

ReadName	Read (with APP)	Mate (novel site)	Read orientation
SRR8898224.96962287	CGTGCTGGTGCATCTTGGAG	GCCTCATGTTGCTCATTGGT	R1R2
SRR8898224.107824814	CTTCCCCGTCATCATCGGCT	GAGTGGGATGCCACATGTC	R1R2
SRR8898224.20867379	CTCCACCTCAGCCTCTTCTI	TAAAATTGAAGTACAGGCTA	F1R2
SRR8898224.118878929	CCTTGATCACTAATCATGT	TGAGAGGAAAAGGCCCTT	F1R2
SRR8898276.166141196	CGCTCCTCTGGGGTGACAG	CAACATCCAATCATGTATAA	F1R2
SRR8898224.107643979_mate	GCGAGTGGGATCCGCCGCC	GAAGGCCCTGGAAACCGAC	F2R1
SRR8898224.27622836_mate	CCGTCCCCTGTCACTGGG	GGGGTGAAGGAGGTGCCA	F2R1
SRR8898224.49640101_mate	TTACCAATTCTGCCTCCTGTI	CCTGGGACTGCTCCTTTACT	F2R1
SRR8898224.96736610_mate	ACAATGTCTTTTAAATTAATA	CCTCTTCCTTCACACCACC	F1R2
SRR8898268.233861544_mate	CAGCAACCAAGGCTCATACT	GCTCTGGAAACAGGAAGAA	F2R1

Read location on APP	Mate location	Sample ID	Region type	Intersected Gene
18/17	chr3:72631698-72631798	AD304 HIF	intergenic	intergenic
6/5	chr13:37663681-37663781	AD304 HIF	Intron	TRPC4
6/5	chr5:140870048-140870148	AD304 HIF	Intron	PCDHA1
14/13	chr1:155946754-155946854	AD304 HIF	3'UTR	ARHGEF2
18/17	chr6:72497946-72498046	AD315 blood	intergenic	intergenic
5'UTR	chr1:148953252-148953352	AD304 HIF	Intron	PDE4DIP
3'UTR	chr12:7210081-7210181	AD304 HIF	5'UTR	PEX5
3'UTR	chr3:172916391-172916491	AD304 HIF	Exon	SPATA16
3'UTR	chr9:112879022-112879122	AD304 HIF	3'UTR	SLC46A2
3'UTR	chr10:43845520-43845620	AD317 HIF	Intron	LINC00619