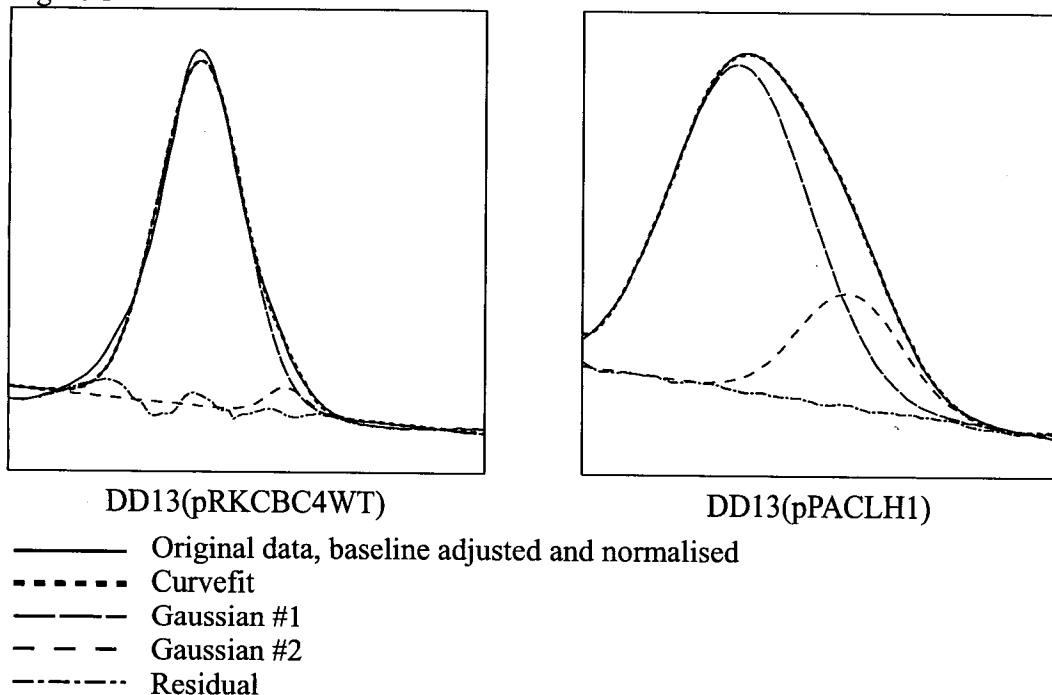


Supplementary Information

Figure 1



The deconvolutions of the WT and LH1 C-terminal swap mutant are shown as representative of all the deconvolutions for which the data is given below. Whilst the fit for the DD13(pPACLH1) spectrum is good with a small residual, that for DD13(pRKCBC4WT) is a poor fit, especially on the blue side of the peak. The fits were performed on the part of the 80K absorbance spectrum from 812-920 nm of each strain.

Table 1

	Chi ²	R ²	Std. Error	Gaussian	Area	Centre	Height	Width
DD13(RKCBC4WT)	44.938	0.996	0.026	#1	30.22	855.37	1.27	22.40
				#2	1.12	875.01	0.10	10.75
DD13(PACLH1)	0.829	1.0	0.003	#1	24.40	847.58	0.62	37.35
				#2	6.34	872.69	0.22	27.57
DD13(PACLH2mol)	20.244	1.0	0.008	#1	21.58	840.30	0.68	30.28
				#2	1.47	864.96	0.08	18.10
DD13/DG2(RKCBC4WT)	24.135	0.996	0.030	#1	33.17	857.17	1.35	23.04
				#2	1.29	877.77	0.10	12.15
DD13/DG2(PACLH1)	6.859	0.999	0.005	#1	20.28	844.71	0.60	31.97
				#2	1.07	869.57	0.06	17.62
DD13/DG2(PACLH2mol)	23.646	0.999	0.007	#1	19.24	844.20	0.56	32.28
				#2	0.64	869.52	0.04	15.01