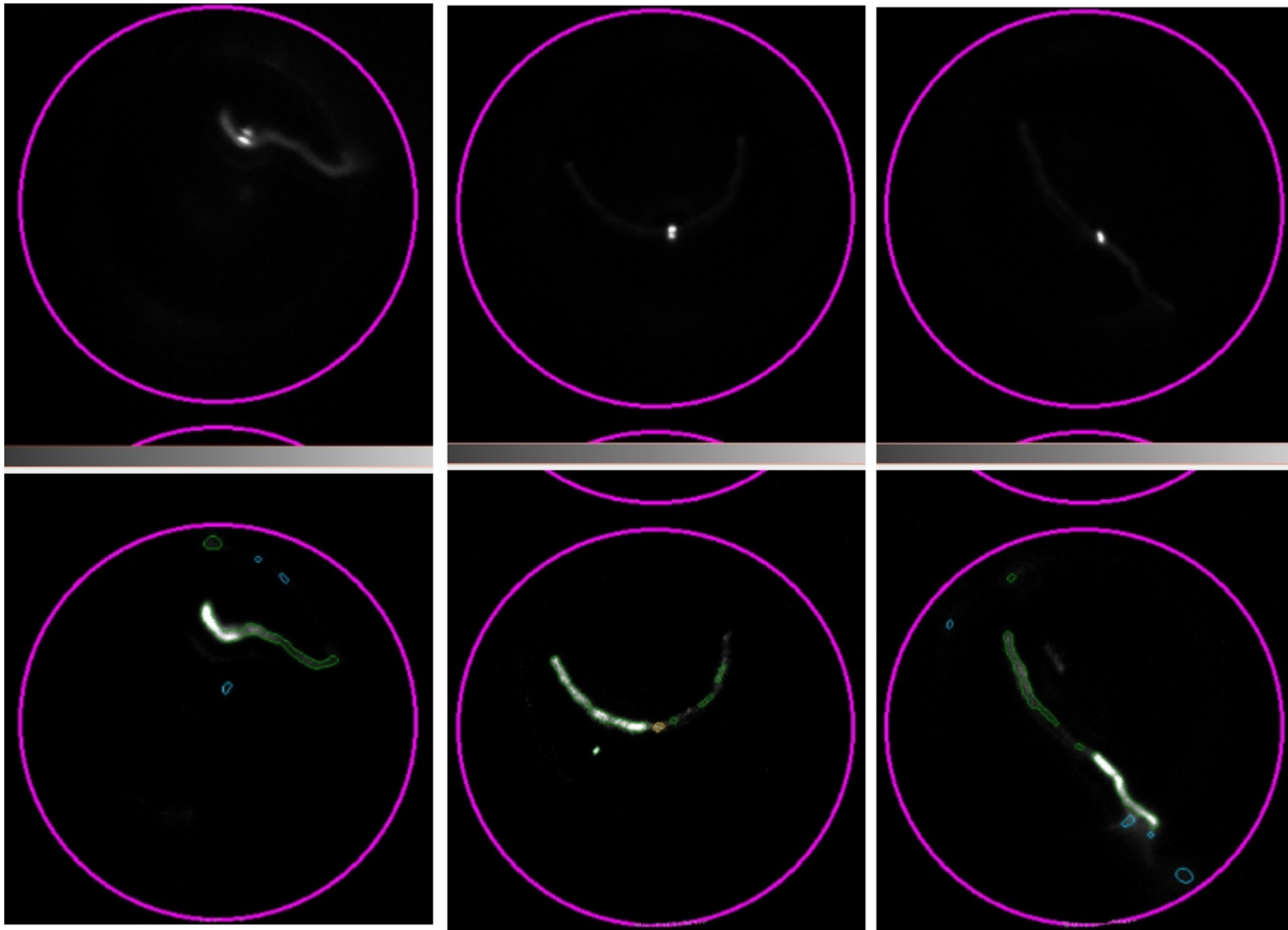
