

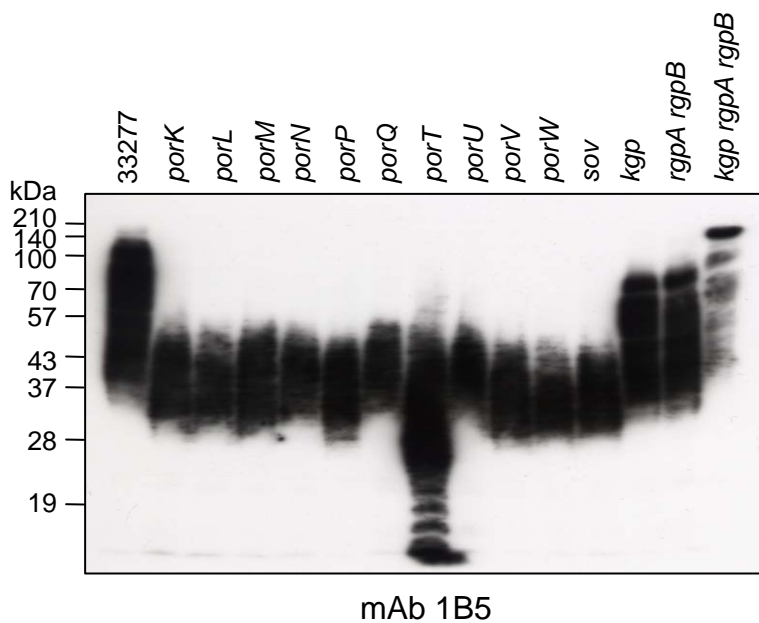
# Supplemental 1

## TM1

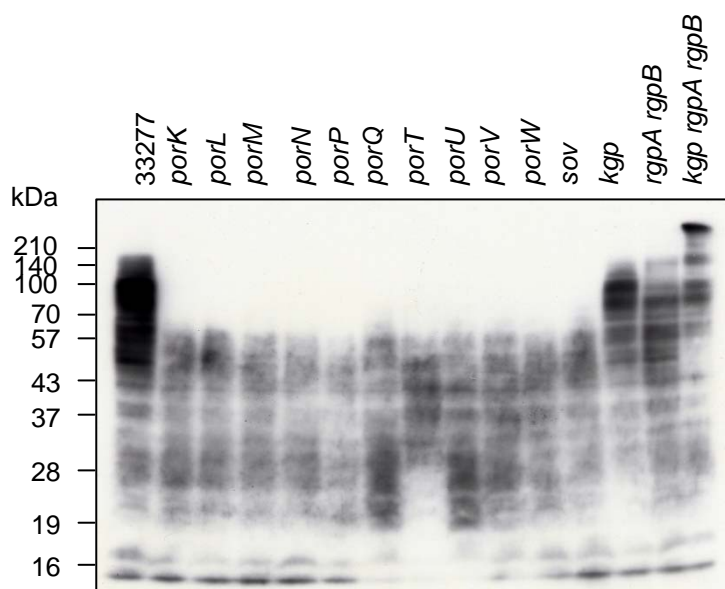
Poras_0604	MTQSSLPNRAVYNEPTRSDEGTRPFTFSQILRLILKQWYWFVLSFVLFVVLGKIVADHRPL	60
PORUE0001_0693	MTQSSLPNSAVNDQPNYPDEGSRPFTFSQILRLILRQWYWFVIFIAIFVWLGCSIVKYRPL	60
POREN0001_1785	MDSTFSPSKTVLP-----QRMSFSAFVRLVVLNWNWFALSLVVAFGFIKMFNGSSAI	52
PGN_2005	MTEKSFRRSVLPLK-----DSVLTLFRRICLRNWNWILISVVLFAGWGVMVVKYKRAGM	51
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Poras_0604	GRQTYMQQLSSREPHLTPMMLTSDS-----TFKTSPTWPEYIATLNTTTAV	109
PORUE0001_0693	GRQTYMQQLSSREPHLTPMMLTSDS-----IPKTSPTWPEYIASLNTTTAV	109
POREN0001_1785	GNNKYRMAVMTRFPIQTSKSDKVFVDANS---GKEAPLWKHTPAFDAAQIYGWIVSADII	109
PGN_2005	APSTYFTTVMARFPEGVQRASSGGLNPNYVDNYTPRWEGISVLDQNSIFNGLCATSLV	111
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Poras_0604	VEAGRINFQVDYFVKTPWGMRDYINQTPIIIVHFDDLLPTDKVHCIAKLDDPVHPQQVTL	169
PORUE0001_0693	LEAGKRIDFQVDYVWVTPFGMRDYINQTPIIIVRFGNLLPTDKLYCIARLDDPVHPKEVTM	169
POREN0001_1785	YRTGKREGFEVEYAQRSGFSSRDIYNHIFPRLIFPDAADADYFTLVVRQEA----DGLQL	165
PGN_2005	ERVGEKIQYDVNYYLPGKVTNHDFYDHTPIHLIFSPESALSSFTVKMKVEK----EHATI	167
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Poras_0604	SGFLGTAQGISINEP--YDVVIVPGSTQETPVGHVSITLDNPKHHFPYHIDQKHKKIALS	227
PORUE0001_0693	SAFSGVVQGOPLYEP--YDVVIVPGSTQETPVGPIITVTLDDPAQHFPYHIDQYTEIPIT	227
POREN0001_1785	SQIKGVYQKELKGTGSYTILLPNWSTVETPVGKVIQDNPGWEEYGIKRSYALDKPIIIT	225
PGN_2005	LSLKGKHDGEKVSIIK---DIRLPYGISVATPIGELRVEKTPRFDYETSKKDFFSKPIIIV	224
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Poras_0604	YS-TLQDIRAVYETEMQVTMCKADLPSSVMRVEMLSNRSERRCLDLLYQMYLVTDSLWG	286
PORUE0001_0693	YT-SLVEARDIYETEMQVTMCKADLPSSVMRVELLSGRSERRCLSLNAMYVVTDSLWG	286
POREN0001_1785	RR-SVIETRAQYDWMVIDN-----TLPNFLNVEVSTTGSARRAKQILAGMLVDLDSLVR	279
PGN_2005	TKESKDKARVLYDSGLRTEE-----SKGRIEMRITIKRSLGFARDFLDGIIIEFDIQR	278
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Poras_0604	VEQLSDEGVTDSLQGFAG--TVPPAGLSP-----FRLIDEPRIAKDLEPDLFIIAG-	335
