Stem cell Information			
Stem cell line	**CHA-hES15**	Insitute	KSCR
Cell type	**hESC**	Banking year	2016
Banking status	**DCB**		
Passage	**p28**		

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

Experiment of data Analysis

Whole Exome Sequencing

Instrument	Illumina HiSeq2500	Analysis program	GATK (UnifiedCaller, v2.3)
Exome Kit	Agilent SureSelectXT V5+UTR	Analysis document	SOP-BI-01
Read length (bp)	101x2	Reference	hg19

Statistics

Total reads	149,706,296
Total yield (Gbp)	15.1
Throughput mean depth(X)	202
On-targe reads	130,279,595
On-target depth(X)	117

Result of data Analysis

SNV, INDEL call

			Stemness	Differenciation
Total variant		75,973		
	SNV	68,095		
	DEL	4,018		
	INS	3,860		
Coding regions		20,907	11	17
	Inframeshift	191	0	1
	Frameshift	162	0	0
	Missense	9,962	10	16
	Nonsense	77	0	0
	Synonymous	10,515		

* 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	chr1	12186058	rs2230625	A	G	SNP	Heterozygous	missense_variant	TNFRSF8	c.1204A>G	p.Ser402Gly	NM_001243.4
3	chr1	21894735	rs3200254	T	C	SNP	Heterozygous	missense_variant	ALPL	c.787T>C	p.Tyr263His	NM_000478.4
4	chr1	226076669	rs41310561	C	T	SNP	Heterozygous	missense_variant	LEFTY1	c.98G>A	p.Arg33Gln	NM_020997.3
5	chr3	109052732	rs3762648	T	C	SNP	Heterozygous	missense_variant	DPPA4	c.163A>G	p.Ile55Val	NM_018189.3
6	chr4	89061114	rs2231137	C	T	SNP	Heterozygous	missense_variant	ABCG2	c.34G>A	p.Val12Met	NM_004827.2
7	chr5	98192164	rs138635992	AAGG	A	DEL	Heterozygous	inframe_deletion	CHD1	5050_5052delC	p.Pro1684del	NM_001270.2
8	chr7	131195712	rs12670788	G	A	SNP	Heterozygous	missense_variant	PODXL	c.581C>T	p.Ser194Leu	NM_001018111.2
9	chr7	131195959	rs3735035	C	T	SNP	Heterozygous	missense_variant	PODXL	c.334G>A	p.Gly112Ser	NM_001018111.2
10	chr12	7842932	819884;rs386526	C	T	SNP	Heterozygous	missense_variant	GDF3	c.637G>A	p.Gly213Arg	NM_020634.1
11	chr13	28537317	rs1805107	G	A	SNP	Heterozygous	missense_variant	CDX2	c.877C>T	p.Pro293Ser	NM_001265.4

Differenciation gene

	Chr	Chr_start	dbsnp135_full	Ref	Alt	Type	Hom_het	Change	Gene	HGVS_C	HGVS_P	비고
1	chr1	94544234	rs3112831	T	C	SNP	Heterozygous	missense_variant	ABCA4	c.1268A>G	p.His423Arg	NM_000350.2
2	chr1	226076669	rs41310561	C	T	SNP	Heterozygous	missense_variant	LEFTY1	c.98G>A	p.Arg33Gln	NM_020997.3
3	chr2	171225841	rs4668246	A	G	SNP	Homozygous	missense_variant	MYO3B	c.925A>G	p.Lys309Glu	NM_138995.4
4	chr2	171260787	rs6736609	G	A	SNP	Heterozygous	missense_variant	MYO3B	c.2308G>A	p.Val770Ile	NM_138995.4
5	chr2	171356274	rs10185178	G	A	SNP	Homozygous	missense_variant	MYO3B	c.3245G>A	p.Arg1082Lys	NM_138995.4
6	chr2	234863788	rs7593557	G	A	SNP	Heterozygous	missense_variant	TRPM8	c.1256G>A	p.Ser419Asn	NM_024080.4
7	chr3	27763427	2715125;rs18741	G	C	SNP	Heterozygous	missense_variant	EOMES	c.359C>G	p.Ala120Gly	NM_001278182.1
8	chr3	27763427	874198;rs368178	G	GCGGCGC	INS	Homozygous	inframe_insertion	EOMES	58_359insGCGG	119_Ala120insG	NM_001278182.1
9	chr4	55139771	rs35597368	T	C	SNP	Heterozygous	missense_variant	PDGFRA	c.1432T>C	p.Ser478Pro	NM_006206.4
10	chr4	57516896	rs4371677	G	A	SNP	Heterozygous	missense_variant	HOPX	c.281C>T	p.Pro94Leu	NM_001145460.1
11	chr8	97614625	rs3816208	G	A	SNP	Heterozygous	missense_variant&splice_region_variant	SDC2	c.175G>A	p.Ala59Thr	NM_002998.3
12	chr10	72195439	rs1904589	T	C	SNP	Homozygous	missense_variant	NODAL	c.494A>G	p.His165Arg	NM_018055.4
13	chr13	28537317	rs1805107	G	A	SNP	Heterozygous	missense_variant	CDX2	c.877C>T	p.Pro293Ser	NM_001265.4
14	chr14	73711394	rs2280792	A	G	SNP	Heterozygous	missense_variant	PAPLN	c.97A>G	p.Ser33Gly	NM_173462.3
15	chr14	73727509	rs177389	T	G	SNP	Heterozygous	missense_variant	PAPLN	c.1997T>G	p.Met666Arg	NM_173462.3
16	chr14	73729069	rs148072678	C	T	SNP	Heterozygous	missense_variant	PAPLN	c.2176C>T	p.Arg726Trp	NM_173462.3
17	chr16	66432423	049970;rs386513	T	C	SNP	Homozygous	missense_variant	CDH5	c.1550T>C	p.Ile517Thr	NM_001795.4