

Co-infection of Mammalian orthorubulavirus 5 and Mammalian orthoreovirus type-3 in domestic pigs in India

Fateh Singh¹, KATHERUKAMEM RAJUKUMAR¹, Senthilkumar D¹, Venkatesh G¹, Deepali Shrivastava¹, Subbiah Kombiah¹, Sandeep Kumar Jhade¹, and Vijendra Singh¹

¹National Institute of High Security Animal Diseases

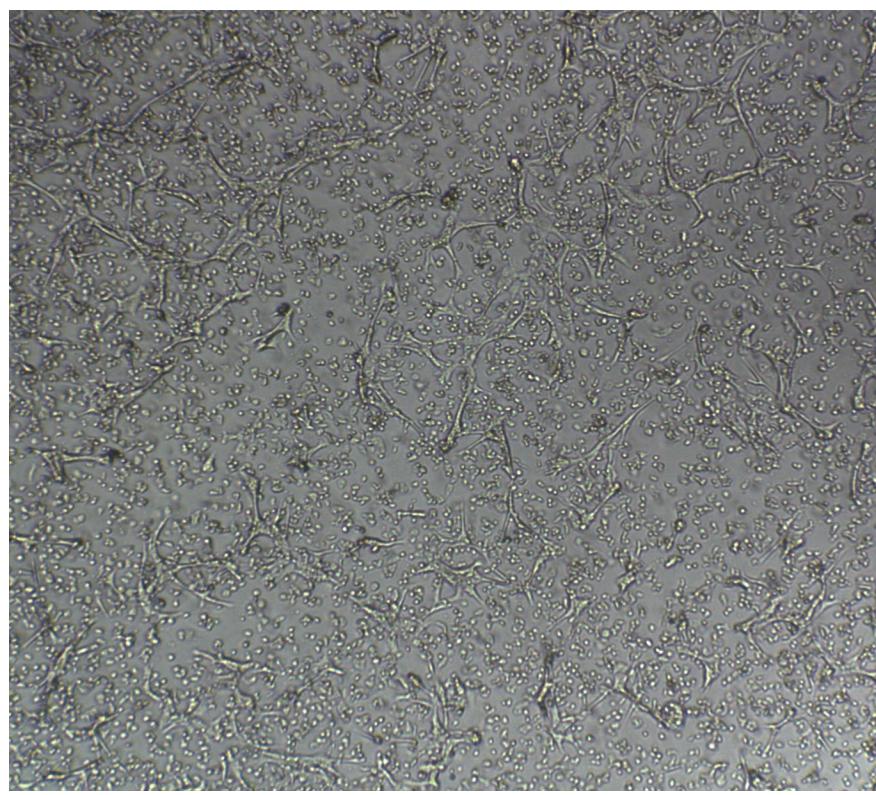
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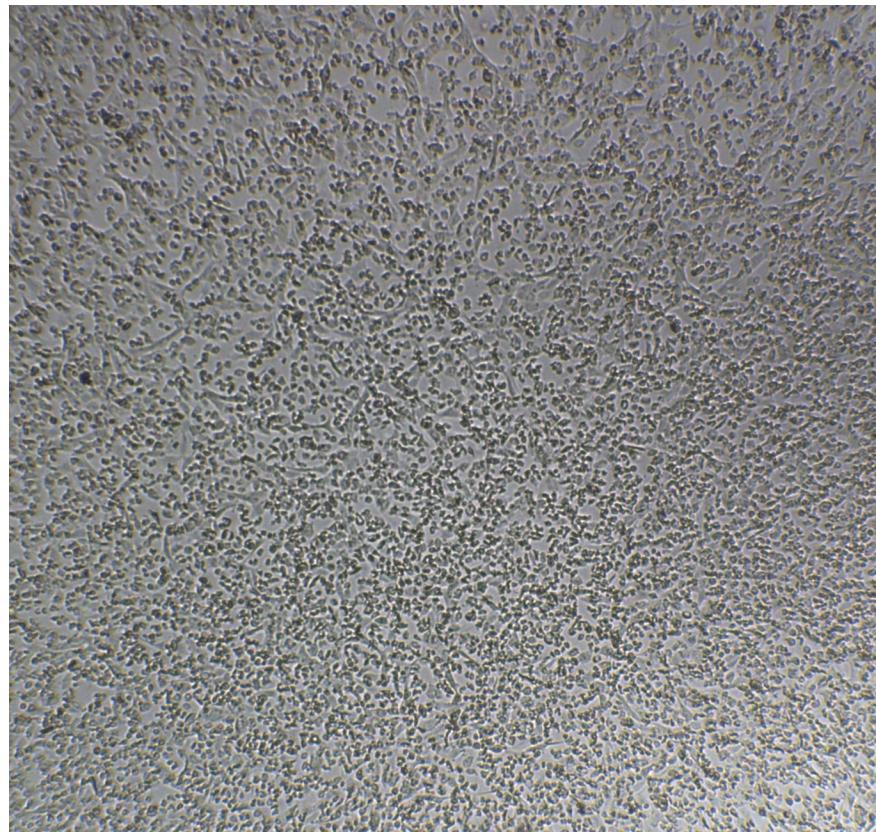
Abstract

