**Supplementary Table 1: Cell line information and Sanger sequence confirmed mutations in each cell line**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sample ID** | **HLA type** | **Non-synon mutations** | **Frameshift mutations** | **Number of total individual epitopes predicted** | **Number of peptides ordered (% total predicted)** |
| **D05** | -A\*02 -B\*27, -B\*44 -Cw02, Cw\*05 | 118 | 5 | 312 | 63 (19.2%) |
| **D14** | -A\*03, -A\*24 -B\*07 Cw15 | 136 | 8 | 319 | 54 (17%) |
| **D41** | A\*01, -A\*02 -B\*08 -Cw07 | 287 | 2 | 756 | 139 (18.4%) |
| **A02** | -A\*02, -A\*31 -B\*14, -B\*27 Cw2 | 238 | 3 | 930 | 184 (19.8%) |
| **A06** | -A\*02, -A\*03 -B\*27, -B\*60 -Cw2, -Cw3 | 262 | 2 | 955 | 202 (21.1%) |