

Supplementary Table 3: Serotyping results for 144 EPEC isolates with a serologically determined O-group

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERR137822	wzx	O165	O165	100	112.949			0	O165
ERR137822	wzy	O165	O165	100	90.823			0	O165
ERS085334	wzx	O118	O118	100	185.592			0	O118
ERS085334	wzy	O118	O151	100	179.838	1snp		0.091	O151
ERS085335	wzx	O55	O55	100	164.306			0	O55
ERS085335	wzy	O55	O55	100	163.968			0	O55
ERS085337	wzx	O123	O123	100	213.728			0	O123
ERS085337	wzy	O123	O186	100	197.228			0	O186
ERS085338	wzx	O171	O70	100	15.907	33snp		2.638	O171
ERS085338	wzy	O171	O70	99.844	16.977	38snp2indel		2.966	O171
ERS085339	wzx	O146	O146	100	184.805	1snp		0.065	O146
ERS085339	wzy	O146	O146	100	172.327			0	O146
ERS085340	wzx	O33 related	O33	100	134.733			0	O33
ERS085340	wzy	O33 related	O33	100	132.765			0	O33
ERS085342	wzx	O118	O118	100	148.132			0	O118
ERS085342	wzy	O118	O151	100	143.012			0	O151
ERS085343	wzx	O103	O111	99.842	12.375	2holes	edge0.0	0	O103
ERS085343	wzy	O103	O111	100	10.716	1snp	edge2.0	0.095	O103
ERS085344	wzx	O33 related	O116	99.3	97.475	144snp2indel9holes		10.148	NC
ERS085344	wzy	O33 related	NC	NA	NA			NA	NC
ERS085345	wzx	O116	O116	98.529	111.498	141snp2indel20holes		10.014	NC
ERS085345	wzy	O116	NC	NA	NA			NA	NC
ERS085346	wzx	O136	O136	100	132.281			0	O136
ERS085346	wzy	O136	O136	100	136.52	1snp		0.081	O136
ERS085347	wzm	O77	O101	100	167.283			0	O101
ERS085347	wzt	O77	O101	100	182.435			0	O101
ERS085348	wzx	O162	O70	100	179.169	33snp		2.638	O70
ERS085348	wzy	O162	O70	99.844	178.105	37snp2indel		2.888	O70

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Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS085350	wzx	O38	O38	100	137.699	3snp		0.229	O38
ERS085350	wzy	O38	O38	100	124.187	6snp		0.489	O38
ERS085351	wzx	O111	O111	99.842	112.908	2holes	edge0.0	0	O111
ERS085351	wzy	O111	O111	100	92.005	1snp		0.095	O111
ERS085352	wzx	O108	O108	100	142.335			0	O108
ERS085352	wzy	O108	O108	100	141.842	1snp		0.081	O108
ERS085353	wzx	O63	O63	100	113.752	2snp		0.158	O63
ERS085353	wzy	O63	O63	100	94.793	3snp		0.229	O63
ERS085355	wzx	O45	O45	100	134.852			0	O45
ERS085355	wzy	O45	O45	100	131.066			0	O45
ERS085356	wzx	O116	O116	98.179	125.566	141snp2indel25holes		10.05	NC
ERS085356	wzy	O116	NC	NA	NA			NA	NC
ERS085357	wzx	O128	O128	100	132.409	3snp		0.208	O128
ERS085357	wzy	O128	O128	100	123.338	3snp		0.287	O128
ERS085360	wzx	O84	O84	100	135.411	1snp		0.072	O84
ERS085360	wzy	O84	O84	100	116.192	1snp		0.087	O84
ERS085361	wzx	O55	O55	100	122.443			0	O55
ERS085361	wzy	O55	O55	100	121.221			0	O55
ERS085363	wzx	O71	O71	100	173.924			0	O71
ERS085363	wzy	O71	O71	100	161.957			0	O71
ERS085364	wzx	O88	O88	100	96.795			0	O88
ERS085364	wzy	O88	O88	100	97.726	1snp		0.078	O88
ERS085365	wzx	O80	O80	100	189.065			0	O80
ERS085365	wzy	O80	O80	100	193.123			0	O80
ERS085366	wzx	O84	O84	100	166.837	1snp		0.072	O84
ERS085366	wzy	O84	O84	100	149.542	1snp		0.087	O84
ERS085367	wzx	O161	O161	100	105.712			0	O161
ERS085367	wzy	O161	O161	99.747	109.469	2snp6indel		0.168	O161

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Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS085368	wzx	O71	O71	100	142.809			0	O71
ERS085368	wzy	O71	O71	100	150.859			0	O71
ERS085369	wzx	O85	O85	100	82.267	1snp		0.082	O85
ERS085369	wzy	O85	O85	100	88.481	2snp		0.179	O85
ERS085370	wzx	O88	O88	100	125.925			0	O88
ERS085370	wzy	O88	O88	100	129.744	1snp		0.078	O88
ERS085371	wzx	O114	O114	100	141.433	1snp		0.08	O114
ERS085371	wzy	O114	O114	99.775	142.368	2snp3indel		0.15	O114
ERS085373	wzx	O71	O71	100	117.675			0	O71
ERS085373	wzy	O71	O71	100	113.902			0	O71
ERS085377	wzx	O126	O126	100	130.18	1snp		0.067	O126
ERS085377	wzy	O126	O126	100	139.019	1snp		0.096	O126
ERS085379	wzx	O128	O114	100	130.754	1snp		0.08	O114
ERS085379	wzy	O128	O114	99.775	140.465	2snp3indel		0.15	NC
ERS085380	wzx	O88	O88	100	170.237			0	O88
ERS085380	wzy	O88	O88	100	174.298			0	O88
ERS085382	wzx	O45	O45	100	93.052			0	O45
ERS085382	wzy	O45	O45	100	102.568			0	O45
ERS085383	wzx	O55	O55	100	100.345			0	O55
ERS085383	wzy	O55	O55	100	80.845	1snp		0.102	O55
ERS085384	wzm	O101	O162	100	116.233			0	O162
ERS085384	wzt	O101	O101	100	128.821			0	O101
ERS085385	wzx	O88	O88	100	81.11			0	O88
ERS085385	wzy	O88	O88	99.922	83.011	1indel		0	O88
ERS085386	wzx	O108	O108	100	103.406	2snp		0.166	O108
ERS085386	wzy	O108	O108	100	89.405	1snp		0.081	O108
ERS085389	wzm	O162	O101	100	77.932			0	O101
ERS085389	wzt	O162	O101	100	75.2			0	O101

