Supplemental Digital Content 1

Table S1. Genetic characteristics of the 84 *E. coli* isolated from the blood of the COLIBAFI children.

Center[1]	Isolate ID	Phylogroup[2]	Clonal group[3]	O-type[4]	*neuC* (K1)[5]	*sfa/foc*	*iroN*	*aer*	*iha*	*papC*	*papGII*	*papGIII*	*hlyC*	*cnf1*	*hra*	*sat*	*ireA*	*usp*	*ompT*	*ibeA*	*fyuA*	*irp2*	*traT*	*clbA*	*clbQ*	*afaD*	*eltB* (LT)	*estA* (ST)	*eae*	*aatA*	PAI I_{CFT073}	PAI II_{J96}	PAI III_{536}	PAI IV_{536}	PAI_{gimA}	PAI_{USP}	PAI_{pks}
2	R1B2B1	B2	B2-II	O2a	0	0	1	1	1	1	1	0	0	0	0	1	1	1	1	0	1	1	0	1	1	0	0	0	0	0	0	0	0	1	0	1	1
2	R1B2B4	B2	B2-IX	O1	1	0	1	1	0	1	1	0	0	0	0	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
2	R1B2C1	B2	B2-IX	O1	1	0	1	1	0	1	1	0	0	0	0	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
2	R1B2E11	B2	B2-IX	O1	1	0	0	0	0	1	1	0	0	0	1	0	1	1	1	0	1	1	1	1	1	0	0	0	0	0	0	0	0	1	0	1	1
4	R1B4A1	B2	B2-IX	O1	1	0	1	1	0	1	1	0	0	0	1	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
4	R1B4A2	B2	B2-VII	O75	0	0	0	1	0	1	1	0	0	0	1	1	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
4	R1B4A6	B2	B2-IX	O2a	1	0	0	0	0	1	1	0	0	0	0	0	1	1	1	1	1	1	0	1	1	0	0	0	0	0	0	0	0	1	1	1	1
4	R1B4A7	B2	B2-II	O6a	0	1	1	1	1	1	1	0	1	0	0	1	1	1	1	0	1	1	0	1	1	0	0	0	0	0	1	0	1	1	0	1	1
4	R1B4B3	B2	B2-II	O6a	0	0	0	1	1	1	1	0	1	0	0	1	0	1	1	0	1	1	1	1	1	0	0	0	0	0	1	0	0	1	0	1	1
4	R1B4B4	A	A_1	O6a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	R1B4B5	D	/	O2a	0	0	0	1	0	1	1	0	0	0	0	1	0	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
4	R1B4C2	B2	B2-II	O6a	0	1	1	1	1	1	1	0	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	0	0	0	1	1	1	1	0	1	1
4	R1B4C6	B2	B2-II	O6a	0	1	1	1	1	1	1	0	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	0	0	0	1	1	1	1	0	1	1
4	R1B4C7	B2	B2-IX	O45a	1	1	1	1	1	1	1	0	1	0	0	1	1	1	1	0	1	1	1	0	0	0	0	0	0	0	1	0	1	1	0	1	0
4	R1B4D3	D	CGA	O17	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
4	R1B4D4	F	/	O7	1	0	0	1	1	1	1	0	0	0	1	1	0	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
4	R1B4D5	B2	B2-IX	O45a	1	0	1	1	0	1	1	0	0	0	1	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
4	R1B4E2	B2	B2-IX	O1	1	0	1	1	1	1	1	0	1	0	1	1	1	1	1	0	1	1	1	0	0	0	0	0	0	0	1	0	0	1	0	1	0
4	R1B4E6	D	CGA	O17	0	0	0	1	1	1	1	0	0	0	0	1	1	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
4	R1B4E7	B2	B2-II	O6a	0	1	1	1	1	1	1	0	1	1	1	1	0	1	1	0	1	1	0	1	1	0	0	0	0	0	1	1	1	1	0	1	1
4	R1B4F2	B2	B2-I	O25b	0	0	0	1	1	0	0	0	0	0	1	1	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1	1	1	0
4	R1B4F4	B2	B2-I	O25b	0	0	0	1	1	0	0	0	0	0	1	1	0	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
4	R1B4F5	F	/	O7	1	0	0	1	0	1	1	0	0	0	1	1	1	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
4	R1B4G5	B2	B2-I	NT	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1	1	1	0
4	R1B4G6	B2	B2-IX	O2a	1	0	1	1	0	1	1	0	0	0	0	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
4	R1B4H2	B2	B2-VII	O75	0	0	0	1	0	0	0	0	0	0	0	1	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
4	R1B4H3	F	/	O7	1	0	0	1	1	1	1	0	0	0	1	1	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
4	R1B4H4	B2	B2-IX	O1	1	0	1	1	1	1	1	0	1	0	1	1	1	1	1	0	1	1	1	0	0	0	0	0	0	0	1	0	0	1	0	1	0
4	R1B4I1	B2	B2-IX	O45a	1	0	1	1	0	1	1	0	0	0	1	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
4	R1B4I5	D	CGA	O17	0	0	0	1	1	1	1	0	0	0	0	1	0	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
4	R1B4I6	F	/	O7	1	0	0	1	0	1	1	0	0	0	0	1	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
4	R1B4J2	B2	B2-IX	O1	1	0	1	1	0	1	1	0	0	0	1	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
4	R1B4J3	B2	B2-V	O16	1	0	0	1	1	1	1	0	0	0	1	1	0	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
4	R1B4J4	B2	B2-II	O6a	0	1	1	1	0	0	0	0	0	0	0	1	0	1	1	0	1	1	0	1	1	0	0	0	0	0	0	0	1	1	0	1	1
5	R1B5A1	D	CGA	O77	0	0	0	1	1	1	1	0	0	0	1	1	0	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
5	R1B5A14	B2	B2-II	O6a	0	0	0	1	1	1	1	0	0	0	1	1	1	1	1	0	1	1	1	1	1	0	0	0	0	0	0	0	0	1	0	1	1
5	R1B5A7	B2	B2-IX	O1	1	0	1	1	0	1	1	0	0	0	1	0	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
5	R1B5B10	F	/	O7	1	0	0	1	1	1	1	0	0	0	0	1	0	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
5	R1B5B15	B1	/	O110	0	0	1	1	0	1	1	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
