SUPPLEMENTARY TABLE S2. QUALITY CONTROL STATISTICS FOR DEEP SEQUENCING

Treatment-biological replicate	*Bar code*	*Raw reads*	*Trimmed reads*	*Reads that passed filter*	*Adaptor trimmed reads*	*No. of clusters after elimination of contaminants*	*Percentage of clusters to be aligned to custom database*	*Percentage of reads with one mismatch (index)*	*Percentage of reads with ≥ Q30 bases (PF)*	*No. of clusters that aligned to custom database*	*Percentage of reads that aligned to custom database*	*Normalization factor*
IVV-1	CGATGT	32598850	30613650	29535544	27341339	21027029	64.5	1.4	88.1	11991977	57.0	1.2
IVV-2	AGTCAA	29793359	28438737	27802444	26551191	18436162	61.9	1.5	92.0	10603224	57.5	1.2
IVV-3	CGATGT	26876728	25550604	24823970	23217360	16613297	61.8	1.4	89.6	10442662	62.9	1.2
IVV-4	AGTCAA	17134304	15808972	15414436	10349527	6707522	39.1	1.9	85.9	2303454	34.3	5.5
IVF-1	TGACCA	26824559	24950288	23977905	21015672	15408959	57.4	2.0	86.4	9327788	60.5	1.5
IVF-2	AGTTCC	27779013	26357327	25704109	23477196	16188889	58.3	1.7	90.7	9541494	58.9	1.4
IVF-3	TGACCA	21881741	20647163	20001561	17881148	14447337	66	2.0	88.6	8539187	59.1	1.5
IVF-4	AGTTCC	19149595	18340695	17985493	14808331	10902272	56.9	1.7	89.6	5385298	49.4	2.3
SCNT (No HDACi)-1	ACAGTG	31228786	29422831	28452531	27712154	18690616	59.9	1.5	90.0	10720264	57.4	1.3
SCNT (No HDACi)-2	ATGTCA	27645052	26109546	25419782	22085706	15612588	56.5	1.7	89.4	8627996	55.3	1.4
SCNT (No HDACi)-3	ACAGTG	27009999	25641434	24933643	24013750	18160023	67.2	1.5	90.6	11206656	61.7	1.2
SCNT (No HDACi)-4	ATGTCA	19227656	18405364	18061551	16023185	10570827	55	1.6	91.6	5644160	53.4	2.2
SCNT-ISAHA-1	GCCAAT	29552589	27667301	26717420	26231546	19940709	67.5	1.9	90.0	4282252	21.5	2.1
SCNT-ISAHA-2	CCGTCC	23064651	21811592	21243715	20040497	14995986	65	1.8	90.6	9256350	61.7	1.4
SCNT-ISAHA-3	GCCAAT	31525066	29722167	28852724	28460363	23110278	73.3	1.9	91.1	10657692	46.1	1.3
SCNT-ISAHA-4	CCGTCC	23662743	22591062	22155107	21017262	15228220	64.4	1.7	92.9	5983358	39.3	2.3
SCNT(SAHA)-1	CAGATC	34301495	32204211	31117401	30416697	23065124	67.2	1.8	90.0	11872741	51.5	1.2
SCNT(SAHA)-2	GTCCGC	31786929	30154944	29428549	28470037	20087884	63.2	3.8	91.8	12554050	62.5	1.0
SCNT(SAHA)-3	CAGATC	26290456	24897741	24195499	23452477	19110436	72.7	1.7	90.8	12892505	67.5	1.1
SCNT(SAHA)-4	GTCCGC	15967702	15115938	14774401	10985400	7911761	49.5	3.5	87.5	4048854	51.2	3.3
SCNT(SCRIPTAID)-1	CTTGTA	30620935	28687613	27623144	24578740	18747904	61.2	1.2	87.8	7153506	38.2	2.1
SCNT(SCRIPTAID)-3	CTTGTA	31549878	29882255	29037432	27698666	21302383	67.5	1.1	90.4	13159596	61.8	1.0
SCNT(SCRIPTAID)-4	GTGAAA	24622616	23154793	22705450	21844300	14243636	57.8	1.2	93.3	7732349	54.3	1.8

IVV, *in vivo* blastocyst stage; IVF, *in vitro* fertilization; SCNT, somatic cell nuclear transfer; HDACi, histone deacetylase inhibitor; ISAHA, 4-iodo-suberoylanilide hydroxamic acid; SAHA, suberoylanilide hydroxamic acid.