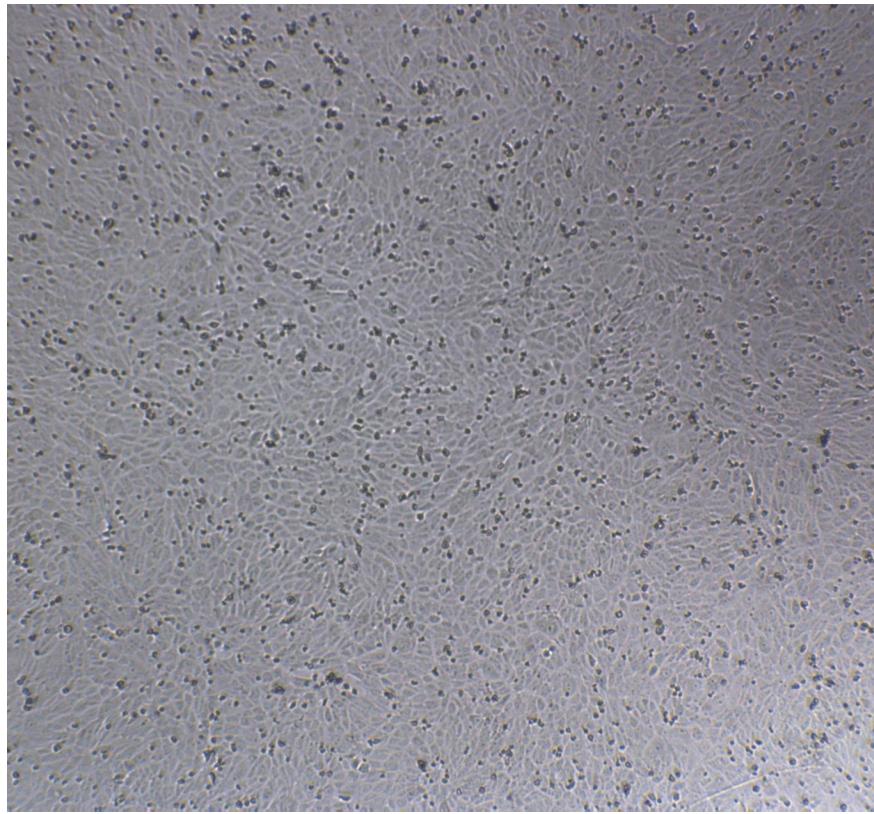
During a routine surveillance for exotic and emerging swine viral diseases in India, five samples (four faecal, one serum) showed cytopathic effects in Vero cells. Transmission electron microscopy of infective cell supernatant revealed the presence of two types of virions. *De novo* metavirome sequencing enabled complete genome assembly of Mammalian orthorubulavirus 5 (MRuV5) and Mammalian orthoreovirus (MRV). The MRuV5 isolates possessed a whole genome of 15246 bp with seven genes (NP, V/P, M, F, SH, HN, L), while the MRV isolates had segmented genome with three large (L1, L2, L3), three medium (M1, M2, M3) and four small (S1, S2, S3, S4) segments. The MRuV5 isolates were genetically grouped with those from various mammalian species reported from South Korea and China. Deduced amino acid sequences of the HN, NP and F gene coding regions of MRuV5 isolates showed the substitutions of three (92L, 111R, 447H), two (86S, 121S) and two (139T, 246T) amino acids, respectively, compared to previously reported strains of the virus. However, they did not reveal any change in predicted amino acid residues at the receptor binding site in HN protein, cleavage site or HN stalk region. S1 gene of the MRV isolates showed the highest nucleotide identity (97.73%) with the MRV3 strain ZJ2013 isolated from pig in China, and these isolates were grouped into MRV type-3. Deduced amino acid sequences of MRV3 S1 gene revealed amino acid residues 198-204NLAIRP, 249I, 340D, 419E known for sialic acid binding site and neurotropism. We report the co-infection of MRuV5 and MRV3 detected incidentally for the first time in domestic pigs in India. Although MRuV5 and MRV3 develop asymptomatic infections or mild disease in animals and humans, continuous monitoring of evolution and spread of such viruses is important in the current global scenario of increasing threats due to emerging novel pathogens.

