

Supplementary Note 1

Transposable elements

BLASTN searches with known fungal transposon sequences¹ revealed degenerate class I and II elements. Among class II homologs were several En/Spm-like sequences distantly related to higher plant transposases. Multiple sequences with similarity to *Fusarium oxysporum* hop1, *F. oxysporum* impala, and *Magnaporthe oryzae* pot2 were also detected. All sequences contained multiple stop codons, and terminal inverted repeats, typical of class II elements, were absent.

Copia class retroelements flanked by near perfect long terminal repeats (LTRs) were located on scaffolds 4 (coordinates 1206479 - 1211609), 42 (56255 - 61289), and 87 (4179 - 9853). Typical of such elements, remnants and “solo LTRs”^{2,3} were distributed on 11 scaffolds. Similarly, a gypsy class retroelement was located on scaffolds 16 (578302-585660), 54 (2146-9683), and 147 (365-7059) with five solo LTRs at separate locations. Again, numerous stop codons were present indicating that *T. reesei* strain QM6a contains no active TEs. As has been repeatedly shown in other Ascomycetes, active processes such as repeat induced point mutation (RIP)⁴ may have attenuated the spread of transposons in *T. reesei*. Base composition ratios, TpA/ApT and (CpA + TpG)/(ApC+Gpt) within degenerate sequences are consistent with such a mechanism.

Scaffolds containing the discovered repeat TTAGGG

The telomeric repeat TTAGGG was identified on the following seven scaffolds in the *T. reesei* genome assembly, identical to the *N. crassa* telomere repeat⁵.

Scaffold
scaffold_31
scaffold_1
scaffold_46
scaffold_45
scaffold_65
scaffold_64
scaffold_87

References:

1. Daboussi, M.J. and Capy, P. Transposable elements in filamentous fungi. *Annu. Rev. Microbiol.* **57**, 275-299 (2003).
2. Goodwin, T.J. and Poulter, R.T. Multiple LTR-retrotransposon families in the asexual yeast *Candida*

albicans. *Genome Res.* **10**, 174-191 (2000).

3. Kim, J.M., Vanguri, S., Boeke, J.D., Gabriel, A., and Voytas, D.F. Transposable elements and genome organization: a comprehensive survey of retrotransposons revealed by the complete *Saccharomyces cerevisiae* genome sequence. *Genome Res.* **8**, 464-478 (1998).
4. Galagan, J.E. and Selker, E.U. RIP: the evolutionary cost of genome defense. *Trends Genet.* **20**, 417-423 (2004).
5. Schechtman, M.G. Characterization of the telomere DNA from *Neurospora crassa*. *Gene* **88**, 159-165 (1990).

Supplementary Note 2

At the more detailed scale of families that compose CAZyme classes we checked whether the general trends observed for the classes could be confirmed. We also looked for CAZyme families that could be significantly divergent in *T. reesei* compared to the other fungi. At the class level, GHs appeared to exhibit higher variability than GTs and this trend was also verified at the family level. The standard deviation for GH families (SD=4.2, average SD per family = 2.1) is higher than for GTs (SD=3, average SD per family = 1.3). Similarly, 60 different GH families are observed in fungi, as compared with 35 GT families. Moreover, despite the higher number of GH than GT families in fungi, more GT families (16) than GH families (11) are universally found in our dataset. *T. reesei* covers 48 families of GHs and 30 families of GTs, which is very close to the Sordariomycetes average repertoire (47 and 30 GH and GT families respectively).

At a higher resolution, we tested whether particular families were specifically present, missing, expanded or reduced in *T. reesei* compared to other fungi (**Supplementary Table 4**). We applied the statistical test described in the **Methods** which takes into account the variability and population size both for species and CAZyme families. For example, *T. reesei* was found to be enriched in seven GH, one GT and one PL families and reduced in two GH and one GT families and the CBMs.

Supplementary Table 1: Libraries used for genome sequencing.

Library Designation	Insert Size	No. Reads	Source
QCAA	3 kb	1317	JGI ^a
UWU	3 kb	197293	JGI
VTN	8 kb	205430	JGI
VTM	37 kb	23034	JGI
BAC Library^b	97-190 kb	6789	NCSU ^c
Total Reads		433863	

^aJoint Genome Institute.

^bLarge insert bacterial artificial chromosome.

^cFungal Genomics Laboratory, North Carolina State University.

