

Additional files

Additional file 1 - Mean features of the Pinot noir genomic contigs [38] that align with SSR markers underlying QTLs: number, length, predicted genes and proteins

SSR	LG	Trait	Contig number	Contig length (nt)	SSR position within contig	Predicted gene position	Chain	Predicted protein length (aa)	Protein similarity	Subcellular localization prediction
VMC5G7	2	F-V	AM426260.2 (CAAP02000071.1)	26662	14770-15156	<u>2488-15183</u>	-	590	Heat shock factor protein hsf8-related [<i>Glycine max</i> , AAS15800]	None
						17802-25590	+	1576	Gag-pol polyprotein-like [<i>Solanum tuberosum</i> , AAU89779]	None/Plastid
VMC2C10.1	2	VT, V-R	AM437882.2 (CAAP02000034.1)	42409	19777-20190	<u>25-12480</u>	-	616	COG6 domain (Golgi complex)	None/Possibly mitochondrial
						<u>17532-24691</u>	+	220	Unknown protein	None
						25695-26921	-	117	Unknown protein	None/Possibly plastid
VVIB23	2	FT, V-R, MSN, MSDW	AM440415.1 (CAAP02004239.1)	64774	38192-38617	3495-6457	+	393	Trehalose-phosphate phosphatase [<i>Nicotiana tabacum</i> , AAU03490]	None
						7743-17562	+	384	Transaldolase ToTAL2 [<i>Lycopersicon esculentum</i> , AAG34725]	Signal peptide/Plastid

						18898-23013	+	661	Vacuolar invertase 2, GIN2 [<i>Vitis vinifera</i> , AAB47172]	Signal anchor/None
						26576-31917	+	560	Copper ion binding [<i>Arabidopsis thaliana</i> , NP_192979]	Signal peptide/ER
						37627-43729	-	272	YABBY-like transcription factor GRAMINIFOLIA [<i>Antirrhinum majus</i> , AAS10177]	Signal anchor/ER
						47472-51589	+	307	Pentapeptide domain Ricin-type beta-trefoil domain	Signal anchor/Plastid
						51769-53143	+	160	Pentapeptide domain	None/Plastid
						53159-55272	-	350	No similarity	None
						56263-58465	-	614	Gag-pol polyprotein [<i>Vitis vinifera</i> , AAF20282]	None
						62047-64593*	-	574	Subtilisin-like protease [<i>Glycine max</i> , AAQ23176]	Possibly mitochondrial
VMC4G6	6	VT, F-V	AM454821.2 (CAAP02000198.1)	41067	28363-28653	*313-6492	+	688	Unknown protein	None
						6612-8295	-	246	Integrase, catalytic region [<i>Medicago truncatula</i> , ABE91551]	None
						8379-16891	-	1242	Reverse transcriptase domain Integrase core domain	None
						17009-19101	+	129	Unknown protein	None

						<u>19461-28624</u>	+	271	Unknown protein	None
						<u>30029-35739</u>	+	280	Unknown protein	None
						35935-40355*	-	1144	Integrase core domain containing protein [<i>Solanum demissum</i> , ABI34329]	None
VMC4H5	6	R, F-R	AM438219.1 (CAAP02000936.1)	20473	17012-17476	6882-9822	+	574	Trehalose-6-phosphate synthase [<i>Ginkgo biloba</i> , AAX16014]	None
						12371-16815	+	238	Unknown protein	None
VMC2H4	12	V-R	AM486664.1 (CAAP02001022.1)	19711	7984-8412	1881-3089	+	173	Putative ripening-related protein [<i>Vitis vinifera</i> , CAB85626]	None
						7347-9086	+	164	Conserved hypothetical protein [<i>Medicago truncatula</i> , ABE79920]	None
						10845-17166	-	1449	Retrotransposon gag protein domain Reverse transcriptase domain Integrase core domain	None
VMC1E11	16	VT, F-V	AM445210.1 (CAAP02001047.1)	32114	26432-26825	817-3807	-	530	Serine/Threonine protein kinase catalytic domain	Signal peptide/ER
						5671-8861	+	547	Tyrosine kinase catalytic domain	Signal peptide/ER
						18105-19513	+	219	DUF1442 domain (unknown function)	Plastid

									ATP binding / protein kinase / protein serine/threonine kinase / protein-tyrosine kinase [<i>Arabidopsis thaliana</i> , NP_199969]	None
					22983-28610	-	798			
VMC7F2	18	MBW, % SDM, MSFW, MSDW	AM464881.2 (CAAP02001498.1)	28046	24475-24950	*1555-9683	+	538	Elongation factor 1-gamma [<i>Prunus avium</i> , Q9FUM1]	None/Possibly plastid
					25131-27824	+	85		MADS-box protein 5 [<i>Vitis vinifera</i> , AAM21345]	None

The predicted genes specifically containing the SSR sequences are in boldface, those with suspect extremely long introns (more than 3000 nt) are underlined, those lacking the transcription start site or the polyA sequence are marked with an asterisk. When two subcellular localization predictions were reported, the first one was obtained with SignalP 3.0 [94], the second one with Predotar 1.03 [93].

In brackets are reported contigs identified after BLASTN alignment against the Whole-Genome Shotgun reads (WGS) database [37]