

Supplementary Table S1A

Sample ID	Sample ID2	Library preparation method	Analysis			Average Depth*	Norm. Std.*
			Ploidy	SNP	CNV/gene depth		
aM P3 Hamster	BPK282siQ17	TruSeq	used	used	used	63.9	0.132
aM P4 Hamster	BPK282siR18	TruSeq	used	used	used	13.7	0.204
ProM (A) R3	BPK282siT20	TruSeq	used	used	used	32.1	0.167
ProM (A) R10	BPK282siA27	TruSeq	used	used	used	13.6	0.181
ProM (P) Sandfly 1	BPK282siU21	TruSeq	used	used	used	46.2	0.143
	BPK282_Fly_P0_1	Nextera	no	used	used	45.7	0.204
ProM (P) Sandfly 2	BPK282siV22	TruSeq	used	used	used	84.3	0.166
	BPK282_Fly_P0_2	Nextera	no	used	used	43.5	0.219
ProM (P) Sandfly 3	BPK282siW23	TruSeq	used	used	used	35.2	0.2
	BPK282_Fly_P0_3	Nextera	no	used	used	60.3	0.201
ProM (A) Sandfly 1	BPK282_Ama_to_fly-1	Nextera	used	used	used	106	0.202
	BPK282siX24	TruSeq	no	used	no	4.7	0.552
ProM (A) Sandfly 2	BPK282_Ama_to_fly-2	Nextera	used	used	used	65.4	0.215
	BPK282siY25	TruSeq	no	used	no	8.2	0.412
ProM (A) Sandfly 3	BPK282_Ama_to_fly-3	Nextera	used	used	used	72.5	0.2
	BPK282siZ26	TruSeq	no	used	no	9.9	0.49
ProM (I) R20	BPK282siP16	TruSeq	used	used	used	65.3	0.375
ProM (I) R22	BPK282siS19	TruSeq	used	used	used	16.3	0.489
	BPK282_Pro_B_fly	Nextera	no	used	used	63	0.347
aM (P/sf) P1 Hamster	BPK282siB28	TruSeq	used	used	no	2.2	0.13
275ProM (I) R33	BPK275si2A1	TruSeq	used	used	used	16.2	0.54
	BPK275_Pro_B_fly	Nextera	no	used	used	13	0.53
275ProM (P) Sandfly 1	BPK275si2B2	TruSeq	used	used	used	52.5	0.16
	BPK275_Fly_P0_1	Nextera	no	used	no	33.3	0.224

275ProM (P) Sandfly 2	BPK275si2C3	TruSeq	no	used	no	13	0.347
	BPK275_Fly_P0_2	Nextera	used	used	used	81.2	0.19
275ProM (P) Sandfly 3	BPK275si2D4	TruSeq	used	used	used	36.5	0.16
	BPK275_Fly_P0_3	Nextera	no	used	no	54.4	0.232
275aM (P/sf) P1 Hamster	BPK275si2E5	TruSeq	used	used	no	4.3	0.414
1SaM P15 Hamster	Ld1S_ama	KAPA Hyper Prep Kit	used	no	no	68.5	0.224
1SProM (A) Sandfly 1	Ld1S_amasf2	KAPA Hyper Prep Kit	used	no	no	109.8	0.203
1SProM (A) Sandfly 2	Ld1S_amasf5	KAPA Hyper Prep Kit	used	no	no	110	0.204
1SProM (A) Sandfly 3	Ld1S_amasf6	KAPA Hyper Prep Kit	used	no	no	74.6	0.239
1SProM (I) R22	Ld1S_p22	KAPA Hyper Prep Kit	used	no	no	81.4	0.204
1SProM (P) Sandfly 1	Ld1S_p22sf5	KAPA Hyper Prep Kit	used	no	no	125	0.194
1SProM (P) Sandfly 2	Ld1S_p22sf7	KAPA Hyper Prep Kit	used	no	no	129.6	0.194
1SProM (P) Sandfly 3	Ld1S_p22sf11	KAPA Hyper Prep Kit	used	no	no	135.5	0.182

*=These values are based on depth without binning to estimate overall sequence quality.

Supplementary Table S1B

Sample ID	Sample ID2	Total (million)	Mapped (million)	(%)	Mapped in pair (million)	(%)	Singletons (million)	(%)	Median depth*	Average depth*	Norm. depth standard deviation*
ProM (I) R20	BPK282RNAsiA1	36	35.29	98	34.67	96.3	0.62	1.7	42.9	49.6	0.69
aM P3 Hamster	BPK282RNAsiB2	38.15	37.31	97.8	36.63	96	0.68	1.8	46.0	52.8	0.70
aM P4 Hamster	BPK282RNAsiC3	18.1	16.31	90.1	15.81	87.3	0.5	2.8	16.3	19.9	0.76
ProM (A) R3	BPK282RNAsiE5	35.4	34.66	97.9	33.98	96	0.67	1.9	35.6	44.2	0.79
ProM (A) R10	BPK282RNAsiF6	30.9	30.22	97.8	29.6	95.8	0.62	2	29.7	38.0	0.83
ProM (P) Sandfly 3	BPK282RNAsiG7	30.12	29.41	97.6	28.9	96	0.51	1.7	33.9	40.6	0.74
aM (P/sf) P1 Hamster	BPK282RNAsiH8	39.82	37.19	93.4	36.55	91.8	0.64	1.6	43.2	50.6	0.73
ProM (A) Sandfly 3	BPK282RNAsiI9	16.25	12.32	75.8	12.02	74	0.3	1.8	6.1	8.0	0.83
275ProM (I) R33	BPK275RNAsiA1	33.15	32.51	98.1	31.95	96.4	0.57	1.7	42.5	47.8	0.67
275ProM (P) Sandfly 2	BPK275RNAsiB2	34.79	34.11	98	33.53	96.4	0.58	1.7	41.0	48.0	0.73
275aM (P/sf) P1 Hamster	BPK275RNAsiC3	18.6	16.35	87.9	16.06	86.4	0.29	1.5	20.8	24.0	0.70
	Total mapped reads	331.3	315.7								
	Average mapped reads	30.1	28.7								

*=These values are based on depth without binning to estimate overall sequence quality.

Read length =75bp