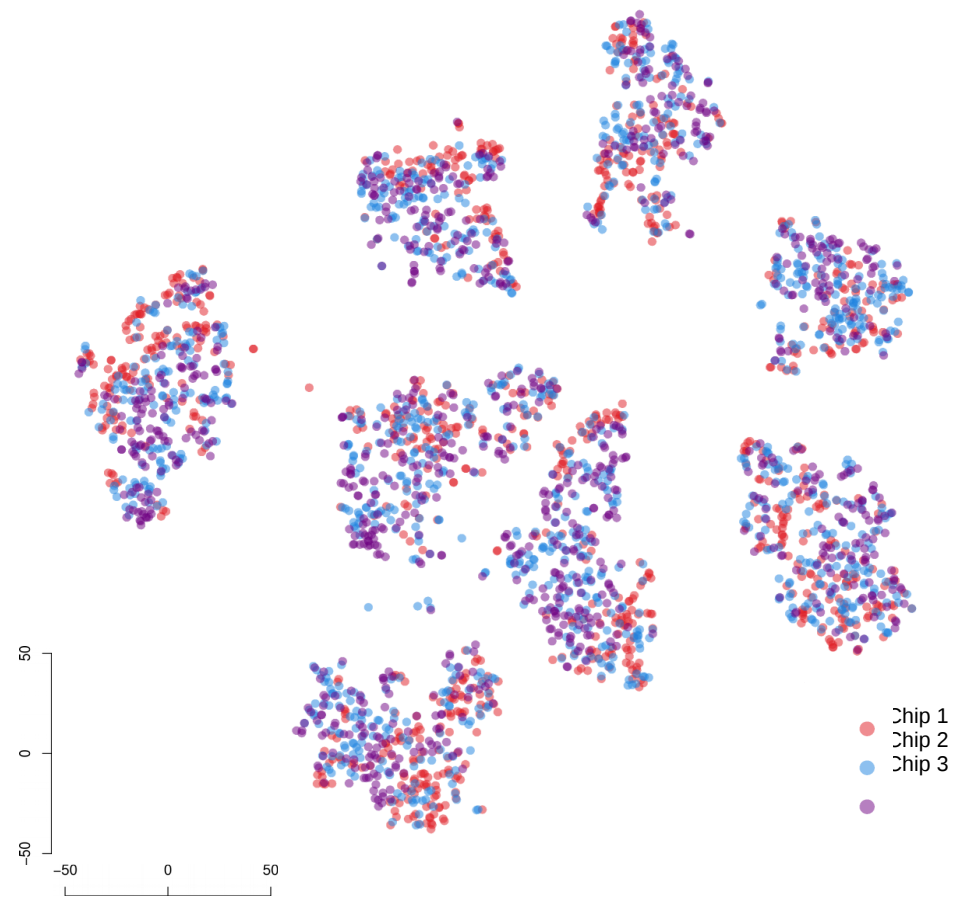


