

**Supplemental Information for *The Genomic Ecosystem of Transposable Elements in Maize*,
Stitzer MC, Anderson SN, Springer NM, and Ross-Ibarra J**

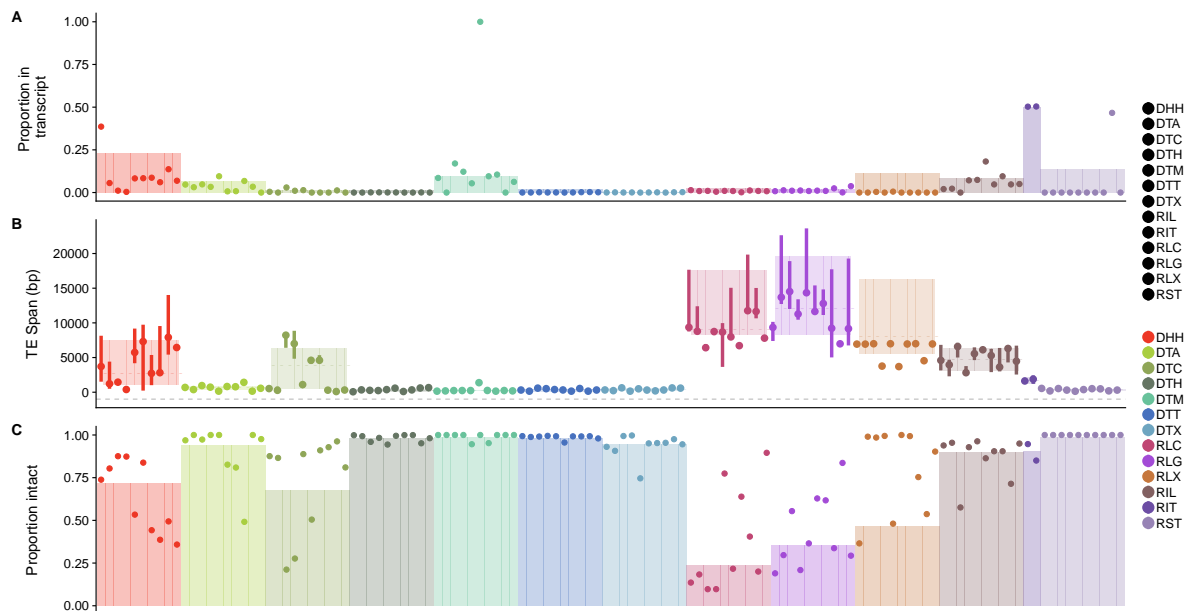


Fig. S1. Family characteristics of each of the largest 10 families of each superfamily with at least 10 copies. (A) Proportion of TEs within the transcript of a gene, including introns and UTRs. (B) TE span along the genome, summing both the base pairs of the TE and the base pairs of the TEs nested within it. (C) Proportion of TEs that are intact, that is, uninterrupted by the insertion of another TE. In (A and C), families are shown as points and superfamily proportions as a barplot, and in (B) families are shown with medians as points and lines representing ranges of upper to lower quartiles, with superfamilies shown as colored rectangles.

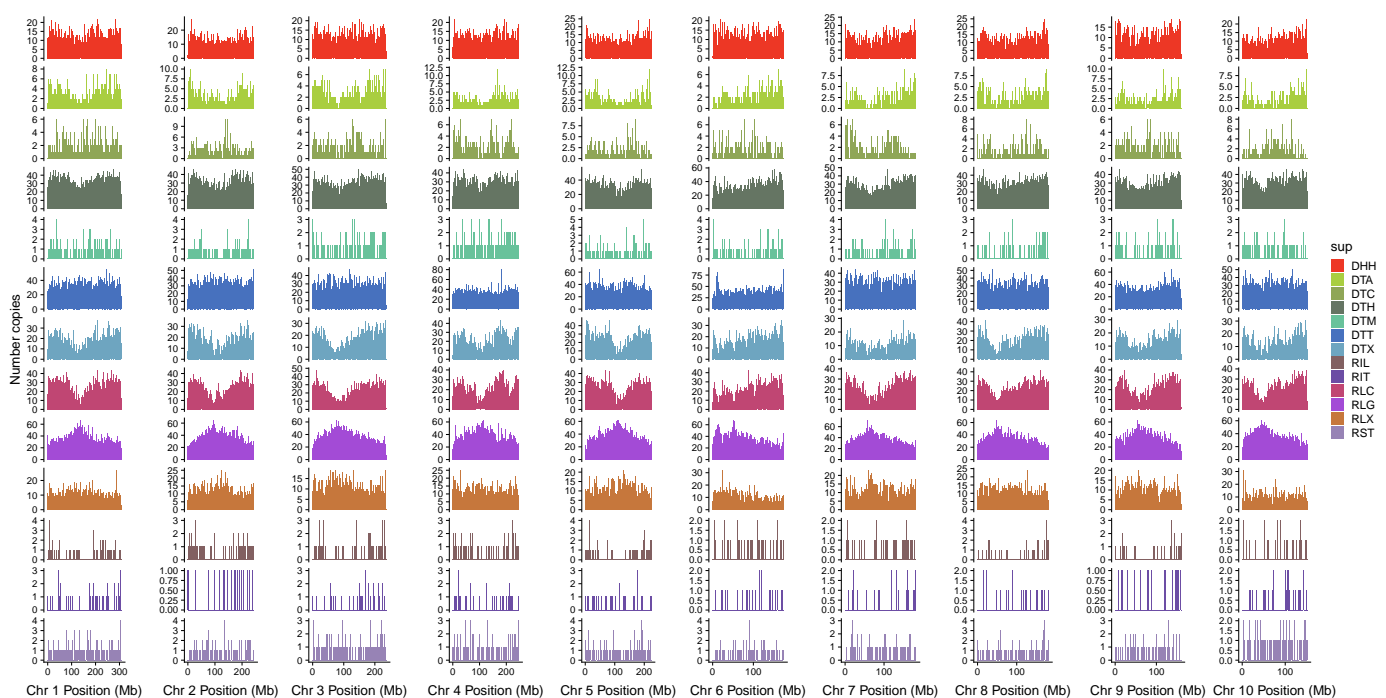


Fig. S2. Chromosomal distribution of superfamilies across all 10 maize chromosomes Count of TE copies of each superfamily in 1 megabase bins across each chromosome.

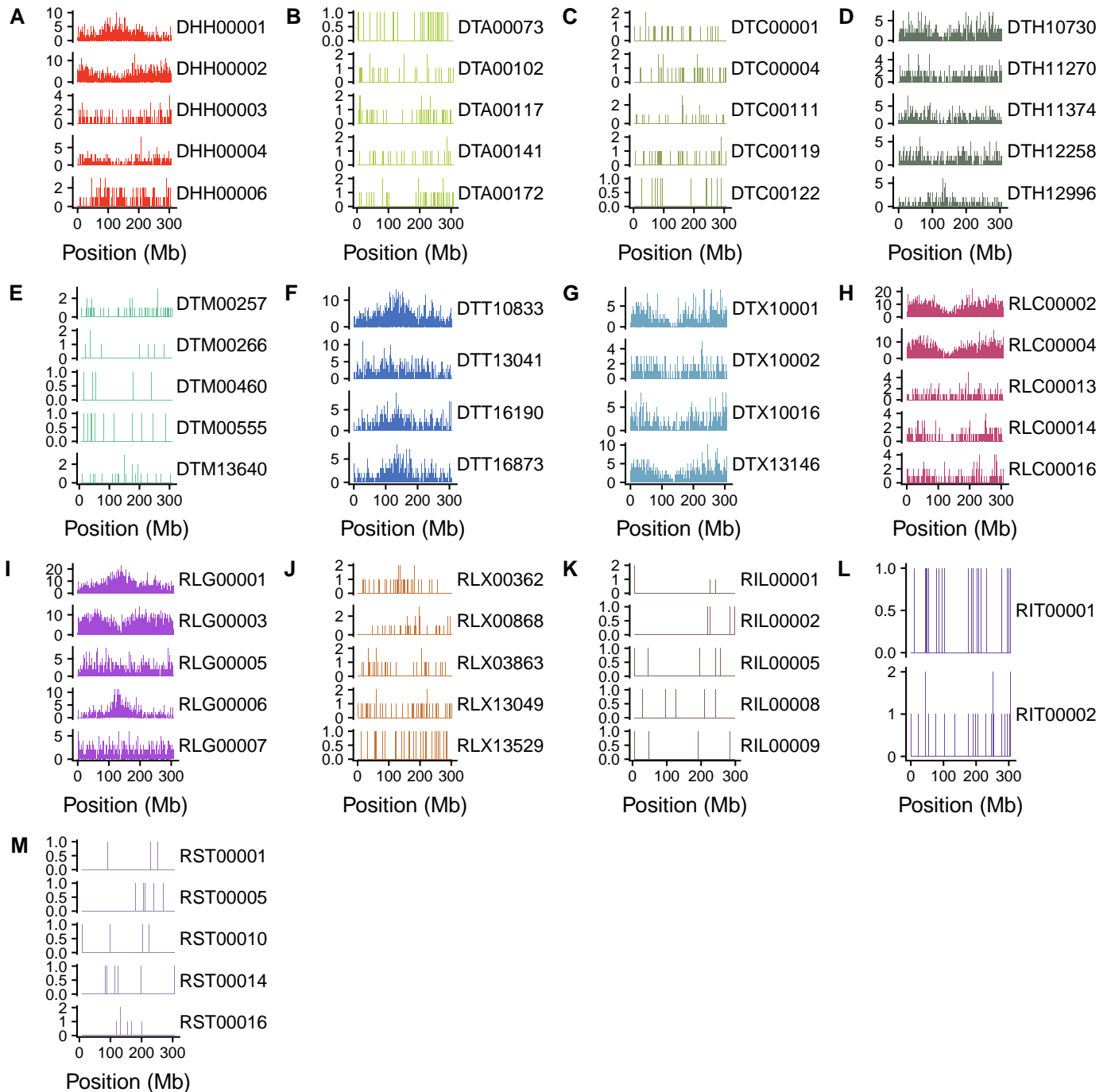


Fig. S3. Distribution on chromosome 1 of five largest families with at least ten copies in each superfamily Count of TE copies in 1 megabase bins along chromosome 1. (A) DHH, (B) DTA, (C) DTC, (D) DTH, (E) DTM, (F) DTT, (G) DTX, (H) RLC, (I) RLG, (J) RLX, (K) RIL, (L) RIT, (M) RST. Note that some families have no copies on chromosome 1, including DTT10880 and DTX10177. Additionally, the RIT superfamily only has two families.

