

Table S7. Allocation of mutational SNPs to lineages by virtual outgroup analysis

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ExPEC Cluster										Outgroup Strains ^g																					
UTI89 ^a	UTI89 site ^b	APEC 01 ^a	APEC 01 site ^b	S88 ^a	S88 site ^b	type ^c	Inferred ancestral base ^d	Lineage inferred to mutate ^e	Support level ^f	CFT073	ED1a	E234869	SMS 3-5	IA139	UMN026	K-12	ATCC 8739	HS	D1 Sd197	CB9615	Sakai	EDL933	IA11	E24377A	SE11	SS Ss046	F2a 301	F2a 2457T	F5 8401	B4 Sb227	B18 BS512
g 975980	a 974947	g 978536	ns	g	APEC	++++	g g g g g	UTI89	++++	c c c c c	536	E234869	SMS 3-5	IA139	UMN026	K-12	ATCC 8739	HS	D1 Sd197	CB9615	Sakai	EDL933	IA11	E24377A	SE11	SS Ss046	F2a 301	F2a 2457T	F5 8401	B4 Sb227	B18 BS512

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ExPEC Cluster										Outgroup Strains ^g																								
UTI89 ^a	UTI89 site ^b	APEC 01 ^a	APEC 01 site ^b	S88 ^a	S88 site ^b	type ^c	Inferred ancestral base ^d	Lineage inferred to mutate ^e	Support level ^f	CFT073	ED1a	E2348/69	SMS 3-5	IA139	UMN026	K-12	ATCC 8739	HS	D1 Sd197	CB96/15	Sakai	EDL933	IA11	E24377A	SE11	SS Ss046	F2a 301	F2a 2457T	F5 8401	B4 Sb227	B18 BS512			
a 3079264	g 3093771	g 3011141	s	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	
g 307927	t 3094434	t 3011804	ns	t	UTI89	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t
t 3080405	t 3094552	g 3011922	ns	t	S88	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	
t 3081153	c 3095660	c 3013030	s	c	UTI89	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	
g 3082908	a 3097415	a 3014785	ns	a	UTI89	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	
a 3094027	t 3108534	a 3025904	ns	a	APEC	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	
t 3098812	a 3113319	a 3030689	ns	t	UTI89	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	
t 3104311	c 3118818	t 3036188	ns	t	APEC	++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	
c 3105017	g 3119524	g 3036894	ns	g	UTI89	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
10 3115492	- 3129998	- 3047368	indel	?	UTI89/AS	+/-																												
t 3119787	t 3134284	a 3051654	s	t	S88	++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	
a 3121450	g 3135947	g 3053317	ns	g	UTI89	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	
c 3123594	c 3140677	t 3055461	ns	c	S88	++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c		
a 3129390	g 3146473	a 3061257	nc	a	APEC	++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	
a 3133250	c 3150333	c 3065117	ns	c	UTI89	+++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c		
c 3133803	t 3150886	t 3065670	s	t	UTI89	+++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t		
- 3137695	3 3154779	- 3069562	ins	3	APEC	-	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3		
- 3137689	- 3154781	3 3069563	ins	3	S88	-	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3			
- 3137690	9 3154782	9 3069566	del	9	UTI89	+++	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9			
t 3139660	c 3156755	c 3071539	ns	c	UTI89	++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c		
g 3145220	a 3162315	g 3077099	ns	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
t 3149493	a 3166588	a 3081372	nc	t	AS	++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t		
g 3155620	a 3172715	g 3087499	s	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
a 3166862	g 3183957	g 3098741	nc	g	UTI89	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
g 3173049	t 3190144	a 3104928	s	g	AS	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
c 3173298	t 3190393	c 3105177	s	c	APEC	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	
a 3174760	a 3191855	t 3106639	nc	a	S88	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	
g 3188210	t 3205305	g 3120089	ns	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
a 3188698	c 3205793	c 3120577	s	c	UTI89	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c		
c 3194119	a 3212114	c 3125998	ns	c	APEC	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c		
g 3197069	a 3214164	a 3128948	s	g	AS	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
g 3199881	a 3216976	g 3131760	s	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
g 3209368	a 3226463	a 3141247	s	s	AS	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
a 3210038	g 3227133	g 3141917	ns	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
c 3225664	t 3242759	c 3157543	ns	c	APEC	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	
a 3229145	c 3246240	c 3161024	ns	c	UTI89	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c		
a 3230093	c 3247188	c 3161972	s	a	AS	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	
t 3242026	c 3259121	c 3173905	ns	c	UTI89	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c		
t 3245947	c 3263042	c 3177826	ns	t	AS	++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t		
t 3248554	g 3265649	g 3180433	s	g	UTI89	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
c 3279697	t 3269792	c 3211576	ns	c	APEC	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	
a 3280580	g 3297675	g 3121459	s	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	
g 3285534	g 3302629	a 3217413	s	g	S88	+++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	
- 3287997	g 3316787	a 3231571	nc	g	S88	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	
- 3287974	a 3324534	g 3239318	nc	g	APEC	+++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	
- 3287974	g 3340695	a 3255479	nc	g	S88	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	
- 3287974	a 3342053	g 3256837	nc	g	APEC	+++	g	g	g	g	g</																							

