

Table S1. Clinical and Demographic Characteristics of Patients Across Four Independent Cohorts.

Characteristic		Age (years), median (IQR)	Female sex, n (%)	ACPA positivity, n (%)	ESR (median, IQR)	CRP (median, IQR)
Cohort A	RA (n=76)	60 (53–66)	61 (80.2%)	53 (70.0%)	60.00 (37.60–85.75)	32.50 (14.50–54.70)
	OA (n=19)	66 (64–71)	15 (78.9%)	0 (0%)	23.00 (15.75–41.50)	17.45 (4.62–65.75)
	HC (n=27)	56 (50–60)	19 (70.3%)	0 (0%)	N/A	N/A
Cohort B	RA (n=40)	52 (42–62)*	27 (67.5%)	25 (62.5%)	44 (28–75)*	24.8 (8.5–65)*
Cohort C	HC (n=29)	52 (40–60)*	20 (69.0%)	0 (0%)	N/A	N/A
	RA (n=37)	56 (52–60)*	29 (78.4%)	37 (100%)	33 (22–45)*	12.1 (7.5–22.5)*
	HC (n=31)	55 (52–59)*	24 (77.4%)	0 (0%)	N/A	N/A
Cohort D	RA, Untreated (n=94)	51 (43-57)	73 (77.7%)	62 (66.0%)	44.00 (23.00-67.00)	14.15 (6.20-38.62)
	RA, Treated (n=41)	53 (41-57)	34 (82.9%)	5 (12.2%)	20.00 (10.00-29.00)	3.34 (1.70-6.60)
	HC (n=97)	43 (37-48)	67 (69.1%)	0 (0.0%)	N/A	N/A

Note: * Values are estimated interquartile ranges (IQR) derived from the reported median and range. The estimation follows the formula: $IQR \approx Range \times 0.34$.

Abbreviations: RA, rheumatoid arthritis; OA, osteoarthritis; HC, healthy controls; ACPA, anti-citrullinated protein antibodies; ESR, erythrocyte sedimentation rate; CRP, C-reactive protein; IQR, interquartile range; N/A, not available.

Table S2. Statistical comparison of alpha diversity metrics across cohorts.

Cohort	Groups	Shannon Index (<i>P</i>)	Simpson Index (<i>P</i>)	Observed Richness (<i>P</i>)	Pielou's Evenness (<i>P</i>)
A	3	0.09	0.10	<0.01	0.18
B	2	0.87	0.95	0.54	0.88
C	2	0.46	0.35	0.65	0.41
D	3	0.43	0.45	0.24	0.58

Note: Data represent the *P*-values derived from statistical comparisons across groups within each cohort (e.g., Kruskal-Wallis test for Cohorts A and D with 3 groups; Wilcoxon rank-sum test for Cohorts B and C with 2 groups). *P* < 0.05 is considered statistically significant.

Abbreviations: P, probability value.

Table S3. Statistical analysis of beta diversity using PERMANOVA and beta dispersion tests.

Cohort	No. of Groups	PERMANOVA			Beta dispersion	
		R ²	F	<i>P</i> -value	F	<i>P</i> -value
A	3	0.04	2.46	<0.01	7.13	<0.01
B	2	0.02	1.17	0.31	4.77	0.03
C	2	0.03	2.32	0.02	2.10	0.15
D	3	0.01	1.16	0.26	0.53	0.59

Note: *P*-values were calculated based on Permutational Multivariate Analysis of Variance (PERMANOVA) using 999 permutations to assess the dissimilarities in microbial community structure between groups. *P* < 0.05 is considered statistically significant.

Abbreviations: R², coefficient of determination; F, F-statistic by permutation; *P*, probability value.

Table S4. Meta-analysis of differentially abundant bacterial species across metagenomic cohorts.

Species	Meta log2FC	SE	95% CI Lower	95% CI Upper	Z-score	P-value	Tau2	I2 (%)	H2	Cochran's Q	P (heterogeneity)	No. of Contributing Cohorts	Shift	Mean log2CPM
Limosilactobacillus fermentum specI_v2_Cluster10 50*	3.42	0.44	2.56	4.29	7.73	<0.01	0.00	0.00	1.00	0.07	0.785	2	Up	5.49
Limosilactobacillus fermentum specI_v2_Cluster48 55*	3.26	0.43	2.41	4.10	7.53	<0.01	0.00	0.00	1.00	0.10	0.748	2	Up	5.36
Scardovia wiggisiae	1.36	0.26	0.85	1.86	5.27	<0.01	0.00	0.00	1.00	2.53	0.283	3	Up	2.09
Lachnospiraceae bacterium	0.89	0.17	0.56	1.22	5.27	<0.01	0.00	0.00	1.00	2.00	0.572	4	Up	7.58
Leuconostoc mesenteroides	1.76	0.35	1.07	2.46	4.98	<0.01	0.00	0.00	1.00	0.77	0.380	2	Up	3.01
Ethanoligenens harbinense	-1.22	0.25	-1.71	-0.73	-4.87	<0.01	0.00	0.00	1.00	1.37	0.713	4	Down	4.23
Serratia liquefaciens	-1.59	0.34	-2.25	-0.92	-4.68	<0.01	0.07	30.38	1.44	1.44	0.231	2	Down	2.15
Leuconostoc citreum	1.58	0.34	0.91	2.24	4.66	<0.01	0.00	0.00	1.00	0.47	0.493	2	Up	3.27
Eggerthella sp.	0.63	0.14	0.36	0.90	4.55	<0.01	0.00	0.00	1.00	2.21	0.530	4	Up	4.78
Lacrimispora saccharolytica	-0.74	0.17	-1.06	-0.41	-4.42	<0.01	0.01	11.63	1.13	4.27	0.234	4	Down	8.91
Staphylococcus aureus	1.22	0.29	0.65	1.80	4.17	<0.01	0.19	61.56	2.60	7.36	0.061	4	Up	4.84
Streptococcus intermedius	1.37	0.33	0.72	2.03	4.12	<0.01	0.22	54.19	2.18	6.83	0.078	4	Up	2.55
Selenomonas sp.	-1.86	0.46	-2.76	-0.96	-4.06	<0.01	0.19	39.65	1.66	1.66	0.198	2	Down	3.50
Bacteroides fragilis	1.12	0.28	0.58	1.65	4.05	<0.01	0.00	0.00	1.00	0.55	0.909	4	Up	14.64

Xanthomonas euvesicatoria	2.17	0.54	1.11	3.23	4.02	<0.01	0.00	0.00	1.00	0.35	0.553	2	Up	3.07
Eubacterium callanderi	0.59	0.15	0.29	0.88	3.91	<0.01	0.00	0.01	1.00	3.16	0.367	4	Up	6.85
Thomasclavelia spiroformis	1.74	0.47	0.82	2.66	3.70	<0.01	0.50	63.74	2.76	9.35	0.025	4	Up	3.76
Streptococcus agalactiae	1.05	0.29	0.49	1.62	3.65	<0.01	0.00	0.00	1.00	0.16	0.689	2	Up	1.25
Actinomyces viscosus	1.47	0.41	0.66	2.28	3.55	<0.01	0.40	69.81	3.31	7.97	0.047	4	Up	1.97
Actinomyces sp.	0.38	0.11	0.16	0.60	3.43	<0.01	0.00	0.00	1.00	0.93	0.819	4	Up	4.70
Pseudomonas syringae	2.10	0.62	0.90	3.31	3.41	<0.01	0.12	16.06	1.19	1.19	0.275	2	Up	2.97
Streptococcus gordonii	1.38	0.41	0.57	2.18	3.33	<0.01	0.38	64.18	2.79	7.54	0.056	4	Up	4.61
Anaerostipes caccae	-1.28	0.39	-2.05	-0.52	-3.29	<0.01	0.00	0.00	1.00	0.02	0.894	2	Down	3.18
Butyricicoccus pulliaecorum	1.05	0.32	0.42	1.67	3.29	<0.01	0.21	59.15	2.45	7.55	0.056	4	Up	3.44
Phocaicola dorei	-0.72	0.24	-1.18	-0.26	-3.04	<0.01	0.06	26.91	1.37	3.43	0.330	4	Down	16.51
Streptococcus vestibularis	1.29	0.44	0.43	2.16	2.94	<0.01	0.42	60.74	2.55	8.19	0.042	4	Up	5.15
Brachyspira pilosicoli	-1.37	0.47	-2.30	-0.44	-2.89	<0.01	0.53	67.96	3.12	10.21	0.017	4	Down	4.34
Parascardovia denticolens	2.02	0.71	0.63	3.41	2.86	<0.01	0.91	66.97	3.03	6.01	0.050	3	Up	2.39
[Ruminococcus] lactaris	1.00	0.35	0.31	1.70	2.83	<0.01	0.00	0.00	1.00	0.00	0.966	2	Up	2.62
Megasphaera elsdenii	1.92	0.70	0.54	3.30	2.73	<0.01	0.95	53.10	2.13	6.43	0.092	4	Up	8.55

Butyrivibrio fibrisolvens	-0.60	0.22	-1.04	-0.17	-2.73	<0.01	0.02	10.81	1.12	1.91	0.385	3	Down	1.90
Streptococcus oralis	0.98	0.37	0.26	1.70	2.68	<0.01	0.17	42.97	1.75	3.38	0.184	3	Up	1.49
Alkaliphilus oremlandii	-0.84	0.31	-1.45	-0.22	-2.68	<0.01	0.08	31.81	1.47	1.47	0.226	2	Down	0.73
Salmonella bongori	0.73	0.27	0.19	1.26	2.67	<0.01	0.00	0.00	1.00	2.17	0.538	4	Up	4.89
Ligilactobacillus ruminis	-1.21	0.47	-2.13	-0.29	-2.57	0.01	0.45	56.36	2.29	7.23	0.065	4	Down	5.93
Dorea longicatena	0.62	0.25	0.13	1.10	2.47	0.01	0.08	33.41	1.50	4.41	0.220	4	Up	7.04
Faecalibacterium prausnitzii	-0.39	0.16	-0.70	-0.08	-2.44	0.01	0.01	8.78	1.10	3.00	0.392	4	Down	8.60
Streptococcus sp. specI_v2_Cluster13 99**	1.56	0.65	0.28	2.84	2.40	0.02	0.85	77.88	4.52	7.31	0.026	3	Up	3.52
Gallibacterium anatis	1.82	0.77	0.31	3.33	2.36	0.02	0.82	67.47	3.07	3.07	0.080	2	Up	2.50
Streptococcus sanguinis	0.87	0.37	0.14	1.60	2.34	0.02	0.32	66.07	2.95	8.16	0.043	4	Up	4.25
Pseudoselenomonas ruminantium	-2.37	1.02	-4.37	-0.37	-2.32	0.02	1.43	77.20	4.39	4.39	0.036	2	Down	4.91
Selenomonas sputigena	-2.08	0.90	-3.85	-0.31	-2.31	0.02	1.11	76.21	4.20	4.20	0.040	2	Down	3.67
Corynebacterium jeikeium	1.21	0.54	0.16	2.27	2.26	0.02	0.54	67.85	3.11	6.88	0.032	3	Up	2.96
Lachnoclostridium phytofermentans	-0.36	0.16	-0.68	-0.05	-2.25	0.02	0.00	0.00	1.00	0.35	0.951	4	Down	3.71
Desulfurispirillum indicum	2.06	0.94	0.23	3.89	2.20	0.03	1.06	61.66	2.61	2.61	0.106	2	Up	2.57

Roseburia hominis	-0.53	0.25	-1.01	-0.04	-2.14	0.03	0.14	63.85	2.77	9.44	0.024	4	Down	13.24
Streptococcus sp. specI_v2_Cluster51 25**	0.76	0.36	0.06	1.47	2.13	0.03	0.27	59.16	2.45	7.31	0.063	4	Up	2.41
Allobaculum stercoricanis	-0.55	0.26	-1.07	-0.04	-2.10	0.04	0.16	64.65	2.83	9.61	0.022	4	Down	5.57
Ruminococcus callidus	-0.86	0.44	-1.72	-0.01	-1.98	0.05	0.29	39.94	1.66	4.95	0.175	4	Down	5.81

Note: Meta-analysis was performed using random-effects models with restricted maximum likelihood (REML) estimation across metagenomic cohorts.

Table S5. Meta-analysis of variable structural variants across metagenomic cohorts.

SV ID	Meta SMD	SE	95% CI Lower	95% CI Upper	P-value	P (heterogeneity)	No. of Contributing Cohorts
Bacteroides uniformis: 3885_3889	-0.30	0.13	-0.56	-0.05	0.02	0.79	4
Bacteroides uniformis: 3889_3890	-0.29	0.13	-0.55	-0.03	0.03	0.86	4
Bacteroides uniformis: 3884_3885	-0.26	0.13	-0.52	0.00	0.05	0.88	4
Bacteroides uniformis: 3880_3883	-0.34	0.13	-0.60	-0.09	0.01	0.75	4
Oscillibacter sp. : 1889_1891	-0.48	0.19	-0.86	-0.10	0.01	0.96	4
Oscillibacter sp. : 1721_1726;1728_1731;210 8_2111;2111_2113	-0.46	0.19	-0.84	-0.07	0.02	0.56	4
Oscillibacter sp. : 1731_1732	-0.48	0.22	-0.92	-0.04	0.03	0.33	4
Oscillibacter sp. : 1726_1728	-0.51	0.25	-0.99	-0.03	0.04	0.25	4
Oscillibacter sp. : 1784_1785	-0.52	0.19	-0.90	-0.14	0.01	0.93	4
Segatella copri: 77_78	-0.58	0.28	-1.13	-0.03	0.04	0.57	4
Faecalibacterium prausnitzii: 2481_2482	0.29	0.15	0.00	0.58	0.05	0.50	4
Faecalibacterium prausnitzii: 1382_1385;1385_1387	-0.37	0.15	-0.66	-0.08	0.01	0.99	4

Ruminococcus sp.: 768_769	-0.94	0.43	-1.78	-0.10	0.03	0.53	2
Parabacteroides merdae: 2404_2410;2410_2422;242 2_2423	-0.35	0.17	-0.69	-0.01	0.04	0.61	4
Parabacteroides merdae: 782_783;2923_2924	-0.45	0.17	-0.79	-0.11	0.01	0.66	4
Roseburia intestinalis: 1845_1851	0.45	0.20	0.05	0.84	0.03	0.51	4
Anaerostipes hadrus: 130_132	0.63	0.32	0.01	1.26	0.05	0.46	2
Anaerostipes hadrus: 2814_2816	0.63	0.32	0.01	1.26	0.05	0.92	2
Ruminococcus callidus: 2759_2760	-0.72	0.32	-1.35	-0.10	0.02	0.97	4
Ruminococcus callidus: 2758_2759;2760_2767	-0.65	0.32	-1.28	-0.03	0.04	0.93	4
Ruminococcus callidus: 2440_2442;2447_2450;245 0_2451	-0.70	0.32	-1.33	-0.07	0.03	0.83	4
Ruminococcus bromii: 97_103	0.59	0.28	0.04	1.14	0.04	0.07	4
Phocaeicola massiliensis: 4194_4195;4195_4196;419 6_4197;4197_4198;4198_4 199;4199_4200;4200_4201; 4201_4202	-0.57	0.24	-1.04	-0.10	0.02	0.91	4
Bacteroides fragilis: 4781_4788	-0.79	0.31	-1.40	-0.18	0.01	0.76	4

Alistipes shahii: 2252_2255;2255_2257;2257_2259;2259_2262;2262_2264;2265_2266	-0.38	0.18	-0.73	-0.03	0.03	0.48	4
[Ruminococcus] lactaris: 1750_1753	1.05	0.38	0.32	1.79	0.01	0.51	3
Parabacteroides distasonis: 4288_4291;4291_4293	0.36	0.16	0.04	0.67	0.03	0.32	4
Bacteroides caccae: 1351_1363	-0.41	0.18	-0.77	-0.05	0.03	0.97	4
Agathobacter rectalis: 585_586	-0.32	0.16	-0.64	-0.01	0.04	0.46	4
Agathobacter rectalis: 461_469	-0.38	0.16	-0.70	-0.07	0.02	0.79	4
Agathobacter rectalis: 3036_3037	-0.39	0.16	-0.71	-0.08	0.01	0.55	4
Agathobacter rectalis: 3102_3105;3105_3106	-0.34	0.16	-0.65	-0.03	0.03	0.85	4
Bacteroides xylanisolvens: 3046_3048;3378_3379	0.44	0.18	0.08	0.80	0.02	0.89	4
Bacteroides xylanisolvens: 4246_4248;4260_4262;4265_4267;4268_4270;4271_4280	0.37	0.18	0.01	0.73	0.04	0.79	4

Note: Meta-analysis was performed using random-effects models with restricted maximum likelihood (REML) estimation across

Table S6. Meta-analysis of deletion structural variants across metagenomic cohorts.

