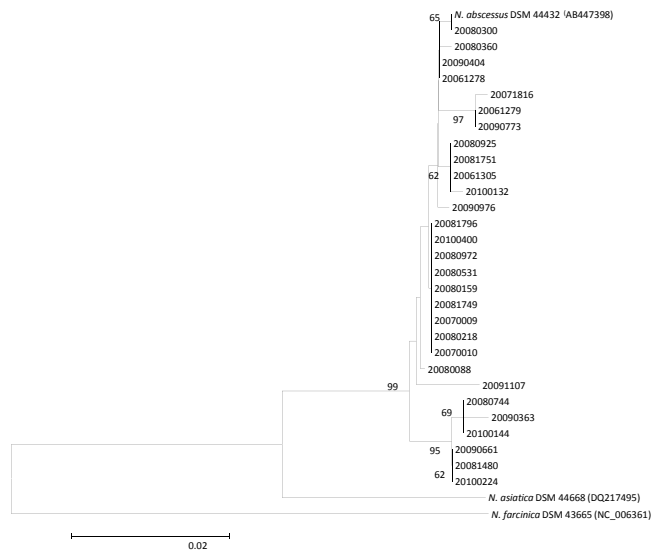
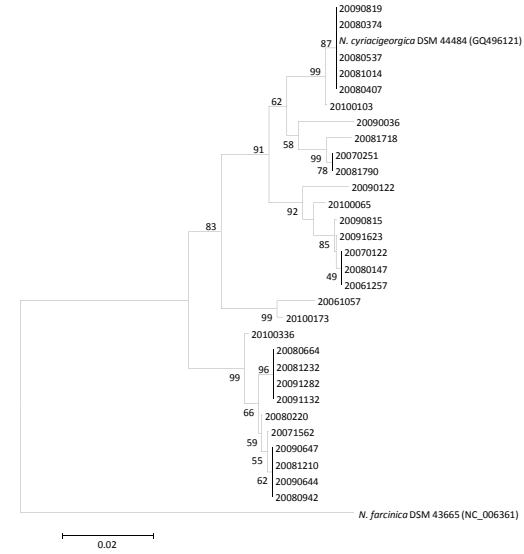


TABLE S1. Strain distribution for each of the studied species of *Nocardia*.

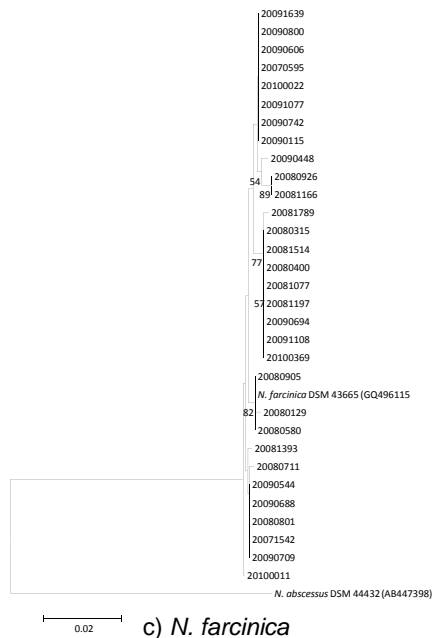
Species (Strain no.)	Spanish provinces (no.)	Clinical origins of the samples
<i>N. abscessus</i> (n=29)	18	24 respiratory system (13 sputum, 3 bronchial alveolar lavage, 6 bronchial alveolar aspirate, 1 nasal aspirate, 1 tracheal aspirate) 2 central nervous system, 2 blood, 1 cutaneous
<i>N. cyriacigeorgica</i> (n=30)	16	24 respiratory system (10 bronchial alveolar aspirates, 8 sputum samples, 4 bronchial alveolar lavages, 1 tracheal aspirate, and 1 pleural fluid sample), 2 central nervous system, 2 genital, 2 blood
<i>N. farcinica</i> (n=31)	18	22 respiratory system (13 sputum, 7 pulmonary abscess, 1 bronchial alveolar lavage, and 1 bronchial alveolar aspirate) 4 skin, 3 central nervous system and 2 blood
<i>N. nova</i> (n=29)	10	26 respiratory system (19 sputum, 4 bronchial alveolar aspirates, 2 pleural fluid and 1 tracheal aspirate) 1 skin and 2 internal tissues



