

Copy number variations within and among diverse cattle breeds

M. Mielczarek^{1,2*}, M. Frąszczak¹, E.L. Nicolazzi³, J. L. Williams⁴, J. Szyda^{1,2}

¹Biostatistics group, Wrocław University of Environmental and Life Sciences; Wrocław, Poland. ²National Research Institute of Animal Production; Cracow-Balice, Poland. ³Council on Dairy Cattle Breeding (CDCB), Bowie, MD 20716, the United States. ⁴Davies Research Centre, University of Adelaide; Adelaide, Australia; *Presenting author, e-mail: magda.mielczarek@upwr.edu.pl

Goals

- describing the CNV landscape in cattle
- assessing the degree of within- and between-breed variability in the CVN length and number

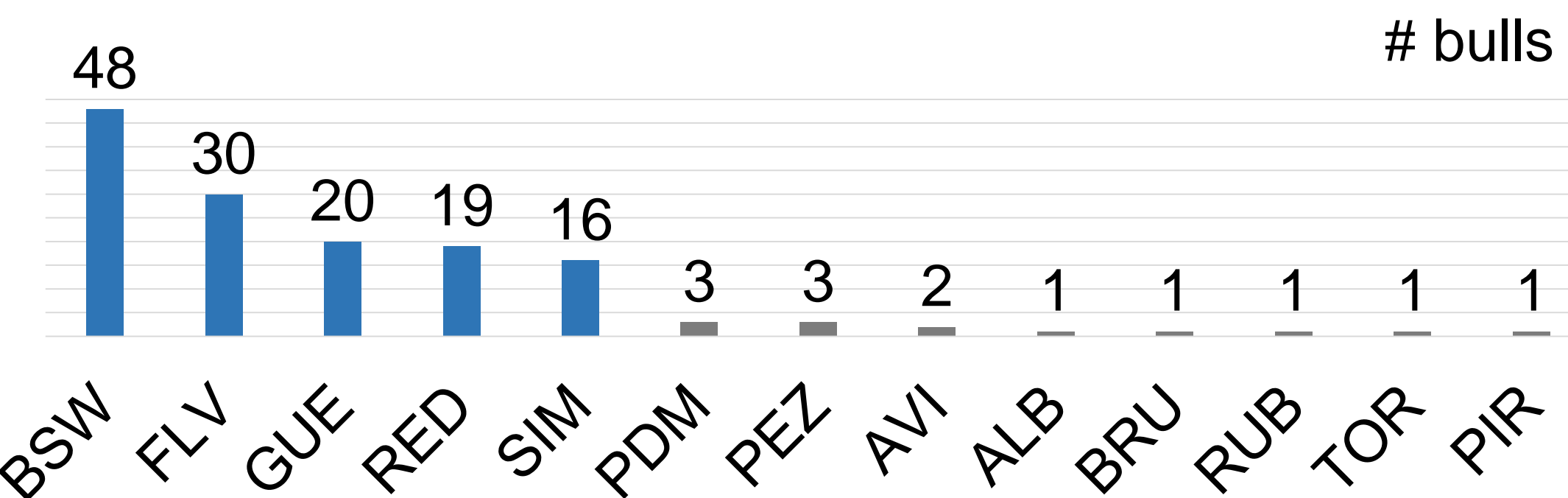
Conclusions

- The CNV landscape in *Bos taurus* genome is highly complex with **inter-breed differences** (may explain some of the phenotypic differences)
- ...but also a significant variation **within breeds** exists (contributes to a within-breed variation available for selection)