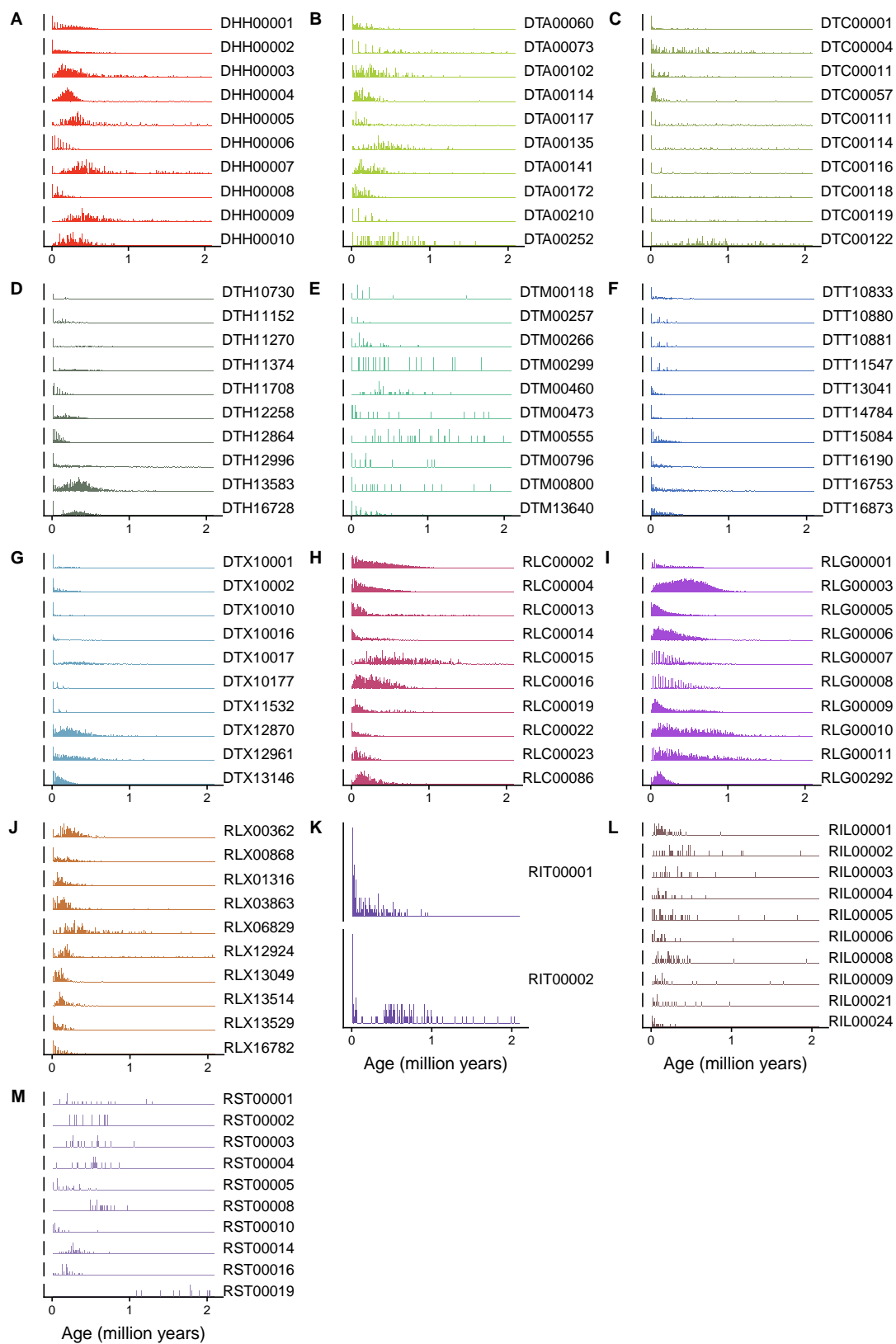


Fig. S4. Ages in 10,000 year bins across each of the largest 10 families of each superfamily with at least 10 copies. (A) DHH, (B) DTA, (C) DTC, (D) DTH, (E) DTM, (F) DTT, (G) DTX, (H) RLC, (I) RLG, (J) RLX, (K) RIL, (L) RIT, (M) RST. The RIT superfamily only contains two families.

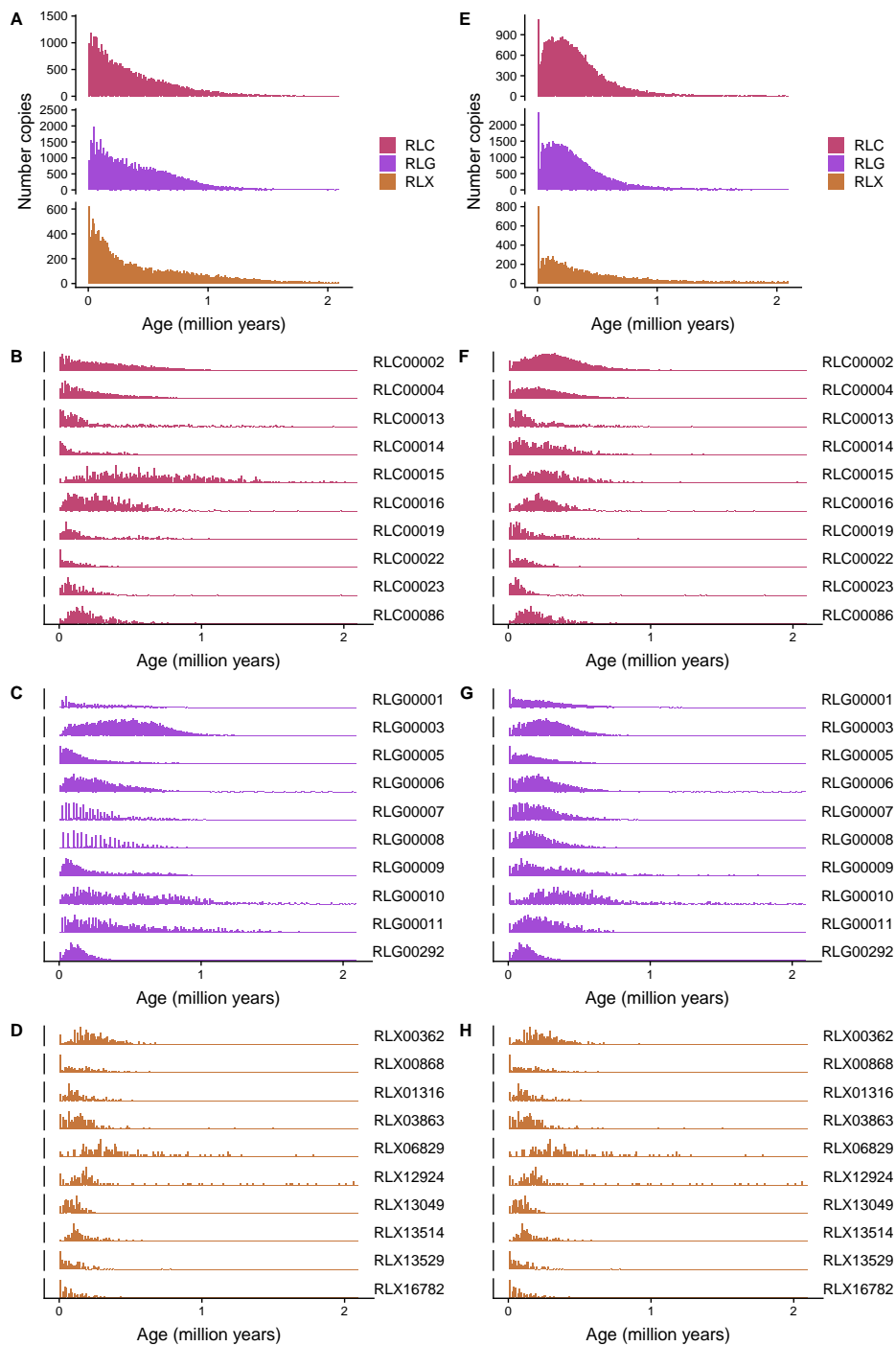


Fig. S5. LTR-LTR ages and terminal branch length ages for LTR retrotransposons. Ages in 10,000 year bins across each of the largest 10 families of each superfamily with at least 10 copies. Left plots (A-D) show LTR-LTR ages, right plots (E-H) show terminal branch length (TBL) ages. (A) all copies, LTR-LTR, (B) all copies, TBL, (C) RLC families, LTR-LTR, (D) RLC families, TBL, (E) RLG families, LTR-LTR, (F) RLG families, TBL, (G) RLX families, LTR-LTR, (H) RLX families, TBL.

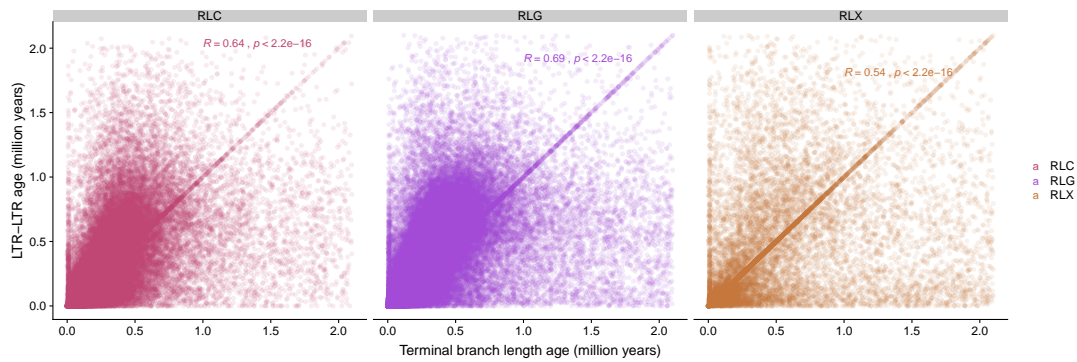


Fig. S6. LTR-LTR ages vs. terminal branch length ages for LTR retrotransposon superfamilies. Spearman's correlation coefficient shown on plot for each superfamily.

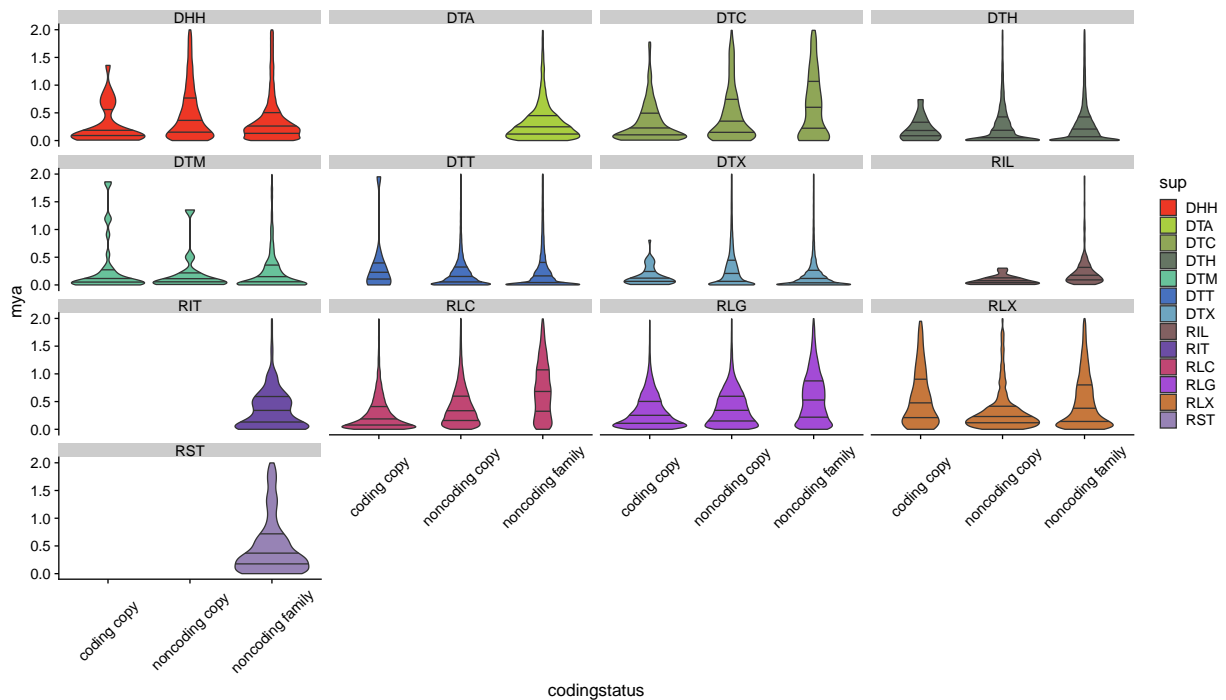


Fig. S7. Age of TE copies split by coding potential of self and family Violin plots with three lines, at median and 25th and 75th percentile. Only ages younger than 2 million years are shown. “Coding copy” refers to those copies that code for protein, “noncoding copy” refers to those copies that don't code for protein, but a family member does, and “noncoding family” refers to copies from families without a coding member in B73.

