

Supporting Table 1. Details of sampling for *Tpi* and *Mpi* loci for *H. erato*, *H. melpomene* and their respective sister and outgroup species. NS = Not Sampled, * = first published in Beltrán et al. (2002) *Mol. Biol. Evol.* **19**, 2176-2190

Species	McMillan Collection #	Study sample #	Sex	Collection locality (Locality, Province, Country)	Aproximate Co-ordinates		No. Alleles TPI	Genbank Accession no.	No. Alleles MPI	Genbank Accession no.
<i>H. erato</i>										
<i>H. e. chesteronii</i>	C65	CHE 1	M	Valle de Cauca, Colombia	76.72W	3.78 N	1	AY319192	NS	
<i>H. e. chesteronii</i>	C140	CHE 2	F	Valle de Cauca, Colombia	76.62 W	3.90 N	1	AY319193	2	AY319856; AY319857
<i>H. e. chesteronii</i>	C188	CHE 3	M	Valle de Cauca, Colombia	76.55 W	3.84 N	1	AY319194	NS	
<i>H. e. chesteronii</i>	C201	CHE 4	F	Valle de Cauca, Colombia	76.43 W	3.88 N	1	AY319195	1	AY319858
<i>H. e. chesteronii</i>	C206	CHE 5	F	Valle de Cauca, Colombia	76.70W	3.73 N	1	AY319196	NS	
<i>E. e. cyrbia</i>	N588	CYR 1	M	Guayquichuma Glen, Loja, Ecuador	79.57 W	3.85 S	NS		2	AY319859; AY319860
<i>E. e. cyrbia</i>	C2861	CYR 2	M	Alluriquin, Pinchincha, Ecuador	79.03 W	0.32 S	2*	AF413758; AF413770	2*	AF413725; AF413728
<i>E. e. cyrbia</i>	PR03	CYR 3	F	Guayquichuma Glen, Loja, Ecuador	79.57 W	3.85 S	1	AY319197	2	AY319861; AY319862
<i>E. e. cyrbia</i>	PR10	CYR 4	F	Guayquichuma Glen, Loja, Ecuador	79.57 W	3.85 S	1	AY319198	NS	
<i>E. e. cyrbia</i>	PR31	CYR 5	F	Guayquichuma Glen, Loja, Ecuador	79.57 W	3.85 S	1	AY319199	2	AY319863; AY319864
<i>E. e. cyrbia</i>	PR43	CYR 6	F	Guayquichuma Glen, Loja, Ecuador	79.57 W	3.85 S	1	AY319200	2	AY319865; AY319866
<i>H. e. petiverana</i>	N7153	PET 1	F	Gamboa, Panama	79.71 W	9.12 N	1	AY319201	2	AY319867; AY319868
<i>H. e. petiverana</i>	N7154	PET 2	F	Gamboa, Panama	79.71 W	9.12 N	1	AY319202	NS	
<i>H. e. petiverana</i>	N7183	PET 3	F	Gamboa, Panama	79.71 W	9.12 N	1	AY319203	2	AY319869; AY319870
<i>H. e. petiverana</i>	C2980	PET 4	M	Gamboa, Panama	79.71 W	9.12 N	2*	AF413752; AF413753	2*	AF413723; AF413724
<i>H. e. petiverana</i>	C2981	PET 5	M	Gamboa, Panama	79.71 W	9.12 N	2*	AF413754; AF413755	NS	
<i>H. e. petiverana</i>	P50	PET 6	F	Gamboa, Panama	79.71 W	9.12 N	1	AY319204	NS	
<i>H. e. petiverana</i>	PR26	PET 7	F	Gamboa, Panama	79.71 W	9.12 N	1	AY319205	2	AY319871; AY319872
<i>H. e. hydara</i>	C454	HY-CO 1	M	Villeta, Colombia	74.56 W	5.07 N	2	AY319206; AY319207	NS	
<i>H. e. hydara</i>	C455	HY-CO 2	M	Villeta, Colombia	74.56 W	5.07 N	1	AY319208	2	AY319873; AY319874
<i>H. e. hydara</i>	C456	HY-CO 3	M	Villeta, Colombia	74.56 W	5.07 N	NS		2	AY319875; AY319876
<i>H. e. hydara</i>	C457	HY-CO 4	F	Villeta, Colombia	74.56 W	5.07 N	1	AY319209	2	AY319877; AY319878
<i>H. e. hydara</i>	TT05	HY-TT 1	F	Maracas, Trinidad	61.26 W	10.85 N	1	AY319210	2	AY319879; AY319880
<i>H. e. hydara</i>	TT06	HY-TT 2	M	Maracas, Trinidad	61.26 W	10.85 N	2	AY319211; AY319212	NS	
<i>H. e. hydara</i>	TT07	HY-TT 3	M	Maracas, Trinidad	61.26 W	10.85 N	2	AY319213; AY319214	NS	
<i>H. e. hydara</i>	TT12	HY-TT 4	F	Braso Seco, Trinidad	61.25 W	10.82 N	1	AY319215	2	AY319881; AY319882
<i>H. e. hydara</i>	C420	HY-FG 1	F	Pt. Macouria, French Guiana	52.36 W	4.91 N	1	AY319216	1	AY319883
<i>H. e. hydara</i>	C440	HY-FG 2	M	Sablance, French Guiana	52.42 W	4.96 N	2	AY319217; AY319218	1	AY319884
<i>H. e. hydara</i>	C442	HY-FG 3	M	Sablance, French Guiana	52.42 W	4.96 N	2	AY319219; AY319220	1	AY319885
<i>H. e. hydara</i>	C444	HY-FG 4	M	Sablance, French Guiana	52.42 W	4.96 N	NS		1	AY319886
<i>H. e. erato</i>	C347	ERA 1	F	Cacao, French Guiana	52.467 W	4.583 N	1	AY319221	1	AY319887
<i>H. e. erato</i>	C348	ERA 2	F	Cacao, French Guiana	52.467 W	4.583 N	1	AY319222	1	AY319888

<i>H. e. erato</i>	C349	ERA 3	M	Cacao, French Guiana	52.467 W	4.583 N	2	AY319223; AY319224	NS	
<i>H. e. emma</i>	JM443	EMM 1	F	Davidcillo, Peru	76.25 W	6.27 N	1	AY319225	2	AY319889; AY319890
<i>H. e. emma</i>	JM1105	EMM 2	F	Davidcillo, Peru	76.25 W	6.27 N	1	AY319226	2	AY319891; AY319892
<i>H. e. etylus</i>	27	ETY 1	F	El Progreso, Rio Zamora, Zamora, Ecuador	78.8 W	3.9 S	1	AY319227	2	AY319893; AY319894
<i>H. e. etylus</i>	101	ETY 2	F	Rio Bombuscaro, Zamora, Ecuador	79.0 W	4.1 S	1	AY319228	2	AY319895; AY319896
<i>H. e. etylus</i>	PR05	ETY 3	F	El Progreso, Rio Zamora, Zamora, Ecuador	78.8 W	3.9 S	1	AY319229	2	AY319897; AY319898
<i>H. e. etylus</i>	PR06	ETY 4	F	El Progreso, Rio Zamora, Zamora, Ecuador	78.8 W	3.9 S	1	AY319230	2	AY319899; AY319900
<i>H. e. favorinus</i>	JM488	FAV 1	F	Chazuta, Peru	76.15 W	6.58 S	1	AY319231	1	AY319901
<i>H. e. favorinus</i>	JM883	FAV 2	F	Chazuta, Peru	76.15 W	6.58 S	1	AY319232	1	AY319902
<i>H. e. favorinus</i>	JM1141	FAV 3	F	Chazuta, Peru	76.15 W	6.58 S	1	AY319233	NS	
<i>H. e. favorinus</i>	JM1908	FAV 4	F	Pachiza, Peru	76.77 W	7.33 S	1	AY319234	1	AY319903
<i>H. e. favorinus</i>	JM1911	FAV 5	F	Pachiza, Peru	76.77 W	7.33 S	1	AY319235	NS	
<i>H. e. latavitta</i>	N2239	LAT 1	M	Sacha Lodge, Rio Napo, Ecuador	76.4 W	0.4 S	NS		1	AY319904
<i>H. e. latavitta</i>	Y30	LAT 2	M	Yasuni, Ecuador	76.4 W	0.7 S	NS		2	AY319905; AY319906
<i>H. e. latavitta</i>	Y31	LAT 3	M	Yasuni, Ecuador	76.4 W	0.7 S	2	AY319236; AY319237	2	AY319907; AY319908
<i>H. e. latavitta</i>	Y34	LAT 4	F	Yasuni, Ecuador	76.4 W	0.7 S	1	AY319238	2	AY319909; AY319910
<i>H. e. notabilis</i>	PR12	NOT 1	M	Puyo, Ecuador	78.0 W	1.5 S	2	AY319239; AY319240	1	AY319911
<i>H. e. notabilis</i>	PR13	NOT 2	F	Puyo, Ecuador	78.0 W	1.5 S	1	AY319241	NS	
<i>H. e. notabilis</i>	PR15	NOT 3	F	Puyo, Ecuador	78.0 W	1.5 S	1	AY319242	2	AY319912; AY319913
<i>H. e. notabilis</i>	PR114	NOT 4	F	Puyo, Ecuador	78.0 W	1.5 S	1	AY319243	2	AY319914; AY319915
<i>H. melpomene</i>										
<i>H. m. cythera</i>	1379	CYTH 1	F	Above La Troncal, Azuay Province	79.3 W	2.5 S	1	AY329803	2	AY332415; AY332416
<i>H. m. cythera</i>	1378	CYTH 2	M	Above La Troncal, Azuay Province	79.3 W	2.5 S	1	AY329802	1	AY332414
<i>H. m. cythera</i>	1051	CYTH 3	M	Tinalandia, Pinchincha Province	79.05 W	0.30 S	1	AY329801	2	AY332412; AY332413
<i>H. m. rosina</i>	C811	ROS 1	M	Gamboa, Panama	79.71 W	9.12 N	2*	AF413782; AF413783	2*	AF413743; AF413744
<i>H. m. rosina</i>	C544	ROS 2	M	Gamboa, Panama	79.71 W	9.12 N	2*	AF413789; AF413790	2	AY332417; AY332418
<i>H. m. rosina</i>	C1652	ROS 3	F	Gamboa, Panama	79.71 W	9.12 N	1	AY329805	2	AY332421; AY332422
<i>H. m. rosina</i>	C841	ROS 4	F	Gamboa, Panama	79.71 W	9.12 N	1	AY329804	2	AY332419; AY332420
<i>H. m. melpomene</i>	C421	MEL-CO 1	F	Villeta, Colombia	74.56 W	5.07 N	1	AY329808	NS	
<i>H. m. melpomene</i>	C422	MEL-CO 2	F	Villeta, Colombia	74.56 W	5.07 N	1	AY329809	2	AY332424; AY332425
<i>H. m. melpomene</i>	C11	MEL-CO 3	F	Guayabetal, Colombia	73.797 W	4.207 N	1	AY329806	1	AY332423
<i>H. m. melpomene</i>	C12	MEL-CO 4	F	Guayabetal, Colombia	73.797 W	4.207 N	1	AY329807	NS	
<i>H. m. melpomene</i>	TT03	MEL-TT 1	F	Maracas, Trinidad	61.26 W	10.85 N	1	AY329810	2	AY332426; AY332427
<i>H. m. melpomene</i>	TT04	MEL-TT 2	F	Maracas, Trinidad	61.26 W	10.85 N	1	AY329811	2	AY332428; AY332429
<i>H. m. melpomene</i>	TT14	MEL-TT 3	F	Braso Seco, Trinidad	61.25 W	10.82 N	1	AY329812	2	AY332430; AY332431
<i>H. m. melpomene</i>	C436	MEL-FG 1	M	Sablance, French Guiana	52.420 W	4.963 N	2	AY329813; AY329814	2	AY332432; AY332433
<i>H. m. melpomene</i>	C437	MEL-FG 2	M	Sablance, French Guiana	52.420 W	4.963 N	2	AY329815; AY329816	1	AY332434
<i>H. m. melpomene</i>	C528	MEL-FG 3	F	Pointe Macouria, French Guiana	52.360 W	4.913 N	1	AY329817	2	AY332435; AY332436
<i>H. m. melpomene</i>	C1384	MEL-FG 4	F	Sablance, French Guiana	52.420 W	4.963 N	1	AY329818	2	AY332437; AY332438
<i>H. m. thelxiopeia</i>	FG82	THEL 1	M	Mariposoula LOC. 72, French Guiana	54.027 W	3.661 N	2	AY329819; AY329820	NS	
<i>H. m. thelxiopeia</i>	FG90	THEL 2	M	Mariposoula LOC. 74, French Guiana	54.031 W	3.634 N	1	AY329821	2	AY332439; AY332440

<i>H. m.thelxiopeia</i>	FG104	THEL 3	M	Mariposoula LOC. 75, French Guiana	54.089 W	3.686 N	2	AY329822; AY329823	2	AY332441; AY332442
<i>H. m.thelxiopeia</i>	FG118	THEL 4	M	Rio Maroni LOC 79, French Guiana	54.392 W	4.292 N	2	AY329824; AY329825	2	AY332443; AY332444
<i>H.m.malletti</i>	N4026	MAL1	M	31 Km down Baeza - Tena Road, Napo, Ecuador	78.8 W	0.9 S	1	AY329826	2	AY332445; AY332446
<i>H.m.malletti</i>	N4027	MAL 2	M	31 Km down Baeza - Tena Road, Napo, Ecuador	78.8 W	0.9 S	NS		2	AY332447; AY332448
<i>H.m.aglaope</i>	JM494	AGLA 1	M	San Juan de Pumayacu, Loreto, Peru	76.2 W	5.9 S	2	AY329827; AY329828	NS	
<i>H.m.aglaope</i>	JM1174	AGLA 2	M	San Juan de Pumayacu, Loreto, Peru	76.2 W	5.9 S	2	AY329829; AY329830	2	AY332449; AY332450
<i>H.m.aglaope</i>	JM1178	AGLA 3	F	San Juan de Pumayacu, Loreto, Peru	76.2 W	5.9 S	1	AY329831	1	AY332451
<i>H. m. amaryllis</i>	JM1916	AMAR 1	M	Pachiza, Peru	76.77 W	7.33 S	NS		1	AY332453
<i>H. m. amaryllis</i>	JM1917	AMAR 2	M	Pachiza, Peru	76.77 W	7.33 S	2	AY329833; AY329834	1	AY332454
<i>H. m. amaryllis</i>	JM1271	AMAR 3	F	Tarapoto, Peru	76.35 W	6.48 S	1	AY329832	1	AY332452
<i>H.m. ecuadoriensis</i>	C428	ECUA 1	F	3.3km S. of Zumba towards Pucupamba, Zamora, Ecuador	79.1 W	4.9 S	1	AY329835	1	AY332455
<i>H.m. ecuadoriensis</i>	C2417	ECUA 2	F	Cumbaratza, Zamora, Ecuador	78.8 W	4.0 S	1	AY329836	2	AY332456; AY332457
<i>H. m. plesseni</i>	N14	PLES 1	M	Rio Quilo, 23km Puyo to Banos, Pastaza	78.1 W	1.5 S	1	AY329837	NS	
<i>H. m. plesseni</i>	C2397	PLES 2	M	Puyo Valley, Ecuador	78.1 W	1.5 S	NS		1	AY332458
<i>H. m. plesseni</i>	C2429	PLES 3	F	Puyo Valley, Ecuador	78.1 W	1.5 S	1	AY329838	2	AY332459; AY332460
Outgroups										
<i>H. himera</i>	N620	HIM 1	F	Vilcabamba, Ecuador	79.212 W	4.264 S	1	AY319244	1	AY319916
<i>H. himera</i>	C2842	HIM 2	M	Catamayo, Ecuador	79.447 W	3.942 S	2	AY319245; AY319246	1*	AF413726
<i>H. himera</i>	PR18	HIM 3	F	Vilcabamba, Ecuador	79.212 W	4.264 S	1	AY319247	2	AY319917; AY319918
<i>H. himera</i>	PR19	HIM 4	F	Vilcabamba, Ecuador	79.212 W	4.264 S	1	AY319248	1	AY319919
<i>H. himera</i>	PR45	HIM 5	M	Vilcabamba, Ecuador	79.212 W	4.264 S	2	AY319249; AY319250	2	AY319920; AY319921
<i>H. himera</i>	JM521	HIM 6	F	10 km S Muyo, near Bagua, Amazonas, Peru	77.4 W	5.8 S	1	AY319251	1	AY319922
<i>H. himera</i>	JM522	HIM 7	M	10 km S Muyo, near Bagua, Amazonas, Peru	77.4 W	5.8 S	2	AY319252; AY319253	NS	
<i>H. clysonimus</i>	C8037		F	Santa Clara, Panama	82.715 W	8.839 N	1	AF413764	1*	AF413720
<i>H. telesiphe</i>	N11		F	Rio Quilo, 23km Puyo to Banos, Pastaza	78.1 W	1.5 S	1	AY319254	1	AY319923
<i>H. cydno chioneus</i>	C553	CYDNO 1	M	Gamboa, Panama	79.71 W	9.12 N	2*	AF413785; AF413786	1	AY332461
<i>H. cydno chioneus</i>	C570	CYDNO 2	M	Gamboa, Panama	79.71 W	9.12 N	1*	AF413787	1*	AF413739
<i>H. cydno chioneus</i>	P40	CYDNO 3	M	Gamboa, Panama	79.71 W	9.12 N	2	AY329839; AY329840	NS	
<i>H. cydno alithea</i>	N1047	CYDNO 4	M	Hacienda La Hesperia, Pinchincha, Ecuador	78.824 W	0.333 S	2	AY329841; AY329842	1	AY332462
<i>H.hecale</i>	Y5		F	Yasuni, Ecuador	76.4 W	0.7 S	1	AY329843	2	AY332463; AY332464

Supporting Figure 1: NEXUS files used for the genealogy estimations of *H. erato* and *H. melpomene* at the nuclear loci *Mannose phosphate isomerase (Mpi)* and *Triose phosphate isomerase (Tpi)*. Alignments were generated using Clustal W (Thompson, J., Higgins, D. & Gibson, T. [1994] *Nucleic Acids Res.* **22**, 4673-4680) and adjusted by eye.

A. Alignment for *H. erato* at the *Mpi* locus

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#NEXUS

BEGIN DATA;
    DIMENSIONS  NTAX=74  NCHAR=611;
    FORMAT DATATYPE=DNA  MISSING=?  GAP=-  MATCHCHAR=.  INTERLEAVE ;
MATRIX

[           10           20           30           40           50]
[           .           .           .           .           .]

CHE2A_C140_A      TTTATCTATT  CAGGCTCATC  CAACTAAGGT  ATGTATCTAA  ATAAAAATTT  [50]
CHE2B_C140_B      .....      .....      .....      .....      .....      [50]
CHE4A_C201_A      .....G...  .....      .....      .....      .....      [50]
CYR1A_N588_A      .....G...  .....      .....      ..A.....  .....      [50]
CYR1B_N588_B      .....G...  .....      ..G.....  ..A.....  .....      [50]
CYR2A_C2861#1     .....      .....      .....      .....      .....      [50]
CYR2B_C2861#2     .....      .....      .....      .....      .....      [50]
CYR3A_PR03_A      .....      .....      .....      .....      .....      [50]
CYR3B_PR03_B      .....      .....      .....      .....      .....      [50]
CYR5A_PR31_A      .....      .....      .....      .....      .....      [50]
CYR5B_PR31_B      .....      .....      .....      .....      .....      [50]
CYR6A_PR43_A      ?????????? ?????????? ??????.....  .....      [50]
CYR6B_PR43_B      ?????????? ?????????? ??.....      .....      [50]
PET1A_N7153_A     .....      .....      .....      .....T...  .....--  [48]
PET1B_N7153_B     .....      .....      .....      .....      .....-  [49]
PET3A_N7183_A     .....      .....      .....      .....      .....      [50]
PET3B_N7183_B     .....      ..A.....  .....      .....T...  .....--  [48]
PET4A_C2980_A     .....G...  .....      .....      .....      .....-  [49]
PET4B_C2980_B     .....      ..A.....  .....      .....T...  .....---  [46]
PET7A_PR26_A      .....G...  .....      .....      .....      .....      [50]
PET7B_PR26_B      .....      .....      .....      .....      .....      [50]
HYCO2A_C455_A     .....      .....      .....      .....      .....      [50]
HYCO2B_C455_B     .....      ..A.....  .....      .....T...  .....--  [48]
HYCO3A_C456_A     .....      ..A.....  ..G.....  .....T...  .....---  [46]
HYCO3B_C456_B     .....      ..A.....  .....      .....T...  .....---  [46]
HYCO4A_C457_A     .....      .....      .....      .....      .....-  [49]
HYCO4B_C457_B     .....      .....      .....      .....      .....-  [48]
HYTT1A_TT05_A     .....      .....      .....      .....      .....      [50]
HYTT1B_TT05_B     ?????????? ?.....      .....      .....      .....      [50]
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HYTT4A_TT12_AA.....T...--	[48]
HYTT4B_TT12_BT...--	[48]
HYFG1A_C420_AT...--	[48]
HYFG2A_C440_A	???..... ..A.....T...--	[48]
HYFG3A_C442_A	[50]
HYFG4A_C444_A	?????????..	[50]
ERA1A_C347_AA.....T...--	[48]
ERA2A_C348_A	??????????? ?--	[47]
EMM1A_JM443_A--	[48]
EMM1B_JM443_B--	[48]
EMM2A_JM1105_AT...--	[48]
EMM2B_JM1105_B-	[49]
ETY1A_N27_AA.....T...--	[48]
ETY1B_N27_BA.....T...--	[48]
ETY2A_N101_A-	[49]
ETY2B_N101_BC...	[50]
ETY3A_PR05_A	[50]
ETY3B_PR05_BA.....T...--	[47]
ETY4A_PR06_AA.....T...--	[48]
ETY4B_PR06_BA.....T...--	[48]
FAV1A_JM488_AA.....T...--	[47]
FAV2A_JM883_AA.....T...--	[48]
FAV4A_JM1908_AA.....T...--	[48]
LAT1A_N2239_AC.....T...--	[48]
LAT2A_Y30_AA.....T...--	[48]
LAT2B_Y30_BA.....CT...G.....--	[48]
LAT3A_Y31_A	[50]
LAT3B_Y31_BC--	[48]
LAT4A_Y34_A-	[49]
LAT4B_Y34_B-	[49]
NOT1A_PR12_AA.....T...--	[48]
NOT3A_PR15_A	[50]
NOT3B_PR15_BA.....T...--	[48]
NOT4A_PR114_A	[50]
NOT4B_PR114_BC.....--	[48]
HIM1A_N620_A	[50]
HIM2A_C2842_1	[50]
HIM3A_PR18_A-	[49]
HIM3B_PR18_B	[50]
HIM4A_PR19_A	[50]
HIM5A_PR45_A	??...G...	[50]
HIM5B_PR45_B	??...G...G.....	[50]
HIM6A_JM521_AG...	[50]
HTELESIPHE_N11A.....G.....--	[48]
HCLYSONIMUS_C3037A..C.....T...--	[48]

[60	70	80	90	100]
[.]