PORUE0001_0693	VEQLTDEGHVDSLQGFVG--TVPPAGLSP-----FRLVDKPRELREIEPDLFVIVG-	335
POREN0001_1785	YNVTLDDLKEQEMIEAALRRLMHPDLSLSPS-----LTAESRTQEIKEQLQRLARTISN	332
PGN_2005	EKYRQVEVEEKIALAEKSLSDLQKSEGPVSDSTLVSLGITEKERNADSEALRKKLVSMINE	338
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	TM2	
Poras_0604	-----MGLLGLLLPLLLMYIYWAIIRGVIYY	360
PORUE0001_0693	-----MGLLGFLLIPLLLLYIYWAILGAIYY	360
POREN0001_1785	REVLRYDHLIE---VTASPAIQSPVGFVSKIIIFLLGLIIPVLIYAWLLRGSVLE	388
PGN_2005	YKVDLLTADASSSLIVLDKTKSVPVSKKDLLLILINLVMGLFFPMIIFVYIVFRNLILV	398
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Poras_0604	VSELPSLLRHRLT--LDLKRGRKGGKPLYPNLEELCALVMPP---QGEPRTIQLATPNST	415
PORUE0001_0693	VCELPRLLRSRLT--LDLQRRHKG-KTLYPHLEELCALVSP---QGEPRAIQLVTPSGT	413
POREN0001_1785	PRQLSPFWQKALISTLRLHRKRGNYSDTPETIDALRFTLQSNLEEDTARPIILFTTPSKS	448
PGN_2005	PSELGEKALKRILALLNGNKKRAATMQRDIDLRLNLTETFLP---DSASSCIILTGMSSGN	455
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Poras_0604	KYHQQLLAEQLQALEQRGISCAVWHLDLAEQKAVSKT--PSDVYHTTITPGLISSSTAFQQ	473
PORUE0001_0693	KYHRQLASELQALQQRGISCAVWYLDLANQKKASKG--SNGVYHTTITPGLIGSSSAFEQ	471
POREN0001_1785	SKAQKRLNKLVDLAASYSLGGNGTGKIVHLLHASNNSVPTLSHARIEQGYWGGKQFSQ	508
PGN_2005	EQTERIATELVSSFERK-----GKNFQILHLEES-----DAALK	489
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Poras_0604	QLKQLQTQHQLTI IASPALMEDPTAYLLSSSVEQSLYCIYRGSTRVRAIKRIVHQLQIRQ	533
PORUE0001_0693	QLKQLQTQHQLTI IVPALT KDPTAYLLN-SLEQSLYCIYRGSTRIGAIKRVVHQLQIRQ	530
POREN0001_1785	DLAPAEAEKKTPTLLIAPFDS---VHLLASQVAQIVVVEQDQSRPTLLSDLEHLSLQGT	565
PGN_2005	EMTALREKGISVFAIAPSVVRSALAVEVSVFVADVSLLLAESMHSKRNDKDEVEAFICQSR	549
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Poras_0604	LLDRSRIEILWIE-----	546
PORUE0001_0693	QLDRSHIHTLWVE-----	543
POREN0001_1785	PP----IHALWVCNIFPFFR	581
PGN_2005	CP----AFVLWLDRY-----	560
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Supplemental 3

A



mAb 1B5

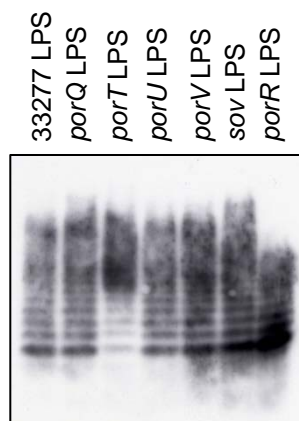


mAb TDC-5-2-1

B



mAb 1B5



mAb TDC-5-2-1