MOLECULAR ECOLOGY
RESOURCES

Supplemental Information for:

Development of DNA methylation-based epigenetic age predictors in loblolly pine (*Pinus taeda*)

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Supplemental Table 1. Top 35 associated (R > |0.5|) CpG cytosines with age

Site	Scaffold	Position	Spearman Correlation	P Value	Cytosine Region	Blast (400 BP Window)	Score	E Value
2285	APFE030121794.1	148	0.733324289	0.200629	Open Sea	gb|AC241290.1| Pinus taeda clone PT_7Ba2797E03, complete sequence	470	0.00E+00
2337	APFE030124122.1	12062	0.785210138	0.039398	Open Sea	gb|BT124256.1| Picea sitchensis clone WS0472_E12 unknown mRNA	70	7.00E-08
2609	APFE030139045.1	4737	-0.701942338	0.163116	Island	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial se...	636	e-178
6977	APFE030396059.1	43236	-0.701776429	0.197521	Open Sea	gb|MG601102.1| Cyanophora sudae strain NIES-764 plastid, complet...	46	1.00E+00
8868	APFE030505808.1	60757	-0.771286772	0.039398	Open Sea	gb|CP025669.1| Ipomoea triloba cultivar NCNSP0323 chromosome 10	46	1.00E+00
9298	APFE030528492.1	85496	-0.7185338	0.259254	Open Sea	gb|AC241325.1| Pinus taeda clone PT_7Ba3500A10, complete sequence	50	6.40E-02
10631	APFE030607390.1	36759	0.733581091	0.152312	Open Sea	gb|CP020627.1| Oryzias latipes strain HSOK chromosome 7	46	1.00E+00
10683	APFE030610080.1	1878	-0.787534698	0.037945	Shore	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial se...	466	0.00E+00
10999	APFE030628375.1	133954	0.745142979	0.087837	Open Sea	gb|BT124256.1| Picea sitchensis clone WS0472_E12 unknown mRNA	54	4.00E-03
12558	APFE030723726.1	3588	0.713815944	0.197521	Open Sea	gb|AC241323.1| Pinus taeda clone PT_7Ba3301B13, complete sequence	242	8.00E-60
13231	APFE030757442.1	2043	-0.772075559	0.039398	Island	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial se...	620	0.00E+00
13232	APFE030757442.1	2050	-0.733794929	0.087837	Island	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial se...	620	0.00E+00
14053	APFE030813233.1	186110	0.724660269	0.234612	Shore	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, ...	244	2.00E-60
14054	APFE030813233.1	186111	0.843901008	0.022294	Shore	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, ...	244	2.00E-60
14822	APFE030850014.1	54663	0.816034678	0.022294	Open Sea	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, ...	180	180
14942	APFE030857403.1	29845	0.735732823	0.180792	Open Sea	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	58	3.00E-04
15815	APFE030906103.1	61	-0.759087976	0.087837	Open Sea	gb|AC241294.1| Pinus taeda clone PT_7Ba2900I02, complete sequence	688	0.00E+00
16078	APFE030921614.1	53438	0.726587083	0.197521	Open Sea	gb|AC241337.1| Pinus taeda clone PT_7Ba3875B09, complete sequence	82	2.00E-11
17458	APFE030995767.1	1961	-0.791747065	0.039398	Island	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial se...	771	0
17856	APFE031018063.1	67260	0.776231876	0.069032	Open Sea	gb|BT124256.1| Picea sitchensis clone WS0472_E12 unknown mRNA	62	2.00E-05
17859	APFE031018063.1	67326	0.797507607	0.037945	Open Sea	gb|BT124256.1| Picea sitchensis clone WS0472_E12 unknown mRNA	62	2.00E-05
17861	APFE031018063.1	67332	0.758537543	0.069032	Open Sea	gb|BT124256.1| Picea sitchensis clone WS0472_E12 unknown mRNA	62	2.00E-05
17863	APFE031018063.1	67347	0.73406183	0.152312	Open Sea	gb|BT124256.1| Picea sitchensis clone WS0472_E12 unknown mRNA	62	2.00E-05
18567	APFE031061272.1	514	-0.708346272	0.152312	Island	gb|KC143594.1| Pinus environmental sample clone CEobese239 18S r...	706	0.00E+00
19887	APFE031135765.1	151	-0.725477173	0.197521	Open Sea	b|DQ987896.1| Pseudolarix amabilis 18S ribosomal RNA gene, part...	729	0.00E+00
22491	APFE031293786.1	340	-0.730607956	0.090228	Open Sea	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial se...	591	0.00E+00
23567	APFE031355998.1	7890	-0.754060344	0.044969	Shore	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial se...	747	0.00E+00
23568	APFE031355998.1	7893	-0.711891658	0.108527	Shore	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial se...	747	0.00E+00
23883	APFE031371374.1	84904	-0.709469987	0.300498	Open Sea	gb|AC241351.1| Pinus taeda clone PT_7Ba4290D18, complete sequence	204	2.00E-48
23905	APFE031373268.1	7107	-0.705844592	0.156773	Shore	gb|AF051798.1|AF051798 Pinus elliottii 18S ribosomal RNA gene, p...	714	0.00E+00
24067	APFE031387609.1	58957	0.779370555	0.037945	Open Sea	gb|CP035221.1| Enterococcus faecium strain SRCM103470 plasmid un...	48	0.25
27180	APFE031573243.1	563	-0.757349385	0.069032	Open Sea	gb|AC241294.1| Pinus taeda clone PT_7Ba2900I02, complete sequence	456	0.00E+00
27813	APFE031614217.1	1073	0.707631993	0.302344	Open Sea	gb|AC241290.1| Pinus taeda clone PT_7Ba2797E03, complete sequence	307	1.00E-79
28563	APFE031657460.1	12503	0.761006635	0.069032	Shore	gb|AC241353.2| Pinus taeda clone PT_7Ba4304M17, complete sequence	143	6.00E-30
5810	APFE030328443.1	923	0.699906162	0.000412	Open Sea	gb|AC241290.1| Pinus taeda clone PT_7Ba2797E03, complete sequence	359	5.00E-95

