

Supplementary Information

1. How are the datasets of DNA methylation preprocessed?

Large datasets like HumanMethylation450 (HM450) and HumanMethylation27 (HM27) contain high-dimensional methylation data, measuring DNA methylation at 485,000 and 27,000 CpG sites, respectively. This results in datasets with an extremely high number of features, which can be computationally challenging to analyze directly. To overcome this, the TCGA-Assembler2 package in R (Wei et al., 2018) provides a streamlined preprocessing pipeline that reduces dimensionality while retaining biologically relevant information. The pipeline assumes that raw beta values have been preprocessed and normalized using external tools, such as SWAN (Subset-quantile Within Array Normalization) or BMIQ (Beta Mixture Quantile Normalization), which are specifically designed for Illumina methylation arrays. These normalization methods correct technical variations, such as batch effects and probe-specific biases, ensuring that the data are comparable across samples and platforms.

A critical step in reducing the high dimensionality of HM450 and HM27 data is the aggregation of methylation values at the gene level. TCGA-Assembler2 uses the `CalculateSingleValueMethylationData` function to summarize methylation beta values for specific genomic regions, such as promoter regions (e.g., TSS1500 and TSS200). For example, methylation levels within TSS1500 (1500 base pairs upstream of the transcription start site) and TSS200 (200 base pairs upstream) are averaged to produce a single gene-level beta value. This approach reduces the number of features from hundreds of thousands of CpG sites to a more manageable number of genes, while preserving the biological significance of methylation patterns in regulatory regions. By focusing on promoter regions, which are critical for gene regulation, this step ensures that the summarized data are both interpretable and relevant for downstream analysis.

Finally, TCGA-Assembler2 addresses the challenge of batch effects and technical variations, which are common in large-scale methylation studies. While the package does not include built-in functions for batch effect correction or quality control (QC), it assumes that users will perform these steps externally using tools like ComBat (for batch effect correction) or the minfi package (for QC). The output of this preprocessing pipeline is a gene-level methylation matrix, where rows represent genes and columns represent samples. This matrix is significantly smaller in size compared to the original dataset, making it computationally efficient for downstream tasks such as identifying differentially methylated genes (DMGs), clustering samples, or integrating methylation data with other omics data. By reducing the dimensionality and improving data quality, TCGA-Assembler2 enables researchers to extract meaningful insights from HM450 and HM27 datasets without being overwhelmed by the high number of features.

[1] Wei, L., Jin, Z., Yang, S., Xu, Y., Zhu, Y., & Ji, Y. (2018). TCGA-assembler 2: software pipeline for retrieval and processing of TCGA/CPTAC data. *Bioinformatics* (Oxford, England), 34(9), 1615–1617. <https://doi.org/10.1093/bioinformatics/btx812>

2. What are the standard preprocessing methods used?
 - a. Samples without valid subtype labels were removed.
 - b. Samples containing >80% zero or missing values were excluded to avoid sparsity-driven biases.
 - c. Classes with fewer than 10 samples were removed to prevent unreliable model training.

Supplementary Table S1: A comprehensive collection of 153 benchmark datasets for cancer molecular subtype classification that encompasses 20 distinct cancers and spans 17 unique data configurations across 8 omics modalities.

| Cancer | Modality | Configuration | Classes | Total Samples | Samples Per Class | No of Features |
|--------|----------|---------------|---------|---------------|-------------------|----------------|
|--------|----------|---------------|---------|---------------|-------------------|----------------|

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|------|---------------|---------------------------|---|-----|---|--------|
| PRAD | miRNA | miRNA HiSeq gene | 8 | 330 | ERG: 151, SPOP: 37, 4 FLI1: 4, Other: 85, FOXA1: 9, ETV1: 27, ETV4: 14, IDH1: 3 | 633 |
| | RNASeq | HiSeqV2 | 8 | 333 | ETV1: 28, ERG: 152, Other: 86, IDH1: 3, ETV4: 14, SPOP: 37, FOXA1: 9, 4 FLI1: 4 | 20530 |
| | | HiSeqV2 PANCAN | 8 | 333 | ETV1: 28, ERG: 152, Other: 86, IDH1: 3, ETV4: 14, SPOP: 37, FOXA1: 9, 4 FLI1: 4 | 20530 |
| | | HiSeqV2 percentile | 8 | 333 | ETV1: 28, ERG: 152, Other: 86, IDH1: 3, ETV4: 14, SPOP: 37, FOXA1: 9, 4 FLI1: 4 | 20501 |
| | Exon | HiSeqV2 exon | 8 | 333 | ETV1: 28, ERG: 152, Other: 86, IDH1: 3, ETV4: 14, SPOP: 37, FOXA1: 9, 4 FLI1: 4 | 239322 |
| | RPPA | RPPA | 8 | 250 | SPOP: 23, ERG: 116, IDH1: 3, ETV1: 23, Other: 65, FOXA1: 7, ETV4: 10, 4 FLI1: 3 | 218 |
| | SNP/ INDEL | mc3 gene level | 8 | 331 | ERG: 151, Other: 86, ETV1: 28, FOXA1: 9, 4 FLI1: 3, ETV4: 14, IDH1: 3, SPOP: 37 | 40543 |
| | CNV | Gistic2 all data by genes | 8 | 333 | ERG: 152, Other: 86, ETV1: 28, FOXA1: 9, 4 FLI1: 4, ETV4: 14, IDH1: 3, SPOP: 37 | 24776 |
| | | Gistic2 all thresholded | 8 | 333 | ERG: 152, Other: 86, ETV1: 28, FOXA1: 9, 4 FLI1: 4, ETV4: 14, IDH1: 3, SPOP: 37 | 24776 |
| | RPPA | RPPA | 5 | 311 | CIN: 178, GS: 39, MSI: 62, EBV: 26, HM SNV: 6 | 218 |
| | SNP/ INDEL | mc3 gene level | 5 | 383 | CIN: 223, GS: 50, MSI: 73, EBV: 30, HM SNV: 7 | 40543 |

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|------|---------------|---------------------------|---|-----|--|--------|
| STAD | CNV | Gistic2 all data by genes | 5 | 383 | CIN: 223, GS: 50, MSI: 73, EBV: 30, HM SNV: 7 | 24776 |
| | | Gistic2 all thresholded | 5 | 383 | CIN: 223, GS: 50, MSI: 73, EBV: 30, HM SNV: 7 | 24776 |
| | Methylation | Human Methylation450 | 5 | 343 | 'GL.CIN': 202, 'GLEBV': 59, 'GL.GS': 29, 'GL.MSI': 46, HM SNV:7 | 20789 |
| PCPG | miRNA | miRNA HiSeq gene | 4 | 173 | Kinase signaling: 68, Wnt altered: 22, Pseudohypoxia: 61, Cortical admixture: 22 | 796 |
| | RNASeq | HiSeqV2 | 4 | 173 | Kinase signaling: 68, Pseudohypoxia: 61, Cortical admixture: 22, Wnt altered: 22 | 20530 |
| | | HiSeqV2 PANCAN | 4 | 173 | Kinase signaling: 68, Pseudohypoxia: 61, Cortical admixture: 22, Wnt altered: 22 | 20530 |
| | | HiSeqV2 percentile | 4 | 173 | Kinase signaling: 68, Pseudohypoxia: 61, Cortical admixture: 22, Wnt altered: 22 | 20501 |
| | Exon | HiSeqV2 exon | 4 | 173 | Kinase signaling: 68, Pseudohypoxia: 61, Cortical admixture: 22, Wnt altered: 22 | 239322 |
| | RPPA | RPPA | 4 | 76 | Pseudohypoxia: 25, Kinase signaling: 34, Wnt altered: 10, Cortical admixture: 7 | 219 |
| | SNP/ INDEL | PCPG mc3 gene level | 4 | 173 | Kinase signaling: 68, Wnt altered: 22, Pseudohypoxia: 61, Cortical admixture: 22 | 40543 |
| | CNV | Gistic2 all data by genes | 4 | 159 | Kinase signaling: 62, Wnt altered: 21, Pseudohypoxia: 54, Cortical admixture: 22 | 24776 |

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|------|-------------|---------------------------|---|-----|--|-------|
| | | Gistic2 all thresholded | 4 | 159 | Kinase signaling: 62, Wnt altered: 21, Pseudohypoxia: 54, Cortical admixture: 22 | 24776 |
| HNSC | RPPA | RPPA | 4 | 200 | Mesenchymal: 58, Classical: 40, Basal: 66, Atypical: 36 | 131 |
| | RPPA | RPPA | 4 | 200 | Basal: 66, Mesenchymal: 58, Atypical: 36, Classical: 40 | 238 |
| | SNP/INDEL | mc3 gene level | 4 | 277 | Mesenchymal: 74, Basal: 87, Atypical: 67, Classical: 49 | 40543 |
| | CNV | Gistic2 all thresholded | 4 | 279 | Mesenchymal: 75, Basal: 87, Atypical: 68, Classical: 49 | 24776 |
| | | Gistic2 all data by genes | 4 | 279 | Mesenchymal: 75, Basal: 87, Atypical: 68, Classical: 49 | 24776 |
| | Methylation | Human Methylation450 | 4 | 279 | Mesenchymal: 75, Basal: 49, Atypical: 87, Classical: 68 | 20789 |
| BLCA | miRNA | miRNA HiSeq gene | 4 | 129 | BLCA.2: 42, BLCA.1: 41, BLCA.3: 31, BLCA.4: 15 | 810 |
| | RNASeq | HiSeqV2 | 4 | 129 | BLCA.2: 42, BLCA.4: 15, BLCA.3: 31, BLCA.1: 41 | 20530 |
| | | HiSeqV2 PANCAN | 4 | 129 | BLCA.2: 42, BLCA.4: 15, BLCA.3: 31, BLCA.1: 41 | 20530 |
| | | HiSeqV2 percentile | 4 | 129 | BLCA.2: 42, BLCA.4: 15, BLCA.3: 31, BLCA.1: 41 | 20501 |

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|------|---------------|---------------------------|---|-----|--|-------|
| | Exon | HiSeqV2 exon | 4 | 129 | BLCA.2: 42, BLCA.1: 41, BLCA.3: 31, BLCA.4: 15 | 78722 |
| | Methylation | Human Methylation450 | 4 | 129 | BLCA.2: 42, BLCA.1: 41, BLCA.3: 31, BLCA.4: 15 | 20789 |
| | RPPA | RPPA | 4 | 118 | BLCA.1: 36, BLCA.4: 15, BLCA.2: 38, BLCA.3: 29 | 131 |
| | | RPPA | 4 | 118 | BLCA.2: 38, BLCA.1: 36, BLCA.3: 29, BLCA.4: 15 | 222 |
| | SNP/ INDEL | mc3 gene level | 4 | 129 | BLCA.1: 41, BLCA.4: 15, BLCA.2: 42, BLCA.3: 31 | 40543 |
| | CNV | Gistic2 all thresholded | 4 | 126 | BLCA.1: 41, BLCA.4: 15, BLCA.2: 41, BLCA.3: 29 | 24776 |
| | | Gistic2 all data by genes | 4 | 126 | BLCA.1: 41, BLCA.4: 15, BLCA.2: 41, BLCA.3: 29 | 24776 |
| SKCM | CNV | Gistic2 all thresholded | 5 | 266 | RAS Hotspot Mutants: 81, Triple WT: 38, BRAF Hotspot Mutants: 118, : 6, NF1 Any Mutants: 23 | 24776 |
| | Methylation | Human Methylation450 | 5 | 333 | RAS Hotspot Mutants: 92, Triple WT: 46, BRAF Hotspot Mutants: 150, : 17, NF1 Any Mutants: 28 | 20789 |
| COAD | miRNA | miRNA GA gene | 4 | 100 | HM SNV: 4, GS: 17, CIN: 62, MSI: 17 | 617 |
| | RNASeq | GAV2 | 4 | 95 | CIN: 59, MSI: 16, GS: 16, HM SNV: 4 | 20530 |

