

Description of variation compared to OXC141 genome

- 1 34kb deletion in SRL1 genome. Corresponds to putative pro-phage sequence. Sequence is entirely removed with cross mapped breakpoints at pro-phage insertion site.
- 2 Deletion involving a non-coding region

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- 3 Poorly resolved area in highly repetitive region of PspA gene. Insufficient information to allow complete sequence to be determined.
- 4 Presence of a full copy of the glutamine ABC transporter permease gene. OXC141 has a deletion in this gene. The 285 bp insertion sequence was reconstructed using reads unmapped to the reference sequence and matched with 100% sequence homology to several published pneumococcal genomes including D39.
- 5 93 bp deletion in a peptide ABC transporter gene. Deletion is not present in any published pneumococcal sequences. Deletion is in-frame and affects the terminal region of the eflux pump. The functional consequence from this limited analysis is not clear.