Stem cell Information			
Stem cell line	**SNU-hES31**	Insitute	KSCR
Cell type	**hESC**	Banking year	2014
Banking status	**DCB**		
Passage	**p34**		

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

Experiment of data Analysis

Whole Exome Sequencing

Instrument	Illumina HiSeq2500	Analysis program	GATK (UnifiedGenotyper, v2.3)
Exome Kit	Agilent SureSelectXT V4+UTR	Analysis document	SOP-BI-01
Read length (bp)	101x2	Reference	hg19

Statistics

Total reads	157,150,812
Total yield (Gbp)	15.7
Throughput mean depth(X)	210
On-targe reads	116,493,973
On-target depth(X)	139

Result of data Analysis

SNV, INDEL call

			Stemness	Differenciation
Total variant		45,091		
	SNV	41,989		
	DEL	1,560		
	INS	1,542		
Coding regions		20,255	8	10
	Inframeshift	183	0	1
	Frameshift	178	0	0
	Missense	9,640	8	9
	Nonsense	76	0	0
	Synonymous	10,178		

* 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	chr3	109052732	rs3762648	T	C	SNP	Homozygous	missense_variant	DPPA4	c.163A>G	p.Ile55Val	NM_018189.3
4	chr4	89052323	rs2231142	G	T	SNP	Heterozygous	missense_variant	ABCG2	c.421C>A	p.Gln141Lys	NM_004827.2
5	chr7	131195712	rs12670788	G	A	SNP	Homozygous	missense_variant	PODXL	c.581C>T	p.Ser194Leu	NM_001018111.2
6	chr7	131195959	rs3735035	C	T	SNP	Homozygous	missense_variant	PODXL	c.334G>A	p.Gly112Ser	NM_001018111.2
7	chr13	28537317	rs1805107	G	A	SNP	Homozygous	missense_variant	CDX2	c.877C>T	p.Pro293Ser	NM_001265.4
8	chr14	76905712	rs143477571	A	G	SNP	Heterozygous	missense_variant	ESRRB	c.16A>G	p.Arg6Gly	NM_004452.3

Differenciation gene

	Chr	Chr_start	dbsnp135_full	Ref	Alt	Type	Hom_het	Change	Gene	HGVS_C	HGVS_P	비고
1	chr1	94496053	rs1800549	G	A	SNP	Heterozygous	missense_variant	ABCA4	c.4283C>T	p.Thr1428Met	NM_000350.2
2	chr2	234863788	rs7593557	G	A	SNP	Heterozygous	missense_variant	TRPM8	c.1256G>A	p.Ser419Asn	NM_024080.4
3	chr3	27763427	874198;rs368178	G	GCGGCGC	INS	Homozygous	inframe_insertion	EOMES	c.358_359insG	p.Ala119_Ala12	NM_001278182.1
4	chr6	106536253	rs2185379	G	A	SNP	Heterozygous	missense_variant	PRDM1	c.220G>A	p.Gly74Ser	NM_001198.3
5	chr6	106554373	rs201512476	A	G	SNP	Heterozygous	missense_variant&splice_reg	PRDM1	c.1901A>G	p.Gln634Arg	NM_001198.3
6	chr8	97614625	rs3816208	G	A	SNP	Heterozygous	missense_variant&splice_reg	SDC2	c.175G>A	p.Ala59Thr	NM_002998.3
7	chr10	72195439	rs1904589	T	C	SNP	Homozygous	missense_variant	NODAL	c.494A>G	p.His165Arg	NM_018055.4
8	chr13	28537317	rs1805107	G	A	SNP	Homozygous	missense_variant	CDX2	c.877C>T	p.Pro293Ser	NM_001265.4
9	chr14	73727509	rs177389	T	G	SNP	Heterozygous	missense_variant	PAPLN	c.1997T>G	p.Met666Arg	NM_173462.3
10	chr16	66432423	049970;rs386513	T	C	SNP	Homozygous	missense_variant	CDH5	c.1550T>C	p.Ile517Thr	