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Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS085391	wzx	O33 related	O33	100	84.819			0	O33
ERS085391	wzy	O33 related	O33	100	98.831			0	O33
ERS085392	wzx	O123	O123	100	121.4			0	O123
ERS085392	wzy	O123	O186	100	116.196			0	O186
ERS085393	wzx	O63	O63	100	85.52	2snp		0.158	O63
ERS085393	wzy	O63	O63	100	73.714	3snp		0.229	O63
ERS085395	wzx	O33 related	O33	100	73.259			0	O33
ERS085395	wzy	O33 related	O33	100	74.158			0	O33
ERS085396	wzm	O101	O162	100	111.087			0	O162
ERS085396	wzt	O101	O101	100	106.607			0	O101
ERS085397	wzx	O137	O114	100	80.48			0	O114
ERS085397	wzy	O137	O114	99.925	92.153	4snp1indel		0.3	O114
ERS085398	wzx	O114	O114	100	89.222			0	O114
ERS085398	wzy	O114	O114	99.925	89.637	4snp1indel		0.3	O114
ERS085399	wzx	O114	O114	100	105.078			0	O114
ERS085399	wzy	O114	O114	99.925	117.226	4snp1indel		0.3	O114
ERS085400	wzx	O124	NC	NA	NA			NA	NC
ERS085400	wzy	O124	NC	NA	NA			NA	NC
ERS085401	wzx	O71	O71	100	110.425			0	O71
ERS085401	wzy	O71	O71	100	103.215			0	O71
ERS085402	wzm	O101	O162	100	79.662			0	O162
ERS085402	wzt	O101	O101	100	79.796			0	O101
ERS085403	wzm	O8	O8	100	159.489	2snp		0.252	O8
ERS085403	wzt	O8	O8	100	176.655	5snp		0.412	O8
ERS085404	wzx	O33	O55	100	71.945			0	O55
ERS085404	wzy	O33	O55	100	61.425			0	O55
ERS085405	wzx	O177	O177	100	84.259	1snp		0.079	O177
ERS085405	wzy	O177	O177	100	80.276	2snp		0.155	O177

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Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS085406	wzx	O55	O33	100	95.3			0	O33
ERS085406	wzy	O55	O33	100	111.178			0	O33
ERS085407	wzx	O171	O171	100	94.443	1snp		0.079	O171
ERS085407	wzy	O171	O171	100	104.074	1snp		0.087	O171
ERS085409	wzx	O51	O51	100	171.801	25snp		1.603	O51
ERS085409	wzy	O51	O51	100	167.488	15snp		1.445	O51
ERS085410	wzx	O45	O45	100	119.45			0	O45
ERS085410	wzy	O45	O45	100	120.542			0	O45
ERS085413	wzx	O82	O82	100	132.968	1snp		0.081	O82
ERS085413	wzy	O82	O82	100	128.09	1snp		0.092	O82
ERS085414	wzx	O123	O123	100	91.091			0	O123
ERS085414	wzy	O123	O186	100	93.73			0	O186
ERS085415	wzx	O45	O45	100	84.781			0	O45
ERS085415	wzy	O45	O45	100	92.248			0	O45
ERS085416	wzx	O45	O45	100	139.063			0	O45
ERS085416	wzy	O45	O45	100	150.374			0	O45
ERS085418	wzx	O82	O82	100	110.738			0	O82
ERS085418	wzy	O82	O82	100	94.282	1snp		0.092	O82
ERS085421	wzx	O2	NC	NA	NA			NA	NC
ERS085421	wzy	O2	NC	NA	NA			NA	NC
ERS085423	wzx	O2	NC	NA	NA			NA	NC
ERS085423	wzy	O2	NC	NA	NA			NA	NC
ERS085424	wzx	O33	O33	100	84.906			0	O33
ERS085424	wzy	O33	O33	100	101.594			0	O33
ERS085425	wzx	O165	O165	100	125.298			0	O165
ERS085425	wzy	O165	O165	100	102.211			0	O165
ERS085426	wzx	O104	O104	100	108.892			0	O104
ERS085426	wzy	O104	O104	100	82.603	4snp		0.359	O104

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Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS085427	wzx	O2	NC	NA	NA			NA	NC
ERS085427	wzy	O2	NC	NA	NA			NA	NC
ERS085428	wzx	O71	O71	100	119.929			0	O71
ERS085428	wzy	O71	O71	100	121.62			0	O71
ERS085429	wzx	O88	O88	100	117.761			0	O88
ERS085429	wzy	O88	O88	100	127.447	2snp		0.157	O88
ERS085434	wzx	O157	O157	100	351.469			0	O157
ERS085434	wzy	O157	O157	100	356.646	1snp		0.084	O157
ERS085435	wzx	O71	O71	100	364.487			0	O71
ERS085435	wzy	O71	O71	100	376.455			0	O71
ERS085436	wzx	O157	O157	100	574.794			0	O157
ERS085436	wzy	O157	O157	100	543.669	1snp		0.084	O157
ERS085437	wzx	O153	O8	100	363.034	27snp		2.273	O8
ERS085437	wzy	O153	O8	99.919	368.318	26snp2indel		2.093	O8
ERS085438	wzx	O88	O88	100	324.358			0	O88
ERS085438	wzy	O88	O88	100	338.088			0	O88
ERS085439	wzx	O88	O88	100	297.404			0	O88
ERS085439	wzy	O88	O88	100	290.496	1snp		0.078	O88
ERS085441	wzx	O114	O114	100	181.433	1snp		0.08	O114
ERS085441	wzy	O114	O114	99.775	158.929	2snp3indel		0.15	O114
ERS139198	wzx	O131	O131	100	46.559	3snp		0.236	O131
ERS139198	wzy	O131	O131	100	45.989			0	O131
ERS139199	wzm	O101	O162	100	71.665			0	O162
ERS139199	wzt	O101	O101	100	62.135			0	O101
ERS139200	wzx	O57	O38	100	94.866	4snp		0.306	O38
ERS139200	wzy	O57	O38	99.919	89.559	5snp1indel		0.407	O38
ERS139201	wzx	O71	O71	100	74.489			0	O71
ERS139201	wzy	O71	O71	100	76.252			0	O71