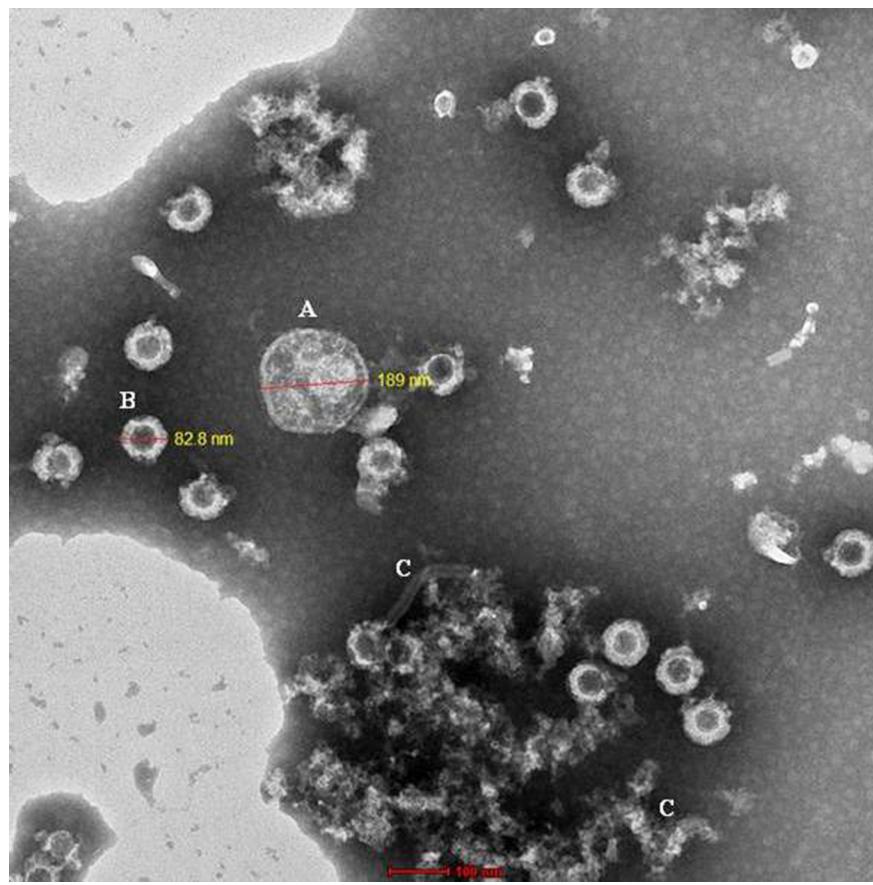
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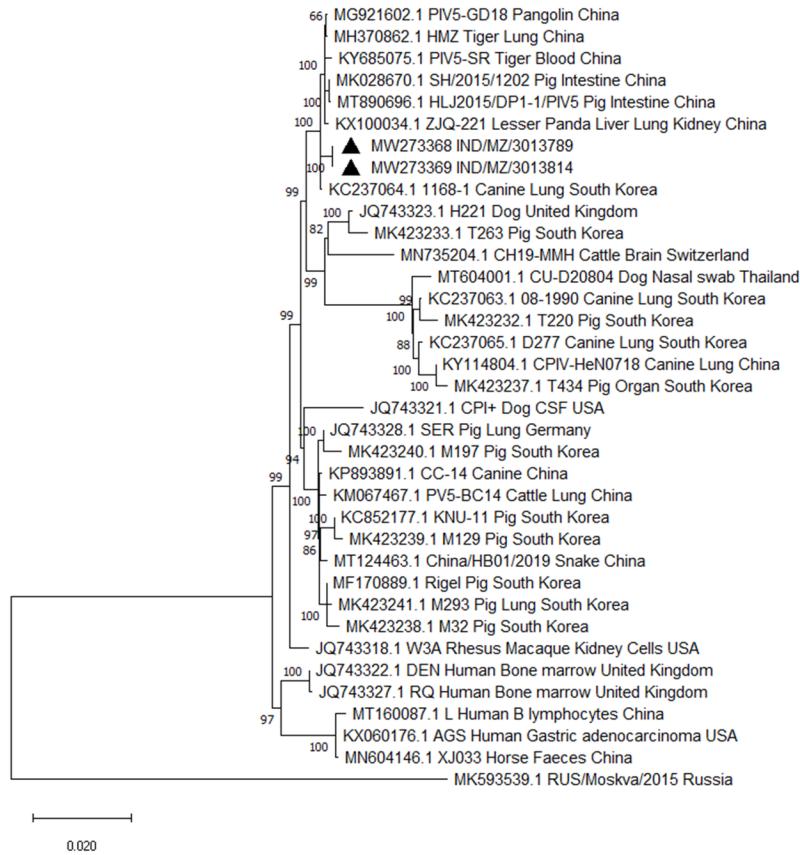
Main Manuscript Document.doc available at <https://authorea.com/users/457645/articles/712715-co-infection-of-mammalian-orthorubulavirus-5-and-mammalian-orthoreovirus-type-3-in-domestic-pigs-in-india>