CHE2A_C140_A	-AAAAAAA--	-----TG	TTTTTA-TTC	TTATCTCAAT	CATTTAATAA	[88]
CHE2B_C140_B	-.....---	-----TTA...	T.....	[88]
CHE4A_C201_A	-.....---	-----	[88]
CYR1A_N588_A	-.....---	-----C.T-CC.	[87]
CYR1B_N588_B	-.....---	-----C.T-CC.	[87]
CYR2A_C2861#1	-.....---	-----	[88]
CYR2B_C2861#2	-.....---	-----C.	..G..T-.C.	S.....	[88]
CYR3A_PR03_A	-.....---	-----C.	..G..T-.C.	A.....	[88]
CYR3B_PR03_B	-.....---	-----C.	..G..T-.C.	A.....	[88]
CYR5A_PR31_A	-.....---	-----C.T-CC.C....	[87]
CYR5B_PR31_B	-.....---	-----	[88]
CYR6A_PR43_A	-.....---	-----	[88]
CYR6B_PR43_B	-.....---	-----C.	..G..T-.C.	A.....	[88]
PET1A_N7153_A	-.....---	-----	..A..TC.C.	[87]
PET1B_N7153_B	-.....A-	-----T-.C.	[87]
PET3A_N7183_A	T.....---	-----	C...T-.C.	[86]
PET3B_N7183_B	-.....---	-----	..A..TC.C.C..	[87]
PET4A_C2980_A	-.....---	-----C.T-CC.	[87]
PET4B_C2980_B	-----	-----	A..A.TC.C.	[77]
PET7A_PR26_A	-.....---	-----C.T-CC.	[87]
PET7B_PR26_B	-.....AA	-----	C...T-.C.	A.....	[88]
HYCO2A_C455_A	T.....---	-----	C...T-.C.	[87]
HYCO2B_C455_B	-.....AA	A-----	..A..TC.C.	[90]
HYCO3A_C456_A	-----	-----CAA..	..A..TC.C.	[81]
HYCO3B_C456_B	-----	-----CAA..	..A..TC.C.	[81]
HYCO4A_C457_A	-.....---	-----C.T-.C.	A.....	[86]
HYCO4B_C457_B	-.....AA	-----CC.T-.C.	[89]
HYTT1A_TT05_A	T.....---	-----	C...T-.C.	[87]
HYTT1B_TT05_B	-.....A-	-----	C...T-.C.	[87]
HYTT4A_TT12_A	-.....AA	-----	..A..TC.C.	[89]
HYTT4B_TT12_B	-.....AA	-----C.T-.C.	[88]
HYFG1A_C420_A	-.....AA	-----	..A..TC.C.	[89]
HYFG2A_C440_A	-.....---	-----	..A..TC.C.	[87]
HYFG3A_C442_A	-.....---	-----C.T-.C.	[88]
HYFG4A_C444_A	T.....---	-----	C...T-.C.	[87]
ERA1A_C347_A	-.....A-	-----	..A..TC.C.C..	[88]
ERA2A_C348_A	-.....---	-----T-.C.A....	[85]
EMM1A_JM443_A	-.....AA	-----CG.TC-	[88]
EMM1B_JM443_B	-.....AA	-----C.T-.C.	[88]
EMM2A_JM1105_A	-.....A-	-----T	..A..TC.C.	[87]
EMM2B_JM1105_B	-.....A-	-----C.T-.C.	[88]
ETY1A_N27_A	-.....AA	TATAA----	---TC.C.	[89]
ETY1B_N27_B	...C...AA	TATAA----	---TC.C.	[89]
ETY2A_N101_A	-.....A-	-----	C...T-.C.	A....T...	[86]
ETY2B_N101_B	-.....---	-----C.T-.C.	[88]
ETY3A_PR05_A	-.....A-	-----	C...T-.C.	[87]
ETY3B_PR05_B	-.....---	-----	..A..TC.C.	[85]
ETY4A_PR06_A	-.....A-	-----	..C..TC.C.	[88]
ETY4B_PR06_B	-.....A-	-----	..A..TC.C.	[88]

FAV1A_JM488_A	-.....----	-----..	..A..TC.C.	[84]
FAV2A_JM883_A	-.....AA	A-----..	..A..TC.C.	[90]
FAV4A_JM1908_A	-.....AA	A-----..	..A..TC.C.	[90]
LAT1A_N2239_A	-.....A-	TAATAA----	----.TC.C.	[88]
LAT2A_Y30_A	-.....AA	-----..	..A..TC.C.	[89]
LAT2B_Y30_B	-.....AA	-----..	..A..TC.C.	[89]
LAT3A_Y31_A	-.....--	-----..-..	[88]
LAT3B_Y31_B	-.....AA	A-----	C....T-.C.	[87]
LAT4A_Y34_A	-.....A-	-----C.T-.C.	[88]
LAT4B_Y34_B	-.....AA	AA-----C.T-.C.C	[91]
NOT1A_PR12_A	-.....AA	-----..	..A..TC.C.	[89]
NOT3A_PR15_A	-.....--	-----C.T-.C.	[88]
NOT3B_PR15_B	-.....AA	-----..	..A..TC.C.	[89]
NOT4A_PR114_A	-.....--	-----C.T-.C.	[88]
NOT4B_PR114_B	-.....----	-----C.T-.C.	[85]
HIM1A_N620_A	-.....----	-----C.T-.CT	[88]
HIM2A_C2842_1	-.....--	-----C.T-.CT	[88]
HIM3A_PR18_A	-.....AA	-----C.T-.CT	[89]
HIM3B_PR18_B	-.....--	-----C.T-.CT	[88]
HIM4A_PR19_A	-.....--	-----C.T-.CT	[88]
HIM5A_PR45_A	-.....----	-----C.T-CC.	[87]
HIM5B_PR45_B	-.....----	-----C.T-CC.	[87]
HIM6A_JM521_A	-.....----	-----C.T-CC.	[87]
HTELESIPHE_N11	-.....GA	-----..	..G..TC.C.	..G.....	[89]
HCLYSONIMUS_C3037	-.....A-	-----..	..AC.TC.C.	..G.....	[88]

[110	120	130	140	150]
[.]

CHE2A_C140_A	TGTGTCATAA	GATAT----	CTT----ATA	AACAAATACA	AAACAATACG	[130]
CHE2B_C140_B	-----.	-----.	[130]
CHE4A_C201_A	-----.	-----.	[130]
CYR1A_N588_AG....TCTT.	-----.T.	[133]
CYR1B_N588_BG....TCTT.	-----.T.	[133]
CYR2A_C2861#1	-----.	-----.	[130]
CYR2B_C2861#2TCTT.	-----.G...T.	[134]
CYR3A_PR03_ATCTT.	-----.G...T.	[134]
CYR3B_PR03_BTCTT.	-----.G...T.	[134]
CYR5A_PR31_AG....TCTT.	-----.T.	[133]
CYR5B_PR31_B	-----.	-----.A	[130]
CYR6A_PR43_A	-----.	-----.A	[130]
CYR6B_PR43_BTCTT.	-----.G...T.	[134]
PET1A_N7153_A	-----.	-----.T.	[129]
PET1B_N7153_BTCTT.	-----.T.	[133]
PET3A_N7183_ATCTT.	-----.	[132]
PET3B_N7183_BT....	-----.	-----.T.	[129]
PET4A_C2980_AG....TCTT.	-----.T.	[133]
PET4B_C2980_BT....	-----.	-----.A	[119]
PET7A_PR26_AG....TCTT.	-----.T.	[133]

PET7B_PR26_BTCTT.----	[134]
HYCO2A_C455_ATCTT.----	[133]
HYCO2B_C455_B	.A.....----T.	[132]
HYCO3A_C456_A--------	..T.....G..	[123]
HYCO3B_C456_B--------	..T.....	[123]
HYCO4A_C457_ATCTT.----T.	[132]
HYCO4B_C457_BTCTT.----	[135]
HYTT1A_TT05_ATCTT.----	[133]
HYTT1B_TT05_BTCTT.----	[133]
HYTT4A_TT12_A--------T.	[131]
HYTT4B_TT12_BTCTT.----	[134]
HYFG1A_C420_A--------T.	[131]
HYFG2A_C440_A	G.....----T.A	[129]
HYFG3A_C442_ATCTT.----T.	[134]
HYFG4A_C444_ATCTT.----	[133]
ERA1A_C347_AT....----T.	[130]
ERA2A_C348_ATCTT.	T.....----	[131]
EMM1A_JM443_A----ACTT.	[134]
EMM1B_JM443_BACTT.----	[134]
EMM2A_JM1105_A--------T.	[129]
EMM2B_JM1105_BA....TCTT.----	[134]
ETY1A_N27_A--------T.	[131]
ETY1B_N27_BG....----T.	[131]
ETY2A_N101_ATCTT.----	[132]
ETY2B_N101_B	.A.A.....TCTT.----T.	[134]
ETY3A_PR05_ATCTT.----	[133]
ETY3B_PR05_B--------T.	[127]
ETY4A_PR06_A--------T.A	[130]
ETY4B_PR06_B--------T.A	[130]
FAV1A_JM488_A--------T.	[126]
FAV2A_JM883_AG....----T.	[132]
FAV4A_JM1908_AG....----T.	[132]
LAT1A_N2239_A	...T.....----T.	[130]
LAT2A_Y30_A--------T.	[131]
LAT2B_Y30_B--------G..T.	[131]
LAT3A_Y31_A--------	[130]
LAT3B_Y31_BTCTT.----C.A	[133]
LAT4A_Y34_ATCTT.----T.	[134]
LAT4B_Y34_BA....TCTT.----A	[137]
NOT1A_PR12_A--------T.	[131]
NOT3A_PR15_A	...A.....TCTT.----T.	[134]
NOT3B_PR15_B--------T.	[131]
NOT4A_PR114_A	...A.....TCTT.----T.	[134]
NOT4B_PR114_BTCTT.----A	[131]
HIM1A_N620_ATCTT.----T.T	[134]
HIM2A_C2842_1TCTT.----T.T	[134]
HIM3A_PR18_ATCTT.----T.T	[135]
HIM3B_PR18_BTCTT.----T.T	[134]
HIM4A_PR19_ATCTT.----T.T	[134]

HIM5A_PR45_AG.....TCTT.	...----...T.	[133]
HIM5B_PR45_BG.....TCTT.	...----...	..G.....T.	[133]
HIM6A_JM521_AG.....TCTT.	...----...R..	[133]
HTELESIPHE_N11TCTT.	...----.A.T	[135]
HCLYSONIMUS_C3037TCTT.	...----.A.TA	[134]

[160	170	180	190	200]
[.]

CHE2A_C140_A	ATCATAATCT	GATAGGACTA	ATACTATGAA	TAATAT----	-----	[166]
CHE2B_C140_B----	-----	[166]
CHE4A_C201_A----	-----	[166]
CYR1A_N588_A	GC.....	...A.....G----	-----	[169]
CYR1B_N588_B	GC.....	...A.....G----	-----	[169]
CYR2A_C2861#1----	-----	[166]
CYR2B_C2861#2	GC.....	...A.....G----	-----	[170]
CYR3A_PR03_A	GC.....	...A.....G----	-----	[170]
CYR3B_PR03_B	GC.....	...A.....G----	-----	[170]
CYR5A_PR31_A	GC.....	...A..A..G----	-----	[169]
CYR5B_PR31_B----	-----	[166]
CYR6A_PR43_A----	-----	[166]
CYR6B_PR43_B	GC.....	...A.....G----	-----	[170]
PET1A_N7153_A	GC.....	...A.....----	-----	[165]
PET1B_N7153_B	GC.....	...A.....G----	-----	[169]
PET3A_N7183_A	GC.....	...A.....G----	-----	[168]
PET3B_N7183_B	GC.....	...A.....----	-----	[165]
PET4A_C2980_A	GC.....	...A.....G----	-----	[169]
PET4B_C2980_B	.C....G...	...A.....----	-----	[155]
PET7A_PR26_A	GC.....	...A.....G----	-----	[169]
PET7B_PR26_B	.C.....	...A..G..G----	-----	[170]
HYCO2A_C455_A	GC.....	...A.....G----	-----	[169]
HYCO2B_C455_B	G.....	...A.....----	-----	[168]
HYCO3A_C456_A	GC.....	...A.....G----	-----	[159]
HYCO3B_C456_B	GC.....	...A.....G----	-----	[159]
HYCO4A_C457_A	GC.....	...A..G..G----	-----	[168]
HYCO4B_C457_B	.C.....	...A..G..G----	-----	[171]
HYTT1A_TT05_A	GC.....	...A.....G----	-----	[169]
HYTT1B_TT05_B	GC.....	...A.....G----	-----	[169]
HYTT4A_TT12_A	G.....	...A.....----	-----	[167]
HYTT4B_TT12_B	GC.....	...A.....G----	-----	[170]
HYFG1A_C420_A	GC.....	...A.....----	-----	[167]
HYFG2A_C440_A	GC.....	...A.....G----	-----	[165]
HYFG3A_C442_A	GC.....	...A.....G----	-----	[170]
HYFG4A_C444_A	GC.....	...A.....G----	-----	[169]
ERA1A_C347_A	GC.....	...A.....----	-----	[166]
ERA2A_C348_A	GC.....	...A.....G----	-----	[167]
EMM1A_JM443_A	GC.....	...A.....G----	-----	[170]
EMM1B_JM443_B	G.....	...A.....G----	-----	[170]
EMM2A_JM1105_A	GC.....	...A.....----	-----	[165]

EMM2B_JM1105_B	GC.....A.....G----	-----	[170]
ETY1A_N27_A	G.....A.....----	-----	[167]
ETY1B_N27_B	G.....A.....----	-----	[167]
ETY2A_N101_A	GC.....A.....G----	-----	[168]
ETY2B_N101_B	GC.....A.....G----	-----	[170]
ETY3A_PR05_A	GC.....A.....G----	-----	[169]
ETY3B_PR05_B	G.....A.....G----	-----	[163]
ETY4A_PR06_A	GC.....A.....G----	-----	[166]
ETY4B_PR06_B	GC.....A.....G----	-----	[166]
FAV1A_JM488_A	G.....A.....G----	-----	[162]
FAV2A_JM883_A	G.....A.....----	-----	[168]
FAV4A_JM1908_A	G.....A.....----	-----	[168]
LAT1A_N2239_A	G.....A.....----	-----	[166]
LAT2A_Y30_A	G.....A.....----	-----	[167]
LAT2B_Y30_B	G.....A.....C....	-----	[167]
LAT3A_Y31_AA.....----	-----	[166]
LAT3B_Y31_B	GC.....A.....G----	-----	[169]
LAT4A_Y34_A	GC.....A.....G----	-----	[170]
LAT4B_Y34_B	GC.....A.....G----	-----	[173]
NOT1A_PR12_A	G.....A.....----	-----	[167]
NOT3A_PR15_A	GC.....A.....G----	-----	[169]
NOT3B_PR15_B	G.....A.....----	-----	[167]
NOT4A_PR114_A	GC.....A.....G----	-----	[170]
NOT4B_PR114_B	GC.....A.....ATATA	ATATGAATAA	[181]
HIM1A_N620_A	GG.....A.....G----	-----	[170]
HIM2A_C2842_1	GG.....A.....G----	-----	[170]
HIM3A_PR18_A	GG.....A.....G----	-----	[171]
HIM3B_PR18_B	GG.....A.....G----	-----	[170]
HIM4A_PR19_A	GG.....A.....G----	-----	[170]
HIM5A_PR45_A	.C.....A.....G----	-----	[169]
HIM5B_PR45_B	.C.....A.....G----	-----	[169]
HIM6A_JM521_A	.C.....A.....G----	-----	[169]
HTELESIPHE_N11	GC.....A.....	..W...G----	-----	[171]
HCLYSONIMUS_C3037	GC.....A.....G----	-----	[170]

[210	220	230	240	250]
[.]

CHE2A_C140_A	---GAGTATT	ATGAATGAGA	TTAAACACTC	AT-----A	GAATTAACTT	[206]
CHE2B_C140_B	---	-----	[206]
CHE4A_C201_A	---	-----	[206]
CYR1A_N588_A	---.T....	..A.....	-----T...	[209]
CYR1B_N588_B	---.T....	..A.....	-----T...	[209]
CYR2A_C2861#1	---C	-----	[206]
CYR2B_C2861#2	---.RT....	..A.....	-----T...	[210]
CYR3A_PR03_A	---.T....	..A.....	-----T...	[210]
CYR3B_PR03_B	---.T....	..A.....	-----T...	[210]
CYR5A_PR31_A	---.T....	G-----T...	[209]
CYR5B_PR31_B	---	-----	[206]

CYR6A_PR43_A	--------	[206]
CYR6B_PR43_B	---	.T....	..A.....-----T...	[210]
PET1A_N7153_A	---	.C....-----	..G.....	[205]
PET1B_N7153_B	---	.T....	G.-----T...	[209]
PET3A_N7183_A	---	.T....	G.-----T...	[208]
PET3B_N7183_B	---	.C....-----	[205]
PET4A_C2980_A	---	.T....T	G.CTAGAAT.T...	[216]
PET4B_C2980_B	---	.C....-----	..G.....	[195]
PET7A_PR26_A	---	.T....C.C....	G.-----T...	[209]
PET7B_PR26_B	---	.T....	G.-----T...	[210]
HYCO2A_C455_A	---	.T....	G.-----T...	[209]
HYCO2B_C455_B	---	.C....A....	..-----	[208]
HYCO3A_C456_A	---	.T....-----T...	[199]
HYCO3B_C456_B	---	.T....-----T...	[199]
HYCO4A_C457_A	---	.T....G...T	G.CTAGAAT.T...	[215]
HYCO4B_C457_B	---	.T....	G.-----T...	[211]
HYTT1A_TT05_A	---	.T....	G.-----T...	[209]
HYTT1B_TT05_B	---	.T....	G.-----T...	[209]
HYTT4A_TT12_A	---	.C....T..	..-----	[207]
HYTT4B_TT12_B	---	.T....	G.-----GT...	[210]
HYFG1A_C420_A	---	.C....-----	..G.....	[207]
HYFG2A_C440_A	---	.C....-----	[205]
HYFG3A_C442_A	---	.T....	G.-----T...	[210]
HYFG4A_C444_A	---	.T....	G.-----T...	[209]
ERA1A_C347_A	---	.C....-----	[206]
ERA2A_C348_A	---	.T....	G.-----GT...	[207]
EMM1A_JM443_A	---	.T....-----	...A.T...	[210]
EMM1B_JM443_B	---	.T....	..A.....-----	...A.T...	[210]
EMM2A_JM1105_A	---	.C....-----	..G.....	[205]
EMM2B_JM1105_B	---	.GT....G...	G.-----	..-----	[202]
ETY1A_N27_A	---	.C....A...	..-----	[207]
ETY1B_N27_B	---	.C....A...	..-----	[207]
ETY2A_N101_A	---	.T....T	G.-----T...	[208]
ETY2B_N101_B	---	.T....	G.-----T...	[210]
ETY3A_PR05_A	---	.T....	G.-----T...	[209]
ETY3B_PR05_B	---	.T....	G.-----GT...	[203]
ETY4A_PR06_A	---	.C....-----	...C....	[206]
ETY4B_PR06_B	---	.C....-----	[206]
FAV1A_JM488_A	---	.T....	G.-----GC...	[202]
FAV2A_JM883_A	---	.C....A...	..-----	[208]
FAV4A_JM1908_A	---	.C....A...	..-----	[208]
LAT1A_N2239_A	---	.C....A...	..-----	[206]
LAT2A_Y30_A	---	.C....T..	..-----	[207]
LAT2B_Y30_B	---	.C....A...	..-----	[207]
LAT3A_Y31_A	--------T...	[206]
LAT3B_Y31_B	---	.T....	G.-----T...	[209]
LAT4A_Y34_A	---	.T....-----T...	[210]
LAT4B_Y34_B	---	.T....	-----T...	[210]
NOT1A_PR12_A	---	.C....A..C.	..-----	[207]

NOT3A_PR15_A	---.T....	G.-----T...	[209]
NOT3B_PR15_B	---A.C....A....	..-----	[207]
NOT4A_PR114_A	---.T....	G.-----T...	[210]
NOT4B_PR114_B	TAG..T....	G.-----T...	[224]
HIM1A_N620_A	---.T....	G.-----T...	[210]
HIM2A_C2842_1	---.T....	G.-----T...	[210]
HIM3A_PR18_A	---.T....	G.-----T...	[211]
HIM3B_PR18_B	---.T....	G.-----T...	[210]
HIM4A_PR19_A	---.T....	G.-----T...	[210]
HIM5A_PR45_A	---.T....	G.-----A.T...	[209]
HIM5B_PR45_B	---.T....	G.-----A.T...	[209]
HIM6A_JM521_A	---.T....	G.-----A.T...	[209]
HTELESIPHE_N11	---.C....T..	..-----	[211]
HCLYSONIMUS_C3037	---.C....-----	[210]

[260	270	280	290	300]
[.]

CHE2A_C140_A	TAAACTCTAC	CAGCAACCAA	CAAATCTTTT	AACTAATTAA	ATGTAAATTC	[256]
CHE2B_C140_B	[256]
CHE4A_C201_A	[256]
CYR1A_N588_A	A.....C.	..G...G..A	[259]
CYR1B_N588_B	A.....C.	..G...G..A	[259]
CYR2A_C2861#1	[256]
CYR2B_C2861#2	A.....C.	..G...G..A	[260]
CYR3A_PR03_A	A.....C.	..G...G..A	[260]
CYR3B_PR03_B	A.....G.C.	..G...G..A	[260]
CYR5A_PR31_A	A.....C.	..G...G..A	[259]
CYR5B_PR31_B	[256]
CYR6A_PR43_A	[256]
CYR6B_PR43_B	A.....C.	..G...G..A	[260]
PET1A_N7153_AT....A..-	---...C..	T.....	[251]
PET1B_N7153_B	A.....--	..G...G..A	[256]
PET3A_N7183_A	C.....C..C.	..GC...G..A	[258]
PET3B_N7183_B	-----	-----	-----	---	[222]
PET4A_C2980_A	A.....C.	..G...G..A	[266]
PET4B_C2980_B--	[241]
PET7A_PR26_A	A.....C.	..G...G..A	[259]
PET7B_PR26_B	C.....C..C.	..GC...G..A	[260]
HYCO2A_C455_A	C.....C..C.	..G...G..A	[259]
HYCO2B_C455_B--	T.....	[256]
HYCO3A_C456_A	C.....C..T..C.	..GC...G..A	[249]
HYCO3B_C456_B	C.....C..T..C.	..GC...G..A	[249]
HYCO4A_C457_A	A.....C.	..G...G..A	[265]
HYCO4B_C457_B	A.....C.	..G...G..A	[261]
HYTT1A_TT05_A	C.....C..C.	..G...G..A	[259]
HYTT1B_TT05_B	C.....C..C.	..GC...G..A	[259]
HYTT4A_TT12_A	-----	-----	-----	---	[224]
HYTT4B_TT12_B	C.....C..G..C.	..GC...G..A	[260]

HYFG1A_C420_AT...G..G...--	-.....T	[253]	
HYFG2A_C440_A	-----	-----	-----	-----	[222]	
HYFG3A_C442_A	A.....--	..G...G..A	[257]	
HYFG4A_C444_A	C.....	C.....C.	..GC...G..A	[259]	
ERA1A_C347_A	-----	-----	-----	-----	[223]	
ERA2A_C348_A	C.....C.	..G...G..	[257]	
EMM1A_JM443_A	C.....	C.....T..C.	..GC...G..A	[260]
EMM1B_JM443_B	C.....	C.....T..C.	..GC...G..A	[260]
EMM2A_JM1105_A--	-.....	[251]	
EMM2B_JM1105_B	--.....C.	..G...G..	C.....A	[250]	
ETY1A_N27_A	G.....	T.....T.	[257]	
ETY1B_N27_B	G.....	T.....T.	[257]	
ETY2A_N101_A	C.....	C.....C.	..GC...G..A	[258]	
ETY2B_N101_B	A.....--	..G...G..A	[257]	
ETY3A_PR05_A	C.....	C.....C.	..GC...G..A	[259]	
ETY3B_PR05_B	C.....C.	..G...G..T	[253]	
ETY4A_PR06_A	-----	-----	-----	-----	[223]	
ETY4B_PR06_B	-----	-----	-----	-----	[223]	
FAV1A_JM488_A	C.....C.	..G...G..T	[252]	
FAV2A_JM883_A--..	T.....G....	[256]	
FAV4A_JM1908_A--..	T.....G....	[256]	
LAT1A_N2239_A--..	T.....	[254]	
LAT2A_Y30_A	-----	-----	-----	-----	[224]	
LAT2B_Y30_B--..	T.....	[255]	
LAT3A_Y31_A	[256]	
LAT3B_Y31_B	C.....G.C.	..G...G..A	[259]	
LAT4A_Y34_A	A.....--	..G...G..A	[257]	
LAT4B_Y34_B	C.....	C.....C.	..GC...G..A	[260]	
NOT1A_PR12_A--..	T.....	[255]	
NOT3A_PR15_A	A.....--	..G...G..A	[256]	
NOT3B_PR15_B	T.....	[257]	
NOT4A_PR114_A	A.....--	..G...G..A	[257]	
NOT4B_PR114_B	C.....	C.....T.C.	..GC...G..A	[273]
HIM1A_N620_A	C.....T.....C.	..G...G..	[260]	
HIM2A_C2842_1	C.....T.....C.	..G...G..	[260]	
HIM3A_PR18_A	C.....T.....C.	..G...G..	[261]	
HIM3B_PR18_B	C.....T.....C.	..G...G..	[260]	
HIM4A_PR19_A	C.....T.....C.	..G...G..	[260]	
HIM5A_PR45_A	A.....C.	..G...G..A	[259]	
HIM5B_PR45_B	A.....C.	..G...G..A	[259]	
HIM6A_JM521_A	A.....C.	..G...G..A	[259]	
HTELESIPHE_N11	C.....	T...TTGTTG	GTTGCTAG..	.TTA.....A	[261]	
HCLYSONIMUS_C3037	T.....	T.....A	[260]	

[310	320	330	340	350]
[.]

