 0.5225 0.82595	AGAGATCCCCAAAACAATACTTGTGATTGAGTACAGTACACTAGGT
plasmid_cp32-9	8236	BB_N12	1.889 ± 0.4424 0.067531	1.871 ± 1.5441 0.42548	0.956 ± 0.0959 0.5071	0.92 ± 0.1406 0.306	GCCCTAATTCTCAAAGATACCTTTGGCCTCAGCAGAACACTCTGAA
plasmid_cp32-9	8452	BB_N13	1.795 ± 0.7596 0.068496	1.841 ± 1.6669 0.50465	1.517 ± 0.9515 0.51145	0.577 ± 0.3506 0.38563	AGCTGTGATTCTCTTAAGTAAACCTCATTAAGCTTAAACAGCGT
plasmid_cp32-9	8593	BB_N13	3.272 ± 1.7946 0.165651	1.242 ± 0.3613 0.42108	1.728 ± 0.5743 0.12104	1.408 ± 0.4336 0.1758	AAAAAGCCCGTTAGTATATTGAGTGAAGTATGAAAATAATGTTGAG
plasmid_cp32-9	8764	BB_N14	1.765 ± 0.4447 0.008008	1.655 ± 1.056 0.26455	1.29 ± 0.4825 0.41303	1.112 ± 0.3467 0.02408	TTGATAAAAGCTATTGCAAGTCTTGTGAGAGACTAGAAAAAATTTAACT
plasmid_cp32-9	8983	IG_211	3.193 ± 1.7299 0.009942	1.703 ± 1.174 0.35361	1.583 ± 0.7696 0.1822	1.136 ± 0.4056 0.87885	AGTCCTCACTGCTAAAATTAACTCATACAATTCTTCTAATTAACTC
plasmid_cp32-9	9158	BB_N15	2.383 ± 1.8508 0.341966	1.867 ± 2.3483 0.58832	0.267 ± 0.1772 0.08861	0.625 ± 0.2814 0.32326	AGTTCTTTCTGTCGACAATTATTTTACAATATCTTAGTGCTA
plasmid_cp32-9	9437	BB_N15	1.450 ± 1.2853 0.661282	2.064 ± 2.0637 0.39182	0.354 ± 0.4031 0.00211	0.05 ± 0.0883 0.06486	GCGTTGCTAACTGATATTCCCTAGGGCACTACCTATGCAATTGGCAAC
plasmid_cp32-9	9683	BB_N15	2.269 ± 0.9055 0.004076	1.214 ± 0.8842 0.48359	0.776 ± 0.3139 0.36498	0.954 ± 0.4428 0.29474	ATTGAAAAACGCGAGTAGAATTGAGTGAAGTATGAAAATAATGTTGAG
plasmid_cp32-9	9764	BB_N15	2.414 ± 0.4417 0.016582	1.777 ± 1.2304 0.36721	1.258 ± 0.3203 0.29617	1.197 ± 0.1686 0.14283	TTAACAGCCTTACTGCATCTCGCTCATAGCACCAGTGGATTAAAGC
plasmid_cp32-9	9802	BB_N15	2.139 ± 0.4392 0.030382	1.332 ± 0.9315 0.57613	0.726 ± 0.2466 0.19521	0.989 ± 0.3161 0.94446	GATCAAAAGACTCATTCATCACCCCCAAGAACACTATTAAACGCCCTTA
plasmid_cp32-9	10057	BB_N15	1.468 ± 0.3529 0.034869	1.284 ± 0.7293 0.48027	0.939 ± 0.1425 0.63957	1 ± 0.2326 0.99454	ACTAATTACTTAAAGACTTACGTTGAAACACATATTGAAACCATA

plasmid_cp32-9	10139	BB_N15	1.429 ± 0.5946 0.012187	1.327 ± 1.1078 0.50422	0.763 ± 0.3484 0.08409	0.819 ± 0.3632 0.12095	ATTATTTCTTGCAAAATTAAAATCGATGCTACCTGGATGGATGGCGGAG
plasmid_cp32-9	10571	BB_N16	0.782 ± 1.0759 0.766948	0.377 ± 0.4736 0.48125	0.652 ± 1.0713 0.02195	2.238 ± 3.1498 0.26317	GAATGGATCTAAAAGGTGGATATGTCCTCAATTGTTTTTAAACAC
plasmid_cp32-9	10739	BB_N16	1.062 ± 0.6449 0.868526	1.767 ± 1.5024 0.45356	0.624 ± 0.5353 0.31738	0.711 ± 0.5773 0.45952	TTTCACCAAGTCATTACCGGATTGAGCTTACATATTCCGCTTCTATCA
plasmid_cp32-9	10742	BB_N16	2.934 ± 1.5709 0.066188	1.536 ± 1.1921 0.3416	0.882 ± 0.501 0.16176	1.019 ± 0.3828 0.84796	TATCATTAACCGTGGAACTAACATCCTTATAAAGGATATGCTTTCT
plasmid_cp32-9	11086	BB_N17	2.697 ± 2.2818 0.137688	2.077 ± 2.0213 0.29144	0.935 ± 0.5586 0.76052	1.542 ± 0.9691 0.13331	GATACATCAAAAAATCCCTGATGGAATTCTTCGCCGAAGAAATTCT
plasmid_cp32-9	11087	BB_N17	1.742 ± 0.984 0.020177	0.469 ± 0.3688 0.33916	0.993 ± 0.5324 0.9609	1.005 ± 0.5501 0.94952	TCTACATTGAGACTCAATTAAAATCATATTGAGTAACAGCATT
plasmid_cp32-9	11090	BB_N17	2.080 ± 1.0217 0.071468	1.894 ± 1.8726 0.39885	0.924 ± 0.3747 0.64472	1.098 ± 0.5289 0.24319	CATAAAAAAATCCCTGATGGAATTCTTCGCCGAAGAAATTCTAA
plasmid_cp32-9	11293	BB_N17	1.629 ± 0.9709 0.409579	1.329 ± 1.4733 0.71836	0.376 ± 0.1297 0.02376	0.531 ± 0.3381 0.05479	AAAATATATTATAAGAAATTGCTCATAAAAAAATTGATTCTATAATG
plasmid_cp32-9	11301	BB_N17	2.024 ± 1.0786 0.100252	1.752 ± 0.8019 0.10836	0.994 ± 0.3853 0.97338	1.104 ± 0.4594 0.71973	ATATATTTACTATATCTCAAATTAAATGTCGTCGGTAGGGTCAAGGG
plasmid_cp32-9	12324	BB_N18	3.089 ± 1.3916 0.034401	2.922 ± 2.7959 0.33567	2.216 ± 1.5055 0.32594	0.96 ± 0.5418 0.72349	CTTAGTGCATTAGCCAAAGACTTAACTAATCTGTGACTGTAAA
plasmid_cp32-9	12328	BB_N18	2.257 ± 0.9378 0.013465	1.956 ± 1.4936 0.25853	1.103 ± 0.365 0.61716	1.11 ± 0.4042 0.47439	GTGCAATTAGCCAAAGACTTAACTAATCTGTGACTGTAAAATT
plasmid_cp32-9	12535	BB_N18	2.564 ± 3.1718 0.150247	2.647 ± 0.4099 0.34117	1.147 ± 1.2722 0.3719	1.135 ± 1.2191 0.56323	ATTATGATTAACAGTTGCTCAAGTAATTGTTGCTAATTATGGTATAAT
plasmid_cp32-9	12833	BB_N19	1.242 ± 1.438 0.773308	1.256 ± 1.4393 0.75649	0.379 ± 0.3157 0.09314	0.563 ± 0.4443 0.16736	AATCTAAGTAAAGCTTTAGATATTCTCATGAAAATAATTTCACAGCGT
plasmid_cp32-9	12876	BB_N19	1.768 ± 0.3764 0.018825	1.566 ± 0.4179 0.18438	1.112 ± 0.469 0.63261	1.768 ± 0.8066 0.18863	TATCCTTTTTCTCAGGCGATGTTGAATATGGAGTTAATTATGAG
plasmid_cp32-9	13140	BB_N20	1.529 ± 0.3813 0.14365	1.43 ± 0.5445 0.35326	1.238 ± 0.6144 0.46981	1.656 ± 0.3166 0.03083	AGTGCACCCGGTTCATTTAGAAAAAGAGATTAAGCTCATTAATT
plasmid_cp32-9	13267	BB_N20	0.408 ± 0.5009 0.106545	0.426 ± 0.5833 0.35824	0.236 ± 0.395 0.33984	0.429 ± 0.4283 0.43563	TGTTGGCTTACAGCTGCACTTTAAATTAGTAGTGTACTCACCTCATCAA
plasmid_cp32-9	13270	BB_N20	1.003 ± 0.9942 0.98761	0.522 ± 0.5829 0.08632	0.902 ± 0.742 0.7311	1.141 ± 0.9341 0.63623	TATCTAATTCTAAAGGAAACTTACTAGACACTAGTAACTACATTAATT
plasmid_cp32-9	13506	BB_N20	1.731 ± 0.9484 0.011602	0.568 ± 0.4902 0.47621	1.002 ± 0.6245 0.95467	0.853 ± 0.435 0.41696	GTTTTAAAGGTCAGTTATACTTACTTCATATAAACATATTCTTT
plasmid_cp32-9	13631	BB_N20	1.193 ± 0.9753 0.75635	0.952 ± 0.7671 0.92107	1.035 ± 0.1904 0.82323	0.507 ± 0.3133 0.07427	AAGGAATTAAAGTTATGAAATAAGTGTGTTAATTAGATAACAGACACTG
plasmid_cp32-9	13772	BB_N20	2.332 ± 1.1543 0.196333	1.661 ± 1.384 0.37552	0.246 ± 0.2607 0.00219	1.332 ± 1.3003 0.68045	TCTGCGTATTGAAAAGTAGCATTTGTCATTAATGGCAATATCTGA
plasmid_cp32-9	13775	BB_N20	1.998 ± 1.4711 0.016922	1.692 ± 2.0025 0.37303	1.207 ± 0.9726 0.52681	1.478 ± 1.328 0.45393	GATTGCTTATTGATATTGGAGTAACTGAAAGATTCACCAATTCTT
plasmid_cp32-9	13936	BB_N21	2.704 ± 1.6841 0.0454	1.626 ± 1.3658 0.25396	0.789 ± 0.4151 0.44207	0.873 ± 0.4566 0.69442	GAAAATATAAAATCAAGAGATATTGCAATATGGATATCTCAAGTTTCT
plasmid_cp32-9	14036	BB_N21	1.166 ± 2.0039 0.761035	0.896 ± 0.9264 0.181662	0.211 ± 0.3486 0.17053	0.091 ± 0.1652 0.17953	ATAGTGTATTGTTCTTACGTCATATTGCACTGATGAGTCATTAGAC
plasmid_cp32-9	14379	BB_N21	1.609 ± 0.8628 0.000695	0.352 ± 0.2631 0.22887	0.85 ± 0.4883 0.29993	0.955 ± 0.599 0.81845	CAGATGGTAAACAATTATAACTTTAACAACTAAGGAGGTTTATGGCTG
plasmid_cp32-9	14388	BB_N21	1.735 ± 0.2102 0.004447	1.269 ± 0.4045 0.35504	1.196 ± 0.1835 0.14085	1.236 ± 0.8078 0.69101	ACAATTATAACTTTAACAACTAAGGAGGTTTATGGCTGATGATCAAG
plasmid_cp32-9	15364	BB_N23	blyA 1.633 ± 1.1199 0.050517	1.717 ± 1.7818 0.33444	0.998 ± 0.631 0.99381	1.142 ± 0.8006 0.23369	AGTTTAATTCTATTAAATTGATAAGAAGTTCTGTTAATTAAATGATCC
plasmid_cp32-9	15450	BB_N23	blyA 1.272 ± 0.3658 0.047634	0.476 ± 0.3913 0.2802	1.092 ± 0.4254 0.18877	1.148 ± 0.4096 0.00875	CAATAGTCAATATGTCCTTAAATAAGGCTTGAAGAAGATTAACACTCTA
plasmid_cp32-9	15538	BB_N24	blyB 2.187 ± 1.7704 0.37625	2.734 ± 3.418 0.474	0.896 ± 0.8213 0.83749	0.718 ± 0.2821 0.15024	0.718 ± 0.2821 0.15024 ATGTTGAGCTTGGACTACGTCCTTACACCCATTGATATTTCTA
plasmid_cp32-9	15799	BB_N24	blyB 1.772 ± 1.486 0.197236	1.978 ± 1.8198 0.23385	0.967 ± 0.7715 0.94165	0.892 ± 0.8081 0.89080	GATATTGAGATTTTCTACAGAAATTAAGTCATGCAATTGATTGATTG
plasmid_cp32-9	15841	BB_N24	blyB 2.754 ± 2.3592 0.295607	0.83 ± 0.2954 0.16262	0.933 ± 0.7685 0.86469	0.847 ± 0.3466 0.62142	AGGAGAAAGAACAAATAATGCAAAATAACACTATTGGTTAGGACTTAAATT
plasmid_cp32-9	15905	BB_N25	0.915 ± 0.8752 0.793443	0.983 ± 0.7617 0.94141	0.634 ± 0.2375 0.14621	0.53 ± 0.2253 0.16005	GTTAACGCTTGTAGATTAATTAGTCCTAAACCAATTAGTGTATTGCTT
plasmid_cp32-9	15989	BB_N25	1.950 ± 1.6932 0.16281	1.917 ± 2.1049 0.33789	0.835 ± 0.5314 0.48595	1.225 ± 0.9267 0.12726	TATGTTGAGTAACTTACTATTACTAAAGTATTGTAATT
plasmid_cp32-9	15991	BB_N25	1.663 ± 0.5827 0.010858	1.362 ± 0.7454 0.24459	0.841 ± 0.3222 0.1767	1.385 ± 0.7616 0.23306	TATATGTTGAGAAAAAAATCTATTACTTACTAAAGTATTGTAATT
plasmid_cp32-9	15992	BB_N25	2.920 ± 1.4441 0.095607	1.405 ± 0.91 0.49128	0.641 ± 0.2536 0.31499	1.346 ± 0.7058 0.56127	TAAGCACACTAAATCTATGGAAACAGCTGAGTCACAAATTGTAAG
plasmid_cp32-9	15994	BB_N25	2.028 ± 1.0149 0.10249	1.678 ± 1.4675 0.41194	1.035 ± 0.4489 0.8214	1.037 ± 0.4096 0.69016	AGCACACAAATCTATGGAAACAGCTGAGTCACAAATTGTAAGAA
plasmid_cp32-9	16433	BB_N26	1.849 ± 0.556 0.059508	1.687 ± 1.3472 0.43206	0.884 ± 0.344 0.68092	0.976 ± 0.2894 0.88322	TGGAGTGTCTTGTAGTCTGATAAGTCTGATAAGGATATTCTGGAT
plasmid_cp32-9	16462	BB_N26	1.005 ± 0.5493 0.979851	0.393 ± 0.3936 0.29273	0.976 ± 0.4541 0.9227	0.686 ± 0.3268 0.29621	TATGTTGATATTGTCCTTACCGCAGTTATGGAGTGTCTTGTAGT
plasmid_cp32-9	16463	BB_N26	1.917 ± 0.6349 0.116708	0.957 ± 1.5824 0.9659	1.408 ± 2.3637 0.79629	1.044 ± 0.8894 0.94339	TATTTAGAGTACATTAACAAACAAACCAATAGCGGAAAAGTCATAAT
plasmid_cp32-9	16509	BB_N26	0.971 ± 0.4938 0.904475	0.545 ± 0.566 0.22696	1.017 ± 0.7667 0.9608	1.097 ± 0.6176 0.33562	AGACTTTTCCGCTATTGGTTTAAATGTCATTAAATGAT
plasmid_cp32-9	16573	IG 212	1.598 ± 0.6788 0.042603	1.642 ± 1.3386 0.3712	0.949 ± 0.3252 0.54898	1.073 ± 0.3823 0.18412	AAATAGAATTCTCTGAAGAAAACACCTTTGTAATTACATTAACTG
plasmid_cp32-9	16576	IG 213	2.209 ± 2.8498 0.062581	3.896 ± 3.0989 0.17978	1.262 ± 0.5698 0.57677	2.028 ± 0.3125 0.26523	CATATAAAATCTCTAACAGCCAATTAACTAAAGTGTATAATGACC
plasmid_cp32-9	16580	IG 214	2.870 ± 2.0168 0.079493	1.504 ± 1.592 0.45763	0.878 ± 0.5308 0.39524	0.906 ± 0.4544 0.81187	AAAAATCTCTAACAGCCAATTAACTAAAGTGTATAATGACCATAA
plasmid_cp32-9	17259	IG 215	1.198 ± 0.5527 0.468828	0.768 ± 0.7183 0.68541	0.899 ± 0.8413 0.89396	1.663 ± 1.1502 0.42171	TTAATACTAAATTTGGATAAACATTATTGTAATTGATGTTTAA
plasmid_cp32-9	17287	IG 216	1.582 ± 0.2579 0.021123	1.199 ± 0.3368 0.50027	0.826 ± 0.1932 0.04066	0.901 ± 0.2403 0.07012	AAAAAGGAATAACAATGAAAATTATCACATTATTGTTTATTGTT
plasmid_cp32-9	17288	IG 217	1.648 ± 0.6625 0.242626	1.054 ± 0.4431 0.89052	0.853 ± 0.3544 0.51468	1.076 ± 0.4385 0.67527	AAAAAGGAATAACAATGAAAATTATCACATTATTGTTTATTGTT
plasmid_cp32-9	17829	BB_N29	2.262 ± 1.0317 0.037917	1.819 ± 1.4259 0.29635	1.124 ± 0.4821 0.34943	1.102 ± 0.4238 0.45405	TTAATGGACTAGGGCCATAAGCAGTCCTCTAACGACACAAACTTCAA
plasmid_cp32-9	17903	BB_N29	3.784 ± 3.3828 0.189866	2.43 ± 2.5805 0.32038	1.391 ± 0.839 0.09534	1.224 ± 0.8406 0.24627	TTATTTCTGAAATAGTTTATACTCCGCCAATAGTTTACTT
plasmid_cp32-9	18033	BB_N29	1.882 ± 0.865 0.131304	2.351 ± 1.3943 0.12706	0.718 ± 0.3312 0.0824	1.427 ± 0.5635 0.01125	TATCTGAAATAAGCTTATTGTTAATTGAGTTTATATTGTT
plasmid_cp32-9	18071	BB_N29	2.717 ± 0.9011 0.086664	2.836 ± 2.9377 0.3991	1.472 ± 0.6924 0.39016	1.655 ± 0.2891 0.06519	TAAACTCAATTACCAAAAGCTTATTGAGATGACCCAAATA

plasmid_cp32-9	18353	BB_N29		1.346 ± 1.4767 0.235652	2.104 ± 2.361 0.3711	0.558 ± 0.7286 0.46995	0.763 ± 0.981 0.8221	ATATAAAAAGC GAAATGGGATCTGATGCACCTATTACAATAATTATG
plasmid_cp32-9	18542	BB_N29		1.435 ± 1.2351 0.648364	0.959 ± 0.4702 0.92193	0.678 ± 0.5904 0.35066	0.641 ± 0.4509 0.41465	TAGTTCATGTTATTAGGACACATTCTACAGCACAAGCAGTGGGTATAGAG
plasmid_cp32-9	18649	BB_N29		1.143 ± 0.8614 0.641332	1.019 ± 0.5838 0.96969	0.713 ± 0.4505 0.32324	0.682 ± 0.4686 0.51389	TCAGGATTTCATGACATATTAGAAGGAAATTGAAAACGTTATTGAAAAGCA
plasmid_cp32-9	18809	IG_218		2.243 ± 0.7657 0.078946	1.406 ± 0.6395 0.40238	1.022 ± 0.2591 0.83102	1.306 ± 0.2394 0.1742	ATAAAATATAAGTATAGC AAAA ACTATT TTG CCAACTTCTTACAAAAAA
plasmid_cp32-9	19020	IG_219		1.915 ± 1.2164 0.045227	1.201 ± 1.3487 0.69949	1.275 ± 0.6507 0.41185	1.024 ± 0.6816 0.70961	TATTTTTACTAA ATTACAAATT TTTTATATTAAATTAAACAAAATTAAATT
plasmid_cp32-9	22293	BB_N34	<i>bdrQ</i>	0.931 ± 1.2842 0.904131	0.662 ± 0.4995 0.29566	0.499 ± 0.438 0.09558	0.452 ± 0.3093 0.03078	ATTACA ACTATGAGGTT TAAAAGGAAAATTGATGAGAAAAGAATT
plasmid_cp32-9	22584	BB_N34	<i>bdrQ</i>	2.275 ± 1.1435 0.124235	1.573 ± 0.6409 0.13127	1.377 ± 0.9351 0.47413	1.058 ± 0.8278 0.89136	TATTTAGCCTAGATAATAAAATAATGTTAAAAAACGA ACTTACTGCAA
plasmid_cp32-9	22849	IG_220		1.779 ± 0.8763 0.201304	1.422 ± 1.3343 0.58605	0.997 ± 0.4258 0.97613	0.948 ± 0.5516 0.88687	GAATTA AAAATT TTTG TATTG TAA AAAAAAGAACCTTTAAATTCT
plasmid_cp32-9	23022	IG_221		0.946 ± 0.4682 0.862626	0.538 ± 0.4537 0.44133	1.07 ± 0.7079 0.74504	1.28 ± 0.975 0.294	GCTAAAAAAATAT TGTCTCA AAAAATCCA ATTAAAGTGGGTTAGCT
plasmid_cp32-9	23219	BB_N35	<i>bppA</i>	1.497 ± 1.4571 0.392884	0.942 ± 0.7971 0.93865	1.031 ± 0.615 0.95357	2.221 ± 1.1333 0.00746	ATCCACAA GAAA ATTCAAGGAGAGCT CAAA ATGATAAGTATTAAACAC
plasmid_cp32-9	23548	BB_N35	<i>bppA</i>	0.058 ± 0.1034 0.049816	0.705 ± 0.7083 0.53294	0.377 ± 0.3693 0.27163	0.415 ± 0.4121 0.26005	TATATGCTCAAGGGCAAAGAGTTAGAGAATT TAGGATTAGAGA
plasmid_cp32-9	23552	BB_N35	<i>bppA</i>	1.140 ± 0.7754 0.784721	0.614 ± 0.4781 0.1065	0.711 ± 0.8514 0.24077	0.513 ± 0.3552 0.24065	TGCTCAAGGGCAAAGAGTTAGAGAATT TAGGATTAGAGA
plasmid_cp32-9	23732	BB_N35	<i>bppA</i>	2.827 ± 2.6101 0.234196	1.303 ± 1.1406 0.53498	1.169 ± 1.0841 0.83795	1.263 ± 0.7677 0.6663	TTAATAAACCGCCATCAATT GTGAGGCCACTAAAGTTCTGAACTGCC
plasmid_cp32-9	23895	BB_N35	<i>bppA</i>	0.462 ± 0.2845 0.239022	0.229 ± 0.2498 0.15076	0.99 ± 0.5968 0.95067	1.07 ± 0.9194 0.79762	CTAACGCCAGTGCTAGCTGTATTGCTGTACATAATATTGAA
plasmid_cp32-9	23920	BB_N35	<i>bppA</i>	3.463 ± 2.5811 0.080509	2.37 ± 2.715 0.33712	1.041 ± 0.6824 0.69869	1.225 ± 0.8096 0.07955	GATGCTG CACCAATTAACTGTAAGATTAAAAGAGATGAGGCC TAAATCA
plasmid_cp32-9	23965	BB_N35	<i>bppA</i>	1.997 ± 1.0621 0.261423	2.031 ± 2.1348 0.48237	1.238 ± 0.7532 0.60521	0.626 ± 0.2975 0.28114	ATATCAAAGT GTTGAATTGTAATAAT GTGAATTAGAAATTATAAAT
plasmid_cp32-9	24026	BB_N35	<i>bppA</i>	1.651 ± 0.428 0.071157	1.642 ± 1.3846 0.50009	0.923 ± 0.1737 0.63921	1.022 ± 0.3509 0.91612	TCTTTTTCAAA TTATAATTCTAATT CACATT TATAACAAATTCAAAC
plasmid_cp32-9	24030	BB_N35	<i>bppA</i>	1.741 ± 0.9853 0.243392	1.037 ± 1.5737 0.97646	0.595 ± 0.5788 0.00165	0.855 ± 0.4955 0.76455	AATATCTTTTCAAATTTATAATTCTAATT CACATT TATAACAAATT
plasmid_cp32-9	24035	BB_N35	<i>bppA</i>	1.611 ± 0.5618 0.140717	0.939 ± 0.3927 0.85157	0.887 ± 0.4393 0.17871	0.877 ± 0.412 0.08171	GTA ACTATAGAGAGGA ACTTAATGGC ACATAATT TAA CGAGGGTACGT
plasmid_cp32-9	24038	BB_N35	<i>bppA</i>	1.942 ± 1.1948 0.103523	1.787 ± 1.7484 0.38351	1.001 ± 0.4318 0.99377	1.034 ± 0.4682 0.79474	ACTATAGAGAGGA ACTTAATGGC ACATAATT TAA CGAGGGTACGT
plasmid_cp32-9	24171	BB_N35	<i>bppA</i>	1.097 ± 0.4422 0.269712	0.871 ± 0.372 0.47512	0.957 ± 0.3876 0.72002	1.175 ± 0.471 0.10133	TTCTATAAACTCTTACCCAATCAACTC CAGA ACTTAA AACAAAT
plasmid_cp32-9	24341	BB_N35	<i>bppA</i>	2.540 ± 1.6035 0.064835	1.618 ± 1.5442 0.37948	0.954 ± 0.4718 0.7621	0.751 ± 0.4397 0.15411	ATATTGTAATTAGCATCTCAACCTTCTTAA TGGGTTCTTCTT
plasmid_cp32-9	24344	BB_N35	<i>bppA</i>	1.872 ± 1.0498 0.327023	2.601 ± 1.579 0.29798	0.615 ± 0.4628 0.38399	1.075 ± 0.4626 0.62713	CGAACATACAT CACTAATT GTGAGCAGTAA ATTATAAATT TGGAGAGTTG
plasmid_cp32-9	24448	BB_N35	<i>bppA</i>	1.186 ± 0.3651 0.456082	1.433 ± 1.0173 0.56569	0.734 ± 0.1516 0.38955	0.966 ± 0.5208 0.90423	CTACCAACAGTGGTACAGTATT TCC TAGCAATATG CATT TGCAAAT
plasmid_cp32-9	24559	IG_222		1.701 ± 0.6095 0.229933	2.272 ± 0.4882 0.02135	0.898 ± 0.6779 0.79662	1.959 ± 0.3896 0.0453	GGAGGATTAA TTAATGCTTATAAAATAA ACAAGATAATAGAACTTT
plasmid_cp32-9	24896	BB_N36	<i>bppB</i>	2.549 ± 0.5231 0.010414	1.478 ± 0.8257 0.45329	1.285 ± 0.3561 0.19646	1.316 ± 0.2777 0.1374	TAAAGT GATAT CATTAA CCTTACCTTAC TCGATT TAACTC GCTT ATT CAAATT
plasmid_cp32-9	24897	BB_N36	<i>bppB</i>	2.326 ± 0.30465 0.529316	0.097 ± 0.1686 0.0044	1.505 ± 1.9273 0.6992	1.838 ± 1.4571 0.41087	TAGCAACAAA AATAAAGAAATTAT TATGATT CACTT GACTGAAACCTC
plasmid_cp32-9	24899	BB_N36	<i>bppB</i>	0.756 ± 0.3064 0.316724	0.641 ± 0.5519 0.46336	1.022 ± 0.2908 0.76637	1.037 ± 0.3735 0.69146	GCAACAAA AATAAAGAAATTAT TATGATT CACTT GACTGAAACCTG
plasmid_cp32-9	26138	IG_223		1.439 ± 0.5049 0.261526	1.358 ± 0.9163 0.49378	1.086 ± 0.4039 0.67268	1.123 ± 0.4984 0.74614	ATT TTGTTACATT CAGCTTACATTAATCAACAA ACTCAA ATGTAATT
plasmid_cp32-9	26255	BB_N38	<i>erpP</i>	3.698 ± 3.119 0.067559	2.005 ± 1.8657 0.06146	1.985 ± 1.6899 0.3034	0.94 ± 0.7195 0.8764	TTCTAGGTGCTTGC CAAATT CACTT CATGATGAGC AAAGTAGTGGT
plasmid_cp32-9	26578	BB_N38	<i>erpP</i>	2.365 ± 2.0978 0.11284	2.166 ± 2.7304 0.37144	1.111 ± 0.9536 0.42215	1.221 ± 0.9061 0.24153	CAAATGTTGTTAA TGTGCG CTTT TAGT CATT GCTT TATAAAGGTATT
plasmid_cp32-9	26940	BB_N39	<i>erpQ</i>	1.156 ± 0.9227 0.79122	1.891 ± 2.0607 0.47684	0.892 ± 0.8728 0.86062	1.54 ± 0.6177 0.21428	TCTTTACTGGTAC TAACTCTT ATTACAA CCTT TAATT TCCC TTCT
plasmid_cp32-9	27669	BB_N39	<i>erpQ</i>	4.328 ± 4.0177 0.28299	4.067 ± 2.9015 0.21359	2.02 ± 0.7089 0.04348	1.993 ± 1.5651 0.35635	TATGGTTATTG CTT CATTAA TTTAGTTG CTTAGC GCGT CCCTAGCATCA
plasmid_cp32-9	27830	IG_224		1.262 ± 0.5919 0.03332	0.71 ± 0.4322 0.52833	1.192 ± 0.6187 0.0616	1.277 ± 0.7125 0.24144	ATTACTGACTGTCA CTGATG TATCCTTAA TTTCTCAA ATT TGAACAA
plasmid_cp32-9	28142	BB_N41		1.899 ± 1.4898 0.128948	2.031 ± 2.1074 0.30731	1.006 ± 0.7062 0.96412	0.845 ± 0.5041 0.45474	TA GCTCTTAA AGCAGCG CAGA ATAC GGA AAAAA ACTGG AAAAGCAC
plasmid_cp32-9	28434	BB_N41		1.609 ± 0.6676 0.179859	1.644 ± 0.8884 0.17492	0.844 ± 0.2459 0.41178	0.723 ± 0.3016 0.38666	ATTGATATTGTTGAA ACTTTT GATAA ATAT GTGTTAAGA ATACCA TAA
plasmid_cp32-9	28459	BB_N41		2.011 ± 1.1872 0.032624	1.375 ± 1.196 0.67903	0.673 ± 0.5154 0.58688	0.906 ± 0.4612 0.71382	TCTTTAACTCTGTTGATCATAATT GTGATT TGTGTTAA CT TTTT
plasmid_cp32-9	28607	IG_225		1.927 ± 1.0938 0.055449	1.559 ± 1.2202 0.26328	1.127 ± 0.6058 0.41081	1.252 ± 0.5816 0.19144	AAAGT CAA AAAA AT CACCA ACAC CTG TCA ATAG AT CAAT AAGA TATAG
plasmid_cp32-9	29064	BB_N42		2.030 ± 1.0985 0.004702	1.395 ± 0.993 0.29471	0.694 ± 0.3647 0.20617	0.966 ± 0.6845 0.69058	TGC CATACTTAA AGGAA ATT GAGGCC AAT GAGC GTT AA TAA AAG
plasmid_cp32-9	29308	BB_N43		1.926 ± 0.689 0.067709	2.062 ± 1.3231 0.23816	0.921 ± 0.3078 0.60675	1.088 ± 0.3598 0.5124	TATCAAACAA ACTTTT CACACT CAAAGGA ATACAA AAAA ATAT
plasmid_cp32-9	29405	BB_N43		3.308 ± 0.5746 0.440605	1.485 ± 0.7228 0.21733	1.04 ± 0.4706 0.87547	1.014 ± 0.3179 0.86786	ATT TGATAAGTTGAA GAAA AACACT GTTAA CT TAAAC AAAA ATGTGA
plasmid_cp32-9	29659	BB_N43		1.421 ± 0.7014 0.431629	1.497 ± 0.9934 0.49241	0.623 ± 0.1554 0.0644	0.905 ± 0.1749 0.27667	TGTAACCTCTTAA CCTT ATAT CCAAGACATACAA ATT CATAT
plasmid_cp32-9	29672	BB_N43		1.934 ± 1.2486 0.036689	2.535 ± 3.6094 0.44581	1.235 ± 0.9606 0.1264	1.139 ± 1.0724 0.59481	AAATCC TTT ATAT CCAAGACATACAA ATT CATAT ATT GTGATT G
plasmid_cp32-9	29783	BB_N43		1.017 ± 0.4648 0.711741	0.468 ± 0.3649 0.2732	0.943 ± 0.4183 0.05588	0.978 ± 0.358 0.69373	C TTCCC TAA ATCTT CAAAC TACT GCGCTT AT CTC CACCAT ATAGATTA
plasmid_cp32-9	29786	BB_N43		1.059 ± 0.8377 0.734276	0.446 ± 0.3776 0.37997	0.948 ± 0.6052 0.87889	0.883 ± 0.6324 0.62994	ATT CAGCACTT ATT GTGTTGAA TGTGAGCT CACAC CAAAGCA ACTT
plasmid_cp32-9	29928	BB_N43		3.100 ± 1.2664 0.046576	1.569 ± 0.5535 0.08419	0.736 ± 0.2286 0.08036	0.942 ± 0.3621 0.86187	ATCG GTT AAA ATAGT GTGCTG GATG CAGGATTAGT CAA AAAA ATAT
plasmid_cp32-9	29931	BB_N43		3.922 ± 2.7306 0.192841	2.975 ± 2.9642 0.34141	1.466 ± 0.8418 0.50656	1.614 ± 0.5741 0.02487	TATG GATAAT ATAGCGACATT AAAGATATA ATT TCAACAACTT GATAA
plasmid_cp32-9	29986	BB_N43		1.887 ± 1.4119 0.284066	0.47 ± 0.3208 0.24251	1.322 ± 0.8694 0.40491	1.422 ± 0.9299 0.33639	GCACATTACATAAGTGTAAA ATTATAT CAAAT GTCGT ATTAT
plasmid_cp32-9	30042	BB_N43		1.780 ± 1.182 0.097431	0.831 ± 0.5684 0.12536	0.759 ± 0.4928 0.11244	0.912 ± 0.5951 0.18953	TGATGGTATCTTATAGAGTTTCTTGTGTTGATAAATCCCTTACT

plasmid_cp32-9	30044	BB_N43	2.175 ± 1.7359 0.06121	1.176 ± 0.9945 0.09672	0.78 ± 0.5098 0.48711	0.873 ± 0.5689 0.63464	TATGATGGTATATCTTATAGAGTTTCTGTGTTCGATAAACCTTTA
plasmid_cp32-9	30122	BB_N43	1.655 ± 0.2793 0.006932	1.619 ± 1.3619 0.4694	0.791 ± 0.202 0.24148	0.792 ± 0.5180 0.449	TAATCATCAGTAATTTATTGTGAAAAATTGAATCAGTGCTGCTATC
plasmid_cp32-9	30134	BB_N43	2.091 ± 1.0261 0.17938	2.198 ± 2.3012 0.46363	0.943 ± 0.8213 0.90657	1.534 ± 0.9428 0.45366	GCCCGATAGCATATTAGACCCAGCATTAGTGTGGAGGGGATAACACTG
plasmid_cp32-9	30190	BB_N43	4.050 ± 2.5519 0.151361	2.063 ± 1.1417 0.22866	2.108 ± 0.5195 0.00205	2.673 ± 1.4068 0.11865	TGTGTTATGGAGCGAGTTGATGATAAGTATTATGCTTTGATTTCAAGAC
plasmid_cp32-9	30215	BB_N43	2.200 ± 1.0538 0.144302	1.301 ± 0.862 0.64653	0.867 ± 0.4434 0.74109	0.751 ± 0.3115 0.24333	AGTATTATGCTTTGATTTCAAGACCAACGACCAGCCAATGATCCTTATA
plasmid_cp32-9	30261	BB_N43	0.516 ± 0.4045 0.093094	0.469 ± 0.3859 0.05542	0.722 ± 0.2708 0.00654	0.848 ± 0.2889 0.34135	AGGATCATGGCTGGCTGGCTTGAATACAAAAGCATATACTTATC
plasmid_cp32-9	30503	BB_N43	0.312 ± 0.4597 0.113528	0.603 ± 0.7168 0.38376	2.224 ± 1.1038 0.08757	0.173 ± 0.112 0.02148	GTTCTCTGTATTTAATGATATTTCGATAAGGGGGATAGCAAACCC
plasmid_cp9	37	IG 226	1.213 ± 1.0272 0.048063	0.795 ± 0.6697 0.54665	0.981 ± 0.8557 0.86579	0.968 ± 0.73 0.933	TATAATATAAAATTGATTATAGTTAACATAGCCTA
plasmid_cp9	1399	BBC02	2.017 ± 2.0823 0.363929	1.041 ± 1.2516 0.84854	1.583 ± 1.4123 0.32624	2.104 ± 1.5027 0.05867	ATGATGGATATTCAAATTAGGAATTGTTAATGTTAAAAAAATCAATT
plasmid_cp9	1854	IG 227	1.205 ± 1.1377 0.559678	1.5 ± 1.4022 0.43278	1.482 ± 1.1559 0.03755	1.183 ± 0.9459 0.4008	ATAAAGGAAATGTTGACAAAAATAAAGGAAATTGGAAAAAAAC
plasmid_cp9	1994	BBC03	0.478 ± 0.7758 0.574043	0.08 ± 0.1645 0.31772	0.18 ± 0.3661 0.39032	0.762 ± 1.2761 0.30938	GTGCTTGTATAAGAAATTTCATTAACTTAACTTGTCAA
plasmid_cp9	1997	BBC03	1.379 ± 1.4645 0.206034	1 ± 1.2191 0.99955	0.913 ± 1.0287 0.43069	1.15 ± 1.2742 0.03686	AAGGAAAAGTGAATGACAATTCCAAAAGAAATATTCCACAGGGTGGAA
plasmid_cp9	2297	BBC03	1.334 ± 1.0861 0.613802	0.672 ± 0.808 0.68298	1.012 ± 0.9211 0.98778	1.27 ± 1.0433 0.66097	TTGGATTTGCCTAGATTTCCTAACGCCGACTTCTTATCTTTATAA
plasmid_cp9	2449	BBC03	0.637 ± 0.1827 0.153958	0.374 ± 0.3251 0.14877	0.985 ± 0.2057 0.93132	1 ± 0.2614 0.99826	GATTTTAGTCTCATTTCTAAAGTTTTAAGAAAATCTTTTG
plasmid_cp9	2774	IG 228	1.650 ± 0.8955 0.331939	0.363 ± 0.1946 0.04349	1.107 ± 0.9402 0.85033	1.622 ± 0.8331 0.28733	TAAGAAAATTATAACTTACGGAGTAAAAAAATGAAAACCGCAAAACAA
plasmid_cp9	2923	BBC05	0.226 ± 0.4822 0.502386	0.17 ± 0.3829 0.47082	0.045 ± 0.0998 0.35167	0.029 ± 0.0666 0.37318	TGGCTATAAGTATCAGAATTCAACGAAATAGCTAGAGAAATTAAAAAGT
plasmid_cp9	2932	BBC05	0.841 ± 0.8882 0.679508	0.847 ± 1.0026 0.33168	1.652 ± 1.4561 0.11876	1.77 ± 1.4111 0.15964	CTTATAGCCATAACCTTAAAGATTTTATCAATCCCCGCAAGTCATCCT
plasmid_cp9	2935	BBC05	0.688 ± 0.6277 0.018325	0.696 ± 0.7415 0.02123	1.159 ± 0.9359 0.15143	1.249 ± 0.909 0.26856	TCAGAATTCAACGAAATAGCTAGAGAAATTAAAAAGTTATTGATAAGCA
plasmid_cp9	3047	BBC05	0.605 ± 0.6185 0.023666	0.931 ± 1.1016 0.86577	1.07 ± 0.789 0.53091	1.073 ± 0.5884 0.8052	GAACCTGTTGCTCCCCACAACGTAAAAGTCGAAATTGCTTAAACATCAA
plasmid_cp9	3050	BBC05	0.588 ± 0.5802 0.015016	0.63 ± 0.6293 0.02945	0.883 ± 0.6067 0.01683	0.968 ± 0.5725 0.71758	CATGTTGAGAACACTCGTTTATAGTACAAACACTGGGTATAAGACTCC
plasmid_cp9	3075	BBC05	2.305 ± 0.177 0.00662	1.564 ± 1.0702 0.03252	1.276 ± 0.297 0.2687	1.508 ± 0.4409 0.19183	CTATAAAACGTTAGTTCTAACACATGTAGAACTTGTGCTCCCCAACACT
plasmid_cp9	3224	BBC05	1.699 ± 1.475 0.475124	0.954 ± 0.9802 0.72082	0.788 ± 0.6577 0.63512	0.863 ± 0.8029 0.59547	GTAGCATATCTAACATAGAGAAGTGGATACTGATGTCAGCTCTT
plasmid_cp9	3274	BBC05	0.264 ± 0.4742 0.043174	0.35 ± 0.4424 0.29731	0.114 ± 0.1647 0.12014	0 ± 0 0.06131	AATAGGAGTCGCATCAGTATCCACTTCTATGTTAAGATATGTCAC
plasmid_cp9	3282	BBC05	1.519 ± 1.1923 0.357859	0.716 ± 0.8573 0.18468	0.906 ± 0.7211 0.73592	0.997 ± 1.0448 0.99589	ACACGAAAATGAAAATTCTATGCCTAGCAAACAGCTGGTTAACAAA
plasmid_cp9	3376	BBC05	1.200 ± 1.016 0.814254	0.892 ± 0.4657 0.62927	0.685 ± 0.3531 0.40963	0.894 ± 0.6158 0.12446	ATACTTCCGGTTTTAACTTTTATCAAAATTTCATTCTGTTGGTT
plasmid_cp9	3473	BBC05	2.038 ± 0.7214 0.081361	1.527 ± 0.517 0.01174	1.227 ± 0.6885 0.64996	0.921 ± 0.6985 0.78566	ATGCCGAATAAGGCATTATATTATTTCTTTCATCATTTACCC
plasmid_cp9	3476	BBC05	1.757 ± 0.1852 0.014645	0.973 ± 0.0858 0.68557	0.965 ± 0.1594 0.47059	1.137 ± 0.0957 0.15856	TGTTTGAATGAGGCGATTAGATGAAATTTTAATGATAATCCTGGG
plasmid_cp9	3596	BBC05	1.601 ± 1.2647 0.455312	1.226 ± 1.2824 0.80247	1.519 ± 0.9065 0.45909	1.653 ± 1.1715 0.38591	GTTCATCTAATTATTAGTTCTGAAATATTCTAAAGAAATTGGCC
plasmid_cp9	3620	BBC05	0.924 ± 0.1404 0.403562	0.803 ± 0.6937 0.66374	1.257 ± 0.2932 0.25244	1.539 ± 0.3006 0.08002	ACTAATACTACGACGTTTATGAAACAACTGCTTGAATTCTTGCATG
plasmid_cp9	3759	IG 229	0.939 ± 0.2618 0.789654	0.998 ± 0.6129 0.99459	1.016 ± 0.4759 0.94723	0.951 ± 0.2467 0.57952	TTAAGATATTGGCTTTCTACTCGCTTATATAATGCTATACAGCC
plasmid_cp9	3797	IG 230	1.670 ± 0.1627 0.010697	0.978 ± 0.1442 0.84928	1.033 ± 0.2061 0.79752	1.197 ± 0.2342 0.1174	GCATTATATAAGCGAGTAGAGAAAGCAAAATATCTAAATTGATTAAT
plasmid_cp9	3800	IG 231	0.652 ± 0.7104 0.616631	0.698 ± 0.7365 0.70935	0.486 ± 0.434 0.32856	0.488 ± 0.4362 0.40793	TCTATACGCCCTCATAAAGGTTAAATTATTCTTTAAAGCTATTAAAAA
plasmid_cp9	3860	BBC06	1.272 ± 0.9523 0.386045	0.986 ± 0.8142 0.9733	0.999 ± 0.9448 0.99627	0.733 ± 0.5873 0.29322	AAGATTAAGTTAAAATAGCTAAAAAGAAATAATTAAACCTTATGA
plasmid_cp9	3888	BBC06	0.172 ± 0.3044 0.138805	0.83 ± 0.7068 0.58797	1.052 ± 1.2696 0.95843	0.294 ± 0.5143 0.02012	TTAAAACAAATTTCGGAGCTTGCCTAAAGGATTAAGTTAAAAATAGCT
plasmid_cp9	4040	BBC06	3.061 ± 3.2674 0.406774	1.707 ± 1.9166 0.58798	2.006 ± 1.6824 0.44628	0.334 ± 0.3311 0.1614	GTCTCATAAAGGGCTATCCAAATTCAATTTCGATTATTAACATTAG
plasmid_cp9	4199	BBC06	1.981 ± 2.0901 0.049646	0.273 ± 0.5327 0.15731	0.75 ± 0.7453 0.59291	0.33 ± 0.5428 0.34113	AAAGCTTTTTGCTAAAGCTCCAGAAATTAGGGGAAGTTAACAAAAAA
plasmid_cp9	4302	BBC06	2.213 ± 1.5582 0.271949	0.795 ± 0.4124 0.36283	0.404 ± 0.4059 0.26432	0.758 ± 0.517 0.21448	TATCTGACTCATAAAGGACTTAACATGCTTAACATAAATAAATAAA
plasmid_cp9	4326	BBC06	1.816 ± 1.1375 0.191252	1.327 ± 0.7119 0.04314	0.803 ± 0.3776 0.49858	0.704 ± 0.3518 0.39509	AATACTGCTTAAACATAAATAAATACAAATAGGCTTATTTCTCA
plasmid_cp9	4379	IG 232	1.912 ± 0.312 0.002474	0.971 ± 0.2826 0.89804	1.067 ± 0.2 0.51501	1.082 ± 0.425 0.65317	TCCTCTCTAGGCTTATTATATACATCTTATTAGCAACTATAAGAA
plasmid_cp9	4396	IG 233	1.797 ± 1.4423 0.348516	0.419 ± 0.5185 0.03656	0.816 ± 0.3487 0.31547	1.114 ± 0.5345 0.77345	ATAAGGCTTAGGAGAGGATATGAGAAAAAAATAGCCTATTGTTATT
plasmid_cp9	4411	IG 234	2.098 ± 1.0646 0.057946	1.149 ± 0.7593 0.58176	1.109 ± 0.664 0.61107	1.631 ± 0.9464 0.33231	ATAAGATGTATAAATAAAGCCTAGGAGGAGATGAGAAAAAAATAGCCT
plasmid_cp9	4575	BBC07	0.837 ± 0.7721 0.612071	0.842 ± 0.8504 0.65565	1.268 ± 0.7303 0.29044	1.198 ± 0.7106 0.52526	TTGTGAAAAGAAAAACACTCTTCTATGGTACGCATTAAATTGTTAAC
plasmid_cp9	4694	BBC07	2.340 ± 1.8765 0.144795	1.216 ± 1.2361 0.77982	1.262 ± 1.45 0.81829	1.281 ± 1.3427 0.74313	GTCTCTAACACAGCAATTTCCTATTAGTGTAGAAAAATTCTTGTGAA
plasmid_cp9	4998	IG 235	1.307 ± 0.5652 0.196801	0.939 ± 0.6528 0.60394	0.799 ± 0.4045 0.63877	1.066 ± 0.4917 0.77749	TTATTGAAAGTAAACATAAAGGAAATTCAAGAAATAGTTATATTTT
plasmid_cp9	5230	IG 236	1.365 ± 2.678 0.717646	0.252 ± 0.4945 0.35952	0.836 ± 1.6399 0.70133	0.262 ± 0.5135 0.42767	TATAAAAACACTAAATTTGACTATATGTCATTAGGCCATTAAAC
plasmid_cp9	5244	IG 237	0.717 ± 0.1835 0.162311	0.42 ± 0.3649 0.15995	0.901 ± 0.1145 0.40223	0.976 ± 0.129 0.548	GTATATCACATTCAGTCTAACCTCCCTGAAACTACCACTTTGTTATT
plasmid_cp9	5336	IG 238	1.489 ± 1.0441 0.144399	1.016 ± 0.9083 0.95874	0.62 ± 0.3994 0.23801	1.349 ± 1.0128 0.22456	GTGCTAACATTAACATAAAGGCTATAGAGTAAACAAACAC
plasmid_cp9	5551	BBC08	1.811 ± 3.0394 0.058387	0.88 ± 1.5316 0.7765	1.028 ± 1.4323 0.97197	1.962 ± 2.7598 0.47132	TAATGAGCATTACTTACAAGTTTATTAAAGGGGGATTATT
plasmid_cp9	5580	BBC08	1.733 ± 1.3289 0.133644	0.914 ± 0.5907 0.38908	1.056 ± 0.5486 0.81004	1.232 ± 0.949 0.23159	TTTATAAAGGGGGATTATTGACTCAATTAAATGATGATACCAT

plasmid_cp9	5624	BBC08	1.359 ± 0.9469 0.05732	0.733 ± 0.639 0.1571	0.72 ± 0.4491 0.38405	1.154 ± 0.7394 0.37672	TATCATCATTAAAATATTGAGTCATAATAAATCCCCCTTATAAATAAAAC
plasmid_cp9	5651	BBC08	1.324 ± 0.6161 0.2539	0.87 ± 0.3712 0.61407	0.945 ± 0.4241 0.6254	1.033 ± 0.5302 0.83518	ATTAGAAAATATGACCAAACCTTGTGCGCTGTGGGGCTAAAATAAACAA
plasmid_cp9	5719	BBC08	1.415 ± 1.707 0.597325	1.015 ± 1.2052 0.86973	1.335 ± 1.6702 0.16314	0.825 ± 0.9363 0.69219	TGGATTAATAGCATTTTATTTGTCTATTTTGGCTATTAGGATTTTC
plasmid_cp9	5723	BBC08	1.377 ± 0.6709 0.270255	0.885 ± 0.5064 0.47084	0.852 ± 0.4389 0.60685	0.984 ± 0.4798 0.95545	ATCCATAATAAGTTTATTTGTCTATTAGCCCACAAGCGACAC
plasmid_cp9	5885	BBC08	1.254 ± 0.6839 0.28598	0.917 ± 1.1802 0.90477	1.18 ± 0.7814 0.2469	1.448 ± 1.0049 0.51117	GTCCTGTTGACTGTTAGTATACTTTTTTGTAATAGATTAAATC
plasmid_cp9	6020	IG 239	1.119 ± 0.7142 0.626351	0.005 ± 0.0089 0.06074	0.222 ± 0.3982 0.05342	1.066 ± 0.9532 0.93599	GTTACAATTCTAATGTCTATAAAAATTAAACCAAAATATAAATATCA
plasmid_cp9	6061	IG 240	2.566 ± 1.5489 0.048488	1.297 ± 0.8145 0.5761	1.302 ± 0.9223 0.67662	2.227 ± 1.4613 0.00313	TATATTTGGTTAATTTATAGACATTAGAAATTGAACTACTATGAA
plasmid_cp9	6070	IG 241	1.695 ± 1.304 0.086797	0.931 ± 0.6817 0.60967	0.905 ± 0.7162 0.33618	1.1 ± 0.8107 0.23315	TGATATTATATATTGGTTAATTTTATAGACATTAGAAATTGAAAC
plasmid_cp9	6075	IG 242	3.039 ± 1.114 0.034635	1.259 ± 1.162 0.76551	0.791 ± 0.5184 0.63643	1.041 ± 0.4202 0.51103	TATATCCTCTAATCTCAAGTTGGGGTTGGCATAAAAGTCTATGTT
plasmid_cp9	6077	IG 243	1.132 ± 0.6194 0.262812	0.847 ± 0.5708 0.08011	0.917 ± 0.7108 0.5042	0.985 ± 0.7039 0.95319	TATCCTCTAATCTCAAGTTGGGGTTGGCATAAAAGTCTATGTTG
plasmid_cp9	6079	IG 244	1.430 ± 1.2785 0.653638	1.055 ± 1.0721 0.93565	0.532 ± 0.6772 0.58275	0.492 ± 0.7031 0.55851	TCCCTCTAATCTCAAGTTGGGGTTGGCATAAAAGTCTATGTTGCGT
plasmid_cp9	6087	IG 245	1.474 ± 0.373 0.067026	1.23 ± 0.2446 0.18017	0.946 ± 0.5103 0.7798	0.927 ± 0.1913 0.5225	ATCTCAAGTTGGGGTTGGCATAAAAGTCTATGTTGCTTTTG
plasmid_cp9	6167	IG 246	1.578 ± 0.8255 0.301895	1.229 ± 1.1773 0.77554	0.865 ± 0.694 0.82937	0.691 ± 0.8896 0.25719	AATTGCTCTAGTGTCTAGCTCAATTGGTACATAATTAAAGTTAGAA
plasmid_cp9	6207	IG 247	1.582 ± 0.2558 0.051851	1.467 ± 0.4626 0.21979	0.995 ± 0.3835 0.97991	1.324 ± 0.646 0.50843	AAGTTAGATAACTATATTAGTGTAGTAATAGATATTATTTAAG
plasmid_cp9	6220	IG 248	1.437 ± 1.132 0.198332	0.964 ± 0.825 0.76741	1.081 ± 0.7269 0.70845	0.86 ± 0.5926 0.45095	AGTTATCTAACCTTAAATTGATGCAAAATTGAGCTAGAGCACTAGAGCA
plasmid_cp9	6281	BBC10	1.616 ± 0.6491 0.066309	1.104 ± 0.5997 0.26385	1.095 ± 0.6436 0.43947	1.204 ± 0.499 0.39217	AATAAAAACAACAAATATTAGCCTAAAGATAAAATCTATTACTAC
plasmid_cp9	6313	BBC10	1.406 ± 0.8959 0.376787	0.735 ± 0.6511 0.31861	0.473 ± 0.2874 0.16807	0.818 ± 0.5199 0.05658	GACAGTATAATAAAATCTGAAGAAGATAAAATAAGAACAAACAAAT
plasmid_cp9	6354	BBC10	1.102 ± 0.6114 0.331682	0.662 ± 0.2809 0.25567	0.906 ± 0.3844 0.53229	0.986 ± 0.4964 0.95751	ATAGCATGGAGTGCAATAGGACTGGTATTACTCCGGCTGATAGAGCTATT
plasmid_cp9	6595	BBC10	1.819 ± 1.1964 0.127575	0.851 ± 0.509 0.00599	1.371 ± 0.6589 0.07461	1.884 ± 0.1047 0.11568	AGCTTATTTCTCTACAATGTTAAATGCAACTTCATCGGCCCTCATCAT
plasmid_cp9	6736	BBC10	1.454 ± 1.0495 0.383044	0.985 ± 0.4641 0.95296	0.595 ± 0.4206 0.33944	1.764 ± 0.9631 0.00749	TTTATAATAAAAAGGAGAGCAACATTACAGAAAACAACAAATAGAAAAA
plasmid_cp9	6739	BBC10	1.457 ± 0.5043 0.090853	0.875 ± 0.4806 0.49797	1.118 ± 0.5021 0.69374	1.329 ± 0.4206 0.05446	GTTCACAAAGATATTACAAATAATGAAAATATTAAATAAAAATTAG
plasmid_cp9	6754	BBC10	4.981 ± 6.4445 0.321029	1.365 ± 2.4634 0.7616	0.433 ± 0.7684 0.0606	4.059 ± 4.428 0.29988	CAAATATGAAAATATTAAATAATAAAAATTAGCTATGTTATT
plasmid_cp9	6901	IG 249	2.968 ± 3.0304 0.391056	0.785 ± 0.7111 0.5827	0.238 ± 0.3163 0.14191	1.613 ± 1.4283 0.46754	TGTATGTTCTATGATATCATAAAATTCTACAAATAATTGAGATTATT
plasmid_cp9	6917	IG 250	5.167 ± 5.3234 0.183428	1.406 ± 1.9629 0.79305	1.731 ± 2.7026 0.66846	2.301 ± 2.0617 0.29748	TTTATATTAATTCTATGTCATAGTTCTATGATATACAAAAATTCACTAA
plasmid_cp9	6920	IG 251	2.889 ± 2.1701 0.007511	0.224 ± 0.411 0.10915	1.779 ± 1.2497 0.12235	0.449 ± 0.539 0.30826	ATATTATTTATTGATATTAAATTGTTGATTTAAAGTGGAGTTAA
plasmid_cp9	6955	IG 252	1.042 ± 0.6491 0.943793	0.42 ± 0.2933 0.09093	0.82 ± 0.6123 0.0803	0.966 ± 0.6587 0.95097	AATCAAACAAAATTAAATCAAATAAAATAATTAAATTATATTAAATT
plasmid_cp9	7061	BBC11	2.185 ± 1.6169 0.068905	0.398 ± 0.4442 0.40891	0.665 ± 0.4686 0.51271	1.596 ± 1.2898 0.28196	TTTGTAGTATTGTTGATTATCCTCGTGAATTTCAGCAACTCTCGCG
plasmid_cp9	7184	BBC11	0.422 ± 0.4476 0.062831	0.386 ± 0.4283 0.08446	0.89 ± 0.7187 0.74057	1.198 ± 1.1096 0.64113	ATTGATTAGTTGGGATTTAAGTACAACTTAGCAGTGGTTAGAATT
plasmid_cp9	7211	BBC11	2.060 ± 0.8891 0.204322	0.671 ± 0.2177 0.26271	1.035 ± 0.3011 0.62744	1.223 ± 0.5218 0.33781	AAACAAATTGACCCAATAGCTGGATGGTTGACACCTACTGTAATACT
plasmid_cp9	7253	BBC11	1.082 ± 0.9764 0.642273	0.829 ± 0.8722 0.33486	0.755 ± 0.814 0.50931	1.04 ± 0.9647 0.41764	CCAGTAGGTGTACAAACCATCCAGTATTGGTCAATTGTTTAATGTC
plasmid_cp9	7339	BBC11	2.241 ± 1.983 0.136666	2.402 ± 2.8016 0.31492	1.094 ± 0.9434 0.26684	0.74 ± 0.5013 0.37797	TAAGTTTCCGGTTGCTAAAAAAAGTTGAAATATCTGCATTITTC
plasmid_cp9	7380	BBC11	2.033 ± 1.993 0.43819	0.72 ± 0.4871 0.34565	0.696 ± 0.5781 0.36699	0.619 ± 0.5503 0.23683	CTTGTACTAGAGAAATTGTTATAACCGAAAAGAATTAACTGCTATTCAA
plasmid_cp9	7419	BBC11	1.208 ± 0.8722 0.630978	1.146 ± 0.8467 0.82929	0.662 ± 0.4655 0.50639	1.041 ± 0.9487 0.96048	ATGCTATTCAAACAAAGTACAGCAAATTACTCAAACAAAGAAAATTCTAATA
plasmid_cp9	7539	BBC11	0.675 ± 0.4263 0.262603	0.37 ± 0.5188 0.33075	0.983 ± 0.7029 0.97455	0.623 ± 0.3458 0.40684	TTGCTAAAAAAATTCAAACAAAGTTACTTAGAAAATGGGTTGAAGCACGTA
plasmid_cp9	7587	BBC11	1.492 ± 0.6245 0.132555	0.833 ± 0.3327 0.4694	0.82 ± 0.3768 0.15509	1.063 ± 0.2261 0.54039	C GTCTCAAACACCCATTCTCAAGTAACCTTTGAATTTTTAGCAATA
plasmid_cp9	7604	BBC11	3.027 ± 4.1706 0.026432	1.12 ± 1.6861 0.91333	1.955 ± 3.3626 0.15353	2.077 ± 3.0187 0.03488	TGTAGAAATTGTTATTCTCAATTAACTTAATGGCTACACTCTTT
plasmid_cp9	7704	BBC11	1.055 ± 0.9122 0.768894	0.819 ± 0.6479 0.21869	0.603 ± 0.4609 0.08243	1.141 ± 0.9208 0.61136	TTTATGGACTATCTCATGCAAGTAAATTCAACCGTATGAGTCATAAAA
plasmid_cp9	7781	IG 253	1.248 ± 1.0479 0.228934	0.809 ± 0.5943 0.53817	0.647 ± 0.4288 0.24044	0.687 ± 0.4736 0.26807	ACTGGTTAACGCTATAAGGCAACTACTTTTATGCACTCATCGCTTGA
plasmid_cp9	7818	IG 254	1.002 ± 0.3329 0.995016	0.691 ± 0.3243 0.34475	0.673 ± 0.3256 0.06769	1.035 ± 0.344 0.83018	TACTCCTTTATACTCCTTACATTGTTATGTTAATCTTAT
plasmid_cp9	7820	IG 255	4.184 ± 3.6731 0.173097	2.007 ± 2.3771 0.3505	1.707 ± 2.1257 0.62162	1.58 ± 1.3005 0.40531	CTCCTTATACTCCTTACATTGTTATGTTAATCTTAT
plasmid_cp9	7827	IG 256	0.698 ± 0.1953 0.183116	0.456 ± 0.411 0.15209	0.917 ± 0.2194 0.40178	0.827 ± 0.1866 0.2473	TAAGGAGTATGTCAAAATAAGGATATTCAACCTTAAAGCTTAACTGG
plasmid_cp9	7883	IG 257	1.482 ± 0.54 0.205898	0.954 ± 0.4153 0.86296	0.851 ± 0.4941 0.03618	0.784 ± 0.3164 0.22418	TTGACTGGACACTGATAAAGATTATTAGAAATACATAAAATGTAAG
plasmid_cp9	7898	IG 258	1.345 ± 0.7364 0.342963	0.566 ± 0.558 0.12817	1.098 ± 1.1561 0.86796	1.075 ± 0.3257 0.19406	GTATCAGTGGCCCTATTGACTGGGACACTGATAAAGATTATTAGAAATACA
plasmid_cp9	8047	BBC12	0.731 ± 0.1699 0.174895	0.457 ± 0.4009 0.19727	0.872 ± 0.142 0.31617	0.915 ± 0.2005 0.08447	AATATCCACTAATAATAATGTAATTAAATTAGAGAATTGTTGTTA
plasmid_cp9	8336	BBC12	0.863 ± 0.591 0.278986	0.614 ± 0.5794 0.04753	1.162 ± 0.7543 0.36433	1.203 ± 0.7693 0.32795	TCTCATATGGGAATAATGACTTTATAATCTGTTCAAGATTAGTA
plasmid_cp9	8611	BBC12	2.663 ± 0.6846 0.008965	1.252 ± 0.796 0.56856	0.799 ± 0.2246 0.10506	1.071 ± 0.3231 0.46105	TGAGTAGTGTCTTGGCTAGTACATAAAATGCAATTGTTAGTAGTA
plasmid_cp9	8726	BBC12	0.960 ± 0.9076 0.655959	0.474 ± 0.3772 0.14284	0.537 ± 0.3653 0.24279	0.791 ± 0.5491 0.50823	TTCAAAAAAATGGGTAGTTACAAACACTTGTGGCTAACAAATTGATGCC
plasmid_cp9	8727	BBC12	1.094 ± 0.5072 0.033336	0.568 ± 0.2604 0.04899	0.691 ± 0.2564 0.16684	0.728 ± 0.4039 0.17989	TTTCAAAAAAATGGGTAGTTACAAACACTTGTGGCTAACAAATTGATGG
plasmid_cp9	8845	BBC12	1.674 ± 1.1677 0.335175	0.648 ± 0.5483 0.18217	0.93 ± 0.7514 0.88892	0.692 ± 0.2577 0.33589	TGCTCAAGGGCAAAGAGTTAGAGAATTAGGTTAGAGAATTAAAG

plasmid_cp9	8848	BBC12	1.251 ± 0.3295 0.202271	0.475 ± 0.1628 0.1123	0.726 ± 0.2335 0.33276	0.886 ± 0.1968 0.41639	TATAAATTCTTCATAAGGCATACTTATACAAAATATTAAGCAGTCTA
plasmid_cp9	8849	BBC12	0.456 ± 0.8365 0.584094	1.097 ± 1.2145 0.9113	1.106 ± 1.3209 0.86341	0.725 ± 0.891 0.6617	TATATGCTCAAGGGCAAAGAGTTAGAGAAATTAGGATTAGAGAAATTATT
plasmid_cp9	8886	BBC12	0.535 ± 0.9648 0.177761	1.75 ± 2.182 0.64941	0.987 ± 1.2334 0.97625	0.799 ± 1.0965 0.82396	TTAACGCAGTCTATTCTCATAAATCTTTAACCCCTACACCCAGCTTAG
plasmid_cp9	9233	IG 259	1.242 ± 0.3609 0.07528	0.707 ± 0.4337 0.22691	0.919 ± 0.3084 0.27771	1.094 ± 0.3046 0.54922	GCAAAAACCTATTTGCCAACTTTTACAAAAAATTTTTATTAAAACAC
plasmid_lp17	439	BB_D01	1.788 ± 1.3645 0.390322	3.397 ± 3.2391 0.31505	1.039 ± 0.2599 0.67941	1.182 ± 0.3708 0.41482	TAGTTAATAGTAGAATTAATTATCATTGGTTAGTAATAATGGTTGAA
plasmid_lp17	459	BB_D01	1.339 ± 0.9953 0.568753	1.689 ± 1.4439 0.41385	0.784 ± 0.7171 0.74574	0.906 ± 0.6862 0.8078	TAGTTGAATAAAGTGGGTAGTTAATAGTAGAATTAATTATCATT
plasmid_lp17	750	BB_D01	1.689 ± 1.6756 0.476507	2.185 ± 2.0046 0.34466	0.908 ± 1.1295 0.87239	2.482 ± 1.5872 0.17364	TATAGTAATAACTACTACTATCAGCATTATTGTTATGCTAGGCATGA
plasmid_lp17	751	BB_D01	2.976 ± 1.2308 0.032901	1.112 ± 0.8094 0.85481	0.961 ± 0.4859 0.91617	0.855 ± 0.7093 0.60687	CCAACTACATAAAATGGAGACAATTGTTAGAATTATTGCAACTTAT
plasmid_lp17	860	IG 260	1.541 ± 1.2021 0.223516	1.397 ± 0.8728 0.02748	0.969 ± 0.5583 0.90364	1.14 ± 0.754 0.15084	TATATAAAAATAGTATTAAATTTCAAGAATATTGTAATTTATAA
plasmid_lp17	861	IG 261	0.819 ± 0.9421 0.741927	0.368 ± 0.6516 0.45791	0.352 ± 0.4226 0.12461	0.708 ± 0.7265 0.2084	CTATAATTTGAAAAAAATCAAACAGTGCCTAGAAATAGAAA
plasmid_lp17	871	IG 262	1.293 ± 1.0209 0.645261	1.153 ± 1.1866 0.85975	1.369 ± 1.0012 0.38866	0.73 ± 0.5772 0.66188	ATGAAAAAAATCAAAACAAAGTGCAGAAATAGAAAAAACACAATT
plasmid_lp17	1035	IG 263	1.197 ± 0.7806 0.48175	1.008 ± 0.5518 0.97419	0.936 ± 0.647 0.83355	0.837 ± 0.7268 0.03951	TATTCATTCTAGATTAAATGTTGTCACATAAAGCAGGCATCCCC
plasmid_lp17	1141	BB_D03	1.164 ± 0.5763 0.698691	1.404 ± 0.6677 0.20003	1.615 ± 1.0522 0.21099	1.486 ± 1.1234 0.31938	AAAACAAAACCATAGTAAACATCTTTAAAACCAGTCACAAATAT
plasmid_lp17	1191	BB_D03	2.000 ± 0.5414 0.008482	1.251 ± 0.4502 0.23325	0.816 ± 0.2848 0.21677	1.28 ± 0.4831 0.21283	TGATTTATTAAATAAATCCTCTAAAGTGTTCGTTCAACAATACAA
plasmid_lp17	1531	BB_D04	1.502 ± 1.4771 0.133001	1.437 ± 1.1602 0.42118	0.936 ± 0.7442 0.86214	0.775 ± 0.5808 0.62499	TAGTATCCAATTITGAATTAGGTCAATGTTGTTAGTGTGAAATA
plasmid_lp17	1578	BB_D04	2.454 ± 3.0428 0.451618	0.728 ± 1.1125 0.75015	0.257 ± 0.3185 0.23113	0.629 ± 0.6729 0.64487	TATTGCAATACTAGTAAAGATATTGAAATAGACATAGCTTAAAG
plasmid_lp17	1587	BB_D04	2.683 ± 0.9707 0.088158	0.865 ± 0.7113 0.71058	1.691 ± 0.579 0.18566	2.166 ± 2.2955 0.42626	TATTGCAATATCTATCTATGTTAAAGTAAACGCACGGCGTATAAGCCC
plasmid_lp17	1777	IG 264	1.814 ± 0.2133 0.020945	2.061 ± 1.992 0.44897	1.314 ± 0.3895 0.36105	1.335 ± 0.4417 0.22847	GATATTAAAAGAGAAACATCTTGTATATTAACTAAAGGTGTTCTCC
plasmid_lp17	1929	IG 265	1.701 ± 0.5349 0.024191	2.013 ± 1.0022 0.08956	1.063 ± 0.4449 0.63287	1.152 ± 0.5244 0.23342	GTGTCATAGGCCATAAAAGAACATAAAACTAAAATATATAAATA
plasmid_lp17	2467	IG 266	1.762 ± 0.4468 0.67539	1.46 ± 0.6321 0.38409	1.157 ± 0.614 0.60255	0.803 ± 0.222 0.1852	TAAAACATAACACATGAAGTTGATTCTAAACCCCTGTTAGAATCTTGA
plasmid_lp17	2722	IG 267	1.596 ± 0.5653 0.114519	1.978 ± 0.9548 0.04507	1.232 ± 0.4229 0.34283	0.97 ± 0.3743 0.80992	TATTAGGCCCTTAATACTCTAGATTATGCTATTTCGAAAAAATT
plasmid_lp17	2885	IG 268	3.073 ± 2.133 0.17603	1.126 ± 0.3526 0.56578	1.065 ± 0.7987 0.91751	0.778 ± 0.4002 0.51073	TAAGTGGCTTAAGGAGATAAGTTACTTAAGGCCCTATCGCATTACT
plasmid_lp17	2936	IG 269	4.261 ± 1.4836 0.00272	2.393 ± 1.5861 0.27602	1.181 ± 0.5648 0.71088	2.481 ± 1.1124 0.05614	TAATTGATATTAAATAGAAAATAGCTAGATATATTAACTAGTAATA
plasmid_lp17	2937	IG 270	0.926 ± 1.3498 0.874742	1.553 ± 2.167 0.20431	0.756 ± 0.9812 0.55526	0.631 ± 0.8191 0.51873	TAATTAGGAAGCATTATGTCCTCAAATGGATGATAACAGATAAAGGGCT
plasmid_lp17	2948	IG 271	2.538 ± 1.3972 0.079649	2.028 ± 1.3022 0.16878	1.802 ± 1.1833 0.37184	1.362 ± 0.5472 0.02718	AAATAGAAAATAAGTCTAGATATTAATCTAGTAATATTCTAAATTATA
plasmid_lp17	2970	IG 272	1.291 ± 1.2068 0.493996	2.084 ± 2.1593 0.37877	0.596 ± 0.337 0.19413	0.797 ± 0.6966 0.58775	TATCTAGACTTATTCTATTAAATACAATTAAATTAGGAAGCATTATG
plasmid_lp17	3207	BB_D05a	2.137 ± 1.6459 0.383718	2.217 ± 0.8495 0.13943	1.191 ± 0.9544 0.79274	0.672 ± 1.0715 0.69303	GGGTTAAATTGGGTACAGAAATTTTATAAGCTTAATTCTCTAAAAAA
plasmid_lp17	3246	BB_D05a	1.458 ± 0.6141 0.040187	1.582 ± 0.981 0.16662	1.01 ± 0.4138 0.90705	0.957 ± 0.4256 0.64668	TATCCTAAAAAGATTTGTCATAGATAAACCAACACTTAAAGAAAAAA
plasmid_lp17	3250	BB_D05a	4.488 ± 5.2176 0.131754	1.352 ± 1.4912 0.57064	5.862 ± 6.912 0.1476	1.48 ± 1.9957 0.23165	CTAAAAAAAGATTGTTACCATAGATAAACCAACACTTAAAGAAAAAAAG
plasmid_lp17	3265	BB_D05a	1.393 ± 0.5095 0.183527	1.5 ± 0.5638 0.18751	0.935 ± 0.1842 0.2	0.945 ± 0.2299 0.51464	TAACAATCTTTTGTAGGATAATAGCTTATAAAATTCTGTACCGGAA
plasmid_lp17	3581	BB_D05a	1.174 ± 0.4308 0.391609	1.009 ± 0.7116 0.97657	0.909 ± 0.4209 0.11472	1.18 ± 0.4676 0.44393	CTTACTAAATCTGTATTGTTCAATTATTATTGGAAAATTTTATCTA
plasmid_lp17	3685	BB_D0027	0.815 ± 0.537 0.382007	0.605 ± 0.5427 0.55509	0.681 ± 0.5125 0.16884	0.804 ± 0.6127 0.21939	TATTGGATAGCTAAATAGAGTTGCTGTCATTTCTGAGACTGTTTT
plasmid_lp17	3798	BB_D0027	0.937 ± 0.7506 0.902774	1.41 ± 1.5225 0.55537	0.799 ± 0.7022 0.64387	0.416 ± 0.2482 0.14865	TTCAATATAGTAGGCCTTAAATTGCTATTGAAATTGTTATAACAAA
plasmid_lp17	3806	BB_D0027	1.969 ± 1.4466 0.190248	1.622 ± 1.4437 0.43109	0.927 ± 0.625 0.84688	0.703 ± 0.4543 0.33132	TATATTGAATATATGTCATTTTTAGTTCTGCTTCTTTCTTCT
plasmid_lp17	3811	BB_D0027	1.742 ± 2.0299 0.274781	2 ± 2.9218 0.44021	0.792 ± 0.6658 0.64318	1.139 ± 1.1283 0.34714	AGCCTTAAATTGCTATTGAAATTGTTATAACAAAGCCTGCTTTAAT
plasmid_lp17	3844	IG 273	2.519 ± 1.2053 0.097641	2.367 ± 1.6661 0.31117	1.221 ± 0.6061 0.41823	0.925 ± 0.5257 0.15507	TATTATAACAAATTCAATATGCAATTAAAGGCTACTATATTGAAATA
plasmid_lp17	3919	IG 274	1.983 ± 2.0828 0.006973	4.432 ± 7.1002 0.33581	0.769 ± 0.769 0.76574	2.626 ± 2.8031 0.03385	AAATTATAGGTTAAATTGTTATCTAGTAAGAATGTTAAACCT
plasmid_lp17	3922	IG 275	1.234 ± 1.0224 0.699548	1.642 ± 1.9083 0.32348	1.055 ± 0.8561 0.81691	1.255 ± 1.0461 0.60642	TAAACTTAACTCTAAATAAAGTAAACTGATGTTCTATAGCTTTAAT
plasmid_lp17	3981	IG 276	4.312 ± 3.2739 0.059536	3.672 ± 2.308 0.05111	2.211 ± 1.7196 0.33133	1.494 ± 0.9155 0.3679	TATTATTAACAAAGATCTATAGAAACATCAGTTACTTATTAGAAT
plasmid_lp17	4164	IG 277	0.963 ± 0.5426 0.88457	0.62 ± 0.5336 0.56161	1.088 ± 0.7262 0.45687	1.129 ± 0.8058 0.15224	ACATGATTACATTCTATTGTTCAATTAGAATTGCTTAAATTAACTT
plasmid_lp17	4496	IG 278	2.162 ± 1.8828 0.14006	1.928 ± 1.694 0.16236	1.086 ± 0.9126 0.80914	1.495 ± 1.8296 0.50112	TATTATATGAGCATTACTTAAGGCATTATTCTAGCTTGAATAATTG
plasmid_lp17	4613	IG 279	0.971 ± 0.5685 0.903651	0.649 ± 0.5826 0.60722	1.084 ± 0.7144 0.51696	1.119 ± 0.7779 0.26993	TATGACAATGATTACATTCTATTGAAATTGCTCCAAATTAA
plasmid_lp17	5046	IG 280	1.705 ± 0.1929 0.026092	1.486 ± 0.7729 0.40175	0.98 ± 0.2794 0.91479	0.863 ± 0.5008 0.68942	TATTATGATAGCAGTCTTGAATAATTAGTAAACCTTTTATAGATT
plasmid_lp17	5074	BB_D09	1.262 ± 0.837 0.013597	1.139 ± 0.8549 0.27077	0.735 ± 0.5077 0.43221	0.866 ± 0.5893 0.39897	AAAAAGTTTTTCTTATTACACAACTTATTATGATAGCAGTCTGAA
plasmid_lp17	5109	BB_D09	1.825 ± 1.8093 0.295818	1.988 ± 1.2842 0.01323	1.56 ± 1.3504 0.60146	1.615 ± 0.8895 0.07033	TATTGCCAATTAAATTAAGAATATAAAAGTTTTT
plasmid_lp17	5122	BB_D09	1.170 ± 0.748 0.110984	0.58 ± 0.4722 0.47847	1.018 ± 0.5552 0.91073	1.017 ± 0.6612 0.67549	TATTGGACATATTGCCAAATTAAATTAAGAATATAAAAGTTTT
plasmid_lp17	5176	BB_D09	0.250 ± 0.3979 0.237965	2.876 ± 4.7856 0.57246	0.035 ± 0.0356 0.07628	1.045 ± 0.8129 0.94725	TAATAAATACCCCTTTAGATTTTAGCTGTTAAATTCATAGT
plasmid_lp17	5893	BB_D10	1.524 ± 0.972 0.200453	1.117 ± 0.8516 0.86814	0.507 ± 0.3212 0.29324	0.892 ± 0.5346 0.82125	TTAACCTTGAATTAACCAAAACTTTAAAGGAATCTTATTA
plasmid_lp17	7724	IG 281	2.291 ± 2.2467 0.352087	1.474 ± 0.9865 0.51705	0.775 ± 0.4468 0.59063	1.656 ± 0.9641 0.208	TATGTTGAATACCTTGTAGGGTGTGCAAGAGCTTATTAGATTGT

