

| | | Variance explained per factor - Sanger&CMRI | | | | | | | | | | | | | | |
|------------------------|-----------------------------|---|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| | | F1 | F2 | F3 | F4 | F5 | F6 | F7 | F8 | F9 | F10 | F11 | F12 | F13 | F14 | F15 |
| Haem | drespo | 0.00 | 0.00 | 0.00 | -0.00 | -0.00 | 0.00 | 0.00 | 0.00 | 0.04 | 0.01 | 0.02 | 0.00 | 0.03 | 0.00 | 0.01 |
| | methylation | -0.00 | 0.00 | 0.10 | 0.02 | 0.08 | 0.00 | 0.00 | -0.00 | 0.09 | 0.00 | 0.00 | 0.00 | 0.04 | 0.00 | 0.00 |
| | proteomics | -0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.11 | 0.00 | 0.00 | 0.04 | 0.00 | 0.02 | 0.00 | 0.04 | 0.00 | 0.00 |
| | transcriptomics | -0.00 | 0.01 | 0.01 | 0.00 | 0.02 | 0.00 | 0.00 | 0.00 | 0.10 | 0.01 | 0.00 | 0.02 | 0.04 | 0.00 | 0.00 |
| Other | drespo | 0.03 | 0.04 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.02 | 0.00 | 0.02 | 0.05 | 0.00 | 0.00 | 0.01 | 0.03 |
| | methylation | 0.11 | 0.04 | 0.08 | 0.05 | 0.06 | 0.00 | 0.02 | 0.02 | 0.00 | 0.01 | 0.01 | 0.00 | 0.01 | 0.01 | 0.01 |
| | proteomics | 0.06 | 0.07 | 0.00 | 0.00 | 0.00 | 0.17 | 0.02 | 0.01 | -0.00 | 0.01 | 0.03 | 0.00 | 0.00 | 0.01 | 0.01 |
| | transcriptomics | 0.13 | 0.10 | 0.01 | 0.02 | 0.01 | 0.00 | 0.03 | 0.02 | 0.00 | 0.02 | 0.02 | 0.02 | 0.01 | 0.01 | 0.01 |
| Features | NProteinsSanger&CMRI | 0.04 | 0.07 | 0.05 | 0.04 | 0.02 | -0.17 | 0.12 | -0.03 | -0.06 | -0.08 | -0.09 | 0.04 | -0.08 | 0.05 | -0.04 |
| | NProteinsBroad | -0.04 | 0.10 | 0.03 | 0.03 | -0.01 | -0.10 | 0.10 | 0.05 | -0.01 | 0.05 | 0.01 | -0.13 | 0.00 | 0.01 | 0.06 |
| | RepsCorrelationSanger&CMRI | -0.14 | 0.13 | -0.09 | -0.00 | 0.05 | 0.10 | -0.08 | 0.08 | 0.08 | -0.02 | 0.08 | -0.05 | 0.07 | -0.08 | -0.02 |
| | Global proteomics | 0.06 | 0.11 | -0.03 | 0.02 | 0.02 | 0.02 | -0.10 | 0.01 | -0.02 | -0.06 | 0.14 | 0.02 | 0.03 | 0.05 | -0.03 |
| | GExpProtCorrSanger&CMRI | 0.26 | 0.07 | 0.08 | 0.05 | -0.02 | -0.57 | 0.13 | -0.05 | 0.00 | -0.05 | -0.11 | 0.14 | 0.01 | 0.12 | 0.03 |
| | GExpProtCorrBroad | 0.24 | -0.17 | 0.19 | 0.15 | 0.05 | -0.25 | 0.17 | -0.06 | -0.06 | 0.02 | 0.19 | 0.11 | 0.02 | -0.10 | -0.01 |
| | SamplesOverlapCorr | -0.05 | 0.07 | -0.01 | 0.07 | 0.03 | 0.02 | 0.03 | 0.08 | 0.06 | -0.07 | 0.07 | 0.01 | 0.06 | -0.05 | 0.08 |
| | Mean IC50 | -0.16 | -0.11 | -0.01 | -0.04 | -0.02 | -0.02 | 0.04 | -0.19 | 0.06 | -0.22 | 0.31 | -0.02 | -0.02 | -0.02 | -0.24 |
| | Binary IC50 | -0.08 | 0.06 | 0.09 | 0.04 | 0.00 | 0.05 | 0.01 | 0.15 | -0.08 | 0.26 | -0.34 | 0.04 | -0.01 | 0.01 | 0.18 |