CHE2A_C140_A	ATATTTTAAA	TAATTTTCAT	GATATGAGAT	GCTCTATTAA	ACAAATGTAA	[306]
CHE2B_C140_B	[306]

CHE4A_C201_A	[306]
CYR1A_N588_A	..G..C....	-.....T.A.....	..C...T...	[308]
CYR1B_N588_B	..G..C....	-.....T.A.....	..C...T...	[308]
CYR2A_C2861#1	[306]
CYR2B_C2861#2	..G..C....	-.....T.A.....	..C...T...	[309]
CYR3A_PR03_A	..G..C....	-.....T.A.....	..C...T...	[309]
CYR3B_PR03_B	..G..C....	-.....T.A.....	..C...T...	[309]
CYR5A_PR31_A	..G.....T.A.....	..C...T...	[309]
CYR5B_PR31_B	[306]
CYR6A_PR43_A	[306]
CYR6B_PR43_B	..G..C....	-.....T.A.....	..C...T...	[309]
PET1A_N7153_AA...G..C...	[301]
PET1B_N7153_B	..G.....-.....	.T.A.....	..C...T...	[305]
PET3A_N7183_A	..G.....T.A.....	..C...T...	[308]
PET3B_N7183_BT..	A.....	..A.....	[272]
PET4A_C2980_A	..G.....T.A...G..C...	[316]
PET4B_C2980_BG.A...G..C...	[291]
PET7A_PR26_A	..G.....T.A.....	..C...T...	[309]
PET7B_PR26_B	..G.....C.....	.T.A.....	..C...T...	[310]
HYCO2A_C455_A	..G.....T.A.....	..C...T...	[309]
HYCO2B_C455_BA.....A.....CG..	[306]
HYCO3A_C456_A	..G.....T.A.....	..C...T...	[299]
HYCO3B_C456_B	..G.....T.A.....	..C...T...	[299]
HYCO4A_C457_A	..G.....	TT.A.....	.TC...T...	[315]
HYCO4B_C457_B	..G..C....	-.....T.A.....	..C...T...	[310]
HYTT1A_TT05_A	..G.....T.A.....	..C...T...	[309]
HYTT1B_TT05_B	..G.....C.....	.T.A.....	..C...T...	[309]
HYTT4A_TT12_AA.....C...	[274]
HYTT4B_TT12_B	..G.....T.A.....T...	[310]
HYFG1A_C420_AT.A...G..C...	[303]
HYFG2A_C440_AA.....	[272]
HYFG3A_C442_A	..G.....-.....	.T.A.....	..C...T...	[306]
HYFG4A_C444_A	..G.....C.....	.T.A.....	..C...T...	[309]
ERA1A_C347_AA.....	[273]
ERA2A_C348_A	..G.....A.....T...	[307]
EMM1A_JM443_A	..G.....T.A.....	..C...T...	[310]
EMM1B_JM443_B	..G.....T.A.....	..C...T...	[310]
EMM2A_JM1105_AA...G..C...	[301]
EMM2B_JM1105_B	..G.....T.A.....	..C...T...	[300]
ETY1A_N27_ACA.....A.....C...	[307]
ETY1B_N27_BCA.....A.....C...	[307]
ETY2A_N101_A	..G.....-.....	.T.A.....	.TC...T...	[307]
ETY2B_N101_B	..G.....-.....	.T.A.....	..C...T...	[306]
ETY3A_PR05_A	..G.....G.....T.A.....	..C...T...	[309]
ETY3B_PR05_B	..G.....T.-----	-----G..	-TG.-----	[287]
ETY4A_PR06_A	A..A.....	[273]
ETY4B_PR06_B	A..A.....	[273]
FAV1A_JM488_A	..G.....A.....T...	[302]
FAV2A_JM883_A	..G.....A.....C	..A.....T...	[306]

FAV4A_JM1908_A	..G.....A.....C	...A.....T...	[306]
LAT1A_N2239_AA.....A.....CG..	[304]
LAT2A_Y30_AA...A.....C...	[274]
LAT2B_Y30_BA.....C	...A.....C...	[305]
LAT3A_Y31_AC..AC.....	[306]
LAT3B_Y31_B	..G.....T..	.T.A.....	..C...T...	[309]
LAT4A_Y34_A	..G.....-.....	.T.A.....	..C...T...	[306]
LAT4B_Y34_B	..G.....C.....	.T.A.....	..C...T...	[310]
NOT1A_PR12_AA.....A.....C...	[305]
NOT3A_PR15_A	..G.....-.....	.T.A.....	..C...T...	[305]
NOT3B_PR15_BA.....A.....C...	[307]
NOT4A_PR114_A	..G.....-.....	.T.A.....	..C...T...	[306]
NOT4B_PR114_B	..G.....T.A.....	..C...T...	[323]
HIM1A_N620_A	..G.....	...C.....	T..A.....T...	[310]
HIM2A_C2842_1	..G.....	...C.....	T..A.....T...	[310]
HIM3A_PR18_A	..G.....	...C.....	T..A.....T...	[311]
HIM3B_PR18_B	..G.....	...C.....	T..A.....T...	[310]
HIM4A_PR19_A	..G.....	...C.....	T..A.....T...	[310]
HIM5A_PR45_A	..G...G..T.A.....	T.C...T...	[309]
HIM5B_PR45_B	..G...G..T.A.....	T.C...T...	[309]
HIM6A_JM521_A	..G...G..T.A.....	T.C...T...	[309]
HTELESIPHE_N11	..G.....C.CT.	.T.A.....	..TT...T...	[311]
HCLYSONIMUS_C3037	..G.....C.TGCT.	.T.A.....	..T...T...	[310]

[360	370	380	390	400]
[.]

CHE2A_C140_A	TAAAAACTTT	AAGTCAAAAA	TTAGACTGAA	ACAATTTAA-	-----	[345]
CHE2B_C140_B-	-----	[345]
CHE4A_C201_A-	-----	[345]
CYR1A_N588_AC.....	T.AA.....	...A.....	.A.G...G-	-----	[347]
CYR1B_N588_BC.....	T.AA.....	...A.....	.A.G...G-	-----	[347]
CYR2A_C2861#1-	-----	[345]
CYR2B_C2861#2	T.AA.....A.G...G-	-----	[348]
CYR3A_PR03_A	T.AA.....A.G...G-	-----	[348]
CYR3B_PR03_B	T.AA.....A.G...G-	-----	[348]
CYR5A_PR31_A	T.AA.....A.G...G-	-----	[348]
CYR5B_PR31_B-	-----	[345]
CYR6A_PR43_A-	-----	[345]
CYR6B_PR43_B	T.AA.....A.G...G-	-----	[348]
PET1A_N7153_AT.A.T	.G.C.----	-----	[336]
PET1B_N7153_B	T.A----A.G...G-	-----	[342]
PET3A_N7183_A	T.AA.....A.G...G-	-----	[347]
PET3B_N7183_BA.....A.....G-	-----	[311]
PET4A_C2980_AT.A.T	.G.C.----	-----	[351]
PET4B_C2980_BT.A.T	.G.C.----	-----	[326]
PET7A_PR26_A	T.AA.....A.G...G-	-----	[348]
PET7B_PR26_B	T.AA.....A.G...G-	-----	[349]
HYCO2A_C455_A	T.AA.....A.G...C.G-	-----	[348]

HYCO2B_C455_BG....	..AC.....A.....G-	-----	[345]
HYCO3A_C456_A	T.AA-.....	...T.....	.A.G....G-	-----	[337]
HYCO3B_C456_B	T.AA-.....	...T.....	.A.G....G-	-----	[337]
HYCO4A_C457_A	T.AA.....A.G....G-	-----	[354]
HYCO4B_C457_B	T.AA.....A.G....G-	-----	[349]
HYTT1A_TT05_A	T.AA.....A.G....G-	-----	[348]
HYTT1B_TT05_B	T.AA.....A.G....G-	-----	[348]
HYTT4A_TT12_AA.....A.....G-	-----	[313]
HYTT4B_TT12_B	...G.....	C.A.....	..----.T..	.A.GG...G-	-----	[345]
HYFG1A_C420_AT.A..A..G-	-----	[342]
HYFG2A_C440_AA.....A.....G-	-----	[311]
HYFG3A_C442_A	T.AA-.....	...T.....	.A.G....G-	-----	[344]
HYFG4A_C444_A	T.AA.....A.G....G-	-----	[348]
ERA1A_C347_AA.....T..A...GA	AATAATTTTG	[323]
ERA2A_C348_A	...G.....	C.A.....	..----.T..	.A.G....G-	-----	[342]
EMM1A_JM443_A	T.AA.....A.....TG-	-----	[349]
EMM1B_JM443_B	T.AA.....A.....TG-	-----	[349]
EMM2A_JM1105_AT.A.T	.G.C.----	-----	[336]
EMM2B_JM1105_B	T.AA.....	..T.....	.AGT...-G-	-----	[338]
ETY1A_N27_A-.....	..A.....	..T.....	.A.G...A.G-	-----	[345]
ETY1B_N27_B-.....	..A.....	..T.....	.A.G...A.G-	-----	[345]
ETY2A_N101_A	T.AA.....A.G....G-	-----	[346]
ETY2B_N101_B	T.AA-.....A.G....G-	-----	[344]
ETY3A_PR05_A	T.AA.....A.G....G-	-----	[348]
ETY3B_PR05_B	-----...C.A.....	..----.T..A.G....G-	-----	[315]
ETY4A_PR06_AA.....A.....G-	-----	[312]
ETY4B_PR06_BA.....A.....G-	-----	[312]
FAV1A_JM488_A	...G.....	C.A.....	..----.T..	.A.G....G-	-----	[337]
FAV2A_JM883_AA.T.....A.....G-	-----	[345]
FAV4A_JM1908_AA.T.....A.....G-	-----	[345]
LAT1A_N2239_AAC.....A.....G-	-----	[343]
LAT2A_Y30_AA.....A.....G-	-----	[313]
LAT2B_Y30_BA.....A.....G-	-----	[344]
LAT3A_Y31_AA.....-	-----	[345]
LAT3B_Y31_B	T.AAT.....A.G....G-	-----	[348]
LAT4A_Y34_A	T.AA-.....A.G....G-	-----	[344]
LAT4B_Y34_B	T.AA.....A.G....G-	-----	[349]
NOT1A_PR12_AA.....T.	..T.....	.A.....G-	-----	[344]
NOT3A_PR15_A	T.AA-.....A.G....G-	-----	[343]
NOT3B_PR15_BA.....A.....G-	-----	[346]
NOT4A_PR114_A	T.AA-.....A.G....G-	-----	[344]
NOT4B_PR114_B	T.AA.....A.G....G-	-----	[362]
HIM1A_N620_A	C.A.....	..----.T..	.A.G....G-	-----	[345]
HIM2A_C2842_1	C.A.....	..----.T..	.A.G....G-	-----	[345]
HIM3A_PR18_A	C.A.....	..----.T..	.A.G....G-	-----	[346]
HIM3B_PR18_B	C.A.....	..----.T..	.A.G....G-	-----	[345]
HIM4A_PR19_A	C.A.....	..T---.-..	.A.G....G-	-----	[345]
HIM5A_PR45_A	T.AA.....A.G....G-	-----	[348]
HIM5B_PR45_B	T.AA.....A.G....G-	-----	[348]

HIM6A_JM521_A	T.AA.....A.G....G-	-----	[348]
HTELESIPHE_N11	C.AA.....A.G....G-	-----	[350]
HCLYSONIMUS_C3037	C.AA.....	..T.....	.A.G....G-	-----	[349]

[410	420	430	440	450]
[.]

CHE2A_C140_A	-----AG	ATAATT----	-TGTGTATGG	TAGGAGTATA	TGGGAGAGAT	[382]
CHE2B_C140_B	-----..----	[382]
CHE4A_C201_A	-----..----	[382]
CYR1A_N588_A	-----G..----C..	...TG....	...G.T.G.	[385]
CYR1B_N588_B	-----G..----C..	...TG....	...G.T.G.	[385]
CYR2A_C2861#1	-----..----	[382]
CYR2B_C2861#2	-----G..----AT.....	..A.G.T.G.	[386]
CYR3A_PR03_A	-----G..----G..	..AT.....	..A.G.T.G.	[386]
CYR3B_PR03_B	-----G..----AT.....	..A.G.T.G.	[386]
CYR5A_PR31_A	-----G..----T.....	...G.T.G.	[386]
CYR5B_PR31_B	-----..----	[382]
CYR6A_PR43_A	-----..----	[382]
CYR6B_PR43_B	-----G..----AT.....	..A.G.T.G.	[386]
PET1A_N7153_A	-----..----	-C.....T.	[373]
PET1B_N7153_B	-----G..----TCT.....	...G.T.G.	[380]
PET3A_N7183_A	-----G..----T.....	...G.T.G.	[385]
PET3B_N7183_B	AAAAAAAG.AAGAA	T.....T.	[361]
PET4A_C2980_A	-----..----T.	[388]
PET4B_C2980_B	-----..----T.	[363]
PET7A_PR26_A	-----G..----AT.....	..A.G.T.G.	[386]
PET7B_PR26_B	-----G..----AT.....	..A.G.T.G.	[387]
HYCO2A_C455_A	-----G..----AT.....	..A.G.T.GA	[386]
HYCO2B_C455_B	-----..A----A.....	...G.T.G.	[382]
HYCO3A_C456_A	-----G..----AT.....	..A.G.TAG.	[375]
HYCO3B_C456_B	-----G..----AT.....	..A.G.TAG.	[375]
HYCO4A_C457_A	-----G..----AT.....	..A.G.T.G.	[392]
HYCO4B_C457_B	-----G..----AT.....	...G.T.G.	[387]
HYTT1A_TT05_A	-----G..----T.....	...G.T.G.	[386]
HYTT1B_TT05_B	-----G..----AT.....	..A.G.T.G.	[386]
HYTT4A_TT12_A	-----..----G.T.	[349]
HYTT4B_TT12_B	-----..A	..C.....----A...G.	[382]
HYFG1A_C420_A	-----..----T.	[379]
HYFG2A_C440_A	-----..A----T.A...	[348]
HYFG3A_C442_A	-----G..----CT.....	...G.T.G.	[382]
HYFG4A_C444_A	-----G..A----AT.....	..A.G.T.G.	[386]
ERA1A_C347_A	AAAGAAAG.AAGAA	T.....T.	[373]
ERA2A_C348_A	-----..A	..C.....----G.	[379]
EMM1A_JM443_A	-----..A----	A.....G.	[386]
EMM1B_JM443_B	-----..A----	A.....G.	[386]
EMM2A_JM1105_A	-----..----	-C.....T.	[373]
EMM2B_JM1105_B	-----G..----AT.....	...T.G.	[376]
ETY1A_N27_A	-----..----AT.....	-..A.G.T.G.	[381]

ETY1B_N27_B	-----..----	-.....	..AT.....	-..A.G.T.G.	[381]
ETY2A_N101_A	-----G..----	-.....	..TT.....	..A.G.T.G.	[384]
ETY2B_N101_B	-----G..----	-.....	..CT.....G.T.G.	[382]
ETY3A_PR05_A	-----G..----	-.....	..AT.....G.T.G.	[386]
ETY3B_PR05_B	-----A	..C.....----	-.....G.	[352]
ETY4A_PR06_A	-----A----	-.....T.A....	[349]
ETY4B_PR06_B	-----A----	-.....T.A....	[349]
FAV1A_JM488_A	-----A	..C.....----	-.....G.	[374]
FAV2A_JM883_A	-----..A----	-.....G.	[382]
FAV4A_JM1908_A	-----..A----	-.....G.	[382]
LAT1A_N2239_A	-----..A----	-.....	..A.....G.	[380]
LAT2A_Y30_A	-----..----	-.....G.T.	[350]
LAT2B_Y30_B	-----..A----	-.....G.	[381]
LAT3A_Y31_A	-----..----	-.....	[382]
LAT3B_Y31_B	-----G..----	-.....	..T.....G.T.G.	[386]
LAT4A_Y34_A	-----G..----	-.....	..CT.....G.T.G.	[382]
LAT4B_Y34_B	-----G..----	-.....	..AT.....	..A.G.T.G.	[387]
NOT1A_PR12_A	-----..A----	-.....	[381]
NOT3A_PR15_A	-----G..----	-.....	..CT.....G.T.G.	[381]
NOT3B_PR15_B	-----..A----	-.....G.	[383]
NOT4A_PR114_A	-----G..----	-.....	..CT.....G.T.G.	[382]
NOT4B_PR114_B	-----G..----	-.....	..AT.....	..A.G.T.G.	[400]
HIM1A_N620_A	-----A	..C.....----	-.....G.	[382]
HIM2A_C2842_1	-----A	..C.....----	-.....G.	[382]
HIM3A_PR18_A	-----A	..C.....----	-.....G.	[383]
HIM3B_PR18_B	-----A	..C.....----	-.....G.	[382]
HIM4A_PR19_A	-----A	..C.....----	-.....G.	[382]
HIM5A_PR45_A	-----G..	..C.....----	-.....	..T.....GG.T.G.	[386]
HIM5B_PR45_B	-----G..	..C.....----	-.....	..C.T.....GG.T.G.	[386]
HIM6A_JM521_A	-----G..	..C.....----	-.....	..T.....GG.T.G.	[386]
HTELESIPHE_N11	-----..	..C.....----	-..C.....T.AG.	[387]
HCLYSONIMUS_C3037	-----..----	-.....A.A....	..C....G.	[386]

[460	470	480	490	500]
[.]

CHE2A_C140_A	ATAATAACAA	AA-----ACA	GTTTGCTAAG	AAA-----	-----	[410]
CHE2B_C140_B-----..-----	-----	[410]
CHE4A_C201_A-----	-----	[410]
CYR1A_N588_AGTCTCT.AT	.C....C..A	..-----	-----	[417]
CYR1B_N588_BGTCTCT.AT	.C....C..A	..-----	-----	[417]
CYR2A_C2861#1-----	-----	[410]
CYR2B_C2861#2GTCTCT...	.C....C..A	..-----	-----	[418]
CYR3A_PR03_AGTCTCT...	.C....C..A	..-----	-----	[418]
CYR3B_PR03_BGTCTCT...	.C....C..A	..-----	-----	[418]
CYR5A_PR31_AGTCTCT...	.C....C..A	..-----	-----	[418]
CYR5B_PR31_B-----..-----	-----	[410]
CYR6A_PR43_A-----	-----	[410]
CYR6B_PR43_BGTCTCT...	.C....C..A	..-----	-----	[418]

PET1A_N7153_A-----A	..-----	-----	[400]
PET1B_N7153_BGTCTCT...	.C....C..A	..-----	-----	[412]
PET3A_N7183_AGTCTCT...	.C....C..A	..-----	-----	[417]
PET3B_N7183_BT.A	..-----	-----	[389]
PET4A_C2980_AA	..-----	-----	[416]
PET4B_C2980_BA	..-----	-----	[391]
PET7A_PR26_AGTCTCT...	.C....C..A	..-----	-----	[418]
PET7B_PR26_BGTCTCT...	.C....C..A	..-----	-----	[419]
HYCO2A_C455_AGTCTCT...	.C....C..A	..-----	-----	[418]
HYCO2B_C455_BA	..A-----	-----	[411]
HYCO3A_C456_AGTCTCT...	AC....C..A	..-----	-----	[407]
HYCO3B_C456_BGTCTCT...	AC....C..A	..-----	-----	[407]
HYCO4A_C457_AGTCTCT...	.C....C..A	..-----	-----	[424]
HYCO4B_C457_BGTATCT...	.C..C..C..A	..-----	-----	[419]
HYTT1A_TT05_AGTCTCT...	.C....C..A	..-----	-----	[418]
HYTT1B_TT05_BGTCTCT...	.C....C..A	..-----	-----	[418]
HYTT4A_TT12_AA	..A-----	-----	[378]
HYTT4B_TT12_BTCT---A	..A-----	-----	[413]
HYFG1A_C420_AA	..-----	-----	[406]
HYFG2A_C440_AA	..-----	-----	[376]
HYFG3A_C442_AGTCTCT...	.C....C..A	..-----	-----	[414]
HYFG4A_C444_AGTCTCT...	.C....C..A	..-----	-----	[418]
ERA1A_C347_AA	..-----	-----	[401]
ERA2A_C348_AG..TCTCT...A	..A-----	-----	[413]
EMM1A_JM443_A	...G.....A	..A-----	-----	[415]
EMM1B_JM443_B	...G.....A	..A-----	-----	[415]
EMM2A_JM1105_AA	..A-----	-----	[402]
EMM2B_JM1105_BGTCTCTT..	.C....C..A	..-----	-----	[408]
ETY1A_N27_AGTCTCT...	.C..AAC..A	..-----	-----	[414]
ETY1B_N27_BGTCTCT...	.C..AAC..A	..-----	-----	[413]
ETY2A_N101_AGTCTCT...	.C..A.C..A	..-----	-----	[416]
ETY2B_N101_BGTCTCT...	.C....C..A	..-----	-----	[414]
ETY3A_PR05_A	...C.---	.GTCTCT...	.C....-.A	..-----	-----	[415]
ETY3B_PR05_BG..TCTCT...A	..A-----	-----	[386]
ETY4A_PR06_AA	..-----	-----	[377]
ETY4B_PR06_BA	..-----	-----	[377]
FAV1A_JM488_AG..TCTCT...A	..A-----	-----	[408]
FAV2A_JM883_AA	..-----	-----	[410]
FAV4A_JM1908_AA	..A-----	-----	[411]
LAT1A_N2239_AA	..-----	-----	[408]
LAT2A_Y30_AA	..-----	-----	[377]
LAT2B_Y30_BA	..-----	-----	[409]
LAT3A_Y31_A-----	-----	[410]
LAT3B_Y31_BGTCTCT...	.C....C..A	..-----	-----	[418]
LAT4A_Y34_AT..GTCTCT...	.C....C..A	..-----	-----	[414]
LAT4B_Y34_BGTCTCT...	.C....C..A	..-----	-----	[419]
NOT1A_PR12_AA	..-----	-----	[409]
NOT3A_PR15_AGTCTCT...	.C....C..A	..-----	-----	[413]
NOT3B_PR15_BT.A	..-----	-----	[411]

NOT4A_PR114_AGTCTCT...C....C..A ..-----	[414]
NOT4B_PR114_BGTCTCT...C....C..A ..-----	[432]
HIM1A_N620_ATCC---...A ..A-----	[413]
HIM2A_C2842_1TCC---...A ..A-----	[413]
HIM3A_PR18_ATCC---...A ..A-----	[414]
HIM3B_PR18_BTCC---...A ..A-----	[413]
HIM4A_PR19_ATCC---...A ..A-----	[413]
HIM5A_PR45_AG..GTCTCT...C....C..A ..--TCTATA CTCTATCTAT	[434]
HIM5B_PR45_BG..GTCTCT...C....C..A ..--TCTATA CTCTATGTAT	[434]
HIM6A_JM521_AG..GTCTCT...C....C..A ..--TCTATA CTCTATCTAT	[434]
HTELESIPHE_N11	T.....G..TCTCT.A.....A ..-----	[420]
HCLYSONIMUS_C3037TTTCT...A.....A ..-----	[419]

[510	520	530	540	550]
[.]

