

Supplementary information

A novel neo-sex chromosome in *Sylvietta brachyura* (Macrosphenidae) adds to the unprecedented avian sex chromosome diversity among Sylvioidea songbirds

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This supplementary information includes **Tables S1-S2** and **Figure S1-S7**.

Table S1. Information on samples and species used for this study.

Species	Common name	Sex	Sample ID	Alias
<i>Argya altirostris</i>	Iraq babbler	female	SJ-2333-IB-2b_S32_L002	A_altirostis_F
<i>Argya altirostris</i>	Iraq babbler	male	SJ-2333-IB-1a_S31_L002	A_altirostis_M
<i>Sylvietta brachyura</i>	Northern Crombec	female	SJ-2333-Sbra-553_S28_L002	S_brachyura_F
<i>Sylvietta brachyura</i>	Northern Crombec	male	SJ-2333-Sbra-878_S26_L002	S_brachyura_M
<i>Pycnonotus barbatus</i>	Common bulbul	female	SJ-2333-Pbar-197_S24_L002	P_barbatus_F
<i>Pycnonotus barbatus</i>	Common bulbul	male	SJ-2333-Pbar-421_S22_L002	P_barbatus_M

Table S2. Mean genome coverage values (total aligned bp / length of reference genome) per sample and reference genome (see Methods). The columns "all", "0-2" and "0" refer to the number of allowed mismatches (see Methods).

Alias	Sample ID	Genome	all	0-2	0
A_altirostis_F	SJ-2333-IB-2b_S32_L002	Turdoides_altirostris	31.5	30.5	25.3
A_altirostis_M	SJ-2333-IB-1a_S31_L002	Turdoides_altirostris	40.5	39.8	34.6
S_brachyura_F	SJ-2333-Sbra-553_S28_L002	Sylvietta_brachyura	28.7	23.2	11.2
S_brachyura_M	SJ-2333-Sbra-878_S26_L002	Sylvietta_brachyura	26.7	24.5	17.6
P_barbatus_F	SJ-2333-Pbar-197_S24_L002	Pycnonotus_barbatus	41.8	37.0	19.2
P_barbatus_M	SJ-2333-Pbar-421_S22_L002	Pycnonotus_barbatus	40.1	37.8	27.8
A_altirostis_F	SJ-2333-IB-2b_S32_L002	Turdoides_altirostris_nonRefAf_consensus	31.5	30.6	26.1
A_altirostis_M	SJ-2333-IB-1a_S31_L002	Turdoides_altirostris_nonRefAf_consensus	40.5	39.7	34.0
S_brachyura_F	SJ-2333-Sbra-553_S28_L002	Sylvietta_brachyura_nonRefAf_consensus	28.7	24.2	14.1
S_brachyura_M	SJ-2333-Sbra-878_S26_L002	Sylvietta_brachyura_nonRefAf_consensus	26.7	24.2	15.4
P_barbatus_F	SJ-2333-Pbar-197_S24_L002	Pycnonotus_barbatus_nonRefAf_consensus	41.5	38.0	24.4
P_barbatus_M	SJ-2333-Pbar-421_S22_L002	Pycnonotus_barbatus_nonRefAf_consensus	39.8	37.3	24.8

