



## ***New Phytologist* Supporting Information Figs S1–S7 and Tables S1–S7, S9 & S10**

Article title: Genome wide association links candidate genes to resistance to *Plum Pox Virus* in apricot (*Prunus armeniaca*)

Authors: Stéphanie Mariette, Fabienne Wong Jun Tai, Guillaume Roch, Aurélien Barre, Aurélie Chague, Stéphane Decroocq, Alexis Groppi, Yec'han Laizet, Patrick Lambert, David Tricon, Macha Nikolski, Jean-Marc Audergon, Albert Glenn Abbott and Véronique Decroocq

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**Table S1** Information for each accession of the study

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**Table S5** Evolution of the mean value of  $\theta$  ( $4N_e\mu$ ) and of  $\varepsilon$  (sequencing error) as a function of minimum coverage

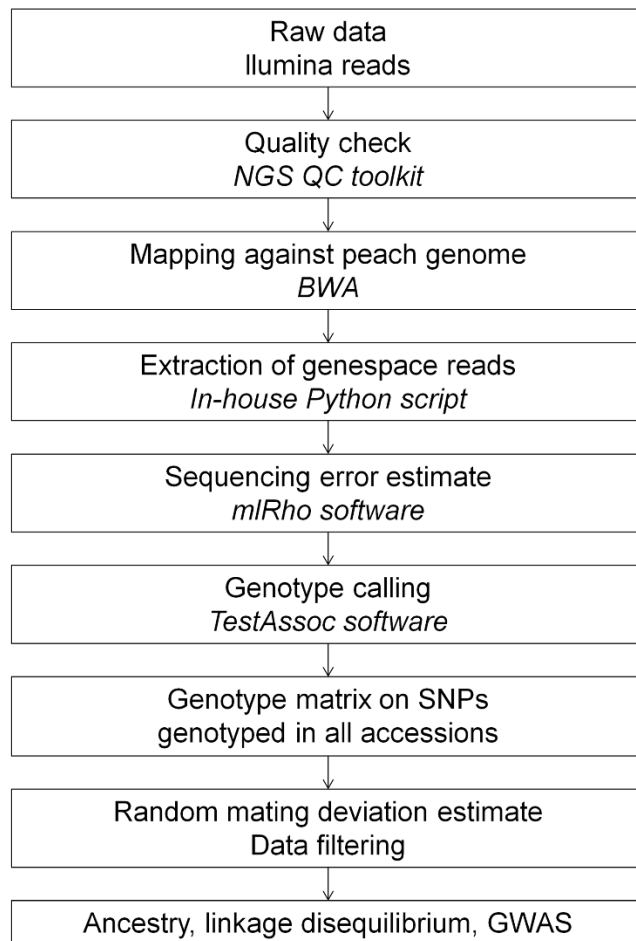
**Table S6** Ancestry of each accession obtained with the *fastStructure* program for  $K = 2$  and for four MAF filterings (MAF\_0, MAF < 0.7%, MAF < 1.4%, MAF < 5%)

**Table S7** Influence of genetic structure and relatedness on interchromosomal and long-range linkage disequilibrium

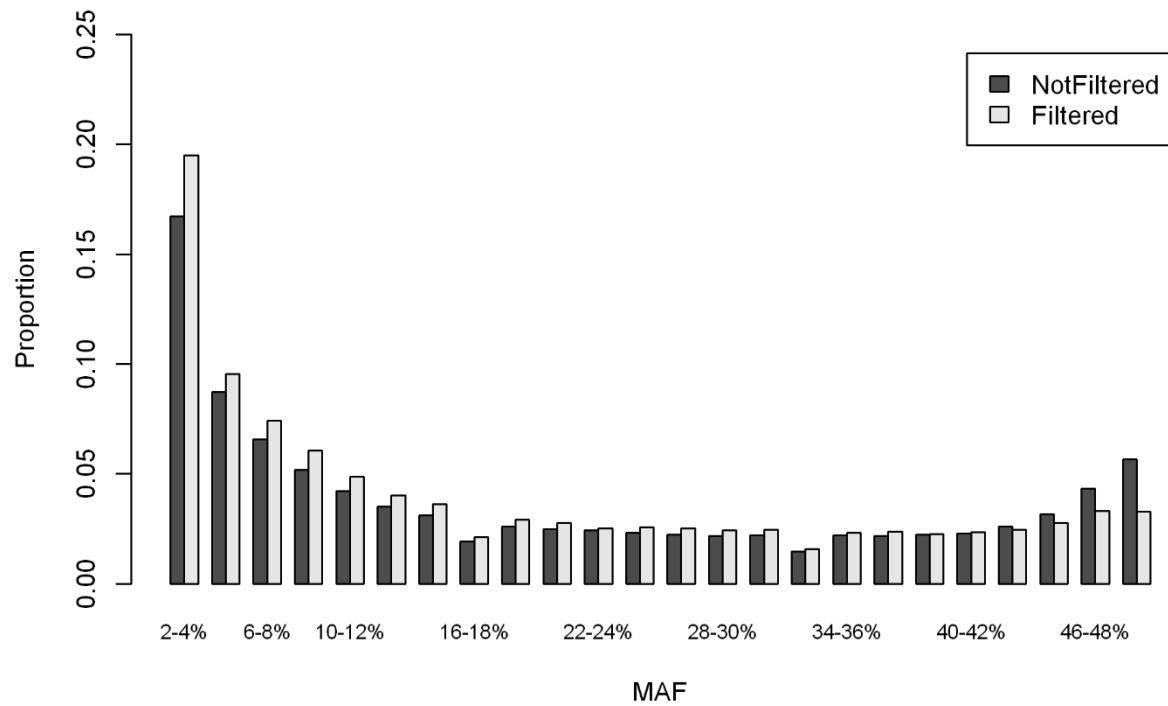
**Table S8** List of significant SNPs obtained with the Q + K model (separate Excel file)

