Table S1. Discordance rates (%) between Illumina WGS and WES data from the same individual

	IL blood (WGS)	IL saliva (WGS)
IL blood Agilent	0.12	0.11
IL blood Nimblegen	0.17	0.16
IL saliva Agilent	0.12	0.11
IL saliva Nimblegen	0.20	0.18

Overall discordance:

Same tissue	0.149
Different tissue	0.152

Table S2. Total number of discordant sites and discordance rate for SNV's (with GQ ≥ 40) called in WGS, Agilent WES and Nimblegen WES data sets from the same individual and tissue type.

	Blood	Saliva	Discordance rate
WGS	33	41	1.36E-04
Agil WES	331	340	1.23E-03
Nimb WES	278	357	1.16E-03
Sites	274866	270885	

Table S3. Examples of how particular variants are classified (for Figure 5). In all cases, we assume the reference allele to be A. Uncalled genotypes are denoted by NN. Platform specific fixed differences are further subdivided into ones where the two IL samples have the non-reference genotype (IL variant) and ones where the two CG samples have the non-reference genotype (CG variant). See text for further discussion of these.

IL blood genotype	IL saliva genotype	CG blood genotype	CG saliva genotype	Called as
AA	AA	AA	AG	False positive (CG sal)
AG	AG	AA	AG	False negative (CG bld)
AG	AT	AG	AG	Miscall (IL sal)
AG	AG	AA	AA	Platform specific FD (IL variant)
AA	AA	AG	AG	Platform specific FD (CG variant)
AA	AG	AG	AA	Other
NN	AA	AA	AG	Platform specific error (CG)
AA	AG	AG	GG	Excluded*

* Sites with more than two observed genotypes are excluded from the analyses

Table S4. Genotype discordance rates for platform-specific fixed differences, stratified by minor allele frequency (MAF)

	IL-variant	CG-variant
Overall	$2.85 * 10^{-4}$	$4.32 * 10^{-3}$
MAF < 0.01	$1.02 * 10^{-2}$	0.168
0.01 ≤ MAF < 0.05	$1.43 * 10^{-4}$	$1.61 * 10^{-3}$
MAF ≥ 0.05	$6.77 * 10^{-5}$	$7.16 * 10^{-4}$

