

Comparative genomics of *Legionella pneumophila* isolates from the West Bank and Germany support molecular epidemiology of Legionnaires' disease
Zayed et al.

SUPPLEMENTARY MATERIALS
TABLES

Table S1: Main features of <i>L. pneumophila</i> isolates and reference strains used in the study.															
Strain designation	GenBank/RefSeq Acc. No:	Sg (mAb) ¹	ST ²	MLV A-8(12) ³	VAC C×	Site of Isolation	Year of Isolation	Source of isolation	Genome Size (bp)	No. of Genes*	Genomic Islands (bp)	Genomic Islands (%)	Coding Sequences*	Contigs	Reason for selection
Genome sequences obtained within this study															
A156_Gt64(74)_Ps	0JAPXIV	6 Dresden	ST7 4	Gt64(74)	VAC C2	Beit Jala, West Bank	2013	Hospital environmental swab	3,366,323	3,049	174,331	5.2	3008	40	Thunderbay branch
A129_Gt64(74)_Ps	0JAPXIU	6 Dresden	ST7 4	Gt64(74)	VAC C2	Beit Jala, West Bank	2013	Hospital environmental swab	3,527,232	3,206	293,904	8.3	3166	56	Thunderbay branch
A15_Gt12(84)_Ps	0JAPXIT	Sg.8	ST1358	Gt12(84)	NA	East Jerusalem, West Bank	2012	Hospital environmental swab	3,495,260	3,088	180,013	5.2	3,053	127	Lorraine branch
A139_Gt4(17)_Ps	0JAPXIS	Sg.1	ST1	Gt4(17)	VAC C1	Nablus, West Bank	2013	Hospital environmental swab	3,579,958	3,242	223,851	6.3	3,205	78	Worldwide present and highest abundance in our collections
A5_Gt4(17)_Ps	0JAPXIR	1 OLDA	ST1	Gt4(17)	VAC C1	East Jerusalem, West Bank	2012	Hospital environmental swab	3,586,669	3,249	225,997	6.3	3,211	80	Worldwide present and highest abundance in our collections

A29_Gt6(18)_Ps	0JAPXIQ	Sg.1	ST1	Gt6(18)	VAC C1	Hebron, West Bank	2012	Hospital environmental swab	3,626,550	3,289	339,005	9.3	3,251	68	Dominant in southern West Bank
A131_Gt6(18)_Ps	0JAPXIP	Sg.1	ST1	Gt6(18)	VAC C1	Hebron, West Bank	2013	Hospital environmental swab	3,548,746	3,206	281,219	7.9	3,169	67	Dominant in southern West Bank
A193_Gt40(47)_Ps	0JAPXIO	6 Dresden	ST3 45	Gt40(47)	VAC C5	Hebron, West Bank	2014	Hospital environmental swab	3,446,379	3,098	185,152	5.4	3,056	33	Alcoy branch, close to Warstein outbreak
A194_Gt40(47)_Ps	CP114578	6 Dresden	ST3 45	Gt40(47)	VAC C5	Hebron, West Bank	2014	Hospital environmental swab	3,467,904	3,121	156,728	4.5	3,071	1	Alcoy branch, close to Warstein outbreak
A195_Gt40(47)_Ps	JAPXIN	6 Dresden	ST3 45	Gt40(47)	VAC C5	Hebron, West Bank	2014	Hospital environmental swab	3,440,802	3,095	167,241	4.9	3,051	42	Alcoy branch, close to Warstein outbreak
A138_Gt9(92)_Ps	JAPXIM	6 Dresden	ST4 61	Gt9(92)	VAC C11	Nablus, West Bank	2013	Hospital environmental swab	3,363,143	3,038	162,571	4.8	2,996	40	Alcoy branch
A112_Gt10(93)_Ps	JAPXIL	6 Dresden	ST4 61	Gt10(93)	VAC C11	Beit Jala, West Bank	2013	Hospital environmental swab	3,362,286	3,030	147,968	4.4	2,990	42	Highly abundant genotype
A114_Gt10(93)_Ps	JAPXIK	6 Dresden	ST4 61	Gt10(93)	VAC C11	Beit Jala, West Bank	2013	Hospital hot water sample	3,362,313	3,033	159,647	4.7	2,989	41	Highly abundant genotype
A127_Gt10(93)_Ps	JAPXIJ	6 Dresden	ST4 61	Gt10(93)	VAC C11	Beit Jala, West Bank	2013	Hospital environmental swab	3,363,025	3,037	142,978	4.3	2,993	38	Highly abundant genotype
A108_Gt10(93)_Ps	JAPXII	6 Dresden	ST4 61	Gt10(93)	VAC C11	Beit Jala, West Bank	2013	Hospital environmental swab	3,291,620	2,949	153,342	4.7	2,907	38	Highly abundant genotype
A166_Gt8(142)_Ps	JAPXIH	Sg.(2-14)	ST1 482	Gt8(142)	VAC C5	Hebron, West Bank	2013	Hospital environmental swab	3,353,128	3,014	204,232	6.1	2,974	28	Alcoy branch
H34_Gt22(102)_D	JAPXIG	Sg.10	NA	Gt22(102)	NA	Braunschweig, Germany	2013	Environmental sample	3,403,136	3,049	160,329	4.7	3,016	64	D7630 branch

H29_Gt22(100)_D	JAPXIF	4 Portland	NA	Gt22(100)	VAC C2	Braunschweig, Germany	2013	Environmental sample	3,403, 391	3,06 1	144,4 15	4.2	3,017	68	D7630 branch
H35_Gt22(102)_D	JAPXIE	Sg.1	NA	Gt22(102)	VAC C5	Braunschweig, Germany	2013	Environmental sample	3,402, 267	3,04 9	166,5 33	4.9	3,013	64	D7630 branch
H39_Gt4(17)_D	JAPXID	4 Portland	NA	Gt4(17)	NA	Braunschweig, Germany	2014	Environmental sample	3,592, 274	3,24 5	226,2 68	6.3	3,202	78	Worldwide present and highest abundance in our collections
H3_Gt14(31)_D	CP11457 6, CP11457 7	6 Chicago	ST1 431	Gt14(31)	VAC C2	Braunschweig, Germany	2009	Environmental sample	3,691, 263	3,38 6	209,8 67	5.7	3,336	2	Alcoy branch
H23_Gt14(30)_D	JAPXIC	6 Chicago	ST1 431	Gt14(30)	VAC C2	Braunschweig, Germany	2013	Environmental sample	3,783, 853	3,48 2	372,7 50	9.9	3,444	130	Alcoy branch
H1_Gt14(31)_D	JAPXIB	6 Chicago	ST1 431	Gt14(31)	VAC C2	Braunschweig, Germany	2009	Environmental sample	3,654, 038	3,35 5	253,0 73	6.9	3,312	69	Alcoy branch
H2_Gt14(31)_D	JAPXIA	6 Chicago	ST1 431	Gt14(31)	VAC C2	Braunschweig, Germany	2009	Environmental sample	3,650, 216	3,34 7	238,6 49	6.5	3,310	64	Alcoy branch
L09-313_Cl_Gt84(116)_D	JAPXHZ	Sg.3	ST9 3	Gt84(116)	VAC C13	Freiburg, Germany	2009	Clinical sample	3,398, 240	3,06 8	160,1 81	4.7	3,027	58	Thunderbay branch
L01-443_Cl_Gt64(74)_D	JAPXHY	1 Knoxville	ST9	Gt64(74)	VAC C13	Herford, Germany	2001	Clinical sample	3,477, 581	3,14 2	225,6 39	6.5	3,099	103	Thunderbay branch
L10-091_Cl_Gt69(69)_D	JAPXHX	1 Philadelphia	ST4 35	Gt69(69)	VAC C2	Erlangen, Germany	2010	Clinical sample	3,687, 459	3,37 3	187,4 40	5.1	3,330	97	Pontiac Branch
L12-317_Cl_Gt72(66)_D	JAPXHW	1 Knoxville	ST4 44	Gt72(66)	VAC C2	Lorrach, Germany	2012	Clinical sample	3,516, 737	3,17 0	186,7 33	5.3	3,133	74	Pontiac Branch
L11-209_Cl_Gt29(27)_D	JAPXHV	1 Knoxville	ST6 2	Gt29(27)	VAC C2	Hannover, Germany	2011	Clinical sample	3,461, 996	3,13 0	96,40 8	2.8	3,085	65	Pontiac Branch
L10-023_Cl_Gt75(49)_D	CP01110 5, CP01110 6	1 Knoxville	ST6 2	Gt75(49)	VAC C2	Ulm, Germany	2010	Clinical sample	3,641, 882	3,42 7	NA	NA	3,377	1	Pontiac Branch

L09-329_Cl_Gt75(49)_D	JAPXHU	1 Philadelphia	ST6_2	Gt75(49)	VAC C2	Trier, Germany	2009	Clinical sample	3,445,544	3,108	117,416	3.4	3,068	76	Pontiac Branch
L02-521_Cl_Gt29(27)_D	JAPXHT	1 Philadelphia	ST6_2	Gt29(27)	VAC C2	Bad Langensalza, Germany	2002	Clinical sample	3,478,585	3,161	118,405	3.4	3,117	72	Pontiac Branch
L02-465_Cl_Gt27(133)_D	JAPXHS	1 Benidorm	ST4_25	Gt27(133)	VAC C1	Berlin, Germany	2002	Clinical sample	3,500,734	3,173	214,498	6.1	3,135	52	Alcoy branch
L04-545_Cl_Gt40(47)_D	JAPXHR	6 Dresden	ST2_92	Gt40(47)	VAC C2	Heide-West, Germany	2004	Clinical sample	3,358,959	3,006	160,642	4.8	2,964	34	Alcoy branch, close to Warstein outbreak
L06-153_Cl_Gt71(135)_D	JAPXHQ	1 OLDA	ST1_69	Gt71(135)	VAC C18	Brandenburg , Germany	2006	Clinical sample	3,405,980	3,074	NA	NA	3,030	39	Alcoy branch
L06-129_Cl_Gt71(135)_D	JAPXHP	1 OLDA	ST1_69	Gt71(135)	VAC C18	Brandenburg , Germany	2006	Clinical sample	3,406,112	3,075	172,495	5.1	3,031	40	Alcoy branch
L04-041_Cl_Gt30(137)_D	JAPXHO	Sg.3	ST8_7	Gt30(137)	NA	Kassel, Germany	2004	Clinical sample	3,522,671	3,206	258,174	7.3	3,165	50	Alcoy branch
L05-341_Cl_Gt8(132)_D	JAPXHN	6 Chicago	ST8_1	Gt8(132)	VAC C16	Darmstadt, Germany	2005	Clinical sample	3,410,856	3,071	219,558	6.4	3,035	31	Alcoy branch
Reference genomes used within this study															
Lpn-LPE509	CP003886	NA	NA	NA	NA	Shanghai, China	2013	Hospital water	3,434,224	3,105	NA	NA	3,055	1	Already published
Lpn-Philadelphia1	NC_002942	1 Philadelphia	ST3_6	Gt64(74)	VAC C2	Philadelphia, USA	1974	Clinical sample	3,397,754	2,943	180,555	5.3	3,023	1	Type strain-well characterized/ cause Philadelphia outbreak/ Already published
Lpn-Thunderbay	CP003730	Sg.6	ST1_87	NA	NA	Thunderbay, Canada	Unkn own	Clinical sample	3,455,167	2,998	NA	NA	3,116	1	Already published

