



The table below provides conversion factors (CF_{CRM}) experimentally determined on certified reference materials (CRM) by using digital PCR by at least three and up to four independent expert laboratories. The expanded uncertainty (U) estimated for each CF_{CRM} has been calculated to allow expressing dPCR results in mass fraction with a reliable uncertainty estimate.

See also : [Corbisier P. and Emons H. \(2019\)](#) and [Corbisier P. et al. \(2022\)](#)

CRM	Species	Event	Transgene method	Endogene method	CF_{CRM}	U (k=2)	Zygoty
ERM®-BF419b	Beta vulgaris (sugar beet)	H71	QT-EVE-BV-001	QT-TAX-BV-013	0.48	0.05	Heterozygous / transgenic parent male
0117-E	Brassica napus (oilseed rape)	LBFLFK1	QT-EVE-BN-012	QT-TAX-BN-001	1.04	0.12	Homozygous
0117-E	Brassica napus (oilseed rape)	LBFLFK2	QT-EVE-BN-013	QT-TAX-BN-001	1.01	0.14	Homozygous
0208-A7	Brassica napus (oilseed rape)	T45	QT-EVE-BN-001	QT-TAX-BN-001	0.97	0.04	Homozygous
0304-B3	Brassica napus (oilseed rape)	GT73	QT-EVE-BN-004	QT-TAX-BN-001	1.03	0.11	Homozygous
0306-F9	Brassica napus (oilseed rape)	MS8	QT-EVE-BN-002	QT-TAX-BN-001	0.484	0.017	Hemizygous
0306-G8	Brassica napus (oilseed rape)	RF3	QT-EVE-BN-003	QT-TAX-BN-001	0.96	0.04	Homozygous
0421-A	Brassica napus (oilseed rape)	MON94100	QT-EVE-BN-014	QT-TAX-BN-001	0.46	0.05	Heterozygous / transgenic parent female
1011-A2	Brassica napus (oilseed rape)	MON88302	QT-EVE-BN-010	QT-TAX-BN-001	1.05	0.06	Homozygous
1116-A	Brassica napus (oilseed rape)	MS11	QT-EVE-BN-011	QT-TAX-BN-001	0.470	0.012	Hemizygous
ERM®-BF434b	Brassica napus (oilseed rape)	73496	QT-EVE-BN-009	QT-TAX-BN-001	1.03	0.07	Homozygous
0711-A4	Brassica napus (swede-rape)	MS1	QT-EVE-BN-005	QT-TAX-BN-001	0.526	0.022	Hemizygous
0711-B3	Brassica napus (swede-rape)	RF1	QT-EVE-BN-006	QT-TAX-BN-001	1.062	0.009	Homozygous
0711-C3	Brassica napus (swede-rape)	RF2	QT-EVE-BN-007	QT-TAX-BN-001	0.99	0.06	Homozygous
0711-D4	Brassica napus (swede-rape)	Topas_19/2	QT-EVE-BN-008	QT-TAX-BN-001	1.06	0.06	Homozygous
0112-A2	Glycine max (soybean)	SYHT0H2	QT-EVE-GM-017	QT-TAX-GM-009	0.97	0.06	Homozygous
0210-A2	Glycine max (soybean)	MON87705	QT-EVE-GM-003	QT-TAX-GM-009	1.01	0.08	Homozygous
0215-A	Glycine max (soybean)	MON87751	QT-EVE-GM-016	QT-TAX-GM-009	1.002	0.021	Homozygous
0311-A2	Glycine max (soybean)	MON87708	QT-EVE-GM-012	QT-TAX-GM-009	1.03	0.06	Homozygous
0610-A6	Glycine max (soybean)	FG72	QT-EVE-GM-001	QT-TAX-GM-009	1.08	0.05	Homozygous
0707-B15	Glycine max (soybean)	A2704-12	QT-EVE-GM-004	QT-TAX-GM-009	0.983	0.010	Homozygous
0707-C9	Glycine max (soybean)	A5547-127	QT-EVE-GM-007	QT-TAX-GM-009	0.99	0.04	Homozygous
0809-A2	Glycine max (soybean)	MON87701	QT-EVE-GM-010	QT-TAX-GM-009	0.96	0.07	Homozygous
0809-B2	Glycine max (soybean)	MON87769	QT-EVE-GM-002	QT-TAX-GM-009	1.01	0.06	Homozygous
0906-B2	Glycine max (soybean)	MON89788	QT-EVE-GM-006	QT-TAX-GM-009	0.979	0.021	Homozygous
0911-D	Glycine max (soybean)	CV127	QT-EVE-GM-011	QT-TAX-GM-009	1.01	0.11	not known
ERM®-BF410bp	Glycine max (soybean)	40-3-2	QT-EVE-GM-005	QT-TAX-GM-009	1.02	0.10	Homozygous
ERM®-BF425d	Glycine max (soybean)	356043	QT-EVE-GM-009	QT-TAX-GM-009	0.98	0.14	Homozygous