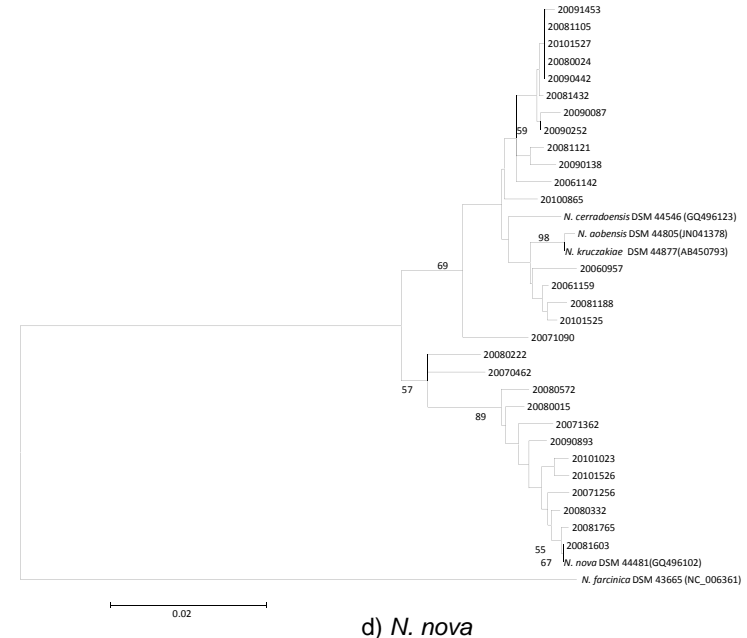
a) *N. abscessus*



b) *N. cyriacigeorgica*

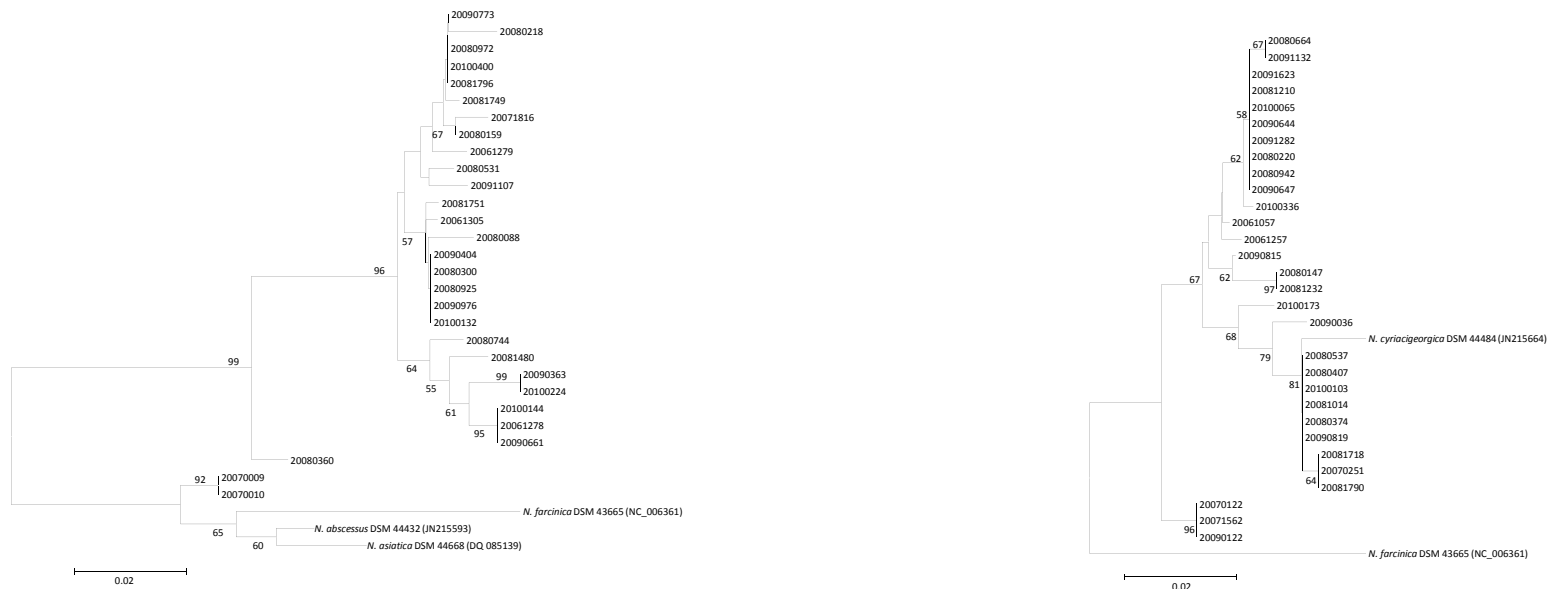


c) *N. farcinica*



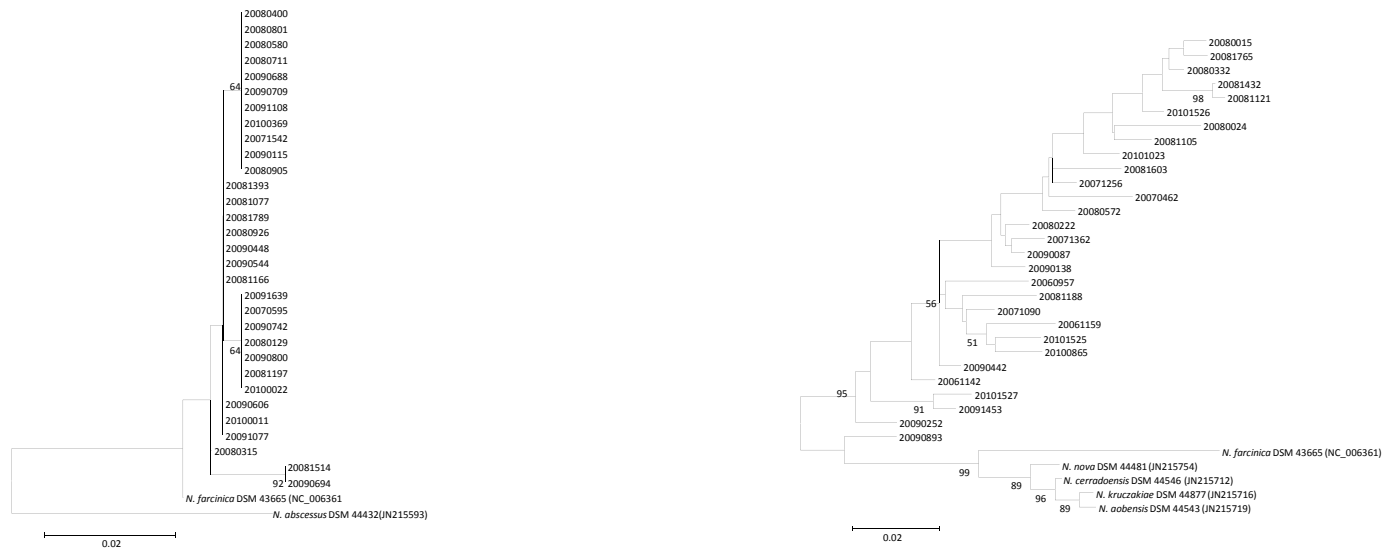
d) *N. nova*

FIG. S1. Phylogenetic trees according to neighbor-joining methods based on *gyrB* gene of *Nocardia* spp. four more prevalent species in Spain. Bootstrap values are expressed as a percentage of 1,000 replications. The scale bar represents 0.02 substitutions per nucleotide position. *N. farcinica* DSM 43665 is used as outgroup, except in case of *N. farcinica* analysis when it is substituted by *N. abscessus* DSM 43665.



a) *N. abscessus*

b) *N. cyriacigeorgica*



c) *N. farcinica*

d) *N. nova*

FIG. S2. Phylogenetic trees according to neighbor-joining methods based on *rpoB* gene of *Nocardia* spp. four more prevalent species in Spain. Bootstrap values are expressed as a percentage of 1,000 replications. The scale bar represents 0.02 substitutions per nucleotide position. *N. farcinica* DSM 43665 is used as outgroup, except in case of *N. farcinica* analysis when it is substituted by *N. abscessus* DSM 44432.

FIG. S3. Polymorphisms in the different GyrB-types found in the *N. nova* population (n=29).