plasmid_lp17	9414	IG 282	1.589 ± 0.5374 0.025443	1.561 ± 0.6657 0.08049	0.958 ± 0.4069 0.74352	1.329 ± 0.5244 0.11018	TATATAATAATACTTTTATATGTAAATAGCAATTATTTGATTAATT
plasmid_lp17	9417	IG 283	3.562 ± 5.2369 0.412614	3.683 ± 4.1172 0.02037	0.578 ± 0.7652 0.42388	2.057 ± 2.414 0.00388	GGCCCTATTCTAAGAATTTTTACTTTAGGAACATTAAATATTTCTT
plasmid_lp17	9479	IG 284	1.494 ± 0.8115 0.035953	1.029 ± 0.7406 0.965	0.619 ± 0.3294 0.19596	0.591 ± 0.5169 0.05325	TATATGAACTGTAAGAAAATATATTAAATGTTCTAAAGTAAAAAAAATTCT
plasmid_lp17	9481	IG 285	1.210 ± 1.4861 0.391913	1.582 ± 2.251 0.43213	0.937 ± 0.9707 0.67607	1.118 ± 1.3455 0.43572	TATATGAACTGTAAGAAAATATATTAAATGTTCTAAAGTAAAAAAAATT
plasmid_lp17	9482	IG 286	2.396 ± 0.7295 0.062242	1.832 ± 0.8598 0.26786	1.556 ± 0.508 0.22797	1.569 ± 0.6205 0.27178	TATATGCATTCTATTAAAAGACACTGAAAACACTCATATTACCAACTAA
plasmid_lp17	9484	IG 287	1.275 ± 0.4883 0.045721	1.4 ± 0.7531 0.26317	0.939 ± 0.3099 0.55581	1.078 ± 0.5284 0.60842	TATGCATTCTATTAAAAGACACTGAAAACACTCATATTACCAACTAAAC
plasmid_lp17	9486	IG 288	1.548 ± 0.2958 0.08646	1.522 ± 0.2621 0.09823	0.926 ± 0.3539 0.70492	0.92 ± 0.2887 0.57769	TGCATTCTATTAAAAGACACTGAAAACACTCATATTACCAACTAAACTA
plasmid_lp17	9820	BB_D15	1.640 ± 0.5582 0.100954	1.584 ± 0.8095 0.27946	1.024 ± 0.389 0.93503	1.158 ± 0.4095 0.40898	TCACAACCCAATATTAAATAAAAAAGTTAATATTATAATAATGAAATA
plasmid_lp17	9859	BB_D15	1.837 ± 1.8613 0.323261	2.862 ± 2.913 0.27732	1.265 ± 1.3026 0.5775	1.345 ± 1.2583 0.45907	TATTATAATATTAACTTTTATTAAATATTGGGTTGTGATTATCAAA
plasmid_lp17	9990	IG 289	4.032 ± 4.5222 0.25246	1.89 ± 3.5114 0.61589	1.18 ± 0.8787 0.50305	2.037 ± 1.8015 0.092	TAACACAATAATGCTTAACCTTAAATTTTAAATGTGTTACTTGTGCTT
plasmid_lp17	9994	IG 290	1.204 ± 0.961 0.411347	0.861 ± 1.1145 0.88653	0.535 ± 0.4202 0.22346	1.025 ± 0.8288 0.86153	TATATACTACAATAATGCTTAACCTTAAATTTTAAATGTGTTACTTGT
plasmid_lp17	10316	IG 291	0.412 ± 0.215 0.088031	0.367 ± 0.3544 0.27917	0.869 ± 0.4352 0.5329	0.809 ± 0.5175 0.12561	TAAACCACCAATATTCTTCTTGCTATACAAAATCTTACAGATCTAAAT
plasmid_lp17	10421	IG 292	1.148 ± 0.8618 0.720026	1.474 ± 0.5069 0.07074	1.381 ± 0.6653 0.50284	1.014 ± 0.6393 0.9703	TAACATAGTTACTTAAATGGAAAAGACTCTATCTGCTTATGTAATAAA
plasmid_lp17	10424	IG 293	2.233 ± 1.8382 0.32674	1.204 ± 0.8089 0.42512	1.2 ± 1.0908 0.7565	0.579 ± 0.526 0.31758	TATGGTATTAAAATACAACCTAAATAAGGAAACCGAGTGGCCTTT
plasmid_lp17	10548	IG 294	1.391 ± 0.8449 0.271304	1.504 ± 0.8174 0.43441	1.413 ± 0.5972 0.14252	1.394 ± 0.6763 0.21384	AGCTAACAGAGCTGCCCTAAGGAGTAGATCATGTATTGGTAAATA
plasmid_lp17	10613	IG 295	0.711 ± 0.3955 0.43132	0.382 ± 0.433 0.26845	1.141 ± 0.5628 0.57131	1.16 ± 0.4573 0.60817	TATTTAAAAGAACAGTATTACCAATACATGATCTAGCCTTAACAGCA
plasmid_lp17	11783	IG 296	1.682 ± 1.42 0.398006	1.76 ± 1.5004 0.34851	0.983 ± 0.7794 0.95663	1.404 ± 0.6011 0.11272	TAAGTTAAATCTACAACAGTTAGAAAAAAACAAAATTAAAATATT
plasmid_lp17	12041	IG 297	1.545 ± 1.2125 0.292606	1.888 ± 1.2904 0.23478	2.094 ± 0.8416 0.07407	2.34 ± 1.6015 0.12961	GTAAGTAAATTCTGGGTATAATGAATTTTATTATCATAATTAAAATT
plasmid_lp17	12167	IG 298	1.151 ± 1.0288 0.724262	0.761 ± 0.6976 0.55742	0.824 ± 0.783 0.81969	0.483 ± 0.5072 0.28447	TATAATGCCAACCTCTCTTGGCCAATAACTTATTATGTTCTTTA
plasmid_lp17	12245	IG 299	1.532 ± 0.3818 0.021476	1.29 ± 0.5749 0.33487	0.91 ± 0.2677 0.5068	1.139 ± 0.3935 0.53695	TATTATAAAAATCTCACACATCTAAATACCTTTAAAGTATTCTTT
plasmid_lp17	12693	BB_D20	1.643 ± 1.3868 0.104396	1.622 ± 1.4507 0.15195	0.965 ± 0.7174 0.79699	1.197 ± 1.0208 0.12184	TATCTTAAATTAAGTCTTCTATTGCTATATTTTAAATAACTTAA
plasmid_lp17	12755	BB_D20	1.954 ± 1.3068 0.282768	1.751 ± 1.433 0.40201	0.889 ± 0.6604 0.20062	1.186 ± 0.9668 0.81275	GTATAATCAGAATGGTATGGATCTTTGTATAAAGTAGGTATATT
plasmid_lp17	12794	BB_D20	2.026 ± 0.3576 0.05435	0.496 ± 0.8619 0.37869	0.852 ± 1.0322 0.82708	0.049 ± 0.0578 0.00496	TACTTATACAAAAGGATCCATACCATTCTGATTACTATAATCGTCT
plasmid_lp17	12939	BB_D20	0.849 ± 0.2836 0.531714	0.549 ± 0.4374 0.35074	0.905 ± 0.2157 0.6049	1.183 ± 0.3550 0.25673	AAGAAATAAAAGCTAACAGACAGGAATTTCGAATTAGGCTTGAATCAT
plasmid_lp17	13007	IG 300	2.103 ± 2.1978 0.341857	1.236 ± 0.2012 0.41382	1.183 ± 0.8333 0.6076	1.534 ± 1.1544 0.33133	TATTTTACACCAATAGCATGATTAACAAGCTAAATTGGAAAATTCTG
plasmid_lp17	13068	IG 301	1.472 ± 0.5738 0.102973	1.537 ± 0.495 0.09584	1.085 ± 0.3263 0.74875	1.036 ± 0.4169 0.71691	TATCTCTATATTACGGCTTGTCTATTCTACGATAACTTTAGTTCT
plasmid_lp17	13082	IG 302	0.742 ± 0.694 0.671434	1.126 ± 1.1974 0.56197	1.259 ± 1.3812 0.7613	0.803 ± 1.014 0.72325	TTTAAGGCCACATCAGATCTAATTCTAAATTTGTAAAGGGGCT
plasmid_lp17	14391	IG 303	1.597 ± 1.3765 0.121741	1.747 ± 1.6778 0.1818	0.95 ± 0.6547 0.84364	1.064 ± 0.9128 0.60318	TATGATTCTGTGAAATTAGGTAGATATGAATTGGTAGATAATGGATT
plasmid_lp17	14497	IG 304	1.516 ± 1.5462 0.539236	1.601 ± 1.6799 0.1416	1.761 ± 2.4208 0.62475	1.214 ± 1.3243 0.62893	TATACTAGAGAGAAAGTTTCCGATATGATCAAAGCATATTGGAAIC
plasmid_lp17	14850	BB_D23	0.815 ± 0.10266 0.565161	0.658 ± 0.8507 0.7376	1.008 ± 1.202 0.9769	0.839 ± 0.9955 0.76295	TATATACTCTTATTATTAATAATTACTTAGTGTATAGGAAATGAGAT
plasmid_lp17	15187	BB_D23	1.342 ± 0.7831 0.451584	1.385 ± 0.3139 0.02914	0.883 ± 0.3861 0.69363	1.172 ± 0.2957 0.45539	GCTTATCATAAAAGGATTGTAAAGTTGTACATAGGATCATTAA
plasmid_lp17	15382	BB_D23	1.106 ± 0.8623 0.565505	0.458 ± 0.3569 0.32925	0.881 ± 0.5801 0.39688	0.882 ± 0.6267 0.51685	TAGAATGATTGTTTACTTCACGACTCTTTTATTATTTTTTAT
plasmid_lp17	15743	BB_D0031	1.907 ± 1.8549 0.319679	2.49 ± 2.8036 0.34626	0.912 ± 0.4728 0.62225	0.974 ± 0.5530 0.78071	TTTGGCGGATGGCCGGCTTAATAAAAATAATTAAAAGTTATCATAT
plasmid_lp17	15958	BB_D24	2.168 ± 2.711 0.50052	1.422 ± 1.4053 0.5527	1.469 ± 1.0931 0.58333	2.438 ± 1.7302 0.19514	AATTAATAGATAAAAATTATTAACATTCTTATTATAAATAAAAAAAT
plasmid_lp17	16058	BB_D24	1.993 ± 1.595 0.028917	1.495 ± 1.9642 0.52429	0.934 ± 0.82 0.83244	0.98 ± 0.7404 0.91674	AAAAACATTTCACAAAATTACAGATTGTTAAAAATGTTTGTATA
plasmid_lp17	16207	IG 305	1.595 ± 0.4164 0.02429	1.918 ± 0.10734 0.19611	0.907 ± 0.3087 0.65997	1.103 ± 0.3705 0.37052	TAAATGCATGTTATAATTAAATTTGAGATGTTTAAATGCCTTTT
plasmid_lp17	16208	IG 306	1.379 ± 1.2642 0.435378	1.634 ± 1.5751 0.27232	1.235 ± 0.8016 0.55421	1.662 ± 1.2128 0.26314	TATATAATGCTACAGAACTATCGATAACAAAATGGAAATTTTTAA
plasmid_lp17	16396	IG 307	1.582 ± 0.5425 0.02029	1.884 ± 0.9099 0.10979	1.07 ± 0.3543 0.62434	1.151 ± 0.4146 0.07985	TATAGATAATACTTATTATTTAATCTAACAGCTAGAAGGAGAAAAA
plasmid_lp17	247	IG 308	1.339 ± 1.258 0.252142	0.399 ± 0.3809 0.3691	1 ± 0.7892 0.99844	0.992 ± 0.8962 0.89502	TATATATGTATAAGTCTGAAAAGAACAGAAAAGGAATAGATCAT
plasmid_lp17	425	BB_U01	1.889 ± 2.1049 0.27337	1.896 ± 2.8511 0.42915	1.015 ± 0.973 0.96863	1.272 ± 1.3156 0.09558	ATATATCAACATAAGAAAATACTTAAATAGGAAATAGGAAAT
plasmid_lp17	469	BB_U01	1.380 ± 1.2019 0.343467	1.845 ± 2.6158 0.48998	0.31 ± 0.2475 0.14638	0.518 ± 0.4518 0.20549	TTCTTTCTCAATTGTTAAGTATTCTGATGATATTACTAG
plasmid_lp17	593	BB_U01	2.088 ± 1.7741 0.210832	0.564 ± 0.7536 0.49787	1.051 ± 0.9647 0.92528	1.191 ± 1.1445 0.60025	AATTGTTTAATTCTTGTAGATAATTCTTATTAGTTAACCAATT
plasmid_lp17	663	IG 309	3.856 ± 3.5073 0.248907	2.383 ± 3.008 0.16583	1.232 ± 0.653 0.65681	1.211 ± 0.6525 0.06812	TATTCCTAAAGTTTGAATAAGATTATTTATAATGTATTACAATAGT
plasmid_lp17	755	BB_U02	3.400 ± 3.7102 0.349131	1.789 ± 1.693 0.44336	1.177 ± 0.6449 0.55345	1.338 ± 0.9156 0.45884	CTCCATCCATAATGAATTAGCCCCCTATTATTTAAATTACCAAT
plasmid_lp17	886	BB_U02	2.181 ± 2.782 0.188152	1.529 ± 0.2034 0.27611	1.208 ± 1.3154 0.24326	1.121 ± 1.3903 0.32741	ATTGTAAGTTTATTGCACTATAAGTAATTCTTATTATGATCTAG
plasmid_lp17	889	BB_U02	2.782 ± 1.3737 0.06447	1.443 ± 0.868 0.24044	1.132 ± 0.4162 0.05612	1.048 ± 0.437 0.02091	TGCTTAAACAAAACATTAAATGAGGCTCTAGAAACACTTAACT
plasmid_lp17	927	BB_U02	0.472 ± 0.2612 0.005929	0.582 ± 0.4813 0.06332	1.368 ± 0.483 0.12005	1.086 ± 0.45 0.21505	AAACTTATCAACTTAGGGTTAATTAAAACCTTATTAGAAATCTGAAA
plasmid_lp17	948	BB_U02	5.077 ± 2.9767 0.062349	2.09 ± 2.2602 0.38761	3.136 ± 2.4967 0.2299	1.817 ± 0.79 0.08172	ATTATAAAACCTTATTAGAAATATTAGAAAAAAATCCAAAAG
plasmid_lp17	954	BB_U02	2.616 ± 0.3191 0.001673	1.088 ± 0.3065 0.64186	0.917 ± 0.2454 0.65471	0.958 ± 0.2689 0.83864	AAACCTTATTAGAAATCTGAAATATTAGAAAAAAATCCAAAAGTAATCT

plasmid_lp21	1053	BB_U02	1.767 ± 2.4911 0.220171	0.384 ± 0.787 0.28882	0.246 ± 0.4328 0.45513	0.761 ± 1.4852 0.31506	CACTCCTTACCTTACGAAAGATTGTTGCATAAAATTATAATTCTCATC
plasmid_lp21	1110	BB_U02	0.664 ± 1.2778 0.75973	0.229 ± 0.4233 0.35332	1.227 ± 1.7561 0.87154	1.109 ± 1.4032 0.81221	TTTAAGCTAATAATACTCAGAAAATTATTTTGCAAAATAGCATAATGCTT
plasmid_lp21	1160	IG 310	4.391 ± 2.4029 0.131202	4.251 ± 4.8174 0.36859	1.767 ± 0.9416 0.32986	1.637 ± 1.2178 0.48226	AAGCATTATGCTATTCGCAAAATAATTCTGGATTATATTAGCTTAA
plasmid_lp21	1163	IG 311	1.854 ± 0.114 0.000215	0.589 ± 0.215 0.09239	1.248 ± 1.0367 0.71332	0.875 ± 0.576 0.7177	GAGTATTAAGGCCATAATAAGAACATAAAACTAAAAAAATATAAATA
plasmid_lp21	1179	IG 312	1.003 ± 0.2651 0.971728	1.437 ± 0.3418 0.03373	0.614 ± 0.2233 0.00241	0.705 ± 0.296 0.38146	TTAGGCCTTAATACTCTAAAGCATTATGCTATTCGCAAAATAATTTC
plasmid_lp21	1207	IG 313	1.200 ± 1.4533 0.146389	0.734 ± 0.8296 0.72574	0.927 ± 1.1505 0.93654	0.152 ± 0.1994 0.29865	TATATTTTAGTTAAATTGTTCTTATTAGGCCCTTAATACTCTAAAGC
plasmid_lp21	1238	IG 314	2.706 ± 2.3247 0.14538	1.593 ± 1.5327 0.29658	1.303 ± 0.8611 0.46673	1.211 ± 0.9741 0.32021	ACATTAATTCTCTAATTACGGTTTATTATATTTTAGTTTAATT
plasmid_lp21	2677	IG 315	3.967 ± 4.633 0.254889	0.969 ± 1.2551 0.97827	1.063 ± 1.2172 0.94861	0.558 ± 0.7399 0.49865	TGTCTATTGTTCTAAATTCCGGCTATTCTATGTTAAAGCATGATAATT
plasmid_lp21	2680	IG 316	3.749 ± 2.1781 0.064614	2.218 ± 1.9904 0.27663	1.499 ± 0.7267 0.06809	1.309 ± 0.7615 0.31121	TATACTTATAGTAAAAGTATCATATAAAGAACATACTTATAAAATGG
plasmid_lp21	3307	BB_U05	1.398 ± 1.2447 0.227603	2.192 ± 2.2681 0.30182	1.502 ± 1.173 0.1563	0.7 ± 0.7923 0.48815	ATATGGCTGTAATTTAAAGGCATTTTAACCAAAAATCTCTATGAGGA
plasmid_lp21	3643	BB_U05	2.000 ± 0.8656 0.019365	1.449 ± 0.8566 0.29541	0.864 ± 0.3502 0.44017	1.266 ± 0.4984 0.39818	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATATAA
plasmid_lp21	3652	BB_U05	2.327 ± 2.6026 0.069335	1.691 ± 2.0553 0.09818	1.277 ± 1.3703 0.47345	1.11 ± 1.3609 0.298	AGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATATAAATAAAATT
plasmid_lp21	3679	IG 317	2.793 ± 0.8336 0.007617	1.132 ± 0.688 0.79011	1.168 ± 0.3516 0.27962	0.864 ± 0.5496 0.79016	CACTCAGTAAACTAACCACTTTACTTATTCTTATGAAATATT
plasmid_lp21	3715	IG 318	0.555 ± 0.3754 0.398419	0.563 ± 0.4309 0.49313	1.005 ± 0.5136 0.98119	0.979 ± 0.5657 0.80884	AGTAAAAGTGGTTAGTTGGAGTGATAATCATAAAAAAATAAATTT
plasmid_lp21	3740	IG 319	1.360 ± 0.1268 0.004951	0.924 ± 0.2399 0.47332	1.12 ± 0.2328 0.26845	1.049 ± 0.5174 0.86714	CACTCCAAAACAACTAACCACTTTACTTATTATGAAATATT
plasmid_lp21	3742	IG 320	2.244 ± 1.2855 0.089728	1.327 ± 0.5896 0.00716	1.395 ± 0.4956 0.12551	1.031 ± 0.5352 0.91668	TACACTCCAAAACAACTAACCACTTTACTTATTATGAAATATT
plasmid_lp21	3776	IG 321	0.626 ± 0.4865 0.536592	0.545 ± 0.458 0.47364	0.952 ± 0.6202 0.77688	0.902 ± 0.6884 0.6389	AGTAAAAGTGGTTAGTTGGAGTGATAATCATATAAATAAATTT
plasmid_lp21	3791	IG 322	2.032 ± 0.3028 0.014341	1.335 ± 0.2296 0.02473	1.069 ± 0.2569 0.43501	1.174 ± 0.1679 0.22447	GTTTGGAGTGATAATCATATAAATAAATTTATAAGAATAAGTAA
plasmid_lp21	3801	IG 323	1.954 ± 0.4115 0.032543	0.961 ± 0.2558 0.85477	1.217 ± 0.5222 0.4787	1.132 ± 0.4117 0.67993	CACTCCAAAACAACTAACCACTTTACTTATTATGAAATATT
plasmid_lp21	3803	IG 324	1.845 ± 0.921 0.123282	1.245 ± 0.5252 0.18316	1.142 ± 0.5269 0.32586	0.914 ± 0.3508 0.47813	TACACTCCAAAACAACTAACCACTTTACTTATTATGAAATATT
plasmid_lp21	3813	IG 325	2.781 ± 0.946 0.002116	1.907 ± 0.6625 0.09517	0.913 ± 0.2946 0.68232	0.828 ± 0.3222 0.52097	TAAATATAATTATTAATAAGAATAAGTAAAGTGGTTAGTTACTGGAGT
plasmid_lp21	3828	IG 326	1.931 ± 0.5924 0.015523	1.127 ± 0.5283 0.46759	0.861 ± 0.3195 0.04595	0.957 ± 0.2426 0.58966	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAA
plasmid_lp21	3834	IG 327	2.744 ± 2.0565 0.276886	1.067 ± 0.7041 0.88992	0.871 ± 0.3761 0.71473	1.069 ± 0.3472 0.55563	TTCTTTATAAAATTATTATGATTATACCTCCAAAACAA
plasmid_lp21	3864	IG 328	2.823 ± 0.7681 0.014777	1.604 ± 0.8556 0.23809	1.155 ± 0.3313 0.1252	1.074 ± 0.4248 0.7916	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	3867	IG 329	1.085 ± 0.5238 0.818951	0.584 ± 0.385 0.27843	0.98 ± 0.5279 0.95847	1.035 ± 0.3459 0.86149	TAAATCATAAAAATAATTTATAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	3901	IG 330	2.975 ± 0.8937 0.054467	1.905 ± 0.666 0.16717	1.636 ± 0.6436 0.12198	1.757 ± 0.7032 0.12032	CTTATTCTTATAAAATTTATTTATGATTTACACTCCAGTAAACT
plasmid_lp21	3912	IG 331	2.894 ± 1.2948 0.050331	1.309 ± 0.4785 0.04175	1.401 ± 0.7193 0.44401	1.451 ± 0.7244 0.14501	AACCACTTTACTTATTCTTATAAAATTTATTTATGATTTACAC
plasmid_lp21	3925	IG 332	3.590 ± 3.891 0.130364	1.887 ± 2.673 0.38558	1.112 ± 1.2734 0.56949	1.285 ± 1.8518 0.57016	GTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	3929	IG 333	2.355 ± 0.5312 0.020289	1.461 ± 0.949 0.49908	0.824 ± 0.1692 0.36552	1.112 ± 0.2363 0.5961	TGTAGCCACTAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	3942	IG 334	1.744 ± 1.142 0.154728	0.576 ± 0.4546 0.50009	0.929 ± 0.769 0.86452	1.393 ± 0.1055 0.21646	TTTATATGATTTATGTTAGTCCTAAACCACTTTACTTATTCTT
plasmid_lp21	3946	IG 335	2.488 ± 2.8598 0.294742	1.482 ± 1.76 0.4592	0.947 ± 0.7779 0.70365	0.888 ± 0.9607 0.42418	TCTATTATGATTTATGTTAGTCCTAAACCACTTTACTTATT
plasmid_lp21	3954	IG 336	1.780 ± 0.753 0.054889	1.153 ± 0.5259 0.26819	0.873 ± 0.3873 0.0826	0.976 ± 0.3509 0.56263	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAA
plasmid_lp21	3990	IG 337	2.924 ± 0.9462 0.0022	1.402 ± 0.8283 0.23902	1.034 ± 0.3366 0.85409	1.246 ± 0.6878 0.5109	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATCTTT
plasmid_lp21	3993	IG 338	1.041 ± 0.562 0.852668	0.562 ± 0.3848 0.32791	0.87 ± 0.5302 0.63771	0.874 ± 0.3758 0.434	TAAATCATAAAATAATTTATAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	4027	IG 339	3.452 ± 0.6223 0.004106	2.132 ± 0.3827 0.02655	1.754 ± 0.6005 0.14865	1.661 ± 0.5231 0.15826	CTTATTCTTATAAAATTTATTTATGATTTACACTCCAGTAAACT
plasmid_lp21	4038	IG 340	3.172 ± 2.1568 0.046691	1.337 ± 0.837 0.15284	1.355 ± 0.9786 0.45369	1.344 ± 1.1018 0.13468	AACCACTTTACTTATTCTTATAAAATTTATTTATGATTTACAC
plasmid_lp21	4051	IG 341	2.718 ± 3.6077 0.075503	1.427 ± 2.488 0.4589	1.115 ± 1.5079 0.74322	1.124 ± 1.8682 0.52794	GTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	4055	IG 342	2.661 ± 1.2102 0.071904	1.586 ± 0.9887 0.3969	0.803 ± 0.3596 0.23605	1.111 ± 0.4549 0.70935	TGTAGCCACTAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	4065	IG 343	5.680 ± 1.8522 0.008917	2.378 ± 0.8652 0.03146	1.501 ± 0.6645 0.20159	1.873 ± 0.6552 0.10225	TAAATATAATTATTAAGAATAAGTAAAGTGGTTAGTTGGAGGT
plasmid_lp21	4067	IG 344	2.494 ± 1.1891 0.151136	1.363 ± 0.4636 0.30548	1.305 ± 0.3923 0.31403	1.242 ± 0.6097 0.58965	AATAATATTTATAAGAATAAGTAAAGTGGTTAGTTGGAGGT
plasmid_lp21	4068	IG 345	1.470 ± 0.7153 0.318856	0.455 ± 0.2679 0.22717	0.932 ± 0.53 0.85503	1.289 ± 0.6138 0.03512	TTTATATGATTTATGTTAGTCCTAAACCACTTTACTTATTCTT
plasmid_lp21	4079	IG 346	3.433 ± 2.5054 0.193814	1.515 ± 0.8437 0.46035	1.929 ± 1.3116 0.21273	1.466 ± 0.9082 0.52598	TAAGATTTATATGATTTATGTTAGTCCTAAACCACTTT
plasmid_lp21	4089	IG 347	0.557 ± 0.3456 0.357884	0.544 ± 0.3806 0.37294	1.034 ± 0.485 0.78176	1.046 ± 0.5909 0.64449	AGTAAAAGTGGTTAGTTGGAGTGATAATCATAAAAATAATT
plasmid_lp21	4114	IG 348	1.986 ± 0.6195 0.015546	1.169 ± 0.5005 0.3955	1.038 ± 0.3361 0.47822	1.155 ± 0.4091 0.52979	CACTCCAAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	4116	IG 349	1.767 ± 0.6199 0.015188	1.282 ± 0.6699 0.25799	1.167 ± 0.3847 0.37636	0.983 ± 0.4311 0.92288	TACACTCCAAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	4117	IG 350	1.097 ± 0.6842 0.758252	0.581 ± 0.399 0.35998	0.946 ± 0.4847 0.84762	1.083 ± 0.4952 0.77957	TAAATCATAAAATAATTTATAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	4128	IG 351	2.967 ± 1.5945 0.159615	1.885 ± 0.8262 0.18941	1.216 ± 0.6354 0.59438	1.265 ± 0.6327 0.52836	AATAATATTTATAAGAATAAGTAAAGTGGTTAGTTGGAGGT
plasmid_lp21	4150	IG 352	0.530 ± 0.3864 0.420371	0.489 ± 0.4271 0.42665	0.963 ± 0.7015 0.72022	0.77 ± 0.6413 0.30996	AGTAAAAGTGGTTAGTTGGAGTGATAATCATATAAAATATT
plasmid_lp21	4162	IG 353	2.711 ± 1.3403 0.037268	1.256 ± 0.4849 0.23871	1.215 ± 0.689 0.54261	1.209 ± 0.5406 0.25133	AACCACTTTACTTATTCTTATAAAATATTATGATTTACAC

plasmid_lp21	4165	IG 354	2.323 ± 0.3404 0.011736	1.412 ± 0.2838 0.01225	1.217 ± 0.2184 0.18346	1.141 ± 0.1587 0.2374	GTTTGGAGGTATAAACATATAAATAATTTATAAAGAATAAGTAA
plasmid_lp21	4175	IG 355	1.608 ± 0.3345 0.025615	1.028 ± 0.1874 0.77133	1.083 ± 0.2577 0.37959	1.031 ± 0.3736 0.88762	CACTCCAAAACAACTAAACCACTTTACTTATTCCTTATAAAATATTATTT
plasmid_lp21	4177	IG 356	1.960 ± 0.8173 0.017354	1.44 ± 0.7082 0.06373	1.289 ± 0.4903 0.25653	1.1 ± 0.5459 0.58727	TACACTCCAAAACAACTAAACCACTTTACTTATTCCTTATAAAATATTATTT
plasmid_lp21	4187	IG 357	5.401 ± 2.7944 0.003759	2.187 ± 1.169 0.01272	1.349 ± 0.8621 0.47186	1.447 ± 0.7118 0.30716	TAATAATATTATAAAGAATAAGTAAAGTGGTTAGTTGGAGTGTT
plasmid_lp21	4189	IG 358	2.595 ± 1.1844 0.148495	1.391 ± 0.6896 0.45072	0.998 ± 0.5666 0.99729	1.324 ± 0.5318 0.43252	AATAATATTATAAAGAATAAGTAAAGTGGTTAGTTGGAGTGTT
plasmid_lp21	4211	IG 359	0.501 ± 0.3254 0.306169	0.535 ± 0.3633 0.35383	0.972 ± 0.449 0.75936	1.03 ± 0.5783 0.65805	ATAAGTAAAGTGGTTAGTTACTGGACTACATAAATCATA
plasmid_lp21	4236	IG 360	2.112 ± 0.6014 0.041403	1.234 ± 0.4544 0.39639	1.042 ± 0.3112 0.47561	1.172 ± 0.4057 0.53883	CACTCCAAAACAACTAAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	4238	IG 361	1.806 ± 0.8338 0.011159	1.344 ± 0.6734 0.02396	1.094 ± 0.4558 0.7122	1.039 ± 0.5559 0.84067	TACACTCCAAAACAACTAAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	4239	IG 362	1.283 ± 0.7012 0.475634	0.553 ± 0.4085 0.35509	0.983 ± 0.4081 0.94647	0.941 ± 0.4491 0.84642	TAATCATAAAAATAATATTATAAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	4269	IG 363	2.593 ± 1.6473 0.017326	2.045 ± 1.8404 0.19895	0.515 ± 0.3486 0.30806	0.888 ± 0.7332 0.74795	ATAAGTAAAGTGGTTAGTTACTGGACTACATAAATCATA
plasmid_lp21	4284	IG 364	2.793 ± 1.4439 0.013777	1.219 ± 0.6115 0.3599	0.983 ± 0.5337 0.96627	1.03 ± 0.6471 0.85773	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	4301	IG 365	1.390 ± 0.6583 0.271274	1.247 ± 0.5563 0.10753	1.308 ± 0.8441 0.58822	1.571 ± 1.1101 0.31037	TGTAGTCCAGTAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	4302	IG 366	1.118 ± 0.6252 0.706066	0.508 ± 0.3544 0.25782	1.024 ± 0.5324 0.94389	1.032 ± 0.4018 0.8702	TAATCATAAAAATAATATTATAAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	4326	IG 367	1.853 ± 0.5514 0.042604	1.132 ± 0.5538 0.59871	0.83 ± 0.2066 0.13023	0.983 ± 0.248 0.49735	TAAGAATAAGTAAAGTGGTTAGTTACTGGAGTGATAAATCATAAAAA
plasmid_lp21	4362	IG 368	3.276 ± 0.742 0.010867	1.756 ± 0.9598 0.22309	1.35 ± 0.2647 0.01449	1.143 ± 0.4397 0.61429	CACTCCAGTAAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	4365	IG 369	1.267 ± 0.8267 0.347072	0.657 ± 0.5165 0.54308	1.053 ± 0.5613 0.77106	1.182 ± 0.5101 0.08942	TAATCATAAAAATAATATTATAAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	4376	IG 370	2.636 ± 1.3641 0.078833	1.72 ± 0.6025 0.04435	1.009 ± 0.5849 0.9652	1.223 ± 0.4337 0.40811	AATAATATTTTATAAAGAATAAGTAAAGTGGTTAGTTGGAGTGTT
plasmid_lp21	4398	IG 371	0.539 ± 0.3166 0.320199	0.565 ± 0.4041 0.40024	0.996 ± 0.4553 0.97074	1.027 ± 0.5314 0.5543	AGTAAAGTGGTTAGTTACTGGAGTGATAAATCATAAAAATAATATT
plasmid_lp21	4399	IG 372	2.632 ± 0.8271 0.027554	1.723 ± 0.7121 0.25825	1.663 ± 1.1213 0.35001	1.74 ± 0.4804 0.11801	CTTATTCTTATAAAATATTATTATTGATTATACACTCCAGTAAACT
plasmid_lp21	4410	IG 373	2.785 ± 1.6003 0.004688	1.356 ± 0.7717 0.43291	1.338 ± 0.8049 0.44297	1.338 ± 0.9476 0.04807	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	4423	IG 374	1.589 ± 0.1522 0.012421	0.987 ± 0.1584 0.89715	0.977 ± 0.1777 0.81328	1.026 ± 0.3128 0.89506	CACTCCAAAACAACTAAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	4425	IG 375	1.757 ± 0.8297 0.017611	1.249 ± 0.6796 0.08459	1.135 ± 0.4915 0.61293	0.936 ± 0.4802 0.67947	TACACTCCAAAACAACTAAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	4426	IG 376	3.315 ± 0.9747 0.534728	0.689 ± 0.6156 0.59978	1.091 ± 0.6452 0.79604	1.207 ± 0.6839 0.43727	TAATCATAAAAATAATATTATAAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	4450	IG 377	1.886 ± 0.8902 0.040632	1.088 ± 0.7179 0.65349	0.901 ± 0.3594 0.34362	0.95 ± 0.3776 0.57603	TAAGAATAAGTAAAGTGGTTAGTTACTGGAGTGATAAATCATAAAA
plasmid_lp21	4471	IG 378	2.553 ± 1.33 0.052878	1.093 ± 0.5704 0.47446	1.055 ± 0.6401 0.69936	1.106 ± 0.5956 0.71909	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	4486	IG 379	2.822 ± 0.826 0.021155	1.608 ± 0.9729 0.27985	1.203 ± 0.2838 0.23965	1.099 ± 0.4657 0.76838	CACTCCAGTAAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	4489	IG 380	1.078 ± 0.5066 0.756306	0.554 ± 0.4557 0.35363	0.985 ± 0.5396 0.97094	0.907 ± 0.3384 0.73963	TAATCATAAAAATAATATTTTATAAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	4522	IG 381	3.631 ± 1.1063 0.043205	1.834 ± 0.8695 0.24409	1.656 ± 1.4053 0.46739	1.713 ± 1.1131 0.42206	AGTAAAGTGGTTAGTTAGTGGACTACATAAATCATAAAAATAATTT
plasmid_lp21	4523	IG 382	2.053 ± 0.7132 0.041181	1.285 ± 0.3966 0.00355	0.929 ± 0.52 0.8692	1.134 ± 0.4702 0.61545	CTTATTCTTATAAAATATTATTATTGATTATACACTCCAGTAAACT
plasmid_lp21	4534	IG 383	3.507 ± 2.7038 0.039492	1.569 ± 1.1276 0.12733	1.661 ± 1.4623 0.37965	1.472 ± 1.3145 0.08788	AACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC
plasmid_lp21	4547	IG 384	2.544 ± 2.8516 0.139437	1.544 ± 2.2261 0.45384	1.094 ± 1.2073 0.66175	1.141 ± 1.5907 0.65129	GTCCACTAAACCAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	4551	IG 385	2.668 ± 1.1816 0.036123	1.66 ± 1.2902 0.36079	0.829 ± 0.2612 0.45888	1.308 ± 0.463 0.41914	TGTAGTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	4552	IG 386	1.236 ± 0.7313 0.499722	0.632 ± 0.3495 0.37221	1.028 ± 0.5347 0.92201	1.1 ± 0.4453 0.64194	TAATCATAAAAATAATATTTTATAAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	4582	IG 387	2.092 ± 1.4782 0.048174	1.831 ± 1.823 0.3044	0.724 ± 0.392 0.45692	0.688 ± 0.4488 0.37375	ATAAGTAAAGTGGTTAGTTACTGGACTACATAAATCATATAAAAT
plasmid_lp21	4586	IG 388	4.009 ± 3.0837 0.023938	2.753 ± 2.7866 0.16801	1.605 ± 1.2337 0.44174	1.537 ± 1.3215 0.02674	CTTATTCTTATAAAATATTATTGATTATGTAGTCCACTAAACT
plasmid_lp21	4614	IG 389	1.681 ± 0.8572 0.263254	1.223 ± 0.3948 0.28385	1.205 ± 0.6623 0.61973	1.856 ± 1.1092 0.22938	TGTAGTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	4624	IG 390	2.883 ± 1.6207 0.015542	1.819 ± 1.1412 0.23432	0.992 ± 0.5458 0.98673	0.731 ± 0.5282 0.58404	TAATAAAATTTATAAAGAATAAGTAAAGTGGTTAGTTACTGGAGT
plasmid_lp21	4636	IG 391	1.256 ± 0.8145 0.614689	1.387 ± 0.6247 0.25186	1.251 ± 0.6226 0.49971	1.715 ± 1.3855 0.40887	AAATATTATTATGATTATGTAGTCCAGTAAACCACTTTAC
plasmid_lp21	4639	IG 392	2.220 ± 0.7409 0.064041	1.319 ± 0.6287 0.37907	1.019 ± 0.2787 0.91292	1.017 ± 0.3088 0.90061	TAAGAATAAGTAAAGTGGTTAGTTACTGGAGTGATAAATCATAAAA
plasmid_lp21	4675	IG 393	2.742 ± 0.756 0.005847	1.494 ± 0.8849 0.28705	1.123 ± 0.3619 0.54128	1.015 ± 0.412 0.94229	CACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	4678	IG 394	1.166 ± 0.7083 0.536433	0.713 ± 0.4693 0.54353	1.083 ± 0.6829 0.8323	1.121 ± 0.4946 0.58908	TAATCATAAAAATAATTTATAAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	4702	IG 395	2.035 ± 0.689 0.016713	1.155 ± 0.5691 0.37678	0.968 ± 0.4421 0.73633	1.014 ± 0.3566 0.90944	TAAGAATAAGTAAAGTGGTTAGTTACTGGAGTGATAAATCATAAAA
plasmid_lp21	4712	IG 396	2.405 ± 0.8789 0.067062	1.5 ± 0.8037 0.21111	1.067 ± 0.7182 0.89886	1.514 ± 0.5153 0.01791	CTTATTCTTATAAAATATTATTGATTATACACTCCAGTAAACT
plasmid_lp21	4723	IG 397	2.702 ± 2.1911 0.060226	1.245 ± 0.8674 0.48136	1.536 ± 1.1454 0.13526	1.099 ± 0.8055 0.73611	AACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC
plasmid_lp21	4738	IG 398	2.854 ± 0.6622 0.016743	1.656 ± 0.9163 0.27786	1.112 ± 0.2879 0.05565	1.071 ± 0.3391 0.74237	CACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	4740	IG 399	1.472 ± 0.8779 0.048947	1.173 ± 0.3653 0.50547	1.104 ± 0.1011 0.81999	0.92 ± 0.5625 0.87636	TACACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	4741	IG 400	1.072 ± 0.5842 0.668494	0.478 ± 0.3522 0.2946	1.026 ± 0.5784 0.94587	1.167 ± 0.4321 0.53084	TAATCATAAAAATAATTTATAAAGAATAAGTAAAGTGGTTAGTT
plasmid_lp21	4765	IG 401	1.961 ± 0.7813 0.060709	1.262 ± 0.695 0.40693	1.119 ± 0.3835 0.31719	1.065 ± 0.4852 0.74267	TAAGAATAAGTAAAGTGGTTAGTTACTGGAGTGATAAATCATAAAA
plasmid_lp21	4775	IG 402	2.509 ± 0.5128 0.036791	1.831 ± 0.3173 0.02656	1.224 ± 0.7556 0.5847	1.291 ± 0.3244 0.22118	CTTATTCTTATAAAATATTATTGATTATACACTCCAGTAAACT

plasmid_lp21	4786	IG 403	2.560 ± 1.8493 0.001155	1.3 ± 0.886 0.456	1.175 ± 0.8976 0.72752	1.033 ± 0.9032 0.78336	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	4801	IG 404	2.915 ± 0.5189 0.003682	1.65 ± 0.8162 0.24487	1.191 ± 0.298 0.11625	1.156 ± 0.4317 0.6141	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	4804	IG 405	1.236 ± 0.7723 0.507286	0.576 ± 0.4479 0.36826	0.936 ± 0.4765 0.78602	1.04 ± 0.3061 0.71325	TAAATCATAAAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	4815	IG 406	2.513 ± 1.3139 0.149255	1.327 ± 0.4784 0.29526	1.021 ± 0.4589 0.9238	1.32 ± 0.4727 0.19787	AATAAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGAT
plasmid_lp21	4837	IG 407	0.534 ± 0.3517 0.355609	0.53 ± 0.3824 0.37442	0.984 ± 0.4416 0.93381	1.046 ± 0.5961 0.43224	AGTAAAAGTGGTTAGTTGGAGTGATATAATCATAAAAAATAAATATT
plasmid_lp21	4849	IG 408	2.187 ± 1.3409 0.022532	0.941 ± 0.5159 0.76136	0.954 ± 0.6793 0.90504	0.913 ± 0.5081 0.65879	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	4862	IG 409	1.584 ± 0.3259 0.02675	1.009 ± 0.1946 0.9382	0.999 ± 0.1985 0.98696	1.043 ± 0.3133 0.75824	CACTCCAAAACAAACCACCTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	4864	IG 410	1.898 ± 0.7533 0.013978	1.391 ± 0.728 0.11164	1.257 ± 0.4956 0.26565	1.054 ± 0.5173 0.69196	TACACTCCAAAACAAACCACCTTTACTTATTCTTATAAAATATT
plasmid_lp21	4865	IG 411	1.198 ± 0.5315 0.444849	0.641 ± 0.4875 0.43043	0.888 ± 0.4601 0.72515	1.072 ± 0.4361 0.78681	TAAATCATAAAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	4889	IG 412	2.187 ± 1.1075 0.050128	1.212 ± 0.5829 0.13811	0.98 ± 0.4449 0.8749	1.097 ± 0.4689 0.30715	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAA
plasmid_lp21	4910	IG 413	2.946 ± 1.4315 0.034499	1.311 ± 0.5738 0.00825	1.371 ± 0.6684 0.44508	1.111 ± 0.7877 0.62008	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	4925	IG 414	2.677 ± 0.6911 0.015106	1.539 ± 0.8211 0.26955	1.204 ± 0.3067 0.06851	1.046 ± 0.4749 0.88892	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	4927	IG 415	1.747 ± 0.4995 0.053965	0.91 ± 0.5089 0.83411	0.815 ± 0.5453 0.29698	0.571 ± 0.2152 0.02726	TACACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	4989	IG 416	2.763 ± 1.0129 0.084599	1.572 ± 0.7177 0.36043	0.786 ± 0.3108 0.23254	1.504 ± 0.6401 0.33106	CATAATCATATAAAATAGATATTCTTATAAAATAAAGTAAAAGTGGTTAG
plasmid_lp21	4990	IG 417	2.820 ± 0.8032 0.001619	1.586 ± 0.6153 0.03982	1.231 ± 0.4436 0.39286	1.251 ± 0.3991 0.08748	TGTAGTCCACTAAACAAACCACTTTACTTATTATTATGAATATT
plasmid_lp21	5003	IG 418	1.730 ± 1.2271 0.450058	0.742 ± 0.3147 0.4014	1.791 ± 0.2098 0.5884	2.252 ± 1.8602 0.33619	TTTATATGATTATGAGTCACAAACTAAACCACTTTACTTATT
plasmid_lp21	5006	IG 419	2.709 ± 0.4216 0.019302	1.723 ± 0.97 0.35551	1.032 ± 0.1876 0.83203	0.942 ± 0.2957 0.80857	GATTTTTATAATAATAAGTAAAAGTGGTTAGTTACTGGACTACATAA
plasmid_lp21	5007	IG 420	2.465 ± 2.7587 0.263539	1.512 ± 1.8528 0.4512	0.997 ± 0.8255 0.98889	0.987 ± 0.10621 0.93476	TCTATTATATGATTATGAGTCACAAACTAAACCACTTTACTTATT
plasmid_lp21	5021	IG 421	2.241 ± 1.3362 0.001003	1.618 ± 1.3027 0.26669	0.614 ± 0.357 0.35995	0.796 ± 0.6934 0.63106	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAAAATCATAAA
plasmid_lp21	5084	IG 422	2.089 ± 1.3815 0.040255	2.088 ± 1.808 0.20791	0.542 ± 0.3557 0.37173	0.777 ± 0.6533 0.581	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAAAATCATAAA
plasmid_lp21	5179	IG 423	2.966 ± 1.1596 0.038888	1.681 ± 0.9807 0.28132	1.239 ± 0.35 0.30467	1.197 ± 0.3556 0.38028	TGTAGTCCACTAAACCACTTTACTTATTCTTATGAAAATATT
plasmid_lp21	5192	IG 424	1.805 ± 1.1735 0.27593	0.622 ± 0.4002 0.47598	1.138 ± 0.7408 0.67399	1.199 ± 0.7031 0.21492	TTTATATGATTATGAGTCACAACTAAACCACTTTACTTATTCTT
plasmid_lp21	5199	IG 425	3.578 ± 2.3084 0.109101	1.734 ± 1.6546 0.36613	1.365 ± 0.6673 0.05447	2.126 ± 0.664 0.26627	TTTATAAAGAATAAGTAAAAGTGGTTAGTTAGTGGAGTGATAATCA
plasmid_lp21	5203	IG 426	3.237 ± 1.9371 0.154544	1.305 ± 0.4478 0.38107	2.032 ± 1.0994 0.1756	2.119 ± 0.5215 0.54366	TAAAATATTATTTATGATTATGAGTCACAAACTAAACCAC
plasmid_lp21	5240	IG 427	2.789 ± 1.7555 0.098152	1.897 ± 1.7668 0.30785	1.054 ± 0.6804 0.65157	1.079 ± 0.9119 0.85147	CACTCCACTAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	5249	IG 428	1.376 ± 1.0786 0.592478	0.364 ± 0.3508 0.32486	1.162 ± 0.8835 0.51582	0.803 ± 0.6736 0.30596	TGATTTATACACTCCACTAAACCACTTTACTTATTCTTATAAA
plasmid_lp21	5251	IG 429	2.489 ± 1.5694 0.14508	1.385 ± 1.1417 0.6015	1.107 ± 0.5028 0.36171	1.022 ± 0.5156 0.94099	TATGATTTATACACTCCACTAAACCACTTTACTTATTCTTATAA
plasmid_lp21	5252	IG 430	4.640 ± 1.677 0.00075	1.983 ± 0.7562 0.00824	1.175 ± 0.655 0.66721	1.391 ± 0.5333 0.2791	TAAAATAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	5254	IG 431	2.249 ± 1.0098 0.134945	1.417 ± 0.4469 0.25654	0.989 ± 0.6661 0.98146	1.069 ± 0.3149 0.79615	AATAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	5259	IG 432	3.472 ± 3.6499 0.35177	2.666 ± 1.7979 0.02647	0.457 ± 0.3681 0.12694	0.593 ± 0.4179 0.34801	TTTATATGATTATGATCACCAACTAAACCACTTTACTTATT
plasmid_lp21	5276	IG 433	0.509 ± 0.3148 0.306584	0.575 ± 0.4388 0.43615	0.948 ± 0.4284 0.71258	1.031 ± 0.572 0.75583	AGTAAAAGTGGTTAGTTGGAGTGATAATCATAAAAAATAATT
plasmid_lp21	5277	IG 434	2.221 ± 1.239 0.143097	1.749 ± 1.2446 0.1708	1.276 ± 0.7703 0.62045	1.137 ± 0.9018 0.67109	CATTATTCTTATAAAATTTTATGATTATACACTCCACAACT
plasmid_lp21	5301	IG 435	2.238 ± 0.6737 0.035143	1.266 ± 0.4391 0.22219	1.143 ± 0.313 0.1001	1.182 ± 0.4935 0.50378	CACTCCAAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	5303	IG 436	1.817 ± 0.7394 0.011742	1.36 ± 0.7034 0.109	1.199 ± 0.4956 0.48157	1.082 ± 0.491 0.6628	TACACTCCAAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	5304	IG 437	1.133 ± 0.5852 0.272008	0.567 ± 0.4143 0.39993	1.04 ± 0.6544 0.90291	0.926 ± 0.439 0.41375	TAAATCATAAAAATAAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	5328	IG 438	2.053 ± 0.9062 0.058968	1.239 ± 0.5891 0.17891	0.959 ± 0.3577 0.56776	1.054 ± 0.4346 0.10148	AAAAGATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAA
plasmid_lp21	5349	IG 439	2.685 ± 1.4357 0.047279	1.156 ± 0.5422 0.40386	1.251 ± 0.7108 0.44191	1.024 ± 0.8961 0.94148	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	5364	IG 440	2.725 ± 0.5375 0.017757	1.582 ± 0.9127 0.33386	1.121 ± 0.1835 0.1941	1.021 ± 0.458 0.94942	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	5369	IG 441	2.675 ± 1.8931 0.113578	2.839 ± 2.7424 0.29003	1.551 ± 1.6724 0.50859	1.533 ± 1.1578 0.53421	AATCATAAAAATAAATTTCTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	5400	IG 442	0.532 ± 0.3361 0.329837	0.547 ± 0.376 0.36683	0.955 ± 0.4232 0.74299	1.074 ± 0.5816 0.20793	AGTAAAAGTGGTTAGTTGGAGTGATAATCATAAAAAATAATT
plasmid_lp21	5425	IG 443	1.649 ± 0.4778 0.073324	0.861 ± 0.2302 0.12273	1.041 ± 0.4116 0.82974	1.253 ± 0.4653 0.32383	CACTCCAAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	5427	IG 444	1.955 ± 1.2629 0.008999	1.257 ± 0.7794 0.56154	1.259 ± 0.8842 0.38391	1.085 ± 0.7627 0.86339	TACACTCCAAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	5428	IG 445	1.091 ± 0.7342 0.784522	0.603 ± 0.413 0.34674	1.031 ± 0.6029 0.93324	0.999 ± 0.601 0.99661	TAAATCATAAAAATAAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	5452	IG 446	2.147 ± 0.8981 0.046398	1.296 ± 0.7009 0.23794	0.999 ± 0.3801 0.99579	1.032 ± 0.3765 0.74996	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAA
plasmid_lp21	5473	IG 447	3.094 ± 2.1048 0.045636	1.125 ± 0.7874 0.4365	1.34 ± 0.9339 0.4312	1.232 ± 0.10421 0.19154	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	5488	IG 448	3.213 ± 0.6962 0.008797	1.66 ± 0.7303 0.17014	1.224 ± 0.2368 0.17313	1.028 ± 0.2988 0.83237	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	5490	IG 449	1.681 ± 0.5316 0.063006	0.879 ± 0.326 0.57968	0.817 ± 0.3473 0.04747	0.844 ± 0.2987 0.58464	TACACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	5491	IG 450	1.258 ± 0.7691 0.523241	0.628 ± 0.4807 0.42572	1.136 ± 0.6428 0.75779	0.935 ± 0.4282 0.81952	TAAATCATAAAAATAAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	5502	IG 451	2.920 ± 1.8416 0.176895	1.715 ± 0.6887 0.21319	0.918 ± 0.3287 0.65655	1.245 ± 0.5256 0.54543	AATAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGAT

plasmid_lp21	5524	IG 452	0.522 ± 0.3507 0.350876	0.556 ± 0.4061 0.41041	0.987 ± 0.4718 0.94505	1.037 ± 0.5806 0.39107	AGTAAAAGGGTTAGTTGGAGGTGTATAAATCATAAAAATAAATTTT
plasmid_lp21	5536	IG 453	2.316 ± 1.2151 0.035621	1.02 ± 0.4193 0.92307	1.105 ± 0.5639 0.69713	0.979 ± 0.7099 0.90074	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	5549	IG 454	1.675 ± 0.3708 0.054674	1.002 ± 0.241 0.98975	1.017 ± 0.208 0.84805	1.068 ± 0.3382 0.73663	CACTCCAAAACAAACCACTTTACTTATTCTTATAAAATTTTATTT
plasmid_lp21	5551	IG 455	1.875 ± 0.7684 0.020405	1.348 ± 0.6738 0.06008	1.212 ± 0.5053 0.28802	0.968 ± 0.5027 0.83767	TACACTCCAAAACAAACCACTTTACTTATTCTTATAAAATTTTATTT
plasmid_lp21	5552	IG 456	1.263 ± 0.8649 0.460936	0.585 ± 0.4631 0.4656	1.092 ± 0.8273 0.82383	1.142 ± 0.6156 0.6309	TAATCATAAAAATAAATTTTATAAAGAATAAGTAAAAGGGTTAGTT
plasmid_lp21	5576	IG 457	1.994 ± 0.4969 0.031935	1.117 ± 0.5378 0.66113	0.996 ± 0.2239 0.93888	1.063 ± 0.2456 0.33308	AAAAGAATAAGTAAAAGGGTTAGTTACTGGAGGTGTATAAATCATAAAA
plasmid_lp21	5597	IG 458	2.790 ± 1.5675 0.048263	1.046 ± 0.4269 0.8487	1.121 ± 0.576 0.70077	0.936 ± 0.7102 0.65472	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	5612	IG 459	2.799 ± 0.8757 0.004112	1.693 ± 1.0061 0.19254	1.14 ± 0.3507 0.40877	1.026 ± 0.4885 0.92811	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTTATTT
plasmid_lp21	5614	IG 460	1.233 ± 0.3867 0.15054	1.098 ± 0.5055 0.82145	1.23 ± 0.8401 0.5473	0.612 ± 0.1858 0.18469	TACACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTTAT
plasmid_lp21	5676	IG 461	2.911 ± 1.0252 0.071896	1.776 ± 0.8975 0.31775	0.862 ± 0.2204 0.44267	1.407 ± 0.5523 0.33199	CATAATCATATAAATAGATTTTATAAATATAAAGTAAAAGGGTTAG
plasmid_lp21	5677	IG 462	2.757 ± 0.7514 0.001258	1.589 ± 0.6285 0.05803	1.235 ± 0.4173 0.32059	1.236 ± 0.3842 0.06441	TGTAGTCCTAAACTAACCACTTTACTTATTATGAAATTTTAT
plasmid_lp21	5693	IG 463	2.658 ± 0.4805 0.027533	1.689 ± 0.9761 0.37616	1.016 ± 0.2379 0.93224	0.888 ± 0.2641 0.6349	GATTTTATAAATAAAGTAAAAGGGTTAGTTACTGGACTACATAA
plasmid_lp21	5694	IG 464	2.253 ± 2.4388 0.305426	1.436 ± 1.6116 0.4853	0.909 ± 0.6781 0.56729	0.902 ± 0.8683 0.50143	TCTATTATGATTATGATTGCTTCACTAAACTAACCACTTTACTTATT
plasmid_lp21	5708	IG 465	1.918 ± 1.5294 0.013547	1.67 ± 1.5185 0.09263	0.454 ± 0.3677 0.39709	0.748 ± 0.6969 0.43475	ATAAGTAAAAGGGTTAGTTACTGGACTACATAAATCATAAAAAAAT
plasmid_lp21	5866	IG 466	3.153 ± 0.8417 0.046	1.69 ± 0.7125 0.26356	1.129 ± 0.1724 0.38939	1.6 ± 0.2961 0.0293	TGTAGTCCTAAACTAACCACTTTACTTATTCTTATGAAATTTTAT
plasmid_lp21	5879	IG 467	1.532 ± 0.9413 0.364235	0.628 ± 0.3671 0.44716	0.865 ± 0.6106 0.7145	1.142 ± 0.6337 0.34704	TTTATATGATTATGATTGCTTCACTAAACTAACCACTTTACTTATTCTT
plasmid_lp21	5886	IG 468	3.493 ± 2.003 0.106957	1.969 ± 1.5593 0.28909	1.362 ± 0.8049 0.42126	1.568 ± 0.9472 0.28695	TTTATAAGAATAAGTAAAAGGGTTAGTTAGTGAGGTGTATAATCA
plasmid_lp21	5890	IG 469	3.635 ± 2.2015 0.166136	1.686 ± 0.5714 0.21293	1.919 ± 0.9509 0.16754	1.462 ± 0.5119 0.31117	AAAATTTTATATGATTGTTAGTGTAGTCCTAAACTAACCACTTT
plasmid_lp21	5927	IG 470	2.543 ± 1.5176 0.106413	1.621 ± 1.5977 0.44012	0.949 ± 0.6228 0.85785	0.781 ± 0.6108 0.35655	CACTCCACTAAACTAACCACTTTACTTATTCTTATAAAATTTTAT
plasmid_lp21	5936	IG 471	1.193 ± 0.9108 0.742445	0.33 ± 0.3167 0.28877	1.068 ± 0.7562 0.80713	0.673 ± 0.5351 0.13919	TGATTATACACTCCACTAAACTAACCACTTTACTTATTCTTATAAA
plasmid_lp21	5938	IG 472	3.182 ± 1.9275 0.102144	1.418 ± 1.113 0.53959	1.381 ± 0.6482 0.1882	1.123 ± 0.665 0.71273	TGTAGTTACACTCCACTAAACTAACCACTTTACTTATTCTTATAAA
plasmid_lp21	5939	IG 473	4.788 ± 1.7633 0.000788	1.989 ± 0.8339 0.00476	1.169 ± 0.5311 0.35566	1.302 ± 0.5589 0.44936	AAATAATTTTATAAAGAATAAGTAAAAGGGTTAGTTGGAGGTGT
plasmid_lp21	5941	IG 474	2.295 ± 1.3381 0.097428	1.499 ± 0.6716 0.02845	0.926 ± 0.3797 0.58206	1.309 ± 0.6509 0.42853	AATAATTTTATAAAGAATAAGTAAAAGGGTTAGTTGGAGGTGT
plasmid_lp21	5946	IG 475	3.192 ± 3.1082 0.333574	2.857 ± 2.1563 0.0566	0.502 ± 0.4078 0.13884	0.574 ± 0.3611 0.3467	TTTATTTATGATTATACCTCCACTAAACTAACCACTTTACTTATT
plasmid_lp21	5963	IG 476	0.515 ± 0.3344 0.325996	0.533 ± 0.3948 0.37634	0.976 ± 0.4501 0.8564	1 ± 0.5912 0.99575	AGTAAAAGGGTTAGTTGGAGGTGTATAAATCATAAAAATAAATTTT
plasmid_lp21	5964	IG 477	2.174 ± 1.1814 0.129111	1.701 ± 1.3394 0.26511	1.251 ± 0.6724 0.58594	1.141 ± 0.8306 0.67662	CTTATTCTTATAAAATTTTATGATTATACACTCCACTAAACT
plasmid_lp21	5988	IG 478	2.130 ± 0.7157 0.016094	1.316 ± 0.5554 0.13756	1.079 ± 0.3962 0.31382	1.22 ± 0.5296 0.32278	CACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATTTTAT
plasmid_lp21	5990	IG 479	1.874 ± 0.7011 0.019344	1.293 ± 0.6294 0.15544	1.18 ± 0.4317 0.41439	1.021 ± 0.4515 0.88447	TACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATTTTAT
plasmid_lp21	5991	IG 480	1.510 ± 1.1671 0.21498	0.582 ± 0.53 0.51841	1.139 ± 0.7462 0.76239	1.108 ± 0.6215 0.73767	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGGGTTAGTT
plasmid_lp21	6015	IG 481	1.987 ± 0.778 0.059044	1.176 ± 0.4157 0.1301	0.974 ± 0.3025 0.77446	1.075 ± 0.3097 0.30898	TAAAGAATAAGTAAAAGGGTTAGTTACTGGAGGTGTATAATCATAAA
plasmid_lp21	6036	IG 482	2.816 ± 1.2555 0.048436	1.253 ± 0.5079 0.15297	1.419 ± 0.7112 0.25482	1.226 ± 0.7088 0.35782	AAACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	6051	IG 483	2.648 ± 0.8033 0.01752	1.514 ± 0.8282 0.21504	1.174 ± 0.3292 0.44228	1.025 ± 0.3892 0.92791	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTTAT
plasmid_lp21	6056	IG 484	2.797 ± 2.0278 0.044559	3.066 ± 2.9487 0.24749	1.638 ± 1.8279 0.5046	1.333 ± 0.9518 0.61649	AATCATAAAAATAATTTCTATAAATAAAGAATAAGTAAAAGGGTTAGTT
plasmid_lp21	6087	IG 485	0.527 ± 0.3362 0.332684	0.531 ± 0.3792 0.36327	0.961 ± 0.4378 0.77812	1.045 ± 0.5961 0.6336	AGTAAAAGGGTTAGTTGGAGGTGTATAAATCATAAAAATAAATTTT
plasmid_lp21	6112	IG 486	1.923 ± 0.7186 0.019636	1.074 ± 0.4967 0.78658	1.099 ± 0.5207 0.67222	1.157 ± 0.5699 0.69783	CACTCCAAAACAACTAACCACTTTACTTATTATGAAATTTTATTT
plasmid_lp21	6114	IG 487	2.173 ± 1.2788 0.023331	1.15 ± 0.8568 0.36615	1.223 ± 0.7237 0.06061	1.048 ± 0.6736 0.88595	TACACTCCAAAACAACTAACCACTTTACTTATTATGAAATTTTATTT
plasmid_lp21	6115	IG 488	1.385 ± 0.6815 0.212079	0.729 ± 0.5668 0.60132	1.025 ± 0.5681 0.93833	1.049 ± 0.4989 0.69159	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGGGTTAGTT
plasmid_lp21	6126	IG 489	2.757 ± 1.2903 0.032693	1.511 ± 0.6798 0.09695	1.182 ± 0.7325 0.53402	1.229 ± 0.7054 0.46803	AATAATTTATAAAGAATAAGTAAAAGGGTTAGTTGGAGGTGT
plasmid_lp21	6148	IG 490	0.645 ± 0.4461 0.525103	0.529 ± 0.4591 0.44983	0.924 ± 0.5845 0.55109	0.845 ± 0.6763 0.40597	AGTAAAAGGGTTAGTTGGAGGTGTATAAATCATAAAAATAAATTTT
plasmid_lp21	6160	IG 491	2.412 ± 1.5821 0.000199	1.055 ± 0.6715 0.85122	1.099 ± 0.8147 0.80682	0.965 ± 0.6353 0.88985	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	6163	IG 492	2.033 ± 0.7737 0.019207	1.361 ± 0.5812 0.18447	1.142 ± 0.4332 0.27178	1.024 ± 0.4255 0.94356	GTTTGGAGGTGTATAAATCATATAAATAAATTTTATAAATAAATGAA
plasmid_lp21	6173	IG 493	1.620 ± 0.3479 0.05725	1.018 ± 0.1885 0.7719	1.013 ± 0.2195 0.92324	1.019 ± 0.317 0.89864	CACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATTTTAT
plasmid_lp21	6175	IG 494	1.854 ± 0.8262 0.027894	1.281 ± 0.6915 0.14158	1.198 ± 0.4658 0.419	0.97 ± 0.4575 0.87003	TACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATTTTAT
plasmid_lp21	6209	IG 495	2.116 ± 2.1241 0.072469	1.518 ± 1.8643 0.24525	0.982 ± 0.9654 0.97057	1.169 ± 1.2554 0.35707	AGTAAAAGGGTTAGTTACTGGAGGTGTATAATCATATAAATAAAT
plasmid_lp21	6221	IG 496	3.621 ± 2.2438 0.09517	1.96 ± 1.8946 0.40236	1.17 ± 0.9134 0.74007	1.198 ± 0.7882 0.64814	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	6236	IG 497	3.967 ± 1.4355 0.004086	1.639 ± 1.1862 0.48551	1.368 ± 0.4983 0.13626	1.265 ± 0.6941 0.63453	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTTAT
plasmid_lp21	6258	IG 498	3.952 ± 2.8058 0.108403	1.932 ± 1.7385 0.24882	1.692 ± 1.2521 0.16621	1.561 ± 1.071 0.11189	TTTATAAAGAATAAGTAAAAGGGTTAGTTACTGGAGGTGTATAAATCA
plasmid_lp21	6299	IG 499	2.822 ± 1.9255 0.098308	1.709 ± 1.7076 0.37598	1.079 ± 0.7755 0.72848	0.883 ± 0.8455 0.72829	CACTCCACTAAACCACTAACCACTTTACTTATTCTTATAAAATTTTAT
plasmid_lp21	6302	IG 500	1.317 ± 0.8216 0.228343	0.636 ± 0.5107 0.51955	1.168 ± 0.6228 0.55236	1.256 ± 0.5887 0.39189	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGGGTTAGTT

plasmid_lp21	6308	IG 501	1.319 ± 1.1552 0.616645	0.372 ± 0.3866 0.38906	1.039 ± 0.9061 0.88485	0.772 ± 0.7432 0.42219	TGATTTATAACACTCCACTAAACTAAACCACCTTACTTATTCTTATAAAA
plasmid_lp21	6310	IG 502	2.829 ± 1.7623 0.08249	1.457 ± 1.159 0.51071	1.272 ± 0.7019 0.21725	1.003 ± 0.52 0.99088	TATGATTTATAACACTCCACTAAACTAAACCACCTTACTTATTCTTATAAA
plasmid_lp21	6313	IG 503	2.707 ± 1.3354 0.127507	1.372 ± 0.2578 0.10205	1.101 ± 0.7267 0.79796	1.088 ± 0.3953 0.76292	AATAAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTTTGAGGTGTAT
plasmid_lp21	6335	IG 504	0.667 ± 0.4794 0.544796	0.543 ± 0.4393 0.43993	1.149 ± 0.6311 0.35262	0.919 ± 0.7282 0.75544	AGTAAAAGTGGTTAGTTGGAGGTGTATAAATCATATAAAATAATTTT
plasmid_lp21	6347	IG 505	3.070 ± 2.742 0.049844	1.581 ± 1.2643 0.41085	1.455 ± 1.1701 0.42446	0.988 ± 0.8757 0.94072	AACCACTTTACTTATTCTTTATAAAATTTTATGATTTACAC
plasmid_lp21	6350	IG 506	2.479 ± 0.4254 0.003041	1.535 ± 0.3156 0.0124	1.274 ± 0.374 0.30829	1.277 ± 0.2601 0.24692	GTTTGGAGGTGTATAAATCATATAAAATAATTTATAAAGAATAAGTAA
plasmid_lp21	6360	IG 507	1.560 ± 0.2957 0.008604	0.929 ± 0.2223 0.46367	1.047 ± 0.2182 0.49757	1.031 ± 0.3761 0.85882	CACTCCAAAACTAAACCACCTTACTTATTCTTATAAAATTTT
plasmid_lp21	6362	IG 508	1.955 ± 0.7751 0.045793	1.305 ± 0.6578 0.28541	1.203 ± 0.4012 0.41023	1.085 ± 0.5395 0.46259	TACACTCCAAAACTAAACCACCTTACTTATTCTTATAAAATTTT
plasmid_lp21	6372	IG 509	4.669 ± 1.9244 0.006198	2.209 ± 0.9496 0.01106	1.383 ± 0.6371 0.27534	1.37 ± 0.5343 0.30953	TAATAAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGGTGT
plasmid_lp21	6374	IG 510	2.764 ± 1.2754 0.071415	1.63 ± 0.584 0.03532	1.158 ± 0.5397 0.41947	1.336 ± 0.5251 0.32912	TAATAAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGGTGTAT
plasmid_lp21	6393	IG 511	2.938 ± 3.1779 0.401687	1.295 ± 1.2866 0.76876	0.777 ± 0.4787 0.66269	0.98 ± 0.5812 0.96681	TTCTTATAAAATTTTATGATTTACACTCCAAAACTAAACCA
plasmid_lp21	6396	IG 512	0.567 ± 0.4395 0.467359	0.491 ± 0.4188 0.42118	1.008 ± 0.6866 0.95443	0.923 ± 0.7614 0.67307	AGTAAAAGTGGTTAGTTGGAGGTGTATAAATCATATAAAATTTT
plasmid_lp21	6411	IG 513	2.198 ± 0.3323 0.025752	1.469 ± 0.2156 0.05031	1.264 ± 0.2425 0.04425	1.345 ± 0.1745 0.0077	GTTTGGAGGTGTATAAATCATATAAAATTTTATAAAGAATAAGTAA
plasmid_lp21	6421	IG 514	2.120 ± 0.5822 0.019761	1.198 ± 0.5635 0.48921	1.014 ± 0.3029 0.67879	1.194 ± 0.4249 0.40479	CACTCCAAAACTAAACCACCTTACTTATTCTTATAAAATTTT
plasmid_lp21	6423	IG 515	1.747 ± 0.6826 0.011299	1.313 ± 0.7565 0.24442	1.13 ± 0.4022 0.48207	0.988 ± 0.4867 0.95938	TACACTCCAAAACTAAACCACTTACTTATTCTTATAAAATTTT
plasmid_lp21	6433	IG 516	2.896 ± 0.7494 0.003744	1.787 ± 0.6235 0.16484	1.049 ± 0.3457 0.68404	0.801 ± 0.2701 0.03892	TAATAAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGT
plasmid_lp21	6448	IG 517	2.109 ± 0.9628 0.022608	1.248 ± 0.7048 0.24082	1.019 ± 0.4819 0.84141	0.994 ± 0.5297 0.92602	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGGTGTATAAATCATAAA
plasmid_lp21	6454	IG 518	3.339 ± 3.4854 0.349825	1.26 ± 1.1033 0.75556	0.894 ± 0.5552 0.82486	0.929 ± 0.5163 0.82448	TTCTTATAAAATTTTATGATTTACACTCCAAAACTAAACCA
plasmid_lp21	6484	IG 519	2.906 ± 0.7569 0.013145	1.773 ± 0.8775 0.17168	1.172 ± 0.2147 0.27798	1.095 ± 0.4734 0.71854	CACTCCAGTAAACTAAACCACCTTACTTATTCTTATAAAATTTT
plasmid_lp21	6487	IG 520	1.203 ± 0.824 0.487946	0.556 ± 0.455 0.45263	1.231 ± 0.7162 0.51215	1.197 ± 0.6991 0.31327	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	6521	IG 521	2.518 ± 1.3207 0.048459	1.509 ± 0.8295 0.04196	1.263 ± 0.6656 0.54514	1.117 ± 0.5589 0.79911	CTTATTCTTATAAAATTTTATGATTTACACTCCAGTAAACT
plasmid_lp21	6532	IG 522	2.731 ± 1.6202 0.05833	0.89 ± 0.5499 0.33298	1.508 ± 0.9963 0.34261	1.126 ± 0.728 0.42024	AACCACTTTACTTATTCTTATAAAATTTTATGATTTACAC
plasmid_lp21	6545	IG 523	2.596 ± 3.2692 0.175238	1.519 ± 2.3073 0.43796	0.984 ± 1.184 0.94772	1.023 ± 1.4348 0.83574	GTCCCACTAAACCACCTTACTTATTCTTATAAAATTTT
plasmid_lp21	6549	IG 524	2.821 ± 0.86 0.046416	1.721 ± 0.8787 0.31462	1.006 ± 0.2971 0.96374	1.36 ± 0.3228 0.14364	TGTAGTCCACTAAACTAAACCACCTTACTTATTCTTATAAAATTTT
plasmid_lp21	6562	IG 525	1.559 ± 0.7769 0.348982	0.576 ± 0.2093 0.19222	0.887 ± 0.6395 0.80354	1.345 ± 0.5793 0.17016	TTTATATGATTTATGAGTCACCAAACCACTTACTTATTCTT
plasmid_lp21	6566	IG 526	2.590 ± 2.9217 0.270756	1.524 ± 1.8128 0.43288	0.99 ± 0.7708 0.94983	0.918 ± 0.9757 0.51916	TCTATTATATGATTTATGAGTCACCAAACCACTTATT
plasmid_lp21	6611	IG 527	2.696 ± 0.977 0.073499	1.617 ± 0.10195 0.46382	0.756 ± 0.301 0.1935	1.3 ± 0.4934 0.43607	CATAATCATATAAAATAGATTTTATAAATAAGTAAAAGTGGTTAG
plasmid_lp21	6612	IG 528	2.369 ± 0.826 0.07989	1.607 ± 0.851 0.33907	0.99 ± 0.2812 0.94831	1.222 ± 0.285 0.32373	TGTAGTCCACTAAACTAAACCACCTTACTTATTCTTATAAAATATCTAT
plasmid_lp21	6624	IG 529	5.162 ± 4.5372 0.174109	2.731 ± 3.0444 0.3254	1.781 ± 1.1462 0.22894	1.731 ± 0.8904 0.00341	AATAGATATTTTATAAATAAGTAAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	6625	IG 530	1.720 ± 0.9559 0.261544	0.596 ± 0.3135 0.34792	1.009 ± 0.703 0.98604	1.426 ± 0.7467 0.08173	TTTATATGATTTATGAGTCACCAAACCACTTATTCTT
plasmid_lp21	6628	IG 531	2.254 ± 0.7898 0.040267	1.544 ± 0.6941 0.10522	0.955 ± 0.6556 0.84533	0.578 ± 0.4264 0.34924	GATATTATATAAAATAAGTAAAAGTGGTTAGTTGGAGTGTATAAAAT
plasmid_lp21	6629	IG 532	2.361 ± 2.5413 0.295965	1.459 ± 1.6818 0.49618	0.875 ± 0.6856 0.40471	0.872 ± 0.8853 0.42967	TCTATTATATGATTTATGAGTCACCAAACCACTTATT
plasmid_lp21	6646	IG 533	0.529 ± 0.3449 0.345792	0.566 ± 0.413 0.41688	0.938 ± 0.4357 0.7428	0.974 ± 0.5205 0.41203	AGTAAAAGTGGTTAGTTGGAGGTATAAATCATAAAAATAATTTT
plasmid_lp21	6671	IG 534	1.887 ± 0.5502 0.117472	0.86 ± 0.2717 0.53105	0.966 ± 0.1129 0.64085	1.008 ± 0.3605 0.97791	CACTCCAAAACCAACCACTTATTCTTATAAAATATCTATT
plasmid_lp21	6673	IG 535	1.993 ± 1.0021 0.033051	1.164 ± 0.6669 0.14707	1.199 ± 0.4754 0.37056	1.019 ± 0.4977 0.9322	TACACTCCAAAACCAACCACTTATTCTTATAAAATATCTATT
plasmid_lp21	6674	IG 536	1.070 ± 0.7123 0.846189	0.573 ± 0.5247 0.45737	0.978 ± 0.5251 0.94866	0.994 ± 0.4946 0.97813	TAATCATAAAAATAAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	6685	IG 537	2.542 ± 1.2953 0.065334	1.352 ± 0.7195 0.18844	1.061 ± 0.5598 0.71182	1.305 ± 0.6103 0.3794	AATAATATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTAT
plasmid_lp21	6707	IG 538	0.544 ± 0.3456 0.35289	0.532 ± 0.3915 0.37427	0.992 ± 0.4522 0.9495	1.065 ± 0.5927 0.17954	AGTAAAAGTGGTTAGTTGGAGGTATAAATCATAAAAATAATTTT
plasmid_lp21	6719	IG 539	2.479 ± 1.0778 0.003915	1.33 ± 0.5483 0.17781	1.265 ± 0.8522 0.61814	1.007 ± 0.64 0.93723	AACCACTTTACTTATTCTTATAAAATTTTATGATTTACAC
plasmid_lp21	6732	IG 540	1.687 ± 0.3773 0.043108	1.064 ± 0.2245 0.60185	1.093 ± 0.1959 0.28875	1.087 ± 0.3568 0.66279	CACTCCAAAACCAACCACTTATTCTTATAAAATTTT
plasmid_lp21	6734	IG 541	1.779 ± 0.8467 0.018149	1.254 ± 0.7067 0.03242	1.114 ± 0.499 0.65752	1.023 ± 0.5577 0.89283	TACACTCCAAAACCAACCACTTATTCTTATAAAATTTT
plasmid_lp21	6735	IG 542	1.307 ± 0.7325 0.264793	0.52 ± 0.4234 0.39425	1.036 ± 0.6489 0.90732	1.011 ± 0.5339 0.96736	TAATCATAAAAATAAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	6746	IG 543	2.715 ± 1.5822 0.111899	1.595 ± 0.7174 0.0633	1.026 ± 0.4957 0.91544	1.249 ± 0.5331 0.09737	AATAATATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTAT
plasmid_lp21	6768	IG 544	0.631 ± 0.4757 0.538003	0.493 ± 0.4385 0.42086	1.053 ± 0.645 0.76716	0.877 ± 0.6327 0.22354	AGTAAAAGTGGTTAGTTGGAGGTATAAATCATATAAAATTTT
plasmid_lp21	6780	IG 545	2.396 ± 1.7396 0.015069	1.298 ± 0.8398 0.49362	1.138 ± 0.9135 0.7231	0.9 ± 0.7382 0.65601	AACCACTTTACTTATTCTTATAAAATTTTATGATTTACAC
plasmid_lp21	6783	IG 546	2.294 ± 0.2514 0.00342	1.323 ± 0.1766 0.03973	1.154 ± 0.2494 0.33692	1.132 ± 0.1477 0.34478	GTTTGGAGGTGTATAAATCATATAAAATTTTATAAAGAATAAGTAA
plasmid_lp21	6793	IG 547	1.604 ± 0.2756 0.013164	1.03 ± 0.1637 0.65177	0.99 ± 0.2415 0.94447	1.056 ± 0.3498 0.69166	CACTCCAAAACCAACCACTTATTCTTATAAAATTTT
plasmid_lp21	6795	IG 548	1.971 ± 0.8222 0.023668	1.434 ± 0.7294 0.11747	1.273 ± 0.437 0.22204	1.053 ± 0.5284 0.79447	TACACTCCAAAACCAACCACTTATTCTTATAAAATTTT
plasmid_lp21	6815	IG 549	3.134 ± 1.7299 0.011725	1.662 ± 1.2111 0.32663	1.35 ± 0.664 0.2244	1.232 ± 0.6984 0.40358	TTTTAAGAATAAGTAAAAGTGGTTAGTTGGAGGTATAAATCA

plasmid_lp21	6856	IG 550	2.887 ± 2.1374 0.133386	1.678 ± 1.8126 0.40406	1.104 ± 0.7673 0.70786	0.962 ± 0.7862 0.89048	CACTCCACTAAACCACTTTACTTATTCTTATAAAATATTCTT
plasmid_lp21	6859	IG 551	1.224 ± 0.5939 0.459414	0.598 ± 0.4632 0.42876	0.996 ± 0.6193 0.99305	1.01 ± 0.4373 0.96633	TAAATCATAAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	6865	IG 552	1.330 ± 0.9395 0.531876	0.361 ± 0.317 0.29738	1.04 ± 0.8064 0.82955	0.794 ± 0.6755 0.04758	TGATTATACCTCCACTAAACCACTTTACTTATTCTTATAAA
plasmid_lp21	6867	IG 553	3.230 ± 2.2115 0.118297	1.808 ± 1.3784 0.36793	1.392 ± 0.7469 0.22355	1.33 ± 0.8768 0.38403	TATGATTATACCTCCACTAAACCACTTTACTTATTCTTATAAA
plasmid_lp21	6892	IG 554	3.597 ± 1.217 0.057314	1.672 ± 1.1023 0.43092	1.346 ± 0.8516 0.49478	1.609 ± 1.1694 0.48361	AGTAAAAGTGGTTAGTTAGTGGACTACATAAAATCATAAAATATT
plasmid_lp21	6904	IG 555	2.779 ± 2.6207 0.025632	1.557 ± 1.571 0.21599	1.514 ± 1.4923 0.53415	1.203 ± 1.1627 0.61243	AACCACTTTACTTATTCTTATAAAATATTATTATGATTATACAC
plasmid_lp21	6917	IG 556	2.548 ± 2.9368 0.117199	1.505 ± 2.3643 0.50098	1.023 ± 1.2241 0.91089	1.031 ± 1.4639 0.85742	GTCCACTAAACCAACCACTTTACTTATTCTTATAAAATATTCTT
plasmid_lp21	6921	IG 557	3.124 ± 0.8523 0.05285	1.959 ± 0.6674 0.14919	1.203 ± 0.1717 0.05066	1.276 ± 0.1653 0.07913	TGTAGTCCACTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	6922	IG 558	1.241 ± 0.5358 0.394937	0.591 ± 0.4084 0.30903	1.005 ± 0.4615 0.98387	0.927 ± 0.3088 0.66068	TAATCATAAAAATAAATATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	6952	IG 559	2.531 ± 1.4025 0.01995	2.042 ± 1.9621 0.31773	0.746 ± 0.3507 0.45648	1.036 ± 0.7812 0.94615	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAAAATCAT
plasmid_lp21	6956	IG 560	3.802 ± 2.4637 0.024617	2.776 ± 2.9302 0.25681	1.429 ± 0.8724 0.46965	1.357 ± 1.0024 0.04242	CTTATTCTTATAAAATATTATTATGATTATGAGTCACAACT
plasmid_lp21	6984	IG 561	1.689 ± 0.6734 0.217705	1.188 ± 0.5911 0.48831	1.406 ± 0.6092 0.2327	1.627 ± 0.9579 0.28547	TGTAGTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	6994	IG 562	2.789 ± 0.9401 0.031315	2.04 ± 0.5761 0.0082	0.866 ± 0.3017 0.25527	1.114 ± 0.5195 0.66762	TAATAAATATTTTATAAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGT
plasmid_lp21	7009	IG 563	1.952 ± 0.8102 0.073879	1.078 ± 0.675 0.73704	0.887 ± 0.2654 0.25795	0.993 ± 0.3265 0.91971	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATAAAA
plasmid_lp21	7045	IG 564	2.799 ± 0.946 0.004974	1.578 ± 0.9297 0.21093	1.057 ± 0.361 0.65224	0.908 ± 0.375 0.75202	CACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7047	IG 565	1.437 ± 0.8336 0.304628	0.693 ± 0.4297 0.53676	0.902 ± 1.1433 0.73991	1.069 ± 0.6244 0.84528	TACACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7048	IG 566	1.378 ± 0.8867 0.363288	0.681 ± 0.4945 0.53895	1.065 ± 0.4898 0.81124	1.182 ± 0.4771 0.12917	TAATCATAAAAATAAATATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	7072	IG 567	2.056 ± 0.6433 0.028327	1.185 ± 0.6035 0.46953	1 ± 0.3328 0.98846	1.117 ± 0.2935 0.11692	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATAAAA
plasmid_lp21	7082	IG 568	2.108 ± 0.3866 0.01614	1.168 ± 0.3713 0.53835	1.206 ± 0.6216 0.58063	0.969 ± 0.2414 0.84823	CTTATTCTTATAAAATATTATTATGATTATACCTCCAGTAAACT
plasmid_lp21	7093	IG 569	3.010 ± 2.0255 0.008547	1.379 ± 0.8448 0.30886	1.417 ± 1.0005 0.51548	1.274 ± 0.9250 0.20979	AACCACTTTACTTATTCTTATAAAATATTATTATGATTATACAC
plasmid_lp21	7108	IG 570	2.674 ± 0.5321 0.010027	1.423 ± 0.8827 0.44752	1.056 ± 0.2855 0.43882	1.057 ± 0.4315 0.85792	CACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7110	IG 571	1.767 ± 0.774 0.207733	1.181 ± 0.4503 0.61233	1.386 ± 0.10849 0.39653	0.868 ± 0.3143 0.46619	TACACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7111	IG 572	1.061 ± 0.6519 0.773734	0.535 ± 0.3922 0.32009	1 ± 0.461 0.99842	1.05 ± 0.4431 0.72396	TAATCATAAAAATAAATATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	7135	IG 573	1.872 ± 0.5552 0.075745	1.116 ± 0.6137 0.73674	0.916 ± 0.2163 0.59063	0.943 ± 0.2818 0.69379	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATAAAA
plasmid_lp21	7145	IG 574	2.731 ± 1.2731 0.15272	1.592 ± 0.7316 0.2044	1.699 ± 1.1646 0.41552	1.187 ± 0.4229 0.55081	CTTATTCTTATAAAATATTATTATGATTATACACTCCAGTAAACT
plasmid_lp21	7156	IG 575	3.089 ± 1.5262 0.036854	1.303 ± 0.6258 0.3219	1.411 ± 0.8827 0.48446	1.367 ± 0.7981 0.15458	AACCACTTTACTTATTCTTATAAAATATTATTATGATTATACAC
plasmid_lp21	7171	IG 576	3.052 ± 0.92 0.012052	1.642 ± 0.8216 0.14985	1.236 ± 0.4181 0.21761	1.136 ± 0.456 0.60663	CACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7173	IG 577	1.407 ± 0.4867 0.317795	1.162 ± 0.397 0.62213	0.97 ± 0.6072 0.90245	0.667 ± 0.2575 0.19382	TACACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7204	IG 578	2.477 ± 0.6141 0.030153	1.671 ± 0.7558 0.19147	1.249 ± 0.4287 0.38305	0.921 ± 0.3223 0.74967	TTCTTATGAAATATTATTATGATTATACACTCCAGTAAACAC
plasmid_lp21	7207	IG 579	0.583 ± 0.4357 0.465251	0.515 ± 0.4512 0.4375	0.987 ± 0.5494 0.95103	0.872 ± 0.6635 0.32673	AGTAAAAGTGGTTAGTTGGAGTGTATAATCATATAAAATATT
plasmid_lp21	7222	IG 580	2.225 ± 0.2467 0.000727	1.345 ± 0.3148 0.11021	1.256 ± 0.2306 0.0322	1.289 ± 0.14 0.03368	GTTTGGAGTGTATAATCATATAAAATATTTTATAAAAGAATAAGTAA
plasmid_lp21	7232	IG 581	1.941 ± 0.6676 0.122733	1.113 ± 0.281 0.57397	1.163 ± 0.3189 0.40568	1.205 ± 0.4842 0.53378	CACTCCAAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7234	IG 582	2.188 ± 0.885 0.036165	1.415 ± 0.7448 0.19375	1.398 ± 0.4672 0.16643	1.044 ± 0.5184 0.86084	TACACTCCAAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7244	IG 583	5.072 ± 2.6381 0.00014	2.305 ± 1.2777 0.00344	1.481 ± 0.7863 0.26266	1.453 ± 0.7983 0.25105	TAATAAATATTTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	7246	IG 584	2.755 ± 1.2097 0.110048	1.759 ± 0.5268 0.09776	1.175 ± 0.2806 0.20741	1.351 ± 0.4347 0.20774	AATAAATATTTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTAT
plasmid_lp21	7268	IG 585	0.595 ± 0.4059 0.454592	0.501 ± 0.431 0.41466	1.029 ± 0.6188 0.81022	0.864 ± 0.5631 0.44606	AGTAAAAGTGGTTAGTTGGAGTGTATAATCATATAAAATATT
plasmid_lp21	7283	IG 586	2.178 ± 0.2972 0.015763	1.335 ± 0.1932 0.03867	1.2 ± 0.2453 0.06984	1.094 ± 0.1525 0.2212	GTTTGGAGTGTATAATCATATAAAATATTTTATAAAAGAATAAGTAA
plasmid_lp21	7293	IG 587	2.296 ± 0.6361 0.023154	1.305 ± 0.4868 0.25829	1.136 ± 0.3448 0.1907	1.28 ± 0.4415 0.30287	CACTCCAAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7295	IG 588	1.878 ± 0.8137 0.02973	1.393 ± 0.7172 0.12751	1.187 ± 0.4623 0.45991	1.059 ± 0.5201 0.66676	TACACTCCAAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7329	IG 589	3.440 ± 1.1361 0.068598	1.32 ± 0.799 0.57944	0.993 ± 0.5816 0.98991	1.492 ± 0.1069 0.52197	AGTAAAAGTGGTTAGTTGGAGTGTATAATCATATAAAATATT
plasmid_lp21	7358	IG 590	3.005 ± 1.1504 0.079883	1.813 ± 1.0426 0.31918	0.977 ± 0.1977 0.83332	1.304 ± 0.3017 0.01481	TGTAGTCCACTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7419	IG 591	3.415 ± 0.8636 0.039006	1.5 ± 0.619 0.34186	1.061 ± 0.4671 0.85126	1.394 ± 0.6649 0.3828	CACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7446	IG 592	1.953 ± 0.9234 0.057439	1.295 ± 0.6122 0.09649	0.959 ± 0.4375 0.69105	1.148 ± 0.4525 0.02116	TAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTATAATCATAAAA
plasmid_lp21	7452	IG 593	2.375 ± 0.8612 0.032707	1.732 ± 0.853 0.18715	1.368 ± 0.7564 0.52838	0.926 ± 0.3918 0.82656	TTCTTATGAAATATTTTATGATTATACACTCCAGTAAACAA
plasmid_lp21	7482	IG 594	3.927 ± 1.4103 0.010268	1.567 ± 0.9366 0.29866	1.405 ± 0.4588 0.08217	1.515 ± 0.8859 0.47775	CACTCCAGTAAACCAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	7515	IG 596	2.166 ± 1.351 0.033107	1.875 ± 0.10161 0.15329	1.278 ± 0.6737 0.67358	1.022 ± 0.4188 0.63172	ATAAGTAAAAGTGGTTAGTTGGAGTGTATAATCATATAAAATAA
plasmid_lp21	7515	IG 595	2.510 ± 1.0577 0.062838	1.928 ± 1.766 0.14961	0.802 ± 0.498 0.51511	0.818 ± 0.7673 0.94669	TTCTTATGAAATATTTTATGATTATACACTCCAGTAAACAC
plasmid_lp21	7557	IG 597	5.015 ± 2.0171 0.013015	2.065 ± 0.8322 0.00572	1.201 ± 0.7153 0.63759	1.66 ± 0.5908 0.13181	AATAAATATTTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	7559	IG 598	2.948 ± 1.7111 0.144879	1.86 ± 0.6514 0.11258	1.202 ± 0.5121 0.38239	1.278 ± 0.6683 0.33082	AATAAATATTTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGT

