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Anotación y validación del genoma de levadura cervecera tipo lager *Saccharomyces pastorianus* 790

Por

QFB PATRICIA MARCELA DE LEÓN MEDINA

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Anotación y validación del genoma de levadura cervecera tipo lager *Saccharomyces pastorianus* 790

Comité de Tesis

Dr. Luis J. Galán Wong
Director

Dr. Benito Pereyra Alférez
Secretario

Dra. Katiushka Arévalo Niño
Vocal

Dr. Hugo A. Luna Olvera
Vocal

Dra. Lilia H. Morales Ramos
Vocal

Dr. Luis C. Damas Buenrostro
Asesor Externo

Junio 2016

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LISTA DE SÍMBOLOS Y ABREVIATURAS

790: Cepa cervecera tipo lager en estudio.

Contig: Conjunto de dos o más lecturas ensambladas.

Mpb: Mega pares de bases (1x10^6 pb).

pb: Pares de bases.

PCR: Reacción en Cadena de la Polimerasa.

Scaffold: Conjunto de dos o más contigs ensamblados, con ubicación y dirección.

Software: Programa de cómputo.

RESUMEN

Las levaduras para la producción de cerveza tipo lager, son de relevancia económica que representan la producción de cerveza lager en México ocupa el total de las ventas, sin embargo, por su uso específico en la industria existe poca información disponible del genoma de estas. Se conoce que el genoma de este tipo de levadura es un hibrido entre *Saccharomyces cerevisiae* y *Saccharomyces eubayanus* pero el contenido de cada uno difiere de cepa a cepa dando como resultados diferentes características en las cervezas. En base a los datos semi ensamblados proporcionados por estudios previos, el genoma de una levadura cervecera tipo lager fue anotado en este estudio con la herramienta computacional Maker. El tamaño de este genoma es de 22.7 Mbp contenidos en 133 scafolds. Se localizaron 7328 genes los cuales fueron sometidos a un alineamiento local y obteniendo los promedios de identidad en cada scaffold encontrando que aproximadamente el 96.8% del genoma fue anotado, 53.93% pertenece al genoma de *S. cerevisiae*, 42.86% pertenece al genoma de *S. eubayanus* mientras que el 3.20% no fue anotado. Estos resultados confirman la característica híbrida de la cepa lager, además que, con la ubicación de los genes en cada uno de los scaffolds, se propone un nuevo ensamblaje para la levadura usada en este estudio.

SUMMARY

The yeast for lager beer production in Mexico is economically relevant, however, due to the specific use in industry there is little information available. It is known that the genome of such yeast is a hybrid between *Saccharomyces cerevisiae* and *Saccharomyces eubayanus* but the content of each strain is variable in every lager yeast giving them a different fermentative profile. Using the semi assembled data from previous studies, the genome of the brewing lager yeast, for this study, was annotated by the computational tool Maker. The size of this genome is 22.7 Mbp contained in 133 scafolds and, the annotation yielded 7328 genes. Those genes were submitted to a local alignment obtaining identity averages in each scaffold. Approximately 96.8% of the genome was annotated; 53.93% corresponded to *S. cerevisiae*, 42.86% were non-*cerevisiae* and 3.20% remained un-annotated. These results confirm the hybrid genome of the lager strain with a bigger quantity of *S. cerevisiae* also, with the gene location ofeach scaffold, a new assembly for the yeast used in this study was proposed.

1. Introducción

La evidencia de la producción y uso bebidas fermentadas en Egipto data de la era predinástica 5500-3100 a.C. (Hornsey 2003), es una tecnología antigua marca el inicio de la era biotecnológica.

La especie *Saccharomyces cerevisiae* es por excelencia el microorganismo más usado y más estudiado en el proceso de fermentación alcohólica (Lodolo *et al.* 2008; Förster *et al*. 2003; Wu *et al*. 2002). En la industria cervecera, este microorganismo es un ingrediente importante e indispensable para la producción de bebidas alcohólicas.

Saccharomyces sensu stricto es un complejo de especies que incluye la mayoría de las cepas de levadura de importancia industrial y en ciencia básica como *S. cerevisiae, S. pastorianus, S. bayanus, S. cariocanus, S. kudriavzevii, S. mikatae y S. paradoxus* (Naumova *et al.* 2003). Actualmente, hay deficiencias para la clasificación de las cepas, las menores diferencias entre las especies que los taxonomistas puedan menospreciar pueden ser de suma importancia técnica para la industria, por lo que la taxonomía que rodea al género *Saccharomyces* es confusa y cambiante (Priest y Graham 2006).

De forma general, la levadura cervecera se encuentra divida en dos grupos: para producción de cerveza tipo ale (*S. cerevisiae*) y para cerveza tipo lager (*S. pastorianus* conocida también como *S. carlsbergensis*).

La levadura cervecera tipo lager es de relevancia económica a nivel industrial para la producción de cerveza; sin embargo, su genoma no ha sido totalmente caracterizado debido a su complejidad y a la ausencia del conocimiento en su estructura (Nakao *et al*. 2009). Es de consideración que cada cepa cervecera es única y ha surgido a través un largo periodo de domesticación.

Se han reportado en la literatura al menos dos genomas completos de levadura tipo lager usada en la industria cervecera, en 2008 la levadura *Saccharomyces pastorianus* Weihenstephan 37/70 (Nakao *et al.* 2009) y en 2014 la levadura *Saccharomyces carlsbergensis* (Walther *et. al* 2014).

En 2014 Elizondo-Gonzalez secuenció y ensambló la primer levadura tipo lager proveniente de la industria cervecera en México (Elizondo-Gonzalez 2014), la cual será usada en este trabajo para llevar a cabo la anotación.

El objetivo de este trabajo es anotar el genoma de una levadura tipo lager, lo que significa: i) determinar la posición de las secuencias codificantes y no codificantes; ii) construir una base de datos para futuras investigaciones sobre su comportamiento genético; iii) determinación de su origen; iv) modificaciones genéticas y predicción de futuros cambios que puedan impactar las características industriales de este tipo de microorganismos.

Consideramos que el conocimiento fundamental de la secuencia nucleotídica del genoma y el arreglo fundamental de los cromosomas, nos colocará en la posibilidad de diseñar procesos más racionales.

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2. Antecedentes

2.1 Características del genero *Saccharomyces*

Saccharomyces pertenece el reino de los hongos y es un ascomiceto unicelular que fermenta los azucares para producir etanol y dióxido de carbono. El arte de producir cerveza data del año 3500 a.C., siendo un producto de consumo diario en Mesopotamia. En la edad media la elaboración de cerveza fue considerada un misterio, cuyos detalles eran celosamente guardados por los maestros cerveceros y sus gremios. Fue hasta el siglo XIX cuando se pudo explicar por primera vez el proceso de fermentación. La mayor parte de las cervezas producidas desde la edad media eran fermentadas por levaduras "altas" ya que al termino de la fermentación la levadura flotaba y se podían "desnatar", por lo que se les confirió el término de cerveza tipo *ale;* hasta el siglo XV en Bavaria se comenzaron a emplear levaduras "bajas"; una diferencia observable es que estas se hunden y van al fondo del tanque además el proceso de elaboración incluye un paso de maduración llamado "lagering", este tipo de cerveza se conoce como lager (Hornsey 2003; Nelson 2005; Brews 2014).

Una característica relevante para el mecanismo de transporte de azucares entre las levaduras tipo ale y lager es que la segunda requiere temperaturas de fermentación bajas de 6 a 14 °C, mientras que las ale requieren de una temperatura de alrededor de 15 a 25°C. (Vidgren *et al*. 2010). La cerveza tipo ale se produce a partir de la levadura *Saccharomyces cerevisiae* mientras que las levaduras lager son criotolerantes y fermentan más lentamente. (Libkind *et al*. 2011).

2.2 Genoma de levadura

En 1996 se publicó el genoma completo de *Saccharomyces cerevisiae* con un tamaño de 12,068,000 pares de bases contenidos en un total de 16 cromosomas y 5885 marco abierto de lectura (ORFs. Por sus siglas en inglés) (Goffeau *et al*. 1996). Durante los años subsecuentes, la información fue depositada en la base de datos acceso *Saccharomyces* Genome Database (SGD) (http://www.yeastgenome.org/. Revisado abril de 2016) con 6,604 ORFs de los cuales 5,138 están verificados, 682 no caracterizados y 784 dudosos (Fig.1).

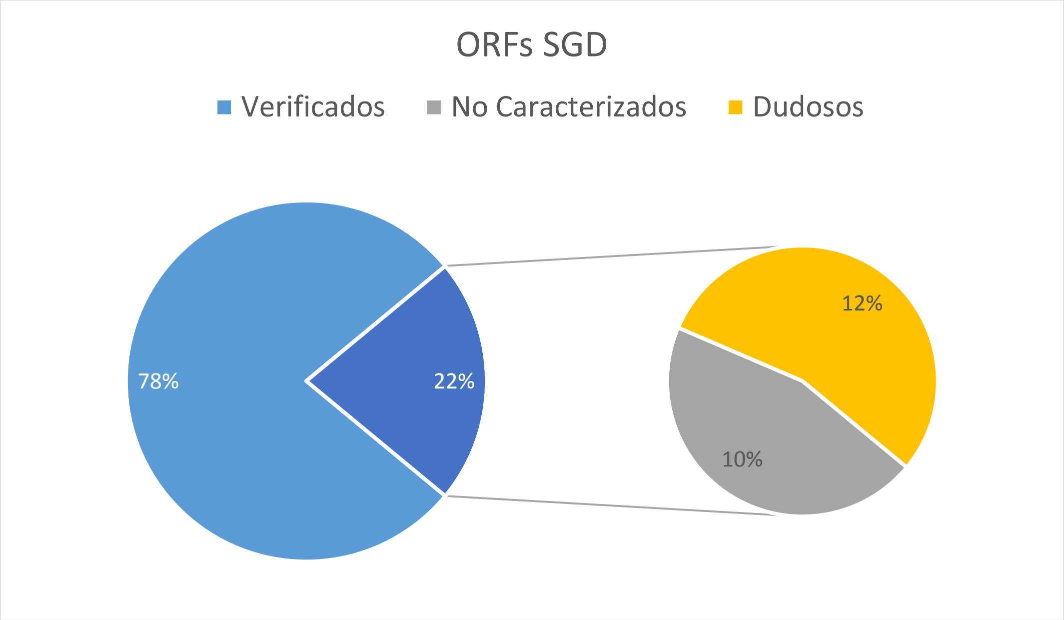


Figura 1. Relación de los ORFs en el genoma de *S. cereviciae*

El primer genoma secuenciado y ensamblado de una levadura lager fue publicado en 2009 por Nakao y colaboradores, la cepa *S. pastorianus* Weihenstephan 37/70, teniendo un tamaño de genoma nuclear de 25 Mpb que corresponde a un hibrido de *S. cerevisiae* y *S. bayanus;* con un genoma mitocondrial proveniente de *S. bayanus*, se encontraron además 8 cromosomas con translocaciones de ambos genomas (Nakao *et al.* 2009).

En 2014, se publicó la secuencia nucleotídica del genoma de una segunda cepa cervecera, *S. carlsbergensis* (*S. pastorianus*). Su genoma nuclear mide 19.5 Mpb con 29 cromosomas (Walther *et. al* 2014) confirmando que se trata de un genoma hibrido entre *S. cerevisiae* y *S. eubayanus*. Esta última levadura fue descubierta en los bosques de la Patagonia en Sur América (Libkind *et al*. 2011) y, recientemente, encontrada también en Norte América (Peris *et al*. 2014) y Asia (Bing *et al.* 2014).

Las levaduras lager se originaron en diferentes tiempos y distintos lugares por lo que los eventos de hibridación son distintos, esto se comprobó más tarde dando lugar a dos grupos de levaduras: Grupo 1 o Saaz y Grupo 2 o Frohberg.

El Grupo 1 se compone de levaduras halodiploides originarias de la fusión de una cepa haploide de *S. cerevisiae* y una cepa haploide de *S. eubayanus,* los re arreglos cromosomales de este grupo resultaron en una pérdida del genoma, en su mayoría proveniente de *S. cerevisiae,* se cree que este grupo procede de Dinamarca probablemente de cervecerías como Carlsberg, la cual produce cerveza tipo Saaz. El Grupo 2 surge de la fusión de una cepa diploide de *S. cerevisiae* con una haploide de *S. eubayanus* conservando ambos genomas y la pérdida del cromosoma 1 de *S. eubayanus,* este grupo podría tener procedencia en Holanda y de cervecerías como Heineken y Oranjeboom (Dunn y Sherlock 2008; Bond *et al*. 2004).

2.3 Herramientas bioinformáticas de anotación

El siguiente paso a al ensamblaje de un genoma es la anotación. La anotación consiste en la búsqueda de secuencias genómicas de relevancia biológica dentro de un genoma (Stein 2001) y puede dividirse en dos fases: i) anotación estructural y ii) anotación funcional (Azevedo *et al*. 2011). La primera se basa en encontrar los sitios de relevancia biológica y conferir una ubicación dentro del genoma, obteniendo como resultado un modelo o un posible marco abierto de lectura (ORF por sus siglas en inglés), esto se logra mediante predicciones de genes *ab-initio* y alineamiento de secuencias homólogas. Por otra parte, en la anotación funcional, los modelos son alineados a secuencias de organismos homólogos para asignarles funciones biológicas, roles en rutas metabólicas y características funcionales. (Rouzé *et al* 1999; Stein 2001; Azevedo *et al*. 2011; Haas *et al*. 2011; Reed *et al*. 2006)

Maker es una herramienta bioinformática desarrollada en el Departamento de Genética Humana de la Universidad de Utah por Mark Yandell y col. (Cantarel *et al*. 2008). Entre los genomas anotados por esta herramienta se encuentran: i) *Schmidtea mediterranea* - Planaria (A Alvarado, Stowers Institute); ii) *Pythium ultimum* - Pudrición rosada (R Buell, Michigan State Univ.); iii) *Pinus taeda* - Pino (A Stambolia-Kovach, Univ. California Davis); iv) *Atta cephalotes* – Hormiga cortadora de hojas (C Currie, Univ. Wisconsin, Madison); v) *Linepithema humile* – Hormiga argentina (CD Smith, San Francisco State Univ.); vi) *Pogonomyrmex barbatus* – Hormiga cosechadora roja (J Gadau, Arizona State Univ.); vii) *Conus bullatus* - Conos (B Olivera Univ. Utah); viii) *Petromyzon marinus* – Lamprea marina (W Li, Michigan State); ix) *Fusarium circinatum* – Chancro recinoso del pino (B Wingfield, Univ. Pretoria); x) *Cardiocondyla obscurior* – Hormiga trampa (J Gadau, Arizona State Univ.); xi) *Columba livia* – Paloma (M Shapiro, Univ. Utah); xii) *Megachile routundata* – Abeja cortadora de hojas de alfalfa; xiii) *Latimeria menadoensis* – Celacanto de Comores; xiv) *Nannochloropsis* - Micro alga (SH Shiu, Michigan State Univ.); xv) *Arabidopsis* thaliana - Arabidopsis re-anotacion (E Huala, TAIR); xvi) *Cronartium quercuum* – Roya fusiforme de pinos y robles (JM Davis, Univ. Florida); xvii) *Ophiophagus hannah* – Cobra rey (T. Castoe, Univ. Colorado); xviii) *Python molurus* – Pitón de la india (T. Castoe, Univ. Colorado); xix) *Lactuca sativa* – Lechuga (RW Michelmore); xx) *Diabrotica virgifera* – Gusano alfilerillo (H Robertson, Univ. Illinois); xxi) *Oryza sativa* - Arroz re-anotación (R Buell, MSU); xxii) *Zea mays* - Maíz re-anotación (C Lawrence, MaizeGDP); xxiii) *Cephus cinctus* – Troncha espigas (H Robertson, Univ. Illinois); xxiv) *Rhagoletis pomonella* – Mosca de la manzana (H Robertson, Univ. Illinois)

2.3.1 Enmascaramiento de repeticiones

La identificación de repeticiones y el enmascaramiento es el primer paso bioinformática de la anotación. Los genomas eucariotas contienen una gran cantidad de transposiciones y elementos interpuestos cortos y largos (Por sus siglas en inglés, SINE´s y LINE´s, respectivamente) que ayudan a la regulación de genes y juegan un papel importante en la evolución (Cooper 2000). El enmascaramiento consiste en cambiar a "N" estos elementos para evitar la obtención de modelos "falsos" (Tarailo-graovac y Chen 2009).

2.3.2 Predicciones *ab-initio*

Los predictores *ab-initio* se basan en los modelos ocultos de Markov los cuales utilizan matrices estocásticas obtenidas en una fase de entrenamiento previa a la predicción, en esta etapa de entrenamiento se alimenta el programa con un juego de genes con estructura conocida de un organismo homologo al secuenciado; con esta información, el programa bioinformático es capaz de predecir secuencias de genes dentro de un genoma. (Haussler et. al 1996; Stanke et. al 2003; Pachter et. al 2002; Korf 2004). Maker requiere de al menos tres predictores *ab-initio* para mejorar la selección de los modelos.

2.3.3 Alineamiento de evidencia

El penúltimo paso de la anotación es el alineamiento de proteínas y secuencias cortas de expresión (EST´s) del mismo organismo u organismos homólogos. Se construyen bases de datos locales con información proveniente de

UnirprotKB/Swissprot (http://www.uniprot.org/) para proteínas y del NCBI (http://www.ncbi.nlm.nih.gov/) para EST´s. BLAST (Camacho *et al*. 2009) es la herramienta bioinformática usada para realizar los alineamientos y se filtran los resultados en base a porcentaje de identidad y porcentaje de similitud.

2.3.4 Maker

Por último, Maker realiza una selección automática de los modelos de anotación como se muestra en la Figura 2:

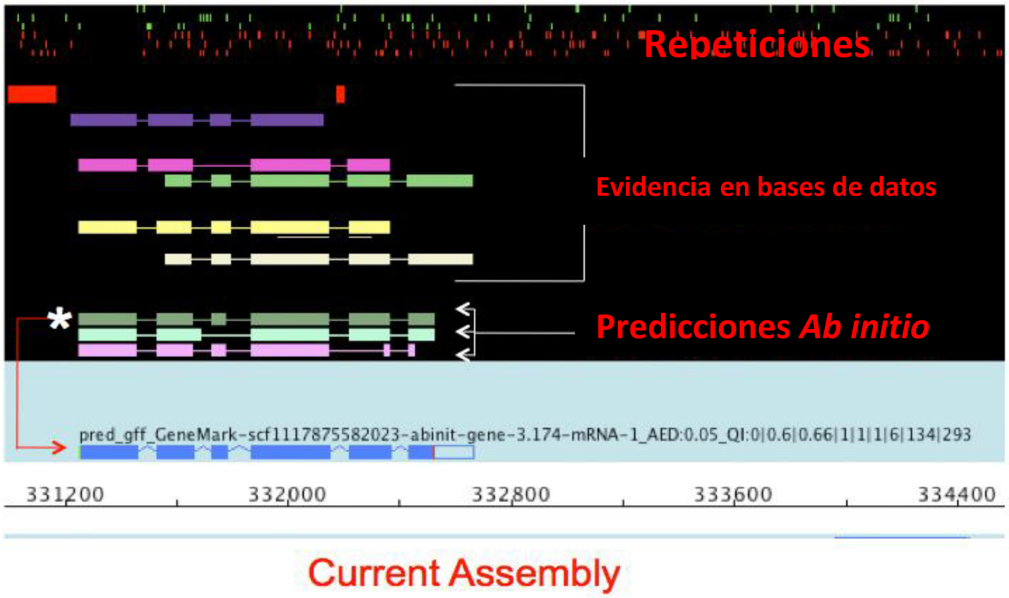


Fig.2: Para obtener el modelo de gen (parte azul), debe existir concordancia entre la evidencia y las predicciones *ab-initio* para obtener el modelo final.

3. HIPOTESIS

La anotación nos permitirá construir un modelo y asignar un objeto (gen/sitio) a una posición dentro del genoma de la levadura lager para la producción de cerveza.

4. Objetivos

4.1 OBJETIVO GENERAL

Ubicar la posición de los genes y sitios de relevancia biológica dentro del genoma de la levadura cervecera tipo lager.

4.2 OBJETIVOS PARTICULARES

1. Anotar el genoma de la levadura cervecera 790.
2. Comprobar que el genoma es un híbrido entre *S. cerevisiae* y *S. eubayanus.*
3. Determinar el porcentaje de cada genoma.
4. Validar la información obtenida de la anotación con técnicas experimentales de biología molecular.

5. Justificación

Las levaduras tipo lager surgieron a través de la domesticación del género *Saccharomyces* para la producción de cerveza, cada empresa cervecera cuenta con un ejemplar único de levadura que se ha adaptado a lo largo del tiempo a las condiciones de fermentación, materia prima empleada y región en la que se encuentra.

El avance tecnológico en el área de la bioinformática permite realizar análisis computacionales exhaustivos y profundos. Con estas herramientas es posible secuenciar y determinar la posición de los genes en genomas completos y complejos como los eucariotas. Anotar y analizar el genoma de levadura cervecera ayudará al mejor entendimiento de la función de los genes involucrados en las rutas metabólicas.

La anotación tiene la finalidad de aportar la información necesaria de estas cepas únicas para poder describir, entender y predecir su comportamiento, ayudando a mejorar la producción y disminución costos.

6. Material y método

Las secuencias semi ensambladas de la levadura *Saccharomyces* sp. 790 fueron proporcionadas por Cuauhtémoc Moctezuma y son resultado del trabajo realizado por Elizondo-González 2014 el cual se muestra en la tabla 1 (Elizondo-Gonzalez 2014). Se usaron como referencia las secuencias nucleotidicas de *S. cerevisiae* S288c obtenidas de base de datos *Saccharomyces* genome database (http://www.yeastgenome.org) y las secuencias nucleotídicas de *S. eubayanus* proporcionadas por Cuauhtémoc Moctezuma para realizar los análisis comparativos.

En la tabla 1 se muestran los resultados de la secuenciación y ensamblaje:

Tabla 1: Resultados de la secuenciación de la levadura *Saccharomyces* sp. 790.

Lecturas ensambladas	17034361
Profundidad	~70x
Tamaño estimado del Genoma (Mb)	22.7
Número de *contigs/scaffolds*	133
Tamaño promedio de *contigs/scaffolds* (pb)	170,987
***Contig/scaffold* de mayor tamaño (pb)**	1,404,408
N50	568,800
Ns	399,699

El análisis bioinformático se llevó a cabo en un servidor con las características mostradas en la Tabla 2.

Tabla 2: Características del servidor usado para la anotación.

Computadora / Servidor	Memoria RAM	CPU	Sistema operativo
HP xw4600 Workstation (Servidor)	4 GB	Intel® Core™2 Quad CPU Q9300 2.50GHz x 4	Linux / Ubuntu Server 64-bit

La instalación de la versión Maker 2.31.8 se llevó a cabo siguiendo las instrucciones del desarrollador.

El programa Maker hace uso de otras herramientas bioinformáticas (Fig. 3) para obtener los probables ORF's; para el enmascaramiento de secuencias repetitivas se utilizó la herramienta RepeatMasker (Smit et. al 1996), en la predicción de genes se requirieron de tres herramientas bioinformáticas, Snap (Korf 2004), Augustus (Mario Stanke *et al*. 2006) y GeneMark (Besemer et. al 2005); para el alineamiento de evidencia se usaron las herramientas de Blast (Camacho *et al*. 2009) y Exonerate (Slater et. al 2005).

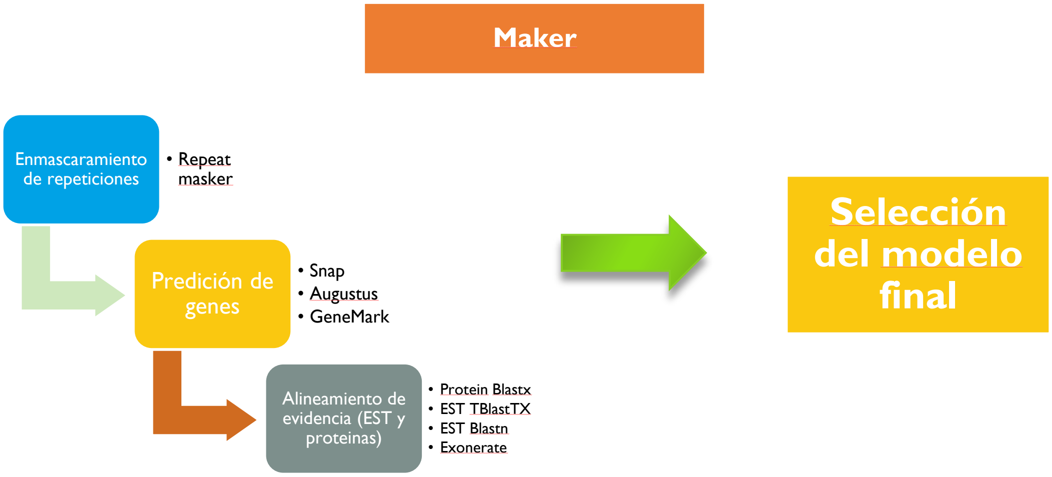


Figura 3. Diagrama de flujo en donde se muestran los programas requeridos para cada proceso dentro del programa bioinformático Maker

Se construyeron dos bases de datos locales de proteínas y secuencias cortas de expresión (EST) obtenidas de la base de datos Uniprot (http://www.uniprot.org/) y del NCBI (http://www.ncbi.nlm.nih.gov), se descargaron un total de 7185 secuencias proteicas, 6629 provenientes de *S. cerevisiae*, 289 de *S. bayanus*, 191 de *S. pastorianus*, 64 de *S. uvarum* y 14 de *S. eubayanus* y para la segunda base de datos se descargaron 34,915 secuencias EST. Esta informacion en conjunto con genoma semiensamblado se uso como entrada para el programa Maker.

La anotación se llevó a cabo en dos fases:

1) Anotación estructural el cual es el resultado del análisis de Maker, se obtienen todas las ubicaciones de los posibles genes dentro del genoma semi ensamblado y además dos archivos de transcritos y proteínas correspondientes a cada gen.

2) Anotación funcional en donde los modelos obtenidos se someten a Blast para otorgarle una identidad relacionada a un organismo homologo (*S. cerevisiae*), conferirle la nomenclatura sistémica y con base en esta información otorgar a estos modelos una posición dentro de los scaffolds

La comprobación experimental de la anotación y ensamblaje se realizó con la técnica de PCR diseñando 2 pares de cebadores como se muestra en la fig. 4, ubicados en 8 puntos de re arreglos (Tabla 3).

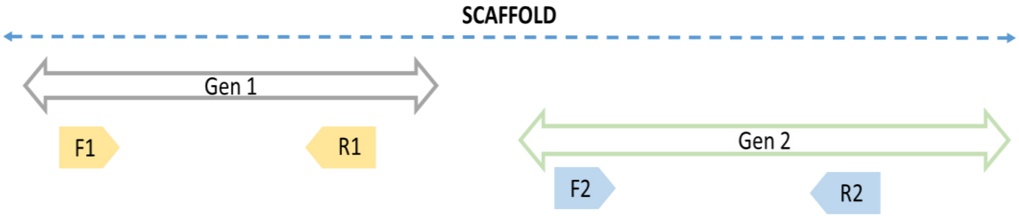


Figura. 4 Representación de la ubicación de los pares de cebadores diseñados. F1 y R1, primer par; F2 y R2, segundo par.

Tabla 3: Pares de cebadores diseñador para los re arreglos encontrados en el genoma de *Saccharomyces* sp. 790

Scaffold 1
YAL007C_YLL024C

CROMOSOMA	FORWARD		REVERSE		
	Código	***Secuencia***	***Código***	***Secuencia***	*Amplicón*
1	Chr1FW	CATGTTTCTCCATTCTCTAGCTCTC	Chr1RV	TATGCTCCAGTTGCTATCACTTTGC	429 pb
12	Chr12FW	CTTCAAAGAGTAAGCAATGGATTCC	Chr12RV	TTTGTCTTCTTCCGCTCAAACTTCC	913 pb
Breakpoint	Chr1FW	CATGTTTCTCCATTCTCTAGCTCTC	Chr12RV	TTTGTCTTCTTCCGCTCAAACTTCC	3355 pb

Scaffold 3

YOR018W_YHR015W

Cromosoma	Forward		Reverse		
	Código	*Secuencia*	*Código*	*Secuencia*	*Amplicón*
15	Chr15FW	CCCAAATAAAGAAGAGAAGAAGCCT	Chr15RV	TGTCAGTTGTTGTAATGATACCGAG	1265 pb
8	Chr8FW	CCTCACTTCAAGTAACAGTAACGAA	Chr8RV	CAAGACTTTCAGCAGCCTTAATGAT	290 pb
Breakpoint	Chr15FW	CCCAAATAAAGAAGAGAAGAAGCCT	Chr8RV	CAAGACTTTCAGCAGCCTTAATGAT	5679 pb

YHR157W_YML091C

Cromosoma	Forward		Reverse		
	Código	*Secuencia*	*Código*	*Secuencia*	*Amplicón*
8	Chr8FW2	CTCTATCTCTTCCTTTTGTCTTTGG	Chr8RV2	GACTGCTAAACTGAAATATGCTTCC	310 pb
13	Chr13FW	ATCTCAAAATATCTGCGTACTTACC	Chr13RV	TTGGATACCTGAGTTCTCTTACGAA	1331 pb
Breakpoint	Chr8FW2	CTCTATCTCTTCCTTTTGTCTTTGG	Chr13RV	TTGGATACCTGAGTTCTCTTACGAA	2766 pb

Scaffold 4
SuYHR014W_YOR019W

Cromosoma	Forward		Reverse		
	Código	*Secuencia*	*Código*	*Secuencia*	*Amplicón*
8	Chr8FW3	ACCCTGTATTTCTGACACCGTGCTA	Chr8RV3	AGTTTGAGAATCTCTTATTGCTTGG	279 pb
15	Chr15FW2	TCCAGAATATGACTTAAAGACCTGC	Chr15RV2	TAGTCTCTCCTTACGATTTTCCCAT	441 pb
Breakpoint	Chr8FW3	ACCCTGTATTTCTGACACCGTGCTA	Chr15RV2	TAGTCTCTCCTTACGATTTTCCCAT	2494 pb

Scaffold 6
YLR288C_YOR182C

Cromosoma	Forward		Reverse		
	Código	*Secuencia*	*Código*	*Secuencia*	*Amplicón*
12	Chr12FW	TGGACAACTATGGTGTACTATTCCT	Chr12RV	CACATCATTGAATCTTGTATCGTCG	976 pb
15	Chr15FW3	CTCGTGCTGGTAAGGTTAAGTCTC	Chr15RV3	TGGACCTGGGTTCATTCTTCTC	155 pb
Breakpoint	Chr12FW	TGGACAACTATGGTGTACTATTCCT	Chr15RV3	TGGACCTGGGTTCATTCTTCTC	2283 pb

Scaffold 11
YPL091W_YBR181C

Cromosoma	Forward		Reverse		
	Código	*Secuencia*	*Código*	*Secuencia*	*Amplicón*
16	Chr16FW	GATGTTGTATTTGGATGGGCTAGAT	Chr16RV	TTCTCCTTACCGTACTTTTCAATGG	803 pb
2	Chr2FW	AGAAGCTCTTCTCTTTCTGATTTCG	Chr2RV	CATTGTCAAGAAGGGTGAACAAGAA	361 pb
Breakpoint	Chr16FW	GATGTTGTATTTGGATGGGCTAGAT	Chr2RV	CATTGTCAAGAAGGGTGAACAAGAA	1770 pb

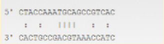
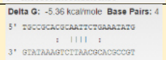
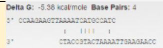
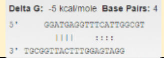
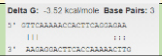
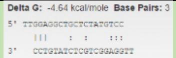
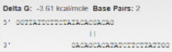
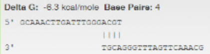
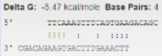
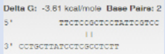
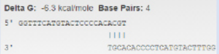
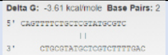
Scaffold 17
YDR262W_YBL099W

Cromosoma	Forward		Reverse		
	Código	*Secuencia*	*Código*	*Secuencia*	*Amplicón*
4	Chr4FW	ATATCATCTAAATTCACTGCGGGTC	Chr4RV	ATTCAATCTACCTGTTAGTGTGCTG	243 pb
2	Chr2FW2	CACAGAAGTTTCCTCCATCTTAGAG	Chr2RV2	TGACGATCACCAATAATCAACTCTC	501 pb
Breakpoint	Chr4FW	ATATCATCTAAATTCACTGCGGGTC	Chr2RV2	ATATCATCTAAATTCACTGCGGGTC	2479 pb

Scaffold 22
YER102W_YBL071W-A

Cromosoma	Forward		Reverse		
	Código	*Secuencia*	*Código*	*Secuencia*	*Amplicón*
5	Chr5FW	ATTCTTCACCTTCCAAGATGTAACC	Chr5RV	ATGGGTATTTCTCGTGATTCTCGTC	644 pb
2	Chr2FW3	GAGCCTGAAAATCAAATGTTCACCT	Chr2RV3	GTACTCAGCCAAGTCTTCTTTATCG	156 pb
Breakpoint	Chr5FW	ATTCTTCACCTTCCAAGATGTAACC	Chr2RV3	GTACTCAGCCAAGTCTTCTTTATCG	1693 pb

Tabla 4: Segundo diseño de cebadores para la comprobación del re ensamblaje manual.

Sitio	Clave	Secuencia	Inicio	Tamaño (pb)	Tm (según OligoAnalyzer)	%GC	Hairpin (ΔG/°C)	Homodímero	Amplicón
YOR018W	Chr15FW	CTACCAAATGCAGCCGTCAC	544	20	59.55°C	55	1.45/-8.4°C	 Delta G: -7.05 kcal/mole Base Pairs: 4 5' CTACCAAATGCAGCCGTCAC 3' CACTGCCGACGTAAACCATC	612 pb
	Chr15RV	TGCCGCACGCAATTCTGAAATATG	1155	24	63.01°C	45.8	-1.03/39.7°C	 Delta G: -5.36 kcal/mole Base Pairs: 4 5' TGCCGCACGCAATTCTGAAATATG 3' GTATAAAGTCTTAACGCACGCCGT	
YHR015W	Chr8FW	CCAAGAAGTTAAAATCATGCCATC	552	24	56.86°C	37.5	0.71/15.3°C	 Delta G: -5.38 kcal/mole Base Pairs: 4 5' CCAAGAAGTTAAAATCATGCCATC 3' CTACCGTACTAAAATTGAAGAACC	1125 pb
	Chr8RV	GGATGAGGTTTCATTGGCGT	1676	20	58.54°C	50	-1/38.7°C	 Delta G: -5 kcal/mole Base Pairs: 4 5' GGATGAGGTTTCATTGGCGT 3' TGCGGTTACTTTGGAGTAGG	
SuYHR014W	Chr8FW2	GTTCAAAAACCACTTCAGGAGAA	64	23	57.42°C	39.1	-0.78/37.6°C	 Delta G: -3.52 kcal/mole Base Pairs: 3 5' GTTCAAAAACCACTTCAGGAGAA 3' AAGAGGACTTCACCAAAAACTTG	340 pb
	Chr8RV2	TTGGAGGCTGCTCTATGTCC	403	20	59.17°C	55	-1.31/38.4°C	 Delta G: -4.64 kcal/mole Base Pairs: 3 5' TTGGAGGCTGCTCTATGTCC 3' CCTGTATCTCGTCGGAGGTT	
YOR019W	Chr15FW	GGTTATTCTTCTATACACGACAG	172	23	54.43°C	39.1	1.01/6.4°C	 Delta G: -3.61 kcal/mole Base Pairs: 2 5' GGTTATTCTTCTATACACGACAG 3' GACAGCACATATCTTCTTATTGG	1151 pb
	Chr15RV	GCAAACTTGATTTGGGACGT	1766	20	57.21°C	45	-1.9/41.8°C	 Delta G: -6.3 kcal/mole Base Pairs: 4 5' GCAAACTTGATTTGGGACGT 3' TGCAGGGTTTAGTTCAAACG	
YBR031W	Chr2FW	TTCAAAGTTTCAGTGAAGACAGC	11	23	57.76°C	39.1	0.12/23.7°C	 Delta G: -5.47 kcal/mole Base Pairs: 4 5' TTCAAAGTTTCAGTGAAGACAGC 3' CGACAGAAGTGACTTTGAAACTT	323 pb
	Chr2RV	TTCTCCGCTCCTATTCGTCC	333	20	58.97°C	55	0.32/20.9°C	 Delta G: -3.61 kcal/mole Base Pairs: 2 5' TTCTCCGCTCCTATTCGTCC 3' CCTGCTTATCCTCGCCTCTT	
YDR011W	Chr4FW	GGTTTCATGTACTCCCCACACGT	275	23	62.68°C	52.2	0.58/16.7°C	 Delta G: -6.3 kcal/mole Base Pairs: 4 5' GGTTTCATGTACTCCCCACACGT 3' TGCACACCCCTCATGTACTTTGG	1388 pb
	Chr4RV	CAGTTTTCTGCTCGTATGCGTC	1662	22	60.22°C	50	-1.63/35.8°C	 Delta G: -3.61 kcal/mole Base Pairs: 2 5' CAGTTTTCTGCTCGTATGCGTC 3' CTGCGTATGCTCGTCTTTTGAC	

7. Resultados

El genoma de la levadura *Saccharomyces* sp. 790 fue analizado por la herramienta de anotación Maker obteniendo 9939 modelos de genes, transcritos y proteínas, la ubicación de cada gen fue determinada dentro de los 133 scaffolds de la levadura y cada uno de los genes fue identificado con su nomenclatura sistemática con el objetivo de dar una orientación a los scaffolds (Tabla 5).

Tabla 5: Modelos sometidos al análisis de Blast e identificados con su nombre sistemático (columna Gen).

Nombre	Gen	%Id	E-value	Tamaño	Promedio Scaffold
scaffold1%7Csize712480-gene-0.15	YAL051W	81.82	0	2573	83.04
scaffold1%7Csize712480-gene-0.17	YAL048C	82.28	0	1688	
scaffold1%7Csize712480-gene-0.19	YAL046C	82.9	5.00E-75	278	
scaffold1%7Csize712480-gene-0.22	YAL043C	78	0	1458	
scaffold1%7Csize712480-gene-0.23	YAL042W	80.64	0	965	
scaffold1%7Csize712480-gene-0.24	YAL041W	80.92	0	2001	
scaffold1%7Csize712480-gene-0.25	YAL040C	80.38	0	1310	
scaffold1%7Csize712480-gene-0.27	YAL038W	96.07	0	2449	
scaffold1%7Csize712480-gene-0.29	YAL036C	85.68	0	1170	
scaffold1%7Csize712480-gene-0.30	YAL035W	83.81	0	2800	
scaffold1%7Csize712480-gene-0.32	YAL034C	80.96	0	963	
scaffold1%7Csize712480-gene-0.33	YAL033W	85.16	4.00E-118	422	
scaffold1%7Csize712480-gene-0.37	YAL029C	77.4	0	2514	
scaffold1%7Csize712480-gene-0.38	YAL031C	77.65	0	1349	
scaffold1%7Csize712480-gene-0.42	YAL034W-A	79.66	7.00E-177	617	
scaffold1%7Csize712480-gene-0.6	YAL062W	81.51	0	1125	
scaffold1%7Csize712480-gene-0.69	YAL056W	76.77	0	1439	
scaffold1%7Csize712480-gene-0.7	YAL061W	80.78	0	981	
scaffold1%7Csize712480-gene-0.88	YAR042W	82.66	0	1640	
scaffold1%7Csize712480-gene-0.9	YAL059W	84.99	1.00E-117	420	
scaffold1%7Csize712480-gene-1.0	YAL023C	83.89	0	2172	
scaffold1%7Csize712480-gene-1.1	YAL022C	80.79	0	1171	

De los 9930 modelos de gen, 7328 obtuvieron un porcentaje de alineamiento resultado del alineamiento local esta cantidad de genes identificados es coherente debido a que el tamaño del genoma de *Saccharomyces* sp. 790 es aproximadamente 35% mas grande que el *S. cerevisiae* cuyo genoma es de 16 Mb.

