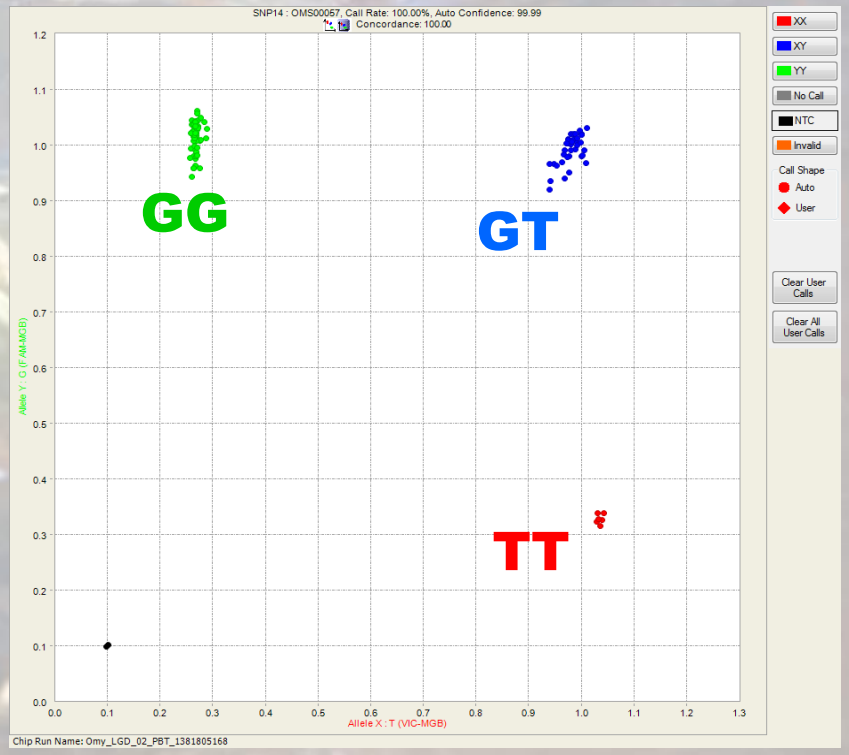
Collaboration of Two Innovative Technologies for VSP Monitoring of the Snake River Steelhead DPS



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2014 Pacific Coast Steelhead Management Meeting

Collaborators

CRITFC
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IDFG
- Matt Campbell
- Matt Corsi
- Tim Copeland
- Bill Schrader
- Lance Hebdon

NOAA
- Chris Jordan
- Darren Ogden

NPT
- Jay Hesse
- Jason Vogel

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- Chris Beasley

SBT
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- Kurt Tardy

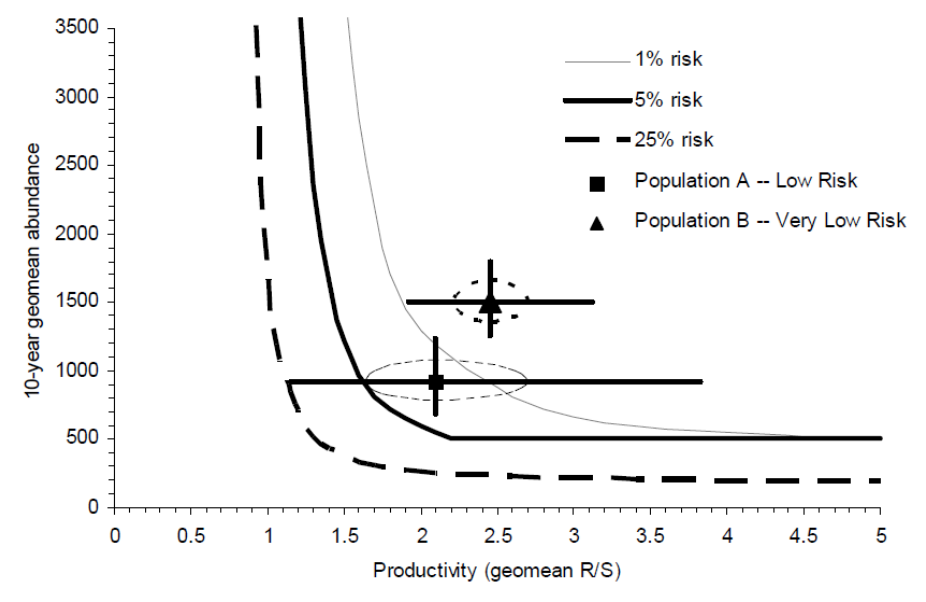
WDFW
- Joe Bumgarner
- Ethan Crawford

VSP Monitoring

- Four key parameters are needed to evaluate a population's viability (McElhany et al. 2000):
  1. Abundance
  2. Population Growth Rate (i.e. recruits per female)
  3. Spatial Structure
  4. Diversity (life-history and genetic)

- Estimates of abundance (combined with sex & age data) over time allows estimation of productivity

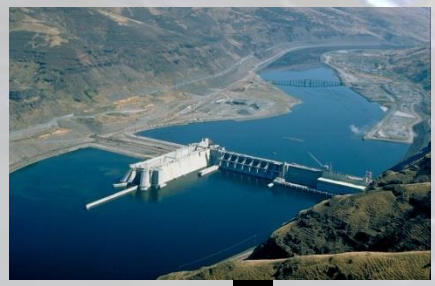
- Abundance & productivity provide indicators of resiliency
  - Extinction risk analysis



Lower Granite Dam (The Mark)

- Intercept 10 – 20% of All Adults
- All Ad-Intact Adults PIT Tagged and Bio-sampled

IPTDS (The Recapture)