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|------|---------------|---------------------------|---|-----|--|--------|
| | Exon | GAV2 exon | 4 | 95 | CIN: 59, MSI: 16, GS: 16, HM SNV: 4 | 239322 |
| | RPPA | RPPA | 4 | 245 | CIN: 152, MSI: 45, GS: 43, HM SNV: 5 | 131 |
| | SNP/ INDEL | mc3 gene level | 4 | 268 | CIN: 178, MSI: 50, GS: 34, HM SNV: 6 | 40543 |
| | CNV | Gistic2 all thresholded | 4 | 341 | CIN: 226, MSI: 60, GS: 49, HM SNV: 6 | 24776 |
| | | Gistic2 all data by genes | 4 | 341 | CIN: 226, MSI: 60, GS: 49, HM SNV: 6 | 24776 |
| LAML | miRNA | miRNA GA gene | 8 | 187 | NA: 9, 7: 20, 4: 37, 1: 14, 2: 21, 6: 35, 3: 18, 5: 33 | 544 |
| | RNASeq | HiSeqV2 PANCAN | 7 | 172 | 3: 18, 4: 35, 1: 14, 5: 32, 6: 35, 2: 20, 7: 18 | 20530 |
| | | GA | 7 | 178 | 6: 35, 5: 33, 1: 14, 2: 21, 7: 20, 4: 37, 3: 18 | 20113 |
| | | HiSeqV2 percentile | 7 | 172 | 3: 18, 4: 35, 1: 14, 5: 32, 6: 35, 2: 20, 7: 18 | 20501 |
| | | HiSeqV2 | 7 | 172 | 3: 18, 4: 35, 1: 14, 5: 32, 6: 35, 2: 20, 7: 18 | 20530 |
| | Exon | GA exon | 7 | 178 | 3: 18, 4: 37, 1: 14, 5: 33, 6: 35, 2: 20, 7: 20 | 219296 |

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|------|---------------|---------------------------|---|-----|--|--------|
| | | HiSeqV2 exon | 7 | 172 | 3: 18, 4: 35, 1: 14, 5: 32, 6: 35, 2: 20, 7: 18 | 155775 |
| | SNP/ INDEL | mutation wustl gene | 8 | 184 | NA: 9, 3: 18, 5: 32, 4: 37, 6: 34, 1: 13, 2: 21, 7: 20 | 43785 |
| | CNV | Gistic2 all data by genes | 8 | 178 | 3: 18, 5: 31, 4: 36, 6: 33, 1: 13, 2: 19, 7: 20, NA: 8 | 24776 |
| | | Gistic2 all thresholded | 8 | 178 | 3: 18, 5: 31, 4: 36, 6: 33, 1: 13, 2: 19, 7: 20, NA: 8 | 24776 |
| LGG | SNP/ INDEL | LGG mc3 gene level | 6 | 511 | G high: 234, Mesenchymal like: 45, Codel: 173, Classic like: 23, G low: 12, PA like: 24 | 40543 |
| | CNV | Gistic2 all thresholded | 7 | 513 | G high: 233, Mesenchymal like: 45, Codel: 172, Classic like: 23, G low: 12, PA like: 25, NA: 3 | 24776 |
| | | Gistic2 all data by genes | 7 | 513 | G high: 233, Mesenchymal like: 45, Codel: 172, Classic like: 23, G low: 12, PA like: 25, NA: 3 | 24776 |
| READ | miRNA | miRNA HiSeq gene | 4 | 84 | CIN: 74, MSI: 2, GS: 6, HM SNV: 2 | 773 |
| | RPPA | RPPA | 4 | 89 | CIN: 77, GS: 7, MSI: 3, HM SNV: 2 | 222 |
| | RPPA | RPPA | 4 | 88 | CIN: 76, GS: 7, HM SNV: 2, MSI: 3 | 131 |
| | SNP/ INDEL | mc3 gene level | 4 | 84 | CIN: 74, GS: 6, MSI: 2, HM SNV: 2 | 40543 |

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| | CNV | Gistic2 all data by genes | 4 | 118 | CIN: 102, GS: 9, HM SNV: 4, MSI: 3 | 24776 |
| | | Gistic2 all thresholded | 4 | 118 | CIN: 102, GS: 9, HM SNV: 4, MSI: 3 | 24776 |
| UCEC | miRNA | miRNA GA gene | 5 | 126 | CN LOW: 53, MSI: 32, NA: 6, POLE: 16, CN HIGH: 19 | 618 |
| | RPPA | RPPA | 5 | 431 | CN HIGH: 126, MSI: 95, POLE: 68, CN LOW: 116, NA: 26 | 222 |
| | | RPPA | 5 | 397 | POLE: 61, NA: 26, CN HIGH: 110, MSI: 89, CN LOW: 111 | 131 |
| | SNP/ INDEL | mc3 gene level | 5 | 444 | CN HIGH: 143, CN LOW: 115, POLE: 69, NA: 15, MSI: 102 | 40543 |
| | CNV | Gistic2 all data by genes | 5 | 530 | CN HIGH: 160, CN LOW: 144, POLE: 79, MSI: 124, NA: 23 | 24776 |
| | | Gistic2 all thresholded | 5 | 530 | CN HIGH: 160, CN LOW: 144, POLE: 79, MSI: 124, NA: 23 | 24776 |
| | Methylation | Human Methylation27 | 5 | 117 | CN HIGH: 21, CN LOW: 42, POLE: 15, MSI: 32, NA: 7 | 12778 |
| Methylation | Human Methylation450 | 5 | 423 | CN HIGH: 140, CN LOW: 102, POLE: 64, MSI: 93, NA: 24 | 20789 | |
| ACC | miRNA | miRNA HiSeq gene | 3 | 79 | intermediate: 27, high: 20, low: 32 | 774 |

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|------|---------------|------------------------------|---|-----|--|-------|
| | RNASeq | HiSeqV2 PANCAN | 3 | 78 | intermediate: 27, high: 19, low: 32 | 20530 |
| | | HiSeqV2 | 3 | 78 | intermediate: 27, high: 19, low: 32 | 20530 |
| | | HiSeqV2 percentile | 3 | 78 | intermediate: 27, high: 19, low: 32 | 20501 |
| | Methylation | Human Methylation450 | 3 | 79 | intermediate: 27, low: 32, high: 20 | 20789 |
| | SNP/ INDEL | ACC mc3 gene level | 4 | 91 | high: 20, low: 32, intermediate: 27, NA: 12 | 40543 |
| | CNV | Gistic2 all data by genes | 4 | 89 | high: 20, low: 32, intermediate: 25, NA: 12 | 24776 |
| | | Gistic2 all thresholded | 4 | 78 | high: 18, low: 28, intermediate: 22, NA: 10 | 24776 |
| LUAD | RPPA | RPPA | 6 | 181 | 2: 28, 5: 42, 1: 19, 6: 32, 4: 22, 3: 38 | 238 |
| | | RPPA | 6 | 181 | 5: 42, 1: 19, 4: 22, 3: 38, 2: 28, 6: 32 | 131 |
| | SNP/ INDEL | mc3 gene level | 6 | 226 | 5: 51, 6: 41, 1: 22, 2: 31, 3: 49, 4: 32 | 40543 |
| | CNV | Gistic2 all data by genes | 6 | 230 | 5: 52, 6: 41, 1: 22, 2: 32, 3: 51, 4: 32 | 24776 |

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|------|---------------|-------------------------|---|-----|--|--------|
| | | Gistic2 all thresholded | 6 | 230 | 5: 52, 6: 41, 1: 22, 2: 32, 3: 51, 4: 32 | 24776 |
| | Methylation | Human Methylation450 | 6 | 188 | 5: 44, 6: 35, 1: 18, 2: 22, 3: 42, 4: 27 | 20789 |
| LIHC | miRNA | miRNA HiSeq gene | 4 | 191 | iCluster:2: 55, iCluster:3: 63, iCluster:1: 65, NA: 8 | 747 |
| | RNASeq | HiSeqV2 | 4 | 193 | iCluster:2: 55, iCluster:3: 63, iCluster:1: 65, NA: 10 | 20530 |
| | | HiSeqV2 percentile | 4 | 193 | iCluster:2: 55, iCluster:3: 63, iCluster:1: 65, NA: 10 | 20501 |
| | | HiSeqV2 PANCAN | 4 | 193 | iCluster:2: 55, iCluster:3: 63, iCluster:1: 65, NA: 10 | 20530 |
| | Exon | HiSeqV2 exon | 4 | 193 | iCluster:2: 55, iCluster:3: 63, iCluster:1: 65, NA: 10 | 239322 |
| | Methylation | Human Methylation450 | 4 | 196 | iCluster:2: 55, iCluster:3: 63, iCluster:1: 65, NA: 13 | 20789 |
| | RPPA | RPPA | 4 | 162 | iCluster:1: 56, iCluster:3: 48, iCluster:2: 46, NA: 12 | 219 |
| | SNP/ INDEL | mc3 gene level | 4 | 182 | iCluster:3: 58, iCluster:1: 60, iCluster:2: 52, NA: 12 | 40543 |
| | CNV | Gistic2 all thresholded | 4 | 191 | iCluster:1: 65, iCluster:3: 63, iCluster:2: 55, NA: 8 | 24776 |

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|------|-------------------------|---------------------------|-----|--|---|--------|
| | | Gistic2 all data by genes | 4 | 191 | iCluster:1: 65, iCluster:3: 63, iCluster:2: 55, NA: 8 | 24776 |
| THCA | miRNA | miRNA HiSeq gene | 6 | 493 | 1: 133, 5: 91, NA: 14, 2: 67, 4: 106, 3: 82 | 763 |
| | RNASeq | HiSeqV2 percentile | 6 | 494 | 2: 67, 5: 93, 4: 106, 1: 134, 3: 82, NA: 12 | 20501 |
| | | HiSeqV2 PANCAN | 6 | 494 | 2: 67, 5: 93, 4: 106, 1: 134, 3: 82, NA: 12 | 20530 |
| | | HiSeqV2 | 6 | 494 | 2: 67, 5: 93, 4: 106, 1: 134, 3: 82, NA: 12 | 20530 |
| | Exon | HiSeqV2 exon | 6 | 494 | 2: 67, 5: 93, 4: 106, 1: 134, 3: 82, NA: 12 | 239322 |
| | Methylation | Human Methylation450 | 6 | 496 | 1: 134, 4: 106, 5: 93, 3: 82, 2: 67, NA: 14 | 20789 |
| | RPPA | RPPA | 6 | 368 | 1: 108, 4: 75, 5: 72, 2: 45, 3: 57, NA: 11 | 260 |
| | SNP/ INDEL | mc3 gene level | 6 | 481 | 1: 127, 2: 66, 4: 103, 3: 79, 5: 93, NA: 13 | 40543 |
| | CNV | Gistic2 all data by genes | 6 | 492 | 1: 132, 2: 67, 3: 82, 4: 105, NA: 14, 5: 92 | 24776 |
| | Gistic2 all thresholded | 6 | 492 | 1: 132, 2: 67, 3: 82, 4: 105, NA: 14, 5: 92 | 24776 | |

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|------|---------------|---------------------------|---|-----|--|-------|
| GBM | Array | AgilentG4502A 072 | 6 | 473 | Mesenchymal like: 135, NA: 194, G low: 8, LGm6 GBM: 26, Classic like: 99, G high: 11 | 17814 |
| | | HT HG U133A | 7 | 529 | Classic like: 99, LGm6 GBM: 37, Mesenchymal like: 144, NA: 223, G low: 13, G high: 12, Codel: 1 | 12042 |
| | | AgilentG4502A 071 | 7 | 101 | Classic like: 15, NA: 41, LGm6 GBM: 12, G low: 5, Mesenchymal like: 25, G high: 2, Codel: 1 | 17814 |
| | Methylation | Human Methylation450 | 5 | 141 | LGm6 GBM: 13, NA: 13, Mesenchymal like: 56, Classic like: 53, G high: 6 | 20789 |
| | RPPA | RPPA | 6 | 215 | Mesenchymal like: 71, NA: 50, LGm6 GBM: 14, G low: 5, Classic like: 71, G high: 4 | 131 |
| | SNP/ INDEL | mc3 gene level | 6 | 314 | Mesenchymal like: 117, LGm6 GBM: 22, G low: 6, Classic like: 99, NA: 62, G high: 8 | 40543 |
| | CNV | Gistic2 all thresholded | 7 | 577 | Mesenchymal like: 164, Classic like: 120, G low: 13, LGm6 GBM: 40, NA: 224, Codel: 1, G high: 15 | 24776 |
| | | Gistic2 all data by genes | 7 | 577 | Mesenchymal like: 164, Classic like: 120, G low: 13, LGm6 GBM: 40, NA: 224, Codel: 1, G high: 15 | 24776 |
| ESCA | RPPA | RPPA | 5 | 116 | ESCC: 72, CIN: 40, MSI: 1, GS: 1, HM SNV: 2 | 219 |
| | SNP/ INDEL | mc3 gene level | 5 | 169 | CIN: 74, HM SNV: 2, ESCC: 90, GS: 1, MSI: 2 | 40543 |