**Table S9** List of validated SNPs

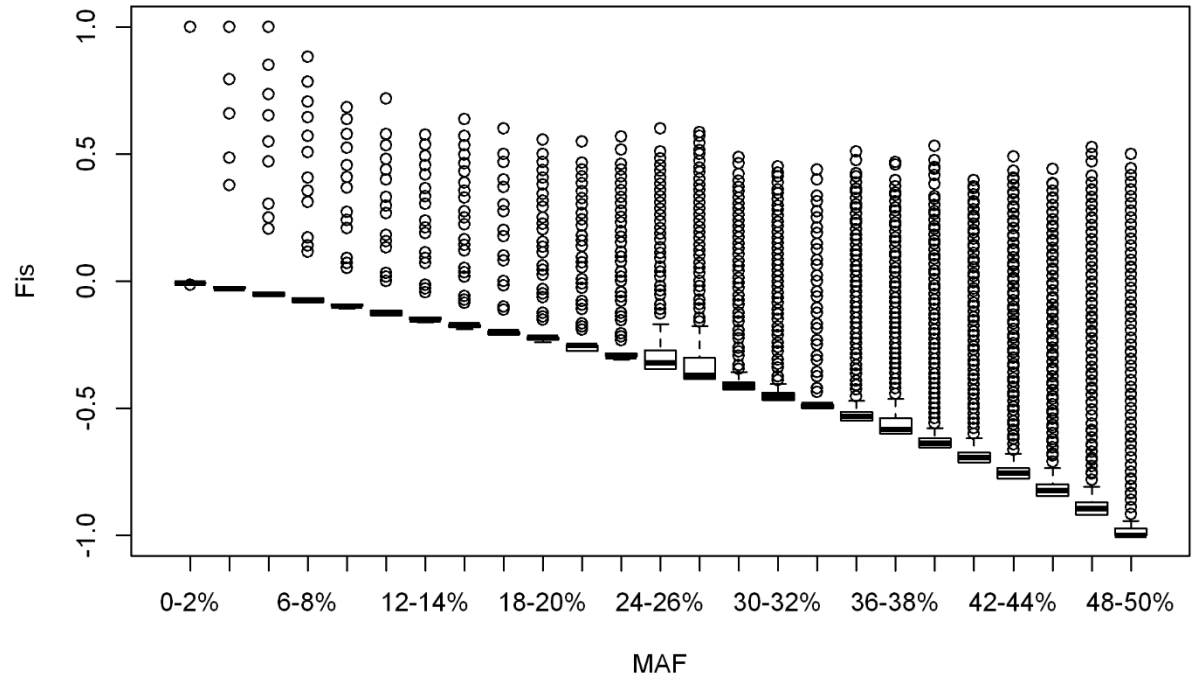
**Table S10** Pairwise linkage disequilibrium on linkage group one



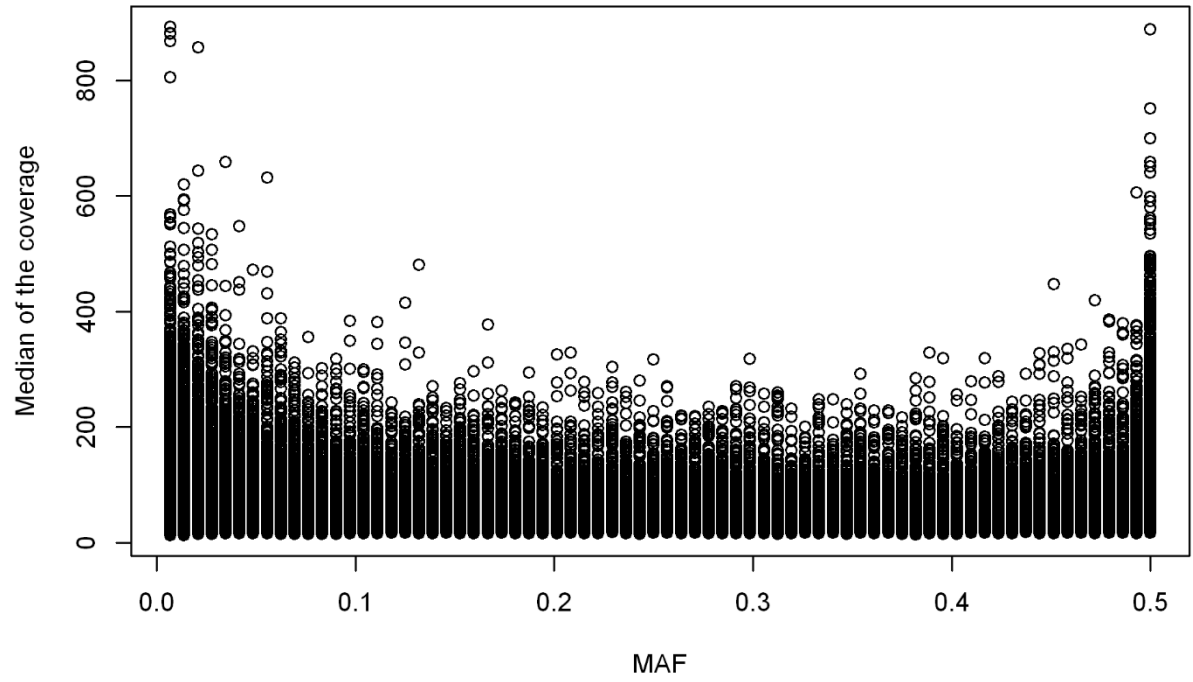
**Fig. S1** Flow chart for the bioinformatics pipeline.



