

Table S7 Segregating sites in tested upstream regions and their frequencies in a Dutch and a Zambian population

Gene	Position ^a	Variant ^b		Frequency Ancestral Variant ^c	
		ZI418	S58	ZI	NL
<i>Cyp6a20</i>	52	C	T	0.765	0.000
	105	C	A	0.633	1.000
	251	G	T	0.510	0.000
	285	T	A	0.913	0.818
	558	A	G	0.138	0.091
	573	A	G	0.510	1.000
	699*	G	C	0.918	0.800
	746	T	C	0.638	1.000
<i>Cyp6t1</i>	19	C	G	0.592	0.667
	63	C	T	0.872	0.100
	79	A	G	0.888	0.727
	122	C	A	0.469	0.182
	213	A	C	0.893	0.727
	226	C	T	0.893	0.727
	256	C	A	0.893	0.727
	284	G	T	0.124	0.000
	286	A	G	0.893	0.727
	309	A	C	0.893	0.727
	319	C	T	0.893	0.727
	333	T	A	0.878	0.727
	373	T	C	0.893	0.727
	404	C	A	0.878	0.727
	572	G	A	1.000	0.400
	622	C	T	0.985	0.200
	630	C	T	0.888	0.700
	646	A	C	0.980	0.200
	710	A	T	0.036	0.455
	772	C	T	0.980	0.273
	863	A	T	1.000	1.000
	864	A	C	1.000	1.000
	1174	A	G	0.291	0.182
	1318	C	T	0.607	0.636
	1408	G	T	0.985	0.182
	1409	C	A	0.985	0.182
	1488	A	G	0.930	0.182
	1588	C	T	0.990	0.091
	1600	G	A	0.653	0.100

	1609	G	A	0.995	0.182
	1614	G	A	0.510	0.727
	1735	C	G	0.000	0.000
<i>Cyp12a4</i>	34	G	T	0.537	0.909
	136	T	A	0.878	0.455
	147	T	G	0.846	1.000
	229	A	T	0.862	1.000
	257	C	T	0.681	0.300
	263	A	C	0.691	0.300
	314	G	A	0.775	1.000
	316	T	A	0.774	1.000
	360	C	A	0.840	1.000
	362	G	A	0.929	1.000
	372	G	T	1.000	1.000
	472	G	A	0.069	0.636
	524	G	T	0.591	0.091
<i>Cyp12a5</i>	56	C	A	0.513	0.364
	189	A	G	0.755	1.000
	414	A	G	0.653	0.091
	504	T	C	0.554	0.818
	537	C	A	0.533	0.200
	667	C	T	0.750	0.000
	774	A	T	0.626	0.091
	775	C	T	0.839	0.091
	777	A	C	0.795	0.091
	781	C	A	0.190	0.909
	903	C	T	0.599	1.000
	904	T	C	0.599	1.000
	972	A	G	0.595	0.909
	1003	C	A	0.503	0.182
	1099	G	T	0.711	0.000
	1106	T	C	0.959	0.100
	1117	T	A	0.593	0.909
	1136	A	C	0.772	1.000
<i>Cyp12b2</i>	46	C	T	0.595	1.000
	118	A	G	0.071	1.000
	140	G	T	0.964	1.000
	157	G	A	0.726	0.000
	172	C	T	0.329	1.000
	203	C	T	0.883	1.000
	290	G	C	0.995	0.700
	298	A	T	0.751	0.000
	353	C	A	0.832	0.000

	423	C	G	0.766	1.000
	147	A	A	0.883	0.700
	187	G	G	0.843	0.700
	193	A	C	0.526	0.900
	252	A	G	0.599	0.900
	366	T	A	0.655	1.000
	442	G	A	0.731	0.600
	482	C	T	0.822	0.800
	563	G	T	0.863	1.000
	569	G	A	0.812	1.000
	594	T	C	0.959	1.000

Cyp28a5

^aPosition in alignment of Zambian and Dutch populations of tested upstream region.

Positions shown in red overlap with at least one predicted transcription factor binding site with predicted differential binding between Z418 and S58. Asterisk indicates that site that corresponds to female *cis*-eQTL identified by Massouras *et al.* (2012).

^bSNP variant in tested upstream regions. The ancestral variant is shown in bold and was inferred from an alignment with *D. simulans*, *D. sechelia*, and *D. yakuba*.

^cFrequency of the ancestral variant in Zambian (ZI) and Dutch (NL) populations. When the ancestral variant could not be inferred, the frequency of Zambian variant is shown.