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|------|---------------|---------------------------|---|-----|---|-------|
| | CNV | Gistic2 all thresholded | 5 | 169 | CIN: 74, HM SNV: 2, ESCC: 90, GS: 1, MSI: 2 | 24776 |
| | | Gistic2 all data by genes | 5 | 169 | CIN: 74, HM SNV: 2, ESCC: 90, GS: 1, MSI: 2 | 24776 |
| KIRC | miRNA | miRNA GA gene | 5 | 233 | 1: 69, 2: 52, 3: 49, 4: 52, NA: 11 | 581 |
| | RPPA | RPPA | 5 | 408 | 3: 89, 1: 137, 2: 87, NA: 23, 4: 72 | 131 |
| | | RPPA | 5 | 408 | 4: 72, 1: 137, 2: 87, 3: 89, NA: 23 | 232 |
| | SNP/ INDEL | mc3 gene level | 5 | 294 | 3: 59, 1: 109, 2: 50, NA: 21, 4: 55 | 40543 |
| | CNV | Gistic2 all thresholded | 5 | 436 | 1: 145, 3: 92, 2: 90, NA: 23, 4: 86 | 24776 |
| | | Gistic2 all data by genes | 5 | 436 | 1: 145, 3: 92, 2: 90, NA: 23, 4: 86 | 24776 |
| | Methylation | Human Methylation450 | 5 | 253 | 1: 91, 3: 53, 2: 36, NA: 19, 4: 54 | 20789 |
| KIRP | RPPA | RPPA | 4 | 125 | C1: 71, C2a: 27, C2c CIMP: 9, C2b: 18 | 220 |
| | SNP/ INDEL | mc3 gene level | 4 | 158 | C2a: 34, C1: 93, C2c CIMP: 9, C2b: 22 | 40543 |

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|------|-------------|---------------------------|---|------|--|--------|
| | CNV | Gistic2 all data by genes | 4 | 161 | C2a: 35, C1: 95, C2c CIMP: 9, C2b: 22 | 24776 |
| | CNV | Gistic2 all thresholded | 4 | 161 | C2a: 35, C1: 95, C2c CIMP: 9, C2b: 22 | 24776 |
| BRCA | miRNA | miRNA HiSeq gene | 5 | 747 | LumA: 390, Basal: 131, Her2: 58, LumB: 136, Normal: 32 | 707 |
| | | miRNA GA gene | 5 | 319 | LumA: 167, LumB: 70, Basal: 51, Her2: 23, Normal: 8 | 593 |
| | RNASeq | HiSeqV2 | 5 | 1097 | Basal: 192, Her2: 82, LumA: 566, LumB: 217, Normal: 40 | 20530 |
| | | HiSeqV2 percentile | 5 | 1097 | Basal: 192, Her2: 82, LumA: 566, LumB: 217, Normal: 40 | 20501 |
| | | HiSeqV2 PANCAN | 5 | 1097 | Basal: 192, Her2: 82, LumA: 566, LumB: 217, Normal: 40 | 20530 |
| | Exon | HiSeqV2 exon | 5 | 1097 | Basal: 192, Her2: 82, LumA: 566, LumB: 217, Normal: 40 | 239322 |
| | Array | AgilentG4502A 073 | 5 | 529 | Her2: 46, LumA: 268, Basal: 96, LumB: 108, Normal: 11 | 17814 |
| | Methylation | Human Methylation27 | 5 | 314 | LumA: 146, Her2: 36, LumB: 70, Basal: 56, Normal: 6 | 12778 |
| | | Human Methylation450 | 5 | 781 | LumA: 418, Her2: 46, LumB: 147, Basal: 136, Normal: 34 | 20789 |

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|-----|---------------|---------------------------|---|------|--|-------|
| | RPPA | RPPA | 5 | 742 | LumA: 358, Basal: 130, Her2: 67, LumB: 167, Normal: 20 | 131 |
| | | RPPA | 5 | 885 | Basal: 157, LumA: 439, LumB: 184, Her2: 75, Normal: 30 | 222 |
| | SNP/ INDEL | mc3 gene level | 5 | 789 | LumA: 413, Her2: 54, LumB: 145, Normal: 32, Basal: 145 | 40543 |
| | CNV | Gistic2 all data by genes | 5 | 1078 | LumA: 556, Her2: 81, LumB: 216, Normal: 39, Basal: 186 | 24776 |
| | | Gistic2 all thresholded | 5 | 1078 | LumA: 556, Her2: 81, LumB: 216, Normal: 39, Basal: 186 | 24776 |
| USC | miRNA | miRNA GA gene | 4 | 107 | secretory: 20, classical: 44, primitive: 14, basal: 29 | 660 |
| | Array | HT HG U133A | 4 | 104 | classical: 37, primitive: 16, secretory: 21, basal: 30 | 12042 |
| | | AgilentG4502A 073 | 4 | 121 | classical: 45, primitive: 19, secretory: 25, basal: 32 | 17814 |
| | RPPA | RPPA | 4 | 112 | classical: 38, basal: 28, secretory: 28, primitive: 18 | 131 |
| | | RPPA | 4 | 112 | classical: 38, primitive: 18, basal: 28, secretory: 28 | 238 |
| | SNP/ INDEL | mc3 gene level | 4 | 173 | basal: 41, classical: 63, secretory: 42, primitive: 27 | 40543 |

| | | | | | | |
|--|-----|---------------------------|---|-----|--|-------|
| | CNV | Gistic2 all data by genes | 4 | 178 | basal: 43, classical: 65, secretary: 43, primitive: 27 | 24776 |
| | | Gistic2 all thresholded | 4 | 178 | basal: 43, classical: 65, secretary: 43, primitive: 27 | 24776 |

Supplementary Table S2: (Fig. 2.) MACC values of top performing classifiers in terms of 20 different configurations of 8 distinct omics modalities across 20 different cancers.

| Cancer | Modality | Scale | Type | Classifier | ACC | PR | RE | F1 | MCC | AUROC |
|--------|----------|---------------------------|------|------------|------|------|------|------|------|-------|
| ACC | Meth. | HumanMethylation450 | ML | HGB | 1 | 1 | 1 | 1 | 1 | 1 |
| ACC | CNV | Gistic2-all-data-by-genes | DL | RESNET34 | 0.87 | 0.9 | 0.87 | 0.87 | 0.94 | 0.95 |
| ACC | CNV | Gistic2-all-thresholded | DL | NN | 0.69 | 0.71 | 0.69 | 0.7 | 0.85 | 0.75 |
| ACC | RNASeq | HiSeqV2 | ML | SVM | 0.83 | 0.9 | 0.83 | 0.84 | 0.93 | 0.95 |
| ACC | RNASeq | HiSeqV2-PANCAN | ML | SVM | 0.83 | 0.9 | 0.83 | 0.84 | 0.93 | 0.95 |
| ACC | RNASeq | HiSeqV2-percentile | DL | RESNET18 | 0.8 | 0.8 | 0.8 | 0.8 | 0.9 | 0.92 |
| ACC | SNP | mc3-gene-level | ML | CNB | 0.53 | 0.3 | 0.53 | 0.37 | 0.74 | 0.67 |
| ACC | miRNA | miRNA-HiSeq-gene | ML | BNB | 0.8 | 0.85 | 0.8 | 0.82 | 0.9 | 0.9 |
| BLCA | Meth. | HumanMethylation450 | ML | HGB | 0.79 | 0.79 | 0.79 | 0.79 | 0.93 | 0.93 |
| BLCA | CNV | Gistic2-all-data-by-genes | DL | NN | 0.66 | 0.71 | 0.66 | 0.67 | 0.87 | 0.81 |
| BLCA | CNV | Gistic2-all-thresholded | ML | SVM | 0.57 | 0.55 | 0.57 | 0.55 | 0.85 | 0.76 |
| BLCA | RNASeq | HiSeqV2 | ML | SVM | 0.94 | 0.95 | 0.94 | 0.94 | 0.97 | 0.99 |
| BLCA | RNASeq | HiSeqV2-PANCAN | ML | SVM | 0.94 | 0.95 | 0.94 | 0.94 | 0.97 | 0.99 |
| BLCA | Exon | HiSeqV2-exon | ML | HGB | 0.89 | 0.94 | 0.89 | 0.9 | 0.98 | 0.99 |
| BLCA | RNASeq | HiSeqV2-percentile | ML | CNB | 0.93 | 0.95 | 0.93 | 0.93 | 0.97 | 0.98 |
| BLCA | RPPA | RPPA | DL | CNN | 0.77 | 0.78 | 0.77 | 0.77 | 0.93 | 0.88 |
| BLCA | RPPA | RPPA-RBN | ML | XGB | 0.76 | 0.87 | 0.76 | 0.77 | 0.94 | 0.89 |
| BLCA | SNP | mc3-gene-level | DL | RESNET152 | 0.39 | 0.36 | 0.39 | 0.36 | 0.82 | 0.55 |

| | | | | | | | | | | |
|------|--------|---------------------------|----|----------|-------|-------|-------|-------|-------|------|
| BLCA | miRNA | miRNA-HiSeq-gene | DL | RESNET18 | 0.97 | 0.97 | 0.97 | 0.97 | 0.99 | 1 |
| BRCA | Array | AgilentG4502A-07-3 | ML | BNB | 0.87 | 0.77 | 0.87 | 0.8 | 0.96 | 0.96 |
| BRCA | Meth. | HumanMethylation27 | ML | HGB | 0.76 | 0.86 | 0.76 | 0.79 | 0.92 | 0.93 |
| BRCA | Meth. | HumanMethylation450 | ML | GNB | 0.642 | 0.593 | 0.642 | 0.603 | 0.902 | 0.79 |
| BRCA | CNV | Gistic2-all-data-by-genes | ML | GNB | 0.65 | 0.58 | 0.65 | 0.57 | 0.9 | 0.79 |
| BRCA | CNV | Gistic2-all-thresholded | ML | GNB | 0.59 | 0.52 | 0.59 | 0.49 | 0.88 | 0.77 |
| BRCA | RNASeq | HiSeqV2 | DL | CNN | 0.8 | 0.85 | 0.8 | 0.82 | 0.97 | 0.98 |
| BRCA | RNASeq | HiSeqV2-PANCAN | DL | CNN LSTM | 0.79 | 0.79 | 0.79 | 0.79 | 0.96 | 0.96 |
| BRCA | Exon | HiSeqV2-exon | ML | LR | 0.81 | 0.84 | 0.81 | 0.82 | 0.96 | 0.99 |
| BRCA | RNASeq | HiSeqV2-percentile | ML | LR | 0.83 | 0.83 | 0.83 | 0.83 | 0.97 | 0.99 |
| BRCA | RPPA | RPPA | DL | CNN LSTM | 0.65 | 0.63 | 0.65 | 0.64 | 0.93 | 0.9 |
| BRCA | RPPA | RPPA-RBN | DL | RESNET34 | 0.7 | 0.74 | 0.7 | 0.71 | 0.93 | 0.9 |
| BRCA | SNP | mc3-gene-level | ML | RF | 0.37 | 0.25 | 0.37 | 0.29 | 0.88 | 0.68 |
| BRCA | miRNA | miRNA-GA-gene | ML | SVM | 0.88 | 0.81 | 0.88 | 0.83 | 0.95 | 0.94 |
| BRCA | miRNA | miRNA-HiSeq-gene | ML | SVM | 0.75 | 0.79 | 0.75 | 0.77 | 0.95 | 0.96 |
| COAD | Meth. | HumanMethylation450 | ML | QDA | 0.93 | 0.88 | 0.93 | 0.89 | 0.93 | 0.93 |
| COAD | RNASeq | GAV2 | ML | LR | 0.86 | 0.82 | 0.86 | 0.84 | 0.96 | 0.87 |
| COAD | Exon | GAV2-exon | ML | SVM | 1 | 1 | 1 | 1 | 1 | 1 |
| COAD | CNV | Gistic2-all-data-by-genes | ML | RF | 0.8 | 0.83 | 0.8 | 0.81 | 0.92 | 0.93 |
| COAD | CNV | Gistic2-all-thresholded | ML | CB | 0.8 | 0.82 | 0.8 | 0.8 | 0.92 | 0.93 |
| COAD | RPPA | RPPA-RBN | ML | SVM | 0.65 | 0.66 | 0.65 | 0.65 | 0.83 | 0.79 |
| COAD | SNP | mc3-gene-level | DL | RESNET50 | 0.73 | 0.71 | 0.73 | 0.72 | 0.86 | 0.79 |
| COAD | miRNA | miRNA-GA-gene | DL | DEEPGENE | 0.752 | 0.786 | 0.752 | 0.763 | 0.885 | 0.94 |
| ESCA | CNV | Gistic2-all-data-by-genes | DL | CNN | 1 | 1 | 1 | 1 | 1 | 1 |
| ESCA | CNV | Gistic2-all-thresholded | DL | DEEPGENE | 1 | 1 | 1 | 1 | 1 | 1 |
| ESCA | RPPA | RPPA | DL | CNN LSTM | 1 | 1 | 1 | 1 | 1 | 1 |

