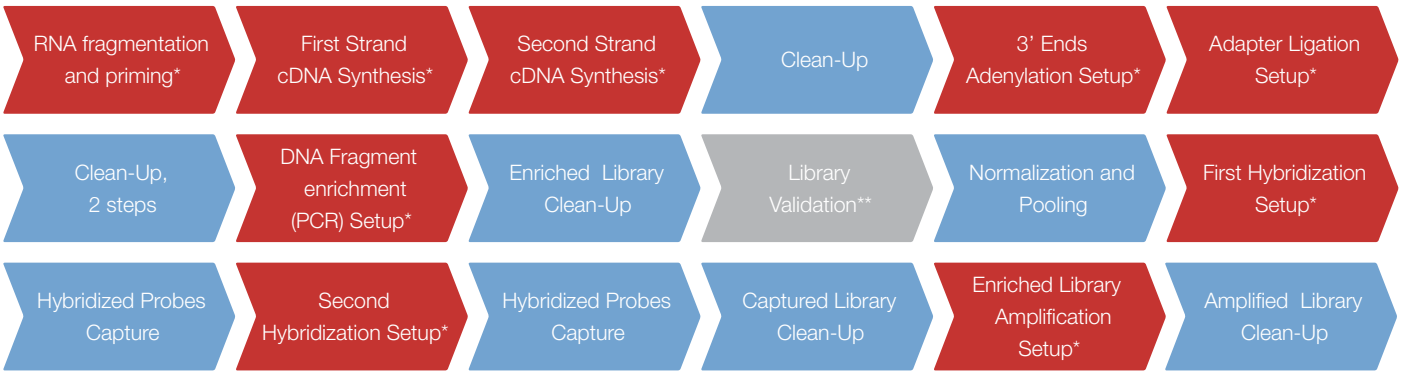
Illumina TruSeq RNA Access

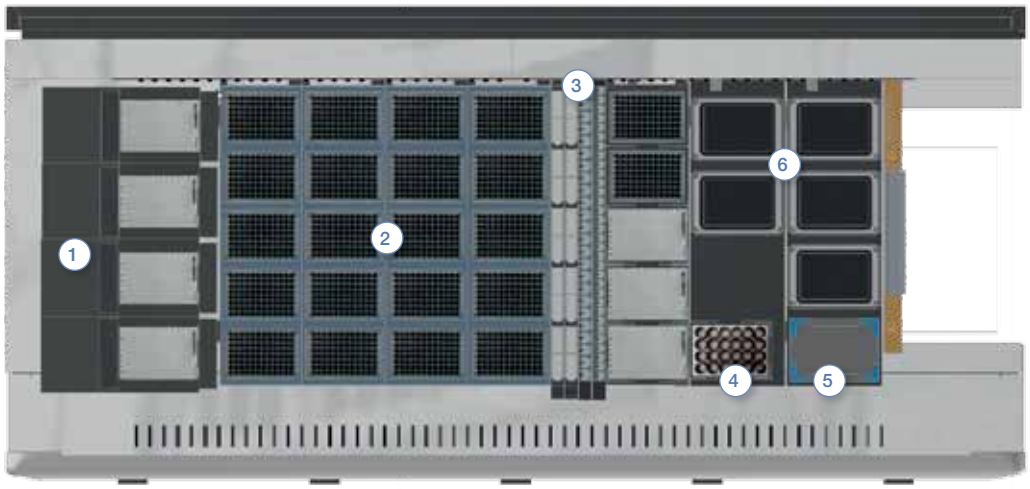
Description and Workflow

This protocol converts total RNA into a library of template molecules of known strand origin and then captures the coding regions of the transcriptome. The resulting library is suitable for subsequent cluster generation and sequencing. The RNA is fragmented into small pieces using divalent cations under elevated temperature. cDNA is generated from the cleaved RNA fragments using random priming during first and second strand synthesis and sequencing adapters are ligated to the resulting double-stranded cDNA fragments. The coding regions of the transcriptome are then captured from this library using sequence-specific probes to create the final library.



** Incubations are performed on Hamilton Heater Shakers (HHS) set at different temperatures. PCR amplification is performed off line. Optional on-line Thermal Cycling with ODTC.*
*** Library Validation is performed off-line on 3rd party devices.*

Deck Layout



1. Plate Stackers
2. Tips
3. Reagents
4. Magnet
5. CPAC
6. Hamilton Heater Shakers (5)

Recommended Platforms

Platform	Pipetting Channels	96 MPH	Batch size	ODTC *
STARlet	8	No	48 samples	No
STAR	8	No/Yes	96 samples	Yes

** On Deck Thermal Cycler*