Lpn-ATCC43290	CP003192	Sg.12	ST187	NA	NA	USA	1987	Clinical sample	3,359,001	2,926	NA	NA	2,993	1	Already published
Lpn-lpm7613	NZ_LT598657, NZ_LT598658	NA	NA	NA	NA	NA	2000	Clinical sample	3,261,562	2,944	NA	NA	2,894	1	Already published
Lpn-Lens	CR628337, CR628339	Sg.1	ST15	NA	NA	France	2004	Clinical sample	3,345,687	3,004	180,986	5.4	2,956	1	Caused a large outbreak in France/ already published
Lpn-Lorraine	FQ958210	Sg.1	ST47	NA	NA	France	2004	Clinical sample	3,467,254	3,069	NA	NA	3,130	1	In top six strains that cause disease/ already published
Lpn-HL06041035	FQ958211	NA	NA	NA	NA	France	2006	Hospital water	3,492,535	3,184	NA	NA	3,113	1	Already published
Lpn-D7631	CP015343	Sg.1	ST731	NA	NA	NYC, USA	2012	Environmental sample	3,436,178	3,090	NA	NA	3,040	1	Already published
Lpn-D7630	CP015344	Sg.1	ST731	NA	NA	NYC, USA	2012	Clinical sample	3,444,702	3,097	NA	NA	3,047	1	Already published
Lpn-D7632	CP015342	Sg.1	ST731	NA	NA	NYC, USA	2012	Clinical sample	3,435,648	3,087	NA	NA	3,037	1	Already published
Lpn-Paris	CIP107629	1 Philadelphia	ST1	Gt4(17)	VACC1	Paris, France	2004	Clinical sample	3,503,610	3,224	163,637	4.7	3,101	1	Worldwide distributed/ already published/ manually annotated
Lpn-OLDA	CP016030	1 OLDA	ST1	NA	NA	USA	1947	Frozen cell culture	3,486,108	3,144	NA	NA	3,094	1	already published
Lpn-Pontiac	CP016029	1 OLDA	NA	NA	NA	Michigan, USA	1968	Sporadic LD case	3,545,001	3,224	NA	NA	3,174	1	Already published
Lpn-Toronto	CP012019.1	NA	NA	NA	NA	Toronto, Canada	2005	Clinical sample	3,573,898	3,269	NA	NA	3,187	1	Already published

Table S2: The dDDH values among all *L. pneumophila* isolates provided according to TYGS. (Provided in Excel file)

[illegible]

Table S3: Whole-genome SNP comparison of <i>L. pneumophila</i> isolates and reference strains. Numbers indicate SNP different from the reference genome																			
<i>L. pneumophila</i> strain	Lpn-LPE 509	Lpn-Philadelphia 1	Lpn-Thunderbay	Lpn-ATCC 43290	Lpn-lpm7613	Lpn-Lens	Lpn-Lorraine	Lpn-HL060 41035	Lpn-D763 1	Lpn-D763 0	Lpn-D763 2	Lpn-Paris	Lpn-OLD A	Lpn-Pontiac	Lpn-Toronto	Lpn-Alcoy	Lpn-Corby	A194 - Gt40 (47)-Ps	H3-Gt14 (31)-D
Lpn-LPE509	0	7,893	6,607	4,432	5,681	61,660	52,372	55,729	51,231	51,231	51,232	54,130	54,189	54,867	57,050	56,175	56,022	56,954	56,967
Lpn-Philadelphia 1	7,949	0	7,173	6,931	8,114	60,513	52,197	57,012	54,113	54,113	54,114	56,508	56,567	57,130	58,655	59,954	59,707	59,815	59,716
L09-313_C1_Gt84(116)_D	7,497	6,725	<u>3,463</u>	3,736	4,614	60,800	52,184	58,590	52,244	52,244	52,245	59,151	59,210	57,112	58,850	56,022	56,099	56,924	57,071
L01-443_C1_Gt64(74)_D	9,711	8,315	<u>6,283</u>	6,589	7,259	60,203	52,162	58,289	52,019	52,019	52,020	59,314	59,373	57,215	59,036	56,337	56,576	57,346	57,053
Lpn-Thunderbay	6,645	7,122	0	2,376	3,271	60,903	52,499	57,766	50,688	50,688	50,689	58,421	58,480	57,208	58,841	56,525	56,277	57,458	57,151
Lpn-ATCC43290	4,471	6,876	2,376	0	1,663	61,037	52,710	57,620	50,680	50,680	50,681	58,102	58,161	56,886	58,502	56,719	56,690	57,633	57,324
Lpn-lpm7613	5,727	8,062	3,270	1,665	0	60,217	52,715	57,852	51,426	51,426	51,427	58,455	58,518	57,005	58,682	56,692	56,664	57,919	57,438
A156_Gt64(74)_Ps	6,255	5,700	<u>3,018</u>	3,288	4,185	61,079	52,328	58,651	50,720	50,720	50,721	59,348	59,407	57,387	58,767	55,986	55,492	57,772	56,644
A129_Gt64(74)_Ps	6,251	5,700	<u>3,018</u>	3,288	4,185	61,078	52,328	58,651	50,720	50,720	50,721	59,348	59,407	57,387	58,767	55,986	55,492	57,772	56,644
Lpn-Lens	62,174	60,985	61,462	61,608	60,755	0	55,607	68,139	66,603	66,603	66,604	67,884	67,917	62,288	63,962	70,708	71,182	70,922	70,076

Lpn-Lorraine	52,25 2	52,094	52,408	52,634	52,62 4	54,96 8	0	50,857	52,01 9	52,01 9	52,02 0	46,52 0	46,54 7	40,56 6	44,74 5	53,38 0	53,84 8	53,59 6	53,23 6
A15_Gt12(84)_Ps	53,54 4	52,817	52,966	53,275	53,20 8	52,50 6	<u>13,18</u> <u>0</u>	53,553	54,04 3	54,04 3	54,04 4	50,89 5	50,92 2	48,03 5	49,23 6	55,93 1	56,52 7	56,18 3	55,60 5
Lpn-HL06041035	55,33 4	56,644	57,431	57,284	57,50 2	66,96 6	50,33 0	0	28,89 8	28,89 8	28,89 9	32,90 7	32,96 8	39,43 5	40,85 5	47,89 8	48,86 6	48,57 8	45,74 6
Lpn-D7631	50,81 7	53,705	50,323	50,325	51,07 0	65,51 4	51,65 5	29,003	0	0	1	43,82 2	43,88 7	46,21 4	46,96 6	45,67 3	46,29 9	46,04 4	44,30 5
Lpn-D7630	50,81 7	53,705	50,323	50,325	51,07 0	65,51 4	51,65 5	29,003	0	0	1	43,82 2	43,88 7	46,21 4	46,96 6	45,67 3	46,29 9	46,04 4	44,30 5
Lpn-D7632	50,81 8	53,706	50,324	50,326	51,07 1	65,51 5	51,65 6	29,004	1	1	0	43,82 3	43,88 8	46,21 5	46,96 7	45,67 4	46,30 0	46,04 5	44,30 6
H34_Gt22(102)_D	53,85 6	58,095	54,717	54,848	54,85 0	66,80 7	51,79 5	25,429	<u>9,793</u>	<u>9,793</u>	9,794	43,03 4	43,09 5	44,85 2	45,63 1	43,27 2	43,76 1	44,29 1	41,67 0
H29_Gt22(100)_D	53,85 5	58,066	54,688	54,819	54,82 1	66,77 8	51,76 6	25,400	<u>9,764</u>	<u>9,764</u>	9,765	43,00 5	43,06 6	44,82 3	45,60 2	43,24 3	43,73 2	44,26 2	41,64 1
H35_Gt22(102)_D	53,85 5	58,132	54,750	54,885	54,88 7	66,84 4	51,83 2	25,466	<u>9,831</u>	<u>9,831</u>	9,832	43,07 1	43,13 2	44,88 9	45,66 9	43,31 0	43,79 9	44,32 9	41,70 8
H39_Gt4(17)_D	55,36 6	57,545	57,882	57,756	57,89 3	62,81 5	47,91 1	36,501	44,70 9	44,70 9	44,71 0	11,08 4	<u>11,02</u> <u>0</u>	32,76 0	32,36 5	46,51 0	46,59 5	46,61 9	46,25 8
A139_Gt4(17)_Ps	53,87 6	56,316	58,267	57,951	58,29 4	66,87 0	46,17 2	33,110	43,89 3	43,89 3	43,89 4	260	<u>195</u>	28,09 8	29,49 8	46,34 4	46,95 8	46,57 4	46,18 5
Lpn-Paris	53,75 4	56,173	58,128	57,812	58,15 5	66,76 7	46,06 8	32,935	43,74 4	43,74 4	43,74 5	0	90	28,05 7	29,45 7	46,18 8	46,80 2	46,41 7	46,03 3
A5_Gt4(17)_Ps	53,88 1	56,289	58,244	57,928	58,27 1	66,85 1	46,14 7	33,054	43,86 3	43,86 3	43,86 4	147	<u>76</u>	28,08 0	29,48 0	46,30 5	46,91 9	46,53 4	46,15 0
Lpn-OLDA	53,81 7	56,232	58,187	57,871	58,21 4	66,79 4	46,09 2	32,997	43,80 7	43,80 7	43,80 8	89	0	28,02 6	29,42 4	46,24 7	46,86 1	46,47 6	46,09 2
A29_Gt6(18)_Ps	53,00 3	56,351	57,396	57,080	57,41 1	66,65 3	46,11 4	32,784	42,71 1	42,71 1	42,71 2	1,753	<u>1,688</u>	28,11 4	29,41 6	45,06 5	45,63 6	45,37 9	44,98 2
A131_Gt6(18)_Ps	53,00 1	56,347	57,392	57,076	57,40 7	66,65 1	46,11 2	32,782	42,70 9	42,70 9	42,71 0	1,751	<u>1,686</u>	28,11 2	29,41 4	45,06 1	45,63 2	45,37 5	44,97 8

L10-091_Cl_Gt6 9(69)_D	54,31 3	56,966	57,043	56,697	56,89 2	64,69 0	42,65 4	38,454	44,54 1	44,54 1	44,54 2	24,40 7	24,37 7	<u>14,35</u> 8	15,65 7	45,82 5	45,79 6	46,44 8	46,07 7
L12-317_Cl_Gt7 2(66)_D	54,27 9	56,915	56,951	56,621	56,80 1	64,19 1	42,01 8	38,499	44,95 4	44,95 4	44,95 5	25,42 2	25,39 2	<u>14,94</u> 2	16,58 7	45,26 4	45,25 7	46,00 4	45,58 9
L11-209_Cl_Gt2 9(27)_D	54,68 8	56,911	56,569	56,259	56,28 0	60,11 2	40,76 2	40,236	46,18 6	46,18 6	46,18 7	28,69 6	28,66 7	<u>2,704</u>	17,49 8	47,31 1	47,98 1	47,91 2	47,05 0
L10-023_Cl_Gt7 5(49)_D	54,48 3	56,779	56,797	56,483	56,58 6	61,11 7	40,20 7	39,537	46,01 3	46,01 3	46,01 4	27,89 8	27,86 9	<u>823</u>	16,39 3	46,77 4	47,33 9	47,53 9	46,45 3
L09-329_Cl_Gt7 5(49)_D	54,32 7	56,492	56,579	56,342	56,44 5	59,97 5	40,31 6	40,251	46,76 1	46,76 1	46,76 2	29,24 8	29,21 9	<u>2,329</u>	17,79 7	47,54 5	47,96 5	48,20 1	47,33 3
Lpn-Pontiac	54,35 0	56,657	56,744	56,430	56,53 3	61,01 6	39,95 1	39,432	45,99 9	45,99 9	46,00 0	27,95 6	27,92 7	0	16,48 4	46,97 3	47,50 1	47,59 7	46,74 7
L02-521_Cl_Gt2 9(27)_D	54,21 5	56,521	56,608	56,294	56,39 7	60,05 1	40,08 3	40,073	46,57 2	46,57 2	46,57 3	29,08 2	29,05 3	<u>2,030</u>	17,67 0	47,78 7	48,27 3	48,36 3	47,59 5
Lpn-Toronto	56,62 6	58,242	58,470	58,127	58,29 4	62,88 5	44,29 6	40,967	46,90 0	46,90 0	46,90 1	29,47 7	29,44 6	16,65 3	0	46,57 6	47,00 1	47,17 6	46,85 3
L02-465_Cl_Gt2 7(133)_D	56,94 7	59,635	57,486	57,654	57,71 8	67,88 1	51,84 4	43,966	39,93 9	39,93 8	39,93 9	43,40 5	43,46 6	45,84 6	46,26 7	19,76 4	20,12 2	<u>19,03</u> 1	21,14 6
L04-545_Cl_Gt4 0(47)_D	56,22 6	59,148	56,602	56,796	57,08 8	69,34 2	52,78 1	48,072	46,33 7	46,33 6	46,33 7	45,80 8	45,86 9	47,91 8	46,70 0	11,77 6	12,44 8	<u>2,822</u>	15,11 2
A193_Gt40(47)_Ps	56,79 0	59,399	57,082	57,269	57,54 2	69,60 1	53,18 2	48,816	46,12 7	46,12 6	46,12 7	46,65 6	46,71 7	48,22 0	47,51 9	13,00 8	14,26 9	<u>76</u>	16,88 3
A194_Gt40(47)_Ps	55,98 0	58,832	56,516	56,703	56,97 6	69,03 8	52,61 3	48,246	45,54 7	45,54 6	45,54 7	46,08 6	46,14 7	47,65 1	46,95 2	12,62 3	13,69 6	0	16,31 9