plasmid_lp21	7569	IG 599	1.818 ± 1.5323 0.442206	1.984 ± 0.7832 0.1155	1.886 ± 1.0428 0.27321	2.578 ± 1.7368 0.23122	AAATATTATTATGATTATGAGTCAGTAAACTAACCACTTTAC
plasmid_lp21	7581	IG 600	0.526 ± 0.338 0.347993	0.519 ± 0.393 0.38019	0.955 ± 0.4497 0.79172	1.045 ± 0.5917 0.46567	AGTAAAAGTGGTTAGTTGGAGTGATAAATCATAAAAATAATTTT
plasmid_lp21	7606	IG 601	2.313 ± 0.6538 0.011701	1.368 ± 0.5493 0.17452	1.053 ± 0.3119 0.25793	1.249 ± 0.4729 0.31673	CACTCCAAAACAAACCACTTTACTTACTTCTTATAAAATATTATTT
plasmid_lp21	7608	IG 602	1.951 ± 0.8377 0.026485	1.422 ± 0.7673 0.1491	1.277 ± 0.4825 0.26027	1.061 ± 0.5051 0.75818	TACACTCCAAAACAAACCACTTTACTTACTTCTTATAAAATATTATTT
plasmid_lp21	7609	IG 603	1.385 ± 0.6897 0.246183	0.662 ± 0.4452 0.4828	1.163 ± 0.542 0.58144	1.244 ± 0.4614 0.23376	TAATCATAAAAATAATATTATATAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	7633	IG 604	2.086 ± 0.7982 0.038151	1.174 ± 0.5085 0.37233	1.015 ± 0.3852 0.6861	1.075 ± 0.4533 0.14742	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAATCATAAAA
plasmid_lp21	7654	IG 605	2.584 ± 1.2384 9.79E-06	1.08 ± 0.5029 0.83352	1.089 ± 0.639 0.78099	1.126 ± 0.6492 0.2133	AACCACTTTACTTACTTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	7669	IG 606	2.935 ± 0.6482 0.017926	1.598 ± 0.8178 0.26401	1.229 ± 0.2622 0.05435	1.172 ± 0.3492 0.51155	CACTCAGTAAACTAACCACTTTACTTACTTCTTATAAAATATTATTT
plasmid_lp21	7671	IG 607	1.315 ± 0.6557 0.561368	0.891 ± 0.5241 0.56569	1.096 ± 0.7682 0.83076	0.727 ± 0.2171 0.32506	TACACTCCAGTAAACTAACCACTTTACTTACTTCTTATAAAATATTATTT
plasmid_lp21	7672	IG 608	1.355 ± 0.8049 0.406876	0.667 ± 0.4428 0.46244	1.136 ± 0.5707 0.72713	1.195 ± 0.5412 0.45552	TAATCATAAAAATAATATTATATAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	7702	IG 609	2.372 ± 1.3024 0.020779	1.996 ± 1.6379 0.20494	0.655 ± 0.379 0.28856	0.842 ± 0.6976 0.72155	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAAATCATAAAAATAAT
plasmid_lp21	7706	IG 610	2.534 ± 0.5364 0.020764	1.623 ± 0.682 0.18991	1.513 ± 0.584 0.31668	1.62 ± 0.5924 0.1073	CTTATCTTATAAAATATTATTTATGATTATACACTCCAGTAAACT
plasmid_lp21	7717	IG 611	2.592 ± 1.4898 0.001457	1.294 ± 0.7019 0.4712	1.217 ± 0.955 0.5952	1.166 ± 0.9697 0.31636	AACCACTTTACTTACTTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	7734	IG 612	1.972 ± 0.9583 0.175302	1.588 ± 0.7236 0.14532	1.636 ± 0.8082 0.21853	2.211 ± 1.1682 0.1373	TGTAGTCCAGTAAACTAACCACTTTACTTACTTCTTATAAAATATTAT
plasmid_lp21	7735	IG 613	1.372 ± 0.5954 0.257097	0.747 ± 0.4469 0.53527	1.142 ± 0.5786 0.68904	1.185 ± 0.4327 0.54651	TAATCATAAAAATAATATTATATAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	7797	IG 614	1.681 ± 0.8394 0.256577	1.188 ± 0.3926 0.01824	1.391 ± 0.8061 0.4582	1.528 ± 1.2175 0.42622	TGTAGTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	7819	IG 615	1.417 ± 0.9055 0.154463	1.094 ± 0.704 0.83805	1.3 ± 0.6954 0.06066	1.698 ± 1.7642 0.43477	AAATATTATTATATGATTATGATTAGTGTAGTCCAGTAAACTAACCACTTTAC
plasmid_lp21	7831	IG 616	2.711 ± 0.9063 0.089278	1.284 ± 0.8159 0.62296	1.353 ± 0.9949 0.6085	1.379 ± 0.9726 0.58094	AGTAAAAGTGGTTAGTTAGTGGACTACATAAATCATAAAAATAATATT
plasmid_lp21	7860	IG 617	2.634 ± 0.9575 0.086142	1.849 ± 0.9725 0.27053	0.924 ± 0.2086 0.25316	1.164 ± 0.3202 0.30969	TGTAGTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	7861	IG 618	1.249 ± 0.8314 0.511536	0.635 ± 0.4921 0.48587	1.124 ± 0.5971 0.71977	1.157 ± 0.5713 0.39282	TAATCATAAAAATAATTTATAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	7872	IG 619	2.831 ± 1.577 0.17067	1.7 ± 0.5896 0.20621	1.242 ± 0.6556 0.6243	1.487 ± 0.5136 0.29847	AATAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTAT
plasmid_lp21	7894	IG 620	0.536 ± 0.3478 0.344291	0.557 ± 0.4025 0.39678	0.928 ± 0.412 0.61389	1.015 ± 0.5539 0.18727	AGTAAAAGTGGTTAGTTGGAGTGATAAATCATAAAAATAATATT
plasmid_lp21	7919	IG 621	1.683 ± 0.3481 0.026226	1.043 ± 0.2166 0.71452	1.08 ± 0.26 0.54462	1.082 ± 0.3177 0.60268	CACTCAAAACAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	7921	IG 622	1.833 ± 0.6666 0.034266	1.345 ± 0.6395 0.17771	1.186 ± 0.3753 0.42988	1.022 ± 0.4894 0.88269	TAACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	7922	IG 623	1.204 ± 0.8755 0.618738	0.605 ± 0.5599 0.54452	1.144 ± 0.8297 0.76381	1.177 ± 0.726 0.65268	TAATCATAAAAATAATTTATAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	7955	IG 624	3.886 ± 1.3674 0.029999	1.929 ± 1.089 0.31061	1.361 ± 1.1507 0.6013	1.596 ± 0.9363 0.43962	AGTAAAAGTGGTTAGTTAGTGGACTACATAAATCATAAAAATAATATT
plasmid_lp21	7967	IG 625	2.861 ± 1.7768 0.00706	1.236 ± 0.741 0.3619	1.292 ± 0.8331 0.46437	1.078 ± 0.6682 0.72001	AACCACTTTACTTATTCTTATAAAATTTATTTATGATTATACAC
plasmid_lp21	7980	IG 626	2.652 ± 3.1281 0.101225	1.484 ± 2.4813 0.53421	0.887 ± 1.0329 0.65739	1.105 ± 1.5576 0.53607	GTCACCAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	7984	IG 627	2.995 ± 1.4754 0.080141	1.85 ± 1.1556 0.30157	0.78 ± 0.2711 0.39018	1.111 ± 0.4136 0.56157	TGTAGTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	7985	IG 628	1.158 ± 0.6508 0.599085	0.687 ± 0.4986 0.51945	1.109 ± 0.5523 0.78381	1.226 ± 0.5428 0.39333	TAATCATAAAAATAATTTATAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	7996	IG 629	2.493 ± 1.553 0.230615	1.581 ± 0.8166 0.32187	1.226 ± 0.2672 0.172	1.211 ± 0.1824 0.24135	AATAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTAT
plasmid_lp21	8018	IG 630	0.529 ± 0.3928 0.384512	0.57 ± 0.4921 0.47488	0.999 ± 0.5234 0.99095	0.877 ± 0.6806 0.42209	AGTAAAAGTGGTTAGTTGGAGTGATAAATCATATAAAAATAATATT
plasmid_lp21	8019	IG 631	3.648 ± 2.4355 0.018729	3.171 ± 3.2459 0.21713	1.685 ± 1.0431 0.26364	1.432 ± 1.013 0.19934	CTTATTCTTATAAAATTTATTTATGATTATGAGTCACAAACT
plasmid_lp21	8033	IG 632	2.295 ± 0.2142 0.004725	1.447 ± 0.2534 0.04854	1.237 ± 0.1728 0.04009	1.192 ± 0.1511 0.15156	GTTTGGAGTGATAATCATATAAAATATTTTAAAGAATAAGTAA
plasmid_lp21	8043	IG 633	1.624 ± 0.36 0.01314	1.007 ± 0.2 0.95087	1.057 ± 0.2298 0.49216	1.101 ± 0.286 0.45133	CACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	8045	IG 634	1.942 ± 0.7211 0.011348	1.367 ± 0.661 0.12828	1.195 ± 0.4336 0.33708	1.092 ± 0.5112 0.6449	TACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	8055	IG 635	4.897 ± 1.3432 0.005045	1.967 ± 0.7189 0.04278	1.306 ± 0.5136 0.25714	1.448 ± 0.4757 0.24841	TAATAAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	8057	IG 636	2.453 ± 0.868 0.080564	1.359 ± 0.4749 0.24578	1.033 ± 0.345 0.84033	1.158 ± 0.4182 0.42029	AATAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTAT
plasmid_lp21	8079	IG 637	0.535 ± 0.3642 0.355865	0.549 ± 0.4024 0.39043	0.978 ± 0.4105 0.88291	1.042 ± 0.5607 0.28098	AGTAAAAGTGGTTAGTTGGAGTGATAAATCATAAAAATAATATT
plasmid_lp21	8104	IG 638	2.104 ± 0.6585 0.036467	1.286 ± 0.4755 0.20645	1.064 ± 0.3468 0.649	1.192 ± 0.4222 0.32834	CACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	8106	IG 639	1.794 ± 0.7456 0.020756	1.362 ± 0.7444 0.16637	1.117 ± 0.429 0.55994	0.987 ± 0.4952 0.93785	TACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	8107	IG 640	1.032 ± 0.6597 0.905259	0.54 ± 0.4172 0.40116	0.908 ± 0.5623 0.74332	0.905 ± 0.457 0.7211	TAATCATAAAAATAATTTATAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	8118	IG 641	2.366 ± 1.3698 0.206455	1.292 ± 0.5972 0.2727	0.798 ± 0.3839 0.54433	1.338 ± 0.5796 0.1129	AATAAATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTAT
plasmid_lp21	8140	IG 642	0.508 ± 0.3504 0.355378	0.472 ± 0.3787 0.35633	0.983 ± 0.5164 0.91354	0.881 ± 0.6154 0.51557	AGTAAAAGTGGTTAGTTGGAGTGATAAATCATATAAAAATAATATT
plasmid_lp21	8152	IG 643	2.595 ± 1.5906 0.017282	1.109 ± 0.5835 0.74381	1.207 ± 0.7546 0.5599	1.187 ± 0.7566 0.41696	AACCACTTTACTTATTCTTATAAAATTTATTTATGATTATACAC
plasmid_lp21	8155	IG 644	2.064 ± 0.4518 0.023945	1.336 ± 0.3239 0.15487	1.139 ± 0.311 0.06496	1.14 ± 0.2922 0.53489	GTTTGGAGTGATAAATCATATAAAATTTTATAAGAATAAGTAA
plasmid_lp21	8165	IG 645	1.658 ± 0.2918 0.003917	1.014 ± 0.2093 0.73006	1.056 ± 0.2266 0.61015	1.033 ± 0.3061 0.74991	CACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	8167	IG 646	1.864 ± 0.6986 0.016176	1.301 ± 0.6302 0.16012	1.21 ± 0.4198 0.26173	0.964 ± 0.4482 0.82701	TACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	8187	IG 647	3.745 ± 2.2896 0.081792	2.427 ± 1.9533 0.21649	1.66 ± 0.9199 0.09577	1.859 ± 0.79 0.00042	TTTTAAGAATAAGTAAAAGTGGTTAGTTGGAGTGATAAATCA

plasmid_lp21	8201	IG 648	0.743 ± 0.8264 0.310659	0.725 ± 0.4617 0.37125	0.478 ± 0.656 0.51716	0.836 ± 0.9205 0.85226	AGTAAAAGTGGTTAGTTAGGGAGTGATAAAATCATAAAATAAATATT
plasmid_lp21	8228	IG 649	2.890 ± 1.8168 0.139866	1.936 ± 2.012 0.42161	1.188 ± 0.6307 0.56259	1.029 ± 0.8987 0.9507	CACTCCACTAAACTAACCCACTTACTTATTCTTATAAAATATTATT
plasmid_lp21	8231	IG 650	1.375 ± 0.7673 0.192213	0.631 ± 0.4775 0.48557	1.236 ± 0.6362 0.38242	1.334 ± 0.6287 0.13006	TAAATCATAAAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	8237	IG 651	1.220 ± 1.0208 0.714273	0.347 ± 0.3593 0.35519	1.053 ± 0.8728 0.83221	0.816 ± 0.7491 0.37992	TGATTTATACACTCCACTAAACTAACCCACTTACTTATTCTTATAAA
plasmid_lp21	8239	IG 652	2.744 ± 1.7682 0.117901	1.437 ± 1.2626 0.55222	1.281 ± 0.6767 0.21125	1.04 ± 0.6021 0.85616	TATGATTTATACACTCCACTAAACTAACCCACTTACTTATTCTTATAAA
plasmid_lp21	8255	IG 653	2.221 ± 1.583 0.041022	1.153 ± 0.9684 0.05912	0.832 ± 0.5621 0.65716	1.344 ± 0.917 0.50278	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATATAA
plasmid_lp21	8264	IG 654	2.336 ± 2.6808 0.043752	1.902 ± 2.493 0.16397	1.114 ± 1.2991 0.79845	1.37 ± 1.7268 0.0206	AGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATATAAATAAATATT
plasmid_lp21	8276	IG 655	2.638 ± 1.6952 0.016793	1.344 ± 0.7607 0.22414	1.451 ± 1.0115 0.47499	1.172 ± 0.7179 0.37358	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTTACAC
plasmid_lp21	8291	IG 656	2.733 ± 0.4141 0.004646	1.591 ± 0.7796 0.2499	1.152 ± 0.2503 0.24282	0.933 ± 0.2391 0.56027	CACTCCAGTAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8293	IG 657	1.339 ± 0.8843 0.600515	1.188 ± 0.518 0.48926	1.014 ± 0.9539 0.96259	0.644 ± 0.5173 0.43992	TACACTCCAGTAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8303	IG 658	4.949 ± 2.2273 0.010688	2.16 ± 0.8674 0.01627	1.384 ± 0.9375 0.47122	1.785 ± 0.7942 0.06733	TAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	8305	IG 659	2.731 ± 1.7645 0.174056	1.627 ± 0.5674 0.03362	1.112 ± 0.7322 0.73112	1.293 ± 0.6753 0.35953	AATAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	8327	IG 660	0.536 ± 0.3584 0.364865	0.556 ± 0.3998 0.40466	0.962 ± 0.4854 0.76087	1.029 ± 0.5912 0.70977	AGTAAAAGTGGTTAGTTGGAGTGATAAAATCATAAAAATAAATATT
plasmid_lp21	8352	IG 661	2.098 ± 0.632 0.036743	1.236 ± 0.5005 0.35799	1.02 ± 0.3147 0.73909	1.179 ± 0.4145 0.44333	CACTCCAAAACTAACCCACTTACTTATTCTTATAAAATATTATT
plasmid_lp21	8354	IG 662	1.895 ± 0.7533 0.01984	1.414 ± 0.7209 0.09581	1.226 ± 0.4681 0.39936	1.041 ± 0.5079 0.72604	TACACTCCAAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8355	IG 663	1.082 ± 0.6358 0.691686	0.551 ± 0.4163 0.36807	0.944 ± 0.4823 0.76026	0.907 ± 0.3735 0.54907	TAAATCATAAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	8379	IG 664	2.261 ± 0.7962 0.02885	1.164 ± 0.5051 0.33442	1.028 ± 0.343 0.5996	1.139 ± 0.3673 0.03664	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATAAA
plasmid_lp21	8400	IG 665	2.652 ± 1.818 0.002927	1.292 ± 0.8211 0.46327	1.367 ± 0.9534 0.48817	0.973 ± 0.7427 0.92512	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTTACAC
plasmid_lp21	8415	IG 666	3.044 ± 0.8048 0.013271	1.551 ± 0.9455 0.3183	1.332 ± 0.2869 0.06657	1.264 ± 0.5335 0.4017	CACTCCAGTAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8417	IG 667	1.011 ± 0.4106 0.965696	0.678 ± 0.4108 0.20434	0.939 ± 0.7679 0.78673	0.575 ± 0.2450 0.16493	TACACTCCAGTAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8451	IG 668	3.751 ± 1.381 0.045448	1.37 ± 0.7861 0.48866	1.409 ± 1.1190 0.503	1.76 ± 1.3654 0.45036	AGTAAAAGTGGTTAGTTAGTGGACTACATAAAATCATAAAAATAAATATT
plasmid_lp21	8480	IG 669	2.749 ± 0.7036 0.001592	1.608 ± 0.5999 0.04985	1.215 ± 0.4299 0.41325	1.233 ± 0.4017 0.10755	TGTAGTCCACTAAACTAACCCACTTACTTATTATTGAAATAATT
plasmid_lp21	8481	IG 670	1.180 ± 0.7726 0.597992	0.583 ± 0.451 0.43027	1.042 ± 0.6596 0.91406	1.059 ± 0.4558 0.30455	TAATCATAAAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	8492	IG 671	2.343 ± 1.4501 0.141782	1.595 ± 0.9107 0.16992	1.167 ± 0.4403 0.23859	1.144 ± 0.5637 0.42391	AATAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	8514	IG 672	0.507 ± 0.3666 0.350443	0.527 ± 0.3943 0.38657	0.944 ± 0.4617 0.72991	0.99 ± 0.5987 0.89537	AGTAAAAGTGGTTAGTTGGAGTGATAAAATCATAAAAATAAATATT
plasmid_lp21	8515	IG 673	5.007 ± 3.1439 0.021128	3.373 ± 3.344 0.21009	2.343 ± 1.4139 0.14966	1.912 ± 1.1942 0.0041	CTTATTCTTATAAAATATTCTTATTGATTGAGTCCACTAAACT
plasmid_lp21	8539	IG 674	1.639 ± 0.3031 0.022841	0.985 ± 0.1848 0.85667	1.019 ± 0.2081 0.83967	1.074 ± 0.2947 0.64555	CACTCCAAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8541	IG 675	1.841 ± 0.7914 0.019081	1.328 ± 0.7342 0.15152	1.188 ± 0.4608 0.33707	1.023 ± 0.497 0.90925	TACACTCCAAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8542	IG 676	1.279 ± 0.7569 0.500791	0.649 ± 0.4868 0.46247	1.241 ± 0.8314 0.63333	1.068 ± 0.4654 0.7856	TAAATCATAAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	8566	IG 677	2.303 ± 0.9392 0.041393	1.23 ± 0.6684 0.34444	1.004 ± 0.3663 0.97095	1.093 ± 0.5133 0.42229	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATAAA
plasmid_lp21	8587	IG 678	2.586 ± 1.4846 0.024188	1.159 ± 0.6904 0.50982	1.123 ± 0.6916 0.67971	0.952 ± 0.8054 0.73655	AACCACTTTACTTATTCTTATAAAATATTCTTATTGATTTACAC
plasmid_lp21	8602	IG 679	2.769 ± 0.6936 0.009512	1.679 ± 0.9316 0.24331	1.113 ± 0.3509 0.27701	1.089 ± 0.4159 0.75643	CACTCCAGTAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8604	IG 680	1.311 ± 0.3974 0.175086	1.442 ± 0.5314 0.33172	1.186 ± 0.7951 0.5596	0.693 ± 0.4277 0.40529	TACACTCCAGTAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8605	IG 681	1.304 ± 0.9966 0.475063	0.74 ± 0.621 0.67605	1.054 ± 0.7107 0.82235	1.175 ± 0.5608 0.45939	TAAATCATAAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	8638	IG 682	3.559 ± 1.1192 0.040447	1.728 ± 0.926 0.35748	1.567 ± 1.1549 0.49457	1.758 ± 1.1125 0.40292	AGTAAAAGTGGTTAGTTAGTGGACTACATAATCATAAAAATAAATATT
plasmid_lp21	8639	IG 683	2.188 ± 0.8211 0.004557	1.516 ± 0.645 0.24447	1.335 ± 0.6564 0.15054	1.422 ± 0.5717 0.33465	CTTATTCTTATAAAATATTCTTATTGATTTACACTCCAGTAAACT
plasmid_lp21	8650	IG 684	2.552 ± 1.8817 0.000708	1.003 ± 0.7767 0.98766	0.988 ± 0.7345 0.98166	0.95 ± 0.7891 0.81213	AACCACTTTACTTATTCTTATAAAATATTCTTATTGATTTACAC
plasmid_lp21	8663	IG 685	2.641 ± 3.2936 0.063262	1.622 ± 2.6331 0.38487	1.014 ± 1.3373 0.9512	1.04 ± 1.721 0.83721	GTCCACTAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8667	IG 686	2.614 ± 0.5973 0.040209	1.487 ± 1.1177 0.5592	0.842 ± 0.1408 0.2313	1.139 ± 0.2157 0.09021	TGTAGTCCACTAAACTAACCCACTTACTTATTCTTATAAAATATT
plasmid_lp21	8668	IG 687	1.373 ± 0.7755 0.374475	0.76 ± 0.5277 0.58617	1.152 ± 0.6245 0.67501	1.28 ± 0.6059 0.25647	TAATCATAAAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	8698	IG 688	2.141 ± 1.2243 0.004954	2.231 ± 1.9707 0.20262	0.786 ± 0.4713 0.66636	0.769 ± 0.6861 0.42379	ATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATA
plasmid_lp21	8730	IG 689	1.625 ± 0.6309 0.240932	1.38 ± 0.7411 0.31562	1.458 ± 0.7651 0.30556	1.731 ± 1.1757 0.30714	TGTAGTCCAGTAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8740	IG 690	2.701 ± 0.8299 0.007076	2.095 ± 0.5971 0.01352	1.101 ± 0.2994 0.56078	1.074 ± 0.3766 0.75667	TAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGT
plasmid_lp21	8755	IG 691	2.189 ± 0.7586 0.055911	1.188 ± 0.5293 0.48033	1.015 ± 0.3386 0.89864	1.117 ± 0.3655 0.40357	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATAAA
plasmid_lp21	8791	IG 692	2.899 ± 0.4567 0.003918	1.572 ± 0.8944 0.32319	1.226 ± 0.2939 0.1817	1.122 ± 0.4338 0.6937	CACTCCAGTAAACTAACCCACTTACTTATTCTTATAAAATATTTT
plasmid_lp21	8794	IG 693	1.498 ± 1.0952 0.313737	0.684 ± 0.6151 0.61122	1.219 ± 0.7765 0.58086	1.103 ± 0.5027 0.56296	TAAATCATAAAATAAATATTCTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	8818	IG 694	1.970 ± 0.6162 0.071736	1.226 ± 0.5869 0.47778	0.907 ± 0.2059 0.14406	1.064 ± 0.2711 0.47359	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATAAA
plasmid_lp21	8828	IG 695	2.816 ± 0.2108 0.002073	1.548 ± 0.5036 0.16351	1.536 ± 0.4886 0.22977	1.012 ± 0.1211 0.81895	CTTATTCTTATAAAATATTCTTATTGATTTACACTCCAGTAAACT
plasmid_lp21	8839	IG 696	2.381 ± 1.5215 0.075412	1.141 ± 0.6063 0.58565	1.187 ± 0.8817 0.74247	1.097 ± 0.6686 0.07668	AACCACTTTACTTATTCTTATAAAATATTCTTATTGATTTACAC

plasmid_lp21	8854	IG 697	2.663 ± 0.7744 0.013906	1.523 ± 0.6598 0.13745	1.054 ± 0.34 0.21869	0.931 ± 0.3908 0.77847	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT	TATTCTTATAAAATATT
plasmid_lp21	8857	IG 698	1.156 ± 0.73 0.730152	0.607 ± 0.4435 0.34817	1.148 ± 0.68 0.7097	1.112 ± 0.6169 0.78224	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGTGGTTAGTT	
plasmid_lp21	8881	IG 699	1.782 ± 0.5131 0.072201	1.133 ± 0.5176 0.57995	0.897 ± 0.2298 0.30138	0.948 ± 0.2582 0.45452	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAA	
plasmid_lp21	8902	IG 700	2.592 ± 1.8093 0.016821	0.953 ± 0.5854 0.89801	1.416 ± 1.0924 0.52978	0.95 ± 0.6265 0.83389	AACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC	
plasmid_lp21	8917	IG 701	2.827 ± 0.791 0.012389	1.582 ± 0.7897 0.191	1.276 ± 0.35 0.10647	0.991 ± 0.3676 0.96133	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	8920	IG 702	1.348 ± 1.0338 0.320899	0.711 ± 0.5275 0.61311	0.989 ± 0.6211 0.96625	1.153 ± 0.5794 0.64804	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGTGGTTAGTT	
plasmid_lp21	8931	IG 703	2.622 ± 1.4105 0.082616	1.549 ± 0.7487 0.24288	1.307 ± 0.6224 0.35357	1.31 ± 0.618 0.49014	AATAATATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGAT	
plasmid_lp21	8953	IG 704	0.539 ± 0.343 0.358672	0.489 ± 0.3446 0.33162	0.999 ± 0.4839 0.9969	1.015 ± 0.6112 0.66317	AGTAAAAGTGGTTAGTTGGAGTGATAATCATAAAAATAAATATT	
plasmid_lp21	8965	IG 705	3.376 ± 1.7917 0.011186	1.392 ± 0.6623 0.34507	1.781 ± 1.1678 0.17077	1.176 ± 0.7687 0.0761	AACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC	
plasmid_lp21	8978	IG 706	1.711 ± 0.2965 0.026892	1.007 ± 0.1707 0.93117	1.043 ± 0.2108 0.68015	1.053 ± 0.2859 0.74259	CACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	8980	IG 707	1.793 ± 0.7065 0.006684	1.316 ± 0.6765 0.10228	1.19 ± 0.4563 0.39813	1.011 ± 0.4605 0.94414	TACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	8981	IG 708	1.209 ± 0.733 0.317256	0.633 ± 0.5201 0.52938	1.071 ± 0.6039 0.79909	1.06 ± 0.5178 0.79145	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGTGGTTAGTT	
plasmid_lp21	9026	IG 709	2.354 ± 1.6306 0.033107	1.121 ± 0.6843 0.67447	1.164 ± 0.8334 0.66182	0.988 ± 0.6828 0.94477	AACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC	
plasmid_lp21	9043	IG 710	1.564 ± 0.8943 0.16743	1.1 ± 0.5865 0.60699	1.24 ± 0.7207 0.54844	1.566 ± 1.3054 0.31794	TGTAGTCAGTAAACTAAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9044	IG 711	1.154 ± 0.7131 0.665282	0.618 ± 0.4824 0.44607	1.012 ± 0.5889 0.97107	1.025 ± 0.5083 0.93951	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGTGGTTAGTT	
plasmid_lp21	9055	IG 712	2.959 ± 1.6719 0.109968	1.681 ± 0.7135 0.12031	0.863 ± 0.454 0.22728	1.62 ± 0.8178 0.28474	AATAATATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGAT	
plasmid_lp21	9077	IG 713	0.491 ± 0.3106 0.281138	0.49 ± 0.3324 0.29575	0.916 ± 0.4013 0.46365	0.967 ± 0.5218 0.49065	AGTAAAAGTGGTTAGTTGGAGTGATAATCATAAAAATAAATATT	
plasmid_lp21	9102	IG 714	1.618 ± 0.2851 0.027575	0.972 ± 0.1952 0.79322	1.007 ± 0.2154 0.92036	1.055 ± 0.3156 0.78622	CACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9104	IG 715	1.865 ± 0.7321 0.028787	1.372 ± 0.7128 0.15692	1.212 ± 0.4222 0.34278	1.053 ± 0.4525 0.71038	TACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9105	IG 716	1.202 ± 0.7122 0.460165	0.567 ± 0.4723 0.44112	0.967 ± 0.5268 0.91076	1.031 ± 0.4851 0.89405	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGTGGTTAGTT	
plasmid_lp21	9129	IG 717	1.910 ± 0.616 0.068803	1.16 ± 0.4682 0.48727	0.816 ± 0.1789 0.04984	0.955 ± 0.2782 0.69182	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAA	
plasmid_lp21	9150	IG 718	2.669 ± 2.1407 0.008101	0.841 ± 0.6569 0.6413	1.054 ± 0.8569 0.90993	0.994 ± 0.9131 0.96599	AACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC	
plasmid_lp21	9165	IG 719	3.137 ± 0.8786 0.022427	1.571 ± 0.4036 0.38276	1.12 ± 0.3374 0.34478	1.152 ± 0.5296 0.60479	CACTCCAGTAAACTAAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9167	IG 720	1.063 ± 0.4596 0.867079	1.215 ± 0.5349 0.48876	0.881 ± 0.662 0.7388	0.759 ± 0.2462 0.37392	TACACTCCAGTAAACTAAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9168	IG 721	1.198 ± 0.773 0.510838	0.663 ± 0.4892 0.5247	0.984 ± 0.6 0.95136	0.932 ± 0.4128 0.78045	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGTGGTTAGTT	
plasmid_lp21	9192	IG 722	2.064 ± 0.8842 0.020931	1.266 ± 0.6843 0.20998	1.081 ± 0.4262 0.23068	1.056 ± 0.3705 0.6692	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAA	
plasmid_lp21	9213	IG 723	2.668 ± 2.4963 0.007548	1.137 ± 0.5033 0.7265	1.446 ± 1.3127 0.43435	1.45 ± 1.3802 0.10475	AACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC	
plasmid_lp21	9228	IG 724	2.624 ± 0.527 0.010667	1.459 ± 0.7427 0.30173	1.071 ± 0.219 0.25869	0.849 ± 0.2989 0.42007	CACTCCAGTAAACTAAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9231	IG 725	1.270 ± 0.5213 0.280643	0.724 ± 0.4596 0.50803	1.333 ± 0.5381 0.30692	1.05 ± 0.3268 0.69692	TAAATCATAAAAATAATTTTATAAAGAATAAGTAAAAGTGGTTAGTT	
plasmid_lp21	9261	IG 726	1.915 ± 1.1816 0.003041	2.09 ± 1.7136 0.14709	0.634 ± 0.4342 0.46402	0.713 ± 0.7488 0.48851	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAAAATCA	
plasmid_lp21	9265	IG 727	2.860 ± 0.5473 0.008177	1.714 ± 0.5578 0.08833	1.366 ± 0.4725 0.34979	1.658 ± 0.8966 0.247	CTTATTCTTATAAAATATTATTGATTATACACTCCAGTAAACT	
plasmid_lp21	9276	IG 728	1.969 ± 1.2758 0.007024	0.826 ± 0.4832 0.5956	0.867 ± 0.5791 0.74148	0.876 ± 0.6076 0.453	AACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC	
plasmid_lp21	9293	IG 729	1.568 ± 0.8303 0.390026	1.302 ± 0.8302 0.3719	1.204 ± 0.7116 0.19421	1.478 ± 1.0238 0.29343	TGTAGTCAGTAAACTAAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9305	IG 730	1.760 ± 2.635 0.667781	2.109 ± 2.1578 0.46656	0.636 ± 0.4196 0.33959	1.407 ± 0.8067 0.5173	AATAGATATTTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGAT	
plasmid_lp21	9327	IG 731	0.580 ± 0.4333 0.463442	0.485 ± 0.3851 0.37251	0.952 ± 0.5413 0.80761	0.867 ± 0.6285 0.45251	AGTAAAAGTGGTTAGTTGGAGTGATAATCATATAAAATATT	
plasmid_lp21	9342	IG 732	2.193 ± 0.2957 0.012389	1.364 ± 0.1946 0.0719	1.244 ± 0.2073 0.02088	1.207 ± 0.1357 0.12856	GTTTGGAGTGATAATCATATAAAATATTTTATAAGAATAAGTAA	
plasmid_lp21	9352	IG 733	1.647 ± 0.3326 0.042529	0.947 ± 0.2302 0.70261	0.982 ± 0.3387 0.91119	1.039 ± 0.3349 0.85566	CACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9354	IG 734	2.106 ± 1.2329 0.041201	1.281 ± 0.8491 0.06933	1.257 ± 0.7018 0.41617	1.019 ± 0.6304 0.94037	TACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9364	IG 735	5.974 ± 2.5744 0.001145	2.466 ± 1.0541 0.00482	1.311 ± 0.6048 0.22077	1.775 ± 0.807 0.16862	TAAATTAATTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTG	
plasmid_lp21	9366	IG 736	3.165 ± 1.8751 0.173275	1.762 ± 0.4942 0.08509	1.208 ± 0.365 0.31378	1.447 ± 0.6573 0.30415	AATAATTAATTTATAAAGAATAAGTAAAAGTGGTTAGTTGGAGTG	
plasmid_lp21	9388	IG 737	0.568 ± 0.4344 0.470351	0.465 ± 0.4255 0.41325	0.99 ± 0.6828 0.93464	0.93 ± 0.7988 0.71996	AGTAAAAGTGGTTAGTTGGAGTGATAATCATATAAAATATT	
plasmid_lp21	9403	IG 738	2.097 ± 0.31 0.018417	1.31 ± 0.2276 0.10389	1.137 ± 0.2239 0.27105	1.153 ± 0.1395 0.10714	GTTTGGAGTGATAATCATATAAAATATTTTATAAGAATAAGTAA	
plasmid_lp21	9413	IG 739	2.218 ± 0.7259 0.024443	1.264 ± 0.54 0.32534	1.066 ± 0.307 0.24873	1.193 ± 0.4975 0.4834	CACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9415	IG 740	1.829 ± 0.7254 0.010905	1.303 ± 0.721 0.20575	1.125 ± 0.4319 0.60192	1.032 ± 0.5109 0.85036	TACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9425	IG 741	2.888 ± 0.4696 0.0092	2.216 ± 0.674 0.06626	1.069 ± 0.2235 0.70411	0.865 ± 0.2903 0.595	TAAATTAATTTATAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGT	
plasmid_lp21	9440	IG 742	2.172 ± 0.9155 0.062723	1.316 ± 0.6415 0.2354	1.016 ± 0.3089 0.82201	1.155 ± 0.4026 0.03341	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAA	
plasmid_lp21	9476	IG 743	2.775 ± 0.7875 0.003976	1.564 ± 0.9419 0.27988	1.173 ± 0.3494 0.21667	0.946 ± 0.4386 0.84733	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT	
plasmid_lp21	9479	IG 744	1.343 ± 0.8179 0.297865	0.622 ± 0.5175 0.51162	1.008 ± 0.6284 0.98586	1.018 ± 0.46 0.93567	TAAATCATAAAAATAATTTATAAAGAATAAGTAAAAGTGGTTAGTT	
plasmid_lp21	9498	IG 745	3.296 ± 0.2029 0.108286	1.326 ± 0.9211 0.2556	1.532 ± 0.8141 0.16603	1.453 ± 0.7653 0.11307	TTTTATAAAGAATAAGTAAAAGTGGTTAGTTAGTGGAGTGATAAT	CA

plasmid_lp21	9512	IG 746	0.748 ± 0.8136 0.364703	0.902 ± 0.4712 0.81608	0.547 ± 0.8063 0.58889	0.887 ± 0.9417 0.88803	AGTAAAAGTGGTTAGTTAGTGGAGTGATAATCATAAAATAAATATT
plasmid_lp21	9513	IG 747	2.297 ± 0.7307 0.044326	1.435 ± 0.7906 0.18348	1.185 ± 0.8273 0.78409	1.116 ± 0.6013 0.50989	CTTATTCTTATAAAATATTATTTATGATTATACACTCCAGTAAACT
plasmid_lp21	9524	IG 748	2.942 ± 1.9239 0.056387	1.384 ± 0.797 0.23281	1.162 ± 0.805 0.3891	1.206 ± 0.9691 0.41339	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	9539	IG 749	2.810 ± 2.3022 0.103349	1.977 ± 2.3143 0.32274	1.067 ± 0.8217 0.73353	1.069 ± 1.0275 0.75517	CACTCCACTAAACTAAACCCTTTACTTATTCTTATAAAATATTATT
plasmid_lp21	9548	IG 750	1.302 ± 0.8563 0.580198	0.367 ± 0.3156 0.29121	0.955 ± 0.6744 0.85342	0.743 ± 0.5112 0.22053	TGATTTATACACTCCACTAAACTAAACCCTTTACTTATTCTTATAAA
plasmid_lp21	9550	IG 751	3.104 ± 1.9297 0.073683	1.58 ± 1.3424 0.47343	1.437 ± 0.7878 0.05179	1.215 ± 0.6554 0.38617	TATGATTTATACACTCCACTAAACTAAACCCTTTACTTATTCTTATAA
plasmid_lp21	9566	IG 752	1.753 ± 1.1076 0.135665	1.156 ± 0.7157 0.66957	0.867 ± 0.4438 0.72758	0.974 ± 0.5563 0.94486	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATATAA
plasmid_lp21	9572	IG 753	1.994 ± 1.9584 0.151133	0.643 ± 0.5194 0.36612	0.642 ± 0.6187 0.20556	0.489 ± 0.6932 0.16163	TTCTTTATGAAATATTATTTATGATTATACACTCCACTAAACTAAC
plasmid_lp21	9575	IG 754	2.517 ± 2.8072 0.045056	1.903 ± 2.3316 0.11813	1.51 ± 1.7309 0.12928	1.435 ± 1.8254 0.07467	AGTAAAAGTGGTTAGTTACTGGAGTGATAATCATATAAAATAATATT
plasmid_lp21	9602	IG 755	4.012 ± 1.429 0.003759	1.996 ± 1.21 0.25736	1.59 ± 0.7962 0.29551	1.415 ± 0.8395 0.5542	CACTCCAGTAAACTAAACCCTTTACTTATTCTTATGAATATTATT
plasmid_lp21	9614	IG 756	4.583 ± 1.317 0.00587	2.302 ± 0.6499 0.00535	1.401 ± 0.5406 0.17523	1.345 ± 0.3915 0.2295	TAAATAAAATTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	9616	IG 757	2.536 ± 1.4478 0.17922	1.489 ± 0.7243 0.25063	1.125 ± 0.4623 0.66773	1.05 ± 0.4692 0.78709	AATAAAATTTATAAAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTAT
plasmid_lp21	9638	IG 758	0.501 ± 0.348 0.327088	0.523 ± 0.3835 0.3642	0.916 ± 0.4335 0.51431	0.954 ± 0.5489 0.59773	AGTAAAAGTGGTTAGTTGGAGTGATAAAATCATAAAAATAAATATT
plasmid_lp21	9663	IG 759	2.085 ± 0.595 0.028936	1.311 ± 0.5363 0.29358	1.1 ± 0.3167 0.20388	1.244 ± 0.4125 0.32792	CACTCCAAAATAACCACTTTACTTATTCTTATAAAATATTATT
plasmid_lp21	9665	IG 760	2.014 ± 0.8337 0.018665	1.416 ± 0.7705 0.14079	1.255 ± 0.4905 0.35499	1.101 ± 0.4903 0.60323	TACACTCCAAAATAACCACTTTACTTATTCTTATAAAATATTATT
plasmid_lp21	9666	IG 761	1.217 ± 0.755 0.578814	0.608 ± 0.4301 0.39062	1.145 ± 0.492 0.51704	1.05 ± 0.4688 0.83612	TAAATCATAAAATAATATTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	9690	IG 762	2.227 ± 0.9832 0.040902	1.238 ± 0.6781 0.26589	1.062 ± 0.4137 0.63497	1.151 ± 0.5127 0.36552	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAAA
plasmid_lp21	9711	IG 763	3.357 ± 2.2009 0.013368	1.345 ± 0.7953 0.30301	1.526 ± 1.0373 0.22672	1.477 ± 0.1017 0.03021	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTACAC
plasmid_lp21	9726	IG 764	2.650 ± 0.8616 0.008842	1.46 ± 0.9102 0.29562	1.081 ± 0.3838 0.25621	0.986 ± 0.4507 0.9616	CACTCCAGTAAACTAAACCCTTTACTTATTCTTATAAAATATT
plasmid_lp21	9728	IG 765	1.336 ± 0.5271 0.417581	1.139 ± 0.1897 0.3844	0.903 ± 0.6048 0.83846	0.771 ± 0.3456 0.49231	TACACTCCAGTAAACTAAACCCTTTACTTATTCTTATAAAATATT
plasmid_lp21	9729	IG 766	1.414 ± 0.7351 0.29903	0.625 ± 0.5405 0.51285	1.066 ± 0.662 0.87742	1.277 ± 0.6152 0.41376	TAAATCATAAAATAATATTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	9753	IG 767	2.185 ± 0.955 0.090021	1.289 ± 0.6286 0.38268	0.949 ± 0.3144 0.6616	1.097 ± 0.4126 0.37695	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATAAA
plasmid_lp21	9763	IG 768	4.458 ± 1.1876 0.024697	2.499 ± 0.4677 0.02377	1.748 ± 0.9406 0.29738	2.146 ± 0.62 0.0907	CTTATTCTTATAAAATATTATTTATGATTACACTCCAGTAAACT
plasmid_lp21	9774	IG 769	2.084 ± 1.1998 0.054811	0.865 ± 0.3626 0.52649	0.959 ± 0.6953 0.92504	1.132 ± 0.7863 0.43632	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTACAC
plasmid_lp21	9789	IG 770	2.885 ± 0.786 0.01389	1.601 ± 0.9759 0.30959	1.171 ± 0.3215 0.0039	1.045 ± 0.5355 0.91026	CACCCAGTAAACTAAACCCTTTACTTATTCTTATAAAATATT
plasmid_lp21	9791	IG 771	1.869 ± 0.4108 0.056965	1.001 ± 0.4677 0.99927	1.271 ± 0.8071 0.57666	0.706 ± 0.1746 0.10057	TACACTCCAGTAAACTAAACCCTTTACTTATTCTTATAAAATATT
plasmid_lp21	9792	IG 772	1.231 ± 0.9468 0.480368	0.551 ± 0.4687 0.45744	1.092 ± 0.7362 0.77629	1.084 ± 0.5588 0.6885	TAAATCATAAAATAATATTTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	9816	IG 773	1.997 ± 0.8288 0.018571	1.314 ± 0.686 0.18841	1.044 ± 0.4303 0.67331	1.035 ± 0.4975 0.27332	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATAAA
plasmid_lp21	9837	IG 774	2.807 ± 1.7063 0.060735	1.016 ± 0.4416 0.94053	1.273 ± 0.6489 0.54311	1.189 ± 0.7482 0.22824	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTACAC
plasmid_lp21	9852	IG 775	2.792 ± 0.9774 0.018999	1.456 ± 0.8237 0.18685	1.057 ± 0.3991 0.81976	1.003 ± 0.4456 0.99225	CACTCCAGTAAACTAAACCCTTTACTTATTCTTATAAAATATT
plasmid_lp21	9854	IG 776	1.508 ± 0.6425 0.207917	1.097 ± 0.4689 0.79521	0.703 ± 0.5333 0.11038	0.603 ± 0.2588 0.14951	TACACTCCAGTAAACTAAACCCTTTACTTATTCTTATAAAATATT
plasmid_lp21	9888	IG 777	0.799 ± 0.5886 0.730962	0.886 ± 0.7039 0.86154	1.331 ± 0.745 0.16042	1.278 ± 0.8091 0.06818	AGTAAAAGTGGTAGTTGGAGTGATAATCATAAAAATAAATATT
plasmid_lp21	9889	IG 778	2.452 ± 0.4568 0.010894	1.517 ± 0.6712 0.173	1.448 ± 0.6979 0.44893	1.216 ± 0.2813 0.25707	CTTATTCTTATAAAATATTATTTATGATTACACTCCAGTAAACT
plasmid_lp21	9913	IG 779	1.964 ± 1.0604 0.094791	0.983 ± 0.4951 0.90964	1.008 ± 0.5045 0.97126	1.084 ± 0.6791 0.79431	CACTCCAAAACACCCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	9915	IG 780	2.619 ± 0.9089 0.032034	1.612 ± 0.7308 0.1368	1.539 ± 0.5434 0.11515	1.186 ± 0.6557 0.57516	TACACTCCAAAACACCCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	9916	IG 781	1.192 ± 0.7016 0.419388	0.601 ± 0.45 0.43044	1.142 ± 0.6169 0.5694	1.063 ± 0.4936 0.62413	TAAATCATAAAATAATATTTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	9940	IG 782	1.946 ± 0.6558 0.047163	1.165 ± 0.5178 0.3842	1.021 ± 0.2928 0.64633	1.049 ± 0.3924 0.56886	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAAATCATAAA
plasmid_lp21	9946	IG 783	2.578 ± 1.8717 0.084422	1.674 ± 1.1484 0.24218	0.903 ± 0.7277 0.82145	1.212 ± 1.163 0.7545	TTCTTATAAAATATTATTTATGATTACACTCCAAAACACCCA
plasmid_lp21	9961	IG 784	2.485 ± 1.3537 0.017281	0.979 ± 0.5679 0.96316	1.103 ± 0.6449 0.81497	0.96 ± 0.7014 0.70935	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTACAC
plasmid_lp21	9976	IG 785	3.006 ± 0.9184 0.017262	1.781 ± 0.9222 0.1805	1.243 ± 0.399 0.19406	1.087 ± 0.498 0.73955	CACTCCAGTAAACTAAACCCTTTACTTATTCTTATAAAATATT
plasmid_lp21	9978	IG 786	1.890 ± 0.7622 0.112357	1.139 ± 0.4583 0.6422	1.36 ± 1.067 0.54923	0.771 ± 0.3417 0.42798	TACACTCCAGTAAACTAAACCCTTTACTTATTCTTATAAAATATT
plasmid_lp21	9979	IG 787	1.165 ± 0.6962 0.534767	0.687 ± 0.4819 0.51472	0.967 ± 0.4871 0.88943	0.942 ± 0.3725 0.74078	TAAATCATAAAATAATATTTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	9990	IG 788	2.375 ± 1.4371 0.199066	1.416 ± 0.7418 0.46765	1.019 ± 0.3969 0.91769	1.123 ± 0.4877 0.75206	AATAATATTTTATAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTAT
plasmid_lp21	10012	IG 789	0.564 ± 0.4215 0.457679	0.518 ± 0.4441 0.45065	0.889 ± 0.5711 0.64684	0.913 ± 0.6917 0.61677	AGTAAAAGTGGTTAGTTGGAGTGATAATCATATAAAATATT
plasmid_lp21	10013	IG 790	2.441 ± 0.3013 0.013234	1.4 ± 0.2651 0.07034	1.249 ± 0.5259 0.50549	1.296 ± 0.5914 0.50908	CTTATTCTTATAAAATATTATTTATGATTACACTCCAGTAAACT
plasmid_lp21	10024	IG 791	2.446 ± 1.2953 0.114114	1.174 ± 0.373 0.44414	1.16 ± 0.5738 0.46689	0.807 ± 0.3454 0.07515	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTACAC
plasmid_lp21	10027	IG 792	1.972 ± 0.2545 0.015299	1.282 ± 0.1547 0.02646	1.161 ± 0.257 0.19192	1.087 ± 0.1431 0.44707	GTTTTGGAGTGATAATCATATAAAATATTATTTATAAGAATAAGTAA
plasmid_lp21	10037	IG 793	1.701 ± 0.3415 0.015263	0.97 ± 0.1671 0.7202	1.078 ± 0.2568 0.38823	1.092 ± 0.3605 0.63384	CACTCCAAAACAAACCCTTTACTTATTCTTATAAAATATT
plasmid_lp21	10039	IG 794	1.957 ± 0.7936 0.013966	1.313 ± 0.6721 0.10454	1.233 ± 0.4446 0.28848	1.082 ± 0.54 0.69869	TACACTCCAAAACAAACCCTTTACTTATTCTTATAAAATATT

plasmid_lp21	10059	IG 795	3.422 ± 2.3812 0.092041	1.962 ± 1.7024 0.21816	1.857 ± 1.0605 0.03408	1.52 ± 0.808 0.066	TTTATAAAAGAATAAGTAAAAGTGGTTAGTTAGTGGAGTGTATAATCA
plasmid_lp21	10100	IG 796	2.694 ± 1.9326 0.106972	1.584 ± 1.7051 0.40187	0.919 ± 0.7159 0.71191	0.803 ± 0.7461 0.33754	CACTCCACTAACTAACCCATTCTTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10103	IG 797	1.170 ± 0.7778 0.615217	0.641 ± 0.4474 0.45057	1.095 ± 0.5889 0.73894	1.154 ± 0.3898 0.52241	TAAATCATAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	10109	IG 798	1.299 ± 0.9391 0.612511	0.307 ± 0.261 0.2421	0.935 ± 0.6699 0.78412	0.772 ± 0.6379 0.20121	TGATTTACACTCCACTAAACTAACCCATTACTTATTCTTATAAA
plasmid_lp21	10111	IG 799	3.022 ± 1.9045 0.095429	1.553 ± 1.291 0.49909	1.391 ± 0.6957 0.17889	1.165 ± 0.6293 0.6165	TATGATTTACACTCCACTAAACTAACCCATTACTTATTCTTATAAA
plasmid_lp21	10122	IG 800	4.039 ± 2.7506 0.076088	2.297 ± 1.9846 0.18292	1.733 ± 1.2008 0.08358	1.645 ± 1.2497 0.12239	TTTATAAAAGAATAAGTAAAAGTGGTTAGTTAGTGGAGTGTATAATCA
plasmid_lp21	10148	IG 801	2.216 ± 1.1486 0.001204	1.178 ± 0.6999 0.16759	0.936 ± 0.5418 0.83382	0.978 ± 0.7403 0.81875	AACCACTTTACTTATTCTTATAAAATTTTATGATTTACAC
plasmid_lp21	10163	IG 802	2.649 ± 1.8321 0.119445	1.902 ± 0.2048 0.37615	1.026 ± 0.6759 0.89692	0.869 ± 0.9056 0.68603	CACTCCACTAAACTAACCCATTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10172	IG 803	1.285 ± 0.889 0.573659	0.346 ± 0.3352 0.30109	1.076 ± 0.8498 0.69478	0.847 ± 0.673 0.28596	TGATTTACACTCCACTAAACTAACCCATTACTTATTCTTATAAA
plasmid_lp21	10174	IG 804	2.839 ± 1.7533 0.124372	1.302 ± 1.0667 0.61478	1.149 ± 0.4626 0.18032	1.029 ± 0.4785 0.87971	TATGATTTACACTCCACTAAACTAACCCATTACTTATTCTTATAAA
plasmid_lp21	10175	IG 805	2.593 ± 1.2483 0.041897	1.854 ± 0.8689 0.08913	0.667 ± 0.3135 0.36883	0.716 ± 0.5030 0.36983	TAAATAAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGT
plasmid_lp21	10182	IG 806	2.581 ± 3.1073 0.450557	2.133 ± 1.9565 0.16513	0.473 ± 0.4153 0.39307	0.636 ± 0.5932 0.55526	TTTATTATGATTTACACTCCACTAAACTAACCCATTACTTATT
plasmid_lp21	10190	IG 807	1.988 ± 0.613 0.029158	1.214 ± 0.5584 0.37582	1.02 ± 0.3318 0.67936	0.952 ± 0.2916 0.10333	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATAAAA
plasmid_lp21	10200	IG 808	2.039 ± 0.9466 0.140033	1.521 ± 0.8899 0.31741	1.4 ± 0.681 0.43807	0.99 ± 0.7611 0.97569	CTTATTCTTATAAAATTTTATGATTTACACTCCACTAAACT
plasmid_lp21	10226	IG 809	2.750 ± 0.4791 0.011567	1.59 ± 0.7821 0.26851	1.065 ± 0.1505 0.25481	0.983 ± 0.3493 0.93654	CACTCCAGTAAACTAACCCATTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10228	IG 810	1.711 ± 0.7139 0.211454	1.413 ± 0.4791 0.2301	0.988 ± 0.6244 0.97814	0.837 ± 0.5888 0.70919	TACACTCCAGTAAACTAACCCATTACTTATTCTTATAAAATTTTAT
plasmid_lp21	10229	IG 811	1.206 ± 0.6427 0.391571	0.608 ± 0.429 0.42444	1.018 ± 0.6151 0.94294	1.025 ± 0.3719 0.81322	TAAATCATAAAATAAATTTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	10253	IG 812	1.983 ± 0.709 0.036513	1.251 ± 0.6054 0.31472	0.964 ± 0.365 0.64789	1.123 ± 0.4304 0.29942	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATAAAA
plasmid_lp21	10263	IG 813	2.135 ± 0.8703 0.029882	1.192 ± 0.4 0.48453	0.883 ± 0.8408 0.87132	0.869 ± 0.3905 0.11338	CTTATTCTTATAAAATTTTATGATTTACACTCCAGTAAACT
plasmid_lp21	10274	IG 814	3.262 ± 1.9244 0.026544	1.18 ± 0.5843 0.49747	1.346 ± 0.8172 0.37764	1.271 ± 0.7551 0.09399	AACCACTTTACTTATTCTTATAAAATTTTATGATTTACAC
plasmid_lp21	10289	IG 815	2.972 ± 0.8247 0.016591	1.701 ± 0.8822 0.19694	1.202 ± 0.243 0.11093	1.134 ± 0.4821 0.65938	CACTCCAGTAAACTAACCCATTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10292	IG 816	1.264 ± 0.7952 0.490727	0.544 ± 0.3178 0.27572	1.014 ± 0.5607 0.96671	1.1 ± 0.5179 0.69887	TAAATCATAAAATAAATTTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	10316	IG 817	1.940 ± 1.1801 0.071228	1.058 ± 0.6243 0.78618	0.921 ± 0.4379 0.78255	1.309 ± 0.7106 0.4355	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATATAA
plasmid_lp21	10325	IG 818	2.191 ± 2.4668 0.02765	1.721 ± 2.1768 0.07034	1.094 ± 1.2473 0.81334	1.136 ± 1.4085 0.42917	AGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATATAAAATATT
plasmid_lp21	10326	IG 819	2.431 ± 0.6214 0.053994	1.408 ± 0.3271 0.01718	1.399 ± 0.8419 0.50161	1.158 ± 0.4241 0.38982	CTTATTCTTATAAAATTTTATGATTTACACTCCAGTAAACT
plasmid_lp21	10337	IG 820	2.212 ± 1.3441 0.028612	0.879 ± 0.4725 0.73935	1.023 ± 0.5989 0.89103	0.869 ± 0.5469 0.59603	AACCACTTTACTTATTCTTATAAAATTTTATGATTTACAC
plasmid_lp21	10352	IG 821	3.240 ± 0.987 0.013347	1.829 ± 1.2282 0.26173	1.221 ± 0.3286 0.17127	1.19 ± 0.4562 0.43439	CACTCCAGTAAACTAACCCATTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10374	IG 822	3.633 ± 1.9317 0.069588	1.93 ± 1.4037 0.21992	1.412 ± 0.7065 0.12214	1.483 ± 0.7776 0.09069	TTTATAAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGTATAATCA
plasmid_lp21	10415	IG 823	2.603 ± 2.1908 0.129908	1.557 ± 1.8511 0.46566	0.971 ± 0.752 0.94134	1.003 ± 0.1096 0.9917	CACTCCACTAACTAACCCATTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10418	IG 824	1.165 ± 0.6532 0.611154	0.628 ± 0.4252 0.43183	1.015 ± 0.5439 0.95523	0.977 ± 0.3225 0.89001	TAAATCATAAAATAAATTTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	10424	IG 825	1.231 ± 0.8497 0.565468	0.336 ± 0.2768 0.26075	0.952 ± 0.7094 0.84167	0.729 ± 0.6046 0.25959	TGATTTACACTCCACTAAACTAACCCATTACTTATTCTTATAAA
plasmid_lp21	10426	IG 826	2.833 ± 2.1711 0.153858	1.479 ± 1.2354 0.49751	1.226 ± 0.68 0.32593	1.057 ± 0.712 0.86164	TATGATTTACACTCCACTAAACTAACCCATTACTTATTCTTATAAA
plasmid_lp21	10437	IG 827	3.637 ± 2.315 0.148514	2.067 ± 1.6218 0.29917	1.426 ± 0.7152 0.23101	1.353 ± 0.5178 0.0931	TTTATAAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGTATAATCA
plasmid_lp21	10463	IG 828	2.687 ± 2.0458 0.022418	1.452 ± 0.1018 0.38191	1.225 ± 0.9232 0.66061	1.145 ± 0.7051 0.5811	AACCACTTTACTTATTCTTATAAAATTTTATGATTTACAC
plasmid_lp21	10478	IG 829	2.360 ± 1.9703 0.107698	1.684 ± 1.8849 0.31993	0.85 ± 0.6092 0.59534	0.916 ± 0.8811 0.43051	CACTCCACTAACTAACCCATTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10481	IG 830	1.122 ± 0.5627 0.63269	0.514 ± 0.3421 0.27471	1.021 ± 0.4741 0.94267	1.014 ± 0.4535 0.94977	TAAATCATAAAATAAATTTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	10487	IG 831	1.336 ± 1.0292 0.0584881	0.404 ± 0.3706 0.35018	1.023 ± 0.8109 0.92458	0.726 ± 0.6465 0.18471	TGATTTACACTCCACTAAACTAACCCATTACTTATTCTTATAAA
plasmid_lp21	10489	IG 832	3.070 ± 1.8654 0.088264	1.611 ± 1.3508 0.47763	1.306 ± 0.6574 0.2301	1.168 ± 0.6461 0.52609	TATGATTTACACTCCACTAAACTAACCCATTACTTATTCTTATAAA
plasmid_lp21	10505	IG 833	1.847 ± 0.7192 0.011622	1.184 ± 0.6083 0.24354	0.93 ± 0.3447 0.34593	0.949 ± 0.4596 0.54772	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATAAAA
plasmid_lp21	10526	IG 834	2.030 ± 1.1794 0.074966	1.058 ± 0.5068 0.63289	1.106 ± 0.6229 0.68222	0.861 ± 0.5607 0.01336	AACCACTTTACTTATTCTTATAAAATTTTATGATTTACAC
plasmid_lp21	10541	IG 835	3.045 ± 1.113 0.004523	1.633 ± 1.0189 0.18922	1.245 ± 0.4886 0.10974	1.14 ± 0.674 0.74427	CACTCCAGTAACTAACCCATTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10543	IG 836	1.219 ± 0.5231 0.642861	0.959 ± 0.5245 0.92633	0.76 ± 0.8433 0.49886	0.656 ± 0.2666 0.32676	TACACTCCAGTAACTAACCCATTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10544	IG 837	1.264 ± 0.7535 0.446752	0.602 ± 0.4412 0.40018	1.098 ± 0.4179 0.71623	1.108 ± 0.4401 0.66448	TAAATCATAAAATAAATTTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	10568	IG 838	1.713 ± 0.952 0.137181	1.03 ± 0.5376 0.84575	0.796 ± 0.4333 0.31083	0.943 ± 0.451 0.83702	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATATAA
plasmid_lp21	10577	IG 839	2.134 ± 2.337 0.075326	1.489 ± 1.7847 0.14912	1.229 ± 1.2329 0.40823	1.166 ± 1.4296 0.23286	AGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATATAAAATTTT
plasmid_lp21	10589	IG 840	3.287 ± 2.1541 0.018323	1.394 ± 0.8438 0.12732	1.394 ± 1.0538 0.4657	1.196 ± 0.8457 0.07146	AACCACTTTACTTATTCTTATAAAATTTTATGATTTACAC
plasmid_lp21	10604	IG 841	2.563 ± 0.9866 0.032966	1.549 ± 0.897 0.18376	1.064 ± 0.391 0.70453	1.106 ± 0.5003 0.7176	CACTCCAGTAACTAACCCATTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10606	IG 842	1.519 ± 0.4482 0.074266	0.967 ± 0.4586 0.92319	1.206 ± 0.7576 0.72753	0.801 ± 0.359 0.37025	TACACTCCAGTAACTAACCCATTACTTATTCTTATAAAATTTTATT
plasmid_lp21	10637	IG 843	2.326 ± 1.6167 0.004956	2.101 ± 2.1532 0.21736	0.582 ± 0.3725 0.39051	0.86 ± 0.9273 0.68415	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAAAATCAA

plasmid_lp21	10669	IG 844	1.747 ± 1.0782 0.261118	1.247 ± 0.519 0.03165	1.25 ± 0.6284 0.55609	1.734 ± 1.1519 0.18987	TGTAGTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTTAT
plasmid_lp21	10715	IG 845	2.614 ± 1.3057 0.158234	1.39 ± 1.1355 0.5986	1.552 ± 1.1166 0.46905	1.25 ± 0.8924 0.67286	AACCACTTTACTTATTCTTATAAAATTTTATGATTATGTAG
plasmid_lp21	10733	IG 846	1.282 ± 0.798 0.55818	0.624 ± 0.4767 0.43692	1.046 ± 0.5069 0.89014	1.109 ± 0.5202 0.73312	TAAATCATAAAAATAAATTTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	10739	IG 847	1.135 ± 0.9945 0.845798	0.19 ± 0.1911 0.21172	1.008 ± 0.7983 0.96716	0.69 ± 0.6381 0.27964	TGATTATACACTCCACTAAACTAAACCCTTACTTATTCTTATAAA
plasmid_lp21	10741	IG 848	2.544 ± 1.8057 0.171784	1.268 ± 1.166 0.70449	1.167 ± 0.6101 0.0638	0.688 ± 0.3355 0.25239	TATGATTATACACTCCACTAAACTAAACCCTTACTTATTCTTATAAA
plasmid_lp21	10757	IG 849	2.360 ± 0.9563 0.063313	1.256 ± 0.5447 0.24966	1.074 ± 0.353 0.43684	1.248 ± 0.4189 0.17691	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAATCATAAA
plasmid_lp21	10778	IG 850	2.411 ± 0.6589 0.010885	1.157 ± 0.2716 0.45246	1.181 ± 0.4784 0.62775	0.972 ± 0.4624 0.84852	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	10793	IG 851	2.765 ± 0.7156 0.014101	1.635 ± 0.8489 0.20293	1.08 ± 0.2836 0.42573	1.05 ± 0.3731 0.81558	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	10795	IG 852	1.488 ± 0.4766 0.185349	1.194 ± 0.2817 0.33991	1.048 ± 0.9185 0.91628	0.726 ± 0.4478 0.40547	TACACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	10817	IG 853	2.464 ± 3.0448 0.189071	1.301 ± 1.5341 0.11427	0.763 ± 0.7358 0.75827	1.356 ± 1.2146 0.56822	AAATATCTATTCTTATGATTATACACTCCAGTAAACTAACCACTTTAC
plasmid_lp21	10829	IG 854	3.696 ± 0.8294 0.013933	1.644 ± 1.0661 0.45162	1.441 ± 1.1271 0.55581	1.858 ± 1.3104 0.41389	AGTAAAAGTGGTTAGTTAGTGGACTACATAAAATCATAAAATTT
plasmid_lp21	10858	IG 855	2.896 ± 0.6663 0.026766	1.79 ± 0.9693 0.31969	0.862 ± 0.1443 0.16787	1.255 ± 0.2795 0.18846	TGTAGTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATCTAT
plasmid_lp21	10859	IG 856	1.135 ± 0.6153 0.65497	0.527 ± 0.428 0.34167	1.091 ± 0.5798 0.81653	1.045 ± 0.4017 0.84052	TAAATCATAAAAATAAATTTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	10883	IG 857	2.152 ± 0.7341 0.015366	1.271 ± 0.4339 0.2816	0.943 ± 0.2852 0.60683	1.115 ± 0.4562 0.32601	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAATCATAAA
plasmid_lp21	10893	IG 858	4.152 ± 3.013 0.023081	3.101 ± 3.4633 0.23405	1.912 ± 1.3391 0.18986	1.803 ± 1.3392 0.0013	CTTATTCTTATAAAATTTTATGATTATGTAGTCCACTAAACT
plasmid_lp21	10919	IG 859	3.179 ± 0.8942 0.004727	1.756 ± 1.0426 0.2123	1.293 ± 0.4391 0.2554	1.085 ± 0.4364 0.56911	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	10921	IG 860	1.157 ± 0.6838 0.73601	0.869 ± 0.4861 0.66146	0.647 ± 0.4352 0.13847	0.788 ± 0.4757 0.54339	TACACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	10922	IG 861	1.127 ± 0.6323 0.683921	0.582 ± 0.4399 0.36911	1.011 ± 0.6642 0.97726	1.142 ± 0.4911 0.66101	TAAATCATAAAAATAAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	10946	IG 862	2.139 ± 0.6702 0.01086	1.298 ± 0.644 0.26158	1.038 ± 0.3394 0.43515	1.091 ± 0.4182 0.23889	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAATCATAAA
plasmid_lp21	10956	IG 863	2.765 ± 0.4364 0.00029	1.392 ± 0.4669 0.29289	1.42 ± 0.7722 0.41501	1.449 ± 0.47 0.20219	CTTATTCTTATAAAATTTTATGATTATACACTCCAGTAAACT
plasmid_lp21	10967	IG 864	2.443 ± 1.3549 0.080493	1.195 ± 0.4369 0.20871	1.239 ± 0.5287 0.29837	0.842 ± 0.5109 0.35126	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	10982	IG 865	3.079 ± 1.1436 0.04338	1.885 ± 0.9449 0.13602	1.249 ± 0.317 0.1659	1.225 ± 0.4615 0.41418	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	10984	IG 866	1.558 ± 0.6724 0.34971	1.203 ± 0.5287 0.60251	1.092 ± 0.8116 0.79772	0.763 ± 0.2891 0.20072	TACACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	10985	IG 867	1.293 ± 0.88 0.327693	0.597 ± 0.4784 0.47171	0.983 ± 0.6193 0.95569	1.034 ± 0.5455 0.90608	TAAATCATAAAAATAAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	11009	IG 868	2.122 ± 0.9107 0.067608	1.417 ± 0.7105 0.24656	1.062 ± 0.3421 0.50213	1.16 ± 0.3672 0.36043	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAATCATATAA
plasmid_lp21	11018	IG 869	1.997 ± 2.4217 0.015082	1.434 ± 1.8947 0.18334	1.005 ± 1.1981 0.9924	1.083 ± 1.4378 0.71805	AGTAAAAGTGGTTAGTTACTGGAGTGATAAATCATATAAAATTT
plasmid_lp21	11030	IG 870	2.178 ± 0.5657 0.015855	1.059 ± 0.2496 0.4511	1.182 ± 0.5352 0.66259	1.023 ± 0.4817 0.90904	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	11045	IG 871	2.695 ± 0.8327 0.016926	1.715 ± 0.9538 0.2043	1.052 ± 0.3145 0.60216	1.125 ± 0.5116 0.70937	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	11047	IG 872	1.782 ± 0.7719 0.264316	1.076 ± 0.4161 0.39135	1.352 ± 1.024 0.48616	0.762 ± 0.2502 0.38312	TACACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	11096	IG 873	1.538 ± 0.6066 0.020803	1.273 ± 0.535 0.21761	1.17 ± 0.4597 0.40689	0.904 ± 0.3648 0.62584	GTTTAGGAGTGATAAATCATATAAAATTTTATAAAAGAATAAGTAA
plasmid_lp21	11142	IG 874	0.764 ± 0.5124 0.650026	0.647 ± 0.4701 0.52219	1.131 ± 0.474 0.57745	1.151 ± 0.6276 0.10784	AGTAAAAGTGGTTAGTTAGGAGTGATAAATCATAAAAATAAATTTT
plasmid_lp21	11167	IG 875	1.900 ± 0.2129 0.01474	1.007 ± 0.2956 0.97678	1.112 ± 0.4863 0.71729	0.769 ± 0.1362 0.20033	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	11170	IG 876	1.236 ± 0.8258 0.213767	0.624 ± 0.5317 0.55306	1.001 ± 0.6588 0.99348	1.234 ± 0.6525 0.22423	TAAATCATAAAAATAAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	11189	IG 877	3.412 ± 2.275 0.070513	1.685 ± 1.3856 0.21039	1.432 ± 0.7899 0.04397	1.37 ± 0.8575 0.04303	TTTATAAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAATCA
plasmid_lp21	11215	IG 878	2.529 ± 1.242 0.010295	1.252 ± 0.6526 0.22599	1.172 ± 0.6921 0.60305	1.141 ± 0.6509 0.38538	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	11230	IG 879	2.995 ± 2.1343 0.053064	1.962 ± 2.0985 0.27939	1.051 ± 0.8771 0.5596	1.095 ± 0.9962 0.46601	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	11233	IG 880	1.317 ± 0.5899 0.378558	0.68 ± 0.4652 0.4229	0.99 ± 0.3744 0.96602	1.187 ± 0.2613 0.22389	TAAATCATAAAAATAAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	11239	IG 881	1.325 ± 0.8883 0.53125	0.401 ± 0.3445 0.31555	1.088 ± 0.7755 0.68321	0.812 ± 0.6654 0.14033	TGATTATACACTCCAGTAAACTAACCACTTTACTTATTCTTATAAA
plasmid_lp21	11241	IG 882	2.777 ± 1.3852 0.056062	1.456 ± 1.1643 0.48234	1.241 ± 0.6079 0.0851	0.982 ± 0.5172 0.89557	TATGATTATACACTCCAGTAAACTAACCACTTTACTTATTCTTATAA
plasmid_lp21	11266	IG 883	3.321 ± 1.3413 0.05881	1.466 ± 0.7893 0.4609	1.048 ± 0.7916 0.89352	1.489 ± 1.1114 0.57691	AGTAAAAGTGGTTAGTTAGGAGTGATAAATCATAAAAATAAATTTT
plasmid_lp21	11278	IG 884	2.361 ± 1.6619 0.019021	0.959 ± 0.7599 0.85999	1.293 ± 0.9319 0.44389	0.904 ± 0.7429 0.63214	AACCACTTTACTTATTCTTATAAAATTTTATGATTATACAC
plasmid_lp21	11291	IG 885	2.591 ± 3.8193 0.114212	1.773 ± 3.1439 0.35727	0.906 ± 1.2221 0.84247	1.067 ± 1.716 0.50701	GTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	11295	IG 886	3.213 ± 0.5099 0.017259	1.865 ± 0.8968 0.23563	1.039 ± 0.4039 0.22171	1.532 ± 0.3548 0.11673	TGTAGTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	11296	IG 887	1.223 ± 0.6808 0.571983	0.567 ± 0.3912 0.3275	1.051 ± 0.5521 0.85717	0.959 ± 0.34 0.86562	TAAATCATAAAAATAAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	11320	IG 888	2.068 ± 0.7389 0.030172	1.164 ± 0.4947 0.27135	1.004 ± 0.3168 0.85257	1.056 ± 0.4594 0.60063	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAATCATAAA
plasmid_lp21	11330	IG 889	3.260 ± 2.0776 0.001427	2.285 ± 2.4236 0.25667	1.331 ± 0.8416 0.53082	1.077 ± 0.7255 0.65621	CTTATTCTTATAAAATTTTATGATTATGTAGTCCAGTAAACT
plasmid_lp21	11356	IG 890	2.633 ± 0.7485 0.028205	1.438 ± 0.8262 0.37417	1.122 ± 0.3041 0.10716	0.956 ± 0.3564 0.86009	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	11358	IG 891	0.887 ± 0.4775 0.794087	0.911 ± 0.5412 0.82779	0.74 ± 0.6101 0.16481	0.6 ± 0.3354 0.2633	TACACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTT
plasmid_lp21	11359	IG 892	1.576 ± 0.8871 0.276528	0.777 ± 0.625 0.68122	1.398 ± 0.9875 0.48712	1.264 ± 0.547 0.52177	TAAATCATAAAAATAAATTTTATAAAAGAATAAGTAAAAGTGGTTAGTT

plasmid_lp21	11404	IG 893	2.380 ± 1.5711 0.039465	1.005 ± 0.5545 0.98796	1.024 ± 0.6558 0.94326	0.938 ± 0.6978 0.53555	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	11417	IG 894	2.969 ± 3.4873 0.121563	1.793 ± 2.7008 0.39026	1.16 ± 1.4148 0.31744	1.203 ± 1.6058 0.31203	GTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	11421	IG 895	2.944 ± 1.2603 0.077741	1.884 ± 1.3107 0.32406	1.045 ± 0.2477 0.83616	1.117 ± 0.2498 0.58692	TGTAGTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	11431	IG 896	2.526 ± 1.6792 0.170436	1.832 ± 1.2394 0.16251	0.644 ± 0.4271 0.48814	1.096 ± 0.7448 0.85561	TAAATAAATATTCTTATAAAAGATAAGTAAAAGTGGTTAGTTACTGGAGT
plasmid_lp21	11434	IG 897	1.627 ± 0.8246 0.335359	0.585 ± 0.1904 0.1538	0.92 ± 0.5703 0.84464	1.111 ± 0.505 0.57809	TTTATATGATTATGTTAGTCCACTAAACTAACCACTTTACTTATTCTT
plasmid_lp21	11445	IG 898	2.989 ± 2.0654 0.230208	1.335 ± 0.4554 0.40632	1.592 ± 1.1145 0.38735	1.047 ± 0.5964 0.9199	TAAAATATTATATGATTATGTTAGTCCACTAAACTAACCACTTT
plasmid_lp21	11446	IG 899	2.072 ± 0.7658 0.02216	1.207 ± 0.7042 0.44647	0.996 ± 0.3606 0.97035	1.177 ± 0.4366 0.18887	TAAGAATAAGTAAAGTGGTTAGTTACTGGAGTGTATAATCATAAAAA
plasmid_lp21	11482	IG 900	2.805 ± 1.0714 0.022288	1.53 ± 0.9649 0.16688	1.086 ± 0.4222 0.71452	1.052 ± 0.5292 0.88857	CACTCAGTAAACTAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	11485	IG 901	1.160 ± 0.8536 0.636965	0.649 ± 0.4742 0.52175	1.043 ± 0.6703 0.92637	1.021 ± 0.5541 0.95597	TAAATCATAAAAATAATATTCTTATAAAAGATAAGTAAAAGTGGTTAGTT
plasmid_lp21	11518	IG 902	4.257 ± 1.7436 0.049435	1.547 ± 0.8341 0.42437	1.639 ± 1.0967 0.39253	1.918 ± 1.2534 0.37713	AGTAAAAGTGGTTAGTTAGTGGACTACATAATCATAAAAATAATATT
plasmid_lp21	11519	IG 903	2.294 ± 0.5353 0.007736	1.244 ± 0.5941 0.34989	1.386 ± 0.8616 0.57605	1.053 ± 0.2617 0.63771	CTTATTCTTATAAAATATTATTTATGATTATACACTCAGTAAACT
plasmid_lp21	11530	IG 904	2.394 ± 1.5125 0.003453	1.074 ± 0.693 0.67614	1.037 ± 0.6883 0.91412	0.87 ± 0.5742 0.57429	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	11543	IG 905	2.455 ± 2.6997 0.157438	1.421 ± 2.1238 0.55868	0.965 ± 1.0846 0.80344	0.991 ± 1.2284 0.94809	GTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	11547	IG 906	2.966 ± 1.0123 0.061411	1.873 ± 0.9136 0.2697	1.024 ± 0.255 0.83568	1.409 ± 0.425 0.04555	TGTAGTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	11572	IG 907	1.785 ± 0.9977 0.170218	1.307 ± 0.7338 0.23403	0.94 ± 0.3884 0.78376	1.203 ± 0.5325 0.60648	TAAGAATAAGTAAAGTGGTTAGTTACTGGAGTGTATAATCATATAAA
plasmid_lp21	11581	IG 908	2.253 ± 2.2628 0.096819	1.594 ± 1.6985 0.14573	1.125 ± 1.071 0.70306	1.025 ± 1.1624 0.40718	AGTAAAAGTGGTTAGTTACTGGAGTGTATAATCATATAAAATAATT
plasmid_lp21	11608	IG 909	2.739 ± 0.136 0.000288	1.137 ± 0.5658 0.7261	1.177 ± 0.3204 0.46417	1.03 ± 0.5901 0.93467	CACTCAGTAAACTAACCACTTTACTTATTCTTATGAAATATTATTT
plasmid_lp21	11644	IG 910	0.537 ± 0.3452 0.35354	0.526 ± 0.3773 0.36668	0.969 ± 0.4831 0.82852	1.009 ± 0.5816 0.86591	AGTAAAAGTGGTTAGTTGGAGTGTATAATCATAAAAATAATATT
plasmid_lp21	11669	IG 911	1.687 ± 0.6827 0.256976	0.83 ± 0.2987 0.54039	0.829 ± 0.261 0.51202	1.159 ± 0.5579 0.72922	CACTCCAAAACAACTAACCACTTTACTTATTATTATGAAATATTATTT
plasmid_lp21	11671	IG 912	2.754 ± 1.4124 0.030423	1.364 ± 0.8532 0.07498	1.565 ± 0.7471 0.10747	1.323 ± 0.8504 0.46401	TACACTCCAAAACAACTAACCACTTTACTTATTATTATGAAATATT
plasmid_lp21	11705	IG 913	0.516 ± 0.3268 0.320486	0.532 ± 0.4346 0.40849	1.038 ± 0.5302 0.64362	0.841 ± 0.5679 0.38139	AGTAAAAGTGGTTAGTTGGAGTGTATAATCATATAAAATAATTT
plasmid_lp21	11720	IG 914	2.322 ± 0.3483 0.001567	1.436 ± 0.2689 0.10841	1.209 ± 0.2844 0.21458	1.215 ± 0.1905 0.1336	GTTTGGAGTGTATAATCATATAAAATAATTTATAAAAGATAAGTAA
plasmid_lp21	11730	IG 915	1.549 ± 0.4279 0.097222	0.929 ± 0.3167 0.783	0.984 ± 0.2264 0.63899	0.782 ± 0.4588 0.51728	CACTCCAAAACAACTAACCACTTTACTAATTCTTATAAAATATT
plasmid_lp21	11732	IG 916	2.468 ± 1.1647 0.093259	1.998 ± 0.7589 0.048	2.042 ± 1.014 0.12751	1.469 ± 0.5773 0.30993	TACACTCCAAAACAACTAACCACTTTACTAATTCTTATAAAATATT
plasmid_lp21	11742	IG 917	2.465 ± 0.9079 0.057129	1.676 ± 0.7699 0.29401	0.772 ± 0.312 0.49076	0.781 ± 0.2841 0.28785	TAATAAAATATTCTTATAAAAGATAAGTAAAGTGGTTAGTTACTGGAGT
plasmid_lp21	11757	IG 918	1.947 ± 0.905 0.057619	1.187 ± 0.6561 0.32666	0.987 ± 0.3368 0.94169	1.017 ± 0.3602 0.88094	TAAGAATAAGTAAAGTGGTTAGTTACTGGAGTGTATAATCATATAAA
plasmid_lp21	11793	IG 919	3.184 ± 0.6876 0.01405	1.688 ± 0.8835 0.24834	1.416 ± 0.3123 0.00879	1.135 ± 0.4017 0.65325	CACTCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	11796	IG 920	1.176 ± 0.7688 0.658247	0.542 ± 0.3752 0.30293	1.103 ± 0.6234 0.79582	1.179 ± 0.4507 0.43306	TAATCATAAAAATAATATTCTTATAAAAGATAAGTAAAGTGGTTAGTT
plasmid_lp21	11830	IG 921	3.093 ± 0.7497 0.01333	1.587 ± 0.4375 0.14382	1.621 ± 1.3601 0.42448	1.924 ± 0.7385 0.18511	CTTATTCTTATAAAATATTCTTATTGATTATACACTCAGTAAACT
plasmid_lp21	11841	IG 922	2.907 ± 2.8259 0.010337	1.251 ± 1.208 0.61475	1.413 ± 1.2939 0.54341	1.284 ± 1.2042 0.45936	AACCACTTTACTTATTCTTATAAAATATTCTTATTGATTATACAC
plasmid_lp21	11854	IG 923	2.632 ± 3.2852 0.130236	1.554 ± 2.3949 0.40152	0.924 ± 1.1893 0.66883	0.927 ± 1.4453 0.55223	GTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	11858	IG 924	2.830 ± 1.5217 0.115064	1.433 ± 1.0471 0.54447	0.982 ± 0.3444 0.94698	1.451 ± 0.5606 0.26155	TGTAGTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	11871	IG 925	1.676 ± 1.0254 0.248042	0.742 ± 0.4784 0.62617	0.985 ± 0.5767 0.95248	1.286 ± 0.7907 0.01777	TTTATATGATTATGTTAGTCCACTAAACTAACCACTTTACTTCTT
plasmid_lp21	11875	IG 926	2.332 ± 2.5948 0.294238	1.37 ± 1.6264 0.52558	0.861 ± 0.6981 0.31211	0.862 ± 0.864 0.19994	TCTATTCTTATGATTATGTTAGTCCACTAAACTAACCACTTTACTT
plasmid_lp21	11883	IG 927	2.028 ± 0.8389 0.038635	1.207 ± 0.6469 0.33123	1.001 ± 0.3914 0.99194	1.088 ± 0.4682 0.2729	TAAGAATAAGTAAAGTGGTTAGTTACTGGAGTGTATAATCATATAAA
plasmid_lp21	11919	IG 928	2.901 ± 1.0487 0.02867	1.419 ± 0.8449 0.21023	1.197 ± 0.4161 0.48447	1.2 ± 0.6402 0.58499	CACTCAGTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	11922	IG 929	1.184 ± 0.5121 0.294445	0.604 ± 0.4646 0.40873	1.106 ± 0.5987 0.75438	0.999 ± 0.341 0.99356	TAATCATAAAAATAATATTCTTATAAAAGATAAGTAAAGTGGTTAGTT
plasmid_lp21	11956	IG 930	2.688 ± 0.5368 0.001824	1.591 ± 0.5819 0.08107	1.557 ± 1.2785 0.55497	1.268 ± 0.4308 0.33897	CTTATTCTTATAAAATATTCTTATTGATTATACACTCAGTAAACT
plasmid_lp21	11967	IG 931	2.237 ± 1.0943 0.017032	1.067 ± 0.5634 0.59088	1.065 ± 0.6654 0.84213	0.882 ± 0.5489 0.55658	AACCACTTTACTTATTCTTATAAAATATTCTTATTGATTATACAC
plasmid_lp21	11980	IG 932	2.441 ± 2.9857 0.123837	1.479 ± 2.2258 0.40833	1.021 ± 1.2166 0.91574	0.889 ± 1.3236 0.15781	GTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	11984	IG 933	2.403 ± 0.9366 0.073529	1.468 ± 0.8431 0.48751	0.746 ± 0.2366 0.21319	1.221 ± 0.3555 0.18375	TGTAGTCCACTAAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	11994	IG 934	4.716 ± 1.0906 0.000634	2.287 ± 0.5476 0.00013	1.194 ± 0.3399 0.33559	1.383 ± 0.3325 0.12127	TAATATAATTTATAAAAGATAAGTAAAGTGGTTAGTTGGAGTGT
plasmid_lp21	11996	IG 935	2.644 ± 1.4897 0.15186	1.578 ± 0.5777 0.12243	0.929 ± 0.432 0.81637	1.227 ± 0.6219 0.39153	AATAAAATTTATAAAAGATAAGTAAAGTGGTTAGTTGGAGTGTAT
plasmid_lp21	11997	IG 936	1.761 ± 1.0148 0.226235	0.705 ± 0.3677 0.50672	0.931 ± 0.577 0.83081	1.47 ± 0.8021 0.03316	TTTATATGATTATGTTAGTCCACTAAACTAACCACTTTACTTCTT
plasmid_lp21	12008	IG 937	3.254 ± 2.7533 0.163371	1.305 ± 0.9333 0.65955	1.593 ± 1.3465 0.09241	1.121 ± 0.8421 0.8625	TAATATTTATATGATTATGTTAGTCCACTAAACTAACCACTTT
plasmid_lp21	12018	IG 938	0.541 ± 0.3665 0.361634	0.532 ± 0.3947 0.3748	0.938 ± 0.4286 0.68066	1.017 ± 0.5365 0.75536	AGTAAAAGTGGTTAGTTGGAGTGTATAATCATAAAAATAATATT
plasmid_lp21	12043	IG 939	2.165 ± 0.6523 0.023913	1.272 ± 0.5334 0.24864	1.022 ± 0.3158 0.83443	1.214 ± 0.5114 0.37532	CACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12045	IG 940	1.805 ± 0.8447 0.03326	1.286 ± 0.668 0.08851	1.154 ± 0.4599 0.49759	1.027 ± 0.4995 0.87206	TACACTCCAAAACAACTAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12046	IG 941	1.312 ± 0.8533 0.343857	0.585 ± 0.528 0.52512	1.062 ± 0.7807 0.86467	1.053 ± 0.6391 0.86308	TAATCATAAAAATAATTTATAAAAGATAAGTAAAGTGGTTAGTT