SV ID	Meta OR	95% CI Lower	95% CI Upper	P-value	P (heterogeneity)	No. of Contributing Cohorts
Blautia wexlerae: 1054_1055;1598_1602	0.25	0.09	0.71	0.01	0.71	2
Phascolarctobacterium sp.: 0_1;228_230;230_244;340_3 41;891_892	2.20	1.05	4.60	0.04	0.52	2
Oscillibacter sp.: 1356_1357	0.30	0.11	0.81	0.02	0.48	2
Oscillibacter sp.: 557_558;1131_1132	2.26	1.04	4.91	0.04	0.84	2
Anaerostipes hadrus: 1104_1111;1111_1112	0.24	0.07	0.86	0.03	0.79	2
Anaerostipes hadrus: 443_444;903_904	0.09	0.02	0.39	0.00	0.98	2
Anaerostipes hadrus: 895_896;897_898	0.21	0.05	0.90	0.04	0.63	2
Mediterraneibacter gnavus: 637_639;2887_2888	0.19	0.04	0.89	0.04	0.33	2
Bacteroides uniformis: 2461_2495;3120_3121	2.01	1.18	3.43	0.01	0.97	2
Bacteroides uniformis: 2624_2628;4186_4192	1.82	1.03	3.24	0.04	0.73	2
Parabacteroides distasonis: 3054_3055	0.35	0.16	0.76	0.01	0.49	2
[Ruminococcus] lactaris: 320_321;1385_1386	0.10	0.02	0.51	0.01	0.83	2
Bifidobacterium pseudocatenulatum: 130_131;1081_1082	0.27	0.09	0.81	0.02	0.59	2

Bacteroides xylanisolvens: 5601_5602	0.46	0.21	0.98	0.05	0.50	2
Agathobacter rectalis: 662_663	2.49	1.26	4.92	0.01	0.83	3
Ruminococcus bromii: 290_291;972_973;1878_1879	0.34	0.15	0.80	0.01	0.53	3
Ruminococcus bromii: 37_39	3.02	1.31	6.93	0.01	0.47	2
Alistipes shahii: 2840_2842	0.33	0.15	0.71	0.00	0.93	2
Roseburia intestinalis: 2079_2081	3.05	1.17	7.95	0.02	0.31	2
Roseburia intestinalis: 3179_3180	0.24	0.07	0.86	0.03	0.14	2
Barnesiella intestinihominis: 324_326;326_328;328_330	0.17	0.05	0.57	0.00	0.73	2
Barnesiella intestinihominis: 3324_3326	0.30	0.11	0.87	0.03	0.71	2
Faecalibacterium prausnitzii: 537_538	1.89	1.01	3.54	0.05	0.30	2
Faecalibacterium prausnitzii: 781_783	2.35	1.27	4.36	0.01	0.98	3
Faecalibacterium prausnitzii: 847_849	2.47	1.08	5.66	0.03	0.86	2

Note: Meta-analysis was performed using random-effects models with the Mantel-Haenszel (MH) method across metagenomic cohorts. Odds ratio (OR) values were pooled for deletion structural variants (dSVs). $OR > 1$ indicates increased odds/risk in rheumatoid arthritis samples, whereas $OR < 1$ indicates decreased odds.

Abbreviations: SV ID, structural variant identifier; Meta OR, pooled odds ratio; 95% CI, 95% confidence interval; P, probability value; P (heterogeneity), P value for heterogeneity test; No. of Contributing Cohorts, number of cohorts showing consistent direction of effect.

Table S7. Performance evaluation and comparison of machine learning models incorporating species and structural variations.

Model Type	No. of Features	Lambda Value	Test AUC (95% CI)	DeLong's P-value
Species-only ($\lambda.1se$)	3	0.09	0.476 (0.330–0.622)	0.04
Species+SV ($\lambda.1se$)	52	0.02	0.621 (0.480–0.761)	
Species-only ($\lambda.min$)	20	0.03	0.449 (0.308–0.590)	
Species+SV ($\lambda.min$)	58	0.01	0.603 (0.462–0.745)	

Note: Machine learning prediction models were constructed using penalized logistic regression (Lasso) on the training dataset (Cohort B+C). Optimal penalty parameters were selected based on the 1-standard-error rule ($\lambda.1se$) and minimum cross-validation error ($\lambda.min$). Model performance (AUC) and statistical significance of AUC differences (DeLong's test) were independently evaluated on the validation dataset (Cohort D).

Abbreviations: AUC, area under the receiver operating characteristic curve; CI, confidence interval; SV, structural variant; $\lambda.1se$, lambda value corresponding to 1 standard error above the minimum cross-validation error; $\lambda.min$, lambda value that minimizes mean cross-validated error.

Table S8. Feature importance and directional correlation of key structural variants across training and independent validation cohorts.

SV ID	Mean SHAP (Training)	Mean SHAP (Test)	Spearman r (Training)	P-value (Training)	Spearman r (Test)	P-value (Test)	Effect (Training)	Effect (Test)	Directional Consistency
Alistipes shahii: 2252_2255;2255_2257;2 257_2259;2259_2262;22 62_2264;2265_2266	0.03	0.02	0.89	<0.01	0.75	<0.01	Promote RA (Risk)	Promote RA (Risk)	Consistent
Faecalibacterium prausnitzii: 537_538	0.01	0.02	-0.70	<0.01	-0.81	<0.01	Protect against RA (Protective)	Protect against RA (Protective)	Consistent
Ruminococcus bromii: 97_103	0.01	0.01	-0.89	<0.01	-0.84	<0.01	Protect against RA (Protective)	Protect against RA (Protective)	Consistent
Bacteroides uniformis: 3880_3883	0.01	0.01	0.82	<0.01	0.85	<0.01	Promote RA (Risk)	Promote RA (Risk)	Consistent
Faecalibacterium prausnitzii: 781_783	0.01	0.01	-0.71	<0.01	-0.77	<0.01	Protect against RA (Protective)	Protect against RA (Protective)	Consistent
Bacteroides fragilis: 4781_4788	0.01	0.00	0.91	<0.01	0.69	<0.01	Promote RA (Risk)	Promote RA (Risk)	Consistent
Agathobacter rectalis: 3036_3037	0.01	0.00	0.81	<0.01	0.72	<0.01	Promote RA (Risk)	Promote RA (Risk)	Consistent
Agathobacter rectalis: 662_663	0.01	0.01	-0.67	<0.01	-0.77	<0.01	Protect against RA (Protective)	Protect against RA (Protective)	Consistent
Oscillibacter sp.: 557_558;1131_1132	0.01	0.01	-0.76	<0.01	-0.75	<0.01	Protect against RA (Protective)	Protect against RA (Protective)	Consistent
Agathobacter rectalis: 3102_3105;3105_3106	0.00	0.00	0.67	<0.01	0.72	<0.01	Promote RA (Risk)	Promote RA (Risk)	Consistent
Bacteroides xylanisolvens: 5601_5602	0.00	0.00	0.68	<0.01	0.66	<0.01	Promote RA (Risk)	Promote RA (Risk)	Consistent
Parabacteroides merdae: 782_783;2923_2924	0.00	0.00	0.70	<0.01	0.81	<0.01	Promote RA (Risk)	Promote RA (Risk)	Consistent

Note: Key structural variants (SVs) were rigorously filtered based on four consensus criteria: (1) ranking among the top 20 most important features evaluated by mean absolute SHAP values (Mean |SHAP|); (2) demonstrating strong monotonic correlation with rheumatoid arthritis (RA) status ($|\text{Spearman } r| \geq 0.6$); (3) achieving strict statistical significance ($P < 0.001$) in both the training dataset (Cohort B+C) and the independent validation dataset (Cohort D); and (4) showing 100% directional consistency between training and validation cohorts.

Abbreviations: SV ID, structural variant identifier; SHAP, SHapley Additive exPlanations; r, Spearman's rank correlation coefficient; P, probability value; RA, rheumatoid arthritis; Training, Cohort B+C; Test, Cohort D.

Table S9. Genome-wide predicted paired transcriptional repressor binding sites and genomic loci ranked by statistical significance.

Pair ID	Sequence ID	Strand	Start	Stop	Matched_Seq	PWM Score	P Value	q Value	Region Type	Target Locus Tag
Pair_1	NC_021010.1	+	662144	662163	TATGACAAATA AAGTTGTCA	31.98	4.77E-11	0.00	Promoter (-200~+50bp)	EUR_RS03225
Pair_2	NC_021010.1	+	2365586	2365605	GTTGTCAATTA TAGTTGTCA	17.88	3.21E-08	0.09	Promoter (-200~+50bp)	EUR_RS11295
Pair_2	NC_021010.1	-	2365588	2365607	TTTGACAATA TAATTGACA	14.35	9.53E-08	0.14	Promoter (-200~+50bp)	EUR_RS11295
Pair_1	NC_021010.1	-	662146	662165	TTTGACAACCTT ATTTGTCA	14.07	1.03E-07	0.14	Promoter (-200~+50bp)	EUR_RS03225
Pair_3	NC_021010.1	+	371814	371833	AATGGCAAAGA AAGTTGTAA	13.22	1.39E-07	0.14	Exon/CDS; Promoter (-200~+50bp)	EUR_RS01730
Pair_4	NC_021010.1	+	2470954	2470973	AACGATAATTA AAATTGTCA	11.47	2.21E-07	0.18	Promoter (-200~+50bp)	EUR_RS11830
Pair_5	NC_021010.1	+	461743	461762	AATGAAAAATA TATTTGTCC	10.70	3.00E-07	0.18	Promoter (-200~+50bp)	EUR_RS02230
Pair_5	NC_021010.1	-	461745	461764	AAGGACAAATA TATTTTTC	10.70	3.00E-07	0.18	Promoter (-200~+50bp)	EUR_RS02230
Pair_6	NC_021010.1	+	2507016	2507035	TATAACAATAA TAATTTTCA	9.71	4.59E-07	0.23	Exon/CDS; Promoter (-200~+50bp)	EUR_RS12020
Pair_7	NC_021010.1	-	149815	149834	AATGACTACAA AAAGTGTCA	8.32	6.81E-07	0.23	Exon/CDS	EUR_RS00695
Pair_8	NC_021010.1	+	2695357	2695376	AATGACAAAGG TAATTATGA	7.73	8.30E-07	0.23	Exon/CDS; Promoter (-200~+50bp)	EUR_RS12805
Pair_9	NC_021010.1	+	2000441	2000460	GATGAATAAAA TATTTGTCA	7.72	8.34E-07	0.23	Exon/CDS	EUR_RS09620

Pair_10	NC_021010.1	-	1572191	1572210	AATGGCGAGGG TATTTGTCA	7.69	8.39E-07	0.23	Exon/CDS	EUR_RS07695
Pair_11	NC_021010.1	+	2475288	2475307	AATAACAATAA TTATTGTTA	7.37	9.52E-07	0.23	Promoter (- 200~+50bp)	EUR_RS11860
Pair_11	NC_021010.1	-	2475290	2475309	AATAACAATAA TTATTGTTA	7.37	9.52E-07	0.23	Promoter (- 200~+50bp)	EUR_RS11860
Pair_12	NC_021010.1	-	1664787	1664806	TACCACAATGA TTATTGTCA	7.28	9.83E-07	0.23	Exon/CDS	EUR_RS08120
Pair_13	NC_021010.1	-	2416119	2416138	AATTACAATAA TTTTAGTCA	7.24	9.94E-07	0.23	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS11505; EUR_RS11510
Pair_14	NC_021010.1	-	1714033	1714052	ATTGAAAAAAA AAATTATCA	6.94	1.10E-06	0.23	Promoter (- 200~+50bp)	EUR_RS08360; EUR_RS08365
Pair_15	NC_021010.1	-	418464	418483	ATTTACAATAA TATTTGTAA	6.89	1.13E-06	0.23	Exon/CDS	EUR_RS01975
Pair_16	NC_021010.1	-	2436916	2436935	TTTCACAACAG TTTTTGTCA	6.82	1.15E-06	0.23	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS11650; EUR_RS11655
Pair_17	NC_021010.1	+	1274106	1274125	TTTTACAAAGA AAATTATCA	6.56	1.24E-06	0.23	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS06155; EUR_RS06160
Pair_18	NC_021010.1	-	1702766	1702785	TATAAAAAAGG TATTTGTCA	6.44	1.28E-06	0.23	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS08300; EUR_RS08305
Pair_19	NC_021010.1	+	2777557	2777576	TATGGCAAAAA TTATTGTAA	6.41	1.29E-06	0.23	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS13145
Pair_20	NC_021010.1	+	871631	871650	TACCACAAGTA TTTTTGTCA	6.38	1.30E-06	0.23	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS04200; EUR_RS04205

Pair_21	NC_021010.1	-	2388984	2389003	TATGAGAAGTA TTTTTTTCA	6.09	1.38E-06	0.23	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS11405
Pair_22	NC_021010.1	+	2778565	2778584	TATGACATTAA ACATTTTCA	6.06	1.39E-06	0.23	Exon/CDS	EUR_RS13145
Pair_23	NC_021010.1	+	2171960	2171979	AATGACAAGAA TCTGTGTGA	5.98	1.42E-06	0.23	Exon/CDS	EUR_RS10385
Pair_24	NC_021010.1	+	1081970	1081989	TTTGAAAATTA TTGTTCTCA	5.94	1.43E-06	0.23	Promoter (- 200~+50bp)	EUR_RS05190
Pair_25	NC_021010.1	-	1852496	1852515	GACGACAAAGG AAATTGTGA	5.62	1.52E-06	0.24	Exon/CDS	EUR_RS08980
Pair_26	NC_021010.1	+	2375496	2375515	GATGACAACAT TTGTTGTCG	5.00	1.72E-06	0.24	Exon/CDS	EUR_RS11350
Pair_27	NC_021010.1	+	2786416	2786435	AAAGATAATGA GAGTTGTCA	4.94	1.74E-06	0.24	Promoter (- 200~+50bp)	EUR_RS13190
Pair_28	NC_021010.1	-	1725810	1725829	GTTGACAAAAA TAATTGTTT	4.83	1.79E-06	0.24	Promoter (- 200~+50bp)	EUR_RS08430
Pair_26	NC_021010.1	-	2375498	2375517	CTCGACAACAA ATGTTGTCA	4.71	1.83E-06	0.24	Exon/CDS	EUR_RS11350
Pair_28	NC_021010.1	+	1725808	1725827	ATAAACAATTA TTTTTGTCA	4.52	1.92E-06	0.24	Promoter (- 200~+50bp)	EUR_RS08430
Pair_29	NC_021010.1	+	1983200	1983219	TCTGACAAATG ATATTGTCG	4.39	1.98E-06	0.24	Exon/CDS	EUR_RS09530
Pair_15	NC_021010.1	+	418462	418481	ATTTACAAATA TTATTGTAA	4.29	2.04E-06	0.24	Exon/CDS	EUR_RS01975
Pair_9	NC_021010.1	-	2000443	2000462	ATTGACAAATA TTTTATTCA	4.16	2.10E-06	0.24	Exon/CDS	EUR_RS09620
Pair_30	NC_021010.1	-	805977	805996	ATTAACCAATA ATTTTGTCA	4.16	2.10E-06	0.24	Promoter (- 200~+50bp)	EUR_RS03920
Pair_31	NC_021010.1	-	1186369	1186388	TATGGCAAAGG TTACTGTCA	4.18	2.10E-06	0.24	Exon/CDS	EUR_RS05735

