Table S6 TFBS models with predicted differential binding between the tested S58 and Z418 upstream regions

Upstream Region	TF Model[a]	Strand[b]	Start[c]	Positions affected[d]	S58[e] Weight	S58[e] ln(P)	Z418[e] Weight	Z418[e] ln(P)
Cyp6a20	B-H1	-	-521	251	7	-9.263	-	-
Cyp6a20	Ets21C	+	-77	699	9	-10.286	-	-
Cyp6a20	schlank	+	-217	558	-	-	7.9	-10.068
Cyp6t1	cad	-	-1036	710	8	-9.432	-	-
Cyp6t1	cad	-	-152	1588	8.2	-9.65	-	-
Cyp6t1	Cf2	+	-1380	373	-	-	9.2	-11.234
Cyp6t1	Cf2	+	-1378	373	-	-	9.1	-10.96
Cyp6t1	Cf2	-	-1373	373	7.5	-9.363	-	-
Cyp6t1	Cf2	+	-1367	373	7.5	-9.363	-	-
Cyp6t1	ems	-	-1147	indel	-	-	6.9	-9.451
Cyp6t1	eve	-	-1147	indel	-	-	7.3	-9.451
Cyp6t1	hb	-	-1157	indel	-	-	7.7	-11.419
Cyp6t1	pb	-	-1147	indel	-	-	7.5	-9.451
Cyp6t1	schlank	-	-1418	319	7.8	-9.808	-	-
Cyp6t1	sd	+	-1718	indel	-	-	7.5	-10.63
Cyp6t1	sd	-	-18	1 bp indel	6.7	-9.207	-	-
Cyp6t1	zen	-	-1147	373	8.2	-9.451	-	-
Cyp12a4	Vsx2	-	-108	472	7.8	-9.393	-	-
Cyp12a5	BEAF-32	-	-447	774, 775, 777, 781	7.9	-9.687	-	-
Cyp12a5	br(var.3)	+	-449	774, 775, 777, 781	-	-	7.6	-10.608
Cyp12a5	Cf2	-	-799	414	-	-	9.1	-10.96
Cyp12a5	dl	+	-454	774, 775, 777	7.5	-9.444	-	-
Cyp12a5	pnr	+	-447	774, 775, 777, 781	8.3	-10.083	-	-
Cyp12a5	tin	-	-1220	1 bp indel	8.1	-9.774	-	-
Cyp28a5	br	-	-475	147	7.2	-9.286	-	-
Cyp28a5	Mad	+	-27	N/A	8.8	-10.582	6.3	-9.491
Cyp28a5	slp1	+	-472	147	7.9	-9.637	-	-
Cyp28a5	twi	+	-478	147	-	-	7.8	-9.869
Cyp28a5	z	-	-142	482	-	-	7.9	-10.087

[a]Matrix models of predicted transcription factor binding sites (TFBS) in the JASPAR CORE Insecta database (Mathelier *et al.* 2016).

[b]TFBS stand orientations. Same orientation as associated gene, +. Opposite orientation of associated gene, -.
[c]Position of start of TFBS from 3' end of tested upstream region.
[d]Position of segregating sites between Z418 and S58 in the alignment of Zambian and Dutch populations that overlap with the predicted TFBS.
[e]Weight and ln(P) were calculated using the *matrix-scan* program in the Regulatory Sequence Analysis Tools (RSAT) suite (Teratsinze *et al.* 2008).

Literature cited

1. Mathelier A., O. Fornes, D. J. Arenillas, C. Y. Chen, G. Denay, J. Lee *et al.*, 2016 JASPAR 2016: a major expansion and update of the open-access database of transcription factor binding profiles. Nucleic Acids Res. 44: D110-115.

2. Turatsinze, J. V., M. Thomas-Chollier, M. Defrance, and J. van Helden, 2008 Using RSAT to scan genome sequences for transcription factor binding sites and *cis*-regulatory modules. Nat Protoc. 3: 1578–1588.