

Table S7. Erythromycin magic pool bias

Cola_mariner_magic.bias													
name	nReads	nPstEnd	fPstEnd	nLoc	nInGene	fStrAgr	nGenesH	meanLoc	medLoc	locBias	meanRd	medRd	rdBias
__p5.1	12063	109	0.009	53	38	0.3684	38	1	1	1	216.1	59.5	3.63
__p5.15	32120	82	0.0026	85	61	0.5246	58	1.1	1	1.05	326.8	66	4.95
__p5.18	19760	51	0.0026	77	56	0.4821	55	1	1	1.02	311.7	162	1.92
_p3.2_p5.18	29760	110	0.0037	169	135	0.5704	128	1.1	1	1.05	174.8	28.5	6.13
p3.3	6006	186	0.031	101	80	0.5	79	1	1	1.01	62.7	18	3.49
_p3.3_p5.12	5065	83	0.0164	68	58	0.5517	57	1	1	1.02	60.6	19	3.19
_p3.3_p5.17	12481	7	0.0006	166	134	0.5672	128	1	1	1.05	83.4	22	3.79
_p3.3_p5.18	4525	46	0.0102	99	86	0.5465	86	1	1	1	46.1	12.5	3.69
_p3.3_p5.24	9212	150	0.0163	159	128	0.6484	126	1	1	1.02	59.8	24	2.49
_p3.3_p5.3	4110	73	0.0178	118	100	0.59	95	1.1	1	1.05	39.6	16	2.47
p3.5	51209	194	0.0038	134	112	0.5357	110	1	1	1.02	335.4	83.5	4.02
_p3.5_p5.17	19064	105	0.0055	64	54	0.463	53	1	1	1.02	290.5	91	3.19
_p3.5_p5.18	229571	91	0.0004	482	401	0.5337	343	1.2	1	1.17	581.1	158	3.68
_p3.5_p5.21	21314	60	0.0028	51	41	0.5122	38	1.1	1	1.08	378.4	35.5	10.66
_p3.5_p5.24	80771	69	0.0009	185	157	0.5541	143	1.1	1	1.1	493	179	2.75
_p3.5_p5.3	50487	515	0.0102	104	86	0.5698	80	1.1	1	1.07	468.1	87.5	5.35
p2.7_p3.1_	8945	132	0.0148	103	80	0.5375	77	1	1	1.04	83.2	35	2.38
p2.7_p3.1_p5.18	3908	163	0.0417	56	47	0.5745	44	1.1	1	1.07	62.7	23.5	2.67
p2.7_p3.2_	8466	133	0.0157	51	36	0.5556	36	1	1	1	147	37	3.97
p2.7_p3.2_p5.10	12392	20	0.0016	64	49	0.449	49	1	1	1	180	86	2.09
p2.7_p3.2_p5.24	8064	21	0.0026	74	62	0.4839	59	1.1	1	1.05	113.2	44	2.57
p2.7_p3.3_	96422	167	0.0017	251	210	0.4714	194	1.1	1	1.08	431.8	197.5	2.19
p2.7_p3.3_p5.10	19799	16	0.0008	71	55	0.5455	55	1	1	1	243.3	159	1.53
p2.7_p3.3_p5.12	23698	38	0.0016	71	56	0.4821	52	1.1	1	1.08	367.4	209	1.76
p2.7_p3.3_p5.13	27090	0	0	79	65	0.5538	61	1.1	1	1.07	365.5	200	1.83
p2.7_p3.3_p5.15	47691	517	0.0108	130	106	0.4151	103	1	1	1.03	382.8	167	2.29
p2.7_p3.3_p5.17	58817	44	0.0007	151	120	0.4917	118	1	1	1.02	417.6	272.5	1.53
p2.7_p3.3_p5.18	58422	0	0	157	136	0.5147	126	1.1	1	1.08	388	221.5	1.75
p2.7_p3.3_p5.21	25897	54	0.0021	80	62	0.4677	57	1.1	1	1.09	297.7	128	2.33
p2.7_p3.3_p5.24	31633	0	0	100	80	0.3875	76	1.1	1	1.05	320.6	121	2.65
p2.7_p3.3_p5.3	46279	17	0.0004	141	115	0.4522	109	1.1	1	1.06	348	154	2.26
p2.7_p3.3_p5.4	20357	8	0.0004	66	58	0.4483	54	1.1	1	1.07	304	166.5	1.83
