

SUPPLEMENTARY

Statistical modelling of CG interdistance across multiple organisms

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1 Fitting method performance

We generated several sets of 2.000.000 and 10.000.000 random number drawn from a gamma distribution with shape parameter $a = 0.2$ and scale parameter $b = 250$, in order to test the performance of our fitting procedure.

We represented the data by taking the logarithm of y-axis values and applying a non-linear least squares regression (via Matlab `fit` function); we considered firstly the entire distribution, and subsequently a truncated version by removing samples from 95th, 90th and 85th percentile.

1.1 Results

In Table 1 and 2 are shown respectively fit results for the first (2.000.000 gamma random numbers) and the second (10.000.000 gamma random numbers) synthetic dataset. We can see that by removing at least the right 10% tail we obtain a better parameter estimation.

a	b	c	r^2	cutoff
0 ¹	320 ± 5	0.32 ± 0.02	0.965 ± 0.004	none
0.10 ± 0.04	272 ± 6	0.25 ± 0.05	0.983 ± 0.002	95th percentile
0.18 ± 0.04	252 ± 5	0.18 ± 0.03	0.986 ± 0.002	90th percentile
0.21 ± 0.04	245 ± 5	0.16 ± 0.03	0.986 ± 0.002	85th percentile

Table 1: *Gamma fit parameter values obtained by performing non-linear least squares regression on semilogarithmic scale. Errors are estimated at 95% confidence level.*

¹In these simulations the algorithm did not converge.

a	b	c	r^2	cutoff
0^2	292 ± 3	0.41 ± 0.02	0.980 ± 0.002	none
0.15 ± 0.04	258 ± 4	0.23 ± 0.04	0.989 ± 0.001	95th percentile
0.19 ± 0.03	250 ± 4	0.19 ± 0.03	0.990 ± 0.001	90th percentile
0.22 ± 0.03	244 ± 4	0.17 ± 0.03	0.992 ± 0.001	85th percentile

Table 2: *Gamma fit parameter values obtained by performing non-linear least squares regression on semilogarithmic scale. Errors are estimated at 95% confidence level.*

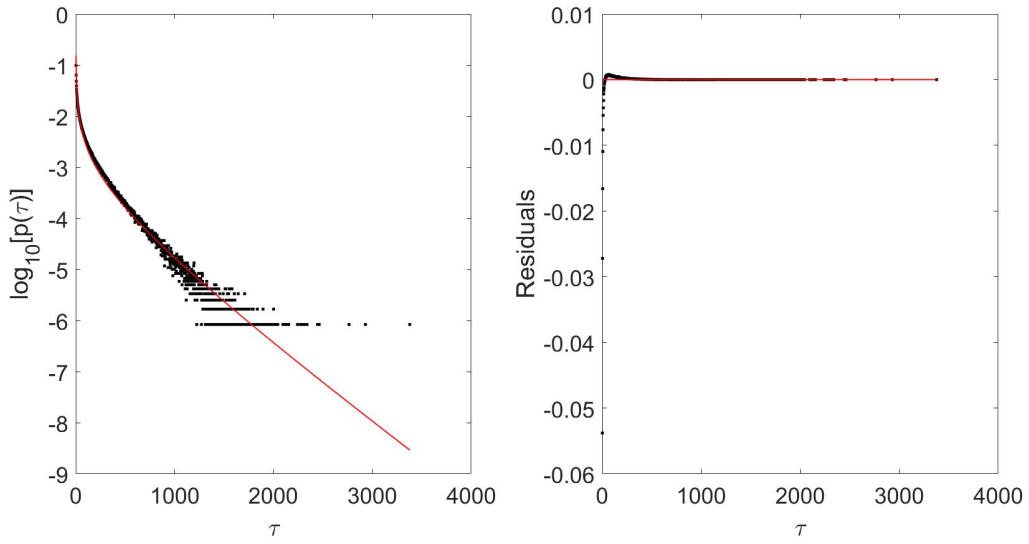


Figure 1: *Gamma fit results for the complete distribution, obtained by 2.000.000 synthetic gamma random numbers (left-hand side), together with residual plot (right-hand side).*

²The algorithm did not converge.

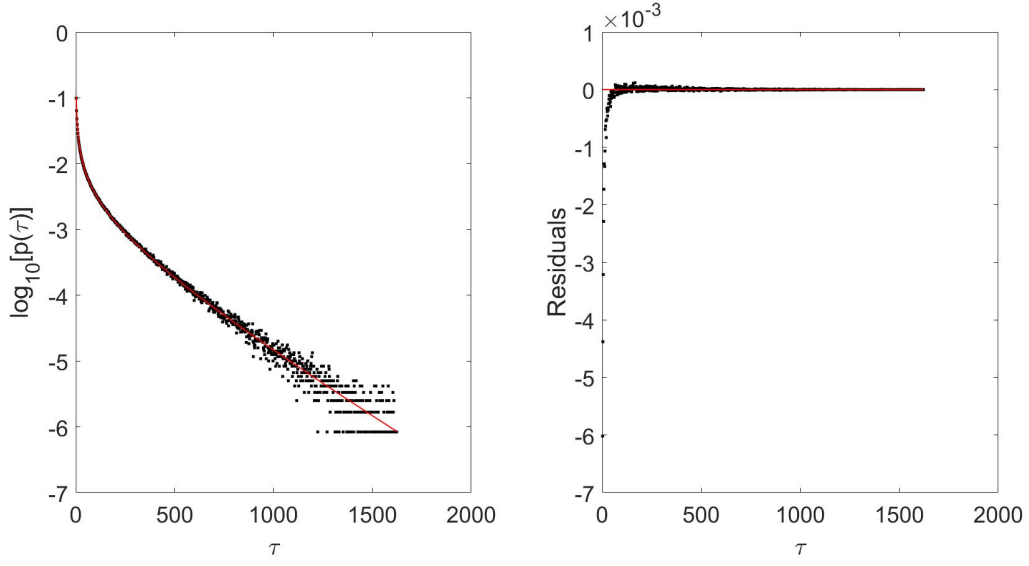


Figure 2: *Gamma fit results for the distribution truncated at 90th percentile and obtained by 2.000.000 synthetic gamma random numbers (left-hand side), together with residual plot (right-hand side).*

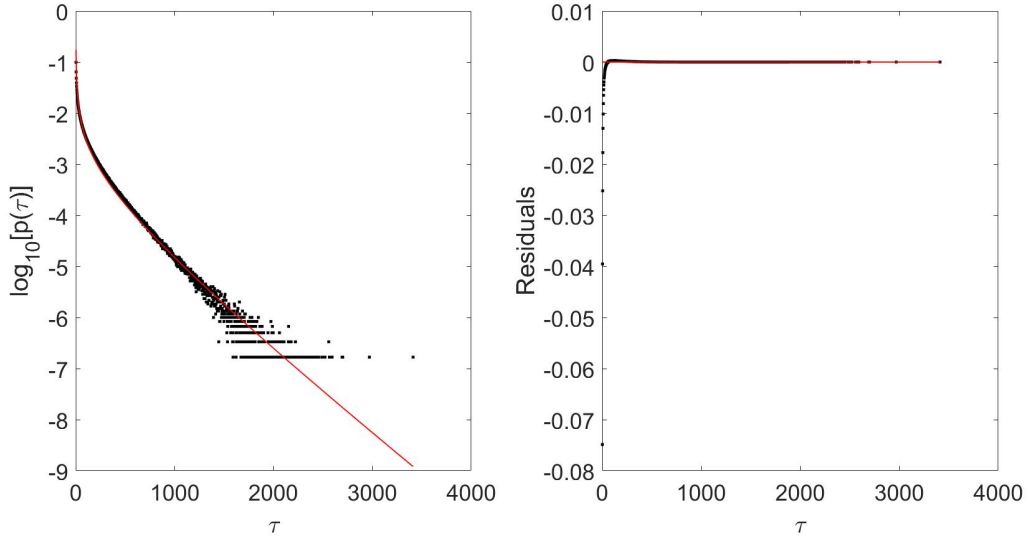


Figure 3: *Gamma fit results for the complete distribution, obtained by 10.000.000 synthetic gamma random numbers (left-hand side), together with residual plot (right-hand side).*

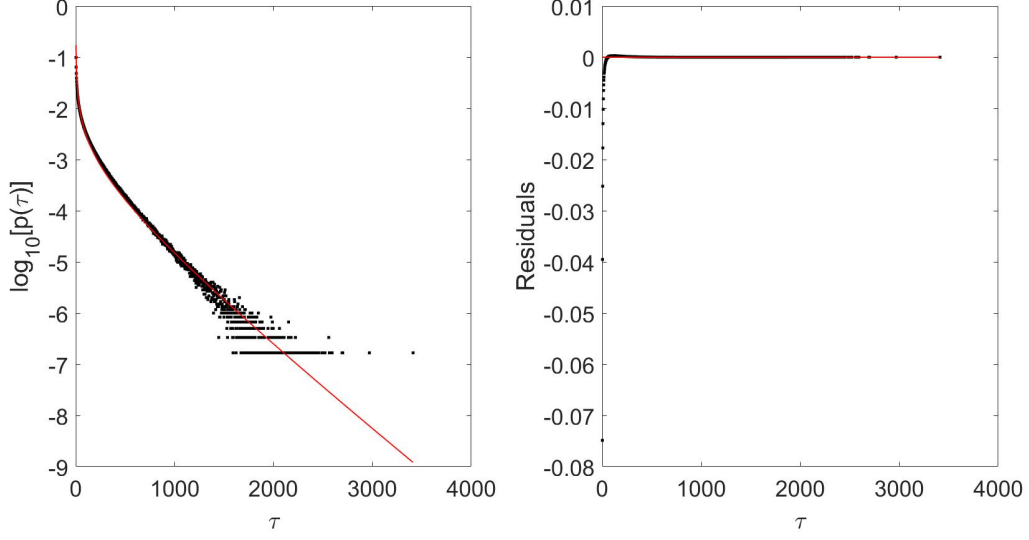


Figure 4: *Gamma fit results for the distribution truncated at 90th percentile and obtained by 10.000.000 synthetic gamma random numbers (left-hand side), together with residual plot (right-hand side).*

2 Fit result plots

We show visually a difference in the goodness of fit between Gamma and Stretched exponential distributions: as it can be seen in Figures. 5,6, the Gamma distribution has a better adherence to real data in the initial part of the distribution, while both distributions have similar performance on the empirical distribution tail.

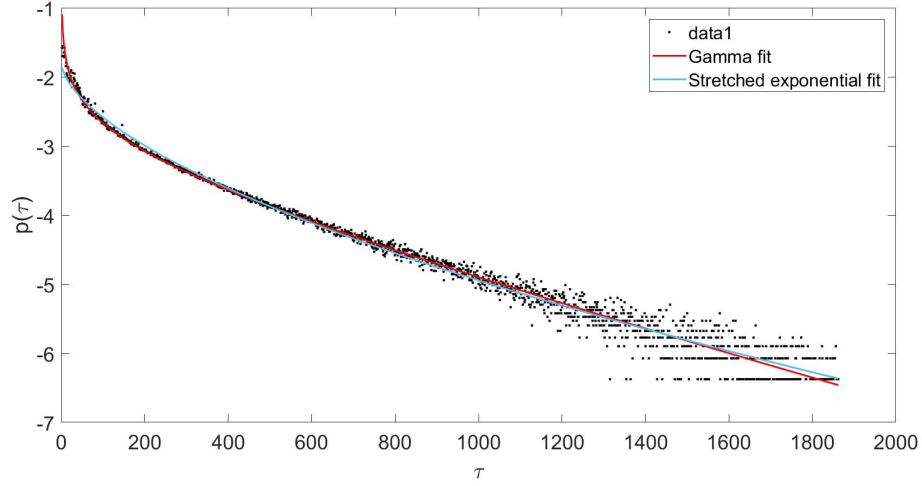


Figure 5: *Gamma (red) and stretched exponential (light blue) fit of Homo sapiens CG interdistance distribution inside chromosome 1.*

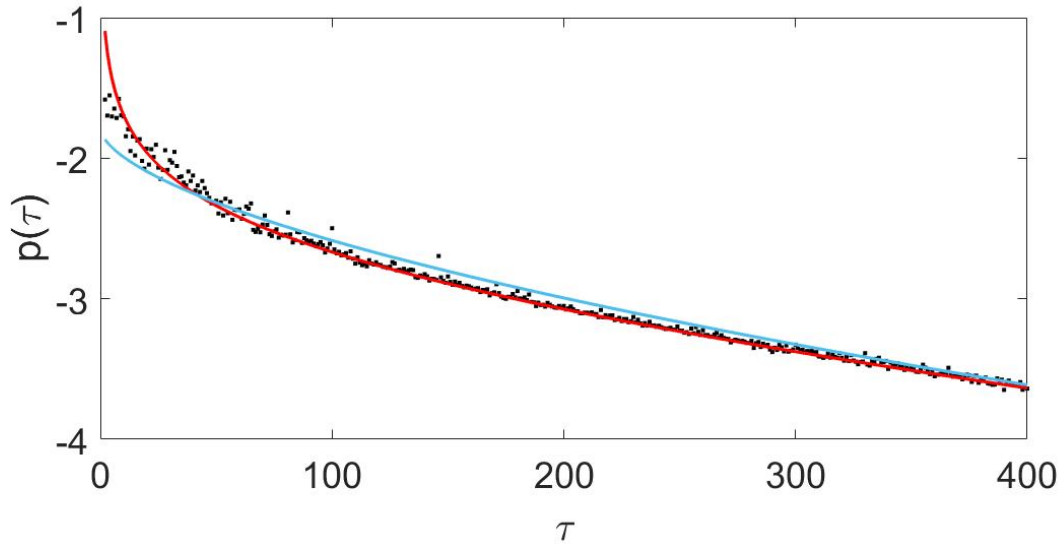


Figure 6: *Zoom of gamma (red) and stretched exponential (light blue) fit of Homo sapiens CG interdistance distribution inside chromosome 1.*

3 Errors on R-squared

For each r^2 value we calculated an error estimate at 95% of confidence interval (see eq. 1), using the following definition:

$$r^2 \pm 2 \cdot SE \quad (1)$$

where SE is the standard error for r^2 , based on Olkin and Finn's approximation:

$$SE = \left(\frac{4r^2(1-r^2)^2(n-k-1)^2}{(n^2-1)(3+n)} \right)^{\frac{1}{2}} \quad (2)$$

where k is the number of predictors in the model and n the total sample size.

Mammal	Gamma	S. Exp	D. Exp	Exp	Q-exp
Bos taurus	0.982 ± 0.002	0.982 ± 0.002	0.981 ± 0.002	0.961 ± 0.004	0.81 ± 0.02
Canis familiaris	0.981 ± 0.002	0.981 ± 0.002	0.977 ± 0.002	0.947 ± 0.005	0.83 ± 0.01
Equus caballus	0.986 ± 0.001	0.987 ± 0.001	0.775 ± 0.002	0.964 ± 0.004	0.80 ± 0.02
Homo sapiens	0.985 ± 0.001	0.985 ± 0.001	0.983 ± 0.002	0.962 ± 0.003	0.80 ± 0.02
Macaca mulatta	0.987 ± 0.001	0.987 ± 0.001	0.986 ± 0.006	0.965 ± 0.003	0.80 ± 0.02
Mus musculus	0.983 ± 0.002	0.985 ± 0.001	0.983 ± 0.002	0.960 ± 0.004	0.80 ± 0.02
Ornithorhynchus anatinus	0.978 ± 0.002	0.981 ± 0.002	0.978 ± 0.002	0.949 ± 0.005	0.83 ± 0.02
Pan troglodytes	0.986 ± 0.001	0.985 ± 0.001	0.984 ± 0.002	0.963 ± 0.003	0.80 ± 0.02
Rattus norvegicus	0.984 ± 0.001	0.987 ± 0.001	0.985 ± 0.001	0.958 ± 0.004	0.80 ± 0.02

Table 3: *R-squared values of gamma, stretched exponential (S. Exp), double exponential (D. Exp), exponential (Exp) and q-exponential (Q-exp) fit for CG interdistance distributions of higher-order organisms. Errors are estimated at 95% confidence interval and rounded to the first significant digit.*

4 Tables containing fit results on 4425 organisms

We provide two tables, one with information on organism type and identification on NCBI website, and the other with all fit parameters of the Gamma distributions, ratio of unknown nucleotides (%N), ratio of CG dinucleotides (%CG) and goodness-of-fit r^2 value.

'CM000719.1'	0.40	0.09	51.79	2.16	0.14	0.04	5674808	0.34	3.09	0.98
'CM000720.1'	0.32	0.10	53.15	2.57	0.17	0.06	5586253	0.41	3.16	0.98
'CM000721.1'	0.29	0.10	54.40	2.76	0.18	0.06	5234797	0.20	3.16	0.97
'CM000722.1'	0.38	0.10	51.29	2.51	0.14	0.05	5246493	0.24	3.09	0.97
'CM000723.1'	0.36	0.10	52.71	2.54	0.15	0.05	5436173	0.34	3.09	0.98
'CM000724.1'	0.36	0.10	51.74	2.43	0.15	0.05	5568034	0.33	3.16	0.98
'CM000725.1'	0.39	0.09	51.84	2.26	0.14	0.04	5576566	0.51	3.10	0.98
'CM000726.1'	0.36	0.10	53.13	2.55	0.15	0.05	5397450	0.22	3.08	0.98
'CM000727.1'	0.32	0.09	54.45	2.45	0.17	0.05	5584055	0.41	3.12	0.98
'CM000728.1'	0.33	0.10	55.87	2.67	0.16	0.05	5859854	0.29	3.04	0.98
'CM000729.1'	0.32	0.09	57.18	2.69	0.17	0.06	5766278	0.35	3.00	0.98
'CM000730.1'	0.24	0.09	57.04	2.74	0.20	0.07	6041497	1.91	3.23	0.98
'CM000731.1'	0.31	0.09	56.90	2.57	0.17	0.05	5878111	0.32	3.04	0.98
'CM000732.1'	0.39	0.09	50.11	2.32	0.14	0.05	5202904	0.37	3.18	0.98
'CM000733.1'	0.44	0.09	46.60	1.91	0.13	0.04	4999804	2.12	3.28	0.98
'CM000734.1'	0.35	0.09	55.82	2.50	0.15	0.05	5769987	0.56	2.98	0.98
'CM000735.1'	0.35	0.09	54.44	2.38	0.15	0.05	5923634	0.30	3.05	0.98
'CM000736.1'	0.32	0.08	59.14	2.54	0.16	0.05	6133179	0.44	2.93	0.98
'CM000737.1'	0.39	0.09	52.83	2.25	0.14	0.04	5799451	0.43	3.06	0.98
'CM000738.1'	0.36	0.10	53.66	2.71	0.15	0.05	5594747	0.57	3.03	0.97
'CM000739.1'	0.33	0.09	53.42	2.52	0.16	0.05	5656704	0.65	3.14	0.98
'CM000740.1'	0.35	0.09	52.96	2.37	0.16	0.05	5789540	0.72	3.10	0.98
'CM000743.1'	0.40	0.09	56.37	2.38	0.13	0.04	5841497	1.05	2.83	0.98
'CM000744.1'	0.39	0.08	56.70	2.38	0.13	0.04	5713954	0.54	2.87	0.98
'CM000745.1'	0.40	0.08	56.33	2.23	0.13	0.04	5782514	0.53	2.85	0.98
'CM000746.1'	0.23	0.10	60.48	3.10	0.21	0.07	5625906	0.39	3.06	0.97
'CM000747.1'	0.37	0.09	54.67	2.47	0.14	0.05	6026843	0.31	2.99	0.98
'CM000748.1'	0.34	0.10	56.54	2.80	0.15	0.05	6323123	0.39	2.96	0.97
'CM000749.1'	0.31	0.10	57.65	2.77	0.17	0.06	6107746	0.79	2.95	0.97
'CM000750.1'	0.34	0.10	54.71	2.72	0.16	0.06	6037513	1.02	3.00	0.97
'CM000751.1'	0.36	0.09	53.90	2.48	0.15	0.05	5527568	0.61	3.04	0.98
'CM000752.1'	0.20	0.09	65.05	3.27	0.22	0.08	6489024	0.39	2.96	0.97
'CM000753.1'	0.33	0.10	57.03	2.85	0.16	0.06	6260142	0.40	2.96	0.97
'CM000754.1'	0.32	0.10	54.30	2.61	0.17	0.06	5488844	0.47	3.13	0.98
'CM000755.1'	0.35	0.09	55.42	2.59	0.15	0.05	6031475	0.31	3.02	0.98
'CM000756.1'	0.26	0.08	63.24	2.86	0.18	0.06	6231196	0.45	2.91	0.98
'CM000757.1'	0.26	0.10	59.63	3.03	0.19	0.07	6002603	0.43	3.04	0.97
'CM000758.1'	0.23	0.09	65.33	3.11	0.20	0.07	6731790	0.36	2.86	0.97
'CM000759.1'	0.34	0.08	58.06	2.39	0.15	0.04	6612432	0.58	2.91	0.98
'CM000776.2'	0.60	0.08	89.10	5.06	0.05	0.02	1623845	0.05	1.62	0.95
'CM000787.2'	0.34	0.22	8.55	0.58	0.49	0.24	4397373	0.31	12.68	0.99
'CM000788.2'	0.34	0.22	8.55	0.58	0.49	0.24	4397242	0.93	12.57	0.99
'CM000789.2'	0.34	0.22	8.55	0.58	0.49	0.24	4397243	0.68	12.61	0.99
'CM000913.1'	0.00	-1.00	8.85	0.32	0.79	0.16	6760392	0.37	14.48	0.98
'CM000854.1'	0.53	0.09	111.35	7.30	0.05	0.02	1702833	1.66	1.38	0.94
'CM000855.1'	0.58	0.08	111.85	6.50	0.05	0.01	1710125	1.38	1.32	0.95
'CM001834.1'	0.08	0.20	16.06	1.17	0.57	0.30	5868202	1.84	8.81	0.98
'CM001149.1'	0.02	0.28	7.73	0.69	0.90	0.53	5259057	0.07	15.36	0.99
'CM000920.1'	0.00	0.22	24.15	2.35	0.31	0.19	3636659	2.46	9.36	0.97
'KN196458.1'	0.37	0.05	539.21	42.78	0.05	0.01	3349855	0.79	0.46	0.89
'KE950501.1'	0.23	0.06	454.22	34.41	0.09	0.02	4032379	0.40	0.67	0.91
'DS362266.1'	0.34	0.07	171.88	12.39	0.09	0.03	1977105	21.67	0.98	0.94
'KB632434.1'	0.16	0.04	311.88	8.72	0.15	0.03	38452041	3.01	0.86	0.97
'DG000025.1'	0.00	-1.00	107.34	1.59	0.20	0.01	45064769	18.15	3.33	0.98
'GL530680.1'	0.06	0.17	88.64	23.41	0.27	0.14	96315	4.22	3.47	0.91
'KI635855.1'	0.44	0.05	111.03	3.21	0.08	0.02	18507834	2.29	1.55	0.98
'CM000436.1'	0.27	0.08	217.05	20.21	0.11	0.04	1344712	0.75	1.10	0.91
'AAGK0100000	0.45	0.09	84.70	4.79	0.09	0.03	2540030	0.00	1.99	0.96
'AAXT0100000	0.50	0.11	39.54	2.05	0.12	0.04	2593320	0.00	3.57	0.98
'CT867985.1'	0.60	0.08	224.02	21.01	0.03	0.01	981684	0.11	0.75	0.87
'CM007668.1'	0.00	0.03	404.92	8.09	0.23	0.04	159902609	2.66	1.05	0.98
'CP000395.1'	0.68	0.09	148.64	13.24	0.03	0.01	905394	0.00	0.97	0.88
'CM001022.1'	0.58	0.28	11.74	1.04	0.24	0.16	2630170	0.00	8.72	0.97
'GL537212.1'	0.59	0.18	20.28	1.82	0.15	0.07	300442	0.01	6.09	0.97
'GL538361.1'	0.00	-1.00	886.77	329.48	0.03	0.01	1422600	2.04	4.18	0.69
'GL541643.1'	0.35	0.17	16.04	1.19	0.29	0.13	867920	3.47	8.34	0.98
'CM001403.1'	0.28	0.12	32.93	1.62	0.24	0.09	8408322	0.01	4.77	0.98
'CM001023.1'	0.79	0.07	53.09	1.79	0.04	0.01	4787724	0.02	2.19	0.98
'CM001025.1'	0.13	0.19	14.29	0.95	0.53	0.26	6270867	0.18	9.76	0.99
'AABW0100000	0.34	0.12	67.02	5.23	0.14	0.06	1250021	0.00	2.69	0.95
'AACF0100000	0.56	0.12	67.71	6.55	0.07	0.03	279155	0.00	2.28	0.94
'AACG0200000	0.68	0.15	38.29	3.42	0.07	0.03	363585	0.00	3.28	0.95
'AACh0100000	0.80	0.23	37.44	8.09	0.05	0.03	45066	0.00	3.26	0.85
'JH797040.1'	0.49	0.23	54.85	15.34	0.10	0.06	54254	0.01	3.25	0.84
'GL985056.1'	0.00	0.28	96.09	19.19	0.05	0.06	3756989	0.09	6.23	0.78
'AAQW0100000	0.00	-1.00	14.15	0.58	0.44	0.09	6492423	0.00	12.09	0.97
'AASL0100000	0.57	0.09	102.91	6.32	0.05	0.02	1616175	0.00	1.46	0.94
'AAXK0100263	0.71	0.16	>1000	>1000	0.03	0.02	10877	0.00	1.27	0.43
'GL636486.1'	0.00	-1.00	>1000	396.62	0.02	0.00	3473653	0.48	4.67	0.64
'ABCY0200000	0.73	0.08	139.52	10.62	0.02	0.01	913294	0.00	0.98	0.91
'ABDF0200000	0.00	-1.00	37.78	1.25	0.45	0.05	3456807	0.00	5.37	0.97
'ABIZ01000001	0.11	0.21	17.40	1.28	0.53	0.31	8220857	0.00	7.88	0.98
'JH597776.1'	0.31	0.15	26.24	1.87	0.25	0.10	1234263	4.55	5.64	0.98
'ABYD0100000	0.78	0.11	33.49	1.76	0.06	0.02	1043181	0.00	3.38	0.98
'ABYE0100000	0.78	0.11	33.62	1.78	0.06	0.02	1043182	0.00	3.38	0.98
'ABYF0100000	0.78	0.10	33.39	1.70	0.06	0.02	1048006	0.00	3.38	0.98
'ABYG0100000	0.78	0.10	33.42	1.72	0.06	0.02	1046064	0.00	3.38	0.98
'ACDA0100504	0.66	0.36	>1000	>1000	0.06	0.05	2193	0.05	3.60	0.31
'ACFJ0100000	0.78	0.10	33.44	1.73	0.06	0.02	1042757	0.00	3.38	0.98
'ACFK0100000	0.53	0.09	109.13	9.04	0.06	0.02	642011	0.00	1.51	0.93
'ACUJ01000001	0.74	0.12	33.72	1.96	0.07	0.02	1076624	0.00	3.45	0.97
'ACUJ0100000	0.77	0.10	36.18	1.82	0.06	0.02	1088736	0.02	3.17	0.98
'CM001368.1'	0.00	-1.00	17.39	0.97	0.31	0.08	4102695	0.00	11.26	0.95
'CM001435.1'	0.00	0.14	34.32	2.19	0.49	0.21	5049928	0.01	5.60	0.98
'HE602535.1'	0.02	0.06	106.56	3.65	0.31	0.08	23260604	3.62	2.63	0.98
'ADBW0100000	0.38	0.23	85.83	39.23	0.11	0.07	23943	0.00	3.04	0.80
'AAXM0100000	0.94	0.28	>1000	>1000	0.04	0.03	2670	0.00	1.65	0.06
'CAAE0101458	0.02	0.07	96.80	4.51	0.31	0.08	7611840	10.69	2.62	0.98
'ADBV0100000	0.37	0.18	121.68	42.98	0.09	0.05	62423	0.00	2.23	0.81
'AAXL0100000	0.56	0.36	>1000	>1000	0.07	0.06	2821	0.00	3.40	0.44
'AASU0100786	0.00	0.29	153.87	219.49	0.29	0.19	11390	0.00	4.75	0.83
'AASW0101622	0.00	-1.00	88.46	21.69	0.31	0.06	26222	0.00	4.64	0.88
'AAXN0100000	0.97	0.12	>1000	>1000	0.05	0.02	2132	0.28	1.17	0.06
'KQ034056.1'	0.60	0.06	69.03	2.03	0.06	0.01	13425595	13.29	1.77	0.98
'BABP0100221	0.43	0.12	162.48	30.76	0.07	0.03	202166	0.00	1.40	0.85
'GL739410.1'	0.00	0.10	193.69	33.27	0.26	0.10	470468	2.12	2.04	0.92

'KE123882.1'	0.63	0.07	224.58	18.19	0.02	0.01	1763222	26.77	0.52	0.88
'KE124552.1'	0.57	0.09	426.73	106.99	0.02	0.01	410486	27.52	0.49	0.73
'CM001871.1'	0.00	-1.00	11.92	0.49	0.66	0.14	4908255	0.29	11.99	0.98
'KE124775.1'	0.51	0.09	39.23	1.82	0.11	0.03	2174208	5.99	3.54	0.98
'DF238808.1'	0.49	0.20	13.87	1.04	0.25	0.13	1398671	0.04	8.52	0.98
'CM001880.1'	0.04	0.05	207.76	6.29	0.26	0.06	42436413	2.78	1.39	0.98
'CM001897.1'	0.00	-1.00	12.13	0.50	0.63	0.13	4928563	0.12	12.00	0.98
'CM001890.1'	0.00	-1.00	12.19	0.50	0.62	0.13	4920230	0.11	12.01	0.98
'CM001889.1'	0.00	0.29	8.11	0.71	0.93	0.60	8496762	1.02	14.67	0.99
'APFE0311456	0.01	0.09	298.68	42.42	0.25	0.09	1058009	6.72	1.25	0.91
'CM001972.1'	0.00	-1.00	28.41	1.20	0.31	0.05	4693747	0.11	7.85	0.96
'CM001904.1'	0.00	-1.00	29.33	1.35	0.24	0.04	4549457	0.06	8.70	0.95
'CM001973.2'	0.00	-1.00	28.13	1.22	0.33	0.06	4264625	0.13	7.67	0.96
'CM001974.1'	0.00	-1.00	28.59	1.22	0.26	0.04	4669628	0.12	8.69	0.96
'CM001975.1'	0.00	-1.00	30.12	1.12	0.31	0.05	4214632	0.14	7.62	0.97
'CM001976.1'	0.00	-1.00	26.97	1.22	0.24	0.04	4829443	0.08	9.41	0.95
'CM001977.1'	0.00	-1.00	30.20	1.49	0.25	0.05	4552467	0.09	7.91	0.94
'CM001978.1'	0.00	-1.00	27.41	1.36	0.23	0.05	4802068	0.15	9.45	0.95
'CM001979.1'	0.00	-1.00	26.40	1.33	0.23	0.05	4993902	0.09	9.58	0.95
'CM001980.1'	0.00	-1.00	24.76	0.91	0.41	0.06	4622940	0.06	7.90	0.97
'CM001981.1'	0.00	-1.00	28.68	1.49	0.24	0.05	4681779	0.15	8.78	0.94
'CM001982.1'	0.00	-1.00	26.32	1.32	0.24	0.05	4781918	0.07	9.48	0.95
'CM001983.1'	0.00	-1.00	30.55	1.39	0.29	0.05	4306477	0.37	7.58	0.95
'CM001984.1'	0.00	-1.00	26.75	1.24	0.24	0.04	4905506	0.09	9.57	0.95
'CM001985.1'	0.00	0.22	26.53	2.53	0.35	0.23	4658967	0.07	7.90	0.96
'CM004347.1'	0.56	0.12	13.97	0.60	0.21	0.06	2618838	0.55	8.49	0.99
'KE145367.1'	0.30	0.12	32.93	1.78	0.23	0.09	3594336	0.46	4.72	0.98
'CM001948.2'	0.28	0.03	259.99	4.62	0.10	0.02	139301422	0.82	0.91	0.98
'CP004010.2'	0.82	0.16	13.61	0.77	0.12	0.05	1139633	0.00	7.51	0.99
'CP004011.1'	0.82	0.16	13.63	0.78	0.12	0.05	1139569	0.02	7.50	0.99
'CM004641.1'	0.33	0.14	16.48	0.88	0.31	0.11	2652413	1.11	8.44	0.99
'KE147309.1'	0.39	0.16	15.66	1.04	0.28	0.11	1354531	2.90	8.47	0.99
'KE148146.1'	0.00	0.13	31.21	1.98	0.46	0.19	4381405	0.34	6.58	0.98
'CM007249.1'	0.55	0.15	13.73	0.74	0.22	0.09	2596710	0.45	8.64	0.99
'AIJO01004611	0.24	0.29	29.02	6.80	0.26	0.19	71563	0.00	6.02	0.91
'KE158016.1'	0.12	0.11	149.64	21.06	0.20	0.08	514026	6.47	1.89	0.92
'KE156110.1'	0.20	0.10	78.05	5.46	0.20	0.07	1746141	3.61	2.61	0.96
'KE151199.1'	0.00	0.09	178.33	17.80	0.28	0.10	1494055	4.39	1.90	0.94
'KE159915.1'	0.66	0.13	22.80	1.34	0.11	0.04	832916	0.92	5.27	0.98
'ALWZ04S2422	0.09	0.08	243.49	24.94	0.20	0.07	1653216	12.37	1.16	0.92
'CM001986.1'	0.10	0.18	15.02	0.95	0.55	0.26	6077542	0.49	9.35	0.99
'CP006026.1'	0.18	0.14	28.60	1.94	0.31	0.12	1597628	0.00	6.47	0.98
'KE161240.1'	0.10	0.04	318.70	11.36	0.18	0.04	22122726	3.37	0.97	0.97
'CM002276.1'	0.24	0.13	38.13	2.40	0.25	0.10	2699012	7.04	4.07	0.97
'KE332545.1'	0.03	0.07	151.10	9.08	0.26	0.07	4533011	7.36	2.05	0.96
'KL558888.1'	0.00	-1.00	126.63	8.57	0.21	0.02	648085	5.71	3.20	0.92
'KE346217.1'	0.18	0.08	112.97	7.01	0.18	0.06	3477367	3.47	2.07	0.96
'ASJL0101749C	0.38	0.23	99.30	57.26	0.10	0.06	23157	0.00	3.00	0.78
'KE362319.1'	0.40	0.25	37.24	10.16	0.16	0.09	29239	0.09	4.74	0.90
'KE361623.1'	0.00	-1.00	19.00	1.61	0.28	0.09	1975278	0.36	10.90	0.91
'CM002022.1'	0.33	0.22	8.55	0.58	0.50	0.24	4391869	0.54	12.66	0.99
'KE370772.1'	0.00	-1.00	106.40	4.02	0.24	0.02	3017511	25.79	2.52	0.95
'KE374994.1'	0.32	0.12	43.67	2.78	0.19	0.07	5203757	57.48	1.64	0.97
'CP006567.1'	0.00	-1.00	8.73	0.29	0.88	0.17	12700734	2.48	13.70	0.99
'KE382941.1'	0.33	0.05	467.27	23.43	0.06	0.01	8324132	2.14	0.49	0.93
'KE384729.1'	0.38	0.13	24.24	1.35	0.22	0.08	2704444	0.16	5.98	0.98
'KE385298.1'	0.35	0.18	24.99	2.41	0.22	0.11	468691	0.01	6.09	0.97
'HF951689.1'	0.59	0.15	15.27	0.78	0.19	0.07	3437861	0.31	7.43	0.99
'FP885895.1'	0.00	-1.00	10.67	0.38	0.68	0.12	3596030	0.06	13.44	0.98
'CM002023.1'	0.00	-1.00	28.35	1.30	0.23	0.04	4662278	0.11	9.20	0.95
'KE391414.1'	0.30	0.22	17.01	2.05	0.31	0.16	171320	0.05	8.62	0.97
'KE392324.1'	0.52	0.21	100.97	41.62	0.06	0.04	57883	26.53	1.64	0.75
'ATLZ0100126C	0.06	0.29	46.13	18.17	0.32	0.23	30512	0.22	5.79	0.89
'CM002024.1'	0.05	0.26	12.73	1.19	0.66	0.41	2938080	0.05	10.64	0.98
'KE444511.1'	0.24	0.25	28.17	6.20	0.26	0.16	47541	1.95	6.41	0.94
'CP004849.1'	0.63	0.13	21.23	1.00	0.13	0.05	4321296	0.00	5.51	0.99
'CP006618.1'	0.79	0.12	34.84	1.97	0.06	0.02	1473302	0.01	3.19	0.97
'KE504634.1'	0.00	-1.00	159.48	4.93	0.24	0.02	4597586	17.51	2.01	0.96
'KE523052.1'	0.83	0.23	27.09	4.96	0.06	0.03	33513	0.04	4.05	0.90
'KE525347.1'	0.00	-1.00	41.29	1.06	0.38	0.04	5918260	0.59	5.67	0.98
'KE526711.1'	0.66	0.14	35.06	3.38	0.08	0.03	169254	0.00	3.66	0.96
'KE525743.1'	0.42	0.14	25.75	1.83	0.19	0.08	937461	0.00	5.62	0.98
'KE537387.1'	0.22	0.16	18.09	1.28	0.37	0.15	1294371	4.20	8.30	0.99
'KE561209.1'	0.39	0.11	75.15	6.35	0.11	0.04	719121	8.85	2.10	0.95
'KE546965.1'	0.00	-1.00	68.35	4.17	0.18	0.03	2816824	0.16	4.75	0.90
'KE549796.1'	0.57	0.17	36.80	3.79	0.10	0.05	345515	2.08	3.62	0.94
'KE558520.1'	0.00	-1.00	182.61	4.80	0.18	0.01	11539319	1.82	2.39	0.95
'KE557376.1'	0.18	0.07	312.18	30.94	0.13	0.04	1713168	0.43	0.98	0.92
'GK000053.2'	1.52	0.51	39.37	10.66	0.00	0.00	5400307	0.24	1.44	0.41
'ATMH0100992	0.00	-1.00	86.58	26.07	0.24	0.05	23937	0.03	6.09	0.85
'ATMG010145E	0.75	0.30	15.57	2.98	0.13	0.08	30297	0.24	6.94	0.93
'CM002081.1'	0.00	-1.00	175.41	2.29	0.24	0.01	68435666	21.46	1.69	0.98
'CAUG0100063	0.74	0.23	11.27	1.03	0.17	0.09	347077	0.03	9.00	0.98
'CM002048.1'	0.33	0.22	8.55	0.58	0.50	0.24	4398504	0.41	12.68	0.99
'HG316454.1'	0.80	0.10	31.43	1.46	0.06	0.02	1686157	0.14	3.57	0.98
'CM002049.1'	0.34	0.22	8.55	0.58	0.49	0.24	4402571	0.78	12.61	0.99
'CM002050.1'	0.34	0.22	8.54	0.57	0.49	0.24	4408178	0.72	12.63	0.99
'CM002258.1'	0.02	0.28	12.69	1.30	0.71	0.48	2856286	0.02	10.69	0.98
'CM002051.1'	0.40	0.22	8.31	0.55	0.45	0.22	4408147	1.28	12.56	0.99
'KE561408.1'	0.44	0.18	14.68	1.04	0.26	0.12	1220848	1.09	8.69	0.98
'KE581409.1'	0.44	0.23	20.95	3.21	0.20	0.11	76007	1.67	6.62	0.95
'CM002052.1'	0.33	0.22	8.56	0.58	0.49	0.24	4397671	0.90	12.60	0.99
'CM002053.1'	0.34	0.22	8.54	0.57	0.49	0.23	4408813	1.33	12.52	0.99
'CM002054.1'	0.34	0.22	8.50	0.57	0.49	0.24	4404319	0.54	12.67	0.99
'CM002055.1'	0.34	0.22	8.54	0.58	0.49	0.24	4393994	1.48	12.49	0.99
'CM002057.1'	0.34	0.22	8.55	0.57	0.49	0.24	4408133	0.39	12.68	0.99
'CM002056.1'	0.33	0.23	8.58	0.60	0.50	0.25	4398802	0.66	12.65	0.99
'CM002058.1'	0.34	0.22	8.55	0.57	0.49	0.24	4393218	0.57	12.64	0.99
'CM002059.1'	0.34	0.22	8.55	0.57	0.49	0.24	4404835	0.64	12.65	0.99
'CM002060.1'	0.34	0.22	8.55	0.57	0.49	0.24	4404586	0.68	12.64	0.99
'CM002061.1'	0.34	0.22	8.55	0.58	0.49	0.24	4402591	0.70	12.63	0.99
'CM002062.1'	0.35	0.22	8.53	0.58	0.48	0.23	4405148	2.88	12.25	0.99
'CM002063.1'	0.34	0.22	8.54	0.58	0.49	0.24	4403568	0.09	12.72	0.99
'CM002064.1'	0.34	0.22	8.54	0.58	0.49	0.24	4404247	1.50	12.48	0.99
'CM002065.1'	0.41	0.21	8.26	0.52	0.44	0.20	4400856	1.31	12.56	0.99
'CM002066.1'	0.34	0.22	8.55	0.58	0.49	0.24	4412421	0.84	12.60	0.99