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Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS139202	wzx	O160	O160	100	65.863	4snp		0.321	O160
ERS139202	wzy	O160	O160	100	66.193	5snp		0.454	O160
ERS139203	wzx	O160	O160	100	65.914	4snp		0.321	O160
ERS139203	wzy	O160	O160	100	64.546	5snp		0.454	O160
ERS139205	wzx	O103 related	O103	100	87.824	2snp		0.158	O103
ERS139205	wzy	O103 related	O103	100	93.853	1snp		0.087	O103
ERS139207	wzx	O71	O71	100	61.414	4snp		0.314	O71
ERS139207	wzy	O71	O71	100	56.909	6snp		0.465	O71
ERS139209	wzx	O88	O88	100	67.546			0	O88
ERS139209	wzy	O88	O88	100	64.71	1snp		0.078	O88
ERS139211	wzx	O61	O61	100	63.755			0	O61
ERS139211	wzy	O61	O61	100	64.548	1snp		0.086	O61
ERS139214	wzx	O153	O8	100	33.144	28snp		2.357	O8
ERS139214	wzy	O153	O8	100	37.183	27snp2indel		2.174	O8
ERS139217	wzx	O88	O88	100	77.126			0	O88
ERS139217	wzy	O88	O88	100	75.905	1snp		0.078	O88
ERS139218	wzm	O8	O8	100	40.244	2snp		0.252	O8
ERS139218	wzt	O8	O8	100	55.521	5snp		0.412	O8
ERS139221	wzx	O101	O88	100	39.964			0	O88
ERS139221	wzy	O101	O88	100	39.427	1snp		0.078	O88
ERS139222	wzx	O111	O111	99.842	82.914	2holes	edge0.0	0	O111
ERS139222	wzy	O111	O111	100	83.139	1snp		0.095	O111
ERS139223	wzm	O88	O162	100	85.424			0	O162
ERS139223	wzt	O88	O101	100	74.106			0	O101
ERS139225	wzx	O88	O88	100	46.978			0	O88
ERS139225	wzy	O88	O88	100	50.15	1snp		0.078	O88
ERS139226	wzx	O55	O55	99.922	27.74	1indel		0	O55
ERS139226	wzy	O55	O55	100	28.609			0	O55

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Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS139227	wzx	O88	O88	100	23.499			0	O88
ERS139227	wzy	O88	O88	100	30.194	1snp		0.078	O88
ERS139228	wzx	O51	O51	100	44.089	25snp		1.603	O51
ERS139228	wzy	O51	O51	100	40.676	15snp		1.445	O51
ERS139229	wzx	O51	O51	100	35.722			0	O51
ERS139229	wzy	O51	O51	100	40.405			0	O51
ERS139230	wzx	O88	O88	100	34.82			0	O88
ERS139230	wzy	O88	O88	100	34.741	1snp		0.078	O88
ERS139231	wzx	O157	O157	100	100.149			0	O157
ERS139231	wzy	O157	O157	100	89.687	1snp		0.084	O157
ERS139232	wzx	O33	O33	100	85.668			0	O33
ERS139232	wzy	O33	O33	100	77.169			0	O33
ERS139233	wzx	O33	O33	100	60.876			0	O33
ERS139233	wzy	O33	O33	100	59.713			0	O33
ERS139234	wzx	O26	O26	100	41.118			0	O26
ERS139234	wzy	O26	O26	100	49.239			0	O26
ERS139235	wzm	O128	O8	100	53.283	2snp		0.252	O8
ERS139235	wzt	O128	O8	100	55.052	5snp		0.412	O8
ERS139236	wzx	O128	O128	100	38.141	5snp		0.347	O128
ERS139236	wzy	O128	O128	100	38.345	3snp		0.287	O128
ERS139239	wzx	O21	O21	100	56.879			0	O21
ERS139239	wzy	O21	O21	100	57.756			0	O21
ERS139241	wzx	O88	O88	100	41.772			0	O88
ERS139241	wzy	O88	O88	100	39.458	1snp		0.078	O88
ERS139243	wzx	O88 related	O88	100	46.203	1snp		0.069	O88
ERS139243	wzy	O88 related	O88	100	43.503			0	O88
ERS139244	wzx	O88	O88	100	55.416			0	O88
ERS139244	wzy	O88	O88	100	61.061	1snp		0.078	O88

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Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS139247	<i>wzm</i>	O8	O8	100	46.715	2snp		0.252	O8
ERS139247	<i>wzt</i>	O8	O8	100	56.016	5snp		0.412	O8
ERS139248	<i>wzx</i>	O153	O178	100	36.47			0	O178
ERS139248	<i>wzy</i>	O153	O178	100	36.591	trun		0	O178
ERS139249	<i>wzx</i>	O51	O51	100	37.165			0	O51
ERS139249	<i>wzy</i>	O51	O51	100	33.913			0	O51
ERS139251	<i>wzx</i>	O33	O33	100	32.823			0	O33
ERS139251	<i>wzy</i>	O33	O33	100	25.849			0	O33
ERS139252	<i>wzx</i>	O157	O157	100	48.776			0	O157
ERS139252	<i>wzy</i>	O157	O157	100	47.832	1snp		0.084	O157
ERS139253	<i>wzx</i>	O33	O33	100	29.705			0	O33
ERS139253	<i>wzy</i>	O33	O33	100	34.061			0	O33
ERS139254	<i>wzx</i>	O45	O45	100	30.064			0	O45
ERS139254	<i>wzy</i>	O45	O45	100	32.091			0	O45
ERS139255	<i>wzx</i>	O88	O88	100	26.664			0	O88
ERS139255	<i>wzy</i>	O88	O88	100	30.75			0	O88
ERS139256	<i>wzx</i>	O103	O88	96.433	1.848	52holes	edge0.0	0	O103
ERS139256	<i>wzy</i>	O103	O103	100	64.73	3snp		0.261	O103
ERS139258	<i>wzx</i>	O71	O71	100	51.35			0	O71
ERS139258	<i>wzy</i>	O71	O71	100	61.423			0	O71
ERS139262	<i>wzx</i>	O109	O109	100	29.755	3snp		0.22	O109
ERS139262	<i>wzy</i>	O109	O109	100	34.03	4snp		0.328	O109
ERS139263	<i>wzm</i>	O8	O8	100	32.877	2snp		0.252	O8
ERS139263	<i>wzt</i>	O8	O8	100	33.834	5snp		0.412	O8
ERS139264	<i>wzx</i>	O82	O82	100	57.328			0	O82
ERS139264	<i>wzy</i>	O82	O82	100	50.77			0	O82
ERS139265	<i>wzx</i>	O153	NC	NA	NA			NA	NC
ERS139265	<i>wzy</i>	O153	NC	NA	NA			NA	NC

Supplementary Table 3: Serotyping results for 144 EPEC isolates with a serologically determined O-group