Por las características hibridas de este genoma, para obtener el tamaño de las regiones que pertenecen a *S. cerevisiae y S. eubayanus*, se calcula el promedio de los genes contenidos en cada scaffold y se analiza cada uno de los scaffolds en base a la siguiente lógica:

Si %Id ≥ 99% y E value ≤ 10^{-6} = El scaffold pertenece a *S. cerevisiae*

Si %Id ≤ 86% y E value ≤ 10^{-6} = El scaffold pertenece a *S. eubayanus*

Si 99% > %Id > 86% y E value ≤ 10^{-6} = El scaffold es un hibrido entre *S. cerevisiae* y *S. eubayanus*

Esta lógica se comprobó alineando los genomas de *S. cerevisiae y S. eubayanus* encontrado una homología aproximada al 80% (Anexo 1).

Los resultados obtenidos de este análisis se pueden observar en la tabla 6. El porcentaje de genoma no anotado corresponde a lo observado por diferentes autores, menos del 5% del genoma de la levadura contiene intrones (Spingola *et al*. 1999; Parenteau *et al*. 2008).

Tabla 6: Resultados obtenidos de la anotación y el alineamiento contra el genoma de referencia *S. cerevisiae*

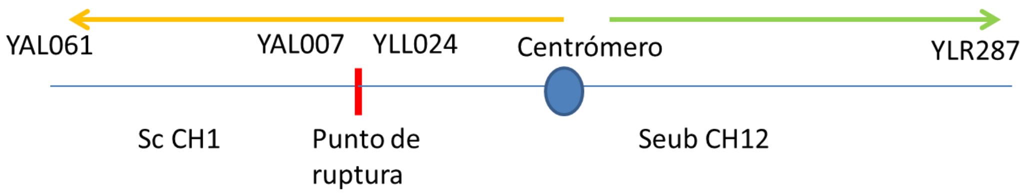
Genoma de *Saccharomyces* sp 790	
Tamaño de genoma	21.64 Mb
Total de genes identificados	7328
Promedio de tamaño de genes	1550 bp
Scaffolds anotados	97 / 133
Tamaño de genoma anotado	96.80%
Porcentaje proveniente de *S. cerevisiae*	53.93%
Porcentaje proveniente de *S. eubayanus*	42.86%
Porcentaje no anotado	3.20%

Se revisaron las ubicaciones de los genes en base a los promedios de identidad para los scaffolds híbridos encontrando 9 puntos de ruptura en 8 scaffolds (Tabla 7) de los cuales 8 puntos son recombinaciones homologas *S.cerevisiae* - *S.cerevisiae* o *S. eubayanus* - *S. eubayanus*, 1 punto de ruptura restante es una translocación *S. eubayanus* - *S.cerevisiae* (Fig. 5).

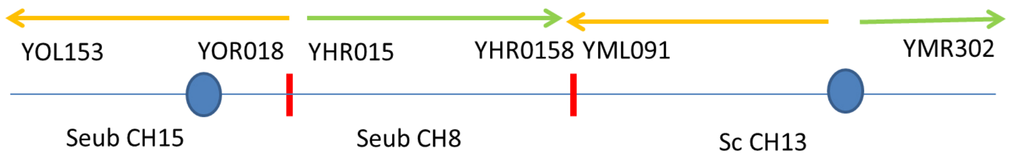
Tabla 7: Puntos de ruptura encontrados en 10 scaffolds

Puntos de ruptura *Saccharomyces* sp 790		
Scaffold	**Nombre sistemático/Nombre común**	**Tipo**
1	YAL007/ERP2 - YAL24C/SSA2	Sb - Sb
3	YOR018W/ROD1 - YHR015W/MIP6	Sb - Sb
3	YHR157W/REC104 - YML091C/RPM2	Sb - Sc
4	YHR014W - YOR019W	Sc - Sc
6	YHR288C/MEC3 - YOR182C/RPS30B	Sc - Sc
11	YPL091W/GLR1 - YBR181C/RPS6B	Sc -Sc
16	YDR013W/PSF1 – YBR021W/FUR4	Sb - Sb
17	YDR262W/FAS1 - YBL099W/ATP1	Sc - Sc
22	YER102W/RPS8B - YBL071W/KTI11	Sc - Sc

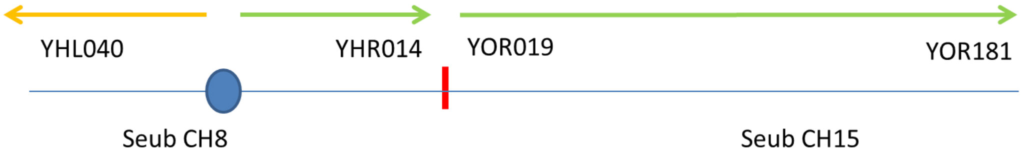
Scaffold 1



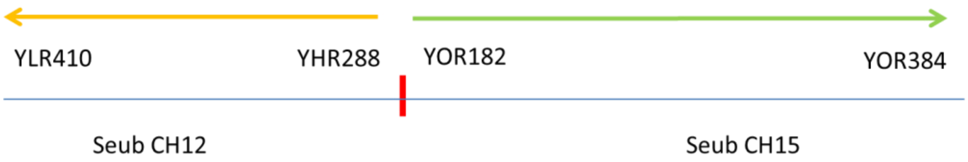
Scaffold 3



Scaffold 4



Scaffold 6



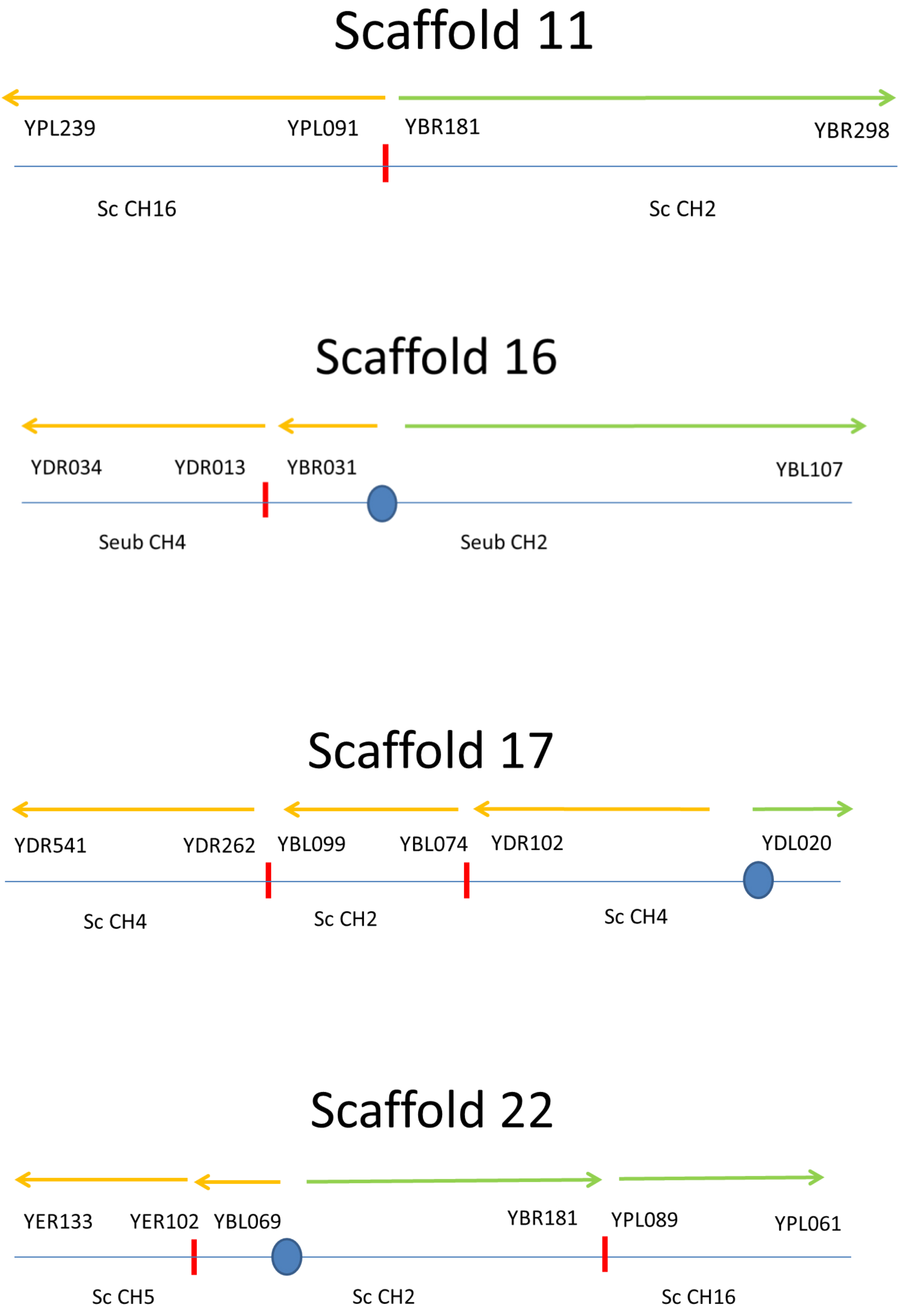
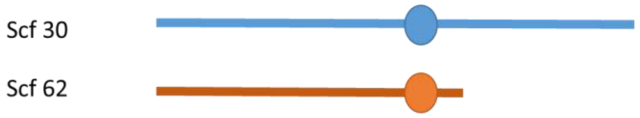
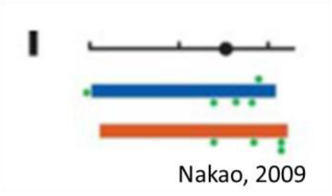


Figura 5: Representación gráfica de los scaffolds con los puntos de ruptura localizados. Los scaffolds 6 y 11 carecen de centrómero.

De los cebadores diseñados para comprobar los puntos de ruptura, ninguno amplificó, por lo que manualmente se separaron estos puntos y se propuso un nuevo re-ensamblaje (Fig. 6), basado en la anotación y comparado con lo encontrado por Nakao y sus colaboradores (Nakao *et al*. 2009) de la levadura cervecera *S. Weihenstephan* 34/70. Esta propuesta se realizó en colaboración con el Instituto Potosino de Investigación Científica y Tecnológica (Gómez-Muñoz 2015) utilizando la técnica de mapeo físico descrita en la tesis de Gómez-Muñoz para la validación experimental.

CH1





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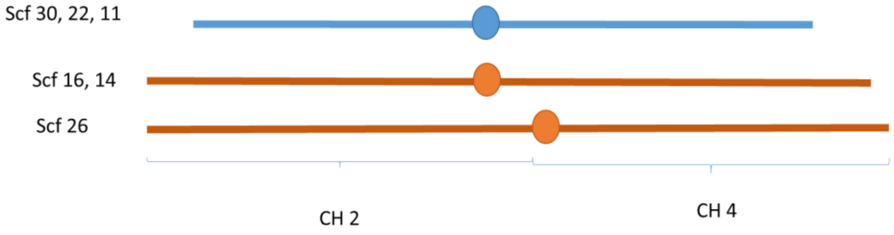
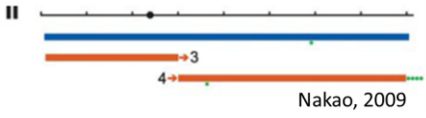
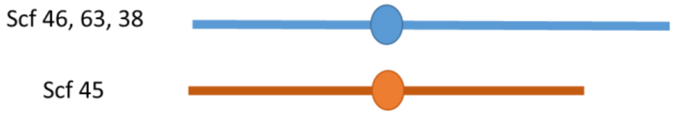
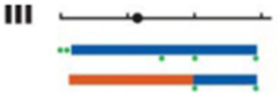




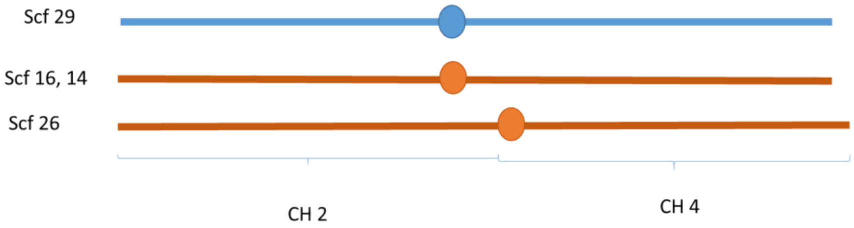
CH3

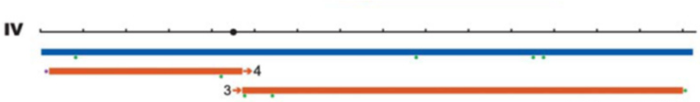




Nakao, 2009

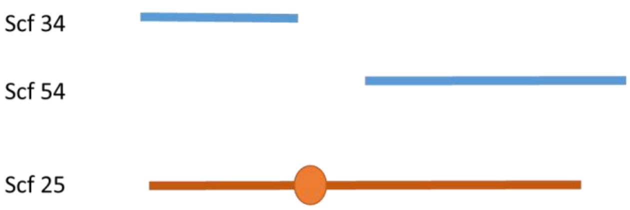
CH4

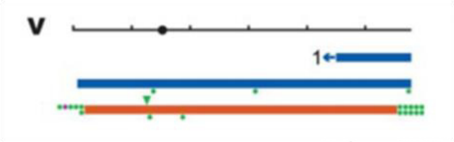




Nakao, 2009

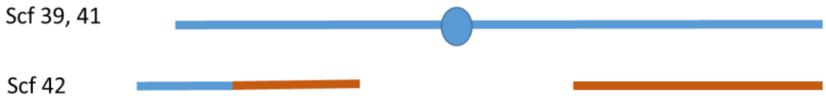
CH5





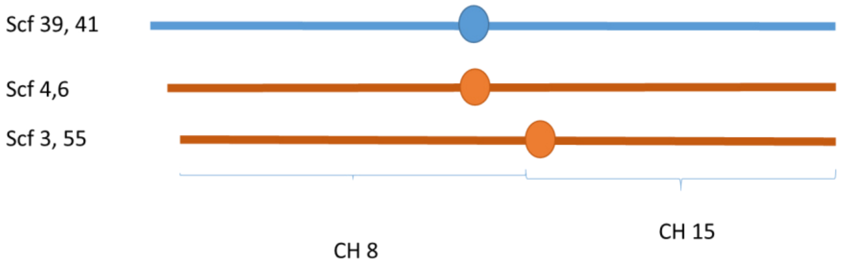
Nakao, 2009

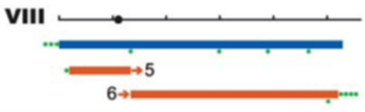
CH7



Nakao, 2009

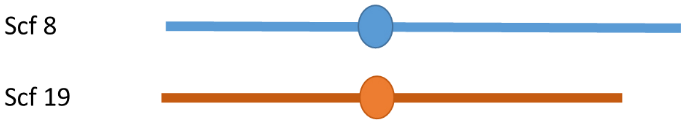
CH8

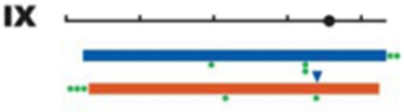




Nakao, 2009

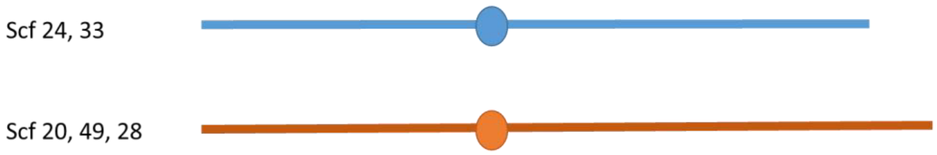
CH9

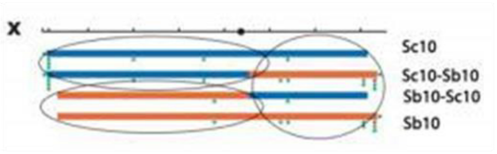




Nakao, 2009

CH10





Nakao, 2009

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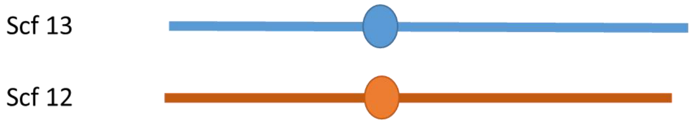

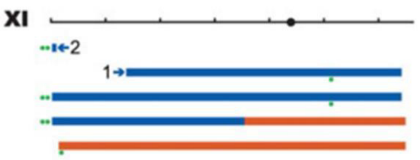

Nakao, 2009

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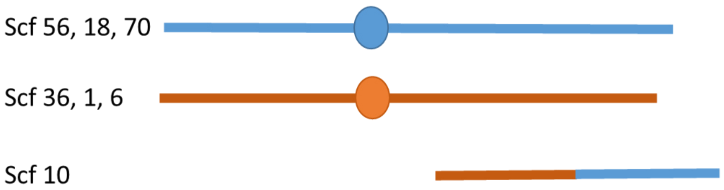

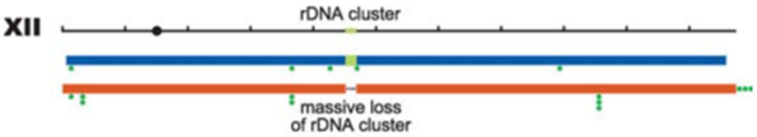

Nakao, 2009

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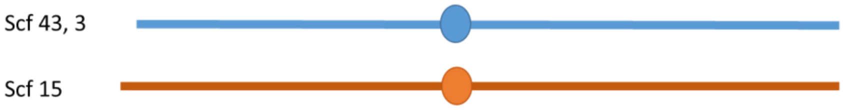
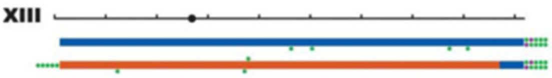
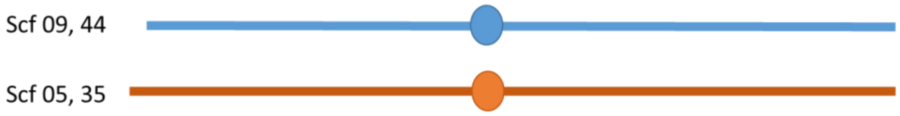
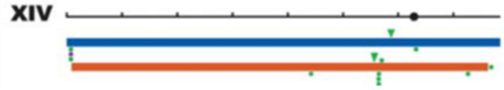




Nakao, 2009

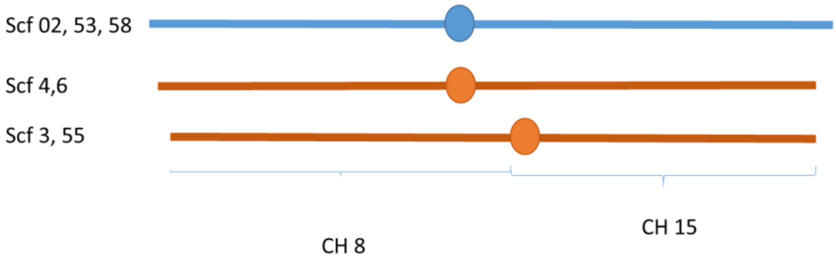
CH14

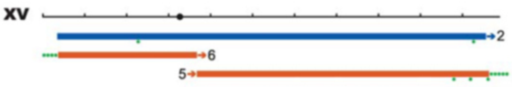




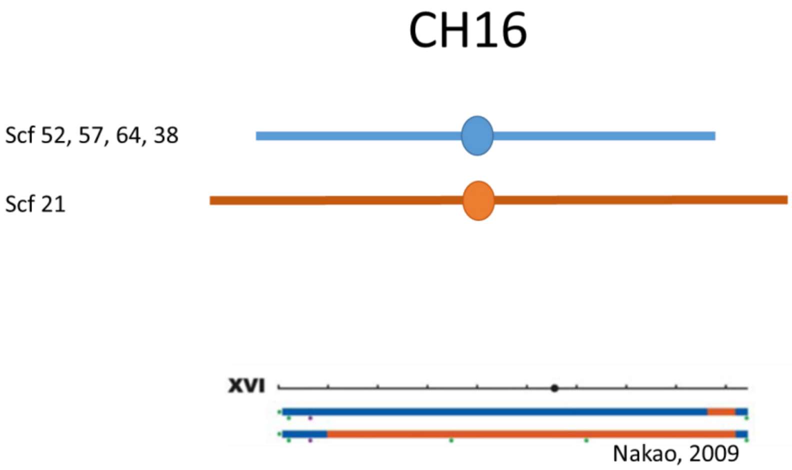
Nakao, 2009

CH15





Nakao, 2009



Nakao, 2009

Fig.6: Ensamblaje basado en la anotación del genoma de *Saccharomyces* sp. 790. La línea azul representa los cromosomas o porciones que pertenecen al genoma de *S. cerevisiae* mientras que la línea naranja representa el genoma de *S. eubayanus.*

Además de la comprobación mediante el mapeo físico, se diseñaron tres juegos de cebadores nuevos basados en este nuevo ensamblaje (Tabla 4) correspondientes a los cromosomas 4 y 8 (scaffold 3, 4 y 26) mostrando amplificación y corroborando estos re arreglos del genoma. Los productos amplificados se muestran en la figura 7.

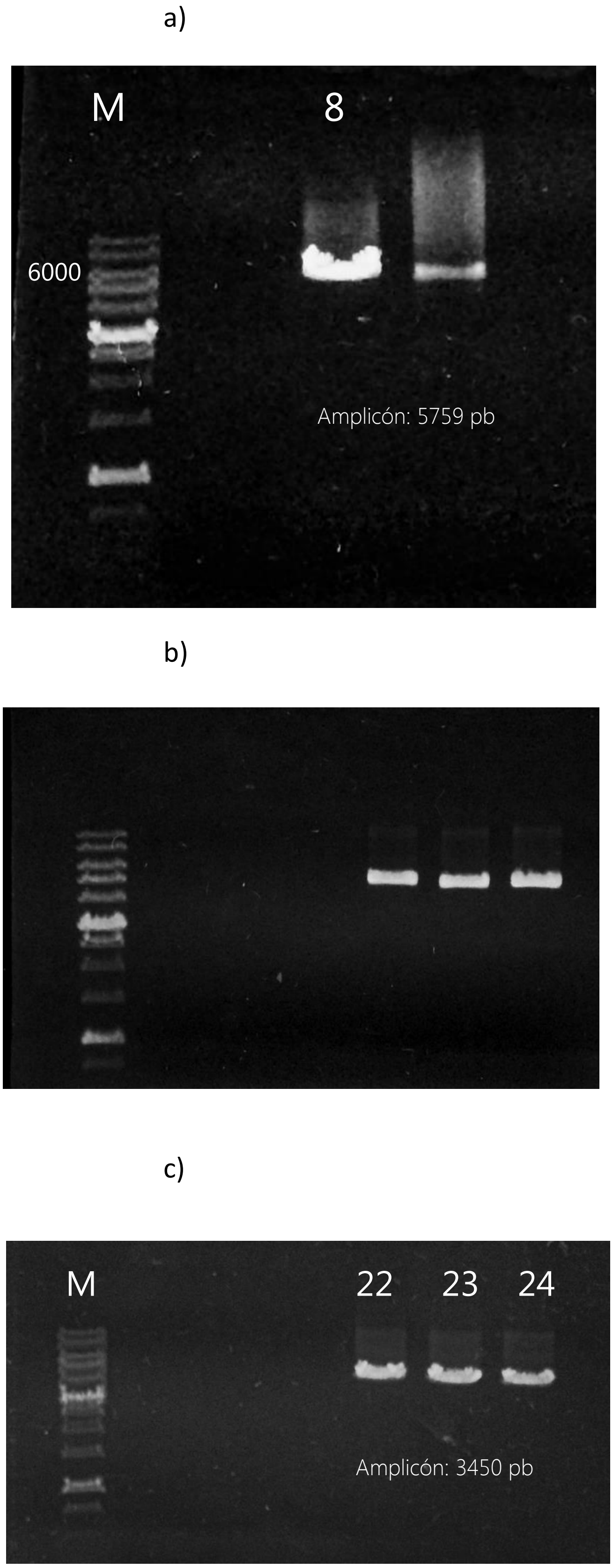


Figura 7: amplificación de los puntos de ruptura; a) amplificación del punto de ruptura en el cromosoma 8, scaffold 3 y 55 (carril 8); b) amplificación del punto de ruptura en el cromosoma 8, scaffolds 4 y 6 (carriles 16,17 y 18); c) amplificación del punto de ruptura en el cromosoma 4, scaffold 26 (carriles 22, 23 y 24)

8. Discusión

Con el desarrollo de nuevas herramientas bioinformáticas y la disminución de los costos de secuenciación, es posible ubicar y determinar las secuencias de genes dentro de genomas completos recién ensamblados, los flujos de trabajo cada vez son más robustos y sencillos, pero requieren de conocimiento informático para la instalación y preparación de estas herramientas. Hasta hace algunos años, el interés de la industria por conocer lo mecanismos biológicos de la producción de ciertos alimentos y bebidas ha ido creciendo y cada vez es más la información disponible para realizar análisis comparativos bioinformáticos.

Según los resultados obtenidos en este estudio, se pudo comprobar que el genoma de la levadura cervecera es un hibrido entre dos especies de *Saccaromyces*: *S. cerevisiae - S. eubayanus* y el tamaño calculado del genoma de 21.64 Mb coincide con lo reportado previamente para otras levaduras utilizadas en la industria cervecera, *S. weihenstephan* (985 scaffolds, ~29 cromosomas y 22.9 Mpb) (Nakao *et al*. 2009) y *S. carlsbergensis* (78 *scaffolds,* 29 cromosomas con 19.5 Mpb de longitud) (Walther et. al 2014).

Uno de los hallazgos relevantes en este estudio fue la homología que presentan las cepas de *S. cerevisiae* y *S. eubayanus* que es cercana al 80%, no se encontró literatura al respecto debido a la poca información sobre el genoma de *S. eubayanus*. Esta información nos ayudó a diferenciar las regiones del genoma de cada una de las especies.

Los alineamientos locales con las cepas de referencias, mostraron un porcentaje de identidad superior al 99%, esto nos indica que el genoma de *Saccharomyces* sp. 790 se ha encontrado conservado a lo largo del tiempo.

Además de conocer la posición de los genes dentro del genoma, la anotación de los genes nos permitió encontrar errores y re-ensamblar el genoma manualmente para así tener 16 cromosomas. De los 133 scaffolds, 70 no pudieron ser ensamblados manualmente ya que sus tamaños son menores a 2000 pb y la suma de estos equivalen al 0.7% del genoma de *Saccharomyces* sp. 790.

El número de copias de cada cromosoma no pudo ser identificado ya que en el ensamblaje las lecturas de las regiones similares son ensambladas en un mismo contig como se muestra en la figura 8, por lo tanto, todas las copias se ensamblan en un solo cromosoma.

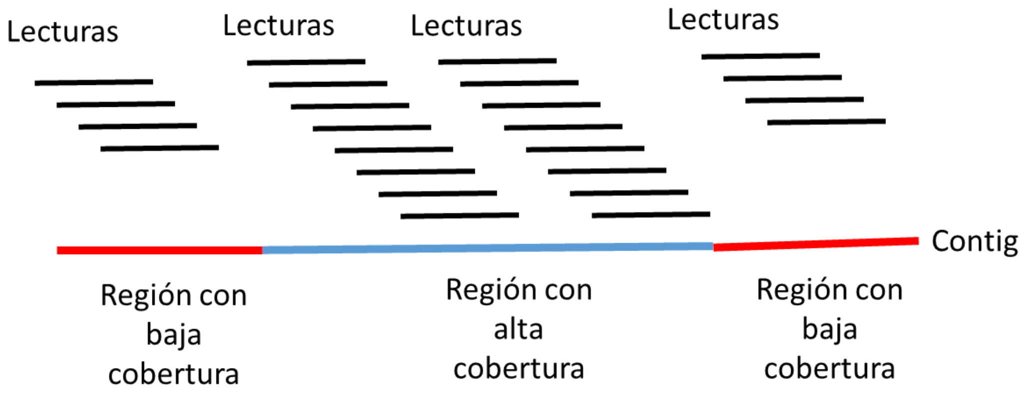


Fig.8: Empalme de las lecturas de secuenciación en regiones similares del genoma.

Contrario a lo reportado por Dunn y Sherlock, en el genoma de la cepa *Saccharomyces* sp. 790 se encontró el cromosoma I de *S. eubayanus*, reportado también por Nakao y colaboradores. Para hacer la diferenciación de grupos en esta cepa se requiere la información del número de copias, pero considerando solo el porcentaje de los genomas, posiblemente sea parte del grupo 2 o Frohberg procedente de Holanda. Cabe la aclaración que esta cepa ha sido usada por más de 100 años en México, por lo cual esta domesticada al tipo de fermentación para la cual es usada.

Además de obtener la posición de los genes en los scaffolds del genoma de la levadura *Saccharomyces* sp 790, la anotación nos ayudó a localizar errores en el ensamblaje y re ensamblar manualmente para obtener un genoma ensamblado a nivel cromosomal sin considerar ploidía.

9. Conclusiones

Los objetivos planteados se cumplieron encontrando lo siguiente:

1. El genoma de la cepa 790 es un hibrido entre *S. cerevisiae* (53.93%) y *S. eubayanus* (42.86%)

2. El porcentaje de identidad entre *S. cerevisiae* y *S. eubayanus* es aproximadamente el 80%.

3. Anotamos el genoma completo de la levadura cervecera *Saccharomyces* sp 790, se obtuvieron 7328 marcos abiertos de lectura.

4. Los scaffolds no ensamblados equivalen al 0.7% del total del genoma.

5. Se identificaron errores de ensamblaje los cuales pudieron detectados con la anotación y re ensamblados manualmente.

6. El mapeo físico es un elemento clave para comprobar el re-ensamblaje manual.

7. Los resultados encontrados son consistentes con lo reportados por otros autores para levaduras cerveceras tipo lager.

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Anexo

Resultados del alineamiento local de *S. eubayanus* vs *S. cervesiae* S288C

Name	Gene	%Id	E-value
scaffold1-gene-0_12-mRNA-1	YEL061C	82.06	0
scaffold1-gene-0_13-mRNA-1	YEL060C	84.86	0
scaffold1-gene-0_16-mRNA-1	YEL056W	81.7	0
scaffold1-gene-0_18-mRNA-1	YEL054C	93.79	0
scaffold1-gene-0_19-mRNA-1	YEL053C	77.44	0
scaffold1-gene-0_20-mRNA-1	YEL052W	83.01	0
scaffold1-gene-0_21-mRNA-1	YEL051W	88.04	0
scaffold1-gene-0_23-mRNA-1	YLR037C	84.96	2.00E-104
scaffold1-gene-0_26-mRNA-1	YEL046C	83.93	0
scaffold1-gene-0_28-mRNA-1	YEL043W	78.71	0
scaffold1-gene-0_3-mRNA-1	YLL062C	79.2	0
scaffold1-gene-0_32-mRNA-1	YEL039C	84.97	2.00E-94
scaffold1-gene-0_34-mRNA-1	YEL037C	80.54	0
scaffold1-gene-0_35-mRNA-1	YEL036C	83.99	0
scaffold1-gene-0_36-mRNA-1	YEL034W	92.63	0
scaffold1-gene-0_37-mRNA-1	YEL032W	82.92	0
scaffold1-gene-0_4-mRNA-1	YLL061W	81.58	0
scaffold1-gene-0_40-mRNA-1	YEL058W	80.71	0
scaffold1-gene-0_5-mRNA-1	YOR386W	77.2	0
scaffold1-gene-0_6-mRNA-1	YEL070W	82.29	0
scaffold1-gene-0_9-mRNA-1	YEL064C	82.11	0
scaffold1-gene-1_0-mRNA-1	YEL024W	87.27	0
scaffold1-gene-1_1-mRNA-1	YEL023C	79.56	0
scaffold1-gene-1_12-mRNA-1	YEL020W-A	87.98	7.00E-83
scaffold1-gene-1_13-mRNA-1	YEL021W	82.84	0
scaffold1-gene-1_137-mRNA-1	YER003C	85.06	0
scaffold1-gene-1_14-mRNA-1	YEL009C	81.57	0
scaffold1-gene-1_141-mRNA-1	YEL012W	84.29	7.00E-176
scaffold1-gene-1_143-mRNA-1	YER007C-A	85.79	8.00E-160
scaffold1-gene-1_15-mRNA-1	YEL007W	78.26	0
scaffold1-gene-1_16-mRNA-1	YEL006W	82.72	0
scaffold1-gene-1_19-mRNA-1	YEL002C	83.3	0
scaffold1-gene-1_2-mRNA-1	YEL022W	83.8	0
scaffold1-gene-1_21-mRNA-1	YER001W	78.06	0
scaffold1-gene-1_24-mRNA-1	YER005W	80.37	0
scaffold1-gene-1_25-mRNA-1	YER006W	86.02	0
scaffold1-gene-1_28-mRNA-1	YER008C	79.62	0
scaffold1-gene-1_28-mRNA-1	YER008C	82.45	0
scaffold1-gene-1_3-mRNA-1	YEL011W	84.44	0

scaffold1-gene-1_31-mRNA-1	YER011W	79.92	3.00E-150
scaffold1-gene-1_33-mRNA-1	YER013W	81.47	0
scaffold1-gene-1_34-mRNA-1	YER014W	79.41	0
scaffold1-gene-1_36-mRNA-1	YPL282C	90.45	5.00E-140
scaffold1-gene-1_38-mRNA-1	YEL031W	85.56	0
scaffold1-gene-1_39-mRNA-1	YEL030W	81.06	0
scaffold1-gene-1_41-mRNA-1	YEL027W	94.01	0
scaffold1-gene-1_42-mRNA-1	YEL026W	93.18	5.00E-160
scaffold1-gene-1_5-mRNA-1	YEL013W	86.72	0
scaffold1-gene-1_6-mRNA-1	YEL015W	81.77	0
scaffold1-gene-1_7-mRNA-1	YEL016C	77.54	0
scaffold1-gene-2_1-mRNA-1	YER024W	81.73	0
scaffold1-gene-2_13-mRNA-1	YER036C	88.36	0
scaffold1-gene-2_14-mRNA-1	YER037W	82	0
scaffold1-gene-2_156-mRNA-1	YER056C-A	94.85	6.00E-146
scaffold1-gene-2_156-mRNA-1	YER056C-A	97.3	3.00E-10
scaffold1-gene-2_158-mRNA-1	YER060W-A	85.64	0
scaffold1-gene-2_17-mRNA-1	YER040W	81.19	0
scaffold1-gene-2_19-mRNA-1	YER042W	83.57	2.00E-146
scaffold1-gene-2_2-mRNA-1	YER025W	88.52	0
scaffold1-gene-2_20-mRNA-1	YER043C	90.69	0
scaffold1-gene-2_26-mRNA-1	YER048C	82.14	0
scaffold1-gene-2_28-mRNA-1	YER049W	83.82	0
scaffold1-gene-2_31-mRNA-1	YER052C	85.48	0
scaffold1-gene-2_35-mRNA-1	YER056C	85.08	0
scaffold1-gene-2_39-mRNA-1	YER059W	78.92	0
scaffold1-gene-2_4-mRNA-1	YER027C	82.37	0
scaffold1-gene-2_42-mRNA-1	YER061C	81.42	0
scaffold1-gene-2_43-mRNA-1	YIL053W	85.03	0
scaffold1-gene-2_45-mRNA-1	YER064C	77.2	0
scaffold1-gene-2_46-mRNA-1	YER065C	83.87	0
scaffold1-gene-2_47-mRNA-1	YER017C	82.56	0
scaffold1-gene-2_48-mRNA-1	YER019W	80	0
scaffold1-gene-2_50-mRNA-1	YER020W	82.25	0
scaffold1-gene-2_51-mRNA-1	YER021W	83.7	0
scaffold1-gene-2_8-mRNA-1	YER031C	87.54	0
scaffold1-gene-2_80-mRNA-1	YER039C	80.37	3.00E-134
scaffold1-gene-3_0-mRNA-1	YER071C	76.63	1.00E-46
scaffold1-gene-3_1-mRNA-1	YER072W	87.76	3.00E-128
scaffold1-gene-3_10-mRNA-1	YER082C	83.66	0
scaffold1-gene-3_116-mRNA-1	YER102W	93.55	0
scaffold1-gene-3_12-mRNA-1	YER086W	86.69	0
scaffold1-gene-3_127-mRNA-1	YER083C	78.77	2.00E-157

scaffold1-gene-3_13-mRNA-1	YER087W	79.52	0
scaffold1-gene-3_139-mRNA-1	YER074W	97.54	0
scaffold1-gene-3_17-mRNA-1	YER090W	84.08	0
scaffold1-gene-3_18-mRNA-1	YER091C	90.54	0
scaffold1-gene-3_2-mRNA-1	YER073W	83.9	0
scaffold1-gene-3_22-mRNA-1	YER095W	82.6	0
scaffold1-gene-3_24-mRNA-1	YER098W	77.34	0
scaffold1-gene-3_29-mRNA-1	YER103W	83.63	0
scaffold1-gene-3_31-mRNA-1	YER105C	76.33	0
scaffold1-gene-3_33-mRNA-1	YER107C	85.77	0
scaffold1-gene-3_34-mRNA-1	YER109C	74.93	0
scaffold1-gene-3_35-mRNA-1	YER110C	85.99	0
scaffold1-gene-3_36-mRNA-1	YER111C	81.98	0
scaffold1-gene-3_4-mRNA-1	YER075C	79.76	0
scaffold1-gene-3_42-mRNA-1	YER069W	81.18	0
scaffold1-gene-3_43-mRNA-1	YER070W	85.86	0
scaffold1-gene-3_5-mRNA-1	YER077C	77.05	0
scaffold1-gene-3_65-mRNA-1	YER078C	83.41	0
scaffold1-gene-3_7-mRNA-1	YER079W	78.98	2.00E-116
scaffold1-gene-3_8-mRNA-1	YER080W	80.57	0
scaffold1-gene-3_9-mRNA-1	YER081W	86.9	0
scaffold1-gene-4_0-mRNA-1	YER122C	80.07	0
scaffold1-gene-4_1-mRNA-1	YER123W	85.11	0
scaffold1-gene-4_10-mRNA-1	YER132C	77.93	0
scaffold1-gene-4_10-mRNA-1	YER132C	79.63	1.00E-166
scaffold1-gene-4_114-mRNA-1	YER151C	81.59	0
scaffold1-gene-4_124-mRNA-1	YER152C	81.01	1.00E-91
scaffold1-gene-4_137-mRNA-1	YER117W	94.64	8.00E-165
scaffold1-gene-4_137-mRNA-1	YER117W	95.92	3.00E-15
scaffold1-gene-4_138-mRNA-1	YER133W	90.73	0
scaffold1-gene-4_138-mRNA-1	YER133W	92.93	4.00E-71
scaffold1-gene-4_14-mRNA-1	YER136W	87.82	0
scaffold1-gene-4_17-mRNA-1	YER139C	83.5	0
scaffold1-gene-4_19-mRNA-1	YER141W	84.05	0
scaffold1-gene-4_20-mRNA-1	YER142C	81	0
scaffold1-gene-4_23-mRNA-1	YER145C	84.98	0
scaffold1-gene-4_25-mRNA-1	YER147C	78.1	0
scaffold1-gene-4_26-mRNA-1	YER148W	88.4	0
scaffold1-gene-4_3-mRNA-1	YER125W	86.42	0
scaffold1-gene-4_30-mRNA-1	YER152C	79.31	0
scaffold1-gene-4_32-mRNA-1	YER154W	81.97	0
scaffold1-gene-4_33-mRNA-1	YER155C	79.65	0
scaffold1-gene-4_36-mRNA-1	YER158C	78.96	2.00E-175