Detections = 10
Efficiency = 1.00

$TR_{LGR} = 0.10$

$$\hat{N} = \frac{\hat{T}_{IPTDS}}{TR_{LGR}}$$

where

$\hat{N}$ = Estimated tributary abundance

$\hat{T}_{IPTDS}$ = Estimated tags at IPTDS

TR_{LGR} = Tagging rate at LGR

$$\hat{T}_{IPTDS} = \frac{Detections_{IPTDS}}{Efficiency_{IPTDS}}$$

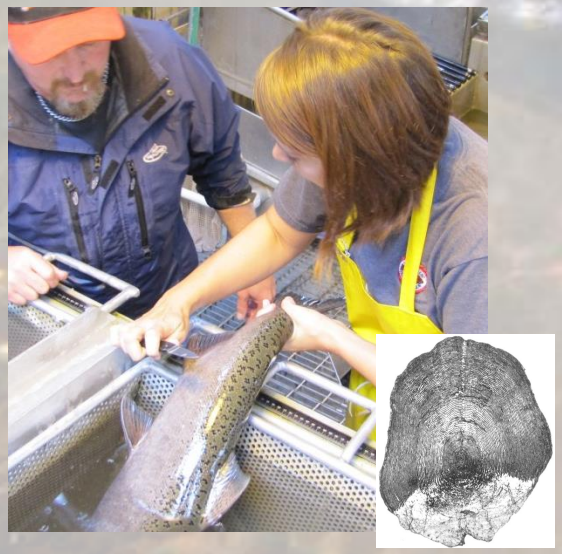
$$TR_{LGR} = \frac{\sum PIT_{Fish}}{TotalPassage_{LGR}}$$

LGR Bio-sampling

PIT Tag

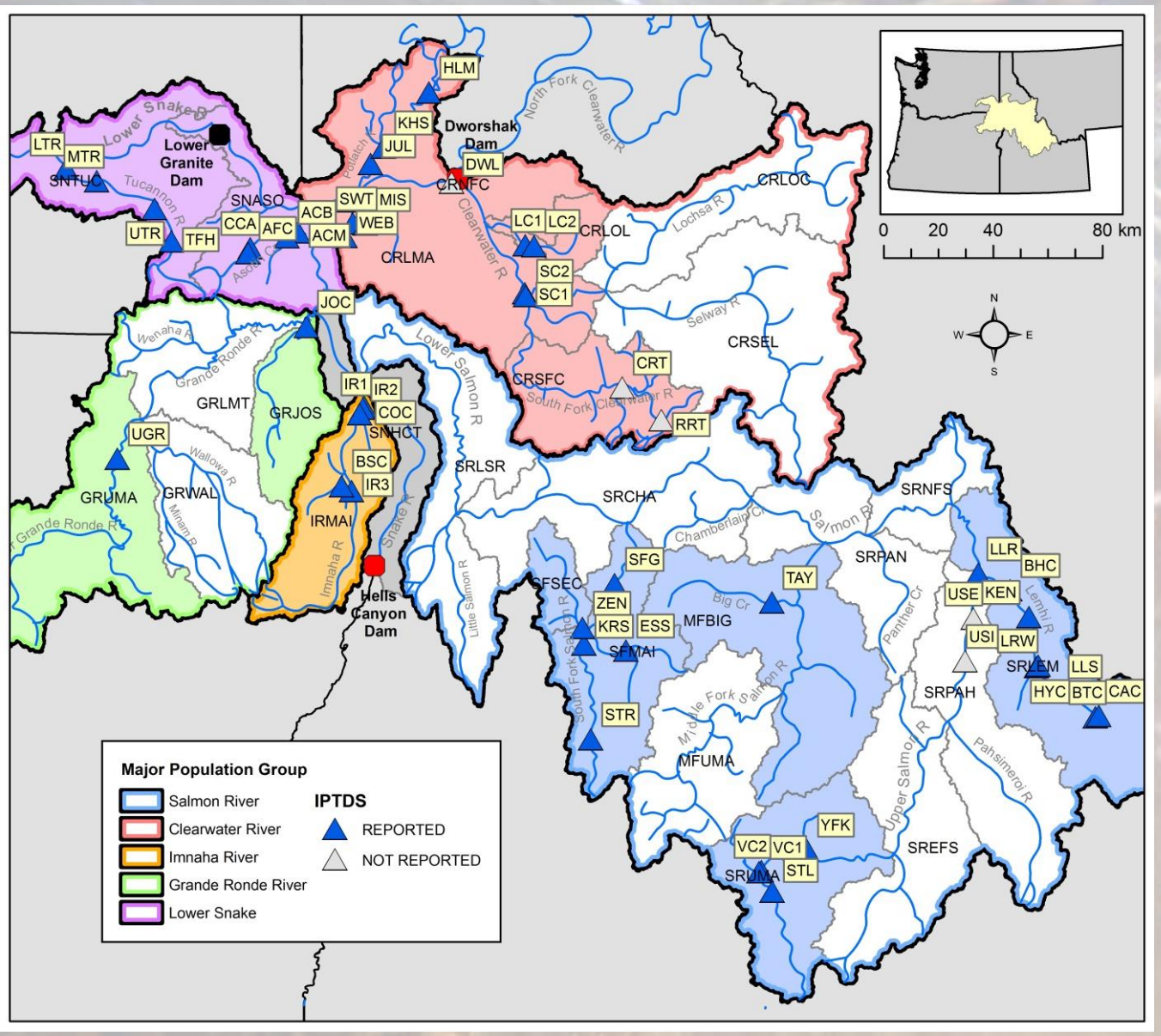
Tissue (Sex and Genotype)

Scale (Age)



Length

Snake River Steelhead DPS



24 Extant Populations

48 Total IPTDS (as of SY2012)

We report on :