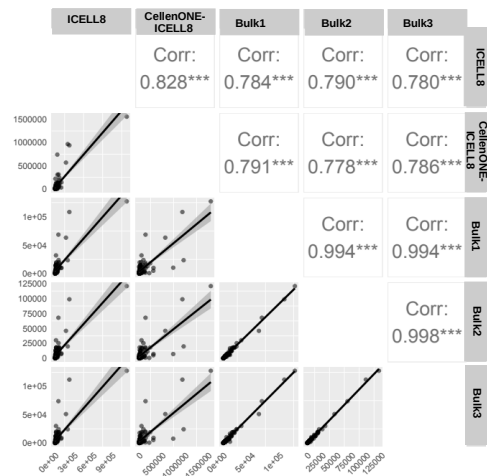


Supplementary Figure 1: dispensing of Schwann cells exhibiting axonic regrowing forms and sizing of 200-500 μm into a Takara ICELL8 5,184 nano-well chip. Cells were fluorescent-labelled with live/dead stain, Hoechst 33342 and propidium iodide (NucBlue Cell Stain Reagent, Thermo Fisher Scientific). Living and single cells were visualized and selected using the CellSelect Software (Takara Bio).

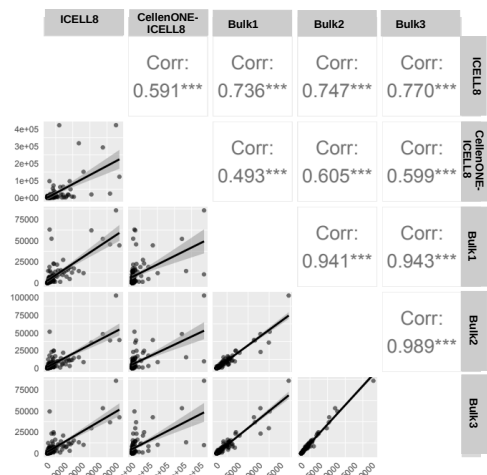


Supplementary Figure 2: t-SNE visualization of the three ICELL8 chips, showing how single cells from all 3 chips overlap with each other and showing no batch effect between them.