A195_Gt40(47)_Ps	56,04 4	58,896	56,580	56,767	57,04 0	69,10 1	52,67 7	48,309	45,61 2	45,61 1	45,61 2	46,15 0	46,21 1	47,71 5	47,01 6	12,68 6	13,75 9	<u>69</u>	16,38 3
A138_Gt9(2)_Ps	55,38 7	58,320	56,257	56,577	56,77 1	69,09 3	52,30 4	47,447	46,59 5	46,59 4	46,59 5	45,20 0	45,26 2	47,41 4	47,23 0	11,67 4	12,97 7	<u>9,235</u>	15,49 7
A112_Gt10(93)_Ps	55,39 1	58,287	56,228	56,579	56,77 3	69,03 5	52,11 9	47,331	46,56 2	46,56 1	46,56 2	45,02 3	45,08 5	47,00 6	46,83 2	12,08 0	13,38 7	<u>9,737</u>	15,66 8
A114_Gt10(93)_Ps	55,39 7	58,293	56,234	56,585	56,77 9	69,04 1	52,12 5	47,337	46,56 8	46,56 7	46,56 8	45,02 9	45,09 1	47,01 2	46,83 8	12,08 6	13,39 3	<u>9,743</u>	15,67 4
A127_Gt10(93)_Ps	55,39 8	58,324	56,265	56,616	56,81 0	69,07 3	52,15 7	47,369	46,60 0	46,59 9	46,60 0	45,06 1	45,12 3	47,04 4	46,87 0	12,11 9	13,42 6	<u>9,776</u>	15,70 7
A108_Gt10(93)_Ps	55,40 0	58,296	56,237	56,588	56,78 2	69,04 4	52,12 8	47,340	46,57 1	46,57 0	46,57 1	45,03 2	45,09 4	47,01 5	46,84 1	12,08 9	13,39 6	<u>9,746</u>	15,67 7
H3_Gt14(31)_D	55,59 9	58,312	55,793	55,969	56,07 3	67,76 5	51,96 0	45,184	43,50 2	43,50 1	43,50 2	45,49 9	45,56 0	46,69 4	46,41 4	12,70 9	13,93 2	15,99 7	0
H23_Gt14(30)_D	55,60 5	58,318	55,799	55,975	56,07 9	67,77 1	51,96 6	45,190	43,50 8	43,50 7	43,50 8	45,50 5	45,56 6	46,70 0	46,42 0	12,71 5	13,93 8	16,00 3	<u>8</u>
H1_Gt14(31)_D	55,60 2	58,315	55,796	55,972	56,07 6	67,76 8	51,96 3	45,187	43,50 5	43,50 4	43,50 5	45,50 2	45,56 3	46,69 7	46,41 7	12,71 2	13,93 5	16,00 0	<u>5</u>
H2_Gt14(31)_D	55,60 2	58,315	55,796	55,972	56,07 6	67,76 8	51,96 3	45,187	43,50 5	43,50 4	43,50 5	45,50 2	45,56 3	46,69 7	46,41 7	12,71 2	13,93 5	16,00 0	<u>5</u>
Lpn-Alcoy	55,19 1	58,936	55,551	55,754	55,71 5	68,79 6	52,37 3	47,589	45,17 3	45,17 2	45,17 3	45,88 9	45,95 0	47,05 9	46,34 9	0	8,536	12,57 5	12,99 2
Lpn-Corby	54,76 0	58,420	55,226	55,457	55,42 8	69,10 5	52,66 7	48,358	45,61 4	45,61 3	45,61 4	46,31 1	46,37 2	47,41 8	46,60 5	8,569	0	13,66 9	14,24 0
L06-153_Cl_Gt71(135)_D	56,43 5	60,030	56,786	57,052	57,08 5	70,19 7	53,88 3	49,343	46,57 9	46,57 8	46,57 9	46,68 8	46,74 9	48,43 6	47,56 9	11,96 0	12,20 3	<u>11,75</u> <u>5</u>	15,63 7
L06-129_Cl_Gt71(135)_D	56,43 2	60,027	56,783	57,049	57,08 2	70,19 4	53,88 0	49,340	46,57 6	46,57 5	46,57 6	46,68 5	46,74 6	48,43 3	47,56 6	11,95 7	12,20 0	<u>11,75</u> <u>2</u>	15,63 4
A166_Gt8(142)_Ps	56,73 4	59,717	57,005	57,273	57,50 6	69,64 8	53,33 1	48,134	44,94 9	44,94 8	44,95 0	45,39 0	45,45 1	47,60 8	46,77 5	13,65 0	13,57 2	<u>11,52</u> <u>2</u>	16,01 0

L04-041_CI_Gt30(137)_D	55,304	58,994	55,498	55,768	55,990	68,718	52,568	45,987	42,328	42,327	42,328	45,102	45,163	46,619	46,345	14,500	14,015	<u>13,882</u>	15,584
L05-341_CI_Gt8(132)_D	56,279	59,240	56,383	56,663	56,758	69,406	52,920	47,086	45,076	45,075	45,076	45,359	45,418	47,058	46,395	13,146	13,809	<u>11,468</u>	14,975
Sum of SNPs	2,578,310	2,701,132	2,617,760	2,616,399	2,630,850	3,523,725	2,659,278	2,398,444	2,314,928	2,314,907	2,314,961	2,175,712	2,177,492	2,223,081	2,313,226	<u>1,930,136</u>	1,983,096	1,943,366	1,962,137
A color represents relative number of SNPs differences. Each branch has specific color code as given in Figure 1. Bold and <u>Underlined</u> = Least No. of SNPs																			

Table S4: Genome-wide quantification of SNPs against <i>L. pneumophila</i> strain Alcoy					
<i>L. pneumophila</i> isolates	SNPs count (bp)	SNPs count (Mbp)	Genome size (bp)	Genome size (Mbp)	SNPs/Mbp
Lpn-LPE509	56,175	0.056	3,434,224	3.43	0.016
Lpn-Philadelphial	59,954	0.060	3,397,754	3.40	0.018
L09-313_Cl_Gt84(116)_D	56,022	0.056	3,398,240	3.40	0.016
L01-443_Cl_Gt64(74)_D	56,337	0.056	3,477,581	3.48	0.016
Lpn-Thunderbay	56,525	0.057	3,455,167	3.46	0.016
Lpn-ATCC43290	56,719	0.057	3,359,001	3.36	0.017
Lpn-lpm7613	56,692	0.057	3,261,562	3.26	0.017
A156_Gt64(74)_Ps	55,986	0.056	3,366,323	3.37	0.017
A129_Gt64(74)_Ps	55,986	0.056	3,527,232	3.53	0.016
Lpn-Lens	70,708	0.071	3,345,687	3.35	0.021
Lpn-Lorraine	53,380	0.053	3,467,254	3.47	0.015
A15_Gt12(84)_Ps	55,931	0.056	3,495,260	3.50	0.016
Lpn-HL06041035	47,898	0.048	3,492,535	3.49	0.014
Lpn-D7631	45,673	0.046	3,436,178	3.44	0.013
Lpn-D7630	45,673	0.046	3,444,702	3.44	0.013
Lpn-D7632	45,674	0.046	3,435,648	3.44	0.013
H34_Gt22(102)_D	43,272	0.043	3,403,136	3.40	0.013
H29_Gt22(100)_D	43,243	0.043	3,403,391	3.40	0.013
H35_Gt22(102)_D	43,310	0.043	3,402,267	3.40	0.013
H39_Gt4(17)_D	46,510	0.047	3,592,274	3.59	0.013
A139_Gt4(17)_Ps	46,344	0.046	3,579,958	3.58	0.013
Lpn-Paris	46,188	0.046	3,503,610	3.50	0.013
A5_Gt4(17)_Ps	46,305	0.046	3,586,669	3.59	0.013
Lpn-OLDA	46,247	0.046	3,486,108	3.49	0.013
A29_Gt6(18)_Ps	45,065	0.045	3,626,550	3.63	0.012
A131_Gt6(18)_Ps	45,061	0.045	3,548,746	3.55	0.013
L10-091_Cl_Gt69(69)_D	45,825	0.046	3,687,459	3.69	0.012
L12-317_Cl_Gt72(66)_D	45,264	0.045	3,516,737	3.52	0.013

L11-209_Cl_Gt29(27)_D	47,311	0.047	3,461,996	3.46	0.014
L10-023_Cl_Gt75(49)_D	46,774	0.047	3,641,882	3.64	0.013
L09-329_Cl_Gt75(49)_D	47,545	0.048	3,445,544	3.45	0.014
Lpn-Pontiac	46,973	0.047	3,545,001	3.55	0.013
L02-521_Cl_Gt29(27)_D	47,787	0.048	3,478,585	3.48	0.014
Lpn-Toronto	46,576	0.047	3,573,898	3.57	0.013
L02-465_Cl_Gt27(133)_D	19,764	0.020	3,500,734	3.50	0.006
L04-545_Cl_Gt40(47)_D	11,776	0.012	3,358,959	3.36	0.004
A193_Gt40(47)_Ps	13,008	0.013	3,446,379	3.45	0.004
A194_Gt40(47)_Ps	12,623	0.013	3,467,904	3.47	0.004
A195_Gt40(47)_Ps	12,686	0.013	3,440,802	3.44	0.004
A138_Gt9(92)_Ps	11,674	0.012	3,363,143	3.36	0.003
A112_Gt10(93)_Ps	12,080	0.012	3,362,286	3.36	0.004
A114_Gt10(93)_Ps	12,086	0.012	3,362,313	3.36	0.004
A127_Gt10(93)_Ps	12,119	0.012	3,363,025	3.36	0.004
A108_Gt10(93)_Ps	12,089	0.012	3,291,620	3.29	0.004
H3_Gt14(31)_D	12,709	0.013	3,691,263	3.69	0.003
H23_Gt14(30)_D	12,715	0.013	3,783,853	3.78	0.003
H1_Gt14(31)_D	12,712	0.013	3,654,038	3.65	0.003
H2_Gt14(31)_D	12,712	0.013	3,650,216	3.65	0.003
Lpn-Corby	8,569	0.009	3,576,470	3.58	0.009
L06-153_Cl_Gt71(135)_D	11,960	0.012	3,405,980	3.41	0.012
L06-129_Cl_Gt71(135)_D	11,957	0.012	3,406,112	3.41	0.012
A166_Gt8(142)_Ps	13,650	0.014	3,353,128	3.35	0.014
L04-041_Cl_Gt30(137)_D	14,500	0.015	3,522,671	3.52	0.015
L05-341_Cl_Gt8(132)_D	13,146	0.013	3,410,856	3.41	0.013