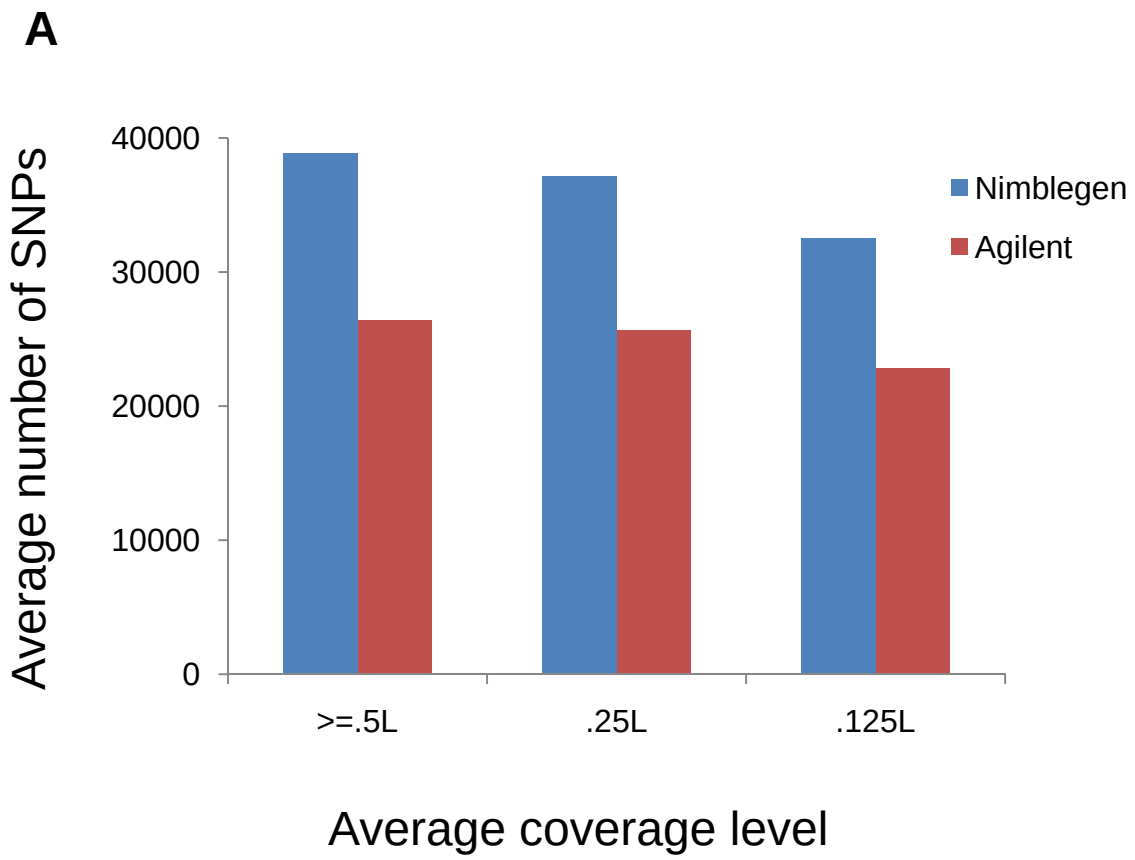
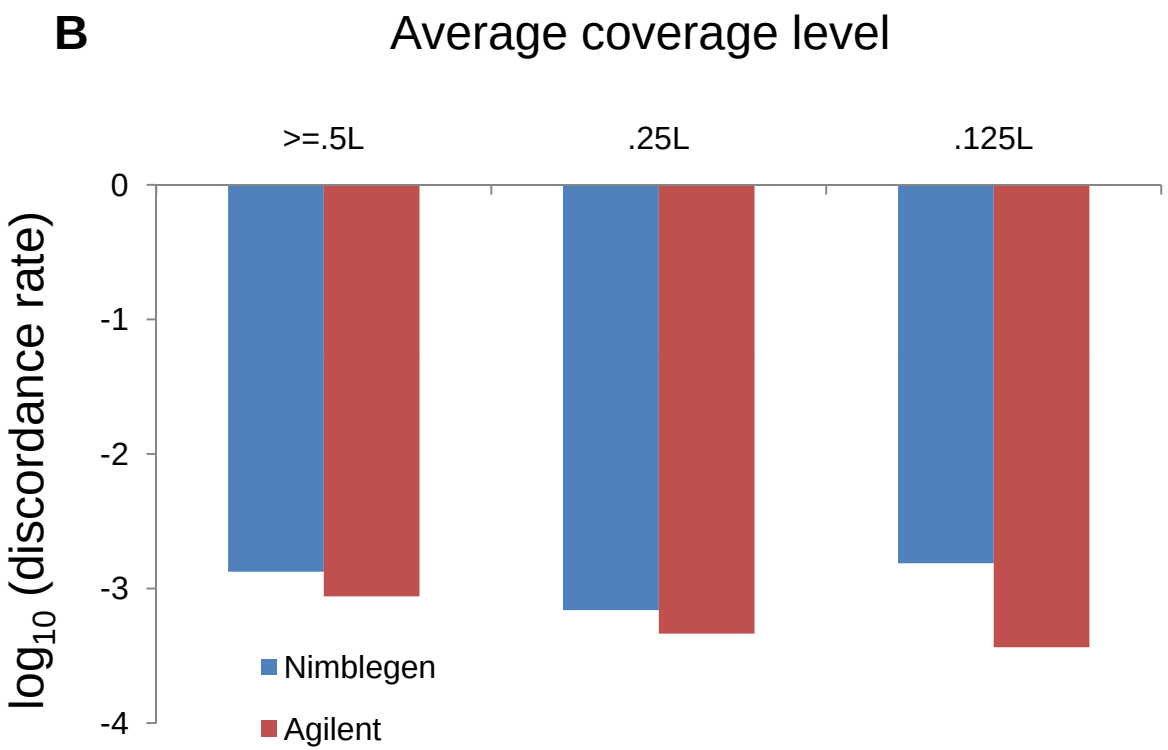


Figure S1. Average number of SNPs called per sample (**A**) and discordance rate (**B**) for exome data, stratified by average coverage level (xL refers to x lanes of coverage).