Supplemental Table 2. Top 35 associated (R > |0.5|) CHG cytosines with age

Site	Scaffold	Position	Spearman Correlation	P Value	Cytosine Region	Blast (400 BP Window)	Score	E Value
202	APFE030007596.1	38804	-0.806365265	0.020114	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	68	3.00E-07
220	APFE030007596.1	38951	-0.821055717	0.004205	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	68	3.00E-07
3482	APFE030156380.1	346800	-0.806273887	0.00961	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	131	2.00E-26
3483	APFE030156380.1	346815	-0.809991495	0.008432	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	131	2.00E-26
3484	APFE030156380.1	346822	-0.857443238	0.002486	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	131	2.00E-26
3492	APFE030156380.1	346895	-0.811874711	0.004205	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	131	2.00E-26
5613	APFE030266102.1	32477	0.865293812	0.002336	Open Sea	gb|EU367255.1| Rhopalosoma nearcticum elongation factor 1-alpha ...	56	0.001
5614	APFE030266102.1	32482	0.831553804	0.004205	Open Sea	gb|JQ519677.1| Rhopalosoma sp. SK-2012 voucher DM400 elongation ...	56	1.00E-03
6868	APFE030325783.1	180321	-0.826493806	0.007519	Open Sea	gb|AC241340.1| Pinus taeda clone PT_7Ba3966E14, complete sequence	230	3.00E-56
7022	APFE030333153.1	146989	0.826364455	0.004205	Open Sea	gb|CP028303.1| Acidovorax avenae subsp. avenae strain SH7 chromo...	48	0.25
7023	APFE030333153.1	146995	0.852965503	0.002336	Open Sea	gb|CP028303.1| Acidovorax avenae subsp. avenae strain SH7 chromo...	48	0.25
7147	APFE030338471.1	63835	-0.800726612	0.01105	Open Sea	gb|AC241283.1| Pinus taeda clone PT_7Ba0038G01, complete sequence	129	9.00E-26
15504	APFE030760562.1	10243	0.805669114	0.020114	Open Sea	gb|AC241316.1| Pinus taeda clone PT_7Ba3194A17, complete sequence	66	1.00E-06
18359	APFE030912860.1	23919	-0.819701284	0.003041	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17
18362	APFE030912860.1	23950	-0.847644292	0.001927	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17
18363	APFE030912860.1	23958	-0.843464441	0.001927	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17
19149	APFE030954374.1	218	0.79762914	0.023837	Open Sea	gb|AC210511.1| Populus trichocarpa clone POP088-A15, complete se...	52	1.60E-02
19270	APFE030960074.1	37277	-0.827238542	0.004542	Open Sea	gb|AC241357.1| Pinus taeda clone PT_7Ba4350E08, complete sequence	466	0
20097	APFE030995986.1	235730	-0.891783455	0.000285	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	88	3.00E-13
20098	APFE030995986.1	235737	-0.806875406	0.004205	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	101	2.00E-17
23311	APFE031152219.1	76212	-0.797666493	0.023837	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	68	3.00E-07
23312	APFE031152219.1	76219	-0.882396735	0.002457	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	68	3.00E-07
23313	APFE031152219.1	76224	-0.860356057	0.004205	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	68	3E-07
23314	APFE031152219.1	76230	-0.860145005	0.004205	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	68	3E-07
23582	APFE031170467.1	52691	-0.827317018	0.003178	Island	gb|AC241357.1| Pinus taeda clone PT_7Ba4350E08, complete sequence	196	4.00E-46
25825	APFE031280591.1	16883	0.814571901	0.010805	Open Sea	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, ...	335	7.00E-88
26765	APFE031328690.1	28908	-0.791872159	0.007471	Open Sea	gb|CP027084.1| Bos mutus isolate yakQH1 chromosome 16	52	2.00E-02
29521	APFE031468650.1	339818	-0.807382534	0.020114	Shore	gb|AC241351.1| Pinus taeda clone PT_7Ba4290D18, complete sequence	444	0.00E+00
29826	APFE031487846.1	62273	-0.795522724	0.024835	Island	gb|CP009524.1| Methanosarcina sp. Kolksee, complete genome	62	2.00E-05
32186	APFE031612942.1	217743	-0.829381363	0.007132	Open Sea	gb|AC241277.1| Pinus taeda clone PT_7Ba0032C08, complete sequence	353	3.00E-93
32194	APFE031612942.1	217788	-0.828561852	0.004205	Open Sea	gb|AC241277.1| Pinus taeda clone PT_7Ba0032C08, complete sequence	353	3.00E-93
32195	APFE031612942.1	217808	-0.791428701	0.010481	Open Sea	gb|AC241277.1| Pinus taeda clone PT_7Ba0032C08, complete sequence	442	0.00E+00
32376	APFE031619745.1	77331	-0.821466976	0.003948	Shore	gb|AC241270.1| Pinus taeda clone PT_7Ba0014H13, complete sequence	242	8.00E-60
32502	APFE031626435.1	55430	-0.83043222	0.004205	Open Sea	gb|JQ262265.1| Pinus radiata isolate 5586 anonymous locus 0_1789...	101	2.00E-17
33496	APFE031678658.1	149227	-0.857466165	0.004205	Open Sea	gb|FJ111945.1| Pinus taeda isolate 4476 anonymous locus UMN_3406...	180	3.00E-41

