

Table S1. Pluripotency related genes expression in hHFMSCs, adherent hHFMSCs<sup>OCT4</sup> and floating hHFMSCs<sup>OCT4</sup>.

Cell type	LEFTY2	SOX18	SEMA4D	POU3F2	POU5F1
hHFMSC_1	0	0	0	0	0.073
hHFMSC_2	0	0	0	0	0.020
hHFMSC_3	0	0	0	0	0.087
hHFMSC <sup>OCT4</sup> -adherent_1	23.1801	2.573	0.142	0.132	305.831
hHFMSC <sup>OCT4</sup> -adherent_2	21.978	3.509	0.094	0.062	375.245
hHFMSC <sup>OCT4</sup> -adherent_3	15.004	0.879	0.155	0.021	224.463
hHFMSC <sup>OCT4</sup> -floating_1	2.389	2.644	0.224	0.166	504.263
hHFMSC <sup>OCT4</sup> -floating_2	1.659	1.758	0.089	0.180	469.818
hHFMSC <sup>OCT4</sup> -floating_3	8.693	1.849	0.112	0.178	367.820

Table S2. Differentiation and development relative GO terms enriched of upregulated DEGs in adherent hHFMSCs<sup>OCT4</sup> versus hHFMSCs.

id	Term	Count	Genes	P-value	Enrichment score
GO:0046548	retinal rod cell development	3	NAGLU, TRPM1, RORB	0	8.1412
GO:0060351	cartilage development involved in endochondral bone morphogenesis	3	SHOX2, TRPV4, COL2A1	0	8.1412
GO:0061005	cell differentiation involved in kidney development	2	GLI3, GLIS2	0	8.1412
GO:0060538	skeletal muscle organ development	2	PAX3, CNTFR	0	8.1412
GO:0061153	trachea gland development	2	EDA, LEF1	0	8.1412
GO:0071599	otic vesicle development	2	AHI1, COL2A1	0	8.1412
GO:0061309	cardiac neural crest cell development involved in outflow tract morphogenesis	2	HES1, HAND2	0	8.1412
GO:0060873	anterior semicircular canal development	1	GLI3	0	8.1412
GO:0060875	lateral semicircular canal development	1	GLI3	0	8.1412
GO:1903010	regulation of bone development	1	GLI3	0	8.1412

*P*-value is a measurement of enrichment of the GO analysis.

Table S3. Differentiation and development relative GO terms enriched of upregulated DEGs in floating hHFMSCs<sup>OCT4</sup> versus adherent hHFMSCs<sup>OCT4</sup>.

id	Term	Count	Genes	P-value	Enrichment score
GO:0021541	ammon gyrus development	1	LRP8	0	23.8456
GO:2000287	positive regulation of myotome development	1	DMRT2	0	23.8456
GO:2000355	negative regulation of ovarian follicle	1	HYAL3	0	23.8456

	development				
GO:1903011	negative regulation of bone development	1	RGN	0	23.8456
GO:0072076	nephrogenic mesenchyme development	1	FOXD1	0	23.8456
GO:0072213	metanephric capsule development	1	FOXD1	0	23.8456
GO:0043009	chordate embryonic development	1	CENPU	0	23.8456
GO:0043045	DNA methylation involved in embryo development	2		0.0024	11.9228
			ZFP57, TRIM28		
GO:0001890	placenta development	4	CCNF, PHLDA2, ASCL2, LHX4	0.0083	4.7691
GO:0003431	growth plate cartilage chondrocyte development	1		0.0083	11.9228
			POC1A		

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*P*-value is a measurement of enrichment of the GO analysis.