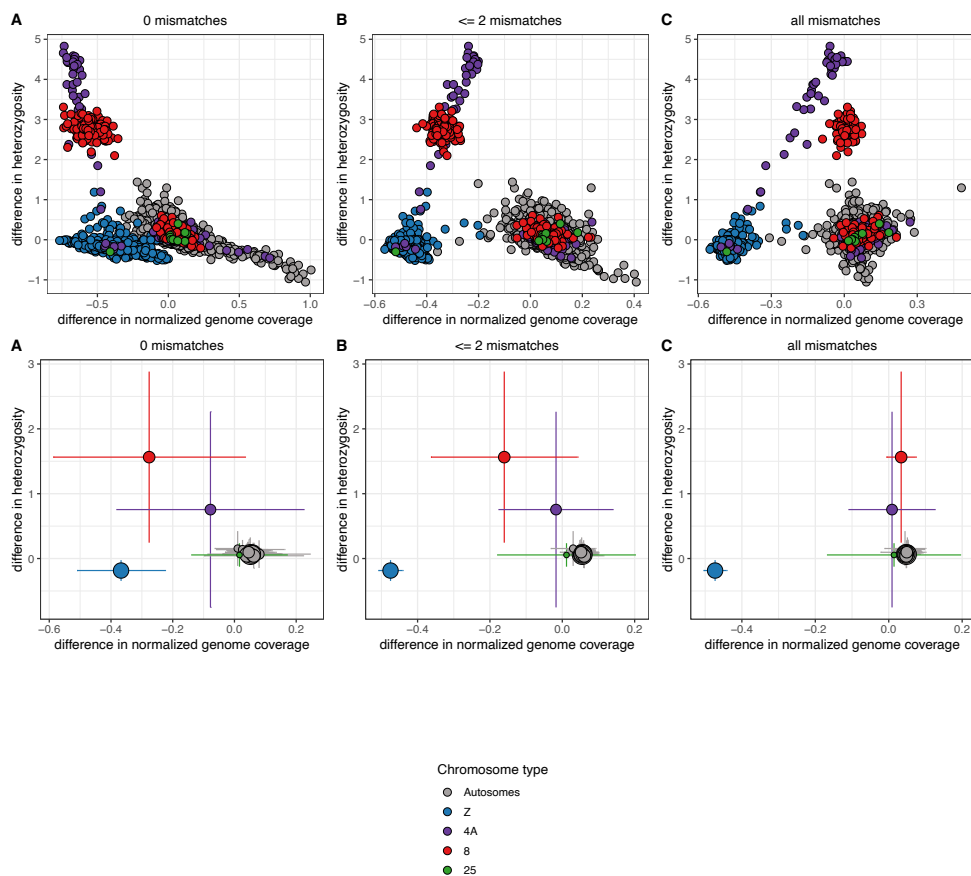


Figure S1. *Sylvieta brachyura*. Genome coverage and heterozygosity values (mean \pm standard deviation across 100 kb windows) per chromosome.

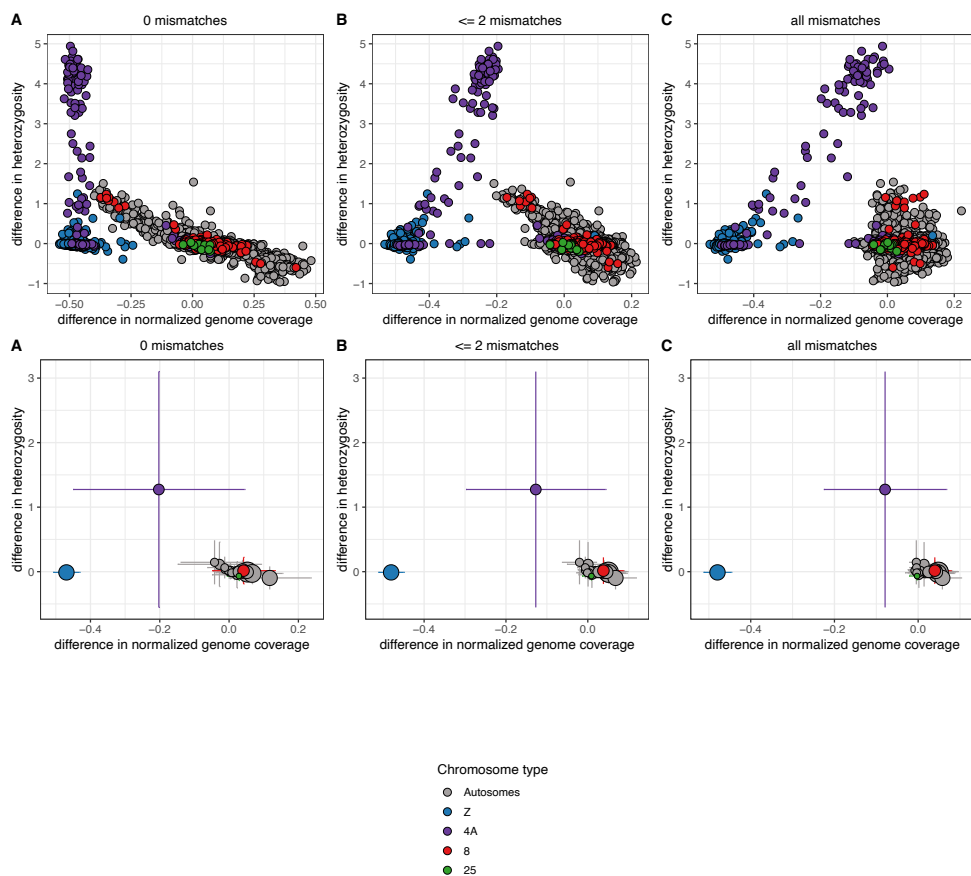


Figure S2. *Argya altirostris*. Genome coverage and heterozygosity values (mean \pm standard deviation across 100 kb windows) per chromosome.

