

Supplementary Information

Genome-wide patterns of genetic variation among elite maize inbreds

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SUPPLEMENTARY FIGURES

Figure S1. Pattern of genome-wide SNP distribution. SNP rates were counted in each 1Mb window across the genome. Regions having the same SNP rates were counted and plotted in the picture. Regions with rates lower than 0.0025 are more than expected in the normal distribution.

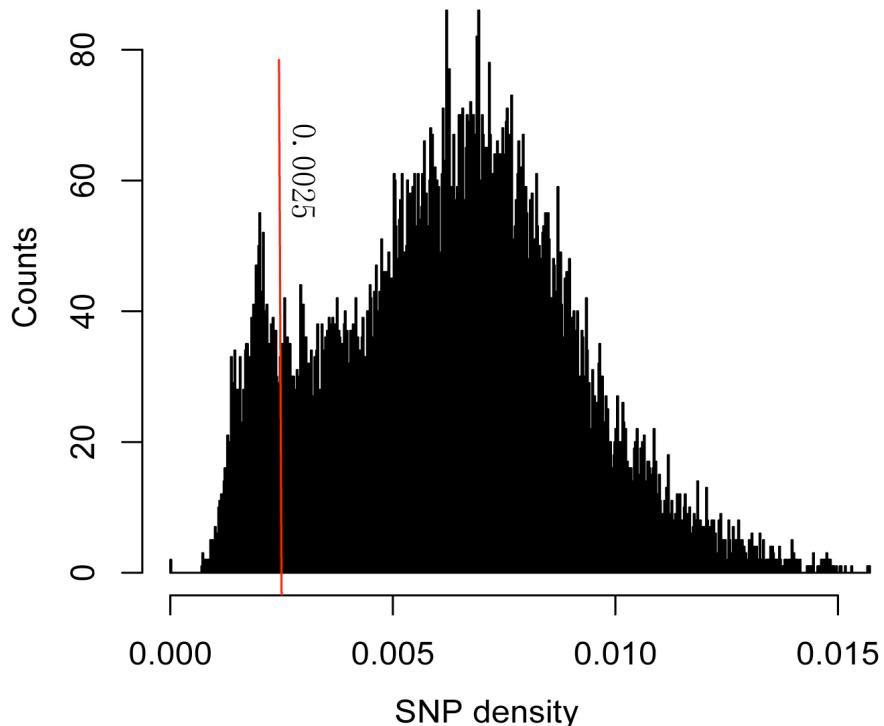


Figure S2. Genome-wide distribution of divergence rate, gene density, zero diversity genes and selected genes on each chromosome. SNP density (black line), π (orange line) and gene density (grey polygon) are plotted using 1-Mb sliding windows. Zero diversity genes are shown by vertical blue bars at the bottom of the plot. Red asterisks mark the position of known selection genes.

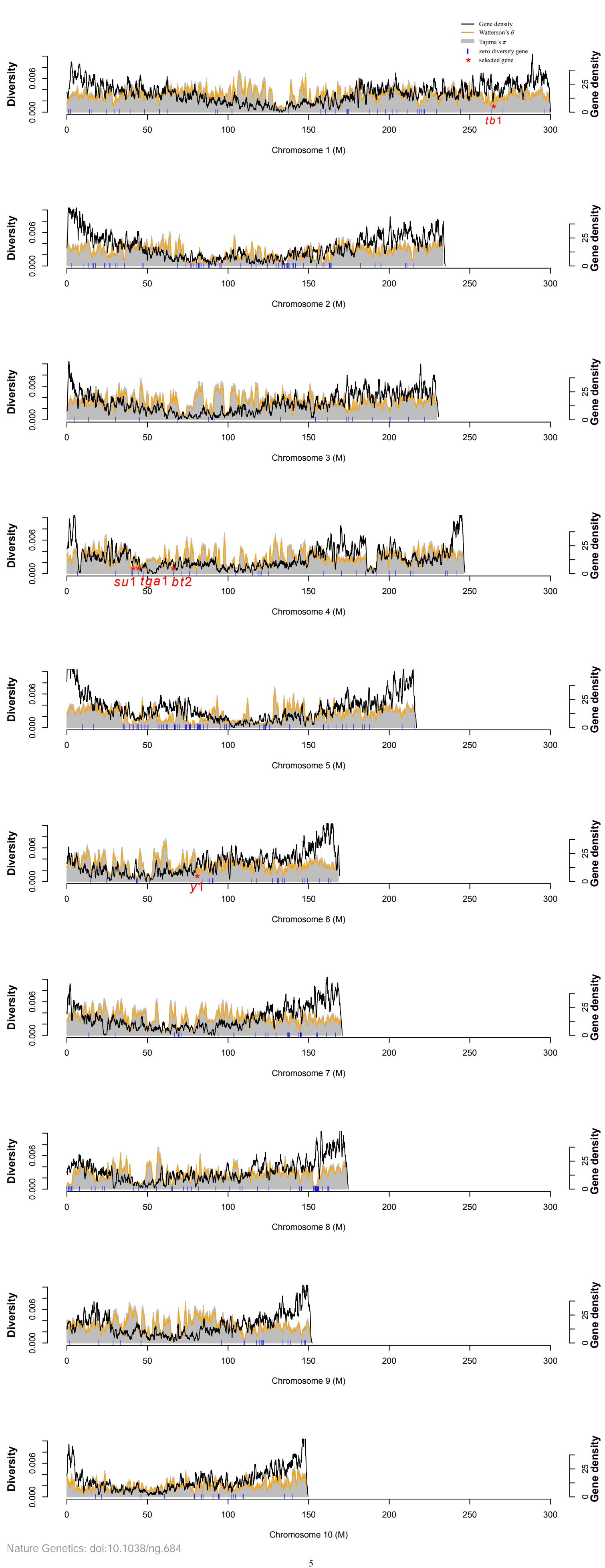
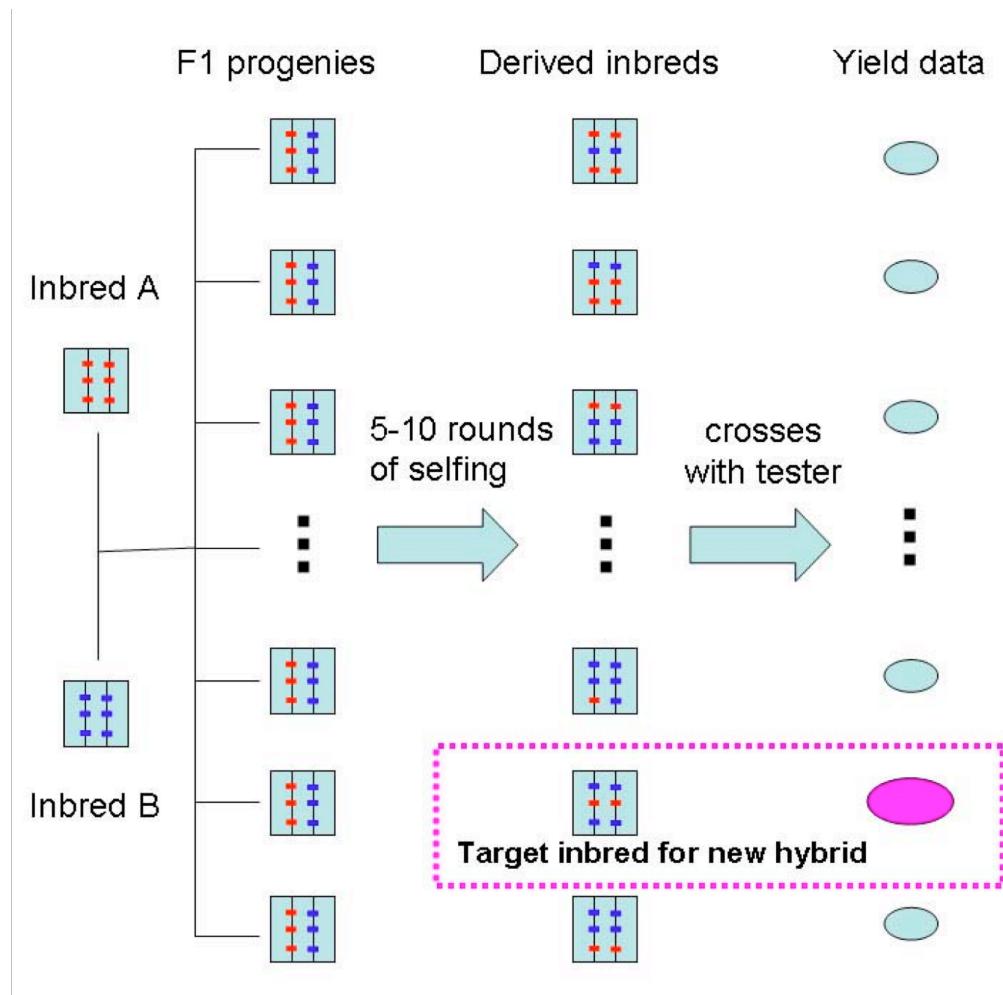


Figure S3. Pedigree Breeding. Inbred A and B from same heterotic group are crossed to produce F1 progenies, which are then selfed for 5 to 10 generations. The derived inbreds are then crossed with tester from another heterotic group. New inbred lines are selected based on the yield performance of the hybrids resulting from these test crosses.



SUPPLEMENTARY TABLES

Table S1. Summary of re-sequencing coverage.

Inbred Names	Yield (Giga base)	% Bases mapped	%Genome coverage	% Gene region coverage	Effective Depth (X)
Zheng 58	12,463,247,122	81.85	85.90	88.96	4.98
Chang7-2	13,463,549,694	75.88	82.99	84.72	4.99
178	13,514,836,532	77.05	83.93	86.06	5.08
5003	13,422,191,476	78.82	86.67	89.13	5.17
478	13,744,504,166	78.73	84.35	85.92	5.28
MO17	17,078,047,650	82.75	86.91	88.82	6.90

Table S2. Summary of indels in genic region.

	total	6bp	5bp	4bp	3bp	2bp	1bp
CDS	663	88	13	19	253	45	245
intron	10436	270	333	649	1029	1888	6267
Promoter	16546	525	579	1056	1887	2965	9534
UTR	2533	86	120	193	321	502	1311

Table S3. Low SNP diversity chromosomal blocks.

chromosomes	start(Mb)	end(Mb)	Length of block(Mb)	average SNP density
chr0	0.3	1.7	1.4	0.00183
chr0	2.1	3.2	1.1	0.00207
chr0	11	15	4	0.00197
chr1	123.8	125.5	1.7	0.00194
chr1	128.1	138.9	10.8	0.00192
chr1	142.3	143.6	1.3	0.00217
chr1	152.2	153.5	1.3	0.00208
chr1	218.5	219.8	1.3	0.00208
chr1	299.6	300.9	1.3	0.00201
chr2	35.4	36.6	1.2	0.00207
chr2	65.4	67.7	2.3	0.00199
chr2	72.7	82.6	9.9	0.00146
chr2	83.2	89.7	6.5	0.00153
chr2	94	98.3	4.3	0.00144
chr2	99.2	101.9	2.7	0.00181
chr2	105.3	106.5	1.2	0.00191
chr2	108.6	109.6	1	0.00214
chr2	121.2	122.9	1.7	0.00222
chr2	124	126	2	0.00193
chr2	128.5	130.3	1.8	0.00191
chr2	131	138.1	7.1	0.00137
chr2	153.4	155.6	2.2	0.00205
chr2	158.2	160.6	2.4	0.00135
chr2	160.8	162	1.2	0.00202
chr2	162.4	164.2	1.8	0.00126
chr3	25.9	27.2	1.3	0.00161
chr3	51.5	52.8	1.3	0.00211
chr3	60.9	63.1	2.2	0.00194
chr3	70.3	74.8	4.5	0.00193
chr3	87.9	89.3	1.4	0.00197
chr3	98.1	101.6	3.5	0.00188
chr3	139.8	141.3	1.5	0.00211
chr4	39.7	41.7	2	0.00168
chr4	45.5	46.8	1.3	0.002
chr4	47.3	49.5	2.2	0.00211
chr4	64.8	66.5	1.7	0.00162
chr4	71.4	73	1.6	0.00216
chr4	79.7	81.8	2.1	0.00185
chr4	95.1	97.4	2.3	0.00185
chr4	99.7	102.1	2.4	0.00181

chr4	104.3	107.7	3.4	0.0021
chr4	112.8	117.2	4.4	0.00161
chr4	118.3	119.4	1.1	0.00193
chr4	119.8	121.7	1.9	0.00204
chr4	124.6	126.2	1.6	0.00194
chr4	166.5	167.6	1.1	0.00187
chr4	186.3	193.1	6.8	0.00198
chr4	199.5	200.5	1	0.00188
chr5	34.3	36.3	2	0.00148
chr5	37.8	41.8	4	0.0014
chr5	42.3	45.4	3.1	0.00156
chr5	47.8	50.7	2.9	0.00205
chr5	56.1	57.3	1.2	0.00197
chr5	58.8	61.1	2.3	0.00204
chr5	62.3	63.6	1.3	0.00176
chr5	66.2	68.4	2.2	0.00188
chr5	72.4	73.4	1	0.00225
chr5	75.3	83.3	8	0.00149
chr5	86.8	88.7	1.9	0.00178
chr5	94.3	96.2	1.9	0.00159
chr5	97.9	99.6	1.7	0.00163
chr5	99.7	103	3.3	0.00199
chr5	104.6	106.1	1.5	0.00217
chr5	113.2	126.6	13.4	0.00153
chr5	127.1	128.6	1.5	0.00197
chr5	131.8	134.8	3	0.00173
chr5	148.1	149.5	1.4	0.00212
chr5	151.8	154.3	2.5	0.00193
chr5	160.3	161.9	1.6	0.00193
chr6	27.4	28.7	1.3	0.00215
chr6	32.5	34	1.5	0.00194
chr6	39.4	45.2	5.8	0.00174
chr6	49.5	53.5	4	0.00163
chr6	134.3	135.5	1.2	0.00204
chr7	38.9	40.9	2	0.00176
chr7	50.3	52.1	1.8	0.00212
chr7	57.9	63.9	6	0.00202
chr7	68.2	71.4	3.2	0.00142
chr7	75.8	79.9	4.1	0.00201
chr7	144.4	145.8	1.4	0.00162
chr7	170.4	171.6	1.2	0.00222
chr8	0	4.1	4.1	0.00178
chr8	40	44.3	4.3	0.00193
chr8	45	47.3	2.3	0.00205

chr8	53.4	55.9	2.5	0.00189
chr8	59.8	61.7	1.9	0.00198
chr8	64.4	66.5	2.1	0.00184
chr8	76.3	77.5	1.2	0.00203
chr8	81.4	82.5	1.1	0.00216
chr8	144.8	145.8	1	0.00216
chr8	152.8	156.3	3.5	0.00134
chr9	51.5	53.3	1.8	0.00215
chr9	64.8	69.2	4.4	0.00199
chr9	109.5	111.6	2.1	0.00177
chr9	151.2	152.9	1.7	0.00186
chr10	31.9	33.3	1.4	0.00205
chr10	42.7	43.7	1	0.00225
chr10	93.6	95.5	1.9	0.00167
chr10	99.7	102.7	3	0.00154
chr10	103.4	105.7	2.3	0.00173
chr10	134.6	135.6	1	0.00214