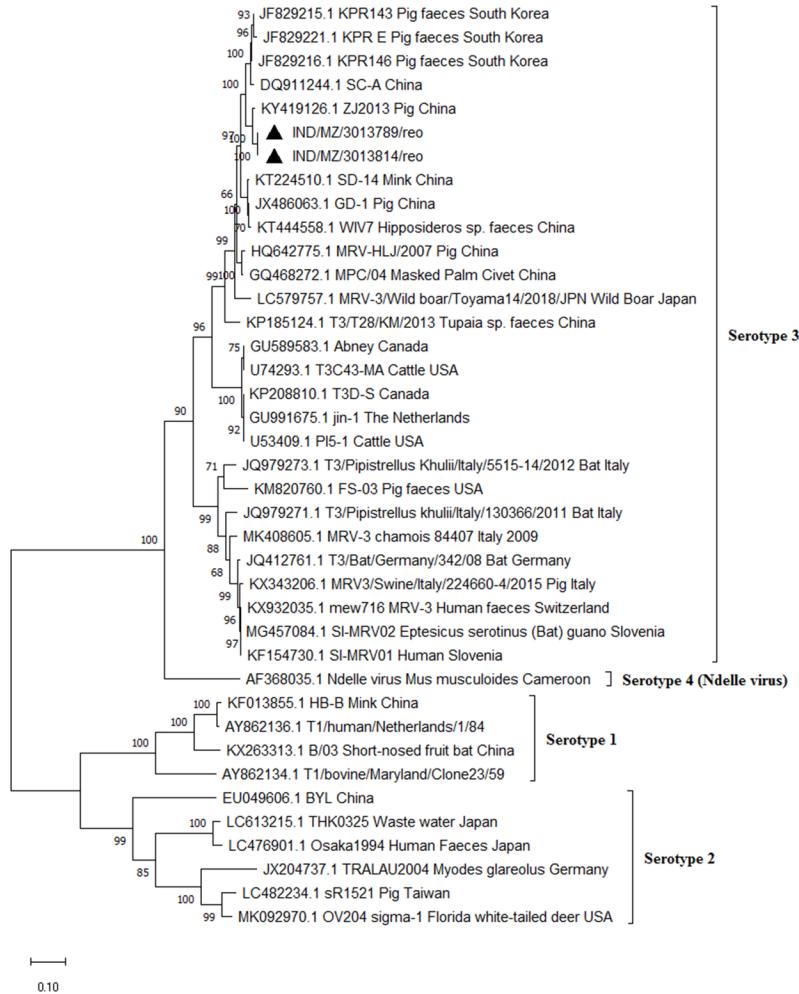


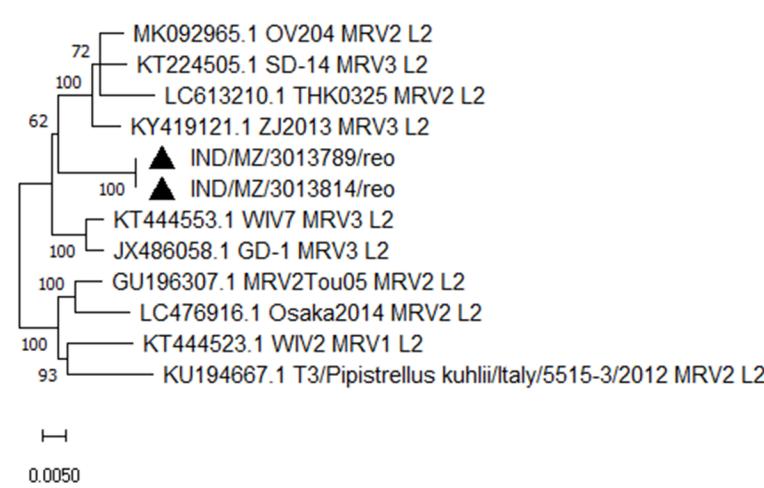


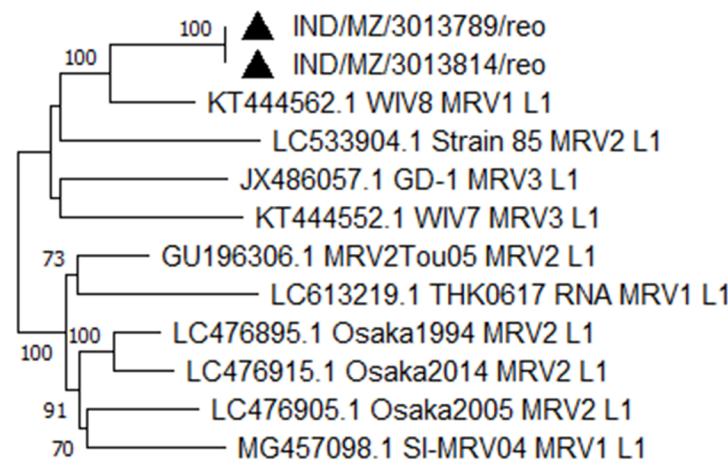






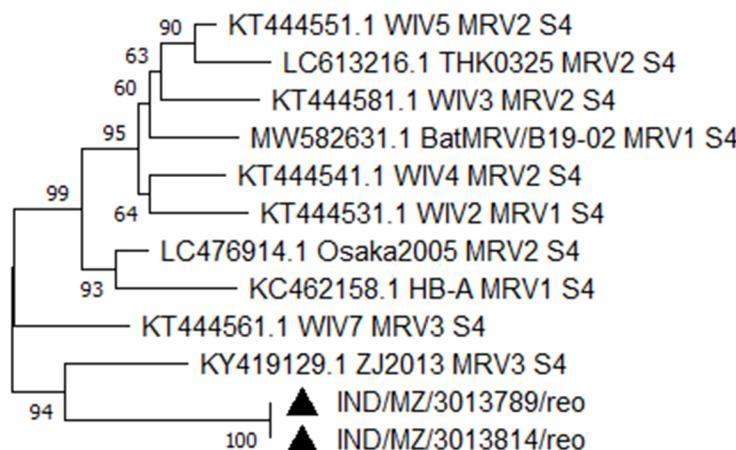




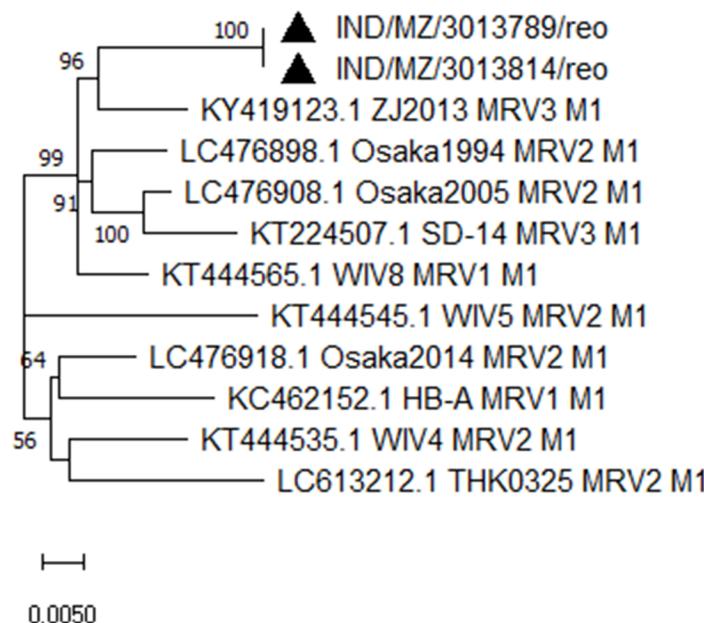


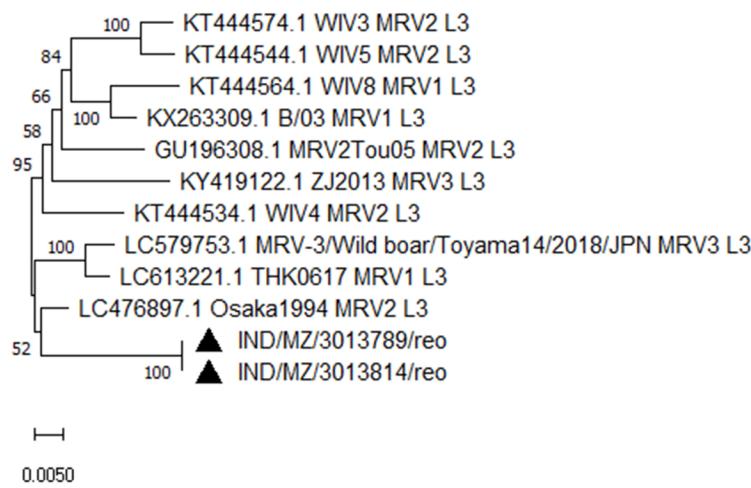