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ExPEC Cluster										Outgroup Strains ^g																							
UTI89 ^a	UTI89 site ^b	APEC 01 ^a	APEC 01 site ^b	S88 ^a	S88 site ^b	type ^c	Inferred ancestral base ^d	Lineage inferred to mutate ^e	Support level ^f	CFT073	ED1a	E234869	SMS 3-5	IA139	UMN026	K-12	ATCC 8739	HS	D1 Sd197	CB9615	Sakai	EDL933	IA11	E24377A	SE11	SS Ss046	F2a 301	F2a 2457T	F5 8401	B4 Sb227	B18 BS512		
g	3816742	g	3849518	a	3764277	ns	g	S88	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g
-	3819082	1	3851868	1	3766627	del	1	UTI89	+++	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
-	3820270	8	3853048	-	3767806	ins	-	APEC	+++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
1	3820615	-	3853399	-	3768150	del	1	AS	+++	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
g	3824281	a	3857065	a	3771816	s	g	AS	+++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g
a	3825492	g	3858276	g	3773027	ns	g	UTI89	+++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g
t	3829512	c	3862296	c	3777047	ns	c	UTI89	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c
a	3831347	g	3864131	g	3778882	s	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	
a	3832427	g	3865211	g	3779962	ns	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
t	3835020	t	3867804	c	3782555	s	t	S88	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t			
g	3843994	t	3876781	t	3791529	nc	AS	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
g	3845773	g	3878560	t	3793308	nc	g	S88	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
c	3853083	t	3885870	c	3800618	ns	c	APEC	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
a	3859041	g	3891828	a	3806576	s	a	APEC	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a			
g	3864493	a	3897280	g	3812028	ns	?	APEC	+/-																								
c	3870043	a	3902838	c	3817578	ns	c	APEC	++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
a	3873522	g	3906317	g	3821057	s	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
t	3876221	c	3909016	t	3823756	s	t	APEC	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t				
a	3877813	a	3910608	t	3825348	ns	a	S88	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a				
g	3880172	g	3912967	a	3827707	ns	g	S88	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
g	3880907	t	3913702	t	3828442	ns	t	UTI89	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t				
a	3881372	g	3914167	g	3828907	ns	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
c	3884077	c	3916872	t	3831612	ns	c	S88	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c				
g	3891483	g	3924278	a	3839018	s	g	S88	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
g	3892367	a	3925162	g	3839902	ns	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
c	3904420	t	3937215	t	3851955	ns	t	UTI89	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t				
a	3908902	g	3941697	a	3856437	ns	a	APEC	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a				
g	3910609	a	3943404	a	3858144	ns	g	AS	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
t	3911193	t	3943988	c	3858728	ns	t	S88	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t				
a	3915496	g	3948291	g	3863031	s	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g				
c	3918150	c	3950945	a	3865685	s	c	S88	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c				
g	3923587	a	3956382	g	3871122	nc	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
a	3928162	g	3960957	g	3875697	ns	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
c	3931406	t	3964201	t	3878941	nc	c	AS	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c				
1	3931749	-	3964543	1	3879284	del	1	APEC	++++	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
a	3932330	a	3965124	c	3879865	ns	a	S88	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a				
g	3942924	g	3975718	a	3890459	ns	g	S88	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g				
t	3947345	t	3980139	g	3894880	ns	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g				
a	3950138	a	3982932	g	3897673	nc	a	S88	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a					
a	3950965	g	3983759	a	3898500	ns	a	APEC	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a					
a	3952712	c	3985506	c	3900247	s	c	UTI89	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c					
1	3961295	1	3994099	-	3908839	del	1	S88	++++	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
t	3964225	t	3997019	s	3911759	s	t	S88	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t					
g	3965091	g	3997885	a	3912625	ns	g	S88	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g				
a	3967376	a	4000170	c	3914910	s	c	S88	-	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c					
g	3969624	a	4002418	a	3917158	s	g	AS	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g				
c	3994180	a	4026974	t	3941714	s	a	UTI89	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a					
g	3995800	a	4028594	g	3943334	ns	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g				
10	4001950	-	4034743	-	3949483	del	10	AS	++++	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10				
-	4001959	10	4034744	-	3949483	ins	10	APEC	-	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10				
1	4001960	1	4034754	-	3949483	del	1	S88	++++																								