p2.7_p3.5_	11390	62	0.0054	70	58	0.431	57	1	1	1.02	168.4	54	3.12
p2.7_p3.5_p5.12	13142	93	0.0071	90	74	0.4865	71	1	1	1.04	158.3	59	2.68
p2.7_p3.5_p5.14	7165	15	0.0021	54	44	0.4773	43	1	1	1.02	134.3	89	1.51
p2.7_p3.5_p5.17	12116	28	0.0023	73	59	0.5254	59	1	1	1	158.9	66	2.41
p2.7_p3.5_p5.18	23387	105	0.0045	121	107	0.486	102	1	1	1.05	195.3	80.5	2.43

p2.7_p3.5_p5.24	15676	76	0.0048	103	83	0.506	81	1	1	1.02	153	85	1.8
p2.8_p3.5_	9134	49	0.0054	67	49	0.6735	47	1	1	1.04	163.4	23	7.11
p2.8_p3.5_p5.17	6858	5	0.0007	51	45	0.4667	44	1	1	1.02	111.2	17	6.54
ponti_mariner_magic.bias													
name	nReads	nPstEnd	fPstEnd	nLoc	nInGene	fStrAgr	nGenesH	meanLoc	medLoc	locBias	meanRd	medRd	rdBias
__p5.1	118675	1083	0.0091	576	421	0.5582	383	1.1	1	1.1	220	103	2.14
__p5.10	8416	24	0.0029	63	49	0.3673	48	1	1	1.02	155.5	56.5	2.75
__p5.14	43518	386	0.0089	187	131	0.4885	125	1	1	1.05	256.2	125	2.05
__p5.15	41699	112	0.0027	206	145	0.4621	141	1	1	1.03	206.9	68	3.04
__p5.18	19499	120	0.0062	84	68	0.5441	66	1	1	1.03	232	69.5	3.34
__p5.2	18682	170	0.0091	55	40	0.425	36	1.1	1	1.11	458.7	117.5	3.9
__p5.4	17669	104	0.0059	127	92	0.5435	89	1	1	1.03	137.9	66	2.09
__p5.6	27863	105	0.0038	147	120	0.6	118	1	1	1.02	193.9	91	2.13
_p3.1_p5.24	16080	162	0.0101	60	46	0.5435	44	1	1	1.05	311.5	134.5	2.32
p3.3	179092	1024	0.0057	1067	775	0.5252	650	1.2	1	1.19	201.5	100	2.01
_p3.3_p5.1	244640	1625	0.0066	1443	1056	0.5369	845	1.2	1	1.25	213.6	88	2.43
_p3.3_p5.10	142459	448	0.0031	723	530	0.5434	467	1.1	1	1.13	236.2	91	2.6
_p3.3_p5.11	43946	605	0.0138	249	168	0.5357	159	1.1	1	1.06	190.3	88	2.16
_p3.3_p5.12	25553	59	0.0023	179	126	0.5	124	1	1	1.02	179	54.5	3.29
_p3.3_p5.13	51313	48	0.0009	216	150	0.4933	144	1	1	1.04	243.1	72	3.38
_p3.3_p5.14	55834	25	0.0004	315	226	0.531	213	1.1	1	1.06	184	86	2.14
_p3.3_p5.15	29139	130	0.0045	216	144	0.5	136	1.1	1	1.06	156.1	76.5	2.04
_p3.3_p5.17	69100	745	0.0108	379	271	0.5646	253	1.1	1	1.07	205.2	98	2.09
_p3.3_p5.18	14733	21	0.0014	96	67	0.6567	65	1	1	1.03	173.2	59	2.94
_p3.3_p5.19	25955	208	0.008	172	118	0.5763	114	1	1	1.04	154.4	66.5	2.32
_p3.3_p5.2	60610	415	0.0068	366	269	0.5762	256	1.1	1	1.05	180.9	64.5	2.8
_p3.3_p5.20	50610	197	0.0039	289	201	0.5075	190	1.1	1	1.06	184.7	88	2.1
_p3.3_p5.21	10115	446	0.0441	82	66	0.5152	65	1	1	1.02	128.5	60	2.14
_p3.3_p5.23	22418	0	0	113	90	0.4889	89	1	1	1.01	202.7	91	2.23