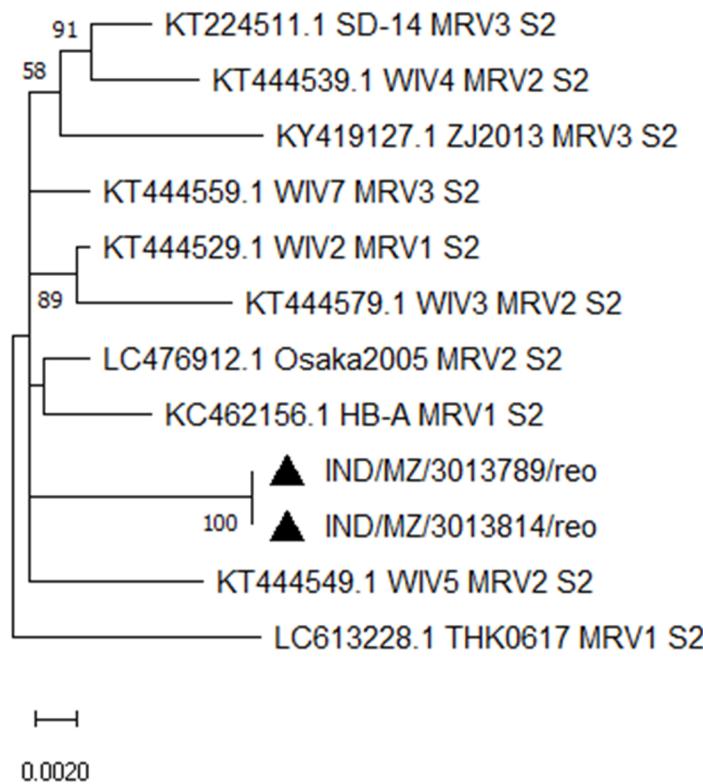


0.0050



0.0050





IND/MC/3013789/reo

	100	200	300	400	500	600	700	800	900	1000
KV419126_1_EJ2013	.A.	.I.	.I.	.Q.						
JFB29216_1_KPR146	.P.IA.	.I.I.	.I.Q.							N.
JFB29215_1_KPR143	.P.IA.	.I.I.	.I.Q.							I.
DQ911244_1_SC-A	.P.IA.	.I.I.	.Q.							N.
JFB29214_1_KPR113	.P.IA.	.I.I.	.Q.							N.
JFB29213_1_KPR110	.P.IA.	.I.R.	.Q.							N.
JFB29221_1_KPR E	.P.IA.	.GI.	.Q.							N.
JX486063_1_GD-1	.A.	.I.	.Q.							N.
KT444558_1_WIVT	.A.	.I.	.Q.							N.
QQ469272_1_MPC/04	G.	.IA.	.I.	.Q.						N.

