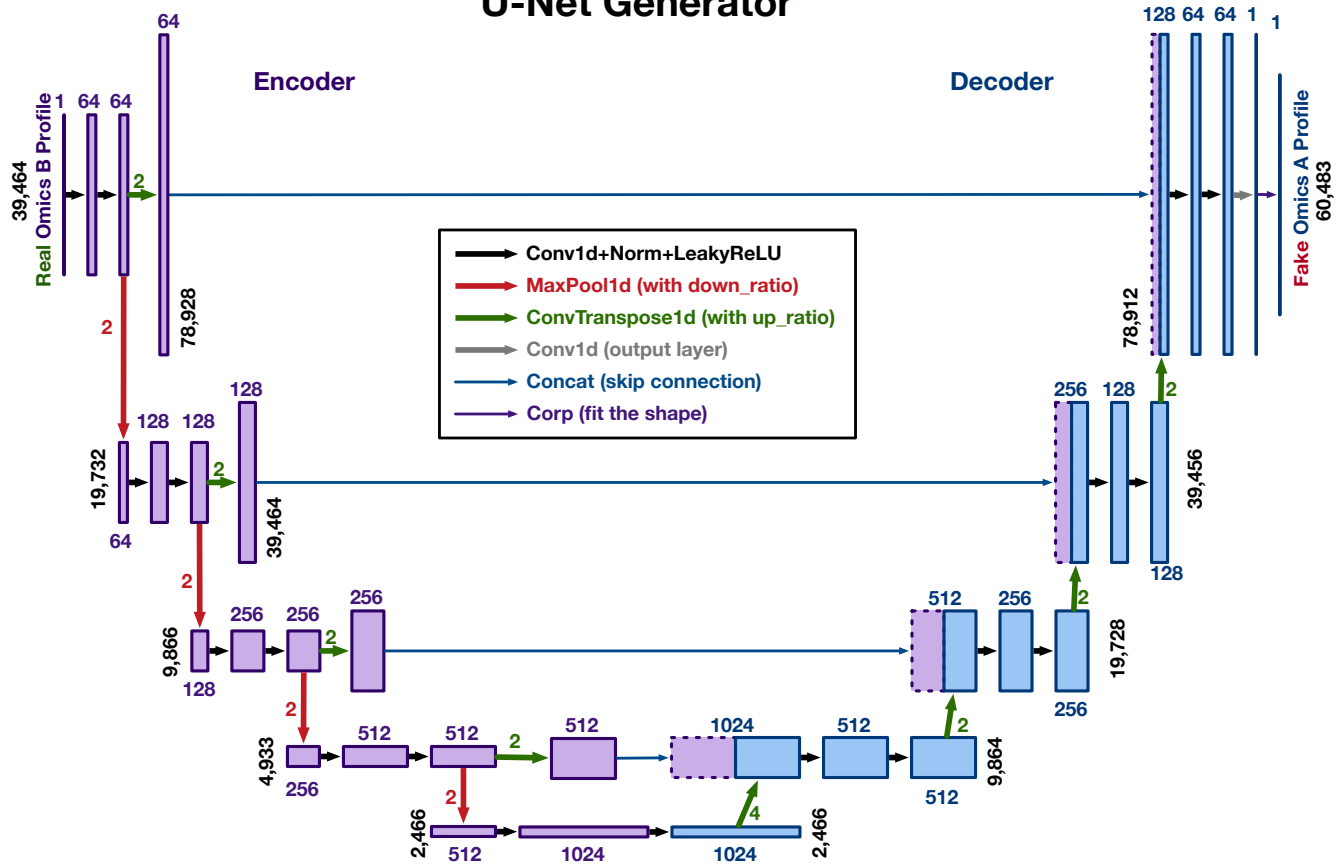
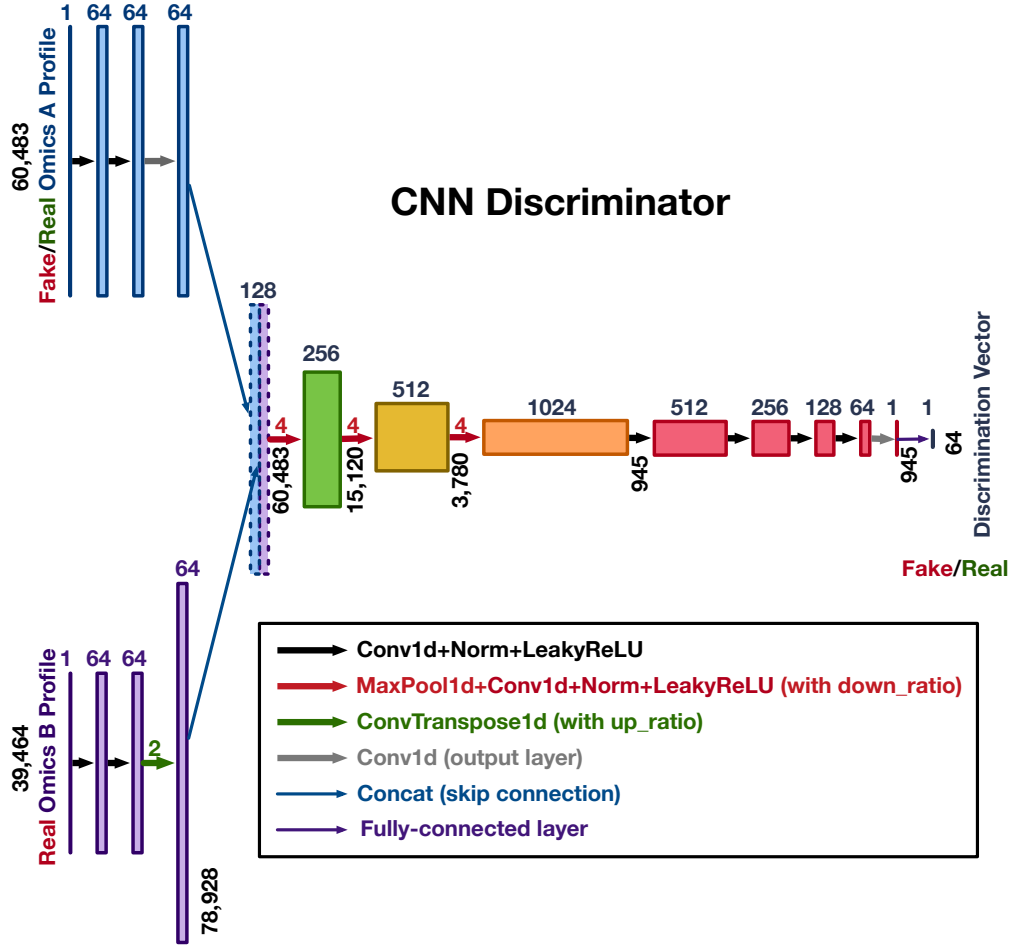