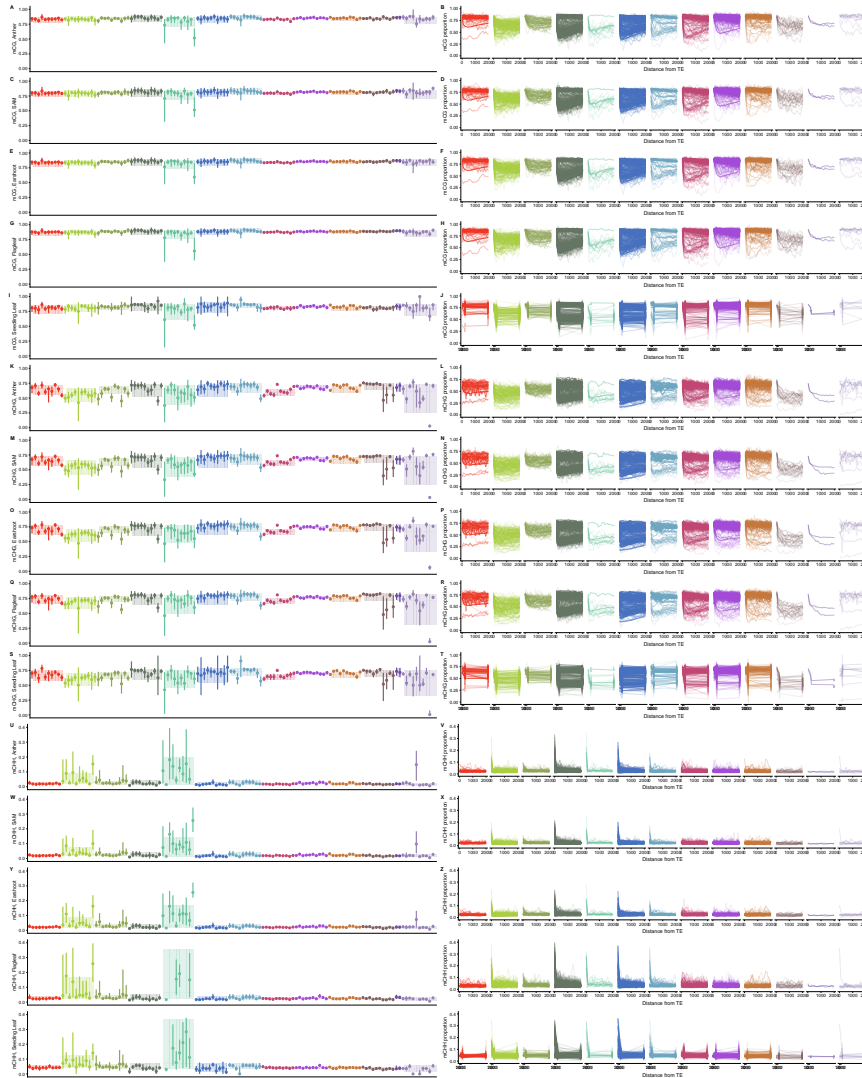


Fig. S8. Methylation in TE and flanking sequence, across tissues. A-J: mCG; K-T: mCHG; U-end mCHH. Tissues on y-axis, from top to bottom: Anther, SAM, Earshoot, Flagleaf, Seedling leaf.

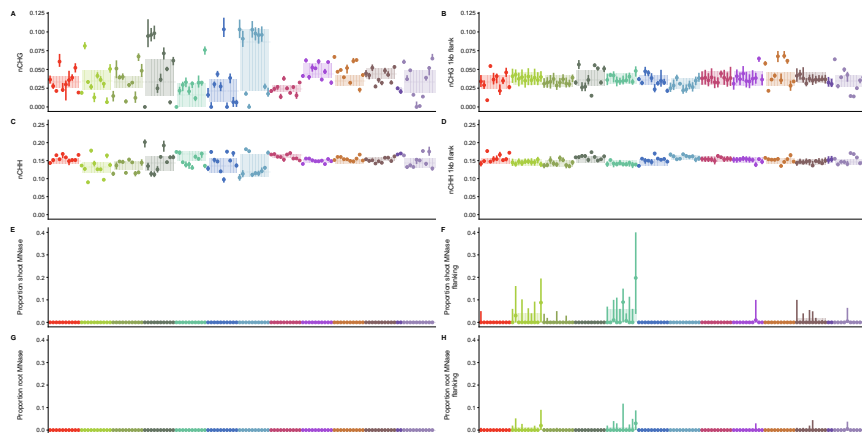


Fig. S9. Features of the TE and flanking sequences. Proportion of sites methylatable in CHG context in the TE (A) and 1kb flanking sequence (B), methylatable in the CHH context in the TE (C) and 1kb flanking sequence (D). Proportion of sites in MNase hypersensitive regions in shoot in TE (E) and 1kb flank (F), and root in TE (G) and 1kb flank (H).

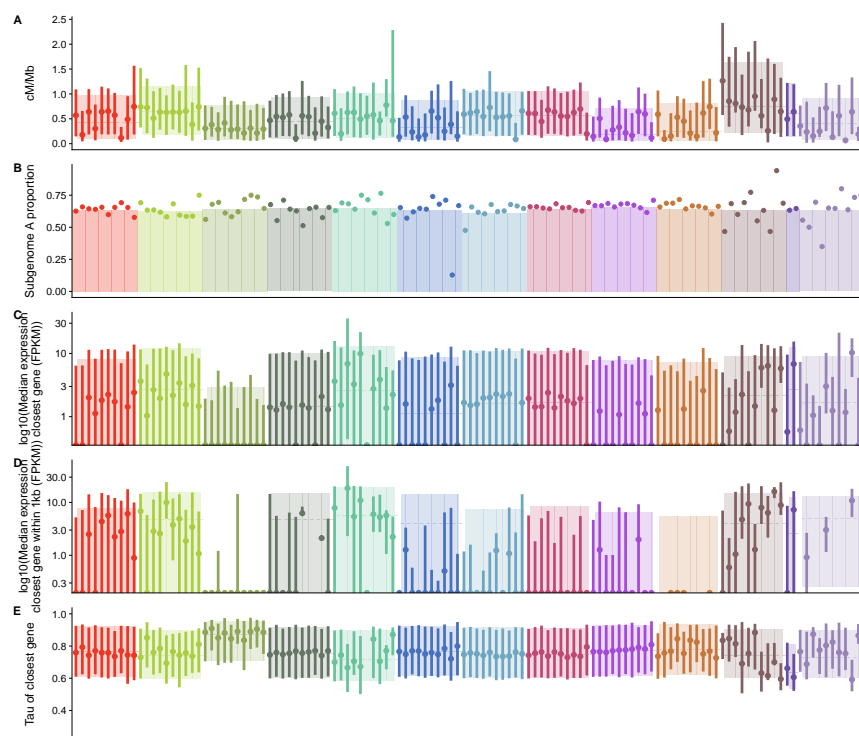


Fig. S10. Recombination, subgenome, and expression of closest gene. (A) Recombination rate across the TE, (B) proportion of TEs in subgenome A, (C) median expression of the closest gene to each TE, (D) median expression of genes within 1kb of the TE (E) Tau of closest gene to each TE.

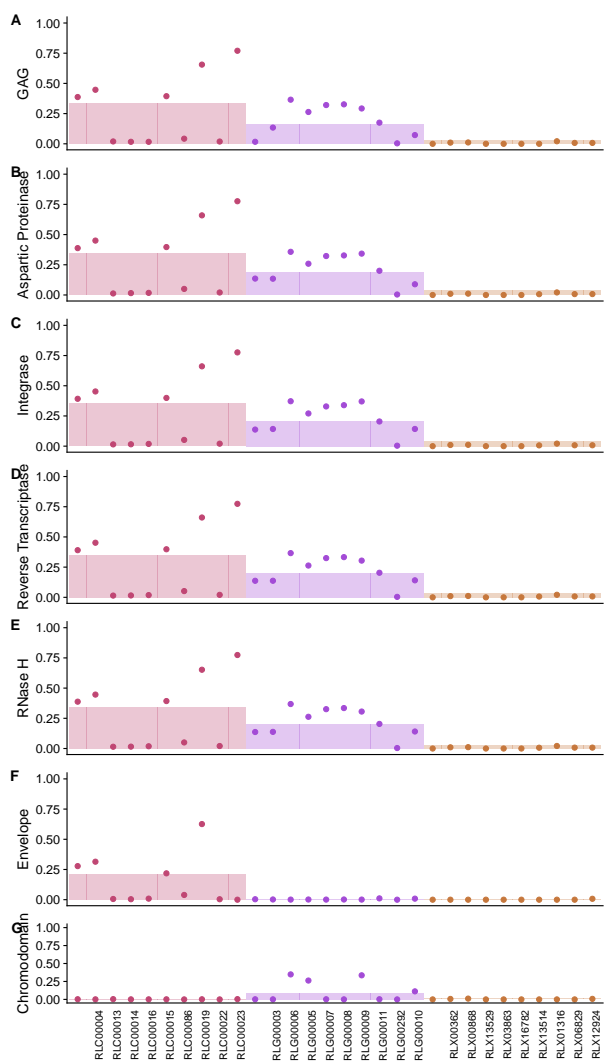


Fig. S11. Protein coding gene presence of individual LTR GAG and POL domains Shown are (A) the proportion of TEs with evidence of agglutination factor (GAG) domain present, (B) aspartic proteinase (AP) domains present, (C) Integrase (INT) domains present, (D) reverse transcriptase (RT) domains present, (E) RNaseH domains present, (F) envelope (ENV) domains present, and (G) chromodomain (CHR) domains present. Families are shown as points and superfamily proportions as barplot.

Table S1. Categories that each feature is classified into.

feature	category
fam	TE_taxonomy
sup	TE_taxonomy
closest	flank_selection
tebp	TE_features
tespan	TE_features
pieces	TE_features
disruptor	TE_features
ingene	flank_selection
helprot	TE_encoded_proteins
rveprot	TE_encoded_proteins
tpaseprot	TE_encoded_proteins
GAG	TE_encoded_proteins
AP	TE_encoded_proteins
INT	TE_encoded_proteins
RT	TE_encoded_proteins
RNaseH	TE_encoded_proteins
ENV	TE_encoded_proteins
CHR	TE_encoded_proteins
pol	TE_encoded_proteins
auton	TE_encoded_proteins
GAGfam	TE_encoded_proteins
APfam	TE_encoded_proteins
INTfam	TE_encoded_proteins
RTfam	TE_encoded_proteins
RNaseHfam	TE_encoded_proteins
ENVfam	TE_encoded_proteins
CHRFam	TE_encoded_proteins
polfam	TE_encoded_proteins
autonfam	TE_encoded_proteins
helprotfam	TE_encoded_proteins
rveprotfam	TE_encoded_proteins
tpaseprotfam	TE_encoded_proteins
orfAA	TE_encoded_proteins
percGC	TE_base_composition
nCG	TE_base_composition
nCHG	TE_base_composition
nCHH	TE_base_composition
percGC_1kbflank	flank_base_composition
nCG_1kbflank	flank_base_composition
nCHG_1kbflank	flank_base_composition
nCHH_1kbflank	flank_base_composition
n_root_hs	TE_methylation_mnase
root_bp	TE_methylation_mnase
root_prop	TE_methylation_mnase
n_shoot_hs	TE_methylation_mnase
shoot_bp	TE_methylation_mnase
shoot_prop	TE_methylation_mnase
flank_n_root_hs	flank_methylation_mnase
flank_root_bp	flank_methylation_mnase
flank_root_prop	flank_methylation_mnase
flank_n_shoot_hs	flank_methylation_mnase
flank_shoot_bp	flank_methylation_mnase
flank_shoot_prop	flank_methylation_mnase
segsites.bp	TE_features

earshoot_flank_chh_800	flank_methylation_mnase
earshoot_flank_chh_900	flank_methylation_mnase
earshoot_flank_chh_1000	flank_methylation_mnase
earshoot_flank_chh_1100	flank_methylation_mnase
earshoot_flank_chh_1200	flank_methylation_mnase
earshoot_flank_chh_1300	flank_methylation_mnase
earshoot_flank_chh_1400	flank_methylation_mnase
earshoot_flank_chh_1500	flank_methylation_mnase
earshoot_flank_chh_1600	flank_methylation_mnase
earshoot_flank_chh_1700	flank_methylation_mnase
earshoot_flank_chh_1800	flank_methylation_mnase
earshoot_flank_chh_1900	flank_methylation_mnase
earshoot_flank_chh_2000	flank_methylation_mnase
flagleaf_avg_cg	TE_methylation_mnase
flagleaf_avg_chg	TE_methylation_mnase
flagleaf_avg_chh	TE_methylation_mnase
flagleaf_flank_cg_100	flank_methylation_mnase
flagleaf_flank_cg_200	flank_methylation_mnase
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flagleaf_flank_cg_400	flank_methylation_mnase
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flagleaf_flank_cg_1200	flank_methylation_mnase
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flagleaf_flank_chh_100	flank_methylation_mnase

