

Supporting Tables

Table S1: Summary of Sequence Reads

Table S1A: Number of Solexa sequence reads for ChIP-seq experiments

Species	Sample	No. of unique reads (in million)	Genome Coverage
<i>D.melanogaster</i>	CTCF1	5.59	1.68
<i>D.melanogaster</i>	CTCF2	5.74	1.72
<i>D.melanogaster</i>	CTCF3	4.44	1.33
<i>D.melanogaster</i>	Input1	7.24	2.17
<i>D.melanogaster</i>	Input2	6.57	1.97
<i>D.melanogaster</i>	Input3	7.3	2.19
<i>D.simulans</i>	CTCF1	5.13	1.68
<i>D.simulans</i>	CTCF2	2.96	0.97
<i>D.simulans</i>	CTCF3	6.82	2.24
<i>D.simulans</i>	Input1	6.26	2.05
<i>D.simulans</i>	Input2	6.26	2.05
<i>D.simulans</i>	Input3	9.41	3.09
<i>D.yakuba</i>	CTCF1	4.38	1.32
<i>D.yakuba</i>	CTCF2	6.32	1.90
<i>D.yakuba</i>	CTCF3	5.75	1.73
<i>D.yakuba</i>	Input1	7.55	2.27
<i>D.yakuba</i>	Input2	7.55	2.27
<i>D.yakuba</i>	Input3	7.55	2.27
<i>D.pseudoobscura</i>	CTCF1	6.11	1.73
<i>D.pseudoobscura</i>	CTCF2	7.59	2.15
<i>D.pseudoobscura</i>	CTCF3	7.48	2.12
<i>D.pseudoobscura</i>	Input1	7.06	2.00
<i>D.pseudoobscura</i>	Input2	7.06	2.00
<i>D.pseudoobscura</i>	Input3	8.37	2.37

Note: Column 3 "No. of unique reads" summarizes the number of sequence reads that are uniquely mapped to certain genome position allowing at most two mismatches. Column 4 "Genome Coverage" are calculated as the read length (36) multiplies the number of unique reads divided by the number of total nucleotides in each sequenced genome .

Table S1B: Number of LiftOver reads of non-*D.melanogaster* species

<i>Species</i>	<i>Sample</i>	<i>No. of LiftOver reads (in million)</i>
<i>D.simulans</i>	CTCF1	5.02
<i>D.simulans</i>	CTCF2	2.89
<i>D.simulans</i>	CTCF3	6.71
<i>D.simulans</i>	input1	6.1
<i>D.simulans</i>	input2	6.1
<i>D.simulans</i>	input3	9.26
<i>D.yakuba</i>	CTCF1	4.1
<i>D.yakuba</i>	CTCF2	5.94
<i>D.yakuba</i>	CTCF3	5.3
<i>D.yakuba</i>	input1	7.03
<i>D.yakuba</i>	input2	7.03
<i>D.yakuba</i>	input3	7.03
<i>D.pseudoobscura</i>	CTCF1	4.75
<i>D.pseudoobscura</i>	CTCF2	5.62
<i>D.pseudoobscura</i>	CTCF3	5.11
<i>D.pseudoobscura</i>	input1	5.68
<i>D.pseudoobscura</i>	input2	5.68
<i>D.pseudoobscura</i>	input3	6.81

Table S1C: Number of Solexa Sequencing reads for RNA-seq experiments

Species	Sample	Number of unique reads mapped to Flybase annotated gene coding regions (in million)
<i>D.melanogaster</i>	WPP1	15.53
<i>D.melanogaster</i>	WPP2	16.77
<i>D.melanogaster</i>	WPP3	12.58
<i>D.simulans</i>	WPP1	15.98
<i>D.simulans</i>	WPP2	11.75
<i>D.simulans</i>	WPP3	9.25
<i>D.yakuba</i>	WPP1	14.80
<i>D.yakuba</i>	WPP2	13.37
<i>D.yakuba</i>	WPP3	12.60