Supplemental Table 3. CpG elastic net model

Site	Robustness	Scaffold	Position	Pearson Correlation	P Value	Cytosine Region	Blast (400 BP Window)	Score	E Value	Model Coefficient
1363	0	APFE030080639.1	200083	-0.6543418	0.6348307	Open Sea	ref|XM_014455775.2| PREDICTED: Myotis lucifugus helicase like transcription factor (HLTF)	46	1	-0.137325946
1467	4	APFE030085865.1	142328	0.6758028	0.6348307	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	62	2.00E-05	0.018496764
1921	1	APFE030116671.1	2305	-0.7126756	0.5844494	Shore	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	448	e-122	-4.19E-05
5733	37	APFE030361284.1	36063	0.6357583	0.6791496	Island	gb|AC241362.1| Pinus taeda clone PT_7Ba4455I19, complete sequence	311	1.00E-80	0.002094687
6241	9	APFE030396059.1	43218	-0.7723175	0.461431	Open Sea	ref|NC_038215.1| Cyanophora sudae strain NIES-764 plastid, complete genome	46	1	-0.015519385
6673	2	APFE030428449.1	50471	0.7102763	0.5844494	Open Sea	ref|XM_009907161.1| PREDICTED: Picoides pubescens sirtuin 1 (SIRT1), partial mRNA	46	1.00E+00	0.015477022
7261	1	APFE030463969.1	274227	0.6338211	0.6868999	Open Sea	gb|AC241310.1| Pinus taeda clone PT_7Ba3100G06, complete sequence	174	2.00E-39	0.032544356
7785	3	APFE030499242.1	23944	-0.7073769	0.5844494	Open Sea	gb|BT109694.1| Picea glauca clone GQ03211_I21 mRNA sequence	321	1.00E-83	-0.01383886
8217	0	APFE030526453.1	7058	-0.6899176	0.6348307	Island	gb|KF357095.1| Uncultured eukaryote clone 58 isolation-source soil oxic incubation T0h 18S ribosomal RNA gene	517	e-143	-0.012800373
8273	3	APFE030528492.1	85496	-0.7445607	0.5844494	Open Sea	gb|AC241325.1| Pinus taeda clone PT_7Ba3500A10, complete sequence	50	6.40E-02	-0.055725197
10300	0	APFE030660856.1	46646	-0.7060463	0.5844494	Island	ref|XM_015758670.2| PREDICTED: Oryza sativa Japonica Group proline-rich protein 36	46	1.00E+00	-0.049986507
10301	8	APFE030660856.1	46656	-0.6761235	0.6348307	Island	ref|XM_015758670.2| PREDICTED: Oryza sativa Japonica Group proline-rich protein 37	46	1.00E+00	-0.000208769
10304	68	APFE030660856.1	46679	-0.7025156	0.6147431	Island	ref|XM_015758670.2| PREDICTED: Oryza sativa Japonica Group proline-rich protein 38	46	1.00E+00	-0.021961049
11268	0	APFE030730360.1	106703	0.5990105	0.7699768	Open Sea	gb|KM672426.1| Pinus strobus NADH dehydrogenase subunit 4 (nad4) gene, complete cds; mitochondril	66	1.00E-06	0.017162217
11723	0	APFE030757442.1	2036	-0.731721	0.5844494	Island	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	620	e-174	-0.000172028
11724	0	APFE030757442.1	2043	-0.7375678	0.5844494	Island	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	620	e-174	-0.002173156
12446	58	APFE030813233.1	186110	0.7973113	0.3468524	Shore	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, partial cds	244	2.00E-60	0.038300859
12447	80	APFE030813233.1	186111	0.7573683	0.5844494	Shore	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, partial cds	244	2.00E-60	0.051582229
12490	0	APFE030814641.1	247938	0.5675825	0.8206907	Open Sea	emb|CR854964.10| Zebrafish DNA sequence from clone DKEY-58J19 in linkage group 1, complete	48	2.50E-01	0.009373239
12872	0	APFE030835997.1	139	0.510232	0.8206907	Open Sea	gb|AC241320.1| Pinus taeda clone PT_7Ba3204L22, complete sequence	139	9.00E-29	0.212277493
13691	0	APFE030886677.1	538	-0.6668645	0.6348307	Island	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	771	0.00E+00	-0.011321856
14607	11	APFE030948861.1	29216	-0.6849999	0.6348307	Open Sea	ref|XM_023867035.1| PREDICTED: Cryptotermes secundus E3 ubiquitin-protein ligase RAD18-like, transcript variant X2	54	4.00E-03	-0.023048274
15749	86	APFE031018063.1	67326	0.7986305	0.3468524	Open Sea	gb|BT124256.1| Picea sitchensis clone WS0472_E12 unknown mRNA	62	2.00E-05	0.096983584
15751	45	APFE031018063.1	67332	0.7723404	0.461431	Open Sea	gb|BT124256.1| Picea sitchensis clone WS0472_E12 unknown mRNA	62	2.00E-05	0.033412522
16108	0	APFE031042600.1	129199	-0.6525636	0.6422765	Open Sea	gb|AC241350.1| Pinus taeda clone PT_7Ba4261L04, complete sequence	145	1.00E-30	-0.015568055
19071	10	APFE031250081.1	44978	-0.6397717	0.6791496	Open Sea	gb|AC241293.1| Pinus taeda clone PT_7Ba2900E24, complete sequence	141	2.00E-29	-0.018881856
19089	26	APFE031252417.1	24795	0.6642303	0.6348307	Open Sea	emb|AM458575.2| Vitis vinifera contig VV78X161277.5, whole genome shotgun sequence	52	1.60E-02	0.080967158
19759	83	APFE031293786.1	333	-0.8095382	0.3468524	Open Sea	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	605	e-169	-0.016476236
19760	80	APFE031293786.1	340	-0.8168549	0.3468524	Open Sea	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	605	e-169	-0.017965071
20699	35	APFE031355998.1	7890	-0.7457455	0.5844494	Shore	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	747	0.00E+00	-0.021921399
22259	0	APFE031461857.1	98665	-0.6296329	0.6902063	Open Sea	gb|AC241316.1| Pinus taeda clone PT_7Ba3194A17, complete sequence	222	8.00E-54	-0.02126557
24048	6	APFE031593997.1	48022	-0.6481513	0.6604906	Open Sea	emb|LR132053.1| Anabas testudineus genome assembly, chromosome: 2	46	1.00E+00	-0.003077815
24772	31	APFE031643940.1	37940	-0.5982827	0.7699768	Open Sea	ref|XM_008462945.2| PREDICTED: Cucumis melo uncharacterized LOC103499830 (LOC103499830), mRNA	46	1.00E+00	-0.000930533
26419	0	APFE031751617.1	8348	-0.6759993	0.6348307	Open Sea	gb|AC241283.1| Pinus taeda clone PT_7Ba0038G01, complete sequence	137	4.00E-28	-0.043467286
Avg Robustness	20.21 (+/- 4.99)								Intercept	25.05316718

