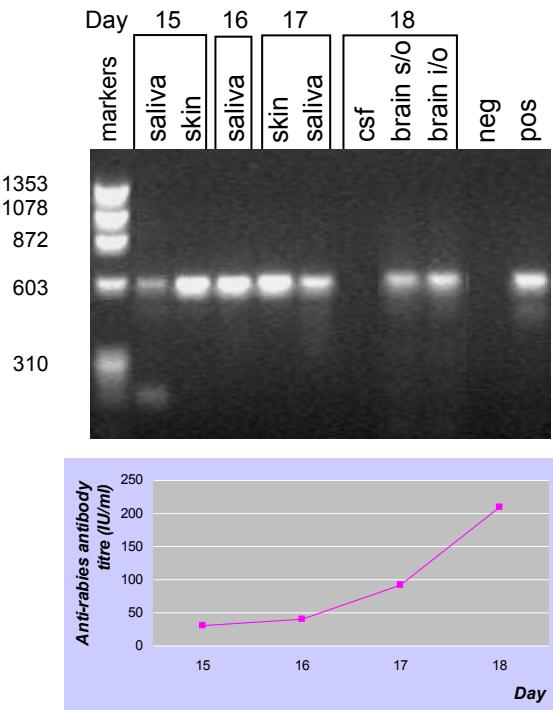


Posted as supplied by author.

Further details about figure 2: This neighbour joining phylogenetic tree is based on 400 nucleotides of the nucleoprotein gene, and shows that the strain we detected was most closely related to GER005 which was isolated from a human who developed rabies in Germany, after a dog bite in India. Bootstrap values over 70% are considered significant and are included within the figure. Accession numbers for the strains of virus used are as follows: THA1013 - AB178892, 8677MAL - U22916, RV69 - AY102995, AF374721 - AF374721, RV341 - AY102998; RV1112 - tbc, 94260NEP - U22918, 9141RUS - U22656, Komatsugawa - AB178890, RV277 - AY062069, RV61 - AY102993, RV193 - AY102996, RV1964 - DQ146162, GER05 - AY956319, RV642 - DQ146161, 93291SR - U22850, 8681IRA - U22482, RV643 - DQ146160, Pasteur Virus - M13215, CVS-11 - AY102992, Takamen - AB178891



Posted as supplied by author.

Supplementary figure. Top: Hemi-nested RT-PCR on diagnostic samples. The day of illness, and nature of the sample is shown; the brain biopsy specimens were taken via the supra-orbital (s/o), or infra-occipital (i/o) routes; neg is a negative control, pos is a positive control virus – strain CVS. The left hand lane shows the size of the molecular weight markers, and the samples which are positive have a band at approximately 400 base pairs.

Bottom: Anti-rabies antibody titres, measured in serum by the fluorescent virus neutralization assay (4) are elevated, and increasing through the course of the hospital admission. This is the expected response in a patient who has received no vaccine.