Table S4. PAV genes list and their pattern of deletion in six inbred lines.

gene ID	chromosome	Zheng58	Chang7-2	178	5003	478	Mo17
GRMZM2G703469	1	-	-	+	+	+	-
GRMZM2G465680	1	+	+	-	+	+	+
GRMZM2G703478	1	+	+	+	+	+	-
GRMZM2G343767	1	-	+	+	+	+	+
GRMZM2G378130	1	+	+	-	+	+	+
GRMZM2G445630	1	+	+	+	+	+	-
GRMZM2G109586	1	+	+	+	+	+	-
GRMZM2G031560	1	+	+	+	+	+	-
GRMZM2G305267	1	-	+	+	+	-	+
GRMZM2G335358	1	-	+	-	+	+	+
GRMZM2G064597	1	-	+	-	+	+	+
GRMZM2G417867	1	+	+	-	+	+	+
GRMZM2G021433	1	-	+	+	+	-	+
GRMZM2G703646	1	+	+	-	+	+	+
GRMZM2G004041	1	+	-	+	+	+	+
GRMZM2G067370	1	+	-	+	+	+	+
GRMZM2G125052	1	+	+	+	+	+	-
GRMZM2G166234	1	+	+	-	+	+	+
GRMZM2G428599	1	-	+	+	+	+	+
GRMZM2G399325	1	-	+	+	+	+	+
GRMZM2G104494	1	+	-	+	+	+	+
GRMZM2G350793	1	+	-	+	-	+	+
GRMZM2G115952	1	+	-	+	+	+	+
GRMZM2G126574	1	+	+	+	-	+	-
GRMZM2G013842	1	+	-	+	+	+	+
GRMZM2G136277	1	+	+	-	+	+	+
GRMZM2G129597	1	+	-	-	+	+	-
GRMZM2G153404	1	+	+	+	+	-	+
GRMZM2G116254	1	+	+	+	+	-	+
GRMZM2G386460	1	+	+	+	+	-	+
GRMZM2G703888	1	+	+	+	+	-	+
GRMZM2G115961	1	+	-	+	-	-	+
GRMZM2G704039	1	+	+	+	-	-	+
GRMZM2G100726	1	-	+	-	-	-	+
GRMZM2G155738	1	-	+	+	+	+	+
GRMZM2G155760	1	+	-	+	+	-	+
AC200627.3_FG005	1	+	-	+	+	+	+
GRMZM2G108828	1	-	+	-	-	+	-
GRMZM2G143317	1	-	-	-	+	+	+
GRMZM2G392563	1	+	-	-	+	+	+
GRMZM2G159353	1	-	+	+	-	-	+

AC203966.5_FG002	1	+	+	+	+	+	-	+
GRMZM2G463280	2	+	+	+	-	+	+	-
GRMZM2G039961	2	+	+	-	+	+	+	+
AC217283.2_FG004	2	+	-	+	+	+	+	+
GRMZM2G108698	2	+	+	-	+	+	-	-
GRMZM2G159896	2	+	+	+	+	+	+	-
GRMZM2G116701	2	-	+	-	+	+	+	-
GRMZM2G115630	2	+	-	+	+	+	+	+
GRMZM2G007256	2	-	+	+	+	+	+	+
GRMZM2G463267	2	+	+	+	-	+	+	-
GRMZM2G162266	2	+	+	+	-	+	+	-
GRMZM2G162230	2	+	+	+	-	+	+	-
GRMZM2G702948	2	+	+	+	+	+	+	-
GRMZM2G148147	2	+	+	-	+	+	+	+
GRMZM2G309188	2	+	+	+	+	+	+	-
GRMZM2G450496	2	+	+	+	-	-	-	-
GRMZM2G020183	2	+	-	+	+	+	+	+
GRMZM2G703190	2	+	-	+	+	+	+	+
GRMZM2G164704	2	+	-	+	+	+	+	+
GRMZM2G346757	2	+	+	-	+	+	+	+
AC195825.3_FG001	2	-	+	-	+	-	+	+
GRMZM2G036547	2	+	-	+	+	+	+	+
GRMZM2G115388	2	+	-	+	+	+	+	+
GRMZM2G025971	2	+	+	-	+	+	+	+
GRMZM2G587376	2	+	+	+	+	+	-	-
GRMZM2G351827	2	-	+	+	+	+	+	+
GRMZM2G119241	2	+	+	+	+	+	+	-
GRMZM2G449669	2	-	-	-	-	-	-	-
GRMZM2G044438	2	-	+	+	+	+	+	+
GRMZM2G358619	2	+	+	+	+	+	-	-
GRMZM2G038024	2	+	+	+	+	+	-	+
GRMZM2G372058	2	+	-	+	+	+	+	+
GRMZM2G428659	2	+	+	+	+	+	+	-
GRMZM2G513206	2	+	+	+	+	+	-	-
GRMZM2G140665	2	+	-	+	+	+	+	+
AC217293.3_FG007	2	+	-	+	+	+	+	+
GRMZM2G007860	2	-	-	-	+	-	-	-
GRMZM2G309503	2	-	-	-	+	-	-	-
GRMZM2G094662	2	-	-	-	+	-	-	-
GRMZM2G396357	2	+	-	-	+	-	-	+
GRMZM2G106493	3	+	+	+	-	-	-	+
AC209243.2_FG002	3	+	+	-	+	-	-	-
GRMZM2G102770	3	+	+	+	+	+	+	-
GRMZM2G338721	3	+	-	+	+	+	+	+

GRMZM2G429964	3	+	+	+	+	-	+
AC229993.1_FG009	3	-	-	+	+	-	+
GRMZM2G019965	3	+	+	+	+	-	+
GRMZM2G146708	3	-	+	+	+	+	+
GRMZM2G364410	3	+	-	+	+	-	-
GRMZM2G016351	3	+	+	-	+	+	+
GRMZM2G144189	3	+	-	+	+	+	+
GRMZM2G360579	3	+	+	-	-	-	+
GRMZM2G044503	3	+	+	-	+	+	+
GRMZM2G042855	3	-	+	-	+	+	+
GRMZM2G129403	3	-	-	-	-	-	-
GRMZM2G701738	3	+	+	+	+	+	-
GRMZM2G016598	3	+	-	+	+	+	+
GRMZM2G701746	3	-	+	+	+	+	+
GRMZM2G104523	3	+	-	+	+	+	+
GRMZM2G041544	3	-	+	+	+	+	+
GRMZM2G470731	3	+	+	+	+	+	-
GRMZM2G396418	3	-	-	+	-	-	+
GRMZM2G180509	3	+	-	+	+	+	+
GRMZM2G162274	3	+	-	+	+	+	+
GRMZM2G077375	3	-	+	-	+	-	-
GRMZM2G348434	3	-	+	-	+	+	+
GRMZM2G007666	4	+	-	+	+	+	+
GRMZM2G007583	4	+	-	+	+	+	+
GRMZM2G702403	4	-	-	-	+	+	-
GRMZM2G054415	4	-	+	-	+	+	+
AC196974.3_FG008	4	+	-	+	+	+	+
GRMZM2G316553	4	+	-	+	+	+	+
GRMZM2G358153	4	-	+	+	+	+	+
GRMZM2G469499	4	+	-	+	+	+	+
GRMZM2G702379	4	-	+	-	+	+	-
GRMZM2G324671	4	+	+	+	-	+	+
GRMZM2G123257	4	+	+	+	+	-	+
GRMZM2G043162	4	-	-	+	+	+	+
GRMZM2G326560	4	+	-	+	+	+	+
AC191692.3_FG001	4	-	-	-	+	+	+
AC208920.3_FG001	4	+	+	+	+	-	+
GRMZM2G498141	4	-	+	+	+	+	+
GRMZM2G127690	4	-	+	+	+	+	-
GRMZM2G313854	4	-	+	+	+	+	+
GRMZM2G542205	4	+	+	+	+	+	-
GRMZM2G071396	4	-	-	+	+	-	-
GRMZM2G109830	4	+	+	+	+	-	+
GRMZM2G042181	4	+	-	-	-	-	+

GRMZM2G332697	4	+	+	+	+	+	-	+
GRMZM2G454184	4	+	+	+	-	-	-	+
GRMZM2G316555	4	+	+	+	+	-	-	-
GRMZM2G702761	4	+	+	+	+	-	-	+
GRMZM2G702783	4	-	+	-	+	-	-	+
AC209971.4_FG003	4	+	-	+	+	+	+	+
GRMZM2G130256	4	+	-	+	+	+	-	-
GRMZM2G025931	4	-	-	-	-	-	-	-
GRMZM2G470863	4	+	+	+	+	-	-	+
GRMZM2G054422	5	+	-	+	+	+	+	+
AC190834.3_FG005	5	-	+	+	+	-	-	+
GRMZM2G309624	5	-	+	+	+	-	-	-
GRMZM2G030821	5	-	+	+	-	-	-	-
GRMZM2G144024	5	+	+	-	+	+	+	+
GRMZM2G012865	5	-	+	+	-	-	-	+
GRMZM2G350471	5	+	-	+	+	+	+	+
AC190526.3_FG004	5	+	+	+	+	+	+	-
GRMZM2G351716	5	+	+	+	+	+	-	-
GRMZM2G317610	5	+	+	+	+	+	+	-
GRMZM2G051673	5	+	+	-	+	+	+	+
GRMZM2G362609	5	+	+	+	+	+	+	-
GRMZM2G701395	5	+	-	+	+	+	+	+
GRMZM2G701452	5	-	-	-	-	-	-	+
GRMZM2G054805	5	-	+	-	+	+	+	-
AC196025.3_FG009	5	+	+	+	+	-	-	+
GRMZM2G432266	5	+	+	-	+	+	+	+
GRMZM2G702064	5	+	+	+	+	+	+	-
GRMZM2G456268	5	-	-	+	-	-	-	+
GRMZM2G465957	5	+	+	+	+	+	+	-
AC212667.3_FG005	5	+	-	+	+	+	+	+
GRMZM2G037595	5	-	+	+	+	+	+	+
GRMZM2G175875	5	+	+	-	+	+	+	+
AC195458.3_FG001	5	-	+	+	-	-	-	+
GRMZM2G481049	5	+	+	-	+	+	+	+
GRMZM2G325623	6	+	-	+	+	+	+	+
GRMZM2G161761	6	+	+	+	+	+	+	-
GRMZM2G378167	6	+	+	+	-	+	+	+
GRMZM2G160853	6	-	+	-	+	+	+	+
GRMZM2G098226	6	+	+	-	+	+	+	+
GRMZM2G047382	6	+	+	-	+	+	+	+
GRMZM2G356378	6	+	+	+	+	+	+	-
GRMZM2G003461	6	+	+	+	+	+	+	-
GRMZM2G134020	6	+	+	+	+	+	+	-
GRMZM2G403828	6	+	+	+	+	+	+	-

GRMZM2G403813	6	+	+	+	+	+	+	-
GRMZM2G451679	6	+	+	+	+	+	+	-
GRMZM2G150524	6	+	+	+	+	+	+	-
GRMZM2G050768	6	+	+	+	+	+	+	-
GRMZM2G390512	6	+	+	+	+	+	+	-
GRMZM2G066978	6	+	+	+	+	+	+	-
GRMZM2G066932	6	+	+	+	+	+	+	-
GRMZM2G048791	6	+	+	+	+	+	+	-
GRMZM2G122520	6	+	+	+	+	+	+	-
GRMZM2G076943	6	+	+	+	+	+	+	-
GRMZM2G051686	6	+	+	+	+	+	+	-
GRMZM2G156578	6	+	+	+	+	+	+	-
GRMZM2G009792	6	+	+	+	+	+	+	-
GRMZM2G082560	6	+	+	+	+	+	+	-
GRMZM2G320152	6	+	+	+	+	+	+	-
GRMZM2G134749	6	+	-	+	+	+	+	+
GRMZM2G471970	6	+	+	+	+	+	+	-
GRMZM2G428420	6	+	-	+	+	+	+	+
GRMZM2G412577	6	+	-	+	+	+	+	+
GRMZM2G700957	6	+	+	-	+	+	+	+
GRMZM2G434561	6	+	-	+	+	+	+	+
GRMZM2G700968	6	+	-	+	-	+	+	-
AC200287.4_FG006	6	+	-	+	+	+	+	+
GRMZM2G034469	6	+	-	+	+	+	+	+
GRMZM2G169376	6	+	-	+	+	+	+	+
GRMZM2G300080	6	+	-	+	+	+	+	+
GRMZM2G300077	6	+	-	+	+	+	+	+
GRMZM2G303865	6	+	-	+	+	+	+	+
GRMZM2G016727	6	+	+	+	+	+	-	+
GRMZM2G331316	6	-	+	-	+	-	-	-
GRMZM2G476323	6	+	+	-	+	+	+	+
AC194824.2_FG003	6	+	+	-	+	+	+	+
GRMZM2G445881	6	+	+	-	+	+	+	+
GRMZM2G129166	6	+	-	+	+	+	+	+
GRMZM2G041694	6	+	-	-	-	-	+	+
AC205122.4_FG006	7	+	+	+	-	-	+	+
GRMZM2G096868	7	+	-	+	+	+	+	+
GRMZM2G030189	7	+	-	+	+	+	+	+
GRMZM2G117281	7	+	+	+	-	+	+	+
GRMZM2G700149	7	-	-	+	+	-	-	-
GRMZM2G129092	7	+	-	-	+	+	-	-
GRMZM2G083285	7	+	+	+	-	-	-	-
GRMZM2G382273	7	+	+	+	-	-	-	-
GRMZM2G055009	7	-	-	+	-	-	-	-

