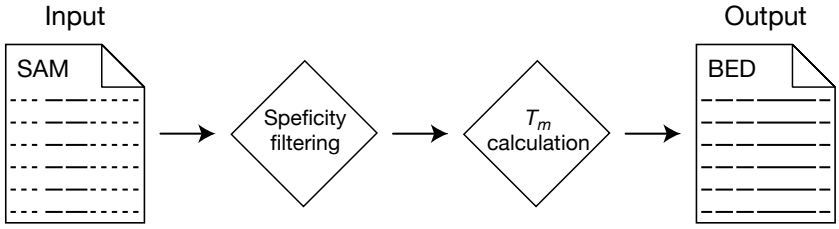
Figure S2

A *outputClean.py*



B

Option	Default	Usage
-f /--file	None	**Required**. Specifies the SAM file to process.
-l /--lda	True	Filter the SAM file using the LDA model.
-u /--unique	False	Filter using unique mode; only keep candidates with 1 reported alignments.
-0 /--zero	False	Filter using zero mode; only keep candidates with 0 reported alignments.
-p /--prob	0.5	The probability threshold for classifying a candidate probe as likely to have off-target binding using the LDA model. Selecting larger values will improve precision (fewer false positives), but at the expense of recall (more false negatives). Selecting lower values will improve recall at the expense of precision.
-T /--Temp	42	The temperature-specific LDA model to use (32, 37, 42, 47, 52, or 57).
-s /--salt	390	The mM Na^+ concentration, default is 390 to match 2X SSC.
-F /--formamide	50	The percent formamide being used.
-R /--Report	False	Writes detailed log file about the behavior of the script if flagged.
-D /--Debug	False	Prints detailed info about the behavior of the script as it runs if flagged.
-M /--Meta	False	Writes a small summary file describing the outcome of the run if flagged.
-o /--output	False	Specifies the stem of the output filename.