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ExPEC Cluster										Outgroup Strains ^g																			
UTI89 ^a	UTI89 site ^b	APEC 01 ^a	APEC 01 site ^b	S88 ^a	S88 site ^b	type ^c	Inferred ancestral base ^d	Lineage inferred to mutate ^e	Support level ^f	CFT073	ED1a	E234869	SMS 3-5	IA139	HS	D1 Sd197	CB9615	Sakai	EDL933	IA11	SE11	SS Ss046	F2a 301	F2a 2457T	F5 8401	B4 Sb227	B18 BS512		
1	4124218	1	4157025	-	4071738	del	1	S88	++++	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
g	4133561	a	4166358	a	4081071	ns	a	UTI89	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a		
a	4138967	a	4171764	g	4086477	s	a	S88	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a		
g	4157079	t	4189876	t	4104589	s	g	AS	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g		
c	4158139	t	4190936	c	4105649	ns	c	APEC	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
g	4158435	g	4191232	a	4105945	nc	-	S88	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
5	4158742	-	4191538	-	4106251	ins	-	UTI89	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
c	4160304	g	4193096	g	4107809	ns	-	UTI89	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a			
g	4168607	g	4201399	a	4116112	s	g	S88	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
a	4172397	g	4205189	g	4119902	nc	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
-	4172678	5	4205471	-	4120183	ins	-	APEC	+++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
c	4173610	t	4206407	t	4121115	ns	c	AS	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
g	4173711	t	4206508	g	4121216	ns	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
t	4174585	a	4207382	a	4122090	nc	t	AS	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t			
g	4176975	a	4209772	g	4124480	s	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
c	4179841	a	4212638	s	4127346	s	a	UTI89	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a			
g	4183713	g	4216510	t	4131218	nc	g	S88	++	a	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
a	4187124	g	4219921	g	4134629	ns	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
c	4202885	a	4235682	a	4150390	nc	c	AS	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
g	4204502	a	4237299	a	4152007	nc	a	UTI89	++	a	u	g	a	g	a	a	a	a	a	a	a	a	a	a	a	a			
a	4204544	g	4237341	g	4152049	nc	a	AS	++	a	a	a	a	a	-	a	a	a	a	a	a	a	a	a	a	a			
c	4204887	c	4237684	t	4152392	ns	c	S88	++	c	c	c	c	c	c	t	c	c	c	c	c	t	t	t	t	t			
a	4207259	g	4240056	g	4154764	nc	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
g	4208037	t	4240834	g	4155542	ns	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
c	4214370	c	4247167	t	4161875	ns	c	S88	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
t	4216893	g	4249690	t	4164398	ns	t	APEC	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t			