_p3.3_p5.24	38241	408	0.0107	303	221	0.5339	210	1.1	1	1.05	139	64.5	2.16
_p3.3_p5.3	40815	2361	0.0578	278	196	0.5102	179	1.1	1	1.09	165.5	82	2.02
_p3.3_p5.4	23791	147	0.0062	145	103	0.5728	102	1	1	1.01	167.7	96	1.75
_p3.3_p5.6	27514	1	0	151	109	0.5321	106	1	1	1.03	187.5	95	1.97
_p3.3_p5.8	10935	0	0	84	62	0.4839	62	1	1	1	152	49	3.1
p3.5	58323	144	0.0025	251	181	0.4586	173	1	1	1.05	258.8	109	2.37
_p3.5_p5.1	64086	336	0.0052	351	246	0.5569	233	1.1	1	1.06	203.5	99	2.06
_p3.5_p5.10	199253	1168	0.0059	813	600	0.5083	507	1.2	1	1.18	293.6	122	2.41
_p3.5_p5.11	86657	255	0.0029	337	240	0.5125	227	1.1	1	1.06	275.6	124	2.22
_p3.5_p5.12	15137	142	0.0094	66	48	0.5625	46	1	1	1.04	260.4	115	2.26
_p3.5_p5.13	22771	181	0.0079	111	84	0.5119	83	1	1	1.01	233.9	103	2.27
_p3.5_p5.14	66966	414	0.0062	336	253	0.5455	234	1.1	1	1.08	235.1	121.5	1.93
_p3.5_p5.15	15336	178	0.0116	87	63	0.5873	60	1.1	1	1.05	177	60.5	2.93
_p3.5_p5.17	24371	171	0.007	111	77	0.5065	74	1	1	1.04	245.1	95	2.58
_p3.5_p5.18	112488	510	0.0045	423	295	0.5458	272	1.1	1	1.08	273.7	109.5	2.5
_p3.5_p5.19	63812	306	0.0048	263	189	0.455	177	1.1	1	1.07	273.3	111	2.46

_p3.5_p5.2	79727	286	0.0036	358	245	0.498	232	1.1	1	1.06	235.2	100	2.35
_p3.5_p5.20	48674	589	0.0121	220	162	0.4691	149	1.1	1	1.09	236	96	2.46
_p3.5_p5.21	19898	207	0.0104	81	65	0.6308	64	1	1	1.02	272.7	82.5	3.31
_p3.5_p5.24	72597	275	0.0038	363	250	0.468	235	1.1	1	1.06	208.8	88	2.37
_p3.5_p5.3	33876	33	0.001	164	123	0.626	120	1	1	1.02	232.7	102.5	2.27
_p3.5_p5.4	14983	215	0.0143	92	72	0.4583	69	1	1	1.04	161	69	2.33
_p3.5_p5.6	80235	163	0.002	395	298	0.4966	271	1.1	1	1.1	218.3	86	2.54
_p3.5_p5.8	13778	62	0.0045	50	35	0.5714	34	1	1	1.03	213.8	132	1.62
_p3.5_p5.9	8592	0	0	54	38	0.5789	38	1	1	1	134.3	58.5	2.3
p2.7_p5.2	12891	19	0.0015	57	41	0.439	39	1.1	1	1.05	265.9	82	3.24
p2.7_p3.2_	14484	104	0.0072	116	91	0.4725	85	1.1	1	1.07	151.2	50	3.02
p2.7_p3.2_p5.1	16822	11	0.0007	176	145	0.4414	142	1	1	1.02	99.6	46	2.16
p2.7_p3.2_p5.10	30620	147	0.0048	278	189	0.4815	182	1	1	1.04	109.4	56	1.95
p2.7_p3.2_p5.11	8633	206	0.0239	115	86	0.5116	86	1	1	1	76	42.5	1.79
p2.7_p3.2_p5.12	4938	6	0.0012	54	41	0.4878	38	1.1	1	1.08	110.6	53.5	2.07
p2.7_p3.2_p5.14	6504	0	0	65	46	0.5435	46	1	1	1	100.8	58.5	1.72
p2.7_p3.2_p5.19	10741	130	0.0121	120	93	0.4624	91	1	1	1.02	82.7	44	1.88
p2.7_p3.2_p5.2	8691	58	0.0067	109	77	0.4805	75	1	1	1.03	85.1	30	2.84