'CM002638.1'	0.00	-1.00	11.94	0.41	0.67	0.12	5053472	0.02	11.96	0.98
'CP006672.1'	0.78	0.10	33.42	1.69	0.06	0.02	1042619	0.02	3.38	0.98
'CP006675.1'	0.78	0.10	33.44	1.66	0.06	0.02	1043010	0.10	3.37	0.98
'CP006677.1'	0.78	0.11	33.41	1.85	0.06	0.02	1041595	0.03	3.38	0.97
'CP006678.1'	0.79	0.11	33.25	1.82	0.06	0.02	1043181	0.00	3.38	0.98
'CP006679.1'	0.78	0.12	33.31	1.98	0.06	0.02	1042783	0.10	3.38	0.97
'CM002782.1'	0.36	0.12	31.75	1.70	0.19	0.07	4204192	2.03	4.72	0.98
'KK076539.1'	0.00	0.09	178.30	13.52	0.28	0.11	7289689	25.66	1.28	0.93
'JELW0100000	0.00	0.18	30.72	2.50	0.50	0.28	5053378	0.01	5.97	0.97
'JAQW0100000	0.25	0.14	215.93	87.35	0.12	0.06	79274	0.00	1.84	0.83
'JAQX0100000	0.18	0.15	488.07	442.29	0.14	0.06	69844	0.01	1.73	0.80
'JAQY0100000	0.16	0.14	266.42	112.62	0.15	0.07	107227	0.00	1.77	0.84
'JAQZ0100000	0.25	0.13	129.72	26.72	0.14	0.06	171681	0.03	2.04	0.89
'JARA0100000	0.26	0.13	123.73	22.20	0.14	0.06	208614	0.00	1.98	0.89
'JARB0100000	0.27	0.13	121.94	21.75	0.13	0.06	214169	0.00	1.95	0.89
'JEMT0102776	0.05	0.13	217.72	59.79	0.23	0.10	198953	0.01	1.93	0.88
'CM002651.1'	0.14	0.13	35.25	1.95	0.34	0.15	11267849	0.26	4.91	0.98
'AWGT0100040	0.35	0.08	386.47	70.58	0.06	0.02	600658	5.49	0.76	0.84
'AWGU010318	0.88	0.17	14.92	1.19	0.10	0.04	163812	0.00	6.57	0.98
'KK082680.1'	0.00	0.11	91.54	6.12	0.17	0.08	8792355	7.22	4.10	0.95
'KK088411.1'	0.20	0.13	33.71	2.35	0.28	0.12	1563877	0.12	5.33	0.98
'KK090061.1'	0.46	0.17	24.15	2.01	0.18	0.09	768125	0.13	5.63	0.97
'KK090494.1'	0.00	-1.00	134.03	3.14	0.27	0.02	7482359	4.06	2.41	0.97
'HF972804.1'	0.49	0.17	21.43	1.72	0.18	0.08	619733	1.46	6.18	0.97
'HF970592.1'	0.38	0.17	25.31	2.29	0.21	0.10	588491	0.59	5.96	0.97
'HF975737.1'	0.43	0.17	23.82	2.09	0.19	0.08	522423	2.40	5.98	0.97
'HF979336.1'	0.54	0.19	20.49	1.88	0.17	0.08	402084	2.42	6.12	0.97
'CAOW0100960	0.92	0.12	>1000	>1000	0.01	0.00	36400	1.44	0.60	0.12
'CM002678.1'	0.21	0.14	108.21	22.35	0.16	0.07	135362	0.00	2.56	0.90
'KK100010.1'	0.58	0.13	30.49	2.24	0.11	0.04	618369	3.18	4.26	0.97
'KK106941.1'	0.31	0.14	28.99	1.73	0.24	0.10	3800214	2.05	5.05	0.98
'KK106981.1'	0.00	-1.00	>1000	269.00	0.01	0.00	10671843	0.72	4.52	0.72
'KK107063.1'	0.00	-1.00	43.71	1.38	0.23	0.03	4675608	1.37	7.47	0.97
'KK115971.1'	0.00	-1.00	115.15	3.98	0.29	0.03	4549800	1.08	2.48	0.95
'KK198108.1'	0.00	-1.00	42.76	1.24	0.31	0.03	6439362	6.63	5.79	0.97
'CM002679.1'	0.00	0.05	152.38	3.59	0.30	0.06	147124936	7.53	1.91	0.98
'KK198755.1'	0.11	0.05	93.49	2.24	0.25	0.05	80079441	8.76	2.48	0.99
'HG803548.1'	0.36	0.16	27.31	2.04	0.22	0.11	1771200	0.18	5.31	0.97
'CBZK0100000	0.21	0.08	>1000	>1000	0.09	0.03	391865	8.26	0.68	0.79
'HG805809.1'	0.68	0.14	29.95	2.24	0.09	0.03	533758	0.00	4.07	0.97
'HG934063.1'	0.37	0.10	31.56	1.43	0.19	0.06	4142257	0.00	4.82	0.99
'KK203934.1'	0.34	0.16	32.23	2.88	0.20	0.10	685249	0.00	4.89	0.96
'KK204238.1'	0.40	0.22	31.26	5.52	0.17	0.10	100620	0.00	5.17	0.93
'KK207357.1'	0.45	0.18	29.25	2.98	0.16	0.08	502909	0.00	4.91	0.96
'KK207889.1'	0.44	0.16	29.92	2.62	0.16	0.07	598948	0.00	4.87	0.97
'KK208427.1'	0.43	0.15	29.97	2.54	0.17	0.07	664234	0.00	4.94	0.97
'KK208846.1'	0.44	0.16	30.44	2.59	0.16	0.07	596576	0.00	4.72	0.97
'KK209394.1'	0.43	0.15	29.89	2.50	0.17	0.07	667787	0.00	4.93	0.97
'KK209984.1'	0.57	0.13	27.72	1.78	0.12	0.05	825833	0.00	4.75	0.98
'KK210299.1'	0.45	0.13	28.60	1.70	0.16	0.06	1440740	0.03	4.98	0.98
'KK210757.1'	0.50	0.14	28.10	1.98	0.15	0.06	795547	0.00	4.88	0.97
'KL203742.1'	0.47	0.04	393.10	13.74	0.04	0.01	15899586	5.73	0.45	0.95
'CP007270.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685848	0.87	8.45	0.96
'CP007274.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685841	0.87	8.45	0.96
'CP007266.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685848	0.84	8.45	0.96
'CP007362.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685841	0.87	8.45	0.96
'CP007363.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685901	0.87	8.45	0.96
'CP007364.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685846	0.87	8.45	0.96
'CP007289.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685775	0.84	8.45	0.96
'CP007290.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685848	0.81	8.45	0.96
'CP007293.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685838	0.87	8.45	0.96
'CP007294.2'	0.00	-1.00	28.24	1.20	0.29	0.05	4685658	0.00	8.51	0.96
'CP007295.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4686394	0.86	8.45	0.96
'CP007277.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685848	0.87	8.45	0.96
'CP007278.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685847	0.87	8.45	0.96
'CP007279.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685848	0.81	8.45	0.96
'CP007281.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685848	0.84	8.45	0.96
'CP007284.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685849	0.85	8.45	0.96
'CP007320.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4686535	0.88	8.45	0.96
'CP007321.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685850	0.84	8.45	0.96
'CP007322.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685850	0.84	8.45	0.96
'CP007300.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685839	0.88	8.45	0.96
'CP007301.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685841	0.87	8.45	0.96
'CP007302.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685836	0.87	8.45	0.96
'CP007303.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685905	0.87	8.45	0.96
'CP007304.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685845	0.88	8.45	0.96
'CP007305.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685907	0.87	8.45	0.96
'CP007306.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685844	0.87	8.45	0.96
'CP007307.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685841	0.87	8.45	0.96
'CP007308.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685842	0.88	8.45	0.96
'CP007309.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685844	0.87	8.45	0.96
'CP007310.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685841	0.87	8.45	0.96
'CP007311.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685841	0.82	8.45	0.96
'CP007313.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685848	0.85	8.45	0.96
'CP007314.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685842	0.87	8.45	0.96
'CP007315.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685836	0.87	8.45	0.96
'CP007316.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685844	0.87	8.45	0.96
'CP007334.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685836	0.87	8.45	0.96
'CP007317.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685843	0.87	8.45	0.96
'CP007318.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685844	0.87	8.45	0.96
'CP007319.2'	0.00	-1.00	28.25	1.20	0.29	0.05	4685849	0.00	8.51	0.96
'CP007323.2'	0.00	-1.00	28.18	1.19	0.29	0.05	4686198	0.85	8.45	0.96
'CP007324.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685845	0.87	8.45	0.96
'CP007325.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685847	0.87	8.45	0.96
'CP007326.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685846	0.87	8.45	0.96
'CP007327.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685848	0.84	8.45	0.96
'CP007328.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685845	0.87	8.45	0.96
'CP007330.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685974	0.87	8.45	0.96
'CP007331.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685849	0.84	8.45	0.96
'CP007344.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685846	0.84	8.45	0.96
'CP007345.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685842	0.87	8.45	0.96
'CP007346.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4685832	0.87	8.45	0.96
'CP007347.2'	0.00	-1.00	28.28	1.21	0.29	0.05	4685839	0.91	8.44	0.96
'CP007348.2'	0.00	-1.00	28.27	1.21	0.29	0.05	4686185	0.87	8.45	0.96
'CP007349.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685845	0.87	8.45	0.96
'CP007350.2'	0.00	-1.00	28.26	1.21	0.29	0.05	4685847	0.87	8.45	0.96

'LRVB0100019	0.80	0.12	38.77	2.55	0.05	0.02	887480	0.38	2.91	0.96
'LSRZ0100000	0.36	0.14	144.47	36.75	0.09	0.04	108686	0.53	1.78	0.83
'CM004174.1'	0.00	-1.00	108.36	9.33	0.02	0.00	12542233	0.15	8.06	0.79
'CM004278.1'	0.00	0.11	275.33	20.16	0.10	0.05	51465339	6.01	1.72	0.87
'LUGF01000840	0.19	0.09	59.15	3.43	0.23	0.07	1966717	5.37	3.41	0.98
'LFIV01000001	0.21	0.18	25.14	2.33	0.32	0.16	861708	0.00	6.67	0.97
'LFIW01002504	0.50	0.16	20.47	1.45	0.18	0.08	1081293	0.00	6.55	0.98
'KV411306.1'	0.00	-1.00	147.36	3.27	0.21	0.01	11880239	0.83	2.75	0.97
'KV416798.1'	0.00	-1.00	150.74	6.29	0.23	0.02	2131707	1.08	2.57	0.94
'LVCR0100126	0.11	0.10	>1000	>1000	0.11	0.04	262077	6.35	0.88	0.77
'CP015162.1'	0.84	0.15	13.43	0.70	0.12	0.04	1139223	1.17	7.43	0.99
'CP014266.1'	0.19	0.12	51.98	3.36	0.25	0.11	3976746	16.96	2.89	0.97
'KV417480.1'	0.00	-1.00	49.82	3.53	0.19	0.04	1754491	2.31	6.21	0.90
'KV417266.1'	0.00	-1.00	25.76	1.82	0.40	0.09	1238575	0.10	7.76	0.93
'JYNV0100029	0.00	-1.00	45.70	3.97	0.18	0.04	1160210	0.11	6.71	0.88
'LWBM0100000	0.00	-1.00	29.01	0.87	0.49	0.06	2751756	1.40	6.72	0.98
'LWAD0100000	0.14	0.18	26.25	2.52	0.37	0.19	796877	0.01	6.49	0.97
'LVYW0100000	0.06	0.14	24.83	1.42	0.44	0.18	6771991	0.03	7.58	0.98
'LVYX0100000	0.03	0.12	25.57	1.31	0.47	0.17	9646222	0.06	7.59	0.99
'KV419394.1'	0.69	0.17	18.64	1.25	0.13	0.06	1464488	0.07	5.91	0.98
'LNAU0100047	0.56	0.16	23.15	2.08	0.14	0.06	163649	0.25	5.68	0.97
'LNAR0100210	0.50	0.17	25.24	2.75	0.15	0.07	158618	0.00	5.60	0.97
'LMYD0100027	0.26	0.16	30.04	2.85	0.26	0.11	370448	0.00	5.69	0.97
'LNAS0100006	0.17	0.17	34.14	3.23	0.31	0.15	896619	0.00	5.32	0.96
'LTAH0113137	0.00	-1.00	>1000	>1000	0.18	0.03	42897	0.30	2.74	0.75
'CP015286.1'	0.00	-1.00	31.89	1.01	0.43	0.06	5897585	0.00	6.16	0.97
'KV429032.1'	0.44	0.18	16.19	1.15	0.25	0.12	1367360	0.16	7.74	0.98
'KV428004.1'	0.90	0.17	16.65	1.12	0.08	0.04	793452	0.00	5.89	0.98
'KV427605.1'	0.00	0.31	84.46	19.61	0.06	0.06	2261102	1.18	6.80	0.78
'KV425882.1'	0.58	0.20	11.69	0.78	0.24	0.11	1669733	0.16	9.76	0.99
'KV425551.1'	0.49	0.17	20.10	1.38	0.19	0.09	1528150	0.47	6.26	0.98
'KV423914.1'	0.32	0.18	17.46	1.48	0.31	0.14	592208	0.33	8.18	0.98
'KV424459.1'	0.51	0.20	14.79	1.25	0.23	0.11	847827	0.02	8.37	0.98
'LRGB0100051	0.00	-1.00	68.10	3.05	0.24	0.03	3718170	15.50	3.71	0.94
'CM004194.1'	0.22	0.03	331.42	5.75	0.12	0.02	194908223	9.15	0.68	0.98
'CM004215.1'	0.22	0.03	331.19	5.96	0.12	0.02	208915005	16.13	0.63	0.98
'CM004235.1'	0.22	0.03	331.80	5.86	0.12	0.02	200880650	12.38	0.66	0.98
'CM004256.1'	0.21	0.03	333.89	6.03	0.12	0.02	203663563	14.39	0.64	0.98
'LWBB0100002	0.22	0.11	27.88	1.33	0.30	0.10	4887614	0.20	5.93	0.99
'LKCNO100000	0.00	-1.00	43.39	1.53	0.24	0.03	5272936	5.77	6.88	0.97
'LUCG0100659	0.36	0.15	741.13	>1000	0.07	0.03	55679	0.01	1.42	0.70
'LRBV0100011	0.17	0.08	269.53	35.63	0.14	0.05	861014	1.35	1.21	0.91
'KV775244.1'	0.00	-1.00	95.47	6.56	0.22	0.03	503854	11.22	3.99	0.93
'CM004297.1'	0.77	0.11	40.02	2.11	0.05	0.02	1556355	0.32	2.84	0.97
'CM004191.1'	0.00	-1.00	8.86	0.35	0.64	0.13	3380454	0.00	16.70	0.98
'AZGY0100000	0.00	-1.00	30.55	1.73	0.30	0.07	4538731	0.39	7.16	0.93
'AZGZ0100000	0.00	-1.00	48.47	2.67	0.34	0.06	1592427	1.67	4.77	0.93
'AZHB0100000	0.00	0.15	27.35	1.88	0.49	0.22	3594368	0.09	7.50	0.98
'AZHA0100000	0.00	0.26	73.76	12.72	0.09	0.09	2279171	0.18	6.52	0.85
'AZHC0100000	0.00	-1.00	55.94	6.17	0.14	0.04	2401918	0.05	6.00	0.82
'AZHF0100000	0.00	0.27	35.76	4.23	0.24	0.21	6903712	0.01	7.07	0.92
'AZHD0100000	0.00	-1.00	25.95	0.59	0.44	0.04	3551027	0.19	8.47	0.99
'KV440971.1'	0.10	0.08	117.53	7.00	0.24	0.08	4452461	1.71	2.13	0.96
'CP014501.1'	0.49	0.09	37.14	1.52	0.12	0.04	5930846	0.00	4.06	0.98
'KV441051.1'	0.00	0.15	33.99	2.60	0.49	0.23	2667860	0.00	5.60	0.97
'LXGT0100000	0.42	0.12	33.53	2.51	0.16	0.06	458991	0.00	4.76	0.97
'LXGU0100000	0.41	0.15	34.56	3.24	0.16	0.07	473958	0.01	4.52	0.96
'LLXD0100009	0.31	0.05	187.51	5.89	0.09	0.02	18910200	0.00	1.19	0.97
'CP014278.2'	0.62	0.09	50.95	2.59	0.07	0.02	1811936	0.01	2.62	0.97
'KV441386.1'	0.00	-1.00	56.05	2.61	0.29	0.04	2552699	0.00	4.92	0.94
'LVLJ01002295	0.00	-1.00	153.23	10.90	0.14	0.02	1551447	6.33	3.18	0.88
'LWCA0100000	0.59	0.13	112.18	18.39	0.05	0.02	159981	0.00	1.54	0.86
'KV441548.1'	0.14	0.17	22.84	1.52	0.42	0.20	5402283	0.73	6.99	0.98
'KV441469.1'	0.69	0.12	18.24	0.78	0.13	0.04	2531235	0.00	6.25	0.99
'LSBG0100045	0.35	0.18	73.87	18.30	0.12	0.07	65819	0.06	2.97	0.88
'LTDL01000014	0.63	0.15	29.72	2.26	0.10	0.05	651558	0.00	4.14	0.96
'LTDK0100017	0.38	0.12	128.09	17.91	0.09	0.04	377182	0.01	1.60	0.89
'LWRU0100016	0.00	0.22	47.45	6.62	0.29	0.20	900278	0.03	5.53	0.92
'LWRT0100020	0.29	0.17	28.95	2.59	0.24	0.12	813103	0.00	5.62	0.97
'LSRY0100000	0.38	0.11	83.96	8.96	0.11	0.04	397962	0.49	2.30	0.94
'LWKT0100000	0.52	0.07	44.49	1.27	0.11	0.03	24575218	0.25	3.25	0.99
'LFJK01000005	0.60	0.07	42.95	1.24	0.08	0.02	18579143	2.98	3.09	0.99
'KV441705.1'	0.17	0.14	24.94	1.51	0.37	0.16	3247906	0.38	6.36	0.98
'KV441636.1'	0.00	0.17	31.71	2.52	0.50	0.26	3419696	0.19	6.00	0.97
'CM004348.2'	0.00	-1.00	180.56	3.68	0.06	0.00	310925244	1.85	4.30	0.94
'LWDD0100000	0.26	0.28	18.93	2.85	0.32	0.22	203074	2.16	7.82	0.95
'LWDF0100000	0.18	0.28	22.51	3.67	0.35	0.25	303331	0.36	7.21	0.94
'LWDE0100000	0.45	0.16	84.86	16.94	0.08	0.04	113829	0.00	2.35	0.87
'LWDG0100000	0.48	0.21	17.35	1.81	0.21	0.11	260180	0.30	7.44	0.97
'LVCJ01000000	0.59	0.13	20.07	1.08	0.15	0.05	1192800	0.00	6.14	0.99
'LVCIO1000064	0.64	0.15	19.09	1.19	0.14	0.05	1047054	0.00	6.17	0.98
'LTAE01000000	0.00	-1.00	330.37	57.75	0.19	0.02	249015	3.30	2.15	0.87
'LVCG0100000	0.00	-1.00	161.44	21.93	0.21	0.02	143306	0.45	3.37	0.90
'LVCH0100005	0.00	0.14	256.29	124.28	0.22	0.10	81532	0.59	2.95	0.89
'LWBQ0100000	0.00	0.20	25.72	2.44	0.42	0.24	1919695	3.82	7.66	0.97
'LVTN0100000	0.00	-1.00	290.18	15.77	0.17	0.01	1648447	2.44	1.97	0.93
'CM004386.1'	0.03	0.24	12.35	1.06	0.69	0.41	3003247	0.00	11.04	0.98
'LWHD0100000	0.14	0.06	150.66	5.96	0.19	0.04	11911191	3.21	1.78	0.97
'KV441875.1'	0.13	0.14	31.01	2.43	0.33	0.14	1252801	2.77	6.25	0.98
'LXWW0100020	0.00	-1.00	29.99	1.83	0.46	0.07	286747	2.45	6.82	0.96
'LVKQ01S0010	0.27	0.06	384.36	34.41	0.08	0.02	2424496	0.62	0.71	0.90
'KV442011.1'	0.37	0.11	33.81	1.88	0.18	0.06	1526291	0.03	4.61	0.98
'LHPN0100000	0.00	-1.00	43.35	1.51	0.42	0.05	4062027	0.27	4.82	0.97
'LHPM0100001	0.21	0.13	35.03	2.07	0.28	0.12	4066456	0.08	4.78	0.98
'CM004359.1'	0.10	0.07	104.51	3.56	0.26	0.07	29387870	0.93	2.29	0.98
'LVYIO1000001	0.51	0.14	20.32	1.04	0.18	0.07	4892217	0.05	6.32	0.99
'LSNX0103146	0.00	-1.00	40.52	1.22	0.30	0.03	3675446	1.83	6.70	0.98
'KV442483.1'	0.36	0.11	30.49	1.43	0.20	0.07	4225797	0.25	4.98	0.99
'CP015814.2'	0.27	0.16	26.84	1.88	0.27	0.13	3550837	0.01	5.58	0.97
'CM004372.1'	0.00	-1.00	112.79	1.96	0.15	0.01	65039919	1.43	4.29	0.97
'BDDP0100362	0.65	0.22	23.10	3.02	0.11	0.06	118917	0.08	5.23	0.95
'LSBH0100000	0.00	0.39	34.73	5.95	0.12	0.15	6692040	0.18	8.67	0.86
'LUKN0100319	0.62	0.20	18.53	1.98	0.15	0.07	134276	1.27	6.38	0.97
'LSBJ01000000	0.19	0.16	29.92	1.92	0.33	0.16	7099765	0.18	5.33	0.97
'LSBIO1000001	0.00	-1.00	31.20	2.30	0.17	0.05	5703399	0.11	8.63	0.89
'CP014639.1'	0.77	0.11	43.37	2.51	0.05	0.02	1113233	0.01	2.71	0.97

'CP019434.1'	0.00	-1.00	13.79	0.57	0.58	0.11	3448835	0.17	11.62	0.98
'MSZU0100007	0.09	0.16	20.61	1.33	0.47	0.21	4877926	0.92	8.21	0.98
'CP019124.1'	0.31	0.27	9.02	0.78	0.51	0.31	3192699	0.30	12.41	0.98
'CP019093.1'	0.00	-1.00	209.15	7.04	0.09	0.01	14772968	7.49	3.13	0.93
'MQVM0100000	0.68	0.11	52.67	3.65	0.06	0.02	782669	0.01	2.46	0.95
'MIPV0100804'	0.00	-1.00	60.95	8.28	0.34	0.06	84164	6.74	4.34	0.89
'MEHY0100001	0.78	0.16	18.71	1.40	0.10	0.04	276830	0.00	5.73	0.98
'CP019420.1'	0.76	0.19	7.25	0.36	0.25	0.11	6407860	0.00	12.33	0.99
'CP019490.1'	0.68	0.11	33.76	1.69	0.08	0.03	2110500	0.00	3.62	0.98
'MTKA0100063	0.11	0.05	351.06	23.07	0.16	0.04	4235486	0.01	0.98	0.94
'CP011180.1'	0.00	-1.00	10.92	0.51	0.73	0.17	4106424	0.00	13.18	0.97
'CP015999.1'	0.00	-1.00	9.54	0.36	0.69	0.13	3241870	0.00	15.32	0.99
'CP018344.1'	0.76	0.08	99.74	5.71	0.03	0.01	1656133	0.01	1.24	0.94
'CP018345.1'	0.76	0.08	100.21	5.77	0.03	0.01	1657699	0.01	1.25	0.94
'CP018346.1'	0.76	0.08	99.82	5.73	0.03	0.01	1656322	0.01	1.24	0.94
'CP011458.1'	0.34	0.14	28.16	1.68	0.23	0.10	3468040	14.45	4.43	0.98
'CP010036.1'	0.14	0.14	32.76	2.22	0.36	0.16	3060958	6.69	4.82	0.97
'CP011466.1'	0.34	0.15	27.49	1.71	0.23	0.10	3190451	11.65	4.63	0.98
'CP010046.1'	0.12	0.15	33.37	2.35	0.37	0.17	3060867	6.45	4.82	0.97
'CP010034.1'	0.13	0.15	32.98	2.27	0.36	0.16	3060738	6.45	4.82	0.97
'CP011470.1'	0.15	0.15	32.61	2.27	0.35	0.16	3060857	9.78	4.65	0.97
'CP010032.1'	0.17	0.14	32.12	2.06	0.33	0.14	3060702	3.99	4.96	0.98
'CP010030.1'	0.13	0.14	33.04	2.10	0.36	0.15	3060902	3.52	4.97	0.98
'CP010040.1'	0.13	0.14	33.03	2.10	0.36	0.15	3060815	3.57	4.97	0.98
'CP011462.1'	0.28	0.14	30.08	1.88	0.25	0.11	3440457	9.06	4.64	0.98
'CP010042.1'	0.13	0.15	32.97	2.29	0.36	0.16	3060835	6.36	4.83	0.97
'CP011468.1'	0.13	0.14	33.15	2.24	0.36	0.16	3060915	6.64	4.81	0.97
'CP011472.1'	0.23	0.15	30.48	1.99	0.29	0.13	2979966	3.06	5.00	0.98
'CP010038.1'	0.14	0.15	32.79	2.24	0.35	0.16	3060807	3.29	4.98	0.97
'CP010044.1'	0.13	0.15	32.95	2.27	0.36	0.17	3060464	4.36	4.93	0.97
'CP019545.1'	0.37	0.17	15.75	1.02	0.29	0.12	2714535	8.12	7.95	0.99
'CP018604.1'	0.38	0.18	15.65	1.07	0.29	0.13	2743999	9.12	7.86	0.98
'CP010084.1'	0.26	0.14	30.32	1.94	0.27	0.12	3326187	6.83	4.76	0.98
'CP011475.1'	0.12	0.15	33.00	2.27	0.37	0.17	3060914	3.36	4.98	0.97
'CP010082.1'	0.16	0.14	32.32	2.16	0.34	0.15	3061930	6.48	4.82	0.97
'CP010076.1'	0.16	0.14	32.22	2.15	0.34	0.15	3060713	3.85	4.96	0.97
'CP010291.1'	0.14	0.15	32.93	2.26	0.36	0.16	3060833	6.34	4.83	0.97
'CP010078.1'	0.15	0.14	32.51	2.12	0.35	0.15	3060699	4.20	4.94	0.98
'CP011438.1'	0.14	0.15	32.79	2.24	0.35	0.16	3060807	3.29	4.98	0.97
'CP019634.1'	0.23	0.14	28.82	1.79	0.30	0.13	3515540	0.19	5.37	0.98
'CP011464.1'	0.20	0.14	30.80	2.07	0.31	0.14	3123307	8.43	4.79	0.98
'CP008702.1'	0.34	0.22	8.54	0.58	0.49	0.24	4411532	1.19	12.54	0.99
'CP009198.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	0.41	12.66	0.99
'CP009199.1'	0.34	0.22	8.54	0.58	0.49	0.24	4411532	1.02	12.58	0.99
'CP009200.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	0.41	12.67	0.99
'CP009201.1'	0.34	0.22	8.52	0.58	0.49	0.24	4411532	0.38	12.66	0.99
'CP009202.1'	0.34	0.23	8.49	0.60	0.49	0.25	4411532	0.04	12.73	0.99
'CP009203.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	0.59	12.64	0.99
'CP009204.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	0.71	12.62	0.99
'CP009205.1'	0.35	0.21	8.48	0.55	0.48	0.23	4411532	0.64	12.64	0.99
'CP009206.1'	0.33	0.21	8.58	0.57	0.50	0.24	4411532	0.54	12.65	0.99
'CP009207.1'	0.34	0.22	8.52	0.58	0.49	0.24	4411532	0.67	12.62	0.99
'CP009172.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	0.37	12.67	0.99
'CP009173.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	0.49	12.65	0.99
'CP009174.1'	0.34	0.22	8.51	0.58	0.49	0.24	4411532	0.49	12.65	0.99
'CP009175.1'	0.36	0.22	8.44	0.57	0.47	0.24	4411532	1.01	12.60	0.99
'CP009176.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	1.04	12.56	0.99
'CP009177.1'	0.34	0.22	8.52	0.58	0.49	0.24	4411532	0.41	12.67	0.99
'CP009178.1'	0.33	0.21	8.56	0.56	0.50	0.23	4411532	0.81	12.60	0.99
'CP009179.1'	0.34	0.22	8.54	0.58	0.49	0.24	4411532	0.75	12.64	0.99
'CP009180.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	0.12	12.72	0.99
'CP009181.1'	0.40	0.21	8.29	0.53	0.45	0.21	4411532	1.10	12.59	0.99
'CP009182.1'	0.35	0.21	8.48	0.55	0.48	0.23	4411532	0.78	12.60	0.99
'CP009184.1'	0.33	0.23	8.56	0.59	0.50	0.25	4411532	0.45	12.66	0.99
'CP009185.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	0.08	12.72	0.99
'CP009186.1'	0.34	0.22	8.54	0.58	0.49	0.24	4411532	0.82	12.60	0.99
'CP009188.1'	0.34	0.22	8.52	0.58	0.49	0.24	4411532	0.68	12.61	0.99
'CP009189.1'	0.34	0.22	8.52	0.58	0.49	0.24	4411532	0.81	12.59	0.99
'CP009194.1'	0.33	0.23	8.55	0.59	0.50	0.25	4411532	0.35	12.69	0.99
'CP009196.1'	0.39	0.21	8.35	0.53	0.45	0.21	4411532	1.12	12.58	0.99
'CP009197.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	0.99	12.57	0.99
'CP009190.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	1.12	12.55	0.99
'CP009191.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	0.33	12.69	0.99
'CP009193.1'	0.33	0.22	8.58	0.57	0.50	0.24	4411532	1.03	12.56	0.99
'CP011436.1'	0.13	0.15	33.08	2.31	0.36	0.17	3060756	6.38	4.83	0.97
'CP019666.1'	0.00	-1.00	10.13	0.46	0.46	0.11	6028390	0.00	16.55	0.97
'CP019678.1'	0.00	-1.00	9.28	0.36	0.62	0.12	3818057	0.00	16.42	0.98
'CP009192.1'	0.34	0.22	8.54	0.58	0.49	0.24	4411532	0.23	12.71	0.99
'CP009195.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	1.02	12.56	0.99
'CP009187.1'	0.36	0.23	8.43	0.58	0.47	0.24	4411532	0.41	12.68	0.99
'CP009183.1'	0.34	0.22	8.53	0.58	0.49	0.24	4411532	1.19	12.53	0.99
'CP019726.1'	0.39	0.09	49.45	2.11	0.14	0.04	5209112	0.00	3.22	0.98
'CCYD0100061	0.54	0.11	25.11	1.16	0.14	0.05	3420761	12.06	4.63	0.99
'CCYT0100000	0.56	0.09	58.69	2.99	0.08	0.03	2399970	2.37	2.42	0.97
'CCYA0100026	0.48	0.18	16.05	1.10	0.23	0.11	1618306	3.95	7.25	0.98
'LK022890.1'	0.74	0.07	110.72	5.03	0.03	0.01	2616835	0.00	1.14	0.95
'LK023128.1'	0.75	0.07	117.50	5.68	0.02	0.01	2504534	0.48	1.06	0.95
'LM993667.1'	0.65	0.07	139.80	7.50	0.03	0.01	2795668	0.03	1.00	0.94
'LK934641.1'	0.65	0.07	140.91	7.52	0.03	0.01	2639166	1.32	0.99	0.94
'CVKT0100758	0.60	0.12	38.90	2.74	0.09	0.03	573988	0.00	3.50	0.97
'CVR0100004'	0.55	0.08	55.19	2.18	0.08	0.02	5381421	0.70	2.56	0.98
'HG983337.1'	0.22	0.14	28.41	1.96	0.29	0.12	1466191	0.79	5.96	0.98
'HG975513.1'	0.00	-1.00	176.46	2.53	0.32	0.02	90311507	4.63	1.50	0.97
'FAXB0100000	0.35	0.21	16.33	1.71	0.29	0.15	262854	0.00	8.56	0.98
'CZCC0100000	0.24	0.23	17.82	2.19	0.35	0.20	263113	0.00	8.55	0.97
'CZCL0100000	0.49	0.12	42.97	2.76	0.11	0.04	1156483	0.00	3.36	0.97
'CZCD0100000	0.25	0.23	17.63	2.06	0.35	0.19	263072	0.00	8.55	0.97
'CZCM0100000	0.30	0.17	17.53	1.55	0.31	0.12	341788	0.00	8.54	0.98
'CZCO0100000	0.00	0.23	25.31	3.00	0.41	0.26	970878	0.00	8.01	0.96
'CZCK0100000	0.27	0.22	17.20	1.99	0.33	0.18	262052	0.03	8.73	0.97
'CZCE0100000	0.35	0.21	16.35	1.69	0.29	0.15	262595	0.00	8.55	0.98
'CZCP0100000	0.33	0.26	16.86	2.25	0.30	0.18	215875	0.00	8.37	0.96
'CZCN0100000	0.38	0.22	15.79	1.66	0.28	0.15	262886	0.00	8.56	0.97
'LN907826.1'	0.17	0.18	9.34	0.53	0.63	0.25	9022917	0.15	13.05	0.99
'CZCJ0100000	0.37	0.20	16.03	1.58	0.28	0.14	263057	0.00	8.56	0.98
'CZCI01000001	0.17	0.25	18.42	2.48	0.39	0.23	247527	0.00	8.78	0.97

