

Supplementary Information

	10	20	30	40	50	60
MHI241	AESTVKQAPVHAVAKAYNDYEEYSLGPEGLKDAMERTGSNALVMDLYALTIIKQGNVNF					
MHI3178	AESTVKQAPVHAVAKAYNDYEEYSLGPEGLKDAMERTGSNALVMDLYALTIIKQGNVNF					
MHI1440	AESTVKQAPVHAAAKAYNDYEEYSLGPEGLKDAMERTGSNALVMDLYALTIIKQGNVNF					
MHI1541	AESTVKQAPVHAVAKAYNDYEEYSLGPEGLKDAMERTGSNALVMDLYALTIIKQGSVNF					
MHI1668	AESTVKQAPVHAAAKAYNDYEEYSLGPEGLKDAMERTGSNALVMDLYALTIIKQGNVNF					
MHI2970	AESTVKQAPVHAAAKAYNDYEEYSLGPEGLKDAMERTGSNALVMDLYALTIIKQGNVNF					
MHI3173	AESTVKQAPVHAAAKAYNDYEEYSLGPEGLKDAMERTGSNALVMDLYALTIIKQGNVNF					
MHI3225	AESTVNQAPVHAVTKASNDDQEYSLRTRDLNHHAMEIKSSDVLVLDLYTL-----					
MHI1430	AESTVKQAPVHAVAKAYNDYEEYSLGPEGLKDAMERTGSNALVMDLYALTIIKQGNVNF					
MHI1444	AESTVKQAPVHAVAKAYNDYEEYSLGPEGLKDAMERTGSNALVMDLYALTIIKQGNVNF					
MHI1758	AESTVKQAPVHAVAKAYNDYDEYSLGPEGLKDAMERTGSNALVMDLYALTIIKQGNVNF					
N5	-----					
	70	80	90	100	110	120
MHI241	NVSSVDAALKGKVIQHQDTARGNAKQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
MHI3178	NVSSVDAALKGKVIQHQDTARGNAKQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
MHI1440	NVSSVDAALKGKVIQHQDTARGNAKQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
MHI1541	NVSSVDAALKGKVIQHQDTARGNAKQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
MHI1668	NVSSVDAALKGKVIQHQDTARGNAKQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
MHI2970	NVSSVDAALKGKVIQHQDTARGNAKQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
MHI3173	NVSSVDAALKGKVIQHQDTARGNAKQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
MHI3225	-----NAKQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
MHI1430	NVSSVDAALKGKVIQHQDTARGNAKQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
MHI1444	NVSSVDAALKGKVIQHQDTARGNAKQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
MHI1758	NVTSVD TSLKGKVIQHQDTARGNAQWLDVLPQLISTNQNIINYN TKFQNYD TLVAAV					
N5	-----					
	130	140	150	160	170	180
MHI241	DAKDKATLTKGLTRLSSSINENKAQVDQLVEDLKKFRNKMTSDTQNFKGDANQITSILAS					
MHI3178	DAKDKATLTKGLTRLSSSINENKAQVDQLVEDLKKFRNKMTSDTQNFKGDANQITSILAS					
MHI1440	DAKDKATLTKGLTRLSSSINENKTQVDQLVDDLKFRNKMTSDTQNFKGDANQITSILAS					
MHI1541	DAKDKATLTKGLTRLSSSINENKAQVDQLVDDLKFRNKMTSDTQNFKGDANQITSILAS					
MHI1668	DAKDKATLTKGLTRLSSSINENKAQVDQLVDDLKFRNKMTSDTQNFKGDANQITSILAS					
MHI2970	DAKDKATLTKGLTRLSSSINENKAQVDQLVDDLKFRNKMTSDTQNFKGDANQITSILAS					
MHI3173	DAKDKATLTKGLTRLSSSINENKAQVDQLVDDLKFRNKMTSDTQNFKGDANQITSILAS					
MHI3225	DAKD-----TRISSSINENKAQVDQLVDDLKFR-----					
MHI1430	DAKDKATLTKGLTRLSSSINENKAQVDQLVEDLKKFRNKMTSDTQNFKGDANQITSILAS					
MHI1444	DAKDKATLTKGLTRLSSSINENKAQVDQLVEDLKKFRNKMTSDTQNFKGDANQITSILAS					
MHI1758	DAKDKATLTKGLTRLSSSI TENKAQVDKLVEDLKKFRNKMTSDTQNFKGDANQITSILAS					
N5	-----DLKKFRNKMTSDTQNFKGDANQITSILAS					
	190	200	210	220	230	240
MHI241	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLGVALI					
MHI3178	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLGVALI					
MHI1440	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLGVALI					
MHI1541	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLGVALI					
MHI1668	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLGVALI					
MHI2970	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLGVALI					
MHI3173	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLGVALI					
MHI3225	-----IAIIGGAVVIATGAGTPLGVALI					
MHI1430	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLGVALI					
MHI1444	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLGVALI					
MHI1758	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLG IALI					
N5	QDAGIPLLQNQITTYNEAISKYNAIIGSSVATALGPIAII GGAVVIATGAGTPLGVALI					

Figure S1. Cont.

	250	260	270	280	290	300
MHI241	AGGAAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
MHI3178	AGGAAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
MHI1440	AGGAAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
MHI1541	AGGAAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
MHI1668	AGGAAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
MHI2970	AGGTAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
MHI3173	AGGAAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
MHI3225	AGGAAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
MHI1430	AGGTAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
MHI1444	AGGTAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
MHI1758	AGGTAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					
N5xxxx11	AGGAAAVGGGTAGIVLAKKELDNAQAEIQKITGQVTTAQLEVAGLTNIKTQTEYLTNTID					

	310	320	330	340	350	360
MHI241	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
MHI3178	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
MHI1440	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
MHI1541	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
MHI1668	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
MHI2970	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
MHI3173	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
MHI3225	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
MHI1430	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
MHI1444	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
MHI1758	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					
N5xxxx11	TAITALQNISNQWYTMGSKYNSLLQNVDSISPNDLVFIKEDLNIKDSWKNIKDYAEKIY					

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MHI241	AEDIKVVDTKKA
MHI3178	AEDIKVVDTKKA
MHI1440	AEDIKVVDTKKA
MHI1541	AEDIKVVDTKKA
MHI1668	AEDIKVVDTKKA
MHI2970	AEDIKVVDTKKA
MHI3173	AEDIKVVDTKKA
MHI3225	AEDIKVVDTKKA
MHI1430	AEDIKVVDTKKA
MHI1444	AEDIKVVDTKKA
MHI1758	AEDIKVVDTKKA
N5xxxx11	AEDIKVVDTKKA

Figure S1. Complete sequence alignment of all strains under study.