Clustal Consensus

IND/MC/3013789/reo

	110	120	130	140	150	160	170	180	190	200
SVTQLQGRVQQLQETAGLRLRVEYDNILATRVDTAAEIVVLLTSLTLRKVTSIQSDPESRIATERTAVTSAASAPLSIRNNHMTIGLNDGLNVRNNHL										

IND/MC/3013814/reo

	110	120	130	140	150	160	170	180	190	200
KV419126_1_EJ2013	.H.	.T.	.A.	A.	A.	M.	Q.			
JFB29216_1_KPR146	.DH.	.T.	.S.	A.	A.	S.	M.	L.		
JFB29215_1_KPR143	.DH.	.T.	.S.E.S.	A.	V.	S.	M.	L.		
DQ911244_1_SC-A	.H.	.DH.	.T.	S.	A.	A.	S.	M.	L.	
JFB29214_1_KPR113	.DH.	.T.	.S.E.S.	A.	V.	S.	M.	L.		
JFB29213_1_KPR110	.DH.	.T.	.S.E.S.	A.	V.	S.	M.	L.		
JFB29221_1_KPR E	.DH.	.T.	.S.E.S.	A.	V.	S.	M.	L.		
JX486063_1_GD-1	.DH.	.T.	.S.E.S.	A.	A.	S.	M.	L.		
KT444558_1_WIVT	G.	.DH.	.S.	A.	A.	S.	M.	L.		
QQ469272_1_MPC/04	ADH.	.T.S.								

Clustal Consensus

IND/MC/3013789/reo

	210	220	230	240	250	260	270	280	290	300
TRPLPOSTQNLINQNGQQLQPRINTQPOQIVASNLNTLTITFTDSIIMSRISTIQSIVVASVTPBLINSSSTVLM/LMLIDSSTTEINHSQQLAVKASPHLNPVPI										

IND/MC/3013814/reo

	210	220	230	240	250	260	270	280	290	300	
KV419126_1_EJ2013	.Q.					.GA.	A.			V.	X..
JFB29216_1_KPR146	Q.					P...	G.			L.	
JFB29215_1_KPR143	Q.					P...	G.			L.	
DQ911244_1_SC-A	Q.										
JFB29214_1_KPR113	Q.										
JFB29213_1_KPR110	Q.										
JFB29221_1_KPR E	Q.										
JX486063_1_GD-1	N.	N.		P.		P.	G.			T.	
KT444558_1_WIVT	N.	N.		A.		A.					
QQ469272_1_MPC/04	N.			I.P.		V.A.				T.	

Clustal Consensus

IND/MC/3013789/reo

	310	320	330	340	350	360	370	380	390	400
VDLSGSISIQMSPNYRFQPSMIGVSYSGSOLSWNV/VNSDIFIADDYIYHICLPAFDGTDIADGDLSINPVTOILLPLLTGTQDTEPAFHNDVWYTQARTIA										

IND/MC/3013814/reo

	310	320	330	340	350	360	370	380	390	400
KV419126_1_EJ2013	.N.									M.
JFB29216_1_KPR146	.N.									I.
JFB29215_1_KPR143	.N.									I.
DQ911244_1_SC-A	A.									I.
JFB29214_1_KPR113	.T.									I.
JFB29213_1_KPR110	.T.									I.
JFB29221_1_KPR E	.G.									
JX486063_1_GD-1	A.			I..N.						
KT444558_1_WIVT	A.			I..N.						
QQ469272_1_MPC/04	A.V..V.			I..T.						

Clustal Consensus

IND/MC/3013789/reo

	410	420	430	440	450
IGLSSGGAGQMSRNLM/ZM/MDQVFLRLP/BDOGSTTNSM/DM/AM/TSPRSPTX					

IND/MC/3013814/reo

	410	420	430	440	450
KV419126_1_EJ2013	.T.				
JFB29216_1_KPR146	.T.				
JFB29215_1_KPR143	.T.				
DQ911244_1_SC-A	.T.				
JFB29214_1_KPR113	.T.				
JFB29213_1_KPR110	.T..R.				
JFB29221_1_KPR E	.T..R.				

Clustal Consensus