OmiTrans: generative adversarial networks based omics-to-omics translation framework

This document provides the Supplementary Figures and Tables mentioned in the manuscript.

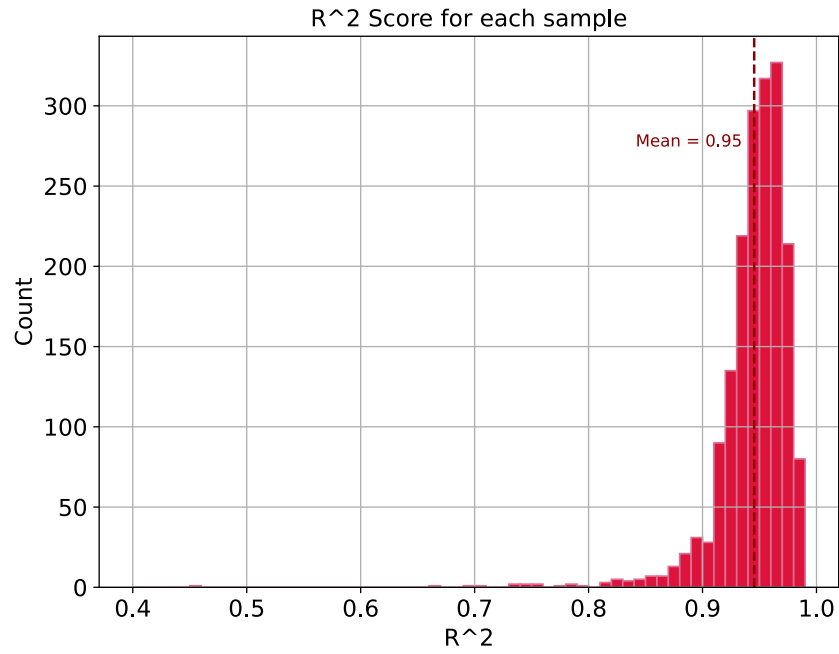




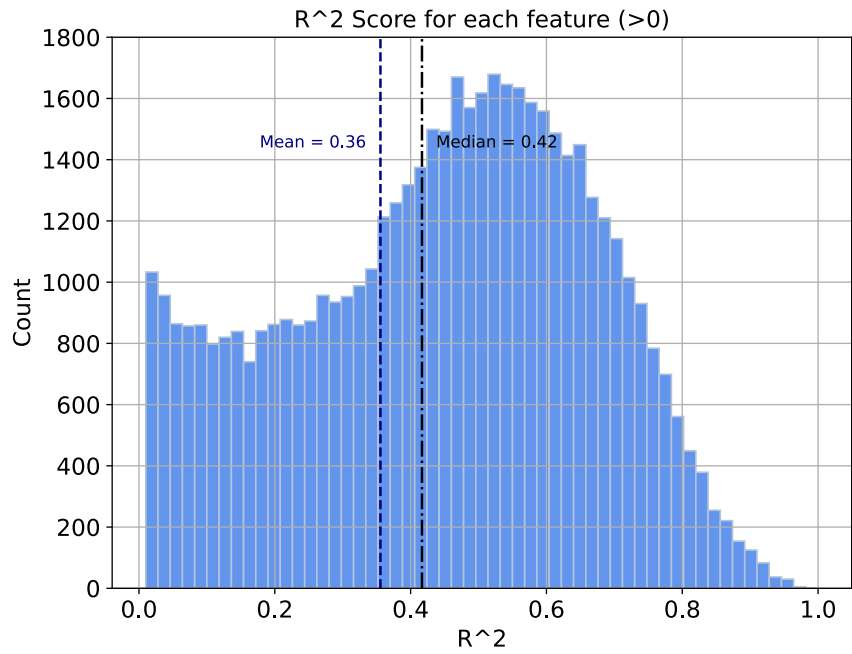
Supplementary Figure 2: The implementation of the OmiTrans discriminator D using a CNN. The channel number and feature number of each tensor in the network were marked in the diagram. Each type of operation group (e.g., conv1D + norm + LeakyReLU) is illustrated using arrows with different colours and thicknesses shown in the legend. The output of the discriminator network is a discrimination vector determining whether the input omics A is fake or real.

Supplementary Table 1: Hyper-parameters used for OmiTrans with the FC-based architecture.