B


Average coverage level
>=.5L
.25L
.125L
0
-1
-2
-3
-4
log10 (discordance rate)
Nimblegen
Agilent

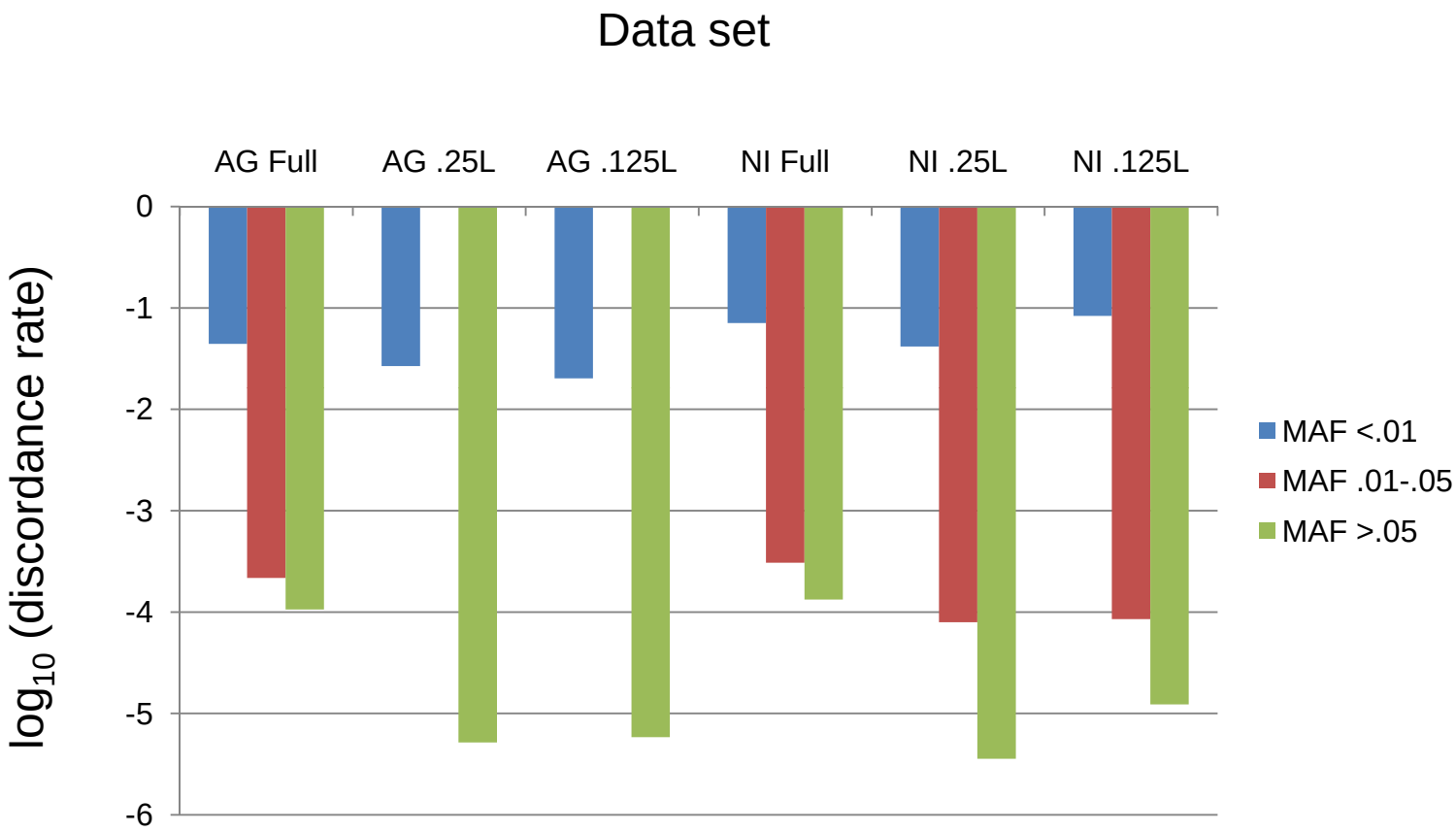


Figure S2. Discordance rate for exome data stratified by minor allele frequency (MAF) for different capture arrays (AG = Agilent, NI = Nimblegen) and