scaffold1-gene-4_38-mRNA-1	YER114C	78.49	0
scaffold1-gene-4_4-mRNA-1	YER126C	88.71	0
scaffold1-gene-4_42-mRNA-1	YER118C	83.2	0
scaffold1-gene-4_44-mRNA-1	YER120W	83.58	0
scaffold1-gene-4_5-mRNA-1	YER127W	80.47	0
scaffold1-gene-4_7-mRNA-1	YER129W	79.05	0
scaffold1-gene-4_9-mRNA-1	YER131W	91.97	2.00E-143
scaffold1-gene-5_0-mRNA-1	YER164W	82.51	0
scaffold1-gene-5_1-mRNA-1	YER165W	92.17	0
scaffold1-gene-5_19-mRNA-1	YER183C	83.36	7.00E-166
scaffold1-gene-5_2-mRNA-1	YER166W	82.96	0
scaffold1-gene-5_20-mRNA-1	YGL256W	87.34	0
scaffold1-gene-5_3-mRNA-1	YER167W	79.55	0
scaffold1-gene-5_32-mRNA-1	YER178W	87.33	0
scaffold1-gene-5_34-mRNA-1	YER175C	79.31	8.00E-169
scaffold1-gene-5_5-mRNA-1	YER169W	81.76	0
scaffold1-gene-5_7-mRNA-1	YER171W	86.34	0
scaffold1-gene-5_8-mRNA-1	YER172C	78.88	0
scaffold1-gene-5_9-mRNA-1	YER173W	76.79	0
scaffold10-gene-0_11-mRNA-1	YJL201W	82.05	0
scaffold10-gene-0_115-mRNA-1	YCR031C	94.63	0
scaffold10-gene-0_116-mRNA-1	YJL177W	94.84	7.00E-137
scaffold10-gene-0_116-mRNA-1	YJL177W	91.87	1.00E-94
scaffold10-gene-0_12-mRNA-1	YJL200C	85.6	0
scaffold10-gene-0_121-mRNA-1	YJL189W	93.75	4.00E-70
scaffold10-gene-0_13-mRNA-1	YJL198W	81.38	0
scaffold10-gene-0_17-mRNA-1	YJL193W	80.02	0
scaffold10-gene-0_18-mRNA-1	YJL192C	83.25	8.00E-161
scaffold10-gene-0_20-mRNA-1	YJL190C	95.67	0
scaffold10-gene-0_22-mRNA-1	YJL186W	79.21	0
scaffold10-gene-0_27-mRNA-1	YJL180C	79.77	0
scaffold10-gene-0_28-mRNA-1	YJL179W	85.45	6.00E-94
scaffold10-gene-0_29-mRNA-1	YJL178C	77.91	5.00E-133
scaffold10-gene-0_3-mRNA-1	YJL212C	85.19	0
scaffold10-gene-0_31-mRNA-1	YJL176C	79.65	0
scaffold10-gene-0_34-mRNA-1	YJL172W	83.92	0
scaffold10-gene-0_37-mRNA-1	YJL168C	81.24	0
scaffold10-gene-0_62-mRNA-1	YJL209W	79.79	0
scaffold10-gene-1_11-mRNA-1	YJL148W	80	2.00E-131
scaffold10-gene-1_12-mRNA-1	YJL147C	74.16	2.00E-119
scaffold10-gene-1_13-mRNA-1	YJL146W	79.86	0
scaffold10-gene-1_135-mRNA-1	YJL138C	94.61	0
scaffold10-gene-1_16-mRNA-1	YJL141C	82.04	0

scaffold10-gene-1_17-mRNA-1	YJL140W	84.51	0
scaffold10-gene-1_2-mRNA-1	YJL159W	81.91	0
scaffold10-gene-1_2-mRNA-1	YJL159W	80.18	8.00E-168
scaffold10-gene-1_2-mRNA-1	YJL159W	89.58	5.00E-90
scaffold10-gene-1_2-mRNA-1	YJL159W	83.43	7.00E-79
scaffold10-gene-1_2-mRNA-1	YJL159W	79.41	3.00E-67
scaffold10-gene-1_22-mRNA-1	YJL133C-A	82.74	8.00E-52
scaffold10-gene-1_23-mRNA-1	YJL133W	85.79	0
scaffold10-gene-1_24-mRNA-1	YJL132W	76.13	0
scaffold10-gene-1_25-mRNA-1	YJL131C	80.91	0
scaffold10-gene-1_26-mRNA-1	YJL130C	86.92	0
scaffold10-gene-1_28-mRNA-1	YJL128C	82.42	0
scaffold10-gene-1_31-mRNA-1	YJL125C	83.05	0
scaffold10-gene-1_36-mRNA-1	YJL117W	82.18	0
scaffold10-gene-1_41-mRNA-1	YJL165C	81	0
scaffold10-gene-1_42-mRNA-1	YJL164C	84.89	0
scaffold10-gene-1_44-mRNA-1	YJL162C	79.65	3.00E-133
scaffold10-gene-1_6-mRNA-1	YJL155C	82.91	0
scaffold10-gene-1_62-mRNA-1	YJL145W	79.6	1.00E-174
scaffold10-gene-1_7-mRNA-1	YJL154C	81.25	0
scaffold10-gene-1_72-mRNA-1	YJL129C	78.34	0
scaffold10-gene-1_82-mRNA-1	YJL167W	86.41	0
scaffold10-gene-2_0-mRNA-1	YJL106W	83.28	0
scaffold10-gene-2_1-mRNA-1	YJL105W	77.58	0
scaffold10-gene-2_10-mRNA-1	YJL095W	82.47	0
scaffold10-gene-2_110-mRNA-1	YJL079C	81.52	1.00E-113
scaffold10-gene-2_13-mRNA-1	YJL092W	79.9	0
scaffold10-gene-2_16-mRNA-1	YJL089W	81.65	6.00E-68
scaffold10-gene-2_18-mRNA-1	YJL087C	79.64	0
scaffold10-gene-2_19-mRNA-1	YJL085W	82.88	0
scaffold10-gene-2_2-mRNA-1	YJL104W	85.71	3.00E-133
scaffold10-gene-2_20-mRNA-1	YJL084C	79.41	0
scaffold10-gene-2_21-mRNA-1	YJL083W	74.5	0
scaffold10-gene-2_22-mRNA-1	YJL082W	83.75	0
scaffold10-gene-2_24-mRNA-1	YJL080C	84.03	0
scaffold10-gene-2_30-mRNA-1	YJL072C	84.02	3.00E-175
scaffold10-gene-2_31-mRNA-1	YJL071W	79.6	0
scaffold10-gene-2_32-mRNA-1	YJL112W	78.82	0
scaffold10-gene-2_33-mRNA-1	YJL111W	87.24	0
scaffold10-gene-2_35-mRNA-1	YJL109C	80.63	0
scaffold10-gene-2_36-mRNA-1	YJL108C	84.11	0
scaffold10-gene-2_5-mRNA-1	YJL101C	81.9	0
scaffold10-gene-2_60-mRNA-1	YJL090C	77.66	0

scaffold10-gene-2_7-mRNA-1	YJL099W	77.55	0
scaffold10-gene-2_8-mRNA-1	YJL098W	76.54	0
scaffold10-gene-3_1-mRNA-1	YJL060W	83.87	0
scaffold10-gene-3_10-mRNA-1	YJL051W	78.9	0
scaffold10-gene-3_11-mRNA-1	YJL050W	85.17	0
scaffold10-gene-3_115-mRNA-1	YJL041W	77.1	0
scaffold10-gene-3_133-mRNA-1	YJL065C	79.8	1.00E-93
scaffold10-gene-3_2-mRNA-1	YJL059W	81.94	0
scaffold10-gene-3_20-mRNA-1	YJL039C	81.23	0
scaffold10-gene-3_24-mRNA-1	YJL036W	85.21	0
scaffold10-gene-3_26-mRNA-1	YJL034W	88.29	0
scaffold10-gene-3_27-mRNA-1	YJL033W	84.01	0
scaffold10-gene-3_29-mRNA-1	YJL030W	84.43	1.00E-162
scaffold10-gene-3_3-mRNA-1	YJL058C	79.21	0
scaffold10-gene-3_31-mRNA-1	YJL026W	87.37	0
scaffold10-gene-3_34-mRNA-1	YJL019W	77.54	0
scaffold10-gene-3_36-mRNA-1	YJL014W	88.05	0
scaffold10-gene-3_37-mRNA-1	YJL070C	80.43	0
scaffold10-gene-3_39-mRNA-1	YJL068C	81.28	0
scaffold10-gene-3_42-mRNA-1	YJL062W-A	88.24	8.00E-82
scaffold10-gene-3_43-mRNA-1	YJL062W	80.4	0
scaffold10-gene-3_7-mRNA-1	YJL054W	76.17	0
scaffold10-gene-3_9-mRNA-1	YJL052W	91.8	0
scaffold10-gene-3_95-mRNA-1	YJL042W	77.6	0
scaffold10-gene-4_0-mRNA-1	YJL008C	86.86	0
scaffold10-gene-4_10-mRNA-1	YJR004C	80.7	0
scaffold10-gene-4_136-mRNA-1	YJR021C	77.84	1.00E-70
scaffold10-gene-4_136-mRNA-1	YJR021C	80.52	1.00E-60
scaffold10-gene-4_14-mRNA-1	YJR007W	89.53	0
scaffold10-gene-4_15-mRNA-1	YJR008W	82.67	0
scaffold10-gene-4_16-mRNA-1	YJR010W	84.92	0
scaffold10-gene-4_17-mRNA-1	YJR011C	79.38	7.00E-152
scaffold10-gene-4_2-mRNA-1	YJL005W	82.27	0
scaffold10-gene-4_27-mRNA-1	YJR024C	84.12	0
scaffold10-gene-4_32-mRNA-1	YJR033C	81.67	0
scaffold10-gene-4_35-mRNA-1	YJR036C	78.67	0
scaffold10-gene-4_37-mRNA-1	YJR040W	82.95	0
scaffold10-gene-4_39-mRNA-1	YJR042W	81.44	0
scaffold10-gene-4_42-mRNA-1	YJL012C	87.03	0
scaffold10-gene-4_44-mRNA-1	YJL010C	83.02	0
scaffold10-gene-4_6-mRNA-1	YJL001W	85.96	4.00E-178
scaffold10-gene-4_6-mRNA-1	YJL001W	95.71	1.00E-24
scaffold10-gene-5_0-mRNA-1	YJR050W	77.82	5.00E-118

scaffold10-gene-5_10-mRNA-1	YJR059W	83.98	0
scaffold10-gene-5_119-mRNA-1	YJR075W	81.34	0
scaffold10-gene-5_12-mRNA-1	YJR061W	75.69	0
scaffold10-gene-5_13-mRNA-1	YJR062C	77	0
scaffold10-gene-5_15-mRNA-1	YJR064W	87.88	0
scaffold10-gene-5_16-mRNA-1	YJR065C	86.32	0
scaffold10-gene-5_17-mRNA-1	YJR066W	82.96	0
scaffold10-gene-5_19-mRNA-1	YJR068W	82.34	0
scaffold10-gene-5_2-mRNA-1	YJR052W	79.21	0
scaffold10-gene-5_20-mRNA-1	YJR069C	82.97	7.00E-151
scaffold10-gene-5_21-mRNA-1	YJR070C	87.7	0
scaffold10-gene-5_22-mRNA-1	YJR072C	84.02	0
scaffold10-gene-5_26-mRNA-1	YJR076C	84.94	0
scaffold10-gene-5_27-mRNA-1	YJR077C	87.06	0
scaffold10-gene-5_29-mRNA-1	YJR080C	79.1	0
scaffold10-gene-5_35-mRNA-1	YJR088C	81.69	0
scaffold10-gene-5_37-mRNA-1	YJR090C	83.44	0
scaffold10-gene-5_38-mRNA-1	YJR091C	81.28	0
scaffold10-gene-5_4-mRNA-1	YJR054W	81.15	0
scaffold10-gene-5_40-mRNA-1	YJR093C	78.2	1.00E-170
scaffold10-gene-5_42-mRNA-1	YJR094W-A	92.78	1.00E-111
scaffold10-gene-5_43-mRNA-1	YJR095W	84.21	0
scaffold10-gene-5_48-mRNA-1	YJR045C	88.31	0
scaffold10-gene-5_49-mRNA-1	YJR046W	78.63	0
scaffold10-gene-5_50-mRNA-1	YJR047C	91.16	0
scaffold10-gene-6_10-mRNA-1	YJR118C	81.43	2.00E-125
scaffold10-gene-6_11-mRNA-1	YJR119C	77.74	0
scaffold10-gene-6_12-mRNA-1	YJR121W	91.36	0
scaffold10-gene-6_14-mRNA-1	YJR123W	97.79	0
scaffold10-gene-6_146-mRNA-1	YJR112W-A	83.8	1.00E-70
scaffold10-gene-6_15-mRNA-1	YJR124C	83.36	0
scaffold10-gene-6_18-mRNA-1	YJR127C	82.32	5.00E-120
scaffold10-gene-6_2-mRNA-1	YJR109C	84.48	0
scaffold10-gene-6_20-mRNA-1	YJR130C	81.93	0
scaffold10-gene-6_22-mRNA-1	YJR132W	81.97	0
scaffold10-gene-6_23-mRNA-1	YJR133W	84.25	9.00E-175
scaffold10-gene-6_27-mRNA-1	YJR136C	77.55	0
scaffold10-gene-6_28-mRNA-1	YJR137C	84.26	0
scaffold10-gene-6_29-mRNA-1	YJR138W	81.19	0
scaffold10-gene-6_3-mRNA-1	YJR110W	81.08	0
scaffold10-gene-6_30-mRNA-1	YJR139C	86.97	0
scaffold10-gene-6_34-mRNA-1	YJR143C	82.82	0
scaffold10-gene-6_36-mRNA-1	YHR203C	95.21	0

scaffold10-gene-6_39-mRNA-1	YAL067C	84.36	0
scaffold10-gene-6_4-mRNA-1	YJR111C	84.15	0
scaffold10-gene-6_45-mRNA-1	YJR104C	84.62	7.00E-130
scaffold10-gene-6_46-mRNA-1	YJR105W	85.77	0
scaffold10-gene-6_9-mRNA-1	YJR117W	86.15	0
scaffold10-gene-6_90-mRNA-1	YJR107W	82.57	0
scaffold10-gene-7_11-mRNA-1	YJR152W	83.21	0
scaffold10-gene-7_29-mRNA-1	YNR072W	82.55	0
scaffold10-gene-7_3-mRNA-1	YHR210C	75.29	6.00E-119
scaffold10-gene-7_7-mRNA-1	YLL025W	79.94	2.00E-59
scaffold11-gene-0_0-mRNA-1	YIL169C	77.09	0
scaffold11-gene-0_10-mRNA-1	YBR289W	84.06	3.00E-110
scaffold11-gene-0_11-mRNA-1	YBR288C	80.34	0
scaffold11-gene-0_12-mRNA-1	YBR287W	82.34	0
scaffold11-gene-0_132-mRNA-1	YBR275C	77.81	0
scaffold11-gene-0_16-mRNA-1	YBR283C	84.5	0
scaffold11-gene-0_17-mRNA-1	YBR282W	82.85	3.00E-108
scaffold11-gene-0_18-mRNA-1	YBR281C	83.05	0
scaffold11-gene-0_23-mRNA-1	YBR274W	82.39	0
scaffold11-gene-0_3-mRNA-1	YFL054C	81.28	0
scaffold11-gene-0_30-mRNA-1	YBR267W	82.17	0
scaffold11-gene-0_32-mRNA-1	YBR263W	87.67	0
scaffold11-gene-0_35-mRNA-1	YBR260C	82.37	0
scaffold11-gene-0_4-mRNA-1	YBR296C	82.58	0
scaffold11-gene-0_41-mRNA-1	YBR255W	79.17	0
scaffold11-gene-0_42-mRNA-1	YBR254C	82.81	1.00E-123
scaffold11-gene-0_5-mRNA-1	YBR294W	80.67	0
scaffold11-gene-0_6-mRNA-1	YBR293W	80.06	0
scaffold11-gene-0_9-mRNA-1	YBR290W	81.94	0
scaffold11-gene-1_10-mRNA-1	YBR234C	83.8	0
scaffold11-gene-1_120-mRNA-1	YBR239C	81.63	0
scaffold11-gene-1_137-mRNA-1	YBR215W	76.3	0
scaffold11-gene-1_15-mRNA-1	YBR229C	78.14	0
scaffold11-gene-1_18-mRNA-1	YBR225W	78.29	0
scaffold11-gene-1_2-mRNA-1	YBR242W	80.84	5.00E-148
scaffold11-gene-1_21-mRNA-1	YBR221C	86.76	0
scaffold11-gene-1_22-mRNA-1	YBR220C	79.89	0
scaffold11-gene-1_23-mRNA-1	YBR218C	85.11	0
scaffold11-gene-1_27-mRNA-1	YBR214W	82.49	0
scaffold11-gene-1_29-mRNA-1	YBR212W	79.09	0
scaffold11-gene-1_3-mRNA-1	YBR241C	81.06	0
scaffold11-gene-1_31-mRNA-1	YBR208C	82.97	0
scaffold11-gene-1_32-mRNA-1	YBR207W	81.99	0

scaffold11-gene-1_33-mRNA-1	YBR205W	83.06	0
scaffold11-gene-1_34-mRNA-1	YBR204C	78.51	0
scaffold11-gene-1_36-mRNA-1	YBR202W	83.8	0
scaffold11-gene-1_38-mRNA-1	YBR200W	82.42	0
scaffold11-gene-1_4-mRNA-1	YBR240C	79.88	0
scaffold11-gene-1_40-mRNA-1	YBR249C	89.73	0
scaffold11-gene-1_41-mRNA-1	YBR248C	82.1	0
scaffold11-gene-1_44-mRNA-1	YBR245C	84.31	0
scaffold11-gene-1_6-mRNA-1	YBR238C	86.56	0
scaffold11-gene-1_6-mRNA-1	YBR238C	82.71	3.00E-65
scaffold11-gene-1_9-mRNA-1	YBR235W	81.23	0
scaffold11-gene-2_0-mRNA-1	YBR192W	85.52	0
scaffold11-gene-2_11-mRNA-1	YBR179C	81.43	0
scaffold11-gene-2_159-mRNA-1	YPL090C	97.45	0
scaffold11-gene-2_16-mRNA-1	YBR172C	74.31	0
scaffold11-gene-2_161-mRNA-1	YBR191W	95.97	0
scaffold11-gene-2_17-mRNA-1	YBR171W	87.18	0
scaffold11-gene-2_18-mRNA-1	YBR170C	82.14	0
scaffold11-gene-2_19-mRNA-1	YBR169C	81.4	0
scaffold11-gene-2_2-mRNA-1	YBR189W	92.06	3.00E-81
scaffold11-gene-2_22-mRNA-1	YBR166C	83.05	0
scaffold11-gene-2_24-mRNA-1	YBR164C	86.18	3.00E-169
scaffold11-gene-2_25-mRNA-1	YBR163W	77.04	0
scaffold11-gene-2_29-mRNA-1	YBR160W	86.24	0
scaffold11-gene-2_30-mRNA-1	YBR159W	82.83	0
scaffold11-gene-2_31-mRNA-1	YBR158W	80.52	0
scaffold11-gene-2_34-mRNA-1	YBR155W	81.2	0
scaffold11-gene-2_35-mRNA-1	YBR154C	89.06	0
scaffold11-gene-2_40-mRNA-1	YBR149W	83.54	0
scaffold11-gene-2_42-mRNA-1	YBR147W	81.31	5.00E-174
scaffold11-gene-2_43-mRNA-1	YBR146W	84.86	0
scaffold11-gene-2_45-mRNA-1	YBR143C	87.31	0
scaffold11-gene-2_48-mRNA-1	YBR198C	83.2	0
scaffold11-gene-2_50-mRNA-1	YBR196C	91	0
scaffold11-gene-2_51-mRNA-1	YBR195C	83.8	0
scaffold11-gene-2_56-mRNA-1	YBR187W	82.97	0
scaffold11-gene-3_10-mRNA-1	YBR125C	83.12	0
scaffold11-gene-3_11-mRNA-1	YBR123C	82.67	0
scaffold11-gene-3_125-mRNA-1	YBR121C	87.19	0
scaffold11-gene-3_144-mRNA-1	YBR093C	83.96	0
scaffold11-gene-3_150-mRNA-1	YBR111W-A	85.61	2.00E-35
scaffold11-gene-3_16-mRNA-1	YBR115C	82.64	0
scaffold11-gene-3_17-mRNA-1	YBR114W	82.6	0

scaffold11-gene-3_18-mRNA-1	YBR112C	83.72	0
scaffold11-gene-3_19-mRNA-1	YBR111C	84.66	0
scaffold11-gene-3_2-mRNA-1	YBR132C	82.08	0
scaffold11-gene-3_24-mRNA-1	YBR106W	87.61	0
scaffold11-gene-3_26-mRNA-1	YBR104W	84.48	0
scaffold11-gene-3_28-mRNA-1	YBR102C	82.14	0
scaffold11-gene-3_31-mRNA-1	YBR097W	79.55	0
scaffold11-gene-3_33-mRNA-1	YBR095C	78.72	0
scaffold11-gene-3_34-mRNA-1	YBR094W	81.93	0
scaffold11-gene-3_4-mRNA-1	YBR130C	78.65	0
scaffold11-gene-3_42-mRNA-1	YBR140C	80.74	0
scaffold11-gene-3_42-mRNA-1	YBR140C	80.53	0
scaffold11-gene-3_43-mRNA-1	YBR139W	82.44	0
scaffold11-gene-3_46-mRNA-1	YBR136W	82.17	0
scaffold11-gene-3_62-mRNA-1	YBR127C	89.42	0
scaffold11-gene-3_75-mRNA-1	YBR118W	96.15	0
scaffold11-gene-3_9-mRNA-1	YBR126C	85.79	0
scaffold11-gene-4_0-mRNA-1	YBR082C	91.54	4.00E-158
scaffold11-gene-4_127-mRNA-1	YBR078W	85.89	0
scaffold11-gene-4_128-mRNA-1	YBR048W	95.09	0
scaffold11-gene-4_130-mRNA-1	YBR069C	83.69	0
scaffold11-gene-4_14-mRNA-1	YBR067C	79.07	9.00E-115
scaffold11-gene-4_19-mRNA-1	YDR037W	88.64	0
scaffold11-gene-4_21-mRNA-1	YBR059C	80.29	0
scaffold11-gene-4_22-mRNA-1	YBR058C	79.07	0
scaffold11-gene-4_24-mRNA-1	YBR056W	82.56	0
scaffold11-gene-4_25-mRNA-1	YBR055C	75.8	0
scaffold11-gene-4_26-mRNA-1	YBR054W	86.29	0
scaffold11-gene-4_29-mRNA-1	YBR050C	73.43	2.00E-84
scaffold11-gene-4_3-mRNA-1	YBR079C	83.8	0
scaffold11-gene-4_30-mRNA-1	YBR049C	82.39	0
scaffold11-gene-4_32-mRNA-1	YBR047W	81.48	8.00E-115
scaffold11-gene-4_33-mRNA-1	YBR046C	78.86	0
scaffold11-gene-4_39-mRNA-1	YBR084C-A	95.44	0
scaffold11-gene-4_40-mRNA-1	YBR084W	84.32	0
scaffold11-gene-4_41-mRNA-1	YBR083W	79.37	0
scaffold11-gene-4_67-mRNA-1	YBR081C	79.8	0
scaffold11-gene-4_67-mRNA-1	YBR081C	81.15	0
scaffold11-gene-4_7-mRNA-1	YBR074W	76.43	0
scaffold11-gene-4_9-mRNA-1	YBR072W	85.09	0
scaffold11-gene-5_0-mRNA-1	YBR036C	81.54	0
scaffold11-gene-5_103-mRNA-1	YDL028C	81.03	0
scaffold11-gene-5_12-mRNA-1	YDR002W	89.44	0

scaffold11-gene-5_13-mRNA-1	YDR001C	86.2	0
scaffold11-gene-5_15-mRNA-1	YDL002C	86.34	0
scaffold11-gene-5_18-mRNA-1	YDL005C	79.78	5.00E-85
scaffold11-gene-5_19-mRNA-1	YDL006W	86.37	0
scaffold11-gene-5_20-mRNA-1	YDL007W	87.46	0
scaffold11-gene-5_23-mRNA-1	YDL010W	79.13	5.00E-133
scaffold11-gene-5_26-mRNA-1	YDL014W	88.24	0
scaffold11-gene-5_31-mRNA-1	YDL019C	80.43	0
scaffold11-gene-5_34-mRNA-1	YDL022W	88.01	0
scaffold11-gene-5_4-mRNA-1	YBR031W	94.05	0
scaffold11-gene-5_41-mRNA-1	YBR041W	83.45	0
scaffold11-gene-5_43-mRNA-1	YBR039W	87.97	0
scaffold11-gene-5_44-mRNA-1	YBR038W	84.74	0
scaffold11-gene-5_45-mRNA-1	YBR037C	81	0
scaffold11-gene-5_5-mRNA-1	YDR011W	84	0
scaffold11-gene-5_7-mRNA-1	YDR007W	77.62	6.00E-97
scaffold11-gene-5_8-mRNA-1	YDR006C	82.72	0
scaffold11-gene-5_89-mRNA-1	YBR043C	81.58	0
scaffold11-gene-6_0-mRNA-1	YDL036C	78.73	0
scaffold11-gene-6_10-mRNA-1	YDL048C	79.37	0
scaffold11-gene-6_11-mRNA-1	YDL049C	80.37	7.00E-167
scaffold11-gene-6_113-mRNA-1	YDL067C	88.46	6.00E-57
scaffold11-gene-6_12-mRNA-1	YDL051W	84.48	0
scaffold11-gene-6_154-mRNA-1	YDL083C	94.61	0
scaffold11-gene-6_155-mRNA-1	YDL029W	86.59	0
scaffold11-gene-6_156-mRNA-1	YDL064W	88.99	2.00E-156
scaffold11-gene-6_157-mRNA-1	YDL075W	96.49	3.00E-133
scaffold11-gene-6_157-mRNA-1	YDL075W	100	4.00E-23
scaffold11-gene-6_16-mRNA-1	YDL055C	89.29	0
scaffold11-gene-6_166-mRNA-1	YMR142C	93.57	0
scaffold11-gene-6_17-mRNA-1	YDL056W	80.92	0
scaffold11-gene-6_19-mRNA-1	YDL058W	75.95	0
scaffold11-gene-6_2-mRNA-1	YDL040C	80.99	0
scaffold11-gene-6_22-mRNA-1	YDL063C	80.14	0
scaffold11-gene-6_25-mRNA-1	YDL066W	86.03	0
scaffold11-gene-6_29-mRNA-1	YDL073W	76.75	0
scaffold11-gene-6_3-mRNA-1	YDL042C	81.15	0
scaffold11-gene-6_30-mRNA-1	YDL074C	81.35	0
scaffold11-gene-6_32-mRNA-1	YDL076C	77.59	1.00E-144
scaffold11-gene-6_33-mRNA-1	YDL077C	79.43	0
scaffold11-gene-6_34-mRNA-1	YDL078C	82.6	0
scaffold11-gene-6_36-mRNA-1	YDL080C	85.14	0
scaffold11-gene-6_37-mRNA-1	YDL081C	91.59	2.00E-124

scaffold11-gene-6_40-mRNA-1	YDL084W	89.5	0
scaffold11-gene-6_41-mRNA-1	YDL085W	80.22	0
scaffold11-gene-6_5-mRNA-1	YDL044C	78.05	0
scaffold11-gene-6_6-mRNA-1	YDL045C	82.63	0
scaffold11-gene-6_61-mRNA-1	YDL070W	84.48	0
scaffold11-gene-6_61-mRNA-1	YDL070W	97.44	7.00E-11
scaffold11-gene-6_77-mRNA-1	YDL087C	82.75	3.00E-169
scaffold11-gene-6_9-mRNA-1	YDL047W	87.3	0
scaffold11-gene-7_0-mRNA-1	YDL097C	84.43	0
scaffold11-gene-7_105-mRNA-1	YDL106C	82.14	0
scaffold11-gene-7_13-mRNA-1	YDL110C	85.65	9.00E-134
scaffold11-gene-7_14-mRNA-1	YDL111C	82.4	0
scaffold11-gene-7_148-mRNA-1	YDL115C	80.35	0
scaffold11-gene-7_151-mRNA-1	YDL108W	84.92	0
scaffold11-gene-7_152-mRNA-1	YDL130W	91.3	2.00E-76
scaffold11-gene-7_152-mRNA-1	YDL130W	96.55	3.00E-49
scaffold11-gene-7_153-mRNA-1	YDL131W	86.32	0
scaffold11-gene-7_17-mRNA-1	YDL114W	77.96	2.00E-147
scaffold11-gene-7_21-mRNA-1	YDL119C	79.87	0
scaffold11-gene-7_24-mRNA-1	YDL122W	80.89	0
scaffold11-gene-7_27-mRNA-1	YDL126C	88.17	0
scaffold11-gene-7_29-mRNA-1	YDL128W	81.66	0
scaffold11-gene-7_3-mRNA-1	YDL100C	86.66	0
scaffold11-gene-7_34-mRNA-1	YDL132W	83.77	0
scaffold11-gene-7_35-mRNA-1	YDL133W	80.21	0
scaffold11-gene-7_37-mRNA-1	YDL135C	86.74	0
scaffold11-gene-7_38-mRNA-1	YDL192W	90.55	0
scaffold11-gene-7_41-mRNA-1	YDL140C	86.8	0
scaffold11-gene-7_41-mRNA-1	YDL140C	87.87	2.00E-179
scaffold11-gene-7_42-mRNA-1	YDL141W	82.27	0
scaffold11-gene-7_45-mRNA-1	YDL091C	79.22	0
scaffold11-gene-7_47-mRNA-1	YDL093W	78.47	0
scaffold11-gene-7_48-mRNA-1	YDL095W	84.48	0
scaffold11-gene-7_54-mRNA-1	YDL116W	80.94	0
scaffold11-gene-7_6-mRNA-1	YDL103C	80.67	0
scaffold11-gene-7_8-mRNA-1	YDL105W	79.1	0
scaffold11-gene-8_1-mRNA-1	YDL149W	79.15	0
scaffold11-gene-8_12-mRNA-1	YDL164C	82	0
scaffold11-gene-8_12-mRNA-1	YDL164C	91.86	6.00E-27
scaffold11-gene-8_127-mRNA-1	YDL199C	79.69	0
scaffold11-gene-8_13-mRNA-1	YDL165W	87.24	0
scaffold11-gene-8_14-mRNA-1	YDL166C	84.16	2.00E-161
scaffold11-gene-8_15-mRNA-1	YDL167C	77.9	0

scaffold11-gene-8_150-mRNA-1	YDL191W	95.24	3.00E-51
scaffold11-gene-8_150-mRNA-1	YDL191W	96	4.00E-40
scaffold11-gene-8_151-mRNA-1	YDL182W	86.03	3.00E-165
scaffold11-gene-8_151-mRNA-1	YDL182W	81.76	1.00E-64
scaffold11-gene-8_16-mRNA-1	YDL168W	84.15	0
scaffold11-gene-8_19-mRNA-1	YDL171C	86.44	0
scaffold11-gene-8_2-mRNA-1	YDL150W	79.48	0
scaffold11-gene-8_22-mRNA-1	YDL176W	80.86	0
scaffold11-gene-8_24-mRNA-1	YDL178W	83.76	0
scaffold11-gene-8_25-mRNA-1	YDL179W	79.25	4.00E-140
scaffold11-gene-8_27-mRNA-1	YDL181W	85.55	2.00E-72
scaffold11-gene-8_29-mRNA-1	YDL183C	79.05	3.00E-176
scaffold11-gene-8_30-mRNA-1	YDL185W	90.86	0
scaffold11-gene-8_30-mRNA-1	YDL185W	90.8	0
scaffold11-gene-8_33-mRNA-1	YDL189W	78.32	0
scaffold11-gene-8_34-mRNA-1	YDL190C	83.06	0
scaffold11-gene-8_36-mRNA-1	YDL192W	93.6	0
scaffold11-gene-8_38-mRNA-1	YDL194W	81.06	0
scaffold11-gene-8_39-mRNA-1	YDL195W	80.51	0
scaffold11-gene-8_41-mRNA-1	YDL198C	85.13	0
scaffold11-gene-8_45-mRNA-1	YDL143W	86.19	0
scaffold11-gene-8_47-mRNA-1	YDL145C	85.33	0
scaffold11-gene-8_48-mRNA-1	YDL146W	80.16	0
scaffold11-gene-8_49-mRNA-1	YDL147W	82.65	0
scaffold11-gene-8_5-mRNA-1	YDL155W	81.17	0
scaffold11-gene-8_7-mRNA-1	YDL157C	86.69	3.00E-102
scaffold11-gene-8_8-mRNA-1	YDL159W	81.87	0
scaffold11-gene-8_9-mRNA-1	YDL160C	87.87	0
scaffold11-gene-9_0-mRNA-1	YDL207W	79.73	0
scaffold11-gene-9_1-mRNA-1	YDL208W	86.84	7.00E-150
scaffold11-gene-9_16-mRNA-1	YDL224C	80.42	0
scaffold11-gene-9_17-mRNA-1	YDL225W	82.6	0
scaffold11-gene-9_18-mRNA-1	YDL226C	81.82	0
scaffold11-gene-9_19-mRNA-1	YDL227C	84.32	0
scaffold11-gene-9_22-mRNA-1	YDL231C	81.26	0
scaffold11-gene-9_23-mRNA-1	YDL233W	78.41	0
scaffold11-gene-9_3-mRNA-1	YDL210W	84.28	0
scaffold11-gene-9_30-mRNA-1	YDL240W	80.92	0
scaffold11-gene-9_34-mRNA-1	YDL201W	85.07	0
scaffold11-gene-9_39-mRNA-1	YDL205C	83.85	0
scaffold11-gene-9_42-mRNA-1	YDL229W	93.5	0
scaffold11-gene-9_42-mRNA-1	YDL229W	97.56	3.00E-33
scaffold11-gene-9_6-mRNA-1	YDL212W	81.62	2.00E-146

scaffold11-gene-9_78-mRNA-1	YDL203C	79.1	0
scaffold11-gene-9_9-mRNA-1	YDL215C	83.48	0
scaffold12-gene-0_10-mRNA-1	YPL265W	84.52	0
scaffold12-gene-0_11-mRNA-1	YPL264C	83.07	0
scaffold12-gene-0_112-mRNA-1	YPL249C-A	96.17	9.00E-132
scaffold12-gene-0_115-mRNA-1	YPL274W	80.95	0
scaffold12-gene-0_12-mRNA-1	YPL263C	82.06	0
scaffold12-gene-0_14-mRNA-1	YPL260W	83.48	0
scaffold12-gene-0_15-mRNA-1	YPL259C	84.66	0
scaffold12-gene-0_16-mRNA-1	YOL055C	80.99	0
scaffold12-gene-0_17-mRNA-1	YPL256C	79.89	0
scaffold12-gene-0_18-mRNA-1	YPL255W	79.55	0
scaffold12-gene-0_19-mRNA-1	YPL254W	81.56	0
scaffold12-gene-0_21-mRNA-1	YPL252C	82.77	5.00E-122
scaffold12-gene-0_22-mRNA-1	YPL250C	80.05	8.00E-79
scaffold12-gene-0_30-mRNA-1	YPL243W	79.85	0
scaffold12-gene-0_31-mRNA-1	YPL242C	79.35	0
scaffold12-gene-0_32-mRNA-1	YPL241C	72.33	2.00E-47
scaffold12-gene-0_33-mRNA-1	YMR186W	88.48	0
scaffold12-gene-0_34-mRNA-1	YPL239W	80.91	2.00E-130
scaffold12-gene-0_35-mRNA-1	YPL237W	89.78	0
scaffold12-gene-0_4-mRNA-1	YPL272C	81.32	0
scaffold12-gene-0_6-mRNA-1	YPL269W	78.51	0
scaffold12-gene-0_7-mRNA-1	YPL268W	79.81	0
scaffold12-gene-0_81-mRNA-1	YPL270W	81.11	0
scaffold12-gene-0_9-mRNA-1	YPL266W	85.18	0
scaffold12-gene-1_13-mRNA-1	YPL217C	82.17	0
scaffold12-gene-1_144-mRNA-1	YPL218W	90.28	0
scaffold12-gene-1_145-mRNA-1	YGL076C	93.62	0
scaffold12-gene-1_16-mRNA-1	YPL214C	82.45	0
scaffold12-gene-1_18-mRNA-1	YPL212C	84.32	0
scaffold12-gene-1_19-mRNA-1	YPL211W	88.87	0
scaffold12-gene-1_2-mRNA-1	YPL228W	84.22	0
scaffold12-gene-1_21-mRNA-1	YPL209C	82.31	0
scaffold12-gene-1_23-mRNA-1	YPL207W	82.11	0
scaffold12-gene-1_24-mRNA-1	YPL206C	79.64	0
scaffold12-gene-1_25-mRNA-1	YPL204W	85.19	0
scaffold12-gene-1_27-mRNA-1	YPL201C	76.13	2.00E-155
scaffold12-gene-1_3-mRNA-1	YPL227C	81.49	0
scaffold12-gene-1_35-mRNA-1	YPL191C	76.73	2.00E-118
scaffold12-gene-1_38-mRNA-1	YPL188W	84.15	0
scaffold12-gene-1_4-mRNA-1	YPL226W	86.27	0
scaffold12-gene-1_41-mRNA-1	YPL184C	82.58	0

scaffold12-gene-1_43-mRNA-1	YPL235W	86.21	0
scaffold12-gene-1_44-mRNA-1	YPL234C	92.14	0
scaffold12-gene-1_45-mRNA-1	YPL233W	80.18	4.00E-133
scaffold12-gene-1_47-mRNA-1	YPL231W	86.87	0
scaffold12-gene-2_1-mRNA-1	YPL175W	84.19	0
scaffold12-gene-2_12-mRNA-1	YPL164C	75.66	0
scaffold12-gene-2_14-mRNA-1	YPL162C	80.07	2.00E-167
scaffold12-gene-2_16-mRNA-1	YPL160W	85.35	0
scaffold12-gene-2_22-mRNA-1	YPL154C	85	0
scaffold12-gene-2_23-mRNA-1	YPL153C	82.98	0
scaffold12-gene-2_26-mRNA-1	YPL150W	82.41	0
scaffold12-gene-2_26-mRNA-1	YPL150W	80.72	0
scaffold12-gene-2_29-mRNA-1	YPL147W	81.54	0
scaffold12-gene-2_30-mRNA-1	YPL146C	80.9	0
scaffold12-gene-2_31-mRNA-1	YPL145C	86.3	0
scaffold12-gene-2_33-mRNA-1	YPL141C	80.59	0
scaffold12-gene-2_35-mRNA-1	YPL139C	77.36	0
scaffold12-gene-2_39-mRNA-1	YPL134C	83.59	0
scaffold12-gene-2_4-mRNA-1	YPL172C	81.97	0
scaffold12-gene-2_41-mRNA-1	YPL132W	86.07	0
scaffold12-gene-2_44-mRNA-1	YPL179W	83.69	0
scaffold12-gene-2_45-mRNA-1	YPL178W	87.58	0
scaffold12-gene-2_7-mRNA-1	YPL169C	82.08	0
scaffold12-gene-2_9-mRNA-1	YPL167C	78.99	0
scaffold12-gene-3_1-mRNA-1	YPL123C	81.64	0
scaffold12-gene-3_10-mRNA-1	YPL113C	77.87	0
scaffold12-gene-3_105-mRNA-1	YPL091W	85.26	0
scaffold12-gene-3_11-mRNA-1	YPL112C	80.58	0
scaffold12-gene-3_11-mRNA-1	YPL112C	90.16	8.00E-14
scaffold12-gene-3_12-mRNA-1	YPL111W	82.11	0
scaffold12-gene-3_13-mRNA-1	YPL110C	79.6	0
scaffold12-gene-3_14-mRNA-1	YPL109C	81.93	0
scaffold12-gene-3_143-mRNA-1	YPL090C	97.45	0
scaffold12-gene-3_17-mRNA-1	YPL106C	87.77	0
scaffold12-gene-3_18-mRNA-1	YPL105C	78.15	0
scaffold12-gene-3_28-mRNA-1	YPL094C	84.35	0
scaffold12-gene-3_29-mRNA-1	YPL093W	89.01	0
scaffold12-gene-3_30-mRNA-1	YPL092W	78.51	0
scaffold12-gene-3_36-mRNA-1	YPL086C	87.79	0
scaffold12-gene-3_40-mRNA-1	YPL082C	83.19	0
scaffold12-gene-3_41-mRNA-1	YPL131W	94.94	0
scaffold12-gene-3_42-mRNA-1	YPL129W	85.09	0
scaffold12-gene-3_44-mRNA-1	YPL127C	78.76	3.00E-141