Supplementary Table 2a. Syntenic blocks in the genomes of *T. reesei*, *F. graminearum* and *N. crassa*.

Organism	No. Blocks	Total Orthologs to <i>T. reesei</i>	% <i>T. reesei</i> genes	Orthologs in synteny	% <i>T. reesei</i> Orthologs
<i>F. graminearum</i>	535	6580	72	5372	81%
<i>N. crassa</i>	538	5624	62	4834	86%

Supplementary Table 2b. General features of *T. reesei* genes in syntenic and non-syntenic regions.

	Organism Compared	G+C %	Length (nucleotide)	No. Genes	Density (Nucl./Gene)	exon length Mean	intron length Mean	Gene Length Mean
Syntenic regions	<i>F. graminearum</i>	54.4%	21.5Mb	6229	3.45 kb	536	119	1844
	<i>N. crassa</i>	54.6%	16.9Mb	4834	3.49 kb	534	121	1876
Gap Regions	<i>F. graminearum</i>	50.2%	11.9Mb	2900	4.11 kb	447	117	1682
	<i>N. crassa</i>	51.9%	16.4Mb	4295	3.82 kb	475	115	1700
conserved Synteny	<i>f. graminearum</i> + <i>N. crassa</i>	54.8%	14.5 Mb	4390	3.31 kb	536	120	1575
conserved Gaps	<i>F. graminearum</i> + <i>N. crassa</i>	49.4%	9.7Mb	2270	4.25 kb	435	115	1645

Supplementary Table 2c. Comparison of domain content (identified by Interpro) in *T. reesei* genes that lie in syntenic blocks vs. gaps. Only the 20 most represented domain are shown.

<i>Regions with Synteny to F. graminearum</i>		
IPR Id	IPR Description	<i>T. reesei</i> Genes with Domain
IPR001680	G-protein beta WD-40 repeat	103
IPR001138	Fungal transcriptional regulatory protein, N-terminal	96
IPR002290	Serine/threonine protein kinase	77
IPR007114	Major facilitator superfamily	69
IPR003593	AAA ATPase	65
IPR007087	Zn-finger, C2H2 type	54
IPR001650	Helicase, C-terminal	53
IPR000504	RNA-binding region RNP-1 (RNA recognition motif)	45
IPR000379	Esterase/lipase/thioesterase	43
IPR000051	SAM (and some other nucleotide) binding motif	34
IPR002110	Ankyrin	33
IPR005225	Small GTP-binding protein domain	33
IPR002048	Calcium-binding EF-hand	28
IPR002198	Short-chain dehydrogenase/reductase SDR	26
IPR001440	TPR repeat	25
IPR001005	Myb, DNA-binding	22
IPR001810	Cyclin-like F-box	21
IPR001623	Heat shock protein DnaJ, N-terminal	21
IPR000205	NAD-binding site	19
IPR002347	Glucose/ribitol dehydrogenase	19

Regions with NO synteny to <i>F. graminearum</i>		
IPR Id	IPR Description	<i>T. reesei</i> Genes with Domain
IPR001138	Fungal transcriptional regulatory protein, N-terminal	98
IPR007114	Major facilitator superfamily	74
IPR000379	Esterase/lipase/thioesterase	52
IPR002347	Glucose/ribitol dehydrogenase	39
IPR002110	Ankyrin	33
IPR000051	SAM (and some other nucleotide) binding motif	31
IPR002198	Short-chain dehydrogenase/reductase SDR	31
IPR003663	Sugar transporter	29
IPR001128	Cytochrome P450	29
IPR003593	AAA ATPase	27
IPR010730	Heterokaryon incompatibility	26
IPR001680	G-protein beta WD-40 repeat	22
IPR007219	Fungal specific transcription factor	20
IPR002290	Serine/threonine protein kinase	19
IPR002293	Amino acid/polyamine transporter I	19
IPR002085	Zinc-containing alcohol dehydrogenase superfamily	18
IPR001810	Cyclin-like F-box	17
IPR000182	GCN5-related N-acetyltransferase	17
IPR001395	Aldo/keto reductase	15
IPR000254	Cellulose-binding region, fungal	14

Supplementary Table 3. Protein families in *T. reesei*.