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all3_flank_chh_1900	flank_methylation_mnase
all3_flank_chh_2000	flank_methylation_mnase
SAM_avg_cg	TE_methylation_mnase
SAM_avg_chg	TE_methylation_mnase
SAM_avg_chh	TE_methylation_mnase
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SAM_flank_chh_2000	flank_methylation_mnase
gene_6_7_internode	flank_closest_gene_expression
gene_7_8_internode	flank_closest_gene_expression
gene_Vegetative_Meristem_16_19_Day	flank_closest_gene_expression
gene_Ear_Primordium_2_4_mm	flank_closest_gene_expression
gene_Ear_Primordium_6_8_mm	flank_closest_gene_expression
gene_Embryo_20_DAP	flank_closest_gene_expression
gene_Embryo_38_DAP	flank_closest_gene_expression
gene_Endosperm_12_DAP	flank_closest_gene_expression
gene_Endosperm_Crown_27_DAP	flank_closest_gene_expression
gene_Germinatin_Kernels_2_DAI	flank_closest_gene_expression
gene_Pericarp_Aleurone_27_DAP	flank_closest_gene_expression
gene_Leaf_Zone_1_Symmetrical_	flank_closest_gene_expression
gene_Leaf_Zone_2_Stomatal_	flank_closest_gene_expression
gene_Leaf_Zone_3_Growth_	flank_closest_gene_expression
gene_Mature_Leaf_8	flank_closest_gene_expression
gene_Primary_Root_5_Days	flank_closest_gene_expression
gene_Root_Cortex_5_Days	flank_closest_gene_expression
gene_Root_Elongation_Zone_5_Days	flank_closest_gene_expression
gene_Root_Meristem_Zone_5_Days	flank_closest_gene_expression
gene_Secondary_Root_7_8_Days	flank_closest_gene_expression
gene_B73_Mature_Pollen	flank_closest_gene_expression
gene_Female_Spikelet_Collected_on_day_as_silk	flank_closest_gene_expression
gene_Silk	flank_closest_gene_expression
famsize	TE_features
gene_coefvar	flank_closest_gene_expression
gene_median	flank_closest_gene_expression

Tefam_ear_primordium.2mm	TE_expression
Tefam_ear_primordium.6mm	TE_expression
Tefam_embryo_20d	TE_expression
Tefam_embryo_38d	TE_expression
Tefam_endosperm_12d	TE_expression
Tefam_endosperm_crown	TE_expression
Tefam_germinating.kernels_2d	TE_expression
Tefam_internode_6to7	TE_expression
Tefam_internode_7to8	TE_expression
Tefam_leaf_8	TE_expression
Tefam_leaf_growth.zone	TE_expression
Tefam_leaf_stomatal.zone	TE_expression
Tefam_leaf_symmetrical.zone	TE_expression
Tefam_meristem_vegetative	TE_expression
Tefam_pollen_mature	TE_expression
Tefam_root_cortex	TE_expression
Tefam_root_elongation.zone	TE_expression
Tefam_root_meristem.zone	TE_expression
Tefam_root_primary	TE_expression
Tefam_root_secondary	TE_expression
Tefam_seed_pericarp.aleurone	TE_expression
Tefam_silk_mature	TE_expression
Tefam_spikelet_female	TE_expression
TefamMedian	TE_expression
TefamMedianPerCopy	TE_expression
TefamMedianPerBp	TE_expression
Tefam_tau	TE_expression
cmmb	flank_selection
subgenome	flank_selection

Table S2. 14 families with at least 10 copies in the B73 genome, with at least 75% of copies coding for transposition related proteins.

sup	fam	propAuton	famsize	medianORF	meanORF
DTC	DTC00001	0.773399014778325	203	614	591.751269035533
DTC	DTC00014	0.8333333333333333	12	678	635.75
DTC	DTC00017	0.9	10	448	453.2
DTC	DTC00027	0.9	20	571.5	580.1
DTC	DTC00041	0.8	10	388	407.4
DTC	DTC00053	0.75	28	745.5	724.821428571429
DTC	DTC00063	0.75	12	495.5	480.916666666667
RLC	RLC00023	0.76878612716763	519	992	941.737769080235
RLC	RLC00074	0.765625	64	901.5	928.3125
RLC	RLC00137	0.857142857142857	28	1287.5	1072.78571428571
RLC	RLC00149	0.777777777777778	27	1253	1103.111111111111
RLC	RLC00158	0.8	25	769	894.84
RLC	RLC00232	0.882352941176471	17	1473	1147.17647058824
RLC	RLC00252	0.8	15	1112	1163.26666666667
RLC	RLC00305	0.909090909090909	11	1008	1009.63636363636
RLC	RLC00367	0.9	10	1616.5	1404.8
RLG	RLG00287	0.846153846153846	13	1173	1101.38461538462
RLG	RLG00363	0.8	10	1442	1235.9

Table S3. 842 families with at least 10 copies in the B73 genome that lack coding representatives.

sup	fam	propAuton	famsize	medianORF	meanORF
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DHH	DHH00001	0	5946	69	170.178694158076
DHH	DHH00003	0	949	541	521.511956521739
DHH	DHH00004	0	1611	369	347.998137802607
DHH	DHH00005	0	265	221	295.777777777778
DHH	DHH00006	0	1013	79	77.5364705882353
DHH	DHH00007	0	403	202.5	238.27380952381
DHH	DHH00008	0	738	739	651.770065075922
DHH	DHH00009	0	283	250	276.218637992832
DHH	DHH00011	0	81	225	266.012345679012
DHH	DHH00012	0	164	226.5	248.440789473684
DHH	DHH00013	0	156	67	145.893203883495
DHH	DHH00014	0	90	402	446.134831460674
DHH	DHH00015	0	119	68	129.794392523364
DHH	DHH00016	0	149	61	90.4491525423729
DHH	DHH00017	0	29	331	325.655172413793
DHH	DHH00018	0	62	988	890.947368421053
DHH	DHH00019	0	110	44.5	133.735294117647
DHH	DHH00020	0	25	232	306
DHH	DHH00021	0	51	388	413.392156862745
DHH	DHH00022	0	35	192	281.318181818182
DHH	DHH00023	0	46	253	227.673913043478
DHH	DHH00024	0	40	49	74.4054054054054
DHH	DHH00025	0	63	121.5	258.648148148148
DHH	DHH00026	0	36	135	149.852941176471
DHH	DHH00027	0	14	64	203
DHH	DHH00028	0	12	218.5	319.416666666667
DHH	DHH00029	0	75	179	242.808219178082
DHH	DHH00030	0	18	322	269.470588235294
DHH	DHH00032	0	68	197	239.754098360656
DHH	DHH00036	0	21	1303	1193.04761904762
DHH	DHH00037	0	16	221	281.933333333333
DHH	DHH00038	0	11	142	214.555555555556
DHH	DHH00040	0	16	306	374.4
DHH	DHH00041	0	16	128.5	184
DHH	DHH00043	0	18	146.5	173.777777777778
DHH	DHH00044	0	15	109.5	130.214285714286
DHH	DHH00045	0	10	81	147.714285714286
DHH	DHH00048	0	24	146	151.434782608696
DHH	DHH00049	0	17	362	318.714285714286
DHH	DHH00050	0	15	54	120.142857142857
DHH	DHH00052	0	13	555	478.666666666667
DHH	DHH00059	0	11	83.5	93.5
DHH	DHH00063	0	10	122	94.1111111111111
DTA	DTA00003	0	12	74	74
DTA	DTA00006	0	12	306	308.75
DTA	DTA00016	0	10	315	322
DTA	DTA00025	0	13	445	405.692307692308
DTA	DTA00029	0	12	307.5	386.166666666667
DTA	DTA00030	0	16	345	383.8125
DTA	DTA00040	0	36	36	36.9285714285714
DTA	DTA00045	0	23	43	46.25
DTA	DTA00046	0	19	27	42.8333333333333
DTA	DTA00049	0	38	30	58.4285714285714
DTA	DTA00051	0	42	39.5	86.6666666666667
DTA	DTA00059	0	12	51	48.1111111111111
DTA	DTA00060	0	120	33	131.263157894737