levels of coverage (.25L refers to .25 lanes of coverage, etc.)

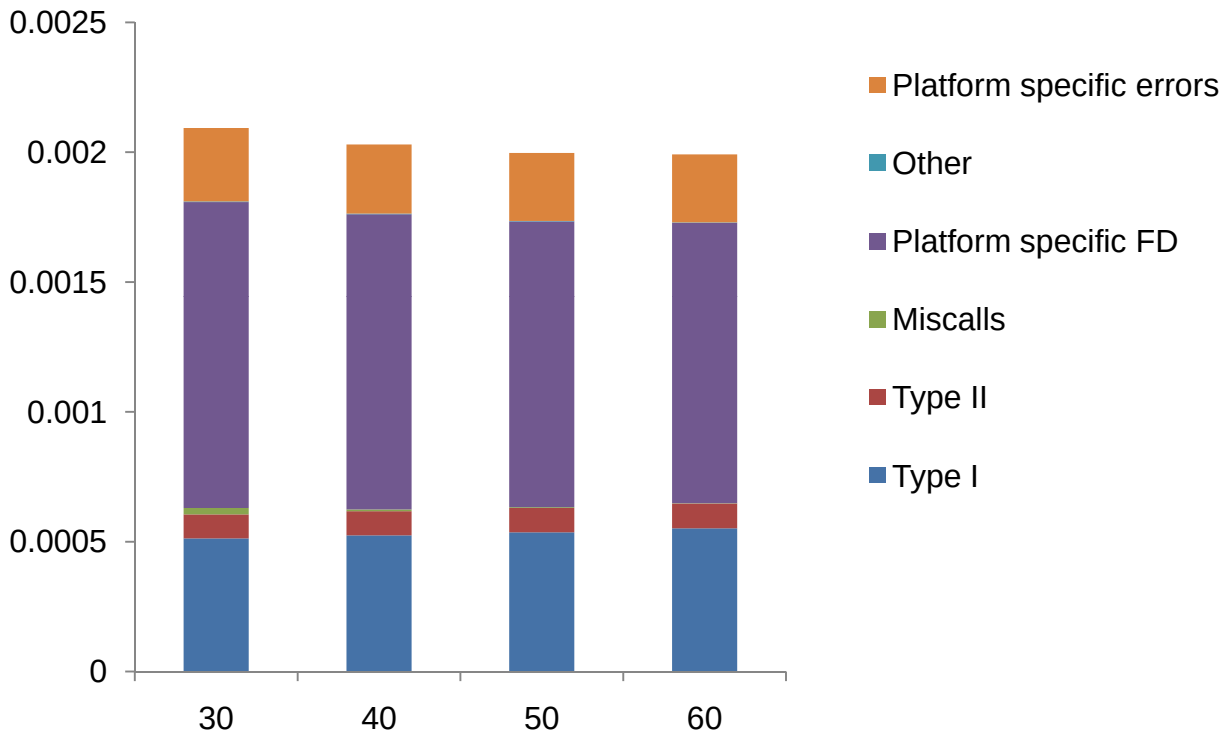


Figure S3. Total error rate for Illumina WGS data with different GQ cutoffs (x-axis). The six different colors represent the 6 different error types described in the main text.