Gene and position	Strains name (Plr+/Plr-)	Distance from dif (kb)	Position (kb) (minute)	Gene function	Filamentation		Viability index	
					Plr+	Plr-	Plr+	Plr-
zch237 *ycgU*	XL215 XL245	-336,2	1252 27	FU	+	+++	96	73
pyrF	XL210 XL240	-248,8	1339,9 28,88	Orotidine-5'-phosphate decarboxylase	+	++	97,5	81,8
zda192 *stfR*	XL236 XL376	-150,9	1438,8 31,01	Phage lambda stf gene homolog in prophage Rac	+	++	92,5	84,9
MR6 *ydbD*	XL157 XL167	-113.5	1473,2 31,75	FU	+	++	92,5	77,7
zdc310 *sfcA*	XL237 XL377	-35,3	1553,5 34,23	Putative malic enzyme, NAD linked	+	++	97,9	81
zdd346 *yneL*		-0,696	1588 34,23	FU				
dif		0	1588,8 34,25	Chromosome dimer resolution site				
zdd347 *hipA*		0,994	1589,7 34,27	probable role in cell division (hipAB operon)				
Sp17 *ydeK*	XL162 XL152	7,3	1596,1 34,32	FU	-	+	100	88,5
zdd370 *yneI*	XL379 XL239	25	1612 34,74	FU	+	++	97,4	77,8
MR4 *ydfE*	XL166 XL156	59.5	1648 35,53	FU	+	++	94,7	81,1
Zdh201 *ydh)*	XL381 XL391	127,6	1716,4 37	FU	+	++	96,8	87,3
Zeq225 *yeaI*	XL385 XL395	280,2	1869 40,28	FU	ND	ND	97	77,8
HisG	XL244 XL214	499,4	2088,2 45,01	ATP phosphoribosyl transferase	++	+++	91,9	76

Table 1: Intra-Ter inversions. Inversions were selected between the *dif* position (*zdd346::lacZ::attB* or *zdd347::lacZ attB* and the indicated *attP* insertion. Given are: the position of *attP* insertion together with the gene concerned, the name of the strains carrying inversion (Plr+ and Plr-), the distance of *attP* from *dif* (negative values for replichore I and positive for replicore II), the position of *attP* on the chromosome map in kb and minutes, the function of the gene disrupted by the *attP* insertion (FU: function unknown; data from the colibri webb site: http://genolist.pasteur.fr/Colibri/). The percentage of filamentous cells in exponentially growing cultures was estimated by FACS as described in Bigot et al., 2004: +++: 20 to 30% filament (as for a *dif* –deleted strain); ++: 10 to 20% filament; +: 1 to 10% filament; -: no filament; ND: not done. The viability index was measured using the co-culture assay (Methods, same values as in Figure 2).

Gene and position	Strains name Plr+/Plr-	Distance from dif (kb)	Position (kb) (minute)	Gene function	Temperature sensitivity Plr+	Plr-	Generation time Plr+	Plr-
metE	XL246 XL216	-2217,4	4010,6 86,45	Tetrahydropteroyltriglutamate methyltransferase	+++	+++	94	180
purA::	XL211 XL241	-1825,5	4402.3 94,89	Adenylosuccinate synthetase	+++	+++	112	220
sp5 (yafT-yafF)	XL161 XL151	-1565	237,3 5,12	FU	+++	+++	92	110
sp39 (ybgS-aroG)	XL154 XL165	-800	784,76 16,92	aroG DAHP synthetase ybgS Function unknown	+	++	75	87
aroA	XL219 XL249	-630,8	958 20,65	3-Enolpyruvylshikimate-5-phosphate synthetase	+	++	70	76,8
napA722	XL383 XL393	707,2	2300,8 49,54	Nitrate redictase homologue	+	++	ND	
pheA	XL244 XL214	1147	2735,8 58,97	Chorismate mutase-P-prephenate dehydratase	+	+++	73	180
sp34 ygcY	XL163 XL153	1330	2918,8 62,89	FU	++	++	ND	
sp122 gspF	XL165 XL155	1868,7	3457,5 74,53	General secretory pathway genes of unknown function	++	++	86	180
malA	XL248 XL218	1962	3550,1 76,47	Maltodextrine phosphatase	++	++	97	196

Table 2: Inter-domain inversions. Inversions were selected between the *dif* position (*zdd346::lacZ::attB* or *zdd347::lacZ attB* and the indicated *attP* insertion. Given are: the position of *attP* insertion with the gene concerned, the name of the strains carrying inversion (Plr+ and Plr-), the distance of *attP* from *dif* (negative values for replichore I and positive for replicore II), the position of *attP* on the chromosome map in kb and minutes, the function of the gene disrupted by the *attP* insertion (FU: function unknown; data from the colibri webb site: http://genolist.pasteur.fr/Colibri/). The level of sensitivity to high temperature is shown (estimated from the ratio of plating efficiency at 42 and 30°C in 10µl spots, Methods and Figure 4): +: ability to form colonies not affected but growth rate on plate reduced (colonies are smaller at 42°C than at 30°C for the same incubation time); ++: plating efficiency 10 to 1000 time reduced; +++: plating efficiency more than 1000 time reduced (only few big colonies corresponding to reverted clones are growing). Generation times in permissive conditions (synthetic medium at 30°C) were calculated from growth curves (ND: not done; Methods).