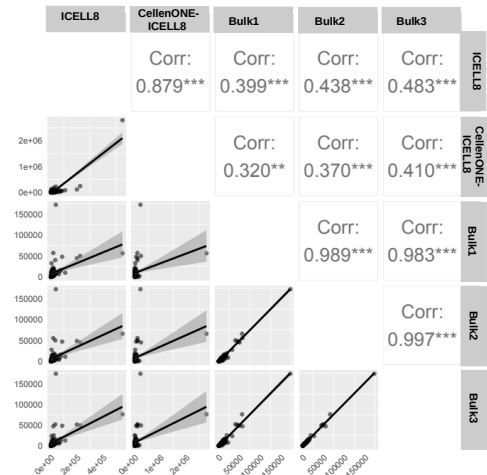
GOE486



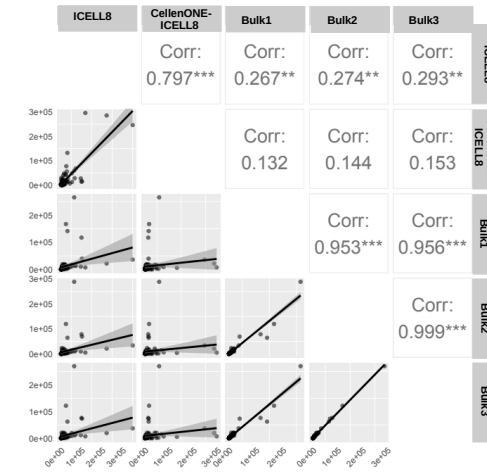
GOE615



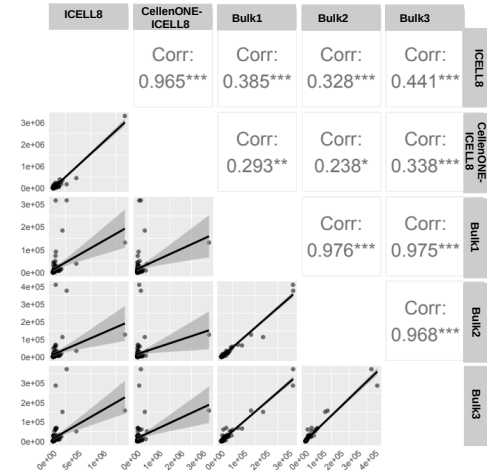
GOE1303



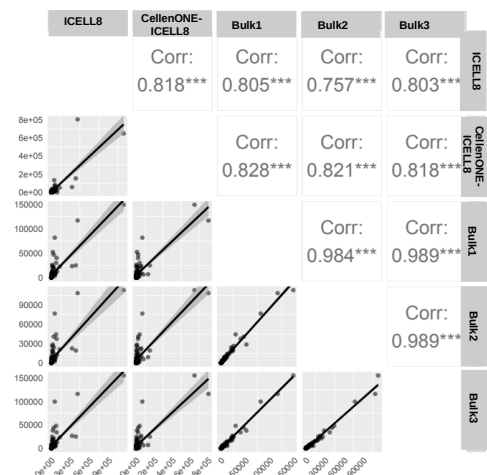
GOE800



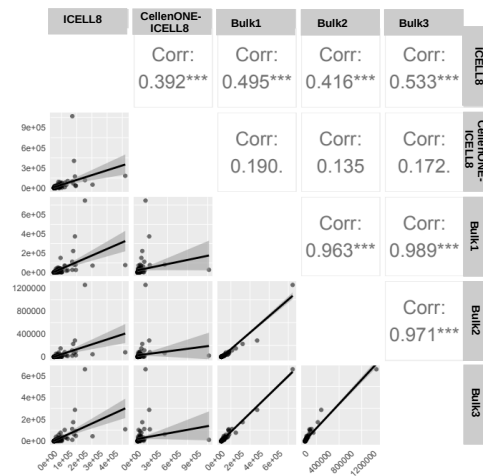
GOE1305



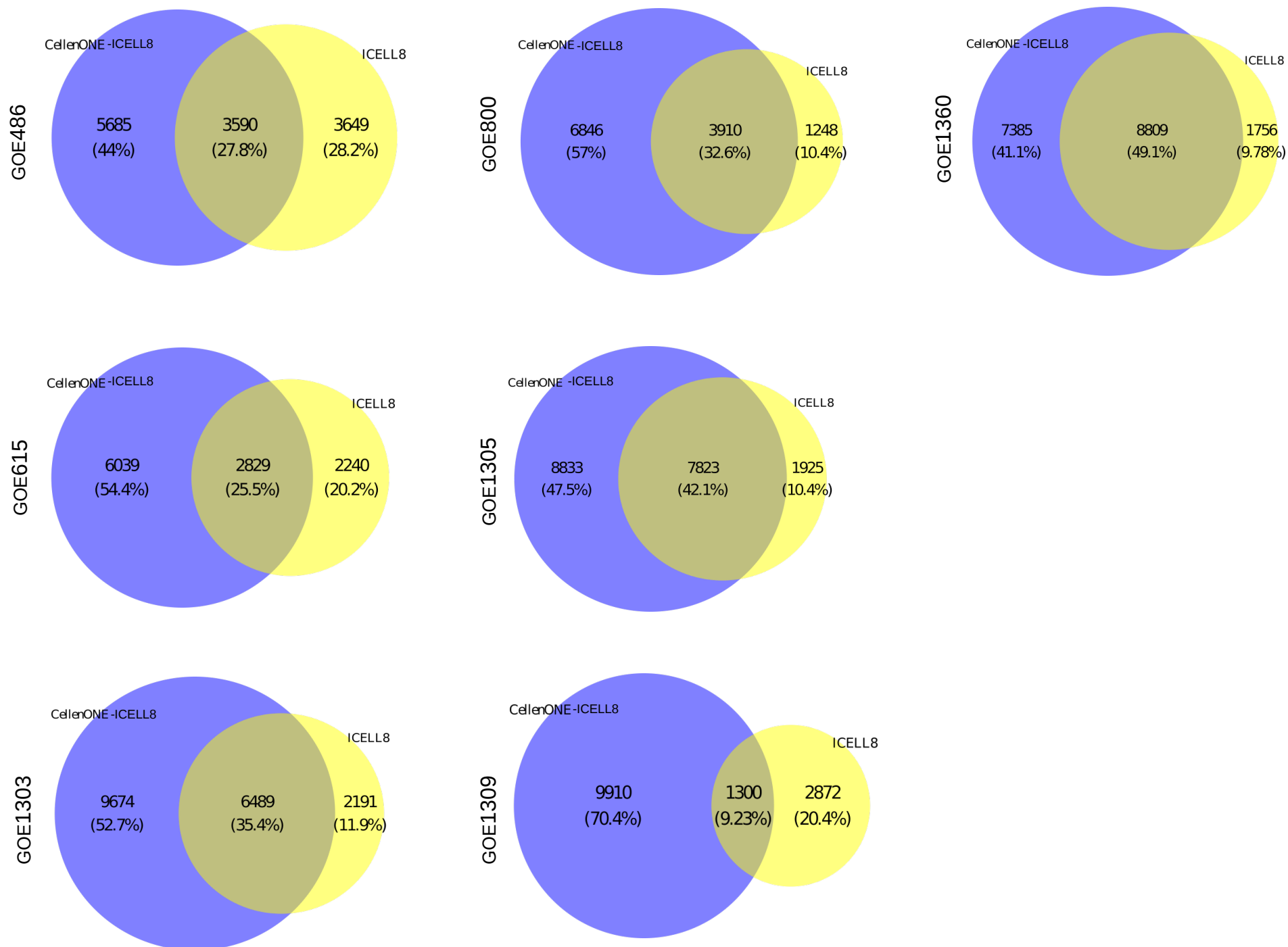