t	4218285	c	4251082	t	4165790	s	t	APEC	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t			
t	4239927	c	4272724	c	4187432	ns	c	UTI89	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
g	4242503	c	4275300	g	4190008	nc	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
6	4247939	-	4280735	-	4195443	del	6	AS	++	6	6	6	6	6	6	-	6	-	-	-	6	6	6	6	6	6	6		
6	4247935	6	4280736	-	4195443	del	6	S88	++	6	6	6	6	6	6	-	6	-	-	-	6	6	6	6	6	6	6		
g	4247989	g	4280780	a	4195482	s	g	S88	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
t	4250508	c	4283299	c	4198001	s	g	UTI89	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
g	4256863	a	4288878	a	4203580	ns	g	AS	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
a	4260364	g	4292379	g	4207081	s	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
g	4261500	g	4293515	a	4208217	ns	s	S88	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
t	4264120	t	4296135	g	4210837	ns	t	S88	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t			
g	4267068	a	4299083	a	4213785	ns	g	AS	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
t	4267978	c	4299993	c	4214695	ns	c	UTI89	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
c	4277937	a	4309952	c	4224505	ns	c	APEC	++	c	c	c	c	c	c	t	t	c	t	t	c	c	c	t	t	t			
g	4282540	t	4231455	t	4229108	ns	g	AS	++	a	g	a	g	a	a	S88	+++	a	a	a	a	a	a	a	a	a	a		
a	4287127	a	4319142	g	4233695	ns	a	UTI89	+++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
c	4288098	t	4320113	t	4234666	ns	c	AS	+++	a	a	a	a	a	a	S88	+++	a	a	a	a	a	a	a	a	a	a		
a	4303644	a	4335659	g	450212	nc	a	UTI89	+++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
t	4308604	c	4340619	c	4255172	ns	c	APEC	+++	a	a	a	a	a	a	UTI89	+++	a	a	a	a	a	a	a	a	a	a		
a	4308862	g	4340877	a	4255430	ns	a	AS	+++	g	g	g	g	g	g	g	UTI89	+++	g	g	g	g	g	g	g	g	g	g	
a	4308923	g	4340938	g	4255491	s	g	UTI89	+++	g	g	g	g	g	g	g	g	UTI89	+++	g	g	g	g	g	g	g	g	g	g
t	4314651	c	4346666	c	4261219	ns	c	APEC	+++	c	c	c	c	c	c	c	c	UTI89	+++	a	a	a	a	a	a	a	a	a	a
t	4319323	a	4351338	a	4265891	ns	a	AS	+++	a	a	a	a	a	a	a	UTI89	+++	a	a	a	a	a	a	a	a	a	a	
1	4321682	1	4353707	-	4268259	del	1	S88	+++	1	1	-	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
-	4323809	-	4355834	17	4270376	ins	17	S88	++	-	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17		
t	4326969	a	4358981	a	4273536	nc	a	UTI89	++	a	a	t	a	a	a	a	UTI89	++	a	a	a	a	a	a	a	a	a	a	
-	4326980	1	4358993	-	4273547	ins	1	APEC	-	1	-	1	1	-	-	1	-	-	-	-	-	-	-	-	-	-			
c	4327063	t	4359077	c	4273630	s	t	APEC	-	t	t	t	t	t	t	t	UTI89	-	t	t	t	t	t	t	t	t	t	t	
g	4327420	a	4359434	g	4273987	s	g	APEC	+++	a	g	g	g	g	g	g	g	UTI89	+++	c	c	c	c	c	c	c	c	c	c
c	4327628	c	4359642	t	4274195	ns	c	S88	+++	c	c	c	c	c	c	c	c	UTI89	+++	c	c	c	c	c	c	c	c	c	c
t	4328003	c	4360017	t	4274570	ns	c	APEC	-	c	c	c	c	c</td															