LT629750.1'	0.32	0.20	9.57	0.59	0.46	0.22	7842044	0.00	12.18	0.99
LT629741.1'	0.83	0.10	43.24	2.02	0.04	0.01	3158583	0.00	2.57	0.97
LT629752.1'	0.59	0.08	99.12	4.55	0.05	0.01	3951560	0.00	1.46	0.96
LT629762.1'	0.00	-1.00	14.60	0.45	0.64	0.09	6092055	0.00	10.63	0.99
LT629740.1'	0.43	0.10	36.31	1.68	0.15	0.05	6014056	0.00	4.00	0.98
LT629771.1'	0.00	-1.00	7.54	0.33	0.73	0.19	7486057	0.00	16.77	0.98
LT629764.1'	0.00	-1.00	29.89	1.01	0.38	0.05	5519819	0.00	7.12	0.97
LT629763.1'	0.27	0.22	14.21	1.09	0.40	0.23	4030203	0.00	9.09	0.98
LT629767.1'	0.17	0.17	14.18	0.86	0.49	0.22	6749275	0.00	9.54	0.99
LT629769.1'	0.22	0.20	13.67	0.95	0.45	0.24	5874625	0.00	9.47	0.98
LT629765.1'	0.00	-1.00	11.28	0.39	0.69	0.11	2633185	0.00	13.23	0.99
LT629766.1'	0.07	0.28	10.22	0.97	0.68	0.44	4023083	0.00	12.50	0.98
LT629770.1'	0.03	0.31	7.47	0.71	0.91	0.57	3552313	0.00	15.48	0.99
LT629772.1'	0.54	0.21	7.04	0.39	0.39	0.18	6733014	0.00	13.57	0.99
LT629775.1'	0.00	-1.00	8.28	0.34	0.81	0.19	9900053	0.00	15.08	0.98
LT629773.1'	0.07	0.12	48.51	3.71	0.34	0.14	1684415	0.01	4.49	0.97
LT629774.1'	0.73	0.08	48.07	1.81	0.05	0.01	3688445	0.00	2.49	0.98
LT629776.1'	0.00	-1.00	7.54	0.34	0.91	0.21	2986943	0.00	16.06	0.98
LT629777.1'	0.00	-1.00	15.83	0.52	0.62	0.10	6529636	0.00	9.68	0.98
LT629778.1'	0.11	0.22	13.17	0.98	0.57	0.32	5943170	0.00	10.55	0.98
LT629779.1'	0.57	0.22	9.60	0.64	0.28	0.14	4459178	0.00	10.91	0.99
LT629801.1'	0.09	0.18	15.29	1.00	0.54	0.25	6417799	0.00	9.59	0.99
LT629784.1'	0.00	-1.00	12.22	0.57	0.51	0.12	4626254	0.00	12.93	0.97
LT630003.1'	0.43	0.11	39.97	1.95	0.14	0.05	5300235	0.00	3.68	0.98
LT629787.1'	0.30	0.18	16.48	1.10	0.35	0.17	3796105	0.00	7.80	0.98
LT629786.1'	0.00	-1.00	18.31	0.72	0.53	0.10	6842016	0.00	9.02	0.97
LT629781.1'	0.00	-1.00	12.81	0.51	0.55	0.10	3763544	0.00	12.50	0.98
LT629793.1'	0.16	0.19	14.46	0.96	0.50	0.25	7087525	0.00	9.38	0.99
LT629799.1'	0.27	0.32	6.19	0.56	0.70	0.44	4405285	0.00	16.29	0.99
LT629782.1'	0.15	0.18	14.63	0.95	0.50	0.24	6130232	0.00	9.64	0.99
LT629788.1'	0.00	0.23	13.99	1.12	0.69	0.40	6092541	0.00	10.46	0.98
LT629800.1'	0.26	0.19	14.43	0.97	0.40	0.21	6032706	0.00	8.99	0.98
LT629803.1'	0.00	-1.00	15.58	0.57	0.61	0.11	6424905	0.00	9.73	0.98
LT629783.1'	0.22	0.19	15.48	1.03	0.43	0.21	5072304	0.00	8.64	0.98
LT629789.1'	0.00	-1.00	8.56	0.30	0.81	0.16	9472622	0.00	14.97	0.99
LT629804.1'	0.30	0.19	20.05	1.55	0.30	0.16	1998342	0.01	7.07	0.98
LT629780.1'	0.00	-1.00	12.43	0.61	0.56	0.13	3191154	0.00	12.61	0.97
LT629791.1'	0.00	-1.00	7.58	0.28	0.84	0.18	7716600	0.00	16.32	0.99
LT629785.1'	0.05	0.22	16.79	1.45	0.60	0.35	3769689	0.00	8.73	0.98
LT629790.1'	0.14	0.20	13.86	0.92	0.53	0.27	6346235	0.00	9.78	0.99
LT629797.1'	0.00	-1.00	15.88	0.65	0.52	0.10	5476367	0.00	10.19	0.97
LT629802.1'	0.27	0.16	13.93	0.75	0.41	0.17	5853167	0.00	9.29	0.99
LT629792.1'	0.33	0.21	12.59	0.93	0.38	0.20	2430293	0.00	9.67	0.98
LT629796.1'	0.22	0.19	13.57	0.86	0.46	0.23	7041758	0.00	9.71	0.99
LT629794.1'	0.70	0.08	76.46	3.36	0.04	0.01	3227923	0.00	1.67	0.97
LT629798.1'	0.16	0.23	14.00	1.11	0.51	0.31	6150838	0.00	9.49	0.98
LT629795.1'	0.33	0.22	15.10	1.14	0.34	0.20	5322478	0.00	8.24	0.98
LT635756.1'	0.51	0.12	40.59	2.20	0.11	0.04	2919042	0.01	3.44	0.97
LT635764.1'	0.63	0.10	37.62	1.60	0.08	0.03	3422859	0.12	3.42	0.98
LT629867.1'	0.16	0.27	7.08	0.56	0.76	0.42	3937879	0.00	15.65	0.99
LT629970.1'	0.27	0.23	11.95	0.91	0.46	0.26	4332289	0.00	10.07	0.98
LT629971.1'	0.16	0.24	7.61	0.54	0.71	0.36	5987931	0.00	14.97	0.99
LT629972.1'	0.00	-1.00	15.96	0.47	0.60	0.09	6592354	0.00	9.70	0.98
*FNXT0100122	0.59	0.11	28.77	1.54	0.11	0.04	1112289	0.12	4.64	0.98
*FNXX0100000	0.00	-1.00	140.86	3.64	0.22	0.02	15208799	2.99	2.49	0.96
LT630002.1'	0.00	0.31	7.72	0.78	0.93	0.60	4141508	0.00	15.47	0.99
LT630032.1'	0.01	0.31	7.72	0.78	0.93	0.60	4141231	0.00	15.47	0.99
*FPAK0100000	0.00	-1.00	114.17	2.20	0.30	0.02	22393718	1.66	2.53	0.97
*FQNF0100000	0.62	0.12	221.18	45.06	0.03	0.01	247000	0.00	0.92	0.75
LT634571.1'	0.00	-1.00	411.56	4.46	0.20	0.01	129927919	0.70	1.10	0.98
LT632320.1'	0.00	0.18	29.97	2.40	0.33	0.19	5174631	0.01	7.37	0.97
LT649234.1'	0.44	0.14	71.14	11.42	0.10	0.04	95011	0.00	2.71	0.92
LT635910.1'	0.46	0.17	78.51	16.72	0.09	0.04	92454	0.18	2.48	0.87
LT658380.1'	0.03	0.22	90.70	38.48	0.30	0.18	91304	0.00	4.02	0.88
LT642146.1'	0.00	-1.00	56.11	5.86	0.35	0.05	88335	0.12	5.07	0.93
LT667505.1'	0.37	0.26	18.34	2.86	0.26	0.15	110906	0.09	7.99	0.96
*QNTN0100167	0.00	0.07	140.24	6.56	0.24	0.07	11737105	6.17	2.57	0.97
LT670849.1'	0.12	0.22	10.39	0.71	0.65	0.34	7525217	0.00	12.34	0.99
LT671675.1'	0.00	-1.00	12.27	0.55	0.61	0.12	2009306	0.11	12.51	0.98
*FTPI01000002	0.24	0.10	115.51	10.99	0.15	0.05	884900	11.30	1.79	0.94
LT671813.1'	0.01	0.15	21.22	1.53	0.52	0.21	1507387	0.00	9.23	0.98
LT671821.1'	0.00	0.14	21.32	1.41	0.52	0.20	1508930	0.00	9.23	0.99
LT671789.1'	0.00	-1.00	21.62	0.65	0.51	0.06	1515123	0.00	9.24	0.99
LT671798.1'	0.00	-1.00	21.09	0.69	0.48	0.06	1509484	0.00	9.63	0.98
LT671805.1'	0.00	0.15	21.57	1.53	0.51	0.21	1509448	0.00	9.22	0.99
LT707061.1'	0.35	0.19	12.93	0.84	0.36	0.17	5729155	0.00	9.34	0.99
LT707063.1'	0.18	0.17	12.70	0.71	0.50	0.21	5897393	0.00	10.42	0.99
LT707062.1'	0.27	0.19	13.45	0.84	0.42	0.21	6077628	0.00	9.43	0.99
LT707064.1'	0.41	0.19	11.59	0.67	0.35	0.17	6090301	0.00	9.84	0.99
LT707065.1'	0.00	0.21	10.81	0.74	0.78	0.39	6227325	0.00	12.99	0.99

AD014297.3 *Drosophila melanogaster* chromosome 3R
 CM000663.2 *Homo sapiens* chromosome 1, GRCh38 reference primary assembly
 CM000313.4 *Pan troglodytes* isolate Yerkes chimp pedigree RC0471 (Clint) chromosome 1, whole genome shotgun sequence
 CM000558.0 *Forpys abelli* chromosome 1
 CM000994.2 *Mus musculus* chromosome 1, GRC primary reference assembly
 CP022684.1 *Arabidopsis thaliana* chromosome 1 sequence
 CM000070.3 *Drosophila pseudoobscura pseudoobscura* strain MV2-25 chromosome 2, whole genome shotgun sequence
 GL010027.1 *Xosetia norvegicus* strain mixed chromosome 1, whole genome shotgun sequence
 GL010027.2 *Loxodonta africana* unplaced genomic scaffold scaffold_0, whole genome shotgun sequence
 D598599.0 *Pericarpium nannifolia* ATCC 14223 scf1 105668343764 genomic scaffold, whole genome shotgun sequence
 CM002888.1 *Danio rerio* chromosome 4, GRCh10 reference primary assembly
 KB941397.1 *Aplysia californica* isolate F4 B8 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence
 CH033449.1 *Homo sapiens* chromosome 2, whole genome shotgun sequence
 CM000463.1 *Homo sapiens* chromosome 2, whole genome shotgun sequence
 BL000001.2 TPA: *Homo sapiens* chromosome 7
 CM000029.2 *Mus musculus* chromosome 1, whole genome shotgun sequence
 BA000047.1 *Pan troglodytes* versus DNA, chromosome V, partial sequence
 CM000054.5 *Stylops mellifera* strain DH4 linkage group 1, whole genome shotgun sequence
 KN913737.1 *Argemone* *argemone* strain Spur 01 unplaced genomic scaffold scaffold2, whole genome shotgun sequence
 CM000308.1 *Macaca mulatta* chromosome 1, whole genome shotgun sequence
 CM000231.2 *Rattus norvegicus* chromosome 1, whole genome shotgun sequence
 CM000411.1 *Onchophanes analatus* chromosome 3, whole genome shotgun sequence
 CM000039.3 *Canis lupus familiaris* chromosome X, whole genome shotgun sequence
 CM000308.3 *Monodelphis domestica* chromosome 1, whole genome shotgun sequence
 CM000377.2 *Equus caballus* chromosome 1, whole genome shotgun sequence
 CM000093.4 *Gallus gallus* isolate RJF #256 breed Red Jungle fow, inbred line UCDD01 chromosome 1, whole genome shotgun sequence
 CM000915.2 *Nasonia vitripennis* chromosome 1, whole genome shotgun sequence
 CM000029.2 *Trichogramma castaneum* strain Georgia GAC linkage group LC3, whole genome shotgun sequence
 CM000455.1 *Plasmodium vivax* chromosome 14, whole genome shotgun sequence
 D554899.0 *Physcomitrella patens* subsp. *patens* PHYPAscaffold1, genomic scaffold, whole genome shotgun sequence
 CH991767.1 *Giardia lamblia* ATCC 50803 SC3, 5775 genomic scaffold, whole genome shotgun sequence
 CH464491.1 *Trypanosoma brucei* brucei strain 92774 GUTa10.1 chromosome 11 chr11_scaffold01 genomic scaffold, whole genome shotgun sequence
 CM001232.1 *Magnaporthe oryzae* 70-15 chromosome 2, whole genome shotgun sequence
 D5382126.1 *Kuyvenomyces ladicis* strain NRRL Y-1140 chromosome F complete sequence
 CR382311.1 *Yarrowia lipolytica* CLUB122 chromosome E complete sequence
 CR380958.2 *Canidia gabriela* strain CBS138 chromosome E complete sequence
 D5496108.1 *Chlamydomonas reinhardtii* strain CC-503 osw2 mt1-CHLREscaffold1, genomic scaffold, whole genome shotgun sequence
 CM000169.1 *Aspergillus fumigatus* A293 chromosome 1, whole genome shotgun sequence
 D5027059.1 *Aspergillus clavatus* NRRL 1 109942828056 genomic scaffold, whole genome shotgun sequence
 FR798432.1 *Leishmania major* strain Friedlin complete genome, chromosome 36
 AE014187.2 *Plasmodium falciparum* 3p76 chromosome 14, complete sequence
 CM000337.2 *Populus trichocarpa* linkage group LG1, whole genome shotgun sequence
 DS113177.1 *Trichomonas vaginalis* GS 1047229024141 genomic scaffold, whole genome shotgun sequence
 CM000894.1 *Eimeria tenella* chromosome 1, ordered contigs
 FR799010.1 *Brucella* *brucella* MHOM/BR/75/M2904 complete genome, chromosome 36
 CM007087.1 *Aspergillus niger* supercontig An02
 FR7991543.1 *Monocystis brevivittis* M1 MONBRAScaffold2, genomic scaffold, whole genome shotgun sequence
 FR799468.1 *Leishmania infantum* JPCM5 genome chromosome 36
 CU328607.1 *Schizosaccharomyces pombe* chromosome 1, complete sequence
 BX24605.5 *Caenorhabditis elegans* chromosome V
 LM857004.1 *Brugia malayi* FR3 supercontig from assembly B_malay3.1 Bmal_v3_scaffold1, whole genome shotgun sequence
 CM000812.5 *Sus scrofa* isolate TJ Tabasco chromosome 1, whole genome shotgun sequence
 GR000001.2 TPA: *Mus* *tarsus* chromosome 1, whole genome shotgun sequence
 CAJ01001934.1 *Plasmodium chabaudi* whole genome shotgun assembly, contig PC_RP2108, whole genome shotgun sequence
 CM000695.1 *Felis catus* breed mixed chromosome A1, whole genome shotgun sequence
 EQ62652.1 *Aspergillus stipitatus* ATCC 10503 scf2_1105507295523 genomic scaffold, whole genome shotgun sequence
 CM000781.2 *Sorghum bicolor* cultivar BTX6600 chromosome 2, whole genome shotgun sequence
 CM000774.0 *Brucella melitensis* strain H97 complete genome, whole genome shotgun sequence
 CM000441.2 *Clostridium difficile* QCC-66/26 chromosome 1, whole genome shotgun sequence
 CR940347.1 *Theileria annulata* strain Ankara isolate clone C9, *** SEQUENCING IN PROGRESS ***
 CH776615.1 *Onocarpus reesi* 1704 scaffold1, genomic scaffold, whole genome shotgun sequence
 EQ999973.1 *Blastomycosis dermatitidis* ER-3 genomic scaffold supercont1.1, whole genome shotgun sequence
 GL014402.1 *Saccharomyces kowilevskii* unplaced genomic scaffold scaffold25907, whole genome shotgun sequence
 CM000791.1 *Oryzodictya cunicularis* chromosome 1, whole genome shotgun sequence
 CM000714.1 *Basillus cereus* M1293 chromosome, whole genome shotgun sequence
 FN597038.1 *Vitis vinifera*, whole genome shotgun sequence of line PNA0024, unoriented chromosome 14, chr14
 GG66612.1 *Branchiostoma floridae* genomic scaffold BRAFLScaffold1_196, whole genome shotgun sequence
 GL048076.1 *Clavospora lusitanae* ATCC 42720 scaffold1, genomic scaffold, whole genome shotgun sequence
 G0657448.1 *Blastomycosis glabrata* SLH1408 genomic scaffold supercont1.1, whole genome shotgun sequence
 G0657448.2 *Basillus mycoides* DSM 2048 chromosome 1, whole genome shotgun sequence
 CM000741.1 *Basillus cereus* AH1273 chromosome, whole genome shotgun sequence
 CH477178.1 *Aedes aegypti* strain Liverpool supercont1.1 genomic scaffold, whole genome shotgun sequence
 GL048072.1 *Macropus eugenii* unplaced genomic scaffold scaffold_4001, whole genome shotgun sequence
 CM000294.1 *Cucumis sativus* cultivar 9930 chromosome 3, whole genome shotgun sequence
 GL020027.1 *Hydra magnipapillata* strain 105 unplaced genomic scaffold HYDRAScaffold_39356, whole genome shotgun sequence
 CM000831.1 *Drosophila virilis* strain 15510 chromosome 6
 KE546988.1 *Hydrogarnipapillata* *hydra* OY26 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
 GL044473.1 *Xenopus tropicalis* strain Nigerian chromosome 1, whole genome shotgun sequence
 CM388813.1 *Arabidopsis lyrata* subsp. *lyrata* unplaced genomic scaffold ARALYScaffold1, whole genome shotgun sequence
 GL192338.1 *Alouatta melanoleuca* unplaced genomic scaffold scaffold292, whole genome shotgun sequence
 GL000721.2 *Glycine max* cultivar Williams 82 chromosome 16, whole genome shotgun sequence
 FR947122.1 *Phaeocharitophila brigatae* complete genome, chrX, whole genome shotgun sequence
 CM000126.1 *Oryza sativa* (indica cultivar-group) chromosome 1, whole genome shotgun sequence
 CM000856.1 *Calithrix jacchus* chromosome 1, whole genome shotgun sequence
 CM000151.3 *Dicystoselium discoideum* AX4 chromosome 2, whole genome shotgun sequence
 GL277768.1 *Nasonia glauca* strain RV2xU4 unplaced genomic scaffold SCAFFOLD1, whole genome shotgun sequence
 GL277950.1 *Nasonia longipennis* strain IVU4 unplaced genomic scaffold SCAFFOLD1, whole genome shotgun sequence
 AE008081.1 *Polychaeta griseivitta* strain Tai18E2 genomic scaffold FPL_scaffold2, whole genome shotgun sequence
 KE141673.1 *Homo sapiens* unplaced genomic scaffold scaffold34, whole genome shotgun sequence
 G0738845.1 *Naegleria gruberi* genomic scaffold NAEGRAScaffold1, whole genome shotgun sequence
 CM000747.1 *Zea mays* cultivar B73 chromosome 1, whole genome shotgun sequence
 CH902611.1 *Drosophila ananassae* strain TSCF14024-0371.133 scaffold, 13340 genomic scaffold, whole genome shotgun sequence
 GH547177.1 *Drosophila erecta* strain TSCF14021-0224.01 scaffold, 4929 genomic scaffold, whole genome shotgun sequence
 CH902611.2 *Drosophila ananassae* strain TSCF14024-0371.133 scaffold, 15110 genomic scaffold, whole genome shotgun sequence
 CH933806.1 *Drosophila mojavensis* strain TSCF15081-1352.22 scaffold, 6540 genomic scaffold, whole genome shotgun sequence
 CH791979.1 *Drosophila persimilis* strain MSH-3 chromosome 0, genomic scaffold, whole genome shotgun sequence
 CH480815.1 *Drosophila sechellia* strain Robc-3 scaffold 0, genomic scaffold, whole genome shotgun sequence
 CH480461.1 *Drosophila virilis* strain TSCF15010-1051.87 scaffold, 13049 genomic scaffold, whole genome shotgun sequence
 BA0000720.1 *Plasmodium berghei* whole genome shotgun assembly, contig PB_RF0829, whole genome shotgun sequence
 AE008720.2 *Oryza sativa* japonica strain Tai18E2 chromosome 3R, whole genome shotgun sequence
 G0505806.1 TPA, asm: *Homo sapiens* unplaced genomic scaffold scaffold1475, whole genome shotgun sequence
 CM000880.2 *Brachyodiplosis distachyon* strain Bd21 chromosome 1, whole genome shotgun sequence
 CM000885.1 *Ovis aries* chromosome 1, whole genome

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X59720.2	S.cerevisiae chromosome III complete DNA sequence	fungi'
AP006502.2	Cyanidioschyzon merolae strain 10D DNA, chromosome 20, complete genome	plants'
AL590450.1	chromosome XI of strain GB-M1 of Encephalitozoon cuniculi (Microspora)	fungi'
FN692037.1	Lactobacillus crispatus 5711 complete genome, strain 5711	bacteria'
CP000581.1	Ostreococcus lucimarinus CCE9901 chromosome 1, complete sequence	plants'
CU928171.1	Lachancea thermotolerans CBS 6340 chromosome G complete sequence	fungi'
GL349433.1	Thecamonas trahens ATCC 50062 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	protozoa'
DS028118.1	Phytophthora infestans T30-4 supercont1.1 genomic scaffold, whole genome shotgun sequence	protozoa'
GL349630.1	Acyrtosiphon pisum unplaced genomic scaffold Scaffold10, whole genome shotgun sequence	invertebrates'
GL376636.1	Pythium ultimum DAOM BR144 unplaced genomic scaffold scf_1117875582039, whole genome shotgun sequence	fungi'
GL629765.1	Grosmannia clavigera kw1407 unplaced genomic scaffold GCSC_140, whole genome shotgun sequence	fungi'
GG742441.1	Grosmannia clavigera kw1407 genomic scaffold scaffold_2, whole genome shotgun sequence	fungi'
GL377302.1	Schizophyllum commune H4-8 unplaced genomic scaffold SCHOCscaffold_1, whole genome shotgun sequence	fungi'
CH408029.1	Chaetomium globosum CBS 148.51 scaffold_1 genomic scaffold, whole genome shotgun sequence	fungi'
GL377338.1	Alta cephalotes unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	invertebrates'
GL377565.1	Selaginella moellendorffii unplaced genomic scaffold SELMOscaffol_0, whole genome shotgun sequence	plants'
GL378233.1	Volvox carteri f. nagariensis unplaced genomic scaffold VOLCA scaffold_1, whole genome shotgun sequence	plants'
JH798064.1	Botryotinia fuckeliana B05.10 unplaced genomic scaffold B0510_SuperContig_J3_V4, whole genome shotgun sequence	fungi'
DS547091.1	Laccaria bicolor S238N-H82 LACBIscaffold_1 genomic scaffold, whole genome shotgun sequence	fungi'
CM000961.1	Corynebacterium genitalium ATCC 33030 chromosome, whole genome shotgun sequence	bacteria'
GL379786.1	Caenorhabditis bremeri unplaced genomic scaffold Scd002_0, whole genome shotgun sequence	invertebrates'
GL365395.1	Gaeumannomyces graminis var. tritici R3-111a-1 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
BK006938.2	TPA, inf. Saccharomyces cerevisiae S288c chromosome IV, complete sequence	fungi'
CP001952.1	Encephalitozoon intestinalis ATCC 50506 chromosome XI, complete sequence	fungi'
CM000962.2	Meleagris gallopavo isolate NT-WF06-2002-E0010 breed Aviagen turkey brand Nicholas breeding stock chromosome 1, whole genome shotgun sequence	vertebrates_non_mammals'
CM000960.1	Escherichia coli str. K-12 substr. MG1655star chromosome, whole genome shotgun sequence	bacteria'
CM001648.1	Nomascus leucogenys chromosome 2, whole genome shotgun sequence	vertebrates_mammals'
CH445325.1	Parastagonospora nodorum SN15 scaffold_1, whole genome shotgun sequence	fungi'
CH476621.1	Sclerotinia sclerotiorum 1980 scaffold_1 genomic scaffold, whole genome shotgun sequence	fungi'
GL429767.1	Myotis lucifugus unplaced genomic scaffold scaffold_0, whole genome shotgun sequence	vertebrates_mammals'
GL475358.1	Caenorhabditis japonica strain DF5081 unplaced genomic scaffold Scaffold18210, whole genome shotgun sequence	invertebrates'
GL438234.1	Camponotus floridanus unplaced genomic scaffold scaffold107, whole genome shotgun sequence	invertebrates'
GL451853.1	Harpegnathos saltator unplaced genomic scaffold scaffold271, whole genome shotgun sequence	invertebrates'
JH119215.1	Wickerhamomyces anomalus NRRL Y-366 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	fungi'
GL455988.1	Oryza glaberrima chromosome 3 short arm genomic scaffold glaberrima_chr3	plants'
GL433353.1	Chlorelia variabilis unplaced genomic scaffold CHLNCscaffold_1, whole genome shotgun sequence	plants'
CM001015.1	Streptomyces clavuligerus ATCC 27064 chromosome, whole genome shotgun sequence	bacteria'
CM001020.1	Pseudomonas aeruginosa 39016 chromosome, whole genome shotgun sequence	bacteria'
CM001040.1	Malus x domestica chromosome 15, whole genome shotgun sequence	plants'
GL476399.1	Petromyzon marinus unplaced genomic scaffold scaffold_71, whole genome shotgun sequence	vertebrates_non_mammals'
CS697331.1	Glomerella griseoviridis M1 001 genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
GL501517.1	Mayella destructor strain Kansas Great Plain chromosome X1 unlocalized genomic scaffold X1.7, whole genome shotgun sequence	invertebrates'
CH236920.1	Aspergillus nidulans FGSC A4 chromosome VIII scaffold_1, whole genome shotgun sequence	fungi'
CM000694.1	Saccharomyces kluyveri NRRL Y-12651 chromosome H, whole genome shotgun sequence	fungi'
CP003820.1	Cryptococcus neoformans var. grubii H99 chromosome 1, complete sequence	fungi'
CH003412.1	Ciona savignyi psa_67 genomic scaffold, whole genome shotgun sequence	invertebrates'
CM000138.1	Oryza sativa Japonica Group chromosome 1, whole genome shotgun sequence	plants'
CH476732.1	Rhizopus oryzae RA 99-880 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
GG704911.1	Coccidioides immitis RS genomic scaffold supercont3.1, whole genome shotgun sequence	fungi'
CH408043.1	Saccharomyces cerevisiae RM11-1a scaffold_1 genomic scaffold, whole genome shotgun sequence	fungi'
CM000040.1	Cryptococcus neoformans var. neoformans B-3501A chromosome 1, whole genome shotgun sequence	fungi'
CM000638.1	Thalassiosira pseudonana CCMP1135 chromosome 1, whole genome shotgun sequence	protozoa'
CH408155.1	Pichia guilliermondii ATCC 6260 scaffold_1 genomic scaffold, whole genome shotgun sequence	fungi'
CH872346.1	Candida albicans WO-1 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
KQ410567.1	Cryptococcus gattii R265 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
CH396049.1	Drosophila pseudoobscura pseudoobscura strain MVZ-25_scf_89412 genomic scaffold, whole genome shotgun sequence	invertebrates'
DS268407.1	Caenorhabditis remanei Scd02_0 genomic scaffold, whole genome shotgun sequence	invertebrates'
CM000578.1	Fusarium verticillioides 7600 chromosome 1, whole genome shotgun sequence	fungi'
CH476655.1	Ajiellomyces capsulatus Nam1 scaffold_1 genomic scaffold, whole genome shotgun sequence	fungi'
CH476594.1	Aspergillus fumigatus H9-824 scaffold_1 genomic scaffold, whole genome shotgun sequence	fungi'
DS027696.1	Neosartorya fischeri NRRL 181 1099437636264 genomic scaffold, whole genome shotgun sequence	fungi'
CH871918.1	Plasmodium falciparum HB3 supercont1.1 genomic scaffold, whole genome shotgun sequence	protozoa'
CH981524.1	Lodderomyces elongisporus NRRL YB-4239 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
KE387274.1	Toxoplasma gondii GT1 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	protozoa'
DS565998.1	Phytophthora ramorum strain Pr102 Scaffold1 genomic scaffold, whole genome shotgun sequence	protozoa'
JH159151.1	Phytophthora sojae unplaced genomic scaffold PHYSOscaffold_1, whole genome shotgun sequence	protozoa'
CH890625.1	Azocerospora apis USDA-ARS671408 SCACFFOLD1 genomic scaffold, whole genome shotgun sequence	protozoa'
DS016058.1	Plasmodium falciparum Dd2 supercont1.1 genomic scaffold, whole genome shotgun sequence	protozoa'
DS016981.1	Coccidioides immitis H538.4 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
KE651166.1	Schizosaccharomyces japonicus yFS275 unplaced genomic scaffold supercont5.1, whole genome shotgun sequence	fungi'
DS022300.1	Batrachochytrium dendrobatidis JEL423 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DSU26053.1	Coccidioides immitis RMSCC Z594 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS178262.1	Puccinia graminis f. sp. tritici CRL 75-36-700-3 supercont2.1 genomic scaffold, whole genome shotgun sequence	fungi'
CM000589.1	Fusarium oxysporum f. sp. lycopersici 4287 chromosome 1, whole genome shotgun sequence	fungi'
DS231615.1	Pyrenophora tritici-repentis Pt-1C-BFP supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
KI544492.1	Toxoplasma gondii VEG unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	protozoa'
DS480378.1	Vanderwaltozyma polyspora DSM 70294 KpolScaffold1018 genomic scaffold, whole genome shotgun sequence	fungi'
DS2681109.1	Coccidioides posadasii RMSCC 3488 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS268118.1	Coccidioides posadasii RMSCC 3703 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
GG663963.1	Ajiellomyces capsulatus J198AR genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
DS499594.1	Aspergillus fumigatus A1163 scf_000001 genomic scaffold, whole genome shotgun sequence	fungi'
DS544195.1	Coccidioides posadasii RMSCC 2133 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS544250.1	Coccidioides posadasii RMSCC 3700 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS544493.1	Coccidioides posadasii CPA 0001 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS985241.1	Trichophyton adhaerens TRADscaffold_1 genomic scaffold, whole genome shotgun sequence	invertebrates'
DS499746.1	Plasmodium falciparum VSJ1 supercont1.2 genomic scaffold, whole genome shotgun sequence	protozoa'
DS050602.1	Plasmodium falciparum Senegal_V34.04 supercont1.2 genomic scaffold, whole genome shotgun sequence	protozoa'
DS050930.1	Plasmodium falciparum RO-33 supercont1.1 genomic scaffold, whole genome shotgun sequence	protozoa'
DS514921.1	Plasmodium falciparum K1 supercont1.1 genomic scaffold, whole genome shotgun sequence	protozoa'
DS519693.1	Plasmodium falciparum FCC-2Hainan supercont1.1 genomic scaffold, whole genome shotgun sequence	protozoa'
DS526469.1	Plasmodium falciparum D10 supercont1.1 genomic scaffold, whole genome shotgun sequence	protozoa'
DS529121.1	Plasmodium falciparum D6 supercont1.2 genomic scaffold, whole genome shotgun sequence	protozoa'
KE123623.1	Plasmodium falciparum 7G8 unplaced genomic scaffold supercont1.57, whole genome shotgun sequence	protozoa'
KE123511.1	Plasmodium falciparum Santa Lucia unplaced genomic scaffold supercont1.50, whole genome shotgun sequence	protozoa'
KN305531.1	Paracoccidioides brasiliensis Pb03 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
KE503206.1	Schizosaccharomyces octosporus yFS286 unplaced genomic scaffold supercont6.1, whole genome shotgun sequence	fungi'
DS981520.1	Carica papaya supercontng_0 genomic scaffold, whole genome shotgun sequence	plants'
DS560032.1	Coccidioides posadasii RMSCC 1037 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS560667.1	Coccidioides posadasii RMSCC 1038 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS561724.1	Coccidioides posadasii CPA 0020 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS562368.1	Coccidioides posadasii CPA 0066 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS572695.1	Verticillium dahliae VdLs.17 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
KN293992.1	Paracoccidioides sp. lutzi P016 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
KQ275957.1	Paracoccidioides brasiliensis Pb18 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
EQ090207.1	Anopheles gambiae M scf_1925401379 genomic scaffold, whole genome shotgun sequence	invertebrates'
EQ099730.1	Anopheles gambiae S scf_1106392397136 genomic scaffold, whole genome shotgun sequence	invertebrates'
DS572940.1	Heterodera glycines HG2_15 genomic scaffold, whole genome shotgun sequence	invertebrates'
DS985214.1	Verticillium albo-atrum VaMs.102 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
EQ151724.1	Mchenga conophoros CCONA1000001 genomic scaffold, whole genome shotgun sequence	vertebrates_non_mammals'
EQ169210.1	Labetotropheus tscheltorini LFUEA1000001 genomic scaffold, whole genome shotgun sequence	vertebrates_non_mammals'
EQ165432.1	Melanochlamys auratus MAURA1000001 genomic scaffold, whole genome shotgun sequence	vertebrates_non_mammals'
EQ202275.1	Maylandia zebra MZEB1000001 genomic scaffold, whole genome shotgun sequence	vertebrates_non_mammals'
EQ220184.1	Rhamphochromis esox RESOA1000001 genomic scaffold, whole genome shotgun sequence	vertebrates_mammals'
CM000605.1	Phaeodactylum tricornutum CCAP 10551 chromosome 1, whole genome shotgun sequence	protozoa'
DS989822.1	Anthroderna gypseum CBS 118893 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS990636.1	Ajiellomyces capsulatus H88 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
GG992419.1	Ajiellomyces capsulatus H143 genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
HF943549.1	Blumeria graminis f. sp. hordei DH14 genomic scaffold, sca005486, whole genome shotgun sequence	fungi'
DS995701.1	Microsporium canis CBS 113480 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
DS995718.1	Trichophyton equinum CBS 127.97 supercont1.1 genomic scaffold, whole genome shotgun sequence	fungi'
GG663735.1	Micromonas pusilla CCMP1545 genomic scaffold MICPUscscaffold_1, whole genome shotgun sequence	plants'
GG745328.1	Alomyces macrogynus ATCC 38327 genomic scaffold supercont3.1, whole genome shotgun sequence	fungi'
KE346360.1	Capaspora owczarskii ATCC 30864 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	invertebrates'
GG698996.1	Nectria haematococca mpII/77-13-4 chromosome 1 genomic scaffold NECHAcasa_1_chr1_3_0, whole genome shotgun sequence	fungi'
GG700648.1	Trichophyton rubrum CBS 118892 genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
GG698477.1	Trichophyton tonsurans CBS 112818 genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
CM000924.1	Saccharomyces cerevisiae Sigma1278b chromosome 4, whole genome shotgun sequence	fungi'
ACYE01000120.1	Trichophyton verrucosum HKI 0517 confg02026_1.f1.exp, whole genome shotgun sequence	fungi'
ADA502000001.1	Puccinia tritici-1 BB60 Race 1 supercont2.1, whole genome shotgun sequence	fungi'
KN583189.1	Saprolengia parasitica CBS 223.65 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	protozoa'
JH379045.1	Epilchloa festucae E2368 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	fungi'
GG749407.1	Blastomyces dermatitidis ATCC 18188 supercont1.1, whole genome shotgun sequence	fungi'
DF090316.1	Bombyx mori DNA, scaffold: Bm_scaf1, strain: p507/Dazao	invertebrates'
FN429986.1	Tuber melanosporum whole genome shotgun sequence assembly, scaffold_1, strain Mel28	fungi'
FN686538.1	Blastoscytis hominis, Singapore isolate B (sub-type 7) whole genome shotgun sequence assembly, scaffold_0	protozoa'
EQ973772.1	Rhinus communis genomic scaffold scf_1106159304512, whole genome shotgun sequence	plants'
CH375957.1	Bombyx mori strain Dazao Scaffold000001 genomic scaffold, whole genome shotgun sequence	invertebrates'
DS562855.1	Cavia porcellus supercont2_0 genomic scaffold, whole genome shotgun sequence	vertebrates_mammals'
FN330975.1	Schistosoma japonicum isolate Anhui clone SJC_S000000, complete sequence, whole genome shotgun sequence	invertebrates'
CM000518.1	Taeniopygia guttata chromosome 2, whole genome shotgun sequence	vertebrates_non_mammals'
DF000001.1	Oryzias latipes DNA, scaffold01, strain: HNI	vertebrates_non_mammals'
KN525718.1	Pteropus vampyrus isolates Shaw unplaced genomic scaffold Scaffold1, whole genome shotgun sequence	vertebrates_mammals'
JH472452.1	Turicops truncatus unplaced genomic scaffold Scaffold8, whole genome shotgun sequence	vertebrates_mammals'
KN672347.1	Dipodomys ordii isolate 6190 unplaced genomic scaffold Scaffold1, whole genome shotgun sequence	vertebrates_mammals'
FR853080.2	Gorilla gorilla gorilla genome chromosome, chr1, whole genome shotgun sequence	vertebrates_mammals'

