Additional file 2: pVACview inputs

Tool/Package Name		**pVACtools**	**NeoFox**	**Vaxrank**	**Antigen.garnish**	**NeoPredPipe**
Variant Level Inputs	Genomic Coordinates	🟩	🟨	🟩	🟥	🟩
	Mutation Position	🟩	🟩	🟥	🟩	🟩
	Gene Name	🟩	🟩	🟩	🟥	🟩
	Amino Acid Change	🟩	🟨	🟥	🟩	🟥
	DNA Depth	🟩	🟨	🟥	🟥	🟥
	DNA VAF	🟩	🟨	🟥	🟥	🟥
	Gene Expression	🟩	🟨	🟥	🟥	🟩
	RNA VAF	🟩	🟨	🟩 Provides "Variant allele RNA read count"	🟥	🟥
	RNA Depth	🟩	🟨		🟥	🟥
Transcript Level Inputs	Transcript Expression	🟩	🟨	🟥	🟥	🟥
	Transcript Support Level	🟩	🟨	🟥	🟥	🟥
	Biotype	🟩	🟨	🟥	🟥	🟥
	Length	🟩	🟨	🟥	🟥	🟥
	Location of variant in transcript	🟩	🟨	🟥	🟩	🟥
Peptide Level Inputs	Minimum Peptide Sequence and matched HLA	🟩	🟩	🟩	🟩	🟩
	Peptide sequences (from different registers of same variant)	🟩	🟥	🟩	🟩	🟩
	Peptides from different transcripts	🟩	🟥	🟥	🟨 The tool will only predict peptides derived from user-input transcript.	🟥
	Predicted Binding Affinities	🟩	🟩	🟩	🟩	🟩
	Multiple prediction algorithms	🟩	🟩	🟩 User needs to compile from multiple output files (each corresponding to one algorithm)	🟩	🟥
	Class I and Class II prediction algorithms	🟩	🟩	🟩	🟩	🟩
	Multiple binding measurements (e.g. IC50, precentile) available	🟩	🟩	🟥	🟩	🟥
	Algorithms with different training data (e.g. in vitro binding, elution data)	🟩	🟥	🟥	🟩	🟩 Uses netMHCpan-4.1
	Binding results for both wildtype and mutant peptides	🟩	🟩	🟩	🟥	🟥
	Binding results available for multiple HLA alleles (not solely best binding HLA allele)	🟩	🟥	🟩	🟩	🟩

Generated by tool with input data (or part of required input)	🟩
Can be added by user as annotation but can't be generated by tool	🟨
Does not exist in output file	🟥