scaffold12-gene-3_45-mRNA-1	YPL126W	81.2	0
scaffold12-gene-3_46-mRNA-1	YPL125W	83.66	0
scaffold12-gene-3_5-mRNA-1	YOR204W	76.88	0
scaffold12-gene-3_6-mRNA-1	YPL118W	84.66	0
scaffold12-gene-3_8-mRNA-1	YPL116W	83.95	0
scaffold12-gene-3_9-mRNA-1	YPL115C	78.21	0
scaffold12-gene-4_0-mRNA-1	YPL074W	81.51	0
scaffold12-gene-4_118-mRNA-1	YPL061W	88.73	0
scaffold12-gene-4_125-mRNA-1	YPL038W	79.12	6.00E-91
scaffold12-gene-4_13-mRNA-1	YPL058C	85.53	0
scaffold12-gene-4_156-mRNA-1	YBR189W	94.15	0
scaffold12-gene-4_157-mRNA-1	YPL079W	96.19	0
scaffold12-gene-4_19-mRNA-1	YPL051W	88.76	0
scaffold12-gene-4_22-mRNA-1	YPL048W	78.33	0
scaffold12-gene-4_24-mRNA-1	YPL046C	82.83	2.00E-68
scaffold12-gene-4_26-mRNA-1	YPL043W	82.47	0
scaffold12-gene-4_27-mRNA-1	YPL042C	84.54	0
scaffold12-gene-4_3-mRNA-1	YPL070W	82.21	0
scaffold12-gene-4_30-mRNA-1	YPL039W	77.3	7.00E-133
scaffold12-gene-4_32-mRNA-1	YPL037C	92	0
scaffold12-gene-4_33-mRNA-1	YGL008C	85.92	0
scaffold12-gene-4_37-mRNA-1	YPL031C	83.41	0
scaffold12-gene-4_39-mRNA-1	YPL029W	79.95	0
scaffold12-gene-4_4-mRNA-1	YPL069C	81.82	0
scaffold12-gene-4_40-mRNA-1	YPL028W	87.12	0
scaffold12-gene-4_42-mRNA-1	YPL026C	85.67	5.00E-86
scaffold12-gene-4_43-mRNA-1	YPL024W	81.78	1.00E-169
scaffold12-gene-4_44-mRNA-1	YPL023C	83.07	0
scaffold12-gene-4_45-mRNA-1	YPL022W	80.61	0
scaffold12-gene-4_51-mRNA-1	YPL075W	81.37	0
scaffold12-gene-5_0-mRNA-1	YPL015C	81.4	0
scaffold12-gene-5_104-mRNA-1	YPR008W	84.1	0
scaffold12-gene-5_11-mRNA-1	YPL004C	84.77	0
scaffold12-gene-5_13-mRNA-1	YPL002C	83.9	0
scaffold12-gene-5_15-mRNA-1	YPR001W	80.2	0
scaffold12-gene-5_16-mRNA-1	YPR002W	81.04	0
scaffold12-gene-5_17-mRNA-1	YPR003C	81.88	0
scaffold12-gene-5_23-mRNA-1	YPR010C	87.4	0
scaffold12-gene-5_25-mRNA-1	YPR015C	81.27	5.00E-168
scaffold12-gene-5_26-mRNA-1	YPR016C	90.27	0
scaffold12-gene-5_29-mRNA-1	YPR019W	84.79	0
scaffold12-gene-5_3-mRNA-1	YPL012W	82.35	0
scaffold12-gene-5_31-mRNA-1	YPR021C	82.06	0

scaffold12-gene-5_33-mRNA-1	YPL019C	81.07	0
scaffold12-gene-5_36-mRNA-1	YPL016W	78.87	0
scaffold12-gene-5_6-mRNA-1	YPL009C	80.41	0
scaffold12-gene-5_85-mRNA-1	YPR009W	79.01	5.00E-148
scaffold12-gene-5_9-mRNA-1	YPL006W	81.91	0
scaffold12-gene-6_10-mRNA-1	YPR036W	84.98	0
scaffold12-gene-6_14-mRNA-1	YPR041W	87.01	0
scaffold12-gene-6_149-mRNA-1	YPR026W	82.66	0
scaffold12-gene-6_15-mRNA-1	YPR042C	78.24	0
scaffold12-gene-6_155-mRNA-1	YPR043W	96.77	9.00E-132
scaffold12-gene-6_18-mRNA-1	YPR046W	78.47	2.00E-91
scaffold12-gene-6_19-mRNA-1	YPR047W	81.27	0
scaffold12-gene-6_23-mRNA-1	YPR052C	92.06	7.00E-108
scaffold12-gene-6_24-mRNA-1	YPR054W	81.58	0
scaffold12-gene-6_25-mRNA-1	YPR055W	81.58	0
scaffold12-gene-6_26-mRNA-1	YPR056W	84.12	0
scaffold12-gene-6_28-mRNA-1	YPR058W	85.59	0
scaffold12-gene-6_3-mRNA-1	YPR029C	79.2	0
scaffold12-gene-6_30-mRNA-1	YPR061C	79.46	2.00E-178
scaffold12-gene-6_31-mRNA-1	YPR062W	83.55	1.00E-121
scaffold12-gene-6_34-mRNA-1	YPR066W	80.57	0
scaffold12-gene-6_37-mRNA-1	YPR069C	87.67	0
scaffold12-gene-6_38-mRNA-1	YPR070W	79.38	0
scaffold12-gene-6_39-mRNA-1	YPR072W	82.11	0
scaffold12-gene-6_41-mRNA-1	YPR074C	88.98	0
scaffold12-gene-6_45-mRNA-1	YBR118W	96.38	0
scaffold12-gene-6_46-mRNA-1	YPR022C	79.68	0
scaffold12-gene-6_48-mRNA-1	YPR024W	82.86	0
scaffold12-gene-6_5-mRNA-1	YPR031W	78.25	0
scaffold12-gene-6_6-mRNA-1	YPR032W	80.34	0
scaffold12-gene-6_9-mRNA-1	YPR035W	88.72	0
scaffold12-gene-7_1-mRNA-1	YPR093C	76.16	2.00E-112
scaffold12-gene-7_10-mRNA-1	YPR105C	80.61	0
scaffold12-gene-7_130-mRNA-1	YPR107C	86.98	0
scaffold12-gene-7_14-mRNA-1	YPR110C	85.49	0
scaffold12-gene-7_141-mRNA-1	YPR132W	98.15	0
scaffold12-gene-7_141-mRNA-1	YPR132W	100	2.00E-27
scaffold12-gene-7_16-mRNA-1	YPR112C	80.87	0
scaffold12-gene-7_19-mRNA-1	YPR115W	78.58	0
scaffold12-gene-7_2-mRNA-1	YPR095C	75.71	0
scaffold12-gene-7_21-mRNA-1	YPR117W	80.16	0
scaffold12-gene-7_22-mRNA-1	YPR118W	80	0
scaffold12-gene-7_24-mRNA-1	YPR120C	81.51	0

scaffold12-gene-7_28-mRNA-1	YPR127W	81.77	0
scaffold12-gene-7_3-mRNA-1	YPR097W	80.34	0
scaffold12-gene-7_30-mRNA-1	YPR129W	78.15	3.00E-176
scaffold12-gene-7_33-mRNA-1	YPR133C	84.59	0
scaffold12-gene-7_35-mRNA-1	YPR135W	80.8	0
scaffold12-gene-7_37-mRNA-1	YPR138C	83.62	0
scaffold12-gene-7_39-mRNA-1	YPR081C	78.46	0
scaffold12-gene-7_41-mRNA-1	YPR083W	79.48	0
scaffold12-gene-7_42-mRNA-1	YPR084W	80.04	0
scaffold12-gene-7_44-mRNA-1	YPR086W	86.21	0
scaffold12-gene-7_45-mRNA-1	YPR088C	87.75	0
scaffold12-gene-7_46-mRNA-1	YPR089W	80.47	0
scaffold12-gene-7_5-mRNA-1	YPR100W	86.62	1.00E-131
scaffold12-gene-7_7-mRNA-1	YPR102C	92.6	0
scaffold12-gene-7_8-mRNA-1	YPR103W	87.31	0
scaffold12-gene-7_94-mRNA-1	YPR104C	78.75	0
scaffold12-gene-8_0-mRNA-1	YPR147C	79.42	5.00E-179
scaffold12-gene-8_1-mRNA-1	YPR148C	82.35	1.00E-47
scaffold12-gene-8_11-mRNA-1	YPR159W	83.23	0
scaffold12-gene-8_12-mRNA-1	YPR160W	85.38	0
scaffold12-gene-8_13-mRNA-1	YPR161C	80.5	0
scaffold12-gene-8_14-mRNA-1	YPR163C	85.84	0
scaffold12-gene-8_14-mRNA-1	YPR163C	87.8	5.00E-79
scaffold12-gene-8_153-mRNA-1	YPR187W	90.65	2.00E-170
scaffold12-gene-8_154-mRNA-1	YPR170W-B	91.28	1.00E-52
scaffold12-gene-8_154-mRNA-1	YPR170W-B	91.74	2.00E-36
scaffold12-gene-8_18-mRNA-1	YPR167C	84.06	0
scaffold12-gene-8_2-mRNA-1	YPR149W	85.74	7.00E-155
scaffold12-gene-8_20-mRNA-1	YPR169W	78	0
scaffold12-gene-8_25-mRNA-1	YPR175W	80.47	0
scaffold12-gene-8_30-mRNA-1	YPR181C	85.75	0
scaffold12-gene-8_33-mRNA-1	YPR184W	80.94	0
scaffold12-gene-8_38-mRNA-1	YPR189W	81.11	0
scaffold12-gene-8_38-mRNA-1	YPR189W	81.23	0
scaffold12-gene-8_39-mRNA-1	YPR190C	82.71	0
scaffold12-gene-8_40-mRNA-1	YPR191W	81.36	0
scaffold12-gene-8_41-mRNA-1	YPR192W	80.66	0
scaffold12-gene-8_43-mRNA-1	YPR194C	80.5	0
scaffold12-gene-8_45-mRNA-1	YPR141C	81.72	0
scaffold12-gene-8_48-mRNA-1	YPR145W	87.03	0
scaffold12-gene-8_6-mRNA-1	YPR154W	79.6	6.00E-127
scaffold12-gene-8_76-mRNA-1	YPR165W	92.37	0
scaffold12-gene-8_8-mRNA-1	YPR156C	85.71	0

scaffold12-gene-8_9-mRNA-1	YPR157W	80.79	0
scaffold13-gene-0_0-mRNA-1	YIR042C	87.88	0
scaffold13-gene-0_1-mRNA-1	YOL161C	92.05	5.00E-145
scaffold13-gene-0_10-mRNA-1	YLR450W	82.44	0
scaffold13-gene-0_11-mRNA-1	YLR449W	80.94	0
scaffold13-gene-0_13-mRNA-1	YLR447C	87.82	0
scaffold13-gene-0_14-mRNA-1	YLR446W	77.76	0
scaffold13-gene-0_18-mRNA-1	YLR441C	95.57	0
scaffold13-gene-0_20-mRNA-1	YLR439W	80.41	0
scaffold13-gene-0_22-mRNA-1	YLR438W	86.7	0
scaffold13-gene-0_26-mRNA-1	YLR433C	83.4	0
scaffold13-gene-0_27-mRNA-1	YLR432W	88.4	0
scaffold13-gene-0_28-mRNA-1	YLR431C	77.76	0
scaffold13-gene-0_29-mRNA-1	YLR430W	82.46	0
scaffold13-gene-0_5-mRNA-1	YLR455W	80.46	0
scaffold13-gene-0_6-mRNA-1	YLR454W	79.61	0
scaffold13-gene-0_67-mRNA-1	YLR443W	80.65	0
scaffold13-gene-0_8-mRNA-1	YLR452C	79.08	0
scaffold13-gene-0_9-mRNA-1	YLR451W	82.67	0
scaffold13-gene-0_90-mRNA-1	YOL159C-A	92.91	2.00E-108
scaffold13-gene-0_94-mRNA-1	YLR448W	90.52	0
scaffold13-gene-1_0-mRNA-1	YLR422W	80.36	0
scaffold13-gene-1_11-mRNA-1	YLR409C	83.15	0
scaffold13-gene-1_124-mRNA-1	YLR425W	79.96	0
scaffold13-gene-1_126-mRNA-1	YDL075W	93.64	4.00E-118
scaffold13-gene-1_130-mRNA-1	YLR426W	79.35	8.00E-177
scaffold13-gene-1_17-mRNA-1	YLR403W	80.19	0
scaffold13-gene-1_18-mRNA-1	YLR401C	79.34	0
scaffold13-gene-1_20-mRNA-1	YLR398C	82.59	0
scaffold13-gene-1_26-mRNA-1	YLR392C	80	0
scaffold13-gene-1_3-mRNA-1	YLR419W	80.42	0
scaffold13-gene-1_30-mRNA-1	YLR387C	80.85	0
scaffold13-gene-1_31-mRNA-1	YLR386W	82.73	0
scaffold13-gene-1_33-mRNA-1	YLR384C	83.54	0
scaffold13-gene-1_34-mRNA-1	YLR383W	82.98	0
scaffold13-gene-1_35-mRNA-1	YLR382C	80.61	0
scaffold13-gene-1_37-mRNA-1	YLR429W	82.12	0
scaffold13-gene-1_38-mRNA-1	YLR427W	80.83	0
scaffold13-gene-1_40-mRNA-1	YLR424W	75.14	0
scaffold13-gene-1_41-mRNA-1	YLR423C	79.36	0
scaffold13-gene-1_49-mRNA-1	YLR410W	82.46	0
scaffold13-gene-1_6-mRNA-1	YLR414C	79.98	2.00E-161
scaffold13-gene-1_7-mRNA-1	YLR413W	77.52	0

scaffold13-gene-2_0-mRNA-1	YLR371W	83.05	0
scaffold13-gene-2_14-mRNA-1	YLR359W	86.91	0
scaffold13-gene-2_144-mRNA-1	YLR367W	91.42	1.00E-87
scaffold13-gene-2_144-mRNA-1	YLR367W	89.63	3.00E-43
scaffold13-gene-2_15-mRNA-1	YLR357W	84.11	0
scaffold13-gene-2_153-mRNA-1	YOR071C	72.63	5.00E-28
scaffold13-gene-2_17-mRNA-1	YLR355C	94.54	0
scaffold13-gene-2_18-mRNA-1	YLR354C	86.87	0
scaffold13-gene-2_20-mRNA-1	YLR352W	81.66	0
scaffold13-gene-2_21-mRNA-1	YLR351C	83.86	0
scaffold13-gene-2_24-mRNA-1	YLR347C	84.87	0
scaffold13-gene-2_26-mRNA-1	YLR345W	83.11	0
scaffold13-gene-2_27-mRNA-1	YGR034W	93.82	5.00E-160
scaffold13-gene-2_28-mRNA-1	YLR343W	77.55	0
scaffold13-gene-2_29-mRNA-1	YLR342W	84.84	0
scaffold13-gene-2_31-mRNA-1	YLR340W	91.43	0
scaffold13-gene-2_33-mRNA-1	YLR336C	80.08	0
scaffold13-gene-2_35-mRNA-1	YGR027C	92.97	5.00E-135
scaffold13-gene-2_36-mRNA-1	YLR332W	75.39	1.00E-141
scaffold13-gene-2_41-mRNA-1	YLR326W	80.86	2.00E-127
scaffold13-gene-2_42-mRNA-1	YLR378C	85.46	0
scaffold13-gene-2_45-mRNA-1	YLR375W	83.62	0
scaffold13-gene-2_5-mRNA-1	YLR237W	82	0
scaffold13-gene-2_9-mRNA-1	YLR363C	84.47	0
scaffold13-gene-3_117-mRNA-1	YLR316C	85.22	3.00E-26
scaffold13-gene-3_12-mRNA-1	YLR308W	75.21	9.00E-22
scaffold13-gene-3_121-mRNA-1	YOR182C	95.21	2.00E-81
scaffold13-gene-3_14-mRNA-1	YLR305C	81.82	0
scaffold13-gene-3_15-mRNA-1	YLR304C	88.01	0
scaffold13-gene-3_16-mRNA-1	YLR303W	90.94	0
scaffold13-gene-3_17-mRNA-1	YLR301W	80.54	8.00E-156
scaffold13-gene-3_18-mRNA-1	YLR300W	85.84	0
scaffold13-gene-3_22-mRNA-1	YLR295C	81.2	6.00E-80
scaffold13-gene-3_23-mRNA-1	YLR293C	93.33	0
scaffold13-gene-3_26-mRNA-1	YLR290C	79.15	2.00E-157
scaffold13-gene-3_27-mRNA-1	YLR289W	83.14	0
scaffold13-gene-3_28-mRNA-1	YLR288C	81.57	0
scaffold13-gene-3_30-mRNA-1	YLR286C	84.63	0
scaffold13-gene-3_34-mRNA-1	YLR278C	81.46	0
scaffold13-gene-3_34-mRNA-1	YLR278C	84	4.00E-61
scaffold13-gene-3_35-mRNA-1	YLR277C	82.76	0
scaffold13-gene-3_36-mRNA-1	YLR276C	84.92	0
scaffold13-gene-3_38-mRNA-1	YLR274W	85.25	0

scaffold13-gene-3_4-mRNA-1	YLR314C	81.29	0
scaffold13-gene-3_40-mRNA-1	YLR272C	82.72	0
scaffold13-gene-3_41-mRNA-1	YLR325C	98.31	7.00E-117
scaffold13-gene-3_45-mRNA-1	YLR320W	76.45	0
scaffold13-gene-3_46-mRNA-1	YLR319C	79.61	0
scaffold13-gene-3_6-mRNA-1	YLR312W-A	80.87	8.00E-161
scaffold13-gene-3_8-mRNA-1	YLR310C	80.62	0
scaffold13-gene-3_9-mRNA-1	YLR309C	77.01	0
scaffold13-gene-4_1-mRNA-1	YLR262C	86.52	0
scaffold13-gene-4_100-mRNA-1	YLR262C-A	91.41	6.00E-72
scaffold13-gene-4_107-mRNA-1	YLR243W	87.38	0
scaffold13-gene-4_11-mRNA-1	YLR249W	92.61	0
scaffold13-gene-4_12-mRNA-1	YLR248W	82.84	0
scaffold13-gene-4_13-mRNA-1	YLR247C	78.49	0
scaffold13-gene-4_13-mRNA-1	YLR247C	77.08	0
scaffold13-gene-4_15-mRNA-1	YLR244C	83.8	0
scaffold13-gene-4_17-mRNA-1	YLR241W	82.25	0
scaffold13-gene-4_18-mRNA-1	YLR240W	82.97	0
scaffold13-gene-4_19-mRNA-1	YLR239C	82.72	0
scaffold13-gene-4_20-mRNA-1	YLR238W	79.47	0
scaffold13-gene-4_21-mRNA-1	YLR237W	84.28	0
scaffold13-gene-4_22-mRNA-1	YLR234W	82.77	0
scaffold13-gene-4_23-mRNA-1	YLR233C	73.04	4.00E-148
scaffold13-gene-4_25-mRNA-1	YLR229C	88.58	0
scaffold13-gene-4_26-mRNA-1	YDR213W	76.47	2.00E-52
scaffold13-gene-4_28-mRNA-1	YLR226W	83.1	0
scaffold13-gene-4_29-mRNA-1	YLR225C	81.29	0
scaffold13-gene-4_3-mRNA-1	YLR259C	87.15	0
scaffold13-gene-4_30-mRNA-1	YLR224W	79.2	0
scaffold13-gene-4_31-mRNA-1	YLR223C	79.46	0
scaffold13-gene-4_35-mRNA-1	YLR219W	75.14	0
scaffold13-gene-4_4-mRNA-1	YLR258W	85.63	0
scaffold13-gene-4_43-mRNA-1	YLR266C	74.47	0
scaffold13-gene-4_45-mRNA-1	YLR264W	95.1	1.00E-88
scaffold13-gene-4_5-mRNA-1	YLR257W	83.09	0
scaffold13-gene-4_6-mRNA-1	YLR256W	81.82	0
scaffold13-gene-5_0-mRNA-1	YLR208W	87	0
scaffold13-gene-5_1-mRNA-1	YLR207W	79.83	0
scaffold13-gene-5_12-mRNA-1	YLR193C	83.11	1.00E-133
scaffold13-gene-5_139-mRNA-1	YLR185W	95.79	6.00E-118
scaffold13-gene-5_16-mRNA-1	YLR189C	82.17	0
scaffold13-gene-5_19-mRNA-1	YLR186W	86.93	0
scaffold13-gene-5_22-mRNA-1	YLR182W	81.18	0

scaffold13-gene-5_23-mRNA-1	YLR181C	79.93	3.00E-117
scaffold13-gene-5_24-mRNA-1	YLR180W	88.73	0
scaffold13-gene-5_27-mRNA-1	YLR177W	79.79	0
scaffold13-gene-5_29-mRNA-1	YLR175W	88.34	0
scaffold13-gene-5_32-mRNA-1	YLR172C	82.89	0
scaffold13-gene-5_34-mRNA-1	YLR168C	85.47	0
scaffold13-gene-5_35-mRNA-1	YLR166C	82.06	0
scaffold13-gene-5_4-mRNA-1	YLR203C	83.84	0
scaffold13-gene-5_43-mRNA-1	YLR210W	80.28	0
scaffold13-gene-5_44-mRNA-1	YLR209C	84.69	0
scaffold13-gene-5_52-mRNA-1	YLR159C-A	100	3.00E-49
scaffold13-gene-5_6-mRNA-1	YLR200W	82.98	5.00E-80
scaffold13-gene-5_8-mRNA-1	YLR197W	88.71	0
scaffold13-gene-5_9-mRNA-1	YLR196W	82.83	0
scaffold14-gene-0_1-mRNA-1	YNR067C	82.43	0
scaffold14-gene-0_10-mRNA-1	YNR056C	81.77	0
scaffold14-gene-0_11-mRNA-1	YNR055C	82.94	0
scaffold14-gene-0_12-mRNA-1	YJL223C	89.46	7.00E-129
scaffold14-gene-0_120-mRNA-1	YNR053C	85.53	0
scaffold14-gene-0_16-mRNA-1	YNR052C	84.05	0
scaffold14-gene-0_18-mRNA-1	YNR050C	85.62	0
scaffold14-gene-0_21-mRNA-1	YNR047W	80.54	0
scaffold14-gene-0_26-mRNA-1	YNR041C	82.18	0
scaffold14-gene-0_32-mRNA-1	YNR035C	85.22	0
scaffold14-gene-0_34-mRNA-1	YNR034W	84.17	0
scaffold14-gene-0_38-mRNA-1	YNR031C	82.94	0
scaffold14-gene-0_39-mRNA-1	YNR030W	81.24	0
scaffold14-gene-0_40-mRNA-1	YNR029C	79.53	0
scaffold14-gene-0_9-mRNA-1	YNR057C	86.02	0
scaffold14-gene-0_96-mRNA-1	YNR041C	80.99	3.00E-88
scaffold14-gene-1_1-mRNA-1	YNR017W	80.7	3.00E-130
scaffold14-gene-1_13-mRNA-1	YNR004W	80.09	1.00E-86
scaffold14-gene-1_157-mRNA-1	YNL004W	82.54	0
scaffold14-gene-1_16-mRNA-1	YNR001C	86.66	0
scaffold14-gene-1_163-mRNA-1	YNL012W	81.31	0
scaffold14-gene-1_163-mRNA-1	YNL012W	90.16	3.00E-14
scaffold14-gene-1_18-mRNA-1	YNL002C	83.68	0
scaffold14-gene-1_19-mRNA-1	YNL003C	85.42	0
scaffold14-gene-1_2-mRNA-1	YNR016C	87.4	0
scaffold14-gene-1_25-mRNA-1	YNL009W	84.09	0
scaffold14-gene-1_26-mRNA-1	YNL010W	87.65	0
scaffold14-gene-1_27-mRNA-1	YNL011C	83.38	0
scaffold14-gene-1_29-mRNA-1	YNL014W	83.94	0

scaffold14-gene-1_31-mRNA-1	YNL016W	87.06	0
scaffold14-gene-1_34-mRNA-1	YNL020C	73.88	3.00E-39
scaffold14-gene-1_36-mRNA-1	YNL022C	83.73	0
scaffold14-gene-1_37-mRNA-1	YNL023C	80.34	0
scaffold14-gene-1_38-mRNA-1	YNL024C	82.13	4.00E-174
scaffold14-gene-1_41-mRNA-1	YNL027W	79.82	0
scaffold14-gene-1_45-mRNA-1	YNR026C	81.46	0
scaffold14-gene-1_5-mRNA-1	YNR013C	81.59	0
scaffold14-gene-1_50-mRNA-1	YNR020C	82.2	1.00E-159
scaffold14-gene-1_51-mRNA-1	YNR019W	80.96	0
scaffold14-gene-1_6-mRNA-1	YNR012W	82.99	0
scaffold14-gene-1_7-mRNA-1	YNR011C	82.29	0
scaffold15-gene-0_1-mRNA-1	YCR104W	90.21	2.00E-138
scaffold15-gene-0_12-mRNA-1	YGR276C	80.13	0
scaffold15-gene-0_14-mRNA-1	YGR274C	81.58	0
scaffold15-gene-0_16-mRNA-1	YGR271C-A	83.47	4.00E-154
scaffold15-gene-0_17-mRNA-1	YGR271W	82.57	0
scaffold15-gene-0_18-mRNA-1	YGR270W	86.96	6.00E-45
scaffold15-gene-0_20-mRNA-1	YGR267C	87.89	0
scaffold15-gene-0_22-mRNA-1	YGR264C	85.2	0
scaffold15-gene-0_23-mRNA-1	YGR263C	79.4	0
scaffold15-gene-0_25-mRNA-1	YGR261C	80.36	0
scaffold15-gene-0_26-mRNA-1	YGR260W	85.23	0
scaffold15-gene-0_27-mRNA-1	YGR258C	76.82	0
scaffold15-gene-0_29-mRNA-1	YGR256W	83.37	0
scaffold15-gene-0_3-mRNA-1	YGR285C	86.78	0
scaffold15-gene-0_31-mRNA-1	YGR253C	89.17	0
scaffold15-gene-0_32-mRNA-1	YGR252W	85.09	0
scaffold15-gene-0_4-mRNA-1	YGR284C	87.63	0
scaffold15-gene-0_6-mRNA-1	YGR282C	87.84	0
scaffold15-gene-0_7-mRNA-1	YGR281W	82.62	0
scaffold15-gene-0_9-mRNA-1	YGR279C	83.52	0
scaffold15-gene-1_10-mRNA-1	YGR229C	84.07	0
scaffold15-gene-1_150-mRNA-1	YGR214W	93.41	0
scaffold15-gene-1_150-mRNA-1	YGR214W	97.83	7.00E-39
scaffold15-gene-1_151-mRNA-1	YGR225W	80.61	0
scaffold15-gene-1_16-mRNA-1	YGR218W	85.91	0
scaffold15-gene-1_17-mRNA-1	YGR217W	81.63	0
scaffold15-gene-1_18-mRNA-1	YGR216C	78.81	0
scaffold15-gene-1_24-mRNA-1	YGR210C	85.51	0
scaffold15-gene-1_25-mRNA-1	YGR209C	86.54	2.00E-94
scaffold15-gene-1_26-mRNA-1	YGR208W	81.01	0
scaffold15-gene-1_30-mRNA-1	YGR204W	84.14	0

scaffold15-gene-1_32-mRNA-1	YGR202C	80.86	0
scaffold15-gene-1_34-mRNA-1	YGR200C	81.32	0
scaffold15-gene-1_36-mRNA-1	YGR198W	79.81	0
scaffold15-gene-1_37-mRNA-1	YGR197C	78.58	0
scaffold15-gene-1_39-mRNA-1	YGR195W	84.21	0
scaffold15-gene-1_42-mRNA-1	YJR009C	96.3	0
scaffold15-gene-1_43-mRNA-1	YGR246C	82.27	0
scaffold15-gene-1_44-mRNA-1	YGR245C	84.58	0
scaffold15-gene-1_48-mRNA-1	YGR240C	88.97	0
scaffold15-gene-1_6-mRNA-1	YGR233C	79.29	0
scaffold15-gene-1_7-mRNA-1	YGR232W	83.38	4.00E-178
scaffold15-gene-1_8-mRNA-1	YGR231C	85.63	0
scaffold15-gene-1_86-mRNA-1	YGR205W	80.55	3.00E-177
scaffold15-gene-2_0-mRNA-1	YGR186W	82.86	0
scaffold15-gene-2_0-mRNA-1	YGR186W	86.21	4.00E-163
scaffold15-gene-2_1-mRNA-1	YGR185C	83.75	0
scaffold15-gene-2_10-mRNA-1	YGR174C	82.8	1.00E-97
scaffold15-gene-2_11-mRNA-1	YGR173W	85.59	0
scaffold15-gene-2_116-mRNA-1	YGR157W	81.9	0
scaffold15-gene-2_12-mRNA-1	YGR172C	84.67	0
scaffold15-gene-2_13-mRNA-1	YGR171C	78.4	0
scaffold15-gene-2_131-mRNA-1	YGL031C	94.38	1.00E-65
scaffold15-gene-2_14-mRNA-1	YGR170W	79.84	0
scaffold15-gene-2_2-mRNA-1	YGR184C	81.77	0
scaffold15-gene-2_20-mRNA-1	YGR165W	84.19	0
scaffold15-gene-2_21-mRNA-1	YGR163W	86.13	0
scaffold15-gene-2_22-mRNA-1	YGR162W	87.09	0
scaffold15-gene-2_25-mRNA-1	YGR159C	83.95	0
scaffold15-gene-2_25-mRNA-1	YGR159C	85.82	7.00E-34
scaffold15-gene-2_28-mRNA-1	YGR156W	81.41	0
scaffold15-gene-2_29-mRNA-1	YGR155W	84.85	0
scaffold15-gene-2_31-mRNA-1	YGR152C	82.9	0
scaffold15-gene-2_36-mRNA-1	YGR146C	81.11	2.00E-141
scaffold15-gene-2_37-mRNA-1	YGR145W	84.95	0
scaffold15-gene-2_38-mRNA-1	YGR144W	87.95	0
scaffold15-gene-2_39-mRNA-1	YGR143W	80.42	0
scaffold15-gene-2_40-mRNA-1	YGR142W	74.53	1.00E-131
scaffold15-gene-2_41-mRNA-1	YGR191W	83.08	0
scaffold15-gene-2_43-mRNA-1	YGR188C	80.36	0
scaffold15-gene-2_5-mRNA-1	YGR180C	86.6	0
scaffold15-gene-2_7-mRNA-1	YGR178C	81.39	0
scaffold15-gene-2_8-mRNA-1	YGR177C	77.3	0
scaffold15-gene-2_9-mRNA-1	YGR175C	88.83	0

scaffold15-gene-3_10-mRNA-1	YGR123C	84.29	0
scaffold15-gene-3_115-mRNA-1	YGR105W	81.62	4.00E-50
scaffold15-gene-3_118-mRNA-1	YGR133W	78.73	3.00E-84
scaffold15-gene-3_13-mRNA-1	YGR120C	79.85	2.00E-157
scaffold15-gene-3_130-mRNA-1	YPR132W	97.1	7.00E-62
scaffold15-gene-3_130-mRNA-1	YPR132W	96.92	1.00E-24
scaffold15-gene-3_14-mRNA-1	YGR119C	79.26	0
scaffold15-gene-3_17-mRNA-1	YGR116W	85.33	0
scaffold15-gene-3_22-mRNA-1	YGR109C	79.58	0
scaffold15-gene-3_23-mRNA-1	YGR108W	80.39	0
scaffold15-gene-3_26-mRNA-1	YGR103W	84.61	0
scaffold15-gene-3_29-mRNA-1	YGR100W	83.49	0
scaffold15-gene-3_31-mRNA-1	YGR098C	77.89	0
scaffold15-gene-3_32-mRNA-1	YGR097W	81.36	0
scaffold15-gene-3_35-mRNA-1	YGR094W	85.51	0
scaffold15-gene-3_38-mRNA-1	YGR140W	78.42	0
scaffold15-gene-3_39-mRNA-1	YGR138C	86.81	0
scaffold15-gene-3_40-mRNA-1	YGR136W	87.9	4.00E-35
scaffold15-gene-3_41-mRNA-1	YGR135W	87.69	0
scaffold15-gene-3_42-mRNA-1	YGR134W	77.73	0
scaffold15-gene-3_68-mRNA-1	YGR112W	79.29	0
scaffold15-gene-3_8-mRNA-1	YGR125W	82.78	0
scaffold15-gene-3_9-mRNA-1	YGR124W	85.67	0
scaffold15-gene-4_0-mRNA-1	YLR044C	76.36	0
scaffold15-gene-4_12-mRNA-1	YGR075C	80.14	1.00E-148
scaffold15-gene-4_13-mRNA-1	YGR072W	78.37	0
scaffold15-gene-4_156-mRNA-1	YGR034W	95.93	7.00E-171
scaffold15-gene-4_16-mRNA-1	YGR068C	77.85	0
scaffold15-gene-4_17-mRNA-1	YGR067C	74.2	0
scaffold15-gene-4_2-mRNA-1	YGR085C	92.41	0
scaffold15-gene-4_22-mRNA-1	YGR061C	85.85	0
scaffold15-gene-4_23-mRNA-1	YGR060W	90.79	0
scaffold15-gene-4_25-mRNA-1	YGR058W	85.79	2.00E-172
scaffold15-gene-4_27-mRNA-1	YGR056W	81.3	0
scaffold15-gene-4_28-mRNA-1	YGR055W	85.51	0
scaffold15-gene-4_29-mRNA-1	YGR054W	83.39	0
scaffold15-gene-4_3-mRNA-1	YGR084C	80.29	0
scaffold15-gene-4_32-mRNA-1	YGR049W	82.39	2.00E-136
scaffold15-gene-4_34-mRNA-1	YGR047C	82.47	0
scaffold15-gene-4_35-mRNA-1	YGR046W	83.4	0
scaffold15-gene-4_37-mRNA-1	YGR043C	81.87	0
scaffold15-gene-4_42-mRNA-1	YGR036C	82.1	1.00E-164
scaffold15-gene-4_45-mRNA-1	YGR092W	84.43	0

scaffold15-gene-4_47-mRNA-1	YGR090W	84.23	0
scaffold15-gene-4_49-mRNA-1	YGR088W	83.39	0
scaffold15-gene-4_5-mRNA-1	YGR082W	86.85	1.00E-172
scaffold15-gene-4_7-mRNA-1	YGR080W	76.96	9.00E-152
scaffold15-gene-4_8-mRNA-1	YGR079W	77.23	5.00E-139
scaffold15-gene-5_1-mRNA-1	YGR027C	96.64	5.00E-155
scaffold15-gene-5_12-mRNA-1	YGR013W	77.1	0
scaffold15-gene-5_141-mRNA-1	YGR004W	83.5	0
scaffold15-gene-5_15-mRNA-1	YGR009C	79.28	0
scaffold15-gene-5_19-mRNA-1	YGR005C	86.11	0
scaffold15-gene-5_2-mRNA-1	YGR026W	82.24	0
scaffold15-gene-5_21-mRNA-1	YGR002C	81.09	0
scaffold15-gene-5_23-mRNA-1	YGL001C	86.75	0
scaffold15-gene-5_25-mRNA-1	YGL003C	83.97	0
scaffold15-gene-5_27-mRNA-1	YGL005C	77.23	3.00E-121
scaffold15-gene-5_28-mRNA-1	YGL006W	80.86	0
scaffold15-gene-5_29-mRNA-1	YGL008C	93.4	0
scaffold15-gene-5_30-mRNA-1	YGL009C	86.12	0
scaffold15-gene-5_33-mRNA-1	YGL013C	82.07	9.00E-37
scaffold15-gene-5_34-mRNA-1	YGL014W	79.35	0
scaffold15-gene-5_34-mRNA-1	YGL014W	83.98	0
scaffold15-gene-5_36-mRNA-1	YGL016W	82.76	0
scaffold15-gene-5_42-mRNA-1	YGL022W	84.81	0
scaffold15-gene-5_43-mRNA-1	YGR033C	83.47	3.00E-160
scaffold15-gene-5_44-mRNA-1	YGR032W	84.22	0
scaffold15-gene-5_45-mRNA-1	YGR031W	79.05	2.00E-167
scaffold15-gene-5_6-mRNA-1	YGR021W	79.52	1.00E-164
scaffold15-gene-5_7-mRNA-1	YGR020C	88.8	2.00E-123
scaffold15-gene-5_8-mRNA-1	YGR019W	86.34	0
scaffold15-gene-5_81-mRNA-1	YGR003W	77.19	0
scaffold15-gene-5_9-mRNA-1	YGR017W	81.2	0
scaffold15-gene-6_1-mRNA-1	YGL030W	98.7	3.00E-156
scaffold15-gene-6_11-mRNA-1	YGL043W	84.08	0
scaffold15-gene-6_12-mRNA-1	YGL044C	86.18	1.00E-100
scaffold15-gene-6_15-mRNA-1	YGL048C	86.61	0
scaffold15-gene-6_158-mRNA-1	YGL076C	93.94	0
scaffold15-gene-6_158-mRNA-1	YGL076C	96.77	6.00E-38
scaffold15-gene-6_16-mRNA-1	YGL049C	82.22	0
scaffold15-gene-6_166-mRNA-1	YGL033W	78.94	4.00E-104
scaffold15-gene-6_19-mRNA-1	YGL055W	87.7	0
scaffold15-gene-6_2-mRNA-1	YGL031C	94.66	0
scaffold15-gene-6_22-mRNA-1	YGL058W	87	3.00E-159
scaffold15-gene-6_26-mRNA-1	YGL062W	84.12	0