BM676130.1 *Procvacia capensis* atlas Dallas Zoo Isls #01D731 unplaced genomic scaffold Scaffold1, whole genome shotgun sequence
CM000438.1 *Burkholderia thailandensis* DSM 70038 chromosome 1, whole genome shotgun sequence
CM000287.4 *Clostridium difficile* QCD-32g56 chromosome, whole genome shotgun sequence
CM000296.1 *Congrebractia litoralis* KT71 chromosome, whole genome shotgun sequence
CM000440.1 *Funaria hygrometrica* subsp. *proserpinacoides* ATCC 30961 chromosome, whole genome shotgun sequence
CM000637.1 *Clostridium difficile* QCD-63g42 chromosome, whole genome shotgun sequence
CM000661.1 *Clostridium difficile* QCD-76w55 chromosome, whole genome shotgun sequence
CM000657.1 *Clostridium difficile* QCD-97b34 chromosome, whole genome shotgun sequence
CM000658.1 *Clostridium difficile* QCD-37x79 chromosome, whole genome shotgun sequence
CM000917.1 *Hoefelia photophila* DFL-43 chromosome, whole genome shotgun sequence
CM000446.1 *Streptococcus pneumoniae* ATCC 25466 chromosome, whole genome shotgun sequence
CM000511.1 *Streptomyces sveticus* ATCC 29083 chromosome, whole genome shotgun sequence
CM000604.1 *Clostridium difficile* ATCC 43255 chromosome, whole genome shotgun sequence
CM000659.1 *Clostridium difficile* CIP 107932 chromosome, whole genome shotgun sequence
CM000660.1 *Clostridium difficile* QCD-23m63 chromosome, whole genome shotgun sequence
CM000662.1 *Escherichia coli* O157:H7 str. TW14588 chromosome, whole genome shotgun sequence
CM000971.1 *Bacillus subtilis* subsp. *subtilis* str. 168 chromosome, whole genome shotgun sequence
CM000498.1 *Bacillus subtilis* subsp. *subtilis* str. JH42 chromosome, whole genome shotgun sequence
CM000490.1 *Bacillus subtilis* subsp. *subtilis* str. SMY chromosome, whole genome shotgun sequence
CM000953.1 *Lactobacillus jensenii* JV-116 chromosome, whole genome shotgun sequence
CM000955.1 *Finegoldia magna* ATCC 53516 chromosome, whole genome shotgun sequence
CM000952.1 *Staphylococcus aureus* subsp. *aureus* S818 chromosome, whole genome shotgun sequence
CM000770.1 *Rickettsia endosymbiont* of *Ixodes trianguliceps* chromosome, whole genome shotgun sequence
CM000241.1 *Aeromonas salmonicida* DSM 15272 chromosome, whole genome shotgun sequence
CM000715.1 *Bacillus cereus* ATCC 10876 chromosome, whole genome shotgun sequence
CM000716.1 *Bacillus cereus* BGSC 6E1 chromosome, whole genome shotgun sequence
CM000717.1 *Bacillus cereus* 172560W chromosome, whole genome shotgun sequence
CM000718.1 *Bacillus cereus* MM3 chromosome, whole genome shotgun sequence
CM000719.1 *Bacillus cereus* AH621 chromosome, whole genome shotgun sequence
CM000720.1 *Bacillus cereus* F309803 chromosome, whole genome shotgun sequence
CM000721.1 *Bacillus cereus* ATCC 4342 chromosome, whole genome shotgun sequence
CM000722.1 *Bacillus cereus* m1550 chromosome, whole genome shotgun sequence
CM000723.1 *Bacillus cereus* BORD-ST24 chromosome, whole genome shotgun sequence
CM000724.1 *Bacillus cereus* BORD-ST196 chromosome, whole genome shotgun sequence
CM000725.1 *Bacillus cereus* BORD-Cat4 chromosome, whole genome shotgun sequence
CM000726.1 *Bacillus cereus* 958201 chromosome, whole genome shotgun sequence
CM000727.1 *Bacillus cereus* 958201 chromosome, whole genome shotgun sequence
CM000728.1 *Bacillus cereus* Rock1-3 chromosome, whole genome shotgun sequence
CM000729.1 *Bacillus cereus* Rock1-15 chromosome, whole genome shotgun sequence
CM000730.1 *Bacillus cereus* Rock3-28 chromosome, whole genome shotgun sequence
CM000731.1 *Bacillus cereus* Rock3-29 chromosome, whole genome shotgun sequence
CM000732.1 *Bacillus cereus* Rock3-42 chromosome, whole genome shotgun sequence
CM000733.1 *Bacillus cereus* Rock3-44 chromosome, whole genome shotgun sequence
CM000734.1 *Bacillus cereus* Rock4-2 chromosome, whole genome shotgun sequence
CM000735.1 *Bacillus cereus* Rock4-18 chromosome, whole genome shotgun sequence
CM000736.1 *Bacillus cereus* F65185 chromosome, whole genome shotgun sequence
CM000737.1 *Bacillus cereus* AH603 chromosome, whole genome shotgun sequence
CM000486.1 *Bacillus cereus* AH716 chromosome, whole genome shotgun sequence
CM000738.1 *Bacillus cereus* AH1271 chromosome, whole genome shotgun sequence
CM000740.1 *Bacillus cereus* AH1272 chromosome, whole genome shotgun sequence
CM000743.1 *Bacillus mycoides* Rock1-4 chromosome, whole genome shotgun sequence
CM000744.1 *Bacillus mycoides* Rock3-17 chromosome, whole genome shotgun sequence
CM000745.1 *Bacillus pseudomyoides* DSM 12442 chromosome, whole genome shotgun sequence
CM000746.1 *Bacillus thuringiensis* serovar *tchongiensis* BGSC 4Y11 chromosome, whole genome shotgun sequence
CM000747.1 *Bacillus thuringiensis* serovar *belov* BGSC 4Y10 chromosome, whole genome shotgun sequence
CM000748.1 *Bacillus thuringiensis* serovar *thuringiensis* str. T10101 chromosome, whole genome shotgun sequence
CM000749.1 *Bacillus thuringiensis* serovar *solis* str. T04001 chromosome, whole genome shotgun sequence
CM000750.1 *Bacillus thuringiensis* serovar *kurstaki* str. T13001 chromosome, whole genome shotgun sequence
CM000751.1 *Bacillus thuringiensis* serovar *pastoris* str. T03A01 chromosome, whole genome shotgun sequence
CM000752.1 *Bacillus thuringiensis* serovar *montreux* BGSC 4A11 chromosome, whole genome shotgun sequence
CM000753.1 *Bacillus thuringiensis* ATCC 10792 chromosome, whole genome shotgun sequence
CM000754.1 *Bacillus thuringiensis* serovar *auisensis* BGSC 4AW1 chromosome, whole genome shotgun sequence
CM000755.1 *Bacillus thuringiensis* serovar *pudloensis* BGSC 4AB1 chromosome, whole genome shotgun sequence
CM000756.1 *Bacillus thuringiensis* serovar *hazhongensis* BGSC 4BD1 chromosome, whole genome shotgun sequence
CM000757.1 *Bacillus thuringiensis* serovar *pulsans* BGSC 4AC1 chromosome, whole genome shotgun sequence
CM000758.1 *Bacillus thuringiensis* IBL 200 chromosome, whole genome shotgun sequence
CM000759.1 *Bacillus thuringiensis* IBL 422 chromosome, whole genome shotgun sequence
CM000776.2 *Helicobacter canadensis* MT 98-549 chromosome, whole genome shotgun sequence
CM000777.2 *Mycobacterium tuberculosis* KZN 4207 chromosome, whole genome shotgun sequence
CM000788.2 *Mycobacterium tuberculosis* KZN V2475 chromosome, whole genome shotgun sequence
CM000789.2 *Mycobacterium tuberculosis* KZN R506 chromosome, whole genome shotgun sequence
CM000913.1 *Streptomyces clavuligerus* ATCC 27064 chromosome, whole genome shotgun sequence
CM000436.1 *Campylobacter jejuni* subsp. *jejuni* 1336 chromosome, whole genome shotgun sequence
CM000855.1 *Campylobacter jejuni* subsp. *jejuni* 414 chromosome, whole genome shotgun sequence
CM001834.1 *Pseudomonas savastanoi* pr. *savastanoi* NCPPB 3335 chromosome, whole genome shotgun sequence
CM000141.1 *Rhodococcus equi* ATCC 33707 chromosome, whole genome shotgun sequence
CM000920.1 *Glucanacetobacter Hansenii* ATCC 23769 chromosome, whole genome shotgun sequence
KN196488.1 *Cholepus hoffmanni* isolate OR478-KB448 unplaced genomic scaffold Scaffold264165, whole genome shotgun sequence
KG955901.1 *Tritonia synthica* isolate Sama-C Tc951 unplaced genomic scaffold Scaffold6316281, whole genome shotgun sequence
KG955906.1 *Ochotona montanus* scaffold 9 per chromosome, whole genome shotgun sequence
KB632434.1 *Vigna pusa* unplaced genomic scaffold Scaffold0, whole genome shotgun sequence
DG000255.1 *Oryza sativa* Japonica Group DNA, chromosome 1, cultivar: Koshihikari, whole genome shotgun sequence
LSG30680.1 *Craen salix* sp. PS1010 unplaced genomic scaffold ps1010ref1, scaffoldRNAPATH22055, whole genome shotgun sequence
KG63855.1 *Callorhynchus pilula* isolate IMCB204 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
CM000436.1 *Cryptosporidium parvum* Izo2 chromosome, whole genome shotgun sequence
CM000750.1 *Thalassiosira weissflogii* strain *Mugga* chromosome 1, whole genome shotgun sequence
AACT1000001.1 *Ibabelia bolina* strain *TZBo* chromosome 3, whole genome shotgun sequence
T867785.1 *Paramecium tritarsale* chromosome undetermined scaffold_1, whole genome shotgun sequence
CM000768.1 *Microbium minus* isolate *mixed* chromosome 8, whole genome shotgun sequence
CP000395.1 *Borrelia azzeli* Plc, complete genome
CM001022.1 *Aminomonas paucivirans* DSM 12260 chromosome, whole genome shotgun sequence
LSG3121.1 *Hydrophilum* sp. series O-1 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
LSG3836.1 *Acanthamoeba dermatidis* ATCC 26199 unplaced genomic scaffold supercont1, whole genome shotgun sequence
LSG1463.1 *Microbacterium lychnidis-dolicus* strain L1 Lamole unplaced genomic scaffold supercont1, whole genome shotgun sequence
CM001403.1 *Mycobacterium goodii* DSM 18603 chromosome, whole genome shotgun sequence
CM001023.1 *Algoriphagus* sp. FR1 chromosome, whole genome shotgun sequence
CM001025.1 *Pseudomonas fluorescens* WH6 chromosome, whole genome shotgun sequence
AA80100001.1 *Rickettsia sibirica* bayanus chromosome, complete genome, whole genome shotgun sequence
AACT100001.1 *Neisseria meningitidis* NRFL-12350 Y476-C872 chromosome, whole genome shotgun sequence
AACG0200001.1 *Saccharomyces bayanus* 623-G6 YM491-Contig2,678, whole genome shotgun sequence
AACT1000001.1 *Saccharomyces mikatae* IO 1615 YM490-Contig2900, whole genome shotgun sequence
JH977040.1 *Saccharomyces kudriavzevii* IF02 unplaced genomic scaffold c2070, whole genome shotgun sequence
LG985056.1 *Trichoderma reesei* QM6a unplaced genomic scaffold TRIREscaffold_1, whole genome shotgun sequence
AACT1000001.1 *Pseudomonas aeruginosa* PACS2 chromosome, whole genome shotgun sequence
AACT100001.1 *Campylobacter jejuni* subsp. *jejuni* 81-176 chromosome, whole genome shotgun sequence
AAAX1002635.1 *Malassezia restricta* KS8 7877 MRE_CONTIG_2694, whole genome shotgun sequence
LBG6486.1 *Coccidioides posadasii* str. *Silveria* unplaced genomic scaffold supercont2, whole genome

[illegible]

KQ257450.1 Spizellomyces punctatus DAOM BR117 chromosome Unknown supercont1.1, whole genome shotgun sequence	fungi'
CP001408.1 Burkholderia pseudomallei MSHR346 chromosome I, complete sequence	bacteria'
HE505206.1 Candida parapsilosis strain CDC317 annotated contig 005809	fungi'
CAB102000001.1 Soridia macrospora k-hel. WGS project CAB100000000 data, contig 2.1, whole genome shotgun sequence	fungi'
CP020338.1 Lactobacillus amylovorus HRL 1112, complete genome	bacteria'
CM002236.1 Neurospora crassa OR74A linkage group I, whole genome shotgun sequence	fungi'
CP017623.1 Candida albicans SC5314 chromosome 1 sequence	fungi'
ABRE01017988.1 Monilophthora perniciosa FA553 Contig18273, whole genome shotgun sequence	fungi'
AAB501000001.1 Ciona intestinalis cion0001, whole genome shotgun sequence	invertebrates'
CM001487.1 Eubacterium cellulosolvens 6 chromosome, whole genome shotgun sequence	bacteria'
JH712066.1 Loa loa unplaced genomic scaffold supercont3.1, whole genome shotgun sequence	invertebrates'
CM001046.1 Listeria monocytogenes FSL F2-208 chromosome, whole genome shotgun sequence	bacteria'
CM001048.1 Listeria innocua FSL S4-378 chromosome, whole genome shotgun sequence	bacteria'
CM001049.1 Listeria innocua FSL J1-023 chromosome, whole genome shotgun sequence	bacteria'
CM001050.1 Listeria ivanovi FSL F6-596 chromosome, whole genome shotgun sequence	bacteria'
CM001051.1 Listeria seeligeri FSL N1-067 chromosome, whole genome shotgun sequence	bacteria'
CM001052.1 Listeria seeligeri FSL S4-171 chromosome, whole genome shotgun sequence	bacteria'
CM001043.1 Mycobacterium tuberculosis HN878 chromosome, whole genome shotgun sequence	bacteria'
CM001044.1 Mycobacterium tuberculosis X122 chromosome, whole genome shotgun sequence	bacteria'
CM001045.1 Mycobacterium tuberculosis R1207 chromosome, whole genome shotgun sequence	bacteria'
GL573169.1 Geomyces destructans 20631-21 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
CM001058.1 Fragaria vesca subsp. vesca linkage group LG6, whole genome shotgun sequence	plants'
BA000049.1 Aspergillus oryzae RIB40 DNA chromosome 1	fungi'
GL577060.1 Apis florea unplaced genomic scaffold scaffold02040, whole genome shotgun sequence	invertebrates'
JH801365.1 Mus musculus strain C57BL/6J unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	vertebrates_mammals'
GL589130.1 Mus musculus strain C57BL/6J unplaced genomic scaffold scaffold_0, whole genome shotgun sequence	vertebrates_mammals'
GL582980.1 Homo sapiens unplaced genomic scaffold scaffold_0, whole genome shotgun sequence	vertebrates_mammals'
CP000289.1 Cryptococcus gattii VM276 chromosome D, complete sequence	fungi'
GG663757.1 Plasmodium falciparum RA-1116 genomic scaffold supercont1.2, whole genome shotgun sequence	protozoa'
GG664659.1 Plasmodium falciparum IGH-CR14 genomic scaffold supercont1.1, whole genome shotgun sequence	protozoa'
CM000488.1 Bacillus subtilis subsp. subtilis str. NCIB 3610 chromosome, whole genome shotgun sequence	bacteria'
KE952971.1 Python bivittatus unplaced genomic scaffold Scaffold0, whole genome shotgun sequence	vertebrates_non_mammals'
GL637601.1 Caenorhabditis tropicalis strain JU1373 unplaced genomic scaffold Scaffold029, whole genome shotgun sequence	invertebrates'
GL833120.1 Aureococcus anophagefferens unplaced genomic scaffold AURANscaffold_1, whole genome shotgun sequence	protozoa'
AEU02000001.1 Ascaris suum AG00001, whole genome shotgun sequence	invertebrates'
CM002306.1 Ogateaea pangopolymorpha DL-1 chromosome VII, whole genome shotgun sequence	fungi'
GL698470.1 Metarhizium acridum CQMa 102 unplaced genomic scaffold Scf_001, whole genome shotgun sequence	fungi'
ADN.J02000001.1 Metarhizium robertsii ARSEF 23 MAa_Scf_1, whole genome shotgun sequence	fungi'
CM001062.1 Salmonella enterica subsp. enterica serovar Choleraesuis str. A50 chromosome, whole genome shotgun sequence	bacteria'
GL732523.1 Daphnia pulex unplaced genomic scaffold DAPPUscfaffold_1, whole genome shotgun sequence	invertebrates'
GL738599.1 Paganomys hartwegi unplaced genomic scaffold scf7180000035380, whole genome shotgun sequence	invertebrates'
AEU102000001.1 Streptococcus parauberis NCFD 2020 chromosome, whole genome shotgun sequence	bacteria'
GL764026.1 Solenopsis invicta unplaced genomic scaffold Sl_gnG.scaffold02694, whole genome shotgun sequence	invertebrates'
JH157811.1 Bombus impatiens unplaced genomic scaffold scf_0102, whole genome shotgun sequence	invertebrates'
CM001064.2 Solanum lycopersicum cultivar Heinz 1706 chromosome 1, whole genome shotgun sequence	plants'
CM001450.1 Oreochromis niloticus linkage group LG7, whole genome shotgun sequence	vertebrates_non_mammals'
CM001076.1 Streptococcus dysgalactiae subsp. dysgalactiae ATCC 27957 chromosome, whole genome shotgun sequence	bacteria'
GL828951.1 Solingopeca sp. ATCC 50818 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	invertebrates'
GL849905.1 Sarcophilus harrisii chromosome 3 unlocalized genomic scaffold Chr3_supercontlig_000000383, whole genome shotgun sequence	vertebrates_mammals'
GG662845.1 Tetrahymena thermophila SB210 genomic scaffold scf_8254803, whole genome shotgun sequence	protozoa'
CM001081.1 Saccharomyces cerevisiae AWRI796 chromosome IV, whole genome shotgun sequence	fungi'
CM001097.1 Saccharomyces cerevisiae Vin13 chromosome IV, whole genome shotgun sequence	fungi'
CM001129.1 Saccharomyces cerevisiae VL3 chromosome IV, whole genome shotgun sequence	fungi'
CM001113.1 Saccharomyces cerevisiae FostersB chromosome IV, whole genome shotgun sequence	fungi'
GL870876.1 Nematocida parisi ERTm3 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
GL870941.1 Dictyostelium purpureum unplaced genomic scaffold DICPUscfaffold_1, whole genome shotgun sequence	protozoa'
CM001142.1 Escherichia fergusonii ECD227 chromosome, whole genome shotgun sequence	bacteria'
CM001148.1 Parascardovia denticolens DSM 10105 chromosome, whole genome shotgun sequence	bacteria'
CM001151.1 Salmonella enterica subsp. enterica serovar Dublin str. 3246 chromosome, whole genome shotgun sequence	bacteria'
CM001153.1 Salmonella enterica subsp. enterica serovar Gallinarum str. 9 chromosome, whole genome shotgun sequence	bacteria'
GL874531.1 Saccharomyces cerevisiae Y10 unplaced genomic scaffold Scfd1, whole genome shotgun sequence	fungi'
GL873277.1 Saccharomyces cerevisiae CBS 7960 unplaced genomic scaffold Scaffold1, whole genome shotgun sequence	fungi'
GL875079.1 Saccharomyces cerevisiae CLIB324 unplaced genomic scaffold Scfd0, whole genome shotgun sequence	fungi'
GL875736.1 Saccharomyces cerevisiae YJM269 unplaced genomic scaffold Scfd1, whole genome shotgun sequence	fungi'
GL875962.1 Saccharomyces cerevisiae FL100 unplaced genomic scaffold Scaffold1, whole genome shotgun sequence	fungi'
GL876586.1 Saccharomyces cerevisiae CLIB215 unplaced genomic scaffold Scaffold01, whole genome shotgun sequence	fungi'
GL877404.1 Vavraia culicis subsp. foridensis unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
GL877354.1 Acanthamoeba castellanii strain Naef unplaced genomic scaffold SCAFFOLD1185, whole genome shotgun sequence	protozoa'
GL876966.1 Magnaporthe poae ATCC 64411 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
CM000832.1 Burkholderia pseudomallei 1710a chromosome I, whole genome shotgun sequence	bacteria'
CM000774.1 Burkholderia pseudomallei 1106b chromosome I, whole genome shotgun sequence	bacteria'
CM001156.1 Burkholderia pseudomallei BpC2 chromosome I, whole genome shotgun sequence	bacteria'
GL865897.1 Ralstonia solanaceum CFPB267 chromosome complete genome	genome
GL862879.1 Batrachyhyrium dendrobatis JAM81 unplaced genomic scaffold BATDEscfaffold_1, whole genome shotgun sequence	fungi'
GL883010.1 Dictyostelium fasciculatum unplaced genomic scaffold Scf_Dfasci-F-a-25c12.r2-5, whole genome shotgun sequence	protozoa'
GL883090.1 Melampsora larici-populina 98AG31 unplaced genomic scaffold MELLAscaffold_1, whole genome shotgun sequence	fungi'
GL888128.1 Acromyrmex echinatior unplaced genomic scaffold scaffold244, whole genome shotgun sequence	invertebrates'
DS891538.1 Ixodes scapularis 1108463063928 genomic scaffold, whole genome shotgun sequence	invertebrates'
DF1573670.1 Daesopus novius unplaced genomic scaffold Scaffold3024, whole genome shotgun sequence	bacteria'
DF145384.1 Jatropha curcas DNA, scaffold. JorAS00002, strain: Palawan, whole genome shotgun sequence	plants'
LT594789.1 Theobroma cacao genome assembly, chromosome: II	plants'
FR823391.1 Neospora caninum Liverpool complete genome, chromosome X	protozoa'
DS571145.1 Entamoeba histolytica HM-1:IMSS scf_1104750518587 genomic scaffold, whole genome shotgun sequence	protozoa'
CH473309.1 Trypanosoma cruzi strain CL Brener 1047053157087 genomic scaffold, whole genome shotgun sequence	protozoa'
DS448800.1 Entamoeba dispar SAW1760 scf_1105229459701 genomic scaffold, whole genome shotgun sequence	protozoa'
CM000437.1 Pichia stipitis CBS 6054 chromosome 1, whole genome shotgun sequence	fungi'
DS231813.1 Culex pipiens quinquefasciatus supercont3.1 genomic scaffold, whole genome shotgun sequence	invertebrates'
DS469507.1 Nematostella vectensis NEMVscfaffold_1 genomic scaffold, whole genome shotgun sequence	invertebrates'
GL889000.1 Saccharomyces cerevisiae PW5 unplaced genomic scaffold Scfd20, whole genome shotgun sequence	fungi'
GL889064.1 Saccharomyces cerevisiae UC5 unplaced genomic scaffold Scfd39, whole genome shotgun sequence	fungi'
GL889345.1 Saccharomyces cerevisiae T73 unplaced genomic scaffold Scfd294, whole genome shotgun sequence	fungi'
GL889895.1 Saccharomyces cerevisiae CLIB382 unplaced genomic scaffold Scfd402, whole genome shotgun sequence	fungi'
GL890460.1 Saccharomyces cerevisiae T7 unplaced genomic scaffold Scfd0, whole genome shotgun sequence	fungi'
CH991540.1 Enterocytozoon bienersi H348 SC_2496 genomic scaffold, whole genome shotgun sequence	fungi'
FN653015.1 Okolopeura dioica, whole genome shotgun assembly, reference scaffold set, scaffold scaffold_1, whole genome shotgun sequence	invertebrates'
FN654275.1 Okolopeura dioica, whole genome shotgun assembly, allelic scaffold set, scaffold scaffoldA_1, whole genome shotgun sequence	invertebrates'
BX526834.1 Cryptosporidium parvum chromosome 6, complete sequence	protozoa'
AP009608.1 Mycoplasma fermentans PG18 DNA, nearly complete genome	bacteria'
FP929036.1 Bulynikibria fibrilolvens 1614 draft genome	bacteria'
FP929053.1 Ruminococcus sp. SR1/5 draft genome	bacteria'
FP929046.1 Faecalibacterium prausnitzii SL3/3 draft genome	bacteria'
FP929051.1 Ruminococcus bromii L2-63 draft genome	bacteria'
FP929062.1 Clostridiales sp. SS3/4 draft genome	bacteria'
FP929044.1 Eubacterium siraeum T03 draft genome	bacteria'
FP929042.1 Eubacterium rectale DSM 17629 draft genome	bacteria'
FP929043.1 Eubacterium rectale M104/1 draft genome	bacteria'
FP929048.1 Megamonas hypermegale ART12/1 draft genome	bacteria'
FP929049.1 Roseburia intestinalis M50/1 draft genome	bacteria'
FP929054.1 Ruminococcus obeum A2-162 draft genome	bacteria'
FP929055.1 Ruminococcus torques L2-14 draft genome	bacteria'
FP929047.1 Gordonia bacter pameliae 7-10-1-4 draft genome	bacteria'
FP929033.1 Bacteroides xylanisolvens XB1A draft genome	bacteria'
FP929052.1 Ruminococcus champanellensis type strain 18P13T draft genome	bacteria'
FP929058.1 Enterococcus sp. 7L76 draft genome	bacteria'
FN554974.1 Trypanosoma brucei gambiense DAL972 chromosome 11, complete sequence	protozoa'
FN645450.1 Triticum aestivum chromosome 3B-specific BAC library, contig ctg0011b	plants'
AP011615.1 Arthrospira platensis NIES-39, "" SEQUENCING IN PROGRESS "" , 19 ordered pieces	bacteria'
FN668375.1 Clostridium difficile M68, complete genome	bacteria'
FP929037.1 Clostridium saccharolyticum-like K10 draft genome	bacteria'
FP929038.1 Coprococcus catus GD/7 draft genome	bacteria'
FP929032.1 Alistipes shahii WAL 8301 draft genome	bacteria'
FP929039.1 Coprococcus sp. ART59/1 draft genome	bacteria'
FP929041.1 Eubacterium cylindroides T2-87 draft genome	bacteria'
FP929059.1 Eubacterium siraeum V105c8a draft genome	bacteria'
FP929050.1 Roseburia intestinalis XB6B4 draft genome	bacteria'
FP929060.1 Clostridiales sp. SM4/1 draft genome	bacteria'
FP929061.1 Anaerostipes hadrus draft genome	bacteria'
FP929056.1 Fretibacterium fastidiosum draft genome	bacteria'
FP929045.1 Faecalibacterium prausnitzii L26 draft genome	bacteria'
FP929034.1 Bifidobacterium longum subsp. longum F8 draft genome	bacteria'
FP929040.1 Enterobacter cloacae subsp. cloacae NCTC 8394 draft genome	bacteria'
FR720325.1 Listeria monocytogenes serotype 7 str. SLCC2482 complete genome	bacteria'
FQ482149.1 Chlamydomophila psittaci RD1 genome	bacteria'
BA000015.5 Arabidopsis thaliana DNA, chromosome 5, complete sequence	plants'
ADN.L01003213.1 Astrammia rara contig02625, whole genome shotgun sequence	protozoa'
CM001159.1 Listeria monocytogenes str. Scott A chromosome, whole genome shotgun sequence	bacteria'
CM001161.1 Rhodobacter sphaeroides WSN8 chromosome chl, whole genome shotgun sequence	bacteria'
CM001167.1 Bacteroides coprosus DSM 18011 chromosome, whole genome shotgun sequence	bacteria'
CM000492.1 Homo sapiens chromosome 2, whole genome shotgun sequence	vertebrates_mammals'
CM001165.1 Streptomyces sp. Tu6071 chromosome, whole genome shotgun sequence	bacteria'
GL891382.1 Neurospora tetrasperma FGSC 2508 unplaced genomic scaffold NEUTE1scaffold_81, whole genome shotgun sequence	fungi'
GL890999.1 Neurospora tetrasperma FGSC 2509 unplaced genomic scaffold NEUTE2scaffold_1, whole genome shotgun sequence	fungi'
CM001168.1 Chlamydomophila abortus LLG chromosome, whole genome shotgun sequence	bacteria'
CAID01000001.2 Ostreococcus tuai WGS project CAID00000000 data, contig chromosome 01, whole genome shotgun sequence	plants'
CM001175.1 Bombus terrestris linkage group LG B07, whole genome shotgun sequence	invertebrates'

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NC020423.1 *Heterophasia glaber* plasmid genomic scaffold scaffold00001, whole genome shotgun sequence
CM003021.1 *Bos indicus* isolate QUIL738 breed Nelore chromosome 1, whole genome shotgun sequence
CM001990.1 *Ficoidia albicollis* isolate OCG2 chromosome 2, whole genome shotgun sequence
JH604633.1 *Nematocitis* sp. 1 ERTm2 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
CM001468.1 *Loxia monacolyptera* FSL J1-208 chromosome, whole genome shotgun sequence
JH605122.1 *Leishmania major* strain SD-72 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence
K0273609.1 *Toxoplasma gondii* AR1 unplaced genomic scaffold scaffold00003, whole genome shotgun sequence
JH605023.1 *Saccharomyces pastinii* ERTm1 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
CM001471.1 *Salmonella enterica* subsp. *houthausen* str. ATCC BAA-1581 chromosome, whole genome shotgun sequence
CM004092.1 *Homo sapiens* chromosome 2, whole genome shotgun sequence
CM001474.1 *Shigella flexneri* 5a str. M807 chromosome, whole genome shotgun sequence
JH605123.1 *Xenobolus nematophila* ATCC 19061 chromosome, complete genome
FR845807.1 *Mycolasma leachi* 99.01A16 complete genome
JF475956.1 *Thiomonas* sp. str. 35a chromosome, complete genome
FR845719.1 *Streptomyces venezuelae* ATCC 10712 complete genome
JH621224.1 *Metschnikowia octodentis* unplaced genomic scaffold scf718000007524, whole genome shotgun sequence
CM001457.1 *Rickettsia helvetica* CAP8 chromosome, whole genome shotgun sequence
JH605124.1 *Cistidium perlegrum* F262 chromosome, whole genome shotgun sequence
JH622822.1 *Saccharomyces kudzuzei* FM1056 unplaced genomic scaffold c2070, whole genome shotgun sequence
K0983268.1 *Toxoplasma gondii* scf2CAPR2c2 unplaced genomic scaffold scaffold00002, whole genome shotgun sequence
JH624522.1 *Saccharomyces kudzuzei* FM1057 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH625338.1 *Saccharomyces kudzuzei* FM1066 unplaced genomic scaffold c2072, whole genome shotgun sequence
JH628928.1 *Saccharomyces kudzuzei* FM1062 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH631522.1 *Saccharomyces kudzuzei* FM1073 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH634452.1 *Saccharomyces kudzuzei* FM1074 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH632993.1 *Saccharomyces kudzuzei* FM1072 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH628500.1 *Saccharomyces kudzuzei* FM1069 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH638420.1 *Saccharomyces kudzuzei* FM1076 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH635991.1 *Saccharomyces kudzuzei* FM1075 unplaced genomic scaffold c2072, whole genome shotgun sequence
JH634542.1 *Saccharomyces kudzuzei* FM1074 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH634412.1 *Saccharomyces kudzuzei* FM1075 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH644817.1 *Saccharomyces kudzuzei* FM1077 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH646584.1 *Saccharomyces kudzuzei* FM1078 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH645006.1 *Saccharomyces kudzuzei* FM1079 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH641959.1 *Saccharomyces kudzuzei* ZP591 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH641353.1 *Saccharomyces kudzuzei* FM1083 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH634493.1 *Saccharomyces kudzuzei* FM1081 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH633923.1 *Saccharomyces kudzuzei* FM1090 unplaced genomic scaffold c2070, whole genome shotgun sequence
JH929243.1 *Entamoeba nutalli* P19 unplaced genomic scaffold asmb1_8287, whole genome shotgun sequence
KL544027.1 *Haemophilus* *Haemophilus* strain H.34 unplaced genomic scaffold asmb1, whole genome shotgun sequence
CP012110.1 *Bacillus licheniformis* U92 genome
CM003385.1 *Pan paniscus* isolate WX-0 chromosome 2B, whole genome shotgun sequence
JH605125.1 *Streptococcus aureus* subsp. *aureus* 71193, complete genome
CM001453.1 *Rhodospirillum thermoglucosidans* TMO-09.020 chromosome, whole genome shotgun sequence
JH650723.1 *Geobacillus* *Geobacillus* MTCC 4759 unplaced genomic scaffold contig610, whole genome shotgun sequence
CM001666.1 *Drosophila simulans* strain wh1501 chromosome 3R, whole genome shotgun sequence
CM003064.1 *Drosophila simulans* chromosome 3R, whole genome shotgun sequence
CP003426.1 *Borella crocidurae* str. *Acherna*, complete genome
JH658587.1 *Fusarium oxysporum* f. sp. *lychnidis* MN25 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
JH650968.1 *Fusarium oxysporum* f. sp. *pisae* DV247 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
JH651225.1 *Tetrahymena borealis* unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
JH651385.1 *Fusarium oxysporum* f. sp. *radixis-lychnidis* 26381 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
JH657918.1 *Fusarium oxysporum* f. sp. *vasinfectum* 25433 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
JH658872.1 *Fusarium oxysporum* f. sp. *cubense* tropical race 4 54006 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
JH658979.1 *Fusarium oxysporum* f. sp. *conglutinans* race 2 54008 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
K024040.1 *Staphylococcus aureus* strain 12228 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence
JH651516.1 *Octodon degus* unplaced genomic scaffold scaffold00001, whole genome shotgun sequence
JH658878.1 *Condylura cristata* unplaced genomic scaffold scaffold00001, whole genome shotgun sequence
JH659320.1 *Fusarium oxysporum* f. sp. *melonis* 26406 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
DG000040.1 *Saccharomyces cerevisiae* *Kyokai* no. 7 (K7) DNA, chromosome IV scaffold, whole genome shotgun sequence
JH658960.1 *Tetrahymena thermophila* SB210 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence
K024040.1 *Staphylococcus aureus* strain 12228 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence
CM001486.1 *Thermoplasma acidophilum* SR4 chromosome, whole genome shotgun sequence
CM001489.1 *Frankia* sp. OX3 chromosome, whole genome shotgun sequence
JH668279.1 *Manduca sexta* unplaced genomic scaffold scaffold00001, whole genome shotgun sequence
JH660758.1 *Gardneria lucida* Xiangrong No.1 unplaced genomic scaffold scaffold_80, whole genome shotgun sequence
JH660948.1 *Phlebotomus papatasi* unplaced genomic scaffold scaffold001, whole genome shotgun sequence
CM001515.1 *Mycobacterium tuberculosis* H37Rv chromosome, whole genome shotgun sequence
CM003586.1 *Setaria italica* strain Yugli chromosome IX, whole genome shotgun sequence
JH668223.1 *Walleria* *Walleria* CBS 633.62 unplaced genomic scaffold WALScaffold_1, whole genome shotgun sequence
CM001513.1 *Pseudomonas fluorescens* S5101 chromosome, whole genome shotgun sequence
CM001512.1 *Pseudomonas fluorescens* Q8r1-96 chromosome, whole genome shotgun sequence
CM001514.1 *Pseudomonas syringae* B3G3R chromosome, whole genome shotgun sequence
CM001501.1 *Pseudomonas chlororhagae* O6 chromosome, whole genome shotgun sequence
CM001493.1 *Paecilomyces* *Paecilomyces* chromosome 1, whole genome shotgun sequence
JH687370.1 *Sternum hirsutum* FP-91666 S51 unplaced genomic scaffold STEHscaffold_1, whole genome shotgun sequence
JH687538.1 *Punctulatia strigosa* NHHB-1173 S55 unplaced genomic scaffold PUNTScaffold_1, whole genome shotgun sequence
JH687733.1 *Auricularia subulatra* TB-10046 S55 unplaced genomic scaffold AURDscaffold_1, whole genome shotgun sequence
CP003563.1 *Sinorhizobium fredii* USDA 257, complete genome
JH689321.1 *Lutzomyia longipalpis* unplaced genomic scaffold Scaffold01, whole genome shotgun sequence
CM001518.2 *Drosophila miranda* strain M52 chromosome 2, whole genome shotgun sequence
AKB01000001.1 *Rhodobacter sphaeroides* 2.4.1 chromosome 1, complete sequence, whole genome shotgun sequence
AKB01000001.1 *Escherichia coli* str. K-12 substr. MG1655 chromosome, whole genome shotgun sequence
CM001525.1 *Saccharomyces cerevisiae* CEN3K 311-7D chromosome IV, whole genome shotgun sequence
AP012200.1 *Melissococcus plutonius* ATCC 35311 DNA, complete genome
FN66894.1 *Cistidium* *Cistidium* B19 chromosome
CM005058.1 *Lactobacillus pentosus* KCA1 chromosome, whole genome shotgun sequence
JH711783.1 *Trametes versicolor* FP-101664 S51 unplaced genomic scaffold TRAVEScaffold_1, whole genome shotgun sequence
JH717967.1 *Fomitiporia mediterranea* F3J22 unplaced genomic scaffold FOMMEScaffold_1, whole genome shotgun sequence
JH71573.1 *Coniophora puteana* RWD-64-598 S52 unplaced genomic scaffold CONPUScaffold_1, whole genome shotgun sequence
JH71528.1 *Trametes versicolor* F3J22 unplaced genomic scaffold TREMEScaffold_1, whole genome shotgun sequence
JH717986.1 *Fusarium oxysporum* f. sp. *undulatum* unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
JH717839.1 *Fusarium oxysporum* FOSC-3 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
CM001557.1 *Bartonella birtles* IB5 325 chromosome, whole genome shotgun sequence
AKVX01000001.1 *Rhodobacter sphaeroides* 2.4.1 chromosome 1, complete sequence, whole genome shotgun sequence
AKVX01000001.1 *Escherichia coli* str. K-12 substr. MG1655 chromosome, whole genome shotgun sequence
AKVX01000001.1 *Streptococcus pneumoniae* TIGR4 chromosome, whole genome shotgun sequence
JH72767.1 *Streptococcus*