Data set

- WGS of 146 bulls
- DNA-seq (Illumina HiSeq 2000)
- genome coverage 7 – 28 x

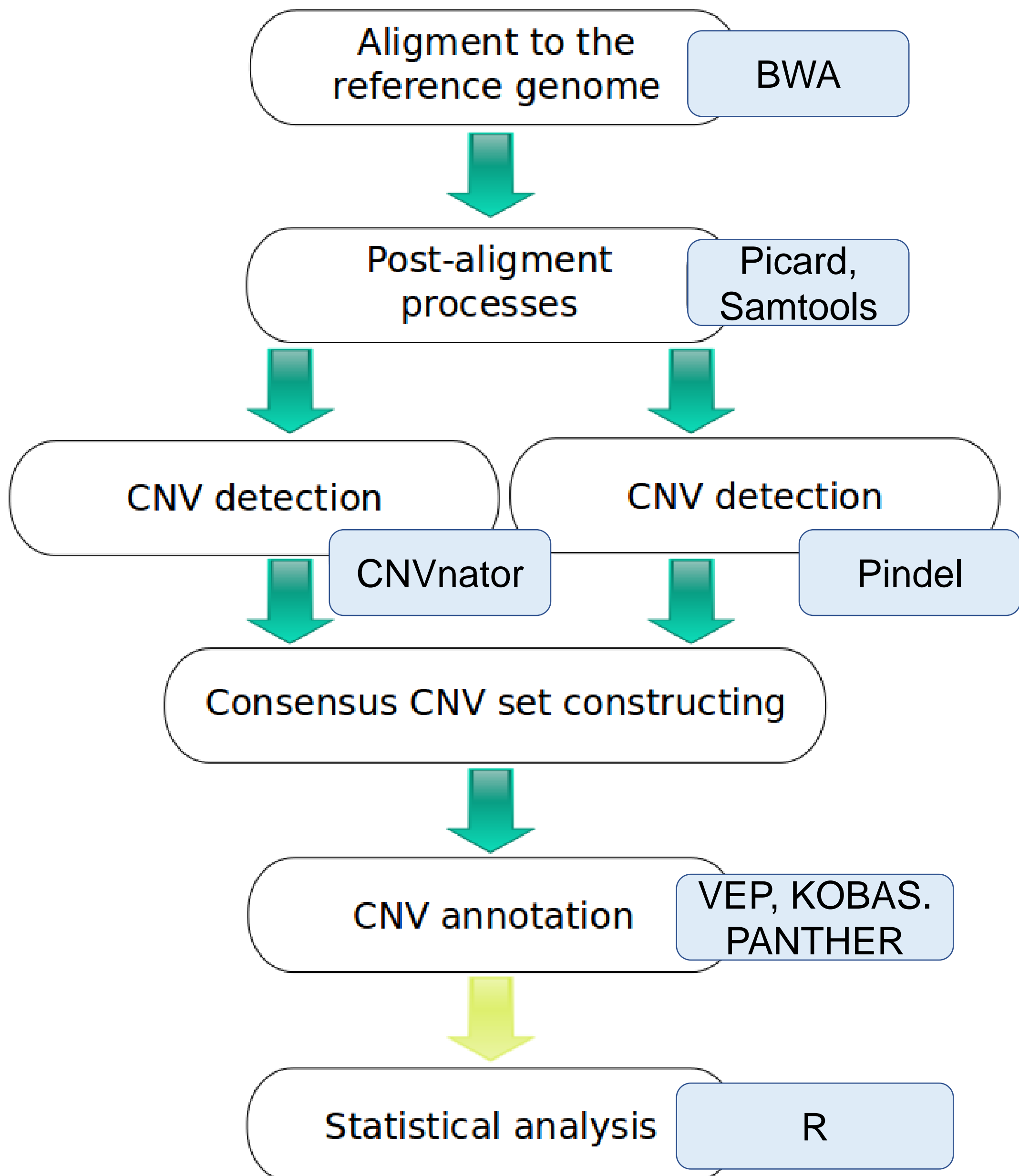


BSW: Brown Swiss, FLV: Fleckvieh, RED: Norwegian Red, GUE: Guernsey, SIM: Simmental, PDM: Parda de la Montaña, PEZ: Pezzata Rossa Italiana, AVI: Avileña, BRU: Bruna Italiana, ALB: Albera, RUB: Rubia Gallega, TOR: Toro de Lidia and PIR: Pirenaica

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Methods



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CNV landscape

• Deletions:

