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Protocol

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Robust scoring of selective drug responses for patient-tailored therapy selection

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Supplementary Information for

Robust scoring of selective drug responses for patient-tailored therapy selection

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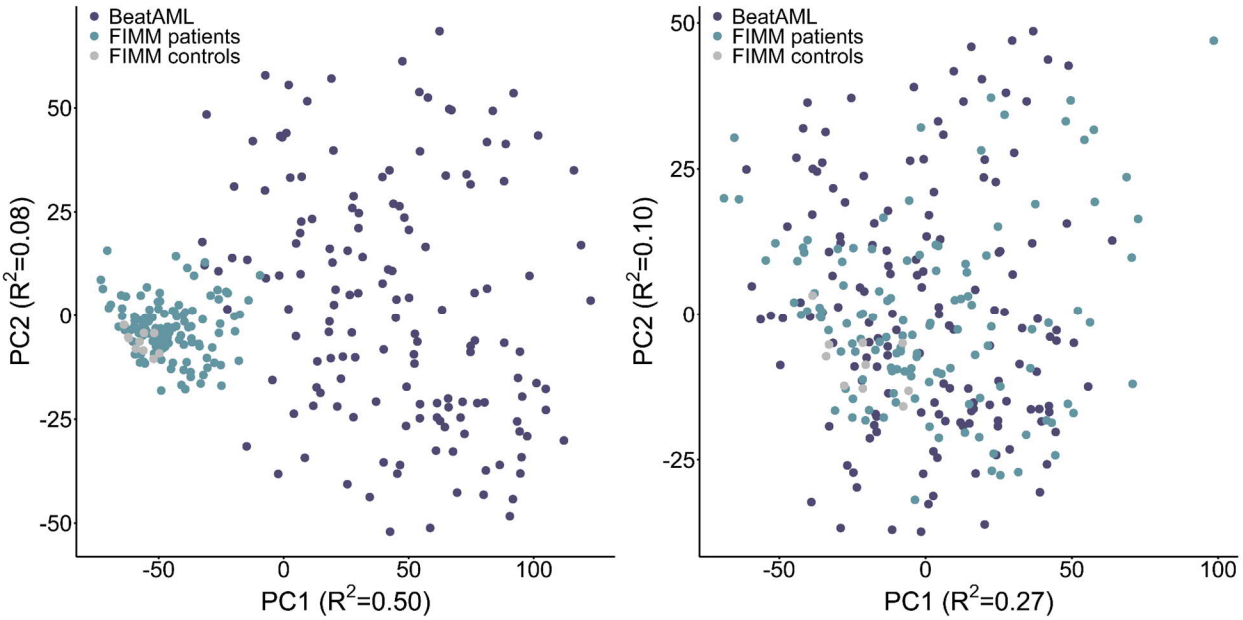
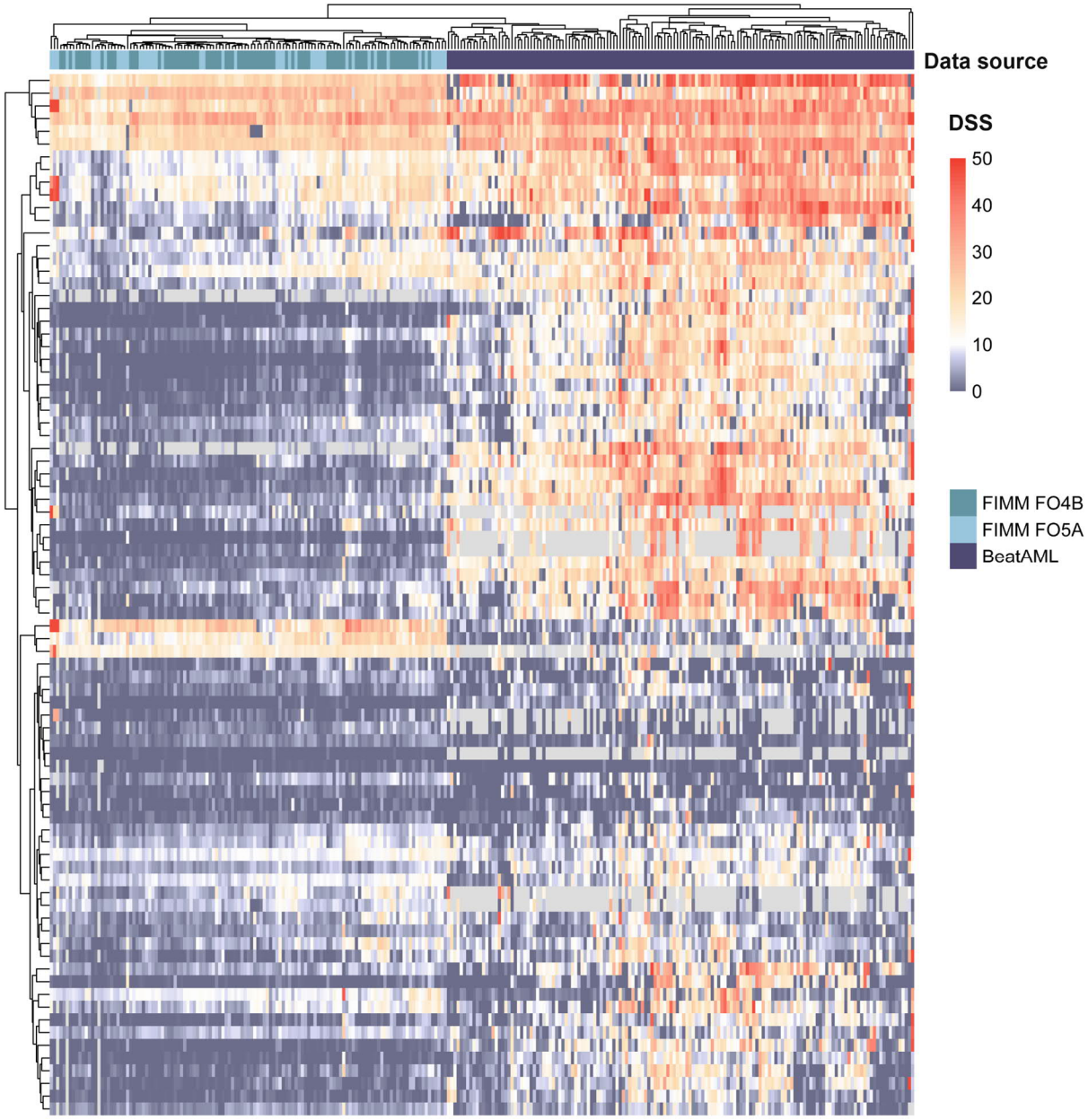
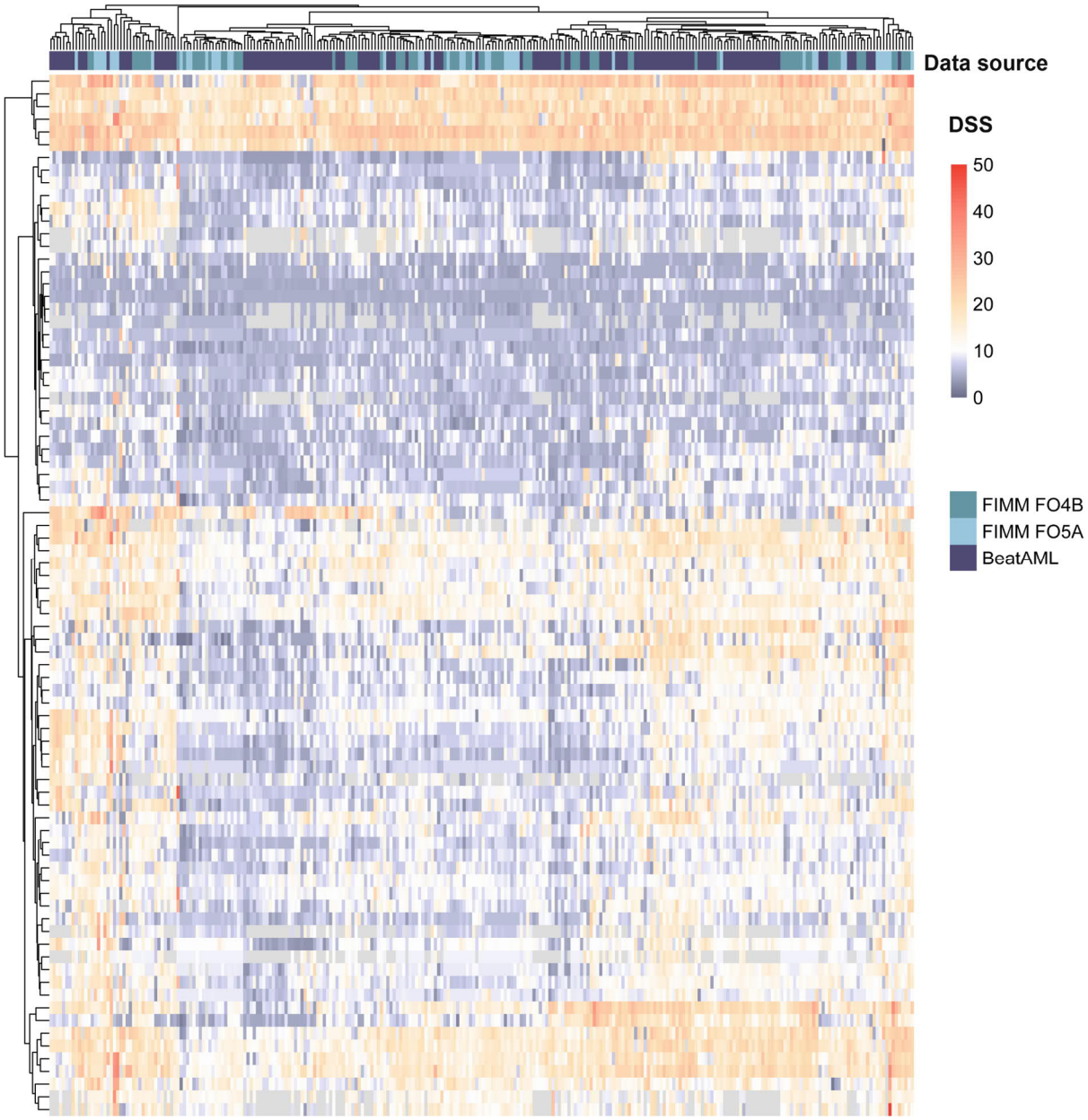


