Stem cell Information			
Stem cell line	**CMC-iPSC-011**	Insitute	KSCR
Cell type	**hiPSC**	Banking year	2017
Banking status	**PCB**		
Passage	**p26**		

Single Nucleotide Variation(SNV), short Insert/Deletion(INDEL) analysis

Experiment of data Analysis

Whole Exome Sequencing

Instrument	Illumina HiSeq2500	Analysis program	GATK (v3.5)
Exome Kit	Agilent SureSelectXT V5+UTR	Analysis document	SOP-BI-01
Read length (bp)	101x2	Reference	hg19

Statistics

Total reads	192,696,964
Total yield (Gbp)	19.40
Throughput mean depth(X)	258
On-targe reads	99,790,708
On-target depth(X)	135

Result of data Analysis

SNV, INDEL call

			Stemness	Differenciation
Total variant		102,380		
	SNV	92,395		
	DEL	4,978		
	INS	5,007		
Coding regions		22,581	12	14
	Synonymous	10,361	-	-
	Missense	9,775	12	14
	Inframeshift	172	-	-
	Frameshift	138	-	-
	Nonsense	121	-	-
	SpliceRegion	2,014	-	-

* Variant calling condition: GATK, DP(>=10)+MQ(>=58)+AF(>=0.3)

Stemness gene

	Chr	Chr_start	dbsnp135_full	Ref	Alt	Type	Hom_het	Change	Gene	HGVS_C	HGVS_P	비고
1	4	89061114	rs2231137	C	T	SNP	`0/1	missense_variant	ABCG2	c.34G>A	`p.Val12Met	NM_001257386.1
2	4	89052323	rs2231142	G	T	SNP	`0/1	missense_variant	ABCG2	c.421C>A	`p.Gln141Lys	NM_001257386.1
3	1	21894735	rs3200254	T	C	SNP	`1/1	missense_variant	ALPL	c.556T>C	`p.Tyr186His	NM_001177520.1
4	13	28537317	rs1805107	G	A	SNP	`1/1	missense_variant	CDX2	c.877C>T	`p.Pro293Ser	NM_001265.4
5	3	109052732	rs3762648	T	C	SNP	`0/1	missense_variant	DPPA4	c.163A>G	`p.Ile55Val	NM_018189.3
6	2	47601106	rs1126497	T	C	SNP	`0/1	missense_variant	EPCAM	c.344T>C	`p.Met115Thr	NM_002354.2
7	1	63789015	rs2274188	G	T	SNP	`0/1	missense_variant	FOXD3	c.286G>T	`p.Val96Leu	NM_012183.2
8	1	226076669	rs41310561	C	T	SNP	`0/1	missense_variant	LEFTY1	c.98G>A	`p.Arg33Gln	NM_020997.3
9	7	131195712	rs12670788	G	A	SNP	`1/1	missense_variant	PODXL	c.581C>T	`p.Ser194Leu	NM_005397.3
10	7	131195959	rs3735035	C	T	SNP	`1/1	missense_variant	PODXL	c.334G>A	`p.Gly112Ser	NM_005397.3
11	1	12186058	rs2230625	A	G	SNP	`0/1	missense_variant	TNFRSF8	c.871A>G	`p.Ser291Gly	NM_001281430.2
12	1	12175729	rs1763642	C	T	SNP	`1/1	missense_variant	TNFRSF8	c.556C>T	`p.Arg186Cys	NM_001281430.2

Differenciation gene

	Chr	Chr_start	dbsnp135_full	Ref	Alt	Type	Hom_het	Change	Gene	HGVS_C	HGVS_P	비고
1	1	94544234	rs3112831	T	C	SNP	`0/1	missense_variant	ABCA4	c.1268A>G	`p.His423Arg	NM_000350.2
2	18	59174759	rs1943330	C	A	SNP	`0/1	missense_variant	CDH20	c.983C>A	`p.Pro328His	NM_031891.2
3	16	66432423	rs1049970	T	C	SNP	`0/1	missense_variant	CDH5	c.1550T>C	`p.Ile517Thr	NM_001795.4
4	13	28537317	rs1805107	G	A	SNP	`1/1	missense_variant	CDX2	c.877C>T	`p.Pro293Ser	NM_001265.4
5	14	38061742	rs7144658	C	T	SNP	`1/1	missense_variant	FOXA1	c.247G>A	`p.Ala83Thr	NM_004496.3
6	1	226076669	rs41310561	C	T	SNP	`0/1	missense_variant	LEFTY1	c.98G>A	`p.Arg33Gln	NM_020997.3
7	2	171260787	rs6736609	G	A	SNP	`1/1	missense_variant	MYO3B	c.2308G>A	`p.Val770Ile	NM_001083615.3
8	2	171356274	rs10185178	G	A	SNP	`1/1	missense_variant	MYO3B	c.3245G>A	`p.Arg1082Lys	NM_001083615.3
9	2	171225841	rs4668246	A	G	SNP	`0/1	missense_variant	MYO3B	c.925A>G	`p.Lys309Glu	NM_001083615.3
10	10	72195439	rs1904589	T	C	SNP	`1/1	missense_variant	NODAL	c.494A>G	`p.His165Arg	NM_018055.4
11	4	71068489	rs3196714	T	C	SNP	`0/1	missense_variant	ODAM	c.665T>C	`p.Ile222Thr	NM_017855.3
12	14	73727509	rs177389	T	G	SNP	`0/1	missense_variant	PAPLN	c.1997T>G	`p.Met666Arg	NM_173462.3
13	14	73711394	rs2280792	A	G	SNP	`0/1	missense_variant	PAPLN	c.97A>G	`p.Ser33Gly	NM_173462.3
14	11	31814819	.	C	T	SNP	`0/1	missense_variant	PAX6	c.1199G>A	`p.Ser400Asn	NM_001310159.1