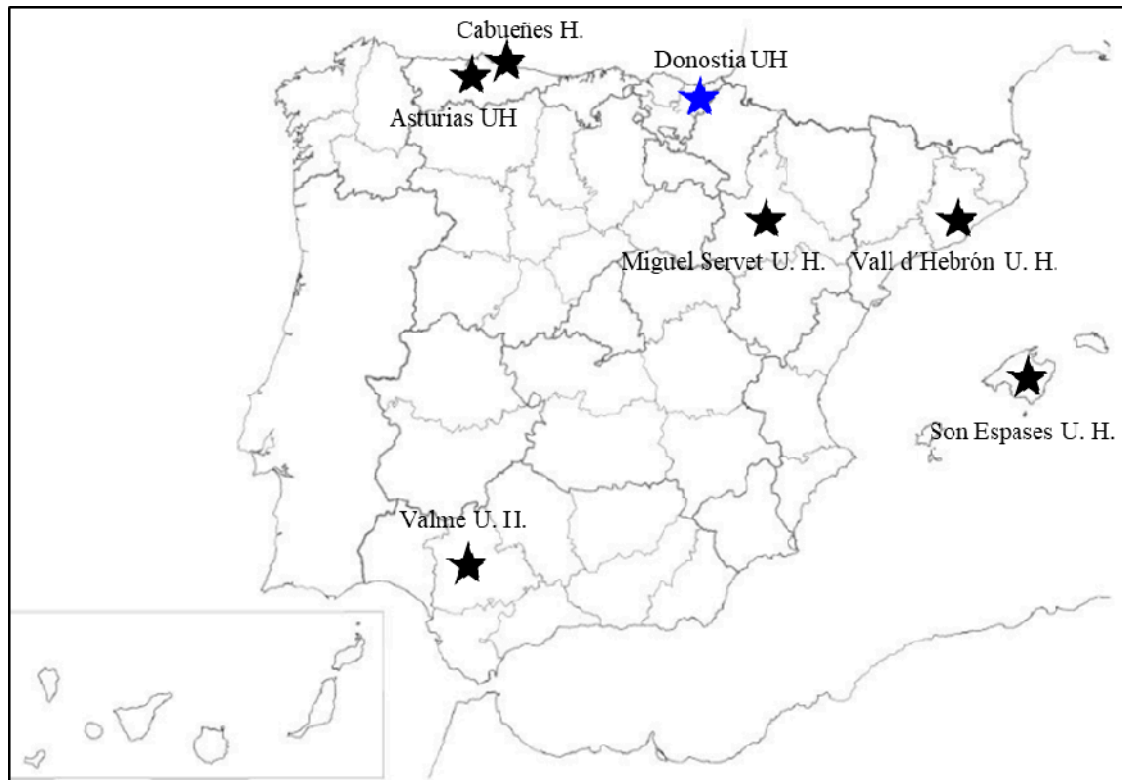