Interpro entry	Peizizomycotina					Saccharomycotina					Category	Interpro entry name	Reason for Interpro entry count difference <i>T. reesei</i> versus <i>Peizizomycotina</i>			
	<i>Aspergillus fumigatus</i>	<i>Aspergillus nidulans</i>	<i>Fusarium graminearum</i>	<i>Trichoderma reesei</i>	<i>Magnaporthe grisea</i>	<i>Neurospora crassa</i>	<i>Ashyba gossypii</i>	<i>Candida albicans</i>	<i>Candida glabrata</i>	<i>Debaryomyces hansenii</i>				<i>Kluyveromyces lactis</i>	<i>Saccharomyces cerevisiae</i>	<i>Yarrowia lipolytica</i>
IPR003117	0	0	0	1	0	0	1	1	1	1	1	1	1	Signal transduction	cAMP-dependent protein kinase regulator, type II PKA R subunit	Mutation
IPR004202	0	0	0	1	0	0	1	0	0	1	1	1	1	Mitochondrion	Cytochrome c oxidase subunit VIIc	Mutation
IPR004556	0	0	0	1	0	0	1	1	1	1	1	1	1	Methylation	Modification methylase HemK	Mutation
IPR002315	1	1	1	3	1	1	1	1	1	2	1	2	1	Protein biosynthesis	Glycyl-tRNA synthetase, alpha-2	Mutation/Presence
IPR002413	0	1	0	3	1	1	1	0	1	1	0	0	0	Secreted?	Ves allergen	Mutation/Presence
IPR012734	1	1	0	3	0	0	1	1	0	0	0	0	0	Carbohydrate metabolism	Dihydroxycetone kinase	Mutation/Presence
IPR010636	0	0	1	6	2	1	0	0	0	0	0	0	0	Hydrophobin	Hydrophobin 2 (i.e. class II)	Presence
IPR006710	15	13	14	2	15	5	0	0	0	0	0	0	0	Plant biomass degradation	Glycoside hydrolase, family 43	Mutation
IPR001077	10	15	8	3	12	8	0	0	0	1	0	0	0	2ndary metabolism	O-methyltransferase, family 2	Mutation
IPR001000	5	5	9	1	5	10	1	2	2	0	0	2	1	Glycoside hydrolase	Glycoside hydrolase, family 10	Mutation
IPR011118	5	7	7	0	9	1	0	0	0	1	0	0	0	Plant biomass degradation	Tannase and feruloyl esterase	Absence
IPR002022	6	8	9	0	2	1	0	0	0	0	0	0	0	Plant biomass degradation	Pectate lyase/Amb allergen	Mutation
IPR001557	3	4	3	1	4	3	2	3	3	3	3	3	2	Glycolysis	L-lactate/malate dehydrogenase	Mutation/Absence
IPR004898	3	5	7	0	1	1	0	0	0	0	0	0	0	Plant biomass degradation	Pectate lyase	Absence
IPR000421	2	1	4	0	3	6	0	0	0	1	0	0	1	Secreted?	Coagulation factor 5/8 type, C-terminal	Mutation
IPR011251	3	2	3	0	2	4	1	2	0	1	1	0	6	Monooxygenase	Bacterial luciferase-like	Mutation
IPR000070	5	3	2	0	2	2	0	0	0	0	0	0	0	Plant biomass degradation	Pectinesterase	Mutation
IPR008701	2	2	4	0	4	1	0	0	0	0	0	0	0	Plant infection	Necrosis inducing	Mutation/Absence
IPR008279	4	1	2	0	2	2	0	0	1	1	1	1	1	Phosphorylation	PEP-utilising enzyme, mobile region	Mutation
IPR004199	1	2	3	0	3	2	0	0	0	1	1	0	0	Glycoside hydrolase	Glycoside hydrolase, family 42, domain 5	Mutation
IPR000383	1	3	4	0	2	1	0	0	0	0	0	0	0	Protein degradation	Peptidase S15	Mutation
IPR001425	1	1	5	0	1	2	0	1	3	1	0	4	0	Opsins	Bacterial rhodopsin	Mutation
IPR010720	2	3	2	0	2	1	0	0	0	1	0	0	0	Glycoside hydrolase	Alpha-L-arabinofuranosidase, C-terminal	Absence
IPR001338	4	3	1	0	1	1	0	0	0	0	0	1	0	Hydrophobin	Fungal hydrophobin (i.e. class I)	Absence
IPR010126	1	1	3	0	2	3	0	0	0	0	0	0	0	Plant biomass degradation	Esterase, PHB depolymerase	Mutation
IPR002229	2	1	3	0	1	2	0	0	1	0	0	0	0	Secreted?	Blood group Rhesus C/E and D polypeptide	Mutation
IPR005914	2	2	1	0	1	2	0	0	0	0	0	0	0	Lipid metabolism	Acetoacetyl-CoA synthase	Mutation
IPR001106	1	2	1	0	1	1	0	0	0	0	0	0	0	Amino acid metabolism	Phenylalanine/histidine ammonia-lyase	Absence
IPR012104	1	1	1	0	1	1	2	2	3	2	2	3	1	Cell cycle	Cyclin, fungal Pcl/HCS26	Mutation
IPR008076	1	1	1	0	1	1	0	0	0	0	0	0	0	Cyanate metabolism	Cyanase	Absence
IPR012235	1	1	1	0	1	1	1	1	1	1	1	1	1	Leucine biosynthesis	3-isopropylmalate dehydratase, fus small/large subunits	Mutation
IPR003702	1	1	1	0	1	1	1	1	1	1	1	1	1	Acetyl-CoA metabolism	Acetyl-CoA hydrolase/transferase	Absence
IPR004235	1	1	1	0	1	1	0	0	0	0	0	0	0	Melanin biosynthesis	Scytalone dehydratase	Mutation
IPR011683	1	1	1	0	1	1	0	0	0	0	0	0	0	Glycoside hydrolase	Glycosyl hydrolase 53	Absence
IPR005874	1	1	1	0	1	1	3	1	1	1	1	1	1	Translation	Eukaryotic translation initiation fac SU1	Mutation