p2.7_p3.2_p5.20	10301	144	0.014	112	90	0.5556	88	1	1	1.02	82	46	1.78
p2.7_p3.2_p5.24	14004	23	0.0016	150	108	0.5093	103	1	1	1.05	100.3	46	2.18
p2.7_p3.2_p5.6	16059	277	0.0172	174	128	0.4609	125	1	1	1.02	94.5	50	1.89
p2.7_p3.3_	272615	636	0.0023	1142	853	0.5064	725	1.2	1	1.18	288.7	117	2.47
p2.7_p3.3_p5.1	132339	1	0	532	409	0.4719	373	1.1	1	1.1	282.7	114	2.48
p2.7_p3.3_p5.10	173579	423	0.0024	607	438	0.484	388	1.1	1	1.13	324.7	123	2.64
p2.7_p3.3_p5.11	74081	50	0.0007	339	250	0.54	240	1	1	1.04	230	132.5	1.74
p2.7_p3.3_p5.12	44312	115	0.0026	167	127	0.5591	122	1	1	1.04	289.8	77.5	3.74
p2.7_p3.3_p5.13	58430	63	0.0011	200	134	0.5224	129	1	1	1.04	273.9	112	2.45
p2.7_p3.3_p5.14	104374	16	0.0002	425	300	0.5233	279	1.1	1	1.08	259.9	123	2.11
p2.7_p3.3_p5.15	46011	54	0.0012	174	124	0.4839	116	1.1	1	1.07	308.6	150.5	2.05
p2.7_p3.3_p5.16	20769	122	0.0059	73	57	0.4912	57	1	1	1	294.4	185	1.59
p2.7_p3.3_p5.17	58647	66	0.0011	274	203	0.4729	190	1.1	1	1.07	237.4	111.5	2.13
p2.7_p3.3_p5.18	41156	118	0.0029	173	124	0.4758	120	1	1	1.03	234	115.5	2.03
p2.7_p3.3_p5.19	68495	138	0.002	292	207	0.4928	198	1	1	1.05	242.9	91.5	2.66
p2.7_p3.3_p5.2	88882	73	0.0008	400	305	0.4754	279	1.1	1	1.09	229.5	112	2.05
p2.7_p3.3_p5.20	107743	67	0.0006	547	386	0.4845	343	1.1	1	1.13	230	108	2.13
p2.7_p3.3_p5.21	13046	52	0.004	68	56	0.5536	54	1	1	1.04	208.6	80.5	2.59
p2.7_p3.3_p5.24	75384	4	0.0001	303	223	0.5022	202	1.1	1	1.1	288.9	118	2.45

p2.7_p3.3_p5.3	56488	13	0.0002	248	185	0.4865	177	1	1	1.05	259.4	89	2.92
p2.7_p3.3_p5.4	116519	73	0.0006	440	303	0.4851	281	1.1	1	1.08	285.1	119	2.4
p2.7_p3.3_p5.6	38842	0	0	175	129	0.4419	123	1	1	1.05	194.5	97	2
p2.7_p3.3_p5.8	76806	20	0.0003	303	215	0.5442	203	1.1	1	1.06	291.5	100	2.91
p2.7_p3.3_p5.9	26582	60	0.0023	95	70	0.4	67	1	1	1.04	275.4	84	3.28
p2.7_p3.5_	26880	149	0.0055	231	175	0.52	165	1.1	1	1.06	124.3	57	2.18
p2.7_p3.5_p5.1	31424	1	0	224	160	0.4375	155	1	1	1.03	141.4	70	2.02
p2.7_p3.5_p5.10	19788	1	0.0001	156	100	0.43	96	1	1	1.04	129.4	62	2.09
p2.7_p3.5_p5.11	14684	221	0.0151	113	84	0.4524	82	1	1	1.02	152.4	57.5	2.65
p2.7_p3.5_p5.12	24115	91	0.0038	192	140	0.4714	136	1	1	1.03	141.8	51	2.78
p2.7_p3.5_p5.13	7433	13	0.0017	57	40	0.475	40	1	1	1	105.8	65	1.63
p2.7_p3.5_p5.14	38599	181	0.0047	343	243	0.5267	232	1	1	1.05	133.7	65.5	2.04
p2.7_p3.5_p5.17	14842	50	0.0034	157	119	0.5462	116	1	1	1.03	104.8	51.5	2.04