AC202110.3_FG004	7	-	+	-	+	+	+	-
GRMZM2G334162	7	-	+	-	+	+	+	-
GRMZM2G329334	7	+	+	+	+	+	+	-
GRMZM2G435015	7	+	+	+	+	+	-	+
GRMZM2G351484	7	+	+	+	+	+	-	+
GRMZM2G336694	8	+	+	-	+	+	+	+
GRMZM2G006290	8	+	-	+	+	+	+	+
GRMZM2G700603	8	+	+	+	+	+	+	-
GRMZM2G405844	8	+	+	-	+	+	-	-
GRMZM2G009732	8	+	+	-	+	+	+	+
GRMZM2G402708	8	+	+	-	+	+	+	+
GRMZM2G061403	8	+	+	-	+	+	+	+
GRMZM2G132088	8	+	+	+	+	+	+	-
GRMZM2G172396	8	+	+	+	+	+	-	-
GRMZM2G171346	8	+	-	+	+	+	+	+
GRMZM2G162727	8	+	-	+	+	+	+	+
GRMZM2G083875	8	+	+	+	-	+	+	+
GRMZM2G356523	8	+	+	-	+	+	+	+
GRMZM2G303168	8	+	-	+	+	+	+	+
GRMZM2G043855	8	+	+	-	+	+	+	+
GRMZM2G700664	8	+	-	+	+	+	+	-
GRMZM2G458650	8	-	+	+	+	+	+	+
GRMZM2G307756	8	+	-	+	+	+	+	+
GRMZM2G101053	8	+	+	-	+	+	+	+
GRMZM2G101080	8	+	+	-	+	+	+	+
GRMZM2G700756	8	+	+	-	+	+	+	+
AC233916.1_FG002	8	+	+	-	+	+	+	+
GRMZM2G439238	8	+	+	+	+	+	+	-
GRMZM2G700765	8	-	+	+	+	+	+	+
GRMZM2G700803	8	-	+	+	+	+	+	+
GRMZM2G120951	8	+	+	+	-	+	+	+
AC188583.4_FG003	9	+	-	-	+	+	+	+
GRMZM2G703044	9	+	-	+	+	+	+	-
GRMZM2G703370	9	+	-	+	+	+	+	-
GRMZM2G096464	9	+	+	+	-	+	+	+
GRMZM2G703552	9	+	+	-	+	+	+	-
GRMZM2G015645	9	+	+	+	+	+	+	-
GRMZM2G109399	9	+	+	-	+	+	+	+
GRMZM2G704171	9	+	-	+	+	+	-	+
GRMZM2G134049	9	+	+	-	+	+	+	+
GRMZM2G416535	9	+	-	+	+	+	+	+
GRMZM2G148216	9	+	+	+	-	+	+	+
GRMZM2G078924	9	-	-	+	-	+	-	-
GRMZM2G457428	9	+	-	+	+	+	+	+

GRMZM2G124409	9	+	-	+	+	+	+	+
GRMZM2G134279	9	+	+	+	-	+	+	+
GRMZM2G036349	9	+	-	+	+	+	+	+
GRMZM2G438606	9	+	+	+	+	+	+	-
AC234175.1_FG009	10	+	+	+	+	+	+	-
GRMZM2G005134	10	+	+	-	+	-	+	+
GRMZM2G084278	10	+	+	-	+	+	+	+
AC214791.2_FG002	10	+	+	+	+	+	+	-
GRMZM2G440965	10	+	-	+	+	+	+	+
GRMZM2G440972	10	+	-	+	+	+	+	+
GRMZM2G700927	10	+	+	+	+	+	+	-
GRMZM2G117319	10	-	+	-	+	+	+	-
GRMZM2G008977	10	-	+	-	+	+	+	-
GRMZM2G074309	10	-	+	-	+	+	+	-
AC193645.3_FG006	10	+	+	-	+	+	+	+
GRMZM2G451765	10	-	-	+	+	+	+	+
GRMZM2G098677	10	+	+	-	+	+	+	+
GRMZM2G098697	10	+	+	-	+	+	+	+
GRMZM2G397785	10	+	+	-	+	+	+	+
GRMZM2G157448	10	+	+	+	+	+	-	+
AC217051.3_FG002	10	+	+	-	+	+	+	+
GRMZM2G042811	10	+	-	+	+	+	+	+
GRMZM2G418875	10	+	-	+	+	+	+	+
AC219002.2_FG004	10	+	-	+	+	+	+	+
GRMZM2G168263	10	+	-	+	+	+	+	+
GRMZM2G435924	10	+	-	+	+	+	+	+
GRMZM2G135378	10	+	-	+	+	+	+	+
GRMZM2G125476	10	+	+	+	+	+	-	+
GRMZM2G107299	10	+	-	+	+	+	+	-
GRMZM2G054591	10	-	-	+	+	+	+	-
GRMZM2G031280	10	-	+	+	+	+	+	-
GRMZM2G456618	10	+	-	+	+	+	+	+
GRMZM2G438178	10	+	+	+	+	+	-	+
GRMZM2G480282	10	-	+	+	+	+	+	+
GRMZM2G370905	10	+	-	+	+	+	+	+

Note: “+” means present, and “-”means absent

Table S5. Novel Genes missing in the B73 reference genome.

Gene_name	Gene_leng(CDS)	Fragment_name	fragment length	similarity with Bacteria protein	similarity with plant protein	similarity with B73 genome (protein)	depth in resequencing	mean depth for paralog region on genome	coverage for paralog region on genome	Function
BGIB73PAVG000440	150	BGIZmNSC003266	1157	-	68.42	87.18	16.19	20.72	100	-
BGIB73PAVG000003	165	BGIZmNSC004712	4627	-	85.45	-	41.32	-	-	-
BGIB73PAVG000047	2280	BGIZmNSC004708	4549	-	68.76	-	22.02	-	-	-
BGIB73PAVG000273	3693	BGIZmNSC004711	4378	-	59.98	-	36.75	-	-	IPR001320; Ionotropic glutamate receptor; IPR001828; Extracellular ligand-binding receptor
BGIB73PAVG000035	231	BGIZmNSC004710	4377	100	55.26	-	27.22	-	-	IPR000477; RNA-directed DNA polymerase (reverse transcriptase); IPR000953; Chromo domain; IPR001584; Integrase, catalytic core; IPR005162; Retrotransposon gag protein
BGIB73PAVG000054	519	BGIZmNSC004710	4377	61.29	54.9	-	23.7	-	-	IPR020040; Ribosomal protein L6, alpha-beta domain
BGIB73PAVG000060	285	BGIZmNSC004710	4377	100	51.06	-	23.61	-	-	IPR005484; Ribosomal protein L18/L5
BGIB73PAVG000171	378	BGIZmNSC004710	4377	60.94	-	-	26.79	-	-	IPR000630; Ribosomal protein S8
BGIB73PAVG000573	588	BGIZmNSC004710	4377	-	60.78	-	29.48	-	-	IPR000218; Ribosomal protein L14b/L23e
BGIB73PAVG000574	465	BGIZmNSC004710	4377	78.21	58.82	-	27.43	-	-	IPR002132; Ribosomal protein L5
BGIB73PAVG000208	3216	BGIZmNSC004705	4258	-	60.71	-	18.43	-	-	IPR000477; RNA-directed DNA polymerase (reverse transcriptase); IPR000953; Chromo domain; IPR001584; Integrase, catalytic core
BGIB73PAVG000572	300	BGIZmNSC004695	3764	-	-	-	16.08	-	-	-
BGIB73PAVG000095	381	BGIZmNSC004700	3693	-	-	-	19.81	-	-	-
BGIB73PAVG000190	603	BGIZmNSC004701	3682	-	54.69	-	45.51	-	-	-
BGIB73PAVG000050	1083	BGIZmNSC004693	3418	-	99.72	-	24.5	-	-	-
BGIB73PAVG000117	1185	BGIZmNSC004692	3408	-	100	-	26.27	-	-	IPR001932; Protein phosphatase 2C-related; IPR014045; Protein phosphatase 2C, N-terminal
BGIB73PAVG000215	1647	BGIZmNSC004687	3264	-	100	-	24.72	-	-	IPR002921; Lipase, class 3
BGIB73PAVG000167	210	BGIZmNSC004684	3038	-	66.67	-	19.23	-	-	-
BGIB73PAVG000076	1401	BGIZmNSC004680	2985	-	80	85.92	28.7	33.61	100	-
BGIB73PAVG000224	2538	BGIZmNSC004677	2949	-	68.54	-	29.84	-	-	IPR008587; Protein of unknown function DUF869, plant
BGIB73PAVG000290	2691	BGIZmNSC004671	2912	-	56.84	83.39	21.15	49.88	100	IPR000477; RNA-directed DNA polymerase (reverse transcriptase); IPR001584; Integrase, catalytic core
BGIB73PAVG000192	771	BGIZmNSC004673	2906	-	56.12	-	17.9	-	-	IPR001584; Integrase, catalytic core
BGIB73PAVG000024	690	BGIZmNSC004675	2903	-	81.08	92.63	27.43	44.28	100	-
BGIB73PAVG000028	2805	BGIZmNSC004674	2896	-	52.35	-	17.1	-	-	IPR000719; Protein kinase, catalytic domain; IPR001611; Leucine-rich repeat; IPR002290; Serine/threonine-protein kinase domain; IPR003591; Leucine-rich repeat, typical subtype; IPR017442; Serine/threonine-protein kinase-like domain; IPR020635; Tyrosine-protein kinase subgroup, catalytic domain
BGIB73PAVG000570	657	BGIZmNSC004670	2847	50.86	-	-	19.64	-	-	IPR000847; HTH transcriptional regulator, LysR; IPR005119; LysR, substrate-binding
BGIB73PAVG000571	909	BGIZmNSC004670	2847	-	-	-	19.12	-	-	IPR000477; RNA-directed DNA polymerase (reverse transcriptase)
BGIB73PAVG000275	1407	BGIZmNSC004676	2817	-	51.74	-	39.64	-	-	-
BGIB73PAVG000569	267	BGIZmNSC004665	2778	-	52.08	91.34	21.63	50.61	100	-
BGIB73PAVG000568	1800	BGIZmNSC004663	2762	-	-	-	20.61	-	-	IPR001736; Phospholipase D/Transphosphatidylase
BGIB73PAVG000122	204	BGIZmNSC004661	2749	-	-	83.17	15.06	34.07	100	-
BGIB73PAVG000040	1098	BGIZmNSC004662	2748	-	57.6	-	26.21	-	-	IPR001433; Oxidoreductase FAD/NAD(P)-binding; IPR008333; Oxidoreductase FAD-binding region; IPR017927; Ferredoxin reductase-type FAD-binding
BGIB73PAVG000128	378	BGIZmNSC004662	2748	-	-	84.94	18.53	11.69	100	-
BGIB73PAVG000567	1107	BGIZmNSC004660	2742	-	-	-	24.05	-	-	IPR001001; DNA polymerase III, beta chain
BGIB73PAVG000566	417	BGIZmNSC004657	2705	-	-	-	19.94	-	-	-
BGIB73PAVG000565	1062	BGIZmNSC004655	2668	-	76.78	-	24.76	-	-	IPR000210; BTB/POZ-like; IPR013069; BTB/POZ
BGIB73PAVG000564	240	BGIZmNSC004658	2668	-	100	-	22.58	-	-	-
BGIB73PAVG000058	1920	BGIZmNSC004653	2651	-	82.74	-	24.98	-	-	Trehalose-phosphatase
BGIB73PAVG000563	1428	BGIZmNSC004647	2624	-	-	-	19.74	-	-	IPR005656; MngE/PrpD
BGIB73PAVG000101	258	BGIZmNSC004645	2619	-	-	85.71	17.65	12.64	100	-
BGIB73PAVG000562	1287	BGIZmNSC004650	2604	-	-	-	24.07	-	-	IPR000583; Mannose-6-phosphate isomerase, type II, C-terminal; IPR005835; Nucleotidyl transferase
BGIB73PAVG000561	516	BGIZmNSC004644	2600	-	100	-	22.2	-	-	IPR001179; Peptidyl-prolyl cis-trans isomerase, FKBP-type
BGIB73PAVG000560	486	BGIZmNSC004638	2567	-	-	-	19.2	-	-	IPR001140; ABC transporter, transmembrane region; IPR003439; ABC transporter-like; IPR017940; ABC transporter integral membrane type 1
BGIB73PAVG000559	597	BGIZmNSC004637	2540	-	89.52	-	34.3	-	-	-
BGIB73PAVG000558	558	BGIZmNSC004639	2525	-	86.11	-	35.91	-	-	-
BGIB73PAVG000556	270	BGIZmNSC004635	2411	53.33	-	-	27.87	-	-	-
BGIB73PAVG000557	738	BGIZmNSC004635	2411	-	-	-	23.93	-	-	IPR000524; HTH transcriptional regulator, GntR; IPR011663; UbiC transcription regulator-associated
BGIB73PAVG000555	222	BGIZmNSC004626	2370	-	53.85	-	29.02	-	-	-
BGIB73PAVG000154	1134	BGIZmNSC004605	2269	-	99.74	-	30.26	-	-	IPR007657; Glycosyltransferase AER61, uncharacterised
BGIB73PAVG000554	378	BGIZmNSC004597	2219	-	-	82.05	26.09	36.32	100	-
BGIB73PAVG000553	588	BGIZmNSC004589	2180	-	75.38	-	34.85	-	-	IPR003128; Villin headpiece
BGIB73PAVG000143	483	BGIZmNSC004583	2156	-	62.6	86.6	26.96	35.55	100	-
BGIB73PAVG000015	231	BGIZmNSC004577	2141	-	98.51	91.69	21.95	48.41	100	IPR007238; DNA primase, large subunit, eukaryotic/archaeal
BGIB73PAVG000552	909	BGIZmNSC004573	2137	50.31	-	-	20.6	-	-	IPR000847; HTH transcriptional regulator, LysR; IPR005119; LysR, substrate-binding
BGIB73PAVG000109	135	BGIZmNSC004570	2129	-	76.09	-	23.24	-	-	-
BGIB73PAVG000549	282	BGIZmNSC004566	2107	-	-	-	22.24	-	-	-
BGIB73PAVG000550	864	BGIZmNSC004566	2107	-	-	-	25.08	-	-	-
BGIB73PAVG000551	492	BGIZmNSC004566	2107	57.47	-	-	17.51	-	-	-
BGIB73PAVG000548	981	BGIZmNSC004563	2102	-	-	-	22.23	-	-	-
BGIB73PAVG000131	645	BGIZmNSC004557	2096	-	78.7	-	20.15	-	-	IPR004883; Lateral organ boundaries, LOB
BGIB73PAVG000077	1440	BGIZmNSC004558	2095	-	88.22	85.62	21.87	25.7	100	IPR001106; Phenylalanine/histidine ammonia-lyase
BGIB73PAVG000547	249	BGIZmNSC004547	2078	-	63.16	84.17	30.09	5.55	100	IPR005202; GRAS transcription factor
BGIB73PAVG000200	1086	BGIZmNSC004528	2018	-	77.65	-	28.13	-	-	IPR001611; Leucine-rich repeat; IPR003591; Leucine-rich repeat, typical subtype; IPR013210; Leucine-rich repeat, N-terminal
BGIB73PAVG000079	1836	BGIZmNSC004551	2074	-	99.44	-	30.63	-	-	IPR006108; 3-hydroxyacyl-CoA dehydrogenase, C-terminal
BGIB73PAVG000546	327	BGIZmNSC004548	2070	-	75.93	-	22.54	-	-	IPR013103; Reverse transcriptase, RNA-dependent DNA polymerase
BGIB73PAVG000183	306	BGIZmNSC004550	2070	-	67.19	84.29	19.06	9.5	100	-
BGIB73PAVG000087	264	BGIZmNSC004542	2059	-	-	81.41	14.46	41.68	100	-
BGIB73PAVG000012	999	BGIZmNSC004539	2056	-	90.03	-	23.48	-	-	-
BGIB73PAVG000114	1710	BGIZmNSC004541	2050	-	99.82	-	34.13	-	-	IPR005202; GRAS transcription factor
BGIB73PAVG000544	1005	BGIZmNSC004540	2046	-	-	-	19.09	-	-	IPR000847; HTH transcriptional regulator, LysR; IPR005119; LysR, substrate-binding
BGIB73PAVG000545	222	BGIZmNSC004540	2046	-	-	-	14.56	-	-	-
BGIB73PAVG000543	1497	BGIZmNSC004532	2042	-	68.88	-	36.41	-	-	IPR001611; Leucine-rich repeat
BGIB73PAVG000019	480	BGIZmNSC004531	2026	-	99.38	-	30.74	-	-	IPR003406; Glycosyl transferase, family 14
BGIB73PAVG000542	1155	BGIZmNSC004529	2020	-	-	-	25.01	-	-	-
BGIB73PAVG000541	528	BGIZmNSC004526	2018	62	-	-	22.89	-	-	IPR002539; MaoC-like dehydratase
BGIB73PAVG000200	1086	BGIZmNSC004528	2018	-	77.65	-	28.13	-	-	IPR002528; Multi antimicrobial extrusion protein MatE

