**Supplementary Table S2: Differentially expressed genes according to treatment response**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| SYMBOL | logFC | AveExpr | t | P.Value | adj.P.Val | B | ENTREZID | GENENAME |
| TAP1 | 1.004 | 8.7386 | 4.3962 | 1.92E-05 | 0.0209 | 2.6235 | 6890 | transporter 1, ATP binding cassette subfamily B member |
| GBP1 | 1.0142 | 9.7533 | 4.1957 | 4.34E-05 | 0.0209 | 1.8958 | 2633 | guanylate binding protein 1 |
| HLA-A | 0.8198 | 12.9362 | 4.0429 | 0.0001 | 0.0209 | 1.3596 | 3105 | major histocompatibility complex, class I, A |
| ITGA2 | -0.8284 | 6.3596 | -3.9938 | 0.0001 | 0.0209 | 1.1908 | 3673 | integrin subunit alpha 2 |
| HLA-B | 0.85 | 13.515 | 3.9747 | 0.0001 | 0.0209 | 1.1256 | 3106 | major histocompatibility complex, class I, B |
| STAT1 | 0.8466 | 10.7274 | 3.9519 | 0.0001 | 0.0209 | 1.0482 | 6772 | signal transducer and activator of transcription 1 |
| CXCL10 | 1.2756 | 8.8884 | 3.9464 | 0.0001 | 0.0209 | 1.0294 | 3627 | C-X-C motif chemokine ligand 10 |
| CD38 | 1.1362 | 6.3107 | 3.7433 | 0.0002 | 0.0392 | 0.3561 | 952 | CD38 molecule |
| CXCL13 | 1.3186 | 6.0197 | 3.6044 | 0.0004 | 0.0521 | -0.0873 | 10563 | C-X-C motif chemokine ligand 13 |
| PDCD1LG2 | 0.7926 | 5.8827 | 3.6035 | 0.0004 | 0.0521 | -0.09 | 80380 | programmed cell death 1 ligand 2 |
| LAG3 | 0.8877 | 6.4371 | 3.5459 | 0.0005 | 0.0582 | -0.2699 | 3902 | lymphocyte activating 3 |
| GNLY | 1.0426 | 7.0858 | 3.4938 | 0.0006 | 0.064 | -0.4301 | 10578 | granulysin |
| IFI27 | 0.9158 | 9.5944 | 3.4511 | 0.0007 | 0.0678 | -0.56 | 3429 | interferon alpha inducible protein 27 |
| DDX58 | 0.694 | 8.1883 | 3.433 | 0.0007 | 0.0678 | -0.6147 | 23586 | DExD/H-box helicase 58 |
| ETV7 | 0.7182 | 6.9431 | 3.4095 | 0.0008 | 0.0686 | -0.6853 | 51513 | ETS variant transcription factor 7 |
| IRF7 | 0.7306 | 7.2571 | 3.3893 | 0.0009 | 0.0689 | -0.7455 | 3665 | interferon regulatory factor 7 |
| TAP2 | 0.5993 | 7.568 | 3.3683 | 0.0009 | 0.0692 | -0.808 | 6891 | transporter 2, ATP binding cassette subfamily B member |
| HIST1H3H | 0.7932 | 9.7112 | 3.3519 | 0.001 | 0.0692 | -0.8564 | 8357 | histone h3.1 |
| MX1 | 0.9357 | 9.8757 | 3.3375 | 0.001 | 0.0692 | -0.899 | 4599 | MX dynamin like GTPase 1 |
| CD274 | 0.7524 | 5.9604 | 3.3069 | 0.0011 | 0.0729 | -0.9885 | 29126 | CD274 molecule |
| TIMP3 | -0.6716 | 10.6326 | -3.2761 | 0.0013 | 0.0769 | -1.078 | 7078 | TIMP metallopeptidase inhibitor 3 |
| THBS4 | -0.9461 | 6.0107 | -3.2521 | 0.0014 | 0.0795 | -1.1471 | 7060 | thrombospondin 4 |
| CCL4 | 0.7586 | 6.7832 | 3.1969 | 0.0017 | 0.0912 | -1.3044 | 6351 | C-C motif chemokine ligand 4 |
| SLAMF7 | 1.0653 | 7.3133 | 3.1759 | 0.0018 | 0.0936 | -1.3637 | 57823 | SLAM family member 7 |
| ISG15 | 0.8621 | 9.8997 | 3.1377 | 0.002 | 0.1017 | -1.4707 | 9636 | ISG15 ubiquitin like modifier |
| CCL5 | 0.8853 | 8.3973 | 3.0133 | 0.003 | 0.1399 | -1.8112 | 6352 | C-C motif chemokine ligand 5 |
| COL1A1 | -0.7136 | 14.0758 | -2.9256 | 0.0039 | 0.1658 | -2.0434 | 1277 | collagen type I alpha 1 chain |