Supplemental Table 4. CHG elastic net model

Site	Robustness	Scaffold	Position	Pearson	P Value	Genomic Region	Blast (400 BP Window)	Score	E Value	Model Coefficient
179	0	APFE030007596.1	38804	-0.819627	0.05246022	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	68	3.00E-07	-0.007445384
2281	6	APFE030117462.1	121500	0.6722937	0.43912359	Open Sea	ref|XM_019687934.1| PREDICTED: Aedes albopictus eukaryotic translation initiation factor	48	0.25	0.008808399
3115	28	APFE030156380.1	346869	-0.8233699	0.05246022	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	141	2.00E-29	-0.012793687
3124	11	APFE030156380.1	346924	-0.8222629	0.05246022	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	141	2.00E-29	-0.005433015
3125	3	APFE030156380.1	346933	-0.7972243	0.07600326	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	141	2.00E-29	-0.007152663
3587	78	APFE030180286.1	185036	0.5912766	0.79690452	Open Sea	gb|CP023124.1| Lupinus angustifolius cultivar Tanjil chromosome LG-12	48	0.25	0.023924566
4242	31	APFE030221227.1	21877	0.6609115	0.5067384	Open Sea	gb|CP022743.1| Mucilaginibacter sp. BJC16-A31, complete genome	46	1	0.024174066
4243	15	APFE030221227.1	21909	0.6524559	0.5535547	Open Sea	gb|CP022743.1| Mucilaginibacter sp. BJC16-A31, complete genome	46	1	0.029399465
4690	0	APFE030242985.1	23615	-0.7661441	0.12831023	Shelf	gb|AC241357.1| Pinus taeda clone PT_7Ba4350E08, complete sequence	74	4.00E-09	-0.00856212
8659	55	APFE030474771.1	62256	-0.8139916	0.05805196	Open Sea	gb|AC241319.2| Pinus taeda clone PT_7Ba3200G14, complete sequence	129	9.00E-26	-0.042836361
9941	66	APFE030550909.1	450854	-0.8182333	0.05246022	Shore	gb|HQ396778.1| Maullinia ectocarpi clone c5 polyubiquitin gene, partial sequence	66	1.00E-06	-0.013008002
11405	0	APFE030630843.1	23995	0.726926	0.23982717	Open Sea	gb|BT118267.1| Picea glauca clone GQ04004_G10 mRNA sequence	86	1.00E-12	0.006253003
16108	30	APFE030899769.1	30167	-0.7815293	0.10631385	Open Sea	gb|KF418024.1| Pinus yunnanensis microsatellite PyG21R sequence	222	8.00E-54	-0.007856223
16261	100	APFE030912860.1	23919	-0.8501721	0.03482505	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17	-0.038099147
16265	100	APFE030912860.1	23958	-0.8630101	0.02957533	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17	-0.028198307
16266	4	APFE030912860.1	23963	-0.7263384	0.23982717	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17	-0.000451613
17019	71	APFE030960074.1	37304	-0.8023064	0.07593744	Shore	gb|AC241357.1| Pinus taeda clone PT_7Ba4350E08, complete sequence	434	e-117	-0.013703889
17723	100	APFE030995986.1	235730	-0.8929755	0.00904229	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	88	3.00E-13	-0.089877676
19149	0	APFE031074694.1	203390	-0.7787887	0.10631385	Open Sea	gb|AC241340.1| Pinus taeda clone PT_7Ba3966E14, complete sequence	168	1.00E-37	-0.027049412
20441	26	APFE031148608.1	70419	0.6716662	0.43912359	Shelf	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, partial cds	287	2.00E-73	0.000185507
23239	7	APFE031308732.1	4957	-0.675735	0.43422847	Shelf	gb|KF418024.1| Pinus yunnanensis microsatellite PyG21R sequence	230	3.00E-56	-0.036838213
23550	57	APFE031328690.1	28908	-0.8555158	0.03313625	Shelf	gb|CP027084.1| Bos mutus isolate yakQH1 chromosome 16	52	1.60E-02	-0.030942121
23986	14	APFE031352602.1	177331	0.7678366	0.12525176	Open Sea	gb|CP003742.1| Octadecabacter arcticus 238, complete genome	50	6.40E-02	0.000114774
24753	2	APFE031397079.1	20243	-0.8184794	0.05246022	Shore	gb|AC241270.1| Pinus taeda clone PT_7Ba0014H13, complete sequence	301	1.00E-77	-0.001620236
25692	5	APFE031453673.1	12701	0.5691848	0.79690452	Open Sea	gb|CP023766.1| Solanum lycopersicum cultivar I-3 chromosome 10	48	2.50E-01	0.009796582
25943	46	APFE031468650.1	339818	-0.8888931	0.00904229	Shore	gb|AC241351.1| Pinus taeda clone PT_7Ba4290D18, complete sequence	444	e-120	-0.034185619
26577	100	APFE031511386.1	11914	0.7886135	0.09263071	Open Sea	dbj|AP015040.1| Vigna angularis var. angularis DNA, chromosome 7, almost complete sequence	48	2.50E-01	0.043460084
28205	5	APFE031612942.1	217743	-0.7607781	0.1359269	Open Sea	gb|AC241277.1| Pinus taeda clone PT_7Ba0032C08, complete sequence	353	3.00E-93	-0.005599988
28364	1	APFE031619745.1	77331	-0.794486	0.07870818	Shore	gb|AC241270.1| Pinus taeda clone PT_7Ba0014H13, complete sequence	2.42E+02	8.00E-60	-0.009614305
28669	0	APFE031637427.1	115414	-0.5714462	0.79690452	Open Sea	gb|KY964286.1| Pinus taeda chloroplast, complete genome	228	1.00E-55	-0.003027496
29048	60	APFE031660503.1	89970	0.8109091	0.0614307	Open Sea	_013188231.1| Anser cygnoides domesticus sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein), transcript variant x	46	1.00E+00	0.099306863
29392	6	APFE031681806.1	197213	-0.6394637	0.60091529	Open Sea	gb|KF418024.1| Pinus yunnanensis microsatellite PyG21R sequence	167	4.00E-37	-3.61E-05
29550	47	APFE031693069.1	277919	-0.581322	0.79690452	Open Sea	gb|AC241279.1| Pinus taeda clone PT_7Ba0032H02, complete sequence	52	1.60E-02	-3.48E-05
29552	64	APFE031693069.1	277928	-0.7440746	0.18704229	Open Sea	gb|AC241279.1| Pinus taeda clone PT_7Ba0032H02, complete sequence	52	1.60E-02	-0.007204891
29742	0	APFE031700512.1	50272	0.2495901	0.87345139	Shelf	emb|LR031576.1| Brassica rapa genome, scaffold: A04	54	4.00E-03	0.001320484
Avg Robustness	32.51 (+/- 5.86)								Intercept	38.1914076

