**Additional File 3: In silico secretome analysis approach for next generation sequencing transcriptomic data**

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Table S3- Represented KEGG BRITE objects found in ES proteins predicted by KAAS

| BRITE object | Number of ES proteins represented |
|---|---|
| Enzymes | 282 |
| Spliceosome | 49 |
| Chaperons and folding catalysts | 44 |
| Peptidases | 44 |
| Protein kinases | 43 |
| Ubiquitin system | 37 |
| Chromosome | 34 |
| Cytoskeleton proteins | 27 |
| DNA repair and recombination proteins | 21 |
| GTP-binding proteins | 19 |
| Proteasome | 18 |
| Transcription factors | 17 |
| Ribosome biogenesis | 16 |
| Translation factors | 11 |
| DNA replication proteins | 9 |
| Transporters | 8 |
| Glycan Binding proteins | 7 |
| Cellular antigens | 7 |
| Glycosyltransferases | 6 |
| Secretion system proteins | 5 |
| CAM ligands | 5 |
| Ion Channels | 4 |
| Ribosome | 4 |
| Bacterial motility proteins | 3 |
| Lipid biosynthesis proteins | 2 |
| Proteoglycans | 2 |
| Cytokines | 2 |
| Nuclear receptors | 1 |
| G protein-Coupled Receptors | 1 |
| Cell adhesion molecules (CAMs) | 1 |