

## Epigenetic regulation of *Verticillium dahliae* virulence: does DNA methylation level play a role?

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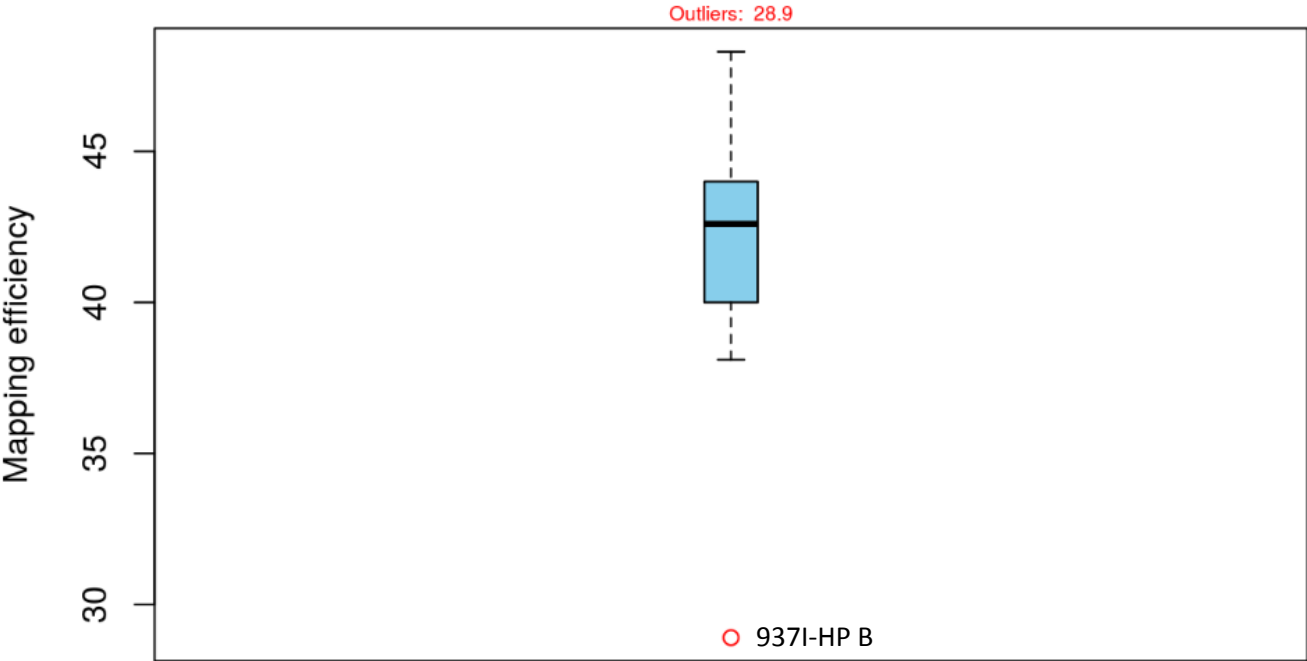