| | | | | | | | | | | |
|------|-------|---------------------------|----|-----------|-------|-------|-------|-------|-------|------|
| ESCA | SNP | mc3-gene-level | DL | MLP | 0.85 | 0.85 | 0.85 | 0.85 | 0.85 | 0.85 |
| GBM | Array | AgilentG4502A-07-1 | DL | NN | 0.73 | 0.77 | 0.73 | 0.74 | 0.93 | 0.94 |
| GBM | Array | AgilentG4502A-07-2 | ML | XGB | 0.75 | 0.8 | 0.75 | 0.76 | 0.94 | 0.91 |
| GBM | Meth. | HumanMethylation450 | ML | DT | 0.57 | 0.59 | 0.57 | 0.57 | 0.89 | 0.73 |
| GBM | CNV | Gistic2-all-data-by-genes | ML | BNB | 0.5 | 0.34 | 0.5 | 0.35 | 0.86 | 0.73 |
| GBM | CNV | Gistic2-all-thresholded | ML | SVM | 0.4 | 0.42 | 0.4 | 0.4 | 0.85 | 0.7 |
| GBM | Array | HT-HG-U133A | ML | HGB | 0.449 | 0.478 | 0.449 | 0.457 | 0.922 | 0.9 |
| GBM | RPPA | RPPA-RBN | DL | MLP | 0.49 | 0.65 | 0.49 | 0.53 | 0.82 | 0.73 |
| GBM | SNP | mc3-gene-level | DL | RESNET18 | 0.37 | 0.41 | 0.37 | 0.34 | 0.81 | 0.71 |
| HNSC | Meth. | HumanMethylation450 | ML | CNB | 0.63 | 0.67 | 0.63 | 0.62 | 0.87 | 0.81 |
| HNSC | CNV | Gistic2-all-data-by-genes | ML | RF | 0.64 | 0.65 | 0.64 | 0.64 | 0.89 | 0.82 |
| HNSC | CNV | Gistic2-all-thresholded | ML | RF | 0.51 | 0.52 | 0.51 | 0.51 | 0.84 | 0.69 |
| HNSC | RPPA | RPPA | ML | GNB | 0.71 | 0.71 | 0.71 | 0.7 | 0.9 | 0.85 |
| HNSC | RPPA | RPPA-RBN | ML | HGB | 0.53 | 0.55 | 0.53 | 0.53 | 0.84 | 0.76 |
| HNSC | SNP | mc3-gene-level | ML | RF | 0.38 | 0.3 | 0.38 | 0.31 | 0.79 | 0.64 |
| KIRC | Meth. | HumanMethylation450 | DL | RESNET101 | 0.34 | 0.25 | 0.34 | 0.27 | 0.83 | 0.66 |
| KIRC | CNV | Gistic2-all-data-by-genes | DL | MLP | 0.34 | 0.34 | 0.34 | 0.34 | 0.84 | 0.6 |
| KIRC | CNV | Gistic2-all-thresholded | ML | HGB | 0.34 | 0.32 | 0.34 | 0.33 | 0.85 | 0.57 |
| KIRC | RPPA | RPPA | DL | DEEPGENE | 0.467 | 0.465 | 0.467 | 0.459 | 0.876 | 0.7 |
| KIRC | RPPA | RPPA-RBN | DL | CNN LSTM | 0.41 | 0.38 | 0.41 | 0.38 | 0.87 | 0.68 |
| KIRC | SNP | mc3-gene-level | DL | RESNET50 | 0.27 | 0.16 | 0.27 | 0.2 | 0.83 | 0.55 |
| KIRC | miRNA | miRNA-GA-gene | DL | CNN | 0.539 | 0.55 | 0.539 | 0.536 | 0.909 | 0.81 |
| KIRP | CNV | Gistic2-all-data-by-genes | DL | DEEPGENE | 0.887 | 0.871 | 0.887 | 0.875 | 0.946 | 0.89 |
| KIRP | CNV | Gistic2-all-thresholded | DL | CNN RNN | 0.74 | 0.72 | 0.74 | 0.73 | 0.9 | 0.94 |
| KIRP | RPPA | RPPA | DL | MLP | 0.77 | 0.89 | 0.77 | 0.8 | 0.91 | 0.93 |
| KIRP | SNP | mc3-gene-level | ML | DT | 0.61 | 0.67 | 0.61 | 0.62 | 0.81 | 0.71 |

| | | | | | | | | | | |
|------|--------|---------------------------|----|-----------|-------|-------|-------|-------|-------|-------|
| LAML | miRNA | GA | ML | SVM | 0.77 | 0.829 | 0.77 | 0.759 | 0.957 | 0.96 |
| LAML | Exon | GA-exon | ML | LR | 0.73 | 0.78 | 0.73 | 0.73 | 0.96 | 0.96 |
| LAML | CNV | Gistic2-all-data-by-genes | DL | RESNET50 | 0.32 | 0.28 | 0.32 | 0.21 | 0.89 | 0.67 |
| LAML | CNV | Gistic2-all-thresholded | ML | GNB | 0.25 | 0.2 | 0.25 | 0.21 | 0.87 | 0.56 |
| LAML | RNASeq | HiSeqV2 | ML | RF | 0.69 | 0.69 | 0.69 | 0.67 | 0.96 | 0.94 |
| LAML | RNASeq | HiSeqV2-PANCAN | ML | RF | 0.69 | 0.69 | 0.69 | 0.67 | 0.96 | 0.94 |
| LAML | Exon | HiSeqV2-exon | ML | HGB | 0.71 | 0.7 | 0.71 | 0.69 | 0.96 | 0.96 |
| LAML | RNASeq | HiSeqV2-percentile | ML | HGB | 0.7 | 0.66 | 0.7 | 0.68 | 0.96 | 0.94 |
| LAML | miRNA | miRNA-GA-gene | ML | HGB | 0.63 | 0.64 | 0.63 | 0.62 | 0.94 | 0.9 |
| LAML | SNP | mutation-wustl-gene | DL | CNN | 0.267 | 0.41 | 0.267 | 0.273 | 0.879 | 0.558 |
| LGG | CNV | Gistic2-all-data-by-genes | DL | NN | 0.65 | 0.65 | 0.65 | 0.65 | 0.97 | 0.89 |
| LGG | CNV | Gistic2-all-thresholded | DL | MLP | 0.66 | 0.58 | 0.66 | 0.61 | 0.97 | 0.91 |
| LGG | SNP | mc3-gene-level | DL | DEEPGENE | 0.633 | 0.669 | 0.633 | 0.645 | 0.964 | 0.95 |
| LIHC | Meth. | HumanMethylation450 | DL | LSTM | 0.69 | 0.64 | 0.69 | 0.66 | 0.95 | 0.82 |
| LIHC | CNV | Gistic2-all-data-by-genes | ML | LR | 0.67 | 0.67 | 0.67 | 0.67 | 0.84 | 0.77 |
| LIHC | CNV | Gistic2-all-thresholded | DL | LSTM | 0.65 | 0.64 | 0.65 | 0.64 | 0.82 | 0.77 |
| LIHC | RNASeq | HiSeqV2 | ML | CB | 0.69 | 0.66 | 0.69 | 0.67 | 0.95 | 0.81 |
| LIHC | RNASeq | HiSeqV2-PANCAN | DL | NN | 0.73 | 0.74 | 0.73 | 0.73 | 0.93 | 0.89 |
| LIHC | Exon | HiSeqV2-exon | ML | CB | 0.63 | 0.6 | 0.63 | 0.61 | 0.93 | 0.84 |
| LIHC | RNASeq | HiSeqV2-percentile | ML | CB | 0.69 | 0.65 | 0.69 | 0.67 | 0.95 | 0.85 |
| LIHC | RPPA | RPPA | DL | RNN | 0.45 | 0.45 | 0.45 | 0.42 | 0.84 | 0.78 |
| LIHC | SNP | mc3-gene-level | ML | DT | 0.46 | 0.464 | 0.46 | 0.382 | 0.809 | 0.635 |
| LIHC | miRNA | miRNA-HiSeq-gene | ML | SVM | 0.86 | 0.86 | 0.86 | 0.86 | 0.93 | 0.92 |
| LUAD | Meth. | HumanMethylation27 | DL | RESNET101 | 1 | 1 | 1 | 1 | 1 | 1 |
| LUAD | Meth. | HumanMethylation450 | ML | RF | 0.79 | 0.83 | 0.79 | 0.8 | 0.96 | 0.94 |
| LUAD | CNV | Gistic2-all-data-by-genes | DL | NN | 0.69 | 0.7 | 0.69 | 0.66 | 0.94 | 0.91 |