Strain ID ^{1,2}	Position ³									Similarity Identity (%) ^{4,5}	GenBank acc. no.
	4 8	1 0 1	1 0 5	1 2 5	1 2 8	1 2 9'	1 3 1	1 5 7	2 1 5		
<i>N. nova</i> DSM 44481 ^T	G	E	D	A	A	–	E	P	V	100	GQ496102
CNM20101526	–	.	.	.	100 (100)	KC631363
CNM20071362	.	.	E	.	.	–	.	.	.	100 (99.6)	KC631362
CNM20080015	–	.	A	.	99 (100)	KC631361
CNM20080222	P	P	A	.	98 (99.8)	KC631360
<i>N. cerradoensis</i> DSM44546 ^T	.	.	E	T	T	P	P	A	.	96 (98.1)	AB450777
<i>N. aobensis</i> DSM 44805 ^T	.	Q	E	S	.	P	P	A	.	96 (97.9)	AB447401
<i>N. kruczakiae</i> DSM 44877 ^T	.	Q	E	S	.	P	P	A	.	96 (98.1)	AB450793
CNM20061159	.	Q	E	S	.	P	P	A	.	97 (99.2)	KC631359
CNM20060957	D	Q	E	S	.	P	P	A	.	97 (99.2)	KC631358
CNM20081188	.	Q	E	N	.	P	P	A	.	97 (99.2)	KC631357
CNM20090138	.	Q	E	T	.	P	R	A	.	97 (100)	KC631356
CNM20061142	S	Q	E	T	.	P	P	A	.	97 (100)	KC631355
CNM20081105	.	Q	E	T	.	P	P	A	.	97 (99.8)	KC631354
CNM20071090	.	Q	E	T	.	P	P	A	F	97 (99.6)	KC631353

¹Identification of the reference/studied strains; ²Strains representatives of the different GyrB-types mentioned in Figure S1; ³Positions of the amino acid change respect to *N. nova* DSM 44481^T; ^{4,5}Similarity identity coefficient, expressed as percentage, respect to *N. nova* DSM 44481^T GyrB protein sequence (CV89659) and 16S (GQ376190).