Table S1. ERAP2 (A) and ERAP1  (B) peptides identified by LC-MS/MS analysis, performed on gel bands in the range 105-120 KDa, digested with trypsin.

### A

| Sequence   | Start position | End position | Mass      | Missed cleavages | Charges | Score | Posterior Error Probability (PEP) |
|------------|----------------|--------------|-----------|------------------|---------|-------|-----------------------------------|
| FDLGSYDIR  | 887            | 895          | 1084.5189 | 0                | 2       | 54.157 | 0.031258                          |
| ILAVTDFEPTQAR | 193   | 205          | 1459.7671 | 0                | 2       | 78.934 | 0.00030139                        |
| ILYALSTSK  | 824            | 832          | 994.5699  | 0                | 2       | 69.423 | 0.013583                          |
| LIELGMEGK  | 840            | 848          | 988.52632 | 0                | 2       | 82.426 | 0.003614                          |
| LNIPTDVLK  | 784            | 792          | 1011.5964 | 0                | 2       | 80.438 | 0.011098                          |
| TDTLDLPEK  | 609            | 617          | 1030.5183 | 0                | 2       | 72.23  | 0.010143                          |
| TQNLAALLHAIAR | 852   | 864          | 1390.8045 | 0                | 3       | 26.124 | 0.040988                          |
| YYVAMDFQAK | 162            | 171          | 1234.5692 | 0                | 2       | 72.547 | 0.0016477                         |

Protein: ERAP2_HUMAN Endoplasmic reticulum aminopeptidase 2  
Accession number: Q6P179  
N° of identified peptides: 8  Unique peptides: 8

### B

| Sequence   | Start position | End position | Mass      | Missed cleavages | Charges | Score | Posterior Error Probability (PEP) |
|------------|----------------|--------------|-----------|------------------|---------|-------|-----------------------------------|
| ASLINNAFQLVSIGK | 637   | 651          | 1573.883  | 0                | 2       | 59.542 | 0.000012376                      |
| DMNEVETQFK  | 691            | 700          | 1239.544  | 0                | 2       | 41.448 | 0.02147                          |
| EMFDDVSYDK  | 431            | 440          | 1247.502  | 0                | 2       | 45.137 | 0.014643                         |
| ESALLFDAEK  | 329            | 338          | 1121.561  | 0                | 2       | 57.55  | 0.026351                         |
| EYLSADAFK   | 450            | 458          | 1042.497  | 0                | 2       | 62.546 | 0.021959                         |
| HLAIISNMPLVK | 213            | 223          | 1221.69   | 0                | 2       | 78.334 | 0.00038694                      |
| ILASTQFEPTAAR | 176   | 188          | 1403.741  | 0                | 2       | 78.934 | 0.00030139                      |
| MAFPCDDEPAFK | 189            | 200          | 1458.631  | 0                | 2       | 57.859 | 0.0012734                       |
| SGIVQYLQK   | 459            | 467          | 1034.576  | 0                | 2       | 60.895 | 0.023789                         |
| SQIEFALCR   | 799            | 807          | 1122.549  | 0                | 2       | 98.299 | 0.0062316                       |
| TQEFQQLTIGR | 829            | 841          | 1514.846  | 0                | 2       | 45.359 | 0.0061572                       |
| YQFSLSSTEK  | 789            | 798          | 1188.566  | 0                | 2       | 117.89 | 0.00061685                      |

Protein: ERAP1_HUMAN Endoplasmic reticulum aminopeptidase 1  
Accession number: Q9NZ08  
N° of identified peptides: 12  Unique peptides: 12