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Supplemental Table 5. Combined CpG and CHG elastic net model

Site	Context	Robustness	Scaffold	Position	Pearson Correlation	P Value	Cytosine Region	Blast (400 BP Window)	Score	E Value	Model Coefficient
4044	CpG	16	APFE030247699.1	1141	-0.6166899	0.71166098	Open Sea	dbj|D38246.1| Pinus luchuensis gene for 18S rRNA	660	0	-0.014690729
10300	CpG	0	APFE030660856.1	46646	-0.7060463	0.38363995	Island	ref|XM_015758670.2| PREDICTED: Oryza sativa Japonica Group proline-rich protein 36	46	1.00E+00	-0.006552247
10836	CpG	32	APFE030701677.1	156970	-0.7089463	0.38316459	Open Sea	gb|CP027083.1| Bos mutus isolate yakQH1 chromosome 15	46	1.30E+00	-0.013530092
12446	CpG	2	APFE030813233.1	186110	0.8384045	0.05596322	Shore	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, partial cds	244	2.00E-60	0.018384386
14607	CpG	4	APFE030948861.1	29216	-0.671841	0.49346882	Open Sea	ref|XM_023867035.1| PREDICTED: Cryptotermes secundus E3 ubiquitin-protein ligase	54	4.00E-03	-0.007251235
17327	CpG	6	APFE031127834.1	4424	-0.6709793	0.49346882	Shore	gb|AC241294.1| Pinus taeda clone PT_7Ba2900I02, complete sequence	381	e-102	-0.013427725
19759	CpG	22	APFE031293786.1	333	-0.8151544	0.07674729	Open Sea	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	605	e-169	-0.024244335
19760	CpG	21	APFE031293786.1	340	-0.8236261	0.07136371	Open Sea	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	605	e-169	-0.022969672
19761	CpG	4	APFE031293786.1	347	-0.7616778	0.21996887	Open Sea	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	605	e-169	-3.19E-06
20699	CpG	84	APFE031355998.1	7890	-0.7457455	0.27281301	Shore	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	747	0.00E+00	-0.001246402
26417	CpG	11	APFE031751617.1	8319	0.7624409	0.21996887	Open Sea	gb|AC241283.1| Pinus taeda clone PT_7Ba0038G01, complete sequence	137	4.00E-28	0.032530321
197	CHG	45	APFE030007596.1	38951	-0.8365761	0.05596322	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	68	3.00E-07	-0.007290976
2212	CHG	2	APFE030114720.1	66598	0.6199171	0.70354547	Open Sea	gb|KY964286.1| Pinus taeda chloroplast, complete genome	458	e-125	0.103090424
2281	CHG	2	APFE030117462.1	121500	0.6722937	0.49346882	Open Sea	ref|XM_019687934.1| PREDICTED: Aedes albopictus eukaryotic translation initiation factor	48	2.50E-01	0.003565166
3115	CHG	35	APFE030156380.1	346869	-0.8207599	0.07136371	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	141	2.00E-29	-0.012602914
3124	CHG	11	APFE030156380.1	346924	-0.822286	0.07136371	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	141	2.00E-29	-0.003528854
4242	CHG	21	APFE030221227.1	21877	0.6066647	0.74662545	Open Sea	gb|CP022743.1| Mucilaginibacter sp. BJC16-A31, complete genome	46	1.00E+00	0.002829825
4243	CHG	10	APFE030221227.1	21909	0.601406	0.76414416	Open Sea	gb|CP022743.1| Mucilaginibacter sp. BJC16-A31, complete genome	46	1.00E+00	0.010099597
4692	CHG	10	APFE030242985.1	42486	0.6858277	0.45547678	Open Sea	gb|AC241283.1| Pinus taeda clone PT_7Ba0038G01, complete sequence	274	2.00E-69	0.024580632
