

Additional file 1: Table S1 - Published QTLs for berry weight and seed traits in *Vitis*

Trait	LG	Doligez et al., 2002	Fischer et al., 2004 ¹	Cabezas et al., 2006	Mejia et al., 2007	Costantini et al., 2008 ²
MBW	1					18
	5		? ⁴			
	12					9
	13		? ⁴			
	15			19		
	18-7F2	38²		44	67	43
	18-N83			23		
MSN	2		nr			23
	8	11				
	11			67		
	18-7F2	48³			48	
TSFW	1		nr	15		nr
	10			33		
	18-7F2	49³		63	84	
MSFW	6		nr	nr	nr	21
	10					13
	13					16⁵
	15					13
	18-7F2	38³				28
%SDM	18-7F2	40³	nr		64	91

QTLs detected with a genome-wide first-type error rate of 5%. The reported number is the maximum % of total variance explained among years and maps (parental and consensus), in bold when the QTL was present in at least 2 years. nr: trait not reported.

The results of Fanizza et al. (2005) were not included because they were based on a subset of the data reported in Costantini et al. (2008); those of Mejia et al. (2011) were not included because the QTLs on LGs others than LG 18 were not reported.

MBW: mean berry weight; MSN: mean seed number; TSFW: total seed fresh weight; MSFW: mean seed fresh weight; %SDM: seed dry matter percentage; RESN: residual berry weight unexplained by seed number; RESFW: residual berry weight unexplained by total seed fresh weight

¹ Complex hybrid cross including up to seven American *Vitis* species

² LOD threshold was extrapolated from the available chromosome-wide values to 3.5 for parental maps and 4.5 for consensus map, to reflect usual values of genome-wide values

³ LG determined according to Doligez et al., 2010

⁴ Stable QTL detected but magnitude of effect not reported

⁵ Doubtful QTL (in a large gap of 26.4 cM, with no strong significance of KW test)