CHE2A_C140_A	-----TCTT TGATATATAG AATATTAA-G TAATTTCTTC TCATTACATA	[453]
CHE2B_C140_B	-----... ..-	[453]
CHE4A_C201_A	-----... ..-	[453]
CYR1A_N588_A	-----...A-..C.....C.T..C..G	[449]
CYR1B_N588_B	-----...A-..C.....C.T..C..G	[449]
CYR2A_C2861#1	-----... ..-	[453]
CYR2B_C2861#2	-----...A-..C.....T.....G	[461]
CYR3A_PR03_A	-----...A-..C.....T.....G	[461]
CYR3B_PR03_B	-----...A-..C.....T.....G	[461]
CYR5A_PR31_A	-----C..A-..C.....T..C..G	[460]
CYR5B_PR31_B	-----... ..-	[453]
CYR6A_PR43_A	-----... ..-	[453]
CYR6B_PR43_B	-----...A-..C.....T.....G	[461]
PET1A_N7153_A	-----... ..G.....-..C.....TT..C..G	[443]
PET1B_N7153_B	-----...A-..C.....T.....G	[455]
PET3A_N7183_A	-----...A-..C.....T.....G	[460]
PET3B_N7183_B	-----... ..-	[432]
PET4A_C2980_A	-----... ..-C..C.....T.....G	[459]
PET4B_C2980_B	-----... ..-C..C.....T.....G	[434]
PET7A_PR26_A	-----...A-..C.....T..TT.....G	[461]
PET7B_PR26_B	-----...A-..C.....T.....G	[462]
HYCO2A_C455_A	-----...A-..C.....T.....G	[461]
HYCO2B_C455_B	-----... ..-A..C.....T.....G	[453]
HYCO3A_C456_A	-----...A-..C.....T.....G	[450]
HYCO3B_C456_B	-----...A-..C.....T.....G	[450]
HYCO4A_C457_A	-----...A-..C.....T.....G	[467]
HYCO4B_C457_B	-----...A-..GC.....TT..C..G	[462]
HYTT1A_TT05_A	-----C..A-..C.....T..C..G	[460]
HYTT1B_TT05_B	-----T.A-..C.....T.....G	[461]
HYTT4A_TT12_A	-----... ..-A..C.....T.....G	[420]
HYTT4B_TT12_B	-----... ..-..C.....T..TT.....G	[455]
HYFG1A_C420_A	-----... ..-..C.....TT..C..G	[449]
HYFG2A_C440_A	-----... ..-..C.....T.....G	[419]

HYFG3A_C442_A	-----..A	-----..C.....T ..T.....G	[457]
HYFG4A_C444_A	-----..A	-----..C.....T ..T.....G	[461]
ERA1A_C347_A	-----.....	-----..C.....T ..T.....G	[444]
ERA2A_C348_A	-----.....	-----..C.....T ..T.....G	[455]
EMM1A_JM443_A	-----.....	-----A ..C.....T ..T.....C	[457]
EMM1B_JM443_B	-----.....	-----A ..C.....T ..T.....C	[457]
EMM2A_JM1105_A	-----..C.....	-----A ..C.....T ..T.....G	[444]
EMM2B_JM1105_B	-----..A	-----..C.....T ..T.....G	[451]
ETY1A_N27_A	-----..A	-----..C.....T ..T.....G	[457]
ETY1B_N27_B	-----..A	-----..C.....T ..T.....G	[456]
ETY2A_N101_A	-----..A	-----..C.....T ..T.....G	[459]
ETY2B_N101_B	-----..A	-----..C.....T ..T.....G	[457]
ETY3A_PR05_A	-----..A	-----..C.....T ..T.....G	[458]
ETY3B_PR05_B	-----.....	-----..C.....TT..C..G	[428]
ETY4A_PR06_A	-----..C	-----..C.....T ..T.....G	[420]
ETY4B_PR06_B	-----.....	-----..C.....T ..T.....G	[420]
FAV1A_JM488_A	-----.....	-----..C.....TT..C..G	[450]
FAV2A_JM883_A	-----.....	-----A ..C.....T ..T.....G	[452]
FAV4A_JM1908_A	-----.....	-----A ..C.....T ..T.....G	[453]
LAT1A_N2239_A	-----.....	-----A ..C.....T ..T.....G	[450]
LAT2A_Y30_A	-----.....	-----..C.....T ..T.....G	[420]
LAT2B_Y30_B	-----.....	-----A ..C.....T ..T.....G	[452]
LAT3A_Y31_A	-----.....	-----.....	[453]
LAT3B_Y31_B	-----..A	-----..C.....T ..T.....G	[461]
LAT4A_Y34_A	-----..A	-----..C.....T ..T.....G	[457]
LAT4B_Y34_B	-----..A	-----..C.....T ..T.....G	[462]
NOT1A_PR12_A	-----.....	-----A ..C.....T ..T.....G	[452]
NOT3A_PR15_A	-----..A	-----..C.....T ..T.....G	[456]
NOT3B_PR15_B	-----.....	-----A ..C.....T ..T.....G	[454]
NOT4A_PR114_A	-----..A	-----..C.....T ..T.....G	[457]
NOT4B_PR114_B	-----..A	-----..C.....T ..T.....G	[475]
HIM1A_N620_A	-----.....	-----..CC..T.- -TT.....G	[453]
HIM2A_C2842_1	-----.....	-----..CC..T.- -TT.....G	[453]
HIM3A_PR18_A	-----.....	-----A ..CC.--..T ..TT.....G	[455]
HIM3B_PR18_B	-----.....	-----..CC.--..T ..TT.....G	[453]
HIM4A_PR19_A	-----.....	-----..CC..T.- -T.....G	[452]
HIM5A_PR45_A	AATCTA...A	-----..C.....C.T..C..G	[472]
HIM5B_PR45_B	AATCTA...A	-----..C.....C.T..C..G	[472]
HIM6A_JM521_A	AATCTA...A	-----..C.....C.T..C..G	[472]
HTELESIPHE_N11	-----.....	-----..C..G....T ..T.....G	[463]
HCLYSONIMUS_C3037	-----..... G.....	-----T ..C..G...T ..T.....G	[462]

[560	570	580	590	600]
[.]

CHE2A_C140_A	ATAGCAAT-- ATTTTATTAC AGAACCATGC CGAACAACTT CATAAGAGCT	[501]
CHE2B_C140_BA--	[501]
CHE4A_C201_A--	[501]
CYR1A_N588_A	.C.A...A-- ..A..G.... A.....	[497]

CYR1B_N588_B	.C.A...A-- ..A..G....	A.....	[497]
CYR2A_C2861#1A--	[501]
CYR2B_C2861#2	...A...A--C.....T....	A.....	[509]
CYR3A_PR03_A	...A...A--C.....T....	A.....	[509]
CYR3B_PR03_B	...A...A--C.....T....	A.....	[509]
CYR5A_PR31_A	.C.A...C-- ..A..G....	A.....	[508]
CYR5B_PR31_BA--	[501]
CYR6A_PR43_AA--	[501]
CYR6B_PR43_B	...A...A--C.....T....	A.....	[509]
PET1A_N7153_A	...A...A--	A.....	[491]
PET1B_N7153_B	...AA..ATA T.....T....	A..C.....	[505]
PET3A_N7183_A	...A...A--	A.....	..C.....	[508]
PET3B_N7183_B	...A...A--T....	A.....	..C.....	[480]
PET4A_C2980_A	...A...A--T....	A.....C..	[507]
PET4B_C2980_B	...A...A--	A.....	..C.....	[482]
PET7A_PR26_A	...A...A--	A.....	..C.....	[509]
PET7B_PR26_B	...A...A--C.....T....	A.....	[510]
HYCO2A_C455_A	...A...A-- ..A.CG....	A.....	..C.....	[509]
HYCO2B_C455_BA--G....	A.....	[501]
HYCO3A_C456_A	...A...A--C.....T....	A.....	..C.....	[498]
HYCO3B_C456_B	...A...A--C.....	G...T....	A.....	..C.....	[498]
HYCO4A_C457_A	...A...A--C.....T....	A.....	[515]
HYCO4B_C457_B	...A...A--	A.....	..C.....	[510]
HYTT1A_TT05_A	.C.A...C-- ..A..G....	A.....	[508]
HYTT1B_TT05_B	...A...A--T....	A.....	[509]
HYTT4A_TT12_AT..A-- ..G.....	A.....	[468]
HYTT4B_TT12_B	...A...A-- ..G.....	A.....	[503]
HYFG1A_C420_A	...A.T.A--	A.....	[497]
HYFG2A_C440_A	?????????? ???? ?????? ?????????? ??????????	[469]
HYFG3A_C442_A	...AA..ATAT....	A.....	[507]
HYFG4A_C444_A	...A...A--T....	A.....	[509]
ERA1A_C347_A	...A...A--G....	A.....A..	[492]
ERA2A_C348_A	...A...A--	A.....	[503]
EMM1A_JM443_A	...A...A--	A.....	[505]
EMM1B_JM443_B	...A...A--	A.....	[505]
EMM2A_JM1105_AA--	A.....	..C.....	[492]
EMM2B_JM1105_B	...A...A-- G.....T....	A.....	[499]
ETY1A_N27_A	...A...A--	[505]
ETY1B_N27_B	...A...A--	[504]
ETY2A_N101_A	...A...A--T....	A.....	[507]
ETY2B_N101_B	...AA..ATA T.....T....	A.....	[507]
ETY3A_PR05_A	...A...A--T....	A.....	[506]
ETY3B_PR05_B	...A.T.A--	A.....	..C.....	[476]
ETY4A_PR06_A	...A...A--G....	A.....	[468]
ETY4B_PR06_B	...A...A--	A.....	[468]
FAV1A_JM488_A	...A.T.A--	A.....	..C.....	[498]
FAV2A_JM883_AA--T....	A.....	[500]
FAV4A_JM1908_AA--T....	A.....	[501]
LAT1A_N2239_AA--	A.....	[498]

LAT2A_Y30_A	...A...A--C..T.....	A.....	[468]
LAT2B_Y30_BA--	A.....	[500]
LAT3A_Y31_AA--	A.....	[501]
LAT3B_Y31_B	...AA..ATA	A.....	[511]
LAT4A_Y34_A	...AA..ATAT.....	A.....	[507]
LAT4B_Y34_B	...A...A--T.....	A.....	[510]
NOT1A_PR12_AA--	A.....	[500]
NOT3A_PR15_A	...AA..ATAT.....	A.....	[506]
NOT3B_PR15_BCTA--	A.....C.....	[502]
NOT4A_PR114_A	...AA..ATAT.....	A.....	[507]
NOT4B_PR114_B	...A...A--C.....T.....	A.....	[523]
HIM1A_N620_A	...A...A--	A.....C.....	[501]
HIM2A_C2842_1	...A...A--	A.....	[501]
HIM3A_PR18_A	...A...A--	A.....C.....	[503]
HIM3B_PR18_B	...A...A--	A.....C.....	[501]
HIM4A_PR19_A	...A...A--	A.....C.....	[500]
HIM5A_PR45_A	.C.A...A--	..A..G....	A.....	[520]
HIM5B_PR45_B	.C.A...A--	..A..G....	A.....	[520]
HIM6A_JM521_A	.C.A...A--	..A..G....	A.....	[520]
HTELESIPHE_N11	...A...A--	A.....	[511]
HCLYSONIMUS_C3037	...A...A--	A.....A	[510]

[610]
[.]

CHE2A_C140_A	TTCCTGACAT G	[512]
CHE2B_C140_B	[512]
CHE4A_C201_A	[512]
CYR1A_N588_A	[508]
CYR1B_N588_B	[508]
CYR2A_C2861#1	[512]
CYR2B_C2861#2TG	[520]
CYR3A_PR03_A	[520]
CYR3B_PR03_B	[520]
CYR5A_PR31_A	[519]
CYR5B_PR31_B	[512]
CYR6A_PR43_A	[512]
CYR6B_PR43_B	[520]
PET1A_N7153_A	[502]
PET1B_N7153_B	...G.....	[516]
PET3A_N7183_A	[519]
PET3B_N7183_B	[491]
PET4A_C2980_AG	[518]
PET4B_C2980_BG	[493]
PET7A_PR26_A	[520]
PET7B_PR26_B	[521]
HYCO2A_C455_A	[520]
HYCO2B_C455_B	[512]
HYCO3A_C456_A	[509]

HYCO3B_C456_B	[509]
HYCO4A_C457_A	[526]
HYCO4B_C457_B	[521]
HYTT1A_TT05_A	[519]
HYTT1B_TT05_B	[520]
HYTT4A_TT12_A	[479]
HYTT4B_TT12_B	[514]
HYFG1A_C420_A	[508]
HYFG2A_C440_A	????????? ?	[480]
HYFG3A_C442_A	[518]
HYFG4A_C444_A	[520]
ERA1A_C347_A	[503]
ERA2A_C348_A	[514]
EMM1A_JM443_A	..????????? ?	[516]
EMM1B_JM443_B	[516]
EMM2A_JM1105_A	[503]
EMM2B_JM1105_BT..	[510]
ETY1A_N27_A	[516]
ETY1B_N27_B	[515]
ETY2A_N101_A	[518]
ETY2B_N101_B	[518]
ETY3A_PR05_A	[517]
ETY3B_PR05_B	[487]
ETY4A_PR06_A	[479]
ETY4B_PR06_B	[479]
FAV1A_JM488_A	[509]
FAV2A_JM883_A	[511]
FAV4A_JM1908_A	[512]
LAT1A_N2239_A	[509]
LAT2A_Y30_A	[479]
LAT2B_Y30_B	[511]
LAT3A_Y31_A	[512]
LAT3B_Y31_BT..	[522]
LAT4A_Y34_A	[518]
LAT4B_Y34_B	[521]
NOT1A_PR12_A	[511]
NOT3A_PR15_A	[517]
NOT3B_PR15_B	[513]
NOT4A_PR114_A	.????????? ?	[518]
NOT4B_PR114_B	[534]
HIM1A_N620_A	[512]
HIM2A_C2842_1	[512]
HIM3A_PR18_A	[514]
HIM3B_PR18_B	[512]
HIM4A_PR19_A	[511]
HIM5A_PR45_A	[531]
HIM5B_PR45_B	[531]
HIM6A_JM521_A	[531]
HTELESIPHE_N11	[522]


```

HCLYSONIMUS_C3037      .....   [521]
;
END;
BEGIN paup;
exclude 43-77 257-258 278-280 466-476 484-515;
Lset Base=(0.4223 0.1137 0.1189) Nst=6 Rmat=(0.8892 2.5421 0.4409 1.8449 3.6626) Rates=gamma Shape=0.6013 Pinvar=0;
END;

```

B. Alignment for *H. erato* at the *Tpi* locus

```
#NEXUS
```

```
BEGIN DATA;
```

```
    DIMENSIONS NTAX=70 NCHAR=433;
```

```
    FORMAT DATATYPE=DNA MISSING=? GAP=- MATCHCHAR=. INTERLEAVE ;
```

```
MATRIX
```

	10	20	30	40	50]	
[.]	
CHE1A_C65_A	TGGTGAAAAG	GATGATCTGG	TTGCTGAAAA	GGTAAAACAA	GCTTTT----	[46]
CHE2A_C140_A----	[46]
CHE3A_C188_A----	[46]
CHE4A_C201_A----	[46]
CHE5A_C206_A----	[46]
CYR2A_C2861_1----	[46]
CYR2B_C2861_2----	[46]
CYR3A_PR03_A----	[46]
CYR4A_PR10_A----	[46]
CYR5A_PR31_A----	[46]
CYR6A_PR43_A----	[46]
PET1A_N7153_AACTTA	[50]
PET2A_N7154_AACTTA	[50]
PET3A_N7183_AG.----	[46]
PET4A_C2980_1----	[46]
PET4B_C2980_2----	[46]
PET5A_C2981_1----	[46]
PET5B_C2981_2G.----	[46]
PET6A_P50_A----	[46]
PET7A_PR26_A----	[46]
HYC01A_C454_AG.----	[46]
HYC01B_C454_BA.----	[46]
HYC02A_C455_AG.----	[46]
HYC04A_C457_A----	[46]
HYTT1A_TT05_A----	[46]
HYTT2A_TT06_A----	[46]
HYTT2B_TT06_B----	[46]
HYTT3A_TT07_A----	[46]

HYTT3B_TT07_BG..----	[46]
HYTT4A_TT12_AG..----	[46]
HYFG1A_C420_AG..----	[46]
HYFG2A_C440_A----	[46]
HYFG2B_C440_B----	[46]
HYFG3A_C442_A----	[46]
HYFG3B_C442_B----	[46]
ERA1A_C347_AG..----	[46]
ERA2A_C348_AA----	[46]	
ERA3A_C349_A----	[46]
ERA3B_C349_BG..----	[46]
EMM1A_JM443_AC----	[46]	
EMM2A_JM1105_A----	[46]
ETY1A_N27_A----	[46]
ETY2A_N101_A----	[46]
ETY3A_PR05_AA----	[46]	
ETY4A_PR06_A----	[46]
FAV1A_JM488_A----	[46]
FAV2A_JM883_AA----	[46]
FAV3A_JM1141_A	...C.....G..----	[46]
FAV4A_JM1908_A----	[46]
FAV5A_JM1911_AA----	[46]	
LAT3A_Y31_A----	[46]
LAT3B_Y31_B----	[46]
LAT4A_Y34_A----	[46]
NOT1A_PR12_AA----	[46]	
NOT1B_PR12_BA----	[46]	
NOT2A_PR13_AA----	[46]	
NOT3A_PR15_A----	[46]
NOT4A_PR114_AA----	[46]	
HIM1A_N620_A----	[46]
HIM2A_C2842_1----	[46]
HIM2B_C2842_2T....----	[46]
HIM3A_PR18_A----	[46]
HIM4A_PR19_A----	[46]
HIM5A_PR45_AA.....----	[46]
HIM5B_PR45_BT....----	[46]
HIM6A_JM521_A----	[46]
HIM7A_JM522_A----	[46]
HIM7B_JM522_B----	[46]
H.CLYSONIMUS_C3037_1----	[46]
H.TELESIPHE_N11_A----	[46]

[60	70	80	90	100]
[.]

CHE1A_C65_A	-----	-----AAGA	CAGCA-----	-AAGTTAAAT	TTATTGT-TA	[73]
CHE2A_C140_A	-----	-----	-----T..	[74]
CHE3A_C188_A	-----	-----	-----T..	[74]

CHE4A_C201_A	-----	-----	-----	-.....T..	[74]
CHE5A_C206_A	-----	-----	-----	-.....T..	[74]
CYR2A_C2861_1	-----	-----	-----	-.....T..	[74]
CYR2B_C2861_2	-----	-----	-----	-.....T..	[74]
CYR3A_PR03_A	-----	-----	..C.	.TA.T	-----	-.....A..C..	[74]
CYR4A_PR10_A	-----	-----	-----	-.....T..	[74]
CYR5A_PR31_A	-----	-----	-----	-.....T..	[74]
CYR6A_PR43_A	-----	-----	..C.	.TA.T	-----	-.....A..C..	[74]
PET1A_N7153_A	ACTTTACTTA	ACAAGC	-----	-.....T..	[94]
PET2A_N7154_A	ACTTTACTTA	ACAAGC	-----	-.....T..	[94]
PET3A_N7183_A	-----	-----	.T.	-----	-.....T..	[74]
PET4A_C2980_1	-----	-----	..G	-----	-.....T..	[74]
PET4B_C2980_2	-----	-----	T....	-----	-.....T..	[74]
PET5A_C2981_1	-----	-----	-----	-.....T..	[74]
PET5B_C2981_2	-----	-----	.T.	-----	-.....T..	[74]
PET6A_P50_A	-----	-----	-----	-.....T..	[74]
PET7A_PR26_A	-----	-----	-----	-.....T..	[74]
HYCO1A_C454_A	-----	-----	.T.	-----	-.....T..	[74]
HYCO1B_C454_B	-----	-----	-----	-.....T..	[74]
HYCO2A_C455_A	-----	-----	.T.	-----	-.....T..	[74]
HYCO4A_C457_A	-----	-----	-----	-.....T..	[74]
HYTT1A_TT05_A	-----	-----	-----	-.....T..	[74]
HYTT2A_TT06_A	-----	-----	-----	-.....T..	[74]
HYTT2B_TT06_B	-----	-----	-----	-.....T..	[74]
HYTT3A_TT07_A	-----	-----	-----	-.....T..	[74]
HYTT3B_TT07_B	-----	-----	-----	-.....T..	[74]
HYTT4A_TT12_A	-----	-----	.T.	-----	-.....T..	[74]
HYFG1A_C420_A	-----	-----	.T.	-----	-.....T..	[74]
HYFG2A_C440_A	-----	-----	-----	-.....T..	[74]
HYFG2B_C440_B	-----	-----	-----	-.....T..	[74]
HYFG3A_C442_A	-----	-----	-----	-.....C..	[74]
HYFG3B_C442_B	-----	-----	-----	-.....T..	[74]
ERA1A_C347_A	-----	-----	.TA.	-----	-.....T..	[74]
ERA2A_C348_A	-----	-----	-----	-.....T..	[74]
ERA3A_C349_A	-----	-----	-----	-.....T..	[74]
ERA3B_C349_B	-----	-----	-----	-.....T..	[74]
EMM1A_JM443_A	-----	-----	-G..	-----	-.....T..	[74]
EMM2A_JM1105_A	-----	-----	-----	-.....T..	[74]
ETY1A_N27_A	-----	-----	-----	-.....T..	[74]
ETY2A_N101_A	-----	-----	..G	-----	-.....T..	[74]
ETY3A_PR05_A	-----	-----	-----	-.....T..	[74]
ETY4A_PR06_A	-----	-----AA.GACAA	A.....	-.....T..	[80]
FAV1A_JM488_A	-----	-----	-----	-.....C..	[74]
FAV2A_JM883_A	-----	-----	-----	-.....A.T..	[74]
FAV3A_JM1141_A	-----	-----	.T.	-----	-.....T..	[74]
FAV4A_JM1908_A	-----	-----AA.GACAA	A.....	-.....T..	[80]
FAV5A_JM1911_A	-----	-----	-----	-.....T..	[74]
LAT3A_Y31_A	-----	-----	-----	-.....T..	[74]
LAT3B_Y31_B	-----	-----	..G	-----	-.....T..	[74]

LAT4A_Y34_A	-----	-----	-----	-..A.....T..	[74]
NOT1A_PR12_A	-----	-----	-----	-.....T..	[74]
NOT1B_PR12_B	-----	-----	-----	-.....T..	[74]
NOT2A_PR13_A	-----	-----	-----	-.....T..	[74]
NOT3A_PR15_A	-----	-----	-----	-.....T..	[74]
NOT4A_PR114_A	-----	-----	-----	-.....T..	[74]
HIM1A_N620_A	-----	-----	-----	-.....C..	[74]
HIM2A_C2842_1	-----	-----	-----	-.....C..	[74]
HIM2B_C2842_2	-----	-----	-----	-.....	C.....C..	[74]
HIM3A_PR18_A	-----	-----	-----	-.....C..	[74]
HIM4A_PR19_A	-----	-----	-----	-.....C..	[74]
HIM5A_PR45_A	-----	-----	-----	-.....C..	[74]
HIM5B_PR45_B	-----	-----	-----	-.....C..	[74]
HIM6A_JM521_A	-----	-----	-----	-.....C..	[74]
HIM7A_JM522_A	-----	-----	-----	-.....C..	[74]
HIM7B_JM522_B	-----	-----	-----	-.....C..	[74]
H. CLYSONIMUS_C3037_1	-----	-----	..C.	-----	-..G.....C..	[74]
H. TELESIPHE_N11_A	-----	-----	..C.	-----	-.....C..	[74]

[110	120	130	140	150]
[.]

CHE1A_C65_A	GTATTTTCTA	TGAATTACTA	TAACAATTGT	ATAAATAAGT	TCACAAATGC	[123]
CHE2A_C140_A	[124]
CHE3A_C188_A	[124]
CHE4A_C201_A	[124]
CHE5A_C206_A	[124]
CYR2A_C2861_1T..	..C.....	[124]
CYR2B_C2861_2T..	..C.....	[124]
CYR3A_PR03_AT..	..C.....	[124]
CYR4A_PR10_AT..	..C.....	[124]
CYR5A_PR31_AT..	..C.....	[124]
CYR6A_PR43_AT..	..C.....	[124]
PET1A_N7153_AT..	..C.....	[144]
PET2A_N7154_AT..	..C.....	[144]
PET3A_N7183_AT..	..C.....	[124]
PET4A_C2980_1T..	..C.....T..	[124]
PET4B_C2980_2	..G.....T..	..T.....	[124]
PET5A_C2981_1T..	..C.....	[124]
PET5B_C2981_2T..	..C.....	[124]
PET6A_P50_AT..	..C.....	[124]
PET7A_PR26_AT..	..C.....	[124]
HYC01A_C454_AT..	..C.....	[124]
HYC01B_C454_BA....T..	..C.....T.	[124]
HYC02A_C455_AT..	..C.....	[124]
HYC04A_C457_AT..	..C.....A.	...T.....	[124]
HYTT1A_TT05_AT..	..C.....A.	[124]
HYTT2A_TT06_A	[124]
HYTT2B_TT06_B	[124]

HYTT3A_TT07_A	[124]
HYTT3B_TT07_B	[124]
HYTT4A_TT12_AT.	..C.	[124]
HYFG1A_C420_AT.	..C.	[124]
HYFG2A_C440_AT.	..C.	[124]
HYFG2B_C440_BT.	..C.	[124]
HYFG3A_C442_AT.	..C.	[124]
HYFG3B_C442_BT.	..TC.	[124]
ERA1A_C347_AT.	..C.	[124]
ERA2A_C348_AA.....	..C.T.	[124]
ERA3A_C349_AA.....	[124]
ERA3B_C349_BT.A.	[124]
EMM1A_JM443_AT.	..C.	[124]
EMM2A_JM1105_A	[124]
ETY1A_N27_AT.	..C.	[124]
ETY2A_N101_AT.	..C.T.	[124]
ETY3A_PR05_AA.....	..T.	..C.T.	[124]
ETY4A_PR06_A	A.....T.	..C.	[130]
FAV1A_JM488_AT.	..C.	[124]
FAV2A_JM883_AT.A.T.	[124]
FAV3A_JM1141_AT.	..C.	[124]
FAV4A_JM1908_A	A.....T.	..C.	[130]
FAV5A_JM1911_AA.....	..T.	..C.T.	[124]
LAT3A_Y31_AT.	..C.	[124]
LAT3B_Y31_BT.G	..C.T.	[124]
LAT4A_Y34_AT.	..C....	--- --	-----	[101]
NOT1A_PR12_AA.....	..T.	..C.T.	[124]
NOT1B_PR12_BA.....	..T.	..C.T.	[124]
NOT2A_PR13_AA.....	..T.	..C.T.	[124]
NOT3A_PR15_AT.	[124]
NOT4A_PR114_AA.....	..T.	..C.T.	[124]
HIM1A_N620_AT.	..C.	[124]
HIM2A_C2842_1T.	..C.	[124]
HIM2B_C2842_2T.	..C.	[124]
HIM3A_PR18_AT.	..C.	[124]
HIM4A_PR19_AT.	..C.	[124]
HIM5A_PR45_AT.	..C.	[124]
HIM5B_PR45_BT.	..C.	[124]
HIM6A_JM521_AT.	..C.	[124]
HIM7A_JM522_AT.	..C.	[124]
HIM7B_JM522_BT.	..C.	[124]
H.CLYSONIMUS_C3037_1TC.	..C.K.G.....	[124]
H.TELESIPHE_N11_AT.	..C.A.	[124]

[160	170	180	190	200]
[.]