scaffold15-gene-6_29-mRNA-1	YGL065C	80.74	0
scaffold15-gene-6_33-mRNA-1	YGL070C	87.26	3.00E-118
scaffold15-gene-6_34-mRNA-1	YGL071W	78.84	0
scaffold15-gene-6_35-mRNA-1	YGL073W	80.62	0
scaffold15-gene-6_38-mRNA-1	YGL077C	83.08	0
scaffold15-gene-6_39-mRNA-1	YGL078C	83.19	0
scaffold15-gene-6_40-mRNA-1	YGL079W	78.46	6.00E-112
scaffold15-gene-6_45-mRNA-1	YGL084C	81.59	0
scaffold15-gene-6_48-mRNA-1	YGL087C	89.11	2.00E-141
scaffold15-gene-6_49-mRNA-1	YGL023C	79.93	3.00E-49
scaffold15-gene-6_5-mRNA-1	YGL036W	75.65	0
scaffold15-gene-6_50-mRNA-1	YGL025C	74.74	2.00E-134
scaffold15-gene-6_51-mRNA-1	YGL026C	85.87	0
scaffold15-gene-6_52-mRNA-1	YGL027C	81.73	0
scaffold15-gene-6_53-mRNA-1	YGL028C	82.64	0
scaffold15-gene-6_7-mRNA-1	YGL038C	77.6	0
scaffold15-gene-6_77-mRNA-1	YGL056C	81.65	0
scaffold15-gene-6_82-mRNA-1	YGL066W	82.36	0
scaffold15-gene-6_9-mRNA-1	YGL040C	83.82	0
scaffold15-gene-7_0-mRNA-1	YGL094C	82.8	0
scaffold15-gene-7_10-mRNA-1	YGL104C	82.23	0
scaffold15-gene-7_11-mRNA-1	YGL105W	87.79	0
scaffold15-gene-7_126-mRNA-1	YGL103W	95.28	3.00E-173
scaffold15-gene-7_126-mRNA-1	YGL103W	100	1.00E-18
scaffold15-gene-7_13-mRNA-1	YGL107C	79.64	0
scaffold15-gene-7_17-mRNA-1	YGL112C	84.5	0
scaffold15-gene-7_19-mRNA-1	YGL114W	83.45	0
scaffold15-gene-7_20-mRNA-1	YGL115W	85.42	0
scaffold15-gene-7_21-mRNA-1	YGL116W	84.47	0
scaffold15-gene-7_24-mRNA-1	YGL120C	85.31	0
scaffold15-gene-7_26-mRNA-1	YGL122C	80.83	0
scaffold15-gene-7_27-mRNA-1	YGL123W	95.06	0
scaffold15-gene-7_29-mRNA-1	YGL125W	82.2	0
scaffold15-gene-7_3-mRNA-1	YGL097W	83.49	0
scaffold15-gene-7_31-mRNA-1	YGL128C	75.34	1.00E-105
scaffold15-gene-7_32-mRNA-1	YGL129C	81.24	0
scaffold15-gene-7_34-mRNA-1	YGL131C	76.98	0
scaffold15-gene-7_37-mRNA-1	YPL187W	78.82	2.00E-26
scaffold15-gene-7_37-mRNA-1	YPL187W	86.09	2.00E-26
scaffold15-gene-7_5-mRNA-1	YGL098W	78.48	1.00E-125
scaffold15-gene-7_6-mRNA-1	YGL099W	85.24	0
scaffold15-gene-7_7-mRNA-1	YGL100W	85.67	0
scaffold15-gene-7_81-mRNA-1	YGL093W	79.78	0

scaffold16-gene-0_1-mRNA-1	YAL062W	81.66	0
scaffold16-gene-0_10-mRNA-1	YAL051W	82.18	0
scaffold16-gene-0_12-mRNA-1	YAL048C	82.54	0
scaffold16-gene-0_14-mRNA-1	YAL046C	83.44	1.00E-76
scaffold16-gene-0_17-mRNA-1	YAL043C	78.24	0
scaffold16-gene-0_18-mRNA-1	YAL042W	80.84	0
scaffold16-gene-0_19-mRNA-1	YAL041W	81.19	0
scaffold16-gene-0_2-mRNA-1	YAL061W	81.26	0
scaffold16-gene-0_20-mRNA-1	YAL040C	80.96	0
scaffold16-gene-0_22-mRNA-1	YAL038W	96.01	0
scaffold16-gene-0_24-mRNA-1	YAL036C	85.78	0
scaffold16-gene-0_25-mRNA-1	YAL035W	83.83	0
scaffold16-gene-0_27-mRNA-1	YAL034C	81.3	0
scaffold16-gene-0_28-mRNA-1	YAL033W	85.3	4.00E-118
scaffold16-gene-0_32-mRNA-1	YAL029C	77.88	0
scaffold16-gene-0_35-mRNA-1	YAL026C	84.52	0
scaffold16-gene-0_37-mRNA-1	YAL031C	77.97	0
scaffold16-gene-0_4-mRNA-1	YAL059W	85.3	3.00E-119
scaffold16-gene-0_6-mRNA-1	YAL056W	77.26	0
scaffold16-gene-1_0-mRNA-1	YAL019W	80.58	0
scaffold16-gene-1_12-mRNA-1	YAL007C	83.05	2.00E-166
scaffold16-gene-1_13-mRNA-1	YAL005C	91.57	0
scaffold16-gene-1_130-mRNA-1	YAL003W	90.93	0
scaffold16-gene-1_130-mRNA-1	YAL003W	96.25	1.00E-30
scaffold16-gene-1_131-mRNA-1	YAR035W	83.42	0
scaffold16-gene-1_18-mRNA-1	YAR002C-A	83.11	9.00E-170
scaffold16-gene-1_19-mRNA-1	YAR003W	84.52	0
scaffold16-gene-1_20-mRNA-1	YAR007C	84.84	0
scaffold16-gene-1_21-mRNA-1	YAR008W	79.57	6.00E-163
scaffold16-gene-1_23-mRNA-1	YAR014C	78.55	3.00E-149
scaffold16-gene-1_23-mRNA-1	YAR014C	83	8.00E-56
scaffold16-gene-1_24-mRNA-1	YAR015W	85.82	0
scaffold16-gene-1_3-mRNA-1	YAL016W	84.69	0
scaffold16-gene-1_35-mRNA-1	YAL024C	79.84	0
scaffold16-gene-1_36-mRNA-1	YAL023C	84.27	0
scaffold16-gene-1_37-mRNA-1	YAL022C	81.1	0
scaffold16-gene-1_38-mRNA-1	YAL021C	83.18	0
scaffold16-gene-1_39-mRNA-1	YAL020C	76.34	9.00E-142
scaffold16-gene-1_65-mRNA-1	YAL013W	81.97	0
scaffold16-gene-1_8-mRNA-1	YAL011W	78.39	0
scaffold17-gene-0_0-mRNA-1	YGL136C	82.18	0
scaffold17-gene-0_11-mRNA-1	YGL147C	91.33	0
scaffold17-gene-0_117-mRNA-1	YGL137W	85.58	0

scaffold17-gene-0_120-mRNA-1	YGL178W	82.6	0
scaffold17-gene-0_13-mRNA-1	YGL150C	83.36	0
scaffold17-gene-0_18-mRNA-1	YGL156W	84.38	0
scaffold17-gene-0_20-mRNA-1	YGL158W	74.64	4.00E-97
scaffold17-gene-0_28-mRNA-1	YGL167C	84.28	0
scaffold17-gene-0_3-mRNA-1	YGL139W	82.9	0
scaffold17-gene-0_30-mRNA-1	YGL170C	79.18	2.00E-174
scaffold17-gene-0_31-mRNA-1	YGL171W	83.03	0
scaffold17-gene-0_32-mRNA-1	YGL172W	80.22	0
scaffold17-gene-0_33-mRNA-1	YGL173C	83.19	0
scaffold17-gene-0_36-mRNA-1	YGL176C	72.73	3.00E-114
scaffold17-gene-0_4-mRNA-1	YGL140C	81.55	0
scaffold17-gene-0_5-mRNA-1	YGL141W	79.95	0
scaffold17-gene-0_55-mRNA-1	YGL142C	79.03	0
scaffold17-gene-0_8-mRNA-1	YGL144C	80.29	0
scaffold17-gene-1_10-mRNA-1	YGL197W	79.9	0
scaffold17-gene-1_101-mRNA-1	YGL194C-A	85.19	2.00E-33
scaffold17-gene-1_12-mRNA-1	YGL200C	83.93	2.00E-166
scaffold17-gene-1_120-mRNA-1	YGL192W	78.76	0
scaffold17-gene-1_13-mRNA-1	YGL201C	85.05	0
scaffold17-gene-1_13-mRNA-1	YGL201C	84.46	1.00E-94
scaffold17-gene-1_17-mRNA-1	YGL206C	83.88	0
scaffold17-gene-1_18-mRNA-1	YGL207W	84.58	0
scaffold17-gene-1_2-mRNA-1	YGL187C	88.35	7.00E-160
scaffold17-gene-1_22-mRNA-1	YGL211W	83.06	0
scaffold17-gene-1_23-mRNA-1	YGL212W	79.04	3.00E-171
scaffold17-gene-1_24-mRNA-1	YGL213C	82.2	0
scaffold17-gene-1_28-mRNA-1	YGL220W	86.59	8.00E-77
scaffold17-gene-1_29-mRNA-1	YGL221C	81.31	0
scaffold17-gene-1_3-mRNA-1	YGL189C	97.78	2.00E-178
scaffold17-gene-1_30-mRNA-1	YGL222C	83.15	1.00E-63
scaffold17-gene-1_33-mRNA-1	YGL225W	86.13	0
scaffold17-gene-1_34-mRNA-1	YLR037C	86.29	3.00E-112
scaffold17-gene-1_38-mRNA-1	YGL179C	77.93	0
scaffold17-gene-1_39-mRNA-1	YGL180W	82.57	0
scaffold17-gene-1_4-mRNA-1	YGL190C	87.15	0
scaffold17-gene-1_8-mRNA-1	YGL195W	81.99	0
scaffold17-gene-1_89-mRNA-1	YGL198W	79.34	2.00E-79
scaffold17-gene-1_9-mRNA-1	YGL196W	78.96	0
scaffold17-gene-2_0-mRNA-1	YGL236C	79.98	0
scaffold17-gene-2_1-mRNA-1	YGL237C	78.66	4.00E-139
scaffold17-gene-2_16-mRNA-1	YGL253W	89.99	0
scaffold17-gene-2_18-mRNA-1	YGL255W	80.17	0

scaffold17-gene-2_19-mRNA-1	YLR460C	76.34	5.00E-160
scaffold17-gene-2_2-mRNA-1	YGL238W	84.68	0
scaffold17-gene-2_25-mRNA-1	YGL227W	80.22	0
scaffold17-gene-2_27-mRNA-1	YGL229C	78.61	0
scaffold17-gene-2_31-mRNA-1	YGL234W	85.08	0
scaffold17-gene-2_8-mRNA-1	YGL245W	88.04	0
scaffold17-gene-2_9-mRNA-1	YGL246C	83.29	0
scaffold17-gene-2_97-mRNA-1	YGL251C	79.14	0
scaffold18-gene-0_1-mRNA-1	YCR095C	81.46	0
scaffold18-gene-0_10-mRNA-1	YCR086W	82.76	1.00E-143
scaffold18-gene-0_11-mRNA-1	YCR084C	84.17	0
scaffold18-gene-0_110-mRNA-1	YOL155C	79.29	1.00E-168
scaffold18-gene-0_15-mRNA-1	YCR077C	83.19	0
scaffold18-gene-0_16-mRNA-1	YCR076C	76.49	1.00E-99
scaffold18-gene-0_18-mRNA-1	YCR075C	78.09	2.00E-126
scaffold18-gene-0_20-mRNA-1	YCR073C	75.41	0
scaffold18-gene-0_21-mRNA-1	YCR072C	86.17	0
scaffold18-gene-0_24-mRNA-1	YCR068W	80.04	0
scaffold18-gene-0_27-mRNA-1	YCR065W	79.37	0
scaffold18-gene-0_28-mRNA-1	YCR063W	83.23	3.00E-118
scaffold18-gene-0_3-mRNA-1	YCR093W	82.15	0
scaffold18-gene-0_3-mRNA-1	YCR093W	82.68	0
scaffold18-gene-0_3-mRNA-1	YCR093W	83.76	0
scaffold18-gene-0_31-mRNA-1	YCR059C	84.17	0
scaffold18-gene-0_32-mRNA-1	YCR057C	82.64	0
scaffold18-gene-0_65-mRNA-1	YEL073C	90.57	1.00E-96
scaffold18-gene-0_79-mRNA-1	YCR091W	79.6	0
scaffold18-gene-0_79-mRNA-1	YCR091W	77.61	1.00E-43
scaffold18-gene-0_8-mRNA-1	YCR088W	79.18	0
scaffold18-gene-0_9-mRNA-1	YCR087C-A	77.38	2.00E-66
scaffold18-gene-1_1-mRNA-1	YCR038C	81.07	9.00E-179
scaffold18-gene-1_11-mRNA-1	YCR028C	81.54	0
scaffold18-gene-1_137-mRNA-1	YCR031C	95.1	0
scaffold18-gene-1_15-mRNA-1	YCR023C	81.6	0
scaffold18-gene-1_19-mRNA-1	YCR020C	80.55	7.00E-136
scaffold18-gene-1_2-mRNA-1	YJL198W	75.87	2.00E-152
scaffold18-gene-1_20-mRNA-1	YCR019W	75.27	6.00E-134
scaffold18-gene-1_22-mRNA-1	YCR017C	81.31	0
scaffold18-gene-1_26-mRNA-1	YCR012W	94.48	0
scaffold18-gene-1_27-mRNA-1	YCR011C	82.93	0
scaffold18-gene-1_30-mRNA-1	YCR008W	81.93	0
scaffold18-gene-1_33-mRNA-1	YCR004C	85.49	0
scaffold18-gene-1_34-mRNA-1	YCR003W	80.73	2.00E-116

scaffold18-gene-1_35-mRNA-1	YCR053W	86.29	0
scaffold18-gene-1_4-mRNA-1	YCR035C	82.49	0
scaffold18-gene-1_40-mRNA-1	YCR046C	82.6	1.00E-122
scaffold18-gene-1_5-mRNA-1	YCR034W	86.8	0
scaffold18-gene-1_6-mRNA-1	YCR033W	76.24	4.00E-120
scaffold18-gene-1_9-mRNA-1	YCR030C	79.6	0
scaffold18-gene-2_12-mRNA-1	YCL025C	82.33	0
scaffold18-gene-2_16-mRNA-1	YCL029C	82.75	0
scaffold18-gene-2_17-mRNA-1	YCL030C	85.72	0
scaffold18-gene-2_172-mRNA-1	YCL011C	84.29	0
scaffold18-gene-2_173-mRNA-1	YCL005W-A	89.06	2.00E-39
scaffold18-gene-2_18-mRNA-1	YCL031C	85.67	0
scaffold18-gene-2_23-mRNA-1	YCL036W	79.19	0
scaffold18-gene-2_24-mRNA-1	YCL037C	83.98	0
scaffold18-gene-2_26-mRNA-1	YCL039W	79.14	0
scaffold18-gene-2_27-mRNA-1	YCL040W	81.68	0
scaffold18-gene-2_28-mRNA-1	YCL043C	82.86	0
scaffold18-gene-2_29-mRNA-1	YCL044C	81.39	0
scaffold18-gene-2_30-mRNA-1	YCL045C	79.51	0
scaffold18-gene-2_30-mRNA-1	YCL045C	79.65	0
scaffold18-gene-2_32-mRNA-1	YCL048W	80.55	0
scaffold18-gene-2_35-mRNA-1	YCL050C	87.25	0
scaffold18-gene-2_38-mRNA-1	YCL054W	86.41	0
scaffold18-gene-2_39-mRNA-1	YCL055W	83.86	0
scaffold18-gene-2_41-mRNA-1	YCL057W	82.14	0
scaffold18-gene-2_44-mRNA-1	YCL059C	86.14	0
scaffold18-gene-2_48-mRNA-1	YCR040W	82.78	8.00E-130
scaffold18-gene-2_49-mRNA-1	YCR039C	99.21	0
scaffold18-gene-2_5-mRNA-1	YCL014W	79.1	0
scaffold18-gene-2_5-mRNA-1	YCL014W	73.04	2.00E-95
scaffold18-gene-2_51-mRNA-1	YCR002C	86.58	0
scaffold18-gene-2_53-mRNA-1	YCL001W	85.14	8.00E-165
scaffold18-gene-2_55-mRNA-1	YCL005W	76.43	1.00E-109
scaffold18-gene-2_7-mRNA-1	YCL017C	84.75	0
scaffold18-gene-2_8-mRNA-1	YCL018W	88.54	0
scaffold19-gene-0_11-mRNA-1	YFL041W	82.89	0
scaffold19-gene-0_121-mRNA-1	YFL039C	94.8	0
scaffold19-gene-0_122-mRNA-1	YFL034C-B	85.95	0
scaffold19-gene-0_15-mRNA-1	YFL037W	87.54	0
scaffold19-gene-0_16-mRNA-1	YFL036W	82.02	0
scaffold19-gene-0_19-mRNA-1	YFL034W	81.89	0
scaffold19-gene-0_2-mRNA-1	YFL050C	77.53	0
scaffold19-gene-0_20-mRNA-1	YFL033C	80.76	0

scaffold19-gene-0_21-mRNA-1	YFL031W	83.02	4.00E-178
scaffold19-gene-0_22-mRNA-1	YFL030W	81.11	0
scaffold19-gene-0_27-mRNA-1	YFL025C	78.35	0
scaffold19-gene-0_28-mRNA-1	YFL024C	82.88	0
scaffold19-gene-0_3-mRNA-1	YFL049W	78.79	0
scaffold19-gene-0_30-mRNA-1	YFL022C	82.58	0
scaffold19-gene-0_31-mRNA-1	YFL021W	78.4	0
scaffold19-gene-0_33-mRNA-1	YFL018C	85.38	0
scaffold19-gene-0_36-mRNA-1	YFL016C	81.25	0
scaffold19-gene-0_58-mRNA-1	YFL044C	82.61	0
scaffold19-gene-0_7-mRNA-1	YFL045C	89.32	0
scaffold19-gene-0_99-mRNA-1	YFL047W	81.74	0
scaffold19-gene-1_0-mRNA-1	YFL005W	87.98	0
scaffold19-gene-1_1-mRNA-1	YFL004W	84.32	0
scaffold19-gene-1_10-mRNA-1	YFR006W	82.17	0
scaffold19-gene-1_14-mRNA-1	YFR015C	84.05	0
scaffold19-gene-1_16-mRNA-1	YFR013W	80.87	0
scaffold19-gene-1_2-mRNA-1	YFL003C	81.67	0
scaffold19-gene-1_20-mRNA-1	YFR009W	85	0
scaffold19-gene-1_23-mRNA-1	YFR019W	81.58	0
scaffold19-gene-1_23-mRNA-1	YFR019W	82.91	0
scaffold19-gene-1_23-mRNA-1	YFR019W	79.94	2.00E-131
scaffold19-gene-1_3-mRNA-1	YFL002C	82.92	0
scaffold19-gene-1_30-mRNA-1	YFR027W	84.49	0
scaffold19-gene-1_31-mRNA-1	YFR028C	84.72	0
scaffold19-gene-1_32-mRNA-1	YFR029W	79.19	0
scaffold19-gene-1_34-mRNA-1	YFL010C	78.25	4.00E-98
scaffold19-gene-1_36-mRNA-1	YFL008W	82.46	0
scaffold19-gene-1_37-mRNA-1	YFL007W	82.17	0
scaffold19-gene-1_56-mRNA-1	YFR024C-A	82.29	0
scaffold19-gene-1_6-mRNA-1	YFR002W	83.03	0
scaffold19-gene-1_8-mRNA-1	YFR004W	86.64	0
scaffold19-gene-1_87-mRNA-1	YFR023W	83.01	0
scaffold19-gene-1_96-mRNA-1	YFR010W	86.3	0
scaffold19-gene-2_1-mRNA-1	YFR040W	80.78	0
scaffold19-gene-2_12-mRNA-1	YFR053C	87.21	0
scaffold19-gene-2_17-mRNA-1	YFR031C	81.34	0
scaffold19-gene-2_19-mRNA-1	YFR032C	77.68	6.00E-108
scaffold19-gene-2_21-mRNA-1	YFR033C	80.71	7.00E-90
scaffold19-gene-2_23-mRNA-1	YFR036W	76.84	8.00E-49
scaffold19-gene-2_24-mRNA-1	YFR037C	82.14	0
scaffold19-gene-2_43-mRNA-1	YFR048W	80.37	0
scaffold19-gene-2_68-mRNA-1	YFR032C-A	96.13	3.00E-80

scaffold19-gene-2_83-mRNA-1	YIL018W	95.96	0
scaffold19-gene-2_83-mRNA-1	YIL018W	88.31	3.00E-75
scaffold2-gene-0_0-mRNA-1	YAL063C	79.12	6.00E-74
scaffold2-gene-0_16-mRNA-1	YKR086W	79.15	0
scaffold2-gene-0_2-mRNA-1	YKR100C	82.1	0
scaffold2-gene-0_20-mRNA-1	YKR082W	79.45	0
scaffold2-gene-0_21-mRNA-1	YKR081C	87.48	0
scaffold2-gene-0_22-mRNA-1	YKR080W	83.97	0
scaffold2-gene-0_3-mRNA-1	YKR099W	80.74	0
scaffold2-gene-0_31-mRNA-1	YKR070W	81.97	0
scaffold2-gene-0_32-mRNA-1	YKR069W	81.38	0
scaffold2-gene-0_34-mRNA-1	YKR067W	80.06	0
scaffold2-gene-0_37-mRNA-1	YKR064W	77.99	0
scaffold2-gene-0_5-mRNA-1	YKR097W	85.91	0
scaffold2-gene-0_8-mRNA-1	YKR095W	76.31	0
scaffold2-gene-0_9-mRNA-1	YKR093W	84.59	0
scaffold2-gene-1_1-mRNA-1	YKR054C	78.28	0
scaffold2-gene-1_1-mRNA-1	YKR054C	79.32	0
scaffold2-gene-1_1-mRNA-1	YKR054C	75.17	0
scaffold2-gene-1_11-mRNA-1	YKR043C	85.33	0
scaffold2-gene-1_13-mRNA-1	YKR041W	88.61	1.00E-19
scaffold2-gene-1_13-mRNA-1	YKR041W	83.84	5.00E-19
scaffold2-gene-1_14-mRNA-1	YKR039W	83.88	0
scaffold2-gene-1_16-mRNA-1	YKR037C	81.66	0
scaffold2-gene-1_18-mRNA-1	YKR035W-A	83.63	9.00E-165
scaffold2-gene-1_19-mRNA-1	YKR034W	81.37	0
scaffold2-gene-1_2-mRNA-1	YKR053C	77.62	0
scaffold2-gene-1_20-mRNA-1	YKR031C	81.23	0
scaffold2-gene-1_21-mRNA-1	YKR029C	75.03	0
scaffold2-gene-1_22-mRNA-1	YKR028W	80.26	0
scaffold2-gene-1_22-mRNA-1	YKR028W	84.96	1.00E-30
scaffold2-gene-1_24-mRNA-1	YKR026C	86.49	0
scaffold2-gene-1_26-mRNA-1	YKR024C	82.24	0
scaffold2-gene-1_27-mRNA-1	YKR023W	77.62	0
scaffold2-gene-1_3-mRNA-1	YKR052C	85.43	0
scaffold2-gene-1_31-mRNA-1	YKR019C	76.19	0
scaffold2-gene-1_32-mRNA-1	YKR018C	82.9	0
scaffold2-gene-1_34-mRNA-1	YKR016W	81.33	0
scaffold2-gene-1_35-mRNA-1	YKR015C	80.41	3.00E-168
scaffold2-gene-1_36-mRNA-1	YKR014C	83.78	0
scaffold2-gene-1_40-mRNA-1	YKR062W	83.56	0
scaffold2-gene-1_41-mRNA-1	YKR061W	82.85	0
scaffold2-gene-1_42-mRNA-1	YKR060W	82.16	0

scaffold2-gene-1_43-mRNA-1	YKR059W	93.88	0
scaffold2-gene-1_45-mRNA-1	YKR057W	93.75	7.00E-100
scaffold2-gene-1_5-mRNA-1	YKR050W	77.34	0
scaffold2-gene-1_8-mRNA-1	YKR046C	84.56	0
scaffold2-gene-2_1-mRNA-1	YKR002W	85.56	0
scaffold2-gene-2_11-mRNA-1	YKL009W	88.02	0
scaffold2-gene-2_12-mRNA-1	YKL010C	81.68	0
scaffold2-gene-2_14-mRNA-1	YKL012W	79.03	0
scaffold2-gene-2_147-mRNA-1	YHL001W	96.22	3.00E-134
scaffold2-gene-2_147-mRNA-1	YHL001W	92.42	2.00E-47
scaffold2-gene-2_150-mRNA-1	YKL006C-A	86.72	3.00E-77
scaffold2-gene-2_16-mRNA-1	YKL014C	78.3	0
scaffold2-gene-2_17-mRNA-1	YKL015W	80.7	0
scaffold2-gene-2_17-mRNA-1	YKL015W	82.61	2.00E-68
scaffold2-gene-2_18-mRNA-1	YKL016C	86.72	6.00E-166
scaffold2-gene-2_2-mRNA-1	YKR001C	86.18	0
scaffold2-gene-2_20-mRNA-1	YKL018W	83.61	0
scaffold2-gene-2_23-mRNA-1	YKL021C	83.09	0
scaffold2-gene-2_24-mRNA-1	YKL022C	81.3	0
scaffold2-gene-2_26-mRNA-1	YKL024C	82.05	2.00E-146
scaffold2-gene-2_27-mRNA-1	YKL025C	80.12	0
scaffold2-gene-2_3-mRNA-1	YKL001C	85.9	0
scaffold2-gene-2_30-mRNA-1	YKL027W	81.87	0
scaffold2-gene-2_31-mRNA-1	YKL028W	84.87	0
scaffold2-gene-2_33-mRNA-1	YKL032C	77.15	0
scaffold2-gene-2_34-mRNA-1	YKL033W	76.58	0
scaffold2-gene-2_36-mRNA-1	YKL034W	82.06	0
scaffold2-gene-2_37-mRNA-1	YKL035W	86.45	0
scaffold2-gene-2_39-mRNA-1	YKL039W	83.83	0
scaffold2-gene-2_4-mRNA-1	YKL002W	86.54	0
scaffold2-gene-2_40-mRNA-1	YKL040C	84.69	0
scaffold2-gene-2_41-mRNA-1	YKR010C	77.71	5.00E-78
scaffold2-gene-2_43-mRNA-1	YKR008W	81.62	0
scaffold2-gene-2_6-mRNA-1	YKL004W	85.07	0
scaffold2-gene-3_10-mRNA-1	YKL058W	86.07	2.00E-109
scaffold2-gene-3_12-mRNA-1	YKL060C	94.84	0
scaffold2-gene-3_14-mRNA-1	YKL062W	78.68	0
scaffold2-gene-3_155-mRNA-1	YKL081W	84.78	0
scaffold2-gene-3_156-mRNA-1	YKL096W-A	85.95	4.00E-81
scaffold2-gene-3_25-mRNA-1	YKL075C	82.15	0
scaffold2-gene-3_27-mRNA-1	YKL078W	82.65	0
scaffold2-gene-3_29-mRNA-1	YKL080W	87.61	0
scaffold2-gene-3_31-mRNA-1	YKL082C	82.61	0

scaffold2-gene-3_33-mRNA-1	YKL086W	85.19	1.00E-107
scaffold2-gene-3_36-mRNA-1	YKL089W	80.9	0
scaffold2-gene-3_39-mRNA-1	YKL092C	77.54	0
scaffold2-gene-3_46-mRNA-1	YKL042W	78.74	0
scaffold2-gene-3_49-mRNA-1	YKL046C	86.51	0
scaffold2-gene-3_50-mRNA-1	YKL047W	76.51	0
scaffold2-gene-3_6-mRNA-1	YKL054C	84.03	0
scaffold2-gene-3_66-mRNA-1	YKL094W	81.92	0
scaffold2-gene-3_70-mRNA-1	YKL088W	79.23	0
scaffold2-gene-3_8-mRNA-1	YKL056C	94.27	0
scaffold2-gene-3_9-mRNA-1	YKL057C	80.46	0
scaffold2-gene-4_0-mRNA-1	YKL103C	80.27	0
scaffold2-gene-4_1-mRNA-1	YKL104C	86	0
scaffold2-gene-4_10-mRNA-1	YKL114C	83.05	0
scaffold2-gene-4_11-mRNA-1	YKL116C	80.23	0
scaffold2-gene-4_12-mRNA-1	YKL117W	87.45	5.00E-173
scaffold2-gene-4_14-mRNA-1	YKL120W	85.96	0
scaffold2-gene-4_15-mRNA-1	YKL121W	78.51	0
scaffold2-gene-4_17-mRNA-1	YKL124W	82.42	0
scaffold2-gene-4_19-mRNA-1	YKL127W	82.97	0
scaffold2-gene-4_21-mRNA-1	YKL129C	81.58	0
scaffold2-gene-4_25-mRNA-1	YKL134C	83	0
scaffold2-gene-4_26-mRNA-1	YKL135C	83.27	0
scaffold2-gene-4_28-mRNA-1	YKL138C	84.96	1.00E-111
scaffold2-gene-4_3-mRNA-1	YKL106W	81.55	0
scaffold2-gene-4_33-mRNA-1	YKL142W	81.15	3.00E-145
scaffold2-gene-4_34-mRNA-1	YKL143W	81.42	0
scaffold2-gene-4_36-mRNA-1	YKL145W	87.06	0
scaffold2-gene-4_37-mRNA-1	YKL146W	80.24	0
scaffold2-gene-4_38-mRNA-1	YKL148C	85.34	0
scaffold2-gene-4_42-mRNA-1	YKL152C	93.72	0
scaffold2-gene-4_46-mRNA-1	YKL099C	85.43	0
scaffold2-gene-4_48-mRNA-1	YKL101W	82.48	9.00E-98
scaffold2-gene-4_8-mRNA-1	YKL112W	80.02	0
scaffold2-gene-4_9-mRNA-1	YKL113C	84.58	0
scaffold2-gene-5_130-mRNA-1	YKL180W	97.74	6.00E-152
scaffold2-gene-5_130-mRNA-1	YKL180W	94.72	2.00E-106
scaffold2-gene-5_14-mRNA-1	YKL179C	80.86	0
scaffold2-gene-5_16-mRNA-1	YKL181W	86.89	0
scaffold2-gene-5_17-mRNA-1	YKL182W	87.64	0
scaffold2-gene-5_18-mRNA-1	YKL183W	83.74	0
scaffold2-gene-5_20-mRNA-1	YKL185W	81.94	0
scaffold2-gene-5_22-mRNA-1	YKL187C	77.87	0

scaffold2-gene-5_24-mRNA-1	YKL189W	82.81	0
scaffold2-gene-5_29-mRNA-1	YKL194C	82.11	0
scaffold2-gene-5_3-mRNA-1	YKL165C	82.53	0
scaffold2-gene-5_31-mRNA-1	YKL196C	85.64	0
scaffold2-gene-5_33-mRNA-1	YKL197C	75.49	0
scaffold2-gene-5_35-mRNA-1	YKL201C	79.06	0
scaffold2-gene-5_36-mRNA-1	YKL156W	88.31	1.00E-80
scaffold2-gene-5_37-mRNA-1	YKL157W	84.54	0
scaffold2-gene-5_4-mRNA-1	YKL166C	84.66	0
scaffold2-gene-5_40-mRNA-1	YKL161C	77.82	0
scaffold2-gene-5_49-mRNA-1	YKL178C	79.21	0
scaffold2-gene-5_7-mRNA-1	YKL171W	78.49	0
scaffold2-gene-5_9-mRNA-1	YKL173W	78	0
scaffold2-gene-5_96-mRNA-1	YKL188C	80.21	0
scaffold2-gene-6_1-mRNA-1	YKL209C	77.87	0
scaffold2-gene-6_11-mRNA-1	YKL203C	82.27	0
scaffold2-gene-6_12-mRNA-1	YKL204W	81.38	0
scaffold2-gene-6_13-mRNA-1	YKL205W	84.65	0
scaffold2-gene-6_2-mRNA-1	YKL210W	84.46	0
scaffold2-gene-6_3-mRNA-1	YKL211C	83.15	0
scaffold2-gene-6_4-mRNA-1	YKL212W	83.01	0
scaffold2-gene-6_7-mRNA-1	YKL215C	81.86	0
scaffold2-gene-6_8-mRNA-1	YKL216W	85.74	0
scaffold20-gene-0_2-mRNA-1	YHR206W	81.12	0
scaffold20-gene-0_31-mRNA-1	YHR205W	78.76	0
scaffold20-gene-0_31-mRNA-1	YHR205W	88.42	3.00E-93
scaffold20-gene-0_4-mRNA-1	YHR208W	87.4	0
scaffold21-gene-0_1-mRNA-1	YOR388C	83.3	0
scaffold21-gene-0_2-mRNA-1	YDR539W	82.49	0
scaffold21-gene-0_4-mRNA-1	YDR536W	84.62	0
scaffold22-gene-0_0-mRNA-1	YEL071W	82.64	0
scaffold23-gene-0_1-mRNA-1	YIL169C	80.85	0
scaffold24-gene-0_7-mRNA-1	Q0075	91.83	5.00E-117
scaffold24-gene-0_8-mRNA-1	Q0045	91.94	4.00E-95
scaffold26-gene-0_1-mRNA-1	YOL158C	87.83	0
scaffold27-gene-0_2-mRNA-1	R0040C	75	5.00E-64
scaffold3-gene-0_105-mRNA-1	YIL156W-B	89.1	3.00E-70
scaffold3-gene-0_106-mRNA-1	YIL133C	91.45	0
scaffold3-gene-0_106-mRNA-1	YIL133C	100	3.00E-10
scaffold3-gene-0_11-mRNA-1	YIL154C	83.57	0
scaffold3-gene-0_12-mRNA-1	YIL153W	82.1	0
scaffold3-gene-0_13-mRNA-1	YIL152W	77.25	4.00E-69
scaffold3-gene-0_14-mRNA-1	YIL151C	80.56	0

scaffold3-gene-0_15-mRNA-1	YIL150C	79.56	0
scaffold3-gene-0_16-mRNA-1	YIL149C	73.25	0
scaffold3-gene-0_17-mRNA-1	YIL147C	80.2	0
scaffold3-gene-0_18-mRNA-1	YIL146C	78.15	0
scaffold3-gene-0_2-mRNA-1	YIL164C	80.53	4.00E-125
scaffold3-gene-0_21-mRNA-1	YIL143C	85.55	0
scaffold3-gene-0_22-mRNA-1	YIL142W	85.11	0
scaffold3-gene-0_24-mRNA-1	YIL139C	79.87	5.00E-148
scaffold3-gene-0_26-mRNA-1	YIL137C	79.57	0
scaffold3-gene-0_28-mRNA-1	YIL135C	81.76	0
scaffold3-gene-0_3-mRNA-1	YIL162W	85.24	0
scaffold3-gene-0_32-mRNA-1	YIL131C	82.37	0
scaffold3-gene-0_4-mRNA-1	YIL161W	74.19	7.00E-57
scaffold3-gene-0_5-mRNA-1	YIL160C	83.43	0
scaffold3-gene-1_12-mRNA-1	YIL115C	76.08	6.00E-164
scaffold3-gene-1_120-mRNA-1	YIL126W	82.23	0
scaffold3-gene-1_17-mRNA-1	YIL110W	79.17	0
scaffold3-gene-1_18-mRNA-1	YIL109C	84.72	0
scaffold3-gene-1_19-mRNA-1	YIL108W	80.35	0
scaffold3-gene-1_2-mRNA-1	YIL125W	84.52	0
scaffold3-gene-1_20-mRNA-1	YIL107C	82.99	0
scaffold3-gene-1_22-mRNA-1	YIL105C	82.98	0
scaffold3-gene-1_23-mRNA-1	YIL104C	80.35	0
scaffold3-gene-1_24-mRNA-1	YIL103W	83.74	0
scaffold3-gene-1_25-mRNA-1	YIL101C	77.83	0
scaffold3-gene-1_28-mRNA-1	YIL097W	78.61	0
scaffold3-gene-1_3-mRNA-1	YIL124W	80.42	0
scaffold3-gene-1_30-mRNA-1	YIL095W	85.73	0
scaffold3-gene-1_31-mRNA-1	YIL094C	85.89	0
scaffold3-gene-1_32-mRNA-1	YIL093C	83.83	0
scaffold3-gene-1_34-mRNA-1	YIL091C	80.4	0
scaffold3-gene-1_4-mRNA-1	YIL123W	86.78	0
scaffold3-gene-1_4-mRNA-1	YIL123W	86.55	1.00E-47
scaffold3-gene-1_40-mRNA-1	YIL084C	83.52	0
scaffold3-gene-1_42-mRNA-1	YIL129C	83.48	0
scaffold3-gene-1_5-mRNA-1	YIL122W	76.65	4.00E-155
scaffold3-gene-1_91-mRNA-1	YIL083C	83.86	0
scaffold3-gene-2_1-mRNA-1	YIL072W	80.89	0
scaffold3-gene-2_112-mRNA-1	YIL049W	81.16	8.00E-166
scaffold3-gene-2_14-mRNA-1	YIL056W	79.72	0
scaffold3-gene-2_15-mRNA-1	YIL055C	75.39	0
scaffold3-gene-2_152-mRNA-1	YIL069C	93.55	0
scaffold3-gene-2_153-mRNA-1	YIL052C	96.67	6.00E-156

scaffold3-gene-2_153-mRNA-1	YIL052C	100	6.00E-12
scaffold3-gene-2_16-mRNA-1	YIL053W	93.76	0
scaffold3-gene-2_18-mRNA-1	YIL051C	86.62	1.00E-136
scaffold3-gene-2_20-mRNA-1	YIL048W	84.85	0
scaffold3-gene-2_21-mRNA-1	YIL047C	82.41	0
scaffold3-gene-2_22-mRNA-1	YIL046W	80.96	0
scaffold3-gene-2_23-mRNA-1	YIL045W	76.94	0
scaffold3-gene-2_27-mRNA-1	YIL041W	86	0
scaffold3-gene-2_31-mRNA-1	YIL035C	86.76	0
scaffold3-gene-2_32-mRNA-1	YIL034C	82.22	0
scaffold3-gene-2_33-mRNA-1	YIL033C	82.58	0
scaffold3-gene-2_35-mRNA-1	YIL030C	80.35	0
scaffold3-gene-2_35-mRNA-1	YIL030C	86.34	0
scaffold3-gene-2_37-mRNA-1	YIL027C	82.06	4.00E-92
scaffold3-gene-2_41-mRNA-1	YIL022W	84.85	0
scaffold3-gene-2_42-mRNA-1	YIL021W	86.84	0
scaffold3-gene-2_43-mRNA-1	YIL078W	86.68	0
scaffold3-gene-2_44-mRNA-1	YIL077C	75.87	2.00E-118
scaffold3-gene-2_47-mRNA-1	YIL075C	84.16	0
scaffold3-gene-2_6-mRNA-1	YIL067C	81.73	0
scaffold3-gene-2_64-mRNA-1	YIL063C	78.88	5.00E-131
scaffold3-gene-2_65-mRNA-1	YIL039W	82.06	0
scaffold3-gene-2_7-mRNA-1	YIL066C	86.41	0
scaffold3-gene-3_1-mRNA-1	YIL013C	82.15	0
scaffold3-gene-3_13-mRNA-1	YIL002C	85.66	0
scaffold3-gene-3_15-mRNA-1	YIR001C	80.17	2.00E-141
scaffold3-gene-3_16-mRNA-1	YIR002C	83.85	0
scaffold3-gene-3_184-mRNA-1	YIR019C	74.36	4.00E-29
scaffold3-gene-3_184-mRNA-1	YIR019C	72.74	2.00E-26
scaffold3-gene-3_184-mRNA-1	YIR019C	73.87	2.00E-26
scaffold3-gene-3_184-mRNA-1	YIR019C	73.65	5.00E-23
scaffold3-gene-3_184-mRNA-1	YIR019C	76.44	2.00E-16
scaffold3-gene-3_184-mRNA-1	YIR019C	79.23	9.00E-16
scaffold3-gene-3_184-mRNA-1	YIR019C	82.29	1.00E-14
scaffold3-gene-3_184-mRNA-1	YIR019C	82.29	1.00E-14
scaffold3-gene-3_184-mRNA-1	YIR019C	82.29	1.00E-14
scaffold3-gene-3_184-mRNA-1	YIR019C	84.21	2.00E-12
scaffold3-gene-3_184-mRNA-1	YIR019C	84.42	2.00E-12
scaffold3-gene-3_184-mRNA-1	YIR019C	84.42	2.00E-12
scaffold3-gene-3_20-mRNA-1	YIR006C	79.72	0
scaffold3-gene-3_20-mRNA-1	YIR006C	79.4	0
scaffold3-gene-3_21-mRNA-1	YIR007W	80.11	0
scaffold3-gene-3_22-mRNA-1	YIR008C	84.01	0