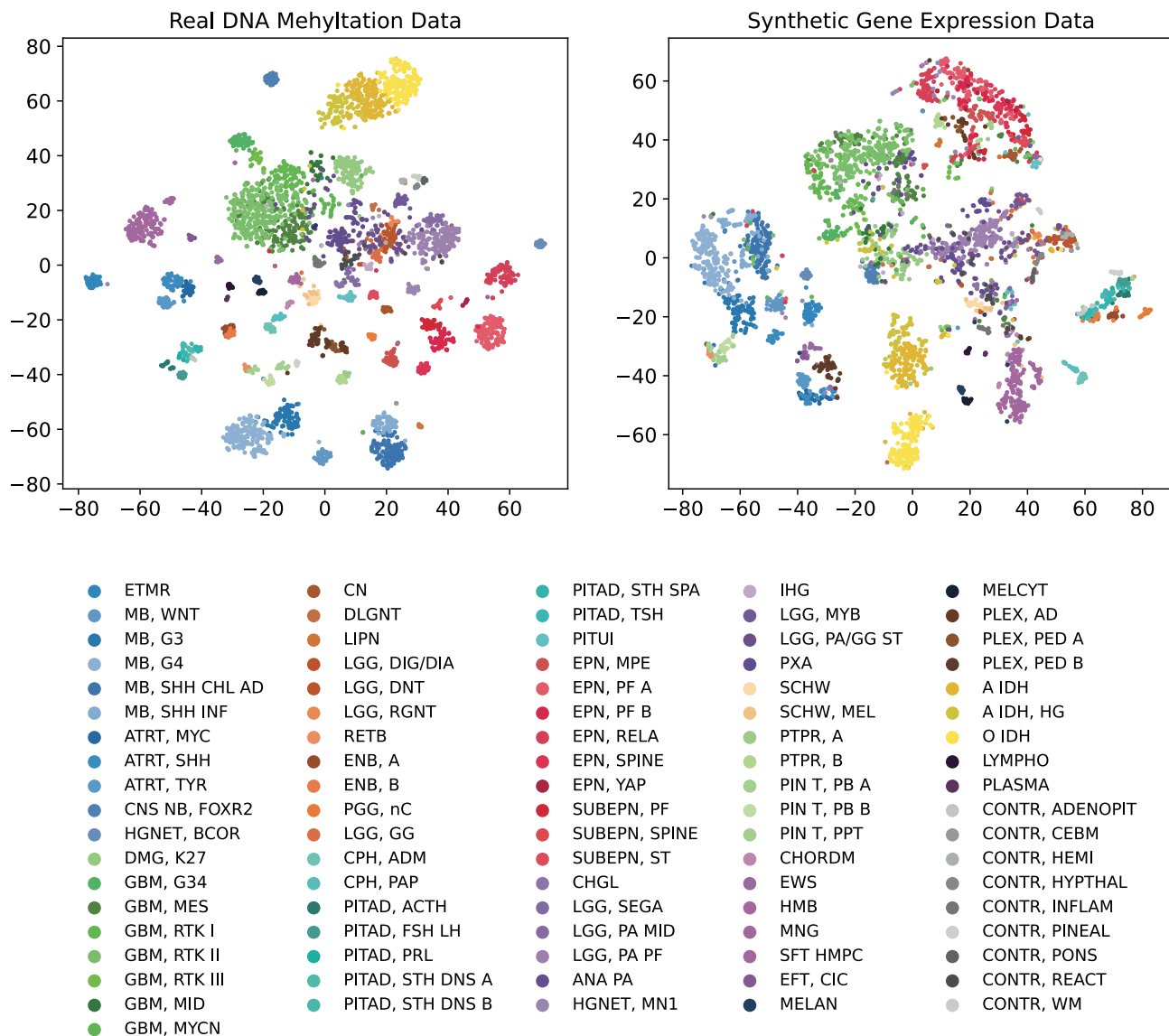
| Hyper-parameter | Value |
|--|--------------------|
| Latent dimension | 256 |
| Learning rate of the generator G | 1×10^{-4} |
| Learning rate of the discriminator D | 1×10^{-4} |
| Batch size | 128 |
| Epoch number - total | 800 |
| Epoch number - decay | 100 |
| Dropout rate | 0.2 |



Supplementary Figure 3: Histogram of the samplewise R^2 scores (R_s^2).



Supplementary Figure 4: Histogram of the featurewise R^2 scores (R_f^2) that larger than zero.



Supplementary Figure 5: The scatter graphs of the original DNA methylation data of the BTM dataset, the fake gene expression data of BTM synthesised by a OmiTrans generator trained on the GDC training set. Samples with different brain tumour types or normal control regions were marked with different colours, brain tumour types and normal control regions belonging to the same upper-level class were marked in similar colours, as shown in the legend. Full name of each brain tumour type and normal control region is listed in Supplementary Table 3.

Supplementary Table 2: Tumour type information of the multi-omics datasets from Genomic Data Commons (GDC). Sample numbers of each tumour type and the normal control for RNA-Seq gene expression profiling (A) and DNA methylation profiling (B) are shown in corresponding columns.

| Tumour Type | Abbreviation | Count A | Count B |
|--|--------------|---------|---------|
| Breast invasive carcinoma | BRCA | 1,104 | 794 |
| Brain lower grade glioma | LGG | 529 | 534 |
| Thyroid carcinoma | THCA | 510 | 515 |
