A

LINE	UAS-DS6K	ap-Gal4	UAS-dE/D3E	Chsome	Map	nucleotide	gene
14,020	A/P up - -	A/P up - - -	A/P up - -	X	2F	2211773	
25,179	TV down ++	(----)	TV down ++	X	3C	3057186	
25,198	TV down ++	TV (----)	TV down +	X	3C	3057186	
25,159	down +++	(----)	down ++	X	3F	3690485	
26,187	down +++	(----)	down ++	X	5E	6177714	
22,155	down ++++	down +	down +++	X	11B	12365975	rab 40
25,175	down +++	(----)	down ++	X	12E	14215238	
11,018	down +++	(----)	down +++	X	12F	14726697	
20,167	A/P down +++	A/P down ++	A/P down +++	X	18B	19154193	
12,002	down +++	(----)	down ++	X			
13,036	down +++	(----)	down +++	X			
18,250	down ++++	down +	down +++	X			
24,183	down +++	(----)	down +	X			
18,113	down +++	(----)	down ++	2	24E	4282935	
26,080	blister up - -	blister up - -	blister up - -	2	28A	7576629	
23,024	down ++++	(----)	down ++	2	28D	7991728	peste
28,133	down +++	(----)	down ++	2	28D	7991787	peste
16,219	addV down +++	addV	addV down +++	2	29A	8271542	
13,148	down +++	(----)	down ++	2	30D	9782358	
24,188	up - -	up - -	up - -	2	34C	13549293	
27,136	down ++++	(----)	down ++++	2	38C	20310996	spir
15,196	down +++	(----)	down +++	2	38C	20311312	spir
19,020	down ++++	(----)	down ++++	2	38C		spir
25,010	down +++	(----)	down ++	2	41F	1509876	
12,177	fold down +++	fold	fold down +++	2	44B	4119835	
28,122	fold down +++	fold+	fold down ++	2	44D	4558214	
13,116	up -	up - - - -	up -	2	45F	5440342	
23,014	down ++++	(----)	down +++	2	46F	6107230	DHR3
12,218	down ++++	(----)	down +++	2	46F	6107302	DHR3
25,138	up - - - -	up - - - -	up - - - -	2	47A	6366134	
8,195	down +++	(----)	down ++	2	47A	6414247	
26,092	addV down +++	addV +	addV down ++	2	47F	7339990	
16,217	A/P up - -	A/P up - - -	A/P up - -	2	49B	8474745	
11,124	fold down ++++	fold down ++	fold down ++++	2	50C	9894698	
17,074	A/P up - - - -	blister up - - - -	A/P up - - - -	2	50F	10155404	
12,190	A/P up - -	A/P up - - -	A/P up - -	2	54B	13307092	
27,116	A/P up - - - -	blister up - - - -	A/P up - - - -	2	54B	13307828	
23,174	A/P up - -	A/P up - - - -	A/P up - -	2	54B	13307943	
13,211	blister up -	blister up - -	blister up -	2	54B	13308389	
24,095	blister up -	A/P up - -	blister up -	2	54B	13308443	
12,205	fold down ++++	fold down ++	fold down ++++	2	54C	13345933	
20,100	down +++	(----)	down ++	2	56D	15245342	
9,100	fold down +++	fold down +	fold down +++	2	56D	15519538	
4,035	addV down +++	addV	addV down ++	2			
7,064	down +++	(----)	down ++	2			
10,118	fold down +++	fold down +	fold down +++	2			
11,051	A/P down ++	(----)	A/P down ++	2			
20,176	up -	up - -	up -	2			
26,015	fold down ++++	fold down ++++	fold down ++++	2			
26,057	down +++	(----)	down ++	2			
27,110	up - -	up - - - -	up - -	2			
15,239	down +++	down +	down +	3	61A	131411	PDK1
15,235	down ++++	down +	down ++	3	61A	131694	PDK1
26,020	down ++++	down +	down +++	3	61A	131712	PDK1
14,342	down ++++	down +	down ++	3	61A	131771	PDK1
22,068	down ++++	down +	down +++	3	61A	131771	PDK1
25,092	down ++++	down +	down ++	3	61A	131781	PDK1
21,024	down ++++	down +	down +++	3	61A	131783	PDK1
18,193	down ++++	down +	down +++	3	61A	131807	PDK1
5,045	down ++++	down +	down ++	3	61A	131885	PDK1
23,180	down ++++	down +	down +++	3	61A	131955	PDK1
28,118	A/P down ++	A/P down +	A/P down ++	3	61D	883054	
21,121	up -	up - -	up -	3	64C	4750797	
17,251	down +++	(----)	down ++	3	66A	7798582	
24,061	down ++++	down +	down +++	3	66E	8942100	CPEB
25,112	down +++	(----)	down +++	3	69A	12259860	
18,100	fold down ++++	fold +	fold down ++	3	71E	15586673	
22,048	A/P down ++++	A/P down +	A/P down ++++	3	76D	19889519	

