

**Development of genic and genomic SSR markers of robusta coffee (*Coffea canephora* Pierre ex A. Froehner)**

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**Table S4: Inter-species and inter-generic transferability of the new EST-SSRs and genomic SSR markers**

Species	<i>Coffea</i> spp.															<i>Psilanthus</i> spp.			Average Average $C_{taxa}$ for all coffees		
	Erythrocoffea		Mozamicroffea				Melanocoffea	Pachycoffea					Average $C_{taxa}$ ( <i>Coffea</i> )	Paracoffea		Average $C_{taxa}$ ( <i>Psilanthus</i> )					
Primer name	<i>C. arabica</i>	<i>C. congensis</i>	Average $C_{taxa}$	<i>C. eugeniooides</i>	<i>C. kapakata</i>	<i>C. racemosa</i>	<i>C. salavatrix</i>	Average $C_{taxa}$	<i>C. stenophylla</i>	<i>C. excelsa</i>	<i>C. litorica</i>	<i>C. aeokatae</i>	<i>C. deweyrei</i>	<i>C. arnoldiana</i>	<i>C. ariawemiensis</i>	Average $C_{taxa}$	Average $C_{taxa}$ ( <i>Coffea</i> )	<i>P. engatensis</i>	<i>P. wightiana</i>	Average $C_{taxa}$ ( <i>Psilanthus</i> )	
a. EST-SSRs ( <i>in-silico</i> EST database)																					
<b>All the CCESSRs</b>	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	$1.00(C_{taxa-mark})/1.00(C_{mark-taxa})$
b. genomic-SSRs (SSR enrichment approach)																					
CCRM06, CCRM14, CCRM16, CCRM17, CCRM19, CCRM21, CCRM23, CCRM24, CCRM28, CCRM31, CCRM33 to CCRM38, CCRM40, CCRM42, CCRM45	+	+	1.00	+	+	+	+	1.00	+	+	+	+	+	+	+	1.00	1.00	+	+	1.00	1.00
CCRM02	+	+	1.00	+	+	+	+	1.00	+	+	+	+	+	-	+	0.83	0.85	+	+	1.00	0.87
CCRM07	+	-	0.50	+	+	+	+	1.00	+	+	+	+	+	-	+	0.83	0.77	+	+	1.00	0.80
CCRM10	+	+	1.00	+	+	+	+	1.00	+	+	+	+	+	+	+	1.00	0.92	-	-	0.00	0.80
CCRM15	+	+	1.00	-	+	-	+	0.50	-	-	+	+	+	+	-	0.67	0.69	-	-	0.00	0.60
CCRM22	+	+	1.00	+	+	+	-	0.75	+	+	+	+	+	+	-	0.83	0.77	+	+	1.00	0.80
CCRM41	+	+	1.00	+	-	+	+	0.75	-	+	+	-	+	+	+	0.83	0.85	+	+	1.00	0.87
<b>Average <math>T_{mark}</math></b>	1.00	0.96	0.98	0.96	0.96	0.96	0.96	0.96	0.92	0.96	1.00	0.96	1.00	0.92	0.92	0.96	0.96	0.92	0.92	0.92	$0.95(C_{taxa-mark})/0.94(C_{mark-taxa})$

+/-: Indicates 'amplification'/'No amplification' and are given a weightage of 1 and 0 for transferability/conservation calculations respectively;  $T_{mark}$ : Marker transferability over all the taxa;  $C_{taxa}$ : Marker conservation over all the taxa;  $T_{mark-taxa}$ : Marker transferability of all the markers over all the taxa;  $C_{taxa-mark}$ : Primer conservation across all the taxa over all the markers.