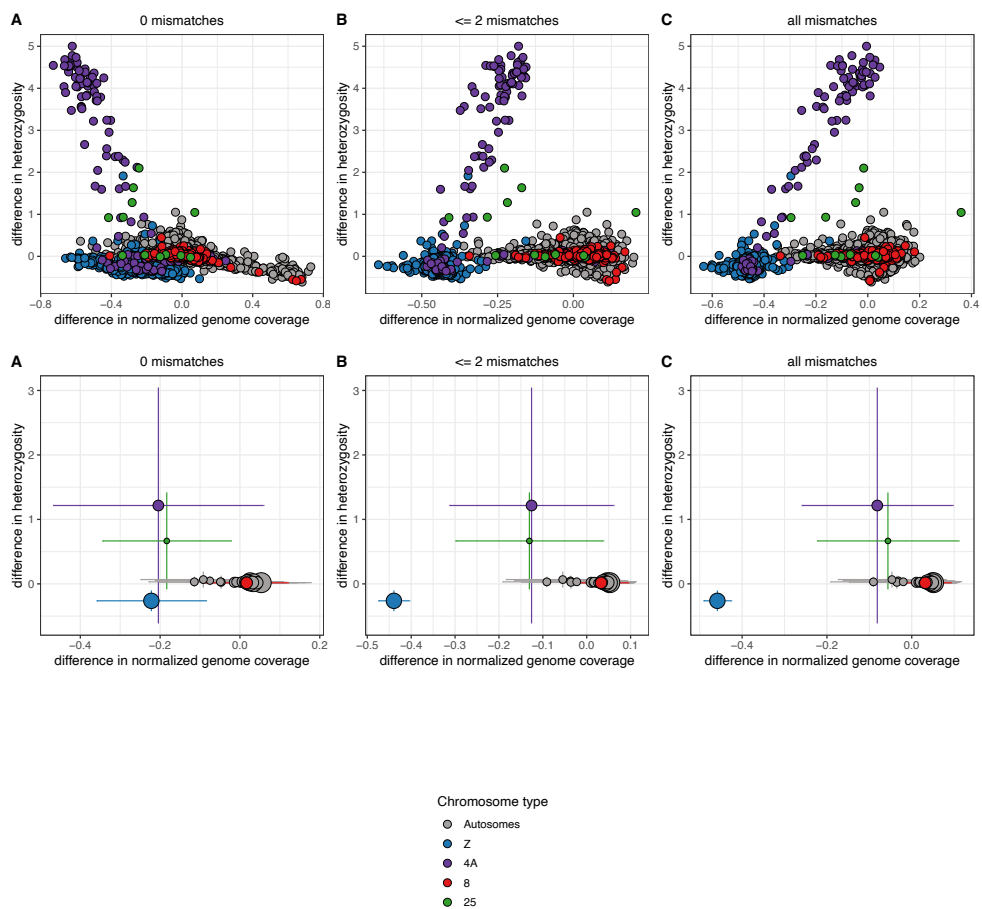


Figure S3. *Pycnonotus barbatus*. Genome coverage and heterozygosity values (mean \pm standard deviation across 100 kb windows) per chromosome.