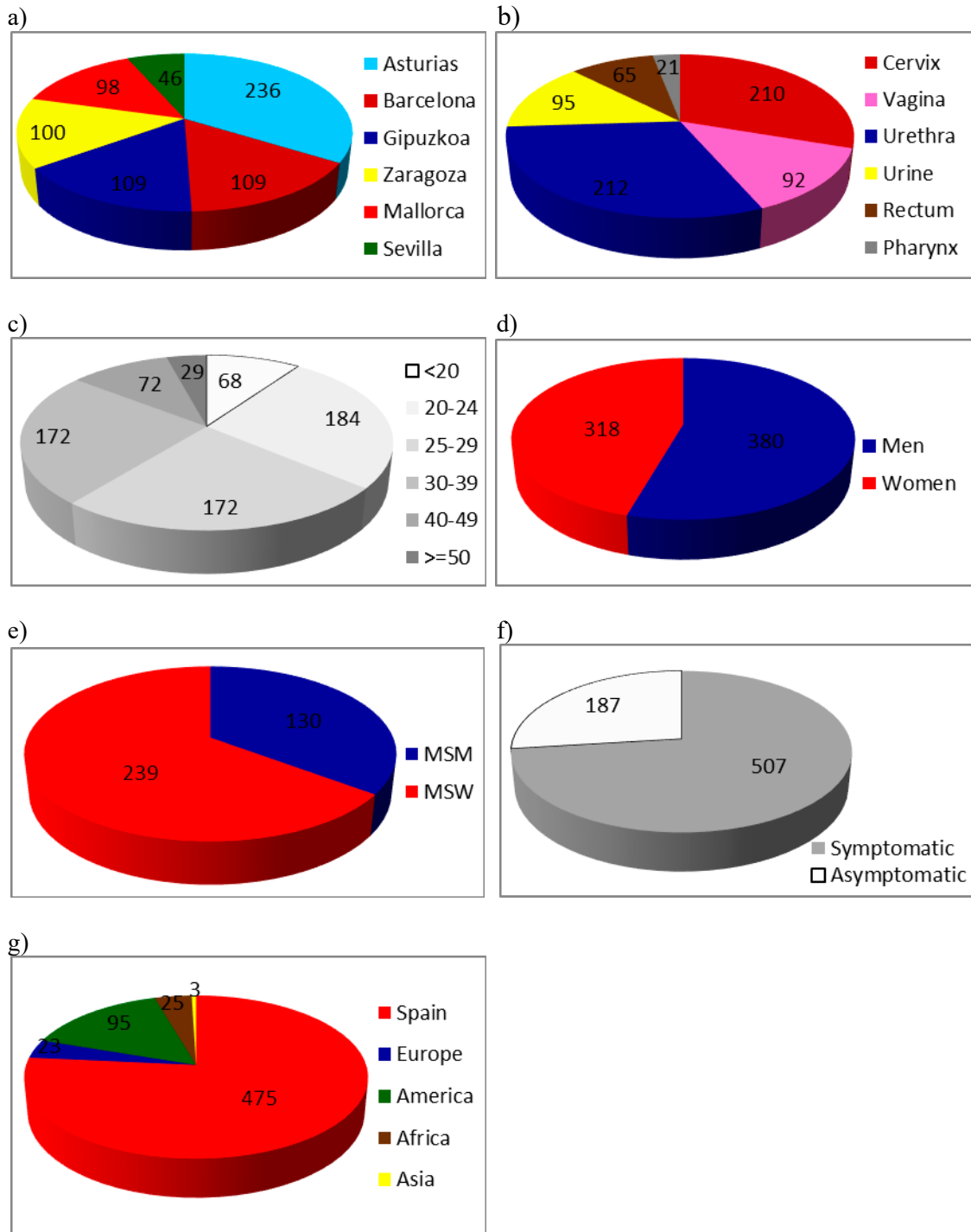


