Table S1 Ribosome profiling data generated for studying species divergence in levels of protein translation.

| ID | mapped count | proportion > Q30 | species |
|---|---|---|---|
| **C18358** | 7,393,603 | 0.971 | chimpanzee |
| **C18359** | 15,478,039 | 0.970 | chimpanzee |
| **C3659** | 20,284,521 | 0.972 | chimpanzee |
| **CPt91** | 10,079,028 | 0.970 | chimpanzee |
| **R181-96** | 12,599,203 | 0.979 | rhesus macaque |
| **R249-97** | 12,040,159 | 0.974 | rhesus macaque |
| **R265-95** | 12,063,859 | 0.979 | rhesus macaque |
| **R290-96** | 10,491,523 | 0.977 | rhesus macaque |
| **H19127** | 8,984,640 | 0.977 | human |
| **H19137** | 9,754,058 | 0.977 | human |
| **H19144** | 12,835,528 | 0.974 | human |
| **H19147** | 14,949,479 | 0.977 | human |

* mapped count: total number of uniquely mapped reads for each sample after removing rRNA, tRNA and snoRNA reads.

* proportion > Q30: proportion of sequencing reads that have a Phred quality score greater than 30.

Table S2 Enrichment of nonsynonymous substitutions in post-translationally buffered genes.

| | **HvC.cor** | **HvC.p.value** | **RvC.cor** | **RvC.p.value** | **RvH.cor** | **RvH.p.value** |
|---|---|---|---|---|---|---|
| **Ka** | - | 0.93 | - | 0.17 | + | 0.63 |
| **Ka/Ks** | - | 0.87 | - | 0.14 | + | 0.68 |

* HvC: human vs. chimpanzee, RvC: rhesus macaque vs. chimpanzee, RvH: rhesus macaque vs. human.

*cor: direction of correlation, + enrichment, - depletion.

*p.value: probability of observing the correlation when there is no enrichment in the feature of interest in post-translationally buffered gene identified between each pair of species.

Table S3 Enrichment of protein modifications in post-translationally buffered genes.

| PTM type | HvC.cor | HvC.p.value | RvC.cor | RvC.p.value | RvH.cor | RvH.p.value |
|---|---|---|---|---|---|---|
| **Ubiquitination** | + | 2.20E-16 | + | 6.66E-16 | + | 2.20E-16 |
| **Phosphorylation** | + | 2.51E-08 | + | 1.29E-02 | + | 4.40E-06 |
| **Acetylation** | + | 2.20E-16 | + | 7.74E-08 | + | 2.39E-10 |
| **Methylation** | + | 4.76E-05 | + | 1.34E-02 | + | 1.84E-04 |
| **Sumoylation** | + | 3.74E-07 | + | 1.14E-03 | + | 2.07E-04 |
| **O-GalNAc** | - | 3.76E-01 | - | 2.99E-01 | + | 7.98E-01 |
| **O-GlcNAc** | - | 9.86E-01 | + | 6.18E-01 | + | 4.93E-02 |

* HvC: human vs. chimpanzee, RvC: rhesus macaque vs. chimpanzee, RvH: rhesus macaque vs. human.

*cor: direction of correlation, + enrichment, - depletion.

*p.value: probability of observing the correlation when there is no enrichment in the feature of interest in post-translationally buffered gene identified between each pair of species.

Table S4 Enrichment of sub-cellular locations for post-translationally buffered genes.

| SubCellLoc | NO. of genes associated | HvC.cor | RvC.cor | HvR.cor | HvC.p.value | RvC.p.value | HvR.p.value |
|---|---|---|---|---|---|---|---|
| **Cytoplasm** | 1393\|1773 | - | + | + | 3.53E-01 | 6.12E-01 | 9.61E-01 |
| **Endoplasmic** | 263\|2903 | - | + | + | 1.55E-01 | 2.04E-01 | 7.06E-01 |
| **Golgi** | 222\|2944 | - | - | - | 2.16E-03 | 2.28E-01 | 1.55E-01 |
| **Cytosol** | 136\|3030 | - | - | - | 1.96E-01 | 1.50E-02 | 1.87E-01 |
| **Nucleus** | 1239\|1927 | + | + | + | 1.32E-05 | 3.30E-01 | 5.34E-01 |
| **Lysosome** | 64\|3102 | - | - | - | 2.59E-01 | 3.19E-01 | 7.65E-01 |
| **Mitochondrion** | 426\|2740 | - | - | - | 7.03E-03 | 2.30E-04 | 7.20E-02 |
| **Peroxisome** | 26\|3140 | - | - | - | 5.92E-01 | 4.41E-01 | 9.96E-01 |
| **Membrane** | 232\|2934 | - | - | + | 4.24E-02 | 7.37E-01 | 2.88E-01 |
| **Endosome** | 112\|3054 | - | - | - | 2.01E-02 | 7.26E-02 | 1.06E-02 |
| **Secreted** | 55\|3111 | - | - | + | 6.67E-01 | 5.81E-01 | 1.61E-01 |
| **P-body** | 24\|3142 | - | + | + | 9.73E-01 | 2.46E-01 | 4.84E-01 |

* HvC: human vs. chimpanzee, RvC: rhesus macaque vs. chimpanzee, HvR: rhesus macaque vs. human.

*cor: direction of correlation, + enrichment, - depletion.