scaffold3-gene-3_24-mRNA-1	YIR010W	81.29	0
scaffold3-gene-3_25-mRNA-1	YIR011C	80.75	0
scaffold3-gene-3_31-mRNA-1	YIR017C	80.12	3.00E-99
scaffold3-gene-3_32-mRNA-1	YIR018W	76.46	6.00E-53
scaffold3-gene-3_41-mRNA-1	YIR028W	84.04	0
scaffold3-gene-3_42-mRNA-1	YIR029W	82.7	0
scaffold3-gene-3_46-mRNA-1	YIR033W	80.69	0
scaffold3-gene-3_47-mRNA-1	YIR034C	86.23	0
scaffold3-gene-3_5-mRNA-1	YHR096C	74.24	5.00E-57
scaffold3-gene-3_53-mRNA-1	YIL019W	79.06	0
scaffold3-gene-3_54-mRNA-1	YIL018W	97.76	3.00E-153
scaffold3-gene-3_54-mRNA-1	YIL018W	100	2.00E-34
scaffold3-gene-3_57-mRNA-1	YIL015W	79.5	0
scaffold3-gene-3_87-mRNA-1	YIL003W	81.84	0
scaffold34-gene-0_1-mRNA-1	Q0120	90.81	3.00E-65
scaffold36-gene-0_0-mRNA-1	YKR105C	81.27	0
scaffold39-gene-0_0-mRNA-1	YIL169C	77.14	3.00E-21
scaffold4-gene-0_0-mRNA-1	YOL157C	84.96	0
scaffold4-gene-0_10-mRNA-1	YML128C	81.44	0
scaffold4-gene-0_104-mRNA-1	YML108W	86.55	1.00E-86
scaffold4-gene-0_11-mRNA-1	YML127W	83	0
scaffold4-gene-0_12-mRNA-1	YML126C	89.6	0
scaffold4-gene-0_127-mRNA-1	YML085C	81.68	0
scaffold4-gene-0_15-mRNA-1	YML123C	85.7	0
scaffold4-gene-0_16-mRNA-1	YML121W	83.37	0
scaffold4-gene-0_17-mRNA-1	YML120C	82.32	0
scaffold4-gene-0_19-mRNA-1	YML118W	78.28	0
scaffold4-gene-0_2-mRNA-1	YBR298C	82.67	0
scaffold4-gene-0_20-mRNA-1	YML117W	78.6	0
scaffold4-gene-0_21-mRNA-1	YML116W	82.2	0
scaffold4-gene-0_22-mRNA-1	YML115C	83.44	0
scaffold4-gene-0_26-mRNA-1	YML111W	82.52	0
scaffold4-gene-0_28-mRNA-1	YML109W	75.88	0
scaffold4-gene-0_28-mRNA-1	YML109W	85.66	3.00E-71
scaffold4-gene-0_31-mRNA-1	YML106W	88.84	0
scaffold4-gene-0_32-mRNA-1	YML105C	83.39	0
scaffold4-gene-0_33-mRNA-1	YML104C	78.44	0
scaffold4-gene-0_34-mRNA-1	YML103C	77.21	0
scaffold4-gene-0_40-mRNA-1	YML099C	79.52	0
scaffold4-gene-0_41-mRNA-1	YML098W	80.55	3.00E-104
scaffold4-gene-0_9-mRNA-1	YML129C	88.73	7.00E-67
scaffold4-gene-1_10-mRNA-1	YML077W	85.63	1.00E-141
scaffold4-gene-1_12-mRNA-1	YML075C	84.48	0

scaffold4-gene-1_13-mRNA-1	YML074C	82.63	1.00E-166
scaffold4-gene-1_13-mRNA-1	YML074C	84.74	5.00E-150
scaffold4-gene-1_140-mRNA-1	YML094W	85.59	2.00E-131
scaffold4-gene-1_143-mRNA-1	YML073C	95.36	0
scaffold4-gene-1_16-mRNA-1	YML072C	82.23	0
scaffold4-gene-1_17-mRNA-1	YML071C	80.16	0
scaffold4-gene-1_24-mRNA-1	YML064C	84.1	0
scaffold4-gene-1_25-mRNA-1	YML063W	96.74	0
scaffold4-gene-1_27-mRNA-1	YML061C	82.53	0
scaffold4-gene-1_29-mRNA-1	YML059C	80.77	0
scaffold4-gene-1_30-mRNA-1	YML058W-A	87.56	4.00E-59
scaffold4-gene-1_31-mRNA-1	YML058W	82.97	1.00E-76
scaffold4-gene-1_32-mRNA-1	YML057W	83.53	0
scaffold4-gene-1_33-mRNA-1	YLR432W	81.79	0
scaffold4-gene-1_36-mRNA-1	YML053C	85.33	4.00E-48
scaffold4-gene-1_37-mRNA-1	YML052W	81.6	0
scaffold4-gene-1_44-mRNA-1	YML093W	81.6	0
scaffold4-gene-1_45-mRNA-1	YML092C	87.28	0
scaffold4-gene-1_46-mRNA-1	YML091C	81.25	0
scaffold4-gene-1_5-mRNA-1	YML082W	81.86	0
scaffold4-gene-1_7-mRNA-1	YML080W	83.33	0
scaffold4-gene-1_75-mRNA-1	YML085C	87.58	0
scaffold4-gene-1_9-mRNA-1	YML078W	87.45	0
scaffold4-gene-2_0-mRNA-1	YML041C	82.54	0
scaffold4-gene-2_1-mRNA-1	YML038C	78.14	0
scaffold4-gene-2_10-mRNA-1	YML028W	90.89	0
scaffold4-gene-2_107-mRNA-1	YML010W	83.96	0
scaffold4-gene-2_112-mRNA-1	YML017W	78.28	0
scaffold4-gene-2_128-mRNA-1	YML009C	88.79	3.00E-70
scaffold4-gene-2_149-mRNA-1	YML042W	81.8	0
scaffold4-gene-2_153-mRNA-1	YML034W	81.83	1.00E-134
scaffold4-gene-2_154-mRNA-1	YML024W	95.85	0
scaffold4-gene-2_155-mRNA-1	YML026C	93.92	8.00E-171
scaffold4-gene-2_155-mRNA-1	YML026C	94.12	5.00E-14
scaffold4-gene-2_156-mRNA-1	YML025C	84.29	0
scaffold4-gene-2_163-mRNA-1	YMR006C	82.78	0
scaffold4-gene-2_163-mRNA-1	YMR006C	74.22	4.00E-175
scaffold4-gene-2_17-mRNA-1	YML021C	80.29	0
scaffold4-gene-2_18-mRNA-1	YML020W	83.03	0
scaffold4-gene-2_22-mRNA-1	YML016C	82.22	0
scaffold4-gene-2_29-mRNA-1	YML008C	85.71	0
scaffold4-gene-2_30-mRNA-1	YML007W	89.3	2.00E-71
scaffold4-gene-2_31-mRNA-1	YML006C	77.36	0

scaffold4-gene-2_32-mRNA-1	YML005W	76.72	0
scaffold4-gene-2_33-mRNA-1	YML004C	83.16	0
scaffold4-gene-2_34-mRNA-1	YML002W	79.68	0
scaffold4-gene-2_35-mRNA-1	YML001W	90.72	0
scaffold4-gene-2_36-mRNA-1	YMR001C	86.92	0
scaffold4-gene-2_37-mRNA-1	YMR002W	83.54	1.00E-121
scaffold4-gene-2_38-mRNA-1	YMR004W	82.62	0
scaffold4-gene-2_4-mRNA-1	YML035C	84.46	0
scaffold4-gene-2_43-mRNA-1	YMR010W	82.92	0
scaffold4-gene-2_44-mRNA-1	YML049C	77.4	0
scaffold4-gene-2_45-mRNA-1	YML048W	81.16	0
scaffold4-gene-2_6-mRNA-1	YML032C	79.01	0
scaffold4-gene-2_7-mRNA-1	YML031W	78.79	0
scaffold4-gene-3_0-mRNA-1	YMR015C	87.85	0
scaffold4-gene-3_12-mRNA-1	YMR027W	81.74	0
scaffold4-gene-3_128-mRNA-1	YMR040W	80.24	2.00E-79
scaffold4-gene-3_146-mRNA-1	YMR033W	82.99	0
scaffold4-gene-3_147-mRNA-1	YMR042W	84.44	9.00E-45
scaffold4-gene-3_15-mRNA-1	YMR030W	76.51	6.00E-154
scaffold4-gene-3_17-mRNA-1	YMR032W	78.9	3.00E-134
scaffold4-gene-3_19-mRNA-1	YMR034C	81.57	0
scaffold4-gene-3_29-mRNA-1	YMR047C	75.41	0
scaffold4-gene-3_31-mRNA-1	YMR049C	85.31	0
scaffold4-gene-3_35-mRNA-1	YMR053C	80.89	0
scaffold4-gene-3_36-mRNA-1	YMR054W	83.09	0
scaffold4-gene-3_39-mRNA-1	YMR058W	84.15	0
scaffold4-gene-3_4-mRNA-1	YMR019W	78.53	0
scaffold4-gene-3_42-mRNA-1	YMR061W	84.53	0
scaffold4-gene-3_44-mRNA-1	YMR011W	85.84	0
scaffold4-gene-3_45-mRNA-1	YMR012W	82.84	0
scaffold4-gene-3_46-mRNA-1	YMR013C	80.69	0
scaffold4-gene-3_47-mRNA-1	YMR014W	78.26	0
scaffold4-gene-3_5-mRNA-1	YMR020W	80.2	0
scaffold4-gene-3_6-mRNA-1	YMR021C	81.33	0
scaffold4-gene-3_82-mRNA-1	YMR056C	82.34	2.00E-110
scaffold4-gene-3_9-mRNA-1	YMR024W	82.6	0
scaffold4-gene-4_1-mRNA-1	YMR071C	86.63	1.00E-157
scaffold4-gene-4_10-mRNA-1	YMR080C	84.53	0
scaffold4-gene-4_12-mRNA-1	YMR083W	85.45	0
scaffold4-gene-4_13-mRNA-1	YMR085W	75.31	1.00E-143
scaffold4-gene-4_136-mRNA-1	YMR086W	75.39	2.00E-122
scaffold4-gene-4_16-mRNA-1	YMR088C	84.11	0
scaffold4-gene-4_17-mRNA-1	YMR089C	84.35	0

scaffold4-gene-4_21-mRNA-1	YMR093W	86.14	0
scaffold4-gene-4_24-mRNA-1	YMR096W	84.44	0
scaffold4-gene-4_26-mRNA-1	YMR098C	75.58	0
scaffold4-gene-4_27-mRNA-1	YMR099C	84.33	0
scaffold4-gene-4_28-mRNA-1	YMR100W	80.27	0
scaffold4-gene-4_29-mRNA-1	YMR101C	80.21	0
scaffold4-gene-4_30-mRNA-1	YMR102C	80.05	0
scaffold4-gene-4_32-mRNA-1	YMR105C	85.43	0
scaffold4-gene-4_36-mRNA-1	YMR109W	85.16	0
scaffold4-gene-4_38-mRNA-1	YMR111C	78.95	0
scaffold4-gene-4_40-mRNA-1	YMR113W	80.02	0
scaffold4-gene-4_41-mRNA-1	YMR114C	81.4	0
scaffold4-gene-4_48-mRNA-1	YMR068W	79.39	0
scaffold4-gene-4_5-mRNA-1	YMR075W	79.98	0
scaffold4-gene-4_6-mRNA-1	YMR076C	81.07	0
scaffold4-gene-4_8-mRNA-1	YMR078C	79.21	0
scaffold4-gene-4_9-mRNA-1	YMR079W	87.91	0
scaffold4-gene-4_91-mRNA-1	YMR065W	80.33	0
scaffold4-gene-4_94-mRNA-1	YMR063W	81.26	5.00E-163
scaffold4-gene-5_14-mRNA-1	YMR136W	78.09	2.00E-135
scaffold4-gene-5_149-mRNA-1	YMR143W	96.46	8.00E-174
scaffold4-gene-5_150-mRNA-1	YMR116C	96.28	0
scaffold4-gene-5_150-mRNA-1	YMR116C	96.71	0
scaffold4-gene-5_151-mRNA-1	YMR142C	94.82	0
scaffold4-gene-5_17-mRNA-1	YMR139W	84.58	0
scaffold4-gene-5_2-mRNA-1	YMR124W	77.31	1.00E-129
scaffold4-gene-5_22-mRNA-1	YMR145C	84.25	0
scaffold4-gene-5_23-mRNA-1	YMR146C	87.67	0
scaffold4-gene-5_3-mRNA-1	YMR125W	82.89	0
scaffold4-gene-5_37-mRNA-1	YMR162C	82.08	0
scaffold4-gene-5_39-mRNA-1	YMR164C	76.62	5.00E-98
scaffold4-gene-5_40-mRNA-1	YMR165C	79.38	0
scaffold4-gene-5_41-mRNA-1	YMR166C	82.57	0
scaffold4-gene-5_42-mRNA-1	YMR167W	81.44	0
scaffold4-gene-5_47-mRNA-1	YMR120C	85.95	0
scaffold4-gene-5_48-mRNA-1	YLR029C	94.81	0
scaffold4-gene-5_5-mRNA-1	YMR127C	82.2	0
scaffold4-gene-5_6-mRNA-1	YMR128W	81.39	0
scaffold4-gene-5_61-mRNA-1	YMR153W	77.78	4.00E-107
scaffold4-gene-5_7-mRNA-1	YMR129W	81.52	0
scaffold4-gene-5_9-mRNA-1	YMR131C	85.55	0
scaffold4-gene-6_11-mRNA-1	YMR187C	80.27	0
scaffold4-gene-6_126-mRNA-1	YMR192W	76.83	0

scaffold4-gene-6_129-mRNA-1	YMR177W	83.62	0
scaffold4-gene-6_13-mRNA-1	YMR189W	83.53	0
scaffold4-gene-6_130-mRNA-1	YMR214W	83.16	0
scaffold4-gene-6_14-mRNA-1	YMR190C	81.91	0
scaffold4-gene-6_142-mRNA-1	YMR194W	94.46	1.00E-125
scaffold4-gene-6_20-mRNA-1	YMR196W	83.94	0
scaffold4-gene-6_21-mRNA-1	YMR197C	83.16	9.00E-170
scaffold4-gene-6_23-mRNA-1	YMR199W	85.05	0
scaffold4-gene-6_26-mRNA-1	YMR202W	85.63	0
scaffold4-gene-6_27-mRNA-1	YMR203W	87.83	0
scaffold4-gene-6_28-mRNA-1	YMR204C	77.8	2.00E-134
scaffold4-gene-6_29-mRNA-1	YMR205C	90.14	0
scaffold4-gene-6_32-mRNA-1	YMR208W	80.58	0
scaffold4-gene-6_36-mRNA-1	YMR212C	82.66	0
scaffold4-gene-6_43-mRNA-1	YMR171C	80.22	0
scaffold4-gene-6_5-mRNA-1	YMR181C	82.98	2.00E-115
scaffold4-gene-6_7-mRNA-1	YPL232W	79.27	1.00E-100
scaffold4-gene-6_78-mRNA-1	YMR186W	88.77	0
scaffold4-gene-6_78-mRNA-1	YMR186W	89.69	0
scaffold4-gene-6_9-mRNA-1	YMR185W	75.79	0
scaffold4-gene-7_0-mRNA-1	YMR220W	80.48	0
scaffold4-gene-7_109-mRNA-1	YMR242C	94.8	0
scaffold4-gene-7_127-mRNA-1	YMR256C	87.5	3.00E-55
scaffold4-gene-7_14-mRNA-1	YMR234W	79.78	1.00E-145
scaffold4-gene-7_141-mRNA-1	YOR293W	94.01	9.00E-113
scaffold4-gene-7_141-mRNA-2	YOR293W	94.01	1.00E-112
scaffold4-gene-7_142-mRNA-1	YMR221C	80.27	0
scaffold4-gene-7_15-mRNA-1	YMR235C	83.27	0
scaffold4-gene-7_17-mRNA-1	YMR237W	83.87	0
scaffold4-gene-7_18-mRNA-1	YMR238W	83.73	0
scaffold4-gene-7_21-mRNA-1	YMR241W	86.52	0
scaffold4-gene-7_23-mRNA-1	YMR243C	83.2	0
scaffold4-gene-7_26-mRNA-1	YMR246W	79.68	0
scaffold4-gene-7_28-mRNA-1	YMR250W	80.25	0
scaffold4-gene-7_32-mRNA-1	YMR253C	83.06	0
scaffold4-gene-7_35-mRNA-1	YMR257C	77.59	0
scaffold4-gene-7_38-mRNA-1	YMR260C	93.3	0
scaffold4-gene-7_39-mRNA-1	YMR261C	82.94	0
scaffold4-gene-7_42-mRNA-1	YMR264W	82.05	9.00E-145
scaffold4-gene-7_43-mRNA-1	YMR265C	77.29	7.00E-129
scaffold4-gene-7_45-mRNA-1	YMR217W	89.26	0
scaffold4-gene-7_8-mRNA-1	YMR228W	82.43	0
scaffold4-gene-7_9-mRNA-1	YMR229C	82.89	0

scaffold4-gene-8_12-mRNA-1	YMR285C	82.39	0
scaffold4-gene-8_13-mRNA-1	YMR287C	79.28	0
scaffold4-gene-8_138-mRNA-1	YMR291W	82.91	0
scaffold4-gene-8_14-mRNA-1	YMR288W	81.26	0
scaffold4-gene-8_16-mRNA-1	YMR290C	87.34	0
scaffold4-gene-8_22-mRNA-1	YMR297W	84.26	0
scaffold4-gene-8_23-mRNA-1	YMR298W	83.44	5.00E-116
scaffold4-gene-8_25-mRNA-1	YMR300C	85.99	0
scaffold4-gene-8_26-mRNA-1	YMR301C	81.44	0
scaffold4-gene-8_27-mRNA-1	YMR302C	83.26	0
scaffold4-gene-8_28-mRNA-1	YOL086C	87.03	0
scaffold4-gene-8_29-mRNA-1	YMR304W	82.58	0
scaffold4-gene-8_3-mRNA-1	YMR275C	80.64	0
scaffold4-gene-8_30-mRNA-1	YMR305C	82.03	0
scaffold4-gene-8_31-mRNA-1	YMR306W	83.49	0
scaffold4-gene-8_32-mRNA-1	YMR307W	82.03	0
scaffold4-gene-8_33-mRNA-1	YMR308C	86.06	0
scaffold4-gene-8_34-mRNA-1	YMR309C	86.88	0
scaffold4-gene-8_40-mRNA-1	YMR269W	78.96	2.00E-112
scaffold4-gene-8_6-mRNA-1	YMR278W	82.05	0
scaffold4-gene-8_77-mRNA-1	YMR310C	80.56	0
scaffold4-gene-8_79-mRNA-1	YMR295C	86.84	2.00E-180
scaffold4-gene-8_8-mRNA-1	YMR280C	78.6	0
scaffold4-gene-9_1-mRNA-1	YMR318C	83.98	0
scaffold4-gene-9_23-mRNA-1	YPL274W	80.04	8.00E-115
scaffold4-gene-9_8-mRNA-1	YMR314W	87.75	0
scaffold4-gene-9_9-mRNA-1	YMR315W	83.57	0
scaffold5-gene-0_10-mRNA-1	YHR193C	88.76	0
scaffold5-gene-0_13-mRNA-1	YHR190W	86.92	0
scaffold5-gene-0_15-mRNA-1	YHR188C	80.6	0
scaffold5-gene-0_17-mRNA-1	YHR186C	83.44	0
scaffold5-gene-0_18-mRNA-1	YHR185C	82.45	8.00E-176
scaffold5-gene-0_20-mRNA-1	YHR183W	90.55	0
scaffold5-gene-0_22-mRNA-1	YHR181W	84.68	0
scaffold5-gene-0_23-mRNA-1	YHR179W	85.64	0
scaffold5-gene-0_24-mRNA-1	YHR178W	84.58	0
scaffold5-gene-0_3-mRNA-1	YHR200W	83.9	0
scaffold5-gene-0_31-mRNA-1	YHR170W	86.84	0
scaffold5-gene-0_32-mRNA-1	YHR169W	84.25	0
scaffold5-gene-0_35-mRNA-1	YHR166C	83.7	0
scaffold5-gene-0_36-mRNA-1	YHR165C	84.45	0
scaffold5-gene-0_38-mRNA-1	YHR164C	78.65	9.00E-153
scaffold5-gene-0_4-mRNA-1	YHR199C	78.49	2.00E-162

scaffold5-gene-0_49-mRNA-1	YHR174W	93.69	1.00E-41
scaffold5-gene-0_6-mRNA-1	YHR197W	80.51	0
scaffold5-gene-0_9-mRNA-1	YHR194W	82.84	0
scaffold5-gene-1_11-mRNA-1	YHR142W	82.99	0
scaffold5-gene-1_12-mRNA-1	YNL162W	96.86	1.00E-151
scaffold5-gene-1_160-mRNA-1	YHR155W	77.36	0
scaffold5-gene-1_2-mRNA-1	YHR151C	78.53	0
scaffold5-gene-1_21-mRNA-1	YHR132W-A	85.86	4.00E-117
scaffold5-gene-1_22-mRNA-1	YHR132C	81.55	0
scaffold5-gene-1_24-mRNA-1	YHR129C	81.29	0
scaffold5-gene-1_25-mRNA-1	YHR128W	87.69	0
scaffold5-gene-1_28-mRNA-1	YHR124W	82.21	0
scaffold5-gene-1_33-mRNA-1	YHR119W	79.55	0
scaffold5-gene-1_37-mRNA-1	YHR115C	81.96	0
scaffold5-gene-1_38-mRNA-1	YHR114W	81.26	0
scaffold5-gene-1_4-mRNA-1	YHR149C	76.23	1.00E-157
scaffold5-gene-1_4-mRNA-1	YHR149C	82.76	9.00E-150
scaffold5-gene-1_45-mRNA-1	YHR107C	85.48	0
scaffold5-gene-1_5-mRNA-1	YHR148W	85.56	8.00E-165
scaffold5-gene-1_54-mRNA-1	YHR154W	77.16	1.00E-169
scaffold5-gene-1_6-mRNA-1	YHR147C	81.94	9.00E-155
scaffold5-gene-2_0-mRNA-1	YHR098C	83.69	0
scaffold5-gene-2_10-mRNA-1	YHR085W	80.83	0
scaffold5-gene-2_11-mRNA-1	YHR084W	82.01	0
scaffold5-gene-2_13-mRNA-1	YHR082C	80.95	0
scaffold5-gene-2_132-mRNA-1	YHR094C	87.76	0
scaffold5-gene-2_132-mRNA-1	YHR094C	84.68	5.00E-172
scaffold5-gene-2_132-mRNA-1	YHR094C	81.11	1.00E-133
scaffold5-gene-2_134-mRNA-1	YHR077C	80	0
scaffold5-gene-2_17-mRNA-1	YHR079C	80.59	0
scaffold5-gene-2_22-mRNA-1	YHR075C	78.61	0
scaffold5-gene-2_23-mRNA-1	YHR074W	85.54	0
scaffold5-gene-2_28-mRNA-1	YHR069C	82.91	0
scaffold5-gene-2_29-mRNA-1	YHR068W	88.66	0
scaffold5-gene-2_31-mRNA-1	YDR312W	81.6	0
scaffold5-gene-2_32-mRNA-1	YHR065C	84.2	0
scaffold5-gene-2_33-mRNA-1	YHR064C	86.9	0
scaffold5-gene-2_34-mRNA-1	YHR063C	80.5	0
scaffold5-gene-2_38-mRNA-1	YHR059W	83.93	5.00E-86
scaffold5-gene-2_39-mRNA-1	YHR102W	79.03	0
scaffold5-gene-2_42-mRNA-1	YHR099W	83.95	0
scaffold5-gene-2_8-mRNA-1	YHR087W	84.09	2.00E-79
scaffold5-gene-2_9-mRNA-1	YHR086W	80.47	0

scaffold5-gene-2_98-mRNA-1	YHR089C	86.68	0
scaffold5-gene-3_1-mRNA-1	YHR047C	79.98	0
scaffold5-gene-3_11-mRNA-1	YHR037W	83.94	0
scaffold5-gene-3_112-mRNA-1	YOR016C	84.78	3.00E-179
scaffold5-gene-3_119-mRNA-1	YOR017W	80.19	0
scaffold5-gene-3_12-mRNA-1	YHR036W	79.61	0
scaffold5-gene-3_140-mRNA-1	YHR056C	78.05	0
scaffold5-gene-3_144-mRNA-1	YHR041C	82.85	3.00E-155
scaffold5-gene-3_145-mRNA-1	YHR021C	97.17	4.00E-117
scaffold5-gene-3_146-mRNA-1	YHR016C	83.62	0
scaffold5-gene-3_15-mRNA-1	YHR033W	81.92	0
scaffold5-gene-3_16-mRNA-1	YHR032W	79.1	0
scaffold5-gene-3_18-mRNA-1	YHR030C	84.33	0
scaffold5-gene-3_20-mRNA-1	YHR028C	79.43	0
scaffold5-gene-3_21-mRNA-1	YHR027C	85.23	0
scaffold5-gene-3_22-mRNA-1	YHR026W	91.76	0
scaffold5-gene-3_23-mRNA-1	YHR025W	86.44	0
scaffold5-gene-3_25-mRNA-1	YHR023W	80.08	0
scaffold5-gene-3_27-mRNA-1	YHR020W	86.08	0
scaffold5-gene-3_29-mRNA-1	YHR018C	85.45	0
scaffold5-gene-3_30-mRNA-1	YHR017W	79.74	0
scaffold5-gene-3_32-mRNA-1	YHR015W	77.36	2.00E-16
scaffold5-gene-3_33-mRNA-1	YOR018W	77.88	0
scaffold5-gene-3_36-mRNA-1	YOR014W	82.3	0
scaffold5-gene-3_38-mRNA-1	YOR011W	83.97	0
scaffold5-gene-3_39-mRNA-1	YOR010C	76.8	5.00E-108
scaffold5-gene-3_43-mRNA-1	YHR052W	80.56	0
scaffold5-gene-3_44-mRNA-1	YHR051W	87.89	8.00E-149
scaffold5-gene-3_5-mRNA-1	YHR042W	83.26	0
scaffold5-gene-3_7-mRNA-1	YHR040W	78.17	0
scaffold5-gene-3_74-mRNA-1	YHR019C	85.22	0
scaffold5-gene-3_8-mRNA-1	YHR039C-A	87.25	7.00E-109
scaffold5-gene-3_9-mRNA-1	YHR039C	84.88	0
scaffold5-gene-4_1-mRNA-1	YOR003W	77.85	0
scaffold5-gene-4_12-mRNA-1	YOL009C	81.43	0
scaffold5-gene-4_13-mRNA-1	YOL010W	86.86	0
scaffold5-gene-4_14-mRNA-1	YOL011W	83.97	0
scaffold5-gene-4_15-mRNA-1	YOL012C	87.65	4.00E-132
scaffold5-gene-4_16-mRNA-1	YOL013C	82.9	0
scaffold5-gene-4_2-mRNA-1	YOR002W	84.43	0
scaffold5-gene-4_21-mRNA-1	YOL018C	82.66	0
scaffold5-gene-4_24-mRNA-1	YOL021C	84.05	0
scaffold5-gene-4_25-mRNA-1	YOL022C	81.32	0

scaffold5-gene-4_26-mRNA-1	YOL023W	82.16	0
scaffold5-gene-4_3-mRNA-1	YOR001W	76.5	0
scaffold5-gene-4_30-mRNA-1	YOL027C	80.4	0
scaffold5-gene-4_32-mRNA-1	YOL030W	82.34	0
scaffold5-gene-4_36-mRNA-1	YOL034W	80.66	0
scaffold5-gene-4_37-mRNA-1	YOL036W	75.88	0
scaffold5-gene-4_39-mRNA-1	YOL039W	94.39	5.00E-140
scaffold5-gene-4_40-mRNA-1	YOL040C	95.1	0
scaffold5-gene-4_42-mRNA-1	YOL042W	84.21	0
scaffold5-gene-4_45-mRNA-1	YOR009W	82.72	2.00E-94
scaffold5-gene-4_47-mRNA-1	YOR007C	84.44	0
scaffold5-gene-4_49-mRNA-1	YOR005C	78.81	0
scaffold5-gene-4_5-mRNA-1	YOL002C	82.37	0
scaffold5-gene-4_7-mRNA-1	YOL004W	82.63	0
scaffold5-gene-4_85-mRNA-1	YOL032W	83.42	0
scaffold5-gene-4_9-mRNA-1	YOL006C	82.74	0
scaffold5-gene-5_0-mRNA-1	YOL052C	79.57	0
scaffold5-gene-5_10-mRNA-1	YOL062C	83.34	0
scaffold5-gene-5_12-mRNA-1	YOL064C	83.77	0
scaffold5-gene-5_13-mRNA-1	YOL065C	79.08	0
scaffold5-gene-5_16-mRNA-1	YOL068C	81.11	0
scaffold5-gene-5_17-mRNA-1	YOL069W	81.9	0
scaffold5-gene-5_20-mRNA-1	YOL072W	79.41	0
scaffold5-gene-5_22-mRNA-1	YOL075C	82.06	0
scaffold5-gene-5_23-mRNA-1	YOL076W	79.08	0
scaffold5-gene-5_26-mRNA-1	YOL078W	80.06	0
scaffold5-gene-5_28-mRNA-1	YOL081W	80.47	0
scaffold5-gene-5_3-mRNA-1	YOL055C	82.81	0
scaffold5-gene-5_32-mRNA-1	YOL086C	94.02	0
scaffold5-gene-5_37-mRNA-1	YOL045W	81.18	0
scaffold5-gene-5_41-mRNA-1	YOL051W	79.49	0
scaffold5-gene-5_6-mRNA-1	YOL058W	86.93	0
scaffold5-gene-5_7-mRNA-1	YOL059W	87.31	0
scaffold5-gene-5_8-mRNA-1	YOL060C	81.88	0
scaffold5-gene-5_8-mRNA-1	YOL060C	76.93	2.00E-97
scaffold5-gene-5_9-mRNA-1	YOL061W	84.4	0
scaffold5-gene-6_1-mRNA-1	YOL101C	82.35	0
scaffold5-gene-6_12-mRNA-1	YOL115W	82.18	0
scaffold5-gene-6_124-mRNA-1	YOL144W	80.61	2.00E-104
scaffold5-gene-6_15-mRNA-1	YOL119C	81.24	0
scaffold5-gene-6_177-mRNA-1	YOL096C	79.68	2.00E-173
scaffold5-gene-6_178-mRNA-1	YOL120C	95.56	0
scaffold5-gene-6_178-mRNA-1	YOL120C	100	1.00E-54

scaffold5-gene-6_179-mRNA-1	YOL121C	94.99	0
scaffold5-gene-6_18-mRNA-1	YOL122C	79.9	0
scaffold5-gene-6_180-mRNA-1	YOL127W	96.64	0
scaffold5-gene-6_19-mRNA-1	YOL123W	85.01	0
scaffold5-gene-6_2-mRNA-1	YOL102C	78.94	5.00E-123
scaffold5-gene-6_20-mRNA-1	YOL124C	84.05	0
scaffold5-gene-6_22-mRNA-1	YOL126C	83.58	0
scaffold5-gene-6_24-mRNA-1	YOL128C	81.69	0
scaffold5-gene-6_25-mRNA-1	YOL129W	83.42	8.00E-145
scaffold5-gene-6_26-mRNA-1	YFL050C	80.48	0
scaffold5-gene-6_28-mRNA-1	YOL132W	81.22	0
scaffold5-gene-6_31-mRNA-1	YOL136C	81.38	0
scaffold5-gene-6_34-mRNA-1	YOL139C	93.3	0
scaffold5-gene-6_37-mRNA-1	YOL142W	81.81	2.00E-171
scaffold5-gene-6_38-mRNA-1	YOL143C	86.42	9.00E-159
scaffold5-gene-6_40-mRNA-1	YOL145C	80.83	0
scaffold5-gene-6_42-mRNA-1	YOL147C	82.02	8.00E-171
scaffold5-gene-6_43-mRNA-1	YOL148C	80.97	0
scaffold5-gene-6_44-mRNA-1	YOL149W	82.36	2.00E-171
scaffold5-gene-6_48-mRNA-1	YKL221W	80.77	0
scaffold5-gene-6_50-mRNA-1	YOL090W	82.82	0
scaffold5-gene-6_51-mRNA-1	YOL091W	77.24	0
scaffold5-gene-6_54-mRNA-1	YOL094C	85.71	0
scaffold5-gene-6_55-mRNA-1	YOL095C	78.87	0
scaffold5-gene-6_57-mRNA-1	YOL097C	86.36	0
scaffold5-gene-6_58-mRNA-1	YOL098C	81.41	0
scaffold50-gene-0_2-mRNA-1	YNR072W	83.7	0
scaffold52-gene-0_0-mRNA-1	Q0130	97.4	3.00E-110
scaffold56-gene-0_0-mRNA-1	YGR287C	84.36	0
scaffold59-gene-0_0-mRNA-1	YOL157C	79.91	6.00E-132
scaffold6-gene-0_1-mRNA-1	YLR153C	88.87	0
scaffold6-gene-0_15-mRNA-1	YLR138W	82.33	0
scaffold6-gene-0_17-mRNA-1	YLR136C	78.84	6.00E-148
scaffold6-gene-0_19-mRNA-1	YLR134W	91.3	0
scaffold6-gene-0_2-mRNA-1	YLR152C	84.91	6.00E-146
scaffold6-gene-0_20-mRNA-1	YLR133W	81.08	0
scaffold6-gene-0_22-mRNA-1	YLR131C	77.17	0
scaffold6-gene-0_27-mRNA-1	YLR126C	80.85	4.00E-164
scaffold6-gene-0_32-mRNA-1	YLR118C	81.18	8.00E-146
scaffold6-gene-0_33-mRNA-1	YLR117C	80.54	0
scaffold6-gene-0_35-mRNA-1	YLR115W	79.78	0
scaffold6-gene-0_36-mRNA-1	YLR114C	80.63	0
scaffold6-gene-0_37-mRNA-1	YLR113W	84.13	0

scaffold6-gene-0_4-mRNA-1	YLR150W	91.09	0
scaffold6-gene-0_4-mRNA-1	YLR150W	85.56	1.00E-44
scaffold6-gene-0_5-mRNA-1	YLR149C	82	0
scaffold6-gene-0_6-mRNA-1	YLR148W	80.61	0
scaffold6-gene-0_88-mRNA-1	YLR142W	81.68	0
scaffold6-gene-1_0-mRNA-1	YLR106C	82.17	0
scaffold6-gene-1_0-mRNA-1	YLR106C	78.72	0
scaffold6-gene-1_119-mRNA-1	YDR343C	77.39	0
scaffold6-gene-1_13-mRNA-1	YLR092W	80.82	0
scaffold6-gene-1_17-mRNA-1	YLR088W	81.71	0
scaffold6-gene-1_18-mRNA-1	YLR087C	82.38	0
scaffold6-gene-1_18-mRNA-1	YLR087C	82.25	0
scaffold6-gene-1_2-mRNA-1	YLR104W	82.06	4.00E-77
scaffold6-gene-1_21-mRNA-1	YLR084C	76.98	0
scaffold6-gene-1_29-mRNA-1	YLR075W	94.31	0
scaffold6-gene-1_32-mRNA-1	YLR072W	79	0
scaffold6-gene-1_33-mRNA-1	YLR110C	93.8	3.00E-173
scaffold6-gene-1_37-mRNA-1	YLR107W	79.26	0
scaffold6-gene-1_5-mRNA-1	YLR100W	81.01	0
scaffold6-gene-1_7-mRNA-1	YLR098C	84.65	0
scaffold6-gene-1_9-mRNA-1	YLR096W	78.34	0
scaffold6-gene-1_94-mRNA-1	YLR089C	84.73	0
scaffold6-gene-2_0-mRNA-1	YLR061W	95.13	4.00E-156
scaffold6-gene-2_1-mRNA-1	YLR060W	85.74	0
scaffold6-gene-2_112-mRNA-1	YLR014C	78.28	0
scaffold6-gene-2_16-mRNA-1	YLR045C	81.06	0
scaffold6-gene-2_165-mRNA-1	YLR054C	78.94	0
scaffold6-gene-2_167-mRNA-1	YLR048W	96.26	0
scaffold6-gene-2_167-mRNA-1	YLR048W	94.57	5.00E-34
scaffold6-gene-2_17-mRNA-1	YLR044C	95.22	0
scaffold6-gene-2_18-mRNA-1	YLR043C	89.14	2.00E-108
scaffold6-gene-2_19-mRNA-1	YLR042C	77.8	8.00E-75
scaffold6-gene-2_23-mRNA-1	YKL224C	91.11	9.00E-138
scaffold6-gene-2_25-mRNA-1	YLR035C	75.59	0
scaffold6-gene-2_26-mRNA-1	YLR034C	84.21	0
scaffold6-gene-2_27-mRNA-1	YLR033W	81.64	0
scaffold6-gene-2_28-mRNA-1	YLR032W	79.77	0
scaffold6-gene-2_3-mRNA-1	YLR058C	91.08	0
scaffold6-gene-2_30-mRNA-1	YLR029C	97.24	0
scaffold6-gene-2_31-mRNA-1	YLR028C	83.73	0
scaffold6-gene-2_32-mRNA-1	YLR027C	82.75	0
scaffold6-gene-2_33-mRNA-1	YLR026C	84.11	0
scaffold6-gene-2_35-mRNA-1	YLR024C	80.75	0

scaffold6-gene-2_35-mRNA-1	YLR024C	80.46	0
scaffold6-gene-2_37-mRNA-1	YLR022C	85.34	0
scaffold6-gene-2_39-mRNA-1	YLR020C	83.79	0
scaffold6-gene-2_4-mRNA-1	YLR057W	77.8	0
scaffold6-gene-2_44-mRNA-1	YLR015W	79.76	0
scaffold6-gene-2_46-mRNA-1	YLR071C	83.7	0
scaffold6-gene-2_48-mRNA-1	YLR069C	84.26	0
scaffold6-gene-2_5-mRNA-1	YLR056W	84.8	0
scaffold6-gene-2_50-mRNA-1	YLR067C	81.7	0
scaffold6-gene-2_51-mRNA-1	YLR066W	84.33	1.00E-142
scaffold6-gene-2_6-mRNA-1	YLR055C	82.96	0
scaffold6-gene-2_6-mRNA-1	YLR055C	89.58	2.00E-45
scaffold6-gene-2_9-mRNA-1	YLR052W	81.83	1.00E-178
scaffold6-gene-3_0-mRNA-1	YLR004C	86.14	0
scaffold6-gene-3_1-mRNA-1	YLR003C	82.63	0
scaffold6-gene-3_13-mRNA-1	YLL010C	82.26	4.00E-176
scaffold6-gene-3_131-mRNA-1	YLL024C	94.27	0
scaffold6-gene-3_131-mRNA-1	YLL024C	92.45	9.00E-111
scaffold6-gene-3_14-mRNA-1	YLL011W	85.27	0
scaffold6-gene-3_18-mRNA-1	YLL015W	80.27	0
scaffold6-gene-3_20-mRNA-1	YLL018C	86.89	0
scaffold6-gene-3_21-mRNA-1	YLL018C-A	84.27	9.00E-63
scaffold6-gene-3_22-mRNA-1	YLL019C	82.14	1.00E-104
scaffold6-gene-3_23-mRNA-1	YLL021W	81.7	6.00E-120
scaffold6-gene-3_25-mRNA-1	YLL023C	82.15	0
scaffold6-gene-3_27-mRNA-1	YOL161C	87.73	7.00E-119
scaffold6-gene-3_28-mRNA-1	YLL026W	86.55	0
scaffold6-gene-3_31-mRNA-1	YLL029W	80.95	0
scaffold6-gene-3_32-mRNA-1	YLL031C	83.62	0
scaffold6-gene-3_33-mRNA-1	YLL032C	77.32	0
scaffold6-gene-3_35-mRNA-1	YLL034C	83.76	0
scaffold6-gene-3_38-mRNA-1	YLR009W	91.04	0
scaffold6-gene-3_4-mRNA-1	YLL001W	85.8	0
scaffold6-gene-3_41-mRNA-1	YLR006C	79.3	0
scaffold6-gene-3_7-mRNA-1	YLL004W	82.03	0
scaffold6-gene-3_8-mRNA-1	YLL005C	79.64	0
scaffold6-gene-3_9-mRNA-1	YLL006W	81.46	0
scaffold6-gene-3_91-mRNA-1	YLL002W	78.37	0
scaffold6-gene-3_94-mRNA-1	YLL008W	83.95	0
scaffold6-gene-4_0-mRNA-1	YLL041C	85.66	0
scaffold6-gene-4_18-mRNA-1	YLL058W	74.36	0
scaffold6-gene-4_2-mRNA-1	YLL043W	84.16	0
scaffold6-gene-4_23-mRNA-1	YLL040C	81.86	0