| Head and neck squamous cell carcinoma | HNSC | 502 | 530 |
| Prostate adenocarcinoma | PRAD | 499 | 503 |
| Lung adenocarcinoma | LUAD | 526 | 471 |
| Skin cutaneous melanoma | SKCM | 471 | 473 |
| Uterine corpus endometrial carcinoma | UCEC | 548 | 436 |
| Bladder urothelial carcinoma | BLCA | 411 | 416 |
| Liver hepatocellular carcinoma | LIHC | 374 | 380 |
| Lung squamous cell carcinoma | LUSC | 501 | 370 |
| Stomach adenocarcinoma | STAD | 375 | 395 |
| Kidney renal clear cell carcinoma | KIRC | 535 | 323 |
| Cervical squamous cell carcinoma and endocervical adenocarcinoma | CESC | 306 | 309 |
| Colon adenocarcinoma | COAD | 471 | 309 |
| Kidney renal papillary cell carcinoma | KIRP | 289 | 276 |
| Sarcoma | SARC | 263 | 265 |
| Pheochromocytoma and paraganglioma | PCPG | 183 | 184 |
| Pancreatic adenocarcinoma | PAAD | 178 | 185 |
| Esophageal carcinoma | ESCA | 162 | 186 |
| Testicular germ cell tumours | TGCT | 156 | 156 |
| Thymoma | THYM | 119 | 124 |
| Acute myeloid leukemia | LAML | 151 | 140 |
| Rectum adenocarcinoma | READ | 167 | 99 |
| Mesothelioma | MESO | 86 | 87 |
| Uveal melanoma | UVM | 80 | 80 |
| Adrenocortical carcinoma | ACC | 79 | 80 |
| Kidney chromophobe | KICH | 65 | 66 |
| Uterine carcinosarcoma | UCS | 56 | 57 |
| Lymphoid neoplasm diffuse large B-cell lymphoma | DLBC | 48 | 48 |
| Cholangiocarcinoma | CHOL | 36 | 36 |
| Ovarian serous cystadenocarcinoma | OV | 379 | 10 |
| Glioblastoma multiforme | GBM | 168 | 153 |
| Normal control | | 741 | 746 |
| Total | | 11,068 | 9,736 |

