[GradientBoostingClassifier] Hypergeometric test: Collapsing analysis vs mantis-ml predictions
Dom_LoF vs shuffle p-value:8.248327651812533e-157

>> Focusing on significant area only:

Dom_LoF -- area: 396.55
Dom_coding -- area: 129.88
Dom_not_benign -- area: 179.13
Rec_coding -- area: 0.0
shuffle -- area: 0.0
> primary / synonymous ratio: 2.21
> primary / shuffle ratio: NA

>> Entire area:

Dom_LoF -- area: 1018.03
Dom_coding -- area: 628.19
Dom_not_benign -- area: 772.99
Rec_coding -- area: 245.38
shuffle -- area: 124.54
> primary / synonymous ratio: 1.32
> primary / shuffle ratio: 8.17

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

X-axis: Top 5.0% mantis-ml predicted genes
Y-axis: Phred score from hypergeometric test (significance increasing in positive direction)