*p.value: probability of observing the correlation when there is no enrichment in the feature of interest in post-translationally buffered gene identified between each pair of species.

Table S5 Enrichment of functional categories for post-translationally buffered genes.

| GO.ID | Term | NO. of genes associated | HvC.fdr | RvC.fdr | HvR.fdr |
|---|---|---|---|---|---|
| **GO:0000184** | nuclear-transcribed mRNA catabolic process & nonsense-mediated decay | 51\|3115 | 2.29E-13 | 8.13E-13 | 1.52E-13 |
| **GO:0003723** | RNA binding | 192\|2974 | 5.09E-07 | 2.59E-03 | 1.08E-05 |
| **GO:0003735** | structural constituent of ribosome | 90\|3076 | 2.11E-09 | 2.09E-03 | 3.73E-10 |
| **GO:0006364** | rRNA processing | 107\|3059 | 2.29E-13 | 8.80E-06 | 1.52E-13 |
| **GO:0006412** | translation | 91\|3075 | 9.45E-08 | 3.77E-05 | 3.92E-10 |
| **GO:0006413** | translational initiation | 59\|3107 | 2.29E-13 | 2.29E-13 | 1.52E-13 |
| **GO:0006614** | SRP-dependent cotranslational protein targeting to membrane | 40\|3126 | 2.29E-13 | 2.29E-13 | 1.52E-13 |
| **GO:0015935** | small ribosomal subunit | 5\|3161 | 5.08E-05 | 3.19E-06 | 3.07E-03 |
| **GO:0019083** | viral transcription | 54\|3112 | 2.29E-13 | 2.29E-13 | 1.52E-13 |
| **GO:0022625** | cytosolic large ribosomal subunit | 23\|3143 | 2.29E-13 | 1.26E-04 | 1.52E-13 |
| **GO:0022627** | cytosolic small ribosomal subunit | 13\|3153 | 1.46E-04 | 2.29E-13 | 1.52E-13 |
| **GO:0030529** | ribonucleoprotein complex | 56\|3110 | 6.29E-05 | 7.29E-03 | 1.95E-03 |

* HvC: human vs. chimpanzee, RvC: rhesus macaque vs. chimpanzee, HvR: rhesus macaque vs. human.

*fdr: False discovery rates (Benjamini-Hochberg) of enrichment in the feature of interest in post-translationally buffered gene identified between each pair of species * Only GO terms that pass a 1% false discovery rate cutoff are presented.

* All associations reported in this table are positive correlations (i.e. enrichment)

Table S6 Post-translationally buffered genes have more variable transcript expression levels in an YRI population.

| feature | HvC.cor | HvC.p.value | RvC.cor | RvC.p.value | HvR.cor | HvR.p.value |
|---|---|---|---|---|---|---|
| **RNA.mean** | + | 2.02E-03 | + | 5.76E-01 | - | 7.29E-01 |
| **RNA.sd** | + | 4.47E-07 | + | 5.44E-05 | + | 1.50E-07 |
| **RNA.TMM.mean** | + | 2.02E-03 | + | 5.76E-01 | - | 7.29E-01 |
| **RNA.TMM.sd** | + | 1.17E-06 | + | 1.05E-04 | + | 1.29E-06 |
| **RNA.QN.mean** | + | 1.82E-03 | + | 5.70E-01 | - | 7.38E-01 |
| **RNA.QN.sd** | + | 1.72E-08 | + | 1.18E-05 | + | 2.40E-08 |

* HvC: human vs. chimpanzee, RvC: rhesus macaque vs. chimpanzee, HvR: rhesus macaque vs. human.

*cor: direction of correlation, + enrichment, - depletion.

*p.value: probability of observing the correlation when there is no enrichment in the feature of interest in post-translationally buffered gene identified between each pair of species.

*mean: average transcript levels across YRI individuals

*sd: standard deviation of transcript levels across YRI individuals

*TMM: trimmed-mean normalized

*QN: quantile normalized

Table S7 Additional ribosome profiling data used for batch effect adjustment and for joint analysis with RNA seq and quantitative mass spec data.

| ID | mapped count | proportion > Q30 | species | batch |
|---|---|---|---|---|
| **C4973** | 14,640,312 | 0.979 | chimpanzee | mm8 |
| **H18505** | 11,952,124 | 0.919 | human | mm1 |
| **H18507** | 7,864,959 | 0.947 | human | mm1 |
| **H18516** | 5,009,693 | 0.923 | human | mm1 |
| **H19193** | 10,081,244 | 0.919 | human | mm1 |
| **H19204** | 15,820,298 | 0.975 | human | mm2 |
| **H19238** | 8,941,143 | 0.984 | human | mm7 |
| **R150-99** | 14,008,661 | 0.978 | rhesus macaque | mm8 |
| **H18909** | 11,532,097 | 0.973 | human | mm2 |
| **H19099** | 13,030,793 | 0.973 | human | mm2 |
| **H19143** | 8,312,531 | 0.973 | human | mm2 |
| **H19201** | 18,731,551 | 0.986 | human | mm7 |
| **H19210** | 12,817,715 | 0.986 | human | mm7 |
| **H19223** | 10,814,930 | 0.985 | human | mm7 |

* mapped count: total number of uniquely mapped reads for each sample after removing rRNA, tRNA and snoRNA reads.

* proportion > Q30: proportion of sequencing reads that have a Phred quality score greater than 30.