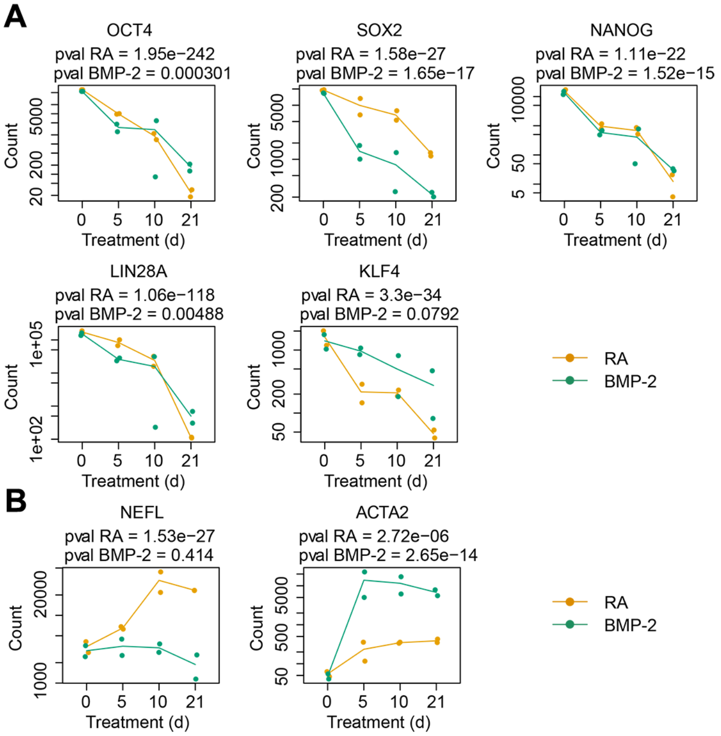
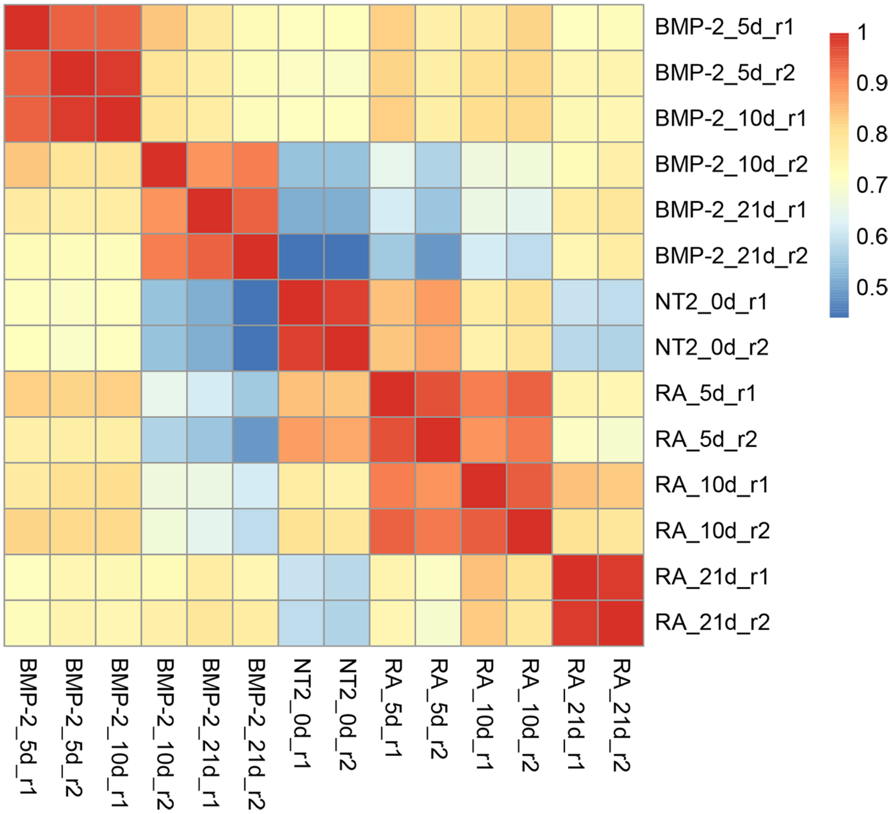
Supplementary Figure 1



Supporting Information Fig. S1. Transcriptional regulation of stem cells markers and lineage-specific genes during differentiation. *A,* Gradual shutdown of OCT4, SOX2, NANOG, LIN28A and KLF4 genes over differentiation of NT2 cells into neurons and muscle cells. *B,* NEFL and ACTA2 genes were upregulated during the neuronal and epithelial differentiation, respectively.

Supplementary Figure 2



Supporting Information Fig. S2. Spearman correlation distance of RNA RPKM from top 2000 highly variable genes.

sample_name	sample	fastq_name	treatment	day	replicate	Assigned	Unassigned_Ambiguity	Unassigned_NoFeatures	Assigned.p	Unassigned_Ambiguity.p	Unassigned_NoFeatures.p	percent_non_zero_genes
BMP-2-5-1	MD5R1	MD5R1_1.fq.gz	BMP-2	5	1	57594587	4234163	5826192	0.851	0.063	0.086	0.6456
BMP-2-5-2	MD5R2	MD5R2_1.fq.gz	BMP-2	5	2	63551060	4582833	8000563	0.835	0.06	0.105	0.6786
BMP-2-10-1	MD10R1	MD10R1_1.fq.gz	BMP-2	10	1	57223052	4307880	5338072	0.856	0.064	0.08	0.6499
BMP-2-10-2	MD10R2	MD10R2_1.fq.gz	BMP-2	10	2	49066318	3500812	5578384	0.844	0.06	0.096	0.644
BMP-2-21-1	MD21R1	MD21R1_1.fq.gz	BMP-2	21	1	52664006	3556318	6612348	0.838	0.057	0.105	0.6511
BMP-2-21-2	MD21R2	MD21R2_1.fq.gz	BMP-2	21	2	52318324	3430236	5395248	0.856	0.056	0.088	0.6429
NT2-0-1	NT2R1	NT2R1_1.fq.gz	NT2	0	1	50877250	3721760	6630658	0.831	0.061	0.108	0.6467
NT2-0-2	NT2R2	NT2R2_1.fq.gz	NT2	0	2	76307589	5594828	9009601	0.839	0.062	0.099	0.6502
RA-5-1	RD5R1	RD5R1_1.fq.gz	RA	5	1	49840958	3886661	4981513	0.849	0.066	0.085	0.6381
RA-5-2	RD5R2	RD5R2_1.fq.gz	RA	5	2	67624047	5090528	8216545	0.836	0.063	0.102	0.677
RA-10-1	RD10R1	RD10R1_1.fq.gz	RA	10	1	46217247	3581885	5859242	0.83	0.064	0.105	0.7059
RA-10-2	RD10R2	RD10R2_1.fq.gz	RA	10	2	61473430	4448407	9131715	0.819	0.059	0.122	0.7149
RA-21-1	RD21R3	RD21R3_1.fq.gz	RA	21	1	62268782	4840911	10494865	0.802	0.062	0.135	0.7357
RA-21-2	RD21R4	RD21R4_1.fq.gz	RA	21	2	70255788	5492259	10249361	0.817	0.064	0.119	0.7235

Supporting Information Table S1. Sample information for RNA-seq. The numbers of assigned and unassigned reads, as well as the percentage of genes with non-zero read counts from FeatureCounts, are reported.