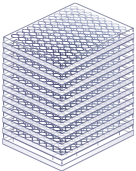
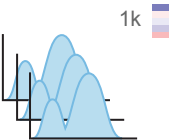
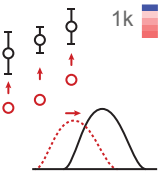
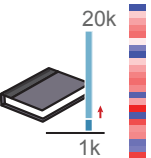
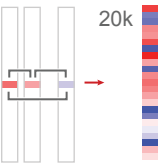
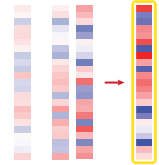










SCAN	DECONVOLUTION	NORMALIZATION	INFERENCE	DIFFERENTIAL EXPRESSION	CONSENSUS	RELATIONSHIPS
 <p>Scan 384-well plates</p>	 <p>Deconvolute 500 colors to 1000 genes</p>	 <p>Scale 80 control genes</p>	 <p>Use landmarks to infer entire transcriptome</p>	 <p>Compare replicate treatments to control</p>	 <p>Collapse multiple shRNA to consensus signatures</p>	 <p>Compute correlation across entire signature data set</p>
LXB 	GEX 	QNORM 	INF DATA 	SIG 	CGS 	GRAPH 
$y = ax^b + c$ $x_{norm} = F_2(F_1(x))$ $g_k = w_0 + \sum_{i=1}^{978} w_i l_i$				$z_i = \frac{x_i - \text{median}(X)}{MAD(X) \times 1.4826}$		$P_{hit}(S, i) = \sum_{\substack{g_j \in S \\ j \leq i}} \frac{ r_j ^p}{N_R}$ $P_{miss}(S, i) = \sum_{\substack{g_j \notin S \\ j \leq i}} \frac{1}{N - N_H}$
$MODZ = \frac{w_a \cdot z_a + w_b \cdot z_b + w_c \cdot z_c + \dots}{w_a + w_b + w_c + \dots}$				$P_{hit} - P_{miss}$		