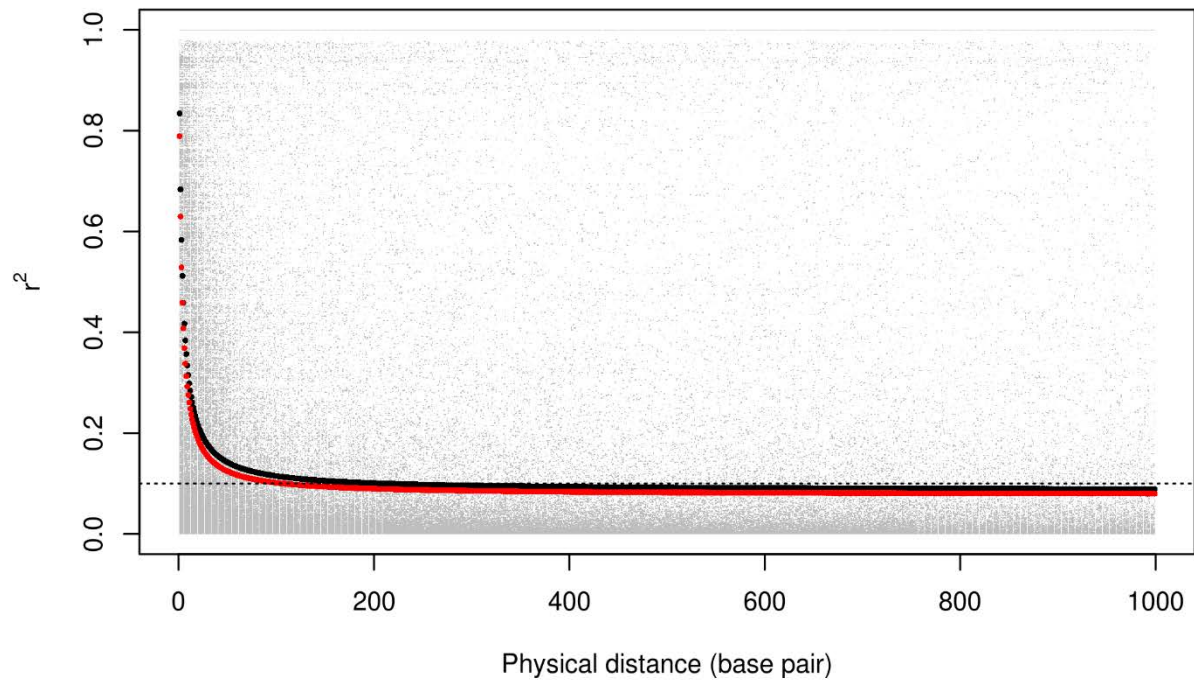
**Fig. S2** Minor allele frequency for the filtered and not filtered data. For clarity of the figure, MAF inferior to 2% were removed.



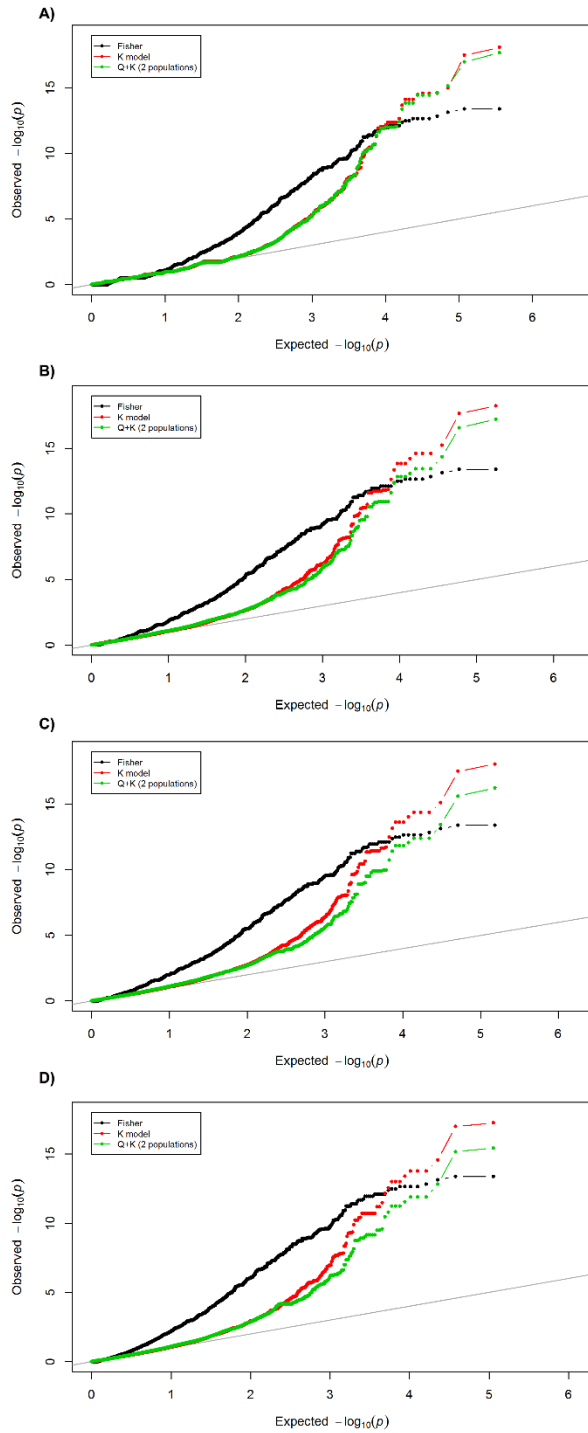
**Fig. S3**  $F_{IS}$  assessed as  $1-H_O/H_E$  as a function of MAF for the not filtered data.