| CD8A | 0.7469 | 7.1559 | 2.9242 | 0.0039 | 0.1658 | -2.0473 | 925 | CD8a molecule |
| ALDH1A3 | -0.6386 | 7.4648 | -2.8856 | 0.0044 | 0.1805 | -2.1475 | 220 | aldehyde dehydrogenase 1 family member A3 |
| PLAT | -0.5323 | 7.5388 | -2.8437 | 0.005 | 0.1925 | -2.2551 | 5327 | plasminogen activator, tissue type |
| EDIL3 | -0.8957 | 6.5925 | -2.8404 | 0.005 | 0.1925 | -2.2635 | 10085 | EGF like repeats and discoidin domains 3 |
| CD79A | 0.8798 | 6.2933 | 2.8265 | 0.0053 | 0.1925 | -2.2989 | 973 | CD79a molecule |
| EGFR | -0.5863 | 7.7635 | -2.8238 | 0.0053 | 0.1925 | -2.3057 | 1956 | epidermal growth factor receptor |
| HEY2 | -0.8171 | 5.8489 | -2.7967 | 0.0057 | 0.2028 | -2.3741 | 23493 | hes related family bHLH transcription factor with YRPW motif 2 |
| SPARC | -0.518 | 11.7881 | -2.7522 | 0.0066 | 0.2125 | -2.4849 | 6678 | secreted protein acidic and cysteine rich |
| IDO1 | 0.8239 | 6.2191 | 2.7514 | 0.0066 | 0.2125 | -2.4868 | 3620 | indoleamine 2,3-dioxygenase 1 |
| C1QA | 0.6519 | 9.8797 | 2.7427 | 0.0067 | 0.2125 | -2.5085 | 712 | complement C1q A chain |
| ICAM1 | 0.5548 | 7.9627 | 2.7422 | 0.0067 | 0.2125 | -2.5096 | 3383 | intercellular adhesion molecule 1 |
| IRF4 | 0.946 | 6.1895 | 2.7364 | 0.0069 | 0.2125 | -2.5238 | 3662 | interferon regulatory factor 4 |
| CTSS | 0.5674 | 9.2116 | 2.7163 | 0.0073 | 0.2199 | -2.5733 | 1520 | cathepsin S |
| CDKN2A | 0.8676 | 7.0094 | 2.7068 | 0.0075 | 0.2208 | -2.5964 | 1029 | cyclin dependent kinase inhibitor 2A |
| IRS1 | -0.5913 | 6.7376 | -2.6691 | 0.0083 | 0.2376 | -2.6877 | 3667 | insulin receptor substrate 1 |
| APOL3 | 0.5671 | 8.0372 | 2.6513 | 0.0088 | 0.2376 | -2.7306 | 80833 | apolipoprotein L3 |
| IRF1 | 0.5173 | 6.3321 | 2.6502 | 0.0088 | 0.2376 | -2.7331 | 3659 | interferon regulatory factor 1 |
| COL1A2 | -0.6124 | 11.5034 | -2.6236 | 0.0095 | 0.2407 | -2.7963 | 1278 | collagen type I alpha 2 chain |
| COL5A1 | -0.5388 | 10.2128 | -2.5845 | 0.0106 | 0.2634 | -2.8885 | 1289 | collagen type V alpha 1 chain |
| IL2RG | 0.6389 | 7.6772 | 2.5775 | 0.0108 | 0.2635 | -2.9049 | 3561 | interleukin 2 receptor subunit gamma |
| CXCL9 | 0.9892 | 9.2842 | 2.553 | 0.0115 | 0.271 | -2.9617 | 4283 | C-X-C motif chemokine ligand 9 |
| SOCS1 | 0.5283 | 8.133 | 2.55 | 0.0116 | 0.271 | -2.9687 | 8651 | suppressor of cytokine signaling 1 |
| CCL7 | 0.702 | 5.2559 | 2.5327 | 0.0122 | 0.2721 | -3.0085 | 6354 | C-C motif chemokine ligand 7 |
| ACSL5 | 0.5907 | 6.3616 | 2.5164 | 0.0128 | 0.2721 | -3.0457 | 51703 | acyl-CoA synthetase long chain family member 5 |
| IL2RB | 0.5982 | 7.1456 | 2.5139 | 0.0129 | 0.2721 | -3.0513 | 3560 | interleukin 2 receptor subunit beta |
| COL3A1 | -0.605 | 13.4832 | -2.5051 | 0.0132 | 0.2741 | -3.0713 | 1281 | collagen type III alpha 1 chain |
| OAS1 | 0.6435 | 7.1465 | 2.4719 | 0.0144 | 0.2816 | -3.1462 | 4938 | 2'-5'-oligoadenylate synthetase 1 |
| FGF13 | -0.5434 | 6.5717 | -2.4646 | 0.0147 | 0.2816 | -3.1627 | 2258 | fibroblast growth factor 13 |