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS139266	wzx	O108	O108	100	69.731			0	O108
ERS139266	wzy	O108	O108	100	69.748	1snp		0.081	O108
ERS139268	wzx	O146	O146	100	39.058			0	O146
ERS139268	wzy	O146	O146	100	35.492			0	O146
ERS139272	wzm	O8	O8	100	33.407	2snp		0.252	O8
ERS139272	wzt	O8	O8	100	41.621	5snp		0.412	O8
ERS139273	wzx	O88	O88	100	68.782			0	O88
ERS139273	wzy	O88	O88	100	61.943	1snp		0.078	O88
ERS139274	wzx	O111	O111	99.842	69.857	2holes	edge0.0	0	O111
ERS139274	wzy	O111	O111	100	67.549	1snp		0.095	O111
ERS139276	wzx	O103	O103	100	61.95	1snp		0.079	O103
ERS139276	wzy	O103	O103	100	51.525	3snp		0.261	O103
ERS139277	wzx	O128	O128	100	70.758	3snp		0.208	O128
ERS139277	wzy	O128	O128	100	66.856	3snp		0.287	O128
ERS139278	wzx	O80	O80	100	34.913			0	O80
ERS139278	wzy	O80	O80	100	34.86			0	O80
ERS150871	wzm	O162	O162	100	97.968			0	O162
ERS150871	wzt	O162	O101	100	85.523			0	O101
ERS150876	wzx	O177	O177	100	44.159	1snp		0.079	O177
ERS150876	wzy	O177	O177	100	51.03	2snp		0.155	O177
ERS150879	wzx	O114	O114	100	94.324			0	O114
ERS150879	wzy	O114	O25	95.104	2.236	44snp1indel52holes	edge1.0	4.356	O114
ERS150882	wzx	O153	O8	100	69.525	27snp		2.273	O8
ERS150882	wzy	O153	O8	100	67.056	27snp1indel		2.174	O8
ERS150883	wzx	O103	O103	100	76.353	2snp		0.158	O103
ERS150883	wzy	O103	O103	100	76.555	1snp		0.087	O103
ERS150902	wzx	O108	NC	NA	NA			NA	NC
ERS150902	wzy	O108	NC	NA	NA			NA	NC

Supplementary Table 3: Serotyping results for 144 EPEC isolates with a serologically determined O-group

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS150905	wzx	O55	O55	100	44.542	18snp		1.408	O55
ERS150905	wzy	O55	O55	100	37.443	22snp		2.249	O55
ERS150906	wzx	O153	O8	100	97.331	27snp		2.273	O8
ERS150906	wzy	O153	O8	100	98.554	27snp1indel		2.174	O8
ERS150986	wzx	O33 related	O33	100	49.852			0	O33
ERS150986	wzy	O33 related	O33	100	46.057			0	O33
ERS150987	wzx	O88	O88	100	67.388			0	O88
ERS150987	wzy	O88	O88	100	62.401	1snp		0.078	O88

NC = No in silico call was made

NA = Not available

Coverage = percentage of the gene length that was covered

Depth = mean read depth across the length of all alleles which were assigned a top scoring allele number

Diffs = differences between the detected allele and the best scoring allele.

Uncertainty = details of parts of the top scoring alleles for which the depth of coverage was too low to give confidence in the result

Divergence = divergence of allele detected to sequence database (ran with option to report <10% divergence)

Reported =reported phenotype of the isolate

SRST2 = call from short read data and the EcOH database

BLAST+ = call from BLAST analysis of Velvet assemblies and the EcOH database

Supplementary Table 4: Serotyping results for 128 EPEC isolates with a serologically determined H-type

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERR137822	<i>fliC</i>	H9	H9	100	114.419	24snp		1.192	H9
ERS085336	<i>fliC</i>	H6	H6	100	173.978	6snp		0.364	H6
ERS085337	<i>fliC</i>	H19	H19	99.945	207.113	1snp1holes		0.055	H19
ERS085338	<i>fliC</i>	H19	H19	99.945	163.106	1snp1holes		0.055	H19
ERS085339	<i>fliC</i>	H21	H21	100	160.369			0	H21
ERS085340	<i>fliC</i>	H34	H34	100	108.13	10snp		0.611	H34
ERS085344	<i>fliC</i>	H6	H9	100	140.062	24snp		1.192	H9
ERS085346	<i>fliC</i>	H51	H51	100	113.062			0	H51
ERS085347	<i>fliC</i>	H33	H33	100	178.785			0	H33
ERS085348	<i>fliC</i>	H33	H40	100	170.619			0	H40
ERS085349	<i>fliC</i>	H33	H33	100	208.251			0	H33
ERS085351	<i>fliC</i>	H19	H19	99.945	112.3	1snp1holes		0.055	H19
ERS085352	<i>fliC</i>	H21	H21	100	119.367			0	H21
ERS085353	<i>fliC</i>	H6	H6	100	110.337	8snp		0.486	H6
ERS085354	<i>fliC</i>	H21	H21	100	132.103			0	H21
ERS085356	<i>fliC</i>	H9	H9	100	215.2	24snp		1.192	H9
ERS085357	<i>fliC</i>	H8	H8	100	158.268	1snp		0.068	H8
ERS085358	<i>fliC</i>	H51	H51	100	126.42	18snp		0.99	H51
ERS085360	<i>fliC</i>	H14	H14	100	125.137	19snp		1.149	H14
ERS085362	<i>fliC</i>	H21	H21	100	148.133	20snp		1.449	H21
ERS085363	<i>fliC</i>	H19	H19	99.945	157.474	1snp1holes		0.055	H19
ERS085365	<i>fliC</i>	H2	H2	100	183.736	12snp		0.803	H2
ERS085367	<i>fliC</i>	H21	H21	100	109.038	20snp		1.449	H21
ERS085368	<i>fliC</i>	H19	H19	99.945	134.475	1snp1holes		0.055	H19
ERS085369	<i>fliC</i>	H31	H31	100	111.102	57snp		3.417	H31
ERS085370	<i>fliC</i>	H25	H25	100	108.609	9snp		0.752	H25
ERS085371	<i>fliC</i>	H2	H2	100	124.914			0	H2
ERS085372	<i>fliC</i>	H21	H21	100	142.293	20snp		1.449	H21

Supplementary Table 4: Serotyping results for 128 EPEC isolates with a serologically determined H-type