CHE1A_C65_A	CATGAAAATG	TGCAGGAGGA	ATAATGTGGG	TGGGCCAAGT	TGTTCAAATG	[173]
CHE2A_C140_A	[174]

CHE3A_C188_A	[174]
CHE4A_C201_A	[174]
CHE5A_C206_A	[174]
CYR2A_C2861_1C.....	[174]
CYR2B_C2861_2	.T.....T.....	[174]
CYR3A_PR03_AT.AA.	[174]
CYR4A_PR10_AC.....	[174]
CYR5A_PR31_A	[174]
CYR6A_PR43_AT.AA.	[174]
PET1A_N7153_ACA.....	[194]
PET2A_N7154_ACA.....	[194]
PET3A_N7183_AA.....	[174]
PET4A_C2980_1C.....	[174]
PET4B_C2980_2	[174]
PET5A_C2981_1A.....	[174]
PET5B_C2981_2	[174]
PET6A_P50_A	[174]
PET7A_PR26_AG.....	[174]
HYCO1A_C454_A	[174]
HYCO1B_C454_B	T.....	[174]
HYCO2A_C455_A	[174]
HYCO4A_C457_AA	[174]
HYTT1A_TT05_AA	[174]
HYTT2A_TT06_A	T.....A.....	[174]
HYTT2B_TT06_B	T.....G.....A.....	[174]
HYTT3A_TT07_A	T.....A.....	[174]
HYTT3B_TT07_B	T.....A.....	...C.....	[174]
HYTT4A_TT12_A	[174]
HYFG1A_C420_A---	[171]
HYFG2A_C440_AT.AA.A	[174]
HYFG2B_C440_BA...G	-....A....	...A.....	[173]
HYFG3A_C442_AT.AA.A	[174]
HYFG3B_C442_BA...G	-....A....	...A.....	[173]
ERA1A_C347_AG.....	[174]
ERA2A_C348_A	T.....	[174]
ERA3A_C349_AA.....	[174]
ERA3B_C349_BC.A.....	[174]
EMM1A_JM443_AG.....	[174]
EMM2A_JM1105_AA.....	[174]
ETY1A_N27_A	[174]
ETY2A_N101_AC.....A.....G.....	[174]
ETY3A_PR05_A	T.....	[174]
ETY4A_PR06_AA----	[176]
FAV1A_JM488_AC.A.....	[174]
FAV2A_JM883_A--	-----	[165]
FAV3A_JM1141_AA.....C.....	[174]
FAV4A_JM1908_AA.....	[180]
FAV5A_JM1911_A	T.....	[174]
LAT3A_Y31_A	[174]

LAT3B_Y31_BC.....	[174]
LAT4A_Y34_A	---...G.A....	[147]
NOT1A_PR12_A	T.....AA	[174]
NOT1B_PR12_B	T.....C.A.	[174]
NOT2A_PR13_A	T.....	[174]
NOT3A_PR15_AA.-..	[173]
NOT4A_PR114_A	T.....	[174]
HIM1A_N620_AT.AA.T...A	[174]
HIM2A_C2842_1T.AA.A	[174]
HIM2B_C2842_2T.AA.T...A	[174]
HIM3A_PR18_AT.AA.T...A	[174]
HIM4A_PR19_AT.AA.T...A	[174]
HIM5A_PR45_AT.AA.T...A	[174]
HIM5B_PR45_BT.AA.A	[174]
HIM6A_JM521_AT.AA.T...A	[174]
HIM7A_JM522_AT.AA.T...A	[174]
HIM7B_JM522_BT.AA.A	[174]
H.CLYSONIMUS_C3037_1CA..	[174]
H.TELESIPHE_N11_AAC...	[174]

[210	220	230	240	250]
[.]

CHE1A_C65_A	AGTAATTGTT	AAGTTGGTCA	ATATTTGCAT	AA-----	-----	[205]
CHE2A_C140_A-----	-----	[206]
CHE3A_C188_A-----	-----	[206]
CHE4A_C201_A-----	-----	[206]
CHE5A_C206_A-----	-----	[206]
CYR2A_C2861_1C...-----	-----	[206]
CYR2B_C2861_2-----	-----	[206]
CYR3A_PR03_A	..C.....GCATTGCT	GTATATTACA	[224]
CYR4A_PR10_A-----	-----	[206]
CYR5A_PR31_A-...T...-----	-----	[205]
CYR6A_PR43_A	..C.....GCATTGCT	GTATATTACA	[224]
PET1A_N7153_A-----	-----	[226]
PET2A_N7154_A-----	-----	[226]
PET3A_N7183_A-----	-----	[206]
PET4A_C2980_1A...	..-----	-----	[206]
PET4B_C2980_2	..C.-.....A....A	..TCAATGCT	GTAT--TAC-	[220]
PET5A_C2981_1C.	..-----	-----	[206]
PET5B_C2981_2-----	-----	[206]
PET6A_P50_A-----	-----	[206]
PET7A_PR26_AC.	..-----	-----	[206]
HYC01A_C454_A-----	-----	[206]
HYC01B_C454_BC...-----	-----	[206]
HYC02A_C455_AG.	..-----	-----	[206]
HYC04A_C457_A	..C.....A....A	..TCAATGCT	GTAT--TAC-	[221]
HYTT1A_TT05_AA....	..G.....A	..TCAATGCT	GTAT--TAC-	[221]
HYTT2A_TT06_A-----	-----	[206]

HYTT2B_TT06_B-----	-----	[206]
HYTT3A_TT07_A-----	-----	[206]
HYTT3B_TT07_B-----	-----	[206]
HYTT4A_TT12_A-----	-----	[206]
HYFG1A_C420_A-----	-----	[203]
HYFG2A_C440_AC.	..-----	-----	[206]
HYFG2B_C440_B-----	-----	[205]
HYFG3A_C442_AC.	..-----	-----	[206]
HYFG3B_C442_B	..C.....-----	-----	[205]
ERA1A_C347_A-----	-----	[206]
ERA2A_C348_AC.-----	-----	[206]
ERA3A_C349_ATG.	..-----	-----	[206]
ERA3B_C349_BT.-----	-----	[206]
EMM1A_JM443_A-----	-----	[206]
EMM2A_JM1105_A-----	-----	[206]
ETY1A_N27_A-----	-----	[206]
ETY2A_N101_AA.T.-----	-----	[206]
ETY3A_PR05_A-----	-----	[206]
ETY4A_PR06_A-----	-----	[208]
FAV1A_JM488_A	..C.....A.A	..TCAATGCT	GTATATTACA	[224]
FAV2A_JM883_A-----	-----	[197]
FAV3A_JM1141_A-----	-----	[206]
FAV4A_JM1908_A-----	-----	[212]
FAV5A_JM1911_AT.TG.	.G-----	-----	[206]
LAT3A_Y31_AA.-----	-----	[206]
LAT3B_Y31_BA	..-----	-----	[206]
LAT4A_Y34_AC.C.	..-----	-----	[179]
NOT1A_PR12_A-----	-----	[206]
NOT1B_PR12_B	..C.....A.A	..TCAATGCT	GTAT--TAC-	[221]
NOT2A_PR13_A-----	-----	[206]
NOT3A_PR15_A-----	-----	[205]
NOT4A_PR114_A-----	-----	[206]
HIM1A_N620_AC.	..-----	-----	[206]
HIM2A_C2842_1C.	..-----	-----	[206]
HIM2B_C2842_2C.	..-----	-----	[206]
HIM3A_PR18_AC.	..-----	-----	[206]
HIM4A_PR19_AC.	..-----	-----	[206]
HIM5A_PR45_AC.	..-----	-----	[206]
HIM5B_PR45_BC.	..-----	-----	[206]
HIM6A_JM521_AC.	..-----	-----	[206]
HIM7A_JM522_AC.	..-----	-----	[206]
HIM7B_JM522_BC.	..-----	-----	[206]
H.CLYSONIMUS_C3037_1	G.....GCATTGCT	GTAT--TAC-	[221]
H.TELESIPHE_N11_A	..C.....C.GCAATGCT	GTAT--TAC-	[221]

[260	270	280	290	300]
[.]

CHE1A_C65_A	-----CAG	GCATATAATA	TTTAAACTAA	TATATTAAAA	ATAAACTAAT	[248]
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CHE2A_C140_A	-----	[249]
CHE3A_C188_A	-----	[249]
CHE4A_C201_A	-----	[249]
CHE5A_C206_A	-----	[249]
CYR2A_C2861_1	----------	-....A...	...G.....	[240]
CYR2B_C2861_2	----------	-....A...	...G.....	[240]
CYR3A_PR03_A	TTACACA...T....	...G.....	[274]
CYR4A_PR10_A	-----G.....	[249]
CYR5A_PR31_A	----------	-....G.....	[239]
CYR6A_PR43_A	TTACACA...T....	...G.....	[274]
PET1A_N7153_A	-----C....G.....	[269]
PET2A_N7154_A	-----C....G.....	[269]
PET3A_N7183_A	-----A....	...G.....	[249]
PET4A_C2980_1	-----G.....	[249]
PET4B_C2980_2	----CA...G.....	[265]
PET5A_C2981_1	-----G.....	[249]
PET5B_C2981_2	-----	...	A.....A....	...G.....	[249]
PET6A_P50_A	----------	-....G.....	[240]
PET7A_PR26_A	-----G.....	[249]
HYCO1A_C454_A	-----	...	A.....A....	..CG.....	[249]
HYCO1B_C454_B	-----A.....	...G...C...	[249]
HYCO2A_C455_A	-----G.....	[249]
HYCO4A_C457_A	----CA...G.-....T....	[265]
HYTT1A_TT05_A	----CA...G.....T....	[266]
HYTT2A_TT06_A	-----G...G.....	[249]
HYTT2B_TT06_B	-----G...G.....	[249]
HYTT3A_TT07_A	-----G...G.....	[249]
HYTT3B_TT07_B	-----G...G.....	[249]
HYTT4A_TT12_A	-----A....	...G.....	[249]
HYFG1A_C420_A	-----G.....	[246]
HYFG2A_C440_A	-----C....	...G.....	[249]
HYFG2B_C440_B	-----T.....G.....	[248]
HYFG3A_C442_A	-----G.....	[249]
HYFG3B_C442_B	-----T.....G.....	[248]
ERA1A_C347_A	----------	-....G.....	[240]
ERA2A_C348_A	-----A.....	...G...C...	[249]
ERA3A_C349_A	-----G.....	[249]
ERA3B_C349_B	-----G.....	[249]
EMM1A_JM443_A	-----G.....	[249]
EMM2A_JM1105_A	-----G.....	[249]
ETY1A_N27_A	-----G.....	[249]
ETY2A_N101_A	-----G.....	[249]
ETY3A_PR05_A	-----A.....	...G...C...	[249]
ETY4A_PR06_A	-----G.....	[251]
FAV1A_JM488_A	TTACACA...A....	...G.....	[274]
FAV2A_JM883_A	-----C....	...G.....	[240]
FAV3A_JM1141_A	-----G.....	[249]
FAV4A_JM1908_A	-----G.....	[255]
FAV5A_JM1911_A	-----G.....G.....	[249]

LAT3A_Y31_A	-----G.....	[249]
LAT3B_Y31_B	-----G.....	[249]
LAT4A_Y34_A	-----G.....	[222]
NOT1A_PR12_A	-----A.....	...G...C...	[249]
NOT1B_PR12_B	-----CA..G.....	[266]
NOT2A_PR13_A	-----A.....	...G...C...	[249]
NOT3A_PR15_A	-----G.....	[248]
NOT4A_PR114_A	-----A.....	...G...C...	[249]
HIM1A_N620_A	-----G.....	[249]
HIM2A_C2842_1	-----G.....	[249]
HIM2B_C2842_2	-----G.....	[249]
HIM3A_PR18_A	-----G.....	[249]
HIM4A_PR19_A	-----G.....	[249]
HIM5A_PR45_A	-----G.....	[249]
HIM5B_PR45_B	-----G.....	[249]
HIM6A_JM521_A	-----G.....	[249]
HIM7A_JM522_A	-----G.....	[249]
HIM7B_JM522_B	-----G.....	[249]
H.CLYSONIMUS_C3037_1	-----CA..C.....	...G..G...	[266]
H.TELESIPHE_N11_A	-----AA..C.....	...G..G...	[266]

[310	320	330	340	350]
[.]

CHE1A_C65_A	ATATTTTCAGG	TGGCCCATGC	CCTTGAATGT	GGTTTAAAAG	TGATTGCCTG	[298]
CHE2A_C140_A	[299]
CHE3A_C188_A	[299]
CHE4A_C201_A	[299]
CHE5A_C206_A	[299]
CYR2A_C2861_1	[290]
CYR2B_C2861_2	[290]
CYR3A_PR03_A	[324]
CYR4A_PR10_A	[299]
CYR5A_PR31_A	[289]
CYR6A_PR43_A	[324]
PET1A_N7153_A	[319]
PET2A_N7154_A	[319]
PET3A_N7183_AG.....	[299]
PET4A_C2980_1	[299]
PET4B_C2980_2G.....A.....	[315]
PET5A_C2981_1G..	[299]
PET5B_C2981_2G....	[299]
PET6A_P50_A	[290]
PET7A_PR26_A	[299]
HYCO1A_C454_AG....	[299]
HYCO1B_C454_BA..	[299]
HYCO2A_C455_AG..	[299]
HYCO4A_C457_A	...C.....G.....A.....	[315]
HYTT1A_TT05_A	...C.....G.....A.....	[316]

HYTT2A_TT06_A	[299]
HYTT2B_TT06_B	[299]
HYTT3A_TT07_A	[299]
HYTT3B_TT07_B	[299]
HYTT4A_TT12_AG.....	[299]
HYFG1A_C420_A	[296]
HYFG2A_C440_AC.....	[299]
HYFG2B_C440_BC.....	[298]
HYFG3A_C442_AC.....	[299]
HYFG3B_C442_BC.....	[298]
ERA1A_C347_AG.....	[290]
ERA2A_C348_AA.....	[299]
ERA3A_C349_A	.C.....	[299]
ERA3B_C349_B	.C.....	[299]
EMM1A_JM443_A	[299]
EMM2A_JM1105_AT.....G.....	[299]
ETY1A_N27_A	[299]
ETY2A_N101_AA.....	[299]
ETY3A_PR05_AA.....	[299]
ETY4A_PR06_A	[301]
FAV1A_JM488_A	[324]
FAV2A_JM883_AT.....G.....	[290]
FAV3A_JM1141_A	[299]
FAV4A_JM1908_AC.....	[305]
FAV5A_JM1911_AA.....	[299]
LAT3A_Y31_AG.....	[299]
LAT3B_Y31_B	[299]
LAT4A_Y34_A	[272]
NOT1A_PR12_AA.....	[299]
NOT1B_PR12_BA.....	[316]
NOT2A_PR13_AA.....	[299]
NOT3A_PR15_A	[298]
NOT4A_PR114_AA.....	[299]
HIM1A_N620_A	T.....	[299]
HIM2A_C2842_1	T.....	[299]
HIM2B_C2842_2	T.....	[299]
HIM3A_PR18_A	T.....	[299]
HIM4A_PR19_A	T.....	[299]
HIM5A_PR45_A	T.....	[299]
HIM5B_PR45_B	T.....	[299]
HIM6A_JM521_A	T.....	[299]
HIM7A_JM522_A	T.....G.....	[299]
HIM7B_JM522_B	T.....	[299]
H.CLYSONIMUS_C3037_1	[316]
H.TELESIPHE_N11_AG.....	[316]

[360	370	380	390	400]
[.]

CHE1A_C65_A	CATAGGTGAA	ACTTTAGAAG	AAAGGGAGGC	GGGTAAAAC	GAGGAAGTGG	[348]
CHE2A_C140_A	[349]
CHE3A_C188_A	T.....	[349]
CHE4A_C201_A	[349]
CHE5A_C206_A	[349]
CYR2A_C2861_1G...	[340]
CYR2B_C2861_2G...	[340]
CYR3A_PR03_A	[374]
CYR4A_PR10_AG..A...	...C....	[349]
CYR5A_PR31_AG..A...	[339]
CYR6A_PR43_A	[374]
PET1A_N7153_AG..A...	...C....	[369]
PET2A_N7154_AG..A...	...C....	[369]
PET3A_N7183_A	T.....	C....G...	.G.....	[349]
PET4A_C2980_1C....	[349]
PET4B_C2980_2G.....	[365]
PET5A_C2981_1	T.....G.....	...C....	[349]
PET5B_C2981_2	T.....	C....G...	.G.....	[349]
PET6A_P50_AG...	[340]
PET7A_PR26_A	T.....G.....	...C....	[349]
HYCO1A_C454_A	T.....	C....G...	.G.....	[349]
HYCO1B_C454_BG.....	[349]
HYCO2A_C455_A	[349]
HYCO4A_C457_AG.....	A.....	[365]
HYTT1A_TT05_AG.....	A.....	[366]
HYTT2A_TT06_AG.....	A.....	[349]
HYTT2B_TT06_BG.....	A.....	[349]
HYTT3A_TT07_AG.....	A.....	[349]
HYTT3B_TT07_BC....	.G.....	A.....	[349]
HYTT4A_TT12_A	T.....	C....G...	.G.....	[349]
HYFG1A_C420_AG.....	...C....	[346]
HYFG2A_C440_AT...	.G.....	...G...	[349]
HYFG2B_C440_BG.....	[348]
HYFG3A_C442_AG.....	[349]
HYFG3B_C442_BG.....	[348]
ERA1A_C347_A	T.....	C....	.G.....	[340]
ERA2A_C348_AG.....	[349]
ERA3A_C349_A	[349]
ERA3B_C349_B	[349]
EMM1A_JM443_A	...T.....G..A...	...C....	[349]
EMM2A_JM1105_A	T.....	C....	.G.....	[349]
ETY1A_N27_AG..A...	...C....	[349]
ETY2A_N101_AG.....	A.....	[349]
ETY3A_PR05_AG.....	[349]
ETY4A_PR06_AG.....	...C....	[351]
FAV1A_JM488_AG..A...	...C....	[374]
FAV2A_JM883_A	T.....	C....	.G.....	[340]
FAV3A_JM1141_AG.....	...A.....	[349]
FAV4A_JM1908_AG.....	...C....	[355]

FAV5A_JM1911_A	T.....	.G..A.....	...C.....	[349]
LAT3A_Y31_A	T....C...	.G.....	A.....	[349]
LAT3B_Y31_BG.....	...C.....	[349]
LAT4A_Y34_AG.....	A.....	[322]
NOT1A_PR12_AG.....	[349]
NOT1B_PR12_BG.....	A.....	[366]
NOT2A_PR13_AG.....	[349]
NOT3A_PR15_A	[348]
NOT4A_PR114_AG.....	[349]
HIM1A_N620_AG.....	[349]
HIM2A_C2842_1G.....T	[349]
HIM2B_C2842_2G.....	[349]
HIM3A_PR18_AG.....	[349]
HIM4A_PR19_AG.....	[349]
HIM5A_PR45_AG.....	[349]
HIM5B_PR45_BG.....	[349]
HIM6A_JM521_AG.....	[349]
HIM7A_JM522_AG.....	[349]
HIM7B_JM522_BG.....	[349]
H.CLYSONIMUS_C3037_1G....A..	A.....C.	[366]
H.TELESIPHE_N11_AG..A.....	A.....	[366]

[410	420	430]
[.	.	.]

CHE1A_C65_A	TGTT	CAGACA	AACTAAGGCT	CTATTGCCTG	CTA	[381]
CHE2A_C140_A		[382]
CHE3A_C188_A		[382]
CHE4A_C201_A		[382]
CHE5A_C206_A		[382]
CYR2A_C2861_1		[373]
CYR2B_C2861_2		[373]
CYR3A_PR03_AC.		[407]
CYR4A_PR10_AA		[382]
CYR5A_PR31_AAC.		[372]
CYR6A_PR43_AC.		[407]
PET1A_N7153_AA		[402]
PET2A_N7154_AA		[402]
PET3A_N7183_AC.		[382]
PET4A_C2980_1C.....	...		[382]
PET4B_C2980_2		[398]
PET5A_C2981_1AC.		[382]
PET5B_C2981_2C.		[382]
PET6A_P50_AAC.		[373]
PET7A_PR26_AAC.		[382]
HYC01A_C454_AC.		[382]
HYC01B_C454_B		[382]
HYC02A_C455_A		[382]
HYC04A_C457_AC.		[398]

HYTT1A_TT05_AC.	[399]
HYTT2A_TT06_A	[382]
HYTT2B_TT06_B	[382]
HYTT3A_TT07_A	[382]
HYTT3B_TT07_B	[382]
HYTT4A_TT12_AC.	[382]
HYFG1A_C420_AC.	[379]
HYFG2A_C440_AG.G.	...	[382]
HYFG2B_C440_B	[381]
HYFG3A_C442_A	[382]
HYFG3B_C442_B	[381]
ERA1A_C347_A	[373]
ERA2A_C348_AAC.	[382]
ERA3A_C349_A	[382]
ERA3B_C349_B	[382]
EMM1A_JM443_AC.	[382]
EMM2A_JM1105_AC.	[382]
ETY1A_N27_AAC.	[382]
ETY2A_N101_A	[382]
ETY3A_PR05_AAC.	[382]
ETY4A_PR06_A	[384]
FAV1A_JM488_A	[407]
FAV2A_JM883_A	G.....C.	[373]
FAV3A_JM1141_AAC.	[382]
FAV4A_JM1908_A	[388]
FAV5A_JM1911_AAC.	[382]
LAT3A_Y31_A	[382]
LAT3B_Y31_BT.....AC.	[382]
LAT4A_Y34_AC.	[355]
NOT1A_PR12_AAC.	[382]
NOT1B_PR12_BC.	[399]
NOT2A_PR13_AAC.	[382]
NOT3A_PR15_AAC.	[381]
NOT4A_PR114_AAC.	[382]
HIM1A_N620_AC.	[382]
HIM2A_C2842_1C.	[382]
HIM2B_C2842_2C.	[382]
HIM3A_PR18_AC.	[382]
HIM4A_PR19_AC.	[382]
HIM5A_PR45_AC.	[382]
HIM5B_PR45_BC.	[382]
HIM6A_JM521_AC.	[382]
HIM7A_JM522_AC.	[382]
HIM7B_JM522_BC.	[382]
H.CLYSONIMUS_C3037_1C.	[399]
H.TELESIPHE_N11_AC.	[399]
;					
END;					
BEGIN PAUP;					

```
Lset Base=(0.3765 0.1271 0.1897) Nst=6 Rmat=(1.0000 4.0187 1.0000 1.0000 8.0465) Rates=gamma Shape=0.8850
Pinvar=0.3402;
END;
```

C. Alignment for *H. melpomene* at the *Mpi* locus

```
#NEXUS
```

```
BEGIN DATA;
```

```
  DIMENSIONS NTAX=56 NCHAR=498;
```

```
  FORMAT DATATYPE=DNA MISSING=? GAP=- MATCHCHAR=. INTERLEAVE ;
```

```
MATRIX
```

```
[
[      10      20      30      40      50]
[      .      .      .      .      .]

CYTH1A_N1379_A  TTTATCCATT CAAGCTCATC CAACTAAGGT ATGTATGATG TATAAAAATA [50]
CYTH1B_N1379_B  .....G. .... . . . . . [50]
CYTH2A_N1378_A  ..... . . . . . [50]
CYTH3A_N1051_A  ..... . . . . . [50]
CYTH3B_N1051_B  ..... . . . .CTAA ATA..... [50]
ROS1A_C811#1    ..... . . . . . [50]
ROS1B_C811#2    ..... . . . .CTAA ATA..... [50]
ROS2A_C544_A    ..... . . . . . [50]
ROS2B_C544_B    ..... . . . . . [50]
ROS3A_C1652_A   ..... . . . .CTAA ATA..... [50]
ROS3B_C1652_B   ..... . . . . . [50]
ROS4A_C841_A    ..... . . . .--- . [47]
ROS4B_C841_B    ..... . . . . . [50]
MELCO2A_C422_A  ..... . . . . . [50]
MELCO2B_C422_B  ..... . . . . . [50]
MELCO3A_C11_A   ..... . . . . . [50]
MELTT1A_TT03_A  ..... . . . .--- . [47]
MELTT1B_TT03_B  ...G..... . . . .--- . [47]
MELTT2A_TT04_A  ..... . . . .--- . [47]
MELTT2B_TT04_B  ...G..... . . . .--- . [47]
MELTT3A_TT14_A  ..... . . . .--- . [47]
MELTT3B_TT14_B  ..... . . . .--- . [47]
MELFG1A_C436_A  ...G..... . . . .--- . [47]
MELFG1B_C436_B  ...G..... . . . .--- . [47]
MELFG2A_C437_A  ...G..... . . . .--- . [47]
MELFG3A_C528_A  ...G..... . . . .--- . [47]
MELFG3B_C528_B  ...G..... . . . .--- . [47]
MELFG4A_C1384_A ..... . . . .--- . [47]
MELFG4B_C1384_B ..... . . . .--- . [47]
THEL4A_FG118_A  ..... . . . .--- . [47]
THEL4B_FG118_B  ...G..... . . . .--- .G.... [47]
THEL2A_FG90_A   ..... . . . .--- . [47]
THEL2B_FG90_B   ...G..... . . . .--- . [47]
```

THEL3A_FG104_A	---	[47]
THEL3B_FG104_B	---	[47]
MAL1A_N4026_A	---	[47]
MAL1B_N4026_BGT.....	---	[47]
MAL2A_N4027_A	---	[47]
MAL2B_N4027_B	---	[47]
ECUA1A_C428_A	---	[47]
ECUA2A_C2417_A	---	[47]
ECUA2B_C2417_B	---	[47]
AMAR1A_JM1916_A	---	[47]
AMAR2A_JM1917_A	---	[47]
AMAR3A_JM1271_A	---	[47]
AGLA2A_JM1174_A	---	[47]
AGLA2B_JM1174_B	...G.....	---	[47]
AGLA3A_JM1178_A	---	[47]
PLES2A_C2397_A	---	[47]
PLES3A_C2429_A	---	[47]
PLES3B_C2429_B	[50]
CYDNO1A_553_A	[50]
CYDNO2A_570_A	...G.....	---	[47]
CYDNO4A_N1047_A	[50]
H.HECALE_Y5_AC.....	---	[47]
H.HECALE_Y5_AC.....	---	[47]

[60	70	80	90	100]
[.]