DTA	DTA00061	0	54	20	54.8
DTA	DTA00062	0	10	131	131
DTA	DTA00064	0	19	104	161.333333333333
DTA	DTA00065	0	19	37	42.5
DTA	DTA00066	0	35	29.5	33.7
DTA	DTA00073	0	148	49.5	46.25
DTA	DTA00076	0	55	42	42
DTA	DTA00077	0	15	433	432.727272727273
DTA	DTA00078	0	26	35	30.625
DTA	DTA00080	0	72	106	129.1875
DTA	DTA00085	0	15	417	455.6
DTA	DTA00089	0	19	87.5	101.75
DTA	DTA00090	0	23	84	169.285714285714
DTA	DTA00091	0	30	86	95.6923076923077
DTA	DTA00092	0	70	26	102.454545454545
DTA	DTA00099	0	19	65	88.4
DTA	DTA00102	0	157	29.5	37.5853658536585
DTA	DTA00104	0	36	90	286
DTA	DTA00106	0	31	58.5	134.230769230769
DTA	DTA00114	0	147	65	79.5365853658537
DTA	DTA00115	0	12	94.5	219.25
DTA	DTA00117	0	234	31.5	40.3809523809524
DTA	DTA00118	0	11	33	355.333333333333
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DTA	DTA00120	0	25	88	137.714285714286
DTA	DTA00124	0	13	41	41
DTA	DTA00126	0	20	24	24
DTA	DTA00131	0	46	88	101.555555555556
DTA	DTA00133	0	14	82	95
DTA	DTA00135	0	132	56	53.8064516129032
DTA	DTA00136	0	40	131	156.782608695652
DTA	DTA00138	0	15	78	95
DTA	DTA00141	0	192	43	50.8
DTA	DTA00142	0	16	47	51
DTA	DTA00143	0	35	36	42.5
DTA	DTA00144	0	24	48.5	54
DTA	DTA00148	0	10	58	118.8
DTA	DTA00149	0	58	20	47.3529411764706
DTA	DTA00151	0	20	47	97.3333333333333
DTA	DTA00152	0	17	60	56.75
DTA	DTA00153	0	11	19	19
DTA	DTA00154	0	14	609.5	512.25
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DTA	DTA00156	0	22	55	52.4
DTA	DTA00159	0	11	110	101.142857142857
DTA	DTA00164	0	10	69	146.285714285714
DTA	DTA00167	0	11	254	254
DTA	DTA00169	0	12	41	40.3333333333333
DTA	DTA00171	0	38	38	90.5
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DTA	DTA00174	0	18	21	31
DTA	DTA00179	0	19	25	25
DTA	DTA00180	0	16	NA	NaN
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DTA	DTA00191	0	17	20.5	20.5
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DTA	DTA00199	0	13	121.5	231.5
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DTA	DTA00210	0	88	NA	NaN
DTA	DTA00217	0	77	22	35.9
DTA	DTA00219	0	11	NA	NaN
DTA	DTA00224	0	13	84	96
DTA	DTA00227	0	13	29	30.6
DTA	DTA00238	0	19	NA	NaN
DTA	DTA00239	0	17	33.5	33.5
DTA	DTA00242	0	11	82.5	72
DTA	DTA00243	0	13	NA	NaN
DTA	DTA00245	0	28	138	297.8
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DTA	DTA00252	0	89	65	53.551724137931
DTA	DTA00253	0	34	28	58.48
DTA	DTA00256	0	15	461.5	406.166666666667
DTA	DTA00267	0	11	23	37.1428571428571
DTA	DTA00283	0	17	33	34.3333333333333
DTA	DTA00286	0	17	27	30.9
DTA	DTA00289	0	11	26	71.8
DTA	DTA00291	0	42	39	50.9230769230769
DTA	DTA00293	0	29	64	53.1578947368421
DTA	DTA00295	0	16	28	25.3333333333333
DTA	DTA00299	0	23	NA	NaN
DTA	DTA00301	0	11	33	105.4
DTA	DTA00307	0	62	25	30.2
DTA	DTA00312	0	18	59	72.5
DTA	DTA00313	0	11	NA	NaN
DTA	DTA00323	0	16	25	34.5
DTA	DTA00339	0	12	45.5	45.5
DTA	DTA00345	0	16	22	22
DTA	DTA00346	0	11	48	48
DTA	DTA00348	0	15	NA	NaN
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DTA	DTA13185	0	35	43	42.9333333333333
DTC	DTC00109	0	10	39	44.4
DTC	DTC00111	0	228	32	35.2894736842105
DTC	DTC00112	0	67	32	40.2857142857143
DTC	DTC00113	0	61	87.5	94.8125
DTC	DTC00114	0	86	29	31.4444444444444
DTC	DTC00115	0	20	37.5	58.75
DTC	DTC00116	0	80	40.5	42.6666666666667
DTC	DTC00118	0	79	24	35.0645161290323
DTC	DTC00122	0	143	42	49.3695652173913
DTC	DTC00126	0	10	NA	NaN
DTC	DTC10850	0	15	30	32
DTC	DTC12155	0	62	29	28.4090909090909
DTC	DTC15669	0	14	35	43
DTH	DTH00004	0	11	345	322.181818181818
DTH	DTH00010	0	17	344	302.882352941176
DTH	DTH00011	0	11	251	255.363636363636
DTH	DTH00012	0	11	198	167.272727272727
DTH	DTH00015	0	10	418	397.6
DTH	DTH00024	0	17	186	279.058823529412
DTH	DTH00032	0	11	219	238.636363636364
DTH	DTH00037	0	97	35	40.2631578947368
DTH	DTH00040	0	48	39	44.1666666666667

DTH	DTH00041	0	21	69	67.8571428571429
DTH	DTH00042	0	11	29	33
DTH	DTH00043	0	15	46.5	46.5
DTH	DTH00044	0	20	43	44.3333333333333
DTH	DTH00046	0	13	43	52.25
DTH	DTH00049	0	46	28	44.8333333333333
DTH	DTH00050	0	16	36	47
DTH	DTH00051	0	27	118	134.714285714286
DTH	DTH00053	0	10	NA	NaN
DTH	DTH00054	0	190	34	40.1351351351351
DTH	DTH00057	0	181	67	58.7205882352941
DTH	DTH00058	0	72	63	84.2
DTH	DTH00062	0	29	27	26
DTH	DTH00067	0	602	36	65.5
DTH	DTH00071	0	11	NA	NaN
DTH	DTH00073	0	122	42	128.777777777778
DTH	DTH00076	0	29	45	50.0909090909091
DTH	DTH00084	0	10	57	54
DTH	DTH00090	0	214	32	35.4545454545455
DTH	DTH00093	0	65	21	24
DTH	DTH00098	0	495	26	29.0246305418719
DTH	DTH00102	0	1291	44	40.5723684210526
DTH	DTH00114	0	25	46	52.5
DTH	DTH00118	0	397	37	41.1511627906977
DTH	DTH00119	0	124	29	31.8235294117647
DTH	DTH00127	0	164	25	30.6923076923077
DTH	DTH00129	0	86	31	35.3636363636364
DTH	DTH00135	0	38	34	40.2727272727273
DTH	DTH00139	0	125	30	31.1315789473684
DTH	DTH00145	0	19	46	46.3333333333333
DTH	DTH00153	0	93	24	27.5
DTH	DTH00154	0	606	33	34.3125
DTH	DTH00160	0	196	35	37.2962962962963
DTH	DTH00162	0	72	79	125.8
DTH	DTH00163	0	968	38	34.8842105263158
DTH	DTH00178	0	10	38.5	38.5
DTH	DTH00180	0	16	34	33.1666666666667
DTH	DTH00181	0	44	40.5	42.75
DTH	DTH00184	0	26	42	39.0588235294118
DTH	DTH00194	0	118	38	55.0618556701031
DTH	DTH00198	0	17	54	54
DTH	DTH00202	0	44	29	42.6
DTH	DTH00220	0	10	42	40.7
DTH	DTH00226	0	40	40	41
DTH	DTH00233	0	292	33	38.804347826087
DTH	DTH00241	0	35	39.5	39.5
DTH	DTH00244	0	11	30	30
DTH	DTH00273	0	11	34	84.6666666666667
DTH	DTH00280	0	289	53	50.9074074074074
DTH	DTH00292	0	10	116	116
DTH	DTH00307	0	20	NA	NaN
DTH	DTH00311	0	79	53	68.75
DTH	DTH00314	0	10	NA	NaN
DTH	DTH00320	0	95	23	27.4
DTH	DTH00326	0	56	33	33
DTH	DTH00327	0	481	40	60.0769230769231
DTH	DTH00335	0	32	21	21.7272727272727

DTH	DTH00337	0	75	32	64.4
DTH	DTH00340	0	27	49	47.93333333333333
DTH	DTH00347	0	14	124	110.2
DTH	DTH00351	0	153	26.5	32.25
DTH	DTH00355	0	67	44.5	47.875
DTH	DTH00361	0	85	27	36.125
DTH	DTH00364	0	76	43	51.0869565217391
DTH	DTH00367	0	10	60.5	60.5
DTH	DTH00382	0	13	24	24.5
DTH	DTH00385	0	82	22.5	28.85
DTH	DTH00389	0	212	26	34.48
DTH	DTH00409	0	748	27	55.68
DTH	DTH00410	0	76	20	30.66666666666667
DTH	DTH00412	0	52	215.5	178.6666666666667
DTH	DTH00418	0	111	39	44.4705882352941
DTH	DTH00431	0	74	43	42.86666666666667
DTH	DTH00434	0	347	27	44.45454545454545
DTH	DTH00437	0	152	49	60.1071428571429
DTH	DTH00442	0	74	36	55
DTH	DTH00453	0	18	31.5	31.5
DTH	DTH00460	0	81	37	30.4
DTH	DTH00463	0	18	33	33
DTH	DTH00471	0	42	32	99.33333333333333
DTH	DTH00485	0	58	37.5	40
DTH	DTH00486	0	16	21	21
DTH	DTH00489	0	99	23	27.1428571428571
DTH	DTH10044	0	86	40	41.75
DTH	DTH10047	0	169	30.5	42.9375
DTH	DTH10048	0	13	52.5	50.75
DTH	DTH10060	0	11	34.5	37.25
DTH	DTH10064	0	28	20	20
DTH	DTH10085	0	20	44	53.5714285714286
DTH	DTH10107	0	290	44	45.2631578947368
DTH	DTH10113	0	37	45	45
DTH	DTH10153	0	61	43	43.5454545454545
DTH	DTH10158	0	98	29	55.4090909090909
DTH	DTH10176	0	146	32	38.9245283018868
DTH	DTH10182	0	26	27.5	46
DTH	DTH10187	0	80	29	29.1153846153846
DTH	DTH10226	0	15	31	33
DTH	DTH10230	0	107	28	30.3888888888889
DTH	DTH10239	0	25	41	43.25
DTH	DTH10248	0	21	26.5	33
DTH	DTH10268	0	516	46	42.5354838709677
DTH	DTH10298	0	21	33.5	33.8333333333333
DTH	DTH10310	0	106	42	40.4390243902439
DTH	DTH10314	0	13	44	46.75
DTH	DTH10328	0	82	40.5	37.9705882352941
DTH	DTH10339	0	13	38	36.5555555555556
DTH	DTH10363	0	1053	41	39.4405594405594
DTH	DTH10364	0	36	34	41.7857142857143
DTH	DTH10379	0	42	35	36.6153846153846
DTH	DTH10380	0	33	31.5	36.7777777777778
DTH	DTH10388	0	43	41.5	52.75
DTH	DTH10391	0	13	26	33.3333333333333
DTH	DTH10406	0	20	28	38
DTH	DTH10440	0	14	37	37

DTH	DTH10442	0	25	36	36.8571428571429
DTH	DTH10444	0	959	31	31.5714285714286
DTH	DTH10445	0	312	30	52.3333333333333
DTH	DTH10454	0	44	45	52.8421052631579
DTH	DTH10481	0	16	38	40.7777777777778
DTH	DTH10483	0	180	27	37.6727272727273
DTH	DTH10494	0	17	39	43.4285714285714
DTH	DTH10560	0	30	42.5	48.5
DTH	DTH10573	0	104	35	36.3103448275862
DTH	DTH10659	0	10	NA	NaN
DTH	DTH10699	0	10	32	30.4
DTH	DTH10700	0	368	33	33.4689655172414
DTH	DTH10715	0	86	34	33.5471698113208
DTH	DTH10741	0	10	31	31
DTH	DTH10775	0	910	134	128.749152542373
DTH	DTH10781	0	12	44.5	42.25
DTH	DTH10818	0	14	31	31
DTH	DTH10852	0	15	34	34
DTH	DTH10855	0	659	28	29.8343558282209
DTH	DTH10856	0	126	28	31.3870967741935
DTH	DTH10946	0	179	25	30.0425531914894
DTH	DTH11074	0	33	35	41.1111111111111
DTH	DTH11101	0	409	21	26.9003984063745
DTH	DTH11152	0	1624	34	54.9435431537962
DTH	DTH11199	0	93	52	58.3793103448276
DTH	DTH11200	0	52	50	58.7894736842105
DTH	DTH11203	0	513	74	78
DTH	DTH11206	0	176	135.5	141.850574712644
DTH	DTH11207	0	245	123	118.725738396624
DTH	DTH11208	0	187	38	43.7260273972603
DTH	DTH11209	0	107	44	53.6944444444444
DTH	DTH11211	0	13	38	44
DTH	DTH11238	0	894	38	45.7435897435897
DTH	DTH11239	0	1029	37	42.6699029126214
DTH	DTH11253	0	30	20	20
DTH	DTH11350	0	75	46	52.8125
DTH	DTH11351	0	29	19	49.25
DTH	DTH11388	0	16	31.5	37.875
DTH	DTH11403	0	79	44	42.4210526315789
DTH	DTH11404	0	10	37.5	37
DTH	DTH11419	0	172	45	41.1692307692308
DTH	DTH11440	0	10	49	49
DTH	DTH11441	0	28	25	27.3333333333333
DTH	DTH11449	0	935	90	80.3986784140969
DTH	DTH11450	0	449	90	79.4233409610984
DTH	DTH11457	0	64	62	69.7924528301887
DTH	DTH11481	0	35	21.5	21.5
DTH	DTH11482	0	24	29.5	28
DTH	DTH11541	0	464	83	77.7443365695793
DTH	DTH11542	0	567	77	78.0234741784038
DTH	DTH11594	0	65	19	19.2727272727273
DTH	DTH11602	0	73	38	39.4358974358974
DTH	DTH11614	0	14	53	53.2
DTH	DTH11708	0	1556	111	105.549578742709
DTH	DTH11714	0	90	36	45.3829787234043
DTH	DTH11715	0	14	46	44.4
DTH	DTH11798	0	14	54	54