GOE1309



GOE1360

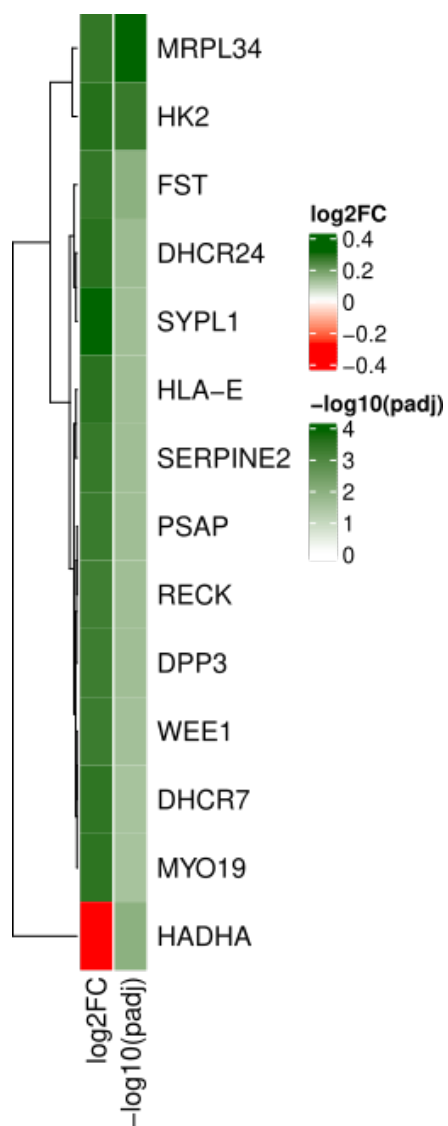


Supplementary Figure 3: Correlations of normalized expressions of the top 100 markers from samples in the scRNA-Seq platforms and bulk RNA-seq datasets, with the correlation coefficients indicated in the upper triangle.