0 - 3,960 (1,708 ± 700)

77.22 % private

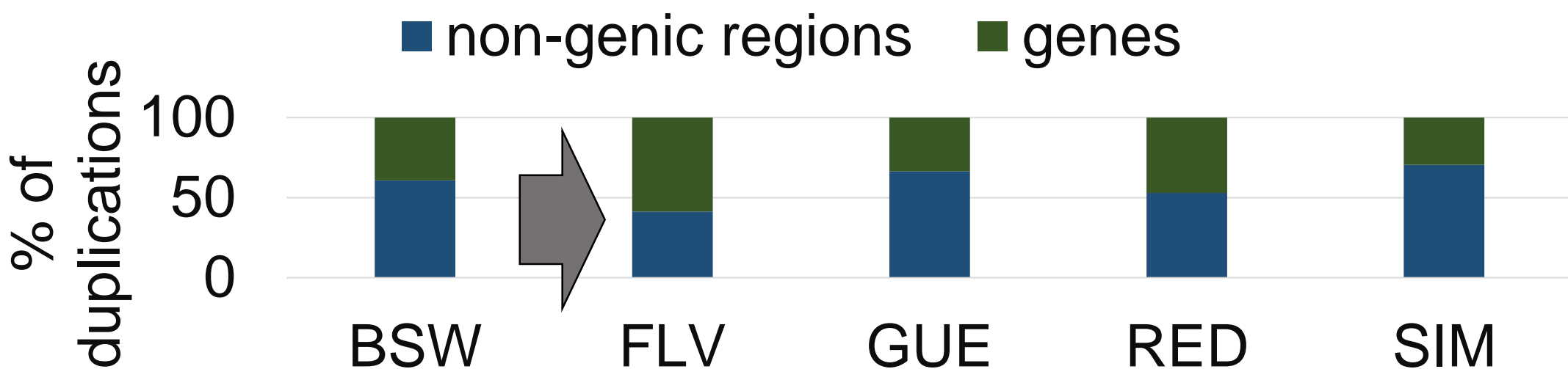
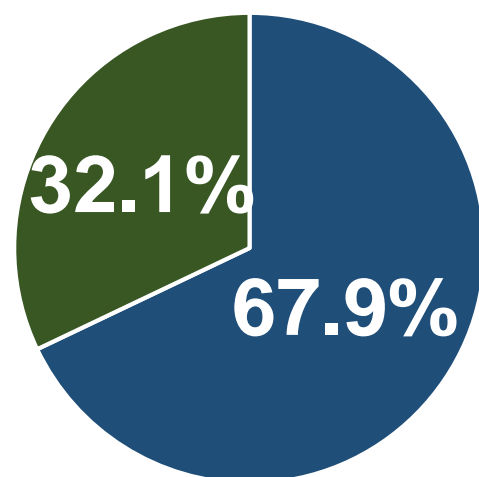
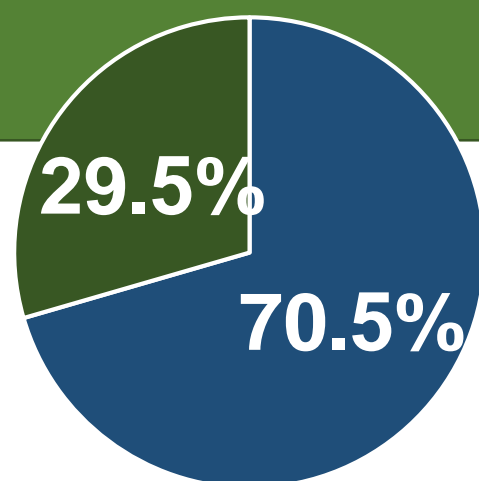
200 - 4,536,800 bp (10,836 ± 53,724)

• Duplications:

12 - 11,704 (1,343 ± 1,086)

84.85 % private

200 - 4,992,800 bp (31,018 ± 169,307)



duplications (in millions)