Table S5: Specific genes for each *L. pneumophila* isolate (hypothetical proteins were excluded)

Isolate designation	Gene No.	Protein function
L09-313_C1_Gt8		
4(116)_D	O6C93_01440	TolC family protein
L01-443_C1_Gt6		
4(74)_D	O6D81_11770	IS6 family transposase
	O6D81_12360	PHA synthase
	O6D81_12420	c-type cytochrome
	O6D81_12425	c-type cytochrome
	O6D81_12430	c-type cytochrome
	O6D81_12440	TerC family protein
	O6D81_12455	reverse transcriptase domain-containing protein
	O6D81_12640	MBL fold metallo-hydrolase
	O6D81_12660	heavy metal-binding domain-containing protein
	O6D81_12690	TolC family protein
	O6D81_12705	efflux RND transporter permease subunit
	O6D81_12815	MBL fold metallo-hydrolase
	O6D81_12840	GGDEF domain-containing protein
	O6D81_12860	TolC family protein
	O6D81_12870	efflux RND transporter permease subunit
	O6D81_12935	efflux RND transporter permease subunit
	O6D81_12945	efflux RND transporter permease subunit
	O6D81_12955	TolC family protein
	O6D81_12520	2Fe-2S iron-sulfur cluster-binding protein
	O6D81_12955	TolC family protein
	O6D81_15015	efflux RND transporter permease subunit
A129_Gt64		
(74)_Ps	O6D13_00025	Antitoxin igA-2
	O6D13_00035	Tyrosine recombinase XerC
	O6D13_00040	ORF6N domain protein
	O6D13_00085	GGDEF domain-containing protein
	O6D13_00090	Tn3 family transposase
	O6D13_00095	recombinase family protein
	O6D13_00100	alpha/beta hydrolase
	O6D13_00115	response regulator
	O6D13_00125	zinc ribbon domain-containing protein
	O6D13_00140	efflux RND transporter periplasmic adaptor subunit

	O6D13_10510	TolC family protein
	O6D13_00230	ParB/RepB/Spo0J family partition protein
	O6D13_00290	carbon storage regulator CsrA
	O6D13_00355	TIGR03752 family integrating conjugative element protein
	O6D13_00365	conjugative transfer ATPase
	O6D13_00375	TIGR03756 family integrating conjugative element protein
	O6D13_00380	integrating conjugative element protein
	O6D13_00385	conjugal transfer protein TraG N-terminal domain-containing protein
	O6D13_00410	DNA topoisomerase III
	O6D13_00470	integrase domain-containing protein
	O6D13_03035	integrase domain-containing protein
	O6D13_03065	ATP-binding cassette domain-containing protein
	O6D13_03090	efflux RND transporter periplasmic adaptor subunit
	O6D13_03095	efflux RND transporter permease subunit
	O6D13_03150	tyrosine-type recombinase/integrase
	O6D13_03225	DUF4156 domain-containing protein
	O6D13_13310	single-stranded DNA-binding protein
	O6D13_13975	lpg2844 family Dot/Icm T4SS effector
	O6D13_14710	IS21 family transposase
H29_Gt22(100)_D	O6D14_10380	HipA N-terminal domain-containing protein
H39_Gt4(17)_D	O6D15_00630	ACR3 family arsenite efflux transporter
	O6D15_00635	arsenate reductase ArsC
	O6D15_00640	ArsI/CadI family heavy metal resistance metalloenzyme
	O6D15_00645	metalloregulator ArsR/SmtB family transcription factor
	O6D15_06785	Tn3 family transposase
A139_Gt4(17)_Ps	O6D12_04050	cell division protein FtsI/penicillin binding protein 2
A5_Gt4(17)_Ps	O6C87_09020	SdhB protein, substrate of the Dot/Icm system
A29_Gt6(18)_Ps	O6D23_02780	cation diffusion facilitator family transporter
	O6D23_02795	type II toxin-antitoxin system HicB family antitoxin
	O6D23_02850	patatin-like phospholipase family protein
	O6D23_02855	DUF3734 domain-containing protein
	O6D23_02870	helix-turn-helix transcriptional regulator
	O6D23_02910	ATP-binding protein
	O6D23_02915	ParA family protein
	O6D23_02945	TraY domain-containing protein
	O6D23_05230	MFS transporter
L09-329_Cl_Gt75(49)_D	O6C51_05560	HNH endonuclease signature motif containing protein

L11- 209_C1_Gt2 9(27)_D	O6C51_05570	helix-turn-helix transcriptional regulator
	O6C51_14225	BREX-1 system adenine-specific DNA-methyltransferase PglX
	O6C51_14230	BREX-1 system phosphatase PglZ type A
L02- 521_C1_Gt2 9(27)_D	O6D35_07945	DNA repair exonuclease
	O6D35_07950	AAA family ATPase
	O6D35_10455	septation initiation protein
L12- 317_C1_Gt7 2(66)_D	L02_521_01364	type IV pilus biogenesis protein PilQ
	O6D27_09325	pilus assembly protein FimV
	O6D27_13310	T4SS effector NAD-dependent ubiquitin ligase SdeA
L10- 091_C1_Gt6 9(69)_D	L02_521_02661	SidE phosphodiesterase domain-containing protein
	O6D34_00100	ATP-binding protein
	O6D34_07330	helicase-related protein
L10- 091_C1_Gt6 9(69)_D	O6D34_07345	DEAD/DEAH box helicase family protein
	O6E59_01085	macro domain-containing protein
	O6E59_10395	GNAT family N-acetyltransferase
	O6E59_10490	diguanylate cyclase
	O6E59_10495	CZB domain-containing protein
	O6E59_10500	GGDEF domain-containing protein
	O6E59_10515	class I SAM-dependent methyltransferase
	O6E59_10550	FIST C-terminal domain-containing protein
	O6E59_10555	DHA2 family efflux MFS transporter permease subunit
	O6E59_10560	HlyD family secretion protein
	O6E59_10565	MarR family transcriptional regulator
	O6E59_10570	efflux transporter outer membrane subunit
	O6E59_10575	sodium:calcium antiporter
	O6E59_10585	HlyD family efflux transporter periplasmic adaptor subunit
	O6E59_10590	ribosome-associated ATPase/putative transporter RbbA
	O6E59_10595	ABC transporter permease
	O6E59_10625	Hsp20/alpha crystallin family protein
	O6E59_10645	class I SAM-dependent methyltransferase
	O6E59_10650	type II toxin-antitoxin system PemK/MazF family toxin
	O6E59_13710	GNAT family N-acetyltransferase
L10- 023_C1_Gt7 5(49)_D	Lpn-L10-023_00139	SdhB protein, substrate of the Dot/Icm system
	Lpn-L10-023_00204	N-6 DNA Methylase

Lpn-L10-023_00228	Inner membrane protein YedI
Lpn-L10-023_00286	heme oxygenase
Lpn-L10-023_00290	heavy metal transporting P-type ATPase, cation transporting
Lpn-L10-023_00336	nicotinate phosphoribosyltransferase
Lpn-L10-023_00381	translation elongation factor Tu (EF-Tu)
Lpn-L10-023_00444	SdhA, substrate of the Dot/Icm system
Lpn-L10-023_00468	signal recognition particle protein Ffh
Lpn-L10-023_00607	dihydrolipoamide succinyltransferase
Lpn-L10-023_00761	DNA topoisomerase IV subunit B
Lpn-L10-023_00967	A/G specific adenine glycosylase
Lpn-L10-023_00995	penicillin binding protein 1A
Lpn-L10-023_01186	DNA integration/recombination/inversion protein
Lpn-L10-023_01251	permeases of drug/transporter
Lpn-L10-023_01275	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase
Lpn-L10-023_01447	thymidylate kinase
Lpn-L10-023_01448	thymidylate kinase
Lpn-L10-023_01576	(type IV) pilus assembly protein PilC
Lpn-L10-023_01578	type 4 (IV) prepilin-like protein leader peptide processing enzyme PilD
Lpn-L10-023_01590	glutamate-1-semialdehyde-2,1-aminomutase
Lpn-L10-023_01637	TolA colicin import membrane protein
Lpn-L10-023_02146	transporter, Zip family
Lpn-L10-023_02235	membrane protein
Lpn-L10-023_02328	sensory box histidine kinase/response regulator
Lpn-L10-023_02334	polyketide synthase, type I
Lpn-L10-023_02335	polyketide synthase, type I
Lpn-L10-023_02336	polyketide synthase, type I
Lpn-L10-023_02370	purine NTPase, putative
Lpn-L10-023_02384	3-oxoacyl-(acyl carrier protein) synthase III
Lpn-L10-023_02501	hypothetical protein
Lpn-L10-023_02530	Legionella vir region protein
Lpn-L10-023_02531	global regulator (carbon storage regulator)
Lpn-L10-023_02560	cellulose synthase subunit BcsC
Lpn-L10-023_02566	Na(+)/H(+) antiporter 1 (Sodium/proton antiporter 1)
Lpn-L10-023_02568	integral membrane protein
Lpn-L10-023_02572	OsmC-like protein
Lpn-L10-023_02574	potassium efflux system KefA
Lpn-L10-023_02575	copper efflux ATPase
Lpn-L10-023_02657	Na(+)/H(+) antiporter 1 (Sodium/proton antiporter 1)
Lpn-L10-023_02720	hypothetical, patatin-like phospholipase
Lpn-L10-023_02756	glutathione S-transferase

	Lpn-L10-023_02780	hydrogenase expression/formation protein
	Lpn-L10-023_02781	hydrogenase expression/formation protein
	Lpn-L10-023_02834	outer membrane efflux protein (RND multidrug efflux)
	Lpn-L10-023_02847	hypothetical protein with coiled coil domain protein
	Lpn-L10-023_02848	hypothetical protein with coiled coil domain protein
	Lpn-L10-023_03007	phospho-N-acetylmuramoyl- pentapeptidetransferase
	Lpn-L10-023_03012	chromosome segregation SMC protein
	Lpn-L10-023_03084	cation transporting ATPase PacS
	Lpn-L10-023_03135	uroporphyrinogen III methylase
	Lpn-L10-023_03137	protoporphyrinogen IX and coproporphyrinogen III oxidase HemY
	Lpn-L10-023_03338	outer membrane efflux protein
	Lpn-L10-023_03386	peroxynitrite reductase, AhpC/Tsa family
	Lpn-L10-023_03416	tetrapyrrole (corrin/porphyrin) methylase
	Lpn-L10-023_03423	GTP binding protein in thiophene and furan oxidation (GTPase)
H23_Gt14(30)_D	O6C86_14460	efflux RND transporter permease subunit
	O6C86_14460	efflux RND transporter permease subunit
	O6C86_10150	conjugal transfer protein TraH
	O6C86_09200	TraU family protein
	O6C86_09230	TraE/TraK family type IV conjugative transfer system protein
	O6C86_09235	TraE/TraK family type IV conjugative transfer system protein
	O6C86_10150	conjugal transfer protein TraH
	O6C86_17105	LuxR C-terminal-related transcriptional regulator
	O6C86_17105	LuxR C-terminal-related transcriptional regulator
	H23_02368	lipolytic enzyme
	O6C86_17085	DNA adenine methylase
		NADPH-dependent 7-cyano-7-deazaguanine reductase
	O6C86_17090	QueF
H3_Gt14(31)_D	LpnH3D14_00327	SdbA protein, putative substrate of the Dot/Icm system
	LpnH3D14_01633	TnpA transposase
H1_Gt14(31)_D	O6C83_15670	integrase domain-containing protein
	O6C83_15670	integrase domain-containing protein
L04-041_Cl_Gt30(137)_D	L04_041_00187	cadmium translocating P-type ATPase CadA
	O6C82_01235	conjugative coupling factor TraD, PFGI-1 class
	L04_041_00251	conjugative coupling factor TraD
	O6C82_01990	ABC transporter permease
	O6C82_02290	AAA family ATPase
	O6C82_03960	(outer) membrane protein
	O6C82_13255	GIY-YIG nuclease superfamily protein