CRM	Species	Event	Transgene method	Endogene method	CF _{CRM}	U (k=2)	Zygosity
ERM®-BF426d	Glycine max (soybean)	305423	QT-EVE-GM-008	QT-TAX-GM-009	0.93	0.11	Homozygous
ERM®-BF432d	Glycine max (soybean)	DAS68416	QT-EVE-GM-013	QT-TAX-GM-009	1.17	0.19	Homozygous
ERM®-BF436b	Glycine max (soybean)	DAS44406	QT-EVE-GM-015	QT-TAX-GM-009	1.00	0.06	Homozygous
ERM®-BF437b	Glycine max (soybean)	DAS81419	QT-EVE-GM-014	QT-TAX-GM-009	0.96	0.04	Homozygous
ERM®-BF443b	Glycine max (soybean)	GMB151	QT-EVE-GN-018	QT-TAX-GM-009	1.05	0.13	Homozygous
0113-A2	Gossypium hirsutum (cotton)	MON88701	QT-EVE-GH-010	QT-TAX-GH-018	1.04	0.04	Homozygous
0306-E4	Gossypium hirsutum (cotton)	LLCotton25	QT-EVE-GH-002	QT-TAX-GH-018	1.06	0.03	Homozygous
0804-B2	Gossypium hirsutum (cotton)	MON1445	QT-EVE-GH-003	QT-TAX-GH-018	1.05	0.06	Homozygous
0804-C2	Gossypium hirsutum (cotton)	MON531	QT-EVE-GH-004	QT-TAX-GH-018	0.97	0.06	Homozygous
0804-D2	Gossypium hirsutum (cotton)	MON15985	QT-EVE-GH-005	QT-TAX-GH-018	0.91	0.10	Homozygous
0906-D2	Gossypium hirsutum (cotton)	MON88913	QT-EVE-GH-007	QT-TAX-GH-018	1.03	0.08	Homozygous
1012-C2	Gossypium hirsutum (cotton)	COT102	QT-EVE-GH-012	QT-TAX-GH-018	1.08	0.10	Homozygous
1108-A7	Gossypium hirsutum (cotton)	GHB614	QT-EVE-GH-006	QT-TAX-GH-018	1.09	0.04	Homozygous
ERM®-BF422b	Gossypium hirsutum (cotton)	281-24-236	QT-EVE-GH-001a	QT-TAX-GH-018	1.02	0.05	Homozygous
ERM®-BF422b	Gossypium hirsutum (cotton)	3006-210-23	QT-EVE-GH-001b	QT-TAX-GH-018	1.00	0.09	Homozygous
ERM®-BF428c	Gossypium hirsutum (cotton)	GHB119	QT-EVE-GH-008	QT-TAX-GH-018	0.96	0.12	Homozygous
ERM®-BF429c	Gossypium hirsutum (cotton)	T304-40	QT-EVE-GH-009	QT-TAX-GH-018	1.27	0.16	Homozygous
ERM®-BF440b	Gossypium hirsutum (cotton)	DAS81910	QT-EVE-GH-011	QT-TAX-GH-018	1.01	0.09	Homozygous
ERM®-BF442b	Gossypium hirsutum (cotton)	GHB811	QT-EVE-GH-013	QT-TAX-GH-018	0.94	0.07	Homozygous
0306-I9	Oryza sativa (rice)	LLRICE62	QT-EVE-OS-002	QT-TAX-OS-017	0.84	0.13	Homozygous
0215-B	Zea mays (maize)	MON87411	QT-EVE-ZM-024	QT-TAX-ZM-002	0.59	0.04	Heterozygous / transgenic parent female
0216-A	Zea mays (maize)	MON87403	QT-EVE-ZM-025	QT-TAX-ZM-002	0.622	0.021	Heterozygous / transgenic parent female
0306-H11*	Zea mays (maize)	T25	QT-EVE-ZM-011	QT-TAX-ZM-002	0.938	0.025	Homozygous
0406-D2	Zea mays (maize)	MON88017	QT-EVE-ZM-016	QT-TAX-ZM-002	0.51	0.07	Heterozygous / transgenic parent female
0407-B	Zea mays (maize)	GA21	QT-EVE-ZM-007	QT-TAX-ZM-002	0.35	0.06	Heterozygous / transgenic parent male
0411-D2	Zea mays (maize)	5307	QT-EVE-ZM-002	QT-TAX-ZM-002	0.34	0.05	Heterozygous / transgenic parent male
0512-A2	Zea mays (maize)	MON87427	QT-EVE-ZM-003	QT-TAX-ZM-002	0.604	0.019	Heterozygous / transgenic parent female
0709-A2	Zea mays (maize)	MON87460	QT-EVE-ZM-005	QT-TAX-ZM-002	0.38	0.05	Heterozygous / transgenic parent male
0906-E2	Zea mays (maize)	MON89034	QT-EVE-ZM-018	QT-TAX-ZM-002	0.36	0.05	Heterozygous / transgenic parent male
1114-B2	Zea mays (maize)	MZIR098	QT-EVE-ZM-028	QT-TAX-ZM-002	0.36	0.05	Heterozygous / transgenic parent male
1114-C	Zea mays (maize)	MZHGOJG	QT-EVE-ZM-027	QT-TAX-ZM-002	0.37	0.06	Heterozygous / transgenic parent male
ERM®-BF411g	Zea mays (maize)	Bt176	QT-EVE-ZM-023	QT-TAX-ZM-002	0.69	0.08	Heterozygous / transgenic parent male
ERM®-BF412bk	Zea mays (maize)	Bt11	QT-EVE-ZM-015	QT-TAX-ZM-002	0.364	0.025	Heterozygous / transgenic parent male

