Edinburgh Genome Foundry
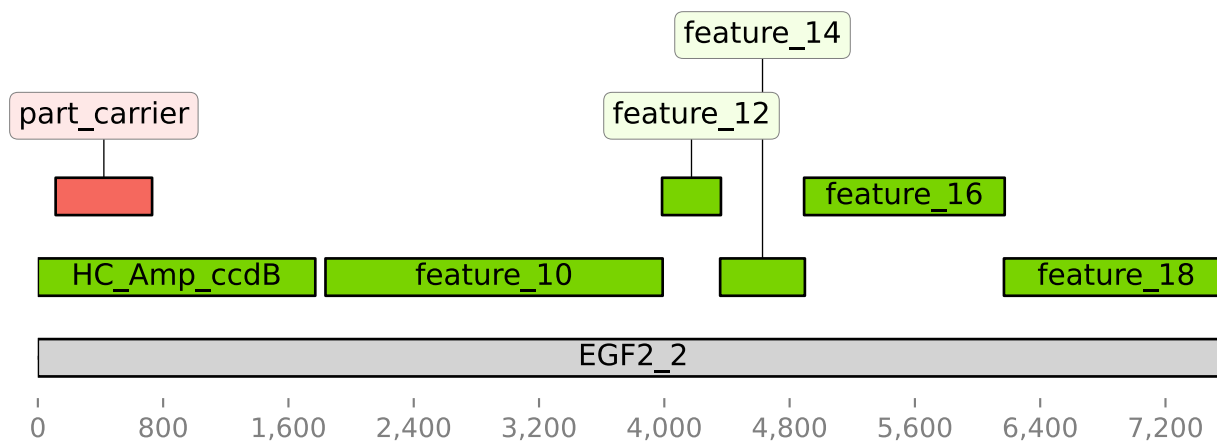
Assembly analysis report

This document reports the sequencing results of the **EGF demo review** project. Each chapter details the results of a plasmid (assembly). Please see the Appendix on the last page for an explanation of the report.
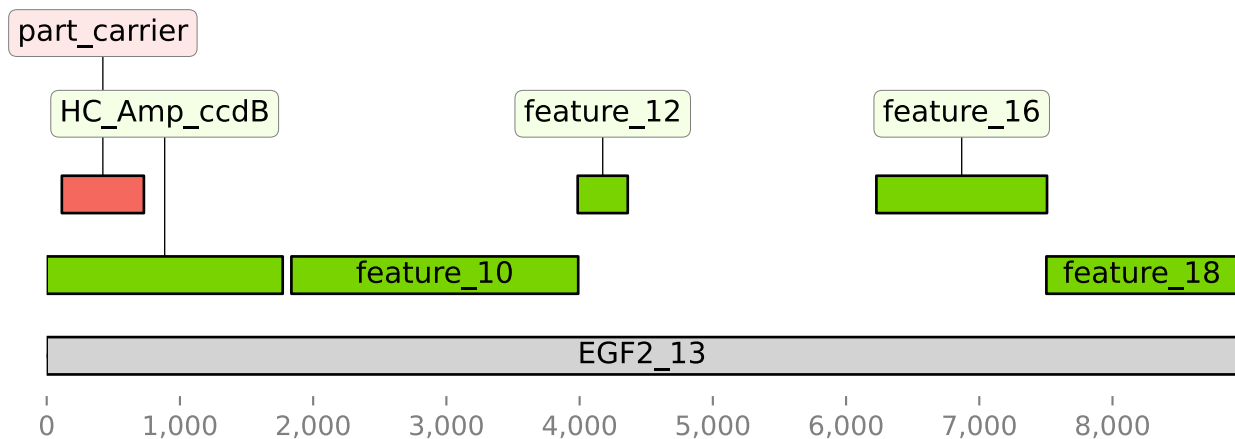
EGF2_2

Plot of the aligning parts:

Alignment table:

Name	Length	Start	End	Strand	T Start	T End	Matches	Size	Quality
EGF2_2	7604	0	7604	+	0	7603	7603	7604	60
HC_Amp_ccdB	2721	949	2721	+	0	1772	1772	1772	60
feature_10	2166	6	2159	+	1837	3990	2153	2153	60
feature_12	390	7	383	+	3986	4362	376	376	60
feature_14	554	6	547	+	4357	4898	541	541	60
feature_16	1294	6	1287	+	4893	6174	1281	1281	60
feature_18	1451	6	1440	+	6169	7603	1434	1434	60
part_carrier	2329	235	852	-	114	730	615	617	60

EGF2_13

Plot of the aligning parts:

Alignment table:

Name	Length	Start	End	Strand	T Start	T End	Matches	Size	Quality
EGF2_13	8939	0	8939	+	0	8938	8938	8939	60
HC_Amp_ccdB	2721	949	2721	+	0	1772	1772	1772	60
feature_10	2166	6	2159	+	1837	3990	2153	2153	60
feature_12	390	7	383	+	3986	4362	376	376	60
feature_16	1294	6	1287	+	6228	7509	1281	1281	60
feature_18	1451	6	1440	+	7504	8938	1434	1434	60
part_carrier	2329	235	852	-	114	730	615	617	60

Appendix

Each chapter describes results on a plasmid sequence (*de novo* assembly). The provided (part) sequences were aligned against the sequence assembled from the reads. The plot shows alignment regions as annotations. If there are unannotated segments, then none of the parts aligned there. If an assembly plan is provided, then annotations are coloured based on whether they are expected in the plasmid: green: part is expected in the construct; red: part shouldn't be in the construct. Grey is the reference expected sequence for the plasmid. The alignments are provided in a PAF (pairwise mapping format) table. The columns of the table are:

- Name: Query sequence name
- Length: Query sequence length
- Start: Query start coordinate
- End: Query end coordinate
- Strand: `+` if query and target on the same strand; `−` if opposite
- T Start: Target start coordinate on the original strand
- T End: Target end coordinate on the original strand
- Matches: Number of matching bases in the mapping (includes mismatches but not indels)
- Size: Number bases, including gaps (indels), in the mapping
- Quality: Mapping quality (0–255 with 255 for missing)