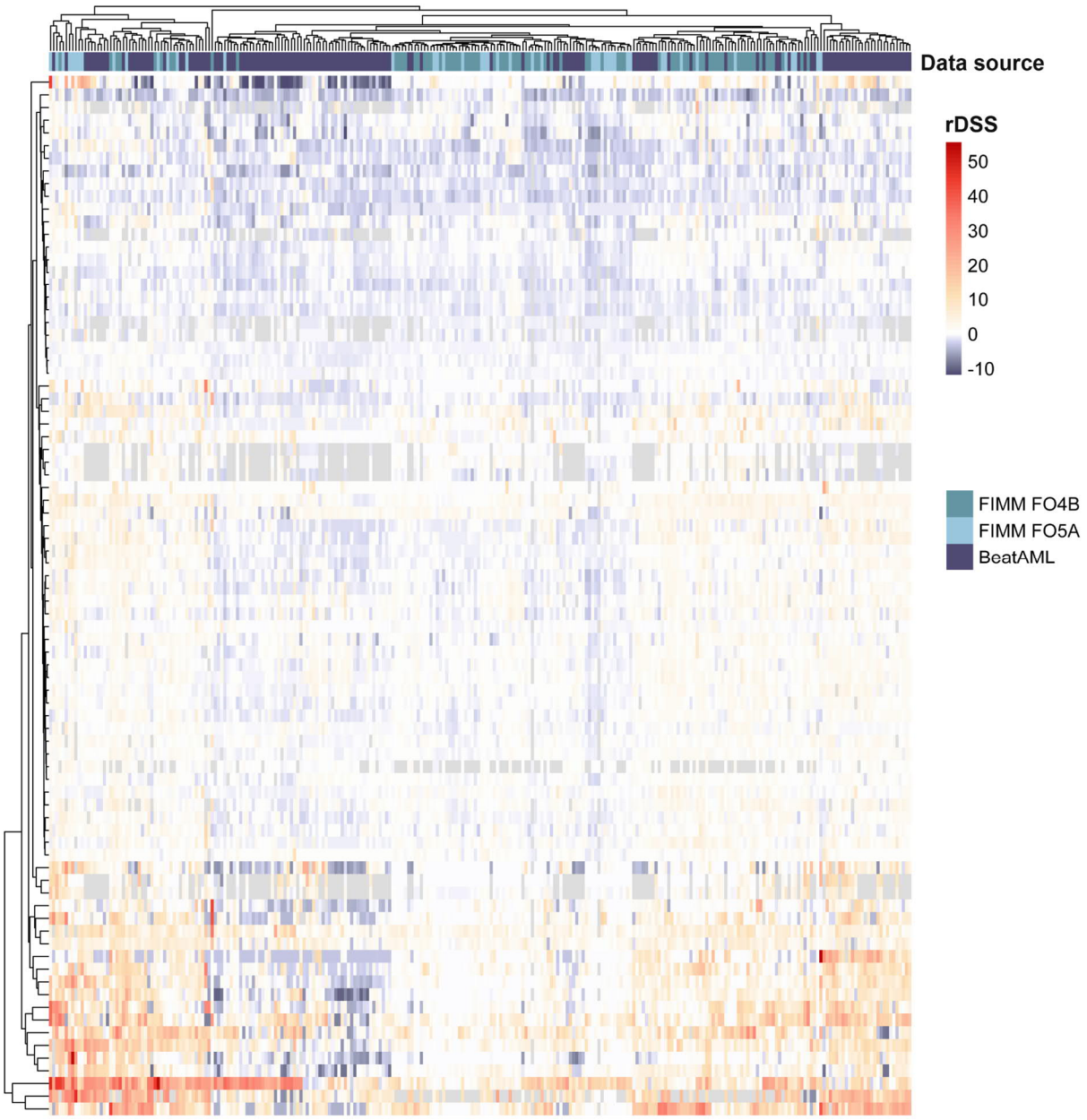
Supplementary Figure 1 | Batch effect correction when combining drug response data from BeatAML patients (n = 147), FIMM-AML patients (n=79 for FO4B compound collection; n=46 for FO5A collection), and FIMM healthy control samples (n = 10, FO5A compound collection). Probabilistic principal component analysis (PPCA) was used, since the BeatAML and FIMM-AML drug response profiles contain missing values (5.29%). *Left panel*: PPCA of non-selective DSS profiles, showing batch effects between the FIMM and BeatAML patients. *Right panel*: PPCA of ComBat-corrected DSS profiles, where the batch variable was sample source (BeatAML samples vs. FIMM patients/controls; see **Procedure 2** for details). The coefficient of determination (R^2) shows the proportion of variance explained by each PC.