[illegible]

JH878907.1	<i>Ascaris suum</i> unplaced genomic scaffold Scaffold122, whole genome shotgun sequence	invertebrates'
JH921428.1	<i>Marraschia brunnea</i> f. sp. 'multigermibut' MB_m1 unplaced genomic scaffold M6_S00001, whole genome shotgun sequence	fungi'
JH947130.1	<i>Elephantulus edwardsi</i> unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	vertebrates_mammals'
K0039398.1	<i>Kluyveromyces marxianus</i> var. <i>marxianus</i> KCTC 17555 unplaced genomic scaffold KM1_scaffold1, whole genome shotgun sequence	fungi'
JH925096.1	<i>Trichosporon asahi</i> var. <i>asahi</i> CBS 8904 unplaced genomic scaffold scaffold00190, whole genome shotgun sequence	fungi'
JH971395.1	<i>Agaricus bisporus</i> var. <i>burnettii</i> JB137-SF unplaced genomic scaffold AGAB11 scaffold_1, whole genome shotgun sequence	fungi'
CP015457.1	<i>Agaricus bisporus</i> var. <i>bisporus</i> H97 chromosome 1 sequence	fungi'
JH930468.1	<i>Phanerochaete carmosa</i> HHB-10118-sp unplaced genomic scaffold PHACAscaffold_1, whole genome shotgun sequence	invertebrates'
KE388890.1	<i>Anopheles stephensi</i> strain Indian Wild Type (Walter Reed) unplaced genomic scaffold scaffold_00001, whole genome shotgun sequence	fungi'
JH932235.1	<i>Passalora fulva</i> CBS 131901 unplaced genomic scaffold scf7180000130789, whole genome shotgun sequence	invertebrates'
JH932306.1	<i>Alelomyces dermatidis</i> ATCC 18187 unplaced genomic scaffold scaffold001, whole genome shotgun sequence	fungi'
CM003198.1	<i>Fusarium pseudograminearum</i> GS3085 chromosome 1, whole genome shotgun sequence	fungi'
CP003064.1	<i>Treponema pallidum</i> subsp. <i>pallidum</i> str. Mexico A, complete genome	bacteria'
HE650821.1	<i>Kazachastania africana</i> CBS 2517 chromosome 1, complete genome	fungi'
HE608151.1	<i>Mycobacterium tuberculosis</i> UT205 complete genome	bacteria'
CM001609.2	<i>Homo sapiens</i> chromosome 1, whole genome shotgun sequence	vertebrates_mammals'
CP003876.1	<i>Actinobacillus suis</i> H91-0380, complete genome	bacteria'
CM003225.1	<i>Artibeus platensis</i> C1 chromosome, whole genome shotgun sequence	bacteria'
JH977611.1	<i>Epilissus fuscus</i> unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	vertebrates_mammals'
CM001772.1	<i>Acetobacter vinelandii</i> VE-C3 chromosome, whole genome shotgun sequence	bacteria'
CM001633.1	<i>Oscillatoria cyanobacterium</i> JSC-12 chromosome, whole genome shotgun sequence	bacteria'
CM001642.1	<i>Brassica rapa</i> chromosome A9, whole genome shotgun sequence	plants'
FN649727.1	<i>Ecocarpus siliculosus</i> strain Ec 32, whole genome shotgun sequence assembly, chromosome LG02	protozoa'
CP003920.1	<i>Candidatus Sulfohalobium</i> sp. RIFRC-1, complete genome	bacteria'
KB01937.1	<i>Canis ferus</i> unplaced genomic scaffold scaffold05573, whole genome shotgun sequence	vertebrates_mammals'
HE965032.1	<i>Tapirina deformans</i> PYCC 5710 genomic scaffold, scaffold00001, whole genome shotgun sequence	fungi'
HF534880.1	<i>Cucumis melo</i> genomic scaffold, scaffold00004, whole genome shotgun sequence	plants'
KB007974.1	<i>Acanthamoeba castellanii</i> str. Neff unplaced genomic scaffold scf7180000084599, whole genome shotgun sequence	protozoa'
HE97160.1	<i>Fibroporia radiculosa</i> TFFH 294 genomic supercontigs, scaffold8592, whole genome shotgun sequence	fungi'
CAF201000001.1	<i>Perforomusca indica</i> DSM 11827, WGS project CAF201000000 data, contig: PIR1_contig_0001, whole genome shotgun sequence	invertebrates_non_mammals'
CA0020015.1	5 days late fecal DNA, chromosome 1, strain: Hd-rR	fungi'
CAC02001347.1	<i>Colletotrichum higginsianum</i> IMI 349063 WGS project CAC0200000000 data, contig: cont1.1, whole genome shotgun sequence	fungi'
HE671591.1	<i>Heliconia melampome</i> melampome genomic scaffold, scf7180001250781, whole genome shotgun sequence	invertebrates'
HE813982.1	<i>Musa acuminata</i> subsp. <i>malaccensis</i> Doubled-haploid Pahang (DH-Pahang) genomic chromosome, chr8	plants'
JH980293.1	<i>Echinops telfairii</i> isolate 266 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	vertebrates_mammals'
CM001774.1	<i>Providencia rettgeri</i> Dme1 chromosome, whole genome shotgun sequence	bacteria'
CM001773.1	<i>Providencia stuartii</i> DSM 19867 chromosome, whole genome shotgun sequence	bacteria'
KB205985.1	<i>Fusarium fujikuroi</i> B14 unplaced genomic scaffold KF1_scaffold029, whole genome shotgun sequence	fungi'
JH994112.1	<i>Pyrus x bretschneideri</i> cultivar Dangshansuli unplaced genomic scaffold scaffold1.0.1, whole genome shotgun sequence	plants'
JH992965.1	<i>Guillardia theta</i> CCMPT212 unplaced genomic scaffold GUITHscaffold_1, whole genome shotgun sequence	protozoa'
JH993675.1	<i>Penicillium digitatum</i> Pd1 unplaced genomic scaffold Scaffold_42, whole genome shotgun sequence	fungi'
JH993736.1	<i>Penicillium digitatum</i> PH026 unplaced genomic scaffold Scaffold_50, whole genome shotgun sequence	fungi'
HE68170.1	<i>Genethopopsis</i> Co 10/25 chromosome 1 draft sequence	fungi'
FO082046.1	<i>Pichia sorbitophila</i> strain CBS 7064 chromosome N complete sequence	fungi'
HE806316.1	<i>Tetrapispora blatae</i> CBS 6284 chromosome 1, complete genome	fungi'
JH993832.1	<i>Trachipleistophora hominis</i> chromosome Unknown scaffold00035, whole genome shotgun sequence	bacteria'
CP003600.1	<i>Chamaesiphon minutus</i> PCC 6605, complete genome	bacteria'
CM001672.1	<i>Microtus ochrogaster</i> chromosome 1, whole genome shotgun sequence	vertebrates_mammals'
CM001705.1	<i>Cytisus sinensis</i> chromosome 5, whole genome shotgun sequence	plants'
CP003642.1	<i>Cylindrocapsa stagnalis</i> PCC 7417, complete genome	bacteria'
KB209920.1	<i>Ophiostoma novo-ulmi</i> H327 unplaced genomic scaffold scaffold00005, whole genome shotgun sequence	fungi'
CM001710.2	<i>Capra hircus</i> breed Yunnan black goat chromosome 1, whole genome shotgun sequence	vertebrates_mammals'
HF545614.1	<i>Chlamydia psittaci</i> 01DC12 complete genome	bacteria'
AMZP02007909.1	<i>Phytophthora lateralis</i> MPF4 scf_22317_100921.contig_1, whole genome shotgun sequence	protozoa'
HE601810.1	<i>Chlamydia trachomatis</i> A/5291 complete genome	bacteria'
HE601798.1	<i>Chlamydia trachomatis</i> D/SotonD1 high quality draft genome sequence	bacteria'
HE601799.1	<i>Chlamydia trachomatis</i> D/SotonD5 complete genome	bacteria'
HE601800.1	<i>Chlamydia trachomatis</i> D/SotonD6 high quality draft genome sequence	bacteria'
HE601802.1	<i>Chlamydia trachomatis</i> E/SotonE4 complete genome	bacteria'
HE601803.1	<i>Chlamydia trachomatis</i> E/SotonE8 high quality draft genome	bacteria'
HE601806.1	<i>Chlamydia trachomatis</i> F/SotonF3 high quality draft genome sequence	bacteria'
HE601807.1	<i>Chlamydia trachomatis</i> G/SotonG1 complete genome	bacteria'
HE601794.1	<i>Chlamydia trachomatis</i> K/SotonK1 complete genome	bacteria'
HE601958.1	<i>Chlamydia trachomatis</i> L2b/LST high quality draft genome sequence	bacteria'
HE601960.1	<i>Chlamydia trachomatis</i> L2b/CV204 high quality draft genome sequence	bacteria'
HE601959.1	<i>Chlamydia trachomatis</i> L2b/Ams1 complete genome	bacteria'
HE601961.1	<i>Chlamydia trachomatis</i> L2b/Ams2 high quality draft genome sequence	bacteria'
HE601961.99	<i>Chlamydia trachomatis</i> L2b/Ams3 high quality draft genome sequence	bacteria'
HE601964.1	<i>Chlamydia trachomatis</i> L2b/Ams4 high quality draft genome sequence</	

CM001785.1 *Vibrio cholerae* O1 str. In G4222 chromosome 1, whole genome shotgun sequence
KB423929.1 *Lupinus angustifolius* unplaced genomic scaffold scaffold45357, whole genome shotgun sequence
CM001787.1 *Bacillus cereus* F chromosome, whole genome shotgun sequence
AHN02000026.1 *Phytophthora lateralis* MPF6 unplaced genomic scaffold scaffold1, whole genome shotgun sequence
K049425.1 *Phytophthora lateralis* SMST21 unplaced genomic scaffold scaffold1, whole genome shotgun sequence
KB444497.1 *Entamoeba histolytica* KUT2 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence
CM002524.1 *Oryza meridionalis* cultivar OR44 (W2121) chromosome 1, whole genome shotgun sequence
KB445550.1 *Baudinia panamensis* UAMH 10762 unplaced genomic scaffold BAUCOscscaffold_1, whole genome shotgun sequence
KB445569.1 *Cochliobolus heterostrophus* C5 unplaced genomic scaffold COCHIEscscaffold_1, whole genome shotgun sequence
KB445637.1 *Cochliobolus sativus* ND90P unplaced genomic scaffold COCCASccaffold_1, whole genome shotgun sequence
K049425.1 *Phytophthora lateralis* SMST21 unplaced genomic scaffold scaffold1, whole genome shotgun sequence
KB445551.1 *Phytophthora lateralis* SMST21 unplaced genomic scaffold scaffold1, whole genome shotgun sequence
KB445552.1 *Phytophthora lateralis* SMST21 unplaced genomic scaffold scaffold1, whole genome shotgun sequence
CM007313.1 *Leishmania braziliensis* MHOMBR/75/MA2903 chromosome 35, whole genome shotgun sequence
VJ87145.1 *Phytophthora ramorum* strain UET 2275 unplaced genomic scaffold scaffold53, whole genome shotgun sequence
CM001792.1 *Oceanobacillus kimchi* X50 chromosome, whole genome shotgun sequence
KB453278.1 *Leishmania panamensis* MHOMCOL/81/13 unplaced genomic scaffold Scaffold01, whole genome shotgun sequence
KB016762.1 *Yersinia brasiliensis* unplaced genomic scaffold scaffold14203, whole genome shotgun sequence
CF7205.2 *Neisseria meningitidis* CGM584 chromosome 14, whole genome shotgun sequence
CM001794.1 *Treponea denticula* H-T1 chromosome, whole genome shotgun sequence
CM001795.1 *Treponea denticula* H-22 chromosome, whole genome shotgun sequence
CM003613.1 *Cajanus cajan* chromosome 11, whole genome shotgun sequence
CM001796.1 *Treponea denticula* ATCC 35404 chromosome, whole genome shotgun sequence
CM001797.1 *Treponea denticula* OTK chromosome, whole genome shotgun sequence
CM001798.1 *Treponea denticula* AL-2 chromosome, whole genome shotgun sequence
KB454422.1 *Dekkera bruxellensis* CBS 2499 unplaced genomic scaffold DEKBRscscaffold_1, whole genome shotgun sequence
KB454484.1 *Gallieria sulphuraria* unplaced genomic scaffold scaffold_0, whole genome shotgun sequence
KB455460.1 *Paranailurus redivivus* unplaced genomic scaffold scaffold823, whole genome shotgun sequence
F0203427.1 *Desulfotolbrivio piezophilus* C1TLV30 complete genome
HF683636.1 *Magasella salicaria* Durham, NC isolate 2 – Nor lab genomic scaffold, scaffold9542, whole genome shotgun sequence
KB455681.1 *Cephus circeus* unplaced genomic scaffold scaffold168, whole genome shotgun sequence
CM001804.1 *Chlamydia thuringiensis* DR4 11934 chromosome chromosome, whole genome shotgun sequence
CM001805.1 *Vibrio vulnificus* VVyb(BT3) chromosome 1, whole genome shotgun sequence
CP001669.1 *Babesia equi* strain WA chromosome 1, complete sequence
KB467406.1 *Aethalia rosea* unplaced genomic scaffold Scaffold10, whole genome shotgun sequence
CM001824.1 *Stenotrophomonas maltophilia* EPMT1 chromosome, whole genome shotgun sequence
KB467407.1 *Stenotrophomonas maltophilia* EPMT1 chromosome, whole genome shotgun sequence
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KB467486.1 *Stenotrophomonas maltophilia* EPMT1 chromosome, whole genome shotgun sequence
KB467487

CM002109.1 Mycobacterium tuberculosis PanR0708 chromosome, whole genome shotgun sequence	bacteria'
CM002112.1 Mycobacterium tuberculosis PanR0801 chromosome, whole genome shotgun sequence	bacteria'
CM002108.1 Mycobacterium tuberculosis PanR0803 chromosome, whole genome shotgun sequence	bacteria'
CM002110.1 Mycobacterium tuberculosis PanR0804 chromosome, whole genome shotgun sequence	bacteria'
CM002107.1 Mycobacterium tuberculosis PanR0805 chromosome, whole genome shotgun sequence	bacteria'
CM002106.1 Mycobacterium tuberculosis PanR0902 chromosome, whole genome shotgun sequence	bacteria'
CM002105.1 Mycobacterium tuberculosis PanR0903 chromosome, whole genome shotgun sequence	bacteria'
CM002104.1 Mycobacterium tuberculosis PanR0904 chromosome, whole genome shotgun sequence	bacteria'
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CM002103.1 Mycobacterium tuberculosis PanR0907 chromosome, whole genome shotgun sequence	bacteria'
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CM002098.1 Mycobacterium tuberculosis PanR1007 chromosome, whole genome shotgun sequence	bacteria'
CM002099.1 Mycobacterium tuberculosis PanR1101 chromosome, whole genome shotgun sequence	bacteria'
CM002097.1 Mycobacterium tuberculosis PanR1006 chromosome, whole genome shotgun sequence	bacteria'
KE947164.1 <i>Neseria apis</i> DRI_01 unplaced genomic scaffold scf7180000046862, whole genome shotgun sequence	fungi'
KE50805.1 <i>Candida albicans</i> A123 unplaced genomic scaffold supercont1.48, whole genome shotgun sequence	fungi'
KE50838.1 <i>Candida albicans</i> A82 unplaced genomic scaffold supercont1.30, whole genome shotgun sequence	fungi'
KE50869.1 <i>Candida albicans</i> A203 unplaced genomic scaffold supercont1.32, whole genome shotgun sequence	fungi'
KE50910.1 <i>Candida albicans</i> A67 unplaced genomic scaffold supercont1.7, whole genome shotgun sequence	fungi'
KE50951.1 <i>Candida albicans</i> A48 unplaced genomic scaffold supercont1.55, whole genome shotgun sequence	fungi'
KE51002.1 <i>Candida albicans</i> CHN1 unplaced genomic scaffold supercont1.7, whole genome shotgun sequence	fungi'
KE51000.1 <i>Candida albicans</i> A20 unplaced genomic scaffold supercont1.6, whole genome shotgun sequence	fungi'
KE51071.1 <i>Candida albicans</i> 3153A unplaced genomic scaffold supercont1.58, whole genome shotgun sequence	fungi'
KE51119.1 <i>Candida albicans</i> A155 unplaced genomic scaffold supercont1.60, whole genome shotgun sequence	fungi'
KE51128.1 <i>Candida albicans</i> A84 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
KV447881.1 <i>Phytophthora kernoviae</i> strain CBS 122049 unplaced genomic scaffold scaffold58756, whole genome shotgun sequence	protozoa'
KE860611.1 <i>Cricetus griseus</i> strain 17AGY chromosome 6 unlocalized genomic scaffold chr1_scaffold_0, whole genome shotgun sequence	vertebrates_mammals'
KE552172.1 <i>Ophiodysops sinensis</i> CO19 unplaced genomic scaffold scaffold OCS_Sel_1, whole genome shotgun sequence	fungi'
CM002128.1 <i>Streptococcus</i> sp. HSISM1 chromosome, whole genome shotgun sequence	bacteria'
CM002129.1 <i>Enterococcus</i> sp. HSIEG1 chromosome, whole genome shotgun sequence	bacteria'
CM002130.1 <i>Streptococcus</i> sp. HSIS53 chromosome, whole genome shotgun sequence	bacteria'
CM002131.1 <i>Streptococcus</i> sp. HSISB1 chromosome, whole genome shotgun sequence	bacteria'
CM002132.1 <i>Streptococcus</i> sp. HSIS51 chromosome, whole genome shotgun sequence	bacteria'
CM002133.1 <i>Streptococcus</i> sp. HSIS52 chromosome, whole genome shotgun sequence	bacteria'
CM002135.1 <i>Viellorella parvula</i> HSIVP1 chromosome, whole genome shotgun sequence	bacteria'
CM002136.1 <i>Xanthomonas citri</i> pv. <i>malvacearum</i> X18 chromosome, whole genome shotgun sequence	bacteria'
CM002029.1 <i>Xanthomonas citri</i> pv. <i>malvacearum</i> X20 chromosome, whole genome shotgun sequence	bacteria'
CM002139.1 <i>Xanthomonas cassavae</i> CFBP 4642 chromosome, whole genome shotgun sequence	bacteria'
KE895867.1 <i>Alligator sinensis</i> unplaced genomic scaffold scaffold442, 1, whole genome shotgun sequence	vertebrates_non_mammals'
KE706420.1 <i>Bomphalopsis platensis</i> B02 unplaced genomic scaffold LGUN_random_Scaffold1, whole genome shotgun sequence	invertebrates'
KE705278.1 <i>Cleome hassleriana</i> unplaced genomic scaffold Cleome1, whole genome shotgun sequence	plants'
KE720815.1 <i>Endocarpus pusillus</i> Z07020 unplaced genomic scaffold C734253, whole genome shotgun sequence	fungi'
KE722155.1 <i>Panthera tigris</i> altaica isolate TaeGuk unplaced genomic scaffold scaffold53, whole genome shotgun sequence	vertebrates_mammals'
KE728806.1 <i>Melampsora piniroqua</i> Mpin7 unplaced genomic scaffold scaffold1661264, whole genome shotgun sequence	fungi'
KE744832.1 <i>Cronartium comandrae</i> C4 unplaced genomic scaffold scaffold1895657, whole genome shotgun sequence	fungi'
KE747824.1 <i>Pyrenophora seminispora</i> CCB06 unplaced genomic scaffold scaffold00028, whole genome shotgun sequence	fungi'
KE749393.1 <i>Eidolon helvum</i> unplaced genomic scaffold EH1_scaffold_2191, whole genome shotgun sequence	bacteria'
KI026023.1 <i>Megaderma lyra</i> unplaced genomic scaffold MI_scaffold_38462, whole genome shotgun sequence	vertebrates_mammals'
KI197197.1 <i>Vigna angularis</i> var. <i>angularis</i> cultivar IT213134 unplaced genomic scaffold scaffoldk_135, whole genome shotgun sequence	plants'
KE856091.1 <i>Pteronotus parnellii</i> unplaced genomic scaffold PP_scaffold_55135, whole genome shotgun sequence	vertebrates_mammals'
KI127945.1 <i>Rhinolophus ferrumequinum</i> unplaced genomic scaffold RF_scaffold_2952, whole genome shotgun sequence	vertebrates_mammals'
KE905672.1 <i>Lethenteron camtschaticum</i> unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	vertebrates_non_mammals'
KI242139.1 <i>Lagenaria siceraria</i> unplaced genomic scaffold scaffold46847, whole genome shotgun sequence	plants'
KV744154.1 <i>Phytophthora cryptogaea</i> strain CBS 418.71 unplaced genomic scaffold scaffoldd829328, whole genome shotgun sequence	protozoa'
CP005585.1 <i>Desulfovibrio gigas</i> DSM 1382 = ATCC 19364 genome	bacteria'
CP006705.1 <i>Pseudomonas aeruginosa</i> PAO581 genome	bacteria'
CP006728.1 <i>Pseudomonas aeruginosa</i> c7447m genome	bacteria'
KI273213.1 <i>Apis dorsalis</i> unplaced genomic scaffold scaffold_74, whole genome shotgun sequence	invertebrates'
HF855115.1 <i>Haemerichus corbtorus</i> ISEI genomic scaffold scaffold_pathogens_Hcorbtorus_scaffold_1, whole genome shotgun sequence	invertebrates'
LN902841.1 <i>Echinococcus multilocularis</i> genomic scaffold, pathogen_EmW_scaffold_01, whole genome shotgun sequence	bacteria'
LN903629.1 <i>Hymenolepis microstoma</i> genomic scaffold, pathogens_HYM_scaffold_0001, whole genome shotgun sequence	invertebrates'
HG326877.1 <i>Campylobacter coli</i> 76339, complete genome	bacteria'
KI304388.1 <i>Anguilla japonica</i> unplaced genomic scaffold scaffold_1, whole genome shotgun sequence	vertebrates_non_mammals'
CM002176.1 <i>Leishmania donovani</i> strain BH1 1220 chromosome 36, whole genome shotgun sequence	protozoa'
CM002177.1 <i>Rhodococcus</i> sp. B6A chromosome, whole genome shotgun sequence	bacteria'
KI419148.1 <i>Bubalus bubalis</i> breed Mediterranean unplaced genomic scaffold scf7180021618025, whole genome shotgun sequence	vertebrates_mammals'
KI397412.1 <i>Amborella trichopoda</i> unplaced genomic scaffold AnTr_v1.0_scaffold00001, whole genome shotgun sequence	plants'
KI402176.1 <i>Physeler calodon</i> unplaced genomic scaffold Scaffold0, whole genome shotgun sequence	vertebrates_mammals'
KI916183.1 <i>Anopheles sinensis</i> strain SINENSIS unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	invertebrates'
AOR002004902.1 <i>Sus scrofa</i> breed Tibetan scaffold487.1, whole genome shotgun sequence	vertebrates_mammals'
KI419149.1 <i>Drosophila suzukii</i> unplaced genomic scaffold scaffold1, whole genome shotgun sequence	invertebrates'
KI433418.1 <i>Anopheles maculatus</i> strain maculatus3 unplaced genomic scaffold supercont1.2, whole genome shotgun sequence	invertebrates'
KI422464.1 <i>Anopheles culicifacies</i> strain species A-37_1 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	invertebrates'
KI915040.1 <i>Anopheles farauti</i> strain FAR1 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	invertebrates'
KI421882.1 <i>Anopheles atroparvus</i> strain EBRO unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	invertebrates'
KI919284.1 <i>Anopheles melas</i> strain CM1001059_A unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	invertebrates'
KI915156.1 <i>Anopheles merus</i> strain MAF unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	invertebrates'
CM002796.1 <i>Mesochorus ca161</i> chromosome chr, whole genome shotgun sequence	invertebrates'
KI440842.1 <i>Sporothrix schenckii</i> ATCC 98251 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
KI516373.1 <i>Puccinia striiformis</i> f. sp. <i>tritici</i> CY32 unplaced genomic scaffold scaffold_2555, whole genome shotgun sequence	fungi'
ATN01000586.1 <i>Magnaporthe oryzae</i> HN19311 NODE_1728_length_698218_cov_2.626876, whole genome shotgun sequence	fungi'
KI472552.1 <i>Diaphorina citri</i> unplaced genomic scaffold scaffold1, whole genome shotgun sequence	invertebrates'
KI441020.1 <i>Sebastes rubrivinctus</i> unplaced genomic scaffold scaffold78, whole genome shotgun sequence	vertebrates_non_mammals'
AUPR02500001.1 <i>Sebastes nigropunctus</i> scaffold_0, whole genome shotgun sequence	vertebrates_non_mammals'
ARW01000001.1 <i>Staphylococcus pseudintermedius</i> E140 chromosome, whole genome shotgun sequence	bacteria'
ARW001000001.1 <i>Serratia plymuthica</i> RVH1 C786_chromosome1.1_C, whole genome shotgun sequence	bacteria'
KI517384.1 <i>Eutrema salusigneum</i> unplaced genomic scaffold scaffold_1, whole genome shotgun sequence	plants'
KI911141.1 <i>Cladonia metacoralifera</i> KoLR002260 unplaced genomic scaffold scaffold6, whole genome shotgun sequence	fungi'
CP006831.1 <i>Pseudomonas aeruginosa</i> PAO1-VE2 genome	bacteria'
CP006832.1 <i>Pseudomonas aeruginosa</i> PAO1-VE13 genome	bacteria'
KI519610.1 <i>Poecilia formosa</i> unplaced genomic scaffold Scaffold0, whole genome shotgun sequence	vertebrates_non_mammals'
KI714883.1 <i>Priapulus caudatus</i> unplaced genomic scaffold Scaffold1, whole genome shotgun sequence	invertebrates'
CM002264.1 <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> CFBP 7119 chromosome, whole genome shotgun sequence	bacteria'
CM002261.1 <i>Xanthomonas alfalfae</i> subsp. <i>alfalfae</i> CFBP 3836 chromosome, whole genome shotgun sequence	bacteria'
KI536661.1 <i>Citrus clementina</i> cultivar <i>Clemenulens</i> unplaced genomic scaffold scaffold_3, whole genome shotgun sequence	plants'
HG428755.1 <i>Escherichia coli</i> PMV-1 main chromosome, complete genome	bacteria'
KI537055.1 <i>Balaenophora aculeolata</i> scopriani unplaced genomic scaffold scaffold1, whole genome shotgun sequence	bacteria_mammals'
CP006844.1 <i>Streptococcus pneumoniae</i> A026 genome	bacteria'
KI538821.1 <i>Populus euphratica</i> unplaced genomic scaffold scaffold1.1, whole genome shotgun sequence	plants'
CM002268.1 <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> CFBP 2526 chromosome, whole genome shotgun sequence	bacteria'
CP006846.1 <i>Anaplasma marginale</i> str. Gypsy Plains genome	bacteria'
CP006847.1 <i>Anaplasma marginale</i> str. Dawn genome	bacteria'
CM002271.1 <i>Streptomyces</i> sp. GBA 94-10 chromosome, whole genome shotgun sequence	bacteria'
CM002273.1 <i>Streptomyces</i> sp. PVA 94-07 chromosome, whole genome shotgun sequence	bacteria'
AUU01000001.1 <i>Carnelina sativa</i> scaffold00001, whole genome shotgun sequence	plants'
KI545873.1 <i>Pseudozyma brasiliensis</i> GHG001 unplaced genomic scaffold PSEUBRA_SCAF3, whole genome shotgun sequence	fungi'
KV441991.1 <i>Candida glabrata</i> CCTCC M202019 chromosome C unlocalized genomic scaffold CGRCMScaffold_02, whole genome shotgun sequence	fungi'
KI546166.1 <i>Spiroplasma salmonicida</i> unplaced genomic scaffold scf7180000020683, whole genome shotgun sequence	protozoa'
CM002277.1 <i>Burkholderia dolosa</i> PC543 chromosome 1 chr1, whole genome shotgun sequence	bacteria'
KI546415.1 <i>Amanita jacksonii</i> TRTC16811 unplaced genomic scaffold V175_0106, whole genome shotgun sequence	fungi'
CM004511.1 <i>Fusarium circinatum</i> strain FSP 34 chromosome 1, whole genome shotgun sequence	fungi'
CM002280.1 <i>Streptomyces niveus</i> NCIMB 11891 chromosome, whole genome shotgun sequence	bacteria'
CM002285.1 <i>Streptomyces roseochromogenes</i> subsp. <i>oscitans</i> DS 12.976 chromosome, whole genome shotgun sequence	bacteria'
KI547134.1 <i>Spathaspora arborariae</i> UFMG-19.1A unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	fungi'
CM002287.1 <i>Bifidobacterium longum</i> E18 chromosome, whole genome shotgun sequence	bacteria'
ATN01000407.1 <i>Magnaporthe oryzae</i> F-81271 NODE_1454_length_675449_cov_14.228848, whole genome shotgun sequence	fungi'
AYR002012334.1 <i>Diaporthe longicolla</i> MSPL 10-6 scaffold17, whole genome shotgun sequence	protozoa'
AWXF01000040.1 <i>Naegleria fowleri</i> strain ATCC 30863 Nfow_contig_40, whole genome shotgun sequence	protozoa'
HG723041.1 <i>Eimeria necatrix</i> Houghton genomic scaffold, Enh_scaff1, whole genome shotgun sequence	protozoa'
HG738137.1 <i>Onchocerca volvulus</i> assembly O_volvulus_Cameroon_v3 genomic scaffold, OVOC_OM1b, whole genome shotgun sequence	invertebrates'
HG670307.1 <i>Eimeria acervulina</i> Houghton genomic scaffold, Eah_scaff1, whole genome shotgun sequence	protozoa'
HG686746.1 <i>Eimeria praecox</i> Houghton genomic scaffold, Eph_scaff1, whole genome shotgun sequence	protozoa'
HF969015.2 <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Bovismorbificans</i> str. 3114 complete genome	protozoa'
HG673746.1 <i>Eimeria tenella</i> Houghton genomic scaffold, Eth_scaff1, whole genome shotgun sequence	protozoa'
HG530631.1 <i>Cryptococcus gattii</i> CBS 7750 genomic scaffold, supercontig_1_01_of_Cryptococcus_neoformans_Serotype_B_CBS7750_SOAP_DE_NOVO, whole genome shotgun sequence	fungi'
HG718748.1 <i>Eimeria maxima</i> Weybridge genomic scaffold, Emw_scaff1, whole genome shotgun sequence	protozoa'
HG738131.1 <i>Elaeophora elaphi</i> genomic scaffold, EEL_scaffold_00001_1478205, whole genome shotgun sequence	invertebrates'
HG710173.1 <i>Eimeria brunetti</i> Houghton genomic scaffold, Ebn_scaff1, whole genome shotgun sequence	protozoa'
HG678410.1 <i>Eimeria mitis</i> Houghton genomic scaffold, Emi_scaff1, whole genome shotgun sequence	protozoa'
CM002295.1 <i>Phaseolus vulgaris</i> cultivar G19833 chromosome 8, whole genome shotgun sequence	plants'
KV724674.1 <i>Phytophthora lateralis</i> strain CBS 168.42 unplaced genomic scaffold scaffold144566, whole genome shotgun sequence	protozoa'
KV737129.1 <i>Phytophthora pinifolia</i> strain CBS 122922 unplaced genomic scaffold scaffold948885, whole genome shotgun sequence	protozoa'
KI570111.1 <i>Cronartium ribicola</i> 11-2 unplaced genomic scaffold scaffold2067960, whole genome shotgun sequence	fungi'
KI578484.1 <i>Leptinotarsa decemlineata</i> unplaced genomic scaffold Scaffold02, whole genome shotgun sequence	invertebrates'
KI615321.1 <i>Peromyscus maniculatus</i> bairdii unplaced genomic scaffold Scaffold4, whole genome shotgun sequence	vertebrates_mammals'
KI603969.1 <i>Cronartium quercuum</i> f. sp. <i>banksianae</i> CqE3WM unplaced genomic scaffold scaffold0044139, whole genome shotgun sequence	fungi'
KI614512.1 <i>Endocronartium harknessii</i> PHW480C unplaced genomic scaffold scaffold971408, whole genome shotgun sequence	fungi'
KI628541.1 <i>Sclerotinia borealis</i> F-4128 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	fungi'
KI629971.1 <i>Ceratostolen solmsi</i> marchali unplaced genomic scaffold scaffold10, whole genome shotgun sequence	invertebrates'
KI630171.1 <i>Mimulus guttatus</i> cultivar IM62 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence	plants'
KI635462.1 <i>Leucanosticta asiatica</i> CBS 871.95 unplaced genomic scaffold scaffold59593, whole genome shotgun sequence	fungi'
AWYD01000740.1 <i>Pseudocercospora pini-desulfuratae</i> CBS 125139 contig101650_0, whole genome shotgun sequence	fungi'
KI633359.1 <i>Mycosphaerella laricina</i> CBS 326.52 unplaced genomic scaffold scaffold90652, whole genome shotgun sequence	fungi'
KI633058.1 <i>Mycosphaerella</i> sp. Ston1 unplaced genomic scaffold scaffold279717, whole genome shotgun sequence	fungi'