4868	CHG	35	APFE030255408.1	6179	-0.6973797	0.40891398	Open Sea	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	98	3.00E-16	-0.022840831
8659	CHG	24	APFE030474771.1	62256	-0.7971943	0.11024773	Open Sea	gb|AC241319.2| Pinus taeda clone PT_7Ba3200G14, complete sequence	129	9.00E-26	-0.0289986
9941	CHG	22	APFE030550909.1	450854	-0.8182333	0.07136371	Shore	gb|HQ396778.1| Maullinia ectocarpi clone c5 polyubiquitin gene, partial sequence	66	1.00E-06	-0.003448074
16261	CHG	91	APFE030912860.1	23919	-0.8501721	0.04730297	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17	-0.034710315
16264	CHG	85	APFE030912860.1	23950	-0.799363	0.11024773	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17	-0.011814445
16265	CHG	100	APFE030912860.1	23958	-0.8630101	0.04730297	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17	-0.034618833
16266	CHG	17	APFE030912860.1	23963	-0.7263384	0.34830679	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17	-0.009208997
16641	CHG	1	APFE030938563.1	91250	-0.6048775	0.75191834	Open Sea	ref|XM_018854053.1| Metschnikowia bicuspidata var. bicuspidata NRRL YB-4993 hypothetical protein (METBIDRAFT_116685), mRNA	52	1.60E-02	-0.000957479
17019	CHG	11	APFE030960074.1	37304	-0.7988719	0.11024773	Shore	gb|AC241357.1| Pinus taeda clone PT_7Ba4350E08, complete sequence	434	e-117	-0.010445391
17723	CHG	100	APFE030995986.1	235730	-0.9065709	0.0048033	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	88	3.00E-13	-0.08792942
20779	CHG	30	APFE031170467.1	52691	-0.8369123	0.05596322	Island	gb|AC241357.1| Pinus taeda clone PT_7Ba4350E08, complete sequence	196	4.00E-46	-0.008197411
20780	CHG	4	APFE031170467.1	52713	-0.7981939	0.11024773	Open Sea	gb|AC241357.1| Pinus taeda clone PT_7Ba4350E08, complete sequence	196	4.00E-46	-0.007110912
23550	CHG	58	APFE031328690.1	28908	-0.8555158	0.04730297	Shelf	gb|CP027084.1| Bos mutus isolate yakQH1 chromosome 16	52	1.60E-02	-0.014444269
25943	CHG	68	APFE031468650.1	339818	-0.9055554	0.0048033	Shore	gb|AC241351.1| Pinus taeda clone PT_7Ba4290D18, complete sequence	444	e-120	-0.041425247
26577	CHG	0	APFE031511386.1	11914	0.8246048	0.07136371	Open Sea	dbj|AP015040.1| Vigna angularis var. angularis DNA, chromosome 7, almost complete sequence	48	2.50E-01	0.043957927
28213	CHG	0	APFE031612942.1	217788	-0.832742	0.05628182	Open Sea	gb|AC241277.1| Pinus taeda clone PT_7Ba0032C08, complete sequence	418	e-113	-0.012395417
29724	CHG	0	APFE031699699.1	101384	0.6829002	0.45677828	Open Sea	ref|NC_037753.1| Bretschneidera sinensis chloroplast, complete genome	52	1.60E-02	0.00169185
30205	CHG	0	APFE031729853.1	48198	-0.7309376	0.32194597	Open Sea	gb|AC241337.1| Pinus taeda clone PT_7Ba3875B09, complete sequence	155	2.00E-33	-0.00368355
30400	CHG	0	APFE031742049.1	13035	-0.716403	0.37593467	Open Sea	emb|LK612858.1| Dicrocoelium dendriticum genome assembly D_dendriticum_Leon_v1_0_4	48	2.50E-01	-0.007650197
	Avg Robustness	25.89 (+/- 5.00)								Intercept	44.5080323