	L04_041_02904	SdcA
	L04_041_02906	SidC protein (substrate of the Dot/Icm system)
L02-465_Cl_Gt27(133)_D	O6D28_09245	ATP-binding protein
	O6D28_09275	MFS transporter
	O6D28_09280	peptide deformylase
	O6D28_14745	alpha/beta fold hydrolase
	O6D28_10135	FAD-binding oxidoreductase
	O6D28_10265	GGDEF domain-containing protein
	O6D28_10270	diguanylate cyclase
	O6D28_10315	cation-translocating P-type ATPase
	O6D28_05830	ISAs1 family transposase
	O6D28_10095	F0F1 ATP synthase subunit beta
	O6D28_14780	F0F1 ATP synthase subunit A
	O6D28_14785	F0F1 ATP synthase subunit A
A194_Gt40(47)_Ps	LpnA194_02940	hypothetical histidine-rich protein
A193_Gt40(47)_Ps	O6C92_00445	translocation/assembly module TamB domain-containing protein
	O6C92_09225	amino acid dehydrogenase
	A193_02478	Primosomal protein N' (replication factor Y)
	O6C92_15530	HslU--HslV peptidase ATPase subunit
L05-341_Cl_Gt8(132)_D	O6C52_01120	AAA family ATPase
	O6C52_06635	cyclic nucleotide-binding domain-containing protein
	O6C52_11395	Vir protein
	L05_341_02307	type I restriction enzyme EcoKI subunit R
	L05_341_02308	Plasmid maintenance system killer protein
	O6C52_11530	helix-turn-helix domain-containing protein
	O6C52_11540	nucleotide-binding protein
L06-153_Cl_Gt71(135)_D	O6D25_07255	tetratricopeptide repeat protein
A138_Gt9(92)_Ps	A138_02923	Multifunctional virulence effector protein DrrA
A127_Gt10(93)_Ps	O6D26_08745	NAD-dependent formate dehydrogenase
	O6D26_08750	NAD-dependent formate dehydrogenase
	A127_02037	sensory box protein, EAL domain, GGDEF domain, signal transduction protein
A166_Gt8(142)_Ps	O6C96_02340	IcmE (DotG)
	O6C96_02805	cyclic nucleotide-binding domain-containing protein
	O6C96_10115	serine/threonine protein kinase

L04- 545_C1_Gt4 0(47)_D	O6C96_10125	serine/threonine-protein kinase
	O6C96_13195	hypothetical histidine-rich protein
	O6D22_05960	Ankyrin repeats
	O6D22_07115	septation initiation protein

Table S6: Nucleotide Polymorphisms in cluster six of <i>L. pneumophila</i> isolates H1, H2, and H23 from the HZI DWSS relative to the H3 PacBio reference sequence obtained.							
Nucleotide Polymorphism	Label (locus tag) ref genome	<i>L. pneumophila</i> Isolate	Gene Name	Gene Product	Gene Function	Length (bp)	Virulence Similarity (%)
A → T	LpnH3 D14_00006	H2	<i>ppeA</i>	Biosynthetic arginine decarboxylase	Intracellular Growth	1,891	NV
C → T	LpnH3 D14_00027	H23	<i>yhdG_1</i>	Amino acid transporter	Survival <i>in vivo</i>	1,391	NV
C → T	LpnH3 D14_00935	H1, H2, H23	<i>bepC</i>	Outer membrane efflux protein	Survive inside the host cells, restores drug efflux	1,724	NV
T → G	LpnH3 D14_00978	H1	<i>mmgC</i>	Acyl-CoA dehydrogenase		1,154	NV
A → G	LpnH3 D14_01656	H23		Alpha/beta hydrolase		983	NV
C → T	LpnH3 D14_02694	H1, H2, H23	<i>ankF</i>	Dot/Icm type IV secretion system effector (Ankyrin repeats)	Host microbe interaction, Intracellular replication	2,765	96
G → T	LpnH3 D14_02706	H23		Aspartyl/Asparaginyl beta hydrolase		719	NV
C → T	LpnH3 D14_02929	H1, H2, H23	<i>dotA</i>	Phagosome trafficking protein DotA	Bacterial replication, virulence, Evasion of Endocytic pathway	3,119	79

C → T	LpnH3 D14_03 123	H23		Hypothetical protein		1,289	NV
NV: Non-Virulence Gene							

Table S7: Gene content according to MAUVE aligner in the studied areas. Hypothetical proteins were excluded

Locus Tag	Gene Name	Product	Length (bp)
Area 1			
LpnA194_02079		Acetyltransferase (GNAT) family protein	437
LpnA194_02080	dpnM	Modification methylase DpnIIA	1,412
LpnA194_02081	dlpA_1	DlpA protein	719
LpnA194_02082		Phosphotransferase enzyme family protein	968
LpnA194_02083		aminoglycoside phosphotransferase	1,436
LpnA194_02085		shikimate kinase	779
LpnA194_02086		Enterochelin esterase	1,415
LpnA194_02088	abcT3_4	ABC transporter, ATP binding protein	1,547
LpnA194_02090		transcriptional regulator, MerR family, mercury resistance	944
LpnA194_02091		beta-lactamase AmpS	800
LpnA194_02092	ftsI4_2	cell division protein FtsI/penicillin binding protein 2	1,922
LpnA194_02093	mecI_2	Methicillin resistance regulatory protein mecI	422
LpnA194_02094		transcriptional regulator SkgA, mercury resistance	749
LpnA194_02097		acetyltransferase, GNAT family	602
LpnA194_02098		reverse transcriptase	1,556
LpnA194_02100		acetyltransferase, GNAT family	482
LpnA194_02101	grpB_2	glutamate rich protein GrpB	956
LpnA194_02102		nucleotidyltransferase PLUS glutamate rich protein GrpB PLUS ribosomal protein alanine acetyltransferase	794
LpnA194_02104		pyridoxamine 5'-phosphate oxidase	581
LpnA194_02105		phage repressor	622
LpnA194_02106	lvrA_2	Legionella vir region protein	872
LpnA194_02107	lvrC	Legionella vir region protein	197
LpnA194_02108		putative exported protein	434
LpnA194_02121		Type IV secretory protein VirB4 component	2,774
LpnA194_02122		TraU protein	995
LpnA194_02123		membrane protein, Tfp pilus assembly, pilus retraction ATPase PilT	1,382
LpnA194_02127		conjugative coupling factor TraD	2,006
LpnA194_02129		Putative HTH-type transcriptional regulator/MT0914	572

LpnA194_02130		Avidin family protein	413
LpnA194_02132		putative secreted esterase	1,556
LpnA194_02133		Bacterial regulatory proteins, luxR family	800
LpnA194_02134	murE3_1	UDP-N-acetylmuramyl tripeptide synthase	1,226
LpnA194_02137	aph_2	spectinomycin phosphotransferase	995
LpnA194_02138		glyoxylase domain hypothetical protein	365
LpnA194_02139		short chain dehydrogenase	734
LpnA194_02140	yafP	putative N-acetyltransferase YafP	1,697
LpnH3D14_02136	fni	isopentenyl-diphosphate delta-isomerase	1,028
LpnH3D14_02137	mvaA	hydroxymethylglutaryl CoA reductase	1,298
LpnH3D14_02139		tRNA-Lys	75
LpnH3D14_02140		tRNA-Lys	75
LpnH3D14_02141		tRNA-Arg	76
LpnH3D14_02142		site specific recombinase	1,160
LpnH3D14_02143	nucS	Endonuclease NucS	1,004
LpnH3D14_02144		Acetyltransferase (GNAT) family protein	485
LpnH3D14_02145		proline/betaine transport protein like protein	1,274
LpnH3D14_02146		putative acetyltransferase	512
LpnH3D14_02147		lipolytic enzyme	686
LpnH3D14_02148		transcription regulator protein, response regulator containing CheY-like receiver domain and HTH DNA-binding domain	803
LpnH3D14_02150	tylM1	dTDP-3-amino-3,6-dideoxy-alpha-D-glucopyranose N,N-dimethyltransferase	824
LpnH3D14_02152		topology modulation protein	542
LpnH3D14_02154		aminoglycoside 6'-N-acetyltransferase	545
LpnH3D14_02155		acetyltransferase, GNAT family	554
LpnH3D14_02156		transcriptional regulator, MerR family, mercury resistance	1,040
LpnH3D14_02157		methyltransferase	881
LpnH3D14_02158		Acetyltransferase (GNAT) family protein	419
LpnH3D14_02159		recombination protein F	1,160
LpnH3D14_02160		Cupin domain protein	386
LpnH3D14_02162		O-antigen acetylase	1,148
LpnH3D14_02163		serine/threonine protein kinase	1,001
LpnH3D14_02164	phaB_4	acetoacetyl CoA reductase	782
LpnH3D14_02165		sepiapterin reductase	794
LpnH3D14_02165	dpmM	Modification methylase DpmM	1,412
LpnH3D14_02168	dlpA_1	DlpA protein	716
LpnH3D14_02169		Phosphotransferase enzyme family protein	968

LpnH3D14_02170		aminoglycoside phosphotransferase	1,436
LpnH3D14_02172	aroK_2	shikimate kinase	779
LpnH3D14_02173	mdtK	Multidrug resistance protein MdtK	1,364
LpnH3D14_02174		transcriptional regulator, LysR family	863
LpnH3D14_02175		major facilitator superfamily transporter	1,175
LpnH3D14_02176		Peptidase family S41	1,337
LpnH3D14_02177		phage repressor	662
LpnH3D14_02178	lvrA_2	Legionella vir region protein	872
LpnH3D14_02179	lvrC_2	Legionella vir region protein	197
LpnH3D14_02180		putative exported protein	434
LpnH3D14_02193		Type IV secretory protein VirB4 component	2,774
LpnH3D14_02194		TraU protein	977
LpnH3D14_02195		membrane protein, Tfp pilus assembly, pilus retraction ATPase PilT	1,382
LpnH3D14_02196		membrane protein	1,568
Table S7: Gene content according to MAUVE aligner in the studied areas. Hypothetical proteins were excluded (Area 2)			
Locus Tag	Gene Name	Product	Length (bp)
corby_02494		lipolytic enzyme	683
corby_02495		transcription regulator protein, response regulator containing CheY-like receiver domain and HTH DNA-binding domain	803
Corby_02499	cadA_2	cadmium translocating P-type ATPase CadA	503
Corby_02500		cadmium efflux ATPase	1,433
Corby_02502	cadA_3	cadmium translocating P-type ATPase CadA	2,135
Corby_02503	helA_2	cobalt/zinc/cadmium efflux RND transporter, permease protein HelA	3,149
Corby_02504	helB_2	cation efflux system HelB	1,256
Corby_02505	helC_2	cobalt/zinc/cadmium efflux RND transporter, outer membrane protein	1,244
Corby_02506		reverse transcriptase	1,364
Corby_02511		reverse transcriptase	1,199
Corby_02512		transposase IS4	1,460
Corby_02513		phage repressor	662
Corby_02514	lvrA_2	Legionella vir region protein	872
Corby_02515	lvrB_2	Legionella vir region protein	383
Corby_02516	lvrC	Legionella vir region protein	197
Corby_02517		putative exported protein	434
Corby_02528		exported membrane protein	1,313
Corby_02530		Type IV secretory protein VirB4 component	2,774