CYTH1A_N1379_A	---ATTTATG	ATATTTCTCC	TTGTGTCAAT	CATTTAATGT	TTCATAA---	[94]
CYTH1B_N1379_B	---.....---	[94]
CYTH2A_N1378_A	---.....---	[94]
CYTH3A_N1051_A	---.....---	[93]
CYTH3B_N1051_B	TAT.....	T.....	...C.....	-----	G.....---	[92]
ROS1A_C811#1	---.....---	[94]
ROS1B_C811#2	TAT.....	T.....	...C.....	-----	G.....---	[92]
ROS2A_C544_A	---.....---	[94]
ROS2B_C544_B	---.....---	[94]
ROS3A_C1652_A	TAT.....	T.....	...C.....	-----	G.....---	[92]
ROS3B_C1652_B	---.....---	[94]
ROS4A_C841_A	---.....	T.....TAT	[94]
ROS4B_C841_B	---.....---	[93]
MELCO2A_C422_A	---.....C.....---	[94]
MELCO2B_C422_B	---.....---	[94]
MELCO3A_C11_A	---.....C.....---	[94]
MELTT1A_TT03_A	---.....	T.....	..A.....---	[91]
MELTT1B_TT03_B	---.....---	[91]
MELTT2A_TT04_A	---.....	T.....	..A.....---	[91]
MELTT2B_TT04_B	---.....---	[91]
MELTT3A_TT14_A	---.....	T.....	..A.....---	[91]
MELTT3B_TT14_B	---.....	T.....	..A.....---	[91]

MELFG1A_C436_A	---	---	[91]
MELFG1B_C436_B	---	---	[91]
MELFG2A_C437_A	---	---	[91]
MELFG3A_C528_A	---	---	[91]
MELFG3B_C528_B	---	---	[91]
MELFG4A_C1384_A	---	T.....A	---	[91]
MELFG4B_C1384_B	---	---	[91]
THEL4A_FG118_A	---	T.....A	---	[91]
THEL4B_FG118_B	---	---	[91]
THEL2A_FG90_A	---	T.....A	---	[91]
THEL2B_FG90_B	---C.....	---	[91]
THEL3A_FG104_A	---	T.....A	---	[91]
THEL3B_FG104_B	---	T.....A	---	[91]
MAL1A_N4026_A	---	T.....A	---	[91]
MAL1B_N4026_B	---	T.....A	---	[91]
MAL2A_N4027_A	---	T.....A	---	[91]
MAL2B_N4027_B	---	T.....AAT....	---	[91]
ECUA1A_C428_A	---	...A...	T.....A	---	[91]
ECUA2A_C2417_A	---	T.....A	---	[91]
ECUA2B_C2417_B	---	T.....A	---	[91]
AMAR1A_JM1916_A	---	T.....A	---	[91]
AMAR2A_JM1917_A	---	...A...	T.....A	---	[91]
AMAR3A_JM1271_A	---	T.....A	---	[91]
AGLA2A_JM1174_A	---	T.....A	---	[91]
AGLA2B_JM1174_B	---	...A...	T.....A	---	[91]
AGLA3A_JM1178_A	---	T.....A	---	[91]
PLES2A_C2397_A	---	T.....A	---	[91]
PLES3A_C2429_A	---	T.....AAT....	---	[91]
PLES3B_C2429_B	---C.....	---	[94]
CYDNO1A_553_A	---	---	[94]
CYDNO2A_570_A	---	T.....TAT	---	[94]
CYDNO4A_N1047_A	---	---	---	[91]
H.HECALE_Y5_A	---	T.....	---	[91]
H.HECALE_Y5_A	---	T.....	.A.....	---	[91]

[110	120	130	140	150]
[.]

CYTH1A_N1379_A	-----	-----	-----	-----	-----	[94]
CYTH1B_N1379_B	-----	-----	-----	-----	-----	[94]
CYTH2A_N1378_A	-----	-----	-----	-----	-----	[94]
CYTH3A_N1051_A	-----	-----	-----	-----	-----	[93]
CYTH3B_N1051_B	-----	-----	-----	-----	-----	[92]
ROS1A_C811#1	-----	-----	-----	-----	-----	[94]
ROS1B_C811#2	-----	-----	-----	-----	-----	[92]
ROS2A_C544_A	-----	-----	-----	-----	-----	[94]
ROS2B_C544_B	-----	-----	-----	-----	-----	[94]
ROS3A_C1652_A	-----	-----	-----	-----	-----	[92]
ROS3B_C1652_B	-----	-----	-----	-----	-----	[94]

ROS4A_C841_A	CTTATTATTC	TTTCCATACA	ACGTGACATT	GGCCATATAT	CAAGAATTCA	[144]
ROS4B_C841_B	-----	-----	-----	-----	-----	[93]
MELCO2A_C422_A	-----	-----	-----	-----	-----	[94]
MELCO2B_C422_B	-----	-----	-----	-----	-----	[94]
MELCO3A_C11_A	-----	-----	-----	-----	-----	[94]
MELTT1A_TT03_A	-----	-----	-----	-----	-----	[91]
MELTT1B_TT03_B	-----	-----	-----	-----	-----	[91]
MELTT2A_TT04_A	-----	-----	-----	-----	-----	[91]
MELTT2B_TT04_B	-----	-----	-----	-----	-----	[91]
MELTT3A_TT14_A	-----	-----	-----	-----	-----	[91]
MELTT3B_TT14_B	-----	-----	-----	-----	-----	[91]
MELFG1A_C436_A	-----	-----	-----	-----	-----	[91]
MELFG1B_C436_B	-----	-----	-----	-----	-----	[91]
MELFG2A_C437_A	-----	-----	-----	-----	-----	[91]
MELFG3A_C528_A	-----	-----	-----	-----	-----	[91]
MELFG3B_C528_B	-----	-----	-----	-----	-----	[91]
MELFG4A_C1384_A	-----	-----	-----	-----	-----	[91]
MELFG4B_C1384_B	-----	-----	-----	-----	-----	[91]
THEL4A_FG118_A	-----	-----	-----	-----	-----	[91]
THEL4B_FG118_B	-----	-----	-----	-----	-----	[91]
THEL2A_FG90_A	-----	-----	-----	-----	-----	[91]
THEL2B_FG90_B	-----	-----	-----	-----	-----	[91]
THEL3A_FG104_A	-----	-----	-----	-----	-----	[91]
THEL3B_FG104_B	-----	-----	-----	-----	-----	[91]
MAL1A_N4026_A	-----	-----	-----	-----	-----	[91]
MAL1B_N4026_B	-----	-----	-----	-----	-----	[91]
MAL2A_N4027_A	-----	-----	-----	-----	-----	[91]
MAL2B_N4027_B	-----	-----	-----	-----	-----	[91]
ECUA1A_C428_A	-----	-----	-----	-----	-----	[91]
ECUA2A_C2417_A	-----	-----	-----	-----	-----	[91]
ECUA2B_C2417_B	-----	-----	-----	-----	-----	[91]
AMAR1A_JM1916_A	-----	-----	-----	-----	-----	[91]
AMAR2A_JM1917_A	-----	-----	-----	-----	-----	[91]
AMAR3A_JM1271_A	-----	-----	-----	-----	-----	[91]
AGLA2A_JM1174_A	-----	-----	-----	-----	-----	[91]
AGLA2B_JM1174_B	-----	-----	-----	-----	-----	[91]
AGLA3A_JM1178_A	-----	-----	-----	-----	-----	[91]
PLES2A_C2397_A	-----	-----	-----	-----	-----	[91]
PLES3A_C2429_A	-----	-----	-----	-----	-----	[91]
PLES3B_C2429_B	-----	-----	-----	-----	-----	[94]
CYDNO1A_553_A	-----	-----	-----	-----	-----	[94]
CYDNO2A_570_A	CTTATTATTC	TTTCCATACA	ACGTGACATT	GGCCAAATAT	CAAGAATTCA	[144]
CYDNO4A_N1047_A	-----	-----	-----	-----	-----	[91]
H.HECALE_Y5_A	-----	-----	-----	-----	-----	[91]
H.HECALE_Y5_A	-----	-----	-----	-----	-----	[91]

[160	170	180	190	200]
[.]

CYTH1A_N1379_A	-----	-GATATTCTT	ATTTATAAAT	AAGTACATAA	CAATATGGCC	[133]
CYTH1B_N1379_B	-----	-.....	[133]
CYTH2A_N1378_A	-----	-.....	[133]
CYTH3A_N1051_A	-----	-.....T.....T.	[132]
CYTH3B_N1051_B	-----	-.....C	[131]
ROS1A_C811#1	-----	-.....	[133]
ROS1B_C811#2	-----	-.....C	[131]
ROS2A_C544_A	-----	-.....	[133]
ROS2B_C544_B	-----	-.....	[133]
ROS3A_C1652_A	-----	-.....C	[131]
ROS3B_C1652_B	-----	-.....	[133]
ROS4A_C841_A	-----	ATTCAATTCA	A.....	.G.....C	[194]
ROS4B_C841_B	-----	-.....T.....	[132]
MELCO2A_C422_A	-----	-.....	[133]
MELCO2B_C422_B	-----	-.....	[133]
MELCO3A_C11_A	-----	-.....	[133]
MELTT1A_TT03_A	-----	-.....G.C	[130]
MELTT1B_TT03_B	-----	-.....C	[130]
MELTT2A_TT04_A	-----	-.....G.C	[130]
MELTT2B_TT04_B	-----	-.....C	[130]
MELTT3A_TT14_A	-----	-.....G.C	[130]
MELTT3B_TT14_B	-----	-.....G.C	[130]
MELFG1A_C436_A	-----	-.....C	[130]
MELFG1B_C436_B	-----	-.....C	[130]
MELFG2A_C437_A	-----	-.....C	[130]
MELFG3A_C528_A	-----	-.....C	[130]
MELFG3B_C528_B	-----	-.....C	[130]
MELFG4A_C1384_A	-----	-.....G.CG.....	[130]
MELFG4B_C1384_B	-----	-.....C	[130]
THEL4A_FG118_A	-----	-.....G.C	[130]
THEL4B_FG118_B	-----	-.....C	[130]
THEL2A_FG90_A	-----	-.....G.CG.....	[130]
THEL2B_FG90_B	-----	-.....C	[130]
THEL3A_FG104_A	-----	-.....G.C	[130]
THEL3B_FG104_B	-----	-.....G.C	[130]
MAL1A_N4026_A	-----	-.....C	[130]
MAL1B_N4026_B	-----	-.....C	[130]
MAL2A_N4027_A	-----	-.....C	[130]
MAL2B_N4027_B	-----	-.....C	[130]
ECUA1A_C428_A	-----	-.....C	[130]
ECUA2A_C2417_A	-----	-.....C	[130]
ECUA2B_C2417_B	-----	-.....C	[130]
AMAR1A_JM1916_A	-----	-.....C	[130]
AMAR2A_JM1917_A	-----	-.....C	[130]
AMAR3A_JM1271_A	-----	-.....C	[130]
AGLA2A_JM1174_A	-----	-.....C	[130]
AGLA2B_JM1174_B	-----	-.....C	[130]
AGLA3A_JM1178_A	-----	-.....G.C	[130]
PLES2A_C2397_A	-----	-.....C	[130]

PLES3A_C2429_A	-----	-.....C	[130]
PLES3B_C2429_B	-----	-.....C	[133]
CYDNO1A_553_A	-----	-.....	[133]
CYDNO2A_570_A	ATTCAATTCA	A.....	.G.....C	[194]
CYDNO4A_N1047_A	-----	-.....CT.	[130]
H.HECALE_Y5_A	-----	-.....C	[130]
H.HECALE_Y5_A	-----	-.....C	[130]

[210	220	230	240	250]
[.]

CYTH1A_N1379_A	ATAATCTGAT	AAGACTAATT	CTATCAATAA	TAGGACTATT	ATGAATCATA	[183]
CYTH1B_N1379_B	[183]
CYTH2A_N1378_A	.C.....	[183]
CYTH3A_N1051_A	[180]
CYTH3B_N1051_BA..G.....GT.G	[181]
ROS1A_C811#1	C.....	[183]
ROS1B_C811#2A..G.....GT.G	[181]
ROS2A_C544_A	[183]
ROS2B_C544_B	[183]
ROS3A_C1652_AA..G.....GT.G	[181]
ROS3B_C1652_B	[183]
ROS4A_C841_AT..	[244]
ROS4B_C841_B	[182]
MELCO2A_C422_A	[183]
MELCO2B_C422_B	[183]
MELCO3A_C11_A	[183]
MELTT1A_TT03_A	...T.....	[180]
MELTT1B_TT03_BA.....T	[180]
MELTT2A_TT04_A	...T.....	[180]
MELTT2B_TT04_BA.....T	[180]
MELTT3A_TT14_A	...T.....	[180]
MELTT3B_TT14_B	...T.....G..	[180]
MELFG1A_C436_AA.....T	[180]
MELFG1B_C436_BA.....T	[180]
MELFG2A_C437_AA.....T	[180]
MELFG3A_C528_AA.....T	[180]
MELFG3B_C528_BA.....---T	[177]
MELFG4A_C1384_A	...T.....	[180]
MELFG4B_C1384_BA.....T	[180]
THEL4A_FG118_A	...T.....	[180]
THEL4B_FG118_BA.....T	[180]
THEL2A_FG90_A	...T.....	[180]
THEL2B_FG90_BA.....T	[180]
THEL3A_FG104_A	...T.....	[180]
THEL3B_FG104_B	...T.....	[179]
MAL1A_N4026_A	...T.....	[180]
MAL1B_N4026_B	...T.....--.	[178]
MAL2A_N4027_A	...T.....	[180]

MAL2B_N4027_B	...T.....					[180]
ECUA1A_C428_A	...T.....					[180]
ECUA2A_C2417_A	...T.....					[180]
ECUA2B_C2417_B	...T.....					[180]
AMAR1A_JM1916_A	...T.....					[180]
AMAR2A_JM1917_A	...T.....					[180]
AMAR3A_JM1271_A	...T.....					[180]
AGLA2A_JM1174_A	...T.....					[180]
AGLA2B_JM1174_B	...T.....					[180]
AGLA3A_JM1178_A	...T.....					[180]
PLES2A_C2397_A	...T.....					[180]
PLES3A_C2429_A	...T.....					[180]
PLES3B_C2429_B					[183]
CYDNO1A_553_A					[183]
CYDNO2A_570_AT.....					[244]
CYDNO4A_N1047_A					[180]
H.HECALE_Y5_A					[180]
H.HECALE_Y5_A					[180]

[260	270	280	290	300]
[.]

CYTH1A_N1379_A	ACAAATCTTT	CAACTAATTA	AATGTAAATT	CATGTTTAA	ATAATTAAAA	[233]
CYTH1B_N1379_B	T.....	[233]
CYTH2A_N1378_A	...T.....	T.....	[233]
CYTH3A_N1051_A	T.....	[230]
CYTH3B_N1051_BG....	T.....T.	.A..AAT..T	[231]
ROS1A_C811#1	T.....	[233]
ROS1B_C811#2G....	T.....A..AAT.TT	[231]
ROS2A_C544_A	T.....	[233]
ROS2B_C544_B	T.....	[233]
ROS3A_C1652_AG....	T.....A..AAT.TT	[231]
ROS3B_C1652_B	T.....	[233]
ROS4A_C841_A	G.....	[294]
ROS4B_C841_B	T.....	[232]
MELCO2A_C422_A	T.....	[233]
MELCO2B_C422_B	T.....	[233]
MELCO3A_C11_A	T.....	[233]
MELTT1A_TT03_A	T.....	[230]
MELTT1B_TT03_B	T.....	[230]
MELTT2A_TT04_A	T.....	[230]
MELTT2B_TT04_B	T.....	[230]
MELTT3A_TT14_A	T.....	[230]
MELTT3B_TT14_B	T.....	[230]
MELFG1A_C436_A	T.....	[230]
MELFG1B_C436_B	T.....	[230]
MELFG2A_C437_A	T.....	[230]
MELFG3A_C528_A	T.....	[230]
MELFG3B_C528_B	T.....	[227]

MELFG4A_C1384_AT.....	[230]
MELFG4B_C1384_BT.....	[230]
THEL4A_FG118_AT.....	[230]
THEL4B_FG118_BT.....	[230]
THEL2A_FG90_AT.....	[230]
THEL2B_FG90_BT.....	[230]
THEL3A_FG104_AT.....	[230]
THEL3B_FG104_BT.....	[229]
MAL1A_N4026_AT.....	[230]
MAL1B_N4026_BT.....	[228]
MAL2A_N4027_AT.....	[230]
MAL2B_N4027_BT.....	[230]
ECUA1A_C428_AT.....	[230]
ECUA2A_C2417_AT.....	[230]
ECUA2B_C2417_BT.....	[230]
AMAR1A_JM1916_AT.....	[230]
AMAR2A_JM1917_AT.....	[230]
AMAR3A_JM1271_AT.....	[230]
AGLA2A_JM1174_AT.....	[230]
AGLA2B_JM1174_BT.....	[230]
AGLA3A_JM1178_AT.....	[230]
PLES2A_C2397_AT.....	[230]
PLES3A_C2429_AT.....	[230]
PLES3B_C2429_BT.....A.....	[233]
CYDNO1A_553_AT.....	[233]
CYDNO2A_570_AG.....	[294]
CYDNO4A_N1047_AT.....A.....	[230]
H.HECALE_Y5_AC..T.G.....	[230]
H.HECALE_Y5_AC..T.....	[230]

[310	320	330	340	350]
[.]

CYTH1A_N1379_A	ATTTAATT-T	GTATATGAGG	GAGAGTTGTT	ATTAC-ACAC	A---TCTCTA	[278]
CYTH1B_N1379_B--	[278]
CYTH2A_N1378_A--	[278]
CYTH3A_N1051_A--	[275]
CYTH3B_N1051_B	T.....A.	A....G.--TT....	.ATA.....	[279]
ROS1A_C811#1--	[278]
ROS1B_C811#2	T.....A.	A....G.--TT..G.	.ATA.....	[278]
ROS2A_C544_A--	[278]
ROS2B_C544_B	.AA.....A..-	[278]
ROS3A_C1652_A	T.....A.	A....G.--TT....	.ATA.....	[279]
ROS3B_C1652_B--	[278]
ROS4A_C841_A-A	---.-.....	.ACAG.....	[339]
ROS4B_C841_B--	[277]
MELCO2A_C422_A---	[277]
MELCO2B_C422_B--	[278]
MELCO3A_C11_A--	[278]

MELTT1A_TT03_A-	---.....	.ACA.....	[276]
MELTT1B_TT03_B- ..T.....	A-.....	.ACA.....	[278]
MELTT2A_TT04_A-	---.....	.ACA.....	[276]
MELTT2B_TT04_B- ..T.....	A-.....	.ACA.....	[278]
MELTT3A_TT14_A-	---.....	.ACA.....	[276]
MELTT3B_TT14_B-	---.....	.ACA.....	[276]
MELFG1A_C436_A-	A-.....	.ACA.....	[278]
MELFG1B_C436_B-	A-.....	.ACA.....	[278]
MELFG2A_C437_A- ..T.....	A-.....	.ACA.....	[278]
MELFG3A_C528_A- ..T.....	A-.....	.ACAA.....	[278]
MELFG3B_C528_B-	A-.....	.ACA.....	[275]
MELFG4A_C1384_A-	---.....	.ATA.....	[276]
MELFG4B_C1384_B- ..T.....	A-.....	.ACA.....	[278]
THEL4A_FG118_A-	---.....	.ACA.....	[276]
THEL4B_FG118_B- ..T.....	A-.....	.ACA.....	[278]
THEL2A_FG90_A-	---.....	.ATA.....	[276]
THEL2B_FG90_B-	A-.....	.ACA.....	[278]
THEL3A_FG104_A-	---.....	.ACA.....	[276]
THEL3B_FG104_B-	---.....	.ACA.....	[275]
MAL1A_N4026_A-	---.....	.ACA.....	[276]
MAL1B_N4026_B-	---.....	.ACA.....	[274]
MAL2A_N4027_A-	-----.....	.ACA.....	[274]
MAL2B_N4027_B-	---.....	.ACA.....	[276]
ECUA1A_C428_A-	---.....	.ACA.....	[276]
ECUA2A_C2417_A-	---.....	.ACA.....	[276]
ECUA2B_C2417_B-	---.....	.ACA.....	[276]
AMAR1A_JM1916_A-	---.....	.ACA.....	[276]
AMAR2A_JM1917_A-	---.....	.ACA.....	[276]
AMAR3A_JM1271_A-	---.....	.ACA.....	[276]
AGLA2A_JM1174_A-	---.....	.ACA.....	[276]
AGLA2B_JM1174_B-	---.....	.ACA.....	[276]
AGLA3A_JM1178_A-	---.....	.ACA.....	[276]
PLES2A_C2397_A-	---.....	.ACA.....	[276]
PLES3A_C2429_A-	--	T.....-.....	.ACA.....	[276]
PLES3B_C2429_B-	A	A.....-.....	.ACA.....	[281]
CYDNO1A_553_A-	---.....	[278]
CYDNO2A_570_A-	ACACA-CA..	---G.....	[339]
CYDNO4A_N1047_A-	A-.....	.ACA.....	[278]
H.HECALE_Y5_A-	A	---.....	.ACA.....	[275]
H.HECALE_Y5_A-	A	---.....G.	.ACA.....	[275]

[360	370	380	390	400]
[.]

