Stem cell Information			
Stem cell line	**CMC-iPSC-005**	Insitute	KSCR
Cell type	**hiPSC**	Banking year	2017
Banking status	**PCB**		
Passage	**p20**		

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	178,280,472
Total yield (Gbp)	18.0
Throughput mean depth(X)	240
On-targe reads	102,371,128
On-target depth(X)	139

Result of data Analysis

SNV, INDEL call

			Stemness	Differenciation
Total variant		103,098		
	SNV	93,085		
	DEL	5,015		
	INS	4,998		
Coding regions		22,516	12	17
	Synonymous	10,405	-	-
	Missense	9,739	12	17
	Inframeshift	152	-	-
	Frameshift	133	-	-
	Nonsense	120	-	-
	SpliceRegion	1,967	-	-

* 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	Het	missense	ABCG2	c.34G>A	`p.Val12Met	NM_001257386.1
2	4	89052323	rs2231142	G	T	SNP	Het	missense	ABCG2	c.421C>A	`p.Gln141Lys	NM_001257386.1
3	1	21894735	rs3200254	T	C	SNP	Het	missense	ALPL	c.556T>C	`p.Tyr186His	NM_001177520.1
4	13	28537317	rs1805107	G	A	SNP	Hom	missense	CDX2	c.877C>T	`p.Pro293Ser	NM_001265.4
5	3	109052732	rs3762648	T	C	SNP	Het	missense	DPPA4	c.163A>G	`p.Ile55Val	NM_018189.3
6	2	47601106	rs1126497	T	C	SNP	Hom	missense	EPCAM	c.344T>C	`p.Met115Thr	NM_002354.2
7	2	47604176	rs74531854	C	T	SNP	Het	missense	EPCAM	c.515C>T	`p.Thr172Met	NM_002354.2
8	12	7842932	rs12819884	C	T	SNP	Hom	missense	GDF3	c.637G>A	`p.Gly213Arg	NM_020634.1
9	7	131193739	rs3212298	C	T	SNP	Het	missense	PODXL	c.976G>A	`p.Val326Ile	NM_005397.3
10	6	31133943	rs3130932	C	A	SNP	Hom	missense	POU5F1.7	c.2G>T	`p.Arg1Met	NM_001285987.1.4
11	1	12175729	rs1763642	C	T	SNP	Hom	missense	TNFRSF8	c.556C>T	`p.Arg186Cys	NM_001281430.2
12	10	135044009	rs11599284	G	A	SNP	Het	missense	UTF1	c.217G>A	`p.Gly73Arg	NM_003577.2

Differenciation gene

	Chr	Chr_start	dbsnp135_full	Ref	Alt	Type	Hom_het	Change	Gene	HGVS_C	HGVS_P	비고
1	16	66434892	.	A	G	SNP	Het	missense	CDH5	c.1810A>G	`p.Ile604Val	NM_001795.4
2	16	66432423	rs1049970	T	C	SNP	Het	missense	CDH5	c.1550T>C	`p.Ile517Thr	NM_001795.4
3	13	28537317	rs1805107	G	A	SNP	Hom	missense	CDX2	c.877C>T	`p.Pro293Ser	NM_001265.4
4	12	48367976	rs2070739	C	T	SNP	Hom	missense	COL2A1	c.4006G>A	`p.Gly1336Ser	NM_033150.2
5	14	38061742	rs7144658	C	T	SNP	Hom	missense	FOXA1	c.247G>A	`p.Ala83Thr	NM_004496.3
6	4	57516896	rs4371677	G	A	SNP	Het	missense	HOPX	c.281C>T	`p.Pro94Leu	NM_001145460.1
7	2	171260787	rs6736609	G	A	SNP	Hom	missense	MYO3B	c.2308G>A	`p.Val770Ile	NM_001083615.3
8	2	171356274	rs10185178	G	A	SNP	Hom	missense	MYO3B	c.3245G>A	`p.Arg1082Lys	NM_001083615.3
9	2	171225841	rs4668246	A	G	SNP	Het	missense	MYO3B	c.925A>G	`p.Lys309Glu	NM_001083615.3
10	10	72195439	rs1904589	T	C	SNP	Hom	missense	NODAL	c.494A>G	`p.His165Arg	NM_018055.4
11	14	73727509	rs177389	T	G	SNP	Hom	missense	PAPLN	c.1997T>G	`p.Met666Arg	NM_173462.3
12	14	73711394	rs2280792	A	G	SNP	Hom	missense	PAPLN	c.97A>G	`p.Ser33Gly	NM_173462.3
13	14	73727926	rs2242616	G	C	SNP	Hom	missense	PAPLN	c.2088G>C	`p.Gln696His	NM_173462.3
14	14	73733285	rs61745771	G	A	SNP	Hom	missense	PAPLN	c.3259G>A	`p.Ala1087Thr	NM_173462.3
15	6	31133943	rs3130932	C	A	SNP	Hom	missense	POU5F1.7	c.2G>T	`p.Arg1Met	NM_001285987.1.4
16	17	64783081	rs6504459	G	A	SNP	Hom	missense	PRKCA	c.1702G>A	`p.Val568Ile	NM_002737.2
17	8	55372118	.	A	T	SNP	Het	missense	SOX17	c.808A>T	`p.Met270Leu	NM_022454.3