Pair_32	NC_021010.1	-	1191130	1191149	TATGGCAAAGG T TACTGTCA	4.18	2.10E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS05760
Pair_33	NC_021010.1	+	2588553	2588572	TATGACCATGG T TTTTGCCA	4.13	2.13E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS12355; EUR_RS12360
Pair_34	NC_021010.1	+	2821162	2821181	AAAGACAAAAA CAGTTGTAA	4.07	2.16E-06	0.24	Exon/CDS	EUR_RS13360
Pair_13	NC_021010.1	+	2416117	2416136	ATTGACTAAAA T TATTGTAA	3.99	2.21E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS11505; EUR_RS11510
Pair_19	NC_021010.1	-	2777559	2777578	ATTTACAATAA T TTTTGCCA	3.94	2.25E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS13145
Pair_35	NC_021010.1	+	3025225	3025244	AATGACAATGA TAGATGCAA	3.94	2.25E-06	0.24	Exon/CDS	EUR_RS14250
Pair_36	NC_021010.1	+	731069	731088	AAAGACAAAGA TACTTATCA	3.85	2.31E-06	0.24	Exon/CDS	EUR_RS03545
Pair_37	NC_021010.1	+	547177	547196	CATGACAAAAA TAGTTGGTA	3.83	2.32E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS02630
Pair_38	NC_021010.1	-	2826608	2826627	TTTGGCAAAAA T TATTGTCT	3.39	2.62E-06	0.24	Exon/CDS	EUR_RS13375
Pair_39	NC_021010.1	-	2220399	2220418	AATAAAAAATA TAGTAGTCA	3.37	2.64E-06	0.24	Intergenic	-
Pair_40	NC_021010.1	+	2956488	2956507	AATAAGAATGA TAGTTATCA	3.37	2.64E-06	0.24	Exon/CDS	EUR_RS13920
Pair_41	NC_021010.1	-	2416191	2416210	TTTTCCTAAAAG TAATTGTCA	3.32	2.67E-06	0.24	Promoter (- 200~+50bp)	EUR_RS11510

Pair_42	NC_021010.1	-	2948571	2948590	TTTCACCAAAA ATATTGTCA	3.10	2.81E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS13875; EUR_RS13880
Pair_43	NC_021010.1	+	504306	504325	TTTTACAAATA ATTTTTTCA	2.99	2.89E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS02410; EUR_RS02415
Pair_44	NC_021010.1	+	3336541	3336560	GATGAGAACGA TTATAGTCA	2.91	2.93E-06	0.24	Exon/CDS	EUR_RS16020
Pair_45	NC_021010.1	+	884039	884058	TTTGAAAAAAA ATATTTTCA	2.82	3.00E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS04250
Pair_46	NC_021010.1	-	1787203	1787222	TATGACATTAA AACTTATCA	2.81	3.00E-06	0.24	Promoter (- 200~+50bp)	EUR_RS08670; EUR_RS08675
Pair_37	NC_021010.1	-	547179	547198	GATACCAACTA TTTTTGTCA	2.57	3.15E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS02630
Pair_20	NC_021010.1	-	871633	871652	TATGACAAAAA TACTTGTGG	2.45	3.24E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS04200; EUR_RS04205
Pair_47	NC_021010.1	+	2359184	2359203	ATTGACAACGA ATATAGTCT	2.29	3.33E-06	0.24	Exon/CDS	EUR_RS11245
Pair_6	NC_021010.1	-	2507018	2507037	GTTGAAAATTA TTATTGTTA	2.24	3.37E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS12020
Pair_21	NC_021010.1	+	2388982	2389001	TATGAAAAAAA TACTTCTCA	2.16	3.43E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS11405
Pair_4	NC_021010.1	-	2470956	2470975	AATGACAATTT TAATTATCG	1.96	3.56E-06	0.24	Promoter (- 200~+50bp)	EUR_RS11830
Pair_48	NC_021010.1	-	3298562	3298581	AATGGCAATTT TAATTGTTA	1.96	3.56E-06	0.24	Promoter (- 200~+50bp)	EUR_RS15840

Pair_49	NC_021010.1	+	1222838	1222857	TATGACACTTA CATTTGGCA	1.82	3.68E-06	0.24	Exon/CDS	EUR_RS05890
Pair_50	NC_021010.1	+	3009326	3009345	AATGATACTGA TAATTGTCG	1.76	3.74E-06	0.24	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS14160; EUR_RS14165
Pair_51	NC_021010.1	+	2949500	2949519	AGTGACAATGA AAATTATAA	1.60	3.88E-06	0.25	Exon/CDS	EUR_RS13880
Pair_16	NC_021010.1	+	2436914	2436933	CATGACAAAAA CTGTTGTGA	1.59	3.89E-06	0.25	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS11650; EUR_RS11655
Pair_52	NC_021010.1	+	3131343	3131362	AATGCCAAATA AAATTGTAC	1.47	4.04E-06	0.25	Promoter (- 200~+50bp)	EUR_RS14975
Pair_53	NC_021010.1	+	2901010	2901029	CATCTCAAATG TAGTTGTCA	1.39	4.15E-06	0.25	Exon/CDS	EUR_RS13685
Pair_54	NC_021010.1	-	528391	528410	ATTTGCAACAG AATTTGTCA	1.30	4.25E-06	0.25	Exon/CDS	EUR_RS02525
Pair_55	NC_021010.1	+	1344985	1345004	CATAAAAATAA AATTTGTCA	1.31	4.25E-06	0.25	Promoter (- 200~+50bp)	EUR_RS06565
Pair_56	NC_021010.1	+	360639	360658	AAAGACAGTGA ATCTTGTCA	1.26	4.34E-06	0.25	Exon/CDS	EUR_RS01685
Pair_57	NC_021010.1	-	3310762	3310781	ATTGTCAATTG ACTTTGTCT	1.08	4.59E-06	0.25	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS15895; EUR_RS15900
Pair_48	NC_021010.1	+	3298560	3298579	TGTAACAATTA AAATTGCCA	1.07	4.60E-06	0.25	Promoter (- 200~+50bp)	EUR_RS15840
Pair_58	NC_021010.1	-	1473081	1473100	AATGACAATAA TAATCATAA	0.96	4.81E-06	0.25	Exon/CDS	EUR_RS07150
Pair_59	NC_021010.1	-	1237303	1237322	TGTGACATTGA AATTAGTCA	0.88	4.94E-06	0.26	Exon/CDS	EUR_RS05955
Pair_60	NC_021010.1	+	2979523	2979542	AATCACAAATT ATCTTGTCA	0.82	5.06E-06	0.26	Exon/CDS	EUR_RS14045

Pair_23	NC_021010.1	-	2171962	2171981	AATCACACAGA TTCTTGTC	0.61	5.43E-06	0.27	Exon/CDS	EUR_RS10385
Pair_61	NC_021010.1	-	2371119	2371138	AATCAAAAAA TAATTGTCC	0.60	5.45E-06	0.27	Exon/CDS	EUR_RS11325
Pair_62	NC_021010.1	-	1597133	1597152	GTTGACAACAG GAATTGTCT	0.59	5.47E-06	0.27	Promoter (- 200~+50bp)	EUR_RS07815
Pair_63	NC_021010.1	-	1183660	1183679	TATCACGTAA TAATTGTCA	0.36	5.94E-06	0.27	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS05720
Pair_7	NC_021010.1	-	2135843	2135862	TATAACACGGA TAAATGTCA	0.31	6.05E-06	0.27	Exon/CDS	EUR_RS10240
Pair_64	NC_021010.1	+	149813	149832	TATGACACTTTT TGTAAGTCA	0.31	6.05E-06	0.27	Exon/CDS	EUR_RS00695
Pair_65	NC_021010.1	+	1834013	1834032	TATGACAAATA TAAGTATGA	0.30	6.06E-06	0.27	Exon/CDS	EUR_RS08900
Pair_66	NC_021010.1	+	2216865	2216884	AATGATAAAAG TACTTTTCA	0.03	6.59E-06	0.29	Intergenic	-
Pair_67	NC_021010.1	-	3200161	3200180	TGTGACCATGA TTGTTGTGA	-0.05	6.75E-06	0.29	Exon/CDS	EUR_RS15330
Pair_68	NC_021010.1	-	1329949	1329968	TCTCACAAATG AAGTCGTCA	-0.12	6.87E-06	0.29	Exon/CDS	EUR_RS06510
Pair_69	NC_021010.1	-	1629514	1629533	TATGTCTAATA TTGTTGCCA	-0.18	6.99E-06	0.29	Exon/CDS	EUR_RS07955
Pair_60	NC_021010.1	-	2979525	2979544	TGTGACAAGAT AATTTGTGA	-0.35	7.29E-06	0.30	Exon/CDS	EUR_RS14045
Pair_43	NC_021010.1	-	504308	504327	TATGAAAAAAT TATTTGTAA	-0.56	7.69E-06	0.31	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS02410; EUR_RS02415
Pair_70	NC_021010.1	-	1824287	1824306	AGTGACAAAGG CATTCGTCA	-0.61	7.78E-06	0.31	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS08850

Pair_71	NC_021010.1	+	1005023	1005042	TATTACAATAA TATTTATTA	-0.62	7.80E-06	0.31	Promoter (- 200~+50bp)	EUR_RS04830
Pair_72	NC_021010.1	-	1763793	1763812	TTTTACAAATA TAGTTAACA	-0.83	8.16E-06	0.31	Exon/CDS	EUR_RS08585
Pair_73	NC_021010.1	-	532403	532422	GATAAAAATGA TAATTGCCA	-0.93	8.36E-06	0.31	Exon/CDS	EUR_RS02550
Pair_74	NC_021010.1	+	1283571	1283590	TATGATAATAA TTGATTTC	-0.98	8.45E-06	0.31	Exon/CDS	EUR_RS06200
Pair_75	NC_021010.1	-	320127	320146	GACGACAAATA TATCTGTGA	-1.34	9.23E-06	0.33	Exon/CDS	EUR_RS01500
Pair_38	NC_021010.1	+	2826606	2826625	CAAGACAATAA TTTTTGCCA	-1.36	9.27E-06	0.33	Exon/CDS	EUR_RS13375
Pair_76	NC_021010.1	+	3182850	3182869	TATGTCAATGA CTTTTGCCA	-1.49	9.63E-06	0.33	Promoter (- 200~+50bp)	EUR_RS15225; EUR_RS15230
Pair_77	NC_021010.1	+	1943150	1943169	AAGGAATATTG TATTTGTCA	-1.60	9.91E-06	0.33	Exon/CDS	EUR_RS09360
Pair_78	NC_021010.1	-	286236	286255	TATGACACCGA TAATTGCCG	-1.70	1.02E-05	0.33	Exon/CDS	EUR_RS01330
Pair_79	NC_021010.1	-	41902	41921	GATAACAGGAA TAACTGTCA	-1.71	1.02E-05	0.33	Exon/CDS	EUR_RS00195
Pair_33	NC_021010.1	-	2588555	2588574	AATGGCAAAAA CCATGGTCA	-1.77	1.04E-05	0.33	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS12355; EUR_RS12360
Pair_80	NC_021010.1	-	2741708	2741727	TTGTACAATTA CATTTGTCA	-1.78	1.04E-05	0.33	Promoter (- 200~+50bp)	EUR_RS12980
Pair_81	NC_021010.1	+	1376771	1376790	AATTGCAATTA TTTTTGCA	-1.82	1.05E-05	0.33	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS06730; EUR_RS06725
Pair_82	NC_021010.1	+	1173587	1173606	ATTGACATATA AAATTGAGA	-1.84	1.07E-05	0.33	Promoter (- 200~+50bp)	EUR_RS05700

Pair_83	NC_021010.1	+	617470	617489	GATGATGAAAA TATTTGACA	-1.92	1.09E-05	0.34	Promoter (- 200~+50bp)	EUR_RS02990
Pair_84	NC_021010.1	-	284336	284355	ACTGACAGTTG TTGTTGTAA	-2.11	1.16E-05	0.34	Exon/CDS	EUR_RS01320
Pair_85	NC_021010.1	+	1943583	1943602	AATGACAAAGA GCTTTTTGA	-2.23	1.20E-05	0.34	Exon/CDS	EUR_RS09360
Pair_86	NC_021010.1	-	1438649	1438668	TATAACAATGT TTAATGTCA	-2.23	1.20E-05	0.34	Promoter (- 200~+50bp)	EUR_RS07005
Pair_34	NC_021010.1	-	2821164	2821183	TTTTACAAGTGT TTTTGTCT	-2.24	1.21E-05	0.34	Exon/CDS	EUR_RS13360
Pair_36	NC_021010.1	-	731071	731090	CATGATAAGTA TCTTTGTCT	-2.33	1.24E-05	0.34	Exon/CDS	EUR_RS03545
Pair_87	NC_021010.1	-	1785141	1785160	TATAACAGCAG CAGTTGTCA	-2.34	1.24E-05	0.34	Exon/CDS	EUR_RS08665
Pair_88	NC_021010.1	-	1803551	1803570	AATGACAAAAA TTATAGTAT	-2.35	1.25E-05	0.34	Promoter (- 200~+50bp)	EUR_RS08745
Pair_89	NC_021010.1	-	2537103	2537122	TATCACAAGTGA TTAATGTCA	-2.37	1.26E-05	0.34	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS12140; EUR_RS12135
Pair_88	NC_021010.1	+	1803549	1803568	AAATACTATAA TTTTTGTCA	-2.40	1.27E-05	0.34	Promoter (- 200~+50bp)	EUR_RS08745
Pair_90	NC_021010.1	+	785820	785839	AATGATACATA TTTTTCTCA	-2.46	1.29E-05	0.34	Exon/CDS	EUR_RS03820
Pair_91	NC_021010.1	+	2451409	2451428	ATTTACAAAGA TAATTATGA	-2.48	1.30E-05	0.34	Promoter (- 200~+50bp)	EUR_RS11745
Pair_92	NC_021010.1	+	2070736	2070755	TTCGACATTTAT ATTGGCA	-2.49	1.31E-05	0.34	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS09960; EUR_RS09965
Pair_93	NC_021010.1	+	2049400	2049419	TGTGATAAATA ATATTGACA	-2.52	1.32E-05	0.34	Promoter (- 200~+50bp)	EUR_RS09850