| IFIT2 | 0.6132 | 7.7455 | 2.4632 | 0.0148 | 0.2816 | -3.1657 | 3433 | interferon induced protein with tetratricopeptide repeats 2 |
| MLPH | -0.7169 | 6.3298 | -2.4606 | 0.0149 | 0.2816 | -3.1716 | 79083 | melanophilin |
| PAX6 | 0.8315 | 4.1896 | 2.4517 | 0.0152 | 0.2842 | -3.1915 | 5080 | paired box 6 |
| CCR5 | 0.5444 | 6.7585 | 2.4449 | 0.0155 | 0.2852 | -3.2065 | 1234 | C-C motif chemokine receptor 5 (gene/pseudogene) |
| PDCD1 | 0.6019 | 5.4694 | 2.4053 | 0.0172 | 0.3084 | -3.2939 | 5133 | programmed cell death 1 |
| SFRP4 | -0.6199 | 8.2487 | -2.4022 | 0.0174 | 0.3084 | -3.3005 | 6424 | secreted frizzled related protein 4 |
| BCL2A1 | 0.5562 | 7.2982 | 2.3866 | 0.0181 | 0.3084 | -3.3345 | 597 | BCL2 related protein A1 |
| GZMA | 0.6315 | 6.2529 | 2.384 | 0.0182 | 0.3084 | -3.3402 | 3001 | granzyme A |
| PIM2 | 0.6123 | 7.8212 | 2.3414 | 0.0204 | 0.3231 | -3.4316 | 11040 | Pim-2 proto-oncogene, serine/threonine kinase |
| SFRP2 | -0.6452 | 10.6621 | -2.3282 | 0.0211 | 0.3239 | -3.4598 | 6423 | secreted frizzled related protein 2 |
| PRF1 | 0.5868 | 6.5615 | 2.3267 | 0.0211 | 0.3239 | -3.463 | 5551 | perforin 1 |
| OASL | 0.6012 | 6.3576 | 2.3263 | 0.0212 | 0.3239 | -3.4639 | 8638 | 2'-5'-oligoadenylate synthetase like |
| THBS1 | -0.5572 | 10.5237 | -2.2472 | 0.0259 | 0.378 | -3.6288 | 7057 | thrombospondin 1 |
| CD27 | 0.6981 | 6.3957 | 2.2355 | 0.0267 | 0.3823 | -3.6527 | 939 | CD27 molecule |
| LYZ | 0.6933 | 11.4721 | 2.2333 | 0.0268 | 0.3823 | -3.6573 | 4069 | lysozyme |
| CA9 | 0.7034 | 5.8046 | 2.2291 | 0.0271 | 0.3823 | -3.6657 | 768 | carbonic anhydrase 9 |
| SPDEF | -0.9031 | 5.7095 | -2.2084 | 0.0285 | 0.3957 | -3.7078 | 25803 | SAM pointed domain containing ETS transcription factor |
| PRR15L | -0.5907 | 6.8748 | -2.1851 | 0.0302 | 0.3982 | -3.7545 | 79170 | proline rich 15 like |
| MDK | 0.5135 | 9.7867 | 2.177 | 0.0308 | 0.3982 | -3.7708 | 4192 | midkine |
| SPRY2 | -0.5578 | 6.4125 | -2.1724 | 0.0312 | 0.3982 | -3.7798 | 10253 | sprouty RTK signaling antagonist 2 |
| GZMB | 0.6469 | 6.9477 | 2.1622 | 0.032 | 0.3982 | -3.8002 | 3002 | granzyme B |
| ACTA2 | -0.5451 | 8.6603 | -2.121 | 0.0353 | 0.4235 | -3.8808 | 59 | actin alpha 2, smooth muscle |
| CTGF | -0.5281 | 9.8999 | -2.0969 | 0.0375 | 0.4309 | -3.9274 | 1490 | cellular communication network factor 2 |
| AREG | -0.7151 | 4.5927 | -2.0472 | 0.0422 | 0.445 | -4.0219 | 374 | amphiregulin |
| INHBB | -0.5829 | 6.4414 | -2.0425 | 0.0426 | 0.445 | -4.0308 | 3625 | inhibin subunit beta B |
| CXCR3 | 0.5965 | 5.7989 | 2.0395 | 0.0429 | 0.445 | -4.0362 | 2833 | C-X-C motif chemokine receptor 3 |
| WNT7B | -0.5045 | 6.3711 | -2.0197 | 0.045 | 0.445 | -4.0732 | 7477 | Wnt family member 7B |
| GZMH | 0.5047 | 5.5735 | 2.0148 | 0.0455 | 0.445 | -4.0824 | 2999 | granzyme H |
| FZD8 | -0.5186 | 7.3162 | -1.9785 | 0.0495 | 0.4644 | -4.1488 | 8325 | frizzled class receptor 8 |

Differential gene expression analysis according to pathologic complete response after neoadjuvant chemotherapy with durvalumab. Included are genes with an absolute log-fold-change > 0.5 and P < 0.05.