Stem cell Information			
Stem cell line	**NCRM5AS-iCAGcGFP.c9**	Insitute	KSCR
Cell type	**hiPSC**	Banking year	2015
Banking status	**PCB**		
Passage	**p70**		

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

Experiment of data Analysis

Whole Exome Sequencing

Instrument	Illumina HiSeq2500	Analysis program	GATK (haplotypeCaller, v3.2)
Exome Kit	Agilent SureSelectXT V5+UTR	Analysis document	SOP-BI-01
Read length (bp)	101x2	Reference	hg19

Statistics

Total reads	153,790,292
Total yield (Gbp)	15.4
Throughput mean depth(X)	208
On-targe reads	76,023,867
On-target depth(X)	103

Result of data Analysis

SNV, INDEL call

			Stemness	Differenciation
Total variant		46,497		
	SNV	43,506		
	DEL	1,469		
	INS	1,522		
Coding regions		10,255	8	11
	Inframeshift	185	1	1
	Frameshift	185	0	0
	Missense	9,974	7	10
	Nonsense	76	0	0
	Synonymous	10,422		

* 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	chr1	12175729	rs1763642	C	T	SNP	Homozygous	missense_variant	TNFRSF8	c.889C>T	p.Arg297Cys	NM_001243.4
2	chr12	7842932	819884;rs386526	C	T	SNP	Heterozygous	missense_variant	GDF3	c.637G>A	p.Gly213Arg	NM_020634.1
3	chr13	28537317	rs1805107	G	A	SNP	Homozygous	missense_variant	CDX2	c.877C>T	p.Pro293Ser	NM_001265.4
4	chr3	109052732	rs3762648	T	C	SNP	Homozygous	missense_variant	DPPA4	c.163A>G	p.Ile55Val	NM_018189.3
5	chr4	55593464	rs3822214	A	C	SNP	Heterozygous	missense_variant	KIT	c.1621A>C	p.Met541Leu	NM_000222.2
6	chr5	98192164	rs138635992	AAGG	A	DEL	Heterozygous	inframe_deletion	CHD1	5050_5052delC	p.Pro1684del	NM_001270.2
7	chr7	131195712	rs12670788	G	A	SNP	Heterozygous	missense_variant	PODXL	c.581C>T	p.Ser194Leu	NM_001018111.2
8	chr7	131195959	rs3735035	C	T	SNP	Heterozygous	missense_variant	PODXL	c.334G>A	p.Gly112Ser	NM_001018111.2

Differenciation gene

	Chr	Chr_start	dbsnp135_full	Ref	Alt	Type	Hom_het	Change	Gene	HGVS_C	HGVS_P	비고
1	chr10	72195439	rs1904589	T	C	SNP	Heterozygous	missense_variant	NODAL	c.494A>G	p.His165Arg	NM_018055.4
2	chr12	48391657	rs34392760	T	A	SNP	Heterozygous	missense_variant	COL2A1	c.426A>T	p.Glu142Asp	NM_001844.4
3	chr13	28537317	rs1805107	G	A	SNP	Homozygous	missense_variant	CDX2	c.877C>T	p.Pro293Ser	NM_001265.4
4	chr14	73711394	rs2280792	A	G	SNP	Heterozygous	missense_variant	PAPLN	c.97A>G	p.Ser33Gly	NM_173462.3
5	chr14	73717720	rs741842	G	A	SNP	Heterozygous	missense_variant	PAPLN	c.571G>A	p.Ala191Thr	NM_173462.3
6	chr14	73727509	rs177389	T	G	SNP	Heterozygous	missense_variant	PAPLN	c.1997T>G	p.Met666Arg	NM_173462.3
7	chr16	66432423	049970;rs386513	T	C	SNP	Heterozygous	missense_variant	CDH5	c.1550T>C	p.Ile517Thr	NM_001795.4
8	chr20	43042364	rs1800961	C	T	SNP	Heterozygous	missense_variant	HNF4A	c.416C>T	p.Thr139Ile	NM_000457.4
9	chr3	27763427	874198;rs368178	G	GCGGCGC	INS	Heterozygous	inframe_insertion	EOMES	58_359insGCGC	119_Ala120insG	NM_001278182.1
10	chr6	106547372	rs811925	C	G	SNP	Heterozygous	missense_variant	PRDM1	c.609C>G	p.Asp203Glu	NM_001198.3
11	chr8	97614661	rs1042381	T	A	SNP	Heterozygous	missense_variant	SDC2	c.211T>A	p.Ser71Thr	NM_002998.3