plasmid_lp21	12057	IG 942	2.534 ± 1.2939 0.16296	1.449 ± 0.4987 0.28116	1.008 ± 0.3652 0.9762	1.187 ± 0.5515 0.66875	AATAAATTTATAAAGAATAAGTAAAGGGTTAGTTGGAGTGAT
plasmid_lp21	12079	IG 943	0.499 ± 0.3251 0.339092	0.492 ± 0.4367 0.41081	0.924 ± 0.5309 0.65778	0.998 ± 0.7041 0.99266	AGTAAAAGTGTAGTTGGAGTGATAAATCATATAAAATATT
plasmid_lp21	12091	IG 944	2.451 ± 1.1381 0.018175	1.174 ± 0.489 0.25762	1.091 ± 0.5209 0.70134	0.916 ± 0.739 0.69306	AACCACTTTACTTATTCTTATAAAATATTATTTGATTATACAC
plasmid_lp21	12094	IG 945	2.238 ± 0.4441 0.028702	1.333 ± 0.3127 0.06068	1.147 ± 0.2849 0.00769	1.273 ± 0.2425 0.046	GTTTGGAGTGATAAATCATATAAAATATTTATAAAGAATAAGTAA
plasmid_lp21	12104	IG 946	1.663 ± 0.3862 0.02237	1.006 ± 0.226 0.961	0.988 ± 0.2135 0.89084	1.099 ± 0.371 0.58732	CACTCCAAAACAAACCACCTTTACTTATTCTTATAAAATATT
plasmid_lp21	12106	IG 947	1.826 ± 0.7645 0.009737	1.343 ± 0.6365 0.03499	1.133 ± 0.4472 0.53443	0.995 ± 0.5087 0.9762	TACACTCCAAAACAAACCACCTTTACTTATTCTTATAAAATATT
plasmid_lp21	12116	IG 948	5.449 ± 2.0758 0.003911	2.391 ± 1.0949 0.01991	1.49 ± 0.6283 0.29857	1.598 ± 0.6248 0.2198	TAAATAATTTATAAAGAATAAGTAAAGGGTTAGTTGGAGTGT
plasmid_lp21	12118	IG 949	2.702 ± 1.5136 0.147935	1.367 ± 0.5672 0.23847	1.126 ± 0.3729 0.32941	1.315 ± 0.5869 0.33149	AATAAATTTATAAAGAATAAGTAAAGGGTTAGTTGGAGTGTAT
plasmid_lp21	12140	IG 950	0.548 ± 0.3608 0.38167	0.523 ± 0.3888 0.38376	1.01 ± 0.5261 0.94595	1.007 ± 0.5858 0.90729	AGTAAAAGTGTAGTTGGAGTGATAAATCATAAAAAATATT
plasmid_lp21	12165	IG 951	2.051 ± 0.6344 0.020231	1.257 ± 0.5366 0.30931	1.073 ± 0.3444 0.15299	1.231 ± 0.4578 0.2993	CACTCCAAAACAAACCACCTTTACTTATTCTTATAAAATATT
plasmid_lp21	12167	IG 952	1.838 ± 0.712 0.028031	1.36 ± 0.6402 0.12383	1.183 ± 0.3783 0.38973	1.032 ± 0.4863 0.82492	TACACTCCAAAACAAACCACCTTTACTTATTCTTATAAAATATT
plasmid_lp21	12168	IG 953	1.364 ± 0.8219 0.286557	0.682 ± 0.53 0.55379	1.114 ± 0.462 0.6331	1.108 ± 0.4543 0.30189	TAAATCATAAAAATATAAATTTATAAAGAATAAGTAAAGGGTTAGT
plasmid_lp21	12198	IG 954	2.310 ± 0.7026 0.017652	1.937 ± 1.7578 0.40874	0.662 ± 0.2738 0.32	0.787 ± 0.6179 0.59106	ATAAGTAAAAGTGTAGTTACTGGACTACATAAAATCAA
plasmid_lp21	12213	IG 955	2.507 ± 1.8023 0.033228	1.177 ± 0.7738 0.44521	1.383 ± 0.9052 0.3853	1.172 ± 0.8612 0.47928	ACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC
plasmid_lp21	12230	IG 956	1.454 ± 0.6586 0.344977	0.986 ± 0.325 0.82542	1.063 ± 0.55 0.82539	1.509 ± 0.1091 0.40657	TGTAGTCAGTAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12231	IG 957	1.146 ± 0.7718 0.700781	0.646 ± 0.5178 0.47297	0.98 ± 0.4358 0.93842	0.992 ± 0.4601 0.96624	TAAATCATAAAAATAATATTTTATAAAGAATAAGTAAAGGGTTAGT
plasmid_lp21	12255	IG 958	1.985 ± 0.9031 0.043013	1.054 ± 0.4816 0.67087	0.929 ± 0.4314 0.68788	1.009 ± 0.4153 0.959	TAAAGAATAAGTAAAGGGTTAGTTACTGGAGTGATAAATCATAAA
plasmid_lp21	12291	IG 959	3.071 ± 0.9105 0.003416	1.628 ± 0.9523 0.20963	1.256 ± 0.3876 0.29375	1.055 ± 0.4882 0.83858	CACTCCAGTAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12294	IG 960	1.335 ± 0.767 0.311682	0.753 ± 0.5799 0.63242	1.213 ± 0.7609 0.61609	1.288 ± 0.7646 0.38928	TAAATCATAAAAATAATATTTTATAAAGAATAAGTAAAGGGTTAGT
plasmid_lp21	12305	IG 961	2.575 ± 1.3415 0.125364	1.732 ± 0.5803 0.06451	1.152 ± 0.3522 0.41628	1.186 ± 0.3984 0.34455	AATAAATTTATAAAGAATAAGTAAAGGGTTAGTTGGAGTGAT
plasmid_lp21	12327	IG 962	0.544 ± 0.3674 0.370208	0.573 ± 0.425 0.42934	1.004 ± 0.4745 0.97779	1.063 ± 0.573 0.14822	AGTAAAAGTGTAGTTGGAGTGATAAATCATAAAAATAATATT
plasmid_lp21	12328	IG 963	3.028 ± 0.4937 0.014634	1.035 ± 0.331 0.81433	1.174 ± 0.7932 0.76143	1.156 ± 0.191 0.12713	CTTATTCTTATAAAATATTATTGATTATCCTCAGTAAAC
plasmid_lp21	12339	IG 964	3.106 ± 1.8129 0.024225	1.473 ± 0.7724 0.26254	1.409 ± 0.8462 0.28967	1.299 ± 0.8471 0.4023	ACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC
plasmid_lp21	12352	IG 965	1.658 ± 0.2534 0.01335	1.001 ± 0.1794 0.98906	0.999 ± 0.2003 0.9907	1.039 ± 0.2934 0.78241	CACTCCAAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12354	IG 966	1.989 ± 0.8601 0.009719	1.406 ± 0.732 0.065	1.276 ± 0.5386 0.37268	1.079 ± 0.5209 0.63376	TACACTCCAAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12355	IG 967	1.141 ± 0.7542 0.58154	0.65 ± 0.5011 0.5291	1.023 ± 0.6092 0.93781	0.949 ± 0.4632 0.76066	TAAATCATAAAAATAATATTTTATAAAGAATAAGTAAAGGGTTAGT
plasmid_lp21	12379	IG 968	2.069 ± 0.7559 0.021696	1.187 ± 0.6234 0.3549	1.051 ± 0.3255 0.48076	1.092 ± 0.3927 0.22726	TAAAGAATAAGTAAAGGGTTAGTTACTGGAGTGATAAATCATAAA
plasmid_lp21	12400	IG 969	2.737 ± 1.2439 0.00914	1.154 ± 0.4873 0.36312	1.123 ± 0.6153 0.78763	1.009 ± 0.5281 0.97075	ACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC
plasmid_lp21	12415	IG 970	2.856 ± 0.7123 0.029333	1.625 ± 0.826 0.2821	1.108 ± 0.2282 0.20102	1.04 ± 0.3452 0.88821	CACTCCAGTAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12417	IG 971	1.190 ± 0.5564 0.597261	0.598 ± 0.2508 0.05811	0.934 ± 0.5682 0.83974	0.651 ± 0.2677 0.32942	TACACTCCAGTAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12418	IG 972	1.096 ± 0.7541 0.79877	0.502 ± 0.3492 0.27651	1.021 ± 0.5706 0.95187	1.013 ± 0.392 0.93403	TAATCATAAAAATAATATTTTATAAAGAATAAGTAAAGGGTTAGT
plasmid_lp21	12451	IG 973	3.243 ± 1.0487 0.07024	1.425 ± 0.6451 0.41668	1.114 ± 0.4535 0.7075	1.563 ± 1.362 0.57936	AGTAAAAGTGTAGTTAGTTACTGGACTACATAAAATCATAAAATAATT
plasmid_lp21	12463	IG 974	2.187 ± 1.1354 0.001695	0.914 ± 0.5336 0.59768	1.139 ± 0.7329 0.76088	0.916 ± 0.677 0.16126	AACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC
plasmid_lp21	12476	IG 975	2.493 ± 3.1496 0.0913	1.444 ± 2.3572 0.4465	1 ± 1.2355 0.99833	1.194 ± 1.81 0.40084	GTCCACTAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12480	IG 976	2.021 ± 0.7134 0.139657	1.181 ± 0.6056 0.70658	0.607 ± 0.3089 0.02324	0.779 ± 0.1827 0.16175	TGTAGTCAGTAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12481	IG 977	1.215 ± 0.6987 0.308081	0.536 ± 0.4513 0.39396	1.04 ± 0.5429 0.78358	0.962 ± 0.3799 0.74077	TAAATCATAAAAATAATATTTTATAAAGAATAAGTAAAGGGTTAGT
plasmid_lp21	12511	IG 978	2.526 ± 1.4871 0.035583	1.732 ± 1.4757 0.25172	0.51 ± 0.2836 0.29991	0.59 ± 0.6073 0.17265	ATAAGTAAAGTGTAGTTACTGGACTACATAAAATCATAAAATAAT
plasmid_lp21	12515	IG 979	3.132 ± 1.997 0.049343	2.59 ± 2.5416 0.25404	1.342 ± 0.7162 0.51753	1.2 ± 0.6652 0.22037	CTTATTCTTATAAAATATTATTGATTATGATTGTAGTCAGTAAAC
plasmid_lp21	12543	IG 980	1.636 ± 0.2637 0.067446	1.13 ± 0.3291 0.56671	1.409 ± 0.4963 0.26546	1.816 ± 1.3396 0.40265	TGTAGTCAGTAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12553	IG 981	2.700 ± 1.3064 0.03441	2.177 ± 1.0674 0.03386	0.955 ± 0.4196 0.84831	0.954 ± 0.5774 0.92039	TAATCATAAAAATAATATTTTATAAAGAATAAGTAAAGGGTTAGT
plasmid_lp21	12568	IG 982	1.965 ± 0.7931 0.079698	1.175 ± 0.5562 0.4119	0.983 ± 0.3586 0.90525	1.125 ± 0.3996 0.33253	TAAGAATAAGTAAAGGGTTAGTTACTGGAGTGATAAATCATAAA
plasmid_lp21	12604	IG 983	2.825 ± 0.6508 0.013939	1.57 ± 0.8558 0.29379	1.147 ± 0.2461 0.08183	1 ± 0.3239 0.99957	CACTCCAGTAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12606	IG 984	1.420 ± 0.2199 0.042627	0.979 ± 0.2254 0.8749	0.992 ± 0.5829 0.98115	0.861 ± 0.1142 0.29059	TACACTCCAGTAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12607	IG 985	1.355 ± 0.9098 0.436384	0.632 ± 0.5312 0.52026	0.954 ± 0.5625 0.8788	1.043 ± 0.516 0.88721	TAAATCATAAAAATAATATTTTATAAAGAATAAGTAAAGGGTTAGT
plasmid_lp21	12631	IG 986	2.309 ± 0.9872 0.029351	1.189 ± 0.6007 0.28334	1.055 ± 0.4651 0.18328	1.112 ± 0.4793 0.27034	TAAGAATAAGTAAAGGGTTAGTTACTGGAGTGATAAATCATAAA
plasmid_lp21	12641	IG 987	2.418 ± 0.6445 0.032232	1.573 ± 0.3571 0.13921	1.493 ± 1.2119 0.5054	1.145 ± 0.258 0.42442	CTTATTCTTATAAAATATTATTGATTATCAGTAAAC
plasmid_lp21	12652	IG 988	2.668 ± 1.6717 0.064245	1.09 ± 0.5339 0.73072	1.229 ± 0.7063 0.44613	1.201 ± 0.8552 0.32386	AACCACTTTACTTATTCTTATAAAATATTATTGATTATACAC
plasmid_lp21	12667	IG 989	2.809 ± 0.6615 0.006805	1.651 ± 0.8819 0.20323	1.197 ± 0.2972 0.2611	0.989 ± 0.3393 0.94435	CACTCCAGTAAACAAACCACTTTACTTATTCTTATAAAATATT
plasmid_lp21	12669	IG 990	1.878 ± 0.8696 0.225424	1.38 ± 0.5498 0.32237	1.16 ± 0.7816 0.65555	0.81 ± 0.3166 0.49107	TACACTCCAGTAAACAAACCACTTTACTTATTCTTATAAAATATT

plasmid_lp21	12670	IG 991	1.078 ± 0.802	0.823004	0.562 ± 0.361	0.33074	0.857 ± 0.4456	0.41872	0.951 ± 0.3489	0.78299	TAAATCATAAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	12715	IG 992	2.663 ± 1.889	0.105291	1.041 ± 0.5881	0.92706	1.402 ± 0.8845	0.48729	1.177 ± 0.6717	0.1101	AACCACTTTACTTATTCTTATAAAATTTATTTATGATTATACAC
plasmid_lp21	12732	IG 993	1.692 ± 0.6263	0.224062	1.25 ± 0.3849	0.30307	1.417 ± 0.709	0.34848	1.819 ± 1.1203	0.30296	TGTAGTCCAGTAAACTAAACCACCTTTACTTATTCTTATAAAATTTAT
plasmid_lp21	12733	IG 994	1.403 ± 0.8256	0.379388	0.752 ± 0.6429	0.67872	1.06 ± 0.6624	0.87155	1.255 ± 0.5044	0.30452	TAAATCATAAAAATAAATTTATAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	12757	IG 995	1.940 ± 0.6924	0.03624	1.101 ± 0.5468	0.64269	0.94 ± 0.2975	0.54326	1.023 ± 0.3262	0.84464	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAAA
plasmid_lp21	12793	IG 996	2.556 ± 0.8115	0.003418	1.503 ± 0.805	0.12787	1.187 ± 0.4108	0.42302	0.824 ± 0.4413	0.46773	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	12796	IG 997	1.319 ± 0.9516	0.455795	0.551 ± 0.4127	0.37632	1.095 ± 0.6615	0.80997	0.964 ± 0.494	0.90652	TAAATCATAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	12820	IG 998	1.920 ± 0.677	0.051707	1.155 ± 0.4889	0.37444	0.926 ± 0.3519	0.59389	0.909 ± 0.3834	0.38285	TAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAATCATAAAA
plasmid_lp21	12830	IG 999	2.473 ± 0.9311	0.03701	1.402 ± 0.5627	0.26615	1.44 ± 1.2069	0.59379	1.422 ± 0.6203	0.08179	CTTATTCTTATAAAATTTATTTATGATTACACTCCAGTAAACT
plasmid_lp21	12841	IG 1000	2.309 ± 1.3602	0.024203	1.003 ± 0.5447	0.99045	1.014 ± 0.6184	0.96961	0.836 ± 0.4741	0.55389	AACCACTTTACTTATTCTTATAAAATTTATTTATGATTATACAC
plasmid_lp21	12856	IG 1001	3.040 ± 0.3829	0.005099	1.564 ± 0.865	0.34215	1.291 ± 0.177	0.10732	1.033 ± 0.4312	0.89563	CACTCCAGTAAACTAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	12859	IG 1002	1.316 ± 0.7020	0.181121	0.759 ± 0.5749	0.66167	1.076 ± 0.664	0.80958	1.059 ± 0.5772	0.73694	TAAATCATAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	12870	IG 1003	2.614 ± 1.6812	0.168408	1.497 ± 0.6129	0.13519	1.114 ± 0.5602	0.52082	1.264 ± 0.4323	0.23053	AATAATATTTATAAGAATAAGTAAAAGTGGTTAGTTGGAGTGAT
plasmid_lp21	12892	IG 1004	0.518 ± 0.3201	0.314765	0.538 ± 0.3855	0.37373	0.934 ± 0.4428	0.62787	0.968 ± 0.5562	0.50706	AGTAAAAGTGGTTAGTTAGTTGGAGTGATAATCATAAAAATAAATTT
plasmid_lp21	12904	IG 1005	3.262 ± 2.0563	0.000224	1.447 ± 0.881	0.2812	1.427 ± 0.9603	0.35971	1.444 ± 0.2092	0.01117	AACCACTTTACTTATTCTTATAAAATTTATTTATGATTATACAC
plasmid_lp21	12917	IG 1006	1.609 ± 0.3487	0.020931	0.946 ± 0.1763	0.39319	1.045 ± 0.2615	0.73987	1.049 ± 0.3559	0.76377	CACTCCAAAACAAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	12919	IG 1007	1.896 ± 0.6791	0.021159	1.274 ± 0.6269	0.22052	1.228 ± 0.4094	0.32749	1.065 ± 0.498	0.74936	TACACTCCAAAACAAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	12920	IG 1008	1.132 ± 0.7649	0.47479	0.658 ± 0.5494	0.57626	0.968 ± 0.5932	0.80742	1.12 ± 0.6497	0.62891	TAAATCATAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	12953	IG 1009	3.948 ± 2.0778	0.061868	2.137 ± 1.3792	0.29576	1.811 ± 1.3628	0.3915	2.04 ± 1.9618	0.48803	AGTAAAAGTGGTTAGTTAGTTAGGGACTACATAATCATAAAAATAAATTT
plasmid_lp21	12965	IG 1010	3.129 ± 1.7265	0.015935	1.228 ± 0.5775	0.46247	1.351 ± 0.474	0.40828	1.284 ± 0.8496	0.14454	AACCACTTTACTTATTCTTATAAAATTTATTTATGATTATACAC
plasmid_lp21	12978	IG 1011	2.579 ± 3.5031	0.12824	1.509 ± 2.4159	0.36335	0.969 ± 1.4019	0.86932	1.002 ± 1.4978	0.95346	GTCCACTAAACTAAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	12982	IG 1012	2.762 ± 1.1249	0.074484	1.685 ± 0.9774	0.3483	0.889 ± 0.3022	0.65587	1.351 ± 0.456	0.3618	TGTAGTCCACTAAACTAAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	12983	IG 1013	1.312 ± 0.8321	0.313117	0.694 ± 0.4604	0.54871	1.135 ± 0.6231	0.62577	1.15 ± 0.5539	0.48356	TAAATCATAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	13017	IG 1014	4.068 ± 2.3734	0.033188	3.119 ± 2.9741	0.22899	1.832 ± 1.2143	0.38232	1.575 ± 0.9593	0.06169	CTTATTCTTATAAAATTTATTTATGATTATGTAGTCCACTAAACT
plasmid_lp21	13041	IG 1015	3.050 ± 3.9858	0.116977	1.691 ± 2.6143	0.30596	1.13 ± 1.5214	0.60004	1.112 ± 1.6811	0.34379	GTCCACTAAACTAAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	13045	IG 1016	3.183 ± 0.7468	0.039372	1.983 ± 0.9563	0.23926	1.053 ± 0.3168	0.79443	1.647 ± 0.2162	0.00833	TGTAGTCCACTAAACTAAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	13055	IG 1017	4.270 ± 0.8324	0.00952	1.946 ± 0.3335	0.04018	1.165 ± 0.3158	0.26365	1.429 ± 0.283	0.07617	TAAATAAATTTTATAAGAATAAGTAAAAGTGGTTAGTTGGAGTGAT
plasmid_lp21	13057	IG 1018	2.875 ± 1.5041	0.146999	1.617 ± 0.6597	0.23242	1.071 ± 0.3879	0.75076	1.051 ± 0.3312	0.86196	AATAATTTTATAAGAATAAGTAAAAGTGGTTAGTTGGAGTGAT
plasmid_lp21	13058	IG 1019	1.680 ± 0.71	0.109268	0.735 ± 0.2887	0.444	1.152 ± 0.7109	0.69407	1.361 ± 0.6494	0.09128	TTTATATGTTTGTAGTCCACTAAACTAAACCACTTTACTTATTCTT
plasmid_lp21	13069	IG 1020	3.175 ± 2.0187	0.15957	1.26 ± 0.5344	0.51224	1.7 ± 1.204	0.31902	1.311 ± 0.4993	0.38105	TAAATATTTTATGTTATGTTAGTTAGTCCACTAAACCACTTT
plasmid_lp21	13079	IG 1021	0.539 ± 0.3693	0.36839	0.539 ± 0.3835	0.3795	0.969 ± 0.4478	0.81921	1.018 ± 0.5396	0.62815	AGTAAAAGTGGTTAGTTGGAGTGATAATCATAAAAATAAATTTTT
plasmid_lp21	13104	IG 1022	2.281 ± 0.7112	0.013884	1.399 ± 0.6361	0.22939	1.144 ± 0.3994	0.13183	1.3 ± 0.5682	0.34918	CACTCCAAAACAAACCACTTTACTTATTCTTATAAAATTTATTTAT
plasmid_lp21	13106	IG 1023	1.815 ± 0.7428	0.028217	1.305 ± 0.6701	0.1465	1.182 ± 0.4631	0.47025	0.998 ± 0.4816	0.99114	TACACTCCAAAACAAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	13107	IG 1024	1.288 ± 0.6612	0.451564	0.499 ± 0.3409	0.17917	0.899 ± 0.4166	0.73798	0.874 ± 0.2614	0.46418	TAAATCATAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	13140	IG 1025	3.115 ± 1.2179	0.050286	1.207 ± 0.8224	0.75829	1.03 ± 0.854	0.94448	1.53 ± 1.311	0.60785	AGTAAAAGTGGTTAGTTAGGGACTACATAATCATAAAAATAAATTT
plasmid_lp21	13152	IG 1026	2.742 ± 1.8058	0.035603	1.365 ± 0.742	0.25337	1.099 ± 0.7222	0.75161	1.3 ± 0.7998	0.07517	AACCACTTTACTTATTCTTATAAAATTTATTTATGATTATACAC
plasmid_lp21	13165	IG 1027	2.704 ± 3.1141	0.163193	1.624 ± 2.4695	0.47943	1.178 ± 1.3357	0.52226	1.241 ± 1.6854	0.50346	GTCCACTAAACCACTTTACTTATTCTTATAAAATTTATTTAT
plasmid_lp21	13169	IG 1028	2.474 ± 0.6154	0.045465	1.467 ± 0.7888	0.45301	0.891 ± 0.1336	0.30182	1.203 ± 0.2403	0.1523	TGTAGTCCACTAAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	13170	IG 1029	1.343 ± 0.9495	0.242124	0.6 ± 0.5285	0.53658	1.112 ± 0.887	0.76403	0.966 ± 0.5537	0.88737	TAAATCATAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	13203	IG 1030	3.449 ± 0.9791	0.032202	1.584 ± 1.0212	0.47845	1.34 ± 0.6962	0.48905	1.439 ± 1.2407	0.64282	AGTAAAAGTGGTTAGTTAGGGACTACATAATCATAAAAATAAATTT
plasmid_lp21	13204	IG 1031	4.693 ± 3.2515	0.044694	3.897 ± 3.9422	0.20827	1.987 ± 1.1388	0.06911	1.959 ± 1.3793	0.03116	CTTATTCTTATAAAATTTATTTATGATTATGTAGTCCACTAAAC
plasmid_lp21	13228	IG 1032	3.473 ± 4.116	0.158899	1.75 ± 2.7705	0.46509	1.232 ± 1.5201	0.30249	1.248 ± 1.7457	0.49584	GTCCACTAAACCACTTTACTTATTCTTATAAAATTTATTTAT
plasmid_lp21	13232	IG 1033	2.955 ± 0.9876	0.020887	2.087 ± 1.2944	0.3133	1.183 ± 0.3943	0.37367	1.123 ± 0.3822	0.53417	TGTAGTCCACTAAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	13295	IG 1034	2.503 ± 0.9063	0.014644	1.301 ± 0.4893	0.0698	1.061 ± 0.4387	0.61347	1.042 ± 0.4989	0.90733	TGTAGTCCACTAAACCACTTTACTTATTCTTATAAAATTTATTT
plasmid_lp21	13319	IG 1035	3.490 ± 2.3351	0.171798	1.675 ± 0.9383	0.38547	1.868 ± 1.4499	0.24098	1.41 ± 0.8492	0.56256	TAAATTTATGATTATGTAGTCCACTAAACCACTTT
plasmid_lp21	13329	IG 1036	0.524 ± 0.3284	0.330421	0.542 ± 0.3876	0.38101	0.954 ± 0.4279	0.79637	0.993 ± 0.5702	0.87972	AGTAAAAGTGGTTAGTTGGAGTGATAATCATAAAAATAAATTTAT
plasmid_lp21	13341	IG 1037	3.796 ± 2.083	0.103665	1.613 ± 1.1678	0.35959	1.125 ± 0.5534	0.68085	1.347 ± 0.6407	0.19596	AACCACTTTACTTATTCTTATAAAATTTATGATTATGTAGTAG
plasmid_lp21	13354	IG 1038	2.093 ± 0.8585	0.127531	1.136 ± 0.4077	0.61275	1.043 ± 0.2612	0.71469	1.18 ± 0.6124	0.69541	CACTCCAAAACCACTTTACTTATTCTTATAAAATTTATTTAT
plasmid_lp21	13356	IG 1039	2.925 ± 1.6723	0.005738	1.771 ± 1.1869	0.04413	1.644 ± 0.9939	0.08551	1.318 ± 0.8436	0.43274	TACACTCCAAAACCACTTTACTTATTCTTATAAAATTTATTTAT

plasmid_lp21	13357	IG 1040	1.015 ± 0.8055 0.943085	0.555 ± 0.3958 0.37635	1.1 ± 0.5892 0.67604	0.994 ± 0.3922 0.97824	TAAATCATAAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	13390	IG 1041	3.691 ± 0.7444 0.024867	1.85 ± 0.8284 0.21672	1.335 ± 0.8106 0.57654	1.987 ± 1.2928 0.30586	AGTAAAAGTGGTTAGTTAGTGGACTACATAAATCATAAAATAAATATT
plasmid_lp21	13402	IG 1042	2.511 ± 1.7516 4.73E-05	1.191 ± 0.8218 0.55479	1.028 ± 0.7568 0.9595	1.008 ± 0.7737 0.97443	AACCACTTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	13415	IG 1043	2.831 ± 3.3227 0.102842	1.764 ± 2.7074 0.393	1.066 ± 1.3129 0.72474	1.077 ± 1.6164 0.73692	GTCCACTAAACTAAACCACCTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	13419	IG 1044	2.594 ± 0.9375 0.083988	1.814 ± 0.9687 0.30735	0.875 ± 0.2345 0.11593	1.423 ± 0.3209 0.10566	TGTAGTCCACTAAACTAAACCACCTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	13453	IG 1045	3.531 ± 0.9406 0.042305	1.735 ± 1.0006 0.32729	1.351 ± 0.8235 0.53727	1.581 ± 1.2552 0.5043	AGTAAAAGTGGTTAGTTAGTGGACTACATAAATCATAAAATAAATATT
plasmid_lp21	13465	IG 1046	2.916 ± 1.608 0.144685	1.534 ± 0.9071 0.34751	1.507 ± 1.7338 0.63309	1.423 ± 0.8141 0.40259	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATGTAG
plasmid_lp21	13482	IG 1047	2.601 ± 1.0302 0.015761	1.353 ± 0.6288 0.11635	1.036 ± 0.4342 0.83708	1.072 ± 0.5602 0.84875	TGTAGTCCACTAAACTAAACCACCTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	13543	IG 1048	3.719 ± 1.4643 0.054744	1.775 ± 1.2867 0.40711	1.445 ± 0.5166 0.03329	0.955 ± 0.4438 0.91528	CACTCCAGTAAACTAAACCACCTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	13546	IG 1049	1.219 ± 0.8105 0.557288	0.592 ± 0.4786 0.47437	1.142 ± 0.6722 0.6982	1.061 ± 0.5178 0.81424	TAAATCATAAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	13579	IG 1050	2.045 ± 0.9747 0.199447	0.682 ± 0.3436 0.45175	0.501 ± 0.3678 0.32638	1.059 ± 1.3864 0.95456	AGTAAAAGTGGTTAGTTAGTGGACTACATAAATCATAAAATAAATAGATATT
plasmid_lp21	13591	IG 1051	2.272 ± 1.0511 0.056313	1.059 ± 0.3436 0.56555	1.056 ± 0.5492 0.80474	1.181 ± 0.5575 0.19046	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	13604	IG 1052	2.491 ± 2.8172 0.102558	1.614 ± 2.3233 0.38993	0.965 ± 1.1866 0.90989	0.945 ± 1.4099 0.7539	GTCCACTAAACTAAACCACCTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	13608	IG 1053	2.746 ± 0.9502 0.056664	1.743 ± 0.7639 0.23367	0.847 ± 0.239 0.38715	1.293 ± 0.3833 0.35969	TGTAGTCCACTAAACTAAACCACCTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	13633	IG 1054	1.985 ± 0.6903 0.062752	1.299 ± 0.62 0.32372	1.026 ± 0.2755 0.54896	0.994 ± 0.305 0.8784	TAAAGAATAAGTAAAAGTGGTTAGTTACTGGAGTGATAAATCATAAAA
plasmid_lp21	13669	IG 1055	3.343 ± 0.9118 0.006837	1.526 ± 0.884 0.28705	1.425 ± 0.6277 0.08607	1.173 ± 0.5021 0.62089	CACTCCAGTAAACTAAACCACTTTACTTATTCTTATAAAATATCTATT
plasmid_lp21	13765	IG 1056	2.264 ± 1.3284 0.078351	1.818 ± 1.4079 0.23809	0.508 ± 0.241 0.12545	0.875 ± 0.75 0.65973	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAAATCATAAAAAATAAATATT
plasmid_lp21	13831	IG 1057	2.895 ± 1.1092 0.081277	1.447 ± 0.0486 0.59667	1.079 ± 0.758 0.86228	1.299 ± 0.7483 0.63386	AGTAAAAGTGGTTAGTTAGTGGACTACATAAATCATAAAAAATAAATATT
plasmid_lp21	13860	IG 1058	3.013 ± 1.1586 0.024078	1.711 ± 0.7588 0.1541	1.149 ± 0.3927 0.49824	1.305 ± 0.4707 0.41321	TGTAGTCCACTAAACTAAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	13861	IG 1059	1.156 ± 0.6435 0.0708656	0.54 ± 0.3551 0.20066	1.106 ± 0.5462 0.76667	1.072 ± 0.3818 0.74906	TAAATCATAAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	13872	IG 1060	3.095 ± 1.6723 0.118597	1.995 ± 0.6224 0.03846	1.313 ± 0.6556 0.31365	1.395 ± 0.5634 0.27825	AATAAAATTTTATAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTTAT
plasmid_lp21	13894	IG 1061	0.512 ± 0.3174 0.299285	0.514 ± 0.3577 0.3305	0.941 ± 0.4089 0.56526	1.026 ± 0.5771 0.77351	AGTAAAAGTGGTTAGTTGGAGTGATAAATCATAAAAAATAAATATT
plasmid_lp21	13919	IG 1062	1.711 ± 0.343 0.043465	0.985 ± 0.1903 0.89433	1.055 ± 0.2163 0.5975	1.121 ± 0.313 0.55502	CACTCCAAAATAACCAACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	13921	IG 1063	1.829 ± 0.7436 0.023323	1.369 ± 0.7098 0.14087	1.232 ± 0.4788 0.40898	1.06 ± 0.4906 0.7067	TACACTCCAAAATAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	13922	IG 1064	1.199 ± 0.7651 0.608008	0.598 ± 0.5059 0.4824	1.08 ± 0.6302 0.84025	1.009 ± 0.4636 0.97217	TAAATCATAAAAATAAATTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	13952	IG 1065	2.522 ± 1.3128 0.003362	1.953 ± 1.2403 0.04691	0.792 ± 0.4042 0.53543	0.755 ± 0.6546 0.58728	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAAATCATATAAATAGAT
plasmid_lp21	13967	IG 1066	2.455 ± 1.4602 0.011177	1.061 ± 0.6007 0.86672	1.199 ± 0.7046 0.66485	1.057 ± 0.6607 0.57937	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	13984	IG 1067	1.989 ± 0.7217 0.132718	1.445 ± 0.4843 0.19557	1.734 ± 0.8806 0.23362	1.842 ± 0.8697 0.18907	TGTAGTCCAGTAAACTAAACCACTTTACTTATTCTTATAAAATATTAT
plasmid_lp21	14018	IG 1068	4.028 ± 1.1615 0.023682	2.198 ± 1.3152 0.27505	1.365 ± 1.0182 0.52761	1.842 ± 1.413 0.43634	AGTAAAAGTGGTTAGTTAGTGGACTACATAAATCATAAAATAAATATT
plasmid_lp21	14047	IG 1069	2.500 ± 0.7938 0.046913	1.353 ± 0.7985 0.55846	0.787 ± 0.22 0.38995	1.1 ± 0.3189 0.65439	TGTAGTCCACTAAACTAAACCACTTTACTTATTCTTATAAAATATTCTAT
plasmid_lp21	14048	IG 1070	1.238 ± 0.9179 0.499085	0.656 ± 0.4688 0.51317	1.122 ± 0.6475 0.65146	1.098 ± 0.4209 0.6103	TAAATCATAAAAATAAATATTCTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	14059	IG 1071	2.664 ± 1.3201 0.0109475	1.682 ± 0.5635 0.02666	1.158 ± 0.4851 0.40663	1.192 ± 0.4684 0.59112	AATAAAATTTTATAAGAATAAGTAAAAGTGGTTAGTTGGAGTGTT
plasmid_lp21	14081	IG 1072	0.526 ± 0.3556 0.351569	0.521 ± 0.3829 0.36572	0.948 ± 0.4609 0.72373	0.984 ± 0.5784 0.71259	AGTAAAAGTGGTTAGTTGGAGTGATAAATCATAAAAAATAAATATT
plasmid_lp21	14082	IG 1073	3.462 ± 2.1803 0.035082	2.188 ± 2.4932 0.35663	1.654 ± 0.9918 0.24371	1.408 ± 0.9777 0.05272	CTTATTCTTATAAAATATTATTTATGATTATGTAGTCCACTAAACT
plasmid_lp21	14106	IG 1074	1.709 ± 0.3488 0.016814	1.032 ± 0.2307 0.73854	1.073 ± 0.2523 0.42633	1.141 ± 0.3402 0.45096	CACTCCAAAATAACCAACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	14108	IG 1075	1.850 ± 0.7017 0.013123	1.398 ± 0.7336 0.16357	1.257 ± 0.4735 0.22895	1.125 ± 0.5041 0.47463	TACACTCCAAAATAACCACTTTACTTATTCTTATAAAATATTATTT
plasmid_lp21	14109	IG 1076	1.171 ± 0.6358 0.534559	0.618 ± 0.4565 0.42908	1.098 ± 0.5331 0.7432	1.092 ± 0.5193 0.77114	TAAATCATAAAAATAAATATTCTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	14139	IG 1077	1.887 ± 0.5976 0.002269	1.508 ± 0.9727 0.34767	0.578 ± 0.2537 0.2645	0.62 ± 0.4356 0.32638	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAAATCATATA
plasmid_lp21	14154	IG 1078	2.310 ± 1.3876 0.070785	0.951 ± 0.4016 0.86524	1.048 ± 0.4555 0.88051	0.899 ± 0.5672 0.63742	AACCACTTTACTTATTCTTATAAAATATTATTTATGATTATACAC
plasmid_lp21	14171	IG 1079	1.699 ± 0.7723 0.241085	1.185 ± 0.9295 0.39304	1.313 ± 0.6867 0.51497	1.474 ± 0.9257 0.43491	TGTAGTCCAGTAAACTAAACCACCTTTACTTATTCTTATAAAATATT
plasmid_lp21	14205	IG 1080	3.274 ± 0.8825 0.041278	1.709 ± 1.0437 0.38219	1.343 ± 0.7687 0.48821	1.553 ± 1.1553 0.52877	AGTAAAAGTGGTTAGTTAGTGGACTACATAAATCATAAAAAATAAATATT
plasmid_lp21	14234	IG 1081	2.777 ± 0.7045 0.007604	1.775 ± 0.8586 0.23014	0.999 ± 0.2287 0.99531	1.182 ± 0.3284 0.49311	TGTAGTCCACTAAACTAAACCACTTTACTTATTCTTATAAAATATTCTAT
plasmid_lp21	14235	IG 1082	1.149 ± 0.5814 0.642251	0.598 ± 0.3913 0.31595	1.057 ± 0.4876 0.84975	0.983 ± 0.4195 0.94917	TAAATCATAAAAATAAATATTCTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	14269	IG 1083	4.194 ± 2.5134 0.030085	2.786 ± 2.7197 0.23945	1.819 ± 0.9926 0.23449	1.672 ± 1.0581 0.02639	CTTATTCTTATAAAATATTATTTATGATTATGTAGTCCACTAAACT
plasmid_lp21	14297	IG 1084	1.747 ± 0.9627 0.135356	1.331 ± 0.5694 0.19452	1.416 ± 0.8993 0.43561	1.919 ± 1.3579 0.18667	TGTAGTCCAGTAAACTAAACCACCTTTACTTATTCTTATAAAATATT
plasmid_lp21	14331	IG 1085	3.255 ± 0.811 0.036452	1.614 ± 0.6384 0.22025	1.493 ± 0.9136 0.45605	1.526 ± 1.2203 0.51952	AGTAAAAGTGGTTAGTTAGTGGACTACATAAATCATAAAAAATAAATATT
plasmid_lp21	14360	IG 1086	3.257 ± 0.9697 0.04407	2.053 ± 0.6421 0.08151	1.237 ± 0.2076 0.25964	1.426 ± 0.424 0.27406	TGTAGTCCACTAAACTAAACCACCTTTACTTATTCTTATAAAATATTCTAT
plasmid_lp21	14424	IG 1087	1.359 ± 0.6012 0.199218	0.621 ± 0.4871 0.464	1.158 ± 0.5924 0.64194	1.061 ± 0.422 0.77487	TAAATCATAAAAATAAATATTCTTATAAGAATAAGTAAAAGTGGTTAGTT
plasmid_lp21	14454	IG 1088	2.142 ± 1.1461 0.019305	2.265 ± 1.829 0.22129	0.574 ± 0.3264 0.32751	0.793 ± 0.6092 0.62823	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAAATCATATAAATAGAT

plasmid_lp21	14486	IG 1089	1.633 ± 0.9219 0.311729	1.065 ± 0.5112 0.44951	1.284 ± 0.763 0.49071	1.36 ± 0.701 0.16587	TGTAGTCCAGTAAACTAACCACTTTACTTATTCTTATAAAAATTTAT
plasmid_lp21	14498	IG 1090	1.808 ± 2.4752 0.632432	2.065 ± 1.8215 0.42978	0.597 ± 0.2948 0.18216	1.391 ± 0.6351 0.46132	AATAGATATTATAAAGAATAAGTAAAAGTGGTTAGTTTGGAGTGTAT
plasmid_lp21	14520	IG 1091	0.520 ± 0.3314 0.316184	0.52 ± 0.3365 0.31974	0.986 ± 0.4207 0.91695	1.013 ± 0.5653 0.84628	AGTAAAAGTGGTTAGTTTGGAGTGTATAATCATAAAAATAAATTTT
plasmid_lp21	14545	IG 1092	1.964 ± 0.5169 0.03481	1.109 ± 0.235 0.27363	1.137 ± 0.311 0.25749	1.158 ± 0.312 0.36106	CACTCCAAAACAAACCACTTTACTTATTCTTATAAAAATCTATT
plasmid_lp21	14547	IG 1093	1.839 ± 0.95 0.071128	1.189 ± 0.6902 0.1087	1.127 ± 0.5007 0.55266	0.968 ± 0.5535 0.83505	TACACTCCAAAACAAACCACTTTACTTATTCTTATAAAAATCTATT
plasmid_lp21	14578	IG 1094	3.142 ± 1.7752 0.068781	1.989 ± 1.5464 0.23225	0.975 ± 0.4796 0.9065	1.196 ± 0.6343 0.09	ATAAGTAAAAGTGGTTAGTTACTGGACTACATAATATGACATAATTAA
plasmid_lp21	14593	IG 1095	4.512 ± 2.7672 0.091998	1.598 ± 0.8707 0.10125	1.754 ± 1.3311 0.28341	1.976 ± 1.1957 0.162	AACCACCTTTACTTATTATAAAAATTTTATGATTACAC
plasmid_lp21	14644	IG 1096	6.934 ± 5.8395 0.217531	1.596 ± 0.4712 0.0318	1.606 ± 1.0636 0.43941	1.732 ± 0.9163 0.24041	TATATCCTCACACATACTTAATTATGTCATATTATGAGTCCAGAACTA
plasmid_lp21	15138	BB_U06	3.602 ± 3.7185 0.195312	1.034 ± 1.4215 0.97876	0.784 ± 0.8094 0.75487	2.138 ± 2.8954 0.26734	TCTGCTTACAACATTATCATATAATTCTTATCCCTCATAAAATTCTAATA
plasmid_lp21	15341	IG 1097	2.682 ± 1.9106 0.085289	1.657 ± 1.7229 0.37715	0.957 ± 0.5154 0.91437	1.124 ± 0.8996 0.54085	AAGACTATGATCGAAATACTAAACCATAAAAAGAACCGAAATTAAAG
plasmid_lp21	16004	BB_U08	3.161 ± 2.2506 0.078341	1.468 ± 1.3268 0.31417	1.119 ± 0.7568 0.64113	1.304 ± 1.305 0.49088	TTTCTACAAACACTGATTATGTTTTCCGAATTATAAGTTTTAT
plasmid_lp21	16145	IG 1098	1.945 ± 1.0689 0.243036	1.455 ± 0.691 0.39935	0.973 ± 0.4148 0.92903	1.115 ± 0.4918 0.75898	TATTACTAATAGGATAATATTACACAAATTAAATAAATTAGCTAAT
plasmid_lp21	16146	IG 1099	3.452 ± 1.6512 0.09494	2.048 ± 1.7308 0.35029	1.108 ± 0.2972 0.23821	1.149 ± 0.4067 0.22194	TATATATCTAGATTCTTTAAGAATTGGTTAGGCAATTAGAAG
plasmid_lp21	16191	IG 1100	3.393 ± 3.5929 0.280637	1.487 ± 2.3339 0.71187	1.494 ± 0.8857 0.42194	0.817 ± 0.8407 0.75368	ATATTGCTAACAAACAAATTCTTAAAGAAAATCTAGATATATATT
plasmid_lp21	16312	BB_U09	0.816 ± 0.3336 0.552261	1.897 ± 0.9352 0.23934	1.441 ± 0.8475 0.16769	1.113 ± 0.4917 0.77599	TAACATACAGTTCTATTACACATAAAATCTGAACTCTAAATA
plasmid_lp21	16356	BB_U09	3.254 ± 1.6852 0.089815	1.766 ± 1.7494 0.55176	1.363 ± 0.7849 0.10779	0.691 ± 0.4791 0.53245	GGAGTTCACAGATTATGTTAGTAAATAGGAACCTGGATGTATACCTA
plasmid_lp21	16405	BB_U09	0.398 ± 0.2592 0.059089	1.394 ± 1.0561 0.64412	0.405 ± 0.3454 0.00805	0.444 ± 0.4998 0.28633	GTTTCGGTTGTTATTCTGACCCCGAAGAAATACAACTCAGCATC
plasmid_lp21	16602	IG 1101	2.618 ± 2.5347 0.222421	1.601 ± 1.3155 0.22046	0.689 ± 0.5569 0.40413	0.969 ± 0.9876 0.94276	GTTGTATTCTTATTGAACAACTAAAAAGAAAACAAATTGAAATTCT
plasmid_lp21	16719	BB_U10	4.333 ± 6.0373 0.17872	1.443 ± 1.618 0.58545	1.103 ± 1.5296 0.61471	1.592 ± 1.7713 0.27423	TATGCCAAATATTGTTGTTATTATTTTGGTTATTCAAATATT
plasmid_lp21	16720	BB_U10	2.860 ± 2.048 0.14962	1.737 ± 0.8001 0.02621	1.156 ± 0.6028 0.43315	1.369 ± 0.5849 0.01559	TATTATCTGAATTACTAGAATAAATAGAAAACATGATCTAAAT
plasmid_lp21	16868	IG 1102	0.727 ± 0.7854 0.489914	0.334 ± 0.4867 0.03513	1.289 ± 1.1083 0.63849	0.686 ± 0.5662 0.20825	TGGAATAATTCTGATTCTGAACTCAATTCTGCACTAATCAAATAAAC
plasmid_lp21	17219	BB_U11	3.208 ± 1.6741 0.070227	1.592 ± 0.7476 0.26533	1.207 ± 0.5843 0.43049	1.025 ± 0.4839 0.91544	GATACAGTGGCAATAAGAACATACCAAAATAAAACCGCATTAAATT
plasmid_lp21	17574	BB_U11	5.771 ± 5.1582 0.130802	2.428 ± 2.548 0.33781	1.77 ± 1.2953 0.2538	1.71 ± 1.7646 0.44085	TAAGAAAACATTTTTAAAGTCTATTGTTCCCTTGCATAATTACT
plasmid_lp21	17640	BB_U11	3.077 ± 3.6687 0.386232	0.461 ± 0.8487 0.06067	0.822 ± 0.9053 0.73678	0.091 ± 0.1687 0.09894	TTCTGTTTAAATATTCTTATGTTATCCCCGTTTAAATGATGGACA
plasmid_lp21	17714	BB_U11	3.684 ± 2.8674 0.197024	1.787 ± 1.5138 0.36895	1.277 ± 0.6643 0.2833	1.264 ± 0.7939 0.4177	TAATATTTTTATCCATAAAAACACTAAAAAATTTAAAGTGT
plasmid_lp21	17717	BB_U11	0.785 ± 0.412 0.222236	0.439 ± 0.1926 0.15411	0.295 ± 0.1718 0.15245	0.551 ± 0.411 0.34212	TTATTCGATTCTTAATAGAATATGCAGAAAATCTTATAAGAGCTAGTA
plasmid_lp21	17919	BB_U12	1.903 ± 1.9165 0.467627	3.017 ± 3.9348 0.30347	0.655 ± 0.5987 0.4082	0.406 ± 0.531 0.33094	TGTTCCCATATATAATGAAAACATTTCTGAGTACTAAAATTAAATGCC
plasmid_lp21	18212	BB_U12	1.476 ± 0.2854 0.123679	1.221 ± 0.2916 0.38449	1.061 ± 0.3052 0.72832	0.944 ± 0.1697 0.69524	TTTATGTTGATGATGTTGTTATTCTTGTATGTTGCTGTTGATAA
plasmid_lp21	18444	IG 1103	2.632 ± 2.5585 0.307889	2.355 ± 2.6152 0.4148	0.928 ± 0.4687 0.7547	1.208 ± 0.9249 0.68036	TTATCTATTGTAATACAGATTCACTGGTTGTTGAGTAAAG
plasmid_lp25	835	BB_E02	2.284 ± 1.0511 0.081724	1.984 ± 1.3322 0.23589	0.856 ± 0.3392 0.02775	0.912 ± 0.3171 0.29937	AATGATGAGAAAACACCAATATCTTATAAAAATTATTATCT
plasmid_lp25	957	BB_E02	3.051 ± 1.4666 0.00448	2.31 ± 1.8379 0.19837	1.076 ± 0.4738 0.72791	1.024 ± 0.5418 0.76219	AGAGTACCAATATCAACCCGAAAGAGTATTATAGGCAATTGCAAGCA
plasmid_lp25	1487	BB_E02	0.770 ± 0.7307 0.616776	4.256 ± 4.7032 0.25819	0.742 ± 0.6107 0.68257	0.616 ± 0.4807 0.51147	GTTAACGTTATGCGAGCAAATATGTTCTAGTATTCTAGAACTAGA
plasmid_lp25	1507	BB_E02	1.753 ± 0.9427 0.284113	1.475 ± 1.0599 0.57723	0.957 ± 0.9193 0.95715	0.782 ± 0.4894 0.67183	TTTGCTCGTATAACCTAACTATATTCAATTGAAAACAAAAAGA
plasmid_lp25	1928	BB_E02	1.327 ± 0.4891 0.04748	0.959 ± 0.5236 0.8021	0.101 ± 0.178 0.02258	0.679 ± 0.8327 0.65789	GCTACTTAATTCTAATTCTTCTTCTACTAGTTCAGTAAAG
plasmid_lp25	3901	BB_E02	1.894 ± 1.4544 0.176353	2.457 ± 1.9343 0.0996	1.037 ± 0.7598 0.93997	1.363 ± 1.168 0.24713	CTCTAGACTCCACTCTTCTATTGACCGGCTTTGTTACTGAAT
plasmid_lp25	4450	IG 1104	3.093 ± 0.7706 0.014484	1.848 ± 1.3627 0.43042	0.889 ± 0.5052 0.55791	1.208 ± 0.5139 0.6418	AGGCTTCCGGAATACTGTCTAAATAGTAAAGTAAATTTTCTTATAAA
plasmid_lp25	4486	IG 1105	2.279 ± 1.3142 0.064929	1.362 ± 0.732 0.10727	0.894 ± 0.5022 0.59469	0.861 ± 0.6252 0.69595	GAGATGATTCTATTGATCATACAAAAGTATTCAAAACAAACAAAT
plasmid_lp25	4683	IG 1106	1.235 ± 0.9656 0.460181	0.984 ± 1.0364 0.9608	0.98 ± 0.6901 0.93503	1.068 ± 0.5961 0.83553	ATTAACTTACAAATAATTAATCAAAATTAAATAAAACAAAT
plasmid_lp25	4909	IG 1107	2.650 ± 1.6352 0.021966	1.739 ± 1.4412 0.25497	1.075 ± 0.6476 0.89247	1.408 ± 0.7247 0.29082	CTCACTGGCAACTATGTTCAATTCTCCTAAATGGCTATAAAAGGA
plasmid_lp25	5003	IG 1108	1.603 ± 0.8135 0.105377	1.306 ± 0.4122 0.16199	0.86 ± 0.3208 0.54004	1.109 ± 0.5483 0.54578	GATATGGAAAAGTGCATCGCAGCTTACATGCCTATAATTCAATATT
plasmid_lp25	5011	IG 1109	2.483 ± 1.6755 0.179095	3.492 ± 3.3406 0.30756	1.401 ± 0.8205 0.43806	1.265 ± 1.0074 0.75153	ATTGTTCTTCAATTCTCAAAATATTAGTATATTGATTCTTATAAA
plasmid_lp25	5049	IG 1110	2.479 ± 1.9367 0.221657	2.342 ± 2.8386 0.4415	0.901 ± 0.5713 0.6904	1.096 ± 0.5556 0.62075	TTGATTCTCATATAATAGATCAGTCTTCCAACATTAAACCTTAA
plasmid_lp25	5155	IG 1111	2.548 ± 2.0206 0.225707	1.738 ± 1.4676 0.35617	0.691 ± 0.4718 0.58324	1.286 ± 0.7679 0.49861	TCAAATAACATTGCAATAAAGGCTTCTAAATCAAGATAGGCAGGACAAT
plasmid_lp25	5223	IG 1112	2.227 ± 1.71 0.116546	0.803 ± 0.5206 0.35302	0.299 ± 0.1686 0.15373	1.24 ± 0.8404 0.57422	CAAAGCTAAAATTATCTAAAAGCAATTCTTACATACATGTCAGAT
plasmid_lp25	5728	BB_E05	2.139 ± 1.9059 0.056922	1.382 ± 1.2125 0.53476	0.696 ± 0.6882 0.44727	0.773 ± 0.7309 0.74701	TGGTTGTTAGCCGGATGTTAAAGTTTGTAGATTTAAATATCATT
plasmid_lp25	6031	IG 1113	2.071 ± 1.1669 0.050691	1.802 ± 1.4979 0.27778	0.792 ± 0.4656 0.03439	1.099 ± 0.6569 0.31011	AGAAGAGTTAAAAGTGTAAATTACAAACAGCTAAAATTGTTGAT
plasmid_lp25	6081	IG 1114	3.040 ± 2.0564 0.174787	1.236 ± 0.5903 0.28648	0.985 ± 0.4291 0.96132	1.058 ± 0.5386 0.82281	AATCTTAAAGTCTAAATCAACTGAAATTACGATTATTGTTAGT
plasmid_lp25	6098	IG 1115	1.926 ± 1.4359 0.133272	1.582 ± 1.344 0.26677	0.954 ± 0.7109 0.49261	1.152 ± 0.0005 0.55816	AATCTAATACTGAATATTAGTATTCTATATAATT
plasmid_lp25	6107	IG 1116	1.470 ± 1.6804 0.563455	1.562 ± 1.8689 0.63418	0.837 ± 1.0586 0.51711	0.603 ± 0.7794 0.0494	CTGAATATTACGATTATTGTTATCATATAATTAAAAAAATA

plasmid_lp25	6139	IG 1117	2.799 ± 1.1666 0.042014	2.14 ± 1.0798 0.22413	0.758 ± 0.5823 0.50083	0.654 ± 0.6645 0.58776	TAATTTAAAAAAATATTCAACCTTATTAACTTCTTATTAA
plasmid_lp25	6736	IG 1118	2.750 ± 2.0393 0.118976	2.451 ± 2.7558 0.25359	0.951 ± 0.862 0.88126	1.038 ± 0.7772 0.93112	TATAAATTATTTACAATATTCTAACAAATTCTAAAAGTTAACAGGTC
plasmid_lp25	6913	BB_E09	2.788 ± 2.3058 0.211368	2.834 ± 2.5907 0.25741	1.215 ± 0.5047 0.29676	1.942 ± 1.2115 0.15053	TATATTCGAATATAATTCTTATACCATATTCTCGTTTTTG
plasmid_lp25	6914	BB_E09	1.890 ± 0.6446 0.090217	1.797 ± 0.7128 0.11882	1.118 ± 0.2602 0.22906	1.04 ± 0.2962 0.8679	TATATGCTTTGCATAAAATTCTCCTATTACCTTGATCAAAGTCAGA
plasmid_lp25	7082	BB_E09	2.171 ± 1.4432 0.285266	2.179 ± 2.9575 0.56961	1.135 ± 0.5696 0.73744	0.883 ± 0.6375 0.67058	ATATTGCTTACTTTAAGGAACCGAATTAAATGAAATAAGAAGGG
plasmid_lp25	7085	BB_E09	2.099 ± 1.7927 0.397553	1.917 ± 0.9125 0.23483	0.824 ± 0.2666 0.22346	0.824 ± 0.7205 0.7313	TTTGTCTTACTTTAAGGAACCGAATTAAATGAAATAAGAAGGGAGG
plasmid_lp25	7186	BB_E09	0.423 ± 0.2621 0.031177	2.016 ± 1.1133 0.20531	0.373 ± 0.3394 0.02111	0.805 ± 0.8342 0.76234	AATCACAGATTTGCCATGTAACATAACCATTGCAAGTATTCAAACA
plasmid_lp25	7248	BB_E09	1.259 ± 0.6169 0.254837	1.342 ± 0.6246 0.1538	1.047 ± 0.5425 0.89774	1.285 ± 0.7256 0.20532	AGAAACTTAAAGCTCTAAGATCTCAATTAAATTATTCTT
plasmid_lp25	7903	IG 1119	2.313 ± 0.7923 0.009196	1.9 ± 1.2476 0.21477	0.965 ± 0.3247 0.79234	1.083 ± 0.4305 0.22017	CTTGGTTTTCAATACCAACTTTAAATCAACAAGTAAAACCTC
plasmid_lp25	8055	IG 1120	4.555 ± 2.9229 0.062368	2.897 ± 2.2125 0.16181	1.276 ± 0.7513 0.08757	1.698 ± 1.5329 0.34059	ATATTATTATTAATAACATACCTAGATTTTACAAACTTAAAGGG
plasmid_lp25	8077	IG 1121	1.174 ± 0.2826 0.490003	0.845 ± 0.3022 0.13971	1.065 ± 0.3721 0.56048	1.108 ± 0.2808 0.13424	TACCTAGATTTCACAACTTAAAGGAGCTGGGTATAATGGAAAAC
plasmid_lp25	8555	IG 1122	2.150 ± 2.2073 0.258318	4.724 ± 6.1513 0.30257	0.813 ± 0.924 0.68024	1.33 ± 1.3734 0.64969	TATCTCCCCTTACCATATTCTTGTATGTTACAATAATTATCTCA
plasmid_lp25	9127	IG 1123	0.454 ± 0.5489 0.260196	0.675 ± 0.7223 0.12915	0.656 ± 0.8527 0.24247	0.875 ± 0.1092 0.84947	TTAATTCTCTAAATTAGGCATTGTTGAATTCTTACTCTATT
plasmid_lp25	9308	IG 1124	2.238 ± 0.8738 0.049695	1.813 ± 0.1078 0.00908	0.981 ± 0.4209 0.8807	1.2 ± 0.5541 0.37738	AAACGAATAACCTAGAACAGGGTGGCAATTGTTATTAAAACCTTAAA
plasmid_lp25	9528	IG 1125	2.804 ± 2.085 0.031963	2.382 ± 2.7242 0.29351	1.068 ± 0.7397 0.70538	1.19 ± 0.0994 0.26102	GAATTAAAACACACTGTTTAAATTCAATTAAAGATTGTA
plasmid_lp25	9579	BB_E16	1.915 ± 0.9743 0.13279	1.507 ± 0.8125 0.04395	0.812 ± 0.3725 0.27103	1.806 ± 1.542 0.31964	TTTGGCAAAAATTCTATCTATTCTCTGTCTCATTAGA
plasmid_lp25	9769	BB_E16	3.194 ± 1.2777 0.009078	1.768 ± 1.4527 0.28873	1.299 ± 0.5266 0.38119	1.046 ± 0.481 0.64674	ACATTGGTGTGATCGAATATAATGAAAAGTTTCTATTAGAATTCC
plasmid_lp25	9989	BB_E16	2.793 ± 1.4341 0.103438	2.739 ± 2.2356 0.29267	1.034 ± 0.611 0.92161	1.427 ± 0.7545 0.18679	TAAGCTGTGATTTTATAAAAACCAATTCTTCAAATTACTATCTTAAA
plasmid_lp25	10044	BB_E16	2.743 ± 2.5431 0.337182	2.018 ± 1.5528 0.38803	0.648 ± 0.7899 0.35729	0.938 ± 0.8314 0.9348	TGTATAGTTTACAAACAAAATTATCATCAAACTTCAACAAATT
plasmid_lp25	10723	IG 1126	2.505 ± 1.2192 0.102696	1.638 ± 1.2377 0.40099	0.838 ± 0.5965 0.53047	1.245 ± 0.8780 0.6047	TAATAAATAAAGGTATGAAAGTAATAATTGTTAATTCTTATTAA
plasmid_lp25	10871	IG 1127	1.730 ± 1.4951 0.531309	1.161 ± 0.4114 0.63042	0.817 ± 0.6264 0.62928	0.828 ± 0.4117 0.64399	GACCGATCTAAAGGATCTTAAAGCTGTATCATTAGATAAGCAATA
plasmid_lp25	11084	IG 1128	1.824 ± 1.442 0.413514	0.636 ± 0.5455 0.58783	0.901 ± 1.2404 0.90877	0.851 ± 0.8681 0.48135	TAAAAGATTCTTCAATATCGATTGTTGATTATTATTGGTATA
plasmid_lp25	11307	IG 1129	2.498 ± 0.8653 0.090441	1.658 ± 0.3997 0.09183	0.997 ± 0.1546 0.97432	1.33 ± 0.2937 0.15534	TTTATTATAAAATTCTTTAAAATTACTTACTTACTTATTGATTATT
plasmid_lp25	11520	BB_E18	3.728 ± 1.2772 0.049863	1.853 ± 0.5288 0.12436	0.959 ± 0.245 0.84459	1.323 ± 0.3361 0.0014	AGGAGTGTAAAAAATATAATTAAAATTATAGATAATTGTGTCGA
plasmid_lp25	11614	BB_E18	1.483 ± 2.06 0.089368	0.422 ± 0.4882 0.50872	0.943 ± 1.3208 0.71118	1.141 ± 1.6842 0.15776	TATTACAAATCAAAGCAAGATTACTAGTTTGTCTAGAAAATTACT
plasmid_lp25	11617	BB_E18	1.739 ± 1.475 0.311777	1.002 ± 0.5282 0.9965	0.649 ± 0.3311 0.19034	0.832 ± 0.3488 0.62042	TGTATGCATCTCTGTTAAGCTGAATCTTAATGGCCTGATAAAATTTC
plasmid_lp25	11621	BB_E18	1.945 ± 2.2835 0.543205	2.286 ± 3.4706 0.48613	0.424 ± 0.7102 0.38311	0.741 ± 0.8032 0.69093	TGATCTCTGTTTAAAGCTGAATCTTAATGGCCTGATAAAATTGCTT
plasmid_lp25	14855	IG 1130	1.658 ± 1.3589 0.283571	2.856 ± 3.4011 0.37055	0.779 ± 0.3666 0.32278	1.193 ± 0.6724 0.5648	AATGTAACATGATCTTAAATTCTTACTAAGAAGTAAAACCAAGG
plasmid_lp25	14861	IG 1131	2.223 ± 1.0901 0.035757	1.671 ± 1.1354 0.21411	0.996 ± 0.4365 0.98381	1.13 ± 0.5108 0.09271	ACTATGAATCTTAAATTCTTACTAAGAAGTAAAACCAAGGAAAAG
plasmid_lp25	15049	BB_E22	2.147 ± 2.2794 0.45596	2.552 ± 2.7942 0.29175	1.306 ± 1.0807 0.69233	1.852 ± 1.3569 0.38024	ATATATAAAACCATTAAGTAGTTAATTAGAAAACTATTATAA
plasmid_lp25	15167	BB_E22	4.223 ± 2.6658 0.086037	1.863 ± 1.8274 0.50124	1.348 ± 0.8588 0.44096	1.241 ± 0.6744 0.51852	ATAACAGATGCTACAAGAGCATACATCTCTGAATTATAATCG
plasmid_lp25	15562	IG 1132	2.605 ± 2.1895 0.284493	1.595 ± 1.4338 0.52324	0.121 ± 0.2109 0.06774	0.202 ± 0.3528 0.01052	CTGTTAGATCTGGCAAGTGCCTGATTCTAAATTCTTATATCT
plasmid_lp25	15685	IG 1133	1.039 ± 0.7161 0.913943	0.874 ± 1.0719 0.89914	1.35 ± 1.0336 0.06566	1.146 ± 1.097 0.20821	TATTCTGTATTAAATATCTCTAAGGAGGTTTATTAAATAATAG
plasmid_lp25	15697	IG 1134	2.443 ± 1.119 0.033712	1.895 ± 1.1573 0.14084	0.994 ± 0.3839 0.95461	1.143 ± 0.492 0.01363	TATTAGGCAATATCCCTTGATACAACTTTGTCATAATTATATTGGG
plasmid_lp25	15938	IG 1135	0.739 ± 0.6689 0.687494	0.675 ± 0.8645 0.70295	0.672 ± 0.4939 0.41625	0.574 ± 0.4598 0.49896	TTATAATAATTAAATTATAGTATAATCGAAAATTGTTACATATTG
plasmid_lp25	16170	IG 1136	2.496 ± 1.4858 0.168929	2.122 ± 2.3389 0.45732	0.672 ± 0.846 0.47284	0.812 ± 0.2343 0.26108	AAGCCCTAATAGCAAGGTTTTCCGATCTATAAGTTAAACTATTGAA
plasmid_lp25	16421	IG 1137	4.134 ± 3.372 0.027816	3.878 ± 4.4963 0.22079	1.057 ± 0.783 0.86692	2.109 ± 2.1238 0.13326	CATATTTTAAATAAAAGTGTATTAAAAAATAAAAAAGAGAA
plasmid_lp25	16503	IG 1138	2.228 ± 0.9168 0.024094	2.137 ± 1.8533 0.31583	0.726 ± 0.2379 0.1518	0.809 ± 0.473 0.35633	AACTAAAAAATGCAAATTTGTAATTGAAAACACTTATTGG
plasmid_lp25	16859	IG 1139	4.743 ± 1.9082 0.002005	3.534 ± 3.095 0.22041	0.72 ± 0.4417 0.31242	1.471 ± 0.7128 0.1905	TTAAAAAAAGGATTAATAATTCTTAAATTAGAAAATTCAATAATAG
plasmid_lp25	17120	IG 1140	1.323 ± 1.1352 0.503824	1.315 ± 0.8617 0.13138	0.871 ± 0.6184 0.3487	0.97 ± 0.6306 0.76245	TCCTTTAAAAAAATAGTATACCGTTGATTCTGCCTTC
plasmid_lp25	17202	IG 1141	1.902 ± 1.2843 0.357187	1.001 ± 0.3237 0.99535	0.755 ± 0.2063 0.22419	0.954 ± 0.2031 0.66186	TGTATGCATCTCTGTTAAGCTGAATCTTAATGGCCTGATAAAATTG
plasmid_lp25	17205	IG 1142	1.345 ± 1.8202 0.032621	0.373 ± 0.4294 0.46881	0.831 ± 1.125 0.487	1.085 ± 1.5875 0.15614	TATTACAAATCAAATCAAGATTACTAGTTTGTCTAGAAAATTACT
plasmid_lp25	17439	IG 1143	0.957 ± 0.7222 0.793653	0.885 ± 0.837 0.66034	0.945 ± 0.5457 0.32983	1.073 ± 0.5632 0.47504	TTAAATCATAAATGTCAAAAATCGGGTAGTAAAGTAAAAGTAAA
plasmid_lp25	17972	IG 1144	2.893 ± 1.6882 0.170438	2.527 ± 1.9189 0.27912	0.819 ± 0.3867 0.42967	1.388 ± 0.7336 0.38798	TTTAAAGGTATTGTTAAATTCTCATATAGAATTCTTATTGGAAT
plasmid_lp25	18136	IG 1145	1.323 ± 0.5261 0.05109	0.932 ± 0.742 0.9184	1.111 ± 0.6277 0.46307	1.313 ± 0.8235 0.25615	GAAAAAAATCATTAATTTAATAATCATATAAGTAAAATTAAATAAG
plasmid_lp25	18137	IG 1146	1.422 ± 0.5235 0.048291	1.037 ± 0.8279 0.95701	1.23 ± 0.6673 0.27738	1.578 ± 0.9741 0.21679	AAAAAAAATCATTAATTTAATAATCATATAAGTAAAATTAAATAAG
plasmid_lp25	18414	IG 1147	1.391 ± 1.0763 0.573152	1.959 ± 1.9536 0.47885	1.91 ± 1.5784 0.29233	1.942 ± 1.3612 0.2002	GTTTATTGCTAGTTGTAACACTAAATTACTTATAGATATTGAGCT
plasmid_lp25	18569	IG 1148	2.879 ± 1.171 0.052618	1.97 ± 1.9802 0.43664	0.785 ± 0.2918 0.31184	1.1 ± 0.7177 0.84158	AATAAAGTGGAAATCTGTGATTTTATTGTTGCATTAAATTGCTT
plasmid_lp25	18747	IG 1149	2.544 ± 2.415 0.110365	1.699 ± 1.8035 0.20923	0.973 ± 0.8657 0.88043	1.074 ± 1.076 0.34438	CCTATATTACATATAAAAGCTAAAGCAATTAAATTACATTCACACT

plasmid_lp25	18754	IG 1150	4.700 ± 5.4837 0.071451	3.016 ± 3.0536 0.1085	1.19 ± 1.259 0.75607	1.874 ± 2.1892 0.24078	ATATATTCTAAAGCTGGTGGGATAATTAGAGGAAAAGTTACTATGTC
plasmid_lp25	18798	IG 1151	2.452 ± 1.0311 0.119589	2.11 ± 0.704 0.03082	1.044 ± 0.3243 0.85386	1.2 ± 0.8176 0.67479	GTAAACCTTTCTCATATAATTATCCACCAAGCTTAGGAATATTTAAATA
plasmid_lp25	18913	IG 1152	2.117 ± 1.5111 0.215737	1.912 ± 1.5723 0.30549	0.658 ± 0.4399 0.05851	0.95 ± 0.4855 0.58607	TCTATAAAACTAAAAATTCTTAGCTGTTTTAAATCTTATTCTAA
plasmid_lp25	19832	BB_E29	1.938 ± 1.6302 0.341932	2.393 ± 3.0211 0.47139	0.866 ± 0.9683 0.81736	1.118 ± 1.1605 0.69966	GTACACTTCTATTGGGTGTAAGTTTATTGTTAACAGTTACATAAGGC
plasmid_lp25	20049	BB_E29	1.491 ± 0.5581 0.260427	1.444 ± 0.6187 0.33258	0.866 ± 0.3907 0.46827	1.149 ± 0.4083 0.62911	CTAAAAAATGCTATGGTTGAATGTTAATGGTCCCTATGTTAGTTGAT
plasmid_lp25	20091	BB_E29	3.303 ± 3.9062 0.099752	2.495 ± 3.4505 0.23149	1.184 ± 1.2866 0.57242	0.945 ± 0.9683 0.91042	CATAAGGAACCATTAAACATCAGACATTTAAGTATGTGAA
plasmid_lp25	20094	BB_E29	1.127 ± 0.7361 0.604378	0.659 ± 0.6035 0.63365	1.071 ± 0.8893 0.07764	1.225 ± 1.1308 0.23838	GTTGATCATTTAAAGCCAAGTCATAATTGAAAAGAAAAATTGTCAGCACA
plasmid_lp25	20495	BB_E29	1.613 ± 0.7215 0.025314	1.037 ± 0.6348 0.09092	1.426 ± 0.556 0.09746	1.136 ± 0.4345 0.68728	TCATAACAAACAAATGGACCTTGACAAGGTGGCATTAGGAGGTGAGA
plasmid_lp25	20989	IG 1153	1.543 ± 1.2013 0.160117	1.179 ± 0.9022 0.83568	0.438 ± 0.5136 0.13792	0.856 ± 0.6136 0.80497	CATATTCAAAGAAGAATATGCTATAAACATTATAATCTAGGTGAAAGATT
plasmid_lp25	20990	IG 1154	3.419 ± 5.2267 0.106034	4.327 ± 8.0973 0.30399	0.35 ± 0.5812 0.41229	1.32 ± 2.0924 0.26008	TGAAATTCTAAGCTTATTAAAGCTTTCTGTATAGTCATTAG
plasmid_lp25	21123	BB_E29a	0.051 ± 0.0663 0.087565	0.556 ± 0.5857 0.42685	1.081 ± 0.6079 0.8305	0.711 ± 0.5036 0.61661	GGTTATTGGCGAGATTATTACTCTAAAATAAGGAGTTGAG
plasmid_lp25	21214	BB_E29a	3.568 ± 0.8758 0.036477	1.695 ± 0.8947 0.29452	1.102 ± 0.2512 0.32778	1.248 ± 0.2135 0.01909	TCTCAATTCTTAAATATTTTATATCTGGCTACTACAACTCC
plasmid_lp25	21923	IG 1155	2.884 ± 0.5778 0.016415	2.406 ± 1.314 0.17859	0.934 ± 0.1926 0.57828	1.269 ± 0.2786 0.07526	ATATAATTCTTAAACATGACTTAAAGGTTGCTTATTGACAATATGTTA
plasmid_lp25	22734	IG 1156	1.615 ± 1.3632 0.463789	2.091 ± 1.3104 0.26207	0.418 ± 0.1904 0.17619	0.759 ± 0.3378 0.51219	ATACTAATTATTAAATTATATTATTGATTATATTAGTTAAGGAGA
plasmid_lp25	23344	IG 1157	3.730 ± 2.8901 0.163572	3.323 ± 3.1523 0.26448	1.005 ± 0.852 0.99192	0.705 ± 0.6795 0.52769	AAGGTGTTCCCTGTAATATTATAGTCGATTAGTAGTCG
plasmid_lp28-1	17	BB_F001	3.961 ± 1.9599 0.103139	3.136 ± 1.032 0.00647	2.206 ± 0.9545 0.08616	3.242 ± 2.0572 0.20902	CATCTACTATTACAAATTAAATTCAAATTTTTAATGAAAATGAGCTT
plasmid_lp28-1	136	BB_F001	1.143 ± 0.4463 0.25462	1.836 ± 0.845 0.1915	0.885 ± 0.4003 0.41724	1.167 ± 0.5661 0.41872	CTTGAAATTGCAAAACAAATTATATCTAAAATTTTTCTGATTAGG
plasmid_lp28-1	1694	IG 1158	0.757 ± 0.7183 0.023813	2.457 ± 2.323 0.20104	0.699 ± 0.4251 0.47183	0.991 ± 0.7484 0.97536	CTAAACAACTAAAATTATTCTTGTGATTACTAGGGCAAAAGAACAC
plasmid_lp28-1	1873	BB_F02	2.080 ± 0.8532 0.090949	1.774 ± 1.6258 0.42718	1.225 ± 0.5059 0.59992	1.33 ± 0.5887 0.23104	GATTATTGATTGAGCTTAAAGGTGCGAATGACTGATATTGAGCT
plasmid_lp28-1	1907	BB_F02	3.991 ± 1.5239 0.072635	2.957 ± 0.5469 0.02319	1.888 ± 0.5122 0.07247	3.216 ± 1.8547 0.17915	CATCTACTATTACAAATTAAATTCAAATTTTTAATGAAAATGAGCTT
plasmid_lp28-1	2562	BB_F03	1.320 ± 0.9992 0.484001	1.076 ± 0.4613 0.84012	1.16 ± 0.5949 0.31688	1.242 ± 0.8986 0.5222	GTTCATGTAAATAATCTTTGACAAATCTGAGCTTATTGTTCCCA
plasmid_lp28-1	2656	IG 1159	1.383 ± 0.9863 0.498975	1.221 ± 1.113 0.77848	1.427 ± 0.9218 0.30352	0.863 ± 0.6258 0.82458	TTATGAAAAAAACAAACAAAGTCGCTCAGAAATAGAAAACACAAAT
plasmid_lp28-1	2986	BB_F05	0.975 ± 0.5424 0.688858	2.053 ± 1.6404 0.26277	1.111 ± 0.5476 0.20243	1.187 ± 0.7689 0.48694	TTATAAAATTAAATTACCCCCCTTAAAGTGTGTTCAACAAATACAAGACTA
plasmid_lp28-1	3410	IG 1160	1.642 ± 0.8743 0.274458	3.421 ± 2.5356 0.20785	1.707 ± 0.7152 0.16798	1.63 ± 0.8152 0.1843	AGTGTCTATGCTTCTTGAAGCTACACTAGCTAAGTTCTACTACTTAA
plasmid_lp28-1	3448	IG 1161	2.248 ± 1.4727 0.200346	0.975 ± 0.4194 0.94145	1.586 ± 0.6581 0.19325	1.547 ± 0.1019 0.37324	TTTTGTAAAATCCAAAAGCTCTTATTATAAGTAAGTCATGTCTT
plasmid_lp28-1	3530	IG 1162	0.916 ± 0.5094 0.86828	1.037 ± 1.0863 0.91965	0.521 ± 0.3929 0.25539	0.327 ± 0.3607 0.1778	AATGAATTACTTACCGGGAGCTTAAATATTCTTAAAGAAATAGGAA
plasmid_lp28-1	3623	IG 1163	0.619 ± 0.8996 0.406834	0.17 ± 0.2034 0.32118	0.253 ± 0.299 0.39275	1.325 ± 1.5062 0.72023	TTGTTACTATAACAAAATTGAACTTAAACATATTACTTTAAA
plasmid_lp28-1	3629	IG 1164	0.969 ± 0.3288 0.332781	1.299 ± 0.6062 0.27706	0.782 ± 0.2182 0.23228	0.793 ± 0.2166 0.20405	GTAACAAATAGTGCCTAAGAAAGAACATTAAATTAAAAATTAAAT
plasmid_lp28-1	3685	BB_F08	1.075 ± 1.6795 0.951709	0.128 ± 0.2281 0.11681	1.097 ± 1.7253 0.90782	1.986 ± 1.5262 0.34175	TAGGAGCTTAAAGCTTAAACAAACTTATTACCAATTATATATA
plasmid_lp28-1	3700	BB_F08	0.482 ± 0.3534 0.21945	1.118 ± 0.7105 0.61188	0.932 ± 0.7056 0.80014	0.876 ± 0.6139 0.82417	AAGCTTAAACAACTTATTACCAATTATATCTCTTAT
plasmid_lp28-1	3729	BB_F08	1.177 ± 0.6611 0.62672	2.253 ± 1.8296 0.32987	0.937 ± 0.2857 0.64032	1.218 ± 0.2807 0.26203	TATATGGTAAAAAAATAGTTGTTAACAGCTTATAAGCATCTCTATAAGTA
plasmid_lp28-1	4315	BB_F0034	1.474 ± 0.8138 0.3568	2.595 ± 3.0178 0.43979	1.089 ± 0.4061 0.6139	1.111 ± 0.6153 0.73604	GCTTCAGAGTTCTTAAAGAGCATTTTGTAGCTAAGTTGTA
plasmid_lp28-1	4522	BB_F10	0.817 ± 0.325 0.430001	1.099 ± 1.2906 0.87359	0.652 ± 0.4617 0.19757	0.65 ± 0.3292 0.31433	AGATGGCTGGCTTGGCTTAAAGTCATTTCCATTAATAAAAGATCTG
plasmid_lp28-1	4675	BB_F10	0.539 ± 0.6843 0.544289	1.391 ± 1.3104 0.19375	0.58 ± 0.7137 0.23463	1.183 ± 1.6603 0.86999	AGACTACTAAGCTTGTATCTATAAAACATCTTAAAGAGATTGGTT
plasmid_lp28-1	4890	BB_F10	0.616 ± 0.5619 0.462245	1.414 ± 1.2212 0.64892	0.546 ± 0.2096 0.14493	1.461 ± 1.3451 0.62569	GTTTAATGATAAGATAAGCTTGTAGCTACCTCTTCTTAGTAACTCCATCAA
plasmid_lp28-1	4936	BB_F10	1.197 ± 0.5238 0.206306	1.627 ± 1.2667 0.36873	0.848 ± 0.245 0.23463	1.013 ± 0.3217 0.93483	GCCTTGCTACTATACTTAAATGACTTAAAGAGATGCCAATATAAC
plasmid_lp28-1	4985	BB_F10	0.757 ± 0.5148 0.615862	3.715 ± 2.2255 0.17575	1.139 ± 0.6674 0.80191	1.371 ± 0.3215 0.68935	ACTGACACAAATATTCTTATTTTAAAAGCCTAAGTACTTATCT
plasmid_lp28-1	5024	IG 1165	1.248 ± 1.887 0.718998	0.44 ± 0.6759 0.54849	1.572 ± 1.8685 0.31826	1.065 ± 1.2021 0.86548	CTTAGGCTTTAAAATAAGAAGATATTGTTGCTAGTTATTGATT
plasmid_lp28-1	5033	IG 1166	2.349 ± 1.2529 0.097718	2.541 ± 1.8545 0.11127	1.624 ± 1.8584 0.47454	1.472 ± 1.1833 0.3377	TCTTAGGCTTTAAAATAAGCTTCTTAGACCTCTTGTAGATA
plasmid_lp28-1	5129	IG 1167	0.982 ± 0.2716 0.187577	1.005 ± 0.6625 0.98696	0.676 ± 0.1787 0.1337	0.975 ± 0.2626 0.79754	AGTGTACTTACCTTCTAGCATTAATTCTTAAACAGTTATTATTA
plasmid_lp28-1	5198	IG 1168	0.961 ± 0.5688 0.793991	2.206 ± 2.2112 0.28381	1.005 ± 0.5176 0.98284	0.952 ± 0.5739 0.86474	TAATCTTCTAAGGAAATATTATAAGAAATTAAGACCTTAAA
plasmid_lp28-1	5277	IG 1169	1.392 ± 0.65 0.412481	2.296 ± 1.4894 0.28527	0.924 ± 0.532 0.84873	1.611 ± 0.6919 0.15585	AAGTAATTITGAATATAGAAAAATAATTAAAGGTCTATTAAATT
plasmid_lp28-1	6677	BB_F13	0.950 ± 0.2437 0.790685	1.776 ± 1.4182 0.35188	1.001 ± 0.4797 0.99811	0.829 ± 0.2997 0.10348	TTATCAAGAAATTAAGAAAACCTTGAAGAGATTTCTTATAATGAA
plasmid_lp28-1	6714	BB_F13	1.630 ± 1.0735 0.091104	1.739 ± 1.2977 0.08354	0.853 ± 0.5641 0.65329	1.343 ± 1.2799 0.38506	TAACTAAAAGACTCGAACCTCTTCAAGAGAAATATTATAAGAAATTA
plasmid_lp28-1	6742	BB_F13	1.262 ± 0.5297 0.080321	1.73 ± 0.7057 0.18983	1.172 ± 0.4371 0.36911	1.187 ± 0.6073 0.32579	CATTTTATAATAGTATAAAAGTCTTATAACTAAAGACTCGAACCTTCT
plasmid_lp28-1	6770	BB_F13	0.944 ± 0.6443 0.753752	1.276 ± 0.7843 0.14184	0.663 ± 0.3256 0.23625	0.926 ± 0.4311 0.83409	TTCTTATGAATCAGATTCTTACTCTTTAAAGAATATTCTTATT
plasmid_lp28-1	7196	BB_F13	2.855 ± 2.3375 0.200878	2.389 ± 1.3295 0.00446	1.148 ± 0.9582 0.67582	3.668 ± 3.7808 0.24502	TGTTTCGGCGTCAGGAATACTTGGTAAAGAATCTG
plasmid_lp28-1	7718	BB_F14	2.101 ± 1.1945 0.030135	6.744 ± 4.2346 0.05972	1.13 ± 1.1771 0.88697	2.773 ± 1.4766 0.02637	AATTTTAAATTCTAGTTCTAGCTTGTGTTGAGCTTAAAGGAA
plasmid_lp28-1	7971	IG 1170	0.042 ± 0.0436 0.025365	0.698 ± 0.9584 0.71242	0.032 ± 0.0561 0.0283	0.246 ± 0.1735 0.01631	AATATGTAAGCTTAAAGTAAATAATTAAAGTTCTAGTTGAAAG