CYTH1A_N1379_A	CAGTTTGCTA AATTTTTTTTG ATAAATGG--	-----	-----	[306]
CYTH1B_N1379_B	-----	-----	[306]
CYTH2A_N1378_A	-----	-----	[306]
CYTH3A_N1051_A	-----	-----	[303]
CYTH3B_N1051_BA.C..A.--	-----	-----	[307]

ROS1A_C811#1	--	-----	-----	[306]
ROS1B_C811#2A.C..A.	--	-----	-----	[306]
ROS2A_C544_A	--	-----	-----	[306]
ROS2B_C544_BT.....	--	-----	-----	[306]
ROS3A_C1652_AA.C..A.	--	-----	-----	[307]
ROS3B_C1652_B	--	-----	-----	[306]
ROS4A_C841_A	--	-----	-----	[367]
ROS4B_C841_B	--	-----	-----	-----	[295]
MELCO2A_C422_A	--	-----	-----	[305]
MELCO2B_C422_B	--	-----	-----	[306]
MELCO3A_C11_A	--	-----	-----	[306]
MELTT1A_TT03_AA.	..A.....	...C..A.	--	-----	-----	[304]
MELTT1B_TT03_BA.....	...C..A.	--	-----	-----	[305]
MELTT2A_TT04_AA.	..A.....	...C..A.	--	-----	-----	[304]
MELTT2B_TT04_BA.....	...C..A.	--	-----	-----	[305]
MELTT3A_TT14_AA.	..A.....	...C..A.	--	-----	-----	[304]
MELTT3B_TT14_BA.	..A.....	...C..A.	--	-----	-----	[304]
MELFG1A_C436_AA.....	...C..A.	--	-----	-----	[305]
MELFG1B_C436_BA.....	...C..A.	--	-----	-----	[305]
MELFG2A_C437_AA.....	...C..A.	--	-----	-----	[305]
MELFG3A_C528_AA.....	...C..A.	--	-----	-----	[305]
MELFG3B_C528_BA.....	...C..A.	--	-----	-----	[302]
MELFG4A_C1384_AA.	..A.....	...C..A.	--	-----	-----	[304]
MELFG4B_C1384_B	...C.....	..A.....	...C..A.	--	-----	-----	[305]
THEL4A_FG118_AA.	..A.....	...C..A.	--	-----	-----	[304]
THEL4B_FG118_BA.....	...C..A.	--	-----	-----	[305]
THEL2A_FG90_AA.	..A.....	...C..A.	--	-----	-----	[304]
THEL2B_FG90_BA....C-	...C..A.	--	-----	-----	[305]
THEL3A_FG104_AA.	..A.....	...C..A.	--	-----	-----	[304]
THEL3B_FG104_BA.	..A.....	...C..A.	--	-----	-----	[303]
MAL1A_N4026_AA.	..A.....	...C..A.	--	-----	-----	[304]
MAL1B_N4026_BA.....	...C..A.	--	-----	-----	[302]
MAL2A_N4027_AA.	..A.....	...C..A.	--	-----	-----	[302]
MAL2B_N4027_BA.	..A.....	...C..A.	--	-----	-----	[304]
ECUA1A_C428_AA.	..A.....	...C..A.	--	-----	-----	[304]
ECUA2A_C2417_AA.....	...C..A.TA	CTGTGTA	ACT	ACTATACTAT	[325]
ECUA2B_C2417_BA.	..A.....	...C..A.	--	-----	-----	[304]
AMAR1A_JM1916_AA.	..A.....	...C..A.	--	-----	-----	[304]
AMAR2A_JM1917_AA.	..A.....	...C..A.	--	-----	-----	[304]
AMAR3A_JM1271_AA.	..A.....	...C..A.	--	-----	-----	[304]
AGLA2A_JM1174_AA.	..A.....	...C..A.	--	-----	-----	[304]
AGLA2B_JM1174_BA.	..A.....	..A.C..A.	--	-----	-----	[304]
AGLA3A_JM1178_AA.	..A.....	...C..A.	--	-----	-----	[304]
PLES2A_C2397_AA.	..A.....	...C..A.	--	-----	-----	[304]
PLES3A_C2429_AA.	..A.....	...C..A.	--	-----	-----	[304]
PLES3B_C2429_BT.....	--	-----	-----	[309]
CYDNO1A__553_A	--	-----	-----	[306]
CYDNO2A_570_A	--	-----	-----	[367]
CYDNO4A_N1047_A	--	-----	-----	[306]

H.HECALE_Y5_A	T.....	..A.....	...C..A.--	-----	-----	[303]
H.HECALE_Y5_A	T.....	..A.....	...C..A.--	-----	-----	[303]

[410	420	430	440	450]
[.]

CYTH1A_N1379_A	-----	AATACTAAGT	ACTTTCTTCT	CTTTCACAA	AAACTAAATT	[346]
CYTH1B_N1379_B	-----	[346]
CYTH2A_N1378_A	-----	[346]
CYTH3A_N1051_A	-----	[343]
CYTH3B_N1051_B	-----	TT.....	[347]
ROS1A_C811#1	-----	[346]
ROS1B_C811#2	-----	TT.....	[346]
ROS2A_C544_A	-----	[346]
ROS2B_C544_B	-----	[346]
ROS3A_C1652_A	-----	TT.....	[347]
ROS3B_C1652_B	-----A.	--...--	-----	[333]
ROS4A_C841_A	-----	T.....	[407]
ROS4B_C841_B	-----	---	[332]
MELCO2A_C422_A	-----	[345]
MELCO2B_C422_B	-----	[346]
MELCO3A_C11_A	-----	[346]
MELTT1A_TT03_A	-----CT....	T.....	[344]
MELTT1B_TT03_B	-----	T....G....	T.....	[345]
MELTT2A_TT04_A	-----CT....	T.....	[344]
MELTT2B_TT04_B	-----	T....G....	T.....	[345]
MELTT3A_TT14_A	-----CT....	T.....	[344]
MELTT3B_TT14_B	-----CT....	T.....	[344]
MELFG1A_C436_A	-----	T....A....	T.....	[345]
MELFG1B_C436_B	-----	T....G....	T.....	[345]
MELFG2A_C437_A	-----	T....G....	T.....	[345]
MELFG3A_C528_A	-----	T....G....	T.....T..	[345]
MELFG3B_C528_B	-----	T....G....	T.....	[342]
MELFG4A_C1384_A	-----CT....	T.....	[344]
MELFG4B_C1384_B	-----	T....G....	T.....	[345]
THEL4A_FG118_A	-----CT....	T.....	[344]
THEL4B_FG118_B	-----	T....G....	T.....	[345]
THEL2A_FG90_A	-----CT....	T.....	[344]
THEL2B_FG90_B	-----	T....G....	T.....	[345]
THEL3A_FG104_A	-----CT....	T.....	[344]
THEL3B_FG104_B	-----CT....	T.....	[343]
MAL1A_N4026_A	-----CT....	T.....	[344]
MAL1B_N4026_B	-----CT....	T.....	[342]
MAL2A_N4027_A	-----CT....	T.....	[342]
MAL2B_N4027_B	-----CT....	T.....	[344]
ECUA1A_C428_A	-----CT....	T.....	[344]
ECUA2A_C2417_A	AGTAGTTAGTCT....	T.....	[375]
ECUA2B_C2417_B	-----CT....	T.....	[344]
AMAR1A_JM1916_A	-----CT....	T.....	[344]

AMAR2A_JM1917_A	-----CT....	T.....	[344]
AMAR3A_JM1271_A	-----CT....	T.....	[344]
AGLA2A_JM1174_A	-----CT....	T.....	[344]
AGLA2B_JM1174_B	-----CT....	T.....	[344]
AGLA3A_JM1178_A	-----CT....	T.....	[344]
PLES2A_C2397_A	-----CT....	T.....	[344]
PLES3A_C2429_A	-----CT....	T.....	[344]
PLES3B_C2429_B	-----	T.....	[349]
CYDNO1A_553_A	-----	[346]
CYDNO2A_570_A	-----	[407]
CYDNO4A_N1047_A	-----	T.....	[346]
H.HECALE_Y5_A	-----C....	...G....	T.....	[343]
H.HECALE_Y5_A	-----C....	...G....	T.....	[343]

[460	470	480	490]
[.	.	.	.]

CYTH1A_N1379_A	TTATTTTCAGG	ACCATGCAGA	ACAACTTCAT	AAGAGCTTTC	CGAACATG	[394]
CYTH1B_N1379_B	[394]
CYTH2A_N1378_A	[394]
CYTH3A_N1051_A	[391]
CYTH3B_N1051_BAT...TG....	[395]
ROS1A_C811#1	[394]
ROS1B_C811#2AT...TG....	[394]
ROS2A_C544_A	[394]
ROS2B_C544_B	[394]
ROS3A_C1652_AAT...G..TG....	[395]
ROS3B_C1652_B	[381]
ROS4A_C841_ATG....	[455]
ROS4B_C841_B	[380]
MELCO2A_C422_A	[393]
MELCO2B_C422_B	[394]
MELCO3A_C11_A	[394]
MELTT1A_TT03_ACA...	.TG....	[392]
MELTT1B_TT03_BA.....	.TG....	[393]
MELTT2A_TT04_ACA...	.TG....	[392]
MELTT2B_TT04_BA.....	.TG....	[393]
MELTT3A_TT14_ACA...	.TG....	[392]
MELTT3B_TT14_BCA...	.TG....	[392]
MELFG1A_C436_AA.....	.TG....	[393]
MELFG1B_C436_BA.....	.TG....	[393]
MELFG2A_C437_AA.....	.TG....	[393]
MELFG3A_C528_AA.....	.TG....	[393]
MELFG3B_C528_BA.....	.TG....	[390]
MELFG4A_C1384_ACA...	.TG....	[392]
MELFG4B_C1384_BA.....	.TG....	[393]
THEL4A_FG118_ACA...	.TG....	[392]
THEL4B_FG118_BA.....	.TG....	[393]
THEL2A_FG90_ACA...	.TG....	[392]

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THEL2B_FG90_B      ..... ..A..... .TG..... [393]
THEL3A_FG104_A     ..... ..CA..... .TG..... [392]
THEL3B_FG104_B     ..... ..CA..... .TG..... [391]
MAL1A_N4026_A      ..... ..CA..... .TG..... [392]
MAL1B_N4026_B      ...A..... ..T.. ..CA..... .TG..... [390]
MAL2A_N4027_A      ..... ..CA..... .TG..... [390]
MAL2B_N4027_B      ..... ..CA..... .TG..... [392]
ECUA1A_C428_A      ..... ..CA..... .TG..... [392]
ECUA2A_C2417_A     ..... ..CA..... .TG..... [423]
ECUA2B_C2417_B     ..... ..CA..... .TG..... [392]
AMAR1A_JM1916_A    ..... ..CA..... .TG..... [392]
AMAR2A_JM1917_A    ..... ..CA..... .TG..... [392]
AMAR3A_JM1271_A    ..... ..CA..... .TG..... [392]
AGLA2A_JM1174_A    ..... ..CA..... .TG..... [392]
AGLA2B_JM1174_B    ..... ..CA..... .TG..... [392]
AGLA3A_JM1178_A    ..... ..CA..... .TG..... [392]
PLES2A_C2397_A     ..... ..CA..... .TG..... [392]
PLES3A_C2429_A     ..... ..CA.G.. .TG..... [392]
PLES3B_C2429_B     .....A..... ..TG..... [397]
CYDNO1A__553_A     ..... ..C..... ..C..... [394]
CYDNO2A_570_A      ..... ..TG..... [455]
CYDNO4A_N1047_A    .....A..... ..TG..... [394]
H.HECALE_Y5_A      ..... ..TG..... [391]
H.HECALE_Y5_A      ..... ..C..... ..TG..... [391]
;
END;

```

```
BEGIN paup;
```

```

exclude 38-40 289-304 317-325 342-344 359-369;
lset Base=(0.3489 0.1647 0.1150) Nst=6 Rmat=(1.0000 2.9379 1.0000 1.0000 1.5587) Rates=equal Pinvar=0.4376;
END;

```

D. Alignment for *H. melpomene* at the *Tpi* locus

```
#NEXUS
```

```
BEGIN DATA;
```

```
    DIMENSIONS NTAX=50 NCHAR=623;
```

```
    FORMAT DATATYPE=DNA MISSING=? GAP=- MATCHCHAR=. INTERLEAVE ;
```

```
MATRIX
```

```

[           10           20           30           40           50]
[           .           .           .           .           .]

```

