Table S1 Fold-changes in *lacZ* reporter gene expression

Promoter	Comparison		Fold-change
	between	within	
ph-p	BR/MG	17°C & NL	2.67
		17°C & ZK	3.08 **
		28°C & NL	4.28 **
		28°C & ZK	6.81 **
	17°C/28°C	BR & NL	0.77
		BR & ZK	1.09
		MG & NL	1.24
		MG & ZK	2.41 **
	NL/ZK	17°C & BR	0.74
		17°C & MG	0.85
		28°C & BR	1.03
		28°C & MG	1.64*
CG3835	BR/MG	17°C & NL	0.33 **
		17°C & ZK	0.21 *
		28°C & NL	0.61 *
		28°C & ZK	0.40 *
	17°C/28°C	BR & NL	0.89
		BR & ZK	0.70
		MG & NL	1.08
		MG & ZK	2.03
	NL/ZK	17°C & BR	1.04
		17°C & MG	0.67
		28°C & BR	0.82
		28°C & MG	1.27

mRNA abundance was measured via RT-qPCR in brains (BR) and midguts (MG) of third instar larvae reared at 17°C or 28°C. *lacZ* reporter gene expression was either driven by the promoter of *ph-p* or the *CG3835* promoter. Promoter and adjacent regulatory regions were either derived from a European strain from the Netherlands (NL) or an African one from Zimbabwe (ZK). Statistical testing included t-tests and correction for multiple testing. *P<0.05, **P<0.01 (FDR=0.05).

Table S2 ***BayeScan*** **outlier SNPs**

Sample	Number of Populations	Position on X chromosome	Posterior Probability	Posterior Odds $\log_{10}$(PO)	alpha	F_{ST}
Europe-Africa	7	2,054,375	1.000	3.699	1.834	0.739
		2,035,164	**0.926**	**1.095**	**1.700**	**0.712**
		2,173,611	0.928	1.111	1.677	0.709
		2,035,208	**0.917**	**1.042**	**1.676**	**0.708**
		2,034,789	**0.919**	**1.054**	**1.665**	**0.706**
		2,032,933	**0.921**	**1.064**	**1.661**	**0.706**
		2,035,090	**0.920**	**1.059**	**1.641**	**0.702**
		2,054,995	0.996	2.442	1.502	0.687
		2,039,998	0.990	1.996	1.449	0.678
		2,055,053	0.988	1.930	1.438	0.676
		1,999,363	0.976	1.617	1.391	0.668
		2,053,119	0.976	1.617	1.379	0.666
		2,056,220	0.972	1.537	1.369	0.664
		2,054,347	0.966	1.448	1.337	0.658
		1,907,955	0.955	1.329	1.248	0.643
		2,056,678	0.933	1.141	1.248	0.642
		2,055460	0.911	1.012	1.246	0.642
		1,905,431	0.955	1.329	1.231	0.640
		1,999,517	0.950	1.275	1.222	0.639
		1,974,821	0.946	1.242	1.216	0.638
		1,903117	0.942	1.212	1.202	0.635
		1,974,723	0.923	1.081	1.162	0.628
		2,090,045	0.901	0.958	-1.521	0.181
		2,179,117	0.926	1.095	-1.573	0.174
		2,136,315	0.941	1.203	-1.584	0.171
		1,963,657	0.928	1.108	-1.609	0.170
		2,181,270	0.948	1.257	-1.589	0.170
		1,984,277	0.933	1.147	-1.644	0.166
		2,171,163	0.953	1.309	-1.626	0.166
		1,994,497	0.961	1.394	-1.673	0.160
		2,069,894	0.954	1.315	-1.691	0.160
		2,179,478	0.973	1.550	-1.702	0.157
		2,141,928	0.976	1.606	-1.733	0.153
		2,153,801	0.973	1.557	-1.742	0.153
		1,965,347	0.979	1.669	-1.782	0.148
		2,139,505	0.971	1.525	-1.846	0.144

Africa	5	2,054,375	0.998	2.698	1.731	0.674
		1,972,008	0.959	1.365	1.343	0.599
		1,972,114	0.958	1.354	1.335	0.598
		2,054,995	0.955	1.331	1.324	0.595
		2,112,292	0.945	1.238	1.290	0.589
		2,141,480	0.939	1.190	1.296	0.590
		2,053,119	0.899	0.951	1.215	0.573
		1,944,464*	0.880	0.864	1.178	0.566
		2,039,998*	0.865	0.807	1.140	0.558

BayeScan analyses were run on a X-chromosomal 300-kb sequence window around the *ph* locus. Significant outlier SNPs at an FDR of 5% are shown here. For the African-exclusive analysis, also outliers at an FDR of 7% are given (marked by asterisks). Six outlier SNPs are located in the region of significant CLR values. Bold font highlights the five outlier SNPs that are located in *ph-p/CG3835* intergenic region and that are not already significantly segregating when only African populations are considered. The SNP at X-chromosomal position 2,039,998 (FlyBase release 5) is located within in the region of significant CLR values, but not between *ph-p* and *CG3835*.