

Fig. S1. Sequences of transgenes and probes used in Fujioka et al., 2012.

transgenes and probes	relative to TSS of <i>slp1</i> (nt)		R. enzyme sites		Flybase (r5.22) coordinates		sequence of: 5' end	3' end, reverse complement
			5'	3'				
u8766	-8713	-6509			3816967	3819171	TAGAGCCTTCAAAGGTTTGCTAAAAGTTT	GGCTAACTGACTCAAGTACTAGTTGAAATC
u8781	-8713	-8072		Bgl2	3816967	3817608	TAGAGCCTTCAAAGGTTTGCTAAAAGTTT	GATCTTCAATCACATCCCCTTGGC
u8172	-8075	-7148	Bgl2	EcoRI	3817605	3818532	GATCTTCAGGATATTCAGCACATGCAT	AATTCGTCGCAGTCTGAGGATTTTC
u8166	-8075	-6509	Bgl2		3817605	3819171	GATCTTCAGGATATTCAGCACATGCAT	GGCTAACTGACTCAAGTACTAGTTGAAATC
u8159	-8075	-5868	Bgl2	Pvu2	3817605	3819812	GATCTTCAGGATATTCAGCACATGCAT	CTGGCAAATTTTGTGATGACCAATGGTTGAG
u7250	-7174	-4993			3818506	3820687	GTGAAAATCCTAGCACTGCGACGAATTC	CGCCTTATCATCGTCGCCGTGATTTTC
u5534	-5512	-3440			3820168	3822240	GCGTCCACAGTCCACAGTCCGCAGGA	CTGCACTTCAGGTAGTGGGGTAAATC
u5547	-5512	-4671		Nhe1	3820168	3821009	GCGTCCACAGTCCACAGTCCGCAGGA	CTAGCTCCCTTCACTCTTCTCGAT
u4734	-4675	-3440	Nhe1		3821005	3822240	GCTAGCTGGGAGATTGATCTACGAAT	CTGCACTTCAGGTAGTGGGGTAAATC
u4739	-4675	-3937	Nhe1	Nsi1	3821005	3821743	GCTAGCTGGGAGATTGATCTACGAAT	TAAAACTGGAAGGATCTCGTCGGCT
u3918	-3929	-1777			3821751	3823903	TGTCGGCAATCCCAGTGCCAACCGCA	ACAATGGAGGAGTTGGGAAGAAAAA
u3925	-3929	-2522		Aat2	3821751	3823158	TGTCGGCAATCCCAGTGCCAACCGCA	CGTGGTAAAACGAATTGATTAGCGA
u3931	-3929	-3056			3821751	3822624	TGTCGGCAATCCCAGTGCCAACCGCA	ATCTTCGCATTTGTCGCGCACAGC
B1	-3929	-3750			3821751	3821930	TGTCGGCAATCCCAGTGCC	GCCTTTGACAACCTTATAGC
B1a	-3911	-3869			3821769	3821811	<i>CCAACCGCATGGACAACCTTAATCAATAAGTCGCAGTCGCGCC</i>	
B1 mut a							<i>CCAACCGCATGGCCAACTCGCGCAATAAGTCGCAGTCGCGCC</i>	
B1b	-3841	-3800			3821839	3821880	<i>GTGCCTCGGTGTGGAAGTATCAATTATAGTGGGTGTGACT</i>	
B1 mut b							<i>GTGCCTCGGTGTGGAAGTCGCAGCATAGTGGGTGTGACT</i>	
B2	-3809	-3630			3821871	3822050	GGTGTGACTGTACGCTTGG	ATGTTCTCCTCTTCAAAGCC
B3	-3689	-3519			3821991	3822161	TTGACACACATATGGTTAGG	GAATGAGCATCTCGAAAGCC
B4	-3569	-3402			3822111	3822278	CATATTTATGTTTGAAGTC	GCCTTACGATCTGGTTTAC
B5	-3454	-3270			3822226	3822410	CTACCTGAAGTGAGATTGGC	ATCAGGTCCTTCACTCGGGC
u3118	-3055	-1777	EcoRV		3822625	3823903	ATCCTGCTGATGTCGAGCCATGTGACA	ACAATGGAGGAGTTGGGAAGAAAAA
u3125	-3055	-2522	EcoRV	Aat2	3822625	3823158	ATCCTGCTGATGTCGAGCCATGTGACA	CGTGGTAAAACGAATTGATTAGCGA
u3923	-3929	-2303			3821751	3823377	TGTCGGCAATCCCAGTGCCAACCGCA	GCACACTGCATAGAGTAATGGGTAATTCGA
u3725	-3679	-2522	Nde1	Aat2	3822001	3823158	TATGGTTAGAAATAAAAATAAAATTTAGAT	CGTGGTAAAACGAATTGATTAGCGA