8g0000050.1	5'-AMP-activated protein kinase subunit gamma	2194	26,5	1,207839562	8g0000050.1	2194	-67	-3,053783045	8g0000050.1	2194	59	2,689152233	8g0000050.1	2194	-77,5	-3,532360985
8g0000180.1	Cutinase	967	63	6,514994829	8g0000180.1	967	-32	-3,309203723	8g0000180.1	967	10	1,034126163	8g0000180.1	967	-17,5	-1,809720786
8g0000310.1	Nicotianamine synthase	1309	27	2,062643239	8g0000310.1	1309	-61	-4,660045837	8g0000310.1	1309	16,5	1,260504202	8g0000310.1	1309	-24,5	-1,871657754
8g0000370.1	Ribosomal RNA large subunit methyltransferase E	466	22,5	4,82832618	8g0000370.1	466	-7	-1,502145923	8g0000370.1	466	11	2,360515022	8g0000370.1	466	-24,5	-5,25751073
8g0000420.1	ATP synthase subunit alpha	509	23	4,518664047	8g0000420.1	509	-33	-6,483300589	8g0000420.1	509	9,5	1,866404715	8g0000420.1	509	-13	-2,554027505
904g0000030.1	CAP-Gly domain-containing linker protein 4	847	10,5	1,239669422	904g0000030.1	847	-27,5	-3,246753247	904g0000030.1	847	46,5	5,489964581	904g0000030.1	847	-23	-2,715466352
918g0000010.1	Transcriptional regulator of yeast form adherence 3	1982	41	2,068617558	918g0000010.1	1982	-53	-2,674066599	918g0000010.1	1982	66	3,329969728	918g0000010.1	1982	-25,5	-1,286579213
91g0000070.1	WD repeat-containing protein 1	3284	43,5	1,324604141	91g0000070.1	3284	-171,5	-5,22228989	91g0000070.1	3284	84,5	2,573081608	91g0000070.1	3284	-89	-2,710109622
925g0000010.1	Meiotically up-regulated gene 9 protein	1651	40	2,422774076	925g0000010.1	1651	-72,5	-4,391278013	925g0000010.1	1651	43,5	2,634766808	925g0000010.1	1651	-38,5	-2,331920049
92g0000170.1	Unknown protein	786	27,5	3,498727735	92g0000170.1	786	-25	-3,180661578	92g0000170.1	786	34,5	4,389312977	92g0000170.1	786	-45	-5,72519084
932g0000010.1	Solute carrier family 2, facilitated glucose transporter member 2	1952	37,5	1,921106557	932g0000010.1	1952	-73	-3,739754098	932g0000010.1	1952	38	1,946721312	932g0000010.1	1952	-28,5	-1,460040984
944g0000020.1	Protein VTS1	2006	23,5	1,171485543	944g0000020.1	2006	-128	-6,380857428	944g0000020.1	2006	25,5	1,271186441	944g0000020.1	2006	-69,5	-3,464606182
957g0000030.1	Esterase	1882	98	5,207226355	957g0000030.1	1882	-98,5	-5,233793836	957g0000030.1	1882	41,5	2,205100956	957g0000030.1	1882	-26,5	-1,408076514
95g0000040.1	50S ribosomal protein L21	932	40	4,291845494	95g0000040.1	932	-36,5	-3,916309013	95g0000040.1	932	12,5	1,341201717	95g0000040.1	932	-26	-2,789699571
95g0000170.1	1D-myo-inositol 2-acetamido-2-deoxy-alpha-D-glucopyranoside deacetylase	450	15,5	3,444444444	95g0000170.1	450	-15,5	-3,444444444	95g0000170.1	450	21,5	4,777777778	95g0000170.1	450	-6	-1,333333333
95g0000230.1	ATP-dependent RNA helicase DHX8	2791	52,5	1,88104622	95g0000230.1	2791	-125,5	-4,496596202	95g0000230.1	2791	69	2,472232175	95g0000230.1	2791	-64	-2,293084916
965g0000020.1	Unknown protein	789	85	10,77313055	965g0000020.1	789	-51	-6,463878327	965g0000020.1	789	39,5	5,006337136	965g0000020.1	789	-38,5	-4,879594423
97g0000010.1	Nucleoporin GLE1	1709	24,5	1,433586893	97g0000010.1	1709	-122,5	-7,167934465	97g0000010.1	1709	39,5	2,311293154	97g0000010.1	1709	-30,5	-1,784669397
97g0000090.1	Unconventional myosin-XV	1274	33	2,590266876	97g0000090.1	1274	-93	-7,299843014	97g0000090.1	1274	27	2,119309262	97g0000090.1	1274	-16	-1,25588697
97g0000140.1	DNA-directed RNA polymerase subunit beta	334	55,5	16,61676647	97g0000140.1	334	-16,5	-4,940119761	97g0000140.1	334	12,5	3,74251497	97g0000140.1	334	-24	-7,185628743
97g0000160.1	U3 small nucleolar RNA-associated protein 13	2824	38	1,345609065	97g0000160.1	2824	-209	-7,400849858	97g0000160.1	2824	106,5	3,771246459	97g0000160.1	2824	-63,5	-2,248583569
987g0000030.1	Unknown protein	1220	14,5	1,18852459	987g0000030.1	1220	-57,5	-4,713114754	987g0000030.1	1220	39	3,196721312	987g0000030.1	1220	-13	-1,065573771
996g0000010.1	Unknown protein	952	82,5	8,665966387	996g0000010.1	952	-42	-4,411764706	996g0000010.1	952	41,5	4,359243698	996g0000010.1	952	-30,5	-3,203781513
99g0000050.1	Unknown protein	1715	22,5	1,311953353	99g0000050.1	1715	-107,5	-6,268221574	99g0000050.1	1715	46	2,682215743	99g0000050.1	1715	-23,5	-1,370262391
99g0000140.1	Unknown protein	475	56,5	11,89473684	99g0000140.1	475	-14,5	-3,052631579	99g0000140.1	475	20	4,210526316	99g0000140.1	475	-6	-1,263157895
9g0000220.1	Unknown protein	2602	41,5	1,594926979	9g0000220.1	2602	-79	-3,036126057	9g0000220.1	2602	51,5	1,979246733	9g0000220.1	2602	-36	-1,383551115
9g0000240.1	Unknown protein	764	35,5	4,646596859	9g0000240.1	764	-41	-5,366492147	9g0000240.1	764	25,5	3,337696335	9g0000240.1	764	-26,5	-3,468586387





**Figure S1** Mapping efficiency of bisulfite treated PE reads with its own genome.



**Figure S2** GO term analysis of the 831 genes selected.

