Supplementary Table 1. Sequencing and mapping summary

Cell line	hESC		Fibro		hESC-Fibro	
Description	undifferentiated hESC		neonatal foreskin fibroblast		hESC differentiated into fibroblast-like cells	
# of runs	6		5		6	
run type	2x 51, 2x76 mix		2x 51, 2x76, 2x99 mix		2x 51, 2x76 mix	
	reads	bases (Gb)	reads	bases (Gb)	reads	bases (Gb)
Pass filtered	858,141,016	63.2	958,424,656	69.8	816,830,044	63.4
Mapped	523,457,901	34.1	595,846,336	37.3	507,178,044	35.4
Mapping rate	61.0%		62.2%		62.1%	
Uniquely mapped	407,608,000	26	460,830,001	28	337,179,056	22.9
Redundancy	28.4%		29.3%		50.4%	
Effective coverage	**9.1X**		**9.8X**		**8.0X**	
Conversion rate	98.5%		99.3%		99.2%	
# of C covered per strand (covered by at least 1 read)	516,837,311		524,002,293		486,542,051	
% of C covered	88.5%		89.8%		83.4%	
# of C within CpG covered per strand (covered by at least 1 read)	26,179,206		26,361,395		25,394,948	
% of C within CpG covered	94.0%		94.6%		91.2%	
CpG methylation rate	57.4%		52.5%		58.5%	