u2316	-2324	-1648		EcoRV	3823356	3824032	CCCATTACTCTATGCAGTGTGCATAAA	ATCTTAGACAACCTTGACAAAACATCA
u1609	-1647	-941	EcoRV	Nru1	3824033	3824739	ATCAAACGCACAGTCCGCCGACAAGTA	CGACAGATTTGCGAATTAGTTCTGGG
u0900	-940	121	Nru1		3824740	3825800	CGAAACTAGAACAAATCCCGG	ATTTCACTTTTACCATTTTTCTGATT
<i>slp1</i> mRNA	1	1458			3825680	3827137		
A0	1515	1692			3827194	3827371	TTGGATCGAGTTATCGACAC	(C)GCTGGAGGAGCTGGGTAAATA
A0-1	1531	1560			3827210	3827239	ACACTTGAAAAATATTCATCAGTGAATAAG	
A0-2	1618	1647			3827297	3827326	TCTTTTCCGTTGACCATCAGCTGCTGTCC	
A0-3	1515	1562			3827194	3827241	TTGGATCGAG	
A0-4	1559	1618			3827238	3827297	AGACTTAATG	
A0-5	1642	1692			3827321	3827371	GCTGTCCAGC	
A1	1601	1800			3827280	3827479	CTGAGAACTCAGCAGTCTCT	TTTTGAACCTCATCCTCTGGC
A1a	1689	1730			3827368	3827409	CAGCAACTTGCTTTCATCCTGATGACTTAATTAGTTGTTGC	
A1a'	1695	1737			3827374	3827416	CTTGCTTTCA	
A1-1	1672	1768			3827351	3827447	ATTTACCCAG	
A2	1739	1898			3827418	3827577	GCGGCAACATGAAAATGATTC	CGGATCGTACCTGCGGTGCC
A2a	1788	1829			3827467	3827508	ATGAGGTTCAAATGAGCCATCACCCATTGACTCGATTTGT	
A2a-mut							ATGAGGTTCC CGACTGAGCAGGCACCCAGGTTCTCGATCGTGT	
A2-1	1815	1897			3827494	3827576	TTGACTCGAT	
A3	1841	2020			3827520	3827699	CATGCCAGTGACAACCTCC	AGTGTGCCCGTGGACAGAG
A4	1961	2108			3827640	3827787	CATGAACCCAGCCAGGCC	CCCAGTGTAGCGCACATATTAG
A5	2081	2284			3827760	3827963	TCTTAACTAATATGTGCGC	GTCCCTGGCTTACGCTGTG
i1523	1517	2293		Stu1	3827196	3827972	GGATCGAGTTATCGACACTTGAAAAA	CCTAGAAAAGTCCCTGGCTTACGCT
i2330	2291	3007		Stu1	3827970	3828686	AGGCCTCAATTTGAAAGATG	GGTAACCCCAACCTGTTAACTGATTTA

p-hs-FLAG-eve sequence of coding region 5' end *AGATCTCCAACATGACTACAAGGACGACGATGACAAGGCTAGCATGCACGGATACCGA...*
in pCaSpeR-hs Bgl2 **Met** FLAG Nhe1 **Met-eve** coding

Column headings indicate the information contained therein. For B1a, *italicized* sequences are included in the transgene of Fig. 7 but not the probes of Fig. 6C,D. For B1a mut a, mutations (indicated by **bold, underlined**) were incorporated into the probes of Fig. 6B and within the u4734-mut transgene in Fig. 5. For B1b, *italicized* sequences are included in the transgene of Fig. 7 but not the probes used to test binding *in vitro*. For B1 mut b, mutations (**bold, underlined**) were incorporated into the probes of Fig. 6B. For A1a, *italicized* sequences are included in the transgene of Fig. 7 but not in the probes used in Fig. 3B,D. For A2a, *italicized* sequences are included in the transgene of Fig. 7 but not in the probe used in Fig. 3E. For A2a-mut, mutations (**bold, underlined**) were incorporated into the A2a-mut and the A1a-A2a-mut transgenes in Fig. 4.