- **43** IPTDS
- **13** populations

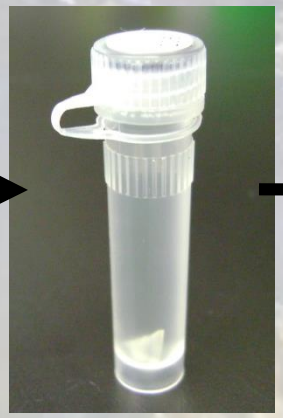
5 MPGs

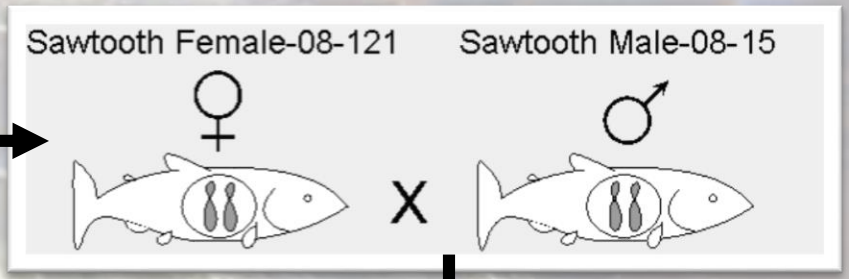
• Salmon	5/12
• Clearwater	3/5
• Imnaha	1/1
• Grande Ronde	2/4
• Lower Snake	2/2

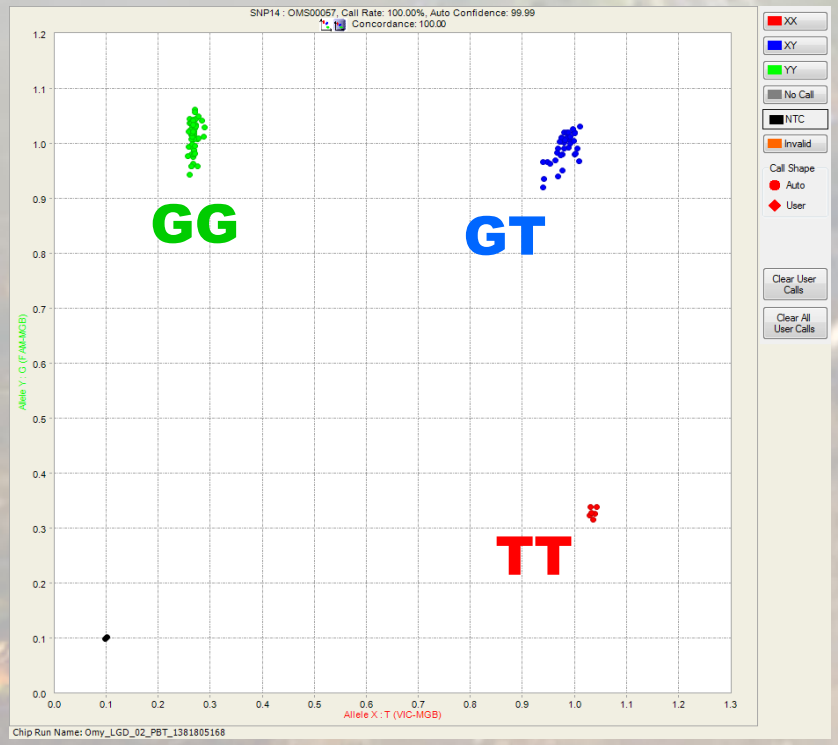
IPTDS Detections, SY2010 - 2012

Spawn Year	Total Tags	Total Pre-tagged Tags	Total IPTDS Detections	Unique Tags Detected
2010	4,043	77 (1.9%)	700	505 (12.5%)
2011	4,646	161 (3.5%)	1,903	1,142 (24.6%)
2012	4,366	110 (2.5%)	2,319	1,374 (31.5%)
Total	**13,055**	**348 (2.7%)**	**4,922**	**3,021 (23.1%)**

Parentage Based Tagging (PBT)