```

CYTH1A_N1379_A      TGGTGAAAAG GACGATCTGG TTGCTGATAA GGTAACAAAAA A-TGACTCTT [49]
CYTH2A_N1378_A      ..... ..TG..... [49]

```

CYTH3A_N1051_A	[49]
ROS1A_C811_1	[49]
ROS1B_C811_2	[49]
ROS2A_C544_1	[49]
ROS2B_C544_2A.....	[50]
ROS3A_C1652_A	[49]
ROS4A_C841_A	[49]
MELCO1A_C421_A	[49]
MELCO2A_C422_A	[49]
MELCO3A_C11_A	[49]
MELCO4A_C12_A	[49]
MELTT1A_TT03_AA.....	[50]
MELTT2A_TT04_AA.....	[50]
MELTT3A_TT14_AA.....	[50]
MELFG1A_C436_1A.....	[50]
MELFG1B_C436_2T.....A.....	[50]
MELFG2A_C437_1A.....	[50]
MELFG2B_C437_2A.....	[50]
MELFG3A_C528_AA.....	[50]
MELFG4A_C1384_AA.....A.....	[50]
THEL1A_FG82_AA.....	[50]
THEL1B_FG82_BA.....	[50]
THEL2A_FG90_AA.....	[50]
THEL3A_FG104_AA.....	[50]
THEL3B_FG104_BA.....	[50]
THEL4A_FG118_AG..	.A.....	[50]
THEL4B_FG118_BA.....	[50]
MAL1A_N4026_AT.....A..	--.....	[48]
AGLA1A_JM494	AT.GTG...A	.GACGATCT.	G.TGCTGAT.	A.GT.....	.AATGACTC.	[50]
AGLA1B_JM494_BT.....A..	--.....	[48]
AGLA2A_JM1174_AT.....A..	--.....	[48]
AGLA2B_JM1174_BT.....A..	--.....	[48]
AGLA1A_JM1178_AC	..T.....A..	--.....	[48]
AMAR2A_JM1917_AT.G.....A..	--.....	[48]
AMAR2B_JM1917_BT.....A..	--.....	[48]
AMAR3A_JM1271_AT.....A..	--.....	[48]
ECUA1A_C428_AT.....A..	--.....	[48]
ECUA2A_C2417_AT...G...A..	--.....	[48]
PLES1A_N14_AT.....A..	--.....	[48]
PLES3A	C.?G???.TG.	TGAA.AGGAT	GAT...G.TG	CTG...GGT	.AAA.AA--.	[48]
CYDNO1A_553_1	???????????	???	[49]
CYDNO1B_553_2	???????????	???	--.....	[48]
CYDNO2A_570_1	[49]
CYDNO4A_N1047_A	--.....	[48]
CYDNO4B_N1047_B	--.....	[48]
CYDNO3A_P40_AA..	--.....T..	[48]
CYDNO3B_P40_B	[49]
H.HECALE_Y5_AA..	--.....	[48]

	60	70	80	90	100]
[.]
CYTH1A_N1379_A	TATACAATAC	AGTAAGAGAA	ATATTTGTCAT	AATCAAATCA	TAGGTTTCAGC [99]
CYTH2A_N1378_A	[99]
CYTH3A_N1051_A	[99]
ROS1A_C811_1T..	[99]
ROS1B_C811_2	[99]
ROS2A_C544_1	[99]
ROS2B_C544_2	[100]
ROS3A_C1652_A	[99]
ROS4A_C841_A	[99]
MELCO1A_C421_A	[99]
MELCO2A_C422_A	[99]
MELCO3A_C11_A	[99]
MELCO4A_C12_A	[99]
MELTT1A_TT03_A	[100]
MELTT2A_TT04_A	[100]
MELTT3A_TT14_A	[100]
MELFG1A_C436_1	[100]
MELFG1B_C436_2	[100]
MELFG2A_C437_1	[100]
MELFG2B_C437_2	[100]
MELFG3A_C528_A	[100]
MELFG4A_C1384_A	[100]
THEL1A_FG82_A	[100]
THEL1B_FG82_B	[100]
THEL2A_FG90_A	[100]
THEL3A_FG104_A	[100]
THEL3B_FG104_B	[100]
THEL4A_FG118_A	[100]
THEL4B_FG118_B	[100]
MAL1A_N4026_A	[98]
AGLA1A_JM494	.TATAC.ATA	CAGT.AGAG.	.ATA..TGCA	T.ATC..ATC	ATA.G.TCAG [100]
AGLA1B_JM494_BT.....	[98]
AGLA2A_JM1174_A	G.....	[98]
AGLA2B_JM1174_BT.....	[98]
AGLA1A_JM1178_A	[98]
AMAR2A_JM1917_AA.....	[98]
AMAR2B_JM1917_BT.....	[98]
AMAR3A_JM1271_AT.....	[98]
ECUA1A_C428_AT.....	[98]
ECUA2A_C2417_AT.....	[98]
PLES1A_N14_A	?.....?	[98]
PLES3A	G.CT.TT..T	.CA.TACATT	.AGAGAAATA	TT.GC.TAAT	C.AA.CATAG [98]
CYDNO1A_553_1GC.	..G..... [99]
CYDNO1B_553_2GC.	..G..... [98]
CYDNO2A_570_1GT.	...A..... [99]
CYDNO4A_N1047_AGT. [98]

CYDNO4B_N1047_BGT.	[98]
CYDNO3A_P40_AGT.	[98]
CYDNO3B_P40_BGC.	[99]
H.HECALE_Y5_AG		[98]

[110	120	130	140	150]
[.]

CYTH1A_N1379_A	CATACATATA	TCTCCATAGA	GAAATAGGAC	ATGGGGGATTA	ACA-GTCTTG	[148]
CYTH2A_N1378_A-.....	[148]
CYTH3A_N1051_A-.....	[148]
ROS1A_C811_1-.....	[148]
ROS1B_C811_2T....-.....	[148]
ROS2A_C544_1-.....	[148]
ROS2B_C544_2T....A.....	..-.....	[149]
ROS3A_C1652_AT-.....	[148]
ROS4A_C841_A-.....	[148]
MELCO1A_C421_A-.....	[148]
MELCO2A_C422_AT....-.....	[148]
MELCO3A_C11_AT....-.....	[148]
MELCO4A_C12_AT....-.....	[148]
MELTT1A_TT03_A	...G.....	..T....C-.....	[149]
MELTT2A_TT04_A	...G.....	..T....C-.....	[149]
MELTT3A_TT14_A	...G.....	..T....C-.....	[149]
MELFG1A_C436_1	...G.....	..T....C-.....	[149]
MELFG1B_C436_2	...G.....	..T....TC-.....	[149]
MELFG2A_C437_1	...G.....	..T....C-.....	[149]
MELFG2B_C437_2-.....	[149]
MELFG3A_C528_A	...G.....	..T....C-.....	[149]
MELFG4A_C1384_A	...G.....	..T....C-.....	[149]
THEL1A_FG82_A	...G.....	..T....C-.....	[149]
THEL1B_FG82_B	...G.....	..T....C-.....	[149]
THEL2A_FG90_A	...G.....	..T....C-.....	[149]
THEL3A_FG104_A	...G.....	..T....C-.....	[149]
THEL3B_FG104_B	...G.....	..T....C-.....	[149]
THEL4A_FG118_A-.....	[149]
THEL4B_FG118_B	...G.....	..T....C-.....	[149]
MAL1A_N4026_AT.....	[148]
AGLA1A_JM494	.CATACATAT	ATCT.TATAG	AG..ATA.GA	CAT...GA.T	..CA-GTC.T	[149]
AGLA1B_JM494_BT.....	[148]
AGLA2A_JM1174_AT....A	[148]
AGLA2B_JM1174_BGT.....	[148]
AGLA1A_JM1178_AA.....	..T.....	[148]
AMAR2A_JM1917_AT.....	[148]
AMAR2B_JM1917_BT.....	[148]
AMAR3A_JM1271_AT.....	[148]
ECUA1A_C428_AT.....	[148]
ECUA2A_C2417_AT....A....	..-.....	[147]
PLES1A_N14_AT.....	[148]

PLES3A	GT.CAGCCAT	A.ATATATCT	CC.TAGA..A	..A..ACA.G	GGGAT.AACA	[148]
CYDNO1A_553_1T.....	...-.....	[148]
CYDNO1B_553_2-.....	[147]
CYDNO2A_570_1-.....	[148]
CYDNO4A_N1047_A-.....	[147]
CYDNO4B_N1047_BG.....-.....	[147]
CYDNO3A_P40_A-.....	[147]
CYDNO3B_P40_B-.....A	[148]
H.HECALE_Y5_AC.....-.....	[147]

[160	170	180	190	200]
[.]

CYTH1A_N1379_A	GACACATACT	TTTTT-ATCT	ATTGTTTCATT	AGATTGAAAC	TCTTATTAAT	[197]
CYTH2A_N1378_A-	[197]
CYTH3A_N1051_A-	[197]
ROS1A_C811_1-	[197]
ROS1B_C811_2-	[197]
ROS2A_C544_1-	[197]
ROS2B_C544_2CC..	...--.....	[196]
ROS3A_C1652_AA.....-	[197]
ROS4A_C841_A-	[197]
MELCO1A_C421_A-	[197]
MELCO2A_C422_A-	[197]
MELCO3A_C11_A-	[197]
MELCO4A_C12_A-C.....	[197]
MELTT1A_TT03_A-	[198]
MELTT2A_TT04_A-	[198]
MELTT3A_TT14_A-	[198]
MELFG1A_C436_1T..-	[198]
MELFG1B_C436_2-	[198]
MELFG2A_C437_1-	[198]
MELFG2B_C437_2-	[198]
MELFG3A_C528_A?-	[198]
MELFG4A_C1384_A-	[198]
THEL1A_FG82_A-	[198]
THEL1B_FG82_B-C	[198]
THEL2A_FG90_AT..-	[198]
THEL3A_FG104_A-	[198]
THEL3B_FG104_BT..-	[198]
THEL4A_FG118_A-	[198]
THEL4B_FG118_B-	[198]
MAL1A_N4026_AT....	[198]
AGLA1A_JM494	.GACACATACT-ATC	TA.TG.TCA.	TAGA.TG..A	CT--TA.T.A	[196]
AGLA1B_JM494_B-	[197]
AGLA2A_JM1174_A	.G.....T....	[198]
AGLA2B_JM1174_BT...C	[198]
AGLA1A_JM1178_AT....	[198]
AMAR2A_JM1917_AT....C.....	[198]

AMAR2B_JM1917_BT...C	[198]	
AMAR3A_JM1271_AT....	[198]	
ECUA1A_C428_AT....	[198]	
ECUA2A_C2417_A-----A.-----	-----A.A.---			[175]	
PLES1A_N14_AT....	[198]	
PLES3A	TGTCTTGGAC	ACA.ACT.T.	T..A.CT...	GTTCATT.GA	.TGA.ACTC.	[198]
CYDNO1A_553_1-....	[197]	
CYDNO1B_553_2-....	[196]	
CYDNO2A_570_1-....	[197]	
CYDNO4A_N1047_AT.---	[195]	
CYDNO4B_N1047_B----	[195]	
CYDNO3A_P40_AT.---	[196]	
CYDNO3B_P40_B-....	[197]	
H.HECALE_Y5_A-....	...T.....G...	.T.....	[196]	

[210	220	230	240	250]
[.]

CYTH1A_N1379_A	ATTGTATATT	TCTTACATAG	AAAGGACAAC	AT-----G	CATACATTTA	[240]
CYTH2A_N1378_A	-----	[240]
CYTH3A_N1051_A	-----	[240]
ROS1A_C811_1	-----	[240]
ROS1B_C811_2	-----	[240]
ROS2A_C544_1	-----	[240]
ROS2B_C544_2	-----	[239]
ROS3A_C1652_A	-----	[240]
ROS4A_C841_A	-----	[240]
MELCO1A_C421_A	-----	[240]
MELCO2A_C422_A	-----	[240]
MELCO3A_C11_A	-----	[240]
MELCO4A_C12_A	-----	[240]
MELTT1A_TT03_ACAATGTAT.	..-...C..	[247]
MELTT2A_TT04_ACAATGTAT.	..-...C..	[247]
MELTT3A_TT14_ACAATGTAT.	..-...C..	[247]
MELFG1A_C436_1CAATGTAT.	..-...C..	[247]
MELFG1B_C436_2CAATGTAT.	..-...C..	[247]
MELFG2A_C437_1CAATGTAT.	..-...C..	[247]
MELFG2B_C437_2	-----	[241]
MELFG3A_C528_ACAATGTAT.	..-...C..	[247]
MELFG4A_C1384_ACAATGTAT.	..-...C..	[247]
THEL1A_FG82_ACAATGTAT.	..-...C..	[247]
THEL1B_FG82_BCAATGTAT.	..-...C..	[247]
THEL2A_FG90_ACAATGTAT.	..-...C..	[247]
THEL3A_FG104_ACAATGTAT.	..-...C..	[247]
THEL3B_FG104_BCAATGTAT.	..-...C..	[247]
THEL4A_FG118_A	-----	[241]
THEL4B_FG118_BCAATGTAT.	..-...C..	[247]
MAL1A_N4026_A	-----	-----G.-	-----	-----	[214]
AGLA1A_JM494	TA.TGTATA.	.TC.TACATA	G..A.GAC.A	CA-----	GCATACA..T	[238]

AGLA1B_JM494_B-----	-----	.G.-	-----	-----	[213]
AGLA2A_JM1174_AA...	..-----	-----	.G.-	-----	-----	[214]
AGLA2B_JM1174_B-----	-----	.G.-	-----	-----	[214]
AGLA1A_JM1178_A-----	-----	.G.-	-----	-----	[214]
AMAR2A_JM1917_A-----	-----	.G.-	-----	-----	[214]
AMAR2B_JM1917_B-----	-----	.G.-	-----	-----	[214]
AMAR3A_JM1271_A	[241]
ECUA1A_C428_A-----	-----	.G.-	-----	-----	[214]
ECUA2A_C2417_A	[218]
PLES1A_N14_A-----	-----	.G.-	-----	-----	[214]
PLES3A	TA.TA....	GTA..TT.C-	-----	--ACGA--	-----	-----	[221]
CYDNO1A_553_1	G.....TC.	[240]
CYDNO1B_553_2	G.....	[239]
CYDNO2A_570_1	G.....	[240]
CYDNO4A_N1047_A	G.....	[238]
CYDNO4B_N1047_B	G.....	[238]
CYDNO3A_P40_A	G.....	[239]
CYDNO3B_P40_B	G.....	[240]
H.HECALE_Y5_A	G.....	[239]

[260	270	280	290	300]
[.]

CYTH1A_N1379_A	GACAATTTTA	ATTAAGATTG	CACTTTTACA	CAGCAAAGTT	AAATTTAGTG	[290]
CYTH2A_N1378_A	[290]
CYTH3A_N1051_A	[290]
ROS1A_C811_1	[290]
ROS1B_C811_2C	[290]
ROS2A_C544_1	[290]
ROS2B_C544_2C	[289]
ROS3A_C1652_A	[290]
ROS4A_C841_A	[290]
MELCO1A_C421_A	[290]
MELCO2A_C422_AC	[290]
MELCO3A_C11_AC	[290]
MELCO4A_C12_AC	[290]
MELTT1A_TT03_A	[297]
MELTT2A_TT04_A	[297]
MELTT3A_TT14_A	[297]
MELFG1A_C436_1	[297]
MELFG1B_C436_2	[297]
MELFG2A_C437_1	[297]
MELFG2B_C437_2C	[291]
MELFG3A_C528_A	[297]
MELFG4A_C1384_A	[297]
THEL1A_FG82_AC.	[297]
THEL1B_FG82_B	[297]
THEL2A_FG90_A	[297]
THEL3A_FG104_A	[297]

THEL3B_FG104_B	[297]
THEL4A_FG118_AC	[291]
THEL4B_FG118_B	[297]
MAL1A_N4026_A	-----	---	[251]
AGLA1A_JM494	AGAC.A...T	.A.T.AGA.T	GCAC..CTAC	ACAGC..AG.	T..A..TAGT	[288]
AGLA1B_JM494_B	-----	---	[250]
AGLA2A_JM1174_A	-----	---	[251]
AGLA2B_JM1174_B	-----	---	[251]
AGLA1A_JM1178_A	-----	---	[251]
AMAR2A_JM1917_A	-----	---	[251]
AMAR2B_JM1917_B	-----	---	[251]
AMAR3A_JM1271_A	[291]
ECUA1A_C428_A	-----	---	[251]
ECUA2A_C2417_A	[268]
PLES1A_N14_A	-----	---	[251]
PLES3A	-----	-----	A.GA..GCAC	TTTT.C.CAG	C..AG.TAAA	[251]
CYDNO1A_553_1A	[290]
CYDNO1B_553_2	T.....	[289]
CYDNO2A_570_1	[290]
CYDNO4A_N1047_A	T.....	[288]
CYDNO4B_N1047_B	[288]
CYDNO3A_P40_A	T.....	[289]
CYDNO3B_P40_BA	[290]
H.HECALE_Y5_AA.....C.	[289]

[310	320	330	340	350]
[.]

CYTH1A_N1379_A	TCTAGTATTT	TCTATGAATT	ATCATACCA-	-----	-----	[319]
CYTH2A_N1378_A-	-----	-----	[319]
CYTH3A_N1051_A-	-----	-----	[319]
ROS1A_C811_1-	-----	-----	[319]
ROS1B_C811_2T.....-	-----	-----	[319]
ROS2A_C544_1-	-----	-----	[319]
ROS2B_C544_2-	-----	-----	[318]
ROS3A_C1652_A-	-----	-----	[316]
ROS4A_C841_A-	-----	-----	[319]
MELCO1A_C421_A-	-----	-----	[319]
MELCO2A_C422_AT.....-	-----	-----	[319]
MELCO3A_C11_AT.....-	-----	-----	[319]
MELCO4A_C12_AT.....-	-----	-----	[319]
MELTT1A_TT03_AT.....-	-----	-----	[326]
MELTT2A_TT04_AT.....-	-----	-----	[326]
MELTT3A_TT14_AT.....-	-----	-----	[326]
MELFG1A_C436_1T.....-	-----	-----	[326]
MELFG1B_C436_2T.....-	-----	-----	[326]
MELFG2A_C437_1T.....-	-----	-----	[326]
MELFG2B_C437_2-	-----	-----	[320]
MELFG3A_C528_AT.....-	-----	-----	[326]

MELFG4A_C1384_AT.....	-	-----	-----	[326]
THEL1A_FG82_A	C.....T.....	-	-----	-----	[326]
THEL1B_FG82_BT.....	-	-----	-----	[326]
THEL2A_FG90_AT.....	-	-----	-----	[326]
THEL3A_FG104_AT.....	-	-----	-----	[326]
THEL3B_FG104_BT.....	-	-----	-----	[326]
THEL4A_FG118_A	-	-----	-----	[320]
THEL4B_FG118_BT.....	-	-----	-----	[326]
MAL1A_N4026_A	-	-----	-----	[280]
AGLA1A_JM494	GTCTAGTA..TCTATG.A.TATCATA.CA	-	-----	-----	[318]
AGLA1B_JM494_BC.....	-	-----	-----	[279]
AGLA2A_JM1174_A	-	-----	-----	[280]
AGLA2B_JM1174_B	-	-----	-----	[280]
AGLA1A_JM1178_A	-	-----	-----	[280]
AMAR2A_JM1917_A	-	-----	-----	[280]
AMAR2B_JM1917_B	-	-----	-----	[280]
AMAR3A_JM1271_A	-	-----	-----	[320]
ECUA1A_C428_A	-	-----	-----	[280]
ECUA2A_C2417_A	-	-----	-----	[297]
PLES1A_N14_A	-	-----	-----	[280]
PLES3A	.T....G.C. AG...TTTC. .G.ACTATC ATACCA	-	-----	-----	[287]
CYDNO1A_553_1A	TT	-----	-----	[322]
CYDNO1B_553_2A.....	-	-----	-----	[318]
CYDNO2A_570_1A	TT	-----	-----	[322]
CYDNO4A_N1047_AA.....	-	-----	-----	[317]
CYDNO4B_N1047_BA	TT	-----	-----	[320]
CYDNO3A_P40_ACA.....	-	-----	-----	[318]
CYDNO3B_P40_BA	TT	-----	-----	[322]
H.HECALE_Y5_AA	TTGTATAAAT	AAGTTCACAA		[339]

[360	370	380	390	400]
[.]

CYTH1A_N1379_A	-----	-----	-----	-----	[319]
CYTH2A_N1378_A	-----	-----	-----	-----	[319]
CYTH3A_N1051_A	-----	-----	-----	-----	[319]
ROS1A_C811_1	-----	-----	-----	-----	[319]
ROS1B_C811_2	-----	-----	-----	-----	[319]
ROS2A_C544_1	-----	-----	-----	-----	[319]
ROS2B_C544_2	-----	-----	-----	-----	[318]
ROS3A_C1652_A	-----	-----	-----	-----	[316]
ROS4A_C841_A	-----	-----	-----	-----	[319]
MELCO1A_C421_A	-----	-----	-----	-----	[319]
MELCO2A_C422_A	-----	-----	-----	-----	[319]
MELCO3A_C11_A	-----	-----	-----	-----	[319]
MELCO4A_C12_A	-----	-----	-----	-----	[319]
MELTT1A_TT03_A	-----	-----	-----	-----	[326]
MELTT2A_TT04_A	-----	-----	-----	-----	[326]
MELTT3A_TT14_A	-----	-----	-----	-----	[326]

MELFG1A_C436_1	-----	-----	-----	-----	-----	[326]
MELFG1B_C436_2	-----	-----	-----	-----	-----	[326]
MELFG2A_C437_1	-----	-----	-----	-----	-----	[326]
MELFG2B_C437_2	-----	-----	-----	-----	-----	[320]
MELFG3A_C528_A	-----	-----	-----	-----	-----	[326]
MELFG4A_C1384_A	-----	-----	-----	-----	-----	[326]
THEL1A_FG82_A	-----	-----	-----	-----	-----	[326]
THEL1B_FG82_B	-----	-----	-----	-----	-----	[326]
THEL2A_FG90_A	-----	-----	-----	-----	-----	[326]
THEL3A_FG104_A	-----	-----	-----	-----	-----	[326]
THEL3B_FG104_B	-----	-----	-----	-----	-----	[326]
THEL4A_FG118_A	-----	-----	-----	-----	-----	[320]
THEL4B_FG118_B	-----	-----	-----	-----	-----	[326]
MAL1A_N4026_A	-----	-----	-----	-----	-----	[280]
AGLA1A_JM494	-----	-----	-----	-----	-----	[318]
AGLA1B_JM494_B	-----	-----	-----	-----	-----	[279]
AGLA2A_JM1174_A	-----	-----	-----	-----	-----	[280]
AGLA2B_JM1174_B	-----	-----	-----	-----	-----	[280]
AGLA1A_JM1178_A	-----	-----	-----	-----	-----	[280]
AMAR2A_JM1917_A	-----	-----	-----	-----	-----	[280]
AMAR2B_JM1917_B	-----	-----	-----	-----	-----	[280]
AMAR3A_JM1271_A	-----	-----	-----	-----	-----	[320]
ECUA1A_C428_A	-----	-----	-----	-----	-----	[280]
ECUA2A_C2417_A	-----	-----	-----	-----	-----	[297]
PLES1A_N14_A	-----	-----	-----	-----	-----	[280]
PLES3A	-----	-----	-----	-----	-----	[287]
CYDNO1A_553_1	-----	-----	-----	-----	-----	[322]
CYDNO1B_553_2	-----	-----	-----	-----	-----	[318]
CYDNO2A_570_1	-----	-----	-----	-----	-----	[322]
CYDNO4A_N1047_A	-----	-----	-----	-----	-----	[317]
CYDNO4B_N1047_B	-----	-----	-----	-----	-----	[320]
CYDNO3A_P40_A	-----	-----	-----	-----	-----	[318]
CYDNO3B_P40_B	-----	-----	-----	-----	-----	[322]
H.HECALE_Y5_A	ATACCTTGAA	AATATGCAGA	ATGAATAATG	CAGGTGGGCC	AAGTTAATGT	[389]

[410	420	430	440	450]
[.]

CYTH1A_N1379_A	-----	-----	-----	-----C	ACTACCACAG	[330]
CYTH2A_N1378_A	-----	-----	-----	-----.	[330]
CYTH3A_N1051_A	-----	-----	-----	-----.	[330]
ROS1A_C811_1	-----	-----	-----	-----.	[330]
ROS1B_C811_2	-----	-----	-----	-----.	..G.....	[330]
ROS2A_C544_1	-----	-----	-----	-----.	[330]
ROS2B_C544_2	-----	-----	-----	-----.	..C.....	[329]
ROS3A_C1652_A	-----	-----	-----	-----.	[327]
ROS4A_C841_A	-----	-----	-----	-----.	[330]
MELCO1A_C421_A	-----	-----	-----	-----.	[330]
MELCO2A_C422_A	-----	-----	-----	-----.	..G.....	[330]

MELCO3A_C11_A	-----	-----	-----	-----	..G.....	[330]
MELCO4A_C12_A	-----	-----	-----	-----	..G.....	[330]
MELTT1A_TT03_A	-----	-----	-----	-----	..A.....	[337]
MELTT2A_TT04_A	-----	-----	-----	-----	..G.....	[337]
MELTT3A_TT14_A	-----	-----	-----	-----	..A.....	[337]
MELFG1A_C436_1	-----	-----	-----	-----	..G.....	[337]
MELFG1B_C436_2	-----	-----	-----	-----	..G.....	[337]
MELFG2A_C437_1	-----	-----	-----	-----	..G.....	[337]
MELFG2B_C437_2	-----	-----	-----	-----	[331]
MELFG3A_C528_A	-----	-----	-----	-----	..A.....	[337]
MELFG4A_C1384_A	-----	-----	-----	-----	..G.....	[337]
THEL1A_FG82_A	-----	-----	-----	-----	..A.....	[337]
THEL1B_FG82_B	-----	-----	-----	-----	..G.....	[337]
THEL2A_FG90_A	-----	-----	-----	-----	..G.....	[337]
THEL3A_FG104_A	-----	-----	-----	-----	..G.....	[337]
THEL3B_FG104_B	-----	-----	-----	-----	..G.....	[337]
THEL4A_FG118_A	-----	-----	-----	-----	[331]
THEL4B_FG118_B	-----	-----	-----	-----	..G.....	[337]
MAL1A_N4026_A	-----	-----	-----	-----	[291]
AGLA1A_JM494	-----	-----	-----	-----	CACTA.CACA	[328]
AGLA1B_JM494_B	-----	-----	-----	-----	..C.....	[290]
AGLA2A_JM1174_A	-----	-----	-----	-----	[291]
AGLA2B_JM1174_B	-----	-----	-----	-----	[291]
AGLA1A_JM1178_A	-----	-----	-----	-----	[291]
AMAR2A_JM1917_A	-----	-----	-----	-----	[291]
AMAR2B_JM1917_B	-----	-----	-----	-----	[291]
AMAR3A_JM1271_A	-----	-----	-----	-----A	[331]
ECUA1A_C428_A	-----	-----	-----	-----	[291]
ECUA2A_C2417_A	-----	-----	-----	-----	[308]
PLES1A_N14_A	-----	-----	-----	-----	[291]
PLES3A	-----	-----	-----	-----	-----CACC	[291]
CYDNO1A_553_1	-----	-----	---GCAATA	TTTGCACTGT	.T.-G..-..	[346]
CYDNO1B_553_2	-----	-----	-----	-----	..C.....	[329]
CYDNO2A_570_1	-----	-----	---GCAATA	TTTGCACTGT	.T.....	[348]
CYDNO4A_N1047_A	-----	-----	-----	-----	..C.....	[328]
CYDNO4B_N1047_B	-----	-----	---GCAATG	TTTGCACTGT	.T.....	[346]
CYDNO3A_P40_A	-----	-----	-----	-----	..C.....	[329]
CYDNO3B_P40_B	-----	-----	---GCAATA	TTTGCACTGT	.T.....	[348]
H.HECALE_Y5_A	TTAAATAAGC	AATTGTTAAG	TTGGGCAATA	TTTGCACTGT	.T.....T..	[439]

[460	470	480	490	500]
[.]

CYTH1A_N1379_A	GCATATAATA	TTCAAACATA	TATGATAAAA	ATAAACTGAT	ATATTTCAGG	[380]
CYTH2A_N1378_A	[380]
CYTH3A_N1051_A	[380]
ROS1A_C811_1	[380]
ROS1B_C811_2	[380]
ROS2A_C544_1	[380]

ROS2B_C544_2							[379]
ROS3A_C1652_A							[377]
ROS4A_C841_A							[380]
MELCO1A_C421_A							[380]
MELCO2A_C422_A							[380]
MELCO3A_C11_A							[380]
MELCO4A_C12_A							[380]
MELTT1A_TT03_A							[387]
MELTT2A_TT04_A							[387]
MELTT3A_TT14_A							[387]
MELFG1A_C436_1		C.					[387]
MELFG1B_C436_2		C.					[387]
MELFG2A_C437_1							[387]
MELFG2B_C437_2							[381]
MELFG3A_C528_A							[387]
MELFG4A_C1384_A							[387]
THEL1A_FG82_A							[387]
THEL1B_FG82_B							[387]
THEL2A_FG90_A							[387]
THEL3A_FG104_A							[387]
THEL3B_FG104_B							[387]
THEL4A_FG118_A							[381]
THEL4B_FG118_B							[387]
MAL1A_N4026_A							[341]
AGLA1A_JM494	.GCATAT.AT	A.TC..ACT.	ATATGAT...	.AT..ACTGA	TATA..TCA.		[378]
AGLA1B_JM494_B							[340]
AGLA2A_JM1174_A							[341]
AGLA2B_JM1174_B							[341]
AGLA1A_JM1178_A							[341]
AMAR2A_JM1917_A							[341]
AMAR2B_JM1917_B							[341]
AMAR3A_JM1271_A							[381]
ECUA1A_C428_A					C.		[341]
ECUA2A_C2417_A					?		[358]
PLES1A_N14_A					?		[341]
PLES3A	A.CACAGGC.	.AT..TA.TC	A.ACTA.T.T	GAT...AAATA	.AC.GAT.TA		[341]
CYDNO1A_553_1					A.		[396]
CYDNO1B_553_2				T	A.		[379]
CYDNO2A_570_1					A.		[398]
CYDNO4A_N1047_A		T					[378]
CYDNO4B_N1047_B					A.		[396]
CYDNO3A_P40_A		T					[379]
CYDNO3B_P40_B					A.		[398]
H.HECALE_Y5_A			T		T		[489]

CYTH1A_N1379_A TGGCCCATGC CCTTGAATGT GGTTTAAAAG TGATTGCCTG TATAGGTGAA [430]

CYTH2A_N1378_A	[430]	
CYTH3A_N1051_A	[430]	
ROS1A_C811_1	[430]	
ROS1B_C811_2	[430]	
ROS2A_C544_1	[430]	
ROS2B_C544_2	[429]	
ROS3A_C1652_A	[427]	
ROS4A_C841_A	[430]	
MELCO1A_C421_A	[430]	
MELCO2A_C422_A	[430]	
MELCO3A_C11_A	[430]	
MELCO4A_C12_A	[430]	
MELTT1A_TT03_A	[437]	
MELTT2A_TT04_A	[437]	
MELTT3A_TT14_A	[437]	
MELFG1A_C436_1	[437]	
MELFG1B_C436_2	[437]	
MELFG2A_C437_1	[437]	
MELFG2B_C437_2	[431]	
MELFG3A_C528_A	[437]	
MELFG4A_C1384_A	[437]	
THEL1A_FG82_AA....	[437]	
THEL1B_FG82_B	[437]	
THEL2A_FG90_A	[437]	
THEL3A_FG104_A	[437]	
THEL3B_FG104_B	[437]	
THEL4A_FG118_A	[431]	
THEL4B_FG118_B	[437]	
MAL1A_N4026_A	[391]	
AGLA1A_JM494	GT.G..CATG	..C.TG.ATG	T.G..T...A	GTGA.TG.CT	GTATA.GTG.	[428]
AGLA1B_JM494_B	[390]
AGLA2A_JM1174_A	[391]
AGLA2B_JM1174_B	[391]
AGLA1A_JM1178_A	[391]
AMAR2A_JM1917_A	[391]
AMAR2B_JM1917_B	[391]
AMAR3A_JM1271_A	[431]
ECUA1A_C428_A	[391]
ECUA2A_C2417_A	[408]
PLES1A_N14_A	[391]
PLES3A	.TT.AGG..G	..CATGCCC.	T.AA.GTGGT	.T.AAAGTGA	.TGCCTGT.T	[391]
CYDNO1A_553_1	[446]
CYDNO1B_553_2	[429]
CYDNO2A_570_1	[448]
CYDNO4A_N1047_A	[428]
CYDNO4B_N1047_B	[446]
CYDNO3A_P40_A	[429]
CYDNO3B_P40_B	[448]
H.HECALE_Y5_A	C.....	[539]

[560	570	580	590	600]
[.]

CYTH1A_N1379_A	ACTTTAGAAG	AGAGGGAGGC	GGGTAAAACT	GAGGAAGTGG	TGTTTCAGGCA	[480]
CYTH2A_N1378_A	[480]
CYTH3A_N1051_A	[480]
ROS1A_C811_1	[480]
ROS1B_C811_2	[480]
ROS2A_C544_1	[480]
ROS2B_C544_2	[479]
ROS3A_C1652_A	[477]
ROS4A_C841_A	[480]
MELCO1A_C421_A	[480]
MELCO2A_C422_A	[480]
MELCO3A_C11_A	[480]
MELCO4A_C12_A	[480]
MELTT1A_TT03_A	[487]
MELTT2A_TT04_A	[487]
MELTT3A_TT14_A	[487]
MELFG1A_C436_1	[487]
MELFG1B_C436_2	[487]
MELFG2A_C437_1A.	[487]
MELFG2B_C437_2	[481]
MELFG3A_C528_A	[487]
MELFG4A_C1384_AA.	[487]
THEL1A_FG82_AA.	[487]
THEL1B_FG82_B	[487]
THEL2A_FG90_A	[487]
THEL3A_FG104_AA.	[487]
THEL3B_FG104_BG.	[487]
THEL4A_FG118_A	[481]
THEL4B_FG118_B	[487]
MAL1A_N4026_AA.	[441]
AGLA1A_JM494	.AC..TAG.A	GAGA..GA.G	C..GT...AC	TGA.G.AGT.	GTG.TCA.GC	[478]
AGLA1B_JM494_B	[440]
AGLA2A_JM1174_A	[441]
AGLA2B_JM1174_B	[441]
AGLA1A_JM1178_AA.	[441]
AMAR2A_JM1917_AA.	[441]
AMAR2B_JM1917_B	[441]
AMAR3A_JM1271_A	[481]
ECUA1A_C428_A	[441]
ECUA2A_C2417_A	[458]
PLES1A_N14_A?	[441]
PLES3A	.GG.G.A.CT	TT..AAGA.A	...AGGCGGG	T.AA.CTGA.	GAAGTG.TGT	[441]
CYDNO1A_553_1????	???????????	???????????	???????????	[496]
CYDNO1B_553_2	[479]
CYDNO2A_570_1	[498]

CYDNO4A_N1047_A	[478]
CYDNO4B_N1047_B	[496]
CYDNO3A_P40_A	[479]
CYDNO3B_P40_B	[498]
H.HECALE_Y5_A	[589]

[610	620]
[.	.]

CYTH1A_N1379_A	AACTAAGGCT CTATTGCCTG CCA	[503]
CYTH2A_N1378_A	[503]
CYTH3A_N1051_A	[503]
ROS1A_C811_1T.....	[503]
ROS1B_C811_2T.....	[503]
ROS2A_C544_1	[503]
ROS2B_C544_2	[502]
ROS3A_C1652_A	[500]
ROS4A_C841_A	[503]
MELCO1A_C421_A	[503]
MELCO2A_C422_A	[503]
MELCO3A_C11_A	[503]
MELCO4A_C12_A	[503]
MELTT1A_TT03_A	[510]
MELTT2A_TT04_A	[510]
MELTT3A_TT14_A	[510]
MELFG1A_C436_1	[510]
MELFG1B_C436_2	[510]
MELFG2A_C437_1	[510]
MELFG2B_C437_2	[504]
MELFG3A_C528_A	[510]
MELFG4A_C1384_A	[510]
THEL1A_FG82_A	[510]
THEL1B_FG82_B	[510]
THEL2A_FG90_A	[510]
THEL3A_FG104_A	[510]
THEL3B_FG104_B	[510]
THEL4A_FG118_A	[504]
THEL4B_FG118_B	[510]
MAL1A_N4026_A	[464]
AGLA1A_JM494	..ACT.A.GC TCTA.TG.CT G.C	[501]
AGLA1B_JM494_B	[463]
AGLA2A_JM1174_A	[464]
AGLA2B_JM1174_B	[464]
AGLA1A_JM1178_A	[464]
AMAR2A_JM1917_A	[464]
AMAR2B_JM1917_B	[464]
AMAR3A_JM1271_A	[504]
ECUA1A_C428_A	[464]
ECUA2A_C2417_A	[481]

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PLES1A_N14_A      ..... [464]
PLES3A            TCAGGCAAAC TA.GGCT..A TTG [464]
CYDNO1A_553_1     ?????????? ??????????? ??? [519]
CYDNO1B_553_2     ?????????? ??????????? ??? [502]
CYDNO2A_570_1     ....??????? ??????????? ??? [521]
CYDNO4A_N1047_A   ..... [501]
CYDNO4B_N1047_B   ..... [519]
CYDNO3A_P40_A     ..... [502]
CYDNO3B_P40_B     ..... [521]
H.HECALE_Y5_A     ..... [612]
;
END;

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