scaffold6-gene-4_3-mRNA-1	YLL045C	92.64	0
scaffold6-gene-4_5-mRNA-1	YLL048C	83.5	0
scaffold6-gene-4_62-mRNA-1	YER187W	93.4	1.00E-179
scaffold6-gene-4_9-mRNA-1	YLL053C	84.75	3.00E-126
scaffold62-gene-0_2-mRNA-1	YCR097W	85.94	6.00E-70
scaffold62-gene-0_2-mRNA-1	YCR097W	91.43	2.00E-34
scaffold62-gene-0_2-mRNA-1	YCR097W	100	8.00E-09
scaffold63-gene-0_0-mRNA-1	YJL223C	92.31	8.00E-107
scaffold68-gene-0_0-mRNA-1	YAR050W	79.74	9.00E-40
scaffold7-gene-0_10-mRNA-1	YDR524C-B	94.61	8.00E-86
scaffold7-gene-0_124-mRNA-1	YDR524C	78.25	0
scaffold7-gene-0_13-mRNA-1	YDR522C	79.12	0
scaffold7-gene-0_141-mRNA-1	YDR500C	93.1	6.00E-105
scaffold7-gene-0_18-mRNA-1	YDR516C	84.01	0
scaffold7-gene-0_25-mRNA-1	YDR508C	81.77	0
scaffold7-gene-0_26-mRNA-1	YDR507C	83.44	0
scaffold7-gene-0_29-mRNA-1	YDR502C	89.21	0
scaffold7-gene-0_32-mRNA-1	YDR499W	80.27	0
scaffold7-gene-0_34-mRNA-1	YDR497C	82.94	0
scaffold7-gene-0_36-mRNA-1	YDR495C	77.92	0
scaffold7-gene-0_40-mRNA-1	YDR490C	76.73	0
scaffold7-gene-0_45-mRNA-1	YDR485C	78.07	2.00E-162
scaffold7-gene-0_8-mRNA-1	YDR528W	77.2	0
scaffold7-gene-0_91-mRNA-1	YDR505C	78.9	3.00E-170
scaffold7-gene-1_14-mRNA-1	YDR460W	86.71	0
scaffold7-gene-1_141-mRNA-1	YDR447C	96.21	0
scaffold7-gene-1_143-mRNA-1	YDR450W	94.68	8.00E-176
scaffold7-gene-1_143-mRNA-1	YDR450W	94.44	1.00E-15
scaffold7-gene-1_17-mRNA-1	YDR457W	83.15	0
scaffold7-gene-1_17-mRNA-1	YDR457W	83.33	0
scaffold7-gene-1_18-mRNA-1	YDR456W	82.49	0
scaffold7-gene-1_24-mRNA-1	YDR449C	82.78	0
scaffold7-gene-1_25-mRNA-1	YDR448W	84.45	0
scaffold7-gene-1_28-mRNA-1	YDR444W	81.28	0
scaffold7-gene-1_29-mRNA-1	YDR443C	79.79	0
scaffold7-gene-1_33-mRNA-1	YDR438W	76.56	4.00E-151
scaffold7-gene-1_37-mRNA-1	YDR434W	82.17	0
scaffold7-gene-1_38-mRNA-1	YDR432W	86.93	0
scaffold7-gene-1_38-mRNA-1	YDR432W	78.76	1.00E-11
scaffold7-gene-1_39-mRNA-1	YDR484W	80.43	0
scaffold7-gene-1_4-mRNA-1	YHR010W	93.19	1.00E-159
scaffold7-gene-1_42-mRNA-1	YDR481C	79.88	0
scaffold7-gene-1_46-mRNA-1	YDR477W	84.55	0

scaffold7-gene-1_65-mRNA-1	YDR472W	81.29	0
scaffold7-gene-1_7-mRNA-1	YDR468C	82.4	3.00E-164
scaffold7-gene-1_8-mRNA-1	YDR466W	80.18	0
scaffold7-gene-1_9-mRNA-1	YDR465C	81.5	0
scaffold7-gene-1_98-mRNA-1	YDR437W	82.37	6.00E-100
scaffold7-gene-10_1-mRNA-1	YBR021W	84.46	0
scaffold7-gene-10_10-mRNA-1	YBR010W	94.16	6.00E-180
scaffold7-gene-10_11-mRNA-1	YNL030W	96.15	4.00E-145
scaffold7-gene-10_13-mRNA-1	YBR006W	84.08	0
scaffold7-gene-10_16-mRNA-1	YBR003W	84.18	0
scaffold7-gene-10_18-mRNA-1	YBR001C	82.59	0
scaffold7-gene-10_20-mRNA-1	YDR224C	91.24	3.00E-148
scaffold7-gene-10_21-mRNA-1	YDR225W	93.23	3.00E-168
scaffold7-gene-10_22-mRNA-1	YBL004W	80.85	0
scaffold7-gene-10_25-mRNA-1	YBL007C	88.41	2.00E-98
scaffold7-gene-10_27-mRNA-1	YBL009W	76.09	0
scaffold7-gene-10_30-mRNA-1	YBL013W	75.6	1.00E-111
scaffold7-gene-10_32-mRNA-1	YBL015W	84.7	0
scaffold7-gene-10_36-mRNA-1	YBR029C	84.15	0
scaffold7-gene-10_39-mRNA-1	YBR025C	87.34	0
scaffold7-gene-10_41-mRNA-1	YBR023C	84.64	0
scaffold7-gene-10_5-mRNA-1	YBR017C	84.19	0
scaffold7-gene-10_86-mRNA-1	YBL010C	82.12	2.00E-143
scaffold7-gene-10_9-mRNA-1	YBR011C	90.55	0
scaffold7-gene-11_0-mRNA-1	YBL025W	81.94	1.00E-101
scaffold7-gene-11_10-mRNA-1	YBL035C	78.74	0
scaffold7-gene-11_12-mRNA-1	YBL037W	81.25	0
scaffold7-gene-11_13-mRNA-1	YBL038W	84.72	2.00E-171
scaffold7-gene-11_14-mRNA-1	YBL039C	86.37	0
scaffold7-gene-11_144-mRNA-1	YBL059C-A	86.29	5.00E-87
scaffold7-gene-11_146-mRNA-1	YBL027W	96.3	0
scaffold7-gene-11_149-mRNA-1	YBL040C	85.13	0
scaffold7-gene-11_150-mRNA-1	YBL026W	87.77	4.00E-72
scaffold7-gene-11_16-mRNA-1	YBL041W	86.5	0
scaffold7-gene-11_17-mRNA-1	YBL042C	82.48	0
scaffold7-gene-11_20-mRNA-1	YBL045C	82.72	0
scaffold7-gene-11_22-mRNA-1	YBL047C	79.01	0
scaffold7-gene-11_25-mRNA-1	YBL051C	80.14	0
scaffold7-gene-11_26-mRNA-1	YBL052C	76.99	0
scaffold7-gene-11_29-mRNA-1	YBL056W	83.22	0
scaffold7-gene-11_34-mRNA-1	YBL061C	79.61	0
scaffold7-gene-11_35-mRNA-1	YBL063W	77.58	0
scaffold7-gene-11_36-mRNA-1	YBL064C	82.93	0

scaffold7-gene-11_37-mRNA-1	YBL066C	78.88	0
scaffold7-gene-11_39-mRNA-1	YBL068W	85.38	0
scaffold7-gene-11_4-mRNA-1	YBL029W	78.5	0
scaffold7-gene-11_42-mRNA-1	YBL072C	95.37	0
scaffold7-gene-11_43-mRNA-1	YBL020W	82.71	0
scaffold7-gene-11_45-mRNA-1	YBL022C	82.21	0
scaffold7-gene-11_46-mRNA-1	YBL023C	85.06	0
scaffold7-gene-11_47-mRNA-1	YBL024W	85.94	0
scaffold7-gene-11_5-mRNA-1	YBL030C	89.79	0
scaffold7-gene-12_0-mRNA-1	YBL080C	79.16	0
scaffold7-gene-12_12-mRNA-1	YBL092W	94.67	5.00E-175
scaffold7-gene-12_13-mRNA-1	YBL093C	85.97	0
scaffold7-gene-12_15-mRNA-1	YBL097W	78.39	0
scaffold7-gene-12_17-mRNA-1	YBL099W	89.4	0
scaffold7-gene-12_21-mRNA-1	YBL104C	82.6	0
scaffold7-gene-12_23-mRNA-1	YBL106C	79.55	0
scaffold7-gene-12_27-mRNA-1	YJL221C	87.82	5.00E-156
scaffold7-gene-12_29-mRNA-1	YBL075C	84.69	0
scaffold7-gene-12_30-mRNA-1	YBL076C	85.38	0
scaffold7-gene-12_31-mRNA-1	YBL078C	87.29	2.00E-113
scaffold7-gene-12_32-mRNA-1	YBL079W	81.65	0
scaffold7-gene-12_38-mRNA-1	YBL105C	81.33	0
scaffold7-gene-12_39-mRNA-1	YBL091C-A	80.78	3.00E-59
scaffold7-gene-12_4-mRNA-1	YBL085W	78.81	0
scaffold7-gene-12_40-mRNA-1	YBR298C	79.76	0
scaffold7-gene-12_6-mRNA-1	YBL087C	95.16	4.00E-168
scaffold7-gene-12_6-mRNA-1	YBL087C	100	2.00E-12
scaffold7-gene-12_7-mRNA-1	YBL088C	77.63	0
scaffold7-gene-12_7-mRNA-1	YBL088C	76.86	0
scaffold7-gene-2_1-mRNA-1	YDR419W	79.7	0
scaffold7-gene-2_11-mRNA-1	YDR407C	79.11	0
scaffold7-gene-2_12-mRNA-1	YDR406W	83.13	0
scaffold7-gene-2_164-mRNA-1	YDR397C	86.45	1.00E-124
scaffold7-gene-2_18-mRNA-1	YDR399W	86	0
scaffold7-gene-2_2-mRNA-1	YDR418W	95.98	0
scaffold7-gene-2_21-mRNA-1	YDR395W	84.25	0
scaffold7-gene-2_22-mRNA-1	YDR394W	88.85	0
scaffold7-gene-2_23-mRNA-1	YDR393W	81.97	0
scaffold7-gene-2_27-mRNA-1	YDR389W	82.3	0
scaffold7-gene-2_28-mRNA-1	YDR388W	84.2	0
scaffold7-gene-2_28-mRNA-1	YDR388W	81.68	6.00E-70
scaffold7-gene-2_3-mRNA-1	YDR416W	76.48	0
scaffold7-gene-2_30-mRNA-1	YDR386W	78.96	0

scaffold7-gene-2_31-mRNA-1	YOR133W	96.11	0
scaffold7-gene-2_32-mRNA-1	YDR384C	80.71	0
scaffold7-gene-2_34-mRNA-1	YDR382W	95.83	6.00E-154
scaffold7-gene-2_42-mRNA-1	YDR375C	82.57	0
scaffold7-gene-2_47-mRNA-1	YDR429C	89.9	0
scaffold7-gene-2_52-mRNA-1	YDR421W	80.74	0
scaffold7-gene-2_6-mRNA-1	YDR412W	83.03	3.00E-180
scaffold7-gene-2_80-mRNA-1	YDR404C	88.95	0
scaffold7-gene-3_0-mRNA-1	YDR364C	82.63	0
scaffold7-gene-3_1-mRNA-1	YDR363W-A	89.47	9.00E-92
scaffold7-gene-3_128-mRNA-1	YDR342C	90.08	1.00E-178
scaffold7-gene-3_128-mRNA-1	YDR342C	87.96	8.00E-150
scaffold7-gene-3_128-mRNA-1	YDR342C	85.89	5.00E-147
scaffold7-gene-3_128-mRNA-1	YDR342C	86.15	4.00E-118
scaffold7-gene-3_13-mRNA-1	YDR350C	78.91	0
scaffold7-gene-3_17-mRNA-1	YDR346C	81.09	0
scaffold7-gene-3_23-mRNA-1	YDR338C	83.06	0
scaffold7-gene-3_24-mRNA-1	YDR337W	83.71	0
scaffold7-gene-3_26-mRNA-1	YDR335W	85.64	0
scaffold7-gene-3_27-mRNA-1	YDR334W	79.17	0
scaffold7-gene-3_3-mRNA-1	YDR362C	80.72	0
scaffold7-gene-3_32-mRNA-1	YDR329C	78.43	0
scaffold7-gene-3_34-mRNA-1	YDR326C	80.12	0
scaffold7-gene-3_35-mRNA-1	YDR372C	84.45	0
scaffold7-gene-3_4-mRNA-1	YDR361C	84.86	0
scaffold7-gene-3_41-mRNA-1	YDR365C	80.96	0
scaffold7-gene-3_6-mRNA-1	YDR358W	76.46	0
scaffold7-gene-3_8-mRNA-1	YDR356W	77.01	0
scaffold7-gene-3_9-mRNA-1	YDR354W	78.55	0
scaffold7-gene-4_121-mRNA-1	YDR310C	77.07	0
scaffold7-gene-4_124-mRNA-1	YDR293C	82.54	0
scaffold7-gene-4_15-mRNA-1	YDR303C	79.59	0
scaffold7-gene-4_17-mRNA-1	YDR301W	82.06	0
scaffold7-gene-4_18-mRNA-1	YDR300C	84.18	0
scaffold7-gene-4_19-mRNA-1	YDR299W	79.31	0
scaffold7-gene-4_2-mRNA-1	YDR316W	81.16	0
scaffold7-gene-4_20-mRNA-1	YDR298C	86.12	0
scaffold7-gene-4_21-mRNA-1	YDR297W	82.25	0
scaffold7-gene-4_24-mRNA-1	YDR294C	82.36	0
scaffold7-gene-4_27-mRNA-1	YDR291W	82.49	0
scaffold7-gene-4_30-mRNA-1	YDR287W	79.08	6.00E-168
scaffold7-gene-4_31-mRNA-1	YDR285W	76.64	0
scaffold7-gene-4_33-mRNA-1	YDR283C	84.96	0

scaffold7-gene-4_36-mRNA-1	YDR280W	84.34	0
scaffold7-gene-4_38-mRNA-1	YDR277C	81.32	0
scaffold7-gene-4_39-mRNA-1	YDR325W	81.4	0
scaffold7-gene-4_40-mRNA-1	YDR324C	83.87	0
scaffold7-gene-4_43-mRNA-1	YDR322W	80.91	0
scaffold7-gene-4_6-mRNA-1	YDR312W	81.65	0
scaffold7-gene-4_87-mRNA-1	YDR321W	82.23	0
scaffold7-gene-5_112-mRNA-1	YDR258C	82.94	0
scaffold7-gene-5_15-mRNA-1	YDR248C	81.2	8.00E-125
scaffold7-gene-5_18-mRNA-1	YDR245W	83.82	0
scaffold7-gene-5_19-mRNA-1	YDR244W	79.72	0
scaffold7-gene-5_2-mRNA-1	YDR262W	76.09	6.00E-108
scaffold7-gene-5_21-mRNA-1	YDR242W	80.98	0
scaffold7-gene-5_22-mRNA-1	YDR240C	77.18	0
scaffold7-gene-5_24-mRNA-1	YDR238C	85.4	0
scaffold7-gene-5_29-mRNA-1	YDR233C	86.5	0
scaffold7-gene-5_30-mRNA-1	YDR232W	84.82	0
scaffold7-gene-5_31-mRNA-1	YDR231C	80.98	2.00E-136
scaffold7-gene-5_32-mRNA-1	YDR229W	79.03	0
scaffold7-gene-5_33-mRNA-1	YDR228C	81.09	0
scaffold7-gene-5_35-mRNA-1	YDR226W	87.54	0
scaffold7-gene-5_36-mRNA-1	YDR225W	93.23	3.00E-168
scaffold7-gene-5_37-mRNA-1	YDR224C	93.72	5.00E-170
scaffold7-gene-5_40-mRNA-1	YDR221W	78.63	5.00E-63
scaffold7-gene-5_40-mRNA-1	YDR221W	76.8	5.00E-48
scaffold7-gene-5_47-mRNA-1	YDR270W	79.11	0
scaffold7-gene-5_48-mRNA-1	YDR268W	82.25	0
scaffold7-gene-5_49-mRNA-1	YDR267C	85.08	0
scaffold7-gene-5_50-mRNA-1	YDR266C	80.43	0
scaffold7-gene-5_51-mRNA-1	YDR265W	77.12	1.00E-155
scaffold7-gene-5_60-mRNA-1	YDR236C	81.29	4.00E-148
scaffold7-gene-5_65-mRNA-1	YDR235W	80.59	0
scaffold7-gene-5_8-mRNA-1	YDR256C	83.64	0
scaffold7-gene-6_1-mRNA-1	YDR208W	82.69	0
scaffold7-gene-6_12-mRNA-1	YDR195W	80.52	0
scaffold7-gene-6_17-mRNA-1	YDR190C	85.15	0
scaffold7-gene-6_20-mRNA-1	YDR186C	77.38	0
scaffold7-gene-6_21-mRNA-1	YDR185C	81.25	6.00E-121
scaffold7-gene-6_26-mRNA-1	YDR180W	77.67	0
scaffold7-gene-6_3-mRNA-1	YDR206W	89.4	6.00E-48
scaffold7-gene-6_31-mRNA-1	YDR176W	79.06	0
scaffold7-gene-6_33-mRNA-1	YDR174W	87.21	0
scaffold7-gene-6_34-mRNA-1	YDR173C	78.33	7.00E-178

scaffold7-gene-6_35-mRNA-1	YDR172W	83.49	0
scaffold7-gene-6_37-mRNA-1	YDR170C	84.11	0
scaffold7-gene-6_38-mRNA-1	YDR169C	81.18	0
scaffold7-gene-6_39-mRNA-1	YDR168W	81.68	0
scaffold7-gene-6_41-mRNA-1	YDR166C	79.83	0
scaffold7-gene-6_42-mRNA-1	YDR165W	77.21	0
scaffold7-gene-6_43-mRNA-1	YDR216W	77.14	0
scaffold7-gene-6_45-mRNA-1	YDR213W	82.2	0
scaffold7-gene-6_46-mRNA-1	YDR212W	86.37	0
scaffold7-gene-6_5-mRNA-1	YDR204W	83.23	0
scaffold7-gene-6_56-mRNA-1	YDR189W	83.5	0
scaffold7-gene-6_6-mRNA-1	YDR202C	82.74	0
scaffold7-gene-6_7-mRNA-1	YDR201W	79.92	4.00E-98
scaffold7-gene-6_9-mRNA-1	YDR198C	75.63	0
scaffold7-gene-6_98-mRNA-1	YDR175C	80.92	1.00E-180
scaffold7-gene-7_0-mRNA-1	YDR158W	86.19	0
scaffold7-gene-7_10-mRNA-1	YDR145W	85.12	1.00E-167
scaffold7-gene-7_12-mRNA-1	YDR143C	79.64	8.00E-105
scaffold7-gene-7_12-mRNA-1	YDR143C	73.19	1.00E-88
scaffold7-gene-7_124-mRNA-1	YDR129C	85.54	0
scaffold7-gene-7_14-mRNA-1	YDR141C	81.72	0
scaffold7-gene-7_18-mRNA-1	YDR135C	82.35	0
scaffold7-gene-7_2-mRNA-1	YDR155C	91.63	0
scaffold7-gene-7_24-mRNA-1	YDR127W	84.33	0
scaffold7-gene-7_25-mRNA-1	YDR126W	80.1	0
scaffold7-gene-7_26-mRNA-1	YDR125C	79.28	0
scaffold7-gene-7_28-mRNA-1	YDR123C	77.12	6.00E-138
scaffold7-gene-7_29-mRNA-1	YDR122W	81.75	0
scaffold7-gene-7_3-mRNA-1	YDR153C	82.02	0
scaffold7-gene-7_36-mRNA-1	YDR163W	86.99	2.00E-32
scaffold7-gene-7_37-mRNA-1	YDR162C	82.69	1.00E-134
scaffold7-gene-7_5-mRNA-1	YDR151C	77.41	2.00E-138
scaffold7-gene-7_7-mRNA-1	YDR148C	88.11	0
scaffold7-gene-7_71-mRNA-1	YDR142C	80.86	0
scaffold7-gene-8_0-mRNA-1	YDR108W	81.8	0
scaffold7-gene-8_1-mRNA-1	YDR107C	80.3	0
scaffold7-gene-8_10-mRNA-1	YDR097C	80.87	0
scaffold7-gene-8_11-mRNA-1	YDR096W	79.88	0
scaffold7-gene-8_12-mRNA-1	YDR093W	80.38	0
scaffold7-gene-8_14-mRNA-1	YDR091C	89.53	0
scaffold7-gene-8_16-mRNA-1	YDR089W	77.23	0
scaffold7-gene-8_17-mRNA-1	YDR088C	77.96	0
scaffold7-gene-8_22-mRNA-1	YDR083W	82.63	0

scaffold7-gene-8_23-mRNA-1	YDR082W	74.49	4.00E-147
scaffold7-gene-8_25-mRNA-1	YDR080W	80.81	0
scaffold7-gene-8_27-mRNA-1	YDR079W	87.28	1.00E-105
scaffold7-gene-8_29-mRNA-1	YDR077W	84.85	9.00E-131
scaffold7-gene-8_29-mRNA-1	YDR077W	91.74	3.00E-41
scaffold7-gene-8_29-mRNA-1	YDR077W	85.37	1.00E-29
scaffold7-gene-8_30-mRNA-1	YDR076W	78.7	0
scaffold7-gene-8_31-mRNA-1	YDR075W	87.19	0
scaffold7-gene-8_32-mRNA-1	YDR074W	83.74	0
scaffold7-gene-8_34-mRNA-1	YDR072C	77.38	0
scaffold7-gene-8_37-mRNA-1	YDR069C	80.41	0
scaffold7-gene-8_39-mRNA-1	YDR067C	83.03	3.00E-169
scaffold7-gene-8_46-mRNA-1	YDR110W	83.29	0
scaffold7-gene-8_6-mRNA-1	YDR101C	84.01	0
scaffold7-gene-8_8-mRNA-1	YDR099W	88.03	0
scaffold7-gene-9_1-mRNA-1	YDR055W	80.28	0
scaffold7-gene-9_10-mRNA-1	YDR044W	88.89	0
scaffold7-gene-9_110-mRNA-1	YDR036C	79.87	0
scaffold7-gene-9_12-mRNA-1	YDR041W	81.15	2.00E-127
scaffold7-gene-9_147-mRNA-1	YDR063W	79.82	4.00E-87
scaffold7-gene-9_151-mRNA-1	YDR059C	87.13	4.00E-128
scaffold7-gene-9_153-mRNA-1	YDR025W	95.33	0
scaffold7-gene-9_155-mRNA-1	YDR064W	93.82	0
scaffold7-gene-9_16-mRNA-1	YDR035W	88.02	0
scaffold7-gene-9_19-mRNA-1	YDR033W	84.68	0
scaffold7-gene-9_2-mRNA-1	YDR054C	85.4	0
scaffold7-gene-9_20-mRNA-1	YDR032C	87.5	0
scaffold7-gene-9_21-mRNA-1	YDR031W	84.21	1.00E-96
scaffold7-gene-9_23-mRNA-1	YDR028C	84.62	0
scaffold7-gene-9_23-mRNA-1	YDR028C	77.19	0
scaffold7-gene-9_24-mRNA-1	YDR027C	79.29	0
scaffold7-gene-9_25-mRNA-1	YDR026C	77.92	0
scaffold7-gene-9_27-mRNA-1	YDR023W	86.55	0
scaffold7-gene-9_28-mRNA-1	YDR022C	76.39	3.00E-80
scaffold7-gene-9_29-mRNA-1	YDR021W	86.79	0
scaffold7-gene-9_32-mRNA-1	YDR018C	76.71	6.00E-169
scaffold7-gene-9_33-mRNA-1	YDR017C	77.79	0
scaffold7-gene-9_39-mRNA-1	YBR031W	94.41	0
scaffold7-gene-9_4-mRNA-1	YDR051C	84.45	0
scaffold7-gene-9_40-mRNA-1	YBR030W	77.79	0
scaffold7-gene-9_43-mRNA-1	YDR062W	83.48	0
scaffold7-gene-9_44-mRNA-1	YDR061W	80.62	0
scaffold7-gene-9_45-mRNA-1	YDR060W	80.69	0

scaffold7-gene-9_47-mRNA-1	YDR058C	81.23	0
scaffold7-gene-9_48-mRNA-1	YDR057W	78.14	0
scaffold7-gene-9_5-mRNA-1	YDR050C	96.25	0
scaffold7-gene-9_7-mRNA-1	YDR047W	85.01	0
scaffold8-gene-0_1-mRNA-1	YAR071W	92.31	0
scaffold8-gene-0_13-mRNA-1	YHL034C	86.95	0
scaffold8-gene-0_14-mRNA-1	YHL033C	92.77	0
scaffold8-gene-0_15-mRNA-1	YHL030W	79.16	0
scaffold8-gene-0_16-mRNA-1	YHL029C	79.98	0
scaffold8-gene-0_21-mRNA-1	YHL024W	81.24	0
scaffold8-gene-0_21-mRNA-1	YHL024W	83.11	0
scaffold8-gene-0_25-mRNA-1	YHL020C	81.55	0
scaffold8-gene-0_47-mRNA-1	YHL023C	79.02	0
scaffold8-gene-0_7-mRNA-1	YDR533C	81.53	2.00E-162
scaffold8-gene-1_1-mRNA-1	YHL008C	81.8	0
scaffold8-gene-1_10-mRNA-1	YHR003C	80.11	0
scaffold8-gene-1_12-mRNA-1	YHR005C	83.87	0
scaffold8-gene-1_126-mRNA-1	YOR028C	75.64	3.00E-111
scaffold8-gene-1_15-mRNA-1	YHR007C	88.98	0
scaffold8-gene-1_16-mRNA-1	YHR008C	87.22	0
scaffold8-gene-1_17-mRNA-1	YHR009C	82.39	0
scaffold8-gene-1_2-mRNA-1	YHL007C	81.25	0
scaffold8-gene-1_21-mRNA-1	YHR013C	85.71	0
scaffold8-gene-1_24-mRNA-1	YOR020C	87.54	3.00E-102
scaffold8-gene-1_35-mRNA-1	YOR033C	76.89	2.00E-57
scaffold8-gene-1_39-mRNA-1	YOR038C	80.71	0
scaffold8-gene-1_4-mRNA-1	YHL003C	83.05	0
scaffold8-gene-1_40-mRNA-1	YOR039W	86.65	0
scaffold8-gene-1_43-mRNA-1	YOR043W	83.77	0
scaffold8-gene-1_44-mRNA-1	YHL016C	85.7	0
scaffold8-gene-1_45-mRNA-1	YHL015W	95.63	3.00E-167
scaffold8-gene-1_46-mRNA-1	YHL014C	83.91	0
scaffold8-gene-1_47-mRNA-1	YHL013C	81.87	0
scaffold8-gene-1_49-mRNA-1	YHL011C	89.24	0
scaffold8-gene-1_5-mRNA-1	YHL002W	79.92	0
scaffold8-gene-1_6-mRNA-1	YKL006W	94.52	7.00E-126
scaffold8-gene-1_63-mRNA-1	YOR037W	77.72	2.00E-150
scaffold8-gene-1_77-mRNA-1	YHR010W	96.77	1.00E-176
scaffold8-gene-1_77-mRNA-1	YHR010W	93.65	3.00E-18
scaffold8-gene-1_9-mRNA-1	YHR002W	84.17	0
scaffold8-gene-2_0-mRNA-1	YOR051C	80.61	0
scaffold8-gene-2_1-mRNA-1	YOR052C	87.31	1.00E-146
scaffold8-gene-2_10-mRNA-1	YOR063W	94.6	0

scaffold8-gene-2_12-mRNA-1	YOR065W	86.94	0
scaffold8-gene-2_120-mRNA-1	YOR058C	77.55	0
scaffold8-gene-2_13-mRNA-1	YOR066W	77.22	0
scaffold8-gene-2_14-mRNA-1	YOR067C	83.58	0
scaffold8-gene-2_15-mRNA-1	YOR069W	78.78	0
scaffold8-gene-2_155-mRNA-1	YOR096W	96.94	0
scaffold8-gene-2_155-mRNA-1	YOR096W	97.92	3.00E-66
scaffold8-gene-2_16-mRNA-1	YOR070C	82.75	0
scaffold8-gene-2_18-mRNA-1	YOR074C	85.21	0
scaffold8-gene-2_19-mRNA-1	YOR075W	81.42	0
scaffold8-gene-2_25-mRNA-1	YOR081C	79.39	0
scaffold8-gene-2_29-mRNA-1	YOR086C	83.26	0
scaffold8-gene-2_30-mRNA-1	YOR087W	82.38	0
scaffold8-gene-2_32-mRNA-1	YOR090C	81.38	0
scaffold8-gene-2_34-mRNA-1	YOR092W	81.13	0
scaffold8-gene-2_35-mRNA-1	YOR093C	81.89	0
scaffold8-gene-2_37-mRNA-1	YOR095C	83.72	0
scaffold8-gene-2_4-mRNA-1	YOR057W	75.3	6.00E-144
scaffold8-gene-2_41-mRNA-1	YOR099W	83.56	0
scaffold8-gene-2_44-mRNA-1	YOR103C	84.27	4.00E-101
scaffold8-gene-2_47-mRNA-1	YOR046C	84.6	0
scaffold8-gene-2_48-mRNA-1	YOR047C	80.37	0
scaffold8-gene-2_49-mRNA-1	YOR048C	83.53	0
scaffold8-gene-2_7-mRNA-1	YOR060C	79.62	5.00E-153
scaffold8-gene-3_1-mRNA-1	YOR112W	80.37	0
scaffold8-gene-3_12-mRNA-1	YOR124C	80.53	0
scaffold8-gene-3_125-mRNA-1	YOR141C	80.68	0
scaffold8-gene-3_131-mRNA-1	YOR122C	88.89	9.00E-128
scaffold8-gene-3_15-mRNA-1	YOR127W	75.87	0
scaffold8-gene-3_18-mRNA-1	YOR130C	80.34	0
scaffold8-gene-3_2-mRNA-1	YOR113W	80.28	0
scaffold8-gene-3_20-mRNA-1	YOR132W	80.89	0
scaffold8-gene-3_21-mRNA-1	YOR133W	94.87	0
scaffold8-gene-3_28-mRNA-1	YOR142W	84.38	0
scaffold8-gene-3_29-mRNA-1	YOR145C	85.48	0
scaffold8-gene-3_30-mRNA-1	YOR147W	79.82	0
scaffold8-gene-3_32-mRNA-1	YOR149C	75.87	0
scaffold8-gene-3_33-mRNA-1	YOR150W	83.54	9.00E-124
scaffold8-gene-3_34-mRNA-1	YOR151C	88.93	0
scaffold8-gene-3_36-mRNA-1	YOR153W	81.4	0
scaffold8-gene-3_39-mRNA-1	YOR108W	83.93	0
scaffold8-gene-3_40-mRNA-1	YOR109W	82.56	0
scaffold8-gene-3_5-mRNA-1	YOR116C	86.15	0

scaffold8-gene-3_6-mRNA-1	YOR117W	86.75	0
scaffold8-gene-3_99-mRNA-1	YOR125C	84.06	2.00E-175
scaffold8-gene-4_11-mRNA-1	YOR173W	83.57	0
scaffold8-gene-4_13-mRNA-1	YOR175C	82.77	0
scaffold8-gene-4_16-mRNA-1	YOR178C	80.1	3.00E-80
scaffold8-gene-4_18-mRNA-1	YOR180C	79.77	3.00E-156
scaffold8-gene-4_19-mRNA-1	YOR181W	79.17	0
scaffold8-gene-4_2-mRNA-1	YOR162C	74.14	0
scaffold8-gene-4_2-mRNA-1	YOR162C	82.4	2.00E-22
scaffold8-gene-4_20-mRNA-1	YOR184W	84.85	0
scaffold8-gene-4_21-mRNA-1	YOR185C	86.79	0
scaffold8-gene-4_23-mRNA-1	YOR187W	86.47	0
scaffold8-gene-4_24-mRNA-1	YOR188W	78.88	0
scaffold8-gene-4_26-mRNA-1	YOR190W	80.96	0
scaffold8-gene-4_27-mRNA-1	YOR191W	81.71	0
scaffold8-gene-4_29-mRNA-1	YOR194C	79.69	2.00E-168
scaffold8-gene-4_33-mRNA-1	YOR198C	87.46	0
scaffold8-gene-4_36-mRNA-1	YOR204W	87.15	0
scaffold8-gene-4_39-mRNA-1	YOR207C	86.31	0
scaffold8-gene-4_4-mRNA-1	YOR164C	84.56	0
scaffold8-gene-4_46-mRNA-1	YOR160W	80.97	0
scaffold8-gene-4_5-mRNA-1	YOR165W	81.44	0
scaffold8-gene-4_7-mRNA-1	YOR167C	97.54	2.00E-96
scaffold8-gene-4_8-mRNA-1	YOR168W	85.2	0
scaffold8-gene-4_9-mRNA-1	YOR171C	79.85	0
scaffold8-gene-5_0-mRNA-1	YOR215C	83.66	4.00E-148
scaffold8-gene-5_10-mRNA-1	YOR227W	79.34	0
scaffold8-gene-5_11-mRNA-1	YOR228C	77.79	2.00E-147
scaffold8-gene-5_14-mRNA-1	YOR231W	79.81	0
scaffold8-gene-5_169-mRNA-1	YPL143W	93.44	8.00E-128
scaffold8-gene-5_18-mRNA-1	YOR236W	77.71	2.00E-101
scaffold8-gene-5_2-mRNA-1	YOR217W	81.78	0
scaffold8-gene-5_22-mRNA-1	YOR241W	81.41	0
scaffold8-gene-5_25-mRNA-1	YOR244W	83.04	0
scaffold8-gene-5_3-mRNA-1	YOR219C	78.03	0
scaffold8-gene-5_34-mRNA-1	YOR254C	82.87	0
scaffold8-gene-5_35-mRNA-1	YOR255W	77.35	3.00E-101
scaffold8-gene-5_37-mRNA-1	YOR257W	86.65	3.00E-153
scaffold8-gene-5_39-mRNA-1	YOR259C	85.77	0
scaffold8-gene-5_4-mRNA-1	YOR220W	79.28	4.00E-154
scaffold8-gene-5_40-mRNA-1	YOR260W	83.02	0
scaffold8-gene-5_41-mRNA-1	YOR261C	85.36	0
scaffold8-gene-5_42-mRNA-1	YOR262W	83	0

scaffold8-gene-5_43-mRNA-1	YOR264W	72.8	3.00E-93
scaffold8-gene-5_46-mRNA-1	YOR267C	83.11	0
scaffold8-gene-5_48-mRNA-1	YOR270C	86.65	0
scaffold8-gene-5_49-mRNA-1	YOR271C	83.03	0
scaffold8-gene-5_5-mRNA-1	YOR221C	82.38	0
scaffold8-gene-5_50-mRNA-1	YOR272W	84.34	0
scaffold8-gene-5_51-mRNA-1	YOR209C	81.92	0
scaffold8-gene-5_53-mRNA-1	YOR211C	82.04	0
scaffold8-gene-5_54-mRNA-1	YOR212W	83.26	0
scaffold8-gene-5_59-mRNA-1	YOR239W	87.25	0
scaffold8-gene-5_6-mRNA-1	YOR222W	86.18	0
scaffold8-gene-5_7-mRNA-1	YOR223W	80.94	0
scaffold8-gene-5_9-mRNA-1	YOR226C	83.76	7.00E-125
scaffold8-gene-6_107-mRNA-1	YOR312C	96.03	0
scaffold8-gene-6_11-mRNA-1	YOR294W	85.97	0
scaffold8-gene-6_13-mRNA-1	YOR296W	80.57	0
scaffold8-gene-6_151-mRNA-1	YOR293W	95.91	5.00E-122
scaffold8-gene-6_151-mRNA-1	YOR293W	100	2.00E-20
scaffold8-gene-6_20-mRNA-1	YOR304W	83.54	0
scaffold8-gene-6_23-mRNA-1	YOR306C	81.62	0
scaffold8-gene-6_24-mRNA-1	YOR307C	78.57	0
scaffold8-gene-6_26-mRNA-1	YOR310C	87.04	0
scaffold8-gene-6_27-mRNA-1	YOR311C	83.69	0
scaffold8-gene-6_32-mRNA-1	YOR317W	80.46	0
scaffold8-gene-6_35-mRNA-1	YOR321W	80.17	0
scaffold8-gene-6_36-mRNA-1	YOR322C	80.58	0
scaffold8-gene-6_39-mRNA-1	YOR326W	82.42	0
scaffold8-gene-6_40-mRNA-1	YOR327C	84.57	5.00E-95
scaffold8-gene-6_41-mRNA-1	YOR328W	79.84	0
scaffold8-gene-6_42-mRNA-1	YOR273C	81.01	0
scaffold8-gene-6_45-mRNA-1	YOR276W	86.49	9.00E-149
scaffold8-gene-6_49-mRNA-1	YOR281C	82.62	0
scaffold8-gene-6_66-mRNA-1	YOR283W	85.61	0
scaffold8-gene-6_7-mRNA-1	YOR290C	82.84	0
scaffold8-gene-7_10-mRNA-1	YOR348C	81.09	0
scaffold8-gene-7_11-mRNA-1	YOR349W	74.29	0
scaffold8-gene-7_15-mRNA-1	YOR353C	77.82	0
scaffold8-gene-7_17-mRNA-1	YOR355W	80.29	0
scaffold8-gene-7_18-mRNA-1	YOR356W	81.87	0
scaffold8-gene-7_19-mRNA-1	YOR357C	87.91	1.00E-162
scaffold8-gene-7_21-mRNA-1	YOR359W	81.69	0
scaffold8-gene-7_23-mRNA-1	YOR361C	84.92	0
scaffold8-gene-7_28-mRNA-1	YOR367W	80.98	1.00E-132