Sawtooth

BY2008

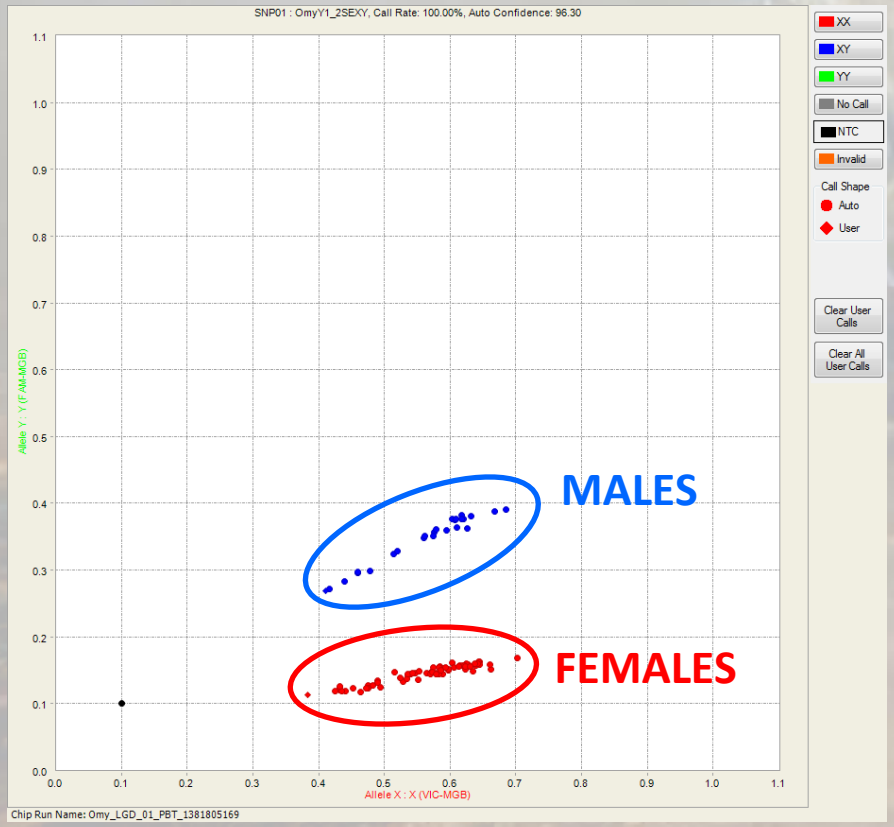
Abundance

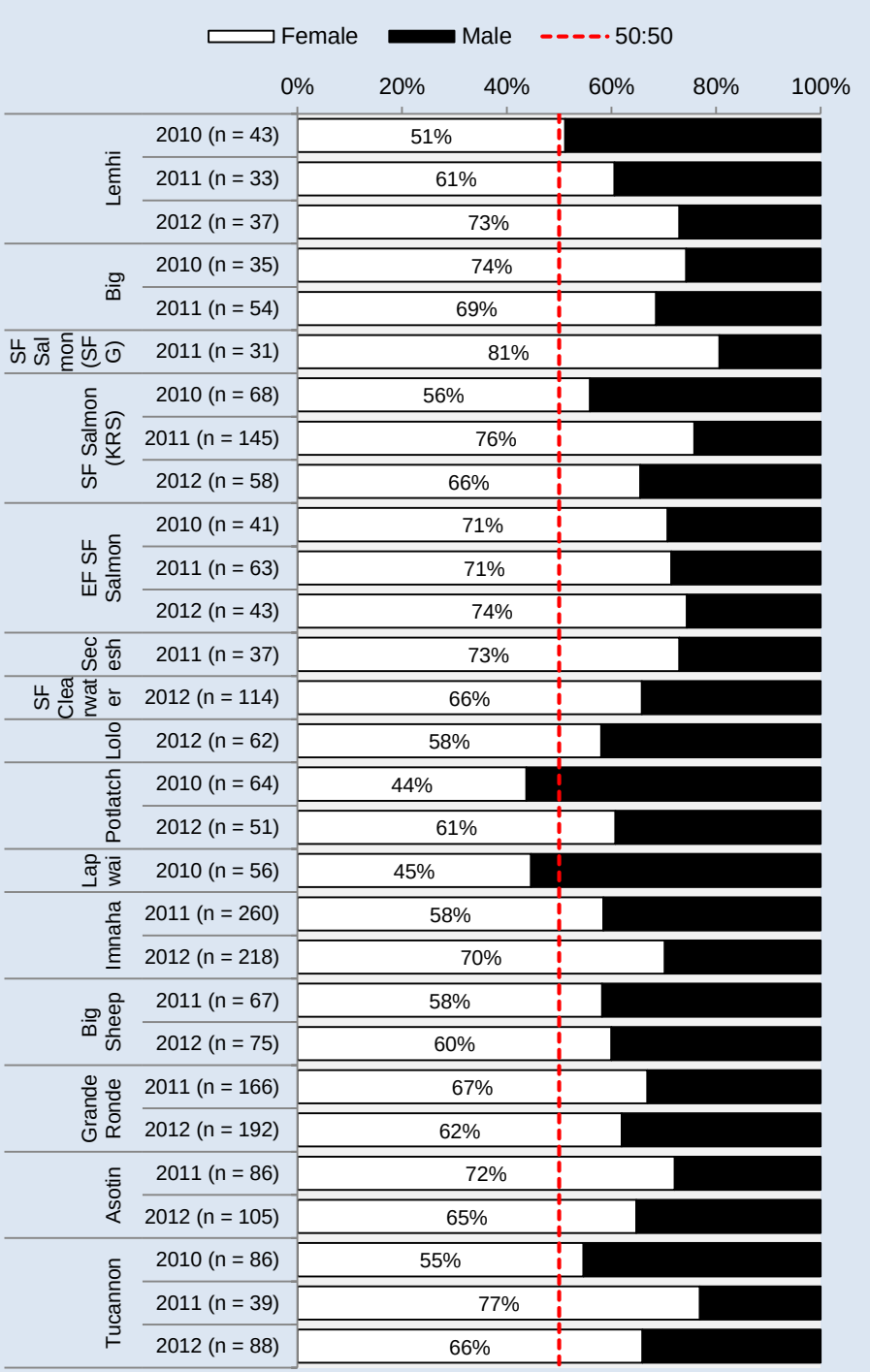
Run-Year	MPG	Population	Subpopulation	Fraction sampled	Escapement	CV	±95% CI
2009-2010	Salmon River	South Fork		90%	1,497	9.1%	268
2009-2010		Secesh		100%	298	22.1%	129
2009-2010		Middle Fork	Big Creek	100%	753	21.8%	322
2009-2010		Upper Salmon	Valley Creek	100%	237	17.7%	82
2009-2010		Lemhi River		95%	630	14.2%	175
2010-2011	Grande Ronde	Joseph Creek		100%	1,627	1.4%	45
2010-2011	Imnaha River	Imnaha River		100%	3,298	1.5%	97
2010-2011		Imnaha River	Cow Creek	100%	147	1.4%	4
2010-2011		Imnaha River	Big Sheep Creek	100%	765	2.2%	33
2010-2011	Salmon River	South Fork		90%	2,540	1.9%	93
2010-2011		Secesh		100%	397	3.1%	24
2010-2011		Middle Fork	Big Creek	100%	687	1.6%	22
2010-2011		Upper Salmon	Valley Creek	100%	232	1.5%	7
2010-2011		Lemhi River		95%	428	1.7%	14
2011-2012	Grande Ronde	Joseph Cr.		100%	1,974	8.0%	310
2011-2012	Imnaha	Imnaha		100%	2,984	4.0%	234
2011-2012		Imnaha	Cow Cr.	100%	131	28.0%	72
2011-2012		Imnaha	Big Sheep Cr.	100%	901	11.0%	194
2011-2012	Salmon	South Form Mainstem*		90%	1,510	9.0%	266
2011-2012		Secesh River		100%	202	24.0%	95
2011-2012		Middle Fork	Big Cr.	100%	490	35.0%	336
2011-2012		Upper Salmon	Valley Cr.	100%	290	18.0%	102
2011-2012		Lemhi River		95%	421	18.0%	149
2011-2012	Clearwater	SF Clearwater		100%	1,201	9.5%	224
2011-2012		Lolo Creek		100%	680	12.0%	160

