Table 8. Intergenic mutations in CF airways isolates from 29 different patients

Type of mutation	Gene with 5' untranslated region containing the mutation ^{†‡}	Distance from mutation to transcription start site of gene, bp	Nucleotide prior to mutation	Nucleotide after mutation	Patient no.	Mutated isolate(s), named by patient age (yr) when isolate was collected	Isolate(s) not containing the mutation, named by patient age (yr) when isolate was collected [§]
intergenic SNP	probable permease of ABC transporter (PA0313)	12	Т	С	10	15.4A, 15.4B	6.7
intergenic 1-bp deletion	*transcriptional regulator <i>vfr</i> (PA0652)	105-110	GGGGGG	GGGGG	21	14.3	0.5, 10.7, 15.2, 19.5
	hypothetical protein (PA0653)	162-167					
intergenic SNP	probable acyl-CoA dehydrogenase (PA0507)	23	С	Т	4	9.1A	3.0, 9.1B
intergenic SNP	RND multidrug efflux membrane fusion protein <i>mexE</i> precursor (PA2493)	115	С	Т	21	19.5	0.5, 10.7, 14.3, 15.2
intergenic SNP	probable major facilitator superfamily (MFS) transporter (PA3573)	317	Т	С	19	7.2	16.4, 22.5

Type of mutation	Gene with 5' untranslated region containing the mutation ^{†‡}	Distance from mutation to transcription start site of gene, bp	Nucleotide prior to mutation	Nucleotide after mutation	Patient no.	Mutated isolate(s), named by patient age (yr) when isolate was collected	Isolate(s) not containing the mutation, named by patient age (yr) when isolate was collected [§]
	*probable transcriptional regulator <i>nalD</i> (PA3574)	48					
intergenic SNP	probable aldehyde dehydrogenase (PA0366)	227	A	G	20	17.3	9.9
	probable transcriptional regulator (PA0367)	63					
intergenic 1bp deletion	hypothetical protein (PA1333)	41	ccccc	cccc	20	17.3	9.9
Intergenic SNP	* transcriptional regulator of anaerobic metabolism <i>anr</i> (PA1544)	65	С	Т	23	6.2	10.0, 14.0
	hypothetical protein (PA1545)	181					
intergenic SNP	transcriptional regulator <i>rhIR</i> (PA3477)	103	С	Т	14	13.1B	4.3, 13.1A

SNP, single-nucleotide polymorphism.

†Genes with names preceded by an asterisk were chosen for sequencing on the basis of other studies. The remaining 24 genes were mutated in the 96-month isolate of patient 1.

[‡]Two genes are listed for a single intergenic mutation when both genes are transcribed in opposite orientations and share the intergenic region in their transcription start sites.

§For each mutation, all isolates listed are clonally related and are from the same patient.