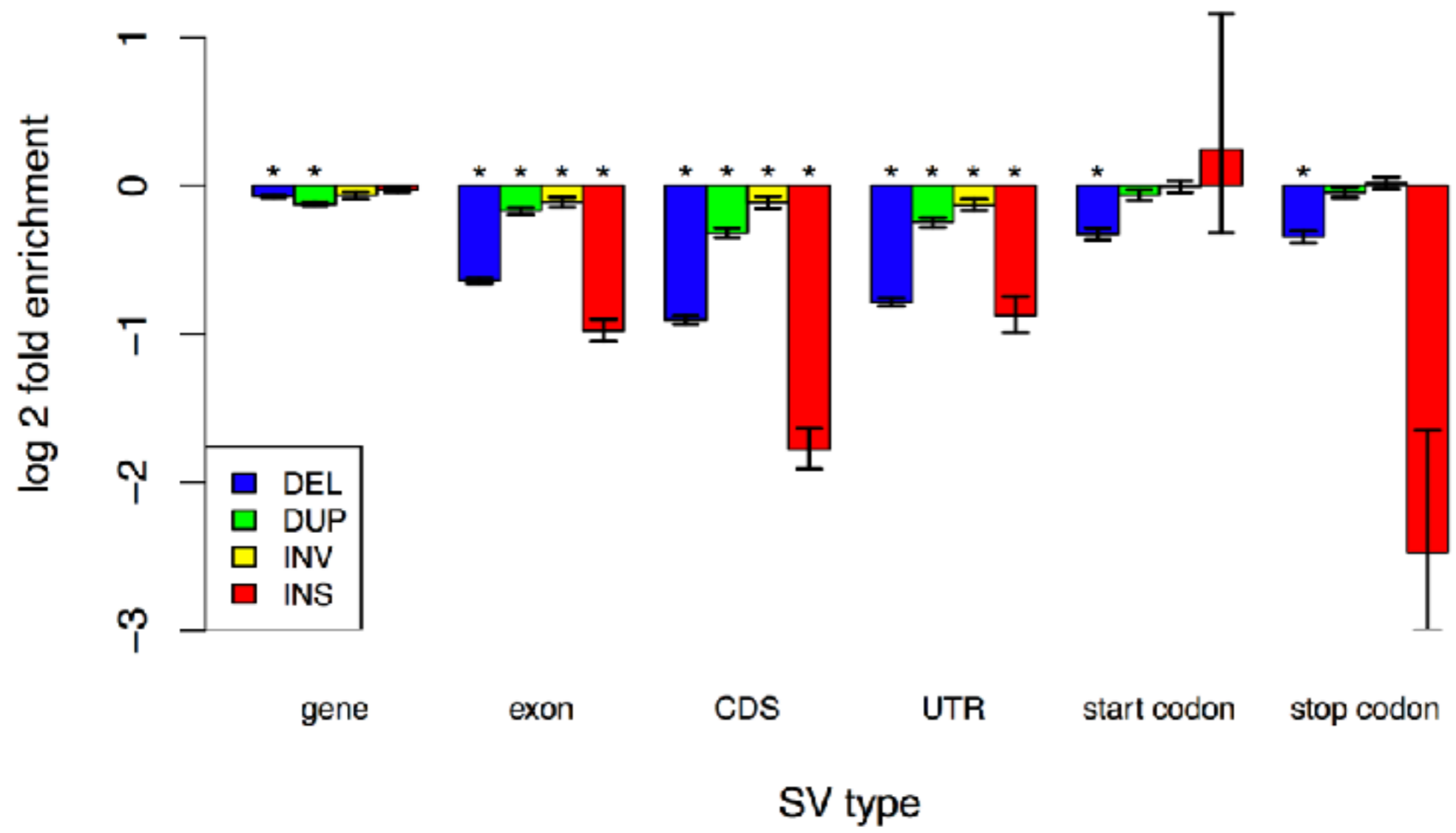
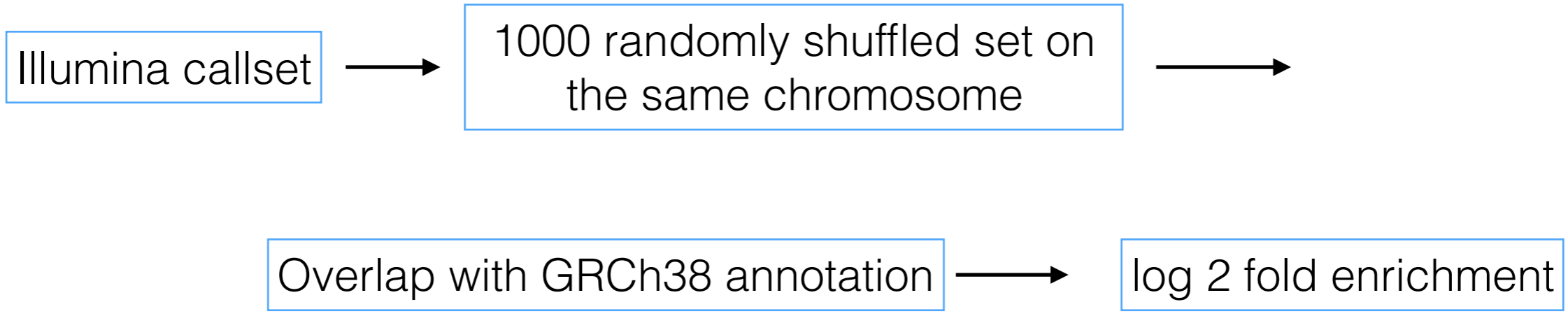