The cells are coloured based on the number of occurrences (0 is white, 1 and 2 are yellow, 3 is orange, and 4 or more is red).

Interpro entry names are taken from Interpro and each category represents a classification by the authors. The column labeled

“Reason for Interpro entry count difference in *T. reesei* versus euascomycetes” is explained in the text.

Supplementary Table 4. CAZyme families having a statistically different distribution in *T. reesei* compared to other fungal genomes. The highest and lowest number of entries in each category is indicated in red and blue. *T. reesei* appears in bold.

Family ^a	GH	GH	GH	GH	GH	GH	GH	GH	GH	GH	GT	GT	GT	PL	PL	PL
	18	13	43	92	27	95	64	30	32	89	71	64	5	1	7	8
Species ^b																
A.nid	19	13	15	5	3	3	0	0	2	0	2	0	2	8	0	0
A.fum	18	16	18	4	5	2	0	1	4	1	3	0	3	6	0	0
A.ory	18	17	20	6	3	3	0	0	4	1	5	0	3	12	1	0
M.gris	14	10	19	6	4	1	1	1	5	0	4	0	1	2	0	0
N.cra	12	10	7	2	0	0	2	1	1	0	1	0	2	1	0	0
T.ree	20	5	2	7	8	4	3	2	0	2	1	2	0	0	2	1
F.gra	19	8	16	0	2	2	2	0	5	0	4	2	0	9	0	0
C.alb	5	4	0	1	0	0	0	0	0	0	12	0	0	0	0	0
S.cer	2	8	0	0	0	0	0	0	1	0	6	0	0	0	0	0
C.gla	2	2	0	0	0	0	0	0	0	0	15	0	0	0	0	0
S.pom	1	12	0	0	1	0	0	0	2	0	0	0	5	0	0	0
C.neo	4	11	0	1	0	0	0	0	1	0	2	0	1	0	0	0
P.chr	11	9	4	4	3	1	0	1	0	2	0	0	1	0	0	1

^aEnzymes abbreviated based on CAZyme classification.

^bSpecies abbreviations: A.nid (*Aspergillus nidulans*), A.fum (*Aspergillus fumigatus*), A.ory (*Aspergillus oryzae*), M.gris (*Magnaporthe grisea*), N.cra (*Neurospora crassa*), T.ree (*Trichoderma reesei*), F.gram (*Fusarium graminearum*), C.alb (*Candida albicans*), S.cer (*Saccharomyces cerevisiae*), C.gla (*Candida glabrata*), S.pom (*Schizosaccharomyces pombe*), C.neo (*Cryptococcus neoformans*), P.chr (*Phanerochaete chrysosporium*).

References as in text.