p2.7_p3.5_p5.18	20040	79	0.0039	150	109	0.5229	105	1	1	1.04	130.4	59	2.21
p2.7_p3.5_p5.2	17067	6	0.0004	209	155	0.471	151	1	1	1.03	83.8	33	2.54
p2.7_p3.5_p5.20	18823	212	0.0113	162	122	0.5246	119	1	1	1.03	122.3	72	1.7
p2.7_p3.5_p5.21	3447	19	0.0055	55	42	0.4286	40	1.1	1	1.05	73.1	31	2.36
p2.7_p3.5_p5.24	31728	404	0.0127	254	189	0.4656	184	1	1	1.03	128.8	59.5	2.16
p2.7_p3.5_p5.3	9713	118	0.0121	80	64	0.5	62	1	1	1.03	115.1	37.5	3.07
p2.7_p3.5_p5.4	22451	21	0.0009	183	124	0.4274	122	1	1	1.02	141.3	66.5	2.12
p2.7_p3.5_p5.6	12439	0	0	91	69	0.4058	67	1	1	1.03	150.5	80	1.88
p2.7_p3.5_p5.9	5634	0	0	52	39	0.3077	37	1.1	1	1.05	129.2	65	1.99
Pedo557_mariner_magic.bias													
name	nReads	nPstEnd	fPstEnd	nLoc	nInGene	fStrAgr	nGenesH	meanLoc	medLoc	locBias	meanRd	medRd	rdBias
_p3.2_p5.18	34973	4	0.0001	61	52	0.5962	47	1.1	1	1.11	680.4	105	6.48
p3.3	75731	7	0.0001	62	55	0.4727	46	1.2	1	1.2	1432.1	883	1.62
_p3.3_p5.17	72144	0	0	53	40	0.5	33	1.2	1	1.21	1744.6	1010	1.73
_p3.3_p5.21	49292	0	0	52	43	0.6279	36	1.2	1	1.19	1178.2	116	10.16
_p3.3_p5.3	69081	1	0	92	74	0.5135	60	1.2	1	1.23	958.4	196	4.89
_p3.5_p5.18	82676	2	0	121	104	0.5385	94	1.1	1	1.11	735.2	298	2.47
p2.7_p3.3_	46193	12	0.0003	53	44	0.4091	40	1.1	1	1.1	1037.8	420.5	2.47
Cola_Tn5_magic.bias													
name	nReads	nPstEnd	fPstEnd	nLoc	nInGene	fStrAgr	nGenesH	meanLoc	medLoc	locBias	meanRd	medRd	
__p5.11	25178	5410	0.2149	152	139	0.5468	135	1	1	1.03	134.8	30.0	
__p5.23	7142	2050	0.287	87	77	0.5844	77	1	1	1	61.8	12.0	
__p5.5	30285	5969	0.1971	148	127	0.5354	124	1	1	1.02	169.5	57.5	

_p3.2_p5.11	6807	2852	0.419	53	48	0.5833	47	1	1	1.02	74.1	10.0
_p3.2_p5.23	6545	3433	0.5245	81	70	0.5857	69	1	1	1.01	38.6	9.0
_p3.2_p5.7	4374	2275	0.5201	71	60	0.6	58	1	1	1.03	33.7	11.0
p3.3	22457	19685	0.8766	99	91	0.5055	87	1	1	1.05	30	10.0
_p3.3_mult	11088	8615	0.777	52	48	0.5208	46	1	1	1.04	48.3	12.5
_p3.3_p5.11	6307	3931	0.6233	85	79	0.7468	78	1	1	1.01	23.1	11.0
_p3.3_p5.18	5694	3670	0.6445	59	56	0.7143	56	1	1	1	34.2	9.0
_p3.3_p5.20	12547	8704	0.6937	123	114	0.5351	108	1.1	1	1.06	34	11.0
_p3.3_p5.23	3098	1242	0.4009	70	63	0.6508	63	1	1	1	27.9	10.0
_p3.3_p5.4	10423	6203	0.5951	90	87	0.5862	83	1	1	1.05	49.5	13.0
_p3.3_p5.5	13972	5182	0.3709	264	243	0.5473	232	1	1	1.05	35.1	11.0
p3.5	78102	36411	0.4662	259	232	0.5216	220	1.1	1	1.05	158.8	36.0
