

Table S1: Genome characteristics of 18 <i>Pseudomonas</i> genomes along with metagenomic recruitment data.																		
Genome Features	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
G+C Difference	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
Codon Bias	0.11	0.13	0.12	0.12	0.12	0.11	0.15	0.14	0.13	0.13	0.14	0.09	0.12	0.10	0.11	0.10	0.12	0.1
Genome size (In Mb)	3.80	5.07	6.74	6.72	6.85	6.40	4.53	4.71	4.70	4.65	4.57	6.58	7.01	5.07	5.43	5.10	4.63	5.70
Meta_1KM	3,855	788	1,503	0	0	186	105	183	1,095	103	807	107	3,421	151	134	1	0	3
Meta_5Km	2,161	474	491	0	0	156	81	82	299	65	474	71	1,373	0	0	0	0	0
Meta_DS	6,473	3,415	3,101	11	1	1,006	455	1,006	2,133	604	2,613	358	6,389	1	121	12	14	53
Meta_solexa_DS	63	87,681	43,046	91	14	13,328	12,627	19,523	15,393	6,517	46,599	3,702	88,432	11	3	1	0	4
Meta_Pond	292,290	195,770	200,842	308	12	56,037	46,344	65148	57,526	26,055	192,949	22,054	3,44,108	156	178	0	1	3
Pathways reconstructed	89	97	101	101	101	97	99	86	92	91	90	99	93	69	69	72	67	77
MGE	24	42	30	27	28	36	25	41	39	12	70	8	56	3	2	21	82	26
IS elements	13	3	11	11	11	14	34	24	0	8	28	3	18	11	1	16	31	2

GSMer 1km	2	1	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
GSMer 5km	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
GSMer DS	0	3	0	0	0	0	0	2	0	1	0	0	0	3	0	0	0	0
GSMer solexaDS	230	917	25	28	19	2	297	181	305	67	87	5	0	0	0	0	0	0
GSMer pond	1425	2	3	1	1	0	5	14	16	20	4	0	0	0	0	0	0	0

Genomes are labeled as numbers from 1 to 18; numbers correspond to the serial number of genomes as they appear in Table 2 in the main article text.

Meta_1km, Meta_5km, Meta_DS, Meta_Pond, represents metagenomic reads recruitment from 1km, 5Km, Dumpsite and pond data on 1-13 genomes. Similarly, GSMer 1km, GSMer 5km, GSMer DS, GSMer pond, represents metagenomic recruitment of GSMs of 1-18 genomes.