plasmid_lp28-1	7999	IG 1171	1.245 ± 0.5247 0.138654	2.024 ± 1.1918 0.12697	1.024 ± 0.4512 0.93318	1.262 ± 0.5064 0.12618	ATTATTTACTTAAACAAGCTACATATTACATTACAAGTAATAAACAT
plasmid_lp28-1	8109	IG 1172	1.046 ± 0.987 0.886727	2.844 ± 2.1387 0.2373	1.184 ± 0.5487 0.59999	1.44 ± 0.7113 0.37237	TATCAGAACTGGTAGATTGCTATGTTTAAAGTAAGTATTAGAATAGCTT
plasmid_lp28-1	8428	BB_F16	1.020 ± 0.6618 0.914236	0.909 ± 1.1505 0.77339	0.615 ± 0.414 0.25939	0.833 ± 1.093 0.58356	CTATACTATTAAATAAGAGAAAAATTATTATCACTAACTATTAAAGCTTG
plasmid_lp28-1	8433	BB_F16	1.702 ± 0.4054 0.094361	2.068 ± 1.4768 0.34439	0.991 ± 0.2691 0.95223	1.495 ± 0.3477 0.17575	GTATAGTAATGATATCCAAAGTATCAAGGGGCCATTATTCTCATTAGATA
plasmid_lp28-1	8492	BB_F16	0.957 ± 0.2732 0.790145	1.034 ± 0.4122 0.92594	0.921 ± 0.2432 0.67992	0.961 ± 0.3013 0.8664	AATAGGGAAAAAACAGCTTAATATTGAGGTATAAAATTTCTCT
plasmid_lp28-1	8529	BB_F16	1.125 ± 0.8442 0.696977	2.212 ± 2.5548 0.43472	0.828 ± 0.5647 0.60734	1.376 ± 1.2735 0.60086	AGATCAAGTAAATTAAATTGGATAGTAAATATTAAAGGGGAAAAAA
plasmid_lp28-1	8563	BB_F16	0.661 ± 0.6813 0.336302	0.518 ± 0.4347 0.39167	0.999 ± 0.4935 0.99826	0.634 ± 0.2928 0.20852	TATGAGGAGTGACTIONAGCTTGAAGCTTATGAAAGTATTAAATTAAAC
plasmid_lp28-1	8602	BB_F16	1.445 ± 1.3509 0.452695	1.698 ± 2.3908 0.57503	0.887 ± 0.9566 0.8129	0.753 ± 0.8376 0.22508	TTAATTAAAACGTAGTTAGAAAAGCAATCTAGATTAGTATGAAAAAC
plasmid_lp28-1	8741	IG 1173	0.563 ± 0.6931 0.044199	1.504 ± 0.9183 0.08731	0.631 ± 0.5179 0.50369	0.771 ± 0.6573 0.7236	TGTTAAAAGGTTTTATTCAAACGTAAAATGGTAAAGTAAAAGGCC
plasmid_lp28-1	8797	BB_F17	0.513 ± 0.9035 0.324174	0.475 ± 0.8179 0.2489	0.023 ± 0.0405 0.04039	0.99 ± 0.9497 0.98559	GCTATATTAAATATGGTAGAGATAATCAGCTTAATGTAGAAAGATA
plasmid_lp28-1	8803	BB_F17	1.687 ± 1.7406 0.423131	1.317 ± 0.7882 0.23828	0.984 ± 0.8228 0.93856	1.097 ± 0.8071 0.71783	ATATAGCTAAGCGCTTTTAACTTTACCCATATTTCAGTTGAATAAA
plasmid_lp28-1	8818	BB_F17	1.051 ± 0.3022 0.055291	1.756 ± 0.7014 0.24299	0.907 ± 0.2068 0.37311	1.095 ± 0.3723 0.19897	TCTCTACCATTTAAATAGCTAAGCGCTTTAACCTTACCCATATT
plasmid_lp28-1	8832	BB_F17	1.249 ± 1.1362 0.266574	1.648 ± 1.4866 0.26971	0.431 ± 0.3795 0.12732	0.563 ± 0.6746 0.43947	CATTAGGCTGATTATCTCACCATTAAATAGCTAAGCGCTTTAA
plasmid_lp28-1	9104	IG 1174	1.072 ± 0.6694 0.373409	1.942 ± 2.0095 0.37729	0.898 ± 0.5365 0.26006	1.082 ± 0.7078 0.62257	CTTATCTAATTAGTAGATTAGCTCTATTCAAGCGCTTATTCCTTAT
plasmid_lp28-1	9491	IG 1175	5.726 ± 6.729 0.030216	2.941 ± 4.4356 0.45242	1.889 ± 2.7119 0.58037	4.872 ± 7.5087 0.35269	AAAAGAGAAAAGAGAATCGACAGAATAAATAAAAAAGAAGAGAACAGC
plasmid_lp28-1	9917	BB_F18	0.591 ± 0.7611 0.151001	1.255 ± 1.4799 0.74615	0 ± 0 0.12451	0.383 ± 0.4638 0.15958	TATGATGTTAGTAGCTATTAAAGATGGCTCTAAATTAGTGAT
plasmid_lp28-1	9920	BB_F18	1.370 ± 0.8978 0.311048	2.076 ± 1.9476 0.34384	0.967 ± 0.5721 0.76243	0.913 ± 0.4125 0.56035	CATATAAACTAAATGGTATGGATCTGCTTGTATAAGTAGATAGAT
plasmid_lp28-1	10055	BB_F19	1.548 ± 0.2737 0.017653	2.484 ± 0.8724 0.07838	1.194 ± 0.3556 0.32973	1.116 ± 0.422 0.67899	GAACCTTTGCTTTTGATAGTTTCTTGGTATTAAAGTTTAA
plasmid_lp28-1	10296	BB_F19	1.190 ± 0.7988 0.561235	1.723 ± 0.9939 0.1978	1.852 ± 0.9536 0.23873	1.081 ± 0.3973 0.67396	AAATAGAGTTTAAAGTTAGTCTATAATATTATTTCAATAACAGT
plasmid_lp28-1	10309	BB_F19	1.754 ± 0.9779 0.069579	1.688 ± 1.5609 0.3863	1.324 ± 0.6573 0.0881	2.241 ± 1.4291 0.14695	TATAACCTTTTATTCTTATTAGTTGATTATTAGTTCTATAAG
plasmid_lp28-1	10347	BB_F19	1.082 ± 0.6823 0.569526	1.758 ± 1.6301 0.36939	0.95 ± 0.4545 0.37662	1.197 ± 0.6803 0.17082	ATAATCAAAAACATCAATAGGAATAAAATGGTTATATAAGCTACCTA
plasmid_lp28-1	10404	BB_F19	0.884 ± 0.4631 0.763246	1.139 ± 0.7572 0.7873	0.973 ± 0.3178 0.92613	1.238 ± 0.3941 0.4969	GAACACAGGATTCTCAAATATAAAAGTAAGAAAAATAGGGAACTTAA
plasmid_lp28-1	10529	BB_F19	1.832 ± 0.967 0.296282	3.689 ± 3.5787 0.26446	2.002 ± 1.9402 0.50307	2.298 ± 3.1548 0.21502	TTCTATGTTAATAGCTTTTAAACCCATATTCTTATTATTTATAAT
plasmid_lp28-1	10560	IG 1176	0.713 ± 0.4763 0.279597	1.472 ± 1.6769 0.51955	0.764 ± 0.4891 0.50826	0.854 ± 0.6513 0.53423	TATGGGTGTTAATAAAGCTTATAAGCATAGATAATATCATATAAGAAGAA
plasmid_lp28-1	10578	IG 1177	1.227 ± 0.997 0.349852	2.762 ± 2.4782 0.20806	0.989 ± 0.5144 0.95254	1.484 ± 0.8835 0.06039	TTATAAAATAATAGAAATATGGGTGTTAATAAAGCTTATAAGCATAGAAT
plasmid_lp28-1	10807	BB_F20	0.740 ± 0.6105 0.677996	0.971 ± 1.2184 0.97726	0.578 ± 0.2797 0.14219	0.123 ± 0.1259 0.0761	GAATTTTAACTATAGCCTATTAACTAAACATTATAATTGAATTA
plasmid_lp28-1	10934	BB_F19a	0.170 ± 0.1226 0.169325	0.578 ± 0.4344 0.34147	0.327 ± 0.4498 0.22108	0.309 ± 0.3239 0.32756	ATACTAACAGAAGGCTAATTTGTAGATAATAATGAAATAGAAAATT
plasmid_lp28-1	11081	BB_F19a	1.212 ± 0.6355 0.486531	1.61 ± 0.8978 0.1804	1.102 ± 0.6971 0.73427	1.239 ± 0.6029 0.49689	GTAGGCCTATTGCAACAAGCATGACTATTATTTATGTAAATAA
plasmid_lp28-1	11497	IG 1178	0.969 ± 0.4526 0.936835	2.026 ± 1.1135 0.22485	0.878 ± 0.2034 0.38747	0.984 ± 0.3652 0.94871	GTAATATTCTTAAATGTGAATCTCTAAATCTGCGCATACATTAAAGT
plasmid_lp28-1	11723	IG 1179	1.082 ± 0.6326 0.795966	2.181 ± 1.6542 0.2082	0.779 ± 0.331 0.20793	1.305 ± 0.536 0.02762	AGCTCTTCGAGGTTTAAATTAAATTATTATTTGCTTTTATAGGCCTT
plasmid_lp28-1	11882	IG 1180	0.635 ± 0.5607 0.150074	0.642 ± 0.4054 0.12356	0.549 ± 0.5864 0.3132	0.731 ± 0.3862 0.1623	ACAAACTTGTATGTTGATAGAAGAATCTAGGTTAACGAAATAAAAGAAG
plasmid_lp28-1	16261	IG 1181	1.185 ± 0.7673 0.686027	1.362 ± 0.7287 0.3393	0.965 ± 0.3008 0.78461	1.496 ± 0.4189 0.10123	TTAGAGCTTAAATAGCATTACACGGAGCAAAGACTTAAAGCTCAA
plasmid_lp28-1	16416	IG 1182	1.267 ± 0.4314 0.443525	1.668 ± 0.9693 0.37321	1.154 ± 0.8024 0.78671	1.239 ± 0.6011 0.59434	TGATTGTTGAAATTGTTGATTATTGCTTTTAAATTGGTGTATCCT
plasmid_lp28-1	16918	IG 1183	0.628 ± 0.3556 0.063526	0.739 ± 0.5612 0.63912	1.224 ± 0.8002 0.3967	1.336 ± 0.8924 0.37472	TTACTTTATAATTGTCGGCGTGGACAGTTTATGGGGGTTCCAT
plasmid_lp28-1	17291	BB_F30	0.928 ± 0.3974 0.839761	2.68 ± 1.0754 0.00968	0.809 ± 0.3328 0.53394	1.464 ± 0.5692 0.23805	TTAAGCTGTATAATGTCAAATGGCTAGGTTAAATCCTAATTCTA
plasmid_lp28-1	17909	IG 1184	1.113 ± 0.4813 0.183627	1.688 ± 1.2405 0.25805	1.026 ± 0.4926 0.50111	1.196 ± 0.6421 0.23109	TTGTGTTAAAGTAGATAGGAATAATTGCGTTTCTATTGAAATTAAATA
plasmid_lp28-1	17993	IG 1185	1.079 ± 0.5246 0.402647	1.631 ± 1.2912 0.3311	0.871 ± 0.3654 0.18998	1.08 ± 0.5225 0.15991	CTTAACATATTATTGAAACAATTAAAATTTGAAATTGACAATGAA
plasmid_lp28-1	18136	IG 1186	1.318 ± 1.1845 0.126396	1.677 ± 1.79 0.31789	0.986 ± 0.7581 0.95634	1.193 ± 1.1601 0.40106	AAATGAGGCTTATTGTTGATTGAAATACATTTAAAAGTCTTTCT
plasmid_lp28-1	18167	IG 1187	1.147 ± 0.3875 0.197164	1.664 ± 0.9238 0.19808	1.078 ± 0.5473 0.64155	1.414 ± 0.5399 0.11444	CATTTTAAAGCTTTCTTCTAGTTCTTTTATTAGTCCTTCTTTAA
plasmid_lp28-1	18591	BB_F32	0.473 ± 0.5077 0.521567	0.965 ± 1.18 0.91491	0.22 ± 0.2506 0.27358	0.803 ± 0.8544 0.72022	TCTGCTCCCACAAAGCACGACCGCCGCTTGTAGCAGCTTCAGT
plasmid_lp28-1	18764	BB_F32	0.939 ± 0.3727 0.762826	1.658 ± 1.2936 0.47517	0.874 ± 0.2548 0.38047	1.015 ± 0.4435 0.95609	AGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGAGTGAAGAGCTGAAG
plasmid_lp28-1	18815	BB_F32	1.173 ± 1.0962 0.806171	1.556 ± 1.0726 0.4711	0.638 ± 0.7417 0.43211	0.97 ± 0.4805 0.87603	TCAGCCACAACTCTCCAATTGCACTAGTACCACTTGAAGCCCCCTCAGCT
plasmid_lp28-1	18997	BB_F32	0.675 ± 0.3765 0.189601	0.594 ± 0.5172 0.52057	0.975 ± 0.5407 0.85686	1.119 ± 0.7518 0.41908	TTGCTTTAGGGGGATGGCTAAGGATTTGCTGTGAAGAGTGGT
plasmid_lp28-1	19151	BB_F32	0.604 ± 0.2386 0.147688	0.479 ± 0.4043 0.16791	0.829 ± 0.3189 0.54657	1.123 ± 0.4493 0.72889	ATATCTGCTCCCACAAAGCACAACAGCACCAGCCGCTTGTAGCAG
plasmid_lp28-1	19154	BB_F32	0.538 ± 0.775 0.454333	2.2 ± 2.7292 0.5354	0.745 ± 0.2553 0.27438	0.436 ± 0.2382 0.06798	TCTGCTCCCACAAAGCACAACAGCACCAGCCGCTTGTAGCAGCT
plasmid_lp28-1	19339	BB_F32	0.602 ± 0.3646 0.407552	1.652 ± 1.8271 0.61821	0.652 ± 0.5999 0.05032	0.778 ± 0.5553 0.71039	AGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGAGTGAAGAGCTGA
plasmid_lp28-1	19393	BB_F32	1.384 ± 1.0385 0.374091	3.536 ± 4.5189 0.35183	0.966 ± 0.6544 0.91842	1.543 ± 1.9684 0.56796	TCCACAACTTCCAATTGCACTAGTACCAATTGAAAGCCCCCTCAGCT
plasmid_lp28-1	19489	BB_F32	1.174 ± 0.4282 0.333449	1.685 ± 0.7542 0.0873	1.137 ± 0.348 0.33755	1.298 ± 0.5108 0.07003	ATAGCCCCCTCAGCTTCCCTTCAACCACACTTCAACAGCAAAC
plasmid_lp28-1	19567	BB_F32	0.687 ± 0.3819 0.202296	0.605 ± 0.5246 0.5331	0.985 ± 0.5416 0.91897	1.142 ± 0.767 0.36444	TTGCTTTAGGGGGATGGCTAAGGATTTGCTGTGAAGAGTGGT

plasmid_lp28-1	19736	BB_F32	0.522 ± 0.251 0.153736	0.53 ± 0.4029 0.36946	0.822 ± 0.4023 0.4381	0.951 ± 0.4593 0.89012	ATATCTGCTCCCCACTAACAGCACTAACAGCACCGCCGCTTGTAGCAG
plasmid_lp28-1	19739	BB_F32	0.459 ± 0.6335 0.290048	2.067 ± 2.4868 0.53787	0.906 ± 0.4233 0.74102	0.362 ± 0.123 0.03137	TCTGCTCCCCACTAACAGCACTAACAGCACCGCCGCTTGTAGCAGCCT
plasmid_lp28-1	19921	BB_F32	1.075 ± 0.4673 0.442647	1.619 ± 1.1951 0.33501	0.811 ± 0.3102 0.07104	1.06 ± 0.551 0.79269	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGGAGTGAAGAGCTGAAAG
plasmid_lp28-1	20151	BB_F32	0.669 ± 0.3609 0.170354	0.599 ± 0.5158 0.51885	0.966 ± 0.5105 0.80365	1.126 ± 0.75 0.42402	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGAGTGGTG
plasmid_lp28-1	20320	BB_F32	0.403 ± 0.4416 0.471404	1.079 ± 1.2706 0.84292	0.194 ± 0.2346 0.27732	0.819 ± 0.9195 0.76191	TCTGCTCCCCACTAACAGCACCGCCGCTTGTAGCAGCCTACTGTCCC
plasmid_lp28-1	20493	BB_F32	0.718 ± 0.3277 0.44104	1.802 ± 1.7542 0.53136	0.594 ± 0.4902 0.03596	0.829 ± 0.5615 0.75777	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGGAGTAAAAGCTGAAAG
plasmid_lp28-1	20646	BB_F32	1.017 ± 0.569 0.95009	1.877 ± 1.3576 0.2403	0.887 ± 0.4624 0.26437	1.056 ± 0.4335 0.82174	GCCCCCTCAGCCTTCCTTCTCATTATTATCCTCTCACAGCAAACCTT
plasmid_lp28-1	20724	BB_F32	0.621 ± 0.4753 0.145374	0.619 ± 0.326 0.34022	0.867 ± 0.3457 0.00953	0.981 ± 0.4105 0.94044	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGAAGGATA
plasmid_lp28-1	20881	BB_F32	0.543 ± 0.1952 0.07919	0.5 ± 0.2676 0.18373	0.794 ± 0.3316 0.15428	1.208 ± 0.3548 0.42848	ATATCTGCTCCCCACTAACAGCACTAACAGCACCGCCGCTTGTAGCAG
plasmid_lp28-1	20884	BB_F32	0.350 ± 0.4849 0.271329	1.648 ± 2.0999 0.64768	0.667 ± 0.3152 0.16132	0.318 ± 0.2296 0.03107	TCTGCTCCCCACTAACAGCACTAACAGCACCGCCGCTTGTAGCAGCCT
plasmid_lp28-1	21066	BB_F32	1.040 ± 0.4953 0.712339	1.575 ± 1.203 0.37453	0.781 ± 0.2981 0.04074	1.022 ± 0.5821 0.92671	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGGAGTGAAGAGCTGAAAG
plasmid_lp28-1	21111	BB_F32	1.229 ± 1.28 0.752348	1.321 ± 0.9818 0.61004	0.584 ± 0.6567 0.27213	0.863 ± 0.4685 0.36045	TCAGCCACAACCTCTCCAATTGTCATCGTACCACTTGAAGGCCCTCAGC
plasmid_lp28-1	21288	BB_F32	0.690 ± 0.4382 0.187418	0.641 ± 0.3973 0.44318	0.828 ± 0.4298 0.0837	0.909 ± 0.3642 0.74366	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGAATGATG
plasmid_lp28-1	21654	BB_F32	0.637 ± 0.2926 0.325471	1.716 ± 1.7239 0.57968	0.56 ± 0.4195 0.06532	0.874 ± 0.5463 0.81479	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGGAGTAAAAGCTGAAAG
plasmid_lp28-1	21777	BB_F32	0.334 ± 0.3116 0.168743	0.705 ± 0.5813 0.64281	1.321 ± 0.6298 0.27015	0.831 ± 0.6394 0.77128	AGCTGGTAAAAGCTGTAAGAACAGCTGAGGGGGCTAACCGGTACTGATG
plasmid_lp28-1	21885	BB_F32	0.749 ± 0.439 0.161768	0.716 ± 0.4094 0.54455	0.893 ± 0.4062 0.34385	1.011 ± 0.5098 0.96682	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGAGTAATG
plasmid_lp28-1	22045	BB_F32	0.489 ± 0.2507 0.089035	0.65 ± 0.5401 0.17373	1.08 ± 0.6574 0.29603	1.247 ± 0.6583 0.88872	ATATCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAG
plasmid_lp28-1	22045	BB_F32	0.451 ± 0.2481 0.253028	0.414 ± 0.2326 0.57562	0.698 ± 0.3131 0.46731	0.958 ± 0.3984 0.24227	TAAAGTGCATTGTTACGGCTCGGGCTGCTGGTAGCAGGATGGAGAGAAG
plasmid_lp28-1	22048	BB_F32	0.496 ± 0.6556 0.26912	1.573 ± 1.707 0.58927	0.663 ± 0.2781 0.17569	0.358 ± 0.2264 0.04648	TCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAGCCT
plasmid_lp28-1	22233	BB_F32	1.087 ± 0.4666 0.390364	1.63 ± 1.2311 0.35811	0.812 ± 0.3066 0.08784	1.066 ± 0.567 0.75411	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGGAGTGAAGAGCTGAAAG
plasmid_lp28-1	22392	BB_F32	0.600 ± 0.3352 0.108704	0.717 ± 0.3571 0.4901	0.911 ± 0.4716 0.32719	1.031 ± 0.3865 0.84441	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGGGTAATA
plasmid_lp28-1	22546	BB_F32	0.612 ± 0.1862 0.186657	0.512 ± 0.2067 0.11952	0.943 ± 0.2385 0.78741	1.296 ± 0.3781 0.20088	ATATCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAG
plasmid_lp28-1	22549	BB_F32	0.451 ± 0.5366 0.14318	2.281 ± 2.7673 0.49025	0.867 ± 0.3416 0.6303	0.504 ± 0.532 0.33193	TCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAGCCT
plasmid_lp28-1	22728	BB_F32	1.180 ± 0.6543 0.743607	1.67 ± 1.1581 0.4617	0.607 ± 0.2557 0.13014	0.885 ± 0.4366 0.76911	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGGAGTGAAGAGCTGAAAG
plasmid_lp28-1	22950	BB_F32	0.650 ± 0.3952 0.238096	0.787 ± 0.4778 0.66777	0.881 ± 0.4279 0.32157	1.091 ± 0.4635 0.72238	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGGGTAATA
plasmid_lp28-1	23110	BB_F32	0.534 ± 0.1701 0.127081	0.47 ± 0.3185 0.19665	0.632 ± 0.2041 0.20708	0.978 ± 0.3677 0.94701	ATATCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAG
plasmid_lp28-1	23113	BB_F32	0.357 ± 0.4036 0.187026	1.866 ± 2.0503 0.56082	0.741 ± 0.3421 0.32615	0.441 ± 0.2513 0.00773	TCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAGCCT
plasmid_lp28-1	23292	BB_F32	1.085 ± 0.4753 0.358957	1.627 ± 1.2084 0.32087	0.775 ± 0.3113 0.11957	1.086 ± 0.6215 0.72793	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGGAGTGAAGAGCTGAAAG
plasmid_lp28-1	23454	BB_F32	0.648 ± 0.4884 0.200612	0.707 ± 0.4532 0.5683	0.883 ± 0.5044 0.09467	1.002 ± 0.5088 0.99571	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGAATGATG
plasmid_lp28-1	23617	BB_F32	0.740 ± 0.313 0.204226	0.595 ± 0.4769 0.44924	0.847 ± 0.4161 0.24691	1.053 ± 0.4096 0.78914	ATATCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAG
plasmid_lp28-1	23709	BB_F32	0.842 ± 0.359 0.565927	1.93 ± 1.135 0.28428	1.003 ± 0.7415 0.99317	1.279 ± 0.9162 0.67447	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGACAGTGGCTGCTAGCA
plasmid_lp28-1	23826	BB_F32	0.764 ± 0.2833 0.158863	1.132 ± 0.6449 0.73048	1.351 ± 0.5239 0.30454	1.127 ± 0.5126 0.55195	AGCTGGTAAAAGCTGTAAGAACAGCTGAGGGGGCTAACGTGTTACTGCTG
plasmid_lp28-1	23931	BB_F32	1.354 ± 0.9767 0.428785	2.963 ± 3.1849 0.32188	1.12 ± 0.7662 0.59057	1.626 ± 1.018 0.43293	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGGATGGTG
plasmid_lp28-1	24396	BB_F32	0.794 ± 0.2936 0.229714	1.148 ± 0.6591 0.70599	1.366 ± 0.5568 0.32861	1.142 ± 0.5027 0.49493	AGCTGGTAAAAGCTGTAAGAACAGCTGAGGGGGCTAACGTGTTACTGCTG
plasmid_lp28-1	24498	BB_F32	0.617 ± 0.3894 0.13029	0.633 ± 0.3836 0.41468	0.833 ± 0.3292 0.0449	0.889 ± 0.3976 0.73437	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGAAGGATG
plasmid_lp28-1	24664	BB_F32	0.523 ± 0.1898 0.081801	0.38 ± 0.3013 0.14581	0.763 ± 0.2616 0.39062	1.018 ± 0.4411 0.96512	ATATCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAG
plasmid_lp28-1	24667	BB_F32	0.500 ± 0.6003 0.348994	1.942 ± 2.4192 0.57758	0.669 ± 0.2623 0.18569	0.427 ± 0.2672 0.18535	TCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAGCCT
plasmid_lp28-1	24771	BB_F32	0.169 ± 0.2399 0.080397	0.691 ± 0.6916 0.1226	0.659 ± 0.9015 0.50615	1.288 ± 0.8182 0.41603	AAGAGGCCAGGGAAAGTTGTTGGGAAGGCTGTGCTGATGTAATGGGACA
plasmid_lp28-1	24849	BB_F32	1.093 ± 0.464 0.263066	1.542 ± 1.1404 0.35123	0.778 ± 0.3083 0.05672	1.029 ± 0.5879 0.90375	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGGAGTGAAGAGCTGAAAG
plasmid_lp28-1	24966	BB_F32	0.345 ± 0.2824 0.126861	0.913 ± 0.4273 0.80931	1.288 ± 0.5552 0.38268	1.056 ± 0.8708 0.92544	AGCTGGTAAAAGCTGTAAGAACAGCTGAGGGGGCTAACGTGTTACTGATG
plasmid_lp28-1	25071	BB_F32	1.408 ± 1.0523 0.374976	2.907 ± 3.1103 0.31217	1.086 ± 0.7504 0.65174	1.627 ± 1.0539 0.43891	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGGATGGTG
plasmid_lp28-1	25167	BB_F32	1.245 ± 1.0276 0.671904	1.935 ± 1.5337 0.32256	1.013 ± 0.3496 0.94881	2.064 ± 1.474 0.264	CAAATCCGATTGCTGCTGATTGGGAAGGTAATGAGGAGAATGGTGCGG
plasmid_lp28-1	25231	BB_F32	0.575 ± 0.1899 0.157929	0.536 ± 0.2971 0.25842	0.746 ± 0.2753 0.42972	1.081 ± 0.3862 0.79262	ATATCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAG
plasmid_lp28-1	25234	BB_F32	0.430 ± 0.583 0.248303	1.845 ± 2.2183 0.58074	0.639 ± 0.2408 0.12234	0.411 ± 0.3248 0.07331	TCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAGCCT
plasmid_lp28-1	25419	BB_F32	1.077 ± 0.5015 0.552665	1.616 ± 1.2291 0.35849	0.819 ± 0.3211 0.03512	1.04 ± 0.5664 0.86974	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGGAGTGAAGAGCTGAAAG
plasmid_lp28-1	25542	BB_F32	0.385 ± 0.3294 0.112439	0.851 ± 0.3924 0.64685	1.35 ± 0.5658 0.42059	1.165 ± 0.9099 0.7917	AGCTGGTAAAAGCTGTAAGAACAGCTGAGGGGGCTAACGTGTTACTGATG
plasmid_lp28-1	25650	BB_F32	0.674 ± 0.3669 0.193154	0.6 ± 0.5242 0.52727	0.985 ± 0.5332 0.91415	1.135 ± 0.7529 0.38737	TTGCTTGAGGGGGATGGCTAAGGATGAAAAGTTGCTGTGAAGAGTGGTG
plasmid_lp28-1	25819	BB_F32	0.515 ± 0.2333 0.051969	0.475 ± 0.2885 0.18289	0.768 ± 0.3628 0.54706	1.073 ± 0.412 0.83004	ATATCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAG
plasmid_lp28-1	25822	BB_F32	0.430 ± 0.6425 0.315285	1.898 ± 2.0067 0.53575	0.772 ± 0.1061 0.0497	0.632 ± 0.3807 0.15017	TCTGCTCCCCACTAACAGCACTAACAGCACCGCCCTTGTAGCAGCCT

plasmid_lp28-1	26001	BB_F32	0.713 ± 0.3761 0.505892	2.107 ± 1.9565 0.44548	0.698 ± 0.5455 0.21892	0.946 ± 0.6106 0.92411	AGGGGATAAAAGGAGATTGTTGAAGCTGCTGGGGGGAGTAAAAGCTGAAAG
plasmid_lp28-1	26124	BB_F32	0.787 ± 0.2799 0.254064	1.09 ± 0.5942 0.80117	1.338 ± 0.4715 0.28754	1.126 ± 0.4767 0.57315	AGCTGGTAAAGCTGTAAGACAGCTGAGGGGGCTCAAGTGTACTGCTG
plasmid_lp28-1	26226	BB_F32	0.691 ± 0.5881 0.271193	0.706 ± 0.4709 0.58368	0.956 ± 0.5623 0.36595	1.11 ± 0.5873 0.78846	TTGCTTGAGGGGGATGGCTAAGGATGGAAAGTTGCTGTGAAGAATGATG
plasmid_lp28-1	26383	BB_F32	0.614 ± 0.2109 0.160262	0.443 ± 0.2685 0.18346	0.747 ± 0.3129 0.18814	1.041 ± 0.3873 0.84851	ATATCTGCTCCCCTAACAAGCAGCTAACAGCACCGCCCTGCTAGCAG
plasmid_lp28-1	26386	BB_F32	0.417 ± 0.5554 0.303337	1.706 ± 2.2278 0.65856	0.541 ± 0.1822 0.09861	0.398 ± 0.2676 0.06845	TCTGCTCCCACTAACAGCACTAACAGCACCGCCCTGCTAGCAGCCT
plasmid_lp28-2	219	BB_G01	1.711 ± 1.2123 0.103113	1.982 ± 1.7124 0.22719	0.9 ± 0.4576 0.72922	1.216 ± 0.642 0.41735	ATGAAAAGAAGTTGCAATAGTGTCAAGAAGATGGCTTAATGATTAT
plasmid_lp28-2	1027	IG_1188	2.615 ± 0.6074 1.48E-05	1.758 ± 0.8282 0.29926	0.798 ± 0.238 0.26638	1.053 ± 0.2795 0.2773	TAGGTTGGAAATTCTTGTATTTCATTGAGACTTCTAAACAGTTT
plasmid_lp28-2	1034	IG_1189	2.030 ± 2.1488 0.229876	3.406 ± 4.8188 0.30783	1.035 ± 1.311 0.94379	1.156 ± 1.6937 0.66404	GAAATTATAGGTGGAATATTCTTGTATTTCATTGAGACTTCTAAA
plasmid_lp28-2	1216	BB_G02	1.188 ± 1.6102 0.721972	0.519 ± 0.8272 0.62834	0.706 ± 0.8921 0.61695	0.556 ± 0.7251 0.48326	TGTTTCATTATTTATAACCAGGCTAATTATGACCCCCCTATTTCAGAG
plasmid_lp28-2	1464	BB_G02	3.211 ± 3.2426 0.151471	1.709 ± 2.3184 0.34675	1.246 ± 1.2749 0.08666	1.072 ± 1.1116 0.61689	CTTGGCTATATTAGCCTTAACTTCAAATATCTATCGAGATAGATT
plasmid_lp28-2	1572	BB_G02	1.287 ± 0.6197 0.193124	0.649 ± 0.554 0.57302	1.102 ± 0.6371 0.06306	1.238 ± 0.8488 0.22944	TTTGTAAACACTTGGCAAACCTTGGAAAGCATCTCATTAATTCTCATTTAGTA
plasmid_lp28-2	1762	BB_G02	2.398 ± 1.0502 0.154602	1.538 ± 1.1674 0.5493	1.757 ± 0.8165 0.20556	3.392 ± 1.3486 0.07633	AATCTAGAAGTTGGTTATAGTAAAGCTTCATTGTCTTCTTATAAAA
plasmid_lp28-2	1827	BB_G02	3.975 ± 1.5946 0.069688	1.876 ± 1.1665 0.29327	1.203 ± 0.6375 0.66009	0.993 ± 0.2374 0.9366	AGTAACCTTTAGAGTTGCCAACCTCCAAATAGTATAGTTACACCTCTT
plasmid_lp28-2	2351	BB_G03	2.706 ± 4.4874 0.490375	2.557 ± 4.262 0.50227	0.489 ± 0.5922 0.05228	0.772 ± 1.0464 0.39796	AGTATTCTTCAAGCACTTGGAGAGCCAAGTAGTGCACCCACCAATATA
plasmid_lp28-2	2374	BB_G03	1.945 ± 1.2532 0.233441	1.651 ± 1.4782 0.36112	0.736 ± 0.5376 0.25058	0.932 ± 0.5964 0.83241	CGATCATGTGTCAGGCCATTATAAGTATTCTTCAAGCACTTGGAGAGCCA
plasmid_lp28-2	2867	IG_1190	1.892 ± 0.8788 0.008936	1.564 ± 0.9415 0.06397	0.796 ± 0.3639 0.42701	1.053 ± 0.5066 0.80211	GCTTTTAGGCTCTAAAGAACGGTCACTCCACTAGAGCATGGTCCACAAGC
plasmid_lp28-2	3151	BB_G05	2.620 ± 0.9072 0.034748	1.926 ± 1.4236 0.30298	0.932 ± 0.2247 0.37281	1.044 ± 0.3258 0.54969	TCATACAAATCAGAGTGGTATGGATCCTCTTGTATAAAGTAGATAGAGAT
plasmid_lp28-2	8045	BB_G10	1.246 ± 1.9196 0.426687	1.34 ± 1.4157 0.47068	0.354 ± 0.4696 0.48394	0.294 ± 0.39 0.41462	AAACAAAAAAAGATATAGAACCCACCAACTACTAACAGACCGAAGAGGCTA
plasmid_lp28-2	8543	BB_G10	1.860 ± 0.6239 0.020496	1.592 ± 0.8235 0.166	0.742 ± 0.1876 0.15885	1.015 ± 0.2924 0.83236	TCTTCATAAAGCCTTAAAGACATTAGGCCGTCTATCATGCTGTCA
plasmid_lp28-2	9092	BB_G10	0.982 ± 1.2388 0.069228	1.696 ± 2.1185 0.32666	0.912 ± 1.3031 0.93909	1.43 ± 1.9322 0.73158	ACTCCAATTATGATTGTAATGAGTACCAAATTACTAAAGAAAAAG
plasmid_lp28-2	11445	BB_G12	0.853 ± 0.9473 0.806847	1.172 ± 1.1568 0.59033	0.629 ± 0.737 0.66264	1.031 ± 1.0601 0.96854	TCCCAGACTATTAGAAACGCCAGGAAAAGATCAAAGAAGAGAAGAGAAG
plasmid_lp28-2	12129	BB_G13	2.165 ± 1.3419 0.153073	1.48 ± 0.9136 0.28109	0.871 ± 0.6398 0.59873	1.119 ± 0.7286 0.74552	GCGAATGCTTTAGGGTTAAAAAGATTGATTCTAACTCAAACTTACAT
plasmid_lp28-2	12340	BB_G14	2.496 ± 1.9577 0.146267	2.218 ± 3.0132 0.55719	0.881 ± 0.6245 0.80324	1.13 ± 1.3087 0.88315	13.13 ATGAACTCAGCGCCATTCTACTAACTCCAAATGTTGAATCAACCAATGTT
plasmid_lp28-2	12539	BB_G14	1.896 ± 3.4224 0.179708	2.189 ± 3.6595 0.11488	0.561 ± 0.826 0.66649	0.697 ± 1.0322 0.73018	TGAACTTGGACACAAAAGCATCGAGTAATTGGCAATGATTAGAATT
plasmid_lp28-2	12699	BB_G14	1.852 ± 1.1485 0.017853	2.315 ± 1.4032 0.09129	1.143 ± 0.8148 0.83153	2.292 ± 1.6375 0.23118	CTTGGCTACTTGTAAACAAACACACAAAAGTATATTACAAGTCTGAAAT
plasmid_lp28-2	12847	BB_G15	4.043 ± 1.3348 0.017694	2.98 ± 1.1331 0.08357	2.236 ± 1.4036 0.29759	2.092 ± 1.2178 0.22302	CTGCTGAGGATTCTATACCTTATATGTCGCCAACCTTGTATTGTTA
plasmid_lp28-2	12924	BB_G15	1.941 ± 0.3729 0.010325	1.44 ± 0.3092 0.45862	0.86 ± 0.2515 0.36347	0.924 ± 0.3785 0.67469	TATGCTGCTCTGAGTCTAGAAATTCAAGAAGAGGGAGCTACCTTACT
plasmid_lp28-2	13362	BB_G16	1.807 ± 0.4755 0.088793	1.284 ± 0.6444 0.32676	0.837 ± 0.4289 0.38165	0.939 ± 0.3126 0.8358	GATATGCAAAATCTTTGGCCCTGACCAAATGGGAGTTGCTTACAATA
plasmid_lp28-2	13681	BB_G17	1.914 ± 2.4885 0.62253	3.724 ± 4.4042 0.34733	0.802 ± 0.9325 0.70897	0.735 ± 0.8951 0.55435	CTTTATCAACCAAATCCAGAAAGTTGTCATTGTCAGGAAATA
plasmid_lp28-2	13757	BB_G17	2.653 ± 2.7004 0.373347	0 ± 0 0.08025	0.441 ± 0.7972 0.26872	0.133 ± 0.1583 0.09042	TGTAACAGTTAAAGAACGGCTAGATTAGAGATCATAAAGTGTAACTTCGGT
plasmid_lp28-2	13902	BB_G17	1.010 ± 0.9079 0.982867	1.26 ± 1.9642 0.79999	0.931 ± 0.9368 0.84665	0.955 ± 1.4748 0.96474	CTATGGATATACGTTGATGAAAGTAGACTTGTGCAAAACGTGAAGCAG
plasmid_lp28-2	14401	BB_G18	1.844 ± 1.465 0.125773	1.492 ± 1.4203 0.3343	0.963 ± 0.8435 0.91842	0.936 ± 0.9853 0.76243	GACTCAAACCTAGGGCCAAATTAAACATCAAGCAAAACTACTTGTATT
plasmid_lp28-2	14441	BB_G18	3.594 ± 3.7526 0.174278	0.534 ± 0.6181 0.56597	1.025 ± 1.4032 0.9819	0.689 ± 0.6984 0.67915	CTTGGCTATTGCACTAACACTCTTGTATTCTCCAACTTGCACAC
plasmid_lp28-2	16230	BB_G20	1.513 ± 1.4736 0.110082	1.66 ± 1.8942 0.28925	0.699 ± 0.5722 0.3835	0.866 ± 0.6859 0.65969	GTAGTTCCAGATTCCGATGTCACACAAAGCCACTAAAAAGGGTTCT
plasmid_lp28-2	16234	BB_G20	2.051 ± 1.1742 0.007416	2.39 ± 2.1308 0.20474	0.856 ± 0.5586 0.61974	1.107 ± 0.6222 0.4857	TATAGTAGTCCAGATTCCGATGTCACACAAAGCCACTAAAAAGGGTT
plasmid_lp28-2	16723	BB_G21	1.842 ± 1.4773 0.193944	1.748 ± 1.7236 0.355	0.658 ± 0.3439 0.36423	0.755 ± 0.6721 0.29731	CTTGGCTTGTGCAAAACACGAAATCTTGTATTCTACTCAGACTTTGATT
plasmid_lp28-2	18055	BB_G22	2.385 ± 2.6741 0.021701	1.756 ± 2.2158 0.10098	0.934 ± 1.0248 0.87401	0.76 ± 0.9676 0.4356	TATCTTTTACAGATACTGACATTAGGAGAAAATTATGGACAATTACAA
plasmid_lp28-2	18057	BB_G22	2.161 ± 0.6553 0.003673	1.522 ± 1.0387 0.37902	0.777 ± 0.4472 0.11873	1.551 ± 0.4321 0.14996	TATATCTTTTACAGATACTGACATTAGGAGAAAATTATGGACAATTAC
plasmid_lp28-2	18116	BB_G22	2.587 ± 0.9964 0.020725	1.399 ± 0.6713 0.13775	0.897 ± 0.2625 0.63264	1.018 ± 0.3826 0.35954	TTACCCACCTTCAACAGTGTCAAGGAAACAAACCTTACAA
plasmid_lp28-2	18145	BB_G22	1.433 ± 1.8607 0.450544	1.956 ± 2.6821 0.10606	0.668 ± 0.8085 0.5641	0.914 ± 1.0092 0.91216	GTTATGAGAGATAGACCCCGAAATTATACACCTTCAACAGTCAA
plasmid_lp28-2	18147	BB_G22	0.498 ± 0.3649 0.266264	1.305 ± 1.5556 0.678	0.789 ± 0.4504 0.66366	0.469 ± 0.5356 0.00822	TAGTTATGAGAGATAGACCCCGAAATTATACACCTTCAACAGTCAA
plasmid_lp28-2	18331	BB_G22	2.618 ± 1.299 0.115713	2.519 ± 2.1214 0.34667	0.94 ± 0.5389 0.89582	1.881 ± 0.6604 0.04734	CCGTCAAGAACGGTGGAGCCGCCAGAACATAGTGTCTCAAGAATCTGCC
plasmid_lp28-2	18864	BB_G23	2.997 ± 1.9188 0.031593	2.584 ± 2.1943 0.11451	0.889 ± 0.6321 0.69543	0.9 ± 0.5472 0.81222	TATTCATTCAGATGATGGTAGTAAATCAATGATAACACAAACAA
plasmid_lp28-2	19017	BB_G23	1.373 ± 0.7002 0.020958	1.075 ± 0.8674 0.77282	0.646 ± 0.3408 0.12581	0.732 ± 0.4241 0.04418	ATCAGTCACAAGTCGCCCTCGCAGACTATCCAACAGCTCAAGTCA
plasmid_lp28-2	19120	BB_G23	2.615 ± 1.0609 0.098834	2.467 ± 1.9588 0.33913	0.923 ± 0.4211 0.82957	1.729 ± 0.511 0.07945	CCGTCAAGAACGGTGGAGCCGCCAGAACATAGTGTCTCAAGAATCTGCC
plasmid_lp28-2	19297	BB_G23	2.017 ± 3.9272 0.691517	1.059 ± 1.484 0.94335	0.205 ± 0.2964 0.28988	1.674 ± 2.6214 0.27684	TATCAAGAAGCAAGTGTACAAGCTTGTGAGAAGATACTAAAATTGTA
plasmid_lp28-2	20219	BB_G24	0.608 ± 0.2466 0.283512	0.513 ± 0.4291 0.3422	0.933 ± 0.4778 0.32729	1.006 ± 0.4994 0.94221	CAACAGCGGGCTGTGAAAGCTTGTCTAGTAAGGTGCCAGTCT
plasmid_lp28-2	20324	BB_G24	1.885 ± 1.8496 0.048924	0.887 ± 1.2584 0.50358	0.65 ± 0.722 0.68959	0.473 ± 0.5897 0.26286	TATGACTCCAGAAAGCCTGAAATGATTCTGTGATGAAATATGTTAG
plasmid_lp28-2	20368	BB_G24	1.537 ± 0.7414 0.007289	1.646 ± 1.7736 0.47465	0.613 ± 0.5413 0.02845	0.861 ± 0.5563 0.10213	TGTTAGAAAACCCGTGCTTATGAAACACTCGTCATCGCCTCGATT

plasmid_lp28-2	20806	BB_G24	3.099 ± 1.7642 0.144362	0.929 ± 0.9018 0.91604	0.606 ± 0.2089 0.17906	0.87 ± 1.2554 0.89721	TTTAGATTCTGCATTGACCTAAATTAAACAATAGTGTCCCTTGACACGT
plasmid_lp28-2	20919	BB_G24	1.819 ± 0.8109 0.242533	1.279 ± 0.3838 0.41316	0.998 ± 0.6027 0.99648	1.096 ± 0.1804 0.55176	CACAAACAGATTCACTTTTCCGAAGATTCAAGCATTAAGACTTTGAAATT
plasmid_lp28-2	21296	BB_G24	2.623 ± 3.3977 0.339132	0.261 ± 0.3768 0.33937	1.181 ± 1.3228 0.86067	0.577 ± 0.783 0.33192	CGCCTTTTGAAGAACCTGCAACGTACAGTGCACCATCGGTACCGAACAT
plasmid_lp28-2	21710	BB_G24	2.754 ± 1.5075 0.096269	2.857 ± 2.4881 0.26037	0.988 ± 0.3219 0.93286	1.558 ± 0.6886 0.06183	ATAGAAAAAAACTAAACTAAAGACCTTATTGATGATGATGCTAGCGAAGCA
plasmid_lp28-2	22159	BB_G24	2.132 ± 2.6693 0.361448	1.755 ± 2.3489 0.44316	1.381 ± 2.0736 0.65907	0.7 ± 0.6818 0.49928	CATGGAAAATTGACTCTTGGGCTTGATATTGATTCTACACGGACG
plasmid_lp28-2	22294	BB_G25	1.767 ± 0.6619 0.051217	1.17 ± 0.5298 0.21216	0.851 ± 0.3767 0.68923	1.076 ± 0.3987 0.22252	CAAAAATACAGCAGAAGATAAGGATTGATTAAGTTGAAGATCAAGACA
plasmid_lp28-2	23052	BB_G27	2.259 ± 1.422 0.134713	1.246 ± 0.8239 0.18506	1.16 ± 1.045 0.84168	1.649 ± 1.054 0.33966	TTTCAAAATTGCACTGTAAAATTCTAGTCTATCCTTACCGCTCTAA
plasmid_lp28-2	23664	BB_G27	2.279 ± 0.8274 0.049015	1.512 ± 1.1202 0.34957	1.068 ± 0.455 0.03808	1.052 ± 0.4363 0.58203	AAGTAGTCTTCAAAGTTGAGAAAAAATTGTAATGCTACAAAAACATT
plasmid_lp28-2	24057	BB_G28	2.829 ± 3.4506 0.235172	2.156 ± 1.8699 0.02061	1.236 ± 1.5446 0.38899	1.597 ± 2.2516 0.42673	GCATTGCTACATGCTGCCATAATATTATTGTTTTACTCTGTCA
plasmid_lp28-2	24235	IG_1191	1.737 ± 0.7979 0.052541	0.816 ± 0.3691 0.63006	1.11 ± 0.5526 0.07027	1.1 ± 0.4789 0.36892	TTACATTATTAGTATTCTGAATTGATTAACGTTTTGCTAAAAATCAA
plasmid_lp28-2	24537	BB_G29	2.350 ± 0.5358 0.052847	1.713 ± 0.7556 0.25665	1.03 ± 0.167 0.82683	1.032 ± 0.1696 0.8268	CATGAATTGCTACCAAATTGTAGCTTAAACAGTAAAAAGAACACTGT
plasmid_lp28-2	24748	BB_G29	2.199 ± 0.7414 0.068487	1.691 ± 1.1981 0.38626	1.026 ± 0.3321 0.89269	1.174 ± 0.315 0.3015	GACTGGTTGCTGTGCTCAAAAGATGGCAAAAGGTTGTTAGTGTGC
plasmid_lp28-2	25212	BB_G29	1.452 ± 1.1932 0.25623	1.43 ± 1.5551 0.32328	0.792 ± 0.702 0.58685	1.052 ± 0.9245 0.91948	ACTAATCAGGATGTTGACAGTCGCACCAATGTCGCCACTCGCCACCG
plasmid_lp28-2	25298	BB_G29	1.035 ± 0.6842 0.787315	1.385 ± 0.8148 0.36957	0.71 ± 0.6104 0.06343	0.698 ± 0.4685 0.40399	TTATAAGAATTCAAAGAATTCTTATGTAATTCAAACAAACAA
plasmid_lp28-2	26295	BB_G30	2.370 ± 1.9779 0.216801	3.667 ± 5.1225 0.38296	1.235 ± 1.5605 0.67469	1.43 ± 1.1372 0.34239	TTCTTGGCAGGTTGCAAAAAGAATGTTGCTGGTCACAAGCGGGATCGGG
plasmid_lp28-2	26984	BB_G31	1.972 ± 1.8178 0.074798	2.441 ± 3.1418 0.2523	0.8 ± 0.7603 0.73946	1.564 ± 1.6389 0.1225	TAATACCTTCGCCCCGGGATTCAAATCTGCACCATAAAACCTTAAACTC
plasmid_lp28-2	27408	BB_G32	1.078 ± 0.5325 0.653328	0.556 ± 0.4585 0.35514	0.772 ± 0.2248 0.22789	0.834 ± 0.5644 0.48287	TCAGTCGCTAAATAAAAGTGAACGGACCTTACCATAAATCAGTTCTG
plasmid_lp28-2	27645	BB_G32	1.247 ± 1.4129 0.421081	0.58 ± 0.5659 0.57403	0.948 ± 0.6904 0.87752	1.152 ± 1.116 0.24042	ATATACGTTGCTTGCACCTGAATTGAAATTCCAATAATAGTTGTATCTC
plasmid_lp28-2	27683	BB_G32	3.588 ± 3.1211 0.032996	2.769 ± 2.9257 0.09625	1.152 ± 1.0024 0.79372	1.351 ± 1.5171 0.03888	TTATTGAAATTCCAAGTCAAGTCAAGGAAACGTATTACGACTCAA
plasmid_lp28-2	28939	BB_G34	2.563 ± 1.4709 0.063135	2.213 ± 1.8648 0.20854	0.926 ± 0.6578 0.23403	1.52 ± 0.8752 0.10697	ATGCTAACCTAAAAAAACTGGGAATCTCAAACAAACTTGAATTACAAA
plasmid_lp28-3	498	BB_H02	1.768 ± 1.4291 0.428204	3.219 ± 2.6906 0.27751	1.071 ± 0.2101 0.54774	1.033 ± 0.3317 0.82585	GTTAATAGTAGAATTAAATTATCATTGGTTAGTAATAATGGTTGAAACG
plasmid_lp28-3	518	BB_H02	1.236 ± 1.102 0.746637	1.472 ± 1.5167 0.59314	0.661 ± 0.6552 0.59516	0.606 ± 0.5364 0.38466	GTTGAATATAAGGTTGGTAGTTAATAGTAAATTATCATTGG
plasmid_lp28-3	804	BB_H02	2.887 ± 0.9203 0.052821	2.107 ± 0.7383 0.72205	1.027 ± 0.4871 0.92835	0.935 ± 0.724 0.87911	TACCAACTACATAAAATAGGAGACAATTGTTAAGAATTATTAGCAACTT
plasmid_lp28-3	924	IG_1192	1.362 ± 1.0142 0.536742	1.272 ± 1.2814 0.73716	1.491 ± 1.048 0.25656	0.829 ± 0.6395 0.78589	TTATGAAAAAAATCAAAAACAAGTGCCTAGAAATAGAAAAACACAAAT
plasmid_lp28-3	1088	BB_H04	1.638 ± 1.0932 0.149829	1.272 ± 0.7149 0.30839	1.297 ± 0.8056 0.10389	1.184 ± 0.8581 0.08101	TTCAATTCTAGATTTAATAATGTATTGTCACATAAAGCAGGCATACCCAG
plasmid_lp28-3	1195	BB_H04	1.067 ± 0.557 0.86485	1.383 ± 0.713 0.37496	1.694 ± 1.0959 0.13679	1.307 ± 0.9478 0.21598	GAAAAAAACAAAACCATAGTAAACAACTATCTTAAACACCAGTCAAATAT
plasmid_lp28-3	1322	BB_H04	2.147 ± 1.3276 0.293402	1.449 ± 0.7854 0.28143	1.706 ± 0.7403 0.25806	1.597 ± 1.096 0.39067	TCTGTTATTGTTGATAGTAGCTTGTATTGTTGAAACACACTTAAAGG
plasmid_lp28-3	1587	BB_H05	1.478 ± 1.3827 0.108043	1.353 ± 1.0876 0.36014	0.784 ± 0.6753 0.462	0.805 ± 0.6422 0.64076	GTATCCAATATTGTTGAATTAGGTCATTAGTTGTTAGTGTAAATAAG
plasmid_lp28-3	1672	BB_H05	2.011 ± 1.3627 0.25515	1.423 ± 0.9665 0.47252	0.845 ± 0.2929 0.33706	1.131 ± 0.7411 0.81984	TAAAGAATAAGTAAAGACTGGTAGTTACTGGAGTATTATCT
plasmid_lp28-3	1677	BB_H05	3.018 ± 1.3543 0.133954	2.845 ± 2.0531 0.24781	1.151 ± 0.2047 0.35555	1.509 ± 0.6746 0.22885	TTTATAAGAATAAGTAAAGACTGGTAGTTACTGGAGTATTAT
plasmid_lp28-3	2049	IG_1193	1.528 ± 1.2467 0.238304	1.997 ± 1.952 0.29286	1.039 ± 0.6478 0.59557	1.181 ± 0.802 0.09269	TAAGCAATAATTATTTTAAATGTAATAAGGAGAGTATGTAATTATTT
plasmid_lp28-3	2181	IG_1194	4.470 ± 4.3551 0.147689	5.994 ± 8.6254 0.35524	2.509 ± 2.6252 0.04421	2.732 ± 2.9487 0.21564	TGCAAGATGTTTAAACCAAGAACATGCCCTCTTTGATAAAATTGG
plasmid_lp28-3	2285	BB_H06	2.740 ± 3.2611 0.182901	3.201 ± 4.5672 0.31933	1.218 ± 1.5555 0.50716	2.263 ± 1.9699 0.02075	AAGCTTAAAGCAAACCTTTATTAGATCACAAAGGTATAAAATTAGGCTT
plasmid_lp28-3	2387	BB_H06	0.948 ± 1.0997 0.932779	0.549 ± 0.6327 0.25245	0.96 ± 0.3987 0.77169	0.83 ± 0.7522 0.69306	TGGTTAATGATAGGGAAATAATTCAAGAAGCAGGTATAAATTTTATA
plasmid_lp28-3	2603	BB_H06	2.474 ± 2.7443 0.447375	1.709 ± 1.8255 0.59689	0.859 ± 0.9682 0.63503	0.496 ± 0.3314 0.29375	ATGATGTTGCTAATGCCAGACATGTTGCTATTCTATAAAACCTAGAA
plasmid_lp28-3	2800	BB_H06	1.214 ± 1.3606 0.35561	0.778 ± 0.7822 0.7042	0.923 ± 0.9597 0.83794	0.959 ± 1.0835 0.83663	TAATGATATTGACTTATTGCGGAGGTACATTCTGATCAAAGTAAGGT
plasmid_lp28-3	2848	BB_H06	2.655 ± 0.8909 0.03838	3.043 ± 1.4379 0.04251	2.319 ± 0.9857 0.02838	2.865 ± 1.1334 0.0498	ATACTTGGCTTTCACAAAAATTAGTCATTAATTTCTGATT
plasmid_lp28-3	2925	BB_H06	0.639 ± 0.9266 0.46041	0.408 ± 0.3886 0.25592	0.31 ± 0.3716 0.07372	0.593 ± 0.9887 0.4416	AACCTTATTGAAATTACATGTTGATATTGATAAAAACCTTTTCTATTT
plasmid_lp28-3	3106	BB_H07	0.707 ± 0.398 0.440295	1.436 ± 1.3102 0.64281	0.71 ± 0.5822 0.49912	0.833 ± 0.5555 0.69099	TTAAAGAATAAGCAATTTTTAAATAAAATGCAAAACAAAAAA
plasmid_lp28-3	3436	BB_H07	1.250 ± 0.1548 0.010165	2.064 ± 0.9217 0.19029	1.02 ± 0.2858 0.90947	0.952 ± 0.1771 0.69342	TGTTTTTCAATTCTTTGAAATTAGCTTTAAGTTCTAAATCATTTA
plasmid_lp28-3	3600	IG_1195	1.438 ± 0.6834 0.016307	1.657 ± 1.4167 0.3442	0.954 ± 0.4459 0.7629	1.256 ± 0.6333 0.07426	ATTGCTAAATCATCTCTTTGCTATATGTAAGTAAAGTCTACCAATA
plasmid_lp28-3	3626	IG_1196	1.559 ± 0.9465 0.158161	2.005 ± 0.9624 0.05212	1.254 ± 0.6854 0.13836	1.344 ± 0.8002 0.45672	TATAGCAAAAGAAGATGATTAGCAATTATGTAATTATAAAAGAGT
plasmid_lp28-3	3684	IG_1197	4.707 ± 5.3426 0.296291	9.766 ± 11.435 0.22836	1.827 ± 2.1481 0.60552	2.716 ± 2.6974 0.28612	AAGCTTTTATTCTAATGTTTAGCTTTATAAAACACCAACATGACA
plasmid_lp28-3	3841	IG_1198	1.775 ± 0.9807 0.070152	1.828 ± 1.7071 0.39427	1.018 ± 0.5949 0.77753	1.437 ± 1.2566 0.46641	AATGATGAAAAGGTTATTCTGGTGAAGTGTATTCTAAACAGAGCCT
plasmid_lp28-3	3896	BB_H09	2.705 ± 2.2229 0.172965	2.577 ± 2.4786 0.27525	1.527 ± 1.3668 0.6134	0.887 ± 0.7164 0.68446	ATTAAGCATTAAATAGATTAAATAAATTCTTAGCAAGAAAACATT
plasmid_lp28-3	4317	BB_H09	1.352 ± 0.7456 0.339888	1.695 ± 1.2087 0.33878	0.953 ± 0.2959 0.62228	1.094 ± 0.2896 0.07547	AATAAGTCAAAACAAATGAATTAAAATAGATATAAAATTCTTAT
plasmid_lp28-3	4343	BB_H09	0.295 ± 0.3464 0.061517	0.356 ± 0.3025 0.05162	0.622 ± 0.2646 0.14108	0.021 ± 0.0367 0.00061	TTTTAATTCTGATTAGTAAAGAAGATTGCTTAAAGCA
plasmid_lp28-3	4402	BB_H09	0.756 ± 0.8913 0.454401	2.324 ± 2.3246 0.40202	0.752 ± 0.9823 0.47391	2.468 ± 1.559 0.20945	TATGTAGAAACACAATAACAAATTCTAGGAGATAAGTACTAATCATGGT
plasmid_lp28-3	4458	BB_H09	2.280 ± 1.337 0.126376	2.492 ± 2.5099 0.34951	1.496 ± 0.9448 0.27372	1.332 ± 0.9479 0.52718	TATCTGATTCTGCACTCTTATATAATTCTTCTATTGACT

plasmid_lp28-3	4655	BB_H09	1.013 ± 0.4626 0.95437	1.255 ± 0.9826 0.75358	0.758 ± 0.4115 0.19848	0.93 ± 0.5618 0.11219	ATAATGAAAATTTATTTCTTATTCTGGAGCTAATTACATCAGTTA
plasmid_lp28-3	4681	BB_H09	1.831 ± 1.5504 0.355132	2.377 ± 2.0619 0.29529	1.094 ± 0.3096 0.70505	1.296 ± 0.6036 0.25379	CTTGTAAATTAGCCCTACTCCAAAATTAAATATTCTCACTAACAGT
plasmid_lp28-3	4730	BB_H09	2.377 ± 2.7427 0.481762	0.513 ± 0.5385 0.50175	1.506 ± 1.0748 0.44892	1.304 ± 1.1376 0.73961	CTCTTAGTGAAGAATATATAATTNTGGAGTAGGGCTAAATTAAACAAAGT
plasmid_lp28-3	4733	BB_H09	1.653 ± 1.7428 0.485795	2.689 ± 4.1522 0.51607	1.669 ± 1.4324 0.20172	1.571 ± 1.2752 0.49219	CTAAATTGCTAAACATTTGTTAATTAAAGATAAGCTTTACTATCTTA
plasmid_lp28-3	5421	BB_H09	1.139 ± 0.5369 0.609672	0.585 ± 0.5146 0.43922	1.172 ± 0.3996 0.1363	1.329 ± 0.7862 0.36622	CAATATCAAATCTTCTGAATATCTGAAACTCAATTCCATAATGGAAAA
plasmid_lp28-3	5663	BB_H09	0.555 ± 0.5558 0.101928	0.376 ± 0.3199 0.31084	0.871 ± 0.7446 0.23723	0.828 ± 0.9927 0.38595	TATTACTTCTCATATTCTTGTATATCTTTAGTCATTTCTATATCT
plasmid_lp28-3	5768	BB_H09	0.693 ± 0.597 0.248384	0.954 ± 0.7863 0.89256	1.052 ± 0.4955 0.81491	1.326 ± 0.5287 0.48218	GTTGAATTCTTAAATTCTTTAAATAAAGAAAATCCACCTTCAAAT
plasmid_lp28-3	5795	BB_H09	1.202 ± 1.0124 0.70087	0.543 ± 0.6537 0.31356	1.327 ± 1.5014 0.15137	0.673 ± 0.844 0.39972	AATAAAGAAAATCCACTTCAAATTCTTTGCAATATCAAAAGATTCA
plasmid_lp28-3	5997	BB_H09	2.414 ± 3.1249 0.262912	2.159 ± 2.5333 0.35428	1.979 ± 2.0211 0.13263	1.369 ± 1.505 0.75455	AAGAGGTGTTATGTTGATTAATCCATTTCGTTGAAATTACT
plasmid_lp28-3	6210	BB_H09	0.905 ± 0.7899 0.789582	0.799 ± 0.7438 0.59712	0.822 ± 0.2647 0.22303	1.042 ± 0.3049 0.8473	GATAAAAAAATCATTGATAATTCTTGTGATCAGGGCATTTAAATTCT
plasmid_lp28-3	6286	BB_H09	1.657 ± 1.2112 0.353258	1.174 ± 1.4474 0.79041	0.97 ± 0.4554 0.89653	0.563 ± 0.2678 0.17581	TTATACCTCAGATGTTAACTGATTATGTTATATCATCAATTGAGA
plasmid_lp28-3	6349	BB_H09	1.487 ± 1.2038 0.004715	2.687 ± 3.5834 0.36097	1.117 ± 1.3345 0.80239	1.498 ± 1.1362 0.38685	TGTGCAATTGTTACTTATTGTTCAAGCTCTTCTGAGTACGAAT
plasmid_lp28-3	6921	BB_H09	1.206 ± 0.6559 0.261985	1.606 ± 1.283 0.35102	0.835 ± 0.3255 0.1469	0.994 ± 0.5234 0.93921	CTTAAATTGCTATATATTGCAATTAAACTATAGAAAT
plasmid_lp28-3	6988	BB_H09	0.739 ± 0.2178 0.099115	0.536 ± 0.4069 0.32506	0.966 ± 0.4278 0.84438	1.176 ± 0.5376 0.34229	AAGATCTCTAAGAGTTTGAATTATCTTTCTTGATATTG
plasmid_lp28-3	7533	BB_H09	0.393 ± 0.3141 0.280225	0.162 ± 0.2187 0.19919	0.77 ± 0.9336 0.75189	1.365 ± 1.611 0.71313	GCAAAGACTCTATTGCTCTGTTGAATTGTCATCTAGCTGAATT
plasmid_lp28-3	7661	BB_H09	1.364 ± 0.5614 0.320168	1.295 ± 0.7286 0.45945	0.903 ± 0.2525 0.69256	0.761 ± 0.1299 0.13442	TAAAGAGATACATTGGATCATTGTTATAATGAATCGGCTTCATTG
plasmid_lp28-3	7815	IG_1199	1.912 ± 1.4323 0.287591	4.08 ± 5.3966 0.40071	1.141 ± 0.3421 0.61573	1.29 ± 0.6432 0.23616	AGATTAGTTTTAATTAAAAAAACTAATCTTAGAGTACATTGAGT
plasmid_lp28-3	7876	IG_1200	2.596 ± 1.7154 0.01682	0.958 ± 0.704 0.82494	1.037 ± 0.919 0.93357	0.809 ± 0.683 0.49848	GAATAAGCTGTTAAAATTATTCTCACTTTCTCAATTAAATTAAAGT
plasmid_lp28-3	8158	BB_H09a	1.347 ± 0.4468 0.349561	1.828 ± 1.2958 0.36985	0.851 ± 0.2848 0.58213	1.431 ± 0.555 0.31759	AGTTCTTAAAATTGGCATCTTGTGCTTGCATGATTGAGCAA
plasmid_lp28-3	9050	IG_1201	1.060 ± 0.3619 0.467637	1.3 ± 0.4725 0.43568	0.331 ± 0.3271 0.02444	0.412 ± 0.1717 0.08514	TAGCTTTGCTTTAAAGCAGTAGTCTATAGTATTTGAAAATTTA
plasmid_lp28-3	9318	IG_1202	1.177 ± 0.5549 0.61041	1.652 ± 1.0274 0.29837	0.957 ± 0.3564 0.42662	0.974 ± 0.6578 0.94901	TTTATTATCTTAAAGACTTCTAGTATAAAGCGTTTCTGACTCT
plasmid_lp28-3	10392	BB_H13	2.041 ± 0.8136 0.096559	2.751 ± 1.5873 0.16165	0.817 ± 0.3524 0.56533	1.379 ± 0.6906 0.3701	CATAGAGATTGGAAAATTAGAAAACAATTGGTATAAGGTCGAGA
plasmid_lp28-3	11113	IG_1203	0.695 ± 0.218 0.011859	1.29 ± 0.746 0.48666	1.41 ± 0.4211 0.28764	0.591 ± 0.5001 0.40546	GGGATAAACAAAAAAAGTACACAAAAAAAGTCAAGAAGGCCATTAG
plasmid_lp28-3	11803	IG_1204	1.410 ± 1.1036 0.423538	2.284 ± 2.1655 0.33742	0.621 ± 0.2864 0.12305	1.173 ± 0.5192 0.48612	TAGGGTTCTCTGCATGGGGCTGCTAAGCTTGTATGCCACCTTA
plasmid_lp28-3	11851	BB_H17	1.800 ± 0.9243 0.032828	0.53 ± 0.922 0.48937	1.197 ± 0.8967 0.36298	0.783 ± 0.5347 0.41632	ATGGTGGCATATCAAGTCTAGGCAGCCCCATGCAGAAAGAACCCCTATA
plasmid_lp28-3	12082	IG_1205	0.757 ± 0.2138 0.135197	0.62 ± 0.5288 0.42787	0.915 ± 0.4745 0.6976	1.055 ± 0.3065 0.67501	AATATAATGGAAATTCAAATCTCACTACGTGTTATTGCA
plasmid_lp28-3	12190	BB_H18	1.362 ± 0.7349 0.19078	1.857 ± 1.0254 0.2093	0.739 ± 0.5629 0.64078	0.849 ± 0.5055 0.58324	GTTCCCAGTCGAACCAACTATTAAATTAAACCCTGAATATAAAA
plasmid_lp28-3	12396	BB_H18	0.575 ± 0.8473 0.146968	0.302 ± 0.544 0.27506	0.264 ± 0.2769 0.22288	0.375 ± 0.6486 0.40127	ATCTCAAATGAGAAAGCCATAGCTCAAGCAAAGTAGATTAAAGAC
plasmid_lp28-3	12511	BB_H18	1.233 ± 0.4309 0.532305	1.613 ± 1.8756 0.65002	0.802 ± 0.3288 0.531	1.017 ± 0.3242 0.95046	CTACTACTGAGATAGTGTGAAGTTTATCAATTGAAAACCAAGAGTGGC
plasmid_lp28-3	12514	BB_H18	0.494 ± 0.8444 0.615982	1.07 ± 1.6561 0.92769	0.481 ± 0.7702 0.44236	0.342 ± 0.5349 0.54668	CTACTGAAGATAGTGTGAAGTTTATCAATTGAAAACCAAGAGTGGCTTA
plasmid_lp28-3	12562	BB_H18	0.636 ± 0.285 0.107056	0.76 ± 0.5372 0.6537	1.023 ± 0.3966 0.91373	1.074 ± 0.5226 0.2042	AGCCACTTGGTTTCAATTGATAAAAACACTTCACTTCTAGTAGTA
plasmid_lp28-3	12673	BB_H18	1.033 ± 0.4832 0.915986	2.051 ± 1.4862 0.31076	1.025 ± 0.4065 0.73958	1.076 ± 0.5686 0.77482	GTAACTTCAATGGGAAAGAAAATTATTAGTTAAGGAAGAAATTACA
plasmid_lp28-3	12793	BB_H18	0.557 ± 0.5117 0.5052	1.85 ± 2.0998 0.58871	0.72 ± 0.5505 0.53535	0.082 ± 0.1256 0.09134	GTATCTTATAATGAATTCTTGTACTATGGAATTTTGTTGATGCCT
plasmid_lp28-3	13036	BB_H18	1.461 ± 2.916 0.814401	0.115 ± 0.2059 0.30643	1.526 ± 1.8277 0.63303	0.742 ± 1.004 0.62012	TTAGCAGGTCACCAATTGACCTTGCCTTACTCTATTGTCATACCTT
plasmid_lp28-3	13215	BB_H18	0.783 ± 0.6122 0.659427	1.028 ± 0.5114 0.94968	0.992 ± 0.5316 0.98567	1.218 ± 0.6728 0.65974	GGCTAATACCAATTGTCACAAATCTTTTAAATTCTTCTAATAGCTTT
plasmid_lp28-3	13342	IG_1206	0.530 ± 0.1338 0.088036	0.391 ± 0.3772 0.19403	1.132 ± 1.2415 0.83833	1.048 ± 0.4871 0.66767	TGACCTTTGTTGTTTAAATTAAAGTCAATTGAAATTCTTCTAAGTAAATTAAA
plasmid_lp28-3	13699	IG_1207	1.689 ± 0.9667 0.393337	1.483 ± 1.1937 0.47766	1.697 ± 0.6158 0.14908	1.088 ± 0.1008 0.91434	AATACTATCATAACACAGCCTGGAGAGGGATAATTAACTCAAGCAA
plasmid_lp28-3	13846	BB_H20	1.426 ± 0.6406 0.11538	1.941 ± 1.5694 0.27648	1.244 ± 0.5655 0.59284	1.348 ± 0.5461 0.20314	TATGAGATAGTGTGAATGCAGACTTAAATTAAAGTAAACCAAGAAAA
plasmid_lp28-3	13968	BB_H20	0.531 ± 0.3673 0.003493	0.795 ± 0.2903 0.49079	0.986 ± 0.7948 0.96408	1.109 ± 0.8559 0.78964	GACTAAAAACATCAATTAAATATTGACCTTGGCCCTTAAAC
plasmid_lp28-3	13984	BB_H20	2.891 ± 1.1316 0.075008	1.609 ± 1.6679 0.57069	1.379 ± 1.2555 0.64029	4.122 ± 2.6196 0.16657	TTAATGATTTTAAAGTCTAAGTCTATCAAATAAGGATCAAGCAGTGGCAA
plasmid_lp28-3	14132	BB_H20	0.579 ± 0.5913 0.525906	0.951 ± 0.8758 0.94975	0.83 ± 0.7421 0.79837	0.514 ± 0.252 0.26588	ATGTCAAAATACCTCCAAAATAAGGAAATTAGAATTGACAAAAAGA
plasmid_lp28-3	14416	BB_H20	1.620 ± 0.7745 0.060807	1.661 ± 1.1847 0.27008	0.905 ± 0.413 0.61428	1.221 ± 0.5916 0.00953	AATTAGGGAGAGTGTAAAAGAATCACTTCTTAGTTAATTAATTACTGA
plasmid_lp28-3	15846	IG_1208	1.648 ± 1.2695 0.165068	2.994 ± 3.1043 0.25808	1.208 ± 0.7903 0.61442	1.265 ± 0.8609 0.3072	CCACTAGATTCTTGTACACATTATTGATCTGTGATCACATGAGTAACA
plasmid_lp28-3	15965	IG_1209	1.638 ± 0.5727 0.094142	2.798 ± 2.906 0.40366	1.066 ± 0.5919 0.89383	1.764 ± 0.1035 0.36738	AGCAGCAGGTGTTTTAGGTCTTTCTTGTCAATCTGTATACTATA
plasmid_lp28-3	16174	IG_1210	0.665 ± 1.1852 0.782404	1.292 ± 1.4216 0.74326	0.994 ± 1.2628 0.99604	1.992 ± 0.2062 0.13867	AAGACTGCAAAAAACACATTCTAAACATGTAACACTTGTGCTGGTGA
plasmid_lp28-3	20387	IG_1211	0.827 ± 0.4601 0.255475	0.431 ± 0.3098 0.2806	0.838 ± 0.4977 0.06725	0.987 ± 0.6943 0.88962	AGTAGCCTGCTGAAGTGTGAAATTCTTCAAGAGTATTATTTGTAAGC
plasmid_lp28-3	20810	BB_H30	0.894 ± 0.6686 0.381557	0.526 ± 0.4535 0.45954	0.972 ± 0.7366 0.78246	1.125 ± 0.963 0.26877	TTATGTTAAGTATATTTCAGCATCATATAAAATAATTAGGAAAG
plasmid_lp28-3	20818	BB_H30	1.731 ± 1.1771 0.034556	2.344 ± 2.447 0.46725	0.702 ± 0.4855 0.43733	1.695 ± 1.1962 0.12344	AGTATATATTTCAGCATCATATAAAATAATTAGGAAAGCTGTT
plasmid_lp28-3	20826	BB_H30	1.091 ± 0.5829 0.439704	1.604 ± 1.3956 0.28675	0.802 ± 0.4211 0.34142	1.043 ± 0.5572 0.76139	TTTCAGCATCATATAAAATAATTAGGAAAGCTGTTCAATGATT

