

依頼書記載名称	Cas9-attP40	Cas9-attP2	19A	40A	42	80B	82B	G13	2A
申請書記載名称	<i>y<sup>1</sup> w<sup>1118</sup> ; attP40 (nos-Cas9)/CyO</i>	<i>y<sup>1</sup> w<sup>1118</sup> ; attP2 (nos-Cas9)/TM6B</i>	<i>y<sup>1</sup> w<sup>1118</sup> FRT19A ; attP40 (nos-Cas9)/CyO</i>	<i>y<sup>1</sup> w<sup>1118</sup> ; FRT40A ; attP2 (nos-Cas9)/TM6B</i>	<i>y<sup>1</sup> w<sup>1118</sup> ; FRT42D ; attP2 (nos-Cas9)/TM6B</i>	<i>y<sup>1</sup> w<sup>1118</sup> ; attP40 (nos-Cas9)/CyO ; FRT80B</i>	<i>y<sup>1</sup> w<sup>1118</sup> ; attP40 (nos-Cas9)/CyO ; FRT82B</i>	<i>w* ; FRTG13</i>	<i>w* ; FRT2A</i>
	PG2865_01_a	PG2865_02_a	PG2865_03_a	PG2865_04_a	PG2865_05_a	PG2865_06_a	PG2865_07_a	PG2865_08_a	PG2865_09_a
Total input reads	109911194	93624018	99050810	104820950	112395906	95661502	141999070	87671340	89019546
Number of duplicate reads (marked)	23448741	18620279	19227231	21720011	24097522	19945735	36145817	17058396	18357011
Number of duplicate reads (marked)(%)	21.33	19.89	19.41	20.72	21.44	20.85	25.45	19.46	20.62
Number of unique reads	86462453	75003739	79823579	83100939	88298384	75715767	105853253	70612944	70662535
Number of unique reads(%)	78.67	80.11	80.59	79.28	78.56	79.15	74.55	80.54	79.38
Reads with mate sequenced	109911194	93624018	99050810	104820950	112395906	95661502	141999070	87671340	89019546
Reads with mate sequenced(%)	100	100	100	100	100	100	100	100	100
Reads without mate sequenced	0	0	0	0	0	0	0	0	0
Reads without mate sequenced(%)	0	0	0	0	0	0	0	0	0
QC-failed reads	0	0	0	0	0	0	0	0	0
QC-failed reads(%)	0	0	0	0	0	0	0	0	0
Mapped reads	106199641	90413141	93339913	101125425	108458107	92174294	136800736	84747518	85774095
Mapped reads(%)	96.62	96.57	94.23	96.47	96.5	96.35	96.34	96.67	96.35
Number of unique & mapped reads (excl. dups)	82750900	71792862	74112682	79405414	84360585	72228559	100654919	67689122	67417084
Number of unique & mapped reads (excl. dups)(%)	75.29	76.68	74.82	75.75	75.06	75.5	70.88	77.21	75.73
Unmapped reads	3711553	3210877	5710897	3695525	3937799	3487208	5198334	2923822	3245451
Unmapped reads(%)	3.38	3.43	5.77	3.53	3.5	3.65	3.66	3.33	3.65
Singleton reads (itself mapped; mate unmapped)	220213	189979	226601	190253	208337	193912	262348	154446	183605
Singleton reads (itself mapped; mate unmapped)(%)	0.2	0.2	0.23	0.18	0.19	0.2	0.18	0.18	0.21
Paired reads (itself & mate mapped)	105979428	90223162	93113312	100935172	108249770	91980382	136538388	84593072	85590490
Paired reads (itself & mate mapped)(%)	96.42	96.37	94.01	96.29	96.31	96.15	96.15	96.49	96.15
Properly paired reads	104227044	88851518	91740524	99537970	106734550	90627226	134745616	83372398	84304752
Properly paired reads(%)	94.83	94.9	92.62	94.96	94.96	94.74	94.89	95.1	94.7