BGIB73PAVG000210	957	BGIZmNSC004524	2013	-	83.78	-	22.69	-	-	-	IPR009730; Micro-fibrillar-associated 1, C-terminal
BGIB73PAVG000540	258	BGIZmNSC004516	2005	-	88.37	-	25.27	-	-	-	-
BGIB73PAVG000237	1674	BGIZmNSC004513	2004	-	78.32	90.33	20.78	40.47	100	-	IPR000571; Zinc finger, CCCH-type
BGIB73PAVG000539	1500	BGIZmNSC004518	2004	-	-	-	25.73	-	-	-	-
BGIB73PAVG000538	1386	BGIZmNSC004515	2002	-	-	-	20.87	-	-	-	-
BGIB73PAVG000274	1728	BGIZmNSC004511	1999	-	-	-	19.94	-	-	-	IPR000477; RNA-directed DNA polymerase (reverse transcriptase); IPR005135;
BGIB73PAVG000158	888	BGIZmNSC004509	1985	-	-	-	20.42	-	-	-	Endonuclease/exonuclease/phosphatase
BGIB73PAVG000254	552	BGIZmNSC004506	1981	-	56.41	-	36.91	-	-	-	IPR000873; AMP-dependent synthetase/ligase
BGIB73PAVG000537	771	BGIZmNSC004496	1956	-	-	-	24.76	-	-	-	IPR000847; HTH transcriptional regulator, LysR;
BGIB73PAVG000205	1284	BGIZmNSC004500	1954	-	68.21	-	33.39	-	-	-	IPR005119; LysR, substrate-binding
BGIB73PAVG000001	957	BGIZmNSC004487	1942	-	-	-	29.17	-	-	-	IPR001128; Cytochrome P450
BGIB73PAVG000535	603	BGIZmNSC004485	1937	-	-	-	19.92	-	-	-	IPR008713; Bacteriophage lambda NinG
BGIB73PAVG000536	381	BGIZmNSC004485	1937	-	-	-	19.3	-	-	-	-
BGIB73PAVG000534	405	BGIZmNSC004483	1909	-	-	-	28.18	-	-	-	-
BGIB73PAVG000260	210	BGIZmNSC004480	1908	-	72.86	87.86	30.38	51.73	100	-	IPR006564; Zinc finger, PMZ-type; IPR007527; Zinc finger, SWIM-type
BGIB73PAVG000159	432	BGIZmNSC004477	1903	-	75	-	34	-	-	-	IPR003676; Auxin responsive SAUR protein
BGIB73PAVG000282	129	BGIZmNSC004468	1895	-	59.18	-	19.05	-	-	-	-
BGIB73PAVG000209	1239	BGIZmNSC004463	1886	-	100	-	30.09	-	-	-	IPR001296; Glycosyl transferase, group 1
BGIB73PAVG000271	585	BGIZmNSC004467	1886	-	-	-	40.12	-	-	-	IPR005135; Endonuclease/exonuclease/phosphatase
BGIB73PAVG000102	258	BGIZmNSC004458	1882	-	-	93.8	9.19	6.79	100	-	-
BGIB73PAVG000120	1140	BGIZmNSC004454	1880	-	85.53	-	18.75	-	-	-	IPR005299; SAM dependent carboxyl methyltransferase
BGIB73PAVG000216	321	BGIZmNSC004456	1876	96.55	62.96	-	20	-	-	-	IPR000440; NADH:ubiquinone/plastoquinone oxidoreductase, chain 3
BGIB73PAVG000147	162	BGIZmNSC004453	1870	-	57.41	91.98	29.02	17.13	100	-	-
BGIB73PAVG000278	141	BGIZmNSC004453	1870	-	70.83	89.58	27.09	8.32	100	-	-
BGIB73PAVG000533	606	BGIZmNSC004451	1864	-	-	-	22.55	-	-	-	IPR019302; Nucleotide-binding protein, predicted, TIR-like
BGIB73PAVG000532	348	BGIZmNSC004446	1860	52.24	-	-	18.41	-	-	-	-
BGIB73PAVG000242	561	BGIZmNSC004449	1860	-	52.88	-	37.07	-	-	-	-
BGIB73PAVG000529	285	BGIZmNSC004433	1840	58.62	-	-	21.95	-	-	-	-
BGIB73PAVG000530	501	BGIZmNSC004433	1840	-	-	-	18.66	-	-	-	IPR007481; Stringent starvation protein B
BGIB73PAVG000531	804	BGIZmNSC004435	1840	-	90.05	90.64	29.32	50.82	100	-	IPR000719; Protein kinase, catalytic domain;
BGIB73PAVG000055	330	BGIZmNSC004439	1837	98.33	56.48	-	30.93	-	-	-	IPR002290; Serine/threonine-protein kinase domain;
BGIB73PAVG00201	318	BGIZmNSC004439	1837	100	61.9	-	21.25	-	-	-	IPR001971; Ribosomal protein S11
BGIB73PAVG00170	1386	BGIZmNSC004432	1835	-	74.78	-	32.41	-	-	-	IPR022885; Pentatricopeptide repeat
BGIB73PAVG000528	663	BGIZmNSC004423	1832	-	-	-	19.07	-	-	-	IPR008775; Phytanoyl-CoA dioxygenase
BGIB73PAVG000526	225	BGIZmNSC004426	1826	-	-	-	19.5	-	-	-	-
BGIB73PAVG000527	201	BGIZmNSC004426	1826	-	98.15	85.89	19.53	43.95	100	-	-
BGIB73PAVG00195	405	BGIZmNSC004422	1818	-	59.48	82.46	39.4	42.73	100	-	-
BGIB73PAVG000227	1185	BGIZmNSC004416	1815	-	60.1	-	16.75	-	-	-	IPR001128; Cytochrome P450
BGIB73PAVG000525	543	BGIZmNSC004415	1813	-	-	-	22.53	-	-	-	-
BGIB73PAVG000111	465	BGIZmNSC004414	1812	61.11	-	-	25.5	-	-	-	IPR001790; Ribosomal protein L10
BGIB73PAVG000127	891	BGIZmNSC004413	1808	-	52.24	-	16.9	-	-	-	IPR001810; Cyclin-like F-box
BGIB73PAVG000133	246	BGIZmNSC004410	1807	-	-	-	30.42	-	-	-	-
BGIB73PAVG000119	312	BGIZmNSC004409	1806	-	-	71.43	-	19.94	-	-	-
BGIB73PAVG000524	888	BGIZmNSC004400	1781	-	-	-	24.94	-	-	-	IPR000073; Alpha/beta hydrolase fold-1
BGIB73PAVG000523	702	BGIZmNSC004387	1768	-	98.28	-	26.02	-	-	-	IPR001305; Heat shock protein DnaJ, cysteine-rich region; IPR002939; Chaperone DnaJ, C-terminal
BGIB73PAVG000113	258	BGIZmNSC004381	1747	100	61.54	-	22.34	-	-	-	IPR007644; RNA polymerase, beta subunit, protrusion;
BGIB73PAVG000118	351	BGIZmNSC004381	1747	95.16	55.17	-	25.75	-	-	-	IPR007645; RNA polymerase Rpb2, domain 3
BGIB73PAVG000136	360	BGIZmNSC004381	1747	93.75	51.67	-	26.63	-	-	-	IPR007120; DNA-directed RNA polymerase, subunit 2, domain 6
BGIB73PAVG000110	264	BGIZmNSC004370	1738	-	60.56	-	24.02	-	-	-	IPR007120; DNA-directed RNA polymerase, subunit 2, domain 6
BGIB73PAVG000231	1215	BGIZmNSC004373	1737	-	50.72	-	24.04	-	-	-	-
BGIB73PAVG000090	288	BGIZmNSC004368	1732	-	-	-	34.36	-	-	-	-
BGIB73PAVG000144	945	BGIZmNSC004363	1724	-	-	-	23	-	-	-	IPR001005; SANT, DNA-binding; IPR014778; Myb, DNA-binding; IPR017930; Myb-type HTH DNA-binding domain
BGIB73PAVG000522	1326	BGIZmNSC004360	1722	-	-	-	17.48	-	-	-	IPR011701; Major facilitator superfamily MFS-1
BGIB73PAVG000521	264	BGIZmNSC004362	1721	-	91.76	-	33.68	-	-	-	IPR000477; RNA-directed DNA polymerase (reverse transcriptase)
BGIB73PAVG000174	1602	BGIZmNSC004352	1714	-	55.62	82.1	26.92	52.06	100	-	-
BGIB73PAVG00243	213	BGIZmNSC004347	1710	-	54	85.37	16.05	59.54	100	-	-
BGIB73PAVG000520	876	BGIZmNSC004346	1704	-	-	-	22.62	-	-	-	IPR003675; Abortive infection protein
BGIB73PAVG000014	348	BGIZmNSC004339	1697	-	75.29	87.69	31.42	41.57	100	-	-
BGIB73PAVG000235	927	BGIZmNSC004343	1696	-	-	-	43.21	-	-	-	-
BGIB73PAVG000056	726	BGIZmNSC004337	1693	-	98.74	-	20.84	-	-	-	IPR000836; Phosphoribosyltransferase
BGIB73PAVG000123	336	BGIZmNSC004331	1692	-	75.23	83.78	16.31	17.79	100	-	IPR008906; HAT dimerisation
BGIB73PAVG000519	585	BGIZmNSC004330	1685	-	-	-	21.36	-	-	-	IPR007210; ABC-type glycine betaine transport system, substrate-binding region
BGIB73PAVG000220	1122	BGIZmNSC004323	1677	-	62.37	-	30.46	-	-	-	IPR001810; Cyclin-like F-box
BGIB73PAVG000517	924	BGIZmNSC004315	1669	-	-	-	23.56	-	-	-	IPR002872; Proline dehydrogenase
BGIB73PAVG000518	339	BGIZmNSC004315	1669	-	-	-	17.22	-	-	-	IPR005119; LysR, substrate-binding
BGIB73PAVG000516	480	BGIZmNSC004309	1661	67.07	65	-	21.8	-	-	-	IPR009783; Protein of unknown function DUF1348
BGIB73PAVG000515	615	BGIZmNSC004296	1644	63.21	50.45	-	21.16	-	-	-	IPR001750; NADH:ubiquinone/plastoquinone oxidoreductase
BGIB73PAVG000514	1416	BGIZmNSC004291	1640	-	-	-	25.45	-	-	-	-
BGIB73PAVG000238	468	BGIZmNSC004278	1620	-	-	-	25.45	-	-	-	IPR001912; Ribosomal protein S4; IPR002942; RNA-binding S4
BGIB73PAVG000513	1296	BGIZmNSC004276	1619	-	51.13	-	17.88	-	-	-	IPR011766; Thiamine pyrophosphate enzyme, C-terminal TPP-binding; IPR012000; Thiamine pyrophosphate enzyme, central region; IPR012001; Thiamine pyrophosphate enzyme, N-terminal TPP binding region
BGIB73PAVG000225	1356	BGIZmNSC004265	1612	-	-	-	23.31	-	-	-	IPR004217; Mitochondrial inner membrane translocase complex, Tim8/9/10/13-zinc finger-like
BGIB73PAVG000132	192	BGIZmNSC004262	1607	-	100	94.76	19.28	49.78	100	-	IPR001901; Protein secE/secG-gamma protein; IPR005824; KOW; IPR00645; Transcription antitermination protein, NusG, N-terminal
BGIB73PAVG000513	846	BGIZmNSC004254	1601	-	-	-	23.09	-	-	-	-
BGIB73PAVG000045	459	BGIZmNSC004255	1598	-	87.96	89.83	17.79	22.09	100	-	-
BGIB73PAVG000511	801	BGIZmNSC004253	1597	-	-	-	18.62	-	-	-	IPR007833; Capsule polysaccharide biosynthesis
BGIB73PAVG000512	474	BGIZmNSC004253	1597	-	-	-	20.75	-	-	-	IPR001451; Bacterial transferase hexapeptide repeat
BGIB73PAVG000510	414	BGIZmNSC004252	1596	-	-	-	18.66	-	-	-	-
BGIB73PAVG000065	462	BGIZmNSC004259	1588	-	100	-	27.23	-	-	-	IPR000916; Bet v 1 allergen
BGIB73PAVG000508	726	BGIZmNSC004241	1588	-	-	-	24.43	-	-	-	IPR002198; Short-chain dehydrogenase/reductase SDR
BGIB73PAVG000509	528	BGIZmNSC004241	1588	-	-	-	22.86	-	-	-	IPR001647; Transcriptional regulator, TetR-like, DNA-binding, bacterial/archaeal
BGIB73PAVG000507	735	BGIZmNSC004243	1580	-	-	-	47.64	-	-	-	-
BGIB73PAVG000506	573	BGIZmNSC004226	1577	-	100	-	26.28	-	-	-	IPR006636; Heat shock chaperonin-binding; IPR015360; XPC-binding domain
BGIB73PAVG000505	1224	BGIZmNSC004227	1576	-	-	-	22.16	-	-	-	-
BGIB73PAVG000504	537	BGIZmNSC004219	1569	-	-	-	20.64	-	-	-	IPR003779; Carboxymuconolactone decarboxylase
BGIB73PAVG000223	915	BGIZmNSC004214	1567	-	55.56	-	21.48	-	-	-	IPR000836; Phosphoribosyltransferase
BGIB73PAVG000503	216	BGIZmNSC004215	1567	-	100	-	33.62	-	-	-	IPR010608; Protein of unknown function DUF1195