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS085373	<i>fliC</i>	H19	H19	99.945	101.517	1snp1holes		0.055	H19
ERS085374	<i>fliC</i>	H21	H21	100	95.861	20snp		1.449	H21
ERS085375	<i>fliC</i>	H40	H40	100	123.574			0	H40
ERS085376	<i>fliC</i>	H40	H40	100	137.395			0	H40
ERS085379	<i>fliC</i>	H2	H2	100	127.609			0	H2
ERS085380	<i>fliC</i>	H25	H25	100	156.99	9snp		0.752	H25
ERS085385	<i>fliC</i>	H25	H25	100	77.449	9snp		0.752	H25
ERS085386	<i>fliC</i>	H9	H9	100	97.948	29snp		1.441	H9
ERS085387	<i>fliC</i>	H40	H40	100	84.296			0	H40
ERS085389	<i>fliC</i>	H33	H33	100	93.409			0	H33
ERS085390	<i>fliC</i>	H4	H4	100	87.688	1snp		0.095	NC
ERS085391	<i>fliC</i>	H6	H6	100	104.914	7snp		0.425	NC
ERS085393	<i>fliC</i>	H6	H6	100	117.772	8snp		0.486	H6
ERS085394	<i>fliC</i>	H21	H21	100	106.933			0	H21
ERS085397	<i>fliC</i>	H6	H2	100	106.635			0	H2
ERS085400	<i>fliC</i>	H2	H2	100	172.988	12snp		0.803	H2
ERS085401	<i>fliC</i>	H19	H19	99.945	126.692	1snp1holes		0.055	H19
ERS085403	<i>fliC</i>	H19	H19	99.945	186.835	1snp1holes		0.055	H19
ERS085405	<i>fliC</i>	H9	H9	100	84.758	29snp		1.441	H9
ERS085407	<i>fliC</i>	H19	H19	99.945	123.681	1snp1holes		0.055	H19
ERS085408	<i>fliC</i>	H40	H40	100	141.429			0	H40
ERS085409	<i>fliC</i>	H40	H40	100	170.563			0	H40
ERS085412	<i>fliC</i>	H21	H21	100	145.696			0	H21
ERS085414	<i>fliC</i>	H19	H19	99.945	105.247	1snp1holes		0.055	H19
ERS085417	<i>fliC</i>	H40	H40	100	110.286			0	H40
ERS085419	<i>fliC</i>	H40	H40	100	134.646			0	H40
ERS085420	<i>fliC</i>	H40	H40	100	104.118			0	H40
ERS085423	<i>fliC</i>	H40	H40	100	148			0	H40

Supplementary Table 4: Serotyping results for 128 EPEC isolates with a serologically determined H-type

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS085425	<i>fliC</i>	H9	H9	100	128.043	24snp		1.192	H9
ERS085426	<i>fliC</i>	H7	H7	100	120.367			0	H7
ERS085428	<i>fliC</i>	H19	H19	99.945	126.366	1snp1holes		0.055	H19
ERS085429	<i>fliC</i>	H25	H25	100	126.467	9snp		0.752	H25
ERS085430	<i>fliC</i>	H2	H2	100	240.047			0	H2
ERS085432	<i>fliC</i>	H40	H40	100	398.368			0	H40
ERS085435	<i>fliC</i>	H40	H40	100	387.068			0	H40
ERS085438	<i>fliC</i>	H25	H25	100	327.584	9snp		0.752	H25
ERS085439	<i>fliC</i>	H25	H25	99.916	318.988	8snp1indel		0.668	H25
ERS085441	<i>fliC</i>	H2	H2	100	306.997			0	H2
ERS139198	<i>fliC</i>	H31	H31	100	38.851	57snp		3.417	H31
ERS139200	<i>fliC</i>	H19	H19	99.945	78.876	1snp1holes		0.055	H19
ERS139201	<i>fliC</i>	H19	H19	99.945	70.117	1snp1holes		0.055	H19
ERS139202	<i>fliC</i>	H19	H19	99.945	55.277	1snp1holes		0.055	H19
ERS139203	<i>fliC</i>	H19	H19	99.945	55.449	1snp1holes		0.055	H19
ERS139204	<i>fliC</i>	H21	H21	100	79.899			0	H21
ERS139205	<i>fliC</i>	H2	H2	100	82.368			0	H2
ERS139206	<i>fliC</i>	H33	H33	100	38.133			0	H33
ERS139209	<i>fliC</i>	H25	H25	100	61.726	9snp		0.752	H25
ERS139216	<i>fliC</i>	H6	H9	100	57.168	37snp		1.838	H9
ERS139217	<i>fliC</i>	H25	H25	100	63.371	9snp		0.752	H25
ERS139218	<i>fliC</i>	H19	H19	99.945	50.072	1snp1holes		0.055	H19
ERS139219	<i>fliC</i>	H19	H2	100	95.907			0	H2
ERS139223	<i>fliC</i>	H25	H33	100	80.138			0	H33
ERS139224	<i>fliC</i>	H21	H21	100	53.241			0	H21
ERS139225	<i>fliC</i>	H25	H25	100	44.457	9snp		0.752	H25
ERS139227	<i>fliC</i>	H25	H25	100	29.315	9snp		0.752	H25
ERS139228	<i>fliC</i>	H40	H40	100	37.992			0	H40

Supplementary Table 4: Serotyping results for 128 EPEC isolates with a serologically determined H-type

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS139229	<i>fliC</i>	H7	H7	100	34.308			0	H7
ERS139230	<i>fliC</i>	H25	H25	100	31.622	9snp		0.752	H25
ERS139233	<i>fliC</i>	H6	H6	100	55.582	7snp		0.425	NC
ERS139234	<i>fliC</i>	H11	H11	100	45.769			0	H11
ERS139235	<i>fliC</i>	H2	H19	99.945	55.682	1snp1holes		0.055	H19
ERS139236	<i>fliC</i>	H2	H2	100	35.768			0	H2
ERS139238	<i>fliC</i>	H5	H5	99.924	49.68	2snp1holes		0.153	H5
ERS139240	<i>fliC</i>	H6	H6	100	68.671	6snp		0.364	H6
ERS139241	<i>fliC</i>	H4	H40	93.78	3.176	6snp92holes	edge1.0	0.433	NC
ERS139242	<i>fliC</i>	H40	H40	100	61.721			0	H40
ERS139243	<i>fliC</i>	H25	H25	100	44.645	9snp		0.752	H25
ERS139244	<i>fliC</i>	H25	H25	100	54.93	9snp		0.752	H25
ERS139247	<i>fliC</i>	H19	H19	99.945	55.241	1snp1holes		0.055	H19
ERS139248	<i>fliC</i>	H6	H7	100	34.656	1snp		0.057	H7
ERS139249	<i>fliC</i>	H7	H7	100	35.269			0	H7
ERS139250	<i>fliC</i>	H40	H40	100	38.836			0	H40
ERS139251	<i>fliC</i>	H6	H6	100	33.115	7snp		0.425	NC
ERS139253	<i>fliC</i>	H6	H6	100	29.189	7snp		0.425	NC
ERS139255	<i>fliC</i>	H25	H25	100	29.05	9snp		0.752	H25
ERS139258	<i>fliC</i>	H19	H19	99.945	49.813	1snp1holes		0.055	H19
ERS139259	<i>fliC</i>	H6	H6	100	44.882	7snp		0.425	NC
ERS139260	<i>fliC</i>	H5	H5	99.924	52.611	2snp1holes		0.153	H5
ERS139262	<i>fliC</i>	H21	H21	100	31.652			0	H21
ERS139263	<i>fliC</i>	H19	H19	99.945	40.015	1snp1holes		0.055	H19
ERS139265	<i>fliC</i>	H19	H19	99.945	53.035	1snp1holes		0.055	H19
ERS139266	<i>fliC</i>	H21	H21	100	64.765			0	H21
ERS139267	<i>fliC</i>	H40	H40	100	75.001			0	H40
ERS139268	<i>fliC</i>	H21	H21	100	38.091			0	H21