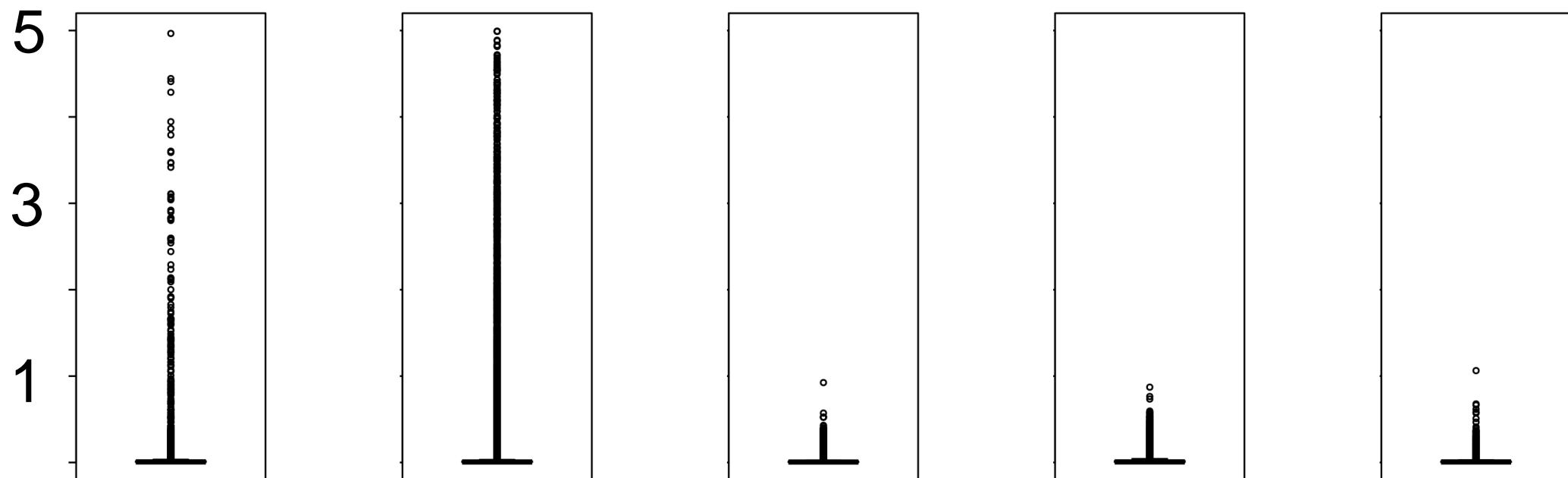
BSW

FLV

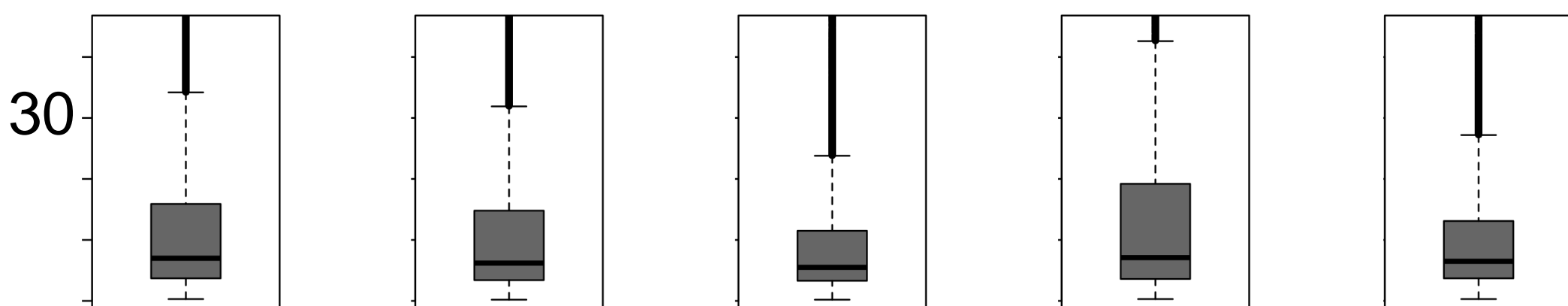
GUE

RED

SIM