BGIB73PAVG000501	597	BGIZmNSC004222	1566	53.77	67.71	-	86.19	-	-	IPR001584; Integrase, catalytic core
BGIB73PAVG000502	267	BGIZmNSC004222	1566	100	77.91	-	81.39	-	-	IPR002514; Transposase IS3/IS911
BGIB73PAVG000500	996	BGIZmNSC004207	1561	-	100	-	22.37	-	-	IPR000719; Protein kinase, catalytic domain;
BGIB73PAVG000499	1257	BGIZmNSC004202	1555	-	-	-	19.39	-	-	IPR002290; Serine/threonine-protein kinase domain;
BGIB73PAVG000497	690	BGIZmNSC004191	1553	-	-	-	17.6	-	-	IPR017442; Serine/threonine-protein kinase-like domain;
BGIB73PAVG000498	750	BGIZmNSC004191	1553	-	-	-	20.65	-	-	IPR020635; Tyrosine-protein kinase, subgroup, catalytic
BGIB73PAVG000212	1002	BGIZmNSC004182	1545	-	99.7	-	18.48	-	-	domain
BGIB73PAVG000116	789	BGIZmNSC004179	1543	-	99.57	-	29.85	-	-	IPR000583; Glutamine amidotransferase, class-II;
BGIB73PAVG000121	666	BGIZmNSC004177	1542	-	100	-	23.58	-	-	IPR01962; Asparagine synthase; IPR017932;
BGIB73PAVG000085	303	BGIZmNSC004175	1538	-	-	87.57	21.17	26.43	100	IPR0010546; Protein of unknown function DUF1120
BGIB73PAVG000218	579	BGIZmNSC004165	1532	-	97.93	-	20.69	-	-	IPR000073; Alpha/beta hydrolase fold-1
BGIB73PAVG000018	303	BGIZmNSC004167	1530	-	100	94.09	25.34	48.47	100	IPR001199; Cytochrome b5
BGIB73PAVG000496	216	BGIZmNSC004162	1529	50.85	-	-	19.27	-	-	IPR001236; Lactate/malate dehydrogenase
BGIB73PAVG000142	276	BGIZmNSC004164	1529	-	100	90.99	27.82	36.93	100	IPR006912; Protein of unknown function DUF635
BGIB73PAVG000073	189	BGIZmNSC004156	1521	79.41	100	-	28.14	-	-	IPR003673; CoA-transferase family III
BGIB73PAVG000165	543	BGIZmNSC004154	1516	-	51.2	83.38	34.06	20.89	100	IPR003377; Trehalose-phosphatase
BGIB73PAVG000083	357	BGIZmNSC004141	1506	-	-	86.81	20.24	23.11	100	IPR001210; Cyclin-like F-box
BGIB73PAVG000495	1017	BGIZmNSC004122	1496	-	-	-	20.33	-	-	IPR005135; Endonuclease/exonuclease/phosphatase
BGIB73PAVG000031	237	BGIZmNSC004109	1491	-	83.54	-	27.96	-	-	IPR001789; Signal transduction response regulator, receiver region
BGIB73PAVG000494	294	BGIZmNSC004105	1486	-	80.39	87.58	27.32	37.13	100	IPR001810; Cyclin-like F-box
BGIB73PAVG000493	324	BGIZmNSC004102	1485	-	-	-	19.19	-	-	IPR003400; Biopolymer transport protein ExbD/TolR
BGIB73PAVG000492	384	BGIZmNSC004088	1474	84.06	-	-	27.78	-	-	IPR001584; Integrase, catalytic core
BGIB73PAVG000211	669	BGIZmNSC004082	1471	-	100	86.47	20.24	42.21	100	IPR001789; Histone-like bacterial DNA-binding protein
BGIB73PAVG000490	702	BGIZmNSC004076	1467	-	-	-	17.75	-	-	IPR002683; Photosystem II oxygen evolving complex protein PsbP
BGIB73PAVG000491	327	BGIZmNSC004076	1467	-	-	-	23.84	-	-	IPR000043; S-adenosyl-L-homocysteine hydrolase; IPR015878; S-adenosyl-L-homocysteine hydrolase
BGIB73PAVG000488	453	BGIZmNSC004068	1463	-	-	-	22.09	-	-	IPR001849; Pleckstrin homology
BGIB73PAVG000489	375	BGIZmNSC004071	1463	75.76	-	-	23.87	-	-	IPR004827; Basic-leucine zipper (bZIP) transcription factor; IPR011700; Basic leucine zipper
BGIB73PAVG000199	198	BGIZmNSC004056	1457	-	61.54	83.1	20.9	18.39	100	IPR002171; Ribosomal protein L2
BGIB73PAVG000112	1236	BGIZmNSC004055	1456	-	-	-	18.97	-	-	IPR013025; Ribosomal protein L25/L23
BGIB73PAVG000072	432	BGIZmNSC004041	1451	-	-	-	16.67	-	-	IPR0005135; Endonuclease/exonuclease/phosphatase
BGIB73PAVG000189	630	BGIZmNSC004044	1451	-	57.14	-	31.63	-	-	IPR001170; Basic leucine zipper
BGIB73PAVG000486	393	BGIZmNSC004035	1449	-	78.26	-	22.35	-	-	IPR001236; Lactate/malate dehydrogenase
BGIB73PAVG000487	210	BGIZmNSC004039	1449	-	-	-	18.88	-	-	IPR001789; Signal transduction response regulator, receiver region
BGIB73PAVG000033	480	BGIZmNSC004032	1446	-	63.35	80.92	22.77	34.16	100	IPR001810; Cyclin-like F-box
BGIB73PAVG000256	615	BGIZmNSC004020	1440	-	57.62	-	35.88	-	-	IPR001210; Cyclin-like F-box
BGIB73PAVG000161	684	BGIZmNSC004013	1439	-	-	-	12.71	-	-	IPR001789; Histone-like bacterial DNA-binding protein
BGIB73PAVG000485	396	BGIZmNSC004008	1437	-	-	-	16.79	-	-	IPR001810; Cyclin-like F-box
BGIB73PAVG000484	360	BGIZmNSC004010	1435	-	90.2	-	24.02	-	-	IPR001789; Histone-like bacterial DNA-binding protein
BGIB73PAVG000483	375	BGIZmNSC004005	1432	-	51.43	87.08	24.06	0.76	33.24	IPR001810; Cyclin-like F-box
BGIB73PAVG000141	753	BGIZmNSC004003	1431	-	99.6	-	21.77	-	-	IPR001210; Cyclin-like F-box
BGIB73PAVG000169	699	BGIZmNSC003985	1423	57.14	58.37	-	18.48	-	-	IPR001789; Histone-like bacterial DNA-binding protein
BGIB73PAVG000482	315	BGIZmNSC003985	1423	100	-	-	24.84	-	-	IPR001810; Cyclin-like F-box
BGIB73PAVG000267	396	BGIZmNSC003986	1423	-	70.45	-	31.52	-	-	IPR001789; Histone-like bacterial DNA-binding protein
BGIB73PAVG000126	531	BGIZmNSC003983	1420	-	-	-	28.26	-	-	IPR001810; Cyclin-like F-box
BGIB73PAVG000481	1167	BGIZmNSC003977	1418	-	-	-	22.55	-	-	IPR001789; Histone-like bacterial DNA-binding protein
BGIB73PAVG000480	237	BGIZmNSC003976	1417	97.96	-	-	16.33	-	-	IPR0000119; Histone-like bacterial DNA-binding protein
BGIB73PAVG000175	612	BGIZmNSC003966	1411	-	100	-	28.71	-	-	IPR002683; Photosystem II oxygen evolving complex protein PsbP
BGIB73PAVG000479	264	BGIZmNSC003964	1409	-	94.32	88.35	29.98	33.41	100	IPR000043; S-adenosyl-L-homocysteine hydrolase; IPR015878; S-adenosyl-L-homocysteine hydrolase
BGIB73PAVG000478	351	BGIZmNSC003941	1388	90	-	-	23.39	-	-	IPR000043; S-adenosyl-L-homocysteine hydrolase; IPR015878; S-adenosyl-L-homocysteine hydrolase
BGIB73PAVG000477	528	BGIZmNSC003929	1381	-	83.94	-	27.49	-	-	IPR000043; S-adenosyl-L-homocysteine hydrolase; IPR015878; S-adenosyl-L-homocysteine hydrolase
BGIB73PAVG000476	1233	BGIZmNSC003915	1368	-	99.27	-	19.9	-	-	IPR000043; S-adenosyl-L-homocysteine hydrolase; IPR015878; S-adenosyl-L-homocysteine hydrolase
BGIB73PAVG000475	354	BGIZmNSC003906	1363	-	100	-	26.73	-	-	IPR000043; S-adenosyl-L-homocysteine hydrolase; IPR015878; S-adenosyl-L-homocysteine hydrolase
BGIB73PAVG000007	1350	BGIZmNSC003893	1357	-	65.91	-	19.98	-	-	NAD binding
BGIB73PAVG000474	606	BGIZmNSC003875	1349	-	100	-	34.23	-	-	IPR001563; Peptidase S10, serine carboxypeptidase
BGIB73PAVG000226	873	BGIZmNSC003869	1346	-	-	-	20.02	-	-	IPR001810; Cyclin-like F-box
BGIB73PAVG000473	558	BGIZmNSC003848	1336	-	-	-	26.89	-	-	IPR000043; S-adenosyl-L-homocysteine hydrolase; IPR015878; S-adenosyl-L-homocysteine hydrolase
BGIB73PAVG000089	240	BGIZmNSC003826	1328	-	-	-	30.35	-	-	IPR001810; Cyclin-like F-box
BGIB73PAVG000029	327	BGIZmNSC003821	1326	-	100	91.33	26.56	44.95	100	IPR001848; Ribosomal protein S10
BGIB73PAVG000472	402	BGIZmNSC003823	1325	-	77.78	87.87	19.35	29.7	100	IPR003851; Zinc finger, Dof-type
BGIB73PAVG000094	264	BGIZmNSC003818	1323	-	-	-	23.9	-	-	IPR000719; Protein kinase, catalytic domain; IPR002290; Serine/threonine-protein kinase domain; IPR017442; Serine/threonine-protein kinase-like domain; IPR020635; Tyrosine-protein kinase, subgroup, catalytic
BGIB73PAVG000471	1041	BGIZmNSC003793	1315	-	72.73	-	27.94	-	-	IPR000511; ATP-citrate lyase/succinyl-CoA ligase; IPR013650; ATP-grasp fold, succinyl-CoA synthetase-type
BGIB73PAVG000020	957	BGIZmNSC003796	1315	-	60.37	-	18.97	-	-	IPR000477; RNA-directed DNA polymerase (reverse transcriptase)
BGIB73PAVG000193	411	BGIZmNSC003794	1314	-	57.97	81.85	31.64	47.86	100	IPR001720; DNA-directed RNA polymerase, subunit 2, domain 6; IPR007641; RNA polymerase Rpb2, domain 7
BGIB73PAVG000178	450	BGIZmNSC003754	1302	-	62.99	90.67	15.88	7.7	100	IPR006912; Protein of unknown function DUF635
BGIB73PAVG000064	273	BGIZmNSC003758	1301	-	-	86.25	23.82	28.14	100	IPR001810; Cyclin-like F-box
BGIB73PAVG000270	636	BGIZmNSC003750	1300	60.53	55.41	-	23.31	-	-	IPR001810; Cyclin-like F-box
BGIB73PAVG000164	555	BGIZmNSC003748	1299	-	71.12	86.89	17.97	33.21	100	IPR001810; Cyclin-like F-box
BGIB73PAVG000264	336	BGIZmNSC003725	1291	-	-	-	22.31	-	-	IPR001810; Cyclin-like F-box
BGIB73PAVG000286	195	BGIZmNSC003725	1291	-	55.38	-	21.34	-	-	IPR001810; Cyclin-like F-box
BGIB73PAVG000470	534	BGIZmNSC003707	1284	-	81.65	88.21	23.4	52.64	100	IPR001810; Cyclin-like F-box
BGIB73PAVG000152	246	BGIZmNSC003706	1282	-	61.64	90.69	38.98	45.11	100	IPR001810; Cyclin-like F-box
BGIB73PAVG000469	435	BGIZmNSC003685	1274	70.67	-	-	18.43	-	-	IPR006657; Molybdopterin dinucleotide-binding region
BGIB73PAVG000106	303	BGIZmNSC003686	1273	-	-	-	33.79	-	-	IPR001881; EGF-like calcium-binding; IPR006210; EGF-like; IPR013091; EGF calcium-binding
BGIB73PAVG000041	1047	BGIZmNSC003687	1273	-	51.02	-	24.6	-	-	IPR005134; Uncharacterised protein family UPF0114, prokaryotic
BGIB73PAVG000468	426	BGIZmNSC003676	1271	53.52	-	-	22.97	-	-	IPR0017867; Protein-tyrosine phosphatase, low molecular weight
BGIB73PAVG000135	663	BGIZmNSC003679	1271	-	-	87.48	26.07	29.75	100	IPR001881; EGF-like calcium-binding; IPR006210; EGF-like; IPR013091; EGF calcium-binding
BGIB73PAVG000467	228	BGIZmNSC003670	1270	-	-	93.57	27.88	10.2	94.57	IPR005134; Uncharacterised protein family UPF0114, prokaryotic
BGIB73PAVG000026	183	BGIZmNSC003640	1262	-	96.72	94.22	21.43	41.51	100	IPR005493; Ribonuclease E inhibitor
BGIB73PAVG000466	384	BGIZmNSC003644	1261	54.93	-	-	23.61	-	-	IPR0005493; Ribonuclease E inhibitor
BGIB73PAVG000246	213	BGIZmNSC003635	1259	-	56.34	-	19.67	-	-	RRA0/Dimethylmenaquinone methyltransferase
BGIB73PAVG000465	294	BGIZmNSC003639	1259	-	-	-	20.04	-	-	IPR005134; Uncharacterised protein family UPF0114, prokaryotic
BGIB73PAVG000005	375	BGIZmNSC003632	1258	73.02	-	-	15.45	-	-	IPR0005493; Ribonuclease E inhibitor
BGIB73PAVG000239	555	BGIZmNSC003608	1252	-	56.76	-	17.16	-	-	IPR0005493; Ribonuclease E inhibitor
BGIB73PAVG000139	261	BGIZmNSC003594	1246	-	62.07	85.71	34.4	57.84	100	IPR0005493; Ribonuclease E inhibitor
BGIB73PAVG000464	291	BGIZmNSC003567	1240	90	-	-	19.06	-	-	IPR0005493; Ribonuclease E inhibitor
BGIB73PAVG000059	213	BGIZmNSC003557	1237	-	98.57	92.92	18.67	23.98	100	IPR0005493; Ribonuclease E inhibitor
BGIB73PAVG000277	150	BGIZmNSC003547	1236	-	62	90.67	20.37	15.55	100	IPR0005493; Ribonuclease E inhibitor
BGIB73PAVG000168	450	BGIZmNSC003553	1236	-	87.18	-	24.55	-	-	IPR001153; Barwin
BGIB73PAVG000202	324	BGIZmNSC003554	1236	-	68.57	83.47	14.			