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Supplemental Table 6. CpG Pearson models (5 and 10 cytosines)

Site	Robustness	Scaffold	Position	Pearson Correlation	P Value	Cytosine Region	Blast (400 BP Window)	Score	E Value	Top 5 Model Coefficient	Top 10 Model Coefficient	Intercept
19760	80	APFE031293786.1	340	-0.8168549	0.3468524	Open Sea	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	605	e-169	-0.15482	-0.878	
15749	86	APFE031018063.1	67326	0.7986305	0.3468524	Open Sea	gb|BT124256.1| Picea sitchensis clone WS0472_E12 unknown mRNA	62	2.00E-05	0.2903	-0.2809	
12446	58	APFE030813233.1	186110	0.7973113	0.3468524	Shore	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, partial cds	244	2.00E-60	0.10704	0.1992	
6241	9	APFE030396059.1	43218	-0.7723175	0.461431	Open Sea	ref|NC_038215.1| Cyanophora sudae strain NIES-764 plastid, complete genome	46	1	0.02812	-0.0971	
20699	35	APFE031355998.1	7890	-0.7457455	0.5844494	Shore	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	747	0.00E+00	-0.13621	0.5696	Top 5: 22.79397
8273	3	APFE030528492.1	85496	-0.7445607	0.5844494	Open Sea	gb|AC241325.1| Pinus taeda clone PT_7Ba3500A10, complete sequence	50	6.40E-02		-0.3472	
11132	5	APFE030723726.1	3588	-0.6481513	0.6604906	Open Sea	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, partial cds	182	7.00E-42		-0.2695	
11724	0	APFE030757442.1	2043	-0.7375678	0.5844494	Island	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	620	e-174		-0.9322	
23380	0	APFE031541527.1	75437	-0.5982827	0.7699768	Shore	gb|KY860920.1| Pinus resinosa 26S ribosomal RNA gene, partial sequence	644	0.00E+00		0.794	
18276	12	APFE031192863.1	106705	-0.6759993	0.6348307	Open Sea	emb|HE574558.1| Pinus pinaster mRNA for pinoresinol-lariciresinol reductase (plr gene)	194	2.00E-45		0.1276	Top 10: 52.8028
Avg Robustness (Top 5)	53.6 (+/- 14.32)											
Avg Robustness (Top 10)	28.8 (+/- 10.72)											