DTH	DTH11817	0	346	33	33.7368421052632
DTH	DTH11830	0	140	25	30.4347826086957
DTH	DTH11834	0	71	26	26.0909090909091
DTH	DTH11854	0	104	115	113.7
DTH	DTH11856	0	60	19	30.8571428571429
DTH	DTH11862	0	53	44	49.1176470588235
DTH	DTH11932	0	44	42	43.1111111111111
DTH	DTH11948	0	17	33	30.6666666666667
DTH	DTH11949	0	14	40	37
DTH	DTH12058	0	11	NA	NaN
DTH	DTH12059	0	13	20	20
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DTH	DTH12191	0	43	NA	NaN
DTH	DTH12217	0	58	34	109.2
DTH	DTH12228	0	26	62	62
DTH	DTH12232	0	109	67.5	70.3448275862069
DTH	DTH12250	0	215	63	51.8571428571429
DTH	DTH12251	0	132	60	66.7368421052632
DTH	DTH12258	0	2623	58	69.0553449583017
DTH	DTH12289	0	13	22	30.6666666666667
DTH	DTH12290	0	46	106	76.7179487179487
DTH	DTH12298	0	203	34	37.8190476190476
DTH	DTH12305	0	50	24	59.7142857142857
DTH	DTH12326	0	267	24	45.75
DTH	DTH12381	0	108	26	27.4117647058824
DTH	DTH12383	0	10	22	45.3333333333333
DTH	DTH12388	0	110	29	34.3
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DTH	DTH12390	0	296	27.5	28.2
DTH	DTH12393	0	153	40	110.3
DTH	DTH12412	0	492	34	39.0961538461538
DTH	DTH12419	0	24	73	58.6666666666667
DTH	DTH12507	0	113	41	46.0491803278689
DTH	DTH12534	0	259	43	47.9195402298851
DTH	DTH12537	0	22	35	41.125
DTH	DTH12555	0	18	25	28.25
DTH	DTH12617	0	34	23	25.875
DTH	DTH12628	0	24	37	56.5384615384615
DTH	DTH12645	0	17	77	76
DTH	DTH12694	0	14	43	42.6
DTH	DTH12697	0	21	38	44.1111111111111
DTH	DTH12711	0	19	38	33.3333333333333
DTH	DTH12718	0	186	30.5	151.375
DTH	DTH12769	0	211	63.5	64.551724137931
DTH	DTH12801	0	232	154	144.188340807175
DTH	DTH12838	0	350	81.5	77.9065040650407
DTH	DTH12839	0	90	72.5	75.3103448275862
DTH	DTH12973	0	325	28	40.7692307692308
DTH	DTH12996	0	1844	32	37.4453870625663
DTH	DTH12997	0	280	31	37.7747747747748
DTH	DTH13012	0	22	63.5	63.5
DTH	DTH13063	0	32	41	48.1111111111111
DTH	DTH13110	0	577	55	60.1994884910486
DTH	DTH13117	0	450	121	126.732426303855
DTH	DTH13200	0	147	30	36.2727272727273
DTH	DTH13235	0	84	190	186.024096385542

DTH	DTH13261	0	28	27	33.2
DTH	DTH13439	0	13	24	25.66666666666667
DTH	DTH13583	0	1462	41	48.6263383297645
DTH	DTH13597	0	21	57	57
DTH	DTH13636	0	22	72	71.88888888888889
DTH	DTH13647	0	39	37	40.125
DTH	DTH13657	0	74	38.5	46.1785714285714
DTH	DTH13748	0	10	65	55
DTH	DTH13854	0	120	47	59.5116279069767
DTH	DTH13942	0	166	62	68.2527472527473
DTH	DTH13989	0	33	45	47.1176470588235
DTH	DTH13990	0	30	46	47.22222222222222
DTH	DTH14072	0	14	21	21
DTH	DTH14130	0	11	28	28
DTH	DTH14236	0	234	25	25.8771929824561
DTH	DTH14279	0	32	58	56.3636363636364
DTH	DTH14804	0	1175	118	118.327630453379
DTH	DTH14898	0	121	80.5	84.7307692307692
DTH	DTH15065	0	78	28	37.8571428571429
DTH	DTH15116	0	12	45	55.3333333333333
DTH	DTH15132	0	235	42	47.1702127659574
DTH	DTH15139	0	12	24	26.3333333333333
DTH	DTH15158	0	79	56	55.5348837209302
DTH	DTH15299	0	255	67	79.0152671755725
DTH	DTH15300	0	100	64	75.1636363636364
DTH	DTH15301	0	45	61.5	83.7
DTH	DTH16098	0	90	57	79.2631578947368
DTH	DTH16099	0	56	61	87.6
DTH	DTH16100	0	40	105	92.7777777777778
DTH	DTH16163	0	12	NA	NaN
DTH	DTH16174	0	211	50	53.9
DTH	DTH16203	0	29	27.5	27.5
DTH	DTH16233	0	867	30	38.0476190476191
DTH	DTH16329	0	598	70	87.0020325203252
DTH	DTH16351	0	11	106	97
DTH	DTH16373	0	611	74	94.4440559440559
DTH	DTH16443	0	98	28	39.1282051282051
DTH	DTH16563	0	263	121	132.171875
DTH	DTH16728	0	1322	30	51.3277693474962
DTH	DTH16758	0	768	31	37.1825396825397
DTH	DTH16778	0	561	91	98.0576923076923
DTH	DTH16779	0	108	90	90.890625
DTH	DTH16783	0	149	39	44.5581395348837
DTH	DTH16799	0	317	172	154.546391752577
DTH	DTH16801	0	14	22	22
DTM	DTM00118	0	19	22	22.3
DTM	DTM00257	0	376	50	48.3404255319149
DTM	DTM00266	0	47	64	470.3333333333333
DTM	DTM00299	0	22	26	26
DTM	DTM00460	0	41	34	34
DTM	DTM00473	0	30	51	54.8235294117647
DTM	DTM00555	0	37	24	24
DTM	DTM00796	0	16	50.5	46.4
DTM	DTM00800	0	17	41	41
DTM	DTM01654	0	13	61	50.2307692307692
DTM	DTM02275	0	10	NA	NaN
DTM	DTM13640	0	178	59	54.7647058823529

DTT	DTT00008	0	32	23	30.25
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DTT	DTT00010	0	932	26	29.015037593985
DTT	DTT00011	0	519	30	37.6666666666667
DTT	DTT00012	0	395	34	190
DTT	DTT00013	0	137	28.5	37.375
DTT	DTT00015	0	234	26	37.4242424242424
DTT	DTT00016	0	632	32.5	51.5634920634921
DTT	DTT00019	0	12	21	21
DTT	DTT00022	0	232	26	35.5689655172414
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DTT	DTT00026	0	1409	32	39.6736111111111
DTT	DTT00027	0	316	32	38.4411764705882
DTT	DTT00031	0	28	22.5	24.8333333333333
DTT	DTT00032	0	291	40	44.9076923076923
DTT	DTT00033	0	53	38	34.4
DTT	DTT00034	0	80	29.5	34.7
DTT	DTT00038	0	15	29	29
DTT	DTT00040	0	13	28	28
DTT	DTT00041	0	57	37	32.6666666666667
DTT	DTT00042	0	429	30	42.1818181818182
DTT	DTT00044	0	127	28	30.4375
DTT	DTT00046	0	95	38.5	46
DTT	DTT00049	0	23	64.5	61.25
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DTT	DTT00054	0	28	22	22
DTT	DTT00056	0	301	25	28.3863636363636
DTT	DTT10003	0	47	39	42.9285714285714
DTT	DTT10009	0	702	34.5	63.9333333333333
DTT	DTT10033	0	52	38	38.5
DTT	DTT10037	0	93	20	20
DTT	DTT10038	0	74	26	26
DTT	DTT10054	0	55	23	28.3333333333333
DTT	DTT10062	0	273	39.5	37.5
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DTT	DTT10115	0	160	28.5	31.28125
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DTT	DTT10125	0	32	25	25.4285714285714
DTT	DTT10171	0	72	30	33.3333333333333
DTT	DTT10172	0	73	24	28.5714285714286
DTT	DTT10193	0	59	20	20
DTT	DTT10253	0	29	49.5	46.6666666666667
DTT	DTT10254	0	384	47	52.6157894736842
DTT	DTT10260	0	125	NA	NaN
DTT	DTT10319	0	26	29	28.6666666666667
DTT	DTT10370	0	21	24	24
DTT	DTT10404	0	13	25	29.7142857142857
DTT	DTT10422	0	11	24	32.3333333333333
DTT	DTT10423	0	18	38	38
DTT	DTT10433	0	21	34.5	35
DTT	DTT10449	0	11	39.5	39.5
DTT	DTT10459	0	43	36	37.375
DTT	DTT10475	0	148	24	27.9016393442623
DTT	DTT10539	0	22	51	48.2857142857143
DTT	DTT10540	0	13	44	37.4285714285714
DTT	DTT10577	0	806	34	35.7627118644068

DTT	DTT10584	0	16	NA	NaN
DTT	DTT10594	0	15	55	55
DTT	DTT10647	0	12	NA	NaN
DTT	DTT10693	0	79	31	35.6666666666667
DTT	DTT10706	0	204	22	22
DTT	DTT10724	0	58	99	77.2727272727273
DTT	DTT10738	0	51	24	29
DTT	DTT10742	0	15	20	20
DTT	DTT10797	0	889	29	27.8618421052632
DTT	DTT10806	0	18	25	25
DTT	DTT10833	0	9953	37	44.4548395123165
DTT	DTT10841	0	28	NA	NaN
DTT	DTT10864	0	113	41	41.6481481481481
DTT	DTT10865	0	56	30	31
DTT	DTT10873	0	122	26	33.3478260869565
DTT	DTT10880	0	6151	33	37.9612289685443
DTT	DTT10889	0	267	28	36.7959183673469
DTT	DTT10892	0	69	41	46.3636363636364
DTT	DTT10893	0	39	28.5	32.5
DTT	DTT10906	0	19	24	24
DTT	DTT10907	0	15	22	22
DTT	DTT10927	0	277	25	31.3125
DTT	DTT10937	0	25	38.5	38.5
DTT	DTT10986	0	20	37.5	43
DTT	DTT11051	0	51	34.5	39.0769230769231
DTT	DTT11056	0	231	34	34.7121212121212
DTT	DTT11071	0	16	30.5	30.5
DTT	DTT11073	0	199	33	36
DTT	DTT11075	0	41	29	38.4375
DTT	DTT11090	0	169	49	48.7777777777778
DTT	DTT11146	0	48	32	37.2
DTT	DTT11147	0	12	45	41.6666666666667
DTT	DTT11169	0	39	24	24
DTT	DTT11170	0	51	47.5	47.5
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DTT	DTT11230	0	53	35	37.5555555555556
DTT	DTT11244	0	56	47	41.1333333333333
DTT	DTT11258	0	15	33	30
DTT	DTT11275	0	16	24	23.3333333333333
DTT	DTT11278	0	50	30	41.3333333333333
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DTT	DTT11292	0	73	22.5	25.6875
DTT	DTT11306	0	21	33	33.2
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DTT	DTT11338	0	296	59.5	61.9918032786885
DTT	DTT11408	0	48	50	51
DTT	DTT11421	0	14	100.5	92.5
DTT	DTT11451	0	88	47.5	51.8
DTT	DTT11452	0	10	48	48
DTT	DTT11463	0	45	34	35.2
DTT	DTT11547	0	1825	38	49.8983050847458
DTT	DTT11587	0	98	28.5	31.875
DTT	DTT11612	0	53	35	41.8666666666667
DTT	DTT11681	0	44	44	39.6
DTT	DTT11719	0	69	46	52.8181818181818
DTT	DTT11766	0	11	39	39
DTT	DTT11806	0	37	37	48.4285714285714