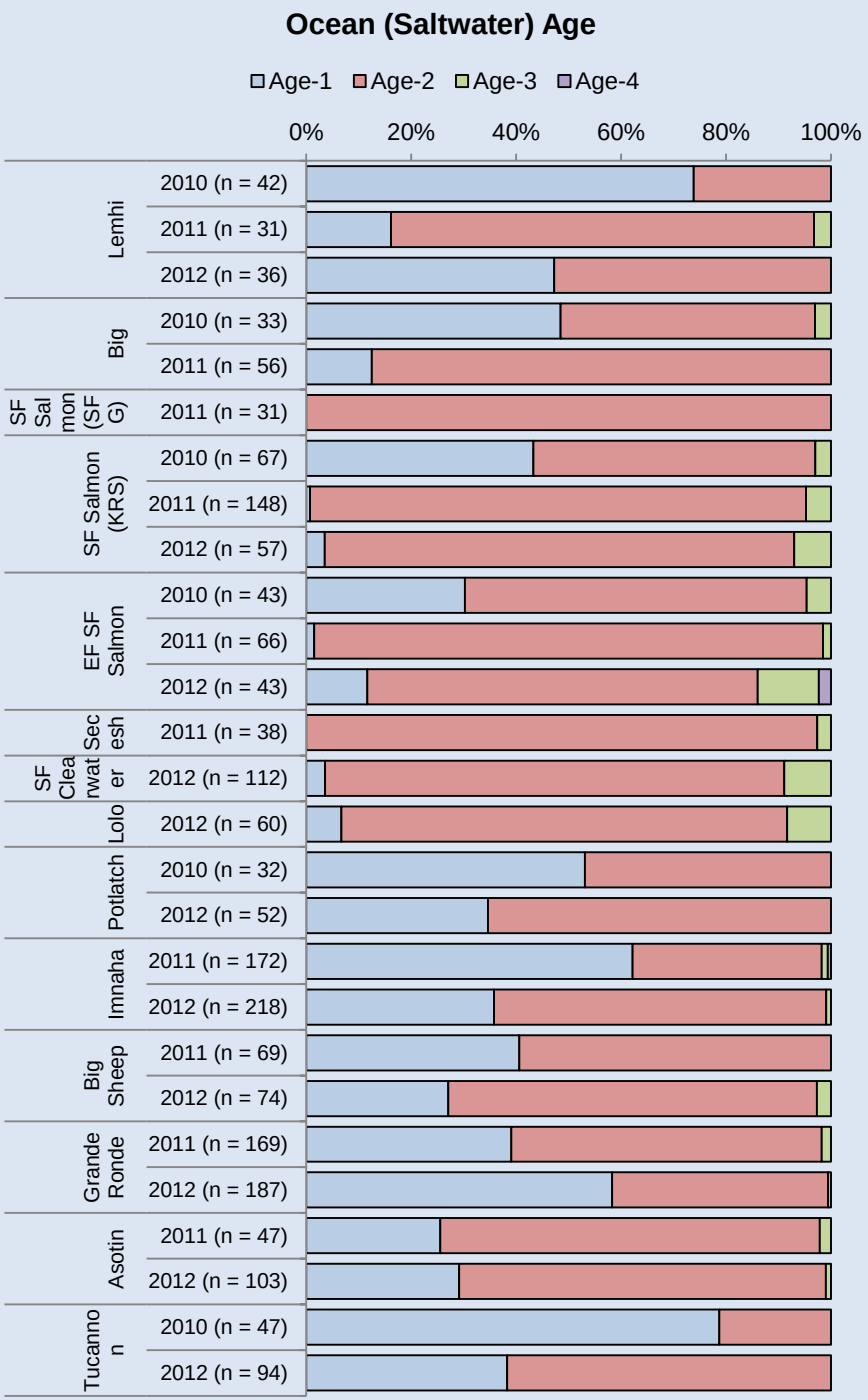
*Includes Secesh River escapement, by subtraction the estimate would be 1,308.

Sex Ratios

- Tissue sample provides sex
- Annual estimates of sex ratio and female/male abundance by population