plasmid_lp28-3	21412	IG 1212	0.972 ± 0.4857 0.929988	2.05 ± 1.2759 0.22859	0.934 ± 0.1669 0.54128	0.806 ± 0.3252 0.39147	CATAATATTAGGATATAAAATAACATGAAAATTAAAGTAAGGAG
plasmid_lp28-3	21416	IG 1213	1.781 ± 0.6417 0.031966	2.591 ± 1.8965 0.21521	1.359 ± 0.5101 0.31988	1.481 ± 0.3842 0.03834	ATATTATAGGATATAAAATAACATGAAAATTAAAGTAAGGAGAATA
plasmid_lp28-3	22210	BB_H32	1.389 ± 0.834 0.550906	3.427 ± 1.9434 0.07743	2.255 ± 1.151 0.02983	1.898 ± 0.9453 0.18933	TACCCCTTAAAGGGTATATATCCACTTCTGAGTCATATTGGCATCCT
plasmid_lp28-3	22230	IG 1214	1.212 ± 0.3732 0.118992	1.925 ± 1.4337 0.29939	0.933 ± 0.2635 0.74148	0.958 ± 0.3284 0.85879	TATCCACTTCTGAGTCATATTGGCATCCTTCTCGGCAGCAGAACTA
plasmid_lp28-3	22622	IG 1215	2.048 ± 2.0496 0.489749	1.5 ± 1.0743 0.09004	1.597 ± 1.333 0.38758	1.388 ± 1.0519 0.49255	TTACAAATAATAACAAATATGTTGAAAATAATTAAATAAAATAC
plasmid_lp28-3	22700	BB_H33	1.556 ± 0.932 0.003284	1.291 ± 1.1296 0.7555	0.936 ± 0.494 0.82009	0.679 ± 0.7691 0.67965	GCTTCAATTAAACAAATTCTATTATTCCTCTTATAAAAACCTTTAT
plasmid_lp28-3	22834	BB_H33	0.957 ± 0.4226 0.914687	1.14 ± 0.6268 0.63234	3.215 ± 4.6934 0.50617	0.947 ± 0.6252 0.82719	TATGTGCATCAATAACCTGGCAATATATACATCTAATATTGCTAA
plasmid_lp28-3	22837	BB_H33	1.111 ± 0.656 0.564169	1.895 ± 1.7478 0.36934	1.083 ± 0.375 0.65944	1.01 ± 0.4252 0.92009	CATATAGAACGTTCTTTTTATTCCATCAAACCTTACGCTTGGTAGTT
plasmid_lp28-3	22930	BB_H33	1.727 ± 1.448 0.40639	2.49 ± 2.8129 0.36224	1.29 ± 1.1863 0.73886	1.503 ± 1.0334 0.21747	CTATTCATGAGGATCGCTAATTGTCGCCACAGTGCTATGTTGAACTACCA
plasmid_lp28-3	22979	IG 1216	2.045 ± 1.0727 0.079707	1.932 ± 1.5733 0.26182	1.588 ± 0.8166 0.03973	1.329 ± 0.5417 0.32141	GATTTTCAATCCTTACTGCCCTTTAAATGCGGAAAAAACCTTACT
plasmid_lp28-3	23006	IG 1217	1.254 ± 1.6579 0.58523	3.558 ± 4.0306 0.10612	1.057 ± 0.9776 0.94617	1.468 ± 1.2049 0.37114	TGAAAGGTTTTATTGTTAAATTAAATTAGGAGCTTAAATTATGCTAA
plasmid_lp28-3	23049	IG 1218	1.030 ± 0.538 0.896958	1.185 ± 1.2918 0.76564	0.745 ± 0.2972 0.28756	0.598 ± 0.2969 0.05233	TATGTCTAAAGGAAGGTTAAAGGTTATTGCTATAATGGAATAAGGAATTAA
plasmid_lp28-3	23075	IG 1219	1.363 ± 0.5855 0.213515	1.699 ± 0.8702 0.1935	0.766 ± 0.3975 0.15583	1.114 ± 0.6991 0.75124	TTGCTATAATGGAATAAGGAATAAGGTGGTTGGGGCAACTGCCCCGAAG
plasmid_lp28-3	23969	IG 1220	1.010 ± 0.4015 0.970602	3.15 ± 3.1031 0.28318	0.499 ± 0.3433 0.00486	0.916 ± 0.3489 0.61697	TTAAGCACTATTGGTTGGTAAAGGAAAAAAATGAACGCTCACTATTATGC
plasmid_lp28-3	24529	IG 1221	1.408 ± 0.8159 0.219085	1.769 ± 1.3087 0.2644	1.163 ± 0.5732 0.32622	1.144 ± 0.4957 0.33442	CTATATAATGCTACTACTAATTTTATATACTTCCAATATTCTTTT
plasmid_lp28-3	25520	BB_H37	1.186 ± 0.6732 0.703586	1.54 ± 1.4579 0.6218	0.514 ± 0.3136 0.08308	0.963 ± 0.6204 0.93623	TTCTCTAAAAAGGTGAGGCAATAGGAAGAAGAGCTTATAAAAGAAGT
plasmid_lp28-3	26221	BB_H37	0.858 ± 1.0283 0.775165	2.114 ± 2.4721 0.1144	1.014 ± 1.2186 0.98859	1.216 ± 1.3027 0.7427	AATGGCCTCAAGAAATGCTTAAATAATTATGGAATAAAAAAGAA
plasmid_lp28-3	28301	IG 1222	1.776 ± 1.0208 0.104856	3.085 ± 2.4027 0.2026	1.56 ± 0.7885 0.26081	1.627 ± 1.3916 0.44535	AGATGCTCAACAACATCTAAAAAAATTCAATTCCAAAATAAACTCTAA
plasmid_lp28-3	28407	IG 1223	2.197 ± 0.8818 0.031554	2.045 ± 1.4617 0.37344	1.328 ± 1.7035 0.72931	0.824 ± 0.4142 0.55691	TCTAGATTTGGTTCTGATTGCTTAAAGGTTGACTGAATTCTTAT
plasmid_lp28-4	237	BB_I01	1.366 ± 1.2988 0.23145	0.382 ± 0.3603 0.35713	0.996 ± 0.8046 0.98398	0.982 ± 0.9044 0.76529	TATATTATGATAAGTCTGAAAGAACAAAGAAAAAGGAATAGATCAT
plasmid_lp28-4	583	BB_I01	2.152 ± 1.9085 0.211246	0.519 ± 0.6733 0.46523	1.03 ± 0.8912 0.9506	1.144 ± 1.0341 0.56062	AATTGTTTAACTTGTGAGATAATTCTTGTGTTAAACCAATTTTT
plasmid_lp28-4	653	IG 1224	3.805 ± 3.4063 0.249918	2.319 ± 1.2709 0.18885	1.304 ± 0.8086 0.64712	1.197 ± 0.6696 0.30492	TATTCTAAAGTTGAGATAATTCTTGTGTTAAACCAATTAAAGT
plasmid_lp28-4	745	BB_I02	3.199 ± 3.3448 0.355186	1.79 ± 1.6065 0.44857	2.128 ± 0.7207 0.60485	1.403 ± 0.8195 0.4113	CTCCATCCATAATGAAATTAGCCCCTATTATTAATTAAATTACCAAT
plasmid_lp28-4	876	BB_I02	2.304 ± 3.0071 0.194568	1.613 ± 2.1573 0.2482	1.328 ± 1.4535 0.10898	1.186 ± 1.5081 0.24889	ATTGTAAGTTTATTGCACTATAAGTAATTCTTATTATGATGATCTAG
plasmid_lp28-4	879	BB_I02	2.773 ± 1.3519 0.06711	1.441 ± 0.8578 0.25043	1.122 ± 0.404 0.05601	1.052 ± 0.4296 0.07973	TGTCTTAATACAAAACAATTAAATGAGGCTCTAGTAAACCTTACACT
plasmid_lp28-4	917	BB_I02	0.477 ± 0.2709 0.006996	0.578 ± 0.4826 0.06276	1.376 ± 0.4995 0.13266	1.097 ± 0.4549 0.19532	AAACTTATCAACTTGGGTTATTATAAAACCTTATTAGAATATCTGAAA
plasmid_lp28-4	938	BB_I02	5.746 ± 3.5045 0.065618	2.868 ± 3.0448 0.31218	3.687 ± 2.6733 0.1748	2.058 ± 0.9781 0.02681	ATTATAAAACCTTATTAGAATATCTGAAATATTAGAAAAAAATCCAAAAG
plasmid_lp28-4	944	BB_I02	2.635 ± 0.3459 0.002793	1.07 ± 0.32 0.69052	0.918 ± 0.2478 0.62435	0.938 ± 0.2273 0.69171	AAACCTTATTAGAATATCTGAAATATTAGAAAAAAATCCAAAAGTAATCT
plasmid_lp28-4	1186	IG 1225	1.548 ± 1.5877 0.662317	0.351 ± 0.6377 0.40954	2.559 ± 3.2017 0.38998	1.45 ± 1.3156 0.63033	TTATAGGCCATAATACTAGGATAGATTTGGTTACTATTATATAATC
plasmid_lp28-4	1232	IG 1226	3.185 ± 2.2017 0.093968	1.648 ± 0.982 0.3672	1.184 ± 0.7261 0.65395	1.177 ± 0.72 0.55364	CCAATATAAAAGCTTAAACAAATAATTCAATATATCTTAAATTCTAGA
plasmid_lp28-4	1355	IG 1227	3.196 ± 3.895 0.043283	1.028 ± 1.9374 0.91039	1.255 ± 2.0479 0.84722	0.748 ± 1.1109 0.69744	ACACTTAACTTCCAGTTAGTTTATTGTTGGGACTATAATAAGT
plasmid_lp28-4	24209	IG 1228	0.927 ± 0.499 0.496848	0.654 ± 0.3664 0.42603	0.937 ± 0.5087 0.52444	1.201 ± 0.6784 0.44608	TTTTTTATTAGATTAACTAGCTGGTTAGTAGATAAAGAGGATGGGAA
plasmid_lp28-4	24325	BB_I39	0.676 ± 0.2192 0.123675	0.704 ± 0.4476 0.5178	1.025 ± 0.3509 0.79011	1.196 ± 0.5256 0.2155	CAATAAAAATGTTGATAACATTAAATAGATAATAAGCGTAGCAAACAA
plasmid_lp28-4	24460	BB_I39	1.509 ± 1.4692 0.549428	1.361 ± 1.4016 0.66348	1.3 ± 0.532 0.26905	1.561 ± 0.5826 0.04692	CGTGTCTCTAGATGAGTTGAATATCCCTTGTGTTCTAAAAATTGACC
plasmid_lp28-4	24641	BB_I39	1.351 ± 0.7475 0.402256	1.161 ± 0.53 0.56345	0.791 ± 0.3781 0.4944	1.25 ± 0.327 0.36316	AAAACATCATCTGTTAAGTTAAAGTCTCTAGAAAATCATTTAGCA
plasmid_lp28-4	26279	IG 1229	1.156 ± 0.5921 0.28517	1.957 ± 1.0049 0.06092	0.878 ± 0.4729 0.59573	0.992 ± 0.675 0.94676	AATGTTAAATAAAATAGCTGTTAGATAACCTGTATTTACACAGATTA
plasmid_lp28-4	26402	BB_I42	0.852 ± 0.7402 0.660447	1.214 ± 1.1953 0.27132	0.613 ± 0.4815 0.43076	0.718 ± 0.6794 0.64598	TTGGGTTGTTATTGCTGATAATCAGGAAACAGCTGTTCAAACCTTTTTT
plasmid_lp28-4	26738	BB_I42	0.877 ± 0.9939 0.829849	0.766 ± 0.4614 0.40865	0.268 ± 0.3423 0.08904	1.054 ± 0.6145 0.73703	TACGCATAAAATTATTATGTTCTGCTCATTTTACCATATAAAACACT
plasmid_lp28-4	26928	BB_I43	2.122 ± 2.5037 0.558348	1.161 ± 1.184 0.87204	0.518 ± 0.3348 0.16402	0.469 ± 0.3482 0.14085	GGAGTTCACAGTTTATGTTAGGTAAATAGGAACCTGGTCTATTATAAT
plasmid_lp28-4	26977	BB_I43	0.365 ± 0.2504 0.080736	1.325 ± 0.8114 0.63302	0.435 ± 0.3073 0.03072	0.468 ± 0.6616 0.35685	GTTTCTGGTTATTCTGTTACCCCGCAAGAAATACACCTCAGCATC
plasmid_lp36	9	IG 1230	1.351 ± 0.861 0.370375	1.515 ± 1.3457 0.47961	0.77 ± 0.396 0.11339	1.153 ± 0.6315 0.47456	ATTTATATAATCTTTCACTTAACATTGTTATACAAAATCTTAAATAT
plasmid_lp36	528	BB_K01	2.210 ± 2.1305 0.442218	2.169 ± 2.7843 0.57645	1.65 ± 1.2536 0.51591	3.217 ± 3.1019 0.28616	CTAATGAAGAAAAGGAAGCTGATGCAGCAATTAAATTAGAAAGAAAATA
plasmid_lp36	640	BB_K01	0.864 ± 0.7905 0.699867	1.158 ± 0.4701 0.4646	0.489 ± 0.4618 0.31729	0.47 ± 0.3748 0.22802	TGCTTAAATAAAAGCTGATTGATGTAATTGAAAGATTAACAAATAA
plasmid_lp36	780	BB_K01	1.112 ± 1.0874 0.240892	1.521 ± 1.7381 0.34507	0.729 ± 0.7219 0.1053	0.941 ± 0.9711 0.29731	GTGAACCTGAGCAGCTTAAATATGATTGATATGGCAGAAAATGAATAA
plasmid_lp36	906	BB_K01	1.516 ± 1.153 0.519457	1.939 ± 1.1561 0.17753	1.355 ± 0.842 0.24359	1.463 ± 0.9412 0.00938	TTTTACTCTAATCTTTAATATGCTTCTTTAACCTTTCTGAGCG
plasmid_lp36	1220	BB_K02a	0.987 ± 1.1943 0.98989	1.005 ± 1.1115 0.99578	0.397 ± 0.4111 0.4124	0.867 ± 1.1021 0.82236	ATGCAGCTAAATAGATTGATGAGCCTGTTGTGAAAGTCTGAGTTT
plasmid_lp36	1239	BB_K02a	0.035 ± 0.0675 0.188896	0.166 ± 0.3145 0.12215	0.079 ± 0.1011 0.16977	0.116 ± 0.1459 0.22164	AGAAGAATGGATAAGCATAATGCAGCGTAATAGATTGATGAGCCTCTG
plasmid_lp36	1540	BB_K02a	0.365 ± 0.3162 0.032411	0.646 ± 0.6226 0.02822	0.75 ± 0.5037 0.03917	0.908 ± 0.6086 0.30527	CTTAACCTTAGCTAAAACACTCCTTGCTAATAGTTAAAATGATCCCGA
plasmid_lp36	1982	BB_K02a	1.342 ± 0.6873 0.085022	1.501 ± 1.2056 0.54354	1.003 ± 0.5544 0.99495	1.124 ± 0.7188 0.77054	TATTCTTATACAGTGCCTTACATTGTTAAATTAGTCCTCTAA

plasmid_lp36	2002	BB_K02a	1.014 ± 0.6786 0.862206	2.204 ± 1.6396 0.11536	1.17 ± 0.747 0.67433	1.294 ± 0.8553 0.19705	TAAGGCAGTGATAAAGAAATAATAATGAAAAATTATTCGTATT
plasmid_lp36	2744	BB_K02a	1.054 ± 0.8722 0.939389	0.392 ± 0.5697 0.17434	1.408 ± 0.9422 0.6	1.15 ± 1.1413 0.87273	CAATATCAAATCTTCTTGAATATCTGAAACTCAATTCCATAGTAAAAA
plasmid_lp36	3053	BB_K02a	0.695 ± 0.1938 0.101114	0.898 ± 0.2465 0.56279	0.874 ± 0.3402 0.16177	1.005 ± 0.5261 0.97422	ATTATACCATAAAGAAGATTAGAAAATCTAAAAGATATACAAGAAAT
plasmid_lp36	3359	BB_K02a	1.281 ± 0.8265 0.500227	1.656 ± 1.7519 0.27484	0.631 ± 0.5548 0.16589	0.787 ± 0.8224 0.07389	TACTGTCTGAATTATATTATTTAGCTTTATAACATTCTATACT
plasmid_lp36	3535	BB_K02a	0.674 ± 0.6656 0.471648	0.568 ± 0.4734 0.33068	0.742 ± 0.2136 0.03745	0.882 ± 0.2151 0.46499	GATATAAAAATCATTGATAATTCTGTGGATCGGGAAATTTTAATTCT
plasmid_lp36	4189	IG_1231	2.306 ± 3.5439 0.156862	1.589 ± 2.2262 0.67015	1.014 ± 1.2565 0.98837	1.62 ± 2.1111 0.60591	GTTTAAATCAATTCAATCCCATTGAGTATTITACACCATTTATAAGTT
plasmid_lp36	4342	IG_1232	1.231 ± 0.6634 0.493185	1.311 ± 1.136 0.29652	0.794 ± 0.4811 0.36773	0.886 ± 0.6081 0.79183	GATACAAAAAACTTTGAGATGTCTATCAGTCATCTAGTTAATGTC
plasmid_lp36	4345	IG_1233	1.479 ± 0.3186 0.007631	1.43 ± 1.1219 0.52482	0.649 ± 0.2117 0.16656	0.718 ± 0.1439 0.13948	ATCAAATAATTAAAATAATTAGTTATGATAAATTGACTTCCAAAATT
plasmid_lp36	4791	IG_1234	1.064 ± 0.266 0.594969	1.221 ± 0.8245 0.59836	0.739 ± 0.1413 0.12055	0.873 ± 0.3094 0.42455	GATATTATCGATACCGTGAATGGAATTGATCTGAAATTGACTTCAAAAAT
plasmid_lp36	4948	IG_1235	1.215 ± 0.96 0.788161	1.348 ± 2.1744 0.78598	0.336 ± 0.3226 0.10595	0.292 ± 0.3787 0.06293	GTATATATGATGTTGGGCTCTCTAAAGTTAGTGTGTTCTATTGTC
plasmid_lp36	4952	IG_1236	0.805 ± 0.184 0.14529	1.134 ± 0.1555 0.32581	0.757 ± 0.0586 0.01997	0.912 ± 0.1603 0.50147	TATACATTATTCCTTATGCACTAACAGTGGAAAGCAAAATCAAATATAG
plasmid_lp36	4953	IG_1237	1.200 ± 0.6173 0.100399	2.082 ± 1.8592 0.26872	0.988 ± 0.5382 0.92274	1.108 ± 0.7177 0.64508	TATGATGGTTGGGCTCTCTAAAGTTAGTGTGTTCTATTGTCATTAA
plasmid_lp36	5111	IG_1238	0.737 ± 0.6867 0.329558	1.03 ± 1.015 0.94725	0.468 ± 0.3485 0.11053	0.785 ± 0.5363 0.37595	TGAGGTTAAAATAATGATAAATCAAAAATTCAAAACCTCTTATAGTA
plasmid_lp36	5623	BB_K07	0.780 ± 1.1145 0.402861	2.536 ± 3.7617 0.39109	0.933 ± 1.0758 0.8756	1.238 ± 1.548 0.43965	AAGAGTGTGAAATTACTGGATGAGTTGCTAAAATATCGTAAGTAGCAAT
plasmid_lp36	5674	BB_K07	0.443 ± 0.2307 0.050178	0.154 ± 0.146 0.06019	0.829 ± 0.4695 0.2558	1.035 ± 0.5887 0.83417	TATTAATTAGTGTGTTGAAAACCGAATCAATTCTGATGAATTCTTAA
plasmid_lp36	5676	BB_K07	1.284 ± 1.2873 0.614931	1.08 ± 0.9947 0.9232	0.796 ± 0.4059 0.55471	0.52 ± 0.4015 0.10734	ATATAGGTTATAATGCTACCTATGCAGC AAAAGTAATTGAGAATGGAC
plasmid_lp36	5683	BB_K07	0.613 ± 0.7077 0.224174	0.826 ± 0.8715 0.63091	0.973 ± 0.3484 0.89208	0.778 ± 0.5763 0.2505	GTGTTGAAAACCGAATCAATTCTCTGATGAATTCTTAATCAATTG
plasmid_lp36	5755	BB_K07	0.789 ± 0.1761 0.20206	0.644 ± 0.5616 0.46578	0.706 ± 0.1472 0.05389	0.675 ± 0.1362 0.10398	CTTCTATGTTTTACTTCCCTGGTATTGATCTCAATTCTTTT
plasmid_lp36	5895	BB_K07	0.926 ± 0.5243 0.773267	1.402 ± 0.5866 0.30801	0.708 ± 0.2644 0.22874	1.058 ± 0.3308 0.64879	CAGGCTAAAGTCGGAAAAAAATCACAAAATTAACTCCGGAAGAGCTAGAAA
plasmid_lp36	6010	BB_K07	1.081 ± 0.6573 0.216269	1.551 ± 1.6119 0.4648	0.697 ± 0.3296 0.22492	0.932 ± 0.4768 0.46746	CTGCTAATAATTCTGTAATGGCATGAGACAATCCATTGATGAAGCA
plasmid_lp36	6364	IG_1239	0.745 ± 0.5627 0.471492	1.381 ± 1.1711 0.58926	0.599 ± 0.678 0.53402	1.004 ± 0.8127 0.99589	AGATATTAAAAGTTAAAATCAAAATAGTTGAGTGTGATCAAGACCGAA
plasmid_lp36	6706	IG_1240	1.294 ± 0.6969 0.375241	1.392 ± 1.1833 0.57809	0.825 ± 0.3926 0.599	1.138 ± 0.7493 0.79361	GTGCAAGAACCCCCCTGGCAAAAGAAAATATTCTCTTCTTTTATT
plasmid_lp36	7307	IG_1241	1.277 ± 1.0889 0.250147	1.697 ± 2.1069 0.46773	0.886 ± 0.6457 0.22385	0.988 ± 0.6286 0.9434	TAACTACACGCCCTAAAGGAGTTACAAAGTGTGAAATATTGGCAAT
plasmid_lp36	7365	BB_K12	1.020 ± 0.6214 0.339349	1.544 ± 1.5577 0.43291	0.704 ± 0.3638 0.21591	0.92 ± 0.5188 0.33457	CTGCTAATAATTCTGTAATGGTAGACAATACCATTGATGAAGCA
plasmid_lp36	7458	BB_K12	0.884 ± 1.0308 0.873439	2.156 ± 2.5577 0.53096	0.769 ± 0.8781 0.72042	0.316 ± 0.3535 0.018	TTAGATGAGATAAGTGAAGGCCACAGGCCCTAAGTCGGAAAAAAATCACAAA
plasmid_lp36	7480	BB_K12	0.807 ± 0.6266 0.292517	0.9 ± 0.9523 0.79774	0.514 ± 0.2147 0.11642	1.068 ± 0.4343 0.44237	CAGGCCCTAAGTCGGAAAAAAATCACAAAATTAACTCCGGAAGAGCTAGAAA
plasmid_lp36	7620	BB_K12	0.998 ± 0.2122 0.989326	0.549 ± 0.4818 0.31015	0.633 ± 0.1268 0.06511	0.823 ± 0.2446 0.46166	CTTCTATGTTTTACTTCCCTGGTATTGATCTCAATTCTTTT
plasmid_lp36	7692	BB_K12	1.113 ± 0.581 0.645502	1.941 ± 1.7673 0.41466	0.96 ± 0.286 0.75713	1.236 ± 0.6021 0.41151	GTGTTGAAAACCGAATCAATTCTCTGATGAATTCTTATCAATTG
plasmid_lp36	7699	BB_K12	1.126 ± 1.3782 0.783851	1.139 ± 1.082 0.87881	0.868 ± 0.5158 0.71403	0.631 ± 0.7057 0.17024	ATATAGGTTATAATGCTACCTATGCAGC AAAAGTAATTGAGAATGGAC
plasmid_lp36	7701	BB_K12	0.480 ± 0.2369 0.006608	0.241 ± 0.2913 0.10316	1.148 ± 0.7268 0.65159	1.24 ± 0.7371 0.49106	TATTAATTAGTGTGTTGAAAACCGAATCAATTCTCTGATGAATTCTTA
plasmid_lp36	7752	BB_K12	1.078 ± 1.4467 0.885355	2.804 ± 3.893 0.39706	0.988 ± 0.9883 0.98178	1.087 ± 1.2953 0.80482	AAGATGGTAAATTACTGGATGAGTTGCTAAAATATCGTAAGTAGCAAT
plasmid_lp36	7968	BB_K12	1.425 ± 1.0929 0.143475	2.64 ± 2.9028 0.2822	1.22 ± 0.9129 0.28088	1.259 ± 0.9358 0.43787	CACCTTAAAGTGTGTTCTACATTCTCATAAGAGTTGAATACATT
plasmid_lp36	7981	BB_K12	1.032 ± 1.2942 0.94391	1.516 ± 2.5129 0.33274	0.93 ± 1.8797 0.79881	1.522 ± 1.823 0.41722	AGTTCGCTGCATACACCTTCAAAGTGTGTTCTACATTCTCATAAGAGTT
plasmid_lp36	8078	IG_1242	0.808 ± 0.5044 0.717579	0.964 ± 0.4549 0.92703	0.297 ± 0.426 0.14807	0.365 ± 0.5211 0.06886	TGCTTCAATTAGGTGTAGATCGCGTCATGGTATGAAACCGCAAGCTATT
plasmid_lp36	8395	BB_K13	0.778 ± 0.9133 0.500504	1.222 ± 1.3661 0.58263	0.701 ± 0.5344 0.51294	0.8 ± 0.5957 0.55067	CTTGTGACAATATTATGATATAAAGCCGAAATGTTAGCAGATTCAATTAG
plasmid_lp36	8651	BB_K13	1.505 ± 2.3647 0.677506	0.385 ± 0.7587 0.3541	0.52 ± 0.762 0.57196	0.56 ± 0.9159 0.59773	TTAATATCATTATAGTGTGTTACGGGTTAAGCTGTATCTAACCCCCAACTA
plasmid_lp36	8702	BB_K13	0.917 ± 0.5669 0.822037	0.653 ± 0.4337 0.25712	0.811 ± 0.5043 0.28482	1.118 ± 0.6074 0.55487	GAAGACGTTGATAAAAATTCTCTCGTAAGCCCTTACCGTAATATAA
plasmid_lp36	8798	BB_K13	0.832 ± 0.2616 0.415912	0.936 ± 0.1953 0.58009	0.843 ± 0.1184 0.08552	0.918 ± 0.2175 0.29987	ATTGATGATATAACAAAAGTAACGAAAATACAAGAAAATATTTCTT
plasmid_lp36	8861	IG_1243	1.131 ± 2.1125 0.163493	2.026 ± 2.7907 0.3939	0.814 ± 1.0028 0.79085	1.407 ± 1.1999 0.182	GATTGACCTTCTAAAAGCAATATAATTAAATTACTGTGATTAACTCTTAA
plasmid_lp36	9128	IG_1244	1.285 ± 1.5931 0.659333	2.367 ± 3.0711 0.19256	1.079 ± 1.3003 0.62581	0.911 ± 1.0877 0.89158	TTTGAAATGTTAAATTATGTTGCTATTCTAAACACAAGATTAAAAAA
plasmid_lp36	9239	IG_1245	1.212 ± 0.5375 0.090666	1.268 ± 0.5883 0.58635	0.437 ± 0.1833 0.16137	0.743 ± 0.2757 0.36413	AGGGCTTTATTATGTTAAAATTAATTATTAATCAATTCTTTT
plasmid_lp36	9425	BB_K15	1.091 ± 1.3746 0.778249	1.263 ± 1.7975 0.8156	0.213 ± 0.2633 0.21224	0.801 ± 0.1087 0.7523	ACTTCTACAAAATTATTATCCAAGATAAAAAGTTCTACATTCTTCCCGC
plasmid_lp36	9479	BB_K15	1.224 ± 0.7033 0.585491	1.647 ± 1.2652 0.19608	0.985 ± 0.6199 0.9691	1.114 ± 0.6688 0.67059	ATCAATATACTTCCATTAAAATGTTAGTTGATACACTAAGGAAA
plasmid_lp36	9647	BB_K15	0.241 ± 0.1652 0.007366	1.831 ± 0.2519 0.03049	0.259 ± 0.4203 0.09977	0.769 ± 1.1841 0.77435	GCATTAAGAAGATTGCTAATAAAATTATGCAAATGC GGCGATAGAATTCC
plasmid_lp36	9674	BB_K15	1.249 ± 0.6268 0.074807	2.179 ± 2.0405 0.28111	0.975 ± 0.5021 0.79423	1.149 ± 0.5396 0.42901	TGCAAATGCGGGCATAGAATTCCAATTAGTTGAGGCAATAATGAGGC
plasmid_lp36	9727	BB_K15	0.778 ± 0.821 0.111182	1.411 ± 1.0403 0.42675	0.789 ± 0.6251 0.74101	0.863 ± 0.6545 0.74003	ACAGCCTATTGCTCAAATTTAGGAATTCTATGCCGCATT
plasmid_lp36	9734	BB_K15	1.007 ± 0.2717 0.090411	1.31 ± 0.5764 0.19188	0.733 ± 0.1742 0.12796	0.937 ± 0.2785 0.29445	TCAAGTAACAGCCTCATTATGCTCAAATCAAATTGGAATTCTATGCC
plasmid_lp36	10199	IG_1246	1.069 ± 0.1955 0.379579	1.376 ± 0.5901 0.24403	0.844 ± 0.2093 0.00118	1.033 ± 0.2769 0.55857	CAGTTGCAATTAAATATACTGGCATTGCGTATAATTAGTTAAAGA
plasmid_lp36	10457	BB_K17	1.230 ± 1.348 0.385555	1.906 ± 2.5568 0.24413	0.517 ± 0.5325 0.42816	0.989 ± 0.9661 0.9809	TATGCGCATCAATAACCTTGGCAGCACATATTCTACCAATGTCGCTAA

plasmid_lp36	10550	BB_K17	1.163 ± 1.2114 0.563057	1.827 ± 2.6607 0.44073	0.772 ± 0.7533 0.53828	1.387 ± 1.3049 0.07602	TTTCATGAGGATCGCTTATTGTAGCCACAGTGCGTGTGCAACTACTAAAT
plasmid_lp36	10584	BB_K17	0.487 ± 0.1477 0.032825	1.078 ± 1.0315 0.8871	0.521 ± 0.3795 0.23085	0.924 ± 0.5151 0.65972	AAATTGATGCCATCAATACCATTAACATTGGCTATTCTAGGAGATCGCTT
plasmid_lp36	10596	BB_K17	1.090 ± 0.5622 0.086531	1.984 ± 1.9413 0.36161	0.957 ± 0.353 0.82245	1.247 ± 0.7680 0.28127	ATTCTAAAAAAACCGAGTTAAATTCTTGGAGCTCCTCTTGTGTC
plasmid_lp36	10728	BB_K17	0.673 ± 0.9447 0.299205	0.562 ± 0.9284 0.61995	1.343 ± 0.8466 0.53189	1.415 ± 1.0622 0.46772	TTTACTATTGGCTGAAGTAATGGATTAAAGGCGTGAATTAACAAGATA
plasmid_lp36	10873	BB_K17	3.777 ± 3.188 0.186823	6.858 ± 10.856 0.42137	1.732 ± 1.3213 0.42078	2.163 ± 2.3704 0.50863	TGCATCTCAGGCATTAGCACTGATCATGAATGTTAACATAGAAGATGC
plasmid_lp36	10955	BB_K17	0.526 ± 0.3491 0.127739	0.793 ± 0.3575 0.5885	0.333 ± 0.2289 0.1745	0.885 ± 0.4331 0.78139	GTATTTCATGCCAAAGATAATTATCTTCATCTTATGTTAACAC
plasmid_lp36	11336	BB_K17	1.100 ± 0.5472 0.200027	1.574 ± 1.3055 0.31381	0.723 ± 0.3582 0.14404	1.114 ± 0.6027 0.17082	AACAATTAAATTGTAGCAAAAATCTATTGGATTAAATTTCACACT
plasmid_lp36	11630	BB_K17	0.921 ± 0.6507 0.868965	1.091 ± 0.9026 0.89027	0.5 ± 0.3107 0.17313	0.995 ± 0.3374 0.98415	CTTGTGGAAGCAATGATGAATATTGTGAAAGCGGCAAATACAATCATC
plasmid_lp36	11650	BB_K17	0.915 ± 0.3639 0.738892	1.448 ± 0.5305 0.14869	1.361 ± 0.5087 0.31465	1.425 ± 0.5546 0.08452	TTCATCATTGCTTCAACAAGATGATGTTGAGAACATGAGCAACTGT
plasmid_lp36	12037	IG_1247	1.066 ± 0.3518 0.679922	1.401 ± 0.5422 0.27777	0.901 ± 0.2129 0.12574	1.013 ± 0.1779 0.76919	TCTATTAAAGGATTATTAAATTGTGCTGGAGTTTTTATTAAAAAATT
plasmid_lp36	12038	IG_1248	1.065 ± 0.4284 0.817497	1.479 ± 1.1156 0.35128	0.764 ± 0.5107 0.43463	1.059 ± 0.439 0.72596	GATAATAACAGACAAAAACTTTGAGTTCTTACAATTTTATCGCTTA
plasmid_lp36	12054	IG_1249	0.941 ± 0.1025 0.912578	1.4 ± 1.6268 0.66927	0.924 ± 0.9352 0.9052	1.753 ± 1.1084 0.33111	ATTGTGTCCTGGCAGTTTTTATTAAATTATGCTTAACATCCTT
plasmid_lp36	12156	IG_1250	0.553 ± 0.3744 0.104757	0.615 ± 0.5397 0.25574	0.764 ± 0.1135 0.02588	0.98 ± 0.1307 0.76518	ATATCCTGTAATAACGCAAACGTTACTATTGATTAAATTGAGAACCA
plasmid_lp36	12163	IG_1251	0.832 ± 0.7801 0.444795	1.575 ± 2.3328 0.63749	0.855 ± 0.7219 0.78174	0.842 ± 0.5172 0.31383	CAGGAGATTATTATGGCTTGTGCCAACAGCAATCAAACACT
plasmid_lp36	12376	IG_1252	1.760 ± 1.461 0.174394	1.481 ± 1.6562 0.35766	1.273 ± 1.1944 0.407	1.247 ± 1.2382 0.61522	CATCTAAAATAATCAATAAAAATCATTTTGTTCGGCTCGCTTTA
plasmid_lp36	12513	IG_1253	1.996 ± 1.2106 0.319978	1.428 ± 0.4981 0.28559	1.004 ± 0.5466 0.99287	1.755 ± 0.3539 0.05022	ATTAATAAAATATCTTTTAAATAAAATTATAGAGGTAATAAAAAAA
plasmid_lp36	12615	BB_K19	0.906 ± 0.7161 0.883929	0.726 ± 0.416 0.14169	0.675 ± 0.4389 0.52484	0.845 ± 0.3511 0.54965	ATATATTTTCAATTATAACTCTTAATTAAATTTACTTTTAA
plasmid_lp36	12995	BB_K19	2.197 ± 2.3467 0.434041	1.863 ± 1.7428 0.14631	1.022 ± 0.8982 0.97689	0.268 ± 0.2449 0.22019	TCTTATTATCTTAAATTCTAATAAAATGATCATTATGTTTTTATGG
plasmid_lp36	13002	BB_K19	0.950 ± 0.0956 0.294315	1.495 ± 0.8616 0.41031	0.699 ± 0.0845 0.00895	0.934 ± 0.0771 0.28942	TAATTCGATTATCTGAACTAAAAACATTACTAAAGCAAGAAAAAAC
plasmid_lp36	13248	IG_1254	1.299 ± 0.9991 0.314265	2.307 ± 2.5259 0.33657	0.905 ± 0.6248 0.08175	1.239 ± 0.9265 0.24175	CTACATTCCAATAAAATAAAAGACGCCCTAAATAGGGCTCTTTATT
plasmid_lp36	13370	IG_1255	0.550 ± 0.6021 0.490652	1.126 ± 1.9368 0.70397	0.719 ± 0.9242 0.46608	1.162 ± 1.3539 0.84903	TTAAAATACAACTTAAATTAAAGTGTATTCTTGGATTACAGTGGCT
plasmid_lp36	15971	IG_1256	1.238 ± 0.9867 0.767596	2.106 ± 2.7229 0.47115	1.158 ± 0.7772 0.80591	1.468 ± 1.322 0.56705	GAATAATAAAATAACACGAGGTGTAATAATCAAACAACTTAA
plasmid_lp36	17085	IG_1257	1.364 ± 0.4297 0.070372	1.661 ± 1.136 0.35251	0.763 ± 0.2102 0.18636	0.938 ± 0.3032 0.78391	ATAAGCTCTCATACTATGTTTATAATTACTACAAAGTAAGAAATA
plasmid_lp36	17929	BB_K55	1.182 ± 0.4687 0.604844	0.895 ± 0.0907 0.80831	0.843 ± 0.2905 0.60355	0.732 ± 0.4864 0.53187	TAAGAGATACATTGGATCATTTGTTTATAATGTAATCGG
plasmid_lp36	18045	BB_K55	1.167 ± 0.8074 0.653774	1.752 ± 1.4793 0.05115	0.868 ± 0.6688 0.71616	1.448 ± 1.0741 0.18602	TATTGCTTGTGTAATTATCATCTATTGAAGAAAGTTTTTATAA
plasmid_lp36	18380	BB_K55	1.003 ± 1.1688 0.996796	0.068 ± 0.1269 0.16043	0.358 ± 0.4024 0.23386	0.718 ± 1.3343 0.80078	TAAGCTCCATACCTTCCATTGAAAGTATTCTCATATGTTGATATTG
plasmid_lp36	18489	IG_1258	0.766 ± 0.6569 0.557412	1.372 ± 1.8019 0.40716	0.617 ± 0.5625 0.3782	0.889 ± 0.9298 0.50901	GCTAAATAAAATAACACCATTCTTGTATTGTTATTCTTCAAT
plasmid_lp36	18492	IG_1259	0.736 ± 0.9769 0.598091	1.488 ± 2.1937 0.70179	0.744 ± 0.5463 0.49553	0.819 ± 0.9029 0.7083	TATTATAAGAAAAGAACTCTAAAAACAGTAATAGCAGTGTG
plasmid_lp36	18669	IG_1260	0.860 ± 0.9858 0.265891	1.158 ± 1.2156 0.42018	0.787 ± 0.5503 0.56689	0.867 ± 0.6830 0.6158	CTTTAAATTCTTGTCTATATAATTCTTAACTTAAATTACTATAGA
plasmid_lp36	18694	IG_1261	1.897 ± 0.8378 0.113308	1.159 ± 0.5636 0.69874	1.103 ± 0.6387 0.85132	1.503 ± 1.3853 0.4006	TAACGAGTAATTCTTGTCTGATACTTTAAATTCTTGTCTATATTT
plasmid_lp36	18949	IG_1262	0.494 ± 0.4764 0.064968	1.232 ± 1.5406 0.77648	0.772 ± 0.9057 0.26512	0.887 ± 0.5955 0.56181	TTGTAGAAGATAAGGTTAAATTATGTAATGAAAGTTGCTAAGTATT
plasmid_lp36	19271	IG_1263	0.945 ± 0.8788 0.723489	1.061 ± 1.1229 0.86545	0.708 ± 0.4545 0.4323	1.172 ± 1.1039 0.34992	TATTACTCTTCTCATATTCTTGTATGTAAGTAGCACTTGTACT
plasmid_lp36	19562	IG_1264	0.289 ± 0.2583 0.07531	0.677 ± 0.1042 0.50524	0.548 ± 0.3744 0.22759	0.526 ± 0.399 0.41633	AGTATTCTTGTCTTATTCTTGTCTTGTCTGCTTCTGTAG
plasmid_lp36	19578	IG_1265	1.144 ± 1.1418 0.860552	1.275 ± 1.2707 0.77881	0.696 ± 0.689 0.64346	0.666 ± 0.466 0.56149	TTTATTGTTCTTATGCTTAGTCTTGTAGCTAGGAATATGTTT
plasmid_lp36	19612	IG_1266	1.073 ± 0.5967 0.824346	0.994 ± 0.2697 0.93819	0.95 ± 0.3248 0.57668	1.093 ± 0.3433 0.59618	GCTAGGAATATGTTTGGAGAAGAACTCTGATTCTAAACTAGTTCTC
plasmid_lp36	19737	IG_1267	0.971 ± 1.1043 0.9753	2.252 ± 3.7962 0.63902	1.416 ± 0.9359 0.42604	0.816 ± 0.932 0.79428	AAATTCTTCACTATGGAATTGAGTTCCAGATGTTAGGAAGGTTGAT
plasmid_lp36	19833	IG_1268	0.714 ± 0.9117 0.305678	1.1 ± 0.9128 0.89308	0.965 ± 0.736 0.95777	0.779 ± 0.64 0.42047	TCTGCAATACTAATTCTGTTTAACTTGTGTTACTGAACTTGTACT
plasmid_lp36	19875	IG_1269	1.105 ± 0.611 0.786457	1.343 ± 0.5532 0.40625	0.85 ± 0.2751 0.49959	1.019 ± 0.8065 0.97251	TTTGCTAATTATAAACTTAACATATTCAATTCTAAACAAACTAAAGA
plasmid_lp36	20108	IG_1270	0.573 ± 0.419 0.431772	0.632 ± 0.5576 0.39955	0.318 ± 0.2251 0.22925	0.593 ± 0.4096 0.42463	CATTAAACTTTTCAATTCTTAAATTGAGTTTAAAGATCTGTTT
plasmid_lp36	20412	BB_K32	1.268 ± 0.8053 0.254242	2.285 ± 1.7421 0.18456	0.901 ± 0.4679 0.51708	1.042 ± 0.496 0.82679	TTGGCTTGGGATTACTTTGGTTTATAAGTGTGATTCTCATCTT
plasmid_lp36	20510	BB_K32	0.982 ± 0.1792 0.370954	1.188 ± 0.2414 0.57307	0.834 ± 0.1308 0.02754	0.97 ± 0.115 0.73702	GAGTTCCCTTCAATAAAAGCCAGGGGATTCTCTTCTTATCTT
plasmid_lp36	21039	BB_K32	0.314 ± 0.5033 0.220102	1.208 ± 1.3971 0.7367	0.464 ± 0.5144 0.47318	0.795 ± 0.1038 0.80972	TTAACACCTCTAGATAAGATGATATGCTTATCTTCTC
plasmid_lp36	21079	BB_K32	0.766 ± 0.6267 0.532292	1.253 ± 1.1716 0.56764	0.96 ± 0.6932 0.93022	0.808 ± 0.6677 0.75895	TATAACTTACATATTCTCAACAAAGCTAACCCAAATGTTCTAC
plasmid_lp36	21354	BB_K32	1.025 ± 0.4754 0.830891	1.096 ± 0.4912 0.58455	0.858 ± 0.285 0.35827	1.226 ± 0.3718 0.308	TAAATTAGATTGTTCTTGTGATTCTGCAATTAAAGTTTATTCTGCTTC
plasmid_lp36	21368	BB_K32	0.896 ± 0.5818 0.553055	1.962 ± 2.1893 0.36044	0.735 ± 0.4942 0.17856	0.734 ± 0.5051 0.43009	AAGCAATAGTAACGTCATCTTAAATGAGGGATTCTTAAAGAAGTGC
plasmid_lp36	21494	IG_1271	0.069 ± 0.0713 0.024611	0.692 ± 0.8704 0.68804	0.045 ± 0.0797 0.02915	0.308 ± 0.2336 0.00655	AATATGTAAGTGTAAAGATAAAATTAAGAAGTTCTAGTTGAAAAAG
plasmid_lp36	21522	IG_1272	1.136 ± 0.4769 0.308833	1.936 ± 1.2293 0.19077	0.796 ± 0.2874 0.46273	1.164 ± 0.4129 0.58522	ATTATTCTAAACAGTCACATTTACATATTGTA
plasmid_lp36	21686	IG_1273	0.549 ± 0.6447 0.087267	0.291 ± 0.3986 0.3142	1.245 ± 1.2064 0.39622	0.51 ± 0.5781 0.54327	GTAAAAGCTATTCTAAATACTTACTTAAACATGGCAATCTACCAATTCT
plasmid_lp36	21702	IG_1274	1.037 ± 0.7527 0.93841	1.105 ± 0.5505 0.74553	0.657 ± 0.5648 0.4411	1.339 ± 0.3167 0.23026	CAAAATGGTATTGTCAGCTGATTCTAACATTCTTATTCACACT

plasmid_lp36	21951	BB_K34	0.964 ± 0.5675 0.770495	0.885 ± 1.1051 0.77559	0.75 ± 0.4142 0.18435	0.911 ± 1.0513 0.80638	CTATACTATTTAATAAGAGAAAAATTATTTACTCAATATTAAAGCTG
plasmid_lp36	21956	BB_K34	1.758 ± 0.2884 0.046757	2.134 ± 1.5522 0.33899	1.03 ± 0.27 0.86215	1.511 ± 0.3139 0.14019	GTATAGTAATGATATCCAAAGTACAAGGGGCCATTATTCATTAGATA
plasmid_lp36	22015	BB_K34	0.957 ± 0.3165 0.845443	1.003 ± 0.4489 0.99354	0.883 ± 0.2651 0.61652	0.932 ± 0.3257 0.79335	AATAGGGGAAAAAAACAAGCTTAATATTGAGTGATAAATAAATTTCCTT
plasmid_lp36	22052	BB_K34	0.896 ± 0.6734 0.330964	1.923 ± 2.1103 0.40732	0.76 ± 0.5372 0.17381	1.333 ± 1.2479 0.5457	AATATCAAGTAAATTAAATTGGATAGTAAATAATAGGGGAAAAAA
plasmid_lp36	22263	IG 1275	0.588 ± 0.8241 0.058612	1.66 ± 1.1677 0.05283	0.554 ± 0.5536 0.44263	0.821 ± 0.6985 0.79511	TGTTAAAAGGTTTATTCAAACGTAAAAATATGGTAAAGTAAAAAGCC
plasmid_lp36	22323	BB_K35	1.492 ± 0.5663 0.299506	2.081 ± 1.3402 0.30689	0.978 ± 0.2384 0.91595	1.185 ± 0.3267 0.3497	TATTTAAATATGGTAGAGATAATCAGCTTAATGAGAAGTAAAGATAGAA
plasmid_lp36	22325	BB_K35	1.786 ± 1.772 0.393033	1.391 ± 0.8688 0.27278	0.967 ± 0.7968 0.88363	1.199 ± 0.9489 0.60039	ATATAGCTAACGGCTTTAACTTACCCATATTTCAGTTGAATAAA
plasmid_lp36	22337	BB_K35	1.166 ± 0.8478 0.492649	0.99 ± 0.7078 0.91422	0.347 ± 0.1817 0.11011	0.701 ± 0.405 0.17351	GAGATAATCAGCTTAATGAGAAGGTAAGATAGAAATCATAGATGTGA
plasmid_lp36	22340	BB_K35	1.076 ± 0.3168 0.014443	1.732 ± 1.0403 0.23806	0.915 ± 0.2116 0.36883	1.104 ± 0.3753 0.16254	TCTCTACCATATTAATAGCTAACGGCTTTAACTTACCCATATT
plasmid_lp36	22598	IG 1276	1.064 ± 0.5359 0.890441	1.962 ± 1.2749 0.31888	0.818 ± 0.2693 0.41546	1.23 ± 0.4946 0.43362	GTAATATTCAATGTGAATCTCAATCTGGCATACTTTAAATGT
plasmid_lp36	22910	IG 1277	6.684 ± 6.397 0.255189	0 ± 0.01495	0.216 ± 0.3779 0.11409	1.812 ± 3.1626 0.67781	ATTAATCATTTAAATATTATGGTTTATTGTAAAGCCAAACTA
plasmid_lp36	23014	IG 1278	1.449 ± 1.0926 0.430879	1.907 ± 1.2237 0.1504	0.927 ± 0.7187 0.75946	1.234 ± 0.8142 0.56772	GTAGGCTCTATTGCAACAAGCATGACTAATTITATCTTTATGTAAATAAA
plasmid_lp36	23131	BB_K37	0.663 ± 0.4882 0.339721	0.322 ± 0.4138 0.12262	0.676 ± 0.4523 0.44492	1.291 ± 0.995 0.70022	TTATCTACATAATTAGCCTCTTGTAGTATTAGGTTGTGATTGTCAAGC
plasmid_lp36	23334	BB_K37	1.541 ± 1.1263 0.419317	2.089 ± 1.2567 0.13996	0.737 ± 0.7876 0.64569	1.452 ± 0.8409 0.38808	TGCTCTCTTAAATGTTGCTATGTTGATGCAACTTCTTAGAAAAGC
plasmid_lp36	24166	BB_K0058	1.151 ± 0.7873 0.713643	1.524 ± 1.719 0.51782	1.263 ± 1.6112 0.7675	0.862 ± 0.5324 0.76192	CCTCTCTTGTAGCCAAATTAAAGAACAGCTAGAAGGATAGAGGCAGGT
plasmid_lp36	24285	IG 1279	1.223 ± 0.8823 0.719325	1.672 ± 2.3465 0.58319	0.965 ± 0.7961 0.94049	1.744 ± 0.9956 0.29149	AGTAGCATATGCTTACTATAAAAATTAGAAATGGCAAAAGAAAGTGGCC
plasmid_lp36	24294	BB_K39	0.894 ± 0.2269 0.516836	0.755 ± 0.1485 0.03513	0.59 ± 0.057 0.00787	0.652 ± 0.0694 0.00579	TGCTCTACTATAAAAATTAGAAATGGCAAAAGAAAGTGGCTTAAGCATG
plasmid_lp36	24297	BB_K39	1.483 ± 0.8336 0.058176	1.359 ± 0.8697 0.59236	0.763 ± 0.5825 0.05218	0.795 ± 0.6833 0.05533	AGCATATGCTACTTACCCGTCTTAAGATTATTTAAAGTGTCTCTGCTA
plasmid_lp36	24522	BB_K39	1.016 ± 1.0032 0.983765	1.1 ± 1.0953 0.73436	0.764 ± 1.0005 0.80203	1.041 ± 1.1666 0.95051	TCGAAAAAAGGCTTCTACTTTCCCATTAACCCAGTTACACACTCCCTA
plasmid_lp36	24785	IG 1280	0.757 ± 0.6539 0.624905	0.693 ± 0.5621 0.635	0.466 ± 0.4422 0.35484	0.534 ± 0.4575 0.46906	GTTTAGGGTCTTATGCTAGTTGCTATGAGCTACAGAGAACTAGTA
plasmid_lp36	24833	IG 1281	0.781 ± 0.3462 0.252072	0.971 ± 0.9271 0.9436	0.591 ± 0.3796 0.1185	0.904 ± 0.4695 0.57478	CTAGTCTCTGATGCTCATGAAACACTAGACATAAGAACCCCTAAACTA
plasmid_lp36	24947	IG 1282	1.734 ± 1.0743 0.177607	2.607 ± 3.4634 0.41911	1.125 ± 1.1189 0.81371	1.836 ± 1.43 0.04212	CTAATACTAAAGATGACTTAGAAAGAACCTTGTACTAGCTT
plasmid_lp36	25003	IG 1283	0.941 ± 0.5093 0.704865	1.535 ± 1.2238 0.38715	0.827 ± 0.3109 0.39339	1.058 ± 0.7776 0.78353	GGTTGTCAAAGCTAGTGACAAATCAAGTCTTCTAAGTCATTTAG
plasmid_lp36	25064	IG 1284	2.044 ± 2.1274 0.395501	2.91 ± 3.4011 0.27374	1.447 ± 1.5194 0.27968	1.759 ± 2.5224 0.40763	GATAACAAAAGTAGTTAAATGAGCTAGAAAGGAGGGTTATGAGTAATT
plasmid_lp36	25376	BB_K40	0.944 ± 0.4996 0.269367	1.179 ± 0.91 0.56487	0.626 ± 0.279 0.18578	0.753 ± 0.3007 0.236	AAAGACAGTAAGAAGTGAGCTTAAGGGTGAGATAGTAAAGTTAGATGAAAGA
plasmid_lp36	25591	BB_K40	1.747 ± 0.7519 0.216858	1.749 ± 0.4295 0.06652	1.175 ± 0.185 0.10667	1.559 ± 0.5736 0.21783	AAATGGATATATCAAGCTTTTATATGCGAGTTCTCACTCTTATITC
plasmid_lp36	25669	IG 1285	0.973 ± 0.2812 0.057936	1.03 ± 0.5725 0.89821	0.662 ± 0.1679 0.15015	0.97 ± 0.2968 0.73008	AGTGTACTTACCCATTAGCTTAATTATTTAAAGTATTATTA
plasmid_lp36	25765	IG 1286	2.510 ± 0.8588 0.003157	3.905 ± 3.8927 0.31105	2.231 ± 2.6721 0.49615	2.166 ± 1.9986 0.38955	TCTTCTGCTTTAAATTCCTGCTTCTAGCCATTCTGATCATA
plasmid_lp36	25774	IG 1287	0.677 ± 0.6784 0.360209	0.32 ± 0.4742 0.40769	1.07 ± 1.2323 0.76138	0.87 ± 0.9446 0.55874	CTTAGGCTTTAAATAAGAAGATATTGTTGCTAGTTATTGATT
plasmid_lp36	25813	BB_K41	0.813 ± 0.5307 0.541661	2.071 ± 1.3832 0.03845	0.852 ± 0.5793 0.73644	1.307 ± 0.9045 0.09998	ACTAGCACAAACATCTTCTTAAAGCCTAAAGTACTGTACT
plasmid_lp36	25853	BB_K41	1.586 ± 1.4675 0.501858	1.595 ± 1.9611 0.2805	0.611 ± 0.6751 0.43415	0.535 ± 0.8889 0.64795	GTAGCAAGGCTACCTTACTATCATCATTATAAAATTATGTTGTTG
plasmid_lp36	25862	BB_K41	1.380 ± 0.6847 0.199055	1.663 ± 1.2423 0.33632	0.817 ± 0.2819 0.17827	1.057 ± 0.3311 0.78262	GCCTTGCTACTATCTAATGACTTAGAAAGGATGCAAATCAATAAAC
plasmid_lp36	25908	BB_K41	0.574 ± 0.6193 0.46354	0.891 ± 0.8977 0.88244	0.645 ± 0.4144 0.31668	1.133 ± 1.1508 0.8507	GTTTAATGATAAGATAAGCTTGAGCTACCTCTTTAGTAACCCATCAA
plasmid_lp36	26123	BB_K41	0.365 ± 0.4265 0.418517	1.236 ± 1.2845 0.61433	0.701 ± 0.8658 0.57949	1.06 ± 1.634 0.95996	AGACTACTAAGCTTGTATCTATAAAACATCTTAAAGAGATTGGTT
plasmid_lp36	26276	BB_K41	1.001 ± 0.4572 0.998153	1.211 ± 1.461 0.773	0.769 ± 0.663 0.39869	0.807 ± 0.4201 0.57515	AGATGGCTGGCTTGGAGGCTTATAGCATTTCCATAAAATTAAAGCTT
plasmid_lp36	26452	IG 1288	1.245 ± 0.6933 0.156025	2.307 ± 2.6584 0.39224	0.941 ± 0.4985 0.63944	1.065 ± 0.777 0.70184	GCTTCAAGGTTCTTAATAAGAGCATTTTTGAGTCTAAGTTGTA
plasmid_lp36	26932	BB_K42a	1.160 ± 0.4457 0.416591	2.061 ± 1.6693 0.26662	0.986 ± 0.4383 0.87029	1.292 ± 0.6854 0.1372	GTTTATGTTCTAGCAATTATGCTCTTTATTAGAAAATTCAACTACT
plasmid_lp36	27034	BB_K42a	1.061 ± 0.5511 0.286491	1.776 ± 1.417 0.27967	0.869 ± 0.3999 0.36404	1.19 ± 0.6732 0.3456	TATTTGTTAAAATAAGAAGATTTGTTAAGCTTATAAGCATCTCTATAAGT
plasmid_lp36	27078	BB_K42a	0.448 ± 0.2682 0.135637	1.121 ± 0.8102 0.14737	0.599 ± 0.3074 0.26247	0.806 ± 0.5219 0.62492	TAGGAGCTTATAAGCTTAAACAACTTATTTCACCAATATATC
plasmid_lp36	27134	IG 1289	0.841 ± 0.2768 0.192931	1.272 ± 0.6083 0.33589	0.727 ± 0.1635 0.18574	0.787 ± 0.1884 0.10173	GTAACAATATGTCGTAACTAGAAAAGAACATTAAATTAAAGATTAAT
plasmid_lp36	27233	IG 1290	0.822 ± 0.5669 0.723512	0.951 ± 0.8269 0.83909	0.481 ± 0.413 0.21026	0.295 ± 0.3072 0.11494	ATATGTTACCTTACAGGGAGCTTAAATTTATCTAGAAAATATGGA
plasmid_lp36	27315	IG 1291	2.140 ± 1.2838 0.073167	0.957 ± 0.5242 0.9121	1.175 ± 0.5108 0.25541	1.361 ± 0.7621 0.36181	TTTTGTTAAAATCCAAAAGCTTCTTATTATAAGTAAGTGTATGCTT
plasmid_lp36	27399	BB_K45	1.101 ± 0.5777 0.822927	1.953 ± 1.0159 0.21937	1.099 ± 0.5498 0.66834	1.493 ± 1.1274 0.42875	CTTAAAGCAGCTTCATGCTTATTAACTCTCAAACCTTTTGT
plasmid_lp36	27542	BB_K45	0.003 ± 0.005 0.165318	0.125 ± 0.2313 0.22628	0.438 ± 0.5313 0.17746	0.699 ± 0.86 0.52762	TATGAATGATGCTAAAGAAGCAATGGGAGGGCTAAAGTGCCTTAAG
plasmid_lp36	27687	BB_K45	0.874 ± 0.7198 0.295257	1.492 ± 1.5554 0.39732	0.715 ± 0.5084 0.1622	0.869 ± 0.5969 0.39239	ACTCTAATTATTCAGATGCGTAAGTGCCTTAAAGATTCAGACGATT
plasmid_lp36	27690	BB_K45	1.441 ± 0.9431 0.153902	1.792 ± 1.4325 0.17399	0.977 ± 0.6218 0.9587	1.435 ± 0.8292 0.43641	GCATAAGCATGGCTGCTACTACTTGCAGAATAGCTGATGCAAGTTAGG
plasmid_lp36	27705	BB_K45	1.107 ± 0.6285 0.551511	1.252 ± 1.2362 0.66965	0.564 ± 0.3132 0.21103	1.117 ± 0.3357 0.5924	GCAGCCATGCTTATGCTAATTCAGATGCAAGTGCAGTAAGTGCCTAA
plasmid_lp36	27852	BB_K45	1.736 ± 0.8904 0.068883	2.075 ± 1.8804 0.27256	1.357 ± 0.7646 0.26356	1.363 ± 0.6089 0.26101	CAGATTAGAAACAAATAAGCTAAGACTTAAATAAAAAGTAAAGTTG
plasmid_lp36	28178	BB_K45	0.996 ± 0.9719 0.991517	0.14 ± 0.164 0.19718	0.647 ± 0.5664 0.39708	0.89 ± 0.9311 0.3534	TAGCTGCAAGAGATAAAAGCTTAAACTGAATATAACTTAATTTAAT

plasmid_lp36	28248	BB_K45	1.086 ± 0.439 0.641341	1.215 ± 0.3575 0.28721	0.904 ± 0.2597 0.64676	1.162 ± 0.2063 0.3022	ACTTTATGCAAAAATAGAGTATTATTGTAATACAATATCATTATATTACAT
plasmid_lp36	28332	IG_1292	1.529 ± 1.4573 0.429876	1.957 ± 1.7606 0.26624	0.861 ± 0.8885 0.72346	1.217 ± 1.1299 0.74715	ACATATAACCTCATATTCTGATTACTAATAATAAATGTAATATAATGATAT
plasmid_lp36	28445	BB_K46	0.956 ± 0.8739 0.936696	1.594 ± 1.7316 0.66278	0.449 ± 0.6848 0.51747	1.332 ± 1.4189 0.76656	TCAGGCAAATGCAGACTTGAAGAGCTAAATAAAGCATATGAAGCTGCTTA
plasmid_lp36	28533	BB_K46	0.989 ± 0.508 0.917376	1.453 ± 1.2747 0.46695	0.711 ± 0.3432 0.3894	0.99 ± 0.5545 0.97222	TAATGACGCCAAAGATGCAATGGAGAGGGCTAAAGAGATGCTAGATAAACG
plasmid_lp36	28852	BB_K46	1.181 ± 0.6661 0.3654	1.228 ± 0.823 0.46682	0.77 ± 0.3271 0.16982	0.817 ± 0.4104 0.04527	GTCTAGCGCACTCTCTGTAAGAGATTCAATTCCCTCATATAATTACTAT
plasmid_lp36	29013	BB_K46	1.177 ± 0.3837 0.260266	1.507 ± 0.8432 0.45431	0.918 ± 0.4233 0.74485	0.946 ± 0.4871 0.78375	TGAAACAAAACATAGACAAAAATCATTAGTTGAGATATGCAAAATG
plasmid_lp36	29095	BB_K46	0.537 ± 1.0585 0.697038	4.132 ± 6.8012 0.46971	1.127 ± 1.4615 0.91763	1.404 ± 1.4722 0.40891	GACAACAACAAGCTTTAATACCTTAAAGCAGCAATGAGAGTAGAAAGT
plasmid_lp36	29213	IG_1293	1.329 ± 0.6672 0.518324	1.572 ± 0.7199 0.20137	0.695 ± 0.622 0.51996	1.029 ± 0.6651 0.94686	GATGAATTAAATTGCTAAATTATTATCCACTTGTGTTCAATTCC
plasmid_lp36	29299	IG_1294	0.643 ± 0.555 0.42699	0.934 ± 1.359 0.94436	0.24 ± 0.2302 0.23643	0.874 ± 0.969 0.87979	TTTTCTATTTTATAATGTGATATTTTTAAGAATAAAGCATA
plasmid_lp36	29402	IG_1295	1.444 ± 1.2473 0.650687	1.921 ± 1.8833 0.36181	0.672 ± 0.7659 0.34997	1.52 ± 1.5686 0.49741	TATAAGCTTTCTAGAAAGATGGGATTATATGAGTAGAGATATTAAG
plasmid_lp36	29403	IG_1296	3.223 ± 2.9664 0.25779	0.567 ± 0.7438 0.53167	1.059 ± 1.1522 0.91868	2.44 ± 2.7944 0.4672	TATATGCCCTACCTAAATTACTATTCACTTCCCTTGTGCTTACAAG
plasmid_lp36	29428	IG_1297	1.159 ± 0.2367 0.142795	1.362 ± 0.3307 0.22503	0.855 ± 0.1683 0.37923	1.075 ± 0.2787 0.24924	ATCCCACATCTTACTAGAAAAGCTTATATCGGCTTACCTAAATTAACTAT
plasmid_lp36	29493	BB_K47	1.344 ± 0.6407 0.396328	2.1 ± 2.0177 0.36987	1.133 ± 0.8292 0.75538	1.65 ± 0.7407 0.13905	TTTCTATTCTTTTGCAAGAATTCCCTGTTGAAGATAATCAACTG
plasmid_lp36	29552	BB_K47	0.823 ± 0.4638 0.420706	0.523 ± 0.4362 0.19823	0.64 ± 0.1818 0.19517	1.324 ± 0.4692 0.06064	TACACAAAAGCTTATTGATTATCTCAACAGGGAAATTCTGCAAAAAGA
plasmid_lp36	29670	BB_K47	1.356 ± 0.3517 0.249864	1.736 ± 1.2955 0.46183	0.61 ± 0.2006 0.2105	1.167 ± 0.4552 0.63048	AAAGACTATACAATGGCAATTACACGGTTGGCAGTTAACGGAC
plasmid_lp36	29673	BB_K47	0.958 ± 0.7028 0.9307	0.335 ± 0.4483 0.20307	0.476 ± 0.5864 0.52509	0.957 ± 1.1699 0.96885	TAAATAGATTCTGCTAGTTATCCTAGCCTCATCTAGCCTTAGCA
plasmid_lp36	30012	BB_K47	1.121 ± 0.6141 0.648407	1.265 ± 0.935 0.55049	0.81 ± 0.3691 0.50053	1.038 ± 0.6399 0.79717	TTCCCTCAGAAGAAGAAATTAAAGCTAACCTTAGATGAATTGACAAG
plasmid_lp36	30139	BB_K47	1.157 ± 0.7394 0.403102	1.85 ± 1.9557 0.40584	0.736 ± 0.4167 0.06318	1.011 ± 0.6534 0.94318	AAAATGACTCGCATGCTCAAATAATGTAAGATGGAAGAAAATAATCA
plasmid_lp36	30142	BB_K47	1.082 ± 1.2397 0.823599	0.587 ± 0.6182 0.47877	0.957 ± 1.2682 0.96866	1.159 ± 1.457 0.80384	TTATTGCTGACTTGAATTGGTAGGGATTCTTATTAGCACCAAGGAT
plasmid_lp36	30183	BB_K47	1.320 ± 1.5561 0.786588	0.888 ± 1.2156 0.84047	0 ± 0 0.03866	0.662 ± 0.6576 0.37317	GCACCAAGGATCATCTGACATATGTTGATTAGAACCTACTTGTAGATTGGA
plasmid_lp36	30226	BB_K47	1.255 ± 0.3058 0.044776	1.144 ± 0.426 0.67279	0.845 ± 0.2475 0.24964	1.046 ± 0.3378 0.67585	AGATGGATCATAAGTTTTTATTGATGATGTAACGTCTTAGGGAGATT
plasmid_lp36	30312	BB_K47	1.318 ± 0.6915 0.243501	1.792 ± 1.3143 0.29009	0.901 ± 0.2629 0.60434	1.163 ± 0.4448 0.06098	GTAGTATTCTTATTCTGTGATGATCTTTAATGCTAACGAAACTGTTCT
plasmid_lp36	30361	BB_K47	1.158 ± 0.5175 0.17455	1.892 ± 1.0652 0.14921	0.948 ± 0.3109 0.66756	1.165 ± 0.417 0.16172	GAACAGTTGCATTAGCATTAAAAGATCATCAAGAAAATAAAATACT
plasmid_lp36	30544	IG_1298	2.011 ± 1.1632 0.261901	1.384 ± 0.5475 0.27566	1.073 ± 0.612 0.81565	1.065 ± 0.6138 0.88204	TATTATAATTATTAAATAGATATTCTGTATATAAGTACATAACAA
plasmid_lp36	30615	IG_1299	1.464 ± 0.7568 0.102791	1.738 ± 0.669 0.17582	0.78 ± 0.3493 0.50659	1.621 ± 0.7375 0.17051	AAGTTAAGAGAAAATAAGTGTGTTAGAAAAGAGTATTATAACAAAG
plasmid_lp36	30723	BB_K48	1.276 ± 1.3532 0.790579	0.348 ± 0.6395 0.3656	0.89 ± 0.6976 0.68581	2.02 ± 1.8995 0.22911	GATAAGTAAAAGTAAATAATTAAAGACAAGCCAGACAATCTTATGAGGT
plasmid_lp36	30751	BB_K48	0.375 ± 0.6217 0.348118	0.32 ± 0.3295 0.14432	0.163 ± 0.2465 0.00998	0.236 ± 0.4162 0.16384	TATAAAAAAATTGCAAGATATGGACTCTAGATAAGTAAAAGATAATTAA
plasmid_lp36	30777	BB_K48	1.328 ± 0.7323 0.421201	1.771 ± 1.5229 0.42878	0.828 ± 0.3904 0.31897	1.237 ± 0.5839 0.42493	AAGACTTCAAGAGTAAATGATATATAAAAATTGCAAGATATGGACT
plasmid_lp36	30902	BB_K48	1.027 ± 0.843 0.893451	1.335 ± 0.956 0.23314	0.616 ± 0.3642 0.13645	0.731 ± 0.5799 0.03512	GTAGCTCTCATGCCCTGAGCATCTTACTTAATGCTTCTTCAAAGC
plasmid_lp36	31078	BB_K48	1.224 ± 0.7699 0.484972	0.843 ± 0.9446 0.49373	1.271 ± 0.6755 0.55651	1.24 ± 0.6811 0.44164	GGCTAGGCAATAAGCTAACCTGTTACTAGATCCCACCTCTTGTAG
plasmid_lp36	31263	BB_K48	0.563 ± 0.9431 0.031126	0.762 ± 1.0534 0.34783	0.362 ± 0.4528 0.38355	0.825 ± 0.9694 0.82844	GCTTCACTGCTTCAATTCTGGATATAACTGTGAGTATGGTTGCTG
plasmid_lp36	31272	BB_K48	1.730 ± 1.492 0.166024	2.173 ± 2.4025 0.32063	1.129 ± 0.6911 0.72432	2.117 ± 1.5257 0.01125	GCTTCATTATCTGGATATAACTTGTAGAGTATGGTTGCTACTTAA
plasmid_lp36	31290	BB_K48	0.442 ± 0.3683 0.28736	0.391 ± 0.4162 0.01268	0.348 ± 0.4511 0.25764	0.777 ± 0.4063 0.17969	ATATCCAAGATAATGAAGCTAGTGAAGCTAGAACATTATGACGGAAATTG
plasmid_lp36	31579	BB_K48	0.822 ± 0.8402 0.705797	1.26 ± 1.2975 0.72061	0.754 ± 0.3754 0.01335	0.719 ± 0.5447 0.16374	AATTCACCTTAACTCTCTTAAAGCTGATATTCTTATAAAAGAA
plasmid_lp36	31763	IG_1300	1.235 ± 1.0423 0.6858	1.833 ± 1.902 0.56023	0.631 ± 0.5092 0.16225	0.431 ± 0.4049 0.36961	AAAAAACTTATATCAGCTTACCTAAATAACTATCTCACTCTTGTG
plasmid_lp36	31835	BB_K49	1.570 ± 2.1339 0.221981	0.639 ± 0.8853 0.59084	0.731 ± 1.1034 0.55648	0.481 ± 0.7707 0.37043	AAGCTTTAAACTCCAGTGTAGGCTTAACTTGTAGATGCTTAACTCA
plasmid_lp36	31902	BB_K49	1.073 ± 0.2378 0.375945	1.587 ± 0.9391 0.32256	0.784 ± 0.3097 0.05469	1.054 ± 0.429 0.79837	TATGAAAATGCTTGTAGGTTCTTAAATGGAAATTCTGAGAAAAGA
plasmid_lp36	31905	BB_K49	0.921 ± 0.4938 0.57225	1.484 ± 1.2265 0.29029	0.824 ± 0.4787 0.1622	0.981 ± 0.6054 0.67436	TTTATGCTTCAATTGCAAGATCTAGTGTAGCTTGTAACTCTGTAT
plasmid_lp36	31931	BB_K49	0.581 ± 0.5927 0.205787	1.164 ± 1.1485 0.39238	0.637 ± 0.667 0.31131	1.031 ± 1.0626 0.87456	TAGCTCTTGTGAACTCTGTATATTGCTTGTGTTAAATTACTGCTTA
plasmid_lp36	32041	BB_K49	0.650 ± 0.4768 0.271838	0.79 ± 0.7126 0.64201	1.171 ± 0.5666 0.67904	1.458 ± 0.6347 0.16723	TCTCGAGCCAACTCATCTGTAGCATCTTGTAGCAGACCCCCAAGAATTGCT
plasmid_lp36	32260	BB_K49	1.124 ± 0.6113 0.595969	1.896 ± 1.4673 0.24663	0.719 ± 0.3709 0.14593	0.718 ± 0.4964 0.08239	ATTCTGAAAATAACTTAAACAAATACACTCTTGTAGTTAAAGAATTTCATC
plasmid_lp36	32498	BB_K49	1.169 ± 0.7639 0.39757	1.814 ± 1.9049 0.41342	0.722 ± 0.4055 0.04784	0.998 ± 0.6394 0.98674	CAAATGACTCGCATGCTCAAATAATGTAAGATGGAAGAAAATAATCA
plasmid_lp36	32542	BB_K49	1.218 ± 1.3582 0.84568	1.003 ± 1.4582 0.9953	0.032 ± 0.0418 0.12114	0.682 ± 0.7396 0.33067	GCACCAAGGATCATCTGACATATGTTGATTAGAACCTACTTGTAGATTGGA
plasmid_lp36	32585	BB_K49	1.285 ± 0.357 0.067855	1.188 ± 0.4853 0.62476	0.871 ± 0.2749 0.33516	1.073 ± 0.3889 0.58922	AGATTGGATCATAAGTTTTTATTGATGATGTAACGTCTTGGAGATT
plasmid_lp36	32671	BB_K49	1.292 ± 0.651 0.28273	1.738 ± 1.2525 0.31606	0.877 ± 0.2239 0.45428	1.16 ± 0.4158 0.14649	GTAGTATTCTTGTGATGATCTTTAATGCTAACGAAACTGTTCT
plasmid_lp36	32720	BB_K49	1.087 ± 0.4635 0.318756	1.915 ± 0.9859 0.12882	0.944 ± 0.2839 0.63339	1.19 ± 0.3724 0.11192	GAACAGTTGCATTAGCATTAAAAGATCATCAAGAAAATAAAATACT
plasmid_lp36	32831	IG_1301	1.690 ± 1.1461 0.060567	1.558 ± 1.5514 0.50087	0.8 ± 0.5296 0.54617	1.37 ± 0.9778 0.35571	TATTCCTTTAAATAAAACTTGTGTTAGTATGCTTATATGCAAATAATTC
plasmid_lp36	33116	BB_K50	1.750 ± 0.4932 0.05221	1.691 ± 0.6213 0.02505	1.474 ± 0.7538 0.45151	1.306 ± 0.4923 0.46388	TATCATTTACTCTGAAAGCTTATTGCTTAGTCAATTTCATTAA
plasmid_lp36	33139	BB_K50	1.238 ± 0.8779 0.50936	1.657 ± 1.4896 0.40781	0.705 ± 0.3754 0.00125	1.121 ± 0.6477 0.49295	AGGACTTCAAGAGTAAATGATATATAAAAATTGCAAAGATATGGACT

plasmid_lp36	33232	BB_K50	1.467 ± 1.4969 0.689801	1.336 ± 1.2215 0.6629	0.344 ± 0.4999 0.07254	1.459 ± 1.1982 0.58814	ATGCTAATGATGCAATGGAGAGTGCTAAAGTTGCTAGAGGTTGCTAAGA
plasmid_lp36	33235	BB_K50	1.246 ± 0.5692 0.166695	1.451 ± 1.2212 0.43928	0.812 ± 0.2708 0.39149	1.163 ± 0.4672 0.18176	TTTATCGGTAAATGGTAAAGATAATTGACCCCTAAATGAGGTATATCT
plasmid_lp36	33396	BB_K50	1.512 ± 0.8239 0.349518	1.483 ± 0.8258 0.39908	0.508 ± 0.1762 0.07202	0.792 ± 0.7308 0.5705	TGCCCTCTTAAATGTTGCTACTGATGCAATTGCTGCTTAGCAAAGC
plasmid_lp36	33403	BB_K50	0.633 ± 0.6854 0.086756	0.299 ± 0.2144 0.17546	0.278 ± 0.3062 0.08965	0.419 ± 0.6248 0.20727	GTAGTTATGCCTCTTAAATGTTGCTACTGATGCAATTGCTGCTTAG
plasmid_lp36	33604	BB_K50	0.729 ± 0.3782 0.440898	0.683 ± 0.5458 0.2682	0.672 ± 0.5797 0.58692	0.511 ± 0.3445 0.25492	TACAAAAGCTTCACTCTTAAAGAGCTGAGAAAGTAAATGCGACTT
plasmid_lp36	33787	BB_K50	0.968 ± 0.9105 0.935673	1.096 ± 1.7305 0.94386	1.012 ± 1.2593 0.98886	1.01 ± 0.9442 0.98923	TTTGTGTTGATCATTCGTTTGTATTACTTCTTTACCCCAATTCT
plasmid_lp36	34079	BB_K50	1.124 ± 0.1725 0.424899	0.952 ± 0.4637 0.86861	0.817 ± 0.0929 0.15355	1.136 ± 0.0898 0.11469	ATGAATTAAATAATTAAAGTGATGTTGATATCCAGTTTTCTAGCTT
plasmid_lp36	34081	IG_1302	1.027 ± 1.1037 0.948319	0.287 ± 0.369 0.28472	0.785 ± 0.4496 0.42014	0.844 ± 0.558 0.27197	TAATGAATTAAATAATTAAAGTGATGTTGATATCCAGTTTTCTAGCT
plasmid_lp36	34137	IG_1303	0.709 ± 0.4736 0.318172	1.208 ± 1.0969 0.75839	1.077 ± 0.7661 0.38915	0.813 ± 0.4903 0.64822	TATGTGATATAATGATAAAATTCTATAATATTCTATTAGATAGAGG
plasmid_lp36	34754	BB_K52	0.670 ± 0.5503 0.56384	0.841 ± 0.6826 0.75401	0.458 ± 0.386 0.2735	0.651 ± 0.5637 0.36047	TATGCCCTCATATCTTACTATAAAAGATAAAGAACCGATAATATAAAAC
plasmid_lp36	34992	BB_K52	1.179 ± 0.7483 0.394775	1.529 ± 1.2227 0.31951	0.751 ± 0.533 0.29973	0.905 ± 0.4144 0.76193	AGATAATAGCATTGAACTAACAGAGTTGAAAAAAATACGAAATAA
plasmid_lp36	35088	BB_K52	1.203 ± 0.377 0.386388	2.075 ± 2.1246 0.24852	0.447 ± 0.1678 0.02379	0.974 ± 0.3736 0.89956	TTTTTCACCCCATTCGATTCAAAACTTTTGTATTAAATTAGCATT
plasmid_lp36	35090	BB_K52	1.308 ± 0.5819 0.277808	1.546 ± 0.4829 0.04809	0.893 ± 0.27 0.15363	1.258 ± 0.6544 0.41849	TATTTTTCACCCCATTCGATTCAAAACTTTTGTATTAAATTAGCATT
plasmid_lp36	35093	BB_K52	1.170 ± 0.433 0.369635	1.592 ± 0.911 0.18997	0.974 ± 0.3474 0.88721	1.232 ± 0.5052 0.1798	AGAGTACCTAAGTCTCAAGTCTCAATTAAATTGTTATTCTT
plasmid_lp36	35180	BB_K52	1.543 ± 0.4454 0.136957	2.366 ± 1.3227 0.16592	1.1 ± 0.4061 0.75222	1.105 ± 0.8283 0.80682	TGTTACATGGGAAATCTGGTGACTTAAGGGTTAAAGATAAAATAA
plasmid_lp36	35218	BB_K52	1.217 ± 1.4859 0.615975	1.163 ± 1.2002 0.8661	0.852 ± 0.8587 0.81057	1.253 ± 1.1814 0.55886	AAAGAGGGGGACGTGCTGTAATTACTTGAGGTGTTATGTCATGGCA
plasmid_lp36	35787	IG_1304	1.267 ± 0.6037 0.259544	2.009 ± 0.9646 0.09395	0.897 ± 0.409 0.61302	0.999 ± 0.6187 0.99368	AATGTTAAATAAAATAGTGTAGAAACTGTATATTACAACAGATTA
plasmid_lp36	35913	BB_K53	0.930 ± 0.7327 0.833799	1.361 ± 1.2901 0.09453	0.663 ± 0.5068 0.41027	0.733 ± 0.678 0.64826	TTGGGTTGTATTGCTGATAATCAGGAAACAGCTGTTCAAAC
plasmid_lp36	36249	BB_K53	0.793 ± 0.7975 0.702946	0.604 ± 0.4493 0.18295	0.265 ± 0.343 0.11887	1.06 ± 0.541 0.47201	TACGCATAAAATTATTATTGTCATTTTACCATATAAAACACT
plasmid_lp36	36485	IG_1305	0.408 ± 0.2344 0.106184	1.43 ± 0.9595 0.56156	0.453 ± 0.3312 0.04536	0.508 ± 0.6374 0.45946	GTTTCGTTTGTATTCTGACCCCGCAAGAAATAACATCAGCATC
plasmid_lp38	425	IG_1306	1.149 ± 0.6376 0.273402	1.715 ± 1.4628 0.33156	0.509 ± 0.2311 0.09512	0.738 ± 0.3364 0.09222	ATACTAATTATTTAATTAGTATTAGTATTGCTTATATTAGGAGA
plasmid_lp38	1575	BB_J02a	1.775 ± 0.9014 0.144942	1.883 ± 1.9787 0.43554	0.992 ± 0.4149 0.96152	1.753 ± 0.7294 0.02557	TTGCAGCGTAATGAAATAGGAAAGCGAAAAGCACCGTATTACTAT
plasmid_lp38	1625	BB_J02a	0.625 ± 0.463 0.222765	0.848 ± 0.6819 0.68652	0.86 ± 0.2347 0.12771	1.088 ± 0.2129 0.44567	TAACCTTTAAATGCTTGTACTTGAAGATAGGATCTTTTGGCC
plasmid_lp38	2072	BB_J02a	1.645 ± 2.9993 0.562201	1.094 ± 1.3788 0.79773	1.058 ± 1.3072 0.95323	1.025 ± 1.2694 0.97699	ATACCATTAGAAATCAAATTAAAGAAATGGCTCTTGGTTATA
plasmid_lp38	2876	BB_J05	0.970 ± 1.0199 0.952309	1.438 ± 1.5539 0.36779	0.475 ± 0.4965 0.22741	0.684 ± 0.6841 0.43432	TTTCCATCAATTAAACTATGCGTAGTTGCCACATTAAATGACTCTAA
plasmid_lp38	3318	BB_J05	0.724 ± 0.3172 0.097649	1.74 ± 1.3469 0.39908	0.604 ± 0.2546 0.01262	0.767 ± 0.2584 0.07477	GATACTAAATAACAGTGAACACTAAAGGCAATAAAAGAGATTTGGT
plasmid_lp38	3493	BB_J05	1.379 ± 0.7395 0.210708	1.935 ± 2.1538 0.37227	1.116 ± 0.6456 0.39357	1.243 ± 0.7543 0.12657	ATAATCAAAAAAACTCAATAAGAATGGAAATTGTATATAAGCTATCTA
plasmid_lp38	3527	BB_J05	1.294 ± 0.3702 0.081372	1.726 ± 1.0781 0.28084	0.807 ± 0.2008 0.08076	1.116 ± 0.2947 0.10133	TGAAAGTAAGAAAATAAACTTTAGAAGTAATAATCAAAAAAACTCA
plasmid_lp38	3549	BB_J05	0.789 ± 0.6311 0.001414	0.948 ± 0.9319 0.79895	1.004 ± 0.6961 0.87788	1.065 ± 0.6917 0.26795	GAACACAAATAATTCTAAATGAAAGTAAGAAAATAAAACTTTAG
plasmid_lp38	3552	BB_J05	0.859 ± 0.7034 0.105993	0.945 ± 0.9399 0.81821	1.016 ± 0.6461 0.90607	0.894 ± 0.5855 0.42811	TTTCCTTTTAAATTCTAAATGAAAGTATTGAGCTTAAAGGAGA
plasmid_lp38	3680	BB_J05	0.516 ± 0.8126 0.568179	1.357 ± 1.0391 0.60274	1.244 ± 1.7853 0.86585	1.166 ± 1.2573 0.78312	TTACCTATCCAAGTAATAATAAGAATTTCTAAAGAAAGATTA
plasmid_lp38	3828	BB_J05	1.598 ± 0.8982 0.380487	2.408 ± 2.1163 0.34971	0.898 ± 0.5288 0.51542	1.214 ± 0.8853 0.46157	ATTAGCGTAATAAAAGCTTAAAGCATAGAATATCTAACCGCAATCAA
plasmid_lp38	3856	IG_1307	1.375 ± 1.4923 0.317973	2.392 ± 3.3046 0.39048	0.819 ± 0.7652 0.17224	0.815 ± 0.5694 0.7086	CTTAAGCGTATATGTCACAGAAGATAACCCATAATACTGTGTATATT
plasmid_lp38	3946	IG_1308	0.322 ± 0.2385 0.106933	0.489 ± 0.4332 0.23586	0.748 ± 0.2549 0.20041	0.673 ± 0.3679 0.0426	TGCCTATATTAGTAACTAAACTAGGTGATAATTGAATATACACAG
plasmid_lp38	4159	IG_1309	1.968 ± 1.2462 0.079477	1.711 ± 1.8424 0.47337	0.736 ± 0.3907 0.32825	1.759 ± 0.1015 0.22072	CTTATTTAGATAAGTATTGCTGAAACACCTTATTGTTGCTAGAGCTT
plasmid_lp38	4221	IG_1310	1.245 ± 1.1496 0.534735	2.303 ± 1.7414 0.25241	0.689 ± 0.5609 0.34583	0.811 ± 0.555 0.67569	TAGAGATAAGCAATAGCTTCTAGACCAAAATAAGGTTTCAAGCTAAACT
plasmid_lp38	4289	IG_1311	1.400 ± 0.516 0.273548	0.992 ± 0.392 0.98111	0.961 ± 0.3446 0.85165	1.344 ± 0.4237 0.12409	TTAGCAAATTATCTCCACCTAAATTCTAGAAATTATAGGTGAAGATT
plasmid_lp38	4388	IG_1312	0.830 ± 0.3489 0.24469	1.288 ± 0.564 0.32341	0.818 ± 0.5366 0.42626	0.545 ± 0.4097 0.32707	TTTCCTACGAAAGAAATTACAAGTGTGTTAACTAAAGTAACAAAGAA
plasmid_lp38	4624	BB_J08	0.889 ± 0.8394 0.599102	2.201 ± 2.7084 0.434	0.875 ± 0.4022 0.61298	1.263 ± 0.668 0.40237	GATTCTAAATTGCCTAAATAAGGAAACAAATGATATAAGGAA
plasmid_lp38	4895	BB_J08	0.590 ± 0.5408 0.490269	1.508 ± 1.4868 0.4951	0.387 ± 0.4115 0.1185	0.722 ± 0.6471 0.29343	CTAACCTTATTAGCGAGATGTCCTAAAGACATACATGCCCTACAGGGAGG
plasmid_lp38	5225	BB_J08	1.147 ± 1.0856 0.732689	0.509 ± 0.5715 0.00247	1.582 ± 1.7458 0.67265	0.766 ± 0.7905 0.15266	ATTCATCATGAGTCTTCAACTATCTTAAATTATTGCAATTGTTAGT
plasmid_lp38	5753	IG_1313	1.482 ± 0.4549 0.001797	1.736 ± 1.2809 0.43354	0.904 ± 0.366 0.71211	1.258 ± 0.6441 0.51712	ATAATAAGTCTTAAAATGATAGTAAAGATGTTGCTCTAATAATT
plasmid_lp38	5767	IG_1314	1.701 ± 0.9016 0.037533	2.131 ± 1.3919 0.09459	1.018 ± 0.4951 0.89408	1.491 ± 0.6463 0.1314	GCAAGCTTATCTAATAAAAGTCTTAAAGATGAGTAAAGATGTTG
plasmid_lp38	5776	IG_1315	0.795 ± 0.3653 0.415541	0.83 ± 0.7231 0.74501	1.025 ± 0.6002 0.95967	0.94 ± 0.6925 0.92329	TAATAGCTTTACATAGTTAGATAACACCGCAAATTAAAGACAAATT
plasmid_lp38	6110	BB_J09	1.356 ± 1.123 0.005327	2.612 ± 2.6627 0.20835	0.919 ± 0.6142 0.81397	1.038 ± 0.973 0.68524	CTACTGTTAAGTTTATTTGCTCTAAATCTGTGTTATGATAAA
plasmid_lp38	6257	BB_J09	0.492 ± 0.3932 0.016074	0.998 ± 0.9972 0.9947	0.946 ± 0.7576 0.73185	1.488 ± 1.2346 0.36549	ATATGCTGTTTGTGATTGTAATTGGAATTGCGCTTCATTATCTA
plasmid_lp38	6737	BB_J09	1.704 ± 0.7935 0.207924	1.489 ± 0.5659 0.18381	0.947 ± 0.3456 0.70989	0.916 ± 0.1551 0.24154	TTTATCCAAATGCTCTTGTACTGTTACATCAATTCT
plasmid_lp38	7780	BB_J11	0.124 ± 0.1558 0.16462	0.31 ± 0.3594 0.16114	0.291 ± 0.3161 0.11218	0.353 ± 0.2387 0.24281	ACAGTCCTACTGCAGGGTATAACGATCATTACTATGCTGGATAAAATG
plasmid_lp38	7922	BB_J11	0.840 ± 0.3136 0.487152	0.708 ± 0.9519 0.60747	0.629 ± 0.1266 0.08356	0.597 ± 0.583 0.30051	TGTATATTGTTGATACATAAGTACAAAAACTTAAACACCTGGGGC