BGIB73PAVG000463	714	BGIZmNSC003552	1233	-	82.7	92.51	29.82	55.86	100	IPR00403; Phosphatidylinositol 3-/4-kinase, catalytic
BGIB73PAVG000461	402	BGIZmNSC003536	1227	-	97.73	-	22.33	-	-	IPR005123; Oxoglutarate/iron-dependent oxygenase
BGIB73PAVG000069	1101	BGIZmNSC003512	1220	-	-	-	19.75	-	-	IPR004115; GAD domain; IPR004364; Aminoacyl-tRNA synthetase, class II (D/K/N); IPR004365; Nucleic acid binding, OB-fold, tRNA/helicase-type; IPR006195; Aminoacyl-tRNA synthetase, class II, conserved region
BGIB73PAVG000084	387	BGIZmNSC003507	1219	-	-	82.59	25.97	39.97	100	-
BGIB73PAVG000459	243	BGIZmNSC003504	1218	91.38	-	-	19.67	-	-	-
BGIB73PAVG000460	234	BGIZmNSC003504	1218	-	-	-	22.75	-	-	-
BGIB73PAVG000458	324	BGIZmNSC003499	1216	-	-	80.85	40.22	17.58	94.7	-
BGIB73PAVG000457	246	BGIZmNSC003489	1215	-	96.34	90.47	23.26	9.81	94.19	IPR000375; Dynamin central region
BGIB73PAVG000163	249	BGIZmNSC003461	1207	-	80.95	87.3	14.23	19.46	100	-
BGIB73PAVG000456	312	BGIZmNSC003454	1205	51.92	98.77	-	20.43	-	-	IPR003348; ATPase, anion-transporting
BGIB73PAVG000188	558	BGIZmNSC003462	1205	-	50.24	84.11	21.87	32.28	100	IPR000953; Chromo domain
BGIB73PAVG000455	798	BGIZmNSC003444	1200	-	82.71	-	26.23	-	-	IPR000719; Protein kinase, catalytic domain; IPR002290; Serine/threonine-protein kinase domain; IPR017442; Serine/threonine-protein kinase-like domain; IPR020635; Tyrosine-protein kinase, subgroup, catalytic domain
BGIB73PAVG000454	516	BGIZmNSC003430	1198	-	100	-	28.16	-	-	IPR006553; Leucine-rich repeat, cysteine-containing subtype
BGIB73PAVG000453	690	BGIZmNSC003426	1197	-	98.82	-	17.14	-	-	-
BGIB73PAVG000452	213	BGIZmNSC003429	1192	-	-	-	42.69	-	-	-
BGIB73PAVG000450	291	BGIZmNSC003404	1188	-	-	-	15.41	-	-	-
BGIB73PAVG000451	606	BGIZmNSC003406	1188	-	-	-	15.69	-	-	-
BGIB73PAVG000013	336	BGIZmNSC003389	1183	59.02	-	-	23.02	-	-	IPR006140; D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
BGIB73PAVG000448	324	BGIZmNSC003372	1182	-	-	-	15.72	-	-	-
BGIB73PAVG000446	498	BGIZmNSC003369	1181	-	-	-	19.75	-	-	-
BGIB73PAVG000447	267	BGIZmNSC003378	1181	-	-	-	30.37	-	-	-
BGIB73PAVG000075	132	BGIZmNSC003361	1177	-	-	90.32	16.15	11.08	100	-
BGIB73PAVG000449	309	BGIZmNSC003345	1174	-	-	-	15.22	-	-	-
BGIB73PAVG000444	795	BGIZmNSC003344	1172	-	-	-	30.34	-	-	IPR000525; Initiator Rep protein
BGIB73PAVG000443	447	BGIZmNSC003336	1171	-	100	-	24.19	-	-	IPR002885; Penatricopeptide repeat
BGIB73PAVG000067	234	BGIZmNSC003323	1170	-	89.61	91.76	16.09	38.05	100	IPR003388; Reticulon
BGIB73PAVG000023	324	BGIZmNSC003330	1170	-	-	91.67	28.87	28.84	100	-
BGIB73PAVG000442	432	BGIZmNSC003325	1169	-	100	88.63	25.09	47.13	100	IPR013746; Hydroxymethylglutaryl-coenzyme A synthase C-terminal
BGIB73PAVG000184	345	BGIZmNSC003294	1162	54.1	67.26	87.69	28.02	43.67	100	IPR013103; Reverse transcriptase, RNA-dependent DNA polymerase
BGIB73PAVG000182	300	BGIZmNSC003291	1161	64.29	73.27	91.09	32.86	45.48	100	IPR013103; Reverse transcriptase, RNA-dependent DNA polymerase
BGIB73PAVG000257	198	BGIZmNSC003291	1161	-	75.76	93.01	31.49	62.94	100	IPR013103; Reverse transcriptase, RNA-dependent DNA polymerase
BGIB73PAVG000140	234	BGIZmNSC003283	1160	-	60.26	91.3	16.51	31.54	100	-
BGIB73PAVG000137	306	BGIZmNSC003284	1160	-	61.76	86.22	24.34	43.47	100	-
BGIB73PAVG000268	393	BGIZmNSC003284	1160	-	54.55	93.47	25.1	30.5	100	-
BGIB73PAVG000441	435	BGIZmNSC003287	1160	54.55	52.43	-	21.49	-	-	IPR001196; Ribosomal protein L15
BGIB73PAVG000289	156	BGIZmNSC003278	1159	-	-	90.38	18.07	25.02	100	-
BGIB73PAVG000293	141	BGIZmNSC003281	1159	-	-	72.92	-	25.33	-	-
BGIB73PAVG000036	303	BGIZmNSC003217	1145	-	67.27	84.79	23.8	39.4	100	IPR002222; Ribosomal protein S19/S15
BGIB73PAVG000438	198	BGIZmNSC003199	1143	97.87	-	-	18.56	-	-	-
BGIB73PAVG000439	366	BGIZmNSC003199	1143	88.52	-	-	17.93	-	-	IPR003489; Ribosomal protein S30Ae/sigma 54 modulation protein
BGIB73PAVG000436	771	BGIZmNSC003194	1142	-	-	-	22.13	-	-	IPR001034; HTH transcriptional regulator, DeoR N-terminal; IPR014056; HTH transcriptional regulator, DeoR
BGIB73PAVG000437	474	BGIZmNSC003196	1142	-	-	89.34	15.25	20.37	100	-
BGIB73PAVG000115	501	BGIZmNSC003191	1141	-	-	-	14.34	-	-	IPR002219; Protein kinase C-like, phorbol ester/diacylglycerol binding; IPR011424; C1-like
BGIB73PAVG000433	408	BGIZmNSC003185	1139	79.17	-	-	16.42	-	-	IPR006656; Molybdopterin oxidoreductase; IPR006963; Molybdopterin oxidoreductase Fe4S4 region
BGIB73PAVG000434	651	BGIZmNSC003190	1139	-	-	-	22.97	-	-	IPR005838; Type III secretion system inner membrane P protein
BGIB73PAVG000435	225	BGIZmNSC003190	1139	97.87	-	-	20.8	-	-	IPR002191; Bacterial export protein Flq, family 3
BGIB73PAVG000071	96	BGIZmNSC003174	1137	-	81.25	94.74	17.35	35.64	100	-
BGIB73PAVG000432	939	BGIZmNSC003175	1137	-	-	-	16.87	-	-	IPR000847; HTH transcriptional regulator, LysR; IPR005119; LysR, substrate-binding
BGIB73PAVG000431	273	BGIZmNSC003158	1134	-	-	89.14	21.49	3.85	91.4	-
BGIB73PAVG000430	327	BGIZmNSC003159	1134	-	-	-	26.81	-	-	-
BGIB73PAVG000429	432	BGIZmNSC003135	1129	-	85.82	-	20.84	-	-	-
BGIB73PAVG000428	1014	BGIZmNSC003125	1127	-	-	-	20.65	-	-	IPR002656; Acetyltransferase 3
BGIB73PAVG000287	213	BGIZmNSC003118	1126	-	63.38	-	17.46	-	-	-
BGIB73PAVG000088	291	BGIZmNSC003107	1124	-	-	89.64	27.89	5.19	100	-
BGIB73PAVG000427	1011	BGIZmNSC003101	1122	-	-	-	15.82	-	-	IPR000015; Fimbrial biogenesis outer membrane usher protein
BGIB73PAVG000425	426	BGIZmNSC003091	1120	-	-	92.65	17.81	5.42	82.43	-
BGIB73PAVG000426	417	BGIZmNSC003093	1120	-	100	91.44	30.6	48.34	100	IPR000910; High mobility group, HMG1/HMG2
BGIB73PAVG000424	771	BGIZmNSC003083	1119	-	-	-	18.91	-	-	IPR013189; Glycosyl hydrolase family 32, C-terminal
BGIB73PAVG000263	303	BGIZmNSC003086	1119	-	53.12	-	26.41	-	-	-
BGIB73PAVG000241	540	BGIZmNSC003077	1117	-	-	-	15	-	-	-
BGIB73PAVG000422	384	BGIZmNSC003068	1116	-	-	82.63	22.49	11.98	100	IPR003245; Plastocyanin-like
BGIB73PAVG000423	933	BGIZmNSC003070	1116	-	66.99	90.55	13.76	16.94	100	IPR001128; Cytochrome P450
BGIB73PAVG000221	540	BGIZmNSC003054	1115	-	66.07	88.51	14.77	30.58	100	IPR000504; RNA recognition motif, RNP-1
BGIB73PAVG000173	432	BGIZmNSC003031	1112	-	73.79	84.92	20.06	41.25	100	IPR005162; Retrotransposon gag protein
BGIB73PAVG000009	819	BGIZmNSC003036	1112	-	58.87	-	25.16	-	-	IPR002182; NB-ARC
BGIB73PAVG000420	360	BGIZmNSC003041	1112	90.16	-	-	29.14	-	-	-
BGIB73PAVG000418	303	BGIZmNSC003026	1111	-	-	85.81	15.93	24.63	100	-
BGIB73PAVG000419	756	BGIZmNSC003027	1111	-	-	-	20.17	-	-	IPR011701; Major facilitator superfamily MFS-1
BGIB73PAVG000417	816	BGIZmNSC003014	1109	-	62.06	-	31.89	-	-	IPR011684; Kipf1-like
BGIB73PAVG000074	438	BGIZmNSC003012	1108	65.85	-	-	19.14	-	-	IPR000664; Cystathione beta-synthase, core
BGIB73PAVG000416	507	BGIZmNSC002992	1105	-	-	-	19.15	-	-	-
BGIB73PAVG000415	507	BGIZmNSC002983	1104	-	-	-	20.08	-	-	IPR011747; Conserved hypothetical protein CHP02241, phage tail region protein
BGIB73PAVG000414	504	BGIZmNSC002981	1103	55.06	-	-	21.03	-	-	IPR008514; Virulence factor, secretion apparatus
BGIB73PAVG000108	702	BGIZmNSC002977	1102	-	-	-	38.06	-	-	IPR004330; Transcription factor, FAR1-related
BGIB73PAVG000412	459	BGIZmNSC002946	1097	-	-	-	26.89	-	-	IPR000182; GCN5-related N-acetyltransferase
BGIB73PAVG000413	333	BGIZmNSC002949	1097	-	100	-	29.31	-	-	-
BGIB73PAVG000411	336	BGIZmNSC002938	1096	-	100	-	23.08	-	-	-
BGIB73PAVG000409	261	BGIZmNSC002926	1094	-	-	-	16.9	-	-	-
BGIB73PAVG000410	405	BGIZmNSC002926	1094	-	-	-	23.38	-	-	-
BGIB73PAVG000039	588	BGIZmNSC002914	1092	59	54.46	-	23.32	-	-	IPR000866; Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen; IPR017936; Thioredoxin-like; IPR019479; Peroxiredoxin, C-terminal
BGIB73PAVG000048	1086	BGIZmNSC002900	1090	-	-	-	15.72	-	-	IPR004099; Pyridine nucleotide-disulphide oxidoreductase, dimerisation; IPR013027; FAD-dependent pyridine nucleotide-disulphide oxidoreductase
BGIB73PAVG000408	447	BGIZmNSC002891	1087	-	99.31	-	28.54	-	-	IPR013748; Replication factor C
BGIB73PAVG000197	423	BGIZmNSC002879	1086	-	-	-	25.33	-	-	-
BGIB73PAVG000407	309	BGIZmNSC002872	1085	-	100	-	18	-	-	IPR010608; Protein of unknown function DUF1195
BGIB73PAVG000006	141	BGIZmNSC002875	1084	-	89.13	83.49	33.29	39.55	100	-
BGIB73PAVG000269	396	BGIZmNSC002867	1083	-	63.64	84.24	28.41	26.72	100	-