Supplementary Table 5. Comparison of the abundance of families of pectin-degrading enzymes predicted from the genome sequences of 13 fungal species. Abbreviations: GH, glycoside hydrolases; PL, polysaccharide lyases; CE8, pectin methylesterases. The highest and lowest number of entries in each family is indicated in red and blue. *T. reesei* appears in bold.

Family ^a Species ^b	GH2 8	GH88	GH105	PL1	PL3	PL4	PL9	CE8	Total
A.nid	9	2	3	8	5	4	1	3	35
A.fum	14	2	2	6	3	3	1	6	37
A.ory	20	3	2	12	3	4	1	5	50
M.gris	3	1	3	2	1	1	0	1	12
N.cra	2	0	1	1	1	1	0	1	7
T.ree	4	0	1	0	0	0	0	0	5
F.gra	6	1	3	9	7	3	1	5	35
C.alb	0	0	0	0	0	0	0	0	0
S.cer	1	0	0	0	0	0	0	0	1
C.gla	0	0	0	0	0	0	0	0	0
S.pom	0	0	0	0	0	0	0	0	0
C.neo	1	0	1	0	0	1	0	0	3
P.chr	4	1	0	0	0	0	0	2	7

^aEnzymes abbreviated based on CAZyme classification³³.

^bSpecies abbreviations: A.nid (*Aspergillus nidulans*), A.fum (*Aspergillus fumigatus*), A.ory (*Aspergillus oryzae*), M.gris (*Magnaporthe grisea*), N.cra (*Neurospora crassa*), T.ree (*Trichoderma reesei*), F.gra (*Fusarium graminearum*), C.alb (*Candida albicans*), S.cer (*Saccharomyces cerevisiae*), C.gla (*Candida glabrata*), S.pom (*Schizosaccharomyces pombe*), C.neo (*Cryptococcus neoformans*), P.chr (*Phanerochaete chrysosporium*).

Supplemental Table 6. Genes encoding components of the *T. reesei* secretion pathway.

Distribution of transport-related small GTPases.

<i>T. reesei</i> ^a	<i>N. crassa</i> ^b	<i>S. cerevisiae</i> ^c	Mammals ^d	Proposed role ^e
Rab proteins				
Found in <i>S. cerevisiae</i> and filamentous fungi				
YPT1	NCU08477.1	Ypt1p	Rab1	ER-GA, IGA, GA-ER
tre44010	NCU06404.1	Sec4p	Rab8	LGA-PM
tre43000	NCU01532.1	Ypt31/32p	Rab11	IGA, LGA-PM?
tre42061	NCU05234.1	Ypt6p	Rab6	IGA, LGA-LE, LE-LGA
tre17707	NCU03711.1	Ypt7p	Rab7	LE-V
tre44333, tre42834	NCU00895.1 NCU06410.1	Ypt51/52/53p	Rab5	PM-EE, EE-LE
Not found in <i>S. cerevisiae</i>				
tre24935 tre29515	NCU00889.1		Rab4	EE-PM
tre31007	NCU01647.1		Rab2	ER-GA, GA-ER
tre33269	NCU08271.1		Rab5?	PM-EE?, EE-LE?
	NCU01453.1		Rab18?	PM-EE?, EE-PM?
Arf and Arf-like proteins				
Found in <i>S. cerevisiae</i> and filamentous fungi				
tre43177	NCU08340.1	Arf1/2p	Arf1	GA-ER, IGA, LGA, PM
tre28367	NCU08989.1	Arl1p	Arl1	LGA
tre38187	NCU00333.1	Arl3p	Arl3	LGA
tre298890	NCU00218.1	Arf3p	Arl2	?
SAR1	NCU00381.1	Sar1p	Sar1	ER-GA
Not found in <i>S. cerevisiae</i>				
tre42316	NCU07173.1		Arf6	PM-EE
tre45468	NCU08618.1		Arl10	?

^a*T. reesei* gene model number. ^b*N. crassa* gene model. ^c*S. cerevisiae* gene designation. ^dFunctional equivalent in mammals. ^eAbbreviations used: ER, endoplasmic reticulum; GA, Golgi apparatus; IGA, intermediate Golgi apparatus; LGA, late Golgi apparatus; PM, plasma membrane; EE, early endosome, LE, late endosome, V, vacuole, ?, uncertain or unknown.

Supplementary Table 7. Scaffold locations of “CAZy clusters.” With regard to G+C content, there seems to be no significant deviation from the mean in any cluster and the furthest deviation from the mean is a cluster on scaffold_33, with a G+C content of 39%. This seems to be due to a Copia transposable element in the intergenic space in the cluster.