Pair_94	NC_021010.1	-	1251846	1251865	TATGAGAAAAA GTATTATCA	-2.52	1.32E-05	0.34	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS06040
Pair_95	NC_021010.1	-	2602751	2602770	GATGACAAAAA TTGCTCACA	-2.56	1.34E-05	0.34	Exon/CDS	EUR_RS12415
Pair_96	NC_021010.1	+	450837	450856	TCTGACAAATG AAATTTTAA	-2.59	1.34E-05	0.34	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS02175
Pair_97	NC_021010.1	-	1886244	1886263	TATGATTTTTAT TTTTGTCA	-2.70	1.39E-05	0.34	Exon/CDS	EUR_RS09100
Pair_98	NC_021010.1	+	238359	238378	TTCGACAATTA TATTTGGGA	-2.78	1.42E-05	0.34	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS01095; EUR_RS01100
Pair_99	NC_021010.1	+	1899673	1899692	TATTCCTATGAT TTTTGTCA	-2.78	1.42E-05	0.34	Exon/CDS	EUR_RS09175
Pair_100	NC_021010.1	+	113607	113626	TATGCCATATA TTTTTGACA	-2.78	1.42E-05	0.34	Exon/CDS	EUR_RS00560
Pair_54	NC_021010.1	-	1344987	1345006	TATGACAAATT TTATTTTAA	-2.81	1.43E-05	0.34	Promoter (- 200~+50bp)	EUR_RS06565
Pair_56	NC_021010.1	-	360641	360660	AATGACAAGAT TCACTGTCT	-2.84	1.45E-05	0.34	Exon/CDS	EUR_RS01685
Pair_101	NC_021010.1	-	1256807	1256826	CATATCAAGAA TCTTTGTCA	-2.91	1.47E-05	0.34	Exon/CDS	EUR_RS06065
Pair_59	NC_021010.1	+	1180058	1180077	TTTGAAAATAA AAATAGTCT	-2.95	1.49E-05	0.34	Exon/CDS	EUR_RS05710
Pair_102	NC_021010.1	+	1237301	1237320	TATGACTAATT TCAATGTCA	-2.94	1.49E-05	0.34	Exon/CDS	EUR_RS05955
Pair_103	NC_021010.1	-	489219	489238	ATTGAAAAAAT TATTTTCA	-2.98	1.50E-05	0.34	Intergenic	-
Pair_104	NC_021010.1	-	3031941	3031960	TTTTGGAAATA TAATTGTCA	-3.01	1.51E-05	0.34	Exon/CDS	EUR_RS14280

Pair_105	NC_021010.1	-	481121	481140	TTTGACAAAAA GATTCTAA	-3.00	1.51E-05	0.34	Exon/CDS	EUR_RS02315
Pair_106	NC_021010.1	+	852423	852442	AATGACACCTG GAATTGTTA	-3.05	1.53E-05	0.34	Exon/CDS	EUR_RS04120
Pair_107	NC_021010.1	+	1835407	1835426	AATGACAATAA TCTTTGCGC	-3.10	1.55E-05	0.34	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS08905
Pair_108	NC_021010.1	-	581083	581102	TTTGCCAAAAG CAGTTCTCA	-3.14	1.57E-05	0.34	Intergenic	-
Pair_109	NC_021010.1	+	1795094	1795113	TATCACAACAA AATGTTTCA	-3.19	1.58E-05	0.34	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS08700
Pair_110	NC_021010.1	-	275763	275782	TTTGAAAAAGA TATTAGCCA	-3.20	1.59E-05	0.34	Exon/CDS	EUR_RS01275
Pair_111	NC_021010.1	+	2342117	2342136	TCTTACAATTAT CTTAGTCA	-3.28	1.61E-05	0.34	Intergenic	-
Pair_112	NC_021010.1	-	2841731	2841750	TATGCCACATA TCATTATCA	-3.36	1.65E-05	0.34	Exon/CDS	EUR_RS13420
Pair_94	NC_021010.1	+	1251844	1251863	TATGATAATAC TTTTTCTCA	-3.44	1.67E-05	0.34	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS06040
Pair_86	NC_021010.1	+	1438647	1438666	TCTGACATTAA ACATTGTTA	-3.45	1.68E-05	0.34	Promoter (- 200~+50bp)	EUR_RS07005
Pair_113	NC_021010.1	-	109854	109873	TATGTCAAGTA TCATTTTCG	-3.56	1.71E-05	0.34	Promoter (- 200~+50bp)	EUR_RS00545
Pair_114	NC_021010.1	-	3178859	3178878	TATGACAATA TCGATGTGT	-3.67	1.75E-05	0.35	Exon/CDS	EUR_RS15215
Pair_115	NC_021010.1	-	630061	630080	TTTGATAATTAT TGTTTTCT	-3.70	1.76E-05	0.35	Exon/CDS	EUR_RS03050
Pair_116	NC_021010.1	-	2679130	2679149	TATGATAAGAA TTATTGCTA	-3.72	1.77E-05	0.35	Exon/CDS	EUR_RS12740

Pair_117	NC_021010.1	+	2938963	2938982	TATGAAAAAAG TTCTTGACA	-3.81	1.79E-05	0.35	Intergenic	-
Pair_118	NC_021010.1	+	3297624	3297643	TATGAAAAAAG TTCTTGACA	-3.81	1.79E-05	0.35	Intergenic	-
Pair_49	NC_021010.1	-	2835730	2835749	TGTGATATGTA TCTTTGTCA	-3.84	1.80E-05	0.35	Exon/CDS	EUR_RS13400
Pair_119	NC_021010.1	-	1222840	1222859	CTTGCCAAATG TAAGTGTCA	-3.82	1.80E-05	0.35	Exon/CDS	EUR_RS05890
Pair_100	NC_021010.1	-	1899675	1899694	TATGACAAAAA TCATAGGAA	-3.94	1.84E-05	0.35	Exon/CDS	EUR_RS09175
Pair_85	NC_021010.1	-	1943585	1943604	TATCAAAAAGC TCTTTGTCA	-3.99	1.85E-05	0.35	Exon/CDS	EUR_RS09360
Pair_90	NC_021010.1	-	785822	785841	TTTGAGAAAAA TATGTATCA	-4.00	1.86E-05	0.35	Exon/CDS	EUR_RS03820
Pair_120	NC_021010.1	-	1564375	1564394	GATGATAACAA AAAGAGTCA	-4.01	1.86E-05	0.35	Exon/CDS	EUR_RS07650
Pair_66	NC_021010.1	-	2216867	2216886	GATGAAAAGTA CTTTTATCA	-4.06	1.87E-05	0.35	Intergenic	-
Pair_87	NC_021010.1	-	2909698	2909717	ATTGACATCGA TAATGGTCT	-4.12	1.89E-05	0.35	Exon/CDS	EUR_RS13715
Pair_121	NC_021010.1	+	1785139	1785158	AATGACAACCTG CTGCTGTTA	-4.10	1.89E-05	0.35	Exon/CDS	EUR_RS08665
Pair_122	NC_021010.1	+	1237196	1237215	ATTTGCAATCA TCATTGTCA	-4.13	1.90E-05	0.35	Exon/CDS	EUR_RS05955
Pair_123	NC_021010.1	-	3196728	3196747	GATGAGAGTTA TTTTTGTCT	-4.21	1.93E-05	0.36	Exon/CDS	EUR_RS15315
Pair_115	NC_021010.1	+	630059	630078	GAAGAAAACAA TAATTATCA	-4.30	1.96E-05	0.36	Exon/CDS	EUR_RS03050
Pair_124	NC_021010.1	+	3161131	3161150	GATGACAAAGA TTTAGGCT	-4.36	1.98E-05	0.36	Exon/CDS	EUR_RS15125

Pair_125	NC_021010.1	-	781637	781656	GATGAAAAGTA GCATTCTCA	-4.36	1.98E-05	0.36	Exon/CDS	EUR_RS03790
Pair_126	NC_021010.1	+	2539409	2539428	ATTGACACCGA AAAGTATCA	-4.41	1.99E-05	0.36	Exon/CDS	EUR_RS12145
Pair_24	NC_021010.1	-	1081972	1081991	CTTGAGAACAA TAATTTTCA	-4.45	2.01E-05	0.36	Promoter (- 200~+50bp)	EUR_RS05190
Pair_70	NC_021010.1	-	1972392	1972411	TTTTTCAAATAT CGTAGTCA	-4.48	2.02E-05	0.36	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS09475; EUR_RS09480
Pair_127	NC_021010.1	-	3188401	3188420	TTTGCCAAATA ACGTTACCA	-4.48	2.02E-05	0.36	Exon/CDS	EUR_RS15280
Pair_128	NC_021010.1	+	1824285	1824304	ACTGACGAATG CCTTTGTCA	-4.48	2.02E-05	0.36	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS08850
Pair_129	NC_021010.1	-	402626	402645	AATCACAGTGG TTATTGCCA	-4.50	2.03E-05	0.36	Exon/CDS	EUR_RS01890
Pair_130	NC_021010.1	+	1042453	1042472	ATTGACACCAA AAAATGTCT	-4.63	2.08E-05	0.36	Exon/CDS	EUR_RS05000
Pair_42	NC_021010.1	+	2948569	2948588	GATGACAATAT TTTTGGTGA	-4.66	2.10E-05	0.36	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS13875; EUR_RS13880
Pair_131	NC_021010.1	+	2930983	2931002	GATGAGACCAA TATTTTTC	-4.70	2.11E-05	0.36	Exon/CDS	EUR_RS13795
Pair_104	NC_021010.1	+	481119	481138	GATTAGAAATC TTTTTGTCA	-4.72	2.12E-05	0.36	Exon/CDS	EUR_RS02315
Pair_127	NC_021010.1	+	1972390	1972409	ATTGACTACGA TATTTGAAA	-4.82	2.16E-05	0.36	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS09475; EUR_RS09480
Pair_27	NC_021010.1	-	2786418	2786437	AATGACAATCT TCATTATCT	-4.84	2.17E-05	0.36	Promoter (- 200~+50bp)	EUR_RS13190

Pair_132	NC_021010.1	+	414890	414909	AATGACAATTG TTTTGGTTT	-4.84	2.17E-05	0.36	Exon/CDS	EUR_RS01960
Pair_133	NC_021010.1	-	1700333	1700352	GTTTAAAAAGA TAATTTTCA	-4.88	2.19E-05	0.36	Intergenic	-
Pair_41	NC_021010.1	+	2416189	2416208	TTTGACAATTA CTTTTGGAA	-5.01	2.25E-05	0.36	Promoter (- 200~+50bp)	EUR_RS11510
Pair_58	NC_021010.1	-	861544	861563	GCTGACAACAG TAGTTCTGA	-5.00	2.25E-05	0.36	Exon/CDS	EUR_RS04160
Pair_134	NC_021010.1	+	1473079	1473098	ATTTATGATTAT TATTGTCA	-5.00	2.25E-05	0.36	Exon/CDS	EUR_RS07150
Pair_40	NC_021010.1	+	2220397	2220416	ATTGACTACTA TATTTTTTA	-5.03	2.26E-05	0.36	Intergenic	-
Pair_72	NC_021010.1	-	3182852	3182871	CATGGCAAAG TCATTGACA	-5.03	2.26E-05	0.36	Promoter (- 200~+50bp)	EUR_RS15225; EUR_RS15230
Pair_76	NC_021010.1	+	1763791	1763810	ATTGTAACTA TATTTGTAA	-5.03	2.26E-05	0.36	Exon/CDS	EUR_RS08585
Pair_89	NC_021010.1	+	2537101	2537120	GATGACATTAA TCAGTGTGA	-5.09	2.29E-05	0.36	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS12140; EUR_RS12135
Pair_8	NC_021010.1	-	2695359	2695378	ATTCATAATTA CCTTTGTCA	-5.11	2.30E-05	0.36	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS12805
Pair_135	NC_021010.1	-	2209221	2209240	TTTCACTATAA CTATTGTCA	-5.18	2.33E-05	0.36	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS10535; EUR_RS10540
Pair_136	NC_021010.1	-	694742	694761	GCTGACAAATG TCGAGGTCA	-5.29	2.39E-05	0.36	Exon/CDS	EUR_RS03375
Pair_137	NC_021010.1	-	390444	390463	TTTGACTGCTAT ATTGGTCA	-5.35	2.42E-05	0.36	Exon/CDS	EUR_RS01820
Pair_106	NC_021010.1	+	1975608	1975627	TTTGATAATTGT AAACGTCA	-5.39	2.45E-05	0.36	Promoter (- 200~+50bp)	EUR_RS09495

Pair_138	NC_021010.1	-	852425	852444	TATAACAATTC CAGGTGTCA	-5.39	2.45E-05	0.36	Exon/CDS	EUR_RS04120
Pair_18	NC_021010.1	+	1702764	1702783	ATTGACAAATA CCTTTTTTA	-5.47	2.49E-05	0.37	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS08300; EUR_RS08305
Pair_139	NC_021010.1	-	211700	211719	ATTGACAAATA ATTATTTTCG	-5.48	2.49E-05	0.37	Promoter (- 200~+50bp)	EUR_RS16110; EUR_RS16275
Pair_140	NC_021010.1	+	2950597	2950616	TATGGCAATTA CAGGTATCA	-5.52	2.52E-05	0.37	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS13890
Pair_63	NC_021010.1	+	1183658	1183677	TTTGACAATTA TTAACGTGA	-5.60	2.57E-05	0.37	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS05720
Pair_119	NC_021010.1	+	2835728	2835747	ACTGACAAAGA TACATATCA	-5.66	2.60E-05	0.37	Exon/CDS	EUR_RS13400
Pair_141	NC_021010.1	+	1444118	1444137	TTTGACAATTG TAATCATAA	-5.67	2.61E-05	0.37	Promoter (- 200~+50bp)	EUR_RS07040
Pair_135	NC_021010.1	+	2209219	2209238	TCTGACAATAG TTATAGTGA	-5.77	2.66E-05	0.38	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS10535; EUR_RS10540
Pair_142	NC_021010.1	-	1624193	1624212	TTTGACAAGAA CTATTGGGA	-5.74	2.66E-05	0.38	Exon/CDS	EUR_RS07925
Pair_47	NC_021010.1	-	2359186	2359205	GTAGACTATAT TCGTTGTCA	-5.80	2.69E-05	0.38	Exon/CDS	EUR_RS11245
Pair_45	NC_021010.1	+	2320364	2320383	TAAGATAAAGG CCTTTGTCA	-5.86	2.73E-05	0.38	Exon/CDS	EUR_RS11055
Pair_143	NC_021010.1	-	884041	884060	ATTGAAAATAT TTTTTTTCA	-5.86	2.73E-05	0.38	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS04250
Pair_144	NC_021010.1	-	1058936	1058955	TTTGCCAAATG TGTTTGTAA	-5.95	2.78E-05	0.38	Exon/CDS	EUR_RS05075