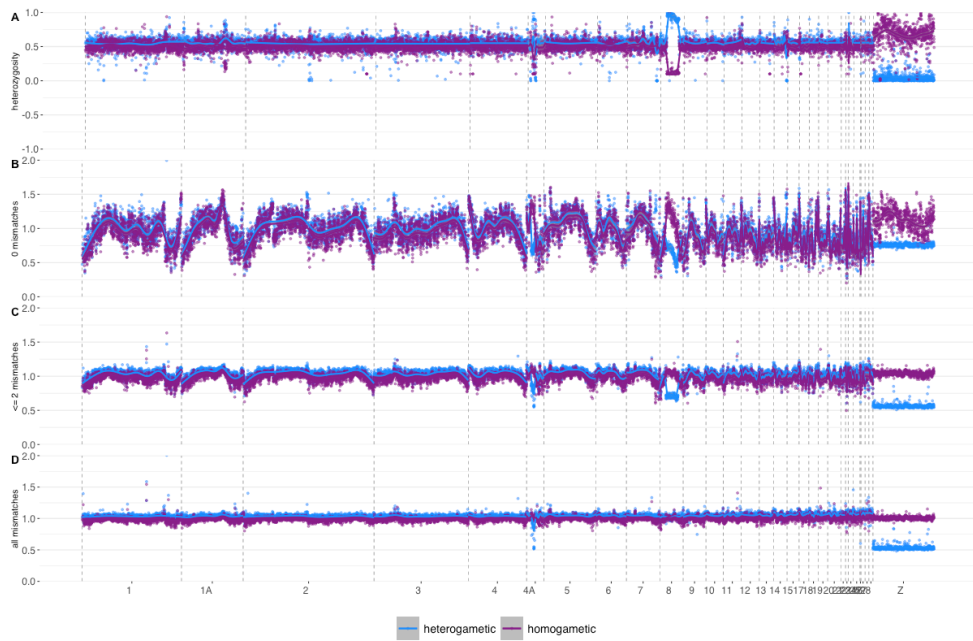


Figure S4. *Sylvietta brachyura*. Genome-wide heterozygosity and genome coverage values, binned into 100 kb windows.

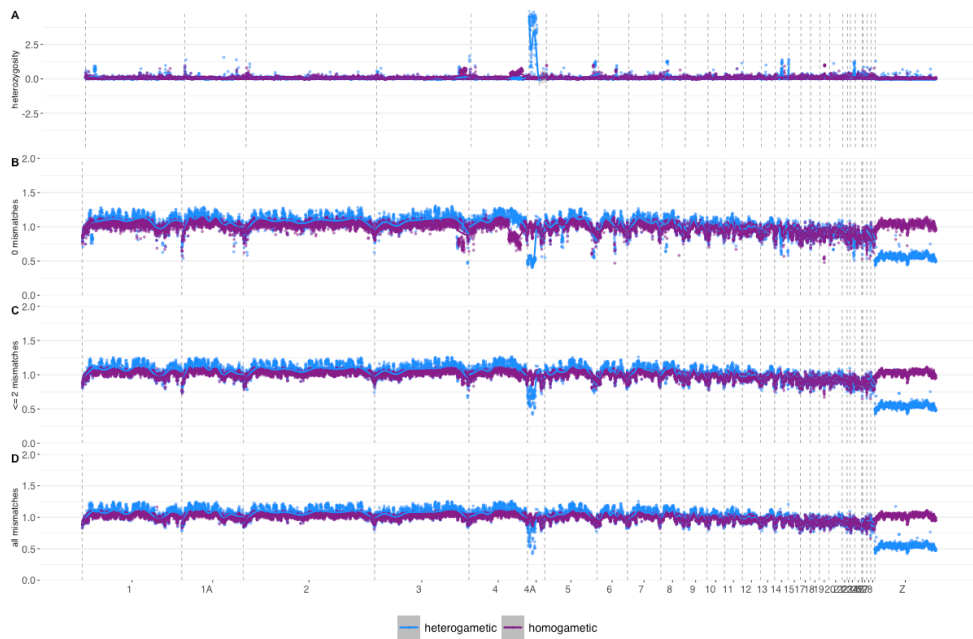


Figure S5. *Argya altirostris*. Genome-wide heterozygosity and genome coverage values, binned into 100 kb windows.

