[XGBoost] Hypergeometric test: Collapsing analysis vs mantis-ml predictions
Dom_LoF vs shuffle p-value:7.54164644641e-142

>> Focusing on significant area only:

Dom_LoF -- area: 41.24
Dom_coding -- area: 0.0
Dom_not_benign -- area: 0.0
Rec_coding -- area: 0.0
shuffle -- area: 0.0
> primary / synonymous ratio: NA
> primary / shuffle ratio: NA

>> Entire area:

Dom_LoF -- area: 469.73
Dom_coding -- area: 123.47
Dom_not_benign -- area: 146.46
Rec_coding -- area: 126.58
shuffle -- area: 90.98
> primary / synonymous ratio: 3.21
> primary / shuffle ratio: 5.16

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