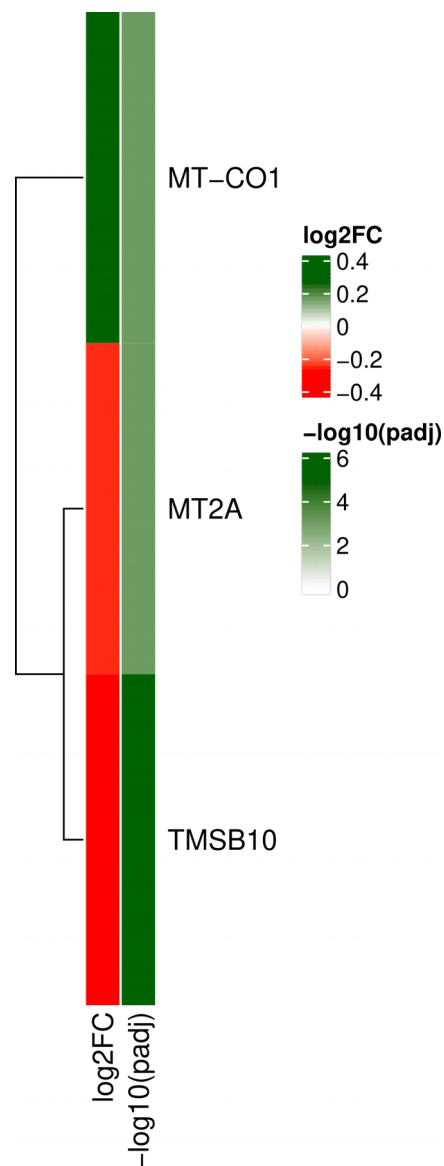


Supplementary Figure 4: Venn diagram of all significant markers detected for samples in both scRNA-Seq platforms.

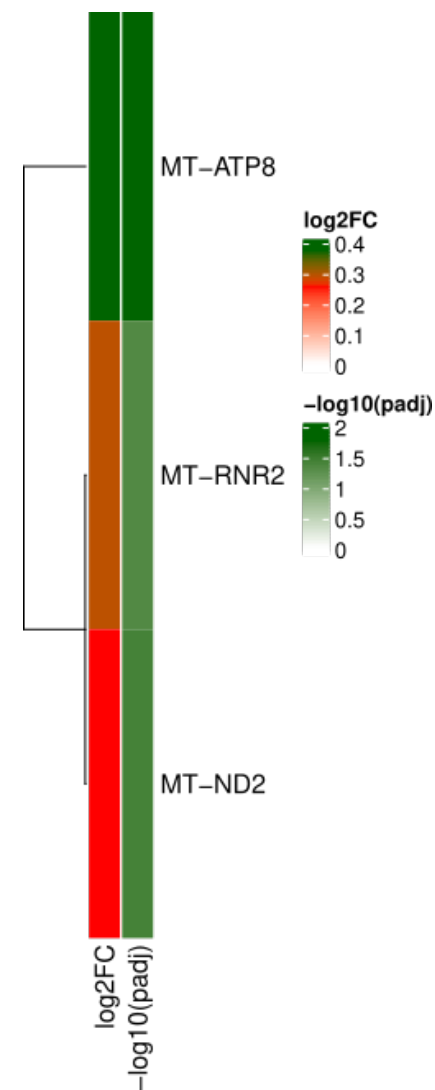
a)

MRPL34^{A74V}

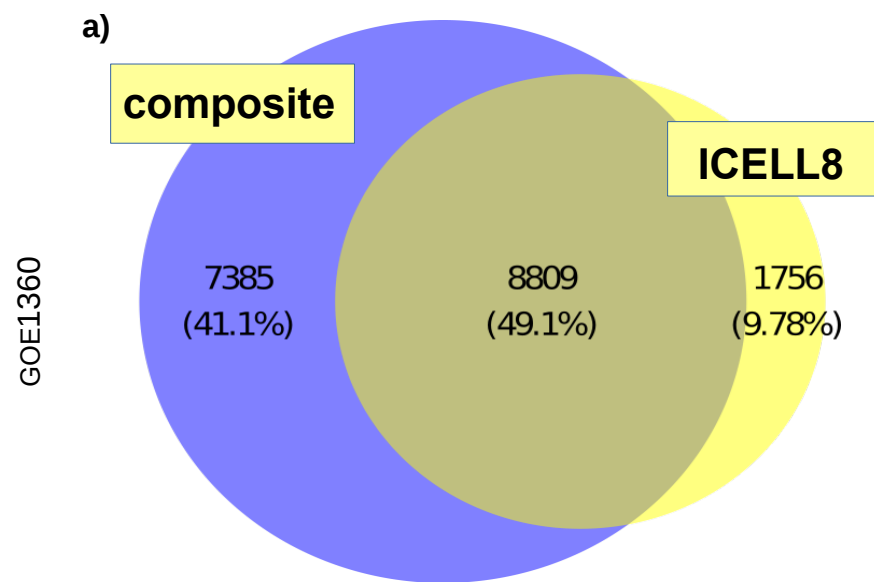
b)

