nature genetics

SUPPLEMENTARY INFORMATION

https://doi.org/10.1038/s41588-018-0283-9

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Accounting for proximal variants improves neoantigen prediction

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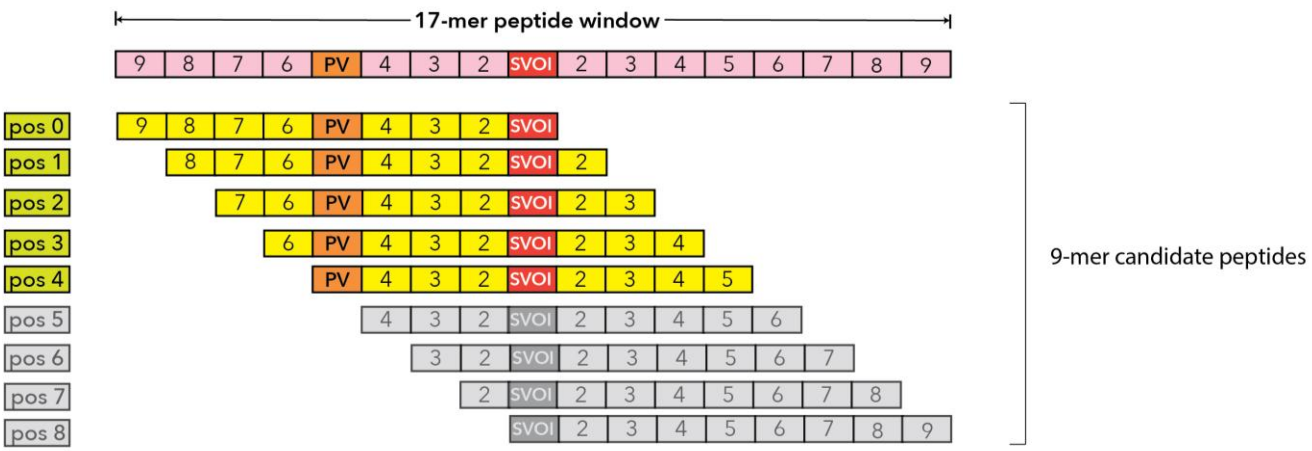
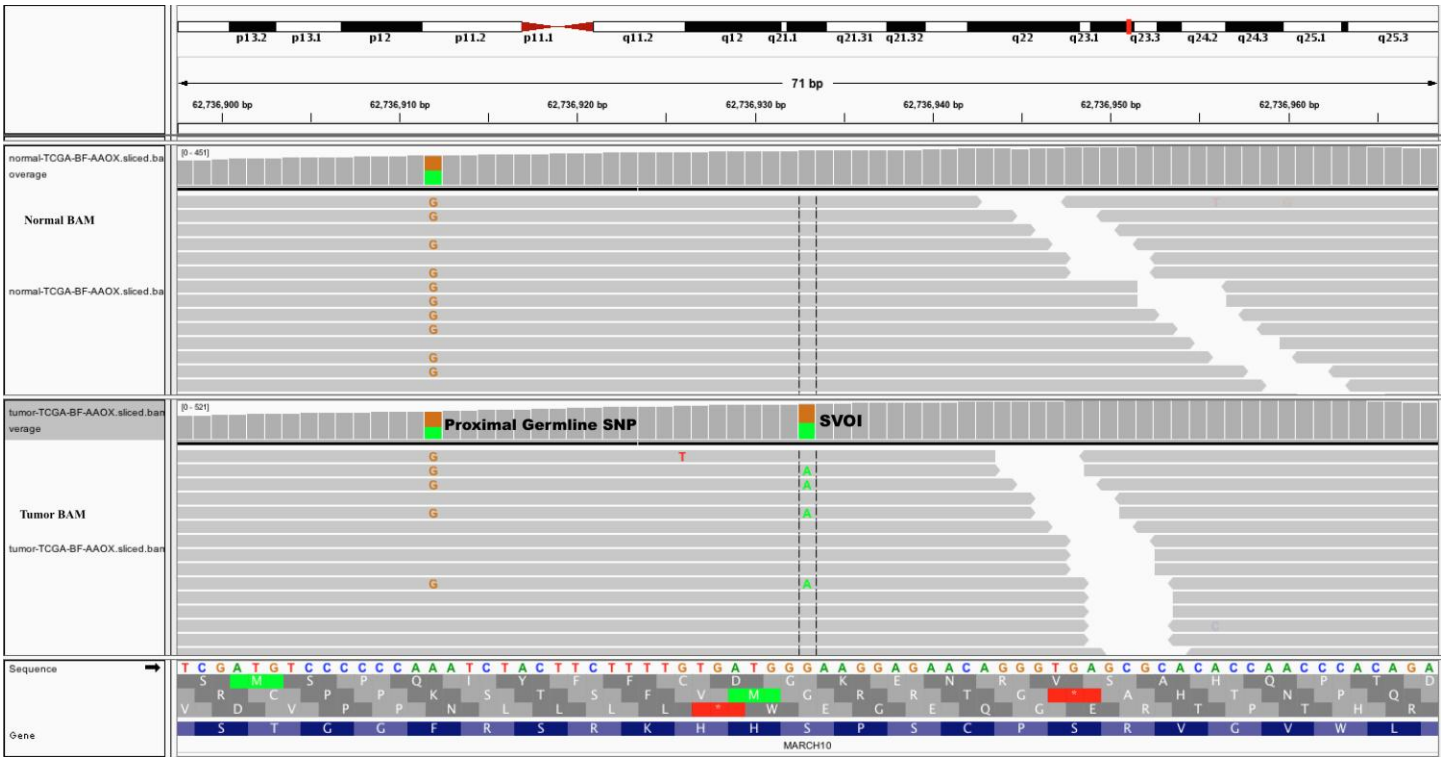

17-mer peptide window
9 8 7 6 PV 4 3 2 SVOI 2 3 4 5 6 7 8 9
pos 0
pos 1
pos 2
pos 3
pos 4
pos 5
pos 6
pos 7
pos 8
9-mer candidate peptides

Supplementary Figure 1

Example of candidate neoantigen evaluation.

This figure shows the possible sub-peptide registers for selection of a candidate neoantigen of length 9. The 17-mer peptide window for a 9-mer candidate is selected by scanning 8 amino acids on each side of the mutated amino acid resulting from the SVOI (red box). Only those registers that contain amino acid changes resulting from both—the proximal variant (PV; orange box), as well as the SVOI (red box)—were considered for this analysis (five peptides shown in yellow for this example). The remaining registers shown (gray boxes) contain the SVOI but are not affected by the proximal variant.



Supplementary Figure 2

Example of a germline SNP within the proximity of a somatic SNV.

An example from one of the TCGA melanoma samples with a missense SNV that overlaps a germline SNP (dbSNP ID: rs9891498), 21 nucleotides upstream. When translated, the germline SNP results in the S357F (NP_001275708.1:p.Phe357Ser) alteration and is 7 amino acids downstream of the missense somatic variant F350S (NP_001275708.1:p.Ser350Phe) in *MARCH10*.