KI635736.1	Plasmodium yoelli 17X unplaced genomic scaffold supercont2.21, whole genome shotgun sequence	protozoa'
CM002307.1	Xanthomonas hortorum pv. carotae str. M081 chromosome, whole genome shotgun sequence	bacteria'
KI636951.1	Staineriema monticolum unplaced genomic scaffold MONTI_736, whole genome shotgun sequence	invertebrates'
CP006735.1	Thermoplasma coccineum sp. NK55 genome	bacteria'
KI652990.1	Ephemera danica unplaced genomic scaffold Scaffold28, whole genome shotgun sequence	invertebrates'
DF239015.1	Symbiodinium minutum Mf 1.05b.01 DNA, scaffold: scaffold2.1, whole genome shotgun sequence	invertebrates'
KI657455.1	Necator americanus unplaced genomic scaffold N_americanus-1.0_Cont1, whole genome shotgun sequence	fungi'
KI669492.1	Kwoniella heveanensis BCC8396 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
KI669518.1	Kwoniella heveanensis CBS 569 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
KI669472.1	Kwoniella mangroviensis CBS 8507 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
KI669547.1	Kwoniella mangroviensis CBS 8885 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
KI669459.1	Kwoniella mangroviensis CBS 10435 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
CM002308.1	Chlamydia pecorum DBDeUG chromosome, whole genome shotgun sequence	bacteria'
CM002309.1	Chlamydia pecorum IPTaLE chromosome, whole genome shotgun sequence	bacteria'
CM002310.1	Chlamydia pecorum MCMarsBar chromosome, whole genome shotgun sequence	bacteria'
CM002311.1	Chlamydia pecorum VPr629 chromosome, whole genome shotgun sequence	bacteria'
DF396901.1	Saccharomyces cerevisiae NAM34-4C DNA, contig: scaffold0021, whole genome shotgun sequence	fungi'
DF396954.1	Saccharomyces cerevisiae IR-2 DNA, contig: scaffold018, whole genome shotgun sequence	fungi'
KI685158.1	Phytophthora parasitica strain CJ0283 unplaced genomic scaffold supercont1.1353, whole genome shotgun sequence	protozoa'
KI671675.1	Phytophthora parasitica strain CJ0565 unplaced genomic scaffold supercont1.1407, whole genome shotgun sequence	protozoa'
KI678687.1	Phytophthora parasitica strain CHvinca01 unplaced genomic scaffold supercont1.1606, whole genome shotgun sequence	protozoa'
KI691933.1	Phytophthora parasitica strain IAC_D1955 unplaced genomic scaffold supercont1.1639, whole genome shotgun sequence	protozoa'
KI697133.1	Beta vulgaris subsp. vulgaris cultivar KWS_DH1440 unplaced genomic scaffold scaffold651, whole genome shotgun sequence	plants'
KI744491.1	Beta vulgaris subsp. vulgaris cultivar STROGA6001 unplaced genomic scaffold scaffold603, whole genome shotgun sequence	plants'
KI723259.1	Beta vulgaris subsp. vulgaris cultivar SynMono DH unplaced genomic scaffold scaffold8048, whole genome shotgun sequence	plants'
KI784202.1	Beta vulgaris subsp. vulgaris cultivar SynTilling DH unplaced genomic scaffold scaffold1035, whole genome shotgun sequence	plants'
CM002317.1	Beta vulgaris subsp. vulgaris cultivar KWS2320 chromosome 6, whole genome shotgun sequence	plants'
KQ207791.1	Spinacia oleracea cultivar SynViroflay unplaced genomic scaffold scaffold77373, whole genome shotgun sequence	plants'
CM002326.2	Beta vulgaris subsp. vulgaris chromosome 6, whole genome shotgun sequence	plants'
BASJ00200084.1	Coturnix japonica DNA, scaffold: scaffold328_cov160, strain: L, whole genome shotgun sequence	vertebrates_non_mammals'
BATS01000001.1	Fragaria x ananassa DNA, contig: FANhyb_rscf000000001.1, whole genome shotgun sequence	plants'
DF277777.1	Fragaria x ananassa DNA, scaffold: FAN_iscf00031532.1, whole genome shotgun sequence	plants'
BATU01046052.1	Fragaria linumae DNA, contig: FL_iscf00046135.1, whole genome shotgun sequence	plants'
BATW01092732.1	Fragaria nubiola DNA, contig: FNU_iscf00093430.1, whole genome shotgun sequence	plants'
BATV01027002.1	Fragaria nipponica DNA, contig: FNI_iscf00027903.1, whole genome shotgun sequence	plants'
KI867152.1	Capsicum annuum cultivar CM334 unplaced genomic scaffold PGAV_1.5_scaffold1, whole genome shotgun sequence	plants'
CM002330.1	Pseudomonas moraviensis R28-S chromosome, whole genome shotgun sequence	bacteria'
DF340865.1	Dianthus caryophyllus DNA, scaffold: scaffold2, whole genome shotgun sequence	plants'
KI894027.1	Cryptococcus dejecticola CBS 10117 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
KI894018.1	Cryptococcus beslioi CBS 10118 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
KI894007.1	Cryptococcus pinus CBS 10737 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	fungi'
CM002361.1	Sesamum indicum cultivar Zhongzhi No. 13 linkage group LG6, whole genome shotgun sequence	plants'
HG380758.1	Adineta vaga genomic scaffold, scaffold_1, whole genome shotgun sequence	invertebrates'
HG792015.1	Penicillium roqueforti FM164 genomic scaffold, ProqFM164S01, whole genome shotgun sequence	fungi'
HG793134.1	Penicillium camemberti str. FM013, whole genome shotgun sequence	fungi'
CBVU01000006.1	Erwinia amylovora LA637 WGS project CBVU0000000000 data, contig LA637_CONTIG_6, whole genome shotgun sequence	bacteria'
CBVT01000006.1	Erwinia amylovora LA636 WGS project CBVT0000000000 data, contig LA636_CONTIG_6, whole genome shotgun sequence	bacteria'
CBVS01000006.1	Erwinia amylovora LA635 WGS project CBVS0000000000 data, contig LA635_CONTIG_6, whole genome shotgun sequence	bacteria'
KI911130.1	Trichoderma reesei RUT C-30 unplaced genomic scaffold TRIREscaffold_1, whole genome shotgun sequence	fungi'
AZIM01000080.1	Ophiophagus hannah scaffold80.1, whole genome shotgun sequence	vertebrates_non_mammals'
KI912109.1	Pestalotiopsis fici W106-1 unplaced genomic scaffold PFICI_Scf_1, whole genome shotgun sequence	fungi'
BATX01138262.1	Fragaria orientalis DNA, contig: FOR_iscf00143214.1, whole genome shotgun sequence	plants'
AWN01000008.1	Moeszomyces aphidis DSM 70725 Seq17, whole genome shotgun sequence	fungi'
KI894189.1	Limulus polyphemus unplaced genomic scaffold scaffold0, whole genome shotgun sequence	invertebrates'
KI913114.1	Aphanomyces astaci strain APO3 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	protozoa'
KI913954.1	Aphanomyces invadans strain NJM9701 unplaced genomic scaffold supercont1.3, whole genome shotgun sequence	protozoa'
DF260912.1	Rhodovulum sulfidophilum DSM 1374 DNA, scaffold: scaffoldContig1, whole genome shotgun sequence	bacteria'
KI925184.1	Plasmodium falciparum Vietnam Oak-Knoll (FVO) unplaced genomic scaffold supercont1.178, whole genome shotgun sequence	protozoa'
KI925625.1	Plasmodium falciparum MailPS096_E11 unplaced genomic scaffold supercont1.157, whole genome shotgun sequence	protozoa'
KI926445.1	Plasmodium falciparum Tansania D000708 unplaced genomic scaffold supercont1.196, whole genome shotgun sequence	protozoa'
KI926126.1	Plasmodium falciparum NF135/5 C10 unplaced genomic scaffold supercont1.111, whole genome shotgun sequence	protozoa'
KI927384.1	Plasmodium falciparum Palo Alto/Uganda unplaced genomic scaffold supercont1.147, whole genome shotgun sequence	protozoa'
KI927620.1	Plasmodium falciparum CAMP/Malaysia unplaced genomic scaffold supercont1.165, whole genome shotgun sequence	protozoa'
KI928025.1	Plasmodium falciparum FCH44 unplaced genomic scaffold supercont2.239, whole genome shotgun sequence	protozoa'
CM002372.1	Streptococcus thermophilus M17PTZA96 chromosome, whole genome shotgun sequence	bacteria'
CM002369.1	Streptococcus thermophilus TH1435 chromosome, whole genome shotgun sequence	bacteria'
CM002370.1	Streptococcus thermophilus TH1436 chromosome, whole genome shotgun sequence	bacteria'
CM002371.1	Streptococcus thermophilus MTH17CL396 chromosome, whole genome shotgun sequence	bacteria'
BASO01002930.1	Arabidopsis halleri subsp. germifera DNA, contig: scaffold2930, whole genome shotgun sequence	plants'
CM002373.1	Cynoglossus semilaevis isolate Cse_v1.0 chromosome 1, whole genome shotgun sequence	vertebrates_non_mammals'
KI964537.1	Bipolaris zeicola 26-R-13 unplaced genomic scaffold scaffold_0, whole genome shotgun sequence	fungi'
KI963918.1	Bipolaris oryzae ATCC 44580 unplaced genomic scaffold scaffold_0, whole genome shotgun sequence	fungi'
KI963911.1	Penicillium chrysogenum NCCT00086 unplaced genomic scaffold NCCT00086_scaf146, whole genome shotgun sequence	fungi'
KI965460.1	Plasmodium inui San Antonio 1 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	protozoa'
KI965394.1	Plasmodium vinckei petteri strain CR unplaced genomic scaffold supercont1.1, whole genome shotgun sequence	protozoa'
JATN01000322.1	Rhizoctonia solani AG-3 Rhs1AP strain AG-3 scf119142671170, whole genome shotgun sequence	fungi'
BASP01010265.1	Arabidopsis lyrata subsp. petraea DNA, contig: scaffold10265, whole genome shotgun sequence	plants'
KI96371.1	Drechlerella stenobrocha 248 unplaced genomic scaffold DRE_Scf_1, whole genome shotgun sequence	fungi'
JAQJ01010622.1	Drosophila simulans strain Dros11saisaaze sim_ext_low_EstContig_13582, whole genome shotgun sequence	invertebrates'
JAQR01002560.1	Drosophila sechellia strain 14021-0248.25 Sec_plus_rsq_contig_326, whole genome shotgun sequence	invertebrates'
KI968691.1	Bipolaris victorialis F13 unplaced genomic scaffold scaffold_0, whole genome shotgun sequence	fungi'
HG803175.1	Brucella canis str. Oliveri chromosome I, genome	fungi'
CBTC010000046.1	Zygosaccharomyces bailii ISA1307 WGS project CBTC0000000000, contig ZBAI_A_scaffold_046, whole genome shotgun sequence	fungi'
HG530068.1	Pseudomonas aeruginosa PA38182, complete genome	bacteria'
HG509299.1	Serinus canaria genomic scaffold, SCA1_01, whole genome shotgun sequence	vertebrates_non_mammals'
CM002401.1	Bacillus anthracis 8903-G chromosome, whole genome shotgun sequence	bacteria'
CM002398.1	Bacillus anthracis 9808-G chromosome, whole genome shotgun sequence	bacteria'
CM002395.1	Bacillus anthracis 52-G chromosome, whole genome shotgun sequence	bacteria'
CP006940.1	Listeria monocytogenes serotype 1/2a str. 01-1280 genome	bacteria'
CM002407.1	Saccharomyces cerevisiae R008 chromosome IV, whole genome shotgun sequence	fungi'
CM002425.1	Saccharomyces cerevisiae P301 chromosome IV, whole genome shotgun sequence	fungi'
CM002335.1	Saccharomyces cerevisiae P263 chromosome IV, whole genome shotgun sequence	fungi'
CM002441.1	Saccharomyces cerevisiae R103 chromosome IV, whole genome shotgun sequence	fungi'
CP005829.1	Borrelia anserina BA2, complete genome	bacteria'
CP004146.1	Borrelia hermsii YOR, complete genome	bacteria'
CP004217.2	Borrelia miyamotoi FR64b, complete genome	bacteria'
CP004267.1	Borrelia crocidurae DOU, complete genome	bacteria'
CP005851.2	Borrelia parkeri G.U.O, complete genome	bacteria'
CP005745.1	Borrelia coriaceae Co53, complete genome	bacteria'
CP005706.1	Borrelia hermsii YBT, complete genome	bacteria'
CP005680.1	Borrelia hermsii MTW, complete genome	bacteria'
CM004551.1	Nannochloropsis gaditana strain B-31 chromosome 1, whole genome shotgun sequence	protozoa'
KQ464259.1	Microplitis demolitor strain Queensland-Clemson subculture unplaced genomic scaffold Mdem_scaffold_0079, whole genome shotgun sequence	invertebrates'
CM003136.1	Streptococcus thermophilus TH1982 chromosome, whole genome shotgun sequence	bacteria'
CM003135.1	Streptococcus thermophilus TH1477 chromosome chr, whole genome shotgun sequence	bacteria'
KQ60624.1	Schmidtea mediterranea strain CIW4 unplaced genomic scaffold scaffold7446, whole genome shotgun sequence	invertebrates'
CM002488.1	Oryza punctata chromosome 1, whole genome shotgun sequence	plants'
CM002500.1	Oryza nivara chromosome 1, whole genome shotgun sequence	plants'
CM002512.1	Oryza glumipatula chromosome 1, whole genome shotgun sequence	plants'
CP007225.1	Agrobacterium tumefaciens LBA4213 (Ach5) circular chromosome	bacteria'
CP006963.1	Acinetobacter baumannii PK4807 genome	bacteria'
HG793125.1	Kuraishia capsulata CBS 1993 genomic scaffold, Kuraishia_capsulata_scaffold_1, whole genome shotgun sequence	fungi'
HG814183.1	Penicillium fuscoglaucum FM041 genomic scaffold, PluFM041S001, whole genome shotgun sequence	fungi'
HG916852.1	Rhizobium sp. LPU83 main chosome complete genome	bacteria'
HG815136.1	Penicillium nalgioense FM193 genomic scaffold, PnaFM193S001, whole genome shotgun sequence	fungi'
HG816029.1	Penicillium cameum LCP05634 genomic scaffold, PcarLCP05634S001, whole genome shotgun sequence	fungi'
HG813308.1	Penicillium panem FM227 genomic scaffold, PpanFM227S001, whole genome shotgun sequence	fungi'
HG813601.1	Penicillium bifforme FM169 genomic scaffold, PhIFM169S001, whole genome shotgun sequence	fungi'
HF95061.1	Phytomonas sp. isolate EM1 genomic scaffold, scaffold_1, whole genome shotgun sequence	protozoa'
CBMN010001971.1	Hordeum pubiflorum WGS project CBMN0000000000 data, cultivar BCC2028, contig Hpubiflorum_contig_1971, whole genome shotgun sequence	plants'
JARH01000012.1	Coletotrichum fioriniae PJ7 Scaffold_1008.1, whole genome shotgun sequence	fungi'
CP007236.1	Enheffer adhaerens OV14 chromosome 1 sequence	bacteria'
CP007268.1	Haltodrosipira halochloris str. A genome	bacteria'
CP006980.1	Pseudomonas aeruginosa LESlike5 sequence	bacteria'
CP006981.1	Pseudomonas aeruginosa LESlike7 sequence	bacteria'
CP006982.1	Pseudomonas aeruginosa LES400 sequence	bacteria'
CP006983.1	Pseudomonas aeruginosa LESB65 sequence	bacteria'
CP006984.1	Pseudomonas aeruginosa LESlike1 sequence	bacteria'
CP006985.1	Pseudomonas aeruginosa LESlike6 sequence	bacteria'
AMGQX01000001.1	Cladophialophora yegresii CBS 114405 acc2N-supercont1.1, whole genome shotgun sequence	fungi'
AMGX01000001.1	Cladophialophora psammophila CBS 110553 acc2L-supercont1.1, whole genome shotgun sequence	fungi'
AMGY01000001.1	Capronia epimyces CBS 606.96 acc2Q-supercont1.1, whole genome shotgun sequence	fungi'
AMWN01000001.1	Capronia coronata CBS 617.96 acc2CG-supercont1.1, whole genome shotgun sequence	fungi'
AZCJ01000001.1	Saccharomyces pastorianus CBS 1513 scaffold00001, whole genome shotgun sequence	fungi'
KQ076434.1	Mucor irregularis B50 unplaced genomic scaffold scaffold12.1, whole genome shotgun sequence	fungi'
CM002545.1	Xanthomonas campestris pv. campestris str. CFBP 1869 chromosome, whole genome shotgun sequence	bacteria'
CM002673.1	Xanthomonas campestris pv. campestris str. CFBP 5817 chromosome, whole genome shotgun sequence	bacteria'
CM002635.1	Xanthomonas campestris pv. incanae strain CFBP 1606R chromosome, whole genome shotgun sequence	bacteria'
CM002636.1	Xanthomonas campestris pv. incanae strain CFBP 2527R chromosome, whole genome shotgun sequence	bacteria'
CM002637.1	Xanthomonas campestris pv. raphani strain CFBP 5828R chromosome, whole genome shotgun sequence	bacteria'
CM002638.1	Xanthomonas campestris strain CFBP 5826R chromosome, whole genome shotgun sequence	bacteria'
CP006672.1	Chlamydia trachomatis strain F12-93 genome	bacteria'
CP006675.1	Chlamydia trachomatis strain E12-94 genome	bacteria'
CP006677.1	Chlamydia trachomatis strain D14-96 genome	bacteria'
CP006678.1	Chlamydia trachomatis strain la20-97 genome	bacteria'

CP006679.1 Chlamydia trachomatis strain J/27-97 genome	bacteria'
CM002782.1 Yarrowia lipolytica PO11 chromosome E, whole genome shotgun sequence	fungi'
KX076539.1 Eurytemora affinis strain Atlantic clade unplaced genomic scaffold Scaffold1, whole genome shotgun sequence	invertebrates'
JELW01000001.1 Metarhizium robertsii ATCC RSEF 2575 contig001, whole genome shotgun sequence	fungi'
JAQW01000001.1 Rhizophagus irregularis DAOM 197198w isolate N31 N31_scaffold1, whole genome shotgun sequence	fungi'
JAQX01000001.1 Rhizophagus irregularis DAOM 197198w isolate N33 N33_scaffold1, whole genome shotgun sequence	fungi'
JAQY01000001.1 Rhizophagus irregularis DAOM 197198w isolate N36 N36_scaffold1, whole genome shotgun sequence	fungi'
JAQZ01000001.1 Rhizophagus irregularis DAOM 197198w isolate N6 Scaffold1, whole genome shotgun sequence	fungi'
JAR01000001.1 Rhizophagus irregularis DAOM 197198w isolate DNA1 scaffold1, whole genome shotgun sequence	fungi'
JARB01000001.1 Rhizophagus irregularis DAOM 197198w isolate DNA2 scaffold1, whole genome shotgun sequence	fungi'
EMT01027768.1 Rhizophagus irregularis DAOM 197198w jcf7180003193370, whole genome shotgun sequence	fungi'
CM026551.1 Fusarium graminearum strain CS3005 chromosome 1, whole genome shotgun sequence	fungi'
AWGT01000406.1 Colinus virginianus strain Texas NorthernBobwhite_ScaffoldedDeNovo_contig_406, whole genome shotgun sequence	vertebrates_non_mammals'
AWGU01031816.1 Colinus virginianus strain Texas NorthernBobwhite_SimpleDeNovo_contig_31816, whole genome shotgun sequence	vertebrates_non_mammals'
KX082860.1 Trichogramma pretiosum unplaced genomic scaffold Scaffold1, whole genome shotgun sequence	invertebrates'
KX084111.1 Aspergillus niger CBS 352690 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	fungi'
KX090611.1 Pyrenochaeta lycopersica CRA-PAV_ER 1211 unplaced genomic scaffold NODE_58991_length_788071_cov_66.298904, whole genome shotgun sequence	fungi'
KX090494.1 Brassica oleracea var. capitata cultivar line 02-12 unplaced genomic scaffold Scaffold000002, whole genome shotgun sequence	plants'
HF972804.1 Neurospora sublineolata FGSC 5508 genomic scaffold, SC_118, whole genome shotgun sequence	fungi'
HF970592.1 Neurospora africana FGSC 1740 genomic scaffold, SC_2, whole genome shotgun sequence	fungi'
HF975737.1 Neurospora panamonica FGSC 7221 genomic scaffold, SC_82, whole genome shotgun sequence	fungi'
HF979336.1 Neurospora terricola FGSC 1859 genomic scaffold, SC_130, whole genome shotgun sequence	fungi'
CACW010096036.1 Camelus bactrianus WGS project CACW000000000 data, contig_113605, whole genome shotgun sequence	vertebrates_mammals'
CM02678.1 Monoraphidium neglectum strain SAG 48.67 chloroplast CP, complete sequence, whole genome shotgun sequence	plants'
KK100010.1 Rhizomucor miehei CAU432 unplaced genomic scaffold RhzM_scaffold1, whole genome shotgun sequence	fungi'
KK106941.1 Endocarpon pusillum strain KoLRI No. LF000583 unplaced genomic scaffold Scaffold_1, whole genome shotgun sequence	fungi'
KK106981.1 Umbilicaria muelhlenbergii strain KoLRI No. LF000956 unplaced genomic scaffold Scaffold_1, whole genome shotgun sequence	fungi'
KK107063.1 Cerapachys biroi unplaced genomic scaffold scaffold52, whole genome shotgun sequence	invertebrates'
KK115971.1 Stegodyphus mimosarum unplaced genomic scaffold scaffold1156, whole genome shotgun sequence	invertebrates'
KK198108.1 Orussus abietinus isolate OAB1.00-Male unplaced genomic scaffold Scaffold1, whole genome shotgun sequence	invertebrates'
CM02679.1 Gossypium arboreum cultivar Shixiya1 chromosome 1, whole genome shotgun sequence	plants'
KX198755.1 Eucalyptus grandis cultivar BRASU21 unplaced genomic scaffold scaffold_3, whole genome shotgun sequence	plants'
HG803543.1 Trichuris muris Edinburgh genomic scaffold, scaffold1, whole genome shotgun sequence	invertebrates'
CBZK010000001.2 Unus arctos WGS project CBZK000000000 data, contig scaffold_297, whole genome shotgun sequence	vertebrates_mammals'
HG805809.1 Trichuris trichiur genomic scaffold, TTRE_000001, whole genome shotgun sequence	invertebrates'
HG834063.1 Yarrowia lipolytica WSH-206 complete genome, chromosome YAL0E	fungi'
KK203934.1 Trichophyton rubrum MR850 unplaced genomic scaffold supercont1.232, whole genome shotgun sequence	fungi'
KK204238.1 Trichophyton interdigittale H6 unplaced genomic scaffold supercont2.1, whole genome shotgun sequence	fungi'
KK207357.1 Trichophyton rubrum CBS 100081 chromosome Unknown supercont1.289, whole genome shotgun sequence	fungi'
KK207889.1 Trichophyton rubrum CBS 288.86 unplaced genomic scaffold supercont1.271, whole genome shotgun sequence	fungi'
KK208427.1 Trichophyton rubrum CBS 289.86 unplaced genomic scaffold supercont1.270, whole genome shotgun sequence	fungi'
KK208846.1 Trichophyton soudanense CBS 452.61 unplaced genomic scaffold supercont1.168, whole genome shotgun sequence	fungi'
KK209384.1 Trichophyton rubrum MR1448 unplaced genomic scaffold supercont1.296, whole genome shotgun sequence	fungi'
KK209984.1 Trichophyton rubrum MR1459 unplaced genomic scaffold supercont1.314, whole genome shotgun sequence	fungi'
KK210299.1 Trichophyton rubrum CBS 735.88 unplaced genomic scaffold supercont1.143, whole genome shotgun sequence	fungi'
KK210757.1 Trichophyton rubrum CBS 202.88 unplaced genomic scaffold supercont2.259, whole genome shotgun sequence	fungi'
KL203742.1 Nanospoxalax gallii isolate Female K2095 unplaced genomic scaffold scaffold140, whole genome shotgun sequence	vertebrates_mammals'
CP007270.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121176 genome	bacteria'
CP007274.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093266 genome	bacteria'
CP007266.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110223 genome	bacteria'
CP007362.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120544 genome	bacteria'
CP007363.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120548 genome	bacteria'
CP007364.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120555 genome	bacteria'
CP007289.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19682831 genome	bacteria'
CP007290.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19683126 genome	bacteria'
CP007293.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20083456 genome	bacteria'
CP007294.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20083636, complete genome	bacteria'
CP007295.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20084384 genome	bacteria'
CP007277.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19930684 genome	bacteria'
CP007278.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19942384 genome	bacteria'
CP007279.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19943269 genome	bacteria'
CP007281.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19961622 genome	bacteria'
CP007284.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19971331 genome	bacteria'
CP007320.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090135 genome	bacteria'
CP007321.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090193 genome	bacteria'
CP007322.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090332 genome	bacteria'
CP007300.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20090877 genome	bacteria'
CP007301.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20091739 genome	bacteria'
CP007302.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093421 genome	bacteria'
CP007303.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093430 genome	bacteria'
CP007304.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093538 genome	bacteria'
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CP007306.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093784 genome	bacteria'
CP007307.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093788 genome	bacteria'
CP007308.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093950 genome	bacteria'
CP007309.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093977 genome	bacteria'
CP007310.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094079 genome	bacteria'
CP007311.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094350 genome	bacteria'
CP007313.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094363 genome	bacteria'
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CP007316.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094642 genome	bacteria'
CP007334.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20092320 genome	bacteria'
CP007317.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094803 genome	bacteria'
CP007319.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20095309 genome	bacteria'
CP007319.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20095440, complete genome	bacteria'
CP007323.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110222 genome	bacteria'
CP007324.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111514 genome	bacteria'
CP007325.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111515 genome	bacteria'
CP007326.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111554 genome	bacteria'
CP007327.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111561 genome	bacteria'
CP007328.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111576 genome	bacteria'
CP007330.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120003 genome	bacteria'
CP007331.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120007 genome	bacteria'
CP007344.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120213 genome	bacteria'
CP007345.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120219 genome	bacteria'
CP007346.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120229 genome	bacteria'
CP007347.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120240 genome	bacteria'
CP007348.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120356 genome	bacteria'
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CP007351.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120497 genome	bacteria'
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CP007354.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120528 genome	bacteria'
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CP007367.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121541 genome	bacteria'
CP007368.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121542 genome	bacteria'
CP007369.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121671 genome	bacteria'
CP007370.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121672 genome	bacteria'
CP007371.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121689 genome	bacteria'
CP007372.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20121703 genome	bacteria'
CP007373.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121744 genome	bacteria'
CP007374.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121746 genome	bacteria'
CP007395.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121748 genome	bacteria'
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CP007398.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121753 genome	bacteria'
CP007400.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120734 genome	bacteria'
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CP007406.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120776 genome	bacteria'
CP007407.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120917 genome	bacteria'
CP007408.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120918 genome	bacteria'
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CP007376.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120927 genome	bacteria'
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CP007378.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120968 genome	bacteria'
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CP007380.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120970 genome	bacteria'
CP007381.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121812 genome	bacteria'
CP007382.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121825 genome	bacteria'
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CP007384.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121969 genome	bacteria'
CP007385.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121970 genome	bacteria'
CP007296.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20090419 genome	bacteria'
CP007297.2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20090435 genome	bacteria'
CP007298.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090539 genome	bacteria'
CP007355.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100098 genome	bacteria'
CP007356.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100089 genome	bacteria'
CP007335.2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120580 genome	bacteria'

CP007336.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021020581 genome
CP007337.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021020590 genome
CP007338.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021020597 genome
CP007339.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021020685 genome
CP007340.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021020686 genome
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CP007362.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021021976 genome
CP007426.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SAZ0008585, complete genome
CP007432.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021021985 genome
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CP007433.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021020051 genome
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CP007412.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021022022 genome
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CP007418.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021030346 genome
CP007419.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021033046 genome
CP007423.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021030347 genome
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CP007420.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021001013 genome
CP007421.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC020900884 genome
CP007422.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC020900931 genome
CP007436.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021020099 genome
CP007453.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021020929 genome
CP007464.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021022033 genome
CP007465.1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA19490457 genome
CP007466.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SAZ00084644 genome
CP007467.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SAZ00084824 genome
CP007468.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SAZ00084777 genome
CP007469.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SAZ00094301 genome
CP007493.2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC021011510 genome
CP007724.1 *Pseudomonas aeruginosa* PA96 genome
CM002692.1 *Geobacillus stearothermophilus* N316321 isolate 9A5 chromosome, whole genome shotgun sequence
CM002694.1 *Oryza minuta* chromosome C3 short arm, whole genome shotgun sequence
KK214010.1 *Aspergillus niger* SH-2 uncultured genomic scaffold contig1, whole genome shotgun sequence
CM002705.1 *Flammulium velutipes* KAC4C2780 chromosome 11, whole genome shotgun sequence
CM002707.1 *Phaeoacremonia relictus* strain Cuauapio linkage group LG2, whole genome shotgun sequence
KK214785.1 *Chlamydomonas reinhardtii* strain 121 uncultured genomic scaffold10850, whole genome shotgun sequence
CM002739.1 *Camellia sativa* cultivar DH55 chromosome 11, whole genome shotgun sequence
CP007430.3 *Persea pyramidalis* strain V4 genome
CA011008.1 *Coprosma floridanum* isolate CFLO 00-Male uncultured genomic scaffold Scaffold3, whole genome shotgun sequence
CA244455.1 *Coleus lecticularis* isolate CLEC.00 strain Harlan uncultured genomic scaffold Scaffold1, whole genome shotgun sequence
KK245107.1 *Onchophagus laevis* bured non- domesticated insect uncultured genomic scaffold Scaffold05, whole genome shotgun sequence
CM002742.1 *Chlamydomonas reinhardtii* strain 121 uncultured genomic scaffold10850, whole genome shotgun sequence
CM002739.1 *Camellia sativa* cultivar DH55 chromosome 11, whole genome shotgun sequence
CP007430.3 *Persea pyramidalis* strain V4 genome
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KK245107.1 *Onchophagus laevis* bured non- domesticated insect uncultured genomic scaffold Scaffold05, whole genome shotgun sequence
CM002742.1 *Chlamydomonas reinhardtii* strain 121 uncultured genomic scaffold10850, whole genome shotgun sequence
CM002739.1 *Camellia sativa* cultivar DH55 chromosome 11, whole genome shotgun sequence
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KK245107.1 *Onchophagus laevis* bured non- domesticated insect uncultured genomic scaffold Scaffold05, whole genome shotgun sequence
CM002742.1 *Chlamydomonas reinhardtii* strain 121 uncultured genomic scaffold10850, whole genome shotgun sequence
CM002739.1 *Camellia sativa* cultivar DH55 chromosome 11, whole genome shotgun sequence
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CM002742.1 *Chlamydomonas reinhardtii* strain 121 uncultured genomic scaffold10850, whole genome shotgun sequence
CM002739.1 *Camellia sativa* cultivar DH55 chromosome 11, whole genome shotgun sequence
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KK245107.1 *Onchophagus laevis* bured non- domesticated insect uncultured genomic scaffold Scaffold05, whole genome shotgun sequence
CM002742.1 *Chlamydomonas reinhardtii* strain 121 uncultured genomic scaffold10850, whole genome shotgun sequence
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KK245107.1 *Onchophagus laevis* bured non- domesticated insect uncultured genomic scaffold Scaffold05, whole genome shotgun sequence
CM002742.1 *Chlamydomonas reinhardtii* strain 121 uncultured genomic scaffold10850, whole genome shotgun sequence
CM002739.1 *Camellia sativa* cultivar DH55 chromosome 11, whole genome shotgun sequence
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CA011008.1 *Coprosma floridanum* isolate CFLO 00-Male uncultured genomic scaffold Scaffold3, whole genome shotgun sequence
CA244455.1 *Coleus lecticularis* isolate CLEC.00 strain Harlan uncultured genomic scaffold Scaffold1, whole genome shotgun sequence
KK245107.1 *Onchophagus laevis* bured non- domesticated insect uncultured genomic scaffold Scaffold05, whole genome shotgun sequence
CM002742.1 *Chlamydomonas reinhardtii* strain 121 uncultured genomic scaffold10850, whole genome shotgun sequence
CM002739.1 *Camellia sativa*