**Fig. S4** Depth of coverage of each SNP as a function of MAF for the not filtered data.

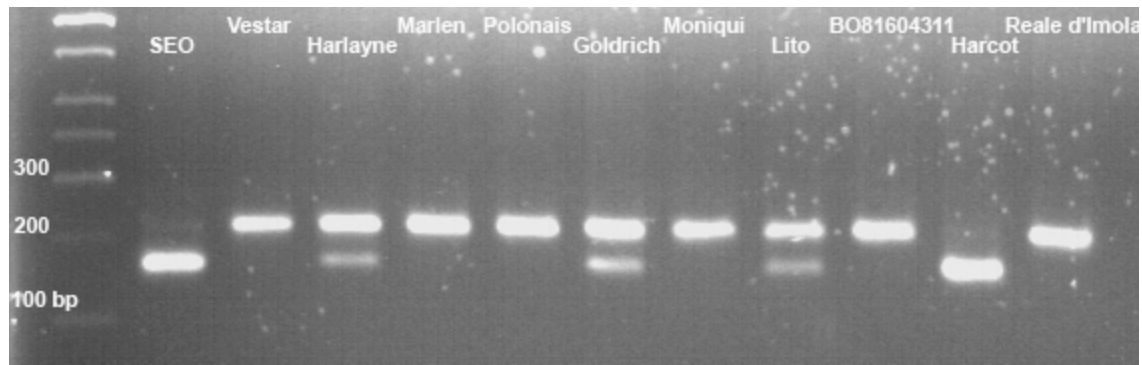


**Fig. S5** Decrease of linkage disequilibrium with the physical distance for the  $r^2$  estimate (black line) and for the  $r^2$  estimate corrected by genetic structure and genetic relatedness (red line). Those estimates were obtained with the LDcorSV R library for the whole sample of 72 accessions. All pairwise values for a physical distance inferior to 1 kb were considered. All  $r^2$  values (not corrected) are represented on the figure.



**Fig. S6** QQ-plot for tested GWAS model using *fastStructure*. Polymorphic loci used in the *fastStructure* analysis were either (a) not filtered (MAF\_0), or selected after removing any SNP with (b) MAF < 0.7%, (c) MAF < 1.4% or (d) removing anything with a MAF < 5%.





**Fig. S7** Polymorphism of the SNP LG1\_11196394. DNA fragments were separated by agarose gel electrophoresis. The upper lane is depicting susceptible apricot accessions while the lower lane is showing pattern for resistant accessions. PCR fragments were digested with the Nde1 restriction enzyme. 'BO81604311' is a variety obtained by the University of Bologna and is originating from a cross between 'Reale d'Imola' and 'San Castrese'.

**Table S1** Information for each accession of the study

Accession number	Accession registered name	Synonym*	Origin	Phenotyping data	Reference for phenotype
A0010	SUCRE DE HOLUB		Hungary	2	This work
A0039	PRECOCE AMPUIS		France	2	This work
A0076	PECHE DE NANCY		France	2	This work
A0157	ROUGE DU ROUSSILLON		France	2	This work
A0300	MEI HWANG		Chine	2	This work
A0500	MONIQUI		Spain	2	This work
A0539	POIZAT		France	2	This work
A0544	CAFONA		Italy	2	Martinez-Gomez <i>et al.</i> (2000)
A0634	HENDERSON		USA	1	This work
A0654	PAVIOT		France	2	Martinez-Gomez <i>et al.</i> (2000)
A0660	BERGERON		France	2	This work
A0665	LUIZET		France	2	Martinez-Gomez <i>et al.</i> (2000)
A0682	MORDEN 604		Canada	2	This work
A0804	SCREARA		France	2	This work
A0862	PSEUDO ROYAL		USA	1	This work
A0882	MADARSKA NARIJLEPSIA		Slovakia	2	This work
A0892	SILISTRA X ANANAS		Romania	2	This work
A1236	MANICOT		France	2	This work
A1267	BADAMI		Iran	2	This work
A1314	ARROGANTE		Spain	2	Martinez-Gomez <i>et al.</i> (2000)
A1343	CANINO		Spain	2	This work
A1453	PERFECTION		USA	2	This work
A1693	NIKITSKII		Ukraine	1	This work
A1710	SUPER ROUGE		France	2	This work
A1711	AVIKALINE		France	2	This work
A1793	TARDIF DE BORDANEIL		France	2	This work
A1809	PRECOCE DE TYRINTHE		Greece	2	This work
A1811	HARCOT		Canada	1	This work
A1813	LAYCOT		Canada	1	This work
A1814	HARGRAND		Canada	2	This work
A1956	PALSTEYN	Palstein	South Africa	2	Martinez-Gomez <i>et al.</i> (2000)
A2065	MAROUCHE n4		Morocco	2	This work
A2067	MAROUCHE n°14		Morocco	2	This work