Table S7. Allocation of mutational SNPs to lineages by virtual outgroup analysis

Table S7. Allocation of mutational SNPs to lineages by virtual outgroup analysis

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ExPEC Cluster							Outgroup Strains ^g																											
UTI89 ^a	UTI89 site ^b	APEC 01 ^a	APEC 01 site ^b	S88 ^a	S88 site ^b	type ^c	Inferred ancestral base ^d	Lineage inferred to mutate ^e	Support level ^f	CFT073	ED1a	536	E2348/69	SMS 3-5	IA139	UMN026	K-12	ATCC 8739	HS	D1 Sd197	CB96/15	Sakai	EDL933	IA11	E24377A	SE11	SS Ss046	F2a 301	F2a 2457T	F5 8401	B4 Sb227	B18 BS512		
g	4913801	t	4930030	t	4891877	ns	t	UTI89	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t		
c	4919522	t	4935751	t	4899954	s	t	UTI89	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t			
c	4945745	t	4961974	c	4911459	s	c	APEC	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
c	4949832	a	4966061	c	4918134	s	c	APEC	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
t	4974091	g	4990320	t	4940268	ns	t	APEC	++++	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t				
c	4974109	t	4990338	c	4940286	s	c	APEC	++++	c	c	c	c	t	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c			
a	4976994	g	4993223	g	4943169	s	a	AS	++	a	a	a	a	g	a	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g			
a	4983543	g	4999772	g	4949716	s	a	AS	++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a			
a	4983865	g	5000094	a	4950038	nc	a	APEC	++++	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a				
t	4986069	g	5002299	g	4952310	s	g	UTI89	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g				
g	4988688	a	5004918	a	4954929	nc	?	UTI89/AS	+-																									
a	4988713	g	5004943	g	4954954	nc	?	UTI89/AS	+-																									
c	4989741	t	5005971	c	4955982	ns	?	APEC	+-																									
g	4989979	a	5006209	a	4956220	s	?	UTI89/AS	+-																									
c	4990632	t	5006862	t	4956873	ns	c	AS	++																									
a	4992238	g	5007574	g	4957585	ns	g	UTI89	++++																									
g	4996702	a	5012038	a	4962049	s	g	AS	++	g				g																		t		
g	5001290	g	5015977	t	4965987	s	g	S88	++	g	g																				t			
a	5009646	g	5026944	a	4976954	ns	a	APEC	+			a		a	a																			
g	5024687	g	5041982	a	4991992	s	g	S88	++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g					
g	5037621	a	5053886	g	5003896	s	g	APEC	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g					
c	5040452	t	5056717	c	5006930	s	c	APEC	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c						
c	5051251	t	5067516	c	5017778	s	c	APEC	++++	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c						
g	5051312	g	5067577	t	5017839	ns	g	S88	++++	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g						

^aNumbers in place of bases indicates number of bases where >2 bases inserted or deleted. In these cases "-" indicates absence of these bases.^bFor indels the base indicated is the base before the insertion or deletion in the strain.^c s: synonymous; ns: non-synonymous; nc: in non-coding gene; i: intergenic; ins: small insert; del: small deletion; indel: the small indels that can't be allocated^d The base in the common ancestor of the 3 ExPEC strains as inferred from outgroup analysis.^e AS: allocated to the lineage to the common ancestor of APEC 01 and S88; UTI89/AS: allocated to the divergence between UTI89 and the common ancestor of APEC 01 and S88 (strain not specified); APEC/S88: allocated to the divergence between APEC 01 and S88 lineages (lineage not specified)..^f Level of support for allocation of mutation as given in previous column⁺⁺⁺ agreement is high - 8 or more outgroup strains with expected base and at most 1 with an alternative base, and at least 2 of the CFT073, ED1a and 536 support the expected base)⁺⁺ agreement good - 4 or more outgroup strains with expected base and at most 1 with an alternative base, and at least 2 of the CFT073, ED1a and 536 support the expected base)⁺⁺ supported by at least 2 of the CFT073, ED1a and 536 regardless of situation with other outgroup strains

+ no conflict but very limited support as either site absent or conflict in all of CFT073, ED1a and 536, or conflict among them, and/or support is less than required for any of the higher levels of support.

+/- no conflict but no support (base not present in any outgroup OR base when present is not that in any of the ExEPEC strains OR both alternative lineages supported equally).

- conflict data implies 2 mutations at that site - eg in the ancestor of 3 ExEPEC strains before isolation and again in one of the lineages.

^g Base, number or "-" indicates the base type or absence of the base. Blank means the site not present.