|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Blood-derived DC treated patient~ | NY-ESO-1 specific SKILs | MAGE-C2 specific SKILs | MUC1 specific SKILs | NY-ESO-1 expression^(%) | MAGE-C2 expression^(%) | MUC1 expression^(%) | IFN-γ+ SKILs  | NY-ESO-1 expression post-vac (%)() | MAGE-C2 expression post-vac (%)() | MUC1expression post-vac (%)() | PD-L1expression post-vac (%)() | TML& | Microsatellite status\* |
| mDC-01mDC-02mDC-03mDC-04mDC-05mDC-06mDC-07pDC-01pDC-02pDC-03pDC-04pDC-05pDC-06pDC-07combiDC-01combiDC-02combiDC-03combiDC-04combiDC-05combiDC-06combiDC-07 | +++++-++--+-++-+++-++ | ++++------+-++-+++-++ | --+-------+--+---+-+- | 00000na00na0000000040na00 | 00000na200na10560000000na00 | 1105<10na1000na005255<130190na1010 | ++--++-++--+--------+ | 0nananana0nana0nananananana na<1na00na | 0nananana0nana0nananananana na<1na00na | 0nananana10nana10nananananana na2na00na | 060na00nanana5<1na0nanana0nanana00 | 28nana25na47nana5646nanananana10526na113474 | MSSMSSnaMSSnanananaMSSMSSnaMSSnananaMSSMSSnaMSSMSSMSS |

**Additional file 8: Table S1. Immunological, immunohistochemical and whole genome sequencing data.**

DC: dendritic cells; Dm: dextramer; LN: lymph nodes; MSI: microsatellite instable; MSS: microsatellite stable; na: not available; post-vac: post-vaccination; SKILs: skin-infiltrating lymphocytes; TML: tumor mutational load.

^ immunohistochemical staining for NY-ESO-1, MAGE-C2 and MUC1 performed on primary prostate biopsies, prostatectomy tissue or lymph nodes metastases all sampled prior to the start of DC vaccinations.

 () immunohistochemical staining for NY-ESO-1, MAGE-C2, MUC1 and PD-L1 performed on lymph nodes metastases or bone metastases all sampled after progression on DC vaccination therapy.

& microsatellite stability score represents the number of somatic inserts and deletions in short repeat sections across the whole genome of the tumor per megabyte.

\* tumor mutational load represents the total number of somatic missense variants across the whole genome of the tumor.