

Table S5 The number of raw reads, filtered reads, and mean length of the reads of formalin-fixed paraffin-embedded tissue samples of wild pigeons collected in the U.S. between 2010 and 2016 sequenced by next-generation sequencing (a continuation of Table 1).

SEPRL ID^a	Raw reads^b	Filtered reads^c	Mean fragment length^d
1177-1	281,595	101,867	127
1177-2	298,765	133,479	134
1177-3	273,772	97,573	124
1178-2	348,758	107,760	99
1178-3	492,731	79,840	118
1179-1	468,373	142,832	134
1179-2	349,992	122,874	99
1179-3	371,462	113,878	85
1180-1	323,798	82,303	146
1180-2	373,021	63,076	154
1180-3	261,102	58,969	160
1181-1	789,277	358,603	226
1181-2	118,942	45,840	189
1181-3	728,732	209,985	143
1182-1	282,145	74,144	201
1182-2	139,459	20,759	156
1182-3	296,801	83,712	167
1183-1	102,912	18,295	135
1183-3	577,717	111,807	96
1184-1	447,260	120,181	160
1184-2	675,639	196,080	99
1184-3	260,637	59,975	86
1185-1	383,615	114,210	149
1185-2	441,925	120,749	96
1185-3	465,822	127,284	103
1187-1	221,880	67,423	103
1187-2	535,022	169,400	107
1187-3	276,923	97,278	81
1188-1	761,054	192,584	121
1188-2	662,055	146,393	120
1188-3	261,977	53,863	158
1189-1	467,073	178,877	213
1189-2	70,355	20,726	93

1189-3	241,116	54,204	126
1191-1	474,651	226,018	213
1191-2	142,706	39,172	189
1191-3	216,770	58,841	167
1192-1	274,143	37,064	162
1192-2	252,619	71,948	85
1192-3	478,451	109,171	92
1193-1	131,923	62,997	197
1193-2	512,056	82,248	122
1194-1	308,540	75,551	170
1194-2	357,966	49,016	135
1194-3	320,925	87,458	91
1195-1	324,745	52,308	178
1195-2	152,545	46,335	176
1195-3	5,988	1,976	127

^a positive samples are in bold font.

^b all reads assigned to each sample

^c the number of paired reads remaining after host and internal control filtering

^d Average fragment size of the reads in each library