Stem cell Information			
Stem cell line	**hUSiPS2**	Insitute	KSCR
Cell type	**hiPSC**	Banking year	2015
Banking status	**MCB**		
Passage	**p25**		

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	164,461,740
Total yield (Gbp)	16.44
Throughput mean depth(X)	222
On-targe reads	101,267,068
On-target depth(X)	137

Result of data Analysis

SNV, INDEL call

			Stemness	Differenciation
Total variant		47,525		
	SNV	44,174		
	DEL	1,682		
	INS	1,669		
Coding regions		21,030	8	10
	Inframeshift	176	0	0
	Frameshift	172	0	0
	Missense	10,043	8	10
	Nonsense	92	0	0
	Synonymous	10,547		

* 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	21894735	rs3200254	T	C	SNP	Heterozygous	missense_variant	ALPL	c.787T>C	p.Tyr263His	NM_000478.4
2	chr1	12175729	rs1763642	C	T	SNP	Homozygous	missense_variant	TNFRSF8	c.889C>T	p.Arg297Cys	NM_001243.4
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	Heterozygous	missense_variant	DPPA4	c.163A>G	p.Ile55Val	NM_018189.3
5	chr4	89052323	rs2231142	G	T	SNP	Heterozygous	missense_variant	ABCG2	c.421C>A	p.Gln141Lys	NM_004827.2
6	chr4	55593464	rs3822214	A	C	SNP	Heterozygous	missense_variant	KIT	c.1621A>C	p.Met541Leu	NM_000222.2
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	chr1	94574258	rs201150919	T	A	SNP	Heterozygous	missense_variant	ABCA4	c.317A>T	p.Tyr106Phe	NM_000350.2
2	chr10	72195439	rs1904589	T	C	SNP	Homozygous	missense_variant	NODAL	c.494A>G	p.His165Arg	NM_018055.4
3	chr12	48367976	rs2070739	C	T	SNP	Heterozygous	missense_variant	COL2A1	c.4213G>A	p.Gly1405Ser	NM_001844.4
4	chr13	28537317	rs1805107	G	A	SNP	Homozygous	missense_variant	CDX2	c.877C>T	p.Pro293Ser	NM_001265.4
5	chr14	73711394	rs2280792	A	G	SNP	Heterozygous	missense_variant	PAPLN	c.97A>G	p.Ser33Gly	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	Homozygous	missense_variant	CDH5	c.1550T>C	p.Ile517Thr	NM_001795.4
8	chr18	59174759	rs1943330	C	A	SNP	Heterozygous	missense_variant	CDH20	CDH20	p.Pro328His	NM_031891.2
9	chr2	234863788	rs7593557	G	A	SNP	Heterozygous	missense_variant	TRPM8	c.1256G>A	p.Ser419Asn	NM_024080.4
10	chr8	97614661	rs1042381	T	A	SNP	Heterozygous	missense_variant	SDC2	c.211T>A	p.Ser71Thr	NM_002998.3