[Stacking] Hypergeometric test: Collapsing analysis vs mantis-ml predictions
Dom_LoF vs shuffle p-value:6.680631893052539e-212

>> Focusing on significant area only:

Dom_LoF -- area: 676.66
Dom_coding -- area: 14.4
Dom_not_benign -- area: 0.32
Rec_coding -- area: 0.0
shuffle -- area: 0.0
> primary / synonymous ratio: 2114.56
> primary / shuffle ratio: NA

>> Entire area:

Dom_LoF -- area: 1224.21
Dom_coding -- area: 332.59
Dom_not_benign -- area: 189.11
Rec_coding -- area: 132.83
shuffle -- area: 48.97
> primary / synonymous ratio: 6.47
> primary / shuffle ratio: 25.0

Legend:
- - - p-val: 0.05
—— Dom_LoF
—— Dom_coding
—— Dom_not_benign
—— Rec_coding
—— shuffle

Y-axis: Phred score from hypergeometric test (significance increasing in positive direction)

X-axis: Top 5.0% mantis-ml predicted genes