| | | | | | | | | | | |
|------|--------|---------------------------|----|-----------|-------|-------|-------|-------|-------|-------|
| LUAD | CNV | Gistic2-all-thresholded | ML | GNB | 0.62 | 0.68 | 0.62 | 0.61 | 0.92 | 0.78 |
| LUAD | RPPA | RPPA | ML | SVM | 0.63 | 0.74 | 0.63 | 0.64 | 0.93 | 0.9 |
| LUAD | RPPA | RPPA-RBN | DL | RESNET18 | 0.52 | 0.58 | 0.52 | 0.54 | 0.9 | 0.76 |
| LUAD | SNP | mc3-gene-level | ML | LR | 0.35 | 0.45 | 0.35 | 0.34 | 0.88 | 0.72 |
| LUSC | Array | AgilentG4502A-07-3 | ML | HGB | 0.85 | 0.9 | 0.85 | 0.84 | 0.96 | 0.99 |
| LUSC | CNV | Gistic2-all-data-by-genes | ML | GNB | 0.59 | 0.59 | 0.59 | 0.58 | 0.87 | 0.75 |
| LUSC | CNV | Gistic2-all-thresholded | ML | XGB | 0.6 | 0.63 | 0.6 | 0.61 | 0.86 | 0.77 |
| LUSC | Array | HT-HG-U133A | DL | RESNET34 | 0.92 | 0.97 | 0.92 | 0.93 | 0.98 | 0.92 |
| LUSC | RPPA | RPPA | DL | RNN | 0.594 | 0.51 | 0.594 | 0.544 | 0.895 | 0.865 |
| LUSC | RPPA | RPPA-RBN | ML | AB | 0.36 | 0.43 | 0.36 | 0.35 | 0.78 | 0.6 |
| LUSC | SNP | mc3-gene-level | ML | HGB | 0.4 | 0.4 | 0.4 | 0.39 | 0.79 | 0.59 |
| LUSC | miRNA | miRNA-GA-gene | ML | SVM | 0.67 | 0.57 | 0.67 | 0.61 | 0.92 | 0.9 |
| PCPG | CNV | Gistic2-all-data-by-genes | ML | RF | 0.56 | 0.49 | 0.56 | 0.52 | 0.9 | 0.84 |
| PCPG | CNV | Gistic2-all-thresholded | ML | XGB | 0.64 | 0.68 | 0.64 | 0.64 | 0.88 | 0.89 |
| PCPG | RNASeq | HiSeqV2 | DL | RESNET18 | 0.94 | 0.96 | 0.94 | 0.94 | 0.99 | 1 |
| PCPG | RNASeq | HiSeqV2-PANCAN | DL | DEEPPGENE | 0.95 | 0.981 | 0.95 | 0.962 | 0.989 | 1 |
| PCPG | Exon | HiSeqV2-exon | ML | SVM | 0.94 | 0.96 | 0.94 | 0.94 | 0.99 | 0.98 |
| PCPG | RNASeq | HiSeqV2-percentile | DL | MLP | 1 | 1 | 1 | 1 | 1 | 1 |
| PCPG | RPPA | RPPA | ML | SVM | 0.95 | 0.94 | 0.95 | 0.94 | 0.96 | 0.93 |
| PCPG | SNP | mc3-gene-level | DL | CNN GRU | 0.5 | 0.52 | 0.5 | 0.5 | 0.87 | 0.7 |
| PCPG | miRNA | miRNA-HiSeq-gene | ML | HGB | 0.98 | 0.96 | 0.98 | 0.97 | 0.99 | 1 |
| PRAD | CNV | Gistic2-all-data-by-genes | DL | MLP | 0.5 | 0.45 | 0.5 | 0.47 | 0.88 | 0.71 |
| PRAD | CNV | Gistic2-all-thresholded | DL | CNN LSTM | 0.45 | 0.38 | 0.45 | 0.39 | 0.87 | 0.68 |
| PRAD | RNASeq | HiSeqV2 | ML | HGB | 0.99 | 0.99 | 0.99 | 0.99 | 1 | 1 |
| PRAD | RNASeq | HiSeqV2-PANCAN | ML | HGB | 0.99 | 0.99 | 0.99 | 0.99 | 1 | 1 |
| PRAD | Exon | HiSeqV2-exon | ML | XGB | 0.93 | 0.91 | 0.93 | 0.92 | 0.98 | 0.98 |

| | | | | | | | | | | |
|------|--------|---------------------------|----|-----------|-------|-------|-------|-------|-------|-------|
| PRAD | RNASeq | HiSeqV2-percentile | ML | HGB | 0.93 | 0.98 | 0.93 | 0.95 | 0.99 | 0.99 |
| PRAD | RPPA | RPPA | ML | SVM | 0.44 | 0.37 | 0.44 | 0.39 | 0.9 | 0.7 |
| PRAD | SNP | mc3-gene-level | ML | SVM | 0.42 | 0.4 | 0.42 | 0.4 | 0.85 | 0.63 |
| PRAD | miRNA | miRNA-HiSeq-gene | DL | MLP | 0.48 | 0.51 | 0.48 | 0.46 | 0.89 | 0.77 |
| SKCM | Meth. | HumanMethylation450 | DL | RESNET34 | 0.39 | 0.43 | 0.39 | 0.37 | 0.86 | 0.62 |
| SKCM | CNV | Gistic2-all-thresholded | DL | RNN | 0.46 | 0.41 | 0.46 | 0.43 | 0.85 | 0.73 |
| STAD | Meth. | HumanMethylation450 | DL | DEEPPGENE | 0.838 | 0.819 | 0.838 | 0.827 | 0.933 | 0.93 |
| STAD | CNV | Gistic2-all-data-by-genes | DL | CNN_GRU | 0.76 | 0.77 | 0.76 | 0.76 | 0.94 | 0.94 |
| STAD | CNV | Gistic2-all-thresholded | DL | CNN_GRU | 0.68 | 0.73 | 0.68 | 0.7 | 0.91 | 0.89 |
| STAD | RPPA | RPPA | DL | RNN | 0.717 | 0.763 | 0.717 | 0.734 | 0.905 | 0.879 |
| STAD | SNP | mc3-gene-level | ML | HGB | 0.77 | 0.76 | 0.77 | 0.76 | 0.93 | 0.92 |
| THCA | Meth. | HumanMethylation450 | ML | SVM | 0.67 | 0.65 | 0.67 | 0.65 | 0.96 | 0.81 |
| THCA | CNV | Gistic2-all-data-by-genes | DL | MLP | 0.3 | 0.32 | 0.3 | 0.3 | 0.87 | 0.6 |
| THCA | CNV | Gistic2-all-thresholded | DL | LSTM | 0.27 | 0.23 | 0.27 | 0.22 | 0.87 | 0.67 |
| THCA | RNASeq | HiSeqV2 | ML | LR | 0.77 | 0.75 | 0.77 | 0.76 | 0.98 | 0.94 |
| THCA | RNASeq | HiSeqV2-PANCAN | DL | CNN | 0.77 | 0.74 | 0.77 | 0.75 | 0.98 | 0.95 |
| THCA | Exon | HiSeqV2-exon | ML | HGB | 0.83 | 0.91 | 0.83 | 0.85 | 0.98 | 0.99 |
| THCA | RNASeq | HiSeqV2-percentile | DL | RESNET18 | 0.76 | 0.76 | 0.76 | 0.76 | 0.98 | 0.92 |
| THCA | RPPA | RPPA | DL | MLP | 0.54 | 0.53 | 0.54 | 0.53 | 0.93 | 0.82 |
| THCA | SNP | mc3-gene-level | ML | HGB | 0.32 | 0.16 | 0.32 | 0.21 | 0.88 | 0.67 |
| THCA | miRNA | miRNA-HiSeq-gene | DL | RESNET18 | 0.687 | 0.689 | 0.687 | 0.68 | 0.965 | 0.934 |
| UCEC | Meth. | HumanMethylation27 | DL | LSTM | 0.881 | 0.937 | 0.881 | 0.9 | 0.965 | 0.956 |
| UCEC | Meth. | HumanMethylation450 | ML | HGB | 0.636 | 0.613 | 0.636 | 0.621 | 0.943 | 0.84 |
| UCEC | CNV | Gistic2-all-data-by-genes | DL | RNN | 0.48 | 0.49 | 0.48 | 0.47 | 0.89 | 0.77 |
| UCEC | CNV | Gistic2-all-thresholded | DL | CNN_LSTM | 0.45 | 0.49 | 0.45 | 0.41 | 0.89 | 0.78 |
| UCEC | RPPA | RPPA | DL | CNN_GRU | 0.573 | 0.555 | 0.573 | 0.56 | 0.918 | 0.813 |

| | | | | | | | | | | |
|------|-------|----------------|----|-----|------|------|------|------|------|------|
| UCEC | RPPA | RPPA-RBN | DL | GRU | 0.59 | 0.58 | 0.59 | 0.58 | 0.92 | 0.8 |
| UCEC | SNP | mc3-gene-level | ML | XGB | 0.7 | 0.71 | 0.7 | 0.71 | 0.96 | 0.89 |
| UCEC | miRNA | miRNA-GA-gene | ML | HGB | 0.67 | 0.83 | 0.67 | 0.71 | 0.9 | 0.81 |

Supplementary Table S3: MACC of top performing classifier-modality combination across 20 different cancers in terms of 8 distinct omics modalities. (b) PR-RC difference of top performing classifier-modality combination for a cancer. A larger PR-RC difference indicates a higher degree of bias in the molecular subtype classification results for the corresponding cancer.

| Cancer | Modality | Scale | Type | Classifier | MACC | PR | RE | F1 | MCC | AUROC | PR-RC |
|--------|----------|---------------------------|------|------------|-------|-------|-------|-------|-------|-------|-------|
| ACC | SNP | mc3-gene-level | ML | CNB | 0.53 | 0.3 | 0.53 | 0.37 | 0.74 | 0.67 | |
| BLCA | CNV | Gistic2-all-thresholded | DL | NN | 0.48 | 0.54 | 0.48 | 0.49 | 0.82 | 0.72 | |
| BRCA | Meth. | HumanMethylation450 | ML | HGB | 0.626 | 0.85 | 0.626 | 0.66 | 0.933 | 0.88 | |
| COAD | Meth. | HumanMethylation450 | ML | QDA | 0.93 | 0.88 | 0.93 | 0.89 | 0.93 | 0.93 | |
| ESCA | CNV | Gistic2-all-data-by-genes | DL | CNN | 1 | 1 | 1 | 1 | 1 | 1 | |
| GBM | Array | AgilentG4502A-07-1 | ML | XGB | 0.7 | 0.87 | 0.7 | 0.73 | 0.92 | 0.91 | |
| HNSC | SNP | mc3-gene-level | ML | RF | 0.38 | 0.3 | 0.38 | 0.31 | 0.79 | 0.64 | |
| KIRC | SNP | mc3-gene-level | DL | RESNET50 | 0.27 | 0.16 | 0.27 | 0.2 | 0.83 | 0.55 | |
| KIRP | RPPA | RPPA | DL | MLP | 0.77 | 0.89 | 0.77 | 0.8 | 0.91 | 0.93 | |
| LAML | SNP | mutation-wustl-gene | DL | CNN | 0.267 | 0.41 | 0.267 | 0.273 | 0.879 | 0.558 | |
| LGG | SNP | mc3-gene-level | DL | DEEPPGENE | 0.633 | 0.669 | 0.633 | 0.645 | 0.964 | 0.95 | |
| LIHC | Meth. | HumanMethylation450 | DL | LSTM | 0.69 | 0.64 | 0.69 | 0.66 | 0.95 | 0.82 | |
| LUAD | RPPA | RPPA | ML | SVM | 0.63 | 0.74 | 0.63 | 0.64 | 0.93 | 0.9 | |
| LUSC | miRNA | miRNA-GA-gene | ML | SVM | 0.67 | 0.57 | 0.67 | 0.61 | 0.92 | 0.9 | |
| PCPG | RNASeq | HiSeqV2 | DL | MLP | 0.61 | 0.88 | 0.61 | 0.63 | 0.87 | 0.99 | |
| PRAD | RPPA | RPPA | ML | SVM | 0.44 | 0.37 | 0.44 | 0.39 | 0.9 | 0.7 | |
| SKCM | CNV | Gistic2-all-thresholded | DL | RNN | 0.46 | 0.41 | 0.46 | 0.43 | 0.85 | 0.73 | |
| STAD | CNV | Gistic2-all-thresholded | DL | CNN GRU | 0.68 | 0.73 | 0.68 | 0.7 | 0.91 | 0.89 | |
| THCA | SNP | mc3-gene-level | ML | HGB | 0.32 | 0.16 | 0.32 | 0.21 | 0.88 | 0.67 | |
| UCEC | miRNA | miRNA-GA-gene | ML | HGB | 0.67 | 0.83 | 0.67 | 0.71 | 0.9 | 0.81 | |

