Sequences producing significant alignments Download \checkmark New Select columns \checkmark Show 10 \checkmark @												
	select all 10 sequences selected	GenBank	GenBank Graphics			Distance tree of results Mew MSA Vi						
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession			
	Leptospira interrogans serovar Canicola strain 611 chromosome 1, complete sequence	Leptospira interrogans serovar C	510	510	100%	2e-143	100.00%	4255595	CP044513.1			
	Leptospira interrogans serovar Canicola strain LJ178 chromosome 1, complete sequence	Leptospira interrogans serovar C	510	510	100%	2e-143	100.00%	4259066	CP044509.1			
	Leptospira interrogans serovar Canicola strain 114 chromosome I sequence	Leptospira interrogans serovar C	510	510	100%	2e-143	100.00%	4218946	CP022883.1			
	Leptospira interrogans serovar Linhai str. 56609 chromosome 1, complete sequence	Leptospira interrogans serovar Li	510	510	100%	2e-143	100.00%	4331770	CP006723.1			
	Leptospira interrogans serovar Gem strain Simon secY gene, partial sequence	Leptospira interrogans serovar G	510	510	100%	2e-143	100.00%	1408	EU358039.1			
	Leptospira interrogans serovar Pomona strain LT 1026 SecY (secY) gene, partial cds	Leptospira interrogans serovar P	510	510	100%	2e-143	100.00%	1375	EU358017.1			
	Leptospira interrogans serovar Monjakov SecY (secY) gene, partial cds	Leptospira interrogans serovar M	510	510	100%	2e-143	100.00%	1386	EU358014.1			
	Leptospira interrogans serovar Pomona SecY (secY) gene, partial cds	Leptospira interrogans serovar P	510	510	100%	2e-143	100.00%	1382	EU358013.1			
	Leptospira interrogans serovar Medanensis strain Hond HC SecY (secY) gene, partial cds	Leptospira interrogans serovar M	510	510	100%	2e-143	100.00%	1386	EU357984.1			
<	Leptospira interrogans serovar Bratislava strain Jez Bratislava SecY (secY) gene, partial cds	Leptospira interrogans serovar Br	510	510	100%	2e-143	100.00%	1386	EU357939.1			
*	Download GenBank Graphics											

Leptospira interrogans serovar Gem strain Simon secY gene, partial sequence Sequence ID: EU358039.1 Length: 1408 Number of Matches: 1

Cases		Eveneet	Identifies	Cana	Chrond	_
Score 510 bits	(276)	Expect 2e-143	Identities 276/276(100%)	Gaps 0/276(0%)	Strand Plus/Plus	
)uery	1	CTTGTTCCTGCCCT	TCaaaaacttcaaaaagaa	ggagaagaaggaag	aaaaaaaaTTGGT	60
Sbjct	163			<u>TTITIITIITIIT</u>		222
)uery	61	CAATATACTAAGTA	TGGAACCGTAATTCTTTGT	GCGATTCAATCTTT	AGCAGTGATCCAA	120
Sbjct	223	CAATATACTAAGTA	TGGAACCGTAATTCTTTGT	GCGATTCAATCTTT	AGCAGTGATCCAA	282
Query	121	CTCGCAAAGGGCTG	GTCTACCGGCACGGAACTT	GAGCCTGCGCGTTA	CCCGGGCTTAATC	180
Sbjct	283	CTCGCAAAGGGCTG	GTCTACCGGCACGGAACTT	GAGCCTGCGCGTTA	 CCCGGGCTTAATC	342
)uery	181	AATTCTTCTGTTGT	TCCTTATTTTTATTTAATC	GGAATCTTATCCAT	TACTACCGGAACC	240
Sbjct	343	AATTCTTCTGTTGT	 ТССТТАТТТТТАТТТААТС	GGAATCTTATCCAT	 TACTACCGGAACC	402
Query	241	GTTCTTCTCATTTG	GTTAGGAGAACAGATCACC	GAA 276		
Sbjct	403	GTTCTTCTCATTTG		 GAA 438		

Figure S6. Sequencing and BLAST analysis of PCR reaction products from clinical urine samples (Sample 019).