Supplementary Table 4: Serotyping results for 128 EPEC isolates with a serologically determined H-type

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS139269	<i>fliC</i>	H21	H21	100	63.781	20snp		1.449	H21
ERS139271	<i>fliC</i>	H7	H7	100	69.198			0	H7
ERS139272	<i>fliC</i>	H19	H19	99.945	38.592	1snp1holes		0.055	H19
ERS139273	<i>fliC</i>	H25	H25	100	59.432	9snp		0.752	H25
ERS139274	<i>fliC</i>	H19	H19	99.945	64.004	1snp1holes		0.055	H19
ERS139275	<i>fliC</i>	H5	H5	99.924	33.633	2snp1holes		0.153	H5
ERS139277	<i>fliC</i>	H8	H8	100	65.095	1snp		0.068	H8
ERS150870	<i>fliC</i>	H21	H21	100	43.797			0	H21
ERS150873	<i>fliC</i>	H5	H5	99.924	77.59	2snp1holes		0.153	H5
ERS150876	<i>fliC</i>	H11	H11	100	44.584			0	H11
ERS150880	<i>fliC</i>	H6	H6	100	69.189	7snp		0.425	NC
ERS150902	<i>fliC</i>	H21	H21	100	72.473			0	H21
ERS150903	<i>fliC</i>	H21	H21	100	77.35			0	H21
ERS150905	<i>fliC</i>	H21	H21	100	38.736			0	H21
ERS150986	<i>fliC</i>	H6	H6	100	45.471	8snp		0.486	H6
ERS150987	<i>fliC</i>	H25	H25	100	57.923	9snp		0.752	H25

Coverage = percentage of the gene length that was covered

Depth = mean read depth across the length of all alleles which were assigned a top scoring allele number

Diffs = differences between the detected allele and the best scoring allele.

Uncertainty = details of parts of the top scoring alleles for which the depth of coverage was too low to give confidence in the result

Divergence = divergence of allele detected to sequence database (ran with option to report <10% divergence)

Reported =reported phenotype of the isolate

SRST2 = call from short read data and the EcOH database

BLAST+ = call from BLAST analysis of Velvet assemblies and the EcOH database

Supplementary Table 5: Serotyping results for Ont, O-rough and H non-motile EPEC isolates

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS085336	wzx	Ont	NC	NA	NA			NA	NC
ERS085336	wzy	Ont	NC	NA	NA			NA	NC
ERS085341	wzx	Ont	O70	100	185.571	33snp		2.638	O70
ERS085341	wzy	Ont	O70	99.844	197.629	38snp2indel		2.966	O70
ERS085354	wzx	Ont	O109	100	134.956	3snp		0.22	O109
ERS085354	wzy	Ont	O109	100	141.635	4snp		0.328	O109
ERS085358	wzx	Ont	O76	100	120.394	5snp		0.404	O76
ERS085358	wzy	Ont	O76	100	114.389	7snp		0.568	O76
ERS085359	wzx	Ont	O26	100	154.225	1snp		0.079	O26
ERS085359	wzy	Ont	O26	100	148.533			0	O26
ERS085362	wzx	Ont	NC	NA	NA			NA	NC
ERS085362	wzy	Ont	O64	100	158.971			0	O64
ERS085372	wzx	Ont	NC	NA	NA			NA	NC
ERS085372	wzy	Ont	O64	100	140.513			0	O64
ERS085374	wzx	Ont	NC	NA	NA			NA	NC
ERS085374	wzy	Ont	O64	100	101.947			0	O64
ERS085375	wzx	Ont	O70	100	129.649	33snp		2.638	O70
ERS085375	wzy	Ont	O70	100	136.112	39snp		3.044	O70
ERS085376	wzx	Ont	O114	100	5.664			0	O70
ERS085376	wzy	Ont	O114	99.399	5.322	3snp8holes		0.227	O70
ERS085381	wzx	Ont	O34	100	130.231			0	O34
ERS085381	wzy	Ont	O34	100	89.523			0	O34
ERS085387	wzx	Ont	O90	100	72.689			0	O90
ERS085387	wzy	Ont	O127	100	65.123			0	O127
ERS085390	wzx	Ont	O88	100	87.992			0	O88
ERS085390	wzy	Ont	O88	100	96.843	1snp		0.078	O88
ERS085394	wzx	Ont	O109	99.927	92.018	2snp1indel		0.147	O109
ERS085394	wzy	Ont	O109	100	81.336	4snp		0.328	O109
ERS085408	wzx	Ont	O70	100	141.529	33snp		2.638	O70
ERS085408	wzy	Ont	O70	99.922	136.988	39snp1indel		3.044	O70

Supplementary Table 5: Serotyping results for Ont, O-rough and H non-motile EPEC isolates

