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EP155 MASMTLQQICQSTICNTIPVGCRRKRTSPAQHGSTSLKESVSESQCETICAOVWDSLSKEQKAITAQPTEFMGTQYEITLKRDSVAELGDNA--VM 88
EP146 MS---LORKCOATPDTRICSGEHRVVVRHDSASIQKSVEDRCYICARVWNSLSEEQKAVCKRPTFEGIVYKMYTRDQSYGGSNAHSRPIL 87

AGLMQEEFG--DDLYECEEYKVVGGWWRGFTGQFSILNPAKFPVDPKVVDFPETTNHPSQWNTVAKWVENCRSNHKTCDLHQGTGWLFPKRLVD 177
AQLLCCQPAKDDLYDCDDYNEVGGWWRNEAGAFALNPSIFPVHEVVELSDSTNDSSSWVSVTWIERCRSEHKTCSESYKTDWVETRLVD 177

LENYGDCQVRVVLSSALEFGNQDVRYLALSHCWGRTPFLVLDGHEELFANGVLVTSLAQNFQDALFATGKLGFRYIWIWDSLCLIQGSRDD 267
VSQFEQYVVCVYTTSGLEPQPRGHPYLALSHCWGKKRFLVFNEETKAKFESGVAISSLAQNFQDAIFTHRLGFRYIWIWDSLCLIQGSRKD 267

WMQQAPLMNKVYRNASTLTCATASPDHGGFFCNREPAFVRBHPFTLRTEAEGLVEGLIKSDFWETDIRRAPINQRAWVWQERLLAPRS 357
WAEQAAPLMNKVYKNAVLTLCAMASAEAEAGGFFRSRDEPKIRECPFRVNTSEGLLDCLVVKSDFWETEVLHAPISKRAWVWQERLLAPRS 357

LCFGQNQLEWECQELQACEVFPNGIPKEEISDIQHPDTIDAVSIKAFRRTISWLADPTIDKTYAD-PELDTMRWYDPSYQVWDEILQLYS 446
LYFGQSQLYWECQEAFAACEVFPDGVPLAEVSEIADIEAVDVVFPKAFIRTAGALVNPITDQEDAKLHETDLDREYESPQVWNEILHSYV 447

SCALTQGGDKLVAISGIAKDLAVYLDDEYLAGLWRKALMDGLLWRVERDEMTGAYIPAKRPPQRYRAPTWSWASVDAIRTRAHT-AVFGEV 535
RCGLTKPEDKFAISGVVKDFADVVGDEYLAGLWRKNLIDGLLWHVQEEELTGLYVPATRVEPYRAPSWSWASVDSPHVRVQSRALHTYD 537

HDGYTELVDVHVVPKGS-----FTGELDHACL LARGHLVTRRRKPVDPRIARHDLFGTFYPDSYDEVITGDEEYCLPLR 609
DSGYAAIDEVNLVFRNEEEKEEEEGGGGGGAPGFPAGELSHACL RARGYLIRTRPPVDRNA-LGSFCQFYPDT-EALEGDVFEFCWPLR 625

EDLCAKLF---ITGLVLMPPFRDSTVTGFAAAQGAATS-----SCSRCAGKMLLVRICTFETAKGDPLQALGLVKPDNWAECGPEGVHL 690
ERINDGDVSGNYLMGLVLGTHPEAAGEEEEGEDADAATNRKRTSCDRGSGQRVFTRVGTFEIDHGDPLOQLSMKKPNWADWGEKDH 715

WELPDHPVSEFVIL. 705
WEPEDAQPYEIVV. 730

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Figure S5 Amino acid alignment of *vic6* alleles in strain EP155 (*vic6-2*) and in strain EP146 (*vic6-1*). Note the high level of polymorphism that spans nearly all of the predicted protein (53% identity). The conserved HET domain found in this candidate *vic* gene is underlined. Amino acid identity is indicated by the solid background, while dashes indicate indels.