Not properly paired reads (discordant)	1752384	1371644	1372788	1397202	1515220	1353156	1792772	1220674	1285738
Not properly paired reads (discordant)(%)	1.59	1.47	1.39	1.33	1.35	1.41	1.26	1.39	1.44
Reads with MAPQ [40:inf]	92902432	78889105	81104559	87507398	94557098	80154719	119317301	74313523	75858989
Reads with MAPQ [40:inf)(%)	84.52	84.26	81.88	83.48	84.13	83.79	84.03	84.76	85.22
Reads with MAPQ [30:40)	441461	373623	381838	432873	449754	366500	554378	332820	341487
Reads with MAPQ [30:40)(%)	0.4	0.4	0.39	0.41	0.4	0.38	0.39	0.38	0.38
Reads with MAPQ [20:30)	1052171	925895	943278	1067227	1099495	925838	1367915	823611	821131
Reads with MAPQ [20:30)(%)	0.96	0.99	0.95	1.02	0.98	0.97	0.96	0.94	0.92
Reads with MAPQ [10:20)	1537378	1365218	1438953	1633913	1658466	1412830	2058861	1273505	1218365
Reads with MAPQ [10:20)(%)	1.4	1.46	1.45	1.56	1.48	1.48	1.45	1.45	1.37
Reads with MAPQ [ 0:10)	10266199	8859300	9471285	10484014	10693294	9314407	13502281	8004059	7534123
Reads with MAPQ [ 0:10)(%)	9.34	9.46	9.56	10	9.51	9.74	9.51	9.13	8.46
Reads with MAPQ NA (Unmapped reads)	3711553	3210877	5710897	3695525	3937799	3487208	5198334	2923822	3245451

Reads with MAPQ NA (Unmapped reads)(%)	3.38	3.43	5.77	3.53	3.5	3.65	3.66	3.33	3.65
Total alignments	106641377	90756698	93666325	101513297	108895705	92546148	137316623	85092526	86102829
Secondary alignments	0	0	0	0	0	0	0	0	0
Supplementary (chimeric) alignments	441736	343557	326412	387872	437598	371854	515887	345008	328734
Estimated read length	150	150	150	150	150	150	150	150	150
Bases in reference genome	143726002	143726002	143726002	143726002	143726002	143726002	143726002	143726002	143726002
Bases in target bed [% of genome]	NA	NA	NA	NA	NA	NA	NA	NA	NA
Average sequenced coverage over genome	114.71	97.71	103.37	109.4	117.3	99.84	148.2	91.5	92.91
Average alignment coverage over genome	77.76	67.39	69.38	74.32	79.21	67.54	94.21	63.96	64.1
PCT of genome with coverage [100x:inf)	17	2.95	3.92	8.93	17.95	3.15	59.62	1.71	1.69
PCT of genome with coverage [50x:100x)	66.34	79.41	79.23	74.73	66.23	79.05	25.74	79.81	79.6
PCT of genome with coverage [40x:50x)	1.72	2.22	1.88	1.6	1.32	2.03	0.88	2.43	2.64
PCT of genome with coverage [30x:40x)	1.2	1.46	1.27	0.96	0.86	1.32	0.66	1.58	1.67
PCT of genome with coverage [20x:30x)	0.9	0.97	0.92	0.73	0.7	0.9	0.64	0.96	1
PCT of genome with coverage [10x:20x)	0.97	0.97	0.9	0.81	0.76	0.94	0.7	0.92	0.94
PCT of genome with coverage [5x:10x)	0.64	0.62	0.55	0.54	0.52	0.67	0.48	0.61	0.6
PCT of genome with coverage [2x:5x)	0.68	0.67	0.6	0.61	0.63	1.1	0.56	0.68	0.66
PCT of genome with coverage [1x:2x)	0.59	0.59	0.54	0.56	0.69	1.25	0.53	0.7	0.58
PCT of genome with coverage [0x:1x)	9.97	10.14	10.18	10.54	10.33	9.59	10.18	10.59	10.62