Supplementary Figure S1. Map with the seven hospitals in Spain participating in this study: Asturias University Hospital (Oviedo, Asturias), Cabueñes University Hospital (Gijón, Asturias), Donostia University Hospital (San Sebastián, Basque Country), Vall d'Hebrón University Hospital (Barcelona, Catalonia), Miguel Servet University Hospital (Zaragoza, Aragón), Son Espases University Hospital (Palma de Mallorca, Balearic Islands), and Valme University Hospital (Seville, Andalusia).



Star in blue: laboratory where *ompA* genotyping and sequenciotyping was performed.

Supplementary Figure S2. Pie charts of the 698 cases of *Chlamydia trachomatis* infection in Spain (2018-2019) included in the study by a) geographical area; b) anatomical site of sampling; c) age group (years); d) sex; e) sexual behaviour; f) clinical manifestations; and g) place of origin.



MSW: men who have sex with women; MSM: men who have sex with men.

Supplementary Table S1. Distribution of sequence types (STs) by genotype of *Chlamydia trachomatis* in 158 cases of this infection in Spain (2018-2019).

MLST (n)/genotype	E	D	F	G	J	I	H	K	B	Total	(%)
3	2									2	1.3
12		1	2							3	1.9
27,265,279,301,575,578,582				1x7						7	4.4
28				2						2	1.3
30								4		4	2.5
33				5						5	3.2
34,358,577,579								1x4		4	2.5
35		6								6	3.8
52				10						10	6.3
56	1			1						2	1.3
58		2								2	1.3
59	3									3	1.9
64,147,154,573,586	1x5									5	3.2
85,110,231,572			1x4							4	2.5
90		1	3							4	2.5
97							6			6	3.8
100						6				6	3.8
104					2					2	1.3
108					5				1	6	3.8
109		4								4	2.5
112,157,267,583,584,588					1x6					6	3.8
128				3						3	1.9
130,517,581						1x3				3	1.9
136					2					2	1.3
148			5							5	3.2
194,243,420,585,587		1x5								5	3.2
208									1	1	0.6
274						2				2	1.3
275				1		1				2	1.3
276						7				7	4.4
327	3									3	1.9
380								2		2	1.3
443,574,580,590							1x4			4	2.5
497	2									2	1.3
571		4								4	2.5
576					2					2	1.3
589				2						2	1.3
Not able to be typed	2	5	1	3	3		1		1	16	10.1
Total (%)	18 (11.4)	28 (17.7)	15 (9.5)	34 (21.5)	20 (12.7)	19 (12.0)	11 (7.0)	10 (6.3)	3 (1.9)	158	100.0
Genotyped, n (%)	225 (35.4)	119 (18.7)	106 (16.7)	70 (11.0)	47 (7.4)	40 (6.3)	13 (2.0)	13 (2.0)	3 (0.5)	636	

Sequence typed, %	8.0	23.5	14.2	48.6	42.6	47.5	84.6	76.9	100	24.8	
STs/genotype	10/16	11/23	7/14	14/31	10/17	7/19	5/10	6/10	2/2	67/142	vs 9/636
(% diversity)	(62.5)	(47.8)	(50.0)	(45.2)	(58.8)	(36.8)	(50)	(60)	(100)	(47.2)	(1.4)

In bold, the most common STs; in blue, STs found in more than one genotype.

Supplementary Table S2. Distribution of sequence types (STs) by genotype of *Chlamydia trachomatis*, sex and sexual behaviour in 142 cases of this infection in Spain (2018-2019).

Genotype	ST	Woman	Man	MSW	MSM	n/ST
E	59	1	2	1	1	3
	327	0	3	3	0	3
	3	0	2	1	1	2
	497	1	1	1	0	2
	56	0	1	0	1	1
	64	1	0	0	0	1
	147	1	0	0	0	1
	154	0	1	0	1	1
	573	1	0	0	0	1
	586	1	0	0	0	1
D	35	4	2	1	1	6
	109	0	4	1	3	4
	571	0	4	0	4	4
	58	0	2	0	2	2
	12	1	0	0	0	1
	90	0	1	0	1	1
	194	0	1	0	1	1
	243	0	1	0	1	1
	420	0	1	1	0	1
	585	1	0	0	0	1
587	0	1	1	0	1	
F	148	2	3	3	0	5
	90	1	2	2	0	3
	12	1	1	0	1	2
	85	0	1	1	0	1
	110	1	0	0	0	1
	231	0	1	0	1	1
	572	0	1	0	1	1
G	52	1	9	1	8	10
	33	0	5	1	4	5
	128	3	0	0	0	3
	28	2	0	0	0	2
	589	0	2	0	2	2
	27	1	0	0	0	1
	56	1	0	0	0	1
	265	1	0	0	0	1
	275	1	0	0	0	1
	279	1	0	0	0	1
	301	0	1	0	1	1
	575	1	0	0	0	1
	578	0	1	1	0	1
582	0	1	0	1	1	
J	108	0	5	0	5	5
	104	1	1	1	0	2
	136	2	0	0	0	2
	576	1	1	1	0	2
	112	0	1	0	1	1
	157	1	0	0	0	1
	267	0	1	1	0	1
	583	0	1	0	1	1
	584	0	1	0	1	1
	588	1	0	0	0	1
I	276	4	3	3	0	7

	100	5	1	1	0	6
	274	1	1	1	0	2
	130	0	1	0	1	1
	275	1	0	0	0	1
	517	1	0	0	0	1
	581	1	0	0	0	1
H	97	3	3	2	1	6
	443	0	1	1	0	1
	574	1	0	0	0	1
	580	1	0	0	0	1
	590	1	0	0	0	1
K	30	1	3	3	0	4
	380	2	0	0	0	2
	34	1	0	0	0	1
	358	1	0	0	0	1
	577	0	1	1	0	1
	579	0	1	0	1	1
B	108	0	1	0	1	1
	208	0	1	1	0	1
Total		59	83	35	48	142

Different STs, n (%) 39 (66.1) 43 (51.8) 25 (71.4) 26 (54.2) 67/142 (47.2)

MSW: men who have sex with women; MSM: men who have sex with men.

In bold, the most common STs; in blue, STs found in more than one genotype.