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS085412	wzx	Ont	O109	100	162.467	3snp		0.22	O109
ERS085412	wzy	Ont	O109	100	128.314	4snp		0.328	O109
ERS085417	wzx	Ont	O70	100	103.173	33snp		2.638	O70
ERS085417	wzy	Ont	O70	99.844	104.934	38snp2indel		2.966	O70
ERS085419	wzx	Ont	O70	100	126.867	33snp		2.638	O70
ERS085419	wzy	Ont	O70	99.844	112.893	38snp2indel		2.966	O70
ERS085420	wzx	Ont	O70	100	96.098	33snp		2.638	O70
ERS085420	wzy	Ont	O70	99.844	96.757	38snp2indel		2.966	O70
ERS085430	wzx	Ont	O114	100	227.896	1snp		0.08	O114
ERS085430	wzy	Ont	O114	99.925	189.239	3snp1indel		0.225	O114
ERS085431	wzx	Ont	O34	100	190.42			0	O34
ERS085431	wzy	Ont	O34	100	116.44			0	O34
ERS085432	wzx	Ont	O70	99.92	390.332	32snp1indel		2.558	O70
ERS085432	wzy	Ont	O70	99.844	361.153	38snp2indel		2.966	O70
ERS085433	wzx	Ont	O34	100	304.169			0	O34
ERS085433	wzy	Ont	O34	100	307.107			0	O34
ERS085440	wzx	Ont	NC	NA	NA			NA	NC
ERS085440	wzy	Ont	NC	NA	NA			NA	NC
ERS139204	wzx	Ont	O109	100	90.28	3snp		0.22	O109
ERS139204	wzy	Ont	O109	100	78.575	4snp		0.328	O109
ERS139206	wzm	Ont	O9	100	36.751	4snp		0.509	O9
ERS139206	wzt	Ont	O9	100	32.933	39snp		3.009	O9
ERS139208	wzx	Ont	O39	100	105.732	2snp		0.135	O39
ERS139208	wzy	Ont	O88	91.843	2.704	1snp104holes	edge0.0	0.085	O39
ERS139215	wzx	Ont	O34	100	68.153			0	O34
ERS139215	wzy	Ont	O34	100	69.755			0	O34
ERS139219	wzx	Ont	O157	94.971	2.637	70holes	edge0.0	0	O128
ERS139219	wzy	Ont	O128	100	102.856	3snp		0.287	O128
ERS139220	wzx	Ont	O33	100	76.047			0	O33
ERS139220	wzy	Ont	O33	100	83.085			0	O33

Supplementary Table 5: Serotyping results for Ont, O-rough and H non-motile EPEC isolates

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS139224	wzx	Ont	O109	100	61.055	4snp		0.293	O109
ERS139224	wzy	Ont	O109	100	58.426	4snp		0.328	O109
ERS139238	wzx	Ont	NC	NA	NA			NA	NC
ERS139238	wzy	Ont	NC	NA	NA			NA	NC
ERS139240	wzx	Ont	NC	NA	NA			NA	NC
ERS139240	wzy	Ont	NC	NA	NA			NA	NC
ERS139242	wzx	Ont	O70	99.92	60.178	32snp1indel		2.558	O70
ERS139242	wzy	Ont	O70	99.922	58.388	39snp1indel		3.044	O70
ERS139250	wzx	Ont	O90	100	42.056			0	O90
ERS139250	wzy	Ont	O127	100	46.384			0	O127
ERS139257	wzx	Ont	O34	100	50.952			0	O34
ERS139257	wzy	Ont	O34	100	47.025			0	O34
ERS139260	wzx	Ont	NC	NA	NA			NA	NC
ERS139260	wzy	Ont	NC	NA	NA			NA	NC
ERS139261	wzx	Ont	O103	100	34.678	1snp		0.079	O103
ERS139261	wzy	Ont	O103	100	30.137	3snp		0.261	O103
ERS139267	wzx	Ont	O70	100	77.32	33snp		2.638	O70
ERS139267	wzy	Ont	O88	91.373	2.616	110holes	edge0.0	0	O70
ERS139269	wzx	Ont	NC	NA	NA			NA	NC
ERS139269	wzy	Ont	O64	100	57.643			0	O64
ERS139271	wzx	Ont	NC	NA	NA			NA	NC
ERS139271	wzy	Ont	NC	NA	NA			NA	NC
ERS139275	wzx	Ont	NC	NA	NA			NA	NC
ERS139275	wzy	Ont	NC	NA	NA			NA	NC
ERS150870	wzx	Ont	O108	100	44.597			0	O108
ERS150870	wzy	Ont	O108	100	43.803	1snp		0.081	O108
ERS150903	wzx	Ont	O109	99.927	93.275	2snp1indel		0.147	O109
ERS150903	wzy	Ont	O109	100	87.055	4snp		0.328	O109
ERS085349	wzm	OR	O101	100	199.907			0	O101
ERS085349	wzt	OR	O101	100	197.597			0	O101

Supplementary Table 5: Serotyping results for Ont, O-rough and H non-motile EPEC isolates

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS139216	<i>wzx</i>	OR	O34	100	63.952			0	O34
ERS139216	<i>wzy</i>	OR	O34	100	55.308			0	O34
ERS139237	<i>wzx</i>	OR	O137	100	39.501	7snp		0.506	O137
ERS139237	<i>wzy</i>	OR	O137	100	34.768	2snp		0.163	O137
ERS139245	<i>wzm</i>	OR	O162	100	53.544			0	O162
ERS139245	<i>wzt</i>	OR	O101	100	57.154			0	O101
ERS139246	<i>wzm</i>	OR	O162	100	51.044			0	O162
ERS139246	<i>wzt</i>	OR	O101	100	57.466			0	O101
ERS139259	<i>wzx</i>	OR	O33	100	48.576			0	O33
ERS139259	<i>wzy</i>	OR	O33	100	53.975			0	O33
ERS150873	<i>wzx</i>	OR	NC	NA	NA			NA	NC
ERS150873	<i>wzy</i>	OR	NC	NA	NA			NA	NC
ERS150874	<i>wzm</i>	OR	O162	100	83.037			0	O162
ERS150874	<i>wzt</i>	OR	O101	100	70.886			0	O101
ERS150880	<i>wzx</i>	OR	O33	100	76.626			0	O33
ERS150880	<i>wzy</i>	OR	O33	100	84.053			0	O33
ERS085334	<i>fliC</i>	H-	H8	100	171.803			0	H8
ERS085335	<i>fliC</i>	H-	H7	100	164.254			0	H7
ERS085341	<i>fliC</i>	H-	H40	100	164.423			0	H40
ERS085342	<i>fliC</i>	H-	H8	100	123.245			0	H8
ERS085343	<i>fliC</i>	H-	H8	100	137.371			0	H8
ERS085345	<i>fliC</i>	H-	H9	100	166.283	24snp		1.192	H9
ERS085350	<i>fliC</i>	H-	H9	100	133.76	37snp		1.838	H9
ERS085355	<i>fliC</i>	H-	H19	99.945	120.25	1snp1holes		0.055	H19
ERS085359	<i>fliC</i>	H-	H8	100	153.82	1snp		0.068	H8
ERS085361	<i>fliC</i>	H-	H7	100	99.548			0	H7
ERS085364	<i>fliC</i>	H-	H25	100	93.715	9snp		0.752	H25
ERS085366	<i>fliC</i>	H-	H9	99.702	148.351	28snp6indel		1.391	H9
ERS085377	<i>fliC</i>	H-	H2	100	133.426			0	H2
ERS085381	<i>fliC</i>	H-	H9	100	152.894	37snp		1.838	H9