Cluster No.	position	G+C%	Length	# CAZy Genes	CAZy Genes% in cluster	p-value
1	scaffold_1:410000-530000	53%	120000	5	17%	3.02E-003
2	scaffold_1:2250000-2500000	49%	250000	9	13%	5.01E-004
3	scaffold_2:1580000-1855000	54%	275000	8	12%	2.22E-003
4	scaffold_3:8500-238500	53%	230000	10	12%	4.93E-004
5	scaffold_3:1214000-1232000	56%	17692	3	43%	1.34E-003
6	scaffold_3:1755000-1850000	51%	95000	4	14%	1.55E-002
7	scaffold_5:55000-190000	51%	135000	7	15%	9.92E-004
8	scaffold_6:10000-148000	51%	138000	5	13%	9.87E-003
9	scaffold_7:1230000-1400000	50%	170000	6	12%	7.59E-003

Supplementary Table 8. Accession numbers of previously described CAZymes that occur in clustered areas.

Gene	Caazy Family	Function	Accession	EC code
<i>cbh1/cel7a</i>	GH7	Cellobiohydrolase		3.2.1.91
<i>cbh2/cel6a</i>	GH6	Cellobiohydrolase	M16190	3.2.1.91
<i>egl1/cel7b</i>	GH7	Endo-1,4-glucanase	M15665	3.2.1.4
<i>egl2/cel5a</i>	GH5	Endo-1,4-glucanase	M19373	3.2.1.4
<i>egl3/cel12a</i>	GH12	Endo-1,4-glucanase	AB003694	3.2.1.4
<i>egl4/cel61a</i>	GH61	Endo-1,4-glucanase	Y111113	3.2.1.4
<i>bgl1/cel3a</i>	GH3	-Glucosidase	U09580	3.2.1.21
<i>xyn1</i>	GH11	Xylanase	X69574	3.2.1.8
<i>xyn2</i>	GH11	Xylanase	X69573	3.2.1.8
<i>xyn3</i>	GH10	Xylanase	AB036796	3.2.1.8
<i>xyn4</i>	GH5	Xylanase		3.2.1.8
<i>bxl1</i>	GH3	-Xylosidase	Z69257	3.2.1.37
<i>axe1</i>	CE5	Acetyl xylan esterase	Z69256	3.1.1.72
<i>abf1</i>	GH54	Arabinofuranosidase	Z69252	3.2.1.55
<i>agl2</i>	GH36	-Galactosidase	Z69254	3.2.1.22
<i>agl3</i>	GH27	-Galactosidase	Z69255	3.2.1.22
<i>swo1</i>	EXPN	Expansin-like	AJ245918	Unknown
<i>cip1</i>	CBM1	Unknown	AY281370	Unknown
<i>cip2</i>	CBM1	Glucuronoyl esterase	AY281368	Unknown

Supplementary Table 9. Non-ribosomal peptide synthase (NRPS) and polyketide synthase (PKS) genes identified in the *T. reesei* genome.

Type	Genelid	Scaffold position
NRPS	123786	scaffold_26:276842-327620
NRPS	23171	scaffold_24:123560-193077
NRPS	71005	scaffold_46:26764-32978
NRPS	60458	scaffold_7:1346092-1352756
NRPS	69946	scaffold_31:39880-54649
NRPS	68204	scaffold_24:269353-272917
NRPS	81014	scaffold_22:47425-51332
NRPS	24586	scaffold_1:2715190-2721980
NRPS	67189	scaffold_20:536612-542052
NRPS	60751	scaffold_8:523737-526732
PKS	73621	scaffold_1:491045-499127
PKS	65172	scaffold_15:76106-84410
PKS	105804	scaffold_6:62708-69489
PKS	106272	scaffold_7:215526-224521
PKS	82208	scaffold_33:8794-15745
PKS	59482	scaffold_6:489751-496726
PKS	73618	scaffold_1:482161-490277
PKS	60118	scaffold_7:961671-969559
PKS	81964	scaffold_29:36588-42408
PKS	65116	scaffold_15:571323-578930
PKS	65891	scaffold_17:631544-639144
PKS-NRPS	58285	scaffold_5:25620-37773
PKS-NRPS	105864	scaffold_6:241163-242628