Pair_46	NC_021010.1	+	1787201	1787220	TTTGATAAGTTT TAATGTCA	-6.03	2.84E-05	0.38	Promoter (- 200~+50bp)	EUR_RS08670; EUR_RS08675
Pair_145	NC_021010.1	-	789479	789498	GATTAATAATAA TCTTTGTAA	-6.07	2.87E-05	0.38	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS03840
Pair_146	NC_021010.1	+	475402	475421	TCTTACAAAAG ATAGTGTCA	-6.12	2.90E-05	0.38	Exon/CDS	EUR_RS02295
Pair_117	NC_021010.1	-	2938965	2938984	TTTGTCAAGAA CTTTTTTCA	-6.15	2.92E-05	0.38	Intergenic	-
Pair_118	NC_021010.1	-	3297626	3297645	TTTGTCAAGAA CTTTTTTCA	-6.15	2.92E-05	0.38	Intergenic	-
Pair_110	NC_021010.1	+	275761	275780	ATTGGCTAATA TCTTTTTCA	-6.18	2.94E-05	0.38	Exon/CDS	EUR_RS01275
Pair_61	NC_021010.1	+	2371117	2371136	TTGGACAATTA TTTTTTTGA	-6.30	3.02E-05	0.38	Exon/CDS	EUR_RS11325
Pair_147	NC_021010.1	+	2260134	2260153	TATGCCAAATA AACTTGACC	-6.33	3.03E-05	0.38	Exon/CDS	EUR_RS16375
Pair_133	NC_021010.1	+	1700331	1700350	ATTGAAAATTA TCTTTTTAA	-6.40	3.08E-05	0.38	Intergenic	-
Pair_51	NC_021010.1	-	2949502	2949521	TTTTATAATTTT CATTGTCA	-6.46	3.12E-05	0.38	Exon/CDS	EUR_RS13880
Pair_148	NC_021010.1	-	64648	64667	ATTGTAAAATA TCTTTGTAA	-6.47	3.12E-05	0.38	Exon/CDS	EUR_RS00280
Pair_71	NC_021010.1	-	1005025	1005044	TTTAATAAATA TTATTGTAA	-6.53	3.17E-05	0.38	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS04835; EUR_RS04830
Pair_149	NC_021010.1	-	2830336	2830355	ATTGACCTGAA TCATTTTCA	-6.56	3.19E-05	0.38	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS13385; EUR_RS13390
Pair_150	NC_021010.1	-	1803771	1803790	TATGACAGATA TACTCTTCA	-6.61	3.22E-05	0.38	Exon/CDS	EUR_RS08750

Pair_151	NC_021010.1	+	3187880	3187899	AGTTACAAACA TAATTGTCT	-6.76	3.30E-05	0.39	Promoter (- 200~+50bp)	EUR_RS15275
Pair_152	NC_021010.1	+	3189865	3189884	TATGACACATA TAGTAGAAA	-6.88	3.39E-05	0.39	Exon/CDS	EUR_RS15285
Pair_153	NC_021010.1	+	288320	288339	GATGACAACGG GCGGTGTCC	-6.99	3.46E-05	0.39	Exon/CDS	EUR_RS01335
Pair_154	NC_021010.1	-	1377483	1377502	TTTTACAAGAA TTATTATCG	-7.03	3.48E-05	0.39	Exon/CDS	EUR_RS06735
Pair_22	NC_021010.1	-	2778567	2778586	GTTGAAAATGT TTAATGTCA	-7.05	3.49E-05	0.39	Exon/CDS	EUR_RS13145
Pair_155	NC_021010.1	+	1312182	1312201	AATTACCATCA TATTTGTTA	-7.22	3.60E-05	0.39	Exon/CDS	EUR_RS06400
Pair_151	NC_021010.1	-	2429238	2429257	TTTGGCCACAA TCGGTGTCA	-7.28	3.63E-05	0.39	Exon/CDS	EUR_RS11595
Pair_156	NC_021010.1	-	3187882	3187901	CAAGACAATTA TGTTTGTAA	-7.27	3.63E-05	0.39	Promoter (- 200~+50bp)	EUR_RS15275
Pair_91	NC_021010.1	+	2358195	2358214	CATGAAAAAAA GAATTGTAA	-7.29	3.64E-05	0.39	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS11240
Pair_157	NC_021010.1	-	2451411	2451430	TTTCATAATTAT CTTTGTAA	-7.29	3.64E-05	0.39	Promoter (- 200~+50bp)	EUR_RS11745
Pair_62	NC_021010.1	+	1597131	1597150	ACAGACAATTC CTGTTGTCA	-7.32	3.65E-05	0.39	Promoter (- 200~+50bp)	EUR_RS07815
Pair_111	NC_021010.1	-	2342119	2342138	CGTGACTAAGA TAATTGTAA	-7.36	3.67E-05	0.39	Intergenic	-
Pair_140	NC_021010.1	-	2809737	2809756	GATGTCAACAA GCTTTGTGA	-7.36	3.67E-05	0.39	Exon/CDS	EUR_RS13310
Pair_158	NC_021010.1	-	2950599	2950618	ATTGATACCTG TAATTGCCA	-7.36	3.67E-05	0.39	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS13890

Pair_35	NC_021010.1	-	3025227	3025246	GATTGCATCTA TCATTGTCA	-7.37	3.69E-05	0.39	Exon/CDS	EUR_RS14250
Pair_69	NC_021010.1	+	1629512	1629531	GTTGGCAACAA TATTAGACA	-7.44	3.73E-05	0.39	Exon/CDS	EUR_RS07955
Pair_74	NC_021010.1	+	3199080	3199099	GTTTTCAAATG TAATTATCA	-7.54	3.80E-05	0.40	Exon/CDS	EUR_RS15325
Pair_159	NC_021010.1	-	1283573	1283592	GATGAAATCAA TTATTATCA	-7.53	3.80E-05	0.40	Exon/CDS	EUR_RS06200
Pair_108	NC_021010.1	+	1971381	1971400	ACTGACAAGTG CGGCTGTCA	-7.59	3.83E-05	0.40	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS09465; EUR_RS09470
Pair_160	NC_021010.1	+	581081	581100	TATGAGAACTG CTTTTGGCA	-7.58	3.83E-05	0.40	Intergenic	-
Pair_3	NC_021010.1	-	371816	371835	GATTACAACCTT TCTTTGCCA	-7.64	3.86E-05	0.40	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS01730
Pair_57	NC_021010.1	+	3310760	3310779	TAAGACAAAGT CAATTGACA	-7.71	3.91E-05	0.40	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS15895; EUR_RS15900
Pair_161	NC_021010.1	-	1322245	1322264	TATGACTCTTCC ATTTGTCA	-7.69	3.91E-05	0.40	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS06475; EUR_RS06470
Pair_132	NC_021010.1	-	414892	414911	AAAAACCAAAA CAATTGTCA	-7.76	3.95E-05	0.40	Exon/CDS	EUR_RS01960
Pair_67	NC_021010.1	+	3200159	3200178	GGTCACAACAA TCATGGTCA	-7.82	4.00E-05	0.40	Exon/CDS	EUR_RS15330
Pair_39	NC_021010.1	-	2956490	2956509	GATGATAACTA TCATTCTTA	-7.94	4.09E-05	0.40	Exon/CDS	EUR_RS13920
Pair_162	NC_021010.1	+	2309770	2309789	ACGGACAGATA AGTTTGTCA	-7.96	4.11E-05	0.40	Exon/CDS	EUR_RS11020

Pair_163	NC_021010.1	+	1741036	1741055	AATCACTATGT TGTTTGTCA	-7.96	4.11E-05	0.40	Promoter (- 200~+50bp)	EUR_RS08485
Pair_137	NC_021010.1	+	390442	390461	GCTGACCAATA TAGCAGTCA	-7.97	4.12E-05	0.40	Exon/CDS	EUR_RS01820
Pair_97	NC_021010.1	+	1886242	1886261	CATGACAAAAA TAAAAATCA	-8.00	4.14E-05	0.40	Exon/CDS	EUR_RS09100
Pair_141	NC_021010.1	-	1444120	1444139	TATTATGATTA CAATTGTCA	-7.99	4.14E-05	0.40	Promoter (- 200~+50bp)	EUR_RS07040
Pair_164	NC_021010.1	+	1902673	1902692	TATCACAATGA CAATTGATA	-8.06	4.20E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS09190
Pair_52	NC_021010.1	-	3131345	3131364	AAGTACAATTT TATTTGGCA	-8.09	4.23E-05	0.41	Promoter (- 200~+50bp)	EUR_RS14975
Pair_29	NC_021010.1	-	1983202	1983221	TCCGACAATAT CATTTGTCA	-8.14	4.28E-05	0.41	Exon/CDS	EUR_RS09530
Pair_165	NC_021010.1	+	2010959	2010978	CAGGACAATTG TAGTTTTGA	-8.18	4.34E-05	0.41	Exon/CDS	EUR_RS09690
Pair_101	NC_021010.1	-	2320366	2320385	ATTGACAAAGG CCTTTATCT	-8.28	4.43E-05	0.41	Exon/CDS	EUR_RS11055
Pair_143	NC_021010.1	+	1256805	1256824	CATGACAAAGA TTCTTGATA	-8.28	4.43E-05	0.41	Exon/CDS	EUR_RS06065
Pair_166	NC_021010.1	-	744435	744454	GATGTCCAATG TCTTTTCA	-8.30	4.46E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS03630
Pair_167	NC_021010.1	+	11166	11185	TCCGACAATCA TTGTTATCA	-8.34	4.50E-05	0.41	Exon/CDS	EUR_RS00065
Pair_147	NC_021010.1	-	2260136	2260155	AAGGTCAAGTT TATTTGGCA	-8.37	4.53E-05	0.41	Exon/CDS	EUR_RS16375
Pair_10	NC_021010.1	-	2269468	2269487	ACTTACAATTA AATTTGATA	-8.38	4.55E-05	0.41	Intergenic	-

Pair_105	NC_021010.1	+	3031939	3031958	ACTGACAATTA TATTTCCAA	-8.38	4.55E-05	0.41	Exon/CDS	EUR_RS14280
Pair_168	NC_021010.1	+	1572189	1572208	AATGACAAATA CCCTCGCCA	-8.38	4.55E-05	0.41	Exon/CDS	EUR_RS07695
Pair_169	NC_021010.1	+	2581200	2581219	GCTGATAATAG TCTTTGGCA	-8.39	4.57E-05	0.41	Exon/CDS	EUR_RS12325
Pair_130	NC_021010.1	-	1042455	1042474	AAAGACATTTT TTGGTGTCA	-8.45	4.64E-05	0.41	Exon/CDS	EUR_RS05000
Pair_170	NC_021010.1	-	1229860	1229879	TATGACACCTG TTATTTTTA	-8.46	4.66E-05	0.41	Exon/CDS	EUR_RS05920
Pair_95	NC_021010.1	+	2602749	2602768	ATTGTGAGCAA TTTTTGTCA	-8.56	4.78E-05	0.41	Exon/CDS	EUR_RS12415
Pair_92	NC_021010.1	-	2070738	2070757	TCTGCCAAATA TAAATGTCG	-8.64	4.89E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS09960; EUR_RS09965
Pair_149	NC_021010.1	-	1933305	1933324	AATGACCGATA ATCTGGTCA	-8.67	4.95E-05	0.41	Exon/CDS	EUR_RS09335
Pair_171	NC_021010.1	+	2830334	2830353	AATGAAAATGA TTCAGGTCA	-8.67	4.95E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS13385; EUR_RS13390
Pair_172	NC_021010.1	+	1225985	1226004	GTTGACAAGGT TCTTGGTGA	-8.72	5.01E-05	0.41	Exon/CDS	EUR_RS05905
Pair_173	NC_021010.1	-	795992	796011	ACCCACAAATA TATTTGTTA	-8.73	5.03E-05	0.41	Exon/CDS	EUR_RS03870
Pair_113	NC_021010.1	+	109852	109871	ATCGAAAATGA TACTTGACA	-8.74	5.05E-05	0.41	Promoter (- 200~+50bp)	EUR_RS00545
Pair_170	NC_021010.1	+	2428200	2428219	ATTCACAGTAA CAGTTGTGA	-8.81	5.14E-05	0.41	Exon/CDS	EUR_RS11590
Pair_174	NC_021010.1	-	2482101	2482120	AATTACAATGT TTGAAGTCA	-8.81	5.14E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS11905

Pair_175	NC_021010.1	+	1229858	1229877	ATTAAAAATAA CAGGTGTCA	-8.81	5.14E-05	0.41	Exon/CDS	EUR_RS05920
Pair_175	NC_021010.1	+	2482099	2482118	ATTGACTTCAA ACATTGTAA	-8.86	5.21E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS11905
Pair_124	NC_021010.1	-	3161133	3161152	GTAGCCTAAAA TCTTTGTCA	-8.88	5.25E-05	0.41	Exon/CDS	EUR_RS15125
Pair_125	NC_021010.1	+	781635	781654	ATTGAGAATGC TACTTTTCA	-8.90	5.28E-05	0.41	Exon/CDS	EUR_RS03790
Pair_99	NC_021010.1	-	238361	238380	TCTCCCAAATA TAATTGTCG	-8.93	5.30E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS01095; EUR_RS01100
Pair_55	NC_021010.1	+	528389	528408	TATGACAAATT CTGTTGCAA	-8.98	5.40E-05	0.41	Exon/CDS	EUR_RS02525
Pair_82	NC_021010.1	-	1173589	1173608	TATCTCAATTTT ATATGTCA	-8.98	5.40E-05	0.41	Promoter (- 200~+50bp)	EUR_RS05700
Pair_172	NC_021010.1	-	1225987	1226006	CATCACCAAGA ACCTTGTCA	-8.98	5.40E-05	0.41	Exon/CDS	EUR_RS05905
Pair_176	NC_021010.1	-	1832006	1832025	TGTGACCAAAA AGATTGTCT	-9.02	5.46E-05	0.41	Exon/CDS	EUR_RS08890
Pair_112	NC_021010.1	+	2841729	2841748	TCTGATAATGA TATGTGGCA	-9.05	5.51E-05	0.41	Exon/CDS	EUR_RS13420
Pair_177	NC_021010.1	-	2308322	2308341	CATGACAATTG CAATTATCG	-9.08	5.56E-05	0.41	Exon/CDS	EUR_RS11015
Pair_178	NC_021010.1	+	192793	192812	AGTTCCAAATA TTGTTGGCA	-9.09	5.59E-05	0.41	Exon/CDS	EUR_RS00890
Pair_179	NC_021010.1	-	355425	355444	TTTGGCAACAA GCTTTGTGA	-9.15	5.67E-05	0.41	Exon/CDS	EUR_RS01660
Pair_180	NC_021010.1	-	3207726	3207745	TGAAACAATAA TAATTGTCG	-9.15	5.67E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS15375

Pair_181	NC_021010.1	+	2022859	2022878	TCTGACAAGGA TAAATGTAC	-9.20	5.75E-05	0.41	Exon/CDS	EUR_RS09730
Pair_182	NC_021010.1	+	2157906	2157925	ACTGGCAAGAA TATTGGTTA	-9.23	5.81E-05	0.41	Exon/CDS	EUR_RS10315
Pair_44	NC_021010.1	-	3336543	3336562	CGTGACTATAA TCGTTCTCA	-9.27	5.86E-05	0.41	Exon/CDS	EUR_RS16020
Pair_65	NC_021010.1	-	1834015	1834034	TCTCATACTTAT ATTTGTCA	-9.27	5.86E-05	0.41	Exon/CDS	EUR_RS08900
Pair_181	NC_021010.1	-	2022861	2022880	AAGTACATTTA TCCTTGTC	-9.31	5.93E-05	0.41	Exon/CDS	EUR_RS09730
Pair_53	NC_021010.1	-	2901012	2901031	CATGACAATA CATTTGAGA	-9.33	5.95E-05	0.41	Exon/CDS	EUR_RS13685
Pair_131	NC_021010.1	-	2930985	2931004	ACTGAAAAATA TTGGTCTCA	-9.38	6.05E-05	0.41	Exon/CDS	EUR_RS13795
Pair_93	NC_021010.1	-	2049402	2049421	TGTGTCAATAT TATTTATCA	-9.43	6.12E-05	0.41	Promoter (- 200~+50bp)	EUR_RS09850
Pair_116	NC_021010.1	+	2679128	2679147	AATAGCAATAA TTCTTATCA	-9.47	6.19E-05	0.41	Exon/CDS	EUR_RS12740
Pair_79	NC_021010.1	+	41900	41919	TATGACAGTTA TTCCTGTTA	-9.49	6.21E-05	0.41	Exon/CDS	EUR_RS00195
Pair_81	NC_021010.1	+	3196726	3196745	TGAGACAAAAA TAACTCTCA	-9.51	6.25E-05	0.41	Exon/CDS	EUR_RS15315
Pair_123	NC_021010.1	-	1376773	1376792	TGTGCCAAAAA TAATTGCAA	-9.51	6.25E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS06730; EUR_RS06725
Pair_150	NC_021010.1	+	1803769	1803788	TGTGAAGAGTA TATCTGTCA	-9.54	6.31E-05	0.41	Exon/CDS	EUR_RS08750
Pair_144	NC_021010.1	+	1058934	1058953	ATTTACAAACA CATTTGGCA	-9.60	6.40E-05	0.41	Exon/CDS	EUR_RS05075
Pair_120	NC_021010.1	+	795990	796009	TGTAACAAATA TATTTGTGG	-9.62	6.44E-05	0.41	Exon/CDS	EUR_RS03870