5	R1B5C14	C	/	O8	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
5	R1B5C7	D	/	O15	0	0	0	1	1	1	1	0	0	0	0	1	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
5	R1B5D14	D	CGA	O17	0	0	0	1	1	1	1	0	0	0	0	1	1	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
5	R1B5E1	B2	B2-IX	O45a	1	0	1	1	0	1	1	0	0	0	1	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
5	R1B5E6	B2	B2-II	O1	0	1	1	0	0	1	1	0	1	0	1	0	0	1	1	0	1	1	0	1	1	0	0	0	0	0	0	0	1	1	0	1	1
5	R1B5F14	A	/	O55	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	R1B5G1	B2	B2-II	O6a	0	1	1	1	1	0	0	0	1	1	1	1	0	1	1	0	1	1	1	1	1	0	0	0	0	0	0	1	1	1	0	1	1
5	R1B5H10	B2	B2-VI	O4	0	1	1	0	0	1	1	1	1	1	1	0	1	0	1	0	1	1	1	1	1	0	0	0	0	0	0	1	1	1	0	0	1
5	R1B5H14	F	/	O7	1	0	0	1	1	1	1	0	0	0	1	1	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
5	R1B5H7	B2	B2-II	O6a	0	1	1	1	1	1	1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	0	0	0	0	0	1	0	1	1	0	1	1
5	R1B5I13	A	/	NT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	R1B5J14	B2	B2-II	O6a	0	1	1	1	0	1	1	0	0	0	0	1	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	1	1	0	1	0
7	R1B7A13	B2	B2-II	O6a	0	1	1	1	1	1	1	0	1	0	0	1	0	1	1	0	1	1	0	1	1	0	0	0	0	0	1	0	1	1	0	1	1
7	R1B7F12	B2	B2-IV	O2b	1	1	1	0	0	1	0	1	1	1	1	0	0	1	1	0	1	1	0	1	1	0	0	0	0	0	0	1	1	1	0	1	1
7	R1B7G4	D	CGA	O17	0	0	0	1	1	1	1	0	0	0	0	1	0	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
7	R1B7G5	C	/	O78	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
8	R1B8A16	B2	B2-IX	O1	1	0	1	1	1	1	1	0	1	0	1	1	1	1	1	0	1	1	1	0	0	0	0	0	0	0	1	0	0	1	0	1	0
8	R1B8C7	A	/	O5	0	0	1	1	0	1	0	0	0	0	1	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
8	R1B8F19	B2	B2-II	O2a	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	0	0	0	1	1	1	1	0	1	1
8	R1B8H26	B2	B2-II	O6a	0	1	1	1	1	0	0	0	1	1	1	1	0	1	1	0	1	1	0	1	1	0	0	0	0	0	0	1	1	1	0	1	1
8	R1B8I14	D	CGA	O2a	0	0	0	1	1	1	1	0	0	0	0	1	0	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
9	R1B9G4	F	/	O1	1	0	0	1	1	1	1	0	0	0	1	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
10	R1B10D1	B1	/	NT	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11	R1B11A24	B2	B2-IV	O2b	1	1	1	0	0	1	0	1	1	1	1	0	0	1	1	0	1	1	1	1	1	0	0	0	0	0	0	1	1	1	0	1	1
11	R1B11B24	B2	B2-II	O6a	0	0	0	1	1	1	1	0	1	0	0	1	0	1	1	0	1	1	1	1	1	0	0	0	0	0	1	0	0	1	0	1	1
11	R1B11C24	B2	B2-IV	O2b	1	1	1	0	0	1	0	1	1	1	1	0	0	1	1	0	1	1	1	1	1	0	0	0	0	0	0	1	1	1	0	1	1
11	R1B11D13	B2	B2-II	O2a	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	0	0	0	1	1	1	1	0	1	1
11	R1B11D14	B2	B2-IV	O2b	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	1	1	1	1	1	1
11	R1B11H17	B2	B2-IX	O2a	1	0	0	0	0	1	1	0	0	0	1	0	1	1	1	0	1	1	1	1	1	0	0	0	0	0	0	0	0	1	0	1	1
11	R1B11H23	F	/	O1	1	0	1	1	1	1	1	0	0	0	1	1	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
11	R1B11I17	B2	B2-IV	O2b	1	1	1	0	0	1	0	1	1	1	1	0	0	1	1	0	1	1	1	1	1	0	0	0	0	0	0	1	1	1	0	1	1
11	R1B11J5	D	/	O7	0	0	0	1	1	0	0	0	0	0	1	1	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
12	R1B12A21	B2	B2-IX	O1	1	0	1	1	0	1	1	0	0	0	1	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
12	R1B12C19	B1	/	O9	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	R1B12D27	B2	B2-II	O6a	0	1	1	1	1	1	1	0	0	0	0	1	1	1	1	0	1	1	0	1	1	0	0	0	0	0	0	0	1	1	0	1	1
12	R1B12E14	B2	B2-IX	O45a	1	0	1	1	0	1	1	0	0	0	1	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
12	R1B12E8	B2	B2-IX	O1	1	0	1	1	0	1	1	0	0	0	1	0	1	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0
12	R1B12F13	A	/	O11	0	0	1	1	0	1	1	0	0	0	1	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
12	R1B12H28	A	A_1	O153	0	0	0	1	1	1	1	0	1	0	0	1	0	0	0	0	1	1	1	0	0	1	0	0	0	1	1	0	0	1	0	0	0
12	R1B12J2	B2	B2-II	O6a	0	1	1	1	1	1	1	0	1	0	0	1	0	1	1	0	1	1	1	1	1	0	0	0	0	0	1	0	1	1	0	1	1
13	R1B13A1	C	/	O8	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
13	R1B13A2	B2	B2-IX	O1	1	0	1	1	1	1	1	0	1	0	1	1	1	1	1	0	1	1	1	0	0	0	0	0	0	0	1	0	0	1	0	1	0
13	R1B13C1	B2	B2-II	O6a	0	1	1	1	1	1	1	0	1	1	1	1	0	1	1	0	1	1	1	0	0	0	0	0	0	0	1	1	1	1	0	1	0
13	R1B13H3	A	A_1	O1	0	0	0	1	1	1	1	0	1	0	0	1	0	0	0	0	1	1	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0
13	R1B13I10	B2	B2-X	O83	0	0	1	1	0	1	1	1	1	1	1	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	1	1	0	1	1	1	0