Supplementary Table 3: Detailed tumour type information of the GSE109381 Brain Tumour Methylation (BTM) dataset.

| Methylation Class | Abbreviation | Count |
|--|------------------|-------|
| Embryonal tumor with multilayered rosettes | ETMR | 49 |
| Medulloblastoma, WNT | MB, WNT | 48 |
| Medulloblastoma, subclass group 3 | MB, G3 | 99 |
| Medulloblastoma, subclass group 4 | MB, G4 | 181 |
| Medulloblastoma, subclass SHH A (children and adult) | MB, SHH CHL AD | 126 |
| Medulloblastoma, subclass SHH B (infant) | MB, SHH INF | 65 |
| Atypical teratoid/rhabdoid tumor, subclass MYC | ATRT, MYC | 31 |
| Atypical teratoid/rhabdoid tumor, subclass SHH | ATRT, SHH | 51 |
| Atypical teratoid/rhabdoid tumor, subclass TYR | ATRT, TYR | 39 |
| CNS neuroblastoma with FOXR2 activation | CNS NB, FOXR2 | 43 |
| CNS high grade neuroepithelial tumor with BCOR alteration | HGNET, BCOR | 26 |
| Diffuse midline glioma H3 K27M mutant | DMG, K27 | 117 |
| Glioblastoma, IDH wildtype, H3.3 G34 mutant | GBM, G34 | 54 |
| Glioblastoma, IDH wildtype, subclass mesenchymal | GBM, MES | 160 |
| Glioblastoma, IDH wildtype, subclass RTK I | GBM, RTK I | 108 |
| Glioblastoma, IDH wildtype, subclass RTK II | GBM, RTK II | 261 |
| Glioblastoma, IDH wildtype, subclass RTK III | GBM, RTK III | 22 |
| Glioblastoma, IDH wildtype, subclass midline | GBM, MID | 33 |
| Glioblastoma, IDH wildtype, subclass MYCN | GBM, MYCN | 33 |
| Central neurocytoma | CN | 23 |
| Diffuse leptomeningeal glioneuronal tumor | DLGNT | 12 |
| Cerebellar liponeurocytoma | LIPN | 11 |
| Low grade glioma, desmoplastic infantile astrocytoma / ganglioglioma | LGG, DIG/DIA | 8 |
| Low grade glioma, dysembryoplastic neuroepithelial tumor | LGG, DNT | 56 |
| Low grade glioma, rosette forming glioneuronal tumor | LGG, RGNT | 12 |
| Retinoblastoma | RETB | 19 |
| Esthesioneuroblastoma, subclass A | ENB, A | 24 |
| Esthesioneuroblastoma, subclass B | ENB, B | 16 |
| Paranglioma, spinal non-CIMP | PGG, nC | 20 |
| Low grade glioma, ganglioglioma | LGG, GG | 26 |
| Craniopharyngioma, adamantinomatous | CPH, ADM | 25 |
| Craniopharyngioma, papillary | CPH, PAP | 20 |
| Pituitary adenoma, ACTH | PITAD, ACTH | 19 |
| Pituitary adenoma, FSH/LH | PITAD, FSH LH | 23 |
| Pituitary adenoma, prolactin | PITAD, PRL | 8 |
| Pituitary adenoma, STH densely granulated, group A | PITAD, STH DNS A | 9 |
| Pituitary adenoma, STH densely granulated, group B | PITAD, STH DNS B | 13 |
| Pituitary adenoma, STH sparsely granulated | PITAD, STH SPA | 17 |
| Pituitary adenoma, TSH | PITAD, TSH | 11 |
| Pituicytoma / granular cell tumor / spindle cell oncocytoma | PITUI | 30 |
| Ependymoma, myxopapillary | EPN, MPE | 45 |
| Ependymoma, posterior fossa group A | EPN, PF A | 127 |
| Ependymoma, posterior fossa group B | EPN, PF B | 59 |
| Ependymoma, RELA fusion | EPN, RELA | 90 |
| Ependymoma, spinal | EPN, SPINE | 34 |
| Ependymoma, YAP fusion | EPN, YAP | 11 |
| Subependymoma, posterior fossa | SUBEPN, PF | 40 |
| Subependymoma, spinal | SUBEPN, SPINE | 12 |
| Subependymoma, supratentorial | SUBEPN, ST | 20 |
| Chordoid glioma of the third ventricle | CHGL | 12 |
| Low grade glioma, subependymal giant cell astrocytoma | LGG, SEGA | 22 |