Corby_02531		TraU protein	995
Corby_02532		membrane protein, Tfp pilus assembly, pilus retraction ATPase PilT	1,382
Corby_02533		membrane protein	1,568
Corby_02536		conjugative coupling factor TraD	2,006

Table S8: Genes of interest in genomic islands of <i>L. pneumophila</i> isolates as identified by IslandViewer4					
Branch	Isolate	Gene	Locus tag	Gene Length (bp)	Product
3 HL 06041085	H34		H34_02359	965	major outer membrane protein
		<i>tufA_2</i>	H34_02301	917	translation elongation factor Tu (EF-Tu)
			H34_02302	341	preprotein translocase subunit SecE
		<i>nusG</i>	H34_02303	548	transcription antitermination protein NusG
		<i>rplK</i>	H34_02304	434	50S ribosomal protein L11
		<i>rplA</i>	H34_02305	695	50S ribosomal protein L1
		<i>rplJ</i>	H34_02306	533	50S ribosomal protein L10
		<i>rplL</i>	H34_02307	380	50S ribosomal protein L7/L12
		<i>rpoB</i>	H34_02308	4,106	DNA-directed RNA polymerase beta subunit
		<i>rpoC</i>	H34_02309	4,247	DNA-directed RNA polymerase subunit beta'
		<i>rpsL</i>	H34_02310	380	30S ribosomal protein S12
		<i>rpsG</i>	H34_02311	527	30S ribosomal protein S7
		<i>fusA</i>	H34_02312	2,084	translation elongation factor G (EF-G)
	H35	<i>ccmC</i>	H35_00671	755	heme exporter protein CcmC
		<i>ccmD</i>	H35_00670	158	heme exporter protein CcmD
		<i>ccmE</i>	H35_00669	431	cytochrome c-type biogenesis protein CcmE
		<i>ccmF</i>	H35_00668	1,952	cytochrome c-type biogenesis protein CcmF
		<i>ccmG</i>	H35_00667	533	cytochrome C biogenesis protein
		<i>ccmH</i>	H35_00666	401	c-type cytochrome biogenesis protein CcmH
		<i>cycH</i>	H35_00665	686	cytochrome c type biogenesis protein CcmH
4 Paris	A29		A29_00568	206	cold shock domain family protein
	A5		A5_02183	986	Microvirus H protein (pilot protein)
			A5_02184	1,541	Bacteriophage replication gene A protein (GPA)
			A5_02185	260	Phage protein C
			A5_02186	458	Bacteriophage scaffolding protein D
			A5_02187	116	Microvirus J protein
	A139		A139_02127	1,025	Bacteriophage replication gene A protein (GPA)
			A139_02128	260	Phage protein C
			A139_02129	458	Bacteriophage scaffolding protein D
			A139_02130	116	Microvirus J protein
			A139_02131	1,283	Capsid protein (F protein)
			A139_02132	527	Major spike protein (G protein)
			A139_02133	986	Microvirus H protein (pilot protein)

5 Pontiac	L10-091	<i>hspC2_1</i>	L10-091_02122	491	small heat shock protein HspC2		
			L10-091_02123	587	heat shock hsp20		
6 Alcoy	L02-465		L02-465_00734	425	hemin binding protein Hbp		
	A194	<i>cya</i>	A194_00644	15,197	Bifunctional hemolysin/adenylate cyclase precursor		
	A112	<i>chuR</i>	A112_02425	1,475	Anaerobic sulfatase-maturing enzyme		
	H23	<i>ampG</i>	H23_01834	1,247	beta lactamase induction signal transducer AmpG		
			H23_02025	1,361	metallo-beta lactamase family protein		
			H23_01996	1,424	Bacteriophage replication gene A protein (GPA)		
			H23_01997	260	Phage protein C		
			H23_01998	458	Bacteriophage scaffolding protein D		
			H23_01999	116	Microvirus J protein		
			H23_02000	1,283	Capsid protein (F protein)		
			H23_02001	527	Major spike protein (G protein)		
			H23_02002	986	Microvirus H protein (pilot protein)		
			H1	<i>ampG</i>	H1_02766	1,247	beta lactamase induction signal transducer AmpG
					H1_00952	1,361	metallo-beta lactamase family protein
					H1_02730	416	Bacteriophage scaffolding protein D
	H1_02731	116			Microvirus J protein		
	H1_02732	1,283			Capsid protein (F protein)		
	H1_02733	527			Major spike protein (G protein)		
	H1_02734	986			Microvirus H protein (pilot protein)		
	H1_02735	1,541			Bacteriophage replication gene A protein (GPA)		
	H2		H2_02312	1,361	metallo-beta lactamase family protein		
	H3		H3_03288	1,361	metallo-beta lactamase family protein		
	L06-129	<i>htpX_3</i>	L06-129_01854	965	heat shock protein, protease HtpX		
			L06-129_01853	470	Phosphate-starvation-inducible E		
		<i>trxA3_2</i>	L06-129_01852	440	thioredoxin		
			L06-129_01848	569	small HspC2 heat shock protein		
		<i>cas1</i>	L06-129_01845	968	CRISPR-associated endonuclease Cas1		
		<i>cas3</i>	L06-129_01844	3,395	CRISPR-associated nuclease/helicase Cas3 subtype I-F/YPEST		
		<i>csy1</i>	L06-129_01843	1,265	CRISPR-associated protein Csy1		
		<i>htpX_3</i>	L06-129_01854	965	heat shock protein, protease HtpX		
			L06-129_01853	470	Phosphate-starvation-inducible E		
			L06-129_01848	569	small HspC2 heat shock protein		

Table S9. Number and distribution of the 8 most frequently identified eukaryotic motifs and heat shock proteins (HSP) within the 55 *L. pneumophila* strains studied. Numbers represent the number of proteins containing the respective eukaryotic motif.

Strain	Ankyrin repeats	F-box	U-box	P-Kinase	LRR	P450	SET	HAD	HSP
A129_Gt64(74)_Ps	12	3	1	6	6	0	1	1	16
A156_Gt64(74)_Ps	12	3	1	6	6	0	1	1	15
L01-443_Cl_Gt64(74)_D	12	3	1	7	7	1	1	1	15
L09-313_Cl_Gt84(116)_D	12	3	1	6	6	0	1	1	16
Lpn-LPE509	12	3	1	7	6	0	1	1	15
Lpn-lpm7613	11	3	1	7	6	0	1	1	16
Lpn-ATCC43290	12	3	1	6	6	0	1	1	16
Lpn-Philadelphia1	12	3	1	7	6	0	1	1	15
Lpn-Thunderbay	12	3	1	6	6	0	1	1	16
A15_Gt12(84)_Ps	16	1	1	11	7	1	1	1	13
Lpn-Lens	15	1	0	7	5	1	1	1	14
Lpn-Lorraine	14	2	1	9	7	1	1	1	13
H29_Gt22(100)_D	12	2	1	8	3	1	1	1	14
H34_Gt22(102)_D	12	2	1	8	3	1	1	1	14
H35_Gt22(102)_D	12	2	1	8	3	1	1	1	14
Lpn-D7630	12	2	1	8	3	1	1	1	14
Lpn-D7631	12	2	1	8	3	1	1	1	14
Lpn-D7632	12	2	1	8	3	1	1	1	14
Lpn-HL06041035	11	1	1	7	5	1	1	1	15
A5_Gt4(17)_Ps	15	2	1	12	4	1	1	1	13
A29_Gt6(18)_Ps	17	2	1	10	4	1	1	1	13
A131_Gt6(18)_Ps	17	2	1	10	4	1	1	1	13
A139_Gt4(17)_Ps	15	1	1	10	4	1	1	1	13
H39_Gt4(17)_D	17	2	1	9	4	1	1	1	13
Lpn-OLDA	16	2	1	11	4	1	1	1	13
Lpn-Paris	16	2	1	11	4	1	1	1	13
L02-521_Cl_Gt29(27)_D	13	2	1	11	3	1	1	1	13
L09-329_Cl_Gt75(49)_D	13	1	1	11	3	1	1	1	13
L10-091_Cl_Gt69(69)_D	12	2	1	13	3	1	1	1	15
L11-209_Cl_Gt29(27)_D	12	1	1	11	3	1	1	1	13
L12-317_Cl_Gt72(66)_D	11	2	1	12	3	1	1	1	13
L10-023_Cl_Gt75(49)_D	11	1	1	11	3	1	1	1	14
Lpn-Toronto	12	2	0	10	3	1	1	1	14
Lpn-Pontiac	13	3	1	11	3	1	1	1	13
A108_Gt10(93)_Ps	12	1	0	6	3	1	1	1	15

A112 Gt10(93) Ps	12	1	0	6	3	1	1	1	16
A114 Gt10(93) Ps	12	1	0	6	3	1	1	1	16
A127 Gt10(93) Ps	12	1	0	6	3	1	1	1	16
A138 Gt9(92) Ps	12	1	0	6	3	1	1	1	16
A166 Gt8(142) Ps	13	1	0	7	3	1	1	1	15
A193 Gt40(47) Ps	16	1	0	7	3	1	1	1	14
A194 Gt40(47) Ps	16	1	0	7	3	1	1	1	15
A195 Gt40(47) Ps	16	1	0	7	3	1	1	1	15
Lpn-Alcoy 2300/99	14	1	0	7	3	1	1	1	15
Lpn-Corby	14	1	0	8	3	1	1	1	15
H1 Gt14(31) D	14	1	0	8	2	1	1	1	16
H2 Gt14(31) D	14	1	0	8	2	1	1	1	16
H3 Gt14(31) D	14	1	0	8	2	1	1	1	16
H23 Gt14(30) D	15	1	0	10	2	1	1	1	16
L02-465 Cl Gt27(133) D	11	1	0	8	5	1	1	1	14
L04-041 Cl Gt30(137) D	11	1	0	6	3	1	1	1	15
L04-545 Cl Gt40(47) D	16	1	0	6	3	1	1	1	16
L05-341 Cl Gt8(132) D	12	1	0	6	3	1	1	1	15
L06-129 Cl Gt71(135) D	12	1	0	7	3	1	1	1	17
L06-153 Cl Gt71(135) D	12	1	0	7	3	1	1	1	17
Gt, MLVA genotype; _Ps, West Bank; _D, Germany, ANK, ankyrin; F-box, F-box domain; LLR, leucine rich repeats; P450, cytochrome_P450; P-kinases (protein kinases); U-box, U-box domain; HAD, HAD-superfamily hydrolase; SET, SET domain; and HPS, Heat Shock proteins.									

