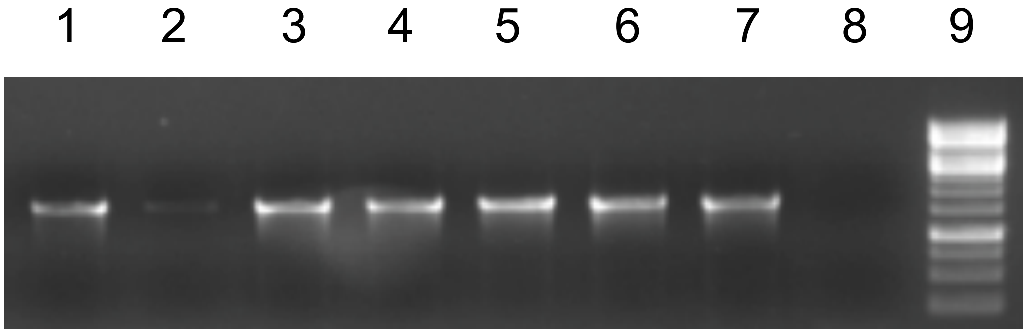
Figure S1: Hybridization data between the DNA of strain ATCC 29059 and the *vmlR* sequence of *Bacillus anthracis* which was tiled onto the PathogenID v.1 microarray.

>BAS2423 (= Truncated *vmlR* of *Bacillus anthracis*)
angccnnngccnnngctncagtaggcnaannntgnacnggtaaanctanagnnnnncacnnnnnnnnnnnnnnnn
nnnngnnnncanntctnnnngcnnntctnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngacnn
nncnnagnnnnnnnnnnnnnnnnnnngcnncanaannnnnnnnnnnnnnnnaannnnnnngnnnnnnnnnn
nnnnnnnnnnnnnncaagtgntgnnccannntnnnnnnnncgatnagnnnnccgnnacnnnnaaannnnnnnn
nnnnnnnnnctnatgannnannnnncganannnnnnnnnnnnnnnnnnnnnnntgnnnnncannnnnnnn
nnnagnnnnnngtacagtt**atcgtcgtatcacatgatcga**nntgtggcnnnnnnnnnggcnnn

Peptide signature (IVVSHDR) of the conserved H-loop motif shared by some categories of ABC proteins

Figure S2: PCR detection of *sal*(A) using P1 and P2 as internal primers



Presence of *sal*(A) was evidenced in all tested strains of *S. sciuri* which are LS_A^R, but not in the type strain of *S. saprophyticus* which is LS_A^S: 1, *S. sciuri* subsp. *rodentium* SVv1 (BM12494); 2, *S. sciuri* subsp. *rodentium* ATCC 700061; 3, *S. sciuri* subsp. *carnaticus* ATCC 700058; 4, *S. sciuri* subsp. *carnaticus* BL2 (BM12489); 5, *S. sciuri* subsp. *sciuri* ATCC 29059; 6, *S. sciuri* subsp. *sciuri* ATCC 29062; 7, *S. sciuri* subsp. *sciuri* SS226 (BM12487); 8, *S. saprophyticus* ATCC 15305; 9, 1-kb ladder.