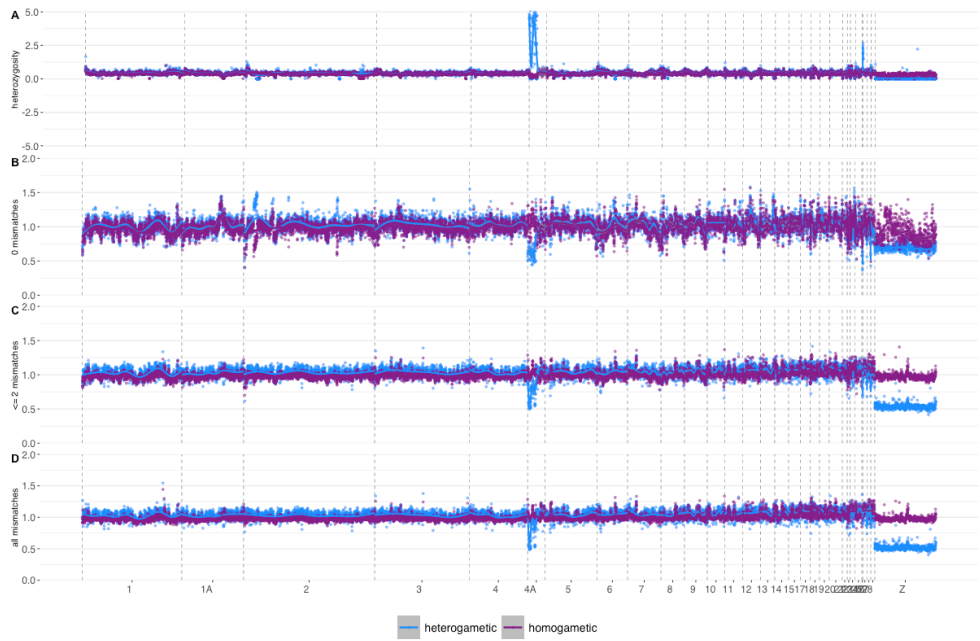


Figure S6. *Pycnonotus barbatus*. Genome-wide heterozygosity and genome coverage values, binned into 100 kb windows.

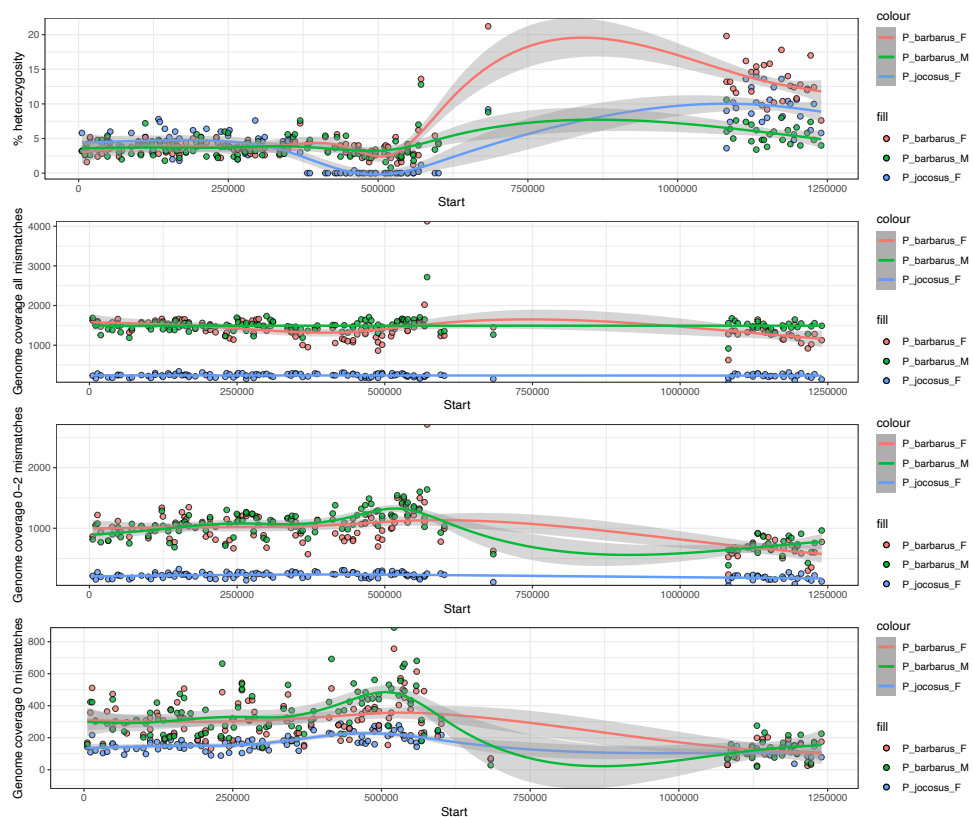


Figure S7. This plot show data from two *P. barbarus* individuals (Table S1) and WGS data from a female *P. jocosus* (NCBI accession code SRR9946586), aligned to the reference genome of the *P. jocosus* individual (NCBI accession code GCA_013400435.1). X-axis: Chromosome position along zebra finch chromosome 25. Y-axes: female-to-male differences in heterozygosity (top row) and genome coverage (from second from top to bottom: with "all", maximum 2 and maximum zero mismatches to the reference genome allowed, respectively).