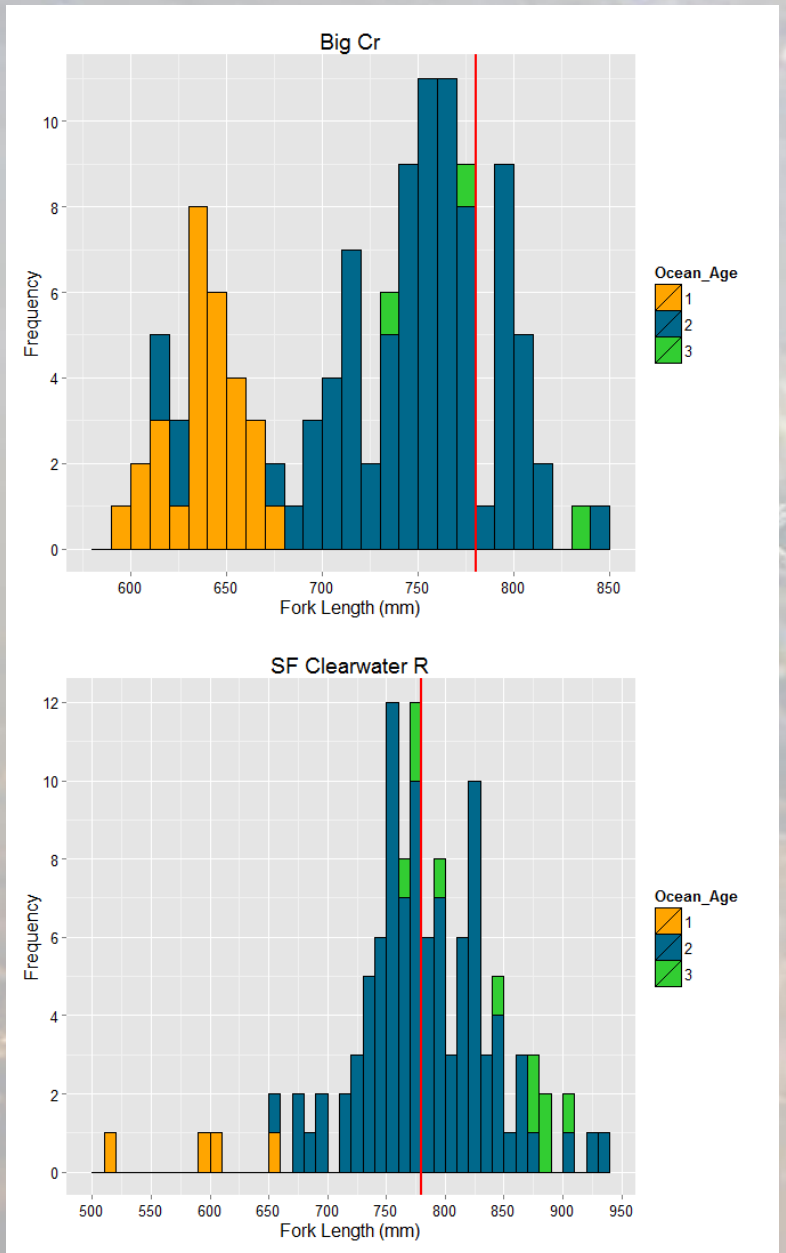


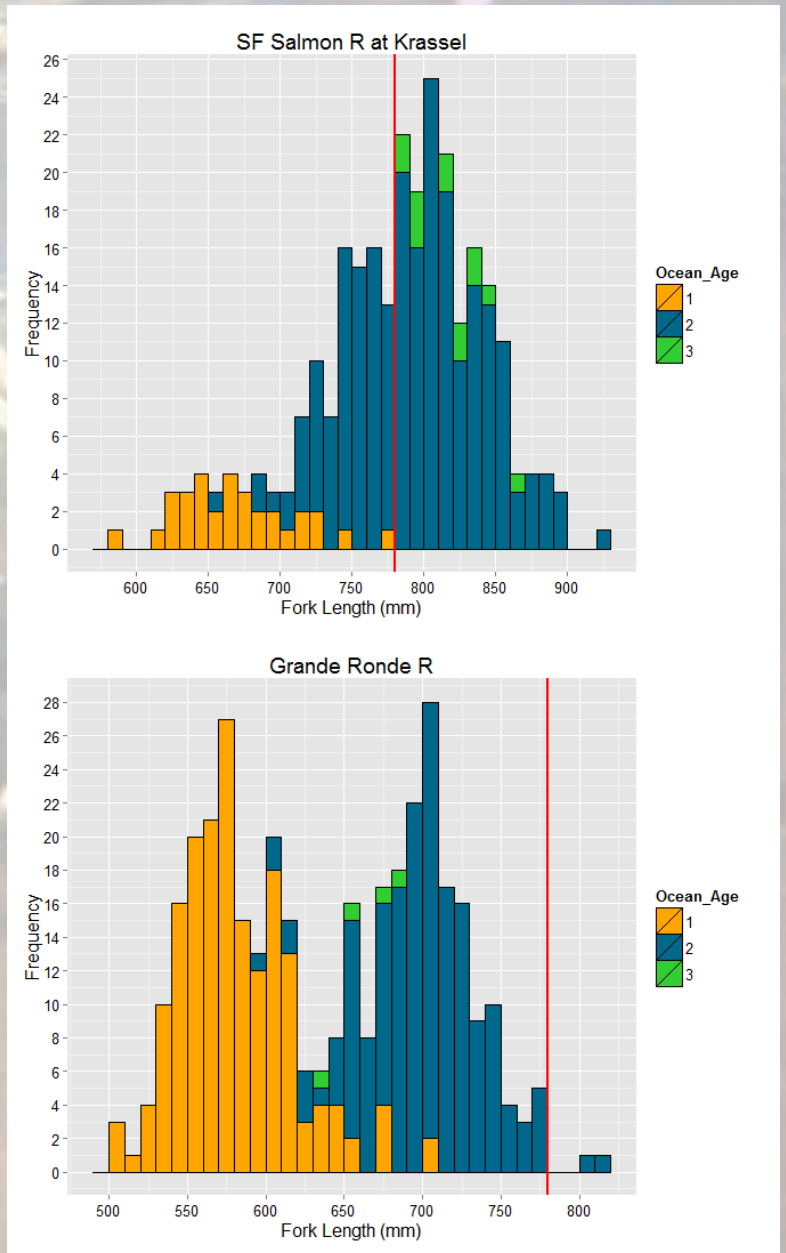


Saltwater Age

- Scale provides age data
- Annual estimates of saltwater, freshwater, and total age by population
- Estimates of abundance by brood year