A2069	CAID AGDZ n2		Morocco	2	This work
A2129	ROUGE DE FOURNES		France	2	This work
A2156	VEECOT		Canada	1	Martinez-Gomez <i>et al.</i> (2000)
A2204	BEBECO	Bebecou	Greece	2	Martinez-Gomez <i>et al.</i> (2000)
A2205	ANDSWEE		Iran	1	This work
A2217	SUNGLO		Canada	1	This work
A2219	VIVAGOLD		Canada	2	This work
A2311	LAMBERTIN n°1		France	2	This work
A2340	SATURN		Romania	2	This work
A2343	OLIMP		Romania	2	This work
A2348	EREVANI		Armenia	2	This work
A2382	STELLA		USA	1	Martinez-Gomez <i>et al.</i> (2000)
A2490	TARDIF DE TAIN		France	2	This work
A2635	MOORPARK		USA	2	Martinez-Gomez <i>et al.</i> (2000)
A2662	ALFRED		USA	1	Martinez-Gomez <i>et al.</i> (2000)
A2734	BOUCHERAN BOUTARD		France	2	This work
A2894	ORANGERED STANDARD	Bahrt or Rutbhart	USA	1	This work
A2928	EARLY BLUSH		USA	1	This work
A3521			Iran	2	This work
A3522			Iran	2	This work
A3698VS	VESTAR		Slovakia	2	This work
A3862	ROBADA		USA	1	This work
A4222	LARCLYD		New-Zeeland	2	This work
A4294	INCOMPARABLE DE MALISSARD	Malissard	France	1	This work
A4316			Italy	1	This work
A4322	PRIBOTO		France	1	This work
A4373	Bo 90 610 010=Bora		Italy	1	Poggi Pollini <i>et al.</i> (2008)
A4374	MURCIANA		Spain	1	This work
A4804			Italy	1	This work
Bulida	BULIDA		Spain	2	Martinez-Gomez <i>et al.</i> (2000)
Goldrich	GOLDRICH		USA	1	This work
Harlayne	HARLAYNE		Canada	1	This work
Monacco_Bello	MONACO BELLO		Italy	2	Martinez-Gomez <i>et al.</i> (2000)
Precoce_d'Imola	PRECOCE D'IMOLA		Italy	2	Martinez-Gomez <i>et al.</i> (2000)
Reale_d'Imola	REALE D'IMOLA		Italy	2	Martinez-Gomez <i>et al.</i>

					<i>al.</i> (2000)
San_Castresse	SAN CASTRESE		Italy	2	Martinez-Gomez <i>et al.</i> (2000)
SEO	STARK EARLY ORANGE	Earle Orange	USA	1	This work
Shalakh	SHALAKH	Yerevani	Armenia	2	Zuriaga <i>et al.</i> (2013)
Velázquez	VELAZQUEZ		Spain	2	Martinez-Gomez <i>et al.</i> (2000)

Accession number, accession registered name, synonym, origin and phenotyping data. \*From UPOV, Technical working party for fruit crops. Thirty-Second Session, Valencia, Spain, 1–5 October 2001.

**Martinez-Gomez P, Dicenta F, Audergon JM. 2000.** Behaviour of apricot (*Prunus armeniaca* L.) cultivars in the presence of sharka (*plum pox potyvirus*): a review. *Agronomie* **20**: 407–422.

**Poggi Pollini C, Bianchi L, Babini AR, Vicchi V, Liverani A, Brandi F, Giunchedi L, Rubies Autonell C, Ratti C. 2008.** Evaluation of *Plum Pox Virus* infection on different Stone Fruit tree varieties. *Journal of Plant Pathology* **90**: S1.27–S21.31.

**Zuriaga E, Soriano JM, Zhebentyayeva T, Romero C, Dardick C, Canizares J, Badenes ML. 2013.** Genomic analysis reveals MATH gene(s) as candidate(s) for *Plum pox virus* (PPV) resistance in apricot (*Prunus armeniaca* L.). *Molecular Plant Pathology* **14**: 663–677.

**Table S2** Phenotypic evaluation method for PPV resistance or susceptibility

	<b>Resistant accession</b>	<b>Susceptible accession</b>
Phenotypic rating	1	2
Symptoms on 'GF305' rootstock	+	+
Symptoms on apricot grafted accession	-*	+ or -
ELISA assay	-	+

\*Sporadic, localized symptoms can be observed on some accessions but they do not generalize.