CRM	Species	Event	Transgene method	Endogene method	CF _{CRM}	U (k=2)	Zygosity
ERM®-BF413gk	Zea mays (maize)	MON810	QT-EVE-ZM-020	QT-TAX-ZM-002	0.36	0.04	Heterozygous / transgenic parent male
ERM®-BF415f	Zea mays (maize)	NK603	QT-EVE-ZM-008	QT-TAX-ZM-002	0.51	0.04	Heterozygous / transgenic parent female
ERM®-BF416d	Zea mays (maize)	MON863	QT-EVE-ZM-009	QT-TAX-ZM-002	0.62	0.08	Heterozygous / transgenic parent female
ERM®-BF418d	Zea mays (maize)	1507	QT-EVE-ZM-010	QT-TAX-ZM-002	0.61	0.09	Heterozygous / transgenic parent female
ERM®-BF420c	Zea mays (maize)	3272	QT-EVE-ZM-019	QT-TAX-ZM-002	0.42	0.06	Heterozygous / transgenic parent male
ERM®-BF423d	Zea mays (maize)	MIR604	QT-EVE-ZM-013	QT-TAX-ZM-002	0.448	0.030	Heterozygous / transgenic parent male
ERM®-BF424d	Zea mays (maize)	DAS59122	QT-EVE-ZM-012	QT-TAX-ZM-002	0.34	0.05	Heterozygous / transgenic parent male
ERM®-BF427d	Zea mays (maize)	98140	QT-EVE-ZM-021	QT-TAX-ZM-002	0.74	0.09	Heterozygous / transgenic parent female
ERM®-BF433d	Zea mays (maize)	DAS40278	QT-EVE-ZM-004	QT-TAX-ZM-002	0.36	0.05	Heterozygous / transgenic parent male
ERM®-BF438b	Zea mays (maize)	VCO1981	QT-EVE-ZM-001	QT-TAX-ZM-002	0.429	0.025	Heterozygous / transgenic parent male
ERM®-BF439b	Zea mays (maize)	4114	QT-EVE-ZM-026	QT-TAX-ZM-002	0.61	0.06	Heterozygous / transgenic parent female
ERM®-BF446b	Zea mays (maize)	MIR162	QT-EVE-ZM-022	QT-TAX-ZM-002	0.57	0.06	Heterozygous / transgenic parent female

Version: 11 Data for CRMs marked in red is either new or has been updated

* The CF_{CRM} for T25 has been established using the ddPCR Supermix for Probes (No dUTP) (Bio-Rad®)