

g172	MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVQPTLYWHVKNKRALLDALAIEML	60
g172T	MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVQPTLYWHVKNKRALLDALAIEML	60
g187	MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVQPTLYWHVKNKRALLDALAIEML	60
g187T	MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVQPTLYWHVKNKRALLDALAIEML	60

g172	DRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL	120
g172T	DRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL	120
g187	DRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL	120
g187T	DRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL	120
	*****:*****	
g172	CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPLLRQAIELFDHQ	180
g172T	CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPLLRQAIELFDHQ	180
g187	CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPLLRQAIELFDHQ	180
g187T	CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPLLRQAIELFDHQ	180

g172	GAEP AFLFGLELIICGLEKQLKCESGS 207	
g172T	GAEP AFLFGLELIICGLEKQLKCESGS 207	
g187	GAEP AFLFGLELIICGLEKQLKCESGS 207	
g187T	GAEP AFLFGLELIICGLEKQLKCESGS 207	

Figure S7. TetR sequence alignment of ATc sensitive pRAB11N-*g172*, *g187* and ATc tolerant pRAB11N-*g172*-T, *g187*-T. Amino acid of interest highlighted in yellow.