VEP: Variant Consequences
Consequences (all), 6 samples

Legend:
- transcript_ablation
- splice_acceptor_variant
- splice_donor_variant
- stop_gained
- frameshift_variant
- inframe_insertion
- missense_variant
- splice_donor_5th_base_variant
- splice_region_variant
- splice_donor_region_variant
- splice_polypyrimidine_tract_variant
- stop_retained_variant
- synonymous_variant
- coding_sequence_variant
- mature_miRNA_variant
- 5_prime_UTR_variant
- 3_prime_UTR_variant
- non_coding_transcript_exon_variant
- intron_variant
- NMD_transcript_variant
- non_coding_transcript_variant
- upstream_gene_variant
- downstream_gene_variant
- regulatory_region_ablation
- regulatory_region_variant
- intergenic_variant
- protein_altering_variant

Samples (y-axis):
- HBRRep1.haplotypecaller.filtered_VEP.ann
- HBRRep2.haplotypecaller.filtered_VEP.ann
- HBRRep3.haplotypecaller.filtered_VEP.ann
- UHRRep1.haplotypecaller.filtered_VEP.ann
- UHRRep2.haplotypecaller.filtered_VEP.ann
- UHRRep3.haplotypecaller.filtered_VEP.ann

x-axis: Consequences (most severe) — 0%, 20%, 40%, 60%, 80%, 100%

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