Supplementary Table S2. Summary of variant calling and effect of filtering for exome sequence data. 1000 exome BAM files were randomly selected from 1000G Phase I data. 10 sample results were averaged over 10 sets of 10 BAM files.

# Sample	Filter		# SNPs total	# avg. SNPs per sample	%dbSNP (v129)	Non-syn.		Synonymous	
						Known Ts/Tv	Novel Ts/Tv	Known Ts/Tv	Novel Ts/Tv
10	None	-	45,403	16,240	70.7	2.15	1.13	5.30	3.23
	SVM	PASS	41,479	14,859	75.3	2.19	1.54	5.38	4.17
		FAIL	3,924	1,381	22.2	1.36	0.47	2.91	1.20
100	None	-	127,664	16,397	41.2	2.18	1.34	5.36	3.63
	SVM	PASS	109,023	14,121	47.2	2.25	1.94	5.44	4.89
		FAIL	18,641	2,586	12.1	1.46	0.48	3.44	1.13
1,000	None	-	399,811	17,174	17.3	2.24	1.61	5.40	4.05
	SVM	PASS	324,381	13,801	20.1	2.33	2.31	5.55	5.49
		FAIL	75,430	3,373	5.2	1.53	0.57	3.32	1.39