Supplementary Table 5: Serotyping results for Ont, O-rough and H non-motile EPEC isolates

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS085382	<i>fliC</i>	H-	H19	99.945	113.356	1snp1holes		0.055	H19
ERS085383	<i>fliC</i>	H-	H7	100	104.609			0	H7
ERS085384	<i>fliC</i>	H-	H33	100	141.447			0	H33
ERS085392	<i>fliC</i>	H-	H19	99.945	148.771	1snp1holes		0.055	H19
ERS085395	<i>fliC</i>	H-	H6	100	133.961	7snp		0.425	NC
ERS085396	<i>fliC</i>	H-	H33	100	118.134			0	H33
ERS085398	<i>fliC</i>	H-	H2	100	95.828			0	H2
ERS085399	<i>fliC</i>	H-	H2	100	130.3			0	H2
ERS085402	<i>fliC</i>	H-	H33	100	82.505			0	H33
ERS085404	<i>fliC</i>	H-	H7	100	77.354			0	H7
ERS085406	<i>fliC</i>	H-	H6	100	125.39	7snp		0.425	NC
ERS085410	<i>fliC</i>	H-	H19	99.945	143.09	1snp1holes		0.055	H19
ERS085413	<i>fliC</i>	H-	H11	100	127.093			0	NC
ERS085415	<i>fliC</i>	H-	H19	99.945	105.188	1snp1holes		0.055	H19
ERS085416	<i>fliC</i>	H-	H19	99.945	162.938	1snp1holes		0.055	H19
ERS085418	<i>fliC</i>	H-	H11	100	96.629			0	NC
ERS085421	<i>fliC</i>	H-	H8	100	138.059			0	H8
ERS085424	<i>fliC</i>	H-	H6	100	106.886	7snp		0.425	NC
ERS085427	<i>fliC</i>	H-	H8	100	124.048			0	H8
ERS085431	<i>fliC</i>	H-	H9	99.95	283.015	36snp1indel		1.788	H9
ERS085433	<i>fliC</i>	H-	H9	100	295.631	37snp		1.838	H9
ERS085434	<i>fliC</i>	H-	H39	100	343.823	1snp		0.077	H39
ERS085436	<i>fliC</i>	H-	H39	100	514.031	1snp		0.077	H39
ERS085437	<i>fliC</i>	H-	H10	100	342.423			0	H10
ERS085440	<i>fliC</i>	H-	H5	99.924	299.827	2snp1holes		0.153	H5
ERS139199	<i>fliC</i>	H-	H33	100	77.114			0	H33
ERS139207	<i>fliC</i>	H-	H8	100	55.726			0	H8
ERS139208	<i>fliC</i>	H-	H25	100	7.046	62snp		5.18	H12
ERS139211	<i>fliC</i>	H-	NC	NA	NA			NA	NC
ERS139214	<i>fliC</i>	H-	H10	100	32.675			0	H10

Supplementary Table 5: Serotyping results for Ont, O-rough and H non-motile EPEC isolates

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
ERS139215	<i>fliC</i>	H-	H9	100	60.308	37snp		1.838	H9
ERS139220	<i>fliC</i>	H-	H6	100	81.875	7snp		0.425	NC
ERS139221	<i>fliC</i>	H-	H25	100	43.863	9snp		0.752	H25
ERS139222	<i>fliC</i>	H-	H19	99.945	79.334	1snp1holes		0.055	H19
ERS139226	<i>fliC</i>	H-	H7	100	32.095			0	H7
ERS139231	<i>fliC</i>	H-	H39	100	81.977	1snp		0.077	H39
ERS139232	<i>fliC</i>	H-	H6	100	76.83	7snp		0.425	NC
ERS139237	<i>fliC</i>	H-	H6	100	32.871	8snp		0.486	H6
ERS139239	<i>fliC</i>	H-	H8	100	50.486			0	H8
ERS139245	<i>fliC</i>	H-	H33	100	52.827			0	H33
ERS139246	<i>fliC</i>	H-	H33	100	59.738			0	H33
ERS139252	<i>fliC</i>	H-	H39	100	44.975			0	H39
ERS139254	<i>fliC</i>	H-	H19	99.945	30.896	1snp1holes		0.055	H19
ERS139256	<i>fliC</i>	H-	NC	NA	NA			NA	NC
ERS139257	<i>fliC</i>	H-	H19	96.508	16.902	27snp64holes		1.526	H9
ERS139261	<i>fliC</i>	H-	H8	100	31.164			0	H8
ERS139264	<i>fliC</i>	H-	H11	100	50.218	1snp		0.073	NC
ERS139276	<i>fliC</i>	H-	H8	100	54.568			0	H8
ERS139278	<i>fliC</i>	H-	H2	100	28.806	12snp		0.803	H2
ERS150871	<i>fliC</i>	H-	H33	100	87.918			0	H33
ERS150874	<i>fliC</i>	H-	H33	100	75.486			0	H33
ERS150879	<i>fliC</i>	H-	H2	100	84.74			0	H2
ERS150882	<i>fliC</i>	H-	H10	100	61.873			0	H10
ERS150883	<i>fliC</i>	H-	H9	100	72.286	29snp		1.441	H9
ERS150906	<i>fliC</i>	H-	H10	100	87.46			0	H10

NC = No in silico call was made

NA = Not available

Ont = O non-typeable

OR = O rough

Supplementary Table 5: Serotyping results for Ont, O-rough and H non-motile EPEC isolates

Isolate	Gene	Reported	SRST2	Coverage	Depth	Diffs	Uncertainty	Divergence	BLAST+
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H- = H non-motile

Coverage = percentage of the gene length that was covered

Depth = mean read depth across the length of all alleles which were assigned a top scoring allele number

Diffs = differences between the detected allele and the best scoring allele.

Uncertainty = details of parts of the top scoring alleles for which the depth of coverage was too low to give confidence in the result

Divergence = divergence of allele detected to sequence database (ran with option to report <10% divergence)

Reported =reported phenotype of the isolate

SRST2 = call from short read data and the EcOH database

BLAST+ = call from BLAST analysis of Velvet assemblies and the EcOH database