DTT	DTT11836	0	16	58.5	58.5
DTT	DTT12019	0	100	42.5	41.75
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DTT	DTT12092	0	33	29	28
DTT	DTT12107	0	55	53	60.8260869565217
DTT	DTT12131	0	69	31.5	38.5
DTT	DTT12147	0	50	35	42.9230769230769
DTT	DTT12149	0	33	28	28.375
DTT	DTT12151	0	43	23	26.08
DTT	DTT12171	0	307	133	122.582644628099
DTT	DTT12202	0	1062	35	42.6472081218274
DTT	DTT12206	0	22	38	38
DTT	DTT12283	0	470	38.5	43.3490566037736
DTT	DTT12293	0	146	43	47.9354838709677
DTT	DTT12378	0	21	40	40.3
DTT	DTT12418	0	1304	138	132.157399486741
DTT	DTT12506	0	1108	37	43.2792792792793
DTT	DTT12510	0	51	22.5	22.5
DTT	DTT12572	0	550	33	36.5084745762712
DTT	DTT12632	0	144	53	58.6521739130435
DTT	DTT12746	0	56	31	39.4285714285714
DTT	DTT12754	0	51	23	22
DTT	DTT12757	0	294	26	33.1
DTT	DTT12762	0	108	50	49.6315789473684
DTT	DTT12764	0	39	27.5	27.5
DTT	DTT12820	0	11	123	121
DTT	DTT12824	0	48	38	38.4
DTT	DTT12825	0	19	33	35
DTT	DTT12875	0	634	31	32.9934640522876
DTT	DTT12876	0	247	29	34.0444444444444
DTT	DTT12955	0	383	27	43.7407407407407
DTT	DTT12967	0	172	28	36.7058823529412
DTT	DTT12974	0	684	35	39.0595238095238
DTT	DTT13041	0	4111	57	55.946103423161
DTT	DTT13098	0	114	26	36.6153846153846
DTT	DTT13262	0	64	32	33.125
DTT	DTT13272	0	58	71	82.8571428571429
DTT	DTT13542	0	21	31	30.75
DTT	DTT13549	0	13	55	49.3333333333333
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DTT	DTT13762	0	41	24	25.5555555555556
DTT	DTT13827	0	16	47	47
DTT	DTT13868	0	12	51	49.7
DTT	DTT13979	0	117	29	35.1333333333333
DTT	DTT14079	0	17	NA	NaN
DTT	DTT14220	0	57	25	31.3333333333333
DTT	DTT14352	0	20	24	29.2
DTT	DTT14358	0	231	41	47.7560975609756
DTT	DTT14774	0	17	30	30
DTT	DTT14784	0	1391	27	32.1055555555556
DTT	DTT15038	0	23	24	24
DTT	DTT15227	0	14	NA	NaN
DTT	DTT15264	0	248	19.5	26.2051282051282
DTT	DTT15335	0	28	26.5	24.625
DTT	DTT15443	0	143	35	38.6739130434783
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DTT	DTT15534	0	48	42	45.6

DTT	DTT15615	0	15	28.5	31
DTT	DTT15785	0	30	27.5	31.25
DTT	DTT15993	0	671	38	44.8076923076923
DTT	DTT16190	0	3555	31	37.0521978021978
DTT	DTT16489	0	414	25.5	25.125
DTX	DTX10013	0	270	34	82.462962962963
DTX	DTX10015	0	46	44.5	47.7777777777778
DTX	DTX10020	0	94	23.5	28.4166666666667
DTX	DTX10023	0	26	26	26.6666666666667
DTX	DTX10031	0	100	70	124.4375
DTX	DTX10032	0	83	71.5	71.7241379310345
DTX	DTX10124	0	56	30	35.6428571428571
DTX	DTX10131	0	120	27	31
DTX	DTX10132	0	90	29	33.75
DTX	DTX10177	0	2850	27	33.3927272727273
DTX	DTX10207	0	108	39	43
DTX	DTX10212	0	101	28	30.9375
DTX	DTX10213	0	15	NA	NaN
DTX	DTX10267	0	51	36	37.84
DTX	DTX10308	0	105	40	43.4285714285714
DTX	DTX10309	0	14	41	39
DTX	DTX10416	0	19	32	36.4444444444444
DTX	DTX10541	0	13	25	31.8
DTX	DTX10542	0	26	31	40.6
DTX	DTX10813	0	20	32	33.5454545454545
DTX	DTX10824	0	38	25	25
DTX	DTX10825	0	41	26	26
DTX	DTX10840	0	243	31	34.0263157894737
DTX	DTX10945	0	10	24	39.6666666666667
DTX	DTX11005	0	33	25	35
DTX	DTX11011	0	75	26	34.625
DTX	DTX11123	0	49	39	50.4814814814815
DTX	DTX11178	0	18	23	22.3333333333333
DTX	DTX11265	0	21	47	49.6363636363636
DTX	DTX11433	0	776	30	39.36
DTX	DTX11622	0	14	40	42.3333333333333
DTX	DTX11661	0	206	61	55.7796610169492
DTX	DTX11816	0	62	26	27.25
DTX	DTX11871	0	273	43	46.4565217391304
DTX	DTX12196	0	26	33	33
DTX	DTX12197	0	141	90	76.2238805970149
DTX	DTX12438	0	23	56	54.5384615384615
DTX	DTX12495	0	281	45	168.875
DTX	DTX12496	0	195	26	49.6031746031746
DTX	DTX12540	0	22	40	40
DTX	DTX12562	0	18	49	62.4
DTX	DTX12870	0	1297	33	38.7846364883402
DTX	DTX12956	0	428	32	36.665306122449
DTX	DTX12962	0	778	45	74.0625
DTX	DTX13146	0	3356	39	49.6301476301476
DTX	DTX13147	0	474	44	52.0334928229665
DTX	DTX13328	0	708	41	51.4421768707483
RIL	RIL00001	0	49	490	594.673469387755
RIL	RIL00002	0	28	231	291.357142857143
RIL	RIL00003	0	21	326	418.952380952381
RIL	RIL00004	0	22	584.5	608.318181818182
RIL	RIL00005	0	33	387	440.878787878788

RIL	RIL00006	0	21	906	822.761904761905
RIL	RIL00007	0	12	503.5	587.916666666667
RIL	RIL00008	0	44	338	344.5
RIL	RIL00009	0	27	658	628.576923076923
RIL	RIL00013	0	10	244	274.5
RIL	RIL00015	0	15	580	696
RIL	RIL00016	0	18	431.5	522.055555555556
RIL	RIL00017	0	16	586.5	618.375
RIL	RIL00019	0	14	572	641.5
RIL	RIL00020	0	10	958.5	771.9
RIL	RIL00021	0	21	608	652.285714285714
RIL	RIL00025	0	17	611	644.235294117647
RIL	RIL00026	0	14	933	900
RIL	RIL00028	0	11	636	750.454545454545
RIT	RIT00001	0	169	280	304.109090909091
RIT	RIT00002	0	129	159	246.258620689655
RLC	RLC00097	0	43	390	401.139534883721
RLC	RLC00116	0	34	339.5	394.625
RLC	RLC00119	0	34	355.5	344.916666666667
RLC	RLC00146	0	26	242.5	305.269230769231
RLC	RLC00148	0	29	155	236.75
RLC	RLC00154	0	26	61	104.923076923077
RLC	RLC00182	0	22	980.5	966.727272727273
RLC	RLC00184	0	23	75	97.7826086956522
RLC	RLC00200	0	12	88	363
RLC	RLC00218	0	17	327	402.764705882353
RLC	RLC00228	0	16	365	378.2
RLC	RLC00247	0	14	313.5	377.5
RLC	RLC00248	0	15	326	369.4
RLC	RLC00250	0	15	213	248.866666666667
RLC	RLC00255	0	13	292	305.153846153846
RLC	RLC00274	0	16	500	536.5
RLC	RLC00279	0	13	579	538.769230769231
RLC	RLC00293	0	11	513	478.545454545455
RLC	RLC00311	0	11	276	356.727272727273
RLC	RLC00340	0	12	660.5	745.5
RLC	RLC00358	0	10	920	905.6
RLC	RLC00375	0	10	471.5	787.9
RLC	RLC00462	0	11	75	189.909090909091
RLC	RLC01304	0	19	660	747.578947368421
RLC	RLC02403	0	51	1064	974.901960784314
RLC	RLC02882	0	33	683	554.272727272727
RLC	RLC06245	0	45	546	495.644444444444
RLC	RLC19829	0	129	728	678.573643410853
RLG	RLG00053	0	121	381.5	392.708333333333
RLG	RLG00077	0	60	42	124.529411764706
RLG	RLG00084	0	51	59	87.8823529411765
RLG	RLG00100	0	55	618	479.137254901961
RLG	RLG00106	0	33	270	304.333333333333
RLG	RLG00114	0	35	300	339.971428571429
RLG	RLG00115	0	34	422	475.411764705882
RLG	RLG00120	0	33	259	289.515151515152
RLG	RLG00131	0	29	385	422.793103448276
RLG	RLG00152	0	26	58.5	81.8076923076923
RLG	RLG00174	0	21	91	173.421052631579
RLG	RLG00181	0	22	304.5	353.272727272727
RLG	RLG00186	0	21	254.5	308

RLG	RLG00191	0	19	225	279.157894736842
RLG	RLG00192	0	20	402	396.1
RLG	RLG00193	0	17	275	318
RLG	RLG00223	0	15	292	328.8
RLG	RLG00226	0	15	278	279.066666666667
RLG	RLG00227	0	14	264.5	300.357142857143
RLG	RLG00237	0	10	231	305.1
RLG	RLG00239	0	16	320	316.4375
RLG	RLG00241	0	15	247	262.733333333333
RLG	RLG00242	0	15	272	337.933333333333
RLG	RLG00251	0	15	276	347
RLG	RLG00261	0	14	77	186.142857142857
RLG	RLG00263	0	14	438	446.571428571429
RLG	RLG00270	0	11	293.5	284.5
RLG	RLG00275	0	11	67	72.2727272727273
RLG	RLG00283	0	13	361	597.538461538462
RLG	RLG00289	0	11	809	752.727272727273
RLG	RLG00306	0	11	238	300.454545454545
RLG	RLG00323	0	12	349.5	362
RLG	RLG00326	0	11	638	638
RLG	RLG00327	0	13	99	147
RLG	RLG00330	0	10	209.5	270.1
RLG	RLG00331	0	11	292	345.090909090909
RLG	RLG00334	0	11	564	557.636363636364
RLG	RLG00342	0	11	302	329.363636363636
RLG	RLG00357	0	10	167.5	184.2
RLG	RLG00376	0	12	345	368.583333333333
RLG	RLG00382	0	15	163	369.866666666667
RLG	RLG00404	0	51	518	560.764705882353
RLG	RLG00417	0	10	341	353.2
RLG	RLG00620	0	198	551	590.89898989899
RLG	RLG01210	0	250	437	497.224
RLG	RLG01224	0	18	356.5	421.944444444444
RLG	RLG01297	0	14	75	169.307692307692
RLG	RLG01328	0	36	399	475.833333333333
RLG	RLG01860	0	18	227	240.833333333333
RLG	RLG02129	0	60	634	683.466666666667
RLG	RLG02424	0	21	242	259.047619047619
RLG	RLG02722	0	131	381	397.885496183206
RLG	RLG04884	0	82	577.5	526.963414634146
RLG	RLG07846	0	156	628	575.532051282051
RLG	RLG07969	0	18	326	348.888888888889
RLG	RLG16490	0	27	478	483.814814814815
RLG	RLG20706	0	34	72	79.0333333333333
RLG	RLG21631	0	68	291	275.602941176471
RLG	RLG22910	0	65	317	311.138461538462
RLG	RLG23054	0	44	969.5	958.363636363636
RLG	RLG23897	0	11	192	197.636363636364
RLX	RLX00065	0	83	264.5	250.175
RLX	RLX00066	0	85	76	82.4939759036145
RLX	RLX00092	0	63	95	114.983870967742
RLX	RLX00094	0	47	306	252.652173913043
RLX	RLX00095	0	44	613	517.790697674419
RLX	RLX00134	0	29	352	493.047619047619
RLX	RLX00144	0	27	238	318.740740740741
RLX	RLX00168	0	24	303	254.04347826087
RLX	RLX00171	0	27	623	534