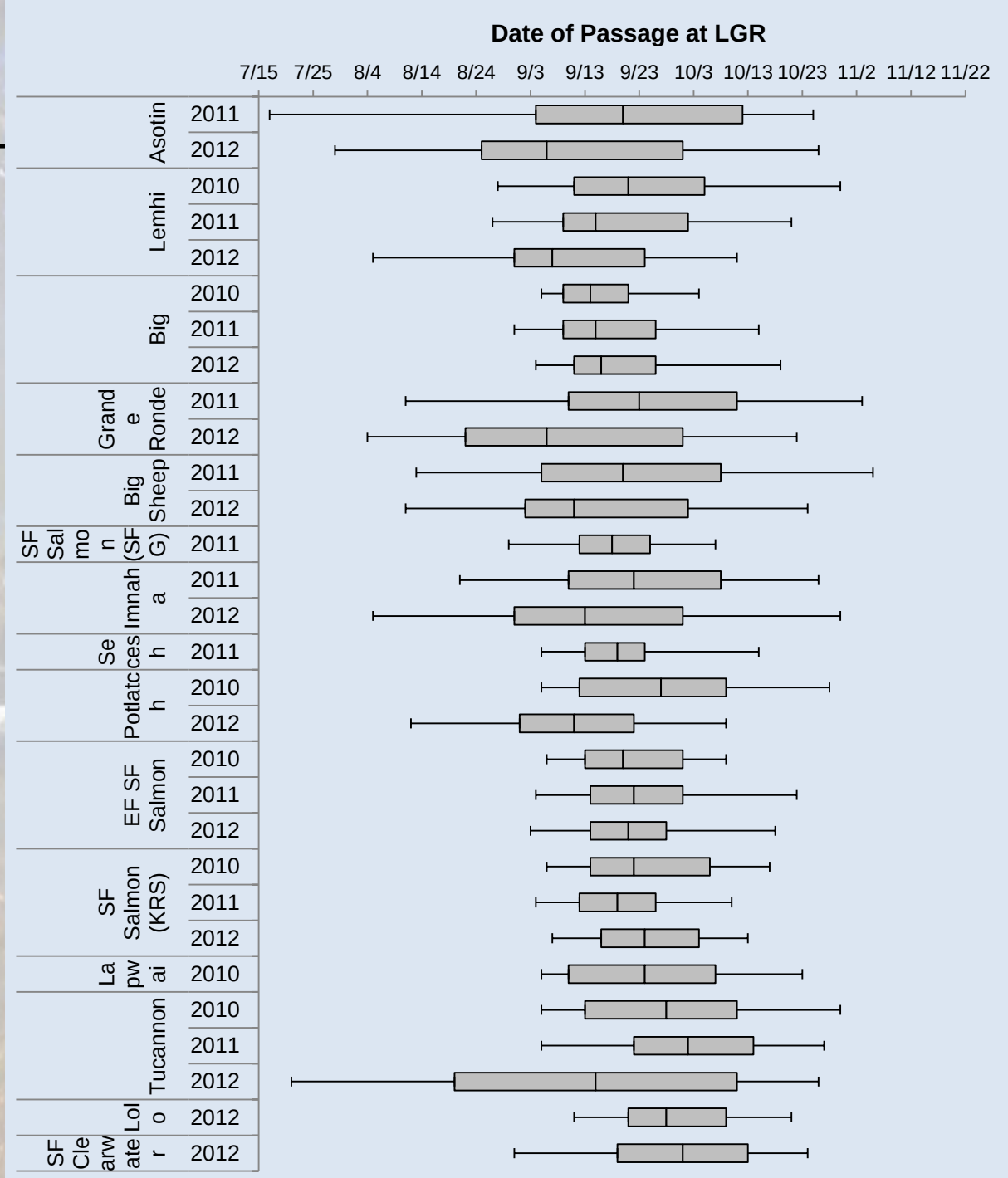
Length at Age





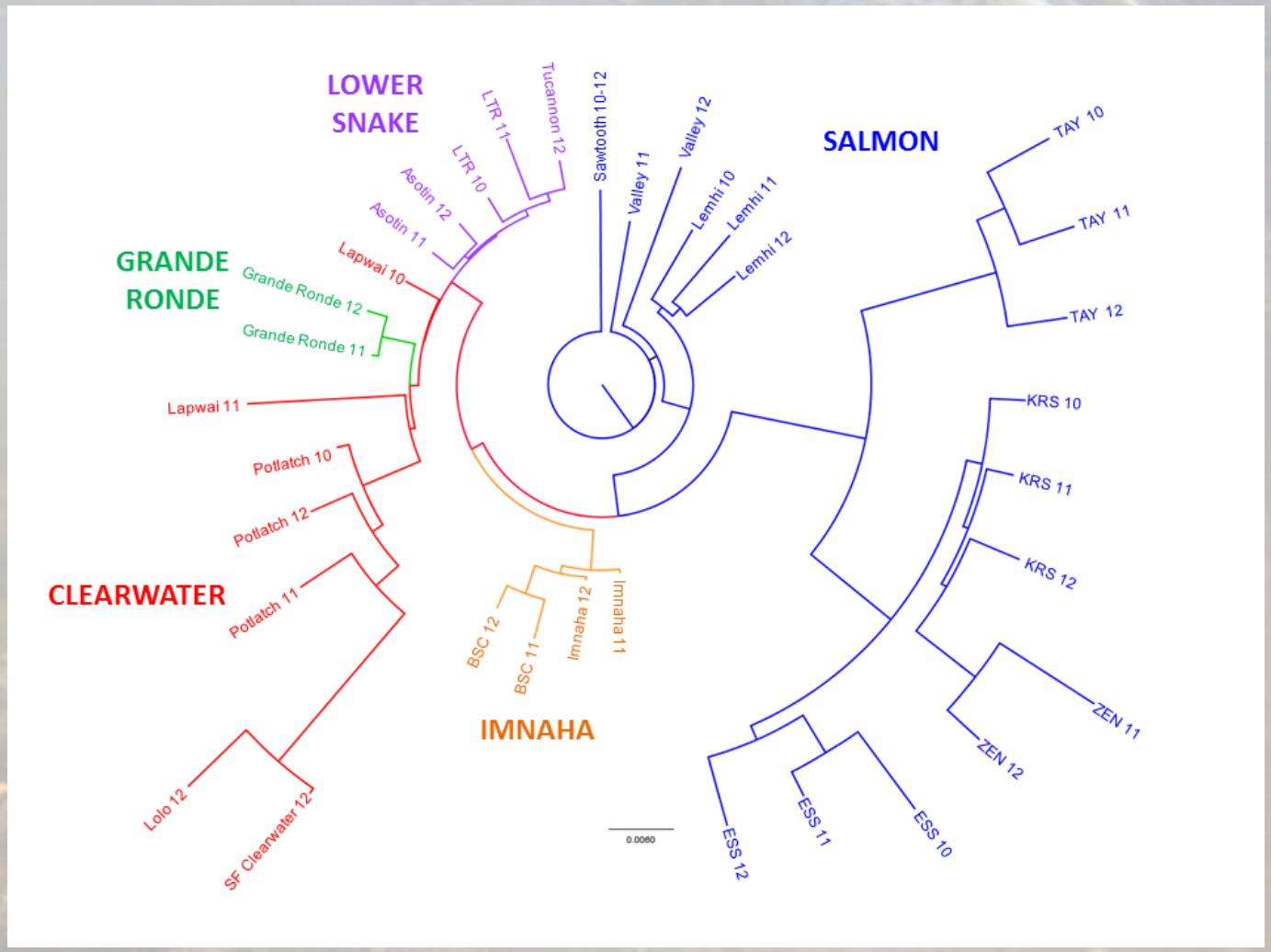
Passage Timing

- Annual monitoring of run-timing by population
- Traditional B-run populations tend to pass later

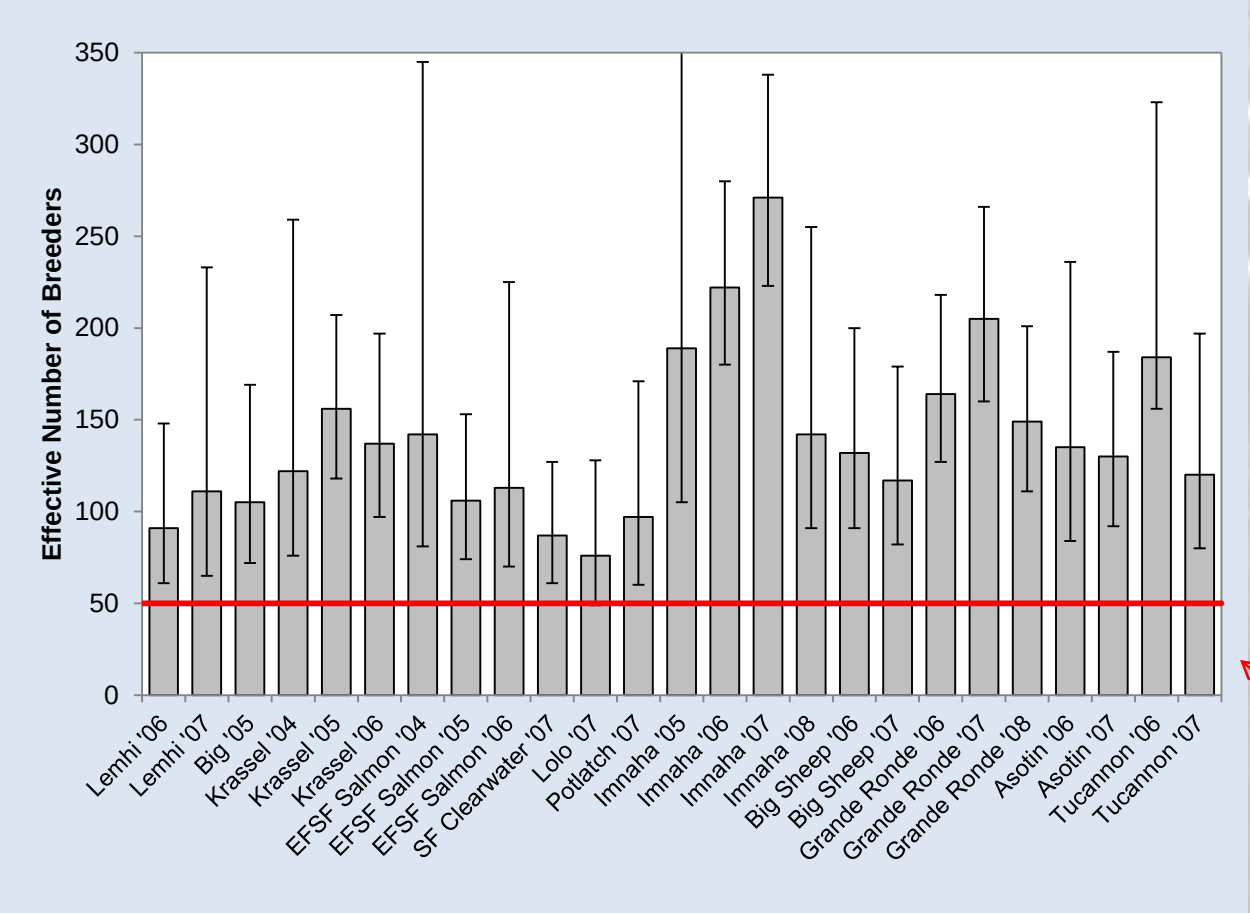


Genetic Structure

- Tissue provides SNP genotype data
- Monitoring of genetic structure over space and time



N_B – Effective Number of Breeders



- Scale age assigns fish back to Brood Year
- Analyze sibship among offspring by BY to estimate N_B
- We're researching effects of sample size on accuracy of estimate

NB > 50 prevents short-term inbreeding and maintenance of genetic diversity

Upper Imnaha River

3D9.1BF2328B20
3D9.QBF1641BB4
3D9.1UF1955DD2
3D9.1BE1970B60
3D9.1BFS971444
3D9.1BF1TE288A
3D9.1BF1AI1964
3D9.1BF232OD0D
3D9.1BF2330NF0
3D9.1BF236AFS8
3D9.1BF23884D?
3D9.1BF23A0EB4