

Table S5. Depth of sequencing coverage for all samples, related to Experimental Procedures.

The number of mapped reads and properly paired reads for each sample replicate. Mean coverage is calculated as (# mapped reads*read length(bp)) / (total sequence length(bp)).

Sample	Total reads	Mapped	Paired	Coverage*
<i>6R_drone</i>	117142832	74702857	64391032	29.38
<i>8B_drone</i>	124991604	85535921	73635406	33.64
<i>6R_queen</i>	114949298	97323965	92094406	41.79
<i>8B_queen</i>	391327620	347122687	332117964	149.05
<i>Instars_A_Blanco</i>	30229044	30229044	26885324	167.53
<i>Instars_B_Blanco</i>	35767847	35767847	31858708	198.22
<i>Instars_A_Rojo</i>	33813595	33813595	29820526	187.39
<i>Instars_B_Rojo</i>	32879078	32879078	29219912	182.21
<i>Guards_1_Blanco</i>	37275881	37275881	32898690	206.58
<i>Guards_2_Blanco</i>	44503015	44503015	38681402	246.63
<i>Guards_1_Rojo</i>	12310104	12310104	10789138	68.22
<i>Guards_2_Rojo</i>	10702645	10702645	9365404	59.31
<i>Brains_1_Blanco</i>	68461783	68461783	57180064	379.41
<i>Brains_2_Blanco</i>	14489590	14489590	12041090	80.30
<i>Brains_3_Blanco</i>	67738004	67738004	56525008	375.39
<i>Brains_1_Rojo</i>	25085265	25085265	20679418	139.02
<i>Brains_2_Rojo</i>	55130044	55130044	46079118	305.52
<i>Brains_3_Rojo</i>	34382456	34382456	28614778	190.54

*Calculated as $(\#reads*length)/genome_length$