**Table S3** Basic bioinformatics results for each accession

Name	Accession_ID	Sequenced by	Number of reads	Number of reads after filtering (FR)	Mapped reads (% of FR)	Mapped reads on genespace (% of FR)
SUCRE DE HOLUB	A0010	Kannapolis	58 735 440	53 893 902	56.11%	26.97%
PRECOCE AMPUIS	A0039*	GATC	179 064 312	143 214 760	49.59%	23.13%
PECHE DE NANCY	A0076*	GATC	122 304 448	105 424 534	52.08%	23.45%
ROUGE DU ROUSSILLON	A0157*	GATC	159 792 028	131 211 302	48.32%	21.95%
MEI HWANG	A0300	GATC	52 549 998	40 400 732	48.39%	22.71%
MONIQUI	A0500*	GATC	104 169 396	84 449 540	50.30%	23.16%
POIZAT AMELIORATION DARNAUD	A0539	GATC	38 313 868	28 905 580	49.94%	22.51%
CAFONA	A0544*	GATC	401 257 350	357 281 758	50.98%	22.24%
HENDERSON	A0634	GATC	58 616 272	45 868 616	49.96%	22.64%
PAVIOT	A0654*	GATC	400 782 048	328 630 160	50.24%	23.19%
BERGERON	A0660	Kannapolis	35 552 638	33 982 888	53.45%	23.11%
LUIZET	A0665	GATC	96 116 902	77 366 990	49.77%	23.37%
MORDEN 604	A0682	Kannapolis	34 946 244	33 427 988	48.62%	20.40%
SCREARA	A0804	GATC	72 393 536	58 061 162	50.45%	23.54%
PSEUDO ROYAL	A0862	GATC	60 015 952	49 843 106	49.67%	21.32%
MADARSKA NARIJLEPSIA	A0882	GATC	56 528 588	42 510 118	50.54%	22.99%
SILISTRA X ANANAS	A0892	GATC	68 210 596	52 205 854	49.59%	23.08%
MANICOT	A1236	GATC	50 402 540	39 784 548	50.65%	22.75%
BADAMI	A1267	Kannapolis	35 527 074	34 001 336	52.58%	22.98%
ARROGANTE	A1314	Kannapolis	57 452 476	51 623 626	55.37%	26.09%
CANINO	A1343*	GATC	148 324 796	121 576 180	48.01%	22.56%
PERFECTION	A1453	Kannapolis	36 536 916	35 117 754	54.44%	23.61%
NIKITSKII	A1693	Kannapolis	65 380 548	58 569 064	55.84%	25.17%
SUPER ROUGE	A1710	GATC	65 760 850	52 573 164	50.37%	24.12%
AVIKALINE	A1711	Kannapolis	64 201 948	57 462 404	56.04%	26.82%
TARDIF DE BORDANEIL TYPE1	A1793	GATC	47 306 978	38 587 884	50.47%	22.60%
PRECOCE DE TYRINTHE	A1809	GATC	81 728 830	65 705 516	50.92%	23.31%
HARCOT	A1811*	GATC	218 574 844	186 464 500	50.43%	21.71%
LAYCOT	A1813	Kannapolis	50 307 744	44 739 638	55.91%	25.71%
HARGRAND	A1814	GATC	42 447 764	32 649 080	50.85%	22.17%
PALSTEYN	A1956	Kannapolis	85 338 108	76 666 958	55.43%	25.61%
MAROUCH n°4	A2065	Kannapolis	71 146 458	64 295 206	55.65%	25.32%
MAROUCH n°14	A2067	GATC	40 076 858	29 955 032	50.82%	23.61%
CAID AGDZ n°2	A2069	Kannapolis	71 314 116	63 899 010	55.72%	25.81%
ROUGE DE FOURNES	A2129	GATC	44 134 376	34 774 394	51.38%	22.93%
VEECOT	A2156	Kannapolis	72 451 224	65 230 908	55.13%	25.88%
BEBECO	A2204*	GATC	151 088 024	121 934 978	49.91%	22.83%
ANDSWEE	A2205	GATC	50 528 126	41 196 216	50.82%	22.83%

SUNGLO	A2217	Kannapolis	59 033 216	52 625 496	55.67%	26.22%
VIVAGOLD	A2219	Kannapolis	70 127 080	63 221 356	56.74%	26.58%
LAMBERTIN n°1	A2311*	GATC	275 826 032	219 922 536	49.70%	22.43%
SATURN	A2340	Kannapolis	68 032 308	61 179 380	56.18%	27.29%
OLIMP	A2343	Kannapolis	66 943 410	61 356 414	55.65%	26.54%
EVERANI	A2348	Kannapolis	64 103 486	58 420 972	55.87%	25.99%
STELLA	A2382	Kannapolis	36 295 238	34 685 342	53.57%	21.35%
TARDIF DE TAIN	A2490	GATC	59 741 380	46 081 886	50.97%	23.47%
MOORPARK	A2635	Kannapolis	66 831 358	60 164 706	55.83%	26.90%
ALFRED	A2662	GATC	54 348 316	42 782 990	51.19%	23.72%
BOUCHERAN BOUTARD	A2734	GATC	78 961 434	62 824 920	50.67%	24.00%
ORANGERED STANDARD	A2894	GATC	38 381 772	27 744 272	50.10%	21.90%
EARLYBLUSH	A2928	GATC	39 650 940	31 114 106	50.78%	23.31%
	A3521	Kannapolis	41 588 794	37 427 124	56.76%	26.92%
	A3522	Kannapolis	69 700 050	60 753 304	55.85%	27.06%
VESTAR	A3698VS	Kannapolis	64 346 216	58 813 854	55.82%	25.69%
ROBADA	A3862	GATC	42 087 168	32 528 844	48.92%	22.09%
LARCLYD	A4222	GATC	54 526 174	42 606 988	51.07%	23.28%
INCOMPARABLE DE MALISSARD	A4294	GATC	45 396 718	35 941 248	49.41%	22.52%
	A4316*	GATC	114 415 466	99 350 894	51.84%	22.58%
PRIBOTO	A4322	Kannapolis	69 470 216	61 228 452	54.66%	25.25%
BO 90 610 010 (BORA)	A4373	GATC	75 344 454	66 764 786	55.30%	25.99%
MURCIANA	A4374	Kannapolis	48 331 824	38 097 616	50.05%	23.68%
	A4804	GATC	64 351 644	53 860 654	50.06%	22.26%
BULIDA	Bulida	Kannapolis	57 137 724	50 416 708	54.88%	24.50%
REALE D'IMOLA	Reale_d'Imola	Kannapolis	78 308 502	70 577 658	51.14%	21.55%
HARLAYNE	Harlayne	Kannapolis	84 499 978	75 374 996	51.43%	20.28%
MONACO BELLO	Monoco_Bello	Kannapolis	61 841 102	56 221 198	56.04%	25.96%
PRECOCE D'IMOLA	Precoce_d'Imola	Kannapolis	73 425 586	65 987 556	55.44%	26.03%
GOLDRICH	Goldrich	Kannapolis	69 675 984	62 114 542	51.99%	21.68%
SAN CASTRESE	San_Castrese	Kannapolis	67 084 194	60 033 208	55.32%	26.06%
STARK EARLY ORANGE	SEO	Kannapolis	48 396 468	43 163 800	50.41%	20.87%
SHALAKH	Shalakh	Kannapolis	77 700 646	70 979 028	52.57%	22.86%
VELAZQUEZ	Velázquez	Kannapolis	46 142 574	42 493 310	55.27%	24.57%