plasmid_lp38	8188	IG 1316	1.020 ± 0.2292 0.892347	1.006 ± 0.1261 0.95357	0.812 ± 0.1985 0.04828	0.98 ± 0.1606 0.884	TGTATGTATAATTAACCTTTAATTAAAAAAATTCTCTAAAAGAAAAATT
plasmid_lp38	8315	IG 1317	0.701 ± 0.3826 0.491187	2.072 ± 2.1371 0.4099	0.676 ± 0.6201 0.55623	0.716 ± 0.5591 0.41773	TTATAAAAATATATTTCACCAAACAAATTATTCAGCTCTCAAAGCTT
plasmid_lp38	8366	IG 1318	1.160 ± 0.7739 0.223809	1.941 ± 2.1602 0.39452	0.814 ± 0.6185 0.08661	1.144 ± 0.7969 0.41921	GAAGCCTTGAGAAGCTTGAATAATTGGTTGATGTGAATATATTTTATA
plasmid_lp38	8932	BB_J13	1.089 ± 0.8997 0.776644	1.836 ± 2.0918 0.24528	0.506 ± 0.4367 0.26515	0.856 ± 0.8148 0.54262	AATAGTATTGATTCTTTCTACTTTCTAGCTCAACACCATTAAA
plasmid_lp38	9387	IG 1319	0.714 ± 0.3717 0.298841	1.777 ± 0.3915 0.09362	1.003 ± 0.3688 0.99096	0.917 ± 1.1547 0.91938	TGCTGTCTCGAGTATTAGTAGCCCATATTGAATGAAATTCAAAAATAA
plasmid_lp38	9654	BB_J15a	0.625 ± 0.2655 0.229382	0.757 ± 0.582 0.08941	0.581 ± 0.4268 0.0121	0.662 ± 0.5427 0.10654	ATGGACGCTATTGATTTTATCACCTTTTATTATATTGAAAAGTT
plasmid_lp38	9690	BB_J15a	1.398 ± 1.1702 0.667636	0.994 ± 0.8649 0.99384	0.868 ± 0.4528 0.71104	1.886 ± 0.998 0.11378	AATAAAAAGGTTGATAAAAATCGAATAGCGTCATTTAAATAATT
plasmid_lp38	9747	BB_J15a	2.671 ± 0.6405 0.012205	2.799 ± 2.2296 0.26445	2.463 ± 1.4556 0.22727	2.048 ± 1.5526 0.35291	TAATTCCAATATACTAATAGATTATTGTTATCAAAAAATACTTTC
plasmid_lp38	9752	BB_J15a	1.161 ± 1.1807 0.770711	1.981 ± 1.6779 0.29071	0.711 ± 0.3294 0.3519	1.113 ± 0.7848 0.61172	TGCACTATTGTTTATCAGATATTAGGGCCTGGATATTAGAAAAAT
plasmid_lp38	9881	BB_J15a	2.689 ± 2.2424 0.221564	1.773 ± 1.6 0.50023	0.595 ± 0.7367 0.63041	1.557 ± 1.4484 0.52868	AATATGAAACTATTAAAACGATAATAAAATATGATAACCAAAGC
plasmid_lp38	9895	BB_J15a	1.113 ± 0.6697 0.705755	1.512 ± 1.1407 0.29432	0.609 ± 0.36 0.29286	1.141 ± 0.757 0.73731	GTAATATATATGAAATATGAAACTATTATTTAAACTGATAATAAAAT
plasmid_lp38	10004	BB_J15a	1.408 ± 0.9474 0.576774	1.261 ± 0.993 0.74885	1.626 ± 0.9208 0.16247	1.299 ± 1.0111 0.48206	CTATTAAATAAAAGGTTGATAGTTACTAACCTTGAATCTATTTTTAA
plasmid_lp38	10040	BB_J15a	1.189 ± 1.4049 0.866528	1.84 ± 2.1631 0.60983	1.099 ± 0.5836 0.79316	1.311 ± 1.4375 0.78497	GTTGGTGTGAAAATGAGAACATGCTGAGACAGACAATGTTAGAAAAAGGT
plasmid_lp38	10045	BB_J15a	1.600 ± 0.8818 0.057185	1.762 ± 1.512 0.3087	0.393 ± 0.1807 0.124	1.165 ± 0.5732 0.16936	TGTTCAATTAAACAATTATAAGTGTCTACAAATACGCCTGTTTATTAA
plasmid_lp38	10113	BB_J15a	0.558 ± 0.5369 0.211274	1.082 ± 0.8407 0.881	0.707 ± 0.2684 0.00265	1.323 ± 0.5253 0.26753	ATGTACAAAAAATAAACATTAATAAAACAGCGTATTGAGCACTTAA
plasmid_lp38	10307	IG 1320	1.379 ± 0.5703 0.072701	1.968 ± 1.193 0.1844	0.961 ± 0.3377 0.33756	1.237 ± 0.4842 0.17924	ACTATTAACTTAACTATTAGTAGATTAGTTAGTTTCCCGACTTAATT
plasmid_lp38	10352	IG 1321	0.039 ± 0.04 0.097087	0.777 ± 0.1039 0.78078	0.018 ± 0.0329 0.09316	0.215 ± 0.3893 0.17123	ATAGTTAATAGTTAATAGTTACTTTGATTAAGATTATATAGCAAAAAA
plasmid_lp38	13526	IG 1322	1.560 ± 1.2547 0.155807	2.313 ± 2.1137 0.12649	1.055 ± 0.8503 0.73592	1.278 ± 1.2556 0.44257	ATAAAAAAATATTAAAAAAATAGAGGTTGAAATTTCATATTATACATA
plasmid_lp38	13731	BB_J0056	1.421 ± 1.0174 0.566421	1.702 ± 0.7624 0.04873	1.288 ± 1.0166 0.70823	1.992 ± 1.3724 0.20207	AATCTGATCTTTAAAGATAAAACTGTTGTTAATAACTAAATAAAACAA
plasmid_lp38	13765	IG 1323	0.460 ± 0.3317 0.024695	1.588 ± 2.3411 0.65295	0.469 ± 0.4114 0.24326	0.685 ± 0.2572 0.20585	TTTTAAGTTAAGGAAATTGAAACAAATCTATTAAATCTGATCTTAAAG
plasmid_lp38	13770	IG 1324	1.276 ± 1.2973 0.34012	2.869 ± 4.1709 0.393778	1.199 ± 1.4571 0.86668	1.377 ± 0.9812 0.4824	GCTCACTTACTTTATTGTTGGTTGATTAAGTGTCTCC
plasmid_lp38	13911	BB_J20	0.785 ± 0.5011 0.68765	1.755 ± 1.4006 0.27709	0.719 ± 0.5569 0.01638	1.586 ± 0.7923 0.17312	GAACCAATTAGGAAATTACTTAATAGCTTAAACAAATGAAATAAAAT
plasmid_lp38	14046	IG 1325	0.286 ± 0.264 0.021242	0.26 ± 0.3022 0.10488	0.187 ± 0.2048 0.06768	0.207 ± 0.1944 0.04528	TTTAAAGACATATGGTTTAAATAATTATATCTTACCTTTATAAA
plasmid_lp38	14113	IG 1326	1.331 ± 0.8976 0.181747	2.675 ± 2.8928 0.25935	1.073 ± 1.1579 0.76358	1.941 ± 1.5218 0.07306	GCTATTGCAATTATCAAGGTTTATAAGTTGTTAATAATTTCACCA
plasmid_lp38	14181	IG 1327	1.359 ± 0.6362 0.31039	1.494 ± 1.0769 0.44808	0.483 ± 0.1168 0.05361	0.826 ± 0.6051 0.5714	TATATGAAGTATTAAAACAATGTCACTTAACTTACTATCAGCTCGGG
plasmid_lp38	14291	IG 1328	0.848 ± 0.2879 0.315202	1.581 ± 0.7921 0.15912	0.534 ± 0.2075 0.09707	0.904 ± 0.2811 0.56607	AAAAGCCTTCAATAATATAATTTAGAAATGCCATTAGCCTC
plasmid_lp38	14650	IG 1329	1.026 ± 1.0418 0.954593	2.066 ± 2.7329 0.42729	0.494 ± 0.4388 0.26531	0.641 ± 0.5081 0.50107	AGGCTGTCACTGGTTATTGATTAAGAAAAGGCATAGAGCTTTTAAAT
plasmid_lp38	14675	IG 1330	0.539 ± 0.4397 0.161163	0.687 ± 0.6887 0.67799	0.872 ± 0.6938 0.47368	0.85 ± 0.6579 0.59136	AAAGGCATAGAGCTTTTAAATAGGCTTTAATTGAAATTGCTTTA
plasmid_lp38	14898	IG 1331	0.450 ± 0.4362 0.171464	1.354 ± 1.9824 0.72968	0.845 ± 0.7487 0.83089	0.346 ± 0.4131 0.22361	GCTATTATTTTTAACTAATTTAAAGGCTATTGCTCTTTTA
plasmid_lp38	15551	BB_J21a	1.424 ± 1.1715 0.204791	1.144 ± 1.2522 0.57529	0.671 ± 0.5172 0.34559	0.964 ± 0.784 0.9456	AAATAGTTTATTAAACCAATTAGTTGTTAATTTAAACCAAGAAAATT
plasmid_lp38	15854	BB_J21a	1.391 ± 1.1249 0.563784	2.112 ± 1.5712 0.20685	1.147 ± 1.4023 0.79268	1.078 ± 0.9094 0.82157	AAATAAAAAAATTACCGCATATTAAACAAATGGTATAAAATAGCTT
plasmid_lp38	16367	IG 1332	1.375 ± 1.3586 0.337188	0.944 ± 1.4003 0.71613	0.664 ± 0.7921 0.36175	0.832 ± 1.048 0.35931	GACCTTGTGTTTAAAGTATGGTTGTTATTGGTTAAGTCAA
plasmid_lp38	16676	BB_J23	3.843 ± 2.6492 0.071267	1.582 ± 1.6063 0.64827	1.739 ± 1.2219 0.38744	1.31 ± 1.4934 0.51525	TATAGACATCTTCATCATTTTTTGACAATTCTCAATTGCGGAAT
plasmid_lp38	17059	BB_J23	0.860 ± 1.133 0.64476	0.748 ± 0.9135 0.1914	1.223 ± 2.2257 0.83359	1.467 ± 2.1303 0.65232	CCAACTTGCAGAGAGTGTGGCAATGAGTTTACTATTAAATTAA
plasmid_lp38	17678	BB_J24	0.851 ± 0.3282 0.184434	1.244 ± 0.7175 0.32251	0.693 ± 0.2865 0.03875	0.953 ± 0.3691 0.79802	CAATGATTGATTCAAAACTAATCGCAATTATAATTGCTTGGTAA
plasmid_lp38	17713	BB_J24	0.243 ± 0.1057 0.096893	0.469 ± 0.5064 0.38644	0.485 ± 0.2022 0.17896	0.581 ± 0.2895 0.10483	ATTGTGCTTGGAAAATTCTTAGAAGATGATAATGTTAGCGGATTATT
plasmid_lp38	17850	BB_J24	0.335 ± 0.413 0.345348	1.14 ± 1.3232 0.64357	2.718 ± 3.0782 0.43615	0.269 ± 0.301 0.10948	AATGCCTCTGGCATTAACAAATAAGAATACATCCTTCTATTGCG
plasmid_lp38	17966	BB_J24	2.087 ± 2.2912 0.124063	0.724 ± 1.1872 0.19472	1.02 ± 1.3551 0.90416	1.436 ± 1.4617 0.54486	GCTTTTGCAATAGAATCTTAAACAAATTCTATTGACACTCTAAGT
plasmid_lp38	20841	BB_J27	2.442 ± 2.3049 0.171844	0.901 ± 1.0486 0.91759	0.564 ± 0.4039 0.35175	1.125 ± 0.7962 0.80248	AGACCAATATAACAAATTGTTCTAGTCATCCCTAAACAGATTAA
plasmid_lp38	21213	BB_J27	0.810 ± 0.2418 0.171488	1.282 ± 0.8288 0.57175	0.797 ± 0.1657 0.01846	0.883 ± 0.2419 0.39964	CCTCTACTACGGATTCTTACTTGCTTGGCTAAATGGCAAAAGAG
plasmid_lp38	21497	BB_J28	1.073 ± 0.6479 0.377247	2.169 ± 1.6461 0.20207	0.998 ± 0.6383 0.99158	1.185 ± 0.6233 0.43723	AAGGGATTTTATGCTAGGAAGACAAGCCAATTAGGTAAAGT
plasmid_lp38	22136	BB_J29	1.066 ± 1.2662 0.815598	1.552 ± 2.5129 0.59722	0.73 ± 0.7675 0.26998	1.008 ± 1.6333 0.98831	CAATTGACAATGAAGCTTATTAGGATTTTAAACTATAAGATTA
plasmid_lp38	22358	BB_J29	1.360 ± 0.7679 0.153331	1.684 ± 1.4282 0.3548	0.836 ± 0.4185 0.08467	1.202 ± 0.8248 0.47594	GAACCGAGAATGGTTTTGAGTTTATTATTTCTAATTCTGTC
plasmid_lp38	22462	BB_J29	0.301 ± 0.3513 0.2946	0.325 ± 0.3822 0.31842	0.559 ± 0.4951 0.49445	0.352 ± 0.1995 0.16822	TTTGGGAGATGAAAATTCTAAGCTTCTTGTCTAACATAGAACCAA
plasmid_lp38	22465	BB_J29	0.587 ± 0.5964 0.045045	0.857 ± 0.8667 0.36726	0.847 ± 0.6531 0.12343	0.97 ± 0.7303 0.75954	TTTATCCCTGGCTTATTCTAAGCATTTAATGAAATTGTTGACT
plasmid_lp38	22725	BB_J29	0.390 ± 0.3624 0.387283	0.782 ± 0.9786 0.80577	2.133 ± 1.8285 0.00515	1.269 ± 1.4876 0.54202	AAAACGTATTCTTCAAGCTAATATACTAAGACCAAGCAAATCTA
plasmid_lp38	22910	BB_J29	0.149 ± 0.1661 0.060683	1.22 ± 1.542 0.81533	0.68 ± 1.1599 0.63844	0.826 ± 0.7676 0.7674	AAGAACATCTTAAAGAATTAAAATTCTTAAAGAACATTAGGAA
plasmid_lp38	22923	BB_J29	0.497 ± 0.46 0.170192	0.504 ± 0.4677 0.25975	0.563 ± 0.3032 0.33602	0.756 ± 0.3962 0.50412	TTTGACACCTTAAAGAACATTCTTAAAGAATTAAAATTCTTCAAA
plasmid_lp38	23061	IG 1333	1.267 ± 0.3031 0.195262	1.644 ± 0.8713 0.31595	0.904 ± 0.2256 0.60551	1.173 ± 0.3096 0.36755	ATACACTCATCTGAAATATAACATGAAAAAATATAACCAACTAGAA

plasmid_lp38	23152	IG 1334	1.151 ± 0.6841 0.748826	1.863 ± 1.4857 0.24914	0.787 ± 0.4914 0.27396	0.967 ± 0.6739 0.95581	TAACAAATAATTGGCAGTTCACTTAACTTACATTGATAGATAAAAATAGA
plasmid_lp38	23300	IG 1335	0.918 ± 0.4366 0.703422	1.712 ± 1.3822 0.26581	1.041 ± 0.5402 0.79851	0.967 ± 0.4915 0.83908	AATATATTTCATCATATTAAACCTCTTACAAGAGTAATTACATCA
plasmid_lp38	23525	BB_J31	1.327 ± 0.7368 0.474187	2.367 ± 3.5463 0.50685	1.11 ± 0.6787 0.58251	0.801 ± 0.7676 0.50763	AGTAGAAAAAGGGGAATGCTAGTAGATAGCATGGGAGAGGTTCCCTACTT
plasmid_lp38	23547	BB_J31	0.572 ± 0.409 0.255135	0.483 ± 0.51 0.46158	1.018 ± 0.7956 0.86616	1.084 ± 0.9841 0.36822	CTAGCATTCCCTTTACTACTTAAACCTTATCTTAGATTCCTGGCA
plasmid_lp38	23644	BB_J31	0.259 ± 0.2768 0.036142	0.232 ± 0.1272 0.03206	0.178 ± 0.2309 0.02104	0.549 ± 0.4524 0.21792	TGATGCCTCATATCCTCTTCAGACAATATGAAGATCGGGATAGGTAGAAT
plasmid_lp38	23738	BB_J31	1.032 ± 0.4262 0.567293	1.142 ± 0.5316 0.24555	0.938 ± 0.3162 0.53425	0.964 ± 0.387 0.16388	AATGATAGCGATAATGATAATTGGATAGATAATAGCTCGAGAAAATAAG
plasmid_lp38	23757	BB_J31	1.622 ± 0.6652 0.225013	2.281 ± 0.1024 0.14878	1.155 ± 0.2037 0.24515	1.328 ± 0.1081 0.00064	ATTTGATGATAATAGCTCGAGAAAATAAGAAAGTGGTAGATGAATTAA
plasmid_lp38	23832	BB_J31	0.719 ± 1.0742 0.711522	1.227 ± 1.4187 0.81919	1.158 ± 1.3295 0.86388	1.032 ± 1.0528 0.73326	GTTGTTCTATAATGAGCTGTAATTCTTACCTAACAGAAAAGGAAAAGATT
plasmid_lp38	24080	BB_J31	1.145 ± 0.1791 0.006239	1.362 ± 0.6787 0.50303	0.728 ± 0.4278 0.41602	0.963 ± 0.1181 0.67299	TATCATAAGCAAGCCGTTACAAGCTCGCTATAGAACCTGGCAGCTTCGC
plasmid_lp38	24115	IG 1336	1.143 ± 0.8534 0.048958	1.99 ± 2.0516 0.28913	0.903 ± 0.5076 0.73261	1.148 ± 0.8298 0.36173	TTAGTGTGTTATTATAGGTGATAAGTTAAAGTACATCTACTGTACTT
plasmid_lp38	24128	IG 1337	0.667 ± 0.5991 0.193359	0.746 ± 0.6552 0.34216	0.794 ± 0.2764 0.16463	1.141 ± 0.3266 0.4166	AATACAACTAACTAATATAATAGATAATTCTATAATATAT
plasmid_lp38	24315	IG 1338	1.340 ± 0.6073 0.150043	1.996 ± 1.297 0.10649	0.765 ± 0.4069 0.29455	1.102 ± 0.6092 0.63316	ATTCTTATAGTAGTAAAGCTTATTGTAAATAAATTAAATAAAAAAGGT
plasmid_lp38	24668	IG 1339	1.043 ± 0.5343 0.392155	2.072 ± 1.8359 0.33882	0.905 ± 0.1066 0.86863	1.307 ± 1.5649 0.71287	AGTCAATAGATAGTGTATTATGTGTAATGTTATTAAATAATTAG
plasmid_lp38	24729	IG 1340	1.980 ± 2.3535 0.403652	1.096 ± 1.3393 0.93408	0.332 ± 0.5536 0.12733	1.098 ± 1.467 0.7376	TTAAAGAGCAGCTTTAATAAAAATCAAATGAAATGTTACTCTGAA
plasmid_lp38	24992	IG 1341	1.398 ± 0.7808 0.221231	2.124 ± 1.757 0.3319	0.985 ± 0.3513 0.93977	1.077 ± 0.3617 0.74424	TATATTTAAAATAAGCCACGATTAAGGATCCAATCCTCTGGGACAACA
plasmid_lp38	25037	IG 1342	1.077 ± 0.3171 0.716231	1.563 ± 0.8196 0.40026	0.765 ± 0.187 0.05906	0.808 ± 0.2111 0.18599	CAAGATATTAAACCATTCTTAGCATTAATATCATTATTATATATT
plasmid_lp38	25204	IG 1343	0.974 ± 0.4668 0.931542	1.238 ± 0.1095 0.74909	0.688 ± 0.4203 0.34161	0.786 ± 0.4048 0.4704	AGTCTATAAAAATATTGTACACAAGACATTCTGTAATCATTATTCT
plasmid_lp38	25209	IG 1344	0.965 ± 0.6597 0.915797	0.807 ± 0.5172 0.45327	1.029 ± 0.4664 0.88454	0.864 ± 0.4618 0.66042	TGTCTATTATATCTATAAAAATAAAACATAATAAAACATAACCAAAT
plasmid_lp38	25215	IG 1345	1.610 ± 0.9677 0.37072	1.789 ± 1.5202 0.50313	0.799 ± 0.453 0.63998	0.629 ± 0.4418 0.43478	TTTATATCTATAAAAATAAAACATAATAAAACATAACCAAATAAAATTAA
plasmid_lp38	25269	IG 1346	0.431 ± 0.7845 0.331577	0.307 ± 0.5597 0.11648	0.818 ± 0.8455 0.78778	0.274 ± 0.4991 0.10099	TACATAATTATTTGGTTATGTTTATTATGTTTATTAGGATA
plasmid_lp38	25377	BB_J34	1.056 ± 0.2397 0.736273	1.438 ± 0.4229 0.19133	1.148 ± 0.3724 0.62999	1.088 ± 0.2289 0.60868	GCTCTTAGCTCTCAATGGCAGACATCATTGCTACCTCCGCACCTTT
plasmid_lp38	25494	BB_J34	0.864 ± 0.5949 0.727544	0.827 ± 0.8946 0.78831	0.645 ± 0.7561 0.62588	0.986 ± 0.5458 0.96512	GCACCCACAAACACATCACACGATGGCTCTTATTGCCATTAGCATAC
plasmid_lp38	25612	BB_J34	1.176 ± 0.7156 0.571434	0.734 ± 0.5371 0.60204	1.016 ± 0.4116 0.94023	1.422 ± 0.8119 0.53893	TAACAGCAAAAGCATTGCCATAAGGCCACACTAGCTTTCTATGGCTTT
plasmid_lp38	25900	BB_J34	1.071 ± 0.9168 0.880078	0.95 ± 0.8837 0.7826	0.798 ± 0.6519 0.74746	1.154 ± 1.0041 0.53417	GTTTATTTCTAGGTGTTAAGGGCTTGACTACGCCCTGAGAAGGGC
plasmid_lp38	26033	BB_J34	1.134 ± 0.3937 0.068485	1.545 ± 1.2034 0.41743	0.776 ± 0.2044 0.10187	0.964 ± 0.3547 0.66566	TAACAAATACAGCCTTATAATACCATTGCAACTTATTGGTTGTGC
plasmid_lp38	26057	BB_J34	1.944 ± 1.7327 0.419315	1.705 ± 1.8348 0.48002	0.717 ± 0.6686 0.50818	2.303 ± 2.1641 0.13826	TCAAGGAGTACTCAATTCTATTATAACAAATACAGCCTTATAATAC
plasmid_lp38	26097	BB_J34	1.047 ± 0.8601 0.932688	1.827 ± 0.9278 0.25967	0.615 ± 0.4976 0.38134	0.897 ± 0.3038 0.6025	TGGATAAGCTTAAAGGCTTTTGTAAAAACATAACATATCAAGGGATAC
plasmid_lp38	26190	BB_J34	1.081 ± 0.5692 0.818456	2.008 ± 1.4651 0.26467	0.852 ± 0.4606 0.59138	1.078 ± 0.5727 0.83943	GCATTTCTGAACTGATCCAAGCACTTACTAGCAGTAGTACACCT
plasmid_lp38	26770	IG 1347	1.367 ± 0.7056 0.363619	1.32 ± 0.8743 0.66123	0.859 ± 0.4236 0.72173	0.685 ± 0.3215 0.32005	TGAGCTACAAAATCTTTAAAAGGCCATATCCAAACTAACTAATTAA
plasmid_lp38	27314	BB_J36	1.621 ± 1.0757 0.246571	1.66 ± 2.1593 0.59667	1.001 ± 0.565 0.99586	1.07 ± 0.7804 0.80281	TTATTAACAAACATCTTGTGAAAGAGCAGCCGATTTGCTATGCTTTG
plasmid_lp38	27490	BB_J36	0.576 ± 0.4029 0.305618	1.233 ± 1.2161 0.81909	0.529 ± 0.3293 0.16524	0.482 ± 0.2636 0.25918	ATACTAGGCACAGCACTCTTAACTTGTGTAAGCTGAGTGTACTTT
plasmid_lp38	27794	BB_J36	0.922 ± 0.3179 0.677789	1.788 ± 1.4908 0.47669	0.975 ± 0.6409 0.96132	1.312 ± 0.4261 0.28813	GTAGTATCATAACAAATAAGGGCATCAGCAAGCATGTAAGGGTACTAGTA
plasmid_lp38	28245	IG 1348	1.409 ± 0.4894 0.093619	1.912 ± 1.2169 0.25721	1.21 ± 0.3305 0.10605	1.339 ± 0.281 0.0632	ATGAAGGGGCAAATTAACAAAGATGACTGTAATTGATAAGTTATGTG
plasmid_lp38	28316	BB_J37	2.802 ± 0.8741 0.046406	2.335 ± 1.6908 0.27605	2.531 ± 1.8072 0.20159	1.75 ± 0.6523 0.21296	GGTGCTATTCTAGTATGGCCTATAATGAATTGTAAGGGGTTCAAAG
plasmid_lp38	28359	BB_J37	0.958 ± 0.1662 0.604649	1.389 ± 0.5474 0.40177	0.819 ± 0.1259 0.01601	1.051 ± 0.2033 0.66657	CTCTCTAGCAGAAACACTAAATCTCAGCAGTTGCCTAAATTCACTAC
plasmid_lp38	28742	IG 1349	0.423 ± 0.5003 0.199674	0.894 ± 0.7856 0.84947	1.045 ± 0.7792 0.94613	1.459 ± 1.3193 0.64904	TTTATTTCTAGATACCCTTATTGTTGTTGCTAAATTACGGATCAAGTT
plasmid_lp38	28966	IG 1350	1.184 ± 0.1794 0.291867	1.664 ± 0.5744 0.20755	0.888 ± 0.0961 0.17894	1.231 ± 0.3339 0.37611	ACTATAGTAAGTTTCTCTAAATAAGATTATCCAAGCTTATTAAAGCT
plasmid_lp38	29134	IG 1351	2.131 ± 2.2334 0.253924	2.344 ± 3.0724 0.37259	1.506 ± 1.3517 0.22966	1.311 ± 1.3574 0.1659	TTACATAACCTAACCAAGAAATTATACGGTTTCTTCTAACAAACTCTT
plasmid_lp38	29137	IG 1352	1.878 ± 2.1555 0.24417	0.533 ± 0.5952 0.40443	0.874 ± 0.821 0.81521	0.752 ± 0.7937 0.30013	CATAACTAACCAAGAAATTATACGGTTTCTTCTAACAAACTCTTCC
plasmid_lp38	29536	IG 1353	1.033 ± 0.5452 0.94048	1.661 ± 1.4865 0.5479	0.819 ± 0.8313 0.7731	1.002 ± 0.9157 0.99758	TTATGCGAAAGCTCTCTAACTTAAATTGGATATTCTGGATT
plasmid_lp38	29537	IG 1354	0.866 ± 0.6237 0.576828	1.011 ± 0.4883 0.93265	0.377 ± 0.3029 0.17396	0.791 ± 0.3143 0.33965	AATATTTATAATTGGATTATACGGCAACTATGTTAAATTACTC
plasmid_lp38	29891	IG 1355	0.924 ± 0.5098 0.48917	0.643 ± 0.3601 0.40935	0.938 ± 0.5099 0.59698	1.182 ± 0.7024 0.505	TTTTTTATTAGATTATACGGTTGTTAGTAGATAAAAGGGATGGGAA
plasmid_lp38	30007	BB_J41	0.667 ± 0.2133 0.100011	0.68 ± 0.436 0.48077	1.018 ± 0.3311 0.74764	1.194 ± 0.5424 0.26925	CAATAAAAATGTTGATAACATTAAAATAGATAATAAGCGCTAGCAAAC
plasmid_lp38	30142	BB_J41	1.468 ± 1.3869 0.556071	1.449 ± 1.4162 0.59818	1.377 ± 0.5947 0.27588	1.617 ± 0.6391 0.09262	CGTGTCTCTAGATGAGTTGAATACCGCTTGTCTAAATTGACC
plasmid_lp38	30323	BB_J41	1.328 ± 0.6093 0.305327	1.183 ± 0.4914 0.45854	0.731 ± 0.3597 0.33323	1.263 ± 0.2595 0.22836	AAAACATCATCTGTTAAAGTTAACTCATTTAGCA
plasmid_lp38	30872	IG 1356	2.852 ± 2.8414 0.28299	3.205 ± 2.4135 0.02968	1.306 ± 1.4781 0.78019	1.451 ± 1.4291 0.53865	ATTTAAGAATTAACTTCATTGATGTTTACGGTAAATTAGATTG
plasmid_lp38	31385	BB_J43	4.508 ± 2.7041 0.083623	2.327 ± 1.3476 0.22302	2.104 ± 1.0185 0.05229	2.104 ± 1.2331 0.25569	TTCTTCAATTAAAGCTTAAATGATTTTATTAAATTAGTAGGCAAAT
plasmid_lp38	31490	BB_J43	1.378 ± 0.795 0.109508	1.731 ± 1.4521 0.30832	0.845 ± 0.4385 0.18788	1.18 ± 0.891 0.52197	GAACCGAGAATGGTTTTGAGTTTATTATTCATAATTCTGTC
plasmid_lp38	31597	BB_J43	0.581 ± 0.5893 0.039578	0.846 ± 0.8536 0.32373	0.851 ± 0.6574 0.10571	0.977 ± 0.7337 0.79145	TTTATCCCCTGGCTTATTTCAGCATTTAATGAGTTACTTACT

plasmid_lp38	31857	BB_J43	0.376 ± 0.3707 0.351477	0.742 ± 0.8863 0.74704	2.118 ± 1.5381 0.01533	1.297 ± 1.3059 0.4944	AAAACGTCACTTCAAAGCTAATATAATCTAAGACCAAGCAAAATCTA
plasmid_lp38	32042	BB_J43	0.150 ± 0.1568 0.117836	1.232 ± 1.5571 0.80413	0.598 ± 0.9896 0.50092	0.79 ± 0.7624 0.74572	AAGAACATTCTTTAAGAATTAAAAATTATTCTAAAGAATTAAAAATTATTTCAGG
plasmid_lp38	32055	BB_J43	0.536 ± 0.5165 0.245917	0.505 ± 0.4871 0.30469	0.583 ± 0.3263 0.37449	0.772 ± 0.4357 0.53734	TTTGACACCTTAAAGAACATTCTTTAAGAATTAAAAATTATTTCAGG
plasmid_lp38	32193	IG 1357	1.705 ± 1.3236 0.315962	1.941 ± 1.5948 0.29915	1.078 ± 0.8778 0.9147	2.268 ± 1.9914 0.40164	ATACACTCATCTGAATATAACATGAAAAAAATAATAATATGCCAAGTAGAAA
plasmid_lp38	32284	IG 1358	1.227 ± 0.6896 0.649941	1.917 ± 1.5359 0.26152	0.789 ± 0.4392 0.22396	0.996 ± 0.6613 0.99417	TAACAAATAATTGGCAGTTCTTTAACCTCTTACAAGAGTAATTACATCA
plasmid_lp38	32432	IG 1359	0.921 ± 0.4675 0.714027	1.69 ± 1.3888 0.26955	1.055 ± 0.5482 0.76435	0.969 ± 0.4978 0.85291	AATATTTTCATCATATTAAACCTCTTACAAGAGTAATTACATCA
plasmid_lp38	32657	BB_J45	1.648 ± 0.9663 0.335421	2.496 ± 3.749 0.49955	1.23 ± 0.7686 0.49585	0.948 ± 0.8947 0.8953	AGTAGAAAAAGGGGAATGCTAGTATAGCATTGGGAGAGGTTCCCTCACTT
plasmid_lp38	32679	BB_J45	0.559 ± 0.3973 0.250303	0.489 ± 0.5178 0.4673	1.039 ± 0.832 0.64369	1.086 ± 0.9774 0.37838	CTAGCATTCCCTTTACTACTAAACCTTATCTTAGATTCCTGGCA
plasmid_lp38	32776	BB_J45	0.286 ± 0.3672 0.046703	0.18 ± 0.08 0.01893	0.194 ± 0.2476 0.01571	0.5 ± 0.4351 0.15339	TGATGCCTCATCTCTTACAGACAATATGAGATCGGGATAGGTAGAAT
plasmid_lp38	32870	BB_J45	1.130 ± 0.4035 0.546915	1.383 ± 0.5902 0.29312	0.962 ± 0.1972 0.47209	1.068 ± 0.2973 0.66467	AATGATGGATAATGATAATTGATGATAATATCGCGAGAAAATAAG
plasmid_lp38	32889	BB_J45	1.159 ± 0.3038 0.121718	1.637 ± 0.9595 0.29339	0.895 ± 0.146 0.29569	1.134 ± 0.2703 0.10962	ATTTGATGATAATCTGGAGAAAATAAGAAGGTGAGATGAATTAA
plasmid_lp38	32964	BB_J45	0.620 ± 0.8925 0.59221	1.078 ± 1.2006 0.93074	0.957 ± 1.0253 0.9316	0.723 ± 0.5733 0.16232	GTTGTTCTATAATGAGCTTGAATTCTTACAGACAAAAGGAAAAGGATT
plasmid_lp38	33247	IG 1360	1.284 ± 1.7484 0.459497	3.492 ± 3.9777 0.14585	1.088 ± 0.941 0.86937	1.824 ± 1.6328 0.03815	ATTAGTGTGTTATTATAGGTGATAAGTTAAAGCACATCTACTGACTT
plasmid_lp38	33260	IG 1361	0.624 ± 0.527 0.162207	0.773 ± 0.6439 0.44008	0.803 ± 0.2673 0.00286	1.073 ± 0.2753 0.3809	AATAACACATAATTAACTACATAAACTAGAAATGATTATTTCATAATAC
plasmid_lp38	33263	IG 1362	0.851 ± 0.8129 0.717336	0.54 ± 0.5143 0.06164	0.764 ± 0.3259 0.49853	0.98 ± 0.4629 0.84879	TATAGGTGATAAGTTAAAGCACATCTACTGACTTTAACATTAGTC
plasmid_lp38	33448	IG 1363	1.378 ± 0.6941 0.183806	1.957 ± 1.4562 0.14108	0.749 ± 0.4582 0.23524	1.072 ± 0.6168 0.77304	ATTCACTTATAGTAAAGCTTTATTGTAATAAATTAAATAAAAAAAAGGT
plasmid_lp38	33610	IG 1364	0.734 ± 0.2984 0.119543	0.926 ± 0.3414 0.48514	0.761 ± 0.2533 0.08219	0.834 ± 0.2726 0.38401	TTGTAAGAAGAAAAGTCGACAATTGATAACTACTAAAGGTTGGATTATT
plasmid_lp38	33827	IG 1365	1.775 ± 1.9325 0.590974	2.089 ± 3.8329 0.66085	2.811 ± 3.4251 0.42493	1.362 ± 1.2758 0.57814	TAATATGCTTTTCTATAAAATTCTCTTGGTAATTTTATATCGCAA
plasmid_lp38	33829	IG 1366	1.356 ± 0.9841 0.106812	1.657 ± 1.4886 0.26538	0.87 ± 0.5976 0.35148	1.064 ± 0.7963 0.5397	TTATATACTTGAACTTATATCATTACTTATTTCGTGTTCT
plasmid_lp38	34175	IG 1367	2.045 ± 1.3316 0.117182	1.873 ± 1.9752 0.42164	0.838 ± 0.4753 0.43146	0.661 ± 0.4737 0.36849	TACTTATAACCTTTAATAAAAACAAAATTATAACCTCAATAA
plasmid_lp38	34398	BB_J46	1.379 ± 1.9694 0.809137	0.236 ± 0.3878 0.16726	0.883 ± 1.0242 0.8985	0.211 ± 0.2374 0.23787	TATGGACTAAAAAAATCCCAAATCTAATGAGTTACACCATTATT
plasmid_lp38	34566	BB_J46	1.054 ± 1.2375 0.922184	1.241 ± 1.8724 0.54149	0.408 ± 0.5024 0.38093	1.025 ± 1.343 0.96562	CATGGCATAATAATCCCATCTTATAAAGAAATTCAAATCACAAC
plasmid_lp38	34632	BB_J46	1.553 ± 0.543 0.25735	1.432 ± 0.4238 0.23287	1.097 ± 0.3958 0.69606	1.31 ± 0.2713 0.18256	TTATGGAGGATGATTAGATGTTAAAATTATCCATATTGTCAGACCT
plasmid_lp38	34709	IG 1368	1.265 ± 0.3147 0.25003	1.237 ± 0.3923 0.19707	0.861 ± 0.4243 0.46883	0.884 ± 0.2796 0.53139	AATATATAGCAATAAAGGCAGTTAGTTTTACATAAAAATTGTTT
plasmid_lp38	34942	BB_J47	2.771 ± 1.6502 0.131928	0.901 ± 0.4801 0.57191	0.977 ± 0.6859 0.96085	1.092 ± 1.1097 0.8647	ATTTCAAACACCAAGAAAAGGAGAATAGTCTACTAAGAAATTAAAGAAT
plasmid_lp38	35218	BB_J47	0.812 ± 1.1213 0.869472	0.369 ± 0.5396 0.54324	0.611 ± 0.9131 0.73604	0.572 ± 0.8608 0.70703	CCATAAAAAAATAACATTAAATTCTTAAATCATTCAACTACG
plasmid_lp38	35318	BB_J47	2.310 ± 2.6563 0.348729	1.278 ± 1.4796 0.76187	1.558 ± 1.7922 0.46684	2.941 ± 2.6286 0.26565	GATAACAAACATCTGCTAACTTCTTACATATGGAGTTGTC
plasmid_lp38	36100	BB_J48	1.407 ± 1.3703 0.436056	2.31 ± 2.7032 0.36793	1.185 ± 0.9824 0.62572	1.311 ± 1.051 0.63196	CTTGTGATGTTAAATCACTCTTGAGGGAAACATAAGGGCTACTA
plasmid_lp38	36259	IG 1369	1.344 ± 1.159 0.232108	1.901 ± 2.0632 0.33473	0.791 ± 0.5913 0.19533	1.091 ± 0.9026 0.38169	AATAAATATGACAAAAAAATTCTTATATATATATTCTTATTAAAAA
plasmid_lp38	36553	BB_J50	1.531 ± 1.0297 0.346394	1.948 ± 1.9187 0.43749	1.287 ± 0.7027 0.36877	1.238 ± 0.6687 0.41147	AATAAGTGTATGTTCCACCATATTTCTATAAAGAAACATTCCA
plasmid_lp38	37386	IG 1370	0.715 ± 0.7129 0.641764	1.631 ± 0.384 0.00626	0.703 ± 0.404 0.19222	0.838 ± 0.4557 0.68838	TTAAAATGCTGTTCTTACATTCTTATTTCAATGTTAGTCTGGCTATT
plasmid_lp38	37527	BB_J51	0.677 ± 0.1137 0.989602	0.792 ± 0.1396 0.06582	0.894 ± 0.2649 0.42096	0.963 ± 0.2682 0.64803	TTATCACCACCACTGGTTTCGACCCATTTCACAGCAAATCCCCG
plasmid_lp38	38593	IG 1371	2.452 ± 1.1498 0.048544	2.806 ± 2.8429 0.31608	1.154 ± 0.5896 0.09648	1.936 ± 1.1654 0.13791	TATACTGAAACTAAAGGGGGGCATATTAGTTAGATAATATTCTTAT
plasmid_lp38	38613	IG 1372	1.929 ± 1.5133 0.302002	4.025 ± 4.044 0.29125	1.041 ± 0.789 0.91252	1.19 ± 0.8198 0.70532	TAGCACTATTATATGATGTTAAAATTATTGATTTGTTAATA
plasmid_lp38	38623	IG 1373	1.612 ± 0.9968 0.130842	2.168 ± 2.3699 0.39343	0.974 ± 0.5641 0.61792	1.228 ± 0.656 0.23907	TAATAGTGTATATGTTGATAATATGCTATATCTGAAACTAAAGGGGG
plasmid_lp5	436	BB_T01	1.793 ± 1.993 0.316885	1.691 ± 2.5346 0.46975	0.926 ± 0.8647 0.84202	1.203 ± 1.2146 0.1239	ATATATCAACATGAAAAAAACTTAAATCAATTAGAAAAGAAATAAAA
plasmid_lp5	480	BB_T01	1.512 ± 1.3425 0.273634	2.146 ± 3.0352 0.43673	0.356 ± 0.3034 0.1509	0.544 ± 0.4348 0.24693	TTTCTTTCTAATTGTTAGTATTCTTCTGATATTACTAG
plasmid_lp5	628	BB_T01	2.336 ± 2.3118 0.416273	1.679 ± 0.7479 0.09317	1.092 ± 0.3513 0.60496	1.047 ± 0.4261 0.89156	ATGTTCTTGTGTTAAATTGTTAAATTCTTGTGAGATTGTTGAGAAT
plasmid_lp5	634	BB_T01	4.454 ± 2.131 0.022631	1.244 ± 1.5402 0.80179	1.59 ± 2.8211 0.71038	0.288 ± 0.5108 0.01963	CTTAAATTGTAATACTTAAATTTAAATCTGCAAATATTGAGAAATAC
plasmid_lp5	693	IG 1374	3.914 ± 0.717 0.01429	2.44 ± 0.1065 0.1255	1.263 ± 0.6481 0.58047	1.252 ± 0.3196 0.23159	AAGATATATATTCTTAAATTTAAATTTAAATTTGCTGGCACATAAT
plasmid_lp5	721	IG 1375	2.614 ± 1.7563 0.227174	2.153 ± 1.6889 0.22865	0.983 ± 1.1142 0.98475	1.358 ± 0.7767 0.51475	TTATTTTTAAATTTAAATTTAAATTTGTTAAATTCTTAAATTTCTAAT
plasmid_lp5	907	BB_T02	1.610 ± 1.4369 0.58142	0.591 ± 0.5097 0.40216	0.262 ± 0.1947 0.12446	0.636 ± 0.3242 0.39467	GATATTGCAATACTGAAAGATATTGAAATAGACATGACTTAATAA
plasmid_lp5	1190	IG 1376	1.306 ± 0.4706 0.401358	1.406 ± 0.7288 0.47901	0.572 ± 0.1213 0.08681	0.767 ± 0.2912 0.06958	ATAGGGGGCTAATTCTTGAATGGAATAATTACGATACACTGGTCGA
plasmid_lp5	1344	BB_T03	2.898 ± 1.6949 0.028507	1.728 ± 1.3691 0.1751	1.086 ± 0.5552 0.75757	1.043 ± 0.96 0.88678	TAATCTTGTGTTCACTATAGAACATTCTGATTGATGTAGTGT
plasmid_lp5	1410	BB_T03	5.695 ± 3.2071 0.068999	2.451 ± 2.5898 0.35956	3.449 ± 2.3467 0.14772	2.057 ± 0.8934 0.10837	ATTATAACACCTTATTAGAATATCTGAAATATTGAAAAAAATCCAAAAG
plasmid_lp5	1416	BB_T03	2.729 ± 0.6105 0.019825	1.171 ± 0.483 0.58267	0.996 ± 0.3458 0.98548	1.058 ± 0.57 0.89306	AAACCTTATTAGAATATCTGAAATATTGAAAAAAATCCAAAAGTAATCG
plasmid_lp5	1658	IG 1377	1.547 ± 1.6854 0.679598	0.313 ± 0.5717 0.38543	2.616 ± 3.5004 0.37814	1.557 ± 1.6366 0.63258	TTATAGGCCATAATTACTAGGATAGATTTGTTACTATTATATAATC
plasmid_lp5	1709	IG 1378	3.276 ± 3.0681 0.323538	1.366 ± 1.0395 0.61829	0.588 ± 0.7673 0.59125	0.576 ± 0.33 0.20094	GTCCTTTATGGATTGATCTTATAGTCATAAATTTCTTATTGGGCTA
plasmid_lp5	1754	IG 1379	2.573 ± 1.297 0.081918	1.571 ± 0.6911 0.11629	0.994 ± 0.3009 0.97715	1.123 ± 0.507 0.26002	CCAATATAAAGCTAAATACAAATAATCTTAAATTCTAGA

plasmid_lp5	1765	IG 1380	1.579 ± 0.7468 0.357344	1.144 ± 1.0372 0.78903	0.559 ± 0.3295 0.06169	0.681 ± 0.2776 0.14618	GCTTTATTTGGTAATTAGTAATTATTTATGTCAAAATCCATAAAAGAC
plasmid_lp5	1877	IG 1381	3.377 ± 4.1599 0.021055	1.088 ± 2.0584 0.77128	1.224 ± 2.091 0.87607	0.822 ± 1.2213 0.78329	ACACTAATTTCCCAGTTAAGTTTATTTGTTGGGCACTATAATAAT
plasmid_lp5	3173	BB_T04	4.789 ± 6.1545 0.202183	1.612 ± 1.6304 0.47033	1.261 ± 1.4489 0.1306	1.628 ± 1.6295 0.10288	TATGCCAAATATTGTTATTTTATTGTTATTCAAATATTTC
plasmid_lp5	3174	BB_T04	3.016 ± 2.2858 0.146225	1.757 ± 0.9587 0.07538	1.168 ± 0.6551 0.45523	1.392 ± 0.6591 0.04085	TATTATCTGAATTACTAGAAATAAAAAAATAGAAAACATGATCTAAAT
plasmid_lp5	3322	IG 1382	0.713 ± 0.75 0.434408	0.338 ± 0.4917 0.03061	1.231 ± 1.0594 0.6796	0.665 ± 0.5559 0.15642	TGGAATAATTCTGATTGGAACTCAATTCTGCACTAATCTAAATAAAC
plasmid_lp5	3673	BB_T06	3.179 ± 1.673 0.070021	1.604 ± 0.7517 0.23976	1.195 ± 0.5948 0.43109	1.002 ± 0.4819 0.9944	GATACAGTGGCAATAAGAATACCCAAAATAAAACCGCATTAATTAATT
plasmid_lp5	4028	BB_T06	5.780 ± 5.0644 0.133248	2.192 ± 2.3241 0.3854	1.84 ± 1.2842 0.20483	1.686 ± 1.6926 0.44753	TAAGAAAACATTTTTTAAAGCTATTGTTCTTGCTATAATTACT
plasmid_lp5	4094	BB_T06	2.420 ± 2.8602 0.439011	0.419 ± 0.7663 0.00914	0.631 ± 0.6851 0.4555	0.048 ± 0.0894 0.10181	TCGTTTTAAATATTCTTATGTTATCCCCGCTTAAATGTATGGACA
plasmid_lp5	4168	BB_T06	3.551 ± 2.8229 0.190719	1.774 ± 1.4483 0.31849	1.239 ± 0.7464 0.33785	1.243 ± 0.862 0.44574	TAATATTTTTATCCATAAAAACAAAAATAAAATTAAAAGGTGT
plasmid_lp5	4171	BB_T06	0.806 ± 0.3975 0.253202	0.469 ± 0.1961 0.1657	0.322 ± 0.1868 0.15859	0.549 ± 0.4617 0.37203	TTATTCGATTCTTAATAGAATATGCAGAAAATCTTATAAAGAGCTAGTA
plasmid_lp5	4666	BB_T07	1.484 ± 0.2615 0.104209	1.239 ± 0.3016 0.36384	1.066 ± 0.3072 0.7164	0.942 ± 0.171 0.67942	TTTATGTCTTGTATGATGATGATTAAACTTTGATGTTGCTTGATAA
plasmid_lp5	4898	IG 1383	2.580 ± 2.496 0.308952	2.363 ± 2.6285 0.41516	0.924 ± 0.4728 0.74059	1.18 ± 0.8992 0.71	TTATCTATTGTAATACAGGTCAGCTTGTATGTTGAGTAAAG
plasmid_lp5	5011	IG 1384	2.478 ± 1.9244 0.294741	2.258 ± 1.4352 0.27195	0.95 ± 0.3415 0.27127	1.073 ± 0.5771 0.88033	CTACTCTAGAAGAGTTCTCCTTATTGAAATTATGACTTTATTATT
plasmid_lp54	325	IG 1385	1.154 ± 0.6865 0.610907	1.973 ± 1.8711 0.41311	0.831 ± 0.2805 0.48082	0.989 ± 0.2454 0.79532	TTTATTATTCTTATTGAGCTTGGATTAACTTTAATTATCTCTT
plasmid_lp54	407	IG 1386	0.765 ± 0.28 0.27991	1.69 ± 1.1357 0.46003	0.934 ± 0.4843 0.88321	1.309 ± 0.8102 0.54946	AATTTCGAAATTAAATTATGGCTCACTTGAACAACTGCTTCAAGCTA
plasmid_lp54	567	IG 1387	0.523 ± 0.1744 0.149728	0.44 ± 0.4003 0.26111	0.933 ± 0.3349 0.40379	0.745 ± 0.2649 0.17775	TGCTTGCAAAATTAATTAAATTATAATTGCGCTAATATTTC
plasmid_lp54	1105	BB_A01	1.153 ± 0.4109 0.523019	1.713 ± 0.6713 0.06053	1.603 ± 0.6175 0.22032	1.623 ± 0.7641 0.08686	GGATTCCAATTATCGTTAAAAAAAGTTAAATTAATAGATAATAA
plasmid_lp54	1458	IG 1388	1.986 ± 0.9238 0.017089	1.149 ± 0.9299 0.70753	0.792 ± 0.6061 0.53232	1.504 ± 0.7751 0.38204	TAGTCTCCTAAAAAGTATTAAATTATTAATTAGTAATTAGCATT
plasmid_lp54	1808	BB_A03	0.687 ± 1.0307 0.680704	1.025 ± 1.7574 0.98214	0.195 ± 0.2881 0.0129	0.261 ± 0.1676 0.04027	TTCATCTCTTCTAGCTCTGATAGAAATTGTACAGATTCTCTATT
plasmid_lp54	2129	BB_A04	0.947 ± 0.9365 0.948923	2.296 ± 3.6814 0.44264	1.079 ± 1.0108 0.86532	1.103 ± 1.2382 0.87541	AAGCTGAGAACTAACGCTAATTCTGAACTTTTATTGATATTG
plasmid_lp54	2796	BB_A04	1.256 ± 0.8589 0.683943	3.859 ± 4.8261 0.41849	0.883 ± 0.5431 0.82739	2.147 ± 1.8919 0.43121	GAGAAAGTGGATCAGATAGGCGGGTCAAGAAAATAGAGCCTTGGGGCGA
plasmid_lp54	2986	IG 1389	1.017 ± 1.0587 0.97298	2.254 ± 3.8108 0.4297	1.412 ± 1.5567 0.06962	0.976 ± 1.0326 0.59003	AAATCAAAATAAAAAACTTAAACGCCCTGCTAATCTTTATCAAGCTT
plasmid_lp54	4436	IG 1390	0.966 ± 0.6157 0.931025	1.438 ± 1.0199 0.25439	0.758 ± 0.5978 0.60228	1.55 ± 1.1515 0.53424	GGCTTAAAATTTTAAAGCTTATTAAATTGTTTATTAAAAAA
plasmid_lp54	4565	IG 1391	0.643 ± 0.9948 0.688675	0.773 ± 1.6268 0.17645	1.021 ± 1.768 0.93799	0.923 ± 1.7036 0.38115	TTGAAAATTAAATTGTAATTAGATTGATGTTAATGTTTAAATT
plasmid_lp54	5150	IG 1392	0.964 ± 1.49 0.409635	1.491 ± 2.3376 0.30263	0.911 ± 1.3586 0.50479	0.89 ± 1.181 0.68049	TGGGAGACGTATGAAAAATATTATTATTGTTATTATTCTTTC
plasmid_lp54	6127	BB_A09	0.915 ± 0.4741 0.660661	1.53 ± 1.1906 0.21429	0.771 ± 0.3968 0.3489	1.13 ± 0.6567 0.17468	TCAATCTCAATGTCGCCCTAAACACTGTTCCGCTTGGCGCTGTAGTAG
plasmid_lp54	6541	BB_A10	0.765 ± 0.5314 0.560399	0.849 ± 0.4569 0.43811	0.53 ± 0.304 0.18776	0.581 ± 0.3702 0.156	TTTGGTATCTTTATTCTATTCTGTTAATAAGAACCTTTG
plasmid_lp54	6963	BB_A10	1.050 ± 0.4254 0.872272	1.386 ± 0.7795 0.44153	0.851 ± 0.2686 0.54002	1.069 ± 0.5666 0.85669	TTAGCAGTTATTGTTAGCTTGTGTTGATTTTGCTGCAATTAAAAT
plasmid_lp54	7499	BB_A11	0.890 ± 0.3923 0.388059	1.373 ± 0.944 0.28226	0.916 ± 0.4152 0.39429	1.07 ± 0.5619 0.11465	ACTTGAACATGATTGATACTGTTAGAAAAGTTAACTCACACT
plasmid_lp54	7563	BB_A11	0.487 ± 0.1384 0.059119	1.17 ± 0.866 0.78715	0.639 ± 0.3748 0.32738	0.745 ± 0.1879 0.2617	AAGCACACAAACACAAAGGCATCTCAAACAAAATTCAATTACA
plasmid_lp54	7841	BB_A11	0.282 ± 0.3475 0.229804	0.305 ± 0.3725 0.25992	0.351 ± 0.5704 0.45434	0.795 ± 0.9808 0.84053	AATTGTAGAGATTCTATTGGTGGCAAGGAAAACCATAGGACTTGGGG
plasmid_lp54	8162	BB_A11	0.677 ± 0.9116 0.744251	0.175 ± 0.3274 0.19771	0.468 ± 0.8775 0.18671	1.55 ± 1.6071 0.66236	TGTTTAAAGTGGGGCATGTTTGGAGAAGAAAATGAAGCTTAAAATT
plasmid_lp54	8485	BB_A13	0.757 ± 0.705 0.500076	2.186 ± 1.3961 0.21716	0.627 ± 0.5133 0.17779	0.65 ± 0.4706 0.16368	TTAAAGCGCTAATGCCAGAGTTGATATTCAATTGTCATT
plasmid_lp54	8595	BB_A13	1.539 ± 1.3198 0.575669	2.041 ± 1.9483 0.48513	1.927 ± 1.0336 0.29322	1.174 ± 0.5591 0.5236	CTTGTAGATGCTATTAGATTGTAAGGATTAAGCCCCAAATATAC
plasmid_lp54	8947	BB_A14	0.915 ± 0.9679 0.851822	0.897 ± 0.4253 0.43004	0.505 ± 0.2147 0.05887	1.004 ± 0.4252 0.93126	TCATCCCCAACAGAGTCACACTAAAGGCTTAAGCTTACGAAGCGCAT
plasmid_lp54	8951	BB_A14	0.554 ± 0.1786 0.104209	0.696 ± 0.504 0.52341	1.26 ± 0.4059 0.36659	1.091 ± 0.4873 0.83137	GATGATGGTCTCTGGAAAGGCTTGTATTGAGAGCATGAAAAATTATA
plasmid_lp54	11279	IG 1393	1.386 ± 0.3275 0.158489	1.699 ± 0.8082 0.30133	0.947 ± 0.2776 0.74606	1.331 ± 0.5126 0.33452	TTCCAGAAGTAACAAATTGAAAAATATAAACTCAATTGTTT
plasmid_lp54	11458	IG 1394	2.833 ± 1.7496 0.010798	2.753 ± 2.4314 0.29936	1.447 ± 1.2783 0.63222	1.03 ± 0.8 0.88233	TTGAATGAGGATAAAATTAATTTCTAAATTCTTAAATTAAATTAA
plasmid_lp54	11518	IG 1395	0.851 ± 0.4197 0.475169	1.754 ± 1.9478 0.46963	0.854 ± 0.4652 0.20104	1.186 ± 0.6189 0.64141	TAGCGATGGGTTAAATTGAGATTATTATTATTATTC
plasmid_lp54	15465	BB_A23	0.709 ± 0.5244 0.248768	1.082 ± 0.8005 0.81665	0.695 ± 0.3102 0.29257	1.204 ± 0.5285 0.48167	AAATATCCAATAGTGCAGGACAAAAATAACATCCGGACTTGGACGTC
plasmid_lp54	15649	BB_A23	0.808 ± 0.9301 0.684838	0.957 ± 1.0836 0.92389	0.397 ± 0.438 0.44262	0.586 ± 0.6787 0.56577	TTGAAATACAGAGATTAGGTTGAAAGATCAGGTTTGTGCATT
plasmid_lp54	15800	BB_A23	0.499 ± 0.8481 0.625234	0.889 ± 1.4184 0.82817	0.844 ± 1.4092 0.89801	1.519 ± 2.04 0.68852	CAAACAAAAAATTTAATCTTTGATGTTATTGGAATTCTTCTT
plasmid_lp54	16256	BB_A24	0.583 ± 0.4273 0.209168	1.349 ± 0.6165 0.47466	0.99 ± 0.7517 0.98722	0.76 ± 0.343 0.39223	TCCAGTTCTTGAGTTAGTAGCTTCTCTTGTATTACGAATT
plasmid_lp54	16973	BB_A25	0.456 ± 0.2019 0.15055	1.284 ± 0.53 0.24895	0.541 ± 0.4061 0.33244	1.097 ± 0.3766 0.59152	TCTATTCTTAAGGAACTTCTGTTCAACATGGCTGTACTTTGCT
plasmid_lp54	17164	BB_A25	3.098 ± 2.3281 0.167475	3.553 ± 5.779 0.52981	1.124 ± 1.4261 0.91404	0.628 ± 0.8152 0.60007	TCTGAATCGCCTCTAAGGTTAAAAACAAAATTTTAAAAAA
plasmid_lp54	17278	IG 1396	0.791 ± 0.9272 0.617165	1.68 ± 2.5557 0.34518	0.932 ± 1.0373 0.89568	1.237 ± 1.7576 0.13902	AATTAGTAAATTAAATTGAAATTTAGGCCACTTTGAAACAAAAT
plasmid_lp54	17877	IG 1397	0.588 ± 0.7868 0.690573	0.107 ± 0.2107 0.32168	0.124 ± 0.2387 0.34845	1.322 ± 2.1123 0.83447	TTGTTCGTTAACACGATTTTGATTTGTTCTGCTTGAGTAA
plasmid_lp54	18257	BB_A30	0.647 ± 0.5392 0.515542	1.184 ± 1.2309 0.04076	0.704 ± 0.5918 0.53646	0.831 ± 1.1375 0.52897	TCCGGTATTGTTGAAAAGATACTTTCTAGCGACCTGGCAGAA
plasmid_lp54	18578	BB_A30	0.937 ± 0.3755 0.165916	1.471 ± 1.3684 0.52689	0.838 ± 0.2708 0.40775	1.254 ± 0.6988 0.57288	AGCCTGAAAGAGAGCTGCTGATAGGTTAAAAGAGAGAGATTGAA

plasmid_lp54	19164	BB_A31	0.794 ± 0.0935 0.112892	1.237 ± 0.447 0.45143	0.753 ± 0.2111 0.04023	1.095 ± 0.1601 0.4798	TTTACGGGGTAAACAGAGATGCTTTCCAAGATTGCTGGGGCAATA
plasmid_lp54	19680	BB_A31	0.734 ± 0.7823 0.457851	1.561 ± 1.6177 0.08415	0.936 ± 0.8811 0.89308	1.333 ± 1.2906 0.55249	GTGATAGTTAATGCTTGTCCATTCAAGTTTAATAGAAAATTCAATG
plasmid_lp54	19700	BB_A31	2.351 ± 1.8852 0.233063	4.626 ± 4.7032 0.28097	1.681 ± 2.2371 0.54436	1.411 ± 1.4805 0.72703	TCCATTCAAGTTTAATAGAAAATTCAATGAAATACCGTTACATTGAG
plasmid_lp54	20553	IG_1398	0.566 ± 0.5935 0.591769	0.749 ± 0.9393 0.70289	1.024 ± 1.0233 0.97385	0.96 ± 1.4778 0.97291	TAAGCTAATTTTTTAAAAGAGAGTTATTTCATCAATTGATTGAGA
plasmid_lp54	21356	BB_A33	0.900 ± 0.5387 0.821773	2.121 ± 1.5071 0.24079	1.133 ± 0.5508 0.46849	1.875 ± 0.8729 0.09443	AAACAAAATATTAGAGATTAAAATACAGCACGGGTTAGTAGAAAAAAAG
plasmid_lp54	21895	BB_A34	0.579 ± 0.273 0.161916	0.451 ± 0.3874 0.33582	0.803 ± 0.512 0.04311	0.945 ± 0.5915 0.14978	AGCTCATCAAGTTCAGGATTGAATATCGTAAGATGCAAAATGTGAGTT
plasmid_lp54	23488	IG_1399	0.634 ± 0.5065 0.310663	1.572 ± 0.7268 0.13652	0.772 ± 0.2755 0.19301	1.28 ± 0.8489 0.65339	CTTAAGGCCTTATTGTAGTTAAAATAAAATGCGTCTTTAACGCCT
plasmid_lp54	23489	IG_1400	0.293 ± 0.3853 0.235887	0.437 ± 0.6268 0.18117	0.481 ± 0.5067 0.4311	1.172 ± 0.9705 0.70148	ACCCATTGTTAGTTAAAAGAAGTTCAATGAAATTGTTGATTATAACA
plasmid_lp54	24047	BB_A36	0.671 ± 0.3078 0.005758	1.357 ± 1.1235 0.54859	0.531 ± 0.2551 0.03849	0.87 ± 0.4607 0.43652	TTTTTGATTGCTTCTAAGGATGTTAACAGACAAAAGAATTATAAGC
plasmid_lp54	25392	IG_1401	0.975 ± 0.6092 0.876772	1.291 ± 0.9594 0.05429	1.123 ± 0.8114 0.53526	1.427 ± 1.2248 0.23418	TTAACACATATTGATATTCAAATGTAATATTAAAATTAAATTGATT
plasmid_lp54	25431	IG_1402	0.769 ± 0.4205 0.594406	1.072 ± 0.6536 0.8624	0.89 ± 0.5644 0.83727	1.379 ± 0.8219 0.06069	GTTTTGATATAATAATGATGATATTAAAATGATTAACGAATT
plasmid_lp54	25596	BB_A38	1.064 ± 0.6474 0.777426	0.733 ± 0.5315 0.64086	0.359 ± 0.1875 0.15004	0.856 ± 0.7759 0.73525	AATTAAATTAAACGCTGCTGAAAAGTCTGCTGAAAGAACGACAGTC
plasmid_lp54	26380	BB_A38	1.753 ± 1.5157 0.473373	1.29 ± 0.914 0.54632	0.455 ± 0.5209 0.39479	1.604 ± 1.1209 0.35557	GAGCCTTAAACCGAACGACTTAAATGAGCACTCAAAGGGCTGGCAGCAGC
plasmid_lp54	26832	BB_A39	0.442 ± 0.487 0.221985	1.09 ± 0.4493 0.72949	0.36 ± 0.1279 0.00413	0.309 ± 0.1233 0.02481	GCAAGATAACTAACTGTTAATTCTCACAATGACTTAAGAGAACT
plasmid_lp54	26934	BB_A39	0.565 ± 0.1972 0.168609	1.047 ± 0.9501 0.90791	0.764 ± 0.407 0.03438	0.926 ± 0.3276 0.38889	GAAAATCTTGTAGCAAAGGGTATTCTTAAAGAGGTTGAAAGGACAA
plasmid_lp54	27125	BB_A39	0.600 ± 0.2539 0.082494	1.282 ± 0.7802 0.25828	0.751 ± 0.2965 0.17122	1.035 ± 0.3888 0.81293	TTCAAGAAAATTCTACAAAGTCATAAATTTCAGAAATAAAATCAGATCA
plasmid_lp54	27359	IG_1403	0.793 ± 0.3773 0.200671	1.114 ± 0.4707 0.34288	0.745 ± 0.3649 0.23959	1.157 ± 0.5091 0.34215	CAAAAAATTAAATTAAAAGAGGATTATTAAATGAGCGATTCAATTGATT
plasmid_lp54	27741	BB_A40	0.212 ± 0.2867 0.275087	1.38 ± 1.3605 0.6676	0.579 ± 0.5496 0.50419	1.103 ± 1.3471 0.92892	AGTCTACACAAACCCATAAGATCACTACCACCGCCTTGCTATTGCA
plasmid_lp54	28205	BB_A41	0.603 ± 0.1728 0.051208	1.163 ± 0.6412 0.51856	0.704 ± 0.1904 0.06357	1.022 ± 0.301 0.886	TAATGATTTAACACAGTCTAACAAATAAGTCCAAAGACAAATAGTAA
plasmid_lp54	28231	BB_A41	0.801 ± 0.8384 0.726001	1.87 ± 2.5383 0.2424	0.986 ± 1.2417 0.94254	1.136 ± 1.3533 0.49992	TAAAGTCCAAAAGACAAAATGTAATAACTTACCTTTCAGTATG
plasmid_lp54	28472	BB_A41	0.749 ± 0.1297 0.162604	1.263 ± 0.2193 0.14843	0.733 ± 0.1213 0.14009	1.127 ± 0.1692 0.273	TATGTACGGACTTTGAATCTTCAACATCAAATAGATAAAACAGTTAACAA
plasmid_lp54	29003	BB_A42	0.120 ± 0.1545 0.012493	0.815 ± 0.8047 0.78543	0.48 ± 0.7271 0.38831	0 ± 0 0.03274	ATTCTCACTTTAGAGTTTAAATTGACTTAAGGCTGTATTGTTATC
plasmid_lp54	29006	BB_A42	0.432 ± 0.2224 0.111352	0.274 ± 0.2688 0.19808	1.624 ± 1.1564 0.41253	0.851 ± 0.9686 0.63081	AGAATCTGCAAAGAGTGTATGAGCAAAACTTAAAGCTTTAATGTTGA
plasmid_lp54	29368	BB_A42	1.009 ± 0.7153 0.696507	1.417 ± 1.0841 0.55021	0.97 ± 0.5747 0.85369	1.047 ± 0.7461 0.91612	AGAGAGCCTTGTCTTAAATCTTAAATCATCCAAGCATTTGCAA
plasmid_lp54	29485	BB_A43	0.636 ± 0.3443 0.117592	1.04 ± 0.4411 0.90372	0.881 ± 0.5317 0.56929	0.644 ± 0.285 0.02891	TATTGGATCTTGTACTCTGAATTACAGAAAAAAGTTCTGTGAATA
plasmid_lp54	29749	BB_A43	1.272 ± 1.3659 0.736115	2.156 ± 1.3689 0.2481	1.717 ± 1.1569 0.36324	2.762 ± 0.5833 0.02626	CTCTTGTGAGTGTAAAGATTAAATTAAAGACATTCTTAAATGAGAA
plasmid_lp54	30034	BB_A44	1.043 ± 0.4694 0.876589	1.239 ± 0.0236 0.7006	0.853 ± 0.2054 0.38705	1.236 ± 0.2306 0.01303	TGGCCTTAAAGCTTTGGACTTAGATCTTGTGATGATAAGTGAAT
plasmid_lp54	30440	BB_A45	1.033 ± 0.4046 0.732187	1.604 ± 1.1257 0.34168	0.878 ± 0.2165 0.26343	0.993 ± 0.25 0.95752	TCGTGAAAAATTCCAAAAGTGTCTACACATTGCAAATGTTCTATAA
plasmid_lp54	30766	BB_A46	0.837 ± 0.6332 0.522172	1.384 ± 1.3723 0.2888	0.627 ± 0.4561 0.3263	0.686 ± 0.6298 0.30178	ATTATTGAAAGCTAGTCTGTTGCAACAAACTAACGCTTATGTTATCTT
plasmid_lp54	31716	BB_A46	1.008 ± 0.6989 0.980898	1.16 ± 2.126 0.87708	0.947 ± 0.6395 0.90434	1.038 ± 0.9699 0.9468	TTAATAGCGTTAATTAAATAACACAAAGAGATAAAACGAATATTAA
plasmid_lp54	31727	BB_A46	0.605 ± 0.3619 0.144079	1.475 ± 1.0066 0.06656	0.75 ± 0.4478 0.20281	0.881 ± 0.518 0.40379	ATTATAATAATAACACAAACAGAGATAAAACGAATATTAAAGGAGAGCATCA
plasmid_lp54	32244	IG_1404	0.332 ± 0.1861 0.07518	1.187 ± 0.7595 0.58047	0.881 ± 0.4728 0.76869	1.176 ± 0.5212 0.29946	AAGGATAAGAATTAAAATGAGATAACAGTTAAAATATTAAACAGAGCCA
plasmid_lp54	32861	BB_A49	0.580 ± 0.3041 0.157957	1.171 ± 0.5747 0.27102	0.937 ± 0.2798 0.73619	0.908 ± 0.3403 0.4851	AATGGGCTACAAGGAGCTGTAGAGGTTAACCGAGTAGCCAATTAAAGCT
plasmid_lp54	32907	BB_A49	0.583 ± 0.3954 0.316945	0.88 ± 0.7911 0.8702	0.216 ± 0.2322 0.08879	1.066 ± 0.7022 0.90502	TTAAATTGGCTACTCGGTTAACCTCTACAGCTCCTGTAGGCCATT
plasmid_lp54	34337	BB_A50	0.843 ± 0.3932 0.360746	1.569 ± 1.3505 0.3454	0.77 ± 0.4454 0.07172	1.028 ± 0.621 0.55875	CTCTGAAATTAAATTCACTAGCGCTATTGCAAATTGTCATGTGCTCAA
plasmid_lp54	36174	BB_A53	0.704 ± 0.2163 0.237602	0.978 ± 0.6456 0.96864	0.5 ± 0.3006 0.0628	0.674 ± 0.3631 0.41293	ATGCTATGCTAACATGTTAAATTCTCAGGTCTTATTAAATTACA
plasmid_lp54	36853	BB_A55	0.668 ± 1.0487 0.684229	1.623 ± 1.7244 0.50734	0.747 ± 1.1866 0.81076	2.773 ± 3.3752 0.07498	AAAACGACATTGTTAAAATTATTATAAAAGTTTCAGTCAGCAA
plasmid_lp54	37748	BB_A56	0.684 ± 0.1442 0.00251	1.507 ± 0.8846 0.38978	0.595 ± 0.4468 0.32571	0.94 ± 0.2508 0.75664	CAAAATTAAAGTTAGATATACTACAGTTACTAATCTAACCTTCGACT
plasmid_lp54	37786	BB_A56	0.991 ± 1.2673 0.97752	1.341 ± 2.0673 0.57799	0.765 ± 0.9329 0.28345	1.126 ± 1.0851 0.73279	TAATTTAATTTTCAAGAAGTGTATAATCATTGATAAAATTAA
plasmid_lp54	37997	BB_A56	1.095 ± 0.9417 0.902541	2.677 ± 3.6538 0.5294	0.749 ± 0.8365 0.71008	1.699 ± 1.5725 0.44428	AAGGATAATGAACTAAGTTGAAAATTCTACATGCACTGGTACTCTA
plasmid_lp54	38387	BB_A57	0.343 ± 0.4792 0.331215	1.188 ± 1.5541 0.8626	0.688 ± 0.8548 0.56456	1.027 ± 1.2081 0.97194	AGTTTCACCAACCCAAAATTACACAAATTGACAGCTCAAGAATATA
plasmid_lp54	38506	BB_A57	0.721 ± 0.4524 0.453609	1.257 ± 0.9923 0.66521	0.681 ± 0.4373 0.37024	1.219 ± 0.8441 0.52054	AAGCTCACTTTGTTAGCTCTCGAGCAATCTGTTTATTATTCTAT
plasmid_lp54	38515	BB_A57	0.723 ± 0.4201 0.18016	1.61 ± 1.0944 0.30051	0.702 ± 0.4299 0.25672	0.866 ± 0.6267 0.64514	TTTGTAGCTCTCGAGCAATCTGTTTATTATTCTATGTTCTCGGT
plasmid_lp54	39016	BB_A57	0.826 ± 0.5941 0.37302	1.784 ± 1.948 0.46121	0.913 ± 0.5994 0.49814	0.86 ± 0.5458 0.37136	AGAAGCTCCAATTAAACAATAATTCTCTGATTTGCAATTCTCTTC
plasmid_lp54	39628	IG_1405	1.252 ± 0.9088 0.503813	3.844 ± 4.714 0.41094	2.372 ± 2.1328 0.30387	1.261 ± 0.6306 0.58867	TAGTGGTGTCTTAAATTCTAAATTTCTAAAGCACCACGACCAATTGCA
plasmid_lp54	40011	BB_A59	0.720 ± 0.1509 0.141831	0.605 ± 0.5465 0.34147	1.132 ± 0.426 0.40671	0.923 ± 0.2089 0.65906	GTGACATTGTTAGAATAGAATCTATTAAACCCACGACCAATTGCACT
plasmid_lp54	40458	BB_A60	0.763 ± 0.2919 0.309524	0.735 ± 0.2656 0.28566	0.602 ± 0.228 0.23762	0.888 ± 0.4193 0.69194	AAGGTCTTTAAATATAATCTTGGGTTTTGGATGTCGTTGGGGGATT
plasmid_lp54	41013	BB_A60	0.916 ± 0.2543 0.180413	1.729 ± 1.5023 0.42009	0.864 ± 0.2729 0.62067	1.06 ± 0.2971 0.41411	AATTGGATCTGTTGATTTATCTATAAAATAAGAACAAAAACCAA
plasmid_lp54	41873	BB_A61	0.744 ± 0.1709 0.051399	1.217 ± 0.2403 0.16095	0.647 ± 0.3487 0.11198	0.914 ± 0.2048 0.26094	GCCTAAATAGTTGCTCTGATTTTATTCTCAATTGCTGCTTTGAATCT