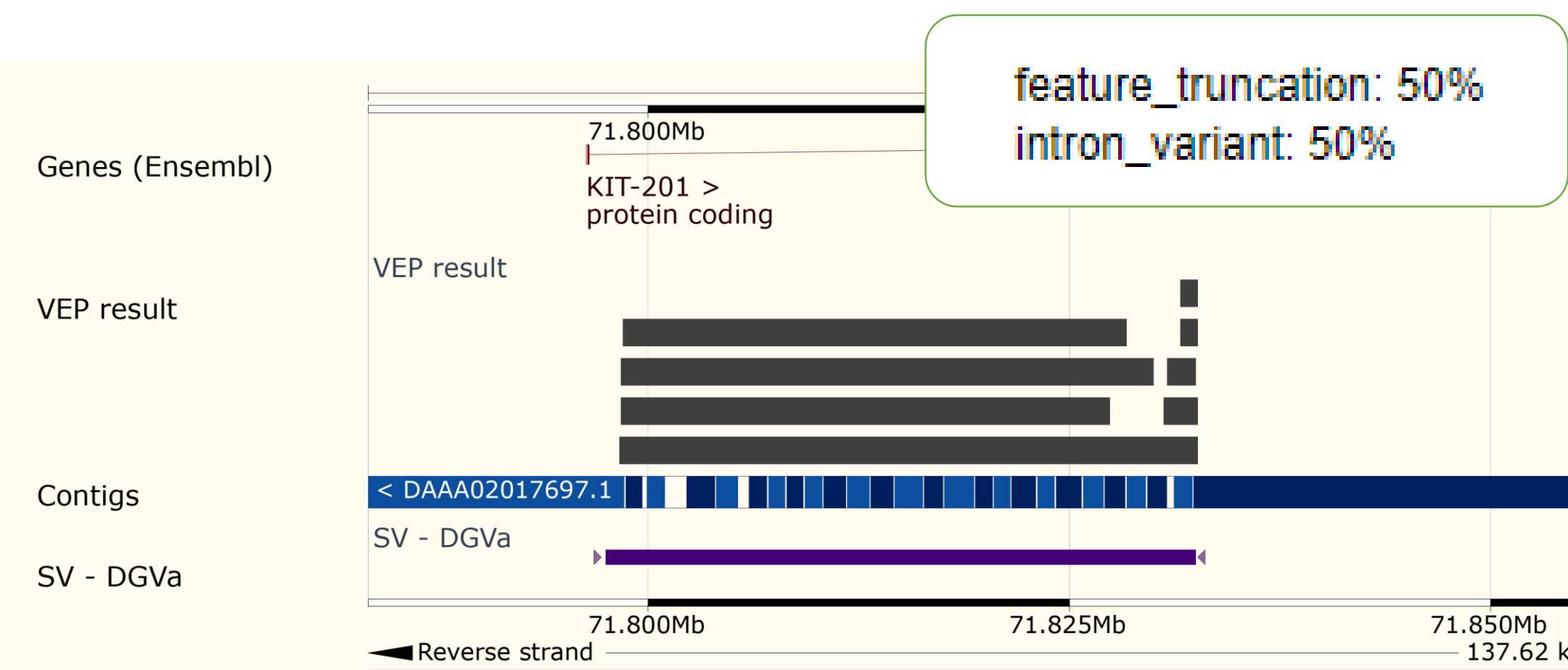
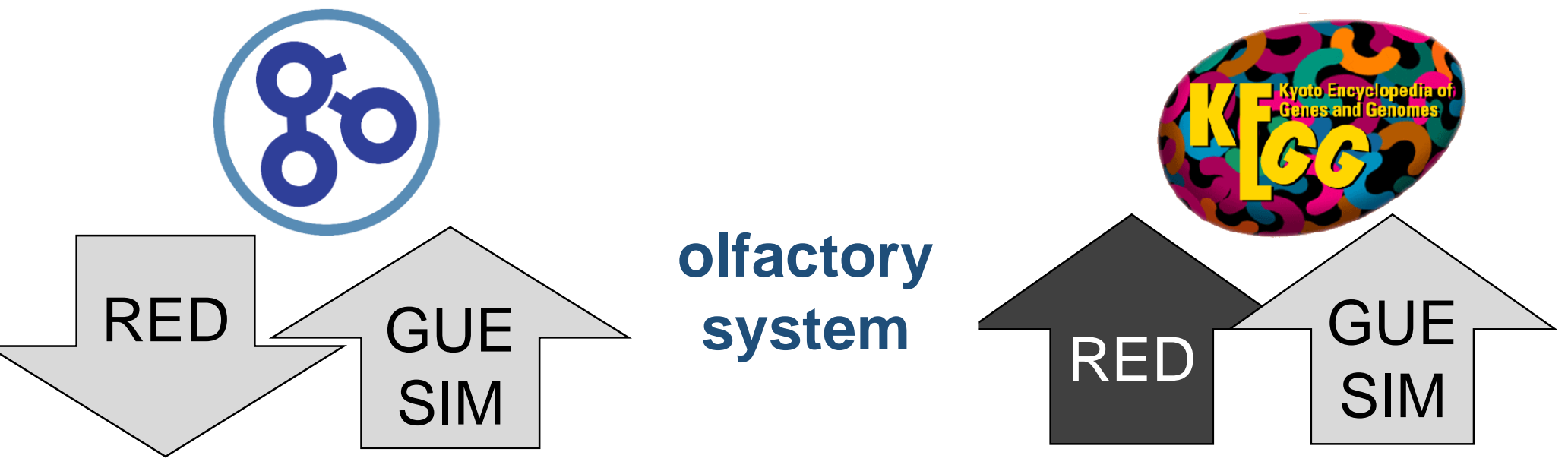
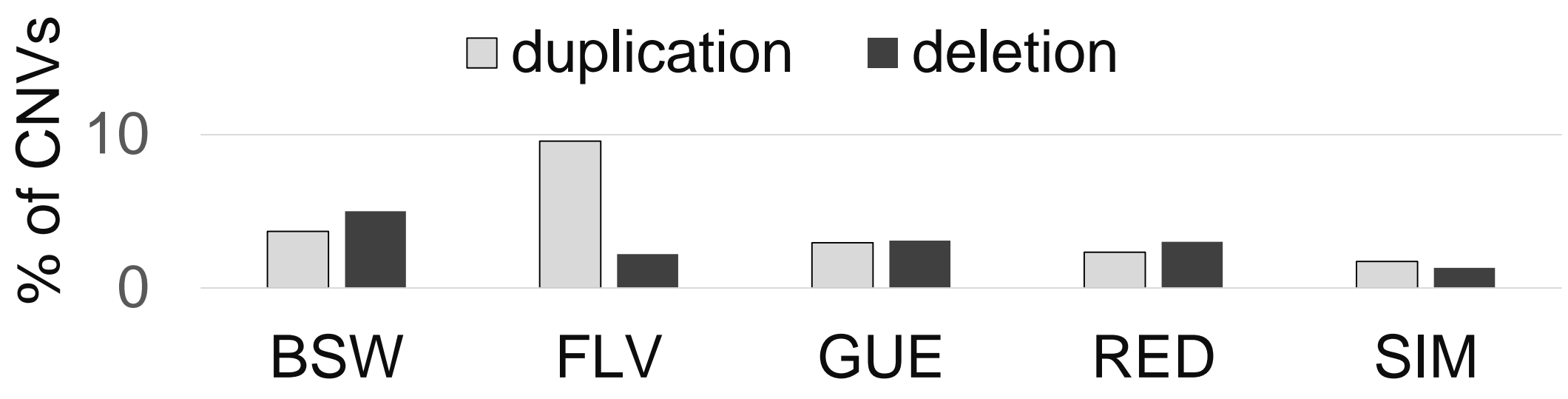
duplications (in thousands)



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Breed specific CNVs



Acknowledgement