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KN151326.1 <i>Steinernema carpocapsae</i> strain ALL unplaced genomic scaffold CARPO_006, whole genome shotgun sequence	invertebrates'
KN151899.1 <i>Nilaparvata lugens</i> isolate NLH13 unplaced genomic scaffold scaffold22, whole genome shotgun sequence	invertebrates'
KN165825.1 <i>Steinernema feltiae</i> strain SN unplaced genomic scaffold FELT_5455, whole genome shotgun sequence	invertebrates'
KN167705.1 <i>Steinernema scaptesis</i> strain FL unplaced genomic scaffold SCAPT_2260, whole genome shotgun sequence	invertebrates'
KN172139.1 <i>Steinernema glaseri</i> strain NC unplaced genomic scaffold GLAS_5991, whole genome shotgun sequence	fungi'
KN173723.1 <i>Nilaparvata lugens</i> yeast-like symbiont strain Hangzhou unplaced genomic scaffold scaffold1.1, whole genome shotgun sequence	fungi'
KN196491.1 <i>Blattella germanica</i> strain American Cyanamid = Orlando Normal breed German cockroach unplaced genomic scaffold Scaffold1, whole genome shotgun sequence	invertebrates'
CM002918.1 <i>Lactobacillus plantarum</i> CMPG5300 chromosome, whole genome shotgun sequence	bacteria'
CP008916.1 <i>Burkholderia</i> sp. BGK chromosome 1, complete sequence	bacteria'
KN214215.1 <i>Castanea mollissima</i> isolate Vianen unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	plants'
JRHR01003679.1 <i>Pythium insidiosum</i> strain CDC B5653 contig3679, whole genome shotgun sequence	protozoa'
QJDR02000001.1 <i>Hyalella azteca</i> isolate HAZT_00-mixed Contig1_fixed, whole genome shotgun sequence	invertebrates'
QJFK01000001.1 <i>Pichia kudriavzevii</i> strain SD108 scaffold00001, whole genome shotgun sequence	fungi'
CCBP01000011.1 <i>Trametes cinnabarina</i> BRFM137 WGS project CCBP0000000000 data, contig scf185007, whole genome shotgun sequence	fungi'
HG918267.1 <i>Capra aegagrus</i> genomic scaffold, scaffold000001, whole genome shotgun sequence	vertebrates_mammals'
H9324983.1 <i>Ovis aries musimon</i> genomic scaffold, scaffold000001, whole genome shotgun sequence	vertebrates_mammals'
CP009578.1 <i>Escherichia coli</i> FAP1 genome	bacteria'
JR1B01000569.1 <i>Saccharomyces cerevisiae</i> strain YS9 scaffold-682, whole genome shotgun sequence	fungi'
JR1C01000262.1 <i>Saccharomyces cerevisiae</i> strain YPS163 scaffold-270, whole genome shotgun sequence	fungi'
JR1E01000200.1 <i>Saccharomyces cerevisiae</i> strain YJM339 scaffold-208, whole genome shotgun sequence	fungi'
JR1D01000075.1 <i>Saccharomyces cerevisiae</i> strain YPS128 scaffold-78, whole genome shotgun sequence	fungi'
JR1F01000017.1 <i>Saccharomyces cerevisiae</i> strain Y35 scaffold-19, whole genome shotgun sequence	fungi'
JR1H01000084.1 <i>Saccharomyces cerevisiae</i> strain SK1 scaffold-103, whole genome shotgun sequence	fungi'
JR1G01000095.1 <i>Saccharomyces cerevisiae</i> strain DBVPG6044 scaffold-99, whole genome shotgun sequence	fungi'
JR1L01000146.1 <i>Saccharomyces cerevisiae</i> strain RedStar scaffold-222, whole genome shotgun sequence	fungi'
JR1I01000088.1 <i>Saccharomyces cerevisiae</i> strain BC187 scaffold-90, whole genome shotgun sequence	fungi'
JR1C01000036.1 <i>Saccharomyces cerevisiae</i> strain YPH499 scaffold-43, whole genome shotgun sequence	fungi'
JR1N01000192.1 <i>Saccharomyces cerevisiae</i> strain FY1679 scaffold-244, whole genome shotgun sequence	fungi'
JR1O01000037.1 <i>Saccharomyces cerevisiae</i> strain 10560-4B scaffold-50, whole genome shotgun sequence	fungi'
JR1R01000143.1 <i>Saccharomyces cerevisiae</i> strain BY4742 scaffold-188, whole genome shotgun sequence	fungi'
JR1Z01000011.1 <i>Saccharomyces cerevisiae</i> strain JK9-3d scaffold-12, whole genome shotgun sequence	fungi'
JR1U01000133.1 <i>Saccharomyces cerevisiae</i> strain W303 scaffold-169, whole genome shotgun sequence	fungi'
JR1V01000074.1 <i>Saccharomyces cerevisiae</i> strain CEN PK2-1Ca scaffold-97, whole genome shotgun sequence	fungi'
JR1T01000140.1 <i>Saccharomyces cerevisiae</i> strain FL100 scaffold-178, whole genome shotgun sequence	fungi'
JR1D01000074.1 <i>Saccharomyces cerevisiae</i> strain X2180-1A scaffold-91, whole genome shotgun sequence	fungi'
JR1Y01000123.1 <i>Saccharomyces cerevisiae</i> strain D273-10B scaffold-169, whole genome shotgun sequence	fungi'
JR1S01000158.1 <i>Saccharomyces cerevisiae</i> strain BY4741 scaffold-202, whole genome shotgun sequence	fungi'
JR1W01000103.1 <i>Saccharomyces cerevisiae</i> strain SEY6210 scaffold-124, whole genome shotgun sequence	fungi'
JR1K01000357.1 <i>Saccharomyces cerevisiae</i> strain L1528 scaffold-371, whole genome shotgun sequence	fungi'
JR1P01000004.1 <i>Saccharomyces cerevisiae</i> strain RM11-1A scaffold-3, whole genome shotgun sequence	fungi'
KN256562.1 <i>Aquila chrysaetos canadensis</i> isolate GSESGE unplaced genomic scaffold Scaffold0, whole genome shotgun sequence	vertebrates_non_mammals'
KN80357.1 <i>Phlebotopus portoricensis</i> strain PP33 unplaced genomic scaffold Scaffold01, whole genome shotgun sequence	fungi'
INBV01000001.1 <i>Taiwanofungus camphoratus</i> strain monokaryon S27 scaf1, whole genome shotgun sequence	invertebrates'
KN266224.1 <i>Dermatophagoides farinae</i> isolate Derf unplaced genomic scaffold scaffold_1, whole genome shotgun sequence	bacteria'
CP007555.1 <i>Coxiella burnetii</i> str. Namibia genome	vertebrates_non_mammals'
FN827340.1 <i>Danio rerio</i> strain Tuebingen, whole genome shotgun sequence assembly, Supercontig_0000001	vertebrates_mammals'
KN266387.1 <i>Vicuña pacos huacaya</i> unplaced genomic scaffold scaffold1, whole genome shotgun sequence	vertebrates_mammals'
KN271213.1 <i>Camelus dromedarius</i> breed Arabia unplaced genomic scaffold scaffold76, whole genome shotgun sequence	vertebrates_mammals'
KN274261.1 <i>Camelus bactrianus</i> breed Alta unplaced genomic scaffold scaffold37, whole genome shotgun sequence	vertebrates_mammals'
JR1U01000167.1 <i>Saccharomyces cerevisiae</i> strain K11 scaffold-173, whole genome shotgun sequence	fungi'
JR1M01000215.1 <i>Saccharomyces cerevisiae</i> strain UWOP505_217_3 scaffold-215, whole genome shotgun sequence	fungi'
KN284664.1 <i>Crocodylus porosus</i> isolate Cpor-Errol unplaced genomic scaffold scaffold-9763, whole genome shotgun sequence	vertebrates_non_mammals'
JR0U00000464.1 <i>Cyclospora cayentanensis</i> strain CHN_HEN01 contig_143, whole genome shotgun sequence	protozoa'
KN296311.1 <i>Rhinophrynus rattus</i> isolate Xiao Hai unplaced genomic scaffold ENSRROG3024130, whole genome shotgun sequence	vertebrates_mammals'
JPYM01000001.1 <i>Fusarium avenaceum</i> strain FA05001 Fave_05001_scaffold1.1, whole genome shotgun sequence	fungi'
CM002938.1 <i>Saccharomyces</i> sp. 'boulardi' strain ATCC MYA-796 chromosome IV, whole genome shotgun sequence	fungi'
PKY01000001.1 <i>Acremonium chrysogenum</i> ATCC 11550 scaffold1, whole genome shotgun sequence	fungi'
JQGE01000019.1 <i>Fusarium avenaceum</i> strain FalLH27 Fave_LH27_contig_3, whole genome shotgun sequence	fungi'
JQGD01000026.1 <i>Fusarium avenaceum</i> strain FalLH03 Fave_LH03_contig_2, whole genome shotgun sequence	fungi'
CP009684.1 <i>Bacillus subtilis</i> strain B-1 genome	bacteria'
CP009656.1 <i>Borrelia burgdorferi</i> strain B31, complete genome	bacteria'
CP009270.1 <i>Burkholderia pseudomallei</i> MSHR2243 chromosome 1, complete sequence	bacteria'
CP009271.1 <i>Burkholderia pseudomallei</i> MSHR1153 chromosome 1, complete sequence	bacteria'
CP009153.1 <i>Burkholderia pseudomallei</i> MSHR3965 chromosome 1 sequence	bacteria'
CM002998.1 <i>Nasalis larvatus</i> isolate Charlie chromosome align_Mm1, whole genome shotgun sequence	vertebrates_mammals'
KN305596.1 <i>Sporisorium scitamineum</i> strain 2014001 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence	fungi'
CM002977.3 <i>Macaca mulatta</i> isolate 17573 chromosome 1, whole genome shotgun sequence	vertebrates_mammals'
AJ1D01000003.1 <i>Candida albicans</i> P78048 supercont1.3, whole genome shotgun sequence	fungi'
AJ1W01000012.1 <i>Candida albicans</i> GC75 supercont1.12, whole genome shotgun sequence	fungi'
AJ1U01000001.1 <i>Candida albicans</i> P37005 supercont1.1, whole genome shotgun sequence	fungi'
AJ1S01000033.1 <i>Candida albicans</i> P94015 supercont1.33, whole genome shotgun sequence	fungi'
AJ1Y01000001.1 <i>Candida albicans</i> P57072 supercont1.1, whole genome shotgun sequence	fungi'
AJ1A01000002.1 <i>Candida albicans</i> P37037 supercont1.2, whole genome shotgun sequence	fungi'
AJ1Q01000005.1 <i>Candida albicans</i> 12C supercont2.5, whole genome shotgun sequence	fungi'
AJ1T01000001.1 <i>Candida albicans</i> P87 supercont2.1, whole genome shotgun sequence	fungi'
JRBH01000517.1 <i>Diospyros lotus</i> cultivar Kunsenshi Contig517, whole genome shotgun sequence	plants'
CM003019.1 <i>Burkholderia pseudomallei</i> MSHR435 chromosome 1, whole genome shotgun sequence	bacteria'
JFP020000002.1 <i>Hanseniaspora uvarum</i> strain 34-9 scaffold_1, whole genome shotgun sequence	fungi'
JPYR01000001.1 <i>Belgian Blue</i> cattle isolate Palmer, Staton, 2011 Ban contig001, whole genome shotgun sequence	invertebrates'
JOT001200203.1 <i>Vaccinium macrocarpon</i> cultivar Ben Lear (CNJ99-125-1 inbred clone) scaffold_3 mitochondrial, whole genome shotgun sequence	plants'
KN323322.1 <i>Gavialis gangeticus</i> isolate Ggan-Ray unplaced genomic scaffold scaffold60, whole genome shotgun sequence	vertebrates_non_mammals'
AJ1V01000007.1 <i>Candida albicans</i> 19F supercont2.7, whole genome shotgun sequence	fungi'
AJ1R01000008.1 <i>Candida albicans</i> L26 supercont2.8, whole genome shotgun sequence	fungi'
AJ1Z01000001.1 <i>Candida albicans</i> P34048 supercont1.1, whole genome shotgun sequence	fungi'
AJ1B01000009.1 <i>Candida albicans</i> P57055 supercont1.9, whole genome shotgun sequence	fungi'
AJ1C01000012.1 <i>Candida albicans</i> P75063 supercont1.12, whole genome shotgun sequence	fungi'
JSU01002258.1 <i>Cyprinodon nevadensis</i> pectoralis isolate South Scruggs Spring subpopulation scaffold2258, whole genome shotgun sequence	vertebrates_non_mammals'
AJ1E01000008.1 <i>Candida albicans</i> P76067 supercont1.8, whole genome shotgun sequence	fungi'
AJ1D01000004.1 <i>Candida albicans</i> P76055 supercont1.4, whole genome shotgun sequence	fungi'
JSXQ01000004.1 <i>Candida albicans</i> P37039 supercont1.4, whole genome shotgun sequence	fungi'
JSXP01000002.1 <i>Candida albicans</i> P36002 supercont1.2, whole genome shotgun sequence	fungi'
JSXR01000016.1 <i>Candida albicans</i> P75010 supercont1.16, whole genome shotgun sequence	fungi'
JPEV01000011.1 <i>Candida albicans</i> P75016 supercont1.11, whole genome shotgun sequence	fungi'
JPEW01000006.1 <i>Candida albicans</i> P78042 supercont1.6, whole genome shotgun sequence	fungi'
AJ1F01000001.1 <i>Candida albicans</i> SC5314 supercont4.1, whole genome shotgun sequence	fungi'
JTBX01000023.1 <i>Candida albicans</i> SC5314 supercont3.23, whole genome shotgun sequence	fungi'
AJ1J01000010.1 <i>Candida albicans</i> Ca6 supercont2.10, whole genome shotgun sequence	fungi'
CP009699.1 <i>Paenibacillus polymyxa</i> strain C706 genome	bacteria'
KN306965.1 <i>Uromyces viciae-fabae</i> strain IZ unplaced genomic scaffold scaffold_1, whole genome shotgun sequence	fungi'
JFWU020000001.1 <i>Phytophthora kernoviae</i> strain NZFS 3630 scf_22359_1.contig_1, whole genome shotgun sequence	fungi'
JFWV020000002.1 <i>Phytophthora kernoviae</i> strain NZFS 2646 scf_22199_2.contig_1, whole genome shotgun sequence	fungi'
JTEQ01000322.1 <i>Piezodorus guildinii</i> isolate RBSS-Aug2013 contig_323, whole genome shotgun sequence	protozoa'
KN707963.1 <i>Homo sapiens</i> unplaced genomic scaffold decoy20001	invertebrates'
LN625285.1 <i>Cryptococcus gattii</i> R265 genomic scaffold, contig_6, whole genome shotgun sequence	vertebrates_mammals'
HG428765.1 <i>Chromomus tentans</i> genomic scaffold, c001_s1, whole genome shotgun sequence	fungi'
KN389625.1 <i>Neurospora crassa</i> strain 73 unplaced genomic scaffold GE21scaffold_1, whole genome shotgun sequence	invertebrates'
KN476293.1 <i>Periopthalmodon Schlosseri</i> unplaced genomic scaffold scaffold2269, whole genome shotgun sequence	fungi'
KN462367.1 <i>Periopthalmodon magnuspinnatus</i> unplaced genomic scaffold scaffold2, whole genome shotgun sequence	vertebrates_non_mammals'
KN493925.1 <i>Scartelaos histophorus</i> unplaced genomic scaffold scaffold2025, whole genome shotgun sequence	vertebrates_non_mammals'
DF837573.1 <i>Acylotestulum subglobosum</i> LB1 DNA, scaffold: scaffold1, whole genome shotgun sequence	protozoa'
DF357216.1 <i>Solanum melongena</i> DNA, scaffold: Sme2.5_00003.1, whole genome shotgun sequence	plants'
KN398398.1 <i>Gossypium arboreum</i> cultivar AKAB401 unplaced genomic scaffold scaffold_14, whole genome shotgun sequence	plants'
KN521806.1 <i>Boleophthalmus pectinirostris</i> unplaced genomic scaffold scaffold1, whole genome shotgun sequence	vertebrates_non_mammals'
JTKG01000001.1 <i>Primula veris</i> cultivar Vogt026P Contig0, whole genome shotgun sequence	plants'
KN536881.1 <i>Oryza longistaminata</i> unplaced genomic scaffold Scaffold119344, whole genome shotgun sequence	plants'
JFBF01000001.1 <i>Bactrocera dorsalis</i> strain Punador scaffold00001, whole genome shotgun sequence	invertebrates'
KN538375.1 <i>Trichuris suis</i> unplaced genomic scaffold T_suis_1_0_Con0, whole genome shotgun sequence	invertebrates'
KN549200.1 <i>Oesophagostomum dentatum</i> strain OD-Hann unplaced genomic scaffold O_dentatum_1_0_Con11, whole genome shotgun sequence	invertebrates'
JNVN01000008.1 <i>Erysiphe necator</i> strain c-c-strain-scaffold_14, whole genome shotgun sequence	fungi'
JNU01000009.1 <i>Erysiphe necator</i> strain branching branching-scaffold_10, whole genome shotgun sequence	fungi'
JNUT01000020.1 <i>Erysiphe necator</i> strain ranch-r ranch9-scaffold_23, whole genome shotgun sequence	fungi'
JNUU01000038.1 <i>Erysiphe necator</i> strain lod lod-scaffold_43, whole genome shotgun sequence	fungi'
KN613455.1 <i>Viper berus berus</i> isolate VBER-BE-female unplaced genomic scaffold scaffold_0, whole genome shotgun sequence	vertebrates_non_mammals'
AJ1U01000001.1 <i>Diaporthe longicolla</i> strain TWH P74 scaffold_1, whole genome shotgun sequence	fungi'
JRUU02000006.1 <i>Raphanus sativus</i> cultivar WK10039 R6, whole genome shotgun sequence	plants'
JPDRO1000001.1 <i>Penicillium chrysogenum</i> strain IB 08921 Pc3_contig_1, whole genome shotgun sequence	fungi'
JWIN01034149.1 <i>Camelus dromedarius</i> breed African isolate Drom800 8669507_scaffold, whole genome shotgun sequence	vertebrates_mammals'
JPKC01022648.1 <i>Toxocara canis</i> isolate PN_DK_2014 scaffold806, whole genome shotgun sequence	invertebrates'
AZHE01000001.1 <i>Metarhizium album</i> ARSEP 1941 scaffold_1, whole genome shotgun sequence	fungi'
JRXU01000010.1 <i>Cryptosporidium hominis</i> isolate 37899 contig_10, whole genome shotgun sequence	protozoa'
KN709239.1 <i>Nelumbo nucifera</i> cultivar Chinese Tai-z lotus unplaced genomic scaffold scaffold396, whole genome shotgun sequence	plants'
KN711236.1 <i>Magnaporthe oryzae</i> strain 98-06 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence	fungi'
KN711580.1 <i>Bactrocera cucurbitae</i> strain USDA-PBARC White Pupae T1 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	invertebrates'
KN713669.1 <i>Fopius arisanus</i> strain USDA-PBARC FA_btor unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	invertebrates'
JRUC01000001.1 <i>Leptographium procenium</i> strain CMW34542 scaffold01, whole genome shotgun sequence	fungi'
CM003052.1 <i>Xanthomonas translucens</i> pv. <i>corallae</i> strain CFBP 2541 chromosome, whole genome shotgun sequence	bacteria'
CP005977.1 <i>Lactobacillus brevis</i> BSO 464 genome	bacteria'
CP010342.1 <i>Bacillus anthracis</i> strain A0157 sequence	bacteria'
KN714663.1 <i>Coccomyxa</i> sp. LA000219 unplaced genomic scaffold scaffold2, whole genome shotgun sequence	plants'
JUDQ01000001.1 <i>Scedosporium aurantiacum</i> strain WM 09.24 scaffold-1, whole genome shotgun sequence	fungi'
JOMC01000025.1 <i>Aspergillus ustus</i> strain 3.3904 AUSC_25, whole genome shotgun sequence	fungi'
AWJAO1004519.1 <i>Rutima echinophylla</i> strain CBS 111549 Joined_contig_4, whole genome shotgun sequence	fungi'
CP007548.1 <i>Trepionema pallidum</i> subsp. <i>endemicum</i> str. Bosnia A genome	bacteria'
KN714666.1 <i>Valsa mali</i> var. <i>pyri</i> strain SXYL134 unplaced genomic scaffold scaffold00001, whole genome shotgun sequence	fungi'
JSSU01001405.1 <i>Ceratocystis albifundus</i> strain CMW17620 scaffold1, whole genome shotgun sequence	fungi'

AZN01000001.1 Metarhizium majus ARSEF 297 Scaffold_1, whole genome shotgun sequence
 AZN01000001.1 Metarhizium guizhouense ARSEF 977 scaffold_1, whole genome shotgun sequence
 AZNG01000001.1 Metarhizium brunneum ARSEF 3297 scaffold_1, whole genome shotgun sequence
 AZNF01000001.1 Metarhizium anisopliae ARSEF 549 scaffold_1, whole genome shotgun sequence
 KN715325.1 *Mutilla frugalis* strain Nwnt-AP1 unplaced genomic scaffold scaffold1, whole genome shotgun sequence
 KN715895.1 *Penicillium chrysogenum* KF-25 unplaced genomic scaffold scaffold5, whole genome shotgun sequence
 KN716150.1 *Dicorycaeus viviparus* strain HannoverDv2000 unplaced genomic scaffold D_viviparus-1.0_Cont1, whole genome shotgun sequence
 KN726132.1 *Ancoylotoma duodenale* strain Zhejiang unplaced genomic scaffold A_duodenale-1.0_Cont1, whole genome shotgun sequence
 CP006902.1 *Clostridium botulinum* Prevot_594 genome
 CBXB01000009.1 *Saprochaete clavata* CNRMA 12.647 WGS project CBXB000000000 data, contig scaffold_9, whole genome shotgun sequence
 HC417165.1 *Oryza sativa* japonica genome assembly, chr01, whole genome shotgun sequence
 CM003064.1 *Oryza sativa* Japonica Group cultivar HEGA isolate HEGA_2.0 chromosome 1, whole genome shotgun sequence
 CM003076.1 *Oryza sativa* Japonica Group cultivar A123 chromosome 1, whole genome shotgun sequence
 CM003098.1 *Valsa mali* strain O3-8 chromosome 1, whole genome shotgun sequence
 JTFG02000001.1 *Ensete ventricosum* cultivar Bedadi scf_6473_1.contig.1, whole genome shotgun sequence
 KN798172.1 *Glossina pallasi* gambiensis isolate 146720 unplaced genomic scaffold scaffold1, whole genome shotgun sequence
 CA003111.1 *Vibrio cholerae* O1 biovar El Tor strain 1-1471 chromosome I, whole genome shotgun sequence
 JROL01007000.1 *Triticum aestivum* cultivar Chinese Spring chromosome 4D map short arm chr4DS00002, whole genome shotgun sequence
 KN805369.1 *Trebouxia gelatinosa* isolate LA002020 unplaced genomic scaffold scaffold1, whole genome shotgun sequence
 KN805370.1 *Schizochytrium* sp. CCTCC M209055 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 JSUV01450192.1 *Apis mellifera* intermissa strain Bida - Haddad scaffold1_size134357, whole genome shotgun sequence
 CP009313.1 *Streptomyces nodosus* strain ATCC 14599 genome
 JACE01000007.1 *Drosophila simulans* strain M252 chromosome 3R, whole genome shotgun sequence
 HG97522.1 *Acinetobacter baumannii* CS01 genomic scaffold, scaffold00001, whole genome shotgun sequence
 HG97528.1 *Acinetobacter baumannii* CR17 genomic scaffold, scaffold00001, whole genome shotgun sequence
 CDMT01009900.1 *Fasciola hepatica* genome assembly Fh_rear10kb, contig contig_9900, whole genome shotgun sequence
 CDHN01000001.1 *Toruella hemipterigena* genome assembly Alpalths-LG, scaffold SCAF1, whole genome shotgun sequence
 CGD01000001.1 *Rhizopus microsporus* genome assembly Rmricr_CBS_344_29, Alpalths-LG, scaffold SCAF1, whole genome shotgun sequence
 CDFH01096868.1 *Acanthamoeba astrosyns* genome assembly Acanthamoeba astrosyns, scaffold 396559, whole genome shotgun sequence
 CDFH01096869.1 *Acanthamoeba culbertsoni* genome assembly Acanthamoeba culbertsoni genome assembly, scaffold 254822, whole genome shotgun sequence
 CDFG01077627.1 *Acanthamoeba lentificata* genome assembly Acanthamoeba lentificata, scaffold 353499, whole genome shotgun sequence
 CDFH01025757.1 *Acanthamoeba healyi* genome assembly Acanthamoeba healyi, scaffold 209159, whole genome shotgun sequence
 CDFD01054303.1 *Acanthamoeba palestensis* genome assembly Acanthamoeba palestensis, scaffold 352945, whole genome shotgun sequence
 CDFK01217088.1 *Acanthamoeba polyphaga* genome assembly Acanthamoeba polyphaga, scaffold 749387, whole genome shotgun sequence
 CDEZ01022494.1 *Acanthamoeba royerba* genome assembly Acanthamoeba royerba, scaffold 139054, whole genome shotgun sequence
 CDFH01096868.1 *Acanthamoeba royerba* genome assembly Acanthamoeba royerba, scaffold 348153, whole genome shotgun sequence
 CDFH01067081.1 *Acanthamoeba divionensis* genome assembly Acanthamoeba divionensis, scaffold 404273, whole genome shotgun sequence
 CDFB01062555.1 *Acanthamoeba lugdunensis* genome assembly Acanthamoeba lugdunensis, scaffold 422590, whole genome shotgun sequence
 CDFN01041723.1 *Acanthamoeba quina* genome assembly Acanthamoeba quina, scaffold 369852, whole genome shotgun sequence
 CDFE01062597.1 *Acanthamoeba mauritanensis* genome assembly Acanthamoeba mauritanensis, scaffold 417904, whole genome shotgun sequence
 CDFL01219416.1 *Acanthamoeba castellanii* genome assembly Acanthamoeba castellanii, scaffold 753047, whole genome shotgun sequence
 CDFJ01214958.1 *Acanthamoeba pearcei* genome assembly Acanthamoeba pearcei, scaffold 744952, whole genome shotgun sequence
 CM003114.1 *Ziziphus jujuba* cultivar Dongzao chromosome 1, whole genome shotgun sequence
 KN805525.1 *Fundulus heteroclitus* isolate Maine unplaced genomic scaffold Scaffold0, whole genome shotgun sequence
 JTL01000001.1 *Basidiobasus undulatus* strain DACM 241956 scaffold1, whole genome shotgun sequence
 CP010455.1 Synthetic *Escherichia coli* C321.deltaA substrain rEc.y.dC.46, complete sequence
 CP010456.1 Synthetic *Escherichia coli* C321.deltaA substrain rEc.b.dC.12, complete sequence
 RJZ01019964.1 *Ermeria meschulizi* isolate Landers Enie_427, whole genome shotgun sequence
 KN839835.1 *Hydromyces pistrini* MD-312 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 KN838536.1 *Laccaria amethystina* LaAM-08-1 unplaced genomic scaffold K443scaffold_1, whole genome shotgun sequence
 KN832554.1 *Plicatropis crispata* FD-325 SS-3 unplaced genomic scaffold PLICrTascaffold_1, whole genome shotgun sequence
 KN837076.1 *Sphaerobolus stellatus* SS14 unplaced genomic scaffold SPHSTascaffold_1, whole genome shotgun sequence
 KN835132.1 *Sullus luteus* UH-Slu-Lm8-n1 unplaced genomic scaffold CY34scaffold_1, whole genome shotgun sequence
 KN834746.1 *Gymnopus luxurians* FD-317 M1 unplaced genomic scaffold GYM.Luscaffold_1, whole genome shotgun sequence
 KN833685.1 *Psilocybe microcarpa* 441 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 KN832970.1 *Ploderma croceum* F.1598 unplaced genomic scaffold scaffold_00001, whole genome shotgun sequence
 KN832870.1 *Oidiodendron maius* Zn unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 KN831944.1 *Psilotus tinctorius* Marx 270 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 KN831768.1 *Hebeloma cylindrosporum* h7 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 KN824824.1 *Paxillus rubicundulus* Ve08.2h10 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 KN824277.1 *Serendipita vermifera* MAFF 305830 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 KN822004.1 *Serendipita citrinum* Foag A unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 KN822942.1 *Tulasnella calospora* MUT 4182 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 KN819323.1 *Paxillus involutus* ATCC 200175 unplaced genomic scaffold PAXINscaffold_1, whole genome shotgun sequence
 KN818222.1 *Amantia muscaria* Koide BX008 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 KN817518.1 *Hypoheloma sublateritium* FD-334 SS-4 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence
 JN7210105339.1 *Thraurhania kawai* isolate Waike scaffold04623, whole genome shotgun sequence
 JLN01012231.1 *Sarcopsis scabiei* isolate Arfan Lab Contig12230, whole genome shotgun sequence
 AP014655.1 *Pseudomonas* sp. MT-1 DNA, nearly complete genome
 DF933830.1 *Talaromyces cellulolyticus* DNA, scaffold: scf_lce0_034, strain Y-94, whole genome shotgun sequence
 LD000290.1 *Humulus lupulus* var. cordifolius DNA, scaffold: KR_scaffold1_size296610, whole genome shotgun sequence
 CP007359.2 *Salmonella enterica* subsp. enterica serovar Enteritidis str. EC20100134 genome
 CP007359.2 *Salmonella enterica* subsp. enterica serovar Enteritidis str. EC20100134 genome
 LD132766.1 *Humulus lupulus* var. lupulus DNA, contig: SW_scaffold1_size296510, whole genome shotgun sequence
 AP014548.1 *Nonlabens marinus* ST-08 DNA, nearly complete genome
 CP010813.1 *Bacillus anthracis* strain Pollino sequence
 KN840438.1 *Phlebiopsis gigantea* 11061_1 CR5-6 unplaced genomic scaffold PHL.GScaffold_1, whole genome shotgun sequence
 CGD01002114.1 *Rhizoctonia solani* AG-1 IB genome assembly 7/3/14, contig contig02187, whole genome shotgun sequence
 CP009805.1 *Botrytis cinerea* B05.10 chromosome 1, complete sequence
 CP010287.1 *Fraxinella tularensis* subsp. tularensis strain Scherm genome
 JSU01000542.1 *Huntella tularensis* strain CMW 11056 scaffold1, whole genome shotgun sequence
 CP009846.1 *Yersinia enterocolitica* strain 8081, complete genome
 CP009996.1 *Yersinia pestis* strain Java9, complete genome
 CP010293.1 *Yersinia pestis* strain Nairobi genome
 CP007299.1 *Mycobacterium tuberculosis* H3b genome
 CP010005.1 *Bacillus thuringiensis* serovar kumari strain HD 1, complete genome
 KN846951.1 *Exophiala sideris* strain CBS 121828 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
 KN846956.1 *Capronia semimera* strain CBS 27337 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
 KN846969.1 *Fonsecaea pedrosoi* CBS 271.37 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
 KN846980.1 *Cladophialophora bartiana* CBS 173.52 unplaced genomic scaffold supercont1.1, whole genome shotgun sequence
 KN847040.1 *Cladophialophora immunda* strain CBS