Pair_173	NC_021010.1	+	1564373	1564392	TATGACTCTTTT TGTTATCA	-9.62	6.44E-05	0.41	Exon/CDS	EUR_RS07650
Pair_98	NC_021010.1	-	113609	113628	TCTGTCAAAAA TATATGGCA	-9.63	6.45E-05	0.41	Exon/CDS	EUR_RS00560
Pair_183	NC_021010.1	+	1584598	1584617	TATTTCCGTAAT ATTTGTCA	-9.69	6.56E-05	0.41	Promoter (- 200~+50bp)	EUR_RS07740
Pair_136	NC_021010.1	+	694740	694759	ACTGACCTCGA CATTTGTCA	-9.73	6.61E-05	0.41	Exon/CDS	EUR_RS03375
Pair_176	NC_021010.1	+	1832004	1832023	AAAGACAATCT TTTTGGTCA	-9.76	6.64E-05	0.41	Exon/CDS	EUR_RS08890
Pair_161	NC_021010.1	+	1322243	1322262	ACTGACAAATG GAAGAGTCA	-9.78	6.67E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS06475; EUR_RS06470
Pair_182	NC_021010.1	-	2157908	2157927	TATAACCAATA TTCTTGCCA	-9.85	6.79E-05	0.41	Exon/CDS	EUR_RS10315
Pair_159	NC_021010.1	-	3199082	3199101	GATGATAATTA CATTTGAAA	-9.91	6.89E-05	0.41	Exon/CDS	EUR_RS15325
Pair_139	NC_021010.1	+	2809735	2809754	TCTCACAAAGC TTGTTGACA	-9.92	6.90E-05	0.41	Exon/CDS	EUR_RS13310
Pair_158	NC_021010.1	+	355423	355442	TCTCACAAAGC TTGTTGCCA	-9.92	6.90E-05	0.41	Exon/CDS	EUR_RS01660
Pair_179	NC_021010.1	+	211698	211717	TACGAAATAAT TATTTGTCA	-9.92	6.90E-05	0.41	Promoter (- 200~+50bp)	EUR_RS16110; EUR_RS16275
Pair_68	NC_021010.1	+	1329947	1329966	AATGACGACTT CATTTGTGA	-9.95	6.94E-05	0.41	Exon/CDS	EUR_RS06510
Pair_165	NC_021010.1	-	2010961	2010980	AATCAAAACTA CAATTGTCC	-9.96	6.96E-05	0.41	Exon/CDS	EUR_RS09690
Pair_78	NC_021010.1	+	286234	286253	TGCGGCAATTA TCGGTGTCA	-10.04	7.07E-05	0.41	Exon/CDS	EUR_RS01330

Pair_166	NC_021010.1	+	744433	744452	GATGAAAAAGA CATTGGACA	-10.05	7.10E-05	0.41	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS03625; EUR_RS03630
Pair_84	NC_021010.1	+	284334	284353	AGTTACAACAA CAACTGTCA	-10.12	7.21E-05	0.42	Exon/CDS	EUR_RS01320
Pair_64	NC_021010.1	+	2135841	2135860	TATGACATTTA TCCGTGTTA	-10.19	7.33E-05	0.42	Exon/CDS	EUR_RS10240
Pair_122	NC_021010.1	-	1237198	1237217	CTTGACAATGA TGATTGCAA	-10.23	7.38E-05	0.42	Exon/CDS	EUR_RS05955
Pair_109	NC_021010.1	-	1795096	1795115	TATGAAACATT TTGTTGTGA	-10.27	7.44E-05	0.42	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS08700
Pair_80	NC_021010.1	-	11168	11187	CATGATAACAA TGATTGTCG	-10.30	7.48E-05	0.42	Exon/CDS	EUR_RS00065
Pair_167	NC_021010.1	+	2741706	2741725	CCTGACAAATG TAATTGTAC	-10.31	7.48E-05	0.42	Promoter (- 200~+50bp)	EUR_RS12980
Pair_180	NC_021010.1	+	3207724	3207743	CACGACAATTA TTATTGTTT	-10.30	7.48E-05	0.42	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS15375
Pair_126	NC_021010.1	-	2539411	2539430	TATGATACTTTT CGGTGTCA	-10.33	7.51E-05	0.42	Exon/CDS	EUR_RS12145
Pair_154	NC_021010.1	+	1377481	1377500	TACGATAATAA TTCTTGTA	-10.36	7.56E-05	0.42	Exon/CDS	EUR_RS06735
Pair_184	NC_021010.1	-	642535	642554	CTTCACAATTC AAATTTTCA	-10.52	7.82E-05	0.43	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS03110
Pair_177	NC_021010.1	+	2308320	2308339	TGCGATAATTG CAATTGTCA	-10.59	7.93E-05	0.43	Exon/CDS	EUR_RS11015
Pair_155	NC_021010.1	-	1312184	1312203	GATAACAAATA TGATGGTAA	-10.65	8.03E-05	0.43	Exon/CDS	EUR_RS06400

Pair_107	NC_021010.1	+	2269466	2269485	GATATCAAATT TAATTGTAA	-10.72	8.16E-05	0.43	Intergenic	-
Pair_168	NC_021010.1	-	1835409	1835428	CAGCGCAAAGA TTATTGTCA	-10.72	8.16E-05	0.43	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS08905
Pair_75	NC_021010.1	+	320125	320144	GGTCACAGATA TATTTGTCG	-10.85	8.39E-05	0.43	Exon/CDS	EUR_RS01500
Pair_14	NC_021010.1	-	2358197	2358216	CATTACAATTC TTTTTTTCA	-10.86	8.40E-05	0.43	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS11240
Pair_157	NC_021010.1	+	1714031	1714050	CATGATAATTT TTTTTTTCA	-10.86	8.40E-05	0.43	Promoter (- 200~+50bp)	EUR_RS08360; EUR_RS08365
Pair_134	NC_021010.1	-	2428202	2428221	ATTCACAACGT TACTGTGA	-10.88	8.42E-05	0.43	Exon/CDS	EUR_RS11590
Pair_174	NC_021010.1	+	861542	861561	ACTCAGAACTA CTGTTGTCA	-10.88	8.42E-05	0.43	Exon/CDS	EUR_RS04160
Pair_146	NC_021010.1	-	475404	475423	AATGACACTAT CTTTTGTAA	-10.91	8.48E-05	0.43	Exon/CDS	EUR_RS02295
Pair_102	NC_021010.1	-	1180060	1180079	AAAGACTATTT TTATTTTCA	-10.92	8.51E-05	0.43	Exon/CDS	EUR_RS05710
Pair_50	NC_021010.1	-	3009328	3009347	CACGACAATTA TCAGTATCA	-11.00	8.67E-05	0.43	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS14160; EUR_RS14165
Pair_138	NC_021010.1	-	1975610	1975629	TTTGACGTTTAC AATTATCA	-11.01	8.68E-05	0.43	Promoter (- 200~+50bp)	EUR_RS09495
Pair_128	NC_021010.1	+	3188399	3188418	AATGGTAACGT TATTTGGCA	-11.02	8.69E-05	0.43	Exon/CDS	EUR_RS15280
Pair_25	NC_021010.1	+	1852494	1852513	AATCACAATTT CCTTTGTCG	-11.03	8.71E-05	0.43	Exon/CDS	EUR_RS08980
Pair_83	NC_021010.1	-	617472	617491	CATGTCAAATA TTTTCATCA	-11.06	8.80E-05	0.43	Promoter (- 200~+50bp)	EUR_RS02990

Pair_160	NC_021010.1	-	1971383	1971402	GATGACAGCCG CACTTGTCA	-11.07	8.81E-05	0.43	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS09465; EUR_RS09470
Pair_163	NC_021010.1	-	2309772	2309791	TTTGACAAACT TATCTGTCC	-11.07	8.81E-05	0.43	Exon/CDS	EUR_RS11020
Pair_152	NC_021010.1	-	288322	288341	AAGGACACCGC CCGTTGTCA	-11.08	8.84E-05	0.43	Exon/CDS	EUR_RS01335
Pair_153	NC_021010.1	-	3189867	3189886	AATTTCTACTAT ATGTGTCA	-11.08	8.84E-05	0.43	Exon/CDS	EUR_RS15285
Pair_185	NC_021010.1	-	129827	129846	TGTGACAAGCA TTATTGCAA	-11.08	8.84E-05	0.43	Exon/CDS	EUR_RS00625
Pair_114	NC_021010.1	+	3178857	3178876	CTACACATCGA TAGTTGTCA	-11.11	8.88E-05	0.43	Exon/CDS	EUR_RS15215
Pair_164	NC_021010.1	-	1902675	1902694	GTTATCAATTG TCATTGTGA	-11.12	8.92E-05	0.43	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS09190
Pair_186	NC_021010.1	+	1079651	1079670	GCTGTCAAATA AATTTTAA	-11.13	8.95E-05	0.43	Exon/CDS	EUR_RS05175
Pair_186	NC_021010.1	-	1079653	1079672	GATTAAAAATT TATTTGACA	-11.13	8.95E-05	0.43	Exon/CDS	EUR_RS05175
Pair_184	NC_021010.1	+	642533	642552	TTTGAAAATTT GAATTGTGA	-11.16	8.99E-05	0.43	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS03110
Pair_148	NC_021010.1	+	64646	64665	GCTTACAAAGA TATTTTACA	-11.20	9.10E-05	0.43	Exon/CDS	EUR_RS00280
Pair_103	NC_021010.1	+	489217	489236	CCTGAAAAATA ATTTTTC	-11.21	9.11E-05	0.43	Intergenic	-
Pair_169	NC_021010.1	-	2581202	2581221	TCTGCCAAAGA CTATTATCA	-11.23	9.14E-05	0.43	Exon/CDS	EUR_RS12325
Pair_73	NC_021010.1	+	532401	532420	CATGGCAATTA TCATTTT	-11.29	9.27E-05	0.43	Exon/CDS	EUR_RS02550

Pair_145	NC_021010.1	+	789477	789496	CATTACAAAGA TTATTTTAA	-11.30	9.28E-05	0.43	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS03840
Pair_30	NC_021010.1	+	1186367	1186386	AGTGACAGTAA CCTTTGCCA	-11.33	9.34E-05	0.43	Exon/CDS	EUR_RS05735
Pair_31	NC_021010.1	+	1191128	1191147	AGTGACAGTAA CCTTTGCCA	-11.33	9.34E-05	0.43	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS05760
Pair_129	NC_021010.1	+	402624	402643	AATGGCAATAA CCACTGTGA	-11.34	9.38E-05	0.43	Exon/CDS	EUR_RS01890
Pair_171	NC_021010.1	+	1933303	1933322	GATGACCAGAT TATCGGTCA	-11.35	9.41E-05	0.43	Exon/CDS	EUR_RS09335
Pair_77	NC_021010.1	-	1943152	1943171	TTTGACAAATA CAATATTCC	-11.37	9.45E-05	0.43	Exon/CDS	EUR_RS09360
Pair_156	NC_021010.1	+	2429236	2429255	ACTGACACCGA TTGTGGCCA	-11.38	9.46E-05	0.43	Exon/CDS	EUR_RS11595
Pair_183	NC_021010.1	-	1584600	1584619	AATGACAAATA TTACGGAAA	-11.41	9.56E-05	0.44	Promoter (- 200~+50bp)	EUR_RS07740
Pair_12	NC_021010.1	+	129825	129844	GTTTGCAATAA TGCTTGTC	-11.45	9.64E-05	0.44	Exon/CDS	EUR_RS00625
Pair_142	NC_021010.1	+	1624191	1624210	CATCCCAATAG TTCTTGTC	-11.45	9.64E-05	0.44	Exon/CDS	EUR_RS07925
Pair_185	NC_021010.1	+	1664785	1664804	CGTGACAATAA TCATTGTGG	-11.45	9.64E-05	0.44	Exon/CDS	EUR_RS08120
Pair_178	NC_021010.1	-	192795	192814	ACTGCCAACAA TATTTGGAA	-11.53	9.86E-05	0.44	Exon/CDS	EUR_RS00890
Pair_121	NC_021010.1	+	2909696	2909715	GCAGACCATTA TCGATGTCA	-11.55	9.92E-05	0.44	Exon/CDS	EUR_RS13715
Pair_17	NC_021010.1	-	1274108	1274127	CATGATAATTT TCTTTGTAA	-11.56	9.96E-05	0.44	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS06155; EUR_RS06160

Pair_96	NC_021010.1	-	450839	450858	TTTTAAAATTTTC ATTTGTCA	-11.57	9.97E-05	0.44	Exon/CDS; Promoter (- 200~+50bp)	EUR_RS02175
Pair_32	NC_021010.1	+	805975	805994	CTTGACAAAAT TATTGGTTA	-11.58	9.98E-05	0.44	Promoter (- 200~+50bp)	EUR_RS03920
Pair_162	NC_021010.1	-	1741038	1741057	TGTGACAAACA ACATAGTGA	-11.58	9.98E-05	0.44	Promoter (- 200~+50bp)	EUR_RS08485

Note: Genome-wide motif scanning for the candidate transcriptional repressor was performed against the reference genome (NC_021010.1) using FIMO with a significance threshold of $p < 1.00E-4$. Complementary reverse-palindromic binding motifs on positive (+) and negative (-) strands within 2bp distance were paired, assigned identical Pair ID identifiers, and ranked in ascending order of their P values. Target genomic regions were annotated as Promoter (defined as -200bp to +50bp relative to the translational start site), Exon/CDS, or Intergenic. False discovery rates (q values) were corrected via the Benjamini-Hochberg procedure.

Abbreviations: PWM, position weight matrix; CDS, coding DNA sequence; FDR, false discovery rate; bp, base pair.

Table S10. Functional annotation and domain architecture of candidate target genes regulated by the transcriptional repressor.

