SNP: Variant counts per approach, by classification category Concordant Discordant extra error prone Discordant extra low coverage 75148 77158 72581 75337 76334 72540 125018 73719 75769 72406 18 13 Discordant extra other Discordant extra repeat Discordant extra total 516 196 391 Calling approach bwa gatk freebayes 177 124 240 bwa gatk gatk Discordant missing error prone Discordant missing low coverage Discordant missing other bwa gkno gatk 607 1460 1142 574 621 887 640 1377 858 Illumina-platinum Discordant missing repeat Discordant shared hethom Discordant missing total 1137 1464 1649 1031 1532 1740 484 311 4709 8300 3370 6781 4133 7408 6137 4707 Discordant shared total Discordant shared vardiff 1001 1594 1671 976 1570 1705 10² 10³ 10⁴ 10⁰ 10⁰ 10¹ 10⁵ 10¹ 10^{2} 10³ 10⁴ 10⁵

Count (log scale)

bwa gatk gatk-haplotype bwa gkno freebayes bwa gkno gatk-haplotype novoalign gatk freebayes novoalign gatk gatk novoalign gatk gatk-haplotype novoalign gkno freebayes novoalign gkno gatk novoalign gkno gatk-haplotype