MT-CO1^{A122T}

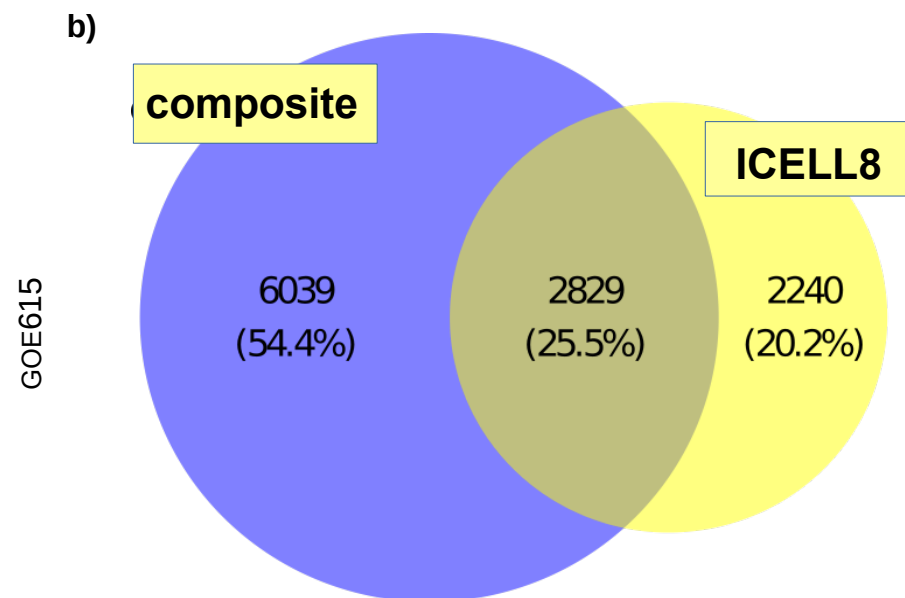
c)

MT-ND5^{T74I}

Supplementary Figure 6: Variant-associated expression signatures in samples (a) GOE247, (b) GOE800 and (c) GOE486. Heatmaps showing log₂FC and -log₁₀ of adjusted p-value for differentially expressed genes between mutant and non-mutant cells for (a) MRPL34^{A74V} variant in sample GOE247 (b) MT-CO1^{A122T} variant in sample GOE800 and (c) MT-ND5^{T74I} variant in sample GOE486.



GOE1360, MT-CYB ^{L236I}	Composite	ICELL8
Mitochondrial respiratory chain complex I	MT-ATP6, MT-ATP8, MT-ND2, MT-ND4, MT-CYB	MT-ATP6, MT-ATP8, MT-ND2, MT-ND4, MT-CYB
Mitochondrial proton-transporting ATP synthase complex		
Transcriptional regulation by MECP2	MET, SLC2A3, SGK1	MET, SLC2A3, SGK1



GOE615, DAXX ^{A486G}	Composite	ICELL8
Transcriptional regulation by TP53	CDKN1A, DAXX, CCNG1, DDIT4, CAPG, TINF2, PPP1CB	CDKN1A, DAXX, CCNG1, DDIT4, CAPG, TINF2, PPP1CB
DNA damage/telomere stress induced senescence	CDKN1A, DAXX	CDKN1A, DAXX
Alternative lengthening of telomeres		

Supplementary Figure 7: Venn diagram of all significant markers detected and regulated in both scRNA-Seq approaches indicating the most relevant genes connecting genetic regulation to phenotype found in both scRNA-Seq approaches (a) sample GOE1360, (b) sample GOE615