RLX	RLX00172	0	23	243	232.47619047619
RLX	RLX00196	0	19	56	97.2105263157895
RLX	RLX00197	0	18	54.5	102
RLX	RLX00210	0	18	138.5	154.666666666667
RLX	RLX00219	0	19	93	111.368421052632
RLX	RLX00220	0	17	220	229.294117647059
RLX	RLX00230	0	16	86	104
RLX	RLX00234	0	16	72.5	101.3125
RLX	RLX00245	0	16	87	113.0625
RLX	RLX00264	0	14	103	178.153846153846
RLX	RLX00299	0	12	63	86.5
RLX	RLX00301	0	12	27	27
RLX	RLX00315	0	13	177	175.076923076923
RLX	RLX00317	0	12	198.5	250.666666666667
RLX	RLX00349	0	10	59	69.3333333333333
RLX	RLX00360	0	10	229.5	298.6
RLX	RLX00369	0	10	178	154.5
RLX	RLX00370	0	10	295	275.5
RLX	RLX00560	0	14	249	247.428571428571
RLX	RLX00647	0	12	765.5	814.916666666667
RLX	RLX00824	0	50	126	165.615384615385
RLX	RLX00910	0	13	536	591.692307692308
RLX	RLX01857	0	36	641	677.944444444444
RLX	RLX01925	0	14	569	563.615384615385
RLX	RLX02412	0	23	897	832.521739130435
RLX	RLX02653	0	15	320	341.733333333333
RLX	RLX02676	0	75	690	653.813333333333
RLX	RLX03238	0	13	252	206.769230769231
RLX	RLX03863	0	183	943	886.07650273224
RLX	RLX04027	0	32	333	300.15625
RLX	RLX06052	0	25	760	760.84
RLX	RLX06850	0	10	505	532
RLX	RLX06925	0	10	416.5	358.8
RLX	RLX07110	0	22	456.5	459
RLX	RLX07511	0	41	60	78.4878048780488
RLX	RLX08341	0	13	265	307.769230769231
RLX	RLX08581	0	28	156	160.607142857143
RLX	RLX09595	0	22	468.5	447.363636363636
RLX	RLX10780	0	13	188	180.307692307692
RLX	RLX10916	0	64	756	715.859375
RLX	RLX11328	0	24	524	484.333333333333
RLX	RLX11700	0	11	212	231.727272727273
RLX	RLX12104	0	32	298.5	355.03125
RLX	RLX12410	0	10	246	284.9
RLX	RLX12632	0	10	34	49.3
RLX	RLX12917	0	43	622	542.46511627907
RLX	RLX13049	0	334	688	673.446107784431
RLX	RLX13352	0	13	364	399.461538461538
RLX	RLX13514	0	153	819	840.843137254902
RLX	RLX13529	0	185	252	230.918918918919
RLX	RLX13698	0	105	627	565.857142857143
RLX	RLX13810	0	12	490.5	483.333333333333
RLX	RLX14021	0	31	458	624.032258064516
RLX	RLX14124	0	28	406.5	438.357142857143
RLX	RLX14762	0	11	442	423.909090909091
RLX	RLX16782	0	168	652	591.690476190476
RLX	RLX17675	0	105	627	665.959595959596

RLX	RLX19305	0	13	150	155.846153846154
RLX	RLX19534	0	21	67.5	67.2777777777778
RLX	RLX19697	0	13	372	406.615384615385
RLX	RLX19762	0	28	278.5	319.107142857143
RLX	RLX22845	0	15	358	355.933333333333
RLX	RLX23205	0	16	294.5	314.625
RLX	RLX23786	0	41	44	51.2564102564103
RST	RST00001	0	22	29	29.25
RST	RST00003	0	17	169	149.352941176471
RST	RST00004	0	18	126	110.0625
RST	RST00005	0	38	50	48.8888888888889
RST	RST00008	0	16	97	100.375
RST	RST00010	0	25	NA	NaN
RST	RST00014	0	41	54	55.6666666666667
RST	RST00016	0	32	27	31.6666666666667
RST	RST00019	0	15	43	43

Table S4. Mean methylation levels across superfamilies, averaged across all tissues, and averaged within a tissue (all3=seedling)

sup	avg_cg	avg_chg	avg_chh	SAM_avg_cg	SAM_avg_chg	SAM_avg_chh	all3_avg_cg	all3_avg_chg	all3_avg_chh	flagleaf_avg_cg	flagleaf_avg_chg	flagleaf_avg_chh	earshoot_avg_cg	earshoot_avg_chg	earshoot_avg_chh	anther_avg_cg	anther_avg_chg	anther_avg_chh
DHH	0.768	0.659	0.034	0.741	0.606	0.025	0.743	0.743	0.050	0.806	0.686	0.036	0.778	0.655	0.028	0.773	0.604	0.028
DTA	0.804	0.607	0.082	0.774	0.519	0.060	0.782	0.782	0.101	0.840	0.637	0.114	0.816	0.575	0.067	0.807	0.524	0.068
DTC	0.833	0.693	0.046	0.799	0.625	0.034	0.811	0.811	0.061	0.875	0.726	0.052	0.843	0.688	0.041	0.837	0.617	0.040
DTH	0.811	0.681	0.062	0.781	0.616	0.046	0.794	0.794	0.085	0.847	0.712	0.079	0.822	0.670	0.047	0.812	0.611	0.052
DTM	0.738	0.595	0.144	0.713	0.525	0.095	0.708	0.708	0.199	0.623	0.195	0.758	0.592	0.104	0.741	0.529	0.128	
DTT	0.801	0.674	0.044	0.773	0.617	0.032	0.775	0.775	0.068	0.839	0.702	0.050	0.813	0.671	0.034	0.803	0.602	0.034
DTX	0.848	0.732	0.041	0.816	0.670	0.033	0.838	0.838	0.060	0.883	0.766	0.042	0.854	0.725	0.034	0.851	0.663	0.034
RIL	0.837	0.687	0.025	0.809	0.617	0.019	0.801	0.801	0.037	0.879	0.700	0.026	0.850	0.677	0.021	0.844	0.639	0.019
RIT	0.850	0.725	0.032	0.822	0.653	0.023	0.824	0.824	0.043	0.891	0.767	0.043	0.861	0.714	0.027	0.854	0.669	0.024
RLC	0.824	0.677	0.027	0.794	0.617	0.021	0.797	0.797	0.047	0.868	0.705	0.027	0.834	0.668	0.022	0.827	0.597	0.020
RLG	0.842	0.735	0.029	0.812	0.681	0.024	0.822	0.822	0.043	0.879	0.762	0.028	0.850	0.736	0.025	0.845	0.673	0.024
RLX	0.806	0.695	0.028	0.776	0.642	0.022	0.784	0.784	0.044	0.844	0.721	0.028	0.815	0.696	0.024	0.808	0.633	0.023
RST	0.740	0.570	0.035	0.716	0.510	0.027	0.716	0.716	0.053	0.773	0.574	0.040	0.755	0.553	0.027	0.742	0.497	0.027

Table S5. TE families that lack methylatable cytosines (presented as family median values).

sup	fam	famsize	tebp	percGC	nCG	nCHG	nCHH
DTH	DTH00067	602	196	0.318	0	0.009	0.139
DTH	DTH00073	122	127	0.441	0	0	0.201
DTH	DTH00090	214	127	0.302	0	0.016	0.120
DTH	DTH00119	124	138	0.388	0	0	0.173
DTH	DTH00163	968	116	0.350	0	0	0.151
DTH	DTH00280	289	200	0.440	0	0.105	0.105
DTH	DTH00320	95	248	0.330	0	0.002	0.154
DTH	DTH00409	748	178	0.296	0	0	0.132
DTH	DTH00410	76	147	0.262	0	0.015	0.105
DTH	DTH00460	81	116	0.364	0	0	0.155
DTH	DTH00486	16	138	0.415	0	0	0.187
DTH	DTH10176	146	160	0.371	0	0	0.175
DTH	DTH10226	15	130	0.354	0.008	0	0.165
DTH	DTH10700	368	103	0.386	0	0	0.190
DTH	DTH10730	3, 113	67	0.412	0	0	0.201
DTH	DTH10855	659	88	0.307	0	0.011	0.142
DTH	DTH10856	126	88	0.308	0	0.011	0.142
DTH	DTH10946	179	87	0.483	0	0.141	0.103
DTH	DTH11101	409	67	0.409	0	0	0.205
DTH	DTH11481	35	52	0.347	0	0.008	0.159
DTH	DTH11817	346	208	0.382	0	0.034	0.156
DTH	DTH12058	11	160	0.373	0	0.006	0.169
DTH	DTH12181	158	354	0.286	0	0.011	0.129
DTH	DTH14130	11	97	0.289	0	0	0.127
DTH	DTH15065	78	275.500	0.244	0	0.001	0.116
DTH	DTH15139	12	358	0.375	0	0.028	0.157
DTM	DTM00257	376	155	0.374	0	0	0.174
DTT	DTT10009	702	147	0.283	0	0.010	0.125
DTT	DTT10797	889	89	0.299	0	0	0.146
DTT	DTT10880	6, 151	156	0.357	0	0	0.174
DTT	DTT10881	2, 514	156	0.357	0	0	0.175
DTT	DTT10986	20	120	0.425	0	0	0.194
DTT	DTT11073	199	143	0.245	0	0	0.108
DTT	DTT11169	39	108	0.290	0	0.008	0.132
DTT	DTT11408	48	109	0.385	0	0	0.183
DTT	DTT11547	1, 825	156	0.359	0	0.006	0.171
DTT	DTT12206	22	190.500	0.229	0	0.011	0.097
DTT	DTT14220	57	157	0.282	0	0.010	0.116
DTT	DTT15443	143	156	0.355	0	0.005	0.168
DTT	DTT15444	519	156	0.353	0	0	0.174
DTX	DTX10131	120	141	0.255	0	0.013	0.110
DTX	DTX10132	90	131.500	0.246	0	0.014	0.105
DTX	DTX10177	2, 850	156	0.357	0	0	0.176
DTX	DTX10212	101	138	0.391	0	0	0.181
DTX	DTX10213	15	138	0.406	0	0	0.188
DTX	DTX10945	10	87	0.451	0	0.126	0.097
DTX	DTX11178	18	72	0.458	0	0	0.212
DTX	DTX12196	26	165	0.273	0	0.024	0.105
DTX	DTX12438	23	275	0.353	0	0.004	0.162
RST	RST00001	22	140	0.349	0.014	0	0.153
RST	RST00010	25	309	0.298	0	0.016	0.132