Number of sequenced reads, number of reads after quality filtering, number of mapped reads, number of reads that fall in the peach gene space. \*These genomes had >2 read files, all the read files were merged which can explain the high number of reads for these genomes.

**Table S4** Number of polymorphic loci identified after each step of filtering

Filtering step	Number of SNPs	Number of covered peach genes**	Length of covered peach genespace	Genespace average SNP density
Unfiltered SNPs restricted to the genespace	over 3,000,000	-	c. 90%	-
Polymorphic loci with complete genotype information*	349,995	17,609 (63.20%)	57,713,320 bp (79.42%)	1 SNP every 165 bp
Depth at the SNP (putative paralogy filtering)	177,599	17,025 (61.10%)	56,668,419 bp (77.99%)	1 SNP every 319 bp
Removing SNPs with MAF < 0.7%	89,261	14,642 (52.55%)	51,290,987 bp (70.59%)	1 SNP every 575 bp
Removing SNPs with MAF < 1.4%	76,921	13,979 (50.17%)	49,625,636 bp (68.29%)	1 SNP every 645 bp
Filtering with a 5% lower limit of MAF	56,708	12,507 (44.89%)	45,570,683 bp (62.71%)	1 SNP every 804 bp

\*Number of loci which were still polymorphic considering a coverage of 8X depth and loci for which we had genotype information for all individuals. \*\*Considering that the 27,864 genes in the peach genome encompass 72,665,440 bp (gff3 file on the GDR [www.rosaceae.org](http://www.rosaceae.org)).



**Table S5** Evolution of the mean value of  $\theta$  ( $4N_e\mu$ ) and of  $\varepsilon$  (sequencing error) as a function of minimum coverage

Minimum coverage	$\theta$ ( $4N_e\mu$ )	Sequencing error
>4X	8.13E-03	2.22E-03
>6X	8.01E-03	2.20E-03
>8X	7.88E-03	2.19E-03
>9X	7.82E-03	2.19E-03
>10X	7.79E-03	2.18E-03
>12X	7.88E-03	2.21E-03
>14X	8.20E-03	2.25E-03

**Table S6** Ancestry of each accession obtained with the fastStructure program for K = 2 and for four MAF filterings (MAF\_0, MAF < 0.7%, MAF < 1.4%, MAF < 5%)

Accession number	Phenotyping data	Ancestry for K = 2			
		MAF_0	MAF < 0.7%	MAF < 1.4%	MAF < 5%
A0634	1	1	Admixed	Admixed	Admixed
A0862	1	1	Admixed	Admixed	Admixed
A1693	1	1	Admixed	Admixed	Admixed
A1811	1	1	Admixed	Admixed	Admixed
A1813	1	1	Admixed	Admixed	Admixed
A2156	1	1	Admixed	Admixed	Admixed
A2205	1	1	Admixed	Admixed	Admixed
A2217	1	1	Admixed	Admixed	Admixed
A2382	1	1	Admixed	Admixed	Admixed
A2662	1	1	1	Admixed	Admixed
A2894	1	Admixed	Admixed	Admixed	Admixed
A2928	1	Admixed	Admixed	2	2
A3862	1	Admixed	Admixed	Admixed	Admixed
A4294	1	1	Admixed	Admixed	Admixed
A4316	1	1	Admixed	Admixed	Admixed
A4322	1	1	Admixed	2	2
A4373	1	1	Admixed	2	2
A4374	1	1	Admixed	Admixed	Admixed
A4804	1	1	Admixed	2	2
Goldrich	1	1	Admixed	2	2
Harlayne	1	1	Admixed	2	2
Stark Early Orange	1	1	Admixed	Admixed	Admixed
A0010	2	1	1	1	1
A0039	2	1	1	1	1
A0076	2	1	1	1	1
A0157	2	1	1	1	1
A0300	2	1	Admixed	Admixed	Admixed
A0500	2	1	1	1	1
A0539	2	Admixed	1	1	1
A0544	2	1	1	1	1
A0654	2	1	1	1	1
A0660	2	1	1	1	1
A0665	2	1	1	1	1
A0682	2	1	1	1	1
A0804	2	1	1	1	1
A0882	2	1	1	1	1
A0892	2	1	1	1	1

