

	Transmembrane domain	Loop 3	Transmembrane domain
MO00014-1_Ng_346	89 TGWGNKQSFVGLKG--GFGTIRAGSLNSPLKNT	89 NVNAWESGKFTGNVLEISGMAQREHRLSVRYDSDP-EFAGFSGSVQYAPKDNSGSGS-----NGES---YHVG	
MO00020-1_Ng_349	89 TGWGNKQSFVGLKG--GFGTIRVGSLSNPLKNTGANVNAWESGKYTGEFLEISKMARREHRLSARYDSDP-EFAGFSGSVQYAPKDNSGSGS-----NGES---YHVG		
MO00023-1_Ng_347	89 TGWGNKQSFVGLKG--GFGTIRVGSLSNPLKNTGANVNAWESGKYTGEFLEISKMARREHRLSARYDSDP-EFAGFSGSVQYAPKDNSGSGS-----NGES---YHVG		
MO00038-1_Ng_349	89 TGWGNKQSFVGLKG--GFGTIRVGSLSNPLKNTGANVNAWESGKYTGEFLEISKMARREHRLSARYDSDP-EFAGFSGSVQYAPKDNSGSGS-----NGES---YHVG		
MO00044-1-3_Ng_348	89 TGWGNKQSFVGLKG--GFGTIRAGSLNSPLKNTGANVNAWESGKFTGNVLEISGMAKREHRLSVRYDSDP-EFAGFSGSVQYAPKDNSGSGS-----NGES---YHVG		
MO0003-1_Nm_332	89 SGWGNRQSFVGLKG--GFGKLRVGRNLNVLKDTG-DINPWEW---KSDYLGVNKAIEPEARLISVRYDSDP-EFAGLSSGSVQYALNDNAGKH-----NSES---YHAG		
MO00012-1_Nm_332	89 SGWGNRQSFVGLKG--GFGKLRVGRNLNVLKDTG-DINPWS---KSDYLGVNKAIEPEARLISVRYDSDP-EFAGLSSGSVQYALNDNAGKH-----NSES---YHAG		
MO00015-1_Nm_330	89 SGWATRESFVGLG--GFGKLRVGRNLNVLKDTG-DINPWS---KSDYLGVNKAIEPEARLISVRYDSDP-EFAGLSSGSVQYALNDNAGRH-----NSES---YHAG		
MO00015-2_Nm_330	89 SGWGNRQSFVGLKG--GFGKLRVGRNLNVLKDTG-DINPWS---KSDYLGVNKAIEPEARLISVRYDSDP-EFAGLSSGSVQYALNDNAGRH-----NSES---YHAG		
MO00021-1_Nm_332	89 SGWGNRQSFVGLKG--GFGKLRVGRNLNVLKDTG-DINPWEW---KSDYLGVNKAIEPEARLISVRYDSDP-EFAGLSSGSVQYALNDNAGKH-----NSES---YHAG		
MO00018-1_No_366	89 SGWATRESFVGLG--GFGKVRAGKLNLTQDK-MDKIDPWEY---KNPALGLGVFTRTGERVVSARYDSDP-VFAGFSANVQTPRDNQAEATGRNT-DYSDTSA---YYAG		
MO00018-1_No_375	91 TNWGSRSFVGLG--GFGKIRAGHMLNLLNE-MDTIDTWLY---KSSALGLGAYVRTGSRTSVRYDSDP-SFGGLKANLQYSPRDNQPRDKNTHAEPGRDQ---YNVG		
MO00032-1_No_366	89 SGWATRESFVGLG--GFGKVRAGKLNLTQDK-MDKIDPWEY---KNPALGLGVFTRTGERVVSARYDSDP-VFAGFSANVQTPRDNQAEATGRNT-DYSDTSA---YYAG		
MO00032-1_No_375	91 TNWGSRSFVGLG--GFGKIRAGHMLNLLNE-MDTIDTWLY---KSSALGLGAYVRTGSRTSVRYDSDP-SFGGLKANLQYSPRDNQPRDKNTHAEPGRDQ---YNVG		
MO00012-2_Nmu_328	82 NGWSTDSYIGLRG--DFGTVRAGWLSTPMHYLTGEQDAFNG---NNHTQTMGRMTFGGREIALNYESKTFDNGFNRYQTAPGANKYK-----DRKRGDWMAGLG		
MO00012-2_Nmu_358	89 KGWGTRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANASVLQFGKLRVDERKVSRYDSDP-VFAGFSASAVQYQPRDNANPEDKHVHDVKTTHS---FDLG		
MO00012-2_Nmu_374	91 QRFGNRSFVGLG--NFGKVRAGNLNMLNE-MDTIDPWY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO00029-2_Nmu_328	82 NGWSTDSYIGLRG--DFGTVRAGWLSTPMHYLTGEQDAFNG---NNHTQTMGRMTFGGREIALNYESKTFDNGFNRYQTAPGANKYK-----DRKRGDWMAGLG		
MO00029-2_Nmu_358	89 KGWGTRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANASVLQFGKLRVDERKVSRYDSDP-VFAGFSASAVQYQPRDNANPEDKHVHDVKTTHS---FDLG		
MO00029-2_Nmu_374	91 QRFGNRSFVGLG--NFGKVRAGNLNMLNE-MDTIDPWY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO00018-2_Nmu_328	82 NGWSTDSYIGLRG--DFGTVRAGWLSTPMHYLTGEQDAFNG---NNHTQTMGRMTFGGREIALNYESKTFDNGFNRYQTAPGANKYK-----DRKRGDWMAGLG		
MO00018-2_Nmu_358	89 KGWGTRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANASVLQFGKLRVDERKVSRYDSDP-VFAGFSASAVQYQPRDNANPEDKHVHDVKTTHS---FDLG		
MO00018-2_Nmu_374	91 QRFGNRSFVGLG--NFGKVRAGNLNMLNE-MDTIDPWY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO0003-2_Ns_332	61 GGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO0003-2_Ns_358	89 SGFANRESFVGLG--GFGKVRAGNLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO0003-2_Ns_372	89 QGFANRDSFVGLG--NFGKVRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO0003-2_Ns_376	94 KEWASRESFVGLG--GFGKIRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO0009-1_Ns_354	85 SGFANRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO0009-1_Ns_357	86 GGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO0009-1_Ns_372	94 KEWASRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO0009-1_Ns_372	89 QGFANRDSFVGLG--NFGKVRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO0009-2_Ns_357	86 GGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO0009-2_Ns_372	89 QGFATRDSFVGLG--NFGKIRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO0009-2_Ns_372	95 SGFANRESFVGLG--GFGKVRAGNLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VFAGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO0009-2_Ns_399	94 KEWASRESFVGLG--GFGKIRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00027-1_Ns_342	59 QGFANRDSFVGLG--NFGKVRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO00027-1_Ns_359	86 NGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO00027-1_Ns_378	100 SGFANRESFVGLG--GFGKVRAGNLNLTQDKNSDSDPWEAG-ANSDVLTGLKFERVDSREVSRYDSDP-VFAGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00027-1_Ns_385	94 KEWASRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VFAGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00027-2_Ns_354	85 SGFANRESFVGLG--GFGKVRAGNLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00027-2_Ns_357	86 GGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO00027-2_Ns_372	89 QGFATRDSFVGLG--NFGKIRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO00027-2_Ns_372	94 KEWASRESFVGLG--GFGKIRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00029-1_Ns_354	85 SGFANRESFVGLG--GFGKVRAGNLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00029-1_Ns_357	86 GGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO00029-1_Ns_372	89 QGFATRDSFVGLG--NFGKIRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO00029-1_Ns_376	94 KEWASRESFVGLG--GFGKIRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00036-1_Ns_357	86 GGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO00036-1_Ns_359	90 SGFANRESFVGLG--GFGKVRAGNLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00036-1_Ns_372	89 QGFATRDSFVGLG--NFGKIRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO00036-1_Ns_376	94 KEWASRESFVGLG--GFGKIRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00036-2_Ns_357	86 GGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO00036-2_Ns_359	90 SGFANRESFVGLG--GFGKVRAGNLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00036-2_Ns_372	89 QGFATRDSFVGLG--NFGKIRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO00036-2_Ns_376	94 KEWASRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00041-1_Ns_354	85 SGFATRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00041-1_Ns_358	86 GGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO00041-1_Ns_372	89 QGFANRDSFVGLG--NFGKVRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO00041-1_Ns_376	94 KEWASRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00045-1_Ns_354	85 SGFATRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00045-1_Ns_357	86 GGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO00045-1_Ns_372	89 QGFANRDSFVGLG--NFGKVRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO00045-1_Ns_376	94 KEWASRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00049-1_Ns_354	85 SGFATRESFVGLG--GFGKVRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YDLG		
MO00049-1_Ns_357	86 GGWGTADSYVALNSYKNLGTVKMGYISTPMN--SIYLNPFDT---NSSILEFGKISRFGQRRVSMAYESP-WKNGQFQFKNVSPGSNAARNNDWNPDKKRGGDWVFGWG		
MO00049-1_Ns_372	89 QGFATRDSFVGLG--NFGKIRAGKLNLMNLTQDK-MDKIDPWEY---KTDAMGLGINTRTGVRITSLRYDSDP-SFGGKFKNVSYAPRDNANPEDKHVHDVKTTHS---YTAG		
MO00049-1_Ns_372	94 KEWASRESFVGLG--GFGKIRAGKLNLTQDKNSDSDPWESSANADTLQGLKIRVDRKVSRYDSDP-VLGGFSASVQYQPRDNANPEDKHVHDVKTTHS---YTAG		

Supplemental Figure 2. Alignment of loop 3 flanking regions of *porB* paralogs found in panel. Loop 3 is boxed (blue) with resistance associated *penB* mutants in *N. gonorrhoeae* strain MO00014-1 colored in red. Transmembrane domains are shaded in grey. Strain number with species; *N. gonorrhoeae* (Ng), *N. meningitidis* (Nm), *N. oralis* (No), *N. mucosa* (Nmu) and *N. subflava* (Ns) and number of amino acids of *porB*.