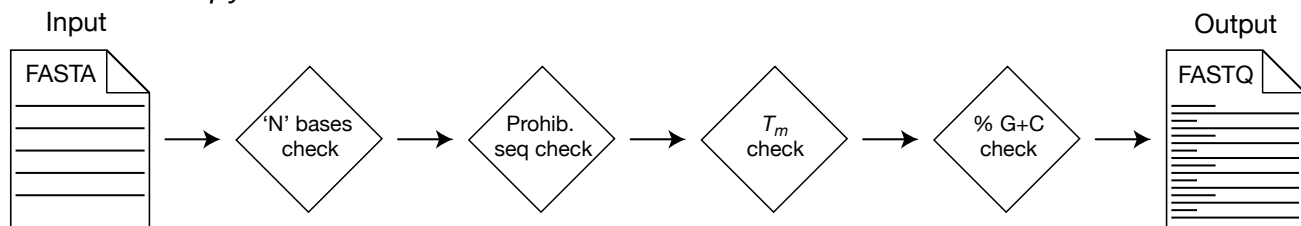


Figure S1**A** *blockParse.py***B**

<u>Option</u>	<u>Default</u>	<u>Usage</u>
-f/--file	None	Required. Specifies the FASTA-formatted file to find candidate probes in.
-l/--minLength	36	The minimum allowed probe length.
-L/--maxLength	41	The maximum allowed probe length.
-g/--min_GC	20	The minimum % G + C bases allowed.
-G/--max_GC	80	The maximum % G + C bases allowed.
-t/--min_Tm	42	The minimum salt + formamide adjusted T_m allowed.
-T/--max_Tm	47	The maximum salt + formamide adjusted T_m allowed.
-X/--prohibitedSeqs	'AAAAA,TTTTT,CCCCC,GGGGG'	Prohibited sequence list (separated by commas with no spaces). Any candidate probe containing one of these sequences will be rejected.
-s/--salt	390	The mM Na ⁺ concentration, default is 390 to match 2X SSC.
-F/--formamide	50	The percent formamide being used.
-S/--Spacing	0	The minimum spacing (bp) between adjacent probes.
-c/--dnac1	25	nM concentration of higher conc. strand (e.g. the probe) for thermo. calcs.
-C/--dnac2	25	nM concentration of lower conc. strand (e.g. the target) for thermo. calcs.
-n/--nn_table	'DNA_NN3'	The Biopython Nearest Neighbor thermodynamic table to use.
-H/--header	None	Specifies a custom FASTA header in the format chr:start-stop.
-b/--bed	False	Writes output as a BED file instead of a FASTQ file if flagged.
-O/--OverlapMode	False	Finds all possible candidate probes and ignores '-S' value if flagged.
-v/--verbose	False	Prints info about probe discovery progress as the script runs if flagged.
-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.