Supplementary Table S4: Modality-wise average MACC values for (a) ML

| Modality | Classifier | MACC | PR | RE | F1 | MCC | AUROC |
|----------|------------|----------|----------|----------|----------|----------|----------|
| Array | AB | 0.457667 | 0.451667 | 0.457667 | 0.433667 | 0.8765 | 0.861667 |
| CNV | AB | 0.403846 | 0.396667 | 0.403846 | 0.361282 | 0.839487 | 0.738462 |
| Exon | AB | 0.665556 | 0.736667 | 0.665556 | 0.674444 | 0.926667 | 0.92 |
| Meth. | AB | 0.484188 | 0.458875 | 0.484188 | 0.447688 | 0.813063 | 0.759 |
| RNASeq | AB | 0.6224 | 0.65012 | 0.6224 | 0.6154 | 0.90512 | 0.86712 |
| RPPA | AB | 0.406522 | 0.387826 | 0.406522 | 0.375217 | 0.825217 | 0.71913 |
| SNP | AB | 0.379105 | 0.365263 | 0.379105 | 0.334842 | 0.808211 | 0.663211 |
| miRNA | AB | 0.472571 | 0.493143 | 0.472571 | 0.456214 | 0.857 | 0.811429 |
| Array | BNB | 0.536167 | 0.515167 | 0.536167 | 0.494833 | 0.877167 | 0.751667 |
| CNV | BNB | 0.434872 | 0.419487 | 0.434872 | 0.405385 | 0.839231 | 0.665641 |
| Exon | BNB | 0.468889 | 0.468889 | 0.468889 | 0.444444 | 0.872222 | 0.703333 |
| Meth. | BNB | 0.263125 | 0.124687 | 0.263125 | 0.163438 | 0.73625 | 0.518125 |
| RNASeq | BNB | 0.5328 | 0.5036 | 0.5328 | 0.5024 | 0.8884 | 0.842 |
| RPPA | BNB | 0.473913 | 0.468261 | 0.473913 | 0.453478 | 0.845652 | 0.764783 |
| SNP | BNB | 0.286368 | 0.177947 | 0.286368 | 0.198053 | 0.771053 | 0.561684 |
| miRNA | BNB | 0.488714 | 0.528143 | 0.488714 | 0.475071 | 0.8615 | 0.816429 |
| Array | CB | 0.489 | 0.454667 | 0.489 | 0.453833 | 0.9 | 0.901667 |
| CNV | CB | 0.435897 | 0.428974 | 0.435897 | 0.401795 | 0.851795 | 0.768974 |
| Exon | CB | 0.547778 | 0.555556 | 0.547778 | 0.52 | 0.905556 | 0.936667 |
| Meth. | CB | 0.5395 | 0.556625 | 0.5395 | 0.5165 | 0.853625 | 0.826 |
| RNASeq | CB | 0.606 | 0.6192 | 0.606 | 0.584 | 0.922 | 0.9332 |
| RPPA | CB | 0.433913 | 0.446522 | 0.433913 | 0.396087 | 0.837826 | 0.786522 |
| SNP | CB | 0.324737 | 0.235316 | 0.324737 | 0.244842 | 0.788421 | 0.655474 |
| miRNA | CB | 0.448214 | 0.451714 | 0.448214 | 0.409643 | 0.845786 | 0.875714 |
| Array | CNB | 0.592 | 0.6155 | 0.592 | 0.598 | 0.9335 | 0.835 |
| Exon | CNB | 0.597778 | 0.661111 | 0.597778 | 0.592222 | 0.915556 | 0.817778 |
| Meth. | CNB | 0.496813 | 0.4725 | 0.496813 | 0.458563 | 0.818188 | 0.759375 |
| RNASeq | CNB | 0.647529 | 0.676588 | 0.647529 | 0.633471 | 0.928353 | 0.881765 |
| SNP | CNB | 0.309684 | 0.290895 | 0.309684 | 0.250263 | 0.780632 | 0.624316 |
| miRNA | CNB | 0.551786 | 0.584929 | 0.551786 | 0.525929 | 0.877571 | 0.835 |
| Array | DT | 0.517333 | 0.536833 | 0.517333 | 0.513 | 0.891 | 0.701667 |
| CNV | DT | 0.418462 | 0.425128 | 0.418462 | 0.412308 | 0.838462 | 0.631538 |
| Exon | DT | 0.638889 | 0.641111 | 0.638889 | 0.634444 | 0.915556 | 0.774444 |
| Meth. | DT | 0.52725 | 0.546813 | 0.52725 | 0.523688 | 0.842688 | 0.685 |
| RNASeq | DT | 0.6572 | 0.6556 | 0.6572 | 0.644 | 0.9036 | 0.7812 |
| RPPA | DT | 0.400435 | 0.413478 | 0.400435 | 0.4 | 0.825217 | 0.613043 |
| SNP | DT | 0.412632 | 0.409684 | 0.412632 | 0.381684 | 0.821526 | 0.615526 |
| miRNA | DT | 0.476929 | 0.484857 | 0.476929 | 0.473786 | 0.841786 | 0.659286 |
| Array | GB | 0.2545 | 0.170167 | 0.2545 | 0.1765 | 0.797167 | 0.825 |
| CNV | GB | 0.299231 | 0.226667 | 0.299231 | 0.230513 | 0.783846 | 0.699487 |
| Exon | GB | 0.395556 | 0.365556 | 0.395556 | 0.352222 | 0.846667 | 0.904444 |
| Meth. | GB | 0.358063 | 0.299937 | 0.358063 | 0.30125 | 0.783688 | 0.759375 |

| | | | | | | | |
|--------|------|----------|----------|----------|----------|----------|----------|
| RNASeq | GB | 0.3664 | 0.324 | 0.3664 | 0.3208 | 0.8212 | 0.8584 |
| RPPA | GB | 0.294348 | 0.211739 | 0.294348 | 0.221739 | 0.773913 | 0.676957 |
| SNP | GB | 0.278158 | 0.215053 | 0.278158 | 0.200211 | 0.767895 | 0.658842 |
| miRNA | GB | 0.313786 | 0.250643 | 0.313786 | 0.254643 | 0.795786 | 0.727143 |
| Array | GNB | 0.638333 | 0.688667 | 0.638333 | 0.639333 | 0.917833 | 0.801667 |
| CNV | GNB | 0.462821 | 0.476667 | 0.462821 | 0.441026 | 0.851282 | 0.669231 |
| Exon | GNB | 0.4 | 0.443333 | 0.4 | 0.37 | 0.852222 | 0.626667 |
| Meth. | GNB | 0.553375 | 0.549187 | 0.553375 | 0.534938 | 0.846 | 0.71125 |
| RNASeq | GNB | 0.3628 | 0.364 | 0.3628 | 0.3232 | 0.8308 | 0.598 |
| RPPA | GNB | 0.477826 | 0.478261 | 0.477826 | 0.458261 | 0.849565 | 0.742609 |
| SNP | GNB | 0.271263 | 0.223421 | 0.271263 | 0.205211 | 0.769 | 0.522737 |
| miRNA | GNB | 0.297857 | 0.300286 | 0.297857 | 0.277143 | 0.785857 | 0.54 |
| Array | HGB | 0.6765 | 0.744667 | 0.6765 | 0.687833 | 0.937 | 0.943333 |
| CNV | HGB | 0.476667 | 0.488974 | 0.476667 | 0.467949 | 0.858974 | 0.769487 |
| Exon | HGB | 0.777778 | 0.823333 | 0.777778 | 0.78 | 0.958889 | 0.963333 |
| Meth. | HGB | 0.624938 | 0.6215 | 0.624938 | 0.606063 | 0.866813 | 0.821875 |
| RNASeq | HGB | 0.7508 | 0.778 | 0.7508 | 0.7524 | 0.9428 | 0.9496 |
| RPPA | HGB | 0.49087 | 0.516087 | 0.49087 | 0.487391 | 0.861304 | 0.785217 |
| SNP | HGB | 0.382842 | 0.336789 | 0.382842 | 0.343263 | 0.802158 | 0.635368 |
| miRNA | HGB | 0.637286 | 0.658214 | 0.637286 | 0.634571 | 0.897929 | 0.862857 |
| Array | KNN | 0.497833 | 0.5645 | 0.497833 | 0.492333 | 0.884667 | 0.853333 |
| CNV | KNN | 0.404359 | 0.423333 | 0.404359 | 0.365385 | 0.829744 | 0.700769 |
| Exon | KNN | 0.564444 | 0.621111 | 0.564444 | 0.557778 | 0.896667 | 0.888889 |
| Meth. | KNN | 0.506688 | 0.570313 | 0.506688 | 0.48425 | 0.837875 | 0.758125 |
| RNASeq | KNN | 0.6364 | 0.7124 | 0.6364 | 0.6396 | 0.9156 | 0.9128 |
| RPPA | KNN | 0.468261 | 0.527826 | 0.468261 | 0.461739 | 0.848696 | 0.748261 |
| SNP | KNN | 0.254211 | 0.140579 | 0.254211 | 0.124842 | 0.754737 | 0.524526 |
| miRNA | KNN | 0.533857 | 0.602143 | 0.533857 | 0.525143 | 0.867286 | 0.836429 |
| Array | LGBM | 0.242833 | 0.145167 | 0.242833 | 0.163167 | 0.792167 | 0.86 |
| CNV | LGBM | 0.287949 | 0.219487 | 0.287949 | 0.214359 | 0.774103 | 0.715641 |
| Exon | LGBM | 0.382222 | 0.336667 | 0.382222 | 0.326667 | 0.847778 | 0.93 |
| Meth. | LGBM | 0.34125 | 0.265625 | 0.34125 | 0.266938 | 0.773625 | 0.780625 |
| RNASeq | LGBM | 0.3604 | 0.3068 | 0.3604 | 0.3092 | 0.826 | 0.8896 |
| RPPA | LGBM | 0.288261 | 0.204348 | 0.288261 | 0.21 | 0.77087 | 0.702609 |
| SNP | LGBM | 0.264368 | 0.15 | 0.264368 | 0.179632 | 0.761579 | 0.637105 |
| miRNA | LGBM | 0.301857 | 0.224286 | 0.301857 | 0.229786 | 0.791929 | 0.776429 |
| Array | LR | 0.672667 | 0.699833 | 0.672667 | 0.670667 | 0.930833 | 0.938333 |
| CNV | LR | 0.486667 | 0.488718 | 0.486667 | 0.475385 | 0.858974 | 0.747949 |
| Exon | LR | 0.747778 | 0.767778 | 0.747778 | 0.748889 | 0.95 | 0.965556 |
| Meth. | LR | 0.652313 | 0.702125 | 0.652313 | 0.659875 | 0.881063 | 0.83875 |
| RNASeq | LR | 0.7728 | 0.7928 | 0.7728 | 0.772 | 0.952 | 0.9524 |
| RPPA | LR | 0.522174 | 0.53913 | 0.522174 | 0.522609 | 0.871304 | 0.797826 |
| SNP | LR | 0.391789 | 0.370368 | 0.391789 | 0.346947 | 0.816895 | 0.691368 |