Locus Tag	Gene Symbol	NCBI Protein ID	COG Category	EC Number	PFAM Domains	Protein Description
EUR_RS00065	-	WP_015515500.1	M	-	Sulfatase	PFAM sulfatase
EUR_RS00195	rpoC	WP_015515518.1	K	2.7.7.6	RNA_pol_Rpb1_1, RNA_pol_Rpb1_2, RNA_pol_Rpb1_3, RNA_pol_Rpb1_4, RNA_pol_Rpb1_5	DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates
EUR_RS00280	yxiO	WP_015515530.1	S	-	ATG22	Psort location CytoplasmicMembrane, score 10.00
EUR_RS00545	cnpD2	WP_012741370.1	T	-	HD,HD_5	PFAM metal-dependent phosphohydrolase, HD sub domain
EUR_RS00560	saeS	WP_015515551.1	T	2.7.13.3	HAMP,HATPase_c, HisKA	Histidine kinase- DNA gyrase B
EUR_RS00625	-	WP_015515561.1	T	2.7.13.3	HAMP,HATPase_c, His_kinase,dCache_1	K07718 two-component system, sensor histidine kinase YesM
EUR_RS00695	msmF	WP_015515575.1	P	-	BPD_transp_1	Psort location CytoplasmicMembrane, score 10.00
EUR_RS00890	-	WP_306779818.1	-	-	-	-
EUR_RS01095	-	WP_012741515.1	S	-	YukD	WXG100 protein secretion system (Wss), protein YukD
EUR_RS01100	yukA	WP_015515625.1	D	-	FHA,FtsK_SpoIIIE, FtsK_SpoIIIE_N	FtsK/SpoIIIE family
EUR_RS01275	-	WP_015515656.1	K	3.6.4.12	AlbA_2,HATPase_c _4,HTH_24,HTH_ DeoR	Putative ATP-dependent DNA helicase recG C-terminal
EUR_RS01320	-	WP_015515664.1	P	-	CbiQ	cobalt transport protein
EUR_RS01330	-	WP_055061104.1	V	-	ABC_membrane,A BC_tran	abc transporter atp-binding protein

EUR_RS01335	-	WP_055061105.1	V	3.6.3.25	ABC_membrane,ABC_tran	abc transporter atp-binding protein
EUR_RS01500	glgX	WP_015515692.1	G	-	GDE_C,GDE_N	Glycogen debranching enzyme
EUR_RS01660	ctpA	WP_015515713.1	M	3.4.21.102	PDZ,PDZ_2,PG_binding_1,Peptidase_S41	Belongs to the peptidase S41A family
EUR_RS01685	pheB	WP_012741625.1	S	5.4.99.5	ACT,ACT_4	Belongs to the UPF0735 family
EUR_RS01730	phbA	WP_012741635.1	I	2.3.1.9	Thiolase_C,Thiolase_N	Belongs to the thiolase family
EUR_RS01820	rimI	WP_012741724.1	K	2.3.1.128,2.3.1.234	Acetyltransf_1,Acetyltransf_10	This enzyme acetylates the N-terminal alanine of ribosomal protein S18
EUR_RS01890	-	WP_015515746.1	S	-	ABC2_membrane_4	ABC-2 family transporter protein
EUR_RS01960	-	WP_015515754.1	-	-	-	-
EUR_RS01975	-	WP_015515758.1	L	-	DUF3427,HIT,Helicase_C,PLDc_2,ResI II	helicase
EUR_RS02175	-	WP_055225040.1	S	-	Fic,HTH_24	Fic/DOC family
EUR_RS02230	-	WP_009265522.1	T	-	Response_reg,Trans_reg_C	Response regulator receiver domain
EUR_RS02295	-	WP_015515804.1	L	-	Phage_int_SAM_4,Phage_integrase	Phage integrase, N-terminal SAM-like domain
EUR_RS02315	-	WP_012744107.1	S	-	AAA-ATPase_like,AAA_21,PDDEXK_9	COG NOG08812 non supervised orthologous group
EUR_RS02410	-	WP_172704783.1	V	-	MatE	MATE efflux family protein
EUR_RS02415	-	WP_012744088.1	-	-	-	-
EUR_RS02525	CP_0318	WP_015515839.1	I	-	PLDc_2	COG1502 Phosphatidylserine phosphatidylglycerophosphate cardiolipin synthases and related enzymes
EUR_RS02550	bioY	WP_012744042.1	S	-	BioY	BioY family
EUR_RS02630	yaaT	WP_015515853.1	K	-	PSP1	domain protein

EUR_RS02990	acpP	WP_012743902.1	IQ	-	PP-binding	Carrier of the growing fatty acid chain in fatty acid biosynthesis
EUR_RS03050	ribD	WP_015515916.1	H	1.1.1.193,3.5.4.26	RibD_C,dCMP_cyt_deam_1	Converts 2,5-diamino-6-(ribosylamino)-4(3h)-pyrimidinone 5'-phosphate into 5-amino-6-(ribosylamino)-2,4(1h,3h)-pyrimidinedione 5'-phosphate
EUR_RS03110	-	WP_015515929.1	-	-	-	-
EUR_RS03225	XK27_07105	WP_015515948.1	K	-	HTH_26,HTH_3	Helix-turn-helix domain
EUR_RS03375	cvaB	WP_015515969.1	V	-	ABC_membrane,A BC_tran,DUF3335, Peptidase_C39	ABC-type bacteriocin transporter
EUR_RS03545	aspC	WP_015515998.1	E	2.6.1.1	Aminotran_1_2	PFAM aminotransferase class I and II
EUR_RS03625	-	WP_007886614.1	S	-	DUF3801	PROTEIN OF UNKNOWN FUNCTION (DUF3801)
EUR_RS03630	-	-	-	-	-	-
EUR_RS03790	-	WP_044926716.1	L	-	DUF3258,Phage_int_SAM_3,Phage_int_egrase	Belongs to the 'phage' integrase family
EUR_RS03820	-	WP_015516010.1	V	-	DUF3578,DUF3883	Domain of unknown function (DUF3883)
EUR_RS03840	-	WP_015516013.1	-	-	-	-
EUR_RS03870	-	WP_012743742.1	O	-	UPF0051	Uncharacterized protein family (UPF0051)
EUR_RS03920	maf	WP_015516027.1	S	-	HD_3	Psort location Cytoplasmic, score
EUR_RS04120	-	WP_015516053.1	S	-	AAA_15,AAA_21,AAA_23	AAA ATPase domain
EUR_RS04160	noIL	WP_015516060.1	G	-	Acyl_transf_3	Acyltransferase family
EUR_RS04200	-	WP_306792023.1	KLT	-	-	serine threonine protein kinase
EUR_RS04205	-	WP_015516067.1	-	-	-	-
EUR_RS04250	-	WP_015516076.1	-	-	-	-

EUR_RS04830	ppaC	WP_015516153.1	C	3.6.1.1	CBS,DHH,DHHA2, DRTGG	domain protein
EUR_RS04835	-	WP_015516154.1	-	-	-	-
EUR_RS05000	ycsE	WP_015516175.1	S	3.1.3.104	Hydrolase_3	Cof-like hydrolase
EUR_RS05075	yocR	WP_015516186.1	S	-	SNF	Belongs to the sodium neurotransmitter symporter (SNF) (TC 2.A.22) family
EUR_RS05175	-	WP_307006156.1	S	-	DUF4071	Tetratricopeptide repeat
EUR_RS05190	-	-	-	-	-	-
EUR_RS05700	-	WP_307006238.1	-	-	-	-
EUR_RS05710	fhcC	WP_307006241.1	M	1.2.7.12	GXGXG	COG3209 Rhs family protein
EUR_RS05720	-	WP_015516281.1	-	-	-	-
EUR_RS05735	-	WP_015516284.1	-	-	-	-
EUR_RS05760	-	WP_306794103.1	-	-	-	-
EUR_RS05890	-	WP_015516300.1	P	-	DUF3887,OAD_ga mma	Oxaloacetate decarboxylase, gamma chain
EUR_RS05905	oadA	WP_012742472.1	C	2.1.3.1,4.1. 1.3,6.4.1.1, 6.4.1.7	Biotin_lipoyl,HMG L-like,PYC_OADA	carboxylase
EUR_RS05920	ytfP	WP_015516303.1	S	-	HI0933_like	Flavoprotein family
EUR_RS05955	rnfD	WP_022293189.1	C	1.6.5.8	NQR2_RnfD_RnfE	Part of a membrane complex involved in electron transport
EUR_RS06040	rodA	WP_015516316.1	D	-	FTSW_RODA_SP OVE	Belongs to the SEDS family
EUR_RS06065	-	WP_015516321.1	S	-	Spore_YtfJ	Sporulation protein YtfJ
EUR_RS06155	rluC	WP_015516332.1	J	5.4.99.23,5. 4.99.24,5.4. 99.28,5.4.9 9.29	PseudoU_synth_2,S 4	Belongs to the pseudouridine synthase RluA family

EUR_RS06160	recU	WP_015516333.1	L	-	RecU	Endonuclease that resolves Holliday junction intermediates in genetic recombination. Cleaves mobile four-strand junctions by introducing symmetrical nicks in paired strands. Promotes annealing of linear ssDNA with homologous dsDNA. Required for DNA repair, homologous recombination and chromosome segregation
EUR_RS06200	rng	WP_015516339.1	J	-	RNase_E_G,S1	ribonuclease, Rne Rng family
EUR_RS06400	-	WP_307006293.1	-	-	-	-
EUR_RS06470	mgsA	WP_012742580.1	G	2.7.1.24,4.2 .3.3	MGS	methylglyoxal synthase
EUR_RS06475	rodA	WP_012742581.1	D	-	FTSW_RODA_SP OVE	Belongs to the SEDS family
EUR_RS06510	radC	WP_015516385.1	E	-	RadC	Belongs to the UPF0758 family
EUR_RS06565	phoH	WP_015516392.1	T	-	PhoH	phosphate starvation-inducible protein
EUR_RS06725	fliR	WP_012742632.1	N	-	Bac_export_1	flagellar biosynthetic protein FliR
EUR_RS06730	fliQ	WP_012742633.1	N	-	Bac_export_3	Flagellar biosynthetic protein FliQ
EUR_RS06735	fliP	WP_012742634.1	N	-	FliP	Plays a role in the flagellum-specific transport system
EUR_RS07005	-	WP_015516442.1	K	-	AAA_16,Abhydrola se_1,BTAD,Trans_r eg_C	Psort location Cytoplasmic, score
EUR_RS07040	-	WP_306781471.1	S	-	Transposase_31	Psort location Cytoplasmic, score
EUR_RS07150	-	WP_015516468.1	-	-	Cna_B,Gram_pos_a nchor	-
EUR_RS07650	cobH	WP_416385941.1	H	5.4.99.60,5. 4.99.61	CbiC,TP_methylase	Precorrin-8X methylmutase
EUR_RS07695	cbiD	WP_015516537.1	HP	2.1.1.195,3. 6.3.34	ABC_tran,CbiD,GA Tase_3,zf-like	ATPases associated with a variety of cellular activities

EUR_RS07740	ydhO1	WP_015516544.1	MT	3.5.1.28	Cu_amine_oxidN1, NLPC_P60,SH3_3	NlpC/P60 family
EUR_RS07815	infC	WP_012742792.1	J	-	IF3_C,IF3_N	IF-3 binds to the 30S ribosomal subunit and shifts the equilibrium between 70S ribosomes and their 50S and 30S subunits in favor of the free subunits, thus enhancing the availability of 30S subunits on which protein synthesis initiation begins
EUR_RS07925	glgA	WP_015516567.1	G	2.4.1.21	Glyco_transf_5,Glycos_transf_1	Synthesizes alpha-1,4-glucan chains using ADP-glucose
EUR_RS07955	-	WP_015516571.1	-	-	-	-
EUR_RS08120	glnQ	WP_015516593.1	E	3.6.3.21	ABC_tran	abc transporter atp-binding protein
EUR_RS08300	-	WP_015516620.1	S	-	Mem_trans	Membrane transport protein
EUR_RS08305	-	WP_307006445.1	K	-	HTH_1,LysR_substrate	LysR substrate binding domain
EUR_RS08360	-	-	-	-	-	-
EUR_RS08365	-	WP_015516629.1	-	-	-	-
EUR_RS08430	-	-	-	-	-	-
EUR_RS08485	-	WP_015516650.1	T	3.6.1.11,3.6.1.40	HD	metal-dependent phosphohydrolase, HD sub domain
EUR_RS08585	-	WP_015516665.1	-	-	-	-
EUR_RS08665	-	WP_015516677.1	S	-	SNF	Sodium:neurotransmitter symporter family
EUR_RS08670	metF	WP_012743035.1	E	1.5.1.20	MTHFR	Methylenetetrahydrofolate reductase
EUR_RS08675	-	WP_015516678.1	V	-	MatE	MATE efflux family protein

EUR_RS08700	nadK	WP_015516683.1	H	2.7.1.23	NAD_kinase	Involved in the regulation of the intracellular balance of NAD and NADP, and is a key enzyme in the biosynthesis of NADP. Catalyzes specifically the phosphorylation on 2'-hydroxyl of the adenosine moiety of NAD to yield NADP
EUR_RS08745	glgC	WP_015516690.1	H	2.7.7.27	Hexapep,NTP_trans ferase	Catalyzes the synthesis of ADP-glucose, a sugar donor used in elongation reactions on alpha-glucans
EUR_RS08750	metAA	WP_012743052.1	E	2.3.1.46	HTS	Transfers an acetyl group from acetyl-CoA to L- homoserine, forming acetyl-L- homoserine
EUR_RS08850	argS	WP_015516702.1	J	6.1.1.19	Arg_tRNA_synt_N, DALR_1,tRNA- synt_1d	Arginyl-tRNA synthetase
EUR_RS08890	ysh1	WP_015516710.1	J	-	Beta- Casp,Lactamase_B, Lactamase_B_2,Lac tamase_B_6,RMMB L	exonuclease of the beta-lactamase fold involved in RNA processing
EUR_RS08900	spoIIIGA	WP_307007086.1	M	-	Peptidase_U4	Psort location CytoplasmicMembrane, score

EUR_RS08905	ftsZ	WP_012743081.1	D	-	FtsZ_C,Tubulin	Essential cell division protein that forms a contractile ring structure (Z ring) at the future cell division site. The regulation of the ring assembly controls the timing and the location of cell division. One of the functions of the FtsZ ring is to recruit other cell division proteins to the septum to produce a new cell wall between the dividing cells. Binds GTP and shows GTPase activity
EUR_RS08980	aha1	WP_015516720.1	P	-	Cation_ATPase_N, E1- E2_ATPase,Hydrolase	ATPase, P-type
EUR_RS09100	-	WP_015516735.1	S	-	-	Psort location CytoplasmicMembrane, score
EUR_RS09175	-	WP_015516747.1	C	1.12.98.1	Fer4,Fer4_7,FrhB_FdhB_C,FrhB_FdhB_N,PS_pyruv_trans	Coenzyme F420 hydrogenase/dehydrogenase, beta subunit C terminus
EUR_RS09190	-	WP_015516750.1	S	-	PS_pyruv_trans,Radical_SAM	Polysaccharide pyruvyl transferase
EUR_RS09335	htpG	WP_015516776.1	O	-	HATPase_c,HATPase_c_3,HSP90	Molecular chaperone. Has ATPase activity

EUR_RS09360	addB	WP_015516781.1	L	3.1.21.3,3.6 .4.12	Exonuc_V_gamma, PDDEXK_1,UvrD_ C	The heterodimer acts as both an ATP- dependent DNA helicase and an ATP- dependent, dual-direction single- stranded exonuclease. Recognizes the chi site generating a DNA molecule suitable for the initiation of homologous recombination. The AddB nuclease domain is not required for chi fragment generation
EUR_RS09465	-	WP_307006529.1	S	-	-	Psort location CytoplasmicMembrane, score
EUR_RS09470	-	WP_008402210.1	-	-	-	-
EUR_RS09475	-	WP_004843525.1	-	-	-	-
EUR_RS09480	-	WP_005608344.1	S	-	DUF1430	Psort location CytoplasmicMembrane, score
EUR_RS09495	-	WP_015516798.1	-	-	-	-
EUR_RS09530	-	WP_055238665.1	S	-	NYN	Conserved Protein
EUR_RS09620	-	WP_012741777.1	S	-	AAA_14,AAA_35, ATPase_2,TniB	PFAM Archaeal ATPase
EUR_RS09690	-	WP_015516822.1	S	-	EamA	Psort location CytoplasmicMembrane, score
EUR_RS09730	-	WP_015516830.1	-	-	-	-
EUR_RS09850	-	-	-	-	-	-
EUR_RS09960	znuB	WP_012741858.1	P	-	ABC-3	ABC 3 transport family
EUR_RS09965	-	WP_015516860.1	-	-	-	-
EUR_RS10240	-	WP_015516903.1	P	-	BPD_transp_1	PFAM binding-protein-dependent transport systems inner membrane component
EUR_RS10315	thrE	WP_015516915.1	K	-	ThrE,ThrE_2	Psort location CytoplasmicMembrane, score

