

Introgressionline	Enzyme	Candidategene	Detected SNPs
IL-1-2	NAD-MDH	Solyc01g090710	M31L, N106D, K234E
IL-2-4	PPi-PFK	Solyc02g081160	A5T, P86S, G149V
IL-3-2	NAD-GIDH	Solyc03g094010	A94T, K205R, S245P, T279M, D300N
IL-4-1	PEPC	Solyc04g006970	D188E, Q332H, H702D, L794F
IL-4-4	NAD-GAPDH	Solyc04g082630	R15G, F62S, R81G, A103V, V403I
IL-7-4	ATP-PFK	Solyc07g045160	N7S, N77D, E350Q
IL-7-4	PPi-PFK	Solyc07g049280	A4T, N60K, K173N, N176D, Q358K
IL-10-3	Invertase	Solyc10g083290	T89I, V205I, E258K, D266N, V270A, N390Y, A432G, N480K, G535E
IL-10-3	Invertase	Solyc10g083300	F4L, F8S, R34K, Y73F, D134N, H202Y, E267K, K296M, I361V, A400E, K461Q, K475N, H477Q
IL-10-3	Invertase	Solyc10g085360	F2V, I9L, L18V, T44I, H48Y, A82S, A141V, I176N, H295R, A336V, R339K, Y410F, D571N, K575R
IL-10-3	Invertase	Solyc10g085640	L19V, F55V, V202M, P210T, R268T, A278T, E379Q, R467S
IL-10-3	Invertase	Solyc10g085650	K139N, D259E, A424V, A452S, N469T, P557T

Indels, Frameshifts	Prosite match	match Region
The reading frame predicted by us starts with an earlier 'ATG' than the ITAG2.3 gene model.	PS00068 - Malate dehydrogenase active site signature	188-200
	No Hits	
	PS00074 - Glu / Leu / Phe / Val dehydrogenases active site	96-109
	PS00781 - Phosphoenolpyruvate carboxylase active site 1	
	PS00393 - Phosphoenolpyruvate carboxylase active site 2	150-161, 708-720
	PS00071 - Glyceraldehyde 3-phosphate dehydrogenase active site	262-269
Insertion at end of Pennellii gene that changes the last two AA from TF to AK; The reading frame predicted by us starts with an earlier 'ATG' than the ITAG2.3 gene model.	No hits	
	No hits	
	PS00609 - Glycosyl hydrolases family 32 active site	56-69
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	No Hits	
	No Hits	
	No hits	

Enzyme	Candidategene	SNPs
TPI	Solyc01g111120	V18A, I58L, A70A, R129K
	Solyc04g011510	T26I, S54N, A142D
	Solyc06g005490	K29E, P90S, G112D, V142A, Q184E, S247T
	Solyc10g054870	A17S, T20S, R39H, M103L
PGI	Solyc04g076090	P12S, E86D, D482N
	Solyc12g014380	Q451R, S480T
UGP	Solyc01g081520	V32I, N192Y, L295F, V342I, S443E, I458V, T511S, R539H, N547S
	?UGP?	none
	?UGP?	K5A A13D T93A V272I A408T V456M I487V S568P D598N
		Q49K, D127A, I244V, D271E, K467E
		G428D
SHKDH	Solyc01g067750	Q35R, P65S, L93M, I132V,
	Solyc06g084460	E83L, D163E, S244P
	Solyc10g038080	A90V, I160T, L232F, N235S, V357L
PGM	Solyc03g006870	NA

Solyc04g005030

NA

Solyc04g045340

I160T, E168D, I174D,
T177S, G575S

Solyc05g026490

R108G, A216V, M376L,
R386G, D613A

Indels, Frameshifts	Prosites Analysis
	PS51440 - Triosephosphate isomerase family profile. PS00171 - Triosephosphate isomerase active site. PS51440 - Triosephosphate isomerase family profile. PS00171 - Triosephosphate isomerase active site. PS51440 - Triosephosphate isomerase family profile. PS00171 - Triosephosphate isomerase active site. PS51440 - Triosephosphate isomerase family profile. PS00171 - Triosephosphate isomerase active site.
	PS51463 - Glucose-6-phosphate isomerase family profile. PS00174 - Phosphoglucose Isomerase signature 2. PS51463 - Glucose-6-phosphate isomerase family profile. PS00765- Phosphoglucose isomerase signature 1. PS00174 - Phosphoglucose Isomerase signature 2.
	no hits
Insertion in Pennellii early in the first exon (5 aa long).	no hits
	no hits
	no hits
	no hits
Two deletions (3nt and 5nt) and an insertion (6nt) from the first exon results in a frameshift mutation. This results in Pennellii reading frame starting 30 aa later. Reading frame at that point is in Sync. It cannot however not be excluded that the Gene model from S.Lyc is incorrect and that the frame only starts from where the Pennellii starts - some support from a multi-alignment of similar genes.	no hits
	no hits
Deletion of 5nt in 1st exon - results in late start of reading frame compared to Lyco (103 aa late)	PS00710 - Phosphoglucomutase and phosphomannomutase phosphoserine signature.

The pennellii acceptor splice site for 6th intron might have a snp. Instead of AG, it is GG. This results in a different splice site in Pennellii and thereby a framshift mutation which results in a later reading frame start in Pennellii (about 246 aa later).

no hits

PS00710 - Phosphoglucomutase and
phosphomannomutase
phosphoserine signature.

no hits

Prosite Analysis location

binding - 82 Binding-84
active site-166 active site
236 active site 234-244
binding - 8 Binding-10 (K at
10 not present) active site-
94 active site 164 active
site 162-172

binding - 10 Binding-12
active site-96 active site-
116 active site 164-174

binding - 68 Binding-70
active site-152 active site-
222 active site 220-230

active site 396(E) active site
425(H) active site 530(K)
PS00174 - 513-530

active site 360(E) active site
391(H) active site 516(K)
PS00765 - 269-282
PS00174 - 499-516

184-193

118-127