| | Global methylation | -0.11 | 0.02 | 0.82 | 0.05 | -0.06 | -0.01 | 0.06 | 0.16 | -0.11 | 0.19 | -0.09 | 0.14 | -0.00 | -0.06 | 0.08 |
| | MSI | -0.08 | 0.15 | 0.16 | -0.03 | -0.09 | 0.04 | 0.19 | 0.07 | 0.01 | 0.15 | -0.05 | 0.06 | -0.01 | 0.00 | 0.09 |
| | MSS | 0.08 | -0.17 | -0.15 | 0.04 | 0.10 | -0.04 | -0.17 | -0.07 | -0.01 | -0.14 | 0.05 | -0.04 | -0.00 | -0.01 | -0.09 |
| | Adherent | -0.15 | -0.20 | 0.04 | -0.01 | -0.01 | 0.14 | 0.01 | -0.05 | 0.02 | 0.05 | -0.02 | 0.08 | -0.04 | -0.06 | -0.07 |
| | Semi-Adherent | 0.02 | 0.16 | -0.04 | -0.03 | 0.03 | -0.05 | 0.03 | 0.04 | 0.01 | -0.01 | 0.03 | 0.01 | -0.10 | 0.06 | -0.06 |
| | Suspension | -0.09 | 0.29 | -0.01 | 0.08 | -0.08 | -0.14 | -0.07 | 0.15 | -0.03 | -0.10 | 0.04 | 0.01 | 0.01 | 0.09 | -0.03 |
| | Unknown | -0.08 | -0.12 | -0.02 | -0.05 | 0.08 | 0.00 | 0.05 | -0.11 | 0.00 | 0.05 | -0.03 | -0.10 | 0.09 | -0.04 | 0.14 |
| | Haematopoietic and Lymphoid | -0.01 | 0.08 | 0.03 | 0.01 | -0.04 | -0.02 | -0.00 | 0.16 | -0.05 | 0.01 | 0.02 | 0.00 | -0.00 | -0.04 | -0.01 |
| | ploidy | -0.05 | -0.10 | 0.03 | 0.07 | 0.08 | 0.04 | -0.11 | -0.04 | -0.04 | -0.01 | 0.04 | 0.02 | 0.01 | 0.04 | -0.06 |
| | mutational_burden | -0.11 | 0.25 | 0.24 | 0.04 | 0.02 | 0.06 | -0.04 | 0.14 | -0.02 | 0.01 | -0.07 | 0.18 | -0.19 | 0.10 | -0.02 |
| | growth | 0.00 | -0.08 | 0.19 | 0.13 | -0.05 | 0.08 | 0.09 | 0.01 | -0.08 | 0.08 | -0.46 | 0.06 | -0.12 | -0.00 | 0.20 |
| | TP53_mut_wes | -0.17 | 0.16 | -0.09 | 0.04 | -0.03 | 0.08 | -0.22 | 0.03 | 0.00 | -0.01 | -0.11 | -0.03 | 0.07 | 0.12 | -0.10 |
| | CDH1_proteomics | -0.44 | -0.16 | 0.16 | 0.09 | -0.06 | -0.05 | -0.17 | 0.17 | -0.10 | 0.29 | 0.12 | 0.01 | 0.13 | -0.14 | 0.01 |
| | VIM_proteomics | 0.51 | -0.61 | 0.05 | 0.01 | 0.05 | -0.17 | 0.21 | -0.34 | -0.09 | -0.02 | 0.10 | 0.05 | -0.14 | 0.15 | -0.01 |
| | BCL2L1_proteomics | -0.12 | -0.16 | -0.00 | 0.01 | -0.07 | -0.23 | 0.04 | -0.21 | 0.01 | -0.22 | 0.20 | -0.04 | 0.18 | -0.13 | -0.21 |
| | CDH1_transcriptomics | -0.70 | 0.22 | -0.00 | -0.06 | -0.04 | 0.18 | -0.18 | 0.19 | 0.10 | -0.12 | 0.09 | -0.14 | 0.03 | -0.12 | -0.01 |
| | VIM_transcriptomics | 0.55 | -0.66 | 0.03 | -0.06 | 0.08 | -0.09 | 0.17 | -0.35 | -0.09 | -0.00 | 0.03 | 0.07 | -0.11 | 0.10 | -0.02 |
| MCL1_transcriptomics | -0.24 | -0.21 | 0.09 | 0.14 | -0.05 | 0.10 | -0.19 | 0.03 | 0.04 | -0.07 | -0.02 | 0.03 | -0.22 | 0.01 | -0.06 | |
| BCL2L1_transcriptomics | -0.46 | -0.22 | 0.12 | 0.08 | -0.14 | -0.00 | 0.01 | -0.21 | -0.00 | -0.28 | 0.12 | 0.02 | 0.14 | -0.20 | -0.17 | |
| SLC5A1_methylation | -0.09 | 0.13 | 0.16 | -0.62 | -0.18 | 0.02 | -0.02 | 0.01 | 0.09 | -0.05 | -0.04 | -0.01 | 0.02 | -0.23 | -0.04 | |