scaffold8-gene-7_30-mRNA-1	YOR369C	94.44	0
scaffold8-gene-7_35-mRNA-1	YOR374W	85.82	0
scaffold8-gene-7_37-mRNA-1	YOR330C	80.3	0
scaffold8-gene-7_4-mRNA-1	YOR340C	85.63	0
scaffold8-gene-7_40-mRNA-1	YOR335C	87.27	0
scaffold8-gene-7_45-mRNA-1	YOR360C	81.97	0
scaffold8-gene-7_5-mRNA-1	YOR341W	86.49	0
scaffold8-gene-7_6-mRNA-1	YOR342C	80.63	0
scaffold8-gene-7_63-mRNA-1	YOR337W	81.58	0
scaffold8-gene-7_7-mRNA-1	YOR344C	83.71	0
scaffold8-gene-7_8-mRNA-1	YOR346W	78.64	0
scaffold8-gene-7_9-mRNA-1	YOR347C	82.56	0
scaffold8-gene-8_0-mRNA-1	YOR381W	80.01	0
scaffold8-gene-8_2-mRNA-1	YOR383C	78.78	4.00E-108
scaffold8-gene-8_24-mRNA-1	YOR380W	82.84	0
scaffold8-gene-8_4-mRNA-1	YFL058W	87.69	0
scaffold8-gene-8_5-mRNA-1	YOR375C	89.42	0
scaffold9-gene-0_0-mRNA-1	YNL031C	93.9	3.00E-177
scaffold9-gene-0_1-mRNA-1	YNL032W	81.59	0
scaffold9-gene-0_104-mRNA-1	YNL070W	87.03	1.00E-53
scaffold9-gene-0_11-mRNA-1	YNL041C	79.1	0
scaffold9-gene-0_134-mRNA-1	YNL069C	92.77	0
scaffold9-gene-0_134-mRNA-1	YNL069C	100	8.00E-07
scaffold9-gene-0_141-mRNA-1	YNL044W	85.43	8.00E-150
scaffold9-gene-0_23-mRNA-1	YNL054W	78.85	0
scaffold9-gene-0_24-mRNA-1	YNL055C	85.88	0
scaffold9-gene-0_27-mRNA-1	YNL059C	82.52	0
scaffold9-gene-0_28-mRNA-1	YNL061W	87.21	0
scaffold9-gene-0_29-mRNA-1	YNL062C	81.52	0
scaffold9-gene-0_31-mRNA-1	YNL064C	87.66	0
scaffold9-gene-0_34-mRNA-1	YNL067W	89.64	0
scaffold9-gene-0_37-mRNA-1	YNL071W	83.06	0
scaffold9-gene-0_4-mRNA-1	YBL019W	78.64	0
scaffold9-gene-0_41-mRNA-1	YNL075W	86.55	0
scaffold9-gene-0_42-mRNA-1	YNL076W	81.23	0
scaffold9-gene-0_97-mRNA-1	YNL048W	82.33	0
scaffold9-gene-1_0-mRNA-1	YNL083W	82.63	0
scaffold9-gene-1_1-mRNA-1	YNL084C	82.18	0
scaffold9-gene-1_10-mRNA-1	YNL094W	79.16	0
scaffold9-gene-1_11-mRNA-1	YNL095C	80.45	0
scaffold9-gene-1_114-mRNA-1	YNL122C	86.84	2.00E-68
scaffold9-gene-1_135-mRNA-1	YNL096C	92.09	1.00E-172
scaffold9-gene-1_135-mRNA-1	YNL096C	92.21	2.00E-56

scaffold9-gene-1_136-mRNA-1	YNL112W	87	0
scaffold9-gene-1_136-mRNA-1	YNL112W	86.51	2.00E-110
scaffold9-gene-1_14-mRNA-1	YNL097C	79.4	0
scaffold9-gene-1_15-mRNA-1	YNL098C	78.78	4.00E-180
scaffold9-gene-1_18-mRNA-1	YNL101W	82.94	0
scaffold9-gene-1_19-mRNA-1	YNL102W	81.64	0
scaffold9-gene-1_2-mRNA-1	YNL085W	83.98	0
scaffold9-gene-1_21-mRNA-1	YNL104C	84.31	0
scaffold9-gene-1_22-mRNA-1	YNL106C	80.6	0
scaffold9-gene-1_25-mRNA-1	YNL110C	83.8	6.00E-177
scaffold9-gene-1_26-mRNA-1	YNL111C	87.47	1.00E-116
scaffold9-gene-1_32-mRNA-1	YNL118C	80.03	0
scaffold9-gene-1_35-mRNA-1	YNL123W	83.73	0
scaffold9-gene-1_36-mRNA-1	YNL124W	76.8	2.00E-175
scaffold9-gene-1_38-mRNA-1	YNL126W	81.58	0
scaffold9-gene-1_39-mRNA-1	YNL077W	76.89	0
scaffold9-gene-1_41-mRNA-1	YNL079C	87.4	0
scaffold9-gene-1_42-mRNA-1	YNL080C	81.28	0
scaffold9-gene-1_44-mRNA-1	YNL082W	76.37	0
scaffold9-gene-1_5-mRNA-1	YNL088W	81.34	0
scaffold9-gene-1_58-mRNA-1	YNL116W	85.85	0
scaffold9-gene-1_7-mRNA-1	YNL091W	76.72	0
scaffold9-gene-1_8-mRNA-1	YNL092W	77.8	0
scaffold9-gene-2_1-mRNA-1	YCR102C	75.84	2.00E-149
scaffold9-gene-2_117-mRNA-1	YNL180C	79.13	0
scaffold9-gene-2_159-mRNA-1	YNL162W	95.91	1.00E-146
scaffold9-gene-2_16-mRNA-1	YNL154C	82.3	0
scaffold9-gene-2_19-mRNA-1	YNL157W	85.68	4.00E-132
scaffold9-gene-2_2-mRNA-1	YNL135C	92.75	4.00E-141
scaffold9-gene-2_22-mRNA-1	YNL160W	81.5	0
scaffold9-gene-2_25-mRNA-1	YNL163C	82.22	0
scaffold9-gene-2_26-mRNA-1	YNL164C	81.89	0
scaffold9-gene-2_28-mRNA-1	YNL166C	87.7	3.00E-33
scaffold9-gene-2_31-mRNA-1	YNL169C	84.54	0
scaffold9-gene-2_32-mRNA-1	YNL172W	80.03	0
scaffold9-gene-2_34-mRNA-1	YNL175C	82.29	0
scaffold9-gene-2_37-mRNA-1	YNL178W	95.16	0
scaffold9-gene-2_4-mRNA-1	YNL137C	81.76	0
scaffold9-gene-2_40-mRNA-1	YNL182C	79.79	0
scaffold9-gene-2_41-mRNA-1	YNL183C	83.59	0
scaffold9-gene-2_42-mRNA-1	YNL185C	83.66	5.00E-121
scaffold9-gene-2_43-mRNA-1	YNL186W	79.79	0
scaffold9-gene-2_43-mRNA-1	YNL186W	83.93	9.00E-36

scaffold9-gene-2_43-mRNA-1	YNL186W	97.62	2.00E-12
scaffold9-gene-2_43-mRNA-1	YNL186W	91.67	9.00E-11
scaffold9-gene-2_46-mRNA-1	YNL127W	81.3	0
scaffold9-gene-2_47-mRNA-1	YNL128W	78.15	0
scaffold9-gene-2_5-mRNA-1	YNL138W	81.35	0
scaffold9-gene-2_50-mRNA-1	YNL131W	83.95	3.00E-123
scaffold9-gene-2_51-mRNA-1	YNL132W	84.84	0
scaffold9-gene-3_10-mRNA-1	YNL207W	82.39	0
scaffold9-gene-3_12-mRNA-1	YDL229W	94.8	0
scaffold9-gene-3_14-mRNA-1	YNL212W	82.13	0
scaffold9-gene-3_17-mRNA-1	YNL216W	82.45	0
scaffold9-gene-3_19-mRNA-1	YNL218W	82.45	0
scaffold9-gene-3_21-mRNA-1	YNL220W	87.36	0
scaffold9-gene-3_23-mRNA-1	YNL222W	90.08	0
scaffold9-gene-3_24-mRNA-1	YNL223W	81.59	0
scaffold9-gene-3_25-mRNA-1	YNL224C	79.02	3.00E-75
scaffold9-gene-3_26-mRNA-1	YNL225C	76.41	0
scaffold9-gene-3_27-mRNA-1	YNL227C	79.43	0
scaffold9-gene-3_29-mRNA-1	YNL230C	77	2.00E-173
scaffold9-gene-3_31-mRNA-1	YNL232W	81.57	0
scaffold9-gene-3_32-mRNA-1	YNL233W	74.78	0
scaffold9-gene-3_34-mRNA-1	YNL236W	83.67	0
scaffold9-gene-3_39-mRNA-1	YNL241C	84.6	0
scaffold9-gene-3_40-mRNA-1	YNL242W	78.12	0
scaffold9-gene-3_42-mRNA-1	YNL244C	88.72	1.00E-110
scaffold9-gene-3_44-mRNA-1	YNL189W	88.73	0
scaffold9-gene-3_45-mRNA-1	YNL190W	83.79	2.00E-161
scaffold9-gene-3_45-mRNA-1	YNL190W	87.45	6.00E-82
scaffold9-gene-3_45-mRNA-1	YNL190W	86.94	4.00E-78
scaffold9-gene-3_45-mRNA-1	YNL190W	88.1	1.00E-64
scaffold9-gene-3_45-mRNA-1	YNL190W	86.54	6.00E-57
scaffold9-gene-3_45-mRNA-1	YNL190W	88.59	1.00E-44
scaffold9-gene-3_45-mRNA-1	YNL190W	88.51	6.00E-22
scaffold9-gene-3_46-mRNA-1	YNL191W	84.09	0
scaffold9-gene-3_47-mRNA-1	YNL192W	81.92	0
scaffold9-gene-3_6-mRNA-1	YNL201C	82.19	0
scaffold9-gene-3_7-mRNA-1	YNL202W	81.56	0
scaffold9-gene-3_9-mRNA-1	YNL206C	80.53	0
scaffold9-gene-4_0-mRNA-1	YNL251C	83.69	0
scaffold9-gene-4_10-mRNA-1	YNL262W	82.47	0
scaffold9-gene-4_14-mRNA-1	YNL267W	81.46	0
scaffold9-gene-4_15-mRNA-1	YNL268W	82.58	0
scaffold9-gene-4_16-mRNA-1	YNL270C	80.89	0

scaffold9-gene-4_17-mRNA-1	YNL271C	80.71	0
scaffold9-gene-4_17-mRNA-1	YNL271C	82.1	0
scaffold9-gene-4_18-mRNA-1	YNL272C	81.54	0
scaffold9-gene-4_20-mRNA-1	YNL274C	82.13	0
scaffold9-gene-4_25-mRNA-1	YNL280C	83.38	0
scaffold9-gene-4_28-mRNA-1	YNL283C	79.03	2.00E-174
scaffold9-gene-4_29-mRNA-1	YNL284C	82.08	0
scaffold9-gene-4_3-mRNA-1	YNL254C	78.07	4.00E-151
scaffold9-gene-4_31-mRNA-1	YNL287W	85.5	0
scaffold9-gene-4_32-mRNA-1	YNL288W	85.13	0
scaffold9-gene-4_33-mRNA-1	YNL289W	83.75	0
scaffold9-gene-4_38-mRNA-1	YNL248C	84.16	0
scaffold9-gene-4_39-mRNA-1	YNL249C	77.73	0
scaffold9-gene-4_4-mRNA-1	YNL256W	79.18	0
scaffold9-gene-4_40-mRNA-1	YNL250W	81.19	0
scaffold9-gene-4_58-mRNA-1	YNL265C	82.77	0
scaffold9-gene-5_0-mRNA-1	YNL298W	80.7	0
scaffold9-gene-5_10-mRNA-1	YNL309W	79.78	0
scaffold9-gene-5_113-mRNA-1	YNL297C	80.61	0
scaffold9-gene-5_117-mRNA-1	YOL120C	94.44	0
scaffold9-gene-5_117-mRNA-1	YOL120C	83.76	6.00E-23
scaffold9-gene-5_118-mRNA-1	YNL302C	96.67	0
scaffold9-gene-5_119-mRNA-1	YNL312W	84.58	0
scaffold9-gene-5_14-mRNA-1	YNL313C	80.24	0
scaffold9-gene-5_18-mRNA-1	YNL317W	84.56	0
scaffold9-gene-5_20-mRNA-1	YNL320W	83.18	0
scaffold9-gene-5_21-mRNA-1	YNL321W	81.29	0
scaffold9-gene-5_22-mRNA-1	YNL322C	74.29	9.00E-97
scaffold9-gene-5_23-mRNA-1	YNL323W	82.19	0
scaffold9-gene-5_24-mRNA-1	YNL325C	82.96	0
scaffold9-gene-5_27-mRNA-1	YNL328C	83.89	1.00E-116
scaffold9-gene-5_29-mRNA-1	YNL330C	87.05	0
scaffold9-gene-5_30-mRNA-1	YDL243C	82.56	0
scaffold9-gene-5_32-mRNA-1	YCR098C	86.74	0
NP_009390_T	YAL012W	88.34	0
NP_010474_T	YDR188W	81.9	0
NP_010628_T	YDR341C	86.45	0
NP_009636_T	YBR080C	87.06	0
NP_012550_T	YJR016C	88.11	0
NP_011105_T	YER178W	87.35	0
NP_011542_T	YGR028W	84.16	0
NP_009685_T	YBR127C	89.4	0
NP_014282_T	YNL117W	83.84	0

NP_012368_T	YJL167W	86.55	0
NP_011262_T	YGL252C	86.27	0
NP_009781_T	YBR222C	82.71	0
NP_011770_T	YHR174W	93.31	0
NP_011831_T	YHL032C	81.81	0
NP_013473_T	YLR369W	82.57	0
NP_010475_T	YDR189W	83.63	0
NP_010632_T	YDR345C	89.68	0
NP_013661_T	YML051W	84.23	0
NP_011962_T	YHR094C	87.75	0
NP_012364_T	YJL171C	84.51	0
NP_009650_T	YBR092C	87.08	0
NP_012044_T	YHR174W	93.31	0
NP_009624_T	YBR068C	80.97	0
NP_013230_T	YLR129W	83.92	0
NP_011964_T	YDR345C	74.68	2.00E-160
NP_011018_T	YER093C	81.89	0
NP_012225_T	YIL039W	82.03	0
NP_009462_T	YBL091C	85.57	0
NP_010167_T	YDL116W	80.95	0
NP_014152_T	YNL247W	83.51	0
NP_015103_T	YPL221W	81.28	0
NP_015077_T	YPL247C	79.69	0
NP_009598_T	YBR042C	81.49	0
NP_013951_T	YMR224C	79.18	1.00E-49
NP_011960_T	YHR092C	87.97	0
NP_013719_T	YMR006C	84.24	0
NP_013958_T	YMR231W	81.14	0
NP_009599_T	YBR043C	81.51	0
NP_012797_T	YKL125W	84.49	0
NP_013948_T	YMR221C	80.27	0
NP_013472_T	YLR368W	79.84	0
NP_010253_T	YDL031W	83.31	0
NP_013721_T	YMR008C	84.02	0
NP_683716_T	YFR048W	80.54	0
NP_014982_T	YOR337W	81.52	0
NP_013102_T	YLR002C	83.25	0
NP_012326_T	YJL209W	79.51	0
NP_010521_T	YDR235W	80.63	0
NP_009421_T	YAR042W	82.51	0
NP_009421_T	YAR042W	84.35	0
NP_014349_T	YNL049C	79.7	0
NP_010920_T	YER005W	80.4	0

NP_009625_T	YBR069C	83.63	0
NP_010982_T	YER060W-A	85.67	0
NP_010933_T	YER017C	82.6	0
NP_012075_T	YHR205W	82.32	0
NP_015129_T	YPL195W	80.93	0
NP_116709_T	YFR051C	82.38	0
NP_012331_T	YJL204C	79.35	0
NP_015130_T	YPL194W	78.82	0
NP_012328_T	YJL207C	79.13	0
NP_011627_T	YGR112W	79.23	0
NP_011373_T	YGL142C	79.03	0
NP_013627_T	YML083C	76.63	0
NP_013934_T	YMR207C	79.35	0
NP_013959_T	YMR232W	79.11	0
NP_012444_T	YJL091C	81.15	0
NP_010630_T	YHR092C	87.97	0
NP_010629_T	YHR092C	87.97	0
NP_011626_T	YGR111W	77.92	0
NP_011853_T	YHL010C	79.53	0
NP_015489_T	YPR163C	85.83	0
NP_015489_T	YPR163C	87.8	2.00E-79
NP_015105_T	YPL219W	80.24	0
NP_116641_T	YFL013C	77.88	0
NP_009714_T	YBR156C	77.09	0
NP_012640_T	YJR106W	78.66	0
NP_012226_T	YIL038C	80.7	0
NP_009371_T	YAL031C	77.99	0
NP_012445_T	YJL090C	77.22	0
NP_011840_T	YHL023C	79.02	0
NP_015076_T	YPL248C	77.27	0
NP_010404_T	YDR119W	77.85	0
NP_013201_T	YLR100W	80.97	0
NP_009918_T	YCL009C	86.55	0
NP_015038_T	YHR174W	93.29	0
NP_015042_T	YHR174W	93.29	0
NP_014056_T	YHR174W	93.29	0
NP_012829_T	YKL094W	81.87	0
NP_009824_T	YBR265W	81.71	0
NP_009825_T	YBR267W	82.43	0
NP_009742_T	YBR183W	81	0
NP_009919_T	YCL008C	78.53	0
NP_116681_T	YFR025C	78.42	1.00E-180
NP_014983_T	YOR338W	78.41	0

NP_014680_T	YOR037W	77.7	4.00E-150
NP_011721_T	YGR205W	80.2	0
NP_116708_T	YFR050C	84.91	0
NP_116610_T	YFL044C	82.61	0
NP_009686_T	YBR128C	78.48	0
NP_009645_T	YBR088C	87.74	0
NP_013772_T	YMR056C	82.34	1.00E-110
NP_012194_T	YIL070C	85.56	0
NP_013055_T	YLL045C	93.03	0
NP_011830_T	YLL045C	93.03	0
NP_013953_T	YMR226C	82.55	0
NP_009522_T	YBL031W	79.7	0
NP_011102_T	YER175C	79.23	3.00E-171
NP_014610_T	YOL032W	83.36	0
NP_014788_T	YOR145C	85.87	0
NP_014926_T	YOR283W	85.47	0
NP_015128_T	YPL196W	81.36	0
NP_011104_T	YER177W	88.7	0
NP_009815_T	YBR256C	79.59	2.00E-141
NP_012828_T	YKL095W	81.22	3.00E-155
NP_011958_T	YHR090C	83.71	0
NP_009917_T	YCL010C	81.72	5.00E-59
NP_011020_T	YER094C	86.13	0
NP_011380_T	YGL135W	94.79	0
NP_015104_T	YGL135W	94.79	0
NP_015491_T	YPR165W	92.34	0
NP_013864_T	YMR144W	80.25	0
NP_009313_T	Q0085	93.7	0
NP_013370_T	YLR268W	86.03	3.00E-179
NP_012201_T	YIL063C	78.7	7.00E-128
NP_014024_T	YMR295C	86.87	3.00E-169
NP_009388_T	YAL014C	78.17	5.00E-118
NP_013884_T	YMR161W	85.44	0
NP_012202_T	YIL062C	84.48	3.00E-128
NP_010962_T	YER044C	87.89	3.00E-148
NP_015195_T	YPL130W	78.18	2.00E-101
NP_010934_T	YER018C	78.37	6.00E-112
NP_012369_T	YJL166W	85.92	9.00E-82
NP_076899_T	YKL018C-A	84.05	1.00E-76
NP_009569_T	YBR013C	83.85	1.00E-101
NP_878098_T	YIL002W-A	86.84	1.00E-54
scaffold9-gene-5_33-mRNA-1	YNL292W	84.75	0
scaffold9-gene-5_34-mRNA-1	YNL293W	80.79	0

scaffold9-gene-5_36-mRNA-1	YNL295W	79.17	0
scaffold9-gene-5_5-mRNA-1	YNL304W	80.03	0
scaffold9-gene-5_8-mRNA-1	YNL307C	87.22	0

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Genome annotation of a *Saccharomyces* sp. lager brewer's yeast

Patricia Marcela De León-Medina [a,b,c], Ramiro Elizondo-González [a,b,c], Luis Cástulo Damas-Buenrostro [c], Jan-Maarten Geertman [d], Marcel Van den Broek [e], Luis Jesús Galán-Wong [a], Rocío Ortiz-López [b], Benito Pereyra-Alférez [a,*]

[a] *Instituto de Biotecnología, Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León. Pedro de Alba y Manuel L. Barragán S/N, Ciudad Universitaria, San Nicolás de los Garza, Nuevo León 66450, Mexico*
[b] *Centro de Investigación y Desarrollo en Ciencias de la Salud, Universidad Autónoma de Nuevo León, Avenida Carlos Canseco s/n esquina con Av. Gonzalitos, Mutualismo, Mitras Centro, 64460 Monterrey, Nuevo León, Mexico*
[c] *Laboratorio de Investigación y Desarrollo, Cervecería Cuauhtémoc Moctezuma S.A. de C.V., Alfonso Reyes Norte Col, Bella Vista, 2202 Monterrey, Nuevo León, Mexico*
[d] *Heineken Supply Chain, Global Research & Development, 2382 PH Zoeterwoude, The Netherlands*
[e] *Department of Biotechnology, Delft University of Technology, Julianalaan 67, 2628 BC Delft, The Netherlands*

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ABSTRACT

The genome of lager brewer's yeast is a hybrid, with *Saccharomyces eubayanus* and *Saccharomyces cerevisiae* as sub-genomes. Due to their specific use in the beer industry, relatively little information is available. The genome of brewing yeast was sequenced and annotated in this study. We obtained a genome size of 22.7 Mbp that consisted of 133 scaffolds, with 65 scaffolds larger than 10 kbp. With respect to the annotation, 9939 genes were obtained, and when they were submitted to a local alignment, we found that 53.93% of these genes corresponded to *S. cerevisiae*, while another 42.86% originated from *S. eubayanus.* Our results confirm that our strain is a hybrid of at least two different genomes.

1. Introduction

The brewing process is probably the most ancient type of biotechnology. There is evidence that the production and consumption of beer began in Egypt in the Early Dynastic Period (5500–3100 BCE) [1]. The first fermentation process was termed “high” because yeast floats to the top of the tank at a temperature between 15 °C and 25 °C during production of ale beer with the yeast *Saccharomyces cerevisiae*. Lager yeast did not emerge until the 15th century. This yeast is capable of fermenting at a temperature lower than 10 °C and flocculates at the bottom of the tank. The fermentation is followed by a maturation process called “lagering” (Masschelein, 1986).

The *Saccharomyces sensu stricto* complex includes six parented species: *S. cerevisiae*, *Saccharomyces bayanus*, *Saccharomyces cariocanus*, *Saccharomyces kudriavzevii*, *S. mikatae* and *S. paradoxus* [2]; however, it has been observed that lager-brewing yeast is a hybrid species of two combined genomes of *S. eubayanus* and *S. cerevisiae* [3–10]. This provides an important source of chromosomal rearrangements, leading to the gene number and the size of the complete genome [11–14]. It has been proposed and recently demonstrated that lager yeast is the product of two independent hybridization events that can be divided into two groups: Saaz and Frohberg, or group I and group II, respectively [15–19].

With the use of next generation sequencing (NGS) technologies, such as the Illumina Platform, 40,175 prokaryote and eukaryotes genomes have been reported, including 210 different strains of the *Saccharomyces* complex (http://www.ncbi.nlm.nih.gov/genome/browse/ - revised July 22, 2015).

To obtain a higher level of understanding of the sequenced organism, the data obtained from NGS has been assembled and annotated.

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[*] Corresponding author at: Pedro de Alba y Manuel L. Barragán S/N, Ciudad Universitaria, San Nicolás de los Garza, Nuevo León 66450, Mexico.
E-mail addresses: bpereyra@gmail.com, benitopereyraal@uanl.edu.mx (B. Pereyra-Alférez).

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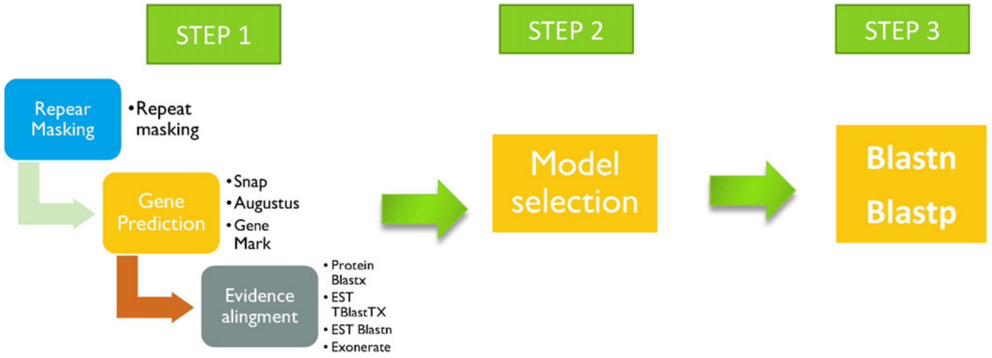

Fig. 1. Maker's annotation pipeline. In step 1, the repetitive sequences are identified and masked; proteins and ESTs are aligned; and using this information, a gene prediction model is made and the structural annotation is completed. Those models are then submitted to a local alignment in Blast for functional annotation.

The annotation process consists of identifying the biological characteristics from sequences of the assembly. This can be performed through gene prediction and homologous sequence alignment [20–22].

Here, we present the analysis of the lager yeast genome *Saccharomyces* sp. strain 790 and its comparison with *S. eubayanus* and *S. cerevisiae* S288c. This study provides information about the genome structure of *Saccharomyces* sp. strain 790.

2. Materials and methods

2.1. Strains and sequences

The brewing yeast *Saccharomyces* sp. strain 790 and a reference sequence of 76 scaffolds from *S. eubayanus* were obtained from the yeast collection of Cervecería Cuauhtémoc Moctezuma S.A. de C.V. The *S. cerevisiae* S288c reference genome sequence was retrieved from the yeast genome database (www.yeastgenome.org).

2.2. Sequencing and genome assembly

The brewing yeast genome was sequenced using the FLX 454 Titanium (Roche) and MiSeq (Illumina) massive sequencing platforms according to the manufacturer's protocols. We obtained 0.8 million reads from FLX 454 Titanium (454 Life Sciences, Branfort, CT) with an average size of 400 bp; 6 million pair-end reads from Illumina (Illumina, San Diego, CA) with an average size of 150 bp; 5 million mate-pair reads from Illumina with an insert size of 350 bp and a size of 101 × 2 bp; and 11.7 million mate-pair reads from Illumina with an insert of 8 kb and a size of 51 × 2 bp. Approximately 454 Illumina pair-end reads were assembled with a Newbler DeNovo Assembler (Roche). Contigs were then processed using SSPACE 1.0 software (Boetzer et al. 2011). This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession LSMH00000000. The version described in this paper is version LSMH01000000.

The sequencing quality data were analyzed with FastQC 0.10.1 software with a value ≥ Q30 [23].

Table 1
Assembly of *Saccharomyces* sp. 790.

Assembled reads	17,034,361
Depth	~70×
Estimated genome size (bp)	22,741,276
Number of scaffolds	133
Average scaffold size (bp)	170,987
Largest scaffold (bp)	1,404,408
N50	568,800
‘Ns’	399,699

Likewise, alignments were made against reference sequences (*S. cerevisiae* S288c and *S. eubayanus*) with the MUMmer 3.23 software package [24].

2.3. Genome annotation

The bioinformatics analysis for the annotation was performed with MAKER v2.31.8 software (University of Utah). MAKER is an integrative tool that yields a putative position of the genes. Fig. 1 depicts the annotation steps [22].

Table 2
Size range among scaffolds.

Size level	Number of scaffolds	Bp	Whole genome proportion (%)	Cumulative % of the whole genome
0:999	47	31,168	0.137	0.137
1 k:9999	21	44,610	0.196	0.333
10 k: 99,999	18	1,063,816	4.678	5.011
100 k 199, 999	11	1,608,982	7.075	12.086
200 k: 299,999	6	1,528,906	6.723	18.809
300 k: 399,999	6	2,092,805	9.203	28.01
400 k: 499, 999	4	1,700,637	7.478	35.490
500 k: 599, 999	7	3,759,004	16.529	52.020
600 k: 699,999	5	3,213,208	14.129	66.149
700 k: 799,999	1	712, 480	3.133	69.282
800 k: 899,999	1	806,158	3.545	72.827
900 k: 999,999	5	4,775,094	20.997	93.824
1;404,408	1	1,404,408	6.176	100
Total	133	22,741,276		

Table 3
Sequenced genome assembly level of *Saccharomyces* species.

Organism	Finished genome	Number of chromosomes	Number of scaffolds	Number of contigs	Size (Mpb)
S. cerevisiae	✓	16	17	–	12.16
S. kudriavzevii	✗	16	2054	–	11.19
S. pastorianus	✗	–	–	2425	24.21
S. paradoxus	✗	16	–	832	11.87
S. mikatae	✗	16	–	1648	11.47
S. bayanus	✗	16	–	586	11.87
S. boulardii	✗	16	48	–	11.64
S. arboricola	✓	16	35	–	11.62
S. uvarum	✗	–	–	3985	11.60
S. carlsbergensis	✗	29	77	–	19.37
S. cerevisiae - S. kudriavzevii	✗	–	60	419	23.37
S. pastorianus —S. weihenstephan 34/70	✗	–	–	1358	22.96
790	✗	**~32**	**133**	–	**22.74**

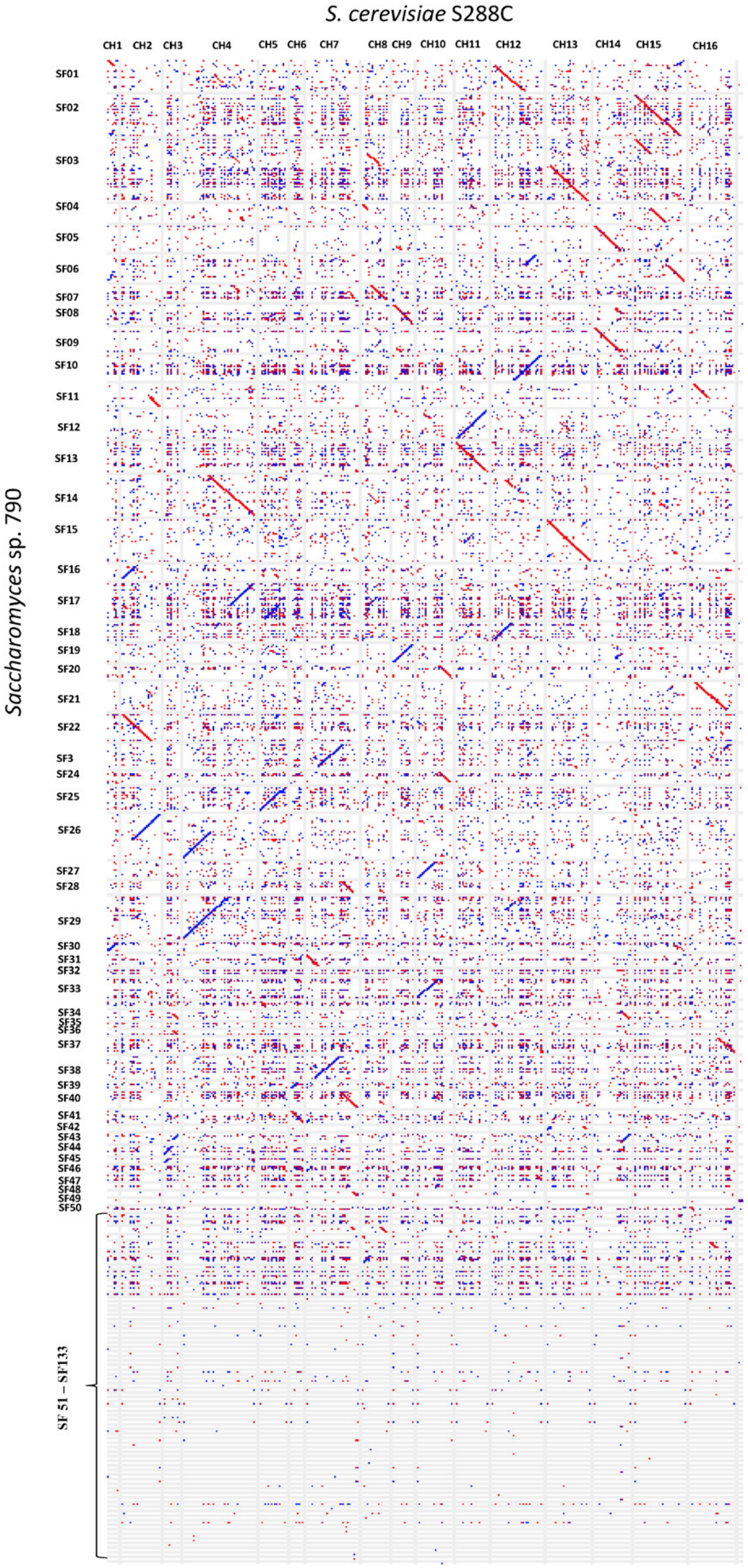

Fig. 2. Alignment dot plot of *Saccharomyces* sp. 790 versus *S. cerevisiae* S288C.

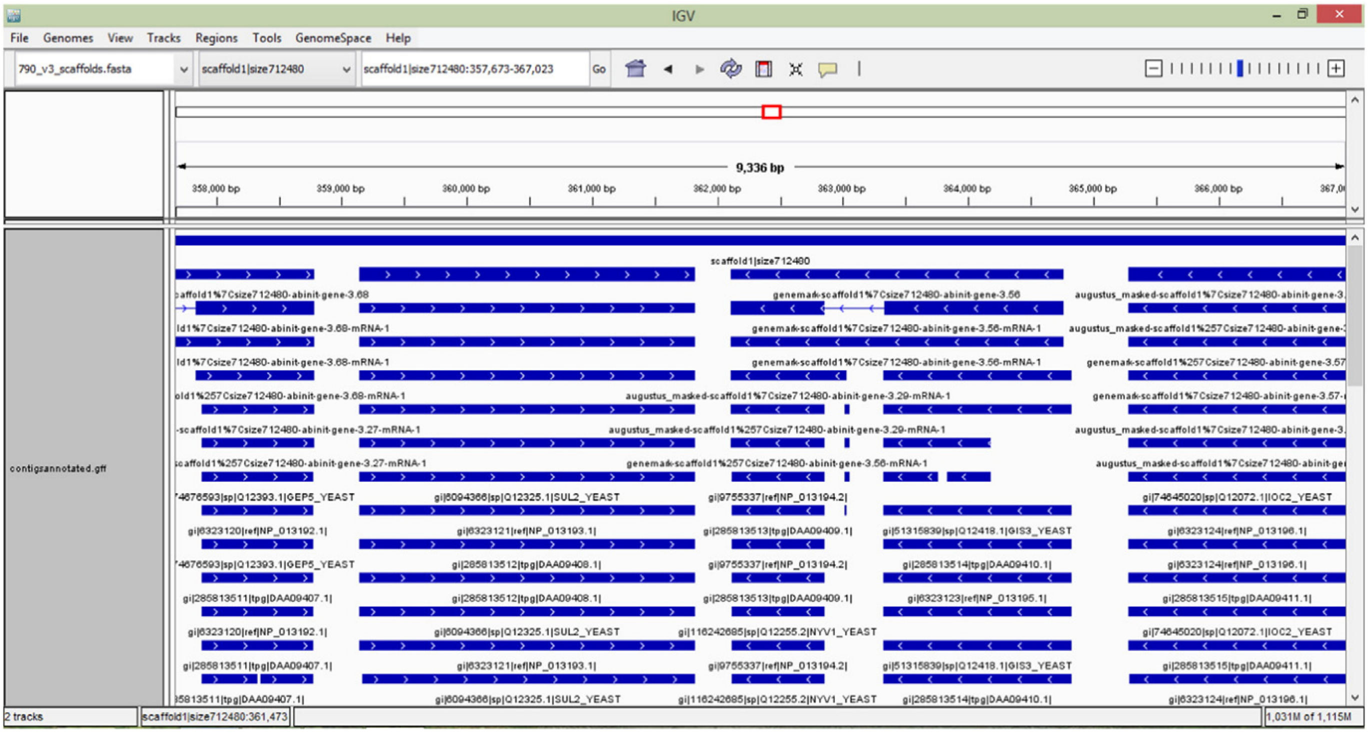

Fig. 3. Visualization of annotations with IGV Tools v2.3 (http://www.broadinstitute.org/software/igv/home). Scaffold 01 alignments and predictions from the Maker's annotation.

3. Results and discussion

The read assembly yielded 133 scaffolds with a ~70× depth and a N50 of 568,800 bp, suggesting a complete genome size of ~22.7 Mbp (Table 1), similar to previous reports of other lager beer yeasts [11,15,25,26]. Approximately 65/133 scaffolds had a size >10 kbp, which represents 99.667% of the assembled genome (Table 2). Table 3 shows a comparison of the assembly level of the sequenced genomes of the *Saccharomyces* species (as of August 2015). It also shows a similar genome size compared to other brewing yeasts [11,26]. The alignments against the reference genome, *S. cerevisiae* S288C, assigned scaffolds to each of its 16 chromosomes, and some scaffolds covered different portions of more than one chromosome; for example, scaffold01 (SF01) aligns with two chromosomes: a small portion with chromosome 1 and with chromosome 12. Scaffold17 (SF17) aligns with chromosomes 4 and 5 (Fig. 2).

The estimated size matches the previous and known information; this is due to the presence of 16 chromosomes of the *S. cerevisiae* subgenome and 16 of *S. eubayanus*. This suggests an overall estimation of 32 chromosomes without considering ploidy. Likewise, its size is close to the sum of the aforementioned genomes (~12 Mbp each). This observation is consistent with the previously reported data by Nakao et al. (2009), Borneman et al. (2011) and Walther et al. (2014), who reported the sequence and assembly of the lager brewing yeast genomes *Saccharomyces carlsbergensis* (78 scaffolds, 29 chromosomes with a 19.5 Mbp length), and *Saccharomyces pastorianus* Weihenstephan 34/70 (985 scaffolds, ~29 chromosomes, and 22.9 Mbp).

The annotation yielded 9939 CDS and a gff file with their locations in the scaffolds of the assembly (Fig. 3). The protein and transcript sequences, were subjected to a local alignment with the Blast tool [27] against a local database using the sequence of *S. cerevisiae* S288C as a reference. The transcripts were considered to be genes because previous reports showed that only approximately 5% of the yeast genome contains introns [28,29].

The scaffolds were classified using the results obtained from Blastn according to the mean identity percentage in all of the genes contained in the same scaffold, as follows (Table 4):

%Id $>$99.0% and E value $<10^{-6}$ = scaffold belongs to *S. cerevisiae.*

%Id $<$90.0% and E value $<10^{-6}$ = scaffold does not belong to *S. cerevisiae.*

99.0% $>$ %Id $>$90.0% and E value $<10^{-6}$ = hybrid scaffold.

Our identity criterion was validated by subjecting the gene sequences from *S. cerevisiae* S288C to a local alignment against *S. eubayanus*, and we found that the %Id between these strains was <90% (Supplementary Table S1) and the average size of the CDS was 1550 bp. Approximately 96.8% of the genome was annotated; 53.93% corresponded to *S. cerevisiae*, 42.86% were non-*cerevisiae* and 3.20% remained un-annotated Fig. 4 (Supplementary Table S2).

4. Conclusions

From the findings in this work, it can be concluded that *Saccharomyces* sp. 790 is a hybrid between *S. cerevisiae* and *S. eubayanus.* Its nuclear genome consists of approximately 32 chromosomes, 16 of which correspond to the *S. cerevisiae* genome and 16 to the *S. eubayanus* genome,

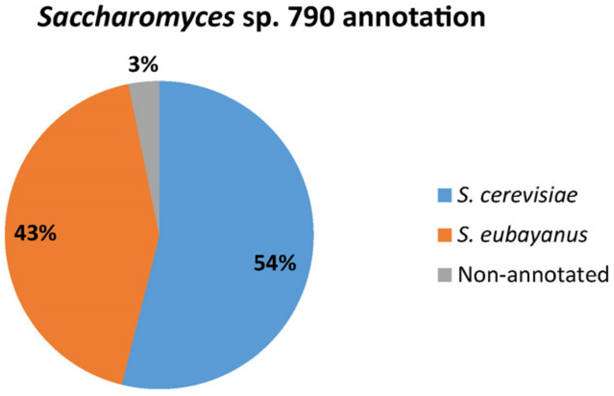

Fig. 4. Schematic representation of *Saccharomyces sp.* 790 annotations. *S. cerevisiae*, *S. eubayanus* and non-annotated proportions are represented in blue, orange and gray, respectively. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

without considering ploidy. A total of 133 scaffolds were obtained in the last version of the assembly. Nine scaffolds presented continuous translocations (scaffolds 1, 4, 6, 23 for the *S. cerevisiae* sub-genome and 26, 11, 17, 22 and 32 for the *S. eubayanus* sub-genome), which indicate homologous recombination events. One scaffold presented a possible recombination event (scaffold 3). Data on the chromosome number and size, as well as the number of scaffolds obtained, are consistent with previous reports on lager yeast [6,15,16]. The next step is to improve the assembly with physical mapping techniques.

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.gdata.2016.05.009.

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