Supplementary Figure 2 | Integrated heatmap of non-selective DSS drug responses for the BeatAML and FIMM-AML cohorts. Columns correspond to 272 patients (147 from BeatAML and 125 from FIMM-AML; n=79 for FO4B compound collection; n=46 for FO5A collection), and rows are 82 overlapping drugs.



Supplementary Figure 3 | Integrated heatmap of ComBat-corrected DSS responses for the BeatAML and FIMM-AML cohorts. Columns correspond to 272 patients (147 from BeatAML and 125 from FIMM-AML; n=79 for FO4B compound collection; n=46 for FO5A collection), and rows are 82 overlapping drugs. Batch effects from the two data sources were adjusted with the non-parametric empirical Bayes method. The ComBat-corrected DSS values were re-scaled to the range of the original DSS values (from 0 to 50).



Supplementary Figure 4 | Integrated heatmap of ComBat-corrected rDSS drug response profiles for the BeatAML and FIMM-AML cohorts. Columns correspond to 272 patients (147 from BeatAML and 125 from FIMM-AML; n=79 for FO4B compound collection; n=46 for FO5A collection), where the selective rDSS normalization was done against the FIMM healthy control samples (n = 10, FO5A compound collection). Rows are 82 overlapping drugs. See **Figure 6** for a version where the drug names are listed.