24,159	fold down ++	fold down +++	fold down +++	3	78C	21233150	
21,070	down +++	down +	down ++	3	79A	21763733	
10,045	down ++++	down +	down ++++	3	85B	4723958	
11,152	down ++++	down ++++	down ++++	3	89B	12106222	
24,034	fold down +++	fold down ++	fold down +++	3	89F	12944822	
26,125	up - -	Up - - - -	up - -	3	93B	16890857	
10,116	down +++	(----)	down ++	3	97D	22702732	
13,123	down +++	(----)	down ++	3	99A	25081089	
13,145	down +++	down +	down ++	3	99C	25585909	
26,094	down +++	(----)	down ++	3	99D	25758758	
17,025	down ++	(----)	down +	3	100F	27677651	
22,067	down ++++	down +	down +++	3	100F	27761974	PTB
26,139	down +++	(----)	down +++	3	100F	27763278	PTB
12,046	down +++	(----)	down +	3	100F	27810394	PTB
6,077	down +++	(----)	down +	3	100F	27811458	PTB
6,027	down ++	(----)	down +	3			
12,100	up -	up - -	up -	3			
12,163	down +++	down +	down +++	3			
16,030	down +++	(----)	down +++	3			
17,203	up - - -	up - - - -	up - - -	3			
19,082	down +++	down +	down ++	3			
19,100	down ++++	(----)	down +++	3			
20,131	down ++++	(----)	down +++	3			
22,105	up -	up -	up -	3			
23,129	down +++	down +	down ++	3			
27,161	down +++	(----)	down +++	3			
26,087	down +++	(----)	down +++	4			

B

Class	**phenotype description**
down ++++	very strong bending down
down +++	strong bending down
down ++	intermediate bending down
down +	bending down as dS6k effect
(----)	flat wing, similar to wild type
Up **-**	wing bent up weakly
Up **- -**	wing bent up strongly
Up **- - - -**	extreme bent up of the wing
A/P	effect following antero-posterior axis (width effect)
TV	veins thicker
fold	wing folded
addV	additional veins
blister	default of wing blades apposition
@	cytogenic location mapped
	irrelevant for dS6K
	effect on wing differentiation
	suppressor
	antero/posterior effect
	similar enhancer with either kinase
	enhancer, greater with dS6K than active-mS6K
	Strong enhancer

Table S1. Screening for modulators of dS6K. (A) The 95 EP lines finally retained are listed. Column legend: **line**, EP number; **UAS-dS6K**, phenotype when co-induced with dS6K; **ap-Gal4**, phenotype when induced alone; **UAS-dE/D3E**, phenotype when co-induced with the active mammalian S6K; **Chsome**, chromosomal location; **Map**, cytological location; **nucleotide**, genomic location according to the flybase consortium; **gene**, potential candidate. (B) Description of the phenotypes indicated in A and of classes of enhancers or suppressors regarding the color usage.