_p3.5_mult	44338	8112	0.183	214	198	0.4899	184	1.1	1	1.08	176.2	48.0
_p3.5_p5.11	20551	3420	0.1664	98	92	0.6196	89	1	1	1.03	173	32.0
_p3.5_p5.14	35273	8376	0.2375	175	160	0.5312	152	1.1	1	1.05	158.4	33.5
_p3.5_p5.18	40169	6900	0.1718	222	195	0.559	177	1.1	1	1.1	170	59.0
_p3.5_p5.20	27254	9211	0.338	120	104	0.5769	101	1	1	1.03	145.6	23.0
_p3.5_p5.23	36601	3640	0.0995	274	250	0.552	242	1	1	1.03	117.7	38.0
_p3.5_p5.4	61668	8805	0.1428	369	334	0.5539	306	1.1	1	1.09	155	35.5
_p3.5_p5.5	44971	3777	0.084	249	227	0.5683	215	1.1	1	1.06	173	55.0
p2.7_p3.1_p5.23	12350	2721	0.2203	59	58	0.569	56	1	1	1.04	168.1	56.5
p2.7_p3.2_p5.11	5469	1024	0.1872	91	82	0.3171	79	1	1	1.04	49.4	24.0
p2.7_p3.2_p5.14	7783	2829	0.3635	76	72	0.4444	69	1	1	1.04	65.8	42.0
p2.7_p3.2_p5.20	11842	4960	0.4188	84	81	0.5062	78	1	1	1.04	85.1	29.0
p2.7_p3.2_p5.5	10910	2416	0.2214	136	121	0.4545	120	1	1	1.01	65.6	22.0
p2.7_p3.3_	45006	20196	0.4487	196	182	0.489	175	1	1	1.04	125.3	34.0
p2.7_p3.3_mult	11539	1937	0.1679	57	52	0.4038	51	1	1	1.02	181	45.0
p2.7_p3.3_p5.11	8245	964	0.1169	74	71	0.4789	69	1	1	1.03	98.3	47.0
p2.7_p3.3_p5.14	13376	2228	0.1666	95	86	0.5698	86	1	1	1	105.2	29.0
p2.7_p3.3_p5.18	5707	1943	0.3405	54	47	0.5319	47	1	1	1	71.9	21.0
p2.7_p3.3_p5.20	24847	4944	0.199	142	125	0.496	123	1	1	1.02	135.2	41.0
p2.7_p3.3_p5.23	38850	4920	0.1266	253	224	0.5357	211	1.1	1	1.06	143.4	47.0
p2.7_p3.3_p5.4	24226	2199	0.0908	167	152	0.4803	143	1.1	1	1.06	141.5	52.0
p2.7_p3.3_p5.5	52398	3078	0.0587	381	338	0.4882	310	1.1	1	1.09	137.3	56.0
p2.7_p3.5_	14060	7843	0.5578	76	72	0.4028	68	1.1	1	1.06	89.3	59.0
p2.7_p3.5_mult	22159	7259	0.3276	166	153	0.3922	145	1.1	1	1.06	95	37.0
p2.7_p3.5_p5.14	8532	3651	0.4279	65	57	0.5614	56	1	1	1.02	81.2	39.5
p2.7_p3.5_p5.18	8451	2715	0.3213	61	56	0.4107	53	1.1	1	1.06	96.6	39.0
p2.7_p3.5_p5.19	11875	3141	0.2645	72	62	0.4516	59	1.1	1	1.05	101.8	27.0
p2.7_p3.5_p5.20	14646	3584	0.2447	97	85	0.5176	84	1	1	1.01	117.7	47.5

p2.7_p3.5_p5.23	7176	1992	0.2776	57	48	0.5	48	1	1	1	77.9	30.5	
p2.7_p3.5_p5.4	40863	5882	0.1439	379	347	0.4582	319	1.1	1	1.09	102.7	39.0	
p2.7_p3.5_p5.5	39169	4776	0.1219	399	358	0.4749	329	1.1	1	1.09	94.4	36.0	
p2.8_p3.2_p5.4	4102	2531	0.617	63	55	0.5091	55	1	1	1	25.8	6.0	
p2.8_p3.5_	15238	6292	0.4129	140	134	0.6269	124	1.1	1	1.08	69	14.0	
p2.8_p3.5_p5.11	9048	1105	0.1221	85	80	0.575	76	1.1	1	1.05	98.1	16.0	
p2.8_p3.5_p5.14	5374	1546	0.2877	78	74	0.5135	74	1	1	1	50.5	11.5	