Functional enrichment analysis & Personalized genomes

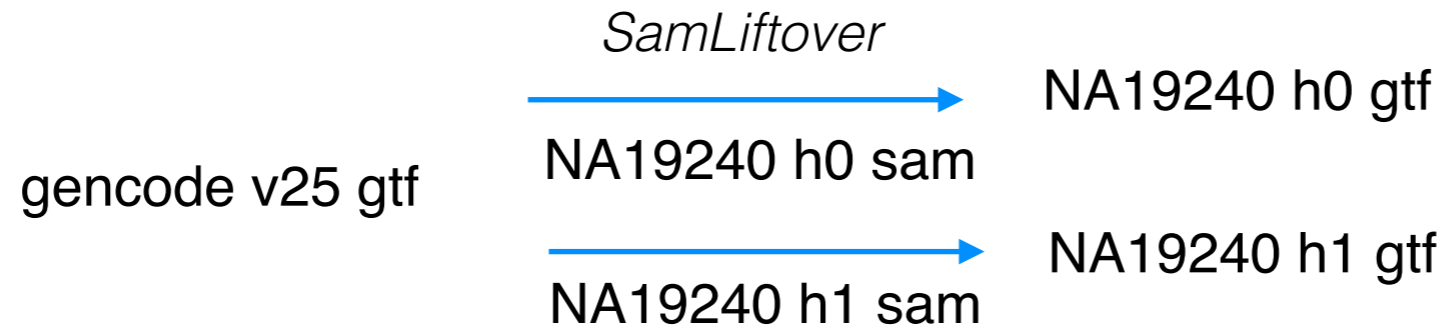
HGSVC April 17, 2017

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Personal genomes in functional genomics analyses: preliminary results for NA19240

- Generate personalized annotation with *SamLiftover* (<https://github.com/mchaisso/mcutils>)



- Map RNA-seq with *STAR* (default params) to GRCh38 and to NA19240 assembled haplotypes

overall mapping statistics

	Uniquely Mapped/%	Multi-mapped/%	Unmapped/%
GRCh38	87.69	10.52	1.78
NA19240 h0	90.20	7.18	2.62
NA19240 h1	89.91	6.71	3.38

