

Table S1. Quantification of repetitive sequence in target *B. anynana* BACs

BAC ID (GenBank)	All repeats			Simple Repeats			Low Complexity Sequence		
	Length (bp)	%	Number	Length (bp)	%	Number	Length (bp)	%	Number [rich in AT/GC/A/G/C/T]
AC239114	3189	2.94	76	655	0.60	14	2534	2.33	62 [59/0/0/2/1/0]
AC239115	3525	2.79	88	283	0.22	8	3242	2.56	80 [77/2/0/0/1/0]
AC239116	3928	3.60	78	627	0.57	15	2992	2.74	63 [57/0/4/1/1/0]
AC239117	2125	2.16	57	247	0.25	8	1878	1.91	49 [49/0/0/0/0/0]
AC239118	3499	2.39	85	864	0.59	16	2635	1.80	69 [65/1/0/0/1/2]
AC239119	4275	3.48	105	790	0.64	16	3485	2.84	89 [85/0/2/1/0/1]
AC239120	2324	2.38	53	411	0.42	8	1913	1.96	45 [42/1/1/0/1/0]
AC239121	3220	2.79	75	1012	0.88	19	2208	1.92	56 [52/2/0/1/1/0]
AC239122	2949	2.31	78	512	0.40	11	2437	1.91	67 [64/0/1/0/1/1]
AC239123	3445	2.67	81	640	0.50	10	2805	2.17	71 [69/1/0/0/1/0]
AC239124	3088	2.54	81	373	0.31	11	2715	2.23	70 [67/0/1/2/0/0]

Identification and characterization of repeated regions was done with RepeatMasker (see Methods). Simple Repeats correspond to duplications of, typically 1-5bases. Low Complexity Sequence corresponds to poly-purine/poly-pyrimidine stretches or regions of >87% AT or >89% GC.