

Table S3. kanamycin magic pool analysis

Brev2_mariner_magic.bias													
name	nReads	nPstEnd	fPstEnd	nLoc	nlnGene	fStrAgr	nGenesH	mean Loc	med Loc	locBias	meanRd	medRd	rdBias
pTGG31	80910	342	0.0042	555	468	0.5214	386	1.2	1	1.21	173	127	1.36
pTGG32	90704	876	0.0097	619	508	0.5276	407	1.2	1	1.25	172.1	118	1.46
pTGG33	116138	105	0.0009	798	664	0.506	512	1.3	1	1.3	182.6	140.5	1.3
pTGG34	160078	609	0.0038	943	798	0.5075	572	1.4	1	1.4	233.8	170.5	1.37
pTGG35	166592	602	0.0036	1117	942	0.4788	658	1.4	1	1.43	206.9	148	1.4
pTGG36	517712	441	0.0009	3089	2579	0.5145	1182	2.2	1	2.18	356.6	224.5	1.59
pTGG37	314744	1519	0.0048	1943	1647	0.5234	914	1.8	1	1.8	287.8	179	1.61
pTGG38	266552	370	0.0014	1581	1316	0.5091	805	1.6	1	1.63	268.2	188	1.43
pTGG39	588471	386	0.0007	3587	2993	0.5058	1301	2.3	2	1.15	372.3	235	1.58
pTGG40	290265	424	0.0015	1853	1543	0.4841	913	1.7	1	1.69	260.3	183	1.42
Sphingo3_mariner_magic.bias													
name	nReads	nPstEnd	fPstEnd	nLoc	nlnGene	fStrAgr	nGenesH	mean Loc	med Loc	locBias	meanRd	medRd	rdBias
pTGG31	355866	182	0.0005	634	531	0.5574	425	1.2	1	1.25	664.6	241	2.76
pTGG32	810892	118	0.0001	1290	1063	0.5428	746	1.4	1	1.42	847.4	340.5	2.49
pTGG33	35614	92	0.0026	74	63	0.6349	55	1.1	1	1.15	542.8	201	2.7
pTGG34	171542	31	0.0002	245	212	0.4811	178	1.2	1	1.19	797.2	297.5	2.68
pTGG35	456342	29	0.0001	742	631	0.5531	495	1.3	1	1.27	696.2	374	1.86
pTGG36	1093305	141	0.0001	2356	1937	0.603	1216	1.6	1	1.59	659	195.5	3.37
pTGG37	1258271	220	0.0002	2706	2230	0.6	1337	1.7	1	1.67	678.7	259	2.62
pTGG38	65228	83	0.0013	136	119	0.6303	109	1.1	1	1.09	486.9	118	4.13
pTGG39	333178	77	0.0002	809	666	0.6096	519	1.3	1	1.28	480.1	176	2.73
pTGG40	321578	71	0.0002	799	653	0.611	522	1.3	1	1.25	439.7	158	2.78
Sphingo4_mariner_magic.bias													
name	nReads	nPstEnd	fPstEnd	nLoc	nlnGene	fStrAgr	nGenesH	mean Loc	med Loc	locBias	meanRd	medRd	rdBias
pTGG31	365810	215	0.0006	87	64	0.6562	19	3.4	3	1.12	15353.8	15215	1.01
pTGG32	1095367	546	0.0005	375	288	0.5208	140	2.1	1	2.06	5403.7	16.5	327.49
pTGG34	197889	226	0.0011	50	42	0.4524	13	3.2	3	1.08	11306.5	13616	0.83
pTGG35	359222	559	0.0016	84	75	0.48	28	2.7	3	0.89	11891.4	10267.5	1.16
pTGG36	669347	427	0.0006	190	154	0.526	68	2.3	2	1.13	7671.6	5226	1.47
pTGG37	905048	844	0.0009	288	242	0.5372	99	2.4	2	1.22	7903.3	6253	1.26

name – name of the transposon vector or the parts combination of the transposon vector
nReads - total reads for the constructs' barcodes (either past-the-end of the transposon or mapped into genome)
nPstEnd - number of reads that corresponded to a strain that has an insertion within the suicide vector instead of within the genome
fPstEnd - fraction of reads for intact vector
nLoc - number of high-confidence insertions
nlnGene - number of insertions within genes
fStrAgr - fraction of time gene strand = insertion strand (for a good vector, will be very close to 50%)
nGenesH - number of different genes with insertions

The remaining statistics are computed while considering only genes that are hit (with at least one insertion):

meanLoc - average of #insertions per gene
medLoc - median of #insertions per gene
locBias - mean/median #insertions per gene
meanRd - average of #reads per gene
medRd - median of #reads per gene
rdBias - mean/median #reads per gene