Table S10 : Nucleotide identity values of orthologous pore-forming activity genes with respect to the BLASTp search against the VFDB using <i>L. pneumophila</i> strain Philadelphia1 as default reference genome												
<i>L. pneumophila</i> strain	<i>Secretion system</i>											<i>Toxin</i>
	Dot/Icm type IVB secretion system											<i>RtxA</i>
	<i>icmT</i>	<i>icmS</i>	<i>icmR</i>	<i>icmQ</i>	<i>icmL/dotI</i>	<i>icmK/dotH</i>	<i>icmE/dotG</i>	<i>icmC/dotE</i>	<i>dotB</i>	<i>dotA</i>	<i>icmW</i>	<i>rtxA</i>
	Id*											
Lpn-Corby	82%	100%	95%	100%	84%	84%	88%	91%	100%	85%	98%	85%
Lpn-Alcoy	82%	100%	95%	100%	84%	84%	88%	99%	100%	81%	98%	85%
L02-465_CI_Gt27(133)_D	82%	100%	95%	100%	84%	84%	88%	99%	100%	81%	99%	85%
L04-545_CI_Gt40(47)_D	82%	100%	95%	100%	84%	84%	88%	99%	100%	81%	98%	84%
A193_Gt40(47)_Ps	82%	100%	95%	100%	84%	84%	88%	99%	100%	78%	98%	84%
A194_Gt40(47)_Ps	82%	100%	95%	100%	84%	84%	88%	99%	100%	78%	98%	84%
A195_Gt40(47)_Ps	82%	100%	95%	100%	84%	84%	88%	99%	100%	78%	98%	84%
A138_Gt9(92)_Ps	82%	100%	95%	100%	84%	83%	88%	99%	100%	78%	98%	75%
A112_Gt10(93)_Ps	82%	100%	95%	100%	84%	83%	88%	99%	100%	78%	98%	75%
A114_Gt10(93)_Ps	82%	100%	95%	100%	84%	83%	88%	99%	100%	78%	98%	75%
A127_Gt10(93)_Ps	82%	100%	95%	100%	84%	83%	88%	99%	100%	78%	98%	75%
A108_Gt10(93)_Ps	82%	100%	95%	100%	84%	83%	88%	99%	100%	78%	98%	75%
H3_Gt14(31)_D	82%	100%	95%	100%	84%	83%	87%	99%	100%	79%	98%	86%
H23_Gt14(30)_D	82%	100%	95%	100%	84%	83%	87%	99%	100%	78%	98%	86%
H1_Gt14(31)_D	82%	100%	95%	100%	84%	83%	87%	99%	100%	78%	98%	86%
H2_Gt14(31)_D	82%	100%	95%	100%	84%	83%	87%	99%	100%	78%	98%	86%
L06-153_CI_Gt71(135)_D	82%	100%	95%	100%	84%	84%	88%	99%	100%	80%	98%	85%
L06-129_CI_Gt71(135)_D	82%	100%	95%	100%	84%	84%	88%	99%	100%	80%	98%	85%

A166_Gt8(142)_Ps	82%	100%	95%	100%	84%	84%	89%	99%	100%	80%	98%	84%
L04-041_CI_Gt30(137)_D	82%	100%	95%	100%	84%	84%	88%	99%	100%	80%	98%	85%
L05-341_CI_Gt8(132)_D	82%	100%	95%	100%	84%	84%	88%	99%	100%	80%	98%	84%
Lpn-Pontiac	82%	100%	96%	99%	84%	82%	88%	100%	100%	88%	99%	80%
L10-091_CI_Gt69(69)_D	82%	100%	96%	99%	84%	82%	88%	100%	100%	81%	99%	75%
L12-317_CI_Gt72(66)_D	82%	100%	96%	99%	84%	82%	88%	100%	100%	81%	99%	75%
L11-209_CI_Gt29(27)_D	82%	100%	96%	99%	84%	82%	88%	100%	100%	81%	99%	80%
L10-023_CI_Gt75(49)_D	82%	100%	96%	99%	84%	82%	88%	100%	100%	81%	99%	80%
L09-329_CI_Gt75(49)_D	82%	100%	96%	99%	84%	82%	88%	100%	100%	81%	99%	80%
L02-521_CI_Gt29(27)_D	82%	100%	96%	99%	84%	82%	88%	100%	100%	81%	99%	80%
Lpn-Paris	82%	100%	96%	99%	84%	82%	89%	100%	99%	81%	99%	83%
H39_Gt4(17)_D	82%	100%	96%	99%	84%	82%	89%	100%	100%	81%	99%	83%
A139_Gt4(17)_Ps	82%	100%	96%	99%	84%	82%	89%	100%	99%	81%	99%	83%
A5_Gt4(17)_Ps	82%	100%	96%	99%	84%	82%	89%	100%	99%	81%	99%	83%
A29_Gt6(18)_Ps	82%	100%	96%	99%	84%	82%	89%	100%	99%	81%	99%	83%
A131_Gt6(18)_Ps	82%	100%	96%	99%	84%	82%	89%	100%	99%	81%	99%	83%
Lpn-HL06041035	82%	99%	97%	99%	84%	82%	87%	99%	100%	81%	99%	85%
H34_Gt22(102)_D	82%	99%	97%	99%	84%	82%	87%	99%	100%	81%	99%	85%
H29_Gt22(100)_D	82%	99%	97%	99%	84%	82%	87%	99%	100%	81%	99%	85%
H35_Gt22(102)_D	82%	99%	97%	99%	84%	82%	87%	99%	100%	81%	99%	85%
Lpn-Lorraine	82%	100%	97%	100%	84%	82%	87%	100%	100%	81%	99%	85%
A15_Gt12(84)_Ps	82%	100%	97%	100%	84%	82%	87%	100%	100%	81%	99%	77%
Lpn-Thunderbay	82%	100%	91%	100%	84%	79%	91%	100%	100%	93%	100%	85%

L09-313 Cl Gt84(116) D	82%	100%	91%	100%	84%	79%	91%	100%	100%	93%	100%	85%
L01-443 Cl Gt64(74) D	82%	100%	91%	100%	84%	79%	91%	100%	100%	93%	100%	85%
A156_Gt64(74)_Ps	82%	100%	91%	100%	84%	79%	91%	100%	100%	93%	100%	85%
A129_Gt64(74)_Ps	82%	100%	91%	100%	84%	79%	91%	100%	100%	93%	100%	85%
* Gene Identity												

Table S11: Summary of main plasmid features in *L. pneumophila* isolates H3, A129, A29, and L10_091.

Isolate designation	No. of base pairs (bp)	No. of CDS*	%GC
H3_Gt14(31)_D	103,432	111	40.0%
A129_Gt64(74)_Ps	72,682	78	38.9%
A29_Gt6(18)_Ps	25,160	27	38.6%
L10-091_Cl_Gt69(69)_D	23,296	25	38.6%

*CDS: Coding DNA Sequence

Table S12: Identification and distribution of prophages in the 55 <i>L. pneumophila</i> strains studied.														
Strain designation	Replicon/Contig	Region	Region Length	Score	Specific Keyword	Region Position	No. tRNA	No. Total Proteins	No. Phage Hit proteins	No. Hypothetical Proteins	% Phages and Hypothetical Proteins	No. Bacterial Proteins	Attachment Site	% GC
Lpn-LPE509	contig000001	1	26Kb	50	Plate, integrase and transposase	2,248,193 - 2,274,256	0	16	9	5	87.5	2	Yes	38.2
Lpn-Philadelphia1	contig000001	1	70.3Kb	70	Plate, integrase and transposase	1,158,151 - 1,188,905	0	26	13	10	88.4	3	Yes	37.2
Lpn-Thunderbay	contig000001	1	70.3Kb	70	Plate, integrase and transposase	1,165,464 - 1,196,215	0	26	13	10	88.4	4	Yes	37.2
Lpn-ATCC43290	contig000001	1	25.1Kb	60	Plate, integrase and transposase	1,118,202 - 1,143,394	0	29	15	11	89.6	3	yes	36.5
	contig000001	2	11.7Kb	70	head, integrase and transposase	2,316,998 - 2,328,793	0	11	7	3	90.9	1	Yes	37.2

Lpn-lpm7613	contig000001	1	11.7Kb	70	head, integrase and transposase	2,316,998 - 2,328,794	0	11	7	3	90.9	1	Yes	37.2
Lpn-Lens	contig000001	1	13.1Kb	30	integrase and plate	1,180,694 - 1,193,879	0	10	6	3	90	1	Yes	38.3
Lpn-Lorraine	contig000001	1	7.6Kb	10	NA	858,707 - 866,331	0	7	6	0	85.7	1	No	36.1
	contig000001	2	16.3Kb	20	integrase	1,107,057 - 1,123,388	0	7	4	0	57.1	3	Yes	37.5
	contig000001	3	22.7Kb	30	integrase and protease	2,553,434 - 2,576,203	1	9	7	1	88.8	1	Yes	40
	contig000001	4	31.9Kb	30	integrase	2,939,178 - 2,971,159	0	9	5	3	88.8	1	Yes	40.4
Lpn-HL06041035	contig000001	1	31.5Kb	50	Plate, and integrase	1,210,553 - 1,242,139	0	19	11	6	89.4	2	Yes	37.5
	contig000001	2	31.5Kb	70	Plate, and transposase	1,225,361 - 1,256,8	0	9	7	1	88.8	1	Yes	36.5

						64								
Lpn-D7631	contig000001	1	27.9K b	40	Plate, integrase and transposa se	1,192,6 48 - 1,220,5 87	0	16	9	7	93.7	1	Yes	38. 6
Lpn-D7630	contig000001	1	27.9K b	40	Plate, integrase and transposa se	1,192,6 48 - 1,220,5 88	0	16	9	7	93.7	1	Yes	38. 6
Lpn-D7632	contig000001	1	27.9K b	40	Plate, integrase and transposa se	1,192,6 48 - 1,220,5 89	0	16	9	7	93.7	1	Yes	38. 6
Lpn-Paris	contig000001	1	18.7K b	30	Plate and integrase	1,185,5 27 - 1,204,2 95	0	15	9	5	93.3	1	Yes	38. 5
Lpn-OLDA	contig000001	1	18.7K b	30	Plate and integrase	1,176,9 98 - 1,195,7 66	0	15	9	5	93.3	1	Yes	38. 5
Lpn-Pontiac	contig000001	1	23.8K b	30	Plate and integrase	1,214,0 34 - 1,237,8 58	0	13	8	4	92.3	1	Yes	37. 8
Lpn-Toronto	contig000001	1	16.2K b	60	Plate, integrase and transposa	1,189,6 58 - 1,214,9	0	10	6	2	80	2	Yes	35. 5

					se	29								
Lpn-Alcoy 2300/99	contig000001	1	19.7Kb	30	Plate and integrase	1,280,061 - 1,299,823	0	12	7	4	91.6	1	Yes	37
Lpn-Corby	contig000001	1	19Kb	30	Plate and integrase	1,286,720 - 1,287,753	0	12	7	4	91.6	1	Yes	38.2
A156_Gt64(74)_ Ps	contig000001	1	20.8Kb	40	Protease, integrase and transposase	222,459 - 243,352	1	17	9	4	76.4	4	Yes	37.4
	contig000002	2	14Kb	30	integrase and transposase	436,455 - 461,457	0	13	8	3	84.6	2	Yes	35.6
A129_Gt64(74)_ Ps	contig000003	1	14Kb	30	integrase and Plate	728 - 14,800	0	12	7	4	91.6	1	Yes	38.4
A15_Gt12(84)_P s		NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
A139_Gt4(17)_P s		NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
A5_Gt4(17)_Ps	contig000001	1	7.6Kb	10	NA	9,003 - 16,627	0	7	6	0	85.7	1	No	36
A29_Gt6(18)_Ps	contig000008	1	19.5Kb	30	integrase and Plate	263,913 - 283,445	0	13	8	4	92.3	1	Yes	37.2

A131_Gt6(18)_Ps	contig000003	1	19.5Kb	30	integrase and Plate	263,913 - 283,445	0	13	8	4	92.3	1	Yes	36.3
	contig000004	2	35.9Kb	30	recombinase	79,639 - 115,554	0	9	6	1	77.7	2	Yes	37.2
A193_Gt40(47)_Ps	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
A194_Gt40(47)_Ps	contig000001	1	13.1Kb	30	integrase and Plate	1,144,101 - 1,157,286	0	10	6	3	90	1	Yes	38.3
A195_Gt40(47)_Ps	contig000002	1	9.7Kb	20	protease	65,660 - 75,400	1	7	6	1	100	0	no	39.6
A138_Gt9(92)_Ps	contig000007	1	20.3K	40	integrase and Plate	25,862 - 46,223	0	12	7	4	91.6	1	Yes	38.4
A112_Gt10(93)_Ps	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
A114_Gt10(93)_Ps	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
A127_Gt10(93)_Ps	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
A108_Gt10(93)_Ps	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
A166_Gt8(142)_Ps	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
H34_Gt22(102)_D	contig000002	1	7.7Kb	20	Plate	236,746 - 244,461	0	11	6	4	90.9	1	No	37.4
H29_Gt22(100)_D	contig000004	1	8.9Kb	30	Plate and integrase	307 - 9,269	0	12	7	4	91.6	1	No	37.7

