Sequences producing significant alignments	
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	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	488	488	100%	7e-137	100.00%	4255595	CP044513.1
	Leptospira interrogans serovar Canicola strain LJ178 chromosome 1, complete sequence	Leptospira interrogans serovar C	488	488	100%	7e-137	100.00%	4259066	<u>CP044509.1</u>
	Leptospira interrogans serovar Canicola strain 114 chromosome I sequence	Leptospira interrogans serovar C	488	488	100%	7e-137	100.00%	4218946	CP022883.1
~	Leptospira interrogans serovar Linhai str. 56609 chromosome 1, complete sequence	Leptospira interrogans serovar Li	488	488	100%	7e-137	100.00%	4331770	CP006723.1
	Leptospira interrogans serovar Gem strain Simon secY gene, partial sequence	Leptospira interrogans serovar G	488	488	100%	7e-137	100.00%	1408	EU358039.1
	Leptospira interrogans serovar Pomona strain LT 1026 SecY (secY) gene, partial cds	Leptospira interrogans serovar P	488	488	100%	7e-137	100.00%	1375	EU358017.1
	Leptospira interrogans serovar Monjakov SecY (secY) gene, partial cds	Leptospira interrogans serovar M	488	488	100%	7e-137	100.00%	1386	EU358014.1
	Leptospira interrogans serovar Pomona SecY (secY) gene, partial cds	Leptospira interrogans serovar P	488	488	100%	7e-137	100.00%	1382	EU358013.1
	Leptospira interrogans serovar Medanensis strain Hond HC SecY (secY) gene, partial cds	Leptospira interrogans serovar M	488	488	100%	7e-137	100.00%	1386	EU357984.1
	Leptospira interrogans serovar Bratislava strain Jez Bratislava SecY (secY) gene, partial cds	Leptospira interrogans serovar Br	488	488	100%	7e-137	100.00%	1386	EU357939.1

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

Range 1	: 164	to 427 GenBank G	raphics		Vext Match	Previous Ma
Score 488 bits	(264)	Expect 7e-137	Identities 264/264(100%)	Gaps 0/264(0%)	Strand Plus/Plus	_
Query	1	TTGTTCCTGCCCTT	Caaaaacttcaaaaaga		aaaaaaa <b>TTGGTC</b>	60
Sbjct	164	TTGTTCCTGCCCTT	CAAAAACTTCAAAAAGA	AGGAGAAGAAGGAAGA	AAAAAAAATTGGTC	223
Query	61	AATATACTAAGTAT	GGAACCGTAATTCTTTG	TGCGATTCAATCTTTA	GCAGTGATCCAAC	120
Sbjct	224	AATATACTAAGTAT	GGAACCGTAATTCTTTC	TGCGATTCAATCTTTA	GCAGTGATCCAAC	283
Query	121	TCGCAAAGGGCTGG	TCTACCGGCACGGAACI	TGAGCCTGCGCGTTAC	CCGGGCTTAATCA	180
Sbjct	284	TCGCAAAGGGCTGG	TCTACCGGCACGGAACI	TGAGCCTGCGCGTTAC	CCGGGCTTAATCA	343
Query	181	ATTCTTCTGTTGTT	CCTTATTTTTATTTAA	CGGAATCTTATCCATT	ACTACCGGAACCG	240
Sbjct	344	ATTCTTCTGTTGTT	CCTTATTTTTATTTAA1	CGGAATCTTATCCATT	ACTACCGGAACCG	403
Query	241	TTCTTCTCATTTGG	TTAGGAGAAC 264			
Sbjct	404	TTCTTCTCATTTGG	TTAGGAGAAC 427			

Figure S5. Sequencing and BLAST analysis of PCR reaction products from clinical urine samples (Sample 005).