plasmid_lp54	42705	BB_A64	0.942 ± 1.2551 0.847531	1.983 ± 3.5177 0.41781	1.017 ± 1.4052 0.96297	1.418 ± 1.6569 0.39946	TGAATTCTTGTCTTAAGGGTCATTTAACGTCAGTTGTAA	
plasmid_lp54	42710	BB_A64	0.916 ± 0.4578 0.797449	1.443 ± 0.843 0.19475	0.871 ± 0.3066 0.52051	1.279 ± 0.7432 0.3148	TTTTGATCTTAAAGGTGTCATTTAATTGAAACGTCAGTTGTAAAGTCAG	
plasmid_lp54	43314	BB_A64	0.680 ± 0.81 0.688974	1.364 ± 1.479 0.70224	0.693 ± 0.7537 0.4924	1.173 ± 1.3139 0.14626	TGAAGCCTTGAATTGCTTATTCTTCAGCTGCGGGCTTGTGGATT	
plasmid_lp54	43703	BB_A65	0.875 ± 0.3457 0.712328	1.669 ± 0.9671 0.40573	0.682 ± 0.2333 0.25958	0.991 ± 0.3911 0.75114	TAAATTAAATAATTAAAAAAATAAGACCTTGACCCAAAGAGAGCGCAT	
plasmid_lp54	43747	BB_A65	1.143 ± 0.809 0.679674	2.048 ± 2.2556 0.25064	0.993 ± 0.6878 0.98827	1.048 ± 0.9584 0.70492	AAAGAGAAATCATAGTATCTTATATGTTGCTCAATGTGTCAGTTAGCT	
plasmid_lp54	43881	BB_A65	0.970 ± 0.466 0.912785	1.216 ± 0.8406 0.67375	1.153 ± 0.6768 0.77751	1.017 ± 0.6249 0.95371	TAATAAAAAGAATGGCTTAGCACAATAGAAACACTAATTAAAGCTCAA	
plasmid_lp54	43967	BB_A65	0.626 ± 0.3074 0.220709	1.191 ± 0.7042 0.15678	0.753 ± 0.3992 0.39056	1.069 ± 0.5205 0.75635	AGCAATCACATGGATAAGCTAAAGCAAATGATTTAACAAAATACTTT	
plasmid_lp54	44265	BB_A65	0.922 ± 0.5162 0.807915	1.516 ± 1.0536 0.20324	0.689 ± 0.3981 0.11083	0.895 ± 0.389 0.77325	TGAAGTTTCTTTTATTATTGTCTTGTCAAATTAACTCAA	
plasmid_lp54	44445	BB_A65	1.124 ± 0.6768 0.522302	1.499 ± 0.8157 0.08435	1.165 ± 0.8867 0.68881	1.306 ± 0.6774 0.24096	TTGTTCTTGTCTTGTAGATCGCAAGAGAAAATGTCGTATC	
plasmid_lp54	44656	IG 1406	0.549 ± 0.5212 0.034755	0.615 ± 0.574 0.01649	0.76 ± 0.4005 0.21516	1.078 ± 0.624 0.37738	TTTGATTAAATAGTTGCAAAATAGTTATTTCTTTAAATAAACTAT	
plasmid_lp54	44658	IG 1407	0.849 ± 0.657 0.25263	2.423 ± 3.0769 0.39217	0.877 ± 0.6414 0.30685	0.975 ± 0.7143 0.65785	TGATTTAAATAGTTGCAAAATAGTTATTTCTTTAAACTATT	
plasmid_lp54	45034	BB_A66	0.721 ± 0.5914 0.357311	1.166 ± 0.8585 0.7547	0.696 ± 0.6316 0.51674	1.057 ± 0.948 0.93324	CCTGATATCATTAATTCTCTTAAAGCTGTGATTGATTCTATTGTAA	
plasmid_lp54	45178	BB_A66	0.598 ± 0.3232 0.377677	1.227 ± 1.2659 0.59619	0.886 ± 0.4982 0.71274	0.692 ± 0.3635 0.4747	GTGTTAGAGTTAACGCTGGCGCGTAACCTCTGCATAAACTTAGCACT	
plasmid_lp54	45450	BB_A66	0.428 ± 0.5238 0.006349	1.951 ± 4.6834 0.49295	0.506 ± 0.5821 0.01978	1.068 ± 1.3238 0.89243	GGCAAAATGTGGCAGCCCGTATTCCTGCTGTTAAAGTTGTATTCC	
plasmid_lp54	46177	IG 1408	0.408 ± 0.4255 0.390767	0.641 ± 0.6468 0.63152	0.738 ± 0.5727 0.54799	1.097 ± 0.6602 0.82476	AAATGAACACAAAAGTAACGTTTCCAGTTAGAAACGCCAATTGTA	
plasmid_lp54	46666	BB_A68	<i>cspA</i>	0.913 ± 0.474 0.762438	1.185 ± 0.5472 0.61764	0.741 ± 0.23 0.11964	1.026 ± 0.2283 0.90048	TAAGTCAGAAGAATCTAAATCATTGCTAATGCAAATAACCAACTTAG
plasmid_lp54	47220	BB_A68	<i>cspA</i>	1.426 ± 0.9786 0.275908	1.23 ± 0.8483 0.65279	0.415 ± 0.4379 0.16008	1.072 ± 0.10387 0.89539	AGCCAAACTAAATATAATCAAGGATTAATATTGCAATGATATTAACTTT
plasmid_lp54	47226	BB_A68	<i>cspA</i>	0.992 ± 0.4499 0.986325	1.444 ± 0.6902 0.41121	0.719 ± 0.3943 0.46334	0.918 ± 0.4556 0.8471	GAAAAAGCCAAACTAAATATAATCAAGGATTAATATTGCAATGATATT
plasmid_lp54	47229	IG 1409		0.653 ± 0.6547 0.471801	0.955 ± 0.975 0.90438	0.654 ± 0.6058 0.3429	0.823 ± 0.6362 0.75396	AATACTCTTATAAACTAATATTAAATTCTAATATAAAAT
plasmid_lp54	48263	BB_A69		1.404 ± 0.4007 0.254683	2.061 ± 1.0934 0.21754	1.28 ± 0.7342 0.58541	0.844 ± 0.3577 0.63701	TTCAAAATACTCTCTTATAAACTTAAACACAGTATTAATTAAATT
plasmid_lp54	48305	IG 1410		0.451 ± 0.6895 0.18355	2.115 ± 2.4973 0.17549	0.781 ± 0.8892 0.58678	0.818 ± 1.0828 0.42427	TTTTAATATAAAATATAATTATAATTATAAAATATTGTCAAATAAT
plasmid_lp54	48639	BB_A70		0.761 ± 0.3765 0.37903	1.868 ± 1.5166 0.42883	0.832 ± 0.2745 0.41724	0.919 ± 0.3382 0.72418	ACAGTTTTCAACAGCTTTGAATTCTTTAGTTAAGTCATA
plasmid_lp54	48752	BB_A70		3.184 ± 3.2875 0.092848	1.445 ± 2.6166 0.68695	3.596 ± 3.4932 0.07827	4.109 ± 5.4459 0.27744	AAAAGAAGATAATTAAACACTCTAACGGAAGAAAATTAAAGAAACTACT
plasmid_lp54	49049	BB_A70		0.346 ± 0.1786 0.157782	0.519 ± 0.4827 0.42329	0.885 ± 0.3998 0.45971	0.909 ± 0.4709 0.48254	AATAGAAAAAAATTACTGCGAAAAGAATCTGATCTTAGAAACTCTGA
plasmid_lp54	49454	BB_A71		0.935 ± 0.4012 0.773401	1.103 ± 0.256 0.07038	0.789 ± 0.2411 0.35373	0.76 ± 0.245 0.37338	AAAACAACTAAACCAATAATATAAGCAACAAACAAATGTCACTTGATA
plasmid_lp54	50033	BB_A0078		0.530 ± 0.5961 0.228728	1.425 ± 0.9799 0.33834	0.716 ± 0.4648 0.03551	0.951 ± 0.9482 0.91984	TAAAGTTAGTATTGTCGAATGATATTAGTTATTGTCAAACACACT
plasmid_lp54	50326	BB_A73		1.052 ± 0.6248 0.885427	0.808 ± 0.6454 0.62142	0.772 ± 0.4799 0.66441	0.743 ± 0.3894 0.34761	AAACACCCTGAAACACCTGTTGACCCACATACACTAAATTGTTGTTGT
plasmid_lp54	50654	BB_A73		0.818 ± 0.7944 0.512352	1.397 ± 1.4388 0.5601	0.38 ± 0.419 0.2534	0.698 ± 0.7118 0.66785	CATTACACACTTATTGGTTAATTGGACAGGATTAAACCAAGAA
plasmid_lp54	50991	BB_A73		0.976 ± 0.5694 0.861827	1.047 ± 0.7221 0.28573	0.888 ± 0.4965 0.78574	0.94 ± 0.5315 0.70202	TTGAAGATTGGGTCTTACATCTTCTGTTTGTAAACCTTTAAT
plasmid_lp54	51432	IG 1411		0.915 ± 0.8488 0.818602	1.384 ± 1.2071 0.4818	0.925 ± 0.6109 0.43564	1.088 ± 0.585 0.70791	TTAAAATTAACACCTTACGCAAACATTGCTTAAAGATCAACTAATTAA
plasmid_lp54	51592	IG 1412		0.895 ± 0.6792 0.07652	1.785 ± 1.7981 0.34424	0.8 ± 0.5024 0.20139	1.092 ± 0.8063 0.38411	GGTCATTCTTAAATTAAACAGTTAATTTATTTATTAAATATGTT
plasmid_lp54	51605	IG 1413		1.260 ± 1.5497 0.647163	2.451 ± 3.0084 0.36624	0.926 ± 1.1417 0.81871	1.126 ± 1.194 0.69332	AATTAAGAATGACCTTAAACAAAGGTTTAATAAGATTAAACACTTA
plasmid_lp54	51658	IG 1414		1.152 ± 1.683 0.098702	0.545 ± 0.725 0.51854	0.942 ± 1.1086 0.95526	0.542 ± 0.6901 0.56157	AACTAAATTAGAATCAATACATATTAAATAAAAAATATAATTAACTTT
plasmid_lp54	51666	IG 1415		1.561 ± 0.296 0.034661	1.878 ± 0.8462 0.19956	1.17 ± 0.2752 0.25518	1.102 ± 0.7223 0.84886	AAAACATAACTAAATTAGAATCAACATATTAAATAAAAAATATAAT
plasmid_lp54	51681	IG 1416		0.471 ± 0.3047 0.109069	2.287 ± 2.9225 0.45262	0.439 ± 0.2897 0.23296	0.57 ± 0.5068 0.50545	AATGTTAAATAAGGAGAAATACAATGACTAAATATTAGTAATTAAAT
plasmid_lp54	51718	BB_A74	<i>osm28</i>	1.732 ± 0.6879 0.069968	1.354 ± 0.8632 0.29125	0.9 ± 0.3963 0.53247	1.141 ± 0.5551 0.32832	ATATTTTAGTATTGTTAATTCTCTTATTAAACATTATTAACTTTATT
plasmid_lp54	51721	BB_A74	<i>osm28</i>	1.404 ± 0.4221 0.245803	1.719 ± 1.0843 0.3709	0.906 ± 0.1309 0.33186	1.076 ± 0.1713 0.54317	AGTAATTAAATAATTAGGATTATTGTTGAGTTAGTTAATGTG
plasmid_lp54	51856	BB_A74	<i>osm28</i>	1.034 ± 0.4677 0.836554	2.413 ± 3.3998 0.30772	0.51 ± 0.4192 0.01645	0.963 ± 0.9145 0.90108	GATCAAAAGATCAGGTTAATCAAGCTTAGATACTTTAACAGGTAAACC
plasmid_lp54	51918	BB_A74	<i>osm28</i>	1.162 ± 0.7559 0.225214	2.468 ± 3.0105 0.40312	0.762 ± 0.9973 0.51684	1.018 ± 1.2162 0.97071	TAGTAAATTAGGGAGTTAGAGAATCATCTTGTAAAGTGGATAACCA
plasmid_lp54	51994	BB_A74	<i>osm28</i>	1.295 ± 1.0295 0.582535	0.995 ± 0.7914 0.98997	0.834 ± 0.1095 0.83903	1.294 ± 1.1246 0.73034	CAAATTTTAACTCTGTCATTTGTTACCAATTCAAGAGATG
plasmid_lp54	52128	BB_A74	<i>osm28</i>	0.581 ± 0.3296 0.054032	1.552 ± 1.928 0.63459	0.567 ± 0.1896 0.00261	0.621 ± 0.4228 0.10692	AGCCTTTAGACATTCAACACCTGTTGACCCCTCAGCAACCATTC
plasmid_lp54	52131	BB_A74	<i>osm28</i>	0.936 ± 0.399 0.091759	1.798 ± 1.4637 0.33846	0.817 ± 0.3349 0.01097	1.089 ± 0.5072 0.38281	TCAAGAAACCCAAAAGCTGTTCTGTTGCTGGTAAGCAACATTAAAT
plasmid_lp54	52138	BB_A74	<i>osm28</i>	1.435 ± 0.2052 0.024005	1.353 ± 0.1842 0.03655	0.855 ± 0.0823 0.0998	1.107 ± 0.1973 0.2192	TTCTTGAACAGCCTTTAGACATTCAACACCTGTTGACCCCTAG
plasmid_lp54	52314	BB_A74	<i>osm28</i>	1.284 ± 0.8403 0.612862	1.359 ± 1.1734 0.7085	1.034 ± 0.6789 0.95432	1.433 ± 0.6671 0.34472	AGAGGCTCAAAAGTCTCAATATGGTTAATGGTTGAATCGTCAAATAA
plasmid_lp54	52403	BB_A74	<i>osm28</i>	1.711 ± 0.1277 0.010185	1.984 ± 0.656 0.12973	1.013 ± 0.0508 0.72147	1.239 ± 0.0862 0.00919	ATAGCCTTGCAACATCTTTGCTAATACTGATCTTATTTGACGGA
plasmid_lp54	52432	BB_A74	<i>osm28</i>	1.225 ± 0.5187 0.363485	1.173 ± 0.5427 0.53882	0.731 ± 0.2054 0.02076	0.943 ± 0.5035 0.79014	CGCCTTGAGCTTAACACATTAGAATGCGTTGCAACATCTTTT
plasmid_lp54	52477	BB_A74	<i>osm28</i>	1.063 ± 1.2639 0.911509	1.223 ± 1.8476 0.8239	0.56 ± 0.5921 0.13521	0.648 ± 0.482 0.48395	TAGTTAGATATAAAATTAAATAATTAGAGGTAAAGCAAAAGGTT
plasmid_lp54	53442	BB_A76	<i>thyX</i>	1.163 ± 1.1269 0.349503	0.303 ± 0.3816 0.36429	0.041 ± 0.0781 0.14939	0.186 ± 0.2245 0.27521	TTTAAATCCAAAGCTTAAATAATTGCAATTATCTTCTGTTGGAAAATCTC
plasmid_lp54	202	IG 1417		2.167 ± 1.9715 0.058637	3.391 ± 3.6107 0.18191	0.482 ± 0.3911 0.36447	1.667 ± 1.4398 0.4733	GTTTACCTGAGTTAAATACCTTAAATTGAGGATTTTAAATTTAAAAA

plasmid_lp56	292	BB_Q01	1.223 ± 1.431 0.655557	2.668 ± 2.3538 0.16432	1.257 ± 2.1747 0.80971	0.852 ± 0.5976 0.78625	TTGCTATTCTGTGGCAAGATTAAAAAGATGCTGAGATTGTATTCCTT
plasmid_lp56	371	BB_Q01	0.594 ± 0.144 0.078448	1.221 ± 0.8381 0.7217	0.363 ± 0.3385 0.01094	0.428 ± 0.5045 0.26307	GTTTTCGGTTGTTATTCTGACTCCGAAGAAATACAAATCAGCATC
plasmid_lp56	420	BB_Q01	1.604 ± 1.4146 0.564604	1.043 ± 1.0673 0.95644	0.406 ± 0.1885 0.0235	0.531 ± 0.3813 0.15803	GGAGTTCACAGATTTTATGTAGGTAATAATAGGAACCTGGTCT
plasmid_lp56	901	BB_Q03	0.767 ± 0.7114 0.603393	1.205 ± 1.2686 0.37823	0.582 ± 0.5223 0.43966	0.671 ± 0.6528 0.60239	TTGGGTTGTTATTGCCTGATAATCAGGAACAAGCTGTTCAAACCTTTT
plasmid_lp56	7211	BB_Q12	1.700 ± 0.9607 0.051905	1.191 ± 1.2767 0.84553	2.071 ± 1.5902 0.38528	2.017 ± 1.462 0.37087	AATAACCCCTCAAATTATTGTAATCGAACATACTGGCTGTTTGCTAA
plasmid_lp56	7397	BB_Q12	1.145 ± 0.2707 0.509624	0.787 ± 0.53 0.59433	1.464 ± 0.3258 0.0941	1.219 ± 0.6298 0.54959	CAGCTTATTCCCAAATCTGCTACTTTATTAAATAAACATCGTACTAA
plasmid_lp56	7503	BB_Q13	3.321 ± 2.6693 0.144823	1.416 ± 1.0581 0.25478	1.521 ± 0.794 0.35649	1.059 ± 0.5977 0.83594	TAATGTATAATGGTTCCGCTGATCAAATTGAAGATGTTGATCTTCAGA
plasmid_lp56	7675	BB_Q13	4.451 ± 3.6105 0.03294	2.045 ± 2.0166 0.07995	1.296 ± 1.7709 0.61317	0.918 ± 0.8592 0.6604	CTTAAAATTACAGTACAAATTAGGCACTTAAAGCAGCGTCTGAAAATT
plasmid_lp56	7703	BB_Q13	2.727 ± 0.4983 0.026227	1.265 ± 0.748 0.59838	0.867 ± 0.123 0.1556	1.061 ± 0.0999 0.28093	AGTGCCTAAATTGTAATGTAATTAGCTTACCACTTCAG
plasmid_lp56	7815	BB_Q13	1.980 ± 0.7038 0.008335	1.203 ± 0.4066 0.37109	1.026 ± 0.4755 0.79232	0.974 ± 0.4272 0.2918	AACTTATAATCACTTGTACTAACAGGCACTGTTCAATTAAAGATG
plasmid_lp56	7900	BB_Q13	0.473 ± 0.5723 0.451791	1.153 ± 1.1453 0.82015	0.409 ± 0.5731 0.11312	0.531 ± 0.5473 0.2467	TGGACTCTTAATATGCCACATCAAGTAAAGAAGTTGCTAGTGGTGA
plasmid_lp56	8267	BB_Q13	1.451 ± 1.8726 0.614781	1.287 ± 1.7054 0.69953	0.536 ± 0.5819 0.00093	0.901 ± 0.7275 0.07106	CCTACACCAAATGAAACAGTGGATAAGGATCAACTGATATTGCTCATTCA
plasmid_lp56	8638	BB_Q14	0.853 ± 0.7168 0.635208	1.242 ± 1.6795 0.80329	0.882 ± 0.6831 0.63319	1.186 ± 0.9819 0.59579	TGGGTTGCAATTAAAGAACAGGGAGTGTGCGAGAATTGAAATTGATA
plasmid_lp56	8737	BB_Q14	0.482 ± 0.2991 0.234416	0.482 ± 0.431 0.33174	0.811 ± 0.4924 0.71508	0.736 ± 0.5661 0.66072	GTAGCAGTGGAGGCGAAGAAGGTGGCGAGGGGGTTGGCTCAAACAAGA
plasmid_lp56	8867	BB_Q14	2.173 ± 1.4266 0.230066	1.413 ± 1.6839 0.692	0.405 ± 0.4373 0.17162	0.369 ± 0.5938 0.4333	ATGAATGGTGTAGAAAAGACTTTCTGATATGTCATTGCGATGATCAAC
plasmid_lp56	9012	BB_Q15	2.909 ± 2.2401 0.0423	0.845 ± 0.7001 0.57825	0.303 ± 0.3039 0.26565	1.156 ± 1.3503 0.76336	AGTACACTGAAATCGCAGGAGTTATTGACATAAGCCACAAGAACCTG
plasmid_lp56	9036	BB_Q15	1.709 ± 0.7542 0.055094	1.642 ± 1.6846 0.48446	0.79 ± 0.2871 0.24429	1.167 ± 0.6183 0.3819	TTATTGACATAAGGCCACAAGAACACTGCAATTCTTATGATTCTGATATGT
plasmid_lp56	9103	BB_Q15	0.496 ± 0.2434 0.101685	0.496 ± 0.4389 0.26388	1.147 ± 0.3211 0.183	1.19 ± 0.4123 0.27232	TTCCAACTTACACATATCAAGACCTTAACATGAACAAAGACCAGAAT
plasmid_lp56	9118	BB_Q15	3.917 ± 2.3666 0.104991	0.773 ± 0.5246 0.46124	1.133 ± 0.5845 0.513	1.223 ± 0.7467 0.67411	TGTGAAAGTTGGAATATCCTTGAATATCAGACATATCAGAACATATAAAG
plasmid_lp56	9387	BB_Q16	2.000 ± 1.244 0.118951	0.771 ± 0.396 0.09602	0.782 ± 0.2948 0.37454	1.174 ± 0.5246 0.0358	TATCAATAATAGCTATAAACTCTAAGTTATCTGACCCCAAATAGGG
plasmid_lp56	9551	BB_Q16	2.738 ± 1.0962 0.066106	1.085 ± 0.6801 0.77752	1.62 ± 0.7268 0.21694	1.039 ± 0.3876 0.90392	CTACCCCTTTAAACTTACTTGTATTAGCCTTAAAGGCTGAGT
plasmid_lp56	9609	BB_Q16	1.949 ± 1.4952 0.302446	1.234 ± 1.4809 0.77564	0.58 ± 0.2748 0.21291	0.7 ± 0.2504 0.0068	TAAGGTAACACTGTAATGATTGTTACTTAGATATGGTATTAAATCATT
plasmid_lp56	9777	BB_Q17	2.009 ± 0.481 0.059984	1.041 ± 0.3561 0.89436	0.756 ± 0.2687 0.34134	0.898 ± 0.1805 0.48182	TTATATTGAGCTGAGCTGTTGATTTGAAAGATATGGTATTGAGT
plasmid_lp56	9842	BB_Q17	2.637 ± 0.9641 0.039344	1.998 ± 2.0076 0.43097	1.04 ± 0.3428 0.87578	1.311 ± 0.6044 0.44374	TGAAAATGCTTGGAAATTAGTATAAATTTCAAATATATTGCAAT
plasmid_lp56	9891	BB_Q17	1.142 ± 0.572 0.520142	1.337 ± 0.7806 0.20255	0.153 ± 0.2227 0.0129	0.298 ± 0.2282 0.10617	TTGCAATAATATATTGAAAATTACTAAATTCCAAAGCATTTTAT
plasmid_lp56	9943	BB_Q17	1.974 ± 1.6579 0.24199	2.955 ± 2.1425 0.14325	0.744 ± 0.7596 0.63713	0.655 ± 0.7298 0.60662	TAAAGCATTAAACATGCGTAATTAGCGTCAAAGTCTTGGCTTAAACACT
plasmid_lp56	9966	BB_Q17	0.752 ± 0.6604 0.342142	0.615 ± 0.5346 0.09435	0.882 ± 0.3295 0.17825	1.048 ± 0.4821 0.48599	CACAATAAAAGCTCATAGTATAATTGCCCAGTCAACACCGACTATATT
plasmid_lp56	10834	BB_Q18	2.557 ± 1.2812 0.065748	2.118 ± 1.9798 0.34498	1.017 ± 0.4891 0.92427	1.012 ± 0.3089 0.95809	ATTGAAAAGTTGGAACTGCAAATTACTTACTTCTTAATGAA
plasmid_lp56	11610	BB_Q19	2.768 ± 0.9505 0.034985	1.679 ± 1.7351 0.53407	1.211 ± 0.5207 0.63745	1.089 ± 0.3274 0.24164	GAAATAATTGGTAGCAATTCTATGTAATGCTAACTCAGCATTTA
plasmid_lp56	11688	BB_Q19	1.888 ± 0.4406 0.067098	1.827 ± 1.5627 0.45085	0.96 ± 0.0967 0.46716	0.937 ± 0.1468 0.48545	GCCCTTAATTCAAAGATACTTTTCCGCTCAGCAGATACTCTGAA
plasmid_lp56	12044	BB_Q20	3.306 ± 1.9999 0.159423	1.533 ± 0.4688 0.22645	1.83 ± 0.7298 0.13972	1.373 ± 0.4474 0.21176	AAAAAGCCGCTTTAGTATTTGAGTGGATGAAATAATGTTGGTGT
plasmid_lp56	12215	BB_Q21	1.813 ± 0.6208 0.012628	1.605 ± 1.2051 0.3071	1.28 ± 0.533 0.42939	1.104 ± 0.4231 0.33645	TTGATAAAGCTATTGCAAGTCTTGTAGGAGACTAGAAATAATTTC
plasmid_lp56	12434	IG 1418	2.210 ± 0.7279 0.045712	1.183 ± 0.6067 0.6632	0.967 ± 0.2883 0.79436	1.013 ± 0.6804 0.98279	AGTCCTACTGCTTAAATTACATACAATTCTTCTAATTTCAT
plasmid_lp56	12437	BB_Q22	2.270 ± 0.7949 0.056651	1.874 ± 0.864 0.19281	1.164 ± 0.3235 0.53006	1.136 ± 0.3073 0.431	GTGAGCGACAATTACCAATTAAATTAAAGGTATTCTGTATGCTGCA
plasmid_lp56	12609	BB_Q22	2.644 ± 2.1966 0.303629	2.173 ± 2.511 0.47441	0.403 ± 0.3902 0.20037	0.715 ± 0.352 0.44001	AGTTCTTTCTGTGCGACAAATTATTTTACAATATCTTGTGCTA
plasmid_lp56	13155	BB_Q22	2.320 ± 0.9336 0.008687	1.284 ± 0.9356 0.42844	0.846 ± 0.377 0.54316	0.956 ± 0.4783 0.32739	ATTGAAAACAGCAGTAGAATTGAGCTATGCTTAAATCCAGTGGTGTCA
plasmid_lp56	13236	BB_Q22	2.464 ± 0.4755 0.021747	1.818 ± 1.2203 0.34388	1.24 ± 0.3148 0.27598	1.215 ± 0.1541 0.05622	TTAACAGCCTTAACTGCACTTCGCTGCTCATAGCACCAACTGGATTAAAGC
plasmid_lp56	13515	BB_Q22	2.573 ± 1.8562 0.006889	1.53 ± 1.4928 0.17422	1.056 ± 0.7383 0.91179	1.863 ± 1.3048 0.22841	TCATTAACCTGATCACCGCTAAATTAAAGGTATTCTGTATGCTGCA
plasmid_lp56	13749	IG 1419	1.551 ± 1.2264 0.023659	1.753 ± 1.9668 0.33498	0.982 ± 0.7321 0.92863	1.008 ± 0.8736 0.73685	ATTACCTTTACCAAATTATGGAGTTGCTGATTGTCTGATTCTCA
plasmid_lp56	14140	BB_Q23	1.393 ± 0.8617 0.321432	1.824 ± 1.2976 0.26606	0.594 ± 0.417 0.00786	0.711 ± 0.5175 0.13572	TGTTCACCGCTTACCACTGGATTGAGCTTACATATTCCGCTTCTATCA
plasmid_lp56	14488	BB_Q24	1.768 ± 1.0236 0.021439	0.474 ± 0.3824 0.35576	0.996 ± 0.5396 0.97988	1.027 ± 0.5722 0.77312	TCTACATTGAGACTCAATTAAATCATATTGAGAACAGCATTTT
plasmid_lp56	14694	BB_Q24	1.712 ± 0.7151 0.24613	1.325 ± 1.3221 0.74175	0.659 ± 0.3937 0.24639	1.11 ± 0.3911 0.68189	AAAATATATTATAAGAAATTGCTCATGAAAAAAATTGATTCATAATG
plasmid_lp56	14702	BB_Q24	2.396 ± 0.9155 0.053469	1.562 ± 0.8991 0.27181	1.007 ± 0.2909 0.95161	1.239 ± 0.4262 0.35243	ATATATTCTACTATCTCAAATTATGTCGCGTGAAGCTAAGGG
plasmid_lp56	15026	BB_Q24	1.295 ± 0.5107 0.509374	0.504 ± 0.2427 0.00397	0.807 ± 0.1923 0.33322	0.961 ± 0.2415 0.86229	TGTTCATACGTAATAGCGATATTGGTACTGGTTACGGGGATATGAATG
plasmid_lp56	15567	BB_Q25	0.945 ± 0.9566 0.898699	0.587 ± 0.3669 0.36204	0.107 ± 0.103 0.0492	1.352 ± 1.273 0.59042	CAATACCCGAATTGAGATTTAGAACACAAAAATCTCTAATA
plasmid_lp56	15612	BB_Q25	1.597 ± 0.5989 0.126441	1.684 ± 1.5304 0.5076	0.813 ± 0.3218 0.00602	1.473 ± 0.4608 0.00871	GAGATATTGAGACTCAATTCTCAAATTGGTATTGTAAC
plasmid_lp56	15725	BB_Q25	3.997 ± 1.4303 0.017351	3.347 ± 3.2297 0.31522	2.283 ± 1.5825 0.32589	1.345 ± 0.7062 0.36706	CTTAGTGCATTAGGCCAAAGACTTAAATCTGATACTGTTAAA
plasmid_lp56	15726	BB_Q25	1.088 ± 0.6338 0.836163	1.348 ± 0.8616 0.52531	1.446 ± 0.7589 0.36349	1.298 ± 0.8769 0.67107	AGTATATAAAATGATGTTGCAAAAGTGAATATGTTATTATCAAA
plasmid_lp56	15729	BB_Q25	2.190 ± 0.804 0.017051	1.843 ± 1.4633 0.32702	0.994 ± 0.2824 0.96732	1.042 ± 0.298 0.74108	GTGCAATTAGCCCAAAGACTTAAATCTGATACTGTTAAAATTA

plasmid_lp56	16027	BB_Q26	2.938 ± 2.6993 0.16018	1.259 ± 1.3553 0.06716	1.91 ± 2.6136 0.60404	0.672 ± 1.0395 0.00432	CCAATTGCAAATTGCTTAATCTTAAATCCATACTAGTAATTATACCAT	
plasmid_lp56	16274	BB_Q26	2.351 ± 0.7097 0.019127	1.176 ± 1.1264 0.79396	0.655 ± 0.2081 0.07119	0.962 ± 0.5333 0.91164	TGTGCTTTGTTGCTGTAGTAGTGAAATATTATTTAAATCTAAGTTA	
plasmid_lp56	16277	BB_Q26	1.959 ± 0.2963 0.007239	1.783 ± 0.3992 0.0915	1.265 ± 0.5917 0.46067	2.065 ± 1.0277 0.18815	TATCCTTTTTCTCAGGCCATGTTGAATATGGAGTTAATTATGAG	
plasmid_lp56	16541	BB_Q27	1.471 ± 0.3331 0.145104	1.27 ± 0.3253 0.17875	1.013 ± 0.4193 0.96057	1.73 ± 0.3637 0.04317	AGTGCACCCGGTTTCACTTTAGAAAAAAAGAGATTAAGCTTATT	
plasmid_lp56	16608	BB_Q27	0.873 ± 0.9009 0.452247	1.218 ± 1.3189 0.60291	0.642 ± 0.5942 0.43721	0.925 ± 0.7908 0.86785	AAGCAGTGCACCGCGCTGTAAGTTGCTTTAGAAGAAATGTGTTCTT	
plasmid_lp56	16705	BB_Q27	1.394 ± 0.3999 0.006152	0.551 ± 0.3777 0.03316	0.447 ± 0.1002 0.03587	0.885 ± 0.4243 0.60424	GTAAATCTAATTTAACTAGTCCTAAATTAAAGCAAACCTTGGAGACAT	
plasmid_lp56	16907	BB_Q27	1.823 ± 1.0735 0.040127	0.66 ± 0.5624 0.58394	1.064 ± 0.6479 0.49279	0.942 ± 0.4736 0.69233	GTTTTAAGGTCAGTTACTTTACTTCATATAAACATTTCTTT	
plasmid_lp56	16942	BB_Q27	4.965 ± 3.0927 0.146931	2.284 ± 1.856 0.33351	1.148 ± 0.5596 0.66258	2.024 ± 0.5603 0.0874	TCCCTAATTGAGAGTCATAATTAAAGTAGAGGAGTTAAAGGTCAGT	
plasmid_lp56	16949	BB_Q27	1.016 ± 0.6722 0.934316	0.307 ± 0.2394 0.17575	1.053 ± 0.5695 0.16014	0.879 ± 0.984 0.74591	TTCTAGGATTATTCAAATAACTATTCTGATATGGAAATCAGCTTGAATA	
plasmid_lp56	17032	BB_Q27	1.055 ± 0.7946 0.937796	0.725 ± 0.6325 0.61696	0.815 ± 0.1709 0.25315	0.457 ± 0.3488 0.20872	AAGGAATTAAGTTATGGAAATAAGTGTGTTATTAAAGATACAGACACTG	
plasmid_lp56	17337	BB_Q28	2.671 ± 1.4285 0.037638	1.619 ± 1.3375 0.29895	0.857 ± 0.4227 0.40907	0.925 ± 0.4146 0.73891	GAAAATAAAATCAAGATATTGCAATATGGATATCTCAAGTTTATCT	
plasmid_lp56	17587	BB_Q28	1.698 ± 1.1929 0.41327	1.679 ± 1.7167 0.56591	0.909 ± 0.2952 0.63847	1.03 ± 0.3542 0.8968	CTACATTATTCGCCTAGCACTAAGAAAGGAAAACGACTAAAAAAAGATAA	
plasmid_lp56	17779	BB_Q28	1.680 ± 0.8831 0.002817	0.374 ± 0.2773 0.24153	0.845 ± 0.4648 0.34831	0.994 ± 0.6017 0.97639	CAGATGTTAACATAATTATAACTTTAACACTAAGGAGGTTTATGGCTG	
plasmid_lp56	17788	BB_Q28	1.636 ± 0.149 0.19652	1.178 ± 0.4194 0.54655	1.015 ± 0.1173 0.85163	1.222 ± 0.7222 0.64378	ACATATTATACTTTAACACTAAGGAGGTTTATGGCTGATGATCAAG	
plasmid_lp56	17813	BB_Q28	1.066 ± 0.9525 0.549535	1.58 ± 2.2069 0.57103	0.635 ± 0.7771 0.10288	1.321 ± 1.3126 0.45795	AGGAGGTTTATGGCTGATGATCAAGAAAATTACTAATTGATGAAGAAGA	
plasmid_lp56	17919	BB_Q29	1.004 ± 0.5178 0.988986	0.535 ± 0.5434 0.48235	1.014 ± 0.6904 0.94942	1.115 ± 0.7244 0.4999	AAAGATCAGTATCGTAACCGTGTACACCTTATTTAAATCTTTATTGAA	
plasmid_lp56	18115	BB_Q29	1.888 ± 1.0338 0.080011	1.609 ± 1.5381 0.43665	0.912 ± 0.4499 0.08884	0.981 ± 0.5013 0.43825	ATTAATTGTCGTTATTAGCATAATTTTCTACAAATCTTATCA	
plasmid_lp56	18267	BB_Q29	1.927 ± 0.7407 0.032716	0.983 ± 0.6363 0.96663	1.259 ± 0.5602 0.09157	0.952 ± 0.4287 0.88392	TATGTTAGGAACGGGTGTTTTGAATAGTATCTGATGAAGGCATTATCA	
plasmid_lp56	18279	BB_Q29	1.972 ± 0.774 0.049873	0.996 ± 0.649 0.98365	0.923 ± 0.3362 0.14293	0.963 ± 0.6124 0.87471	CCATCAAATTACTATGGCAGCATAACTAGAAAGTACTACCTTATCC	
plasmid_lp56	18326	BB_Q29	3.296 ± 1.5021 0.031334	1.808 ± 1.5662 0.37628	1.261 ± 0.4999 0.04822	1.185 ± 0.5135 0.01114	TCCCTCTGACTATGAGAATAAAGCGATATCTTAATATGGAAAGACAATGA	
plasmid_lp56	18668	IG_1420	1.818 ± 0.5673 0.012827	0.669 ± 0.2323 0.28676	1.062 ± 0.3821 0.64541	0.927 ± 0.494 0.8218	TATCAAAATCTGTAATTGCTAACTTGGCTAAAGCTTACAGTTAAAGGATCTG	
plasmid_lp56	18833	BB_Q30	2.447 ± 1.2075 0.106437	1.786 ± 0.7381 0.08793	0.822 ± 0.5237 0.39444	0.774 ± 0.5332 0.31802	AAAGACATATTGACTATTGTAATAGGCAAGATTTTAAGAATGGTAATGGT	
plasmid_lp56	18851	BB_Q30	blyA	1.032 ± 0.4108 0.751532	0.453 ± 0.3784 0.29656	0.932 ± 0.3756 0.48672	0.975 ± 0.4135 0.68639	CAATAGTCATATGCTTTAGTAAAGGCTTGAAGAAGATTAACTCCTA
plasmid_lp56	18854	BB_Q30	blyA	2.480 ± 2.0472 0.323681	1.932 ± 1.6995 0.14718	1.454 ± 0.8892 0.31093	1.57 ± 1.0865 0.05681	ATAGGCAAGATTTTAAGAATGGTATGGAAACAAATCACATTAAA
plasmid_lp56	18939	BB_Q31	blyB	2.237 ± 1.5672 0.293526	2.718 ± 3.014 0.40027	1.008 ± 1.1258 0.99078	0.716 ± 0.3067 0.40611	ATGTTGAGCTTGGACTTACGCTTTATCACACCTTATTGATATTTCTA
plasmid_lp56	19200	BB_Q31	blyB	1.658 ± 1.3684 0.19448	1.778 ± 1.6337 0.18767	1.085 ± 0.9502 0.79198	0.793 ± 0.622 0.73367	GATATTTGAGATTTTTCTACAGAATTAACTAAGTCATGCTTGTGATTG
plasmid_lp56	19242	BB_Q31	blyB	2.946 ± 2.3998 0.25547	0.796 ± 0.3104 0.31114	0.902 ± 0.865 0.8171	0.739 ± 0.3436 0.44535	AGGAAAGAACAAATAATGCAAACAAACACTATTGGTTAGGACTTAATT
plasmid_lp56	19285	BB_Q32		5.349 ± 2.9793 0.063849	1.705 ± 1.2396 0.46825	0.53 ± 0.5388 0.43563	0.846 ± 1.1272 0.82392	AGTCTAACCAATTAGTGTATTGCTTATTGCTTCTTCTTATAGAT
plasmid_lp56	19306	BB_Q32		0.912 ± 0.7261 0.60427	1.075 ± 0.6728 0.73531	0.759 ± 0.4142 0.4315	0.407 ± 0.2584 0.1518	GTTAACGCTGATAGTAAATTAGCTTAAACCAATAGTGTATTGCTT
plasmid_lp56	19390	BB_Q32		1.937 ± 1.5894 0.100428	1.983 ± 2.3213 0.35962	0.738 ± 0.4754 0.34696	1.184 ± 0.9373 0.20945	TATGTTTGTAGAAAAAACTTACTACTAAAGTATTAGTAAATT
plasmid_lp56	19392	BB_Q32		1.716 ± 0.6897 0.007504	1.495 ± 0.9458 0.24165	0.854 ± 0.4825 0.22133	1.287 ± 0.7414 0.24647	TATATGTTTGTAGAAAAAACTTACTACTAAAGTATTAGTAAAT
plasmid_lp56	19393	BB_Q32		2.523 ± 1.4533 0.163978	1.314 ± 0.8374 0.55484	0.609 ± 0.3152 0.37189	1.301 ± 0.7097 0.59845	TAAGCACACTAAATCTATGGAAACAGCTGAGTCACAAATATTGAG
plasmid_lp56	19395	BB_Q32		2.090 ± 0.9455 0.073098	1.728 ± 1.4304 0.37376	1.093 ± 0.483 0.5306	1.071 ± 0.403 0.34931	AGCACACTAAATCTATGGAAACAGCTGAGTCACAAATATTGAGAA
plasmid_lp56	19479	BB_Q32		3.037 ± 1.0164 0.059001	1.322 ± 1.0664 0.63198	0.751 ± 0.1936 0.2848	0.849 ± 0.1453 0.19229	TTATCTAACATGTTATTTAAATGCTTGTATTCTCAAATTTAG
plasmid_lp56	19910	BB_Q33		1.011 ± 0.4886 0.95079	0.567 ± 0.5663 0.19747	0.994 ± 0.7091 0.98212	1.121 ± 0.6505 0.23258	AGTACTTTCCGCTATTGGTTTGTATTAACTAAGTCATATATG
plasmid_lp56	19974	IG_1421		1.618 ± 0.6521 0.039302	1.652 ± 1.375 0.38915	0.962 ± 0.3153 0.60627	1.074 ± 0.3712 0.0703	AAATAGAATTCTTGTCAAGAAAACCTTTGTAAATTACATTTTACTG
plasmid_lp56	19981	IG_1422		2.052 ± 1.128 0.07233	1.544 ± 1.7309 0.53114	0.71 ± 0.4464 0.46024	0.762 ± 0.505 0.61314	AAAAAACTCTAAAGCCAATTACTAAATAGTATATAATGACCATAA
plasmid_lp56	20735	BB_Q34	bdrW	1.793 ± 1.2656 0.340143	1.105 ± 0.7193 0.65994	1.001 ± 0.6557 0.99865	1.206 ± 0.7153 0.70373	TTTAGAAATGAAAGCAAATTAGCCGGCTATCTGTGATAGACATTG
plasmid_lp56	21792	BB_Q37		0.951 ± 0.3623 0.77552	0.881 ± 0.4351 0.50414	0.827 ± 0.3358 0.61936	1.488 ± 1.037 0.55724	TATTATTTTCTCACCTTCATTCACCAATTTTTATTTAAACAGTG
plasmid_lp56	22085	BB_Q37		1.040 ± 0.5595 0.641685	1.028 ± 0.4884 0.94942	1.422 ± 0.4859 0.2087	0.987 ± 0.3729 0.93592	GCTGACCAACAACTGTGGCATTGTATTCAAATTTTAGACCCATTTC
plasmid_lp56	22518	IG_1423		0.920 ± 0.4096 0.752739	0.663 ± 0.5701 0.53146	0.799 ± 0.3987 0.62475	0.94 ± 0.5305 0.88026	GCAAAACATTTTGCCATTTCACAAAATTTTTACAAAAAATAG
plasmid_lp56	24151	BB_Q39		2.495 ± 1.2309 0.123166	1.976 ± 1.1552 0.23027	1.401 ± 1.0138 0.52308	1.004 ± 1.1265 0.99536	GATTATCATGGAGGGCCTTATTAATGGGAAAGAATGTTGAAGAAC
plasmid_lp56	26910	IG_1424		1.807 ± 0.7088 0.157518	1.768 ± 1.8537 0.52239	1.069 ± 0.5486 0.83914	1.224 ± 0.5092 0.41127	GGAGTAAAAGATGGAAAATCTTCAAACAAATAATCCACAAGAAAATA
plasmid_lp56	26946	BB_Q43	bppA	1.369 ± 1.513 0.484346	0.781 ± 0.7297 0.77194	0.997 ± 0.7002 0.99692	1.993 ± 1.2831 0.00407	ATCCACAAGAAAATTCAGGAGAGCTAAATGATAAGTATTACAAAC
plasmid_lp56	27279	BB_Q43	bppA	1.100 ± 0.9204 0.813909	0.558 ± 0.6637 0.45901	0.64 ± 0.8005 0.50895	0.389 ± 0.3102 0.30961	TGCTCAAGGCCAAAGAGTAGAGAATTAGGTTAGAGA
plasmid_lp56	27384	BB_Q43	bppA	0.215 ± 0.3013 0.202738	0.715 ± 0.7489 0.71617	1.831 ± 1.6284 0.3292	0.687 ± 0.5113 0.30014	TCAACACCGTTGGCATTTTATTTATATAATCAATTATCACCG
plasmid_lp56	27513	BB_Q43	bppA	2.664 ± 0.8142 0.011759	1.325 ± 0.7663 0.30229	0.944 ± 0.2579 0.78619	1.203 ± 0.3929 0.3828	TGAGTAGTGTATTGCTGAGTACAATAAAATGGCAATTAAAGCAGT
plasmid_lp56	27647	BB_Q43	bppA	3.269 ± 2.3215 0.09379	2.139 ± 2.3425 0.36579	1.032 ± 0.5916 0.78351	1.178 ± 0.7676 0.39124	GATGCTGCACCAATTACTGTAAGTAAAAGAGATGAGGCTTAATATCA
plasmid_lp56	27753	BB_Q43	bppA	1.826 ± 0.6604 0.069879	1.818 ± 1.6706 0.46174	1.098 ± 0.3574 0.716	1.128 ± 0.4026 0.3689	TCTTTTCAAAATTATAATTCTAATTCAACATTAAACAAAC

plasmid_lp56	27757	BB_Q43	<i>bppA</i>	1.118 ± 0.4876 0.587129	0.914 ± 1.5913 0.94032	0.36 ± 0.3995 0.00283	0.57 ± 0.3148 0.29239	AATATCTTTTCAATTATAATTCTAATTCACATTATAACAAATT
plasmid_lp56	27762	BB_Q43	<i>bppA</i>	1.647 ± 0.4333 0.122985	1.03 ± 0.3616 0.91068	0.888 ± 0.4204 0.36291	0.837 ± 0.2949 0.00297	GTAACATAGAGAGGAATACTTAATGGCACATAATTAAACGAGGATACGT
plasmid_lp56	27765	BB_Q43	<i>bppA</i>	1.871 ± 1.3954 0.180626	1.816 ± 1.6603 0.30956	1.097 ± 0.6002 0.39859	1.042 ± 0.4883 0.84099	ACTATAGAGAGGAATACTTAATGGCACATAATTAAACGAGGATACGT
plasmid_lp56	27896	BB_Q43	<i>bppA</i>	1.051 ± 0.3293 0.771892	2.072 ± 1.7566 0.33431	0.789 ± 0.6708 0.52845	0.701 ± 0.308 0.03418	GAATATGTTGATTGTGCAGACCTTGAAATTAAAGGATAATCAATCTGCTGAA
plasmid_lp56	27898	BB_Q43	<i>bppA</i>	1.069 ± 0.404 0.34762	0.859 ± 0.3393 0.41223	0.925 ± 0.3623 0.50426	1.129 ± 0.4305 0.10545	TTCTATAAATTCTTACCCAACTCAAACACTCAACTCAGAACTTAAAAAATC
plasmid_lp56	28068	BB_Q43	<i>bppA</i>	2.049 ± 0.9377 0.115973	1.401 ± 0.8275 0.43137	0.931 ± 0.3564 0.53283	0.605 ± 0.2411 0.0762	ATATTGAAATTAGCATCTTCACCTATCTTATGGCTTTCTTTTT
plasmid_lp56	28071	BB_Q43	<i>bppA</i>	1.773 ± 1.1792 0.416363	2.37 ± 0.2041 0.34525	0.616 ± 0.4542 0.44469	1.145 ± 0.5687 0.68406	CGAACATATCCACTAATTGAGCAGTTAAATTATAAATTGGAGAGTTG
plasmid_lp56	28387	BB_Q44	<i>bppB</i>	1.694 ± 0.6664 0.246845	1.342 ± 1.3866 0.74582	1.121 ± 0.5144 0.72854	1.535 ± 0.2119 0.57786	TAATAATGAGACACAAAAGTAACACCCCCATTGGTATCTCAGTCTT
plasmid_lp56	28445	BB_Q44	<i>bppB</i>	1.906 ± 1.0591 0.228988	1.629 ± 1.5174 0.53261	0.645 ± 0.4593 0.34241	1.123 ± 0.312 0.64256	TAGTTTATAGGACTGGATATATTAAAGAGCAATTGTTTATTAAATCT
plasmid_lp56	28626	BB_Q44	<i>bppB</i>	0.812 ± 0.2755 0.00345	0.545 ± 0.3469 0.20152	1.015 ± 0.3805 0.93605	0.845 ± 0.5533 0.65926	GCAACAAAAAATAAAGAATATTATGATTCACTTACTAAAGGCCACGT
plasmid_lp56	29064	BB_Q45	<i>bppC</i>	3.181 ± 2.0517 0.107186	2.01 ± 2.1805 0.41384	0.684 ± 0.2648 0.16983	0.915 ± 0.3422 0.75699	TGTGCTGTTGGATAGCCTGAACTCTCTGAGTTGATAACAAATTCTCTA
plasmid_lp56	30975	IG 1425		1.259 ± 0.5835 0.283719	0.641 ± 0.4888 0.43726	0.878 ± 0.5366 0.51412	0.918 ± 0.4856 0.761	ATTACTGACTGTAACGTGATCTCTTAAATTCTCAAATTAGAATTGT
plasmid_lp56	31261	BB_Q48		3.375 ± 0.8836 0.032138	2.447 ± 2.7443 0.44475	1.004 ± 0.2756 0.97152	1.918 ± 0.9502 0.2087	ACTAGCCTAAATAACTCAAACGAAATTACAGTGTGTTGAA
plasmid_lp56	32145	BB_Q49		2.032 ± 0.2015 0.187521	1.381 ± 1.8539 0.58032	1.517 ± 1.3866 0.2554	1.294 ± 1.2358 0.34693	TCTAATTCACTTAAACTTCTAGCGTTACTCTGATCTAAAGGTTG
plasmid_lp56	32442	BB_Q49		1.094 ± 0.454 0.394264	0.454 ± 0.3269 0.21002	0.875 ± 0.2545 0.12052	0.925 ± 0.3157 0.03621	CTATTTTGAGTTGCTTTCAGCCTATTAGCAGTTGAAAGTTT
plasmid_lp56	32539	BB_Q50		1.450 ± 0.7563 0.083033	0.943 ± 0.8036 0.61898	0.577 ± 0.3871 0.35062	0.842 ± 0.5751 0.09324	AAGCTAACAAATTCTCAATTAAATTGATAAGTTGAAGAAGAGCAGCTA
plasmid_lp56	32596	BB_Q50		2.876 ± 3.1574 0.33731	3.022 ± 2.3985 0.18679	1.506 ± 0.7562 0.12602	1.141 ± 0.5477 0.38083	AAACAAAAAAATGTGATAAAAAGCATTAAAAGAATAATGAAAAAAAGATT
plasmid_lp56	32939	BB_Q50		0.887 ± 0.4027 0.130489	0.437 ± 0.4041 0.2936	1.044 ± 0.6342 0.77313	0.936 ± 0.5084 0.19186	CTTCCCCTAAATCTTCAAAATCACTGCTTATCTCACCAGTAGGATTA
plasmid_lp56	32942	BB_Q50		1.151 ± 0.9413 0.421061	0.448 ± 0.3756 0.3846	0.92 ± 0.6101 0.82682	0.872 ± 0.6666 0.55979	ATTAGCAGCTTATTGGTAATGAGGCTACACTTACACAAGCAAACCT
plasmid_lp56	33084	BB_Q50		3.414 ± 1.3548 0.051495	1.711 ± 0.7516 0.15067	0.884 ± 0.2782 0.14411	1.064 ± 0.4367 0.85132	ATCGGTTTAAATAGTGTCTGGATGATCAGGATTAGTACAAAAATAAT
plasmid_lp56	33198	BB_Q50		2.754 ± 1.7612 0.151241	1.123 ± 0.4159 0.02081	0.87 ± 0.5247 0.39284	1.285 ± 0.5216 0.2113	TGATGGTATCTTATAGAGCTTCTTGTGTTGATAAACTCTTACT
plasmid_lp56	33200	BB_Q50		3.989 ± 3.132 0.093326	2.021 ± 1.6096 0.09744	1.194 ± 1.1711 0.46065	1.102 ± 0.7674 0.72085	TATGATGGTATCTTATAGAGCTTCTTGTGTTGATAAACTCTT
plasmid_lp56	33371	BB_Q50		1.146 ± 0.6261 0.790864	1.625 ± 1.5583 0.55485	0.768 ± 0.6668 0.64022	0.402 ± 0.2349 0.05225	AGTATGTTGTTGTATTCAAGACAGCACCAGCCAATGACCGTATA
plasmid_lp56	33680	BB_Q50		0.304 ± 0.3307 0.199897	0.259 ± 0.2462 0.22864	0.462 ± 0.3473 0.21261	0.318 ± 0.4223 0.22695	TTTATTCGATAAAAGGAGATAACAAAACCATGATGATGCTTGTGAA
plasmid_lp56	33767	BB_Q50		2.597 ± 2.6331 0.196594	1.368 ± 1.6389 0.11166	0.667 ± 0.7309 0.57133	1.233 ± 1.2355 0.72369	GAGAGAGAAGTGTCTACTTGGCAATCAAAGATTGTAATTGAA
plasmid_lp56	33903	BB_Q51		3.702 ± 2.4026 0.117423	2.541 ± 1.8232 0.17983	1.42 ± 0.7053 0.27828	1.602 ± 0.8407 0.22691	GATAAAATAAGTCACTAGAACTATATAAACTCAATTGTTTAAAGGAA
plasmid_lp56	34086	BB_Q51		2.372 ± 1.1127 0.059966	1.739 ± 1.2248 0.3058	0.302 ± 0.1011 0.07165	1.093 ± 0.7733 0.84485	AGCTACCCTTTCATGGATGGCTATGTTTAGTGTGAAACCAAAGATACC
plasmid_lp56	34202	BB_Q51		1.783 ± 0.8379 0.229404	1.767 ± 1.1918 0.40088	1.135 ± 0.7361 0.49465	1.147 ± 0.487 0.57271	TTCAATACTAACAGTATTCAAAACCATAGGTAATTCTATTTAACGGCTG
plasmid_lp56	34205	BB_Q51		1.868 ± 0.3236 0.024467	1.499 ± 0.8454 0.3443	0.799 ± 0.2071 0.17898	1.009 ± 0.2656 0.87479	TGTAAGAGATTGGGAGTTGTTGATCTATAACCTATAAGTAAACAA
plasmid_lp56	34206	BB_Q51		1.249 ± 0.3993 0.440262	0.546 ± 0.3942 0.12584	1.088 ± 0.2532 0.65839	1.116 ± 0.3678 0.67184	CATATTCTAACTAACAGTATTCAAAACCATAGGTAATTCTTAAACCG
plasmid_lp56	34234	BB_Q51		2.371 ± 2.8369 0.443999	0.93 ± 0.1091 0.91026	1.289 ± 0.5335 0.49786	1.464 ± 1.5189 0.61383	TGATCAAAATCACTCCAAATCTTACATATTCAAACTAACAGGTTCA
plasmid_lp56	34297	BB_Q51		3.365 ± 1.1827 0.065945	2.213 ± 3.1997 0.56313	0.672 ± 0.5122 0.2756	1.755 ± 0.7964 0.19832	AAAGTCGACTTATCATATGAAACATTGATTATCTAAAGAGATATG
plasmid_lp56	34385	BB_Q51		2.264 ± 1.4737 0.116963	2.556 ± 2.5638 0.30951	0.808 ± 0.4483 0.47658	1.292 ± 0.8741 0.35286	TTTATTTGAAAGAGATAACAAAACCATGATGATGCTTGTGAA
plasmid_lp56	34551	BB_Q51		1.956 ± 0.8192 0.181307	1.946 ± 1.493 0.38839	1.051 ± 0.2343 0.79277	1.11 ± 0.1235 0.11682	TCTTCTTTTGAGAAAACAAACATTCAAACATCATAGAAAGTAA
plasmid_lp56	34851	BB_Q51		3.431 ± 2.5072 0.043007	2.531 ± 3.7191 0.4261	0.997 ± 0.6714 0.99471	1.009 ± 0.8153 0.98944	GGAGTAATTATTACGATTTCTCAAAGGTGTACAAGAACAGTTGAGA
plasmid_lp56	35219	BB_Q52		1.331 ± 0.9379 0.61366	0.979 ± 0.7768 0.8746	0.792 ± 0.6841 0.58027	1.243 ± 0.8531 0.10928	CATCGTTTAAAGAGCAGGCAAATAGTAAATCTAAAGAGACAAGTCGAGA
plasmid_lp56	35440	BB_Q52		0.976 ± 1.1144 0.957844	0.899 ± 1.0038 0.77778	1.049 ± 0.9177 0.85715	1.036 ± 0.8397 0.54671	CATTTAAAGACATTATGCAAGCACACGTAAGAGAACCTTGTACGCAAGT
plasmid_lp56	35445	BB_Q52		2.938 ± 2.0842 0.123142	2.481 ± 3.1003 0.45153	0.806 ± 0.6422 0.71028	0.963 ± 0.6803 0.89366	AAAGACATTATGCAAGCACACGTAAGAGAACCTTGTACGCAAGT
plasmid_lp56	35556	BB_Q52		1.370 ± 0.6568 0.095211	0.326 ± 0.2505 0.16449	0.909 ± 0.7139 0.69414	1.175 ± 0.7389 0.51363	TTAGAGCAACTTGTCTTGTGAAAGTGAATTAAAGGAA
plasmid_lp56	35635	BB_Q52		1.670 ± 0.7944 0.159546	1.399 ± 1.3809 0.60296	1.099 ± 0.3172 0.48495	0.84 ± 0.2027 0.43715	GAGTCACAGAAGAAGAATTGCTACTCGCATTTCTTAAATTATTC
plasmid_lp56	35724	BB_Q52		0.866 ± 1.0617 0.86178	1.547 ± 1.0961 0.40265	0.599 ± 0.7227 0.32073	0.192 ± 0.1948 0.04667	CAAGCGATAAGTAACCTAACAGCAAGGAACTTGTACGCAAGT
plasmid_lp56	36243	BB_Q53		1.531 ± 1.0358 0.204387	1.234 ± 0.5952 0.00164	0.824 ± 0.3512 0.39854	1.02 ± 0.5014 0.93997	ATGCACAAGGAGAGCTGAAAAGAATGGGGAAATGATAAATCTGTTAAT
plasmid_lp56	36477	BB_Q54		4.692 ± 3.3451 0.157777	1.162 ± 0.3079 0.47892	1.25 ± 0.8293 0.56261	1.401 ± 0.4816 0.18731	GGAGCAGCTGAAATTCTGATTCTAACCTTAATTGTGGATTATCATCAAC
plasmid_lp56	36709	BB_Q54		3.603 ± 1.5142 0.000613	1.552 ± 0.6418 0.22212	1.327 ± 0.9022 0.5172	1.204 ± 0.5907 0.57924	TTCTCTTATTGCTGCAAAGCTTGAACATGAAAAGAATAAGCATTAAAC
plasmid_lp56	36894	BB_Q54		1.529 ± 1.151 0.465003	2.361 ± 2.4322 0.36897	0.698 ± 0.596 0.33288	0.754 ± 0.3843 0.52492	ACAAGATACCTTCAAAGTTATTGTAATGAGCAACTACGAGTACTA
plasmid_lp56	36935	BB_Q55		2.405 ± 1.1822 0.055263	1.573 ± 1.5908 0.54041	0.64 ± 0.213 0.17604	0.718 ± 0.311 0.34123	TATCCAAATTCTCCATTAACTCGGATTCTTGTAAACAGATACC
plasmid_lp56	50441	BB_Q0091		3.391 ± 0.7395 5.15E-05	1.104 ± 0.5137 0.55951	1.46 ± 0.7259 0.35144	0.756 ± 0.1708 0.2618	AAACCTGTTAGAATATTGAAAGAAGAATCCAAAAGTAATCTT
plasmid_lp56	50472	IG 1426		1.881 ± 0.8045 0.179795	1.283 ± 0.5755 0.50823	1.135 ± 0.5707 0.60616	0.799 ± 0.3552 0.52518	GCTAAAACAACTAACATGAAGTTGATTCAAACACCTGTTAGAATATCTT
plasmid_lp56	50664	IG 1427		1.050 ± 0.6632 0.946647	1.438 ± 0.9608 0.36175	0.577 ± 0.483 0.08988	0.507 ± 0.1963 0.0949	ATAGGGGCTAATTCTTGGATGGTAATTAACAACTAC

plasmid_lp56	50960	IG 1428	1.928 ± 2.1089	0.210704	0.519 ± 0.5867	0.26573	0.804 ± 0.7808	0.29663	0.684 ± 0.6393	0.67573	TTTATATTTAGTTAATTGTTCTTATTAGGCCTATGAGACACTA
plasmid_lp56	51010	IG 1429	1.959 ± 0.7098	0.006902	2.485 ± 1.359	0.08782	1.152 ± 0.6207	0.36872	1.463 ± 0.6867	0.061	TAGTGTCTCATAGGCCATAAAAGAACATAAAACTAAAAATATATAA
plasmid_lp56	51056	IG 1430	1.660 ± 1.749	0.480967	2.368 ± 2.3884	0.2457	1.269 ± 1.1699	0.66361	0.913 ± 1.0347	0.92321	TAATTTAAATATGGTATCACCCCTTACACCTTAAACACTTTAGA
plasmid_lp56	51163	IG 1431	1.549 ± 0.3761	0.074913	1.877 ± 1.8123	0.47265	1.214 ± 0.2757	0.27175	1.112 ± 0.2622	0.55518	ATGATATTAAGAGAACATCTTAGTATATTACTAAAGGTGTTCTCC
plasmid_lp56	51166	IG 1432	0.622 ± 1.0097	0.705367	0.516 ± 0.6432	0.31041	0.381 ± 0.7367	0.50418	0.871 ± 1.0647	0.80547	TATAGTCTATTAGTGTCAATAATTGTTGTAACATATTAAAGG
plasmid_lp56	51353	BB_Q85	2.012 ± 1.5817	0.367653	0.691 ± 0.4494	0.49228	1.362 ± 0.8993	0.54808	1.632 ± 1.9244	0.58919	TTGAATATCTATCTATGTTAAAGTAAACGCACGGCGTATAAAGCCCCTA
plasmid_lp56	51362	BB_Q85	2.242 ± 2.0813	0.429427	0.701 ± 0.6851	0.63503	0.383 ± 0.2665	0.26278	0.782 ± 0.5729	0.71942	GATATTGCAATACTAGTAAAGATATTGAAATAGACATAGACTTATAATAA
plasmid_lp56	51409	BB_Q85	1.034 ± 0.9973	0.87732	1.062 ± 0.9816	0.82629	0.789 ± 0.7473	0.69429	0.735 ± 0.6695	0.56438	GTATCCAATATTTTGAAATTAGGTCAATGTTGTTAGTGTAAATAAG
plasmid_lp56	51749	IG 1433	1.954 ± 0.5646	0.103424	1.331 ± 0.6742	0.48582	0.856 ± 0.4735	0.66557	1.404 ± 0.4664	0.28808	TATGATTTATAAAATTAAATCCCCCTTAAGTGTTCGTTCAACAATAC
plasmid_lp56	51799	IG 1434	1.619 ± 1.7119	0.601996	1.772 ± 1.643	0.25832	2.134 ± 2.0605	0.19642	1.936 ± 2.0226	0.20657	GAAAAAACAAAACCATACTAGAAAATCTTTAAAAACAGTCAAATAT
plasmid_lp56	51905	IG 1435	1.292 ± 0.674	0.201538	1.045 ± 0.4695	0.84199	0.914 ± 0.5554	0.51956	0.876 ± 0.5306	0.07627	TTCATCTAGATTAAATGATTGTCACATAAGCAGGCATACCCAG
plasmid_lp56	52069	IG 1436	1.385 ± 1.077	0.514898	1.285 ± 1.3103	0.73826	1.621 ± 1.177	0.32104	0.843 ± 0.6685	0.79822	TTATGAAAAAAATCAAAAACAAAGTGCCTAGAAATAGAAAAAACACAAT
plasmid_lp56	52151	BB_Q88	1.211 ± 1.6239	0.804167	1.585 ± 2.4158	0.64593	0.568 ± 0.4882	0.27866	0.696 ± 0.4727	0.49859	ATTCTAACAAATTGTCCTCATTATTGTAGTTGGTATAGTAAACTA
plasmid_lp56	52189	BB_Q88	1.995 ± 1.1786	0.137438	0.795 ± 0.5014	0.47487	0.619 ± 0.4287	0.43144	0.596 ± 0.4473	0.43897	TACCAACTACATAAAATGGAGACAATTGTTAAGAATTATTAGCAACTT
plasmid_lp56	52190	BB_Q88	1.571 ± 1.4973	0.366654	1.668 ± 1.7354	0.37196	0.866 ± 0.9772	0.71408	1.983 ± 1.266	0.02956	TAGATAAACTACTACTATCAGCATTATTGTTAATGCTAGGCATGATT
plasmid_lp56	52481	BB_Q88	1.211 ± 0.9628	0.72228	1.489 ± 1.2763	0.47584	0.736 ± 0.585	0.65952	0.72 ± 0.5959	0.35432	GTTGAATATAAGGTGGTAGTTAATAGTAAATTATTCATTGG
plasmid_lp56	52501	BB_Q88	1.591 ± 1.3063	0.454275	3.075 ± 2.9752	0.32416	1.000 ± 0.2589	0.9917	1.062 ± 0.4755	0.80603	GTTAATAGTAGAATTATATTATCATTTGGTTAGAATAATGGTTAACG

^aSamples with >10 sequences in all 3 glucose cultures

^b% of total reads following growth in specified carbohydrate/% total reads following growth in glucose

^cp-value was obtained using a Ttest

^dA fitness value of 0 indicates that insertions in this gene were not present in the population following growth in GlcNAc

Table S4: Tn-seq and STM results for the transport and lps4 mutants

Location	Position	Locus	Gene	Strand	Mean Fitness Value	Fitness Value Group 1 ^a	Fitness Value Group 2	Group 1			Group 2			STM Data ^b			Plasmid Missing in Arrayed Frozen Stock	Sequence of insertion site			
								# of Sequence Reads	% of Total Sequence Reads	Mouse ^b	Culture ^c			STM Mutant Name	% of Tissues Positive ^d	MFI of All Tissues					
											# of Sequence Reads	% of Total Sequence Reads	Mouse ^b								
chr	41270	BB_0042	phoU	-	0.00	0.000	0.00	3568	0.07	0	0.00	7748	0.15	0	0.00	1057C153	24.79	none	GATGATTATCAGTACGATATTGGAAAGTTTGCAGGAAGAATAATTCGAACT		
chr	48460	BB_0051	-	+	0.01	4.01E-03	0.02	73708	1.52	310	6.08E-03	24814	0.47	263	0.01	T02P01A01	71.28	cp9	TCTATAAAATCACATTAACCTGAAACAAAAAAATATCGAACCT		
chr	11343	BB_0116	malX1	+	9.33E-05	1.87E-04	0.00	20449	0.42	4	7.84E-05	21851	0.42	0	0.00	T08P02E04	38.91	ip28-2, 65	TCTGAAATAACAAAGATCTATAAAAGCCAATAAAAGTAAATAAAAGAG		
chr	113729	BB_0116	malX1	-	4.49E-05	0.00	8.98E-05	26477	0.54	0	0.00	20211	0.39	1	3.44E-05	T067C104	49.57	lps	TGTTGGACTGCCGGAGCATAGGGGTTCAAGGGATTGTCTATG		
chr	114543	BB_0116	malX1	-	8.91E-05	1.42E-04	3.61E-05	87217	1.79	13	2.55E-04	50249	0.96	1	3.44E-05	T067C049	41.67	188.36	none		
chr	141502	BB_0140	besB	+	9.31	5.18	13.45	6511	0.13	35365	0.69	7121	0.14	52790	1.83	T117C33	93.33	3038.00	lps		
chr	142678	BB_0141	besA	-	1.95	0.94	2.95	23359	0.48	23067	0.45	22739	0.43	37005	1.28	T067C059	6.67	45.95	lps		
chr	143042	BB_0142	besC	+	0.00	0.00	0.00	108	0.08	0	0.00	2815	0.00	0	0.00	T107C020	40.00	407.11	lps		
chr	144594	BB_0143	lysA	+	0.08	1.06E-04	1.54E-04	15689	2.23	2896	0.06	15488	0.33	1	3.44E-05	T074C417	13.33	64.91	lps		
chr	154095	BB_0164	-	+	4.99E-05	9.97E-05	0.00	105178	2.11	11	2.15E-04	92377	1.76	0	0.00	T074C009	53.96	cp22-6, 65	GTGCTTAATAATTAAAGGGTTTGGTAGGGCATTCATTAAATTITTTT		
chr	175916	BB_0190	rnfP	-	15.26	10.48	20.04	16329	0.95	50293	0.99	23219	0.44	257625	8.91	T087C379	36.67	290.11	lps		
chr	246891	BB_0241	gfpK	+	15.40	15.56	15.23	27469	0.20	1586807	13.12	56807	1.08	477025	16.50	T087C443	93.33	3579.00	lps		
chr	249604	BB_0243	gfpD	-	0.98	0.56	1.40	24757	5.04	144545	2.83	8.84E-04	1.69	68409	2.37	T047C219	66.67	226.79	none		
chr	325023	BB_0318	mgmA	+	1.87E-04	9.94E-05	2.78E-04	29966	0.62	5	5.88E-05	6.53E-03	0.12	1	3.44E-05	T107C055	0.00	14.39	lps		
chr	335333	BB_0328	oppA1	-	3.52	1.70	5.34	27553	0.56	48801	0.96	21653	0.41	63789	2.21	T037C00	ND	none	TGTTGAGATTATTAATGATCATCATGAGCTTTT		
chr	337852	BB_0329	oppA2	-	8.03E-05	1.61E-04	0.00	11871	0.24	2	3.92E-05	1.01E-04	0.19	0	0.00	T117C145	20.00	186.39	lps		
chr	421166	BB_0408	fruA1	+	0.05	2.25E-04	0.11	16956	0.35	4	7.84E-05	2.14E-04	0.41	1294	0.04	T074C473	0.00	19.75	lps		
chr	586734	BB_0573	-	9.32E-03	0.02	0.00	1995	0.39	7	7.65E-04	1.11E-02	0.23	1762	0.00	T067C301	23.00	24.04	lps			
chr	630318	BB_0604	icp	-	0.00	0.00	0.00	178	3.66E-03	0	0.00	1.58E-02	3.01E-03	0	0.00	T107P01A01	0.00	24.71	ip28		
chr	651136	BB_0629	fruA2	-	0.00	0.00	0.00	11380	0.23	10897	0.00	9.50E-04	0.18	0	0.00	T107P02A09	0.00	34.93	none		
chr	655200	BB_0630	fruA3	-	1.41	0.51	1.31	11166	0.16	31423	0.02	10899	1.30	86829	1.00	T074C459	53.91	100.00	lps		
chr	675846	BB_0637	rnbC1	+	0.00	0.00	0.00	6226	0.13	0	0.00	3250-3	0.04	0	0.00	T047C451	6.57	39.77	lps		
chr	676847	BB_0638	rnbC2	-	3.63E-05	0.00	7.27E-05	22422	0.46	0	0.00	2.50E-04	0.48	1	3.44E-05	T107C062	0.00	28.86	none		
chr	684113	BB_0645	rnsG	+	0.00	0.00	0.00	10825	0.22	0	0.00	8.73E-03	0.17	0	0.00	T107C291	0.00	25.18	ip5, ip28-2		
chr	775398	BB_0733	prbA	+	9.38E-05	1.20E-04	0.00	70718	1.45	5	9.81E-05	3.02E-05	0.58	2	6.92E-05	T119P01A09	0.00	34.77	lps		
chr	861758	BB_0818	panF	-	2.11	2.86	2.16	8616	0.00	4496	0.09	4.16E-03	0.08	6566	0.23	T067C026	66.67	535.18	cp9, ip28		
plasmid	cp26	35042	BB_0804	chbC	-	0.05	0.09	1.40E-03	87262	1.70	8071	0.16	1.72E-02	1.28	133	0.23	T067P01C04	83.33	1795.95	ip21, ip5	
plasmid	cp26	3542	BB_0804	chbC	-	1.79	2.95	0.63	74613	1.53	23178	4.53	123342	2.35	42897	1.48	T097C403	86.67	1067.25	lps	
plasmid	cp26	4228	BB_0805	chbA	-	0.56	0.15	0.98	69686	1.43	10628	0.21	12125	2.31	65357	4.02	T057C26	73.33	1921.04	cp9, ip5	
plasmid	cp26	19120	BB_0822	chbA	+	9.93E-05	1.81E-04	2.71E-05	84083	1.73	30	3.14E-04	210745	4.02	2	6.92E-05	T077C00	0.00	28.14	cp9	
plasmid	cp26	25105	BB_0829	malX2	+	0.01	0.00	0.00	84738	1.32	7444	0.08	10675	2.04	7807	0.09	T077C009	66.67	787.09	none	
plasmid	cp26	32302	BB_0830	malX2	+	3.75E-05	6.08E-05	1.05E-05	151	0.51	10656	0.06	1.56E-04	0.09	1.00	0.00	T047C011	1.57	1.00	lps	
plasmid	ip5	10646	BB_0836	chbA	-	0.00	0.00	0.00	151	0.73	20	6364	0.00	19241	0.37	16191	0.56	T077C045	100.00	425.00	lps
plasmid	ip5	2388	BB_0840	-	0.16	0.32	0.00	14004	0.19	2508	0.05	14913	0.28	0	0.00	T087C141	6.67	22.82	lps		
plasmid	ip5	2796	BB_0840	-	5.46	5.86	5.05	55718	1.15	34245	6.72	84336	1.61	23153	8.13	T097C181	93.33	1360.64	lps		
plasmid	ip5	4123	BB_0840	-	0.19	0.37	6.15E-05	31343	0.64	12170	0.24	29505	0.56	1	3.44E-05	T107C188	53.33	478.43	lps		
plasmid	ip5	4249	BB_0845	-	0.07	2.21E-04	1.58	17280	0.36	4	7.84E-05	21021	0.40	1685	0.06	T047C41	46.67	108.46	cp9		
plasmid	ip5	5049	BB_0807	chpA1	+	1.16	1.31	14269	0.26	52705	0.27	17957	0.34	12974	0.45	T07C018	93.33	2440.71	lps		
plasmid	ip5	5454	BB_0810	-	0.14	0.34	0.00	14241	0.03	3985	0.08	4291	0.08	0	0.00	T077C152	6.67	38.29	cp9, ip28		
plasmid	ip5	5658	BB_0810	-	0.82	1.50	1.41	12641	0.26	19929	0.31	143775	2.74	11481	0.40	T087C084	20.00	82.29	ip21		
plasmid	ip5	5658	BB_0810	-	1.75	1.39	2.11	6205	1.28	10500	1.77	78344	1.49	91132	3.15	T057C040	26.67	203.46	lps		
plasmid	ip5	7241	BB_0811	-	2.44	2.17	2.72	40406	1.11	122972	2.41	75040	1.43	112335	3.88	T07C070	26.67	16.04	lps		
plasmid	ip5	7241	BB_0811	-	0.40	0.34	0.05	10254	0.51	10464	0.08	10254	0.00	10254	0.00	T047C011	1.57	1.00	lps		
plasmid	ip5	10646	BB_0813	-	0.00	0.00	0.00	151	0.73	20	6364	0.00	19241	0.37	16191	0.56	T077C045	100.00	425.00	lps	
plasmid	ip5	14845	BB_0813	-	5.39	3.71	7.07	22335	0.46	68685	1.70	15145	0.60	122860	4.25	T077C167	6.67	113.54	cp9, ip28		
plasmid	ip5	16551	BB_0814	-	6.24-03	0.01	1.84-05	72866	1.50	948	0.02	13633	2.55	6	1.20-04	T097C080	0.00	159.3	cp9, ip28, ip29		
plasmid	ip5	16552	BB_0814	-	0.75	0.84	0.65	55982	1.23	53062	1.04	66480	1.27	23793	0.82	T117C43	40.00	1575.82	ip21, cp9		
plasmid	ip5	16569	BB_0823	chpA	+	0.62	0.47	0.77	168180	3.46	18023	0.25	57977	1.11	4	1.38-04	T07C190	26.67	387.00	cp9	
plasmid	ip5	16452	BB_0824	chpA	-	0.54	0.82	0.35	10506	0.55	1235	0.19	85609	1.63	1.38E-04	0.04	T070C073	0.00	22.57	ip21, cp9	
plasmid	ip5	16504	BB_0824	chpA	-	0.79	0.65	0.00	16931	1.79	68052	1.33	99711	1.90	34899	1.22	T07C188	13.33	17.11	none	
plasmid	ip5	2244	BB_0824	-	0.07	0.61	0.07	26955	0.55	17375	0.34	27116	0.71	1486	0.05	T047C322	73.33	776.71	cp9		
plasmid	ip5	2244	BB_0824	-	0.16	0.17	0.14	27497	0.57	4912	0.10	20549	0.39	1585	0.05	T057C82	40.00	85.21	lps		
plasmid	ip5	32713	BB_0848	-</td																	

Table S5. Tn-seq results for mutants not expected in mouse Tn-seq screen

Location	Insertion Site	Gene Locus	Gene Name	Strand	Mean Fitness Value	Group 1 Culture ^a				Fitness Value ^c	Group 2 Culture ^a				Fitness Value
						# of Sequence Reads	% of Total Sequence Reads	# of Sequence Reads	% of Total Sequence Reads		# of Sequence Reads	% of Total Sequence Reads	# of Sequence Reads	% of Total Sequence Reads	
chromosom	16023	BB_0017		+	2.33E-05	20443	0.42	1	1.96E-05	4.66E-05	19876	0.38	0	0.00	0.00
chromosom	16404	BB_0017		-	0.00 ^d	1146	0.02	0	0.00	0.00	3470	0.07	0	0.00	0.00
chromosom	48358	BB_0051		+	0.77	83829	1.72	72985	1.43	0.83	18577	0.35	7230	0.25	0.71
chromosom	162049	BB_0161		-	16.10	13539	0.28	85169	1.67	6.00	8990	0.17	129877	4.49	26.21
chromosom	203963	BB_0202		+	0.00	3909	0.080	0	0.00	0.00	2487	0.05	0	0	0
chromosom	210905	BB_0208		+	0.00	3974	0.08	0	0.00	0.00	2716	0.05	0	0.00	0.00
chromosom	247158	BB_0241	glpK	-	0.19	4864	0.100	1952	0.04	0.38	3547	0.07	1	3.46E-05	5.11E-04
chromosom	259760	BB_0252		-	1.43E-05	33239	0.68	1	1.96E-05	2.87E-05	14792	0.28	0	0.00	0.00
chromosom	259760	BB_0252		-	1.43E-05	33239	0.683	1	1.96E-05	2.87E-05	14792	0.28	0	0	0
chromosom	278726	BB_0265		-	0.00	243	5.00E-03	0	0.00	0.00	100	1.91E-03	0	0.00	0.00
chromosom	335795	BB_0328		+	0.69	58	1.19E-03	46	9.02E-04	0.76	55	1.05E-03	19	6.57E-04	0.63
chromosom	335960	BB_0328		-	0.98	946	0.02	1092	0.02	1.10	981	0.02	466	0.02	0.86
chromosom	336240	BB_0328		-	0.86	681	0.01	682	0.01	0.96	757	0.01	322	0.01	0.77
chromosom	336408	BB_0328		+	0.92	216	4.44E-03	242	4.75E-03	1.07	202	3.85E-03	86	2.97E-03	0.77
chromosom	336495	BB_0328		+	0.85	23	4.73E-04	22	4.31E-04	0.91	23	4.38E-04	10	3.46E-04	0.79
chromosom	387418	BB_0377	luxS	-	2.75	959	0.02	5529	0.11	5.50	1407	0.03	0	0.00	0.00
chromosom	433284	BB_0420		-	0.00	63085	1.30	3	5.88E-05	4.54E-05	41195	0.79	0	0.00	0.00
chromosom	476098	BB_0456		+	0.00	52	1.07E-03	0	0.00	0.00	645	0.01	0	0.00	0.00
chromosom	576468	BB_0563		-	0.47	33503	0.69	22323	0.44	0.64	36952	0.70	6030	0.21	0.30
chromosom	609976	BB_0591		-	0.66	25027	0.51	4437	0.09	0.17	14410	0.27	9181	0.32	1.16
chromosom	633518	BB_0607	pcrA		0.00	58	1.19E-03	0	0.00	0.00	1138	0.02	0	0.00	0.00
chromosom	644034	BB_0616		-	5.72E-05	8335	0.171	1	1.96E-05	1.14E-04	4126	0.08	0	0	0
chromosom	675579	BB_0637		-	0.00	1404	0.029	0	0.00	0.00	1696	0.03	0	0	0
chromosom	682871	BB_0644		+	3.55E-04	3010	0.06	0	0.00	0.00	2555	0.05	1	3.46E-05	7.10E-04
chromosom	708138	BB_0669		+	0.00	208	4.28E-03	0	0.00	0.00	207	3.95E-03	0	0.00	0.00
chromosom	761926	BB_0723		+	0.05	2812	0.06	0	0.00	0.00	2795	0.05	140	4.84E-03	0.09
chromosom	771307	BB_0731		+	0.00	295	0.01	0	0.00	0.00	164	3.13E-03	0	0.00	0.00
chromosom	774466			+	0.00	1060	0.02	0	0.00	0.00	99	1.89E-03	0	0.00	0.00
chromosom	815254	BB_0773		-	4.34E-03	59435	1.22	289	0.01	4.64E-03	68609	1.31	153	0.01	4.05E-03
chromosom	876597	BB_0830		+	0.01	47911	0.99	61	1.20E-03	1.21E-03	28995	0.55	312	0.01	0.02
chromosom	888240			-	0.00	1584	0.03	0	0.00	0.00	1482	0.03	0	0.00	0.00
chromosom	906090	BB_0848a		+	0.24	10740	0.22	4601	0.09	0.41	7363	0.14	266	0.01	0.07
plasmid_cp32-4	23395	BB_R36	bppA	+	0.32	32131	0.66	4110	0.08	0.12	42482	0.81	12192	0.42	0.52
plasmid_cp32-6	1185	BB_M01		-	2.73	1078	0.02	6163	0.12	5.45	1049	0.02	0	0.00	0.00
plasmid_cp32-7	5135	BB_O07		+	0.09	14957	0.31	2337	0.05	0.15	29260	0.56	601	0.02	0.04
plasmid_cp9	8639	BBC12		-	0.31	23116	0.48	2956	0.06	0.12	30224	0.58	8237	0.28	0.49
plasmid_lp17	12323	BB_D20		-	0.00	351	0.01	0	0.00	0.00	436	0.01	0	0.00	0.00
plasmid_lp21	11096			+	0.26	57	1.17E-03	20	3.92E-04	0.33	72	1.37E-03	7	2.42E-04	0.18
plasmid_lp28-1	4837	BB_F10		+	0.00	1196	0.02	0	0.00	0.00	1601	0.03	0	0.00	0.00
plasmid_lp28-1	8473	BB_F16		+	4.64E-04	1028	0.02	1	1.96E-05	9.28E-04	2808	0.05	0	0.00	0.00
plasmid_lp28-2	13899	BB_G17		-	1.37	4297	0.09	12369	0.24	2.75	5414	0.10	0	0.00	0.00
plasmid_lp28-2	19829	BB_G24		-	5.35	14278	0.29	38441	0.75	2.57	15152	0.29	67868	2.35	8.13
plasmid_lp28-3	20826	BB_H30		+	0.00	173	3.56E-03	0	0.00	0.00	1589	0.03	0	0.00	0.00
plasmid_lp28-3	21777	BB_H32		-	0.00	1645	0.03	0	0.00	0.00	1296	0.02	0	0.00	0.00
plasmid_lp36	21081	BB_K32		+	0.00	1181	0.02	0	0.00	0.00	3674	0.07	0	0.00	0.00
plasmid_lp36	21996	BB_K34		+	3.15E-04	1057	0.02	0	0.00	0.00	2883	0.05	1	3.46E-05	0.00
plasmid_lp36	24374	BB_K39		-	1.82E-04	10482	0.22	4	7.84E-05	3.64E-04	20326	0.39	0	0.00	0.00
plasmid_lp36	25961	BB_K41		-	0.00	975	0.02	0	0.00	0.00	1208	0.02	0	0.00	0.00
plasmid_lp36	30899	BB_K48		+	0.67	1045	0.02	0	0.00	0.00	3219	0.06	2364	0.08	1.33
plasmid_lp38	7922	BB_J11		+	0.00	10833	0.22	0	0.00	0.00	8687	0.17	0	0.00	0.00
plasmid_lp54	5588	BB_A08		-	0.00	455	0.009	0	0.00	0.00	481	0.01	0	0	0
plasmid_lp54	15220	BB_A22		+	7.99E-05	41768	0.859	7	1.37E-04	1.60E-04	43367	0.83	0	0	0
plasmid_lp54	29484	BB_A43		-	1.94	17	3.50E-04	53	1.04E-03	2.97	34	6.48E-04	17	5.88E-04	0.91
plasmid_lp54	43967	BB_A65		-	0.69	20740	0.426	1460	0.03	0.07	26966	0.51	19388	0.67	1.30
plasmid_lp54	44656			+	1.49	11724	0.24	25432	0.50	2.07	17088	0.33	8519	0.29	0.90
plasmid_lp54	45178	BB_A66		+	7.61E-05	6267	0.129	1	1.96E-05	1.52E-04	4912	0.09	0	0	0
plasmid_lp54	46055			-	0.00	1903	0.04	0	0.00	0.00	6513	0.12	0	0.00	0.00
plasmid_lp54	48155	BB_A69		+	0.39	31	6.37E-04	14	2.75E-04	0.43	31	0.00	6	2.08E-04	0.35
plasmid_lp54	52311	BB_A74	osm28	+	0.00	241	0.005	0	0.00	0.00	954	0.02	0	0	0

^a Bacterial population recovered from the mouse inoculum grown in culture^b Bacterial population isolated from organ cultures from infected mice^c % of total reads in population recovered from mice/% total reads in the cultured inoculum^d A fitness value of 0 indicates the insertion sequence was not present in the population following mouse infection

IG, Intergenic

Table S6. Primer sequences used in this study

Primer	Sequence
p408(KpnI)-F	5'-GGGGTACCCAACTGATTATTTAATAATATAAAAATTGTTTACC-3'
ppb407(XbaI)-R	5'-GCTCTAGAGCTTAATTAAAACCAGCAATAAAGC-3'
pMargent1	5'-CGGCAAGTTCATCC TTAGGAGACCGGGG-3'
olj376	5'-GTGACTGGAGTTC AGACGTGTGCTCTTCCGATCTGGGGGGGGGGGGGG-3'
pMargent2	5'-AATGATACGGCGACCACCGAGATCTACACTCTTCCGGGGACTTATCAGCCAACCTGTTA-3'
Indexing Primer	5'-CAAGCAGAAGACGGCATACGAGATNNNNNGTACTGGAGTTCAGACGTGTGCTCTCCGATCT-3'
pMargent3	5'-ACACTCTTCCGGGGACTTATCAGCCAACCTGTTA-3'
recA qPCR For	5'-GTGGATCTATTGATTAGATGAGGCTCTCG-3'
recA qPCR Rev	5'-GCCAAAGTTCTGCAACATTAACACCTAAAG-3'
aacC1 qPCR For	5'-GTTGCCGGATCAAGAGCTA-3'
aacC1 qPCR Rev	5'-GCAGAGCGAGGTATGTAGG-3'
aadA qPCR For	5'-GGCTTGATGAAACAACGGG-3'
aadA qPCR Rev	5'-GTCGTCGTGCACAACAATGG-3'
ermC qPCR For	5'-GAGGTGTAATTCTGTAACTGCC-3'
ermC qPCR Rev	5'-TGGAATTATCGTGATCAACAAG-3'
bb408_For	5'-GGATCTTAATTCCGCCCAATCATA-3'
bb408_Rev	5'-GGATCCTGTTAAGAAAATACAAGTGTGGAG-3'
bbb29_For	5'-GCCTTCATGCTCCAATAGCAC-3'
bbb29_Rev	5'-TCCGCCAGAAAATGTTAGCCA-3'
rrp1_For	5'-AAAGATAAAGCTTTGAAGCAGAGA-3'
rrp1_Rev	5'-TCAAAAAGAATAGCAACTGGCAA-3'