Notes:

[1]Centers are as follow: 2=Necker hospital, Paris; 4=Robert Debré hospital, Paris; 5=Louis Mourier hospital, Colombes; 7=CHU Brest; 8=CHU Caen; 9=CHU Tours; 10=CHU Angers; 11=CHU Dijon; 12=CHU Nantes; 13=CHG Argenteuil.

[2]The phylogroups were determined as in (19).

[3]The clonal groups were delineated by allele specific PCRs for the D (19) and B2 (8,21) phylogroup strains. The correspondences with the ST complexes (STc) using the Achtman MLST scheme (8) are as follow: CGA=STc69, B2I=STc131, B2II=STc73, B2IV=STc141, B2V=STc144, B2VI=STc12, B2VII=STc14, B2IX=STc95, B2X=STc372. A_1 (*chuA* -, *yjaA* +, TspE4.C2 -)=STc10. /=not determined.

[4]The O-types were defined by allele specific PCR as in (22, 23). NT=not typed.

[5]Colors refer to the 7 pathogenicity islands defined as in (24, 25, 26). Blue refers to PAI I_{CFT073}, orange to PAI II_{J96}, green to PAI III_{536}, purple to PAI IV_{536}, yellow to PAI_{gimA}, red to PAI_{USP} and light grey to PAI_{pks}.