BCI001000001.1 Cystobasidiopsis lactophilus DNA, scaffold: scaffold_0, strain: JCM 7595, whole genome shotgun sequence fungi'
BCIP01000001.1 Ambrosiozyma monospora DNA, scaffold: scaffold_0, strain: JCM 7599, whole genome shotgun sequence fungi'
BCI001000001.1 Cryptococcus phenolicus DNA, scaffold: scaffold_0, strain: JCM 11743, whole genome shotgun sequence fungi'
BCIT01000001.1 Holtermanniella nyssorum DNA, scaffold: scaffold_0, strain: JCM 11471, whole genome shotgun sequence fungi'
BCIV01000001.1 Cryptococcus wieringiae DNA, scaffold: scaffold_0, strain: JCM 11695, whole genome shotgun sequence fungi'
BCIW01000001.1 Yarrowia deformans DNA, scaffold: scaffold_0, strain: JCM 1694, whole genome shotgun sequence fungi'
BCIX01000001.1 Bulleromyces albus DNA, scaffold: scaffold_0, strain: JCM 2954, whole genome shotgun sequence fungi'
BCIV01000001.1 Rhodotulula toruloides DNA, scaffold: scaffold_0, strain: JCM 10020, whole genome shotgun sequence fungi'
BCIZ01000001.1 Rhodotulula toruloides DNA, scaffold: scaffold_0, strain: JCM 10021, whole genome shotgun sequence fungi'
BCJAO1000001.1 Rhodotulula toruloides DNA, scaffold: scaffold_0, strain: JCM 10049, whole genome shotgun sequence fungi'
BCJAO1000001.1 Erythrobasidium yunnanense DNA, scaffold: scaffold_0, strain: JCM 10687, whole genome shotgun sequence fungi'
BCJDO1000001.1 Yarrowia keelungensis DNA, scaffold: scaffold_0, strain: JCM 14894, whole genome shotgun sequence fungi'
BCJE01000001.1 Rhodotulula toruloides DNA, scaffold: scaffold_0, strain: JCM 24501, whole genome shotgun sequence fungi'
BCJF01000001.1 Vanrija humicola DNA, scaffold: scaffold_0, strain: JCM 1457, whole genome shotgun sequence fungi'
BCJGO1000001.1 Trichosporon porosum DNA, scaffold: scaffold_0, strain: JCM 1458, whole genome shotgun sequence fungi'
BCJHO1000001.1 Cryptococcus curvatus DNA, scaffold: scaffold_0, strain: JCM 1532, whole genome shotgun sequence fungi'
BCJIO1000001.1 Trichosporon brassicae DNA, scaffold: scaffold_0, strain: JCM 1599, whole genome shotgun sequence fungi'
BCJNO1000001.1 Trichosporon gamsei DNA, scaffold: scaffold_0, strain: JCM 9941, whole genome shotgun sequence fungi'
BCJO01000001.1 Trichosporon gracile DNA, scaffold: scaffold_0, strain: JCM 10018, whole genome shotgun sequence fungi'
BCJOU1000001.1 Meira nashicola DNA, scaffold: scaffold_0, strain: JCM 18503, whole genome shotgun sequence fungi'
BCJVO1000001.1 Candida versatilis DNA, scaffold: scaffold_0, strain: JCM 5958, whole genome shotgun sequence fungi'
BCJW01000001.1 Mrakia frigida DNA, scaffold: scaffold_0, strain: JCM 7857, whole genome shotgun sequence fungi'
BCJX01000001.1 Trichosporon guelhoui DNA, scaffold: scaffold_0, strain: JCM 10690, whole genome shotgun sequence fungi'
BCJZ01000001.1 Xanthophyllomyces dendrorhous DNA, scaffold: scaffold_0, strain: JCM 9681, whole genome shotgun sequence fungi'
BCKC01000001.1 Endocalyx cinctus DNA, scaffold: scaffold_0, strain: JCM 7946, whole genome shotgun sequence fungi'
BCKD01000001.1 Pilasporangium apinafurcum DNA, scaffold: scaffold_0, strain: JCM 30513, whole genome shotgun sequence protozoa'
BCKE01000001.1 Pilasporangium apinafurcum DNA, scaffold: scaffold_0, strain: JCM 30514, whole genome shotgun sequence protozoa'
BCKFO1000001.1 Yarrowia sp. JCM 30694 DNA, scaffold: scaffold_0, strain: JCM 30694, whole genome shotgun sequence fungi'
BCKGO1000001.1 Yarrowia sp. JCM 30695 DNA, scaffold: scaffold_0, strain: JCM 30695, whole genome shotgun sequence fungi'
BCKHO1000001.1 Albophoma yamanashiensis DNA, scaffold: scaffold_0, strain: JCM 11844, whole genome shotgun sequence fungi'
BCKIO1000001.1 Didymobotryum rigidum DNA, scaffold: scaffold_0, strain: JCM 8837, whole genome shotgun sequence fungi'
BCKJO1000001.1 Trichosporon veenhuisii DNA, scaffold: scaffold_0, strain: JCM 10691, whole genome shotgun sequence fungi'
BCKKO1000001.1 Dioszegia crocea DNA, scaffold: scaffold_0, strain: JCM 2961, whole genome shotgun sequence fungi'
BCKLO1000001.1 Leucosporidium creatinivorum DNA, scaffold: scaffold_0, strain: JCM 10699, whole genome shotgun sequence fungi'
BCKNO1000001.1 Dioszegia eurentica DNA, scaffold: scaffold_0, strain: JCM 2956, whole genome shotgun sequence fungi'
BCKOO1000001.1 Milleriomyces acaciae DNA, scaffold: scaffold_0, strain: JCM 10732, whole genome shotgun sequence fungi'
BCKOQ1000001.1 Ascidea asiatica DNA, scaffold: scaffold_0, strain: JCM 7603, whole genome shotgun sequence fungi'
BCKOU1000001.1 Trichosporon cutaneum DNA, scaffold: scaffold_0, strain: JCM 1462, whole genome shotgun sequence fungi'
BCKOV1000001.1 Trichosporon laibachii DNA, scaffold: scaffold_0, strain: JCM 2947, whole genome shotgun sequence fungi'
BCKWO1000001.1 Ogataea methanica DNA, scaffold: scaffold_0, strain: JCM 10240, whole genome shotgun sequence fungi'
BCKX01000001.1 Malassezia dermati DNA, scaffold: scaffold_0, strain: JCM 11348, whole genome shotgun sequence fungi'
BCKYO1000001.1 Malassezia japonica DNA, scaffold: scaffold_0, strain: JCM 11963, whole genome shotgun sequence fungi'
BCKZ01000001.1 Alloscoidea hylecoeti DNA, scaffold: scaffold_0, strain: JCM 7604, whole genome shotgun sequence fungi'
BCLA01000001.1 Malassezia nana DNA, scaffold: scaffold_0, strain: JCM 12085, whole genome shotgun sequence fungi'
BCLC01000001.1 Cryptococcus sp. JCM 24511 DNA, scaffold: scaffold_0, strain: JCM 24511, whole genome shotgun sequence fungi'
BCLD01000001.1 Cryptococcus terricola DNA, scaffold: scaffold_0, strain: JCM 24518, whole genome shotgun sequence fungi'
CM003855.1 Plasmodium reichenowi strain SY57 chromosome 14, whole genome shotgun sequence protozoa'
CM003869.1 Plasmodium gaboni strain SY75 chromosome 14, whole genome shotgun sequence protozoa'
CP014868.1 Pseudomonas fluorescens strain KENGFT3 genome bacteria'
BCLF01000001.1 Zoysia japonica DNA, contig: Zjn_sc00001.1, cultivar: Nagrizaki, whole genome shotgun sequence plants'
BCLGO1000001.1 Zoysia matrella DNA, contig: Zmw_sc00001.1, cultivar: Wakaba, whole genome shotgun sequence plants'
BCLHO1000001.1 Zoysia pacifica DNA, contig: Zpz_sc00001.1, cultivar: Zanza, whole genome shotgun sequence plants'
BDANO1000128.1 Flammulina velutipes DNA, config: NODE_162, strain: TR19, whole genome shotgun sequence fungi'
BCLX01000001.1 Yarrowia sp. JCM 30695 DNA, scaffold: scaffold_1, strain: JCM 30695, whole genome shotgun sequence fungi'
KV388093.1 Lepidothrix coronata isolate B3197 unplaced genomic scaffold Scaffold0, whole genome shotgun sequence fungi'
KV389426.1 Cebus capucinus imitator isolate Cc_AM_T3 unplaced genomic scaffold Scaffold0, whole genome shotgun sequence vertebrates_mammals'
LUEZ01000001.1 Hysipyzgus marmoreus strain 51987-8 scaffold_0, whole genome shotgun sequence fungi'
CP010347.1 Bordetella pertussis strain 1475 genome bacteria'
JSDN015027139.1 Dendrobium catenatum Dcal scaffold_368, whole genome shotgun sequence plants'
LTYT01001188.1 Agallia nitratia isolate Laifall00101-2011 scaffold001188, whole genome shotgun sequence vertebrates_non_mammals'
LQHGO1037208.1 Oryza sativa India Group cultivar Telep OsTET_37363, whole genome shotgun sequence plants'
LQHE01008114.1 Oryza sativa India Group cultivar Co39 OsCo39_8114, whole genome shotgun sequence plants'
LQHF01005255.1 Oryza sativa India Group cultivar Tadukan OsTAD_5256, whole genome shotgun sequence plants'
CP013008.1 Artrosipira platensis YZ genome bacteria'
KV392032.1 Trichosporon cutaneum strain CGMCC 2.1374 unplaced genomic scaffold scaffold1, whole genome shotgun sequence bacteria'
CP015048.1 Leptospira borgpetersenii serovar Hardjo strain BK-30 chromosome 1 sequence bacteria'
CP015052.1 Leptospira borgpetersenii serovar Hardjo strain NVSL S 818 chromosome 1 sequence bacteria'
CP015044.1 Leptospira borgpetersenii serovar Hardjo strain BK-6 chromosome 1 sequence bacteria'
CP015046.1 Leptospira borgpetersenii serovar Hardjo strain BK-9 chromosome 1, complete sequence bacteria'
CP015050.1 Leptospira borgpetersenii serovar Hardjo strain NVSL S 1343 chromosome 1 sequence bacteria'
LFHQ01000537.1 Colletotrichum tofieldiae strain CBS 168.49 contig615, whole genome shotgun sequence fungi'
LHFR01000304.1 Colletotrichum tofieldiae strain CBS 127615 contig369, whole genome shotgun sequence fungi'
LFHP01001266.1 Colletotrichum tofieldiae strain CBS 165.85 contig1635, whole genome shotgun sequence fungi'
LFHS01000445.1 Colletotrichum tofieldiae strain CBS 130851 contig599, whole genome shotgun sequence fungi'
CM003885.1 Oryza sativa India Group cultivar Minghui 63 chromosome 1, whole genome shotgun sequence plants'
CM003897.1 Oryza sativa India Group cultivar Zhenshan 97 chromosome 1, whole genome shotgun sequence plants'
JYHR01000001.1 Drechmeria coniospora strain ATCC 96282 omap49267b, whole genome shotgun sequence fungi'
KV407454.1 Xylaria hevaeae TC161 unplaced genomic scaffold L228scaffold_1, whole genome shotgun sequence fungi'
CM003910.1 Oryza sativa India Group cultivar Zhenshan 97 chromosome 1, whole genome shotgun sequence plants'
CM003922.1 Oryza sativa India Group cultivar Minghui 63 chromosome 1, whole genome shotgun sequence plants'
CP015225.1 Pseudomonas fluorescens strain FW300-N2E2 genome bacteria'
CM003934.1 Mus musculus strain 129S1/SvJmJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM003954.1 Mus musculus strain A/J chromosome 1, whole genome shotgun sequence vertebrates_mammals'
KV409358.1 Scleropages formosus breed green arowana unplaced genomic scaffold scaffold119, whole genome shotgun sequence vertebrates_non_mammals'
KV408664.1 Scleropages formosus breed red arowana unplaced genomic scaffold scaffold42, whole genome shotgun sequence vertebrates_non_mammals'
KV411217.1 Scleropages formosus breed golden arowana unplaced genomic scaffold scaffold72, whole genome shotgun sequence vertebrates_non_mammals'
CM003974.1 Mus musculus strain AKR/J chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM003994.1 Mus musculus strain CAST/EJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004014.1 Mus musculus strain CBA/J chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004034.1 Mus musculus strain DBA/2J chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004074.1 Mus musculus strain FVB/NJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004134.1 Mus musculus strain NZO/SHLJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004154.1 Mus musculus strain NZO/SHLJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004114.1 Mus musculus musculus strain PWK/PhJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004054.1 Mus musculus domesticus strain WBS/EJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004094.1 Mus spretus strain SPRET/EJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
LRVB01000198.1 Saccharomyces sp. 'boulardii' strain ATCC MYA-797 contig_338, whole genome shotgun sequence fungi'
LSRZ01000001.1 Haemophilus tartarophilus strain SISKW1 HNScaffold0001, whole genome shotgun sequence protozoa'
CM004174.1 Drechmeria coniospora strain ARSEF 6962 chromosome 01, whole genome shotgun sequence fungi'
CM004278.1 Daucus carota subsp. sativus cultivar DH1 chromosome 1, whole genome shotgun sequence plants'
LUGF01008404.1 Calycopsis scoprops scaffold1367, whole genome shotgun sequence invertebrates'
LFIV01000001.1 Colletotrichum tofieldiae strain 0861 Cl_v4_contig1, whole genome shotgun sequence fungi'
LFIV01002504.1 Colletotrichum incanum strain MARF 238704 contig2939, whole genome shotgun sequence fungi'
KV411306.1 Branchiostoma belcheri isolate BF01 breed outbred unplaced genomic scaffold scaffold1, whole genome shotgun sequence invertebrates'
KV416798.1 Branchiostoma belcheri isolate BF01 breed outbred unplaced genomic scaffold 220164697062, whole genome shotgun sequence invertebrates'
LVCR01001269.1 Crotalus horridus isolate 016-059-1111 sequence_1269_262077, whole genome shotgun sequence vertebrates_non_mammals'
CP015162.1 Trepnomena pallidum subsp. pallidum strain Amoy genome bacteria'
CP014266.1 Acinetobacter baumannii strain Ab421_GEIH-2010 genome bacteria'
KV417480.1 Fibulorhizodontia sp. CBS 109695 unplaced genomic scaffold FIBSPscaffold_1, whole genome shotgun sequence fungi'
KV417266.1 Calocera viscosa TUF012733 unplaced genomic scaffold CALVIscaffold_1, whole genome shotgun sequence fungi'
JYIV01000290.1 Ascochyta rabiei strain A/OII scaffold_336, whole genome shotgun sequence fungi'
LWBM01000028.1 Aspergillus terreus strain 45A scaffold_26, whole genome shotgun sequence fungi'
LWAD01000001.1 Diaporthe ampelina strain S3MP scaffold_1, whole genome shotgun sequence fungi'
LVYY01000001.1 Sporothrix globosa strain CBS 120340 Scaffold_1, whole genome shotgun sequence fungi'
LVYX01000001.1 Sporothrix globosa strain SS01 Scaffold_1, whole genome shotgun sequence fungi'
KV419394.1 Sclerotremastum niveorenneum HHB9708 unplaced genomic scaffold SISNscaffold_1, whole genome shotgun sequence fungi'
LNAU01000470.1 Pseudogymnoascus sp. GMY116 scaffold469, whole genome shotgun sequence fungi'
LNA01002106.1 Pseudogymnoascus sp. BL549 C15672, whole genome shotgun sequence fungi'
LMYD01000275.1 Pseudogymnoascus sp. BL308 scaffold276, whole genome shotgun sequence fungi'
LNAS01000063.1 Pseudogymnoascus pannorum var. pannorum strain ATCC 16222 scaffold59, whole genome shotgun sequence fungi'
LTAH01131375.1 Oscheius sp. TEL-2014 isolate Inbred line 7 NODE_638708_length_42873_cov_3.493621, whole genome shotgun sequence fungi'
CP015286.1 Paenibacillus glucanolyticus strain 5162 genome bacteria'
KV429032.1 Daedalea quercina 1-15889 unplaced genomic scaffold DAEQUscaffold_1, whole genome shotgun sequence fungi'
KV428004.1 Sclerotremastum suecicum HHB10207 ss-3 unplaced genomic scaffold SISUscaffold_1, whole genome shotgun sequence fungi'
KV427605.1 Laetiporus sulphureus 93-53 unplaced genomic scaffold LAESUscaffold_1, whole genome shotgun sequence fungi'
KV425882.1 Exidia glandulosa HHB12029 unplaced genomic scaffold EXIGLScaffold_1, whole genome shotgun sequence fungi'
KV425551.1 Neolentinus lepideus HHB14362 ss-1 unplaced genomic scaffold NEOLEscaffold_1, whole genome shotgun sequence fungi'
KV423914.1 Calocera cornea HHB12733 unplaced genomic scaffold CALCOscaffold_1, whole genome shotgun sequence fungi'
KV424459.1 Penicillora sp. CONT unplaced genomic scaffold PENSscaffold_1, whole genome shotgun sequence fungi'
LRCB01000512.1 Daphnia magna strain Xin63 scaffold00512, whole genome shotgun sequence invertebrates'
CM004194.1 Mus musculus strain BALB/cJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004215.1 Mus musculus strain C57BL/6NJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004235.1 Mus musculus strain C3H/HeJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
CM004256.1 Mus musculus strain LPJ chromosome 1, whole genome shotgun sequence vertebrates_mammals'
LWBZ01000028.1 Fusarium sp. FS5C_8 Chr_1_0, whole genome shotgun sequence fungi'
LKCNO1000001.1 Ophiostoma polytrichii strain BCC 54312 scaffold11, whole genome shotgun sequence fungi'
LUCGO1000698.1 Carthamus tinctorius cultivar AC SUNSET scaffold6606, whole genome shotgun sequence plants'
LRBV01000112.1 Quercus lobata isolate SW786 scaffold95, whole genome shotgun sequence plants'
KV775244.1 Dichanthelium oligosanthes cultivar Kellogg 1175 unplaced genomic scaffold Do_version_2_scaffold1, whole genome shotgun sequence plants'
CM004297.1 Saccharomyces cerevisiae strain GLBRCY22-3 chromosome IV, whole genome shotgun sequence fungi'
CM004191.1 Burkholderia terrforti strain MSMB2203WGS chromosome 1, complete sequence, whole genome shotgun sequence bacteria'
AZQY01000001.1 Ascochyta albyensis RCEF 2459 scaffold_1, whole genome shotgun sequence fungi'
AZQZ01000001.1 Ascochyta blight ARSEF 7405 Scaffold_1, whole genome shotgun sequence fungi'
AZHB01000001.1 Isaria fumosorosea ARSEF 2679 scaffold_1, whole genome shotgun sequence fungi'
AZHA01000001.1 Cordyceps brongniartii RCEF 3172 Scf_1, whole genome shotgun sequence fungi'

MALM01000147.1 Fusarium oxysporum f. sp. lycopersici strain FoI016 FoI016_contig_147, whole genome shotgun sequence	fungi'
MALQ01000133.1 Fusarium oxysporum f. sp. lycopersici strain FoI038 FoI038_contig_133, whole genome shotgun sequence	fungi'
MALN01000001.1 Fusarium oxysporum f. sp. lycopersici strain FoI029 FoI029_contig_1, whole genome shotgun sequence	fungi'
MALP01000036.1 Fusarium oxysporum f. sp. lycopersici strain FoI069 FoI069_contig_36, whole genome shotgun sequence	fungi'
MALQ01000021.1 Fusarium oxysporum f. sp. lycopersici strain FoI072 FoI072_contig_21, whole genome shotgun sequence	fungi'
MALR01000043.1 Fusarium oxysporum f. sp. lycopersici strain FoI073 FoI073_contig_43, whole genome shotgun sequence	fungi'
MALS01000071.1 Fusarium oxysporum f. sp. lycopersici strain FoI074 FoI074_contig_71, whole genome shotgun sequence	fungi'
MALU01000008.1 Fusarium oxysporum strain FoMN14 FoMN14_contig_8, whole genome shotgun sequence	fungi'
MALT01000041.1 Fusarium oxysporum f. sp. lycopersici strain FoI075 FoI075_contig_41, whole genome shotgun sequence	fungi'
MALW01000040.1 Fusarium oxysporum f. sp. lycopersici strain FoI087 FoI087illumina_contig_40, whole genome shotgun sequence	fungi'
MALY01000048.1 Fusarium oxysporum f. sp. melonis strain Fom005 Fom005pilon_contig_48, whole genome shotgun sequence	fungi'
MALX01000016.1 Fusarium oxysporum f. sp. melonis strain Fom004 Fom004pilon_contig_16, whole genome shotgun sequence	fungi'
MALZ01000010.1 Fusarium oxysporum f. sp. melonis strain Fom006 Fom006pilon_contig_10, whole genome shotgun sequence	fungi'
MAMA01000006.1 Fusarium oxysporum f. sp. melonis strain Fom009 Fom009pilon_contig_6, whole genome shotgun sequence	fungi'
MAMC01000110.1 Fusarium oxysporum f. sp. melonis strain Fom011 Fom011pilon_contig_110, whole genome shotgun sequence	fungi'
MAMB01000046.1 Fusarium oxysporum f. sp. melonis strain Fom010 Fom010pilon_contig_46, whole genome shotgun sequence	fungi'
MAME01000138.1 Fusarium oxysporum f. sp. melonis strain Fom013 Fom013pilon_contig_138, whole genome shotgun sequence	fungi'
MAMD01000116.1 Fusarium oxysporum f. sp. melonis strain Fom012 Fom012pilon_contig_116, whole genome shotgun sequence	fungi'
MAMG01000023.1 Fusarium oxysporum f. sp. lycopersici strain FoI002 FoI002_contig_23, whole genome shotgun sequence	fungi'
MAMF01000123.1 Fusarium oxysporum f. sp. melonis strain Fom016 Fom016pilon_contig_123, whole genome shotgun sequence	fungi'
MABT01000031.1 Fusarium oxysporum f. cucumerinum strain Foc011 Foc011_contig_31, whole genome shotgun sequence	fungi'
LORI01150276.1 Hydrocolea elegans strain CAD11 H_elegans_150303, whole genome shotgun sequence	invertebrates'
CP016880.1 Neisseria meningitidis strain M07165 genome	bacteria'
CP016882.1 Neisseria meningitidis strain M22747 genome	bacteria'
CP016881.1 Neisseria meningitidis strain M07999 genome	bacteria'
CP016883.1 Neisseria meningitidis strain M22790 genome	bacteria'
CP016884.1 Neisseria meningitidis strain M22797 genome	bacteria'
CP016886.1 Neisseria meningitidis strain M25074 genome	bacteria'
CP016885.1 Neisseria meningitidis strain M25073 genome	bacteria'
CM004561.1 Fusarium pseudograminearum strain FBG55266 chromosome 1, whole genome shotgun sequence	fungi'
CM004562.1 Capra hircus breed San Clemente chromosome 1, whole genome shotgun sequence	vertebrates_mammals'
MBPS01000051.1 Fusarium fujikuroi strain CF-295141 Contig0000051, whole genome shotgun sequence	fungi'
CP015855.1 Escherichia coli strain EDL933-1 genome	bacteria'
MAYM01001094.1 Phytophthora kernoviae isolate Chile2 scf_33878_1080.contig.1, whole genome shotgun sequence	protozoa'
LYOV02000019.1 Homo sapiens isolate HX1 Super-Scaffold_28, whole genome shotgun sequence	vertebrates_mammals'
CP014708.1 Komagataella phaffii strain WT chromosome 1 sequence	fungi'
CP014584.1 Komagataella pastoris strain ATCC 28485 chromosome 1 sequence	fungi'
CP016906.1 Enterobacter cloacae isolate SBP-8 genome	bacteria'
KV757199.1 Cutaneotrichosporon curvatus strain ATCC 20509 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence	fungi'
KV757211.1 Solicozozyma terricola strain JCM 24523 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence	fungi'
MBAO01000288.1 Phytophthora sp. Chile scf_39142_635.contig.1, whole genome shotgun sequence	protozoa'
MBAO01000506.1 Phytophthora kernoviae isolate Chile7 scf_14714_984.contig.1, whole genome shotgun sequence	protozoa'
MBAO01000360.1 Phytophthora kernoviae isolate Chile1 scf_19415_347.contig.1, whole genome shotgun sequence	protozoa'
CM004594.1 Homo sapiens isolate KOREF chromosome 2, whole genome shotgun sequence	vertebrates_mammals'
MBDO01000001.1 Phytophthora kernoviae isolate Chile6 scf_58185_5.contig.1, whole genome shotgun sequence	protozoa'
KV757425.1 Phytophthora kernoviae isolate Chile4 unplaced genomic scaffold scf_64197_2, whole genome shotgun sequence	protozoa'
CP013830.1 Pasteurellaceae bacterium N1060 genome	protozoa'
CP016045.1 Treponema pallidum subsp. pallidum strain PT_SIF0897 genome	bacteria'
CP016047.1 Treponema pallidum subsp. pallidum strain PT_SIF0857 genome	bacteria'
CP016049.1 Treponema pallidum subsp. pallidum strain PT_SIF0908 genome	bacteria'
CP016050.1 Treponema pallidum subsp. pallidum strain PT_SIF0954 genome	bacteria'
CP016051.1 Treponema pallidum subsp. pallidum strain PT_SIF1002 genome	bacteria'
CP016052.1 Treponema pallidum subsp. pallidum strain PT_SIF1020 genome	bacteria'
CP016053.1 Treponema pallidum subsp. pallidum strain PT_SIF1063 genome	bacteria'
CP016054.1 Treponema pallidum subsp. pallidum strain PT_SIF1127 genome	bacteria'
CP016055.1 Treponema pallidum subsp. pallidum strain PT_SIF1135 genome	bacteria'
CP016056.1 Treponema pallidum subsp. pallidum strain PT_SIF1140 genome	bacteria'
CP016057.1 Treponema pallidum subsp. pallidum strain PT_SIF1142 genome	bacteria'
CP016058.1 Treponema pallidum subsp. pallidum strain PT_SIF1156 genome	bacteria'
CP016059.1 Treponema pallidum subsp. pallidum strain PT_SIF1167 genome	bacteria'
CP016060.1 Treponema pallidum subsp. pallidum strain PT_SIF1183 genome	bacteria'
CP016061.1 Treponema pallidum subsp. pallidum strain PT_SIF1196 genome	bacteria'
CP016062.1 Treponema pallidum subsp. pallidum strain PT_SIF1200 genome	bacteria'
CP016063.1 Treponema pallidum subsp. pallidum strain PT_SIF1242 genome	bacteria'
CP016064.1 Treponema pallidum subsp. pallidum strain PT_SIF1262 genome	bacteria'
CP016065.1 Treponema pallidum subsp. pallidum strain PT_SIF1261 genome	bacteria'
CP016066.1 Treponema pallidum subsp. pallidum strain PT_SIF1278 genome	bacteria'
CP016067.1 Treponema pallidum subsp. pallidum strain PT_SIF1280 genome	bacteria'
CP016068.1 Treponema pallidum subsp. pallidum strain PT_SIF1299 genome	bacteria'
CP016069.1 Treponema pallidum subsp. pallidum strain PT_SIF1348 genome	bacteria'
LZY001000002.1 Paracoccidioides brasiliensis strain Pb300 supercont1.2, whole genome shotgun sequence	fungi'
LYUC01000001.1 Paracoccidioides brasiliensis strain CNH supercont1.1, whole genome shotgun sequence	fungi'
MCQ002000131.1 Aspergillus fumigatus strain LMB-35A scaffold2_sra2524342, whole genome shotgun sequence	fungi'
CP016975.1 Brucella canis strain 2009013648 chromosome 1 sequence	bacteria'
CP016985.1 Brucella melitensis strain 2010724553 chromosome 1 sequence	bacteria'
CP016632.1 Streptococcus pneumoniae strain D122 genome	bacteria'
CP016633.1 Streptococcus pneumoniae strain D141 genome	bacteria'
CP017004.1 Plasmodium falciparum 3D7 chromosome 14 sequence	protozoa'
MAES001000001.1 Marsus vietnami isolate B01_N305 scaffold_0_1.R, whole genome shotgun sequence	vertebrates_non_mammals'
MAZY01000003.1 Pleurotus eryngii strain 183 scaffold003, whole genome shotgun sequence	fungi'
KV766071.1 Botryosphaeria berengeriana strain LW030101 unplaced genomic scaffold Scaffold1, whole genome shotgun sequence	fungi'
CP017074.1 Luteimonas sp. JM171 genome	bacteria'
JXNT01000001.1 Aspergillus cristatus strain GZAAS20_1005 Scaffold_Scf_1, whole genome shotgun sequence	fungi'
CP016855.1 Staphylococcus aureus subsp. aureus strain 5118 N, complete genome	bacteria'
LHJ401000101.1 Fusarium meridionale strain NRRL28721 contig_131, whole genome shotgun sequence	fungi'
LHT201000026.1 Fusarium asiaticum strain NRRL28720 contig_9, whole genome shotgun sequence	fungi'
LHTY01000088.1 Fusarium asiaticum strain NRRL6101 contig_19, whole genome shotgun sequence	fungi'
LHUB01000118.1 Fusarium meridionale strain NRRL28723 contig_21, whole genome shotgun sequence	fungi'
LHUD01000197.1 Fusarium graminearum strain NRRL28336 contig_3, whole genome shotgun sequence	fungi'
LHUC01000016.1 Fusarium graminearum strain DAOM180378 contig_5, whole genome shotgun sequence	fungi'
LJU01000001.1 Ochreseella cincta OcoN01_Sco001, whole genome shotgun sequence	invertebrates'
MDGX01000001.1 Brettanomyces bruxellensis strain CBS 2795 y81_scaffold1, whole genome shotgun sequence	fungi'
AWGH01000001.1 Tschuyayaea wingfieldii CBS 7118 supercont1.1, whole genome shotgun sequence	fungi'
AWGK01000001.1 Cryptococcus depauperatus CBS 7841 supercont1.1, whole genome shotgun sequence	fungi'
AWGJ01000001.1 Cryptococcus amyloletus CBS 6039 supercont1.1, whole genome shotgun sequence	fungi'
MEKH01000001.1 Cryptococcus amyloletus CBS 6273 supercont2.1, whole genome shotgun sequence	fungi'
AWGL01000001.1 Cryptococcus depauperatus CBS 7855 supercont2.1, whole genome shotgun sequence	fungi'
KV766159.1 Penicillium oxalicum strain HP7-1 unplaced genomic scaffold scaffold_1, whole genome shotgun sequence	fungi'
MEI201000001.1 Globodera affinis isolate Ge_1_G_ellingtonae_scaf_0001, whole genome shotgun sequence	invertebrates'
CP012555.1 Raoultella ornithinolytica strain 18 sequence	bacteria'
CM004629.1 Vigna angularis var. angularis cultivar Kyungwonpat chromosome 6, whole genome shotgun sequence	plants'
MDVQ01000001.1 Crocodylus porosus isolate Cpor-Eor scaffold_1, whole genome shotgun sequence	vertebrates_non_mammals'
MDVQ01000008.1 Gaviais gangeticus isolate Ogan-Ray scaffold_8, whole genome shotgun sequence	vertebrates_non_mammals'
MEDX01000015.1 Fonticula-like sp. SCN 57-25 ABS05_02015, whole genome shotgun sequence	invertebrates'
MEDY01000042.1 Rhyzissia sp. SCN 62-46 ABS51_C0042, whole genome shotgun sequence	protozoa'
CP016418.1 Chlamydia trachomatis strain SB002739 sequence	bacteria'
CP016420.1 Chlamydia trachomatis strain SB006930 sequence	bacteria'
CP016422.1 Chlamydia trachomatis strain SB008107 sequence	bacteria'
CP016424.1 Chlamydia trachomatis strain SB013112 sequence	bacteria'
CP016426.1 Chlamydia trachomatis strain SB013321 sequence	bacteria'
MINI01187594.1 Phormia regina isolate Indy20121 PregJ_Contig_187788, whole genome shotgun sequence	invertebrates'
MINI01166222.1 Phormia regina isolate Indy2012m PregM_Contig_166753, whole genome shotgun sequence	invertebrates'
MEH001000001.1 Lolium perenne isolate 4540-9 Ryegrass_Norm_contig_4785, whole genome shotgun sequence	plants'
CM004674.1 Saccharomyces cerevisiae strain wild007 chromosome IV, whole genome shotgun sequence	fungi'
CM004690.1 Saccharomyces cerevisiae strain wild003 chromosome IV, whole genome shotgun sequence	fungi'
CM004706.1 Saccharomyces cerevisiae strain wild005 chromosome IV, whole genome shotgun sequence	fungi'
CM004738.1 Saccharomyces cerevisiae strain wild004 chromosome IV, whole genome shotgun sequence	fungi'
CM004722.1 Saccharomyces cerevisiae strain wild006 chromosome IV, whole genome shotgun sequence	fungi'
CM004754.1 Saccharomyces cerevisiae strain wild002 chromosome IV, whole genome shotgun sequence	fungi'
CM004770.1 Saccharomyces cerevisiae strain wild001 chromosome IV, whole genome shotgun sequence	fungi'
CM004802.1 Saccharomyces cerevisiae strain wine019 chromosome IV, whole genome shotgun sequence	fungi'
CM004786.2 Saccharomyces cerevisiae strain wine018 chromosome IV, whole genome shotgun sequence	fungi'
CM004818.2 Saccharomyces cerevisiae strain wine017 chromosome IV, whole genome shotgun sequence	fungi'
CM004834.2 Saccharomyces cerevisiae strain wine016 chromosome IV, whole genome shotgun sequence	fungi'
CM004850.2 Saccharomyces cerevisiae strain wine015 chromosome IV, whole genome shotgun sequence	fungi'
CM004866.2 Saccharomyces cerevisiae strain wine014 chromosome IV, whole genome shotgun sequence	fungi'
CM004882.2 Saccharomyces cerevisiae strain wine013 chromosome IV, whole genome shotgun sequence	fungi'
CM004898.1 Saccharomyces cerevisiae strain wine012 chromosome IV, whole genome shotgun sequence	fungi'
CM004914.2 Saccharomyces cerevisiae strain wine011 chromosome IV, whole genome shotgun sequence	fungi'
CM004930.2 Saccharomyces cerevisiae strain wine010 chromosome IV, whole genome shotgun sequence	fungi'
CM004946.2 Saccharomyces cerevisiae strain wine009 chromosome IV, whole genome shotgun sequence	fungi'
CM004962.2 Saccharomyces cerevisiae strain wine008 chromosome IV, whole genome shotgun sequence	fungi'
CM004978.2 Saccharomyces cerevisiae strain wine007 chromosome IV, whole genome shotgun sequence	fungi'
CM004994.2 Saccharomyces cerevisiae strain wine006 chromosome IV, whole genome shotgun sequence	fungi'
CM005010.2 Saccharomyces cerevisiae strain wine005 chromosome IV, whole genome shotgun sequence	fungi'
CM005026.2 Saccharomyces cerevisiae strain wine004 chromosome IV, whole genome shotgun sequence	fungi'
CM005042.2 Saccharomyces cerevisiae strain wine003 chromosome IV, whole genome shotgun sequence	fungi'
CM005058.2 Saccharomyces cerevisiae strain wine002 chromosome IV, whole genome shotgun sequence	fungi'
CM005074.2 Saccharomyces cerevisiae strain wine001 chromosome IV, whole genome shotgun sequence	fungi'
CM005090.1 Saccharomyces cerevisiae strain spirits011 chromosome IV, whole genome shotgun sequence	fungi'
CM005106.1 Saccharomyces cerevisiae strain spirits010 chromosome IV, whole genome shotgun sequence	fungi'
CM005122.1 Saccharomyces cerevisiae strain spirits009 chromosome IV, whole genome shotgun sequence	fungi'
CM005138.1 Saccharomyces cerevisiae strain spirits008 chromosome IV, whole genome shotgun sequence	fungi'
CM005154.1 Saccharomyces cerevisiae strain spirits007 chromosome IV, whole genome shotgun sequence	fungi'
CM005170.1 Saccharomyces cerevisiae strain spirits006 chromosome IV, whole genome shotgun sequence	fungi'

LT629740.1	Mucilaginibacter mallensis strain MP1X4 genome assembly, chromosome: 1	bacteria'
LT629771.1	Jiangella sp. DSM 45060 genome assembly, chromosome: 1	bacteria'
LT629764.1	Paenibacillaceae bacterium GAS479 genome assembly, chromosome: 1	bacteria'
LT629763.1	Pseudomonas sabulnigri strain JCM 14963 genome assembly, chromosome: 1	bacteria'
LT629767.1	Pseudomonas umsongensis strain BS3657 genome assembly, chromosome: 1	bacteria'
LT629769.1	Pseudomonas syringae strain 31R1 genome assembly, chromosome: 1	bacteria'
LT629765.1	Corynebacterium timonense strain DSM 45434 genome assembly, chromosome: 1	bacteria'
LT629766.1	Brevibacterium silguriense strain DSM 23676 genome assembly, chromosome: 1	bacteria'
LT629770.1	Microbacterium paraxoydans strain DSM 15019 genome assembly, chromosome: 1	bacteria'
LT629772.1	Microtholus soli strain DSM 21800 genome assembly, chromosome: 1	bacteria'
LT629775.1	Streptomyces sp. TL1_053 genome assembly, chromosome: 1	bacteria'
LT629773.1	Gardnerella vaginalis strain DSM 4944 genome assembly, chromosome: 1	bacteria'
LT629774.1	Winogradskyella sp. RHA_55 genome assembly, chromosome: 1	bacteria'
LT629776.1	Paraoskovia marina strain DSM 22126 genome assembly, chromosome: 1	bacteria'
LT629777.1	Pseudomonas asplenii strain ATCC 23835 genome assembly, chromosome: 1	bacteria'
LT629778.1	Pseudomonas granadensis strain LMG 27940 genome assembly, chromosome: 1	bacteria'
LT629779.1	Pseudarthrobacter equi strain IMMIB L-1606 genome assembly, chromosome: 1	bacteria'
LT629801.1	Pseudomonas rhodesiae strain BS2777 genome assembly, chromosome: 1	bacteria'
LT629784.1	Stappia sp. ES.058 genome assembly, chromosome: 1	bacteria'
LT630003.1	[Clostridium] sphenoides JCM 1415 strain ATCC 19403 genome assembly, chromosome: 1	bacteria'
LT629787.1	Pseudomonas salegens strain CECT 8338 genome assembly, chromosome: 1	bacteria'
LT629786.1	Pseudomonas syrniantha strain LMG 2190 genome assembly, chromosome: 1	bacteria'
LT629781.1	Vermucomicrobiaceae bacterium GAS474 genome assembly, chromosome: 1	bacteria'
LT629793.1	Pseudomonas yamanorum strain LMG 27247 genome assembly, chromosome: 1	bacteria'
LT629799.1	Friedmanniella sagamiharensis strain DSM 21743 genome assembly, chromosome: 1	bacteria'
LT629782.1	Pseudomonas orientalis strain BS2775 genome assembly, chromosome: 1	bacteria'
LT629788.1	Pseudomonas moraviensis strain BS3668 genome assembly, chromosome: 1	bacteria'
LT629800.1	Pseudomonas brenneri strain BS2771 genome assembly, chromosome: 1	bacteria'
LT629803.1	Pseudomonas vancouverensis strain BS3656 genome assembly, chromosome: 1	bacteria'
LT629783.1	Pseudomonas fragi strain NRRL B-727 genome assembly, chromosome: 1	bacteria'
LT629789.1	Amycolatopsis keratiniphila strain FH 1893 genome assembly, chromosome: 1	bacteria'
LT629804.1	Arcanobacterium phocae strain DSM 10002 genome assembly, chromosome: 1	bacteria'
LT629780.1	Pseudomonas guangdongensis strain CCTCC 2012022 genome assembly, chromosome: 1	bacteria'
LT629791.1	Jiangella alkaliphila strain DSM 45079 genome assembly, chromosome: 1	bacteria'
LT629785.1	Pseudomonas pohangensis strain DSM 17875 genome assembly, chromosome: 1	bacteria'
LT629790.1	Pseudomonas mediterranea strain DSM 16733 genome assembly, chromosome: 1	bacteria'
LT629797.1	Pseudomonas sihuensis strain KCTC 32246 genome assembly, chromosome: 1	bacteria'
LT629802.1	Pseudomonas mucidolens strain LMG 2224 genome assembly, chromosome: 1	bacteria'
LT629792.1	Actinomyces radingae strain DSM 9169 genome assembly, chromosome: 1	bacteria'
LT629796.1	Pseudomonas mandelii strain LMG 21607 genome assembly, chromosome: 1	bacteria'
LT629794.1	Polartibacter sp. He1_33_78 genome assembly, chromosome: 1	bacteria'
LT629798.1	Pseudomonas corrugata strain BS3649 genome assembly, chromosome: 1	bacteria'
LT629795.1	Pseudomonas psychrophila strain BS3667 genome assembly, chromosome: 1	bacteria'
LT635756.1	[Candida] intermedia strain CBS 141442 genome assembly, chromosome: 1	fungi'
LT635764.1	[Candida] intermedia strain PYCC 4715 genome assembly, chromosome: 1	fungi'
LT629867.1	Leifsonia sp. 21MFCrub1.1 genome assembly, chromosome: 1	bacteria'
LT629970.1	Pseudomonas xanithomarina strain LMG 23572 genome assembly, chromosome: 1	bacteria'
LT629971.1	Mycobacterium rutilum strain DSM 45405 genome assembly, chromosome: 1	bacteria'
LT629972.1	Pseudomonas fuscovaginae strain LMG 2158 genome assembly, chromosome: 1	bacteria'
FNXT01001221.1	Tetradasmus obliquus genome assembly, contig: scaf1221, whole genome shotgun sequence	plants'
FNXX01000001.1	Conringia planisliqua genome assembly, contig: scaffold_1, whole genome shotgun sequence	plants'
LT630002.1	Leifsonia sp. 467MF genome assembly, chromosome: 1	bacteria'
LT630032.1	Leifsonia sp. 98AMF genome assembly, chromosome: 1	bacteria'
FPAX01000001.1	Euclidium syriacum genome assembly, contig: scaffold_1, whole genome shotgun sequence	plants'
FQNF01000001.1	Hanseniaspora guilliermondii, strain UTAD222, genome assembly, contig: HGU1_contig_001, whole genome shotgun sequence	fungi'
LT634571.1	Sus scrofa genome assembly, chromosome: X	vertebrates_mammals'
LT632320.1	Escherichia coli strain NCTC 13441 genome assembly, chromosome: 1	bacteria'
LT649234.1	Stramenopiles sp. TOSAG23-2 genome assembly, scaffold: TOSAG23-2_scaffold_1, whole genome shotgun sequence	protozoa'
LT635910.1	Stramenopiles sp. TOSAG23-6 genome assembly, scaffold: TOSAG23-6_scaffold_1, whole genome shotgun sequence	protozoa'
LT665360.1	Stramenopiles sp. TOSAG41-1 genome assembly, scaffold: TOSAG41-1_scaffold_1, whole genome shotgun sequence	protozoa'
LT642146.1	Stramenopiles sp. TOSAG23-3 genome assembly, scaffold: TOSAG23-3_scaffold_1, whole genome shotgun sequence	protozoa'
LT667505.1	Bathycoccus sp. TOSAG39-1 genome assembly, scaffold: TOSAG39-1_scaffold_1, whole genome shotgun sequence	plants'
FQTN01001675.1	Branchiostoma belcheri isolate BF01 genome assembly, contig: scaffold1, whole genome shotgun sequence	invertebrates'
LT670849.1	Bradyrhizobium erythrophlei strain GAS401 genome assembly, chromosome: 1	bacteria'
LT671675.1	Olsenella sp. Marseille-P3237 strain Marseille-P3237T genome assembly, chromosome: scaffold00001	bacteria'
FTP01000002.1	Fraxinus excelsior genome assembly, contig: Contig1, whole genome shotgun sequence	plants'
LT671813.1	Malassezia sympodialis isolate KS292 genome assembly, chromosome: 1	fungi'
LT671821.1	Malassezia sympodialis ATCC 42132 genome assembly, chromosome: 1	fungi'
LT671789.1	Malassezia sympodialis isolate KS024 genome assembly, chromosome: 1	fungi'
LT671798.1	Malassezia sympodialis isolate KS327 genome assembly, chromosome: 2	fungi'
LT671805.1	Malassezia sympodialis isolate KS004 genome assembly, chromosome: 1	fungi'
LT707061.1	Pseudomonas putida strain N1R genome assembly, chromosome: 1	bacteria'
LT707063.1	Pseudomonas sp. B10 genome assembly, chromosome: 1	bacteria'
LT707062.1	Pseudomonas sp. A214 genome assembly, chromosome: 1	bacteria'
LT707064.1	Pseudomonas sp. 7SR1 genome assembly, chromosome: 1	bacteria'
LT707065.1	Achromobacter sp. MFA1 R4 genome assembly, chromosome: 1	bacteria'