| | | |
|--|-----------------|--------------|
| Low grade glioma, subclass hemispheric pilocytic astrocytoma and ganglioglioma | LGG, PA MID | 55 |
| Low grade glioma, subclass midline pilocytic astrocytoma | LGG, PA PF | 154 |
| Anaplastic pilocytic astrocytoma | ANA PA | 46 |
| CNS high grade neuroepithelial tumor with MN1 alteration | HGNET, MN1 | 26 |
| Infantile hemispheric glioma | IHG | 15 |
| Low grade glioma, MYB/MYBL1 | LGG, MYB | 27 |
| Low grade glioma, subclass posterior fossa pilocytic astrocytoma | LGG, PA/GG ST | 45 |
| (Anaplastic) pleomorphic xanthoastrocytoma | PXA | 67 |
| Schwannoma | SCHW | 31 |
| Melanotic schwannoma | SCHW, MEL | 12 |
| Papillary tumor of the pineal region group A | PTPR, A | 9 |
| Papillary tumor of the pineal region group B | PTPR, B | 23 |
| Pineoblastoma group A / intracranial retinoblastoma | PIN T, PB A | 9 |
| Pineoblastoma group B | PIN T, PB B | 23 |
| Pineal parenchymal tumor | PIN T, PPT | 20 |
| Chordoma | CHORDM | 11 |
| Ewing sarcoma | EWS | 17 |
| Hemangioblastoma | HMB | 27 |
| Meningioma | MNG | 149 |
| Solitary fibrous tumor / hemangiopericytoma | SFT HMPC | 18 |
| CNS Ewing sarcoma family tumor with CIC alteration | EFT, CIC | 13 |
| Melanoma | MELAN | 18 |
| Melanocytoma | MELCYT | 19 |
| Plexus tumor, subclass adult | PLEX, AD | 23 |
| Plexus tumor, subclass paediatric A | PLEX, PED A | 16 |
| Plexus tumor, subclass paediatric B | PLEX, PED B | 49 |
| IDH glioma, subclass astrocytoma | A IDH | 172 |
| IDH glioma, subclass high grade astrocytoma | A IDH, HG | 87 |
| IDH glioma, subclass 1p/19q codeleted oligodendroglioma | O IDH | 163 |
| Lymphoma | LYMPHO | 14 |
| Plasmacytoma | PLASMA | 8 |
| Control tissue, pituitary gland anterior lobe | CONTR, ADENOPIT | 9 |
| Control tissue, cerebellar hemisphere | CONTR, CEBM | 8 |
| Control tissue, hemispheric cortex | CONTR, HEMI | 13 |
| Control tissue, hypothalamus | CONTR, HYPTHAL | 9 |
| Control tissue, inflammatory tumor microenvironment | CONTR, INFLAM | 24 |
| Control tissue, pineal gland | CONTR, PINEAL | 12 |
| Control tissue, pons | CONTR, PONS | 12 |
| Control tissue, reactive tumor microenvironment | CONTR, REACT | 23 |
| Control tissue, white matter | CONTR, WM | 9 |
| Total | | 3,905 |