BGIB73PAVG000406	771	BGIZmNSC002831	1076	-	-	-	17.68	-	-	-	
BGIB73PAVG000004	222	BGIZmNSC002827	1075	-	-	85.59	22.24	25.71	100	-	
BGIB73PAVG000405	459	BGIZmNSC002817	1073	58.75	-	-	23.01	-	-	-	
BGIB73PAVG000404	207	BGIZmNSC002803	1070	-	-	83.68	31.33	34.94	100	-	
BGIB73PAVG000081	393	BGIZmNSC002789	1069	-	-	90.73	15.84	12.41	100	-	
BGIB73PAVG000402	375	BGIZmNSC002779	1068	-	-	80.41	14.01	26.66	100	-	
BGIB73PAVG000403	957	BGIZmNSC002780	1068	-	-	18.3	-	-	-		
BGIB73PAVG00068	156	BGIZmNSC002777	1067	-	-	31.38	-	-	-		
BGIB73PAVG000134	222	BGIZmNSC002782	1067	-	-	85.63	21.36	28.26	100	-	
BGIB73PAVG000401	621	BGIZmNSC002761	1065	-	-	21.3	-	-	-		
BGIB73PAVG000400	426	BGIZmNSC002743	1061	-	-	16.14	-	-	-		IPR000644; Cystathione beta-synthase, core
BGIB73PAVG000002	972	BGIZmNSC002750	1061	-	-	59.94	-	-	-		
BGIB73PAVG000397	414	BGIZmNSC002733	1060	-	-	16.09	-	-	-		IPR0006175; Endoribonuclease L-PSP
BGIB73PAVG000398	294	BGIZmNSC002733	1060	63.33	-	-	15.8	-	-	3	IPR001638; Extracellular solute-binding protein, family
BGIB73PAVG000399	555	BGIZmNSC002734	1060	-	-	19.93	-	-	-		
BGIB73PAVG000397	372	BGIZmNSC002742	1060	-	-	88.33	32.66	36.2	100	-	
BGIB73PAVG000017	285	BGIZmNSC002727	1058	-	100	91.29	29.67	48.78	100	-	
BGIB73PAVG000155	327	BGIZmNSC002715	1056	-	67.96	83.7	29.99	32.59	100	-	
BGIB73PAVG000288	195	BGIZmNSC002699	1053	-	-	85.29	29.59	0	0		
BGIB73PAVG000396	306	BGIZmNSC002678	1052	-	-	11.37	-	-	-		
BGIB73PAVG000008	429	BGIZmNSC002679	1051	-	100	-	18.78	-	-		IPR001356; Homeobox; IPR005539; ELK
BGIB73PAVG000205	522	BGIZmNSC002662	1048	-	66.48	84.45	21.14	37.69	100	-	
BGIB73PAVG000395	282	BGIZmNSC002653	1046	-	-	88.7	10.27	9.68	100	-	
BGIB73PAVG000240	492	BGIZmNSC002650	1045	-	59.55	-	25.99	-	-		
BGIB73PAVG000070	96	BGIZmNSC002635	1044	-	84.38	93.67	27.95	5.78	64.56	-	
BGIB73PAVG000393	312	BGIZmNSC002634	1043	-	-	31.92	-	-	-		
BGIB73PAVG000394	681	BGIZmNSC002637	1043	-	-	25.53	-	-	-		IPR018769; Protein of unknown function DUF2345
BGIB73PAVG000279	144	BGIZmNSC002620	1041	-	60.42	87.5	14.07	39.42	100	-	
BGIB73PAVG000392	918	BGIZmNSC002622	1041	-	-	23.05	-	-	-		
BGIB73PAVG000443	288	BGIZmNSC002594	1037	-	100	90.14	30.56	40.35	100		IPR014876; DEK, C-terminal
BGIB73PAVG000251	636	BGIZmNSC002588	1036	-	-	86.21	23.68	22.35	100	-	
BGIB73PAVG000229	288	BGIZmNSC002555	1031	-	-	20.03	-	-	-		
BGIB73PAVG000391	336	BGIZmNSC002545	1030	-	100	88.62	18.49	29.14	100	-	
BGIB73PAVG000250	645	BGIZmNSC002520	1027	-	53.21	-	38.14	-	-		
BGIB73PAVG000266	288	BGIZmNSC002505	1024	-	-	18.52	-	-	-		
BGIB73PAVG000390	585	BGIZmNSC002492	1023	-	-	19.53	-	-	-		
BGIB73PAVG000280	147	BGIZmNSC002494	1023	-	54.17	-	35.39	-	-		
BGIB73PAVG000389	924	BGIZmNSC002496	1022	-	98.31	92.34	29.47	52.96	100	-	
BGIB73PAVG000386	507	BGIZmNSC002477	1021	-	-	18.47	-	-	-		
BGIB73PAVG000387	264	BGIZmNSC002479	1021	72.41	-	-	15.05	-	-		
BGIB73PAVG000388	825	BGIZmNSC002498	1021	-	66.18	-	79.49	-	-		IPR001878; Zinc finger, CCCH-type
BGIB73PAVG000385	354	BGIZmNSC002465	1020	-	-	15.11	-	-	-		IPR009457; Protein of unknown function DUF1084
BGIB73PAVG000232	531	BGIZmNSC002400	1012	-	100	-	16.02	-	-		IPR013103; Reverse transcriptase, RNA-dependent DNA polymerase
BGIB73PAVG000285	165	BGIZmNSC002475	1020	-	83.33	86.99	63.61	8.15	82.11		
BGIB73PAVG000384	846	BGIZmNSC002449	1018	-	-	18.7	-	-			IPR006992; Amidohydrolase 2
BGIB73PAVG000207	429	BGIZmNSC002452	1018	-	52.08	-	25.47	-	-		
BGIB73PAVG000228	237	BGIZmNSC002455	1018	-	100	-	20.35	-	-		IPR003614; Knottin; IPR008176; Gamma thionin
BGIB73PAVG000383	222	BGIZmNSC002439	1017	-	98.28	-	18.71	-	-		
BGIB73PAVG000382	489	BGIZmNSC002427	1015	70.45	-	-	23.22	-	-		IPR008331; Ferritin/Dps protein
BGIB73PAVG000232	531	BGIZmNSC002400	1012	-	100	-	16.02	-	-		
BGIB73PAVG000381	882	BGIZmNSC002394	1011	-	65.65	-	17.95	-	-		IPR002213; UDP-glucuronosyl/UDP-glucosyltransferase
BGIB73PAVG000062	249	BGIZmNSC002395	1011	-	100	-	21.73	-	-		IPR001563; Peptidase S10, serine carboxypeptidase
BGIB73PAVG000380	210	BGIZmNSC002381	1010	-	-	92.59	16.56	24.81	100	-	
BGIB73PAVG000148	210	BGIZmNSC002392	1010	-	58.57	-	22.18	-	-		
BGIB73PAVG000222	327	BGIZmNSC002377	1009	-	100	-	28.92	-	-		
BGIB73PAVG000379	204	BGIZmNSC002373	1008	100	-	-	18.64	-	-		IPR006110; RNA polymerase Rpb6
BGIB73PAVG000377	411	BGIZmNSC002325	1004	-	-	-	11.45	-	-		
BGIB73PAVG000378	219	BGIZmNSC002333	1004	-	-	-	14.28	-	-		
BGIB73PAVG000261	147	BGIZmNSC002319	1003	-	69.39	89.8	13.18	37.24	100	-	
BGIB73PAVG000376	327	BGIZmNSC002309	1001	-	87.07	-	21.49	-	-		IPR002110; Ankyrin repeat; IPR020683; Ankyrin repeat-containing domain
BGIB73PAVG000162	261	BGIZmNSC002286	999	55.17	-	-	12.1	-	-		
BGIB73PAVG000096	285	BGIZmNSC002293	999	-	-	85.91	22.51	26.51	100	-	
BGIB73PAVG000086	363	BGIZmNSC002263	996	-	-	91.48	18.65	8.3	100	-	
BGIB73PAVG000075	309	BGIZmNSC002253	994	-	-	-	22.07	-	-		
BGIB73PAVG000078	915	BGIZmNSC002230	992	-	59.67	-	20.81	-	-		IPR001135; NADH-quinone oxidoreductase, subunit D
BGIB73PAVG000074	369	BGIZmNSC002240	992	92.31	59.5	-	26.97	-	-		IPR005822; Ribosomal protein L13
BGIB73PAVG000010	339	BGIZmNSC002215	990	-	85.34	-	13.15	-	-		IPR001106; Phenylalanine/histidine ammonia-lyase
BGIB73PAVG000373	894	BGIZmNSC002217	990	-	-	-	16.81	-	-		
BGIB73PAVG000181	249	BGIZmNSC002199	989	-	-	-	23.39	-	-		
BGIB73PAVG000027	153	BGIZmNSC002202	989	-	-	95.04	24.18	11.65	97.16		
BGIB73PAVG000372	531	BGIZmNSC002189	988	-	-	-	24.12	-	-		IPR003779; Carboxymuconolactone decarboxylase
BGIB73PAVG000091	390	BGIZmNSC002183	987	-	-	-	17.88	-	-		
BGIB73PAVG000371	510	BGIZmNSC002179	986	-	-	98.82	-	27.87	-		IPR005123; Oxoglutarate/iron-dependent oxygenase
BGIB73PAVG000219	666	BGIZmNSC002180	986	-	-	76.8	-	15.1	-		IPR006747; Protein of unknown function DUF599
BGIB73PAVG000194	432	BGIZmNSC002160	985	-	64.08	84.88	25.37	12.54	100	-	
BGIB73PAVG000370	201	BGIZmNSC002171	985	-	100	-	22.26	-	-		
BGIB73PAVG000368	621	BGIZmNSC002152	983	-	-	-	18.15	-	-		
BGIB73PAVG000369	747	BGIZmNSC002153	983	-	-	-	17.33	-	-		IPR002678; NGG1p interacting factor 3, NIF3
BGIB73PAVG000185	345	BGIZmNSC002120	979	-	78.49	-	12.61	-	-		IPR013103; Reverse transcriptase, RNA-dependent DNA polymerase
BGIB73PAVG000258	198	BGIZmNSC002120	979	-	60.61	-	14.09	-	-		
BGIB73PAVG000367	240	BGIZmNSC002113	978	-	-	89.68	10.93	11.51	100	-	
BGIB73PAVG000252	567	BGIZmNSC002127	978	-	-	-	26.38	-	-		
BGIB73PAVG000366	240	BGIZmNSC002109	977	-	-	88.38	13.35	15.46	100	-	
BGIB73PAVG000365	531	BGIZmNSC002102	976	53.33	83.02	87.01	17.54	32.21	100		IPR000873; AMP-dependent synthetase/ligase
BGIB73PAVG000234	405	BGIZmNSC002104	976	-	-	-	27.79	-	-		
BGIB73PAVG000049	888	BGIZmNSC002081	974	-	62.08	-	18.41	-	-		IPR013149; Alcohol dehydrogenase, zinc-binding;
BGIB73PAVG000172	378	BGIZmNSC002084	974	-	-	93.42	19.99	9.95	100	-	IPR013154; Alcohol dehydrogenase GroE-like
BGIB73PAVG000364	447	BGIZmNSC002082	973	-	76.86	-	22.71	-	-		IPR007491; Protein of unknown function DUF537
BGIB73PAVG000060	147	BGIZmNSC002056	972	-	70.83	91.03	28.26	21.21	100	-	
BGIB73PAVG000030	318	BGIZmNSC002038	969	-	66.04	85.85	20.93	55.82	100		IPR002182; NB-ARC
BGIB73PAVG000092	414	BGIZmNSC002026	968	-	-	83.28	23.32	50.4	100	-	
BGIB73PAVG000151	225	BGIZmNSC002011	967	-	-	-	22.32	-	-		
BGIB73PAVG000363	201	BGIZmNSC002017	967	-	-	-	18.05	-	-		
BGIB73PAVG000362	315	BGIZmNSC001995	964	-	-	-	16.91	-	-		
BGIB73PAVG000360	675	BGIZmNSC001956	960	-	-	-	14.34	-	-		IPR018060; Helix-turn-helix, AraC domain
BGIB73PAVG000361	750	BGIZmNSC001961	960	51.91	-	-	19.07	-	-		IPR011708; Bacterial DNA polymerase III, alpha subunit
BGIB73PAVG000248	174	BGIZmNSC001946	958	-	-	84.69	23.41	45.51	100	-	
BGIB73PAVG000359	684	BGIZmNSC001937	957	-	89.04	92.03	29.66	60.1	100		IPR010918; AIR synthase related protein, C-terminal
BGIB73PAVG000357	339	BGIZmNSC001914	955	94.83	-	-	22.08	-	-		IPR019