| | | | | | | | |
|--------|-----|----------|----------|----------|----------|----------|----------|
| miRNA | LR | 0.688571 | 0.712857 | 0.688571 | 0.685429 | 0.9155 | 0.895714 |
| Array | QDA | 0.261 | 0.2585 | 0.261 | 0.251 | 0.806167 | 0.533333 |
| CNV | QDA | 0.286154 | 0.281282 | 0.286154 | 0.238205 | 0.769231 | 0.527179 |
| Exon | QDA | 0.243333 | 0.235556 | 0.243333 | 0.232222 | 0.793333 | 0.517778 |
| Meth. | QDA | 0.28525 | 0.275375 | 0.28525 | 0.274875 | 0.7525 | 0.51875 |
| RNASeq | QDA | 0.2568 | 0.2532 | 0.2568 | 0.2472 | 0.7756 | 0.5156 |
| RPPA | QDA | 0.268696 | 0.253478 | 0.268696 | 0.246087 | 0.762609 | 0.517826 |
| SNP | QDA | 0.258421 | 0.203158 | 0.258421 | 0.186789 | 0.761105 | 0.507895 |
| miRNA | QDA | 0.228786 | 0.239929 | 0.228786 | 0.223786 | 0.767429 | 0.499286 |
| Array | RF | 0.595 | 0.654333 | 0.595 | 0.603 | 0.923667 | 0.908333 |
| CNV | RF | 0.487949 | 0.516667 | 0.487949 | 0.480769 | 0.86359 | 0.770513 |
| Exon | RF | 0.673333 | 0.725556 | 0.673333 | 0.676667 | 0.934444 | 0.944444 |
| Meth. | RF | 0.602063 | 0.632 | 0.602063 | 0.59325 | 0.87075 | 0.81375 |
| RNASeq | RF | 0.6772 | 0.7312 | 0.6772 | 0.6776 | 0.9332 | 0.9412 |
| RPPA | RF | 0.483478 | 0.508696 | 0.483478 | 0.471739 | 0.854783 | 0.775652 |
| SNP | RF | 0.392105 | 0.366105 | 0.392105 | 0.338842 | 0.812632 | 0.670316 |
| miRNA | RF | 0.560643 | 0.610857 | 0.560643 | 0.551643 | 0.878286 | 0.873571 |
| Array | SVM | 0.689 | 0.736167 | 0.689 | 0.690833 | 0.936667 | 0.941667 |
| CNV | SVM | 0.500513 | 0.495897 | 0.500513 | 0.484103 | 0.862564 | 0.746667 |
| Exon | SVM | 0.748889 | 0.771111 | 0.748889 | 0.748889 | 0.957778 | 0.937778 |
| Meth. | SVM | 0.637063 | 0.678 | 0.637063 | 0.639563 | 0.876688 | 0.81875 |
| RNASeq | SVM | 0.7812 | 0.8056 | 0.7812 | 0.7836 | 0.956 | 0.9388 |
| RPPA | SVM | 0.548261 | 0.564783 | 0.548261 | 0.545652 | 0.876522 | 0.793478 |
| SNP | SVM | 0.387579 | 0.363526 | 0.387579 | 0.342 | 0.814789 | 0.671053 |
| miRNA | SVM | 0.698571 | 0.7085 | 0.698571 | 0.694214 | 0.917643 | 0.878571 |
| Array | XGB | 0.715667 | 0.7625 | 0.715667 | 0.7175 | 0.946333 | 0.941667 |
| CNV | XGB | 0.479744 | 0.489231 | 0.479744 | 0.47359 | 0.86 | 0.778462 |
| Exon | XGB | 0.763333 | 0.824444 | 0.763333 | 0.774444 | 0.947778 | 0.95 |
| Meth. | XGB | 0.595313 | 0.62025 | 0.595313 | 0.589313 | 0.857 | 0.818125 |
| RNASeq | XGB | 0.7016 | 0.706 | 0.7016 | 0.696 | 0.9284 | 0.924 |
| RPPA | XGB | 0.499565 | 0.517391 | 0.499565 | 0.493043 | 0.861739 | 0.775652 |
| SNP | XGB | 0.404158 | 0.407368 | 0.404158 | 0.391158 | 0.817526 | 0.679579 |
| miRNA | XGB | 0.602786 | 0.641143 | 0.602786 | 0.599143 | 0.8815 | 0.859286 |

Supplementary Table S5: Modality-wise average MACC values for DL classifiers.

| Modality | Classifier | ACC | PR | RE | F1 | MCC | AUROC |
|----------|------------|----------|----------|----------|----------|----------|----------|
| Array | CNN | 0.614333 | 0.687 | 0.614333 | 0.613 | 0.912 | 0.926667 |
| CNV | CNN | 0.488205 | 0.506667 | 0.488205 | 0.473846 | 0.864615 | 0.771282 |
| Exon | CNN | 0.269556 | 0.156222 | 0.269556 | 0.180444 | 0.807667 | 0.603667 |
| Meth. | CNN | 0.5495 | 0.556438 | 0.5495 | 0.511 | 0.859 | 0.79375 |
| RNASeq | CNN | 0.64808 | 0.64724 | 0.64808 | 0.62692 | 0.9192 | 0.9104 |

| | | | | | | | |
|--------|-------------|----------|----------|----------|----------|----------|----------|
| RPPA | CNN | 0.521217 | 0.554826 | 0.521217 | 0.521261 | 0.868391 | 0.777435 |
| SNP | CNN | 0.351211 | 0.342263 | 0.351211 | 0.312895 | 0.804789 | 0.653053 |
| miRNA | CNN | 0.605214 | 0.645429 | 0.605214 | 0.597286 | 0.895643 | 0.888786 |
| Array | CNN GRU | 0.286167 | 0.210167 | 0.286167 | 0.2115 | 0.8105 | 0.778333 |
| CNV | CNN GRU | 0.476154 | 0.486154 | 0.476154 | 0.464103 | 0.863846 | 0.762564 |
| Exon | CNN GRU | 0.214444 | 0.085222 | 0.214444 | 0.119778 | 0.785556 | 0.48 |
| Meth. | CNN GRU | 0.286875 | 0.13875 | 0.286875 | 0.180438 | 0.74875 | 0.619188 |
| RNASeq | CNN GRU | 0.316 | 0.20048 | 0.316 | 0.22892 | 0.8066 | 0.68336 |
| RPPA | CNN GRU | 0.492478 | 0.504261 | 0.492478 | 0.473435 | 0.857 | 0.765174 |
| SNP | CNN GRU | 0.384368 | 0.363263 | 0.384368 | 0.353316 | 0.814684 | 0.649474 |
| miRNA | CNN GRU | 0.415429 | 0.346357 | 0.415429 | 0.360286 | 0.8385 | 0.777286 |
| Array | CNN LSTM | 0.257833 | 0.1435 | 0.257833 | 0.173167 | 0.797167 | 0.658333 |
| CNV | CNN LSTM | 0.468462 | 0.460256 | 0.468462 | 0.439744 | 0.859487 | 0.757692 |
| Exon | CNN LSTM | 0.214111 | 0.085889 | 0.214111 | 0.120111 | 0.785889 | 0.493889 |
| Meth. | CNN LSTM | 0.29 | 0.163188 | 0.29 | 0.189188 | 0.754375 | 0.512 |
| RNASeq | CNN LSTM | 0.27184 | 0.1358 | 0.27184 | 0.1726 | 0.78616 | 0.63364 |
| RPPA | CNN LSTM | 0.505652 | 0.512043 | 0.505652 | 0.497783 | 0.864217 | 0.784174 |
| SNP | CNN LSTM | 0.344368 | 0.333947 | 0.344368 | 0.292895 | 0.805579 | 0.649737 |
| miRNA | CNN LSTM | 0.398643 | 0.3295 | 0.398643 | 0.330571 | 0.821429 | 0.808786 |
| Array | CNN RNN | 0.307833 | 0.215167 | 0.307833 | 0.234833 | 0.817167 | 0.678333 |
| CNV | CNN RNN | 0.495128 | 0.504103 | 0.495128 | 0.485128 | 0.866923 | 0.761795 |
| Exon | CNN RNN | 0.214111 | 0.084444 | 0.214111 | 0.120111 | 0.785889 | 0.498444 |
| Meth. | CNN RNN | 0.29875 | 0.165 | 0.29875 | 0.199813 | 0.76375 | 0.641125 |
| RNASeq | CNN RNN | 0.33252 | 0.257 | 0.33252 | 0.2498 | 0.81024 | 0.75312 |
| RPPA | CNN RNN | 0.520261 | 0.544304 | 0.520261 | 0.517565 | 0.869696 | 0.785087 |
| SNP | CNN RNN | 0.368 | 0.33 | 0.368 | 0.325737 | 0.809211 | 0.655211 |
| miRNA | CNN RNN | 0.450714 | 0.399786 | 0.450714 | 0.401 | 0.847857 | 0.823286 |
| Array | DEEPGENE | 0.460333 | 0.474167 | 0.460333 | 0.4445 | 0.879167 | 0.826667 |
| CNV | DEEPGENE | 0.445763 | 0.455974 | 0.445763 | 0.431605 | 0.850789 | 0.726053 |
| Exon | DEEPGENE | 0.25 | 0.09 | 0.25 | 0.132 | 0.75 | 0.529 |
| Meth. | DEEPGENE | 0.463733 | 0.481733 | 0.463733 | 0.4176 | 0.8256 | 0.738 |
| RNASeq | DEEPGENE | 0.52136 | 0.50688 | 0.52136 | 0.49348 | 0.87156 | 0.80448 |
| RPPA | DEEPGENE | 0.447045 | 0.470455 | 0.447045 | 0.436545 | 0.835409 | 0.715273 |
| SNP | DEEPGENE | 0.396789 | 0.387368 | 0.396789 | 0.371789 | 0.820737 | 0.662947 |
| miRNA | DEEPGENE | 0.614214 | 0.64 | 0.614214 | 0.606357 | 0.897286 | 0.880214 |
| Array | DENSENET121 | 0.302333 | 0.266333 | 0.302333 | 0.239333 | 0.811 | 0.653333 |
| CNV | DENSENET121 | 0.328205 | 0.280256 | 0.328205 | 0.27359 | 0.785897 | 0.62 |
| Exon | DENSENET121 | 0.233778 | 0.183667 | 0.233778 | 0.175111 | 0.786 | 0.518222 |
| Meth. | DENSENET121 | 0.32275 | 0.307313 | 0.32275 | 0.256813 | 0.780813 | 0.597438 |
| RNASeq | DENSENET121 | 0.334 | 0.30024 | 0.334 | 0.27136 | 0.80636 | 0.68048 |
| RPPA | DENSENET121 | 0.360739 | 0.352957 | 0.360739 | 0.327174 | 0.807304 | 0.638783 |
| SNP | DENSENET121 | 0.283895 | 0.182 | 0.283895 | 0.178632 | 0.765 | 0.580263 |
| miRNA | DENSENET121 | 0.344429 | 0.319 | 0.344429 | 0.285643 | 0.801143 | 0.6535 |

| | | | | | | | |
|--------|-------------|----------|----------|----------|----------|----------|----------|
| Array | DENSENET161 | 0.299667 | 0.276667 | 0.299667 | 0.228667 | 0.815667 | 0.7 |
| CNV | DENSENET161 | 0.332564 | 0.271538 | 0.332564 | 0.262051 | 0.790513 | 0.628205 |
| Exon | DENSENET161 | 0.231778 | 0.173889 | 0.231778 | 0.151444 | 0.788444 | 0.519444 |
| Meth. | DENSENET161 | 0.294313 | 0.2295 | 0.294313 | 0.2275 | 0.749813 | 0.552313 |
| RNASeq | DENSENET161 | 0.34736 | 0.33696 | 0.34736 | 0.27748 | 0.80864 | 0.66196 |
| RPPA | DENSENET161 | 0.323783 | 0.306348 | 0.323783 | 0.295478 | 0.784174 | 0.580739 |
| SNP | DENSENET161 | 0.2545 | 0.137278 | 0.2545 | 0.157278 | 0.766944 | 0.554611 |
| miRNA | DENSENET161 | 0.336571 | 0.343429 | 0.336571 | 0.274 | 0.796643 | 0.651 |
| Array | DENSENET169 | 0.335333 | 0.3145 | 0.335333 | 0.280333 | 0.830333 | 0.691667 |
| CNV | DENSENET169 | 0.331282 | 0.277179 | 0.331282 | 0.264872 | 0.792308 | 0.627179 |
| Exon | DENSENET169 | 0.231111 | 0.153 | 0.231111 | 0.157667 | 0.788889 | 0.532111 |
| Meth. | DENSENET169 | 0.328563 | 0.324063 | 0.328563 | 0.285313 | 0.7745 | 0.563125 |
| RNASeq | DENSENET169 | 0.35696 | 0.30948 | 0.35696 | 0.27936 | 0.81084 | 0.6792 |
| RPPA | DENSENET169 | 0.343565 | 0.357478 | 0.343565 | 0.315652 | 0.790913 | 0.599217 |
| SNP | DENSENET169 | 0.292263 | 0.206737 | 0.292263 | 0.199895 | 0.774579 | 0.592684 |
| miRNA | DENSENET169 | 0.366571 | 0.343714 | 0.366571 | 0.316214 | 0.807143 | 0.690571 |
| Array | DENSENET201 | 0.312833 | 0.3075 | 0.312833 | 0.256667 | 0.818333 | 0.691667 |
| CNV | DENSENET201 | 0.332821 | 0.285385 | 0.332821 | 0.270769 | 0.791538 | 0.624359 |
| Exon | DENSENET201 | 0.225333 | 0.189111 | 0.225333 | 0.143333 | 0.789 | 0.526778 |
| Meth. | DENSENET201 | 0.267 | 0.228063 | 0.267 | 0.187563 | 0.738813 | 0.543813 |
| RNASeq | DENSENET201 | 0.34416 | 0.29472 | 0.34416 | 0.27232 | 0.8062 | 0.67076 |
| RPPA | DENSENET201 | 0.330261 | 0.308043 | 0.330261 | 0.302174 | 0.793217 | 0.606696 |
| SNP | DENSENET201 | 0.282889 | 0.200278 | 0.282889 | 0.190222 | 0.776722 | 0.533778 |
| miRNA | DENSENET201 | 0.361929 | 0.350571 | 0.361929 | 0.309571 | 0.809 | 0.682786 |
| Array | DENSENET264 | 0.343 | 0.282333 | 0.343 | 0.286667 | 0.8265 | 0.66 |
| CNV | DENSENET264 | 0.320657 | 0.269114 | 0.320657 | 0.253486 | 0.799143 | 0.630543 |
| Exon | DENSENET264 | 0.238667 | 0.176667 | 0.238667 | 0.176111 | 0.790444 | 0.505778 |
| Meth. | DENSENET264 | 0.29 | 0.251063 | 0.29 | 0.234375 | 0.743 | 0.561438 |
| RNASeq | DENSENET264 | 0.36528 | 0.3286 | 0.36528 | 0.29932 | 0.81436 | 0.68588 |
| RPPA | DENSENET264 | 0.344957 | 0.315609 | 0.344957 | 0.309304 | 0.800739 | 0.608478 |
| SNP | DENSENET264 | 0.273833 | 0.169 | 0.273833 | 0.183722 | 0.772 | 0.547389 |
| miRNA | DENSENET264 | 0.341643 | 0.294 | 0.341643 | 0.268286 | 0.802 | 0.659429 |
| Array | GRU | 0.4895 | 0.5285 | 0.4895 | 0.469833 | 0.8755 | 0.823333 |
| CNV | GRU | 0.481282 | 0.497949 | 0.481282 | 0.478974 | 0.863333 | 0.772051 |
| Exon | GRU | 0.214444 | 0.085222 | 0.214444 | 0.119778 | 0.785556 | 0.523444 |
| Meth. | GRU | 0.576 | 0.606938 | 0.576 | 0.559 | 0.864313 | 0.821938 |
| RNASeq | GRU | 0.37424 | 0.2974 | 0.37424 | 0.30588 | 0.82376 | 0.65496 |
| RPPA | GRU | 0.504 | 0.495696 | 0.504 | 0.482435 | 0.863348 | 0.800348 |
| SNP | GRU | 0.315316 | 0.296105 | 0.315316 | 0.280316 | 0.788263 | 0.613526 |
| miRNA | GRU | 0.550714 | 0.572214 | 0.550714 | 0.536357 | 0.874 | 0.862571 |
| Array | LSTM | 0.472833 | 0.481833 | 0.472833 | 0.444833 | 0.872167 | 0.788333 |
| CNV | LSTM | 0.491538 | 0.510513 | 0.491538 | 0.484103 | 0.866923 | 0.785385 |
| Exon | LSTM | 0.214444 | 0.085222 | 0.214444 | 0.118667 | 0.785556 | 0.551444 |

