SNP: Variant counts per approach, by classification category Concordant Discordant extra error prone Discordant extra low coverage 78468 77537 72744 78489 76892 72681 126526 77223 75997 72442 18 13 Discordant extra other Discordant extra repeat Discordant extra total 1017 1084 344 281 278 33 348 417 Calling approach bwa gatk freebayes 421 425 bwa gatk gatk Discordant missing low coverage Discordant missing error prone bwa gatk gatk-haplotype Discordant missing other 1789 2913 6615 bwa gkno freebayes 10. 455 1052 1032 1668 bwa gkno gatk 1865 2612 6607 bwa gkno gatk-haplotype 2081 3206 6084 413 438 832 93 Illumina-platinum novoalign gatk freebayes novoalign gatk gatk novoalign gatk gatk-haplotype Discordant missing total Discordant missing repeat Discordant shared hethom novoalign gkno freebayes 2316 352 1743 1468 novoalign gkno gatk 1659 1464 1547 1748 2571 4086 novoalign gkno gatk-haplotype 191 208 397 Discordant shared total Discordant shared vardiff 1819 1534 1690 1532 1602 1777 68 55 29 1590 1640 1701 10<sup>3</sup> 10<sup>2</sup> 10<sup>4</sup> 10<sup>5</sup> 10<sup>1</sup> 10<sup>3</sup> 10<sup>0</sup> 10<sup>0</sup> 10<sup>1</sup> 10<sup>4</sup> 10<sup>5</sup>

Count (log scale)