Figure S1: Barplot showing offspring contribution to the study population by the parents used in the current study, A) Sires and B) Dams.

Table S1: Wild populations allelic frequencies of 4 of the variants associated with VNN resistance located in the 3'UTR region of the *ENSDLAG00005026832 (IFI27L2A)* gene.

| Variant	Reference (Ref)	Alternative (Alt)	ATL Ref	ATL Alt	WMED Ref	WMED Alt	EMED Ref	EMED Alt
CHR3:10081901	T	G	0.85	0.15	0.87	0.13	0.25	0.75
CHR3:10081923	C	T	0.92	0.08	0.95	0.05	0.27	0.73
CHR3:10082148	C	T	0.77	0.23	0.75	0.25	0.18	0.82
CHR3:10082380	T	C	0.65	0.35	0.80	0.20	0.18	0.82

Alternative allele – VNN resistance allele, Reference allele – susceptible allele, ATL – Atlantic population (susceptible), WMED – West Mediterranean population (susceptible), EMED – East Mediterranean population (resistant).

VARIANT: CHR3:10077301

CCTGGTGAGTACCACT**G**TTACTTTGACAATT>CCTGGTGAGTACCACT**A**TTACTTTGACAATT

TFBS	ModelID	Database	WT score	MT score	WT strand	MT strand	Prediction	Score
KLF15	TFFM0942.1	jaspar2022DetailedTFFMs	0.0225	0.6857	minus	plus	gain	0.8039

*TFBS: Name of the transcription factor, **ModelID**: ID of the model in the source database, **Database**: Source database of the model, **wt_score, mt_score**: The highest score in the reference and mutated sequence, **wt_strand, mt_strand**: Strand of the location with the highest score in the reference and mutated sequence, **Prediction**: Prediction of a gain or loss of TFBS, or NA if not prediction was possible, **Score**: Score of prediction between -1 (likely TFBS loss) and +1 (likely TFBS gain)
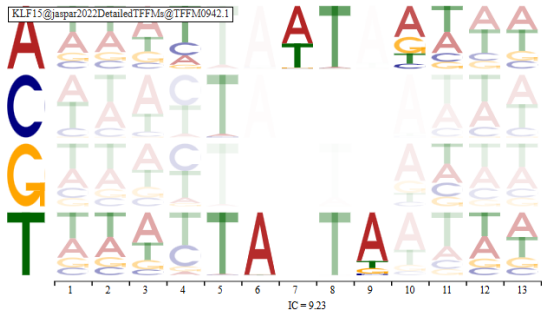
VARIANT: CHR3:10081209

CTGCAGGTTTCACCTCAGCTGGA**G**TAGCTGCAGGCTCCATT>CTGCAGGTTTCACCTCAGCTGGA**A**TAGCTGCAGGCTCCATT

TFBS	ModelID	Database	WT score	MT score	WT strand	MT strand	Prediction	Score
TEAD4	TFFM0110.1	jaspar2022DetailedTFFMs	0.0201	0.7912	minus	plus	gain	0.9392
ZNF140	TFFM0634.1	jaspar2022DetailedTFFMs	0.0132	0.8483	plus	plus	gain	0.9808

*TFBS: Name of the transcription factor, **ModelID**: ID of the model in the source database, **Database**: Source database of the model, **wt_score, mt_score**: The highest score in the reference and mutated sequence, **wt_strand, mt_strand**: Strand of the location with the highest score in the reference and mutated sequence, **Prediction**: Prediction of a gain or loss of TFBS, or NA if not prediction was possible, **Score**: Score of prediction between -1 (likely TFBS loss) and +1 (likely TFBS gain)
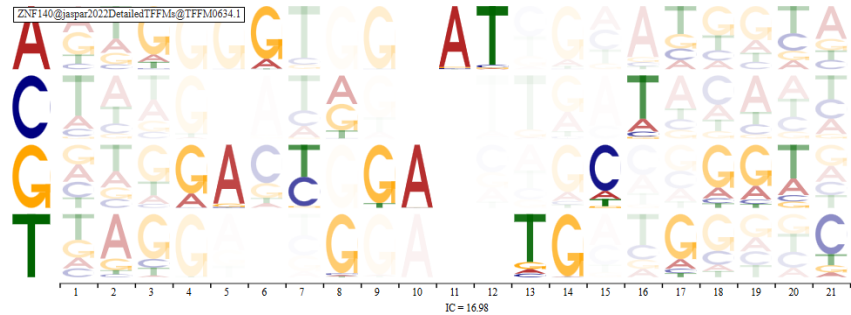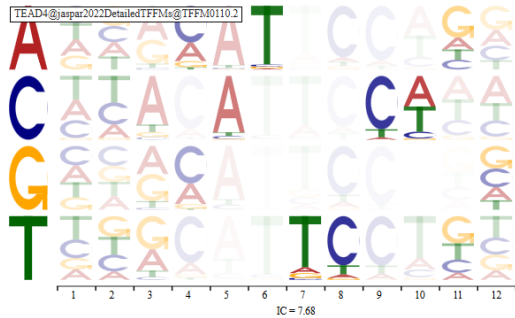

Figure S2: Predicted TFBS loss or gain effect results summary from FABIAN-variant of two putative causal variants (**CHR3:10077301** and **CHR3:10081209**).