p2.8_p3.5_p5.18	3837	999	0.2604	53	48	0.6042	48	1	1	1	55.7	16.0	
p2.8_p3.5_p5.23	7283	636	0.0873	92	80	0.55	79	1	1	1.01	71.7	12.0	
p2.8_p3.5_p5.4	32851	4347	0.1323	375	343	0.5773	318	1.1	1	1.08	83.4	22.0	
p2.8_p3.5_p5.5	22576	2169	0.0961	226	204	0.5882	198	1	1	1.03	93.8	24.0	
p2.8_p3.5_p5.7	9013	521	0.0578	69	63	0.5397	59	1.1	1	1.07	140.6	18.0	
Ponti_Tn5_magic.bias													
name	nReads	nPstEnd	fPstEnd	nLoc	nInGene	fStrAgr	nGenesH	meanLoc	medLoc	locBias	meanRd	medRd	rdBias
__mult	13701	305	0.0223	111	95	0.4842	91	1	1	1.04	107.9	36	3
__p5.11	23105	258	0.0112	124	107	0.6168	104	1	1	1.03	174.9	68	2.57
__p5.19	14025	300	0.0214	96	74	0.4865	72	1	1	1.03	167.6	39.5	4.24
__p5.20	22370	193	0.0086	147	129	0.4264	124	1	1	1.04	159.4	48	3.32
__p5.23	11175	39	0.0035	71	63	0.5714	61	1	1	1.03	177.3	54	3.28
__p5.5	28877	134	0.0046	145	120	0.4667	117	1	1	1.03	203.3	50	4.07
p3.3	42644	651	0.0153	398	337	0.5727	301	1.1	1	1.12	120.6	40	3.02
_p3.3_mult	18558	243	0.0131	186	171	0.5556	164	1	1	1.04	102.5	28	3.66
_p3.3_p5.1	8952	2066	0.2308	64	56	0.6429	55	1	1	1.02	118.2	29	4.08
_p3.3_p5.11	48920	53	0.0011	410	357	0.535	318	1.1	1	1.12	133.5	45.5	2.93
_p3.3_p5.14	10268	75	0.0073	97	77	0.6104	75	1	1	1.03	100	41	2.44
_p3.3_p5.16	11488	59	0.0051	71	62	0.4839	62	1	1	1	164	49	3.35
_p3.3_p5.18	45717	165	0.0036	378	336	0.5506	312	1.1	1	1.08	127.3	37	3.44
_p3.3_p5.19	38939	92	0.0024	266	227	0.5727	212	1.1	1	1.07	163.4	56.5	2.89
_p3.3_p5.20	114564	217	0.0019	803	693	0.5512	589	1.2	1	1.18	167.3	51	3.28
_p3.3_p5.23	42724	40	0.0009	328	287	0.5192	272	1.1	1	1.06	132.5	44	3.01
_p3.3_p5.4	23073	128	0.0055	200	169	0.5976	161	1	1	1.05	124.9	52	2.4
_p3.3_p5.5	83208	157	0.0019	604	511	0.5166	447	1.1	1	1.14	160.1	54	2.96
_p3.3_p5.7	11022	3	0.0003	90	77	0.4935	76	1	1	1.01	119.7	36.5	3.28
p3.5	76888	1212	0.0158	367	321	0.5607	286	1.1	1	1.12	243.1	90.5	2.69
_p3.5_mult	47796	177	0.0037	261	216	0.5741	206	1	1	1.05	188.7	62	3.04
_p3.5_p5.1	10755	36	0.0033	56	51	0.7255	48	1.1	1	1.06	216.2	114	1.9
_p3.5_p5.10	9677	178	0.0184	60	48	0.5208	48	1	1	1	148.9	79	1.89
_p3.5_p5.11	18410	197	0.0107	88	77	0.6104	75	1	1	1.03	202.3	55	3.68
_p3.5_p5.14	15438	225	0.0146	123	112	0.4554	108	1	1	1.04	134.1	65	2.06
_p3.5_p5.16	12415	87	0.007	102	84	0.5833	81	1	1	1.04	122	73	1.67
_p3.5_p5.18	55819	122	0.0022	331	287	0.5226	265	1.1	1	1.08	187.8	64	2.93
