doi:10.1038/nature20781

Supplementary Tables

Table S1. Oligonucleotide sequences. "N" bases represent random bases, with 25% each A,C,G,T.

Oligonucleotide	Sequence
5' adapter, top oligo.	ACA CTC TTT CCC TAC ACG ACG CTC TTC C
5' adapter, bottom oligo.	NNN NNN GGA AGA GCG TCG TGT AGG GAA AGA GTG T*/3SpC3/
3' adapter, top oligo.	/5Phos/AGA TCG GAA GAG CAC ACG TCT GAA CTC CAG TCA C*/3SpC3/
3' adapter, bottom oligo.	GTG ACT GGA GTT CAG ACG TGT GCT CTT CCG ATC TNN NNN* N
Barcoding PCR primer 1	AAT GAT ACG GCG ACC ACC GAG ATC TAC ACT CTT TCC CTA CAC GAC
Barcoding PCR primer 2 (XXXXXX = barcode)	CAA GCA GAA GAC GGC ATA CGA GAT XXX XXX GTG ACT GGA GTT CAG ACG
Re-amplification PCR primer 1	AAT GAT ACG GCG ACC ACC GA
Re-amplifciation PCR primer 2	CAA GCA GAA GAC GGC ATA CGA
Custom Read 1 Primer	ACA CTC TTT CCC TAC ACG ACG CTC TTC C

Table S2. Sequencing depth. Read counts represent aggregate count across technical replicates for each condition.

Library pool	Description	Read Pairs Sequenced	Unique, Filtered Read Pairs
Expt10gy	0gy	31,808,455	21,946,973
Expt1300gy	300gy	229,463,822	124,159,324
Expt1300ctrl	300ctrl	43,929,541	39,634,270
Expt20	0gy	78,57,521	6,888,065
Expt2300	300gy	245,274,091	150,821,920
Expt2300ctrl	300ctrl	39,382,901	33,375,990
Expt30	0gy	7,201,311	5,943,196
Expt3300	300gy	166,062,580	126,897,301
Expt3300ctrl	300ctrl	23,146,100	16,862,506
SizeSel300gy	300gy	13,039,157	2,396,243
SizeSel0gy	0gy	39,061	11,824
SizeSel300ctrl	300ctrl	5,210,567	1,076,867