BGIB73PAVG000350	180	BGIzmnNSC001773	938	-	-	81.01	24.76	48.47	100	-	
BGIB73PAVG000351	291	BGIzmnNSC001773	938	-	-	31.47	-	-	-	-	
BGIB73PAVG000230	381	BGIzmnNSC001750	937	-	100	-	19.69	-	-	IPR012946; X8	
BGIB73PAVG000348	630	BGIzmnNSC001759	937	-	-	-	23.73	-	-	IPR000891; Pyruvate carboxyltransferase	
BGIB73PAVG000177	273	BGIzmnNSC001743	936	57.63	76.09	91.56	21.82	28.5	100	IPR001584; Integrase, catalytic core	
BGIB73PAVG000145	234	BGIzmnNSC001708	932	-	69.44	83.26	23.21	33.91	100	-	
BGIB73PAVG000166	159	BGIzmnNSC001699	931	-	73.58	-	30.79	-	-	-	
BGIB73PAVG000347	393	BGIzmnNSC001693	930	-	-	-	12.22	-	-	-	
BGIB73PAVG000032	237	BGIzmnNSC001687	929	-	51.61	90.72	20.22	15.67	100	-	
BGIB73PAVG000146	231	BGIzmnNSC001653	926	-	85.9	87.03	19.63	39.91	100	-	
BGIB73PAVG000346	576	BGIzmnNSC001653	924	-	-	-	25.94	-	-	-	
BGIB73PAVG000345	699	BGIzmnNSC001620	923	-	-	-	18.34	-	-	IPR001155; NADH:flavin oxidoreductase/NADH oxidase, N-terminal	
BGIB73PAVG000217	678	BGIzmnNSC001629	923	-	-	-	23.86	-	-	IPR002586; Cobyrinic acid a,c-diamide synthase	
BGIB73PAVG000176	234	BGIzmnNSC001552	915	-	63.29	86.88	22.11	49.94	100	IPR004242; Transposon, En/Spm-like	
BGIB73PAVG000063	243	BGIzmnNSC001504	910	-	100	88.3	27.89	44.74	100	IPR001563; Peptidase S10, serine carboxypeptidase	
BGIB73PAVG000344	813	BGIzmnNSC001503	909	-	60.56	-	28.36	-	-	IPR005202; GRAS transcription factor	
BGIB73PAVG000213	579	BGIzmnNSC001490	908	-	99.48	-	33.58	-	-	IPR005527; Septum formation topological specificity factor MinE	
BGIB73PAVG000343	363	BGIzmnNSC001474	907	-	-	84.82	32.23	48.76	100	-	
BGIB73PAVG000130	288	BGIzmnNSC001476	907	-	54.74	87.14	26.27	43.08	100	-	
BGIB73PAVG000150	231	BGIzmnNSC001477	907	-	58.49	-	11.77	-	-	-	
BGIB73PAVG000342	345	BGIzmnNSC001452	905	-	-	-	18.91	-	-	-	
BGIB73PAVG000341	801	BGIzmnNSC001439	903	-	-	-	19.72	-	-	IPR001789; Signal transduction response regulator, receiver region	
BGIB73PAVG000340	726	BGIzmnNSC001410	901	-	-	-	28	-	-	IPR000914; Bacterial extracellular solute-binding protein, family 5	
BGIB73PAVG00053	393	BGIzmnNSC001398	900	-	63.38	86.83	15.46	9.83	100	IPR001813; Ribosomal protein 60S	
BGIB73PAVG000339	267	BGIzmnNSC001400	900	78.33	-	-	15.98	-	-	IPR000847; HTTH transcriptional regulator, LysR	
BGIB73PAVG000125	204	BGIzmnNSC001401	900	-	85.29	89.71	27.89	65.12	100	IPR002885; Pentatricopeptide repeat	
BGIB73PAVG000245	168	BGIzmnNSC001337	894	-	57.14	91.25	30.47	24.24	100	-	
BGIB73PAVG000105	513	BGIzmnNSC001301	891	-	-	-	26.02	-	-	-	
BGIB73PAVG00022	291	BGIzmnNSC001307	891	-	-	88.04	17.81	16.9	100	-	
BGIB73PAVG000016	468	BGIzmnNSC001311	891	-	87.18	-	29.67	-	-	IPR007371; Thiamin pyrophosphokinase, catalytic domain; IPR007373; Thiamin pyrophosphokinase, vitamin B1-binding region	
BGIB73PAVG000337	780	BGIzmnNSC001287	890	-	99.61	-	13.54	-	-	IPR005123; Oxoglutarate/iron-dependent oxygenase	
BGIB73PAVG000052	849	BGIzmnNSC001292	890	-	100	87.6	21.53	53.85	100	IPR000504; RNA recognition motif, RNP-1	
BGIB73PAVG000338	156	BGIzmnNSC001298	890	-	-	95.35	8.9	0	0	-	
BGIB73PAVG000204	669	BGIzmnNSC001299	890	-	64	78.55	23.38	63.65	100	-	
BGIB73PAVG00044	357	BGIzmnNSC001278	889	-	100	90.31	30.45	41.15	100	IPR004038; Ribosomal protein L7Ae/L30e/Gadd45	
BGIB73PAVG000336	606	BGIzmnNSC001281	889	-	-	-	20.55	-	-	-	
BGIB73PAVG000255	585	BGIzmnNSC001277	888	-	-	68.1	80.84	36.8	44.48	100	-
BGIB73PAVG000335	162	BGIzmnNSC001265	887	-	67.86	86.16	15.17	22.72	100	-	
BGIB73PAVG000333	372	BGIzmnNSC001240	886	-	98.37	-	15.68	-	-	-	
BGIB73PAVG000334	306	BGIzmnNSC001254	886	-	-	-	32.71	-	-	-	
BGIB73PAVG000129	291	BGIzmnNSC001219	884	-	54.08	88.95	22.91	36.3	100	-	
BGIB73PAVG000249	165	BGIzmnNSC001220	884	-	54.55	-	11.52	-	-	-	
BGIB73PAVG000332	264	BGIzmnNSC001236	884	-	-	90.7	26.6	3.3	43.5	-	
BGIB73PAVG000331	372	BGIzmnNSC001207	883	-	-	-	14.76	-	-	-	
BGIB73PAVG00284	234	BGIzmnNSC001210	883	53.19	76.74	88.21	19	10.87	100	IPR008906; HAT dimerisation	
BGIB73PAVG000186	300	BGIzmnNSC001202	882	-	-	91.12	23.73	14.45	100	-	
BGIB73PAVG000283	177	BGIzmnNSC001187	881	-	-	86.21	13.94	27.65	100	-	
BGIB73PAVG000021	132	BGIzmnNSC001188	881	-	-	-	28.86	-	-	-	
BGIB73PAVG000265	276	BGIzmnNSC001169	879	-	-	64.13	86.61	35.85	45.78	100	-
BGIB73PAVG000330	297	BGIzmnNSC001148	878	-	-	88.69	25.18	39.17	100	-	
BGIB73PAVG000329	264	BGIzmnNSC001104	874	-	64.46	-	57.52	-	-	-	
BGIB73PAVG000179	309	BGIzmnNSC001079	873	-	71.3	90.59	22.94	6.4	100	IPR013103; Reverse transcriptase, RNA-dependent DNA polymerase	
BGIB73PAVG000328	213	BGIzmnNSC001081	873	-	100	-	19.59	-	-	IPR013650; ATP-grasp fold, succinyl-CoA synthetase-type	
BGIB73PAVG000292	144	BGIzmnNSC001057	871	-	52.08	84.62	17.64	40.34	100	-	
BGIB73PAVG000327	366	BGIzmnNSC001025	869	54.84	-	-	21.21	-	-	-	
BGIB73PAVG000203	345	BGIzmnNSC001034	869	-	51.46	82.35	16.4	32.42	100	-	
BGIB73PAVG000326	648	BGIzmnNSC001015	868	51.56	-	-	14.02	-	-	-	
BGIB73PAVG000236	309	BGIzmnNSC001018	868	-	56.48	91.39	13.67	5.13	100	-	
BGIB73PAVG000324	618	BGIzmnNSC000991	866	-	-	-	21.5	-	-	IPR001123; Lysine exporter protein (LYSE/YGGA)	
BGIB73PAVG000325	795	BGIzmnNSC000996	866	-	-	-	14.7	-	-	IPR003709; Peptidase M15B/M15C, D,D-carboxypeptidase VanY/endolysins	
BGIB73PAVG000099	261	BGIzmnNSC000999	866	-	-	92.25	13.48	9.09	100	-	
BGIB73PAVG000103	180	BGIzmnNSC000999	866	-	-	92.22	13.45	6.51	100	-	
BGIB73PAVG000149	243	BGIzmnNSC000975	865	-	61.84	92.54	15.14	41.62	100	-	
BGIB73PAVG000323	315	BGIzmnNSC000983	865	88.33	-	-	22.23	-	-	-	
BGIB73PAVG000191	780	BGIzmnNSC000969	864	-	72.18	-	76.69	-	-	IPR001584; Integrase, catalytic core	
BGIB73PAVG000322	255	BGIzmnNSC000950	863	-	-	95.22	13.95	24.96	100	-	
BGIB73PAVG000321	654	BGIzmnNSC000941	862	-	-	-	19.69	-	-	IPR011701; Major facilitator superfamily MFS-1	
BGIB73PAVG000320	342	BGIzmnNSC000866	857	-	100	-	27.07	-	-	IPR003864; Protein of unknown function DUF221	
BGIB73PAVG000318	267	BGIzmnNSC000852	856	-	-	88.89	22.65	12.9	100	-	
BGIB73PAVG0008319	600	BGIzmnNSC000860	856	59	-	-	18.9	-	-	IPR000515; Binding-protein-dependent transport systems inner membrane component	
BGIB73PAVG000317	339	BGIzmnNSC000831	854	-	82.79	89.69	36.14	49.51	100	-	
BGIB73PAVG000316	297	BGIzmnNSC000800	852	-	100	-	30.93	-	-	-	
BGIB73PAVG000253	411	BGIzmnNSC000801	852	59.15	-	-	20.77	-	-	IPR001750; NADH:ubiquinone/plastoquinone oxidoreductase	
BGIB73PAVG000315	273	BGIzmnNSC000789	851	93.33	-	-	20.13	-	-	IPR002191; Bacterial export protein FliQ, family 3	
BGIB73PAVG000082	345	BGIzmnNSC000790	851	-	-	83.47	16.19	17.14	100	-	
BGIB73PAVG000104	405	BGIzmnNSC000752	849	-	-	92.21	22.48	6.09	77.92	-	
BGIB73PAVG000111	351	BGIzmnNSC000760	849	-	-	85.08	30.77	20.11	100	IPR007021; Protein of unknown function DUF659	
BGIB73PAVG000314	309	BGIzmnNSC000736	848	80	-	-	19.04	-	-	IPR009799; Ethyl tert-butyl ether degradation EthD	
BGIB73PAVG000124	366	BGIzmnNSC000693	845	-	-	86.25	25.51	56.28	100	-	
BGIB73PAVG000312	573	BGIzmnNSC000677	844	-	-	-	20.26	-	-	IPR000847; HTTH transcriptional regulator, LysR; IPR005119; LysR, substrate-binding	
BGIB73PAVG000313	234	BGIzmnNSC000685	844	-	-	88	53.75	20.57	100	-	
BGIB73PAVG000304	297	BGIzmnNSC000663	843	-	100	-	17.12	-	-	-	
BGIB73PAVG000311	231	BGIzmnNSC000664	843	86.67	-	-	14.65	-	-	IPR004039; Rubredoxin-type Fe(Cys)4 protein	
BGIB73PAVG000259	201	BGIzmnNSC000630	840	-	60	92	18.6	53.2	100	IPR006091; Acyl-CoA oxidase/dehydrogenase, central region; IPR006092; Acyl-CoA dehydrogenase, N-terminal	
BGIB73PAVG000244	213	BGIzmnNSC000595	838	-	63.89	89.05	20.19	4.75	100	-	
BGIB73PAVG000187	258	BGIzmnNSC000596	838	-	88.37	95.69	27.52	87.09	100	IPR005162; Retrotansposon gag protein	
BGIB73PAVG000156	177	BGIzmnNSC000584	837	-	55	93.4	20.77	36.21	100	-	
BGIB73PAVG000042	450	BGIzmnNSC000594	837	-	100	-	33.1	-	-	IPR002530; Zein seed storage protein	
BGIB73PAVG000061	246	BGIzmnNSC000533	834	-	70.73	91.06	19.64	4.71	66.67	-	
BGIB73PAVG000100	234	BGIzmnNSC000535	834	-	-	88.33	19.11	27.88	100	-	
BGIB73PAVG000309	258	BGIzmnNSC000540	834	-	-	87.07	12.33	43.59	100	-	
BGIB73PAVG000247	186	BGIzmnNSC000500	832	-	54.1	-	18.83	-	-	-	
BGIB73PAVG000066	138	BGIzmnNSC000483	831	-	-	89.29	12.41	28.79	100	-	
BGIB73PAVG000093	321	BGIzmnNSC000493	831	-	83.33	90.27	18.99	36.23	100	-	
BGIB73PAVG000308	480	BGIzmnNSC000502	831	-	-	84.57	15.06	16.83	100	-	
BGIB73PAVG000307	501	BGIzmnNSC000477	830	-	-	56.52	89.02	16.37	42.15	100	-
BGIB73PAVG000291	147	BGIzmnNSC000479	830	-	-	-	-	-	-	-	
BGIB73PAVG000046	243	BGIzmnNSC000458	829	-	-	84.29	18.11	29.7	100	-	
BGIB73PAVG000057	285	BGIzmnNSC000437	827	-	85.71	90.24	15.65</				

BGIB73PAVG000196	546	BGIZmNSC000446	827	-	62.6	85.52	15.26	18.89	100	-
BGIB73PAVG000272	330	BGIZmNSC000425	826	98.33	54.05	-	23.27	-	-	IPR007081; RNA polymerase Rpb1, domain 5 IPR013103; Reverse transcriptase, RNA-dependent DNA polymerase
BGIB73PAVG000180	252	BGIZmNSC000415	825	-	65.48	86.43	13.83	16.88	100	-
BGIB73PAVG000306	609	BGIZmNSC000417	825	-	-	-	10.93	-	-	-
BGIB73PAVG000281	252	BGIZmNSC000354	821	-	62.65	87.55	24.01	41.51	100	-
BGIB73PAVG000206	378	BGIZmNSC000304	819	-	56.72	86.01	25.73	13.67	100	-
BGIB73PAVG000233	294	BGIZmNSC000278	817	-	66.67	91.76	31.71	7.21	100	-
BGIB73PAVG000198	441	BGIZmNSC000281	817	-	73.83	87.95	25.99	59.63	100	-
BGIB73PAVG000305	348	BGIZmNSC000250	816	81.67	-	-	19.49	-	-	-
BGIB73PAVG000304	315	BGIZmNSC000253	816	-	62.73	94.17	28.75	57.17	100	-
BGIB73PAVG000107	168	BGIZmNSC000255	816	-	75.61	92.73	31.58	48.25	100	IPR001394; Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2
BGIB73PAVG000157	162	BGIZmNSC000220	814	-	62.26	90.43	9.05	43.24	100	-
BGIB73PAVG000303	480	BGIZmNSC000241	814	-	96.86	89.43	30.5	52.64	100	-
BGIB73PAVG000302	618	BGIZmNSC000191	812	-	51.68	-	21.43	-	-	-
BGIB73PAVG000301	396	BGIZmNSC000193	812	-	-	-	22.55	-	-	-
BGIB73PAVG000299	240	BGIZmNSC000166	811	-	-	90.52	15.71	8	100	-
BGIB73PAVG000300	282	BGIZmNSC000184	811	-	100	84.38	34.6	83.92	100	IPR005135; Endonuclease/exonuclease/phosphatase
BGIB73PAVG000298	348	BGIZmNSC000139	809	83.33	-	-	13.55	-	-	-
BGIB73PAVG000297	645	BGIZmNSC000107	807	-	-	-	14.85	-	-	-
BGIB73PAVG000296	234	BGIZmNSC000076	805	-	-	-	14.67	-	-	-
BGIB73PAVG000138	258	BGIZmNSC000057	804	-	-	88.37	11.35	33.99	100	-
BGIB73PAVG000295	384	BGIZmNSC000020	802	86.76	-	-	15.79	-	-	IPR004690; Malonate transporter MadL subunit IPR005132; Rare lipoprotein A; IPR007112; Expansin 45, endoglucanase-like; IPR007117; Pollen allergen/expansin, C-terminal
BGIB73PAVG000153	576	BGIZmNSC000022	802	-	77.02	-	14.24	-	-	-
BGIB73PAVG000098	462	BGIZmNSC000001	801	-	-	88.89	23.15	16.74	100	-
BGIB73PAVG000294	432	BGIZmNSC000008	801	72.73	-	-	17.19	-	-	-