Supplemental Table 7. CHG Pearson models (5 and 10 cytosines)

Site	Robustness	Scaffold	Position	Pearson Correlation	P Value	Cytosine Region	Blast (400 BP Window)	Score	E Value	Top 5 Model Coefficient	Top 10 Model Coefficient	Intercept
17723	100	APFE030995986.1	235730	-0.8929755	0.00904229	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	88	3.00E-13	-0.20782	-0.41395375	
25943	46	APFE031468650.1	339818	-0.8888931	0.00904229	Shore	gb|AC241351.1| Pinus taeda clone PT_7Ba4290D18, complete sequence	444	e-120	-0.07479	-0.29605558	
16265	100	APFE030912860.1	23958	-0.8630101	0.02957533	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17	-0.15581	-0.12531913	
23550	57	APFE031328690.1	28908	-0.8555158	0.03313625	Shelf	gb|CP027084.1| Bos mutus isolate yakQH1 chromosome 16	52	1.60E-02	-0.17155	-0.25092601	
197	10	APFE030007596.1	38951	-0.581322	0.79690452	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	68	3.00E-07	0.10013	0.0700562	Top 5: 51.04011
1837	2	APFE030092303.1	104992	-0.7440746	0.18704229	Open Sea	gb|AC241340.1| Pinus taeda clone PT_7Ba3966E14, complete sequence	236	5.00E-58		0.2650131	
3115	28	APFE030156380.1	346869	-0.8233699	0.05246022	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	141	2.00E-29		-0.17643639	
20779	15	APFE031170467.1	52691	0.2495901	0.87345139	Island	gb|AC241357.1| Pinus taeda clone PT_7Ba4350E08, complete sequence	196	4.00E-46		0.04057985	
3124	11	APFE030156380.1	346924	-0.8222629	0.05246022	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	141	2.00E-29		0.10968849	
179	0	APFE030007596.1	38804	-0.819627	0.05246022	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	68	3.00E-07		0.30582527	Top 10: 51.52011
Avg Robustness (Top5)	62.6 (+/- 17.13)											
Avg Robustness (Top10)	36.9 (+/- 12.01)											

Supplemental Table 8. Combined CpG and CHG Pearson models (5 and 10 cytosines)

Site	Context	Robustness	Scaffold	Position	Pearson Correlation	P Value	Cytosine Region	Blast (400 BP Window)	Score	E Value	Top 5 Model Coefficient	Top 10 Model Coefficient	Intercept
17723	CHG	100	APFE030995986.1	235730	-0.90657093	0.004803	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	88	3.00E-13	-0.21737	-0.280356	
25943	CHG	68	APFE031468650.1	339818	-0.905555442	0.004803	Open Sea	gb|AC241351.1| Pinus taeda clone PT_7Ba4290D18, complete sequence	444	e-120	-0.1406	-0.16354	
16265	CHG	100	APFE030912860.1	23958	-0.863010148	0.047303	Open Sea	gb|AC241341.1| Pinus taeda clone PT_7Ba4050C22, complete sequence	101	2.00E-17	-0.07848	-0.105378	
5002	CHG	100	APFE030266102.1	32477	0.858565258	0.047303	Open Sea	gb|JQ519677.1| Rhopalosoma sp. SK-2012 voucher DM400 elongation factor 1 alpha	56	0.001	0.03705	-0.006861	
23550	CHG	58	APFE031328690.1	28908	-0.855515837	0.047303	Shelf	gb|CP027084.1| Bos mutus isolate yakQH1 chromosome 16	52	1.60E-02	-0.04465	-0.150913	Top 5 : 48.57360
8273	CpG	9	APFE030528492.1	85496	-0.845328122	0.051005	Open Sea	gb|AC241325.1| Pinus taeda clone PT_7Ba3500A10, complete sequence	50	6.40E-02		-0.134639	
12446	CpG	2	APFE030813233.1	186110	0.838404521	0.055963	Open Sea	gb|HM853297.1| Pinus pinaster malate dehydrogenase (mdhB) gene, partial cds	244	2.00E-60		-0.004067	
20779	CHG	30	APFE031170467.1	52691	-0.836912349	0.055963	Island	gb|AC241357.1| Pinus taeda clone PT_7Ba4350E08, complete sequence	196	4.00E-46		0.028785	
197	CHG	46	APFE030007596.1	38951	-0.836576128	0.055963	Island	gb|AC241265.2| Pinus taeda clone PT_7Ba0002H13, complete sequence	68	3.00E-07		0.064688	
1837	CHG	6	APFE030092303.1	104992	-0.834273616	0.056282	Open Sea	gb|AC241340.1| Pinus taeda clone PT_7Ba3966E14, complete sequence	236	5.00E-58		0.208078	Top 10: 53.340569
	Avg Robustness (Top5)	85.2 (+/- 9.2)											
	Avg Robustness (Top10	51.9 (+/- 12.56)											