H35_Gt22(102)_D	contig000007	1	8.9Kb	30	Plate and integrase	307 - 9,269	0	12	7	4	91.6	1	No	37.7
H39_Gt4(17)_D	contig000002	1	21Kb	30	Protease and integrase	53,825 - 74,871	1	9	7	1	88.8	1	Yes	39.9
H3_Gt14(31)_D	contig000001	1	19.1Kb	40	Plate and integrase	1,235,020 - 1,254,153	0	20	9	8	85	3	Yes	36.3
H23_Gt14(30)_D	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
H1_Gt14(31)_D	contig000001	1	13.1Kb	30	Plate and integrase	140,500 - 153,676	0	10	6	3	90	1	Yes	38.2
H2_Gt14(31)_D	contig000007	1	19.1Kb	40	Plate and integrase	432,357 - 451,502	0	20	9	8	85	3	Yes	36.3
L09-313_Cl_Gt84(116)_D	contig000005	1	7.7Kb	20	Plate	297,105 - 304,820	0	11	6	4	90.9	1	No	37.4
L01-443_Cl_Gt64(74)_D	contig000006	1	25Kb	40	Transposase and integrase	161,092 - 186,094	0	13	8	3	84.6	2	Yes	35.6
	contig000007	2	7.6Kb	10	NA	259,232 - 266,856	0	7	6	0	85.7	1	No	36.2
L10-091_Cl_Gt69(69)_D	contig000002	1	5.6Kb	30	Head	1,954 - 7,588	0	8	6	1	87.5	1	No	36.5
L12-317_Cl_Gt72(66)_D	contig000005	1	7.6Kb	10	NA	43,883 - 51,507	0	7	6	0	85.7	1	no	36.1

L11- 209_Cl_Gt29(27) _D	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
L10- 023_Cl_Gt75(49) _D	contig000001	1	23.8Kb	30	Plate and integrase	1,196,930 - 1,220,754	0	13	8	4	92.3	1	yes	37.8
L09- 329_Cl_Gt75(49) _D	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
L02- 521_Cl_Gt29(27) _D	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
L02- 465_Cl_Gt27(133) _D	contig000007	1	7.6Kb	10	NA	1,196,930 - 1,220,754	0	7	6	0	85.7	1	No	36.2
L04- 545_Cl_Gt40(47) _D	contig000007	1	23Kb	30	Plate and integrase	15,451 - 38,507	0	10	6	3	90	1	Yes	40.3
L06- 153_Cl_Gt71(135) _D	contig000001	1	7.6Kb	10	NA	139,563 - 147,187	0	7	6	0	85.7	1	No	36
L06- 129_Cl_Gt71(135) _D	contig000001	1	7.6Kb	10	NA	2,031 - 9,655	0	7	6	0	85.7	1	No	36
L04- 041_Cl_Gt30(137) _D	contig000002	1	19.8Kb	20	integrase	70,310 - 90,170	0	14	6	5	78.5	3	Yes	36.6
	contig000003	2	7.7Kb	20	Plate	25,004 - 32,719	0	11	6	4	90.9	1	No	37.4

L05- 341_Cl_Gt8(132) D	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	N A
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NA: Not
Available

Comparative genomics of *Legionella pneumophila* isolates from the West Bank and Germany support molecular epidemiology of Legionnaires' disease

Zayed et al.

SUPPLEMENTARY MATERIALS

FIGURES

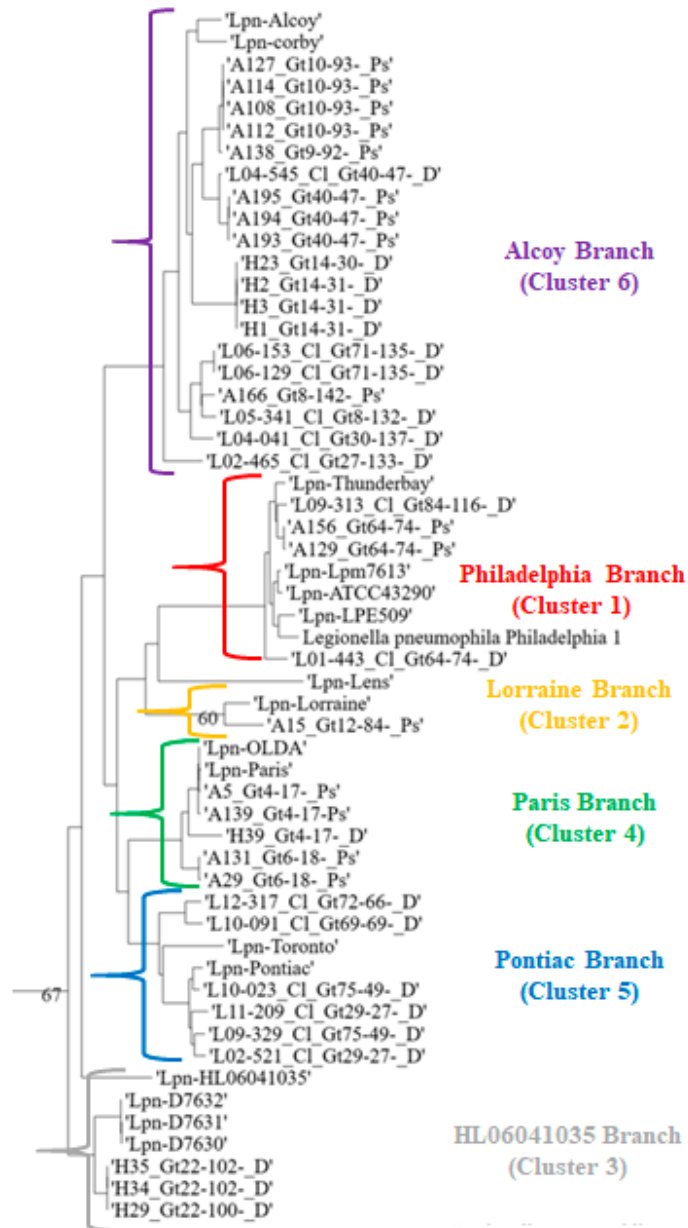


Figure S1. Phylogenomic tree of 55 *L. pneumophila* genomes based on the GBDP phylogenetic analyses retrieved from the TYGS website. The branch lengths are scaled in terms of GBDP distance formula d4. Color coding specific for each *L. pneumophila* branch

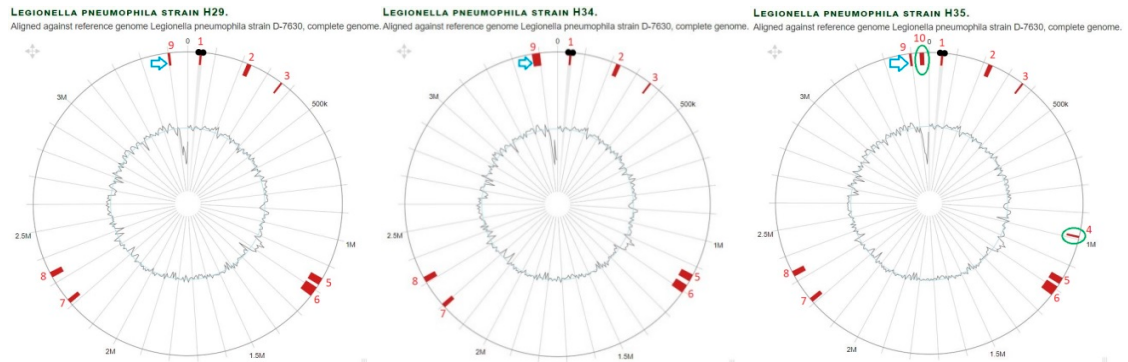
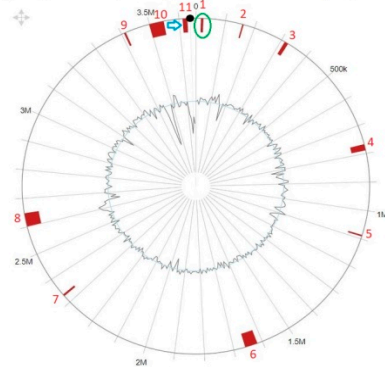


Figure S2: Comparison of Genomic islands in branch HL06041035 of *L. pneumophila* strain H29, H34 and H35 aligned against reference genome *L. pneumophila* strain HL06041035. The outer layers, the circle shows: (i) nucleotide positions in megabase pairs (Mbp) (black); (ii) Island Viewer-annotated potential genomic islands (GI) are labeled accordingly (red); (iii) Extra GIs (marked Green oval); (iv) GI different size (Blue arrow).

LEGIONELLA PNEUMOPHILA STRAIN A139.
Aligned against reference genome Legionella pneumophila str. Paris complete genome.



LEGIONELLA PNEUMOPHILA STRAIN A5.
Aligned against reference genome Legionella pneumophila str. Paris complete genome.

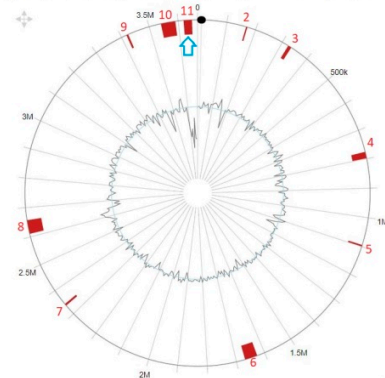
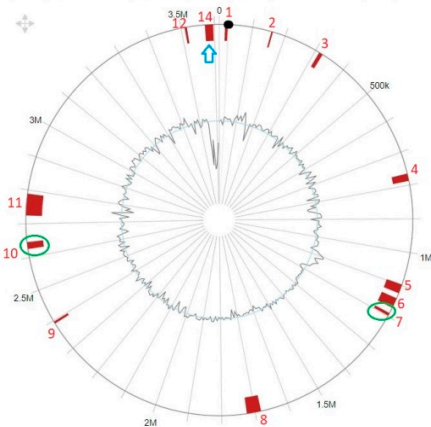


Figure S3: Comparison of Genomic islands in branch Paris of *L. pneumophila* strain A5 and A139 aligned against reference genome *L. pneumophila* strain Paris. The outer layers, the circle shows: (i) nucleotide positions in megabase pairs (Mbp) (black); (ii) Island Viewer-annotated potential genomic islands (GI) are labeled accordingly (red); (iii) Extra GIs (marked Green oval); (iv) GI different size (Blue arrow).

LEGIONELLA PNEUMOPHILA STRAIN A131.
Aligned against reference genome Legionella pneumophila str. Paris complete genome.



LEGIONELLA PNEUMOPHILA STRAIN A29.
Aligned against reference genome Legionella pneumophila str. Paris complete genome.

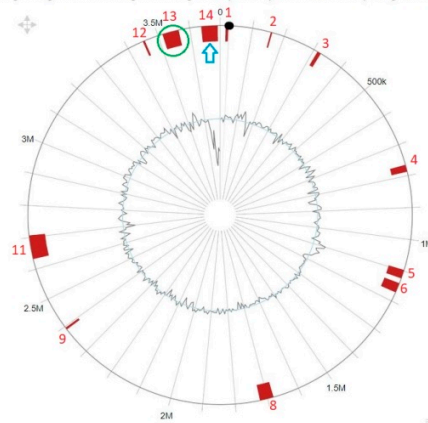


Figure S4: Comparison of Genomic islands in Branch Paris of *L. pneumophila* strain A29 and A131 aligned against reference genome *L. pneumophila* strain Paris. The outer layers, the circle shows: (i) nucleotide positions in megabase pairs (Mbp) (black); (ii) Island Viewer-annotated potential genomic islands (GI) are labeled accordingly (red); (iii) Extra GIs (marked Green oval); (iv) GI different size (Blue arrow).