A1236	2	1	1	1	1
A1267	2	Admixed	Admixed	Admixed	Admixed
A1314	2	1	1	1	1
A1343	2	1	1	1	1
A1453	2	1	Admixed	Admixed	Admixed
A1710	2	1	1	1	1
A1711	2	1	1	1	1
A1793	2	1	1	1	1
A1809	2	1	Admixed	Admixed	Admixed
A1814	2	Admixed	Admixed	Admixed	Admixed
A1956	2	1	Admixed	Admixed	Admixed
A2065	2	1	1	1	1
A2067	2	Admixed	1	1	1
A2069	2	1	1	1	1
A2129	2	1	Admixed	Admixed	Admixed
A2204	2	1	1	1	1
A2219	2	1	Admixed	Admixed	Admixed
A2311	2	1	Admixed	Admixed	Admixed
A2340	2	1	1	1	1
A2343	2	1	1	1	1
A2348	2	1	Admixed	Admixed	Admixed
A2490	2	1	1	1	1
A2635	2	1	1	1	1
A2734	2	1	1	1	1
A3521	2	1	Admixed	Admixed	Admixed
A3522	2	1	Admixed	Admixed	Admixed
A3698VS	2	1	Admixed	Admixed	Admixed
A4222	2	1	Admixed	Admixed	Admixed
Bulida	2	1	1	1	1
Monaco Bello	2	1	1	1	1
Precoce d'Imola	2	1	Admixed	Admixed	Admixed
Reale d'Imola	2	1	1	1	1
San Castrese	2	1	Admixed	Admixed	Admixed
Shalakh	2	Admixed	Admixed	2	2
Velázquez	2	1	1	1	1

**Table S7** Influence of genetic structure and relatedness on interchromosomal and long-range linkage disequilibrium

	Interchromosomal	Long-range (>1 Mb)	Short-range (<1 Mb)
$r^2$	152.686 (25%)	227.859 (38%)	223.518 (37%)
$r^2_{vs}$	18.853 (8%)	59.891 (26%)	152.792 (66%)

**Table S9** List of validated SNPs

SNP	Significance rank in the EMMAX analysis	Name of the SNP marker (dCAPS)	Polymorphic between 11 apricot accessions	Forward primer <sup>1</sup>	Reverse primer <sup>1</sup>	Restriction enzyme
scaffold1_11548906	1	SNP_LG1_11548906	√	TCAATAAGCAAAATGTTTCACTCA	CCTAGATCAGAGTCGAGCTTATTATA	<i>DraI</i>
scaffold1_8157485	2	SNP_LG1_8157485 °	√	GCCAGTTTCCTGTAGCAAAAGTAC	TGGTATGATTATTTCTCTCGTTTCC	<i>ScaI</i>
scaffold1_11199476	3	SNP_LG1_11199476	√	GCTGTCCCCTCTAAAACAGCT	AGTTCAGTGCTTATATTTATGGCA	<i>PvuII</i>
scaffold1_8101365	4	SNP_LG1_8101365	√	CTTCTTCTGGATCAGACACCATCAGTC	GCTTGCCACCAAGATTAAG	<i>BstXI</i>
scaffold1_8104371	6	SNP_LG1_8104371	√	GACACACCCTTACCTCTTAAAAGC	GAAAGGTTAAAGCCYTTTACTAAATA	<i>SspI</i>
scaffold1_8325258	7	SNP_LG1_8325258	√	CTAATAAACTGGACCTGCAGCAT	TTGCAAACATTGCCAAAAGG	<i>SphI</i>
scaffold1_11196394	13	SNP_LG1_11196394	√	GATGAATACTTCCTTTAAATATGCATA	ACCCAACCTTTGCGCTTTGT	<i>NdeI</i>
scaffold1_11164527	15	SNP_LG1_11164527	√	CAGGAAATTGTCTTAATGGTCACCAC	GAAATCTAATGCAATCCCTCAA	<i>DraIII</i>
scaffold1_10867606	19	SNP_LG1_10867606	-*	AGACATATCCTGCACACTGCT	TGCACCGTATATAATCCTCTCAAGC	<i>HindIII</i>
scaffold1_10925115	20	SNP_LG1_10925115	√	GGAAGTTCTTTCTTTCTGAAGGT	ATCGGTACCCAATCAAGCAGTA	<i>AccI</i>
scaffold1_11226179	22	SNP_LG1_11226179	√	AATTGTTGTAGCATTGGCTGT	GATCAGATAATGACACTGACGCG	<i>MluI</i>
scaffold1_11226791	23	SNP_LG1_11226791	√	GCTTCCATTGACACATCTTGC7TA	GCTCTGTTGTTTCTGATGGAG	<i>AflIII</i>
scaffold1_11597307	25	SNP_LG1_11597307	√	GAAGGCTTGCAATTAGAAAATGC	CAGTRGCAGAAGCCCACAAG	<i>AvaiIII (NsiI)</i>
scaffold1_8247948	26	SNP_LG1_8247948	√	ATGTTTGCATGTAAGAAATTTGGAT	AGGAGCTGGAATGTACCATCA	<i>FokI</i>
scaffold1_8406669	27	SNP_LG1_8406669	√	CAAGTCTCCCGTGCCAAGT	TCTCTGAAGAAAACAGGAACCAT	<i>XmnI</i>

√SNP marker tested and polymorphic among 11 apricot accessions. -\*dCAPS marker not functional over the eleven apricot accessions tested (no PCR fragment generated). °Previously developed and tested in segregating populations in Decroocq *et al.* (2014). <sup>1</sup>In italics, nucleotides modified in order to introduce a restriction site.

**Decroocq S, Chague A, Lambert P, Roch G, Audergon JM, Geuna F, Chiozzotto R, Bassi D, Dondini L, Tartarini S *et al.* 2014.** Selecting with markers linked to the PPVres major QTL is not sufficient to predict resistance to *Plum Pox Virus* (PPV) in apricot. *Tree Genetics & Genomes* **10**: 1161–1170.