_p3.5_p5.19	50084	324	0.0065	267	229	0.5022	216	1.1	1	1.06	200.3	80	2.5

_p3.5_p5.20	34352	215	0.0063	218	184	0.5272	180	1	1	1.02	156.5	69.5	2.25
_p3.5_p5.23	70244	79	0.0011	349	299	0.495	273	1.1	1	1.1	223.7	92	2.43
_p3.5_p5.4	46898	201	0.0043	227	201	0.4975	195	1	1	1.03	182.9	85	2.15
_p3.5_p5.5	26231	33	0.0013	138	120	0.5917	118	1	1	1.02	186.8	56	3.34
p2.7_p3.1_p5.23	14077	91	0.0065	63	56	0.625	55	1	1	1.02	247.7	66	3.75
p2.7_p3.2_	5848	131	0.0224	62	52	0.5	51	1	1	1.02	103	43	2.39
p2.7_p3.2_p5.11	4959	25	0.005	57	46	0.5217	46	1	1	1	63.6	32	1.99
p2.7_p3.2_p5.20	13809	90	0.0065	157	142	0.5563	137	1	1	1.04	88.4	37	2.39
p2.7_p3.3_	140077	866	0.0062	771	673	0.4799	576	1.2	1	1.17	215.3	78	2.76
p2.7_p3.3_mult	26381	23	0.0009	137	121	0.5372	116	1	1	1.04	198.5	74.5	2.66
p2.7_p3.3_p5.1	13000	99	0.0076	87	74	0.473	74	1	1	1	142.1	76.5	1.86
p2.7_p3.3_p5.11	42016	27	0.0006	248	205	0.5171	196	1	1	1.05	176.1	75.5	2.33
p2.7_p3.3_p5.13	14697	189	0.0129	124	112	0.5536	103	1.1	1	1.09	132.1	51	2.59
p2.7_p3.3_p5.14	19751	45	0.0023	155	132	0.3864	128	1	1	1.03	131.8	57.5	2.29
p2.7_p3.3_p5.16	10830	41	0.0038	76	68	0.4118	67	1	1	1.01	158.3	65	2.44
p2.7_p3.3_p5.18	48757	172	0.0035	258	212	0.4858	197	1.1	1	1.08	209	99	2.11
p2.7_p3.3_p5.19	47241	56	0.0012	287	248	0.4919	229	1.1	1	1.08	182.2	90	2.02
p2.7_p3.3_p5.20	165039	423	0.0026	956	814	0.4988	682	1.2	1	1.19	202.2	89	2.27
p2.7_p3.3_p5.23	246173	271	0.0011	1246	1066	0.4934	853	1.2	1	1.25	248.4	109	2.28
p2.7_p3.3_p5.4	28762	47	0.0016	215	192	0.4635	180	1.1	1	1.07	138.9	50.5	2.75
p2.7_p3.3_p5.5	126344	104	0.0008	555	470	0.4596	421	1.1	1	1.12	254.1	101	2.52
p2.7_p3.3_p5.9	12152	13	0.0011	93	78	0.4744	75	1	1	1.04	135.1	45	3
p2.7_p3.5_	7368	115	0.0156	93	84	0.4762	83	1	1	1.01	79.5	36	2.21
p2.7_p3.5_mult	20096	165	0.0082	178	145	0.469	138	1.1	1	1.05	110.1	48.5	2.27
p2.7_p3.5_p5.18	10499	74	0.007	117	100	0.32	98	1	1	1.02	94.3	55	1.71
p2.7_p3.5_p5.19	12889	103	0.008	149	131	0.4733	129	1	1	1.02	86.9	39	2.23
p2.7_p3.5_p5.20	16024	496	0.031	178	143	0.4406	138	1	1	1.04	70.3	34	2.07
p2.7_p3.5_p5.23	10817	62	0.0057	123	100	0.42	94	1.1	1	1.06	85.1	48	1.77
p2.7_p3.5_p5.4	16229	114	0.007	176	148	0.5135	142	1	1	1.04	93.9	41.5	2.26
p2.7_p3.5_p5.5	18801	40	0.0021	177	146	0.4521	143	1	1	1.02	111	42	2.64

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

nInGene - 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