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|--------|-----------|----------|----------|----------|----------|----------|----------|
| Meth. | LSTM | 0.554375 | 0.52825 | 0.554375 | 0.520813 | 0.852 | 0.811 |
| RNASeq | LSTM | 0.36944 | 0.2886 | 0.36944 | 0.30228 | 0.82096 | 0.66792 |
| RPPA | LSTM | 0.461087 | 0.462261 | 0.461087 | 0.434826 | 0.849522 | 0.784435 |
| SNP | LSTM | 0.303053 | 0.258947 | 0.303053 | 0.248789 | 0.782947 | 0.602263 |
| miRNA | LSTM | 0.495643 | 0.484429 | 0.495643 | 0.466286 | 0.862571 | 0.869929 |
| Array | MLP | 0.596167 | 0.650167 | 0.596167 | 0.583167 | 0.908833 | 0.905 |
| CNV | MLP | 0.482564 | 0.49 | 0.482564 | 0.473846 | 0.858718 | 0.744872 |
| Exon | MLP | 0.412222 | 0.395556 | 0.412222 | 0.362222 | 0.861111 | 0.728889 |
| Meth. | MLP | 0.570438 | 0.568563 | 0.570438 | 0.55125 | 0.854625 | 0.815625 |
| RNASeq | MLP | 0.5564 | 0.5652 | 0.5564 | 0.5272 | 0.8944 | 0.8172 |
| RPPA | MLP | 0.541739 | 0.555217 | 0.541739 | 0.536957 | 0.877826 | 0.814348 |
| SNP | MLP | 0.365474 | 0.352947 | 0.365474 | 0.327579 | 0.810579 | 0.642211 |
| miRNA | MLP | 0.602643 | 0.626786 | 0.602643 | 0.591 | 0.885929 | 0.870714 |
| Array | NN | 0.6795 | 0.712833 | 0.6795 | 0.684333 | 0.931 | 0.933333 |
| CNV | NN | 0.508718 | 0.503333 | 0.508718 | 0.493077 | 0.866923 | 0.764615 |
| Exon | NN | 0.621222 | 0.640111 | 0.621222 | 0.610889 | 0.907556 | 0.859333 |
| Meth. | NN | 0.632563 | 0.657188 | 0.632563 | 0.630438 | 0.872188 | 0.816125 |
| RNASeq | NN | 0.73872 | 0.75164 | 0.73872 | 0.73876 | 0.94096 | 0.93992 |
| RPPA | NN | 0.428261 | 0.421304 | 0.428261 | 0.39813 | 0.832 | 0.76487 |
| SNP | NN | 0.311842 | 0.323105 | 0.311842 | 0.297474 | 0.784947 | 0.570474 |
| miRNA | NN | 0.555143 | 0.607071 | 0.555143 | 0.554071 | 0.876 | 0.820571 |
| Array | RESNET101 | 0.454833 | 0.470833 | 0.454833 | 0.4075 | 0.867833 | 0.788333 |
| CNV | RESNET101 | 0.350769 | 0.349231 | 0.350769 | 0.296667 | 0.799744 | 0.658718 |
| Exon | RESNET101 | 0.332778 | 0.308889 | 0.332778 | 0.275111 | 0.829111 | 0.744556 |
| Meth. | RESNET101 | 0.556 | 0.596188 | 0.556 | 0.538438 | 0.861625 | 0.8215 |
| RNASeq | RESNET101 | 0.56368 | 0.61524 | 0.56368 | 0.54948 | 0.88688 | 0.88236 |
| RPPA | RESNET101 | 0.364391 | 0.376826 | 0.364391 | 0.348478 | 0.806435 | 0.645913 |
| SNP | RESNET101 | 0.290667 | 0.214 | 0.290667 | 0.224722 | 0.779833 | 0.595111 |
| miRNA | RESNET101 | 0.542643 | 0.562857 | 0.542643 | 0.522643 | 0.876786 | 0.828 |
| Array | RESNET152 | 0.411167 | 0.463 | 0.411167 | 0.387667 | 0.855167 | 0.781667 |
| CNV | RESNET152 | 0.332821 | 0.302821 | 0.332821 | 0.273333 | 0.791795 | 0.636923 |
| Exon | RESNET152 | 0.296889 | 0.254222 | 0.296889 | 0.235667 | 0.812889 | 0.731 |
| Meth. | RESNET152 | 0.446125 | 0.473438 | 0.446125 | 0.406688 | 0.804625 | 0.733563 |
| RNASeq | RESNET152 | 0.48024 | 0.47296 | 0.48024 | 0.42516 | 0.85676 | 0.82608 |
| RPPA | RESNET152 | 0.318783 | 0.315565 | 0.318783 | 0.285348 | 0.782565 | 0.596391 |
| SNP | RESNET152 | 0.308842 | 0.237211 | 0.308842 | 0.250632 | 0.779421 | 0.590368 |
| miRNA | RESNET152 | 0.512 | 0.531071 | 0.512 | 0.475643 | 0.857286 | 0.791214 |
| Array | RESNET18 | 0.599 | 0.656333 | 0.599 | 0.604667 | 0.918 | 0.91 |
| CNV | RESNET18 | 0.359231 | 0.363846 | 0.359231 | 0.320513 | 0.807692 | 0.658205 |
| Exon | RESNET18 | 0.534667 | 0.575 | 0.534667 | 0.497556 | 0.883556 | 0.911222 |
| Meth. | RESNET18 | 0.614 | 0.656063 | 0.614 | 0.606875 | 0.873563 | 0.831313 |
| RNASeq | RESNET18 | 0.689 | 0.72656 | 0.689 | 0.687 | 0.93416 | 0.93584 |
| RPPA | RESNET18 | 0.481435 | 0.526087 | 0.481435 | 0.481304 | 0.847261 | 0.747174 |

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|--------|----------|----------|----------|----------|----------|----------|----------|
| SNP | RESNET18 | 0.322421 | 0.274211 | 0.322421 | 0.263211 | 0.788895 | 0.613632 |
| miRNA | RESNET18 | 0.636786 | 0.6475 | 0.636786 | 0.626857 | 0.898643 | 0.896786 |
| Array | RESNET34 | 0.5735 | 0.630667 | 0.5735 | 0.567833 | 0.905833 | 0.883333 |
| CNV | RESNET34 | 0.360256 | 0.342051 | 0.360256 | 0.313846 | 0.804103 | 0.654359 |
| Exon | RESNET34 | 0.425778 | 0.384222 | 0.425778 | 0.353444 | 0.854889 | 0.829667 |
| Meth. | RESNET34 | 0.581375 | 0.652188 | 0.581375 | 0.57625 | 0.85625 | 0.79975 |
| RNASeq | RESNET34 | 0.63992 | 0.70524 | 0.63992 | 0.63104 | 0.91596 | 0.91944 |
| RPPA | RESNET34 | 0.440957 | 0.453609 | 0.440957 | 0.428522 | 0.833913 | 0.724 |
| SNP | RESNET34 | 0.323684 | 0.313842 | 0.323684 | 0.261368 | 0.773895 | 0.622579 |
| miRNA | RESNET34 | 0.626571 | 0.64 | 0.626571 | 0.616714 | 0.899857 | 0.886786 |
| Array | RESNET50 | 0.474667 | 0.497333 | 0.474667 | 0.441667 | 0.871667 | 0.828333 |
| CNV | RESNET50 | 0.364359 | 0.358205 | 0.364359 | 0.316154 | 0.806154 | 0.65 |
| Exon | RESNET50 | 0.429222 | 0.400556 | 0.429222 | 0.37 | 0.843778 | 0.821778 |
| Meth. | RESNET50 | 0.539563 | 0.561625 | 0.539563 | 0.515625 | 0.846313 | 0.804125 |
| RNASeq | RESNET50 | 0.62832 | 0.70364 | 0.62832 | 0.6294 | 0.9122 | 0.92408 |
| RPPA | RESNET50 | 0.408522 | 0.476783 | 0.408522 | 0.40713 | 0.81887 | 0.697565 |
| SNP | RESNET50 | 0.341526 | 0.302316 | 0.341526 | 0.280368 | 0.790842 | 0.626632 |
| miRNA | RESNET50 | 0.567286 | 0.610071 | 0.567286 | 0.563071 | 0.88 | 0.863929 |
| Array | RNN | 0.5045 | 0.5435 | 0.5045 | 0.4915 | 0.8755 | 0.76 |
| CNV | RNN | 0.492564 | 0.502821 | 0.492564 | 0.485897 | 0.864872 | 0.767949 |
| Exon | RNN | 0.214444 | 0.085222 | 0.214444 | 0.119778 | 0.785556 | 0.507778 |
| Meth. | RNN | 0.495625 | 0.473625 | 0.495625 | 0.454125 | 0.839 | 0.782063 |
| RNASeq | RNN | 0.37892 | 0.29988 | 0.37892 | 0.31316 | 0.8224 | 0.65336 |
| RPPA | RNN | 0.561478 | 0.580174 | 0.561478 | 0.555783 | 0.884957 | 0.821261 |
| SNP | RNN | 0.361421 | 0.370368 | 0.361421 | 0.340737 | 0.808632 | 0.655368 |
| miRNA | RNN | 0.556 | 0.593643 | 0.556 | 0.545071 | 0.8835 | 0.856929 |