EUR_RS10385	-	WP_306775944.1	S	-	CxxCxxCC	N-methylation of lysine residues in flagellin K00599
EUR_RS10535	cobI	WP_015568886.1	H	2.1.1.130,2.1.1.151,4.9.1.3	CbiK,TP_methylase	Cobalt chelatase (CbiK)
EUR_RS10540	-	WP_015516949.1	E	-	HGD-D	2-hydroxyglutaryl-CoA dehydratase, D-component
EUR_RS11015	-	WP_015517030.1	S	-	ABC2_membrane_2	ABC-2 family transporter protein
EUR_RS11020	-	WP_015517031.1	S	-	DUF5050	ABC-2 family transporter protein
EUR_RS11055	asnC	WP_041254504.1	K	-	AsnC_trans_reg,HTH_24,HTH_AsnC-type	Transcriptional regulator, AsnC family
EUR_RS11240	yybN	WP_015517059.1	S	-	DUF2712	PROTEIN OF UNKNOWN FUNCTION (DUF2712)
EUR_RS11245	-	WP_015517060.1	-	-	-	-
EUR_RS11295	-	WP_015517065.1	O	-	Peptidase_M10	Matrixin
EUR_RS11325	-	WP_012742212.1	-	-	-	-
EUR_RS11350	nadE	WP_307006650.1	H	6.3.1.5,6.3.5.1	CN_hydrolase,NAD_synthase	Catalyzes the ATP-dependent amidation of deamido-NAD to form NAD. Uses
EUR_RS11405	-	WP_015517078.1	T	-	Response_reg,Trans_reg_C	Transcriptional regulatory protein, C terminal
EUR_RS11505	pcrA	WP_015517095.1	L	3.6.4.12	UvrD-helicase,UvrD_C	DNA helicase
EUR_RS11510	-	WP_015517096.1	-	-	-	-
EUR_RS11590	-	WP_215677306.1	U	-	T2SSE	Type II IV secretion system protein
EUR_RS11595	-	WP_015517110.1	U	-	T2SSF	Psort location CytoplasmicMembrane, score
EUR_RS11650	-	WP_015517121.1	S	-	-	Psort location CytoplasmicMembrane, score
EUR_RS11655	-	WP_015517122.1	L	2.1.1.37	DNA_methylase	Belongs to the class I-like SAM-binding methyltransferase superfamily. C5-methyltransferase family

EUR_RS11745	-	WP_015517140.1	S	-	-	Psort location Cytoplasmic, score
EUR_RS11830	-	WP_015517153.1	-	-	-	-
EUR_RS11860	-	WP_015517159.1	-	-	-	-
EUR_RS11905	-	WP_012743608.1	S	-	DUF2442	PROTEIN OF UNKNOWN FUNCTION (DUF2442)
EUR_RS12020	-	WP_015517179.1	-	-	-	-
EUR_RS12135	-	WP_307006738.1	S	-	TPM_phosphatase	TPM domain
EUR_RS12140	ybeL	WP_015517198.1	J	1.17.4.1,4.6 .1.1	DUF1451	peptidyl-tyrosine sulfation
EUR_RS12145	trkH	WP_015517199.1	P	-	TrkH	Cation transport protein
EUR_RS12325	glf	WP_015517228.1	M	5.4.99.9	GLF,NAD_binding_8	UDP-galactopyranose mutase
EUR_RS12355	cps3F	WP_015517234.1	-	-	-	-
EUR_RS12360	cpsE	WP_015517235.1	M	-	Bac_transf,CoA_binding_3,STAS	sugar transferase
EUR_RS12415	-	WP_015517245.1	M	3.2.1.21,3.5 .1.28	Amidase_3,CW_binding_1,Fn3-like,Glucosaminidase,Glyco_hydro_3,Glyco_hydro_3_C	N-acetylmuramoyl-L-alanine amidase
EUR_RS12740	-	WP_015517292.1	-	-	-	-
EUR_RS12805	dapB	WP_015517300.1	E	1.17.1.8	DapB_C,DapB_N	Catalyzes the conversion of 4-hydroxy-tetrahydrodipicolinate (HTPA) to tetrahydrodipicolinate
EUR_RS12980	-	WP_015517326.1	S	-	DUF3990	PROTEIN OF UNKNOWN FUNCTION (DUF3990)
EUR_RS13145	xsa	WP_307006813.1	G	3.2.1.55	Alpha-L-AF_C	Alpha-L-arabinofuranosidase
EUR_RS13190	-	WP_015517353.1	-	-	-	-

Phosphorylase is an important allosteric enzyme in carbohydrate metabolism. Enzymes from different sources differ in their regulatory mechanisms and in their natural substrates. However, all known phosphorylases share catalytic and structural properties

Belongs to the 'phage' integrase family

EcoEI R protein C-terminal

Isochorismatase family
Catalyzes the synthesis of beta-nicotinate D- ribonucleotide from nicotinate and 5-phospho-D-ribose 1-phosphate at the expense of ATP

ABC transporter

Belongs to the sodium solute symporter (SSF) (TC 2.A.21) family

Specifically methylates position 2 of adenine 2503 in 23S rRNA and position 2 of adenine 37 in tRNAs

Diguanylate cyclase (GGDEF) domain

SH3 domain protein

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-

-

-

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EUR_RS13890	-	WP_012744368.1	-	-	-	-
EUR_RS13920	-	WP_015517468.1	-	-	-	-
EUR_RS14045	dnaK	WP_015517488.1	O	-	HSP70	Heat shock 70 kDa protein
EUR_RS14160	-	WP_012740974.1	S	-	Flp1_like	Putative Flagellin, Flp1-like, domain
EUR_RS14165	-	WP_307006870.1	S	-	-	Psort location
EUR_RS14250	lysS	WP_015517514.1	J	6.1.1.6	tRNA-synt_2,tRNA_anti-codon,tRNA_bind	Belongs to the class-II aminoacyl-tRNA synthetase family
EUR_RS14280	-	WP_007286197.1	T	-	HATPase_c	His Kinase A (phosphoacceptor) domain
EUR_RS14975	qmoA	WP_015517610.1	C	-	FAD_oxidored,Fer4,Fer4_7,Pyr_redox_2	4Fe-4S dicluster domain
EUR_RS15125	-	WP_015517626.1	V	-	FtsX	Efflux ABC transporter, permease protein
EUR_RS15215	yocS	WP_330361655.1	S	-	SBF	Psort location CytoplasmicMembrane, score 9.99
EUR_RS15225	-	WP_015517645.1	S	-	DegV	EDD domain protein, DegV family
EUR_RS15230	nfo	WP_015517646.1	L	3.1.21.2	AP_endonuc_2	Endonuclease IV plays a role in DNA repair. It cleaves phosphodiester bonds at apurinic or apyrimidinic sites (AP sites) to produce new 5'-ends that are base-free deoxyribose 5-phosphate residues. It preferentially attacks modified AP sites created by bleomycin and neocarzinostatin
EUR_RS15275	-	WP_015517653.1	S	-	DUF3783	Domain of unknown function (DUF3783)
EUR_RS15280	-	WP_012741133.1	T	-	LytTR,Response_re_g	LytTr DNA-binding domain
EUR_RS15285	-	WP_306754280.1	T	-	HATPase_c_5,PAS_9	GHKL domain

EUR_RS15315	-	WP_015517658.1	K	-	AraC_binding,HTH_18,HTH_AraC	COG2207 AraC-type DNA-binding domain-containing proteins
EUR_RS15325	-	WP_022293762.1	S	-	BPD_transp_2	Branched-chain amino acid transport system / permease component
EUR_RS15330	-	WP_012741144.1	S	-	ABC_tran	ATPases associated with a variety of cellular activities
EUR_RS15375	-	WP_015517666.1	-	-	-	-
EUR_RS15840	fumB	WP_015517734.1	C	4.2.1.2	Fumerase_C	Fe-S type, tartrate fumarate subfamily, beta
EUR_RS15895	yidC	WP_015517739.1	U	-	60KD_IMP	Membrane protein insertase, YidC Oxa1 family
EUR_RS15900	jag	WP_012744416.1	S	-	Jag_N,KH_4,R3H	R3H domain protein
EUR_RS16020	amyC	WP_012744388.1	G	-	BPD_transp_1	Binding-protein-dependent transport system inner membrane component
EUR_RS16110	-	WP_307007055.1	S	-	BrnA_antitoxin,Cop G_antitoxin	BrnA antitoxin of type II toxin-antitoxin system
EUR_RS16275	-	-	-	-	-	-
EUR_RS16375	XK27_0050 0	WP_015516983.1	L	-	Eco57I,Helicase_C,N6_Mtase,ResIII,S NF2_N	helicase C-terminal domain protein

Note: Candidate target genes regulated by or containing the identified repressor binding motifs were retrieved and functionally profiled based on NCBI RefSeq annotations and eggNOG-mapper (v2). Functional categories, enzyme commission (EC) numbers, and structural domain architectures were assigned using COG, EC, and Pfam databases, respectively.

Abbreviations: COG, Clusters of Orthologous Groups (e.g., J: Translation/ribosomal structure; K: Transcription; L: Replication, recombination and repair; M: Cell wall/membrane/envelope biogenesis; G: Carbohydrate transport and metabolism; P: Inorganic ion transport and metabolism; S: Function unknown); EC, Enzyme Commission; Pfam, Protein families database; RefSeq, NCBI Reference Sequence Database.

Table S11. Rosetta Energy Breakdown and Scoring Terms for Transcriptional Regulator Dimer–DNA Complexes Across Wild-Type and Mutant Systems.

Target Gene	System Variant	Total Score	van der Waals Attraction (fa_atr)	van der Waals Repulsion (fa_rep)	Electrostatic Interactions (fa_elec)	Solvation Energy (fa_sol)	Sidechain Hydrogen Bonds (hbond_sc)	Backbone Hydrogen Bonds (hbond_bb_sc + hbond_sr_lr_bb)
XK27_07105	Wild-Type (WT)	99.41	-1262.17	133.48	-498.78	1124.56	-133.48	-94.21
	Mutant	762.55	-1385.09	982.55	-309.58	1219.7	-101.85	-75.31
phbA	Wild-Type (WT)	128.57	-1235.16	125.88	-488.14	1149.39	-122.72	-98.64
	Mutant	1252.61	-1341.99	1430.54	-320.36	1180.77	-91.04	-81.85
xsa	Wild-Type (WT)	165.32	-1239.98	132.67	-506.53	1102.47	-133.66	-92.74
	Mutant	1071.71	-1365.75	1221.39	-297.25	1208.37	-80.27	-81.94

Note: All energy terms were calculated using the Rosetta ref2015 energy function following classical molecular mechanics energy minimization in OpenMM. Energy breakdown values are reported in Rosetta Energy Units (REU). Lower (more negative) values indicate thermodynamically more favorable interactions.

Abbreviations: WT, wild-type; REU, Rosetta energy units; fa_atr, full-atom attractive van der Waals energy; fa_rep, full-atom repulsive van der Waals energy; fa_elec, Coulombic electrostatic potential; fa_sol, Lazaridis-Karplus implicit solvation energy; hbond_sc, sidechain-sidechain hydrogen bonds; hbond_bb_sc, backbone-sidechain hydrogen bonds; hbond_sr_bb, short-range backbone-backbone hydrogen bonds; hbond_lr_bb, long-range backbone-backbone hydrogen bonds.

Table S12. Oligonucleotide probe sequences used for surface plasmon resonance (SPR).

Probe Name	Target Gene Locus	Type	5' Modification	Sense Strand Sequence (5' → 3')	Length (nt)
XK27_07105-XK27_07105_WT	EUR_RS03225	Wild-type	5'-Biotin	ATGACAAGAATATAATACATTATGACAAATA AAGTTGTCAAACAGACAAAAATAATTGTC	60
XK27_07105-XK27_07105_Mut	EUR_RS03225	Mutant	5'-Biotin	ATGACAAGAATATAATACATCCGCGCGCGCG CGCGCGCGCAACAGACAAAAATAATTGTC	60
XK27_07105-phbA_WT	EUR_RS01730	Wild-type	5'-Biotin	CAATTTAAAGGAGATAATATAATGGCAAAGA AAGTTGTAATCGCAAGTGCTTGCCGTACA	60
XK27_07105-phbA_Mut	EUR_RS01730	Mutant	5'-Biotin	CAATTTAAAGGAGATAATATCCGCGCGCGCG CGCGCGCGCTCGCAAGTGCTTGCCGTACA	60
XK27_07105-xsa_WT	EUR_RS13145	Wild-type	5'-Biotin	ATAAGAGATAAAGGAGAACTATGGCAAAAA TTATTGTAAATAATGAGAATAAAAAGAGT	60
XK27_07105-xsa_Mut	EUR_RS13145	Mutant	5'-Biotin	ATAAGAGATAAAGGAGAAACCCGCGCGCGCG CGCGCGCGCATAATGAGAATAAAAAGAGT	60

Note: The 5'-biotinylated sense strands and complementary unmodified antisense strands were synthesized and annealed at an equimolar ratio (10 μ mol/L each) in annealing buffer (10 mmol/L Tris-HCl, 50 mmol/L NaCl, 1 mmol/L EDTA, pH 8.0) to generate double-stranded DNA probes.

Mutant probes were generated by substituting the core palindromic binding motifs with GC-rich poly-linkers.

Abbreviations: WT, wild-type; Mut, mutant; nt, nucleotide; SPR, surface plasmon resonance.

Table S13. Key resources and reagents used in this study.

REAGENT or RESOURCE	SOURCE	IDENTIFIER
BL21(DE3) Chemically Competent Cell	Tsingke	Cat#DLC201
IPTG	Sangon Biotech	Cat#A600168
Protease inhibitors	MCE	Cat#HY-K0012
Tris	Sangon Biotech	Cat#A610195
NaCl	Sangon Biotech	Cat#A501218
EDTA	Sangon Biotech	Cat#B540625
Imidazole	Sangon Biotech	Cat#A500529
Ni-NTA beads	Cytiva	Cat#17526801
HBS-EP+ buffer	Cytiva	Cat#BR100669
Biotin-Labeled DNA Probes	Tsingke	N/A
Streptavidin (SA) Probes	Gator	Cat#160002
Regeneration Buffer	Gator	Cat#120012

Note: Commercial reagents, bacterial competent cells, chromatography resins, and biosensor consumables used for recombinant protein expression, purification, and bio-layer interferometry (BLI) binding assays are listed alongside their respective commercial sources and catalog identifiers (Methods). Biotinylated and unmodified oligonucleotide DNA probes were custom-synthesized by Tsingke Biotechnology.

Abbreviations: IPTG, isopropyl beta-D-1-thiogalactopyranoside; Tris, tris(hydroxymethyl)aminomethane; EDTA, ethylenediaminetetraacetic acid; Ni-NTA, nickel-nitrilotriacetic acid; HBS-EP+, 10 mmol/L HEPES, 150 mmol/L NaCl, 3 mmol/L EDTA, and 0.05% (v/v) Surfactant P20; SA, streptavidin; BLI, bio-layer interferometry; MCE, MedChemExpress; N/A, not applicable.