

2-fold dilutions



1.5-fold
decreasing input



	1	2	4	8	16	32	64	128	Dilution
SS-16	423,000	211,500	105,750	52,875	26,438	13,219	6,609	3,305	
SS-60	282,000	141,000	70,500	35,250	17,625	8,813	4,406	2,203	
SS-10	188,000	94,000	47,000	23,500	11,750	5,875	2,938	1,469	
SS-34	125,333	62,667	31,333	15,667	7,833	3,917	1,958	979	
SS-70	83,556	41,778	20,889	10,444	5,222	2,611	1,306	653	
SS-25	55,704	27,852	13,926	6,963	3,481	1,741	870	435	
SS-40	37,136	18,568	9,284	4,642	2,321	1,160	580	290	
SS-19	24,757	12,379	6,189	3,095	1,547	774	387	193	
SS-28	16,505	8,252	4,126	2,063	1,032	516	258	129	
SS-50	11,003	5,502	2,751	1,375	688	344	172	86	
SS-22	7,335	3,668	1,834	917	458	229	115	57	
Oligo									

Supplementary Table 3.1. *Experiment scheme to investigate the performance of data normalization with ERDN controls.* Predetermined fold-change oligos (SS-10 to SS-70, serving here as spike-ins with known differences in RNA input between samples) were randomized and diluted according to the table above using 1.5-fold differences in the number of input molecules between consecutive oligos. From this mix, 2-fold to 128-fold dilutions were made by serial dilution. Values are in zeptomole/ μg total RNA. Each fold-change mix was then combined with a fixed amount of the ERDN mix and added to equal aliquots taken from a single batch of adult male zebrafish total RNA.